# Supporting information

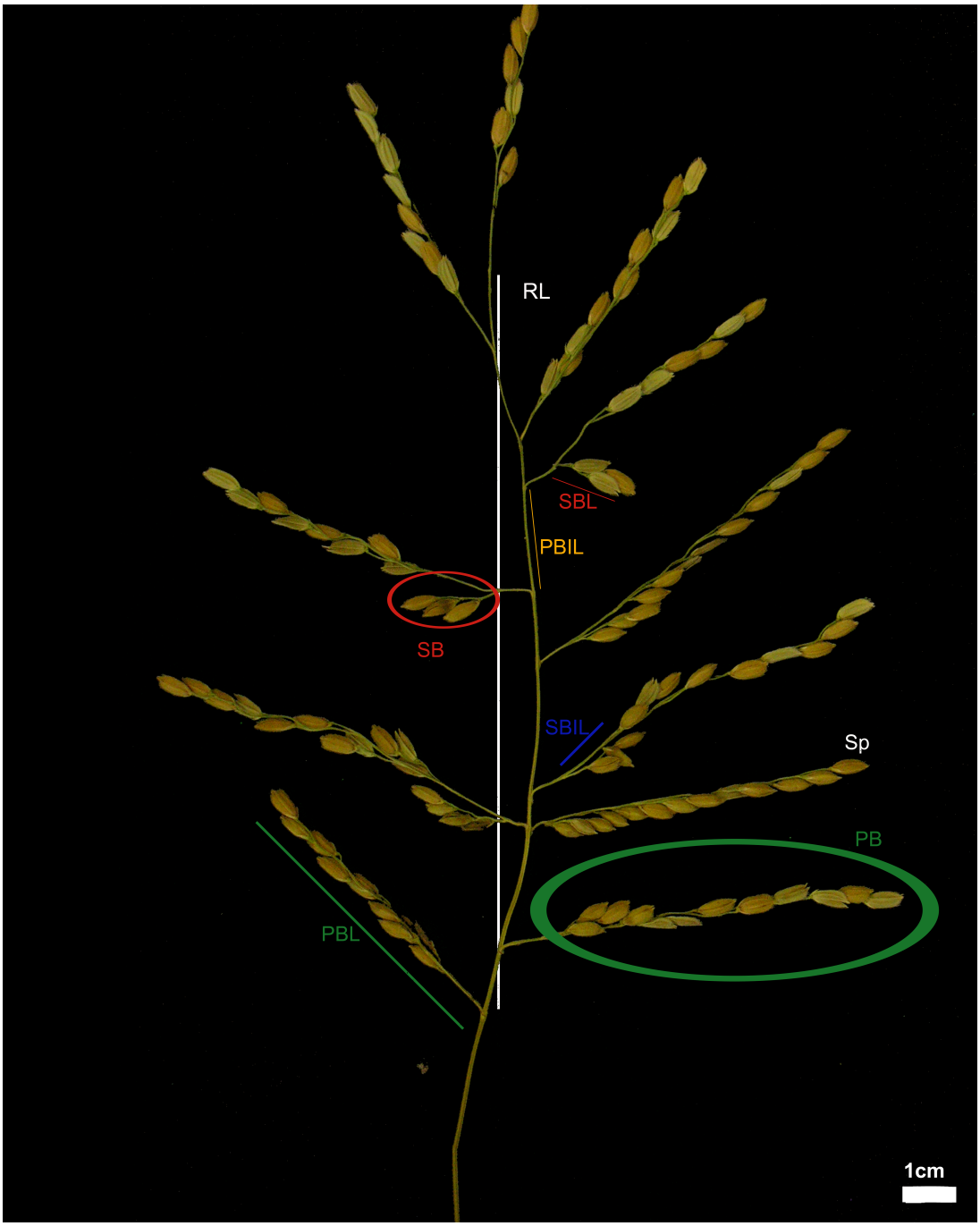


**Figure S1**. Spread mature rice panicle. PB: Primary branch; PBIL: Primary branch internode length; PBL: Primary branch length; RL: Rachis length; SB: Secondary branch; SBIL: Secondary branch internode length; SBL: Secondary branch length; Sp: Spikelet.

