

SUPPLEMENTARY DATA

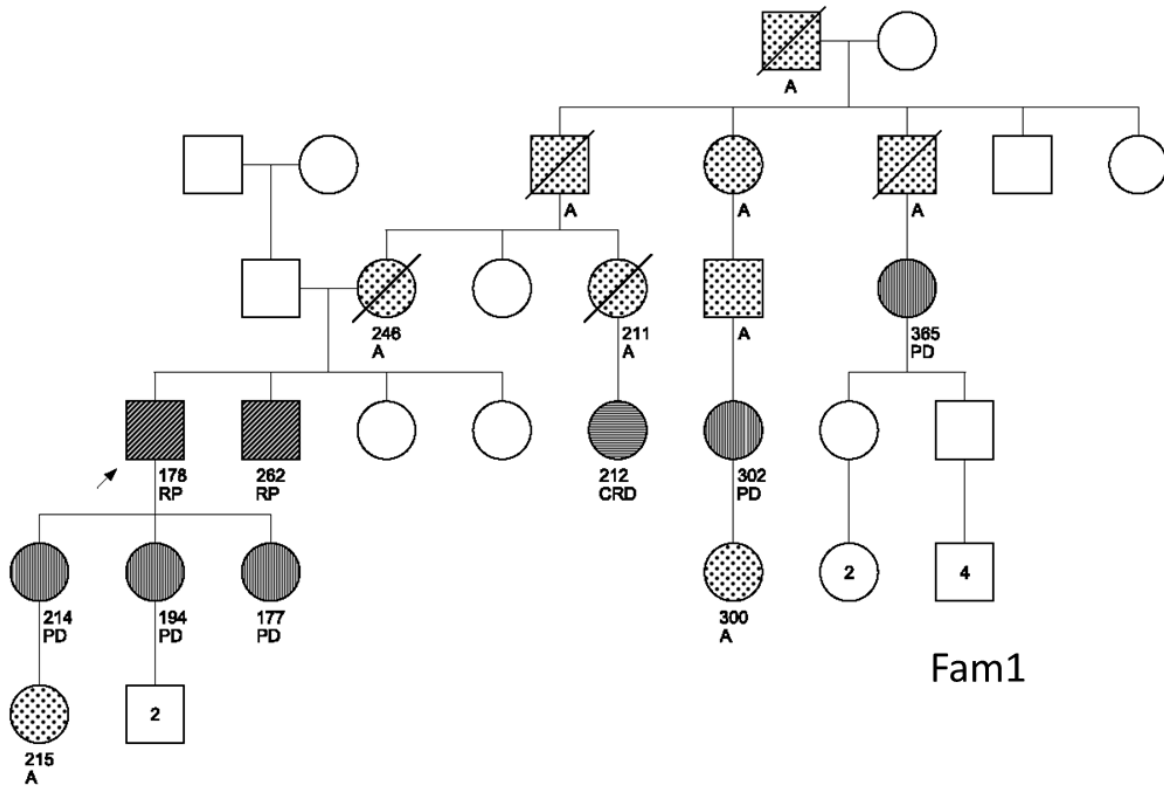
Exon	Primer sequences 5' to 3'	Size in bp
<i>ROM1</i>		
Ex 1A Forward	GGGGCTGACAGGGGGGCG	339
Ex 1A Reverse	GGGGCAGGACAGGGAACTG	
Ex 1B Forward	CCTGTCAGTTCCTGTCCTGC	450
Ex 1B Reverse	GAGGAAGGGAGACGCAAATCAC	
Ex 2 Forward	AGGCCTCTATCTCCAGACAT	450
Ex 2 Reverse	AGTCCCGGGTGGGAGGAGGT	
Ex3 Forward	CAACCCTGGGCCTCTTGGAA	403
Ex3 Reverse	GCCTTGTAAGGAGTTGTGA	
<i>GUCA1</i>		
Ex 3 Forward	ACAGCTCAAGGCTGTAATCC	598
Ex 3 Reverse	GGTCCCTCCAGCACTTCC	
Ex 4 Forward	GCCTGAGGCTGGAGTGAG	285
Ex 4 Reverse	TGTTCTAACCTGGGCTCTC	
Ex 5 Forward	CCCAATCCTACCCCTGAGAT	246
Ex 5 Reverse	CCTCTCCTTTAGTGACCTTCCA	
Ex 6 Forward	TGCTCTGGACTGCAGAAATG	476
Ex 6 Reverse	GCAGAGGGATGTTGAACAGTG	
<i>NXNL1</i>		
Ex 1 Forward	TGAAGTCCTAAGCTGGTTTTCT	489
Ex 1 Reverse	TTCACTTTCAGCGAACATGC	
Ex 2 Forward	GATCCGTCCAGACTGACCTG	384
Ex 2 Reverse	TCATCAACAAACCCCACTCC	

