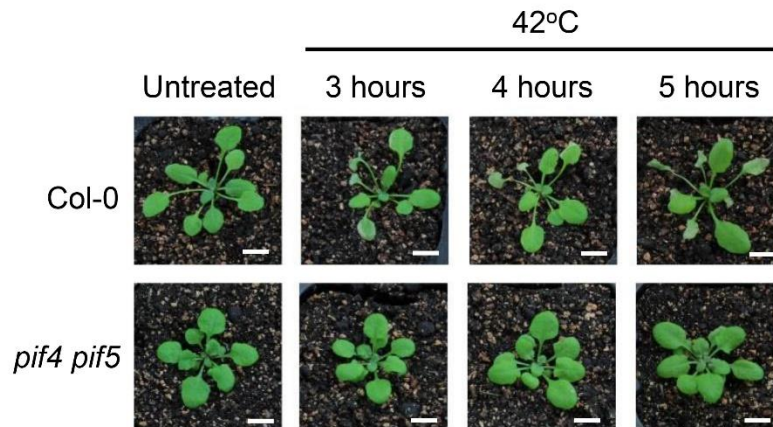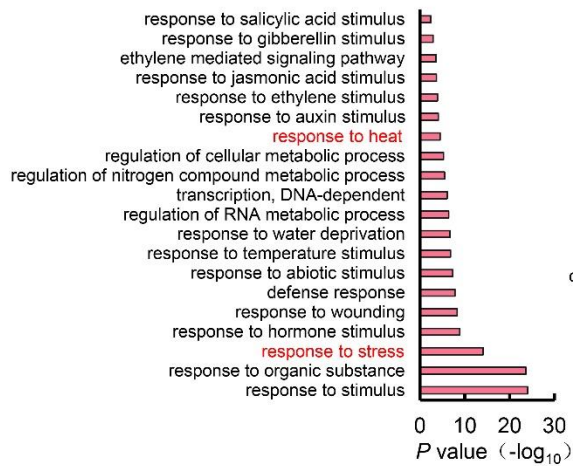# Supplementary data

Fig. S1. Exploration of experimental conditions for heat treatment. Rrepresentative the 3-week-old Col-0 and *pif4-2 pif5-3* grown in soil under the 16h light/8h dark condition after heat treatment at 42 ℃ for 3, 4 and 5 hours respectively and untreated materials. Scale bar, 1 cm.

A Up-regulated genes in *pif4 pif5* heat vs Col-0 heat

response to salicylic acid stimulus
response to gibberellin stimulus
ethylene mediated signaling pathway
response to jasmonic acid stimulus
response to ethylene stimulus
response to auxin stimulus
response to heat
regulation of cellular metabolic process
regulation of nitrogen compound metabolic process
transcription, DNA-dependent
regulation of RNA metabolic process
response to water deprivation
response to temperature stimulus
response to abiotic stimulus
defense response
response to wounding
response to hormone stimulus
response to stress
response to organic substance
response to stimulus

0   10   20   30
P value（-log$_{10}$）

B Down-regulated genes in *pif4 pif5* heat vs Col-0 heat

response to salicylic acid stimulus
cellular catabolic process
homeostatic process
ion homeostasis
peptide transport
response to hydrogen peroxide
response to jasmonic acid stimulus
response to reactive oxygen species
response to water deprivation
response to heat
response to temperature stimulus
response to abscisic acid stimulus
response to osmotic stress
cellular amino acid derivative metabolic process
response to wounding
response to oxidative stress
secondary metabolic process
response to abiotic stimulus
response to stress
response to stimulus
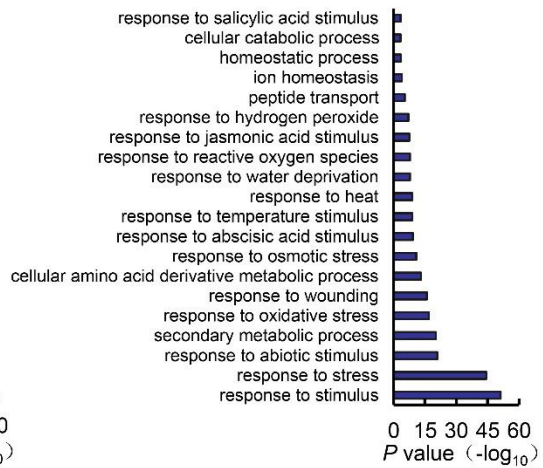
0   15 30 45 60
P value（-log$_{10}$）

Fig. *S2*. **Analysis of down regulated DEGs in Col-0 after heat treatment.**

(A) Gene Ontology analysis of the up regulated genes between wild-type Col-0 and *pif4 pif5* mutant after heat treatment.

