

Table S1 Description of the three reference genes (RG) and their amplified sequences

RG	Gene description	Homological species	Nr-ID	Original sequence CDS	Primer sequences (forward/reverse)	Amplicon sequences (bp)	Amplicon length (bp)	Identity(%)
<i>UBQ14</i>	Polyubiquitin 14	Arabidopsis thaliana	gi 356548684 ref XP_003542730.1	ATGCAGATTTTGTGAAGACCTTGACTGG AAAGACCATCACTTTGGAGGTTGAGAGTT CTGACACGATTGATAATGTTAAAGCCAAGA TTCAGGACAAGGAGGGGATTCCCCAGAT CAGCAGCGTTTGATATTGCTGGGAAGCA GTTGGAGGATGGCCGACTCTTGCAAGTA CAACATTCAAAGGAGTCTACCCTTCACC TTGTGCTTCGTCTCCGTGGTGGG	AAGCCAAGAT TCAGGACAAG /GGAGACGAA GCACAAGGT	AAGCCAAGATTC AGGACAAGGAGG GGATTCCCCCAG ATCAGCAGCGTT TGATATTTGCTGG GAAGCAGTTGGA GGATGGCCGTAC TCTTGCAGATTAC AACATTCAAAG GAGTCTACCCTTC ACCTTGTGCTTCG TCTCC	141	100.00
<i>UBQ4-1</i>	Polyubiquitin 4	Arabidopsis thaliana	gi 357148706 ref XP_003574865.1	GGCCGAACCCTAGCGGATTACAACATCCA AAAGGAGTCCACCCTCCATCTGGTGCTTC GTCTCAGAGGTGGTATGCAGATCTTCGTCA AAACCCTAACAGGCAAAACCATCACCTT GAAGTCGAGAGCTCCGACACCATTGACAA CGTTAAAGCTAAGATTCAAGACAAGGAGG GAATTCCCCCGACCAGCAGAGGCTGATC TTCGCCGCAAGCAATTGGAAGATGGAAG GACCCTTGCCGATTACAACATCCAGAAAG	CCGTCTTCGT GGAGGTAT/CT GTTGGTCTGG TGGAATC	CCGTCTTCGTGGA GGTATGCAGATT TTTGTCAAGACCT CACCGGAAAAAC CATTACTTTGGAA GTGAGAGCTCAG ACACCATTGACA ATGTGAAGGCCA AGATCAGGATAA	139	100.00

				AATCAACTCTTCACTTGGTCCTCCGTCTTC		GGAAGGGATTCC		
				GTGGAGGTATGCAGATTTTTGTCAAGACC		ACCAGACCAACA		
				CTCACCGGAAAAACCATTACTTTGGAAGT		G		
				GGAGAGCTCAGACACCATTGACAATGTGA				
				AGGCCAAGATCCAGGATAAGGAAGGGATT				
				CCACCAGACCAACAGAGGCTGATTTTCGC				
				CGGGAAGCAGCTTGAAGATGGAAGGACG				
				TTGGCAGACTACAACATTCAAAGGAGTC				
				GACTCTCCACTTGGTCCTTCGTCTCCGTGG				
				AGGT				
				ATGGACAACACCTTCTTGTTACCTCAGA				
				GTCAGTGAATGAGGGCCACCCGACAAGC		GCCAAGACCAAC		
				TCTGCGATCAGGTCTCTGATGCTGTGCTCG		CTAGTAATGGTG		
				ACGCTTGCCTGGAGCAGGATCCCAGAGC		TTTGGTGAAATC		
				AAAGTCGCTTGTGAGACTTGTGCCAAGAC		ACCACCAAGGCC		
				CAACCTAGTAATGGTGTTTGGTAAAATCAC	GCCAAGACCA	AAAGTAAACTAC		
<i>SAMS</i>	S-adenosylmet	Phaseolus	gi 75304713 sp	CACCAAGGCCAAAAGTAAACTACGAAAAG	ACCTAGTAAT/	GAAAAGATCGTT	126	100.00
	hionine	lunatus	Q8W3Y4.1 ME	ATCGTTCGTGACACCTGCAGAAATATTGGC	AGCATCAAGA	CGTGACACCTGC		
	synthase		TK_PHALU	TTCGTCTCTCATGATGTTGGTCTTGATGCT	CCAACATCAT	AGAAATATTGGC		
				GACAATTGCAAGGTCTTGGTCCACATTGAT		TTCGTCTCTCATG		
				CAGCAAAGCCCTGATATTGCTCGGGGTGT		ATGTTGGTCTTGA		
				CCATGGTCACAACACCAAACGCCCCGAGG		TGCT		
				AGATT				

Raw sequences of reference genes and their PCR-amplified sequences were identical

Table S2 Specific primers of genes of interest (GOIs) used to validate the RNA-seq data

No.	GOI	Forward primer	Reverse primer
1	CL554.Contig1_All	ACCGTCTAGTCCGTGATG	CGATTCTCCATACCACAAGG
2	CL194.Contig1_All	CTTGCGGAACAGATACTT	TCTTCTATCAGGCGGCTAT
3	CL194.Contig2_All	TCAGAGGAGCAGAGAAGAG	GAGAGCAGAACATCAATCATC
4	CL2377.Contig1_All	CCAAGACAATAGCGAGGAT	ATGAAGGAGTTCTGCCATC
5	CL2671.Contig3_All	GGTTGAGAAGAATAAGGATGG	TGGAGAGTGTGACATTAGAC
6	CL4001.Contig3_All	CTCATCCTCATCTTCCTCAC	GAAGTCGTTCTCTAGCATTG
7	CL4287.Contig2_All	CCTTGTTCTCCTCAATGTATG	AATGCTGTCCTCTGTAATCT
8	CL4799.Contig3_All	GGAGATTAGGAAGGCACAA	TTGGTGATGCGGAAGTAAT
9	CL5341.Contig4_All	GAGAGCGGTGGAATCATG	CTAAGGCGATGCTGATCC
10	CL5399.Contig4_All	AAGTTCAGTAGGAGCCAATG	ACTACAGCCTCAACAATTCC
11	CL5403.Contig3_All	TTGTTCTCGGAGTGTACTACT	GGATGCGGTGGATGATGT
12	CL556.Contig4_All	ACACGAACTCCAACATAGAC	CCTCCAAGAACACGACTG
13	CL8155.Contig1_All	ACCTTGTTTCGTTACTCCATT	CGGCAGACTTGACAGAAT
14	CL8199.Contig1_All	TAGGCTACGGAACCAACT	TAGTGGCAGGAGGAGTAG
15	CL11757.Contig1_All	CAACAACCTCATCATCATCATC	GCACAGGACGGAGTAGTT
16	CL2466.Contig2_All	GCTCACAGGATCATCTACT	TTCTCAACACTCACTCAACT
17	CL2476.Contig1_All	GCCTTCCGTCTTCAGATT	GCTTATCACCTCGCAGTT
18	CL2476.Contig2_All	CATCTGCCAACCGTCTTC	CGTGATATGCTCCAAGTAGT
19	CL4508.Contig1_All	TTCCTCCTCCTCACAGTT	GTCGTTGCTGGAAGTAGT
20	CL5630.Contig4_All	CAGTGGCATAGGCAACTT	AGATGTGGTAGGAGGAGAG
21	CL7754.Contig1_All	AAGTATTGGTGCCGAAGG	ATCTGCTGAGGTGGTAGT
22	Unigene1793_All	GTTGGCGACGGAGATAAG	TCCTTCACCTTCTTCTTCAC
23	Unigene2635_All	GCCGTTGAGTGTAAGTGT	TCTCCTGGTGTGTCATCTCC
24	Unigene3242_All	ATGACACTCTTCCTGATGG	TCACTAAGCCACCGTTCT
25	Unigene4450_All	GGTGACAAGTATGAGAGTATGA	GCCTCCTCAACCACAGTT
26	Unigene6757_All	TACATTCACCGAGTTGGAG	CTTACGACCGAGGTTGAG
27	Unigene7583_All	CACTCTTACATTGCGTCTCT	GACTCCGTGGTGTGATAG
28	Unigene8987_All	TGGAAGCGGTTAGAGATG	TGCCAATCCTACTCAACTC
29	Unigene10228_All	GTCTGAACAAGTGGAGGAG	CCTACTAGCCAGCCTAAGA
30	Unigene12763_All	GCCAGCATCAACAATG	CCATTCTTACAGCACTCCT
31	Unigene12765_All	CATCACAGGAGTTCTTGGAT	CCGCATCACGCCTTATAC
32	Unigene14565_All	AGTGGTGGACAACAAGTTC	GGACAGGAGGAAGCAAGT
33	Unigene14931_All	CCTCGTCATCATCGTTCC	AAGTTGAGGCGGTGTATG
34	Unigene15235_All	GTCCAGTCCTTCTTCAAT	TGGCATTATCAACCTCTTCC
35	Unigene15442_All	CCGTCTCTTCCACTCTTC	ACGAGGAGGAGATTATGATG
36	Unigene17080_All	TCACCACCGCTAATCCTT	ATCATCTCCAACGCTAAGTC
37	Unigene17201_All	ATGCGAAGTGTCCGATT	CATCATTATCCGTGACACAT
38	Unigene18031_All	GCTTAACGAACGGATACCT	CGTCGGTGGTTCTAATGAT

39	Unigene18687_All	CCTCATCCTCAACAACCTAGCC	CCATCGGCGTGCAGAACAT
40	Unigene19181_All	ACTCGCATTCAATCCAACCT	CATTAGTGGTGTGGTAGTGT
41	Unigene19630_All	CTGACACGAACTCCAACAT	CACTACTATCTCTACACGAACT
42	Unigene19863_All	ATGAGGAAGAAGTCGCTTG	CTTCGTAGCACCACAGTT
43	Unigene20977_All	CAACATCAACCATCGTCAT	AGAATTGCTGTAACTTGTC
44	Unigene24860_All	GGTGAAGGACTCGCTATG	GCACATTCCTGTAGATCAAC
45	Unigene25824_All	GAGACTTCCTGCCATTGAT	CTTGACCTGAATCCGTTAATC
46	Unigene25987_All	CCCATCTCTGCGTTACATTCTC	GACATCCTTGCCTCTGTCTATC
47	Unigene39885_All	ACCGCCTCAACCTCCTATCC	TCTCCGATTCCACGCTCTC
48	Unigene40223_All	GCCAGCATCACAACAATG	CCATTCTTACAGCACTCCT
49	Unigene43261_All	TAGGAGGAGGAACGGTCT	AGGCTAAGAACCAACCAAG
50	Unigene43262_All	CGTGGTTGTTACATCAGTTG	GAATGCTCGTGGTGGTTC
51	CL2465.Contig3_All	GGACCACTGGCGTAAGAT	CTGACATCCTCCACAACAC
52	CL422.Contig1_All	GTCACTACAACCTCGGCACCAT	TCAGCATCCTCCACCTCTCG
53	CL1442.Contig1_All	ACCTTCGTTGCCTTCGCTTG	CAGGAGAGGATGGAGGAGATGT
54	CL1442.Contig3_All	TGGCTTGGTCTGGCTCTACTAC	ATGTGGGCGAAGGCGAAGT
55	CL1491.Contig3_All	ACTGGCGAACCTAAGAAG	CCTAAGCGTTTCGGTGAGAT
56	CL1491.Contig4_All	CGTCCAGTGAAAGAGTCAGC	GCCGTGATCTCCCTACAAC
57	CL1912.Contig1_All	GTGAGGTTGGTGGTGTG	CGGCTCTTAGGCATAGTAAT
58	CL2342.Contig9_All	CGAATCCGTAGTTCCTCAT	CGAGTGGTGGTTATGGTT
59	CL2377.Contig3_All	CCGTGACAAGAGCGAGGATT	GGATGGTTGGTTGACGAAGAAG
60	CL4044.Contig3_All	ATCTCACCTACCTCCATTCT	GAAGGAGTGTAAGATGATGATG
61	CL5221.Contig2_All	CCCTCCCTTCTTCGCCTTCT	CGGAGACGATGACGGTGATG
62	CL7434.Contig1_All	TTCTATGGCAGCGGCTCATTG	CGGTTGGAGGTTGTGGAAGAG
63	CL10212.Contig1_All	TGTCCAGTGTGCCCTTTCAAG	AACGACTCCAATGCCGCTAAG
64	CL2342.Contig16_All	TTCTGAACGCTGGAATCTT	TTGGAGGAGAGTGTTGATG
65	Unigene6737_All	CCGTTCTTGAGAGGTTATCT	TATTGCTTGATGGCTTGGT
66	Unigene7711_All	GCCGCTTCCACCTCTTCTCT	TGAGGCAGTAGGAACCGCTAG
67	Unigene19492_All	CGGTGTTGGAAGGAGGAGTT	GGCAGCGTCATCTCAAAGTTCT
68	Unigene20299_All	TTCAGAGGCACAGACACAGTTG	AACAATGGCGGTGAGGTATGG
69	Unigene23516_All	TCGGTGGAGGAGAAGAGCAT	CGGAGTTGAGAAGAGACGGTTC
70	Unigene26381_All	CTCAATCATCACCTACATTCC	CGAAGTTGTTGGCTTGAAT

