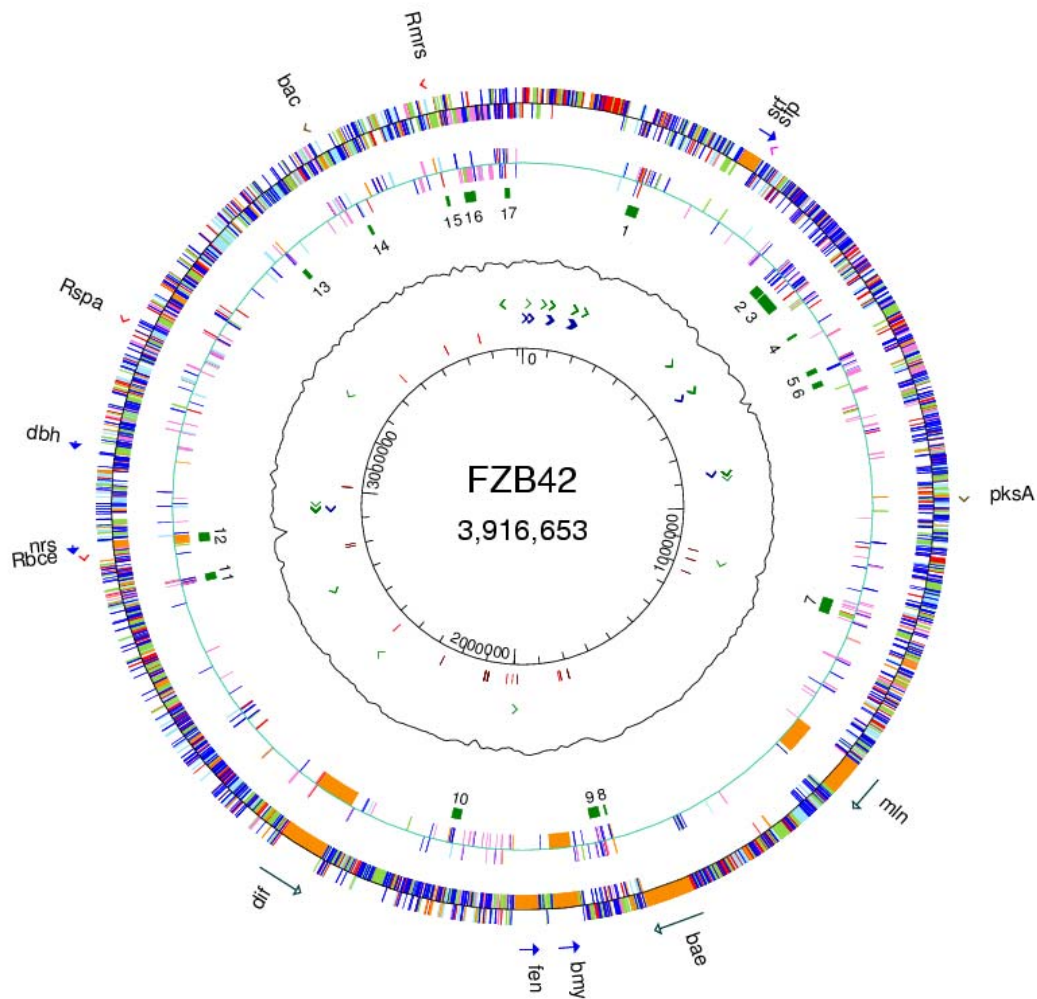
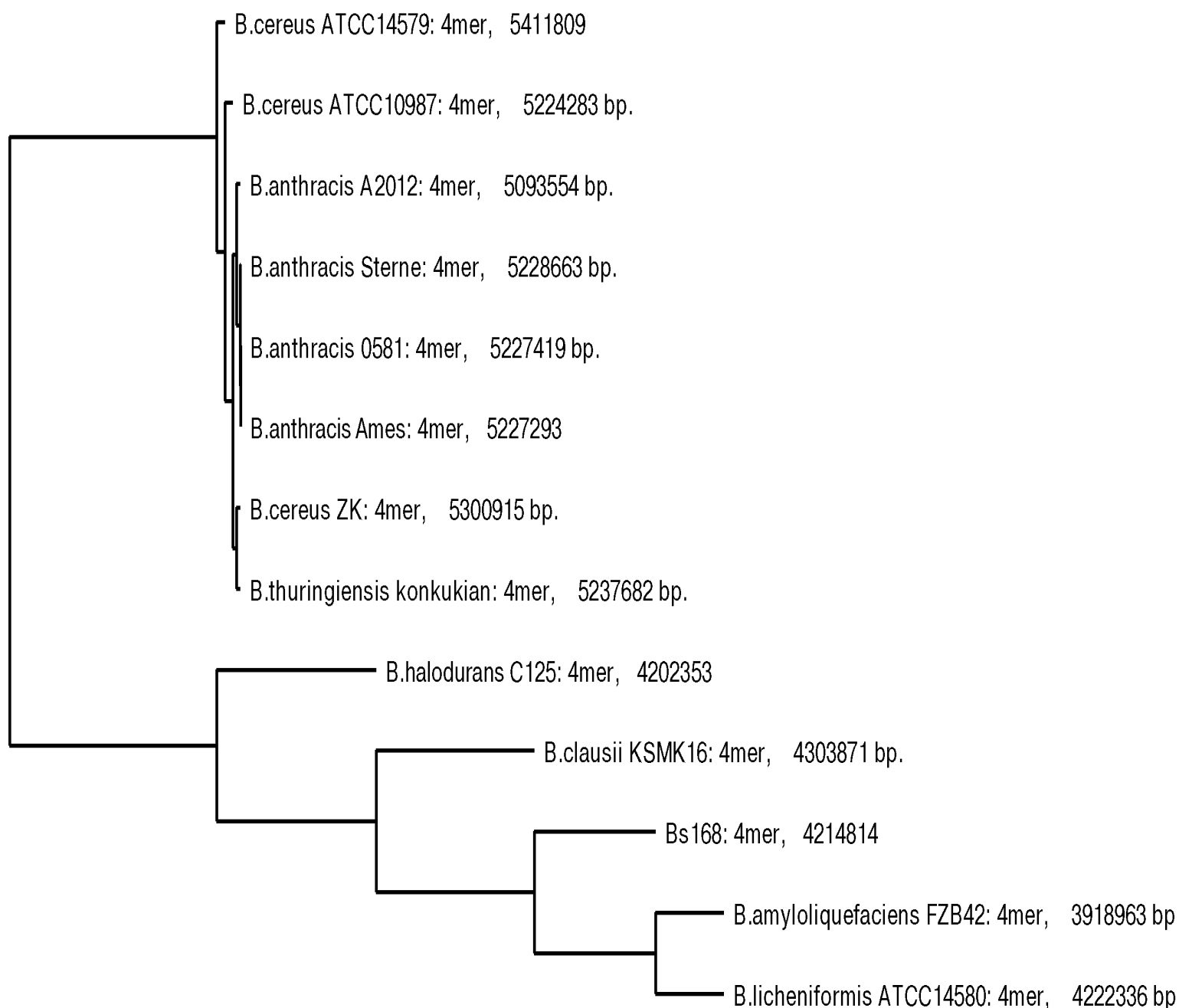
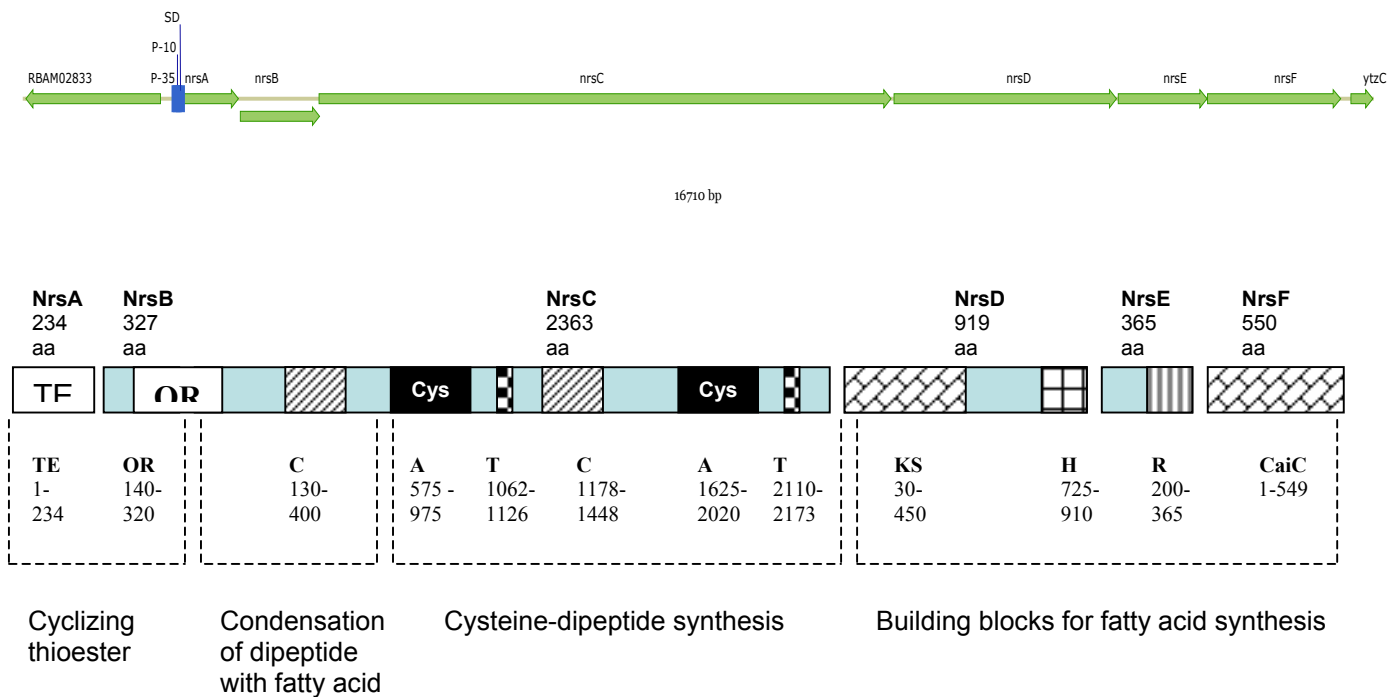




Supplementary Figure 1. The genome of *B. amyloliquefaciens* FZB42. The likely origin of replication was defined by similarities to the corresponding regions in *B. subtilis* and *B. licheniformis*. The first nucleotide pair of the *B. amyloliquefaciens* genome was defined congruent with *B. subtilis* as the A:T nucleotide pair located 412 bps upstream from *dnaA*. Outmost circle: Genes and gene clusters involved in synthesis and export (detoxification) of secondary metabolites: *srf*, surfactin; *sfp*, phospho-pantetheinyl-transferase; *pksA*, regulator polyketide synthesis; *mln*, macrolactin; *bae*, bacillaene, *bmy*, bacillomycin D; *fen*, fengycin; *dif*, difficidin; *Rbce*, bacitracin export; *nrs*, hybrid polyketide/cysteine containing peptide; *dbh*, bacillibactin; *Rspa*, subtilin immunity; *bac*, bacilysin; *Rmrs*, mersacidin immunity. 1st circle: all genes in color code according to their functions: cell envelope and cellular processes, green; information pathways, orange; intermediary metabolism, pink; other functions, red; unknown, black. 2nd circle: Genes not conserved in *B. subtilis* including four giant gene clusters involved in synthesis of secondary metabolites (orange); 3rd circle: the numbered 17 DNA islands (green), 4th circle: GC content profile, 5th circle: rRNAs (green), 6th circle: tRNAs (cyan), 7th circle: prophages (black), transposons, and IS elements (red), 8th circle: scale (bp).



Supplementary Figure 2. Phylogenetic relationship of the *B. amyloliquefaciens* FZB42 genome to other *Bacillus* genomes. Phylogenetic tree was constructed by UPGMA algorithm basing on the matrix of distances D:4mer_n0 between non-normalized tetranucleotide usage patterns calculated for complete genomes. (The algorithms of D-values calculation has been published recently: <http://www.biomedcentral.com/1471-2105/5/90>).



Supplementary Figure 3: The *nrs* gene cluster of FZB42

NrsA, TE: nonintegrated thioesterase II, similar SubT (*B. subtilis*)

NrsB, OR: mcbC like oxydoreductase domain of NRPS predicted to modify polypeptides by cyclizing a thioester to form a ring, FMN dependent „oxidation“ domain

NrsC, NRPS, C(130) pfam 00668 condensation reaction to form peptide bonds in non-ribosomal peptide synthesis

A(575) adenylation, AMP binding, Cys activating, similar SubA and BacA Cys adenylation domains

T(1062) thiolation, PCP, PP-binding pfam 0550

C(1178) pfam 00668 condensation reaction to form peptide bonds in non-ribosomal peptide synthesis

A(1625) adenylation, AMP binding, Cys activating, similar SubA and BacA Cys adenylation domains

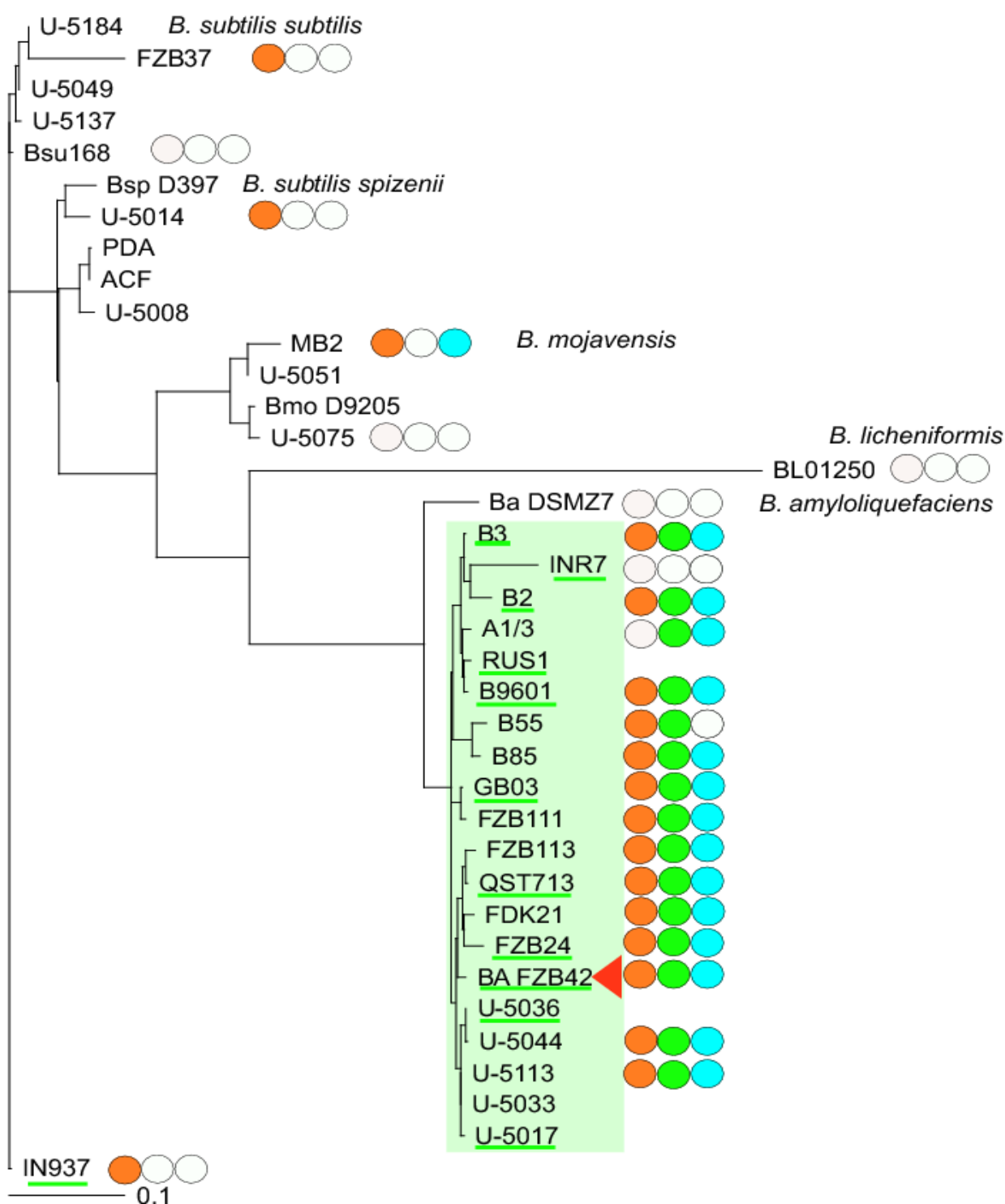
T(2110) thiolation, PCP, PP-binding pfam 0550

NrsD, KS(30) ketosynthase, β -ketoacyl carrier protein (ACP) synthase, responsible for elongation steps in fatty acid synthesis (elongation by Claisen condensatin of malonyl acyl carrier protein (ACP) with acyl ACP)

H(725) gloB, Zn dependent hydrolase, similar hydroxyacylglutathione hydrolase Cl. tetani (31%)

NrsE, R (200) C-terminal part of NrsE resembles regulatory ArsR like protein

NrsF, CaiC, (long chain) acyl CoA synthase, probably involved in fatty acid synthesis.



Supplementary Figure 4. Phylogenetic tree based on partial *cheA* nucleotide sequences. The scale bar indicates 0.1 nucleotide substitutions per nucleotide position. FZB42 (labeled by filled arrowhead) belongs to an ecomorph of plant-associated *B. amyloliquefaciens* strains. Strains with commercial importance are underlined: IN937 and INR7 (J. Kloepper, Auburn AL), FZB24 (Abitep GmbH, Germany and Taegro® Earth Biosciences Inc., USA), GB03 (Kodiak®, Gustafson Biologicals, Plano TX, USA), QST713 (Serenade®, Agraquest Inc., Davis CA, USA), RUS1 (Baksib F®, Siberia, Russia), U-5036 and U-5017 (UCM, Ukrainian Collection of Microorganisms, Kyiv, Ukraine), B9601-Y6 (Yunnan Agricultural University, China), and strains B2 and B3 (Nanjing Agricultural University, China). Polyketide production is indicated by colored filled circles; bacillaene, orange; difficidin, green; macrolactin, cyan; Circles without color indicate that no production of the respective antibiotic was detected. A phylogenetic tree based on partial *gyrA* nucleotide sequences yielded a similar dendrogram (not shown).

