

## ***Supplementary Information***

### **Transposable element polymorphisms improve prediction of complex agronomic traits in rice**

**Supplementary Table 1** Phenotypes used in this study.

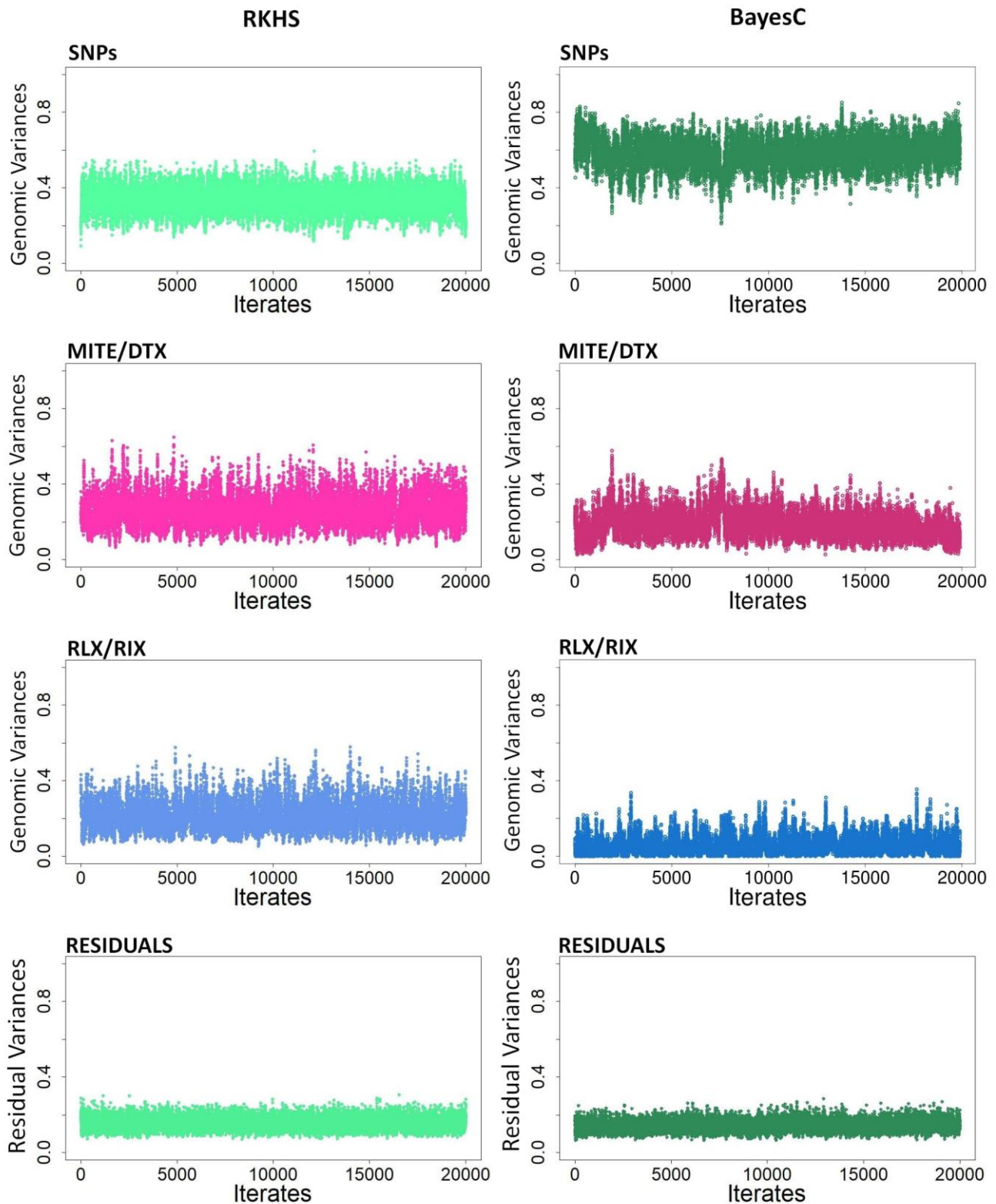
| <b>Phenotype</b>                    | <b>Recoding</b>                                      | <b>N</b> | <b>Mean</b> | <b>SD</b> |
|-------------------------------------|------------------------------------------------------|----------|-------------|-----------|
| <b>Culm Diameter 1<sup>st</sup></b> | None                                                 | 608      | 1.62        | 0.49      |
| <b>Culm strength</b>                | Classes {1,2,3} recoded as {1}, classes {4:9} as {2} | 642      | 1.39        | 0.49      |
| <b>Flag leaf angle</b>              | None                                                 | 639      | 3.89        | 1.68      |
| <b>Grain length</b>                 | None                                                 | 641      | 8.62        | 1.02      |
| <b>Grain width</b>                  | None                                                 | 641      | 3.01        | 0.39      |
| <b>Leaf length</b>                  | None                                                 | 606      | 3.17        | 0.68      |
| <b>Leaf senescence</b>              | Classes {2:9} recoded as {2}                         | 640      | 1.56        | 0.49      |
| <b>Grain weight</b>                 | None                                                 | 641      | 2.47        | 0.49      |
| <b>Salt injury at EC12</b>          | Classes {1:7} recoded as {1}, class {9} as {2}       | 602      | 1.46        | 0.49      |
| <b>Time to flowering</b>            | Log transformation                                   | 642      | 4.59        | 0.23      |
| <b>Panicle Threshability</b>        | Classes {1:5} recoded as {1}, classes {6:9} as {2}   | 639      | 1.43        | 0.49      |

