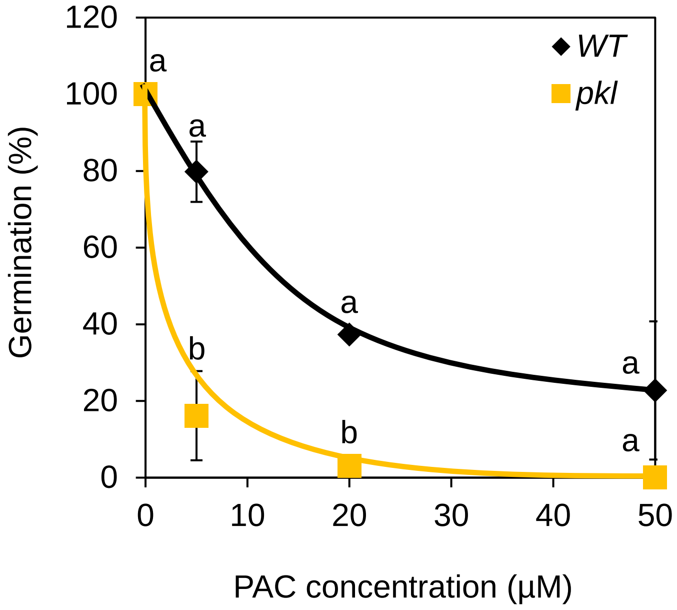
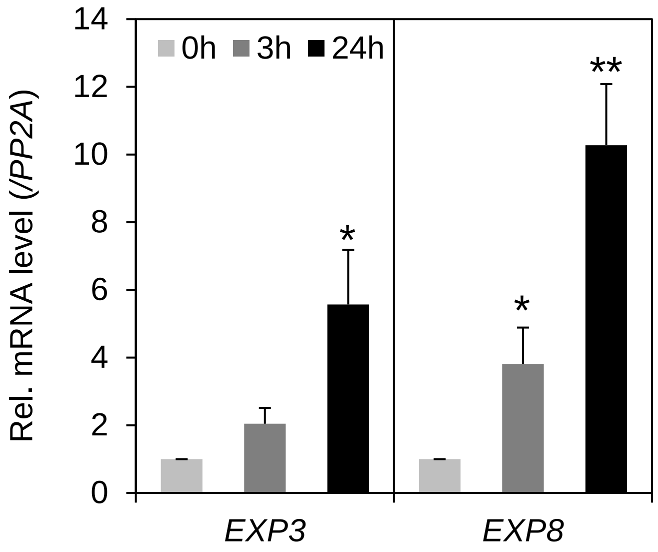
Supplemental Figure 1.



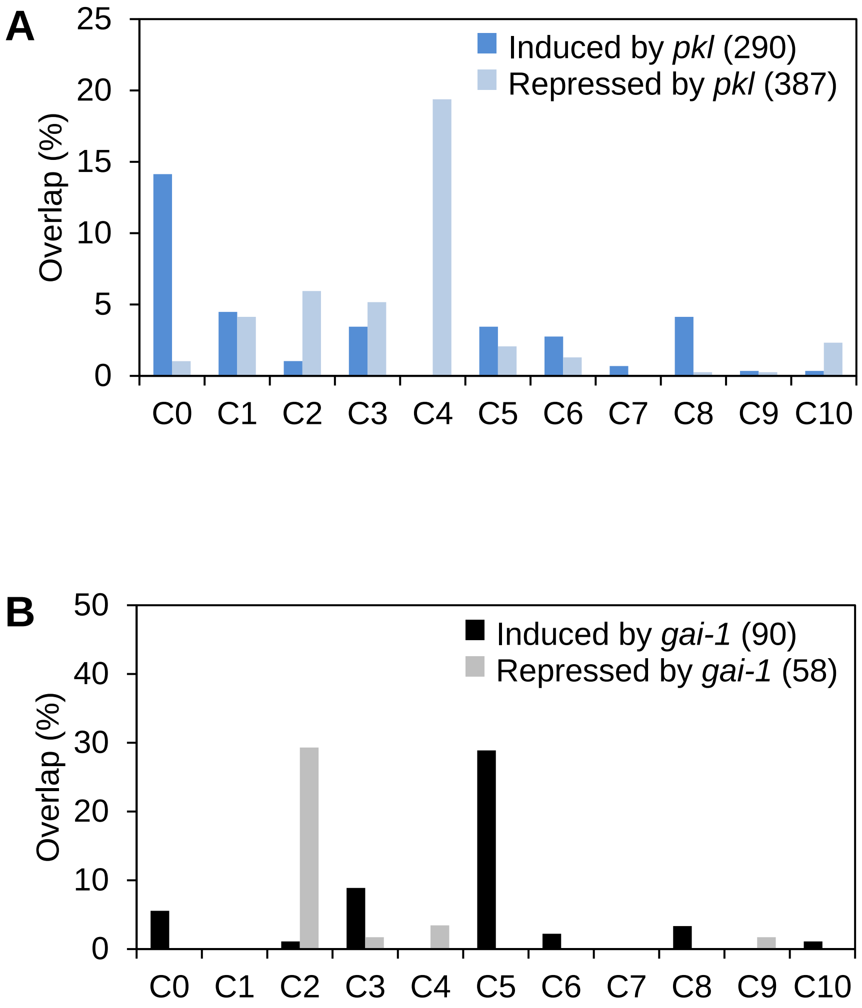
Supplemental Figure 1. *pkl* is more sensitive to PAC than WT in seed germination. Data are means ± SE (3 biological replicates). Different letters above the curves indicate significant differences, $p<0.01$.

