The Shared cM Project Version 4.0 (March 2020)

Blaine T. Bettinger, Ph.D., J.D.

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 nearly 60,000 known relationships were provided.

For more information:

- The Shared cM Project <u>http://thegeneticgenealogist.com/2015/05/29/the-shared-cm-project/</u>
- Bettinger, Blaine T., "The Shared cM Project: A Demonstration of the Power of Citizen Science." *Journal of Genetic Genealogy* (2016): 38-42. <u>http://jogg.info/pages/vol8/editorial/bettinger/bettinger-</u> <u>sharedcMProject.html</u>

To provide your data for subsequent updates:

- The Shared cM Project: <u>https://forms.gle/sg45AMGynMsvxfzU6</u>
- Also consider submitting data to the "Pedigree Collapse, Double/Multiple Cousin, and ROH Shared cM Project": <u>https://forms.gle/zDR49xjgB1nKLpq99</u>

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.

Differences Between Version 3.0 And Version 4.0

There are numerous changes in this version of the Shared cM Project compared to previous versions. These changes were made to improve legibility and presentation of data, to add additional types of data, and to eliminate unnecessary data. Following is a list of some of the major changes to the data analysis and presentation in Version 4.0 of the Shared cM Project:

- Added 32,999 data points thanks to submissions from thousands of generous genealogists, this update represents an increase of 147%;
- Added a methods section a methods section was added to provide information about how the submitted data was processed;
- **Changed "Clusters" to "Groupings"** due to the growing popularity of shared match clustering, I've changed the name of the meiosis clusters in the former Cluster Chart to Meiosis Groupings. A description of meiosis groupings was added;
- Added meiosis grouping histograms and line graphs these provide additional useful information about ranges and relationship overlaps;
- Added standard deviation standard deviations were added to provide additional information about ranges and variation within a relationship range;
- **Standardized histogram bins from random ranges to fixed ranges** the bins for all histograms were previously generated by Excel, but in this version are generated by me in an attempt to have consistent ranges for similar relationships;
- Added several histograms containing multiple relationships these special relationship groupings are common problems for genealogists, and showing the overlap between these relationships provides additional information;
- **Removed company and endogamy breakdowns** these breakdowns were only rarely utilized and did not have a significant impact on relationship predictions; and
- Provided a short description and chart of differences between version 3.0 and version 4.0 regarding the minimum, average, and maximum values – this summary highlights some of the major differences in this new version.

Methods

Data Collection

Data was collected from participants using Google Forms, which collected the submissions into a spreadsheet. The Google Form contained data entry fields for required information ("Known Relationship," "Total Shared cM," "Number of Shared Segments," "Endogamy or Known Cousin Marriage" (YES/NO) and "Source" (23andMe, AncestryDNA, Family Tree DNA, MyHeritage, GEDmatch, or Other)), and optional data entry fields ("Longest Block," "Notes," and "Email Address").

A total of 59,714 submissions were made to the Shared cM Project as of 8 July 2019 (beginning March 4, 2015). For analysis, the submissions were downloaded as an Excel spreadsheet on 8 July 2019.

Initial Data Curation

Because "Known Relationship" was a text entry field, submissions varied considerably regarding the naming of various relationships. In this initial data curation stage, all decipherable relationships were converted to a uniform format (where "C" equals cousin and "R" equals removed). Submissions with indecipherable relationships were eliminated. Submissions with obvious data entry errors were also eliminated, such as those where the longest segment was longer than the total shared cM, or where there was text in the cM field instead of a number.

This initial data curation eliminated a total of 1,739 submissions (2.9%), bringing the total to 57,975 data points used for statistical analysis (although there were submissions included in this total for relationships not analyzed by the project).

A total of 48 different relationships ranging from Parent/Child to 8C were analyzed individually. The total number of submissions for each relationship varied, with a low of 33 for 5C3R, and a high of 5,281 for 2C1R.

