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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.

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	X-ray diffraction data were indexed, integrated, and scaled with XDS (version Jan 31, 2020; built=20200417); CryoEM data were collected using the SerialEM software (version 3.8.7); Biological Image analysis was performed with ImageJ. Data collection from images was entered into Microsoft Excel (version 16.58, 22021501) for analysis. Alignments were done with ClustalOmega (Version 1.2.2). No custom codes were used for data collection.
Data analysis	CryoEM data analysis was conducted using Relion (version 3.1.1), CTFFIND4 (version 4.1.13) and cryoSPARC (version 3.3.1). Model building and refinement for cryoEM and crystal structures were carried out using COOT (version 0.8.9.2) and PHENIX (version 1.19.2-4158), respectively. Mass spectrometry data were analyzed using the Analyst TF1.5 software (version 1.5). X-ray fluorescence data were analyzed using the DppMCA software (version 1.0.0.22). Plotting and statistical analysis of biological data were performed with GraphPad 9 (version 9.0.0 (86)). No custom codes were used for 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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The data supporting the findings of this study are available within the paper and its Supplementary Information. The cryo-EM structures of the apo NPR1, NPR12-

TGA32, and TGA32-NPR12-TGA32, and X-ray crystal structures of the NPR1(del)SBD and TGA3 NID have been deposited to the Protein Data Bank (www.pdb.org) with PDB access codes of 7MK2, 7TAD, 7TAC, 7MK3, 7TAE, respectively. The cryo-EM density maps of apo NPR1, NPR1-SA, NPR12-TGA32, and TGA32-NPR12-TGA32 have been deposited to EMDB under the access codes of EMD-23884, EMD-23885, EMD-25771, and EMD-25769, respectively. The datasets generated and/or analysed during this study are available as Source Data. All source data are included in the paper. There are no restrictions on data availability.
For material requests, please contact the corresponding authors.

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	The appropriate sample size was determined based on previous studies (e.g. Zavaliev et al: Cell 2020, 162, 1-16). Minimum of three plants were sampled per each biological repeat. Samples collected from each biological repeat were pooled to perform statistical analyses.
Data exclusions	No data points were excluded in the biological experiments
Replication	All experiments were repeated at least twice with similar results.
Randomization	Genotypes or expression variants were randomly sampled and the samples were gathered into experimental groups for which the analyses were performed.
Blinding	No blinding was used during experimentation because a specific developmental stage and/or tissue section had to be used for sample collection.

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	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	1) anti-GFP: Clone Living Colors® A.v. Monoclonal Antibody (JL-8), Takara Bio Clontech. Mouse monoclonal Ab (cat# 632381; RRID: AB_2312808; Lot: A80344133). Dilution 1:5000 2) anti-HA BioLegend. Mouse monoclonal Ab, clone 16B12 (cat#901513; RRID:AB_2820200; Lot:B272923). Dilution 1:1000 3) HRP Goat Anti-Mouse IgG (H+L); Abcam, (cat#Ab97040; RRID: AB_2769851; Lot:GR3356071.1). Dilution 1:20000 4) anti-RFP: ChromoTek. Mouse monoclonal Ab (cat# 6G6; RRID: AB_2631395; Lot: 51020014AB). Dilution 1:5000 5) anti-cMyc: Santa Cruz (clone SC-40). Mouse monoclonal Ab(cat# 9E10; RRID: AB_627268; Lot: H0219). Dilution 1:1000 6) anti-GST-HRP. Rabbit polyclonal Ab. Cytiva (cat# RPN1236; RRID: AB_771429; Lot: 17007382). Dilution 1:10000
Validation	1) anti-GFP, Takara. Validation and certificate of analysis: https://www.takarabio.com/documents/Certificate%20of%20Analysis/632380/632380-632381-070313.pdf 2) anti-HA BioLegend. Mouse monoclonal Ab, clone 16B12 (cat#901513; RRID:AB_2820200; Lot:B272923) certificate of analysis: https://www.biolegend.com/Default.aspx?Id=18924 3) anti-RFP ChromoTek, Mouse monoclonal Ab (cat# 6G6; RRID: AB_2631395; Lot: 51020014AB): https://www.chromotek.com/fileadmin/content/PDFs/Data_Sheets/6g6_Datasheet_RFP_antibody__6G6.pdf 4) anti-GST-HRP. https://www.cytivalifesciences.com/en/us/shop/protein-analysis/blotting-and-detection/blotting-standards-and-reagents/anti-gst-hrp-conjugate-p-05747#tech-spec-table 5) anti-cMyc Santa Cruz. https://datasheets.scbt.com/sc-40.pdf

6) HRP Goat Anti-Mouse IgG (H+L); Abcam, (cat#Ab97040) https://www.abcam.com/goat-mouse-igg-hl-hrp-preadsorbed-ab97040.html

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Sf9 (Expression Systems; catalog #: 94-001F) and Tni (Expression Systems; catalog #: 94-002F) insect cells were used for baculovirus amplification and recombinant protein expression respectively.
Authentication	Cells have been authenticated by the vendors. No further authentication was performed for commercially available cell lines.
Mycoplasma contamination	Cells were not tested for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.