

## Supplementary material

### Tables

**Table S1** Primer list used in qPCR for 14 *AcWRKYs* validation. ID, gene's name, primer sequences and expected size for each gene are reported in the table.

Gene ID/reference	Name	Primer	Sequences (5' – 3')
TRINITY_DN15477_c0_g1	<i>AcWRKY1</i>	Forward	GGGTACGGGTTCCAGATCTG
		Reverse	ACCCCACTATGCTGGTTGTG
TRINITY_DN24552_c0_g2	<i>AcWRKY2</i>	Forward	CACTTCTCCGTCACCCATGT
		Reverse	ACGAAGCAAGAATCATCAAAGCA
TRINITY_DN22804_c0_g1	<i>AcWRKY3</i>	Forward	TGAACTCTTACCTGCCGCAG
		Reverse	GCAACCCATGATCCCTGACA
TRINITY_DN33211_c0_g1	<i>AcWRKY9</i>	Forward	AACTCGACCTCAGCGTTGTT
		Reverse	GTCGCCCAAATTCACCATTGA
TRINITY_DN1383_c0_g1	<i>AcWRKY12</i>	Forward	AGCTACTACAGATGCACGCA
		Reverse	TGGACTTCTGAATAGGATGAGTGT
TRINITY_DN6283_c1_g1	<i>AcWRKY17</i>	Forward	ACCTCCTTTTACATTGGAAGTGC
		Reverse	ACGAATTCACAAAAGAGTCCCCT
TRINITY_DN9124_c1_g1	<i>AcWRKY18</i>	Forward	TCCCTTCAACTGCTCGTCG
		Reverse	TCTCTTCAAACCTCGAACTGCCA
TRINITY_DN10137_c1_g1	<i>AcWRKY21</i>	Forward	ATGCTCTTTTGCCCCACTGT
		Reverse	CGTGTATGTGCTCACCTTCG
TRINITY_DN8131_c0_g1	<i>AcWRKY26</i>	Forward	TCCTGAACGGTTGTCATGCA
		Reverse	CCGGTTTTATTCAAGTCCACTCC
TRINITY_DN32880_c0_g1	<i>AcWRKY30</i>	Forward	AGCCTGCACATCGAACTCT
		Reverse	GGAACCTCCGATCAAGGTTGGT
TRINITY_DN15141_c0_g1	<i>AcWRKY32</i>	Forward	CGCTGATCCTAATTCACGGC
		Reverse	ATTGTTGTTGGCACCATTACCA
TRINITY_DN24099_c0_g1	<i>AcWRKY37</i>	Forward	TGCCGAACCTTGATCTTCCCA
		Reverse	CGGTGGAGGAAATATGGGCA
TRINITY_DN13617_c0_g1	<i>AcWRKY46</i>	Forward	CAAACGCTTCCACCTACAAACA
		Reverse	TCTTGATCGTTGCATGAGAAGTC
TRINITY_DN6283_c0_g1	<i>AcWRKY52</i>	Forward	AGAAATGTTCCAAGGCTCGGA
		Reverse	TCCGTGTTCTAGTTCTATGGTACAAA
ADC83988.1 (Khosa et al., 2016)	<i>Actin</i>	Forward	CTGGGATGACATGGAGAAGATT
		Reverse	GTTAAGTGGAGCCTCCGT

**Table S2** ABA concentration (ug/g) in uninfected and OYDV-infected samples at each sampling time (T<sub>1</sub>, T<sub>2</sub>, and T<sub>3</sub>) evaluated by HPLC/MS.

<b>Time</b>	<b>Sample</b>	<b>ABA (ug/g)</b>	<b>St. dev.</b>
T1	Uninfected	0.995	0.147
	OYDV-infected	0.376	0.097
T2	Uninfected	0.269	0.001
	OYDV-infected	0.579	0.004
T3	Uninfected	0.197	0.096
	OYDV-infected	1.311	0.179

**Table S3** Overview of sequencing and assembly output of *A. cepa* bulb transcriptome.

<b>Items</b>	<b>Statistics</b>
Number of contigs	581,029
Number of sequences after cd-hit tool	479,145
Total length (nt) of transcripts	440,954,936
Total number of genes	316,298
Longest sequence (nt)	15,759
Mean sequence length (nt)	920
Median sequence length (nt)	494
N50 sequence length (nt)	1,615
GC-content (%)	36.72
BUSCO Complete	87.71%
BUSCO Complete + Partial	91.88%
BUSCO Missing	8.12%

