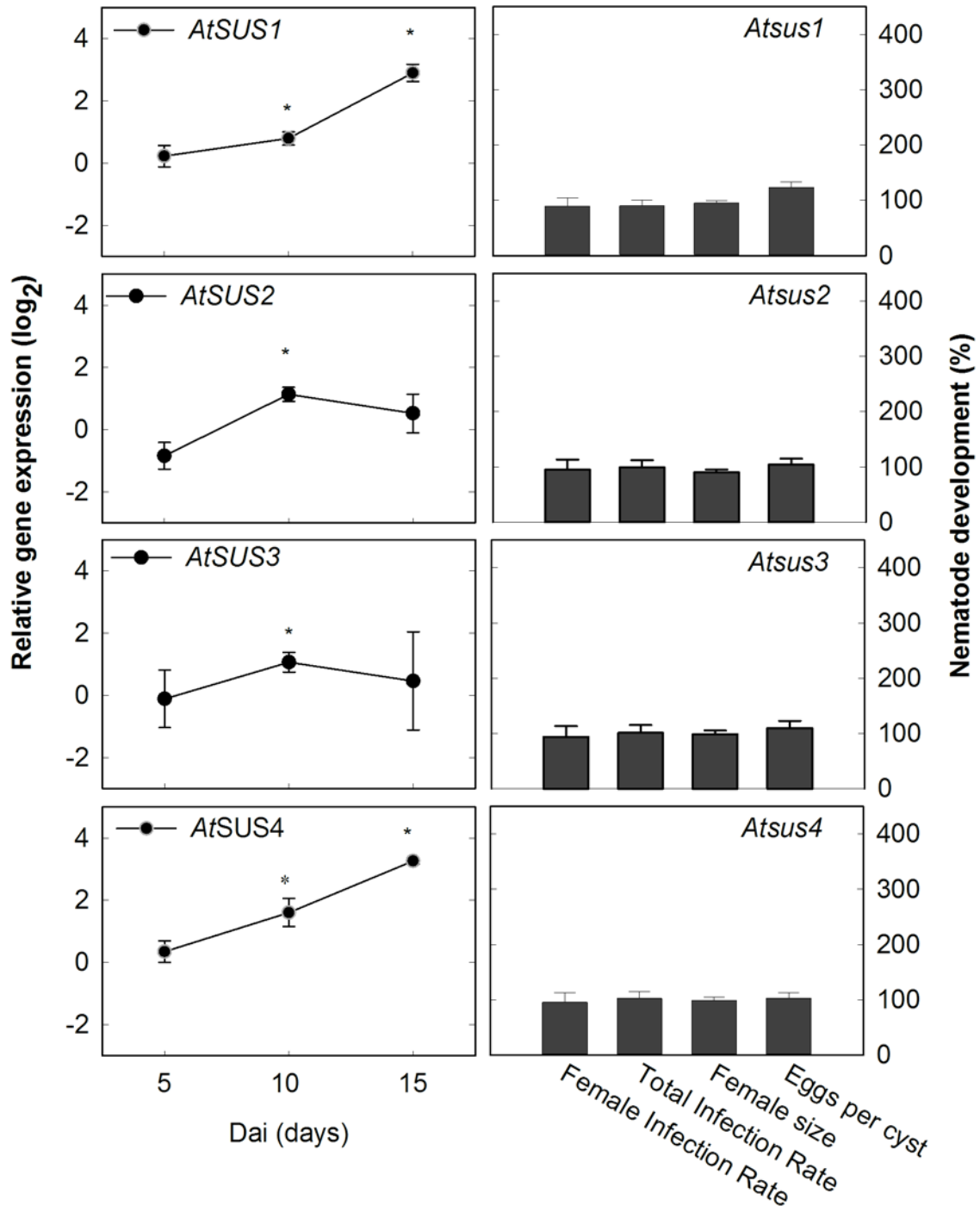