Supplemental Figure 2.



Supplemental Figure 2. GA induction time course of *EXPs*.
Relative transcript levels of *EXP3* and *EXP8* in 7-day-old *ga1-13* seedlings in response to 10µM GA_3 treatment were analyzed by RT-qPCR. Data are means ± SE (3 biological replicates). * $p<0.05$; ** $p<0.01$.

Supplemental Figure 3.



Supplemental Figure 3. Comparison of RNA-Seq data with previous microarray datasets.
(A) Overlap between C0-C10 clusters and *pkl*-responsive genes. The *pkl*-induced and repressed genes were identified by microarray analysis using 14-d-old WT and *pkl-1* mutant seedlings grown on growth media under 24-hr light (Zhang et al. 2012). Numbers in parentheses are the total of *pkl*-induced or -repressed genes in this published dataset.
(B) Overlap between C0-C10 clusters and *gai*-responsive genes. The *gai*-induced and repressed genes were identified by microarray analysis using WT and *HS::gai-1* transgenic line; The 3-d-old WT and *HS::gai-1* seedlings grown on growth media at 22°C under dark conditions were treated for 30 min at 37°C and then incubated at 22°C for up to 4 hr (Gallego-Bartolome et al., 2011). Numbers in parentheses are the total of *gai-1*-induced or -repressed genes in this published dataset.
In (A) and (B), to calculate the % overlap for each gene cluster, we divided the number of overlapping genes in each category by the total number of genes in that same category in the published dataset.

