

The Shared cM Project – Version 3.0 (August 2017)

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. For this update, total shared cM data for more than 25,000 known relationships were provided.

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
- Bettinger, Blaine T., The Shared cM Project: A Demonstration of the Power of Citizen Science. *Journal of Genetic Genealogy*, 2016, pgs. 38-42. <http://jogg.info/pages/vol8/editorial/bettinger-sharedcMProject.html>

To provide your data for subsequent updates:

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

Possible issues with user-provided data:

- **Data entry errors** – some of the information entered by participants is affected by data entry errors (for example, a longest segment greater than the total shared cM). When these entries 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.
- **Endogamy and Pedigree Collapse** - Some relationships will be affected by endogamy and/or pedigree collapse, which will increase the amount of DNA shared by test-takers having a certain genealogical relationship. Although the collection form requests information about known endogamy and/or pedigree collapse, many contributors will not be aware of the endogamy and pedigree collapse in their tree. Additionally, some participants may have selected only one relationship although there were several known relationships.
- **Company Thresholds** – Each of the DNA testing companies applies a different matching threshold to maximize the identification of genetic cousins while minimizing false positives. These thresholds may impact the total amount of DNA shared by two test-takers, especially at more distant relationships.

Using the Shared cM Project

Step 1: How much DNA do two people share?

- Determine how much DNA you share with a genetic match
- In this AncestryDNA example, I share 95 cM with this match

Step 2: Which Cluster(s) does the total shared cM fit into?

- Review the Cluster Chart to see into which Cluster(s) the total shared cM fits, using the 95th percentiles
- In this example, 95 cM fits into each of Clusters #6, 7, and 8 (that is, it falls within the 95th percentile range for each of these Clusters).

Step 3: Which Cluster(s) the total shared cM **best** fits into

- Based on the **average**, which Cluster(s) does the total shared cM most closely match?
- In this example, 95 cM best fits into Clusters #6 and 7 (i.e., 95 cM is closest to the average for these Clusters)

Step 4: Review the **histograms** for the relationships in the best fit Cluster(s)

- Using the relationships listed in the Cluster(s), go to the histograms and see which relationship(s) the total shared cM is nearest the peak of the histogram. Note that this only provides **clues** as to the *most likely* relationships; your actual relationship may vary.
- For this example, for which relationships in Clusters #6 and 7 is 95 cM closest to the peak of the histogram?

This method helps you narrow in on *most likely* relationships,
but does not definitely identify a specific relationship.

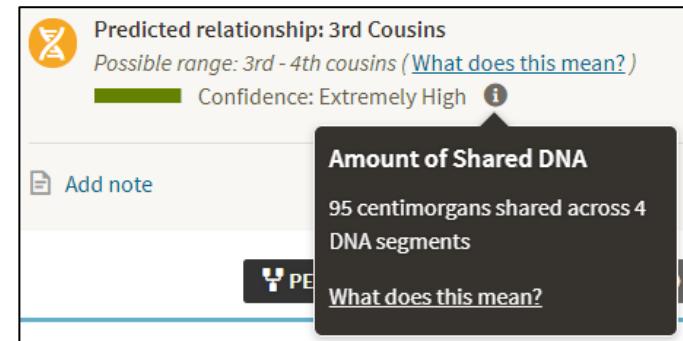


Table 1. The Cluster Chart

The average, minimums, and maximums for each Cluster were calculated using every submission for the relationships within that Cluster, rather than averaging the previously calculated averages for those relationships. Minimums were automatically set to “0 cM” for Clusters 6-10.

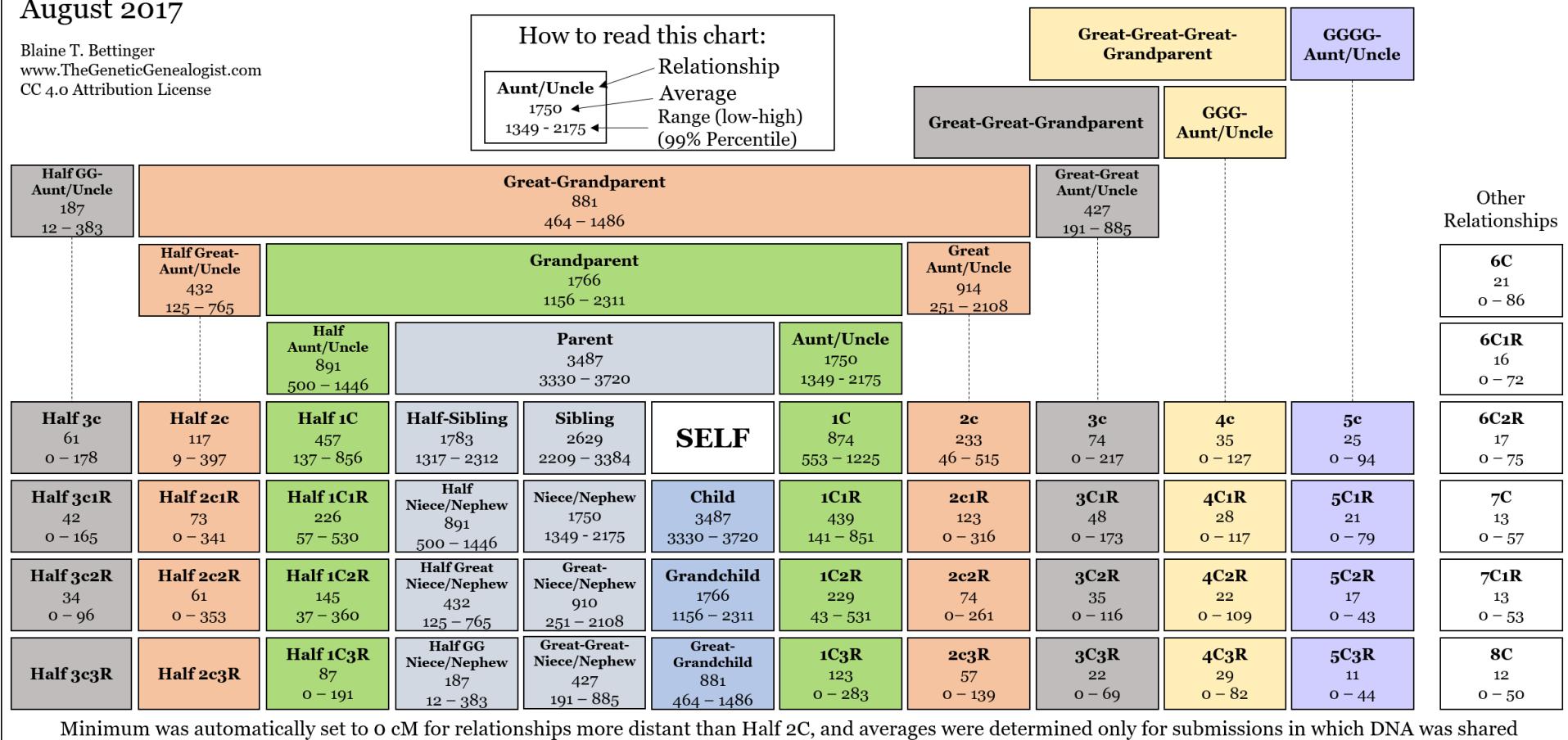
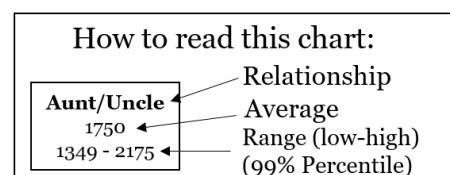
The Shared cM Project – Version 3.0 August 2017		Blaine T. Bettinger www.TheGeneticGenealogist.com CC 4.0 Attribution License		For MUCH more information (including histograms and company breakdowns) see: goo.gl/Z1EcJQ		
Cluster	Relationships	Total #	Average	Range (95 th Percentile)	Range (99th Percentile)	Expected
Cluster #1	Siblings	1345	2629	2342 - 2917	2209 – 3384	2550
Cluster #2	Half Sibling, Aunt/Uncle/Niece/Nephew, and Grandparent/Grandchild	2473	1760	1435 – 2083	1294 – 2230	1700
Cluster #3	1C, Half Aunt/Uncle/Niece/Nephew, Great-Grandparent/Great-Grandchild, and Great-Aunt/Uncle/Niece/Nephew	2261	884	619 – 1159	486 – 1761	850
Cluster #4	1C1R, Half 1C, Half Great- Aunt/Uncle/Niece/Nephew, and Great-Great- Aunt/Uncle/Niece/Nephew	1842	440	235 – 665	131 – 851	425
Cluster #5	1C2R, Half 1C1R, 2C, and Half Great-Great- Aunt/Uncle/Niece/Nephew	2224	232	99 – 397	47 – 517	213
Cluster #6	1C3R, Half 1C2R, Half 2C, and 2C1R	2284	123	0 – 236	0 – 317	106
Cluster #7	Half 1C3R, Half 2C1R, 2C2R, and 3C	2492	75	0 – 158	0 – 229	53
Cluster #8	Half 2C2R, 2C3R, Half 3C, and 3C1R	1864	49	0 – 114	0 – 175	27
Cluster #9	Half 3C1R, 3C2R, and 4C	1528	36	0 – 84	0 – 122	13
Cluster #10	Half 3C2R, 3C3R, Half 4C, and 4C1R	1040	29	0 – 67	0 – 118	7

Figure 1. The Relationship Chart

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For MUCH more information (including histograms and company breakdowns) see: goo.gl/Z1EcJQ



NOTE: for this and other charts or diagrams in this document, the minimum was automatically set to “0 cM” for relationships more distant than Half 2C, and averages were determined only for relationships in which DNA was shared.

Larger version at: https://isogg.org/wiki/Autosomal_DNA_statistics

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Histograms

Histogram = a graphical representation of the distribution of numerical data

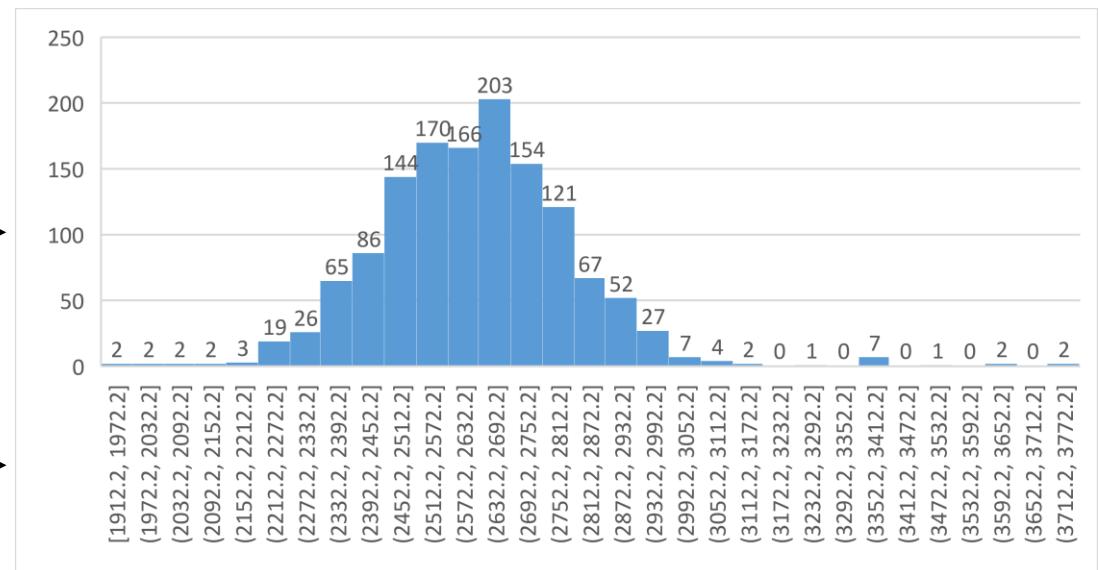
The following steps are followed to create a histogram:

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, 203 data entries are in the interval of 2632.2 to 2692.1 cM.

These are “bins,” ranges of total shared cM. For example, a total of 203 data entries are in the interval of 2632.2 to 2692.1 cM for this relationship (siblings).



