

Relationship	FTDNA / 23andMe / GEDMATCH DNA									ANCESTRY DNA				
	Total cMs (centimorgans)	Longest Segment	Number of Segments	Minimum Total cMs	Maximum Total cMs	Average % Shared DNA	Range % Shared DNA**	Probability of match showing ***		Sample Size	Total cMs	Avg cM	Total Segement	Average of shared Segments
Parent/Child	3539-3748	~285	23 - 34	3539	3748	50.000%	47.29 - 50.66	100%		24	3314-3431	3396	70-106	83
Siblings *	2643- 2802	50 - 141	43 - 67	2643	2802	* 50.000%	* ~37.5	100%	See note below *	14	2282-2695	2536	60-81	71
Nephew, Niece, Uncle, Aunt	1526 - 2082	95 - 163	38 - 52	1526	2082	25.000%	19.43 - 32	100%		22	1360-1873	1602	58-89	70
Half Siblings	1320 - 2100		29 - 33			25.000%	19.42 - 31.39	100%		16	1381-2033	1667	52-85	68
Double first cousins	~ 1500					25.000%		100%						
Grandparent, grandchild	1087 - 2297		20 - 47	1087	2297	25.000%	18.32 - 29.35	100%		2	1822-2091	1957	72-73	73
Great Grandparent, Great grandchild	572 - 1231		15 - 25	572	1231	12.500%		100%		1	636	636	28	28
Great Uncle/Aunt/Niece/Nephew	550 - 860	60 - 135	23 - 30	550	860	12.500%	9.5 - 12.3	100%		2	641-961	801	36-51	44
Half nephew/niece/aunt/uncle	684 - 1122	54 - 112	22 - 47	684	1122	12.500%	9.6 - 15.8	100%		12	528-1078	843	25-46	36
1st cousin	548-1034	50 - 182	17 - 32	530	1128	12.500%	7.31 - 13.8	100%		17	560-1138	859	29-54	43
Half 1st cousin	~325	30 - 35	~21			6.250%	~4 - 7	100%		4	400-596	499	21-26	24
1st cousin 1X	220 - 638	34 - 106	12 - 26	218	638	6.250%	2.88 - 8.41			20	204-536	401	16-32	23
Half 1st cousin 1X	~200	~28	~14			3.125%	~2 - 3.5			4	30-226	99	2-12	6
1st cousin 2X	107 - 426	21 -64		127	139	3.125%	1.42 - 5.68			8	119-233	183	5-17	12
2nd cousins	101-378	31 - 61	10 - 18	73	383	3.125%	2.88 - 5.04	99%		40	99-464	233	8-21	14
2nd cousins 1X	19 - 197	19 - 81	4 - 12	19	197	1.563%	0.25 - 2.54			60	19-435	117	1-28	7
2nd cousins 2X	12 - 72.5		1 - 6	12	72.5	0.781%	0.16 - 2.54			26	10-131	54	1-7	4
3rd cousins	43- 150		2 - 6	8	58	0.781%	0.3 -2.0	90%		77	6-135	50	1-10	4
3rd cousins 1X	11.5- 99		1 - 4	8	58	0.391%	0.11 - 1.32			112	5-202	31	1-8	3
4th cousins	5 - 50	0 - 24	0 - 4	8	58	0.195%	0.07 - 0.66	45 - 50%		71	5-128	26	1-7	2
5th cousins	0 - 33	0 - 10		0	27	0.049%	~0.049	10 - 15%		83	5-63	16	1-4	1
6th cousins							0.001 - 0.012	2 - 5%		31	5-43	12	1-3	1
more distant than 6th cousins								remote - less than 2%						

ANCESTRY PREDICTION CATEGORIES						
	cM Avg	cM Min	Max	Seg Avg	Seg Min	Max
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/