**Table S4** Summary of DEGs ( $P_{adj} < 0.05$ ) extracted between uninfected and OYDV infected samples at T<sub>2</sub>/T<sub>1</sub>, T<sub>3</sub>/T<sub>1</sub>, and T<sub>3</sub>/T<sub>2</sub> comparisons. The total number of DEGs, up (Log<sub>2</sub> fold change > 1) and down (Log<sub>2</sub> fold change < -1) regulated genes were indicated

<b>Sample</b>	<b>Comparison</b>	<b>Number of DEGs</b>	<b>Log<sub>2</sub> fold change &gt; 1</b>	<b>Log<sub>2</sub> fold change &lt; -1</b>
Uninfected	T <sub>2</sub> /T <sub>1</sub>	1,253	325	796
	T <sub>3</sub> /T <sub>1</sub>	2,278	1,129	861
	T <sub>3</sub> /T <sub>2</sub>	1,859	1,326	362
	<i>Total</i>	<i>5,390</i>	<i>2,780</i>	<i>2,019</i>
OYDV-infected	T <sub>2</sub> /T <sub>1</sub>	304	100	189
	T <sub>3</sub> /T <sub>1</sub>	401	191	184
	T <sub>3</sub> /T <sub>2</sub>	617	319	248
	<i>Total</i>	<i>1,322</i>	<i>610</i>	<i>621</i>

**Table S5** List of annotated DEGs, and their fold change (log<sub>2</sub> Fold-Change), isolated at T<sub>2</sub>/T<sub>1</sub>, T<sub>3</sub>/T<sub>1</sub>, and T<sub>3</sub>/T<sub>2</sub>, comparisons, in uninfected and OYDV-infected bulbs using MapMan software. Fold change and annotation is reported for each gene.

**Table S6** List of annotated DEGs, and their fold change (log<sub>2</sub> Fold-Change), isolated at T<sub>2</sub>/T<sub>1</sub>, T<sub>3</sub>/T<sub>1</sub>, and T<sub>3</sub>/T<sub>1</sub>, comparisons, in uninfected and OYDV-infected bulbs using MapMan software. Fold change and annotation is reported for each gene. The present list has been used to develop Figure 2.

**Table S7** List of onion *AcWRKYs* isolated.

**Table S8** Summary of *AcWRKY* DEGs detected in both uninfected and OYDV-infected bulbs in each comparison

<b>Condition</b>	<b>T<sub>2</sub>/T<sub>1</sub></b>	<b>T<sub>3</sub>/T<sub>1</sub></b>	<b>T<sub>3</sub>/T<sub>2</sub></b>
Uninfected	<i>WRKY18, 21 37</i>	<i>WRKY2, 9, 12, 17, 30, 32, 46, 52</i>	<i>WRKY1, 2, 3, 9, 12, 17, 18, 21, 26, 37, 46, 52</i>
OYDV-infected	-	-	-

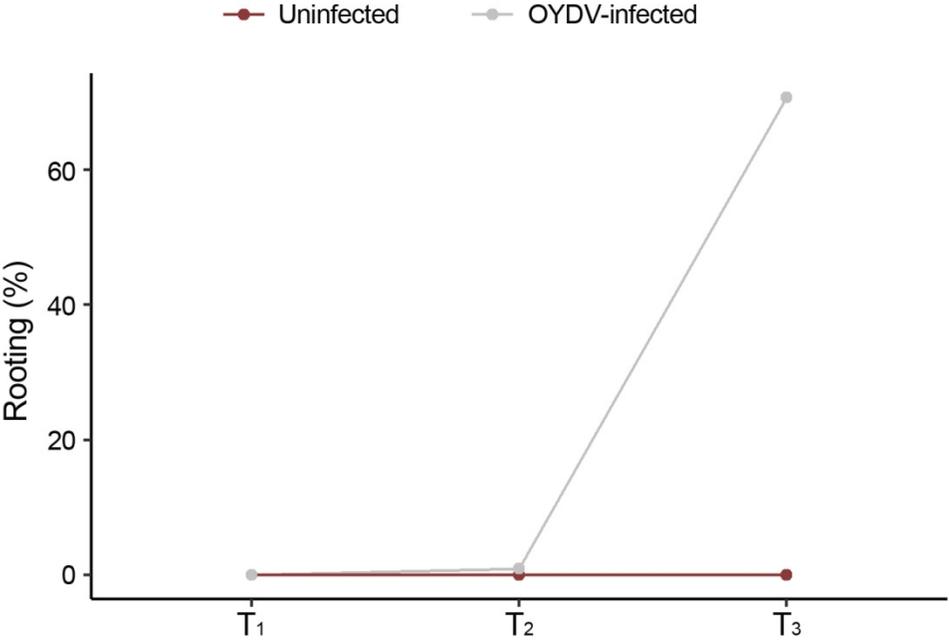
**Table S9** RNASeq (log2 FC) and qPCR ( $2^{-\Delta\Delta Ct}$ ) values for *AcWRKYs* differentially expressed in each comparison, isolated in uninfected samples, were indicated. Expression pattern of *AcWRKYs* extracted were also evaluated for uninfected (U)/OYDV-infected (I) bulbs comparison at T<sub>3</sub>. Genes showing significant differences (p<0.05) between conditions (U and I) by RNASeq and qPCR were underlined. For each *AcWRKY* is reported the transcript ID and its orthologous in *A. thaliana* (*AtWRKY*).