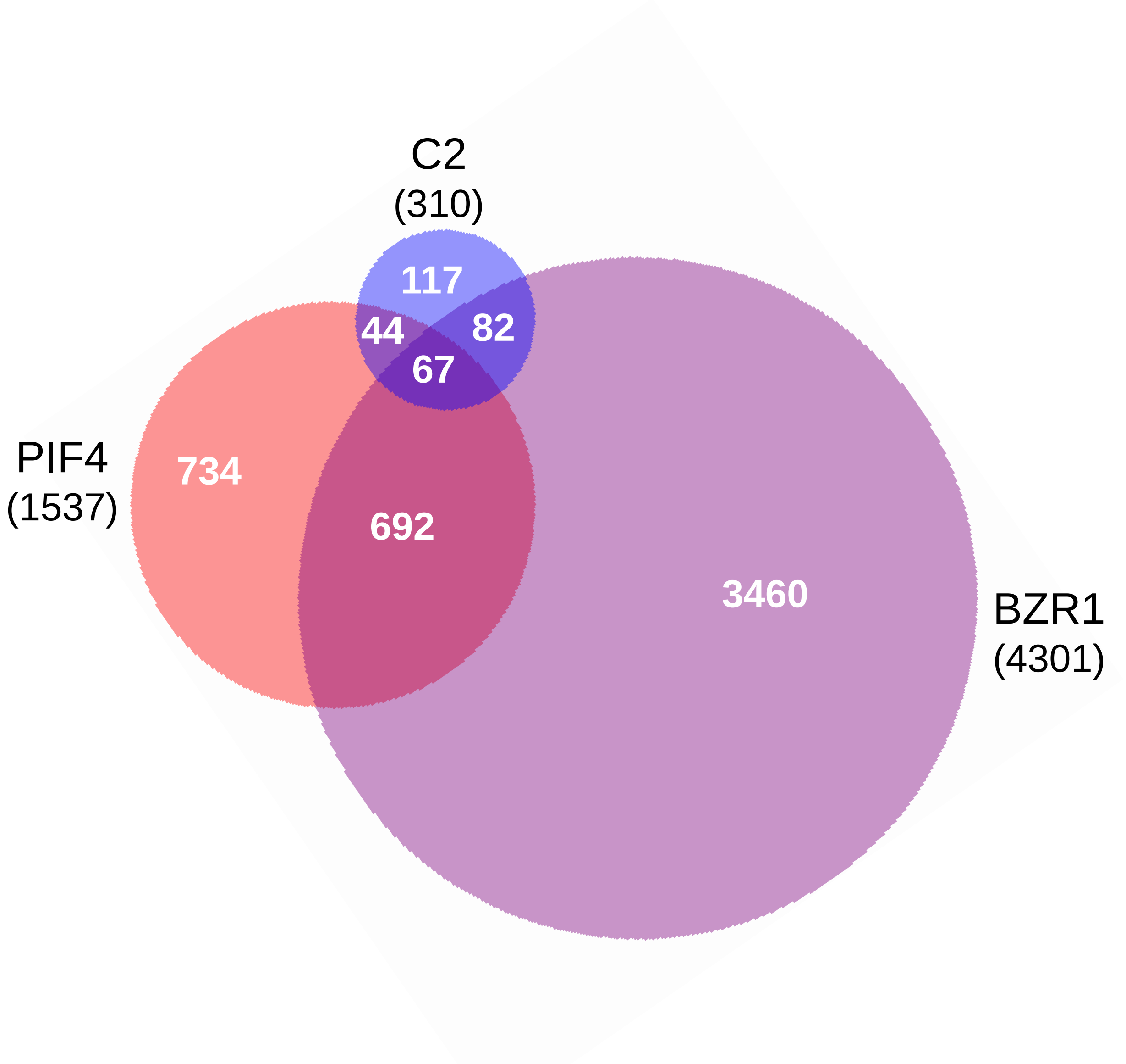
Supplemental Figure 4.

Ribosome-related genes of C7

GA/Mock	*ga1-13*	*ga1-13 pkl*
Up	94% (174)	4% (8)
Down	6% (12)	96% (178)

Supplemental Figure 4. Ribosome-related C7 cluster genes were up-regulated by GA in *ga1*, but down-regulated by GA in *ga1 pkl*.

Supplemental Figure 5.



Supplemental Figure 5. The C2 cluster genes are highly enriched in PIF4- and BZR1-target genes. The Venn diagram shows overlap among our C2 cluster genes and the direct target genes of PIF4 and BZR1 (Oh et al., 2012).

Supplemental Table 1. Summary of GO terms enriched among genes in each cluster.

