Supplemental Figure 1: Selection of 7 environmental covariates for the factorial regression model



DAP = Days after plantation

Period covering the flowering time (under the 4th truss) of the MAGIC population

Supplemental Figure 2: Boxplot distribution of the traits across environments. The colors of the boxplot are according to the groups defined by clustering of the environments

📫 G1 📫 G2 📫 G3 📫 G4



Supplemental Figure 2: Boxplot distribution of the traits across environments. The colors of the boxplot are according to the groups defined by clustering of the environments

firm flw ٠ • 80 100 60 80 60 40 • 40 WDM or 15 WDMor15 HSMor16 HSMor16 LSMor16 LSMor16 HAVI17 HAVI17 Mor15 Mor15 Avi12 Avi17 Avi12 Avi17 fw SSC 125 100 10 75 50 5 25 : 0 HSMor16 WDM or 15 WDMor15 HSMor16 LSMor16 WDIs15 LSMor16 WDIs15 WDIs14 HAVI17 HAVI17 Mor15 Mor15 Avi12 HIs14 Avi12 Avi17 Avi17 Is15 Is14 Is15

🚔 G1 🚔 G2 🚔 G3 븢 G4

Supplemental Figure 3: Heritability in the MAGIC-MET design. For each trait, heritability was computed at every environment and plotted with heritability of the full design H^2 (in green)



Supplemental Figure 4: Proportion of the sum of square attributed to the different factors in the factorial regression model. For each trait, the orange and green stacked bars represent the proportion of the SSq explained by the Genotype and Environment factors in a modified version of model (4) where all environmental covariates have been considered. The remaining colors represent the part of the GxE that could be explained by the different environmental covariates. Stars within the different bars highlighted the significant covariates (α <0.05). The missing bars for some traits denote the covariates that accounted for no variance.



Supplemental Figure 5: Histogram distribution of mean and all plasticity parameters for each trait



Stem diameter (diam)

Supplemental Figure 5: Histogram distribution of mean and all plasticity parameters for each trait



60 -30 · 40 · 20 · . 50 . 75 . 20 . 30 -200 -1

Supplemental Figure 5: Histogram distribution of mean and all plasticity parameters for each trait



Supplemental Figure 6: Physical positions of the MAGIC-MET QTLs for diam, leaf, height, fset, nflw, nfr, firm and SSC. The outer circle with gray font represents the known and cloned QTL/gene for each trait. The following circle with black bars represents the different domestication/improvement sweep regions identified in (Zhu et al. 2018). The other circles plot the CI of QTLs identified on mean, plasticity or with QEI analysis









Supplemental Figure 7: Number of the MAGIC-MET QTLs identified within or outside the domesticated/improved regions. Only the MAGIC-MET QTLs within short CI (lower than 2Mbp) were considered. The response specific category included QEI and plasticity specific QTLs; the common category correspond to QTLs that were commonly identified on mean, plasticity and QEI or at least two of them





Supplemental Figure 9: Correlation between the genotypic sensitivities to environmental covariates from the factorial regression model and slopes from the Finlay-Wilkinson regression model. The negative correlations between "slopes" and "Scv" are an artifact of the analysis due to differences in the order of environments between average performance and the chosen environmental covariates.



Supplemental Figure 10: Venn diagram of the number of QTL specific or commonly detected with mean, PP or using the QEI models.

