Supplementary Table 3. SIFT/PolyPhen predictions for rs1150781 and rs114591848

SNP ID	Chr:Pos	Allele	Consequence	Gene	Transcript ID	Codons (aminoacid)	SIFT consequence (score)	PolyPhen consequence (score)
rs1150781	6:34,214,322	G	Missense variant	*C6orf1* (*SMIM29*)	ENSG00000186577	GGG(Gly150)→ GCG(Ala150)	Deleterious (0)	Benign (0.015)
rs114591848	14:21,550,212	G	Missense variant	*ARHGEF40*	ENSG00000165801	CGG(Arg1062)→ CAG(Gln1062)	Tolerated9 (0.08)	possibly damaging (0.679)

All SNPs were annotated and imported from dbSNP (release 151) in European Molecular Biology Laboratory-European Bioinformatics Institute.
SIFT, sorting intolerant from tolerant; PolyPhen, polymorphism phenotyping; SNP, single nucleotide polymorphism; Chr, chromosome; Pos, position; *SMIM29*, small integral membrane protein 29; *ARHGEF40*, advanced glycosylation end-product specific receptor.

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