Cluster (Gene #)	Enriched GO BP and CC terms	Number of genes in the cluster (%)	Number of genes in the background (%)	FDR
C0 (483)	**response to stimulus**^{BP}	98 (21.1)	4057 (10.7)	3.00E-10
	└ response to stress	67 (14.4)	2320 (6.1)	1.00E-10
	└ defense response	34 (7.3)	766 (2.0)	3.00E-12
	└ response to abscisic acid stimulus	17 (3.7)	378 (1.0)	6.00E-06
	└ regulation of defense response	6 (1.3)	66 (0.2)	5.00E-05
	post-embryonic development^{BP}	28 (6.0)	705 (1.9)	3.00E-08
	└ seed development	22 (4.7)	530 (1.4)	8.00E-07
	lipid localization^{CC}	12 (2.6)	24 (0.1)	9.00E-61
C1 (823)	**metabolic process**^{BP}	292 (36.0)	10614 (28.1)	4.00E-05
	└ protein amino acid phosphorylation	55 (6.8)	946 (2.5)	1.00E-11
	└ sulfate assimilation	5 (0.6)	13 (0.0)	1.00E-09
	response to stimulus^{BP}	172 (21.2)	4057 (10.7)	2.00E-18
	└ response to stress	123 (15.2)	2320 (6.1)	6.00E-22
	└ defense response	58 (7.2)	766 (2.0)	5.00E-20
	└ response to endoplasmic reticulum stress	8 (1.0)	23 (0.1)	2.00E-15
	└ innate immune response	36 (4.4)	347 (0.9)	5.00E-20
	└ systemic acquired resistance	9 (1.1)	54 (0.1)	3.00E-08
	plasma membrane^{CC}	80 (9.9)	1456 (3.9)	2.00E-15
	endoplasmic reticulum^{CC}	40 (4.9)	466 (1.2)	6.00E-17
	proteasome complex^{CC}	11 (1.4)	67 (0.2)	9.00E-11
C2 (310)	**response to stimulus**^{BP}	69 (22.6)	4057 (10.7)	5.00E-09
	└ response to chemical stimulus	44 (14.4)	2085 (5.5)	4.00E-09
	└ response to auxin stimulus	24 (7.9)	360 (1.0)	5.00E-29
	└ response to gibberellin stimulus	8 (2.6)	159 (0.4)	5.00E-06
	developmental growth^{BP}	11 (3.6)	242 (0.6)	2.00E-07
	└ unidimensional cell growth	8 (2.6)	186 (0.5)	7.00E-05
	cell wall^{CC}	27 (8.9)	403 (1.1)	6.00E-34
	anchored to membrane^{CC}	13 (4.3)	272 (0.7)	3.00E-10
	apoplast^{CC}	10 (3.3)	182 (0.5)	2.00E-09
C3 (645)	**metabolic process**^{BP}	258 (40.6)	10614 (28.1)	3.00E-10
	└ photosynthesis	37 (5.8)	162 (0.4)	3.00E-73
	└ photosynthesis, light reaction	23 (3.6)	103 (0.3)	2.00E-43
	└ electron transport chain	13 (2.0)	88 (0.2)	4.00E-15
	└ cellular nitrogen compound metabolic process	29 (4.6)	506 (1.3)	1.00E-09
	└ carbohydrate catabolic process	13 (2.0)	128 (0.3)	9.00E-10
	└ starch catabolic process	5 (0.8)	15 (0.0)	3.00E-11
	response to abiotic stimulus^{BP}	59 (9.3)	1471 (3.9)	7.00E-10
	└ response to light stimulus	29 (4.6)	596 (1.6)	3.00E-07
	└ phototropism	5 (0.8)	25 (0.1)	3.00E-07
	cellular component biogenesis^{BP}	35 (5.5)	571 (1.5)	5.00E-13
	└ ribosome biogenesis	19 (3.0)	241 (0.6)	3.00E-10
	└ protein complex assembly	16 (2.5)	134 (0.4)	9.00E-15
	chloroplast organization^{BP}	12 (1.9)	73 (0.2)	2.00E-15
	protein targeting to chloroplast^{BP}	7 (1.1)	33 (0.1)	4.00E-11
	plastid^{CC}	270 (42.5)	2965 (7.9)	2.00E-210
	└ plastid thylakoid membrane	63 (9.9)	231 (0.6)	1.00E-152
	└ plastid stroma	62 (9.8)	322 (0.9)	2.00E-107
	└ plastid envelope	54 (8.5)	331 (0.9)	2.00E-78
	ribosome^{CC}	41 (6.5)	524 (1.4)	5.00E-24
C4 (420)	**response to stimulus**^{BP}	92 (22.4)	4057 (10.7)	1.00E-11
	└ response to abiotic stimulus	45 (11.0)	1471 (3.9)	1.00E-10
	└ response to radiation	24 (5.9)	613 (1.6)	1.00E-08
	└ response to cold	14 (3.4)	328 (0.9)	2.00E-05
	photosynthesis^{BP}	21 (5.1)	162 (0.4)	2.00E-37
	lipid localization^{BP}	5 (1.2)	24 (0.1)	1.00E-11
	plastid^{CC}	88 (21.5)	2965 (7.9)	3.00E-22
	└ plastid thylakoid	26 (6.3)	293 (0.8)	6.00E-32
	photosynthetic membrane^{CC}	32 (7.8)	273 (0.7)	2.00E-53
	└ photosystem I	8 (2.0)	22 (0.1)	2.00E-35

(continued) Supplemental Table 1. Summary of GO terms enriched among genes in each cluster.

