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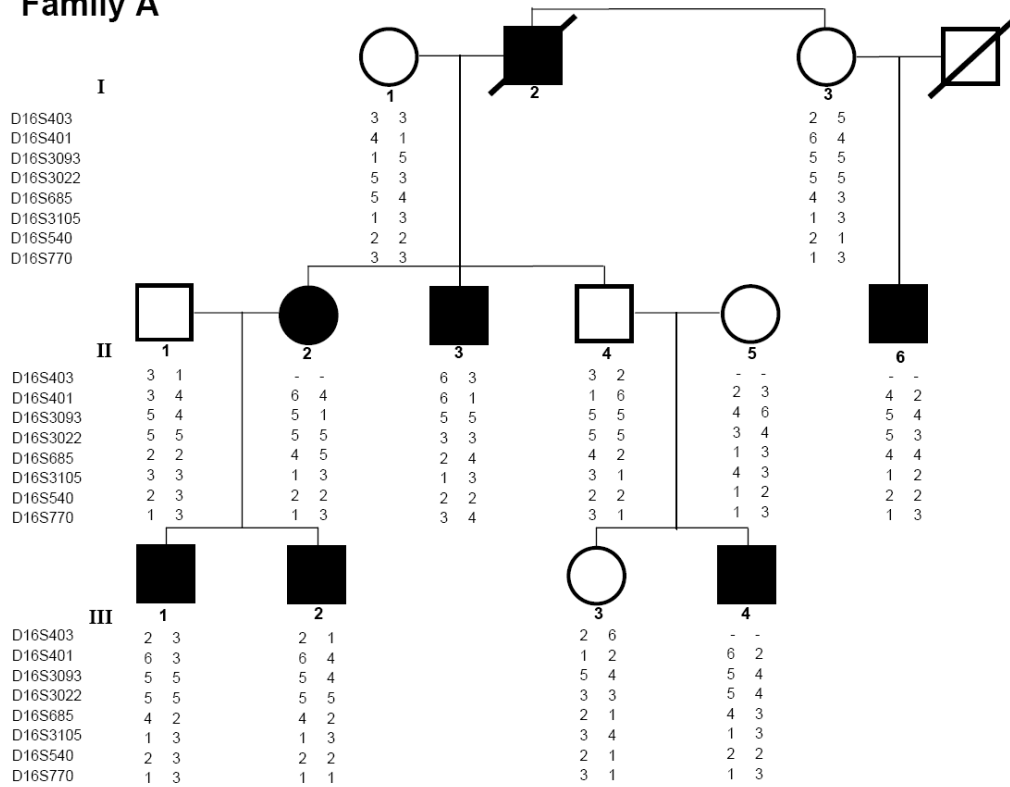
## **Supplemental Data**

### **Familial Pityriasis Rubra Pilaris Is**

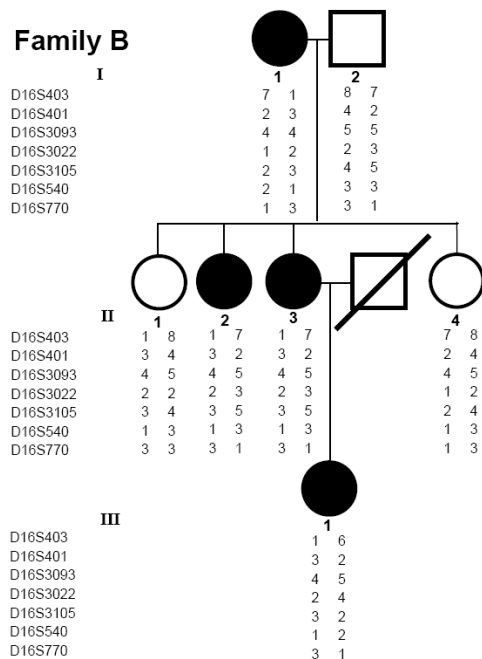
### **Caused by Mutations in *CARD14***

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### Family A



### Family B



### Family C

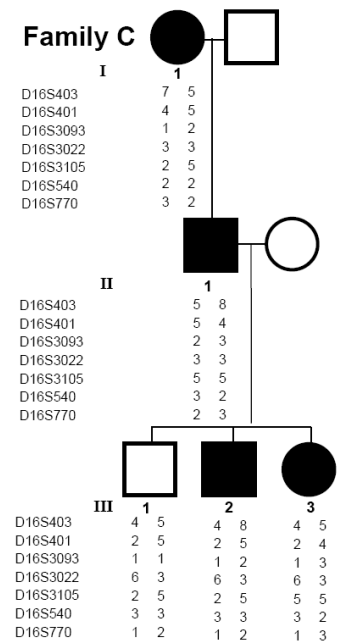


Figure S1. Haplotype Analysis on Chromosome 16

Haplotype analysis with polymorphic markers across the centromeric region of chromosome 16.

Table S1. Exome and Targeted-Capture Next-Generation Sequencing

Sample*	Platform	Total Reads	No. Aligned Reads	% Aligned	% Mapped to Targets	Average Coverage of the Targets	% Targets Covered at Least 10x
III4	Illumina Genome Analyzer IIx	16848189	10163867	60.3	7.2	8.7	25.5
II2	Illumina Genome Analyzer IIx	11595716	6216881	53.6	5.6	4.7	11.4
II4	Illumina Genome Analyzer IIx	15550166	8209894	52.8	3.5	3.9	9.7
II5	Illumina Genome Analyzer IIx	10020725	5876735	58.6	5.4	3.9	9.7
III4	SOLiD 3.5	84143687	63836967	75.9	55.7	41.1	82.6
II2	HiSeq2000	53635584	42157569	78.6	77.6	50.2	94.0

\* Targeted next generation sequencing was performed using DNAs from 4 members of Family A. Aligned reads are those that map to the hg19 reference genome while reads mapped to target are those aligned to the targeting "baits" according to the capture method