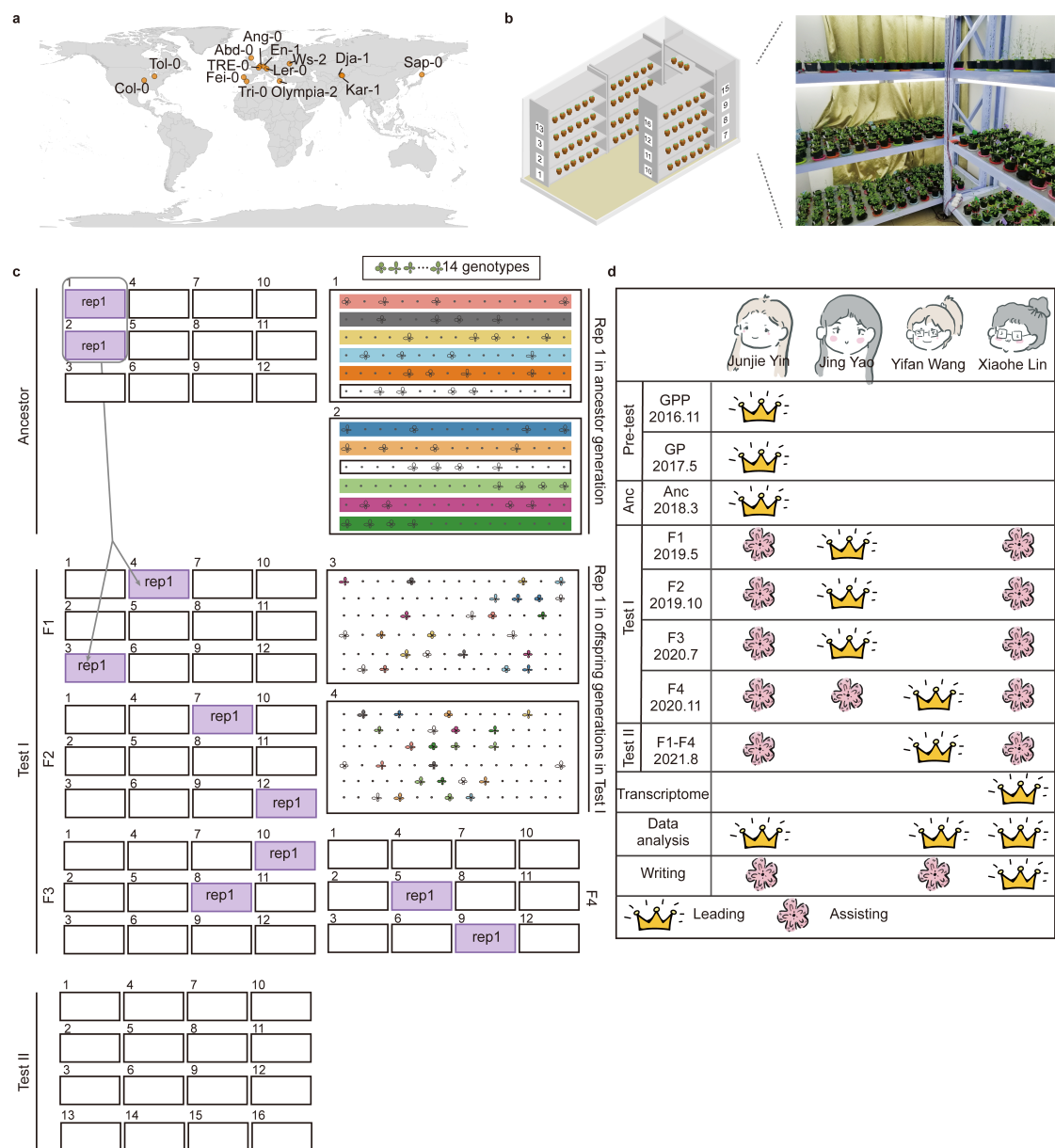


1 **Extended data figures**



2

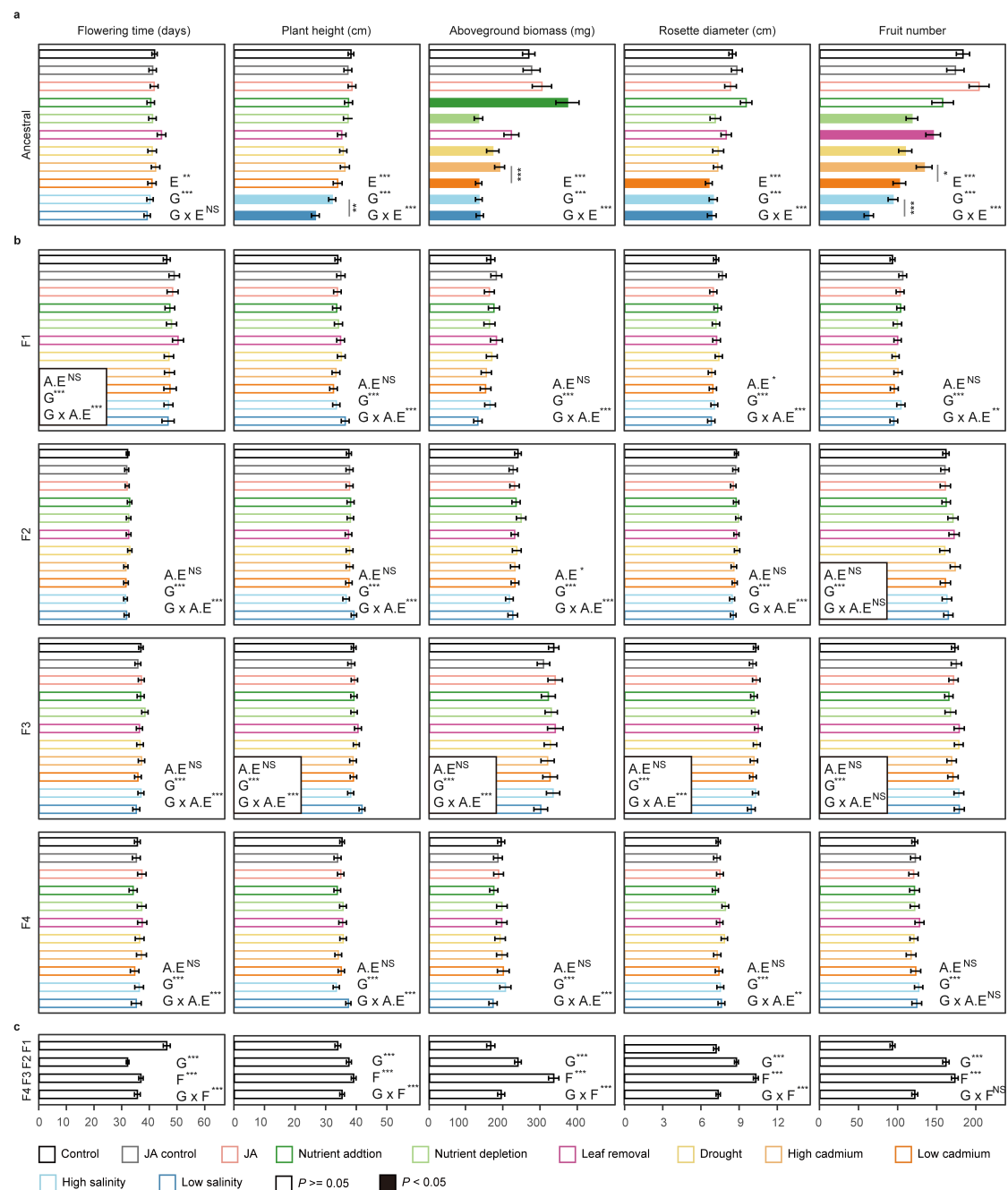
3 **Extended Data Fig. 1| Details of the experimental design.**