Cluster (Gene #)	Enriched GO BP and CC terms	Number of genes in the cluster (%)	Number of genes in the background (%)	FDR
C5 (468)	**response to stimulus**$^{\mathbf{BP}}$	94 (20.9)	4057 (10.7)	6.00E-10
	└ response to chemical stimulus	60 (13.4)	2085 (5.5)	1.00E-10
	└ response to gibberellin stimulus	21 (4.7)	159 (0.4)	4.00E-34
	└ gibberellin signaling pathway	6 (1.3)	40 (0.1)	7.00E-10
	└ response to abscisic acid stimulus	17 (3.8)	378 (1.0)	1.00E-06
	└ response to abiotic stimulus	49 (10.9)	1471 (3.9)	9.00E-12
	└ response to salt stress	18 (4.0)	366 (1.0)	3.00E-08
	└ response to cold	16 (3.6)	328 (0.9)	4.00E-07
	secondary metabolic process$^{\mathbf{BP}}$	21 (4.7)	489 (1.3)	1.00E-07
	└ flavonoid biosynthetic process	9 (2.0)	69 (0.2)	2.00E-13
	└ gibberellin biosynthetic process	6 (1.3)	19 (0.1)	2.00E-19
	polysaccharide metabolic process$^{\mathbf{BP}}$	12 (2.7)	152 (0.4)	3.00E-10
	└ starch metabolic process	8 (1.8)	41 (0.1)	1.00E-17
C6 (269)	**metabolic process**$^{\mathbf{BP}}$	292 (36.0)	10614 (28.1)	4.00E-05
	└ response to chemical stimulus	46 (17.3)	2085 (5.5)	5.00E-14
	└ response to chitin	13 (4.9)	151 (0.4)	1.00E-23
	└ response to abscisic acid stimulus	12 (4.5)	378 (1.0)	3.00E-06
	└ response to stress	40 (15.0)	2320 (6.1)	3.00E-07
	└ defense response to bacterium	7 (2.6)	177 (0.5)	1.00E-04
	└ regulation of defense response	6 (2.3)	66 (0.2)	2.00E-10
	aromatic compound biosynthetic process$^{\mathbf{BP}}$	10 (3.8)	237 (0.6)	2.00E-07
	└ flavonoid biosynthetic process	6 (2.3)	69 (0.2)	5.00E-10
C7 (118)	**metabolic process**$^{\mathbf{BP}}$	95 (80.5)	10614 (28.1)	5.00E-35
	└ translation	68 (57.6)	1445 (3.8)	9.00E-190
	secondary metabolic process$^{\mathbf{BP}}$	13 (11.0)	489 (1.3)	8.00E-18
	└ glucosinolate biosynthetic process	11 (9.3)	41 (0.1)	2.00E-144
	ribosome biogenesis$^{\mathbf{BP}}$	23 (19.5)	241 (0.6)	6.00E-126
	ribosome$^{\mathbf{CC}}$	69 (58.5)	524 (1.4)	0
C9 (113)	**cellular nitrogen compound metabolic process**$^{\mathbf{BP}}$	10 (9.2)	506 (1.3)	7.00E-09
	flower development$^{\mathbf{BP}}$	8 (7.3)	377 (1.0)	1.00E-07
	sulfur compound biosynthetic process$^{\mathbf{BP}}$	5 (4.6)	115 (0.3)	6.00E-10

* C8 and C10: No significant enrichment of GO terms were found.

Supplemental Table 2. List of Primers and Their Uses.

