

# DNA Detectives Autosomal Statistics Chart

Created by Christa Stalcup

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cM (centiMorgans)^		Percentage (%) of Shared DNA^^		Group	Relationship	Notes
Average	Range	Average	Range			
3,600		50%			Parent - Child	
2650	2300 - 3900	37%	32%-54%	Group A	Full Sibling	Ancestry, FTDNA and GEDmatch (HIR only)
3600		50%				23andMe (FIR included)
1800	1300 – 2300	25%	18%-32%	Group B	Half Sibling Aunt/Uncle/Niece/Nephew Double First Cousin Grandparent/Grandchild	3/4 Siblings^^^
900	575 - 1330	12.5%	8%-18.5%	Group C	First Cousin (1C) Half Aunt/Uncle/Niece/Nephew Great-Grandparent/Great-Grandchild Great-Aunt/Uncle/Niece/Nephew	
450	215 - 650	6.25%	3%-9%	Group D	First Cousin Once Removed (1C1R) Half First Cousin (½ 1C) Half Great-Aunt/Uncle/Niece/Nephew	
224	75 - 360	3.125%	1%-5%	Group E	Second Cousin (2C) First Cousin Twice Removed (1C2R) Half First Cousin Once Removed (½1C1R)	
112	30 - 215	1.56%	0.42% - 3%	Group F	Second Cousin Once Removed (2C1R) Half Second Cousin (½ 2C) First Cousin Three Times Removed (1C3R) Half First Cousin Twice Removed (½ 1C2R)	
56	0 - 109*	0.78%	0% - 1.52%	Group G	Third Cousin (3C) Second Cousin Twice Removed (2C2R)	~10% of 3Cs will not share DNA*
30	0 - 75**	0.4%	0%-1%	Group H	Third Cousin Once Removed (3C1R) Other Distant Cousins	~50% of 4Cs will not share DNA**

^cM =Ancestry.com & FTDNA

^^Percentage of DNA = 23AndMe

^^^ 3/4 Siblings are a combination of half siblings and 1<sup>st</sup> cousins, FIRs are included.

Groups A & B: 99% within the ranges given

Groups C – I: 95% within the ranges given

# DNA Detectives Autosomal Statistics Chart Explained

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## Why this chart and not company predictions?

It is preferred that you personally interpret the DNA share vs taking the company's relationship prediction at face value.

## Where to find your DNA share:

**Ancestry:** Click on the match's profile and a little "i" icon will display next to the Confidence Level to give you the cM total (not including X share)

**FTDNA:** Manually calculate the total cM share with the segments 7cM and higher. (Tip, just add up the tiny segments and remove that total)

**23andMe:** Percentage listed on the profile.

**GEDmatch:** Combine autosomal and X DNA share.

## Converting to percentages:

If you prefer working with percentages (most of the admins do), then take the total cM share and divide by 71.6 to get an approximate percentage for FTDNA and GEDmatch. For Ancestry.com, divide by 68.

**Anomalies and Outliers:** It is best if you first look at the average DNA share per relationship (column labeled "Average") while comparing what you share with your DNA match, then proceed to look at the ranges. If you are what we may refer to as an 'in-between' share, then you will need to consider two groups of possible relationships. This is why we have added a new feature called "**groups**". There can be many relationships to consider so having you refer to a chart and providing you a group is easier than typing out every single relationship option here in Facebook. Unfortunately, you seldom are working with only one option of a relationship. There are two major factors that contribute to having more relationships to consider than you hoped for:

1. The randomness of DNA inheritance

95-99% of the time your cM share will fall within the correct groupings. However, there are anomalies occasionally, such as seeing a half 1st cousin (or 1C1R) sharing as high as a full 1st cousin, or seeing a 3rd cousin sharing as high as 2%/150cMs. You will need to consider many relationships and use the amount shared as a guide, you must dig into the tree to see what relationships are possible. If you believe you are dealing with an anomaly or an outlier, the only method to know for certain is to test an additional family member to confirm.

2. Endogamy and pedigree collapse within the population

This is dealt with on a daily basis in genetic genealogy, whether it is a specific known endogamous population or your relatives just decided to never move from that southern mountaintop. Also, consider that you may not have cousin marriages in your tree, but you could instead descend from a "bottle neck" population and you are virtually 5th -7th cousins with all the descendants of the founding families of that area.