The Shared CM Project – Version 2.0 (June 25, 2016)

Blaine T. Bettinger

The Shared cM Project is a collaborative data collection and analysis project created to understand the ranges of shared centimorgans associated with various known relationships. As of June 2016, total shared cM data for more than 10,000 known relationships has been provided. This is the first update to the original data, released in May 2015. In this update there are more than 4,000 new entries. Additionally, the data for each relationship has been analyzed statistically to remove extreme outliers and produce a histogram to show the distribution.

For more information:

- The Shared cM Project - http://thegeneticgenealogist.com/2015/05/29/the-shared-cm-project/
- Autosomal DNA Statistics - http://isogg.org/wiki/Autosomal_DNA_statistics

To provide your data for subsequent updates:

- http://thegeneticgenealogist.com/2015/03/04/collecting-sharing-information-for-known-relationships/

Known issues with the Shared cM Project data:

- **Data entry errors** – some of the information entered by participants is clearly affected by data entry errors (for example, a longest segment begin greater than the total shared cM). When these errors could be *definitively* determined, they were removed.
- **Incorrect relationships (known or unknown)** – some relationships were almost certainly entered incorrectly, which might be due to misunderstandings of "removed" relationships in genealogy. Other relationship errors were clearly due to misattributed parentage events resulting in the believed relationship being incorrect.

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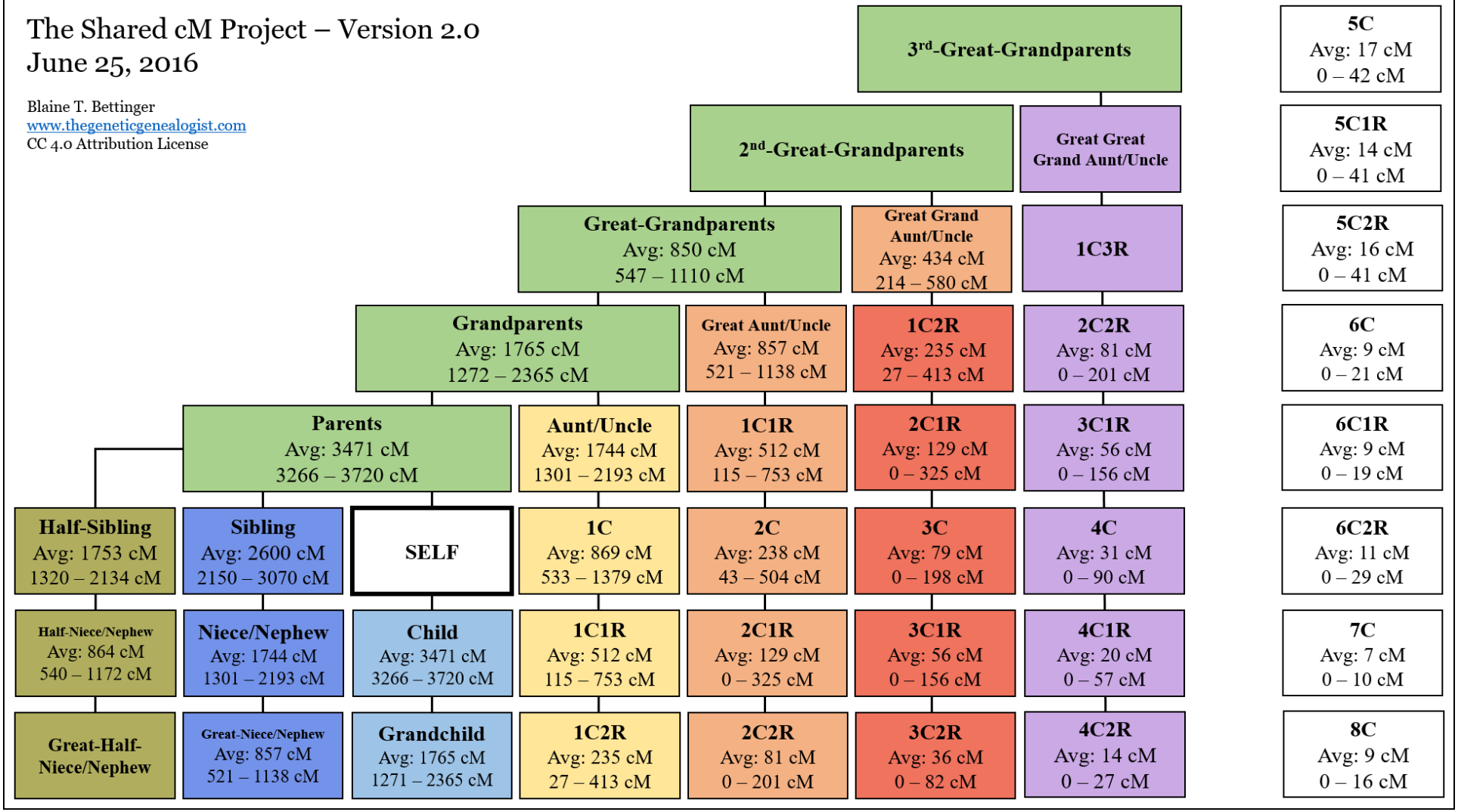

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Histograms

Histogram = a graphical representation of the distribution of numerical data

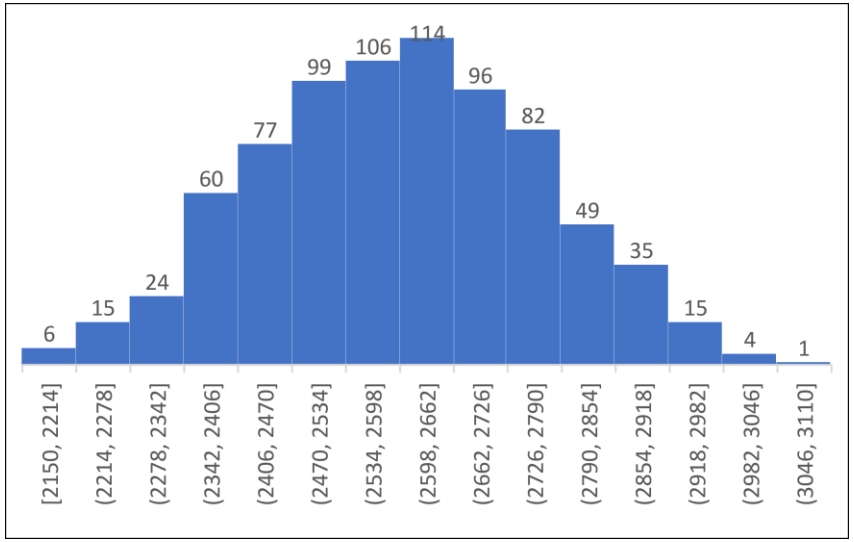
The following steps are followed to create a histogram:

