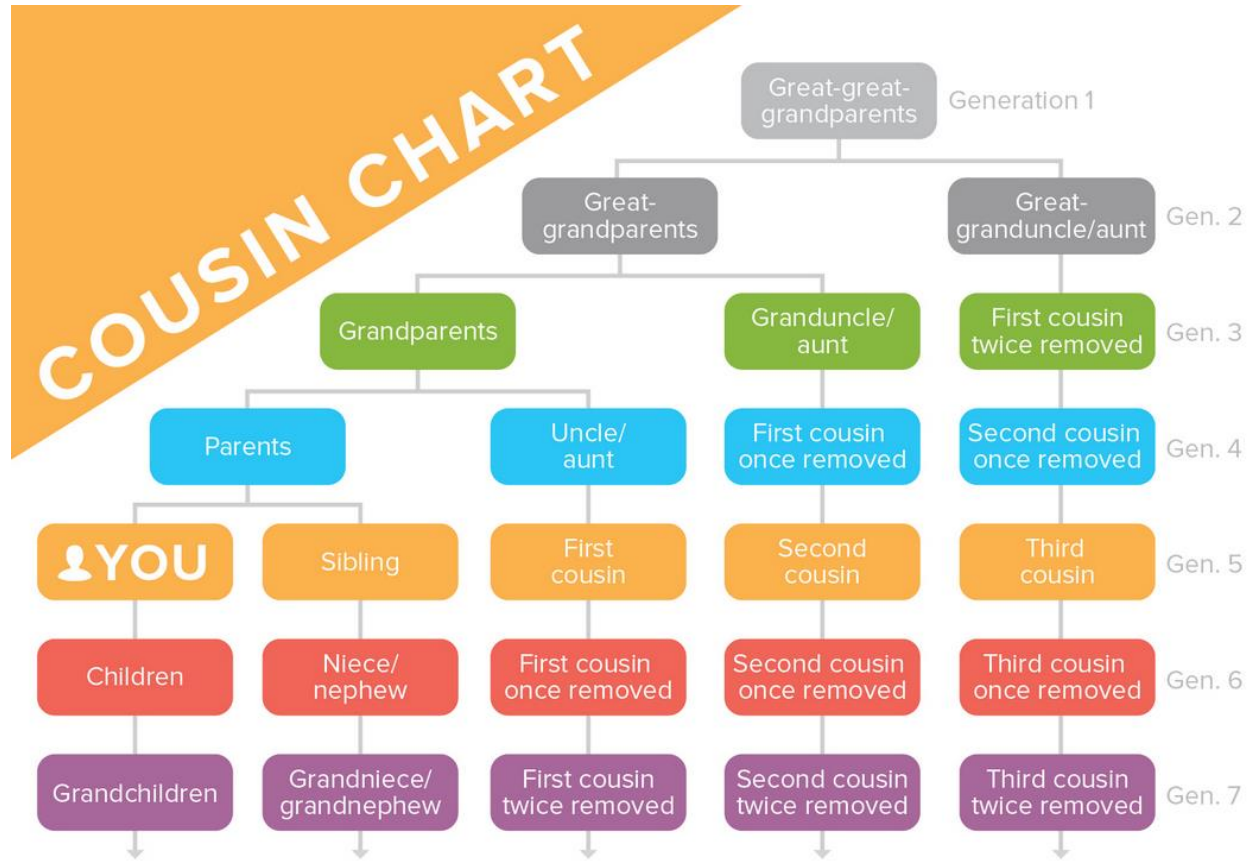


# DNA Relationships Explained: Known Relatives

By Sara Allen



familysearch.org

<https://www.familysearch.org/en/blog/what-is-a-second-cousin>

Instructions for using this chart:

- 1. Across the top row find the common ancestors' relationship to you.
- 2. In the left hand column find the common ancestors' relationship to the other individual.

