Genotype distribution of the study population by gender, family relationship and affected status

	Mothers		Daughters				
Genotype	Affected	Unaffected	Affected	Unaffected	Fathers	Sons	Total
CYP17							
CC	2	10	47	41	6	11	117
CT	8	32	147	108	30	22	347
TT	2	19	107	61	8	18	215
Unknown	64	140	0	0	233	0	437
Total	76	201	301	210	277	51	1116
CYP19 (no. of TTTA repeats)							
7/7	1	15	88	55	7	21	187
7/8	0	10	34	29	4	5	82
7/9	0	0	1	0	1	0	2
7/10	0	1	5	6	2	0	14
7/11	9	19	106	71	14	19	238
7/12	0	2	9	8	0	0	19
7/13	0	0	0	0	1	0	1
8/8	0	0	4	1	0	0	5
8/10	0	1	3	2	0	0	6
8/11	1	2	24	16	1	3	47
8/12	0	0	1	2	0	0	3
8/13	0	0	0	1	0	0	1
9/11	0	0	0	1	0	0	1
10/11	0	0	2	3	0	2	7
11/11	0	5	19	16	1	1	42
11/12	0	1	4	2	0	0	7
11/13	1	0	2	1	1	0	5
11/not 11[a]	1	3	0	0	5	0	9
Unknown	63	143	0	0	241	0	447
Total	76	202	302	214	278	51	1123

[a]Indicates those whose genotype cannot be inferred for both alleles; the other allele could be 7, 8, or 12. Two of these nine observations, one an unaffected mother and the other the father in the same nuclear family, will be excluded when the allele with 10 or more repeats is selected as bad allele, because either them could be 11/12.