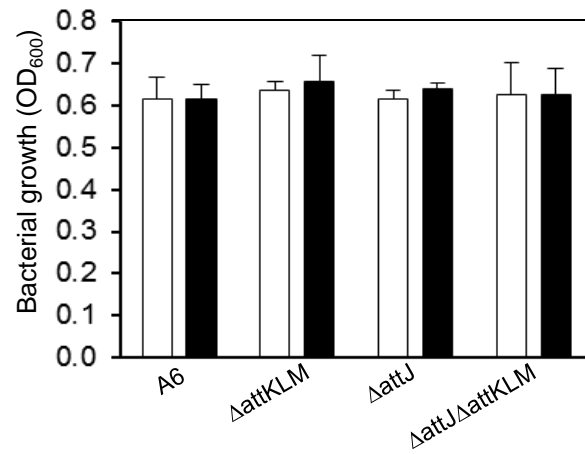


SUPPLEMENTARY INFORMATION (SI)

For

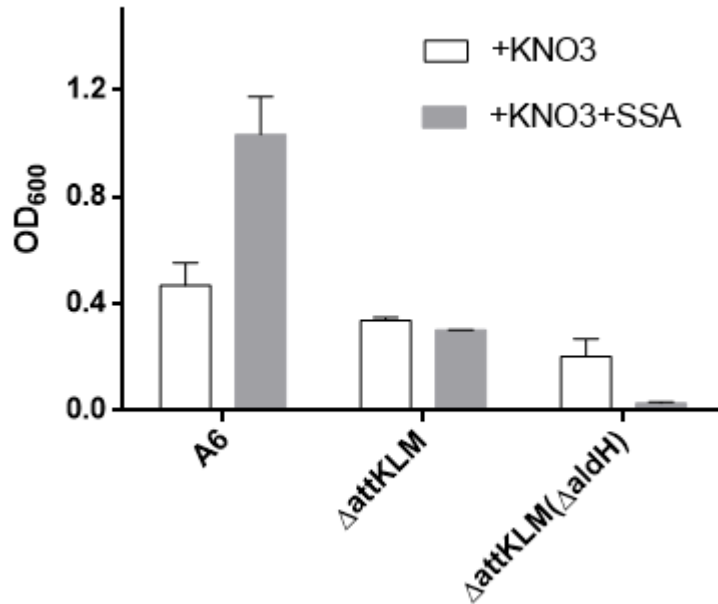
The manuscript of “Succinic Semialdehyde Promotes Pro-survival capability of *Agrobacterium tumefaciens* A6” by *Chao Wang et al.*

Fig. S1



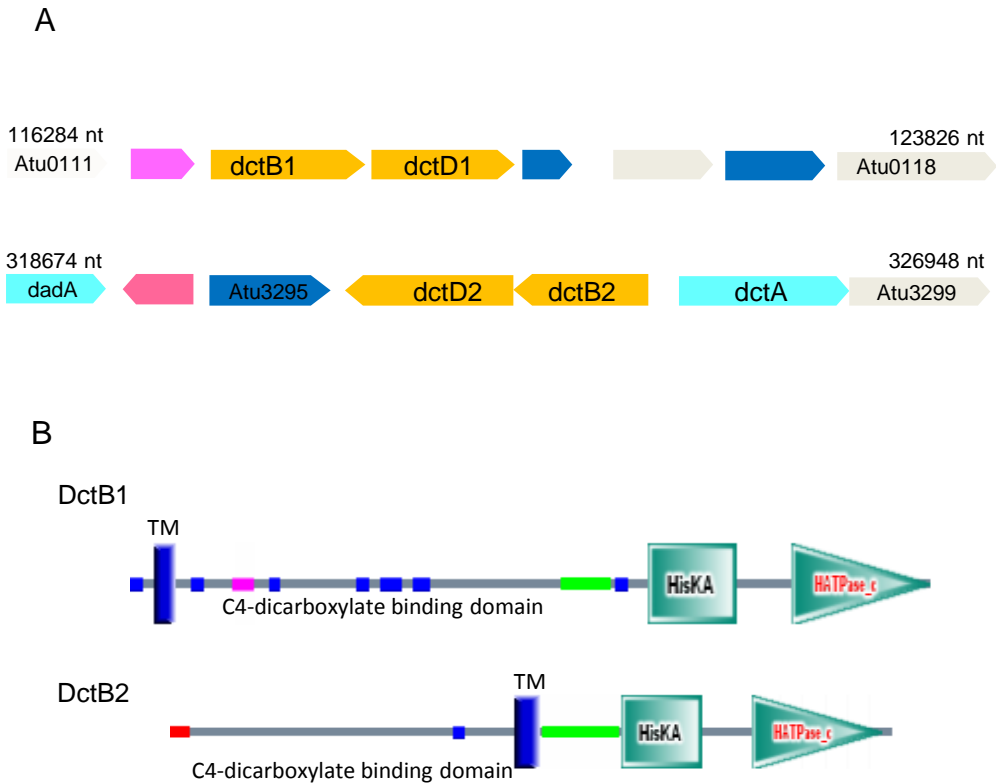
Supplementary Figure S1. Growth of *A. tumefaciens* A6 and related mutants using $(\text{NH}_4)_2\text{SO}_4$ as sole nitrogen source with (filled) and without (open) SSA.

