

Table S1. Metrics for transcripts generated by Illumina sequencing mapping to the *P. vulgaris* genome. Transcript mapping is for mRNA libraries from CBB-susceptible and CBB-resistant RIL plant leaves sampled post-inoculation (PI) with water (mock) and *X. axonopodis* (*Xap*).

RIL	Treatment	PI (h)	Raw reads	Trimmed reads	Total mappings	Single mappings	Multi mappings	Alignment (%)	Transcripts
CBB-susceptible	Mock	0	89002269 (±6.3%)	88980236 (±6.3%)	70938331 (±6.0%)	61690532 (±6.1%)	92477798 (±6.8%)	79.8 (±0.4%)	44182 (±0.7%)
	Mock	8	98043419 (±6.2%)	98018530 (±6.2%)	77433697 (±5.8%)	68355937 (±5.1%)	9077760 (±10.9%)	79.0 (±0.6%)	43538 (±2.5%)
	Mock	24	92254389 (±8.2%)	92229654 (±8.2%)	73059843 (±8.1%)	65787819 (±8.2%)	7272024 (±7.3%)	79.3 (±0.2%)	44632 (±0.8%)
	Mock	48	97238219 (±4.6%)	97212573 (±4.6%)	77152959 (±4.6%)	70954344 (±4.4%)	6198615 (±12.2%)	79.4 (±0.1%)	44663 (±0.4%)
	<i>Xap</i>	0	81708983 (±3.4%)	81686076 (±3.4%)	64649642 (±3.6%)	55136256 (±3.5%)	9513386 (±4.7%)	79.1 (±0.2%)	43583 (±0.2%)
	<i>Xap</i>	8	99910895 (±5.0%)	99883764 (±5.0%)	78824174 (±5.4%)	70007671 (±4.7%)	8816503 (±11.1%)	78.9 (±0.5%)	42190 (±6.1%)
	<i>Xap</i>	24	89059555 (±2.5%)	89035464 (±2.5%)	69870807 (±2.8%)	63016977 (±3.7%)	6853830 (±7.5%)	78.5 (±0.6%)	44580 (±0.5%)
	<i>Xap</i>	48	85520810 (±4.8%)	85499423 (±4.8%)	66745366 (±3.5%)	60319696 (±4.2%)	6425670 (±13.8%)	78.7 (±0.6%)	44452 (±0.3%)
	Mock	0	89306333 (±6.0%)	89285555 (±6.0%)	70294844 (±5.8%)	60446036 (±5.5%)	9848808 (±12.8%)	78.8 (±0.5%)	44022 (±0.1%)
	Mock	8	104029850 (±10.9%)	104004500 (±10.9%)	82477919 (±11.3%)	71323134 (±11.2%)	11154785 (±16.2%)	79.2 (±0.5%)	44590 (±0.4%)
	Mock	24	97594783 (±6.4%)	97572905 (±6.4%)	76965956 (±6.3%)	69518533 (±7.4%)	7447423 (±4.8%)	78.9 (±0.2%)	44897 (±0.5%)
	Mock	48	87986621 (±7.6%)	87966646 (±7.6%)	68734223 (±7.2%)	62959382 (±8.3%)	5774841 (±4.7%)	78.2 (±0.6%)	44044 (±2.0%)
CBB-resistant	<i>Xap</i>	0	77550060 (±8.7%)	77532011 (±8.7%)	61824489 (±8.0%)	52424394 (±7.3%)	9400096 (±13.0%)	79.8 (±0.6%)	35826 (±22.0%)
	<i>Xap</i>	8	94459242 (±5.6%)	94236153 (±5.7%)	74577706 (±5.9%)	64493749 (±6.8%)	10083957 (±7.0%)	79.1 (±0.3%)	43219 (±2.3%)
	<i>Xap</i>	24	84607080 (±3.7%)	84586474 (±3.7%)	60158244 (±10.3%)	54746523 (±9.9%)	5411721 (±14.8%)	79.3 (±1.1%)	37638 (±19.0%)
	<i>Xap</i>	48	90716979 (±1.6%)	90692987 (±1.6%)	70755116 (±2.1%)	65649321 (±1.6%)	5105795 (±12.8%)	78.0 (±0.9%)	45085 (±0.02%)

¹Data represents the mean ± percent standard error (in parentheses) of three experimental replicates.

Tables S2 to S51 list upregulated and/or downregulated *P. vulgaris* genes in leaves of a CBB-resistant RIL and/or a CBB-susceptible RIL following inoculation with *Xanthomonas axonopodis* (*Xap*). Significant DEGs had a q value ≤ 0.05 ; this statistical information is provided in Excel S1 and Excel S2 spreadsheets of the Supplementary Information. **In Tables S2 to S51, the significant upregulated DEGs (as statistically determined in Excel S1 & S2) are shaded dark grey for the *Xap* treatment relative to the light grey mock treatment at the specified PI sampling time; the significant downregulated DEGs (as statistically determined in Excel S1 & S2) are shaded dark grey for the mock treatment relative to light grey for the *Xap* treatment at the specified PI period. Non-shaded data are not significantly different at the specified PI sampling period.**

Table S2. Transcript abundance for genes upregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (*Xap*). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G024200</i>	Domain of unknown function	0.78 ± 0.21	0.75 ± 0.36	1.58 ± 0.24	2.61 ± 0.85	3.44 ± 0.47	0.37 ± 0.23	1.88 ± 0.07	1.06 ± 0.31
<i>Phvul.002G231600</i>	17.6 kDa class I heat shock protein 1-related	2.71 ± 0.83	2.89 ± 0.29	15.88 ± 0.93	24.34 ± 2.67	28.86 ± 14.77	10.36 ± 6.6	20.35 ± 1.8	27.81 ± 5.07
<i>Phvul.002G240100</i>	Receptor like protein 55	0.62 ± 0.37	0.4 ± 0.24	0.81 ± 0.17	0.62 ± 0.1	2.75 ± 0.54	0.56 ± 0.38	0.75 ± 0.17	0.31 ± 0.12
<i>Phvul.003G203400</i>	No functional annotation	2.15 ± 0.38	1.8 ± 0.69	5.56 ± 0.76	4.57 ± 1.4	9.25 ± 3.77	3.82 ± 2.37	5.37 ± 0.96	5.23 ± 0.19
<i>Phvul.004G107700</i>	Heat shock protein 90	51.05 ± 18.33	29.26 ± 7.86	121.17 ± 10.06	112.91 ± 13.09	222.51 ± 80.19	81.13 ± 60.3	130.61 ± 8.42	126.16 ± 20.74
<i>Phvul.007G060900</i>	Protein IQ-domain 19	0.26 ± 0.12	0.38 ± 0.08	0.34 ± 0.09	0.74 ± 0.02	1.07 ± 0.18	0.29 ± 0.2	0.48 ± 0.18	0.46 ± 0.15
<i>Phvul.008G000200</i>	Protein tyrosine kinase / Di-glucose binding within endoplasmic reticulum	0.39 ± 0.06	0.41 ± 0.28	0.44 ± 0.08	0.48 ± 0.09	1.64 ± 0.59	0.51 ± 0.27	0.37 ± 0.09	0.6 ± 0.31
<i>Phvul.009G072700</i>	No functional annotation	0.98 ± 0.42	0.48 ± 0.16	1.65 ± 0.53	0.53 ± 0.12	3.95 ± 1.59	1.16 ± 0.65	1 ± 0.02	0.14 ± 0.05
<i>Phvul.011G183500</i>	Pathogenesis-related protein Bet v I family	0.51 ± 0.14	0.97 ± 0.45	0.21 ± 0.15	0.06 ± 0.06	2.82 ± 1.51	0.56 ± 0.23	0.19 ± 0.18	0 ± 0

Table S3. Transcript abundance for genes upregulated in the CBB-resistant RIL at 8 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G075600</i>	Peroxidase / Lactoperoxidase	0.22 ± 0.11	0.34 ± 0.23	0.16 ± 0.07	0.24 ± 0.12	0.28 ± 0.12	1.76 ± 0.81	0.5 ± 0.32	0.93 ± 0.26

Table S4. Transcript abundance for genes upregulated in the CBB-resistant RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G002200</i>	No functional annotation	3.06 ± 1.25	1.34 ± 0.5	1.53 ± 0.35	7.96 ± 7.03	3.43 ± 0.67	1.48 ± 0.72	12.16 ± 5.77	21.46 ± 12.11
<i>Phvul.001G170800</i>	Zinc finger protein, ZAT11	1.39 ± 0.58	0.49 ± 0.3	0.47 ± 0.15	4.1 ± 3.99	1.17 ± 0.29	0.53 ± 0.1	2.54 ± 1.4	7.92 ± 5.38
<i>Phvul.001G203300</i>	Glutaredoxin-C11-related	0.19 ± 0.18	0 ± 0	0 ± 0	0.44 ± 0.44	0.45 ± 0.45	0.41 ± 0.23	1.11 ± 0.64	0.15 ± 0.16
<i>Phvul.001G243600</i>	Serine/threonine-protein kinase-like protein	0.57 ± 0.22	0.15 ± 0.04	0.21 ± 0.03	0.88 ± 0.79	0.51 ± 0.17	0.61 ± 0.14	0.99 ± 0.44	3.44 ± 1.88
<i>Phvul.002G275000</i>	NAC domain-containing protein 2	3.1 ± 0.5	3.35 ± 0.58	2.37 ± 0.45	9.52 ± 7.16	3.01 ± 0.57	4.14 ± 0.6	10.58 ± 4.02	30.27 ± 9.17
<i>Phvul.002G297100</i>	WRKY DNA -binding domain	3.53 ± 0.96	1.55 ± 0.5	0.89 ± 0.07	8.22 ± 6.7	2.09 ± 0.47	1.89 ± 0.12	17.8 ± 8.44	20.63 ± 14.86
<i>Phvul.003G292400</i>	AP2 domain	0.09 ± 0.09	0 ± 0	0 ± 0	0.14 ± 0.14	0.09 ± 0.05	0 ± 0	0.67 ± 0.41	0.72 ± 0.43
<i>Phvul.003G030601</i>	VQ motif	0.29 ± 0.04	0.26 ± 0.13	0.45 ± 0.21	2.07 ± 1.39	0.25 ± 0.12	0.38 ± 0.1	2.22 ± 0.93	4.22 ± 1.42
<i>Phvul.003G034400</i>	Protein of unknown function	4.07 ± 0.55	3.27 ± 0.8	2.15 ± 0.17	8.42 ± 5.9	4.61 ± 1.07	4.24 ± 0.44	17.2 ± 7.6	29.46 ± 15.72
<i>Phvul.003G048800</i>	No functional annotation	3.6 ± 1.27	2.57 ± 0.55	2.42 ± 0.26	10.53 ± 6.3	5.73 ± 1	4.13 ± 2.02	11.55 ± 4.4	22.15 ± 12
<i>Phvul.003G251200</i>	Glycosyltransferase 8 domain-containing protein	0.41 ± 0.21	0.28 ± 0.13	0.29 ± 0.02	0.2 ± 0.05	0.56 ± 0.14	0.42 ± 0.38	1.41 ± 0.83	1.11 ± 0.88
<i>Phvul.004G162500</i>	Arabinogalactan peptide 16-related	6.83 ± 1.52	5.92 ± 1.15	2.7 ± 0.51	16.81 ± 13.18	10.82 ± 2.16	11.1 ± 2.01	21.87 ± 10.18	65.9 ± 35.02
<i>Phvul.005G057400</i>	Expressed protein	1.24 ± 0.8	1.45 ± 0.55	0.56 ± 0.29	2.17 ± 2.03	1.61 ± 0.54	1.83 ± 0.59	8.08 ± 4.05	15.97 ± 12.08

Table S4 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G079650</i>	No functional annotation	0.91 ±0.57	0.17 ±0.17	0 ±0	0.31 ±0.31	0 ±0	0.3 ±0.3	1.43 ±0.88	3.62 ±3.11
<i>Phvul.005G100600</i>	No functional annotation	6.32 ±0.38	5.91 ±0.6	2.5 ±0.16	6.74 ±3.48	10.15 ±2	7.66 ±1.71	13.02 ±4.95	25.24 ±12.62
<i>Phvul.005G122501</i>	NAC domain-containing protein 61-related	0.54 ±0.23	0.23 ±0.2	0.14 ±0.06	0.39 ±0.32	0.52 ±0.15	0.22 ±0.2	1.96 ±0.85	2.02 ±1.77
<i>Phvul.006G165800</i>	Protein TIFY 5A-related	0.09 ±0.01	0.27 ±0.14	0 ±0	0.1 ±0.06	0.1 ±0.06	0.16 ±0.08	0.71 ±0.53	0.97 ±0.37
<i>Phvul.006G183100</i>	AP2 domain	1.76 ±0.56	1.49 ±0.23	1.17 ±0.13	6.42 ±4.31	1.84 ±0.64	2.03 ±1.03	7.49 ±3.21	22.23 ±8.83
<i>Phvul.006G111700</i>	WRKY DNA-binding domain	5.77 ±1.3	3.91 ±1.18	3.4 ±0.3	9.6 ±6.1	5.47 ±1.06	4.57 ±1.31	15.74 ±5.96	27.1 ±15.65
<i>Phvul.007G035500</i>	Domain of unknown function	1.19 ±0.3	1.01 ±0.38	0.3 ±0.07	2.71 ±2.25	1.37 ±0.54	2 ±0.55	2.13 ±1.07	7.06 ±3.85
<i>Phvul.007G273400</i>	MYB-like DNA-binding protein	2.83 ±0.26	2.69 ±0.04	1.44 ±0.13	6.65 ±4.36	2.29 ±0.87	3.28 ±0.47	8.62 ±3.74	19.2 ±5.59
<i>Phvul.007G066500</i>	Dehydration-responsive element-binding protein 1A-related	0.21 ±0.13	0 ±0	0 ±0	0.07 ±0.08	0.16 ±0.16	0 ±0	1.15 ±1	0.89 ±0.72
<i>Phvul.008G169800</i>	No functional annotation	3.53 ±1.42	2.48 ±0.9	2.49 ±0.39	10.1 ±7.84	4.55 ±1.84	4.05 ±1.78	12.75 ±5.35	38.82 ±19.14
<i>Phvul.008G225500</i>	Hs1pro-1 protein C-terminus	3.31 ±0.66	2.36 ±0.43	1.23 ±0.3	9.65 ±6.92	1.5 ±0.28	2.54 ±0.42	10.38 ±4.99	28.69 ±14.66
<i>Phvul.008G235100</i>	Calcium-binding protein CML24-related	11.71 ±4.09	5.83 ±0.94	4.64 ±0.38	10.07 ±5.42	20.69 ±5.54	12.34 ±3.43	22.38 ±9.39	27.71 ±20.37
<i>Phvul.008G238500</i>	U-Box domain-containing protein 54-related	0.47 ±0.1	0.23 ±0.13	0.23 ±0.07	2.61 ±2.46	0.25 ±0.03	0.2 ±0.06	2.33 ±1.03	6.17 ±3.34
<i>Phvul.008G259800</i>	Protein phosphatase 2C-like protein-related	5.72 ±1.65	3.74 ±0.19	4.7 ±0.42	13.69 ±8.36	4.4 ±0.72	4.21 ±1.07	19.06 ±8.08	33.16 ±20.24

Table S4 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G250400</i>	E3 ubiquitin-protein ligase RNF38/44	10.87 ±2.96	5.59 ±1.15	3.35 ±0.57	10.02 ±5.94	16.63 ±4.79	14.3 ±8.04	21.43 ±9.45	37.04 ±21.33
<i>Phvul.009G045601</i>	No functional annotation	6.03 ±2.59	2.93 ±1.26	0.99 ±0.12	21.51 ±19.06	3.99 ±0.64	3.8 ±1.25	15.24 ±8.21	54.97 ±33.5
<i>Phvul.009G045700</i>	No functional annotation	3.06 ±1.27	1.33 ±0.58	1.72 ±0.1	12.02 ±10.56	2.26 ±0.31	1.95 ±0.59	15.44 ±7.61	42.79 ±26.05
<i>Phvul.009G070800</i>	C2H2-type zinc finger	22.26 ±9.12	8.81 ±3.67	11.06 ±1.33	59.09 ±42.64	21.58 ±4.56	15.63 ±8.53	51.39 ±20.43	142.33 ±63.62
<i>Phvul.009G143800</i>	Solute carrier family 25 (mitochondrial oxoglutarate transporter), member 11	0.44 ±0.01	0.69 ±0.33	0.16 ±0.06	3.21 ±3.03	0.5 ±0.07	0.77 ±0.13	4.83 ±2.61	8.22 ±5.75
<i>Phvul.009G253300</i>	COBRA-like protein 7-related	0.25 ±0.06	0.16 ±0.07	0.16 ±0.02	0.49 ±0.03	0.23 ±0.07	0.2 ±0.01	0.67 ±0.29	0.83 ±0.39
<i>Phvul.010G062500</i>	WRKY transcription factor 33	0.63 ±0.17	0.39 ±0.09	0.27 ±0.09	2.2 ±1.81	0.17 ±0.05	0.44 ±0.1	4.24 ±1.96	5 ±3.24
<i>Phvul.010G120700</i>	F11O4.3-related	0.42 ±0.06	0.45 ±0.13	0.16 ±0.03	0.38 ±0.13	0.87 ±0.1	0.54 ±0.25	0.71 ±0.08	1.09 ±0.38
<i>Phvul.011G003100</i>	Serine/threonine-protein kinase-like protein CCR4	2.76 ±0.88	1.47 ±0.37	0.9 ±0.22	4.46 ±3.59	4.93 ±0.89	2.8 ±1.41	13.81 ±6.67	12.45 ±9.68
<i>Phvul.011G095500</i>	NAC domain-containing protein 61-related	0.92 ±0.25	0.66 ±0.06	1.09 ±0.14	4.19 ±2.01	0.95 ±0.21	0.72 ±0.22	9.54 ±3.71	13.87 ±9.57
<i>Phvul.011G097400</i>	CCR4-associated factor 1 homolog 11-related	34.55 ±5.48	25.29 ±2.22	21.44 ±2.59	63.7 ±39.05	49.54 ±13.17	42.66 ±18.23	90.1 ±32.27	138.53 ±61.98
<i>Phvul.011G036600</i>	SAUR family protein	1.43 ±0.55	0.73 ±0.35	1.06 ±0.36	2.19 ±0.41	1.8 ±0.06	0.98 ±0.28	5.21 ±1.78	1.55 ±0.44
<i>Phvul.011G048800</i>	Domain of unknown function	11.61 ±3.38	5.27 ±1.59	3.84 ±0.83	19.13 ±14.99	6.23 ±1.36	7.9 ±1.93	15.52 ±5.75	37.94 ±21.02

Table S4 continued

		Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.007G074600</i> , <i>Phvul.007G074800</i> , <i>Phvul.007G074900</i> , <i>Phvul.007G075000</i>	Copper transport family protein-related	19.06 ±2.85	13.92 ±3.49	7.49 ±0.83	21.02 ±12.89	20.46 ±3.67	15.55 ±2.8	36.77 ±13.54	58.03 ±33.06
XLOC_025168	No functional annotation	0 ±0	0.26 ±0.26	0 ±0	0.57 ±0.57	0 ±0	0.2 ±0.2	1.41 ±0.29	5.45 ±1.62

Table S5. Transcript abundance for genes upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G019200</i>	MYB-like DNA-binding protein	0.2 ± 0.1	0.4 ± 0.09	0.04 ± 0.04	0.45 ± 0.21	0.05 ± 0.05	0.15 ± 0.09	0.57 ± 0.02	2.51 ± 0.64
<i>Phvul.001G019300</i>	AR781	0.28 ± 0.1	0.14 ± 0.08	0.44 ± 0.09	1.04 ± 0.65	0.19 ± 0.13	0.27 ± 0.02	0.79 ± 0.21	5.14 ± 1.14
<i>Phvul.001G039900</i>	WRKY DNA-binding domain	2.49 ± 0.5	3.36 ± 0.68	2.11 ± 0.35	2.83 ± 0.95	2.56 ± 0.7	3.39 ± 0.17	4.01 ± 1.16	16.61 ± 5.46
<i>Phvul.001G040000</i>	L-type lectin-domain containing receptor kinase ix.1-related	0.17 ± 0.13	0.16 ± 0.05	0.02 ± 0.01	0.07 ± 0.05	0 ± 0	0.15 ± 0.05	0.09 ± 0.02	0.52 ± 0.05
<i>Phvul.001G040700</i>	L-type lectin-domain containing receptor kinase ix.1-related	1.61 ± 0.32	1.99 ± 0.85	2.47 ± 0.54	2.99 ± 0.72	1.95 ± 0.18	1.51 ± 0.33	2.96 ± 0.31	23.94 ± 3.27
<i>Phvul.001G042100</i>	WRKY DNA-binding domain	0.82 ± 0.33	0.65 ± 0.27	0.37 ± 0.18	0.63 ± 0.31	0.19 ± 0.11	0.74 ± 0.23	1.34 ± 0.69	10.69 ± 4.35
<i>Phvul.001G042200</i>	WRKY transcription factor 40-related	1.58 ± 0.24	1.84 ± 0.74	1.04 ± 0.22	1.82 ± 0.79	0.75 ± 0.32	1.45 ± 0.18	2.98 ± 1.22	30.93 ± 17.3
<i>Phvul.001G051000</i>	No functional annotation	0.08 ± 0.05	0.19 ± 0.1	0.12 ± 0.02	0.1 ± 0.03	0.01 ± 0.01	0.06 ± 0.02	0.19 ± 0.13	1.28 ± 0.76
<i>Phvul.001G073600</i>	E3 ubiquitin-protein ligase ATL42-related	0.03 ± 0.01	0.05 ± 0.04	0.1 ± 0.03	0.18 ± 0.05	0 ± 0	0.14 ± 0.04	0.09 ± 0.09	0.98 ± 0.23
<i>Phvul.001G074200</i>	Regulator of chromosome condensation	0 ± 0	0.01 ± 0.01	0.08 ± 0.04	0.08 ± 0.02	0.05 ± 0.03	0.03 ± 0.02	0.05 ± 0.02	0.56 ± 0.24
<i>Phvul.001G088200</i>	WRKY transcription factor 45-related	1.46 ± 0.14	1.61 ± 0.52	3.47 ± 1.35	5.99 ± 1.05	1.02 ± 0.13	0.78 ± 0.05	4.15 ± 1.87	39.03 ± 5.24
<i>Phvul.001G095600</i>	EF-hand calcium-binding domain containing protein	0.06 ± 0.06	0.09 ± 0.09	0.46 ± 0.37	0.58 ± 0.18	0.09 ± 0.09	0.43 ± 0.16	1.06 ± 0.11	9.72 ± 2.1

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G102300</i>	Tetrahydrofolate dehydrogenase	4.13 ±1.1	3.62 ±1.66	2.46 ±0.15	1.61 ±0.21	5.17 ±0.79	2.95 ±0.84	2.75 ±0.69	7.63 ±0.69
<i>Phvul.001G108101</i>	MATE efflux family protein	1.91 ±0.36	1.86 ±0.83	2.97 ±0.68	2.76 ±0.54	2.44 ±0.18	1.43 ±0.29	2.65 ±0.16	11.25 ±3.38
<i>Phvul.001G112400</i>	Shikimate <i>O</i> -hydroxycinnamoyltransferase	0.14 ±0.07	0.05 ±0.04	0.31 ±0.13	0.18 ±0.09	0 ±0	0.15 ±0.08	0.22 ±0.07	5.38 ±0.78
<i>Phvul.001G124700</i> , <i>Phvul.001G124800</i>	Trans-aconitate 3-methyltransferase	4.17 ±1.29	4.04 ±2.26	2.6 ±0.57	2.13 ±0.35	4.59 ±0.59	3.55 ±0.99	4.57 ±1.4	30.48 ±15.91
<i>Phvul.001G130200</i>	Glycosyltransferase	0.3 ±0.16	0.55 ±0.14	0.39 ±0.18	0.57 ±0.29	0.28 ±0.09	0.45 ±0.1	1.05 ±0.41	6.58 ±2.93
<i>Phvul.001G131000</i>	Heat shock transcription factor, other eukaryote	0.14 ±0.06	0.1 ±0.05	0.19 ±0.08	0.18 ±0.05	0.05 ±0.03	0.09 ±0.03	0.33 ±0.16	3 ±0.42
<i>Phvul.001G135200</i>	Raffinose synthase	2.09 ±0.24	2.16 ±0.12	2.33 ±0.2	3.2 ±0.92	1.38 ±0.32	1.64 ±0.24	2.68 ±0.18	18.72 ±11.32
<i>Phvul.001G142000</i>	Late embryogenesis abundant protein 4-5	1.57 ±1.47	2.42 ±1.4	0.17 ±0.06	0 ±0	0.03 ±0.03	2.88 ±1.77	0.42 ±0.29	3.53 ±1.6
<i>Phvul.001G155150</i> , <i>Phvul.001G155201</i>	Cation transporting ATPase, C-terminus / Haloacid dehalogenase-like hydrolase	4.84 ±0.26	5.36 ±1.64	3.88 ±0.81	5.93 ±1.45	3.89 ±0.44	5.09 ±0.16	8.59 ±2.2	32.33 ±8.23
<i>Phvul.001G155400</i>	Calcium binding protein	1.43 ±0.33	1.09 ±0.05	1.5 ±0.09	1.63 ±0.59	0.52 ±0.12	1.75 ±0.39	2.19 ±0.07	12.17 ±2.2
<i>Phvul.001G160100</i>	Ethylene-responsive transcription factor, ERF096	0.26 ±0.18	0.37 ±0.09	0.61 ±0.27	1.48 ±1.3	0.37 ±0.13	0.27 ±0.2	1.26 ±0.54	8.24 ±6.77
<i>Phvul.001G164900</i>	Auxin-responsive protein, IAA10-related	0.64 ±0.14	0.53 ±0.31	0.81 ±0.24	0.68 ±0.03	0.35 ±0.06	0.43 ±0.14	0.97 ±0.14	3.5 ±1.24
<i>Phvul.001G169300</i>	Cation/H ⁽⁺⁾ antiporter 20	0.07 ±0.04	0.08 ±0.07	0.31 ±0.13	0.17 ±0.08	0.28 ±0.12	0.07 ±0.05	0.14 ±0.03	2.26 ±0.42

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G177700</i>	Phenylalanine ammonia-lyase	4.14 ±0.49	4.02 ±2.34	5.06 ±0.21	6.61 ±1.93	3.4 ±0.35	3.53 ±0.79	8.09 ±1.95	37.89 ±3.72
<i>Phvul.001G192000</i>	No apical meristem (NAM) protein	0.47 ±0.18	0.58 ±0.39	0.38 ±0.06	0.7 ±0.27	0.82 ±0.2	0.43 ±0.18	0.75 ±0.16	3.42 ±1.54
<i>Phvul.001G194600</i>	Harpin-induced protein-like-related	3.23 ±0.54	2.73 ±0.46	2.31 ±0.48	3.88 ±1.63	2.39 ±0.11	3.05 ±0.29	6.67 ±2.68	34.47 ±10.59
<i>Phvul.001G223700</i>	Inositol 3- α -galactosyltransferase / UDP- α -D-galactose: myo-inositol 3- α -D-galactosyltransferase	0.57 ±0.18	0.26 ±0.05	0.53 ±0.25	0.58 ±0.2	0.42 ±0.06	0.57 ±0.07	0.52 ±0.19	8.94 ±2.69
<i>Phvul.001G226000</i>	Calmodulin binding protein-like	0.52 ±0.06	0.69 ±0.39	0.42 ±0.1	0.73 ±0.25	0.7 ±0.09	0.52 ±0.22	1.53 ±0.49	13.36 ±3.72
<i>Phvul.001G226100</i>	Calmodulin binding protein-like	3.01 ±0.53	2.66 ±0.13	4.03 ±0.14	3.87 ±1.31	5.37 ±1.22	3.98 ±0.56	8.59 ±2.51	17.12 ±9.05
<i>Phvul.001G258900</i>	NADH-ubiquinone reductase complex 1 MLRQ subunit (B12D)	1.17 ±0.17	1.28 ±0.42	2.12 ±0.49	1.19 ±0.44	1.22 ±0.48	1.48 ±0.81	3 ±1.32	12.66 ±1.82
<i>Phvul.001G264400</i>	K13899 - Cystatin-C (CST3)	0.34 ±0.35	0 ±0	1.41 ±0.59	1.07 ±0.41	0.36 ±0.36	0.08 ±0.08	0.46 ±0.18	4.88 ±2.13
<i>Phvul.002G009700</i>	VQ motif	0.34 ±0.18	0.12 ±0.12	0.31 ±0.18	0 ±0	0 ±0	0.39 ±0.27	0.78 ±0.16	1.43 ±0.59
<i>Phvul.002G014700</i>	Isoflavone 2'-hydroxylase	1.46 ±0.27	1.02 ±0.08	1.37 ±0.45	0.91 ±0.18	0.68 ±0.12	1.52 ±0.63	1.82 ±0.38	9.06 ±1.09
<i>Phvul.002G019100</i>	Heat stress transcription factor B-1	0.49 ±0.05	0.41 ±0.16	1.15 ±0.21	1.3 ±0.23	0.38 ±0.06	0.46 ±0.12	1.53 ±0.45	10.84 ±3.52
<i>Phvul.002G021800</i>	Reticulon-like protein B13	0 ±0	0.02 ±0.02	0 ±0	0 ±0	0 ±0	0.05 ±0.03	0.08 ±0.08	0.72 ±0.69

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G025000</i>	Premnaspirodiene oxygenase	0.1 ±0.03	0.07 ±0.05	0.24 ±0.17	0.27 ±0.08	0.02 ±0.02	0.08 ±0.06	0.61 ±0.28	2.75 ±0.36
<i>Phvul.002G029900</i>	No functional annotation	0.08 ±0.08	0.11 ±0.03	0.14 ±0.09	0.24 ±0.12	0.08 ±0.08	0.05 ±0.02	0.11 ±0.06	10.94 ±9.62
<i>Phvul.002G039100</i> , <i>Phvul.002G039166</i> , <i>Phvul.002G039232</i>	Chalcone synthase	0.4 ±0.13	0.52 ±0.24	0.67 ±0.2	0.43 ±0.15	0.17 ±0.08	0.44 ±0.22	1.64 ±0.87	10.8 ±1.31
<i>Phvul.002G040100</i>	4-Coumaroyl: coenzyme A ligase 1	10.37 ±3.44	8.98 ±3.32	8.9 ±1	6.64 ±0.54	15.25 ±1.89	8.9 ±2.92	10.43 ±1.33	32.89 ±4.72
<i>Phvul.002G044100</i>	Diamine N-acetyltransferase / spermidine N(1)- acetyltransferase	1.04 ±0.27	1.87 ±0.51	1.34 ±0.43	2.58 ±0.64	0.98 ±0.1	1.51 ±0.41	2.95 ±0.78	13.23 ±3.3
<i>Phvul.002G046100</i>	Protein kinase domain // S- locus glycoprotein domain // D-mannose binding lectin	0.16 ±0.05	0.12 ±0.03	0.11 ±0.01	0.23 ±0.03	0.09 ±0.05	0.07 ±0.01	0.19 ±0.08	0.94 ±0.05
<i>Phvul.002G046500</i>	Protein kinase domain // S- locus glycoprotein domain // D-mannose binding lectin	0.22 ±0.02	0.23 ±0.11	0.16 ±0.01	0.56 ±0.34	0.16 ±0.01	0.18 ±0.04	0.46 ±0.14	2.84 ±0.64
<i>Phvul.002G048100</i>	Tryptophan synthase β chain- like protein	1.53 ±0.3	1.99 ±1.46	1.64 ±0.39	1.34 ±0.09	0.99 ±0.18	0.92 ±0.24	2.01 ±0.31	19.36 ±10.16
<i>Phvul.002G075600</i>	No functional annotation	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.61 ±0.33
<i>Phvul.002G075900</i>	No functional annotation	0.02 ±0.02	0 ±0	0.04 ±0.02	0.07 ±0.01	0 ±0	0.11 ±0.03	0.35 ±0.14	0.93 ±0.08
<i>Phvul.002G076500</i>	Neutrophil collagenase / Matrix metalloproteinase 8	0 ±0	0.02 ±0.02	0.03 ±0.03	0 ±0	0 ±0	0 ±0	0.13 ±0.06	3.37 ±0.37

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G076600</i>	Matrilysin / Uterine metalloendopeptidase	0.2 ±0.08	0.02 ±0.02	0.56 ±0.4	0.29 ±0.16	0.09 ±0.05	0.13 ±0.09	0.44 ±0.25	5.64 ±0.88
<i>Phvul.002G082300</i>	Regulator of Vps4 activity in the MVB pathway protein	2.11 ±0.3	2.47 ±0.64	2.17 ±0.12	3.11 ±1.24	3.47 ±0.41	3.16 ±0.39	6.21 ±2.04	17.96 ±8.89
<i>Phvul.002G083900</i>	Calcium-binding protein CML30-related	0.27 ±0.06	0.3 ±0.09	0.37 ±0.14	0.08 ±0.01	0.2 ±0.08	0.4 ±0.08	0.5 ±0.18	3.82 ±0.67
<i>Phvul.002G113000</i>	Amino acid transporter	3.71 ±2.04	6.02 ±1.7	4.66 ±1.31	6.14 ±0.28	1.63 ±0.32	6.41 ±2.39	7.71 ±1.97	27.13 ±0.53
<i>Phvul.002G144600</i>	Cinnamyl alcohol dehydrogenase 6-related	0.21 ±0.09	0.17 ±0.12	0.24 ±0.12	0.3 ±0.17	0 ±0	0.05 ±0.03	0.16 ±0.07	4.41 ±1.04
<i>Phvul.002G154600</i>	MATE efflux family protein	0.01 ±0.01	0.01 ±0.01	0.02 ±0.02	0.14 ±0.14	0.01 ±0.01	0.04 ±0.01	0.17 ±0.12	1.09 ±0.62
<i>Phvul.002G155500</i>	Thaumatococcus family	172.86 ±40.76	185.61 ±21.54	133.5 ±9.89	165.9 ±29.15	162.42 ±39.58	233.18 ±13.23	176.62 ±35.67	941.24 ±138.86
<i>Phvul.002G160600</i>	Protein LURP-one-related 17	1.85 ±0.44	0.96 ±0.23	1.27 ±0	2.25 ±1.18	2.13 ±0.49	1.57 ±0.47	2.27 ±0.67	11.17 ±6.51
<i>Phvul.002G180900</i>	BON1-associated protein 1-related	0.03 ±0.03	0.03 ±0.03	0.22 ±0.17	0.25 ±0.13	0 ±0	0.19 ±0.1	0.39 ±0.2	6.29 ±0.76
<i>Phvul.002G184300</i>	Chalcone synthase	0.22 ±0.09	0.28 ±0.06	0.49 ±0.18	0.37 ±0.04	0.2 ±0.1	0.68 ±0.32	1.32 ±0.65	3.95 ±0.33
<i>Phvul.002G188800</i>	LYSM domain-containing GPI-anchored protein 2	9.97 ±0.54	10.16 ±3.52	8.05 ±0.06	9.97 ±0.59	11.34 ±0.72	11.06 ±1.19	12.56 ±1.65	45.08 ±5.1
<i>Phvul.002G197800</i>	Stress up-regulated Nod 19	3.14 ±1.09	3.23 ±0.9	3.89 ±0.53	4.54 ±0.44	1.67 ±0.38	4.09 ±1.45	4.7 ±0.88	26.44 ±9.34
<i>Phvul.002G199800</i>	Tetrahydroberberine oxidase	0.17 ±0.09	0.04 ±0.02	0.49 ±0.17	0.32 ±0.09	0 ±0	0.06 ±0.01	0.75 ±0.39	22.13 ±1.24
<i>Phvul.002G209400</i>	Pathogenesis-related protein Bet v I family	1.23 ±0.57	1.7 ±0.3	3.24 ±1.24	1.86 ±0.84	0.74 ±0.14	1.49 ±0.6	5.01 ±1.6	56.05 ±1.95

