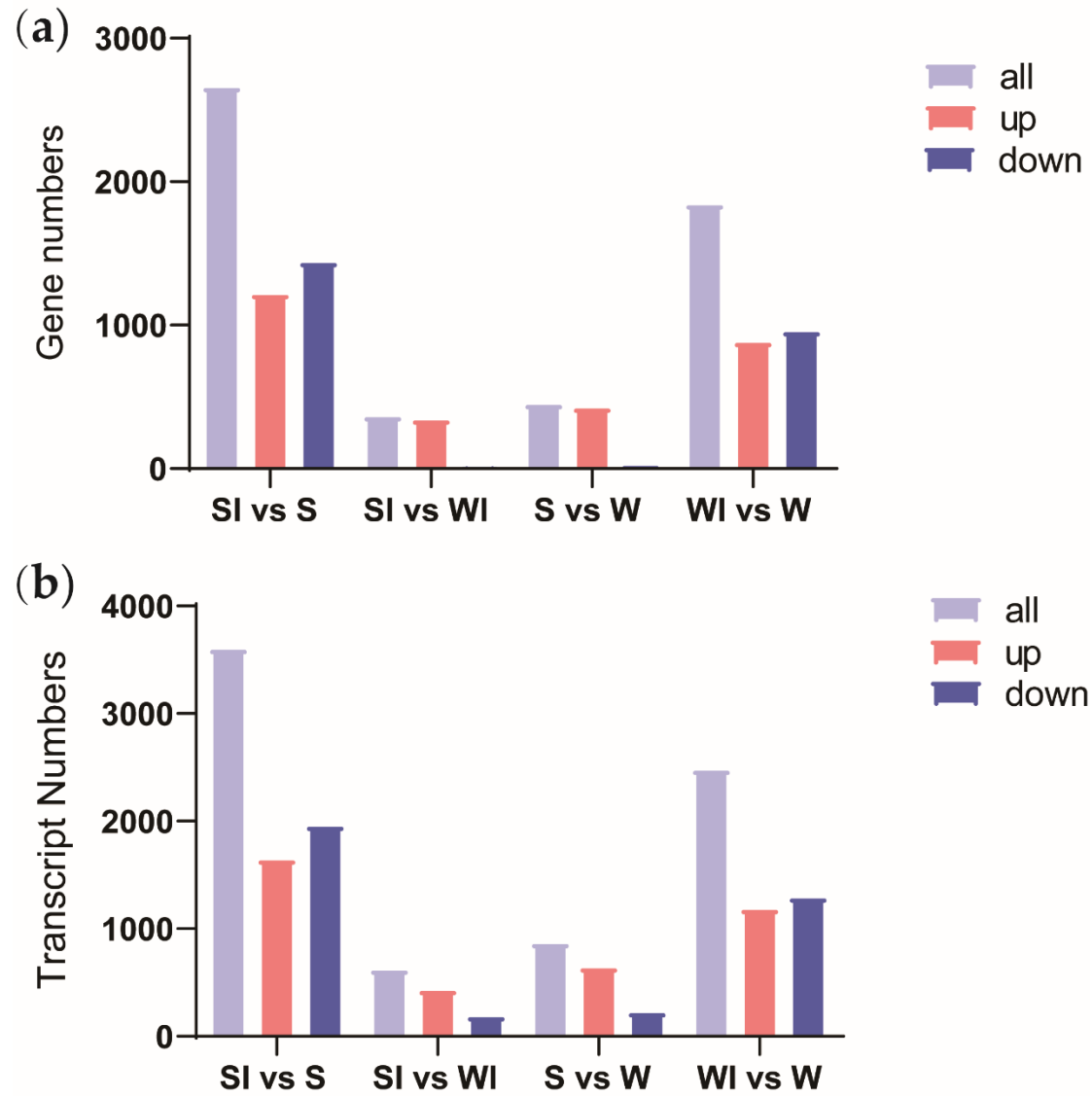
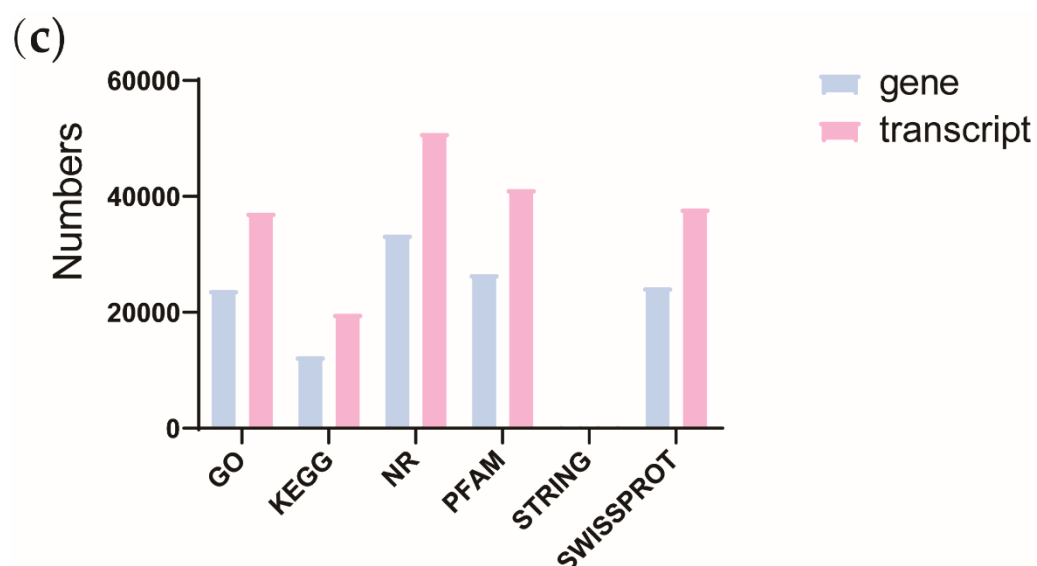


