

# The presence of plasmids in *Lactococcus lactis* IL594 determines changes in the host phenotype and expression of chromosomal genes

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## Supplementary Materials

**Table S1.** Strains and primers used in this study.

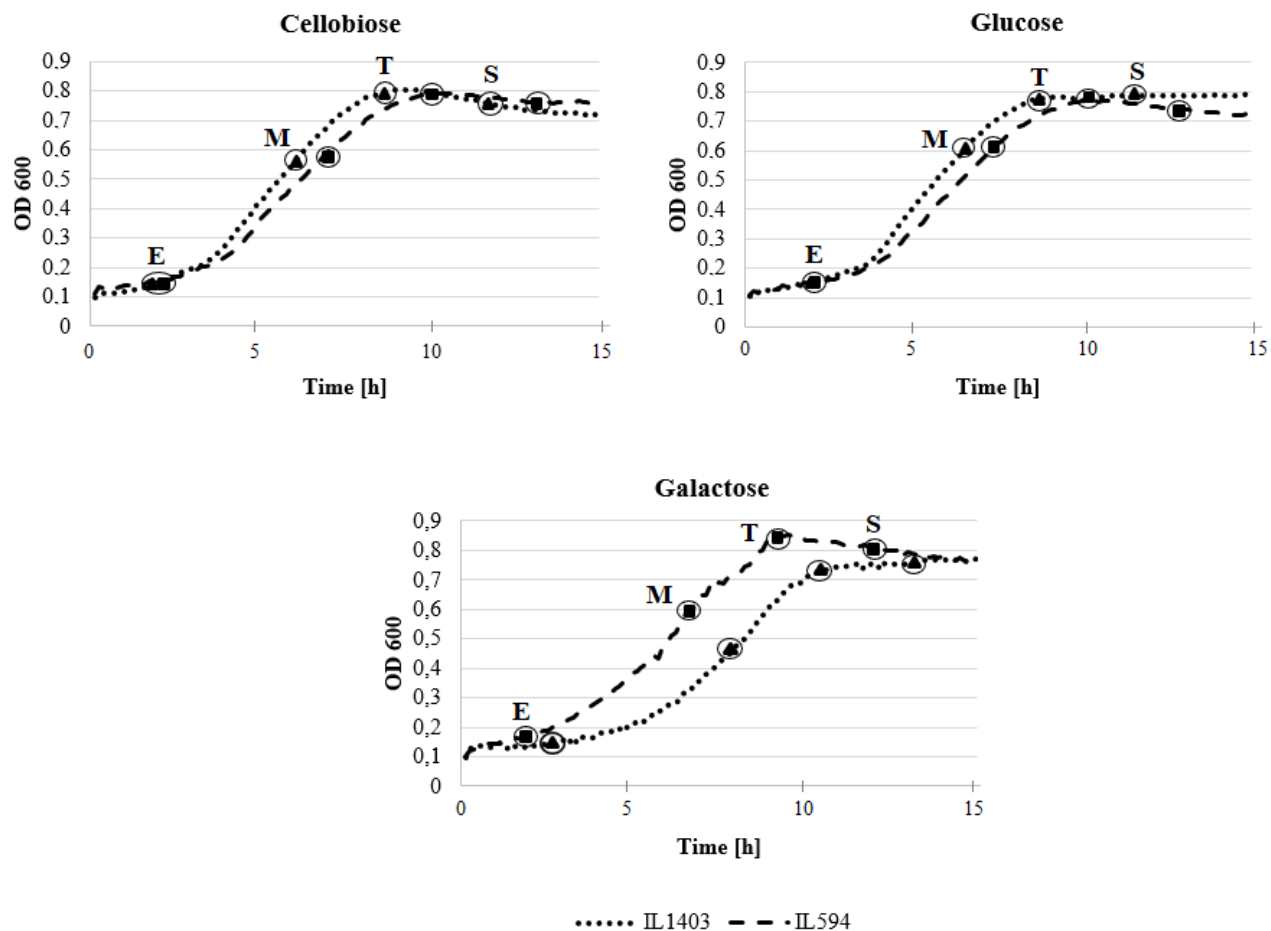
Strain or primer pair	Genotypic characteristics	Source and reference
<i>L. lactis</i>		
IL594	wild-type strain harbouring seven plasmids pIL1-pIL7	INRA [31]
IL1403	plasmid-free strain, derivative of IL594	
Primers <sup>a</sup>		
LIPurMaF / LIPurMaR	<u>ATTGCGTAGCCATGTGCGTC/CTGTTTCTCCACCAATCAGCG</u>	This study
LITufaF / LITufaR	<u>CGTGACCTCTTGAGCGAATACG/GAGTGGTTTGTCACTGTTCGCG</u>	
p1orf3zF / p1orf3zR	<u>CTTGCTGACGAATTAGGAGTTAG/TCAGCGGTTAATAGCTTCATAC</u>	
p1orf6zF / p1orf6zR	<u>CCTTGTTCTGTTGGATTGATTAG/AGAACTCGCTTCTAAATTTGTG</u>	
p2citRzF / p2citRzR	<u>AGGAGACAACAACATGAAAGTC/GAGCGTTTGTCTCCAATCTG</u>	
p2orf2zF / p2orf2zR	<u>AGCTAAACAGACCGTTCAATAC/GTTTAGGACGATCGAACCAC</u>	
p3orf2tF / p3orf2tR	<u>CAACAACAGAACGAAACACAAC/AAGTTCTGTTCTAAGAATACTGACG</u>	
p3orf3zF / p3orf3zR	<u>TCTCAGGTGTTTATCTGGTATTTC/GACAACAAGTCCTACTCCAAAG</u>	
p4or24zF / p4or24zR	<u>GTTTGATCTTACCTTGCTGTTG/GTTACTGGGAACCGATTACG</u>	
p4or49zF / p4or49zR	<u>CCTTACCAATGGTGATGTAATCG/GTCAAAGATACTGGCGGTTTAG</u>	
p5cadAzF / p5cadAzR	<u>GCATCGACGGTTGGTATTG/GTTTGGCGGCTAAGTCTAAC</u>	
p5cadCzF / p5cadCzR	<u>GTTGATAGTCACAAGGATGGTAAG/AATTTACGCCAAGCTCCATAAG</u>	
p6orf6zF / p6orf6zR	<u>TCAGGGAATTCTTTATTAGGTTCTG/CTTGTTTCATCTACCTTAGTCAAGTATC</u>	
p6orf7zF / p6orf7zR	<u>GATATACTGCGACTTCCAGTTG/ATTCTAATGCCACATGGTAAGG</u>	
p7or11zF / p7or11zR	<u>ATCGAACCGCCAATCAAG/CCGTATTGATCCCAGAAGTAAG</u>	
p7orfXzF / p7orfXzR	<u>TGCAGATGAGTTGAGTGTTAC/TGCTACCACCTTCTACTTTACC</u>	

