Suppl. Table II. *NLRP12* variant characteristics

Genomic position [a]	Chr19:54314056
Coding sequence alteration [b]	c.857C>T
Amino acid alteration	p.Pro286Leu
Allele count in the gnomAD database	40
Allele frequency in the gnomAD database	$1.42x10^{-4}$
SIFT [c]	0
LRT [d]	0.015882
GERP++ [e]	4.47
PhyloP [f]	0.944
Polyphen [g]	0.877
CADD [h]	23.1

Predictive analyses were performed with GATK analysis toolkit (Ref PMID: 20644199) and CADD (Ref PMID: 30371827)

[a] Positions refer to Hg19 (GRCh37).

[b] Positions refer to GenBank transcript NM_144687.4.

[c] Function prediction tool based on protein sequence conservation among homologs. Variants with scores between 0 and 0.05 are considered deleterious.

[d] DNA sequence evolutionary model expressed as a p-value.

[e] GERP++NR score: DNA conservation score.

[f] Vertebrate PhyloP scores. Values vary between -20 and +9.873. Sites predicted to be conserved are assigned positive scores, while sites predicted to be fast-evolving are assigned negative scores.

[g] Polyphen2_HDIV_score: variants with scores between 0.85 and 1.0 are predicted to be damaging with high confidence.

[h] CADDv1.3 scores ranges from 1 to 99, with a higher score indicating greater deleteriousness.