Content

Supplementary Table 1: DNA islands and deletions in FZB42. DNA islands were identified by deviating GC and OU patterns.....page 02

Supplementary Table 2. Signal transduction two component systems.....page 04

Supplementary Table 3. Sigma and anti-sigma factors.....page06

Supplementary Table 4. Transport systems in *Bacillus amyloliquefaciens* FZB42.....page08

Supplementary Table 5. Genes probably involved in plant bacterium interactions.....page23

Supplementary Table 6. Secretion proteins with Tat (RR_SP), Sip/SipV, SPase I and SPase II or without known signal peptides.....page28

Supplementary Table 7. Competence genes.....page45

Supplementary Table 8. Regulatory mutants and mutants used to demonstrate production of bacillibactin, bacilysin and macrolactin in FZB42.....page47

Supplementary Table 1. DNA islands and deletions in FZB42. DNA islands were identified by deviating GC and OU patterns.

DNA islands confirmed by OUV and deviation of GC content

No	from	to	size	RBAM	DR	OU	phage	tRNA	remark
01	207129 gmsS	228161 csgA	20132 212	191 212	+	+	Prophage 1	-	RR/HK, detoxification (export antimicrobial peptides), KDPG reductase, RR/HK, ABC transporter; substitution of prophage 1 (deletion 1: 31522 bp)
02	502777 ydcK	521213 cspC	18436 503	485 503	+	+	Prophage 2	Leu	ester cyclase, transporter, MarR regulator (2), NAD dependent dehydrogenase, NADP quinone reductase, TeiR, regulator, oxido reductase (3), fatty acid desaturase, substitution of prophage 2 (deletion 3: 57856 bp)
03	524801 ykeR	560664 ydeR	35863 547	508 547	+	+	Prophage 3	-	Rhodanase, aspartate racemase, PadR regulator, Mannose-6-phosphate isomerase, dihydrodipicolinate synthase, Fe-S-cluster redox enzyme, pyrimidine kinase, sugar phosphatase, arsenite efflux pump, Na ⁺ /H ⁺ antiporter, GnrR regulator, PaB regulator, methyl transferase, RR/HK, substitution of prophage 3 (deletion 4: 30805)
04	622192 groEL	626239 guR	4047 614	613 614	+	+	-	-	Hypothetical proteins
05	698876 yefA	708318 yeeF	8442 689	682 689	+	+	-	-	Type I restriction modification (HsdM, methylase, restrictase)
06	726898 yefO	736787 yml	9889 722	712 722	+	+	-	-	Detoxification: ABC multiring transporter, nitro reductase
07	1164638 yjcJ	1193383 yJB	28745 1206	1178 1206	+	+	Prophage 4	Val	sugar transporter, galR, ganA, galT, galE, galK, ptsI/BC, ptsI/A, P-β-gal, deoR regulator, phosphohexomutase, substitution of prophage 4 (deletion 5: 30805)
08	1793935 glnA	1796733 xynP	2798 1754	1750 1754	+	+	phI105	-	phage integrase, gluconolactonase
09(17)	1808007 pps	1827932 lexA	19925 1786	1761 1786	+	+	Prophage 5	-	homing endonuclease, nuclease inhibitor, dehydrogenase, protein acetyltransferase, chitin binding, transporter, regulator, substitution of prophage 5 (deletion 6:24681)
10(18)	2078498 yocU	2095572 yokA	17074 2015	2005 2015	+	+	SP6C2	-	Replication terminator yodN, phage proteins but lacking major SP6C2, RR/HK, site specific recombinase YokA, , partial substitution of SP6C2 (deletion 8:134339)
11(19)	2791263 ywdH	2804346 tyrS	13083 2759	2741 2759	+	+	+	-	Chemotaxis motB, formiate dehydrogenase, PBSX sigma, flavohemo protein, protease, phage, cation transporter, regulator, aa permease
12(20)	2868866 yfrA	2885172 yqQA	16306 2833	2866 2833	+	+	-	-	Non-ribosomal peptide synthesis:NRPS, PKS, thioesterase, acyl CoA synthetase, permease
13(22)	3453000 ywqL	3460914 ywqJ	7914 3435	3427 3435	+	+	-	-	transposase COG2801, transposase Imo828, hypothetical proteins
14	3606934 rocG	3611924 spSL	4990 3610	3605 3610	-	+	-	-	RR/HK, ABC transport
15	3767647 yxdJ	3772893 fba	5246 fba	mrs	-	+	Imo828	-	Detoxification: mersacidin export and regulation, mrsK, mrsR, mrsF, mrsG, mrsE
16 (23)	3804179 ahpF	3824538 yycP	19359 3834	3814 3834	-	+	-	-	xanthine dehydrogenase, carbon monoxide dehydrogenase, MobA-related protein
17(24)	3882866 yyaT	3891718 yyeL	8852 3899	3891 3899	-	+	-	-	Regulator (LysR), short chain dehydrogenase, protein kinase

Deletions occurring in the FZB42 genome in comparison to *B. subtilis* 168. In some cases DNA islands or small insertions partially substitute the deletions.

Deletion	From	To (BS)	Size (BS)	From	To (BAM)	Size (BAM)	Rearrangement	Insertion	Function (BS)
D01	198829	231336	31507	207129	228161	21032		island 01 (6)	Prophage 1 (glnS...csgA)
D02	277309	281695	4386	258428	263883	5255	ydfM...Q, rtpA	RBAM00245 and 00247	YcbB...ycbP uncharacterised transport
D03	528339	587288	58949	503554	561410	57856		island 02 (7)	Prophage 2
D04	649781	666812	17031	622647	627217	4570		island 03 (8ab)	Prophage 3
D05	1251842	1282647	30805	1154253	1194500	40247		island 06 (12)	YjcA Prophage 4
D06	1892604	1917465	24861	1805625	1829032	23407		island 08 (16)	XylB prophage5 yncF
D07	2027010	2070955	43945	2005338	2006922	1584		RBAM01907...RBAM01909	Prophage 6
D08	2151287	2285626	134339	2079893	2095742	15849		island 09 (17)	PhageSP1C2
D09	2647874	2701917	54043	2521031	2525910	4879	sigK	RBAM02464/02466/02467	Skin element
D10	2706907	2773120	66213	2530861	2545735	14874	yjaC, yjaR, yrdA, manAPR, yjdI, yjbF1	RBAM02477...02480, 02484, 02486	yqeF, spoIVB...spollic,yrkR YrkN...prophage7...levRDEF
D11	3302067	3304627	2560	3042510	3048822	6312	yjkK, dltE	RBAM02992...02997	GsacC...yrtJ GuaC,paIBA,yuIM
D12	3445270	3448651	3381	3188685	3200762	12077	ytnJ, ytmO...I, ytlI	RBAM03155...03158	YvaC...yvaF, multidrug efflux
D13	3721598	3723359	1761	3450564	3450722	158			YwqONM(K)
D14	3834768	3841317	6549	3560740	3560921	181			Lantibiotics:Subtilisin gene cluster: sboAB, albaBCDEF
D15	4034625	4038487	3862	3739282	3743639	4357		RBAM03753...03753	Unknown proteins: YxxED, yxiDCB
D16	4103919	4117974	14055	3801051	3802073	1022		RBAM03810	YxaHGF,yxnA,yxaDCBA,grt
D17	4120077	4127053	6976	3804179	3807467	3288	ydgF	RBAM03814	RKPZ
D18	4129065	4133463	4398	3809392	3823164	13772		island 13(2)	Variable region for integration of RMI: yyDCB

Supplementary Table 2. Signal transduction two component systems

No.	Gene	From	To	Function	Note	Homologous Genes	Identity	Strain
1	RBAM00197	210976	211996	sensor IM-HK	IM-HK	BceR	43%	BSU
	RBAM00196	210296	210977	response regulator		BceS	26%	BSU
2	RBAM00207	221869	222997	Sensor histidine kinase		NP348870	28%	CAC
	RBAM00208	223004	223646	response regulator		NP348816	56%	CAC
3	ycbA	256238	257477	sensor histidine kinase ycbA		ycbA	67%	BSU
	ycbB	257481	258426	response regulator ycbB		ycbB	75%	BSU
	rapJ	280720	281841	RR aspartate phosphatase J	Rap family	rapJ	71%	BSU
4	ydkK	399847	401275	sensor histidine kinase ydkK		ydkK	71%	BSU
	RBAM00430	462135	463268	RR aspartate phosphatase	Rap family	rapH	43%	BSU
	rapC	401430	402681	RR aspartate phosphatase C	Rap family	rapC	82%	BSU
	ykJJ	399174	399855	response regulator ykJJ		ykJJ	89%	BSU
	phrC	402568	402681	Inhibitor of rapC	Rap family	phrC	71%	BSU
5	dcfS	473927	475547	C4-dicarboxylate sensor HK		dcfS	85%	BSU
	dcfR	475524	476193	C4-dicarboxylate RR		dcfR	76%	BSU
6	RBAM00545	558806	559490	response regulator		EAO53033	86%	BTU
	RBAM00546	559489	560560	sensor histidine kinase		EAO053032	64%	BTU
7	ydfI	570006	570639	response regulator		ydfI	82%	BSU
	ydfH	568796	570011	sensor histidine kinase		ydfH	61%	BSU
8	cltT	772497	773175	response regulator cltT		cltT	72%	BSU
	cltS	770896	772498	histidine kinase cltS		cltS	60%	BSU
9	yhcY	938538	939678	sensor histidine kinase yhcY		yhcY	70%	BSU
	yhcZ	939680	940322	response regulator yhcZ		yhcZ	74%	BSU
	rapA	1217119	1218249	RR aspartate phosphatase A	Rap family	rapA	83%	BSU
	phrA	1218239	1218373	Inhibitor of rapA	Rap family	phrA	68%	BSU
10	cheB	1628059	1629124	Chemotaxis RR-glutamate methyltransferase		cheB	75%	BSU
	cheA	1629138	1631148	sensor HK, Chemotaxis protein cheA		cheA	84%	BSU
11	yvrG1	1866835	1868332	sensor kinase yvrG		EAT23926	46%	CPY
	yvrH1	1868335	1869138	response regulator yvrH		EAT23927	55%	CPY
	RBAM0210	2082746	2083882	RR aspartate phosphatase	Rap family	rapA	49%	BSU
12	RBAM02014	2087794	2088372	response regulator		AAU24295	75%	BLI
	RBAM02015	2088365	2089438	histidine kinase		AAU24296	76%	BLI
13	resE	2221192	2222973	sensor histidine kinase		resE	84%	BSU
	resD	2222970	2223692	response regulator		resD	94%	BSU
14	yrkQ	2526372	2527670	sensor histidine kinase		yrkQ	95%	BSU
	yrkP	2527657	2528352	response regulator		yrkP	90%	BSU
15	lysS	2720358	2722139	sensor histidine kinase		lysS	79%	BSU

Supplementary Tables

No	Gene	From	To	Function	Note	Homologous Genes	Identity	Strain
15	lytT	2719646	2720380	response regulator		lytT	80%	BSU
16	phoR	2739951	2741690	Pho regulon HK		phoR	68%	BSU
17	phoP	2741683	2742402	Pho regulon RR		phoP	84%	BSU
	bceS	2860839	2861843	Sensor IM-HK bceS		bceS	76%	BSU
18	bceR	2861836	2862531	Response regulator bceR		bceR	79%	BSU
19	yufL	2978391	2979990	sensor histidine kinase		yufL	79%	BSU
	yufM	2979985	2980690	response regulator		yufM	89%	BSU
20	comp	2993285	2995585	histidine kinase		comp	54%	BSU
	comA	2992560	2993204	response regulator		comA	80%	BSU
21	cssR	3125793	3126468	response regulator		cssR	79%	BSU
	cssS	3126467	3127820	sensor histidine kinase		cssS	765	BSU
22	yvqC	3134530	3135162	response regulator		yvqC	87%	BSU
	yvqE	3135140	3136222	sensor histidine kinase		yvqE	75%	BSU
23	yvrG	3146338	3148080	sensor histidine kinase		yvrG	70%	BSU
	yvrH	3148077	3148796	response regulator		yvrH	81%	BSU
24	RBAM03131	3163318	3163963	response regulator		NP978180	76%	BCE
	RBAM03132	3163962	3165072	sensor histidine kinase		NP978181	50%	BCE
25	spaK	3208488	3209891	subtilin IM-HK spaK		AA891593	54%	BSU
	spaR	3209882	3210544	subtilin RR spaR		AA891594	80%	BSU
26	RBAM03294	3317774	3318835	histidine kinase (IM-HK)		AAPO8928	39%	BCE
	RBAM03295	3318832	3319509	response regulator		AAPO8927	56%	BCE
27	rapD	3473348	3474412	RR aspartate phosphatase		rapD	74%	BSU
	rapB	3498853	3497763	RR aspartate phosphatase B		rapB	74%	BSU
28	rapF	3564414	3565559	RR aspartate phosphatase F		rapF	78%	BSU
	phrF	3565543	3565662	Inhibitor of rapF		phrF	74%	BSU
29	RBAM03606	3608103	3608801	response regulator		YP085861	51%	BCE
	RBAM03605	3607166	3608101	sensor histidine kinase		YP085862	58%	BCE
30	yxdK	3765985	3766935	IM-HK yxdK		yxdK	97%	BSU
	yxdJ	3766959	3767648	response regulator yxdJ		yxdJ	88%	BSU
31	mrsK2	3767798	3769237	sensor histidine kinase		CAB60253	98%	Bsp
	mrsR2	3769234	3769956	response-regulator		CAB60254	99%	Bsp
32	yocG	3791238	3791837	Putative response regulators		yocG	79%	BSU
	yocF	3791834	3792970	sensor histidine kinase		yocF	75%	BSU
33	RBAM03832	3823009	3822011	RR aspartate phosphatase X		YP_080123	48%	BLI
	yycF	3849397	3850107	response regulator		yycF	91%	BSU
34	yycG	3847555	3849390	sensor histidine kinase		yycG	88%	BSU

❖ Abbreviation: BLI, *B. licheniformis*; BSU, *B. subtilis*; Bsp, *Bacillus sp.*; BTU, *B. thuringiensis*; CAC, *Clostridium acetobutylicum*; CPY, *Clostridium phytofermentans*

Supplementary Table 3. Sigma and anti-sigma factors.

<i>No.</i>	<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Product</i>	<i>Note</i>	<i>Function</i>
<i>1</i>	sigH	117336	117990	RNA polymerase sigma-30 factor sigH		Information pathways; RNA synthesis; Initiation
<i>2</i>	sigW	199909	200470	RNA polymerase ECF-type sigma factor sigW	ECF	Information pathways; RNA synthesis; Initiation
	ybbM	200486	201110	Predicted transmembrane transcriptional regulator (anti-sigma W factor) ybbM		Information pathways; RNA synthesis; Initiation
	rsbR	494973	495792	Positive regulator of sigma-B activity rsbR		Other functions; Adaptation to atypical conditions
	rsbS	495799	496162	Negative regulator of sigma-B activity (antagonist of RsbT) rsbS		Other functions; Adaptation to atypical conditions
	rsbT	496167	496566	Serine/threonine-protein kinase rsbT (Switch protein/serine kinase) (Anti-sigma-B factor rsbT)		Other functions; Adaptation to atypical conditions
	rsbU	496580	497585	Sigma factor sigB regulation protein (Phosphoserine phosphatase) rsbU		Other functions; Adaptation to atypical conditions
	rsbV	497651	497978	Anti-anti-sigma factor (antagonist of RsbW) rsbV		Other functions; Adaptation to atypical conditions
	rsbW	497977	498457	Serine-protein kinase rsbW (Anti-sigma-B factor)(Sigma-B negative effector) rsbW		Other functions; Adaptation to atypical conditions
<i>3</i>	sigB	498425	499211	RNA polymerase sigma-B factor (Sigma-37) (General stress protein 84) (GSP84) sigB		Information pathways; RNA synthesis; Initiation
	rsbX	499213	499813	sigma-B activity indirect negative regulator rsbX		Other functions; Adaptation to atypical conditions
	yrbM	639934	640794	Putative anti-sigV factor yrbM		Information pathways; RNA synthesis; Regulation
<i>4</i>	sigV	640794	641291	RNA polymerase ECF (extracytoplasmic function)-type sigma factor sigV	ECF	Information pathways; RNA synthesis; Initiation
<i>5</i>	RBAM00641	655674	656205	Putative sigma factor RBAM00641	ECF	Information pathways; RNA synthesis; Initiation
	RBAM00642	656189	657626	Hypothetical protein RBAM00642		Unknown; No similarity
	yhdK	956006	956296	putative anti-sigma M factor yhdK		Information pathways; RNA synthesis; Regulation
	yhdL	956284	957357	putative anti-sigma M factor yhdL		Information pathways; RNA synthesis; Regulation
<i>6</i>	sigM	957350	957841	RNA polymerase ECF (extracytoplasmic function)-type sigma factor sigM	ECF	Information pathways; RNA synthesis; Initiation
<i>7</i>	sigI	1285554	1286298	RNA polymerase sigma factor sigI		Information pathways; RNA synthesis; Initiation
<i>8</i>	ylaC	1462008	1462527	Putative RNA polymerase sigma-70 factor ylaC	ECF	Information pathways; RNA synthesis; Initiation
<i>9</i>	sigE	1520786	1521503	RNA polymerase sporulation-specific sigma-29 factor sigE		Information pathways; RNA synthesis; Initiation
<i>10</i>	sigG	1521646	1522426	RNA polymerase sporulation-specific sigma factor sigG		Information pathways; RNA synthesis; Initiation
<i>11</i>	sigD	1632815	1633577	RNA polymerase sigma-28 factor sigD		Information pathways; RNA synthesis; Initiation
	rsiX	2219378	2220481	Sigma-X negative effector rsiX		Information pathways; RNA synthesis; Regulation
<i>12</i>	sigX	2220417	2221001	RNA polymerase sigma factor sigX	ECF	Information pathways; RNA synthesis; Initiation
<i>13</i>	sigF	2247703	2248470	RNA polymerase sporulation-specific sigma factor sigF		Information pathways; RNA synthesis; Initiation
	spoilAB	2248482	2248922	Anti-sigma F factor spoilAB		Cell envelope and cellular processes; Sporulation
	spoilAA	2248919	2249272	Anti-sigma F factor antagonist spoilAA		Cell envelope and cellular processes; Sporulation
<i>14</i>	rpoD	2470948	2472069	RNA polymerase major sigma-43 factor (sigma-A) rpoD		Information pathways; RNA synthesis; Initiation

