

Supplementary Table 1. List of co-expression genes for DTX39, which is related to myrosinase-glucosinolate defense system.

Rank	Gene	Function	Gene ID	Z-score*
1	TSA1	TSK-associating protein 1	At1g52410	5.4
2	MVP1	GDSL-like Lipase/Acylhydrolase superfamily protein	At1g54030	5.3
3	MEB1	Vacuolar iron transporter (VIT) family protein	At4g27860	4.8
4		Mannose-binding lectin superfamily protein	At1g52000	4.4
5	MBD1	methyl-CPG-binding domain 11	At3g15790	4.3
6		transmembrane protein: putative (Protein of unknown function: DUF538)	At4g02360	4.3
7	BGLU18	β -glucosidase 18	At1g52400	4.2
8		scorpion toxin-like knottin superfamily protein	At2g43530	4.2
9		Reticulon family protein	At3g10260	4.1
10	TBL26	TRICHOME BIREFRINGENCE-LIKE 26	At4g01080	4.1
11		HXXXD-type acyl-transferase family protein	At5g67150	3.9
12		Major facilitator superfamily protein	At1g72130	3.9
13	AAS	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	At2g20340	3.9
14		MD-2-related lipid recognition domain-containing protein	At5g23820	3.8
15		NAD(P)-binding Rossmann-fold superfamily protein	At3g55290	3.8
16	MEB2	Vacuolar iron transporter (VIT) family protein	At5g24290	3.8
17	CSLA10	cellulose synthase-like A10	At1g24070	3.7
18	MBP1	Myrosinase-binding protein 1	At1g52040	3.7
19		transmembrane protein: putative (DUF677)	At3g28270	3.7
20	CLH1	chlorophyllase 1	At1g19670	3.6
21	HPL1	hydroperoxide lyase 1	At4g15440	3.6
22		FAD-binding Berberine family protein	At2g34810	3.6
23		Alkaline-phosphatase-like family protein	At4g29700	3.5
24	JR1	Mannose-binding lectin superfamily protein	At3g16470	3.5
25	scpl29	serine carboxypeptidase-like 29	At4g30810	3.5
26		B-cell receptor-associated 31-like protein	At1g48440	3.5
27	DET2	3-oxo-5- α -steroid 4-dehydrogenase family protein	At2g38050	3.4
28	MYB47	MYB domain protein 47	At1g18710	3.4
29	PGL5	6-phosphogluconolactonase 5	At5g24420	3.4
30		Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein	At1g63010	3.4
31	DHAR1	dehydroascorbate reductase	At1g19570	3.4
32		GDSL-like Lipase/Acylhydrolase superfamily protein	At1g54020	3.4
33	PBP1	PYK10-binding protein 1	At3g16420	3.4
34		SGNH hydrolase-type esterase superfamily protein	At1g28570	3.4
35	FMO GS-OX2	flavin-monooxygenase glucosinolate S-oxygenase 2	At1g62540	3.4
36	UGT78D1	UDP-glucosyl transferase 78D1	At1g30530	3.3
37	NSP1	nitrile specifier protein 1	At3g16400	3.3
38		Esterase/lipase/thioesterase family protein	At5g41120	3.3
39	MBP2	Myrosinase-binding protein 2	At1g52030	3.3
40	VSP1	vegetative storage protein 1	At5g24780	3.3
41	IGMT5	O-methyltransferase family protein	At1g76790	3.3
42		TRAF-like family protein	At3g28220	3.3
43	CSLA11	cellulose synthase like A11	At5g16190	3.2
44	CSLA01	cellulose synthase-like A01	At4g16590	3.2
45		ion channel POLLUX-like protein: putative (DUF1012)	At5g02940	3.2
46	VSP2	vegetative storage protein 2	At5g24770	3.2
47		ChaC-like family protein	At1g44790	3.2
48		GDSL-like Lipase/Acylhydrolase superfamily protein	At1g54010	3.1
49	CYP79B2	Cytochrome P450: family 79: subfamily B2	At4g39950	3.1
50	CYP79B3	Cytochrome P450: family 79: subfamily B3	At2g22330	3.1
51		Kunitz family trypsin and protease inhibitor protein	At1g73325	3.1
52	CYP96A4	cytochrome P450: family 96: subfamily A: polypeptide 4	At5g52320	3.1
53	COR13	Tyrosine transaminase family protein	At4g23600	3.1
54		ion channel POLLUX-like protein: putative (DUF1012)	At5g43745	3.0
55	NAI1	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	At2g22770	3.0
56		Voltage-gated chloride channel family protein	At5g33280	3.0
57		Embryo-specific protein 3: (ATS3)	At2g41475	3.0
58		AMP-dependent synthetase and ligase family protein	At1g20490	3.0
59		Acyl-CoA thioesterase family protein	At4g00520	3.0
60		Protein kinase superfamily protein	At5g01850	3.0
61		Glycosyl hydrolases family 32 protein	At1g62660	3.0
62		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	At1g06620	3.0
63	CYP83B1	Cytochrome P450: family 83: subfamily B1	At4g31500	3.0
64	KAT5	peroxisomal 3-keto-acyl-CoA thiolase 2	At5g48880	3.0
65	AOS	allene oxide synthase	At5g42650	2.9
66	SPL11	squamosa promoter-like 11	At1g27360	2.9
67		NAD(P)H-quinone oxidoreductase subunit: putative (DUF581)	At3g22550	2.9
68	UBP1B	oligouridylate binding protein 1B	At1g17370	2.9
69		scorpion toxin-like knottin superfamily protein	At2g43550	2.9
70		Regulator of chromosome condensation (RCC1) family protein	At3g02510	2.9
71		UDP-Glycosyltransferase superfamily protein	At4g27560	2.9
72	FLR1	Leucine-rich repeat (LRR) family protein	At3g12145	2.9

