

Report

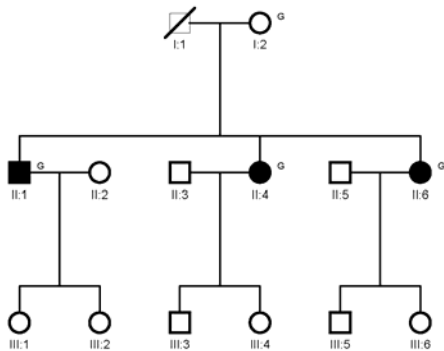
Genome-wide High-Density SNP-Based Linkage Analysis of Infantile Hypertrophic Pyloric Stenosis

Identifies Loci on Chromosomes 11q14-q22 and Xq23

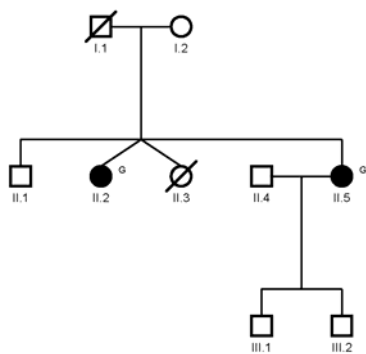
K. Everett, B. Chioza, C. Georgoula, A. Reece, F. Capon, K. Parker, C. Cord-Udy, P. McKeigue, S. Mitton, A. Pierro, P. Puri, H.M. Mitchison, E. Chung, and R.M. Gardiner

Figure S1. Pedigree Diagrams for All Families Included in Analysis, Showing All Individuals on Whom There Is Information