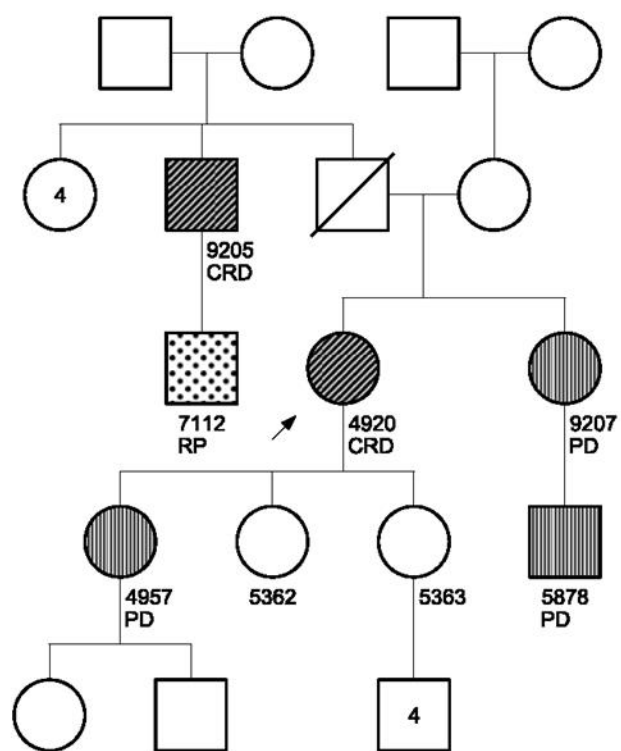
Supplement 1: Primers used for sequencing *ROM1*, *GUCA1*, and *NXNL1* genes.

Supplement 2: Figures for family pedigrees.