The minimum and maximum are for the 99th percentile when available (thus there may be values below the minimum and below the maximum, which should be considered outliers)

Table 2. Relationship Histograms

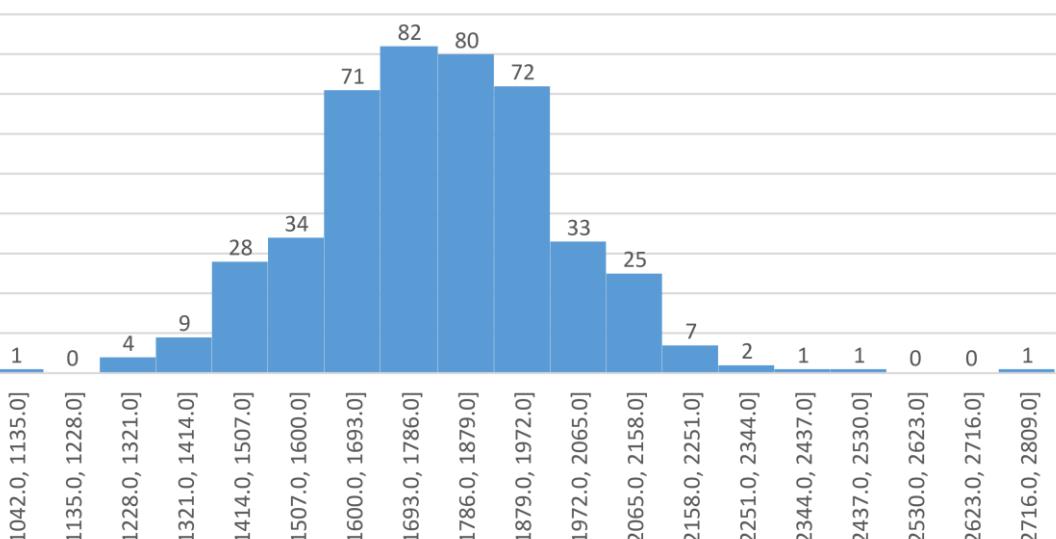
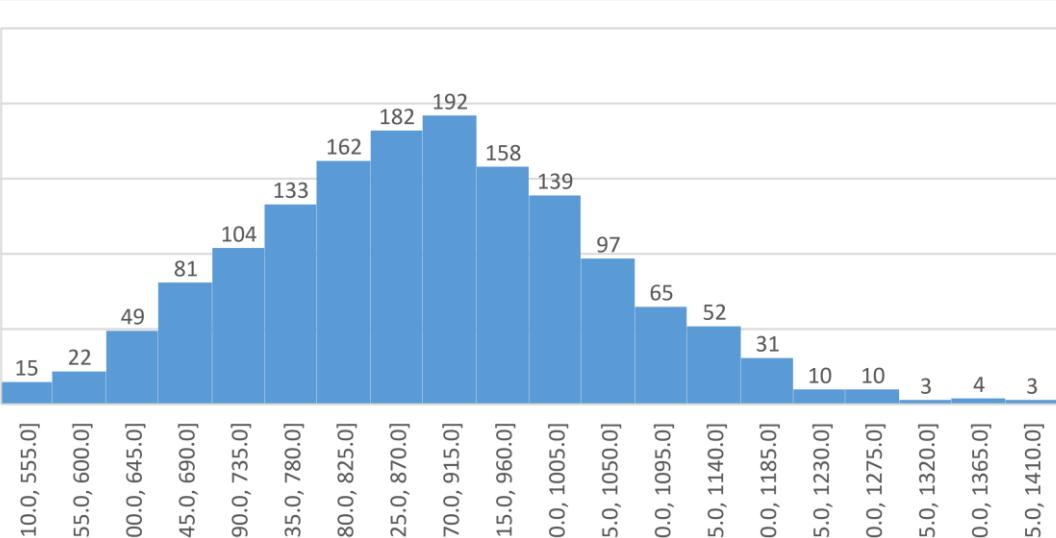
- NOTES:
 - Data for the Min, Average, and Max columns is the 99th percentile where available, otherwise it is the 95th percentile (see Table 3 for more information). The data for the histograms contain all submissions (including outliers) for the relationship.
 - The minimum was automatically set to 0 cM for relationships more distant than Half 2C, and averages were determined only for relationships in which DNA was shared. Because the data is biased toward relationships in which DNA was shared, an analysis of the frequency of submissions in which the shared DNA was 0 cM was not performed.
 - The total number of submissions (provided in the column marked "#") may include MyHeritage submissions, which were not analyzed because there wasn't enough data.

