Supplementary figure S1: Pedigree structure and segregation analysis of identified *ABCA4* sequence variants in the family. Showing segregation of *ABCA4* sequence variants M1: c.157G>A (p.(Glu53Lys)) and M2: c.2267C>T (p.(Ser756Phe)). (-) indicates reference allele, whereas M1 and M2 indicate the mutant alleles. The black arrow represents the patient.