Fig. S2



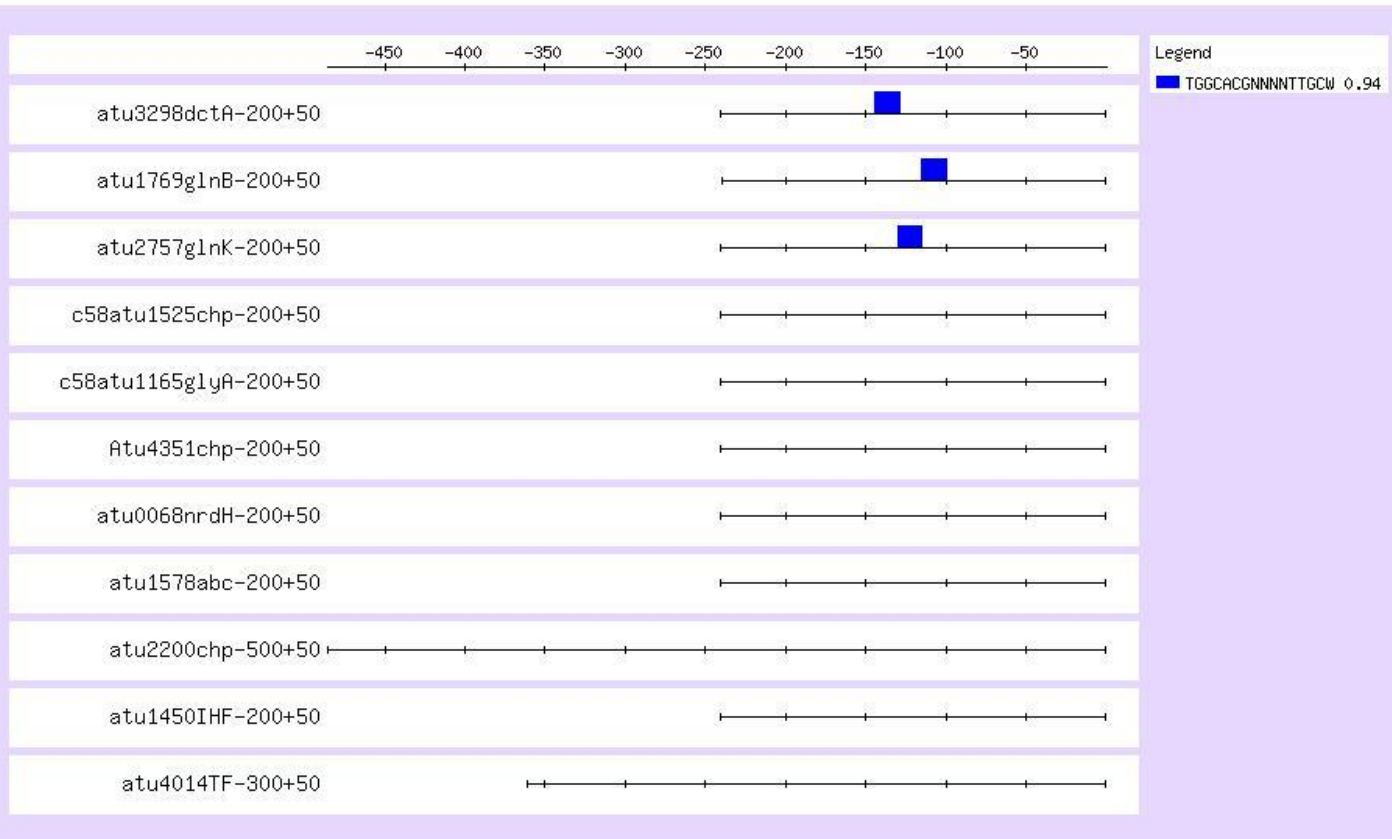
Supplementary Figure S2. Growth of *A. tumefaciens* A6 and related mutants using KNO₃ as sole nitrogen source with (filled) and without (open) SSA.