73	BAM2	beta-amylase 2	At4g00490	2.9
74			At2g41312	2.9
75	NSP4	nitrile specifier protein 4	At3g16410	2.9
76	TLL1	triacylglycerol lipase-like 1	At1g45201	2.9
77	THI2.1	thionin 2.1	At1g72260	2.8
78	GSTF9	glutathione S-transferase PHI 9	At2g30860	2.8
79		MATE efflux family protein	At3g26590	2.8
80	ANNAT4	annexin 4	At2g38750	2.8
81	GGH1	gamma-glutamyl hydrolase 1	At1g78660	2.8
82		Major facilitator superfamily protein	At5g17010	2.8
83	SS2	starch synthase 2	At3g01180	2.8
84		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	At5g05600	2.8
85	JAL34	Mannose-binding lectin superfamily protein	At3g16460	2.8
86	NSH3	inosine-uridine preferring nucleoside hydrolase family protein	At5g18860	2.8
87		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	At3g56080	2.8
88	GGT4	gamma-glutamyl transpeptidase 4	At4g29210	2.7
89	GGH2	gamma-glutamyl hydrolase 2	At1g78680	2.7
90	JAL23	jacalin-related lectin 23	At2g39330	2.7
91	EULS3	hydroxyproline-rich glycoprotein family protein	At2g39050	2.7
92		GDLS-like Lipase/Acylhydrolase superfamily protein	At1g31550	2.7
93	ARGAH2	Arginase/deacetylase superfamily protein	At4g08870	2.7
94		alpha/beta-Hydrolases superfamily protein	At2g24280	2.7
95	GGH3	gamma-glutamyl hydrolase 3	At1g78670	2.7
96		Calcium-dependent phosphotriesterase superfamily protein	At2g47370	2.7
97		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	At1g77260	2.7
98	SFR2	Glycosyl hydrolase superfamily protein	At3g06510	2.7
99		Subtilase family protein	At3g14067	2.7
100	NAI2	TSA1-like protein	At3g15950	2.7

*Correlation coefficients listed in the ATTED-II database version 12.0 (ath-u.4 in <http://atted.jp>). Genes related to glucosinolate biosynthesis and degradation are highlighted with red and blue colors, respectively.

Supplementary Table 2. List of co-expression genes for DTX38, which is related to myrosinase-glucosinolate defense system.