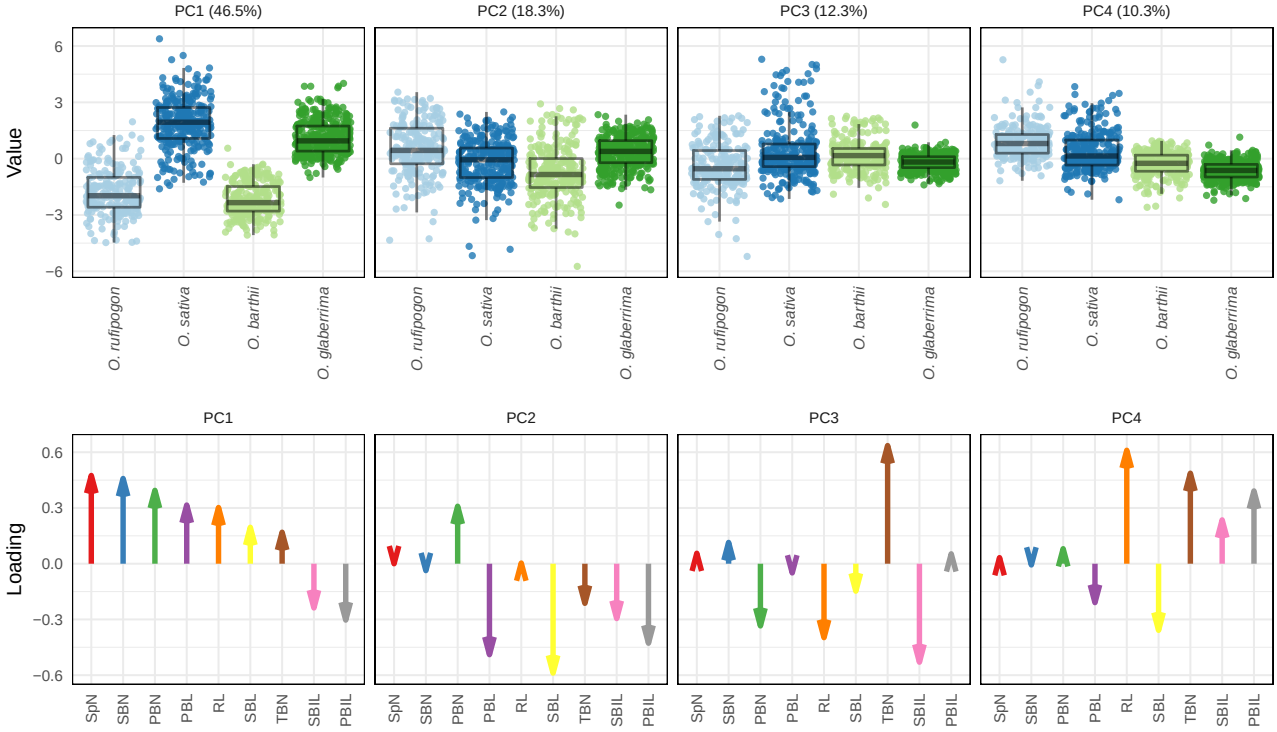


**Figure S2**. Principal component analysis (PCA) of panicle phenotyping data showing components 1–4. PC1 accounts for 46.5% of variability and separates panicles from domesticated and wild accessions. The lower ordinates do not separate panicles by species.