Fig. S3



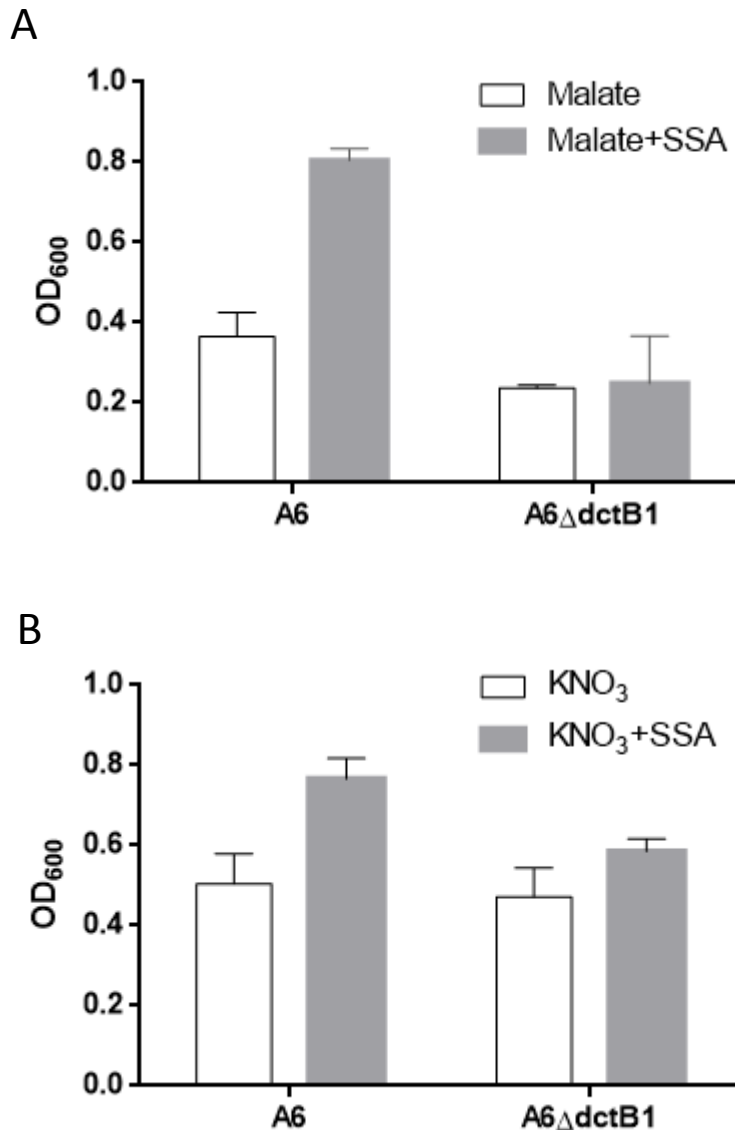
Supplementary Figure S3. Sequence analyses of two-component system DctB/D in *A. tumefaciens*. **(A)** Genetic localization of two copies of DctB/D. DctB: two component sensor kinase for C4-dicarboxylate transport; DctD: two component response regulator for C4-dicarboxylate transport, which is the activator of *rpoN*-dependent promoter. **(B)** Domain analyses of DctB ; the c4-dicarboxylate binding domain and the transmembrane domain are respectively illustrated.

Fig. S4



Supplementary Figure S4. Promoter analyses of genes upregulated by SSA and identification of rpoN-dependent promoter in *glnK*, *glnB* and *dctA*.

Fig. S5



Supplementary Figure S5. Growth of *A. tumefaciens* A6 and its *dctB1* mutant using (A) malate as sole carbon source and (B) KNO₃ as sole nitrogen source with (filled) and without (open) SSA.

Table S1. Bacterial strains and plasmids used in this study

Strain & plasmid	Relevant characteristics ^a	Sources or references
<i>A. tumefaciens</i>		
C58	Wild type nopaline strain of <i>A. tumefaciens</i>	S. Q. Pan
A6	Wild type octopine strain of <i>A. tumefaciens</i>	A. Kerr
A6(Δ <i>dctA</i>)	A6 carrying a in-frame deletion of <i>dctA</i>	This study
A6(Δ <i>dctB1</i>)	A6 carrying a in-frame deletion of <i>dctB1</i>	This study
Δ attJ	A6 with the <i>attJ</i> gene transcriptionally fused with Tn3HoHo1- <i>lacZ</i> , same as A6(<i>attJ::lacZ</i>), Ampr	(1)
Δ attKLM	A6 with the <i>attKLM</i> operon transcriptionally fused with Tn3HoHo1- <i>lacZ</i> , same as A6(<i>attKLM::lacZ</i>), Ampr	(2)
Δ attJ Δ attKLM	Δ attKLM with mutation of <i>attJ</i> by <i>Tn5</i> transposon	This study
Δ attKLM Δ aldH	Δ attKLM with in frame deletion of the <i>aldH</i> gene, same as A6(<i>attKLM::lacZ</i> , Δ <i>aldH</i>), Amp ^r	(3)
<i>E. coli</i>		
DH5 α	supE44 Δ lacU169(Φ 80lacZ Δ M15) hsdR17 λ . <i>pir</i> recA1 endA1 gyrA96 thi-1 relA1	Laboratory collection
S17-1	pro res- mod+ integrated copy of RP4, mob+	A. Kerr
Plasmids		
pK18mobsacB	Mobilization and counter selection vector, oriT (RP4) <i>lacZ</i> α , <i>sacB</i> , Suc ^r	(4)
pK18- Δ <i>dctB1</i>	pK18mobsacB containing part of <i>dctB1</i> and its flanking region for <i>dctB1</i> in-frame deletion, Kan ^r	This study
pK18- Δ <i>dctA</i>	pK18mobsacB containing part of <i>dctA</i> and its flanking region for <i>dctA</i> in-frame deletion, Kan ^r	This study
pLAFR3	IncP, broad host range cosmid vector, Tc ^r	(5)
pLA- <i>aldH</i>	pLAFR3 harbouring the encoding region of <i>aldH</i> , Tc ^r	Wang et al, (2006)