Table S3 Validation of up- or down-regulation of 70 genes of interest (GOIs) obtained from transcriptome sequencing of MeJA root-irrigation-treated samples of *P. multiflorum*

GOI	Expression profile in RNA-seq data	RG	Norm. Expression	Remarks	GOI	Expression profile in RNA-seq data	RG	Norm. Expression	Remarks	GOI	Expression profile in RNA-seq data	RG	Norm. Expression	Remarks
		A	1.6593	Up			A	13.4100	Up			A	0.7917	Down
1	1.0200/Up	B	3.7599	Up	25	1.2038/Up	B	14.5043	Up	48	1.8590/Up	B	0.6090	Down
		C	6.0906	Up			C	28.8255	Up			C	2.3327	Up
		A	1.9789	Up			A	18.7135	Up			A	1.8411	Up
2	2.6674/Up	B	1.9705	Up	26	3.3290/Up	B	20.2406	Up	49	3.1671/Up	B	1.8332	Up
		C	1.2490	Up			C	40.2257	Up			C	1.1619	Up
		A	0.8731	Down			A	2.1345	Up			A	430.7607	Up
3	2.3859/Up	B	0.8307	Down	27	1.1852/Up	B	1.0367	Up	50	3.8210/Up	B	432.2252	Up
		C	1.0088	Up			C	0.5833	Down			C	977.8709	Up
		A	1.0386	Up			A	0.7169	Down			A	0.26250	Down
4	2.1982/Up	B	0.9882	Down	28	2.0610/Up	B	0.7193	Down	51	-1.9211/Down	B	0.3468	Down
		C	1.2001	Up			C	1.6274	Up			C	0.0513	Down
		A	0.9028	Down			A	1.3071	Up			A	0.0513	Down
5	1.2242/Up	B	1.4383	Up	29	1.6990/Up	B	1.0055	Up	52	-2.0226/Down	B	0.0291	Down
		C	2.6741	Up			C	3.8514	Up			C	0.0678	Down
		A	0.9428	Down			A	3.1225	Up			A	0.3165	Down
6	4.9758/Up	B	0.8970	Down	30	3.6982/Up	B	14.7466	Up	53	-1.1219/Down	B	0.6924	Down
		C	1.0894	Up			C	3.3139	Up			C	1.1216	Up
		A	5.5281	Up			A	0.9823	Down			A	0.1291	Down
7	2.009/Up	B	5.2596	Up	31	4.8210/Up	B	4.6390	Up	54	-1.5971/Down	B	0.2824	Down

		C	6.3877	Up		C	1.0425	Up		C	0.4575	Down		
		A	3.3854	Up		A	1.2525	Up		A	0.1400	Down		
8	2.3654/Up	B	4.4728	Up	32	1.0276/Up	B	2.9467	Up	55	-2.4382/Down	B	0.0794	Down
		C	0.2044	Down			C	2.5470	Up			C	0.1851	Down
		A	1.9406	Up			A	0.5454	Down			A	0.4182	Down
9	2.2361/Up	B	3.9834	Up	33	1.2200/Up	B	1.2830	Up	56	-1.3878/Down	B	0.2372	Down
		C	2.2424	Up			C	1.1090	Up			C	0.5531	Down
		A	1.0216	Up			A	0.5882	Down			A	0.5788	Down
10	1.1145/Up	B	4.7823	Up	34	1.2988/Up	B	0.4525	Down	57	-2.6004,Down	B	2.2073	Up
		C	1.0747	Up			C	1.7331	Up			C	1.5850	Up
		A	1.0428	Up			A	1.4319	Up			A	0.0675	Down
11	1.4991/Up	B	1.0383	Up	35	2.0276/Up	B	1.1015	Up	58	-0.1110/Down	B	0.0058	Down
		C	0.8468	Down			C	4.2192	Up			C	0.0342	Down
		A	3.0219	Up			A	1.3831	Up			A	0.0920	Down
12	2.6813/Up	B	4.8143	Up	36	1.5844/Up	B	1.8311	Up	59	-3.8691/Down	B	0.0232	Down
		C	8.9506	Up			C	2.0702	Up			C	0.2252	Down
		A	1.5265	Up			A	1.1087	Up			A	0.0401	Down
13	1.5223/Up	B	2.0168	Up	37	3.4324/Up	B	1.0549	Up	60	-1.4818/Down	B	0.0878	Down
		C	0.3707	Down			C	1.2811	Up			C	0.1422	Down
		A	1.6648	Up			A	0.4384	Down			A	0.0469	Down
14	2.2486/Up	B	2.1996	Up	38	1.0711/Up	B	1.0314	Up	61	-1.3605/Down	B	0.1026	Down
		C	0.0746	Down			C	0.8914	Down			C	0.1662	Down
		A	11.9031	Up			A	1.4056	Up			A	0.0887	Down
15	1.3550/Up	B	15.7265	Up	39	1.7215/Up	B	1.3996	Up	62	-1.1463/Down	B	0.0513	Down

		C	1.3918	Up		C	0.8871	Down		C	0.1196	Down		
		A	3.0541	Up		A	43.1840	Up		A	0.0708	Down		
16	1.7506/Up	B	6.6822	Up	40	2.5695/Up	B	47.8814	Up	63	-1.4925/Down	B	0.1549	Down
		C	10.8243	Up			C	52.1335	Up			C	0.2509	Down
		A	0.4171	Down			A	1.3231	Up			A	0.7239	Down
17	1.0197/Up	B	0.6646	Down	41	2.6666/Up	B	1.3174	Up	64	-0.2074/Down	B	0.9565	Down
		C	1.2355	Up			C	0.8350	Down			C	2.9069	Up
		A	0.4878	Down			A	1.0530	Up			A	0.7579	Down
18	1.7704/Up	B	0.7771	Down	42	3.7158/Up	B	1.0018	Up	65	-1.0285/Down	B	1.0014	Up
		C	1.4448	Up			C	1.2167	Up			C	1.7350	Up
		A	1.3710	Up			A	0.8989	Down			A	0.2313	Down
19	2.0177/Up	B	2.1843	Up	43	3.7129/Up	B	0.6915	Down	66	-1.1136/Down	B	0.5060	Down
		C	4.0609	Up			C	2.6486	Up			C	0.8197	Down
		A	0.3645	Down			A	0.6940	Down			A	2.3093	Up
20	2.3626/Up	B	0.7976	Down	44	2.3679/Up	B	3.2774	Up	67	-1.1661/Down	B	0.1973	Down
		C	1.2920	Up			C	0.7365	Down			C	1.1708	Up
		A	2.8722	Up			A	7.4977	Up			A	0.9220	Down
21	1.6801/Up	B	6.5677	Up	45	1.5964/Up	B	5.7676	Up	68	-2.4393/Down	B	0.5229	Down
		C	10.6390	Up			C	22.0915	Up			C	1.2194	Up
		A	1.0201	Up			A	0.3452	Down			A	1.1705	Up
22	2.2485/Up	B	1.0157	Up	46	2.7215/Up	B	0.7552	Down	69	-1.1914/Down	B	1.1655	Up
		C	1.2533	Up			C	1.2234	Up			C	0.7388	Down
		A	782.4474	Up			A	1.4990	Up			A	0.8349	Down
23	1.6285/Up	B	846.3021	Up	47	1.4991/Up	B	1.4925	Up	70	-1.0103/Down	B	1.1030	Up

		C	1681.9184	Up		C	0.9460	Down		C	3.3007
		A	0.4132	Down							
24	1.0059/Up	B	1.9516	Up							
		C	0.4386	Down							

A, B and C correspond to reference genes (RGs) *UBQ1A*, *UBQ4-1*, and *SAMS*, respectively. GOI serial numbers are the same as in Table S3. Three RGs were selected for validation of the up- or down-regulation of each GOI obtained from transcriptome sequencing. If the normalized expression value of a GOI was greater than 1, the GOI was considered to be up-regulated. Down-regulated genes were those with normalized expression values less than 1

Table S4 Statistical comparison of contigs and unigenes between control and treatment root transcriptome data of *P. multiflorum* seedlings

Gene type	Sample	Total Number	Total Length(nt)	Mean Length(nt)	N50	Total Consensus Sequences	Distinct Clusters	Distinct Singletons
Contig	Control	135,230	48,184,343	356	651	-	-	-
	Treatment	117,736	41,211,915	350	610	-	-	-
Unigene	Control	89,440	57,785,503	646	1024	89,440	31,545	57,895
	Treatment	78,409	47,285,726	603	929	78,409	25,690	52,719
	All	79,565	62,762,185	789	1187	79,565	33,718	45,847

Table S5 Validation of raw sequences of 13 genes of interest (GOI) by sequencing of their PCR products

Gene ID	Nr-ID	Primer sequences (forward/reverse)	Blast cds of raw sequences	Amplicon sequences (bp)	Amplicon length (bp)	Identity(%)
Unigene124 71_All	gi 371534669 gb AE X32786.1	TCCACATCTACT CCCTCAACTCC/ CAGGAACCTCA CCAGCAACT	ACGGAACGGTAGAAGAAGGATTCGACTCA	TTCCACATTCTTACCCTCAACTCCG	736	98.64
			TCGGAGGCGGTGGCGCTGCCGTTCTCCTCG	TCCTCCTCTGCGCCATGAGGGCCGG		
			GGAACAACAGGGCTACCAAAGGGGGTGGT	CAGCGCCGTCCTCCTCGTCCACAAG		
			GCTGACGCACAAGAGTCTGATAACGAGCGT	TTCGAGATCGCCGCCCTGCTCGAGC		
			CGCACAACAAGTGGACGGGAAAACCCGA	AGCTCGAGCGCCACCGCGTCACGG		
			ATCTCTACCTGACCCGGACGATGTCGTTTT	TGGCCGCGTTGTCCCGCCTCTCGT		
			GTGCTTGCTTCCCCTATTCCACATCTACTCCC	CCTGGCCCTCGCCAAGAATCCGAT		
			TCAACTCCGTCCTCCTCTGCGCCATGAGGGC	GGTGGAGAAGTTCGACCTCGGCTC		
			CGGCAGCGCCGTCCTCCTCGTCCACAAGTT	CATCAGGGCGGTGCTCTCCGGGGC		
			CGAGATCGCCGCCCTGCTCGAGCAGCTCGA	GGCGCCGCTTGAAAAGGAGCTCGA		
			GCGCCACCGCGTCACGGTGGCCGCGTTGT	GGACGCCCTCCGGAGTCGGCTCCC		
			CCCGCCTCTCGTCCCTGGCCCTCGCCAAGAAT	GCAGGCCGTTCTCGGTCAGGGTTAT		
			CCGATGGTGGAGAAGTTCGACCTCGGCGCC	GGAATGACGGAGGCAGGGCCAGTG		
			ATCAGGGCGGTGCTCTCCGGGGCGGCGCCG	TTAGCAATGTGCCTGGGATTTGCAA		
			CTTGAAAGGAGCTCGAGGACGCCCTCCGG	AGGAGCCCTTCCCCACCAAGCCCG		
			AGTCGGTCCCGCAGGCCGTTCTCGGTGAG	GCTCTGTGGATCCGTCGTCCGCAA		
			GGTTATGGAATGACGGAGGCAGGGCCAGTG	CGCTGAGATGAAGGTTGTGATCC		
			TTAGCAATGTGCCTGGGATTTGCAAAGGAG	CGAAACCGGATCCTCTCTCGGCTTC		
			CCCTTCCCCACCAAGCCCGGCTCTTGTGGAT	AATCAACCCGGTGAGATCTGCATC		
			CCGTCGTCCGCAACGCTGAGATGAAGGTTG	CGTGGAGATCAGATCATGAAAGGG		
TCGATCCCGAAACCGGATCCTCTCTCGGCTT	TATCTAAACGATGACGCGGCCACA					

			CAATCAACCCGGTGAGATCTGCATCCGTGG	GCTGCAACCATAGACGCCCAAGGC		
			AGATCAGATCATGAAAGGGTATCTAAACGAT	TGGCTTCATACTGGGGACATTGGCT		
			GACGCGGCCACAGCTGCAACCATAGACGCC	ACGTCGATGAAGACATCGAGGTTT		
			CAAGGCTGGCTTCATACTGGGGACATTGGCT	TCATTGTCGACCGAGTAAAGGAGA		
			ACGTCGATGAAGACATCGAGGTTTTTCATTGT	TCATTAATAATCAAAGGATTCCAGGT		
			CGACCGAGTAAAGGAGATCATTAAATTCAA	AGCGCCAGCAGAGCTAGAGGCGCT		
			AGGATTCCAGGTAGCGCCAGCAGAGCTAGA	TCTAGTGAGCCATCCCTCCATAGCC		
			GGCGCTTCTAGTGAGCCATCCCTCCATAGCC	GATGCAGCCGTTGTCCCGCAAAAAG		
			GATGCAGCCGTTGTCCCGCAAAAAGGATGAA	GATGAAGTTGCTGGGAAAGGTTCC		
			GTTGCTGGTGAGGTTCCCTGTGGCGTTTGTGG	TGAA		
			TTCGGTCTGAAGGGTTTGAGCTTACAGAAG			
			ATGCAGTCAAAGAATTCGTAGCAAAGCAGG			
			TGGTTTTCTACAAGAAGCTGCACAAGGTGT			
			ACTTTGTTACGCGATCCCGAAGTCTCCGTC			
			TGGTAAAATCCTGAGGAAAGAGCTCCGAGC			
			TAAGTTGGCT			
		GAGCTAGTAAA	ATAGCAGAGCTAGTAAACCACCCAGACATC	GAGCTAGTAAACCACCCAGACATCC		
Unigene438	gi 314910736 gb AD	CCACCCAGACA/	CAAGCCAAGCTTCGAGCCGAGCTCGATACC	AAGCCAAGCTTCGAGCCGAGCTCG		
41_All	T63059.1	GGTAAGGGAGG	GTCCTGGGCAAAGGAGCCCAGATAACCGAG	ATACCGTCCTGGGCAAAGGAGCCC	110	100.00
		TTGGTGAGAT	CCCGATCTCACCAACCTCCCTTACCTCCAA	AGATAACCGAGCCCGATCTCACCAA		
				CCTCCCTTACCT		
		CCGCAGTTGGA	GAACTCGACACCGTCTCTCGGAAAGGGCGTC	TGAGCCCCGAACACCAAAGACTCCC		
Unigene195	gi 85720056 gb ABC	ACCTGAGAAG/	CAGATAACGGAGCCCGACATCCAAAGACTC	TTACCTTTACGCCGTCATCAAGGAA	452	98.89
56_All	75596.1	AGGCAGAGGCT	CCTTACCTTTACGCCGTCATCAAGGAAGCGC	GCGCTCCGTCTCCGAATGGCAATCC		

