

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 [Authors & Referees](#) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 All commercial DNA and RNA sequencing platforms used in this study are fully described.

Data analysis 2018 versions of, Microsoft Office Excel, MECAT, Quiver, Juicebox, GATK, Joinmap 5.0, MapDisto 2.0, Axiom Analysis Suite Software, Joinmap 4.1, Blast, SINE-finder, MITE-hunter, RepeatMasker, Trinity, Kallisto, MAKER 2.31.9, SNAP, AUGUSTUS, InterProScan, Mummer, Bowtie2 v2.2, DAGchainer, Integrative Genomics Viewer, Samtools, Perl, Biopython, Unix. As cited in manuscript

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/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 datasets generated during and/or analyzed for this study are available in Supplementary Data, the public repository of the National Center for Biotechnology Information (NCBI; <https://www.ncbi.nlm.nih.gov>), the open access internet site PeanutBase (<https://peanutbase.org/>). Genome assemblies and annotations, identified transposable elements, transcript assemblies, base methylation states and map data are available at Peanutbase (https://peanutbase.org/peanut_genome). *Arachis hypogaea* cv. Tifrunner sequence reads are archived in NCBI under BioProject PRJNA419393, the genome assembly has GenBank accession numbers CM009801–CM009820. Small RNA sequences are deposited with NCBI Sequence Read Archives SAMN06658954, SAMN06658955, SAMN06658956. Whole genome sequence data of diverse accessions are deposited in the Sequence Read Archive of NCBI, Bioproject IDs: PRJNA525866, PRJNA511155 and PRJNA490832.

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](https://www.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	Genomes from individual plants were analyzed.
Data exclusions	No data exclusions. Sequencing data was quality filtered, as described in manuscript.
Replication	Genomes from individual plants were analyzed, replication not applicable.
Randomization	Randomization is not relevant to our study. Taxonomic classifications were used for ordering data presentations.
Blinding	Blinding was not applicable for 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 & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	No laboratory animals were used in the study
Wild animals	No wild animals were used in the study
Field-collected samples	Samples were from greenhouse grown plants
Ethics oversight	No ethical approval was required for studying greenhouse grown plants.

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