

Supplementary Table 1. RNA-sequencing reads count and statistics. The total number of paired reads obtained in RNA-sequencing analysis after adapter trimming and quality filtering. Reads were mapped to the genome of *N. benthamiana*. The overall alignment percentage is shown in the last column. OE1 and OE2 are two independent overexpression lines of *Ok4CL11* in *N. benthamiana*. Wild-type (WT) is the non-transformed plant of *N. benthamiana*. Rep 1-3 are three independent biological replicates (n); wherein 3 plants per line were pooled to form a single biological replicate.

Sample name	Total paired reads (filtered)	Overall alignment (%)
<i>Ok4CL11</i> -OE1 Rep 1	38611481	97.68
<i>Ok4CL11</i> -OE1 Rep 2	40957981	97.90
<i>Ok4CL11</i> -OE1 Rep 3	38066763	97.86
<i>Ok4CL11</i> -OE2 Rep 1	39857739	98.00
<i>Ok4CL11</i> -OE2 Rep 2	40049183	96.92
<i>Ok4CL11</i> -OE2 Rep 3	37633735	97.97
Wild-type (WT) Rep 1	29447773	97.91
Wild-type (WT) Rep 2	25830474	98.28
Wild-type (WT) Rep 3	39918389	97.87

Supplementary Table 2. List of primers used in the study.

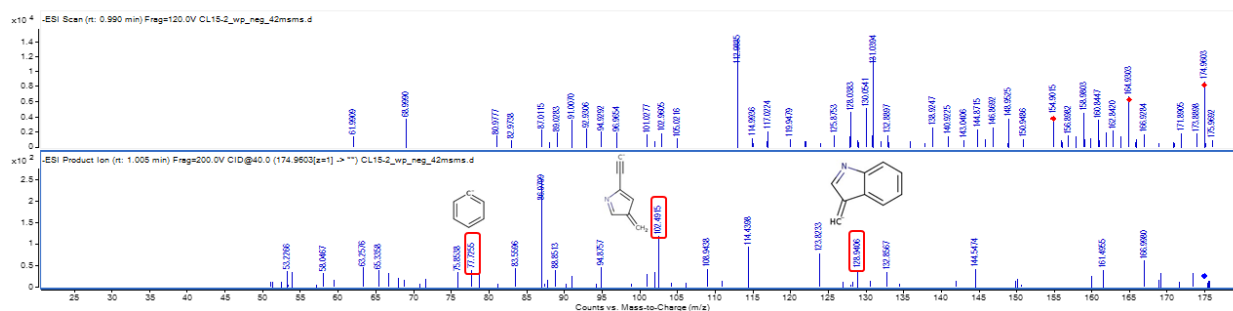
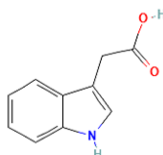
S r.	Primer	Gene	Sequence (5'→3')	Length (bp)	Amplification (bp)	Purpose
1	Ok4CL7 FL- F	<i>Ocimum 4-Coumarate-CoA ligase 7</i>	AATACATATGATGGCTGCATTAAT AAAAGCCC	32	1731	Cloning for Ok4CL7 overexpression construct
2	Ok4CL7 FL- R		AATAGAATTCCTAAAGCCTGGAAA CAAACAAGTTC	35		
3	Ok4CL11 FL- F	<i>Ocimum4-Coumarate-CoA ligase 11</i>	AAAACATATGATGGCTGCATTAAT AAAAGCCC	32	1731	Cloning for Ok4CL11 overexpression construct
4	Ok4CL11 FL- R		AAAAGAATTCAAGCCTTGAAACGA ACAAGTTC	32		
5	Ok4CL15 FL- F	<i>Ocimum 4-Coumarate-CoA ligase 15</i>	AATACATATGATGGAGCTGAAAGA AGAGAAG	31	1608	Cloning for Ok4CL15 overexpression construct
6	Ok4CL15 FL- R		AATAGTCGACTTACATTCTAGCTCT CAGATTCTTCC	36		
7	Ok4CL11 sense F	<i>Ocimum4-Coumarate-CoA ligase 11</i>	AATAGTCGACCATCAGGGCTATC	23	250	Cloning for Ok4CL11 RNAi construct
8	Ok4CL11 sense R		AATAGGTACCGCAGAAAATGCTAG	24		
9	Ok4CL11 antisense F	<i>Ocimum4-Coumarate-CoA ligase 11</i>	AATAGGATCCGCAGAAAATGCTAG	24	250	
10	Ok4CL11 antisense R		AATAGAGCTCCATCAGGGCTATC	23		
11	Ok4CL7 qF	<i>Ocimum 4-Coumarate-CoA ligase 7</i>	TTAGGTAATGCATTGGAGGGTTGC	24	166	RT-qPCR analysis
12	Ok4CL7 qR		AGTATAAAATCGCGGCGGTGTCCT	24		
13	Ok4CL11 qF	<i>Ocimum 4-Coumarate-CoA ligase 11</i>	GTTTTGGATTTGAGCTGTGAGAA	23	136	
14	Ok4CL11 qR		CAGTAGTGCCAGACGAGTAC	20		
15	Ok4CL15 qF	<i>Ocimum 4-Coumarate-CoA ligase 15</i>	ATTTGCCTCAAAGGAAGCTCC	21	239	
16	Ok4CL15 qR		CTCCATATCTGATGCTGCTGT	21		
17	L23 qF	<i>N. benthamiana 60S ribosomal protein L23</i>	AAGGATGCCGTGAAGAAGATGT	21	110	
18	L23 qR		GCATCGTAGTCAGGAGTCAACC	22		
19	LOC107763568 qF	<i>Glycosyltransferase LOC107763568</i>	AACCCCTCAAAGCATCAGGT	20	157	
20	LOC107763568 qR		TTATCCCCTCGCGATTGCG	20		
21	LOC107763569 qF	<i>Glycosyltransferase LOC107763569</i>	AACAACCGTTTACGGCCTCA	20	209	
22	LOC107763569 qR		CCAAGAACGTAACGGGGTGA	20		
23	UGT74F1 qF	<i>Glycosyltransferase UGT74F1</i>	AGGTAAGTATGGATGTCCA	21	172	
24	UGT74F1 qR		ACTGAGCTGATTGGTTGGTGA	21		
25	LOC107831012 qF	<i>Glycosyltransferase LOC107831012</i>	GCGCTGAAGTGAAGAAAGC	20	167	
26	LOC107831012 qR		CCGATCTCCTGTTTGGGACC	20		
27	4CL2-like qF	<i>4-Coumarate-CoA ligase 2 like</i>	TGGCCTTCACAAACAAGGGAT	21	152	
28	4CL2-like qR		TCACAACCTCAGATGCCGTA	20		
29	CHS1 qF	<i>Chalcone synthase 1</i>	AGGAAGTAGTGGTGAAGGGC	20	119	
30	CHS1 qR		CCCACAATATAAGCCCAACCC	21		