Strain & plasmid	Relevant characteristics ^a	Sources or references
pLA- <i>attK</i>	pLAFR3 harbouring the encoding region of <i>attK</i> , Tc ^r	Wang et al, (2006)
pLA- <i>attL</i>	pLAFR3 harbouring the encoding region of <i>attL</i> , Tc ^r	Wang et al, (2006)
pLA- <i>attM</i>	pLAFR3 harbouring the encoding region of <i>attM</i> , Tc ^r	Wang et al, (2006)

^aSuc^r, sucrose resistant; Kan^r, kanamycin resistant; Amp^r, ampicillin resistant; Tc^r, tetracycline resistant.

Reference

1. **Wang C, Yan C, Gao YG, Zhang LH.** 2015. D101 is critical for the function of AttJ, a repressor of quorum quenching system in *Agrobacterium tumefaciens*. *J Microbiol* **53**:623-632.
2. **Zhang HB, Wang C, Zhang LH.** 2004. The quorumone degradation system of *Agrobacterium tumefaciens* is regulated by starvation signal and stress alarmone (p)ppGpp. *Mol Microbiol* **52**:1389-1401.
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4. **Schafer A, Tauch A, Jager W, Kalinowski J, Thierbach G, Puhler A.** 1994. Small mobilizable multi-purpose cloning vectors derived from the *Escherichia coli* plasmids pK18 and pK19: selection of defined deletions in the chromosome of *Corynebacterium glutamicum*. *Gene* **145**:69-73.
5. **Staskawicz B, Dahlbeck D, Keen N, Napoli C.** 1987. Molecular characterization of cloned avirulence genes from race 0 and race 1 of *Pseudomonas syringae* pv. *glycinea*. *J Bacteriol* **169**:5789-5794.

Tab. S2 ORFs up-regulated by SSA (≥ 2 fold)

ORF ^b	Gene	fold ^a	Description
Amino acid biosynthesis/metabolism			
Atu0017	trpF	2.1	N-(5'-phosphoribosyl) anthranilate isomerase
Atu0029	ahcY	2.2	S-adenosylhomocysteine hydrolase
Atu0312	cysK	2.9	cysteine synthase
Atu0380	argB	2.5	acetylglutamate kinase
Atu0817	cysD	3.3	sulfate adenylate transferase, subunit 2
Atu1165	glyA	4.5	serine hydroxymethyltransferase
Atu1332	aroQ	2.4	3-dehydroquinate dehydratase
Atu1770	glnA	7.8	glutamine synthetase I
Atu2019	ilvC	2.6	ketol-acid reductoisomerase
Atu2196	aatA	2.3	aspartate aminotransferase A
Atu2264	leuA	2.1	2-isopropylmalate synthase
Atu2416	glnA	5.8	glutamine synthetase II
Atu2667	argG	2.1	argininosuccinate synthase
Atu2698	tyrA	2.6	chorismate mutase
Atu2709	leuC	2.1	3-isopropylmalate dehydratase, large subunit
Atu2791	leuB	2.0	3-isopropylmalate dehydrogenase
Atu3612	hisC	2.4	histidinol-phosphate aminotransferase
Atu4110	sdh	2.8	serine dehydrogenase
Atu4172	lysC	2.1	aspartate kinase, alpha and beta subunit
Purine, pyrimidine, nucleoside and nucleotide metabolism			
Atu0068	nrdH	3.2	glutaredoxin protein
Atu0069	nrdI	3.1	NrdI protein involved in ribonucleotide reduction
Atu0070	nrdE	2.9	ribonucleoside-diphosphate reductase 2 alpha chain
Atu0071	nrdF	3.4	ribonucleoside-diphosphate reductase 2 beta chain
Atu0132		2.3	2-deoxyribose-5-phosphate aldolase
Atu0135	upp	2.4	uracil phosphoribosyltransferase
Atu0314	dut	2.0	deoxyuridine 5'triphosphate nucleotidohydrolase
Atu1122	ndk	2.3	nucleoside diphosphate kinase
Atu1731	gpt	2.1	xanthine-guanine phosphoribosyltransferase
Atu1850	purL	2.1	phosphoribosylformylglycinamide synthetase II
Atu1926	adk	2.2	adenylate kinase
Atu2170	carA	2.6	carbamoylphosphate synthase small chain

Atu2447	purA	2.1	adenylosuccinate synthetase
Atu3604	hpt	2.2	hypoxanthine phosphoribosyltransferase

