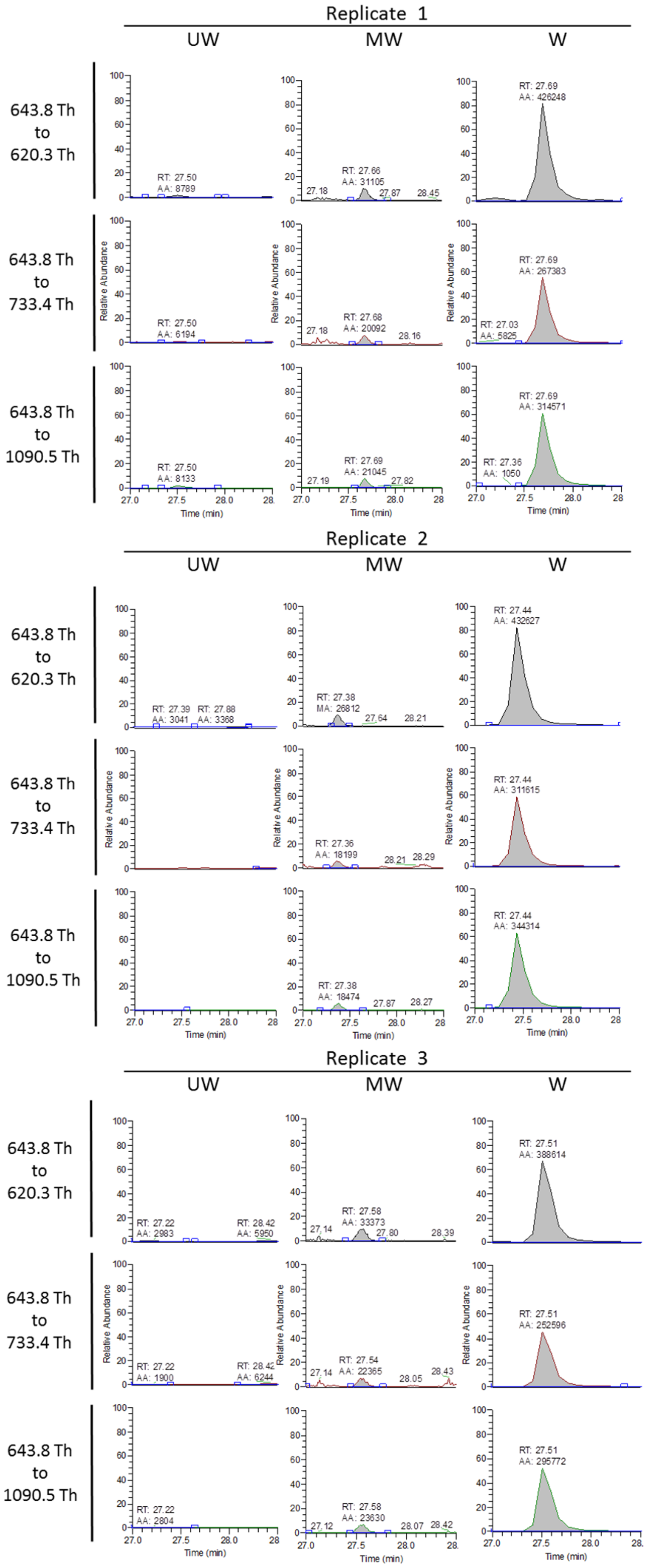
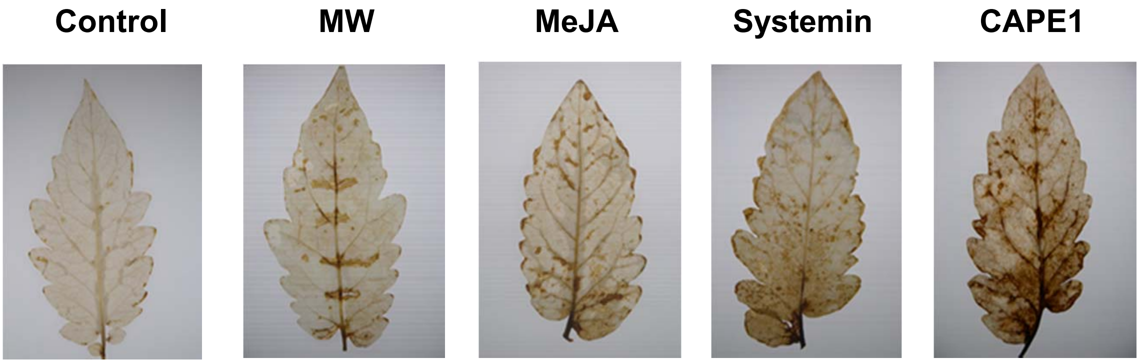
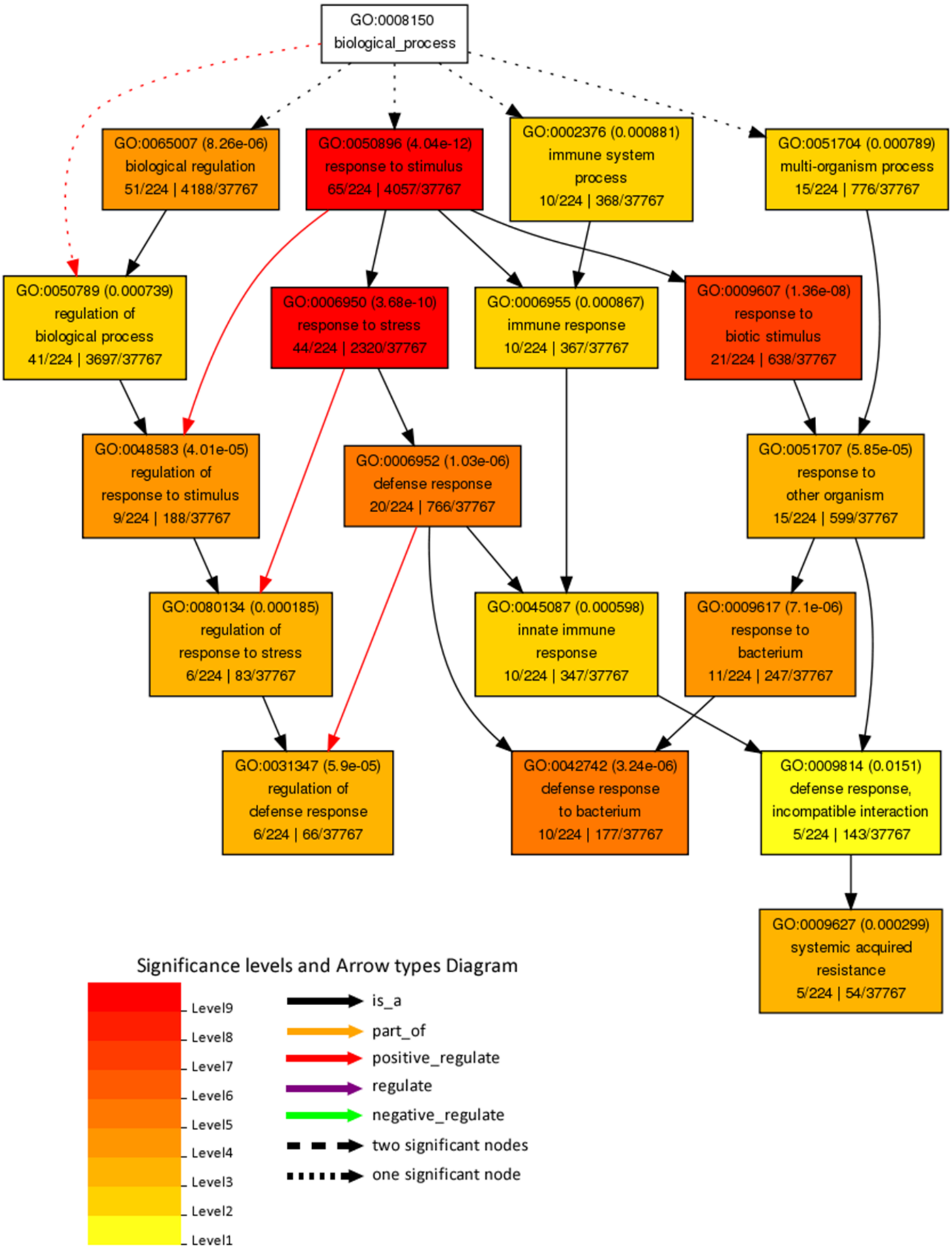