Rank	Gene	Function	Gene ID	Z-score*
1		receptor Serine/Threonine kinase-like protein	At4g18250	4.2
2	ALDH2C4	aldehyde dehydrogenase 2C4	At3g24503	3.9
3		chitin synthase: putative (DUF1218)	At4g19370	3.8
4	SDR3	NAD(P)-binding Rossmann-fold superfamily protein	At2g47130	3.7
5	EDS5	MATE efflux family protein	At4g39030	3.7
6		plant stearyl-acyl-carrier desaturase family protein	At3g02610	3.5
7	IGMT1	O-methyltransferase family protein	At1g21100	3.5
8		P-loop containing nucleoside triphosphate hydrolases superfamily protein	At3g28580	3.5
9	RLP12	receptor like protein 12	At1g71400	3.4
10		glucosyltransferase-like protein	At4g15270	3.4
11	NAC042	NAC domain containing protein 42	At2g43000	3.4
12		Protein kinase superfamily protein	At1g67000	3.3
13	WRKY60	WRKY DNA-binding protein 60	At2g25000	3.2
14		TCP family transcription factor	At1g35560	3.2
15		leucine-rich repeat transmembrane protein kinase family protein	At1g34420	3.2
16		Protein kinase superfamily protein	At2g28940	3.2
17	NAXT1	nitrate excretion transporter1	At3g45650	3.2
18		uncharacterized protein	At1g64405	3.1
19	BEH3	BES1/BZR1 homolog 3	At4g18890	3.1
20		Leucine-rich repeat protein kinase family protein	At1g51890	3.1
21		NAD(P)-linked oxidoreductase superfamily protein	At1g59960	3.1
22	CRCK1	calmodulin-binding receptor-like cytoplasmic kinase 1	At5g58940	3.1
23	IGMT3	O-methyltransferase family protein	At1g21110	3.1
24		Pyridoxamine 5'-phosphate oxidase family protein	At3g21140	3.1
25		Disease resistance protein (TIR-NBS-LRR class) family	At5g38340	3.0
26	HWI1	Receptor-like protein kinase-related family protein	At1g70690	3.0
27	FAH1	ferulic acid 5-hydroxylase 1	At4g36220	3.0
28	YLS5	Class I glutamine amidotransferase-like superfamily protein	At2g38860	3.0
29	RBK1	ROP binding protein kinases 1	At5g10520	2.9
30		Leucine-rich repeat protein kinase family protein	At5g59680	2.9
31		Malectin/receptor-like protein kinase family protein	At5g39020	2.9
32		Phenazine biosynthesis PhzC/PhzF protein	At1g03210	2.9
33		MATE efflux family protein	At2g04090	2.9
34		phospholipase-like protein (PEARL1 4) family protein	At2g20950	2.9
35	CYP83B1	Cytochrome P450: family 83: subfamily B1	At4g31500	2.9
36	KT1	K ⁺ transporter 1	At2g26650	2.8
37		Transmembrane proteins 14C	At2g26240	2.8
38		AlG2-like (avirulence induced gene) family protein	At3g28940	2.8
39		Matrixin family protein	At1g59970	2.8
40		O-glucosyltransferase rumi-like protein (DUF821)	At5g23850	2.7
41		Major facilitator superfamily protein	At3g45660	2.7
42	ABCG24	P-loop containing nucleoside triphosphate hydrolases superfamily protein	At1g53390	2.7
43	ATOBGM	GTP-binding protein Obg/CgtA	At1g07620	2.7
44		GroES-like zinc-binding alcohol dehydrogenase family protein	At1g64710	2.7
45	ATSYTF	C2 domain-containing protein	At3g18370	2.7
46		Ankyrin repeat family protein	At4g14390	2.7
47	MDHAR	monodehydroascorbate reductase	At3g09940	2.7
48	CuAO1	Copper amine oxidase family protein	At1g62810	2.7
49		alpha/beta-Hydrolases superfamily protein	At1g47480	2.7
50		wall-associated receptor kinase-like protein	At4g00955	2.7
51		uncharacterized protein	At2g18210	2.7
52	UGT71C5	UDP-glucosyl transferase 71C5	At1g07240	2.7
53		FAD/NAD(P)-binding oxidoreductase family protein	At5g05320	2.7
54	FMO1	flavin-dependent monooxygenase 1	At1g19250	2.6
55	MES1	methyl esterase 1	At2g23620	2.6
56		Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	At2g46150	2.6
57	CES101	lectin protein kinase family protein	At3g16030	2.6
58		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	At3g13610	2.6
59	CNGC3	cyclic nucleotide gated channel 3	At2g46430	2.6
60		Protein kinase superfamily protein	At5g42440	2.6
61	PAD3	Cytochrome P450 superfamily protein	At3g26830	2.6
62		RING/U-box superfamily protein	At5g53110	2.6
63	MSRB8	methionine sulfoxide reductase B8	At4g21840	2.6
64	CYP79B2	Cytochrome P450: family 79: subfamily B2	At4g39950	2.6
65		EF hand calcium-binding protein family	At3g03000	2.6
66		Exostosin family protein	At2g31990	2.6
67		VQ motif-containing protein	At4g20000	2.6
68		Concanavalin A-like lectin protein kinase family protein	At4g29050	2.5
69		Inositol monophosphatase family protein	At5g09290	2.5
70		uncharacterized protein	At1g23840	2.5
71		Calcium-dependent lipid-binding (CaLB domain) family protein	At3g62780	2.5
72		Cold acclimation protein WCOR413 family	At2g23680	2.5

