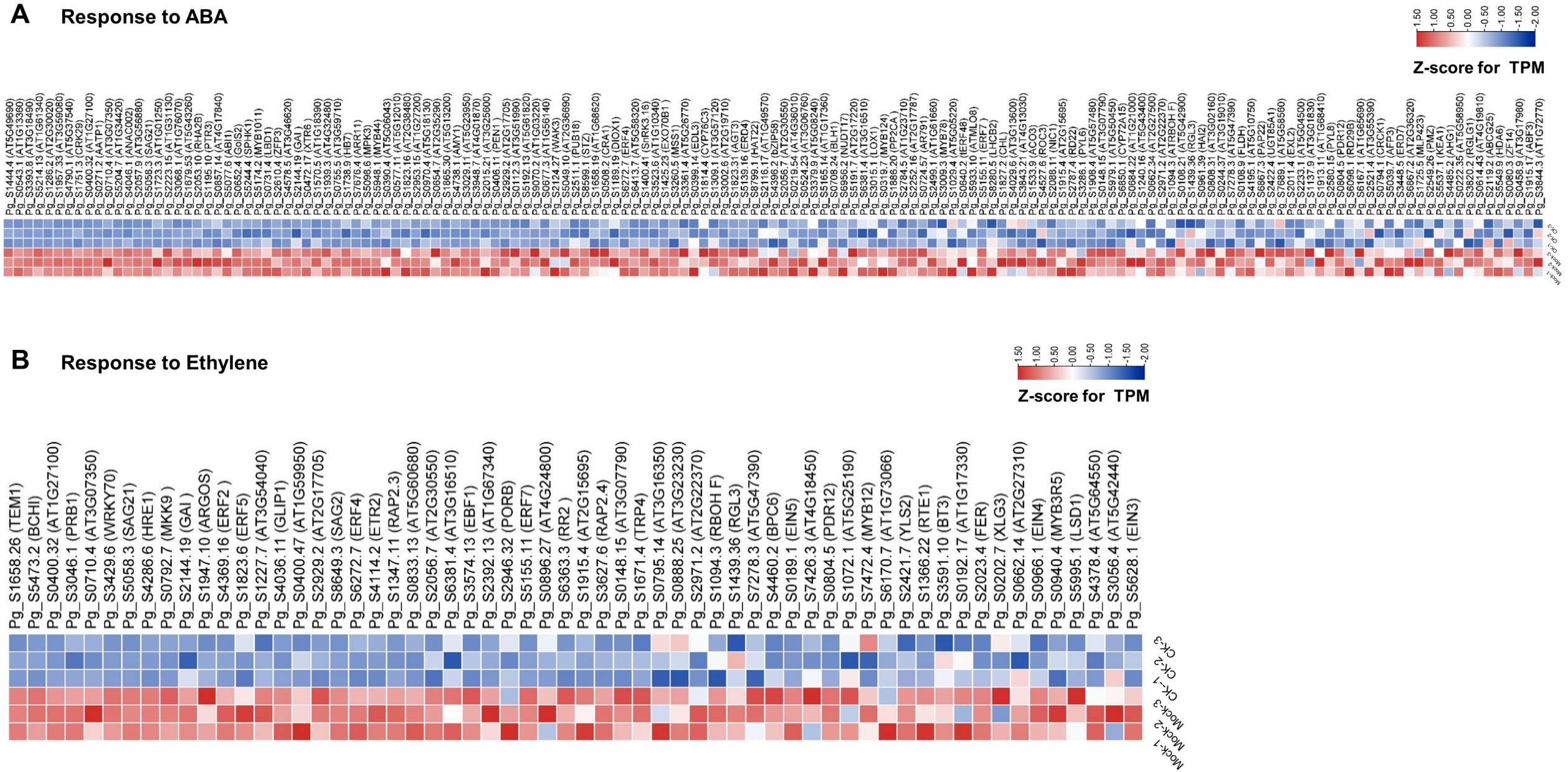
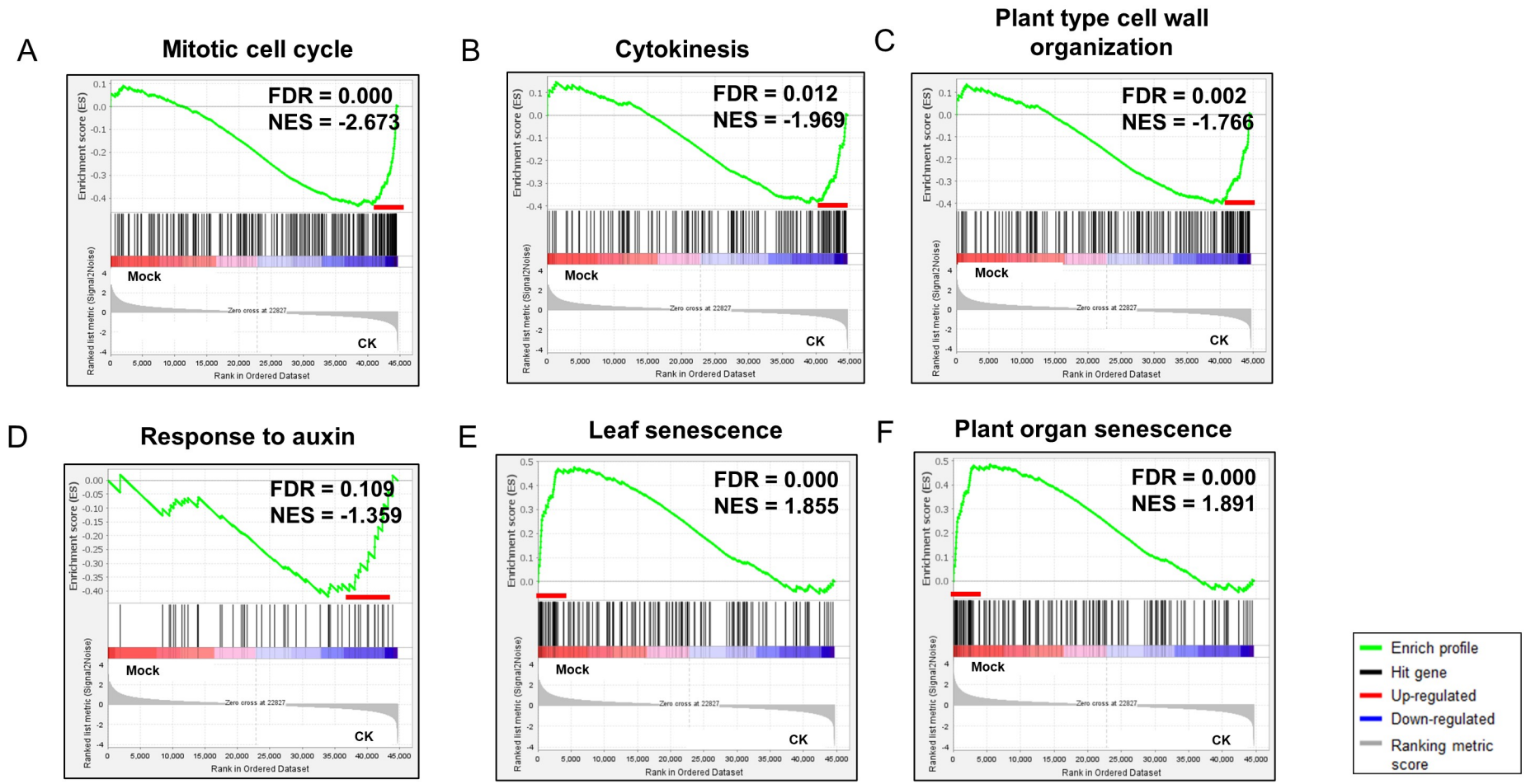
