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CodY, a pleiotropic regulator, influences multicellular behaviour and efficient production of virulence factors in *Bacillus cereus*

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Supporting information

Table S1 Transcriptome analysis of gene expression in the *B. cereus* $\Delta codY$ mutant compared to the wild type strain. Asterisks behind the locus tag indicate the members of the predicted PclR regulon in *B. cereus* ATCC 14579 (Gohar *et al.* 2008).

locus tag	ratio	Bayes.p	function
BC0564	82.1	10^{-15}	hypothetical lipoprotein
BC3585	63.7	$< 10^{-15}$	oligopeptide-binding protein (<i>oppA</i>)
BC2026	62.3	$< 10^{-15}$	oligopeptide-binding protein (<i>oppA</i>)
BC1397	53.4	$< 10^{-15}$	acetolactate synthase large subunit
BC1402	49.6	$< 10^{-15}$	3-isopropylmalate dehydratase large subunit (<i>leuC</i>)
BC1401	48.6	$< 10^{-15}$	3-isopropylmalate dehydrogenase (<i>leuB</i>)
BC1400	41.5	$< 10^{-15}$	2-isopropylmalate synthase
BC1399	39.9	$< 10^{-15}$	ketol-acid reductoisomerase 1 (<i>ilvC</i>)
BC1396	38.7	$< 10^{-15}$	branched-chain amino acid aminotransferase
BC3939	38.3	$< 10^{-15}$	formamidase (<i>amiF</i>)
BC1398	38.2	$< 10^{-15}$	acetolactate synthase small subunit
BC1278	38.0	10^{-14}	signal peptidase I (<i>sipW</i>)
BC1281	34.7	10^{-15}	cell envelope-bound metalloprotease (<i>tapA</i>)
BC5080	34.7	$< 10^{-15}$	Methyltransferase
BC5081	32.1	$< 10^{-15}$	NADH oxidase
BC2287	30.9	$< 10^{-15}$	methylisocitrate lyase
BC1781	29.8	$< 10^{-15}$	threonine dehydratase (<i>ilvA</i>)
BC5079	29.8	$< 10^{-15}$	short chain dehydrogenase
BC2046	25.6	$< 10^{-15}$	CBS domain containing protein
BC1332	24.2	10^{-13}	methylthioribose salvage protein
BC1780	23.7	$< 10^{-15}$	dihydroxy-acid dehydratase (<i>ilvD</i>)
BC4071	22.0	$< 10^{-15}$	Transporter
BC1403	21.6	10^{-19}	3-isopropylmalate dehydratase small subunit (<i>leuD</i>)
BC5082	21.4	$< 10^{-15}$	putative uncharacterized protein
BC3583	20.7	10^{-14}	methyltransferase (<i>yodH</i>)
BC1333	20.6	$< 10^{-15}$	CBS domain containing protein
BC0255	19.7	10^{-15}	amino acid permease (<i>yfnA</i>)
BC1779	19.3	10^{-15}	ketol-acid reductoisomerase 2 (<i>ilvC2</i>)
BC5086	18.8	$< 10^{-15}$	putative lantibiotic biosynthesis protein
BC5083	18.6	$< 10^{-15}$	lantibiotic biosynthesis protein
BC0701	18.4	$< 10^{-15}$	N-acyl-L-amino acid amidohydrolase (<i>yhaA</i>)
BC1777	17.7	$< 10^{-15}$	acetolactate synthase large subunit (<i>ilvB</i>)
BC5085	16.4	$< 10^{-15}$	hypothetical cytosolic protein
BC3678	16.3	10^{-15}	multidrug resistance ABC transporter ATP-binding and permease protein
BC1776	16.2	$< 10^{-15}$	branched-chain amino acid aminotransferase (<i>ilvE</i>)
BC0638	16.0	10^{-15}	Na ⁺ /H ⁺ dependent alanine carrier protein
BC5084	15.7	$< 10^{-15}$	lanthionine biosynthesis protein
BC0819	15.2	$< 10^{-15}$	oligopeptide transport system permease protein (<i>oppC</i>)
BC1072	14.4	$< 10^{-15}$	endonuclease/exonuclease/phosphatase family protein
BC3063	13.5	$< 10^{-15}$	pyrrolidone-carboxylate peptidase (<i>pcp</i>)
BC2958	13.3	$< 10^{-15}$	putative uncharacterized protein
BC2861	12.7	10^{-13}	putative Xaa-Pro dipeptidyl-peptidase (<i>pepX</i>)