Outlier Removal

Each relationship was analyzed individually, and obvious errors were removed (for example, 7 cM for a parent/child relationship). Then, a total of 1% of the submissions for each relationship was removed, removing 0.5% of the submissions at each end of the range. For example, if there were 200 submissions, 2 submissions were removed (the highest submission and the lowest submission).

Data Analysis

The dataset contained 55,418 submissions for the 48 different relationships analyzed by the project. Following outlier removal, the minimum, average, and maximum values of the remaining data points were identified for each relationship using standard methodology. Standard deviation was calculated using Excel.

For relationships where the minimum value was o cM shared, the averages were calculated only for cM amounts greater than o cM. *Accordingly*, these averages represent the average only for cousins sharing a detectable amount of DNA.

A histogram was created for each relationship. The histograms were created in Excel using the data for each relationship after outliers were removed.

	Launch Date	Total Submissions
Version 1.0	May 2015	>6,000
Version 2.0	June 2016	>10,000
Version 3.0	August 2017	>25,000
Version 4.0	March 2020	>59,000

Previous Versions of the Shared cM Project

Thank You

Thank you to EVERYONE that has submitted data to the Shared cM Project, whether one submission or many. YOU make this project possible!

Thank you to members of the write-up review team that provided valuable data consistency checks, documentation and formatting review, and wonderful suggestions for improving this document (B.J. Jamieson, Bob Danovich, Darrin Chambers, Deanna Eckman Korte, Elizabeth Heise, Eva Dahlberg, Fiona Brooker, Graham Hart, Jarrett Ross, Jim Owston, John Collins, Mary Kathryn Crews Kozy, Mia Bennett, Michelle Patient, Paula Williams, R S Vivs Laliberte, Randy W Whited, Rob Warthen). A very special thank you to Anne Bettinger for her generous donation of *many* hours to the project! And a thank you to Jonny Perl for so generously creating and hosting the interactive version of the Shared cM Project at DNA Painter (www.dnapainter.com)!

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) **3rd-4th Cousin** Shared DNA: 95 cM across 4 segments ()

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

- Review the Meiosis Grouping Table to see into which Meiosis Grouping(s) the total shared cM fits (see next page for more information about "Meiosis Groupings")
- In this example, 95 cM fits into each of Meiosis Groupings #5, 6, 7, 8, 9, and 10

Step 3: Which Meiosis Grouping(s) does the total shared cM *best* fit into?

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

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

- Using the relationships listed in the Meiosis Grouping(s), go to the histograms and see for 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 Meiosis Groupings #6 and 7 is 95 cM closest to the peak of the histogram?

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

Meiosis Groupings

In the table on the following page, some of the closest relationships are gathered into Groupings based on the number of separating meioses (which could also be called recombination events or reproductive events) for that relationship. For example, there are two meioses that separate full siblings, and they form their own Meiosis Grouping (Grouping 1). There are three meioses that separate half siblings. Aunts/Uncles/Nieces/Nephews, and Grandparents/Grandchildren, so they form a second Meiosis Grouping (Grouping 2). Since the number of separating meioses are the same for each relationship in the chart, there is expected to be commonality of the minimum, average, and maximum for that group.

In the table, the average, minimum, maximum, and standard deviation values were calculated using the combined submissions for each relationship within that Meiosis Grouping. Minimums were automatically set to 0 cM for Meiosis Grouping 6-10.

Thirty-six of the 48 relationships analyzed by the Shared cM Project were utilized to generate the 10 Meiosis Groupings.

The Expected values in the table are based on perfect 50% inheritance of shared DNA at each generation. For example, the Expected value for half-siblings is 25% (or 1,700 cM). However, the Expected value does not consider the natural variation that occurs in human genetics. A table of expected values with more information can be found at the ISOGG Wiki (https://isogg.org/wiki/Autosomal_DNA_statistics).