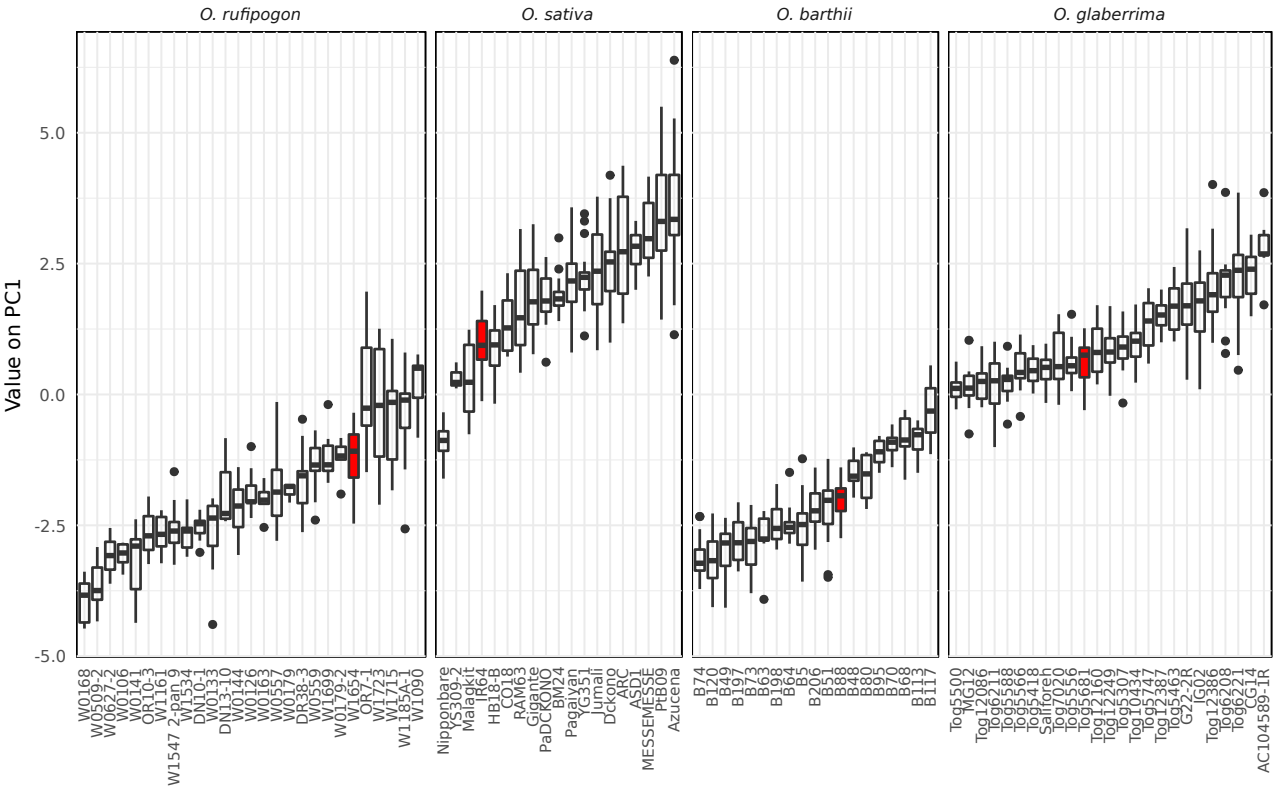


**Figure S3**. The accessions used for RNAseq are consistent with species-wide patterns of panicle architecture. The *y*-axis shows the projection of each panicle on principal component 1 (PC1), which separates wild and domesticated accessions (Fig. 1). The accessions chosen for RNAseq are shown in red. Accessions used for phenotyping are listed in supporting information Table S1.

