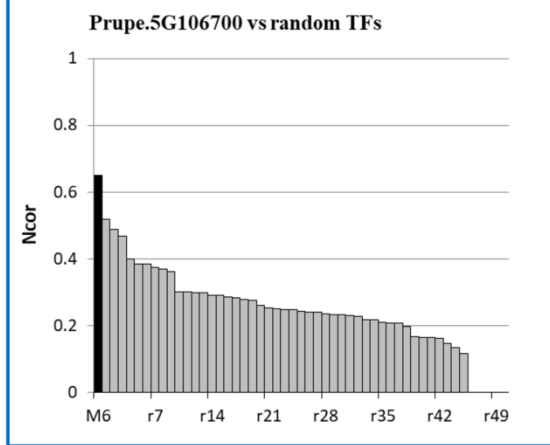
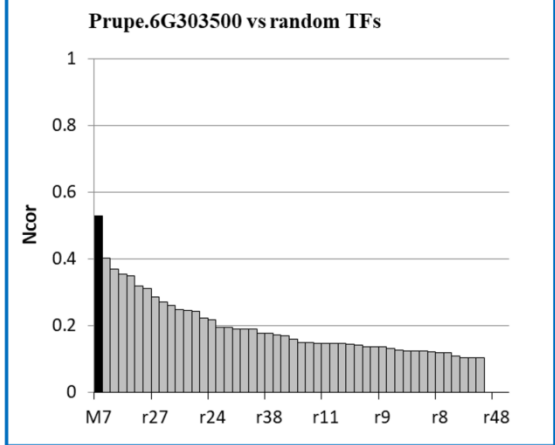