Meiosis Groupings

The Shared cM Project – Version 4.0 March 2020

Blaine T. Bettinger www.TheGeneticGenealogist.com CC 4.0 Attribution License

Grouping	Relationships	Total #	Average	Minimum	Maximum	Standard Deviation	Expected
Grouping #1	Siblings	2465	2613	1613	3488	204	2550
Grouping #2	Half Sibling, Aunt/Uncle/Niece/Nephew, and Grandparent/Grandchild	5067	1749	984	2461	201	1700
Grouping #3	1C, Half Aunt/Uncle/Niece/Nephew, Great-Grandparent/Great-Grandchild, and Great-Aunt/Uncle/Niece/Nephew	5134	865	330	1486	165	850
Grouping #4	1C1R, Half 1C, Half Great-Aunt/Uncle/Niece/Nephew, and Great-Great Aunt/Uncle/Niece/Nephew	4766	435	102	980	124	425
Grouping #5	1C2R, Half 1C1R, 2C, and Half Great-Great-Aunt/Uncle/Niece/Nephew	5998	227	33	592	85	213
Grouping #6	1C3R, Half 1C2R, Half 2C, and 2C1R	6160	122	0	353	59	106
Grouping #7	Half 1C3R, Half 2C1R, 2C2R, and 3C	6686	72	0	244	43	53
Grouping #8	Half 2C2R, 2C3R, Half 3C, and 3C1R	5077	48	0	192	32	27
Grouping #9	Half 3C1R, 3C2R, and 4C	3966	35	0	166	24	13
Grouping #10	Half 3C2R, 3C3R, Half 4C, and 4C1R	2633	28	0	126	19	7

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.



Meiosis Groupings Histograms

On the following pages are histograms for each of the ten Meiosis Groupings from the Meiosis Grouping Table on page 6.





















Meiosis Grouping Line Graphs

These following line graphs are another way to visualize the Meiosis Grouping histogram distributions from the previous pages. In the first graph, all ten Meiosis Groupings are shown. In the second and third graphs, the Meiosis Groupings are broken down in the first five and the last five.







The Relationship Chart

The Shared cM Project – Version 4.0 (March 2020)

Blaine T. Betting www.TheGenetic CC 4.0 Attributic	er Genealogist.com on License			How to read	this chart: Relationship)		Great-Gre Grandj	at-Great- parent	GGGG- Aunt/Uncle	
			Au 12	nt/Uncle ▲ 1741 ▲ 01 - 2282 ◀	- Average Range (min-r	nax)	Great-Great	Grandparent	GGG- Aunt/Uncle		
Half GG- Aunt/Uncle 208 103 - 284			Gi	r eat-Grandpare 887 485 – 1486	nt			Great-Great Aunt/Uncle 420 186 – 713	1C3R 117 25 – 238	2c3R 51 0 - 154	Other Relationships
Half 1C2R 125 16 – 269	Half Great- Aunt/Uncle 431 184 – 668			Grandparent 1754 984 – 2462			Great Aunt/Uncle 850 330 – 1467	1C2R 221 33 - 471	2c2R 71 0- 244	3C2R 36 0 – 166	6C 18 0 - 71
Half 2c1R 66 0 - 190	Half 1C1R 224 62 – 469	Half Aunt/Uncle 871 492 – 1315		Parent 3485 2376 - 3720		Aunt/Uncle 1741 1201 - 2282	1C1R 433 102 – 980	2c1R 122 14 - 353	3C1R 48 0 - 192	4C1R 28 0 - 126	6C1R 15 0 - 56
Half 3c 48 0 - 168	Half 2c 120 10 - 325	Half 1C 449 156 – 979	Half-Sibling 1759 1160 – 2436	Sibling 2613 1613 - 3488	SELF	1C 866 396 - 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 66 0 - 190	Half 1C1R 224 62 – 469	Half Niece/Nephew 871 492 - 1315	Niece/Nephew 1740 1201 - 2282	Child 3487 2376 - 3720	1C1R 433 102 – 980	2c1R 122 14 - 353	3C1R 48 0 – 192	4C1R 28 0 – 126	5C1R 21 0 - 80	7 C 14 0 - 57
Half 3c2R 27 0 - 78	Half 2c2R 48 0 - 144	Half 1C2R 125 16 – 269	Half Great Niece/Nephew 431 184 - 668	Great- Niece/Nephew 850 330 - 1467	Grandchild 1754 984 – 2462	1C2R 221 33 - 471	2c2R 71 0- 244	3C2R 36 0 – 166	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 420 186 – 713	Great- Grandchild 887 485 – 1486	1C3R 117 25 – 238	2c3R 51 0 - 154	3C3R 27 0 – 98	4C3R 19 0 – 60	5C3R 13 0 - 30	8C 11 0 - 42
Minimu	m was automa	tically set to 0	cM for relation	ships more di	stant than Hal	f 2C, and avera	iges were deter	rmined only for	r submissions	in which DNA	was shared