		TACCGTTAGG	TCCGTCTCCGAATGGCAATCCCTCTGCTGGT CCCACACATGAACCTCGACGACGCCAAGCT GGCGGGCTACGACATCCCGGCGGAGAGCAA GATCCTGGTCAACGCCTGGTGGCTGGCAA CAACCCCGACACCTGGAAGAATCCCGAGGA GTTCCGCCCCGAACGCTTCTTGAAGAAGA GTCCAAGGTTGACGCCAACGGTAACGATTT CCGTTACTTGCCGTTTGGCGTCGGACGGAG GAGTTGCCCCGGTATTATTCTGGCCTTGCCTA TTGCGGGAATTACCGTTGGGAGGTTGGTTC AGAATTTGAGCTTCTCCGCCGCCAGGGA AGGACAAGGTTGATACTTCTGAGAAAGCTG GGCAATTTAGCTTGCAGATTCTTAACCACTC CACCATTGTTCTTAAGCCAAGGAGC	CTCTGCTGGTCCCACACATGAACCT CGACGACGCCAAGCTGGCGGGCTA CGACATCCCGGCGGAGAGCAAGAT CCTGGTCAACGCCTGGTGGCTGGCC AACAACCCCGACACCTGGAAGAAT CCCGAGGAGTTCCGCCCCGAACGC TTCTTGAAGAAGAGTCCAAGGTT GACGCCAACGGTAACGATTTCCGTT ACTTGCCGTTTGGCGTCGGMCGGA GGAGTTGCCCCGGTATTATTCTGGC CTTGCCTATTGCGGGAATTACCGTT GGGAGGTTGGTTCAGAATTTGAGC TTCTCCGCCGCCAGGGAAGGACA AGGTTGATACTTCTGAGAAAGCTGG GCAATTTAGCTTGCAGATTCTTAAC CACTCCACCA		
			ATCCCCAGGATCGCCTTCTACACCTCCGGAT CCTTCGTTTCCTCCGTCAGCGCCACTCTGTT	TCCCAGGATTCGCTTCTACACCTCC GGATCCTTCGTTTCCTCCGTCAGCG		
CL2476.Co	gi 223546179 gb EEF	CTTCTACACCT/ TCGTCGAGCCA GCTTAACACCT	TCCGTCCAATTIACCGATCTGCCGCTCCC CTGTTTTCAAGGAGGAGCATCTGCCAACCG TCTTCAGACTCTACAACGAATCCGATCGCAG TTCTCATGCTATCAAGGACGGATTGATGGCG AACTTGTCAGCTGGGGCTGCGTTTACAATT	CCACTCTGTTTTCCGACGTTGCGAG ATTCAAGGCGCTCGATTCCGTCCAA TTTACCGATCTGCCGCGTCCCCTG TTTTCAAGGAGGAGCATCTGCCAAC CGTCTTCAGACTCTACAACGAATCC	411	98.78

		CGTTTCGCGCCCTCGAAGGCGACTACTTGG	GATCGCAGTTTCATGCTATCAAGG		
		AGCATATCACGAAGGTGACCGTCAACGGGA	ACGGATTGATGGCGAACTTGTCCAG		
		GAGTCTACGGCGTCGGTCCGGTTAGTTTGTT	CTGGGGCTGCGTTTACAATTCGTTT		
		CAAGGAATCCGCGACTCTAAGTCGGGTCAA	CGCGCCCTCGAAGGCGACTACTTGG		
		CCCGGATCAGGATGTAACTGCGAGGTGTTA	AGCATATCASGAAGGTGACCGTCAA		
		AGCTGGCTCGACGATTGCCCG	CGGGAGAGTCTACGGCGTCGGTCC		
			GGTTAGTTTGTTCAAGGAATCCGCG		
			ACTCTAAGTCGGGTCAACCCGGATC		
			AGGATGTAACTGCGAGGTGTTAAG		
			CTGGCTCGACGA		
		ATTTCAAAGACGGCAAATCTAGTACTGATCC	TCTCTTCTCAACCAATGGCATCRGA		
		CAGCTCCGGGAATGGGCCACCTTGCCCCG	YWCATYGATATTCYCAAATCGAC		
		CCATAGAGCTGGCCAAGCACCTGGTGGCCC	CTCAAMTYCGCCAGAMCGAGCTTC		
		GGGATCCGCGCCTCTCCATCACCGTCCTCCT	TTGACTCACATGAACGCYTACCAA		
		CATCAAGGGTTTCGTCCCCGAGGAAACGCT	CCCAAAGTCAAGGAAGMCATCGA		
	CTCTCCATCACC	CGAATCTTATATCCTCTCTCTGAAATCCA	GGRTSTYMGATCCGCKGGTCCCYTS		
CL8199.Co	gi 51705413 gb AAU	GTCCTCCT/	CCTCTCTTCTCAACCAAGGCATCGGATTCAT	SCCGTTGCGGGGCTCCTCGTGGACA	
ntig1_All	09444.1	CGTCGAGTTCC	TGATATFCCCCAAATCGACCTCAACTCCGCC	TGTTCTGCACTTCCACGATCGATGT	862
		ATCCACAGT	AGACCGAGCTTCTTGACTCACATGAACGCC	GGCAACAGAGCTTGGGMYASMGTC	94.77
			TACCAACCCAAAGTCAAGGAAGCCATCGAG	TKACGTCTTSTTCACCTCCGGCGCC	
			GGTCTTCGATCCGCGGGTCCCCTGCCCCGTTG	GGCYTTSTCCGCKTGTTTTTCCACC	
			CGGGGCTCCTCGTGGACATGTTCTGCACTTC	TCCATGGATTAGGGGTGATGTGG	
			CACGATCGATGTGGCAACAGAGCTTGGGCT	CGCAGGAATASGATGTGTTCCGGA	
			ACCGTCTTACGTCTTCTTACCTCCGGCGCC	GCCCCGATACGTTGYTGGAGATTC	

GGCCTTCTCCGCATGTTTTCCACCTCCATG CAGGGTTTCGAAATCCGGTGCCGG
GATTAGGGGTCGATGTGGCGCAGGAATACG TGAAAGTTTTGCCGGGGARATTCTT
ATGTCGTTCCGAGCCCGGATACGTTGTTGGA GTCTAAAGACGGTCAGTCATCCAC
GATTCCAGGGTTTCGAAATCCGGTGCCGGT GYTCTTGCGCCTCGYTGACAAGTTC
GAAAGTTTTGCCGGGAGATTCTGTCTAA CGCCAGGCCAAGGGTATTTTSGTAA
AGACGGTCAGTCATCCACGTTCTTGCGCCTC ATACATGCATGGAGATTGATCGGG
GCTGACAAGTTCCGCCAGGCCAAGGGTATT ACYTAATCCAGTCCATGTYGCAGC
TTGGTAAATACATGCATGGAGATTGATCGGG AAGACATCGAAMTCCCACCGATCT
ACTTAATCCAGTCCATGTCGCAGCAAGACAT ACCCGGTGGGGCCCATCCTCAACCT
CGAAATCCCACCGATCTACCCGGTGGGGCC GCCGACYGAAGATGATCATGGTCA
CATCCTCAACCTGCCGACTGAAGATGATCAT TGATGATGACGAGTCCTCCRGAA
GGTCATGATGATGACGAGTCCTCCGGGAAA AGATCCAATCACGAGGTGGCTGGA
GATCCAATCACGAGGTGGCTGGACGACCAG CGACCAGCCGCTCGATCCGTGGT
CCGCCTCGATCCGTGGTGTTCCTCTGCTTCG GTTCCTCTGCTTCRGGAGCAGGGGA
GGAGCAGGGGAACCTTCAACGACACGCAG ACCTTCAACGACACGCASATCAAA
ATCAAAGAGATCGCCGTCGGGCTCGAGCGA GAGATCGCCGTCGGGCTCGAGCGA
AGTGGCCAACGCTTTCTGTGGTCCCTCCGG AGTGGCCAACGCTTTYTGTTGGTCCC
CAACGACCCGGTGAGACCGGGGTCCATTG TCCGGCAACGACCCGGTGAGACCG
GAATTAGATGATCCTAGTAAGGTGTTGCCGG GGGTTCCATTGSAWTTAGATGAKC
AGGGGTTTTTTGAGCGGACAGCCGAGAAAAG CTAGTAAGGTGTTGCCCKGAGGGGT
GGAGGGTCATAGGGTGGGCCCCGAGGCCGA TTTTGTAGCGGACAGCCGAGAAAAG
GGGTGTTGGCCACAAGGCGGTTGGGGCAT GGAGGGTCATA
TCGTGTCGCACTGTGGATGGAACCTCGACG

7_All

B60721.1|

CGAAGTTG/ CCGTTACTCCGT CGTTAGCCT	GTGGGCCATCTCCTCGCCGAAGTTGAGGTT AGCCGGCGAGTCACATCCTTAGACGCCAA ATCTCCATAGCCATCCTCATCCCCAAGCTCC CCGTCCCCAACGAAAACCTCGACGTCTTCA TCAAATCCCTCGACGCCGACCTCCGCCGCG ACCCCGACCCGCGAATCTCCGTCGTCGAGC TTCCGCCGCTGGACGACGTCCCGCCGGAGC TGACCCAACCCGGGAACCACGTCTCCTAG TCGACAGCCTCGCGGGTCTCTACAAGCCGA TCGTGAAGCGCACGGTCGAGGAGCGCCGGC TCCGGCGCAAAACCGCCGGAATCGTCTTCG ACATGTTCTGCGCGCCGATGGTCGACGTGG CGGAGGAGCTCGGCGTGCCGTCTACTTGT TCTACACCTCCGGCGCTAACATGCTCAGCTT AACTCTCAAGCTGGAGTCGCTCGCGGCGGA CGACCTGCCGGCGCTCTTCGAAGGAATGTC GCCGGAGTCAACGCCGGTCGAATTCCCGGG ATTCAAGAATCCCGTGCCGTTGAAGGTCTG GCCCGAGCTCTATCTAAACAAAGGGGCAGC GCTCTGGGCCCACTTCATGCGGTTGCTTCT CAGTATCGCAAAACCAAGGGCATTGTTGTA AATACATTCACCGAGTTGGAGTCGGAACTC CTTAAGTCCTTGAACGAAAACGAACGTTTT CCTCCCGTTTATTCCGTGGGCCCATCCTCA	TCACATCCTTAGMYKSMSMMMTYY YCMKAGCCWTCCTCATCCCCAAGC TCCCCGTCCCCAACGAAAACCTCGR CGTCTTCATCAAATCCCTCGACGCC GACCTCCGCCGCGACCCCGACCCG CGAATCTCCGTCGTCGAGCTTCCGC CGCTGGACGACGTCCCGCCGGAGC TGACCCAACCCGGGAACCACGTCC TCCTAGTCGACAGCCTCGCGGGTCT CTACAAGCCGATCGTGAAGCGCAC GGTCGAGGAGCGCCGGTCCGGCG CAAAACCGCCGGAATCGTCTTCGAC ATGTTCTGCGCGCCGATGGTCGACG TGGCGGAGGAGCTCGGCGTGCCGT CCTACTTGTCTACACCTCCGGCGCT AACATGCTCAGCTTAACTCTCAAGC TGGAGTCGCTCGCGGCGGACGACC TGCCGGCGCTCTTCGAAGGAATGTC GCCGGAGTCAACGCCGGTCGAATT CCCGGATTCAAGAATCCCGTGCCG TTGAAGGTCTGGCCCGAGCTCTATC TAAACAAAGGGGCAGCGCTCTGGG CCCCTTCATGCGGTTGCTTCTCA GTATCGCAAAACCAAGGGCATTGTTG
--	---	--

