CORRECTIONS

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Pischke M.S., Huttlin E.L., Hegeman A.D., and Sussman M.R. A Transcriptome-Based Characterization of Habituation in Plant Tissue Culture.

An Excel sorting error resulted in incorrect reports of the numbers of significantly differentially expressed genes identified by SAM analysis in Table III.

Table III. *Breakdown of significantly differentially expressed genes by test*

Correct numbers of differentially expressed genes identified by SAM analysis are as follows.

Method	Gene Expression Category	FC + BA versus FC − BA	T87 + BA versus T87 − BA	T87 − BA versus FC + BA
SAM	Significantly up-regulated genes	467	0	612
	Significantly down-regulated genes	20	36	1,024
	Total significantly differentially expressed genes	487	36	1,636

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www.plantphysiol.org/cgi/doi/10.1104/pp.109.900300