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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

- |                                     |                                     |                                                                                                                                                                                                                                                            |
|-------------------------------------|-------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement                                                                                                                                    |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly                                                                                                                                    |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of all covariates tested                                                                                                                                                                                                                     |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons                                                                                                                                        |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings                                                                                                                                                           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes                                                                                                                                     |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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 | No commercial, open-source, or custom code was used to collect the data for this study. Data were obtained from publicly available databases, including NCBI.                                                                                                                                                                                                                                                                              |
| Data analysis   | All data processing, modeling, and subsequent analyses were performed using custom code. Various open-source toolkits were used, as described in the manuscript. The core code used in this study is available at GitHub ( <a href="https://github.com/ddxz/DroGeneNet">https://github.com/ddxz/DroGeneNet</a> ) and archived in Zenodo ( <a href="https://doi.org/10.5281/zenodo.19232105">https://doi.org/10.5281/zenodo.19232105</a> ). |

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](#)

All data used in this study are publicly available. The specific sources and accession numbers of the datasets are provided in the Source Data (<https://doi.org/10.5281/zenodo.19245595>).

## 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                                        | No sex- or gender-based analyses were performed in this study, as these factors were not relevant to the research questions. Therefore, sex and gender data were not collected. No specific considerations for sex or gender were made during the study design.              |
| Reporting on race, ethnicity, or other socially relevant groupings | This study did not involve the use of any socially constructed or socially relevant categorization variables. Therefore, no categorization of participants based on factors such as race, ethnicity, gender, socioeconomic status, or other similar variables was performed. |
| Population characteristics                                         | This study did not involve human participants, and therefore no covariate-relevant population characteristics such as age, genotypic information, or past and current diagnoses and treatments are applicable.                                                               |
| Recruitment                                                        | This study did not involve human participants, so issues related to participant recruitment and self-selection bias are not applicable.                                                                                                                                      |
| Ethics oversight                                                   | This study did not require ethical approval, as it did not involve human participants or animal subjects.                                                                                                                                                                    |

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](https://nature.com/documents/nr-reporting-summary-flat.pdf)

## Ecological, evolutionary & environmental sciences study design

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

|                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|--------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Study description        | This study investigates the drought resistance mechanisms in four major Poaceae crops—rice, wheat, maize, and sorghum—by analyzing over 5000 bulk RNA-seq datasets aggregated from diverse geographic environments worldwide. Other crops in Fabaceae and Solanaceae were also included for further validation. The goal is to map the interactions among 130,000 genes by constructing a large-scale gene regulatory network (GRN) that integrates transcriptional, proteomic, and metabolic data. We aimed to identify conserved and divergent drought resistance mechanisms across species.                                                                                                                                                                                                                                                                                                                          |
| Research sample          | This study uses existing RNA-seq datasets aggregated from diverse geographic environments worldwide. The data includes over 5000 bulk RNA-seq samples from four major Poaceae crops: rice, wheat, maize, and sorghum. Soybean in Fabaceae, potato in Solanaceae, as well as foxtail millet and teff, were also used for further validation. These datasets are sourced from public repositories, including NCBI and other public databases. The samples represent a variety of environmental conditions, providing a comprehensive view of the drought resistance mechanisms in these crops. Additionally, the study incorporates 3.3 million gene regulatory interactions, which were obtained from PlantRegMap, STRING, and KEGG databases. These interactions were derived from experimental data and literature reviews, further enriching the understanding of regulatory networks involved in drought resistance. |
| Sampling strategy        | Samples were selected from over 5000 bulk RNA-seq datasets, obtained from public repositories like NCBI, covering a broad range of environmental conditions for four major Poaceae crops: rice, wheat, maize, and sorghum. Soybean in Fabaceae, potato in Solanaceae, as well as foxtail millet and teff, were also used for further validation. The data were chosen to represent diverse geographic locations and varied environmental stressors. No formal sample size calculation was performed, as the large-scale dataset already provided sufficient coverage to capture the genetic and environmental variability relevant to the study's aims. The total number of samples (5000+) ensures that the results are robust and reflective of global drought resistance mechanisms across the studied species.                                                                                                      |
| Data collection          | We collected RNA-Seq data from NCBI for japonica rice, indica rice, wheat, maize, and sorghum under normal and drought stress conditions, and filtered out the data that did not meet the requirements. To ensure the reliability of the results, we further obtained transcriptome data under control and drought conditions for soybean ( <i>Glycine max</i> ) in Fabaceae, potato ( <i>Solanum tuberosum</i> ) in Solanaceae, as well as foxtail millet ( <i>Setaria italica</i> ) and teff ( <i>Eragrostis tef</i> ). Additionally, we downloaded transcriptional regulation, protein interaction, and metabolic regulatory relationship data from PlantRegMap, STRING, and KEGG databases, and performed gene ID conversion and matching.                                                                                                                                                                          |
| Timing and spatial scale | The data collection started in December 2023 and ended in November 2025. The data were sourced from different geographic locations around the world.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Data exclusions          | Genes with expression levels less than or equal to 1 in two-thirds of the samples were excluded from the analysis. Due to inconsistencies in gene counts across different annotation platforms, some genes were excluded during the gene ID conversion process.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

|                 |                                                                                                                                                                                                                                                                                                            |
|-----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Reproducibility | This study is based on publicly available datasets, and all code used is fully reproducible to achieve the research results.                                                                                                                                                                               |
| Randomization   | The data were divided into two groups: a normal group and a drought stress group. These groups were derived from a large number of different experiments, with each sample in the normal group corresponding to a sample in the drought stress group. The sample sizes for both groups were roughly equal. |
| Blinding        | Blinding was not relevant to this study as it is based on publicly available RNA-seq data. Since the analysis involved existing datasets without experimental manipulation, blinding was not applicable.                                                                                                   |

Did the study involve field work? ☐ Yes ☒ No

## 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                                  |
|-------------------------------------|--------------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                    |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input 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 type="checkbox"/>            | <input checked="" type="checkbox"/> Plants             |

### Methods

| n/a                                 | Involved 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 |

## Plants

|                       |                                                                                                                                                                                                                         |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Seed stocks           | All data were sourced from publicly available databases, with specific data links and identifiers provided in the manuscript.                                                                                           |
| Novel plant genotypes | This study does not involve the generation of novel plant genotypes. All data used were derived from publicly available datasets, and no transgenic, gene-edited, or mutagenized plants were involved in this research. |
| Authentication        | This study does not involve the generation of novel plant genotypes or the use of seed stocks, and therefore no authentication procedures or experiments on mutations and secondary effects were conducted.             |