



## Supplementary materials

## Tables

**Table S1.** Summary of RNA-Seq datasets generated from whiteflies fed for 0, 2, 6, 12 or 48 h on TYLCV-infected tomato plants.

Sampla	<b>Total Raw Reads</b>	<b>Total Clean Reads</b>	<b>Total Mapping</b>	Uniquely Mapping			
Sample	(M)	(M)	(%)	(%)			
0 h-1	21.46	21.41	92.04	78.86			
0 h-2	21.47	21.41	92.10	77.55			
0 h-3	21.46	21.32	92.03	77.99			
2 h-1	21.48	21.42	91.60	76.05			
2 h-2	21.48	21.42	91.92	77.43			
2 h-3	21.49	21.42	92.03	79.63			
6 h-1	21.48	21.43	91.94	78.05			
6 h-2	21.48	21.42	91.62	76.24			
6 h-3	21.48	21.42	91.63	76.76			
12 h-1	21.42	21.35	91.11	76.89			
12 h-2	21.43	21.36	91.56	79.10			
12 h-3	21.41	21.33	91.68	79.28			
48 h-1	21.47	21.42	92.03	78.5			
48 h-2	21.47	21.42	92.25	79.88			
48 h-3	21.49	21.3	91.67	77.05			

Gene ID	Accession	Cone Annotation	log2 (Fold change)						
	No.	Gene Annotation	0 h vs. 2 h	0 h vs. 6 h	0 h vs. 12 h	0 h vs. 48 h			
Bta01475	XP_018896 986.1	uncharacterized protein LOC109030464	-1.55	-1.67	-1.29	-1.57			
Bta01655	XP_018906 270.1	rap1 GTPase-activating protein 1 isoform X3	-1.47	-1.21	-1.72	-1.72			
Bta02375	XP_018913 743.1	uncharacterized protein LOC109041776	-1.18	-1.19	-1.57	-1.95			
Bta02580	XP_018905 067.1	fatty acid synthase	-1.31	-1.12	-2.05	-2.02			
Bta03074	XP_018907 085.1	, fatty acid synthase	-1.34	-1.20	-1.76	-1.71			
Bta04016	XP_018917 600.1	ras-like GTP-binding protein RhoL	-1.12	-1.28	-1.07	-1.24			
Bta04099	XP_018907 804.1	acyl-CoA Delta(11) desaturase-like	-1.28	-1.62	-2.37	-3.34			
Bta05107	XP_018895 569.1	protein FAM166B-like isoform X2	-1.21	-1.08	-1.15	-1.31			
Bta05672	XP_018908 790.1	acyl-CoA desaturase-like	-1.92	-1.26	-1.91	-1.48			
Bta06172	XP_018896 161.1	protein sprint	-1.32	-1.18	-1.33	-1.47			
Bta06187	XP_018896 237.1	solute carrier family 2, facilitated glucose transporter member 1-like	-1.32	-1.27	-1.35	-1.40			
Bta06483	XP_018909 499.1	phospholipase A2-like isoform X1	-3.15	-2.25	-2.16	-3.79			
Bta07569	XP_018896 886.1	fatty acid synthase-like	-1.51	-1.31	-2.05	-2.00			
Bta08548	XP_018898 043.1	protein decapentaplegic	-1.77	-2.31	-1.48	-1.41			
Bta08620	XP_018898 020.1	striated muscle-specific serine/threonine-protein kinase-like	-1.26	-1.34	-1.91	-3.07			
Bta09047	XP_018916 310.1	phosphoenolpyruvate carboxykinase [GTP]-like isoform X2	-1.90	-2.26	-2.51	-2.27			
Bta09151	XP_018916 388.1	calcium/calmodulin-dependent protein kinase kinase 1 isoform X1	-1.98	-2.10	-2.43	-2.58			
Bta09156	XP_018916 405.1	insulin-like peptide receptor	-1.95	-1.50	-1.53	-1.34			
Bta09525	XP_002430 571.1	dual specificity protein phosphatase, putative	-1.48	-1.67	-1.96	-2.03			
Bta09906	KPJ01710. 1	Nitric oxide synthase-like protein	-1.30	-1.03	-1.21	-1.18			
Bta10543	XP_023724 614.1	carnitine O-palmitoyltransferase 1, liver isoform isoform X3	-1.17	-1.22	-1.54	-1.64			

 Table S2. Common DEGs involved in signal transduction in virus-infected whiteflies.