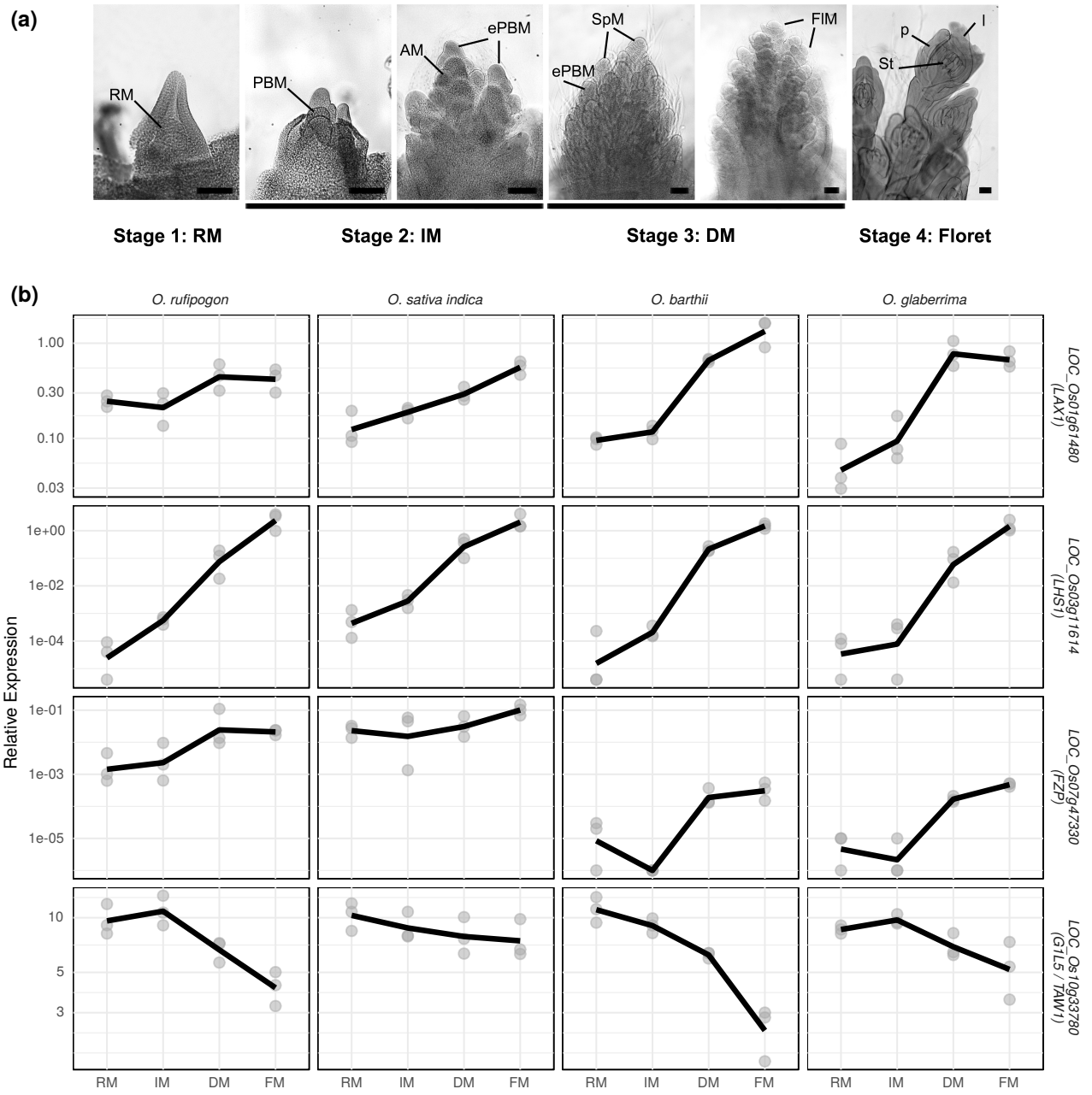


**Figure S4**. Early stages of rice panicle development used for gene expression analysis. (**a**) Developmental stages of immature panicles collected for expression analysis. Stage 1: rachis meristem; Stage 2: indeterminate meristem (IM) stage with formation of primary branch meristems, elongation of primary branch meristem and formation of axillary meristem; Stage 3: determinate meristem (DM) stage with spikelet meristem and floret differentiation; Stage 4: floret displaying early floral organ differentiation. The scale bar indicates 100 µm. (**b**) Quantitative RT-PCR using meristem stage-specific marker genes for validation of staging. AM: axillary meristem; ePBM: elongating primary branch meristem; FlM: floret meristem; l: lemma; p: palea; PBM: primary branch meristem; RM: Rachis meristem; SpM: spikelet meristem; St: stamen.