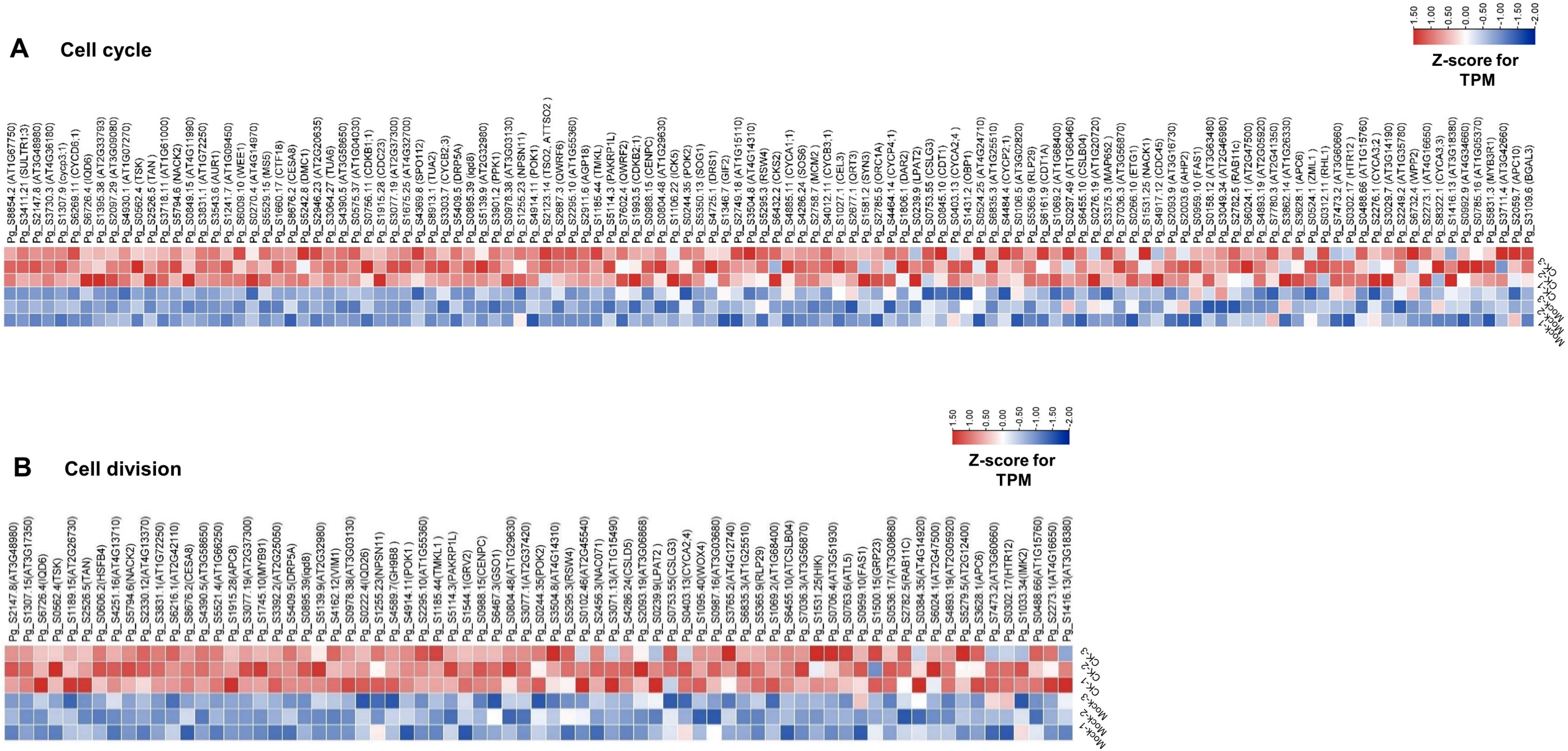