BC0703	12.6	$< 10^{-15}$	Na ⁺ /proline symporter
BC0699	12.5	10^{-15}	arginine permease (<i>rocE</i>)
BC1017	12.5	10^{-14}	putative uncharacterized protein
BC4232	12.3	10^{-13}	shikimate kinase (<i>aroK</i>)

BC4515	12.1	< 10 ⁻¹⁵	Esterase
BC3455	11.8	< 10 ⁻¹⁵	amino acid permease (<i>ybxG</i>)
BC4907	11.7	< 10 ⁻¹⁵	superoxide dismutase (<i>sodC</i>)
BC5343	11.1	< 10 ⁻¹⁵	3-hydroxybutyryl-CoA dehydrogenase (<i>mmgB</i>)
BC0818	11.0	10 ⁻¹³	Oligopeptide transport system permease protein (<i>oppB</i>)
BC1522	10.7	10 ⁻¹²	menaquinol-cytochrome c reductase iron-sulfur subunit (<i>qcrA</i>)
BC3248	10.7	< 10 ⁻¹⁵	D-3-phosphoglycerate dehydrogenase (<i>serA</i>)
BC1524	10.5	< 10 ⁻¹⁵	menaquinol-cytochrome c reductase cytochrome c subunit (<i>qcrC</i>)
BC2984	10.1	< 10 ⁻¹⁵	immune inhibitor A
BC2760	10.1	10 ⁻¹⁵	transcriptional regulator, TetR family
BC3249	9.7	< 10 ⁻¹⁵	phosphoserine aminotransferase (<i>serC</i>)
BC4659	9.7	10 ⁻¹⁴	acetyl-coenzyme A synthetase (<i>acsA</i>)
BC3066	9.3	< 10 ⁻¹⁵	UPF0271 protein
BC5342	8.8	10 ⁻¹²	acyl-CoA dehydrogenase, short-chain specific (<i>mmgC</i>)
BC1523	8.7	< 10 ⁻¹⁵	menaquinol-cytochrome c reductase cytochrome b subunit (<i>qcrB</i>)
BC3062	8.7	< 10 ⁻¹⁵	NAD-dependent deacetylase (<i>npdA</i>)
BC3064	8.6	10 ⁻¹³	Permease
BC2221	8.5	< 10 ⁻¹⁵	oligopeptide transport system permease protein (<i>oppC</i>)
BC3504	8.5	10 ⁻¹⁵	(S)-2-hydroxy-acid oxidase chain D
BC4120	8.5	10 ⁻¹²	putative uncharacterized protein
BC5416	8.3	< 10 ⁻¹⁵	carbon starvation protein A (<i>cstA</i>)
BC1018	8.3	10 ⁻¹⁴	putative uncharacterized protein
BC3942	8.2	< 10 ⁻¹⁵	cytochrome c oxidase polypeptide III (<i>ctaE</i>)
BC5344	8.2	10 ⁻¹⁴	acetyl-CoA acetyltransferase (<i>mmgA</i>)
BC3065	8.1	10 ⁻¹⁴	permease
BC5341	8.0	< 10 ⁻¹⁵	acyl-CoA dehydrogenase, short-chain specific (<i>acdA</i>)
BC0511	8.0	< 10 ⁻¹⁵	glutamate synthase [NADPH] large chain (<i>gltA</i>)
BC1836	7.8	< 10 ⁻¹⁵	branched-chain amino acid transport system carrier protein
BC2757	7.7	< 10 ⁻¹⁵	tryptophan 2,3-dioxygenase
BC2222	7.7	10 ⁻¹⁴	oligopeptide transport system permease protein (<i>oppB</i>)
BC0870	7.7	< 10 ⁻¹⁵	multidrug resistance ABC transporter ATP-binding and permease protein
BC3921	7.5	< 10 ⁻¹⁵	uncharacterized N-acetyltransferase
BC3679	7.5	< 10 ⁻¹⁵	multidrug resistance ABC transporter ATP-binding and permease protein
BC1413	7.4	< 10 ⁻¹⁵	histidinol-phosphatase
BC5452	7.4	10 ⁻¹⁴	GMP reductase (<i>guaC</i>)
BC2045	7.4	10 ⁻¹⁰	putative uncharacterized protein
BC5299	7.4	< 10 ⁻¹⁵	NADH-quinone oxidoreductase
BC3085	7.3	10 ⁻¹⁰	putative lipoprotein
BC2285	7.1	10 ⁻⁹	2-methylcitrate synthase
BC2758	7.1	< 10 ⁻¹⁵	metal-dependent hydrolase
BC3165	7.1	10 ⁻¹⁴	xanthine dehydrogenase subunit
BC1966	7.0	< 10 ⁻¹⁵	homoserine kinase (<i>thrB</i>)
BC3068	6.9	10 ⁻¹⁴	kinase autophosphorylation inhibitor (<i>kipI</i>)
BC5453	6.9	< 10 ⁻¹⁵	oligoendopeptidase F
BC3943	6.9	< 10 ⁻¹⁵	cytochrome c oxidase polypeptide I
BC3247	6.8	10 ⁻¹⁵	pyrophosphatase
BC5300	6.7	10 ⁻¹⁰	NADH-quinone oxidoreductase chain B
BC1410	6.6	< 10 ⁻¹⁵	imidazole glycerol phosphate synthase subunit (<i>hisF</i>)
BC5091	6.6	< 10 ⁻¹⁵	SnoK-like protein
BC1280	6.5	10 ⁻⁹	putative uncharacterized protein (<i>tasA</i>)
BC3067	6.3	< 10 ⁻¹⁵	regulator of kinase autophosphorylation inhibitor
