Appendix 1. Results of *In silico* molecular genetic analysis of *KCNV2* mutations identified

Pt	Exon	Nucleotide substitution	Amino acid change	Hom/ het	Report	SIFT	Polyphen 2		HSF Matrix				Allelic frequency observed by EVS	Reference
						Prediction	Prediction	Hum var score (0-1)	Site affected	Wildtype CV	Mutant CV	CV % variation		
4	1	c.80G>A	p.Arg27His	Hom	This sudy	Intolerant	POD	0.680	Acceptor	85.2	85.69	No change (0.08%)	ND	db SNP (rs145731729)
1, 2, 3	1	c.529T>C	p.Cys177Arg	Het	This sudy	Intolerant	PRD	0.999	Donner	66.29	66.15	No change (-0.02%)	ND	
4	1	c.617G>C	p.Arg206Pro	Hom	This sudy	Intolerant	PRD	0.972	Acceptor	72.3	72.06	No change (-0.34 %)	ND	
1, 2, 3	2	c.1381G>A	p.Gly461Arg	Het	Friedburg *et.al*. 2011[27]	Intolerant	PRD	1.000	Acceptor	53.6	82.55	New site (54.0 %)	6/13006	db SNP (rs149648640)

Pt = patient; Hom = homozygous; Het = heterozygous; SIFT = sorting Intolerant from Tolerance; HSF = human splicing finder program; CV = consensus values; EVS = exome variant server; POD = possibly damaging; PRD = probably damaging; ND = not detected.

SIFT (version 4.0.4) results are reported to be tolerant if tolerance index ≥ 0.05 or intolerant if tolerance index < 0.05. Polyphen-2 (vision 2.1) appraises mutations qualitatively as Benign, Possibly Damaging or Probably Damaging based on the model's false positive rate. The cDNA is numbered according to Ensemble transcript ID ENST00000382082, in which +1 is the A of the translation start codon. Human splicing finder version 2.4.1 was applied to predict the effect of each variant on splicing. The results from HSF matrix indicate the values for the wild type and mutant sequences. The larger difference of values between the wild type and the mutant sequences indicates the greater change that the variant can affect on the splice site. EVS denotes variants in the Exome Variant Server, NHLBI Exome Sequencing Project, Seattle, WA, USA. [accessed 01/12/2012; http://snp.gs.washington.edu/EVS/]