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G209500</i>	Pathogenesis-related protein Bet v I family	3.42 ±1.7	3.55 ±0.1	11.8 ±2.73	9.59 ±2.36	1.46 ±0.21	5.99 ±2.06	16.15 ±2.88	167.31 ±10.04
<i>Phvul.002G209600</i>	Protein of unknown function	0.19 ±0.02	0.29 ±0.09	0.15 ±0.03	0.15 ±0.04	0.44 ±0.12	0.31 ±0.09	0.27 ±0.05	1.42 ±1.03
<i>Phvul.002G215000</i>	Legume lectin domain / Protein tyrosine kinase	0.18 ±0.03	0.17 ±0.03	0.26 ±0.05	0.25 ±0.1	0.13 ±0.04	0.16 ±0.06	0.53 ±0.35	3.3 ±1.62
<i>Phvul.002G215100</i>	Protein tyrosine kinase / Leucine rich repeat N- terminal domain (LRRNT_2)	0.06 ±0.02	0.05 ±0.02	0.11 ±0.03	0.16 ±0.02	0.02 ±0.01	0.06 ±0.01	0.15 ±0.04	1.2 ±0.29
<i>Phvul.002G217900</i>	Protein kinase domain // Leucine rich repeat N- terminal domain (LRRNT_2)	0.08 ±0.05	0.1 ±0.03	0.1 ±0.08	0.36 ±0.11	0.02 ±0.02	0.04 ±0.02	0.18 ±0.08	1.6 ±0.12
<i>Phvul.002G219300</i>	(3S,6E)-Nerolidol synthase	1.85 ±0.16	2.68 ±1.51	2.66 ±0.78	2.27 ±0.56	1.72 ±0.43	1.32 ±0.33	3.22 ±0.7	10.74 ±3.27
<i>Phvul.002G223400</i>	NADH: ubiquinone reductase (non-electrogenic)	0.41 ±0.09	0.36 ±0.15	0.41 ±0.03	0.4 ±0.08	0.39 ±0.08	0.4 ±0.08	1.1 ±0.36	2.78 ±0.65
<i>Phvul.002G239400</i>	Leucine-rich repeat receptor- like protein kinase	1.3 ±0.05	1.44 ±0.26	1.25 ±0.09	1.31 ±0.08	1.28 ±0.32	1.66 ±0.06	1.63 ±0.33	5.26 ±1.56
<i>Phvul.002G258600</i>	Copine (calcium-dependent phospholipid-binding protein) family protein	2.63 ±0.13	3.46 ±0.66	1.74 ±0.07	2.51 ±0.23	2.46 ±0.25	2.92 ±0.28	3.63 ±0.49	11.14 ±2.65
<i>Phvul.002G259900</i>	Protein of unknown function	0.39 ±0.06	0.31 ±0.1	0.22 ±0.05	0.29 ±0.08	0.17 ±0.08	0.48 ±0.13	0.28 ±0.05	1.48 ±0.42
<i>Phvul.002G265400</i>	WRKY transcription factor 50-related	3.76 ±0.21	4.89 ±1.3	3.48 ±0.34	5.48 ±1.73	5.71 ±0.47	5.03 ±0.85	7.63 ±3.24	38.57 ±11.44
<i>Phvul.002G268100</i>	No functional annotation	0.69 ±0.27	0.78 ±0.28	0.32 ±0.13	0.89 ±0.39	1.23 ±0.26	0.9 ±0.35	0.7 ±0.27	4.61 ±2.73

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G269300</i>	Histone H3	8.51 ±1.66	10.18 ±1.74	3.91 ±0.06	2.93 ±0.73	10.44 ±2.1	13.72 ±0.42	5 ±0.98	15.03 ±2.7
<i>Phvul.002G271900</i>	No functional annotation	0.07 ±0.03	0.03 ±0.03	0.03 ±0.02	0 ±0	0 ±0	0 ±0	0 ±0	1.24 ±0.93
<i>Phvul.002G285800</i>	WRKY transcription factor 45-related	0.15 ±0.09	0.13 ±0.01	0.63 ±0.27	1.32 ±0.43	0.12 ±0.13	0.18 ±0.1	1.52 ±0.88	13.62 ±7.11
<i>Phvul.002G286500</i> , <i>Phvul.002G286600</i>	Thaumatococcus family	36.94 ±5.61	40.16 ±14.23	20.53 ±3.79	17.93 ±3.06	42.08 ±7.34	48.86 ±8.22	22.22 ±2.92	121.64 ±6.39
<i>Phvul.002G317000</i>	MYB-like DNA-binding protein	0.23 ±0.08	0.8 ±0.43	1.42 ±0.47	1.42 ±0.63	0.22 ±0.12	0.51 ±0.11	1.92 ±0.72	17.6 ±5.65
<i>Phvul.002G318000</i>	Core-2/I-branching β -1,6-N- acetylglucosaminyltransferase family protein	1 ±0.17	0.93 ±0.08	0.8 ±0.05	0.71 ±0.2	0.86 ±0.27	1.26 ±0.2	1.03 ±0.06	3.04 ±0.51
<i>Phvul.002G318100</i>	Protein SAR deficient 1	3.62 ±0.16	4.43 ±1.45	2.44 ±0.16	3.36 ±1.02	4.28 ±0.51	4.24 ±0.46	5.91 ±1.46	31.67 ±13.13
<i>Phvul.002G318200</i>	Protein tyrosine kinase // Wall-associated receptor kinase C-terminal	1 ±0.06	0.99 ±0.05	0.79 ±0.09	0.83 ±0.19	0.77 ±0.13	0.88 ±0.2	1.03 ±0.17	3.63 ±1.21
<i>Phvul.002G326600</i>	Aminocyclopropane- carboxylate oxidase	6.96 ±1.99	8.24 ±3.67	5.47 ±1.17	8.04 ±3.48	8.25 ±1.63	7.07 ±1.65	12.12 ±4.17	77.29 ±30.27
<i>Phvul.002G329200</i>	RAS-related protein RABA6A-related	0.48 ±0.16	0.27 ±0.08	0.55 ±0.14	0.38 ±0.08	0.47 ±0.12	0.35 ±0.02	0.54 ±0.06	2.15 ±1.1
<i>Phvul.003G012800</i>	AR781	0.2 ±0.06	0.15 ±0.05	0.37 ±0.17	0.33 ±0.18	0.06 ±0.03	0.15 ±0.08	0.37 ±0.17	2.19 ±0.08
<i>Phvul.003G019800</i>	Nudix hydrolase 17, mitochondrial-related	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.05 ±0.05	0.61 ±0.44
<i>Phvul.003G022400</i>	Copper transport protein ATOX1-related	0.3 ±0.08	0.99 ±0.31	0.51 ±0.11	0.56 ±0.17	0.25 ±0.08	0.66 ±0.12	0.74 ±0.32	3.63 ±0.75

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G022500</i>	No functional annotation	8.75 ±1.1	11.88 ±5.05	5 ±0.93	6.72 ±0.49	7.34 ±2.29	8.85 ±1.07	8.42 ±1.26	43.1 ±8.5
<i>Phvul.003G024200</i>	Phospholipid-transporting ATPase 10-related	0.37 ±0.09	0.37 ±0.14	0.46 ±0.07	0.57 ±0.05	0.39 ±0.03	0.37 ±0.05	0.58 ±0.09	3.93 ±0.32
<i>Phvul.003G029400</i>	No functional annotation	0.41 ±0.19	0.23 ±0.18	0.45 ±0.09	0.39 ±0.15	0.09 ±0.02	0.13 ±0.02	0.28 ±0.09	1.7 ±0.96
<i>Phvul.003G034000</i>	E3 ubiquitin-protein ligase RHA2	1.11 ±0.38	1.45 ±0.17	0.59 ±0.23	0.99 ±0.2	0.97 ±0.29	0.27 ±0.14	1.28 ±0.64	5.57 ±2.96
<i>Phvul.003G051900</i>	Auxin response factor 30- related	0.06 ±0.06	0.15 ±0.15	0 ±0	0 ±0	0 ±0	0.42 ±0.36	0.46 ±0.25	1.55 ±0.43
<i>Phvul.003G074000</i>	Isoflavone synthase	0.05 ±0.03	0.19 ±0.03	0.42 ±0.21	0.18 ±0.03	0.1 ±0.03	0.21 ±0.1	0.67 ±0.45	1.23 ±0.18
<i>Phvul.003G079800</i>	Adenylyl-sulfate reductase / Thioredoxin-dependent 5'- adenylylsulfate reductase	0.16 ±0.02	0.16 ±0.04	0.24 ±0.14	0.13 ±0.05	0.29 ±0.12	0.13 ±0.02	0.21 ±0.04	0.96 ±0.48
<i>Phvul.003G088000</i>	Adenine nucleotide α - hydrolases-like superfamily protein	0.09 ±0.02	0.23 ±0.11	0.35 ±0.17	0.22 ±0.08	0.12 ±0.09	0.15 ±0.06	0.28 ±0.09	2.23 ±0.29
<i>Phvul.003G096700</i>	Late embryogenesis abundant 3 family protein	3.13 ±0.21	1.72 ±0.44	7.96 ±2	9.41 ±2.88	2.31 ±0.96	1.68 ±0.18	8.23 ±2.04	89.58 ±60.55
<i>Phvul.003G104400</i>	C2 domain-containing protein-related	14.7 ±9.62	25.73 ±10.15	4.23 ±0.46	9.62 ±2.52	5.04 ±0.86	23.55 ±8.86	11.04 ±2.88	38.95 ±5.38
<i>Phvul.003G107100</i>	E3 ubiquitin-protein ligase ATL41-related	1.13 ±0.32	0.95 ±0.25	1.18 ±0.26	1.46 ±0.14	1.32 ±0.13	1.4 ±0.5	1.19 ±0.35	7.57 ±2.36
<i>Phvul.003G109000</i>	Pathogenesis-related protein Bet V I family	0.51 ±0.12	0.75 ±0.11	1.2 ±0.62	1.24 ±0.38	0.46 ±0.09	1.27 ±0.36	3.2 ±1.65	27.88 ±5.69
<i>Phvul.003G109200</i>	Pathogenesis-related protein Bet V I family	0.49 ±0.48	0.9 ±0.31	0.91 ±0.38	0.73 ±0.11	0.07 ±0.03	0.69 ±0.34	1.46 ±0.76	12.18 ±0.92

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G109300</i>	Pathogenesis-related protein Bet V I family	0 ±0	0.06 ±0.06	0 ±0	0 ±0	0 ±0	0.04 ±0.03	0.02 ±0.02	0.78 ±0.09
<i>Phvul.003G109600</i>	Pathogenesis-related protein Bet V I family	0.1 ±0.05	0.08 ±0.05	0.37 ±0.2	0.2 ±0.11	0 ±0	0.16 ±0.08	0.36 ±0.18	4.18 ±0.33
<i>Phvul.003G109602</i>	Pathogenesis-related protein Bet V I family	0.06 ±0.06	0.08 ±0.04	0.25 ±0.07	0.22 ±0.12	0 ±0	0.14 ±0.08	0.32 ±0.17	5.29 ±0.15
<i>Phvul.003G109603</i>	Pathogenesis-related protein Bet V I family	0.28 ±0.22	0.18 ±0.14	0.14 ±0.08	0.22 ±0.08	0 ±0	0.22 ±0.11	0.43 ±0.23	6.07 ±0.24
<i>Phvul.003G109800</i>	Pathogenesis-related protein Bet V I family	0.03 ±0.03	0.02 ±0.02	0.21 ±0.1	0.19 ±0.1	0 ±0	0.03 ±0.03	0.43 ±0.16	3.8 ±0.47
<i>Phvul.003G126300</i>	Saccharopine dehydrogenase (NADP ⁽⁺⁾ , L-lysine-forming) / Lysine-ketoglutarate reductase	0.69 ±0.08	0.74 ±0.09	0.9 ±0.08	1.52 ±0.19	0.58 ±0.16	0.88 ±0.1	1.34 ±0.34	8.44 ±3.79
<i>Phvul.003G129200</i>	Protein TIFY 10a-related	0.49 ±0.21	0.5 ±0.23	0.92 ±0.11	0.85 ±0.31	0.95 ±0.2	0.76 ±0.25	1.12 ±0.28	3.7 ±1.57
<i>Phvul.003G136400</i>	Gulonolactone oxidase	0.08 ±0.03	0.08 ±0.07	0.12 ±0.04	0.11 ±0.05	0.1 ±0.05	0.1 ±0.06	0.27 ±0.1	2.13 ±0.43
<i>Phvul.003G140800</i>	Helix-loop-helix DNA- binding domain	1.95 ±0.27	3.42 ±0.68	2.42 ±0.06	2.25 ±0.29	2.46 ±0.29	2.31 ±0.18	4.86 ±1.29	9.64 ±2.44
<i>Phvul.003G146700</i>	β-1,3-N- acetylglucosaminyltransferase	0.21 ±0.04	0.1 ±0.02	0.18 ±0.08	0.85 ±0.43	0.45 ±0.12	0.38 ±0.18	1.13 ±0.31	3.48 ±1.23
<i>Phvul.003G154800</i>	Heat shock 70 kDa protein 5	1.42 ±0.62	0.68 ±0.12	5.52 ±1.28	4.69 ±1.69	2.13 ±0.18	0.99 ±0.55	4.69 ±0.55	32.56 ±19.83
<i>Phvul.003G160900</i>	No functional annotation	1.53 ±0.45	1.91 ±0.53	1.01 ±0.13	3.58 ±2.37	0.75 ±0.12	1.84 ±0.42	3.7 ±1.64	20.72 ±11.53
<i>Phvul.003G166700</i> , <i>Phvul.003G166800</i>	Blue copper protein	3.39 ±0.16	4.14 ±0.16	2.97 ±0.3	3.16 ±0.51	2.91 ±0.19	5.02 ±0.69	5.34 ±0.98	19.19 ±5.14

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G182600</i>	Adenine nucleotide α -hydrolases-like protein-related	0.31 ± 0.11	0.38 ± 0.03	0.37 ± 0.08	0.46 ± 0.06	0.1 ± 0.06	0.31 ± 0.05	0.73 ± 0.24	2.5 ± 1.89
<i>Phvul.003G184200</i>	Ninja-family protein AFP1-related	0.06 ± 0.03	0.39 ± 0.26	0.21 ± 0.02	0.22 ± 0.09	0.09 ± 0.09	0.04 ± 0.04	0.29 ± 0.17	3.27 ± 1.56
<i>Phvul.003G187200</i>	Protein kinase domain // Leucine rich repeat (LRR_1) // Leucine rich repeat N-terminal domain (LRRNT_2) // Leucine rich repeat (LRR_8)	0.16 ± 0.01	0.21 ± 0.05	0.2 ± 0.06	0.2 ± 0.09	0.22 ± 0.07	0.24 ± 0.02	0.39 ± 0.12	1.83 ± 0.57
<i>Phvul.003G209101</i>	Malate synthase / Malic-condensing enzyme	0.08 ± 0.05	0.2 ± 0.07	0.39 ± 0.16	0.78 ± 0.53	0.01 ± 0.02	0.11 ± 0.07	1.1 ± 0.61	13.73 ± 9.05
<i>Phvul.003G212600</i>	MATE efflux family protein	0.09 ± 0.02	0.16 ± 0.08	0.12 ± 0.04	0.21 ± 0.18	0.06 ± 0.06	0.22 ± 0.11	0.45 ± 0.27	1.87 ± 0.94
<i>Phvul.003G217100</i>	Probable lipid transfer (LTP_2)	61.06 ± 3.62	64.15 ± 7.3	25.41 ± 2.92	20.88 ± 2.46	68.14 ± 6.93	69.47 ± 2.25	37.52 ± 5.91	99.28 ± 12.11
<i>Phvul.003G237400</i>	Expressed protein	28.25 ± 15.35	9.09 ± 7.95	26.34 ± 8.13	21.15 ± 9.94	31.69 ± 4.55	11.07 ± 10.4	21.35 ± 1.99	95.47 ± 56.71
<i>Phvul.003G238700</i>	Auxin responsive GH3 gene family	0.36 ± 0.22	0.47 ± 0.21	0.66 ± 0.17	1.06 ± 0.17	0.09 ± 0.03	0.41 ± 0.17	1.48 ± 0.85	11.47 ± 1.77
<i>Phvul.003G239800</i>	No functional annotation	1.03 ± 0.58	0.66 ± 0.33	0.93 ± 0.35	1.63 ± 0.91	0.46 ± 0.32	0.65 ± 0.27	2.09 ± 0.58	32.86 ± 9.66
<i>Phvul.003G247500</i>	Leucine-rich repeat-containing protein	0.06 ± 0.02	0.01 ± 0.01	0.18 ± 0.06	0.12 ± 0.05	0.02 ± 0.02	0.04 ± 0.02	0.19 ± 0.12	9.3 ± 1.4
<i>Phvul.003G249400</i>	No functional annotation	4.47 ± 1.72	3.92 ± 1.44	1.63 ± 0.31	0.55 ± 0.28	5.59 ± 1.07	3.33 ± 1.1	1.21 ± 0.1	2.72 ± 1.56
<i>Phvul.003G251000</i>	Calcium-binding protein CML41-related	3.4 ± 0.14	5.27 ± 1.32	5.04 ± 0.77	4.71 ± 0.21	2.74 ± 0.56	2.89 ± 0.28	4.83 ± 0.18	18.85 ± 1.92

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G255300</i>	No functional annotation	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0.12 ±0.08	1.29 ±0.45
<i>Phvul.003G256600</i>	BCS1 AAA-type ATPase	4.93 ±0.88	4.58 ±2.26	2.56 ±0.42	3.96 ±0.69	4.81 ±0.43	4 ±0.69	4.45 ±0.96	20.16 ±7.82
<i>Phvul.003G272900</i>	(-)-Lariciresinol reductase	2.75 ±0.37	3.8 ±0.65	2.46 ±0.22	2.75 ±0.42	2.34 ±0.18	4.02 ±1.17	4.45 ±0.99	12.89 ±1.99
<i>Phvul.003G287400</i> , <i>Phvul.003G287500</i>	Alcohol dehydrogenase related	10.63 ±4.35	8.63 ±5.7	8.51 ±1.26	6.6 ±0.54	11.58 ±1.15	4.87 ±2.32	9.8 ±1.39	39.19 ±21.39
<i>Phvul.004G018900</i>	α-Dioxygenase (DOX1)	0.12 ±0.04	0.1 ±0.05	0.77 ±0.33	0.31 ±0.09	0.01 ±0.01	0.04 ±0.03	0.68 ±0.57	2.52 ±1.05
<i>Phvul.004G044800</i> , <i>Phvul.004G044900</i>	Leucine rich repeat (LRR_1) // Leucine rich repeat N- terminal domain (LRRNT_2) // Leucine rich repeat (LRR_8)	0.15 ±0.03	0.22 ±0.04	0.19 ±0.02	0.14 ±0.05	0.11 ±0.03	0.15 ±0.02	0.35 ±0.01	0.75 ±0.27
<i>Phvul.004G056700</i>	Amino acid transporter	0.63 ±0.18	0.46 ±0.16	0.75 ±0.07	0.61 ±0.06	0.63 ±0.21	0.5 ±0.12	0.93 ±0.32	9.55 ±1.47
<i>Phvul.004G071700</i>	MLO-like protein 12-related	0.14 ±0.08	0.14 ±0.04	0.25 ±0.11	0.35 ±0.05	0.15 ±0.02	0.15 ±0.05	0.46 ±0.12	2.46 ±0.34
<i>Phvul.004G077400</i>	No apical meristem (NAM) protein	0.12 ±0.07	0.21 ±0.1	0.23 ±0.05	0.75 ±0.16	0.07 ±0.03	0.41 ±0.23	0.53 ±0.1	4.72 ±2
<i>Phvul.004G088400</i>	Alliin lyase / L-cysteine sulfoxide lyase	0.46 ±0.16	0.29 ±0.08	1.05 ±0.55	0.54 ±0.21	0.03 ±0.03	0.17 ±0.07	0.98 ±0.33	29.28 ±2.25
<i>Phvul.004G092100</i>	Ethylene-responsive transcription factor 15-related	0.27 ±0.15	0.36 ±0.09	0.45 ±0.17	0.44 ±0.14	0.07 ±0.04	0.61 ±0.33	0.83 ±0.32	2.85 ±1.36

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.004G099100</i>	Leucine rich repeat (LRR_1) // Leucine rich repeat N-terminal domain (LRRNT_2) // Leucine rich repeat (LRR_8)	1.35 ±0.58	1.85 ±0.46	0.68 ±0.09	1.26 ±0.08	0.78 ±0.24	1.45 ±0.5	1.28 ±0.22	9.37 ±2.55
<i>Phvul.004G103900</i>	Isoflavone 7-O-glucosyltransferase	0.34 ±0.12	0.38 ±0.13	0.54 ±0.03	0.26 ±0.02	0.47 ±0.17	0.41 ±0.06	0.69 ±0.36	1.32 ±0.27
<i>Phvul.004G107200</i>	Copper transport family protein-related	8.8 ±0.7	8.99 ±3.99	3.68 ±0.63	5.64 ±1.21	12.74 ±2.11	7.37 ±0.54	7.98 ±1.25	30.51 ±16.6
<i>Phvul.004G115600</i>	Leucine rich repeat (LRR_1) // Leucine rich repeat (LRR_8)	0.22 ±0.04	0.28 ±0.07	0.23 ±0.06	0.22 ±0.04	0.07 ±0.02	0.38 ±0.18	0.23 ±0.03	1.34 ±0.03
<i>Phvul.004G129300</i> , <i>Phvul.004G129400</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // PPR repeat family (PPR_2) // Pentatricopeptide repeat domain (PPR_3)	0.48 ±0.33	0.98 ±0.31	0.82 ±0.14	0.33 ±0.12	0.47 ±0.2	0.98 ±0.39	0.69 ±0.15	1.4 ±0.62
<i>Phvul.004G141200</i>	ADP-ribosylation factor GTPase-activating protein AGD15-related	0.29 ±0.08	0.26 ±0.08	0.27 ±0.06	0.53 ±0.18	0.54 ±0.15	0.34 ±0.07	1.04 ±0.32	2.44 ±0.66
<i>Phvul.004G153056</i>	No functional annotation	0.73 ±0.73	1.48 ±0.77	3.89 ±1.47	2.03 ±1.22	0.31 ±0.31	0.64 ±0.64	7.1 ±2.15	53.29 ±6.4
<i>Phvul.004G155900</i>	Protein SAR deficient 1	0.13 ±0.05	0.2 ±0.08	0.1 ±0.01	0.28 ±0.07	0.08 ±0.08	0.17 ±0.09	0.31 ±0.04	1.2 ±0.17
<i>Phvul.004G157900</i>	Protein NIM1-interacting 2	2.89 ±0.99	3.79 ±0.92	0.88 ±0.08	0.76 ±0.17	1.16 ±0.32	3.04 ±0.87	0.77 ±0.25	3.12 ±0.31
<i>Phvul.005G011100</i>	Phospholipid-transporting ATPase	0.1 ±0.03	0.09 ±0.02	0.28 ±0.05	0.25 ±0.05	0.09 ±0.03	0.06 ±0.01	0.39 ±0.16	1.59 ±0.17

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G024800</i>	VQ motif	1.83 ±0.15	2.33 ±0.59	1.57 ±0.09	2.3 ±1.76	2.27 ±0.42	2.97 ±0.95	3.38 ±0.32	13.41 ±3.57
<i>Phvul.005G042200</i>	No functional annotation	0.33 ±0.18	0.03 ±0.03	0.4 ±0.14	0.54 ±0.46	0 ±0	0.07 ±0.04	0.57 ±0.29	5.27 ±2.15
<i>Phvul.005G057200</i>	Expressed protein	0.82 ±0.42	0.54 ±0.43	0.6 ±0.31	1.31 ±0.89	1.12 ±0.24	1 ±0.17	2.18 ±0.96	17.1 ±11.51
<i>Phvul.005G077501</i>	Oxidoreductase, 2-oxoglutarate-Fe II oxygenase family protein	0.43 ±0.13	0.23 ±0.05	0.78 ±0.13	0.54 ±0.16	0.35 ±0.06	0.25 ±0.1	1.05 ±0.55	3.18 ±1.05
<i>Phvul.005G097500</i>	E3 ubiquitin-protein ligase ATL41	0.58 ±0.2	1.16 ±0.3	0.4 ±0.25	0.65 ±0.19	0.31 ±0.07	0.9 ±0.29	0.89 ±0.21	2.69 ±0.09
<i>Phvul.005G109000</i>	Transferase family	1.35 ±0.13	1.57 ±0.72	0.9 ±0.24	1.57 ±0.46	1.19 ±0.18	0.95 ±0.2	1.73 ±0.44	19.43 ±4.61
<i>Phvul.005G111500</i>	Geranyl diphosphate diphosphatase	0.46 ±0.26	0.29 ±0.21	0.61 ±0.12	0.3 ±0.12	0.6 ±0.14	0.16 ±0.09	0.71 ±0.32	1.59 ±0.72
<i>Phvul.005G136700</i>	MLO protein	0.11 ±0.06	0.19 ±0.03	0.08 ±0.02	0.2 ±0.02	0.14 ±0.08	0.14 ±0.1	0.1 ±0.03	1.49 ±0.18
<i>Phvul.005G137300</i>	LOB domain-containing protein 1-related	0.18 ±0.02	0.29 ±0.06	0.63 ±0.1	0.36 ±0.04	0.16 ±0.06	0.23 ±0.11	0.45 ±0.09	1.66 ±0.12
<i>Phvul.005G155800</i>	Chitinase-related	10.85 ±1.26	10.96 ±3.19	11.57 ±0.56	13.63 ±1.16	12 ±1.04	12.99 ±0.7	19.76 ±1.98	119.1 ±11.06
<i>Phvul.005G158500</i>	β-Fructofuranosidase, insoluble isoenzyme CWINV1-related	1.15 ±0.55	1.28 ±0.15	2.16 ±0.34	2.6 ±0.65	0.66 ±0.03	1.49 ±0.59	2.55 ±0.32	11.17 ±0.72
<i>Phvul.005G166500</i>	ABC transporter G family member 29	0.12 ±0.03	0.17 ±0.06	0.2 ±0.05	0.34 ±0.11	0.16 ±0.01	0.18 ±0.02	0.42 ±0.07	3.87 ±0.32

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G171900</i>	U5 SNRNP-specific protein-like factor and related proteins // G protein β subunit-like protein	2.14 ± 0.5	2.53 ± 1.43	0.52 ± 0.08	0.73 ± 0.29	3.01 ± 0.8	2.22 ± 0.55	1.09 ± 0.33	14.86 ± 4.66
<i>Phvul.005G173000</i>	Auxin-responsive protein IAA15	0.56 ± 0.04	0.57 ± 0.19	0.86 ± 0.16	0.8 ± 0.42	0.65 ± 0.12	0.6 ± 0.16	0.89 ± 0.09	3.96 ± 3.04
<i>Phvul.005G173600</i>	Sulfate-transporting ATPase	1.13 ± 0.25	1.51 ± 0.39	1.93 ± 0.78	1.58 ± 0.23	0.81 ± 0.14	1.7 ± 0.43	2.76 ± 0.98	17.38 ± 2.49
<i>Phvul.006G002700</i>	Genomic DNA, chromosome 3, P1 clone: MKA23	1.92 ± 0.43	2.18 ± 0.51	1.96 ± 0.24	4.21 ± 2.07	0.72 ± 0.15	1.89 ± 0.32	4.46 ± 1.05	17.43 ± 3.6
<i>Phvul.006G020700</i>	Interleukin-1 receptor-associated kinase 4	1.03 ± 0.1	1.11 ± 0.23	0.93 ± 0.21	1.98 ± 0.78	0.9 ± 0.24	1.11 ± 0.21	2.72 ± 1	8.21 ± 0.95
<i>Phvul.006G022800</i>	Aspartyl protease-like protein	0.6 ± 0.14	0.43 ± 0.09	0.43 ± 0.08	1.3 ± 0.83	1.15 ± 0.18	0.56 ± 0.16	1.61 ± 0.54	6.01 ± 2.79
<i>Phvul.006G058700</i>	X-box transcription factor-related	0.1 ± 0.06	0.12 ± 0.03	0.13 ± 0.05	0.12 ± 0.05	0.08 ± 0.02	0.18 ± 0.08	0.22 ± 0.08	1.12 ± 0.06
<i>Phvul.006G074600</i>	WRKY transcription factor 33	0.08 ± 0.02	0.11 ± 0.05	0.18 ± 0.1	0.09 ± 0.02	0.07 ± 0.03	0.04 ± 0.03	0.14 ± 0.08	2.68 ± 0.13
<i>Phvul.006G078300</i>	No functional annotation	0.27 ± 0.14	0.26 ± 0.14	1.1 ± 0.61	0.84 ± 0.58	0 ± 0	0.71 ± 0.43	1.35 ± 0.73	50.32 ± 1.95
<i>Phvul.006G079500</i>	Oxalate-CoA ligase / Oxalyl-CoA synthetase	0.03 ± 0.03	0.01 ± 0.01	0.1 ± 0.06	0 ± 0	0.01 ± 0.01	0.05 ± 0.02	0.22 ± 0.13	0.91 ± 0.53
<i>Phvul.006G079700</i>	Trans-cinnamate 4-monooxygenase / Cinnamic acid 4-monooxygenase	0.18 ± 0.07	0.2 ± 0.06	0.26 ± 0.14	0.32 ± 0.24	0.25 ± 0.06	0.24 ± 0.09	0.59 ± 0.16	4.18 ± 0.49
<i>Phvul.006G085200</i>	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.81 ± 0.25	0.68 ± 0.48	0.58 ± 0.06	0.51 ± 0.07	0.98 ± 0.1	0.48 ± 0.27	0.49 ± 0.08	3.69 ± 0.8

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G086100</i>	AMP-binding enzyme	3.5 ±0.68	5.15 ±0.95	2.01 ±0.22	2.23 ±0.62	2.74 ±0.64	4.98 ±0.66	3.61 ±0.82	18.34 ±7.39
<i>Phvul.006G086200</i> , <i>Phvul.006G086211</i>	No functional annotation	0.82 ±0.28	1.06 ±0.44	0.62 ±0.03	1.25 ±0.46	0.69 ±0.21	1 ±0.25	1.33 ±0.27	6.04 ±1.98
<i>Phvul.006G090200</i>	Respiratory burst oxidase homolog protein B	0.83 ±0.18	0.8 ±0.06	0.76 ±0.15	1.21 ±0.43	1.36 ±0.09	1.44 ±0.22	2.34 ±0.81	6.96 ±3.08
<i>Phvul.006G102200</i>	Hevein-like preproprotein	21.03 ±4.55	28.96 ±4.85	14.63 ±2.89	21.22 ±2.73	16.78 ±2.63	28.09 ±5.79	21.47 ±5.8	127.81 ±17.59
<i>Phvul.006G102300</i>	Hevein-like preproprotein	91.09 ±11.4	92.58 ±21.55	91.71 ±5.23	84.31 ±10.74	81.62 ±18.82	94.07 ±11.93	99.37 ±14.05	513.25 ±9.39
<i>Phvul.006G129500</i>	Peroxidase 22-related	0.4 ±0.31	0.41 ±0.16	1.37 ±0.46	0.87 ±0.04	0.21 ±0.05	0.15 ±0.09	1.79 ±0.53	53.74 ±4.05
<i>Phvul.006G135600</i>	Copper transport protein, ATOX1-related	1.34 ±0.31	1.64 ±1.17	0.54 ±0.13	0.75 ±0.2	1.28 ±0.35	1.02 ±0.35	0.92 ±0.31	11.97 ±6.18
<i>Phvul.006G142300</i>	Auxin-induced in root cultures protein 12	4.62 ±0.53	4.62 ±0.66	4.19 ±0.63	6.16 ±1.74	3.55 ±0.4	5.71 ±0.78	7.83 ±1.73	29.32 ±6.52
<i>Phvul.006G154700</i>	Epididymal membrane protein E9-related	0.73 ±0.1	0.6 ±0.03	1.53 ±0.35	2.53 ±0.43	0.85 ±0.18	0.85 ±0.11	2.58 ±0.73	14.55 ±2.3
<i>Phvul.006G173000</i>	No functional annotation	0.78 ±0.24	1.09 ±0.33	0.37 ±0.13	1 ±0.58	0.21 ±0.11	1.62 ±0.48	1.3 ±0.46	8.35 ±3.12
<i>Phvul.006G178800</i>	E3 ubiquitin-protein ligase ATL41	2.33 ±0.1	2.12 ±0.21	2.6 ±0.37	2.61 ±0.72	2.13 ±0.49	2.28 ±0.06	4.13 ±0.55	11.9 ±1.69
<i>Phvul.006G181300</i>	Glutaredoxin-C9	0.88 ±0.32	0.78 ±0.21	0.56 ±0.06	1.42 ±1.1	0.46 ±0.15	1.4 ±0.07	2.22 ±0.37	12.78 ±6.21
<i>Phvul.006G185300</i>	Lipoxygenase	0.19 ±0.14	0.43 ±0.09	0.11 ±0.05	0.05 ±0.01	0.11 ±0.04	0.3 ±0.08	0.13 ±0.08	2.94 ±2.41
<i>Phvul.006G188900</i>	No apical meristem (NAM) protein	0.02 ±0.02	0.05 ±0.02	0.23 ±0.12	0.27 ±0.2	0.02 ±0.02	0.07 ±0.05	0.13 ±0.05	2 ±1.37

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G192400</i>	EF hand (EF-hand_1) / Pyridine nucleotide- disulphide oxidoreductase	0.31 ±0.1	0.32 ±0.09	0.47 ±0.1	0.43 ±0.06	0.24 ±0.08	0.39 ±0.1	0.73 ±0.22	1.77 ±0.16
<i>Phvul.006G194200</i>	β-Amyrin synthase (LUP4)	1.11 ±0.16	0.68 ±0.19	0.61 ±0.21	0.25 ±0.13	0.8 ±0.06	0.52 ±0.06	0.58 ±0.07	1.17 ±0.97
<i>Phvul.006G194600</i>	Receptor-like serine/ Threonine-protein kinase SD1-6-related	0.18 ±0.08	0.26 ±0.09	0.28 ±0.02	0.26 ±0.08	0.23 ±0.03	0.33 ±0.06	0.42 ±0.13	2.06 ±0.38
<i>Phvul.006G195600</i> , <i>Phvul.006G195700</i>	S-Linalool synthase	5.9 ±1.06	7.77 ±1.41	1.35 ±0.28	0.78 ±0.12	10.4 ±0.63	9.15 ±1.04	2.57 ±1.33	7.22 ±3.2
<i>Phvul.006G198200</i>	Protein kinase domain // Leucine rich repeat N- terminal domain (LRRNT_2) // Leucine rich repeat (LRR 8)	0.58 ±0.16	0.86 ±0.14	0.81 ±0.08	0.84 ±0.05	0.53 ±0.06	0.94 ±0.05	1.08 ±0.17	3.42 ±0.57
<i>Phvul.007G008600</i>	Chalcone isomerase	6.74 ±1.26	7.98 ±1.57	7.3 ±1.5	7.39 ±0.35	7.66 ±1.29	10.73 ±1.64	14.37 ±5.18	74.24 ±2.89
<i>Phvul.007G016100</i>	EamA-like transporter family	0.17 ±0.05	0.25 ±0.12	0.16 ±0.06	0.26 ±0.08	0.14 ±0.12	0.12 ±0.04	0.33 ±0.03	1.32 ±0.65
<i>Phvul.007G022600</i>	Replication factor A3	2.16 ±0.92	3.81 ±0.65	1.98 ±0.29	0.94 ±0.54	2.31 ±0.38	4.11 ±0.62	1.94 ±0.14	3.77 ±0.4
<i>Phvul.007G024900</i>	Monocarboxylate transporter	0.08 ±0.04	0.23 ±0.03	0.36 ±0.08	0.36 ±0.09	0.05 ±0.03	0.3 ±0.13	0.44 ±0.1	6.22 ±0.38
<i>Phvul.007G026700</i>	Genomic DNA, chromosome 3, P1 clone: MPE11	4.22 ±2.18	5.52 ±1.56	1.89 ±0.2	3.45 ±1.15	2.03 ±0.28	5.31 ±1.79	4.06 ±1.15	16.51 ±7.4
<i>Phvul.007G040900</i>	Peptidase of plants and bacteria	37.05 ±3.99	35.39 ±11.93	27.25 ±1.55	33.58 ±9.83	40.3 ±8.69	41.34 ±6.95	41.44 ±9.05	240.01 ±32.57
<i>Phvul.007G041000</i>	Peptidase of plants and bacteria	18.42 ±3.21	16.7 ±6.21	5.6 ±0.32	6.97 ±1.33	17.77 ±4.35	16.75 ±2.32	8.85 ±1.18	36.8 ±2.45

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.007G048500</i> , <i>Phvul.007G048600</i>	Cysteine-rich receptor-like protein kinase 28-related	1.87 ±0.16	2.08 ±0.28	1.28 ±0.11	1.66 ±0.14	2.1 ±0.27	2.45 ±0.44	1.96 ±0.18	10.4 ±2.67
<i>Phvul.007G048800</i>	Cysteine-rich receptor-like protein kinase 28-related	0.31 ±0.06	0.2 ±0.04	0.22 ±0.05	0.27 ±0.1	0.23 ±0.08	0.28 ±0.05	0.37 ±0.12	1.6 ±0.49
<i>Phvul.007G048900</i> , <i>Phvul.007G049100</i> , <i>Phvul.007G049200</i>	Cysteine-rich receptor-like protein kinase 28-related; salt stress response/antifungal	5.06 ±2.01	7.25 ±1.23	2.46 ±0.7	3.25 ±0.61	6 ±0.53	7.58 ±1.1	4.28 ±1.05	14.15 ±1.81
<i>Phvul.007G049700</i>	Cysteine-rich repeat secretory protein 1-related	0.41 ±0.22	0.19 ±0.16	1.89 ±0.88	1.05 ±0.51	0 ±0	0.17 ±0.17	1.74 ±1.18	59.51 ±3.16
<i>Phvul.007G052500</i>	Cysteine-rich receptor-like protein kinase 28-related	0.06 ±0.01	0.12 ±0.05	0.15 ±0.05	0.09 ±0.03	0.13 ±0.01	0.1 ±0.05	0.07 ±0.02	1 ±0.06
<i>Phvul.007G091000</i>	Isoliquiritigenin 2'- <i>O</i> - methyltransferase	0.26 ±0.13	0.43 ±0.09	0.31 ±0.12	0.23 ±0.09	0.11 ±0.06	0.25 ±0.08	0.76 ±0.25	3.77 ±0.11
<i>Phvul.007G101400</i>	No functional annotation	0.43 ±0.13	0.27 ±0.16	0.88 ±0.29	0.84 ±0.13	0.38 ±0.23	0.62 ±0.1	0.92 ±0.21	3.6 ±0.34
<i>Phvul.007G123958</i>	Endoglucanase 7	0.42 ±0.08	0.21 ±0.05	0.39 ±0.08	0.46 ±0.05	0.2 ±0.03	0.25 ±0.01	0.43 ±0.07	3.31 ±0.43
<i>Phvul.007G134700</i>	Glutathione S-transferase, GST, superfamily, GST domain containing	0.92 ±0.61	1.4 ±0.23	1.43 ±0.47	0.84 ±0.28	0.69 ±0.13	1.28 ±0.38	2.02 ±0.25	13.81 ±0.74
<i>Phvul.007G160901</i>	Leucine-rich repeat- containing protein	0.31 ±0.13	0.48 ±0.1	0.12 ±0.03	0.16 ±0.06	0.32 ±0.03	0.44 ±0.14	0.3 ±0.09	0.8 ±0.4
<i>Phvul.007G186900</i>	No functional annotation	0.56 ±0.08	0.49 ±0.18	0.48 ±0.11	0.82 ±0.23	0.71 ±0.18	0.6 ±0.25	0.67 ±0.23	11.68 ±0.72
<i>Phvul.007G211600</i>	Protein NIM1-interacting 1	2.53 ±0.87	2.24 ±0.65	1.02 ±0.09	1.38 ±0.42	1.38 ±0.27	2.61 ±0.88	3.72 ±1.91	22.17 ±13.28