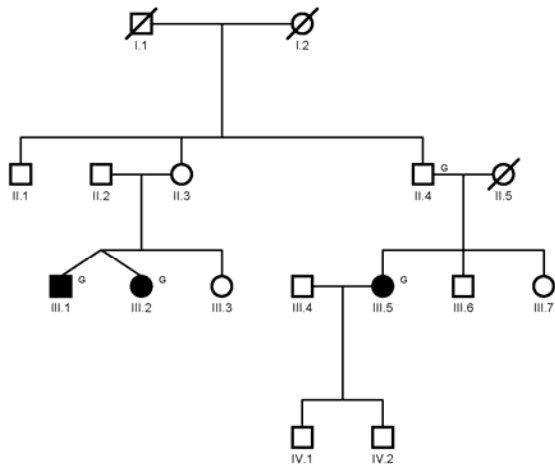
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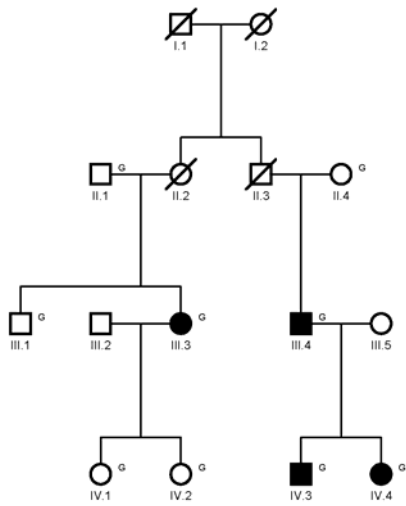
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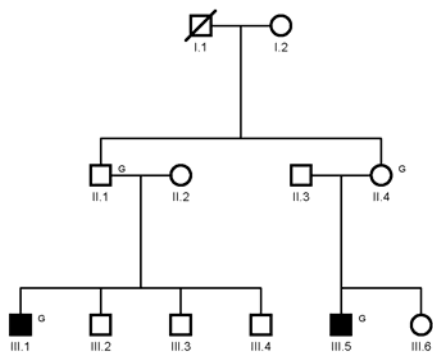
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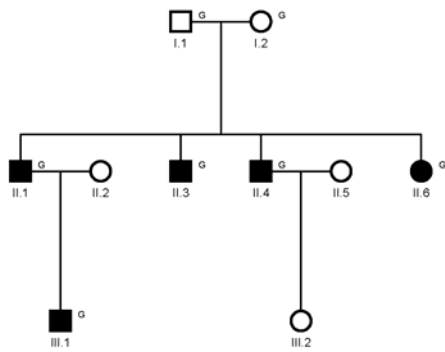
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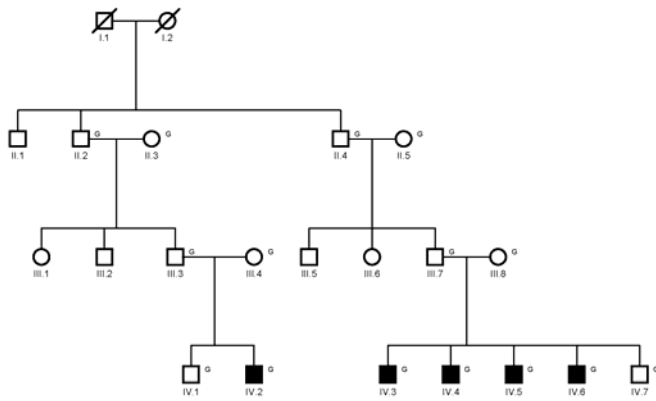
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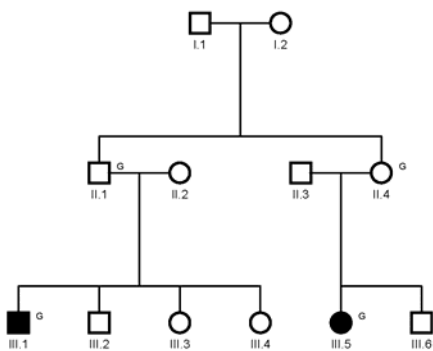
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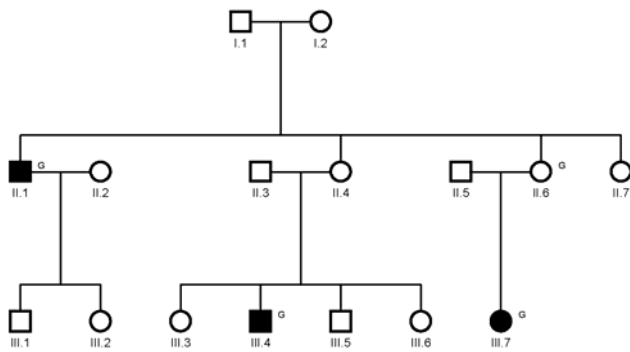
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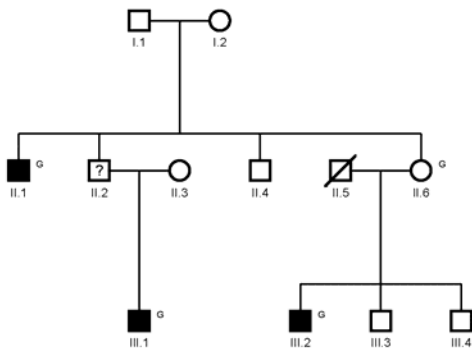
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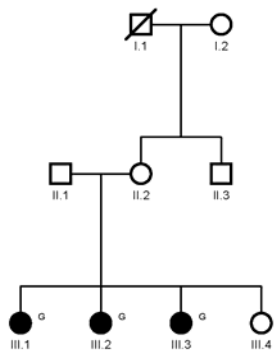
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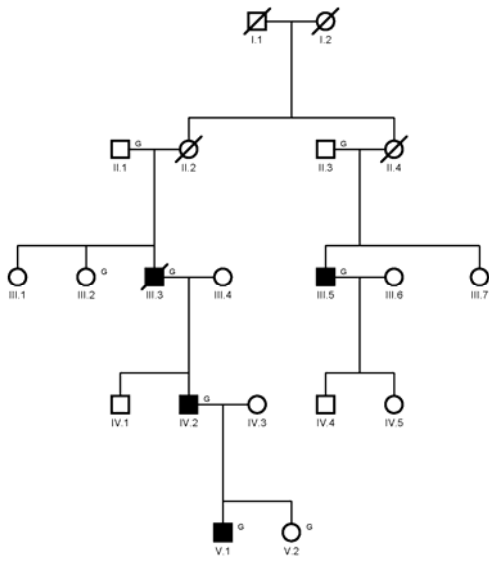
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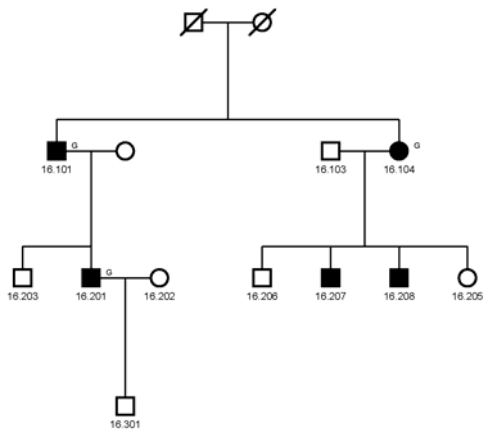
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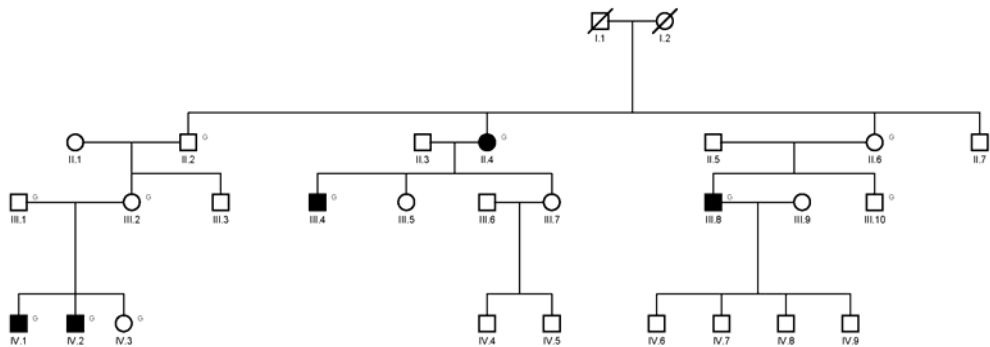
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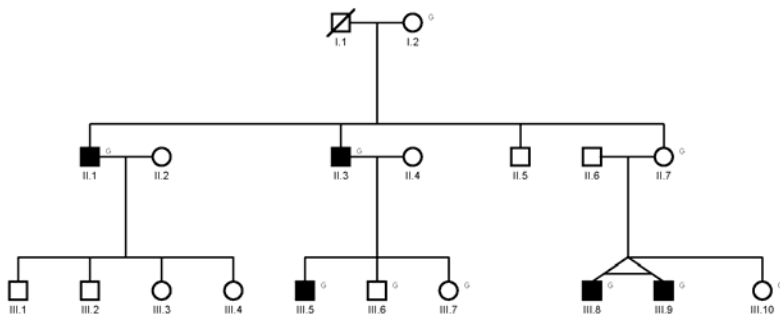
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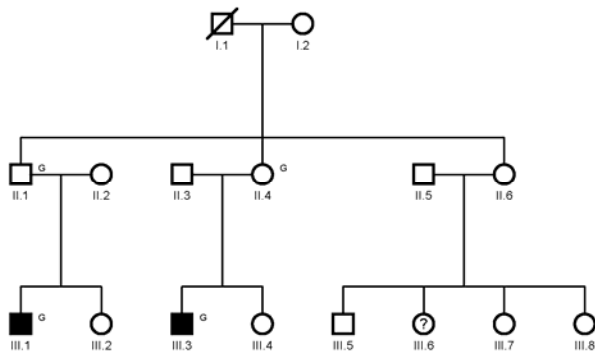
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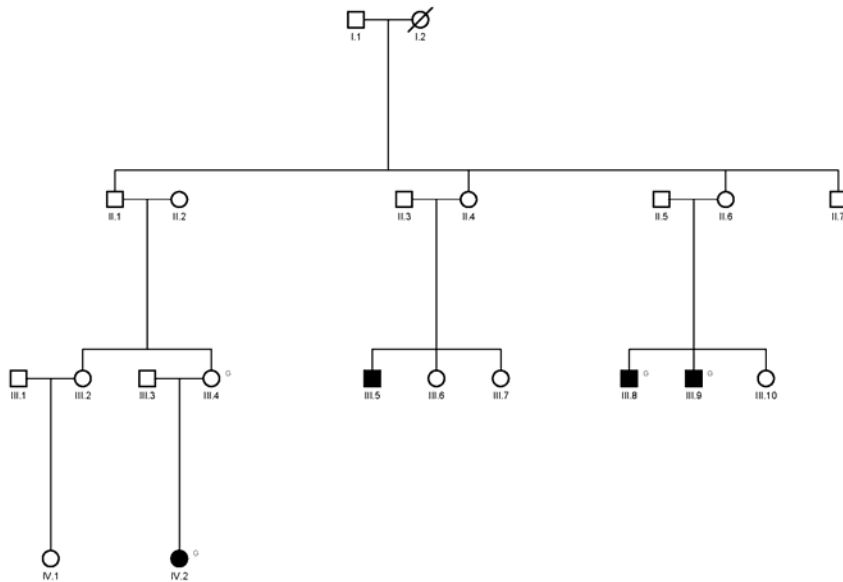
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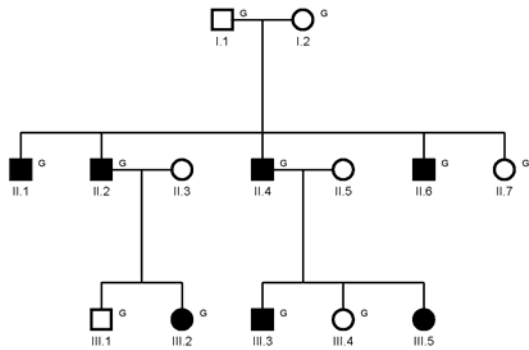