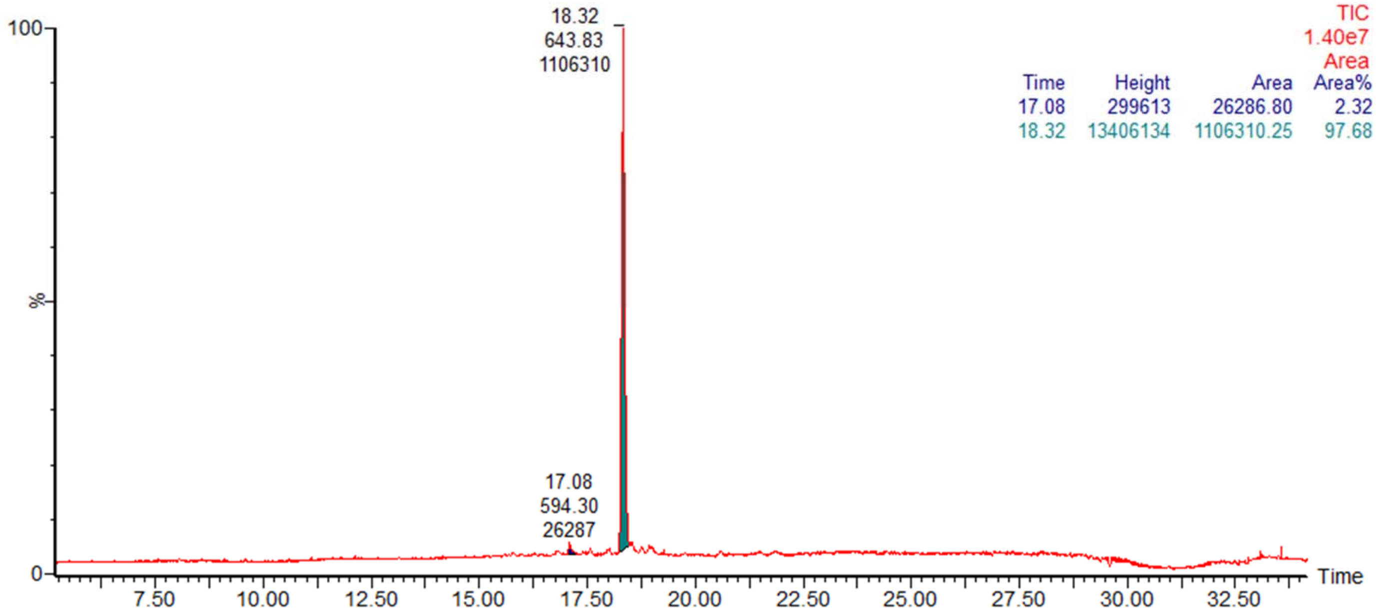
Supplemental Figure 1. Abundances of selected CAPE1 transitions in unwounded (UW), mechanically wounded (MW) and wounded plus MeJA (W) treated tomato. The doubly charged CAPE1 precursor m/z 643.8 was selected and targeted to the fragments of 620.3, 733.4 and 1090.5 using nanoUHPLC-SRM-MS.