Supplementary Tables

No	Gene	From	To	Product	Note	Function
15	sigK	2523058	2523778	RNA polymerase sporulation-specific sigma factor K		Information pathways; RNA synthesis; Initiation
16	sigL	3268056	3269369	RNA polymerase sigma-54 factor sigL		Information pathways; RNA synthesis; Initiation
	figM	3373572	3373638	Negative regulator of flagellin synthesis (Anti-sigma-D factor) figM		Cell envelope and cellular processes; Mobility and chemotaxis

Supplementary Table 4. Transport systems in *Bacillus amyloliquefaciens* FZB42

No.	Gene	From	To	Product	Substrate	Transport System	Family	TC No.	Note
AA1	ybxG	219867	221050	Putative proline-specific permease ybxG	amino acid		2.A.3.1.X		
AA2	ybeC	229443	231078	Hypothetical protein ybeC	amino acid		2.A.3.6.X		
AA3	gltP	248191	249441	Proton/glutamate symport protein gltP	glutamate		2.A.23.1.1		
AA4	ybgF	250919	252322	Putative histidine permease ybgF	histidine		2.A.3.1.X		
AA5	ybgH	253499	254935	Putative sodium/proton-dependent alanine transporter	amino acid		2.A.25.X.X		
AA6	ycgH	309013	310341	Putative Amino acid transporter ycgH	aromatic amino acid		2.A.3.1.X		
AA7	ygoO	321032	322337	Sodium/proline symporter ygoO	amino acid		2.A.21.2.X		
AA8	yveA	599498	601060	Aspartate-proton symporter yveA	amino acid		2.A.3.6.X		
AA9	opuE	688275	689753	Proline transporter opuE	proline		2.A.21.2.1		
AA10	yfnA	746364	747749	Putative metabolite transporter yfnA	cationic amino acid		2.A.3.3.X		
AA11	yhcl	918414	919803	Putative sodium-dicarboxylate symporter yhcl	glutamate		2.A.23.1.X		
AA12	yhdG	953096	954497	Putative amino acid transporter yhdG	cationic amino acid		2.A.3.3.X		
AA13	yhaG	1003365	1003883	Hypothetical protein yhaG	tryptophan		9.A.15.1.1		
AA14	gltT	1023791	1025080	Proton/sodium-glutamate symport protein gltT	glutamate		2.A.23.1.2		
AA15	yHjB	1046432	1047901	Putative metabolite permease yHjB	amino acid		2.A.21.2.X		
AA16	ykbA	1232399	1233715	Putative amino acid permease ykbA	amino acid		2.A.3.3.X		
AA17	alsT	1850139	1851555	Amino acid carrier protein alsT	alanine		2.A.25.1.X		
AA18	yodF	2052689	2054177	Proline permease homolog yodF	amino acid		2.A.21.2.X		
AA19	braB	2782202	2783540	Branched-chain amino acid transport system carrier protein braB	branched-chain amino acid		2.A.26.1.1		
AA20	RBAM02758	2804047	2804776	Putative amino acid permease RBAM02758	unknown		2.A.78.X.X		unique
AA21	opuD	2843073	2844606	Glycine betaine transporter opuD	Glycine betaine		2.A.15.1.1		
AA22	yfnA	2891426	2892829	Putative amino acid permease yfnA	amino acid		2.A.3.1.X		
AA23	yvsH	3156158	3157570	Conserved hypothetical protein yvsH	arginine-ornithine		2.A.3.2.X		
AA24	yvbW	3250396	3251736	Putative amino acid permease yvbW	amino acid		2.A.3.1.X		
AA25	RBAM03574	3575456	3576836	Putative amino acid transporter RBAM03574	amino acid		2.A.3.X.X		unique
AA26	rocC	3600696	3602114	Amino acid permease rocC	amino acid		2.A.3.1.X		

No	Gene	From	To	Product	Substrate	Transport	Family	TC No	Note
AA27	hutM	3751326	3752742	Histidine permease hutM	histidine		2.A.3.1.X		
AA28	ygjF	3805596	3806942	Putative amino acid permease ygjF	amino acid		2.A.3.1.X		
AA29	rocE	3830506	3831906	Amino acid permease rocE	basic amino acid		2.A.3.1.X		
ABC1	msmE	2846094	2847369	Multiple sugar-binding protein msmE	sugar	amyC(M)/amyD(M)/ msmE(B)	3.A.1.X.X		
	amyD	2847368	2848280	Sugar transport protein amyD			3.A.1.X.X		
	amyC	2848279	2849098	Maltose transport protein amyC			3.A.1.X.X		
ABC2	appD	1113562	1114546	Oligopeptide transport ATP-binding protein appD	oligopeptide	appD(A)/appF(A)/app appB(M)/appA(B)	3.A.1.5.X		
	appF	1114545	1115532	Oligopeptide transport ATP-binding protein appF			3.A.1.5.X		
	appA	1115612	1117238	Oligopeptide-binding protein appA precursor			3.A.1.5.X		
	appB	1117307	1118255	Oligopeptide transport system permease protein appB			3.A.1.5.X		
	appC	1118279	1119191	Oligopeptide transport system permease protein appC			3.A.1.5.X		
ABC3	araQ	2704613	2705455	L-arabinose transport system permease protein araQ	sugar	araP(M)/araQ(M)/araN(B)	3.A.1.2.X		
	araP	2705459	2706400	L-arabinose transport system permease protein araP			3.A.1.2.X		
	araN	2706442	2707737	Probable arabinose-binding protein precursor araN			3.A.1.2.X		
ABC4	bceB	2858044	2859984	Bacitracin export permease protein bceB	drug efflux	bceA(A)/bceB(M)	3.A.1		unique
	bceA	2859981	2860733	Bacitracin export ATP-binding protein bceA			3.A.1		unique
ABC5	cydD	3698340	3700070	ABC membrane transporter (ATP-binding protein) cydD	unknown	cydC(AM)/cydD(AM)	3.A.1.X.X		
	cydC	3700067	3701770	ABC membrane transporter (ATP-binding protein) cydC			3.A.1.X.X		
ABC6	dctB	472794	473846	Putative C4-dicarboxylate binding protein dctB	dicarboxylate receptor	dctB(B)	3.A.1.X.X		
ABC7	dppE	1245715	1247332	Dipeptide-binding protein dppE precursor	dipeptide	dppD(A)/dppB(M)/dpp C(M)/dppE(B)	3.A.1.5.2		
	dppC	1243737	1244682	Dipeptide transport system permease protein dppC			3.A.1.5.2		
	dppD	1244690	1245716	Dipeptide transport ATP-binding protein dppD			3.A.1.5.2		
	dppB	1242805	1243729	Dipeptide transport system permease protein dppB			3.A.1.5.2		
ABC8	expZ	573775	575403	ABC transporter, ATPase component expZ	unknown	ecsA(A)/ecsB(M)/exp Z(A)	3.A.1.X.X		
	ecsA	1006147	1006888	ABC-type transporter ATP-binding protein ecsA			3.A.1.X.X		
		1006883	1008107	Hypothetical protein ecsB	unknown		3.A.1.X.X		
ABC9	feuC	186279	187301	Iron-uptake system permease protein feuC	iron	feuB(M)/feuC(M)/feuA (B)	3.A.1.14.X		

<i>No</i>	<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Product</i>	<i>Substrate</i>	<i>Transport</i>	<i>Family TC</i>	<i>No</i>	<i>Note</i>
ABC10	feuB	187291	188298	Iron-uptake system permease protein feuB	iron		3.A.1.14.X		
	feuA	188318	189274	Iron-binding protein feuA	iron		3.A.1.14.X		
ABC11	fhuG	3152767	3153777	Ferrichrome ABC transporter (permease) fhuG	ferrichrome	fhuC(A)/fhuB(M)/fhuG(M)/fhuD(B)	3.A.1.14.3		
	fhuB	3153777	3154844	Ferrichrome ABC transporter (permease) fhuB			3.A.1.14.3		
ABC11	fhuC	3151945	3152748	Ferrichrome ABC transporter (ATP-binding protein) fhuC			3.A.1.14.3		
	fhuD	3155062	3155998	Ferrichrome ABC transporter (ferrichrome binding protein)			3.A.1.14.3		
	ftsX	3357538	3358437	Cell-division protein ftsX	cell division	ftsE(A)/ftsX(M)	3.A.1.X.X		
	ftsE	3358421	3359107	Cell-division ATP-binding protein ftsE			3.A.1.X.X		
ABC12	glnQ	2574222	2574948	Glutamine ABC transporter (ATP-binding protein) glnQ	polar amino acid	glnQ(A)/glnP(M)/glnM(M)/glnH(B)	3.A.1.3.2		
	glnH	2574971	2575796	Glutamine ABC transporter (glutamine-binding protein) glnH			3.A.1.3.2		
	glnM	2575855	2576503	Glutamine ABC transporter (integral membrane protein) glnM			3.A.1.3.2		
	glnP	2576524	2577178	Glutamine ABC transporter (integral membrane protein) glnP			3.A.1.3.2		
ABC13	mrsF	3770199	3771108	Putative ABC transporter, ATP-binding protein mrsF	drug efflux	mrsF(A)/mrsG(M)/mrsE(M)	3.A.1		unique
	mrsG	3771107	3771863	Putative ABC-transporter integral membrane protein mrsG	drug efflux		3.A.1		unique
ABC14	mrsE	3771882	3772614	Putative ABC-transporter integral membrane protein mrsE	drug efflux		3.A.1		unique
	msmX	3706999	3708099	Multiple sugar-binding transport ATP-binding protein msmX	sugar	msmX(A)	3.A.1.1.X		
ABC15	oppD	1126472	1126546	Oligopeptide ABC transporter (ATP-binding protein) oppD	oligopeptide	oppD(A)/oppF(A)/oppB(M)/oppC(M)/oppA(B)	3.A.1.5.1		
	oppF	1126541	1127456	Oligopeptide ABC transporter (ATP-binding protein) oppF			3.A.1.5.1		
	oppA	1121862	1123494	Oligopeptide ABC transporter (binding protein) oppA			3.A.1.5.1		
	oppB	1123603	1124536	Oligopeptide ABC transporter (permease) oppB			3.A.1.5.1		
	oppC	1124542	1125457	Oligopeptide ABC transporter (permease) oppC			3.A.1.5.1		
	opuAA	295622	296876	Glycine betaine ABC transporter (ATP-binding protein) opuAA	glycine-betaine	opuAA(A)/opuAB(M)/opuAC(B)	3.A.1.12.2		
ABC17	opuAB	296879	297725	Glycine betaine ABC transporter (permease) opuAB			3.A.1.12.2		
	opuAC	297727	298606	Glycine betaine ABC transporter (glycine betaine-binding protein) opuAC			3.A.1.12.2		
	opuBD	3212888	3213565	Choline transport system permease protein opuBD	choline	opuBA(A)/opuBB(M)/opuBD(M)/opuBC(B)	3.A.1.12.3		
	opuBC	3213584	3214501	Choline ABC transporter (choline-binding protein) opuBC			3.A.1.12.3		
ABC17	opuBB	3214516	3215169	Choline ABC transporter (membrane protein) opuBB			3.A.1.12.3		
	opuBA	3215186	3216331	Choline ABC transporter (ATP-binding protein) opuBA			3.A.1.12.3		

Supplementary Tables

No	Gene	From	To	Product	Substrate	Transport	Family	TC	No	Note
ABC18	opuCB	3218809	3219462	Glycine betaine/carnitine/choline ABC transporter (permease protein) opuCB	choline/carnitine/ glycine betaine	opuCA(A)/opuCB(M)/ opuCD(M)/opuCC(B)	3.A.1.12.4			
	opuCA	3219483	3220622	Glycine betaine/carnitine/choline ABC transporter (ATP-binding protein) opuCA			3.A.1.12.4			
	opuCC	3217878	3218795	glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein) opuCC			3.A.1.12.4			
	opuCD	3217186	3217860	Glycine betaine/carnitine/choline ABC transporter (permease protein) opuCD			3.A.1.12.4			
ABC19	psBA	2448630	2449436	Phosphate ABC transporter (ATP-binding protein) psBA	phosphate	psBA(A)/psBB(A)/ps IC(M)/psIA(M)/psIS(B)	3.A.1.7.1			
	psA	2449455	2450339	Phosphate ABC transporter (permease) psA			3.A.1.7.1			
	psC	2450339	2451268	Phosphate ABC transporter (permease) yqgH			3.A.1.7.1			
	psS	2451317	2452219	Phosphate ABC transporter (binding protein) psS			3.A.1.7.1			
	psBB	2447836	2448618	Phosphate ABC transporter (ATP-binding protein) psBB			3.A.1.7.1			
	ABC20	RBAM00191	207774	Putative ATP binding protein of ABC transporter	unknown	RBAM00191(A)	3.A.1			unique
ABC21	RBAM00714	728576	729464	Putative ABC transporter (ATP-binding protein)	unknown	RBAM00714(A)/ RBAM00715(M)	3.A.1			unique
	RBAM00715	729481	730219	Putative ABC transporter permease RBAM00715			3.A.1			unique
ABC22	RBAM01170	1158999	1159721	Putative ABC-type multidrug transport system, permease RBAM01170	unknown	RBAM01171(A)/ RBAM01170(M)	3.A.1			unique
	RBAM01171	1159714	1160451	ABC (ATP-binding cassette) transporter nucleotide-binding domain RBAM01171	unknown		3.A.1			unique
ABC23	RBAM02994	3043333	3044037	Putative ABC-transporter ATP-binding protein RBAM02994	unknown	RBAM02994(A)	3.A.1			unique
	RBAM03133	3165194	3166127	Putative multidrug ABC transporter, ATPase component RBAM03133	unknown	RBAM03133(A)/RBAM 03134(M)/RBAM03135	3.A.1			unique
ABC24	RBAM03134	3166163	3167245	Putative multidrug ABC transporter, permease RBAM03134	unknown		3.A.1			unique
	RBAM03135	3167249	3168392	Putative multidrug ABC transporter, permease RBAM03135	unknown		3.A.1			unique
ABC25	RBAM03581	3581332	3582250	Putative ABC transporter ATP-binding protein RBAM03581	unknown	RBAM03581(A)	3.A.1			unique
ABC26	RBAM03610	3610649	3611593	Putative ABC transporter (ATP-binding protein) RBAM03610		unknown	RBAM03610(A)			3.A.1
	unique									
ABC27	RBAM03694	3683843	3684737	Iron compound ABC transporter, substrate-binding protein RBAM03694	ferrichrome	RBAM03692(M)/RBAM 03693(M)/RBAM03694	3.A.1			unique
	RBAM03692	3681784	3682810	Putative ferrichrome transport system permease RBAM03692			3.A.1			unique
ABC28	RBAM03693	3682813	3683824	Putative ferrichrome ABC transporter (permease) RBAM03693			3.A.1			unique
	RBAM03838	3835733	3837358	Putative ABC transporter ATP-binding protein RBAM03838	unknown	RBAM03838(A)	3.A.1			unique
ABC29	rhsA	3432524	3434015	Ribose ABC transporter (ATP-binding protein) rhsA	ribose	rhsA(A)/rhsC(M)/rhsD (M)/rhsB(B)	3.A.1.2.1			
	rhsC	3434007	3434976	Ribose ABC transporter (permease) rhsC			3.A.1.2.1			
	rhsB	3434992	3435907	Ribose ABC transporter (ribose-binding protein) rhsB			3.A.1.2.1			

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ABC30	rlsD	3432112	3432505	Ribose ABC transporter (membrane protein)	rlsD		3.A.1.2.1			
	resC	2224730	2224730	cytochrome c-type synthesis protein	resC	resC(M)	3.A.1.X.X			
ABC31	spaG	3210566	3211336	Lantibiotic ABC transporter permease	spaG	spaF(A)/spaE(M)/spaG(M)	3.A.1			unique
	spaE	3211333	3212067	Lantibiotic ABC transporter permease	spaE		3.A.1			unique
ABC32	spaF	3212064	3212777	Lantibiotic transporter (ATP-binding protein)	spaF		3.A.1			unique
	ssuC	895228	896059	Putative aliphatic sulfonates transport permease	protein ssuC	ssuB(A)/ssuC(M)/ssuA(B)	3.A.1.17.X			
ABC33	ssuA	894239	895226	Putative aliphatic sulfonates binding protein	precursor ssuA		3.A.1.17.X			
	ssuB	893414	894221	Putative aliphatic sulfonates transport ATP-binding protein	ssuB		3.A.1.17.X			
ABC34	tagH	3399741	3401285	Teichoic acids export ATP-binding protein	tagH	tagH(A)/tagG(M)	3.A.1.104.1			
	tagG	3401306	3402133	Teichoic acid translocation permease	protein tagG		3.A.1.104.1			
ABC35	ybaF	152878	153673	Putative ABC transporter (permease)	ybaF	ybaE(A)/ybaX(A)/ybaF(M)	3.A.1.X.X			
	ybaX	151191	152034	putative ABC transporter (ATP-binding protein)	ybaX		3.A.1.X.X			
ABC36	ybaE	152051	152879	Putative ABC transporter (ATP-binding protein)	ybaE		3.A.1.X.X			
	ycdI	285699	286392	Putative ABC transporter (ATP-binding protein)	ycdI	ycdI(A)/ybaE(M)/ybaF(M)	3.A.1.X.X			
ABC37	yceA	286352	287189	Putative zinc ABC transporter, permease	protein		3.A.1.X.X			
	ycdH	284685	285642	Putative high-affinity zinc ABC transporter (Zn (II) -binding lipoprotein)			3.A.1.X.X			
ABC38	yckJ	376630	377319	Putative ABC-type transporter protein, permease	component yckJ	yckI(A)/yckJ(M)/yckK(B)	3.A.1.3.X			
	yckK	377321	378118	Probable amino-acid ABC transporter extracellular binding protein	yckK		3.A.1.3.X			
ABC39	yckI	375874	376617	Putative ABC-type transporter protein, ATPase	component yckI		3.A.1.3.X			
	ydl	397525	398961	Putative ABC transporter (permease)	ydl	ydlH(A)/ydlI(M)	3.A.1.X.X			
ABC40	ydlH	396827	397510	Putative ABC transporter (ATPase component)	ydlH		3.A.1.X.X			
	ydlQ	407462	408404	Putative ferrichrome ABC transporter (periplasmic binding protein)	ydlQ	ydlP(A)/ydlO(M)/ydlN(	3.A.1.14.X			
ABC41	ydlN	404798	405749	Putative ferrichrome ABC transporter (permease)	ydlN		3.A.1.14.X			
	ydlP	406682	407438	Putative ferrichrome ABC transporter (ATP-binding protein)			3.A.1.14.X			
ABC42	ydlO	405741	406686	Putative ferrichrome ABC transporter (permease)	ydlO		3.A.1.14.X			
	ydbA	469744	470548	ABC transporter (binding protein) like protein	ydbA	ydbA(B)/ydbB(M)	3.A.1.X.X			
ABC43	ydbB	471157	471514	Conserved hypothetical protein	ydbB		3.A.1.X.X			
	ydlF	615312	617240	Putative ABC transporter ATP-binding	ydlF	ydbJ(A)/ydbK(M)/ydlF(A)	3.A.1.X.X			