			ACCTCGGTCGTAAGGCTAACGACGGAGTAA	GTAATACATTCACCGAGYWGGAG		
			CGGAATCGCCTCGGGATCCGACGCTGAGTT	TCGGAACTCCWTAAGTCCTTGAAC		
			GGTTAGACGAGCAACCGGCTGGGTTCGGTGG	GAAAACGAACGTTTTCCYCCCGTK		
			TTTCTTCTGCTTCGGGAGCAAG	WWTCCGTGGGCCCCATCCTCAAC		
				CTCGGTCGTAAGGCTAACGCG		
			TCCAAGTTCACATCCTCATGTTCCCGTGGC	GGAAGGCTTCTCTTGGCACCGAG		
			TCGCCATCGGCCACATAACTCCCTACCTCCA	ACTGCCTCGGACGTCCCCATCTCCC		
			CCTCTCCAACAACTCGCCGAAAAAGGCCA	TCACACGCTTTCTCGCCATCGCATT		
			CAAAATCACATTCCTCCTCCCAAACAAGGCT	CGACCTGACGCSCCCMMRWSTYYM		
			CAAGTCCTCCTCCAACACCTCAACCTCCAC	MMAAATCATAACTCGACCTYMAAA		
			CCTTCCCTCATCACTTTCCACCCACTCTCGA	CCCGGATTTCTGTCTTCTACGACTTC		
			TCCCCAAGTGGAAGGCCTTCTCTTGGCA	GCTCACTGGGTCCCCGAGGATCACG		
		ACCCTTCCCTCA	CCGAGACTGCCTCGGACGTCCCCATCTCCCT	TCCAAGCTCGGGATCAAGTCGGTAT		
Unigene154	gi 223537474 gb EEF	TCACTTTCC/	CACACGCTTTCTCGCCATCGCATTTCGACCTG	GKTATWACGTAGTAWGCGCCGSCGC		
30_All	39100.1	GGCATCCTTCA	ACGCGCCCCAAGTCTCACAAATCATACTCG	CCTGGCCCATAACATGGYCCCCGTG	1014	92.13
		CAGCCTTACT	ACCTCAAACCGGATTTCTGTCTTCTACGACTT	CGTTACACTTGTACCCTCCACTTA		
			CGCTCACTGGGTCCCCGAGATCACGTCCAA	CGGCGGCGCAGGTGGAGGAGCTGG		
			GCTCGGGATCAAGTCGGTATGTTATAACGTA	TTGCGCCGCCGCAGRATACCCCAT		
			GTATGCGCCGCCGCCCTGGCCCATAACATGG	GGSGCTTTTGCACAAGCACGAGGSG		
			TCCCCGTGCGTTACTTGTACCCCTCCACT	CGTAAGCTCGKGTTCATGGCCCAAG		
			TACGGCGGAGCAGGTGGAGGAGCTGGTTGC	AATATGGCAGCGGAATCACCTTCTT		
			GCCGCCCCGAGGATACCCCATGGCGCTTTTG	CGAGAGGYTCAACTCGGCACTGAA		
			CACAAGCACGAGGCGGTAAGCTCGTGTTT	GTTGGCCGACGCCATCGCTATCAGG		
			ATGGCCCAAGAATATGGCAGCGGAATCACC	ACTTGCAAGGAGATCGAGGGGAAG		

TTCTTCGAGAGGCTCAACTCGGCACTGAAG	TTCTGTGATTACCTCAGCAGCCAGT
TTGGCCGACGCCATCGCTATCAGGACTTGCA	TTGAGACATCAGKGTACTCACGGG
AGGAGATCGAGGGGAAGTTCTGTGATTACC	CCCCGCGTTGCCGACTTGACCACC
TCAGCAGCCAGTTTGAGACATCAGTGTTACT	ACCGAAGGRACGGCGTTGGATGAG
CACGGGCCCCGTGTTGCCGACTTGACCAC	AAATGGGCGAGCTGGCTCGRAGCC
CACCGAAGGGACGGCGTTGGATGAGAAATG	CACGAACCGGGTTCAGTGATTTACT
GGCGAGCTGGCTCGGAGCCCACGAACCGG	GCGCGTTCGGRACCCAGTGTTTCCT
GTTCAGTGATTTACTGCGCGTTCGGGACCCA	TGACAAGCACCAGTTTCAGGAGATT
GTGTTTCCTTGACAAGCACCAGTATCAGGA	CTTTTAGGGTTCGAGTTAACTGGTTA
GATTCCTTTAGGGTTCGAGTTAACTGGTTAT	TCCGTTCTTTGTGGCCCTAAAGCCT
CCGTTCTTTGTGGCCCTAAAGCCTCCTACGG	CCTACGGGATGCTCGACGATAGAGG
GATGCTCGACGATAGAGGAGGCTTTACCAG	AGGCTTTACCAGAGGGGTTTGARG
AGGGGTTTGAAGAGCGGGTCAGGGGGAAG	AGCGGGTCAGGGGRAAGGGGGKK
GGGGTGGTTTACGGAGGGTGGGACATCCAG	GTTTACGGAGGGTGGGACATCCAGC
CAACCGCTCATACTGGAGCACCCGTCGGTT	AACCGCTCATACTGGAGCACCCGTC
GGGTGCTTCGTGAGCCATTGTGGGTTCGGG	GKKKKGSTKCKTSRKSAYSWKKG
TCCATGTGGGAGTCGCTTATGGGGAAGCCTC	TKSGKKYSRKKYSRWGTCGCTATGG
AAATAGTGTGGTGCCACAGCAGGGTGACC	GAGYYSMWWWGKGKRWGCCTC
AGGTAATGAATACGAGGATCATGGCGCGAG	AAATAGTGTGGTGCCACAGCAGG
AGATGAAGGTGGCAGTGAGGTGGAGAAG	GTGACCAGGTAATGAATACGAGGAT
GACGAGAGTGGGTGGGTTTCAAGGGAGAG	CATGGCGCGAGAGATGAAGGTGGC
CCTGAGTAAGGCTGTGAAGGATGCCATGGAT	AGTGGAGGTGGAGAAGGACGAGA
AAGGAGAGCGTGGTGGGGTGTGTTGATTAGA	GTGGGTG
GAGAACCATGCTAAGTGGAGGGAGGTGTTG	

		GGGAGCCCTGGCTTCATGAGTGGTTATGTTG		
		ACAGCTTTGTGCATCAATTGGAGAGGCTTTT		
		GGAT		
		ATGGCTTCAGAACCCAAAAAAGCCCATTTT	CAGGCACGGCACAACCGTCACCAT	
		GTAGTGTTCATGATGCAACAAGGCCACA	AGTACCACACCTCTCAACGCTCTC	
		TGATCCCAATGGTAGACATCGCAAGGCTCAT	CGTTTCAAAGCCACCCTCGATCACG	
		AGCAAGGCACGGCACAACCGTCACCATAGT	ACGTCGAAACTGAAGCATTGGACA	
		CACCACACCTCTCAACGCTCTCCGTTTCAA	TTCGAGTTGCCGAAATCGAATTCCC	
		GCCACCCTCGATCACGACGTCGAAACTGAA	TTCCAAGGAAGCGGGATTTCCCGA	
		GCATTGGACATTCGAGTTGCCGAAATCGAAT	AGGAATCGAAAATGCCGACATGTT	
		TCCCTTCCAAGGAAGCGGGATTTCCCGAAG	GCCTTCCCTCGGTTTGGTGAATCA	
	AGCCGTTGAGC	GAATCGAAAATGCCGACATGTTGCCTTCCCT	TTCGTCGTTTCCACCAGCTTGCTTC	
CL554.Cont	gi 62241063 dbj BA	TTACAGGTTAC/	ATGATCAATCTGAGAAGCTTTTCTC	
ig1_All	D93688.1	TGGTATCAGTG	AGAGCTTAAGCCCAAACCAACTTG	1264
		GTGTGGAGAGT	CATTTTGTCCGACGTCATATTTTTCAT	99.05
			TGGACAATTGATATTGCTAAGAGG	
			TATGGTGTTCGAAGAATTGTGTTTC	
			ATGGTCTTGGTTGCTTTGCTTTACT	
			CTGCTCTCACAATTTGATCAAGTCT	
			AAGGTTCTTGATAGTATAACCTCTG	
			ACACAGAGCAAGTTGTAGTGCCTG	
			ATCTGCCAGATGAGATTGTTCTTAC	
			CAAAGATCAGCTTCCCAATAGCCTT	
			AGGCCAGGGTCTTCGGCCCTAAAA	

AATCGTTTGGGATTGTAGTGAATCTTTCTGA	GATCGAACTAYGCGTATTAGAGCA
GGAATTGGAGGTGCAATATATGAAGAGATAC	GCTGAAGAAGAATCGTTTGGGATT
AAAGAGGCGAAGTCGCCAAAGAAGGTTTG	GTAGTGAATTCTTTTCGAGGAATTGG
GTTTGTGGTCTGTTTGCTTGAGCAACAAA	AGGTGCAATATATGAAGAGATACA
GATAATGCAAGCAAGGGTGACAGAGGCAAC	AAGAGGCGAAGTCGCCAAAGAAGG
AAATCTTCTGTTGATGGAAATTTATGTTTGA	TTTGGTTTGTGGTCTGTTTGCTTG
AATGGCTTGAGAATCGTGAACCGGGTTCTGT	AGCAACAAAGATAATGCAAGCAAG
AATCTATGCTTGCCATGGAACCTTTGCTCG	GGTGACAGAGGCAACAAATCTTCT
TTCAACACGCGACAAATGATGGAGCTCGGT	GTTGATGGAAATTTATGTTTCAAAT
TTAGGCTTGGAGGAATCGAAAAATCTTTC	GGCTTGAGAATCGTGAACCGGGTT
GTATGGGTTATAAGAAGACGAGACGGGTTG	CTGTAATCTATGCTTGCCATGGAAC
GAGGAACTCGAGAAGTGGATGAAGGAAAG	CCTTTGCTCGTTCAACACGCGACAA
CGGGTTCAAAGAAAGGATTAAGATAGAGC	ATGATGGAGCTCGGTTTAGGCTTGG
ATTAGTGATTTGGGGATGGGCACCACAAGT	AGGAATCGAAAAAATCTTTCGTAT
GTTGATATTGTCACACCCTTCAATAGGTGGA	GGGTTATARGAAGACGAGACGGGT
TTCTTGACACACTGTGGATGGAACCTGACTC	TGGAGGAACTCGAGAAGTGGATGA
TAGAAGGGGTGTGCGCGGGTTTGCCAATGG	RGRAARSSGGKTYRAAGAAAGGA
TGACATGGCCAATGTTTTCGGACCAATTCTA	TTAAAGATAGAGCATTAGTGATTTG
TAATGAGAAGTTGATTACACAAATATGGAAG	GGGATGGGCACCACAAGTGTGAT
ATTGGTGTGACAGTCGGAGTGAAGAGTCCT	ATTGTCACACCCTTCAATAGGTGGA
GTGAAGTTTGAGGAAGAGAAAATGTTGTCT	TTCTTGACACACTGTGGATGGAAC
ATTTTGGTGAAGAAAGAAGACGTTGCGAAG	CGACTCTAGAAGGGGTGTGCGCGG
GCGGTGGAGGCGATAATGGAGGACGGAGA	GTTTGCCAATGGTGACATGGCCAAT
AGAAGGGAGGAAGAGAAAGGAAAGGGCA	GTTTTCGGACCAATTCTATAATGAG

			AGAGAGTTGGGAAATATGGCTAGAGAAGCG	AAGTTGATTACACAAATATGGAAG		
			TTTGGAGAGGGTGGCTCTGCTTATTTGAGTA	ATTGGTGTGACAGTCGGAGTGAAG		
			TGAAATCTTTAATCAACGATATTTTACAACA	AGTCCTGTGAAGTTTGAGGAAGAG		
			A	AAAATGTTGTCTATTTTGGTGAAGA		
				AAGAAGACGTTGCGAAGGCGGTGG		
				AGGCGATAATGGAGGACGGAGAAG		
				AAGGGAGGAAGAGA		
			CTCTTCTTGCAGCTTCTTCTTGCACCTTTTGT	TCCGTCACACGGGGGTCTCACCAGT		
			TGCTTCCTTTATCTTCCTCATAAAAAGAATA	GTGCTCACTACCCTCACTCTAYKW		
			AGAAAAAGCTAGTCAACCTCCGGGGCCAC	WCWWKRCWAWRCMWACKRSSSS		
			CTGGGCTTCCGGTCATCGGTAACCTCCACCA	YYWAWKKYTTGAAACTCGGGTTT		
			GTGTGCTTCCACTACCCTCACCTCTACTTT	GTACMAMCYSTKGTGGTTTCCTCG		
			CATGAACTATGCAAAACCTACGGGCCCTTAA	GCAAAAATGGCCAAGGAAGTACTG		
			TGTCTTTGAAACTCGGGTTTGTACCAACCCT	AAAACCCATGACAACGTCTTCGCT		
		CGGTCATCGGT	TGTGGTTTCCTCGGCAAAAATGGCCAAGGA	AGCAGGCCAAAGTTGTTAAATCAA		
Unigene152	gi 225458057 ref XP	AACCTCCAC/	AGTACTGAAAACCCATGACAACGTCTTCGCT	CAAAAATATTTTACAATGGGTTAA	948	93.54
35_All	_002278387.1	TGTTTCCTTCAC	AGCAGGCCAAAGTTGTTAAATCAACAAAAA	GCATAACCCTATTACCCTATGGCGA		
		CACTGCCTTC	CTATTTTACAATGGGTTAAGCATAACCCTATT	TCACTGGAGAGAAATTAGGAAAGC		
			ACCCTATGGCGATCACTGGAGAGAAATTAG	CTGTATAGTTCATCTCTTTAGTCCT		
			GAAAGCCTGTATAGTTCATCTCTTTAGTCCTA	AAGAGAGTCCAGTCCTTCTCTTCAA		
			AGAGAGTCCAGTCCTTCTCTTCAATTCGAGA	TTCGAGAAGATGAGGTTTATCAGA		
			AGATGAGGTTTATCAGATGACGCGGGAGATA	TGACGCGGGAGATATCGTGTTTGG		
			TCGTGTTTGGGCAATAAAAAGAAGCCGGTA	GCAATAAAAAGAAGCCGGTAAATT		
			AATTTAAGTGAAATGATGATATGCGTTATCA	TAAGTGAAATGATGATATGCGTTAT		