Supplemental Figure 2. Study of CAPE1 bioactivities in the triggering of leaf tissue H_2O_2 production. Detached tomato leaves were treated with water (Control), mechanical wounding (MW), 1.25 mM MeJA, 250 nM systemin and 250 nM CAPE1 peptide for 4 hours, respectively. After the treatment, 1 mg/ml of diaminobenzidine (DAB) was applied to visualize H2O2 accumulation. Images are representative of the results of three biological repeats.



Supplemental Figure 3. Functional categorization of the defense genes induced by CAPE1 using hierarchy of GO categorization analyzed by Blast2GO and agriGO. The significance levels diagram showed the grade of color of a box is positively correlated to the GO enrichment level of the term. Solid, dashed, and dotted lines represent two, one and zero enriched terms at both ends connected by the line, respectively. The rank direction of the graph is set to from top to bottom.



Time	Height	Area	Area%
17.08	299613	26286.80	2.32
18.32	13406134	1106310.25	97.68

Supplemental Figure 4. Purity evaluation of CAPE1 peptide using nanoUHPLC-MS. Synthetic CAPE1 peptide (0.4 pmol) was analyzed by nanoUHPLC-MS with 35 min gradient and the chromatographic peak areas of the CAPE1 and impurities were labeled and integrated. The CAPE1 peptide purity was determined to be 97.68%.

Supplemental Table 1. Total identified and quantified endogenous peptides observed in unwounded and wounded plus MeJA treated tomato.