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.

Individual Relationship Histograms

Relationship	#	Min	Average	Max	SD	Histogram
Parent/Child 2	2412	2376	3485	3720	115	$ \begin{array}{c} 800 & 742 746 733 \\ 700 \\ 600 \\ 500 \\ 400 \\ 300 \\ 200 \\ 200 \\ 0 & 1 2 0 3 3 2 0 2 1 7 \\ 0 & 0 1 2 0 3 3 0 0 \\ 0 & 0 1 0 0 \\ 0 & 0 1 0 0 \\ 0 & 0 1 0 0 \\ 0 & 0 1 0 0 \\ 0 & 0 0 $



















Page **32** of **56**







Relationship	#	Min	Average	Max	SD	Histogram
2C3R (Grouping #8)	163	0	51	154	32	$ \begin{bmatrix} 70 & & & & & & & & & & & & & & & & & & $
3C1R (Grouping #8)	4514	0	48	192	32	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$















Relationship	#	Min	Average	Max	SD	Histogram
6C	441	0	18	71	13	$\begin{bmatrix} 200 \\ 180 \\ 140 \\ 140 \\ 120 \\ 120 \\ 120 \\ 120 \\ 120 \\ 120 \\ 120 \\ 100 \\ 80 \\ 40 \\ 20 \\ 10 \\ 20 \\ 30 \\ 40 \\ 50 \\ 60 \\ 70 \\ 80 \\ 90 \\ 10 \\ 20 \\ 30 \\ 40 \\ 50 \\ 60 \\ 70 \\ 80 \\ 90 \\ 10 \\ 80 \\ 90 \\ 10 \\ 80 \\ 90 \\ 10 \\ 10 \\ 10 \\ 10 \\ 10 \\ 10 \\ 1$
5C3R	34	0	13	30	7	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$





Relationship	#	Min	Average	Max	SD	Histogram
8C	239	0	11	42	5	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$

Histograms with Multiple Relationships (Special Cases)



* This chart suggests that full sibling relationships in the range of 1600 to 2000 or so are likely to be unknown half-sibling relationships (and potentially some full sibling relationships that are believed to be half-sibling relationships).



* This chart suggests that total shared cM cannot be utilized to differentiate between half-sibling and aunt/uncle/niece/nephew relationships.





