

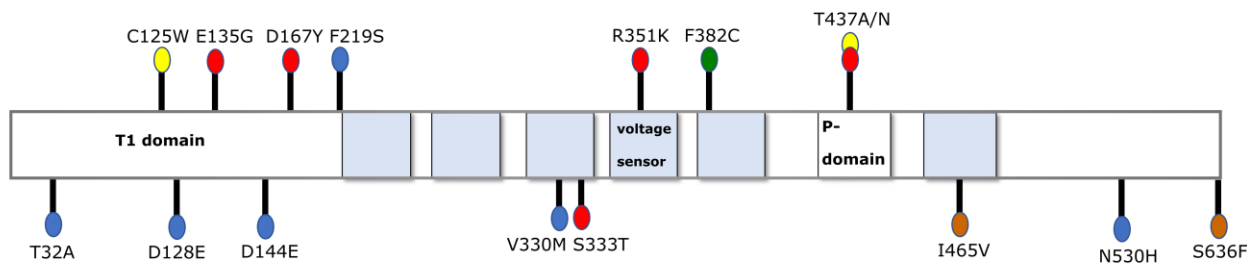
eTable 1: Analysis of the detected *KCNC2* variants (NM_139137) by different prediction tools (marked in bold if deleterious, damaging, possibly damaging or disease causing). Protein variants in bold were functionally analyzed. Cadd phred of 20 or more marked in bold.

| 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 (<i>de novo</i>), 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.

eFigure 1

**Strong pathogenic variants
(group1)**



**Mild pathogenic/modifying variants
(group2)**

- Transmembrane sections of *K_v3.2*
- Variants associated to genetic generalized epilepsy (GGE)
- Variants associated to developmental and epileptic encephalopathy (DEE)
- Variants associated to focal epilepsy (FE)
- Variants associated to early onset absence epilepsy (EOAE)
- Variants associated to Myoclonic-atonic epilepsy (MAE)