nature portfolio

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Last updated by author(s): Jun 30, 2022

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	DNA-seq raw NGS data was generated by sequencing using the Illumina Hiseq 2500 platform. DNA-seq raw pacbio data were generated by sequencing using the Pacbio sequel II. BioNano optical map were generated on the Irys (BioNano Genomics) imaging instrument. RNA-seq raw data were generated by sequencing using the Illumina Hiseq2500 platform.
Data analysis	All softwares used in the present study are publicly available and the corresponding software versions were described in detail in the Methods and Supplementary Text. 1. GenomeScope 2.0 v1.0.0 https://github.com/schatzlab/genomescope 2. fastp v0.20.1 https://github.com/OpenGene/fastp 3. Jellyfish v2.1.3 https://github.com/gmarcais/Jellyfish 4. Canu v2.2 https://canu.readthedocs.io/en/latest/ 5. HERA v1.0 https://github.com/liangclab/HERA 6. BioNano Solve program v3.7.1: https://s3.amazonaws.com/www.bnxinstall.com/access/tools/access.tools.tgz 7. Juicer v1.6: https://github.com/aidenlab/juicer 8. 3D-DNA v180922: https://github.com/aidenlab/3d-dna 9. Juicebox v2.10.01:https://github.com/aidenlab/Juicebox/releases/tag/2.10.01 10. RepeatModeler v1.0.8 http://www.repeatmasker.org/RepeatModeler/ 11. RepeatMasker v4.0.5 http://repeatmasker.org/ 12. LTR_Finder v1.07 https://github.com/xzhub/LTR_Finder 13. LTRharvest in genometools v1.61 https://github.com/genometools/genometools/issues 14. LTR_retriever v2.7 https://github.com/oushujun/LTR_retriever 15. MUSCLE v3.8.31 https://www.ebi.ac.uk/Tools/msa/muscle/

16. EMBOSS v6.6.0 http://emboss.sourceforge.net/
17. Blast2GO v2.5 https://www.blast2go.com/
18. KEGG Automatic Annotation Server V2.1:https://www.genome.jp/kaas-bin/kaas_main
19. BLAST+ v2.2.26 ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/
20. MCScanX v1.0 https://github.com/wyp1125/MCScanx
21. ksrates v1.1.1 https://github.com/VIB-PSB/ksrates
22. mclblastline pipeline v.10-201 https://bioweb.pasteur.fr/docs/modules/mcl/12-068/mclblastline.html
23. BLASTP v.2.6.0+ https://blast.ncbi.nlm.nih.gov/Blast.cgi
24. PAML package V4.9 http://abacus.gene.ucl.ac.uk/software/paml.html
25. wgd V1.01 https://wgd.readthedocs.io/en/latest/index.html
26. Fasttree v2.1.11 http://www.microbesonline.org/fasttree/
27. i-ADHoRe v.3.0.01 https://github.com/VIB-PSB/i-ADHoRe
28. Orthofinder v2.4.0 http://www.stevekellylab.com/software/orthofinder
29. iTAK v18.12 http://itak.feilab.net/cgi-bin/itak/index.cgi
30. HISAT2 v2.1.0 http://daehwankimlab.github.io/hisat2/download/
31. StringTie v1.3.5 https://ccb.jhu.edu/software/stringtie/
32. edgeR R package v3.20.9 https://bioconductor.org/packages/release/bioc/html/edgeR.html
33. WGCNA v1.68 https://horvath.genetics.ucla.edu/html/CoexpressionNetwork/Rpackages/WGCNA/
34. Cytoscape v3.7.1 https://cytoscape.org/
35. InterProscan v5.21-60.0 http://www.ebi.ac.uk/interpro/download/
36. Genewise v2.2.0 https://www.ebi.ac.uk/seqdb/confluence/display/THD/GeneWise
37. PASA v2.4.1 http://pasapipeline.github.io/
38. Augustus v3.2.2 https://github.com/Gaius-Augustus/Augustus
39. GlimmerHMM v3.0.4 http://ccb.jhu.edu/software/glimmerhmm/
40. SNAP v2013-02-16 https://github.com/KorfLab/SNAP
41. EVidenceModeler v1.1.0 https://evidencemodeler.github.io/
42. BLAT https://genome.ucsc.edu/goldenPath/help/blatSpec.html
43. tRNAscan-SE v2.0rc2 https://github.com/UCSC-LoweLab/tRNAscan-SE
44. INFERNAL v1.1.2 http://eddylab.org/infernal/
45. Barrnap v0.9 https://github.com/tseemann/barrnap#barrnap
46. EMBOSS package v6.6.0 http://emboss.sourceforge.net/
47. Hmmer v3.1b1 http://hmmer.org/
48. Coding Potential Calculator v1.0 https://github.com/biocoder/cpc
49. MAFFT v7.471 https://mafft.cbrc.jp/alignment/software/changelog.html
50. trimAL v1.4rev15 https://vicfero.github.io/trimal/
51. Gblock v0.91b http://molevol.cmima.csic.es/castresana/Gblocks/Gblocks_documentation.html
52. IQ-TREE v2.0.3 http://www.iqtree.org/
53. CAFE 3 v4.2.1 https://github.com/hahnlab/CAFE
54. PHYLIP v3.696 https://evolution.genetics.washington.edu/phylip.html

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

The A. capillus-veneris genome assembly, genome annotation, and all of the raw sequencing data have been deposited at NCBI, under the BioProject accession number PRJNA593372 (genome assembly and annotation) and PRJNA593361 (transcriptome raw sequence data). The CDS and peptide files are available from https://figshare.com/s/47be9fe90124b22d3c0e.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	This manuscript does not deal with this issue.
Population characteristics	This manuscript does not deal with this issue.
Recruitment	This manuscript does not deal with this issue.
Ethics oversight	This manuscript does not deal with this issue.

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 establish sample size. For RNA-seq, twenty tissues covering all development stages in A. capillus-veneris, at least three independent biological replicates were analyzed for each tissue. For wounding treatment, five independent biological replicates were detected the contents of jasmonates. For the coronatine treatment, we found large data fluctuation in plant samples with three replicates, which is filed standared, in the pre-test. Therefore, we used five independent biological replicates for metabolome analysis with coronatine treatment.
Data exclusions	No data was excluded.
Replication	For transcriptome analyses, each of the twenty samples had three biological replicates, except for mature sporangium sample and young sporophyte sample that have two biological replicates. All the experiments were successful. For the detection of jasmonates content and the metabolites analyses, five biological replicates were collected for experimental treatment and the following statistically analyses. All the experiments were successful.
Randomization	A. capillus-veneris samples were collected randomly from individuals in the field. All materials were selected randomly for experiments.
Blinding	Experiments was blinded and carried out by different coauthors or other researchers.

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

Methods

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