Supplementary Table 1. In silico prediction of missense variants

Family no.	Gene	Nucleotide change[a]	Protein change[a]	PolyPhen-2[b]	SIFT	PROVEAN[c]
21	*ENG*	c.821C>T	p.Thr274Ile	Probably damaging (0.999)	Predict tolerated	Deleterious (–3.531)
6	*ACVRL1*	c.199C>T	p.Arg67Trp	Probably damaging (0.998)	Predict not tolerated	Deleterious (–3.694)
10	*ACVRL1*	c.925G>A	p.Gly309Ser	Probably damaging (0.999)	Predict not tolerated	Deleterious (–5.959)
12	*ACVRL1*	c.781G>C	p.Ala261Pro	Probably damaging (1.000)	Predict not tolerated	Deleterious (–4.293)
30	*ACVRL1*	c.605T>G	p.Val202Gly	Probably damaging (0.998)	Predict not tolerated	Deleterious (–6.296)
32	*ACVRL1*	c.1124A>G	p.Tyr375Cys	Probably damaging (1.000)	Predict not tolerated	Deleterious (–8.984)
38	*ACVRL1*	c.1005T>G	p.Asn335Lys	Probably damaging (1.000)	Predict not tolerated	Deleterious (–5.957)

[a]Reference sequences to describe variants are NC_000009.12 (*ENG* genomic DNA), NM_000118.3 (*ENG* coding DNA), and NP_000109.1 (ENG protein), NC_000012.12 (*ACVRL* genomic DNA), NM_000020.3 (*ACVRL* coding DNA), and NP_000011.2 (ACVRL protein). [b]The score is indicated in parentheses. [c]The score is indicated in parentheses and the cutoff value is –2.5.