

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm 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 statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

Data analysis

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 Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical methods were used to pre-determine sample sizes but our sample sizes are similar to those reported in previous publications (Refs. 18,31,34,42,48).
Data exclusions	No data were excluded from the analyses, except for patch recordings when experiments were incomplete because the patch had ruptured during the experiments.
Replication	Patch-clamp data derives from independently measured out-side-out patches. Electrophysiology and gating compliance data derives from the same, independently measured animals.
Randomization	Experiments were randomized with respect to genotypes and stimulation amplitudes.
Blinding	Investigators were blinded initially for genotypes during experiment and outcome assessment, yet blinding was given up in the course of the study because it turned out to be in-effective as genotypes could be inferred easily from phenotypes.

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 & experimental systems

n/a	Included in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	FluoTag®-X4 Atto 488nm anti-GFP (1:1000, NanoTag Biotechnologies, N0304) Cy3-conjugated goat anti-HRP (1:300, Jackson ImmunoResearch, 123-165-021) rabbit anti-NOMPC-EC (kindly provided by Yuh-Nung Jan, 1:500) Alexa Fluor 488 goat anti-rabbit (Thermo Fisher Scientific, A-11008, 1:1000)
Validation	anti-NOMPC-EC (Zhang et al., 2015), anti-HRP (Katana et al. 2019), anti-GFP confirmed with in vivo localization of NOMPC in S2 cells and at the tip of the cilium (see Extended Data Figs. 1a and 2).

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	Schneider's Drosophila Line 2 [D. Mel. (2), SL2] (ATTC CRL-1963)
Authentication	Proof of cell line authentication was provided by the vendor (ATCC, CRL-1963). In addition, we examined the morphology of the cells and observed the successful expression of the fusion proteins with the Gal4/UAS-System (Act5c>Gal4 plasmid and UAST-attP-constructs)
Mycoplasma contamination	Mycoplasma contamination is routinely checked every 4 months (MycosPY® Master Mix, Biontex). PCR tests were negative throughout.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in the study.

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	Drosophila melanogaster, adults (2-5 after eclosure)
Wild animals	No wild animals were used in this study.
Reporting on sex	Flies of either sex were used as neither Johnston's organ function nor auditory mechanics seem to be sex-specific.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	Dealing with an invertebrate species, no ethical approval was needed. Experiments were carried out in accordance with German Federal Regulations (license Gen.Az 501.40611/0166/501).

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