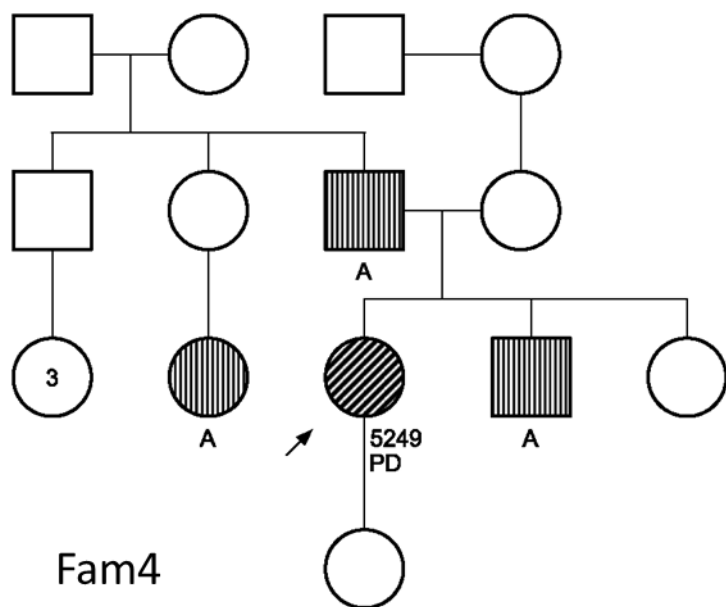
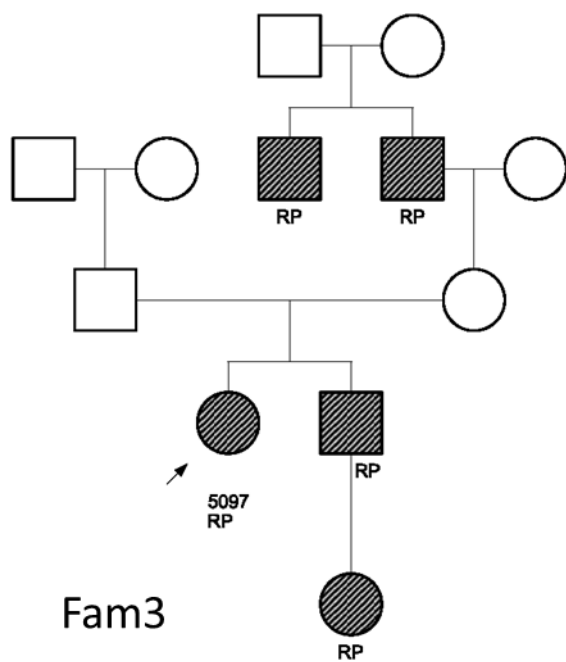
The phenotypes of affected individuals and pedigrees showing autosomal dominant inheritance with variable expressivity for 14 families (Fam1, Fam2, Fam3, Fam4, Fam5, Fam6, Fam7, Fam8, Fam11, Fam12, Fam13, Fam14, Fam15 and Fam16) are shown. Please refer to table 1 for phenotype and haplotype in *trans* data. In some families only single individuals were

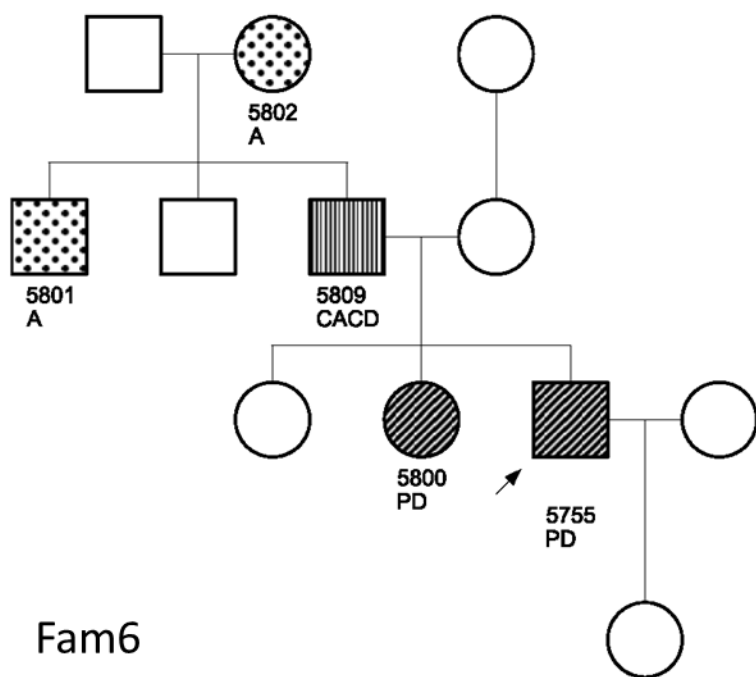
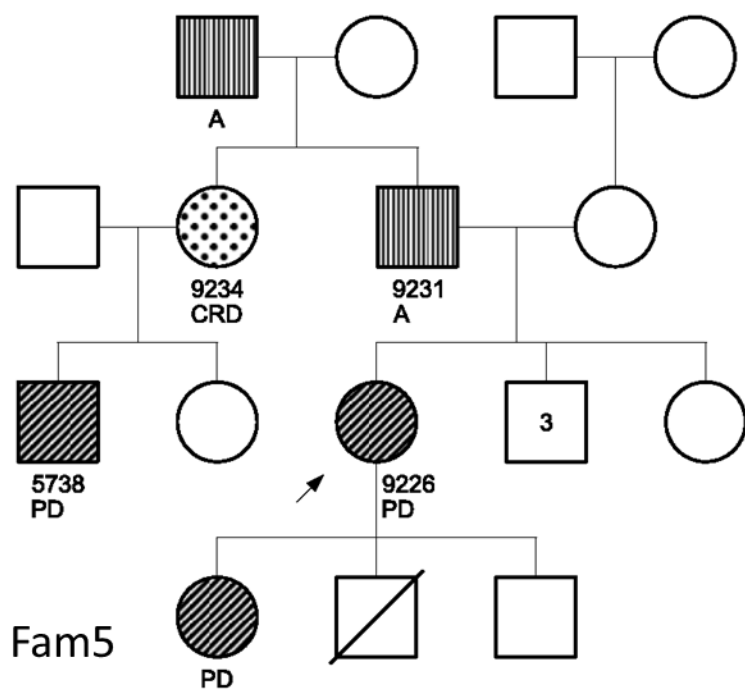
available for the study without pedigree information (Fam9, Fam10, Fam17, Fam18 and Fam19). Phenotypes are represented by PD –Pattern dystrophy, RP- retinitis pigmentosa, CRD – cone rod dystrophy, CACD- central areolar chorioretinal dystrophy, and A –affected, when an affected individual's fundus photo was not available for evaluation.