# Supplementary materials

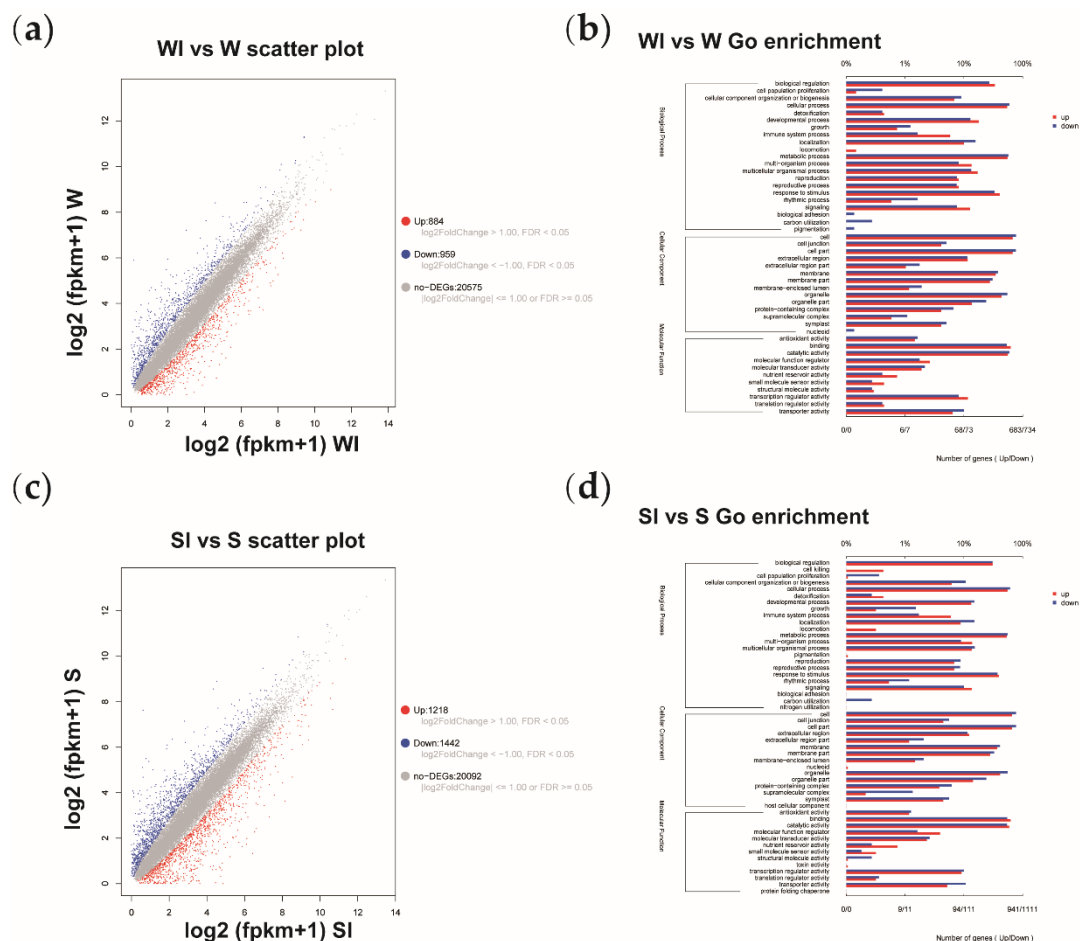
## Supplementary Figures:





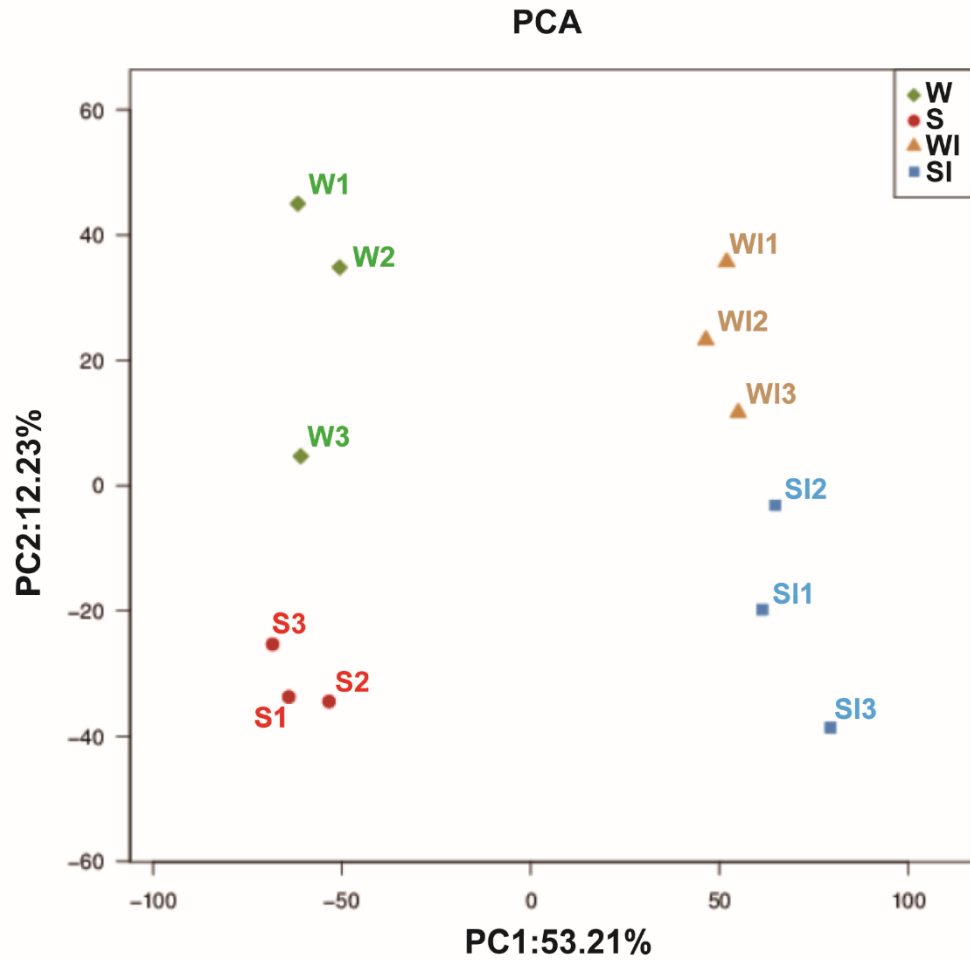
**Figure S1: Statistics of DEGs.**

(a) Statistics of all differential genes and the number of up-regulated and down-regulated differential genes in different groups. (b) Statistics of all differential transcription factors and up-regulated and down-regulated differential transcription factors in different groups. (c) Statistics of the number of differential genes in different annotation analysis. (W represents water feeding; WI represents water feeding then infestation; S represents sorbitol feeding; SI represents sorbitol feeding then infestation.).



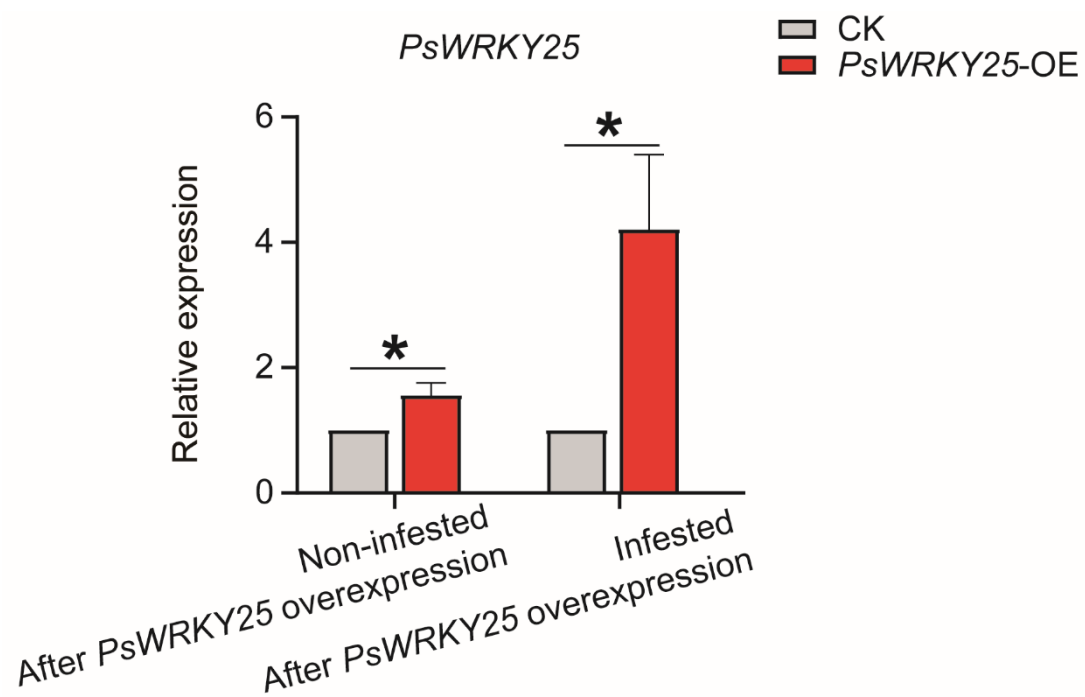
**Figure S2: GO and KEGG enrichment analysis showed that differentially expressed genes between treatments.**

(a) GO enrichment analysis of differential genes between WI and W. (b) KEGG enrichment analysis of differential genes between WI and W. (c) GO enrichment analysis of differential genes between SI and S. (d) KEGG enrichment analysis of differential gene between SI and S. (W represents water feeding; WI represents water feeding then infestation; S represents sorbitol feeding; SI represents sorbitol feeding then infestation.).



**Figure S3: PCA analysis showing intra- sample and inter- sample correlation.**

It shows the PCA analysis of 12 samples. (W represents water feeding; WI represents water feeding then infestation; S represents sorbitol feeding; SI represents sorbitol feeding then infestation. And the 1, 2, 3 represents three biological repetitions.).



