Table S3. *Expected and observed frequencies of functional categories for Cmm-modulated genes*

The distribution in functional categories of annotated genes differentially expressed in response to *Cmm* was compared to that of the approximately 1,000 annotated tomato genes that are available from database. *P* values for differences in the percentage of each category were calculated using a two-sided binomial test followed by false discovery rate correction for multiple testing.

		4 dpi		**8 dpi**	
Functional Category	**Expected %**	**Observed %**	***P* value**	**Observed %**	***P* value**
Defense	6.5	20.5*	$6.2\text{x}10^{-3}$	19.0*	$4.9\text{x}10^{-6}$
Transcription	10.2	10.3	1	11.4	0.71
Oxygen and radical metabolism	2.5	10.3	0.03	11.4*	$2.0\text{x}10^{-5}$
Stress	1.4	12.8*	$4.5\text{x}10^{-4}$	8.6*	$3.7\text{x}10^{-5}$
Signaling	6.3	2.6	0.57	8.6	0.64
Protein degradation	6.9	12.8	0.25	7.6	0.82
Hormone-related	1.2	10.3*	$2.7\text{x}10^{-3}$	6.7*	$6.2\text{x}10^{-4}$
Protein synthesis	11.1	7.7	0.7	5.7	0.1
Lipid metabolism	1.1	0	1	4.8*	0.01
Cell wall-related	2.7	5.1	0.55	3.8	0.59
Carbohydrate metabolism	10.7	2.6	0.13	2.9*	$7.0\text{x}10^{-3}$
Secondary metabolism	6.8	0	0.13	2.9	0.15
Nucleic acid-related	3.9	2.6	1	2.9	0.85
Transport	8.6	2.6	0.28	1.9*	0.01

*Significantly enriched percentages (*P* value < 0.05).