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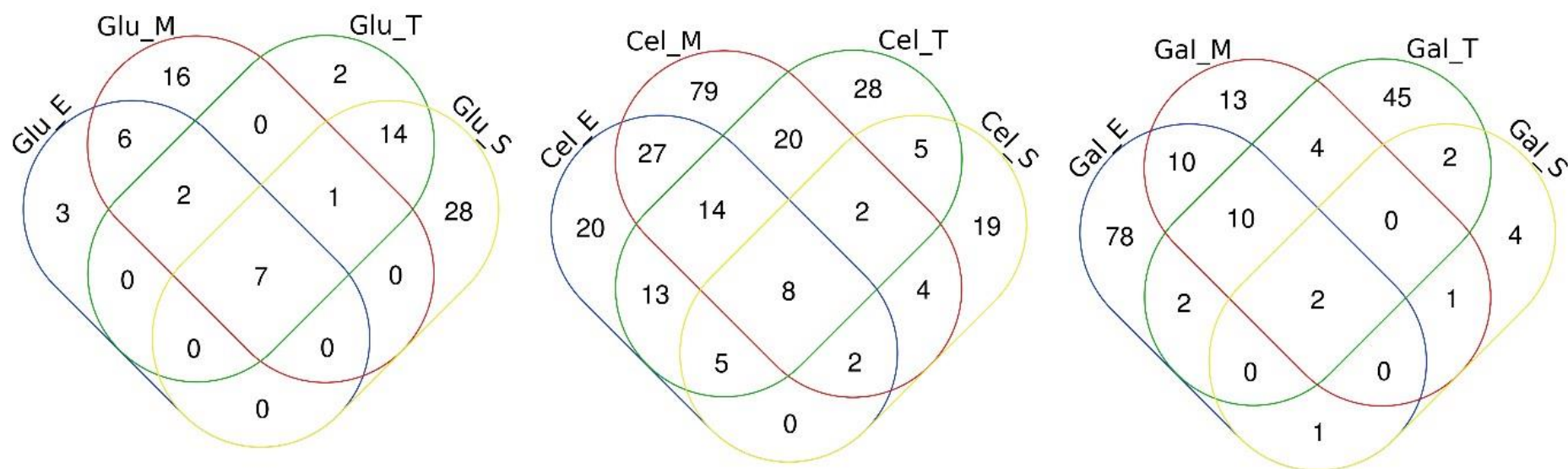
<sup>a</sup>primers were designed on the basis of the *L. lactis* IL594 plasmid nucleotide sequences (NCBI accession no. HM021326, HM021327, HM021328, HM021329, HM021330, HM021331, and HM197723;

<http://www.ncbi.nlm.nih.gov>)

**Figure S1.** Time points of samples collection during growth of *L. lactis* IL594 (---) and IL1403 (•••) in M17 supplemented with different carbon sources. Identified time points of bacterial growth phases: early exponential (E), mid-exponential (M), transition (T), and stationary (S) are presented in circles.



**Figure S2.** Venn diagram of differentially expressed genes in *L. lactis* IL594 in comparison to IL1403 induced by presence of different carbon sources (glucose- “Glu”; cellobiose- “Cel”; galactose- “Gal”). The numbers of genes in the intersection sets are indicated. E refers to the early exponential phase of growth, M - mid-exponential growth phase, T - transition phase and S - stationary phase of growth. Overlapping regions show the number of common genes with an altered expression profile at different growth phases. Numbers in non-overlapping areas of each oval show the number of genes expressed differently only in selected phase of growth unique to each strain. The number of genes expressed commonly in all growth phases included 7 (0.3%), 8 (0.3%), and 2 (0.08%) genes during growth of the strain on glucose, cellobiose, and galactose, respectively. The number of genes expressed differently in all growth phases included 49 (2%), 146 (6%), and 140 (5%) genes during growth of the strain on glucose, cellobiose, and galactose, respectively. The numbers in brackets represents the percentages of all genes annotated in IL1403 genome.



**Table S2 .** Differentially expressed genes in *L. lactis* IL594. A gene was considered to be upregulated between compared *L. lactis* samples if the level of its transcript was elevated by at least 4-fold ( $\text{Log}_2\text{Ratio} \geq 2.0$ ) and downregulated when the level of its transcript was decreased by at least 4-fold ( $\text{Log}_2\text{Ratio} \leq -2.0$ ). The transcription change was recognized as valid when the probability of such a random difference was less than 0.05 ( $p < 0.05$ ).