ID	<i>AcWRKY</i>	<i>AtWRKY</i>	T <sub>2</sub> /T <sub>1</sub>		T <sub>3</sub> /T <sub>1</sub>		T <sub>3</sub> /T <sub>2</sub>		T <sub>3</sub> U/I	
			RNASeq	qPCR	RNASe q	qPCR	RNASe q	qPCR	RNASe q	qPCR
TRINITY_DN15477_c0_g1	<i>AcWRKY1</i>	<i>AtWRKY69</i>	-	-	-	-	1.026	2.126	-	-
TRINITY_DN24552_c0_g2	<u><i>AcWRKY2</i></u>	<u><i>AtWRKY41</i></u>	-	-	1.988	2.744	3.131	4.321	1.101	3.745
TRINITY_DN22804_c0_g1	<i>AcWRKY3</i>	<i>AtWRKY71</i>	-	-	-	-	1.163	2.662	0.845	1.921
TRINITY_DN33211_c0_g1	<i>AcWRKY9</i>	<i>AtWRKY46</i>	-	-	1.410	1.314	2.133	3.988	-	-
TRINITY_DN1383_c0_g1	<i>AcWRKY12</i>	<i>AtWRKY75</i>	-	-	1.522	2.056	1.408	2.901	-	-
TRINITY_DN6283_c1_g1	<i>AcWRKY17</i>	<i>AtWRKY26</i>	-	-	1.008	1.638	1.974	3.208	-	-
TRINITY_DN9124_c1_g1	<i>AcWRKY18</i>	<i>AtWRKY67</i>	-2.155	-2.976	-	-	3.604	5.150	-	-
TRINITY_DN10137_c1_g1	<i>AcWRKY21</i>	<i>AtWRKY40</i>	-2.288	-2.325	-	-	3.047	3.354	-	-
TRINITY_DN8131_c0_g1	<i>AcWRKY26</i>	<i>AtWRKY51</i>	-	-	-	-	2.685	4.836	-	-
TRINITY_DN32880_c0_g1	<u><i>AcWRKY30</i></u>	<u><i>AtWRKY22</i></u>	-	-	3.773	9.114	-	-	4.831	5.001
TRINITY_DN15141_c0_g1	<u><i>AcWRKY32</i></u>	<u><i>AtWRKY6</i></u>	-	-	2.491	7.681	-	-	1.937	1.535
TRINITY_DN24099_c0_g1	<i>AcWRKY37</i>	<i>AtWRKY70</i>	-1.297	-1.186	-	-	1.634	3.335	-	-
TRINITY_DN13617_c0_g1	<i>AcWRKY46</i>	<i>AtWRKY55</i>	-	-	3.477	8.017	4.425	8.202	-	-
TRINITY_DN6283_c0_g1	<i>AcWRKY52</i>	<i>AtWRKY33</i>	-	-	2.441	2.397	3.315	4.454	-	4.856