4 **a**, The geographic origins

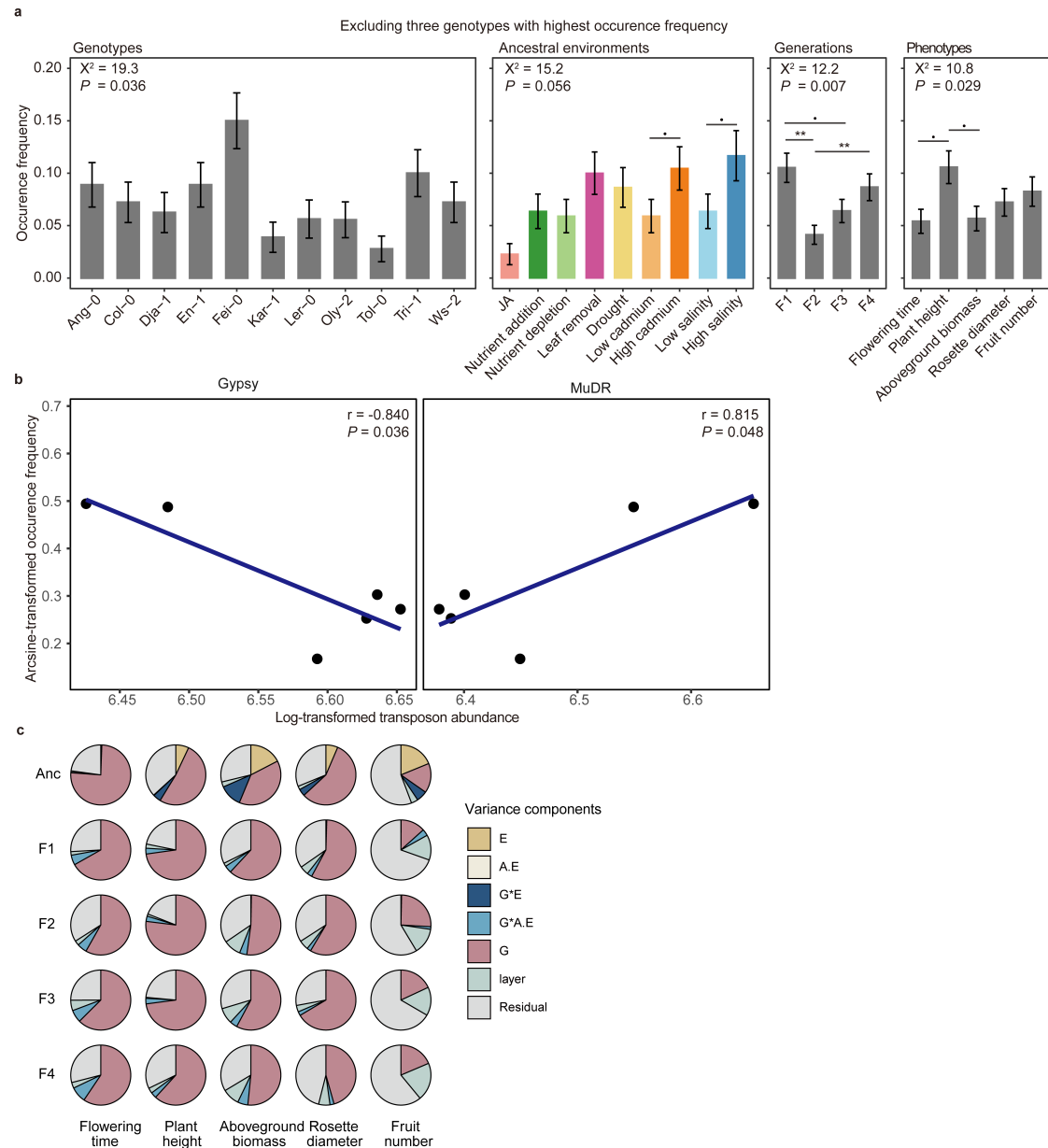
5 of the 14 accessions of *A. thaliana*. **b**, The growth room setup and numbers indicating