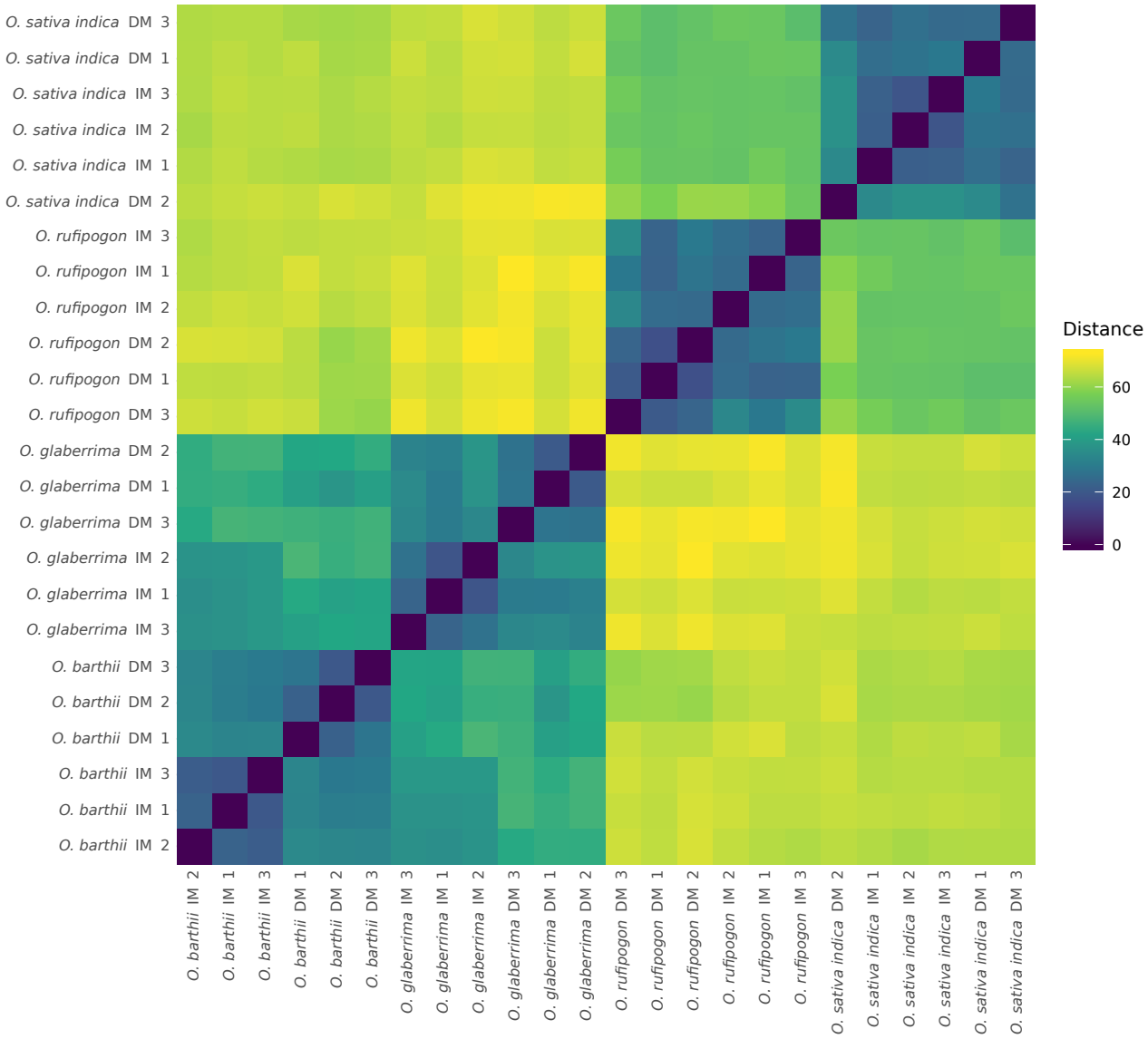


**Figure S5**. Heatmap of pairwise distances between RNAseq samples. Samples group by stage, species and continent. The numbers indicate single samples (three replicates per accession per stage). The axes are ordered by hierarchical clustering of Minkowski distances between samples.

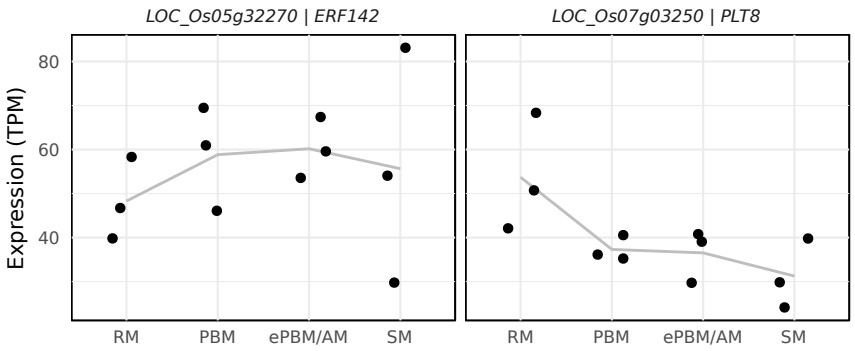


**Figure S6**. Expression of *AP2/EREBP*-like genes in *O. sativa japonica* cv. Nipponbare meristems (data from Harrop *et al.*, 2016). Both genes are expressed at all stages. *PLT8* expression peaks in RM. RM, rachis meristem; PBM, primary branch meristem; ePBM/AM, extending primary branch meristem and axillary meristem; SM, spikelet meristem.

