

## Supplementary Tables

**Supplementary Table S1.** Genetic loci of *D. solani* strain IPO 2222 Tn5 mutants regulated in the presence of *S. dulcamara* tissues

No.	Mutant	Insertion name, Tn5 locus	Protein accession number, protein name	Transcriptional organization (single gene vs. operon)	Entry, KEGG pathway, UniProt-based protein function	Remarks	Homologs in different bacterial species
1	M69	<i>ds69</i> , A4U42_RS11770	WP_022632034, glycosyl transferase	operon, 12 genes: A4U42_RS11790, A4U42_RS11785, A4U42_RS11780, A4U42_RS11775, <b>A4U42_RS11770</b> , A4U42_RS11765, A4U42_RS11760, A4U42_RS11755, A4U42_RS11750, A4U42_RS11745, A4U42_RS11740, A4U42_RS11735	glycosyltransferase family 4 protein, capsular glucan synthase	in operon together with <i>ds271</i> and <i>ds943</i>	
2	M73	<i>ds73</i> , A4U42_RS15630	WP_022632758, mannosyl transferase	single gene	glycosyltransferase family 4 protein		
3	M93	<i>ds93</i> , A4U42_RS01565	WP_022634127, mycocerosate synthase	operon, 2 genes: <b>A4U42_RS01565</b> , A4U42_RS01560	SDR family NAD(P)-dependent oxidoreductase		
4	M106	<i>ds106</i> , A4U42_RS13890	WP_022632437 transcriptional regulator GcvA	single gene	regulation of transcription, LysR family transcriptional regulator, glycine cleavage system transcriptional activator		
5	M115	<i>ds115</i> , A4U42_RS16110	WP_022632856, non-ribosomal peptide synthase	operon, 8 genes: A4U42_RS16130, A4U42_RS16125, A4U42_RS16120, A4U42_RS16115, <b>A4U42_RS16110</b> , A4U42_RS16105, A4U42_RS16100, A4U42_RS16095	no KEGG pathway, non-ribosomal peptide synthase	in operon together with <i>ds255</i>	

6	M119	<i>ds119</i> , A4U42_RS01450	WP_022634107 FMN/FAD transporter	single gene	EmmdR/YeeO family multidrug/toxin efflux MATE transporter		
7	M241	<i>ds241</i> , <i>tgt</i> A4U42_RS14365	WP_022632529, tRNA guanosine transglycosylase Tgt	operon, 2 genes: <i>queA</i> , <i>tgt</i>	queueine tRNA- ribosyltransferase, tRNA guanosine transglycosylase Tgt		
8	M253	<i>ds253</i> , <i>wbeA</i> A4U42_RS06140	WP_022634991 WbeA	operon, 7 genes: <i>gmd</i> <b>A4U42_RS06140</b> A4U42_RS06135 A4U42_RS06130 A4U42_RS06125 A4U42_RS06115 A4U42_RS06110	entry not assigned,		
9	M255	<i>ds255</i> , A4U42_RS16105	WP_022632855, non-ribosomal peptide synthetase	operon, 8 genes: A4U42_RS16130, A4U42_RS16125, A4U42_RS16120, A4U42_RS16115, A4U42_RS16110, <b>A4U42_RS16105</b> , A4U42_RS16100, A4U42_RS16095	non-ribosomal peptide synthetase	in operon together with <i>ds115</i>	
10	M264	<i>ds264</i> , A4U42_RS11855	WP_022632050, hypothetical protein	operon, 3 genes: <b>A4U42_RS11855</b> , A4U42_RS11850, A4U42_RS11845	entry not assigned, contains endonuclease subunit and chromosome segregation ATPase subunit		
11	M271	<i>ds271</i> , A4U42_RS11740	WP_023637586, capsular biosynthesis protein	operon, 12 genes A4U42_RS11790, A4U42_RS11785, A4U42_RS11780, A4U42_RS11775, A4U42_RS11770, A4U42_RS11765, A4U42_RS11760, A4U42_RS11755, A4U42_RS11750, A4U42_RS11745,	polysaccharide biosynthesis protein VpsM, outer membrane beta-barrel protein	in operon together with <i>ds69</i> and <i>ds943</i>	