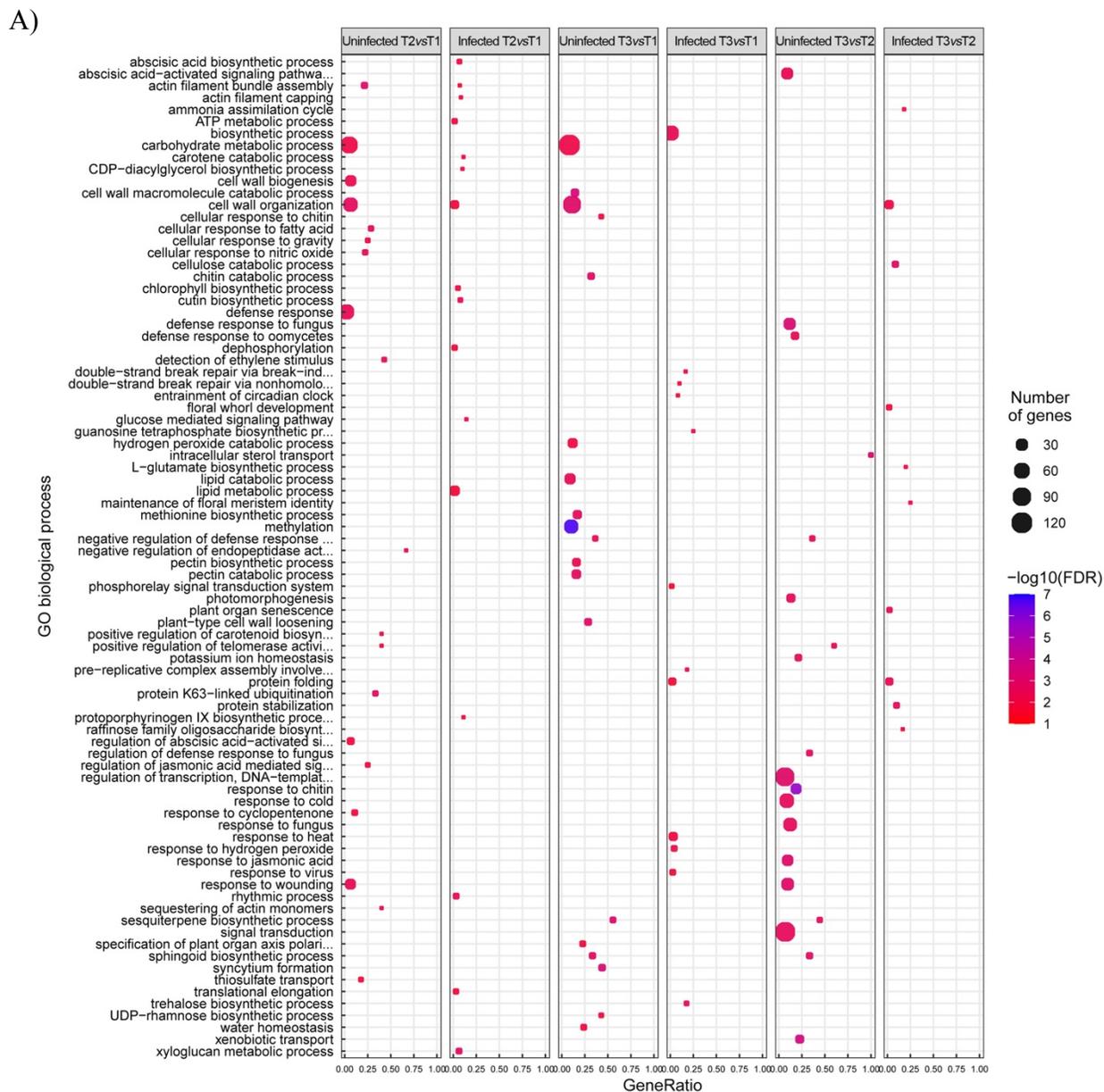
**Table S10** List of genes extracted in Co-expression network analyses by using as baits 3 *AcWRKYs* up-regulated at T<sub>3</sub> in the uninfected/OYDV infected bulbs comparison (*AcWRKY2*, 30, 32).