ACACAATAGTATGTAGAGTTGCTTTTGGGAG CAACACAATAGTATGTAGAGTTGC
GAGGGAAGAGGTTGATAATGCCAAGTATAG TTTTGGGAGGAGGGAAGAGGTTGA
AAGTAATCTCCAAGTCATGCTTAGGGTTATA TAATGCCAAGTATAGAAGTAATCT
CAAGAATTGCTTGTTAGTTTTTCTTTTCCGA CCAAGTCATGCTTAGGGTTATACAA
TTATTTTCCTCTTATGGGTTGGGTGGATAAGA GAATTGCTTGTTAGTTTTTCTTTTTC
TCAGGAGGCTAATGCATCCCCAATTCAATAA CGATTATTTTCCTCTTATGGGTTGG
GGTTTCTATGGAGTTGGATGGCCTTCTTGAG GTGGATAAGATCAGGAGGCTAATG
GAAATCATTGACGAGCATGTGAAGACAAAA CATCCCCAATTCAATAAGGTTTCTA
TCTAGCCGAGAAGAAGAGGAAGACATTGTT TGGAGTTGGATGGCCTTCTTGAGGA
GATGTGCTACTCAGGCTCCAACGACAGAAT AATCATTGACGAGCATGTGAAGAC
TCATTTGGATTTCGACATTAACCGTGATCACA AAAATCTAGCCGAGAAGAAGAGGA
TCAAAGCAACTCTTATGGATTATTCGTGGC AGACATTGTTGATGTGCTACTCAGG
AGGGACAGATACAGCTGCAGGAACAATAGT CTCCAACGACAGAATTCATTTGGAT
TTGGGCAATGACGGAGCTTATGAGGAATCC TCGACATTAACCGTGATCACATCAA
AAAGGCAATGAAGCAACTGCAAGAAGAAG AGCAACTCTTATGGATTTATTCGTG
CAAGAACAACATTGATGGGTAAAGACTA GCAGGGACAGATACAGCTGCAGGA
TAAAAGAAGCAGATCTTGAAAAGCTAGTGT ACAATAGTTTGGGCAATGACGGAG
ATTTGAAGGCAGTGGTGAAGGAAACATTGA CTTATGAGGAATCCAAAGGCAATG
GATTGCACCCGGCAGCTCCATTGCTAGTCCC AAGCAACTGCAAGAAGAAGCAAGA
CCGAGAAGCCAATCAAAGTTGCATAATTGA ACAACATTGATGGGTAAAGACT
CGGGTACGAAATCAAAAAGAAAACCTTAGT ATAAAAGAAGCAGATCTTGAAAGC
CTATGTAAATGCATATGCAATTGGAAGGGAC TAGTGTATTTGAAGGATGTGGG
CCTGAAGCCTGGGAAAACCCGGAT

ntig1_All	_002308860.1	GCGTAATC/ GCAACCTTGGA AGAGGGACT	TCGTCCTCTCCTACCTCCTCTACAACCGCCT CCGGTTCAAGCTCCCGCCGGGCCAAGGCC CTGGCCCGTCGTCGGGAACCTCTACGACAT CAAGCCCGTTCGCTTCCGTTGCTTCCACGAA TGGGCCCAACGCTACGGGCCATCATATCGG TGTGGTTCGGGTCCAACCTCAACGTGATCGT GTCGAACACCGAGCTGGCTCGGGAGGTGCT CAAGGAGAAGGACCAGCAGCTGGCGGACC GCCACCGGAGCCGGTCAGCGGTCCGGTTCA GCCGCAACGGGGCGGATCTCATATGGGCCG ACTACGGGCCTCACTATGTGAAGGTGAGGA AGGTGTGTACGTTGGAGCTTTTTACGCCTAA GAGGCTTGAATCTCTTAGGCCCGTTAGGGA GGATGAGGTTACCGCCATGATTGAATCCATC TACAAAGATTGCACCTCTCATGAAACCCATG GGAAGAGCCTGACGCTGAAGAAATACTTAG GAGCCGTGGCCTTCAACAACATAACAAGGC TCGCCTTTGGGAAGCGGTTTCATGAACGACG AGGGCGTAATCAACAAGCAAGGGCTCGAGT TCAAGGCCATTGTAGCCAACGGCTTGAAGC TTGGGGCGTCTTTGGCCATGTCGGAGCACAT TAACTGGCTCCGGTGGATGTACCCGGTTGAG GAGGAGGCCTTTGCCAAGCACAACGCCCAA AGGGACCGTCTCACAAGGCCATCATGGAT	CAAGGCCATTGTAGCCAACGGCTTG AAGCTTGGGGCGTCTTTGGCCATGT CGGAGCACATTA ACTGGCTCCGGTG GATGTACCCGGTTGAGGAGGAGGC CTTTGCCAAGCACAACGCCCAAAG GGACCGTCTCACAAGGCCATCATG GATGAGCACACCGCCGCTCGCCAA AAGAGTGGTGACACAAAACAACAC TTTGTGATGCTTTGTTGACTCA AGGACAAGTATGATCTTAGTGAAGA CACCATTATTGGACTTCTTTGGGACA TGATCACGGCCGGYATGGACACAAC AGCAATCTCAGTAGAATGGGCCATG GCGGAGCTAATCCGAAACCCAAGG ACCCAACAAAAGGCCAAGAAGAG CTTGACCGGGTCATCGGGCATGAAC GAATCATGATTGAATCCGACATCTC CAACCTCCCTTACTTGCAAGCTGTG GCCAAGGAGGCGCTCAGGCTACAC CCACCAACGCCACTAATGCTCCCCC ACCGAGCCAATGCCAACGTAA AAATCGCGGGCTATGACATCCCGAA AGGCTCCATTGTCCAAGTCAACGTG TGGGCTGTGGCCCGTGACCCGGCT
-----------	--------------	---------------------------------------	--	---

GAGCACACCGCCGCTCGCCAAAAGAGTGGT	GTGTGGAAGGACCCGCTCGAGTTC
GACACAAAACAACACTTTGTTGATGCTTTGT	AGGCCCGAAAGGTACTTTGAGGAG
TGACACTCAAGGACAAGTATGATCTTAGTGA	GATGTTGACATGAAAGGGCACGAC
AGACACCATTATTGGACTTCTTTGGGACATG	TTAGGTTATTGCCTTTCCGGGGCGG
ATCACGGCCGGTATGGATAACAACAGCAATCT	GTCGACGGGTCTGCCAGGTGCC
CAGTAGAATGGGCCATGGCGGAGCTAATCC	AGCTCGGTATAAACTTGGTCACCTC
GAAACCCAAGGACCCAACAAAAGGCCCAA	CATGTTRGGTCATTTGCTGCACCATT
GAAGAGCTTGACCGGGTCATCGGGCATGAA	TTAGCTGGAGCCCGCCCGACGGGCT
CGAATCATGATCGAATCCGACATCTCCAACC	TAAGCCCGAAGAGATCGACATGTCG
TCCCTTACTTGCAAGCTGTGGCCAAGGAGG	GAGAATCCCGGGTTGTTACATATAT
CGCTCAGGCTACACCCACCAACGCCACTAA	GACTTCTCCGTTGCAGACAGTCCTC
TGCTCCCCACCGAGCCAACGCCAACGTAA	TCTCACAAGGTGTGTCCAA
AAATCGGGGGCTATGACATCCCGAAAGGCT	
CCATTGTCCAAGTCAACGTGTGGGCTGTGG	
CCCGTGACCCGGCTGTGTGGAAGGACCCGC	
TCGAGTTCAGGCCCGAAAGGTACTTTGAGG	
AGGATGTTGACATGAAAGGGCACGACTTTA	
GGTTATTGCCTTTCCGGGGCGGGTCGACGGG	
TCTGCCAGGTGCCAGCTCGGTATAAACTT	
GGTCACCTCCATGTTGGGTTCATTTGCTGCAC	
CATTTTAGCTGGAGCCACCCAACGGGCTTA	
AGCCCGAAGAGATTGACATGTCCGAGAATC	
CCGGGTTGGTTACATATATGACTTCTCCGTTG	
CAGACAGTCCCTCTTCCAAGGTTGCCTTCTC	

Unigene198 63_All	gi 401710284 gb AF P97667.1	AGATGAGGAAG AAGTCGCTTGA/ TTCGTAGCACC ACAGTTTCA	AGTTGTACAAAAGGGTACCTGTGGATATG GATGAGATGAGGAAGAAGTCGCTTGAAAAC GGTCAAGCAACCACCGGAGAAGGACTTGA GTGGGGCGTTCTGTTTGGATTGGGCCTGGT ATTACTGTTGAAACTGTGGTGCTACGAAGTG TGCCCATCTTT ATGGAGGCTTCAATTGAGGAGATTAGGAAG GCACAAACACCCGCTACCGTCTGGCCATC GGCACCGCCAACCTCCCAACTGCATGTAC CAAGCCGACTTTCCCGATTACTTCCGCA GAGTGAACACC TCACCCACCTC/ TTCCAAGCTCT GCAACTCCTT	AGGACTTGAGTGGGGCGTTCTGTTT GGATTTGGGCCTGGTATTACTGTTG AAACTGTGGTGCTACGAAA TAAGAGTGAACACCTCACCCACCT CAAGCACAAATTCAAGCGCATTG TGAGAAGTCAATGATCGAGAAGCG TTACCTTCAATTGACGGAAGAAATT CTCAAAGAAAACCCGAATATCGG TGCATACGAGGCACCATCATTGGA TGTAAGACACAAAATTCAGGTGAA AGGAGTTGCAGAGCTTGGGAAA	69	98.55
CL4799.Co ntig3_All	gi 163867088 gb AB Y47640.1	GAGTGAACACC TCACCCACCTC/ TTCCAAGCTCT GCAACTCCTT	GGGAAGAAGAC GACCGGAGAT/ GAATCGGAACA CTTCGCATGAC	GGGAAGAAGACGACCGGAGATGGGTTCTGA GTGGGGCGTCGCGATTGGATTGGGGCCTGG GCTTACCGTTGAGACCGTTGTCATGCGAAGT GTTCCGATTCCG	190	91.05
Unigene172 01_All	gi 91984065 gb ABE 68892.1	GGGAAGAAGAC GACCGGAGAT/ GAATCGGAACA CTTCGCATGAC	GGGAAGAAGACGACCGGAGATGGGTTCTGA GTGGGGCGTCGCGATTGGATTGGGGCCTGG GCTTACCGTTGAGACCGTTGTCATGCGAAGT GTTCCGATTCCG	TGGGGCCTGGGCTTACCGTTGAGA CCGTTGTCATGCGAAGTGTTCGGAT TCA	52	98.08

Shared identities between raw sequences and sequences of their corresponding PCR amplicons varied from 91.05 to 100%