**Figure S4: The relative expression of *PsWRKY25* in different treatment periods.**

The relative expression of *PsWRKY25*. It was measured in leaves during different periods of pathogen infestation. (\* stands for  $p < 0.05$ , with significant difference.).

## Supplementary Tables:

**Table S1: Sequencing raw data statistics.**

Sample ID	Total Reads	Total Bases	Error%	Q20%	Q30%	GC%
WI3	43235154	6485273100	0.0284	96.44	91.37	45.46
WI2	56899720	8534958000	0.0279	96.71	91.7	44.1
WI1	43749624	6562443600	0.0286	96.33	91.21	45.73
W3	42014688	6302203200	0.0271	97.06	92.31	43.99
W2	45163140	6774471000	0.0281	96.64	91.57	44.09
W1	46431786	6964767900	0.028	96.69	91.59	45.12
SI3	48772064	7315809600	0.0277	96.77	91.84	45.37
SI2	53449888	8017483200	0.0273	96.95	92.17	44.23
SI1	48976330	7346449500	0.028	96.64	91.7	44.14
S3	67144730	10071709500	0.0279	96.7	91.66	45.48
S2	58828702	8824305300	0.0281	96.68	91.44	44.43
S1	48403090	7260463500	0.0281	96.58	91.57	44.12

**Table S2: RT-qPCR primer sequences.**

<b>Primer</b>	<b>(5' to 3')</b>	<b>Base</b>
<i>UBQ</i> -qPCR-F	AGACCTACACCAAGCCCAAGAAGAT	25
<i>UBQ</i> -qPCR-R	CCAGCACCGCACTCAGCATTAG	22
<i>PtPR1</i> -like1-qPCR-F	TTTGGCGTAATTCTGCTCGC	20
<i>PtPR1</i> -like1-qPCR-R	TGCCGGGTGGATCATAGTTG	20
<i>PtPR1</i> -like2-qPCR-F	CCACTAACCTGGGACACCAC	20
<i>PtPR1</i> -like2-qPCR-R	CCATGCAAGGTTCTCCCCAT	20
<i>PtCML</i> -qPCR-F	CGGGTGACTGGTCCGATATG	20
<i>PtCML</i> -qPCR-R	TTTCTCGAGACAAGGCCGTC	20
<i>PtCPK</i> -qPCR-F	ACTTGTCAAGGCAGCCAAAT	20
<i>PtCPK</i> -qPCR-R	CCCCTGCACAAAGCTCCATA	20
<i>PtCPK26</i> -qPCR-F	CCTCCAATTCCAAGCGCAAC	20
<i>PtCPK26</i> -qPCR-R	GCTGTCCTTCTTCGGGTTGA	20
<i>PtCEPK1</i> -qPCR-F	TACTCAGGAGTTGCTGCAGC	20
<i>PtCEPK1</i> -qPCR-R	CTTCAAGGGCCGGTAGCTAC	20
<i>PtWRKY25</i> -qPCR-F	ACCACAGCAACAATGGCAAC	20
<i>PtWRKY25</i> -qPCR-R	CGGATGTTGCTGTAGGTGGT	20
<i>PtWRKY33</i> -qPCR-F	GGACAACCTTAGCTGGGGAC	20
<i>PtWRKY33</i> -qPCR-R	GGGGGAGGAGAAAAGGGTTG	20

**Table S3: Vector primer sequences.**

Primer	(5' to 3')	Base
<i>PtWRKY25-F</i>	ATGGCTGCTTCTTCAGGGAG	20
<i>PtWRKY25-R</i>	CTACCAAAACTCTCTACTTCCA	23

**Table S4: GO enrichment data.**

Due to the large amount of data, please see the "Supplementary Table ".

**Table S5: KEGG enrichment data.**

Due to the large amount of data, please see the "Supplementary Table ".

**Table S6: Venn data.**

Due to the large amount of data, please see the "Supplementary Table ".

**Table S7: TF binding sites data.**

Due to the large amount of data, please see the "Supplementary Table ".

**Table S8: DEGs data.**

Due to the large amount of data, please see the "Supplementary Table ".