

Table S1. *In silico* analysis to predict *ABCA1* variant pathogenicity according to AMCG guidelines

Variants <i>ABCA1</i> (NM_005502.4)	Inheritance	Population frequencies			Conservation Scores			Prediction Pathogenicity Scores		
		gnomAD	ExAC	1000 Genomes	GERP	PhyloP100way	PhastCons100way	DANN	Mutation Taster	FATHMM
c.4799A>G	Mother Father	-	-	-	5.20	8.017	1.000	0.9984	DC	D

DC: Disease causing; D: Damaging; WT: Wild Type