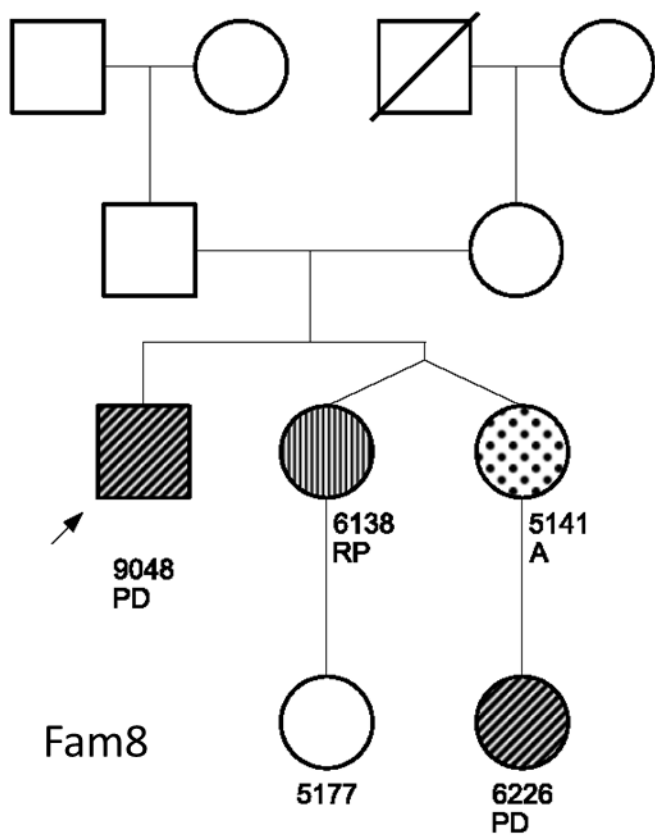
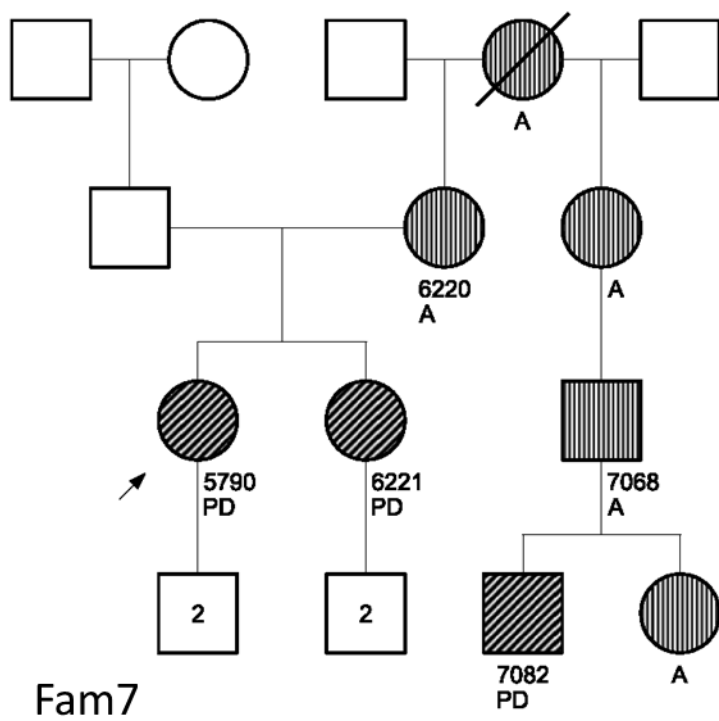