No	Gene	From	To	Product	Substrate	Transport	Family	TC	No	Note
	ydbK	479816	480581	Hypothetical protein ydbK			3.A.1.X.X			
	ydbJ	478897	479821	Putative ABC transporter (ATP-binding protein) ydbJ			3.A.1.X.X			
ABC41	yfC	836473	838288	Hypothetical ABC transporter ATP-binding protein yfC	unknown	yfB(AM)/yfC(AM)	3.A.1.106.X			
	yfB	834759	836490	Putative ABC transporter (ATP binding protein) yfB			3.A.1.106.X			
ABC42	yfL	223789	224722	Putative ABC transporter (ATP-binding protein) yfL	unknown	yfL(A)/yfM(M)/yfN1(M)	3.A.1.X.X			
	yfM	224733	225918	Putative ABC transporter, permease component yfM			3.A.1.X.X			
	yfN1	225917	227057	Putative ABC-type multidrug transport system, permease			3.A.1.X.X			
ABC43	yfmM	756417	757973	Putative ABC transporter (ATP-binding protein) yfmM	unknown	yfmM(A)	3.A.1.X.X			
ABC44	yfmR	752822	754509	Putative ABC transporter (ATP-binding protein) yfmR	unknown	yfmR(A)	3.A.1.X.X			
ABC45	ygaD	870103	871843	Putative ABC transporter ATP-binding protein ygaD	unknown	ygaD(AM)	3.A.1.106.X			
ABC46	yhaQ	991368	992262	Putative ABC transporter (ATP-binding protein) yhaQ	unknown	yhaQ(A)	3.A.1.X.X			
ABC47	yhcH	913805	914720	Putative ABC transporter (ATP-binding protein) yhcH	unknown	yhcG(A)/yhcH(A)/yhcl	3.A.1.X.X			
	yhcl	914715	915660	Conserved hypothetical protein yhcl			3.A.1.X.X			
	yhcJ	916336	917164	Hypothetical lipoprotein yhcJ precursor			3.A.1.X.X			
	yhcG	913070	913802	Putative ABC transporter ATP-binding protein yhcG			3.A.1.X.X			
ABC48	yheI	972874	974629	Putative ABC transporter (ATP-binding protein) yheI	unknown	yheH(MA)/yheI(MA)	3.A.1.106.X			
	yheH	974628	976647	Putative ABC transporter (ATP-binding protein) yheH			3.A.1.106.X			
ABC49	yhiQ	1033280	1034156	Conserved hypothetical protein yhiQ	iron (III)-dicitrate	yhiQ(B)	3.A.1.14.X			
ABC50	yjKB	1204022	1204771	putative amino acid ABC transporter (ATP-binding protein) yjKB	unknown	yjKB(A)	3.A.1.X.X			
ABC51	yKD	1250361	1251330	Putative oligopeptide ABC transporter (ATPase component)yKD	oligopeptide	yKD(A)	3.A.1.5.X			
ABC52	yknY	1370188	1370878	Putative ABC transporter (ATP-binding protein) yknY	unknown	yknY(A)/yknZ(M)	3.A.1.X.X			
	yknZ	1370877	1372068	Putative ABC transporter permease yknZ			3.A.1.X.X			
ABC53	ykoC	1271234	1271995	Conserved hypothetical protein ykoC	unknown	ykoD(A)/ykoC(M)	3.A.1.X.X			
	ykoD	1271970	1273607	Putative cation ABC transporter (ATP-binding protein) ykoD			3.A.1.X.X			
ABC54	ykpA	1377110	1378727	ABC transporter (ATP-binding protein) ykpA	unknown	ykpA(A)	3.A.1.X.X			
ABC55	yimA	1522557	1523352	Putative ABC transporter (ATP-binding protein) yimA	unknown	yimA(A)	3.A.1.X.X			
ABC56	yqiY	2365156	2365815	Putative amino acid ABC transporter (permease) yqiY	polar amino acid	yqiZ(A)/yqiY(M)/yqiX(B)	3.A.1.3.X			

Supplementary Tables

No	Gene	From	To	Product	Substrate	Transport	Family	TC No	Note
	yqIX	2365877	2366644	Putative amino acid ABC transporter (binding protein) yqIX			3.A.1.3.X		
	yqIZ	2364441	2365163	Putative amino acid ABC transporter (ATP-binding protein)			3.A.1.3.X		
ABC57	ytrO	2564673	2565941	Putative protease ytrO	unknown	ytrO(A)	3.A.1.X.X		
ABC58	ytrP	2837673	2838377	Putative ABC transporter (ATP-binding protein) ytrP	unknown	ytrP(A)	3.A.1.X.X		
ABC59	ytrD	2901395	2902205	Putative ABC transporter (permease) ytrD	nitrate	ytrA(A)ytrC(A)ytrD(M)	3.A.1.X.X		
	ytrA	2899622	2900624	Putative ABC-transport system substrate-binding protein ytrA			3.A.1.X.X		
	ytrC	2900638	2901418	Putative ABC-transport system (ATP-binding protein) ytrC			3.A.1.X.X		
ABC60	ytrN	3195247	3196026	putative amino-acid ABC transporter ATP-binding protein ytrN	polar amino acid	ytrN(A)ytrM(M)ytrM(M)ytrK(B)ytrJ(B)	3.A.1.3.X		
	ytrM	3196023	3196730	Putative amino-acid ABC transporter permease protein ytrM			3.A.1.3.X		
	ytrL	3196746	3197468	Putative amino acid ABC transporter (permease) homolog			3.A.1.3.X		
	ytrK	3197491	3198303	Putative amino-acid ABC transporter (extracellular binding protein)			3.A.1.3.X		
	ytrJ	3198329	3199045	Putative amino acid ABC transporter (substrate-binding protein)			3.A.1.3.X		
ABC61	ytrD	2864606	2865586	Hypothetical protein ytrD	unknown	ytrB(A)ytrC1(M)ytrC(M)ytrD(M)	3.A.1.X.X		
	ytrB	2867605	2868483	Putative ABC transporter (ATP-binding protein) ytrB	unknown		3.A.1.X.X		
	ytrC1	2865623	2866609	Hypothetical protein ytrC1	unknown		3.A.1.X.X		
	ytrC	2866625	2867611	Hypothetical protein ytrC	unknown		3.A.1.X.X		
ABC62	ytrF	2862595	2863905	Hypothetical protein ytrF	unknown	ytrE(A)ytrF(M)	3.A.1.X.X		
	ytrE	2863895	2864596	Hypothetical ABC transporter ATP-binding protein ytrE	unknown		3.A.1.X.X		
ABC63	ytrN	2981094	2982165	Hypothetical lipoprotein ytrN	unknown	ytrN(B)	3.A.1.X.X		
ABC64	ytrO	2982309	2983839	Putative ABC transport system, ATPase component ytrO	unknown	ytrO(A)ytrQ(M)ytrP(M)	3.A.1.X.X		
	ytrP	2983834	2984878	Putative ABC transporter permease ytrP	unknown		3.A.1.X.X		
	ytrQ	2984881	2985838	Putative ABC transporter permease ytrQ	unknown		3.A.1.X.X		
ABC65	yurJ	3079610	3080716	Putative multiple sugar ABC transporter (ATP-binding protein) yurJ	sugar	yurJ(A)yurN(M)yurM(M)yurO(B)	3.A.1.X.X		
	yurM	3082493	3083377	Putative sugar ABC transporter permease yurM	sugar		3.A.1.X.X		
	yurN	3083381	3084271	Putative sugar ABC transporter permease protein yurN	sugar		3.A.1.X.X		

Supplementary Tables

No	Gene	From	To	Product	Substrate	Transport	Family	TC	No	Note
ABC66	yurO	3084296	3085582	Multiple sugar-binding extracellular protein yurO	sugar		3.A.1.X.X			
	yusB	3099364	3100032	Putative ABC transporter (permease) yusB	sulfate	yusC(A)/yusB(M)	3.A.1.X.X			
	yusC	3100025	3101050	Putative ABC transporter (ATP-binding protein) yusC	sulfate		3.A.1.X.X			
ABC67	yusV	3119264	3120088	Putative iron(III) ABC transport ATPase component yusV	unknown	yusV(A)	3.A.1.X.X			
ABC68	yycC	3319704	3321473	Putative ABC transporter (ATP-binding protein) yycC	unknown	yycC(MA)	3.A.1.106.X			
ABC69	yvgK	3160718	3161644	Putative molybdenum-binding protein yvgK	molybdenum	yvgM(M)/yvgL(B)/yvgK(B)	3.A.1.8.X			
	yvgL	3161762	3162557	Putative molybdate-binding protein yvgL	molybdenum		3.A.1.8.X			
	yvgM	3162663	3163221	Putative molybdenum transport permease yvgM	molybdenum		3.A.1.8.X			
ABC70	yvrB	3142412	3143458	Putative iron permease yvrB	heme	yvrA(A)/yvrB(M)/yvrC(B)	3.A.1.14.X			
	yvrC	3143421	3144365	Putative iron-binding protein yvrC	heme		3.A.1.14.X			
	yvrA	3141189	3142415	Putative ABC transport system ATP-binding protein yvrA	heme		3.A.1.14.X			
ABC71	ywjA	3544397	3546121	Putative ABC transporter ATP-binding protein ywjA	unknown	ywjA(AM)	3.A.1.106.X			
ABC72	yxdM	3763225	3765093	Hypothetical protein yxdM	unknown	yxdL(A)/yxdM(M?)	3.A.1.106.X			
	yxdL	3765068	3765841	Putative ABC transporter (ATP-binding protein) yxdL	unknown		3.A.1.106.X			
	yxeB	3760564	3761524	putative ABC transporter (binding protein) yxeB	ferriochrome	yxeB(A)	3.A.1.14.X			
ABC74	yxeM	391960	392749	Putative amino-acid ABC transporter binding protein yxeM	polar amino acid	yxeO(A)/yxeN(M)/yxeM(B)	3.A.1.3.X			
ABC75	yxeN	392774	393446	Putative amino acid ABC transporter (permease) yxeN	polar amino acid		3.A.1.3.X			
	yxeO	394209	394209	probable amino acid ABC transporter (ATP-binding protein)	polar amino acid		3.A.1.3.X			
	yurY	3096757	3097542	Putative ABC transporter (ATP-binding protein) yurY	unknown	yurY(A)	3.A.1.X.X			
PST1	ybbF	195617	196984	Putative sucrose phosphotransferase enzyme II ybbF	sucrose		4.A.1.2.1			
PST2	mliA	422209	423640	Phosphotransferase system (PTS) manitol-specific enzyme IIABC component mliA	mannitol		4.A.2.1.2			
PST3	RBAM00392	423668	424097	PTS manitol-specific enzyme IIA component RBAM00392	unknown		unknown			unique
PST4	nagP	780570	781950	Phosphotransferase system (PTS) N-acetylglucosamine-specific enzymeIIICB component nagP	N-acetylglucosamine		4.A.1.1.2			
PST5	treP	786368	787781	Phosphotransferase system (PTS) trehalose-specific enzyme IIIBC component treP	trehalose		4.A.1.2.4			
PST6	glvC	830362	831946	Phosphotransferase system (PTS) maltose-specificenzymelICB component glvC	arbutin		4.A.1.2.X			
PST7	ptsG	1328347	1330441	phosphotransferase system (PTS) glucose-specificenzymelICBA component ptsG	glucose		4.A.1.1.1			

Supplementary Tables

No	Gene	From	To	Product	Substrate	Transport	Family	TC	No	Note
PST8	ptlH	1330540	1330804	Phosphocarrier protein HPr component ptlH	energy coupling		8.A.8			
PST9	ptlI	1330806	1332519	Phosphoenolpyruvate-protein phosphotransferase ptlI	energy coupling		8.A.7			
PST10	fruA	1374030	1375929	phosphotransferase system (PTS) fructose-specific enzyme I IABC component fruA	fructose		4.A.2.1.1			
PST11	ypqE	2143377	2143883	Putative PTS system IIA component ypqE	glucose		4.A.1.1.1			
PST12	manP	2537563	2539521	Phosphotransferase system (PTS) mannose-specific enzyme I IBCA component manP	mannose		4.A.2.1.X			
PST13	sacP	3631105	3632487	Phosphotransferase system (PTS) sucrose-specific enzyme I IBC component sacP	sucrose		4.A.1.2.1			
PST14	ywbA	3663073	3664407	Putative PTS system IIBC component ywbA	diacetylchitobiose		4.A.3.2.X			
PST15	licA	3676561	3676893	Phosphotransferase system (PTS) lichenan specific enzyme IIA component licA	lichenan	licA/licC/licB	4.A.3.2.2			
	licC	3676912	3678270	Phosphotransferase system (PTS) lichenan specific enzyme IIC component licC	oligosaccharide		4.A.3.2.2			
	licB	3678286	3678594	Phosphotransferase system (PTS) lichenan specific enzyme IIB component licB	oligosaccharide		4.A.3.2.2			
PST16	ydhO	3687320	3688637	Putative cellobiose phosphotransferase system enzyme	oligosaccharide	ydhO/ydhM/ydhN	4.A.3.2.1			
	ydhM	3686658	3686967	Putative cellobiose phosphotransferase system enzyme	diacetylchitobiose		4.A.3.2.1			
	ydhN	3686984	3687299	Putative cellobiose phosphotransferase system enzyme	diacetylchitobiose		4.A.3.2.1			
PST17	bgIP	3737447	3739282	Phosphotransferase system (PTS) beta-glucoside-specific enzyme I IBCA component bgIP	β -glucoside		4.A.1.2.X			
	yfkF	805745	806923	Hypothetical protein yfkF	efflux		2.A.1.X.X			
	yhdH	954614	955967	Putative sodium-dependent transporter yhdH	metabolite		2.A.22.4.X			
	gipF	932368	933196	Glycerol uptake facilitator gipF	glycerol facilitator		1.A.8			
	yhcA	909294	910887	Hypothetical transport protein yhcA	multidrug efflux		2.A.1.3.X			
	yfhI	856382	857579	Conserved hypothetical protein yfhI	metabolite efflux		2.A.1.X.X			
	yfiU	847108	848700	Putative multidrug-efflux transporter yfiU	multidrug efflux		2.A.1.X.X			
	yfiQ	813871	814830	Putative divalent cation transport protein yfiQ	Mg2+		9.A.17.1.X			
	yloB	1554264	1556934	Putative calcium-transporting ATPase yloB	calcium efflux		3.A.3			
	yfkE	807082	808135	Putative H ⁺ /Ca2 ⁺ antiporter yfkE	proton cation antiport		2.A.19.X.X			
	bit	1053467	1054663	Multidrug resistance protein II bit	multidrug efflux		2.A.1.2.8			
	yfkL	801994	803187	Conserved hypothetical protein yfkL	unknown		2.A.1.X.X			
	ctm	774345	775641	magnesium citrate secondary transporter ctm	citrate-Mg2 ⁺ -H ⁺ symporter		2.A.11.1.1			

No	Gene	From	To	Product	Substrate	Transport	Family	TC	No	Note
	yflS	763436	764870	Putative 2-oxoglutarate/malate translocator yflS	dicarboxylate		2.A.47.3.X			
	yfmO	755189	756371	Putative multidrug-efflux transporter yfmO	multidrug efflux		2.A.1.X.X			
	yfnC	745017	746246	Putative fosfomycin resistance protein yfnC	multidrug efflux		2.A.1.3.X			
	pbuG	657985	659305	Hypoxanthine/guanine permease pbuG	Hypoxanthine/guanosine		2.A.1.40.2			
	yeaB	648484	649354	Putative transport protein yeaB	metal ion efflux		2.A.4.1.X			
	yfkC	809031	809864	Conserved hypothetical protein yfkC	unknown		1.A.23.X.X			
	ykkD	1255219	1255531	Putative Multidrug resistance protein ykkD	multidrug efflux		2.A.7.1.5			
	cysP	1546969	1548031	Sulfate permease cysP	sulfate		2.A.20.1.X			
	pyrP	1534980	1536288	Uracil permease pyrP	uracil		2.A.40.1.X			
	ykbB	1385230	1385893	conserved hypothetical protein ykbB	potassium		2.A.38.4.4			
	ykuT	1360100	1360906	Conserved hypothetical protein ykuT	osmolyte release following osmotic shift		1.A.23.3.1			
	ykuC	1346872	1348164	Hypothetical protein ykuC	macrolide efflux		2.A.1.21.X			
	ptlI	1330806	1332519	Phosphoenolpyruvate-protein phosphotransferase ptlI	energy coupling		8.A.7			
	ptlH	1330540	1330804	Phosphocarrier protein HPr component ptlH	energy coupling		8.A.8			
	yhdY	966727	967840	Conserved hypothetical protein yhdY	unknown		1.A.23.X.X			
	yjaJ	3894895	3896224	Conserved hypothetical protein yjaJ	unknown		2.A.1.22.X			
	yhaU	988000	989214	Putative Na ⁺ /H ⁺ antiporter yhaU	Na ⁺ /H ⁺ antiport		2.A.37.X.X			
	ykcC	1254881	1255217	Putative Multidrug resistance protein ykcC	multidrug efflux		2.A.7.1.5			
	yubD	1240251	1241808	Conserved hypothetical protein yubD	multidrug efflux		2.A.1.X.X			
	pit	1230485	1231483	Putative low-affinity inorganic phosphate transporter pit	phosphate		2.A.20.1.X			
	yjmB	1210026	1211409	Putative symporter yjmB	sugar		2.A.2.X.X			
	yjbQ	1142207	1144049	Putative Na ⁺ /H ⁺ antiporter yjbQ	Na ⁺ /H ⁺ antiport		2.A.37.X.X			
	yflZ	1096434	1096974	Putative multidrug resistance protein yflZ	multidrug efflux		2.A.1.X.X			
	yqjK	604286	605702	Putative sugar transporter yqjK	sugar		2.A.1.1.X			
	ykrM	1289705	1291055	Putative transporter (membrane component) ykrM	potassium		2.A.38.1.X			
	mdr	305385	306917	Multidrug-efflux transporter mdr	multidrug efflux		2.a.1.2.8			
	gabP	646712	648097	Gamma-aminobutyrate (GABA) permease gabP	γ-aminobutyrate		2.A.3.1.11			