Primer	Forward primer / LP	Reverse primer / RP	Note
Genotyping			
ga1-13	TTGATTTTGGTCGTACATGTGAG	ACGCAAACCCAATCTATCATG	SALK_109115
pkl	AACAGGTTTCCCTGGATGATC	GGAAGATGTGAGCTCTGATGG	SAIL_73_H08
rga-29	ATGAATGATGATTGAAGTGG	CTAAACGAACACCGTTCTCT	SALK_089146
gai-t6	GAAGACGACGGTAACGGCAT	ATAATCGAAATTATCCGGTGC	
rgl1	AAAGTTCGATCATCCGACATG	AAAACTTATCGATGGAACCGG	SALK_136145
rgl2	AAAAACCTTACCAACCCATGAAG	TGAGCGAACTTCAGGTAAGGG	SALK_027654
rgl3-3	ATGAAACGAAGCCATCAAGAAACG	GGGCGAAATTGTCACAAAACGAAAC	CS16355
gai-1	ATGAAGAGAGATCATCATCA	TCAAGCCACGTGTAAAGCTC	CS63
LBb1.3	ATTTTGCCGATTTCGGAAC		LB for SALK lines
LB3	TAGCATCTGAATTTCATAACCAATCTCGATACAC		LB for SAIL lines
Ds5'	TCCGTTCCGTTTTCGTTTTTTAC		LB for *gai-t6*
Quantitative PCR			
PP2A	TATCGGATGACGATTCTTCGTGCAG	GCTTGGTCGACTATCGGAATGAGAG	AT1G13320
LEC1	TACCTCCTCCGGGTCCTTATGGTT	CAAAAGCCGGCATTCCGTTAATGG	AT1G21970
FUS3	CTGTGGTTAACGATCTTCTCCTCC	CGTTGGAGGTAAGAGCCGTCGTG	AT3G26790
ABI3	TCACCTTCAACATGGGTTCCTCCA	GAGTAATCTCTGATCTCTCATTTG	AT3G24650
EXP8	CATGTATGAAGAAAGGAGGAATAAG	AACTGCCAATTAGAAGGAGCCACG	AT2G40610
PRE1	CAGCCTCGAAAGTATTGCAAG	TTCTAATAACGGCGGCTTCAG	AT5G39860
SPL3	TGAGAAGAAGCAAAGCGGAA	TATCCGCGGTACAACTCTCG	AT2G33810
SPL5	ATGCAGCAGGTTTCATGAGC	GCCTGACCCTTCTCCAAAAC	AT3G15270
LFY	CCTAGACGAAGAAGCTTCAAATGC	CAGCCATGACGACAAGCGATGTTC	AT5G61850
FUL	GTCAGCAAGAAGGACAATTAGTCC	GAGAGTTTGGTTCCGTCAACGAC	AT5G60910
GA3OX1	GCTCGTGGTTAACGTTGGTGAC	CGATTCAACGGGACTAACCAGC	AT1G15550
GA20OX1	CAATGGCGCTCCATTCGTCCCAAC	GCTCTCTCGGTGGCGTCACTACTC	AT4G25420
SCL3	CAGCTGAGGCACGTGAGAATGAT	ACCACCATGACCTTTGGAGACAAAC	AT1G50420
GID1A	CGAGCGATGAAGTTAATCT	GAAAACCCCATCAACCG	AT3G05120
GID1B	AGAGGTCAAAGCCTTAAAGGAGTC	CTTCAAGACCAGTCTTCTTAAGCCC	AT3G63010
PAP1	GAGAAATTCCTAGAGGAAAGCCAAG	CACAGTCTCTCCATCGAAAAGACTC	AT1G56650
EXP1	TTACCTTAACGGACAATCTCTCTC	TCTAACTGCTTCTACTGTGAAGGT	AT1G69530
EXP3	TCAGATACTTCAATCTTGTTCTGG	TGCCAGTTCTGTCCCCAGTTCCGA	AT2G37640
XTH8	CCACAACAGAGAATTGGTGGGATC	GGGAACCTCTCACTGTCTTTGC	AT1G11545
XTH16	CGCTGCAGCTTGTACTGTTTCTTC	GCTCATTAGCCACTTGAGATTCAC	AT3G23730
AGP21	GCTCCAAGCCCAACTTCTGATG	TCAAAAGATGAAACCAGATGCC	AT1G55330
PLL20	CGGAGCATTTTTCACACGTTCTGG	ATGGTGCCGACGAGTGAGGATG	AT3G07010
IAA19	GGTGACAACTGCGAATACGTTACCA	CCCGGTAGCATCCGATCTTTTCA	AT3G15540
GH3.3	GAAGTCATGGCTCGGTGCTGCTTG	GTATCTCGAGTGGTCCTATCGAC	AT2G23170
SAUR16	CCTGATCCTTCTTCAACAAGCAGAG	CATCTGATCATGGATGTTAGAGAGAG	AT4G38860
PRE5	GGTACTACAAGAGACATGCAAC	GAGTAAGCTTCTAATCACGGC	AT3G28857
HBI1	GATTTGTCTGCGATAAACCCG	CGAGGCTAGATGTGTTGTAGAGAC	AT2G18300
SPL9	GTAGTGGCACGGCAATGGGTGA	GAAGAGTCATAAGCCCTTGTGTTC	AT2G42200
CYCB1;4	CTCGGAAGATGAGATTATGGAGC	CAACTTCAGCGTTTTCTGAGACAG	AT2G26760
CYCB2;2	GGTGAGACTACATCAGAAAGCTGG	GAGAATCTGACACAAGAAAGTGTGC	AT4G35620