Common Ancestor	Grandparent	Great Grandparent	Great 2 <sup>nd</sup> Grandparent	Great 3 <sup>rd</sup> Grandparent	Great 4 <sup>th</sup> Grandparent	Great 5 <sup>th</sup> Grandparent	Great 6 <sup>th</sup> Grandparent	Great 7 <sup>th</sup> Grandparent	Great 8 <sup>th</sup> Grandparent	Great 9 <sup>th</sup> Grandparent	Great 10 <sup>th</sup> Grandparent
Grandparent	1 <sup>st</sup> cousin	1 <sup>st</sup> cousin once removed	1 <sup>st</sup> cousin 2x removed	1 <sup>st</sup> cousin 3x removed	1 <sup>st</sup> cousin 4x removed	1 <sup>st</sup> cousin 5x removed	1 <sup>st</sup> cousin 6x removed	1 <sup>st</sup> cousin 7x removed	1 <sup>st</sup> cousin 8x removed	1 <sup>st</sup> cousin 9x removed	1 <sup>st</sup> cousin 10x removed
Great Grandparent	1 <sup>st</sup> cousin once removed	2 <sup>nd</sup> cousin	2 <sup>nd</sup> cousin once removed	2 <sup>nd</sup> cousin 2x removed	2 <sup>nd</sup> cousin 3x removed	2 <sup>nd</sup> cousin 4x removed	2 <sup>nd</sup> cousin 5x removed	2 <sup>nd</sup> cousin 6x removed	2 <sup>nd</sup> cousin 7x removed	2 <sup>nd</sup> cousin 8x removed	2 <sup>nd</sup> cousin 9x removed
Great 2 <sup>nd</sup> Grandparent	1 <sup>st</sup> cousin 2x removed	2 <sup>nd</sup> cousin once removed	3 <sup>rd</sup> cousin	3 <sup>rd</sup> cousin once removed	3 <sup>rd</sup> cousin 2x removed	3 <sup>rd</sup> cousin 3x removed	3 <sup>rd</sup> cousin 4x removed	3 <sup>rd</sup> cousin 5x removed	3 <sup>rd</sup> cousin 6x removed	3 <sup>rd</sup> cousin 7x removed	3 <sup>rd</sup> cousin 8x removed
Great 3 <sup>rd</sup> Grandparent	1 <sup>st</sup> cousin 3x removed	2 <sup>nd</sup> cousin 2x removed	3 <sup>rd</sup> cousin once removed	4 <sup>th</sup> cousin	4 <sup>th</sup> cousin once removed	4 <sup>th</sup> cousin 2x removed	4 <sup>th</sup> cousin 3x removed	4 <sup>th</sup> cousin 4x removed	4 <sup>th</sup> cousin 5x removed	4 <sup>th</sup> cousin 6x removed	4 <sup>th</sup> cousin 7x removed
Great 4 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 4x removed	2 <sup>nd</sup> cousin 3x removed	3 <sup>rd</sup> cousin 2x removed	4 <sup>th</sup> cousin once removed	5 <sup>th</sup> cousin	5 <sup>th</sup> cousin once removed	5 <sup>th</sup> cousin 2x removed	5 <sup>th</sup> cousin 3x removed	5 <sup>th</sup> cousin 4x removed	5 <sup>th</sup> cousin 5x removed	5 <sup>th</sup> cousin 6x removed
Great 5 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 5x removed	2 <sup>nd</sup> cousin 4x removed	3 <sup>rd</sup> cousin 3x removed	4 <sup>th</sup> cousin 2x removed	5 <sup>th</sup> cousin once removed	6 <sup>th</sup> cousin	6 <sup>th</sup> cousin once removed	6 <sup>th</sup> cousin 2x removed	6 <sup>th</sup> cousin 3x removed	6 <sup>th</sup> cousin 4x removed	6 <sup>th</sup> cousin 5x removed
Great 6 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 6x removed	2 <sup>nd</sup> cousin 5x removed	3 <sup>rd</sup> cousin 4x removed	4 <sup>th</sup> cousin 3x removed	5 <sup>th</sup> cousin 2x removed	6 <sup>th</sup> cousin once removed	7 <sup>th</sup> cousin	7 <sup>th</sup> cousin once removed	7 <sup>th</sup> cousin 2x removed	7 <sup>th</sup> cousin 3x removed	7 <sup>th</sup> cousin 4x removed
Great 7 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 7x removed	2 <sup>nd</sup> cousin 6x removed	3 <sup>rd</sup> cousin 5x removed	4 <sup>th</sup> cousin 4x removed	5 <sup>th</sup> cousin 3x removed	6 <sup>th</sup> cousin 2x removed	7 <sup>th</sup> cousin once removed	8 <sup>th</sup> cousin	8 <sup>th</sup> cousin once removed	8 <sup>th</sup> cousin 2x removed	8 <sup>th</sup> cousin 3x removed
Great 8 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 8x removed	2 <sup>nd</sup> cousin 7x removed	3 <sup>rd</sup> cousin 6x removed	4 <sup>th</sup> cousin 5x removed	5 <sup>th</sup> cousin 4x removed	6 <sup>th</sup> cousin 3x removed	7 <sup>th</sup> cousin 2x removed	8 <sup>th</sup> cousin once removed	9 <sup>th</sup> cousin	9 <sup>th</sup> cousin once removed	9 <sup>th</sup> cousin 2x removed
Great 9 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 9x removed	2 <sup>nd</sup> cousin 8x removed	3 <sup>rd</sup> cousin 7x removed	4 <sup>th</sup> cousin 6x removed	5 <sup>th</sup> cousin 5x removed	6 <sup>th</sup> cousin 4x removed	7 <sup>th</sup> cousin 3x removed	8 <sup>th</sup> cousin 2x removed	9 <sup>th</sup> cousin once removed	10 <sup>th</sup> cousin	10 <sup>th</sup> cousin once removed
Great 10 <sup>th</sup> Grandparent	1 <sup>st</sup> cousin 10x removed	2 <sup>nd</sup> cousin 9x removed	3 <sup>rd</sup> cousin 8x removed	4 <sup>th</sup> cousin 7x removed	5 <sup>th</sup> cousin 6x removed	6 <sup>th</sup> cousin 5x removed	7 <sup>th</sup> cousin 4x removed	8 <sup>th</sup> cousin 3x removed	9 <sup>th</sup> cousin 2x removed	10 <sup>th</sup> cousin once removed	11 <sup>th</sup> cousin

