

**Supplementary Table 2. Population frequencies and *in silico* pathogenicity predictions for *GGPS1* variants reported in this study**

Gene	<i>GGPS1</i>	<i>GGPS1</i>	<i>GGPS1</i>	<i>GGPS1</i>	<i>GGPS1</i>
<b>Variant</b>	c.269A>G p.(Asn90Ser)	c.439A>G p.(Met147Val)	c.196A>C p.(Ill66Leu)	c.545T>C p.(Leu182Pro)	c.770T>G p.(Phe257Cys)
<b>Transcript</b>	NM_004837.4	NM_004837.4	NM_004837.4	NM_004837.4	NM_004837.4
<b>Rs-ID</b>	rs1012843795	rs1237799550	Absent	Absent	Absent
<b>gnomAD</b>	Absent	1 heterozygous allele out of 251328	Absent	Absent	Absent
<b>Iranome and GME</b>	Absent	Absent	Absent	Absent	Absent
<b>UK Biobank</b>	Absent	2 heterozygous alleles out of 537358	Absent	6 heterozygous alleles out of 537358	Absent
<b>Queen Square Genome database (23 000 exomes)</b>	Absent	Absent	Absent	Absent	Absent
<b>Centogene database</b>	1 heterozygous allele Centogene AF ~5.6 x 10 <sup>(-6)</sup>	2 heterozygous alleles	Absent	Absent	Absent
<b>TOPMed</b>	1 heterozygous allele	1 heterozygous allele	Absent	Absent	Absent
<b>ClinVar</b>	Not reported	Not reported	Not reported	Not reported	Not reported
<b>CADD PHRED score</b>	26.4	25.8	25	26	27.3
<b>GERP</b>	6.17	6.17	5.05	6.17	6.17
<b>SIFT score</b>	0.02 (Deleterious)	0.00 (Deleterious)	0.01 (Deleterious)	0.00 (Deleterious)	0.00 (Deleterious)
<b>PolyPhen score</b>	0.964 (Probably damaging)	0.946 (Probably damaging)	1 (Probably damaging)	0.999 (Probably damaging)	0.994 (Probably damaging)
<b>PROVEAN</b>	-5.0 (Damaging)	-3.73 (Damaging)	-1.88 (Neutral)	-6.55 (Damaging)	-6.98 (Damaging)
<b>FATHMM PRED</b>	Tolerated	Tolerated	Tolerated	Tolerated	Damaging
<b>LRT PRED</b>	Deleterious	Deleterious	Deleterious	Deleterious	Deleterious
<b>MetaLR score</b>	0.5429 (Damaging)	0.5090 (Damaging)	0.4605 (Tolerated)	0.6008 (Damaging)	0.5524 (Damaging)
<b>MutPred score</b>	0.859	0.728	0.776	0.734	0.751

<b>MutationAssessor score</b>	3.42 (High functional impact)	3.765 (High functional impact)	2.845 (Medium functional impact)	3.19 (Medium functional impact)	3.38 (Medium functional impact)
<b>REVEL score</b>	0.624	0.570	0.50	0.7039	0.7179
<b>ACMG</b>	PS4, PP1 (moderate), PM2, PP3 Likely pathogenic	PS4, PP1 (moderate), PM2, PP3 Likely pathogenic	PM2, PP3, PP4 VUS	PM2, PP3 VUS	PM2, PP3 VUS