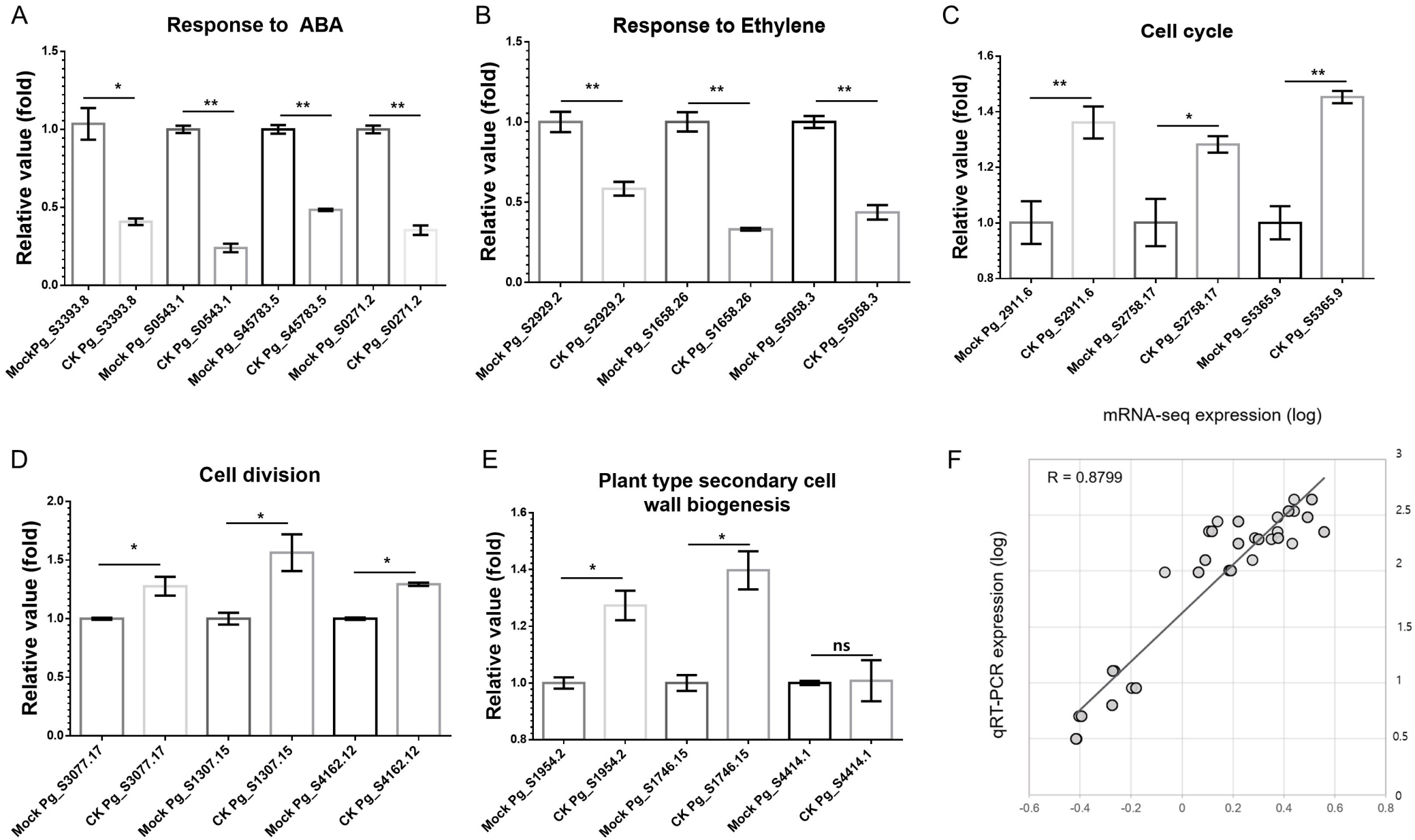
Supplementary figure 1. Expression heatmap of the leading-edge subset genes of (A) Response to ABA and (B) Response to Ethylene presented in Fig. 3C.