BC4645	6.3	10 ⁻¹²	acetyl-coenzyme A synthetase
BC0986	6.2	10 ⁻¹⁵	response regulator aspartate phosphatase
BC3069	6.2	10 ⁻¹⁵	transcriptional regulator (<i>kipR</i>)
BC3051	6.2	10 ⁻¹³	ribosomal-protein-alanine acetyltransferase
BC1408	6.2	< 10 ⁻¹⁵	imidazole glycerol phosphate synthase subunit (<i>hisH</i>)

BC4023	6.1	10^{-14}	acetyl-CoA acetyltransferase
BC3186	6.0	10^{-13}	putative uncharacterized protein
BC3418	6.0	10^{-15}	phenazine biosynthesis protein (<i>phzF</i>)
BC1762	6.0	$< 10^{-15}$	fosmidomycin resistance protein
BC3990	5.9	$< 10^{-15}$	2,4-dienoyl-CoA reductase
BC3938	5.9	10^{-15}	hypothetical cytosolic protein
BC2288	5.9	10^{-14}	acyl-CoA dehydrogenase
BC1406	5.9	10^{-15}	histidinol dehydrogenase
BC4357	5.8	10^{-12}	(R)-specific enoyl-CoA hydratase
BC3416	5.8	10^{-13}	SMS protein
BC1409	5.8	$< 10^{-15}$	imidazole-4- carboxamide isomerase (<i>hisA</i>)
BC2759	5.8	$< 10^{-15}$	L-kynurenine hydrolase
BC1655	5.7	10^{-15}	putative uncharacterized protein
BC1407	5.7	$< 10^{-15}$	imidazoleglycerol-phosphate dehydratase (<i>hisB</i>)
BC3941	5.6	10^{-6}	cytochrome c oxidase polypeptide IVB
BC1339	5.6	$< 10^{-15}$	putative uncharacterized protein
BC3060	5.6	10^{-13}	signal peptidase I
BC5412	5.5	10^{-11}	two-component sensor protein (<i>yhcY</i>)
BC3940	5.5	$< 10^{-15}$	cytochrome aa(3) assembly factor (<i>ctaG</i>)
BC4241	5.5	10^{-10}	putative uncharacterized protein
BC3415	5.3	10^{-15}	putative uncharacterized protein
BC5404	5.2	$< 10^{-15}$	homoserine dehydrogenase
BC3012	5.2	10^{-12}	putative adenine deaminase
BC1411	5.2	10^{-8}	phosphoribosyl-AMP cyclohydrolase (<i>hisI</i>)
BC4662	5.1	10^{-11}	acetoin utilization protein (<i>acuC</i>)
BC0323	5.0	10^{-13}	phosphoribosylaminoimidazole carboxylase catalytic subunit
BC1284	5.0	$< 10^{-15}$	immune inhibitor A
BC1828	5.0	$< 10^{-15}$	Xaa-Pro aminopeptidase
BC5301	4.9	10^{-8}	NADH-quinone oxidoreductase subunit
BC4924	4.9	$< 10^{-15}$	phosphohydrolase
BC0324	4.9	10^{-11}	phosphoribosylaminoimidazole carboxylase ATPase subunit
BC3944	4.9	10^{-12}	cytochrome c oxidase subunit 2
BC1965	4.9	10^{-12}	threonine synthase
BC2848	4.9	10^{-14}	oligopeptide-binding protein (<i>oppA</i>)
BC3958	4.9	$< 10^{-15}$	myo-inositol-1-monophosphatase
BC1785	4.8	10^{-14}	acetyltransferase
BC1405	4.7	10^{-14}	ATP phosphoribosyltransferase (<i>hisG</i>)
BC1569	4.7	10^{-14}	xanthine phosphoribosyltransferase (<i>xpt</i>)
BC2849	4.7	10^{-9}	cell wall-associated hydrolase
BC1380	4.7	10^{-14}	putative uncharacterized protein
BC5297	4.6	10^{-9}	NADH-quinone oxidoreductase subunit H (<i>nuoH</i>)
BC1404	4.6	10^{-14}	ATP phosphoribosyltransferase regulatory subunit (<i>hisZ</i>)
BC0898	4.5	$< 10^{-15}$	3-hydroxybutyryl-CoA dehydratase
BC5092	4.5	10^{-10}	glyoxalase/bleomycin resistance protein
BC3991	4.5	10^{-14}	phosphoesterase
BC3652	4.5	10^{-11}	histidine ammonia-lyase (<i>hutH</i>)
BC5026	4.5	10^{-11}	putative uncharacterized protein
BC3414	4.4	10^{-15}	hydrolase
BC5239	4.4	10^{-13}	cell-wall binding protein
BC1395	4.3	10^{-11}	putative uncharacterized protein
BC4133	4.3	10^{-14}	zinc metallohydrolase
BC4259	4.3	10^{-11}	hypothetical membrane spanning protein
BC1764	4.3	$< 10^{-15}$	Acetyltransferase