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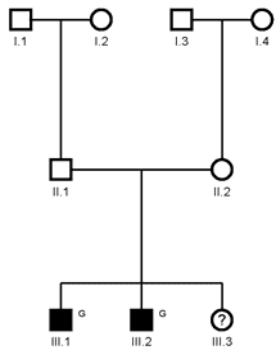
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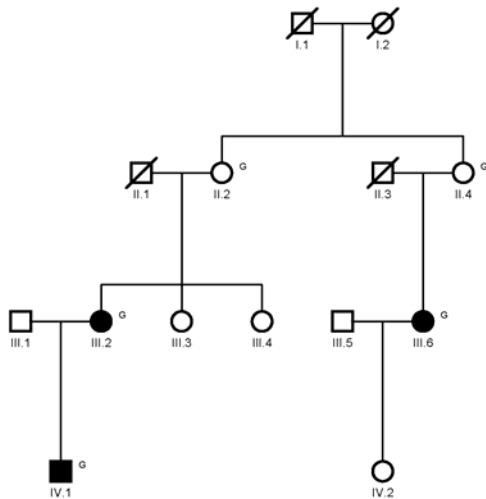
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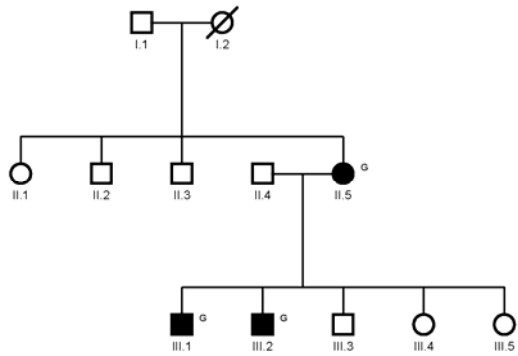
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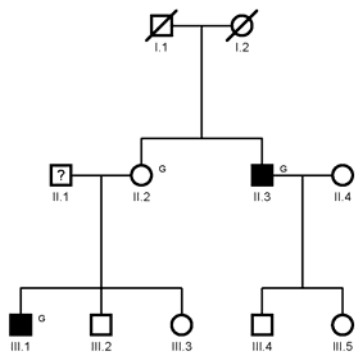
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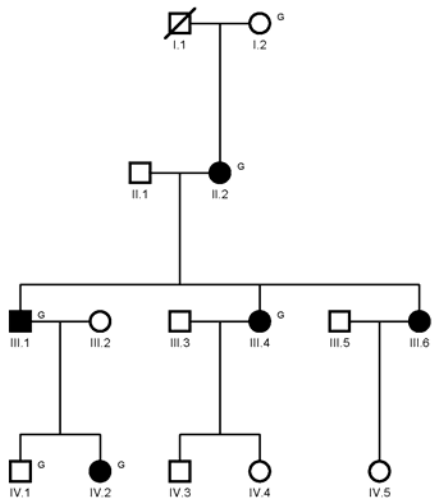
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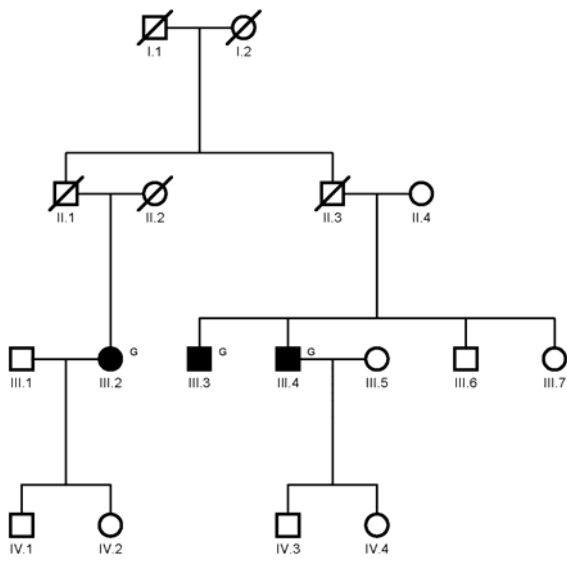
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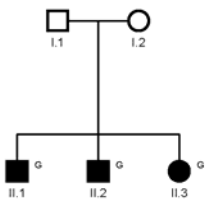
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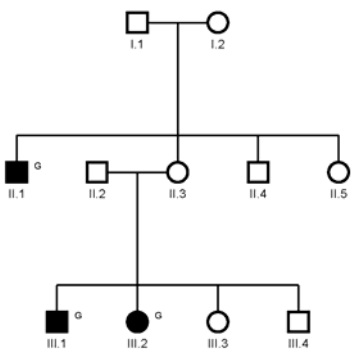
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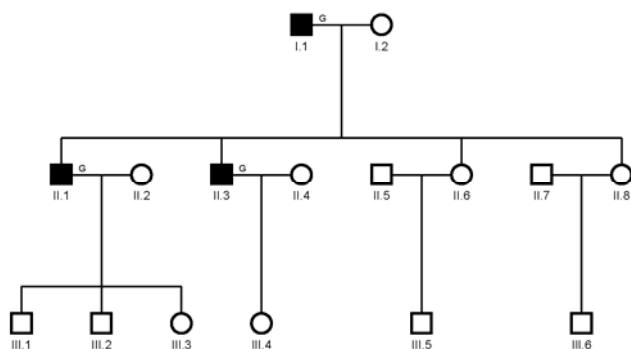
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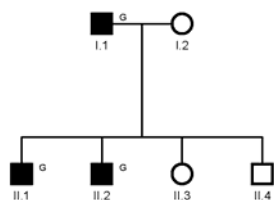
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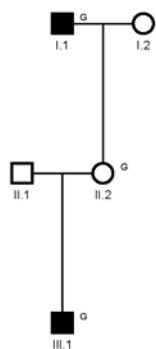
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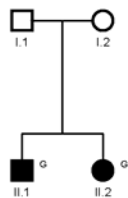
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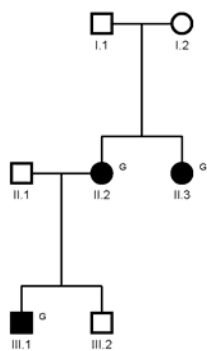
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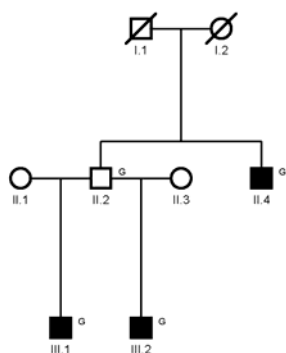
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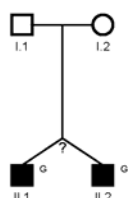
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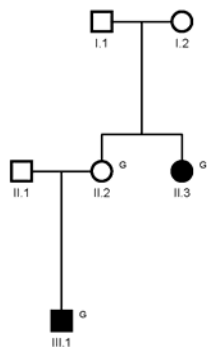