**Figures**

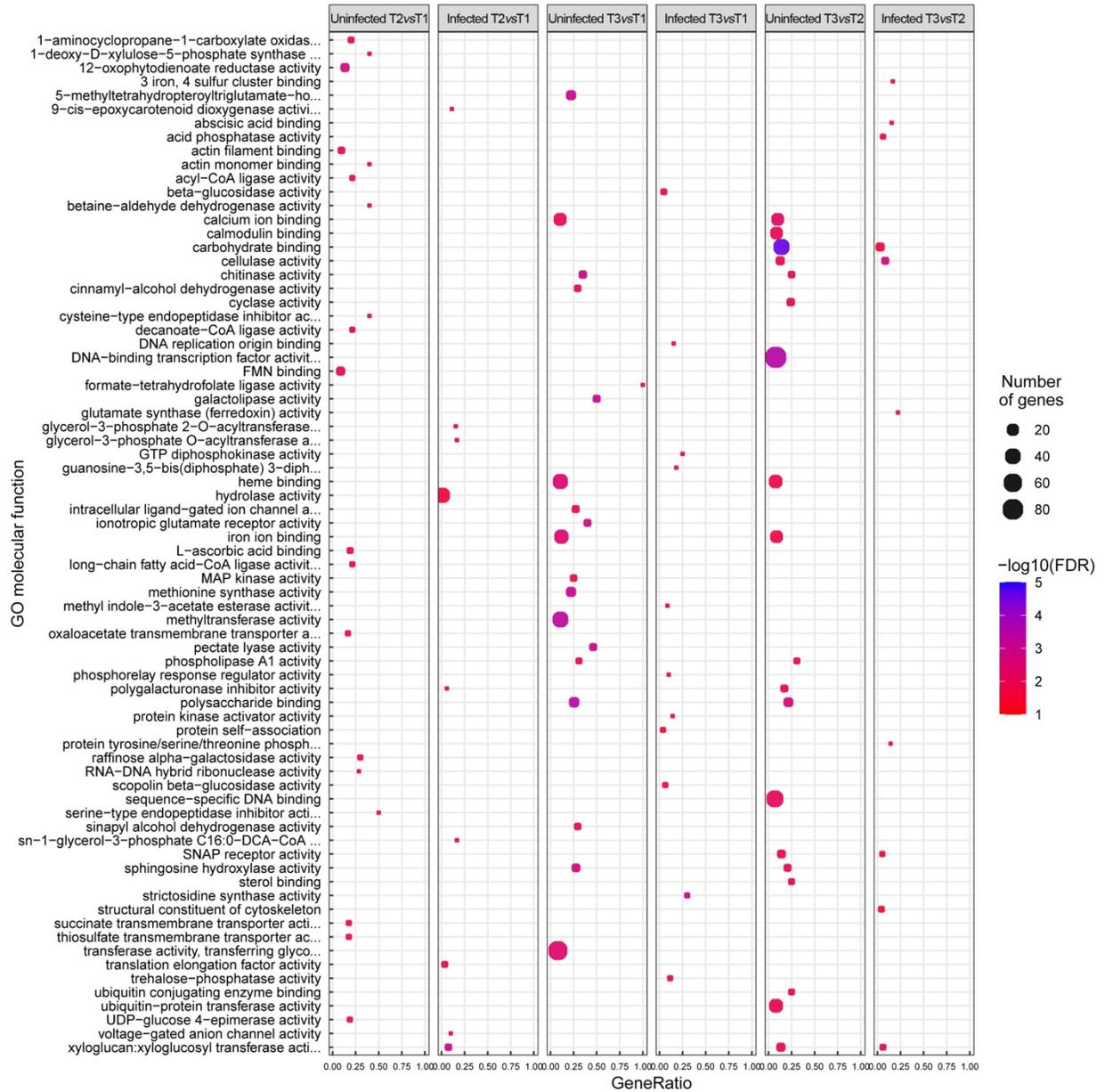
**Figure S1** Rooting evaluation between **A)** uninfected and **B)** OYDV-infected bulbs across sampling time. Percentage is referred to the number of onion which show rooting at the three selected time points.