BC2609	4.3	10^{-15}	cytochrome P450
BC0297	4.3	$< 10^{-15}$	guanine-hypoxanthine permease
BC3501	4.2	10^{-7}	response regulator aspartate phosphatase

BC0688	4.2	10 ⁻¹⁵	proline-specific permease
BC4256	4.2	10 ⁻¹⁴	transcriptional regulator, ArsR family
BC1964	4.2	10 ⁻¹⁴	homoserine dehydrogenase
BC2492	4.2	10 ⁻¹³	putative uncharacterized protein
BC3151	4.2	10 ⁻⁹	zwitermicin A resistance protein (<i>zmaR</i>)
BC1015	4.1	< 10 ⁻¹⁵	choloylglycine hydrolase
BC3077	4.1	10 ⁻¹⁰	hypothetical membrane spanning protein
BC2198	4.1	10 ⁻¹⁴	Sec-independent protein translocase protein (<i>tatC</i>)
BC1784	4.1	10 ⁻¹³	hypothetical membrane spanning protein
BC2063	4.1	< 10 ⁻¹⁵	alanine racemase
BC1412	4.0	10 ⁻⁵	phosphoribosyl-ATP pyrophosphatase (<i>hisE</i>)
BC1763	4.0	< 10 ⁻¹⁵	cysteine synthase
BC0887	4.0	< 10 ⁻¹⁵	collagen adhesion protein
BC3650	4.0	10 ⁻¹³	imidazolonepropionase
BC3178	4.0	10 ⁻¹⁵	lactoylglutathione lyase
BC4288	4.0	10 ⁻¹²	membrane-attached cytochrome c550
BC3968	4.0	10 ⁻¹³	putative uncharacterized protein
BC0328	4.0	10 ⁻⁸	phosphoribosylformylglycinamide synthase 1 (<i>purQ</i>)
BC2229	3.9	< 10 ⁻¹⁵	azoreductase
BC3245	3.9	10 ⁻¹⁰	amino acid permease
BC0676	3.9	10 ⁻⁶	putative uncharacterized protein
BC3651	3.9	10 ⁻¹⁰	urocanate hydratase (<i>hutU</i>)
BC5003	3.9	< 10 ⁻¹⁵	3-ketoacyl-CoA thiolase
BC2175	3.9	10 ⁻¹²	D-beta-hydroxybutyrate permease
BC0944	3.9	< 10 ⁻¹⁵	putative uncharacterized protein
BC4503	3.9	< 10 ⁻¹⁵	cytosine deaminase
BC1765	3.8	< 10 ⁻¹⁵	hypothetical cytosolic protein
BC3612	3.8	10 ⁻¹⁴	thiol:disulfide interchange protein (<i>tlpA</i>)
BC3059	3.8	10 ⁻⁹	putative cephalosporin hydroxylase (<i>cmcl</i>)
BC2147	3.8	10 ⁻¹²	response regulator aspartate phosphatase
BC4550	3.8	10 ⁻¹²	threonine transporter
BC1570	3.8	10 ⁻¹³	xanthine permease
BC5298	3.7	10 ⁻⁶	NADH-quinone oxidoreductase chain D
BC3058	3.7	10 ⁻⁶	phosphohydrolase
BC3960	3.7	10 ⁻⁹	UPF0637 protein
BC3951	3.7	10 ⁻¹⁴	PhoH protein
BC1379	3.6	10 ⁻¹⁰	gentamicin resistance protein
BC4195	3.6	10 ⁻¹¹	ribosomal-protein-alanine acetyltransferase
BC2078	3.6	10 ⁻¹⁵	hypothetical membrane spanning protein
BC4132	3.6	< 10 ⁻¹⁵	hypothetical protein
BC0971	3.6	10 ⁻¹²	carboxylic ester hydrolase
BC3150	3.6	10 ⁻⁸	transcriptional regulator, AraC family
BC5004	3.6	10 ⁻¹⁴	enoyl-CoA hydratase
BC4158	3.6	10 ⁻¹³	2-oxoisovalerate dehydrogenase beta subunit
BC2176	3.6	10 ⁻⁸	1,3-propanediol dehydrogenase
BC1476	3.6	< 10 ⁻¹⁵	cytochrome c assembly protein (<i>resC</i>)
BC0473	3.5	10 ⁻¹¹	arginine utilization regulatory protein (<i>rocR</i>)
BC3829	3.5	10 ⁻¹⁵	integrase/recombinase
BC2209	3.5	10 ⁻¹⁰	D-alanine aminotransferase
BC3623	3.5	10 ⁻¹²	putative uncharacterized protein
BC4768	3.5	10 ⁻¹⁰	putative uncharacterized protein
BC1340	3.5	10 ⁻¹⁰	sensor protein (<i>kinB</i>)
BC1508	3.4	10 ⁻⁶	putative uncharacterized protein
BC3622	3.4	10 ⁻⁸	multidrug resistance protein B
BC3052	3.4	10 ⁻¹⁰	lysine-specific permease
BC1467	3.4	10 ⁻¹²	putative uncharacterized protein

BC2315	3.4	10 ⁻⁹	DNA polymerase (<i>dinB</i>)
BC5295	3.4	10 ⁻⁵	NADH-quinone oxidoreductase chain J
BC3580	3.4	10 ⁻¹⁰	putative uncharacterized protein
BC2240	3.4	10 ⁻¹²	magnesium and cobalt efflux protein (<i>corC</i>)
BC1751	3.4	10 ⁻¹⁰	putative uncharacterized protein
