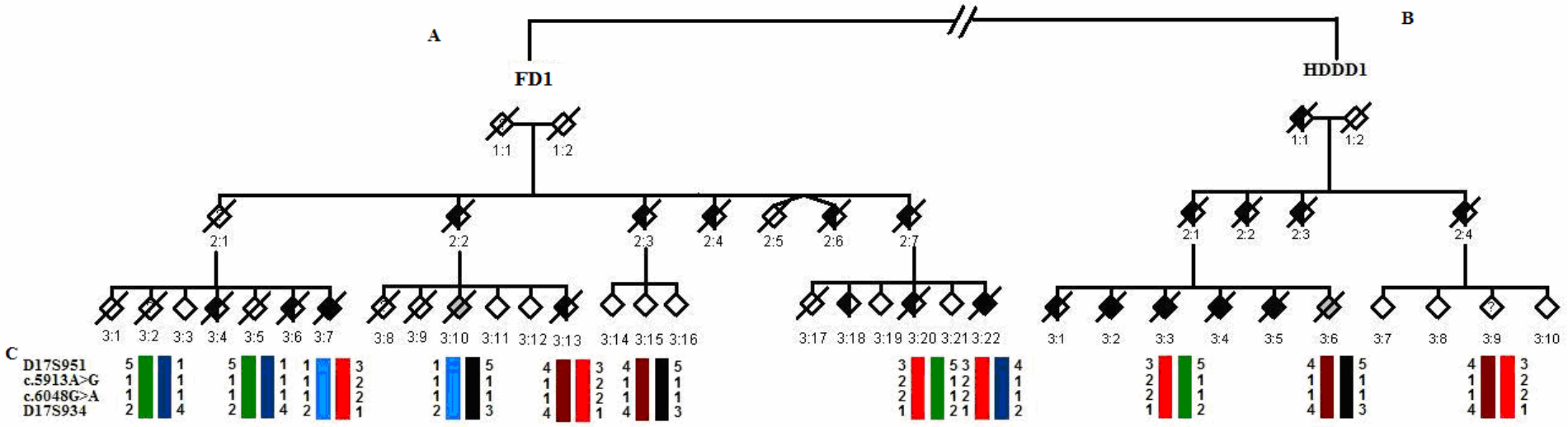
Supplementary Table and Figure

Supplementary Table S1. **List of non-pathogenic variants identified in this study**

Polymorphism	**No. of Subjects**	**Location in gene**
g.4141C>T (p.D33)	1	Ex 1
g.4450G>A	3	IVS 2
g.5059_5060insGTCA	1	IVS 3
g.6048G>A	3	IVS 7
g.77754C>T	7	3'UTR

All mutation numbering is based on the genomic DNA sequence. EnsEMBL gene ID: ENSG00000030582 (NCBI36:17:39778017:39785996:1).



Supplementary Figure S1. Mutational analysis. Segregation analysis of IVS6-2G>A transition within (A) FD1 kindred, (B) HDDD1 kindred. Affected and 50% of the at risk individuals are heterozygous for the mutation, (C) Haplotype analysis using two microsatellite markers flanking *GRN*, the pathogenic g.5913A>G (IVS6-2A>G) and a non-pathogenic variation in intron 7 (IVS7+8A>G) shows an unambiguous disease haplotype shared between the two kindreds**.**