Relationship	#	Min	Average	Max	Histogram																																																																
Parent/Child	1378	3330	3487	3720	(histogram not necessary)																																																																
Sibling (Cluster #1) (Although siblings should share 50% of their DNA, similar to parent/child, the testing companies only report sharing of <i>half-identical regions</i> even though siblings share <i>fully-identical regions</i> . As a result, siblings are incorrectly reported to share less than 50% of their DNA)	1345	2209	2629	3384	<table border="1"> <caption>Data for Sibling Relationship Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Count</th> </tr> </thead> <tbody> <tr><td>[1912,2, 1972,2]</td><td>2</td></tr> <tr><td>[1972,2, 2032,2]</td><td>2</td></tr> <tr><td>[2032,2, 2092,2]</td><td>2</td></tr> <tr><td>[2092,2, 2152,2]</td><td>2</td></tr> <tr><td>[2152,2, 2212,2]</td><td>3</td></tr> <tr><td>[2212,2, 2272,2]</td><td>19</td></tr> <tr><td>[2272,2, 2332,2]</td><td>26</td></tr> <tr><td>[2332,2, 2392,2]</td><td>65</td></tr> <tr><td>[2392,2, 2452,2]</td><td>86</td></tr> <tr><td>[2452,2, 2512,2]</td><td>144</td></tr> <tr><td>[2512,2, 2572,2]</td><td>170</td></tr> <tr><td>[2572,2, 2632,2]</td><td>166</td></tr> <tr><td>[2632,2, 2692,2]</td><td>203</td></tr> <tr><td>[2692,2, 2752,2]</td><td>154</td></tr> <tr><td>[2752,2, 2812,2]</td><td>121</td></tr> <tr><td>[2812,2, 2872,2]</td><td>67</td></tr> <tr><td>[2872,2, 2932,2]</td><td>52</td></tr> <tr><td>[2932,2, 2992,2]</td><td>27</td></tr> <tr><td>[2992,2, 3052,2]</td><td>7</td></tr> <tr><td>[3052,2, 3112,2]</td><td>4</td></tr> <tr><td>[3112,2, 3172,2]</td><td>2</td></tr> <tr><td>[3172,2, 3232,2]</td><td>0</td></tr> <tr><td>[3232,2, 3292,2]</td><td>1</td></tr> <tr><td>[3292,2, 3352,2]</td><td>0</td></tr> <tr><td>[3352,2, 3412,2]</td><td>7</td></tr> <tr><td>[3412,2, 3472,2]</td><td>0</td></tr> <tr><td>[3472,2, 3532,2]</td><td>1</td></tr> <tr><td>[3532,2, 3592,2]</td><td>0</td></tr> <tr><td>[3592,2, 3652,2]</td><td>2</td></tr> <tr><td>[3652,2, 3712,2]</td><td>0</td></tr> <tr><td>[3712,2, 3772,2]</td><td>2</td></tr> </tbody> </table>	cM Range	Count	[1912,2, 1972,2]	2	[1972,2, 2032,2]	2	[2032,2, 2092,2]	2	[2092,2, 2152,2]	2	[2152,2, 2212,2]	3	[2212,2, 2272,2]	19	[2272,2, 2332,2]	26	[2332,2, 2392,2]	65	[2392,2, 2452,2]	86	[2452,2, 2512,2]	144	[2512,2, 2572,2]	170	[2572,2, 2632,2]	166	[2632,2, 2692,2]	203	[2692,2, 2752,2]	154	[2752,2, 2812,2]	121	[2812,2, 2872,2]	67	[2872,2, 2932,2]	52	[2932,2, 2992,2]	27	[2992,2, 3052,2]	7	[3052,2, 3112,2]	4	[3112,2, 3172,2]	2	[3172,2, 3232,2]	0	[3232,2, 3292,2]	1	[3292,2, 3352,2]	0	[3352,2, 3412,2]	7	[3412,2, 3472,2]	0	[3472,2, 3532,2]	1	[3532,2, 3592,2]	0	[3592,2, 3652,2]	2	[3652,2, 3712,2]	0	[3712,2, 3772,2]	2
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Grandparent/Grandchild (Cluster #2)	611	1156	1766	2311	<table border="1"> <caption>Data for Grandparent/Grandchild (Cluster #2) Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[1024.1, 1119.1]</td><td>2</td></tr> <tr><td>(1119.1, 1214.1]</td><td>4</td></tr> <tr><td>(1214.1, 1309.1]</td><td>12</td></tr> <tr><td>(1309.1, 1404.1]</td><td>19</td></tr> <tr><td>(1404.1, 1499.1]</td><td>35</td></tr> <tr><td>(1499.1, 1594.1]</td><td>58</td></tr> <tr><td>(1594.1, 1689.1]</td><td>87</td></tr> <tr><td>(1689.1, 1784.1]</td><td>103</td></tr> <tr><td>(1784.1, 1879.1]</td><td>95</td></tr> <tr><td>(1879.1, 1974.1]</td><td>73</td></tr> <tr><td>(1974.1, 2069.1]</td><td>65</td></tr> <tr><td>(2069.1, 2164.1]</td><td>33</td></tr> <tr><td>(2164.1, 2259.1]</td><td>12</td></tr> <tr><td>(2259.1, 2354.1]</td><td>6</td></tr> <tr><td>(2354.1, 2449.1]</td><td>2</td></tr> <tr><td>(2449.1, 2544.1]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[1024.1, 1119.1]	2	(1119.1, 1214.1]	4	(1214.1, 1309.1]	12	(1309.1, 1404.1]	19	(1404.1, 1499.1]	35	(1499.1, 1594.1]	58	(1594.1, 1689.1]	87	(1689.1, 1784.1]	103	(1784.1, 1879.1]	95	(1879.1, 1974.1]	73	(1974.1, 2069.1]	65	(2069.1, 2164.1]	33	(2164.1, 2259.1]	12	(2259.1, 2354.1]	6	(2354.1, 2449.1]	2	(2449.1, 2544.1]	1														
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Half Sibling (Cluster #2)	451	1317	1783	2312	 <table border="1"> <caption>Data for Half Sibling (Cluster #2) Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[1042.0, 1135.0]</td><td>1</td></tr> <tr><td>(1135.0, 1228.0]</td><td>0</td></tr> <tr><td>(1228.0, 1321.0]</td><td>4</td></tr> <tr><td>(1321.0, 1414.0]</td><td>9</td></tr> <tr><td>(1414.0, 1507.0]</td><td>28</td></tr> <tr><td>(1507.0, 1600.0]</td><td>34</td></tr> <tr><td>(1600.0, 1693.0]</td><td>71</td></tr> <tr><td>(1693.0, 1786.0]</td><td>82</td></tr> <tr><td>(1786.0, 1879.0]</td><td>80</td></tr> <tr><td>(1879.0, 1972.0]</td><td>72</td></tr> <tr><td>(1972.0, 2065.0]</td><td>33</td></tr> <tr><td>(2065.0, 2158.0]</td><td>25</td></tr> <tr><td>(2158.0, 2251.0]</td><td>7</td></tr> <tr><td>(2251.0, 2344.0]</td><td>2</td></tr> <tr><td>(2344.0, 2437.0]</td><td>1</td></tr> <tr><td>(2437.0, 2530.0]</td><td>1</td></tr> <tr><td>(2530.0, 2623.0]</td><td>0</td></tr> <tr><td>(2623.0, 2716.0]</td><td>0</td></tr> <tr><td>(2716.0, 2809.0]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[1042.0, 1135.0]	1	(1135.0, 1228.0]	0	(1228.0, 1321.0]	4	(1321.0, 1414.0]	9	(1414.0, 1507.0]	28	(1507.0, 1600.0]	34	(1600.0, 1693.0]	71	(1693.0, 1786.0]	82	(1786.0, 1879.0]	80	(1879.0, 1972.0]	72	(1972.0, 2065.0]	33	(2065.0, 2158.0]	25	(2158.0, 2251.0]	7	(2251.0, 2344.0]	2	(2344.0, 2437.0]	1	(2437.0, 2530.0]	1	(2530.0, 2623.0]	0	(2623.0, 2716.0]	0	(2716.0, 2809.0]	1		
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¹ C (Cluster #3)	1512	553	874	1225	 <table border="1"> <caption>Data for 1C (Cluster #3) Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[510.0, 555.0]</td><td>15</td></tr> <tr><td>(555.0, 600.0]</td><td>22</td></tr> <tr><td>(600.0, 645.0]</td><td>49</td></tr> <tr><td>(645.0, 690.0]</td><td>81</td></tr> <tr><td>(690.0, 735.0]</td><td>104</td></tr> <tr><td>(735.0, 780.0]</td><td>133</td></tr> <tr><td>(780.0, 825.0]</td><td>162</td></tr> <tr><td>(825.0, 870.0]</td><td>182</td></tr> <tr><td>(870.0, 915.0]</td><td>192</td></tr> <tr><td>(915.0, 960.0]</td><td>158</td></tr> <tr><td>(960.0, 1005.0]</td><td>139</td></tr> <tr><td>(1005.0, 1050.0]</td><td>97</td></tr> <tr><td>(1050.0, 1095.0]</td><td>65</td></tr> <tr><td>(1095.0, 1140.0]</td><td>52</td></tr> <tr><td>(1140.0, 1185.0]</td><td>31</td></tr> <tr><td>(1185.0, 1230.0]</td><td>10</td></tr> <tr><td>(1230.0, 1275.0]</td><td>10</td></tr> <tr><td>(1275.0, 1320.0]</td><td>3</td></tr> <tr><td>(1320.0, 1365.0]</td><td>4</td></tr> <tr><td>(1365.0, 1410.0]</td><td>3</td></tr> </tbody> </table>	cM Range	Frequency	[510.0, 555.0]	15	(555.0, 600.0]	22	(600.0, 645.0]	49	(645.0, 690.0]	81	(690.0, 735.0]	104	(735.0, 780.0]	133	(780.0, 825.0]	162	(825.0, 870.0]	182	(870.0, 915.0]	192	(915.0, 960.0]	158	(960.0, 1005.0]	139	(1005.0, 1050.0]	97	(1050.0, 1095.0]	65	(1095.0, 1140.0]	52	(1140.0, 1185.0]	31	(1185.0, 1230.0]	10	(1230.0, 1275.0]	10	(1275.0, 1320.0]	3	(1320.0, 1365.0]	4	(1365.0, 1410.0]	3
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Relationship	#	Min	Average	Max	Histogram																														