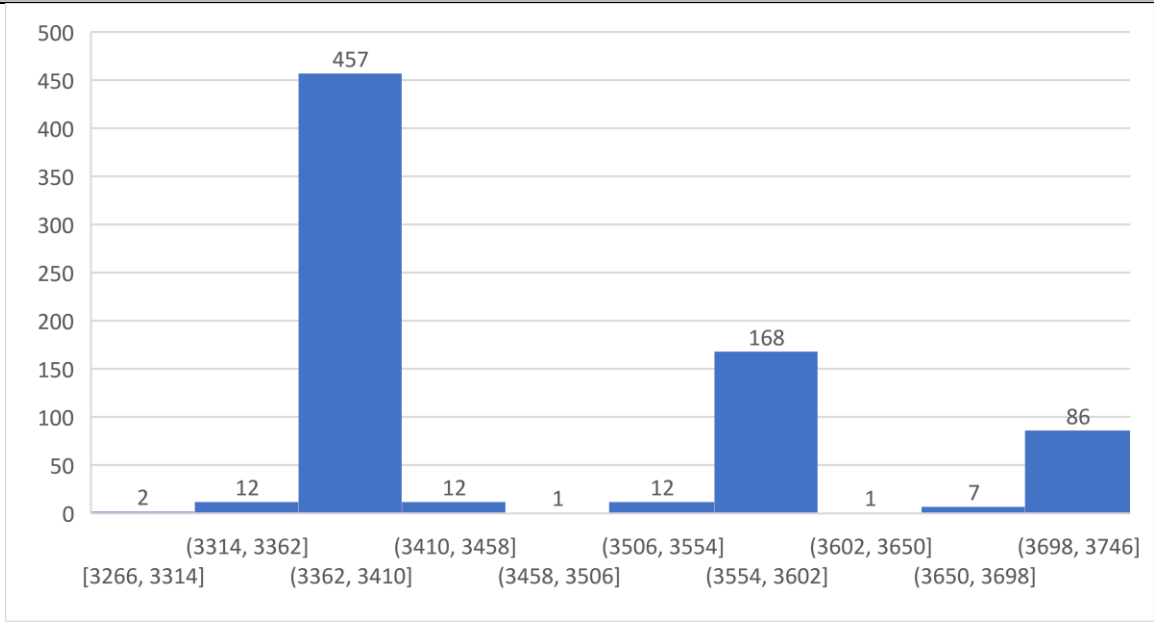
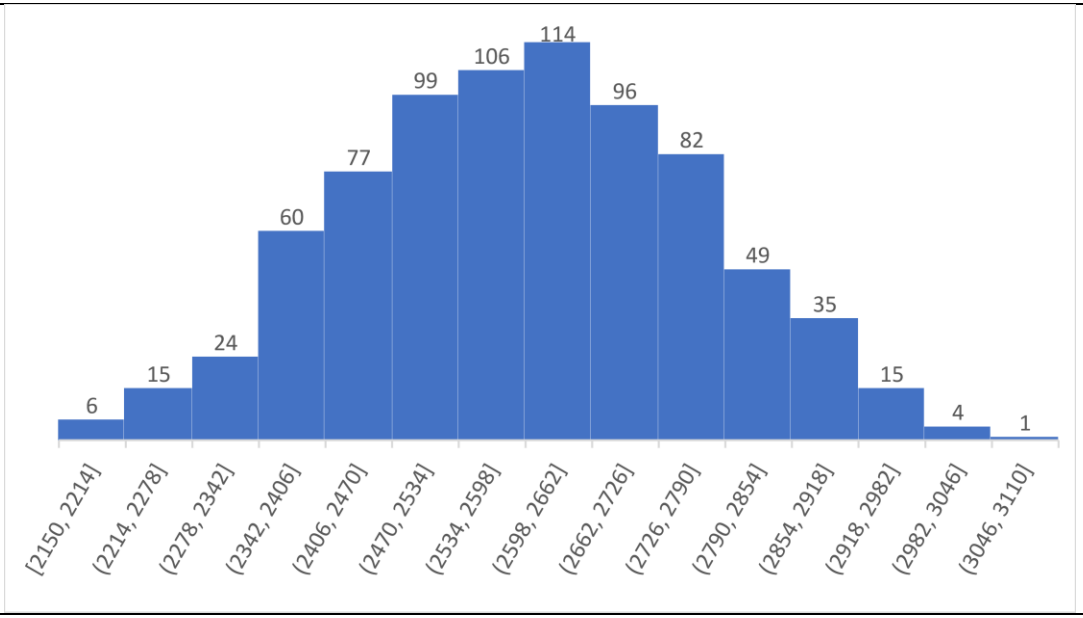
1. Divide entire range of total shared cM (from the smallest amount to the largest amount) into a series of intervals of equal size (called "bins"); and
2. Count how many data points fall within each of the intervals.