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.007G220400</i>	No functional annotation	2.11 ±0.84	1.74 ±1.39	5.08 ±0.29	4.85 ±1.54	2.29 ±0.38	1.14 ±0.12	6.8 ±1.11	27.99 ±9.22
<i>Phvul.007G222500</i>	Ethylene-responsive transcription factor ERF016-related	0.15 ±0.15	0.23 ±0.12	0 ±0	0 ±0	0 ±0	0.05 ±0.02	0 ±0	0.77 ±0.48
<i>Phvul.007G252500</i>	PR5-like receptor kinase-related	0.26 ±0.08	0.19 ±0.06	0.25 ±0.06	0.28 ±0.03	0.18 ±0.04	0.24 ±0.04	0.24 ±0.06	1.21 ±0.36
<i>Phvul.007G259400</i>	Late embryogenesis abundant protein 4-5	0.31 ±0.1	0.18 ±0.07	0.11 ±0.06	0.25 ±0.09	0.48 ±0.12	0.18 ±0.02	0.21 ±0.1	8.3 ±7.11
<i>Phvul.007G260400</i>	L-type lectin-domain containing receptor kinase S.5-related	0.14 ±0.12	0.09 ±0.02	0.18 ±0.05	0.52 ±0.16	0.08 ±0.04	0.23 ±0.1	0.24 ±0.12	2.13 ±0.32
<i>Phvul.007G273000</i>	Ethylene-responsive transcription factor 1B	1.51 ±0.22	1.94 ±0.37	1.12 ±0.14	2.49 ±1.36	1.64 ±0.43	1.88 ±0.32	2.26 ±0.6	14.24 ±2.62
<i>Phvul.007G278900</i>	Calcium binding protein	3.36 ±0.72	3.22 ±1.4	2.97 ±0.88	2.93 ±1.24	3.86 ±0.69	3.89 ±0.59	6.77 ±1.02	31.71 ±11.13
<i>Phvul.008G008800</i>	No functional annotation	0.14 ±0.1	0.08 ±0.08	0.33 ±0.17	0.13 ±0.02	0 ±0	0.13 ±0.07	0.15 ±0.08	1.16 ±0.18
<i>Phvul.008G011400</i>	Heat shock protein 70 kDa	0.27 ±0.03	0.29 ±0.13	0.23 ±0.09	0.29 ±0.04	0.33 ±0.11	0.29 ±0.01	0.3 ±0.05	1.59 ±0.29
<i>Phvul.008G011500</i>	Thioredoxin	0.15 ±0.08	0.17 ±0.09	0.28 ±0.15	0.35 ±0.06	0.31 ±0.03	0.29 ±0.11	0.64 ±0.09	4.07 ±0.4
<i>Phvul.008G011800</i>	Thioredoxin	0.06 ±0.03	0.05 ±0.05	0.14 ±0.03	0.13 ±0.02	0.08 ±0.01	0.13 ±0.05	0.4 ±0.05	4.07 ±0.42
<i>Phvul.008G011900</i>	Heat shock protein 70 kDa	0.29 ±0.08	0.29 ±0.1	0.24 ±0.03	0.2 ±0.03	0.26 ±0.06	0.32 ±0.08	0.36 ±0.09	1.48 ±0.23

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G014600</i>	C2H2-type zinc finger	0.07 ±0.03	0.1 ±0.06	0.37 ±0.03	0.63 ±0.23	0 ±0	0.07 ±0.06	0.5 ±0.24	2.85 ±0.48
<i>Phvul.008G015800</i>	6'-Deoxychalcone synthase	0.89 ±0.83	1.15 ±0.34	0.83 ±0.13	0.9 ±0.23	0.14 ±0.09	1.11 ±0.57	0.92 ±0.09	17.93 ±1.1
<i>Phvul.008G028900</i>	UDP-arabinopyranose mutase	3.46 ±1.37	5.31 ±0.99	1.34 ±0.16	1.73 ±0.56	2.7 ±0.43	5.97 ±1.88	2.24 ±0.26	9.31 ±2.36
<i>Phvul.008G037300</i>	Calmodulin	5.3 ±1.33	3.3 ±1.15	3 ±0.2	8.85 ±5.39	4.35 ±1.43	4.02 ±1.19	9.38 ±2.44	37.89 ±14.74
<i>Phvul.008G040800</i>	ATP-dependent zinc metalloprotease FTSH 6, chloroplastic	0 ±0	0.01 ±0.01	0.07 ±0.01	0.05 ±0.04	0.07 ±0.03	0.02 ±0.02	0.12 ±0.04	0.64 ±0.4
<i>Phvul.008G043400</i>	Receptor like protein 54	0.11 ±0.02	0.07 ±0.01	0.1 ±0.06	0.06 ±0.03	0.03 ±0.03	0.05 ±0.01	0.03 ±0.01	1.04 ±0.63
<i>Phvul.008G044900</i>	AAA-type ATPase family protein-related	1.46 ±0.08	2.38 ±1.02	1.69 ±0.18	2.26 ±0.93	1.22 ±0.24	1.93 ±0.17	2.7 ±0.99	15.86 ±3.86
<i>Phvul.008G048466</i>	Prenylated RAB acceptor 1-related	13.29 ±2.09	13.27 ±4.81	7.31 ±0.28	14.62 ±3.05	9.16 ±3.68	11.2 ±2.44	15.72 ±3.79	59.83 ±23.74
<i>Phvul.008G048532</i>	Prenylated RAB acceptor 1-related	6.56 ±1.32	6.99 ±2.96	5.09 ±0.88	5.97 ±2.06	7.38 ±2.15	7.74 ±0.94	6.18 ±1.55	35.87 ±16.82
<i>Phvul.008G076500</i>	Vestitone reductase	0.52 ±0.06	0.4 ±0.05	1 ±0.3	0.78 ±0.14	0.24 ±0.01	0.68 ±0.27	1.11 ±0.46	7.5 ±0.24
<i>Phvul.008G076600</i>	Vestitone reductase	1.76 ±0.81	2.45 ±0.54	2.43 ±0.52	3.34 ±0.42	0.67 ±0.1	2.54 ±0.82	3.92 ±0.83	36.27 ±0.99
<i>Phvul.008G094400</i>	GRAS domain family	0.05 ±0.04	0.05 ±0.04	0.05 ±0.03	0.15 ±0.1	0.05 ±0.05	0.03 ±0.02	0.11 ±0.06	1.95 ±0.77
<i>Phvul.008G094500</i>	Protein kinase domain / Legume lectin domain	0.38 ±0.14	0.32 ±0.16	0.39 ±0.09	0.82 ±0.41	0.27 ±0.04	0.18 ±0.05	0.6 ±0.08	3.35 ±1.31
<i>Phvul.008G094900</i>	Ammonium transporter 2	1.34 ±0.27	1.19 ±0.16	1.1 ±0.08	1.79 ±0.6	0.98 ±0.22	1.29 ±0.31	3.17 ±1.02	11.57 ±3.68

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G098500</i>	Flavonol synthase	0.02 ±0.02	0.07 ±0.03	0.07 ±0.07	0.09 ±0.06	0 ±0	0.06 ±0.04	0.17 ±0.16	1.22 ±0.55
<i>Phvul.008G112200</i>	Laccase-7-related	0.52 ±0.12	0.6 ±0.2	1.67 ±0.69	0.69 ±0.21	0.24 ±0.05	0.71 ±0.34	1.48 ±0.84	11.42 ±2.63
<i>Phvul.008G114766</i>	No functional annotation	0.4 ±0.27	0.38 ±0.31	0.44 ±0.44	1.14 ±0.76	0.46 ±0.35	0.22 ±0.14	1.95 ±1.03	8.13 ±6.03
<i>Phvul.008G123900</i>	SNARE proteins	0.24 ±0.09	0.21 ±0.08	0.55 ±0.2	0.43 ±0.27	0.27 ±0.11	0.15 ±0.05	1.02 ±0.29	9.73 ±1.48
<i>Phvul.008G127200</i>	Deacetoxyvindoline 4- hydroxylase / Desacetoxyvindoline-17- hydroxylase	0.95 ±0.25	0.7 ±0.14	1.18 ±0.21	1.16 ±0.31	0.63 ±0.1	0.96 ±0.12	1.57 ±0.49	4.71 ±1.41
<i>Phvul.008G139900</i>	No functional annotation	175.27 ±67.05	232.13 ±35.8	116.11 ±20.67	137.25 ±10.28	113.33 ±33.12	261.54 ±64.33	171.45 ±53.6	1151.16 ±76.66
<i>Phvul.008G140113</i>	No functional annotation	7.68 ±4.32	11.59 ±2.25	6.37 ±1.67	7.5 ±1.25	4.61 ±1.62	13.87 ±3.29	10.05 ±3.59	142.24 ±18.43
<i>Phvul.008G140800</i>	Hydroquinone glucosyltransferase	1.06 ±0.3	1.78 ±0.61	2.16 ±0.55	2.31 ±0.59	1.1 ±0.25	1.69 ±0.32	3.64 ±0.93	15.9 ±1.8
<i>Phvul.008G169600</i>	LL-diaminopimelate aminotransferase	0.86 ±0.42	1.54 ±0.33	1.46 ±0.48	1.96 ±1.15	0.44 ±0.15	1.46 ±0.52	2.65 ±1.41	19.04 ±2.33
<i>Phvul.008G172400</i>	Trehalose-phosphate phosphatase D-related	0.23 ±0.04	0.22 ±0.02	0.13 ±0.03	0.14 ±0.05	0.29 ±0.03	0.18 ±0.02	0.29 ±0.07	4.65 ±0.47
<i>Phvul.008G176900</i>	Protein of unknown function	0.64 ±0.2	0.28 ±0.06	0.12 ±0.04	0.45 ±0.24	0.36 ±0.14	0.55 ±0.29	0.36 ±0.03	3.51 ±0.91
<i>Phvul.008G186200</i>	No functional annotation	7.45 ±4.71	2.61 ±0.88	10.46 ±2.42	11.82 ±7.06	5.72 ±1.82	3.62 ±1.69	8.22 ±1.65	73.58 ±44.86
<i>Phvul.008G193900</i>	Aspartyl protease-like protein	1.34 ±0.2	1.11 ±0.09	0.66 ±0.13	1.74 ±0.81	1.16 ±0.23	1.29 ±0.09	2.43 ±0.67	7.57 ±4.05

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G194600</i>	NAC domain-containing protein 6-related	0.28 ±0.13	0.11 ±0.06	0.37 ±0.22	0.25 ±0.07	0.17 ±0.09	0.24 ±0.08	0.36 ±0.06	2.51 ±0.53
<i>Phvul.008G194828</i>	Leucine-rich repeat-containing protein	0.37 ±0.06	0.16 ±0.05	0.34 ±0.11	0.43 ±0.21	0.32 ±0.1	0.19 ±0.08	0.87 ±0.33	1.74 ±1.09
<i>Phvul.008G213914</i>	Aminocyclopropane-carboxylate oxidase	0 ±0	0.04 ±0.01	0.1 ±0.06	0.07 ±0.02	0.05 ±0.05	0.03 ±0.02	0.01 ±0.01	0.86 ±0.43
<i>Phvul.008G223500</i>	Leucoanthocyanidin dioxygenase	0.11 ±0.05	0.09 ±0.06	0.17 ±0.02	0.28 ±0.2	0.05 ±0.05	0.03 ±0.02	0.38 ±0.17	1.14 ±0.49
<i>Phvul.008G224400</i>	α/β -hydrolase related protein	0.13 ±0.02	0.26 ±0.03	0.28 ±0.14	0.84 ±0.05	0.14 ±0.08	0.34 ±0.1	1.3 ±0.21	3.41 ±1.2
<i>Phvul.008G232700</i>	Extended synaptotagmin-related	0.21 ±0.03	0.29 ±0.08	0.35 ±0.08	0.44 ±0.39	0.56 ±0.22	0.28 ±0.15	1.19 ±0.66	5.35 ±2.22
<i>Phvul.008G238200</i>	No functional annotation	36.82 ±4.95	28.34 ±10.25	17.67 ±1.47	39.65 ±21.12	15.9 ±9.1	24.54 ±9.77	30.36 ±13.57	160 ±42.82
<i>Phvul.008G242900</i>	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein-related	0.26 ±0.26	0.32 ±0.12	0.33 ±0.16	0.36 ±0.2	0.11 ±0.07	0.26 ±0.03	0.8 ±0.03	5.77 ±0.28
<i>Phvul.008G248900</i>	CBL-interacting serine/threonine-protein kinase 2	1.17 ±0.51	0.46 ±0.36	0.66 ±0.09	0.71 ±0.16	0.84 ±0.04	0.59 ±0.38	0.79 ±0.17	3.34 ±1.91
<i>Phvul.008G285000</i>	Calcium transporting ATPase	1 ±0.08	0.76 ±0.06	0.89 ±0.02	1 ±0.28	0.61 ±0.12	0.77 ±0.09	1.13 ±0.07	5.1 ±1.25
<i>Phvul.008G288600</i> , <i>Phvul.008G288700</i>	Exosome complex component RRP42; nudix hydrolase related	2.75 ±0.85	3.07 ±0.52	1.69 ±0.02	1.62 ±0.36	2.34 ±0.28	3.55 ±0.78	2.52 ±0.33	6.78 ±0.65
<i>Phvul.008G289200</i>	No functional annotation	0.36 ±0.1	0.63 ±0.25	0.18 ±0.01	0.35 ±0.15	0.25 ±0.13	0.42 ±0.12	0.38 ±0.17	1.59 ±0.27

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G289500</i>	Phenylalanine ammonia-lyase	0.96 ±0.12	0.88 ±0.24	0.88 ±0.24	0.69 ±0.12	0.76 ±0.09	0.94 ±0.1	1.31 ±0.21	4.47 ±0.25
<i>Phvul.009G014800</i>	F14I17.20 protein	0.12 ±0.05	0.1 ±0.04	0.18 ±0.12	0.15 ±0.05	0.1 ±0.05	0.12 ±0.02	0.07 ±0.04	1.07 ±0.16
<i>Phvul.009G032900</i>	No functional annotation	4.95 ±0.24	5.19 ±2.44	3.18 ±0.93	12.1 ±7	4.4 ±0.28	3.51 ±0.43	10.87 ±3.16	74.76 ±28.24
<i>Phvul.009G042800</i>	No functional annotation	0.32 ±0.07	0.17 ±0.1	0.29 ±0.15	0.17 ±0.12	0.13 ±0.13	0.19 ±0.1	0.3 ±0.15	4.79 ±2.37
<i>Phvul.009G043100</i>	WRKY DNA-binding domain	11.61 ±2.04	13.04 ±1.94	6.22 ±0.66	6.25 ±1.33	8.6 ±0.25	12.67 ±2.38	8.61 ±1.51	39.4 ±15.01
<i>Phvul.009G046800</i>	No functional annotation	23.85 ±2.96	17.53 ±2.05	17.8 ±2.3	16.56 ±3.59	15.31 ±2.47	15.04 ±1.1	19.51 ±2.83	205.74 ±4.75
<i>Phvul.009G046900</i>	Leucine rich repeat (LRR_1) // Protein tyrosine kinase // Leucine rich repeat N-terminal domain (LRRNT_2) // Leucine rich repeat (LRR_8)	0.24 ±0.14	0.12 ±0.06	0.18 ±0.04	0.27 ±0.06	0.07 ±0.03	0.2 ±0.1	0.34 ±0.09	6.91 ±0.98
<i>Phvul.009G080000</i>	WRKY DNA-binding domain	0.57 ±0.18	1.07 ±0.16	0.7 ±0.12	0.95 ±0.23	0.41 ±0.17	1.16 ±0.19	1.54 ±0.44	9.84 ±1.87
<i>Phvul.009G087400</i>	WRKY transcription factor 40-related	0.69 ±0.12	0.56 ±0.17	0.64 ±0.02	0.62 ±0.29	0.49 ±0.11	0.84 ±0.09	0.78 ±0.19	10.32 ±2.1
<i>Phvul.009G118800</i>	Expressed protein-related	0.06 ±0.02	0.08 ±0.02	0.16 ±0.08	0.23 ±0.02	0.05 ±0.01	0.12 ±0.03	0.29 ±0.12	2.61 ±0.54
<i>Phvul.009G138900</i>	WRKY DNA-binding domain	5.18 ±0.59	4.85 ±1.41	3.49 ±0.69	7.3 ±1.13	4.91 ±0.33	4.77 ±0.71	7.51 ±1.82	30.67 ±5.29

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G154100</i>	Amino acid transporter	0.26 ±0.19	0.74 ±0.21	0.51 ±0.08	0.42 ±0.05	0.14 ±0.05	0.74 ±0.35	0.59 ±0.21	1.76 ±0.34
<i>Phvul.009G155800</i>	No functional annotation	0.58 ±0.08	0.58 ±0.31	0.53 ±0.1	0.58 ±0.29	0.37 ±0.05	0.5 ±0.01	0.72 ±0.23	3.34 ±1.31
<i>Phvul.009G156300</i>	No apical meristem (NAM) protein	0.78 ±0.47	1.1 ±0.44	0.17 ±0.09	0.54 ±0.1	0.29 ±0.12	1.19 ±0.49	0.51 ±0.16	2.22 ±1.44
<i>Phvul.009G180501</i>	Leucine rich repeat N-terminal domain (LRRNT_2) // Leucine rich repeat (LRR 8)	5.42 ±3.87	9.57 ±4.28	1.21 ±0.43	0.62 ±0.29	1.7 ±0.37	10.52 ±5.47	3.26 ±1.66	2.74 ±1.09
<i>Phvul.009G182300</i>	Aminobutyraldehyde dehydrogenase / γ -guanidinobutyraldehyde dehydrogenase	10.84 ±5.25	12.95 ±3.63	7.68 ±1.02	6.19 ±0.64	6.18 ±0.5	14.36 ±3.83	10.37 ±1.02	40.16 ±16.72
<i>Phvul.009G189300</i>	Molybdate-transporting ATPase	0.19 ±0.03	0.22 ±0.05	0.3 ±0.06	0.3 ±0.12	0.1 ±0.03	0.23 ±0.13	0.34 ±0.04	2.06 ±0.22
<i>Phvul.009G210100</i>	Protein phosphatase 2C	1.58 ±0.28	1.04 ±0.4	1.75 ±0.35	1.73 ±0.33	1.56 ±0.25	0.89 ±0.13	2.05 ±0.26	7.97 ±2.37
<i>Phvul.009G211000</i>	Extensin-like protein repeat	18.39 ±6.69	25.36 ±4.21	51.92 ±9.86	45.25 ±10.73	11.8 ±3.14	31.54 ±9.55	51.53 ±9.19	241.75 ±7.85
<i>Phvul.009G225300</i>	Protein TIFY 10a-related	12.66 ±1.22	10.84 ±1.71	15.8 ±0.98	16.3 ±2.94	14.84 ±2.53	11.56 ±0.76	24.67 ±5.2	81.37 ±35.7
<i>Phvul.009G227001</i>	SER/THR protein kinase ACIK1B	0.04 ±0.02	0.06 ±0.02	0.14 ±0.06	0.24 ±0.03	0.06 ±0.04	0.06 ±0.03	0.2 ±0.06	1.15 ±0.36
<i>Phvul.009G231600</i>	Sterol regulatory element-binding protein	0.69 ±0.17	0.65 ±0.12	0.47 ±0.13	0.75 ±0.11	0.53 ±0.15	0.68 ±0.03	0.86 ±0.2	4.5 ±0.37

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G235700</i>	Helix-loop-helix DNA-binding domain (HLH)	1.43 ±0.06	2.14 ±0.93	1.77 ±0.2	1.15 ±0.2	1.47 ±0.24	1.44 ±0.05	2.86 ±0.91	17.83 ±7.19
<i>Phvul.009G240750</i>	No functional annotation	2.92 ±1.07	2.23 ±1.6	1.89 ±0.53	4.46 ±1.91	1.83 ±1.19	3.33 ±0.44	3.58 ±1.81	30.01 ±9.09
<i>Phvul.009G241900</i>	VQ motif	1.19 ±0.33	1.41 ±0.23	1.61 ±0.32	1.66 ±0.14	0.69 ±0.14	1.56 ±0.47	2.84 ±0.86	14.82 ±1.78
<i>Phvul.009G244200</i>	Isoflavone 2'-hydroxylase	0.28 ±0.14	0.17 ±0.11	0.67 ±0.13	0.86 ±0.06	0.08 ±0.05	0.21 ±0.09	0.83 ±0.06	4.4 ±0.16
<i>Phvul.009G256400</i>	Glucan endo-1,3-β-d-glucosidase / Laminarinase	49.3 ±24.32	72.4 ±26.75	43.1 ±13.16	104.6 ±6.97	25.95 ±6.85	70.12 ±23.73	76.07 ±23.3	547.25 ±144.34
<i>Phvul.009G258600</i>	Anthranilate N-methyltransferase	3.94 ±1.39	4.01 ±0.37	4.55 ±1.18	4.52 ±0.91	1.8 ±0.19	4.02 ±0.91	6.81 ±1.25	64.16 ±2.2
<i>Phvul.009G262300</i>	GDSL esterase/lipase 5-related	0.33 ±0.05	1.03 ±0.5	0.36 ±0.1	0.68 ±0.17	0.82 ±0.21	0.67 ±0.01	0.69 ±0.06	3.23 ±0.36
<i>Phvul.009G262900</i>	Lipoxygenase 3, chloroplastic-related	0.19 ±0.08	0.13 ±0.02	0.24 ±0.09	0.15 ±0.05	0.07 ±0.02	0.27 ±0.1	0.25 ±0.03	2.01 ±0.09
<i>Phvul.010G000300</i>	Leucocyanidin oxygenase	1.43 ±0.48	2.2 ±0.79	1.89 ±0.61	1.43 ±0.13	1 ±0.43	1.49 ±0.4	3.34 ±1.5	6.66 ±2.77
<i>Phvul.010G003400</i>	No functional annotation	0.08 ±0.08	0.13 ±0.08	0.11 ±0.08	0.16 ±0.05	0.09 ±0.05	0.03 ±0.02	0.41 ±0.24	2.75 ±0.45
<i>Phvul.010G005900</i>	Laccase-7-related	0.15 ±0.05	0.02 ±0.02	0.17 ±0.15	0.16 ±0.08	0.02 ±0.02	0.13 ±0.13	0.18 ±0.14	1.25 ±0.29
<i>Phvul.010G006000</i>	PAR1 protein	4.12 ±0.98	3.47 ±1.28	2.88 ±0.4	3.33 ±1.43	3.59 ±0.52	3.49 ±0.57	5.89 ±1.82	33.94 ±11.78
<i>Phvul.010G007400</i>	O-Fucosyltransferase family protein	0.13 ±0.04	0.07 ±0.05	0.1 ±0.06	0.1 ±0.06	0.42 ±0.05	0.18 ±0.06	0.21 ±0.07	0.88 ±0.51
<i>Phvul.010G008800</i>	Glyceollin synthase	0.17 ±0.09	0.12 ±0.06	0.2 ±0.16	0.19 ±0.11	0.03 ±0.03	0.17 ±0.09	0.39 ±0.2	2.14 ±0.68

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.010G016200</i>	Domain of unknown function	0.3 ±0.09	0.21 ±0.1	0.27 ±0.06	0.35 ±0.13	0.35 ±0.14	0.21 ±0.1	0.36 ±0.06	2.19 ±1.31
<i>Phvul.010G021001</i>	GDSL esterase/lipase 5-related	0.38 ±0.17	0.32 ±0.08	0.69 ±0.36	1.16 ±0.39	0.08 ±0.05	0.27 ±0.02	0.83 ±0.38	33.9 ±1.49
<i>Phvul.010G021700</i>	Membrane protein of ER body 2	0.23 ±0.18	0.17 ±0.06	0.44 ±0.16	0.33 ±0.21	0.12 ±0.1	0.42 ±0.12	0.51 ±0.06	2.35 ±0.25
<i>Phvul.010G032000</i>	Protein kinase domain //D-mannose binding lectin	0.2 ±0.04	0.16 ±0.05	0.1 ±0.03	0.12 ±0.03	0.45 ±0.07	0.31 ±0.04	0.11 ±0.01	0.58 ±0.31
<i>Phvul.010G044900</i> , <i>Phvul.010G045200</i>	No functional annotation	2.49 ±0.24	2.75 ±1.06	2.12 ±0.53	2.54 ±0.1	2.11 ±0.42	2.15 ±0.05	3.14 ±0.6	17.96 ±4.46
<i>Phvul.010G045000</i>	No functional annotation	0.65 ±0.15	0.97 ±0.43	0.86 ±0.14	1.13 ±0.1	0.48 ±0.18	0.96 ±0.18	1.1 ±0.1	10.69 ±1.16
<i>Phvul.010G057300</i> , <i>Phvul.010G057500</i> , <i>Phvul.010G057600</i>	Protein kinase domain // S-locus glycoprotein domain // D-mannose binding lectin	0.51 ±0.13	0.6 ±0.07	0.5 ±0.03	0.35 ±0.03	0.37 ±0.1	0.56 ±0.06	0.48 ±0.07	1.56 ±0.14
<i>Phvul.010G059000</i>	Had superfamily, subfamily IIIB acid phosphatase	3.91 ±0.69	4.22 ±1.85	2.39 ±0.2	3.57 ±0.7	4.05 ±0.49	4.4 ±0.79	5.18 ±0.59	19.85 ±4.32
<i>Phvul.010G063600</i>	Dirigent protein 19	7.14 ±3.78	12.75 ±2.53	4.9 ±0.14	5.27 ±0.63	5.03 ±1.29	12.92 ±3.38	12.42 ±1.7	28.7 ±2.59
<i>Phvul.010G063800</i>	Dirigent protein 19	6.7 ±2.04	8.83 ±1.09	9 ±2.14	7.37 ±2.08	3.43 ±0.16	10.32 ±3.47	15.47 ±3.89	72.32 ±13.91
<i>Phvul.010G070250</i>	PTHR36766:SF1 - HR3	1.28 ±0.18	1.11 ±0.32	0.68 ±0.24	1.27 ±0.27	1.41 ±0.59	1.53 ±0.19	1.63 ±0.11	5.34 ±2.45
<i>Phvul.010G073500</i>	Uncharacterized protein	0.19 ±0.1	0.14 ±0.08	0.35 ±0.21	0.28 ±0.14	0.13 ±0.07	0.09 ±0.03	0.32 ±0.06	5.43 ±4.42
<i>Phvul.010G075400</i>	Glutathione S-transferase U1-related	2.85 ±0.55	3.9 ±0.35	3.16 ±0.39	3.92 ±0.61	2.98 ±0.31	3.53 ±0.73	4.4 ±0.77	15.93 ±0.44
<i>Phvul.010G079900</i>	Pectinesterase/pectinesterase inhibitor 17-related	0.76 ±0.1	0.54 ±0.13	1 ±0.33	0.93 ±0.12	0.36 ±0.13	0.69 ±0.15	1 ±0.27	12.4 ±0.65

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.010G089900</i>	BON1-associated protein 1-related	0.49 ±0.03	0.24 ±0.07	0.39 ±0.14	0.51 ±0.1	0.75 ±0.25	0.37 ±0.19	0.67 ±0.13	6.76 ±1.87
<i>Phvul.010G090000</i>	BON1-associated protein 1-related	0.74 ±0.39	1.02 ±0.62	1.03 ±0.07	1.79 ±1.22	0.95 ±0.38	0.78 ±0.24	3.08 ±0.98	19.25 ±10.07
<i>Phvul.010G093400</i>	BON1-associated protein 1-related	0.21 ±0.12	0.17 ±0.13	0.06 ±0.06	0.2 ±0.03	0.33 ±0.08	0.03 ±0.03	0.51 ±0.26	3.53 ±1.04
<i>Phvul.010G112600</i>	CGI-141-related/lipase containing protein	0 ±0	0.01 ±0.01	0.07 ±0.07	0.16 ±0.06	0 ±0	0.01 ±0.01	0.04 ±0.02	0.82 ±0.42
<i>Phvul.010G117200</i>	Homeobox-leucine zipper protein ATHB-12-related	1.58 ±0.79	1.09 ±0.23	1.47 ±0.42	2.89 ±1.64	0.57 ±0.09	1.13 ±0.24	2.34 ±0.42	23.02 ±15.06
<i>Phvul.010G120200</i>	Anthranilate N-methyltransferase	0.14 ±0.09	0.22 ±0.08	0.18 ±0.11	0.14 ±0.09	0.02 ±0.02	0.22 ±0.11	0.37 ±0.2	6.33 ±0.9
<i>Phvul.010G128900</i>	Flavonoid 3'-monooxygenase / Flavonoid 3'-hydroxylase	39.67 ±9	51.76 ±5.85	21.25 ±1.94	21.35 ±2.09	33.68 ±3.12	54.42 ±6.47	33.76 ±7.48	100.49 ±31.46
<i>Phvul.010G134000</i>	Domain of unknown function	5.37 ±2.59	23.37 ±5.46	10.82 ±2.23	15.82 ±5.67	2.14 ±0.96	9.29 ±1.68	23.52 ±8.48	107 ±20.35
<i>Phvul.010G137300</i>	Calmodulin-binding protein	0.08 ±0.03	0.09 ±0.05	0.1 ±0.01	0.14 ±0.06	0.2 ±0.08	0.11 ±0.05	0.14 ±0.04	0.79 ±0.4
<i>Phvul.010G137800</i> , <i>Phvul.010G137900</i>	β-Fructofuranosidase, insoluble isoenzyme CWINV1-related	1.42 ±0.04	1.48 ±0.44	1.8 ±0.36	1.77 ±0.28	1.25 ±0.16	1.45 ±0.23	2.94 ±0.31	43.53 ±3.94
<i>Phvul.010G155100</i>	No functional annotation	2.05 ±0.48	1.91 ±0.55	1.7 ±0.21	2.35 ±1.02	2.32 ±0.92	2.15 ±0.51	3.83 ±1.22	12.2 ±4.05
<i>Phvul.011G013600</i>	α-Farnesene synthase	0.79 ±0.39	0.73 ±0.73	1.28 ±0.22	0.59 ±0.13	1.18 ±0.09	0.24 ±0.24	1.11 ±0.12	2.38 ±1.73
<i>Phvul.011G025100</i>	Amino acid transporter	9.22 ±1.37	8.98 ±4.61	8.45 ±0.62	9.36 ±3.17	13.18 ±2.28	8.37 ±2.73	15.19 ±3.24	41.28 ±9.45
<i>Phvul.011G034800</i>	Senescence-associated protein	1.22 ±0.21	0.72 ±0.06	0.88 ±0.05	0.99 ±0.33	0.6 ±0.06	0.89 ±0.28	3.38 ±1.43	4.47 ±2.71

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G035600</i>	Adenine nucleotide α -hydrolases-domain containing protein kinase-related	0.16 ± 0.14	0.16 ± 0.05	0.14 ± 0.06	0.16 ± 0.05	0.03 ± 0.03	0.22 ± 0.16	0.21 ± 0.09	1.24 ± 0.21
<i>Phvul.011G041400</i>	S-locus glycoprotein domain // D-mannose binding lectin // protein tyrosine kinase	0.26 ± 0.03	0.54 ± 0.16	0.15 ± 0.02	0.25 ± 0.09	0.28 ± 0.03	0.46 ± 0.08	0.3 ± 0.06	1.61 ± 0.47
<i>Phvul.011G043100</i>	BCS1 AAA-type ATPase	5.84 ± 0.29	6.62 ± 1.64	3.59 ± 0.23	4.8 ± 0.83	5.81 ± 0.18	5.74 ± 0.38	6.73 ± 1.49	23.38 ± 7.74
<i>Phvul.011G044500</i>	NAD dependent epimerase/dehydratase	0.28 ± 0.02	0.31 ± 0.12	0.79 ± 0.38	0.26 ± 0.2	0.29 ± 0.02	0.46 ± 0.09	0.78 ± 0.51	4.68 ± 0.76
<i>Phvul.011G051600</i>	No functional annotation	0.18 ± 0.09	0.25 ± 0.09	0.25 ± 0.12	0.64 ± 0.64	0 ± 0	0.15 ± 0.08	0.45 ± 0.31	5.6 ± 1.43
<i>Phvul.011G060300</i>	Glucosyltransferase-like protein-related	0.06 ± 0.06	0.06 ± 0.02	0.14 ± 0.08	0.17 ± 0.05	0.03 ± 0.01	0.05 ± 0.03	0.21 ± 0.08	1.67 ± 0.4
<i>Phvul.011G062900</i>	Putative hydrolase of the HAD superfamily	0.45 ± 0.18	0.53 ± 0.25	0.51 ± 0.1	0.18 ± 0.03	0.35 ± 0.03	0.36 ± 0.03	0.5 ± 0.17	1.46 ± 0.54
<i>Phvul.011G072200</i>	Lob domain-containing protein 1-related	0.85 ± 0.36	1.31 ± 0.28	1.33 ± 0.17	1.51 ± 0.4	0.45 ± 0.08	1.74 ± 0.79	1.62 ± 0.27	8.54 ± 3.1
<i>Phvul.011G077900</i>	Glucan endo-1,3- β -D-glucosidase / Laminarinase	113.58 ± 47.26	113.85 ± 21.75	89.63 ± 16.63	80.81 ± 21.81	78.16 ± 23.53	134.92 ± 24.91	115.59 ± 21.84	671.13 ± 21.22
<i>Phvul.011G089500</i>	γ -Aminobutyrate transporter 1	0.32 ± 0.12	0.33 ± 0.15	0.38 ± 0.15	0.27 ± 0.1	0.15 ± 0.02	0.37 ± 0.08	0.41 ± 0.13	3.6 ± 0.44
<i>Phvul.011G096300</i>	F-box-like	0.4 ± 0.17	0.78 ± 0.15	0.4 ± 0.12	0.49 ± 0.18	0.33 ± 0.06	0.67 ± 0.17	0.87 ± 0.38	3 ± 0.43
<i>Phvul.011G108600</i>	EF-hand calcium-binding domain containing protein	2.2 ± 0.22	2.25 ± 0.94	1.67 ± 0.52	3.33 ± 0.51	3.27 ± 0.86	4.21 ± 1.83	3.66 ± 1.05	18.08 ± 2.4

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G109600</i>	MYB-like DNA-binding protein	0.18 ±0.13	0.22 ±0.12	0.13 ±0.06	0.2 ±0.2	0.02 ±0.02	0.09 ±0.05	0.12 ±0.03	3.84 ±1.86
<i>Phvul.011G147800</i>	NAC domain-containing protein 19-related	0.05 ±0.03	0.08 ±0.06	0.02 ±0.01	0.58 ±0.28	0.03 ±0.03	0.11 ±0.04	0.33 ±0.14	6.47 ±3.31
<i>Phvul.011G148500</i>	No functional annotation	0.09 ±0.09	0.03 ±0.03	0.03 ±0.03	0.61 ±0.54	0 ±0	0.13 ±0.13	0.59 ±0.28	3.13 ±1.81
<i>Phvul.011G150400</i>	Cysteine-rich receptor-like protein kinase 27-related	0.34 ±0.09	0.59 ±0.09	0.28 ±0.05	0.17 ±0.05	0.37 ±0.03	0.5 ±0.02	0.38 ±0.12	1.55 ±0.4
<i>Phvul.011G166500</i>	Trypsin and protease inhibitor	0.95 ±0.23	0.64 ±0.13	1.99 ±0.68	1.18 ±0.07	1.09 ±0.44	0.83 ±0.21	1.53 ±0.55	41.53 ±2.24
<i>Phvul.011G167300</i>	Chitinase	13.43 ±4.41	15.61 ±2.15	13.54 ±2.48	12.81 ±2.57	10.54 ±1.62	16.53 ±1.38	16.43 ±2.67	199.32 ±2.61
<i>Phvul.011G169900</i>	Trypsin and protease inhibitor	0.38 ±0.19	0.3 ±0.11	0.5 ±0.04	0.53 ±0.04	0.43 ±0.08	0.15 ±0.06	0.28 ±0.12	14.3 ±0.89
<i>Phvul.011G176950</i>	Glucan endo-1,3-β-D-glucosidase / Laminarinase	41.53 ±3.63	57.12 ±29.51	23.69 ±0.25	24.91 ±6.13	45.91 ±14.23	55.25 ±7.93	37.77 ±9.5	295.71 ±30.8
<i>Phvul.011G179600</i>	Caspase regulator, RING finger domain-containing	0.4 ±0.08	0.62 ±0.1	0.42 ±0.06	0.37 ±0.1	0.61 ±0.03	0.45 ±0	0.51 ±0.12	2.92 ±0.28
<i>Phvul.011G211600</i>	No functional annotation	0 ±0	0 ±0	0 ±0	0 ±0	0.12 ±0.06	0 ±0	0 ±0	0.87 ±0.79
<i>Phvul.011G214400</i>	Protein kinase domain /D-mannose binding lectin	0.06 ±0.03	0.05 ±0.02	0.06 ±0.03	0.11 ±0.06	0.06 ±0.02	0.04 ±0.02	0.09 ±0.02	1.17 ±0.15
<i>Phvul.L000770</i> , <i>Phvul.L001078</i>	No functional annotation	1.06 ±0.45	1.39 ±0.65	1.53 ±0.54	3.2 ±0.16	1.29 ±0.14	2.01 ±0.73	3.62 ±0.87	28.35 ±15.29
<i>Phvul.L003043</i>	C2H2-type zinc finger family protein-related	0.6 ±0.29	0.7 ±0.2	0.3 ±0.11	0.68 ±0.14	1.18 ±0.34	0.79 ±0.43	0.74 ±0.26	7.24 ±3.97
XLOC_016664	No functional annotation	0.25 ±0.18	0.24 ±0.09	0.22 ±0.03	0.41 ±0.08	0.02 ±0.02	0.28 ±0.14	0.56 ±0.02	2.89 ±0.2