Great-Aunt/Uncle/Niece/Nephew (Cluster #3)	413	251	914	2108	<table border="1"> <caption>Data for Great-Aunt/Uncle/Niece/Nephew (Cluster #3) Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[205.3, 345.3]</td><td>10</td></tr> <tr><td>(345.3, 485.3]</td><td>10</td></tr> <tr><td>(485.3, 625.3]</td><td>26</td></tr> <tr><td>(625.3, 765.3]</td><td>68</td></tr> <tr><td>(765.3, 905.3]</td><td>126</td></tr> <tr><td>(905.3, 1045.3]</td><td>97</td></tr> <tr><td>(1045.3, 1185.3]</td><td>35</td></tr> <tr><td>(1185.3, 1325.3]</td><td>8</td></tr> <tr><td>(1325.3, 1465.3]</td><td>2</td></tr> <tr><td>(1465.3, 1605.3]</td><td>6</td></tr> <tr><td>(1605.3, 1745.3]</td><td>3</td></tr> <tr><td>(1745.3, 1885.3]</td><td>11</td></tr> <tr><td>(1885.3, 2025.3]</td><td>5</td></tr> <tr><td>(2025.3, 2165.3]</td><td>3</td></tr> </tbody> </table>	cM Range	Frequency	[205.3, 345.3]	10	(345.3, 485.3]	10	(485.3, 625.3]	26	(625.3, 765.3]	68	(765.3, 905.3]	126	(905.3, 1045.3]	97	(1045.3, 1185.3]	35	(1185.3, 1325.3]	8	(1325.3, 1465.3]	2	(1465.3, 1605.3]	6	(1605.3, 1745.3]	3	(1745.3, 1885.3]	11	(1885.3, 2025.3]	5	(2025.3, 2165.3]	3
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Great-Grandparent/Great Grandchild (Cluster #3)	61	464	881	1486	(not enough data for a histogram)																														
Half Aunt/Uncle/Niece/Nephew (Cluster #3)	275	500	891	1446	<table border="1"> <caption>Data for Half Aunt/Uncle/Niece/Nephew (Cluster #3) Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[349.0, 440.0]</td><td>1</td></tr> <tr><td>(440.0, 531.0]</td><td>2</td></tr> <tr><td>(531.0, 622.0]</td><td>9</td></tr> <tr><td>(622.0, 713.0]</td><td>36</td></tr> <tr><td>(713.0, 804.0]</td><td>42</td></tr> <tr><td>(804.0, 895.0]</td><td>56</td></tr> <tr><td>(895.0, 986.0]</td><td>55</td></tr> <tr><td>(986.0, 1077.0]</td><td>33</td></tr> <tr><td>(1077.0, 1168.0]</td><td>22</td></tr> <tr><td>(1168.0, 1259.0]</td><td>14</td></tr> <tr><td>(1259.0, 1350.0]</td><td>3</td></tr> </tbody> </table>	cM Range	Frequency	[349.0, 440.0]	1	(440.0, 531.0]	2	(531.0, 622.0]	9	(622.0, 713.0]	36	(713.0, 804.0]	42	(804.0, 895.0]	56	(895.0, 986.0]	55	(986.0, 1077.0]	33	(1077.0, 1168.0]	22	(1168.0, 1259.0]	14	(1259.0, 1350.0]	3						
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Relationship	#	Min	Average	Max	Histogram																																														
1C1R (Cluster #4)	1594	141	439	851	<table border="1"> <caption>Data for 1C1R Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[61.4, 99.4]</td><td>9</td></tr> <tr><td>(99.4, 137.4]</td><td>6</td></tr> <tr><td>(137.4, 175.4]</td><td>17</td></tr> <tr><td>(175.4, 213.4]</td><td>29</td></tr> <tr><td>(213.4, 251.4]</td><td>33</td></tr> <tr><td>(251.4, 289.4]</td><td>73</td></tr> <tr><td>(289.4, 327.4]</td><td>112</td></tr> <tr><td>(327.4, 365.4]</td><td>173</td></tr> <tr><td>(365.4, 403.4]</td><td>204</td></tr> <tr><td>(403.4, 441.4]</td><td>208</td></tr> <tr><td>(441.4, 479.4]</td><td>182</td></tr> <tr><td>(479.4, 517.4]</td><td>154</td></tr> <tr><td>(517.4, 555.4]</td><td>133</td></tr> <tr><td>(555.4, 593.4]</td><td>79</td></tr> <tr><td>(593.4, 631.4]</td><td>73</td></tr> <tr><td>(631.4, 669.4]</td><td>38</td></tr> <tr><td>(669.4, 707.4]</td><td>21</td></tr> <tr><td>(707.4, 745.4]</td><td>13</td></tr> <tr><td>(745.4, 783.4]</td><td>13</td></tr> <tr><td>(783.4, 821.4]</td><td>6</td></tr> <tr><td>(821.4, 859.4]</td><td>3</td></tr> <tr><td>(859.4, 897.4]</td><td>3</td></tr> </tbody> </table>	cM Range	Frequency	[61.4, 99.4]	9	(99.4, 137.4]	6	(137.4, 175.4]	17	(175.4, 213.4]	29	(213.4, 251.4]	33	(251.4, 289.4]	73	(289.4, 327.4]	112	(327.4, 365.4]	173	(365.4, 403.4]	204	(403.4, 441.4]	208	(441.4, 479.4]	182	(479.4, 517.4]	154	(517.4, 555.4]	133	(555.4, 593.4]	79	(593.4, 631.4]	73	(631.4, 669.4]	38	(669.4, 707.4]	21	(707.4, 745.4]	13	(745.4, 783.4]	13	(783.4, 821.4]	6	(821.4, 859.4]	3	(859.4, 897.4]	3
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Great-Great-Aunt/Uncle/Niece/Nephew (Cluster #4)	25	191	427	885	(not enough data for a histogram)																																														
Half 1C (Cluster #4)	177	137	457	856	<table border="1"> <caption>Data for Half 1C Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[88.0, 169.0]</td><td>2</td></tr> <tr><td>(169.0, 250.0]</td><td>6</td></tr> <tr><td>(250.0, 331.0]</td><td>16</td></tr> <tr><td>(331.0, 412.0]</td><td>43</td></tr> <tr><td>(412.0, 493.0]</td><td>47</td></tr> <tr><td>(493.0, 574.0]</td><td>37</td></tr> <tr><td>(574.0, 655.0]</td><td>11</td></tr> <tr><td>(655.0, 736.0]</td><td>10</td></tr> <tr><td>(736.0, 817.0]</td><td>2</td></tr> <tr><td>(817.0, 898.0]</td><td>3</td></tr> </tbody> </table>	cM Range	Frequency	[88.0, 169.0]	2	(169.0, 250.0]	6	(250.0, 331.0]	16	(331.0, 412.0]	43	(412.0, 493.0]	47	(493.0, 574.0]	37	(574.0, 655.0]	11	(655.0, 736.0]	10	(736.0, 817.0]	2	(817.0, 898.0]	3																								
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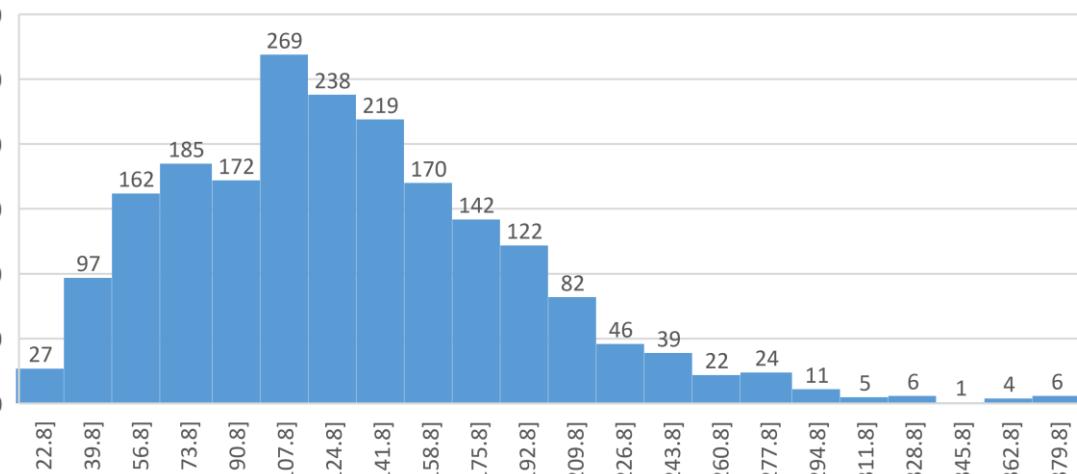
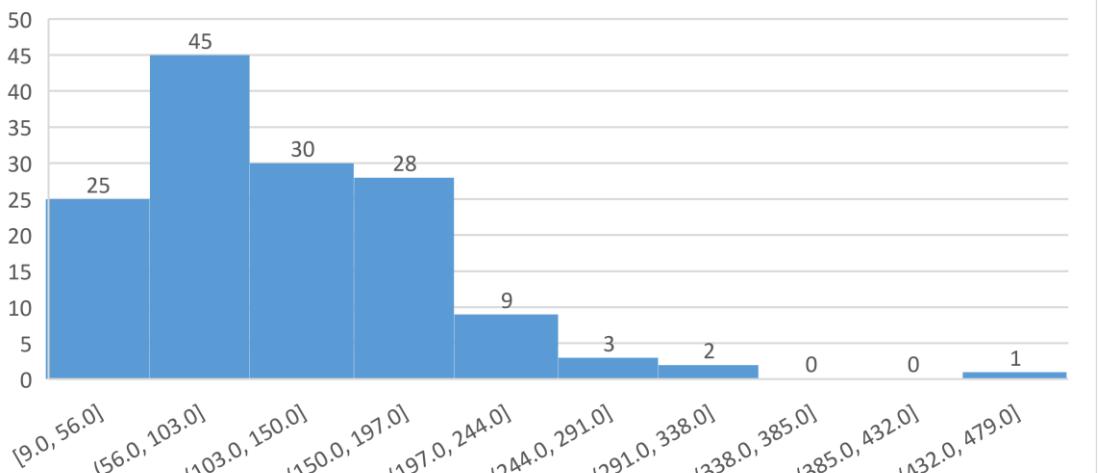
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Half Great-Aunt/Uncle/Niece/Nephew (Cluster #4)	44	125	432	765	(not enough data for a histogram)																																										
1C2R (Cluster #5)	481	43	229	531	<table border="1"> <caption>Data for 1C2R Cluster #5 Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[25.7, 65.7]</td><td>12</td></tr> <tr><td>(65.7, 105.7]</td><td>19</td></tr> <tr><td>(105.7, 145.7]</td><td>56</td></tr> <tr><td>(145.7, 185.7]</td><td>79</td></tr> <tr><td>(185.7, 225.7]</td><td>80</td></tr> <tr><td>(225.7, 265.7]</td><td>81</td></tr> <tr><td>(265.7, 305.7]</td><td>66</td></tr> <tr><td>(305.7, 345.7]</td><td>40</td></tr> <tr><td>(345.7, 385.7]</td><td>25</td></tr> <tr><td>(385.7, 425.7]</td><td>14</td></tr> <tr><td>(425.7, 465.7]</td><td>3</td></tr> <tr><td>(465.7, 505.7]</td><td>1</td></tr> <tr><td>(505.7, 545.7]</td><td>1</td></tr> <tr><td>(545.7, 585.7]</td><td>2</td></tr> <tr><td>(585.7, 625.7]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[25.7, 65.7]	12	(65.7, 105.7]	19	(105.7, 145.7]	56	(145.7, 185.7]	79	(185.7, 225.7]	80	(225.7, 265.7]	81	(265.7, 305.7]	66	(305.7, 345.7]	40	(345.7, 385.7]	25	(385.7, 425.7]	14	(425.7, 465.7]	3	(465.7, 505.7]	1	(505.7, 545.7]	1	(545.7, 585.7]	2	(585.7, 625.7]	1										
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2C (Cluster #5)	1590	46	233	515	<table border="1"> <caption>Data for 2C Cluster #5 Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[22.4, 48.4]</td><td>16</td></tr> <tr><td>(48.4, 74.4]</td><td>17</td></tr> <tr><td>(74.4, 100.4]</td><td>40</td></tr> <tr><td>(100.4, 126.4]</td><td>78</td></tr> <tr><td>(126.4, 152.4]</td><td>137</td></tr> <tr><td>(152.4, 178.4]</td><td>177</td></tr> <tr><td>(178.4, 204.4]</td><td>195</td></tr> <tr><td>(204.4, 230.4]</td><td>184</td></tr> <tr><td>(230.4, 256.4]</td><td>193</td></tr> <tr><td>(256.4, 282.4]</td><td>152</td></tr> <tr><td>(282.4, 308.4]</td><td>132</td></tr> <tr><td>(308.4, 334.4]</td><td>76</td></tr> <tr><td>(334.4, 360.4]</td><td>57</td></tr> <tr><td>(360.4, 386.4]</td><td>35</td></tr> <tr><td>(386.4, 412.4]</td><td>25</td></tr> <tr><td>(412.4, 438.4]</td><td>24</td></tr> <tr><td>(438.4, 464.4]</td><td>17</td></tr> <tr><td>(464.4, 490.4]</td><td>9</td></tr> <tr><td>(490.4, 516.4]</td><td>9</td></tr> <tr><td>(516.4, 542.4]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[22.4, 48.4]	16	(48.4, 74.4]	17	(74.4, 100.4]	40	(100.4, 126.4]	78	(126.4, 152.4]	137	(152.4, 178.4]	177	(178.4, 204.4]	195	(204.4, 230.4]	184	(230.4, 256.4]	193	(256.4, 282.4]	152	(282.4, 308.4]	132	(308.4, 334.4]	76	(334.4, 360.4]	57	(360.4, 386.4]	35	(386.4, 412.4]	25	(412.4, 438.4]	24	(438.4, 464.4]	17	(464.4, 490.4]	9	(490.4, 516.4]	9	(516.4, 542.4]	1
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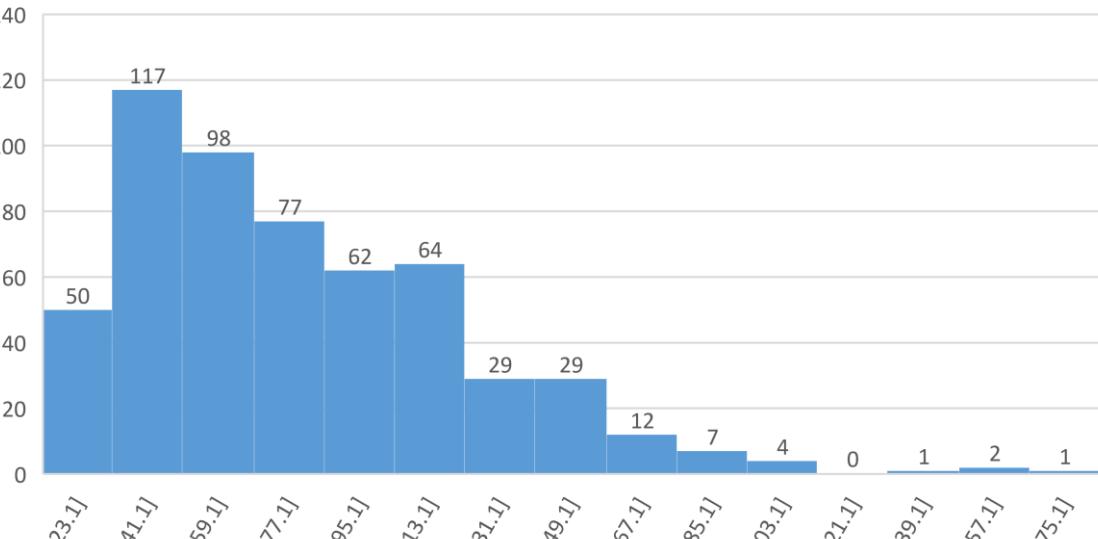
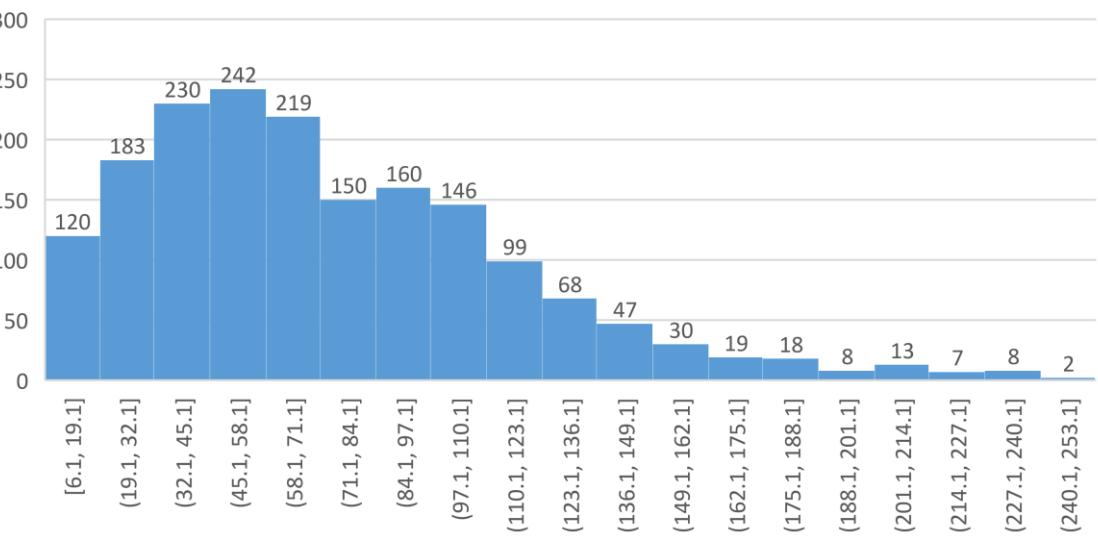
The Shared cM Project – Version 3.0 (August 2017)

