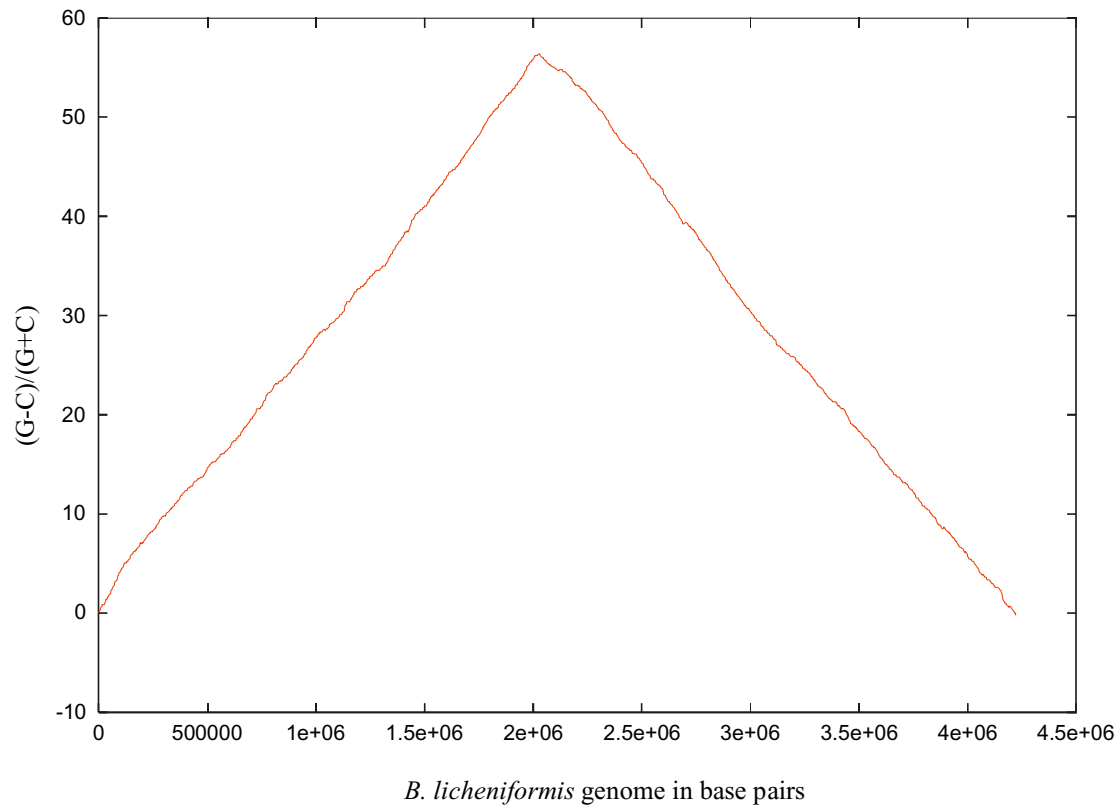
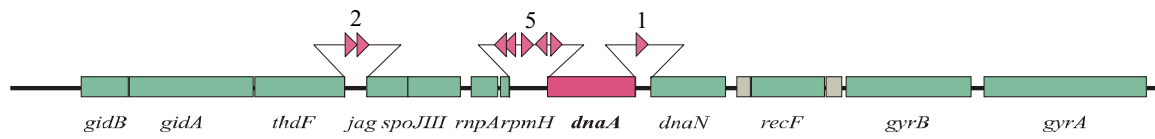


## Supplementary Figure 1



Supplementary Figure 1. Cumulative GC skew of the *B. licheniformis* genome. The origin of replication can be found at the very beginning of the graph, the termination of replication at the peak. The DNA region corresponding to the origin contains the genes and binding motifs typically found at the origin of replication in bacterial genomes.

Supplementary Figure 2.



Supplementary Figure 2. Genes and functional regions surrounding the origin of replication in *B. licheniformis*. Genes are deduced from the DNA sequence and are described by their names. The replication initiation gene *dnaA* is shaded in red, genes of known function in green and genes of unknown function in grey. Eight initially DnaA binding motifs are displayed by arrows, the binding motifs are either perfect or differ not more than one base from the consensus sequence found in *B. subtilis* and *E. coli* (consensus sequence: TTATCCACA).