**Supplementary Table 2** MITE family IDs from Castanera et al. (2021).

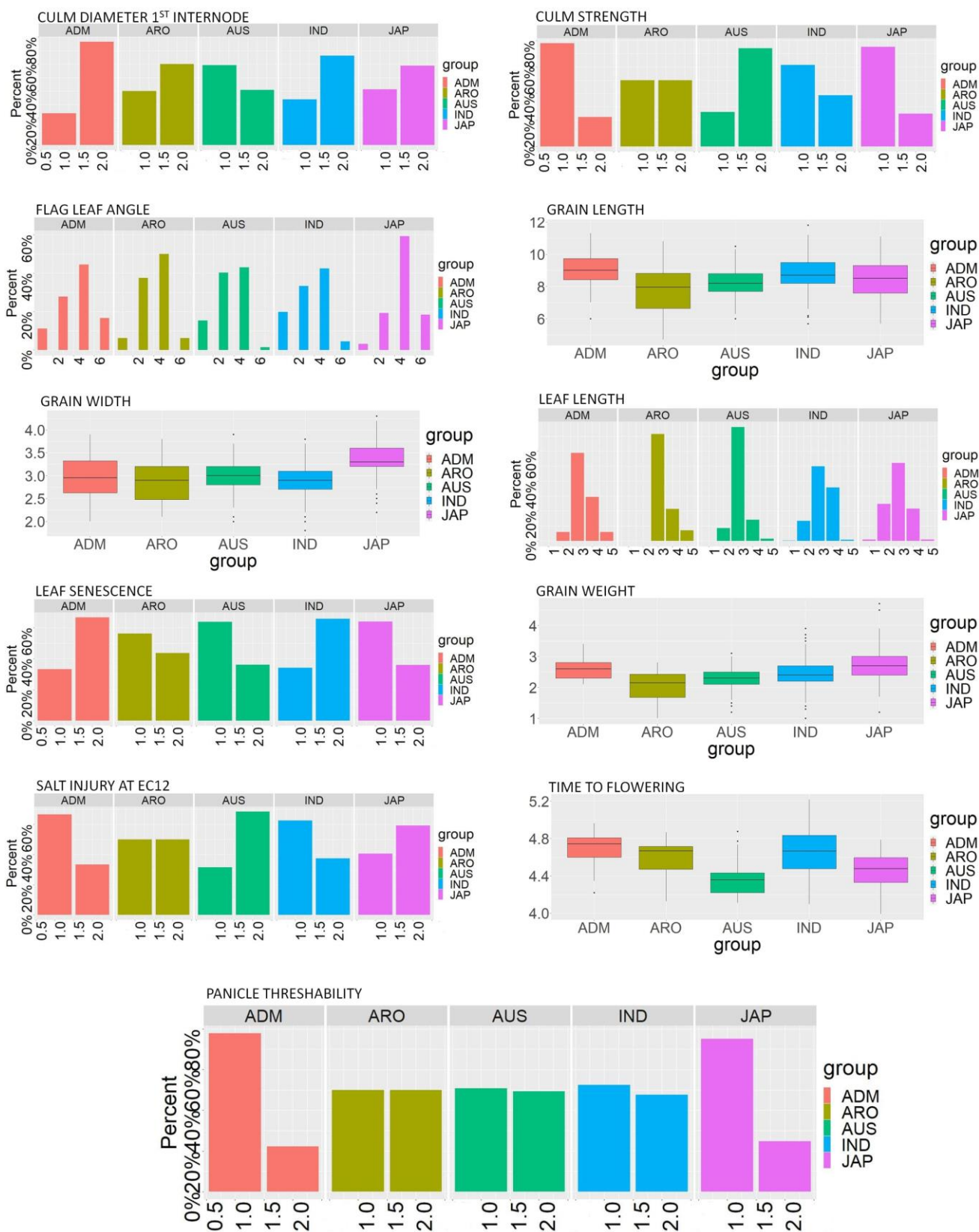
| <b>MITE family*</b>          | <b>MITE type**</b> | <b>TIP number</b> | <b>Genic TIPs</b> | <b>Percentage of genic TIPs</b> |
|------------------------------|--------------------|-------------------|-------------------|---------------------------------|
| <b>MH63fam6_341</b>          | Tourist-like       | 3058              | 942               | 30.8                            |
| <b>MH63fam8_344</b>          | Tourist-like       | 2087              | 657               | 31.5                            |
| <b>MH63fam13_234</b>         | MITE-adh B-like    | 1166              | 475               | 40.7                            |
| <b>MH63fam14_237</b>         | MITE-adh B-like    | 1771              | 603               | 34.0                            |
| <b>MH63fam29_244</b>         | unclassified       | 1850              | 585               | 31.6                            |
| <b>MH63fam32_236</b>         | MITE-adh B-like    | 2185              | 624               | 28.6                            |
| <b>MH63fam47_235</b>         | MITE-adh B-like    | 3627              | 1312              | 36.2                            |
| <b>MH63fam50_219</b>         | MITE-adh M-like    | 1207              | 471               | 39.0                            |
| <b>MH63fam51_257</b>         | unclassified       | 696               | 238               | 34.2                            |
| <b>MH63fam72_365</b>         | Amy/LTP-like       | 971               | 354               | 36.5                            |
| <b>MH63fam73_259</b>         | unclassified       | 1003              | 292               | 29.1                            |
| <b>MH63fam106_364</b>        | Castaway-like      | 1067              | 314               | 29.4                            |
| <b>N22fam5_230</b>           | MITE-adh I-like    | 1093              | 354               | 32.4                            |
| <b>N22fam30_347</b>          | Tourist-like       | 767               | 223               | 29.1                            |
| <b>N22fam34_480</b>          | Ditto-like         | 2615              | 742               | 28.4                            |
| <b>Oryza1fam20_279</b>       | Gaijin/Gaigin-like | 2170              | 690               | 31.8                            |
| <b>SE260500111fam211_334</b> | Tourist-like       | 1019              | 301               | 29.5                            |
| <b>SE260500112fam219_340</b> | Tourist-like       | 2357              | 696               | 29.5                            |

