

Homozygous C-terminal loss-of-function Nav1.4 variant in a patient with congenital myasthenic syndrome

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Supplementary methods

This study was accepted and achieved under the ethical guidelines issued by our institutions for clinical studies and is in compliance with the Helsinki Declaration. Patient gave informed consent.

Targeted exon sequencing of a custom panel of 136 genes implicated in neuromuscular disorders (MYOdiagHTS panel) was performed using SureSelect Agilent capture and HiSeq2500 sequencing (Illumina). Mutation was confirmed by Sanger sequencing.

Long exercise test was performed in accordance with (1, 2).

Cell culture, transient transfections and patch clamp analysis in HEK293T cells were performed as in (3) except that open state inactivation was fitted with single exponential function. For analysis of current density data only cells with current amplitude larger than 100 pA were used. For analysis of biophysical parameters only cells with current amplitude larger than 300 pA were used. T-test and Mann-Whitney test were used for statistical comparisons.

Supplementary references

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2. Arzel-Hezode M, Sternberg D, Tabti N, *et al.* Homozygosity for dominant mutations increases severity of muscle channelopathies. *Muscle nerve*. 2010;41:470-7. doi.org/10.1002/mus.21520
3. Luo S, Sampedro Castaneda M, Matthews E, *et al.* Hypokalaemic periodic paralysis and myotonia in a patient with homozygous mutation p.R1451L in Nav1.4. *Sci Rep* 2018;8:9714. doi.org/10.1038/s41598-018-27822-2