Proprotein Information		Peptide Identification										Peptide Ratio (W/UW)[a]	
Accession Number	**Description**	**Peptide Sequence**	**MD Score**	**MASCOT Score**	**Observed M/Z**	**Z**	**Observed MW**	**Theor. MW**	**Mass Error**	**Scoring Fragments**	**RT (min)**	**Ratio**	**Norm. Ratio**
Internal Standard	β-casien	LLYQEPVLGPVR	36.84~61.66	51.47~78.69	692.42	2	1382.83	1382.79	±0.08	6~10	38.75~40.20	1.63	1.00
Solyc05g051750.2.1	Prosystemin	AVQSKPPSKRDPPKMQTD	21.35	38.18	1005.54	2	2009.07	2009.04	0.04	18	21.52	9999[b]	**9999[b]**
Solyc05g025600.1.1	Chloroplast photosystem II subunit X	VSNFDPVKR	21.71	40.69	531.28	2	1060.55	1060.57	-0.01	5	26.16	9999[b]	**9999[b]**
Solyc00g174340.1.1	Pathogenesis-related protein 1b	PVGNWIGQRPY	41.91	53.37	643.86	2	1285.7	1285.66	0.05	8	36.84	9999[b]	**9999[b]**
Solyc01g007350.2.1	Photosystem I reaction center subunit VIII	ASLFLHVQKNK	38.52	56.85	642.88	2	1283.75	1283.73	0.01	7	29.04	19.08	**11.71**
Solyc12g035280.1.1	Photosystem II CP47 chlorophyll apoprotein	LGDPTTKRQAA	26.31	45.66	579.33	2	1156.65	1156.62	0.03	5	21.47	7.70	**4.72**
Solyc11g071640.1.1	Beta-D-glucosidase	SHNDPLFHFGFGLTTKPVK	45.86	46.63	714.73	3	2141.16	2141.11	0.05	14	41.75	4.43	**2.72**
Solyc01g104170.2.1	Ankyrin repeat domain-containing protein 2	DVLKLLEKDAFL	21.47~32.00	38.68~42.18	702.42	2	1402.82	1402.81	0.01	8	50.47	4.04	**2.48**
Solyc04g082010.1.1	Plastocyanin	LLNAAGETYSVTLSE	30.74~49.74	43.55~59.25	784.4	2	1566.78	1566.78	±0.01	10~11	40.54~40.74	2.37	1.45
Solyc09g059020.2.1	Alcohol dehydrogenase zinc-containing	ENLELIVGLVKEGK	47.66	69.64	770.96	2	1539.91	1539.89	0.02	8	44.17	1.91	1.17
Solyc11g072190.1.1	Elongation factor beta-1	VSVDTLIEERL	33.72~57.55	43.22~81.11	637.35	2	1272.69	1272.69	±0.01	6~8	43.81~44.15	1.27	0.78
Solyc08g007510.2.1	ER-derived vesicles protein ERV14	LAHIIILL	40.23	44.88	453.34	2	904.67	904.61	0.06	5	44.96	0.83	0.51
Solyc06g007800.2.1	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	KLPEWSPIQVL	23.26	38.05	655.39	2	1308.77	1308.74	0.02	5	38.29	0.81	**0.50**
Solyc06g050910.1.1	Unknown Protein	IKLPLILQ	42.56	58.07	469.34	2	936.67	936.64	0.03	6	43.54	0.69	**0.42**
Solyc05g055310.2.1	Copper chaperone	FDIDLKEQK	26.49~29.47	42.12~44.02	568.3	2	1134.59	1134.59	±0.02	8	32.08~32.28	0.13	**0.08**
Solyc05g054070.2.1	60S ribosomal protein L6	KAIEGIPELKAYLSARF	36.14	46.13	636.04	3	1905.1	1905.07	0.03	7	44.69	-9999[c]	**-9999[c]**
Solyc05g056390.2.1	chaperonin	FHLYRDEDILGTL	25.17~35.59	43.33~61.11	796.39	2	1590.76	1590.8	±0.05	6~15	43.57~43.96	-9999[c]	**-9999[c]**
Solyc07g044860.2.1	Oxygen-evolving enhancer protein 2, chloroplastic	KFVENAATSFSI	39.23	49.38	657.35	2	1312.69	1312.67	0.03	8	40.20	111.62	**68.48**
		KFVENAATSFSIA	40.16~58.74	59.38~78.22	692.86	2	1383.7	1383.7	0	9~10	38.47~39.02	1.25	0.77
Solyc06g063370.2.1	Chlorophyll a-b binding protein 1A, chloroplastic	LTVIGGASERVPT	22.63~62.90	41.92~86.53	650.39	2	1298.77	1298.72	±0.05	6~10	33.38~35.15	3.73	**2.29**