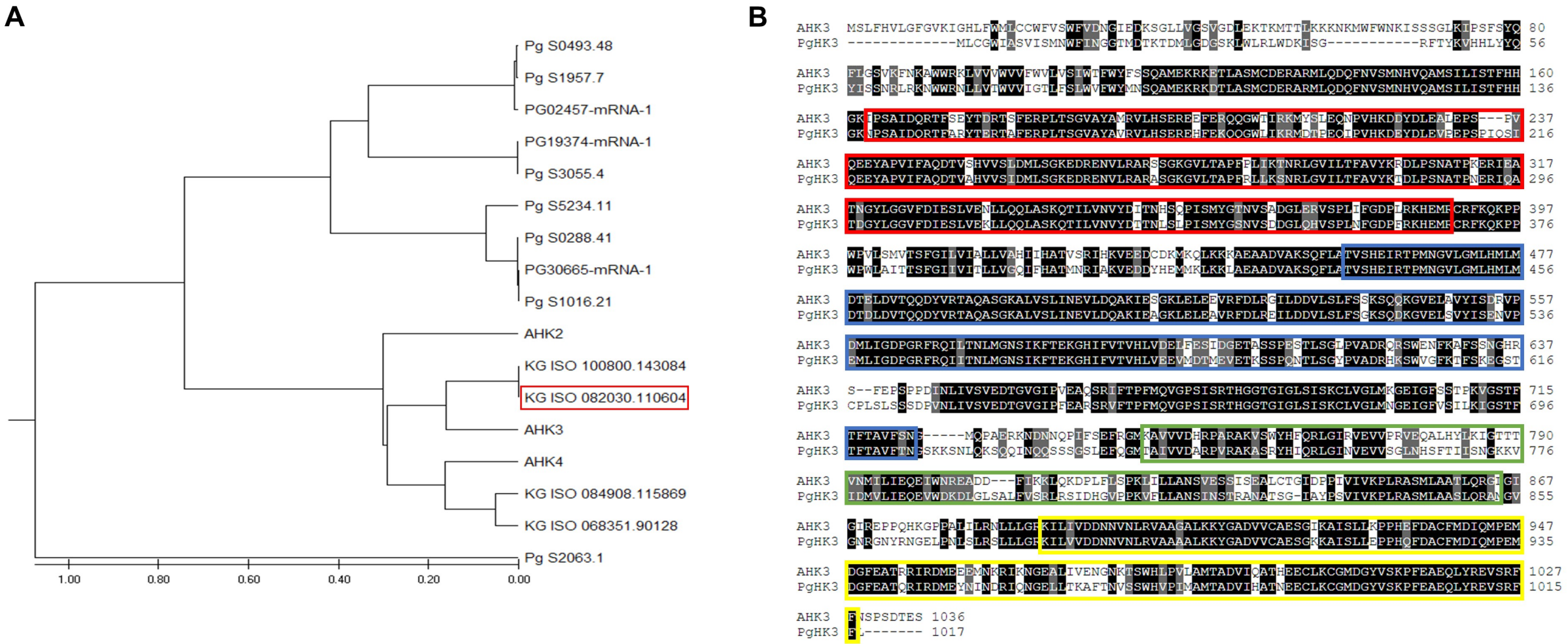
Supplementary figure 2. Enrichment plot for Mitotic cell cycle (FDR = 0.000, NES = -2.6730092), cytokinesis (FDR = 0.012770083, NES = -1.96904), Plant type cell wall organization (FDR = 0.0022396417, NES = -1.7666447), Response to auxin (FDR = 0.109900534, NES = -1.3593768), Leaf senescence (FDR = 0.00014285714, NES= 1.8558527) and Plant organ senescence (FDR = 0.000, NES = 1.8910872) GSEA. In the plot, the red line indicates a leading-edge subset of the enriched gene set group leading to enrichment scores concerning expression changes.