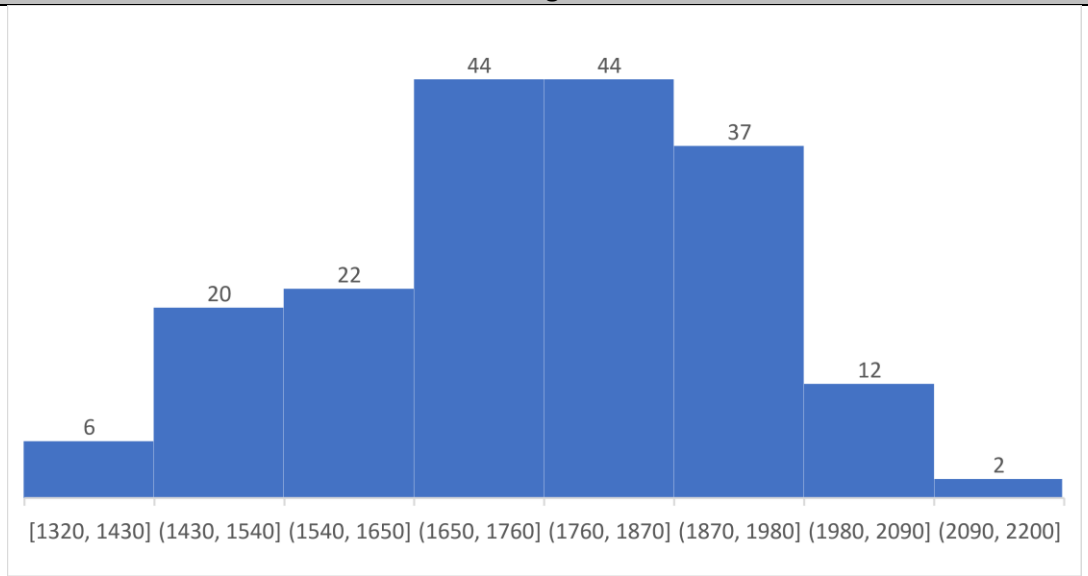
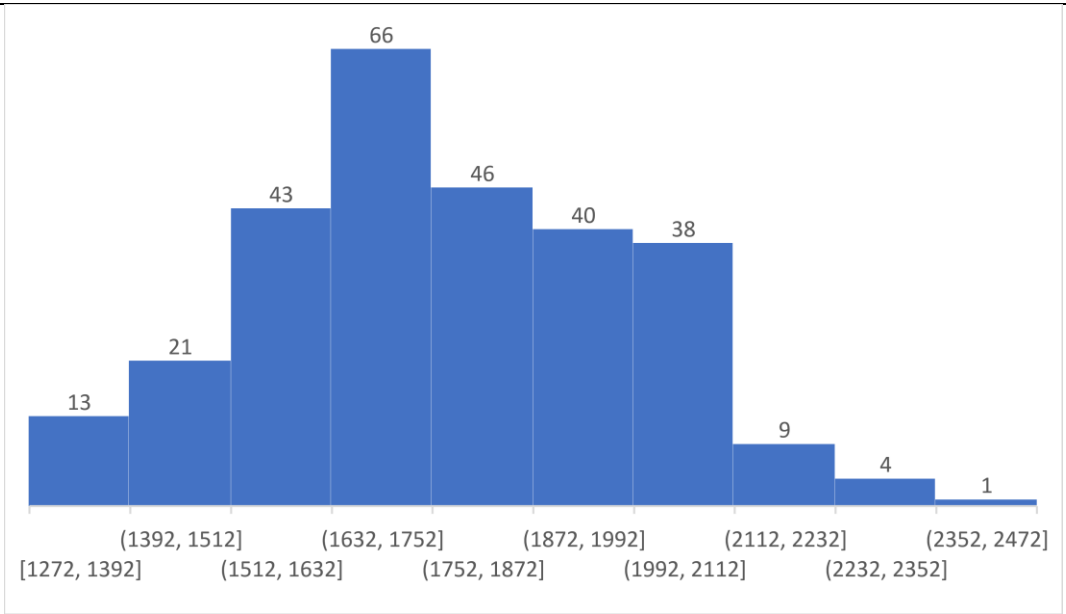
How to read these histograms:

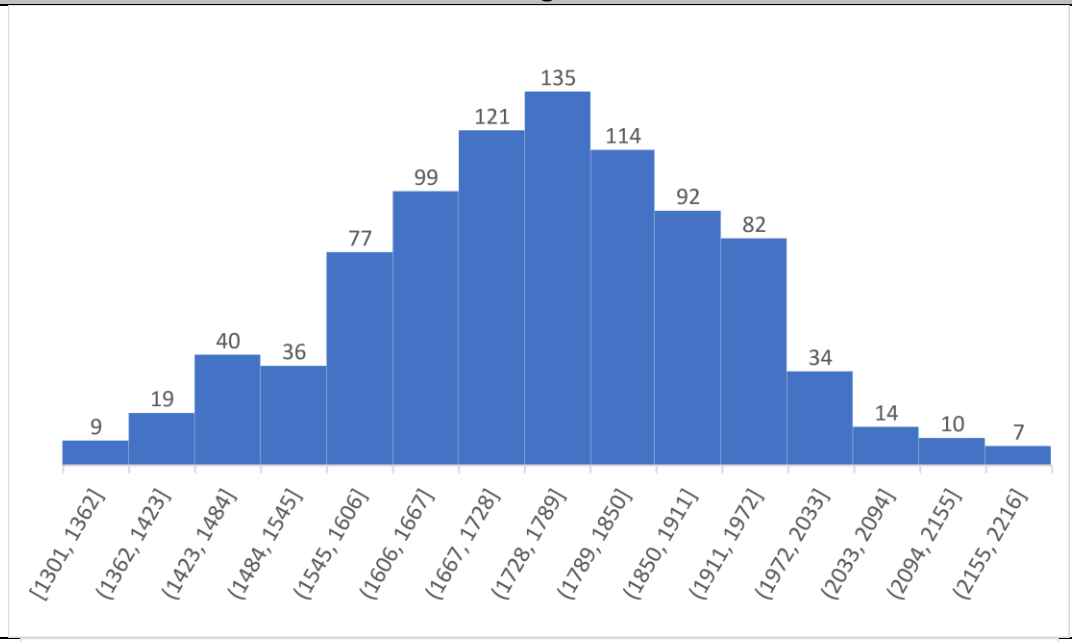
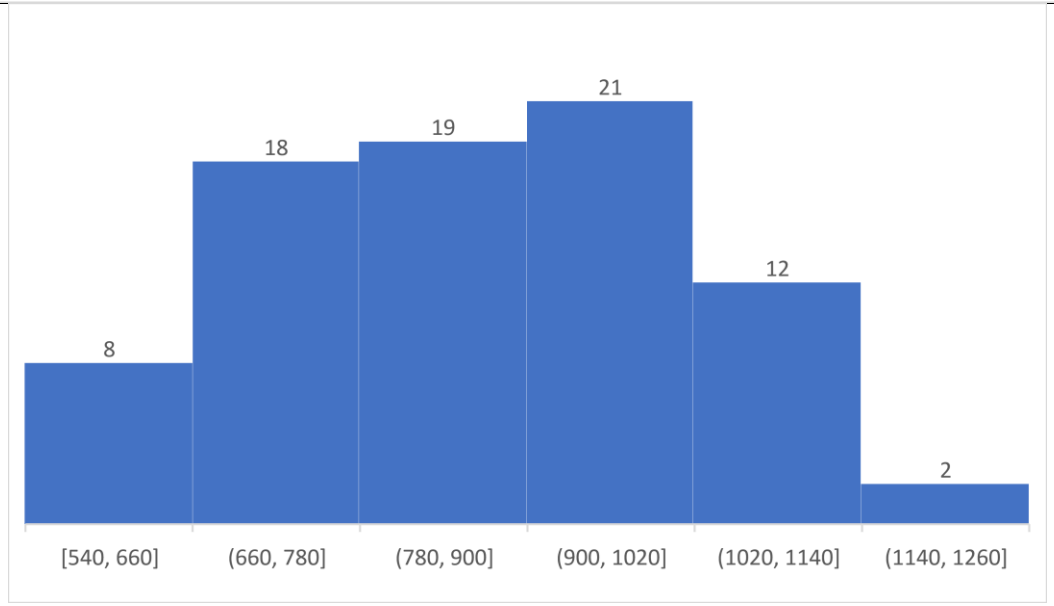
The number at the top of each bar is the total number of data entries for each interval (see "bin," below). For example, six (6) data entries are in the first interval.