				<b>A4U42_RS11740,</b> A4U42_RS11735			
12	M273	<i>ds273, bglF</i> A4U42_RS00580	WP_022633945 PTS beta-glucoside transporter subunit IIABC	operon, 3 genes: <i>bglG,</i> <b><i>bglF,</i></b> <i>ascB</i>	beta-glucoside PTS system EIICBA component [EC:2.7.1.-]		
13	M277	<i>ds277,</i> A4U42_RS04070	WP_022634595, DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid	operon, 3 genes: <b>A4U42_RS04070,</b> A4U42_RS04065, A4U42_RS04060	membrane protein involved in D-alanine export, DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid		
14	M278	<i>ds278,</i> A4U42_RS02215	WP_022634251 glycosyltransferase	single gene	glycosyltransferase, cellulose synthase catalytic subunit (UDP- forming)		
15	M281	<i>ds281,</i> A4U42_RS17100	WP_022633056, predicted transcriptional regulator YheO	single gene	PAS domain-containing protein		
16	M321	<i>ds321,</i> A4U42_RS16640	WP_022632961, D-cysteine desulphydrase	operon, 2 genes: <b>A4U42_RS16640</b> A4U42_RS16645	L-cysteate sulfo-lyase [EC:4.4.1.25]		
17	M327	<i>ds327,</i> A4U42_RS19655	WP_022633559, ClbS/DfsB family four-helix bundle protein	single gene	ClbS/DfsB family four-helix bundle protein		
18	M328 and M880	<i>ds328,</i> A4U42_RS17270	WP_022633089, glucarate transporter	single gene	MFS transporter, ACS family, D- galactonate transporter		
19	M468	<i>ds468,</i> A4U42_RS17435	WP_022633124, conjugal transfer protein TraR	operon, 3 genes: A4U42_RS17445, A4U42_RS17440, <b>A4U42_RS17435</b>	TraR/DksA family transcriptional regulator		
20	M519	<i>ds519, nifN</i> A4U42_RS06315	WP_022635026, nitrogen fixation protein NifN	operon, 3 genes : <i>nifE</i> <b><i>nifN</i></b> A4U42_RS06310	nitrogenase molybdenum-iron protein NifN		
21	M521	<i>ds521,</i> A4U42_RS16075	WP_223849466, polyketide synthase	single gene	SDR family NAD(P)-dependent oxidoreductase		
22	M564	<i>ds564,</i> A4U42_RS04280	WP_022634635, nitrate reductase	single gene	nucleobase:cation symporter-1, NCS1 family		

23	M573	<i>ds573</i> , A4U42_RS11730	WP_022632027, undecaprenyl-phosphate glucose phosphotransferase	single gene	L-talarate/galactarate dehydratase		
24	M578	<i>ds578</i> , A4U42_RS17980	WP_023637770, peptide permease	operon, 4 genes: A4U42_RS17995, A4U42_RS17990, A4U42_RS17985, <b>A4U42_RS17980</b>	peptide/nickel transport system permease protein, ABC transporter permease		
25	M585	<i>ds585</i> , A4U42_RS07980	WP_022635320, phage tail protein	operon, 2 genes: <b>A4U42_RS07980</b> A4U42_RS07975	phage tail protein		
26	M596	<i>ds596</i> , <i>uvrY</i> ( <i>expA</i> , <i>gacA</i> ) A4U42_RS01590	WP_022634131, two-component system response regulator UvrY (GacA)	operon, 2 genes: <i>uvrY</i> , <i>uvrC</i>	two-component system, NarL family, invasion response regulator UvrY, two component system ExpA-ExpS in SRP bacteria		
27	M598 and M980	<i>ds598</i> , A4U42_RS08155	WP_022635352, malate permease	single gene	malate:Na <sup>+</sup> symporter, 2- hydroxycarboxylate transporter family protein		
28	M620 and M940	<i>ds620</i> , <i>dprA</i> A4U42_RS06665	WP_022635094, DNA-protecting protein DprA	single gene	DNA processing protein, DNA-protecting protein DprA		
29	M622	<i>ds622</i> , <i>prfC</i> A4U42_RS11580	WP_022631998, peptide chain release factor 3	single gene	peptide chain release factor 3		
30	M635	<i>ds635</i> , <i>menH</i> A4U42_RS14815	WP_023637673, 2-succinyl-6-hydroxy-2,4- cyclohexadiene-1- carboxylate synthase	operon, 6 genes: <i>menF</i> <i>menD</i> <b><i>menH</i></b> <i>menB</i> <i>menC</i> <i>menE</i>	2-succinyl-6-hydroxy-2,4- cyclohexadiene-1-carboxylate synthase [EC:4.2.99.20]		
31	M652	<i>ds652</i> , <i>sctR</i> A4U42_RS20675	WP_022633761, EscR/YscR/HrcR family type III secretion system export apparatus protein	operon, 11 genes: <i>sctW</i> <i>sctV</i> <i>sctD</i> <i>scN</i> <b><i>sctR</i></b> <i>sctS</i> <i>sctT</i>	type III secretion protein R, type III secretion system export apparatus subunit SctR		