6 different layers. **c**, The design and randomization of the experiment. **d**, The timeline of

this study and the contributions of student authors.

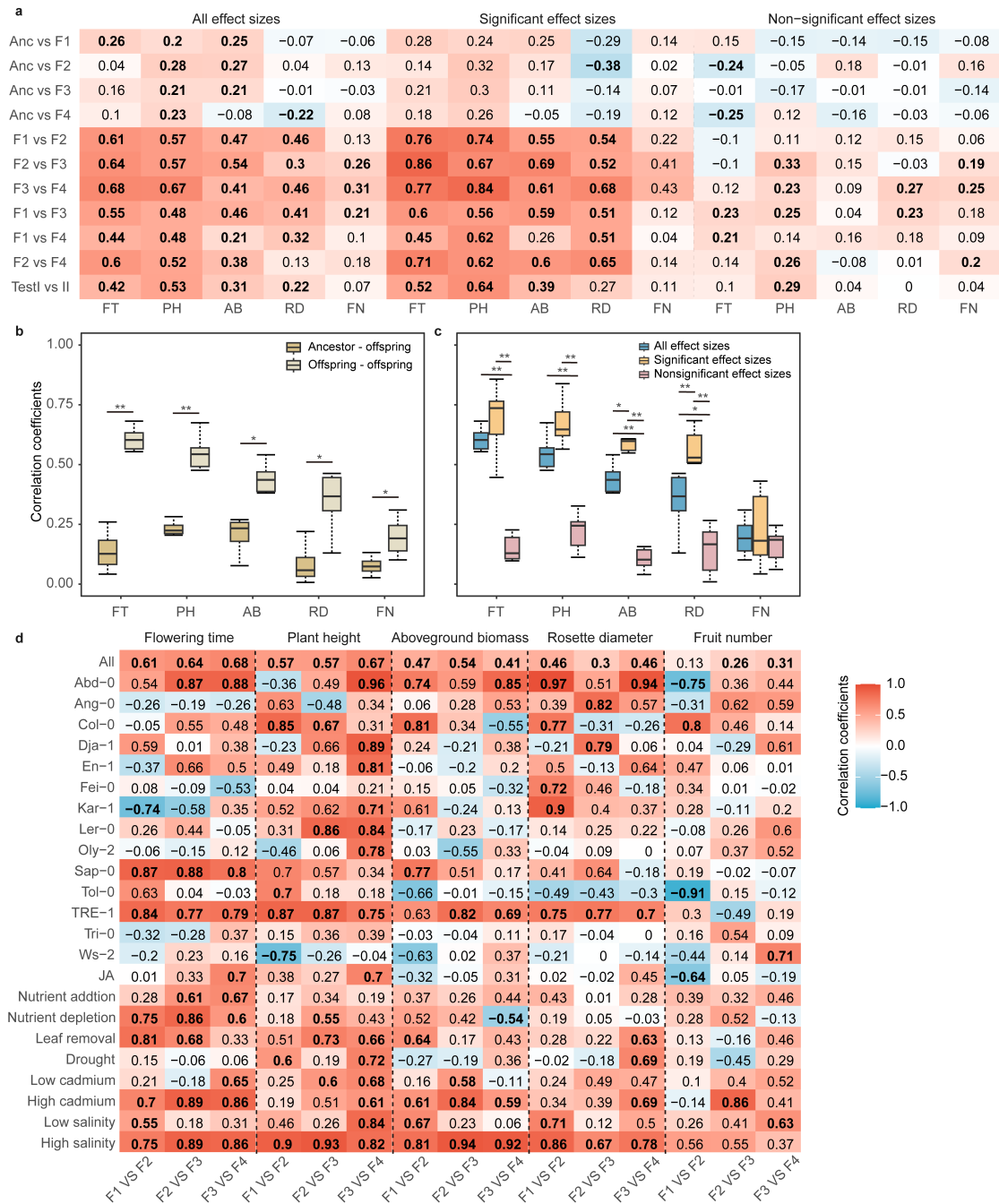


Extended Data Fig. 2| Phenotypes of the ancestral generation and offspring generations (Test I). **a**, Phenotypes of the ancestral generation. Filled bars indicate that the treatment significantly changed the phenotype compared to the control environment. **b**, The phenotypes of offspring generations (F1-F4). All phenotypes were measured in the control environment in Test I. **c**, A comparison between offspring generations of plants derived from the ancestral environment of the control. Details of the statistical results of panels a/b and c are shown in Supplementary Tables 2 and 3. E, A.E, G, and F represent fixed effects of the environment, ancestral environment, genotype and generation. Significance levels: *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.



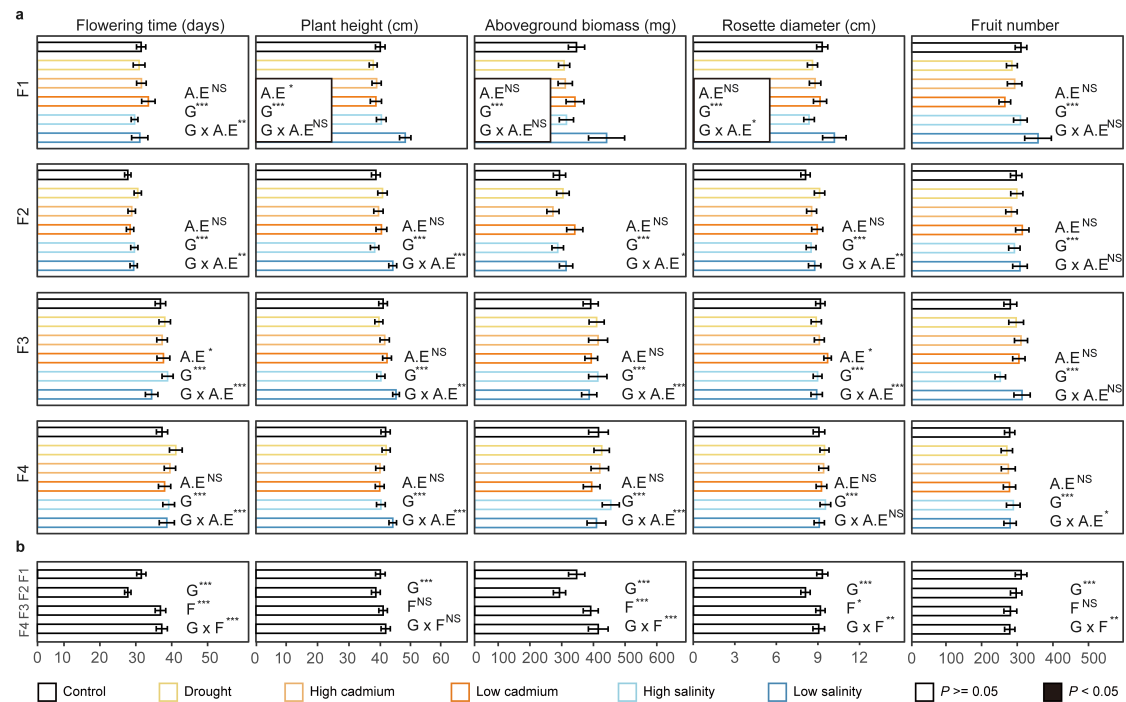
Extended Data Fig. 3 | Predictability of environment-induced phenotypic changes.

a, After excluding the three genotypes with the highest occurrence frequencies, the variation between ancestral environmental treatments became insignificant. Error bars indicate the standard error. **b**, The arcsine regressions transformed occurrence frequency among various genotypes against factors that significantly explained this variance (Fig. 3b). **c**, The partitioning of variance in the linear mixed-effect models.