Table S5 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
XLOC_023524	No functional annotation	0 ±0	1.29 ±1.29	2.03 ±1.3	2 ±0.28	0.71 ±0.71	1.03 ±0.52	1.83 ±1.17	36.2 ±3.05
XLOC_027462	No functional annotation	0 ±0	0 ±0	0.32 ±0.32	0.57 ±0.14	0 ±0	0 ±0	0.24 ±0.08	5.03 ±0.74
XLOC_027490	No functional annotation	0.32 ±0.1	0.52 ±0.09	0.14 ±0.1	0.4 ±0.05	0.13 ±0.01	0.32 ±0.17	0.47 ±0.08	2.75 ±0.54

Table S6. Transcript abundance for genes upregulated in the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G076200</i>	F3I6.5 protein	4.98 ± 1.36	2.76 ± 0.2	5.19 ± 1.14	8.5 ± 3.05	20.63 ± 3.59	2.44 ± 0.25	6.21 ± 1.04	9 ± 3.26
<i>Phvul.002G165800</i>	BCS1 AAA-type ATPase	0.47 ± 0.16	0.1 ± 0.06	0.2 ± 0.04	0.29 ± 0.14	1.88 ± 0.17	0.04 ± 0.04	0.25 ± 0.02	0.27 ± 0.16
<i>Phvul.003G075300</i>	No functional annotation	11 ± 2.47	8.96 ± 0.18	7.68 ± 1.25	4.46 ± 0.76	48.57 ± 4.26	9.46 ± 1.71	6.03 ± 0.65	6.39 ± 2.14
<i>Phvul.003G079900</i>	Glucan endo-1,3- β -glucosidase 1	4.37 ± 1.08	2.21 ± 0.09	2.25 ± 0.23	1.04 ± 0.09	20.32 ± 8.19	2.26 ± 0.44	1.42 ± 0.34	2.11 ± 0.84
<i>Phvul.003G110200</i>	COBRA-like protein 7-related	3.71 ± 0.57	2.83 ± 0.32	1.66 ± 0.25	5.29 ± 3.48	16.3 ± 2.63	2.52 ± 0.07	1.87 ± 0.17	7.14 ± 4.73
<i>Phvul.003G138226</i>	Very-long-chain 3-oxoacyl-CoA synthase	3.19 ± 0.69	2.07 ± 0.39	3.49 ± 0.69	3.36 ± 0.51	17.13 ± 6.83	1.9 ± 0.28	2.82 ± 0.77	3.31 ± 0.52
<i>Phvul.003G140426</i>	No functional annotation	5.51 ± 1.18	4.37 ± 0.35	5.65 ± 0.4	5.11 ± 0.62	23.1 ± 4.88	3.91 ± 0.78	5.08 ± 0.33	4.87 ± 1.09
<i>Phvul.003G147300</i>	Xyloglucan endotransglucosylase/ Hydrolase protein 21-related	0.15 ± 0.08	0.01 ± 0.01	0.1 ± 0.03	0.21 ± 0.13	1.14 ± 0.67	0 ± 0	0.03 ± 0.03	0.04 ± 0.03
<i>Phvul.003G152300</i>	NAD dependent epimerase/dehydratase	36.19 ± 4.07	27.86 ± 0.9	31.2 ± 3.91	39.41 ± 18.99	146.5 ± 30.89	27.39 ± 1.24	29.13 ± 5.24	57.35 ± 23.34

Table S6 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.004G019600</i>	Xyloglucan glycosyltransferase 4	1.97 ±0.31	1.33 ±0.12	1.3 ±0.09	1.12 ±0.21	8.95 ±2.21	1.41 ±0.1	1.5 ±0.17	1.88 ±0.58
<i>Phvul.004G132000</i>	Peroxidase 47	8.04 ±3.45	3.82 ±0.96	4.13 ±0.81	1.45 ±0.2	54.64 ±19.76	2.98 ±1.06	5.9 ±0.94	5.52 ±1.89
<i>Phvul.004G173101</i>	Protein of unknown function	4.65 ±0.16	5.01 ±0.25	2.71 ±0.65	6.11 ±1.85	24.27 ±7.84	3.73 ±0.63	2.3 ±0.17	5.12 ±2.11
<i>Phvul.005G068500</i>	Basic helix-loop-helix domain-containing protein	3.16 ±1.09	3.18 ±0.69	0.45 ±0.24	0.18 ±0.02	20.23 ±11.99	3.54 ±1.13	0.63 ±0.18	0.51 ±0.23
<i>Phvul.005G111300</i>	Xyloglucan endotransglucosylase / Hydrolase protein 9	22.23 ±6.44	17.23 ±0.46	11.41 ±2.32	7.29 ±1.71	139.23 ±91.53	17.06 ±1.01	10.8 ±0.95	10.14 ±2.29
<i>Phvul.006G023000</i>	Zinc finger FYVE domain containing protein	0.39 ±0.2	0.21 ±0.09	0.2 ±0.05	0.05 ±0.05	1.63 ±0.16	0.18 ±0.04	0.09 ±0.07	0.07 ±0.02
<i>Phvul.006G167400</i>	BCL2-associated athanogene	4.63 ±0.58	5.25 ±0.5	3.41 ±0.72	1.47 ±0.19	19.39 ±6.03	4.5 ±0.48	3.01 ±1.1	3.81 ±1.06
<i>Phvul.006G204100</i>	No functional annotation	7.81 ±1.87	4.93 ±0.98	4.05 ±0.24	30.76 ±20.77	35.96 ±8.97	3.86 ±0.95	3.54 ±0.69	20.34 ±12.31
<i>Phvul.007G021700</i>	Cupin domain (Cupin_2)	0.69 ±0.39	0.53 ±0.01	0.56 ±0.08	0.49 ±0.06	3.28 ±0.44	1.37 ±0.03	0.53 ±0.16	0.64 ±0.17
<i>Phvul.007G198400</i>	F-Box protein PP2-B13-related	2.42 ±0.76	0.57 ±0.29	2.85 ±0.48	3.51 ±0.21	10.94 ±1.91	0.92 ±0.11	2.98 ±0.18	3.42 ±0.49
<i>Phvul.008G049600</i>	Cyclin-U4-1	1.46 ±0.79	0.5 ±0.28	1.94 ±0.47	0.52 ±0.23	8.44 ±3.88	0.47 ±0.03	1.16 ±0.28	1.38 ±0.53
<i>Phvul.008G081000</i>	Receptor-like protein kinase feronia	5.86 ±0.52	3.11 ±1.56	4.14 ±0.45	3.73 ±0.44	25.19 ±7.19	4.96 ±0.4	3.89 ±0.29	5.67 ±1.64

Table S6 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G174100</i>	Predicted RNA-binding protein SEB4 (RRM superfamily)	0.23 ±0.05	0.02 ±0.02	0.09 ±0.05	0.01 ±0.01	1.01 ±0.85	0.04 ±0.02	0 ±0	0 ±0
<i>Phvul.008G237500</i>	Glutamine synthetase	0.67 ±0.05	0.68 ±0.4	0.22 ±0.03	0.14 ±0.05	4.21 ±2.71	1.02 ±0.23	0.14 ±0.05	0.13 ±0.08
<i>Phvul.009G074400</i>	Xyloglucan glycosyltransferase 12-related	4.36 ±0.39	2.48 ±1.24	2.21 ±0.36	2.03 ±0.44	18.13 ±6.41	4.07 ±0.45	1.81 ±0.35	3.17 ±1.52
<i>Phvul.009G075801</i>	No functional annotation	683.63 ±56.18	443.46 ±225.4	356.53 ±73.1	206.74 ±7.14	2865.96 ±646.99	590.81 ±71.25	241.43 ±24.29	337.75 ±80.59
<i>Phvul.009G113400</i>	F2J10.8 protein-related	12.99 ±2.38	6.95 ±3.48	9.59 ±1.77	6.11 ±1.24	62.11 ±7.73	11.94 ±0.96	9.04 ±0.85	9.19 ±2.68
<i>Phvul.009G234900</i>	No functional annotation	0 ±0	0.55 ±0.55	3.09 ±0.47	1.97 ±1.13	10.23 ±1.86	0.66 ±0.66	1.61 ±1.61	2.44 ±1.29
<i>Phvul.010G061500</i>	Wound-induced protein WI12	1.03 ±0.53	0.25 ±0.13	2.33 ±1.25	0.79 ±0.12	6.65 ±2.15	0.17 ±0.11	1.17 ±0.4	1.24 ±0.51
<i>Phvul.010G152200</i>	Gibberellin 3-β-dioxygenase 1-related	0.38 ±0.05	0.39 ±0.21	0.35 ±0.08	0.18 ±0.13	2.52 ±1.43	0.39 ±0.07	0.39 ±0.13	0.44 ±0.13
<i>Phvul.011G054100</i>	Calmodulin-like protein 6-related	7.02 ±1.93	2.55 ±1.39	7.15 ±0.92	14.32 ±4.38	37.3 ±4.83	4.14 ±0.66	7.14 ±0.37	14.26 ±4.21
<i>Phvul.011G107000</i>	Xyloglucan endotransglucosylase/ Hydrolase protein 9	5.15 ±2.12	5.36 ±2.8	2.17 ±0.29	1.97 ±0.39	34.64 ±27.35	7.76 ±1.44	2.29 ±0.66	2.69 ±0.68
XLOC_027363	No functional annotation	1.67 ±0.76	0.76 ±0.38	1.44 ±0.16	1.06 ±0.55	7.44 ±0.65	1.66 ±0.31	1.28 ±0.32	1.1 ±0.28

Table S7. Transcript abundance for genes upregulated in the CBB-susceptible RIL at 8 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G127300</i>	Cysteine protease family C1-related	0.48 ± 0.46	0.32 ± 0.18	0.14 ± 0.11	0.05 ± 0.01	0.06 ± 0.03	1.42 ± 0.73	0.22 ± 0.04	0.11 ± 0.03
XLOC_001894	No functional annotation	0.09 ± 0.05	0 ± 0	0 ± 0	0.03 ± 0.03	0.08 ± 0.08	1.07 ± 0.57	0.18 ± 0.1	0.08 ± 0.08

Table S8. Transcript abundance for genes upregulated in the CBB-susceptible RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G012600</i>	Auxin response factor 30-related	0.18 ± 0.02	0.18 ± 0.03	0 ± 0	0.08 ± 0.04	0.06 ± 0.06	0.82 ± 0.49	0.56 ± 0.15	0.31 ± 0.23
<i>Phvul.003G143400</i>	Peroxidase 16-related	0 ± 0	0 ± 0	0 ± 0	0.13 ± 0.07	0 ± 0	0 ± 0	0.6 ± 0.55	0.26 ± 0.25
<i>Phvul.004G059200</i>	Pectate lyase 11-related	1.27 ± 0.46	2 ± 0.11	3.17 ± 0.47	3.75 ± 0.87	0.73 ± 0.31	1.67 ± 0.13	13.34 ± 7.33	11.84 ± 7.47
<i>Phvul.007G021300</i>	Protein trichome birefringence-like 36	0.33 ± 0.05	0.49 ± 0.1	0.19 ± 0.05	0.22 ± 0.06	0.24 ± 0.03	0.4 ± 0.05	0.97 ± 0.5	0.77 ± 0.42
<i>Phvul.009G108300</i>	Adenosylhomocysteine nucleosidase	1.61 ± 0.97	1.82 ± 1.02	2.45 ± 0.49	13.17 ± 2.83	0.53 ± 0.29	1.82 ± 0.4	10.65 ± 6.96	6.96 ± 2.74

Table S9. Transcript abundance for genes upregulated in the CBB-susceptible RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G001500</i>	Multi-copper oxidase type I family protein-related	6.48 ± 0.72	5.54 ± 0.94	1.46 ± 0.79	0.42 ± 0.09	8.77 ± 3.13	5.11 ± 1.6	2.13 ± 0.39	1.71 ± 0.16
<i>Phvul.001G146800</i>	Receptor-like cytoplasmic kinase VIA5	6.06 ± 0.7	5.74 ± 0.27	1.17 ± 0.24	0.2 ± 0.06	10.6 ± 0.43	4.62 ± 0.68	1 ± 0.52	1.23 ± 0.35
<i>Phvul.002G000900</i>	Taxadien-5- α -ol O-acetyltransferase	5.1 ± 1.86	1.59 ± 0.21	4.1 ± 0.18	0.62 ± 0.19	6.69 ± 1.06	1.48 ± 0.14	2.72 ± 1.25	2.59 ± 1.25
<i>Phvul.002G083600</i>	Pollen allergen /Rare lipoprotein A (RlpA)-like double-psi β -barrel	68.8 ± 11.82	57.44 ± 14.71	16.78 ± 6.39	3.84 ± 1.61	38.81 ± 4.27	70.09 ± 4.12	9.09 ± 4.43	18.04 ± 8.05
<i>Phvul.002G153900</i>	Dehydration-responsive element-binding protein 1E-related	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0.39 ± 0.24	0 ± 0	0.05 ± 0.05	0.84 ± 0.84
<i>Phvul.003G080100</i>	Multi-copper oxidase	3.6 ± 0.81	2.1 ± 0.59	1.24 ± 0.25	0.22 ± 0.05	5.94 ± 2.17	1.51 ± 0.2	0.54 ± 0.23	0.87 ± 0.4
<i>Phvul.004G093200</i>	Light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1)	53.17 ± 21.56	11.06 ± 3.83	19.7 ± 5.46	2.23 ± 0.29	80.64 ± 3.96	5.44 ± 2.44	26.74 ± 13.12	21.01 ± 16.71
<i>Phvul.006G207900</i>	Copper transport protein ATOX1-related	12.05 ± 2.66	12.74 ± 1.92	4.47 ± 1.33	0.35 ± 0.03	13.46 ± 2.35	13.77 ± 1.21	2.36 ± 1.18	3.92 ± 1.71
<i>Phvul.007G196500</i>	No functional annotation	0.38 ± 0.39	0 ± 0	0 ± 0	0 ± 0	0.54 ± 0.27	0.16 ± 0.16	0.12 ± 0.12	0.87 ± 0.28
<i>Phvul.008G030300</i>	No functional annotation	45.29 ± 8.15	37.29 ± 19.56	11.61 ± 2.29	1.02 ± 0.7	45.75 ± 8.17	52.63 ± 12.53	6.67 ± 3.44	7.41 ± 3.81
<i>Phvul.008G100300</i>	Embryo-specific protein 3	3.4 ± 0.17	1.62 ± 0.92	4.27 ± 0.51	0.5 ± 0.04	3.13 ± 0.06	2.57 ± 0.4	2.46 ± 0.98	2.42 ± 0.73

Table S9 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G137700</i>	Epidermal patterning factor-like protein 9	11.38 ±2.52	9.36 ±5.91	3.18 ±1.5	0.67 ±0.25	12.41 ±3.56	11.44 ±1.81	1.83 ±0.8	2.8 ±1.45
<i>Phvul.008G248000</i>	Expansin-A8	1.66 ±0.45	1.06 ±0.57	0.49 ±0.09	0 ±0	2.45 ±0.81	1.69 ±0.46	0.71 ±0.52	0.63 ±0.32
<i>Phvul.008G261200</i>	Protein ELF4-like 1	24.67 ±24.54	47.59 ±24.03	0.37 ±0.25	0 ±0	0.34 ±0.07	73.97 ±1.7	0.06 ±0.06	0.69 ±0.15
<i>Phvul.009G187400</i>	Gibberellin-regulated protein 4	161.56 ±64.34	193.6 ±96.9	15.6 ±7.07	2.03 ±0.92	104.6 ±4.81	269.09 ±42.92	8.67 ±4.82	9.62 ±3.6
<i>Phvul.010G129900</i>	Germin-like protein subfamily 3	634.04 ± 469.3	977.85 ± 497.08	51.89 ± 22.68	7.28 ± 1.77	441.73 ± 150.71	1701.17 ± 159.9	24.56 ± 10.55	34.04 ± 13.51
<i>Phvul.011G063800</i>	Expansin-A6	50.07 ±20.99	8.09 ±4.22	9.72 ±2.7	2.26 ±0.35	28.96 ±1.33	9.69 ±2.32	7.71 ±4.27	10.23 ±4.41
<i>Phvul.011G209600</i>	Zinc finger protein-related	585.72 ±142.6 8	250.2 ±134.0 6	600.85 ±34.67	91.94 ±4.43	835.51 ±40.86	365.09 ±78.45	437.27 ±209.5 4	407.22 ±167.51
XLOC_009121	No functional annotation	0 ±0	0.68 ±0.57	0.15 ±0.15	0.06 ±0.06	0.97 ±0.68	0.09 ±0.09	0.58 ±0.2	0.33 ±0.17
XLOC_020711	No functional annotation	0 ±0	0.54 ±0.54	1.13 ±0.57	0 ±0	0 ±0	0.46 ±0.46	1.21 ±0.62	1.89 ±0.99

Table S10. Transcript abundance for genes downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G020100</i>	Galactolipase	31.65 \pm 23.06	51.76 \pm 20.87	5.26 \pm 0.63	5.38 \pm 0.67	7.79 \pm 0.84	51.22 \pm 22.05	7.29 \pm 1.51	11.57 \pm 5.4
<i>Phvul.001G033700</i>	Cytosolic resiniferatoxin binding protein RBP-26	4.12 \pm 3.04	10.22 \pm 5.15	1.41 \pm 0.28	1.29 \pm 0.08	0.85 \pm 0.19	8.2 \pm 3.82	1.29 \pm 0.5	0.86 \pm 0.06
<i>Phvul.001G087300</i>	Zinc finger protein CONSTANS-like 14-related	2.03 \pm 1.89	3.22 \pm 1.54	0.1 \pm 0.03	0.12 \pm 0.04	0.42 \pm 0.03	3.2 \pm 1.35	0.24 \pm 0.06	0.16 \pm 0.04
<i>Phvul.001G154400</i>	Auxin canalisation	0.8 \pm 0.61	1.45 \pm 0.63	0.06 \pm 0.02	0.11 \pm 0.03	0.16 \pm 0.02	1.17 \pm 0.48	0.12 \pm 0.02	0.08 \pm 0.01
<i>Phvul.001G156900</i>	Galactolipase / Triacylglycerol lipase	108.88 \pm 83.07	117.59 \pm 73.13	73.66 \pm 28.83	41.58 \pm 25.8	21.21 \pm 11.89	85.58 \pm 41.27	72.25 \pm 9.1	61.64 \pm 29.15
<i>Phvul.001G255400</i>	SufE-like protein 2, chloroplastic	0.9 \pm 0.36	0.67 \pm 0.24	1.27 \pm 0.35	2.38 \pm 1.39	0 \pm 0	0.59 \pm 0.28	0.81 \pm 0.31	5.63 \pm 0.23
<i>Phvul.001G263300</i>	No functional annotation	4.52 \pm 3.74	7.79 \pm 3.06	4.82 \pm 1.1	11.37 \pm 4.4	0.9 \pm 0.18	7.98 \pm 4.1	6.57 \pm 0.99	10.46 \pm 1.76
<i>Phvul.001G234700</i> , <i>Phvul.001G234800</i>	Tropinone reductase I	8.84 \pm 7.03	11.74 \pm 4.92	2.83 \pm 0.29	2.53 \pm 0.14	2.12 \pm 0.42	12.97 \pm 5.55	2.68 \pm 0.25	2.59 \pm 0.62
<i>Phvul.002G028500</i>	Polyol transporter 3-related	5.23 \pm 4.13	5.11 \pm 1.61	0.43 \pm 0.1	0.66 \pm 0.2	0.82 \pm 0.39	5.82 \pm 2.42	0.72 \pm 0.16	1.03 \pm 0.11
<i>Phvul.002G100501</i>	LOB domain-containing protein 4	1.14 \pm 0.69	1.25 \pm 0.51	0.73 \pm 0.1	0.62 \pm 0.28	0.18 \pm 0.08	1.7 \pm 0.9	2.31 \pm 0.69	0.94 \pm 0.2
<i>Phvul.002G168400</i>	Glycogen phosphorylase	9.21 \pm 7.78	17.11 \pm 8.79	0.74 \pm 0.13	0.59 \pm 0.1	1.39 \pm 0.16	13.5 \pm 6.21	0.83 \pm 0.08	0.74 \pm 0.1
<i>Phvul.002G240900</i>	WRKY transcription factor 65-related	0.68 \pm 0.57	1.18 \pm 0.52	0.12 \pm 0.02	0.19 \pm 0.09	0 \pm 0	1.11 \pm 0.51	0.1 \pm 0.03	0.51 \pm 0.1
<i>Phvul.002G303700</i>	SAUR family protein	9.69 \pm 4.23	15.36 \pm 5.16	7.97 \pm 1.7	8.44 \pm 0.97	1.71 \pm 0.19	12.66 \pm 5.37	6.84 \pm 0.98	7.44 \pm 1.37

Table S10 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G044500</i>	PPR repeat (PPR) // PPR repeat family (PPR_2) // DYW family of nucleic acid deaminases	0.74 ±0.59	0.79 ±0.35	0.3 ±0.06	0.45 ±0.12	0.12 ±0.02	0.98 ±0.44	0.35 ±0.08	0.55 ±0.16
<i>Phvul.003G157900</i>	No functional annotation	4.41 ±1.61	1.53 ±0.79	9.26 ±2.11	0.75 ±0.74	0 ±0	3.77 ±1.44	5.92 ±4.83	2.48 ±0.05
<i>Phvul.003G206400</i>	Cytochrome P450 CYP2 subfamily	1.67 ±1.45	4.84 ±2.48	0.19 ±0.13	0.24 ±0.07	0.14 ±0.05	3.96 ±1.95	0.23 ±0.08	0.28 ±0.02
<i>Phvul.003G255700</i>	No functional annotation	9.62 ±8.27	11.72 ±5.87	1.07 ±0.49	2.04 ±0.57	1.32 ±0.47	12.58 ±5.67	1.49 ±0.43	1.18 ±0.4
<i>Phvul.003G047100</i>	Glucosyl/glucuronosyl transferases	4.06 ±3.06	4.05 ±2.33	14.77 ±4.93	5.3 ±3.07	0.46 ±0.17	4.44 ±2.47	13.2 ±2.74	3.05 ±1.29
<i>Phvul.003G162800</i>	Aspartate racemase	0.7 ±0.44	0.56 ±0.39	0.55 ±0.06	0.42 ±0.19	0.17 ±0.06	0.87 ±0.38	0.33 ±0.18	0.41 ±0.08
<i>Phvul.003G219200</i>	Bifunctional inhibitor/ Lipid-transfer protein/seed storage 2S albumin superfamily protein	1.28 ±1.02	1.57 ±0.61	1.48 ±0.78	1.44 ±0.3	0.23 ±0.07	2.45 ±1.11	3.03 ±0.32	0.91 ±0.48
<i>Phvul.004G137600</i>	DR4 protein-related	22.04 ±18.58	23.79 ±14.25	54.85 ±16.75	20.05 ±10.36	2.78 ±1.15	22.39 ±12.29	59.21 ±15.85	13.59 ±5.68
<i>Phvul.004G135700</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	1.3 ±0.87	1.51 ±0.61	0.46 ±0.05	0.49 ±0.07	0.18 ±0.02	1.4 ±0.5	0.61 ±0.13	0.93 ±0.11
<i>Phvul.004G160800</i>	α/β Hydrolase fold-containing protein	36.74 ±30.46	57.75 ±26.56	11.51 ±1.43	9.38 ±1.94	5.65 ±1.08	58.1 ±27.15	9.1 ±1.1	5.43 ±0.7
<i>Phvul.005G001000</i>	X-Box transcription factor-related	7.39 ±5.89	6.66 ±3.98	21.15 ±7.97	9.03 ±5.16	1.7 ±0.96	7.93 ±4.38	20.28 ±4.91	5.37 ±1.61
<i>Phvul.005G032600</i>	Dirigent protein 20-related	7.52 ±5.04	6.84 ±3.62	31.04 ±9.23	14.7 ±6.08	1.4 ±0.72	7.16 ±3.01	32.1 ±6.03	6.91 ±2.71

Table S10 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G075200</i>	Cathepsin H / N-benzoylarginine- β -naphthylamide hydrolase	0.85 ± 0.22	0.66 ± 0.16	0.82 ± 0.23	0.76 ± 0.21	0.16 ± 0.05	0.43 ± 0.12	0.66 ± 0.16	0.85 ± 0.11
<i>Phvul.005G120400</i>	PPR repeat (PPR) // PPR repeat (PPR_1)	0.88 ± 0.79	1.26 ± 0.61	0.38 ± 0.08	0.45 ± 0.14	0.2 ± 0.07	1.24 ± 0.59	0.56 ± 0.09	0.7 ± 0.14
<i>Phvul.005G156900</i>	Linoleate 9S-lipoxygenase	181.7 ± 141.39	207.98 ± 119.73	290.11 ± 136.69	112.24 ± 69.14	39.2 ± 15.97	233.48 ± 113.2	288.57 ± 71.01	59.56 ± 27.01
<i>Phvul.005G080600</i>	γ -Glutamyl hydrolase	15.27 ± 13.03	16.13 ± 10.37	6.19 ± 3.51	1.4 ± 0.29	1.86 ± 0.33	14.45 ± 8.2	4.02 ± 0.96	1.24 ± 0.22
<i>Phvul.005G156800</i>	Linoleate 9S-lipoxygenase	76.8 ± 65.79	79.03 ± 49.09	140.86 ± 44.72	76.64 ± 38.7	9.12 ± 5.13	97.09 ± 49.93	167.41 ± 43.87	68.4 ± 15.99
<i>Phvul.003G188300</i> , <i>Phvul.003G188400</i>	PPR repeat (PPR) // PPR repeat family (PPR_2) // Pentatricopeptide repeat domain (PPR_3)	11.17 ± 9.38	17.67 ± 8.12	1.55 ± 0.18	1.94 ± 0.08	2.06 ± 0.29	21.38 ± 9.73	1.82 ± 0.12	1.51 ± 0.04
<i>Phvul.006G034000</i>	UDP-glucose 4,6-dehydratase	1.88 ± 1.52	1.54 ± 1.04	5.05 ± 1.76	2.19 ± 1.28	0.17 ± 0.08	1.71 ± 1.11	5.31 ± 0.87	2.15 ± 1.26
<i>Phvul.006G146400</i>	Chitin elicitor receptor kinase 1	1.17 ± 0.88	2.32 ± 1.11	0.27 ± 0.09	0.21 ± 0.05	0.21 ± 0.05	1.83 ± 0.87	0.33 ± 0.03	0.25 ± 0.05
<i>Phvul.007G017600</i>	No functional annotation	1.15 ± 0.48	0.97 ± 0.57	0.19 ± 0.1	0.14 ± 0.08	0.24 ± 0.08	0.66 ± 0.27	0.16 ± 0.05	0.02 ± 0.02
<i>Phvul.007G135800</i>	Glucosyl/glucuronosyl transferases	1.39 ± 1.24	2.98 ± 1.57	0.17 ± 0.06	0.1 ± 0.02	0.2 ± 0.03	1.91 ± 0.81	0.24 ± 0.05	0.09 ± 0.03
<i>Phvul.007G050900</i>	Cysteine-rich receptor-like protein kinase 9-related	7.55 ± 6.18	12.15 ± 5.03	1.78 ± 0.15	3.24 ± 0.39	1.38 ± 0.22	10 ± 4.33	3 ± 0.32	3.74 ± 0.5

Table S10 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G257300</i>	CCT motif	17.09 ±16.99	38.71 ±19.34	0.06 ±0.04	0.06 ±0.03	0.23 ±0.04	34.57 ±17.25	0.09 ±0.09	0.05 ±0.03
<i>Phvul.008G079600</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // Pentatricopeptide repeat domain (PPR_3) // DYW family of nucleic acid deaminases	0.66 ±0.44	1.11 ±0.55	0.4 ±0.08	0.44 ±0.13	0.08 ±0.02	0.95 ±0.43	0.34 ±0.06	0.67 ±0.02
<i>Phvul.008G128700</i>	β-Amyrin 24-hydroxylase / Sophoradiol 24-hydroxylase	9.04 ±7.5	8.51 ±5.32	30.75 ±11.85	8.9 ±4.92	1.61 ±1.01	10.02 ±5.48	27.86 ±5.24	3.63 ±1.55
<i>Phvul.008G152900</i>	Permease of the drug/metabolite transporter (DMT) superfamily	18.65 ±10.57	28.74 ±10.17	8.74 ±1.15	9.11 ±0.7	4.58 ±0.68	29.19 ±11.31	9.85 ±0.08	8.38 ±1.52
<i>Phvul.008G211800</i>	Niemann pick type C2 protein NPC2-related	5.22 ±5.01	5.73 ±4.5	7.79 ±4.61	3.5 ±1.74	0.23 ±0.13	5.22 ±3.03	8.87 ±1.16	1.07 ±0.6
<i>Phvul.009G002200</i>	Amidophosphoribosyl-transferase / Phosphoribosyldiphosphate 5-amidotransferase	39.43 ±28.42	68.34 ±28.52	13.52 ±1.68	21.89 ±1.18	8.53 ±1.25	69.99 ±31.74	16.67 ±1.44	27.26 ±1.09
<i>Phvul.009G146800</i>	Alginate lyase	20.59 ±17.51	45.57 ±20.52	6.15 ±0.98	9.23 ±3.94	2.62 ±0.43	43.42 ±20.38	6.53 ±0.28	14.43 ±6.4
<i>Phvul.010G143100</i>	Leucine-rich repeat protein kinase-related	0.97 ±0.81	1.95 ±0.96	0.13 ±0.01	0.2 ±0.03	0.12 ±0.04	1.67 ±0.74	0.15 ±0.02	0.3 ±0.03
<i>Phvul.010G162600</i>	DnaJ homolog subfamily C member	64.65 ±41.73	129.07 ±52.28	71.22 ±19.4	121.05 ±17.36	10.17 ±1.37	100.59 ±52.37	95.07 ±3.44	128.38 ±26.56
<i>Phvul.011G085200</i>	Xyloglucan:xyloglucosyl transferase	18.66 ±11.69	16.01 ±5.57	17.56 ±2.86	8.62 ±3.06	3.29 ±0.8	18.32 ±6.81	23.96 ±2.08	2.99 ±0.95
<i>Phvul.011G125700</i>	E3 ubiquitin-protein ligase RNF1/2	26.3 ±21.83	39.01 ±18.63	6.07 ±0.47	5.65 ±0.45	4.23 ±0.21	37.29 ±18.37	5.82 ±0.19	7.15 ±0.28

Table S10 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G167000</i>	Chitinase	7.32 ±7.06	6.03 ±4.42	14 ±9.98	2.99 ±2.23	0.17 ±0.1	3.48 ±1.85	9.19 ±1.77	2.54 ±0.46
<i>Phvul.011G018000</i>	Alcohol dehydrogenase related	7 ±5.46	15.56 ±7.1	0.77 ±0.05	0.89 ±0.13	1.61 ±0.31	12.43 ±5.21	0.93 ±0.28	0.7 ±0.16
<i>Phvul.007G276500</i> , <i>Phvul.007G276600</i>	No functional annotation	89.3 ±73.34	75.74 ±47.75	151.45 ±91.16	39.43 ±23.99	15.6 ±6.73	70.5 ±46.32	119.51 ±51.52	137.18 ±62.5
<i>Phvul.004G129600</i> , <i>Phvul.004G129700</i> , <i>Phvul.004G129800</i> , <i>Phvul.004G129900</i> , <i>Phvul.004G130000</i>	DR4 protein-related	25.05 ±21.45	17.98 ±9.37	28.58 ±11.88	12.56 ±7.33	1.81 ±0.96	18.56 ±9.14	32.63 ±7.77	14.44 ±6.13
<i>Phvul.010G134900</i> , <i>Phvul.010G135000</i>	Linoleate 13S-lipoxygenase / Lipoxidase	84.61 ±73.62	77.78 ±49.63	123.84 ±40.64	60.48 ±35.79	12.28 ±6.45	99.21 ±50.37	141.3 ±44.79	45.94 ±19.79
<i>Phvul.008G228814</i> , <i>Phvul.008G229000</i> , <i>Phvul.008G229400</i>	Proprotein convertase subtilisin/ Kexin	16.57 ±14.8	20.03 ±14.98	9.97 ±6.51	2.08 ±0.1	1.7 ±0.47	10.76 ±5.29	7.67 ±0.57	0.94 ±0.23
XLOC_015034	No functional annotation	0.83 ±0.53	0.76 ±0.39	1.25 ±0.44	1.06 ±0.96	0 ±0	0.27 ±0.17	2.48 ±0.31	2.03 ±0.28
XLOC_025196	No functional annotation	1.1 ±0.79	1.88 ±1.14	1.36 ±0.69	3.55 ±2.4	0 ±0	1.19 ±0.79	4.04 ±1.3	6.81 ±0.39

Table S11. Transcript abundance for genes downregulated in the CBB-resistant RIL at 8 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.004G142500</i> , <i>Phvul.004G142600</i> , <i>Phvul.004G142700</i>	Protein phosphatase 1, regulatory subunit, and related proteins; Leucine Rich Repeat (LRR_1) // Leucine rich repeat (LRR_8)	1.38 ± 0.89	0.72 ± 0.25	1.01 ± 0.24	0.57 ± 0.3	0.23 ± 0.18	0.16 ± 0.06	0.64 ± 0.47	1.39 ± 0.45
XLOC_015051	No functional annotation	1.63 ± 0.84	0.84 ± 0.42	1.91 ± 0.23	2.8 ± 0.41	0.41 ± 0.21	0 ± 0	2.78 ± 0.35	1.78 ± 0.95
XLOC_011019	No functional annotation	0.35 ± 0.35	1.41 ± 1.15	0.71 ± 0.4	0 ± 0	0.78 ± 0.39	0 ± 0	0.58 ± 0.58	0.23 ± 0.24

Table S12. Transcript abundance for genes downregulated in the CBB-resistant RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G281200</i>	Strictosidine synthase-related	2.87 ± 1.24	4.35 ± 1.85	0.83 ± 0.54	0.12 ± 0.05	5.01 ± 2.16	3.38 ± 0.62	0.21 ± 0.07	0.07 ± 0.02
XLOC_002678	No functional annotation	0.51 ± 0.26	0.67 ± 0.43	2.07 ± 1.72	0.34 ± 0.33	0.35 ± 0.35	0.81 ± 0.54	0 ± 0	0.45 ± 0.23

Table S13. Transcript abundance for genes downregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G296700</i>	Upstream-binding transcription factor	0.57 ± 0.1	0.52 ± 0.15	0.5 ± 0.04	0.64 ± 0.11	0.51 ± 0.09	0.52 ± 0.05	0.49 ± 0.07	0.12 ± 0.04
<i>Phvul.005G113800</i>	Peroxidase 3-related	4.79 ± 1.66	3.25 ± 0.92	2.31 ± 0.97	2.22 ± 0.66	7.45 ± 0.64	3.56 ± 1.58	1.74 ± 0.28	0.46 ± 0.18
<i>Phvul.006G202700</i>	No functional annotation	912.7 ± 153.9 4	873.97 ± 58.41	211.87 ± 86.13	128.81 ± 29.43	993.88 ± 101.2 6	788.51 ± 36.1	120.08 ± 5.05	31.84 ± 23.56
<i>Phvul.008G037500</i>	Pollen allergen / Rare lipoprotein A (RlpA)-like double-psi β -barrel	3.34 ± 1.28	3.41 ± 0.81	2.78 ± 0.5	1.49 ± 0.14	6.68 ± 2.04	3.52 ± 0.52	1.59 ± 0.2	0.31 ± 0.07
<i>Phvul.008G174800</i>	No functional annotation	0.98 ± 0.4	0.69 ± 0.25	0.31 ± 0.05	1.44 ± 0.62	1.56 ± 1.26	1.19 ± 0.16	0.76 ± 0.16	0.17 ± 0.06
<i>Phvul.008G218500</i>	Peroxidase 52	0.4 ± 0.15	0.23 ± 0.16	1.74 ± 0.51	2.2 ± 1.18	0.46 ± 0.04	0.23 ± 0.13	1.41 ± 0.46	0.32 ± 0.15

