nature portfolio

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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	SerialEM 3.0, EPU 3.1
Data analysis	MotionCor2 1.6.3, cryoSPARC 4, Relion 4, Alphafold 2, COOT 0.9.8, Phenix 1.13, MolProbity 4.2, PyMOL 2.5.4, Prism 9.00, Chimera 1.17, ChimeraX 1.6, ImageJ 1.54f

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

Cryo-EM density maps of VANGL1, VANGL2, VANGL1-PK1, VANGL1-PK1(745-790), and VANGL2-PK1(745-790) have been deposited in the Electron Microscopy Data Bank under the accession codes EMD-61545 [https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-61545], EMD-61546 [https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-61546], EMD-61547 [https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-61547], EMD-61548 [https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-61548], and EMD-61549 [https://www.ebi.ac.uk/pdbe/entry/emdb/EMD-61549]. Their atomic coordinates have been deposited in the Protein Data Bank under accession codes

9JK6 [https://doi.org/10.2210/pdb9JK6/pdb], 9JK7 [https://doi.org/10.2210/pdb9JK7/pdb], 9JK8 [https://doi.org/10.2210/pdb9JK8/pdb], 9JK9 [https://doi.org/10.2210/pdb9JK9/pdb], and 9JKA [https://doi.org/10.2210/pdb9JKA/pdb]. The previously published structure utilized for analysis in this study can be accessed in the Protein Data Bank under accession code 7CHQ [https://doi.org/10.2210/pdb7CHQ/pdb].

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	Statistical methods were not used to determine sample size. The data size for cryo-EM experiments was determined by the availability of microscope time and the particle density on the grids. Sufficient cryo-EM data were collected to achieve the reported resolution of 3D reconstructions. For functional experiments, the sample size was at least three, adhering to common practice in the field and striking a reasonable balance between statistical robustness and practicality.
Data exclusions	Cryo-EM data processing involved removing poor-quality particle images to achieve high-resolution 3D reconstructions through established classification procedures.
Replication	Biochemical experiments, including protein purification and SDS-PAGE analyses, were conducted at least three times. Despite some degree of variability in protein yield, the profiles of chromatography and SDS-PAGE were reproducible. Functional experiments were also repeated at least three times with independent samples, consistently yielding comparable results and reaffirming the reproducibility.
Randomization	Randomization was not used in this study as the specific types of experiments conducted do not necessitate it; they are not influenced by the sample allocation processes common in other research methods.
Blinding	Blinding was not used in this study as subjective analysis was not needed. Each experiment was analyzed using consistent methods. Quantitative measurements using various approaches as described in the methods minimized biased assessment.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	Anti-Paxillin (1:4000, BD, 610052); Goat anti-Mouse IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor™ 647 (1:500, Invitrogen, A21235)
Validation	All the antibodies are commercial and have been validated by the manufacturers. The validation statements are available on each manufacturer's website.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HEK-293S GnTI– (ATCC CRL-3022), Sf9 (ATCC CRL-1711), U2OS (ATCC HTB-96).
Authentication	No further authentication was performed for commercially available cell lines.
Mycoplasma contamination	Periodically test negative.
Commonly misidentified lines (See ICLAC register)	None of the cell lines used is listed in the database of commonly misidentified cell lines maintained by ICLAC.

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A