

Supporting Information

Figure S1. GO annotation of differentially expressed genes in 3-day-old seedlings. AgriGO analysis computes GO term enrichment in one set of genes by comparing it to another set, named the target and reference list, respectively. P-value<0.05, FDR<0.05. The darker of the box, the higher the enrichment of the genes in the pathway.

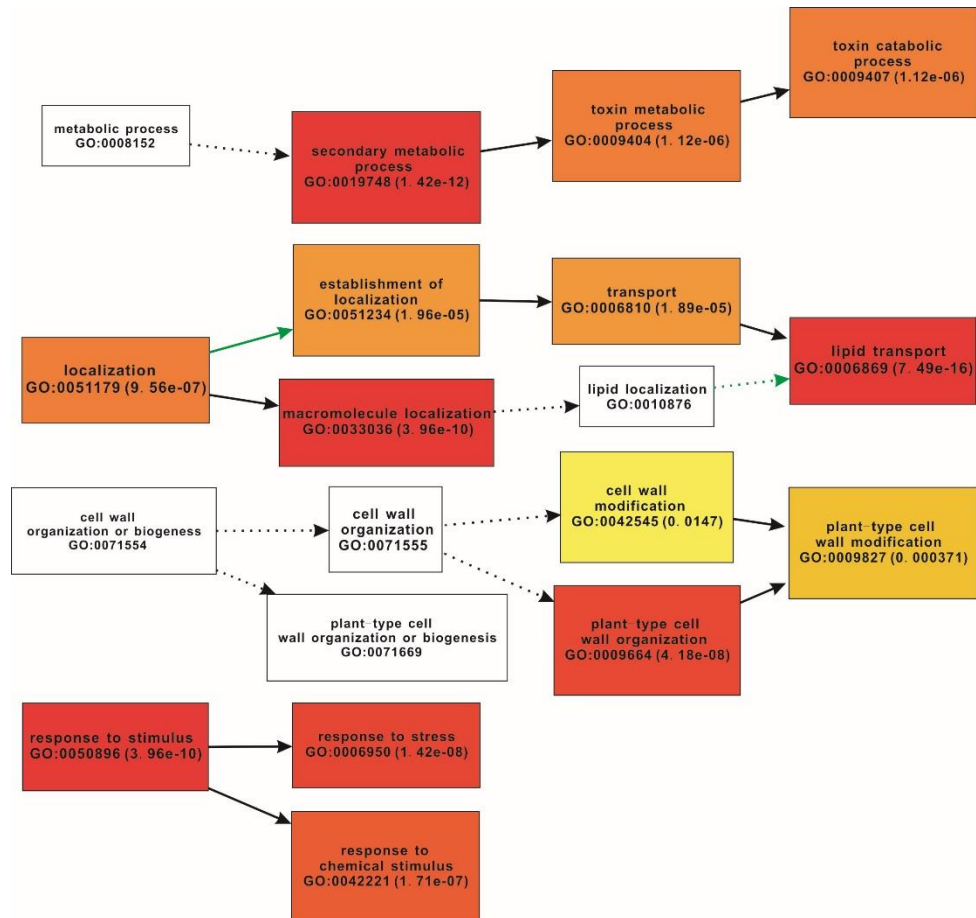


Figure S2. GO annotation of differentially expressed genes in 10-day-old seedlings. AgriGO analysis computes GO term enrichment in one set of genes by comparing it to another set, named the target and reference list, respectively. P-value<0.05, FDR<0.05. The darker of the box, the higher the enrichment of the genes in the pathway.