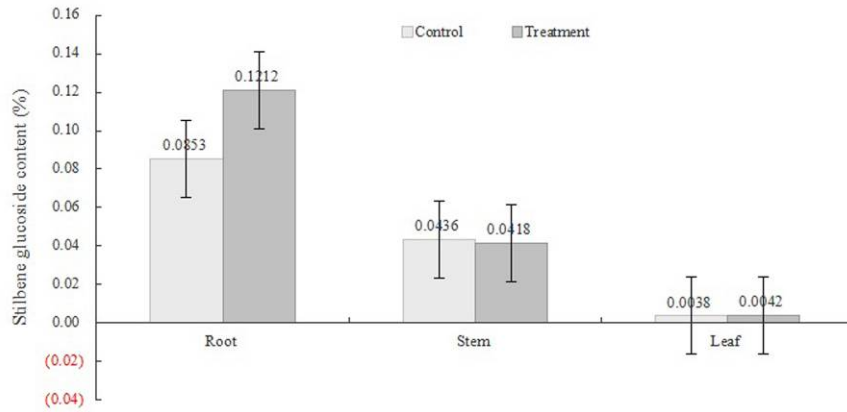


Fig. S1 Effects of MeJA on stilbene glucoside content in *P. multiflorum*

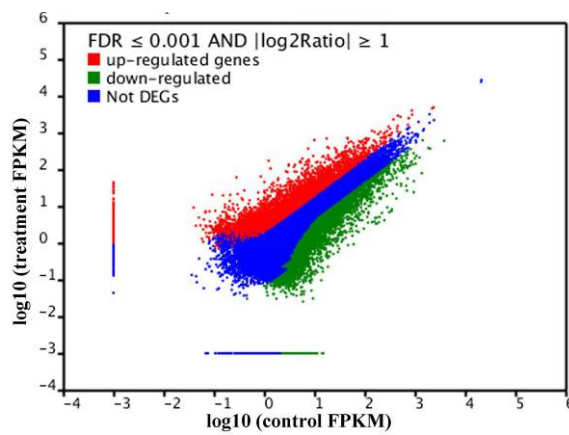


Fig. S2 Expression levels of unigenes in control vs. treatment

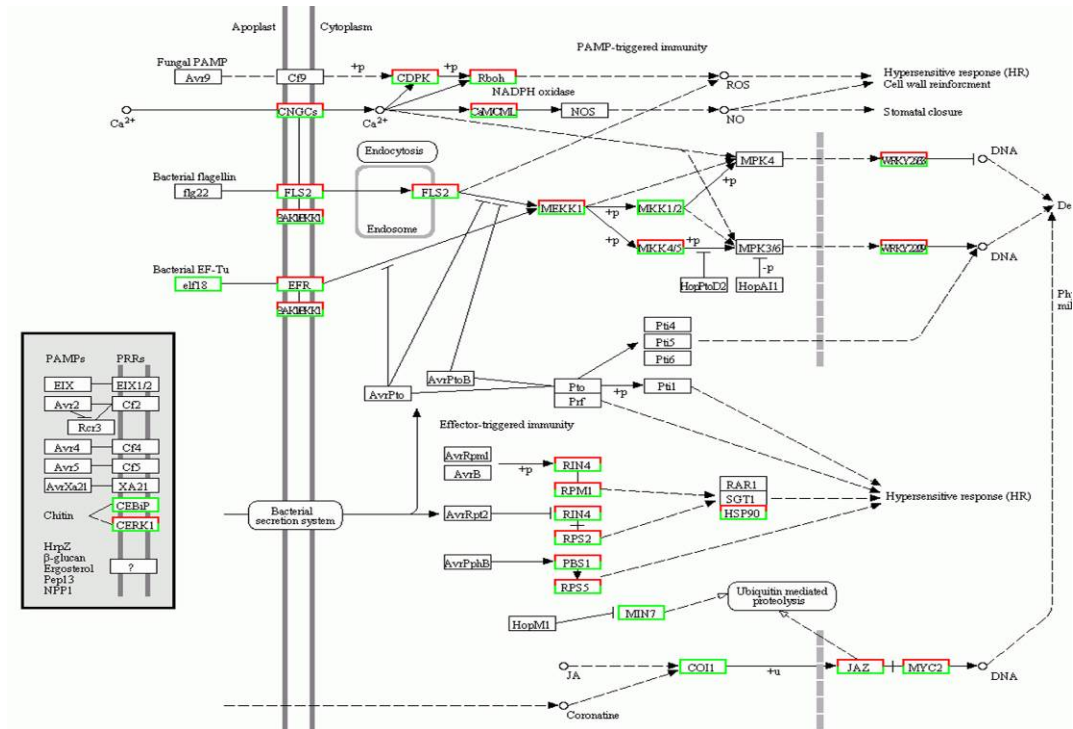


Fig. S3 "Plant-pathogen interaction" metabolic pathway induced by MeJA in *P. multiflorum* Thunb. root transcriptome

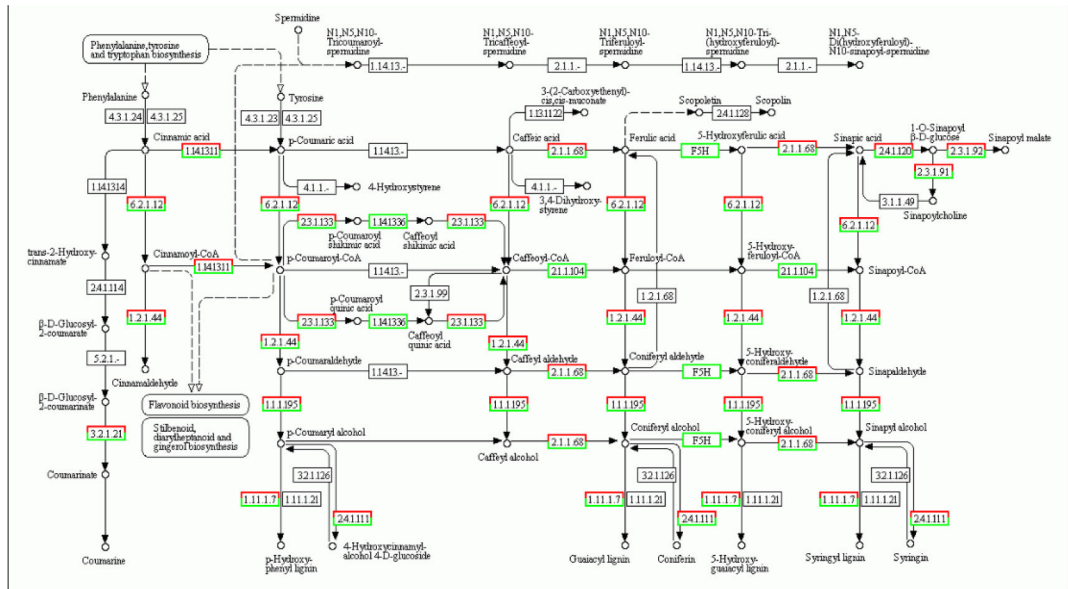


Fig. S4 “Phenylpropanoid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

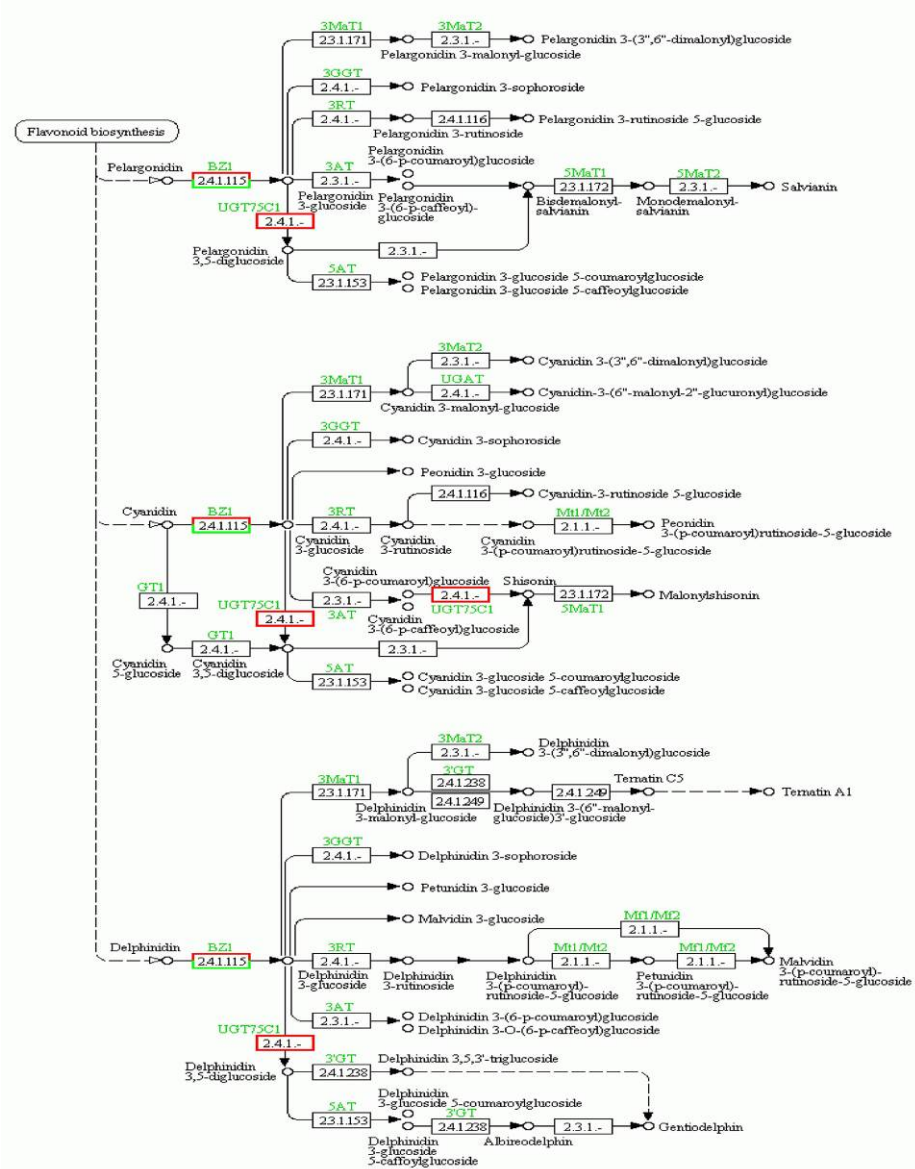


Fig. S5 “Anthocyanin biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

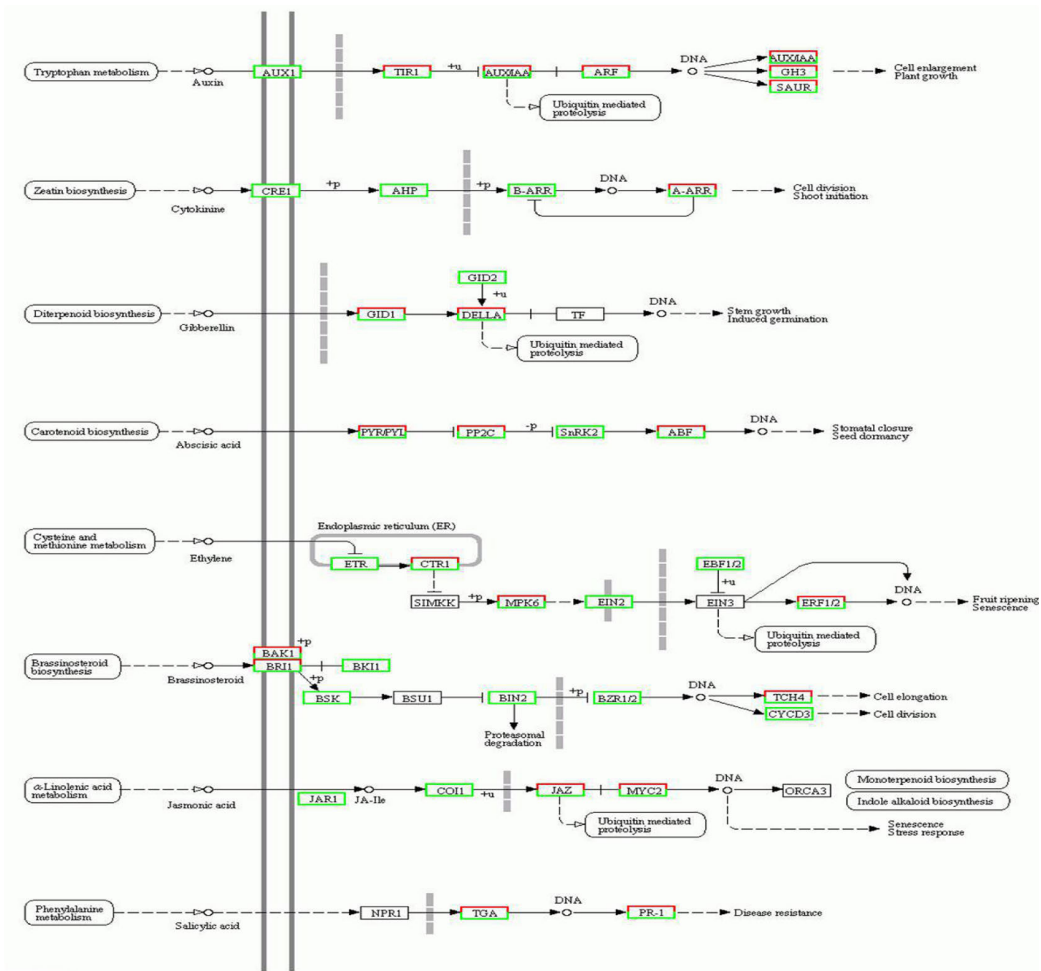


Fig. S6 “Plant hormone signal transduction” pathway induced by MeJA in *P. multiflorum* root transcriptome