		TVIGGASERVPT	24.32~35.54	40.62~47.29	593.83	2	1185.65	1185.64	0.01	7	28.78	0.57	**0.35**
Solyc02g038690.1.1	Histone H2B	IQTAVRLVLPGE	29.2	38.23	648.41	2	1294.8	1294.76	0.04	6	41.81	5.35	**3.28**
		IQTAVRLVLPGEL	28.01~54.30	41.74~67.78	704.94	2	1407.86	1407.84	±0.01	13~15	46.23~46.76	0.27	**0.17**
		EIQTAVRLVLPGEL	29.75~49.83	42.82~62.43	769.44	2	1536.87	1536.89	-0.02	13~17	46.67~46.94	0.80	**0.49**
Solyc01g087520.2.1	Ferredoxin-thioredoxin reductase variable chain	EGRSTPVKFSAHLKEDE	24.72~59.75	37.34~67.73	483.24	4	1928.92	1928.96	-0.04	8	26.67	1.94	1.19
		EGRSTPVKFSAHLKED	27.28	39.74	600.97	3	1799.9	1799.92	-0.02	8	26.58	29.71	**18.23**
		EGRSTPVKFSAHLKEDE	24.72~59.75	37.34~67.73	644.01	3	1929.01	1928.96	±0.05	8~9	26.67~27.01	6.23	**3.82**
		PYKVEFVVDDL	26.93	42.95	662.35	2	1322.68	1322.68	0.01	7	44.66	0.14	**0.09**
		YVAVHKGKQISANLPYKVEFVVDDL	47.47	47.47	708.89	4	2831.51	2831.52	-0.01	10	42.43	0.27	**0.17**
Solyc09g063130.2.1	Photosystem I reaction center subunit IV A	PKTRYPVVVR	20.95~27.72	37.64~46.28	607.86	2	1213.71	1213.73	-0.02	6	25.38	9.90	**6.07**
		NKVNYANVSTN	26.20~33.25	40.05~48.23	612.31	2	1222.6	1222.59	±0.01	6~11	23.52~24.20	0.33	**0.20**
		NKVNYANVSTNNY	23.06	38.75	750.86	2	1499.71	1499.7	0.01	6	28.62	1.40	0.86
		NKVNYANVSTNNYA	31.07~67.87	40.19~73.19	786.4	2	1570.78	1570.74	±0.05	7~11	28.61~28.82	2.46	1.51
		FNKVNYANVSTNNYALDEVEEVK	31.18~85.88	40.12~91.04	887.46	3	2659.37	2659.28	±0.09	8~20	38.14~38.75	20.97	**12.87**
		NKVNYANVSTNNYALDE	40.55~57.53	44.58~63.34	965	2	1927.98	1927.89	±0.09	10~14	32.46~34.21	0.43	**0.26**
		NKVNYANVSTNNYALDEVE	56.12~79.63	57.96~86.34	1079.02	2	2156.03	2156	±0.02	12~14	36.34~36.41	5.70	**3.50**
		FNKVNYANVSTNNYALDEVE	55.72~58.40	55.72~64.74	1152.56	2	2303.11	2303.07	±0.04	10	37.91~37.96	3.25	1.99
		NKVNYANVSTNNYALDEIEEV	49.06~54.60	53.05~61.02	1200.07	2	2398.12	2398.13	±0.02	10	42.06~42.11	0.02	**0.01**
Solyc01g107330.2.1	SWIB/MDM2 domain protein	LEIAGLISPHFLK	26.97~42.08	42.89~78.24	719.44	2	1436.87	1436.84	±0.04	9	46.12~46.68	0.72	**0.44**
		LEIAGLISPHFL	23.09~28.06	37.41~49.38	655.36	2	1308.71	1308.74	±0.03	6	51.77~52.04	2.45	1.50
Solyc04g014720.2.1	60S ribosomal protein L6	AVPDLKGYLSARF	22.52~35.40	38.35~42.62	718.89	2	1435.77	1435.78	-0.01	7~8	42.27~42.56	0.15	**0.09**
		IKAIEAVPDLKGYLSARF	40.77	48.09	664.36	3	1990.05	1990.13	-0.07	17	43.84	0.27	**0.16**
Solyc12g099240.1.1	Huntingtin interacting protein K	LAAVKINAADIDIIANE	28.91	39.53	877.48	2	1752.96	1752.96	-0.01	8	43.82	0.84	**0.52**
		LAAVKINAADIDIIANEL	22.38~73.78	46.63~86.26	934.05	2	1866.09	1866.05	±0.04	11~12	50.69~50.87	0.57	**0.35**
Solyc11g012110.1.1	60S ribosomal protein L6	PELKGYLSARF	29.23	46.33	640.86	2	1279.7	1279.69	0.01	9	40.66	-9999	**-9999[b]**
		AVPELKGYLSARF	32.86~40.56	44.38~51.03	725.88	2	1449.75	1449.8	±0.05	9~10	40.35~40.64	0.37	**0.23**
		IKAIEAVPELKGYLSARF	30.32~37.44	39.62~44.65	669.06	3	2004.16	2004.14	0.02	7	43.27	0.02	**0.01**