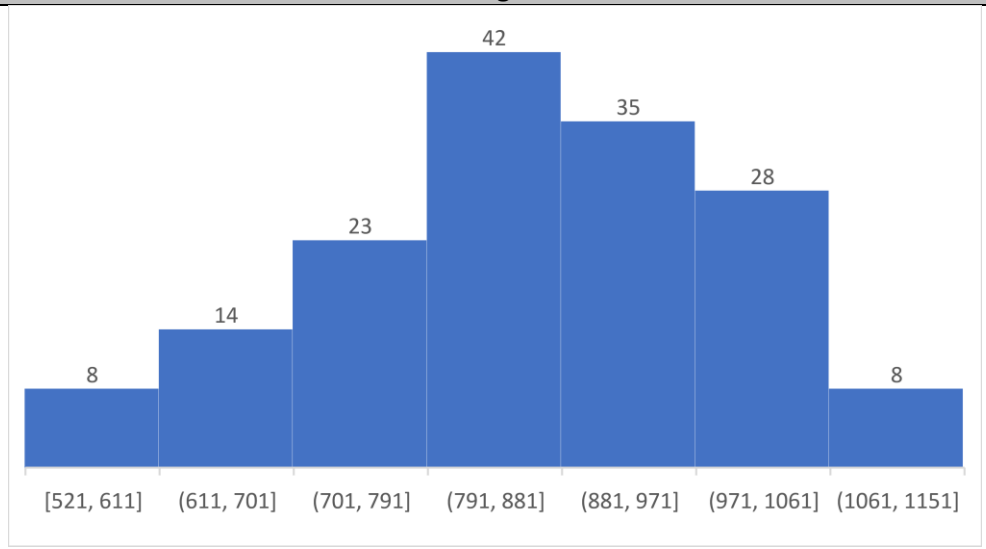
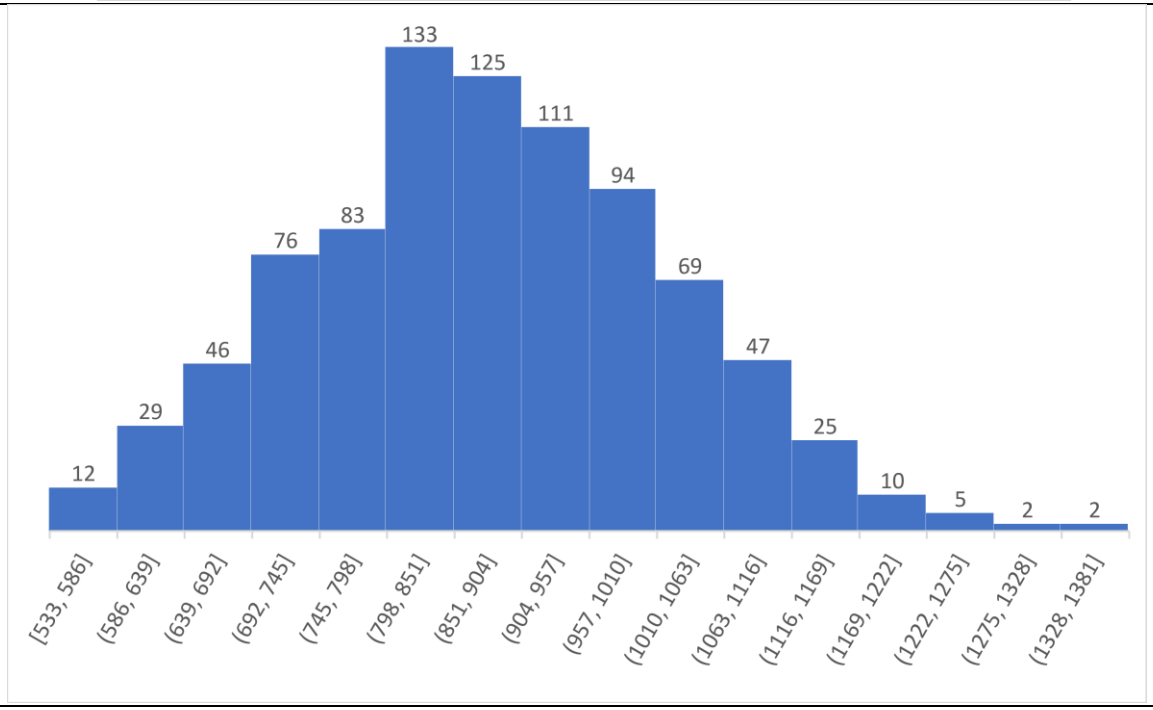
These are "bins," or consecutive non-overlapping ranges of total shared cM. For example, a total of six (6) data entries were within the bin or range of 2150 to 2214 cM for this relationship (siblings).