\* Family IDs from Castanera et al., (2021)

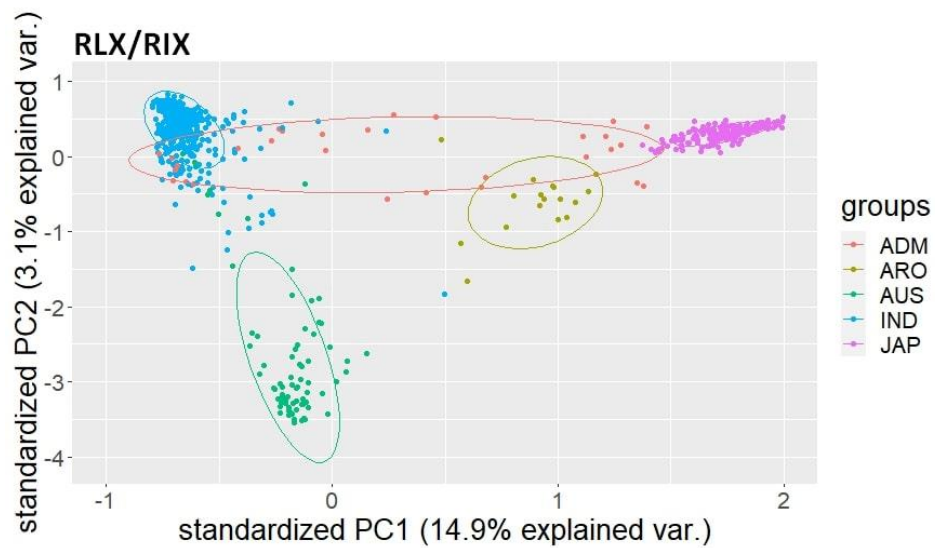
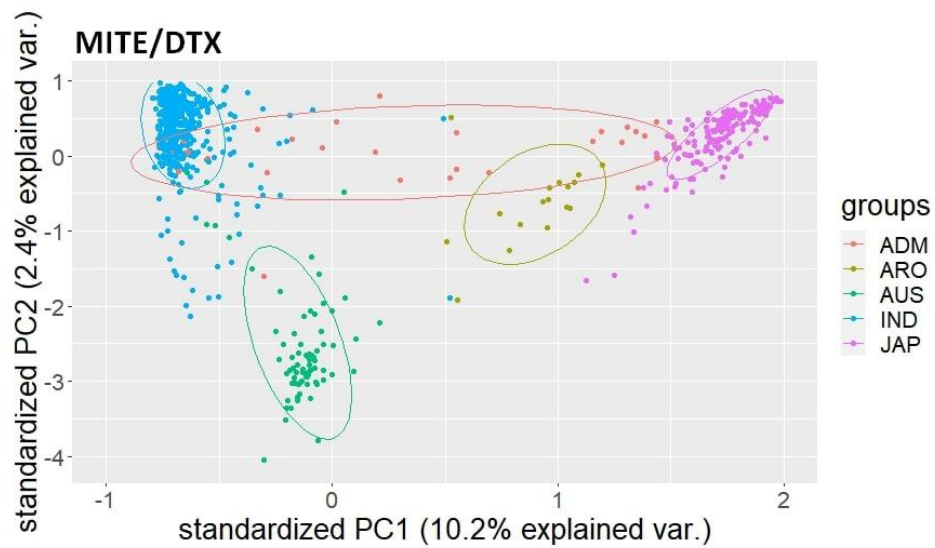
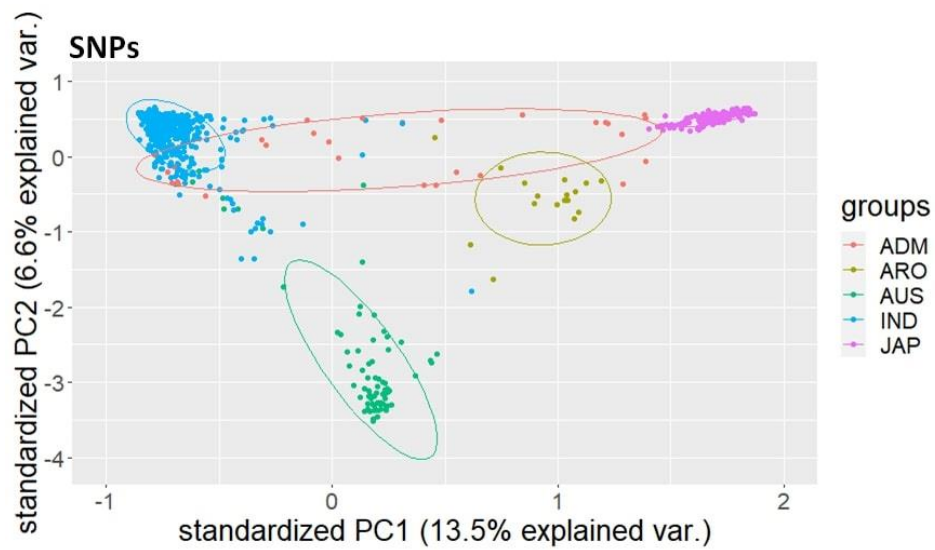
\* Classification based on best BLAST hit to Oryza Repeat Database ([http://rice.uga.edu/annotation\\_oryza.shtml](http://rice.uga.edu/annotation_oryza.shtml))