No	Gene	From	To	Product	Substrate	Transport	Family TC No	Note
	yscG	427759	428971	Conserved hypothetical protein yscG	unknown		2.A55.X.X	
	ycnJ	419272	420900	Putative copper export protein ycnJ	unknown		9.B62.X.X	
	glcU	416933	417794	Glucose uptake protein glcU	sugar		2.a.7.5.X	
	ycnB	408448	409872	Putative multidrug resistance protein ycnB	multidrug efflux		2.A.1.3.X	
	yciF	381998	383476	Putative di-tripeptide ABC transporter, permease yciF	di/tripeptide		2.A.17.1.X	
	ycxC	371986	372948	Conserved hypothetical protein yxC	metabolite-drug efflux		2.A.7.3.X	
	yvaD	468808	469215	Hypothetical protein yvaD	multidrug efflux		2.A.7.1.X	
	ycbE	314185	315493	Putative sugar transport-related protein ycbE	glucarate		2.A.1.14.X	
	yvaE	469212	469577	Putative multidrug-efflux transporter yvaE	multidrug efflux		2.A.7.1.X	
	yceI	294037	295237	Hypothetical transport protein yceI	unknown		2.A.1.2.X	
	lmrB	269539	270972	Drug-export protein lmrB	drug efflux		2.A.1.3.X	
	ydiM	259677	260570	Putative cation efflux transporter ydiM	metal ion efflux		2.A.4.X.X	
	glpT	234302	235636	Glycerol-3-phosphate permease glpT	Glycerol-3-phosphate		2.A.1.4.3	
	ybaS	184558	185539	Putative sodium dependent transporter ybaS	unknown		2.a.21.X.X	
	ybaR	183145	184447	Putative sulfate permease ybaR	sulfate		2.A53.X.X	
	glcP1	178108	178322	Putative glucose/mannose:H ⁺ symporter/glcP1	Glucose-mannose: H ⁺ symporter		2.A.1.7.3	
	nasA	334013	335216	Nitrate transporter nasA	Nitrate efflux		2.A.1.8.2	
	RBAM00541	554168	555455	Putative Na ⁺ /H ⁺ antiporter RBAM00541	unknown		2.A.35.X.X	unique
	ykwW	1322830	1324741	Putative cation transport ATPase ykwW	cadmium efflux		3.A.3	
	yvdS	598399	598728	Conserved hypothetical protein yvdS	metabolite-drug efflux		2.A.7.1.X	
	yvdR	598085	598399	Conserved hypothetical protein yvdR	metabolite-drug efflux		2.A.7.1.X	
	yycB	596811	598023	Conserved hypothetical protein yycB	cyanate		2.A.1.17.X	
	ydhL	593806	594966	Conserved hypothetical protein ydhL	chloramphenicol efflux		2.A.1.X.X	
	yzcE	584734	585604	Hypothetical protein yzcE	metabolite-drug efflux		2.A.7.3.X	
	ydgK	578743	579952	Putative bicyclomycin resistance protein ydgK	multidrug efflux		2.A.1.2.X	
	mntH	466190	467464	Manganese transport protein mntH	manganeses		2.A.55.1.1	
	ydeR	561410	562600	Hypothetical protein ydeR	unknown		2.A.1.X.X	

No	Gene	From	To	Product	Substrate	Transport	Family TC No	Note
	guaA	631030	632404	Probable glucitol transport protein guaA	sugar		2.A.2.X.X	
	trtA	540147	541182	Potassium uptake protein trtA	potassium		2.A.38.X.X	
	czcD	539142	540081	Cation-efflux system membrane protein czcD	metal ion efflux		2.A.4.1.1	
	ybfB	532355	533645	Hypothetical protein ybfB	unknown		2.A.1.1.X	
	RBAM00491	509188	510589	Putative permease RBAM00491	unknown		2.A.1.6.X	unique
	ydbO2	483213	483717	Hypothetical protein ydbO2	metal ion efflux		2.A.4.X.X	
	ydbO1	482827	483211	Hypothetical protein ydbO1	metal ion efflux		2.A.4.X.X	
	dclP	476304	477568	C4-dicarboxylate transport protein dclP	dicarboxylate		2.A.23.X.X	
	YdfJ	570740	572891	Putative antibiotic transport-associated protein YdfJ	unknown		2.a.6.X.X	
	RBAM03275	3301733	3303107	Putative transport protein RBAM03275	sugar		2.A.1.1.X	unique
	yvgP	3170005	3172020	Conserved hypothetical protein yvgP	Nar ⁺ H ⁺ antiport		2.A.36.3.X	
	ywrA	3450028	3450562	Putative chromate transporter ywrA	chromate-sulfate transport		2.A.51.X.X	
	ywrB	3449441	3450029	Putative chromate transporter ywrB	chromate-sulfate transport		2.A.51.X.X	
	ywrK	3441056	3442385	Putative transporter ywrK	arsenite efflux		2.A.45.1.X	
	ywtG	3418149	3419525	Putative transport protein ywtG	sugar		2.A.1.1.X	
	ywtG	3418149	3419525	Putative transport protein ywtG	sugar		2.A.1.1.X	
	tuaB	3389976	3391424	Teichuronic acid biosynthesis protein tuaB	polysaccharide efflux		9.A.1.X.X	
	ywoG	3478466	3479660	Putative transporter ywoG	drug efflux		2.A.1.X.X	
	ykoK	1276629	1277982	Putative divalent cation transporter ykoK	Mg2 ⁺		9.A.19.1.X	
	ywoE	3479698	3481152	Putative allantoin permease (Allantoin transportprotein) ywoE	uracil		2.A.39.X.X	
	RBAM01682	1671661	1672987	Conserved hypothetical protein RBAM01682	unknown		2.A.1.X.X	unique
	yvhH	3266342	3268016	Putative L-lactate permease yvhH	unknown		2.A.14.X.X	
	gntP	3259754	3261080	Gluconate permease gntP	gluconate		2.A.8.1.1	
	yvbV	3249444	3250359	Conserved hypothetical protein yvbV	metabolite-drug efflux		2.A.7.3.X	
	araE	3243969	3245363	Arabinose-proton symporter araE	L-arabinose		2.A.1	
	copA	3183726	3186164	Copper-transporting P-type ATPase copA	Cu2 ⁺		3.A.3.5.1	
	yvgW	3181465	3183576	Putative metal ABC-transporter, ATPase component yvgW	cadium efflux		3.A.3	

No	Gene	From	To	Product	Substrate	Transport	Family TC No	Note
	ywA	3350957	3352292	Conserved hypothetical protein ywA	multidrug efflux		2.A.1.X.X	
	ydiA	3685206	3686502	Puative arsenical pump membrane protein ydiA	arsenite efflux		2.A.45.X.X	
	ybfF	3876926	3878128	Conserved hypothetical protein ybfF	drug efflux		2.A.1.2.X	
	csbC	3786500	3787886	Sugar transporter csbC	sugar		2.A.1.1.X	
	iolF	3776645	3777940	Inositol transport protein iolF	inositol		2.A.1.1.X	
	nupC	3754113	3755294	Pyrimidine-nucleoside transport protein nupC	nucleoside		2.A.41.1.2	
	yxfF	3734444	3735355	Conserved hypothetical protein yxfF	metabolite-drug efflux		2.A.7.3.X	
	ciH	3727277	3724055	Citrate transporter ciH	citrate-Ca2+-H+ symporter		2.A.11.1.2	
	yxA	3717900	3719091	Putative transport protein yxA	nucleoside		2.A.41.1.X	
	mscL	3472276	3472671	Large conductance mechanosensitive channel protein mscL	following osmotic		osmolyte release	1.A.22.1.3
	yxA	3696046	3697402	Putative purine-cytosine permease yxA	purine		2.A.39.X.X	
	ywbF	3296041	3297273	Putative sugar permease ywbF	sugar		2.A.1.X.X	
RBAM03600		3599461	3600661	Putative drug resistance transporter RBAM03600	multidrug efflux		2.A.1.2.X	unique
	ywfA	3598000	3599238	Conserved hypothetical protein ywfA	drug efflux		2.A.1.X.X	
	narK	3557321	3558511	Nitrite extrusion protein narK	nitrite efflux		2.A.1.8.1	
	ywkB	3525757	3526713	Hypothetical protein ywkB	efflux		2.A.69.X.X	
	atpA	3510384	3511892	ATP synthase (subunit alpha) atpA	proton efflux		3.A.2	
	ngA	3483497	3484706	Ammonium transporter ngA	amino acid		2.A.49.1.X	
	ywoD	3481317	3482881	Conserved hypothetical protein ywoD	drug efflux		2.A.1.X.X	
	cinH	3704679	3706020	Putative citrate/malate transporter cinH	L-malate/citrate:H+ symport		2.A.24.2.4	
	yocR	2028187	2029524	Putative sodium-dependent transporter yocR	metabolite		2.A.22.4.X	
	yqeW	2491437	2492370	Conserved hypothetical protein yqeW	phosphate		2.A.53.X.X	
	nhaC	2444110	2445472	Na+/H+ antiporter nhaC	Na+:H+ antiport		2.A.35.1.X	
	yqxL	2434693	2435643	Conserved hypothetical protein yqxL	Mg2+		9.A.17.1.X	
	mieN	2257393	2258799	Malate-H+/Na+-lactate antiporter mieN	Na+:H+ antiport		2.A.35.1.X	
	pbuX	2129300	2130604	Xanthine permease pbuX	xanthine		2.A.40.3.1	
	yqjE	2046866	2047762	Hypothetical protein yqjE	metabolite-drug efflux		2.A.7.3.X	

<i>No</i>	<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Product</i>	<i>Substrate</i>	<i>Transport</i>	<i>Family TC No</i>	<i>Note</i>
yyqJ	3139190	3140458	Conserved hypothetical protein yyqJ	macrolide efflux			2.A.1.21.X	
yybF1	2544377	2545583	Hypothetical transport protein yybF1	drug efflux			2.A.1.2.X	
yydB	3304410	3305999	Putative transporter yydB	sulfate			2.A.53.X.X	
yojI	2043242	2044598	Putative multidrug resistance protein yojI	drug efflux			2.A.66.1.X	
yocB	1999023	2000270	Conserved hypothetical protein yocB	unknown			2.A.1.X.X	
ybcL	1978842	1980017	Conserved hypothetical protein ybcL	efflux			2.A.1.2.X	
yoeA	1973265	1974653	Conserved hypothetical protein yoeA	efflux			2.A.66.2.X	
exuT	1857486	1858752	Hexuronate transporter exuT	glucarate			2.A.1.14.X	
xynP	1798060	1799449	hypothetical symporter xynP	glucuronide			2.A.2.3.X	
ebvA	1779724	1780038	Multidrug resistance protein ebrA	multidrug efflux			2.A.7.1.6	
ebvB	1779353	1779706	Multidrug resistance protein ebrB	multidrug efflux			2.A.7.1.6	
yocS	2029728	2030700	Putative sodium-dependent transporter yocS	metabolite			2.A.28.X.X	
mrpA	2986346	2988746	Na ⁺ /H ⁺ antiporter subunit A (mrpA)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
yhvG	2551270	2552070	Putative formate transporter yhvG	formate			2.A.44.1.X	
RBAM03031	3074660	3075856	Multidrug resistance protein RBAM03031	drug efflux			2.A.1.2.X	unique
yulK	3050239	3051456	Putative Na ⁺ /nucleoside co-transporter yulK	nucleoside			2.A.41.X.X	
mrpG	2991741	2992113	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit G (mrpG)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
mrpF	2991473	2991755	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit F (mrpF)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
mrpE	2990997	2991471	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit E (mrpE)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
mrpD	2989501	2990989	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit D (mrpD)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
mrpB	2988745	2989174	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit B (mrpB)	K ⁺ /Na ⁺ antiport			2.A.63.1.X	
yusP	3111720	3113313	Putative multidrug-efflux transporter yusP	multidrug efflux			2.A.1.X.X	
yuxJ	2974106	2975243	Conserved hypothetical protein yuxJ	multidrug efflux			2.A.1.X.X	
yugO	2958450	2959434	Conserved hypothetical protein yugO	potassium channel			1.A.1	
yuaA	2934572	2935238	Conserved hypothetical protein yuaA	potassium			2.A.38.4.3	
RBAM02833	2884258	2885923	Putative permease MDR type RBAM02833	drug efflux			2.A.1.3.X	unique
yfIB	2855838	2857022	Conserved hypothetical protein yfIB	multidrug efflux			2.A.1.X.X	

Supplementary Tables

No	Gene	From	To	Product	Substrate	Transport	Family TC/No	Note
	ytgP	2839783	2841420	Putative spore cortex protein ytgP	polysaccharide efflux		9.A.1.X.X	
	ytdD	2732693	2733890	Putative arabinose efflux permease ytdD	multidrug efflux		2.A.1.X.X	
	secDF	2598736	2600955	Protein-export membrane protein secDF	protein export		2.A.6.4.1	
	mrpC	2989176	2989515	Na ⁽⁺⁾ /H ⁽⁺⁾ antiporter subunit C (mrpC)	K ⁺ /Na ⁺ antiport		2.A.63.1.X	

- ❖ "Aa" stands for amino acid permease.
- ❖ "ABC" stands for ABC-transporter system; "A" is for ATP binding protein, "W" for the membrane channel (permease) and "B" for binding protein.
- ❖ "PTS" stands for phosphotransferase system.
- ❖ "Unique" means this gene is not presented in *Bacillus subtilis* 168.
- ❖ For more detail about the TC number see http://www.tcdp.org/simple_search.php

Supplementary Table 5. Genes probably involved in plant bacterium interactions.

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Protein</i>	<i>Remark</i>
Root colonization, swarming motility and biofilm formation				
sacB	3869505	3870926	Levan sucrose	Levan is implicated in the aggregation of wheat root-adhering soil ¹
yciH	284685	285644	High affinity zinc ABC transporter lipoprotein	Proposed to be involved in surface adhesion ²
RBAM00754	769334	770713	Collagen like triple helix with GXT repeats5	Proposed to be involved in surface adhesion ³
RBAM00751	767904	769154	Collagen like triple helix with GXT repeats4	Proposed to be involved in surface adhesion ³
RBAM00750	765780	767777	Collagen like triple helix with GXT repeats3	Proposed to be involved in surface adhesion ³
yfiQ	842464	843552	Putative surface adhesion protein	Proposed to be involved in surface adhesion ²
sfp	375046	374372	Phosphopantetheinyl transferase necessary for lipopeptide and polyketide synthesis	Biosurfactant necessary for surface motility and biofilm formation but suppressing biofilm formation in competing microorganisms ^{4,5}
yczE	375792	375145	Integral membrane spanning protein affecting lipopeptide and polyketide synthesis	Biosurfactant necessary for surface motility and biofilm formation but suppressing biofilm formation in competing microorganisms ^{4,5}
srfABCD	343826	369253	Surfactin synthetases	Biosurfactant necessary for surface motility and biofilm formation but suppressing biofilm formation in competing microorganisms ^{4,5}
comP	2993285	2995585	ComX sensor kinase	Regulator of surfactin production ⁶
swrC	2413698	2413141	Multidrug efflux pump	Self-resistance against surfactin ⁶
efp	2413698	2413141	Similar to elongation factor P	Essential for swarming motility ⁶
swrB	1633667	1634074	Swarming protein	Essential for swarming motility ⁶
swrA	3354144	3353791	Swarming protein	Essential for swarming motility ⁶
spo0A	2393886	2393086	Master regulator of initiation of sporulation	Involved in initial stage of biofilm formation ⁷
sigH	117336	117992	Sigma factor H	Involved in initial stage of biofilm formation ⁷
abrB	45895	45611	Transition state regulator	Transcription control of biofilm formation ^{8,9,10}
sigW	199909	200472	ECF sigma factor W	Transcription control of biofilm formation ^{8,9,10}
resE	2222973	2221192	Sensor histidine kinase controlling aerobic and anaerobic respiration	Transcription control of biofilm formation ^{8,9,10}
sinR	2427247	2427588	Master regulator of biofilm formation	Transcription control of biofilm formation ^{8,9,10}
sinI	2427046	2427219	SinR antagonist	Transcription control of biofilm formation ^{8,9,10}
ybdK	479816	480583	Hypothetical protein	Transcription control of biofilm formation ^{8,9,10}
ycbA	256238	257479	Sensor histidine kinase	Transcription control of biofilm formation ^{8,9,10}
lys	2722139	2720358	Sensor histidine kinase controlling autolysis	Transcription control of biofilm formation ^{8,9,10}
epsA-O	3285390	3274560	Operon for capsular poly-saccharide biosynthesis	Exopolysaccharide necessary for biofilm formation controlled by sinR ¹⁰
yixB	936650	938392	Putative phosphohexomutase	Likely involved in exopolysaccharide synthesis ¹¹
yqxM	2429713	2429042	Hypothetical protein	Member of yqxM-sfpW-tasA operon, essential for biofilm formation and controlled by sinR ¹¹
sfpW	2429070	2428486	Type I signal peptidase	Impaired in processing of TasA ¹¹