Gene	NCBI	COGs	Upregulation or downregulation on a sugar source												Protein function
	GeneID		Glucose				Cellobiose				Galactose				
			E	M	T	S	E	M	T	S	E	M	T	S	
<b>Energy production and conversion</b>															
<i>atpC</i>	SPS12515.1	C		2.6				2.8				2.4			F0F1 ATP synthase subunit epsilon
<i>atpD</i>	SPS12514.1	C					2.3		2.5					3.5	F0F1 ATP synthase subunit beta
<i>citB</i>	AAK04769.1	C				2.9	5.5	6.3	7.5	3.8	7.8	8.1	6.0		aconitate hydratase
<i>ldhB</i>	AAK04474.1	C					2.4	3.0							L-lactate dehydrogenase
<i>mleS</i>	AAK04998.1	C			2.1					2.9			2.3	2.1	malate dehydrogenase malic enzyme
<i>noxD</i>	GEB09238.1	C						-4.1	-2.0		-3.6	-4.2			NADH oxidase
<i>ybiE</i>	GFO78088.1	C	2.3					3.3				2.2			oxidoreductase
<i>ycdG</i>	AAK04334.1	C									2.2	4.9			oxidoreductase
<i>yddB</i>	AAK04431.1	C				2.2									oxidoreductase
<i>yfhC</i>	AAK04676.1	C				2.0					2.1				hypothetical protein
<i>yfiJ</i>	AAK04695.1	C	-2.0						-2.5	-2.1	-2.3				NADPH-flavin oxidoreductase
<i>yiaD</i>	AAK04894.1	C						-2.5	-2.0						NADH-flavin reductase
<i>ypjF</i>	AAK05652.1	C						2.7							oxidoreductase
<i>yrjB</i>	AAK05831.1	C		2.1					-2.3						oxidoreductase
<b>Cell cycle control, cell division, chromosome partitioning</b>															
<i>ftsE</i>	SPS11645.1	D					-2.2	-2.2				2.3			cell-division ATP-binding protein
<i>ftsW2</i>	AAK04982.1	D				2.5							3.1		hypothetical protein
<i>gidA</i>	AAK05945.1	D						-2.3							tRNA uridine 5-carboxymethylaminomethyl modification protein GidA
<b>Amino acid transport and metabolism</b>															

<i>arcA</i>	WP_004254504.1	E													-2.9				arginine deiminase				
<i>arcC2</i>	AAK06131.1	E													-2.7				carbamate kinase				
<i>aroD</i>	SPS10137.1	E													-2.3				3-dehydroquinate dehydratase				
<i>asnH</i>	AAK06326.1	E													2.6	2.0				asparagine synthetase			
<i>cysD</i>	AAK04171.1	E													2.5				O-acetylhomoserine sulfhydrylase				
<i>cysK</i>	QOK50869.1	E													-3.5	4.2	-2.3			cysteine synthase serine family			
<i>glnB</i>	AAK05689.1	E	3.0			2.5	3.1			2.4						nitrogen regulatory protein P-II							
<i>glnQ</i>	SPS12229.1	E													-2.4	-2.4				glutamine ABC transporter ATP-binding protein			
<i>gltB</i>	SPS11857.1	E													2.3				glutamate synthase large subunit glutamate family				
<i>hisK</i>	GEB08549.1	E													2.4				histidinol phosphatase histidine family				
<i>homD</i>	CAA65713.1	E													3.7	2.2			homoserine dehydrogenase				
<i>ilvD</i>	SPS12837.1	E													2.2	2.2				dihydroxy-acid dehydratase			
<i>ilvH</i>	SPS12840.1	E													2.0	-2.1				acetolactate synthase 3 regulatory subunit			
<i>oppB</i>	QQF01347.1	E	6.0	6.7	6.3	6.1	6.4	6.8	8.1	3.0	7.0	6.7	5.4	0.8			oligopeptide ABC transporter permease						
<i>oppC</i>	QQF01348.1	E	6.2	6.8	6.7	4.9	3.2	5.4	4.9			5.9	5.6	2.7	2.3			oligopeptide ABC transporter permease					
<i>oppD</i>	QQF01345.1	E	4.2	4.9	3.3			3.2	5.4	4.9			5.9	5.6	2.7	2.2			oligopeptide ABC transporter ATP binding protein				
<i>oppF</i>	QQE99754.1	E	5.0	6.0	5.0	4.0	4.4	6.7	6.4	2.3	6.2	6.2	3.4				oligopeptide ABC transporter ATP binding protein						
<i>optA</i>	GEB08281.1	E													-3.1				oligopeptide ABC transporter				
<i>optB</i>	GEB08280.1	E													-2.6	-2.3				oligopeptide ABC transporter permease			
<i>pepD</i>	AAK04350.1	E													2.8	4.5				dipeptidase			
<i>pepF</i>	CAA83534.1	E													2.7	2.1				oligoendopeptidase F			
<i>pepO</i>	QOK51376.1	E													-3.9	-3.9	-2.8	-3.3	-2.5			neutral endopeptidase	
<i>pepP</i>	AAK04789.1	E													-2.9	-3.0				-2.1			aminopeptidase P
<i>trpC</i>	TRW54532.1	E													-2.0							Indole-3-glycerol phosphate synthase	
<i>ydgB</i>	AAK04453.1	E													2.8							L-asparagine uniporter	

<i>yeyJ</i>	AAK04598.1	E			2.0	hypothetical protein
<i>yfcG</i>	AAK04637.1	E			3.2	oligopeptide ABC transporter ATP binding protein
<i>ygaJ</i>	AE005176.1	E		-2.2		putative peptidase
<i>yhbF</i>	AAK04808.1	E		-2.4		hypothetical protein
<i>yibG</i>	AAK04907.1	E		2.6		L-asparagine uniporter
<i>yrfD</i>	AAK05797.1	E	2.7	4.0		amino acid antiporter
<i>yshA</i>	AAK05907.1	E		2.5		glutamate antiporter
<b>Nucleotide transport and metabolism</b>						
<i>add</i>	AAK04385.1	F		2.2	2.0	adenosine deaminase
<i>dukA</i>	GEB08937.1	F			2.4	deoxynucleoside kinase nucleotide and nucleoside interconversions
<i>pfs</i>	AAK05978.1	F		2.0		5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
<i>xpt</i>	AAK05244.1	F	2.9			xanthine phosphoribosyltransferase
<i>yccE</i>	AAK04320.1	F			-2.1	hypothetical protein   NUDIX hydrolase
<i>yeyD</i>	AAK04591.1	F			-3.4	hypothetical protein   nucleoside 2-deoxyribosyltransferase
<i>yfcD</i>	AAK04634.1	F		2.7		hypothetical protein
<i>ygbG</i>	AAK04728.1	F		2.8		ribonuclease Z
<i>ygiJ</i>	AAK04786.1	F		2.5	-2.1	hypothetical protein   adenylate kinase
<i>ypdB</i>		F	2.0		2.3	ribonuclease
<i>ypdD</i>		F	2.1		2.1	ribonuclease
<b>Carbohydrate transport and metabolism</b>						
<i>bglH</i>	AAK05557.1	G	2.0			beta-glucosidase
<i>deoB</i>	AE005176.1	G		-2.4		phosphopentomutase
<i>dexC</i>	GFO79576.1	G			2.5	neopullulanase degradation of polysaccharides