Supplementary Table 1. SigD binding site

Gene	Promoter sequence <sup>a</sup>	5' UTR <sup>b</sup>
<i>yyyF</i> (BLi03788)	aattagaagc <b>taaa</b> tcaatttt-cttccct <b>gccgata</b> taaaaaatag	35
<i>hag</i> (BLi03780)	atTTTTgctata <b>aa</b> caatttca-aggcacct <b>ccgata</b> taaaatattgt	87
<i>yyyC</i> (BLi03779)	taaagataatt <b>ta</b> atctcattcg--cccttag <b>gccgata</b> taagtttttag	35
<i>mcpA</i> (BLi03295)	aaaatgcata <b>ta</b> aaaaactttta--aaagaat <b>ccgata</b> ttagggatat	36
<i>lytD</i> (BLi03821)	tttttattgt <b>ta</b> aaaaaataat--cggctc <b>gccgata</b> aaaaagagaaa	57
<i>cheV</i> (BLi01614)	agccggagcat <b>ca</b> aacttttaac-aaaagac <b>gccgata</b> taaaaaagtaa	38
<i>motA</i> (BLi01524)	agaaacagcct <b>ta</b> aaagttcctatcacgcaaac <b>accgata</b> tttaacgatatag	39
<i>mcpC</i> (BLi01604)	caggctatct <b>ta</b> atTTTTgcgaa--atTTTT <b>gccgata</b> aaaaagaatat	37
<i>Bacillus licheniformis</i> Consensus	----- <b>TaAa</b> -----N(14-16)----- <b>gCCGATAt</b> -----	35-87
<i>Bacillus subtilis</i> Consensus	----- <b>taaa</b> -----N(14-16)----- <b>gCCGATAt</b> -----	

<sup>a</sup> Consensus elements are in boldface type. Capitals indicate invariant consensus positions. Small letters indicate consensus positions with sporadic variations

<sup>b</sup> **UnTranslated Region**. The distance indicated in base pairs is from the first base after the consensus to the first base of the start codon.

Supplementary Table 2. SigL binding site

Gene	Promoter sequence <sup>a</sup>	5' UTR <sup>b</sup>
<i>levD</i> (BLi02831)	cagtttgt <b>tg</b> gca <b>cgatacttg</b> ca <b>ttataaataaagcgaacg</b>	39
<i>rocD</i> (BLi00422)	attaagagt <b>tg</b> gca <b>cgatacttg</b> ca <b>tataaagatagtgtgaaa</b>	67
<i>acoA</i> (BLi00849)	tgggagagt <b>tg</b> gca <b>cgat</b> tt <b>tttg</b> ca <b>tcataaacgtgtgagtaa</b>	38
<i>ptb</i> (BLi02586)	tttccata <b>ctgg</b> ca <b>cgaaacttg</b> ca <b>tgat</b> atag <b>tg</b> ggcggat	39
<i>yveP</i> (BLi03689)	tgggataca <b>ctgg</b> ca <b>gc-ttcttg</b> ca <b>tc</b> cgccgcttgat <b>ttt</b>	83
<i>Bacillus licheniformis</i> Consensus	----- <b>TGGCA</b> ----- <b>CTTGCAT</b> -----	38-83
<i>Bacillus subtilis</i> Consensus	----- <b>TGGcA</b> ----- <b>CTTGCAT</b> -----	

<sup>a</sup> Consensus elements are in boldface type. Capitals indicate invariant consensus positions. Small letters indicate consensus positions with sporadic variations

<sup>b</sup> UnTranslated Region. The distance indicated in base pairs is from the first base after the consensus to the first base of the start codon.

Supplementary Table 3. ORFs of *B. licheniformis* with putative function without orthologous ORFs in *B. subtilis*

GBK	Annotation
BLi00185	putative phenazine biosynthesis protein phzF
BLi00206	putative transporter
BLi00207	putative ABC transporter ATP-binding protein
BLi00208	putative transcriptional regulator, GntR family
BLi00209	putative transcriptional regulator
BLi00227	putative carboxylase
BLi00228	putative transporter
BLi00242	putative methyltransferase
BLi00243	putative nucleoside-diphosphate-sugar epimerases
BLi00245	putative sodium-dependent phosphate transporter
BLi00258	putative oxidoreductase
BLi00260	putative sugar ABC transporter, periplasmic-binding protein
BLi00263	putative antibiotic hydrolase
BLi00267	putative cellobiose phosphotransferase system
BLi00268	putative enzyme IICB component
BLi00271	putative carbonic anhydrase precursor (EC 4.2.1.1)
BLi00278	regulatory protein blaR1
BLi00279	penicillinase repressor (Regulatory protein blaI) (Beta-lactamase repressor protein)
BLi00290	putative two-component response regulator
BLi00292	putative two-component sensor histidine kinase
BLi00295	putative ABC transporter permease protein
BLi00301	putative serine protease
BLi00312	putative lantibiotic transport ATP-binding protein
BLi00313	putative protein SpaE
BLi00314	putative protein SpaG
BLi00315	putative subtilin biosynthesis regulatory protein
BLi00316	putative subtilin biosynthesis sensor protein spaK (EC 2.7.3.-).
BLi00319	putative acyl carrier protein reductase (EC 1.1.1.100)
BLi00325	putative 6-aminohexanoate-cyclic-dimer hydrolase (EC 3.5.2.12)
BLi00326	putative cellobiose phosphotransferase system enzyme II
BLi00328	putative beta-lactamase protein
BLi00332	putative PTS system, cellobiose-specific enzyme II, B component
BLi00333	putative PTS system, cellobiose-specific enzyme II, A component
BLi00338	putative chitinase (EC 3.2.1.14)
BLi00339	putative chitinase (EC 3.2.1.14)
BLi00344	putative thiosulfate sulfurtransferase protein (EC 2.8.1.1)
BLi00348	putative permease
BLi00350	putative transcriptional regulator
BLi00352	putative transcriptional regulator