Relationship	#	Min	Average	Max	Histogram																		
Half 1C1R (Cluster #5)	138	57	226	530	<table border="1"> <caption>Data for Half 1C1R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[54.0, 120.0]</td><td>18</td></tr> <tr><td>(120.0, 186.0]</td><td>37</td></tr> <tr><td>(186.0, 252.0]</td><td>37</td></tr> <tr><td>(252.0, 318.0]</td><td>24</td></tr> <tr><td>(318.0, 384.0]</td><td>13</td></tr> <tr><td>(384.0, 450.0]</td><td>4</td></tr> <tr><td>(450.0, 516.0]</td><td>3</td></tr> <tr><td>(516.0, 582.0]</td><td>2</td></tr> </tbody> </table>	Bin Range	Frequency	[54.0, 120.0]	18	(120.0, 186.0]	37	(186.0, 252.0]	37	(252.0, 318.0]	24	(318.0, 384.0]	13	(384.0, 450.0]	4	(450.0, 516.0]	3	(516.0, 582.0]	2
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Half Great-Great-Aunt/Uncle/Niece/Nephew (Cluster #5)	15	12	187	383	(not enough data for a histogram)																		
1C3R (Cluster #6)	38	0	123	283	(not enough data for a histogram)																		

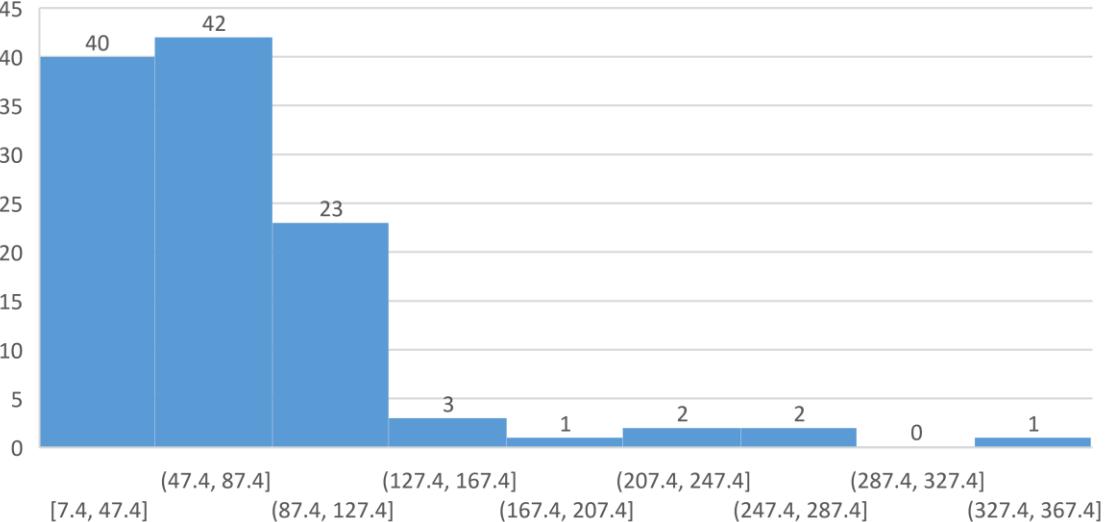
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Relationship	#	Min	Average	Max	Histogram																																														
2C1R (Cluster #6)	2064	0	123	316	 <table border="1"> <caption>Data for 2C1R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.8, 22.8]</td><td>27</td></tr> <tr><td>(22.8, 39.8]</td><td>97</td></tr> <tr><td>(39.8, 56.8]</td><td>162</td></tr> <tr><td>(56.8, 73.8]</td><td>185</td></tr> <tr><td>(73.8, 90.8]</td><td>172</td></tr> <tr><td>(90.8, 107.8]</td><td>269</td></tr> <tr><td>(107.8, 124.8]</td><td>238</td></tr> <tr><td>(124.8, 141.8]</td><td>219</td></tr> <tr><td>(141.8, 158.8]</td><td>170</td></tr> <tr><td>(158.8, 175.8]</td><td>142</td></tr> <tr><td>(175.8, 192.8]</td><td>122</td></tr> <tr><td>(192.8, 209.8]</td><td>82</td></tr> <tr><td>(209.8, 226.8]</td><td>46</td></tr> <tr><td>(226.8, 243.8]</td><td>39</td></tr> <tr><td>(243.8, 260.8]</td><td>22</td></tr> <tr><td>(260.8, 277.8]</td><td>24</td></tr> <tr><td>(277.8, 294.8]</td><td>11</td></tr> <tr><td>(294.8, 311.8]</td><td>5</td></tr> <tr><td>(311.8, 328.8]</td><td>6</td></tr> <tr><td>(328.8, 345.8]</td><td>1</td></tr> <tr><td>(345.8, 362.8]</td><td>4</td></tr> <tr><td>(362.8, 379.8]</td><td>6</td></tr> </tbody> </table>	Bin Range	Frequency	[5.8, 22.8]	27	(22.8, 39.8]	97	(39.8, 56.8]	162	(56.8, 73.8]	185	(73.8, 90.8]	172	(90.8, 107.8]	269	(107.8, 124.8]	238	(124.8, 141.8]	219	(141.8, 158.8]	170	(158.8, 175.8]	142	(175.8, 192.8]	122	(192.8, 209.8]	82	(209.8, 226.8]	46	(226.8, 243.8]	39	(243.8, 260.8]	22	(260.8, 277.8]	24	(277.8, 294.8]	11	(294.8, 311.8]	5	(311.8, 328.8]	6	(328.8, 345.8]	1	(345.8, 362.8]	4	(362.8, 379.8]	6
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Half 1C2R (Cluster #6)	39	37	145	360	(not enough data for a histogram)																																														
Half 2C (Cluster #6)	143	9	117	397	 <table border="1"> <caption>Data for Half 2C Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[9.0, 56.0]</td><td>25</td></tr> <tr><td>(56.0, 103.0]</td><td>45</td></tr> <tr><td>(103.0, 150.0]</td><td>30</td></tr> <tr><td>(150.0, 197.0]</td><td>28</td></tr> <tr><td>(197.0, 244.0]</td><td>9</td></tr> <tr><td>(244.0, 291.0]</td><td>3</td></tr> <tr><td>(291.0, 338.0]</td><td>2</td></tr> <tr><td>(338.0, 385.0]</td><td>0</td></tr> <tr><td>(385.0, 432.0]</td><td>0</td></tr> <tr><td>(432.0, 479.0]</td><td>1</td></tr> </tbody> </table>	Bin Range	Frequency	[9.0, 56.0]	25	(56.0, 103.0]	45	(103.0, 150.0]	30	(150.0, 197.0]	28	(197.0, 244.0]	9	(244.0, 291.0]	3	(291.0, 338.0]	2	(338.0, 385.0]	0	(385.0, 432.0]	0	(432.0, 479.0]	1																								
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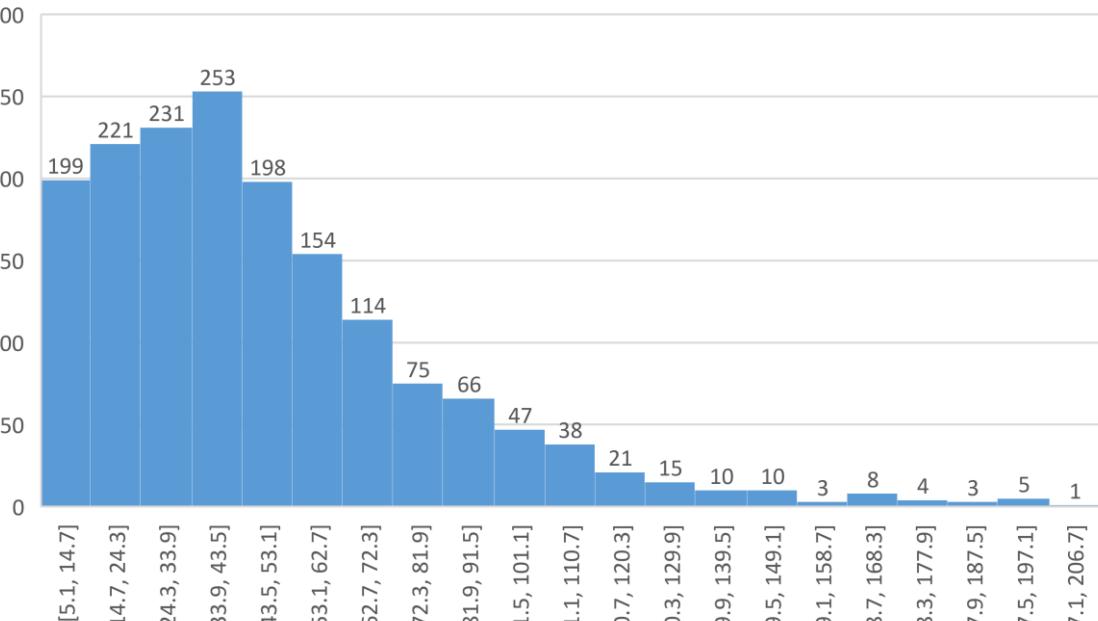
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Relationship	#	Min	Average	Max	Histogram																																								
2C2R (Cluster #7)	564	0	74	261	 <table border="1"> <caption>Data for 2C2R Cluster Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5,1, 23,1]</td><td>50</td></tr> <tr><td>(23,1, 41,1]</td><td>117</td></tr> <tr><td>(41,1, 59,1]</td><td>98</td></tr> <tr><td>(59,1, 77,1]</td><td>77</td></tr> <tr><td>(77,1, 95,1]</td><td>62</td></tr> <tr><td>(95,1, 113,1]</td><td>64</td></tr> <tr><td>(113,1, 131,1]</td><td>29</td></tr> <tr><td>(131,1, 149,1]</td><td>29</td></tr> <tr><td>(149,1, 167,1]</td><td>12</td></tr> <tr><td>(167,1, 185,1]</td><td>7</td></tr> <tr><td>(185,1, 203,1]</td><td>4</td></tr> <tr><td>(203,1, 221,1]</td><td>0</td></tr> <tr><td>(221,1, 239,1]</td><td>1</td></tr> <tr><td>(239,1, 257,1]</td><td>2</td></tr> <tr><td>(257,1, 275,1]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[5,1, 23,1]	50	(23,1, 41,1]	117	(41,1, 59,1]	98	(59,1, 77,1]	77	(77,1, 95,1]	62	(95,1, 113,1]	64	(113,1, 131,1]	29	(131,1, 149,1]	29	(149,1, 167,1]	12	(167,1, 185,1]	7	(185,1, 203,1]	4	(203,1, 221,1]	0	(221,1, 239,1]	1	(239,1, 257,1]	2	(257,1, 275,1]	1								
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3C (Cluster #7)	1791	0	74	217	 <table border="1"> <caption>Data for 3C Cluster Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[6,1, 19,1]</td><td>120</td></tr> <tr><td>(19,1, 32,1]</td><td>183</td></tr> <tr><td>(32,1, 45,1]</td><td>230</td></tr> <tr><td>(45,1, 58,1]</td><td>242</td></tr> <tr><td>(58,1, 71,1]</td><td>219</td></tr> <tr><td>(71,1, 84,1]</td><td>150</td></tr> <tr><td>(84,1, 97,1]</td><td>160</td></tr> <tr><td>(97,1, 110,1]</td><td>146</td></tr> <tr><td>(110,1, 123,1]</td><td>99</td></tr> <tr><td>(123,1, 136,1]</td><td>68</td></tr> <tr><td>(136,1, 149,1]</td><td>47</td></tr> <tr><td>(149,1, 162,1]</td><td>30</td></tr> <tr><td>(162,1, 175,1]</td><td>19</td></tr> <tr><td>(175,1, 188,1]</td><td>18</td></tr> <tr><td>(188,1, 201,1]</td><td>8</td></tr> <tr><td>(201,1, 214,1]</td><td>13</td></tr> <tr><td>(214,1, 227,1]</td><td>7</td></tr> <tr><td>(227,1, 240,1]</td><td>8</td></tr> <tr><td>(240,1, 253,1]</td><td>2</td></tr> </tbody> </table>	cM Range	Frequency	[6,1, 19,1]	120	(19,1, 32,1]	183	(32,1, 45,1]	230	(45,1, 58,1]	242	(58,1, 71,1]	219	(71,1, 84,1]	150	(84,1, 97,1]	160	(97,1, 110,1]	146	(110,1, 123,1]	99	(123,1, 136,1]	68	(136,1, 149,1]	47	(149,1, 162,1]	30	(162,1, 175,1]	19	(175,1, 188,1]	18	(188,1, 201,1]	8	(201,1, 214,1]	13	(214,1, 227,1]	7	(227,1, 240,1]	8	(240,1, 253,1]	2
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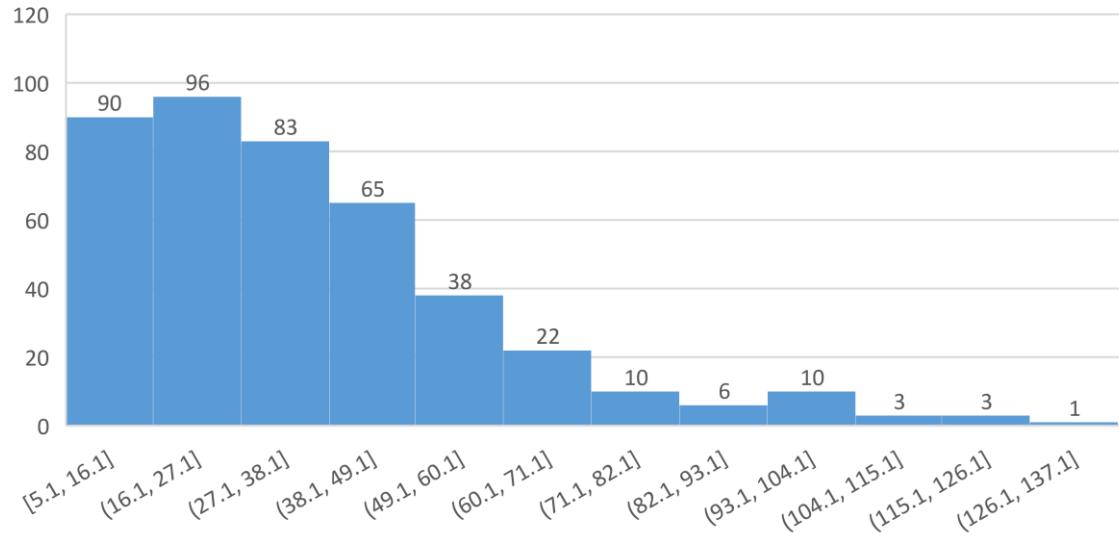
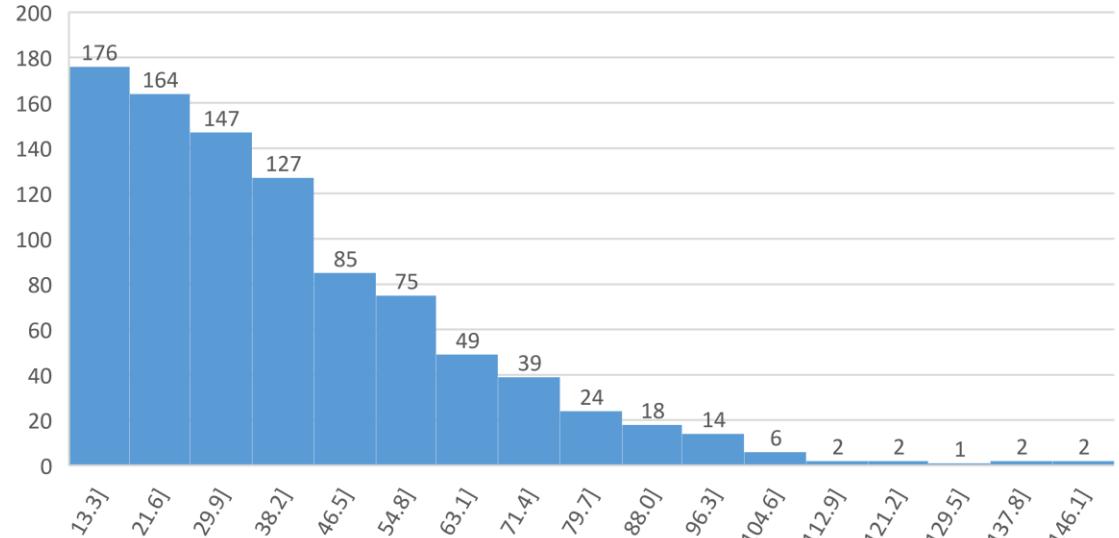
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Relationship	#	Min	Average	Max	Histogram																				
Half 1C3R (Cluster #7)	19	0	87	191	(not enough data for a histogram)																				
Half 2C1R (Cluster #7)	116	0	73	341	 <p>A histogram showing the distribution of values for Half 2C1R (Cluster #7). The x-axis represents value ranges, and the y-axis represents frequency. The distribution is highly skewed to the right, with the highest frequency in the first bin.</p> <table border="1"> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[7.4, 47.4]</td><td>40</td></tr> <tr><td>(47.4, 87.4]</td><td>42</td></tr> <tr><td>(87.4, 127.4]</td><td>23</td></tr> <tr><td>(127.4, 167.4]</td><td>3</td></tr> <tr><td>(167.4, 207.4]</td><td>1</td></tr> <tr><td>(207.4, 247.4]</td><td>2</td></tr> <tr><td>(247.4, 287.4]</td><td>2</td></tr> <tr><td>(287.4, 327.4]</td><td>0</td></tr> <tr><td>(327.4, 367.4]</td><td>1</td></tr> </tbody> </table>	Bin Range	Frequency	[7.4, 47.4]	40	(47.4, 87.4]	42	(87.4, 127.4]	23	(127.4, 167.4]	3	(167.4, 207.4]	1	(207.4, 247.4]	2	(247.4, 287.4]	2	(287.4, 327.4]	0	(327.4, 367.4]	1
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(327.4, 367.4]	1																								
2C3R (Cluster #8)	50	0	57	139	(not enough data for a histogram)																				