Supplementary figure 3. Expression heatmap of the leading-edge subset genes of (A) cell cycle and (B) cell division presented in Fig. 3D.

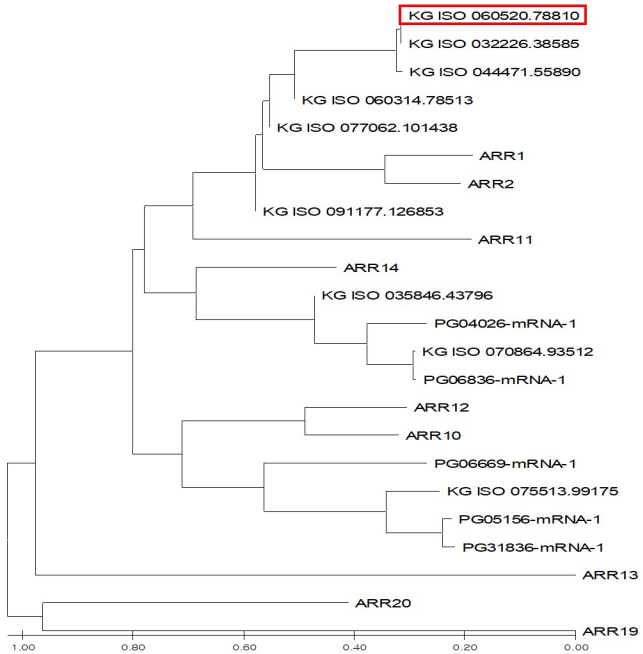

A
Response to ABA
Relative value (fold)
MockPg_S3393.8
CK Pg_S3393.8
Mock Pg_S0543.1
CK Pg_S0543.1
Mock Pg_S45783.5
CK Pg_S45783.5
Mock Pg_S0271.2
CK Pg_S0271.2
B
Response to Ethylene
Relative value (fold)
Mock Pg_S2929.2
CK Pg_S2929.2
Mock Pg_S1658.26
CK Pg_S1658.26
Mock Pg_S5058.3
CK Pg_S5058.3
C
Cell cycle
Relative value (fold)
Mock Pg_2911.6
CK Pg_S2911.6
Mock Pg_S2758.17
CK Pg_S2758.17
Mock Pg_S5365.9
CK Pg_S5365.9
D
Cell division
Relative value (fold)
Mock Pg_S3077.17
CK Pg_S3077.17
Mock Pg_S1307.15
CK Pg_S1307.15
Mock Pg_S4162.12
CK Pg_S4162.12
E
Plant type secondary cell wall biogenesis
Relative value (fold)
ns
Mock Pg_S1954.2
CK Pg_S1954.2
Mock Pg_S1746.15
CK Pg_S1746.15
Mock Pg_S4414.1
CK Pg_S4414.1
F
R = 0.8799
qRT-PCR expression (log)
mRNA-seq expression (log)

Supplementary figure 4. Validation of the transcripts level of GSEA transcriptome data by qRT-PCR. (A) The expression level of Response to ABA related genes. (B) The expression level of Response to Ethylene related genes. (C) The expression level of Cell cycle related genes. (D) The expression level of Cell division related genes. (E) The expression level of Plant type secondary cell wall biogenesis related genes. The expression level was measured by quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR). *PgACT1* was used as an internal control. Error bars indicate SEM (*P < 0.05, **P < 0.01 Student's t-test, n.s., no significance). (F) Analysis between qRT-PCR expression and mRNA-seq data using linear regression. The TPM which is TMM-normalized of target genes divided by that of *PgACT1*, as an internal control, is indicated in the x axis, while relative expression levels of each gene were determined by $2^{-\Delta\Delta CT}$ method, as indicated in the y axis.