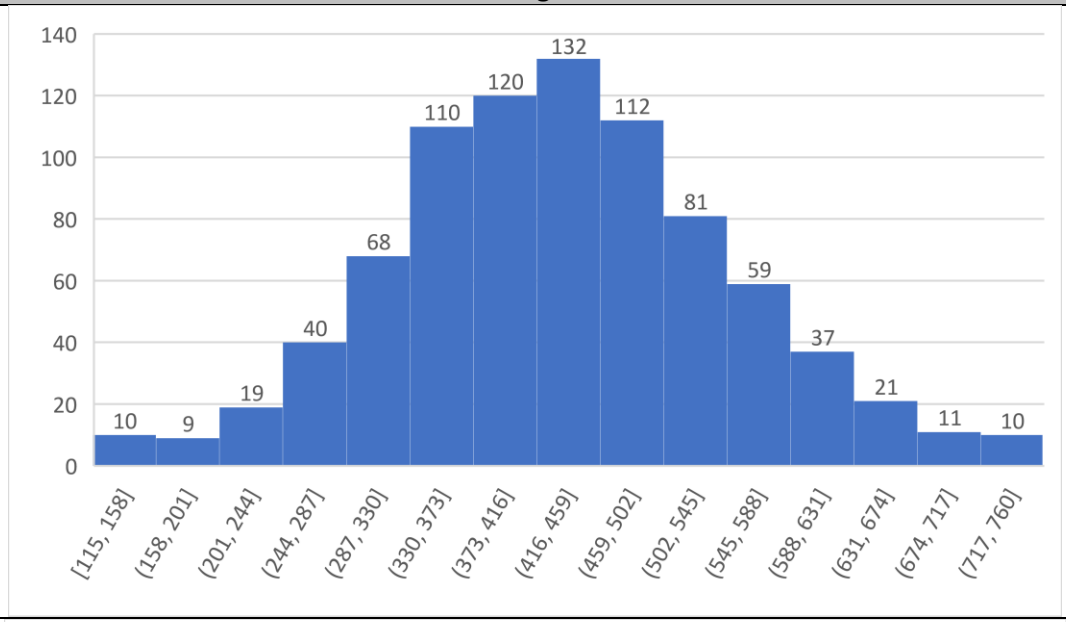
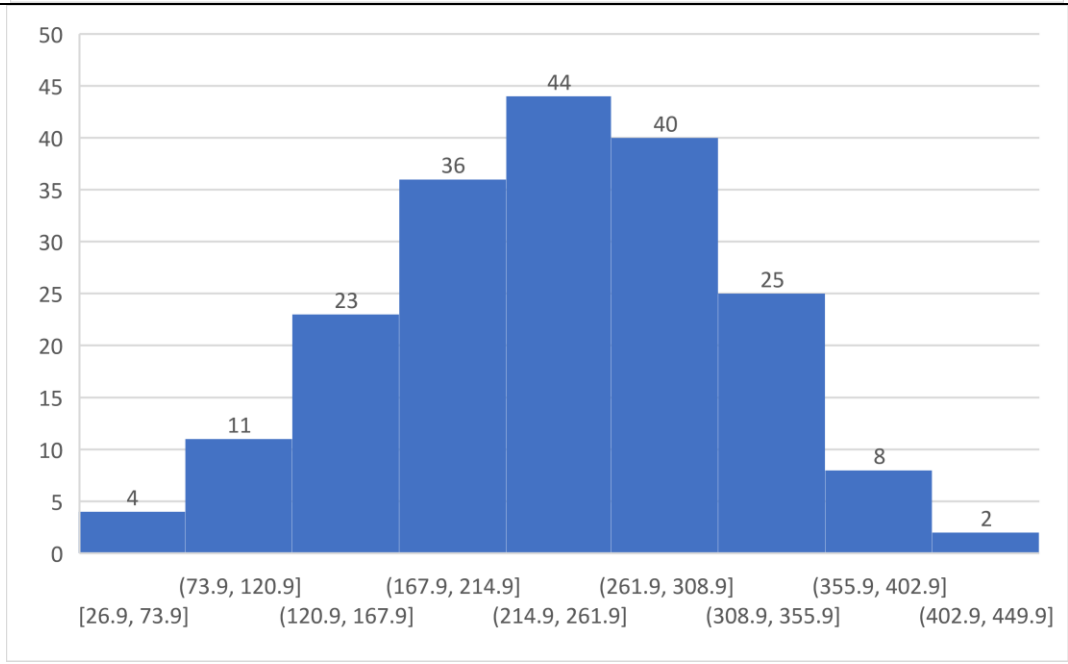


