Supplemental Table 3. Distributions of expression differences of genes in functional categories compared with the overall differences distribution

				Functional category[e]					
Genotype[a]	Infection court[b]	Expression change range[c]	KS test[d]	Disease & defense	Signal transduction	Transcription	Intracellular traffic	Cell structure	Metabolism
Sloan	Lower	Full	n1	850	1,976	2,385	815	1,097	3,337
			n2	23,556	23,556	23,556	23,556	23,556	23,556
			p	<0.0001	<0.0001	<0.0001	0.0008	0.006	<0.0001
		±2X	n1	463	1,470	1,639	640	730	2,230
			n2	16,879	16,879	16,879	16,879	16,879	16,879
			p	0.03	0.0002	<0.0001	0.002	<0.0001	<0.0001
		±1.5X	n1	269	1,006	1,064	484	442	1,420
			n2	11,200	11,200	11,200	11,200	11,200	11,200
			p	0.34	0.018	<0.0001	0.017	0.0003	<0.0001
		±1.2X	n1	92	361	377	195	120	431
			n2	3,947	3,947	3,947	3,947	3,947	3,947
			p	0.57	0.37	0.0008	0.23	0.36	0.0004
	Upper	Full	n1	823	1,878	2,267	784	1,038	3,245
			n2	22,758	22,758	22,758	22,758	22,758	22,758
			p	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
		±2X	n1	505	1,566	1,756	664	776	2,341
			n2	17,787	17,787	17,787	17,787	17,787	17,787
			p	0.094	<0.0001	<0.0001	0.0067	0.094	<0.0001
		±1.5X	n1	327	1,114	1,195	504	529	1,561
			n2	12,361	12,361	12,361	12,361	12,361	12,361
			p	0.21	<0.0001	<0.0001	0.029	0.088	<0.0001
		±1.2X	n1	93	389	391	219	153	501
			n2	4,414	4,414	4,414	4,414	4,414	4,414
			p	0.67	0.0058	0.0011	0.14	0.12	0.0002

Supplemental Table 3 (continued)

				Functional category[e]					
Genotype[a]	Infection court[b]	Expression change range[c]	KS test[d]	Disease & defense	Signal transduction	Transcription	Intracellular traffic	Cell structure	Metabolism
V71-370	Lower	Full	n1	802	1,813	2,228	741	1,015	3,085
			n2	21,772	21,772	21,772	21,772	21,772	21,772
			p	<0.0001	<0.0001	<0.0001	0.0001	0.013	<0.0001
		±2X	n1	524	1,518	1,816	662	772	2,309
			n2	17,661	17,661	17,661	17,661	17,661	17,661
			p	0.18	<0.0001	<0.0001	0.0008	0.099	<0.0001
		±1.5X	n1	359	1,079	1,283	507	538	1,620
			n2	12,925	12,925	12,925	12,925	12,925	12,925
			p	0.17	0.0004	<0.0001	0.0013	0.099	<0.0001
		±1.2X	n1	124	385	476	244	191	513
			n2	4,824	4,824	4,824	4,824	4,824	4,824
			p	0.23	0.02	<0.0001	0.092	0.018	0.01
	Upper	Full	n1	736	1,651	2,044	698	914	2,904
			n2	20,418	20,418	20,418	20,418	20,418	20,418
			p	<0.0001	<0.0001	<0.0001	<0.0001	0.0009	<0.0001
		±2X	n1	530	1,511	1,831	653	764	2,365
			n2	17,960	17,960	17,960	17,960	17,960	17,960
			p	0.12	<0.0001	<0.0001	0.0007	0.01	<0.0001
		±1.5X	n1	398	1,225	1,400	538	570	1,729
			n2	14,034	14,034	14,034	14,034	14,034	14,034
			p	0.15	<0.0001	<0.0001	0.0002	0.22	<0.0001
		±1.2X	n1	143	492	529	275	205	614
			n2	5,438	5,438	5,438	5,438	5,438	5,438
			p	0.51	0.006	<0.0001	0.028	0.029	<0.0001

[a] Genotypes were cultivars Sloan and V71-370. [b] Responses in both upper infection court (Upper vs. Mock) and lower infection court (Lower vs. Mock) were evaluated relative to mock inoculated tissue. [c] The expression changes were calculated by contrast analysis with SAS Proc Mixed using GC-RMA normalized data. “Full” = full range from the greatest down-regulation to the greatest up-regulation; “±2.0X” = from down-regulated 2.0x to up-regulated 2.0x; “±1.5X” = from 1.5x down-regulated to 1.5x up-regulated; “±1.2X” = from 1.2x down-regulated to 1.2x up-regulated. [d] Kolmogorov-Smirnov test for distribution differences between a particular functional category and the whole gene set, for genes with significant infection responses: n1 = number of the significant genes in the functional category; n2 = the number of overall significant genes; p, the p-value generated by 10,000 fold resampling as described in the Methods, and adjusted for false discovery by the TST method. [e] Functional category of each gene drawn from annotation of the Affymetrix GeneChip by the Goldberg group at the University of California, Los Angeles (http://estdb.biology.ucla.edu/seed).