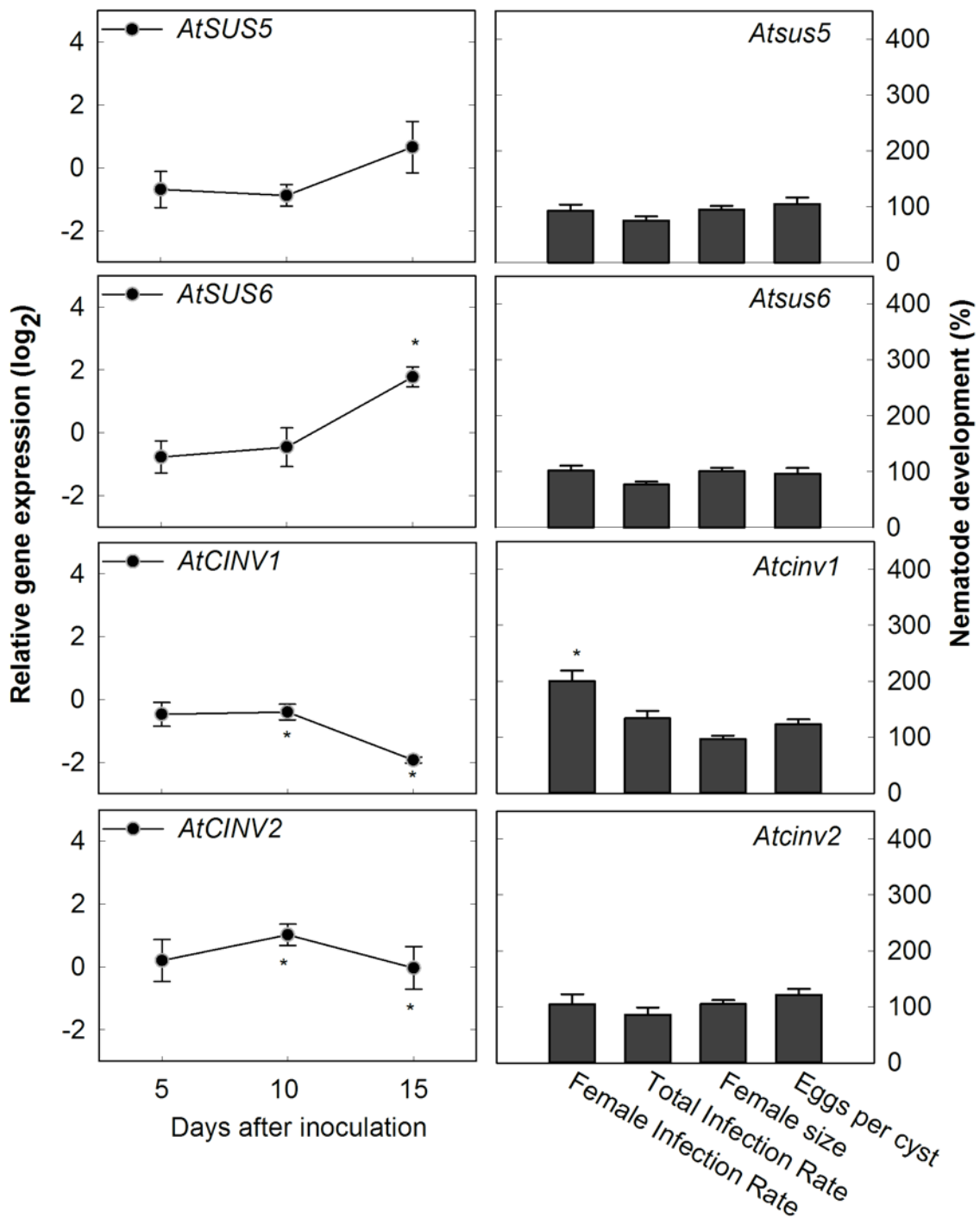