BLi00353	putative transcriptional regulatory protein
BLi00358	putative ATP/GTP-binding protein
BLi00380	putative transcriptional regulator, MarR family
BLi00385	putative flavodoxin
BLi00386	putative ABC-type transporter, ATPase component
BLi00392	putative methyl-accepting chemotaxis protein
BLi00395	putative N-methylhydantoinase A (EC 3.5.2.14)
BLi00396	putative N-methylhydantoinase B (EC 3.5.2.14)
BLi00397	putative spermidine/putrescine-binding periplasmic protein 2 precursor
BLi00398	putative multiple sugar-binding transport ATP-binding protein
BLi00399	putative spermidine/putrescine ABC transporter, permease protein
BLi00400	putative spermidineputrescine ABC transporter permease protein
BLi00401	lichenysin synthetase A
BLi00402	lichenysin synthetase B
BLi00403	lichenysin synthetase C
BLi00404	lichenysin synthetase D
BLi00407	putative phosphopantetheinyl transferase (EC 2.7.8.-)
BLi00409	putative transcriptional regulator
BLi00412	putative ABC transporter subunit
BLi00416	putative 2,4-diaminobutyrate decarboxylase
BLi00417	putative methyl-accepting chemotaxis protein
BLi00439	putative sugar ABC transporter, periplasmic sugar-binding protein
BLi00440	putative ABC transporter (permease)
BLi00441	putative two-component sensor response regulator
BLi00442	putative sugar ABC transporter, periplasmic-binding protein
BLi00444	putative ABC transporter (permease)
BLi00488	putative cotransporter
BLi00489	putative acyl-carrier-protein dehydratase
BLi00493	putative sugar-specific PTS component EIIB
BLi00494	putative membrane protein
BLi00495	putative transketolase (EC 2.2.1.1)
BLi00496	putative transketolase (EC 2.2.1.1)
BLi00506	putative PTS system, mannitol-specific IIA component (EC 2.7.1.69)
BLi00514	putative transcriptional regulator, LytR family
BLi00521	putative chitin binding protein
BLi00522	putative transposase
BLi00523	putative transposase
BLi00532	putative Na <sup>+</sup> /H <sup>+</sup> antiporter
BLi00536	putative H <sup>+</sup> /glutamate symport protein
BLi00545	putative esterase/lipase
BLi00573	putative permease

BLi00575	putative repressor protein
BLi00579	putative dehydrogenase
BLi00584	putative arginase protein (EC 3.5.3.1)
BLi00585	putative ABC transporter (ATP-binding protein)
BLi00588	putative two-component sensor histidine kinase
BLi00590	putative multidrug transporter
BLi00633	putative transcriptional regulator
BLi00639	putative transporter
BLi00644	putative oxidoreductase protein
BLi00647	putative transcriptional regulator
BLi00648	putative required for spore cortex peptidoglycan synthesis
BLi00649	putative sporulation protein
BLi00656	alpha-amylase precursor (EC 3.2.1.1)
BLi00658	maltogenic alpha-amylase (EC 3.2.1.133) (glucan 1,4-alpha- maltohydrolase)
BLi00678	putative transcriptional regulatory protein
BLi00709	putative transposase
BLi00722	putative phosphotriesterase protein
BLi00723	putative phosphotriesterase protein
BLi00724	putative phosphopentomutase
BLi00743	putative type I restriction-modification system specificity subunit
BLi00744	putative type I restriction-modification system methylation subunit
BLi00745	putative type I restriction enzyme specificity protein (EC 3.1.21.3)
BLi00746	putative restriction enzyme type I helicase subunit
BLi00747	putative 5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-)
BLi00750	putative transcription antiterminator
BLi00753	putative methyltransferase
BLi00755	putative repressor protein
BLi00763	putative oxidoreductase (EC 1.1.1.-)
BLi00772	putative sodium channel
BLi00802	putative spore coat polysaccharide synthesis
BLi00803	putative O-acetyl transferase
BLi00805	putative mannosyltransferase B fusion protein
BLi00807	putative lipopolysaccharide biosynthesis glycosyltransferase
BLi00817	putative Na(+)-linked D-alanine glycine permease
BLi00825	putative thioredoxin-like oxidoreductases
BLi00828	putative glycerol dehydrogenase (EC 1.1.1.6)
BLi00848	putative intracellular protease/amidase, ThiJ family
BLi00863	putative 3-hydroxybutyryl-CoA dehydratase
BLi00873	putative nitroreductase
BLi00888	putative small acid-soluble spore protein
BLi00892	putative oligopeptide ABC transporter (ATP-binding protein)