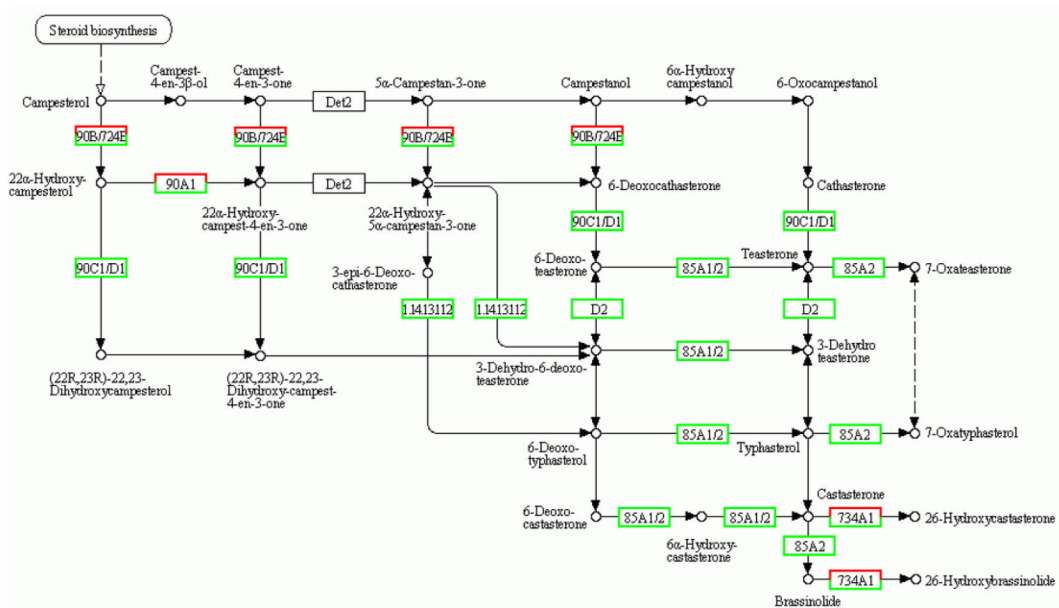


Fig. S7 “Brassinosteroid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

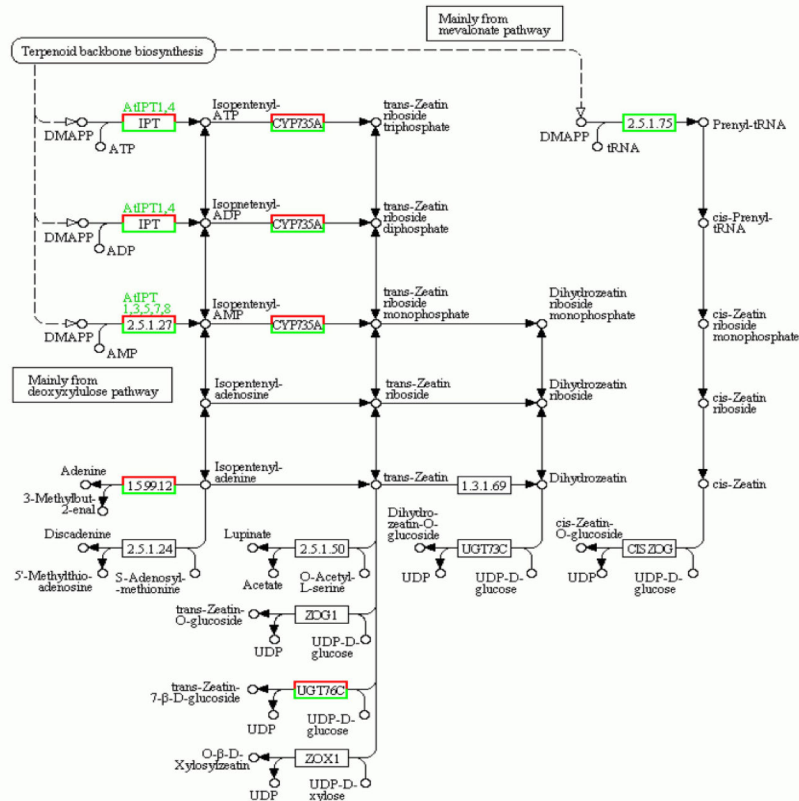


Fig. S8 “Zetin biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

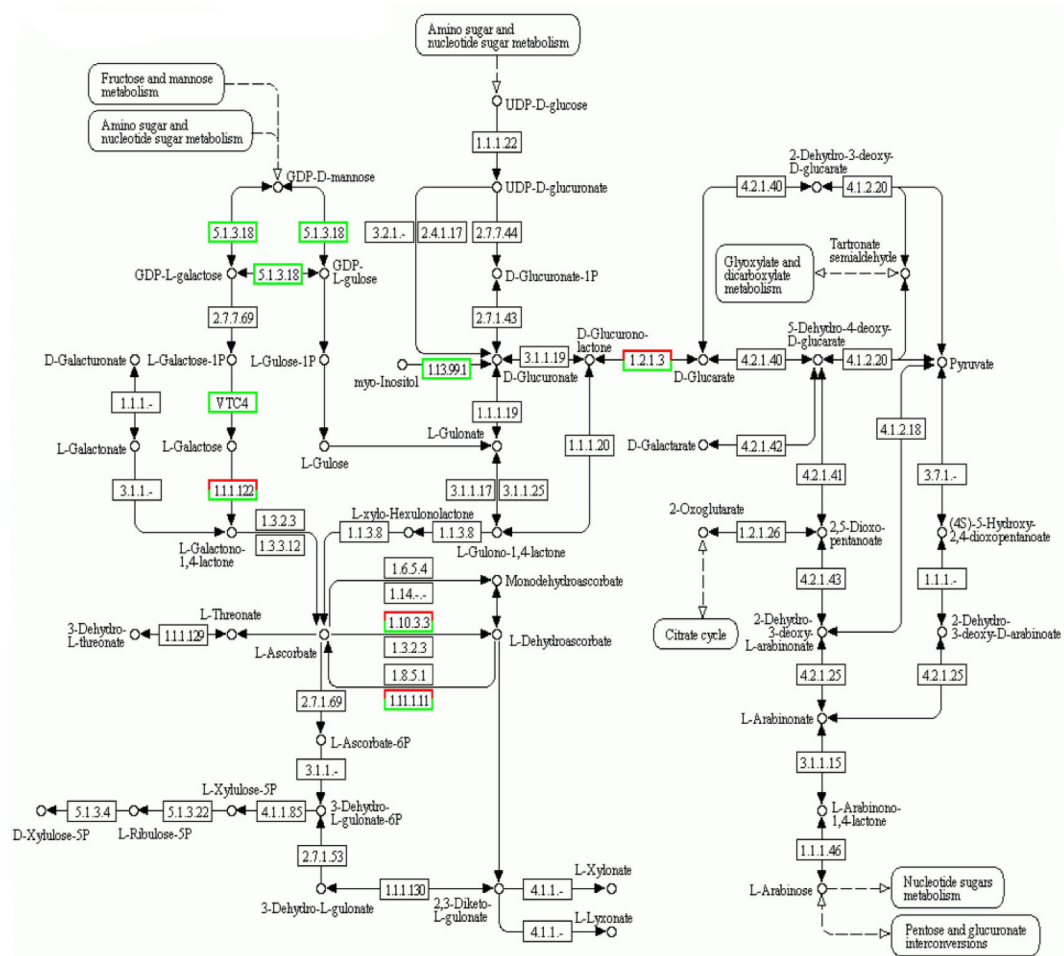


Fig. S9 “Ascorbate and aldarate” pathway induced by MeJA in *P. multiflorum* root transcriptome

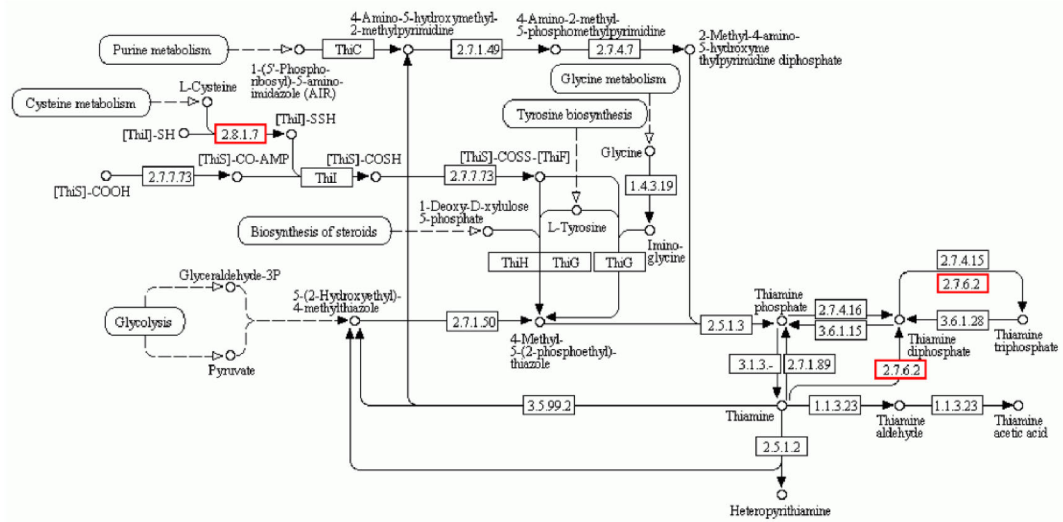


Fig. S10 “Thiamine metabolism” pathway induced by MeJA in *P. multiflorum* root transcriptome

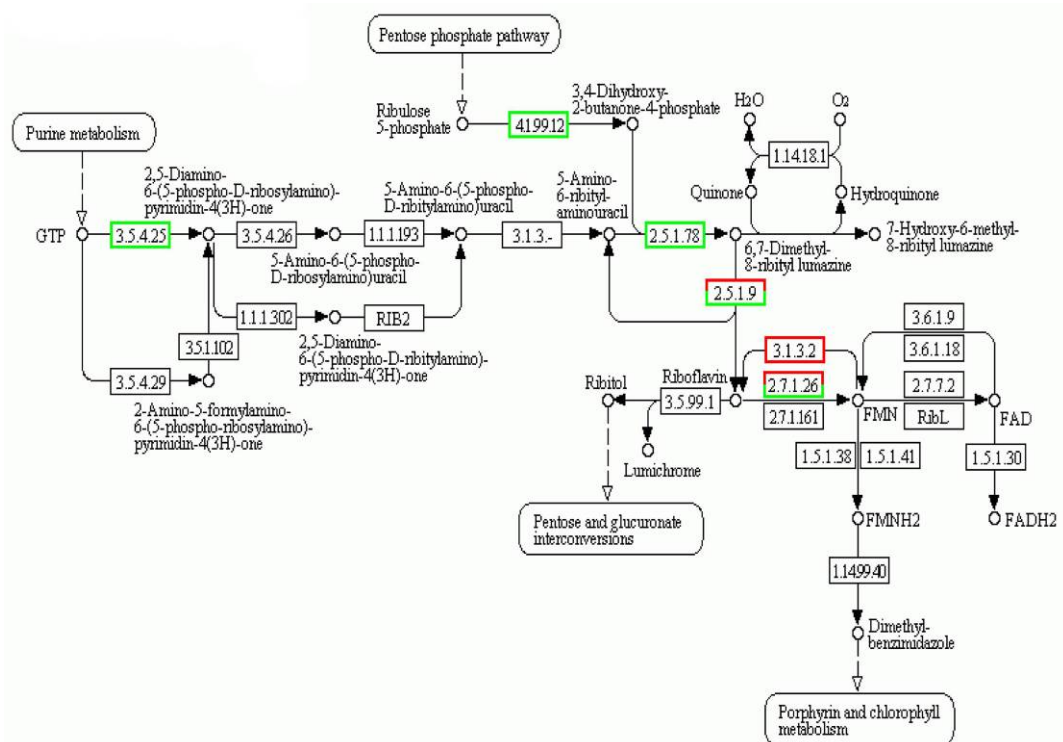


Fig. S11 “Riboflavin metabolism” pathway induced by MeJA in *P. multiflorum* root transcriptome

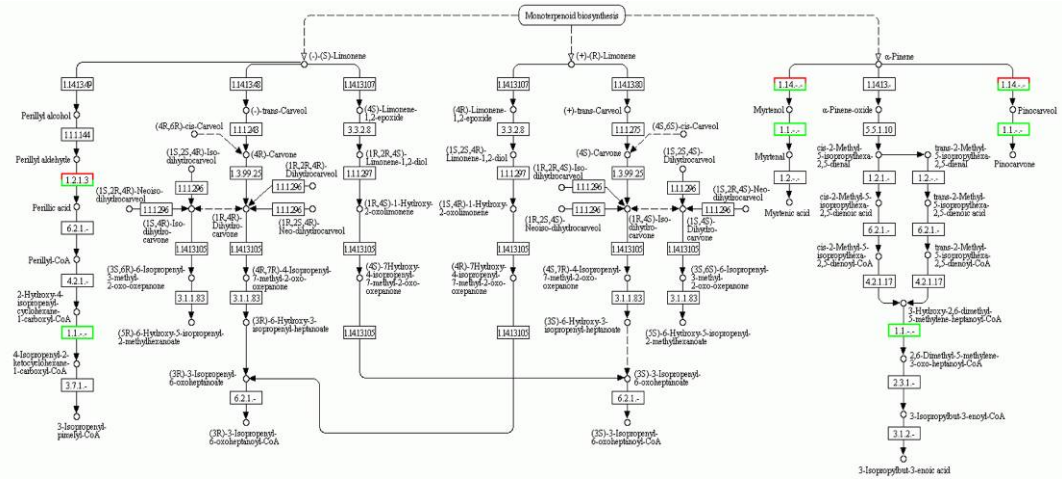


Fig. S16 “Limonene and pinene degradation” pathway induced by MeJA in *P. multiflorum* root transcriptome