BC2082	3.3	10 ⁻¹¹	putative uncharacterized protein
BC4661	3.3	10 ⁻¹⁴	acetoin utilization protein(<i>acuB</i>)
BC3532	3.3	10 ⁻¹⁵	glyoxalase family protein
BC3716	3.3	10 ⁻¹⁴	phosphopantetheine adenyltransferase
BC1282	3.3	10 ⁻⁹	biofilm specific transcriptional regulator (<i>sinR</i>)
BC2290	3.3	10 ⁻¹⁴	methylmalonate-semialdehyde dehydrogenase
BC4762	3.3	10 ⁻¹³	phosphoenolpyruvate carboxykinase (<i>pckA</i>)
BC2190	3.3	10 ⁻⁹	penicillin-binding protein
BC3828	3.2	10 ⁻¹⁴	ATP-dependent protease (<i>hsV</i>)
BC2142	3.2	10 ⁻⁸	stage V sporulation protein S
BC4683	3.2	10 ⁻¹⁵	ribosomal-protein-serine acetyltransferase
BC1315	3.2	10 ⁻¹¹	transcriptional regulator, PadR family (<i>phaQ</i>)
BC1475	3.2	10 ⁻¹²	cytochrome c biogenesis protein (<i>resB</i>)
BC2038	3.2	10 ⁻¹⁴	acyl-CoA hydrolase
BC3776	3.2	10 ⁻¹²	stage V sporulation protein S
BC3775	3.2	10 ⁻¹³	microsomal dipeptidase
BC1313	3.2	10 ⁻⁹	polyhydroxyalkanoic acid inclusion protein (<i>phaP</i>)
BC0602	3.2	10 ⁻¹²	bacillolysin
BC4765	3.1	10 ⁻⁶	transporter, drug/metabolite exporter family
BC1766	3.1	10 ⁻⁷	putative uncharacterized protein
BC4660	3.1	10 ⁻¹²	acetoin utilization protein (<i>acuA</i>)
BC3413	3.1	10 ⁻¹¹	esterase
BC5002	3.1	10 ⁻¹⁰	acyl-CoA dehydrogenase
BC0326	3.0	10 ⁻⁹	phosphoribosylaminoimidazole-succinocarboxamide synthase (<i>purC</i>)
BC1783	3.0	10 ⁻¹⁰	capsule biosynthesis protein (<i>capA</i>)
BC2289	3.0	10 ⁻¹¹	3-hydroxyisobutyrate dehydrogenase
BC1749	3.0	10 ⁻⁸	putative uncharacterized protein
BC4583	3.0	10 ⁻⁸	NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase
BC5340	3.0	10 ⁻⁸	Transcriptional regulator, TetR family
BC1860	0.33	10 ⁻⁵	phage protein
BC1745	0.33	10 ⁻⁹	putative uncharacterized protein
BC0805	0.33	10 ⁻⁹	outer surface protein
BC0990	0.33	10 ⁻¹⁴	putative uncharacterized protein
BC4367	0.33	10 ⁻¹¹	cysteine synthase
BC3980	0.32	10 ⁻¹³	putative N-acetyldiaminopimelate deacetylase
BC2546	0.31	10 ⁻⁷	putative uncharacterized protein
BC1083	0.31	10 ⁻¹⁰	transcriptional regulator, LacI family
BC4366	0.31	< 10 ⁻¹⁵	cystathionine beta-lyase
BC5065	0.31	10 ⁻¹⁵	methyl-accepting chemotaxis protein
BC1852	0.30	10 ⁻⁶	exonuclease SbcC
BC0209	0.30	10 ⁻⁷	oligopeptide transport ATP-binding protein (<i>oppD</i>)
BC0194	0.30	10 ⁻⁷	hypothetical membrane spanning protein
BC4927	0.30	10 ⁻⁹	cell surface protein
BC3747*	0.30	10 ⁻¹⁴	GGDEF family protein
BC0552	0.29	10 ⁻¹²	internalin protein
BC1908	0.29	10 ⁻⁷	phage-related protein
BC0888	0.29	10 ⁻¹⁴	N-acetylmuramoyl-L-alanine amidase
BC5066	0.29	10 ⁻¹⁵	endonuclease/exonuclease/phosphatase family protein
BC0213	0.29	10 ⁻¹⁴	transcriptional regulator, AraC family
BC4789	0.29	10 ⁻¹⁴	S-ribosylhomocysteine lyase (<i>luxS</i>)
BC1433	0.29	10 ⁻¹³	putative uncharacterized protein

BC5243	0.29	10 ⁻⁶	putative uncharacterized protein
BC3161*	0.29	10 ⁻¹⁰	microbial collagenase (<i>colA</i>)
BC1877	0.28	10 ⁻⁶	phage protein
BC0966	0.28	10 ⁻⁸	fimbria associated protein
BC1855	0.28	10 ⁻⁹	chromosome segregation ATPases
BC0491	0.28	10 ⁻⁶	formate acetyltransferase
BC1656	0.28	10 ⁻¹³	flagellin
BC3121	0.28	10 ⁻¹³	5'-nucleotidase
BC4055	0.28	10 ⁻¹²	N-acetylgalactosamine-6-phosphate deacetylase
BC4229	0.28	10 ⁻⁹	putative uncharacterized protein