Gene	From	To	Protein	Remark
tasA	2428421	2427636	Spore coat associated protein	Required for development of complex colony architecture ¹¹ Protein secretion to extracellular matrix ⁸ Predicted role in NAD metabolism ⁸ Control of community development ⁸ Control of community development ⁸
ecsABC	1006147	1008856	ABC multidrug transport	
yqeK	2514458	2513898	Putative HD phosphatase	
yJbF	1485947	1486396	Positive regulator of ComK	
ymcA	1694164	1694595	Hypothetical protein	
Bacterial target molecules for general plant immune response				
flgK	3371542	3375059	Flagellin HAP1	Involved in elicitation of plant basal defence ¹² , repression by exudates ¹⁷
flfD	3366502	3368049	Flagellin HAP2	Involved in elicitation of plant basal defence ¹² , upregulation by exudate ¹⁷
hag	3369130	3368360	Flagellin HAG	Involved in elicitation of plant basal defence ¹² , upregulation by exudate ¹⁷
tufA	133588	134778	Elongation factor EF-Tu	Involved in elicitation of plant basal defence ¹²
RBAM03209- RBAM03201	3234773	3225710	Unknown operon probably involved in lipopoly- saccharide biosynthesis	Involved in elicitation of plant basal defence ¹²
tuaA-tagO	3392102	3382000	Operon involved in teichuronic acid/lipopoly-saccharide biosynthesis	Involved in elicitation of plant basal defence ¹²
Biofertilization: Mineral availability (Iron, phosphate)				
RBAM03694	3683843	3684737	Iron compound ABC transporter	deficient in biofilm formation (A. Bhutari unpublished) Phosphate availability ¹³ , up-regulated by exudates ¹⁷ Transport/binding proteins and lipoproteins
yvC	3143421	3144365	Putative iron binding protein	
yusV	3120088	3119264	Putative iron(III) ABC transport ATPase component	
phy	2077791	2078942	phytase	
ydQ	405741	406688	Ferrichrome ABC transporter	
Breakdown, transport and utilization of plant derived substrates: Celluloses and hemicelluloses				
xynA	1872057	1870519	xylanase	Extracellular degradation of plant cell walls
xynD	3492633	3493274	xylanase	Extracellular degradation of plant cell walls
xynP	1798060	1799451	hypothetical symporter	Transport of oligosaccharides
xynB	1799494	1799451	Xylan beta-1,4-xylosidase	Carbohydrate metabolism
lacR	1183963	1190647	lactose phosphotransferase system repressor protein	COG1349, GlpR ¹⁸
lacG	1189633	1188233	Putative 6-phospho-beta-galactosidase	pfam00232, Glyco_hydro_1, Glycosyl hydrolase family ¹
lacE	1188169	1187855	Phosphotransferase system	cellobiose-specific component IIA
lacF	1187843	1186146	Phosphotransferase system	cellobiose-specific component IIB C
galK1	1186130	1184961	Galactokinase galK1	cellobiose-specific component IIB C
galE1	1184957	1183965	UDP-glucose 4-epimerase	cellobiose-specific component IIB C
galT1	1183963	1182464	Galactose-1-phosphate uridy/transferase	cellobiose-specific component IIB C
ganA	1182412	1181300	arabinogalactan endo-1,4-beta-galactosidase	Extracellular degradation of plant cell walls

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Protein</i>	<i>Remark</i>
pgm	1190656	1191348	Predicted phosphoglucomutase	COG0637, Predicted phosphatase/phosphohexomutase
pel	762046	763311	Pectate lyase	COG3866, PelB, Pectate lyase
yHfE	1022710	1023750	glucanase/aminopeptidase	
bgIC	1866112	1864613	Endo-1,4-beta-glucanase	
ysdC	2715972	2714887	Putative endo-1,4-beta-glucanase	COG1363, FvX, Cellulase M and related proteins
bgIS	3724830	3724099	endo-beta-1,3-1,4 glucanase	plam00722, Glyco_hydro_16, Glycosyl hydrolases family ¹⁷
Breakdown, transport and utilization of plant derived substrates: Chitin, chitosan				
csn	3091485	3092319	chitosanase	Downregulated by exudate
Breakdown, transport and utilization of plant derived substrates: Proteins and peptides				
bpr	1515288	1519581	Bacillopeptidase F	Upregulation by exudate
ggt	1977020	1978793	glutamyltranspeptidase	Upregulation by exudates
Breakdown, transport and utilization of plant derived substrates: Opines				
yckK	378118	377321	Probable amino-acid ABC transporter extracellular binding protein	
yckJ	377319	376630	HisM, ABC-type amino acid transport system, permease	Octopin permease occM (31%)
yckI	376617	375874	ABC-type polar amino acid transport system	OccP A, tumefaciens (43%)
ytmJ	3195045	3198329	amino acid ABC transporter, amino acid-binding protein	periplasmic binding proteins (PBBs)
ytmK	3198303	3197491	amino acid ABC transporter, amino acid-binding protein, periplasmic binding proteins (PBBs)	
ytmL	3196746	3197468	His/Glu/Gln/Arg/opine family putative amino-acid ABC transporter ATP-binding protein	Octopin permease occM (33%)
ytmM	3196730	3196023	Amino acid ABC transporter, permease protein, 3-TM	Octopin permease occM (30%)
ytmN	3196026	3195247	HisP and GlnQ are the ATP-binding components of the bacterial periplasmic histidine and glutamine permeases	
yxeN	3927774	3934448	Amino acid ABC transporter, permease protein, 3-TM region, His/Glu/Gln/Arg/opine	Octopin permease occM (33%)
RBAM03043	3090827	3090108	COG2226, UbiE, Methylase involved in ubiquinone/menaquinone biosynthesis	possible methyltransferase
yurR	3090070	3088955	COG0665, Dada, Glycine/D-amino acid oxidases (deaminating)	22% 48/209 AgaE (A. tumefaciens)
RBAM03038	3086818	3087744	Helix-turn-helix transcription regulator	
yurP	3086621	3085635	AgaS, Predicted phosphosugar isomerase	opine catabolism protein-like [Sinorhizobium medicae] (46%)
yurO	3085582	3084296	ABC-type sugar transport system, periplasmic component	extracellular solute-binding protein, family
yurN	3084271	3083381	ABC sugar transporter, inner membrane subunit	
yurM	3083377	3082493	ABC sugar transporter, inner membrane subunit	UgpE, ABC-type sugar transport system, permease component
yurL	3082479	3081625	cd01940, Fructose-lysine_kinase_like	37% 102/269 chdE (A. tumefaciens), 37% 100/270 mocE [A. tumefaciens]

<i>Gene</i>	<i>To</i>	<i>Protein</i>	<i>Remark</i>
yurK	3080872	pfam00392, GntR, Bacterial regulatory proteins	Transcription regulator
yurJ	3080716	MalK, ABC-type sugar transport systems, ATPase component	COG3839, MalK, ABC-type sugar transport systems,ATPase
Production of phytohormones and other compounds involved in phytostimulation and ISR			
dhaS	2023838	Putative indole-3-acet-aldehyde dehydrogenase	Involved in Trip-dependent IAA synthesis in FZB 42. Knock out mutants in the respective genes were found impaired in IAA synthesis and plant growth ¹⁴
ysnE	3641549	Putative IAA acetyl-transferase	Involved in Trip-dependent IAA synthesis in FZB 42. Knock out mutants in the respective genes were found impaired in IAA synthesis and plant growth ¹⁴
yhcX	928472	nitrilase	Involved in Trip-dependent IAA synthesis in FZB 42. Knock out mutants in the respective genes were found impaired in IAA synthesis and plant growth ¹⁴
alsD	34338021	Acetolactate decarboxylase	Involved in synthesis of 2,3-butanediol ¹⁵
alsS	3439797	Acetolactate synthase S	Involved in synthesis of 2,3-butanediol ¹⁵
alsR	3439951	LysR transcriptional regulator	Regulator of the alsDS operon ¹⁶
Response to environmental stress			
tpx	2771642	Thiol peroxidase	Upregulation by exudate ¹⁷
cspC	522629	Cold shock protein	Adaptation to atypical conditions, involved in elicitation of plant basal defence ¹²
cspB	915954	Major cold shock protein	Adaptation to atypical conditions, involved in elicitation of plant basal defence ¹²
cspD	2114744	Cold shock protein	Adaptation to atypical conditions, involved in elicitation of plant basal defence ¹²
cspR	901609	Putative rRNA methylase	Adaptation to atypical conditions, involved in elicitation of plant basal defence ¹²
sodA	2457322	Superoxide dismutase	repression by exudate ¹⁷
Other genes affected by plant exudate			
pla	3589028	phosphotransacetylase	Strongly upregulated by exudate ¹⁷
ycyO	3826461	Hypothetical protein	Expressed in presence of soil extract ¹⁷
yfE	782563	Hypothetical protein	repression by exudate ¹⁷

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Supplementary Table 6. Secretion proteins with Tat (RR_SP), Sip/SipV, SPase I and SPase II or without known signal peptides

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>2D/MS</i>	<i>Product</i>	<i>Function</i>
<i>RR_SP</i> phoD	264912	266661		Phosphodiesterase/alkaline phosphatase phoD	Intermediary metabolism; Metabolism of phosphate
yeaA lipoproteins	286352	287189		Putative zinc ABC transporter, permease protein	Cell envelope and cellular processes; Transport/binding proteins and
yfjN	793223	797515	x	Putative multifunctional phosphoesterase yfjN	Intermediary metabolism; Metabolism of nucleotides and nucleic acids
yhcR TM	923053	924880	x	Putative 5'-nucleotidase yhcR	Intermediary metabolism; Metabolism of nucleotides and nucleic acids
appB TM lipoproteins	1117307	1118255		Oligopeptide transport system permease protein appB	Cell envelope and cellular processes; Transport/binding proteins and
oppB lipoproteins	1123603	1124536		Oligopeptide ABC transporter (permease) oppB	Cell envelope and cellular processes; Transport/binding proteins and
ykuE	1348809	1349624		putative phosphoesterase ykuE	Unknown; Similar to unknown proteins from B. subtilis
ykpC	1381115	1381249		Hypothetical protein ykpC	Unknown; Similar to unknown proteins from B. subtilis
pbpX	1685646	1686825		Penicillin-binding protein pbpX	Cell envelope and cellular processes; Cell wall
ymaC	1778120	1778825		Phage- replication protein homolog ymaC	Other functions; Phage-related functions
qcrA (electron transport chain and	2172317	2172820		Menaquinol-cytochrome c reductase iron-sulfur subunit	Cell envelope and cellular processes; Membrane bioenergetics
tlpA	2947095	2949083		(Rieske iron-sulfur protein) qcrA	ATP synthase
lipA groups	3063003	3063899		Methyl-accepting chemotaxis protein tlpA	Cell envelope and cellular processes; Mobility and chemotaxis
yvhJ TM	3380681	3381899		Lipoic acid synthetase lipA	Intermediary metabolism; Metabolism of coenzymes and prosthetic
<i>Sip/SipV</i> yfiI lipoproteins	738025	739951		Putative transcriptional regulator yvhJ	Information pathways; RNA synthesis; Regulation
				putative phosphoglycerol transferase yfiI	Cell envelope and cellular processes; Transport/binding proteins and

Supplementary Tables

<i>Gene</i> <i>RR_SP</i>	<i>From</i>	<i>To</i>	<i>2D/MS</i>	<i>Product</i>	<i>Function</i>
dacA	17316	18645		Serine-type D-ala-D-ala carboxypeptidase dacA	Cell envelope and cellular processes; Cell wall
cwlD	157468	158179		N-acetylmuramoyl-L-alanine amidase cwlD	Cell envelope and cellular processes; Cell wall
ybbC	191095	192339		Conserved hypothetical protein ybbC	Unknown; Similar to unknown proteins from B. subtilis
ybbE	194315	195598		Putative beta-lactamase ybbE	Other functions; Detoxification
ybbR	202092	203529		Conserved hypothetical protein ybbR	Unknown; Similar to unknown proteins from B. subtilis
yolA1	227356	227830	x	Hypothetical protein yolA1	Unknown; Similar to unknown proteins from B. subtilis
glpQ	233319	234206	x	Glycerophosphoryl diester phosphodiesterase glpQ	Intermediary metabolism; Metabolism of lipids
RBAM00226	240910	241351	u	Hypothetical protein RBAM00226	Unknown; No similarity
lip	273071	273713	x	Triacylglycerol lipase lip	Intermediary metabolism; Metabolism of lipids
amyE molecules; Specific	302141	304118	x	alpha-amylase amyE	Intermediary metabolism; Metabolism of carbohydrates and related pathways
Mdr lipoproteins	305385	306917		Multidrug-efflux transporter mdr	Cell envelope and cellular processes; Transportbinding proteins and
lci	312066	312350		Putative antimicrobial peptide lci	Other functions; Antibiotic production
yckD	338332	338653		Hypothetical protein yckD	Unknown; Similar to unknown proteins from B. subtilis
ycnI	418648	419259		Conserved hypothetical protein ycnI	Unknown; Similar to unknown proteins from B. subtilis
RBAM00438	468123	468474	u	hypothetical protein RBAM00438	Unknown; Similar to unknown proteins from other organisms
ydbK	479816	480581		Hypothetical protein ydbK	Unknown; Similar to unknown proteins from B. subtilis
RBAM00614	626630	627017	u	Hypothetical protein RBAM00614	Unknown; Similar to unknown proteins from other organisms
ydjH	635897	636656		Conserved hypothetical protein ydjH	Unknown; Similar to unknown proteins from B. subtilis

<i>Gene</i> <i>RR_SP</i>	<i>From</i>	<i>To</i>	<i>2D/MS</i>	<i>Product</i>	<i>Function</i>
ydJM	642884	643250		Hypothetical protein ydJM	Unknown; Similar to unknown proteins from B. subtilis
ydJN	643318	644362		Hypothetical protein ydJN	Unknown; Similar to unknown proteins from B. subtilis
pel molecules: Specific	762046	763309	x	Pectate lyase pel	Intermediary metabolism; Metabolism of carbohydrates and related pathways
ylfE	782563	784500	x	Conserved hypothetical protein ylfE	Unknown; Similar to unknown proteins from B. subtilis
yfKD	808211	809000		Hypothetical protein yfKD	Unknown; Similar to unknown proteins from B. subtilis
pdaA molecules: Specific	811425	812214		Putative polysaccharide deacetylase pdaA	Intermediary metabolism; Metabolism of carbohydrates and related pathways
Mpr molecules	857973	858884		Extracellular metalloprotease precursor mpr	Intermediary metabolism; Metabolism of amino acids and related pathways
yfHK	859709	860234		Conserved hypothetical protein yfHK	Cell envelope and cellular processes; Cell division
yhdC	941296	941617		Hypothetical protein yhdC	Unknown; Similar to unknown proteins from B. subtilis
lyf ^W	941684	943118		Endopeptidase lyfF precursor lyfF	Cell envelope and cellular processes; Cell wall
phoA	946993	948372		Alkaline phosphatase IV precursor (APase IV) phoA	Intermediary metabolism; Metabolism of phosphate
lyfE ^W	948832	949654		cell wall hydrolase phosphatase-associated protein lyfE	Cell envelope and cellular processes; Cell wall
yhaK	1000771	1001301		Conserved hypothetical protein yhaK	Unknown; Similar to unknown proteins from B. subtilis
yhfM	1029796	1030191		Hypothetical protein yhfM	Unknown; Similar to unknown proteins from B. subtilis
aprE molecules	1031642	1032790	x	Serine alkaline protease (subtilisin E) aprE	Intermediary metabolism; Metabolism of amino acids and related pathways
RBAM01125	1127565	1128759	u	Conserved hypothetical protein RBAM01125	Unknown; Similar to unknown proteins from other organisms

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>2D/MS</i>	<i>Product</i>	<i>Function</i>
blm	1158209	1158956	x	Beta-lactamase II precursor (Penicillinase) (Cephalosporinase) blm	Other functions; Detoxification
penP	1177569	1178481	x	Beta-lactamase precursor penP	Other functions; Detoxification
ganA molecules; Specific	1181300	1182412	x, u	Predicted arabinogalactan endo-1,4-beta-galactosidase ganA	Intermediate metabolism; Metabolism of carbohydrates and related pathways
phrA	1218239	1218371		Phosphatase rapA inhibitor phrA	Cell envelope and cellular processes; Sporulation
htrA	1238614	1239966		Putative serine protease do-like htrA	Other functions; Adaptation to atypical conditions
motB	1307170	1307955		motility protein motB	Cell envelope and cellular processes; Mobility and chemotaxis
ykvT	1319951	1320572		Spore cortex-lytic enzyme ykvT	Cell envelope and cellular processes; Germination
stoA	1322093	1322585		Sporulation thiol-disulfide oxidoreductase A precursor stoA	Cell envelope and cellular processes; Sporulation
RBAM01373	1337557	1337946	u	Hypothetical protein RBAM01373	Unknown; No similarity
ykwD	1338334	1339119		Conserved hypothetical protein ykwD	Unknown; Similar to unknown proteins from B. subtilis
yknX	1369051	1370185		Putative secretion protein yknX	Unknown; Similar to unknown proteins from B. subtilis
nprE molecules	1457924	1459489	x	Bacillolysin precursor nprE	Intermediate metabolism; Metabolism of amino acids and related
ylaE	1462857	1463474		Hypothetical protein ylaE	Unknown; Similar to unknown proteins from B. subtilis
yblL	1490278	1491298		conserved hypothetical protein yblL	Unknown; Similar to unknown proteins from B. subtilis
pbpB	1499462	1501604		Penicillin-binding protein IIB pbpB	Cell envelope and cellular processes; Cell wall
bpr molecules	1515288	1519581	x	bacillopeptidase F precursor bpr	Intermediate metabolism; Metabolism of amino acids and related
yxF	1614116	1614728		Conserved hypothetical protein yxF	Unknown; Similar to unknown proteins from B. subtilis
filL	1617573	1617990		Flagellar protein filL	Cell envelope and cellular processes; Mobility and chemotaxis

<i>Gene</i>	<i>From</i>	<i>to</i>	<i>2D/MS</i>	<i>Product</i>	<i>Function</i>
flhZ	1620554	1621205		Flagellar biosynthetic protein flhZ precursor	Cell envelope and cellular processes; Mobility and chemotaxis ylyY 1657809 1658766 Putative deacetylase ylyY Intermediary metabolism; Metabolism of carbohydrates and related pathways
nucB	1774286	1774718		Sporulation-specific extracellular nuclease precursor nucB	Intermediary metabolism; Metabolism of nucleotides and nucleic acids
RBAM01763	1809727	1810149	u	Hypothetical protein RBAM01763	Unknown; Similar to unknown proteins from other organisms
yoaW	1812970	1813213		Hypothetical protein yoaW	Unknown; Similar to unknown proteins from B. subtilis
RBAM01776	1819258	1819876	x, u	Putative chitin binding protein RBAM01776	Unknown; Similar to unknown proteins from other organisms
RBAM01779	1820922	1821458	u	Hypothetical protein RBAM01779	Unknown; Similar to unknown proteins from other organisms
RBAM01786	1828266	1828692	u	Hypothetical protein RBAM01786	Unknown; No similarity
RBAM01835	1862637	1862946	u	Hypothetical protein RBAM01835	Unknown; No similarity
bgIC molecules; Specific	1864613	1866112		Endo-1,4-beta-glucanase bgIC	Intermediary metabolism; Metabolism of carbohydrates and related pathways
ynfF molecules; Specific	1869186	1870457	x	Conserved hypothetical protein ynfF	Intermediary metabolism; Metabolism of carbohydrates and related pathways
yngK	1930425	1931963		Conserved hypothetical protein yngK	Unknown; Similar to unknown proteins from B. subtilis
yoaB	1974882	1975422		Hypothetical protein yoaB	Unknown; Similar to unknown proteins from B. subtilis
ggt groups	1977020	1978793	x	Gamma-glutamyltranspeptidase ggt	Intermediary metabolism; Metabolism of coenzymes and prosthetic
yocA	2013278	2013941		Conserved hypothetical protein yocA	Other functions; Transposon and IS
yocH ^w	2017794	2018663		Putative cell-wall binding protein yocH	Cell envelope and cellular processes; Sensors (signal transduction)
yojL ^w	2039446	2040687		Conserved hypothetical protein yojL	Cell envelope and cellular processes; Cell wall
phy	2077791	2078842	x	3-phylase precursor (Myo-inositol-hexaphosphate 3- phosphohydrolase) phy	Intermediary metabolism; Metabolism of phosphate