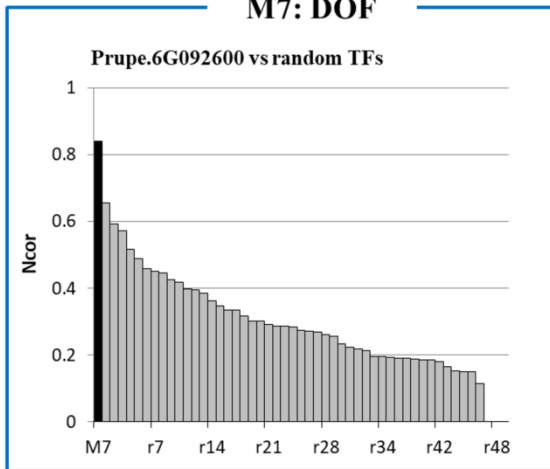
### M6: WRKY



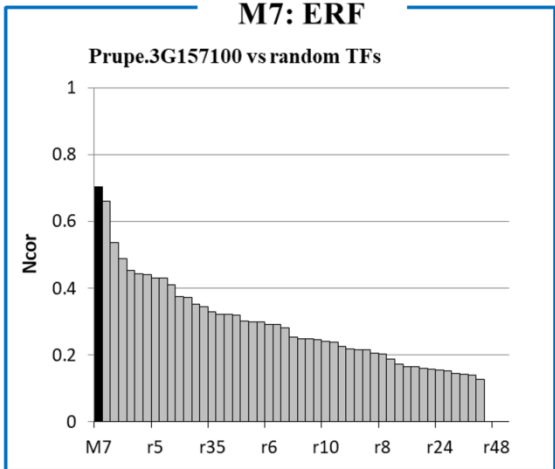
### M7:bHLH

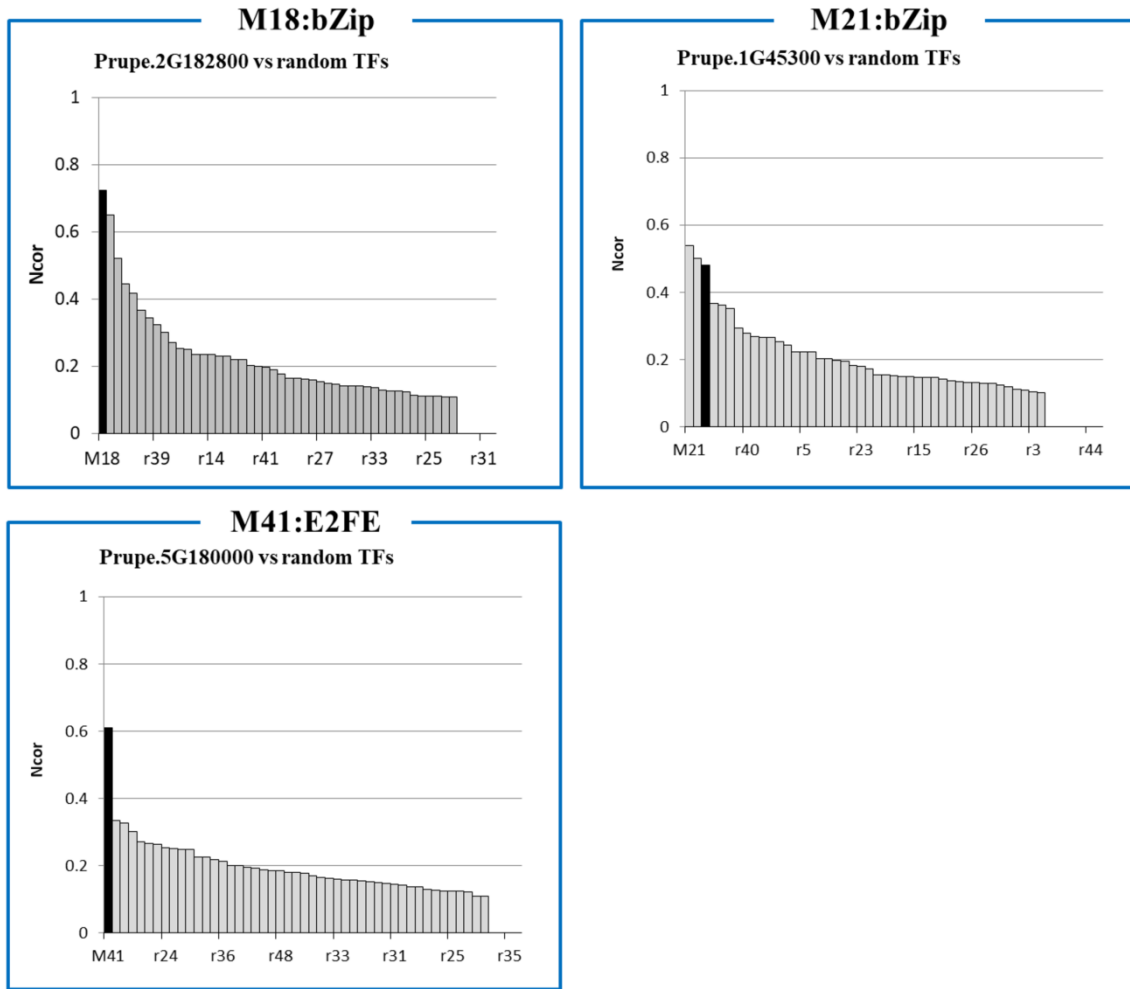


### M7: DOF



### M7: ERF





**Figure S4.** Comparison of the motifs predicted with footprintDB to the corresponding enriched consensus in the promoters of modules M6, M7, M18, M21 and M41, reported on **Table 3**. The x-axis corresponds to the best prediction of a module (black bar) and the predictions of 50 random transcription factors drawn from modules with predicted candidate motifs excluding the module of interest (gray bars). Modules with potential DNA motifs are as follow (M1, M2, M3, M4, M5, M6, M7, M9, M10, M11, M18, M21, M24, M28, M41, M43 and M44). The y-axis shows the Ncor score (from 0 to 1) to score matrix-to-matrix similarities between footprintDB predictions and RSAT enriched motifs. Note that RSAT detects potential motifs from promoter sequences of co-expressed gene modules, whilst with footprintDB motifs are actually predicted from the protein sequence of transcription factors. The gene name in each plot corresponds to the actual TF annotated inside this module. For instance, Prupe.1G106700 in module M6 encodes the WRKY transcription factor.