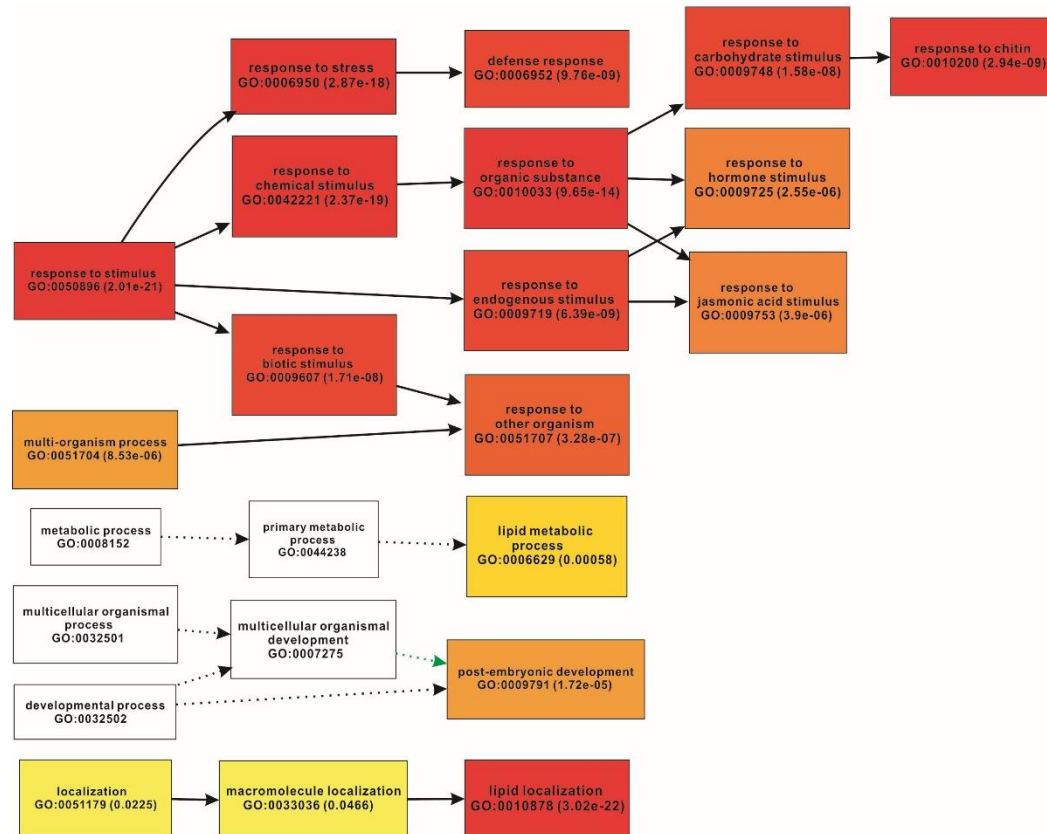


Table S1. Summary of RNA-seq data and mapping statistics.

Sample	Total reads	Reads uniquely mapped	Percent mapped
C31	35386206	33538475	94.8
C32	37995733	37643127	99.1
P31	35886548	34941281	97.4
P32	50683350	49112361	96.9
C101	23634132	23028083	97.4
C102	29894932	27989230	93.6
P101	25570076	25505294	99.7
P102	28890794	28849062	99.8
CS1	31221560	30005422	96.1
CS2	44876299	43017240	95.9
PS1	39051666	37727433	96.6
PS2	37501870	33227329	88.6

Table S2. A subset of flowering-related genes affected by *pkl* mutation.

Gene ID	Annotation	Col-0	<i>pkl-1</i>	log ₂ (fold_change)
AT1G09000	ANP1 (ARABIDOPSIS NPK1-RELATED PROTEIN KINASE 1)	4.87526	1.7659	-1.46508
AT1G10670	ACLA-1; ATP citrate synthase	230.428	166.486	-0.46891
AT1G19180	JAZ1	80.3354	42.7947	-0.90861
AT1G23420	INO (INNER NO OUTER)	3.79992	0.132253	-4.84459
AT1G24260	SEP3 (SEPALLATA3)	5.94192	0.041098	-7.17573
AT1G30330	ARF6 (AUXIN RESPONSE FACTOR 6)	54.2583	32.9931	-0.71768
AT1G52030	MBP2 (MYROSINASE- BINDING PROTEIN 2)	129.129	28.1357	-2.19834
AT1G52150	ATHB-15	50.8615	37.3638	-0.44494
AT1G62360	STM (SHOOT MERISTEMLESS)	28.4466	11.5652	-1.29846
AT1G67260	TCP1	4.32113	0.303007	-3.83399
AT1G69120	AP1 (APETALA1)	9.46002	0	-1.79769e+308
AT1G69180	CRC (CRABS CLAW)	10.2478	0.080233	-6.9969
AT2G28290	SYD (SPLAYED)	24.0555	18.8359	-0.35288
AT2G33810	SPL3	7.35049	1.95678	-1.90936
AT2G45660	AGL20 (AGAMOUS-LIKE 20)	22.2215	8.90424	-1.31939
AT3G02310	SEP2 (SEPALLATA 2)	6.40752	0.025689	-7.9625
AT3G03090	AtVGT1 (<i>Arabidopsis</i> <i>thaliana</i> vacuolar glucose transporter 1)	17.4622	9.40908	-0.89211
AT3G42960	ATA1 (ARABIDOPSIS TAPETUM 1)	5.22014	0	-1.79769e+308