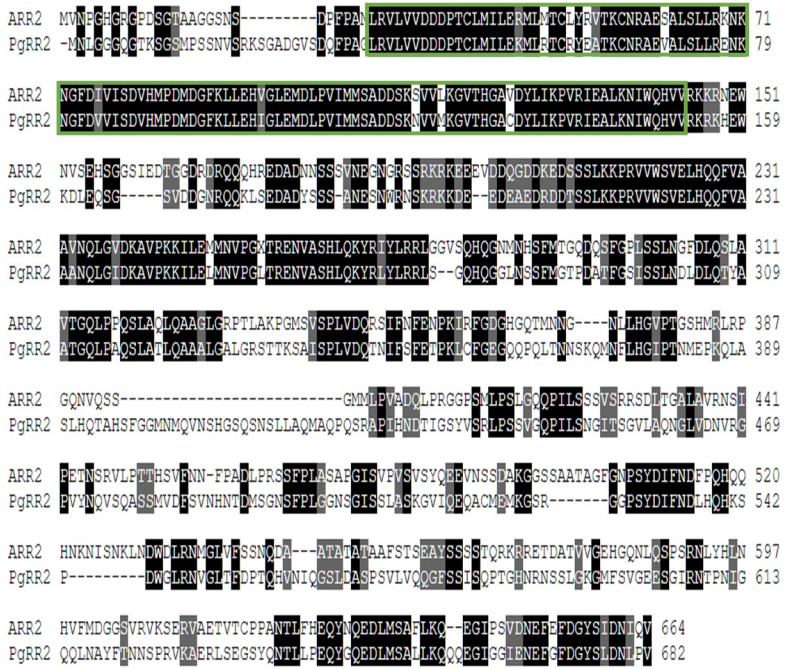


Supplementary figure 5. Identification of putative CK receptor genes in *P. ginseng* (A) Phylogenetic trees of AHK2, AHK3, AHK4 and putative PgHK proteins were analyzed with MEGA 7 program. Tree scale bar: 0.1. (B) CHASE, Histidine kinase and Response regulatory 2 domain were conserved in PgHK3. Conserved domains are CHASE domain in red, Histidine kinase domain in blue, Response regulatory 1 domain in green, Response regulatory 2 in yellow. Identical amino acids were shaded in black, and similar amino acids were shaded in gray.

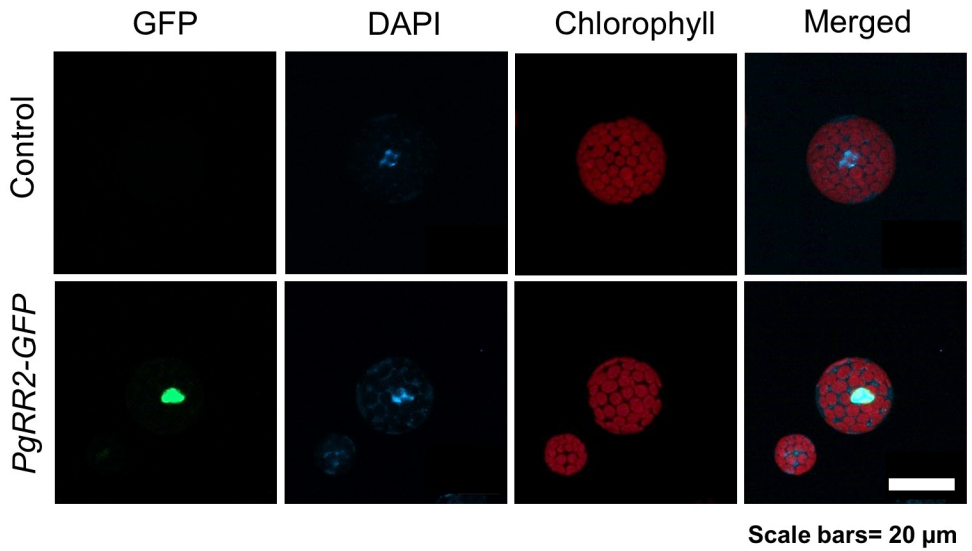
A


KG ISO 060520.78810
KG ISO 032226.38585
KG ISO 044471.55890
KG ISO 060314.78513
KG ISO 077062.101438
ARR1
ARR2
KG ISO 091177.126853
ARR11
ARR14
KG ISO 035846.43796
PG04026-mRNA-1
KG ISO 070864.93512
PG06836-mRNA-1
ARR12
ARR10
PG06669-mRNA-1
KG ISO 075513.99175
PG05156-mRNA-1
PG31836-mRNA-1
ARR13
ARR20
ARR19
1.00
0.80
0.60
0.40
0.20
0.00