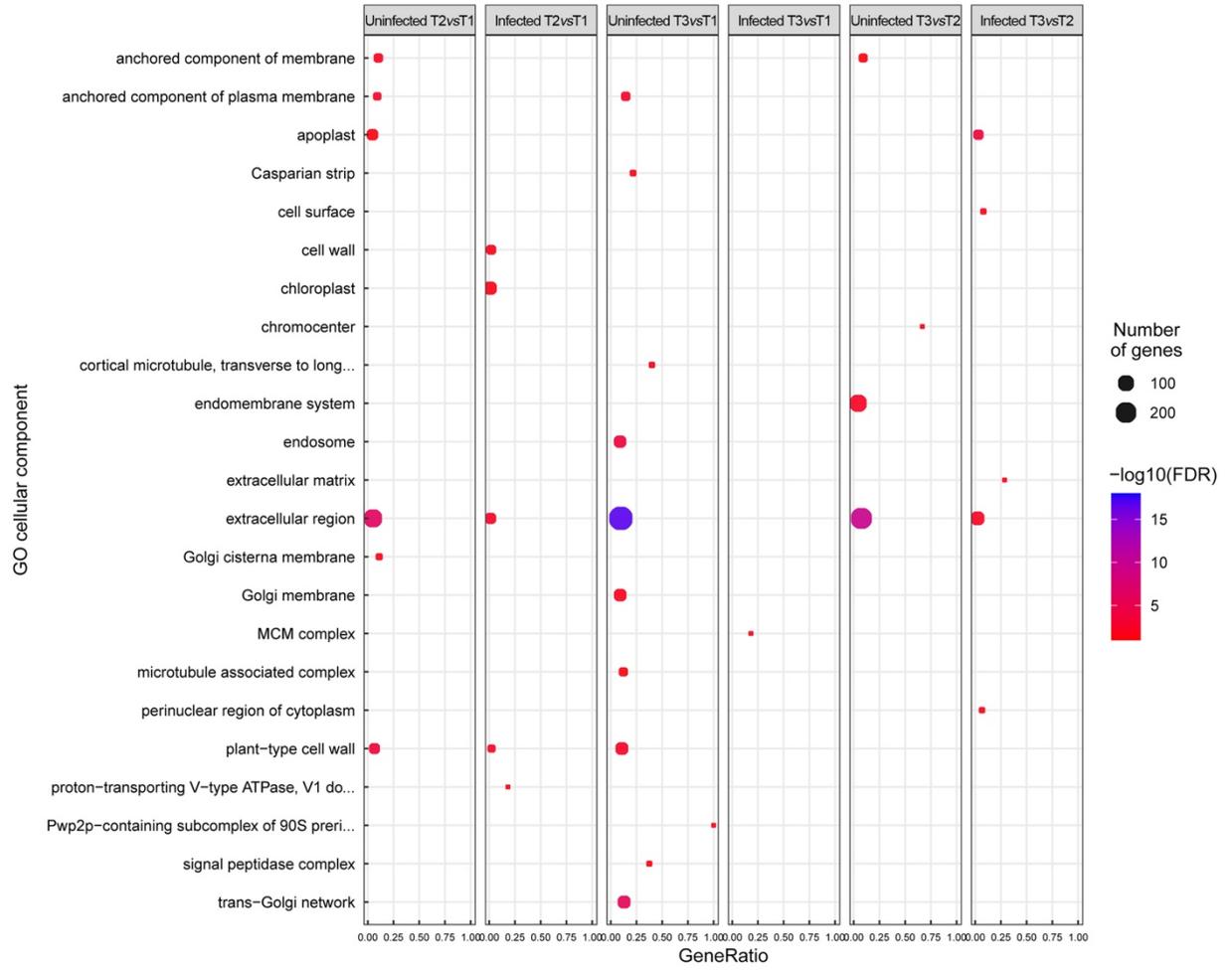
**Figure S2** GO terms enrichment analysis carried out at each sampling times investigated in uninfected and OYVD-infected bulbs. A) Biological Process (BP); B) Molecular Function (MF); C) Cellular Component (CC).



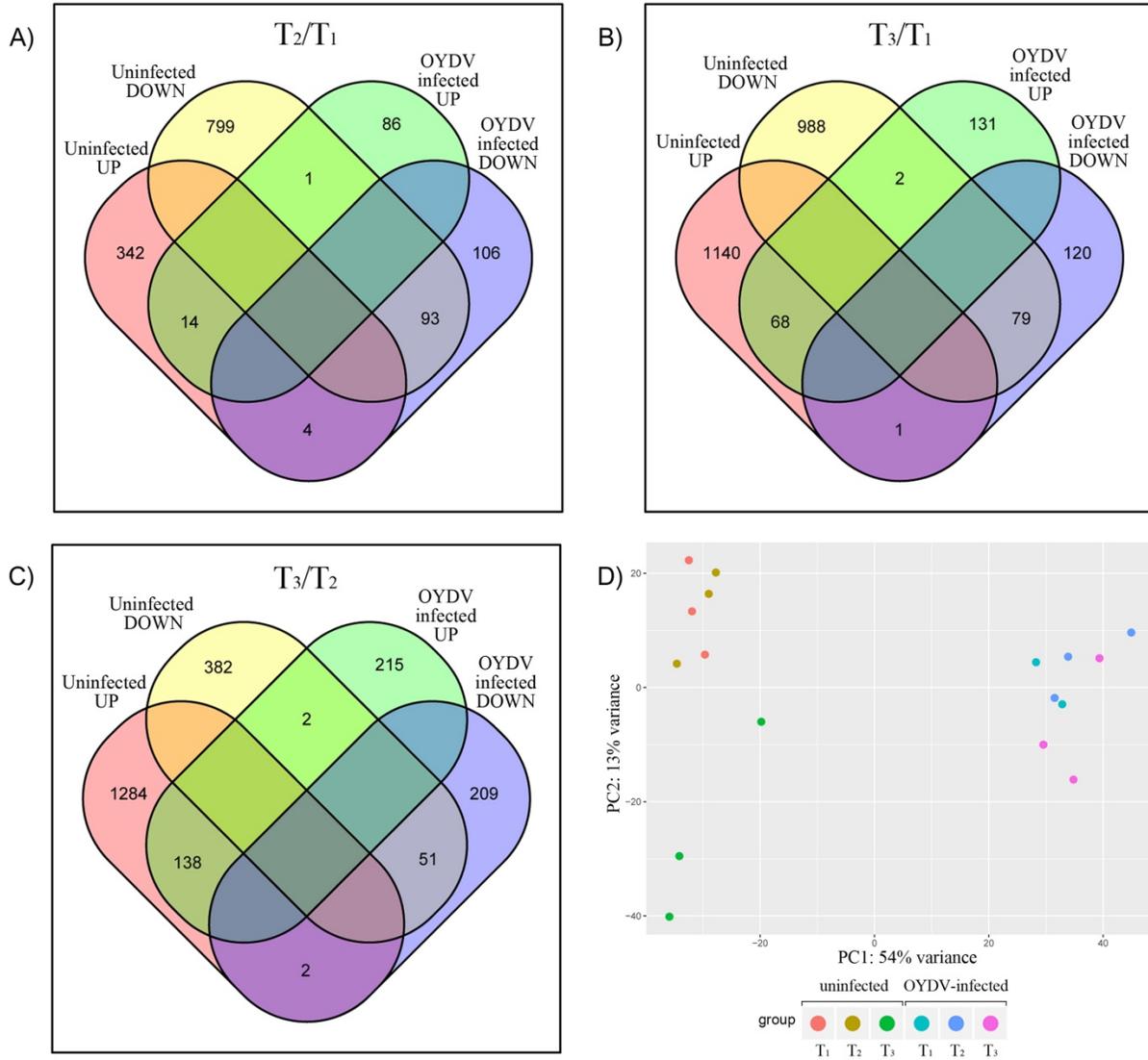
B)