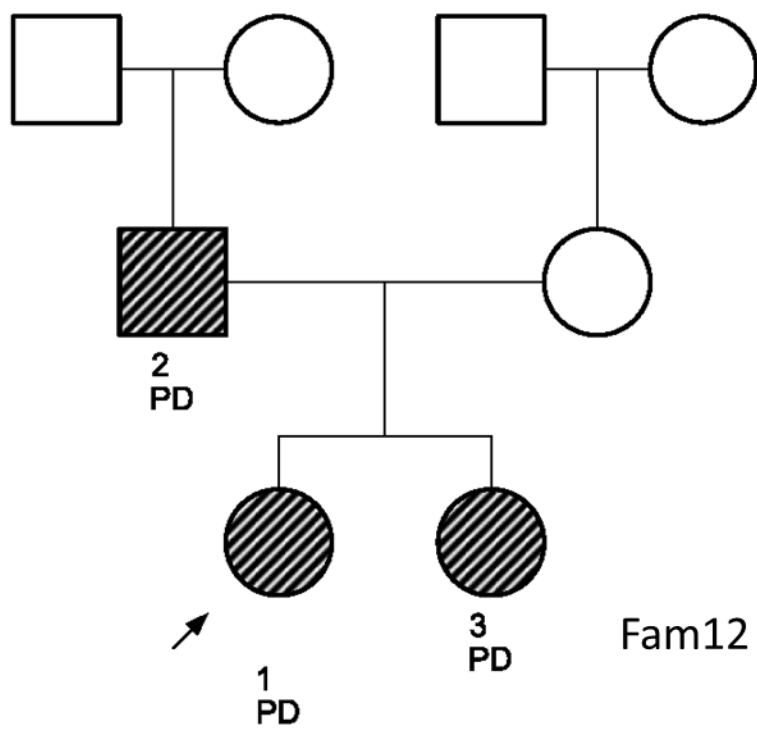
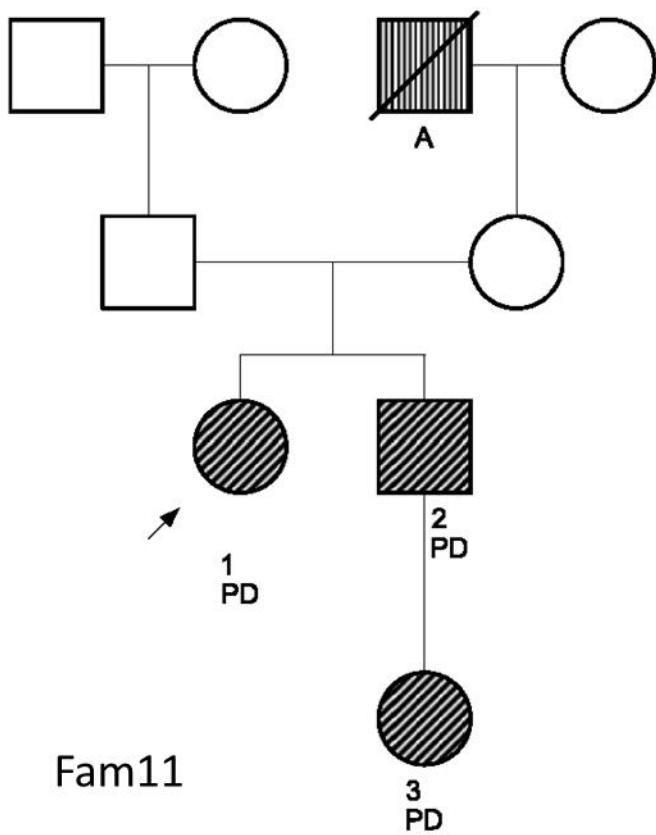


