



Supplemental Figure 2

Diagrams represents the correlation between the expression of the transcription factors identified by SeqEnrich (Becker et al., 2017) and their target genes in 727 *Arabidopsis thaliana* natural variations (Kawakatsu et al., 2017). Colour code (red to blue) depicts highly negative to highly positive Pearson correlation coefficients. Non-significant ($p > 0.05$) correlations are indicated with a cross.