<i>fruA</i>	AAK05057.1	G	2.3													PTS system fructose-specific transporter subunit IIBC
<i>galE</i>	WP_058218180.1	G						2.2								UDP-glucose 4-epimerase
<i>glmM</i>	SPS12287.1	G						-2.0								phosphoglucosamine mutase
<i>gntK</i>	QNL92507.1	G						3.1	5.3	2.9	5.8	4.8	3.6			gluconate kinase energy metabolism, sugars
<i>malE</i>	AAK05781.1	G	-6.1	-5.8	-5.1	-3.1	-6.7	-6.3	-4.9	-2.0		-2.7	-3.0	-3.3		maltose ABC transporter substrate binding protein
<i>malF</i>	AAK05782.1	G	-6.5	-5.7	-5.4	-2.4	-6.5	-5.9	-3.8					-2.0		maltose ABC transporter permease
<i>malG</i>	AAK05783.1	G	-4.7	-5.3	-4.3	-2.2	-6.0	-5.6	-2.5							maltose ABC transporter permease
<i>pgmB</i>	SPS12282.1	G	-3.2	-2.8			-2.3	-2.0	-2.5							beta-phosphoglucomutase
<i>rbsD</i>	SPS10141.1	G			-2.3	-2.1				-2.4			-2.6	-2.1		D-ribose pyranase cytoplasmic mutarotase
<i>rbsK</i>	SPS10140.1	G			-2.5	2.0				-2.2			-2.0	-2.1		ribokinase
<i>xylB</i>	QQE99348.1	G					2.5	2.9			2.7					xylulose kinase
<i>xylT</i>	AAK05601.1	G	2.2													D-xylose proton-symporter
<i>xynD</i>	AAK04381.1	G					2.5		2.3	2.1			2.8			endo-1,4-beta-xylanase D
<i>xynT</i>	AAK05604.1	G				2.3										xyloside transporter
<i>yedF</i>	AAK04525.1	G	2.5				2.0	2.0			2.0	2.0				PTS system beta-glucoside-specific transporter; PTS system
<i>yeeA</i>	AAK04526.1	G	-2.8													hypothetical protein   glycoside (trehalose, maltose) hydrolase
<i>yeeB</i>	AAK04528.1	G				-2.1	-2.3		-3.1							sugar hydrolase
<i>yhgE</i>	AAK04856.1	G			2.4	3.8										hypothetical protein
<i>yjbC</i>	AAK04990.1	G									-3.8					hypothetical protein   hexose phosphatase
<i>yngG</i>	AAK05428.1	G								2.2						sugar ABC transporter permease transport and binding protein

<i>ypdA</i>	AAK05595.1	G	3.2	2.3	2.4	2.0	2.4	2.7	sugar ABC transporter substrate binding protein
<i>yqhA</i>	AAK05727.1	G	2.1	-2.4					hypothetical protein   aldose-1-epimerase
<i>yrgI</i>	AAK05812.1	G	2.7	-2.3					hypothetical protein   phosphoglycerate mutase
<b>Coenzyme transport and metabolism</b>									
<i>dfpA</i>	GEB08447.1	H				-2.2			phosphopantothenoylcysteine decarboxylase
<i>menB</i>	SPS12340.1	H	3.4						naphthoate synthase
<i>menD</i>	SPS12342.1	H				2.2			2-oxoglutarate decarboxylase menaquinone and ubiquinone
<i>nadD</i>	GFO78988.1	H					2.4		nicotinic acid mononucleotide adenylyltransferase
<i>pyrZ</i>	AAK05445.1	H			2.5		2.2		dihydroorotate dehydrogenase electron transfer subunit
<i>ribA</i>	GFO78927.1	H		2.0					3,4-dihydroxy-2-butanone 4-phosphate synthase
<i>yccH</i>	AAK04324.1	H		2.2			2.5		5'nucleosyl;-tetraphosphatase
<i>ychG</i>	AAK04378.1	H				-2.2			hypothetical protein   Protoporphyrinogen oxidase
<i>yjhB</i>	AAK05043.1	H		3.0					hypothetical protein   1,4-dihydroxy-2- naphthoate octaprenyltransferase
<i>yuhD</i>	AAK06091.1	H		2.2					hypothetical protein  methyltransferases
<b>Lipid transport and metabolism</b>									
<i>accD</i>	SPS12911.1	I		-2.4					acetyl-CoA carboxylase subunit beta
<i>fabZ1</i>	AAK04663.1	I		-2.9					(3R)-hydroxymyristoyl-ACP dehydratase
<i>mvaA</i>	PLW59014.2	I		-3.0		-3.3			hydroxymethylglutaryl-CoA reductase
<i>ydhD</i>	AAK04467.1	I	3.5	3.8		2.8			hypothetical protein
<i>yebA</i>	AAK04504.1	I				-2.8			mevalonate kinase