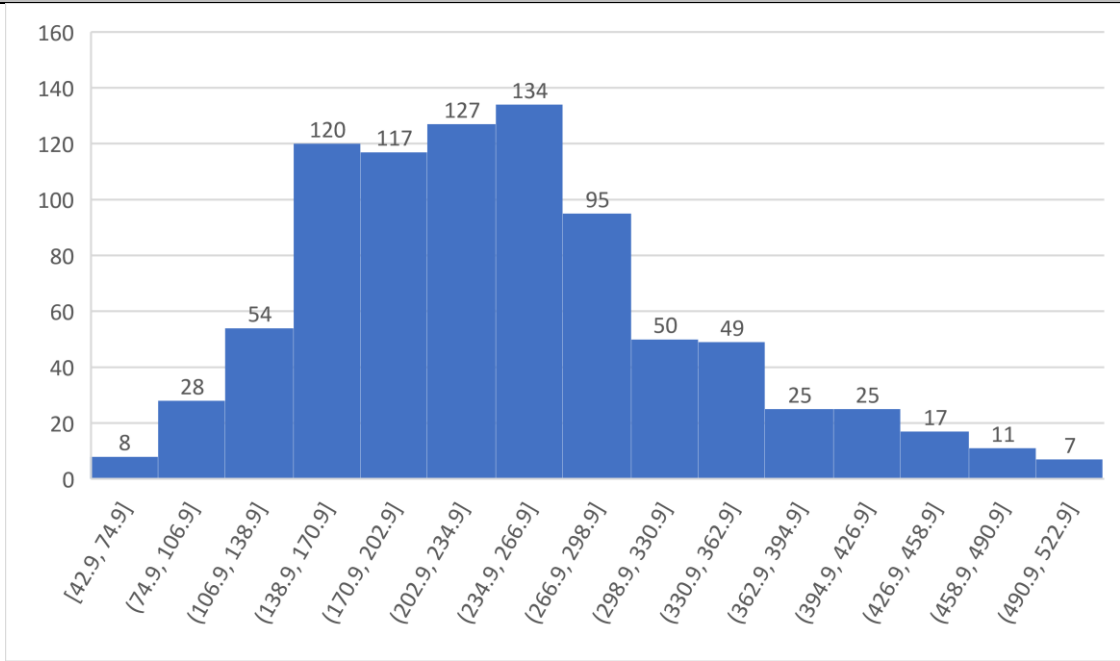
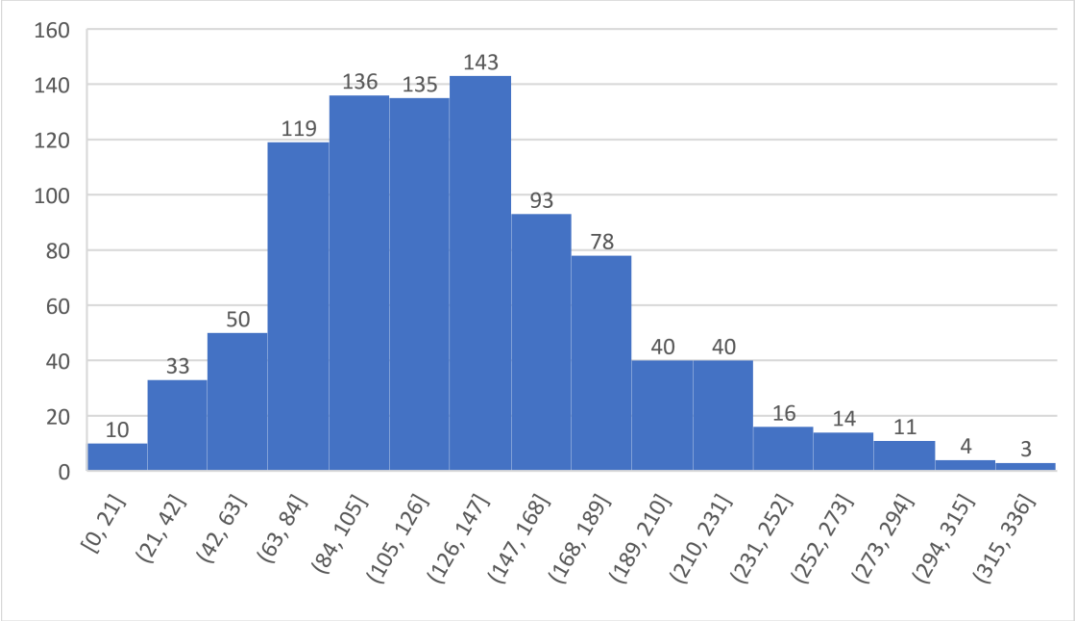
Relationship	#	Min	Average	Max	Histogram
Parent/Child	758	3266	3471	3720	
Siblings	789	2150	2600	3070	

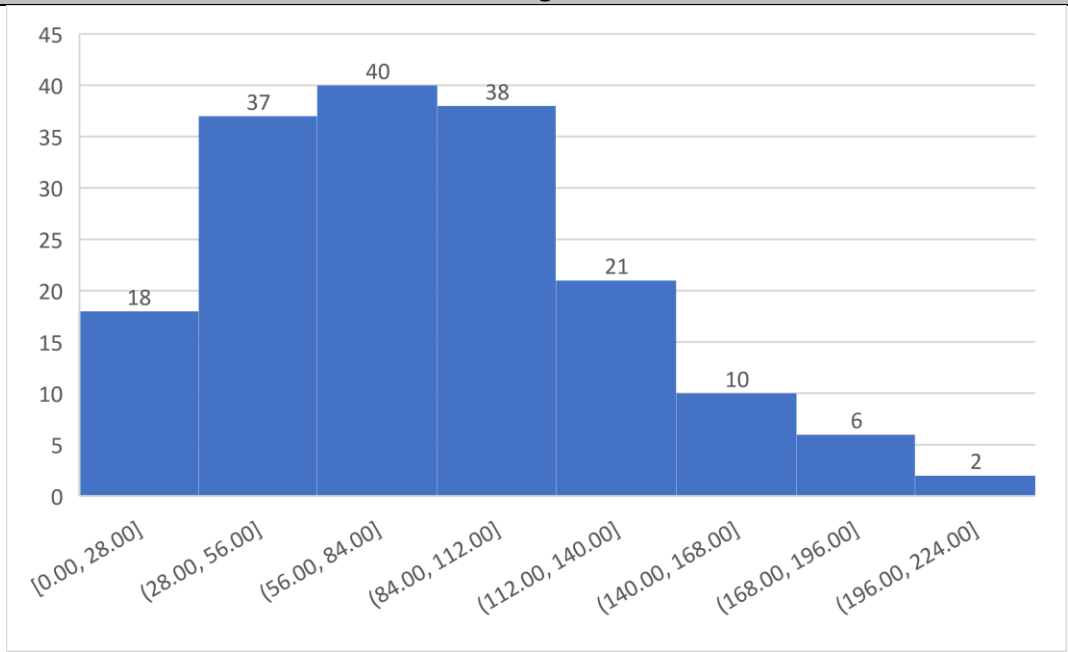
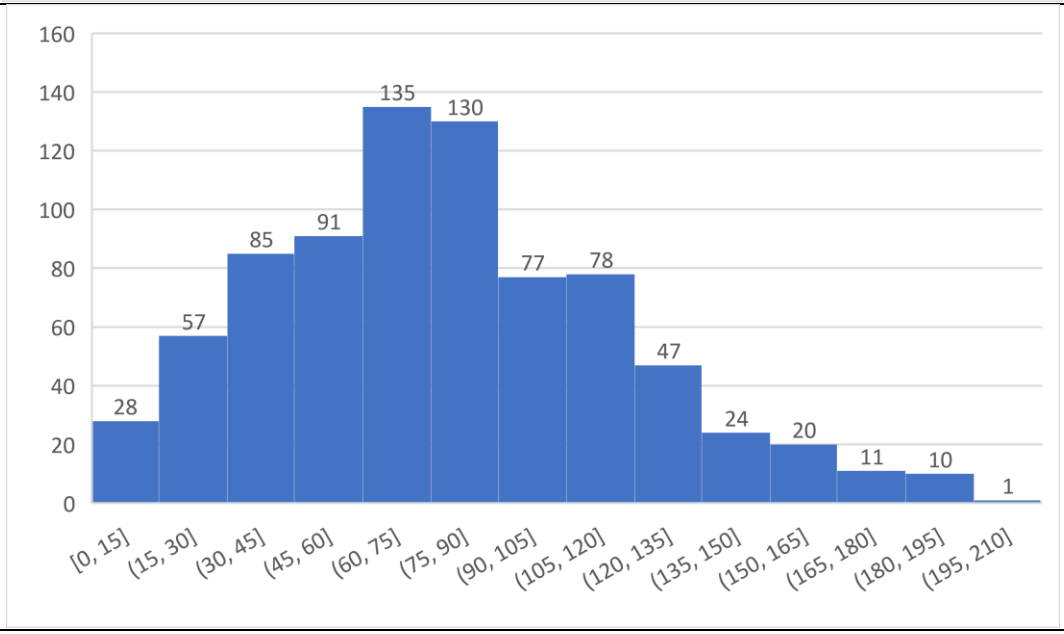
Relationship	#	Min	Average	Max	Histogram
Half Siblings	187	1320	1753	2134	
Grandparent/Grandchild	281	1272	1765	2365	