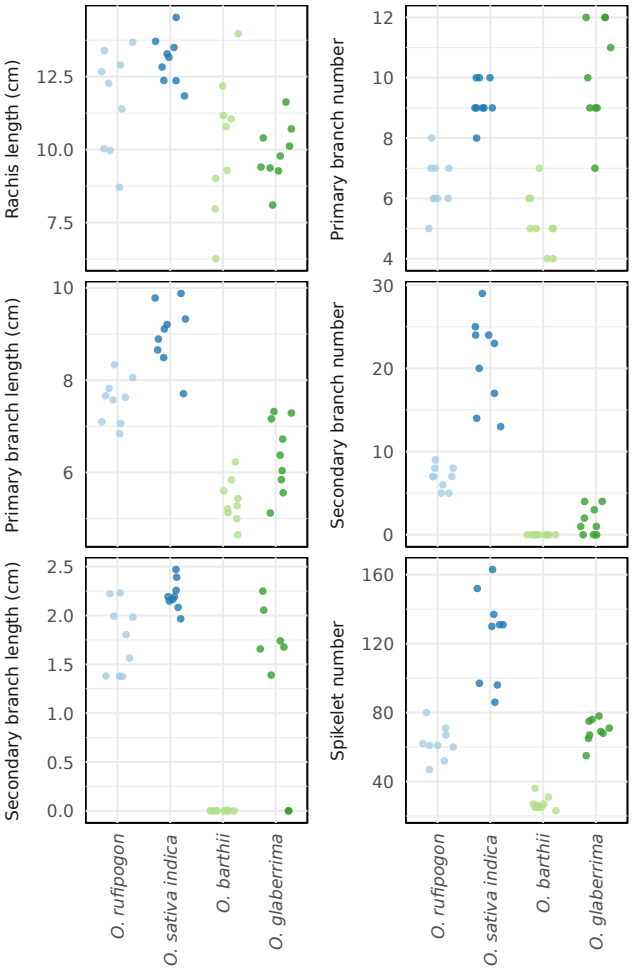


**Figure S7**. Phenotyping of the four *Oryza* accessions used for RNAseq. These plants were grown at the same time and in the same conditions as the plants used for gene expression analysis. The domesticated accessions produce more spikelets and secondary branches than their wild relatives. The domesticated accessions have a similar number of primary branches, but the Asian domesticated species has more secondary branches and spikelets than the domesticated African species.