73		HXXXD-type acyl-transferase family protein	At3g50280	2.5
74		Transducin/WD40 repeat-like superfamily protein	At5g42010	2.5
75	PLDGAMMA1	phospholipase D gamma 1	At4g11850	2.5
76		Concanavalin A-like lectin protein kinase family protein	At5g65600	2.5
77		uncharacterized protein	At5g23510	2.5
78		S-locus lectin protein kinase family protein	At2g19130	2.5
79		uncharacterized protein	At1g23850	2.5
80		Galactose mutarotase-like superfamily protein	At4g25900	2.5
81		hypothetical protein (Protein of unknown function: DUF538)	At5g46230	2.5
82	LBD4	LOB domain-containing protein 4	At1g31320	2.5
83		Serine/Threonine kinase family catalytic domain protein	At1g18390	2.4
84		uncharacterized protein	At1g49000	2.4
85		MATE efflux family protein	At3g26590	2.4
86		enabled-like protein (DUF1635)	At5g22930	2.4
87	MSRB9	methionine sulfoxide reductase B9	At4g21850	2.4
88		Glyceraldehyde-3-phosphate dehydrogenase-like family protein	At1g34200	2.4
89		Leucine-rich repeat protein kinase family protein	At5g49760	2.4
90		calmodulin-binding protein (DUF1645)	At2g15760	2.4
91		beta-1:2-N-acetylglucosaminyltransferase II	At2g05320	2.4
92		Powdery mildew resistance protein: RPW8 domain-containing protein	At3g26470	2.4
93	CRT3	calreticulin 3	At1g08450	2.4
94	CNGC10	cyclic nucleotide gated channel 10	At1g01340	2.4
95		calmodulin-binding family protein	At5g57010	2.4
96		RNI-like superfamily protein	At5g45500	2.4
97		uncharacterized protein	At3g19660	2.4
98	RBOHD	respiratory burst oxidase homologue D	At5g47910	2.4
99	CYP704A2	cytochrome P450: family 704: subfamily A: polypeptide 2	At2g45510	2.4
100	GSTF3	glutathione S-transferase F3	At2g02930	2.3

*Correlation coefficients listed in the ATTED-II database version 12.0 (ath-u.4 in <http://atted.jp>). Genes related to glucosinolate biosynthesis are highlighted with red color.

Supplementary Table 3. List of proteins used in phylogenetic tree analysis in Extended Fig. 1.