AT3G45640	ATMPK3 (MITOGEN- ACTIVATED PROTEIN KINASE 3)	31.855	56.1736	0.818374
AT3G54340	AP3 (APETALA3)	9.14978	0	-1.79769e+308
AT3G55400	OVA1 (OVULE ABORTION 1)	39.8313	54.28	0.446519
AT3G56090	ATFER3 (ferritin 3)	160.172	99.1372	-0.69212
AT3G58780	SHP1 (SHATTERPROOF 1)	2.46869	0	-1.79769e+308
AT4G01500	NGA4 (NGATHA4)	0.93908	0.101652	-3.20761
AT4G18960	AG (AGAMOUS)	2.76238	0.070878	-5.28443
AT4G24540	AGL24 (AGAMOUS-LIKE 24)	109.183	33.7643	-1.69318
AT4G24960	ATHVA22D	166.74	106.652	-0.64468
AT4G31820	ENP (ENHANCER OF PINOID)	35.0728	46.7203	0.413697
AT4G35900	FD	14.2118	6.76736	-1.07043
AT5G01600	ATFER1	21.2919	7.95457	-1.42045
AT5G02030	RPL (REPLUMLESS)	23.6946	13.3304	-0.82983
AT5G03840	TFL1 (TERMINAL FLOWER 1)	7.30515	1.26189	-2.53333
AT5G07180	ERL2 (ERECTA-LIKE 2)	21.3323	14.0623	-0.60121
AT5G13480	FY	49.614	25.0198	-0.98768
AT5G15800	SEP1 (SEPALLATA1)	4.15749	0.023574	-7.46239
AT5G24860	FPF1 (FLOWERING PROMOTING FACTOR 1)	2.15649	0.155621	-3.79257
AT5G37260	RVE2 (REVEILLE 2)	30.4397	77.7443	1.35278
AT5G46845	mirna MIR160/MIR160C (MICRORNA160)	0	2.80363	1.79769e+308
AT5G60910	AGL8 (agamous-like 8)	14.8143	0.94094	-3.97674
AT5G61850	LFY (LEAFY)	2.18216	0.130034	-4.0688
AT5G65050	AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31)	70.9461	43.0345	-0.72123

Table S3. *LFY* and *LFY*-regulated genes affected by *pkl* mutation.

Gene ID	Annotation	Col	<i>pkl-1</i>	log ₂ (fold_change)
<i>AT1G24260</i>	SEP3 (SEPALLATA3)	5.94192	0.041098	-7.17573
<i>AT1G62360</i>	STM (SHOOT MERISTEMLESS)	28.4466	11.5652	-1.29846
<i>AT1G69120</i>	AP1 (APETALA1)	9.46002	0	-1.79769e+308
<i>AT2G33810</i>	SPL3	7.35049	1.95678	-1.90936
<i>AT2G45660</i>	AGL20 (AGAMOUS-LIKE 20)	22.2215	8.90424	-1.31939
<i>AT3G02310</i>	SEP2 (SEPALLATA 2)	6.40752	0.025689	-7.9625
<i>AT4G18960</i>	AG (AGAMOUS)	2.76238	0.070878	-5.28443
<i>AT4G24540</i>	AGL24 (AGAMOUS-LIKE 24)	109.183	33.7643	-1.69318
<i>AT4G35900</i>	FD	14.2118	6.76736	-1.07043
<i>AT5G03840</i>	TFL1 (TERMINAL FLOWER 1)	7.30515	1.26189	-2.53333
<i>AT5G13480</i>	FY	49.614	25.0198	-0.987681
<i>AT5G15800</i>	SEP1 (SEPALLATA1)	4.15749	0.023574	-7.46239
<i>AT5G60910</i>	AGL8 (agamous-like 8)	14.8143	0.94094	-3.97674
<i>AT5G61850</i>	LFY (LEAFY)	2.18216	0.130034	-4.0688
<i>AT5G65050</i>	AGL31 (AGAMOUS LIKE MADS-BOX PROTEIN 31)	70.9461	43.0345	-0.721229
<i>AT3G54340</i>	AP3 (APETALA3)	9.14978	0	-1.79769e+308

Table S4. Primers used in the experiment shown in Figure 4.