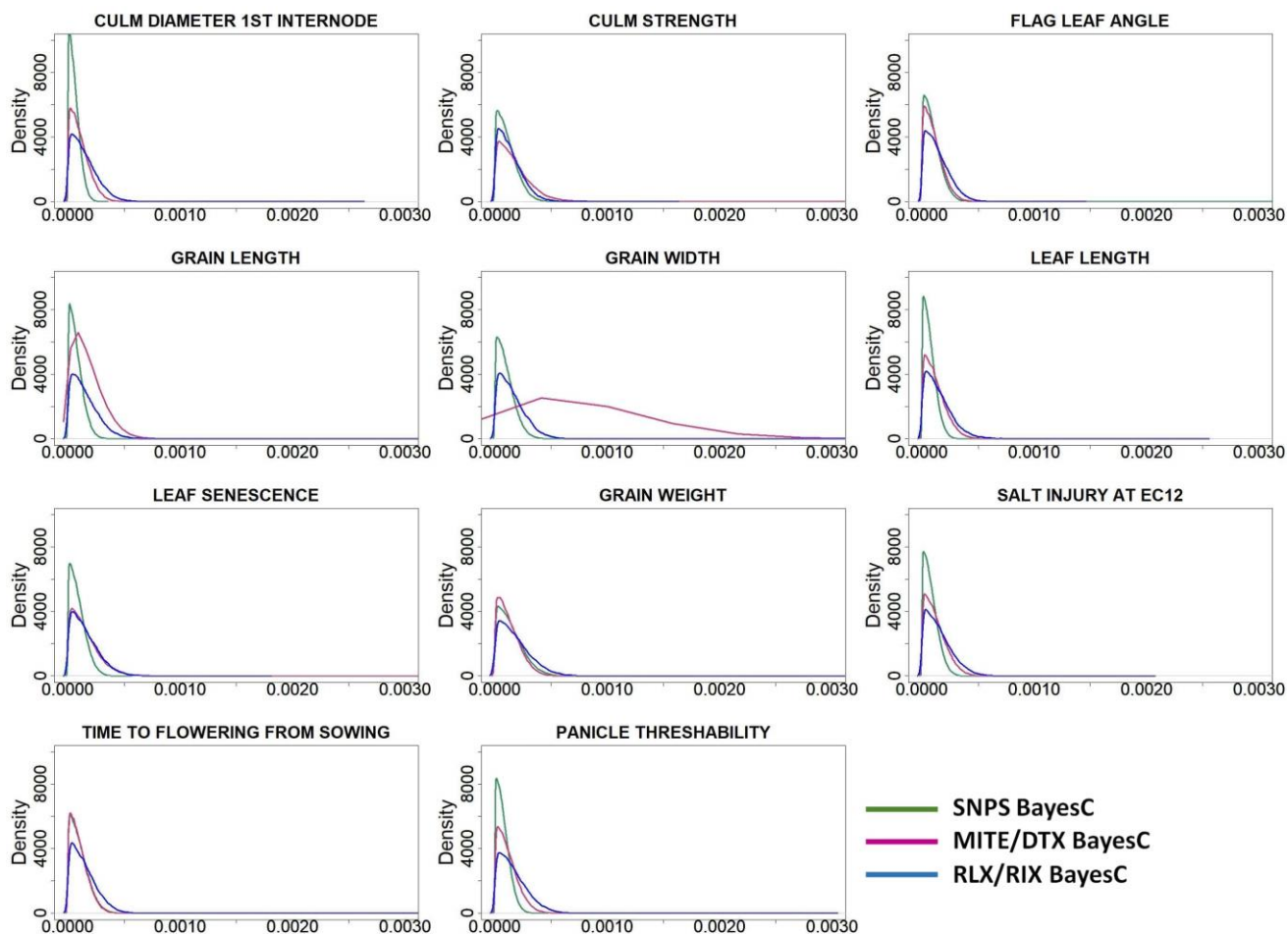
**Supplementary Fig. 1** Plot of variances across iterations to show convergence. Results correspond to “Grain width” under models 1a and 2a. Variances with Bayes C were computed as in <https://github.com/gdlc/BGLR-R/blob/master/inst/md/heritability.md>.