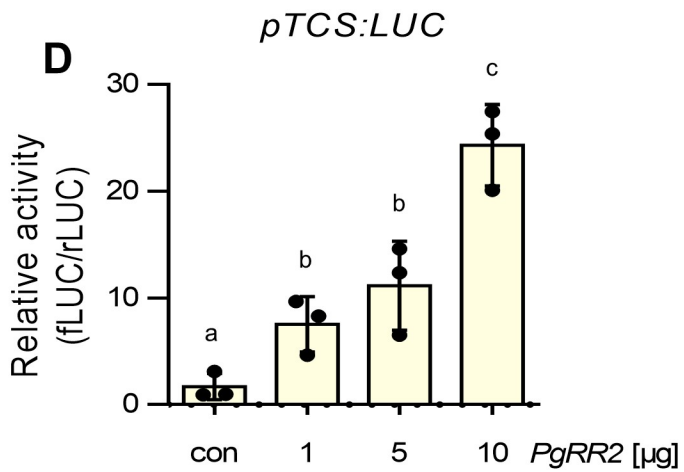
B


ARR2 MVNPGHGRGPDSGTAAGGSNS---------DFFPAMLRVLVVDDDPTCLMILERMLMTCLYRVTKCNRAESALSLLRENK 71
PgRR2 -MNLGPGQGTKSGSMPSSNVSRKSGADGVSDQFPAKLRVLVVDDDPTCLMILEKMLETCEYEATKCNRAEVALSLLRENK 79
ARR2 NGFDIVISDVHMPDMDGFKLLEHVGLEMDLPVIMMSADDSKSVVLKGVTHGAVDYLIKPVRIEALKNIWQHVVRKKRNEW 151
PgRR2 NGFDVVISDVHMPDMDGFKLLEHIGLEMDLPVIMMSADDSKNVVMKGVTHGACDYLIKPVRIEALKNIWQHVVRKRKHEW 159
ARR2 NVSEHSGGSIEDIGGDRDRQQQHFEDADNNSSSVNENERSSRKRKEEEVDDQGDDKEDSSSLKKPRVVWSVELHQQFVA 231
PgRR2 KDLEQSG-----SVDDGNRQQKLSEDADYSSS-ANESNVRNSKRKKDE--EDEAEDRDDTSSLKKPRVVWSVELHQQFVA 231
ARR2 AVNQLGVDKAVPKKILEVMNVPGVTRENVASHLQKYRIYLRRLGGVSQHQGNMNHSFMTGQDQSFGPLSSLNGFDLQSLA 311
PgRR2 AANQLGIDKAVPKKILELMNVPGLTRENVASHLQKYRLYLRRLS--GQHQGGLNSSFMGTPDATFGSLSSLNDLDLQTYA 309
ARR2 VTGQLEPQSLAQLQAAGLGRPTLAKPGMSVSPLVDQRSIFNFENPKIRFGDGHGQTMNNG----NLLHGVPTGSHMRLRP 387
PgRR2 ATGQLEAQSLATLQAAALGALGRSTTKSAISPLVDQTNIFSFETPKLCFGEGQQPQLTNNSKQMNFLHGIPTNMEPKQLA 389
ARR2 GQNVQSS----------GMMLPVADQLPRGGPSMLPSLGQQPILSSSVSRRSDLTGALAVRNSL 441
PgRR2 SLHQTAHSFGGMNMQVNSHGSQSNSLLAQMAQPQSRAPIHNDTIGSYVSRLPSSVGQPILSNGITSGVLAQNGLVDNVRG 469
ARR2 PETNSRVLPTTHSVENN-FPADLPRSSFPLASAEGISVPVSVSYQEEVNSSDAKGSSAATAGFGNPSYDIFNDFPQHQQ 520
PgRR2 PVYNQVSQASSMVDFSVNHNTDMSGNSFPLGGNSGISSLASKGVIQEQACMQMKGSR-------GGPSYDIFNDLHQHKS 542
ARR2 HNKNISNKLNDWDLRNVGLVFSSNQDA---ATATATAAFSTSEAYSSSSTQRKRRETDATVVGEHGQNLQSPSRNLYHIN 597
PgRR2 P---------DWGLRNVGLTGDPTQHVNIQGSLDASPSVLVQQGFSSISQPTGHNRNSSLGKGMFSVGEESGIRNTPNIG 613
ARR2 HVFMDGGSVRVKSERVAETVTCPPANTLFHEQYNQEDLMSAFLKQ--EGIPSVDNEEEFDGYSIDNIQV 664
PgRR2 QQLNAYFNNSPRVKAERLSEGSYQNTLLPEQYGQEDLMSALLKQQQEGIGGIENEEFGFDGYSLDNLEV 682