Relationship Chart

Grouping #	Relationship	#	Min	Average	Max	SD	Expected	
	Parent/Child	2412	2376	3485	3720	115	Varies	
1	Sibling	2465	1613	2613	3488	203	2550	
2	Aunt/Uncle/Niece/Nephew	2695	1201	1741	2282	180	1700	
2	Grandparent/Grandchild	1106	984	1754	2462	236	1700	
2	Half Sibling	1266	1160	1759	2436	207	1700	
3	1C	3337	396	866	1397	161	850	
3	Great- Aunt/Uncle/Niece/Nephew	833	330	850	1467	118	850	
3	Great-Grandparent/Great- Grandchild	149	485	887	1486	181	850	
3	Half Aunt/Uncle/Niece/Nephew	815	492	871	1315	165	850	
4	1C1R	3700	102	433	980	123	425	
4	Great-Great- Aunt/Uncle/Niece/Nephew	137	186	420	713	121	425	
4	Half 1C	691	156	449	979	134	425	
4	Half Great- Aunt/Uncle/Niece/Nephew	238	184	431	668	105	425	
5	1C2R	1187	33	221	471	83	213	
5	2C	4172	41	229	592	86	213	
5	Half 1C1R	605	62	224	469	80	213	
5	Half Great-Great- Aunt/Uncle/Niece/Nephew	34	103	208	284	43	213	
6	1C3R	202	25	117	238	48	106	
6	2C1R	5281	14	122	353	59	106	
6	Half 1C2R	165	16	125	269	54	106	
6	Half 2C	512	10	120	325	62	106	
7	2C2R	1404	0	71	244	42	53	
7	3C	4775	0	73	234	43	53	
7	Half 1C3R	33	0	60	120	32	53	
7	Half 2C1R	474	0	66	190	39	53	
8	2C3R	163	0	51	154	32	27	
8	3C1R	4514	0	48	192	32	27	
8	Half 2C2R	98	0	48	144	32	27	
8	Half 3C	302	0	48	168	33	27	
9	3C2R	965	0	36	166	27	13	
9	4C	2752	0	35	139	23	13	
9	Half 3C1R	249	0	37	139	24	13	
10	3C3R	106	0	27	98	19	7	
10	4C1R	2383	0	28	126	20	7	

Grouping #	Relationship	#	Min	Average	Max	SD	Expected
10	Half 3C2R	55	0	27	78	15	7
10	Half 4C	89	0	30	74	18	7
n/a	4C2R	603	0	22	93	16	3.3
n/a	$5^{\rm C}$	1130	0	25	117	18	3.3
n/a	4C3R	89	0	19	60	12	1.7
n/a	5C1R	975	0	21	80	15	1.7
n/a	5C2R	242	0	18	65	12	0.8
n/a	6C	441	0	18	71	13	0.8
n/a	5C3R	34	0	13	30	7	0.4
n/a	6C1R	441	0	15	56	9	0.4
n/a	6C2R	161	0	13	45	8	0.2
n/a	7C	258	0	14	57	9	0.2
n/a	7C1R	330	0	12	50	7	0.1
n/a	8C	239	0	11	42	5	0.05

Differences in Minimum, Average, and Maximum Values Between Version 3.0 Vs. Version 4.0

There are many changes to the minimum, average, and maximum values for relationships in Version 4.0 of the Shared cM Project relative to the prior Version 3.0. As the number of submissions for a relationship grows, the distribution of cM values for that relationship is more clearly defined. This allows for improved definition and elimination of outliers for each relationship. In some cases, the very large increase in submissions moved the minimum and/or maximum values further outward for a broader distribution in this version, and in other cases it moved the minimum and/or maximum values inward for a tighter distribution in this version.

For example, the large increase in the number of submissions for Great-Aunt/Uncle/Niece/Nephew allowed for significantly better definition of the distribution for that relationship, and thus better definition of outliers. The maximum cM value for that relationship moved from 2,108 cM in Version 3.0 to 1,467 cM in Version 4.0.

Interestingly, the average cM values were very consistent from Version 3.0 to Version 4.0. For the 48 analyzed relationships, only nine changed by more than 10 cM, and only three changed by more than 20 cM.