Table S14. Transcript abundance for genes downregulated in the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G022200</i>	Cold regulated protein 27	17.31 ± 17.05	40.72 ± 2.78	0.09 ± 0.06	0.05 ± 0.03	0.1 ± 0.02	55.98 ± 4.99	0.08 ± 0.08	0.09 ± 0.03
<i>Phvul.001G124300</i>	Pyrroline-5-carboxylate reductase	9.89 ± 7.92	27.61 ± 0.72	1.77 ± 0.4	1.35 ± 0.17	1.9 ± 0.04	26.29 ± 0.28	1.92 ± 0.32	1.59 ± 0.39
<i>Phvul.001G130900</i>	ATP-binding cassette transporter	2.65 ± 1.63	6.01 ± 0.35	1.84 ± 0.14	3 ± 0.69	0.56 ± 0.17	5.87 ± 0.73	2.29 ± 0.92	2.43 ± 1.11
<i>Phvul.001G162800</i>	Long-chain-alcohol oxidase	7.22 ± 6.35	20.9 ± 1.26	0.87 ± 0.21	0.71 ± 0.1	0.92 ± 0.18	23.25 ± 0.98	0.93 ± 0.14	1.1 ± 0.25
<i>Phvul.001G221600</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	0.82 ± 0.57	1.51 ± 0.12	0.42 ± 0.05	0.55 ± 0.14	0.11 ± 0.05	1.83 ± 0.18	0.48 ± 0.19	0.59 ± 0.24
<i>Phvul.001G227500</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	0.79 ± 0.65	1.92 ± 0.06	0.29 ± 0.06	0.53 ± 0.13	0.15 ± 0.02	2.58 ± 0.41	0.57 ± 0.11	0.62 ± 0.11
<i>Phvul.001G247500</i>	SEL1 repeat	7.09 ± 5.66	18.62 ± 1.01	0.71 ± 0.2	0.93 ± 0.21	1.4 ± 0.27	19.47 ± 0.29	1.01 ± 0.17	1.17 ± 0.16
<i>Phvul.002G211500</i>	Oxidoreductase, 2-oxoglutarate-Fe II oxygenase family protein	1.08 ± 0.39	1.2 ± 0.06	0.73 ± 0.05	3.54 ± 1.07	0.23 ± 0.01	1.02 ± 0.23	2.38 ± 1.19	2.58 ± 1.5
<i>Phvul.002G283000</i>	Polynucleotide adenylyltransferase domain and RNA recognition motif-containing protein-related	8.21 ± 6.48	18.62 ± 1.51	4.43 ± 0.27	4.74 ± 0.79	1.99 ± 0.14	20.95 ± 1.97	4.66 ± 0.3	5.62 ± 1.28
<i>Phvul.003G004400</i>	Nicotinamidase 3	8.07 ± 5.91	22.42 ± 0.76	2.56 ± 0.34	2.52 ± 0.21	1.84 ± 0.15	28.23 ± 3.21	2.37 ± 0.17	2.05 ± 0.28

Table S14 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G101100</i>	Nitrate, formate, iron dehydrogenase	3.15 ±1.93	7.36 ±1.09	2.72 ±0.92	8.34 ±1.74	0.55 ±0.16	5.49 ±1.45	8.82 ±6.33	7.69 ±4.1
<i>Phvul.003G157500</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	0.57 ±0.36	1.25 ±0.12	0.3 ±0.03	0.54 ±0.04	0.13 ±0.08	1.25 ±0.18	0.35 ±0.1	0.31 ±0.06
<i>Phvul.003G162300</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // PPR repeat family (PPR_2) // DYW family of nucleic acid deaminases	4.23 ±3.14	10.52 ±0.34	0.88 ±0.3	0.75 ±0.18	0.89 ±0.13	11.33 ±0.48	1 ±0.17	1.01 ±0.22
<i>Phvul.003G189800</i>	PPR repeat (PPR) // PPR repeat family (PPR_2) // DYW family of nucleic acid deaminases	1.09 ±0.77	2.27 ±0.08	0.46 ±0.07	0.81 ±0.21	0.19 ±0.03	2.29 ±0.46	0.62 ±0.2	0.52 ±0.09
<i>Phvul.003G229500</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	36.46 ±29.38	98.5 ±3.26	9.24 ±1.4	11.13 ±2.66	8.84 ±0.23	104.06 ±2.37	12.29 ±2.55	11.2 ±1.32
<i>Phvul.004G047900</i>	Proline dehydrogenase	1.12 ±0.8	2.47 ±0.38	0.57 ±0.23	1.01 ±0.46	0.24 ±0.03	2.88 ±0.1	1.11 ±0.39	0.9 ±0.13
<i>Phvul.004G083200</i>	Acyl-CoA N-acyltransferases superfamily protein	13.38 ±10.01	32.92 ±0.55	1.26 ±0.1	1.4 ±0.25	2.85 ±0.32	33.55 ±0.61	1.28 ±0.18	1.14 ±0.19
<i>Phvul.004G128500</i>	APO protein 1, chloroplastic	5.26 ±4.21	13.62 ±1.02	1.29 ±0.16	2.13 ±0.21	0.94 ±0.08	14.85 ±0.66	1.22 ±0.23	1.51 ±0.21
<i>Phvul.004G133300</i>	No functional annotation	1.27 ±1.11	2.8 ±0.25	0.44 ±0.04	0.6 ±0.16	0.26 ±0.01	3.38 ±0.4	0.61 ±0.22	0.65 ±0.21
<i>Phvul.004G151100</i>	Zinc finger protein	4.66 ±3.97	9.81 ±1.46	2.94 ±0.62	4 ±0.3	1.06 ±0.22	11.69 ±2.02	2.43 ±0.51	3.87 ±0.88
<i>Phvul.004G151525</i>	EF-hand calcium-binding domain containing protein	15.77 ±11.48	34.1 ±2.7	3.12 ±0.58	1.81 ±0.42	3.35 ±0.8	31.25 ±1.19	3.31 ±0.29	1.11 ±0.43

Table S14 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G039200</i>	Vicianin β -glucosidase	39.58 ± 32.27	95.77 ± 12.14	2.5 ± 0.26	1.64 ± 0.21	8.95 ± 1.64	91.11 ± 3.44	2.38 ± 0.2	2.18 ± 0.57
<i>Phvul.005G124400</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	2.66 ± 1.97	6.26 ± 0.55	0.76 ± 0.22	0.82 ± 0.21	0.46 ± 0.1	6.75 ± 0.38	0.75 ± 0.24	0.94 ± 0.08
<i>Phvul.005G159300</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	1.02 ± 0.83	2.16 ± 0.14	0.37 ± 0.02	0.64 ± 0.18	0.24 ± 0.08	2.07 ± 0.19	0.48 ± 0.08	0.53 ± 0.13
<i>Phvul.005G174500</i>	Protein of unknown function	1.85 ± 1.32	3.34 ± 1.22	0.22 ± 0.07	0 ± 0	0.23 ± 0.07	1.67 ± 0.35	0.03 ± 0.01	0.16 ± 0.09
<i>Phvul.006G036400</i>	PPR repeat (PPR) /DYW family of nucleic acid deaminases	0.54 ± 0.46	0.97 ± 0.15	0.18 ± 0.03	0.35 ± 0.04	0.09 ± 0.02	1.13 ± 0.17	0.29 ± 0.02	0.3 ± 0.09
<i>Phvul.007G093600</i>	MLO-like protein 12-related	40.43 ± 28.57	98.75 ± 9.36	7.09 ± 1.42	29.97 ± 8.76	10.04 ± 0.54	107.29 ± 2.22	10.96 ± 2.32	19.69 ± 5.5
<i>Phvul.007G125500</i>	Potato inhibitor I family	1.94 ± 1.94	5.7 ± 0.98	5.74 ± 1.54	2.48 ± 0.94	0 ± 0	6.01 ± 0.27	5.77 ± 2.23	6.06 ± 2.6
<i>Phvul.007G161300</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	0.87 ± 0.7	1.09 ± 0.59	0.39 ± 0.03	0.63 ± 0.06	0.22 ± 0.08	1.71 ± 0.01	0.47 ± 0.16	0.57 ± 0.05
<i>Phvul.007G169400</i>	No functional annotation	8.21 ± 6.19	13.04 ± 6.55	5.07 ± 0.31	7.92 ± 0.62	1.27 ± 0.3	20.88 ± 4.23	5.91 ± 1.35	6.75 ± 1.26
<i>Phvul.007G216700</i>	No functional annotation	16.46 ± 15.17	26.93 ± 13.87	0.16 ± 0.08	0.03 ± 0.03	3.38 ± 1.11	39.89 ± 5.24	0.11 ± 0.06	0.04 ± 0.04
<i>Phvul.007G278100</i>	Chlorophyllase	27.09 ± 23.72	57.23 ± 28.8	3.33 ± 0.57	3.46 ± 0.4	4.32 ± 0.35	84.81 ± 3.71	4.39 ± 0.51	2.97 ± 0.39
<i>Phvul.008G025900</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	4.5 ± 4	9.64 ± 4.88	0.62 ± 0.05	0.72 ± 0.03	0.45 ± 0.13	13.46 ± 0.95	0.65 ± 0.13	0.94 ± 0.09

Table S14 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G046100</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // PPR repeat family (PPR_2)	1.05 ±0.76	1.73 ±0.88	0.71 ±0.04	1.12 ±0.19	0.24 ±0.07	2.68 ±0.28	0.89 ±0.3	0.72 ±0.17
<i>Phvul.008G103900</i>	Cis-zeatin O-glucosyltransferase	0.84 ±0.7	1.07 ±0.55	0.15 ±0.03	0.1 ±0.03	0.06 ±0.02	1.8 ±0.41	0.11 ±0.03	0.13 ±0.06
<i>Phvul.008G105000</i>	Mitochondrial inner membrane protease subunit 2	2.67 ±1.4	3.87 ±1.95	1.25 ±0.35	2.42 ±0.32	0.54 ±0.16	6.02 ±0.91	1.83 ±0.4	1.82 ±0.49
<i>Phvul.008G201000</i>	No functional annotation	0.9 ±0.26	0.15 ±0.15	0.24 ±0.12	0.38 ±0.19	0 ±0	0.26 ±0.15	0.45 ±0.14	0.3 ±0.17
<i>Phvul.008G279800</i>	X-box transcription factor-related	12.28 ±9.2	23.37 ±11.8	4.37 ±0.32	5.16 ±0.47	2.58 ±0.39	38.63 ±2.42	6.81 ±1.62	4.25 ±0.32
<i>Phvul.009G004200</i>	B-box zinc finger	1.16 ±1.02	2.37 ±1.22	0.02 ±0.02	0.02 ±0.02	0 ±0	4.36 ±0.65	0 ±0	0 ±0
<i>Phvul.009G081600</i>	No functional annotation	1.07 ±0.82	1.6 ±0.83	0.24 ±0.12	0 ±0	0.16 ±0.08	2.35 ±0.09	0.08 ±0.02	0.23 ±0.1
<i>Phvul.009G159500</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	0.85 ±0.5	1.36 ±0.69	0.37 ±0.1	0.6 ±0.03	0.19 ±0.03	1.66 ±0.15	0.51 ±0.19	0.65 ±0.11
<i>Phvul.009G169000</i>	Coproporphyrinogen dehydrogenase	3.46 ±2.89	7 ±3.56	0.74 ±0.13	1.35 ±0.24	0.58 ±0.09	10.32 ±1.08	0.93 ±0.16	0.84 ±0.21
<i>Phvul.010G077634</i>	SCY1-like protein 1	11.07 ±8.8	19.06 ±9.69	2.67 ±0.39	2.23 ±0.23	2.18 ±0.16	29.56 ±0.83	2.79 ±0.29	2.34 ±0.42
<i>Phvul.010G093200</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // PPR repeat family (PPR_2)	0.71 ±0.44	1.05 ±0.53	0.35 ±0.12	0.5 ±0.09	0.14 ±0.05	1.47 ±0.06	0.34 ±0.13	0.44 ±0.12
<i>Phvul.010G102700</i>	Domain of unknown function	5.13 ±4.51	10.01 ±5.06	0.35 ±0.09	1.21 ±0.27	0.76 ±0.23	14.42 ±0.24	0.88 ±0.18	0.67 ±0.06
<i>Phvul.010G159900</i>	Complement component 1	1.71 ±0.47	1.57 ±0.79	1.61 ±0.13	2.86 ±0.12	0.38 ±0.14	2.71 ±0.31	2.24 ±0.63	2.56 ±0.23

Table S14 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G006400</i>	PPR repeat (PPR) // PPR repeat (PPR_1) // Pentatricopeptide repeat domain (PPR_3)	0.76 ±0.61	1.22 ±0.63	0.35 ±0.1	0.3 ±0.09	0.09 ±0.05	1.89 ±0.47	0.43 ±0.17	0.31 ±0.16
<i>Phvul.011G033200</i>	Uncharacterized conserved protein	17.33 ±14.86	31.63 ±15.82	2.14 ±0.33	3.34 ±0.43	3.89 ±0.36	50.7 ±2.9	2.49 ±0.5	2.87 ±0.54
<i>Phvul.011G060800</i>	PPR repeat (PPR) // Pentatricopeptide repeat domain (PPR_3)	4.09 ±3.06	6.84 ±3.45	0.81 ±0.14	1.69 ±0.33	0.74 ±0.14	11.46 ±2.01	1.29 ±0.63	1.8 ±0.37
<i>Phvul.011G096800</i>	(+)-Borneol dehydrogenase	6.71 ±6.67	14.44 ±7.22	0.06 ±0.03	0.24 ±0.14	0 ±0	26.75 ±6.91	0.38 ±0.38	0.04 ±0.04
XLOC_012819	No functional annotation	1.01 ±0.25	1.85 ±1.09	0.65 ±0.07	2.14 ±1.07	0 ±0	1.63 ±0.96	0.68 ±0.39	0.72 ±0.46
XLOC_012875	No functional annotation	2.38 ±1.9	3.95 ±0.7	2.25 ±0.93	2.51 ±0.06	0.17 ±0.08	2.93 ±0.66	2.66 ±1.19	2.6 ±0.38
XLOC_022362	No functional annotation	1.08 ±0.37	1.1 ±0.55	0.39 ±0.06	0.35 ±0.14	0.12 ±0.04	2.49 ±0.26	0.61 ±0.02	0.42 ±0.17
XLOC_027366	No functional annotation	1.5 ±1.5	2.44 ±1.28	0 ±0	0 ±0	0 ±0	4.6 ±1.28	0 ±0	0 ±0

Table S15. Transcript abundance for genes downregulated in the CBB-susceptible RIL at 8 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G026900</i> , <i>Phvul.005G026966</i>	No functional annotation	0 ± 0	0.69 ± 0.25	0 ± 0	0.23 ± 0.12	0 ± 0	0 ± 0	0.25 ± 0.13	0.72 ± 0.39
<i>Phvul.005G038300</i>	No functional annotation	2.33 ± 1.57	0.76 ± 0.14	0.63 ± 0.63	1.26 ± 0.63	1.21 ± 0.61	0 ± 0	0.69 ± 0.37	0.46 ± 0.46
<i>Phvul.005G071400</i>	γ -Thionin family	0.15 ± 0.15	0.84 ± 0.46	0 ± 0	0.22 ± 0.14	0.16 ± 0.08	0 ± 0	0.05 ± 0.05	0.3 ± 0.22

Table S16. Transcript abundance for genes downregulated in the CBB-susceptible RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G070100</i>	RING-H2 finger protein	0.18	0	0.76	0.63	0.34	0.21	0	0.73
	ATL66	± 0.1	± 0	± 0.47	± 0.21	± 0.19	± 0.12	± 0	± 0.3
<i>Phvul.008G028100</i>	Hyoscyamine (6S)- dioxygenase	0.11 ± 0.08	0.02 ± 0.02	1.32 ± 0.26	0.58 ± 0.11	0.19 ± 0.12	0.17 ± 0.09	0.28 ± 0.16	0.82 ± 0.12

Table S17. Transcript abundance for genes downregulated in the CBB-susceptible RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G246300</i>	Absciscic acid receptor PYL5	0.02 ± 0.02	0.27 ± 0.27	0.83 ± 0.39	2.15 ± 2.01	0 ± 0	0.14 ± 0.05	2.12 ± 1.55	0.3 ± 0.12
<i>Phvul.003G030000</i>	Protein kinase-like protein	2.29 ± 0.91	0.56 ± 0.06	1.02 ± 0.1	8.16 ± 3.2	1.35 ± 0.12	0.63 ± 0.12	1.81 ± 0.51	2 ± 0.73
<i>Phvul.006G001500</i>	Leucine Rich Repeat (LRR_1) / Leucine rich repeat N-terminal domain (LRRNT_2) / Leucine rich repeat (LRR_8)	2.14 ± 0.87	0.86 ± 0.2	0.74 ± 0.03	4.48 ± 2.45	1.81 ± 0.1	0.86 ± 0.03	0.85 ± 0.18	1.1 ± 0.55
<i>Phvul.006G151500</i>	Glucose-6-phosphate/phosphate translocator 1, chloroplastic-related	0.57 ± 0.24	0.48 ± 0.26	0.64 ± 0.06	5.74 ± 4.98	1.62 ± 0.46	0.36 ± 0.08	0.59 ± 0.14	1.13 ± 0.47
<i>Phvul.007G049900</i>	Cysteine-rich receptor-like protein kinase 28-related	0.44 ± 0.06	0.3 ± 0.06	0.12 ± 0.04	1.53 ± 0.94	0.3 ± 0.08	0.2 ± 0.08	0.23 ± 0.1	0.26 ± 0.06
<i>Phvul.009G133500</i>	Expressed protein	6.4 ± 2.13	4.3 ± 2.19	1.48 ± 0.2	12.9 ± 6.97	2.25 ± 0.48	5.3 ± 0.45	2.49 ± 1.52	2.53 ± 1.18
XLOC_020687	No functional annotation	0.26 ± 0.2	0.1 ± 0.1	0.03 ± 0.03	0.61 ± 0.61	0.02 ± 0.02	0.01 ± 0.01	0 ± 0	0 ± 0

Table S18. Transcript abundance for genes downregulated in the CBB-resistant RIL and the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/treatment/sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G085200	A. thaliana mRNA (ORF19) from chromosome 3	673.81 ±649.02	1421.87 ±692.45	50.54 ±7.56	102.02 ±31.39	25.22 ±3.08	1127.76 ±565.04	89.94 ±7.03	76.61 ±34.87
Phvul.001G220100	Cathepsin B / Cathepsin B1	38.09 ±30.52	72.69 ±32.65	8.44 ±0.7	11.63 ±1.79	7.81 ±0.54	64.64 ±29.19	10.46 ±0.36	14.33 ±1.88
Phvul.001G226300	DnaJ homolog subfamily C member	35.58 ±34.81	67.28 ±32.78	1.72 ±0.07	2.06 ±0.2	1 ±0.16	62.46 ±30.26	1.99 ±0.2	1.97 ±0.1
Phvul.001G242900	Protein early flowering 4	129.46 ±127.77	197.2 ±103.54	2.89 ±0.8	2.92 ±0.65	3.13 ±0.16	255.71 ±130.32	3.07 ±0.18	5.29 ±0.5
Phvul.002G018400	CGI-141-related/lipase containing protein	17.92 ±14.52	30.68 ±14.25	2.79 ±0.1	2.49 ±0.33	3.23 ±0.11	33.13 ±15.32	2.75 ±0.51	4.05 ±0.96
Phvul.002G060000	F5O11.5	1.6 ±1.26	3.46 ±1.2	0.62 ±0.09	1.02 ±0.06	0.28 ±0.17	3.07 ±0.98	0.88 ±0.06	0.8 ±0.17
Phvul.002G084700	PPR repeat (PPR) / DYW family of nucleic acid deaminases	1.25 ±0.98	1.97 ±0.99	0.49 ±0.08	0.7 ±0.17	0.3 ±0.03	2.44 ±0.89	0.78 ±0.18	0.75 ±0.03
Phvul.002G093000	DnaJ homolog subfamily C member	11.35 ±10.95	24.98 ±12.45	0.27 ±0.14	0.42 ±0.06	1.11 ±0.36	25.82 ±12.51	0.26 ±0.04	0.46 ±0.15
Phvul.002G096000	Phosphoglucosyltransferase (α-D-glucose-1,6-bisphosphate-dependent) /	51.69 ±47.49	106.02 ±50.3	3.51 ±1.21	2.7 ±0.66	5.14 ±1.47	92.61 ±43.17	4.52 ±0.29	1.96 ±0.79
Phvul.002G110800	Histone H1	54.71 ±36.73	96.22 ±40.15	44.42 ±12.82	75.18 ±8.01	13.22 ±2.49	72.9 ±27.52	54.05 ±6.75	66.25 ±0.73

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G111900</i>	Ferulate-5-hydroxylase	6.47 ±5.44	10.98 ±4.94	2.43 ±0.27	2.72 ±0.43	1.16 ±0.23	10.15 ±4.24	3.11 ±0.42	3.21 ±0.74
<i>Phvul.002G120500</i>	Pentatricopeptide repeat-containing protein	3.3 ±3.04	4.93 ±2.51	0.98 ±0.2	1.63 ±0.54	0.45 ±0.05	4.87 ±2.48	1.18 ±0.14	2.11 ±0.5
<i>Phvul.002G213300</i>	Nicotinamidase	25.61 ±22.74	50.22 ±24.07	5.53 ±0.87	12.77 ±3.23	2.87 ±0.59	38.29 ±17.51	10.34 ±1.3	14.05 ±4.65
<i>Phvul.002G234400</i>	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	22.73 ±19.38	45.78 ±21.63	5.09 ±0.89	5.31 ±0.48	4.8 ±0.55	44.88 ±20.41	6.37 ±1.03	9.32 ±1.41
<i>Phvul.002G263100</i>	No functional annotation	22.45 ±21.56	59.19 ±29.5	1.22 ±0.55	2.14 ±0.96	1.82 ±0.8	56.76 ±29.67	1.26 ±0.18	1.04 ±0.32
<i>Phvul.002G309600</i>	NADP-dependent malic enzyme 1	38.45 ±30.51	68.07 ±29.46	3.79 ±0.2	3.8 ±0.32	7.35 ±0.61	66.17 ±28.94	4.03 ±0.05	5.45 ±0.91
<i>Phvul.002G314000</i> , <i>Phvul.002G314100</i>	Aldehyde dehydrogenase (NAD(P) ⁽⁺⁾)	21.06 ±16.07	30.24 ±11.82	6.98 ±1.49	12.96 ±2.09	4.39 ±1.17	27.98 ±11.11	10.36 ±0.42	20.64 ±3.49
<i>Phvul.002G321800</i>	Flavin-binding Kelch repeat F-box protein 1 (FKF1)	15.55 ±15.12	33.39 ±16.58	0.31 ±0.09	0.43 ±0.12	0.55 ±0.08	28.49 ±14.03	0.26 ±0.03	0.35 ±0.05
<i>Phvul.002G326700</i>	Multidrug resistance protein	36.15 ±33.95	70.22 ±34.17	1.4 ±0.07	0.81 ±0.31	2.62 ±0.7	66.33 ±32.06	1.69 ±0.17	1.08 ±0.18
<i>Phvul.003G004300</i>	Molecular chaperone (DnaJ superfamily)	155.73 ±154.2	300.71 ±151.93	0.57 ±0.25	0.56 ±0.08	1.04 ±0.25	292.06 ±145.9	0.51 ±0.05	0.62 ±0.12
<i>Phvul.003G022000</i>	Clathrin assembly protein	11.24 ±9.98	21.32 ±10.28	1.34 ±0.18	1.56 ±0.24	1.2 ±0.24	21 ±9.95	1.59 ±0.13	3.83 ±0.33

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G044600</i>	Glutamate formimidoyltransferase	5.56 ±4.72	10.78 ±4.86	0.43 ±0.1	0.52 ±0.04	0.83 ±0.14	9.2 ±4.27	0.55 ±0.2	1.32 ±0.55
<i>Phvul.003G124400</i>	Genomic DNA, chromosome 3, P1 clone: MKP6	6.95 ±3.91	13.64 ±3.91	2.45 ±0.21	3.94 ±0.61	1.19 ±0.46	10.09 ±4.73	3.87 ±1.01	5.04 ±1.56
<i>Phvul.003G131400</i>	Germin-like protein subfamily 3	99.16 ±73.9	170.39 ±71.85	0.63 ±0.22	0.35 ±0.08	22.87 ±4.83	222.61 ±104.5	0.41 ±0.13	0.17 ±0.1
<i>Phvul.003G142200</i>	Delta(4)-3-oxosteroid 5-β-reductase	10.54 ±8.09	11.41 ±5.17	1.06 ±0.61	0.72 ±0.46	2.52 ±0.16	13.57 ±6.2	0.76 ±0.18	0.23 ±0.17
<i>Phvul.003G148400</i>	Allergen V5/TPX-1-related family protein-related	23.87 ±20.45	47.11 ±21.25	2.29 ±0.15	2.19 ±0.63	3.26 ±0.52	39.94 ±20.03	4.28 ±0.82	1.29 ±0.25
<i>Phvul.003G198500</i>	RNA-dependent RNA polymerase 2	1.54 ±1.22	2.64 ±1.06	0.8 ±0.02	0.69 ±0.14	0.34 ±0.03	2.03 ±0.79	0.68 ±0.04	0.81 ±0.06
<i>Phvul.003G209600</i>	β-Lactamase / Penicillinase	14.18 ±11.8	24.69 ±11.56	2.38 ±0.48	2.44 ±0.4	3.14 ±0.35	24.46 ±10.62	2.91 ±0.35	2.54 ±0.15
<i>Phvul.003G249200</i>	No functional annotation	4.39 ±3.43	8.39 ±3.65	2.02 ±0.18	2.15 ±0.5	0.92 ±0.22	7.58 ±3.01	2.14 ±0.2	2.38 ±0.49
<i>Phvul.003G295900</i>	No functional annotation	17.81 ± 116.61	266.35 ±133	1.88 ±0.23	3.69 ±1.03	1.73 ±0.19	224.45 ±116.72	2.91 ±0.94	2.76 ±1
<i>Phvul.004G079500</i>	NDH-dependent cyclic electron flow 5	79.39 ±78.23	165.6 ±81.94	1.85 ±0.36	1.69 ±0.33	2.66 ±0.75	151.29 ±73.91	1.94 ±0.2	1.12 ±0.23
<i>Phvul.004G082300</i>	Tyrosine-specific transport protein	11.46 ±9.73	22.22 ±9.87	1.22 ±0.13	1.42 ±0.31	2.61 ±0.51	20.69 ±9.15	1.31 ±0.16	0.97 ±0.18
<i>Phvul.004G088300</i>	Gigantea	23.93 ±23.16	47.96 ±23.68	0.67 ±0.12	0.74 ±0.13	0.67 ±0.12	43.8 ±21.39	0.59 ±0.06	0.61 ±0.09
<i>Phvul.004G106700</i>	Protein of unknown function	171.12 ±161.43	346.79 ±168.52	2.44 ±0.42	2.47 ±0.59	11.26 ±2.33	328.87 ±158.55	2.72 ±0.28	1.78 ±0.51

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.004G114700</i>	Leucine Rich Repeat (LRR_1) // Leucine rich repeat N-terminal domain (LRRNT_2)	1.92 ±1.77	4.08 ±1.98	0.12 ±0.02	0.36 ±0.16	0.18 ±0.04	4.03 ±1.97	0.19 ±0.07	1.06 ±0.28
<i>Phvul.004G119400</i>	No functional annotation	5.11 ±5.11	6.71 ±3.87	0.06 ±0.06	0.03 ±0.03	0 ±0	7.63 ±4	0 ±0	0.03 ±0.03
<i>Phvul.004G133000</i>	Member of 'GDYG' family of lipolytic enzymes	5.21 ±4.28	9.2 ±4.02	0.5 ±0.06	0.82 ±0.3	0.63 ±0.06	8.65 ±3.94	0.5 ±0.11	0.37 ±0.09
<i>Phvul.005G032700</i>	Dirigent protein 20-related	4.95 ±4.02	6.82 ±3.51	4.28 ±0.99	2.44 ±1.24	0.88 ±0.41	6.83 ±2.72	4.83 ±0.65	2.5 ±0.5
<i>Phvul.005G104600</i>	Expansin-B1-related	19.78 ±12.81	30.7 ±11.32	1.64 ±0.81	0.83 ±0.21	4.88 ±0.44	30.78 ±13.32	1.27 ±0.29	0.43 ±0.13
<i>Phvul.005G174000</i>	ATP:ADP antiporter, AAA family	75.56 ±68.63	148.25 ±69.69	4.85 ±0.7	9.78 ±4.25	8.3 ±0.88	151.45 ±71.25	6.78 ±1.08	5.7 ±2.98
<i>Phvul.006G063800</i>	No functional annotation	127.94 ±127.13	259.59 ±130.39	0.38 ±0.05	0.5 ±0.02	0.81 ±0.23	243.41 ±121.35	0.67 ±0.2	0.46 ±0.08
<i>Phvul.006G064100</i>	α-Glucan phosphorylase 2, cytosolic	63.6 ±58.48	130.93 ±62.67	4.14 ±0.18	4.04 ±0.31	5.38 ±0.32	124.56 ±59.83	4.41 ±0.11	3.42 ±0.16
<i>Phvul.006G065300</i>	Phosphomethyl-pyrimidine synthase	420.23 ±409.6	791.06 ±401.32	8.43 ±1.11	7.22 ±0.52	11.08 ±1.84	735.82 ±363.26	9.17 ±0.79	5.64 ±0.85
<i>Phvul.006G067600</i>	Ring finger protein 41, 151	6.45 ±4.79	12.46 ±5.42	2.38 ±0.77	3.97 ±0.85	1.6 ±0.12	10.3 ±4.77	3.14 ±0.62	3.39 ±1.3
<i>Phvul.006G117800</i>	Pre-mRNA 3'-end-processing factor FIP1	0.85 ±0.8	1.4 ±0.66	0.26 ±0.03	0.29 ±0.02	0.2 ±0.06	1.19 ±0.5	0.34 ±0.04	0.39 ±0.12
<i>Phvul.006G146300</i>	Chaperonin-like RBCX protein	74.85 ±73.93	157.04 ±78.76	0.09 ±0.05	0 ±0	0.5 ±0.2	134.64 ±67.26	0.26 ±0.11	0.14 ±0.08

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G151300</i> , <i>Phvul.006G151400</i>	β -Glucosidase 45-related	2.2 ± 1.96	3.76 ± 1.71	0.77 ± 0.23	0.98 ± 0.08	0.31 ± 0.08	3.72 ± 1.62	0.86 ± 0.09	1.5 ± 0.11
<i>Phvul.006G168800</i>	Proprotein convertase subtilisin/Kexin	2.32 ± 2.19	4.33 ± 2	0.28 ± 0.03	0.26 ± 0.01	0.16 ± 0.05	4.2 ± 1.99	0.32 ± 0.03	0.37 ± 0.02
<i>Phvul.006G183600</i>	Dormancy/auxin associated protein (Auxin repressed)	747.6 ± 677.17	1359.88 ± 644.52	178.44 ± 28.08	371.03 ± 80.11	70.19 ± 14.64	1089.32 ± 506.99	334.91 ± 43.67	414.93 ± 126.65
<i>Phvul.006G207600</i>	DnaJ homolog subfamily C member	6.39 ± 6.23	13.67 ± 6.84	0.08 ± 0.08	0.21 ± 0.12	0.32 ± 0.15	12.22 ± 6.8	0.18 ± 0.04	0.14 ± 0.06
<i>Phvul.007G017500</i>	Major facilitator protein	37.19 ± 33.19	64.76 ± 31.02	2.9 ± 0.68	2.29 ± 0.22	3.78 ± 0.12	66.54 ± 31.23	2.93 ± 0.16	3.36 ± 0.35
<i>Phvul.007G021100</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	26.08 ± 26.02	54.9 ± 27.38	0.02 ± 0.01	0.03 ± 0.02	0.15 ± 0.02	50.46 ± 25.12	0.04 ± 0.02	0.04 ± 0.02
<i>Phvul.007G027200</i>	B-box zinc finger (ZF-B_box) // CCT motif (CCT)	15.39 ± 15.36	30.91 ± 15.39	0.05 ± 0.01	0.06 ± 0.01	0.07 ± 0.03	34.99 ± 18.43	0.04 ± 0.01	0.05 ± 0.02
<i>Phvul.007G042100</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	0.76 ± 0.72	1.01 ± 0.5	0.31 ± 0.02	0.46 ± 0.12	0.11 ± 0.03	1.01 ± 0.46	0.26 ± 0.13	0.51 ± 0.1
<i>Phvul.007G074500</i>	Protein REVEILLE 3-related	0.9 ± 0.66	2.52 ± 1.18	0.33 ± 0.06	0.27 ± 0.09	0.1 ± 0.01	1.74 ± 0.62	0.2 ± 0.03	0.14 ± 0.03
<i>Phvul.007G090100</i>	Isoliquiritigenin 2'-O-methyltransferase	3.97 ± 3.54	10.8 ± 4.91	0.59 ± 0.03	0.53 ± 0.16	0.79 ± 0.27	8.71 ± 3.83	0.72 ± 0.07	0.48 ± 0.23
<i>Phvul.007G091400</i>	No functional annotation	26.15 ± 21.24	48.38 ± 22.07	3.42 ± 0.33	2.15 ± 0.55	5.11 ± 0.86	44.15 ± 18.28	2.75 ± 0.18	1.81 ± 0.61

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.007G135000</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	2.08 ±1.67	3.24 ±1.52	0.69 ±0.1	1 ±0.16	0.41 ±0.1	2.9 ±1.24	0.86 ±0.12	0.95 ±0.17
<i>Phvul.007G146900</i>	PPR repeat (PPR) / DYW family of nucleic acid deaminases	0.7 ±0.55	0.96 ±0.51	0.23 ±0.03	0.67 ±0.24	0.09 ±0.07	0.91 ±0.42	0.46 ±0.13	0.65 ±0.14
<i>Phvul.007G150700</i>	Nucleolin	659.01 ±522.58	1095.81 ±480.8	52.02 ±15.09	49.85 ±9.26	147.75 ±23.13	1188.61 ±518.24	45.37 ±6.63	37.61 ±4.16
<i>Phvul.007G214800</i>	Drought responsive ATP-binding motif containing protein	132.58 ±130.8	227.74 ±114.62	0.63 ±0.14	0.83 ±0.16	1.82 ±0.19	248.29 ±123.38	0.6 ±0.11	0.39 ±0.09
<i>Phvul.008G003500</i>	Protein NRT1/ PTR family 6.1	43.52 ±31.97	82.4 ±35.48	2.49 ±0.76	1.98 ±0.18	10.37 ±0.43	76 ±32.89	2.6 ±0.32	1.56 ±0.49
<i>Phvul.008G048400</i>	PPR repeat (PPR) // PPR repeat family (PPR_2)	3.89 ±3.7	8.92 ±4.36	0.58 ±0.03	0.73 ±0.18	0.22 ±0.06	7.6 ±3.69	0.6 ±0.11	0.98 ±0.27
<i>Phvul.008G148100</i>	F-box associated	9.18 ±7.01	19.85 ±8.64	2.08 ±0.59	4.26 ±0.73	1.4 ±0.47	17.56 ±8.07	3.49 ±0.41	4.89 ±1.21
<i>Phvul.008G222000</i>	Outer membrane protein insertion porin family	3.95 ±3.5	8.5 ±4.12	0.34 ±0.04	0.46 ±0.12	0.69 ±0.18	8.15 ±3.87	0.35 ±0.02	0.52 ±0.16
<i>Phvul.008G225600</i>	No functional annotation	11.27 ±10.94	24.89 ±12.45	0.32 ±0.05	0.52 ±0.23	0.43 ±0.08	23.28 ±12.34	0.46 ±0.03	0.31 ±0.08
<i>Phvul.008G264700</i>	Heat shock protein 42	377.21 ±375.45	755.61 ±381.03	3.84 ±0.14	4.27 ±0.64	2.27 ±0.57	632.39 ±314.98	3.17 ±0.51	3.35 ±0.4
<i>Phvul.009G013600</i>	Cathepsin L	319.35 ±293.42	620.61 ±296.82	35.85 ±2.68	45.18 ±3.62	25.05 ±3.35	520.06 ±244.94	43.82 ±2.85	75.51 ±7.52