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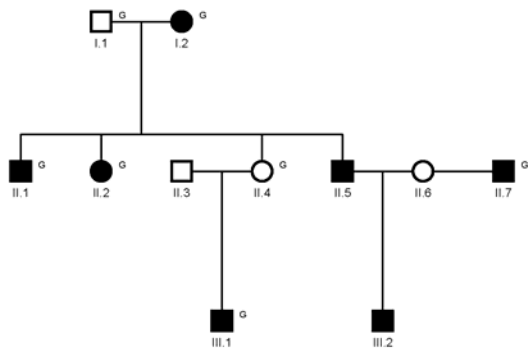
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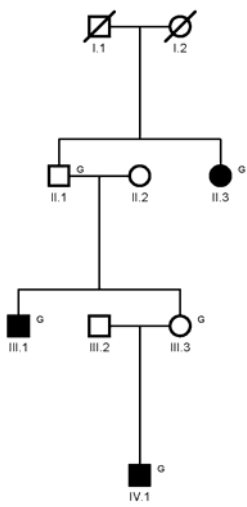
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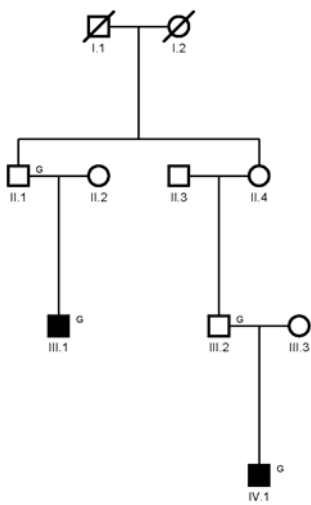
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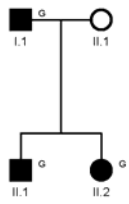
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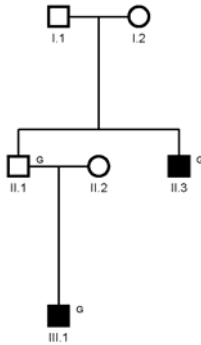
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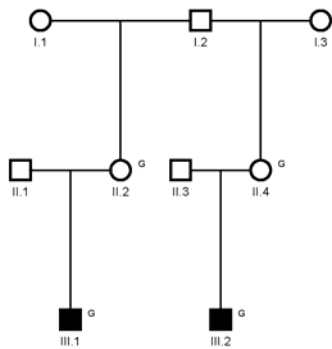
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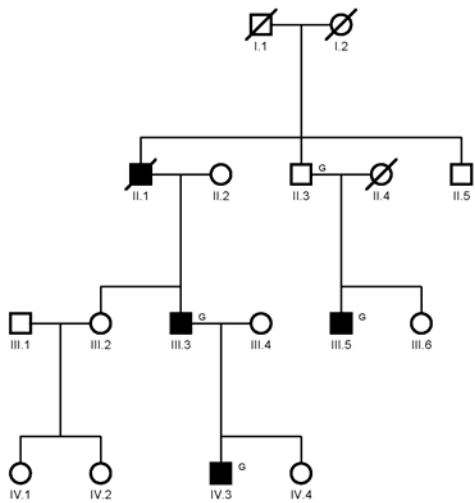
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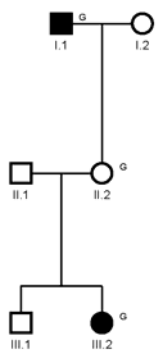
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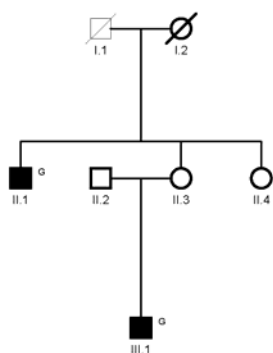
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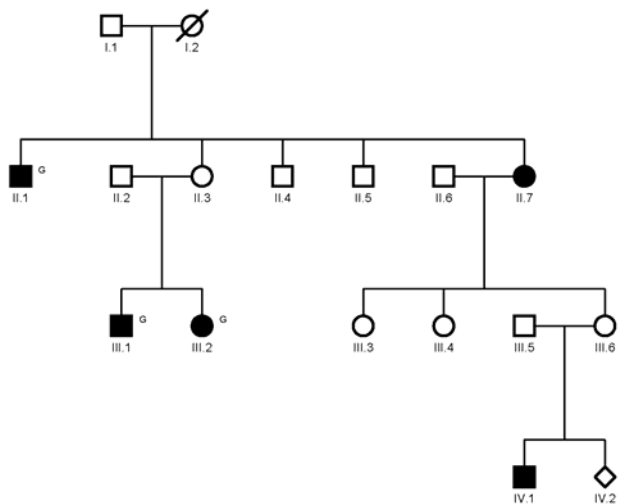
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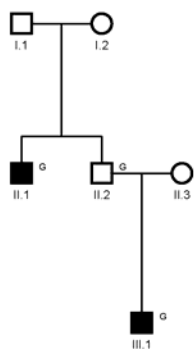
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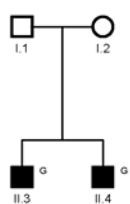
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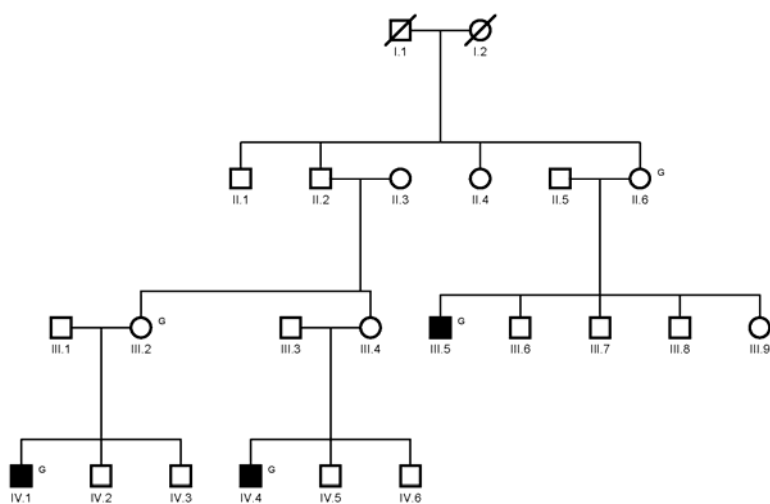
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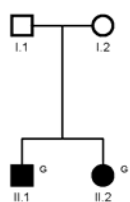
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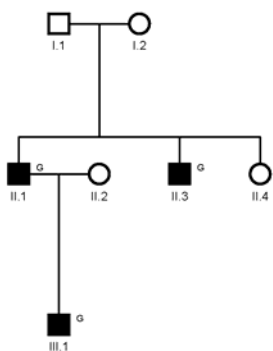
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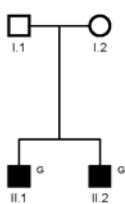