Grouping #	Relationship	Version 3.0 # of Submissions	Version 4.0 # of Submissions	Version 3.0 Min	Version 4.0 Min	Change	Version 3.0 Average	Version 4.0 Average	Change	Version 3.0 Max	Version 4.0 Max	Change
	Parent/Child	1378	2412	3330	2376	-29%	3487	3485	0%	3720	3720	0%
1	Sibling	1345	2465	2209	1613	-27%	2629	2613	-1%	3384	3488	3%
2	Aunt/Uncle/Niece/Nephew	1411	2695	1349	1201	-11%	1750	1741	-1%	2175	2282	5%
2	Grandparent/Grandchild	611	1106	1156	984	-15%	1766	1754	-1%	2311	2462	7%
2	Half Sibling	451	1266	1317	1160	-12%	1783	1759	-1%	2312	2436	5%
3	1C	1512	3337	553	396	-28%	874	866	-1%	1225	1397	14%
3	Great- Aunt/Uncle/Niece/Nephew	413	833	251	330	31%	914	850	-7%	2108	1467	-30%
3	Great-Grandparent/Great- Grandchild	61	149	464	485	5%	881	887	1%	1486	1486	0%
3	Half Aunt/Uncle/Niece/Nephew	275	815	500	492	-2%	891	871	-2%	1446	1315	-9%
4	1C1R	1594	3700	141	102	-28%	439	433	-1%	851	980	15%
4	Great-Great- Aunt/Uncle/Niece/Nephew	25	137	191	186	-3%	427	420	-2%	885	713	-19%
4	Half 1C	177	691	137	156	14%	457	449	-2%	856	979	14%
4	Half Great- Aunt/Uncle/Niece/Nephew	44	238	125	184	47%	432	431	0%	765	668	-13%
5	1C2R	481	1187	43	33	-23%	229	221	-3%	531	471	-11%
5	2C	1590	4172	46	41	-11%	233	229	-2%	515	592	15%
5	Half 1C1R	138	605	57	62	9%	226	224	-1%	530	469	-12%
5	Half Great-Great- Aunt/Uncle/Niece/Nephew	15	34	12	103	758%	187	208	11%	383	284	-26%
6	1C3R	38	202	0	25	n/a	123	117	-5%	283	238	-16%
6	2C1R	2064	5281	0	14	n/a	123	122	-1%	316	353	12%
6	Half 1C2R	39	165	37	16	-57%	145	125	-14%	360	269	-25%
6	Half 2C	143	512	9	10	11%	117	120	3%	397	325	-18%
7	2C2R	564	1404	0	0	n/a	74	71	-4%	261	244	-7%

7	3C	1791	4775	0	0	n/a	74	73	-1%	217	234	8%
7	Half 1C3R	19	33	0	0	n/a	87	60	-31%	191	120	-37%
7	Half 2C1R	116	474	0	0	n/a	73	66	-10%	341	190	-44%
8	2C3R	50	163	0	0	n/a	57	51	-11%	139	154	11%
8	3C1R	1736	4514	0	0	n/a	48	48	0%	173	192	11%
8	Half 2C2R	24	98	0	0	n/a	61	48	-21%	353	144	-59%
8	Half 3C	55	302	0	0	n/a	61	48	-21%	178	168	-6%
9	3C2R	459	965	0	0	n/a	35	36	3%	116	166	43%
9	4C	998	2752	0	0	n/a	35	35	0%	127	139	9%
9	Half 3C1R	71	249	0	0	n/a	42	37	-12%	165	139	-16%
10	3C3R	47	106	0	0	n/a	22	27	23%	48	98	104%
10	4C1R	934	2383	0	0	n/a	28	28	0%	117	126	8%
10	Half 3C2R	26	55	0	0	n/a	34	27	-21%	96	78	-19%
10	Half 4C	32	89	0	0	n/a	36	30	-17%	120	74	-38%
n/a	4C2R	245	603	0	0	n/a	22	22	0%	109	93	-15%
n/a	5C	422	1130	0	0	n/a	25	25	0%	94	117	24%
n/a	4C3R	25	89	0	0	n/a	29	19	-34%	86	60	-30%
n/a	5C1R	354	975	0	0	n/a	21	21	0%	79	80	1%
n/a	5C2R	92	242	0	0	n/a	17	18	6%	43	65	51%
n/a	6C	122	441	0	0	n/a	18	18	0%	86	71	-17%
n/a	5C3R	12	34	0	0	n/a	11	13	18%	44	30	-32%
n/a	6C1R	138	441	0	0	n/a	16	15	-6%	72	56	-22%
n/a	6C2R	59	161	0	0	n/a	17	13	-24%	75	45	-40%
n/a	7C	54	258	0	0	n/a	13	14	8%	57	57	0%
n/a	7C1R	89	330	0	0	n/a	13	12	-8%	53	50	-6%
n/a	8C	80	239	0	0	n/a	12	11	-8%	50	42	-16%
		22419	55418									