Working with DNA Prediction Chart

We have put together a DNA Prediction Chart, combining suggestions from several sources.

This is the way we suggest that you use it.

Here are the FTDNA results that Sandra has with Fred.

	A	B	C	D	E	F	G
1	Profile Name	Full Name	Chromosc	Start	End	cM	SNPS
2	Sandra	Fred	4	126,341,682	164,609,000	35.06	7291
3	Sandra	Fred	2	41,978,630	71,036,408	29.33	8300
4	Sandra	Fred	14	33,846,466	64,353,711	25.9	7400
5	Sandra	Fred	17	4,859,182	14,158,697	23.8	3331
6	Sandra	Fred	98	22,803,814	37,214,111	22.87	2175
7	Sandra	Fred	8	154,984	10,244,874	20.18	4833
8	Sandra	Fred	2	191,676,665	212,090,891	17.61	4084
9	Sandra	Fred	16	83,933,985	88,690,776	14.19	1911
10	Sandra	Fred	98	49,385,222	71,842,330	10.64	1375
11	Sandra	Fred	5	27,863,513	34,771,107	10.03	1748
12	Sandra	Fred	19	211,912	2,664,416	6.94	769
13	Sandra	Fred	5	115,441,855	120,901,846	5.09	1300

First I gather the statistics. We only consider segments 5 cM or over.

The total DNA shared is the total of column F. 221.64 cM

The longest segment is 35.06

The total number of segments is 12

To get the % of DNA, divide the total cMs over 5 by 74.4 if X is included in the total cMs or if results are from 23andme (Otherwise use 68)

In this case 221.64/74.4 = 2.97%

Now bring up the DNA prediction chart. You can print the table and color it in if you wish. I have shaded the areas where Fred's DNA falls.

Relationship	Total cMs (centimor	Longest Segm	Number of Seg	Minimum To	Maximum To	Average % Shar	Range % Share	Probability of match showing
Parent/Child	3539-3748		23 - 34	3539	3748	0.5	47.29 - 50.66	1
Siblings *	2643- 2802	50 - 141	43 - 67	2643	2802	50.000% *	~37.5 See *	1
Nephew, Niece, Uncle, Aunt	1526 - 2082	95 - 163	38 - 52	1526	2082	0.25		1
Half Siblings	~ 1700		29 - 33			0.25	21.74-31.39	1
Double first cousins	~ 1500					0.25		1
Grandparent, grandchild	1087 - 2297		20 - 47	1087	2297	0.25		1
Great Grandparent, Great grandchild	972 - 1231		15 - 25	572	1231	0.125		1
Great Uncle/Aunt/Niece/Nephew	550 - 860	60 - 135	23 - 30	550	860	0.125	9.5 - 12.3	1
1st cousin	548-1034	50 - 182	17 - 32	530	1128	0.125	7.31 - 13.8	1
1st cousin 1X	220 - 638	34 - 106	12 - 23	218	638	0.0625	2.88 - 7.9	
1st cousin 2X	107 - 426	21 -64		127	139	0.03125	1.42 - 5.68	
2nd cousins	101-378	31 - 61	10 - 18	73	383	0.03125	2.88 - 5.04	0.99
2nd cousins 1X	19 - 197	19 - 81	4 - 12	19	197	0.01563	0.25 - 2.54	
2nd cousin 2X	12 - 72.5		1 - 6	12	72.5	0.00781	0.16 - 2.54	
3rd cousins	43- 150		2 - 6	8	58	0.00781	0.3 -2.0	0.9
3rd cousins 1X	11.5- 99		1 - 4	8	58	0.00391	0.11 - 1.32	
4th cousins	5 - 50	0 - 24	0 - 2	8	58	0.00195	.07 - 0.5	45 - 50%
5th cousins	0 - 33	0 - 10		0	27	0.00049	~0.049	10 - 15%
6th cousins and more distant							0.001 - 0.012	2 - 5%

These show a number of ranges. DNA is not 100% predictable so we are working with averages to get a better idea of what the relationship is likely to be. The green is very high for the rest of the data, note that there are no comparable figures for some of the relationships, so discard the high part. Most of the shading falls in about the same area of the chart. Looking at the chart, I would think the chances are pretty high that we are looking at a 2nd cousin, twice removed to a 3rd cousin relationship. This means shared great- great grandparents.

Another example:

Sandra had a cousin match with Carter

Sandra	Carter		5	142,643,609	180,625,733	57.81
Sandra .	Carter		4	170,827,564	173,561,269	2.49
Sandra	Carter		20	31,036,099	33,776,127	2.3
Sandra	Carter		8	91,113,457	94,129,515	2.23
Sandra	Carter		10	117,868,591	119,441,522	1.94
Sandra	Carter		2	82,182,418	85,044,774	1.32

Going to prediction chart:

Relationship	Total cMs (centimorgans)	Longest Segment	Number of Segments	Minimum Total	Maximum Total	Average % Share	Range % Shared	Probability of match
Parent/Child	3539-3748		23 - 34	3539	3748	0.5	47.29 - 50.66	1
Siblings *	2643- 2802	50 - 141	43 - 67	2643	2802	50.000% *	~37.5 See *	1
Nephew, Niece, Uncle, Aunt	1526 - 2082	95 - 163	38 - 52	1526	2082	0.25		1
Half Siblings	~1700		29 - 33			0.25	21.74-31.39	1
Double first cousins	~1500					0.25		1
Grandparent, grandchild	1087 - 2297		20 - 47	1087	2297	0.25		1
Great Grandparent, Great grandchild	972 - 1231		15 - 25	572	1231	0.125		1
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1st cousin	548-1034	50 - 182	17 - 32	530	1128	0.125	7.31 - 13.8	1
1st cousin 1X	220 - 638	34 - 106	12 - 23	218	638	0.0625	2.88 - 7.9	
1st cousin 2X	107 - 426	21 -64		127	139	0.03125	1.42 - 5.68	
2nd cousins	101-378	31 - 61	10 - 18	73	383	0.03125	2.88 - 5.04	0.99
2nd cousins 1X	19 - 197	19 - 81	4 - 12	19	197	0.01563	0.25 - 2.54	
2nd cousin 2X	12 - 72.5		1 - 6	12	72.5	0.00781	0.16 - 2.54	
3rd cousins	43- 150		2 - 6	8	58	0.00781	0.3 -2.0	0.9
3rd cousins 1X	11.5- 99		1 - 4	8	58	0.00391	0.11 - 1.32	
4th cousins	5 - 50	0 - 24	0 - 2	8	58	0.00195	.07 - 0.5	45 - 50%
5th cousins	0 - 33	0 - 10		0	27	0.00049	~0.049	10 - 15%
6th cousins and more distant							0.001 - 0.012	2 - 5%

This single segment is very long, but the number of segments and the percentage are the most important keys here. Look at 3rd cousin and 3rd cousin once removed.

Remember these are just guidelines and suggested areas to explore, you may have to move closer or further out on the tree.

This chart helps you get a picture of what you are dealing with. It is not an absolute.