(B) Gene Ontology analysis of the down regulated genes between wild-type Col-0 and *pif4 pif5* mutant after heat treatment.
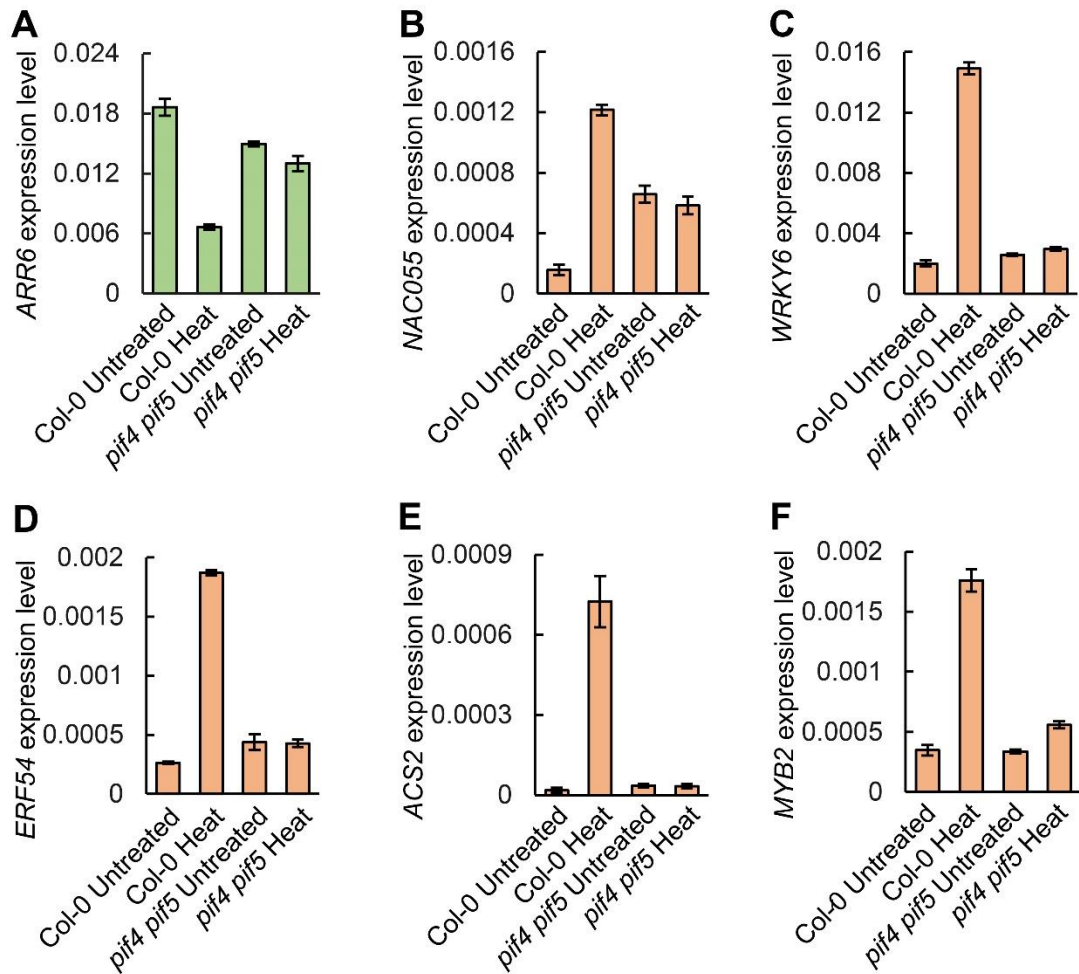
Fig. S3. **The transcript levels of senescence associated genes after heat stress induced senescence.**