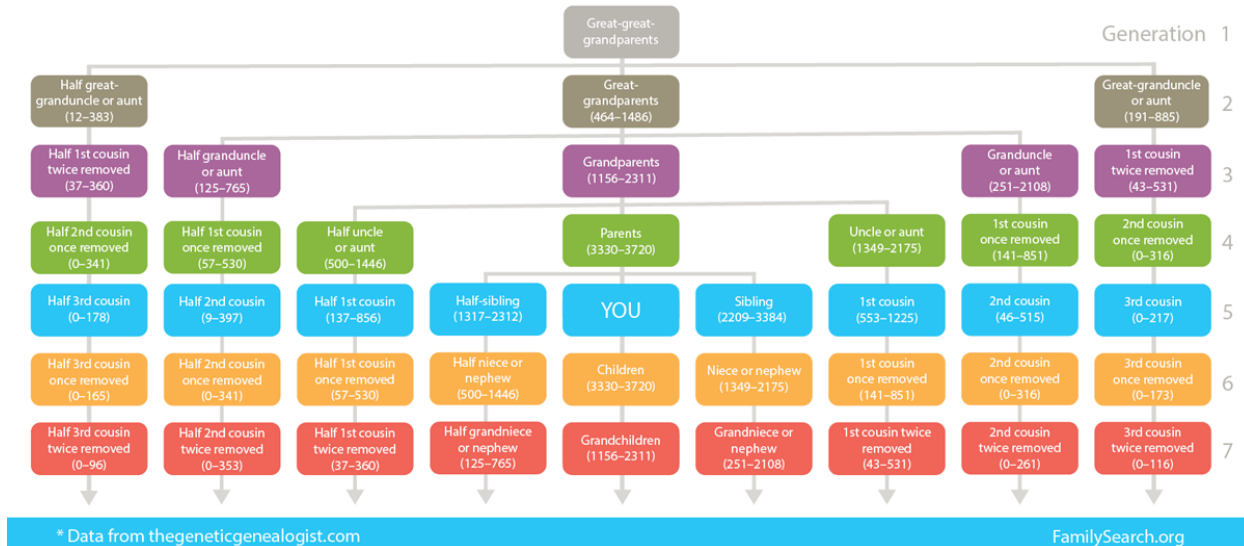
Credit – ISOGG Wiki

<https://isogg.org/wiki/Cousin>

# How Many Centimorgans Do You Share with Your Relatives?

How this chart works

Relationship  
Centimorgan range  
(low to high)