Fatty acid, cofactor and prosthetic group

Atu0066	frcK	2.1	pantothenate kinase
Atu0151	fabA	2.8	D-3-hydroxydecanoyl-(acyl carrier-protein) dehydratase
Atu0757	fabI	2.0	enoyl-(acyl-carrier-protein) reductase [NADH]
Atu1096	acpP	2.9	acyl carrier protein
Atu1169	ribC	2.3	riboflavin synthase alpha chain
Atu1171	ribH	2.1	riboflavin synthase beta chain
Atu1330	accC	2.4	acetyl-CoA carboxylase, biotin carboxylase
Atu1331	accB	2.0	acetyl-CoA carboxylase, biotin carboxyl carrier protein
Atu1383	fabZ	2.1	(3R)-Hydroxymyristoyl-[acyl carrier protein]- Dehydratase
Atu1454	cysG	2.7	siroheme synthase
Atu2613	hemA	2.2	5-aminolevulinate synthase
Atu2805		2.4	cobalamin synthesis related protein
Atu5122	fabG	2.2	3-oxoacyl-(acyl-carrier protein) reductase

Central intermediary metabolism

Atu1456		2.3	sulfite reductase [NADPH] hemoprotein beta-component
Atu1854	grlA	2.2	glutaredoxin-related protein
Atu2405	ureB	2.0	urease beta subunit
Atu2661	ppa	2.4	inorganic pyrophosphatase
Atu2751	fdxA	2.0	Ferredoxin
Atu5296		2.6	arylester hydrolase
Atu5297		2.1	Hydrolase

Energy metabolism

Atu0022	trxA	2.4	thioredoxin C-1
Atu0101	cycM	2.2	cytochrome c
Atu0404	pgi	2.1	glucose-6-phosphate isomerase
Atu0599	pgl	2.2	6-phosphogluconolactonase
Atu0713	atpI	2.0	ATP synthase, subunit I
Atu0714	atpA	2.2	ATP synthase A chain
Atu0715	atpC	2.1	ATP synthase C chain
Atu0717		3.1	ATP synthase B chain
Atu0767	coxB	2.2	cytochrome c oxidase subunit II

Atu0775	thrB	2.0	homoserine kinase
Atu1256		2.1	cytochrome P450 hydroxylase
Atu1268	nuoA	2.5	NADH ubiquinone oxidoreductase chain A
Atu1269	nuoB	2.2	NADH ubiquinone oxidoreductase chain B
Atu1270	nuoC	3.1	NADH ubiquinone oxidoreductase chain C
Atu1274	nuoE	2.1	NADH ubiquinone oxidoreductase chain E
Atu1275	nuoF	2.1	NADH ubiquinone oxidoreductase chain F
Atu1277	nuoH	2.3	NADH ubiquinone oxidoreductase I chain H
Atu1278	nuoI	2.4	NADH ubiquinone oxidoreductase chain I
Atu1279	nuoJ	2.4	NADH ubiquinone oxidoreductase chain J
Atu1281	nuoL	2.7	NADH ubiquinone oxidoreductase chain L
Atu1283	nuoN	2.3	NADH ubiquinone oxidoreductase chain N
Atu1392	cisY	2.1	citrate synthase
Atu1426	eno	2.2	enolase
Atu1429	pdhA	2.5	pyruvate dehydrogenase alpha subunit
Atu1430		2.5	pyruvate dehydrogenase beta subunit
Atu1458	mvrA	2.3	ferredoxin NADP+ reductase
Atu1463	gcvH	2.0	glycine cleavage system component H
Atu1613	rpiA	2.0	ribose 5-phosphate isomerase
Atu2237	fbcC	2.0	cytochrome c1
Atu2239	fbcF	2.1	ubiquinol-cytochrome C reductase iron-sulfur subunit
Atu2621	atpC	2.3	ATP synthase epsilon chain
Atu2623	atpG	2.2	ATP synthase gamma chain
Atu2624	atpA	2.5	ATP synthase alpha chain
Atu2625	atpH	2.5	ATP Synthase delta chain
Atu2637	sucD	2.2	succinyl-CoA synthetase alpha chain
Atu2638	sucC	2.5	succinyl-CoA synthetase beta chain
Atu2645	sdhC	2.3	succinate dehydrogenase cytochrome B-556 subunit
Atu2685	acnA	2.1	aconitate hydratase
Atu3737	gapA	2.2	Glyceraldehyde 3-Phosphate Dehydrogenase
Atu3778	galU	3.0	UTP-glucose-1-phosphate uridylyltransferase
Atu4405	napE	5.2	periplasmic nitrate reductase protein NapE
Atu4406	napF	2.2	periplasmic nitrate reductase protein NapF
Atu4407	napD	3.2	periplasmic nitrate reductase protein NapD
Atu4408	napA	3.0	periplasmic nitrate reductase protein NapA
Atu4409	napB	4.1	periplasmic nitrate reductase small subunit
Atu4410	napC	2.1	periplasmic nitrate reductase small subunit