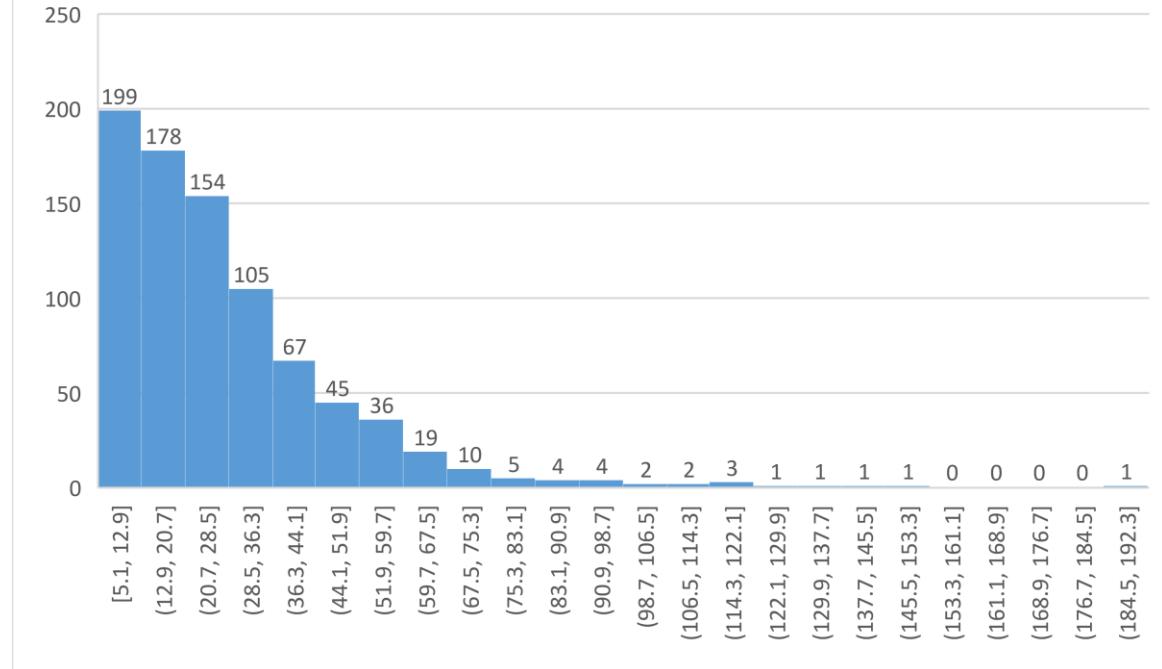
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Relationship	#	Min	Average	Max	Histogram																																												
3C1R (Cluster #8)	1736	0	48	173	 <table border="1"> <caption>Data for 3C1R Histogram</caption> <thead> <tr> <th>cM Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.1, 14.7]</td><td>199</td></tr> <tr><td>(14.7, 24.3]</td><td>221</td></tr> <tr><td>(24.3, 33.9]</td><td>231</td></tr> <tr><td>(33.9, 43.5]</td><td>253</td></tr> <tr><td>(43.5, 53.1]</td><td>198</td></tr> <tr><td>(53.1, 62.7]</td><td>154</td></tr> <tr><td>(62.7, 72.3]</td><td>114</td></tr> <tr><td>(72.3, 81.9]</td><td>75</td></tr> <tr><td>(81.9, 91.5]</td><td>66</td></tr> <tr><td>(91.5, 101.1]</td><td>47</td></tr> <tr><td>(101.1, 110.7]</td><td>38</td></tr> <tr><td>(110.7, 120.3]</td><td>21</td></tr> <tr><td>(120.3, 129.9]</td><td>15</td></tr> <tr><td>(129.9, 139.5]</td><td>10</td></tr> <tr><td>(139.5, 149.1]</td><td>10</td></tr> <tr><td>(149.1, 158.7]</td><td>3</td></tr> <tr><td>(158.7, 168.3]</td><td>8</td></tr> <tr><td>(168.3, 177.9]</td><td>4</td></tr> <tr><td>(177.9, 187.5]</td><td>3</td></tr> <tr><td>(187.5, 197.1]</td><td>5</td></tr> <tr><td>(197.1, 206.7]</td><td>1</td></tr> </tbody> </table>	cM Range	Frequency	[5.1, 14.7]	199	(14.7, 24.3]	221	(24.3, 33.9]	231	(33.9, 43.5]	253	(43.5, 53.1]	198	(53.1, 62.7]	154	(62.7, 72.3]	114	(72.3, 81.9]	75	(81.9, 91.5]	66	(91.5, 101.1]	47	(101.1, 110.7]	38	(110.7, 120.3]	21	(120.3, 129.9]	15	(129.9, 139.5]	10	(139.5, 149.1]	10	(149.1, 158.7]	3	(158.7, 168.3]	8	(168.3, 177.9]	4	(177.9, 187.5]	3	(187.5, 197.1]	5	(197.1, 206.7]	1
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Half 2C2R (Cluster #8)	24	0	61	353	(not enough data for a histogram)																																												
Half 3C (Cluster #8)	55	0	61	178	(not enough data for a histogram)																																												

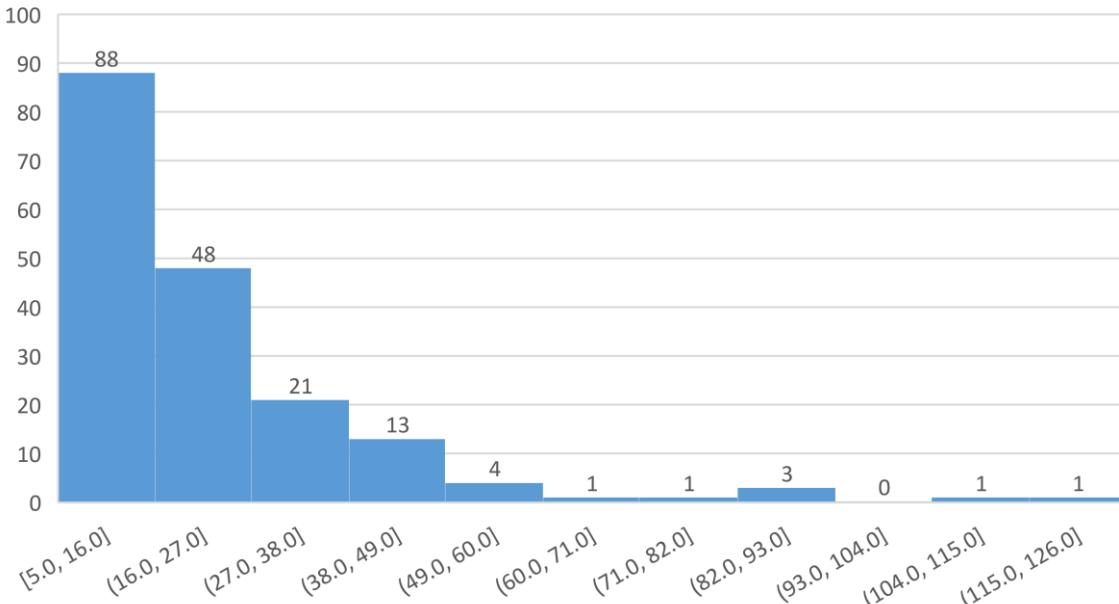
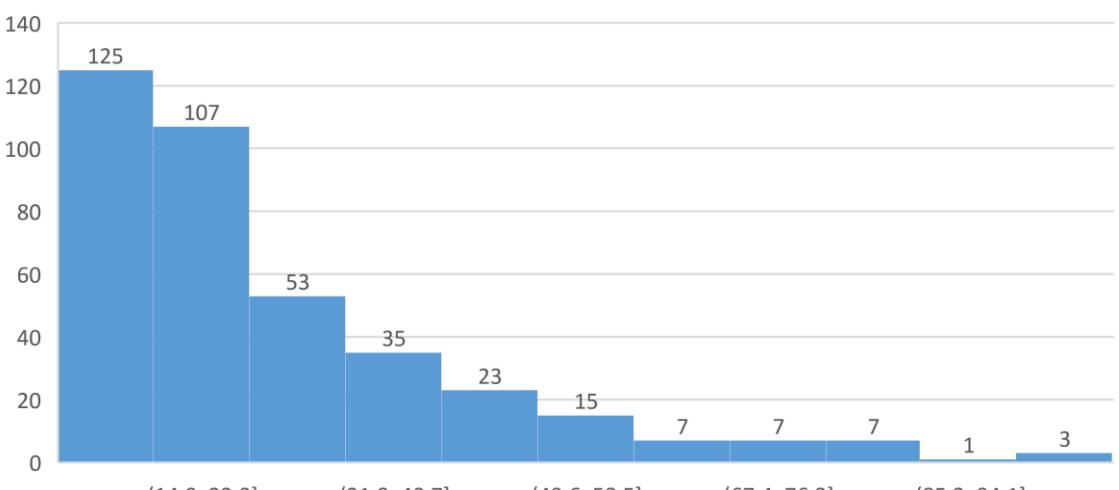
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Relationship	#	Min	Average	Max	Histogram																																				
3C2R (Cluster #9)	459	0	35	116	 <table border="1"> <caption>Data for 3C2R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.1, 16.1]</td><td>90</td></tr> <tr><td>(16.1, 27.1]</td><td>96</td></tr> <tr><td>(27.1, 38.1]</td><td>83</td></tr> <tr><td>(38.1, 49.1]</td><td>65</td></tr> <tr><td>(49.1, 60.1]</td><td>38</td></tr> <tr><td>(60.1, 71.1]</td><td>22</td></tr> <tr><td>(71.1, 82.1]</td><td>10</td></tr> <tr><td>(82.1, 93.1]</td><td>6</td></tr> <tr><td>(93.1, 104.1]</td><td>10</td></tr> <tr><td>(104.1, 115.1]</td><td>3</td></tr> <tr><td>(115.1, 126.1]</td><td>3</td></tr> <tr><td>(126.1, 137.1]</td><td>1</td></tr> </tbody> </table>	Bin Range	Frequency	[5.1, 16.1]	90	(16.1, 27.1]	96	(27.1, 38.1]	83	(38.1, 49.1]	65	(49.1, 60.1]	38	(60.1, 71.1]	22	(71.1, 82.1]	10	(82.1, 93.1]	6	(93.1, 104.1]	10	(104.1, 115.1]	3	(115.1, 126.1]	3	(126.1, 137.1]	1										
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4C (Cluster #9)	998	0	35	127	 <table border="1"> <caption>Data for 4C Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.0, 13.3]</td><td>176</td></tr> <tr><td>(13.3, 21.6]</td><td>164</td></tr> <tr><td>(21.6, 29.9]</td><td>147</td></tr> <tr><td>(29.9, 38.2]</td><td>127</td></tr> <tr><td>(38.2, 46.5]</td><td>85</td></tr> <tr><td>(46.5, 54.8]</td><td>75</td></tr> <tr><td>(54.8, 63.1]</td><td>49</td></tr> <tr><td>(63.1, 71.4]</td><td>39</td></tr> <tr><td>(71.4, 79.7]</td><td>24</td></tr> <tr><td>(79.7, 88.0]</td><td>18</td></tr> <tr><td>(88.0, 96.3]</td><td>14</td></tr> <tr><td>(96.3, 104.6]</td><td>6</td></tr> <tr><td>(104.6, 112.9]</td><td>2</td></tr> <tr><td>(112.9, 121.2]</td><td>2</td></tr> <tr><td>(121.2, 129.5]</td><td>1</td></tr> <tr><td>(129.5, 137.8]</td><td>2</td></tr> <tr><td>(137.8, 146.1]</td><td>2</td></tr> </tbody> </table>	Bin Range	Frequency	[5.0, 13.3]	176	(13.3, 21.6]	164	(21.6, 29.9]	147	(29.9, 38.2]	127	(38.2, 46.5]	85	(46.5, 54.8]	75	(54.8, 63.1]	49	(63.1, 71.4]	39	(71.4, 79.7]	24	(79.7, 88.0]	18	(88.0, 96.3]	14	(96.3, 104.6]	6	(104.6, 112.9]	2	(112.9, 121.2]	2	(121.2, 129.5]	1	(129.5, 137.8]	2	(137.8, 146.1]	2
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Relationship	#	Min	Average	Max	Histogram																																																		
Half 3C1R (Cluster #9)	71	0	42	165	(not enough data for a histogram)																																																		
3C3R (Cluster #10)	47	0	22	48	(not enough data for a histogram)																																																		
4C1R (Cluster #10)	934	0	28	117	 <table border="1"> <caption>Data for 4C1R Histogram</caption> <thead> <tr> <th>Value Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.1, 12.9]</td><td>199</td></tr> <tr><td>(12.9, 20.7]</td><td>178</td></tr> <tr><td>(20.7, 28.5]</td><td>154</td></tr> <tr><td>(28.5, 36.3]</td><td>105</td></tr> <tr><td>(36.3, 44.1]</td><td>67</td></tr> <tr><td>(44.1, 51.9]</td><td>45</td></tr> <tr><td>(51.9, 59.7]</td><td>36</td></tr> <tr><td>(59.7, 67.5]</td><td>19</td></tr> <tr><td>(67.5, 75.3]</td><td>10</td></tr> <tr><td>(75.3, 83.1]</td><td>5</td></tr> <tr><td>(83.1, 90.9]</td><td>4</td></tr> <tr><td>(90.9, 98.7]</td><td>4</td></tr> <tr><td>(98.7, 106.5]</td><td>2</td></tr> <tr><td>(106.5, 114.3]</td><td>2</td></tr> <tr><td>(114.3, 122.1]</td><td>3</td></tr> <tr><td>(122.1, 129.9]</td><td>1</td></tr> <tr><td>(129.9, 137.7]</td><td>1</td></tr> <tr><td>(137.7, 145.5]</td><td>1</td></tr> <tr><td>(145.5, 153.3]</td><td>1</td></tr> <tr><td>(153.3, 161.1]</td><td>0</td></tr> <tr><td>(161.1, 168.9]</td><td>0</td></tr> <tr><td>(168.9, 176.7]</td><td>0</td></tr> <tr><td>(176.7, 184.5]</td><td>0</td></tr> <tr><td>(184.5, 192.3]</td><td>1</td></tr> </tbody> </table>	Value Range	Frequency	[5.1, 12.9]	199	(12.9, 20.7]	178	(20.7, 28.5]	154	(28.5, 36.3]	105	(36.3, 44.1]	67	(44.1, 51.9]	45	(51.9, 59.7]	36	(59.7, 67.5]	19	(67.5, 75.3]	10	(75.3, 83.1]	5	(83.1, 90.9]	4	(90.9, 98.7]	4	(98.7, 106.5]	2	(106.5, 114.3]	2	(114.3, 122.1]	3	(122.1, 129.9]	1	(129.9, 137.7]	1	(137.7, 145.5]	1	(145.5, 153.3]	1	(153.3, 161.1]	0	(161.1, 168.9]	0	(168.9, 176.7]	0	(176.7, 184.5]	0	(184.5, 192.3]	1
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Half 3C2R (Cluster #10)	26	0	34	96	(not enough data for a histogram)																																																		
Half 4C (Cluster #10)	32	0	36	120	(not enough data for a histogram)																																																		