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G023700</i>	RNA recognition motif	337.38 ± 258.23	632.93 ± 273.95	102.56 ± 4.8	119.21 ± 2	71.38 ± 5.34	570.89 ± 248.86	96.69 ± 1.24	108.65 ± 0.56
<i>Phvul.009G045000</i>	Pseudo-response regulator 5	38.36 ± 36.7	78.8 ± 38.74	2.48 ± 0.31	2.54 ± 0.73	1.73 ± 0.25	64.07 ± 31.22	2.22 ± 0.25	1.76 ± 0.35
<i>Phvul.009G090600</i>	No functional annotation	4.16 ± 4.16	11.68 ± 5.84	0 ± 0	0.19 ± 0.11	0.21 ± 0.16	9.58 ± 4.63	0.14 ± 0.07	0.24 ± 0.04
<i>Phvul.009G152200</i>	Filament-like plant protein 3	15.39 ± 12.56	30.53 ± 13.61	3.18 ± 0.51	4.2 ± 1.07	3.68 ± 0.49	27.16 ± 11.82	4.75 ± 0.24	3.89 ± 1.27
<i>Phvul.009G200900</i>	Protein CHUP1, chloroplastic	13.33 ± 12.42	29.49 ± 14.06	0.67 ± 0.21	0.62 ± 0.2	1.69 ± 0.36	26.17 ± 12.42	0.73 ± 0.08	0.41 ± 0.1
<i>Phvul.009G227100</i>	Cathepsin H	1199.97 ± 1047.1	2176.12 ± 1000.87	382.64 ± 59.87	527.25 ± 40.82	185 ± 36.4	1957.83 ± 870.98	530.82 ± 39.68	786.79 ± 103.79
<i>Phvul.009G227800</i>	Germin-like protein subfamily 3	305.85 ± 284.5	675.53 ± 330.61	0.81 ± 0.15	0.73 ± 0.32	26.41 ± 5.02	656.26 ± 314.65	0.67 ± 0.11	0.34 ± 0.07
<i>Phvul.009G257000</i>	Serine/threonine kinase	1.16 ± 0.71	0.82 ± 0.34	0.32 ± 0.09	0.5 ± 0.06	0.2 ± 0.08	1.32 ± 0.53	0.17 ± 0.05	0.54 ± 0.24
<i>Phvul.010G023700</i>	F21O3.2 protein-related	122.77 ± 114.18	258.19 ± 123.99	10.51 ± 2.75	16.12 ± 3.97	9.41 ± 1.45	228.36 ± 109.62	12.77 ± 2.29	13.68 ± 4.26
<i>Phvul.010G097300</i>	Bestrophin, RFP-TM, chloride channel	8.25 ± 6.43	16.59 ± 7.81	2.56 ± 0.33	2.97 ± 0.23	1.36 ± 0.14	13.53 ± 6.21	2.68 ± 0.35	2.81 ± 0.35
<i>Phvul.010G142600</i>	IAA-amino acid hydrolase ILR1-like 1-related	14.47 ± 12.34	25.98 ± 11.34	3.45 ± 0.36	3.19 ± 0.37	2.34 ± 0.43	27.24 ± 12.42	3.67 ± 0.78	3.89 ± 0.41
<i>Phvul.010G156300</i>	Post-illumination chlorophyll fluorescence increase protein	436.85 ± 403.16	856.03 ± 411.4	28.36 ± 4.08	21.94 ± 0.68	38.45 ± 6.62	769.96 ± 365.62	25.71 ± 3.02	16.25 ± 2.07

Table S18 continued

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.010G164200</i>	Bactericidal permeability-increasing BPI protein-related	8.72 ±7.08	17.53 ±7.85	1.88 ±0.12	2.32 ±0.17	1.47 ±0.13	15.58 ±7.05	1.87 ±0.18	2.66 ±0.35
<i>Phvul.011G045100</i>	Transcription termination factor family protein	9.7 ±8.15	17.84 ±8.09	2.26 ±0.39	1.92 ±0.25	2.28 ±0.05	16.48 ±6.95	2.01 ±0.35	1.47 ±0.17
<i>Phvul.011G050000</i>	Expressed protein	117.31 ±113.92	236.62 ±116.38	3.4 ±0.53	5.45 ±0.84	2.13 ±0.62	197.02 ±97.47	5.4 ±0.91	4.97 ±0.93
<i>Phvul.011G056500</i>	Protein C13C4.7	854.87 ±748.9	1685.46 ±856.19	61.81 ±30.64	30.85 ±13.61	95.55 ±12.36	1542.9 ±722.81	85.04 ±30.12	100.18 ±47.3
<i>Phvul.011G056900</i>	Lysine-specific demethylase 8	11.31 ±11.18	21.71 ±10.78	0.24 ±0.02	0.36 ±0.22	0.28 ±0.12	17.73 ±8.81	0.19 ±0.02	0.27 ±0.08
<i>Phvul.011G062100</i>	MYB-like DNA-binding domain	7.93 ±7.79	13.6 ±6.74	0.31 ±0.1	0.13 ±0.05	0.19 ±0.07	14.21 ±6.84	0.41 ±0.11	0.48 ±0.1
<i>Phvul.011G090500</i>	Nucleobase-ascorbate transporter 12	4.02 ±3.41	9.53 ±4.49	0.53 ±0.05	0.45 ±0.03	0.9 ±0.24	8.59 ±3.97	0.49 ±0.1	0.37 ±0.04
<i>Phvul.011G138600</i>	Anthocyanidin 3- <i>O</i> -glucoside 2"- <i>O</i> -glucosyltransferase	9.51 ±9.13	20.42 ±10.01	0.08 ±0.05	0.2 ±0.05	0.52 ±0.1	17.17 ±8.19	0.28 ±0.12	0.1 ±0.01
<i>Phvul.011G163100</i>	Methyltransferase-like protein 20	3.23 ±2.74	5.06 ±2.64	0.46 ±0.09	0.62 ±0.19	0.44 ±0.04	6.71 ±3.04	0.52 ±0.08	0.54 ±0.07
XLOC_006186	No functional annotation	1.22 ±0.45	1.13 ±0.21	1.16 ±0.55	1.25 ±0.14	0 ±0	2.92 ±2	2.86 ±1.25	4.6 ±2.78

Table S18 continued

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-susceptible RIL									
Phvul.001G085200	A. thaliana mRNA (ORF19) from chromosome iii	935.03 ±885.18	2944.13 ±182.69	63.59 ±7.86	55.38 ±27.46	52.52 ±13.07	3098.13 ±77.18	132.07 ±33.56	70.5 ±13.14
Phvul.001G220100	Cathepsin B / Cathepsin B1	41.42 ±32.81	122.34 ±9.35	8.51 ±0.59	8.9 ±0.96	7.48 ±0.93	122.03 ±5.12	9.93 ±1.44	7.81 ±0.7
Phvul.001G226300	DnaJ homolog subfamily C member	24.86 ±23.39	76.17 ±4	0.56 ±0.18	0.77 ±0.16	0.55 ±0.16	77.9 ±2.37	0.67 ±0.04	0.56 ±0.1
Phvul.001G242900	Protein early flowering 4	122.31 ±116.77	311.07 ±17.44	5.13 ±0.46	4.99 ±1.16	2.32 ±0.42	389.03 ±43.28	5.36 ±0.39	3.96 ±0.5
Phvul.002G018400	CGI-141-related/lipase containing protein	20.13 ±17.49	54.52 ±1.13	2.3 ±0.3	2.17 ±0.18	3.05 ±0.17	60.75 ±1.07	2.51 ±0.29	2.28 ±0.21
Phvul.002G060000	F5O11.5	1.74 ±1.25	3.73 ±0.29	0.7 ±0.18	0.66 ±0.03	0.37 ±0.27	4.09 ±0.75	0.97 ±0.1	0.86 ±0.16
Phvul.002G084700	PPR repeat (PPR)/ DYW family of nucleic acid deaminases	1 ±0.88	2.37 ±0.25	0.43 ±0.11	0.63 ±0.06	0.19 ±0.03	3.08 ±0.32	0.63 ±0.14	0.55 ±0.28
Phvul.002G093000	DnaJ homolog subfamily C member	11.38 ±11.18	34.68 ±0.51	0.2 ±0.06	0.11 ±0.03	0.27 ±0.08	37.1 ±1.66	0.14 ±0.08	0.2 ±0.06
Phvul.002G096000	Phosphoglucumutase	45.04 ±42.34	146.65 ±9.64	1.07 ±0.23	1.25 ±0.32	3.91 ±1.02	147.06 ±4.52	1.91 ±0.47	1.76 ±0.05
Phvul.002G110800	Histone H1	75.93 ±58.69	200.11 ±8.89	25.55 ±1.65	47.53 ±9.6	11.28 ±2.69	186.45 ±8.46	43.79 ±13.25	33.29 ±8.39
Phvul.002G111900	Ferulate-5-hydroxylase	6.78 ±5.76	17.19 ±0.53	2.77 ±0.49	3.14 ±0.35	1.25 ±0.38	19.06 ±1.25	3.11 ±0.22	2.98 ±0.25
Phvul.002G120500	Pentatricopeptide repeat-containing protein	2.91 ±2.67	8.16 ±0.49	0.84 ±0.14	1.5 ±0.18	0.38 ±0.07	9.4 ±0.8	1.27 ±0.35	1.07 ±0.44

Table S18 continued

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G213300</i>	Nicotinamidase / Nicotine deamidase	29.79 ±27.15	88.23 ±14.82	3.22 ±0.36	7.44 ±1.72	1.97 ±0.6	93.3 ±1.99	10.02 ±3.72	5.93 ±0.82
<i>Phvul.002G234400</i>	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	21.53 ±18.42	65 ±4.38	3.33 ±0.58	5.42 ±1.4	4.28 ±0.37	65.04 ±2.89	5.71 ±1.48	5.46 ±0.79
<i>Phvul.002G263100</i>	No functional annotation	23.71 ±22	69.17 ±2.63	1.31 ±0.43	1.17 ±0.24	1.4 ±0.19	80.84 ±3.27	0.85 ±0.02	0.72 ±0.23
<i>Phvul.002G309600</i>	NADP-dependent malic enzyme 1	36.83 ±29.7	96.67 ±3.23	3.74 ±0.25	3.35 ±0.18	8.48 ±0.54	99.21 ±1.24	3.97 ±0.64	3.42 ±0.28
<i>Phvul.002G314000</i> , <i>Phvul.002G314100</i>	Aldehyde dehydrogenase (NAD(P) ⁽⁺⁾)	17.27 ±12.96	43.69 ±2.83	5.03 ±0.38	11.72 ±0.33	2.86 ±0.41	41.69 ±3.94	11.09 ±4.89	7.69 ±2.24
<i>Phvul.002G321800</i>	Flavin-binding kelch repeat F-box protein 1	18.12 ±17.59	51.53 ±1.5	0.09 ±0.02	0.14 ±0.02	0.19 ±0.06	51.07 ±2.45	0.16 ±0.06	0.08 ±0.02
<i>Phvul.002G326700</i>	Multidrug resistance protein	32 ±30.11	97.94 ±7.52	0.89 ±0.09	0.96 ±0.31	1.65 ±0.53	104.43 ±4.41	0.86 ±0.11	0.92 ±0.12
<i>Phvul.003G004300</i>	Molecular chaperone (DnaJ superfamily)	118.59 ±115.54	353.86 ±14.75	0.81 ±0.22	1.3 ±0.39	1.59 ±0.24	436.85 ±38.77	0.65 ±0.05	0.81 ±0.14
<i>Phvul.003G022000</i>	Clathrin assembly protein	10.92 ±9.31	29.33 ±1.26	0.97 ±0.21	2.52 ±0.68	1.61 ±0.2	32.74 ±4.51	1.35 ±0.31	1.3 ±0.05
<i>Phvul.003G044600</i>	Glutamate formimidoyltransferase	3.63 ±2.64	8.6 ±0.38	0.41 ±0.15	0.28 ±0.05	0.61 ±0.05	9.15 ±0.98	0.25 ±0.14	0.53 ±0.06
<i>Phvul.003G124400</i>	Genomic DNA, chromosome 3, P1 clone: MKP6	8.81 ±5.68	18.75 ±1.07	1.87 ±0.45	2.9 ±0.8	1.23 ±0.41	18.06 ±1.14	3.41 ±0.52	3.48 ±1.18

Table S18 continued

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G131400</i>	Germin-like protein subfamily 3	76.08 ±69.28	149.08 ±34.8	0.54 ±0.03	0.05 ±0.02	7.82 ±1.52	158.5 ±17.37	0.35 ±0.05	0.44 ±0.19
<i>Phvul.003G142200</i>	Δ(4)-3-oxosteroid 5-β-reductase	4.83 ±3.78	14.48 ±3.75	0.7 ±0.09	0.43 ±0.16	1.2 ±0.42	16.2 ±3.53	0.96 ±0.07	0.94 ±0.47
<i>Phvul.003G148400</i>	Allergen V5/TPX-1-related family protein-related	15.43 ±11.05	32.42 ±5.55	2.18 ±0.57	1.5 ±0.33	2.76 ±0.69	37.27 ±5.54	6.97 ±4.72	5.84 ±3.94
<i>Phvul.003G198500</i>	RNA-dependent RNA polymerase 2	1.21 ±0.83	3.15 ±0.27	0.64 ±0.05	0.8 ±0.13	0.28 ±0.03	3.2 ±0.13	0.63 ±0.16	0.46 ±0.05
<i>Phvul.003G209600</i>	β-lactamase / Penicillinase	12.49 ±10.61	33.23 ±1.48	1.78 ±0.21	2.01 ±0.38	2.18 ±0.3	36.52 ±1.72	2.21 ±0.53	1.85 ±0.16
<i>Phvul.003G249200</i>	No functional annotation	4.46 ±3.66	12.45 ±0.5	1.5 ±0.16	2.03 ±0.42	0.7 ±0.27	11.53 ±0.97	1.99 ±0.63	1.89 ±0.33
<i>Phvul.003G295900</i>	No functional annotation	115.33 ±112.76	383.84 ±30.19	1.77 ±0.31	1.62 ±0.08	1.72 ±0.35	453.7 ±20.73	1.78 ±0.5	1.5 ±0.15
<i>Phvul.004G079500</i>	NDH-dependent cyclic electron flow 5	71.39 ±70	218 ±0.83	0.81 ±0.14	0.73 ±0.02	1 ±0.08	232.96 ±2.38	0.88 ±0.13	0.84 ±0.29
<i>Phvul.004G082300</i>	Tyrosine-specific transport protein	12.24 ±9.34	32.77 ±2.32	1.47 ±0.28	1.32 ±0.23	2.39 ±0.22	34.58 ±0.8	1.3 ±0.22	1.34 ±0.15
<i>Phvul.004G088300</i>	Gigantea (GI)	24.15 ±23.04	71.62 ±1.96	0.6 ±0.04	0.8 ±0.29	1.06 ±0.1	76.31 ±0.81	0.5 ±0.05	0.65 ±0.06
<i>Phvul.004G106700</i>	Protein of unknown function	148.43 ±139.46	446.06 ±4.75	2.88 ±0.27	2.24 ±0.08	9.12 ±0.33	486.81 ±17.67	3.08 ±0.24	2.99 ±0.38
<i>Phvul.004G114700</i>	Leucine Rich Repeat (LRR_1) // Leucine rich repeat N-terminal domain (LRRNT_2)	1.77 ±1.5	4.69 ±0.51	0.13 ±0.02	0.99 ±0.64	0.12 ±0.05	5.47 ±0.38	0.23 ±0.09	0.38 ±0.2
<i>Phvul.004G119400</i>	No functional annotation	2.5 ±2.51	8.97 ±1.2	0 ±0	0 ±0	0 ±0	11.53 ±1.18	0 ±0	0 ±0

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.004G133000</i>	Member of 'GDYG' family of lipolytic enzymes	5.72 ±5.39	19.11 ±1	0.39 ±0.06	0.31 ±0.12	0.51 ±0.25	18.09 ±1.38	0.17 ±0.07	0.59 ±0.13
<i>Phvul.005G032700</i>	Dirigent protein 20-related	2.73 ±1.73	5.94 ±0.34	0.91 ±0.08	0.59 ±0.05	0.6 ±0.15	5.58 ±0.52	1 ±0.12	0.65 ±0.09
<i>Phvul.005G104600</i>	Expansin-B1-related	20.15 ±15.15	31.57 ±6.85	2.43 ±0.46	0.66 ±0.21	4.39 ±0.59	24.97 ±4.26	1.77 ±0.2	1.65 ±0.4
<i>Phvul.005G174000</i>	ATP:ADP antiporter, AAA family	72.19 ±62.22	193.57 ±6.07	4.81 ±0.94	5.43 ±2.78	10.28 ±1.03	210.12 ±4.85	8.02 ±1.94	4.36 ±1.2
<i>Phvul.006G063800</i>	No functional annotation	109.07 ±107.01	311.04 ±14.3	0.63 ±0.16	0.33 ±0.13	1.21 ±0.22	355.65 ±6.16	0.47 ±0.01	0.46 ±0.03
<i>Phvul.006G064100</i>	α-Glucan phosphorylase 2, cytosolic	51.9 ±46.54	159.27 ±7.81	4.3 ±0.16	3.99 ±0.56	5.2 ±0.24	171.81 ±1.85	4.05 ±0.23	3.72 ±0.38
<i>Phvul.006G065300</i>	Phosphomethyl-pyrimidine synthase	335.18 ±321.36	990.33 ±18.39	5.27 ±0.53	4.79 ±0.69	9.7 ±0.35	1117.41 ±41.12	6.23 ±0.31	5.54 ±0.4
<i>Phvul.006G067600</i>	Ring finger protein 41, 151	8.21 ±6.93	23.81 ±2.98	2.07 ±0.4	2.04 ±0.67	1.65 ±0.12	26.18 ±1.59	2.55 ±1.05	1.93 ±0.2
<i>Phvul.006G117800</i>	Pre-mRNA 3'-end-processing factor FIP1 (FIP1L1, FIP1)	0.88 ±0.72	1.98 ±0.23	0.24 ±0.08	0.18 ±0.03	0.08 ±0.02	2.31 ±0.25	0.27 ±0.01	0.3 ±0.05
<i>Phvul.006G146300</i>	Chaperonin-like RBCX protein	60.05 ±57.54	188.11 ±1.23	0.19 ±0.05	0.21 ±0.03	0.89 ±0.13	220.61 ±17.82	0.03 ±0.03	0.12 ±0.08
<i>Phvul.006G151300</i> , <i>Phvul.006G151400</i>	β-glucosidase 45-related	3.22 ±2.72	9.85 ±0.6	0.9 ±0.17	0.94 ±0.17	0.49 ±0.1	10.06 ±1.37	1.32 ±0.39	1.18 ±0.38
<i>Phvul.006G168800</i>	Proprotein convertase subtilisin/kexin	2.94 ±2.68	8.19 ±0.17	0.37 ±0.02	0.35 ±0.01	0.22 ±0.09	8.08 ±0.13	0.26 ±0.04	0.37 ±0.07

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.006G183600</i>	Dormancy/auxin associated protein (Auxin repressed)	858.7 ±781.6	2585.37 ±142.81	142.07 ±27.12	174.1 ±54.63	72.73 ±11.27	2563.23 ±122.83	283.78 ±117.96	176.72 ±22.55
<i>Phvul.006G207600</i>	DnaJ homolog subfamily C member	6.94 ±6.69	19.4 ±1.46	0.1 ±0.01	0.24 ±0.24	0.22 ±0.12	20.76 ±1.44	0.17 ±0.09	0.36 ±0.13
<i>Phvul.007G017500</i>	Major facilitator protein	35.33 ±29.92	98.92 ±6.14	3.73 ±0.3	3.15 ±0.8	4.93 ±0.46	116.81 ±10.78	2.97 ±0.27	3.02 ±0.26
<i>Phvul.007G021100</i>	PPR repeat (PPR) // PPR repeat family (PPR 2)	24.51 ±24.12	72.7 ±3.14	0.07 ±0.03	0.04 ±0.02	0.1 ±0.05	78.12 ±3.04	0.01 ±0.01	0.04 ±0.02
<i>Phvul.007G027200</i>	B-box zinc finger (ZF-B box) // CCT motif	15.47 ±15.33	44 ±1.93	0.06 ±0.03	0.06 ±0.03	0.14 ±0.09	60.23 ±4.64	0.13 ±0.05	0.03 ±0.01
<i>Phvul.007G042100</i>	PPR repeat (PPR) // PPR repeat family (PPR 2)	0.71 ±0.61	1.33 ±0.16	0.22 ±0.1	0.49 ±0.13	0.11 ±0.03	1.62 ±0.31	0.17 ±0.11	0.41 ±0.14
<i>Phvul.007G074500</i>	Protein REVEILLE 3-related	1.23 ±1.07	3.29 ±0.61	0.26 ±0.08	0.23 ±0.03	0.16 ±0.07	3.14 ±0.21	0.27 ±0.05	0.18 ±0.03
<i>Phvul.007G090100</i>	Isoliquiritigenin 2'-O-methyltransferase	2.91 ±2.46	11.69 ±1.48	0.28 ±0.02	0.1 ±0.02	0.42 ±0.16	11.41 ±1.57	0.39 ±0.13	0.27 ±0.09
<i>Phvul.007G091400</i>	No functional annotation	19.85 ±13.38	47.64 ±1.25	3.48 ±0.45	2.51 ±0.49	4.96 ±1.06	57.18 ±8.72	2.22 ±0.45	3.1 ±0.55
<i>Phvul.007G135000</i>	PPR repeat (PPR) // PPR repeat family (PPR 2)	1.68 ±1.41	4.79 ±0.26	0.61 ±0.11	0.74 ±0.15	0.29 ±0.01	5.15 ±0.55	0.56 ±0.17	0.76 ±0.24
<i>Phvul.007G146900</i>	PPR repeat (PPR) / (DYW deaminase)	0.75 ±0.35	1.18 ±0.59	0.21 ±0.12	0.66 ±0.2	0.1 ±0.04	1.61 ±0.27	0.32 ±0.01	0.35 ±0.14
<i>Phvul.007G150700</i>	Nucleolin (NCL, NSR1)	509.71 ±447.24	923.43 ±461.93	35.49 ±4.77	35.08 ±7.33	92.09 ±3.71	1462.25 ±49.26	34.6 ±4.82	39.54 ±8.43

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.007G214800</i>	Drought responsive ATP-binding motif containing protein	81.55 ±78.7	162.28 ±81.17	0.75 ±0.25	0.96 ±0.15	1.48 ±0.35	299.22 ±21.15	0.75 ±0.14	0.71 ±0.12
<i>Phvul.008G003500</i>	Protein NRT1/ PTR family 6.1	46.9 ±37.25	86.77 ±43.54	2.18 ±0.16	1.54 ±0.24	9.72 ±0.21	133.09 ±1.26	2.75 ±0.29	2.19 ±0.32
<i>Phvul.008G048400</i>	PPR repeat (PPR) // PPR repeat family (PPR 2)	4.67 ±4.37	8.72 ±4.36	0.32 ±0.05	0.67 ±0.2	0.22 ±0.05	13.58 ±0.68	0.39 ±0.18	0.5 ±0.16
<i>Phvul.008G148100</i>	F-box associated (FBA 1) // F-box-like	11.04 ±9.08	20.6 ±10.3	2.05 ±0.15	2.57 ±0.23	1.92 ±0.43	32.6 ±0.35	2.45 ±0.57	3.13 ±0.7
<i>Phvul.008G222000</i>	Outer membrane protein insertion porin family (SAM50, TOB55, BamA)	3.94 ±3.55	8.36 ±4.19	0.44 ±0.06	0.41 ±0.05	0.44 ±0.01	13.35 ±0.71	0.35 ±0.08	0.36 ±0.08
<i>Phvul.008G225600</i>	No functional annotation	10.45 ±9.95	19.35 ±9.68	0.3 ±0.05	0.33 ±0.03	0.34 ±0.13	37.37 ±2.59	0.39 ±0.09	0.39 ±0.1
<i>Phvul.008G264700</i>	Heat shock protein 42	328.92 ±321.83	699.76 ±350.95	1.31 ±0.21	1.87 ±0.1	3.26 ±0.38	1194.12 ±95.48	1.82 ±0.51	1.79 ±0.25
<i>Phvul.009G013600</i>	Cathepsin L	323.57 ±288.69	654.49 ±333.05	23.02 ±2.99	32.49 ±3.68	30.87 ±5.55	1051.09 ±36.36	33.45 ±8.51	29.51 ±6.9
<i>Phvul.009G023700</i>	RNA recognition motif	299.87 ±237.27	556.6 ±278.53	70.22 ±2.26	71.01 ±2.57	61.72 ±3.52	835.11 ±9.23	74.65 ±1.89	72.97 ±3.57
<i>Phvul.009G045000</i>	Pseudo-response regulator 5 (PRR5)	44.99 ±41.6	81.96 ±41.04	3.1 ±0.41	2.53 ±0.37	3.51 ±0.41	131 ±3.9	3.2 ±0.09	2.61 ±0.46
<i>Phvul.009G090600</i>	No functional annotation	8.14 ±7.85	16.29 ±8.34	0.22 ±0.12	0.26 ±0.09	0.55 ±0.09	28.75 ±1.47	0.16 ±0.05	0.49 ±0.17

Table S18 continued

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G152200</i>	Filament-like plant protein 3	16.13 ±13.48	28.43 ±14.22	3.51 ±0.19	3.18 ±0.96	3.34 ±0.41	45.77 ±1.33	5.23 ±0.88	3.71 ±0.39
<i>Phvul.009G200900</i>	Protein CHUP1, chloroplastic	11.88 ±11.37	23.27 ±11.64	0.35 ±0.03	0.22 ±0.04	0.76 ±0.14	37.34 ±3.19	0.59 ±0.06	0.55 ±0.05
<i>Phvul.009G227100</i>	Cathepsin H (CTSH)	1190.97 ±1009.11	2332 ±1176.28	270.03 ±35.48	502.68 ±85.24	213.99 ±49.55	3821.31 ±225.14	450.49 ±139.55	437.93 ±166.38
<i>Phvul.009G227800</i>	Germin-like protein subfamily 3	301.5 ±287.71	565.99 ±283.69	0.87 ±0.3	0.51 ±0.09	16.86 ±3.38	876.11 ±87	1.23 ±0.68	0.99 ±0.45
<i>Phvul.009G257000</i>	Serine/threonine kinase	0.82 ±0.47	1.07 ±0.54	0.19 ±0.09	0.31 ±0.12	0.13 ±0.03	1.51 ±0.19	0.23 ±0.08	0.22 ±0.1
<i>Phvul.010G023700</i>	F21O3.2 protein-related	126.49 ±115.58	248.01 ±124.1	10.49 ±1.21	10.4 ±3.37	12.9 ±2.59	416.16 ±10.84	14.67 ±2.62	11.99 ±0.75
<i>Phvul.010G097300</i>	Bestrophin, RFP-TM, chloride channel	7.87 ±6.69	15.25 ±7.75	2.23 ±0.39	2.62 ±0.24	1.41 ±0.07	22.22 ±1.2	1.84 ±0.25	2.2 ±0.42
<i>Phvul.010G142600</i>	IAA-amino acid hydrolase ILR1-like 1-related	13.29 ±9.9	23.02 ±11.55	2.84 ±0.21	3.06 ±0.64	2.71 ±0.42	34.53 ±0.54	3.53 ±0.23	3.01 ±0.22
<i>Phvul.010G156300</i>	Post-illumination chlorophyll fluorescence increase protein	386.94 ±348.79	777.68 ±389.57	25.44 ±1.6	23.7 ±5.09	33.47 ±4.72	1328.07 ±70.19	24.09 ±3.13	26.1 ±2.39
<i>Phvul.010G164200</i>	Bactericidal permeability-increasing BPI protein-related	9.01 ±7.97	17.27 ±8.69	0.77 ±0.16	1.09 ±0.3	1.29 ±0.21	25.48 ±0.66	1 ±0.08	1.22 ±0.05
<i>Phvul.011G045100</i>	Transcription termination factor family protein	7.77 ±6.36	14.17 ±7.09	1.4 ±0.13	1.63 ±0.16	1.72 ±0.1	22.9 ±0.38	1.73 ±0.23	1.63 ±0.23

Table S18 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.011G050000</i>	Expressed protein	109.56 ± 105.68	229.68 ±114.9	1.6 ±0.44	2 ±0.43	1.69 ±0.21	414.39 ±12.14	1.74 ±0.62	1.87 ±0.36
<i>Phvul.011G056500</i>	Protein C13C4.7	719.9 ±634.74	1522.89 ±785.77	26.43 ±8.04	32.64 ±6.7	97.19 ±13.01	2329.47 ±175.92	45.69 ±2.36	52.99 ±6.9
<i>Phvul.011G056900</i>	Lysine-specific demethylase 8 (KDM8, JMJD5)	8.53 ±8.27	19.03 ±9.64	0.16 ±0.03	0.16 ±0	0.2 ±0.08	29.43 ±2.03	0.34 ±0.08	0.19 ±0.03
<i>Phvul.011G062100</i>	MYB-like DNA-binding domain	7.43 ±7.07	12.79 ±6.4	0.3 ±0.1	0.24 ±0.02	0.37 ±0.03	21.99 ±2.2	0.2 ±0.06	0.39 ±0.06
<i>Phvul.011G090500</i>	Nucleobase-ascorbate transporter 12	4.25 ±3.83	7.84 ±3.96	0.23 ±0.01	0.37 ±0.1	0.56 ±0.1	12.39 ±0.68	0.35 ±0.1	0.37 ±0.02
<i>Phvul.011G138600</i>	Anthocyanidin 3- <i>O</i> -glucoside 2"- <i>O</i> -glucosyltransferase	9.09 ±8.57	22.87 ±12.41	0.09 ±0.05	0.1 ±0	0.55 ±0.08	35.3 ±2.56	0.23 ±0.06	0.14 ±0
<i>Phvul.011G163100</i>	Methyltransferase-like protein 20	3.19 ±2.89	4.79 ±2.41	0.49 ±0.06	0.4 ±0.08	0.37 ±0.11	6.83 ±2.1	0.34 ±0.18	0.72 ±0.25
XLOC_006186	No functional annotation	2.82 ±2.62	7.26 ±1.94	0 ±0	0 ±0	0 ±0	10.03 ±1.86	0 ±0	0 ±0

Table S19. Transcript abundance for genes upregulated in the CBB-resistant RIL and the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G157500	Prenylated RAB acceptor 1-related	4.13 ± 1.36	4.92 ±1.11	0.8 ±0.12	0.42 ±0.05	17.7 ±4.15	6.11 ±3.13	0.59 ±0.03	0.4 ±0.05
Phvul.002G077400	Glycosyltransferase 8 domain-containing protein	18.37 ± 3.15	16.06 ±2.06	11.62 ±1.2	9.79 ±0.6	79.39 ±4.49	35.96 ±21.52	13.35 ±2.01	12.71 ±4.3
Phvul.002G142600	No functional annotation	0.5 ± 0.16	0.53 ±0.06	0.63 ±0.1	0.71 ±0.14	2.62 ±0.98	0.79 ±0.47	0.68 ±0.17	0.68 ±0.16
Phvul.003G052400	Xyloglucan endotransglucosylase/ Hydrolase protein 33-related	1.8 ± 0.48	1.83 ±0.42	0.9 ±0.64	0.8 ±0.13	9.76 ±1.8	3.5 ±1.46	1.28 ±0.62	0.58 ±0.24
Phvul.003G053700	No functional annotation	15.23 ± 7.28	10.02 ±6.14	4.7 ±2.22	3.65 ±2.41	77.08 ±15.07	17.73 ±14.67	4.21 ±1.63	2.13 ±1.2
Phvul.003G137600	Xyloglucan:xyloglucosyl transferase	5.41 ± 2.91	5.45 ±2.22	8.27 ±5.31	6.26 ±1.05	32.13 ±6.5	9.41 ±5.78	7.95 ±2.12	8.15 ±0.85
Phvul.003G147600	Xyloglucan endotransglucosylase / Hydrolase protein 25-related	0.8 ± 0.06	1.13 ±0.42	0.52 ±0.25	0.47 ±0.15	11.91 ±4.18	4.17 ±2.98	0.96 ±0.44	1.03 ±0.83
Phvul.003G147700	Xyloglucan endotransglucosylase/ hydrolase protein 25-related	7.13 ± 3.17	15.38 ±5.48	6.94 ±6.66	0.67 ±0.21	68.16 ±9.84	25.49 ±10.15	2.37 ±1.37	1.07 ±0.4
Phvul.003G205700	Plant protein of unknown function	1.14 ± 0.31	1.11 ±0.36	1.11 ±0.21	1.06 ±0.18	5.45 ±0.78	1.95 ±1.11	1.14 ±0.08	0.59 ±0.21

Table S19 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G238200</i>	Lysine-rich arabinogalactan protein 17-related	119.22 ±42.68	94.18 ±35.61	38.48 ±10.12	28.2 ±4.76	477.75 ±77.64	165.36 ±97.56	47.37 ±8.63	14.72 ±2.98
<i>Phvul.005G084800</i>	No functional annotation	8.36 ± 1.96	6.65 ±0.95	5.89 ±0.54	8.47 ±0.97	36.09 ±2.68	15.69 ±10.9	8.54 ±0.48	8.79 ±2.52
<i>Phvul.005G099500</i>	Fasciclin-like arabinogalactan protein 13-related	31.25 ±15.62	25.2 ±8.07	9.81 ±6.34	3.75 ±0.75	152.7 ±18.65	53.35 ±33.94	6.03 ±2.16	2.25 ±0.54
<i>Phvul.007G110600</i>	Phosphate-induced protein 1 conserved region	24.39 ± 6.67	24.71 ±3.24	10.77 ±4.52	8.86 ±1.25	129.74 ±24.32	48.91 ±26.67	10.04 ±1.69	5.77 ±1.59
<i>Phvul.007G186500</i>	Protein NDRG1	12.49 ± 6.91	11.65 ±4.1	5.58 ±3.73	2.76 ±0.59	56.73 ±8.97	15.46 ±9.08	3.38 ±1.03	1.56 ±0.52
<i>Phvul.007G215200</i>	T14P4.7 Protein	5.58 ± 0.96	6.66 ±0.66	2.57 ±0.36	2.26 ±0.12	36.17 ±9.53	11.07 ±5.4	2.57 ±0.46	2.66 ±0.57
<i>Phvul.008G175700</i>	Phosphate-induced protein 1 protein, putative-related	1.11 ± 0.42	0.95 ±0.28	0.58 ±0.21	0.92 ±0.2	7.23 ±1.61	3.67 ±2.93	1.17 ±0.42	0.95 ±0.7
<i>Phvul.009G032100</i>	Phosphate-induced protein 1 protein, putative-related	6.63 ± 1.36	10.4 ±2.92	5.56 ±2.36	6.44 ±1.02	39.58 ±10.76	15.06 ±5.11	6.64 ±2.47	6.48 ±0.31
<i>Phvul.009G173000</i>	Plant protein of unknown function	1.52 ± 0.37	1.98 ±0.35	1 ±0.26	0.65 ±0.16	6.96 ±1.42	2.9 ±1.02	0.89 ±0.12	0.55 ±0.23
<i>Phvul.009G180401</i>	No functional annotation	24.48 ± 5.81	28.35 ±3.88	10.49 ±5.7	13.65 ±1.87	118.55 ±13.45	55.15 ±27.47	13.86 ±2.94	11.76 ±0.96
<i>Phvul.011G024801</i>	Expansin-like A1-related	12.74 ± 2.3	14.6 ±1.08	7.36 ±2.22	8.12 ±0.57	90.05 ±9.32	37.46 ±22.68	16.41 ±5.03	15.99 ±6.32
<i>Phvul.011G055600</i>	No functional annotation	3.7 ± 1.33	2.11 ±0.57	4.04 ±0.5	4.4 ±0.35	16.08 ±3.42	4.51 ±2.81	6.76 ±1.88	3.9 ±1.13
<i>Phvul.011G214200</i>	AXI 1 protein-like protein	1.22 ± 0.45	1.13 ±0.21	1.16 ±0.55	1.25 ±0.14	8.41 ±1.14	2.92 ±2	2.86 ±1.25	4.6 ±2.78

Table S19 continued

Table S13 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-susceptible RIL									
Phvul.001G157500	Prenylated RAB acceptor 1-related	1.59 ±0.38	3.17 ±0.29	0.59 ±0.05	0.48 ±0.15	7.08 ±3.18	2.64 ±0.32	0.49 ±0.25	0.98 ±0.46
Phvul.002G077400	Glycosyltransferase 8 domain-containing protein	14.98 ±1.7	13.44 ±0.69	11.34 ±0.62	10.22 ±1.4	78.62 ±9.1	14.98 ±1.61	10.08 ±1.33	13.56 ±3.01
Phvul.002G142600	No functional annotation	0.67 ±0.15	0.58 ±0.06	0.54 ±0.19	0.58 ±0.16	4.38 ±1.88	0.46 ±0.05	0.86 ±0.1	0.71 ±0.29
Phvul.003G052400	Xyloglucan endotransglucosylase/ Hydrolase protein 33-related	1.28 ±0.18	1 ±0.02	1.05 ±0.42	0.52 ±0.2	14.05 ±6.65	1.33 ±0.22	0.99 ±0.28	1.58 ±1
Phvul.003G053700	No functional annotation	6.85 ±2.68	3.72 ±0.4	3.56 ±1.15	3.08 ±1.82	55.77 ±16.33	1.59 ±0.59	2.07 ±0.69	6.55 ±2.48
Phvul.003G137600	Xyloglucan:xyloglucosyl transferase / Xyloglucan endotransglycosylase	4.49 ±1.44	3.04 ±0.66	5.42 ±1.81	4.69 ±1.11	29.24 ±12.62	2.8 ±0.12	4.32 ±0.64	6.07 ±2.86
Phvul.003G147600	Xyloglucan endotransglucosylase/hydr olase protein 25-related	0.48 ±0.36	0.94 ±0.08	0.27 ±0.1	0.39 ±0.23	9.75 ±3.41	0.83 ±0.2	0.13 ±0.03	1.23 ±1.03
Phvul.003G147700	Xyloglucan endotransglucosylase/hydr olase protein 25-related	4.87 ±3.89	14.79 ±2.47	1.02 ±0.63	0.78 ±0.35	60.41 ±32.59	19.46 ±4.54	0.33 ±0.08	1.55 ±1.22
Phvul.003G205700	Plant protein of unknown function	1.21 ±0.35	0.67 ±0.09	1.66 ±0.22	1.11 ±0.09	5.43 ±0.58	0.8 ±0.1	1.71 ±0.1	1.03 ±0.33
Phvul.003G238200	Lysine-rich arabinogalactan protein 17-related	81.15 ±12.66	52.32 ±5.65	50.42 ±15.18	16.49 ±2.31	448.18 ±162.03	45.52 ±4.8	41.58 ±4.47	48.26 ±15.5
Phvul.005G084800	No functional annotation	6.87 ±0.57	5.76 ±0.65	5.88 ±0.77	7.44 ±0.62	29.93 ±4.77	5.81 ±0.14	5.9 ±0.33	8.61 ±2.42

Table S19 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.005G099500</i>	Fasciclin-like arabinogalactan protein 13-related	11.68 ±2.78	10.84 ±1.84	5.88 ±3.34	1.67 ±0.45	121.41 ±56.13	10.32 ±1.85	3.91 ±0.99	4.95 ±1.87
<i>Phvul.007G110600</i>	Phosphate-induced protein 1 conserved region	16.55 ±2.49	20.82 ±0.91	7.69 ±1.12	6.4 ±1.15	129.75 ±29.88	20.2 ±2.74	8.63 ±1.64	8.68 ±3.13
<i>Phvul.007G186500</i>	Protein NDRG1	5.69 ±0.99	3.63 ±1.85	3.4 ±1.56	1.43 ±0.31	55.95 ±30.64	5.54 ±0.43	2.35 ±0.13	2.55 ±0.78
<i>Phvul.007G215200</i>	T14P4.7 Protein	4.36 ±0.46	3.21 ±1.63	2.67 ±0.62	2.19 ±0.46	46.18 ±25.34	5.11 ±0.44	2.28 ±0.48	2.49 ±0.28
<i>Phvul.008G175700</i>	Phosphate-induced protein 1 protein, putative-related	0.54 ±0.23	0.4 ±0.23	0.38 ±0.17	0.81 ±0.34	5.16 ±1.26	0.64 ±0.18	0.31 ±0.1	1.41 ±0.83
<i>Phvul.009G032100</i>	Phosphate-induced protein 1 protein, putative-related	6.13 ±2.57	8.84 ±4.42	3.79 ±1.3	2.2 ±0.43	44.35 ±14.54	14.04 ±1.14	3.69 ±0.43	4.62 ±1.17
<i>Phvul.009G173000</i>	Plant protein of unknown function	1.21 ±0.35	0.94 ±0.48	0.73 ±0.17	0.63 ±0.18	7.26 ±1.45	1.82 ±0.19	0.8 ±0.09	0.66 ±0.25
<i>Phvul.009G180401</i>	No functional annotation	14.72 ±5.68	17.23 ±8.63	6.6 ±1.76	7.88 ±1.11	101.24 ±16.05	32.66 ±3.07	9.12 ±1.47	9.86 ±1.52
<i>Phvul.011G024801</i>	Expansin-like A1-related	8.57 ±1.7	8.74 ±4.63	7.46 ±1.13	9.51 ±3.99	78.03 ±18.75	13.97 ±0.5	7.28 ±0.73	15.43 ±8.07
<i>Phvul.011G055600</i>	No functional annotation	2.46 ±0.62	1.08 ±0.55	2.3 ±0.17	2.11 ±0.4	14.09 ±5.1	1.54 ±0.21	2.27 ±0.13	5.84 ±3.59
<i>Phvul.011G214200</i>	AXI 1 protein-like protein	0.91 ±0.12	0.48 ±0.25	0.81 ±0.13	1.99 ±1.13	7.93 ±3.03	0.76 ±0.07	0.86 ±0.18	2.36 ±1.41

Table S20. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and 8 h thereafter. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G147400</i>	Xyloglucan endotransglucosylase/ Hydrolase protein 25-related	1.06 ± 0.5	0.12 ± 0.07	0.12 ± 0.07	0.33 ± 0.09	4.94 ± 0.83	2.38 ± 1.98	0.48 ± 0.27	0.91 ± 0.55

Table S21. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated 24 h thereafter.

Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G158300</i>	No functional annotation	6.37 \pm 1.84	0 \pm 0	0 \pm 0	6.18 \pm 2.15	0 \pm 0	0 \pm 0	7.3 \pm 4.25	19.4 \pm 9.54

Table S22. Transcript abundance for genes downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G040300</i>	L-type lectin-domain containing receptor kinase ix.1-related	2.8 ± 2.21	2.97 ± 1.09	0.65 ± 0.05	0.9 ± 0.23	0.55 ± 0.24	2.9 ± 1	1.32 ± 0.31	6.13 ± 1.44
<i>Phvul.001G075400</i>	Protein phosphatase 2	13.09 ± 5.61	10.89 ± 5.63	3.93 ± 1.8	4.9 ± 4.31	3.02 ± 0.79	10.75 ± 3.13	3.23 ± 0.77	54.08 ± 36.1
<i>Phvul.001G145900</i>	Dirigent protein 1-related	1.32 ± 0.9	1.71 ± 0.85	1.54 ± 0.62	2.09 ± 0.57	0 ± 0	1.69 ± 0.71	2.98 ± 1.12	34.15 ± 2.4
<i>Phvul.003G009200</i>	Cytochrome P450	0.66 ± 0.39	0.91 ± 0.33	0.19 ± 0.05	0.24 ± 0.06	0.11 ± 0.02	0.89 ± 0.28	0.34 ± 0.05	3.91 ± 0.63
<i>Phvul.004G138500</i>	Trypsin and protease inhibitor	7.43 ± 5.58	10.07 ± 3.69	2.1 ± 0.55	0.87 ± 0.38	1.56 ± 0.36	8.03 ± 3.35	3.85 ± 1.67	8.75 ± 4.77
<i>Phvul.010G063900</i>	Dirigent protein 19	10.25 ± 5.71	9.19 ± 1.45	9.47 ± 3.86	11.81 ± 2.6	1.74 ± 0.35	10.74 ± 3.74	19.77 ± 3.45	198.38 ± 17.65
<i>Phvul.011G203450</i>	VQ motif	1.13 ± 0.31	0.43 ± 0.12	0.77 ± 0.25	1.2 ± 0.71	0 ± 0	1.38 ± 0.38	3.33 ± 2.22	31.48 ± 4.47

Table S23. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated in the CBB-susceptible RIL 24 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.003G295200	Carboxylesterase 12-related	78.58 ±66.05	112.75 ±44.92	13.62 ±0.54	26.22 ±5.24	13.97 ±1.39	105.44 ±45.14	21.94 ±3.37	70.05 ±16.1
CBB-susceptible RIL									
Phvul.003G295200	Carboxylesterase 12-related	28.9 ±11.37	81.91 ±18.31	5.2 ±1.15	53.37 ±7.86	8.12 ±2.33	69.48 ±6.99	28.54 ±18.45	16.14 ±6.84

Table S24. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated in the CBB-susceptible RIL 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.010G144300	Acid phosphatase-related	139.23 ±138.44	131.59 ±106.68	381.59 ±225.37	79.13 ±69.37	0.6 ±0.32	123.69 ±92.98	249.52 ±63.65	20.73 ±5.36
CBB-susceptible RIL									
Phvul.010G144300	Acid phosphatase-related	6.62 ±3.61	20.28 ±13.99	25.84 ±17.65	3.17 ±2.33	2.82 ±2.34	39.78 ±3.48	16.64 ±7.63	20.68 ±2.73

Table S25. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated 24 and 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G287200</i> , <i>Phvul.008G287300</i>	6'-Deoxychalcone synthase	1.24 \pm 1.15	1.65 \pm 0.35	0.5 \pm 0.18	1 \pm 0.4	0.2 \pm 0.07	1.95 \pm 0.94	2.49 \pm 1.14	27.17 \pm 2.45

Table S26. Transcript abundance for genes upregulated in both RILs at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap), and 8 h PI in the CBB-resistant RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.002G122200	Absciscic acid 8'-hydroxylase 1-related	5.74 ±3.05	2.31 ±1.51	3.34 ±0.74	4.18 ±1.4	53.7 ±10.28	16.42 ±15.09	8.61 ±3.63	8.53 ±4.9
Phvul.002G231500, Phvul.002G231700	17.6 kDa class I heat shock protein 1-related	7.13 ±1.33	5.7 ±0.7	8.83 ±1.2	8.82 ±1.52	71.49 ±40.11	27.17 ±20.85	9.87 ±0.62	14.06 ±4.53
Phvul.002G049700	F2J10.8 protein-related	13.14 ±3.58	9.96 ±2.55	5.84 ±1.51	5.35 ±0.57	189.17 ±29.9	70.09 ±63.58	7.07 ±1.81	6.1 ±2.72
Phvul.003G147500	Xyloglucan endotransglucosylase/ Hydrolase protein 25-related	1.23 ±0.54	0.44 ±0.31	0.13 ±0.06	0.31 ±0.24	18.75 ±4.31	6.79 ±6.55	1.22 ±0.44	1.35 ±0.87
Phvul.004G044100	ATP-dependent CLP protease ATP-binding subunit CLPB	1.07 ±0.28	0.64 ±0.06	1.97 ±0.14	2.55 ±0.35	11.99 ±6.6	4.15 ±3.54	2.51 ±0.28	2.29 ±0.49
Phvul.005G111100	No functional annotation	9.27 ±4.19	5.48 ±3.76	4.37 ±0.83	2.77 ±0.11	87.19 ±6.85	25.68 ±24.16	4.88 ±0.5	2.16 ±0.17
Phvul.008G016500, Phvul.008G016600	IQ calmodulin-binding motif / BAG domain	3.67 ±1.84	1.41 ±0.5	4.02 ±0.34	4.6 ±0.98	60.8 ±31.89	21.84 ±20.7	5.08 ±0.76	5.43 ±0.96
Phvul.008G175800, Phvul.008G175900, Phvul.008G176000	Cysteine-rich receptor-like protein kinase 28-related	28.97 ±11.9	12.23 ±4.77	8.62 ±2.74	9.86 ±4.05	260.69 ±43.9	109.18 ±101.5	23.08 ±10.42	28.77 ±21.06
Phvul.009G152500	17.6 kDa class I heat shock protein 1-related	1.96 ±0.76	0.59 ±0.21	2.02 ±0.4	1.25 ±0.15	17.66 ±8.45	5.56 ±5.25	2.84 ±0.99	2.95 ±0.62
Phvul.010G125400	Auxin responsive protein	0.6 ±0.22	0.5 ±0.16	0.22 ±0.09	0.29 ±0.06	11.99 ±3.85	3.84 ±3.39	0.23 ±0.06	0.24 ±0.12

Table S26 continued

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-susceptible RIL									
Phvul.002G122200	Abscisic acid 8'-hydroxylase 1-related	3.08 ± 1.15	0.74 ± 0.06	3.45 ± 0.52	7.89 ± 4.41	58.93 ± 13.59	1.1 ± 0.12	3.34 ± 0.28	11.08 ± 7
Phvul.002G231500, Phvul.002G231700	17.6 kDa class I heat shock protein 1-related	6.16 ± 0.33	6.15 ± 0.62	5.8 ± 0.91	5.9 ± 0.12	36.48 ± 27.78	7.38 ± 0.5	4.99 ± 0.64	5.62 ± 0.38
Phvul.002G049700	F2J10.8 protein-related	8.19 ± 0.41	6.53 ± 0.35	5.29 ± 0.72	4.64 ± 1.28	186.16 ± 24.66	6.39 ± 0.45	4.56 ± 0.95	9.73 ± 5.59
Phvul.003G147500	Xyloglucan endotransglucosylase/ Hydrolase protein 25-related	0.15 ± 0.15	0.06 ± 0.03	0.11 ± 0.04	0.52 ± 0.39	12.67 ± 3.09	0.08 ± 0.04	0.08 ± 0.08	1.5 ± 1.11
Phvul.004G044100	ATP-dependent CLP protease ATP-binding subunit CLPB	0.9 ± 0.17	0.62 ± 0.05	1.58 ± 0.18	1.5 ± 0.08	6.42 ± 4.12	0.75 ± 0.05	1.49 ± 0.16	1.51 ± 0.08
Phvul.005G111100	No functional annotation	5.53 ± 1.68	3.15 ± 0.23	4.08 ± 0.7	3.51 ± 0.49	70.33 ± 7.1	2.67 ± 0.47	4.23 ± 0.54	5.48 ± 1.11
Phvul.008G016500, Phvul.008G016600	IQ calmodulin-binding motif /BAG domain	3.55 ± 0.91	0.97 ± 0.49	3.33 ± 0.08	3.16 ± 0.33	34.26 ± 20.21	1.3 ± 0.14	3.19 ± 0.66	3.65 ± 0.5
Phvul.008G175800, Phvul.008G175900, Phvul.008G176000	Cysteine-rich receptor-like protein kinase 28-related	18.23 ± 5.77	4.08 ± 2.04	4.97 ± 1.21	13.69 ± 8.38	253.89 ± 20.92	7.23 ± 1.04	5.54 ± 0.4	30.58 ± 21.82
Phvul.009G152500	17.6 kDa class I heat shock protein 1-related	1.16 ± 0.6	0.2 ± 0.12	2.08 ± 0.37	1.98 ± 0.23	7.82 ± 4.9	0.71 ± 0.23	2.07 ± 0.02	2.92 ± 0.66
Phvul.010G125400	Auxin responsive protein	0.57 ± 0.33	0.46 ± 0.24	0.28 ± 0.12	0.27 ± 0.09	10.87 ± 0.99	0.42 ± 0.14	0.27 ± 0.08	0.31 ± 0.12

Table S27. Transcript abundance for genes downregulated at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) in both RILs and upregulated 48 h PI in the CBB-resistant RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G145800	Dirigent protein 1-related	1.91 ±1.37	3.16 ±1.28	2.45 ±0.53	3.06 ±0.64	0.23 ±0.14	3.08 ±1.3	3.81 ±0.72	28.96 ±2.86
Phvul.002G032866	Isoflavone reductase	1.2 ±0.72	1.12 ±0.47	1.39 ±0.7	1.55 ±0.5	0.29 ±0.1	1.79 ±0.85	2.9 ±0.23	30.4 ±2.74
Phvul.003G051700	Isoflavone synthase	2.28 ±1.44	2.45 ±0.87	3.12 ±1.45	3.09 ±1.13	0.33 ±0.12	3.07 ±1.42	5.66 ±2.34	102.17 ±4.19
Phvul.003G109100	Pathogenesis-related protein Bet V I family	248.26 ±196.46	397.11 ±159.63	117.07 ±25.98	143.12 ±17.85	53.8 ±13.12	500.28 ±241.6	235.87 ±63.19	736.34 ±116.98
Phvul.006G069300	Glutamine-dependent asparagine synthetase	3.54 ±2.56	5.52 ±2.42	2.08 ±0.89	2.24 ±0.86	0.59 ±0.27	3.51 ±2.14	3.14 ±1.65	17.76 ±4.93
CBB-susceptible RIL									
Phvul.001G145800	Dirigent protein 1-related	1.76 ±1.44	3.69 ±0.7	1.48 ±0.15	1.79 ±0.47	0.23 ±0.14	3.19 ±0.3	3.11 ±1.09	3.84 ±0.56
Phvul.002G032866	Isoflavone reductase	2.35 ±1.34	2.92 ±0.72	0.57 ±0.17	1.08 ±0.19	0.35 ±0.16	2.53 ±1.13	1.21 ±0.6	2.11 ±0.91
Phvul.003G051700	Isoflavone synthase	2.62 ±1.39	5 ±1.15	0.63 ±0.1	1.38 ±0.48	0.59 ±0.23	2.01 ±0.8	2.15 ±1.13	3.97 ±2.03
Phvul.003G109100	Pathogenesis-related protein Bet V I family	208.02 ±164.91	498.09 ±37.11	94.87 ±14.26	145.84 ±70.05	46.96 ±3.04	390.61 ±56.52	130.24 ±33.47	153.47 ±49.16
Phvul.006G069300	Glutamine-dependent asparagine synthetase	22.4 ±15.7	47.09 ±8.23	3.68 ±1.47	2.77 ±1	2.4 ±0.66	33.35 ±16	4.03 ±1.44	4.92 ±1.93

Table S28. Transcript abundance for a gene upregulated in the CBB-resistant and CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated in the CBB-resistant RIL at 24 and 48 h PI.

Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.009G089300	Ethylene-responsive transcription factor ERF003	3.99 ± 2.11	2.82 ± 2.17	5.67 ± 4.49	1.02 ± 0.24	18.84 ± 4.02	5.28 ± 4.42	1.33 ± 0.23	0.25 ± 0.13
CBB-susceptible RIL									
Phvul.009G089300	Ethylene-responsive transcription factor ERF003	2.65 ± 1.14	0.89 ± 0.44	5.21 ± 1.54	1.84 ± 0.57	24.52 ± 6.14	1.2 ± 0.36	2.65 ± 0.51	5.29 ± 2.53

Table S29. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated 48 h PI, and downregulated in the CBB-susceptible RIL at 0 h PI and upregulated 24 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.006G078400	No functional annotation	43.71 ± 41.03	43.73 ± 19.76	9.36 ± 3.59	11.85 ± 2.07	3.33 ± 0.77	47.71 ± 22.29	10.49 ± 2.18	69.64 ± 10.65
CBB-susceptible RIL									
Phvul.006G078400	No functional annotation	18.58 ± 14.84	76.27 ± 27.64	3.27 ± 0.57	45.25 ± 7.56	1.99 ± 0.52	43.85 ± 9.98	19.35 ± 14.73	14.14 ± 9.16

Table S30. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and at all sampling times thereafter, and upregulated in the CBB-susceptible RIL at 0 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.008G207300	Late embryogenesis abundant hydroxyproline-rich glycoprotein	14.63 ±4.78	6.79 ±2.11	3.51 ±0.14	14.08 ±10.15	58.94 ±12.31	28.52 ±22.4	33.76 ±16.6	61.88 ±45.85
CBB-susceptible RIL									
Phvul.008G207300	Late embryogenesis abundant hydroxyproline-rich glycoprotein	7.6 ±2.92	2.2 ±1.14	2.37 ±1.17	33.92 ±20.27	53.87 ±10.22	3.97 ±0.16	2.76 ±0.37	31.96± 19.49

Table S31. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 8 h and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.008G249900</i>	Peroxidase / Lactoperoxidase	0.41 ± 0.37	0.24 ± 0.1	0.43 ± 0.24	0.27 ± 0.05	0.14 ± 0.11	1.07 ± 0.66	0.93 ± 0.42	3.85 ± 0.92

Table S32. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 8 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated at 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.009G158300</i> , <i>Phvul.009G158400</i>	Calcium/Calmodulin- dependent protein kinase / Microtubule-associated protein 2 kinase	4.41 ± 2.29	4.98 ± 2.17	0.85 ± 0.15	0.85 ± 0.16	4.97 ± 2.93	1.16 ± 0.41	2.42 ± 1.62	3.58 ± 3.13

Table S33. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 8 and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated in the CBB-susceptible RIL at 0 h post-inoculation (PI). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.004G122000	Dehydration-responsive element-binding protein 1a-related	1.42 ±0.88	0.16 ±0.08	0.06 ±0.06	1.65 ±1.54	5.1 ±2.04	2.71 ±2.64	3.57 ±1.99	7.01 ±5.72
CBB-susceptible RIL									
Phvul.004G122000	Dehydration-responsive element-binding protein 1a-related	0.27 ±0.22	0.04 ±0.03	0.04 ±0.02	5.95 ±4.04	5.92 ±2.74	0.07 ±0.03	0.04 ±0.02	4.9 ±3.52

Table S34. Transcript abundance for genes respectively upregulated and downregulated in the CBB-resistant RIL at 24 and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
Gene ID	Gene Annotation	Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
Upregulated									
Phvul.001G087100	GRAM domain	4.89 ±1.11	3.49 ±1.08	3.4 ±0.14	6.09 ±2.62	9.86 ±1.76	5.46 ±2.11	17.87 ±6.66	35.55 ±22.66
Phvul.001G067400	EF-hand calcium-binding domain containing protein	1.61 ±0.87	0.88 ±0.03	0.7 ±0.16	2.57 ±1.74	3.25 ±0.62	2.05 ±1.13	5.26 ±2.13	15.98 ±9.76
Phvul.001G194700, Phvul.001G194900	Harpin-induced protein-like-related	31.28 ±7.01	18.72 ±6.25	11.56 ±1.56	45.65 ±33.12	36.48 ±5.38	30.28 ±10.12	85.5 ±36.2	220.26 ±116.56
Phvul.002G293000	1-Aminocyclopropane-1-carboxylate synthase 2-related	3.23 ±0.5	2.2 ±0.62	1.42 ±0.27	3.07 ±2.27	3 ±0.42	2.71 ±0.75	7 ±3.33	14.69 ±7.89
Phvul.005G115200	No functional annotation	2.62 ±0.29	3.77 ±0.95	0.68 ±0.15	1.77 ±0.48	4.16 ±0.43	4.8 ±0.65	3.15 ±1.11	7.59 ±1.1
Phvul.007G029800	Core-2/I-branching β-1,6-N-acetylglucosaminyltransferase-like protein	0.29 ±0.08	0.14 ±0.02	0.1 ±0.03	0.35 ±0.2	0.08 ±0.06	0.07 ±0.05	0.75 ±0.33	3.05 ±1.34
Phvul.009G167200	No functional annotation	1.79 ±0.51	0.85 ±0.19	0.83 ±0.17	1.85 ±1.21	0.56 ±0.24	0.86 ±0.21	4.76 ±2.24	9.05 ±6.09
Phvul.010G090100	BON1-associated protein 1-related	0.52 ±0.24	0.41 ±0.27	2.82 ±0.71	4.02 ±0.7	0.29 ±0.09	0.38 ±0.09	3.89 ±1.62	10.24 ±5.81
Phvul.010G111900	WRKY DNA -binding domain	11.23 ±1.74	13.44 ±1.39	6.85 ±2.6	11.89 ±7.04	9.7 ±2.04	13.99 ±1.54	20.41 ±7.32	39.81 ±24.09
XLOC_023351	No functional annotation	5.32 ±1.92	4.22 ±1.93	0.24 ±0.1	0.48 ±0.2	7.24 ±0.76	5.46 ±1.64	12.23 ±3.35	24.96 ±15.32
XLOC_023352	No functional annotation	20.69 ±9.43	14.41 ±5.68	3.85 ±0.52	9.44 ±5.06	18.01 ±5.3	15.74 ±4.82	34.27 ±9.71	74.15 ±47.64

Table S34 continued

		Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
Downregulated									
<i>Phvul.008G003200</i>	Pollen proteins Ole e I like	0.02	0.04	0.86	0.95	0.03	0.08	0.21	0.14
		±0.02	±0.03	±0.46	±0.46	±0.03	±0.05	±0.03	±0.03

Table S35. Transcript abundance for genes upregulated in the CBB-resistant RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and at 0 h PI in the CBB-susceptible RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G212300	Domain of unknown function	5.39 ±2.92	1.12 ±0.44	1.42 ±0.1	6.01 ±4.53	6.05 ±1.16	2.62 ±2.2	6.46 ±3.49	12.52 ±7.42
Phvul.003G066700	No functional annotation	3.34 ±1.68	1.11 ±0.42	0.49 ±0.3	4.35 ±4.12	5.6 ±1.24	4.05 ±3.09	7.08 ±3.65	13.66 ±9.72
Phvul.005G088600	Calcium binding protein	28.33 ±9.98	13.32 ±2.59	7.18 ±1.3	31.49 ±25.79	67.07 ±25.89	43.22 ±31.75	46.24 ±21.93	95.93 ±53.37
Phvul.010G062900	Methyltransferase	5.95 ±2.15	3.05 ±0.7	3.69 ±0.46	7.44 ±3.33	21.3 ±2.99	10.71 ±8.26	15.73 ±6.67	22.11 ±14.65
CBB-susceptible RIL									
Phvul.001G212300	Domain of unknown function	2.33 ±0.8	0.56 ±0.28	0.97 ±0.13	5.84 ±4.65	9.82 ±4.09	0.56 ±0.2	0.85 ±0.36	9.06 ±4.82
Phvul.003G066700	No functional annotation	0.7 ±0.42	0.72 ±0.19	0.76 ±0.13	7.4 ±6.48	3.71 ±0.91	0.61 ±0.04	0.55 ±0.25	5.62 ±2.6
Phvul.005G088600	Calcium binding protein	10.6 ±4.46	7.01 ±0.48	3.89 ±1.05	57.68 ±36.25	64.87 ±19.05	7.99 ±0.95	5.5 ±1.48	43.4 ±20.55
Phvul.010G062900	Methyltransferase	4.32 ±1.23	1.53 ±0.8	4.04 ±0.06	11.82 ±7.31	23.72 ±4.99	2.64 ±0.37	3.76 ±0.36	18.5 ±10.78

Table S36. Transcript abundance for genes upregulated in the CBB-resistant RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and in the CBB-susceptible RIL at 48 h PI. Transcript levels for individual genes corresponding to RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.003G212700	AP2 domain	0.12 ±0.12	0 ±0	0 ±0	0 ±0	0 ±0	0.05 ±0.05	0.78 ±0.47	0 ±0
Phvul.004G011800	Pectin lyase-like superfamily protein	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	0 ±0	1.48 ±0.46	0.15 ±0.03
Phvul.007G066520	AP2 domain	1.67 ±0.39	1.06 ±0.17	0.4 ±0.16	0.5 ±0.11	0.97 ±0.2	0.96 ±0.05	3.6 ±1.91	1.35 ±1.01
CBB-susceptible RIL									
Phvul.003G212700	AP2 domain	0 ±0	0.11 ±0.05	0 ±0	0 ±0	0.44 ±0.44	0.09 ±0.09	0.13 ±0.13	1.13 ±1.13
Phvul.004G011800	Pectin lyase-like superfamily protein	0.06 ±0.03	0.02 ±0.01	0.05 ±0.03	0 ±0	0.11 ±0.11	0 ±0	2.09 ±1.62	1.73 ±1.3
Phvul.007G066520	AP2 domain	1.22 ±0.25	1.05 ±0.32	0.6 ±0.14	0.63 ±0.26	3.17 ±2.26	0.86 ±0.07	0.38 ±0.07	4.35 ±3.78

Table S37. Transcript abundance for genes upregulated in the CBB-resistant RIL at 24 and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and at 0 h PI in the CBB-susceptible RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.004G022700	Galacturonosyltransferase-like 8-related	0.95 ±0.33	0.35 ±0.14	0.13 ±0.02	0.82 ±0.73	1.88 ±0.1	1 ±0.61	1.98 ±1.28	4.04 ±2.52
XLOC_009124	No functional annotation	2 ±0.88	0.79 ±0.54	0.24 ±0.02	4.36 ±3.98	1.57 ±0.36	0.99 ±0.53	12.63 ±6.81	30.37 ±20.77
XLOC_023518	No functional annotation	1.85 ±0.6	0.52 ±0.08	0.27 ±0.09	1.14 ±0.78	1.27 ±0.36	1.59 ±0.86	3.57 ±1.95	10.64 ±7.39
CBB-susceptible RIL									
Phvul.004G022700	Galacturonosyltransferase-like 8-related	0.42 ±0.14	0.23 ±0.03	0.21 ±0.07	1.57 ±1.2	2.04 ±1.13	0.17 ±0.06	0.14 ±0.01	1.37 ±0.84
XLOC_009124	No functional annotation	0.52 ±0.21	0.27 ±0.03	0.21 ±0.09	15.41 ±14.6	3.36 ±2.38	0.14 ±0.05	0.19 ±0.05	13.3 ±7.66
XLOC_023518	No functional annotation	0.68 ±0.11	0.31 ±0.16	0.33 ±0.02	5.11 ±4.64	3.12 ±1.47	0.49 ±0.07	0.27 ±0.05	5.22 ±3.75

Table S38. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 24 and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated at 48 h PI in the CBB-susceptible RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.002G177900	Galacturonosyltransferase-like 8-related	0.1 ±0.06	0.55 ±0.33	0.11 ±0.02	0.25 ±0.05	0.24 ±0.08	0.19 ±0.1	0.62 ±0.06	4.71 ±1.74
CBB-susceptible RIL									
Phvul.002G177900	Galacturonosyltransferase-like 8-related	0.19 ±0.02	0.07 ±0.03	0.16 ±0.04	0.68 ±0.35	0.31 ±0.14	0.09 ±0.02	0.06 ±0.03	0.12 ±0.03

Table S39. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and in the CBB-susceptible RIL at 24 and 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.008G144100	β-expansin 6-related	0.13 ±0.13	0.02 ±0.02	0.11 ±0.06	0.16 ±0.09	0 ±0	0.08 ±0.06	7.51 ±1.55	0.96 ±0.19
CBB-susceptible RIL									
Phvul.008G144100	β-expansin 6-related	0.04 ±0.02	0.03 ±0.03	0.2 ±0.05	0.18 ±0.1	0.03 ±0.02	0.05 ±0.05	13.7 ±9	12.07 ±8.83

Table S40. Transcript abundance for a gene upregulated in both RILs at 24 and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
<i>Phvul.007G099700</i>	No functional annotation	0	0.03	0.34	0.86	0.04	0.05	17.6	22.03
		±0	±0.03	±0.12	±0.38	±0.03	±0.05	±5.83	±3.6
CBB-susceptible RIL									
<i>Phvul.007G099700</i>	No functional annotation	0	0.05	0.32	0.16	0	0.03	29.87	15.02
		±0	±0.02	±0.2	±0	±0	±0.02	±25.63	±11.5

Table S41. Transcript abundance for genes upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) *Xanthomonas axonopodis* (Xap) and downregulated in the CBB-susceptible RIL at 0 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G145600	Dirigent protein 1-related	0.31 ±0.13	0.2 ±0.12	0.71 ±0.33	0.26 ±0.13	0.14 ±0.1	0.32 ±0.2	1.94 ±1.4	8.73 ±3.53
Phvul.002G038600, Phvul.002G038700, Phvul.002G038800, Phvul.002G038900, Phvul.002G039000, Phvul.002G039300	Chalcone synthase	1.28 ±0.76	1.49 ±0.14	1.8 ±0.77	1.31 ±0.46	0.34 ±0.05	1.8 ±0.69	4.12 ±1.52	26.91 ±2.34
Phvul.004G085676	Nudix hydrolase related	0.16 ±0.04	0.39 ±0.11	0.48 ±0.14	0.67 ±0.28	0.27 ±0.1	0.31 ±0.13	0.92 ±0.23	13.39 ±4.94
Phvul.006G197100, Phvul.006G197200, Phvul.006G197300	Pathogenesis-related protein 1 (PR1)	11.29 ±3.76	9.58 ±2.62	13.91 ±5.88	10 ±4.91	7.08 ±1.87	11.86 ±1.67	11.94 ±3.66	326.38 ±17.06
Phvul.008G032200	Isoflavone-7- <i>O</i> -β-glucoside 6"- <i>O</i> -malonyltransferase	4.05 ±2.97	7.02 ±2.62	0.71 ±0.08	0.99 ±0.3	1.27 ±0.08	6.37 ±2.71	1.01 ±0.17	4.78 ±1.68
Phvul.009G043200	WRKY transcription factor 38-related	0.32 ±0.18	0.58 ±0.28	0.42 ±0.09	0.37 ±0.14	0.21 ±0.06	0.31 ±0.05	0.33 ±0.09	2.33 ±1.29
Phvul.010G042200	Hydroquinone glucosyltransferase	1.61 ±1.15	2.97 ±1.2	0.87 ±0.27	1.56 ±0.5	0.64 ±0.09	3.22 ±1.59	1.67 ±0.68	8.91 ±2.7
CBB-susceptible RIL									
Phvul.001G145600	Dirigent protein 1-related	0.55 ±0.1	0.3 ±0.2	0.04 ±0.04	0.32 ±0.06	0 ±0	0.06 ±0.06	0.03 ±0.03	0.85 ±0.82

Table S41 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.002G038600</i> , <i>Phvul.002G038700</i> , <i>Phvul.002G038800</i> , <i>Phvul.002G038900</i> , <i>Phvul.002G039000</i> , <i>Phvul.002G039300</i>	Chalcone synthase	1.18 ±0.5	2.04 ±0.31	0.64 ±0.29	0.65 ±0.04	0.16 ±0.05	1.07 ±0.28	0.77 ±0.18	1.33 ±0.67
<i>Phvul.004G085676</i>	Nudix hydrolase related	0.76 ±0.58	0.4 ±0.08	0.18 ±0.03	3.2 ±2	0.13 ±0.04	0.18 ±0.08	0.35 ±0.24	0.89 ±0.7
<i>Phvul.006G197100</i> , <i>Phvul.006G197200</i> , <i>Phvul.006G197300</i>	Pathogenesis-related protein 1 (PR1)	29.26 ±14.35	33.09 ±9.95	16.54 ±14.69	16.99 ±5.87	7.23 ±3.76	14.28 ±5.12	17.66 ±13.68	24.78 ±13.82
<i>Phvul.008G032200</i>	Isoflavone-7- <i>O</i> -β-glucoside 6"- <i>O</i> -malonyltransferase	3.62 ±2.75	7.59 ±3.82	0.49 ±0.04	0.84 ±0.22	0.85 ±0.18	9.19 ±0.48	0.61 ±0.11	1.02 ±0.54
<i>Phvul.009G043200</i>	WRKY transcription factor 38-related	0.61 ±0.48	0.15 ±0.08	0.14 ±0.06	1.35 ±0.61	0.1 ±0.02	0.11 ±0.02	0.13 ±0.07	0.35 ±0.23
<i>Phvul.010G042200</i>	Hydroquinone glucosyltransferase	2.37 ±1.67	2.74 ±1.51	0.3 ±0.02	1.4 ±0.6	0.4 ±0.04	4.23 ±0.33	0.96 ±0.65	1.95 ±1.39

Table S42. Transcript abundance for genes upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated in the CBB-susceptible RIL at 8 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.002G200600	Tetrahydroberberine oxidase	0.28 ±0.13	0.13 ±0.06	1.72 ±1.07	0.56 ±0.13	0 ±0	0.13 ±0.05	1.06 ±0.55	32.71 ±1.73
Phvul.004G098000	Extensin-like region	6.02 ±1.89	3.08 ±1.23	16.74 ±6.93	12.5 ±1.31	3.17 ±0.68	2.01 ±0.5	11.5 ±2.25	255.16 ±7.49
CBB-susceptible RIL									
Phvul.002G200600	Tetrahydroberberine oxidase	0.77 ±0.36	1.28 ±0.13	0.38 ±0.33	0.54 ±0.24	0.05 ±0.05	0.28 ±0.19	0.45 ±0.32	1 ±0.53
Phvul.004G098000	Extensin-like region	8.16 ±1.69	15.51 ±6.44	6.75 ±5.26	13.13 ±4.77	2.66 ±0.82	3.7 ±0.84	19.74 ±15.14	16.31 ±6.8

Table S43. Transcript abundance for genes upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and in the CBB-susceptible RIL at 24 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.006G196900	Pathogenesis-related protein 1 (PR1)	3.93 ±2.54	7.62 ±2.2	1.99 ±0.42	2.32 ±0.19	1.79 ±0.72	9.2 ±2.49	2.75 ±1.06	33.99 ±7.53
Phvul.006G124600, Phvul.006G124700	FAD-binding berberine family protein-related	0.11 ±0.11	0.08 ±0.01	0.33 ±0.13	0.22 ±0.05	0.08 ±0.06	0.12 ±0.03	0.35 ±0.16	1.67 ±0.32
Phvul.001G128500	β-1,3-glucanase 1-related	32.88 ±25.47	40.37 ±14.4	41.76 ±14.98	126.99 ±13.57	8.31 ±2.77	35.24 ±16.65	89.48 ±27.66	559.47 ±136.63
CBB-susceptible RIL									
Phvul.006G196900	Pathogenesis-related protein 1 (PR1)	1.44 ±0.8	1.76 ±0.83	0.66 ±0.25	7.51 ±3.5	0.89 ±0.21	1.35 ±0.36	3.58 ±2.06	2.4 ±1.18
Phvul.006G124600, Phvul.006G124700	FAD-binding berberine family protein-related	0.15 ±0.08	0.16 ±0.04	0.27 ±0.05	1.56 ±0.57	0.02 ±0.02	0.14 ±0.06	1.16 ±0.99	0.49 ±0.28
Phvul.001G128500	β-1,3-glucanase 1-related	22.22 ±13.78	53.86 ±14.8	15.37 ±1.13	110.11 ±54.43	6.18 ±1.02	45.09 ±17.01	96.64 ±74.85	85.44 ±57.83

