

## **Comparison of two different host plant genera responding to grapevine leafroll-associated virus 3 infection**

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## **SUPPLEMENTARY FIGURE LEGENDS**

**Supplementary Figure S1.** RT-qPCR validation of differentially expressed genes. Log<sub>2</sub> fold expression values of (a) seven *Vitis vinifera* and (b) four *Nicotiana benthamiana* RNA-seq-selected genes.

**Supplementary Table S1.** Summary of differentially expressed genes

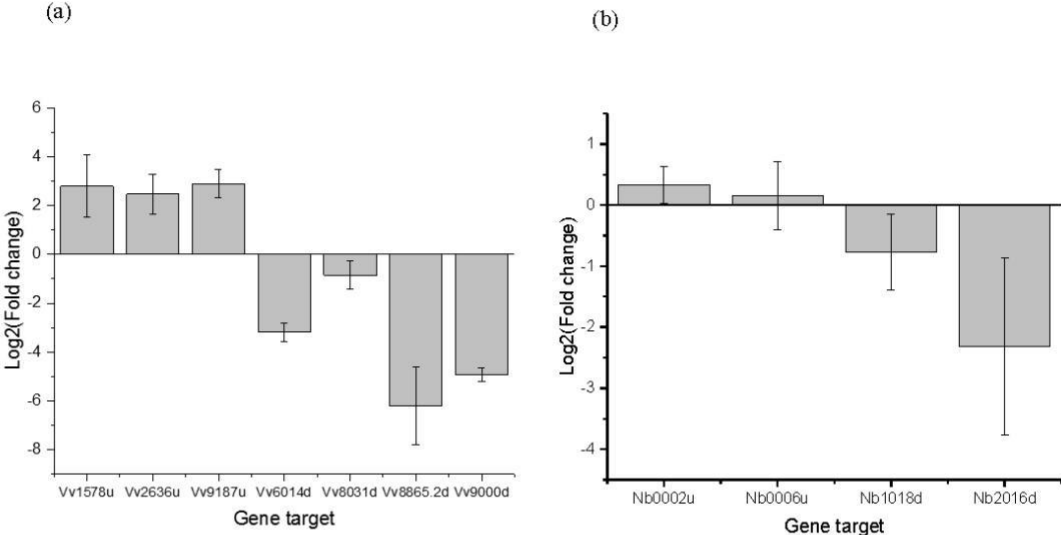
**Supplementary Table S2.** Summary of transcript accumulation

**Supplementary Table S3.** Summary of shared differentially expressed genes found in more than one expression category to be up, down, or stably expressed.

**Supplementary Table S4.** Real-time polymerase chain reaction primers and gene targets.

**Supplementary Table S5.** Summary of viruses and viroids present in plant samples.

Supplementary Figure S1



**Table S3. Summary of shared differentially expressed genes found in more than one expression category to be up, down, or stably expressed.**

**Upregulated**

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Auxin transporter-like protein  
Cytochrome P450  
NAC domain-containing protein  
NAD(P)H-quinone oxidoreductase  
Protein NRT1/ PTR  
Subtilisin-like serine protease  
Sugar transporter protein  
Sulfate transporter  
U-box domain-containing protein  
Zinc finger protein

**Downregulated**

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17.4 kDa class III heat shock protein  
Auxin efflux carrier component  
BAG family molecular chaperone  
regulator  
Chaperone protein  
Copper chaperone  
Cytochrome P450  
Ethylene-responsive transcription factor  
Heat shock cognate 70 kDa  
Homeobox-leucine zipper protein  
Peptidyl-prolyl cis-trans isomerase  
Protein NRT1/ PTR  
Sulfate transporter  
Zinc finger protein

**Stable**

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60S ribosomal protein  
Eukaryotic translation initiation factor  
NAC domain-containing protein

**Table S4. Real-time polymerase chain reaction primers and gene targets.**

Primer name	Nucleotide sequence (5'-3')	Transcript ID	Description
<i>Vitis vinifera</i>			
V8856.2F	AGCTGGTGGGTCATTCACTG	GSVIVG01028856001	heat shock protein 83
V8856.2R	GTACTCCACCTGGTCGTCCT		
V8031F	ACGTAGACAAGAAGCTCGCTGA	GSVIVG01038031001	probable glutathione S-transferase parC
V8031R	AGAGAAGGGCACCAGAGCCA		
V2636F	CAATGTGATGGAGGCGAAGG	GSVIVG01012636001	thiamine thiazole synthase 2, chloroplastic
V2636R	GGTAGGACCCATCCTTGAG		
V1578F	AGCAGGGTATCCTCCACAAC	GSVIVG01015780001	cysteine-rich and transmembrane domain-containing protein A
V1578R	CAAGGCAGCACAACATCCTT		
V9187F	TGGGATTGTCAACAGGCTCT	GSVIVG01009187001	VIN3-like protein 2 isoform X1
V9187R	TCGTATCTGCATCCCTGCTT		
V6014F	TGCGGTTCAAGGCTGGTGTTT	GSVIVG01026014001	stromal 70 kDa heat shock-related protein, chloroplastic
V6014R	TTGCCCATCTGCTGCCGTA		
V9000F	ACAACCCAAGGTGGTAGGTG	GSVIVG01035900001	chaperone protein ClpB4, mitochondrial
V9000R	AATAGTTGCCGCCCAAACCT		
V3149F*	ACTGCGTGTGGAGTAAGGA	GSVIVG01023149001	auxin response factor 1 isoform X1
V3149R*	CGACCGACTTGTTCTTGTTT		
V1341F*	TGGGAAGAGATCCAGGCAGCA	GSVIVG01013410001	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase
V1341R*	GCTCCTCCACCTTGGGCAAT		
<i>Nicotiana benthamiana</i>			
B1018F	TTGCCTTTGGTGTCCCTTGGT	Niben101Scf01182g01018	Bidirectional sugar transporter N3
B1018R	TGAGGAGTGCAGTGTTGGTC		
B2016F	TGCGAGTCGAACGAACCTGCT	Niben101Scf00739g02016	Zinc finger Ran-binding domain-containing protein 2
B2016R	CATACCACATCCAATTCTGCTGC		
B0002F	ACCACCAGGATTTAGGTTCTTTCCT	Niben101Scf03366g00002	NAC domain-containing protein 21/2
B0002R	GCCACCTCAGGAAGTTGCCA		
B0006F	TGTCTCTCAGGCTCACCACGA	Niben101Scf03243g00006	Tubulin alpha chain
B0006R	TTCACGTCCTTGGGCACCAC		
B0009F*	GCTTGGAGAAGCGGTTTGGTC	Niben101Scf07824g00009	cellulose synthase 1
B0009R*	GCCCACCGAAGCACCTCTTT		
B0007F*	TGTCCAGGAGAGATTCGGGTCTG	Niben101Scf06579g00007	Cytochrome b-c1 complex subunit 7
B0007R*	ACACGCACGCTCTGTGTCTC		

\* genes showing stable expression by HTS used to normalize data