UniProt ID *	Gene name	Common name	Species
Q9SIA5	At2g04040	DTX1	<i>Arabidopsis thaliana</i>
Q8GXM8	At2g04080	DTX2	<i>Arabidopsis thaliana</i>
Q9SIA4	At2g04050	DTX3	<i>Arabidopsis thaliana</i>
Q9SIA3	At2g04070	DTX4	<i>Arabidopsis thaliana</i>
Q9SIA1	At2g04090	DTX5	<i>Arabidopsis thaliana</i>
Q8RWF5	At2g04100	DTX6	<i>Arabidopsis thaliana</i>
Q1PFG9	At1g64820	DTX7	<i>Arabidopsis thaliana</i>
F4HQ05	At1g66780	DTX8	<i>Arabidopsis thaliana</i>
Q9C9M8	At1g66760	DTX9	<i>Arabidopsis thaliana</i>
Q8VYL8	At1g15150	DTX10	<i>Arabidopsis thaliana</i>
F4HZH9	At1g15160	DTX11	<i>Arabidopsis thaliana</i>
Q8L731	At1g15170	DTX12	<i>Arabidopsis thaliana</i>
Q94AL1	At1g15180	DTX13	<i>Arabidopsis thaliana</i>
Q9C994	At1g71140	DTX14	<i>Arabidopsis thaliana</i>
F4IHU9	At2g34360	DTX15	<i>Arabidopsis thaliana</i>
Q9FHB6	At5g52450	DTX16	<i>Arabidopsis thaliana</i>
Q9C9U1	At1g73700	DTX17	<i>Arabidopsis thaliana</i>
Q9LUH3	At3g23550	DTX18	<i>Arabidopsis thaliana</i>
Q9LUH2	At3g23560	DTX19/ALF5	<i>Arabidopsis thaliana</i>
F4HPH2	At1g33100	DTX20	<i>Arabidopsis thaliana</i>
Q8W488	At1g33110	DTX21	<i>Arabidopsis thaliana</i>
F4HPH1	At1g33090	DTX22	<i>Arabidopsis thaliana</i>
Q8RXK1	At1g33080	DTX23	<i>Arabidopsis thaliana</i>
F4J158	At3g03620	DTX24	<i>Arabidopsis thaliana</i>
Q8L616	At5g17700	DTX25	<i>Arabidopsis thaliana</i>
Q1PDX9	At5g10420	DTX26	<i>Arabidopsis thaliana</i>
Q9FKQ1	At5g65380	DTX27	<i>Arabidopsis thaliana</i>
Q9FNC1	At5g44050	DTX28	<i>Arabidopsis thaliana</i>
Q38956	At3g26590	DTX29	<i>Arabidopsis thaliana</i>
Q9LS19	At5g38030	DTX30	<i>Arabidopsis thaliana</i>
Q9LPV4	At1g12950	DTX31	<i>Arabidopsis thaliana</i>
F4I4Q3	At1g23300	DTX32	<i>Arabidopsis thaliana</i>
Q9SX83	At1g47530	DTX33	<i>Arabidopsis thaliana</i>
F4JH46	At4g00350	DTX34	<i>Arabidopsis thaliana</i>
F4JTB3	At4g25640	DTX35/FFT	<i>Arabidopsis thaliana</i>
Q9SAB0	At1g11670	DTX36	<i>Arabidopsis thaliana</i>
O80695	At1g61890	DTX37	<i>Arabidopsis thaliana</i>
F4JKB9	At4g21903	DTX38	<i>Arabidopsis thaliana</i>
Q940N9	At4g21910	DTX39	<i>Arabidopsis thaliana</i>
Q9LVD9	At3g21690	DTX40	<i>Arabidopsis thaliana</i>
Q9LYT3	At3g59030	DTX41/TT12	<i>Arabidopsis thaliana</i>
Q9SYD6	At1g51340	DTX42	<i>Arabidopsis thaliana</i>
Q9SFB0	At3g08040	DTX43/FRD3	<i>Arabidopsis thaliana</i>
Q84K71	At2g38330	DTX44	<i>Arabidopsis thaliana</i>
Q9SVE7	At4g38380	DTX45	<i>Arabidopsis thaliana</i>
Q8W4G3	At2g21340	DTX46/EDS5H	<i>Arabidopsis thaliana</i>

Q945F0	At4g39030	DTX47/EDS5	<i>Arabidopsis thaliana</i>
Q9SLV0	At1g58340	DTX48/ABS4	<i>Arabidopsis thaliana</i>
O82752	At4g23030	DTX49	<i>Arabidopsis thaliana</i>
Q9FJ87	At5g52050	DTX50	<i>Arabidopsis thaliana</i>
Q9SZE2	At4g29140	DTX51/ABS3	<i>Arabidopsis thaliana</i>
Q4PSF4	At5g19700	DTX52	<i>Arabidopsis thaliana</i>
Q9ZVH5	At2g38510	DTX53	<i>Arabidopsis thaliana</i>
Q9LE20	At1g71870	DTX54	<i>Arabidopsis thaliana</i>
Q9FH21	At5g49130	DTX55	<i>Arabidopsis thaliana</i>
O49660	At4g22790	DTX56/RHC1	<i>Arabidopsis thaliana</i>
A0A1S4CVU7	LOC107823048	NtJAT1	<i>Nicotiana tabacum</i>
A0A077LAP2	LOC107779024	NtJAT2	<i>Nicotiana tabacum</i>
A3KDM4	LOC107792500	NtMATE1	<i>Nicotiana tabacum</i>
A3KDM5	LOC107807968	NtMATE2	<i>Nicotiana tabacum</i>
A0A1S4AET7	LOC107796897	NtMATE21	<i>Nicotiana tabacum</i>
A0A1S4AL16	LOC107798833	NtMATE22	<i>Nicotiana tabacum</i>
-	Sobic.001G012600	SbMATE2	<i>Sorghum bicolor</i>
Q2QM65	Os12g42130	OsTT12	<i>Oryza sativa</i>
E3SHE0	LOC103443147	MdMATE1	<i>Malus domestica</i>
E3SHE2	LOC11431940	MdMATE2	<i>Malus domestica</i>
C9WSQ2	Mtr5g090290	MtMATE1	<i>Medicago truncatula</i>
F4ZG52	Mtr1g100180	MtMATE2	<i>Medicago truncatula</i>
A0A2H4UZL7	KY851294	FaTT12	<i>Fragaria ananassa</i>
D7F4H6	ACZ55933	ZmMATE2	<i>Zea mays</i>
F6H569	Vitis12g00135	VvMATE1	<i>Vitis vinifera</i>
E0CTZ6	Vitis12g00134	VvMATE2	<i>Vitis vinifera</i>
C1J5V2	LOC100268149	VvAM1	<i>Vitis vinifera</i>
C0JLI5	LOC100256121	VvAM3	<i>Vitis vinifera</i>
Q6V7U8	NP_001234424	LeMTP77	<i>Solanum lycopersicum</i>
A0A5A4LJP6	MH475368	CsMATE1a	<i>Crocus sativus</i>
A0A5A4LIX7	MH475369	CsMATE1b	<i>Crocus sativus</i>
A0A5A4M457	MF966956	CsMATE4	<i>Crocus sativus</i>
A0A0A0LR20	Csa1G044870	CsMATE1	<i>Cucumis sativus</i>
A0A1S3ATX8	Melo3C002190	CmMATE1	<i>Cucumis melo</i>
	Cla008357	CIMATE1	<i>Citrullus lanatus</i>
	XP_002282907	VvDTX41B	<i>Vitis vinifera</i>

