	Ju	JG	SW	E	A	RF	RM	B	Je	MD	TP	J	total
Ju	■		2		1	1	0.5		1				5.5
JG		■	1										1
SW	2	1	■				1		1		1		6
E				■				1					1
A	1				■		0.5						1.5
RF	1					■			1		1		3
RM	0.5		1		0.5		■				1		3
B				1				■					1
Je	1		1			1			■		3		6
MD										■	1	1	2
TP			1			1	1		3	1	■	1	8
J										1	1	■	2
total	5.5	1	6	1	1.5	3	3	1	6	2	8	2	40

Notes:

1. The fractional entries reflect the Cr18 situation where either of the 1st cousins A or Ju are proven to match RM. If needed the same approach could be used to bring many of the unallocated matches into the above chart. For example, where (as is common) there are 4 possible interpretations of one of the rare segment boundary coincidences, each could be assigned the value 1/4.
2. Such a procedure would however introduce error, as is obvious in what we have done in this chart, and may not leave us much better off. A probability estimate of the total fit of each relative can of course be found in our chart listing the 31 rare segment boundary coincidences.
3. It is fortunate here that while JG, E and B show 1 proven match each, there is no real doubt about their family branch/connection.