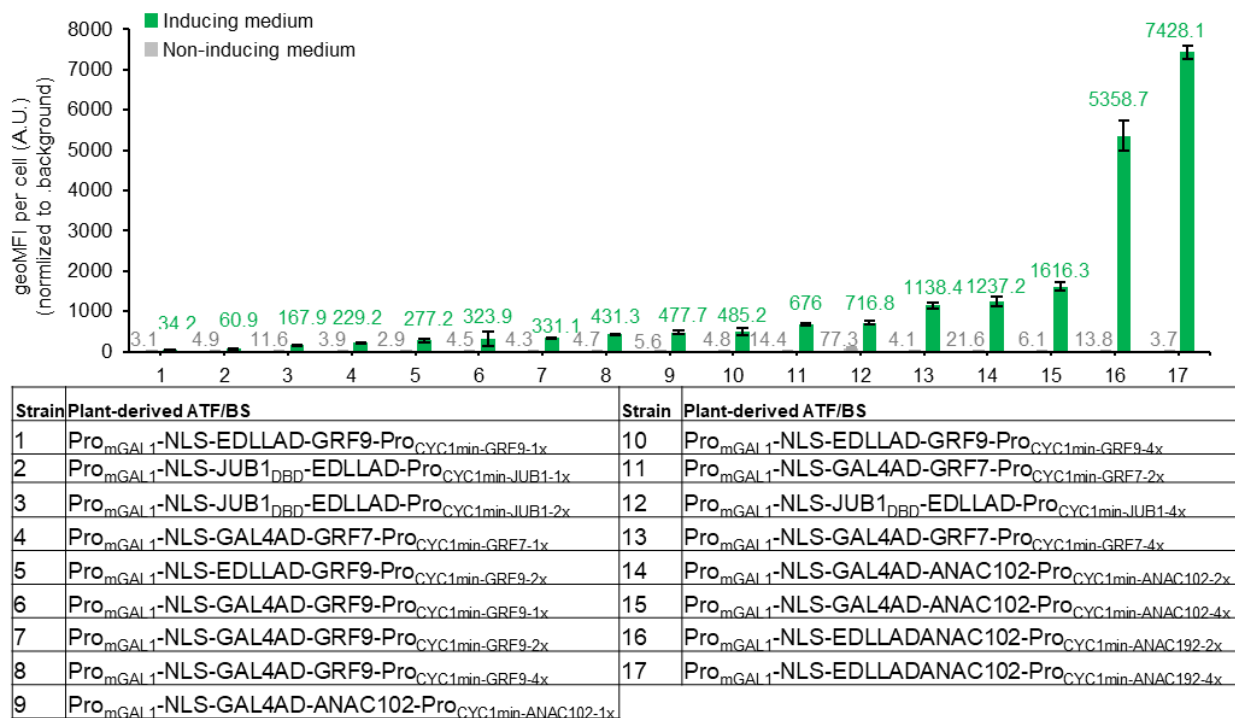


Supplementary Figures



Supplementary Figure 1.

The genome-integrated, plant-based ATFs in *S. cerevisiae*.

A total of 17 different plant-derived ATFs and promoter pair combinations, providing weak (1–7; 0–400 AU), medium (8–13; 400–1,200 AU), and strong (14–17; 1,200–8,000 AU) transcriptional outputs (green) and low basal expression (grey), were selected from the previously characterised library of plant-derived ATF/BS integrated into the *ura3-52* locus. geoMFI, geometric mean fluorescence intensity; AU, arbitrary units, determined using EGFP as a reporter. ANAC102, A NAC domain transcription factor; GRF7, Growth-Regulating Factor 7; GRF9, Growth-Regulating Factor 9; JUB1, JUNGBRUNNEN1; NLS, nuclear localization signal; Pro_{CYC1mini}, *CYC1* minimal promoter; Pro_{mGAL1}, modified *GAL1* promoter. '1X', '2X', and '4X' indicate the number of bindings sites implemented for the ATFs within the *CYC1* minimal promoters. Data are shown in **Data S5**.