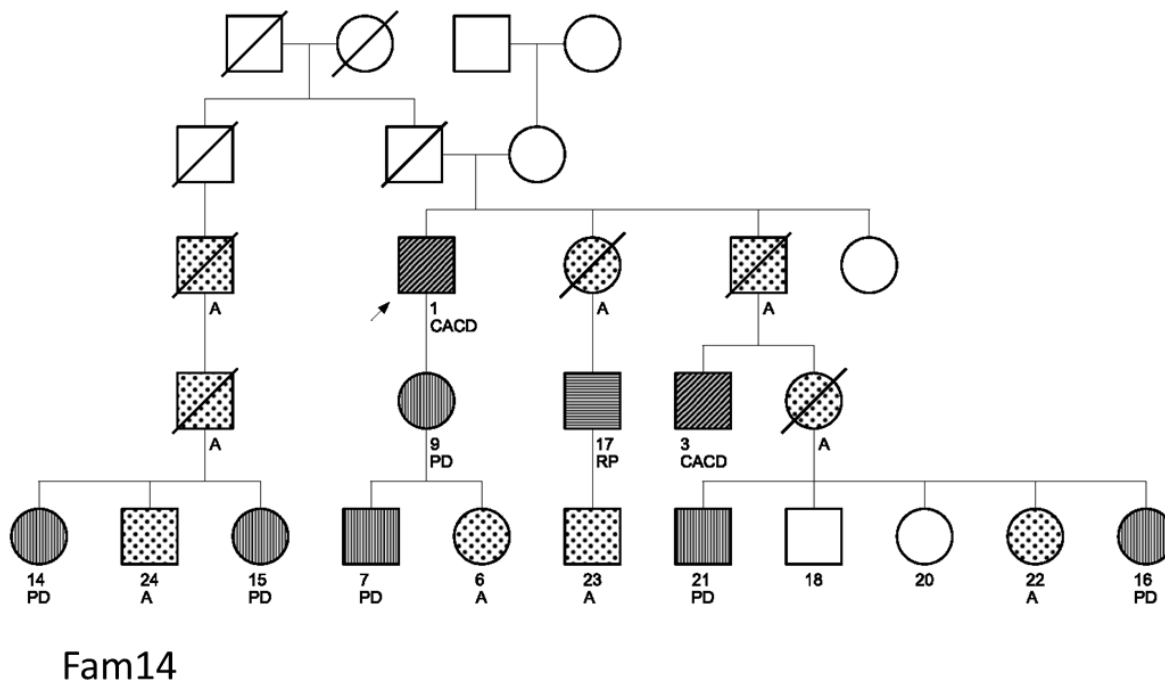
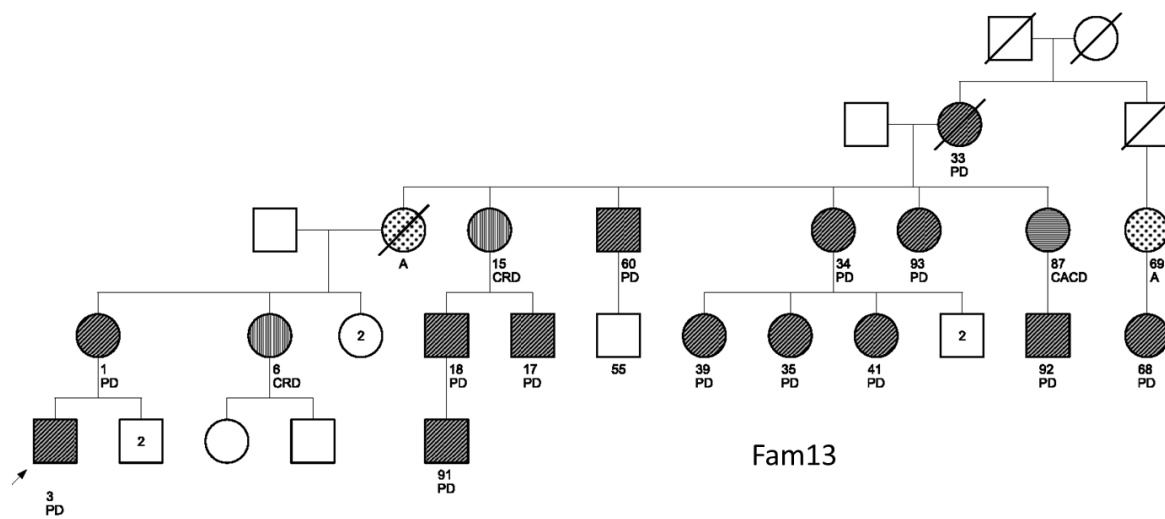
FAM2