* The UniProt database is <https://www.uniprot.org>.

Supplementary Table 4. List of all glucosinolates identified in this study, including their retention times, fragmentation and intensities of signals obtained during LC-MS/MS analyses.

Metabolite name	Abbreviation used in the publication	Rt(min)	Exact mass of [M-H] ⁻		Fragmentation	PubChem CID*	Identification level	biological repetition				biological repetition				
			Measured	Calculated				col0	col0	col0	col0	dtx39-1	dtx39-1	dtx39-1	dtx39-1	dtx39-1
Glucoliberin 3-(methylsulfinyl)propyl glucosinolate	3MSOP	1.7	422.0257	422.0255	422.02; 358.02; 195.97; 96.96	656543	2	25723.63	23893.5	24803.88	26675.75	24223.38	30584	27218.38	18973.63	23683.75
Glucoerucin 4-(methylthio)butyl glucosinolate	4MTB	2.7	420.0453	420.0462	420.05; 259.01; 178.04; 96.96	656539	2	1370351	1414011	1313259	1090182	1109877	1380206	1119479	997176	1088586
Glucoraphanin 4-(methylsulfinyl)butyl glucosinolate	4MSOB	1.75	436.0399	436.0411	436.04; 372.05; 178.02; 96.96	9548634	2	270212	249835.1	286207.5	279275.5	240176.5	304610.3	265927.5	227969.3	294713.9
Glucolalysin 5-(methylsulfinyl)pentyl glucosinolate	5MSOP	1.8	450.0559	450.0568	450.06; 386.06; 285.55; 194.05; 96.96	9589398	2	57245.88	50181	58709.38	42030.75	35636.25	40221.38	34561.88	54502.75	63638.5
Glucoberberoin 5-(methylthio)pentyl glucosinolate	5MTP	4	434.0615	434.0619	434.06; 336.35; 223.05; 164.04; 96.96	9548727	2	703421.3	749633.1	630472	574651.9	564332.1	671336.9	620351.6	533682.6	556772.9
Glucosquerellin 6-(methylthio)hexyl glucosinolate	6MTH	8.6	448.0762	448.0775	448.08; 363.08; 242.96; 141.07; 96.96	46173875	2	175463.5	179998.8	154233.6	151495.3	188596.4	216499.8	203165.3	171782.5	193341.6
Glucosesperin 6-(methylsulfinyl)hexyl glucosinolate	6MSOH	1.9	464.0711	464.0724	464.07; 400.08; 274.60; 229.41; 148.67; 96.96	134160269	2	17122.63	16177.88	22897.38	14937.63	17361.13	20709.75	18229.63	25536	36402
Glucorabishirsutain 7-(methylthio)heptyl glucosinolate	7MTH	9.8	462.0920	462.0932	462.09; 382.13; 274.99; 220.08; 96.96	46173876	2	987954.6	1094279	1008847	948234.9	1162006	1282921	1131595	1076175	1212119
Glucohirsutin 8-(methylsulfinyl)octyl glucosinolate	8MSOO	2.5	492.1032	492.1037	492.10; 428.11; 234.08; 96.96	46173880	2	61671.88	69219.5	69587.63	56283	31399.38	45728.75	32447.25	49679	55478.5
Glucorabishirsuin 8-(methylthio)octyl glucosinolate	8MTO	10.75	476.1095	476.1088	476.11; 274.99; 259.01; 195.03; 96.96	46173877	2	19350.5	20994.5	19523	19787.88	19759.75	24220.5	25342.88	17296.63	28345
Glucobrassicin 3-indolylmethyl glucosinolate	13G	5.2	447.0529	447.0537	447.05; 393.52; 313.18; 259.02; 205.05; 152.40; 96.96	656506	1	3517618	3676707	3868847	3379701	658943	716054.4	839548.3	1241250	1566305
4-Hydroxyglucobrassicin 4-hydroxy-3-indolylmethyl glucosinolate	4OH-13G	2.1	463.0483	463.0487	463.05; 373.83; 221.13; 157.35; 96.96	656561	2	135399.9	146840.1	122646.1	109950.4	21421.25	18535	21953.75	21047	22843.5
Neoglucobrassicin 1-methoxy-3-indolylmethyl glucosinolate	1MO-13G	8.7	477.0640	477.0643	477.06; 446.05; 421.05; 365.04; 341.04; 315.04; 259.01; 96.96	656565	1	417367.9	490604.6	317201.6	350687	713754.1	672374.8	603057	465932.6	503745.9
4-Methoxyglucobrassicin 4-methoxy-3-indolylmethyl glucosinolate	4MO-13G	7.6	477.0657	477.0643	477.07; 425.05; 373.05; 345.04; 307.04; 259.01; 205.05; 96.96	656563	1	2849591	3390411	2971588	3083317	3615479	3559474	3655259	3908446	3978506