3 1	F3H-like qF	<i>Flavonoid 3'-monooxygenase-like</i>	ATGGGCTCACTACACATCCT	20	110	
3 2	F3H-like qR		AGCTATAACAGGAAGCACTTAGG	23		
3 3	PIN2 qF	<i>Auxin efflux carrier PIN2</i>	GCAAGTAGCCATGATTAATGGGA	23	89	
3 4	PIN2 qR		AGCCATAAGCTAAGATCAAAGCAAC	25		
3 5	PIN3 qF	<i>Auxin efflux carrier PIN3</i>	GATAAGTCAGCACCACTGC	21	236	
3 6	PIN3 qR		CCAACGAACAGAACCATAAGCC	22		
3 7	SAUR71-1 qF	<i>Auxin-responsive protein SAUR71-like-1</i>	TTCAGGCCAACATACACCC	20	84	
3 8	SAUR71-1 qR		AGCAAATCATGGAATGAAAGCACA	24		
3 9	SAUR71-2 qF	<i>Auxin-responsive protein SAUR71-like-2</i>	GGCTGAAATGGGTTCAGTA	20	93	
4 0	SAUR71-2 qR		TGGCTATTACCCAAACGCCT	20		
4 1	ARF1 qF	<i>Auxin response factor 1</i>	TGCCAAAACCAGCCAATGTT	20	138	
4 2	ARF1 qR		GGAGTAACTGCAACTGGCCT	20		
4 3	ARF2 qF	<i>Auxin response factor 2</i>	TGCCAAAACCAGCCAATGTT	20	110	
4 4	ARF2 qR		GGAGTAACTGCAACTGGCCT	20		
4 5	ARF4 qF	<i>Auxin response factor 4</i>	CGGAGGACTATTGACTCGCT	20	184	
4 6	ARF4 qR		CTGATCCCCTCTACTGGCCC	20		
4 7	LAX5 qF	<i>Auxin transporter-like protein LAX5</i>	GGTGGAGGGAGTGAAGCATT	20	101	
4 8	LAX5 qR		ACACAGTAACGGCATGTCCC	20		
4 9	LAX3 qF	<i>Auxin transporter-like protein LAX3</i>	ATTTCCAGTCAAAAACCTACCACAT	24	109	
5 0	LAX3 qR		AGAGTGTTAGAGGGTAACATGGAT	24		
5 1	LAX2 qF	<i>Auxin transporter-like protein LAX2</i>	GATACGTTTGGCCTTTTCGCT	21	174	
5 2	LAX2 qR		AGGACATGGTTTGTGACCG	20		
5 3	BIG-like qF	<i>Auxin transport protein BIG-like</i>	ACCATCAGTCCAATGGGTGG	20	188	
5 4	BIG-like qR		CGCCCTCAGAGAAAAGGTCC	20		
5 5	AUX/IAA qF	<i>Auxin response factor (AUX/IAA)</i>	AAGACAATTCCAGCCAACG	20	91	
5 6	AUX/IAA qR		ATCTTCCTTCCAAGTTGATCTGC	23		
5 7	SCR-like 21 qF	<i>Scarecrow-like protein 21</i>	ACCAACAATGGACTCTTGCAT	21	172	
5 8	SCR-like 21 qR		CAAGCCTTGCTCGGTTTCTC	21		
5 9	SCR-like 32_1 qF	<i>Scarecrow-like protein 32_1</i>	TGACTCAAACCAACGCCTCA	20	177	
6 0	SCR-like 32_1 qR		TAGCTCCATTAGCAGCCGTG	20		
6 1	SCR-like 32_2 qF	<i>Scarecrow-like protein 32_2</i>	TACTAGTGCCTCGCCATTCT	20	90	
6 2	SCR-like 32_2 qR		CCTTCAAGTTCATCGGACGG	20		
6 3	SCR-like 28 qF	<i>Scarecrow-like protein 28</i>	TATCACC GCCTCCACCTTTG	20	151	
6 4	SCR-like 28 qR		ACCAAGCCATGACTGTCTAACG	22		