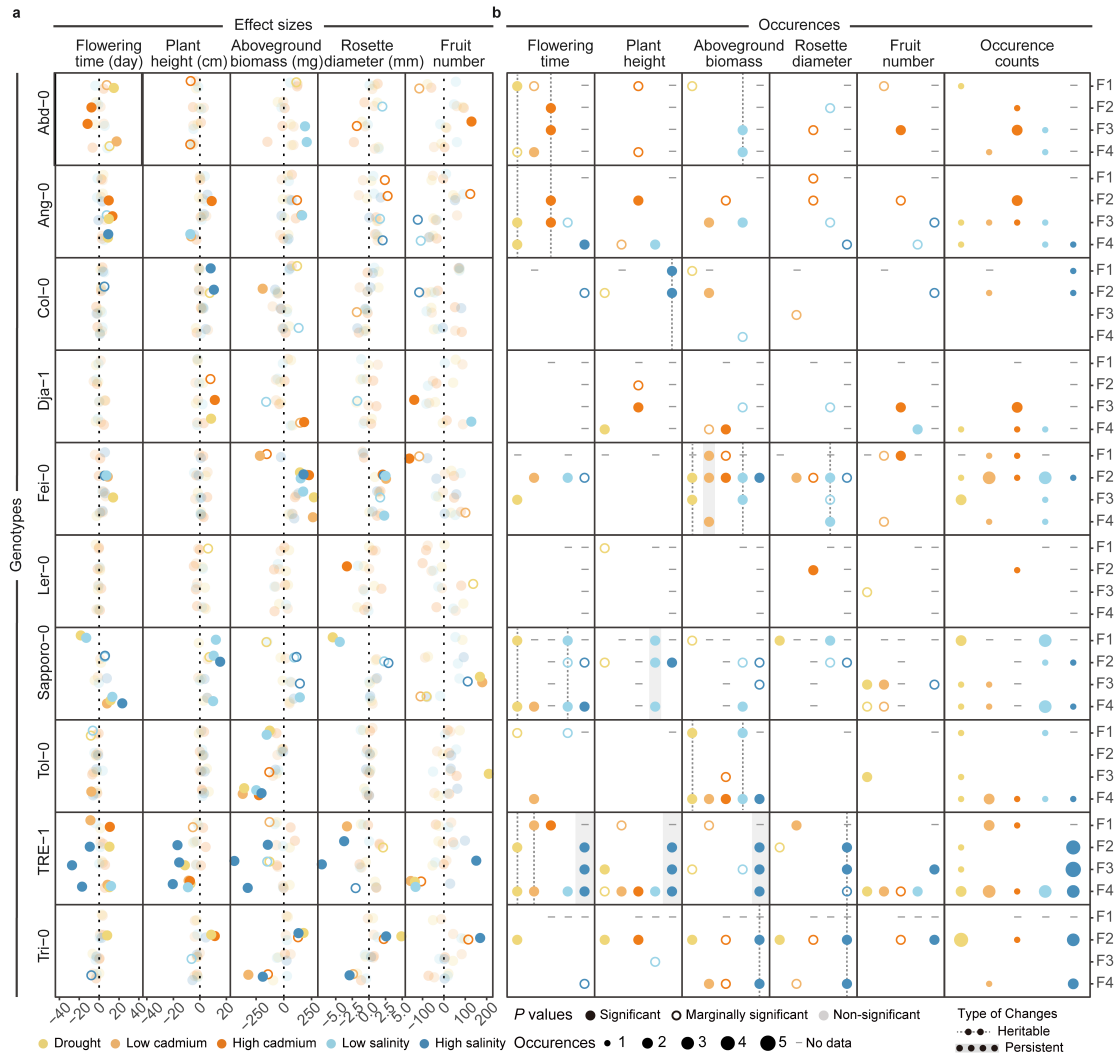


Extended Data Fig. 4 | Reproducibility of effect sizes between generations and tests

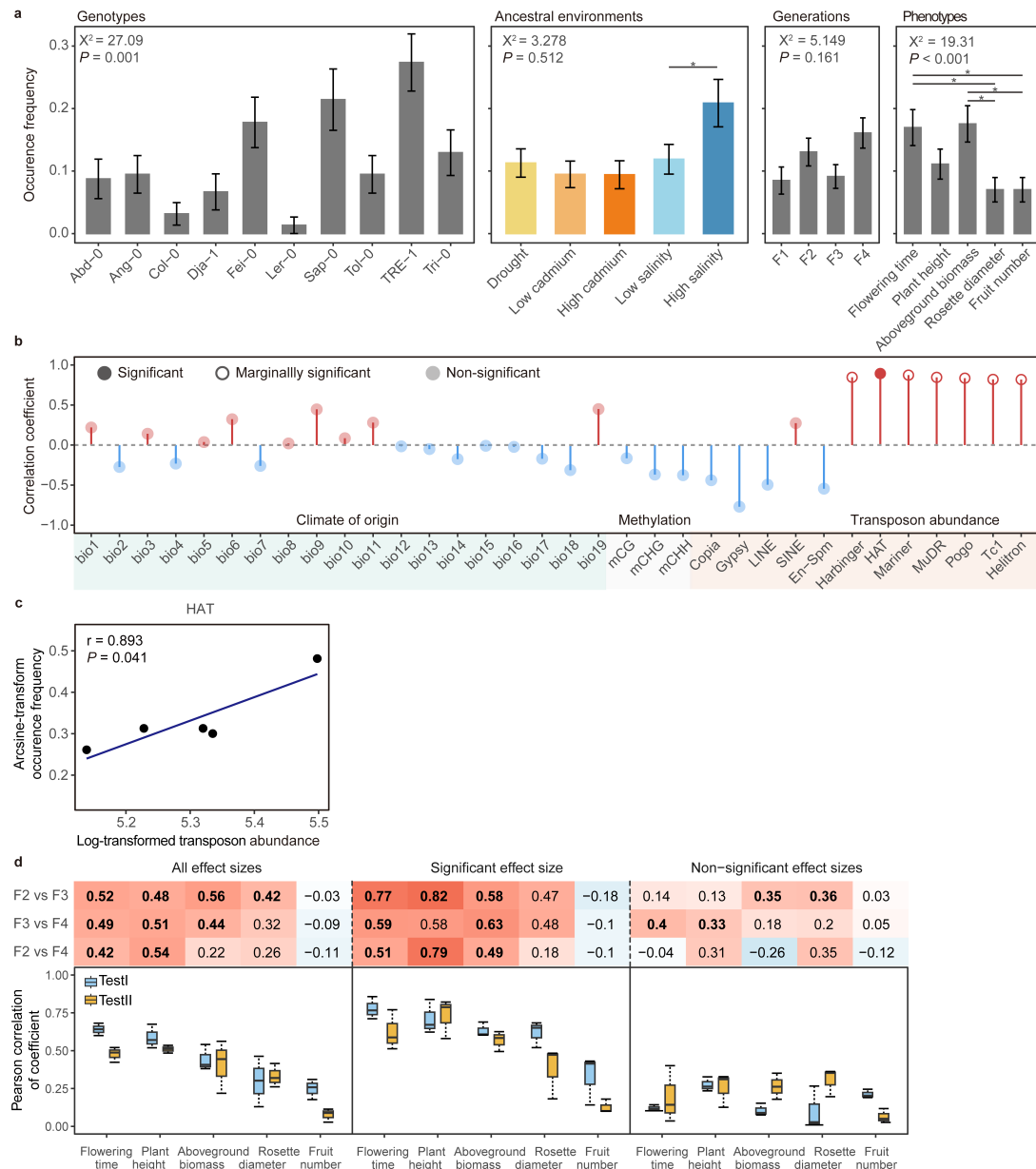
a, The correlation coefficients between ancestral responses and effect sizes of environment-induced changes in offspring generations, between offspring generations, and between tests. **b**, Comparison of correlation coefficients. **c**, The correlation coefficients of effect sizes between offspring generations when we scaled down the experiment to include only one genotype (but multiple treatments) or one treatment (but multiple genotypes). Significance levels: *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.