* Chemical id of compound from PubChem database. m/z measured is a value of m/z detected and processed by MS-Dial from every sample followed by alignment of peaks to one data matrix; error is calculated from equation $\text{error} = (\text{m/z measured} - \text{m/z calculated}) / \text{m/z calculated} \times 10^6$; metabolite identification level according to Metabolomics Standards Initiative recommendation: level 1 - identification based on standard compounds; level 2 - identification based on fragmentation spectra and comparison to available data bases, including PubChem.

Supplementary Table 5. Plasmids used in this study.

name	gene	note	origine
Vectors			
pENTR1 A	-	Gateway entry clone	Thermo Fisher
pGWB604	GFP	T-DNA vector	Nakamura et al. (2010) doi: 10.1271/bbb.100184
pGWB405	GFP	Plant transient expression vector	Nakagawa et al. (2007) doi: 10.1271/bbb.70216
pGWB633	GUS	T-DNA vector	Nakamura et al. (2010) doi: 10.1271/bbb.100184
pCBC-DT1 T2	sgRNA	CRISPR-Cas9 vector	Addgene, #50590
pK11.1R	sgRNA	CRISPR-Cas9 vector	Addgene, #85808
p415-GW	-	Yeast expression vector	Yamada et al. (2012) doi: 10.1104/pp.112.207654
pYES2	-	Yeast expression vector	Thermo Fisher, V82520
pYES2-DEST52	-	Yeast expression vector	Thermo Fisher, 12286019
pAG416GAL-ccdB-EGFP	GFP	Yeast expression vector	Addgene, #14195
pDR196	-	Yeast expression vector	Addgene, #36029
pDR196-ccdB-V5-6×His	V5-6×His	Yeast expression vector	This study
Gateway Entry Clones			
pENTR1 A/DTX38Δstop	DTX38	Entry clone for DTX38 cDNA without stop codon	This study
pENTR1 A/DTX39Δstop	DTX39	Entry clone for DTX39 cDNA without stop codon	This study
pENTR1 A/GTR1	GTR1	Entry clone for GTR1 cDNA with stop codon	This study
pENTR1 A/GTR3	GTR3	Entry clone for GTR3 cDNA with stop codon	This study
pENTR1 A/DTX38	DTX38	Entry clone for DTX38 cDNA with stop codon	This study
pENTR1 A/DTX39	DTX39	Entry clone for DTX39 cDNA with stop codon	This study
pENTR1 A/ProDTX39:DTX39	ProDTX39:DTX39	Entry clone for 2-kb upstream promoter and DTX39 coding region without a stop codon	This study
pENTR1 A/ProDTX39	ProDTX39	Entry clone for 2-kb upstream promoter of DTX39	This study
Others			
pGWB405/Pro35S:DTX38-GFP	Pro35S:DTX38-GFP	Vector for plant transient expression, analysis of DTX38-GFP protein localization	This study
pGWB405/Pro35S:DTX39-GFP	Pro35S:DTX39-GFP	Vector for plant transient expression, analysis of DTX39-GFP protein localization	This study
pGWB604/ProDTX39:DTX39-GFP	ProDTX39:DTX39-GFP	T-DNA vector for constitutive transformation, analysis of DTX39-GFP protein localization/accumulation	This study
pGWB633/ProDTX39:GUS	ProDTX39:GUS	T-DNA vector for constitutive transformation, analysis of DTX39 promoter activity	This study
pK11.1R/DTX38	DTX38 double guide RNA	T-DNA vector for constitutive transformation, produce DTX38 mutant for CRISPR-Cas9 system	This study
p415/GTR1	GTR1	Yeast expression	This study
p415/GTR3	GTR3	Yeast expression	This study
pYES2-DEST52 /DTX38	DTX38	Yeast expression	This study
pYES2-DEST52 /DTX39	DTX39	Yeast expression	This study
pAG416GAL/DTX38-GFP	DTX38-GFP	Yeast expression, analysis of DTX38-GFP protein localization	This study
pAG416GAL/DTX39-GFP	DTX39-GFP	Yeast expression, analysis of DTX39-GFP protein localization	This study
pDR196/DTX39-V5-6×His	DTX39	Yeast expression	This study