<i>yriF</i>	AAK05835.1	I	2.6							hypothetical protein
Translation, ribosomal structure and biogenesis										
<i>def</i>	SPS11935.1	J	-4.2							peptide deformylase
<i>infB</i>	SPS12378.1	J	2.4							translation initiation factor IF-2
<i>infC</i>	SPS12498.1	J	-2.3			-4.1				translation initiation factor IF-3
<i>lysS</i>	SPS12107.1	J	-5.4							lysyl-tRNA synthetase class II
<i>mnmA</i>	SPS12635.1	J	-2.0							tRNA-specific 2-thiouridylase MnmA
<i>rnpA</i>	SPS12578.1	J	2.6	2.8	2.2	2.2				ribonuclease P
<i>rplC</i>	SPS12433.1	J	-2.0							50S ribosomal protein L3
<i>rplD</i>	SPS12434.1	J	-2.1			-2.2				50S ribosomal protein L4
<i>rplT</i>	SPS12500.1	J	2.2							50S ribosomal protein L20
<i>rpmE2</i>	SPS12051.1	J	2.9	5.0	2.2	6.5	5.1	3.3	50S ribosomal protein L31 RpmE2	
<i>rpmI</i>	SPS12499.1	J	2.2							50S ribosomal protein L35 ribosomal proteins
<i>rpsF</i>	SPS10925.1	J	2.3							30S ribosomal protein S6
<i>rpsG</i>	SPS10759.1	J	-2.6							30S ribosomal protein S7
<i>rpsN2</i>	AAK04986.1	J	-2.2							30S ribosomal protein S14
<i>rpsT</i>	AAK05837.1	J	2.0							30S ribosomal protein S20
<i>serS</i>	SPS12712.1	J	-6.1	-5.8	-5.1	-3.1	-6.7	-6.3	-3.9	seryl-tRNA synthetase
<i>ybgE</i>	GFO78072.1	J	2.4							amidase
<i>yhdC</i>	AAK04831.1	J	2.3							acetyl transferase
<i>ylaG</i>	AAK05199.1	J	-4.3							hypothetical protein
<i>ymdC</i>	AAK05309.1	J	2.1							kanamycin kinase
<i>ynjI</i>	AAK05309.1	J	2.5							hypothetical protein
<i>yqfF</i>	AAK05713.1	J	2.1							spermidine acetyltransferase
<i>yyaL</i>	AAK04104.1	J	2.3							GTP-dependent nucleic acid-binding protein EngD
Transcription										



yveF	AAK06157.1	K	2.2	2.3	2.8	-2.1	2.5	hypothetical protein		
Replication, recombination and repair										
dnaB	SPS12362.1	L	2.5					hypothetical protein		
dnaI	WP_060416476.1	L	-3.4	-4.9	-3.4 -3.7 -2.2			primosomal protein DnaI		
dnaN	PS10614.1	L	-3.2					DNA polymerase III subunit beta		
dnaQ	AAK05080.1	L	-2.1					DNA polymerase III subunit epsilon		
mutM	SPS12735.1	L	2.6	2.8	-2.2	formamidopyrimidine-DNA glycosylase				
ogt	PLW60489.1	L	2.0 -3.5					6-O-methylguanine DNA methyltransferase		
polC	AAK06222.1	L	2.4					DNA polymerase III PolC		
recJ	SPS10369.1	L	-2.1 -2.1					ssDNA-specific exonuclease RecJ		
recO	SPS12671.1	L	2.6					DNA repair protein RecO		
sbcC	AAK05419.1	L	2.0					ATP-dependent dsDNA exonuclease degradation of DNA		
scpA	AE005176.1	L	-2.4					segregation and condensation protein A		
tag	AAK05220.1	L	-2.5 2.4					DNA-3-methyladenine glycosidase		
tra1077C	AAK04470.1	L	6.4	6.8	8.1	3.0	7.0	6.7	5.4	IS1077C transposase
tra1077D	AAK04737.1	L	-2.1					IS1077D transposase		
tra1077E	AAK04922.1	L	-3.0					IS1077E transposase		
tra904A	AAK04151.1	L	3.8	5.3	3.4				transposase of IS904A	
tra904B	AAK04235.1	L	3.7	4.8	2.2				transposase of IS904B	
tra904D	AAK04468.1	L	3.8	4.9	3.0	3.1			2.4	transposase of IS904D
tra904E	AAK04735.1	L	3.5	4.2	2.2				transposase of IS904E	
tra983A	AAK04779.1	L	-3.6					transposase of IS983A		
trpB	SPS11791.1	L	3.0					tryptophan synthase subunit beta		
xseA	GEB09426.1	L	5.0					exodeoxyribonuclease VII large subunit		
yafG	AAK04149.1	L	2.0	2.2	3.2	hypothetical protein				
yafI	AAK04152.1	L	3.5	3.9	hypothetical protein					

<i>ybdK</i>	AAK04234.1	L	2.0	3.5	2.7			2.7	2.0	hypothetical protein transposon related function	
<i>ygcE</i>	AAK04738.1	L				2.9	4.4			hypothetical protein	
<i>yidF</i>	AAK04921.1	L		3.6	3.9				2.1	hypothetical protein	
<i>ysiD</i>	AAK05915.1	L				2.7	-2.2			hypothetical protein	
<i>ytfB</i>	AAK05980.1	L				2.9				hypothetical protein	
Cell wall/membrane/envelope biogenesis											
<i>dacB</i>	AAK05048.1	M				2.9				D-alanyl-D-alanine carboxypeptidase murein sacculus and peptidoglycan	
<i>dapA</i>	SPS10159.1	M			2.3		2.4	2.3	2.9	dihydrodipicolinate synthase	
<i>ftsQ</i>	AAK05686.1	M							2.1	hypothetical protein	
<i>glmS</i>	WP_058223713.1	M	2.0							glucosamine--fructose-6-phosphate aminotransferase	
<i>murB</i>	SPS10276.1	M				2.5				UDP-N-acetylenolpyruvoylglucosamine reductase	
<i>pbp2A</i>	AIS04644.1	M				2.9				penicillin-binding protein 2a	
<i>plpB</i>	AAK04417.1	M						2.2		outer membrane lipoprotein	
<i>rgpE</i>	AAK04304.1	M				2.8	-2.2			glycosyltransferase	
<i>ycbF</i>	AAK04311.1	M				2.5				LPS biosynthesis protein	
<i>ycbG</i>	AAK04312.1	M				2.1				LPS biosynthesis protein	
<i>yibC</i>	AAK04903.1	M						-3.9		hypothetical protein	
Cell motility											
<i>acmA</i>	AAK04370.1	N				2.22	-2			autolysin cell wall hydrolase	
Posttranslational modification, protein turnover, chaperones											
<i>ahpC</i>	SPS12269.1	O				-2.5	-2.2	3.2		alkyl hydroperoxide reductase	
<i>gcp</i>	SBW29465.1	O						-4.7		DNA-binding/iron metalloprotein/AP endonuclease	
<i>osmC</i>	PLW60135.1	O		-6.5	-5.7	-5.4	-2.4	-6.5	-5.9	-4.9	osmotically inducible protein