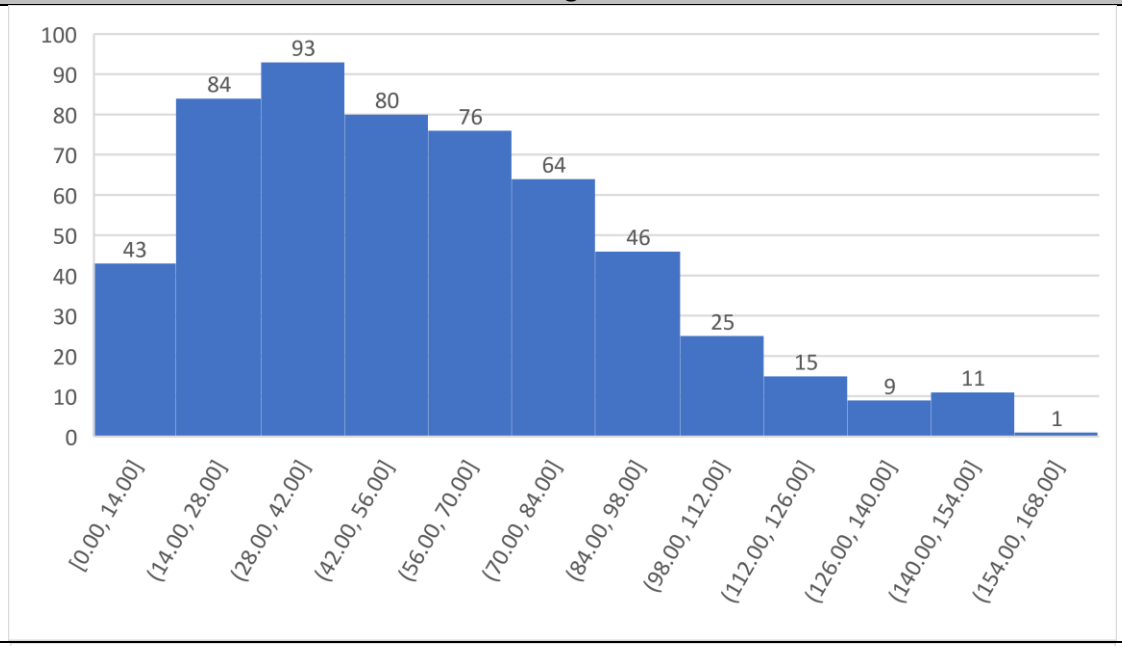
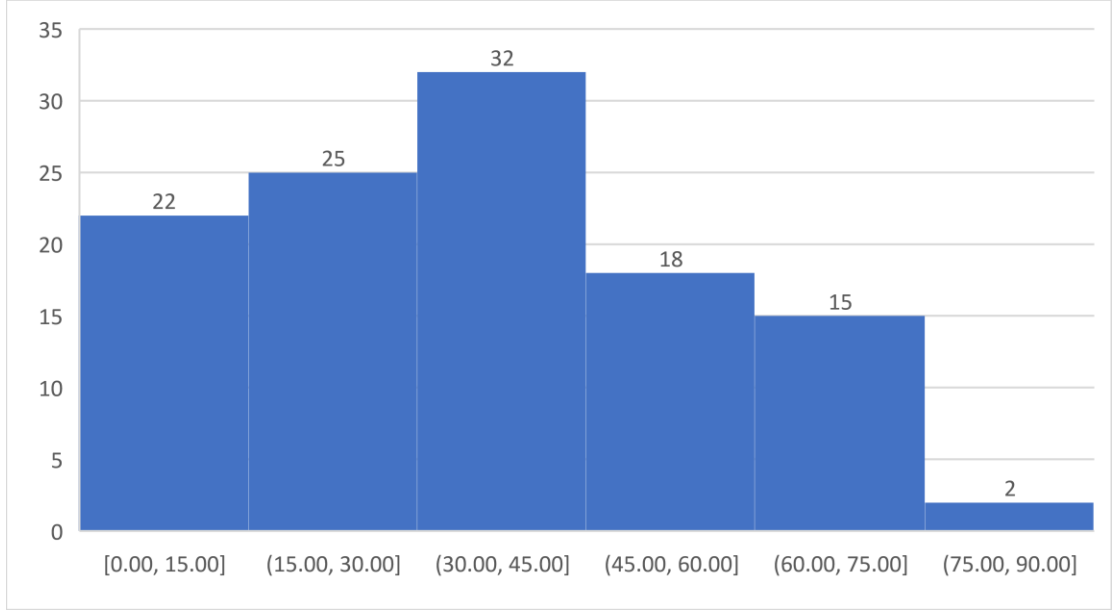
Relationship	#	Min	Average	Max	Histogram
Aunt/Uncle/Niece/Nephew	889	1301	1744	2193	
Half Aunt/Uncle	80	540	863	1172	

