

**Table S1:** *In silico* prediction of the effects of missense *de novo* variant c.1411G>C (p.Val471Leu) in the *KCNC2* (KV3.2) gene.

<i>In silico predictive tool</i>	<i>Prediction/Score/PHRED-scaled</i>
PA_CADD_phred	27.3 (>30 highly pathogenic; >20 pathogenic)
PA_DANN_score	0.998239 (range from 0 to 1) *
PA_FATHMM_pred	DAMAGING
PA_GERP++_RS	6.06 (range from 12.3 to 6.17) *
PA_LRT_pred	Deleterious
PA_M-CAP_pred	DAMAGING
PA_MetaSVM_pred	DAMAGING
PA_MutationAssessor_pred	Low (non-functional)
PA_MutationTaster_pred	DAMAGING
PA_PROVEAN_pred	DAMAGING
PA_Polyphen2_HDIV_pred	Probably Damaging
PA_SIFT_pred	DAMAGING
PA_SiPhy_29way_logOdds	20.6397 (range from 0 to 37.9718) *
PA_fathmm-MKL_coding_pred	DAMAGING

\*A larger number indicates a higher probability to be damaging. Modified from ref. [15].