BLi00893	putative oligopeptide ABC transporter
BLi00894	putative oligopeptide ABC transporter (binding protein) (initiation of sporulation, competence development)
BLi00895	putative oligopeptide ABC transporter (permease)
BLi00896	putative oligopeptide ABC transporter
BLi00922	putative response regulator aspartate phosphatase rapD
BLi00968	putative glycine betaine/L-proline transport
BLi00972	putative ABC transporter ATP-binding protein
BLi00973	putative ABC transporter permease protein
BLi00977	putative acylamino-acid-releasing enzyme
BLi00981	putative two-component hybrid sensor and regulator
BLi00989	putative transporter
BLi00991	putative permease
BLi00999	putative transcriptional repressor, putative
BLi01011	putative oxidoreductase
BLi01014	putative pyridoxalphosphat-dependent decarboxylase
BLi01024	putative acyl-CoA thioesterase (EC 3.1.2.2)
BLi01025	putative transcriptional regulator, AcrR family
BLi01031	putative N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
BLi01038	putative acetyltransferase (EC 2.3.1.-)
BLi01063	putative response regulator aspartate phosphatase A (EC 3.1.-.-)
BLi01105	putative DNA-binding protein
BLi01106	putative amino acid transporter
BLi01107	putative permease
BLi01109	subtilisin carlsberg precursor (EC 3.4.21.62)
BLi01124	putative metabolite transport protein
BLi01125	putative transcriptional regulator, pucR
BLi01127	putative permease
BLi01129	putative ureidoglycolate dehydrogenase (EC 1.1.1.154)
BLi01134	putative carbamate kinase (EC 2.7.2.2)
BLi01135	putative metabolite transport protein
BLi01148	putative malate dehydrogenase
BLi01151	putative two-component sensor histidine kinase
BLi01152	putative two-component response regulator
BLi01175	putative ammonium transporter
BLi01176	putative nitrogen regulatory protein P-II
BLi01184	putative-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-)
BLi01185	putative siderophore biosynthesis protein lucA
BLi01186	putative siderophore biosynthesis protein lucB
BLi01187	putative siderophore biosynthesis protein lucD
BLi01188	putative siderophore biosynthesis protein lucC
BLi01190	putative oxidoreductase



BLi01192	putative 5-methyltetrahydrofolate-homocysteine methyltransferase (EC 2.1.1.13)
BLi01213	putative undecaprenol kinase (EC 2.7.1.66)
BLi01229	putative efflux protein
BLi01244	putative two-component response regulator involved in the response to the environmental Mg-citrate complex
BLi01245	putative sensor kinase (EC 2.7.3.-)
BLi01280	putative UDP-glucose 4-epimerase (EC 5.1.3.2)
BLi01288	putative repressor transcription regulator protein
BLi01292	putative transcriptional regulator, MarR/EmrR family
BLi01309	putative cell wall-binding protein
BLi01319	putative repressor protein
BLi01344	putative phage PBSX protein
BLi01349	putative phage PBSX protein
BLi01350	putative phage PBSX protein
BLi01352	putative cell wall hydrolase
BLi01354	putative transcriptional regulator, GntR family
BLi01358	putative dehydrogenase (EC 1.1.1.-)
BLi01419	putative phosphoglycerate mutase
BLi01428	putative integrase-phage associated
BLi01436	putative phage protein
BLi01437	putative phage protein
BLi01453	putative single-stranded DNA-binding protein
BLi01464	putative multidrug resistance protein
BLi01465	putative portal protein
BLi01466	putative phage protein
BLi01468	putative phage protein
BLi01470	putative phage capsid protein
BLi01471	putative phage protein
BLi01473	putative phage protein
BLi01474	putative phage protein
BLi01475	putative phage protein
BLi01476	putative phage tail protein
BLi01477	putative phage tail protein
BLi01478	putative phage protein
BLi01479	putative phage protein
BLi01480	putative phage protein
BLi01482	putative phage protein
BLi01484	putative phage protein
BLi01486	putative glycosyl hydrolase/lysozyme
BLi01531	putative integrase/recombinase
BLi01547	putative terminase-small subunit
BLi01548	putative terminase