BC3520	0.28	10 ⁻¹¹	methyl-accepting chemotaxis protein
BC1626	0.27	10 ⁻¹⁴	chemotaxis protein (<i>motB</i>)
BC1906	0.27	10 ⁻¹⁰	phage protein
BC1898	0.26	10 ⁻⁹	phage protein
BC1646	0.26	10 ⁻¹⁵	putative uncharacterized protein
BC1185	0.26	10 ⁻⁶	oligopeptide-binding protein (<i>oppA</i>)
BC5123	0.26	10 ⁻⁵	putative uncharacterized protein
BC5018	0.26	10 ⁻¹⁵	hypothetical membrane spanning protein
BC1911	0.25	10 ⁻⁷	N-acetylmuramoyl-L-alanine amidase
BC1627	0.25	10 ⁻¹⁵	chemotaxis protein (<i>cheY</i>)
BC1736	0.24	10 ⁻¹¹	export ABC transporter permease protein
BC1857	0.24	10 ⁻¹⁰	exonuclease (<i>sbcD</i>)
BC3117	0.24	10 ⁻¹²	arsenical pump membrane protein
BC0896	0.24	< 10 ⁻¹⁵	peptidoglycan endo-beta-N- acetylglucosaminidase
BC1893	0.23	10 ⁻⁷	scaffold protein
BC3257	0.23	< 10 ⁻¹⁵	N-acetylmuramoyl-L-alanine amidase
BC3795	0.23	10 ⁻¹⁰	translocation-enhancing protein <i>tepA</i>
BC0860	0.23	10 ⁻¹⁰	multidrug resistance protein B
BC0884	0.23	< 10 ⁻¹⁵	alpha-acetolactate decarboxylase
BC2771	0.23	< 10 ⁻¹⁵	hypothetical exported protein
BC1913	0.22	10 ⁻⁷	phage protein
BC0422	0.22	10 ⁻¹⁴	methyl-accepting chemotaxis protein
BC1880	0.22	10 ⁻⁹	phage protein
BC0421	0.22	10 ⁻⁸	anaerobic C4-dicarboxylate transporter
BC0883	0.22	< 10 ⁻¹⁵	acetolactate synthase large subunit
BC3230	0.22	10 ⁻¹⁰	hypothetical membrane spanning protein
BC4509*	0.22	10 ⁻¹³	sodium export permease protein
BC2678	0.21	10 ⁻¹⁵	putative uncharacterized protein
BC4564	0.21	10 ⁻⁹	metal-dependent phosphohydrolase
BC0211	0.21	10 ⁻¹²	oligopeptide-binding protein (<i>oppA</i>)
BC0907	0.21	< 10 ⁻¹⁵	oligopeptide-binding protein (<i>oppA</i>)
BC2728	0.21	10 ⁻¹⁴	hypothetical cytosolic protein
BC1897	0.20	10 ⁻¹³	phage protein
BC1081*	0.20	10 ⁻¹¹	PlcR-regulated protein (<i>prp2</i>)
BC3639	0.20	10 ⁻¹⁵	hypothetical membrane spanning protein
BC4510*	0.20	< 10 ⁻¹⁵	Na ⁺ export ATP-binding protein
BC1862	0.20	10 ⁻¹²	phage protein
BC5101*	0.20	10 ⁻¹⁵	perfringolysin O
BC1634	0.20	< 10 ⁻¹⁵	chemotaxis protein methyltransferase
BC1921	0.20	10 ⁻⁶	site-specific recombinase
BC1816	0.20	10 ⁻¹¹	UPF0145 protein
BC1894	0.19	10 ⁻¹³	phage protein
BC1889	0.19	10 ⁻¹³	phage protein
BC3663	0.19	10 ⁻¹²	drug/metabolite exporter family
BC3884	0.19	10 ⁻¹⁵	dihydroorotate dehydrogenase (<i>pyrD</i>)
BC1631	0.18	< 10 ⁻¹⁵	putative uncharacterized protein

BC4669	0.18	< 10 ⁻¹⁵	large-conductance mechanosensitive channel (<i>mscL</i>)
BC2466	0.18	< 10 ⁻¹⁵	microbial collagenase
BC5387	0.18	< 10 ⁻¹⁵	phosphate acetyltransferase
BC3857	0.18	10 ⁻¹²	thiamin pyrophosphokinase
BC4999*	0.17	10 ⁻¹⁰	CAAX amino terminal protease family
BC0689	0.17	10 ⁻¹⁵	guanine-hypoxanthine permease
BC1630	0.17	< 10 ⁻¹⁵	putative uncharacterized protein
BC1647	0.17	10 ⁻¹⁵	flagellum-specific ATP synthase
BC1664	0.17	10 ⁻¹¹	flagellar motor switch protein (<i>fliN</i>)
BC1160	0.17	10 ⁻⁷	soluble lytic murein transglycosylase
BC5237	0.17	< 10 ⁻¹⁵	N-acetylglucosaminyltransferase
BC2006	0.16	< 10 ⁻¹⁵	methyl-accepting chemotaxis protein
BC5236	0.16	< 10 ⁻¹⁵	diguanylate cyclase/phosphodiesterase domain 1
BC3891	0.16	< 10 ⁻¹⁵	bifunctional protein (<i>pyrR</i>)
BC1671	0.16	< 10 ⁻¹⁵	flagellar basal-body rod protein (<i>flgG</i>)
BC5116	0.15	10 ⁻⁵	putative uncharacterized protein