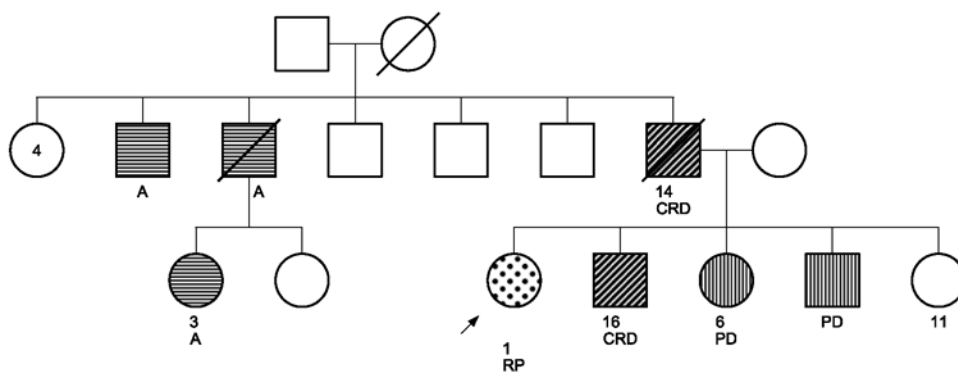




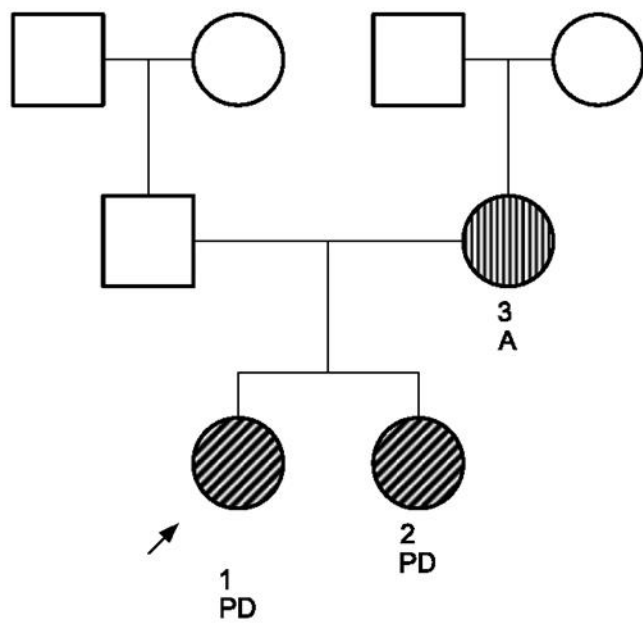








Fam 15



Fam16