

Supplementary Table 1

group name	library name	organism	tissue	genotype	age	treatment	time
WT_seedling	WT	<i>Arabidopsis thaliana</i>	seedling	Col-0	7-day-old	none	0
PSK_0	tpst	<i>Arabidopsis thaliana</i>	seedling	tpst	7-day-old	none	0
PSK_100nM	PSK	<i>Arabidopsis thaliana</i>	seedling	tpst	7-day-old	100 nM PSK	5 hours
PSK_1uM	PSK_10x	<i>Arabidopsis thaliana</i>	seedling	tpst	7-day-old	1 μ M PSK	5 hours
WT_shoot	WL_0	<i>Arabidopsis thaliana</i>	shoot	Col-0	11-day-old	none	0
shoot_0	TL_0	<i>Arabidopsis thaliana</i>	shoot	tpst	11-day-old	none	0
shoot_30m	TL_30m	<i>Arabidopsis thaliana</i>	shoot	tpst	11-day-old	10 nM PSK	30 minutes
shoot_2h	TL_2h	<i>Arabidopsis thaliana</i>	shoot	tpst	11-day-old	10 nM PSK	2 hours
shoot_5h	TL_5h	<i>Arabidopsis thaliana</i>	shoot	tpst	11-day-old	10 nM PSK	5 hours
shoot_11d	TL_11d	<i>Arabidopsis thaliana</i>	shoot	tpst	11-day-old	10 nM PSK	11 days
WT_root	WR_0	<i>Arabidopsis thaliana</i>	root	Col-0	11-day-old	none	0
root_0	TR_0	<i>Arabidopsis thaliana</i>	root	tpst	11-day-old	none	0
root_30m	TR_30m	<i>Arabidopsis thaliana</i>	root	tpst	11-day-old	10 nM PSK	30 minutes
root_2h	TR_2h	<i>Arabidopsis thaliana</i>	root	tpst	11-day-old	10 nM PSK	2 hours
root_5h	TR_5h	<i>Arabidopsis thaliana</i>	root	tpst	11-day-old	10 nM PSK	5 hours
root_11d	TR_11d	<i>Arabidopsis thaliana</i>	root	tpst	11-day-old	10 nM PSK	11 days

Supplementary Table 1. Information of each plant sample and PSK treatment in RNA-seq experiments. Group name of the plant sample was used in differential expression analysis, functional enrichment analysis and transcription factors enrichment analysis.

Supplementary Table 2A

(A)

W-box motifs in down-regulated DEGs promoter regions (1000 bp upstream)						
treatment	oligomer	N in list	N in genome	% in DEG	% in genome	p-value*
PSK 100 nM seedling	TTGACT	28	25580	16/36	17247/34187	0.51
	TTGACC	13	15426	10/36	12035/34187	0.39
PSK 1 μ M seedling	TTGACT	62	25580	48/87	17247/34187	0.39
	TTGACC	31	15426	28/87	12035/34187	0.65
PSK shoot 30 m	TTGACT	68	25580	45/103	17247/34187	0.20
	TTGACC	47	15426	35/103	12035/34187	0.84
PSK shoot 2 h	TTGACT	251	25580	183/380	17247/34187	0.38
	TTGACC	139	15426	111/380	12035/34187	0.015
PSK shoot 5h	TTGACT	1266	25580	836/1661	17247/34187	0.94
	TTGACC	754	15426	583/1661	12035/34187	0.94
PSK shoot 11 d	TTGACT	1078	25580	736/1542	17247/34187	0.031
	TTGACC	646	15426	514/1542	12035/34187	0.12
PSK root 30 m	TTGACT	51	25580	34/69	17247/34187	0.90
	TTGACC	31	15426	25/69	12035/34187	0.90
PSK root 2 h	TTGACT	82	25580	54/127	17247/34187	0.076
	TTGACC	46	15426	34/127	12035/34187	0.050
PSK root 5 h	TTGACT	179	25580	124/279	17247/34187	0.047
	TTGACC	106	15426	87/279	12035/34187	0.17
PSK root 11 d	TTGACT	183	25580	118/240	17247/34187	0.70
	TTGACC	100	15426	79/240	12035/34187	0.50
PSY shoot	TTGACT	191	25580	97/161	17247/34187	0.014
	TTGACC	93	15426	65/161	12035/34187	0.19
PSY root	TTGACT	185	25580	128/279	17247/34187	0.13
	TTGACC	104	15426	80/279	12035/34187	0.023
flg22 seedling	TTGACT	4253	25580	2520/4048	17247/34187	< 2.2e-16
	TTGACC	2590	15426	1843/4048	12035/34187	< 2.2e-16
WCS417 shoot	TTGACT	692	25580	411/694	17247/34187	3.3e-06
	TTGACC	386	15426	289/694	12035/34187	0.00040
WCS417 root	TTGACT	1056	25580	627/1002	17247/34187	5.0e-15
	TTGACC	558	15426	414/1002	12035/34187	4.8e-05

Supplementary Table 2. W-box motifs in the promoter regions of up- and downregulated DEGs. (A) Number of W-box motifs in the promoter regions (1000 bp upstream) of up-regulated DEGs, number of W-box motifs in the promoter regions of all genes in the genome, percentage of DEGs containing W-box motifs among all DEGs, and percentage of genes containing W-box motifs among all genes in each treatment condition.