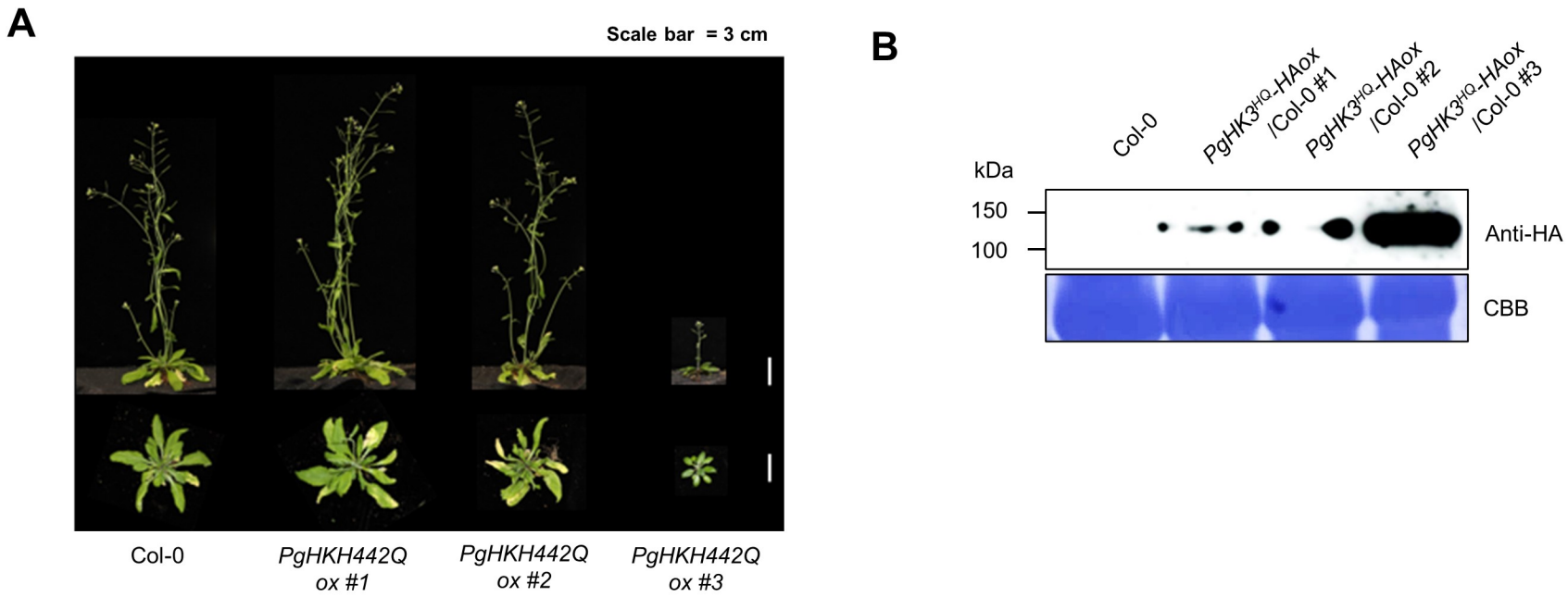
C


GFP
DAPI
Chlorophyll
Merged
Control
PgRR2-GFP
Scale bars= 20 μm

D


pTCS:LUC
Relative activity
(fLUC/rLUC)
30
20
10
0
a
b
b
c
con
1
5
10
PgRR2 [μg]

Supplementary figure 6. Identification of putative type-B response regulator genes in *P. ginseng* genome. (A) Phylogenetic trees of type-B ARRs and putative PgRRs were analyzed with MEGA 7 program. KG ISO 060520.78810 was cloned as a *PgRR2*. (B) Response regulatory domains were conserved in PgRR2. Response regulatory 1 domain is conserved (green box). Identical amino acids were shaded in black, and similar amino acids were shaded in gray. (C) PgRR2 is localized at the nucleus. Scale bar = 20μm. (D) Measurement of transcriptional level of *proTCS::LUC* by *PgRR* concentration (1 – 10 μg). Error bars represent standard error (n=3). Different lowercase letters indicate statistically significant differences $P < 0.05$; one-way ANOVA, followed by Tukey's multiple range test.



Supplementary figure 7. (A) Phenotype of 5-week-old *PgHK3H442Q* overexpressing lines in Col-0 background. Scale bar = 3. (B) The protein expression levels of *PgHK3-H442Q* overexpressing lines. Proteins were detected with an anti-HA antibody.