Atu4464	talB	2.8	transaldolase
Atu4734	acnB	2.1	aconitate hydratase 2

Transport & binding protein

Atu0030	ptsH	2.2	phosphocarrier protein HPr
Atu0031		2.4	PTS system, IIA component
Atu0063	frcB	2.3	ABC transporter, substrate binding protein [sugar]
Atu0064	frcC	2.1	ABC transporter, membrane spanning protein [sugar]
Atu0065	frcA	2.6	ABC transporter, nucleotide binding/ATPase protein [sugar]
Atu0188		2.0	ABC transporter, membrane spanning protein [peptide]
Atu0249		2.2	ABC transporter, substrate binding protein [sugar]
Atu0330	ptsN	2.2	nitrogen regulatory IIA protein
Atu0528	mscL	2.0	large conductance mechanosensitive channel proteins
Atu0820		2.4	ABC transporter, substrate binding protein [sulfate]
Atu0895		3.5	ABC transporter, substrate binding protein
Atu1021		2.0	outer membrane protein
Atu1577		3.1	ABC transporter, substrate binding protein [amino acid]
Atu1578		3.7	ABC transporter, membrane spanning protein [amino acid]
Atu1579		3.0	ABC transporter, membrane spanning protein [amino acid]
Atu1580		4.3	ABC transporter, nucleotide binding/ATPase protein [amino acid]
Atu1879		2.3	ABC transporter, substrate binding protein [amino acid]
Atu2276	braC	2.2	ABC transporter, substrate binding protein [amino acid]
Atu2281		2.0	ABC transporter, substrate binding protein [proline/glycine betaine]
Atu2347	gguA	2.1	ABC transporter, nucleotide binding/ATPase protein [sugar]
Atu2348	chvE	3.1	sugar binding protein
Atu2365		2.7	ABC transporter, substrate binding protein [amino acid]
Atu2422		2.6	ABC transporter, substrate binding protein [amino acid]
Atu2492	mtbA	2.2	MFS permease [sugar]
Atu2561	modA	2.3	ABC transporter, substrate binding protein [molybdate]
Atu2758	amtB	4.8	ammonium transporter
Atu2771	bfr	3.3	bacterioferritin
Atu3170		2.0	ABC transporter, nucleotide binding/ATPase protein
Atu3298	dctA	5.8	C4-dicarboxylate transport protein
Atu3357		3.1	ABC transporter, substrate binding protein [amino acid]
Atu3368		2.7	periplasmic mannitol-binding protein

Atu3396		2.2	ABC transporter, substrate binding protein [iron]
Atu3504		3.5	ABC transporter, substrate binding protein [sulfate]
Atu4033		2.6	ABC transporter, substrate binding protein [sugar]
Atu4431		3.6	ABC transporter, substrate binding protein [oligopeptide]
Atu4447		2.0	ABC transporter, substrate binding protein [sorbitol]
Atu4448		2.9	ABC transporter, membrane spanning protein
Atu4449		2.1	ABC transporter, membrane spanning protein [sorbitol/mannitol]
Atu4488		2.0	ABC transporter, membrane spanning protein
Atu4525		2.3	ABC transporter, substrate binding protein [oligopeptide]
Atu4600		2.3	ABC transporter, nucleotide binding/ATPase protein

DNA/chromosome metabolism

Atu0338	ihfB	2.1	integration host factor, beta subunit
Atu1262		2.6	DNA-binding protein
Atu1359	dksA	2.1	dnaK deletion suppressor protein
Atu1512	ssb	2.9	single-strand DNA binding protein

Transcription

Atu0331		3.3	sigma-54 modulation protein
Atu0385	rnpA	2.1	ribonuclease P protein component
Atu1029	rnpO	2.6	DNA-directed RNA polymerase omega subunit
Atu1339	rne	2.5	ribonuclease E
Atu1923	rpoA	2.0	DNA-directed RNA polymerase alpha subunit
Atu1956	rpoB	2.6	DNA-directed RNA polymerase beta chain
Atu1961	nusG	2.2	transcription antitermination protein NusG
Atu2182	greA	2.5	transcription elongation facto
Atu2700	rimM	2.3	16S rRNA processing protein
Atu2833	rho	2.6	transcription termination factor Rho

Translation

Atu0084	rpsO	2.2	30S ribosomal protein S15
Atu0112	rpmF	2.1	50S ribosomal protein L32
Atu0254	infC	3.3	translation initiation factor 3
Atu0255	rpmI	2.6	50S ribosomal protein L35
Atu0256	rplT	2.4	50S ribosomal protein L20
Atu0258	pheS	2.2	phenylalanyl-tRNA synthetase, alpha-subunit