Supplementary Table 6. Primers used in this study.

name	sequence (5' > 3')
qRT-PCR	
RT-UBQ10_F	GAAGTGGAAGCTCCGACAC
RT-UBQ10_R	TTAGAAACCACCACGAAGACG
RT-DTX38_F	CGTTGGCTTTAATGCTGCTG
RT-DTX38_R	TGACGCAATCACGACAAGTG
RT-DTX39_F	TCGCTTACGCCGTCAACTTC
RT-DTX39_R	ATGCCCATAAAGCCCATGTC
Cloning	
pEN_GTR1_F	GGAACCAATTCAGTCGACATGAAGAGCAGAGTCATTCTTA
pEN_GTR1_R	GAAAGCTGGGTCTAGATTTCAGACAGAGTTCTTGCTCTT
pEN_GTR3_F	GGAACCAATTCAGTCGACATGGAGGTTGAGAAGACAGAG
pEN_GTR3_R	GGGTCTAGATATCTCGATTACACTGACACCTTATCAAACCTC
pEN_DTX38_F	GGAACCAATTCAGTCGACATGAATGGGTCAAATGAGAC
pEN_DTX38_R	AAGAAAGCTGGGTCTAGATTTACTTCATAACAAAATTACTAA
pEN_DTX38_stop_R	GGGTCTAGATATCTCGAATTCTGGAGAGGCTCTTTGTCTG
pEN_DTX39_F	GGAACCAATTCAGTCGACATGGAAGTGCCTAGTGAAAC
pEN_DTX39_R	AAGAAAGCTGGGTCTAGATCTAGTTTTGGAGAGGCTCC
pEN_DTX39_stop_R	CTGGGTCTAGATATCTCGAGTTTTGGAGAGGCTCCTTCTTGTCG
pEN_ProDTX39_F	GGAACCAATTCAGTCGACCAGTCTTCACTCATCAGACCGAAAG
pEN_ProDTX39_R	GGGTCTAGATATCTCGAAGATTGGGAAAAAATTACAAAG
CRISPR_dtx38_F	AGTCGAAGTAGTGATTGGACAAGCGTATGGTGCCACGTTTTAGAGCTAGAAATAGC
CRISPR_dtx38_R	ATTTCTAGCTCTAAAAACATGTCTTTTCTCGCCGTCACAATCTCTTAGTCGACTCTAC
pDR196_5_F	CCCGGGCTGCAGGAATTACAAGTTTGTACAAAAAAGCTGAAC
pDR196_hisV5_R	ACCGGGCCCCCCTCGATCAATGGTGATGGTGATGATGACC
yor1_kanmx4_F	GTAAAGCCGTTGCTATATACGAATATGCGTACGCTGCAGGTCGAC
yor1_kanmx4_R	AATCATGCAACAAATAATATAAATTAATCGATGAATTCGAGCTCG
prb1-hyg_F	AAAACAACTAAACCTAATTCTAACAAGCAAAGATGAAGTTAGAACGTACGCTGCAGGTCGAC
prb1-hyg_R	AAAGCAGCTGAAATTTTTCTAAATGAAGAATTAAATAATATTCAAATCGATGAATTCGAGCTCG
Genotyping	
GABI_100G09_F	TAGCTAACGTAATCACGAA
GABI_100G09_R	TTGTAGTTAGGTATGGGCAGTGCA
DTX39_muant_R	TCCAAGCTCATTACTTGTCCGTAC
DTX38_mutant_F	ATGGGTAGTGC GGTCGAGAC