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
yoqH	2082024	2082476	Hypothetical protein [Bacteriophage SPBcc2] yoqH		Other functions; Phage-related functions
ypmS	2097947	2098510	Hypothetical protein ypmS		Unknown; Similar to unknown proteins from B. subtilis
ypjP	2105538	2106146	Hypothetical protein ypjP		Unknown; Similar to unknown proteins from B. subtilis
ypcP	2117828	2118715	Putative 5'-3' exonuclease ypcP		Information pathways; DNA replication
yqgA	2135748	2136212	Hypothetical protein yqgA		Unknown; Similar to unknown proteins from B. subtilis
aspB molecules	2154218	2155399	Aspartate aminotransferase (Transaminase A) aspB		Intermediary metabolism; Metabolism of amino acids and related
ypmB	2155422	2155907	Hyperthetical protein ypmB		Unknown; Similar to unknown proteins from B. subtilis
ypjB	2169291	2170073	Hypothetical protein ypjB		Unknown; Similar to unknown proteins from B. subtilis
tyrA molecules	2176957	2178063	Prephenate dehydrogenase tyrA		Intermediary metabolism; Metabolism of amino acids and related
sleB ^w	2205742	2206611	Spore cortex-lytic enzyme sleB		Cell envelope and cellular processes; Germination
ypbG	2210755	2211543	Conserved hypothetical protein ypbG		Unknown; Similar to unknown proteins from B. subtilis
dacB	2229164	2230315	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5) dacB		Cell envelope and cellular processes; Cell wall
ypuD	2237654	2237998	Hypothetical protein ypuD		Unknown; Similar to unknown proteins from B. subtilis
ypuA	2240259	2241159	Conserved hypothetical protein ypuA		Unknown; Similar to unknown proteins from B. subtilis
dacF	2249368	2250537	Penicillin binding protein (putative D-alanyl-D-alanine carboxypeptidase) dacF		Cell envelope and cellular processes; Cell wall
yqil	2386582	2387208	Putative N-acetylmuramoyl-L-alanine amidase yqil		Cell envelope and cellular processes; Cell wall
yqjG (electron transport chain and	2389780	2390899	Putative NADH-dependent flavin oxidoreductase yqjG		Cell envelope and cellular processes; Membrane bioenergetics
tasA	2427636	2428421	Spore coat-associated protein N (tasA)		ATP synthase
yqxM	2429042	2429713	Hypothetical protein yqxM		Cell envelope and cellular processes; Sporulation
					Unknown; Similar to unknown proteins from B. subtilis

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
yqzG	2429972	2430299		Hypothetical protein yqzG	Unknown; Similar to unknown proteins from B. subtilis
yqzC	2447273	2447735		Hypothetical protein yqzC	Unknown; Similar to unknown proteins from B. subtilis
pbpA	2453664	2455811		Penicillin-binding protein IIA (pbpA)	Cell envelope and cellular processes; Cell wall
yqzZ	2459590	2459890		Conserved hypothetical protein yqzZ	Unknown; Similar to unknown proteins from B. subtilis
ccaA (electron transport chain and	2470235	2470597		cytochrome c550 ccaA	Cell envelope and cellular processes; Membrane bioenergetics
spolIP	2503961	2505154		Stage II sporulation P (spolIP)	ATP synthase)
yrnS	2560716	2561432		Hypothetical protein yrnS	Cell envelope and cellular processes; Sporulation
yrnR	2561496	2563250		Putative penicillin-binding protein yrnR	Unknown; Similar to unknown proteins from B. subtilis
yrnL groups	2567700	2568791		Conserved hypothetical protein yrnL	Cell envelope and cellular processes; Cell wall
yrnJ	2590376	2591936		Putative N-acetylmuramoyl-L-alanine amidase yrnJ	Intermediary metabolism; Metabolism of coenzymes and prosthetic
mreC	2625522	2626385		Rod shape-determining protein mreC	Cell envelope and cellular processes; Cell wall
abnA molecules; Specific	2713780	2714745		Arabinan-endo 1,5-alpha-L-arabinase abnA	Cell envelope and cellular processes; Cell wall
yuaB	2933863	2934406	x	Hypothetical protein yuaB	Intermediary metabolism; Metabolism of carbohydrates and related pathways
yciN	2938356	2938676		Hypothetical protein yciN	Unknown; Similar to unknown proteins from B. subtilis
pbpD	2975335	2977207		Penicillin-binding protein IV pbpD	Unknown; Similar to unknown proteins from B. subtilis
yunA	3064102	3065077		Conserved hypothetical protein yunA	Cell envelope and cellular processes; Cell wall
yunB	3065117	3065875		Conserved hypothetical protein yunB	Unknown; Similar to unknown proteins from B. subtilis
bsn	3078691	3079558		Putative extracellular ribonuclease precursor bsn	Unknown; Similar to unknown proteins from B. subtilis
csn	3091485	3092319	x	Chitosanase csn	Intermediary metabolism; Metabolism of nucleotides and nucleic acids
					Intermediary metabolism; Metabolism of carbohydrates and related

molecules; Specific pathways				
Gene	From	To	Remark	Product Function
yusW	3120244	3120681	Hypothetical protein yusW	Unknown; Similar to unknown proteins from B. subtilis
ygo	3169480	3169963	Putative stress response protein precursor ygo	Unknown; Similar to unknown proteins from B. subtilis
ywaD yfc	3235039 3272441	3236343 3273049	Putative peptidase ywaD Conserved hypothetical protein yfc	Intermediary metabolism; Metabolism of amino acids and related mol. Intermediary metabolism; Metabolism of carbohydrates and related
yvcE ^w	3314395	3315807	Conserved hypothetical protein yvcE	Cell envelope and cellular processes; Cell wall
yvpB	3328337	3329060	Conserved hypothetical protein yvpB	Unknown; Similar to unknown proteins from B. subtilis
ynb	3335754	3339623	Conserved hypothetical protein ynb	Unknown; Similar to unknown proteins from B. subtilis
ywoF	3356065	3357489	Hypothetical protein ywoF	Unknown; Similar to unknown proteins from B. subtilis
lytC ^w	3392337	3393827	N-acetylmuramoyl-L-alanine amidase (major autolysin) (CWP49) lytC	Cell envelope and cellular processes; Cell wall
lytB ^w	3393849	3395969	Amidase enhancer precursor (Modifier protein of major autolysin) lytB	Cell envelope and cellular processes; Cell wall
lytR	3396500	3397415	Membrane-bound protein lytR	Information pathways; RNA synthesis; Regulation
lytD ^w	3408995	3411640	Beta-N-acetylglucosaminidase (major autolysin) (CWP90) lytD	Cell envelope and cellular processes; Cell wall
ywf	3419828	3420812	Putative transcriptional regulator ywf	Information pathways; RNA synthesis; Regulation
pgdS	3422703	3423938	Gamma-DL-glutamyl hydrolase precursor pgdS	Cell envelope and cellular processes; Cell wall
ywtC	3424089	3424250	Hypothetical protein ywtC	Unknown; Similar to unknown proteins from B. subtilis
ywsB	3435970	3436501	Conserved hypothetical protein ywsB	Unknown; Similar to unknown proteins from B. subtilis
ywqC	3463215	3463961	Conserved hypothetical protein ywqC	Other functions; Adaptation to atypical conditions
spoIIQ	3487554	3488423	Stage II sporulation protein Q (spoIIQ)	Cell envelope and cellular processes; Sporulation
xynA molecules: Specific	3492633	3493272	Endo-1,4-beta-xylanase A precursor xynA	Intermediary metabolism; Metabolism of carbohydrates and related pathways
x				

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
ywmD	3501260	3501940	Conserved hypothetical protein ywmD	Unknown;	Similar to unknown proteins from B. subtilis
ywmC	3502250	3502936	Conserved hypothetical protein ywmC	Unknown;	Similar to unknown proteins from B. subtilis
spolID	3503201	3504232	Stage II sporulation protein D (spolID)	Cell envelope	and cellular processes; Sporulation
ywmB	3505776	3506516	Hypothetical protein ywmB	Unknown;	Similar to unknown proteins from B. subtilis
spolIR	3521072	3521752	Stage II sporulation protein R (spolIR)	Cell envelope	and cellular processes; Sporulation
ywjE	3541811	3543008	Conserved hypothetical protein ywjE	Intermediary metabolism;	Metabolism of lipids
ywdK	3622954	3623325	Conserved hypothetical protein ywdK	Unknown;	Similar to unknown proteins from B. subtilis
ywcl	3633562	3633876	Hypothetical protein ywcl	Unknown;	Similar to unknown proteins from B. subtilis
vpr molecules	3634402	3636811	Minor extracellular protease vpr	Intermediary metabolism;	Metabolism of amino acids and related
epr molecules	3664569	3666312	Minor extracellular protease epr precursor	Intermediary metabolism;	Metabolism of amino acids and related
DlID	3672742	3673918	Undecaprenol-phosphate-poly(glycerophosphate chain) D-alanine transfer protein dlID	Cell envelope	and cellular processes; Cell wall
ydhT molecules; Specific	3691931	3693011	Putative Mannan endo-1,4-beta-mannosidase ydhT	Intermediary metabolism;	Metabolism of carbohydrates and related pathways
yxkC	3710528	3711164	Hypothetical protein yxkC	Unknown;	Similar to unknown proteins from B. subtilis
RBAM03730	3719141	3719815	Hypothetical protein RBAM03730	Unknown;	Similar to unknown proteins from other organisms
citH lipoproteins	3722777	3724055	Citrate transporter citH	Cell envelope	and cellular processes; Transport/binding proteins and
bgIS molecules; Specific	3724099	3724830	endo-beta-1,3-1,4 glucanase bgIS	Intermediary metabolism;	Metabolism of carbohydrates and related pathways
pelB molecules; Specific	3733237	3734301	Pectate lyase pelB	Intermediary metabolism;	Metabolism of carbohydrates and related pathways

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
yxA molecules: Specific	3743639	3745045		Conserved hypothetical protein yxA	Intermediary metabolism; Metabolism of carbohydrates and related pathways
yxaL	3797057	3798304	x	Conserved hypothetical protein yxaL	Information pathways; Protein modification
sacB molecules: Specific	3869505	3870924	x	Levansucrase sacB	Intermediary metabolism; Metabolism of carbohydrates and related pathways
yveB molecules: Specific	3871000	3872542		conserved hypothetical protein yveB	Intermediary metabolism; Metabolism of carbohydrates and related pathways
RBAM03730	3887944	3888439	x, u	Hypothetical protein RBAM03897	Unknown; No similarity
RBAM03897	3887944	3888439	x, u	Hypothetical protein RBAM03897	Unknown; No similarity
<i>SPase II</i> yacD	81431	82319		protein secretion protein prsA homolog yacD	Cell envelope and cellular processes; Protein secretion
gerD	159346	159903		Germination response protein precursor gerD	Cell envelope and cellular processes; Germination
feuA lipoproteins	188318	189274		Iron-binding protein feuA	Cell envelope and cellular processes; Transport/binding proteins and pathways
ybbD molecules: Specific	192355	194268		Putative Beta-hexosaminidase ybbD	Intermediary metabolism; Metabolism of carbohydrates and related pathways
RBAM00219	231612	232812	u	Hypothetical protein RBAM00219	Unknown; Similar to unknown proteins from other organisms
ycbU	268376	269501		Putative selenocysteine lyase ycbU	Other functions; Miscellaneous
yccC molecules	271759	272872		Putative asparaginase yccC	Intermediary metabolism; Metabolism of amino acids and related pathways
ycdA	276029	277024		Hypothetical protein ycdA	Unknown; Similar to unknown proteins from B. subtilis
ycdD	280107	280610		hypothetical protein ycdD	Other functions; Phage-related functions
ycdH lipoproteins	284685	285642		Putative high-affinity zinc ABC transporter (Zn (II) -binding lipoprotein)	Cell envelope and cellular processes; Transport/binding proteins and pathways

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
opuAC lipoproteins	297727	298606	Glycine betaine ABC transporter (glycine betaine-binding protein) opuAC	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
yckK lipoproteins	377321	378118	Probable amino-acid ABC transporter extracellular binding protein yckK	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
gerKC	387563	388787	Germination response protein gerKC	Cell envelope and cellular processes; Germination	Cell envelope and cellular processes; Germination
yxzM lipoproteins	391960	392749	Putative amino-acid ABC transporter binding protein yxmM	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
yclQ lipoproteins	407462	408404	Putative ferrichrome ABC transporter (periplasmic binding protein) ydQ	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
pbpC	433875	435876	Penicillin-binding protein III pbpC	Cell envelope and cellular processes; Cell wall	Cell envelope and cellular processes; Cell wall
ydaJ	448419	449502	Hypothetical protein ydaJ	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
ydcC	491805	492810	Conserved hypothetical protein ydcC	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
ydhK	593155	593752	Hypothetical protein ydhK	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
ydiK	619528	619719	hypothetical lipoprotein ydiK precursor	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
yerB	676867	677860	Hypothetical protein yerB	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
yerH	684995	686189	Hypothetical protein yerH	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
yfnG	740940	741906	Putative CDR-glucose 4,6-dehydratase yfnG	Cell envelope and cellular processes; Cell wall	Cell envelope and cellular processes; Cell wall
ybfJ	857621	858010	Hypothetical protein ybfJ	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis
ssuA lipoproteins	894239	895226	Putative aliphatic sulfonates binding protein precursor ssuA	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
yhcJ lipoproteins	916336	917164	Hypothetical lipoprotein yhcJ precursor	Cell envelope and cellular processes; Transport/binding proteins and	Cell envelope and cellular processes; Transport/binding proteins and
yhdN	920629	921166	Putative lipoprotein yhdN	Unknown; Similar to unknown proteins from B. subtilis	Unknown; Similar to unknown proteins from B. subtilis

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>	yhcS	925103	925697	Conserved hypothetical
protein yhcS	Unknown; Similar to unknown proteins from B. subtilis								
yhaR	990285	991050		Putative enoyl CoA hydratase yhaR	Intermediary metabolism; Metabolism of lipids				
prsA	999128	999979		Foldase protein prsA precursor	Cell envelope and cellular processes; Protein secretion				
yhfQ lipoproteins	1033280	1034156		Conserved hypothetical protein yhfQ	Cell envelope and cellular processes; Transport/binding proteins and				
ypd	1044865	1045578	x	Hypothetical protein ypd	Unknown; Similar to unknown proteins from B. subtilis				
yhjA	1045771	1046038		Hypothetical protein yhjA	Unknown; Similar to unknown proteins from B. subtilis				
RBAM01081	1085066	1086041	u	Conserved hypothetical protein RBAM01081	Unknown; Similar to unknown proteins from other organisms				
Med	1108749	1109700		Transcriptional activator protein med precursor med	Cell envelope and cellular processes; Transformation/competence				
appA lipoproteins	1115612	1117238		Oligopeptide-binding protein appA precursor	Cell envelope and cellular processes; Transport/binding proteins and				
oppA lipoproteins	1121862	1123494	x	Oligopeptide ABC transporter (binding protein) oppA	Cell envelope and cellular processes; Transport/binding proteins and				
yjgB	1195216	1195785		Hypothetical protein yjgB	Unknown; Similar to unknown proteins from B. subtilis				
dppE lipoproteins	1245715	1247332		Dipeptide-binding protein dppE precursor	Cell envelope and cellular processes; Transport/binding proteins and				
ykyA	1391954	1392590		Hypothetical protein ykyA	Unknown; Similar to unknown proteins from B. subtilis				
slp lipoproteins	1451788	1452162		Small peptidoglycan-associated lipoprotein slp	Cell envelope and cellular processes; Transport/binding proteins and				
RBAM01452 molecules: Specific	1452411	1453209	u	Putative polysaccharide deacetylase RBAM01452	Intermediary metabolism; Metabolism of carbohydrates and related pathways				
yjaJ	1466654	1467277		Hypothetical protein yjaJ	Unknown; Similar to unknown proteins from B. subtilis				
ctaC (electron transport chain and	1478095	1479163		Cytochrome c oxidase subunit II precursor ctaC	Cell envelope and cellular processes; Membrane bioenergetics ATP synthase)				
ymzC	1782391	1782664		Hypothetical protein ymzC	Unknown; Similar to unknown proteins from B. subtilis				

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
yoaO	1816094	1816571	Hypothetical protein yoaO	Unknown;	Similar to unknown proteins from B. subtilis
yneA	1829809	1830118	Hypothetical protein yneA	Unknown;	Similar to unknown proteins from B. subtilis
xyuD TM molecules, Specific	1870519	1872057	Endo-1,4-beta-xylanase D precursor xyuD	Intermediary metabolism;	Metabolism of carbohydrates and related pathways
yojM	2038775	2039365	Putative superoxide dismutase yojM	Other functions;	Detoxification
yodJ	2060957	2061775	Putative D-alanyl-D-alanine carboxypeptidase yodJ	Cell envelope and cellular processes;	Cell wall
yobA	2080255	2080608	Hypothetical protein yobA	Unknown;	Similar to unknown proteins from B. subtilis
ypmR	2098520	2099275	Conserved hypothetical protein ypmR	Unknown;	Similar to unknown proteins from B. subtilis
ypmQ (electron transport chain and	2099353	2099976	Conserved hypothetical protein ypmQ	Cell envelope and cellular processes;	Membrane bioenergetics
yphF	2195527	2196261	Hypothetical protein yphF	ATP synthase)	
yqjG TM	2358588	2359422	Putative lipoprotein SpoIIJ-like protein yqjG	Unknown;	Similar to unknown proteins from B. subtilis
yqjX lipoproteins	2365877	2366644	Putative amino acid ABC transporter (binding protein) yqjX	Cell envelope and cellular processes;	Transport/binding proteins and
yqjH lipoproteins	2387227	2387520	Hypothetical protein yqjH	Cell envelope and cellular processes;	Transport/binding proteins and
spoIVB	2394167	2395447	stage IV sporulation protein spoIVB	Cell envelope and cellular processes;	Sporulation
yqhB	2435789	2437088	Conserved hypothetical protein yqhB	Other functions;	Miscellaneous
yqgU	2440386	2441438	Hypothetical protein yqgU	Unknown;	Similar to unknown proteins from B. subtilis
psIS lipoproteins	2451317	2452219	Phosphate ABC transporter (binding protein) psIS	Cell envelope and cellular processes;	Transport/binding proteins and
yqeF	2518636	2519367	Conserved hypothetical protein yqe	Unknown;	Similar to unknown proteins from B. subtilis
glnH lipoproteins	2574971	2575796	Glutamine ABC transporter (glutamine-binding protein) glnH	Cell envelope and cellular processes;	Transport/binding proteins and