Atu0323	rpsT	2.3	30S ribosomal protein S20
Atu0534	infA	3.1	translation initiation factor IF-1
Atu0676	hisS	2.1	histidyl-tRNA synthetase
Atu0689	rluB	2.3	ribosomal large subunit pseudouridine synthase B
Atu0786		2.1	peptidase, family M16
Atu0977	dop	3.0	serine protease DO-like protease
Atu1258	clpP	2.0	ATP-dependent Clp protease, proteolytic subunit
Atu1259	clpX	2.0	ATP-dependent Clp protease, ATP-binding subunit
Atu1261	lon	2.6	ATP-dependent protease LA
Atu1288	proS	2.1	prolyl-tRNA synthetase
Atu1299	rpmG	2.5	50S ribosomal protein L33
Atu1318	gatC	3.9	glutamyl-tRNA-Gln-amidotransferase chain C
Atu1375	tsf	2.1	translation elongation factor Ts
Atu1377	rff	2.7	ribosome recycling factor
Atu1680	ppiB	2.2	peptidyl prolyl cis-trans isomerase
Atu1686	ppiD	2.2	peptidyl-prolyl cis-trans isomerase D
Atu1924	rpsK	2.5	30S ribosomal protein S11
Atu1925	rpsM	2.7	30S ribosomal protein S13
Atu1928	rplO	2.6	50S ribosomal protein L15
Atu1930	rplR	2.5	50S ribosomal protein L18
Atu1931	rplF	2.7	50S ribosomal protein L6
Atu1932	rpsH	2.5	30S ribosomal protein S8
Atu1933	rpsN	2.3	30S ribosomal protein S14
Atu1934	rplE	2.0	50S ribosomal protein L5
Atu1935	rplX	3.5	50S ribosomal protein L24
Atu1936	rplN	3.7	50S ribosomal protein L14
Atu1937	rpsQ	2.4	30S ribosomal protein S17
Atu1938	rplL	2.3	50S ribosomal protein L29
Atu1939	rplP	2.3	50S ribosomal protein L16
Atu1941	rplV	2.5	50S ribosomal protein L22
Atu1942	rpsS	2.2	30S ribosomal protein S19
Atu1944	rplW	2.7	50S ribosomal protein L23
Atu1946	rplC	2.3	50S ribosomal protein L3
Atu1947	rpsJ	2.2	30S ribosomal protein S10
Atu1948	tuf	2.4	elongation factor TU
Atu1949	fusA	2.3	translation elongation factor G
Atu1950	rpsG	2.0	30S ribosomal protein S7

Atu1958	rplJ	2.2	50S ribosomal Protein L10
Atu1959	rplA	2.2	50S ribosomal protein L1
Atu1966	tuf	2.2	elongation factor TU
Atu2044	hflC	2.4	HFLC protein
Atu2227	rplY	2.2	50S ribosomal protein L25
Atu2270	clpP	2.5	ATP-dependent Clp protease, proteolytic subunit
Atu2699	rpsP	2.0	30S ribosomal protein S16
Atu2784	rpmA	2.2	50S ribosomal protein L27
Atu2785	rplU	2.1	50S ribosomal protein L21
Atu3519	ppiD	3.1	peptidyl-prolyl cis-trans isomerase
Atu3617	rpmB	2.1	50S ribosomal protein L28
Atu3637	rpsU	2.1	30S ribosomal protein S21
Atu3743		2.0	50S ribosomal protein L31
Atu4064	rpsU	2.1	30S ribosomal protein S21

Regulator and two-component signaling

Atu0062	frcR	2.4	transcriptional regulator, ROK family
Atu0465		2.5	transcriptional regulator
Atu0484		2.0	two component response regulator
Atu0524	luxR	2.2	transcriptional regulator, LuxR family
Atu0573		2.0	transcriptional regulator
Atu0978	ragA	2.3	two component response regulator
Atu1450	hfq	3.5	host factor I
Atu1769	glnB	8.4	nitrogen regulatory protein PII
Atu1985		2.4	two component response regulator
Atu2020		2.3	transcriptional regulator, TetR family
Atu2278	noIR	2.8	transcriptional regulator, ArsR family
Atu2434	ctrA	2.4	two component response regulator
Atu2757	glnK	9.6	nitrogen regulatory protein PII
Atu2765		2.5	transcriptional regulator, CarD family
Atu3572		2.4	transcriptional regulator, HTH family
Atu3883		3.3	chemotaxis response regulator
Atu4014		3.7	transcriptional regulator

Cell envelope

Atu0126		2.4	membrane lipoprotein
Atu0224	ctpA	2.4	components of type IV pilus, pilin subunit

Atu1131	ropB	2.6	outer membrane protein
Atu1381	omp1	2.2	group 1 outer membrane protein precursor
Atu1500	rlpA	2.0	rare lipoprotein A
Atu1789		2.4	lipoprotein
Atu2100		2.1	penicillin binding protein 2
Atu3708		2.2	outer surface protein
Atu4061	exoX	2.4	exopolysaccharide production repressor protein
Atu4489		2.2	outer membrane lipoprotein
Atu4610		2.6	sugar nucleotide epimerase/dehydratase
Atu4612	wbnE	2.4	glycosyltransferase
Atu4613		2.1	glycosyltransferase
Atu4617	rffB	2.2	dTDP-D-glucose-4,6-dehydratase
Atu4618	rfbC	2.7	dTDP-rhamnose-3,5-epimerase