BC5009	0.15	10 ⁻¹⁴	methyl-accepting chemotaxis protein
BC1746	0.15	10 ⁻¹³	aspartate/ammonia ligase
BC0615	0.15	< 10 ⁻¹⁵	di-/tripeptide transporter
BC1652	0.14	< 10 ⁻¹⁵	putative uncharacterized protein
BC3877	0.14	10 ⁻¹⁵	hypothetical membrane spanning protein
BC3883	0.14	10 ⁻¹⁵	orotidine 5'-phosphate decarboxylase (<i>pyrF</i>)
BC1660	0.14	< 10 ⁻¹⁵	soluble lytic murein transglycosylase
BC1669	0.14	< 10 ⁻¹⁵	flagellar biosynthesis protein (<i>flhA</i>)
BC1653	0.14	< 10 ⁻¹⁵	putative uncharacterized protein
BC5117	0.14	10 ⁻¹⁰	ABC transporter permease protein
BC5241	0.14	10 ⁻¹³	putative uncharacterized protein
BC1709	0.14	< 10 ⁻¹⁵	malate-2H ⁺ /lactate-Na ⁺ antiporter (<i>mleN</i> or <i>nhaC</i>)
BC1663	0.14	10 ⁻⁸	flagellar motor switch protein (<i>fliN</i>)
BC0404	0.13	10 ⁻¹²	methyl-accepting chemotaxis protein (<i>mcpA</i>)
BC1670	0.13	< 10 ⁻¹⁵	flagellar biosynthesis protein (<i>flhF</i>)
BC3880	0.13	10 ⁻¹⁰	hypothetical membrane spanning protein
BC1668	0.13	< 10 ⁻¹⁵	flagellar biosynthetic protein (<i>flhB</i>)
BC1639	0.13	< 10 ⁻¹⁵	flagellar protein (<i>fliS</i>)
BC5380	0.13	< 10 ⁻¹⁵	ferrichrome-binding protein
BC1654	0.13	< 10 ⁻¹⁵	chemotaxis protein (<i>cheV</i>)
BC1667	0.13	< 10 ⁻¹⁵	flagellar biosynthetic protein (<i>fliR</i>)
BC1665	0.13	< 10 ⁻¹⁵	flagellar biosynthetic protein (<i>fliP</i>)
BC0013	0.13	10 ⁻¹⁵	inosine-5'-monophosphate dehydrogenase (<i>guaB</i>)
BC3886	0.13	< 10 ⁻¹⁵	carbamoyl-phosphate synthase large chain (<i>carB</i>)
BC1912	0.12	10 ⁻⁹	phage protein
BC3885	0.12	< 10 ⁻¹⁵	dihydroorotate dehydrogenase electron transfer subunit (<i>pyrK</i>)
BC5242	0.12	10 ⁻¹²	membrane protein with C2C2 zinc finger
BC1635	0.12	< 10 ⁻¹⁵	putative uncharacterized protein
BC1638	0.12	< 10 ⁻¹⁵	flagellar hook-associated protein 2 (<i>fliD</i>)
BC4340	0.12	10 ⁻¹³	NAD(P)H nitroreductase
BC0678	0.11	< 10 ⁻¹⁵	methyl-accepting chemotaxis protein (<i>mcpC</i>)
BC0965	0.11	< 10 ⁻¹⁵	putative uncharacterized protein
BC2538	0.11	10 ⁻¹²	two-component response regulator
BC1848	0.11	< 10 ⁻¹⁵	2-hydroxychromene-2-carboxylate isomerase family protein
BC1643	0.11	10 ⁻¹⁰	flagellar hook-basal body complex protein (<i>fliE</i>)
BC1628	0.11	< 10 ⁻¹⁵	chemotaxis protein (<i>cheA</i>)
BC4512	0.11	< 10 ⁻¹⁵	chemotaxis protein (<i>motB</i>)
BC2735*	0.11	< 10 ⁻¹⁵	bacillolysin (<i>nprE</i>)
BC1637	0.11	< 10 ⁻¹⁵	flagellar hook-associated protein 3 (<i>flgL</i>)
BC5235	0.10	< 10 ⁻¹⁵	nucleoside permease (<i>nupC</i>)

BC1636	0.10	< 10 ⁻¹⁵	flagellar hook-associated protein 1 (<i>flgK</i>)
BC1991	0.10	< 10 ⁻¹⁵	putative murein endopeptidase
BC4513	0.10	< 10 ⁻¹⁵	chemotaxis protein (<i>motA</i>)
BC3887	0.10	10 ⁻¹⁵	carbamoyl-phosphate synthase small chain (<i>carA</i>)
BC4511*	0.10	< 10 ⁻¹⁵	acid phosphatase (<i>lppC</i>)
BC1642	0.09	< 10 ⁻¹⁵	flagellar basal-body rod protein (<i>flgC</i>)
BC0954	0.09	< 10 ⁻¹⁵	<i>tcdA-E</i> operon negative regulator
BC3762*	0.09	< 10 ⁻¹⁵	microbial collagenase (<i>mpbE</i>)
BC0559	0.09	< 10 ⁻¹⁵	methyl-accepting chemotaxis protein (<i>cheW</i>)
BC3102*	0.09	< 10 ⁻¹⁵	hemolysin BL binding component (<i>hblB</i>)
BC3104*	0.09	< 10 ⁻¹⁵	hemolysin BL lytic component L2 (<i>hblC</i>)
BC1625	0.09	< 10 ⁻¹⁵	chemotaxis protein (<i>motA</i>)
BC1648	0.09	< 10 ⁻¹⁵	hypothetical cytosolic protein