Table S44. Transcript abundance for genes that were adversely regulated across both RILs at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL upregulated									
Phvul.001G036600	Fructan β -(2,1)-fructosidase / Inulinase	0.08 ± 0.01	0.11 ± 0.06	0.09 ± 0.02	0.06 ± 0.04	0.15 ± 0.08	0.08 ± 0.03	0.08 ± 0.05	0.7 ± 0.29
Phvul.001G205900	Protein C41G7.9, isoform B	0.24 ± 0.09	0.1 ± 0.05	0.13 ± 0.02	0.18 ± 0.13	0.18 ± 0.12	0.09 ± 0.09	0.18 ± 0.05	8.93 ± 8.64
Phvul.001G255200	RING/U-box domain-containing protein	0.93 ± 0.77	0.1 ± 0.06	0.45 ± 0.25	1.41 ± 1.35	0.85 ± 0.09	0.25 ± 0.18	1.08 ± 0.54	20.25 ± 18.02
Phvul.002G155400	Thaumatococin family	0.64 ± 0.3	0.17 ± 0.04	1.88 ± 0.57	0.75 ± 0.39	0.08 ± 0.04	0.09 ± 0.05	1.35 ± 0.68	21.48 ± 1.55
Phvul.002G309300	Ring zinc finger protein	0.3 ± 0.15	0.23 ± 0.06	0.28 ± 0.14	0 ± 0	0.14 ± 0.07	0.32 ± 0.16	0.06 ± 0.06	0.63 ± 0.27
Phvul.003G128133	Flavin-containing monooxygenase 1-related	0 ± 0	0.08 ± 0.04	0.4 ± 0.3	0.36 ± 0.15	0 ± 0	0.11 ± 0.03	0.41 ± 0.36	5.26 ± 0.34
Phvul.003G131500	12-Oxophytodienoate reductase 3	0.58 ± 0.1	1.55 ± 0.2	0.42 ± 0.08	0.12 ± 0.06	0.64 ± 0.07	0.85 ± 0.08	0.74 ± 0.44	2.59 ± 0.84
Phvul.005G053100	Glutathione S-transferase U21-related	0.64 ± 0.09	0.67 ± 0.21	0.32 ± 0.18	0.55 ± 0.14	0.74 ± 0.13	0.68 ± 0.17	1.21 ± 0.43	5.35 ± 3.44
Phvul.005G108900	Transferase family	1.18 ± 0.16	1.52 ± 0.78	0.58 ± 0.12	1.23 ± 0.14	1.46 ± 0.24	1.16 ± 0.16	0.9 ± 0.16	5.63 ± 1.8
Phvul.007G066300	No functional annotation	0.43 ± 0.25	0.39 ± 0.2	0.29 ± 0.17	1.27 ± 0.31	0.46 ± 0.14	0.44 ± 0.25	0.7 ± 0.27	9.07 ± 4
Phvul.007G111200	Calcium binding protein	1.83 ± 0.37	1.62 ± 0.77	1.14 ± 0.05	1.4 ± 0.24	2.16 ± 0.65	1.52 ± 0.9	1.79 ± 0.47	7.84 ± 4.72
Phvul.010G093500	BON1-associated protein 1-related	0.75 ± 0.14	1.09 ± 0.1	1.02 ± 0.45	0.35 ± 0.31	0.58 ± 0.16	1.1 ± 0.44	2 ± 0.58	3.77 ± 0.51

Table S44 continued

Table S11 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL downregulated									
<i>Phvul.003G169100</i>	Hydrophobic seed protein	40.5 ±15.84	36.23 ±2.21	38.49 ±23.19	17.51 ±4.98	49.37 ±15.77	39.43 ±1.84	23.64 ±3.52	3.65 ±1.59
<i>Phvul.008G076300</i>	4,4-dimethyl-9β,19-cyclopropylsterol-4-α-methyl oxidase (SMO1)	9.38 ±0.39	10.9 ±1.32	3.67 ±1.65	1.82 ±0.84	9.39 ±1.02	11.39 ±0.81	5.63 ±0.57	0.41 ±0.25
<i>Phvul.011G026700</i>	Proline-rich protein 4	1087.49 ±125.66	1139.65 ±82.56	366.15 ±245.7	118.78 ±68.29	1146.18 ±146.68	1076.04 ±33.82	258.72 ±64.09	21.66 ±5.21
CBB-susceptible RIL upregulated									
<i>Phvul.002G155400</i>	Thaumatococin family	0.82 ±0.37	1.11 ±0.2	0.61 ±0.47	0.38 ±0.13	0.25 ±0.15	0.4 ±0.22	0.35 ±0.18	1.83 ±1.2
<i>Phvul.003G131500</i>	12-Oxophytodienoate reductase 3	0.49 ±0.1	0.61 ±0.12	0.2 ±0.02	0.11 ±0.05	0.96 ±0.13	1.01 ±0.27	0.36 ±0.07	0.66 ±0.22
<i>Phvul.003G169100</i>	Hydrophobic seed protein	29.92 ±3.01	29.26 ±4.95	37.43 ±13.05	4.73 ±1.89	36.37 ±5.23	20.98 ±1.5	19.28 ±9.7	21.51 ±9.65
<i>Phvul.008G076300</i>	4,4-dimethyl-9β,19-cyclopropylsterol-4α-methyl oxidase (SMO1)	7.21 ±2.32	7.16 ±3.66	6.54 ±2.22	0.38 ±0.09	6.59 ±1.01	7.39 ±1.52	2.91 ±1.36	3.59 ±1.75
<i>Phvul.010G093500</i>	BON1-associated protein 1-related	0.75 ±0.51	0.72 ±0.39	0.74 ±0.24	0.15 ±0.03	0.45 ±0.13	1.1 ±0.33	0.61 ±0.19	1.57 ±0.58
<i>Phvul.011G026700</i>	Proline-rich protein 4	1004.13 ±58.08	662.57 ±331.68	404.29 ±72.89	24.11 ±4.45	1109.66 ±120.05	863.29 ±204.69	235.91 ±130.63	245.5 ±131.52
CBB-susceptible RIL downregulated									
<i>Phvul.001G036600</i>	Fructan β-(2,1)-fructosidase / Inulinase	0.31 ±0.16	0.18 ±0.12	0.15 ±0.02	1.19 ±0.73	0.13 ±0.05	0.09 ±0.02	0.12 ±0.08	0.3 ±0.17

Table S44 continued

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				<i>Xap</i> inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.001G205900</i>	Protein C41G7.9, isoform B	0.46 ±0.25	0 ±0	0.29 ±0.07	3.35 ±3.09	0.42 ±0.01	0 ±0	0.14 ±0.03	0.52 ±0.53
<i>Phvul.001G255200</i>	RING/U-box domain-containing protein	0.54 ±0.38	0.05 ±0.03	0.39 ±0.18	14.56 ±10.89	0.96 ±0.81	0.03 ±0.02	0.12 ±0.08	1.97 ±1.45
<i>Phvul.002G309300</i>	Ring zinc finger protein	0.14 ±0.14	0.36 ±0.12	0.12 ±0.06	0.61 ±0.24	0.07 ±0.08	0.48 ±0.25	0.2 ±0.2	0 ±0
<i>Phvul.003G128133</i>	Flavin-containing monooxygenase 1-related	0.02 ±0.02	0.01 ±0.01	0.06 ±0.05	1.7 ±1.1	0.05 ±0.03	0.14 ±0.13	0.29 ±0.18	0.34 ±0.23
<i>Phvul.005G053100</i>	Glutathione S-transferase U21-related	0.73 ±0.18	0.15 ±0.02	0.11 ±0.03	2.32 ±1.53	0.44 ±0.09	0.21 ±0.03	0.12 ±0.09	0.29 ±0.1
<i>Phvul.005G108900</i>	Transferase family	1.86 ±1.15	0.53 ±0.07	0.33 ±0.08	3.28 ±1.97	0.75 ±0.27	0.43 ±0.03	0.57 ±0.29	0.57 ±0.32
<i>Phvul.007G066300</i>	No functional annotation	0.75 ±0.4	0.44 ±0.14	0.06 ±0.06	7.59 ±5.42	0.07 ±0.07	0.04 ±0.04	0.73 ±0.38	1.29 ±0.92
<i>Phvul.007G111200</i>	Calcium binding protein	1.25 ±0.48	0.71 ±0.07	0.83 ±0.13	6.86 ±4.51	1.1 ±0.16	0.53 ±0.14	0.59 ±0.22	1.16 ±0.44

Table S45. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated at 0 h PI and upregulated at 24 h PI in the CBB-susceptible RIL.
Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.001G145700	Dirigent protein 1-related	0.64 ±0.42	0.29 ±0.14	0.8 ±0.33	1.13 ±0.33	0.14 ±0.14	0.15 ±0.12	0.25 ±0.11	102.18 ±10.58
CBB-susceptible RIL									
Phvul.001G145700	Dirigent protein 1-related	0.53 ±0.2	0.94 ±0.74	0.27 ±0.12	1.43 ±0.81	0 ±0	0.29 ±0.23	1.38 ±0.96	1.07 ±0.64

Table S46. Transcript abundance for a gene upregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated at 0 h PI and upregulated at 48 h PI in the CBB-susceptible RIL.
Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.009G244100	Isoflavone 2'-hydroxylase	1.6 ±1.35	1.09 ±0.47	1.2 ±0.22	1.13 ±0.24	0.02 ±0.02	1.66 ±0.82	2.04 ±0.53	10.51 ±1.19
CBB-susceptible RIL									
Phvul.009G244100	Isoflavone 2'-hydroxylase	1.34 ±1.28	1.33 ±0.76	0.5 ±0.13	0.21 ±0.08	0.12 ±0.08	1.16 ±0.2	0.87 ±0.2	1.52 ±0.47

Table S47. Transcript abundance for a gene downregulated in the CBB-resistant RIL at 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and downregulated at 24 h PI and upregulated at 48 h PI in the CBB-susceptible RIL. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
CBB-resistant RIL									
Phvul.006G035050,	No functional annotation	0.85	1.09	0.64	3.14	3.11	3.64	0.62	0.52
Phvul.006G035100		±0.16	±0.23	±0.06	±2.29	±2.53	±1.48	±0.04	±0.08
CBB-susceptible RIL									
Phvul.006G035050,	No functional annotation	0.87	2.66	7.26	0.55	0.61	1.36	0.72	2.59
Phvul.006G035100		±0.1	±1.14	±4.39	±0.09	±0.01	±0.16	±0.05	±1.82

Table S48. Transcript abundance for a gene downregulated in the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and upregulated at 8 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
XLOC_008103	No functional annotation	0.66	0	0	0.38	0	0.97	0.41	0
		± 0.66	± 0	± 0	± 0.32	± 0	± 0.54	± 0.41	± 0

Table S49. Transcript abundance for a gene upregulated in the CBB-susceptible RIL at 0 h and 48 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
<i>Phvul.003G268200</i>	No functional annotation	0.42 ± 0.08	0.11 ± 0.01	0.2 ± 0.12	0.28 ± 0.18	2.33 ± 1.13	0.12 ± 0.07	0.07 ± 0.02	1.25 ± 0.94

Table S50. Transcript abundance for a gene upregulated in the CBB-susceptible RIL at 0 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap) and at 8 and 24 h PI and downregulated at 48 h PI. Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

Gene ID	Gene Annotation	Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
		0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
XLOC_015635	No functional annotation	0 ± 0	0 ± 0	0 ± 0	1.8 ± 1.8	2.2 ± 1.1	0.8 ± 0.8	1.09 ± 1.1	0 ± 0

Table S51. Transcript abundance for genes adversely regulated (up or up and down) in the CBB-susceptible RIL at 8 h and 24 h post-inoculation (PI) with *Xanthomonas axonopodis* (Xap). Transcript levels for individual genes corresponding to each RIL/ inoculation treatment/ sampling time PI are represented as FPKM \pm SE of three experimental replicates.

		Transcript levels (FPKM)							
		Mock inoculation				Xap inoculation			
Gene ID	Gene Annotation	0 h PI	8 h PI	24 h PI	48 h PI	0 h PI	8 h PI	24 h PI	48 h PI
Upregulated									
XLOC_020701	No functional annotation	0.7 ±0.35	0 ±0	0 ±0	1.24 ±0.25	0.39 ±0.39	1.36 ±0.39	2.8 ±0.51	1.08 ±0.54
Downregulated 8 h PI and upregulated 24 h PI									
Phvul.004G092694	Light-harvesting complex II chlorophyll a/b binding protein 1 (LHCB1)	5.87 ±3.49	0.66 ±0.33	0.59 ±0.52	0.5 ±0.28	2.6 ±2.03	0 ±0	2.68 ±1.94	1.26 ±1.26

Table S52. Gene ontology (GO) terms enriched across the differentially expressed genes of the CBB-susceptible RIL at 0 h post-inoculation with *Xanthomonas axonopodis* (Xap).

Gene ID	GO Term	Description
<i>Phvul.001G124300</i>	GO:0004616	Phosphogluconate dehydrogenase (decarboxylating) activity
	GO:0004735	Pyrroline-5-carboxylate reductase activity
	GO:0006098	Pentose-phosphate shunt
	GO:0006561	Proline biosynthetic process
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.002G038600</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Metabolic process
	GO:0016020	Membrane
<i>Phvul.002G038700</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Metabolic process
	GO:0016020	Membrane
<i>Phvul.002G038800</i>	GO:0008415	Metabolic process
	GO:0008610	Lipid biosynthetic process
<i>Phvul.002G038900</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Metabolic process
	GO:0016020	Membrane
	GO:0008415	Metabolic process
	GO:0008610	Lipid biosynthetic process
<i>Phvul.002G039300</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Metabolic process
	GO:0016020	Membrane
<i>Phvul.002G077400</i>	GO:0016757	Transferase activity, transferring glycosyl groups
<i>Phvul.002G096000</i>	GO:0005975	Carbohydrate metabolic process
	GO:0016868	Intramolecular transferase activity, phosphotransferases
<i>Phvul.003G052400</i>	GO:0004553	Hydrolase activity, hydrolyzing O-glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G079900</i>	GO:0004553	Hydrolase activity, hydrolyzing O-glycosyl compounds
	GO:0005975	Carbohydrate metabolic process

Table S52 continued

Gene ID	GO term	Description
<i>Phvul.003G137600</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147300</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147500</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147600</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147700</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G152300</i>	GO:0003854	3- β -hydroxy- Δ 5-steroid dehydrogenase activity
	GO:0006694	Steroid biosynthetic process
	GO:0008831	dTDP-4-dehydrorhamnose reductase activity
	GO:0009058	Biosynthetic process
	GO:0016491	Oxidoreductase activity
	GO:0044237	Cellular metabolic process
	GO:0045226	Extracellular polysaccharide biosynthetic process
	GO:0050662	Coenzyme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.004G022700</i>	GO:0016757	Transferase activity, transferring glycosyl groups

Table S52 continued

Gene ID	GO term	Description
<i>Phvul.004G047900</i>	GO:0004657	Proline dehydrogenase activity
	GO:0006537	Glutamate biosynthetic process
	GO:0006562	Proline catabolic process
	GO:0055114	Oxidation-reduction process
<i>Phvul.004G083200</i>	GO:0008080	N-Acetyltransferase activity
	GO:0008152	Metabolic process
<i>Phvul.005G039200</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.005G111300</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.006G064100</i>	GO:0004645	1,4- α -Oligoglucan phosphorylase activity
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.006G065300</i>	GO:0009228	Thiamine biosynthetic process
<i>Phvul.006G069300</i>	GO:0004066	Asparagine synthase (glutamine-hydrolyzing) activity
	GO:0006529	Asparagine biosynthetic process
<i>Phvul.006G151300</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.006G151400</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.008G103900</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups
<i>Phvul.008G237500</i>	GO:0004356	Glutamate-ammonia ligase activity
	GO:0006542	Glutamine biosynthetic process
	GO:0006807	Nitrogen compound metabolic process
<i>Phvul.008G279800</i>	GO:0016020	Membrane
	GO:0016760	Cellulose synthase (UDP-forming) activity
	GO:0030244	Cellulose biosynthetic process
<i>Phvul.010G042200</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups
<i>Phvul.011G107000</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast

Table S52 continued

Gene ID	GO term	Description
<i>Phvul.011G138600</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups

Table S53. Gene ontology (GO) terms enriched across the differentially expressed genes of the CBB-resistant RIL at 0 h post-inoculation with *Xanthomonas axonopodis* (Xap)

Gene ID	GO term	Description
<i>Phvul.001G226300</i>	GO:0031072	Heat shock protein binding
<i>Phvul.002G077400</i>	GO:0016757	Transferase activity, transferring glycosyl groups
<i>Phvul.002G093000</i>	GO:0031072	Heat shock protein binding
<i>Phvul.002G096000</i>	GO:0005975	Carbohydrate metabolic process
	GO:0016868	Intramolecular transferase activity, phosphotransferases
<i>Phvul.002G168400</i>	GO:0004645	1,4- α -Oligoglucan phosphorylase activity
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.003G004300</i>	GO:0031072	Heat shock protein binding
<i>Phvul.003G047100</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups
<i>Phvul.003G052400</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G137600</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147400</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147500</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147600</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process

Table S53 continued

Gene ID	GO term	Description
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.003G147700</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity
	GO:0048046	Apoplast
<i>Phvul.004G129600</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G129700</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G129800</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G129900</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G130000</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G137600</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.004G138500</i>	GO:0004866	Endopeptidase inhibitor activity
<i>Phvul.005G001000</i>	GO:0016020	Membrane
	GO:0016760	Cellulose synthase (UDP-forming) activity
	GO:0030244	Cellulose biosynthetic process
<i>Phvul.005G156800</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.005G156900</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G034000</i>	GO:0003824	Catalytic activity
	GO:0003854	3- β -hydroxy- Δ 5-steroid dehydrogenase activity
	GO:0006694	Steroid biosynthetic process
	GO:0008831	dTDP-4-dehydrorhamnose reductase activity
	GO:0009058	Biosynthetic process
	GO:0044237	Cellular metabolic process
	GO:0045226	Extracellular polysaccharide biosynthetic process

Table S53 continued

Gene ID	GO term	Description
	GO:0050662	Coenzyme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G064100</i>	GO:0004645	1,4- α -Oligoglucan phosphorylase activity
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.006G151300</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.006G151400</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process
<i>Phvul.006G207600</i>	GO:0031072	Heat shock protein binding
<i>Phvul.007G135800</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups
<i>Phvul.009G002200</i>	GO:0004044	Amidophosphoribosyltransferase activity
	GO:0008152	Metabolic process
	GO:0009113	Purine nucleobase biosynthetic process
	GO:0009116	Nucleoside metabolic process
<i>Phvul.010G134900</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.010G135000</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.010G162600</i>	GO:0031072	Heat shock protein binding
<i>Phvul.011G056500</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.011G085200</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005618	Cell wall
	GO:0005975	Carbohydrate metabolic process
	GO:0006073	Cellular glucan metabolic process
	GO:0016762	Xyloglucan:xyloglucosyl transferase activity

Table S53 continued

Gene ID	GO term	Description
	GO:0048046	Apoplast
<i>Phvul.011G138600</i>	GO:0008152	Metabolic process
	GO:0016758	Transferase activity, transferring hexosyl groups
<i>Phvul.011G167000</i>	GO:0004553	Hydrolase activity, hydrolyzing <i>O</i> -glycosyl compounds
	GO:0005975	Carbohydrate metabolic process

Table S54. Gene ontology (GO) terms enriched across the differentially expressed genes of the CBB-resistant RIL at 24 h post-inoculation with *Xanthomonas axonopodis* (Xap)

Gene ID	GO term	Description
<i>Phvul.001G203300</i>	GO:0009055	Electron transfer activity
	GO:0015035	Protein disulfide oxidoreductase activity
	GO:0045454	Cell redox homeostasis
<i>Phvul.002G275000</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.002G297100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.003G212700</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.003G292400</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.006G111700</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.006G183100</i>	GO:0003700	DNA-binding transcription factor activity
<i>Phvul.007G066500</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.007G273400</i>	GO:0003677	DNA binding
<i>Phvul.008G235100</i>	GO:0005509	Calcium ion binding
	GO:0005578	Extracellular matrix
	GO:0007165	Signal transduction
<i>Phvul.009G089300</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.010G062500</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.010G111900</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.010G120700</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.011G095500</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated

Table S55. Gene ontology (GO) terms enriched across the differentially expressed genes of the CBB-resistant RIL at 48 h post-inoculation with *Xanthomonas axonopodis* (Xap)

Gene ID	GO term	Description
<i>Phvul.001G039900</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.001G040000</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.001G040300</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.001G040700</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.001G042100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.001G042200</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.001G088200</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.001G112400</i>	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
<i>Phvul.001G131000</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0005634	Nucleus
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.001G142000</i>	GO:0009790	Embryo development
<i>Phvul.001G160100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.001G164900</i>	GO:0005634	Nucleus
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.001G192000</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.002G014700</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.002G019100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0005634	Nucleus
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.002G025000</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.002G038600</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane
<i>Phvul.002G038700</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane
<i>Phvul.002G038800</i>	GO:0008415	Transferase activity, transferring acyl groups
	GO:0008610	Lipid biosynthetic process
<i>Phvul.002G038900</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane
<i>Phvul.002G039000</i>	GO:0008415	Transferase activity, transferring acyl groups
	GO:0008610	Lipid biosynthetic process
<i>Phvul.002G039100</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane
<i>Phvul.002G039300</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.002G044100</i>	GO:0008080	N-Acetyltransferase activity
	GO:0008152	Metabolic process
<i>Phvul.002G046100</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G046500</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G076500</i>	GO:0004222	Metalloendopeptidase activity
	GO:0006508	Proteolysis
	GO:0008152	Metabolic process
	GO:0008270	Zinc ion binding
<i>Phvul.002G076600</i>	GO:0004222	Metalloendopeptidase activity
	GO:0006508	Proteolysis
	GO:0008152	Metabolic process
	GO:0008270	Zinc ion binding
<i>Phvul.002G144600</i>	GO:0008270	Zinc ion binding
	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
	GO:0048037	Cofactor binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.002G154600</i>	GO:0006855	Drug transmembrane transport
	GO:0015238	Xenobiotic transmembrane transporter activity
	GO:0015297	Antiporter activity
	GO:0016020	Membrane
<i>Phvul.002G184300</i>	GO:0004315	3-Oxoacyl-[acyl-carrier-protein] synthase activity
	GO:0006633	Fatty acid biosynthetic process
	GO:0008415	Transferase activity, transferring acyl groups
	GO:0016020	Membrane
<i>Phvul.002G199800</i>	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity
	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.002G200600</i>	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity
	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.002G209400</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.002G209500</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.002G215000</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G215100</i>	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G217900</i>	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G219300</i>	GO:0000287	Magnesium ion binding
	GO:0008152	Metabolic process
	GO:0010333	Terpene synthase activity
	GO:0016829	Lyase activity
<i>Phvul.002G223400</i>	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process
	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G265400</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.002G285800</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.002G318200</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.002G326600</i>	GO:0016491	Oxidoreductase activity
	GO:0016706	2-Oxoglutarate-dependent dioxygenase activity
	GO:0055114	Oxidation-reduction process

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.003G009200</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.003G022400</i>	GO:0030001	Metal ion transport
	GO:0046872	Metal ion binding
<i>Phvul.003G024200</i>	GO:0000166	Nucleotide binding
	GO:0003824	Catalytic activity
	GO:0008152	Metabolic process
	GO:0046872	Metal ion binding
<i>Phvul.003G051700</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.003G051900</i>	GO:0005507	Copper ion binding
<i>Phvul.003G074000</i>	GO:0009055	Electron transfer activity
	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.003G088000</i>	GO:0006950	Response to stress
<i>Phvul.003G096700</i>	GO:0006950	Response to stress
<i>Phvul.003G109000</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G109100</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G109200</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G109300</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G109600</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G109800</i>	GO:0006952	Defense response
	GO:0009607	Response to biotic stimulus
<i>Phvul.003G126300</i>	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.003G131500</i>	GO:0010181	FMN binding
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.003G136400</i>	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity
	GO:0009690	Cytokinin metabolic process
	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
<i>Phvul.003G140800</i>	GO:0006355	Regulation of transcription, DNA-templated
	GO:0030528	Transcription regulator activity
<i>Phvul.003G154800</i>	GO:0000902	Cell morphogenesis
	GO:0005524	ATP binding
<i>Phvul.003G166700</i>	GO:0005507	Copper ion binding
	GO:0009055	Electron transfer activity
<i>Phvul.003G166800</i>	GO:0005507	Copper ion binding
	GO:0009055	Electron transfer activity
<i>Phvul.003G182600</i>	GO:0006950	Response to stress
<i>Phvul.003G187200</i>	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.003G212600</i>	GO:0006855	Drug transmembrane transport
	GO:0015238	Xenobiotic transmembrane transporter activity
	GO:0015297	Antiporter activity
	GO:0016020	Membrane
<i>Phvul.003G272900</i>	GO:0003824	Catalytic activity
	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
	GO:0044237	Cellular metabolic process
	GO:0050662	Coenzyme binding
<i>Phvul.003G287400</i>	GO:0008270	Zinc ion binding
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.003G287500</i>	GO:0008270	Zinc ion binding
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.004G018900</i>	GO:0004601	Peroxidase activity
	GO:0006979	Response to oxidative stress
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.004G077400</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.004G092100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.004G122000</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.004G141200</i>	GO:0008060	GTPase activator activity
	GO:0008270	Zinc ion binding
	GO:0032312	Transcription regulator activity
<i>Phvul.005G011100</i>	GO:0000166	Nucleotide binding
	GO:0003824	Catalytic activity
	GO:0008152	Metabolic process
	GO:0046872	Metal ion binding
<i>Phvul.005G108900</i>	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
<i>Phvul.005G109000</i>	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
<i>Phvul.005G111500</i>	GO:0000287	Magnesium ion binding
	GO:0008152	Metabolic process
	GO:0010333	Terpene synthase activity
	GO:0016829	Lyase activity
<i>Phvul.005G113800</i>	GO:0004601	Peroxidase activity
	GO:0006979	Response to oxidative stress
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.005G155800</i>	GO:0004568	Chitinase activity
	GO:0006032	Chitin catabolic process
	GO:0008061	Chitin binding
	GO:0016998	Cell wall macromolecule catabolic process
<i>Phvul.005G173000</i>	GO:0005634	Nucleus
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.006G020700</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.006G074600</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.006G079700</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G090200</i>	GO:0005506	Iron ion binding
	GO:0016021	Integral component of membrane
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0050664	Oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor
<i>Phvul.006G102200</i>	GO:0008061	Chitin binding
	GO:0042742	Defense response to bacterium
	GO:0050832	Defense response to fungus
<i>Phvul.006G102300</i>	GO:0042742	Defense response to bacterium
	GO:0050832	Defense response to fungus
<i>Phvul.006G124600</i>	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity
	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G124700</i>	GO:0008762	UDP-N-acetylmuramate dehydrogenase activity
	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G129500</i>	GO:0004601	Peroxidase activity
	GO:0006979	Response to oxidative stress
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G135600</i>	GO:0030001	Metal ion transport
	GO:0046872	Metal ion binding
<i>Phvul.006G181300</i>	GO:0009055	Electron transfer activity
	GO:0015035	Protein disulfide oxidoreductase activity
	GO:0045454	Cell redox homeostasis
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G188900</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.006G192400</i>	GO:0016491	Oxidoreductase activity
	GO:0050660	Flavin adenine dinucleotide binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.006G194600</i>	GO:0004674	Protein serine/threonine kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.006G195600</i>	GO:0000287	Magnesium ion binding
	GO:0008152	Metabolic process
	GO:0010333	Terpene synthase activity
	GO:0016829	Lyase activity
<i>Phvul.006G195700</i>	GO:0000287	Magnesium ion binding
	GO:0008152	Metabolic process
	GO:0010333	Terpene synthase activity
	GO:0016829	Lyase activity
<i>Phvul.006G198200</i>	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G048500</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G048600</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G048800</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G048900</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G049100</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G052500</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.007G222500</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G259400</i>	GO:0009790	Embryo development
<i>Phvul.007G260400</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.007G273000</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.007G278900</i>	GO:0005509	Calcium ion binding
	GO:0005578	Carbohydrate binding
	GO:0007165	Signal transduction
<i>Phvul.008G011400</i>	GO:0000902	Cell morphogenesis
	GO:0005524	ATP binding
<i>Phvul.008G011500</i>	GO:0047134	Protein-disulfide reductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G011800</i>	GO:0047134	Protein-disulfide reductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G011900</i>	GO:0000902	Cell morphogenesis
	GO:0005524	ATP binding
<i>Phvul.008G015800</i>	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G032200</i>	GO:0016747	Transferase activity, transferring acyl groups other than amino-acyl groups
<i>Phvul.008G037300</i>	GO:0005509	Calcium ion binding
	GO:0005578	Carbohydrate binding
	GO:0007165	Signal transduction
<i>Phvul.008G040800</i>	GO:0004222	Metalloendopeptidase activity
	GO:0006508	Proteolysis
	GO:0008270	Zinc ion binding
	GO:0016021	Integral component of membrane
<i>Phvul.008G076300</i>	GO:0005506	Iron ion binding
	GO:0006633	Fatty acid biosynthetic process
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.008G076500</i>	GO:0006694	Steroid biosynthetic process
	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
	GO:0044237	Cellular metabolic process
	GO:0050662	Coenzyme binding
<i>Phvul.008G076600</i>	GO:0006694	Steroid biosynthetic process
	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
	GO:0044237	Cellular metabolic process
	GO:0050662	Coenzyme binding
<i>Phvul.008G094500</i>	GO:0004672	Protein kinase activity
	GO:0005488	Binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.008G098500</i>	GO:0016491	Oxidoreductase activity
	GO:0016706	2-Oxoglutarate-dependent dioxygenase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G112200</i>	GO:0005507	Copper ion binding
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G127200</i>	GO:0016491	Oxidoreductase activity
	GO:0016706	2-Oxoglutarate-dependent dioxygenase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G194600</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.008G218500</i>	GO:0004601	Peroxidase activity
	GO:0006979	Response to oxidative stress
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G223500</i>	GO:0016491	Oxidoreductase activity
	GO:0016706	2-Oxoglutarate-dependent dioxygenase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G248900</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
	GO:0007165	Signal transduction
<i>Phvul.008G249900</i>	GO:0004601	Peroxidase activity
	GO:0006979	Response to oxidative stress
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process

Table S55 Continued

Gene ID	GO term	Description
<i>Phvul.008G285000</i>	GO:0000166	Nucleotide binding
	GO:0046872	Metal ion binding
<i>Phvul.008G287200</i>	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.008G287300</i>	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.009G043100</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.009G043200</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.009G046900</i>	GO:0004672	Protein kinase activity
	GO:0005515	Protein binding
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.009G080000</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.009G087400</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.009G089300</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.009G138900</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.009G156300</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.009G182300</i>	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.009G231600</i>	GO:0006355	Regulation of transcription, DNA-templated
	GO:0030528	Transcription regulator activity
<i>Phvul.009G235700</i>	GO:0006355	Regulation of transcription, DNA-templated
	GO:0030528	Transcription regulator activity
<i>Phvul.009G244100</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.009G244100</i>	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.009G244200</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.009G262900</i>	GO:0005515	Protein binding
	GO:0016702	Oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen
	GO:0046872	Metal ion binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.010G000300</i>	GO:0016491	Oxidoreductase activity
	GO:0016706	2-Oxoglutarate-dependent dioxygenase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.010G005900</i>	GO:0005507	Copper ion binding
	GO:0016491	Oxidoreductase activity
	GO:0055114	Oxidation-reduction process
<i>Phvul.010G032000</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.010G057300</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.010G057500</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.010G057600</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.010G111900</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding

Table S55 continued

Gene ID	GO term	Description
<i>Phvul.010G117200</i>	GO:0003700	DNA-binding transcription factor activity
	GO:0005634	Nucleus
	GO:0006355	Regulation of transcription, DNA-templated
	GO:0043565	Sequence-specific DNA binding
<i>Phvul.010G128900</i>	GO:0009055	Electron transfer activity
	GO:0016705	Oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
	GO:0020037	Heme binding
	GO:0055114	Oxidation-reduction process
<i>Phvul.011G013600</i>	GO:0000287	Magnesium ion binding
	GO:0008152	Metabolic process
	GO:0010333	Terpene synthase activity
	GO:0016829	Lyase activity
<i>Phvul.011G035600</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0006468	Protein phosphorylation
<i>Phvul.011G041400</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.011G044500</i>	GO:0006694	Steroid biosynthetic process
	GO:0016616	Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
	GO:0044237	Cellular metabolic process
	GO:0050662	Coenzyme binding
<i>Phvul.011G147800</i>	GO:0003677	DNA binding
	GO:0006355	Regulation of transcription, DNA-templated
<i>Phvul.011G150400</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation
<i>Phvul.011G179600</i>	GO:0008270	Zinc ion binding
<i>Phvul.011G214400</i>	GO:0004672	Protein kinase activity
	GO:0005524	ATP binding
	GO:0005529	Carbohydrate binding
	GO:0006468	Protein phosphorylation

Table S56. UHPLC-MS/MS identification of flavonols and isoflavones in acidified methanolic extracts of leaves sampled from CBB-resistant and CBB-susceptible *P. vulgaris* leaves.

Compound	Chemical Formula	Retention Time (min)	Parent Ion [M-H] ⁻	Fragment Ion(s) [M-H] ⁻
Quercetin rutinoside-xyloside (1)	C ₃₂ H ₃₈ O ₂₀	22.46	741.1891	609.1483, 301.0355, 300.0278, 178.9989
Quercetin glucoside-xyloside (1)	C ₂₆ H ₂₈ O ₁₆	22.7	595.1309	595.1312, 463.0536, 301.0357, 300.0279
Quercetin glucuronide-xyloside	C ₂₆ H ₂₆ O ₁₇	22.86	609.11	301.0353, 300.0276, 178.9984, 151.0039
Quercetin glucoside-xyloside (2)	C ₂₆ H ₂₈ O ₁₆	22.9	595.1309	595.1309, 463.0536, 301.0356, 300.0278
Kaempferol diglucoside (1)	C ₂₇ H ₃₀ O ₁₆	23.42	609.1466	609.1465, 285.0399, 284.0324
Quercetin rutinoside-xyloside (2)	C ₃₂ H ₃₈ O ₂₀	23.45	741.1891	741.1905, 301.0363, 300.0274
Kaempferol diglucoside (2)	C ₂₇ H ₃₀ O ₁₆	23.68	609.1466	609.1465, 285.0399, 284.0324
Quercetin dixyloside (1)	C ₂₅ H ₂₆ O ₁₅	24.67	565.1202	565.1201, 301.0354, 300.0275, 178.9984
Kaempferol rutinoside-xyloside	C ₃₂ H ₃₈ O ₁₉	24.71	725.1945	725.1941, 593.1503, 285.0403, 284.0325
Quercetin 3- <i>O</i> -galactoside	C ₂₁ H ₂₀ O ₁₂	24.74	463.0882	463.0875, 301.0349, 300.0273, 255.0286

Table S56 continued

Compound	Chemical Formula	Retention Time (min)	Parent Ion [M-H] ⁻	Fragment Ion(s) [M-H] ⁻
Quercetin 3- <i>O</i> -glucuronide	C ₂₁ H ₁₈ O ₁₃	24.91	477.0674	301.0353, 178.9987, 151.0038
Quercetin 3- <i>O</i> -glucoside	C ₂₁ H ₂₀ O ₁₂	24.97	463.0882	463.0880, 301.0352, 300.0274, 271.0250
Quercetin 3- <i>O</i> -rutinoside	C ₂₇ H ₃₀ O ₁₆	25.01	609.1461	609.1465, 301.0352, 300.0274, 178.9977
Kaempferol glucoside-xyloside	C ₃₂ H ₃₈ O ₁₉	25.24	579.1349	579.1351, 447.0923, 285.0403, 284.0326
Quercetin dixyloside (2)	C ₂₅ H ₂₆ O ₁₅	25.28	565.1202	565.1194, 301.0350, 300.0275
Quercetin xyloside	C ₂₀ H ₁₈ O ₁₁	25.59	433.0779	433.0747, 301.0352, 300.0276, 271.0612
Isorhamnetin glucoside-xyloside	C ₂₇ H ₃₀ O ₁₆	25.63	609.1454	609.1470, 315.0512, 314.0432, 300.0276
Kaempferol glucuronide	C ₂₁ H ₁₈ O ₁₂	27.34	461.0729	285.0403, 113.0247, 85.0596, 59.0136
Kaempferol rutinoside	C ₂₇ H ₃₀ O ₁₅	27.53	593.1512	593.1514, 285.0404, 284.0325
Isorhamnetin glucuronide	C ₂₂ H ₂₀ O ₁₃	28.16	491.0832	315.0512, 300.0275, 113.0248, 85.0297
Daidzein	C ₁₅ H ₁₀ O ₄	28.6	253.0506	253.0510, 224.0482, 209.0612

Table S56 continued

Compound	Chemical Formula	Retention Time (min)	Parent Ion [M-H] ⁻	Fragment Ion(s) [M-H] ⁻
Genistein	C ₁₅ H ₁₀ O ₅	31.59	269.0451	269.0457, 224.0475, 133.0293
Coumestrol ¹	C ₁₅ H ₈ O ₅	33.86	267.0299	267.0299, 266.0220, 239.0351, 211.0403
Phaseollinisoflavan	C ₂₀ H ₂₀ O ₄	38.2	323.1295	323.1292, 282.9808, 201.0924, 135.0454

¹ Identified via co-elution with an authentic coumestrol standard. All other compounds were identified on the basis of their MS parent and fragment ion data and compared to a MS/MS library for flavonols and isoflavones, and the scientific literature as described in section 4.5 of the Materials and Methods.

Figure S1. Negative ion UHPLC-MS/MS analysis of the leaves of the CBB-resistant RIL following *X. axonopodis* inoculation detected a peak (retention time = 38.2 min) with MS/MS fragmentation data matching phaseollinisoflavan