<https://www.familysearch.org/en/blog/centimorgan-chart-understanding-dna>

DNA Detectives Autosomal Statistics Chart						
Created by Christa Stalcup			©THEDNADETECTIVES, 2016			
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 (½ 1C1R)	
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	
Created by Christa Stalcup	©THEDNADETECTIVES, 2016
<b>Why this chart and not company predictions?</b> It is preferred that you personally interpret the DNA share vs taking the company's relationship prediction at face value.]	
<b>Where to find your DNA share:</b> <b>Ancestry</b> 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) <b>FTDNA</b> Manually calculate the total cM share with the segments 7cM and higher. (Tip, just add up the tiny segments and remove that total) <b>23andMe</b> Percentage listed on the profile <b>GEDmatch</b> Combine autosomal and X DNA share.	
<b>Converting to percentages:</b> 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.	
<b>Anomalies and Outliers</b> It is best if you first look at the average DNA share per relationship (bright bold red column) 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. <ol style="list-style-type: none"> <li><u>The randomness of DNA inheritance</u> 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.</li> <li><u>Endogamy and pedigree collapse within the population</u> 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.</li> </ol>	

From DNA DETECTIVES  
FACEBOOK Page



# Shared Centimorgan Project > <https://dnainter.com/tools/sharedcmv4>

## The Shared cM Project 4.0 tool v4

Read more about the tool and this update

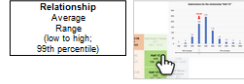
### March 2020

Blaine T. Bettinger  
[www.thegeneticeologist.com](http://www.thegeneticeologist.com)  
 More about this project  
 CC 4.0 Attribution License  
 Interactive version v4 by Jonny Peril at DNA Painter  
 Click here to contribute data to the shared cM project  
 Last updated 28th March 2020

Enter the total number of cM for your match:

or enter %

How to read this chart



Then any relationships that fit will stand out below  
[Read more about cousin relationships](#)

### Other versions

New: with option to add a second amount  
 Beta with updated probabilities  
 With editable boxes  
 Shared cM 3.0 (2017) version

Half GG-Aunt / Uncle 208 103 - 284		Great-Grandparent 381 485 - 1488						Great-Great-Grandparent 420 168 - 713		GGG Aunt / Uncle 117 25 - 238		2C3R 51 0 - 154		Other Relationships									
Half 1C2R 125 10 - 209		Half Great-Aunt / Uncle 451 184 - 888			Grandparent 1754 984 - 2482			Great-Aunt / Uncle 850 330 - 1487		1C2R 221 33 - 471		2C2R 71 0 - 244		3C2R 38 0 - 168		6C 18 0 - 71							
Half 2C1R 96 0 - 190		Half 1C1R 224 62 - 489		Half Aunt / Uncle 871 492 - 1315		Parent 3485 2370 - 3720			Aunt / Uncle 1741 1201 - 2282		1C1R 433 102 - 980		2C1R 122 14 - 353		3C1R 48 0 - 192		4C1R 28 0 - 128		6C1R 15 0 - 56				
Half 3C 48 0 - 168		Half 2C 120 10 - 325		Half 1C 449 158 - 979		Half Sibling 1759 1160 - 2438		Sibling 2813 1613 - 3488		SELF		1C 898 398 - 1397		2C 229 41 - 592		3C 73 0 - 234		4C 35 0 - 139		5C 25 0 - 117		6C2R 13 0 - 45	
Half 3C1R 37 0 - 139		Half 2C1R 98 0 - 190		Half 1C1R 224 62 - 489		Half Niece / Nephew 871 492 - 1315		Niece / Nephew 1740 1201 - 2282		Child 3487 2378 - 3720		1C1R 433 102 - 980		2C1R 122 14 - 353		3C1R 48 0 - 192		4C1R 28 0 - 128		5C1R 21 0 - 80		7C 14 0 - 57	
Half 3C2R 27 0 - 78		Half 2C2R 48 0 - 144		Half 1C2R 125 10 - 209		Half Great-Niece / Nephew 451 184 - 888		Great-Niece / Nephew 850 330 - 1487		Grandchild 1754 984 - 2482		1C2R 221 33 - 471		2C2R 71 0 - 244		3C2R 38 0 - 168		4C2R 22 0 - 93		5C2R 18 0 - 65		7C1R 12 0 - 50	
Half 3C3R		Half 2C3R		Half 1C3R 60 0 - 120		Half GG-Niece / Nephew 208 103 - 284		Great-Great-Niece / Nephew 420 168 - 713		Great-Grandchild 857 485 - 1488		1C3R 117 25 - 238		2C3R 51 0 - 154		3C3R 27 0 - 98		4C3R 19 0 - 60		5C3R 13 0 - 30		8C 11 0 - 42	