



## **DNA and Endogamy: Strategies to Analyze Your DNA Matches**

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- DNA is not a silver bullet
  - DNA doesn't lie, but it can be misinterpreted, especially when dealing with endogamous populations
  - It is very important to build family trees
- Autosomal DNA Testing is the best way to find family
- Definition of Endogamy
  - Endogamy as a continuum- not all endogamy is created equal
  - Examples of endogamous populations (e.g., Ashkenazi Jews, Polynesians, Amish, Acadian, Colonial)
  - Endogamy versus pedigree collapse
- How endogamy affects DNA matches
  - You may have thousands of matches
  - More distant matches will look closer than they actually are because they are comprised of several smaller segments
  - How endogamy manifests can look differently depending on the population as well as what percentage of that population is part of your heritage
- Implications of endogamy on practical genetic genealogy methodology
  - Leeds Method very likely won't work
    - Try adjusting the parameters (e.g., increase minimum threshold)
  - Autoclustering tools won't work well, even with modifications
  - What are the Odds? (WATO) tool very possibly won't work
  - View shared matches with caution
  - Shared cM Project can't really account for endogamy at certain relationships, though this varies according to the endogamous population
- Myth-busting: "Because of endogamy, it's impossible to find family."
  - Ashkenazi Jewish DNA example of around 1000cMs (centimorgans)
  - Tools like the Shared cM Project and the DNA Detective "Green" Chart can still be utilized for closer matches
- Strategies to Mitigate Effects of Endogamy
  - Build your trees
  - Focus on matches with highest number of centimorgans and longest segments
  - Use a chromosome browser when available
  - Target test known family members
  - DNA Painting

- AncestryDNA
  - Timber for <90cMs, weighted versus unweighted
  - No chromosome browser, but largest segment available
  - Look at total centimorgans and number of segments
  - Pro Tools!
- 23andme
  - As of January 2025, the chromosome browser is still disabled, including Advanced DNA Comparison
  - Predictions are especially poor with endogamy and the trees are often wrong
  - Problems with using haplogroups
  - Strategies to use 23andme
    - Look at Relatives in Common against known matches
    - Sort by number of segments
- MyHeritage
  - Chromosome browser that also maps out triangulation
  - Autoclustering tool
  - Beware of effects of imputation
- Family Tree DNA (FTDNA)
  - Can sort by longest segment
  - Unlocking the chromosome browser is a must to view segment sizes, subtract small segments
  - Benefits and limitations of Y-DNA and mtDNA testing are typically population specific
- GEDMatch
  - Are Your Parents Related? (AYPR) tool

Largest segment = 8.5 cM  
Total of segments > 7 cM = 8.5 cM

Important Notice: The traditional charts used by genetic genealogists to predict the relationship between two people who share DNA are not relevant to, or accurate for, interpreting the results from the AYPR tool. The amount of shared DNA between the parents of a person who receives a positive result is approximately four times higher than the total ROH inherited by the user, the result displayed in cMs here, however an accurate and comprehensive interpretation of the data and prediction of the relationship between the parents of the user is complex, and this calculation alone is not a reliable indicator of the parents' relationship.

Interpreting your result:

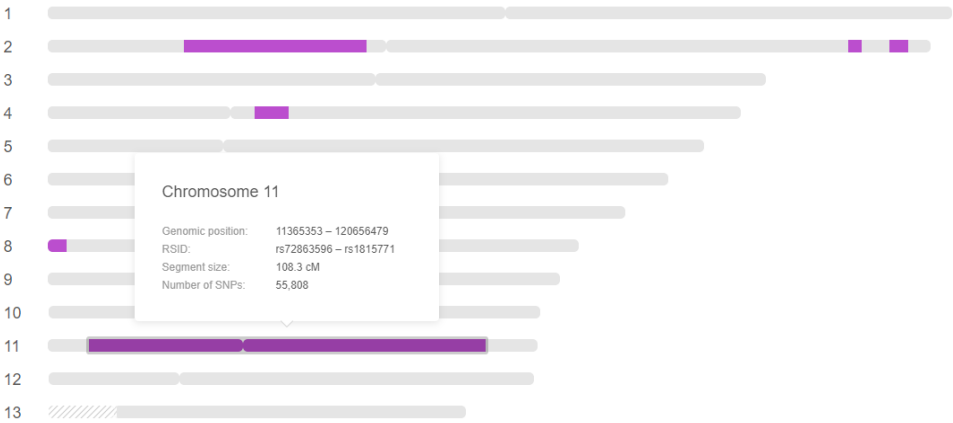
**This analysis indicates that your parents may be distantly related.**