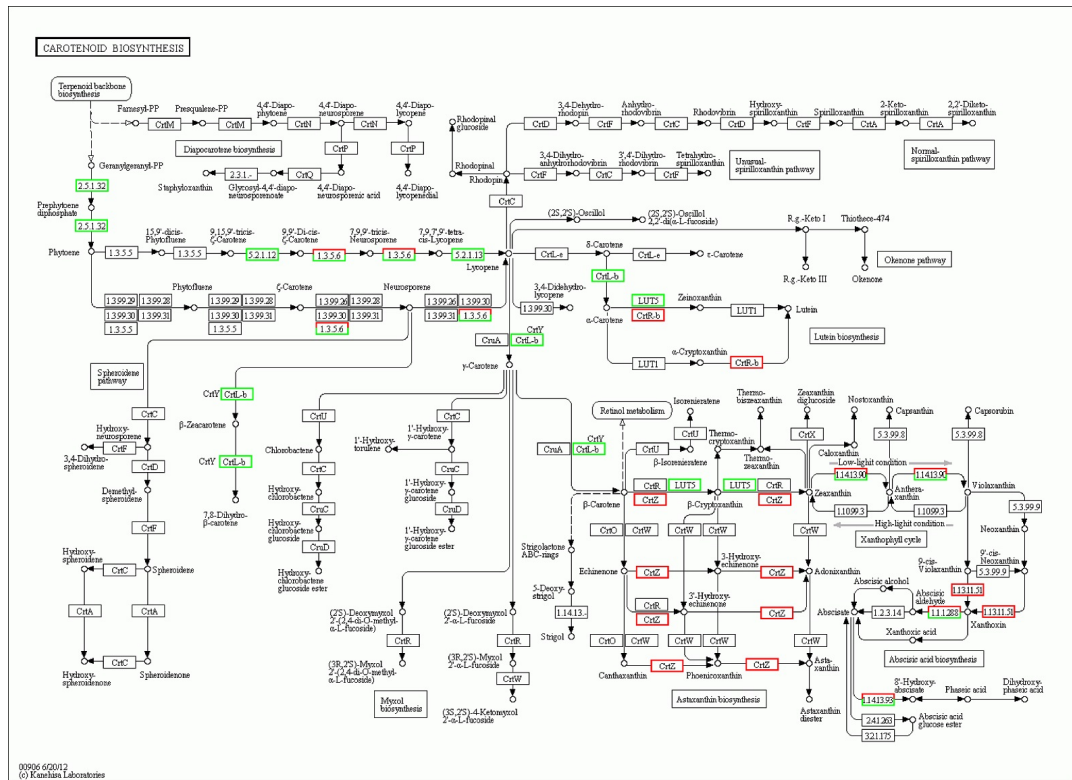


Fig. S17 “Carotenoid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

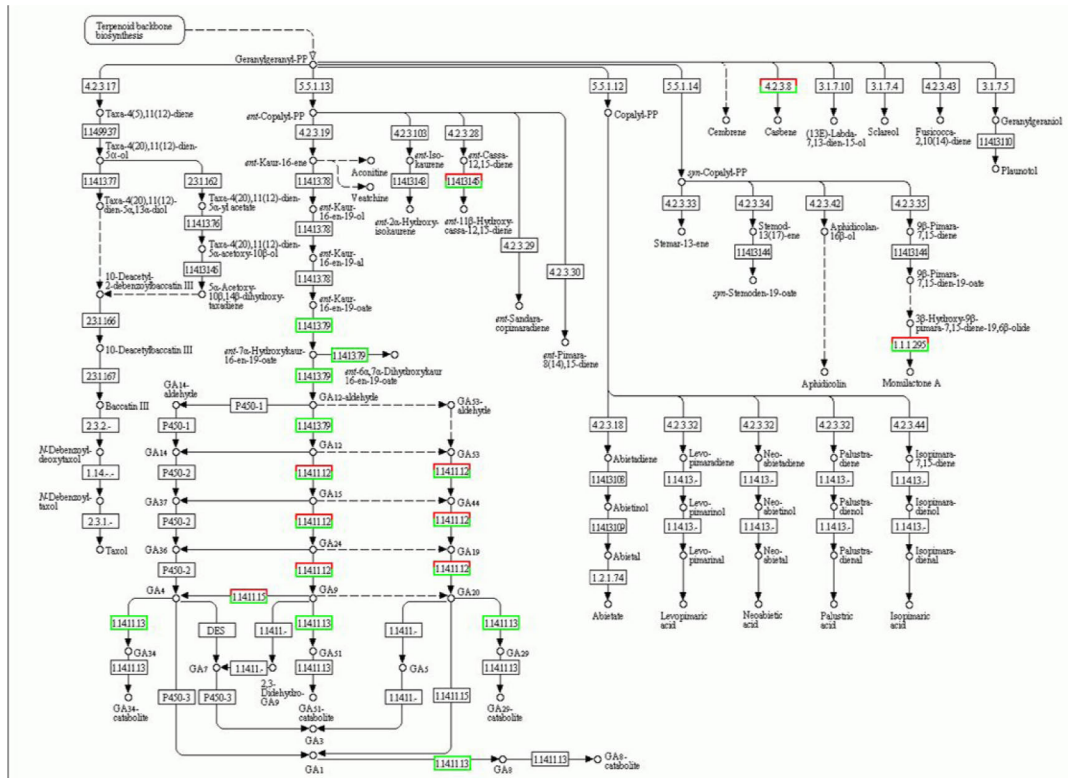


Fig. S18 “Diterpenoid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

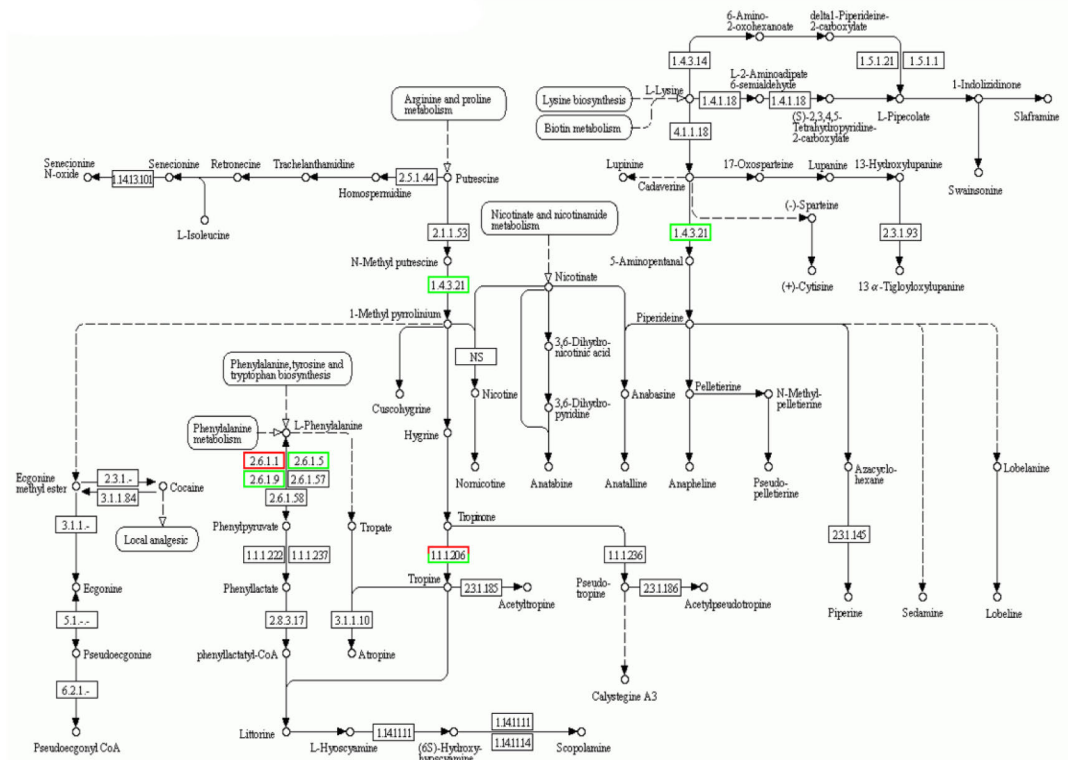


Fig. S19 “Tropane, piperidine and pyridine alkaloid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

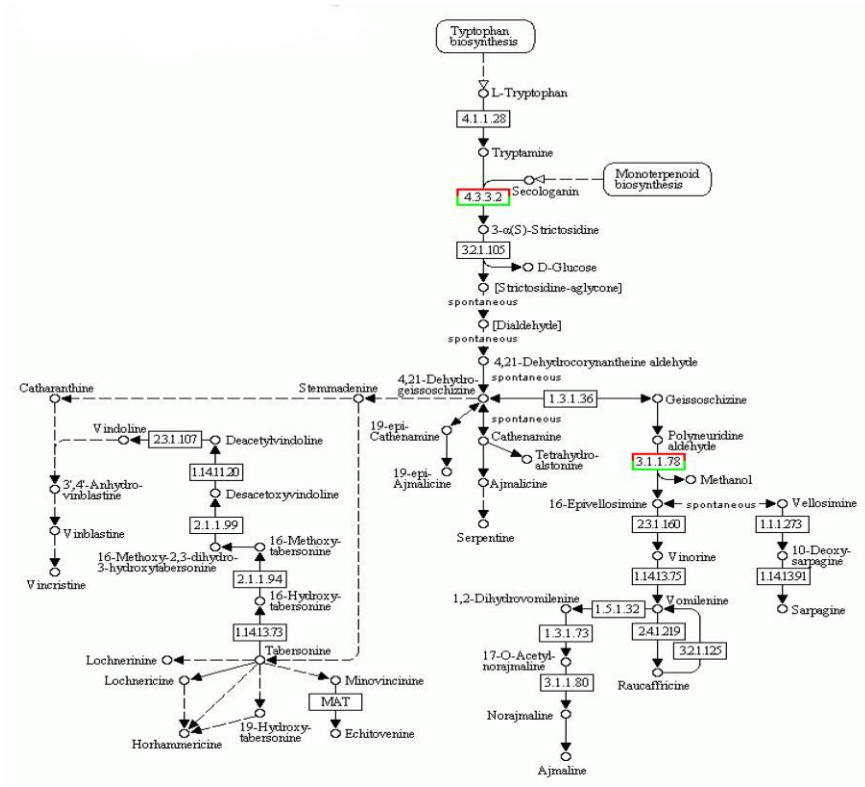


Fig. S21 “Indole alkaloid biosynthesis” pathway induced by MeJA in *P. multiflorum* root transcriptome

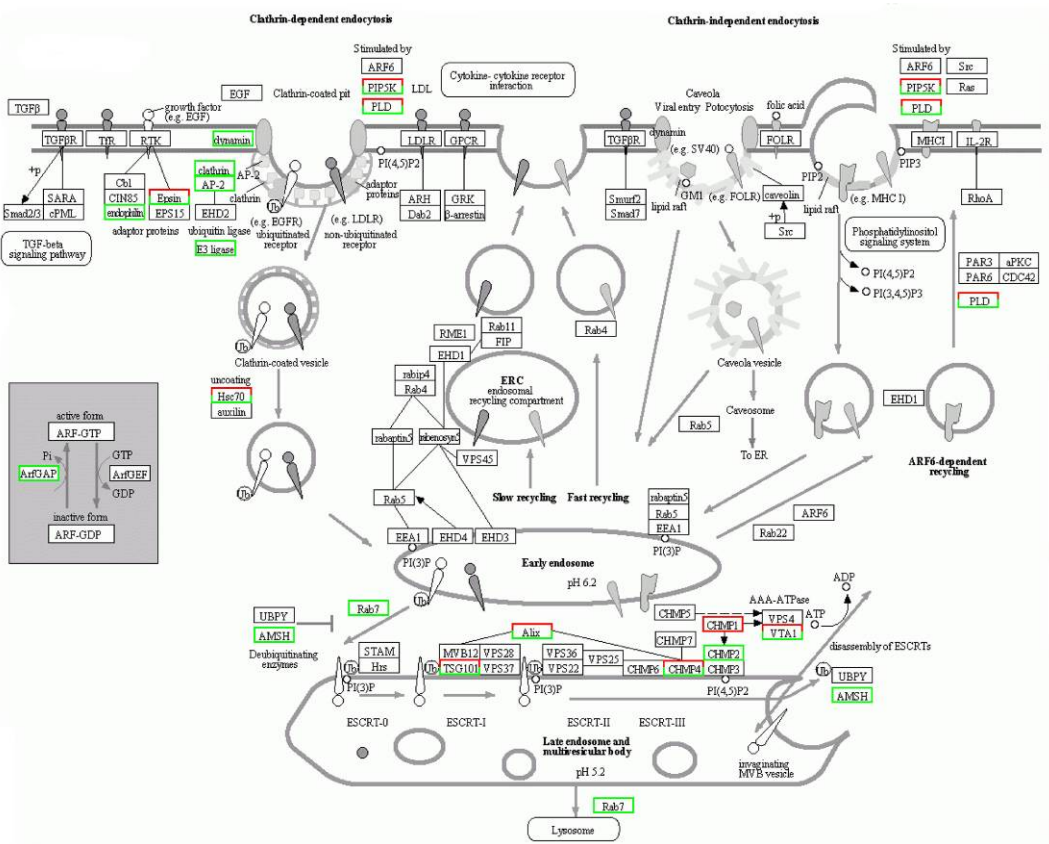


Fig. S22 “Endocytosis” pathway induced by MeJA in *P. multiflorum* root transcriptome