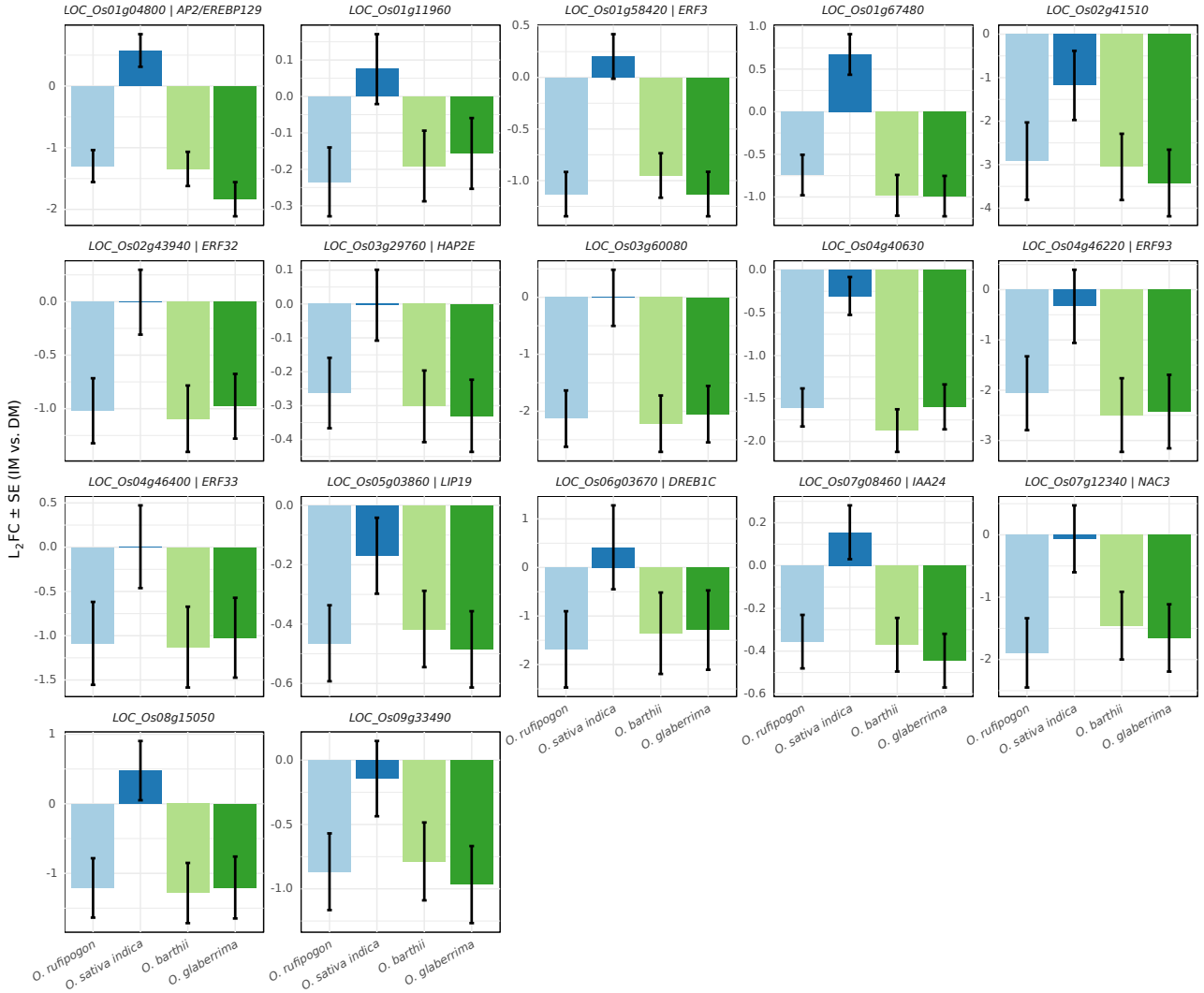


**Figure S8**. Most genes in cluster 5 have negative $L_2$FCs between IM and DM in *O. rufipogon*, *O. barthii* and *O. glaberrima*, but $L_2$FCs in *O. sativa indica* are closer to zero. This cluster has an enrichment of *AP2/EREBP*-like genes.