<i>pflA</i>	QOK49714.1	O			2.8	-2.0			pyruvate-formate lyase activating enzyme		
<i>trxB2</i>	AAK05745.1	O		-2.2	2.2			-3.4	thioredoxin reductase		
<i>ydiE</i>	AAK04480.1	O			2.5	3.6	-2.4	2.6	hypothetical protein		
Inorganic ion transport and metabolism											
<i>amtB</i>	AAK05690.1	P		4.1					ammonium transporter		
<i>cbiO</i>	SBW29503.1	P	2.2			5.8		2.2	3.8	cobalt importer protein; ATP-binding subunit	
<i>dpsA</i>	GFO79963.1	P		-2.0						non-heme iron-binding ferritin	
<i>fhuB</i>	PLW60363.1	P							-2.1	ferrichrome ABC importer permease	
<i>mtsA</i>	AAK05414.1	P	-2.7	-3.4						manganese ABC importer	
<i>mtsB</i>	AAK05416.1	P	-2.2	-3.2						manganese ABC importer	
<i>mtsC</i>	AAK05415.1	P	-2.9	-4.3			-2.3			manganese ABC importer permease	
<i>pacL</i>	AAK04776.1	P							2.3	magnesium-transporting ATPase	
<i>yafB</i>	AAK04148.1	P				2.1	3.0			sulfate permease, MFS superfamily	
<i>ydaE</i>	AAK04406.1	P							2.3	Co/Zn/Cd efflux system component	
<i>yigC</i>	AAK04943.1	P					2.5			arsenate reductase	
<i>yoaB</i>	SPS12037.1	P					2.7			magnesium-transporting ATPase	
<i>yogJ</i>	AAK05544.1	P					2.2			Fe/Co/Zn/Cd efflux system component	
<i>yuhE</i>	AAK06092.1	P					2.6			copper homeostasis protein	
<i>yuiA</i>	AAK06092.1	P					2.6			heavy metal-transporting ATPase	
<i>zitQ</i>	AAK06212.1	P					3.1	-2.3		zinc ABC importer ATP binding protein	
Secondary metabolites biosynthesis, transport and catabolism											
<i>dltA</i>	WP_058205708.1	Q				-2.9		-3.0		-2.0	D-alanine--poly(phosphoribitol) ligase subunit 1
<i>dltC</i>	QQE99144.1	Q				-2.1		-3.6			D-alanine--poly(phosphoribitol) ligase subunit 2
<i>fabF</i>	SPS12386.1	Q		-2.3							3-oxoacyl-ACP synthase fatty acid and phospholipid metabolism

<i>fabG</i>	QNL91178.1	Q	-2.3							3-ketoacyl-ACP reductase
<i>ykaF</i>	AAK05079.1	Q						-2.4	-2.3	hypothetical protein
<b>General function prediction</b>										
<i>comEC</i>	AAK05870.1	R							2.7	hypothetical protein
<i>engA</i>	KWT47845.1	R					2.8			GTP-binding protein EngA
<i>yagB</i>	AIS02642.1	R					2.1			hypothetical protein
<i>ybhD</i>	AAK04270.1	R				-2.2	-2.3			hypothetical protein
<i>yceE</i>	AAK04342.1	R							4.0	hypothetical protein
<i>ycfF</i>	SBW29425.1	R						-3.5	-2.3	hypothetical protein
<i>ydhB</i>	AAK04465.1	R						-2.7		hypothetical protein
<i>yeaA</i>	AAK04493.1	R							-3.0	hypothetical protein
<i>yfgH</i>	AAK04668.1	R					2.8			hypothetical protein
<i>yheB</i>	AAK04833.1	R							2.4	hypothetical protein
<i>yhhD</i>	AAK04860.1	R				2.5				hypothetical protein
<i>yihF</i>	AAK04954.1	R						-2.3		hypothetical protein
<i>ykiF</i>	AAK05173.1	R						2.6		hypothetical protein
<i>ymdE</i>	AAK05315.1	R						-3.2		hypothetical protein
<i>yqeL</i>	AAK04319.1	R				-2.2			4.6	GTP-binding protein YqeH
<i>yqfE</i>	AAK05712.1	R					2.5			hypothetical protein
<i>yqgA</i>	AAK05716.1	R					2.4			hypothetical protein
<i>yrjE</i>	AAK05834.1	R					2.6			transport permease
<i>ysbA</i>	AAK05851.1	R	2.1	2.3	2.9	2.7				hypothetical protein
<i>yseA</i>	AAK05879.1	R						-2.6		hypothetical protein
<i>ytaB</i>	AAK05932.1	R					2.2	2.9		hypothetical protein
<i>ythC</i>	AAK06004.1	R					2.9			hypothetical protein
<i>ywfD</i>	AAK06275.1	R						2.6		hypothetical protein
<i>yxfC</i>	AAK06364.1	R					2.2			hypothetical protein
<b>Function unknown</b>										