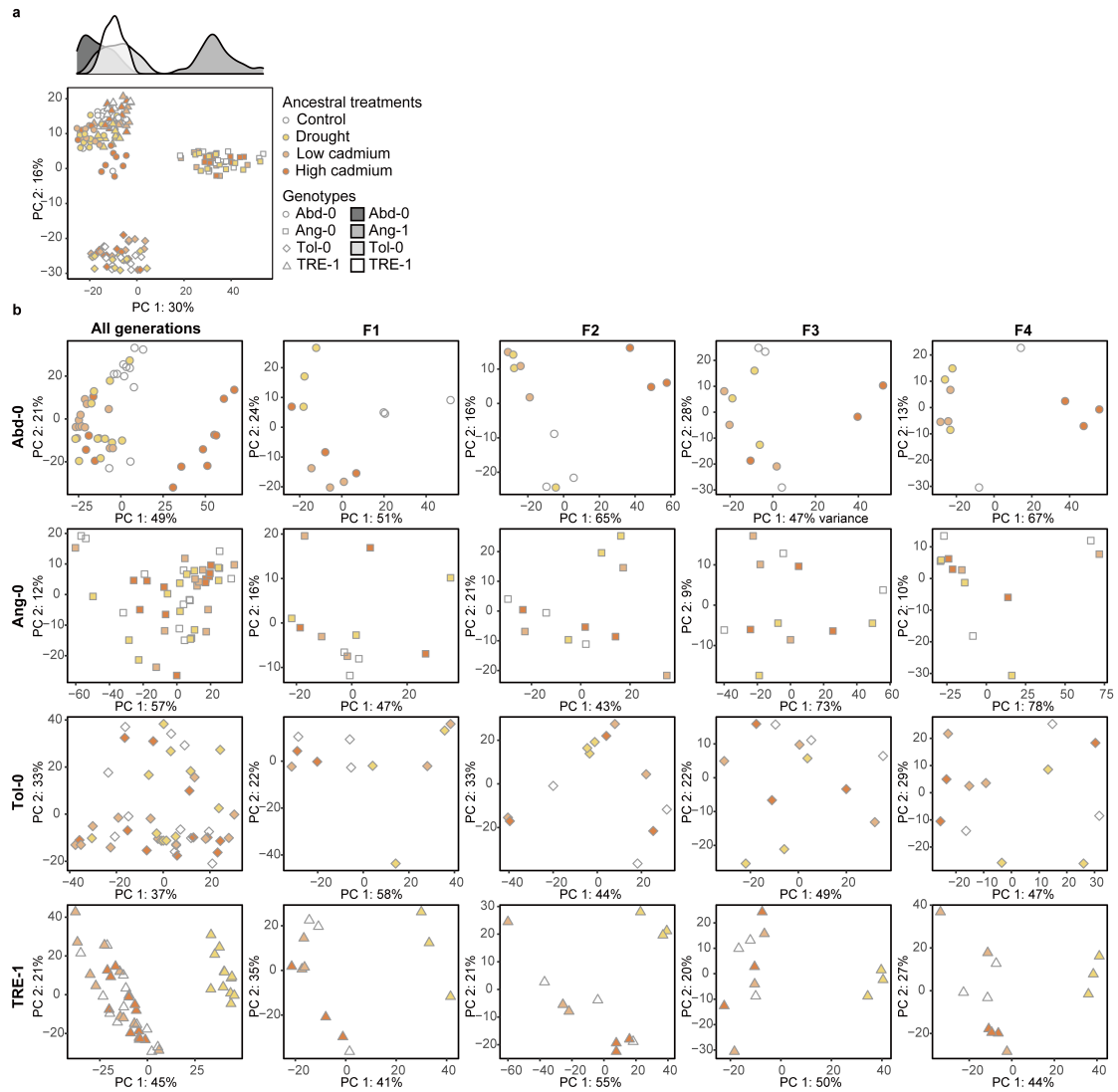
Extended Data Fig. 5 | The phenotypes of the offspring generation in Test II. a, The phenotypes of offspring generations (F1-F4) measured in the control environment. **b,** A comparison between generations of plants derived from the ancestral control environment. Details of the statistical results of panels a and b are shown in Supplementary Tables 5 and 6. E, A.E, G, and F represent fixed effects of the environment, ancestral environment, genotype and generation. The estimates for F1 may be biased due to missing samples. Significance levels: *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.



