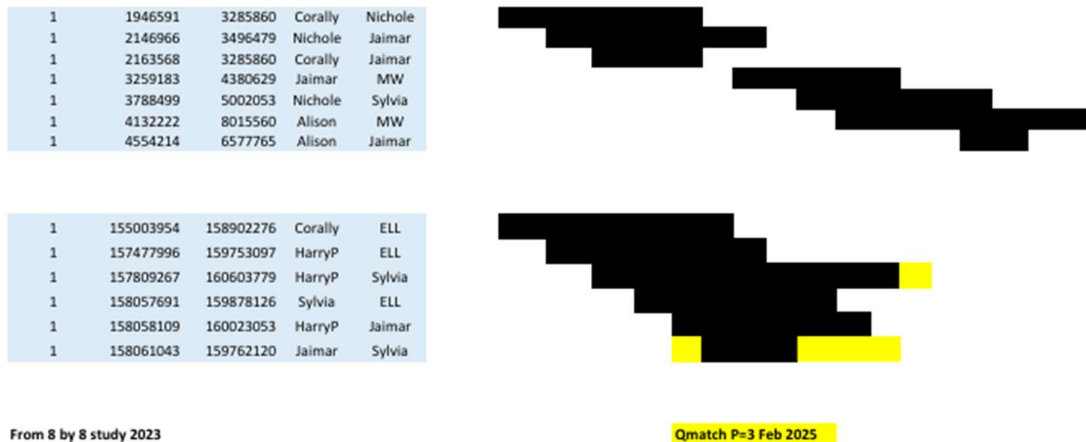Why tests are needed to distinguish family from random multiples

Feb 2025

The diagram below shows 2 amazing multiples arising from the random sample in our 8 by 8 study of 2023. The 1st of them, a 7-match multiple, is revealed by the bar diagram to be little more than a strong triple.

1	1946591	3285860	Corally	Nichole
1	2146966	3496479	Nichole	Jaimar
1	2163568	3285860	Corally	Jaimar
1	3259183	4380629	Jaimar	MW
1	3788499	5002053	Nichole	Sylvia
1	4132222	8015560	Alison	MW
1	4554214	6577765	Alison	Jaimar

1	155003954	158902276	Corally	ELL
1	157477996	159753097	HarryP	ELL
1	157809267	160603779	HarryP	Sylvia
1	158057691	159878126	Sylvia	ELL
1	158058109	160023053	HarryP	Jaimar
1	158061043	159762120	Jaimar	Sylvia

From 8 by 8 study 2023

Qmatch P=3 Feb 2025

However, the 2nd of them, a 6-match multiple, consists of 2 doubly-linked strong triples and looks very impressive. Checking with Qmatch 3cM with P=3 (that is, the same settings used to validate our Cr2, Cr8 and Cr21 Baruch Lousada indicators), makes little difference other than to add a common type of segment boundary coincidence (lower left of bar diagram).

The absence of our improbable segment boundary coincidence allows us to declare that the significance of this intriguing match is that it increases the threshold for genuine family multiples to overcome at the setting used (Qmatch 3cM P=3)!