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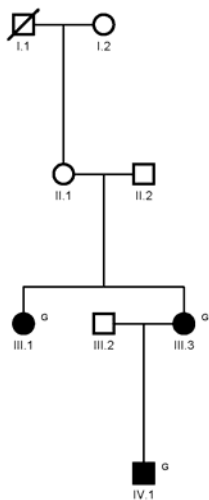
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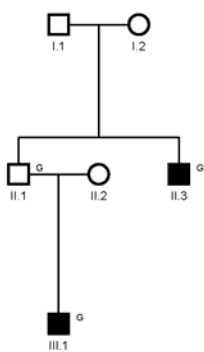
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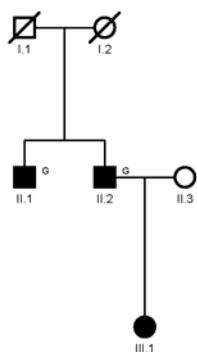
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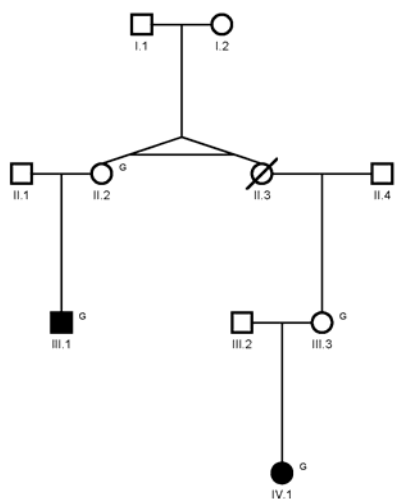
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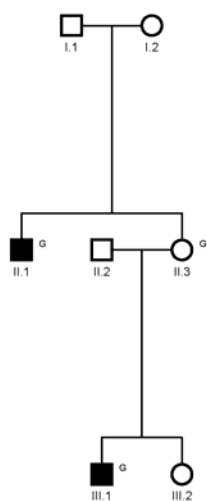
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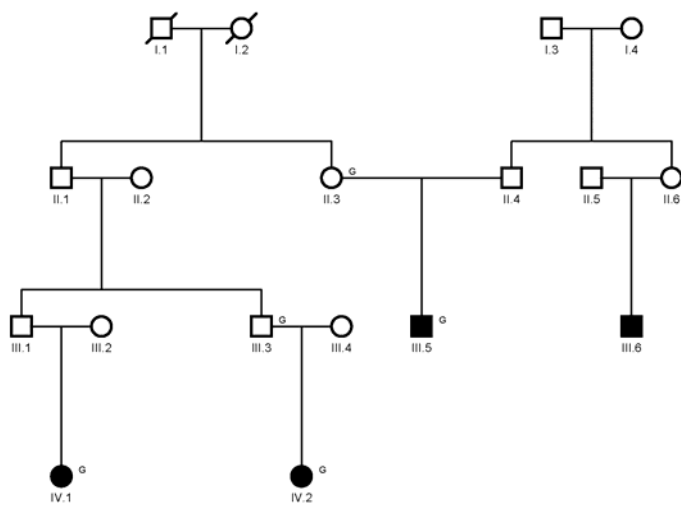
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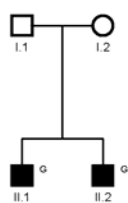
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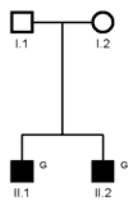
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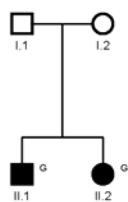
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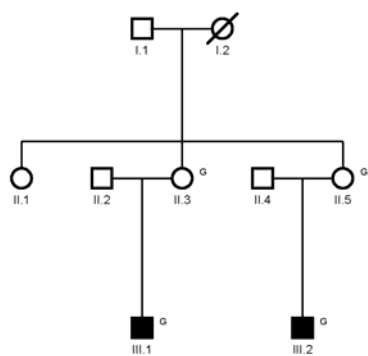
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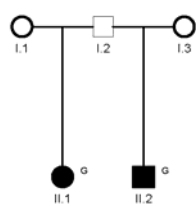
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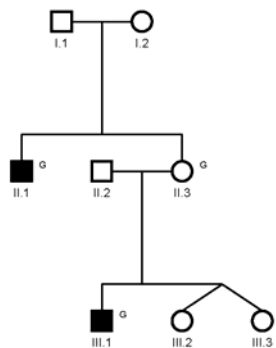
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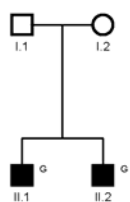
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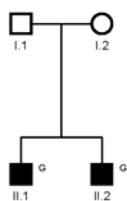
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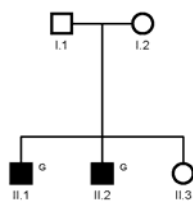