* The p-value represent Fisher's exact test for the overrepresentation of DEGs containing W-box motifs compared to the genome background.

Supplementary Table 2B

(B)

W-box motifs in down-regulated DEGs promoter regions (1000 bp upstream)						
treatment	oligomer	N in list	N in genome	% in DEG	% in genome	p-value*
PSK 100 nM seedling	TTGACT	164	25580	78/102	17247/34187	8.2e-08
	TTGACC	71	15426	50/102	12035/34187	0.0048
PSK 1 μ M seedling	TTGACT	194	25580	91/135	17247/34187	9.0e-05
	TTGACC	83	15426	60/135	12035/34187	0.030
PSK shoot 30 m	TTGACT	140	25580	69/89	17247/34187	1.9e-07
	TTGACC	57	15426	39/89	12035/34187	0.096
PSK shoot 2 h	TTGACT	518	25580	288/455	17247/34187	3.7e-08
	TTGACC	257	15426	182/455	12035/34187	0.034
PSK shoot 5h	TTGACT	1443	25580	933/1796	17247/34187	0.20
	TTGACC	835	15426	644/1796	12035/34187	0.56
PSK shoot 11 d	TTGACT	1227	25580	789/1516	17247/34187	0.21
	TTGACC	728	15426	568/1516	12035/34187	0.061
PSK root 30 m	TTGACT	275	25580	137/182	17247/34187	8.5e-12
	TTGACC	155	15426	105/182	12035/34187	6.6e-10
PSK root 2 h	TTGACT	451	25580	243/360	17247/34187	6.7e-11
	TTGACC	284	15426	187/360	12035/34187	8.0e-11
PSK root 5 h	TTGACT	264	25580	139/218	17247/34187	7.6e-05
	TTGACC	133	15426	90/218	12035/34187	0.064
PSK root 11 d	TTGACT	183	25580	89/147	17247/34187	0.016
	TTGACC	79	15426	54/147	12035/34187	0.73
PSY shoot	TTGACT	401	25580	240/418	17247/34187	0.0043
	TTGACC	207	15426	149/418	12035/34187	0.88
PSY root	TTGACT	817	25580	460/713	17247/34187	2.6e-14
	TTGACC	429	15426	302/713	12035/34187	7.2e-05
fig22 seedling	TTGACT	1721	25580	1249/2774	17247/34187	2.7e-09
	TTGACC	1084	15426	888/2774	12035/34187	0.00024
WCS417 shoot	TTGACT	266	25580	178/381	17247/34187	0.15
	TTGACC	165	15426	123/381	12035/34187	0.24
WCS417 root	TTGACT	329	25580	216/454	17247/34187	0.22
	TTGACC	183	15426	146/454	12035/34187	0.18

Supplementary Table 2. (B) Number of W-box motifs in the promoter regions (1000 bp upstream) of down-regulated DEGs, number of W-box motifs in the promoter regions of all genes in the genome, percentage of DEGs containing W-box motifs among all DEGs, and percentage of genes containing W-box motifs among all genes in each treatment condition.

* The p-value represent Fisher's exact test for the overrepresentation of DEGs containing W-box motifs compared to the genome background.

Supplementary Table 3

Gene ID	Gene name	TTGACT in promoter region*	TTGACC in promoter region*
AT1G08030	TPST	×	√
AT1G13590	PSK1	√	×
AT2G22860	PSK2	√	×
AT3G44735	PSK3	√	×
AT3G49780	PSK4	√	√
AT5G65870	PSK5	√	√
AT2G02220	PSKR1	√	×
AT5G53890	PSKR2	√	×

Supplementary Table 3. W-box motifs presence in the promoter regions of genes involved in PSK signaling.

* √ indicates at least one W-box motif presents in promoter region; × indicates no W-box presents in promoter region.

Supplementary Table 4

data type	geno type	age	tissue	medium	condition	treatment	concentration	time	reference
PSK	tpst	7 d	seedling	liquid 0.5x MS	16 h / 8 h long day	add peptide	100 nM / 1 μ M	5 h	Our data
PSK	tpst	11 d	root / shoot	liquid 0.5x MS	16 h / 8 h long day	replace medium	10 nM	30 m / 2 h / 5 h / 11 d	Our data
PSY	tpst	7 d	root / shoot	liquid B5	continuous light	add peptide	1 μ M	7 d	Ogawa-Ohnishi et al., 2022
flg22	Col-0	12 d	seedling	liquid 1x MS	16 h / 8 h long day	replace medium	1 μ M	2 h	Birkenbihl et al., 2017
WCS417	Col-0	12 d	root / shoot	Solid 0.5x MS	16 h / 8 h long day	contact with root at 5 d	10 μ l 2×10^6 CFU ml ⁻¹	7 dpi	Desrut et al., 2020

Supplementary Table 4. Growth conditions and treatment methods for RNA-seq data used in the comparison of PSK, PSY, flg22 and WCS417 induced DEGs.