(**A-F**) RT-qPCR analysis of *ARR6* (**A**), *NAC055* (**B**), *WRKY6* (**C**), *ERF54* (**D**), *ACS2* (**E**) and *MYB2* (**F**) in Col-0 and *pif4 pif5* of heat treatment and untreated group. 3-week-old wild-type Col-0 and *pif4 pif5* plants grown in soil under the 16h light/8h dark condition and were treated at 42 ℃ for 5 hours. The 3rd and 4th rosette leaves which began to turn yellow at the edge were collected for RNA extraction after 3 days of recovering growth. Three biological replicates were performed. Error bars represent SD.
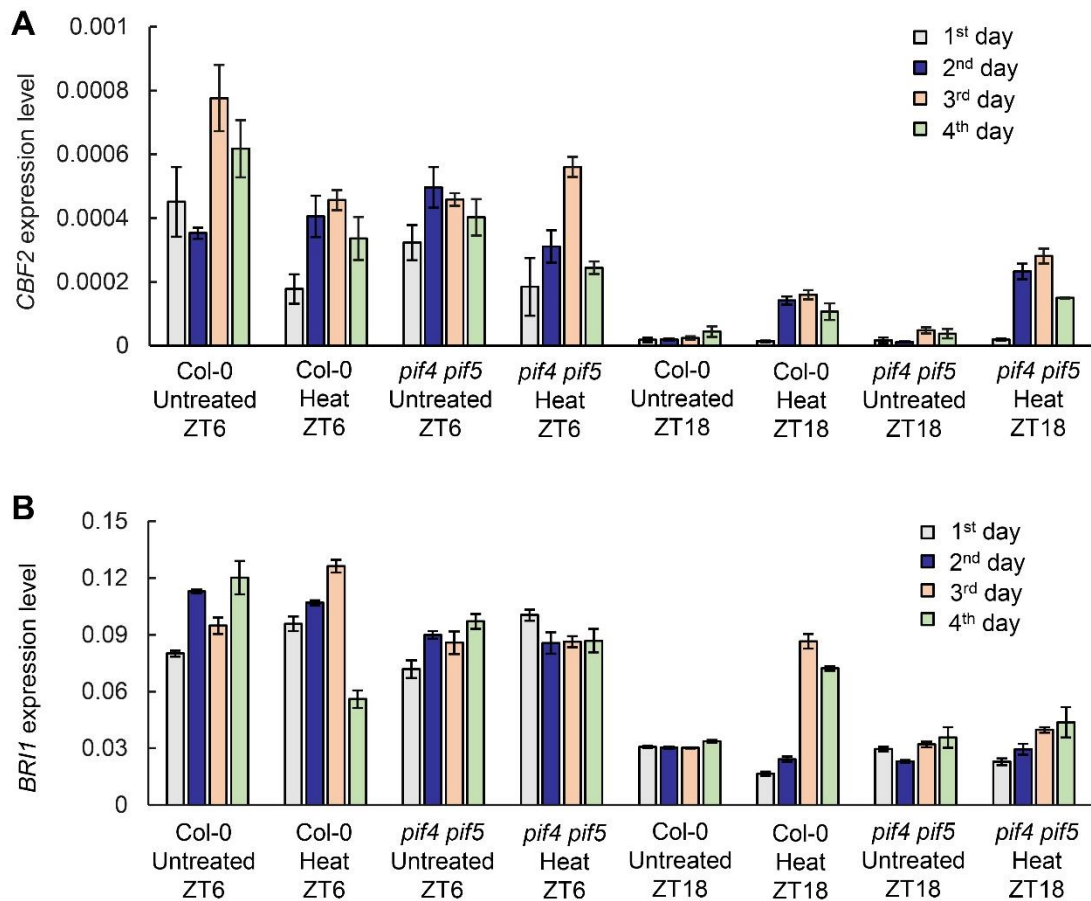
Fig. *S4*. **The change in transcript levels of *CBF2* and *BRI1* during heat stress induced senescence.**

(A-B) The changes in the transcriptional levels of *CBF2* **(A)** and *BRI1* **(B)** during heat stress induced senescence were determined by RT-qPCR. The 3rd and 4th leaves of the heat treated at 42°C for 2 hours and untreated 18-day-old Col-0 and *pif4 pif5* grown in MS with 3% Sucrose agar plate under the LD condition were collected immediately and at the same time points of the day over the next two days at ZT6 and ZT18, respectively. Three biological replicates were performed. Error bars represent SD.

Table S1. Primers used in this study.