Kitty Cooper has a blog article on this program: [When the DNA says your parents are related](#)

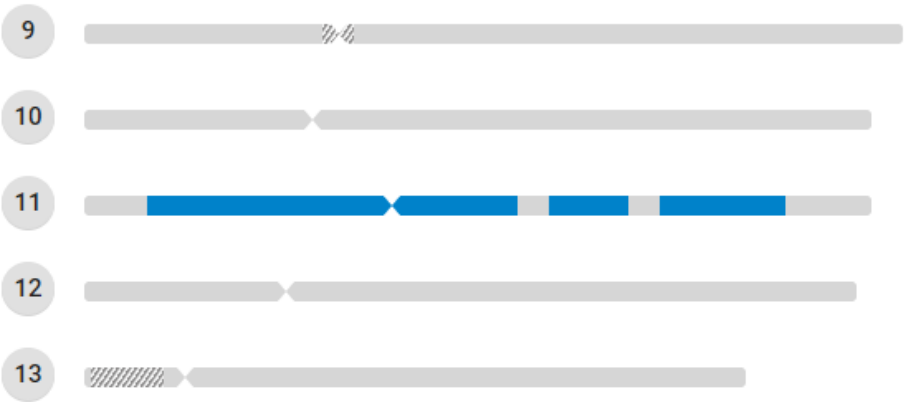
- DNA Painter can be very helpful in determining Identical by Descent (IBD) matches versus Identical by State (IBS) matches
  - Example: For Ashkenazi Jews, I use 10cM segment as a minimum threshold, but segments 10-15cMs have also been endogamous

# Imputation Example

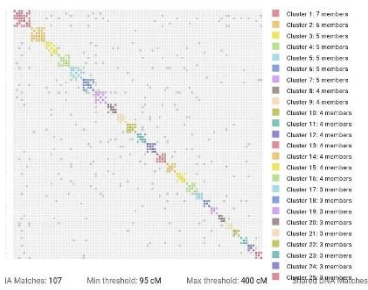
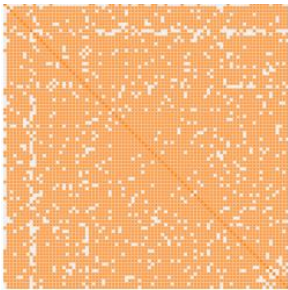
MyHeritage



FTDNA



## Autoclustering Genetic Affairs for 23andme Default Settings and MyHeritage



## Suggested Resources

### **Books**

Blaine T. Bettinger and Debbie Parker Wayne (2016). *Genetic Genealogy in Practice*.  
Roberta Estes (2021). *DNA for Native American Genealogy*.  
Debbie Parker Wayne, editor (2019). *Advanced Genetic Genealogy: Techniques and Case Studies*. “The Challenge of Endogamy and Pedigree Collapse” by Kimberly T. Powell provides helpful methodological strategies.

### **Blogs & Articles**

*The Genetic Genealogist*, Dr. Blaine Bettinger / <https://thegeneticgenealogist.com/>  
*The DNA Geek*, Dr. Leah Larkin / <https://thednageek.com/>  
*DNAeXplained*, Roberta Estes / <https://dna-explained.com/>  
*Kitty Cooper's Blog*, Kitty Cooper / <https://blog.kittycooper.com/>  
*Your DNA Guide*, Diahan Southard / <https://www.yourdnaguide.com/>  
*Behold Genealogy*, Louis Kessler / <https://www.beholdgenealogy.com/blog/>  
“No, You Don’t Really Have 7,900 4th Cousins: Some DNA Basics for Those With Ashkenazi Jewish Heritage,” Jennifer Mendelsohn / <https://clevertitletk.medium.com/no-you-dont-really-have-7-900-4th-cousins-some-dna-basics-for-those-with-jewish-heritage-857f873399ff>

### **Facebook Groups**

All DNA Detective groups  
Genetic Genealogy Tips & Techniques  
Jewish DNA for Genetic Genealogy and Family Research  
(These groups may also lead you to more specialized DNA groups for the respective endogamous population)

### **Other Resources**

Legacy Family Tree Webinars (requires a subscription). I highly recommend Paul Woodbury’s “Dealing with Endogamy” / <https://familytreewebinars.com/webinar/dealing-with-endogamy/>  
Genealogy journals  
Local genealogical societies, including ones with DNA SIGs

Most importantly, practice! Practice will allow you to understand the nuances found within each.