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Relationship	#	Min	Average	Max	Histogram																								
4C2R	245	0	22	109	 <table border="1"> <caption>Data for 4C2R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.0, 16.0]</td><td>88</td></tr> <tr><td>(16.0, 27.0]</td><td>48</td></tr> <tr><td>(27.0, 38.0]</td><td>21</td></tr> <tr><td>(38.0, 49.0]</td><td>13</td></tr> <tr><td>(49.0, 60.0]</td><td>4</td></tr> <tr><td>(60.0, 71.0]</td><td>1</td></tr> <tr><td>(71.0, 82.0]</td><td>1</td></tr> <tr><td>(82.0, 93.0]</td><td>3</td></tr> <tr><td>(93.0, 104.0]</td><td>0</td></tr> <tr><td>(104.0, 115.0]</td><td>1</td></tr> <tr><td>(115.0, 126.0]</td><td>1</td></tr> </tbody> </table>	Bin Range	Frequency	[5.0, 16.0]	88	(16.0, 27.0]	48	(27.0, 38.0]	21	(38.0, 49.0]	13	(49.0, 60.0]	4	(60.0, 71.0]	1	(71.0, 82.0]	1	(82.0, 93.0]	3	(93.0, 104.0]	0	(104.0, 115.0]	1	(115.0, 126.0]	1
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5C	429	0	25	94	 <table border="1"> <caption>Data for 5C Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.1, 14.0]</td><td>125</td></tr> <tr><td>(14.0, 22.9]</td><td>107</td></tr> <tr><td>(22.9, 31.8]</td><td>53</td></tr> <tr><td>(31.8, 40.7]</td><td>35</td></tr> <tr><td>(40.7, 49.6]</td><td>23</td></tr> <tr><td>(49.6, 58.5]</td><td>15</td></tr> <tr><td>(58.5, 67.4]</td><td>7</td></tr> <tr><td>(67.4, 76.3]</td><td>7</td></tr> <tr><td>(76.3, 85.2]</td><td>7</td></tr> <tr><td>(85.2, 94.1]</td><td>1</td></tr> <tr><td>(94.1, 103.0]</td><td>3</td></tr> </tbody> </table>	Bin Range	Frequency	[5.1, 14.0]	125	(14.0, 22.9]	107	(22.9, 31.8]	53	(31.8, 40.7]	35	(40.7, 49.6]	23	(49.6, 58.5]	15	(58.5, 67.4]	7	(67.4, 76.3]	7	(76.3, 85.2]	7	(85.2, 94.1]	1	(94.1, 103.0]	3
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(94.1, 103.0]	3																												
4C3R	25	0	29	86	(not enough data for a histogram)																								

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Relationship	#	Min	Average	Max	Histogram																				
5C1R	354	0	21	79	<table border="1"> <caption>Data for 5C1R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.2, 14.1]</td><td>148</td></tr> <tr><td>(14.1, 23.0]</td><td>59</td></tr> <tr><td>(23.0, 31.9]</td><td>31</td></tr> <tr><td>(31.9, 40.8]</td><td>37</td></tr> <tr><td>(40.8, 49.7]</td><td>9</td></tr> <tr><td>(49.7, 58.6]</td><td>9</td></tr> <tr><td>(58.6, 67.5]</td><td>10</td></tr> <tr><td>(67.5, 76.4]</td><td>5</td></tr> <tr><td>(76.4, 85.3]</td><td>3</td></tr> </tbody> </table>	Bin Range	Frequency	[5.2, 14.1]	148	(14.1, 23.0]	59	(23.0, 31.9]	31	(31.9, 40.8]	37	(40.8, 49.7]	9	(49.7, 58.6]	9	(58.6, 67.5]	10	(67.5, 76.4]	5	(76.4, 85.3]	3
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(76.4, 85.3]	3																								
5C2R	92	0	17	43	(not enough data for a histogram)																				
6C	122	0	21	86	<table border="1"> <caption>Data for 6C Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.0, 16.0]</td><td>68</td></tr> <tr><td>(16.0, 27.0]</td><td>27</td></tr> <tr><td>(27.0, 38.0]</td><td>13</td></tr> <tr><td>(38.0, 49.0]</td><td>3</td></tr> <tr><td>(49.0, 60.0]</td><td>2</td></tr> <tr><td>(60.0, 71.0]</td><td>2</td></tr> <tr><td>(71.0, 82.0]</td><td>1</td></tr> <tr><td>(82.0, 93.0]</td><td>1</td></tr> </tbody> </table>	Bin Range	Frequency	[5.0, 16.0]	68	(16.0, 27.0]	27	(27.0, 38.0]	13	(38.0, 49.0]	3	(49.0, 60.0]	2	(60.0, 71.0]	2	(71.0, 82.0]	1	(82.0, 93.0]	1		
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(71.0, 82.0]	1																								
(82.0, 93.0]	1																								
5C3R	12	0	11	44	(not enough data for a histogram)																				

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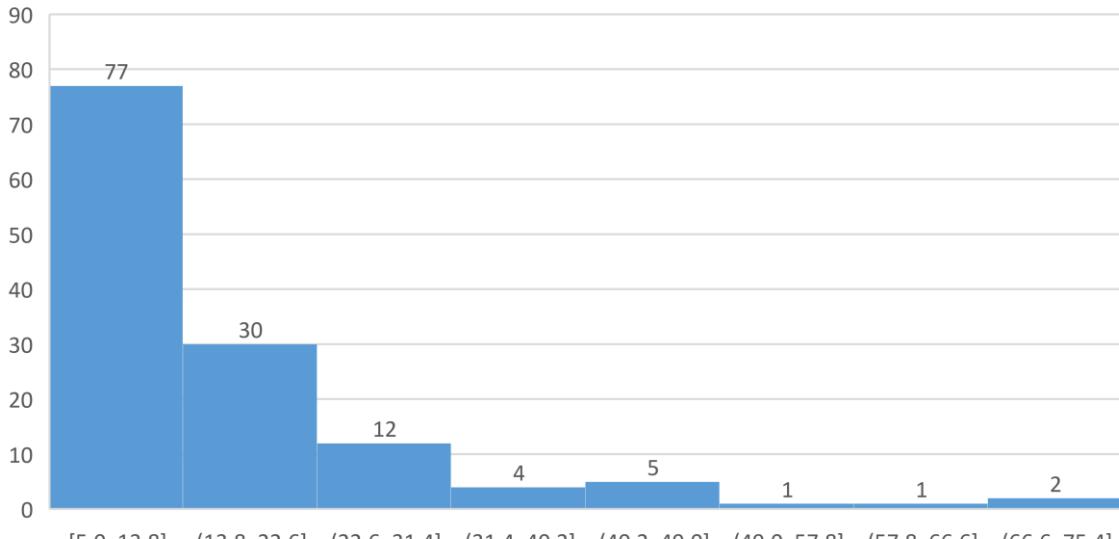
Relationship	#	Min	Average	Max	Histogram																		
6C1R	138	0	16	72	 <table border="1"> <caption>Data for 6C1R Histogram</caption> <thead> <tr> <th>Bin Range</th> <th>Frequency</th> </tr> </thead> <tbody> <tr><td>[5.0, 13.8]</td><td>77</td></tr> <tr><td>(13.8, 22.6]</td><td>30</td></tr> <tr><td>(22.6, 31.4]</td><td>12</td></tr> <tr><td>(31.4, 40.2]</td><td>4</td></tr> <tr><td>(40.2, 49.0]</td><td>5</td></tr> <tr><td>(49.0, 57.8]</td><td>1</td></tr> <tr><td>(57.8, 66.6]</td><td>1</td></tr> <tr><td>(66.6, 75.4]</td><td>2</td></tr> </tbody> </table>	Bin Range	Frequency	[5.0, 13.8]	77	(13.8, 22.6]	30	(22.6, 31.4]	12	(31.4, 40.2]	4	(40.2, 49.0]	5	(49.0, 57.8]	1	(57.8, 66.6]	1	(66.6, 75.4]	2
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6C2R	59	0	17	75	(not enough data for a histogram)																		
7C	54	0	13	57	(not enough data for a histogram)																		
7C1R	89	0	13	53	(not enough data for a histogram)																		
8C	80	0	12	50	(not enough data for a histogram)																		

Table 3. Company and Endogamy Breakdown

NOTES:

- The total number of submissions (marked as "#") may include MyHeritage submissions, which were not analyzed because there wasn't enough data.
- "n/a" indicates that there was not enough data (i.e., not enough submissions) to calculate the percentile.
- For some relationships, there was not enough data to breakdown the submissions into endogamous versus non-endogamous, or into different companies

Relationship		Total #	Average	Median	5th Percentile	95th Percentile	1st Percentile	99th Percentile
Parent/Child	Total	1348	3487	3468	3380	3718	3330	3720
	Non-Endogamous	1246	3490	3469	3380	3718	3343	3720
	Endogamous	102	3445	3395	3283	3671	1752	3850
	23andMe	143	3680	3717	3535	3720	3307	3770
	AncestryDNA	285	3449	3466	3352	3544	3157	3587
	FTDNA	524	3379	3384	3379	3384	3375	3586
	GEDmatch	380	3586	3587	3578	3587	3531	3851
Sibling	Total	1348	2629	2627	2342	2917	2209	3384
	Non-Endogamous	1181	2630	2624	2339	2931	2201	3504
	Endogamous	167	2656	2653	2352	2910	2116	3659
	23andMe	112	2852	2793	2533	3779	2188	3984
	AncestryDNA	190	2585	2583	2309	2841	2032	2922
	FTDNA	644	2563	2558	2302	2812	2213	3381
	GEDmatch	394	2696	2700	2461	2933	2321	3065