Primer name	Sequence	Experiment
*GST-PIF4-Eco*R1-F	CCGCGTGGATCCCCGGAATTCATGGAACACCAAGGTTGGAG	*GST-PIF4*
*GST-PIF4-Xho*1-R	GATGCGGCCGCTCGAGTCGACCTAGTGGTCCAAACGAGAAC	
NAC019-EMSA-G1-F	ATCACGACGATCTAACTGACACACGTGTCAGAATTCAAAAGTGTTTATAGATAAACACAA	EMSA assay
NAC019-EMSA-G1-R	TTGTGTTTATCTATAAACACTTTTGAATTCTGACACGTGTGTCAGTTAGATCGTCGTGAT	
NAC019-EMSA-G2-F	CATTTCAGAAAACCCGTCAACAAAAAACACGTGAAATAAAATATCTCTTCCTTTACCAGT	
NAC019-EMSA-G2-R	ACTGGTAAAGGAAGAGATATTTTATTTCACGTGTTTTTTGTTGACGGGTTTTCTGAAATG	
NAC019-EMSA-G34-F	TTGCGCCTAACTTCTACGATAGACACGTGGACACGTGTCGTCATGATGTAGTTTTGTCCG	
NAC019-EMSA-G34-R	CGGACAAAACTACATCATGACGACACGTGTCCACGTGTCTATCGTAGAAGTTAGGCGCAA	
IAA29-EMSA-G-F	GAGTAGTCACGCACGCACGACTCCGTTCACGTGACATTCACGTTGATATTTCCCCCTCTA	
IAA29-EMSA-G-R	TAGAGGGGGAAATATCAACGTGAATGTCACGTGAACGGAGTCGTGCGTGCGTGACTACTC	
IAA29-EMSA-P-F	GATGTTGGATGTCTAAATTCGTTGAATCATGTGTCTCTTGACGAAATATGCATCTTCTTA	
IAA29-EMSA-P-R	TAAGAAGATGCATATTTCGTCAAGAGACACATGATTCAACGAATTTAGACATCCAACATC	
NAC019-q-F	TTTCTCTCTTCAGCTCATCG	RT-qPCR
NAC019-q-R	ATTTTATCCGTACCCGTAGC	
IAA29-q-F	ACCGAATATGAAGATTGCGA	
IAA29-q-R	GATGAACAGATTCCGCAAAG	
SAG113-q-F	TGTGGAAGAAGACGTGAAAT	
SAG113-q-R	GCATCAGCTTCAAACTCTTC	
CBF2-q-F	GGAAGGAAGAAGTTTCGTGA	
CBF2-q-R	TTTCTTGTTTGGCTCTCTCA	
BRI1-q-F	AATTACCGGAATCTCTGACG	
BRI1-q-R	TGTTCTGAAGGTAAAGCTCC	
PIF4-1222-R	GTTGTTGACTTTGCTGTCCCGC	
PIF4-1184-F	AGATGCAGCCGATGGAGATGTT	
PIF5-1246-R	CGCCGGAGATCCAAATCCCAACAT	
PIF5-1204-F	GCGGGAAATCAGATGCAGACCGTG	
ARR6-q-F	CTTCAAAGTTTGGATCACCG	
ARR6-q-R	TTTCCTCAACATCCAAACCA	
ARR5-q-F	TAGTTCGGTTGGATTTGAGG	

*ARR5*q-R	ATACGAGGCAAGATGTTCTC	
WRKY6-q-F	CTCCGACAAGAAATCTAGGG	
WRKY6-q-R	TTTTTCGCACGCTTATCTTC	
NYE2-q-F	GGAGTTGATGAGAAGAAGCA	
NYE2-q-R	TTCGTCCCGGAACAATTTAT	
ACS2-q-F	CTTGCAGAGAATCAGCTTTG	
ACS2-q-R	AAAAGTCACTCTTCCACCTC	
SAG29-q-F	TGTGTTGCCATTTCTGTTTC	
SAG29-q-R	GCGCTTATAGTGAGGAAGAA	
NAC055-q-F	GGATTATGCATGAGTACCGT	
NAC055-q-R	CGACCACTCGTCATTAGATT	
ERF54-q-F	TAACTTGGAGAGCAAGGAAC	
ERF54-q-R	CCAAATCATCCCAAAGAGGA	
MYB2-q-F	TCCTAGTCAACTTCGTCTCT	
MYB2-q-R	CCTCTTCTAACATCTGGACG	
ACT2-F	GCTGAGAGATTCAGATGCCCA	
ACT2-R	GTGGATTCCAGCAGCTTCCAT	
TUB4-F	AGGGAAACGAAGACAGCAAG	
TUB4-R	GCTCGCTAATCCTACCTTTGG	