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
bofC	2608695	2609204	Bypass-of-forespore protein C (bofC)	Cell envelope and cellular processes; Sporulation	
	2666709	2667794	Germination protein gerM	Cell envelope and cellular processes; Germination	
araN lipoproteins	2706442	2707737	Probable arabinose-binding protein precursor araN	Cell envelope and cellular processes; Transport/binding proteins and	
msmE lipoproteins	2846094	2847369	Multiple sugar-binding protein msmE	Cell envelope and cellular processes; Transport/binding proteins and	
yrfF lipoproteins	2862595	2863905	Hypothetical protein yrfF	Cell envelope and cellular processes; Transport/binding proteins and	
RBAM02837	2887891	2888700	u	Glycerophosphoryl diester phosphodiesterase RBAM02837	Unknown; Similar to unknown proteins from other organisms
yfiA lipoproteins	2899622	2900624		Putative ABC-transport system substrate-binding protein yfiA	Cell envelope and cellular processes; Transport/binding proteins and
yfkA	2904119	2904562		Hypothetical protein yfkA	Unknown; Similar to unknown proteins from B. subtilis
yufN lipoproteins	2981094	2982165		Hypothetical lipoprotein yufN	Cell envelope and cellular processes; Transport/binding proteins and
yuiC	3037172	3037813		Conserved hypothetical protein yuiC	Unknown; Similar to unknown proteins from B. subtilis
yurO lipoproteins	3084296	3085582		Multiple sugar-binding extracellular protein yurO	Cell envelope and cellular processes; Transport/binding proteins and
yusA	3098535	3099350		Conserved hypothetical protein yusA	Unknown; Similar to unknown proteins from B. subtilis
gerAC	3133376	3134486		Spore germination protein A3 (gerAC)	Cell envelope and cellular processes; Germination
yvrC lipoproteins	3143421	3144365		Putative iron-binding protein yvrC	Cell envelope and cellular processes; Transport/binding proteins and
fhuD and lipoproteins	3155062	3155998		Ferrichrome ABC transporter (ferrichrome binding protein) fhuD	Cell envelope and cellular processes; Transport/binding proteins
yvgL lipoproteins	3161762	3162557		Putative molybdate-binding protein yvgL	Cell envelope and cellular processes; Transport/binding proteins and

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
ymk lipoproteins	3197491	3198303	Putative amino-acid ABC transporter (extracellular binding protein) ymk	Cell envelope and cellular processes;	Transport/binding proteins and
ymJ lipoproteins	3198329	3199045	Putative amino acid ABC transporter (substrate-binding protein) ytmJ	Cell envelope and cellular processes;	Transport/binding proteins and
opBC lipoproteins	3213584	3214501	Choline ABC transporter (choline-binding protein) opBC	Cell envelope and cellular processes;	Transport/binding proteins and
opUC lipoproteins	3217878	3218795	glycine betaine/carnitine/choline ABC transporter (osmoprotectant-binding protein) opuCC	Cell envelope and cellular processes;	Transport/binding proteins and
cccB (electron transport chain and	3359326	3359667	Cytochrome c551 (cccB)	Cell envelope and cellular processes;	Membrane bioenergetics
LyfA	3396002	3396319	Membrane bound lipoprotein lyfA	ATP synthase)	
gerBC	3415510	3416638	Spore germination protein BC (gerBC)	Cell envelope and cellular processes;	Protein secretion
gerKC1	3429025	3430156	Putative spore germination protein gerKC1	Cell envelope and cellular processes;	Germination
u				Cell envelope and cellular processes;	Sporulation
rbkB lipoproteins	3434992	3435907	Ribose ABC transporter (ribose-binding protein) rtsB	Cell envelope and cellular processes;	Transport/binding proteins and
ymnJ	3487040	3487462	Conserved hypothetical protein ymnJ	Unknown;	Similar to unknown proteins from B. subtilis
qxAX TM (electron transport chain and	3645580	3646545	Quinol oxidase subunit II precursor qoxA	Cell envelope and cellular processes;	Membrane bioenergetics
RBAM03694 lipoproteins	3683843	3684737	Iron compound ABC transporter, substrate-binding protein RBAM03694	ATP synthase)	
u				Cell envelope and cellular processes;	Transport/binding proteins and
yxkH	3706057	3706899	Conserved hypothetical protein yxkH	Unknown;	Similar to unknown proteins from B. subtilis
yxEF	3758553	3758969	Hypothetical protein yxeF	Unknown;	Similar to unknown proteins from B. subtilis
yxEB	3760564	3761524	putative ABC transporter (binding protein) yxeB	Cell envelope and cellular processes;	Transport/binding proteins and

Supplementary Tables

lipoproteins

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
yxmA	3762864	3763211	Hypothetical protein yxA	Unknown	Similar to unknown proteins from B. subtilis
ycpP	3824538	3825701	Hypothetical protein ycpP	Unknown	Similar to unknown proteins from B. subtilis
ycyO	3825712	3826461	Conserved hypothetical protein ycyO	Unknown	Similar to unknown proteins from B. subtilis
spoIIJ ^{PR} , TM	3914884	3915673	Stage III sporulation protein J (spoIIJ)	Cell envelope and cellular processes; Sporulation	
<i>without signal peptide</i> fusA	133466		Elongation factor G fusA	Information pathways; Protein synthesis; Elongation	
	320791		1-pyrolidine-5-carboxylate dehydrogenase like protein ycgN	Intermediary metabolism; Metabolism of amino acids and related	
ycgN molecules	319246				
groEL	621013	622645	Class I heat-shock protein (chaperonin) groEL	Information pathways; Protein folding	
yhdR molecules	960728	961910	Putative aspartate aminotransferase yhdR	Intermediary metabolism; Metabolism of amino acids and related	
fabF	1111281	1112517	Beta-ketoacyl-acyl carrier protein synthase II fabF	Intermediary metabolism; Metabolism of lipids	
pdhA molecules, Main glycolytic	1446775	1447888	Pyruvate dehydrogenase E1 alpha subunit pdhA	Intermediary metabolism; Metabolism of carbohydrates and related pathways	
pdhB molecules, Main glycolytic	1447894	1448869	Pyruvate dehydrogenase E1 beta subunit pdhB	Intermediary metabolism; Metabolism of carbohydrates and related pathways	
pdhD molecules, Main glycolytic	1450328	1451738	Dihydrolipoamide dehydrogenase E3 subunit pdhD	Intermediary metabolism; Metabolism of carbohydrates and related pathways	
bcd	2374286	2375380	Leucine dehydrogenase bcd	Intermediary metabolism; Metabolism of lipids	
sodA	2457322	2457927	Superoxide dismutase [Mn] sodA	Other functions; Detoxification	
mdh molecules; TCA cycle	2742618	2743556	Malate dehydrogenase mdh	Intermediary metabolism; Metabolism of carbohydrates and related	
tpx	2771642	2772145	Thiol peroxidase tpx	Other functions; Detoxification	

Supplementary Tables

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Remark</i>	<i>Product</i>	<i>Function</i>
ald molecules	3017110	3018238	x Alanine dehydrogenase ald		Intermediary metabolism; Metabolism of amino acids and related
eno molecules; Main glycolytic	3236488	3237780	x Enolase (2-phosphoglycerate dehydratase) eno		Intermediary metabolism; Metabolism of carbohydrates and related pathways
pgm molecules; Main glycolytic	3237808	3239343	x 2,3-bisphosphoglycerate-independent phosphoglycerate mutase pgm		Intermediary metabolism; Metabolism of carbohydrates and related pathways
flhD	3366502	3368049	x Flagellar hook-associated protein II (HAPII) flhD		Cell envelope and cellular processes; Mobility and chemotaxis
hag	3368300	3369130	x Flagellin protein hag		Cell envelope and cellular processes; Mobility and chemotaxis
flgK	3371542	3373059	x Flagellar hook-associated protein I (HAPI) flgK		Cell envelope and cellular processes; Mobility and chemotaxis
RBAM03430	3453269	3453595	x u Hypothetical protein RBAM03430		Unknown; Similar to unknown proteins from other organisms
pta molecules; Specific	3589028	3589999	x Phosphotransacetylase pta		Intermediary metabolism; Metabolism of carbohydrates and related pathways
❖ Proteins lacking a (putative) SPase I cleavage site, some of which contain additional transmembrane domains, are indicated with a superscript TM; Proteins containing cell wall binding repeats are indicated with a superscript W.					
❖ "x" stands for experimental identified by the proteomics; "u" stands for unique gene in comparison with <i>B. subtilis</i> 168.					

Supplementary Table 7. Competence genes.

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Gene Product</i>	<i>Function Category</i>	<i>Identity</i>
<i>structural components</i>					
nin	340236	340634	Inhibitor of the DNA degrading activity of NucA (competence)	Intermediary metabolism; Metabolism of nucleotides and nucleic acids	75%
nucA	340655	341092	Membrane-associated nuclease nucA	Intermediary metabolism; Metabolism of nucleotides and nucleic acids	73%
smf	1599070	2430970	Putative DNA processing protein smf	Cell envelope and cellular processes; Transformation/competence	67%
comGG	2430577	2430954	DNA transport machinery protein comGG	Cell envelope and cellular processes; Transformation/competence	51%
comGF	2430955	2431455	Probably part of the DNA transport machinery comGF	Cell envelope and cellular processes; Transformation/competence	46%
comGE	2431364	2431678	DNA transport machinery protein comGE	Cell envelope and cellular processes; Transformation/competence	42%
comGD	2431662	2432099	DNA transport machinery protein comGD	Cell envelope and cellular processes; Transformation/competence	47%
comGC	2432089	2432397	Exogenous DNA-binding (competence) comGC	Cell envelope and cellular processes; Transformation/competence	62%
comGB	2432402	2433439	DNA transport machinery protein comGB	Cell envelope and cellular processes; Transformation/competence	59%
comGA	2433426	2434496	Protein required for exogenous DNA-binding (competence) comGA	Cell envelope and cellular processes; Transformation/competence	82%
comEC	2508240	2510591	Putative integral membrane protein comEC	Cell envelope and cellular processes; Transformation/competence	50%
comEB	2510592	2511161	Protein required for DNA binding and uptake (competence) comEB	Cell envelope and cellular processes; Transformation/competence	90%
comEA	2511228	2511842	Unspecific high-affinity DNA-binding protein comEA	Cell envelope and cellular processes; Transformation/competence	57%
comER	2511901	2512720	competence protein comER	Cell envelope and cellular processes; Transformation/competence	79%
comC	2630086	2630838	Type 4 prepilin-like proteins leader peptide-processing enzyme comC	Cell envelope and cellular processes; Transformation/competence	54%
comFC	3374401	3375078	Competence protein FC (comFC)	Cell envelope and cellular processes; Transformation/competence	59%
comFB	3375096	3375380	competence protein FB (comFB)	Cell envelope and cellular processes; Transformation/competence	67%
comFA	3375438	3376823	Late competence protein comFA	Cell envelope and cellular processes; Transformation/competence	62%
ssb	3900060	3900578	Single-strand DNA-binding protein (Helix-destabilizing protein) ssb	Information pathways; DNA replication	75%
<i>regulatory components</i>					
abrB	45611	45895	Transcriptional regulator abrB	Information pathways; RNA synthesis; Regulation	98%
clpC	104295	106725	Class III stress response-related ATPase clpC	Other functions; Adaptation to atypical conditions	95%
srfAA	343826	354578	surfactin synthetase A srfAA	Other functions; Antibiotic production; surfactin biosynthesis	72%
srfAB	354602	365360	surfactin synthetase B srfAB	Other functions; Antibiotic production; surfactin biosynthesis	75%
comS	357711	357873	Competence protein S comS	Cell envelope and cellular processes; Transformation/competence	61%
srfAC	365397	369231	surfactin synthetase C srfAC	Other functions; Antibiotic production; surfactin biosynthesis	85%
srfAD	369253	369982	surfactin synthetase D srfAD	Other functions; Antibiotic production; surfactin biosynthesis	79%
rapC	401430	402576	Response regulator aspartate phosphatase rapC	Cell envelope and cellular processes; Sporulation	82%
phrC	402568	402679	phosphatase (RapC) regulator/competence and sporulation stimulating factor (CSF) phrC	Cell envelope and cellular processes; Sporulation	60%
sigB	498425	499211	RNA polymerase sigma-B factor (Sigma-37) (General stress protein 84) (GSP84) sigB	Information pathways; RNA synthesis; Initiation	91%
comK	1042514	1043090	Competence transcription factor (CTF) comK	Information pathways; RNA synthesis; Regulation	82%
med	1108749	1109700	Transcriptional activator protein med precursor med	Cell envelope and cellular processes; Transformation/competence	78%

<i>Gene</i>	<i>From</i>	<i>To</i>	<i>Gene Product</i>	<i>Function Category</i>	<i>Identity</i>
comZ	1109715	1109904	ComG operon repressor comZ	Cell envelope and cellular processes; Transformation/competence	86%
oppA	1121882	1123494	Oligopeptide ABC transporter (binding protein) oppA	Cell envelope and cellular processes; Transport/binding proteins and lipoproteins	86%
oppB	1123603	1124536	Oligopeptide ABC transporter (permease) oppB	Cell envelope and cellular processes; Transport/binding proteins and lipoproteins	80%
oppC	1124542	1125457	Oligopeptide ABC transporter (permease) oppC	Cell envelope and cellular processes; Transport/binding proteins and lipoproteins	87%
oppD	1125472	1126546	Oligopeptide ABC transporter (ATP-binding protein) oppD	Cell envelope and cellular processes; Transport/binding proteins and lipoproteins	90%
oppF	1126541	1127456	Oligopeptide ABC transporter (ATP-binding protein) oppF	Cell envelope and cellular processes; Transport/binding proteins and lipoproteins	95%
mecA	1131012	1131666	Adapter protein mecA	Cell envelope and cellular processes; Transformation/competence	83%
ybfF	1485947	1486394	Conserved hypothetical protein ybfF	Cell envelope and cellular processes; Transformation/competence	87%
codY	1606607	1607384	GTP-sensing transcriptional pleiotropic repressor codY	Information pathways; RNA synthesis; Regulation	90%
pnpA	1655573	1657694	Polynucleotide phosphorylase (PNPase) pnpA	Intermediary metabolism; Metabolism of nucleotides and nucleic acids	95%
cinA	1683014	1684262	Competence-damage inducible protein cinA	Cell envelope and cellular processes; Transformation/competence	86%
ymcA	1694164	1694593	Conserved hypothetical protein ymcA	Unknown; Similar to unknown proteins from B. subtilis	91%
mecB	2210019	2210603	Negative regulator of genetic competence mecB	Cell envelope and cellular processes; Transformation/competence	77%
spo0A	2393086	2393886	Stage 0 sporulation protein A (spo0A)	Information pathways; RNA synthesis; Regulation	92%
sinI	2427046	2427219	SinR antagonist sinI	Cell envelope and cellular processes; Sporulation	70%
sinR	2427247	2427586	HTH-type transcriptional regulator sinR	Information pathways; RNA synthesis; Regulation	98%
lonB	2648735	2650393	Lon-like ATP-dependent protease lonB	Other functions; Adaptation to atypical conditions	89%
clpX	2650543	2651805	ATP-dependent Clp protease ATP-binding subunit (class III heat-shock protein) clpX	Other functions; Adaptation to atypical conditions	87%
comA	2992560	2993204	Two-component response regulator comA	Information pathways; RNA synthesis; Regulation	86%
comP	2993285	2995585	Two-component sensor histidine kinase comP	Cell envelope and cellular processes; Sensors (signal transduction)	52%
comX	2995599	2995772	Competence pheromone precursor comX	Cell envelope and cellular processes; Transformation/competence	24%
comQ	2995741	2996601	transcriptional regulator of late competence operon (comG) and surfactin expression comQ	Information pathways; RNA synthesis; Regulation	35%
degQ	2996809	2996949	Degradation enzyme regulation protein degQ	Other functions; Adaptation to atypical conditions	81%
slr	3285635	3286088	Putative transcriptional regulator slr	Information pathways; RNA synthesis; Regulation	78%
clpP	3298885	3299479	ATP-dependent Clp protease proteolytic subunit (class III heat-shock protein) clpP	Other functions; Adaptation to atypical conditions	95%
degU	3377877	3378566	Two-component response regulator degU	Information pathways; RNA synthesis; Regulation	100%
degS	3378643	3379806	Two-component sensor histidine kinase degS	Information pathways; RNA synthesis; Regulation	89%

Supplementary Table 8. Regulatory mutants and mutants used to demonstrate production of bacillibactin, bacilysin and macrolactin in FZB42

Strain	Description	Source and/or reference
FZB42	Wild type, used to demonstrate production of bacillibactin by mass spectrometry (<i>m/z</i> 905 [M+Na], 921[M+K])	BGSC 10A6, this study
CH3	<i>Δsfp::ermAM</i> , deficient in lipopeptides and polyketides but able to produce bacilysin	6, this study
CH4	<i>ΔyczE::ermAM</i> , impaired in synthesis of bacillomycinD and polyketides	6, this study
CH8	<i>Δpks3KSI::ermAM</i> , no synthesis of diffidin, used to detect bacilysin production by TLC and HPLC ³¹	6, this study
RS2	<i>Δbac::Cm^R Δpks3KSI::ermAM</i> , no synthesis of bacilysin and diffidin, used as negative control for bacilysin production	This study
CH11	<i>Δpks1KSI::cat Δpks3KSI::ermAM</i> , no synthesis of bacillaene and diffidin, used to detect macrolactin production by mass spectrometry	6, this study
CH7	<i>Δpks2KSI::cat</i> , no synthesis of macrolactin	6, this study