BC1641	0.09	< 10 ⁻¹⁵	flagellar basal-body rod protein (<i>flgB</i>)
BC5125	0.08	10 ⁻¹³	putative uncharacterized protein
BC1657	0.08	< 10 ⁻¹⁵	flagellin
BC1649	0.08	< 10 ⁻¹⁵	hypothetical protein
BC3103*	0.08	< 10 ⁻¹⁵	hemolysin BL lytic component L1 (<i>hblD</i>)
BC5119	0.08	10 ⁻¹³	putative uncharacterized protein
BC3888	0.08	< 10 ⁻¹⁵	dihydroorotase (<i>pyrC</i>)
BC1644	0.08	< 10 ⁻¹⁵	flagellar M-ring protein (<i>fliF</i>)
BC1640	0.07	10 ⁻⁶	putative uncharacterized protein
BC0556*	0.07	10 ⁻¹²	microbial collagenase (<i>colC</i>)
BC1811*	0.07	< 10 ⁻¹⁵	non-expressed enterotoxin C (<i>nheC</i>)
BC5121	0.07	10 ⁻⁸	putative uncharacterized protein
BC1810*	0.07	< 10 ⁻¹⁵	non-hemolytic enterotoxin lytic component L1 (<i>nheB</i>)
BC1650	0.07	< 10 ⁻¹⁵	basal-body rod modification protein (<i>flgD</i>)
BC0683	0.07	< 10 ⁻¹⁵	putative uncharacterized protein
BC5351*	0.06	< 10 ⁻¹⁵	Bacillolysin (<i>nprB</i>)
BC5118	0.06	10 ⁻¹³	ABC transporter ATP-binding protein
BC1645	0.06	< 10 ⁻¹⁵	flagellar motor switch protein (<i>fliG</i>)
BC3889	0.06	< 10 ⁻¹⁵	aspartate carbamoyltransferase (<i>pyrB</i>)
BC3890	0.05	< 10 ⁻¹⁵	uracil permease (<i>pyrP</i>)
BC0215	0.05	10 ⁻¹⁵	oligopeptide-binding protein (<i>oppA</i>)
BC1809*	0.05	< 10 ⁻¹⁵	non-hemolytic enterotoxin lytic component L2 (<i>nheA</i>)
BC5122	0.05	< 10 ⁻¹⁵	hypothetical cytosolic protein
BC1659	0.04	< 10 ⁻¹⁵	flagellin
BC1110*	0.04	< 10 ⁻¹⁵	cytotoxin K (<i>cytK</i>)
BC0671*	0.03	< 10 ⁻¹⁵	sphingomyelin phosphodiesterase (<i>sph</i>)
BC5124	0.03	< 10 ⁻¹⁵	putative uncharacterized protein
BC3761*	0.02	< 10 ⁻¹⁵	1-phosphatidylinositol phosphodiesterase (<i>plcA</i>)
BC0670*	0.02	< 10 ⁻¹⁵	phospholipase C (<i>plcB</i>)

Gohar, M., Faegri, K., Perchat, S., Ravnum, S., Okstad, O. A., Gominet, M. et al. (2008) The PlcR virulence regulon of *Bacillus cereus*. *PLoS One* **3**: e2793.

Table S2 Oligonucleotides used

Oligo name	locus tag/gene	Sequence	Restriction site introduced
oligo 1	BC3826/ <i>codY</i>	AGGCACAGCGCTTAATTGAT	
oligo 2	BC3826/ <i>codY</i>	AATTTTCTCGTTTTTGCTAA <u>ACGCGT</u> CATTTCAAAG	MluI
oligo 3	BC3826/ <i>codY</i>	<u>ACGCGT</u> TAAATTTATAAAAACTCTCC	MluI
oligo 4	BC3826/ <i>codY</i>	CGAAACTACAAACGTAGCACCA	
oligo 5	BC3826/ <i>codY</i>	TCCAAGATGCGCTAGGAAGT	
oligo 6	BC3826/ <i>codY</i>	ACCAGCACGAGTTGCTTCTT	
oligo 7	BC1809/ <i>nheA</i>	CAATCGTTTTGTTTCTATCGGTACTT	
oligo 8	BC1809/ <i>nheA</i>	GTTGAATGCGAAGAGCTGCTT	
oligo 9	BC1810/ <i>nheB</i>	TGCGACAGCTCTAGGACCAA	
oligo 10	BC1810/ <i>nheB</i>	TGCTGCACCACCTGCAATTA	
oligo 11	BC0158/ <i>rpoA</i>	ACCGCTTGAGCGTGGATATG	
oligo 12	BC0158/ <i>rpoA</i>	TAGCAGTAACAGCGGCACCA	
oATK344	BC2026/ <i>oppA</i>	CGACGGATCCTTCCCCAATCTATATG	BamHI
oATK345	BC2026/ <i>oppA</i>	TCGTGGAACGGAAGGGTTAG	
oATK346	BC1396/ <i>bcaa</i>	CACGGAATTCGCAGCATTCTACTACC	EcoRI
oATK347	BC1396/ <i>bcaa</i>	CGACGGATCCCGCCTCCTATGTTCTATG	BamHI
oATK348	BC0699/ <i>rocE</i>	CACGGAATTCGCAGCAGCAAGTATAATC	EcoRI
oATK349	BC0699/ <i>rocE</i>	CGACGGATCCCGTATTTTCTTGAATG	BamHI
oATK350	BC1110/ <i>cytK</i>	CACGGAATTCGCATGAAGCCAAACCCATC	EcoRI
oATK351	BC1110/ <i>cytK</i>	CGACGGATCCTTATCTTTGTCGATATATG	BamHI
oATK356	BC1625/ <i>motA</i>	CACGGAATTCGAAAGCCAGCTATGTC	EcoRI
oATK357	BC1625/ <i>motA</i>	CGAGGGATCCGGGCTAGAAATATCAAACCTC	BamHI