**Altered sucrose synthase and invertase expression affects the local and systemic sugar metabolism of nematode-infected *Arabidopsis thaliana* plants**

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**Figure S1.** Fold change ( $\log_2$ ) expression levels of *SUS* and *CINV* genes in *H. schachtii*-induced syncytia compared to non-infected *A. thaliana* wild type roots. Values are means  $\pm$ SE, n=3 (left side). Total and female nematode infection rates, female size and eggs per cyst of *H. schachtii* on single *A. thaliana sus* and *cinv* T-DNA mutant lines relative to the wild type. Values are means  $\pm$ SE, n=14 to 33 (right side). \* indicate significant differences (Student's t-test,  $p \leq 0.05$ ).

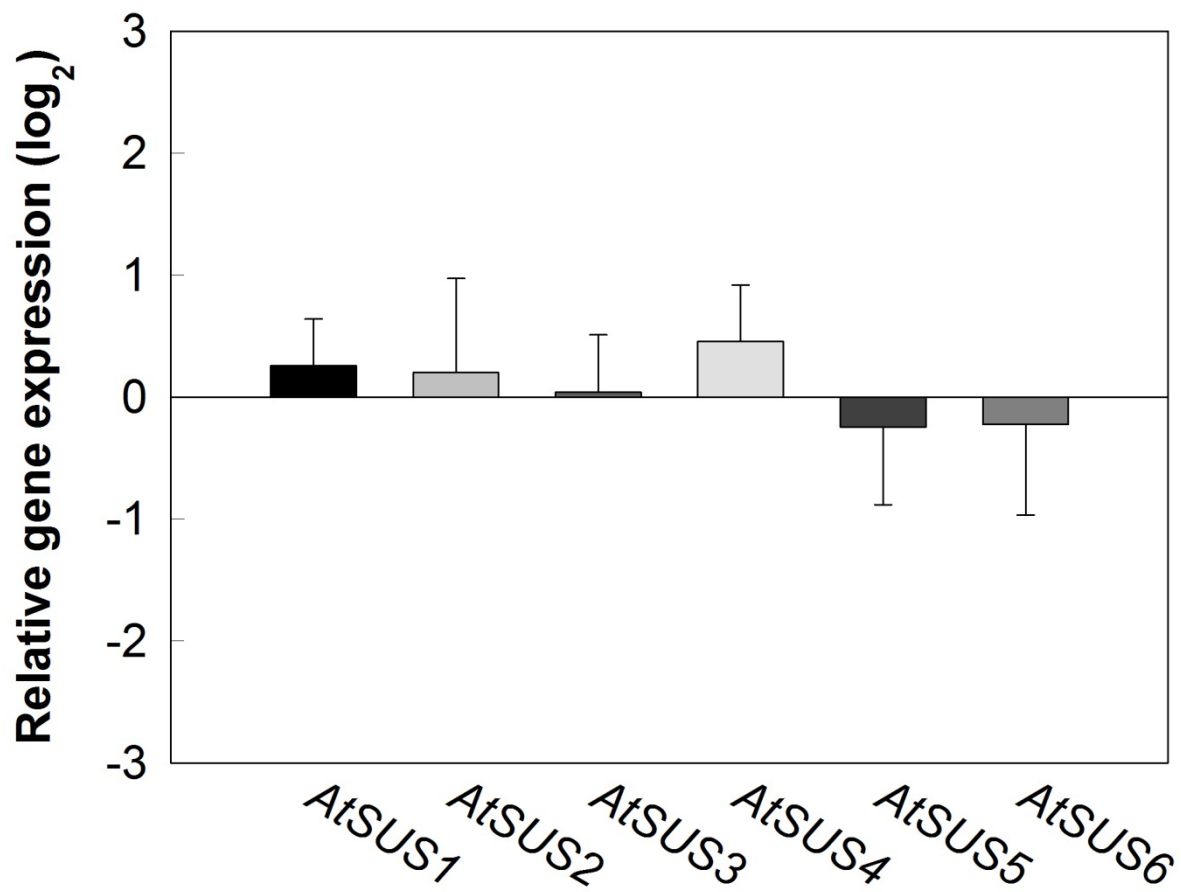




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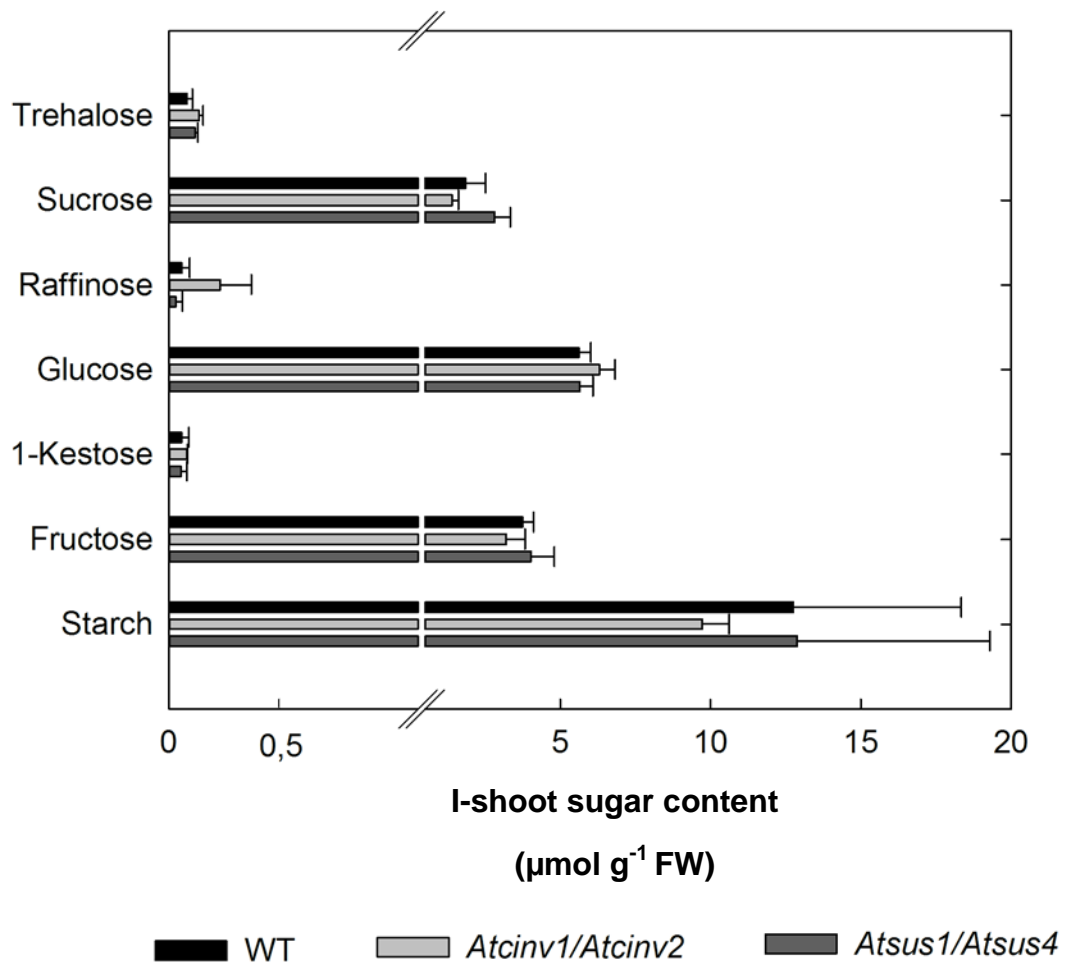
**Figure S2.** Fold change ( $\log_2$ ) expression levels of *SUS* genes in *H. schachtii*-induced syncytia of the *Atcinv1/Atcinv2* line compared to the wild type. Values are means  $\pm$ SE, n=3.



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**Figure S3.** Sugar levels of shoots of nematode-infected wild type, *cinv1/cinv2* and *sus1/sus4* T-DNA insertion lines (15 dai). Values are means  $\pm$ SE, n=3, no significant differences from the wild type were observed (Student's t-test,  $p \leq 0.05$ ).