L200001			S	-4.1		-2.2		-2.6		hypothetical protein similar to prophage bIL312 protein 12					
L200003			S	2.5		3.5				hypothetical protein					
L200005			S	2.5		2.2				hypothetical protein					
L200032			S					2.3		hypothetical protein					
L200034			S			2.8				hypothetical protein					
L200039			S					-2.7		hypothetical protein similar to bacteriophage bIL285					
L200065			S	2.4		2.7		-2.2		2.1		hypothetical protein			
L200074			S	2.9		2.4		2.0		2.5		-2.3	-2.4	2.1	hypothetical protein
L200078			S			2.1		2.7		4.5		4.4		3.7	sodium:solute symporter, former pseudogene
yacI	AAK04112.1	S			2.3								hypothetical protein		
yaiG	AAK04182.1	S			2.7		3.2		-2.2		2.0		hypothetical protein		
yaiJ	BAL52160.1	S			3.3						-3.2		hypothetical protein		
ybaC	AAK04199.1	S			-3.8		2.6		6.1		-2.4		hypothetical protein		
ybbB	SBW29265.1	S					-2.2		-2.6		-4.3		-2.3		hypothetical protein
ybcG	AAK04218.1	S			2.6								hypothetical protein		
ybfA	AAK04251.1	S									3.1		hypothetical protein		
ybgB	GFO78053.1	S			2.6								hypothetical protein		
ybjD	AAK04293.1	S			2.6		2.5						hypothetical protein		
ycbA	AAK04306.1	S							-2.2				hypothetical protein		
ycdB	AAU43207.1	S							-2.1				hypothetical protein		
ycjG	AAK04395.1	S			2.6								hypothetical protein		
ydbD	AAK04412.1	S			2.0				2.2				hypothetical protein		
yedA	AAK04521.1	S			2.8								hypothetical protein		
yfdG	AAK04648.1	S			2.1								hypothetical protein		
yfhH	AAK04680.1	S			-3.6				-2.3				hypothetical protein		

<i>yfiH</i>	AAK04692.1	S		2.2									hypothetical protein
<i>yfiI</i>	AAK04694.1	S		3.0	-2.1								hypothetical protein
<i>ygaD</i>	AAK04713.1	S		-2.4									hypothetical protein
<i>ygfE</i>	AAK04761.1	S							-2.4				magnesium importer and exporter
<i>yghD</i>	AAK04774.1	S							2.3				hypothetical protein
<i>yhbH</i>	AAK04810.1	S							-4.0				hypothetical protein
<i>yhhE</i>	AAK04861.1	S		2.8									hypothetical protein
<i>yhjA</i>	AAK04881.1	S	-2.2						-2.7				hypothetical protein
<i>yibD</i>	AAK04904.1	S							2.2				hypothetical protein
<i>yiiF</i>	AAK04961.1	S							3.6				transporter
<i>yjaE</i>	AAK04980.1	S	3.2										hypothetical protein transmembrane protein
<i>yjhA</i>	AK05042.1	S							-2.7				hypothetical protein
<i>yjjA</i>	AAK05061.1	S							-3.3				hypothetical protein
<i>ykbC</i>	AAK05084.1	S		2.7	4.3								hypothetical protein
<i>ylfI</i>	AAK05242.1	S							2.5				hypothetical protein
<i>ylgB</i>	AAK05246.1	S							-2.2	2.1			hypothetical protein
<i>yliD</i>	AAK05268.1	S	2.1	3.7				-2.1					hypothetical protein
<i>ymeA</i>	AAK05317.1	S		3.5						3.1			hypothetical protein
<i>ymhC</i>	AAK05348.1	S		3.1	-2.5								hypothetical protein
<i>ynbD</i>	AAK05394.1	S							-2.4				hypothetical protein
<i>ynjH</i>	AAK05458.1	S		4.4	6.7	6.4	2.3	6.2	6.2	3.4			hypothetical protein
<i>yogI</i>	AAK05543.1	S	-2.3										phosphate-starvation-inducible protein PsiE
<i>ypgH</i>	AAK05624.1	S		-5.3						-3.3			hypothetical protein
<i>yphH</i>	AAK05632.1	S						2.7					hypothetical protein
<i>yphK</i>	AAK05635.1	S		-2.3					-2.8				hypothetical protein
<i>ypiH</i>	AAK05645.1	S							2.1				hypothetical protein



<i>yqeA</i>	AAK05695.1	S				-3.7		2.0			-2.3	hypothetical protein
<i>yraD</i>	AAK05753.1	S				2.8	4.4					hypothetical protein
<i>yraF</i>	AAK05756.1	S								-2.1		hypothetical protein
<i>yrbB</i>	AAK05760.1	S						-2.3	-2.2	-2.1		hypothetical protein
<i>yrbH</i>	AAK05766.1	S					-2.6		3.2			hypothetical protein
<i>yreD</i>	AAK05787.1	S	3.3	3.8	4.9	3.8						hypothetical protein
<i>yrgE</i>	AAK05807.1	S								2.4		hypothetical protein
<i>yriB</i>	AAK05827.1	S				2.1		2.4			2.9	hypothetical protein
<i>ysbB</i>	AAK05852.1	S					2.8					hypothetical protein
<i>ysbC</i>	AAK05853.1	S			2.0	2.1						hypothetical protein
<i>yseD</i>	AAK05883.1	S				2.7	3.0	-2.2		2.4		hypothetical protein
<i>yshB</i>	AAK05909.1	S					2.7	-2.1				hypothetical protein
<i>ysjF</i>	AAK05925.1	S					3.0	-2.2				hypothetical protein
<i>ytcA</i>	AAK05950.1	S						-2.6	-2.2			hypothetical protein
<i>yuaB</i>	AAK06021.1	S				2.3					3.0	hypothetical protein
<i>yuiE</i>	AAK06109.1	S									2.6	hypothetical protein
<i>yujG</i>	AAK06119.1	S									4.4	hypothetical protein
<i>yvcA</i>	AAK06139.1	S				2.2	2.3					hypothetical protein
<i>yveG</i>	AAK06158.1	S				2.1						hypothetical protein
<i>yviA</i>	AAK06207.1	S				-3.8			-2.2		-2.5	hypothetical protein
<i>yxcE</i>	AAK06341.1	S					2.3					hypothetical protein
<b>Signal transduction mechanisms</b>												
<i>ytaD</i>	AAK05934.1	T				2.3				2.8	2.1	tyrosine phosphatase translation
<i>ythA</i>	AAK06002.1	T				2.3						hypothetical protein
<i>ythB</i>	AAK06003.1	T				2.7	-2.1	-3.0		4.1	-2.2	hypothetical protein
<b>Intracellular trafficking, secretion, and vesicular transport</b>												
<i>clpP</i>	AIS03218.1	U									-2.8	ATP-dependent Clp protease proteolytic subunit