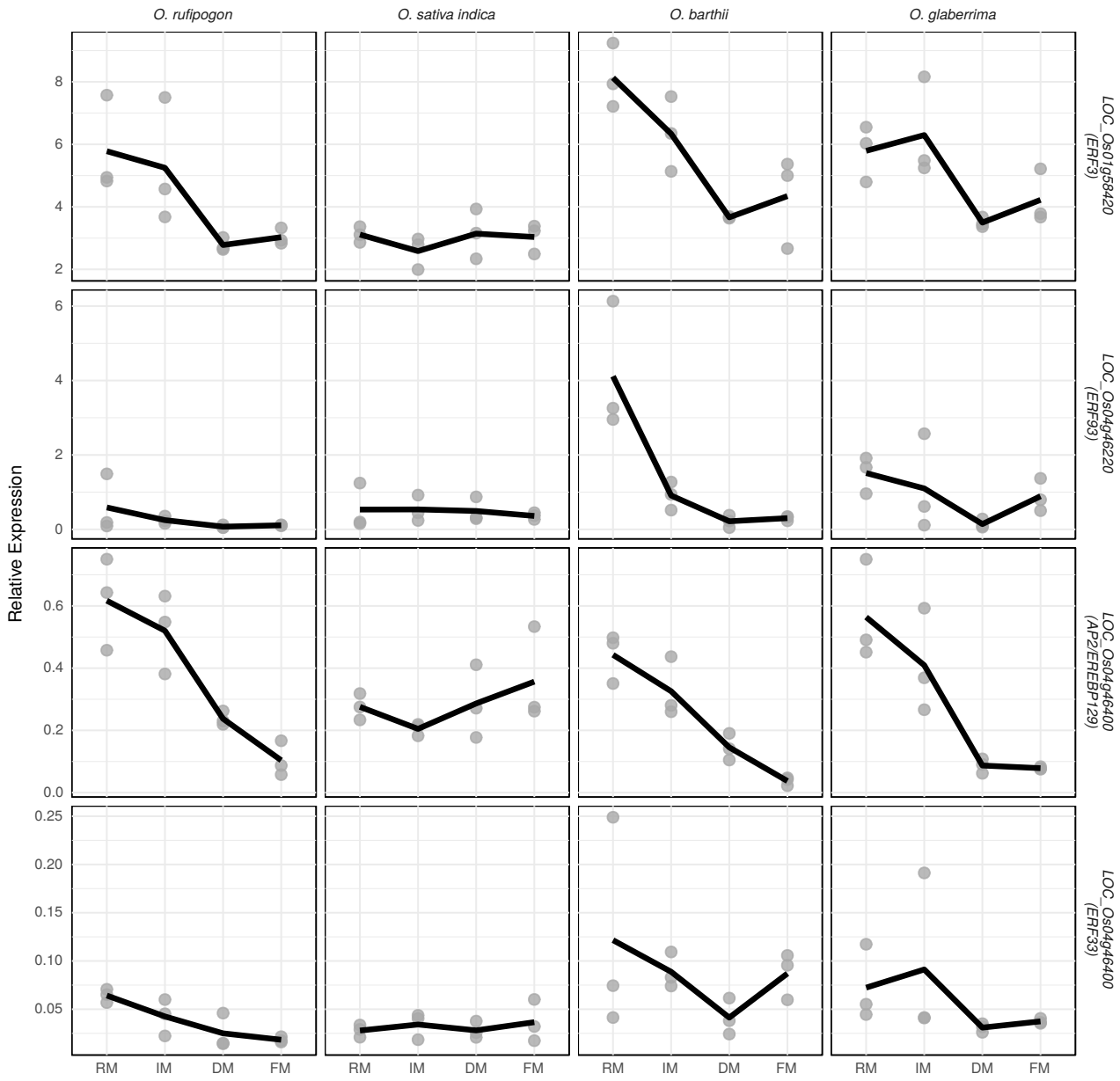


**Figure S9**. Expression analysis along early panicle development of *AP2/EREBP*-like genes present in cluster 5. DM: determinate meristem; FM: floret meristem; IM: indeterminate meristem; RM: rachis meristem.

## Supporting information table captions

**Table S1**. Rice accessions used in this study.

**Table S2**. Sequences of primers used.

**Table S3**. Quantification of panicle traits in 91 accessions from wild and domesticated Asian and African rice species. Ob, *O. barthii*; Og, *O. glaberrima*; Os, *O. sativa*; Or, *O. rufipogon*; PBN, Primary branch; PBIL, Primary branch internode length; PBL, Primary branch length; RL, Rachis length; SBN, Secondary branch; SBIL, Secondary branch internode length; SBL, Secondary branch length; SpN, Spikelet number; TBN, Tertiary branch number.

**Table S4**. Read and mapping statistics for all RNAseq samples.

**Table S5**. Differential expression test results between stages across all species. We used an arbitrary differential expression threshold of 1.5-fold change in expression and adjusted *p*-value (false discovery rate) less than 0.1.

**Table S6**. Transcription factor family enrichment by $L_2$FC.

**Table S7**. Detailed quantification of panicle traits from *crl5* and *smos1* mutants. PBN,Primary branch; PBIL, Primary branch internode length; PBL, Primary branch length; RL, Rachis length; SBN, Secondary branch; SBIL, Secondary branch internode length; SBL,Secondary branch length; SpN, Spikelet number; TBN, Tertiary branch number

**Table S8**. Clustered genes.

**Table S9**. Differential expression test results for the stage × accession interaction in Asian and African accessions.

**Table S10**. Detailed quantification of panicle traits from rice accessions used for sequencing analysis. These plants were grown at the same time and in the same conditions as the plants used for gene expression analysis.

## References

**Harrop TWR, Ud Din I, Gregis V, Osnato M, Jouannic S, Adam H, Kater MM**. 2016. Gene expression profiling of reproductive meristem types in early rice inflorescences by laser microdissection. The Plant Journal **86**, 75–88.