Cell process

Atu0006	secB	3.6	protein-export protein SECB
Atu0542	fla	2.3	flagellin
Atu0553	fliE	2.4	flagellar hook-basal body complex protein
Atu0562	fliN	3.4	flagellar motor switch protein FliN
Atu0574	flgE	2.6	flagellar hook protein
Atu0575	flgK	2.1	hook associated protein I homolog
Atu0577	flaF	2.7	FLAF protein
Atu0578	flbT	2.3	FLBT protein
Atu0682	groEL	3.0	60 KDA chaperonin
Atu0683	groES	2.6	10 KD chaperonin (protein CPN10)
Atu0779	prx	2.1	peroxiredoxin
Atu0876	sodF	2.5	superoxide dismutase
Atu1563	yajC	2.5	preprotein translocase protein
Atu1664	tig	2.0	trigger factor
Atu1706	tatA	2.2	SEC-independent protein translocase protein
Atu1775		2.1	polyketide biosynthesis associated protein
Atu2200	cspA	3.5	cold shock protein
Atu2550	acrA	2.0	acriflavin resistance protein A
Atu2617	cheW	2.0	chemotaxis protein
Atu3121	cspA	2.4	cold shock protein
Atu3247	minE	2.7	cell division topological specificity factor
Atu3249	minC	2.0	bacterial septum site-determining protein

Atu3520	secA	2.7	preprotein translocase SECA subunit
Atu3732	tlyC	2.1	hemolysin
Atu4214	cspA	2.5	cold shock protein

Virulence

Atu2553	chvH	2.2	elongation factor P
Atu4074	exoC	2.3	phosphoglucomutase
Atu5129	attC	2.1	ABC transporter, substrate binding protein [mannopine]
Atu5136	attJ	3.7	transcription regulator, lclR family
Atu5137	attK	9.4	NAD-dependent succinate aldehyde dehydrogenases
Atu5138	attL	13.9	alcohol dehydrogenase
Atu5139	attM	21.1	Zn-dependent hydrolases

a. Fold change represents the average ratio of mRNA transcript levels in SSA-treated to untreated *A. tumefaciens*.

b. Open reading frame (ORF) is as annotated in <http://cancer.lbi.ic.unicamp.br/agroC58/>.

Table S3. Downregulated genes with SSA treatment (≤ -1.5 fold)

ORF ^b	Gene	Fold ^a	Description
Fatty acid metabolism			
Atu1974	cfa	-1.7	cyclopropane-fatty-acyl-phospholipid synthase
Atu1417	fad	-1.5	enoyl-CoA hydratase
Central metabolism			
Atu1535	FixQ	-2.0	cytochrome c oxidase, FixQ chain
Atu1654		-1.8	nitroreductase
Transport & binding protein			
Atu5346		-1.5	ABC transporter, membrane spanning protein [oligopeptide]
Atu1398		-1.5	ABC transporter, membrane spanning protein [amino acid]
Atu5523		-1.6	ABC transporter, membrane spanning protein [amino acid]
Atu3149		-1.5	ABC transporter, membrane spanning protein [sugar]
Atu3187	ugpE	-1.7	ABC transporter, membrane spanning protein [glycerol-3-phosphate]
Atu1736		-1.5	manganese transport protein
Atu2390		-1.5	ABC transporter, membrane spanning protein
Atu4785	afuB	-1.5	ABC transporter, membrane spanning protein [iron]
DNA metabolism			
Atu0840		-1.8	ATP-dependent DNA ligase
Regulator			
Atu4644		-1.5	transcriptional regulator, AraC family
Cell process			
Atu3887	ibpA	-1.6	small heat shock protein
Atu6071	attM	-1.8	Zn-dependent hydrolases
Hypothetical protein			
Atu0117		-1.5	hypothetical protein
Atu0448		-1.5	hypothetical protein
Atu0743		-1.6	hypothetical protein
Atu0868		-1.5	hypothetical protein
Atu0968		-1.5	hypothetical protein
Atu1591		-1.5	hypothetical protein
Atu1886		-1.5	hypothetical protein
Atu2570		-1.5	hypothetical protein
Atu3373		-1.9	hypothetical protein
Atu4016		-1.6	hypothetical protein
Atu4302		-1.5	hypothetical protein
Atu4308		-1.5	hypothetical protein
Atu4353		-1.5	hypothetical protein
Atu4506		-1.7	hypothetical protein
Atu5009		-1.5	hypothetical protein
Atu6137		-1.5	hypothetical protein

a. Fold change represents the average ratio of mRNA transcript levels in SSA-treated strain C58 to untreated strain C58.

b. Open reading frame (ORF) is as annotated in <http://cancer.lbi.ic.unicamp.br/agroC58/>.