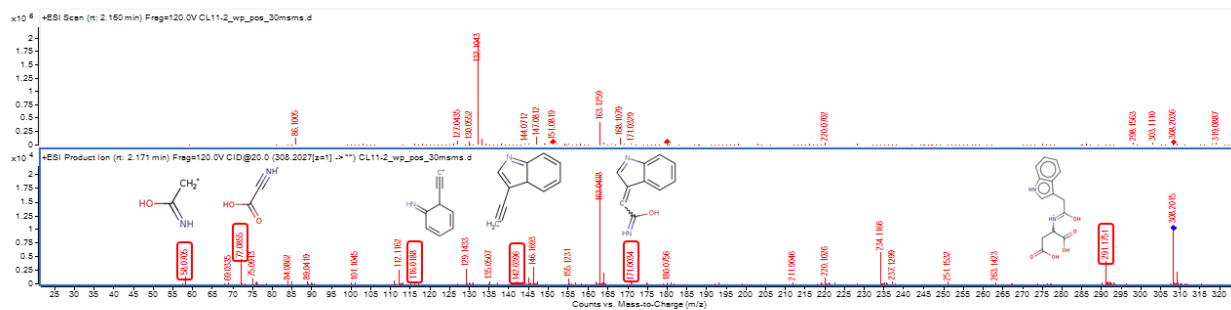
6 5	SHR qF	SHORT-ROOT	ATCCATCTTCGACCCACATCA	21	122	
6 6	SHR qR		AGCTAAAACCACCTACTCCACTT	23		
6 7	LRP1 qF	LATERAL ROOT PRIMORDIUM 1-like 1	GGCTACTGCTAGGAGACTGC	20	145	
6 8	LRP1 qR		ACCGTTACCGATGGTGGTTC	20		
6 9	EIF3e qFP	Eukaryotic Translation Initiation Factor 3 Subunit E	GGAGCACAGGAGAAGATGAAGGA G	24	164	
7 0	EIF3e qRP		CGTTGGTGAATGCGGCAGTAGG	22		
7 1	NOST Rscr	Nopaline synthase terminator	GCAACAGGATTCAATCTTAAG	21		Transgenic line confirmation

Supplementary Table 3. MS/MS fragmentation for IAA, IAA-Asp, K37R and rutin. The structures of these metabolites and their major MS/MS fragments (highlighted by red box) were used to identify the respective metabolites.

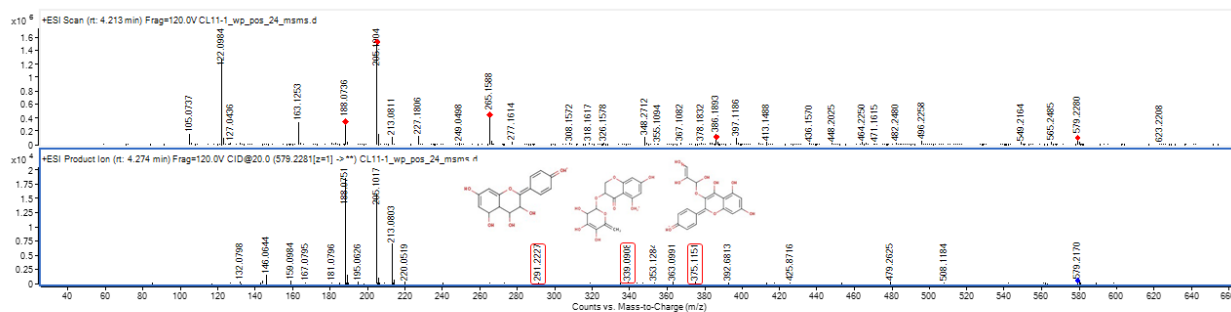
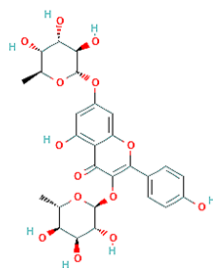
Indole 3- acetic acid (IAA)



Indole 3-acetyl aspartic acid (IAA-Asp)



Kaempferol-3,7-O-bis-alpha-L-rhamnoside (K3,7R)



Rutin (Quercetin-3-O-rutinoside)