Extended Data Fig. 6 | Ancestral environment-induced phenotypic changes assessed by Test II for different genotypes, environmental treatments and offspring generations. a, The effect sizes of phenotypic changes measured in Test II. **b,** The occurrence of significant and marginally significant effect sizes and the sum of occurrence over phenotypes.

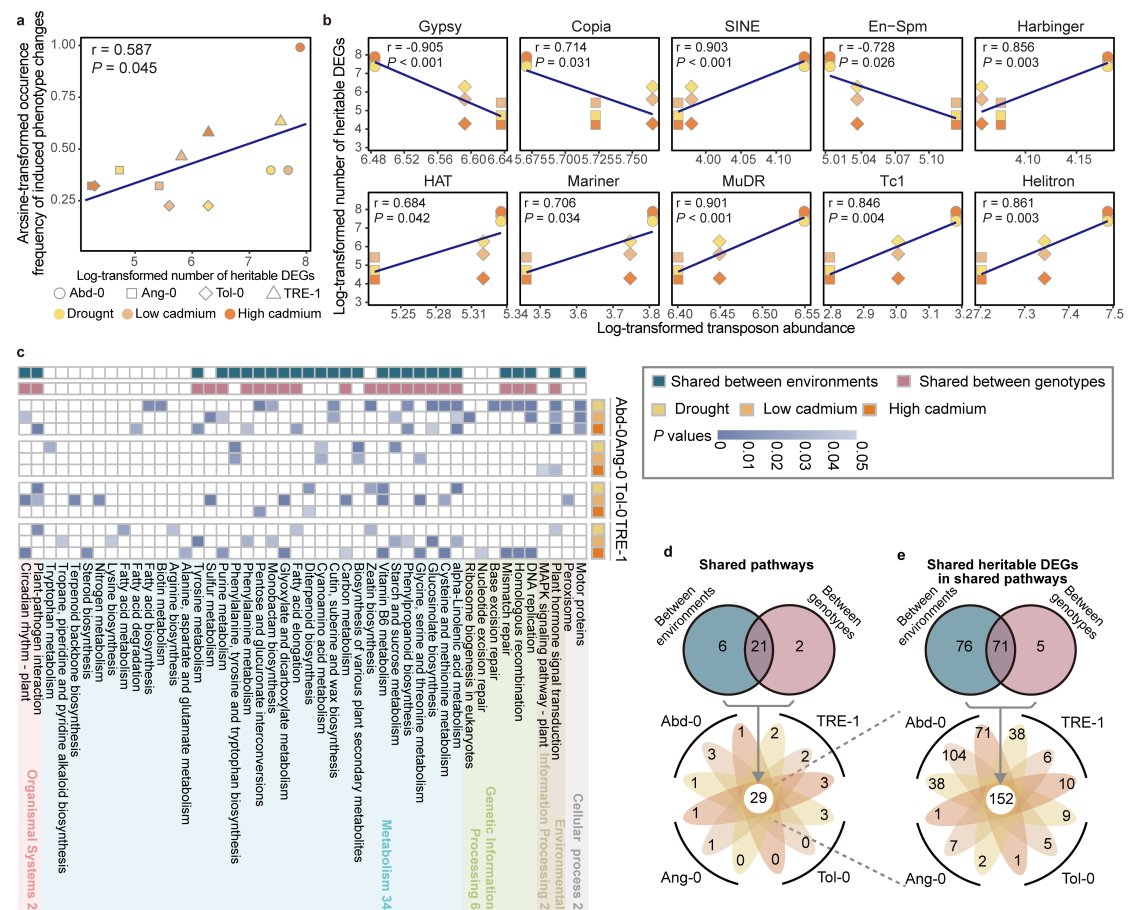


Extended Data Fig. 7 | Predictability and reproducibility analysis of environment-induced changes assessed in Test II. **a**, The occurrence frequency of significant environment-induced changes for different genotypes, environmental treatments, offspring generations and phenotypes. Error bars indicate the standard error. **b**, The correlation coefficients of regressions of occurrence frequency for various genotypes (arcsine transformed) against factors that potentially explain this variance. **c**, The arcsine regressions transformed occurrence frequency of various genotypes against factors that significantly explained this variance. **d**, The correlation coefficients (=reproducibility) of effect sizes between offspring generations and comparisons of reproducibility between Test I and Test II. Significance levels: *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