[a] ratio of the peptide intensity observed in unwounded (UW) and wounded plus MeJA (W) treated plants

[b] the peptide was only detected in wounding plus MeJA (W) treated sample (S/N < 10 in unwounded samples)

[c] the peptide was only detected in unwounded sample (S/N < 10 in wounded plus MeJA (W) treated sample samples)

Supplemental Table 2. Primers used in this study.

Gene	Gene Accession #	Primer (5'->3')	Product size (bp)
Elongation Factor 1α (EF-1α)	X14449	For: CTCCGTCTTCCACTTCAGG Rev: TCAGTTGTCAAACCAGTAGGG	128
Ubiquitin 3 (Ubi3)	X58523	For: ACTCTTGCCGACTACAACATCC Rev: CTCCTTACGAAGCCTCTGAACC	198
Proteinase Inhibitor 1 (PI-1)	K03290	For: CTTCTTCCAACTTCCTTTG Rev: TGTTTTCCTTCGCACATC	110
Proteinase Inhibitor 2 (PI-2)	K03291	For: AATTATCCATCATGGCTGTTCAC Rev: CCTTTTTGGATCAGATTCTCCTT	254
AvrPto-dependent Pto-interacting protein 3 (Adi3)	NM_001247682	For: AGGCAGTTTCCTATAGGGGCTA Rev: TCGACCATCAGGTCTTCTTCC	155
Ethylene response factor 5 (ERF5)	NM_001247583	For: ATGGGTTCTCCACAAGAGAC Rev: GAAGCTTGCGATGTCATCAA	132
Pahtogenesis-related protein 1b (PR-1b)	M69248.1	For: CTCATATGAGACGTCGAGAAG Rev: GGAAACAAGAAGATGCAGTACTTAA	204
beta-1,3-glucanase (PR-2)	NM_001247869.1	For: CAAATAACAGGAGCGCAGCC Rev: GTTACTTCCTTTGAGGGCAT	163
Cys protease (PR-7)	CK574973.1	For: TCAGCACCTCTGGACCTTT Rev: GCTCCTGAAGGCTCTGTTA	141
Class II chitinase (Chi;2)	U30465.1	For: TTTTGGTCGAGGTCCTATCC Rev: GTAATGACATCGTGTGCCGA	186
WRKY transcription factor 53 (WRKY53)	Solyc08g008280.2.1	For: AAATGGATTGTGCATCAAACTGGGA Rev: AGCCACCCCAGTTGAGAATCAACA	189