Primer	Nucleotide sequence
<i>PP2Af</i>	TAACGTGGCCAAAATGATGC
<i>PP2Ar</i>	GTTCTCCACAACCGCTTGGT
<i>AIR1f</i>	TCAATCTCAGCGTACTCCTCAA
<i>AIR1r</i>	GCATCGGTATGATTCGTTTGT
<i>DIR1f</i>	CATGAGCCAGGATGAGTTGA
<i>DIR1r</i>	CTGTTTGGGGAGAGCAGAAG
<i>DOGT1f</i>	GCCTTGTGAGCTGAATCTCC
<i>DOGT1r</i>	TGTTGGTGGATAAAGAAGGAGTG
<i>ELPf</i>	TGGGTATTGGAAGAGAAGACG
<i>ELPr</i>	GGAAGGTACAGTTGAAGGGTTG
<i>LOX4f</i>	CGGACGGATAGAGAAGGAGAT
<i>LOX4r</i>	GGAGCCATCAACTCATACGG
<i>LTP2f</i>	AGGTGCTCCACTTACCCAAG
<i>LTP2r</i>	CTTTAGCGGCAGATTGAAGG
<i>PHE1f</i>	TTAGGAGCACAAACATCAGTGG
<i>PHE1r</i>	CTTG CATGGACAACAACA ACTAC
<i>EDA39f</i>	GCTACAAGCACAAGCACTGG
<i>EDA39r</i>	CGTGGAGACACCCTCACTTT
<i>HSP20f</i>	GATGAGAGCGGTCGAACCTA
<i>HSP20r</i>	GATGGTGGTCATGTCGTCAG
<i>OFPf</i>	CTGACATGGCCGAGTATGTG
<i>OFPr</i>	GTACCCTTGGTGGTGTCTCG
<i>OLEO2f</i>	GGTGATCGGCTTAATGGTTG
<i>OLEO2r</i>	ACATCCCCGAGGCTAAAAAG
<i>SESA3f</i>	ACGGACCATTCCAATCCAG
<i>SESA3r</i>	AAGGAGGGAAGAAAGGGATG
<i>SZF1f</i>	AGTTTCGACTCCTCCGGTTT
<i>SZF1r</i>	ATCTGCTTCCACCATTGAGC
<i>WOX12f</i>	CGAGATTGATTTGGGGTTTG
<i>WOX12r</i>	AAGAGAGGCCGAGGAAAAAG

Table S5. Primers used in the experiment shown in Figures 5 and 6.

Primer	Nucleotide sequence
<i>AGf</i>	AGCTTATGCCACCACCTCAA
<i>AGr</i>	CTAACTGGAGAGCGGTTTGG
<i>AGL20f</i>	TTTTGTTGAGTGGAGATCACTTTC
<i>AGL20r</i>	TGAAGAGAGTAGCCCAAGTTCTG
<i>AGL24f</i>	CAGGGAAGTGTCGGAGTCAT
<i>AGL24r</i>	GTTGGAAAGGGCAAACTGA
<i>AGL31f</i>	CGGAATTATCTGCCACTCAAA
<i>AGL31r</i>	TCCACACTTGCATTATCGACAT
<i>AGL8f</i>	CAAAGCCATCTCTGGAGGAG
<i>AGL8r</i>	AGAAGAAAACGGGTCAGCAA
<i>AP1f</i>	TTAATTGGATGAAAAGAGCCTAGC
<i>AP1r</i>	CCCGTTTACAACCTGCAACCT
<i>AP3f</i>	ACGTGCTTACGCTCTTCGTT
<i>AP3r</i>	CACCAGCAAACCTTTTAGCC
<i>FDf</i>	AGGCAGAAAATGCAAGACTCA
<i>FDr</i>	TGGAAGACCGTTGAAGTGTG
<i>FYf</i>	GTTGAAACCACCACGTCCTT
<i>FYr</i>	CCTCAGATGTCGCAAAGTCA
<i>LFYf</i>	GCTCTCCACTGCCTAGACGA
<i>LFYr</i>	CATGACGACAAGCGATGTTC
<i>SEP1f</i>	GAGCAAATAACTGCGACAACC
<i>SEP1r</i>	TTTGTTGGTGAGCTTTAACACAG
<i>SEP2f</i>	GGGTCTTCGTGGTGTGATCT
<i>SEP2r</i>	AGGCACAAACAAATCCTGAAA
<i>SPL3f</i>	AGGTTTCACGCGCTCAGT
<i>SPL3r</i>	TTTTCCGCCTTCTCTCGTT
<i>STMf</i>	CAAAGCATGGTGGAGGAGA

<i>STMr</i>	GTAATGGACGCAACACATCCT
<i>TFL1f</i>	CAAGGCCAAGCATAGGGATA
<i>TFL1r</i>	GCGACAGGGAGACCAAGAT