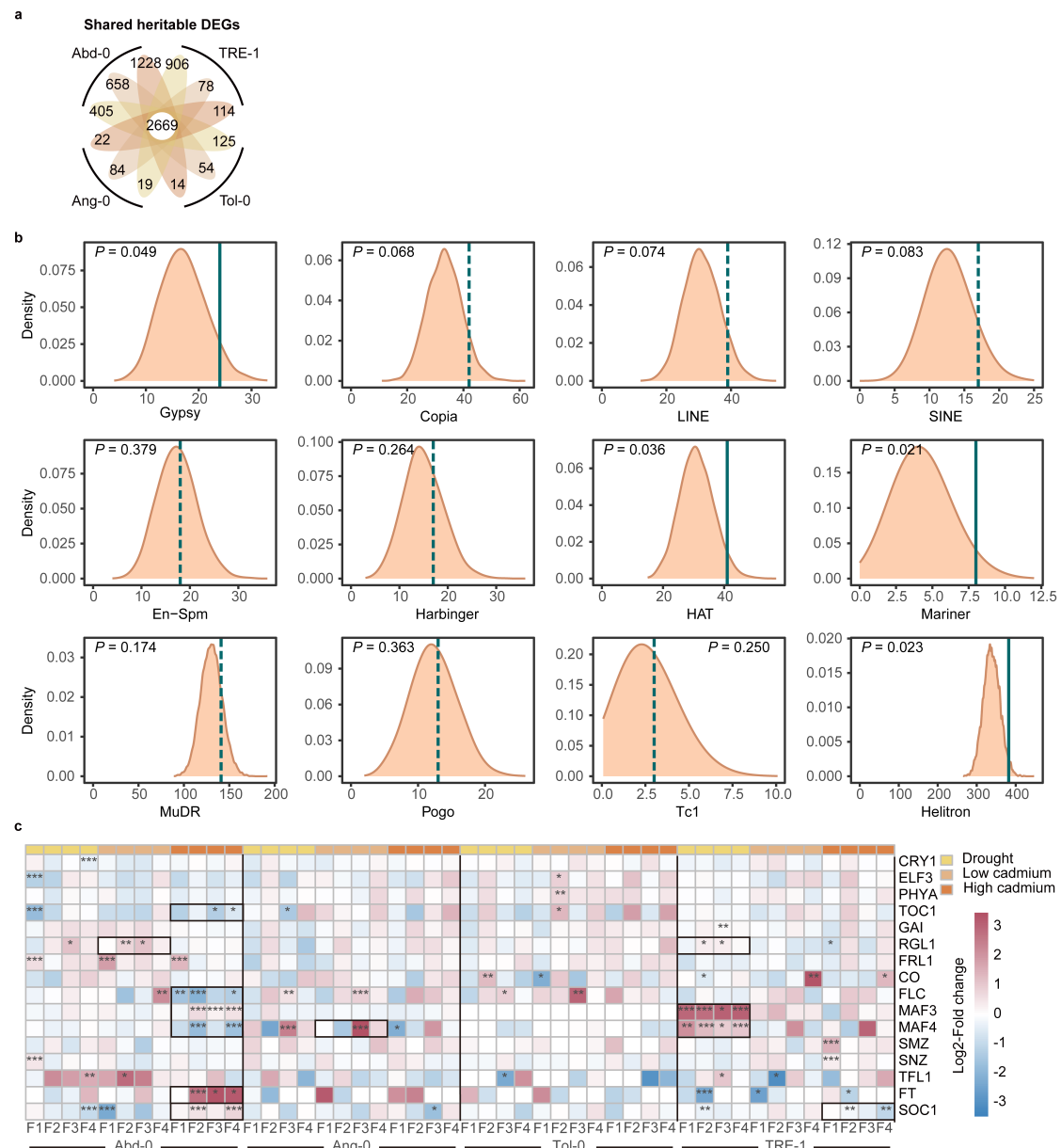


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61 **Extended Data Fig. 8 | Principal component analysis (PCA) of genome-wide gene**
 62 **expression patterns of different samples. a, PCA of all samples, including four**
 63 **genotypes, four environmental treatments, and four offspring generations. b, PCA for**
 64 **each genotype and generation.**



Extended Data Fig. 9: Summary of findings showing the relationships and functions of heritable DEGs. **a**, The significant positive correlations between occurrence frequencies and numbers of heritable DEGs. **b**, Regressions of the number of heritable DEGs against the number of transposons per superfamily. **c**, The results of KEGG enrichment analysis of heritable DEGs. **d**, Venn plot showing the number of significantly enriched pathways shared between genotypes/treatments. **e**, Venn plot of the number of heritable DEGs within the shared pathways.



Extended Data Fig. 10 | Shared heritable DEGs and DEGs related to flowering time. **a**, Venn plot of all heritable DEGs. The number (2669) in the middle circle indicate the number of heritable DEGs that were shared by at least two environments or genotypes. **b**, The null distribution of transposon abundance upstream of genes for different superfamilies. The horizontal lines indicate the observed transposon abundance upstream of the 2669 heritable DEGs shared by at least two environments or genotypes. Significant P values indicate significant enrichment of transposons upstream of heritable DEGs compared with the null expectation. **c**, Heatmap of flowering time-related genes that were DEGs for at least one generation.