BLi01549	putative phage head portal protein
BLi01550	putative phage pi3 protein 23, ATP dependent Clp protease
BLi01554	putative phage protein
BLi01556	putative phage tail protein
BLi01557	putative phage protein
BLi01561	putative phage protein
BLi01562	putative phage protein
BLi01564	putative phage protein
BLi01566	putative phosphodiesterase
BLi01569	putative holin
BLi01574	putative integrase-phage associated
BLi01576	putative response regulator aspartate phosphatase H (EC 3.1.-.-)
BLi01577	putative response regulator aspartate phosphatase H (EC 3.1.-.-)
BLi01578	putative response regulator aspartate phosphatase H (EC 3.1.-.-)
BLi01605	putative acyl carrier protein reductase
BLi01678	putative transposase
BLi01679	putative transposase
BLi01747	putative bacillopeptidase F
BLi01753	putative rRNA (guanine-N1-) methyltransferase
BLi01778	putative phosphoadenosine phosphosulfate reductase (EC 1.8.99.4)
BLi01850	putative flagellar protein
BLi01880	putative endo-1,4-glucanase (EC 3.2.1.4)
BLi01881	putative cellulose 1,4-beta-cellobiosidase
BLi01882	putative cellulase (EC 3.2.1.4)
BLi01883	putative endo-1,4-beta-mannosidase
BLi01908	putative cell wall-binding protein
BLi01909	putative zinc protease (EC 3.4.99.-)
BLi01922	putative dipeptidase
BLi01935	putative phosphinothricin N-acetyltransferase (EC 2.3.1.-)
BLi01937	putative L-amino acid oxidase precursor
BLi01940	putative Na <sup>+</sup> /H <sup>+</sup> antiporter
BLi01941	putative tetracycline resistance protein
BLi01942	putative tetracycline resistance protein
BLi01944	putative hydrolase
BLi01947	putative penicillin-binding protein
BLi01951	putative spore coat protein
BLi01952	putative ABC transporter (ATP-binding protein)
BLi01971	putative transcriptional repressor of the peroxide regulon
BLi01972	putative transcriptional regulator, GntR family
BLi01979	putative transcriptional regulator TetR/AcrR family
BLi01981	putative cytosine permease

BLi01982	putative N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14)
BLi01983	putative N-methylhydantoinase B (EC 3.5.2.14)
BLi01984	putative N-methylhydantoinase B (EC 3.5.2.14)
BLi01995	putative phage protein
BLi01997	putative phage protein
BLi02003	putative short chain dehydrogenase
BLi02012	putative acetyltransferase
BLi02016	putative cytochrome C biogenesis (thioredoxin)
BLi02017	putative manganese-containing catalase
BLi02019	putative acetyl transferase
BLi02022	putative transcriptional regulator MarR family
BLi02062	putative sugar kinase, possible xylulose kinase
BLi02063	putative L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)
BLi02065	putative sugar transporter
BLi02066	putative acetoin reductase (EC 1.1.1.5)
BLi02083	putative transcriptional regulator (Fnr/Crp family)
BLi02084	putative nitric-oxide reductase subunit B (EC 1.7.99.7)
BLi02092	putative pyridine nucleotide-disulphide oxidoreductase
BLi02093	putative methyltransferase
BLi02098	putative transcriptional regulator
BLi02099	putative catabolite repression HPr-like protein
BLi02102	putative enoyl(3-hydroxyisobutryl)-coenzyme A hydratase protein (EC 4.2.1.17)
BLi02103	putative enoyl-CoA hydratase (EC 4.2.1.17)
BLi02105	putative 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
BLi02106	putative butyryl-CoA dehydrogenase
BLi02113	putative ABC transporter ATP-binding protein
BLi02114	putative transcriptional regulator
BLi02115	putative glycerophosphodiester phosphodiesterase
BLi02116	putative D-mannonate dehydratase (EC 4.2.1.8)
BLi02117	putative alpha-glucosidase (EC 3.2.1.20)
BLi02118	putative C4-dicarboxylate transporter, large subunit
BLi02119	putative C4-dicarboxylate transporter, small subunit
BLi02131	putative pyruvate formate-lyase activating enzyme (EC 1.97.1.4)
BLi02132	putative formate acetyltransferase (EC 2.3.1.54)
BLi02138	putative acetyl-coenzyme A synthetase (EC 6.2.1.1)
BLi02142	putative biotin carboxyl carrier protein
BLi02148	putative gamma-glutamyl phosphate reductase (EC 1.2.1.41)
BLi02153	putative sulfate permease
BLi02167	putative transcriptional regulator, MarR/EmrR family
BLi02170	putative cinnamoyl ester hydrolase
BLi02179	putative lipoprotein