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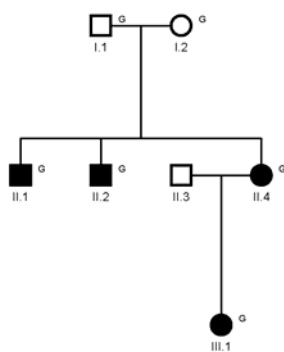
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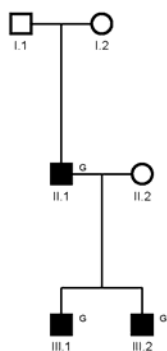
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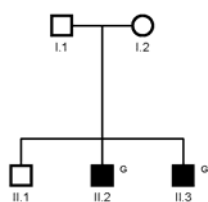
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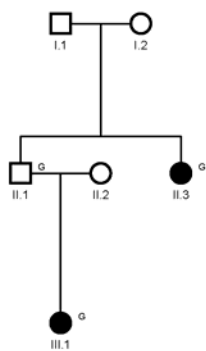
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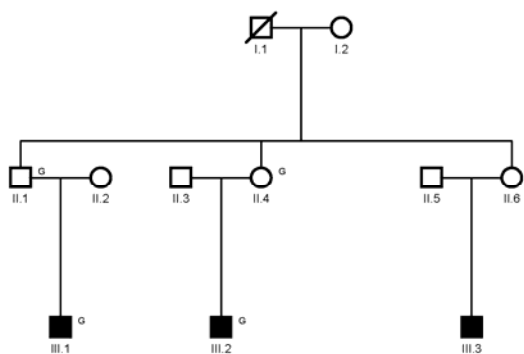
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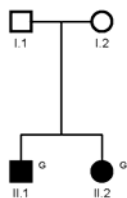
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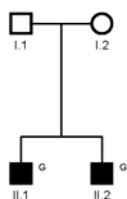
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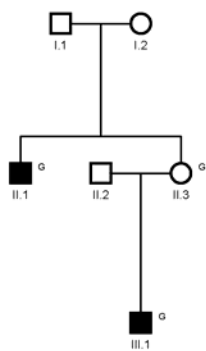
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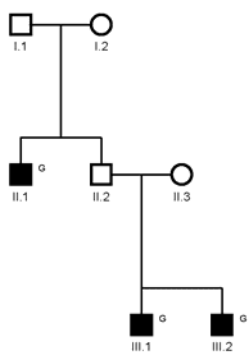
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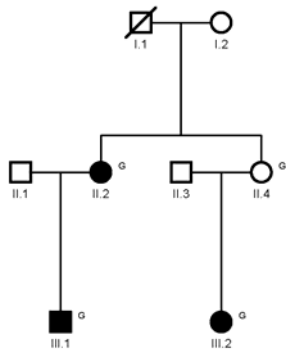
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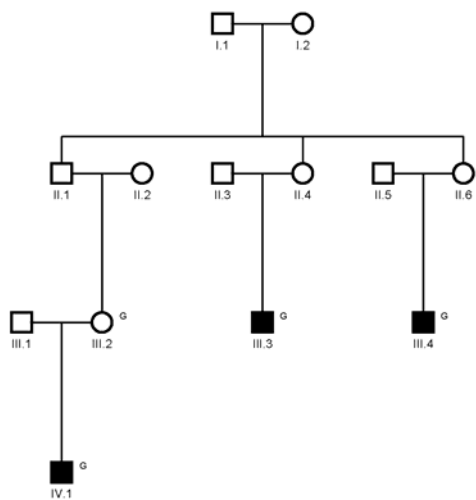
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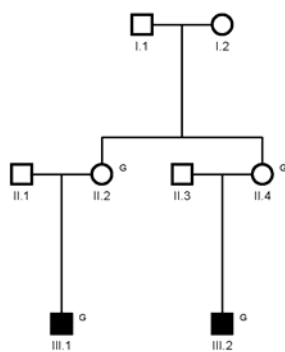
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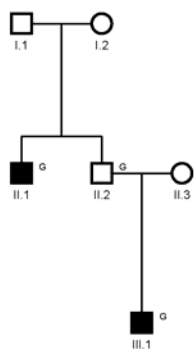
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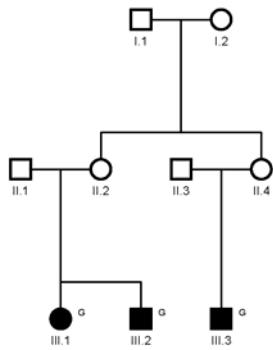
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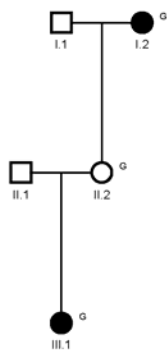
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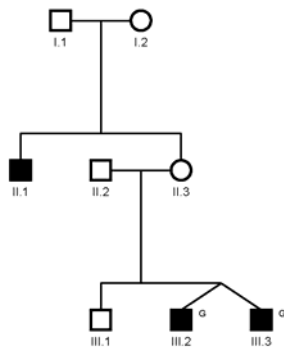
Family 479.