				<i>sctU</i> A4U42_RS20670 A4U42_RS20665 A4U42_RS20660			
32	M702	<i>ds702</i> , A4U42_RS13765	WP_230469717, serine protease	single gene	subtilase-type serine protease [EC:3.4.21.-], autotransporter domain-containing protein		
33	M828	<i>ds828</i> , A4U42_RS16290	WP_022632893, nickel ABC transporter permease subunit NikC	operon, 4 genes: A4U42_RS16300, A4U42_RS16295, <b>A4U42_RS16290</b> , A4U42_RS16285	nickel transport system permease protein, ABC transporter permease subunit		
34	M854	<i>ds854</i> , A4U42_RS09805	WP_022631675, glutathione ABC transporter permease GsiC	operon, 5 genes: A4U42_RS09810, <b>A4U42_RS09805</b> , A4U42_RS09800, A4U42_RS09795, A4U42_RS09790	glutathione transport system permease protein		
35	M884	<i>ds884</i> , A4U42_RS00600	WP_022633948, peptidoglycan-binding protein	single gene	L,D-transpeptidase YcfS		
36	M890	<i>ds890</i> , A4U42_RS09520	WP_022631619, pseudouridine-5-phosphate glycosidase	operon, 2 genes: <b>A4U42_RS09520</b> A4U42_RS09525	pseudouridylate synthase [EC:4.2.1.70], pseudouridine-5'-phosphate glycosidase		
37	M937	<i>ds937</i> , <i>glpX</i> A4U42_RS07915	WP_022635307, fructose 1,6-bisphosphatase	operon, 3 genes: <i>glpK</i> <b><i>glpX</i></b> A4U42_RS07905	fructose-1,6-bisphosphatase II [EC:3.1.3.11], class II fructose-bisphosphatase		
38	M943	<i>ds943</i> , A4U42_RS11735	WP_023637585, undecaprenyl-phosphate glucose phosphotransferase	operon, 12 genes: A4U42_RS11790, A4U42_RS11785, A4U42_RS11780, A4U42_RS11775, A4U42_RS11770, A4U42_RS11765, A4U42_RS11760, A4U42_RS11755, A4U42_RS11750,	undecaprenyl-phosphate glucose phosphotransferase	in operon together with <i>ds271</i> and <i>ds69</i>	

				A4U42_RS11745, A4U42_RS11740, <b>A4U42_RS11735</b>			
39	M945	<i>ds945</i> , A4U42_RS12920	WP_022632248, ferredoxin	operon, 4 genes: A4U42_RS12930, A4U42_RS12925, <b>A4U42_RS12920</b> , A4U42_RS12915	ferredoxin, 2Fe-2S iron-sulfur cluster- binding protein		
40	M946	<i>ds946</i> , A4U42_RS12865	WP_022632237, aminotransferase	operon, 2 genes: <b>A4U42_RS12865</b> A4U42_RS12870	putrescine aminotransferase [EC:2.6.1.82], aminotransferase class III-fold pyridoxal phosphate-dependent enzyme		
41	M955	<i>ds955</i> , <i>fdhF</i> A4U42_RS16455	WP_022632925, formate dehydrogenase subunit alpha	operon, 2 genes: <i>fdhF</i> A4U42_RS16460	formate dehydrogenase (hydrogenase) [EC:1.17.98.4 1.17.98.-], formate dehydrogenase subunit alpha		
42	M1009	<i>ds1009</i> , A4U42_RS16195	WP_022632873, ABC transporter	single gene	ATP-binding cassette, subfamily F, member 3		