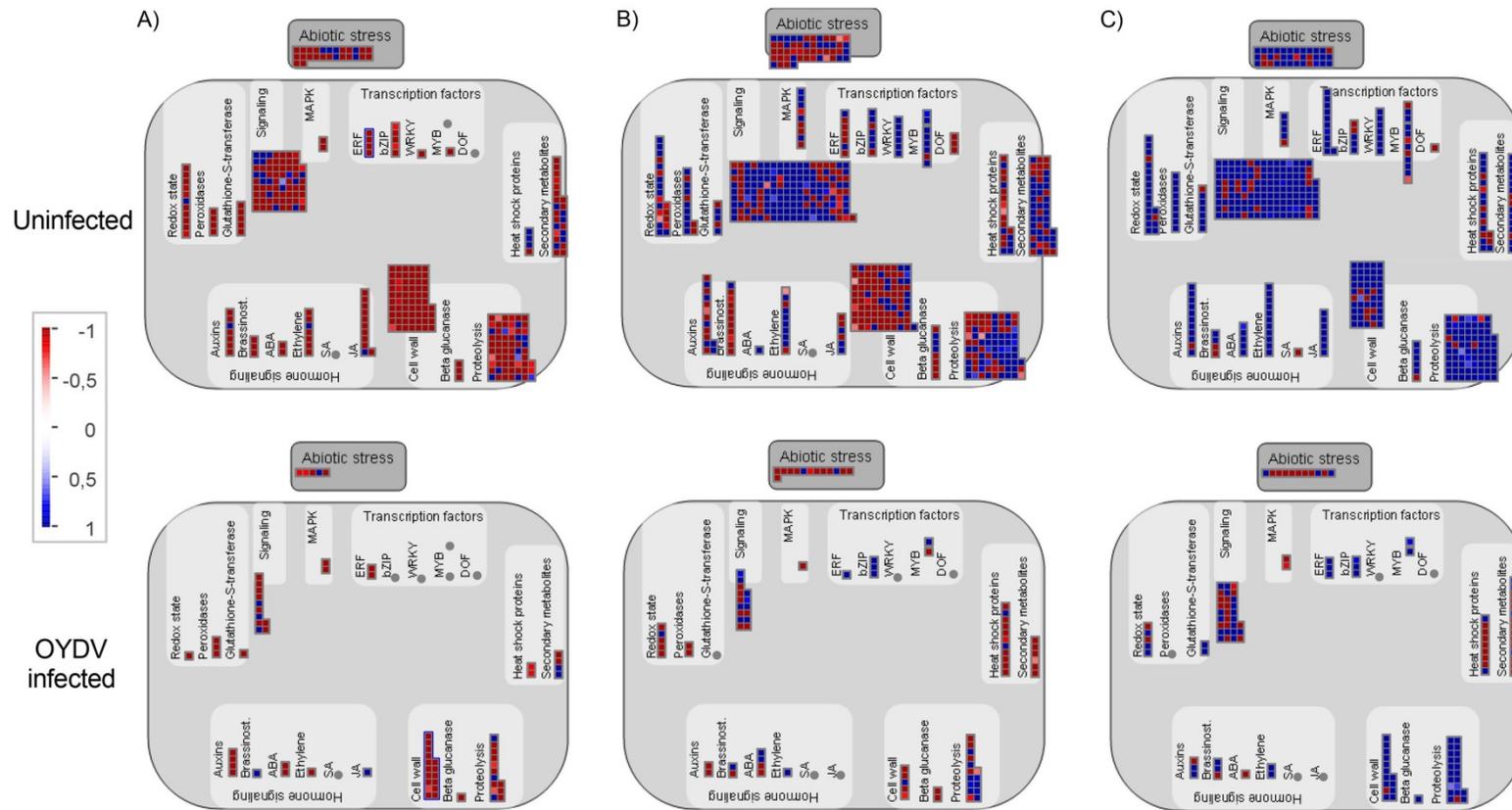
C)