**Supplementary Fig. 2** Raw phenotypic distributions by populations, which are shown with different colors.

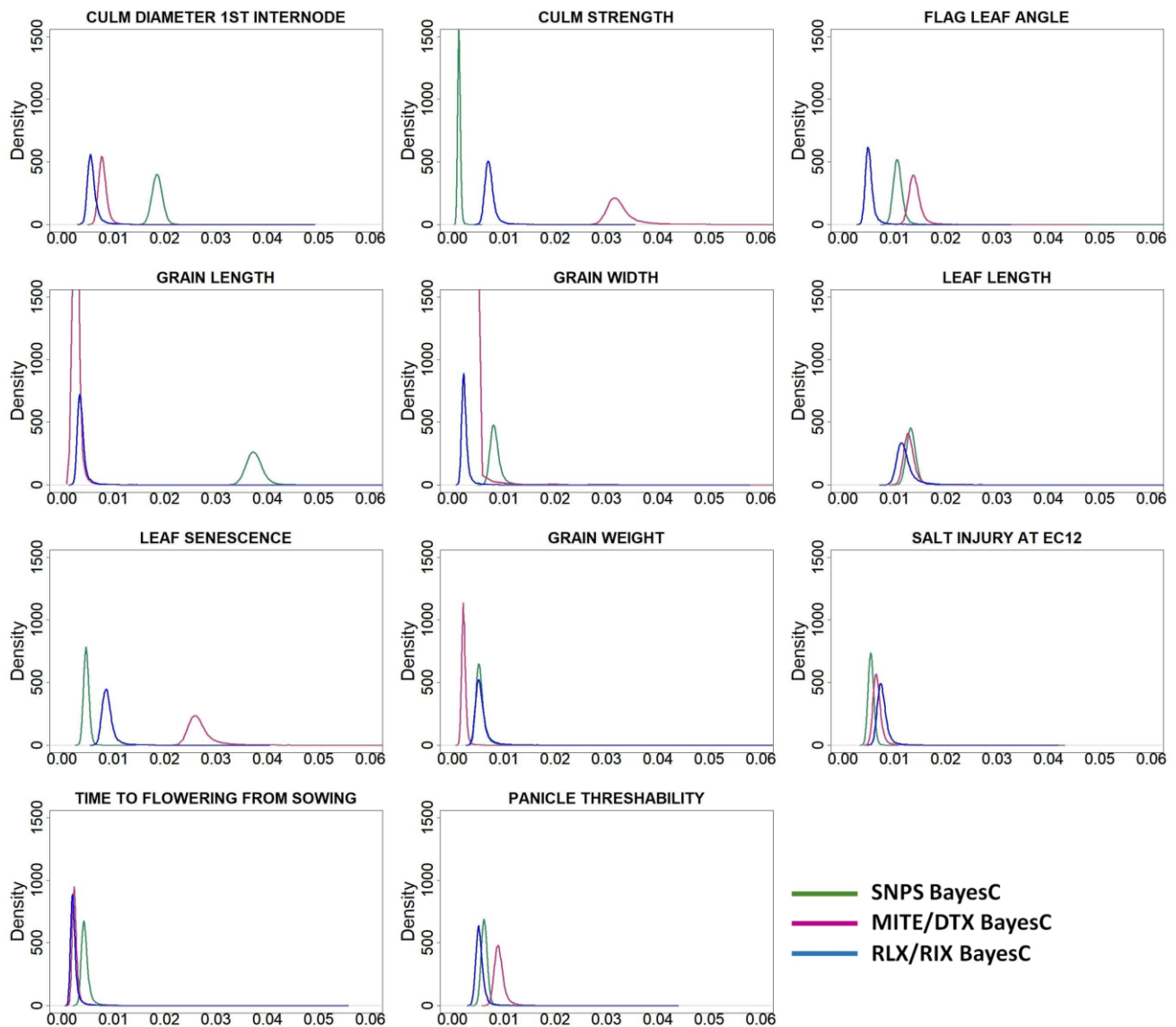


**Supplementary Fig. 3** Principal Component Analysis resulting from each marker set.



**Supplementary Fig. 4** Distributions of estimated marker effects from Bayes C using model 2a in the across population prediction scenario.





**Supplementary Fig. 5** Distributions of marker probabilities entering the model (d) in Bayes C using model 2a in the across population prediction scenario.

**Supplementary Table 3** | Comparison of correlation values of two binary traits under a linear and threshold model.

| Model         |      | Linear       |         |       | Threshold    |         |
|---------------|------|--------------|---------|-------|--------------|---------|
| Phenotype     | SNPs | MITE/DTX     | RLX/RIX | SNPs  | MITE/DTX     | RLX/RIX |
| Culm Diameter | 0.19 | 0.27         | 0.25    | 0.15  | <b>0.29*</b> | 0.15    |
| Culm strength | 0.08 | <b>0.18*</b> | 0.16    | -0.01 | 0.10         | 0.12    |