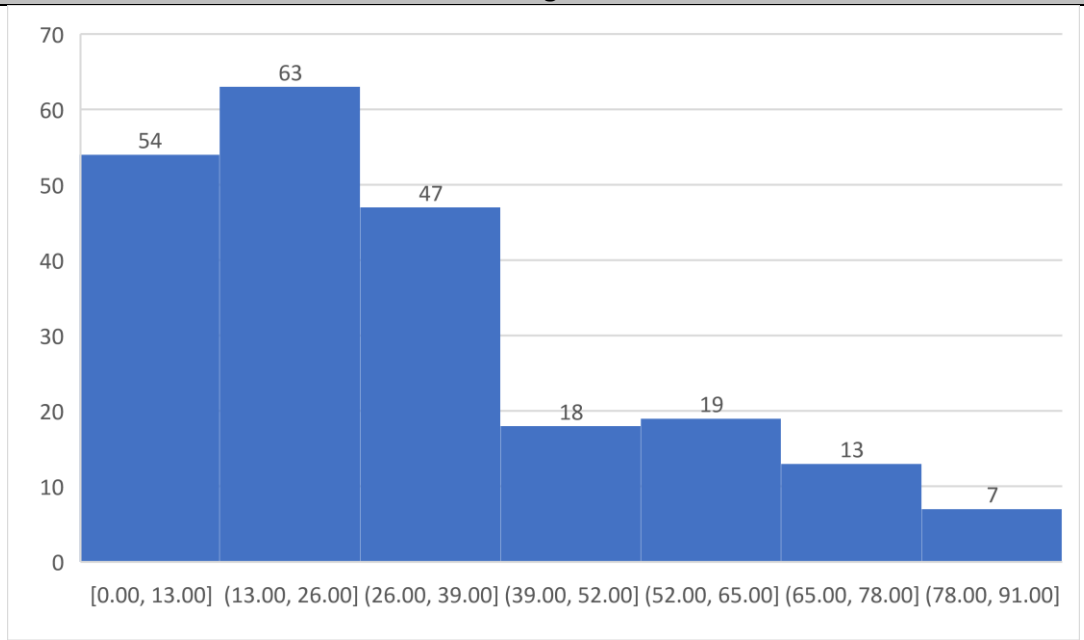
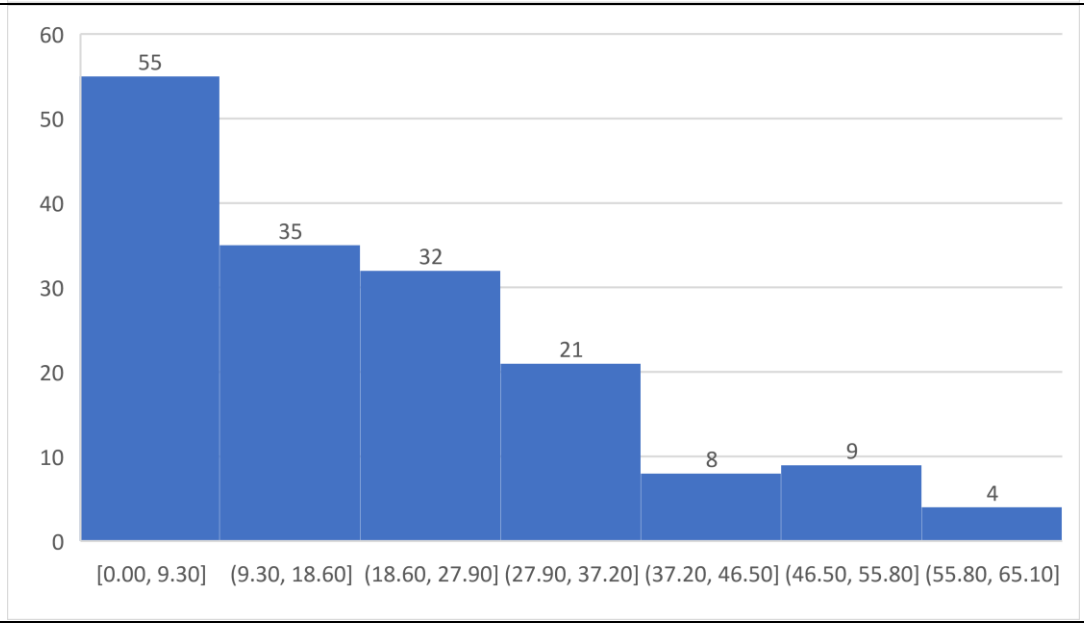
Relationship	#	Min	Average	Max	Histogram
Great Aunt/Uncle	158	521	857	1138	
1C	869	533	869	1379	

Relationship	#	Min	Average	Max	Histogram
1C1R	839	115	512	753	
1C2R	193	27	235	413	

Relationship	#	Min	Average	Max	Histogram
2C	867	43	238	504	
2C1R (the average was calculated only for those sharing DNA)	884	0	129	325	

Relationship	#	Min	Average	Max	Histogram
2C2R (the average was calculated only for those sharing DNA)	172	0	81	201	
3C (the average was calculated only for those sharing DNA)	794	0	79	198	

Relationship	#	Min	Average	Max	Histogram
3C1R (the average was calculated only for those sharing DNA)	547	0	56	156	
3C2R (the average was calculated only for those sharing DNA)	114	0	36	82	

Relationship	#	Min	Average	Max	Histogram
4C (the average was calculated only for those sharing DNA)	221	0	31	90	
4C1R (the average was calculated only for those sharing DNA)	164	0	20	57	

Due to the low number of data entries for the following, histograms were not created:

Relationship	#	Min	Average	Max
Great Grandparent/Grandchild	29	547	850	1110
Great Great Aunt/Uncle	6	214	434	580
Half 1C	23	236	554	704
Half 1C1R	32	78	187	253
Half 2C	51	0	123	245
Half 2C1R	40	0	73	196
4C2R	34	0	14	27
5C	99	0	17	42
5C1R	82	0	14	41
5C2R	25	0	16	41
6C	38	0	9	21
6C1R	46	0	9	19
6C2R	20	0	11	29
7C	19	0	7	10
7C1R	42	0	7	14
8C	25	0	9	16

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3C1R	547	0	56	156
3C2R	114	0	36	82
4C	221	0	31	90
4C1R	164	0	20	57
4C2R	34	0	14	27
5C	99	0	17	42
5C1R	82	0	14	41
5C2R	25	0	16	41
6C	38	0	9	21
6C1R	46	0	9	19
6C2R	20	0	11	29
7C	19	0	7	10
7C1R	42	0	7	14
8C	25	0	9	16