BLi02180	putative long-chain acyl-CoA synthetase
BLi02187	putative transcriptional regulator, TetR family
BLi02198	putative transcriptional regulator, DeoR family
BLi02205	putative UDP-N-acetylglucosamine 4,6-dehydratase (EC 4.2.1.-)
BLi02208	putative glycosyl transferase
BLi02212	putative symporter
BLi02231	putative spore germination protein
BLi02233	putative hydrolase
BLi02238	putative transporter
BLi02239	putative ribosomal protein S14
BLi02257	putative transporter
BLi02273	putative oxidoreductase
BLi02279	putative transposase
BLi02280	putative transposase
BLi02286	putative permease
BLi02300	putative permease
BLi02328	putative formate-tetrahydrofolate ligase (EC 6.3.4.3)
BLi02346	putative acetyltransferase
BLi02426	putative isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2)
BLi02433	putative L-asparaginase (EC 3.5.1.1)
BLi02451	putative peptidoglycan GlcNAc deacetylase
BLi02454	putative two-component sensor histidine kinase
BLi02455	putative two-component response phosphate regulator
BLi02477	putative phosphatase
BLi02478	putative stress response homolog Hsp
BLi02483	putative transposase
BLi02484	putative transposase
BLi02506	putative PTS cellobiose-specific enzyme IIB
BLi02508	putative transcriptional regulator (LysR family)
BLi02509	putative ribosomal protein N-acetyltransferase
BLi02528	putative oligopeptide ABC transporter (permease)
BLi02529	putative oligopeptide ABC transporter (permease)
BLi02530	putative dipeptide ABC transporter
BLi02531	putative oligopeptide ABC transporter, ATP-binding protein
BLi02532	putative DNA-damage-inducible protein
BLi02533	putative fibronectin-binding protein
BLi02541	putative ABC transporter permease protein
BLi02542	putative ABC transporter ATP-binding protein
BLi02553	putative ribosomal protein L33
BLi02561	putative PTS system, cellobiose-specific enzyme II, C component
BLi02562	putative ABC transporter (ATP-binding protein)

BLi02576	putative amino acid ABC transporter (binding protein)
BLi02663	putative mutants lead to the production of immature spores
BLi02688	putative ABC transporter (ATP-binding protein)
BLi02698	putative endonuclease V (EC 3.1.25.1)
BLi02774	putative alanyl-tRNA synthetase (EC 6.1.1.7)
BLi02775	putative amino acid aldolase or racemase
BLi02776	putative translation initiation inhibitor
BLi02779	putative threonine synthase (EC 4.2.3.1)
BLi02785	putative hydrolase
BLi02786	putative flavoprotein reductase
BLi02787	putative two-component response regulator involved in degradative enzyme and competence regulation
BLi02788	putative two-component sensor histidine kinase involved in degradative enzyme and competence regulation
BLi02796	putative S-adenosylmethionine-dependent methyltransferase
BLi02800	putative ABC transporter permease protein
BLi02803	putative delta-aminolevulinic acid dehydratase
BLi02811	putative oligopeptide transporter putative substrate binding domain
BLi02812	putative oligopeptide ABC transporter, permease protein
BLi02813	putative oligopeptide transport system permease protein
BLi02814	putative dipeptide transport ATP-binding protein
BLi02815	putative dipeptide transport ATP-binding protein
BLi02817	putative cation efflux pump
BLi02818	putative transcriptional regulator, AraC family
BLi02819	putative oxidoreductase protein (EC 1.-.-)
BLi02820	putative phosphatase
BLi02821	putative lipase/esterase
BLi02835	putative chloramphenicol acetyltransferase (EC 2.3.1.28)
BLi02850	putative cell wall-associated protease precursor (EC 3.4.21.-)
BLi02851	putative methyltransferase
BLi02927	putative transcriptional regulator
BLi02962	putative branched-chain amino acid aminotransferase (EC 2.6.1.42)
BLi02967	putative phage PBSX protein
BLi02969	putative phage protein
BLi02977	putative ABC transporter (binding protein)
BLi02978	putative response regulator aspartate phosphatase
BLi02990	putative oxidoreductase protein
BLi03013	putative ABC transporter, ATP-binding protein
BLi03103	putative transposase
BLi03104	putative transposase
BLi03154	putative pseudouridylate synthase
BLi03166	putative membrane protein
BLi03172	putative amino acid permease

