**Data availability**

RNASeq Series: GSE124003

**Computational analysis**

RNASeq:

1. Raw reads are aligned to TAIR10, with adapters removed. Transcripts were assembled and quantified with Stringtie. The raw coverage was normalised within each RNA-Seq library into TPM values (transcript-per-million).

2. Prefiltering was performed to remove lowly-expressed transcripts.

3. Temperature perturbation was quantified as log2[ TPMplus1\_27C\_Col-0 / TPMplus1\_22C\_Col-0 ] for each of the 7 time-points.

4. Genotype perturbation was quantified as log2[ TPMplus1\_27C\_pif7-1 + 1 / TPMplus1\_27C\_Col-0 ]

5. Genes were clustered according to the temperature perturbation matrix using XX model.

6. Marker-based target calling: perturbation profiles of a group of 3 marker gene were selected and averaged to generate a signature for each of the perturbation matrix. Within each perturbation matrix, a similarity score is calculated for each gene as the dot product of its profile and the signature profile. The best xx% of the genes are then claimed as transcriptionally perturbed.

ChIP-Seq:

1. Mapped with bowtie2. Doubly mapped reads were discarded.

1. PIF7 binding sites were called from 186CS12 using `callpeak macs2` with a fold-change cut off of 3.25. A gene is classified as a bound target if there is a peak summit within +/- 3000 of its start codon.

1. RPKM values (reads per kilo base-pair per million reads) were estimated from the raw alignments using a bin size of 10bp.

1. RPKM profile was extracted for each peak around the reported summit position. Per-position average and standard deviation was calculated across the peaks.

1. Overlapping ChIP-Seq: two peaks are considered overlapping if their summits were closer than a CUTOFF of 600bp.

Motif analysis:

Functional peaks were defined to be near (+/- 3000bp of start codon) a transcriptionally perturbed gene according to the genotype perturbation matrix. Sequences were extracted around the peak summit for a window of 100bp. Non-novo enrichment was performed using AME against database “ArabidopsisPBM\_20140210.meme” with argument “ame --kmer 2 --control --shuffle-- --hit-lo-fraction 0.25 --evalue-report-threshold 10.0”. De-novo inference of motif was performed using MEME with argument “meme -mod anr -dna -nmotifs 3”.