	VP 018012	odium-coupled neutral amino				
Bta11166	71_010912 277.1	acid transporter 9 homolog	-1.23	-1.24	-1.51	-1.61
	277.1	isoform X1				
	VD 018000	muscle, skeletal receptor				
Bta11403	522 1	tyrosine protein kinase-like	-1.33	-1.13	-1.53	-2.05
	322.1	isoform X1				
Bta11772	XP_022194	sphingomyelin	1.01	1.20	-1.20	1.04
	226.1	phosphodiesterase	-1.01	-1.30		-1.24
Bta12556	XP_018901	senecionine N-oxygenase-like	1.07	-1.17	-1.33	1 1 1
	460.1		-1.37			-1.11
Bta12593	VD 010001	BCL2/adenovirus E1B 19 kDa				
	XP_018901	protein-interacting protein 3	-1.65	-2.00	-2.11	-2.26
	501.1	isoform X1				
Bta15685	XP_018916	ABC transporter G family	1.07	1 (0	1.07	1.00
	054.1	member 23-like	-1.36	-1.60	-1.87	-1.92

## Figures

	0h-1	0h-2	0h-3	2h-1	2h-2	2h-3	6h-1	6h-2	6h-3	12h-1	12h-2	12h-3	48h-1	48h-2	48h-3	
0h-1	1.000	0.994	0.998	0.988	0.977	0.977	0.987	0.991	0.977	0.975	0.972	0.984	0.968	0.971	0.970	1.00
0h-2	0.994	1.000	0.994	0.984	0.979	0.971	0.982	0.983	0.972	0.973	0.964	0.981	0.953	0.955	0.957	
0h-3	0.998	0.994	1.000	0.982	0.970	0.968	0.981	0.987	0.969	0.968	0.963	0.978	0.956	0.959	0.959	
2h-1	0.988	0.984	0.982	1.000	0.994	0.996	0.996	0.994	0.995	0.992	0.992	0.997	0.984	0.985	0.987	0.95
2h-2	0.977	0.979	0.970	0.994	1.000	0.994	0.990	0.984	0.990	0.992	0.990	0.993	0.974	0.970	0.977	0.35
2h-3	0.977	0.971	0.968	0.996	0.994	1.000	0.991	0.987	0.993	0.991	0.994	0.995	0.986	0.984	0.987	
6h-1	0.987	0.982	0.981	0.996	0.990	0.991	1.000	0.998	0.995	0.989	0.991	0.996	0.983	0.984	0.985	0.00
6h-2	0.991	0.983	0.987	0.994	0.984	0.987	0.998	1.000	0.992	0.986	0.988	0.994	0.983	0.986	0.984	0.90
6h-3	0.977	0.972	0.969	0.995	0.990	0.993	0.995	0.992	1.000	0.995	0.998	0.995	0.991	0.991	0.993	
12h-1	0.975	0.973	0.968	0.992	0.992	0.991	0.989	0.986	0.995	1.000	0.996	0.994	0.987	0.982	0.989	
12h-2	0.972	0.964	0.963	0.992	0.990	0.994	0.991	0.988	0.998	0.996	1.000	0.994	0.993	0.989	0.994	
12h-3	0.984	0.981	0.978	0.997	0.993	0.995	0.996	0.994	0.995	0.994	0.994	1.000	0.985	0.985	0.988	
48h-1	0.968	0.953	0.956	0.984	0.974	0.986	0.983	0.983	0.991	0.987	0.993	0.985	1.000	0.997	0.998	
48h-2	0.971	0.955	0.959	0.985	0.970	0.984	0.984	0.986	0.991	0.982	0.989	0.985	0.997	1.000	0.998	
48h-3	0.970	0.957	0.959	0.987	0.977	0.987	0.985	0.984	0.993	0.989	0.994	0.988	0.998	0.998	1.000	

Figure S1. Pearson correlation coefficient of gene expression levels among 15 samples.



**Figure S2.** Common DEGs in viruliferous whiteflies. (A) Venn-diagram showing unique and common DEGs in different comparisons of 0 h vs. 2 h, 0 h vs. 6 h, 0 h vs. 12 h and 0 h vs. 48 h. (B) Hierarchical cluster analysis of 235 identified common DEGs.



**Figure S3.** Time-associated gene clusters. For different treatments, genes with similar expression patterns were clustered into different groups. (A) Hierarchical cluster of 127 up-regulated genes. (B) Hierarchical cluster of 355 down-regulated genes.