BLi03194	putative glucosyl transferase
BLi03198	putative amino acid transporter
BLi03212	putative ABC transporter (amino acid permease)
BLi03257	putative transcriptional regulator
BLi03265	putative oligoendopeptidase
BLi03272	putative high affinity choline transporter
BLi03304	putative sugar hydrolase
BLi03313	putative acetyltransferase
BLi03340	putative transposase
BLi03341	putative transposase
BLi03355	putative transposase
BLi03356	putative transposase
BLi03357	putative two-component sensor histidine kinase involved in early competence (EC 2.7.1.-)
BLi03370	putative lipase/esterase
BLi03371	putative lipase precursor (EC 3.1.1.3)
BLi03380	putative Na(+)-linked D-alanine glycine permease
BLi03406	putative response regulator
BLi03415	putative spore germination protein
BLi03432	putative transcriptional regulator
BLi03444	putative permease
BLi03478	putative penicillin-binding protein 5* (D-alanyl-D-alanine carboxypeptidase) (EC 3.4.16.4)
BLi03498	putative pectin methylesterase
BLi03500	putative acyl carrier protein reductase (EC 1.1.1.100)
BLi03502	putative alcohol dehydrogenase II (EC 1.1.1.1)
BLi03503	putative dihydrodipicolinate synthase
BLi03507	putative transcriptional regulator, GntR family
BLi03510	putative transcriptional regulator of the alpha-acetolactate operon
BLi03511	putative polygalacturonase
BLi03527	putative ABC transporter (ATP-binding protein)
BLi03540	putative ABC transporter sugar binding protein
BLi03541	putative transporter
BLi03543	putative alpha-glucosidase
BLi03544	putative sugar hydrolase
BLi03548	putative transcriptional regulator
BLi03549	putative fructose 1-phosphate kinase
BLi03551	putative phosphotransferase system (PTS) fructose-specific enzyme IIABC component
BLi03552	putative fructose-1,6-bisphosphate aldolase
BLi03556	putative intracellular proteinase I
BLi03562	putative chloramphenicol resistance protein
BLi03563	putative chloramphenicol resistance protein
BLi03571	putative amidase

BLi03576	putative two-component response regulator [YvrG]
BLi03590	putative transposase
BLi03591	putative transposase
BLi03592	putative transcriptional repressor protein
BLi03599	putative phage protein
BLi03600	putative phage protein
BLi03602	putative phage PBSX protein
BLi03604	putative phage autolysin (amidase) homolog
BLi03606	putative phage tail protein
BLi03614	putative phage protein
BLi03616	putative portal protein
BLi03617	putative phage protein
BLi03618	putative terminase large subunit
BLi03619	putative phage terminase protein, small subunit
BLi03622	putative phage protein
BLi03624	putative phage protein
BLi03626	putative phage protein
BLi03627	putative phage protein
BLi03629	putative phage protein
BLi03630	putative phage protein
BLi03631	putative phage protein
BLi03632	putative phage protein
BLi03635	putative phage protein
BLi03637	putative phage protein
BLi03647	putative spore germination protein
BLi03657	putative iron(III) transporter binding protein
BLi03697	putative glucarate transporter
BLi03699	putative pyridoxal phosphate biosynthetic protein
BLi03701	putative alcohol dehydrogenase
BLi03702	putative dihydrodipicolinate synthase
BLi03703	putative sigma-L-dependent transcriptional regulator
BLi03704	putative transcriptional regulator
BLi03719	putative ribonuclease (EC 3.1.27.-)
BLi03755	putative dioxygenase
BLi03767	putative cell wall-binding protein
BLi03803	putative NDP-sugar epimerase (EC 5.1.3.2)
BLi03816	putative CDP-glycerol:polyglycerol phosphate glycerophosphotransferase
BLi03823	putative anaerobic ribonucleoside-triphosphate reductase activating protein
BLi03824	putative anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)
BLi03862	putative fructose-6-phosphate aldolase 2 (EC 4.1.2.-)
BLi03863	putative sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.1.140)

