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## Transcriptome-based discovery of genes and networks related to *R<sub>SC3Q</sub>*-mediated resistance to *Soybean mosaic virus* in soybean

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### Supplemental information

**Table S1.** Primer sequences used for quantitative real-time PCR

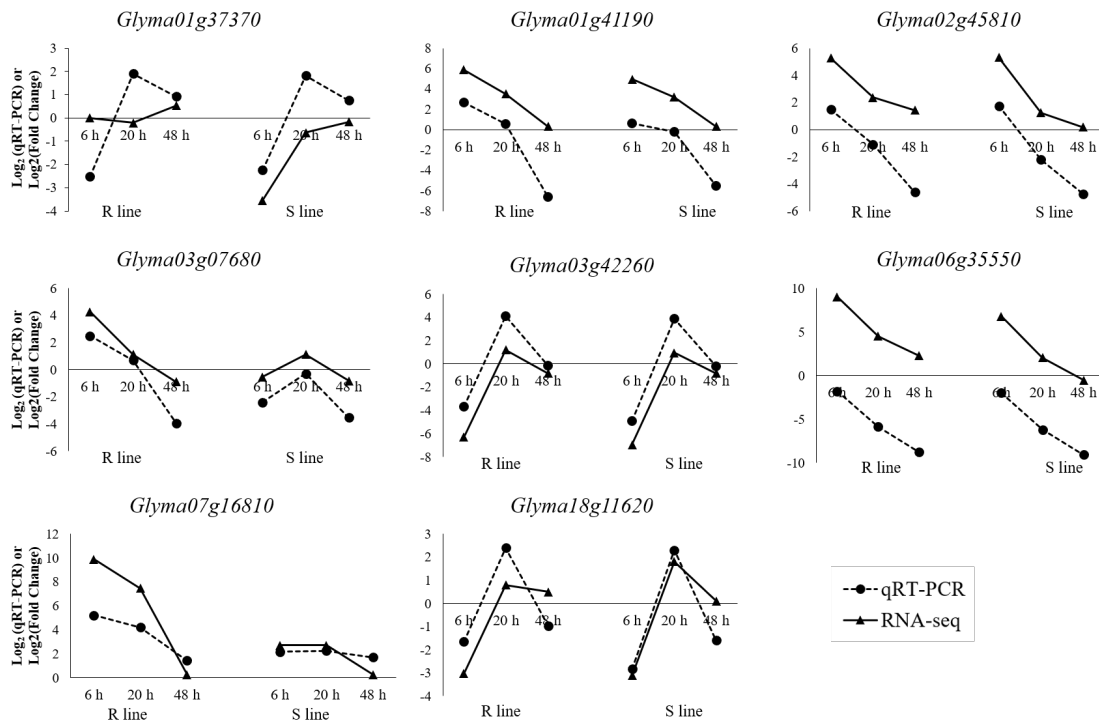
Primer ID	Forward primers (5'-3')	Reverse primers (5'-3')
<i>Glyma03g28650</i>	GACCTCGAGTCGCTTCTCAC	TGAGAGACTCAACCGTGATGC
<i>Glyma11g33790</i>	ATGATGGCGGAGCTTGATCG	CAGCCCGTTCTTGCCAGAT
<i>Glyma19g31395</i>	GGCATCACCGTAGAAAGGCT	AACCCGTCCCCATTTCTGTC
<i>CP</i> (SMV coat protein)	TTCTGAAAGTCCGTATATGCCTAG	GCCTTTCAGTATTTTCGGAGTT
<i>Tubulin</i>	GGAGTTCACAGAGGCAGAG	CACTTACGCATCACATAGCA
<i>Glyma01g37370</i>	AAAATCCGGCTTCACAACCA	TGCCCATCAGCATCAGGTC

<i>Glyma01g41190</i>	CCAACCCATCTTCCGTCTC	AGCGTGAACCTTCTCCCTTT
<i>Glyma02g45810</i>	ACTACCCACGTTCTGCCTATGA	AAAGCCAGTTGAGCCACCC
<i>Glyma03g07680</i>	TACCCTAAGTGCCCACAGCC	ACAGTGACCCAATCTTCTCCTCT
<i>Glyma03g42260</i>	ACCCTGTTCATCTGTATCTTCCG	TGCTTGCCATCATCTATCTCCA
<i>Glyma06g35550</i>	ATAATAAATGGCCTGTGCTACCTTG	TTCCACTTGACCCTCCTCCC
<i>Glyma07g16810</i>	AATGAGCAGCCCATAGCAGA	TTGGACCAGAAACGAGCC
<i>Glyma18g11620</i>	GACAAGCCCAATCCTAAGCC	CTCCCAATGAAATGAGCAAAGT