**Figure S3** Transcriptome relationships among the three time points during onion bulb dormancy of uninfected and OYDV-infected plants. VENN diagrams of transcriptome profiles at T<sub>2</sub>/T<sub>1</sub> (A), T<sub>3</sub>/T<sub>1</sub> (B), and T<sub>3</sub>/T<sub>2</sub> (C) comparisons. PCA (D) developed using five hundred most variable genes.

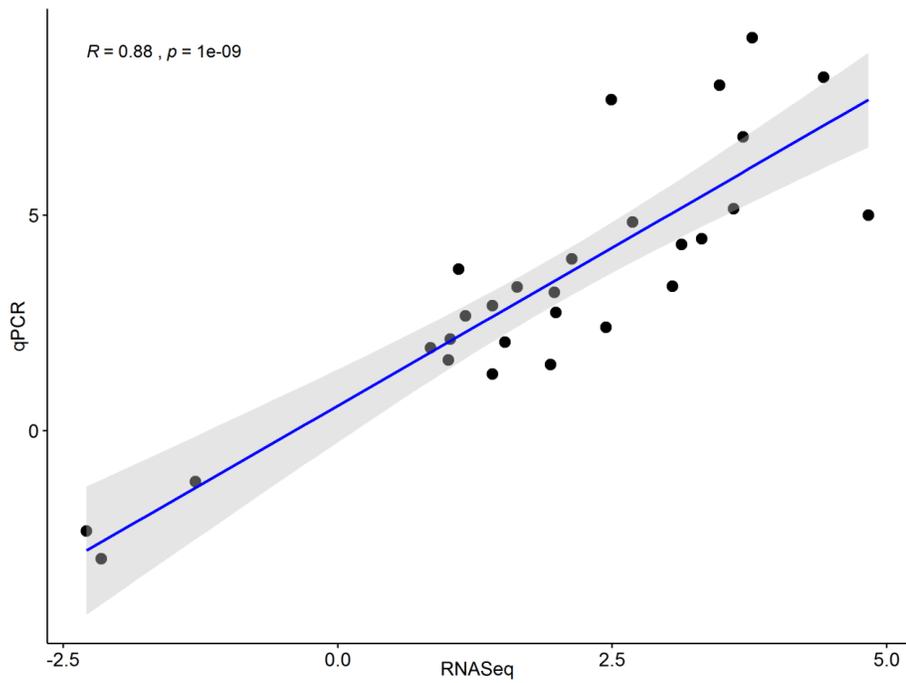


**Figure S4** Overview expression level changes of genes associated to hormone signaling, and some key metabolism pathways involved in dormancy process between uninfected and OYDV infected, following the Mercator annotation. **A)**  $T_2/T_1$ , **B)**  $T_3/T_1$ , and **C)**  $T_3/T_2$  comparisons. Transcription levels with a value  $\log_2 FC \geq 1$  for pairwise comparisons are displayed in colored squares. The blue and red indicate up- and down-regulated genes, respectively. The scale showing the expression level is displayed in the pictures that have been exported from MapMan and their quality was further improved accordingly.





**Figure S6** Correlation analysis between RNA-Seq and qPCR data for *AcWRKYs* differentially expressed in each comparison (Table S9). The same RNAs from NGS experiment were utilized for validation. The Pearson Correlation Coefficient ( $R = 0.88$ ) and the p-value ( $p = 1e-09$ ) were reported.



**Figure S7** Flow chart of the experimental procedure carried out in the present study.