BLi03864 putative PTS system, glucitol/sorbitol-specific IIA component (EC 2.7.1.69)  
BLi03865 putative PTS system, glucitol/sorbitol-specific IIBC component (EC 2.7.1.69)  
BLi03866 putative PTS system, glucitol/sorbitol-specific IIC2 component (EC 2.7.1.69)  
BLi03867 putative sorbitol operon activator  
BLi03868 putative transcriptional repressor  
BLi03877 putative cell shape determining protein  
BLi03891 putative RNA polymerase sigma factor  
BLi03896 putative multidrug efflux protein  
BLi03909 putative transposase  
BLi03910 putative transposase  
BLi03917 putative oxalate:formate antiporter  
BLi03918 putative formate dehydrogenase alpha chain (EC 1.2.1.2)  
BLi03989 putative hydroxybenzoate hydroxylase  
BLi03990 putative benzoate transport protein  
BLi03991 putative aromatic compounds specific dioxygenase  
BLi03992 putative 4-oxalocrotonate tautomerase (EC 5.3.2.-)  
BLi03993 putative decarboxylase/dehydratase  
BLi03995 putative transcriptional regulator  
BLi04004 putative multidrug ABC transporter, permease protein  
BLi04023 putative N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)  
BLi04031 putative ATP-binding protein of ABC transporter  
BLi04032 putative ATP-binding protein of ABC transporter  
BLi04033 putative asparagine synthetase (EC 6.3.5.4)  
BLi04036 putative response regulator  
BLi04048 xylose isomerase (EC 5.3.1.5)  
BLi04055 putative two-component sensor histidine kinase  
BLi04063 putative phosphoglycerate dehydrogenase  
BLi04069 putative galactonate transporter  
BLi04070 putative galactonate dehydratase protein (EC 4.2.1.6)  
BLi04071 putative 2-keto-3-deoxygluconate-6-phosphate aldolase  
BLi04072 putative 2-keto-3-deoxygluconate kinase (EC 2.7.1.45)  
BLi04073 putative transcriptional regulator  
BLi04093 putative transcriptional regulator  
BLi04097 putative chromate transport protein  
BLi04100 putative pectin acetyltransferase (EC 3.1.1.6)  
BLi04103 putative bicyclomycin resistance protein  
BLi04114 putative transcriptional repressor of the peroxide regulon  
BLi04117 putative ABC transporter ATP-binding protein  
BLi04122 putative transcriptional regulator  
BLi04125 putative ABC-transporter, membrane protein  
BLi04126 putative bacteriocin formation protein



BLi04127 putative lantibiotic mersacidin precursor  
BLi04128 putative bacteriocin formation protein  
BLi04129 putative pectate lyase  
BLi04152 putative transcriptional regulator (GntR family)  
BLi04153 putative transcriptional regulator (GntR family)  
BLi04156 putative beta-glucosidase  
BLi04163 arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)  
BLi04164 ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)  
BLi04165 putative sugar permease  
BLi04166 carbamate kinase (EC 2.7.2.2)  
BLi04167 putative transcriptional regulator of anaerobic genes  
BLi04168 putative ABC transporter (ATP-binding protein)  
BLi04169 putative PTS enzyme IIC component  
BLi04171 putative RNA polymerase ECF-type sigma factor  
BLi04172 putative anaerobic ribonucleoside-triphosphate reductase activating protein (EC 1.97.1.4)  
BLi04176 putative cell-division protein / general stress protein (class III heat-shock)  
BLi04178 putative sucrose-6-phosphate hydrolase (EC 3.2.1.26)  
BLi04180 putative sugar ABC transporter, permease  
BLi04182 putative sugar ABC transporter sugar binding protein  
BLi04183 putative repressor  
BLi04190 putative NDP-sugar epimerase (EC 5.1.3.2)  
BLi04199 putative beta-glucosidase (EC 3.2.1.21)  
BLi04205 putative transcriptional regulator  
BLi04207 putative isocitrate lyase (EC 4.1.3.1)  
BLi04208 putative malate synthase (EC 4.1.3.2)  
BLi04224 putative transposase  
BLi04241 putative transporter  
BLi04251 putative methylmalonate-semialdehyde dehydrogenase [acylating] (EC 1.2.1.27)  
BLi04257 putative ABC transporter, ATP-binding protein  
BLi04259 putative glycerol 1-phosphate dehydrogenase  
BLi04265 putative ferrous iron transport protein B  
BLi04274 putative amino acid symporter  
BLi04285 putative transcriptional repressor of the xylose operon  
BLi04290 putative alcohol dehydrogenase/acetaldehyde dehydrogenase  
BLi04307 putative ABC transporter ATP-binding protein  
BLi04314 putative metal-dependent hydrolase  
BLi04315 putative type I restriction enzyme (restriction chain)  
BLi04316 putative type I restriction enzyme hsdS subunit  
BLi04317 putative DNA-binding protein  
BLi04318 putative type I site-specific deoxyribonuclease  
BLi04322 putative site-specific recombinase

BLi04342	putative holin
BLi04349	putative N-acetylglucosamine-6-phosphate isomerase (EC 3.5.99.6)
BLi04351	putative 3-oxoacyl-acyl-carrier protein reductase
BLi04371	putative RNA polymerase sigma factor

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green	Genes involved in transport
orange	Genes involved in regulation
yellow	Genes involved in various enzymatic reactions
pink	Transposases
blue	Phage related genes