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**Table S1:** List of T-DNA insertion lines used in this study and their sources. All lines have the *Arabidopsis* Col0 background.

<b>Name</b>	<b>Locus</b>	<b>Salk line</b>	<b>Source</b>
<i>Atsus1</i>	At5g20830	SALK-014303	NASC
<i>Atsus2</i>	At5g49190	SALK-076303	NASC
<i>Atsus3</i>	At4g02280	SALK-019405	NASC
<i>Atsus4</i>	At3g43190	Arab4	Bieniawska et al., 2007
<i>Atsus5</i>	At1g73370	SAIL-374-D07	NASC
<i>Atcinv1</i>	At1g35580	Salk_095807	NASC
<i>Atcinv2</i>	At4g09510	Sail_518_d02	NASC
<i>Atsus3/Atsus2</i>	At4g02280	Salk_019405	Bieniawska et al., 2007
	At5g49190	Salk_076303	
<i>Atsus5/Atsus6</i>	At5g37180	Salk_152944	Bieniawska et al., 2007
	At1g73370	Salk_107491	
<i>Atsus1/Atsus4</i>	At4g20830	Salk_014303	Bieniawska et al., 2007
	At3g43190	Arab4	
<i>Atcinv1/Atcinv2</i>	At1g35580	Salk_095807	Barratt et al., 2009
	At4g09510	Sail_518_d02	

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**Table S2.** Primer sequence used to identified the correct T-DNA insertion in *SUS* and *CINV* genes