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Aunt/Uncle/Niece/Nephew	Total	1411	1750	1752	1452	2034	1349	2175
	Non-Endogamous	1250	1747	1749	1447	2033	1344	2185
	Endogamous	161	1776	1789	1492	2039	1416	2119
	23andMe	142	1810	1805	1547	2082	1324	2255
	AncestryDNA	226	1720	1725	1428	1998	1275	2156
	FTDNA	617	1711	1709	1437	1965	1351	2108
	GEDmatch	416	1808	1814	1546	2095	1422	2227
Grandparent	Total	611	1766	1770	1360	2136	1156	2311
	Non-Endogamous	579	1764	1770	1353	2136	1144	2306
	Endogamous	32	1797	1773	1371	2403	n/a	n/a
	23andMe	79	1826	1842	1421	2159	n/a	n/a
	AncestryDNA	130	1729	1740	1245	2184	727	2367
	FTDNA	196	1720	1713	1338	2055	1242	2248
	GEDmatch	205	1811	1834	1410	2191	1167	2503
Half Sibling	Total	451	1783	1779	1453	2111	1317	2312
	Non-Endogamous	401	1784	1779	1450	2113	1314	2294
	Endogamous	50	1779	1751	1510	2126	n/a	n/a
	23andMe	43	1887	1868	1367	2421	n/a	n/a
	AncestryDNA	93	1741	1731	1440	2057	n/a	n/a
	FTDNA	141	1730	1722	1442	1997	1343	2176
	GEDmatch	174	1826	1821	1478	2135	1327	2337
1C	Total	1512	874	873	638	1119	553	1225
	Non-Endogamous	1283	867	865	636	1107	556	1209
	Endogamous	229	914	906	650	1207	544	1350
	23andMe	113	895	897	603	1170	524	1341
	AncestryDNA	303	849	843	636	1094	561	1257
	FTDNA	770	872	872	637	1106	558	1213
	GEDmatch	322	898	889	657	1150	549	1295

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Great Aunt/Uncle	Total	413	914	872	487	1770	251	2108
	Non-Endogamous	385	907	866	483	1774	245	2117
	Endogamous	28	1010	940	490	1775	n/a	n/a
	23andMe	42	971	899	550	2154	n/a	n/a
	AncestryDNA	94	876	848	406	1491	n/a	na/
	FTDNA	144	915	871	531	1800	282	1956
	GEDmatch	131	918	891	416	1851	207	2122
Great Grandparent/Great Grandchild	Total	61	881	894	552	1201	n/a	n/a
Half Aunt/Uncle/Niece/Nephew	Total	275	891	875	637	1196	500	1446
	Non-Endogamous	235	888	870	641	1189	496	1610
	Endogamous	40	905	935	595	1205	n/a	n/a
	23andMe	23	949	925	679	1308	n/a	n/a
	AncestryDNA	70	863	867	555	1209	n/a	n/a
	FTDNA	63	872	828	596	1113	n/a	n/a
	GEDmatch	119	905	909	638	1197	510	1657
1C1R	Total	1594	439	430	236	657	141	851
	Non-Endogamous	1402	433	427	227	641	132	770
	Endogamous	192	486	455	264	823	168	1065
	23andMe	147	466	466	249	672	154	885
	AncestryDNA	490	420	405	215	635	148	976
	FTDNA	602	446	434	245	660	132	770
	GEDmatch	350	444	433	243	663	129	938
Great Great Aunt/Uncle/Niece/Nephew	Total	25	427	455	198	797	n/a	n/a

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Half 1C	Total	177	457	449	259	695	137	856
Half Great Aunt/Uncle/Niece/Nephew	Total	44	432	415	175	741	n/a	n/a
1C2R	Total	481	229	221	96	385	43	531
	Non-Endogamous	436	219	228	93	380	42	528
	Endogamous	45	246	245	97	404	n/a	n/a
	23andMe	57	258	255	129	379	n/a	n/a
	AncestryDNA	154	217	203	67	384	35	504
	FTDNA	166	238	228	128	388	73	578
	GEDmatch	103	219	223	84	383	27	521
2C	Total	1590	233	223	102	406	46	515
	Non-Endogamous	1393	227	220	99	391	46	501
	Endogamous	197	274	255	145	466	38	671
	23andMe	156	233	232	92	405	4	498
	AncestryDNA	598	219	208	93	390	41	515
	FTDNA	478	248	238	124	413	87	551
	GEDmatch	358	237	222	102	422	39	647
Half 1C1R	Total	138	226	219	78	397	57	530
Half Great Great Aunt/Uncle/Niece/Nephew	Total	15	187	188	n/a	n/a	n/a	n/a
1C3R	Total	38	123	116	32	240	n/a	n/a

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2C1R	Total	2064	123	116	36	235	20	316
	Non-Endogamous	1888	120	114	35	229	20	298
	Endogamous	176	153	139	62	283	32	387
	23andMe	168	133	132	41	238	19	274
	AncestryDNA	961	112	108	31	221	16	311
	FTDNA	524	136	128	53	245	26	353
	GEDmatch	407	129	120	43	247	22	349
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Half 1C2R	Total	39	145	131	54	279	n/a	n/a
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Half 2C	Total	143	117	105	16	237	9	397
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2C2R	Total	564	74	63	19	157	8	261
	Non-Endogamous	527	71	62	19	142	9	236
	Endogamous	37	119	110	7	271	n/a	n/a
	23andMe	49	76	66	14	153	n/a	n/a
	AncestryDNA	309	64	49	18	141	7	241
	FTDNA	106	94	85	43	162	31	401
	GEDmatch	100	83	72	17	176	n/a	n/a
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3C	Total	1791	74	64	17	155	9	217
	Non-Endogamous	1607	70	63	16	147	9	208
	Endogamous	184	101	101	43	223	43	396
	23andMe	158	73	74	31	170	30	245
	AncestryDNA	853	64	53	14	146	10	207
	FTDNA	406	93	88	46	181	39	233
	GEDmatch	366	76	69	23	155	20	231
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Half 1C3R	Total	19	87	58	n/a	n/a	n/a	n/a

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Half 2C1R	Total	116	73	61	15	193	8	341
2C3R	Total	50	57	48	9	136	n/a	n/a
3C1R	Total	1736	48	41	10	112	7	173
	Non-Endogamous	1616	47	40	9	108	7	153
	Endogamous	120	71	58	14	183	6	292
	23andMe	117	49	41	9	106	7	244
	AncestryDNA	972	39	33	9	100	6	137
	FTDNA	332	74	66	30	147	24	218
	GEDmatch	310	48	43	10	101	8	152
Half 2C2R	Total	24	61	49	2	301	n/a	n/a
Half 3C	Total	55	61	54	9	165	n/a	n/a
3C2R	Total	459	35	31	9	90	6	116
	Non-Endogamous	423	35	31	9	84	6	115
	Endogamous	36	40	30	7	114	n/a	n/a
	23andMe	30	28	27	8	57	n/a	n/a
	AncestryDNA	281	30	25	7	69	6	108
	FTDNA	68	59	54	27	111	n/a	na/
	GEDmatch	79	38	33	10	94	n/a	n/a
4C	Total	998	35	29	7	82	5	127
	Non-Endogamous	905	33	28	7	77	5	104
	Endogamous	93	53	42	9	152	n/a	n/a
	23andMe	34	34	28	10	91	n/a	n/a
	AncestryDNA	584	29	25	7	68	5	96
	FTDNA	134	66	59	18	141	10	255
	GEDmatch	242	33	29	8	71	5	80

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Half 3C1R	Total	71	42	33	8	108	n/a	n/a
3C3R	Total	47	22	19	7	48	n/a	n/a
4C1R	Total	934	28	22	7	65	5	117
	Non-Endogamous	858	27	22	7	59	5	94
	Endogamous	76	45	34	6	135	n/a	n/a
	23andMe	35	32	28	9	81	n/a	n/a
	AncestryDNA	580	22	19	6	50	5	89
	FTDNA	122	61	50	29	124	22	556
	GEDmatch	196	30	26	7	61	6	140
Half 3C2R	Total	26	34	28	9	96	n/a	n/a
Half 4C	Total	32	36	27	7	96	n/a	n/a
4C2R	Total	245	22	17	6	55	5	109
5c	Total	422	25	19	6	66	5	94
	Non-Endogamous	374	24	19	6	58	5	81
	Endogamous	48	33	24	7	89	n/a	n/a
	23andMe	8	n/a	n/a	n/a	n/a	n/a	n/a
	AncestryDNA	250	18	15	6	39	5	78
	FTDNA	60	50	45	22	81	n/a	n/a
	GEDmatch	104	30	25	8	65	n/a	n/a
4C3R	Total	25	29	25	9	82	n/a	n/a

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5C1R	Total	350	21	15	6	61	5	79
	Non-Endogamous	290	20	14	6	57	5	76
	Endogamous	60	30	26	7	70	n/a	n/a
	23andMe	6	25	26	n/a	n/a	n/a	n/a
	AncestryDNA	223	16	12	6	39	5	70
	FTDNA	39	49	42	22	83	n/a	n/a
	GEDmatch	82	29	28	8	62	n/a	n/a
5C2R	Total	92	17	14	6	43	n/a	n/a
6C	Total	122	18	13	6	50	5	86
5C3R	Total	12	11	8	n/a	n/a	n/a	n/a
6C1R	Total	138	16	12	5	44	5	72
6C2R	Total	59	17	14	5	45	n/a	n/a
7C	Total	54	13	9	6	39	n/a	n/a
7C1R	Total	89	13	9	5	39	n/a	n/a
8C	Total	80	12	9	5	29	n/a	n/a

Table 4. Relationship Chart

Cluster #	Relationship	#	Min	Average	Median	Max	Expected
	Parent/Child	1378	3330	3487	3468	3720	Varies
1	Sibling	1345	2209	2629	2627	3384	2550
2	Aunt/Uncle/Niece/Nephew	1411	1349	1750	1752	2175	1700
2	Grandparent/Grandchild	611	1156	1766	1770	2311	1700
2	Half Sibling	451	1317	1783	1779	2312	1700
3	1C	1512	553	874	873	1225	850
3	Great-Aunt/Uncle/Niece/Nephew	413	251	914	872	2108	850
3	Great-Grandparent/Great-Grandchild	61	464	881	894	1486	850
3	Half Aunt/Uncle/Niece/Nephew	275	500	891	875	1446	850
4	1C1R	1594	141	439	430	851	425
4	Great-Great-Aunt/Uncle/Niece/Nephew	25	191	427	455	885	425
4	Half 1C	177	137	457	449	856	425
4	Half Great-Aunt/Uncle/Niece/Nephew	44	125	432	415	765	425
5	1C2R	481	43	229	221	531	213
5	2C	1590	46	233	223	515	213
5	Half 1C1R	138	57	226	219	530	213
5	Half Great-Great-Aunt/Uncle/Niece/Nephew	15	12	187	188	383	213
6	1C3R	38	0	123	116	283	106
6	2C1R	2064	0	123	116	316	106
6	Half 1C2R	39	37	145	131	360	106
6	Half 2C	143	9	117	105	397	106
7	2C2R	564	0	74	63	261	53
7	3C	1791	0	74	64	217	53
7	Half 1C3R	19	0	87	58	191	53
7	Half 2C1R	116	0	73	61	341	53
8	2C3R	50	0	57	48	139	27
8	3C1R	1736	0	48	41	173	27
8	Half 2C2R	24	0	61	49	353	27
8	Half 3C	55	0	61	54	178	27
9	3C2R	459	0	35	31	116	13
9	4C	998	0	35	29	127	13
9	Half 3C1R	71	0	42	33	165	13
10	3C3R	47	0	22	19	48	7
10	4C1R	934	0	28	22	117	7

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Cluster #	Relationship	#	Min	Average	Median	Max	Expected
10	Half 3C2R	26	0	34	28	96	7
10	Half 4C	32	0	36	27	120	7
n/a	4C2R	245	0	22	17	109	3.3
n/a	5C	422	0	25	19	94	3.3
n/a	4C3R	25	0	29	25	86	1.7
n/a	5C1R	354	0	21	15	79	1.7
n/a	5C2R	92	0	17	14	43	0.8
n/a	6C	122	0	18	13	86	0.8
n/a	5C3R	12	0	11	8	44	0.4
n/a	6C1R	138	0	16	12	72	0.4
n/a	6C2R	59	0	17	14	75	0.2
n/a	7C	54	0	13	9	57	0.2
n/a	7C1R	89	0	13	9	53	0.1
n/a	8C	80	0	12	9	50	0.05