Family 481.



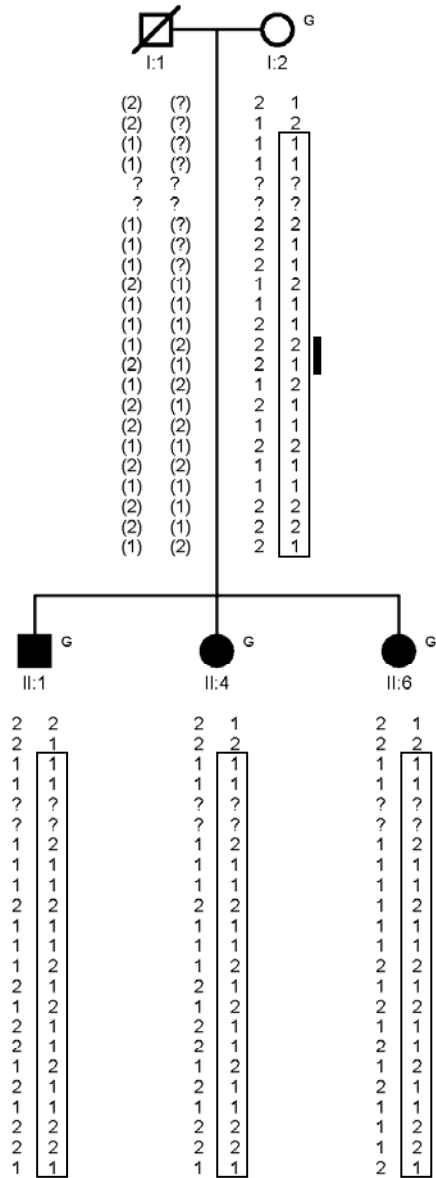
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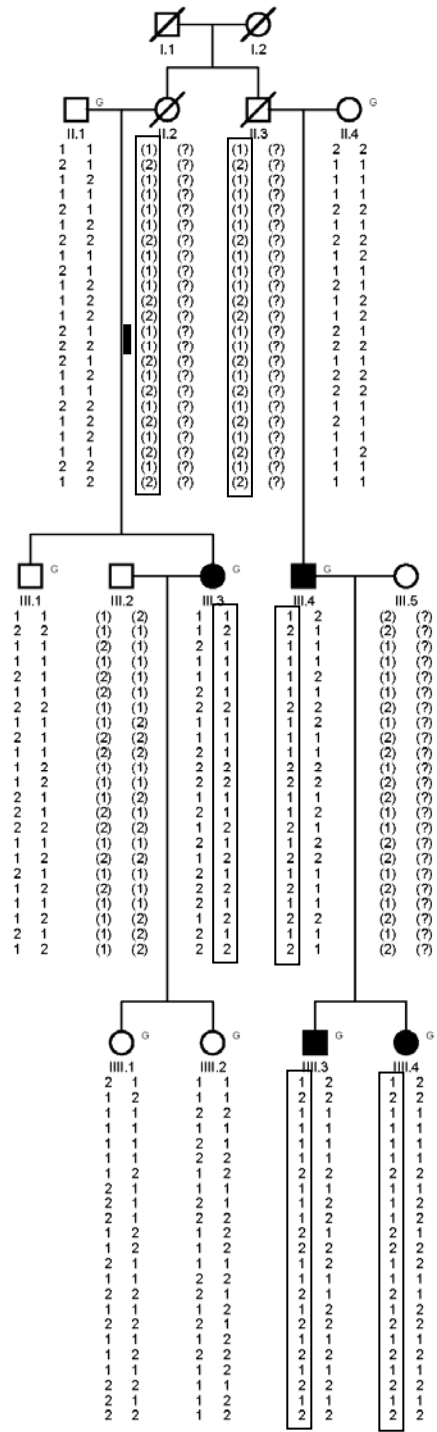
Individuals with a line through them are dead. Individuals marked with a G have been genotyped with the Illumina Linkage IV Panel of SNPs. Shaded individuals are affected. Standard nomenclature is used for the identification of individuals.