<b>Gene</b>	<b>Primer sequence</b>
At1g35580	RP CAATCGACCAAATGAGTGAGG LP CGCTAGACCTAGCCATTAGGG
At4g09510	RP AACGATCTCTTCCGTTTCGATC LP GAGCCACATAATTCAAAGCAAC
At5g20830	RP CGCTTGTTTCTGAGAGAAACG LP TCCCCTCTCAAGACCAATCTC
At5g49190	RP TGCACCATTTCTGAAACCTT LP CATGGGTAATGGTTTTGGTTG
At4g02280	RP TTTCCCGTATTCCGAAGAAAC LP TTGGAGACCAGCGTCTGATAC
At5g37180	RP TTGTTTGGCCAGTTTCTGATC LP ATTTCCCTTTTACCGCACAAG
At1g73370	RP ATCCATCTGAATTTCCCCTTG LP TGACACGGTTAATACCGGAAG

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**Table S3.** Primers sequences, concentrations and MgCl<sub>2</sub> concentrations for q-PCR

Gene	Primer	sequence	Primer (nM)	MgCl <sub>2</sub> (nM)	
At1g35580	<i>AtCINV1</i>	FP	TCGAGGGCCATGAGTGGCGC	300	
		RP	CGCGGTCTTGGCAGTCTGCG		
At4g09510	<i>AtCINV2</i>	FP	CGGTGGATCTTGGCCAGTATTGC	200	
		RP	CCAGCAATCTCGGTGTAGCCGT		
At3g13790	<i>AtCWINV1</i>	FP	GCCAGCTCGTTCCGTGACCC	200	
		RP	ACGAAGACGTTTCCACGCCGTT		
At3g52600	<i>AtCWINV2</i>	FP	CGTGAAGGGTTGGGCCGGAA	200	
		RP	GGACCTCAAAGCGTTGGCCC		
At1g55120	<i>AtCWINV3</i>	FP	ATCTCAACCAACCGTACCGGACC	200	
		RP	CGTGGAGTGTCCCCACACGA		
At2g36190	<i>AtCWINV4</i>	FP	ACCAAAGGTGCGGTTTGGGGT	200	
		RP	TGAACCGGACCATGTACCTCCG		
At3g13784	<i>AtCWINV5</i>	FP	GGTTGGGCCGGTTTACAGGCT	150	
		RP	GGATCGGTCCAGCCCGGTTT		
At5g11920	<i>AtCWINV6</i>	FP	GCATCACTGCTGCCCAAGCA	200	25
		RP	TGCATATCCGTTACCGCGACGA		
At1g62660	<i>AtVACINV1</i>	FP	GGCGAGCACGGAAGCTCTCT	200	
		RP	TCAGCCTTGGAGCCGTCGTG		
At1g12240	<i>AtVACINV2</i>	FP	GTGGACCGGCTCAGCCACAT	200	
		RP	AGGGAGGATACCGGGCGGAG		
At5g20830	<i>AtSUS1</i>	FP	GCGCGTCCACAGCCAACGTG	200	
		RP	ACCAGGCCTTGGCCTCACAGC		
At5g49190	<i>AtSUS2</i>	FP	AGGGTGTACCAAATCTCAT	300	25
		RP	CATAGTCAAAGCTGTGTGG		
At4g02280	<i>AtSUS3</i>	FP	GAGCACGGGCTCTCGGGTTT	200	
		RP	GCCGAGTCTCACGACGCTCC		
At3g43190	<i>AtSUS4</i>	FP	CACACTTCCCGGGTTGTACCGT	350	25
		RP	GCGCAAGCGAGTGTCTTACCG		
At5g37180	<i>AtSUS5</i>	FP	GTCCTCGAAGCTCGGAGGGC	180	
		RP	CTCCCTGCGCTTTCTCCCA		
At1g73370	<i>AtSUS6</i>	FP	CGCCTTGATTGCAAGCCAGACC	200	
		RP	TGGCCTGTCCTTGCTTCCTGC		



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At5g10790	<i>UBP22</i>	FP	ACAACATATGACCCGTTTATCGA	347	30
		RP	TGTTTAGGCGGAACGGATACT		
	<i>18SrRNA</i>	FP	GGTGGTAACGGGTGACGGAGAAT	355	30
		RP	CGCCGACCGAAGGGACAAGCCGA		

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