eTable 1: Analysis of the detected *KCNC2* variants (**NM_139137)** by different prediction tools (marked in bold if deleterious, damaging, possibly damaging or disease causing). Protein variants in bold were functionally analyzed. Cadd phred of 20 or more marked in bold.

Pt. No	Mutations	Protein variants	SIFT (T, tolerated; D, deleterious)	Polyphen2 HVAR (B, benign, P; possibly damaging; D, probably damaging)	Polyphen HDIV (B, benign, P; possibly damaging; D, probably damaging)	MutationTaster (N, neutral; D, disease causing)	CADD phred
Group 1: strong pathogenic variants (*de novo*), 10/27							
1	c.C375G	**p.C125W**	**D**	**D**	**D**	**D**	**26.9**
2	c.A404G	**p.E135G**	T	**D**	**D**	**D**	**27.4**
3	c.G499T	p.D167Y	T	**D**	**P**	**D**	**29.5**
4	c.T656C	**p.F219S**	**D**	**P**	**D**	**D**	**28.2**
5/6	c.G1052A	p.R351K	**D**	**D**	**D**	**D**	**27.8**
7	c.T1145G	p.F382C	**D**	**D**	**D**	**D**	**25.1**
8	c.A1309G	**p.T437A**	**D**	**D**	**D**	**D**	**24.7**
9/10	c.C1310A	p.T437N	**D**	**D**	**D**	**D**	**25.6**
Group 2: mild pathogenic or modifying variants, 8/27							
11	c.A94G	p.T32A	**D**	**P**	**D**	**D**	**25.1**
12	c.C384A	p.D128E	T	**P**	**D**	**D**	**27.8**
13	c.C432G	p.D144E	**D**	**P**	**P**	**D**	**24.2**
14	c.G988A	p.V330M	T	**P**	**P**	**D**	**24.3**
15	c.G998C	p.S333T	T	**P**	**D**	**D**	**24.1**
16	c.A1393G	p.I465V	T	**D**	**D**	**D**	**22.9**
17	c.A1588C	p.N530H	**D**	**P**	**P**	**D**	**21.4**
18	c.C1907T	p.S636F	**D**	**P**	**D**	**D**	**28.2**

eFigure 1: Scheme of *K_V3.2* demonstrating the relation of the described variants including the clinical phenotype to functionally relevant areas of the channel.