Figure S2. Pedigree and Predicted Haplotype Structure of Those Families that Individually Provide the Strongest Evidence for Linkage to Chromosomes 11 and/or the X Chromosome

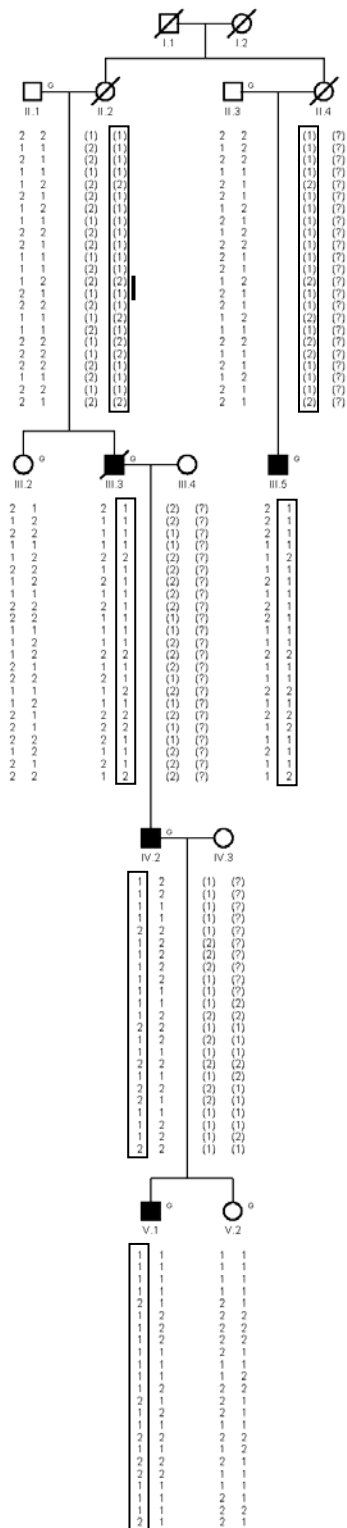
Family 1. Chromosome 11



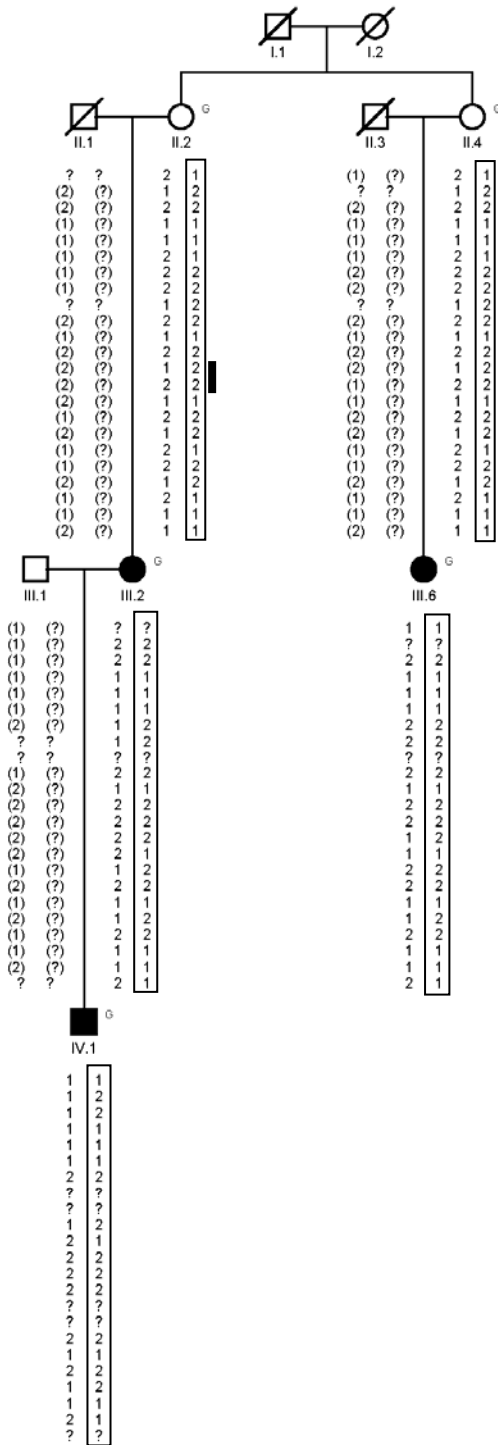
Family 5. Chromosome 11



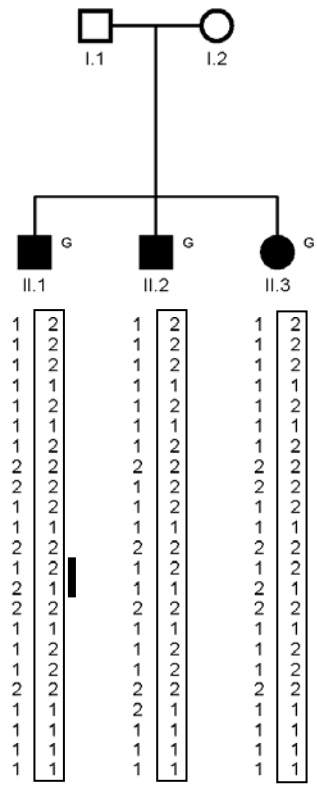
Family 15. Chromosome 11



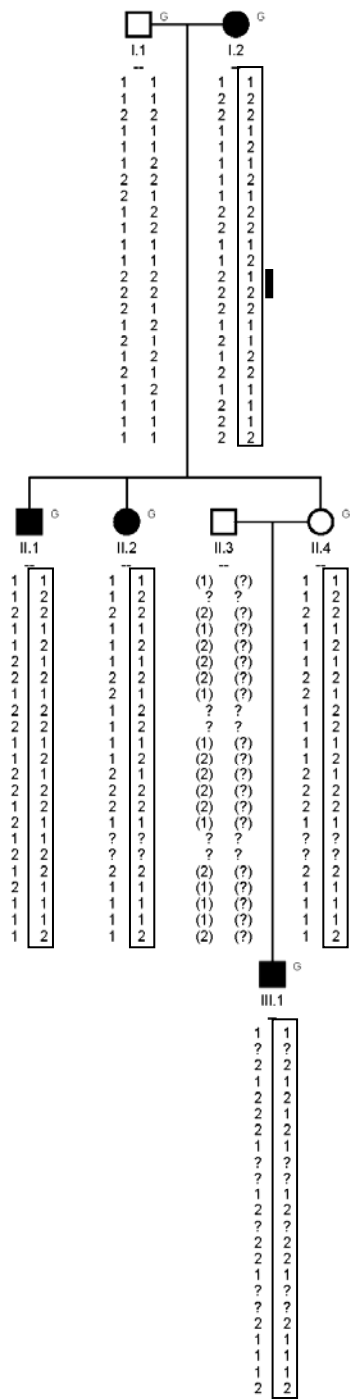
Family 23. Chromosome 11



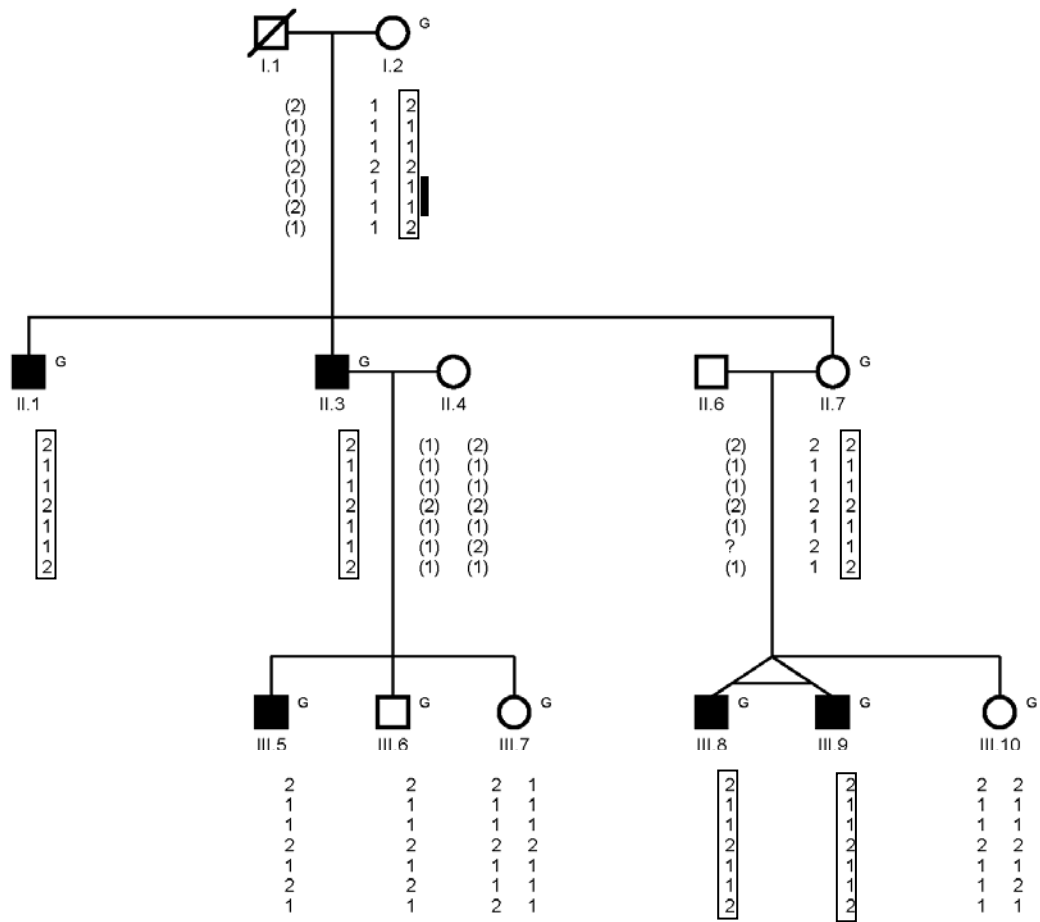
Family 29. Chromosome 11



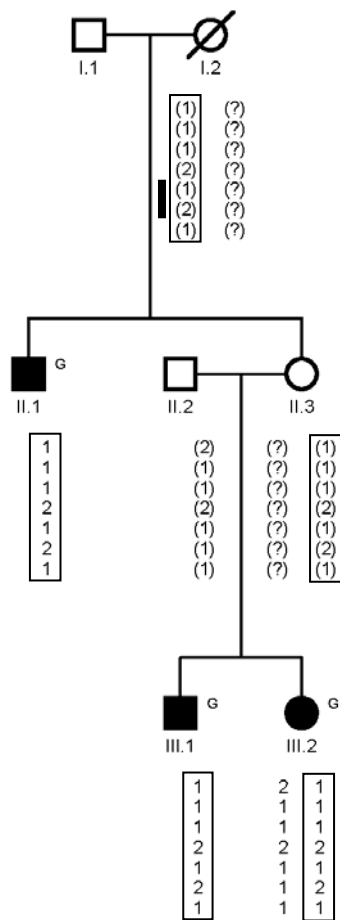
Family 93. Chromosome 11



Family18. X chromosome



Family 170. X chromosome



Genotyped individuals are marked with a G. Alleles in parentheses have been inferred. Genotypes given with question marks are unknown or of unknown phase. Disease-segregating chromosomal regions are boxed. SNPs which flank the proposed candidate genes, *TRPC6*, on chromosome 11, and *TRPC5*, on the X chromosome are shown with a black bar on just one ancestral disease-segregating chromosome.

Table S1. Z_{\max} Scores for All Analyzed Families for the Critical Regions on Chromosome 11 and the X Chromosome

Family Number	Chromosome 11	X Chromosome
1	2.44	-0.43
2	0.18	0.59
3	0.01	1
5	3.51	1
6	-0.54	
7	-0.59	-0.33
9	-0.86	-0.24
10	-0.3	
11	-0.33	0.53
13	0.56	-0.48
14	0.83	-0.35
15	3.43	1.29
16	1.26	1
17	-0.09	0.12
18	-0.2	3.68
19	1.72	
20	0.65	0.65
21	0.25	0.96
22	1.41	1
23	2.5	-0.06
25	1.41	1
26	1	0.12
27	1.76	1
28	1.1	1
29	2.45	-0.47
30	1.86	1.25
32	0	1
34	-0.54	0.51
39	1	1
76	1.41	-0.44
79	1.26	0.73
81	0.56	
84	0.05	0.35
86	1	0.58
93	2.09	-0.3
101	-0.31	-0.57
115	1	
119	0.46	0.42
131	-0.99	
135	0.3	
146	2.45	
162	1	-1
168	0.23	1.73
170	1.7	2.5
175	0.19	

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179	0.06	-0.44
184	-0.14	-0.21
192	-1.26	0.41
204	1.26	1
214	1.41	0.51
215	1.26	0.73
260	0.04	
262	0.64	1
278	0.54	0.8
288	1	-0.24
290	0	1
304	0.11	-0.16
319	1.17	0.52
326	0.05	0.85
327	1.73	1.29
333	-0.89	
345	-0.14	0.5
346	0.8	1
353	0.19	1
360	1.41	0.91
364	1.28	-0.31
365	1.34	-0.07
369	-0.06	0.41
373	-0.01	1
379	-0.45	
389	0.3	1
414	1.41	1
415	-0.97	0.79
420	-0.84	1
435	1.63	-0.41
441	0.02	0.4
457	1.73	-0.77
478	1	
479	1.08	0.64
481	0.99	1
485	0.85	0.51

Z_{\max} scores for the X chromosome are not available for those families not consistent with X-linked inheritance.