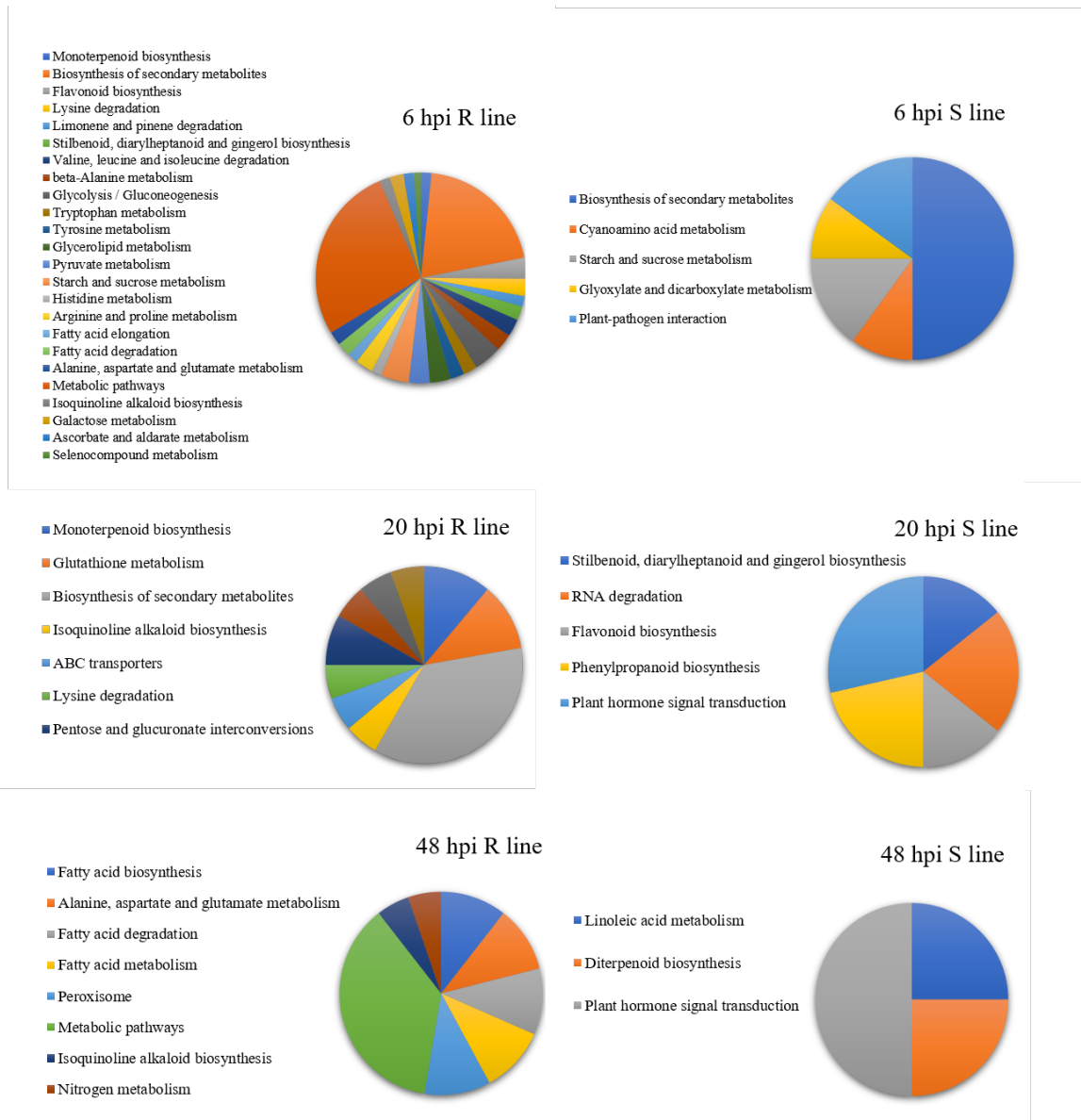
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**Table S2.** Statistical summary of the R and S lines after RNA resequencing

Sample	Clean reads	Mapping reads	Mapping Rate	Map Genes	Total Gene	Map Gene Rate
0R	60693386	56187385	92.57%	40502	46,430	87.23%
0S	58986036	51736666	87.71%	40382	46,430	86.97%
6R	53945472	47571906	88.18%	41309	46,430	88.97%
6S	59174920	50811749	85.86%	40954	46,430	88.21%
20R	55029478	48625219	88.36%	41291	46,430	88.93%
20S	67068306	57550836	85.80%	40620	46,430	87.48%
48R	42969016	36418403	84.75%	39159	46,430	84.33%
48S	63021226	50244246	79.72%	40979	46,430	88.26%



**Figure S1. Quantitative real-time PCR analysis was used to test the reliability of transcriptome analysis.** The expression pattern of eight randomly selected genes were from qPCR analysis and transcriptome data after SC3 inoculation at 0, 6, 24, and 48 h in R and S lines.  $\text{---}\bullet\text{---}$ :  $\text{Log}_2(\text{data of qPCR})$   $\text{---}\blacktriangle\text{---}$ :  $\text{Log}_2(\text{data of fold change from transcriptome})$ .



**Figure S2** Relative distribution of enriched pathways in soybean plants (R and S lines) infected with SC3 at different time points.