**Supplementary Table S2.** Results of BIOLOG phenotypic microarrays GEN III and EcoPlate for 8 mutants expressing no or reduced symptoms on *S. dulcamara* planta

GEN III	IPO2222	M241	M253	M264	M271	M277	M278	M281	M596
D-cellobiose	+	+	-	-	+	+	+	+	+
D-turanose	-	-	-	+	-	-	-	-	-
L-glutamic acid	+	-	-	+	-	+	+	+	+
D-glucuronic acid	+	+	-	+	-	+	+	+	+
pH 5	+	+	+	+	+	+	-	+	+
4% NaCl	-	-	-	-	-	+	-	-	+
8% NaCl	-	-	-	-	-	-	-	-	+
fusidic acid	-	+	-	-	-	+	-	-	+
D-serine	+	+	-	-	-	-	-	-	-
guanidine HCl	+	+	-	+	+	+	+	+	-
lithium chloride	+	+	+	+	-	+	-	+	+
sodium butyrate	-	+	-	-	-	+	-	-	+
EcoPlate	IPO2222	M241	M253	M264	M271	M277	M278	M281	M596
D-xylose	+	+	+	+	+	+	+	-	+
L-asparagine	+	+	+	+	+	+	+	-	+
D-mannitol	+	+	+	+	+	+	-	+	+
L-serine	+	+	+	+	-	+	+	+	+
D-malic acid	-	-	-	+	+	+	+	-	+

“+” – positive result (=change of medium color due to bacterial growth and metabolism)

“-” – negative result (=the lack of change of medium color = no bacterial growth/no bacterial metabolism)

**Supplementary Table S3.** List of PCR primers used in this study with amplification efficiencies in the applied setup

Target locus	Primer name <sup>A</sup>	Primer sequence	Amplicon length (bp)	E <sup>B</sup>	R <sup>2</sup>	Slope	Reference
A4U42_14370	7_M241_F	TATTTGATGGGGGTGGGTAA	150	102.1%	0.998	-3.272	This study
	7_M241_R	GTGTTTGGCGTTACGGATCT					
A4U42_06145	8_M253_F	AGCCGGACTCTATGGCACTA	146	97.5%	0.990	-3.384	This study
	8_M253_R	GAGCCTGTTTAATGGCTTCG					
A4U42_11860	10_V2_M264_F	AAGTGTGTTTGTGGGCATGA	121	100.5%	0.992	-3.311	This study
	10_V2_M264_R	GAGCGACTTCCATCGTCTCT					
A4U42_11745	11_M271_F	TAGGCCGCACAGAGGATATT	140	90.1%	0.997	-3.585	This study
	11_M271_R	CATAAAGCGGTAGCGAAAGC					
A4U42_04075	13_M277_F	GCGCAGAATATTGGCATTTT	127	74.3%	0.997	-4.146	This study
	13_M277_R	ACCACTGAAGCATGTTGTGC					
A4U42_02220	14_M278_F	CTGGGATCACGTTTTCGTTT	132	74.9%	0.996	-4.118	This study
	14_M278_R	TGCAATATAATCGGCATCCA					
A4U42_17105	15_M281_F	GTCGCGTCTCTGTGTCTCAA	147	90.6%	0.973	-3.568	This study
	15_M281_R	CTGATCGATACGCTGACGAA					
A4U42_01595	26_M596_F	CGGTGAAGATGCGGTAAGAT	108	93.8%	0.990	-3.479	This study



	26_M596_R	CGTACAATTTGCGTGTTGC					
A4U42_03695	V2_yhb_F	CAGCACATGGGTCAACAAAC	126	91.1%	0.997	-3.555	This study
	V2_yhb_R	ACATGTACGATTCCGCATCA					
A4U42_05475	lpxC_F	ATGAACAGGTCGCCAATCG	93	84.2%	0.999	-3.771	PMID: 32983224
	lpxC_R	AGATGATTACCGTGTGCTGAAC					

<sup>A</sup> designation of the source Tn mutant is included in the primer name for all genes except for the reference genes *lpxC* and *yhbN*

<sup>B</sup> primer pair efficiency