

**FTDNA / 23andMe / GEDMATCH DNA**

Relationship	Total cMs (centimorgans)	Longest Segment	# of Segments	Minimum Total cMs	Maximum Total cMs	% Shared DNA	Range % Shared DNA**	Probability of match showing ***
Parent/Child	3539-3748	~285	23 - 34	3539	3748	50.000%	29 - 50.66	100%
Siblings *	2643-2802	50 - 141	43 - 67	2643	2802	50.000%	~ 37.5	100%
Nephew, Niece, Uncle, Aunt	1526 - 2082	95 - 163	38 - 52	1526	2082	25.000%	19.43 - 32	100%
Half Siblings	1320 - 2100		29 - 33			25.000%	42 - 31.39	100%
Double first cousins	~ 1500					25.000%		100%
Grandparent, grandchild	1087 - 2297		20 - 47	1087	2297	25.000%	32 - 29.35	100%
Great Grandparent, Great grandchild	572 - 1231		15 - 25	572	1231	12.500%		100%
Great Uncle/Aunt/Niece/Nephew	550 - 860	60 - 135	23 - 30	550	860	12.500%	9.5 - 12.3	100%
Half nephew/niece/aunt/uncle	684 - 1122	54 - 112	22- 47	684	1122	12.500%	9.6 - 15.8	100%
1st cousin	548-1034	50 - 182	17 - 32	530	1128	12.500%	7.31 - 13.8	100%
Half 1st cousin	~325	30 - 35	~21			6.250%	*4 - 7	100%
1st cousin 1X	220 - 638	34 - 106	12 - 26	218	638	6.250%	2.88 - 8.41	
Half 1st cousin 1X	~200	~28	~14			3.125%	*2 - 3.5	
1st cousin 2X	107 - 426	21-64		127	139	3.125%	1.42 - 5.68	
2nd cousins	101-378	31 - 61	10 - 18	73	383	3.125%	2.88 - 5.04	99%
2nd cousins 1X	19 - 197	19 - 81	4 - 12	19	197	1.563%	1.25 - 2.54	
2nd cousins 2X	12 - 72.5		1 - 6	12	72.5	0.781%	0.16 - 2.54	
3rd cousins	43- 150		2 - 6	8	58	0.781%	0.3 - 2.0	90%
3rd cousins 1X	11.5- 99		1 - 4	8	58	0.391%	0.11 - 1.32	
4th cousins	5 - 50	0 - 24	0 - 4	8	58	0.195%	1.07 - 0.66	45 - 50%
5th cousins	0 - 33	0 - 10		0	27	0.049%	*0.049	10 - 15%
6th cousins							0.001 - 0.012	2 - 5%
more distant than 6th cousins								remote - less than 2%

**ANCESTRY DNA**

Sample Size	Total cMs	Avg cM	Total Segment	# of shared Segments
24	3314-3431	3396	70-106	83
14	2282-2695	2536	60-81	71
22	1360-1873	1602	58-89	70
16	1381-2033	1667	52-85	68
2	1822-2091	1957	72-73	73
1	636	636	28	28
2	641-961	801	36-51	44
12	528-1078	843	25-46	36
17	560-1138	859	29-54	43
4	400-596	499	21-26	24
20	204-536	401	16-32	23
4	30-226	99	2-12	6
8	119-233	183	5-17	12
40	99-464	233	8-21	14
60	19-435	117	1-28	7
26	10-131	54	1-7	4
77	6-135	50	1-10	4
112	5-202	31	1-8	3
71	5-128	26	1-7	2
83	5-63	16	1-4	1
31	5-43	12	1-3	1

ANCESTRY PREDICTION CATEGORIES				
	cM Avg	Max-Min	Seg Avg	Max-Min
PARENT_CHILD	3396	3431-3314	83	106 - 70
IMMEDIATE_FAMILY	2536	3695 - 2282	71	80 - 61
CLOSE_FAMILY	1636	2091-1360	68	89 - 52
CLOSE_FAMILY- 1st COUSIN	1737	1850 - 1638	76	82 - 72
FIRST_COUSIN	840	1138 - 418	40	54 - 25
SECOND_COUSIN	290	561 - 144	17	32 - 8
THIRD_COUSIN	98	139 - 72	6	12 - 2
FOURTH_COUSIN	32	71 - 18	3	7 - 1
DISTANT_COUSIN	10	18 - 5	1	4 - 1

\* Everyone has two copies of each chromosome, one from mother, one from father. The DNA companies' matching algorithms do not treat the two copies separately. It is considered a match whether you share DNA on your maternal copy or your paternal copy or both. This is also the reason why full siblings who essentially share ~50%, but only ~37.5% is reported - the "missing" ~12.5% is where siblings match on both the maternal and paternal copies but only one is counted.

\*\* To figure the % of shared DNA - add up the total cMs over 5 cMs and divide by 74, if X is included; by 71 if not. So if the total = 1700, take 1700/74 = 22.97%, and would fit into the range of a half-sibling, or nephew/niece/uncle/aunt or a grandparent!