# nature research

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Last updated by author(s):	Apr 21, 2022

## **Reporting Summary**

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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St	at	ıst	$1 \cap S$

FOI	ali StatiSticai ari	alyses, commit that the following items are present in the figure legend, table legend, main text, or Methods section.		
n/a	Confirmed			
	The exact	sample size $(n)$ for each experimental group/condition, given as a discrete number and unit of measurement		
	🔀 A stateme	ent on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly		
	The statis	tical test(s) used AND whether they are one- or two-sided on tests should be described solely by name; describe more complex techniques in the Methods section.		
$\boxtimes$	A descript	ion of all covariates tested		
	A descript	ion of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons		
	A full desc	cription of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) tion (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)		
	For null hy Give P valu	ypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted es as exact values whenever suitable.		
$\times$	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings			
$\times$	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes			
$\boxtimes$	Estimates of effect sizes (e.g. Cohen's d, Pearson's r), indicating how they were calculated			
	'	Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.		
Software and code				
Policy information about <u>availability of computer code</u>				
Da	ata collection	not applicable		

Electrophysiology data were analysed using Clampfit 9.2 (Molecular Devices). Statistical evaluation of data was performed using GraphPad

#### Data

Data analysis

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

Prism version 9 (La Jolla, CA, USA). Figures were created using Origin 9.0 (Microcal Software Inc., Northampton, MA).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request of any qualified investigator for purposes of replicating procedures and results.

Field-specific reporting				
•		the best fit for your research. If you are not sure, read the appropriate sections before making your selection.		
□ Life sciences	В	ehavioural & social sciences		
For a reference copy of t	he document with a	all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
Life scier	nces stu	ıdy design		
All studies must dis	close on these	points even when the disclosure is negative.		
Sample size		of the biophysical properties of heterologously expressed Nav1.2 channel variants, we collected data from at least three insfections. For each variants, a minimum of six cells were assessed.		
Data exclusions	study; cells expr	r ovarian (CHO) cells of 12–25 pF cell capacitance and expressing 2–10 nA peak Nav1.2 currents (INa) were included in the essing small INa (< 2 nA, ~20 % of cells) or large INa (>10 nA, ~20 %) were excluded, according to a previously published ki et al. 2018. Proc Natl Acad Sci U S A 115, E5516-E5525, doi:10.1073/pnas.1800077115).		
Replication	individual variar	data included in this study is reproducible. This has been confirmed in transfections repeated at least three times for each and included in the study. Notably, the biophysical data obtained for the wild-type (control) Nav1.2 channel in this study is reviously published data (Berecki et al. 2018. Proc Natl Acad Sci U S A 115, E5516-E5525, doi:10.1073/pnas.1800077115).		
Randomization	Individual chanr conditions.	nel variants (mutants) were simultaneously studied with the wild-type Nav1.2 channel to maintain identical experimental		
Blinding	ding Blinding was not used in this study.			
Reporting for specific materials, systems and methods  We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.				
Materials & exp	perimental sy	ystems Methods		
n/a Involved in th	e study	n/a Involved in the study		
Antibodies		ChIP-seq		
Eukaryotic	Eukaryotic cell lines			
	ogy and archaeol			
	Animals and other organisms			
Human research participants  Clinical data				
	search of concer	1		
Eukaryotic c	ell lines			
Policy information a	about <u>cell lines</u>			
Cell line source(s)	)	Chinese hamster ovarian (CHO) cells.		
Authentication CHO cells are commer		CHO cells are commercially available for research and our cells were not specifically authenticated.		
Mycoplasma con	tamination	The CHO cells used tested negative for mycoplasma contamination. In our laboratory, mycoplasma testing is carried out every three months.		
Commonly miside (See <u>ICLAC</u> register)	Commonly misidentified lines (See ICLAC register)			

### Human research participants

Policy information about <u>studies involving human research participants</u>

Population characteristics This information is provided detailed in the Supplementary Data 1 file.

Recruitment The medical literature, the SCN2A International Natural History Study (NHS) database, the Florey Institute's Ion Channels

Recruitment

Laboratory database, and the Simons Searchlight database (SSDb) (https://www.sfari.org/resource/simons-searchlight/) were searched to identify all recurrent SCN2A variants with clinical information available on affected individuals. Details on patient selection are provided in the main manuscript and Supplementary Methods.

Ethics oversight

The study was approved by the Human Research Ethics Committees of the Royal Children's Hospital and Austin Health Melbourne, University Medical Center Groningen, State Medical Association of Berlin, and the Simons Foundation. Written informed consent was obtained for all individuals whose previously unpublished clinical data is presented here.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

#### Clinical data

Policy information about <u>clinical studies</u>

 $All \ manuscripts \ should \ comply \ with \ the \ ICMJE \ \underline{guidelines \ for \ publication \ of \ clinical \ research} \ and \ a \ completed \ \underline{CONSORT \ checklist} \ must \ be \ included \ with \ all \ submissions.$ 

Clinical trial registration	Not applicable
Study protocol	Clinical information was collected as described in Methods of the manuscript.
Data collection	See above (recruitment)
Outcomes	Not applicable