<i>comGA</i>	AAK06221.1	U	2.7	3.0	-2.1	protein ComGA competence protein	
<i>sipL</i>	GFO80241.1	U	2.5			signal peptidase I	
Defence mechanisms							
<i>blt</i>	AAK04221.1	V	2.2			multidrug efflux transporter multidrug resistance	
<i>hsdS</i>	AAK57812.1	V	-3.0	-2.6	-2.1	type I restriction enzyme specificity protein	
<i>lmrA</i>	QQF01231.1	V	2.6			multidrug resistance ABC transporter ATP-binding protein	
<i>lmrP</i>	QQF00039.1	V	2.4			multidrug efflux MFS transporter	
<i>napC</i>	GFO78231.1	V	3.6			multidrug-efflux transporter multidrug resistance	
<i>ycfC</i>	AAK04353.1	V	3.0			ABC transporter permease	
<i>ydaG</i>	AAK04408.1	V	2.3			multidrug resistance ABC transporter ATP-binding protein	
<i>ypbC</i>	AAK05582.1	V	3.3	3.1		MATE family efflux transporter	
<i>ypgD</i>	AAK05620.1	V	-3.4	-2.8	-2.2	multidrug resistance ABC transporter ATP-binding protein	
<i>yvhA</i>	AAK06200.1	V	2.2			MATE family efflux transporter	
<i>ywiG</i>	AAK06301.1	V	2.1	2.0		ABC-type multidrug transport system, ATPase component	
Mobilome:prophages, transposons							
<i>bIL30901</i>		X	-2.3			integrase prophage bIL309 protein 01	
<i>bIL30909</i>		X	2.8			prophage bIL309 protein 09	
<i>bIL30911</i>		X	3.2			recombinase prophage bIL309 protein 11	
<i>bIL30913</i>	GCF_000842505.1	X	-2.1			replisome organizer prophage bIL309 protein 13	
<i>bIL30914</i>		X	2.3			DNA replication protein prophage bIL309 protein 14	
<i>bIL30922</i>		X	2.5	2.2	2.3	2.8	prophage bIL309 protein 22

<u>bIL30923</u>		X			-2.1	-2.1			prophage bIL309 protein 23
<u>bIL30928</u>		X		-5.4	-2.5		2.2	6.7 -3.4	prophage bIL309 protein 28
<u>bIL30929</u>		X		3.0					prophage bIL309 protein 29
<u>bIL30932</u>		X		2.3	3.3		2.4		prophage bIL309 protein 32
<u>bIL30936</u>		X		-2.3	-3.9	-2.2		-3.7 -3.5	prohead protease prophage bIL309 protein 36
<u>bIL30938</u>		X					2.2		prophage bIL309 protein 38
<u>bIL30942</u>		X			-2.2	-2.1			small major structural protein prophage bIL309 protein 42
<u>bIL30943</u>		X			2.3				prophage bIL309 protein 43
<u>bIL30945</u>		X					-2.1		choline ABC transporter permease and substrate binding protein
<u>bIL30949</u>		X					2.1		muramidase prophage bIL309 protein 49
<u>choS</u>	AAK04946.1	X					-2.1		prophage bIL309 protein 45 tail component
<u>pi206</u>		X			3.0				prophage bIL285 protein 06
<u>pi215</u>		X			2.0				prophage bIL285 protein 15
<u>pi240</u>		X			-3.0	-2.1		-2.0	prophage bIL285 protein 40
<u>pi301</u>		X						2.2	prophage bIL286 protein 01
<u>pi308</u>		X			2.6	4.0			prophage bIL286 protein 08
<u>pi319</u>	GCF_000845385.1	X				2.2			prophage bIL286 protein 19 tail component
<u>pi325</u>		X			2.5		-3.2		head-tail joining protein prophage bIL286 protein 25
<u>pi333</u>		X			2.7	2.8	-2.4	2.4	prophage bIL286 protein 33
<u>pi336</u>		X						2.0	prophage bIL286 protein 36
<u>pi338</u>		X				2.0	-2.2		prophage bIL286 protein 38
<u>pi339</u>		X			2.8		2.5 2.4		2.9 prophage bIL286 protein 39
<u>pi341</u>		X						2.4	prophage bIL286 protein 41

<u>pi346</u>	X				2.9	-2.3		DNA replication protein prophage bIL286 protein 46
<u>pi348</u>	X						2.3	single strand binding helix destabilising protein prophage bIL286 protein 48
<u>pi349</u>	X					3.8		prophage bIL286 protein 49
<u>pi360</u>	X					2.8		integrase prophage bIL286 protein 60
<u>ps101</u>	X			3.1		2.3		prophage bIL310 protein 01
<u>ps105</u>	X			2.8	3.7			DNA primase prophage bIL310 protein 05
<u>ps106</u>	X			2.1	3.0			prophage bIL310 protein 06
<u>ps107</u>	X			2.4	2.2	2.8	2.0	prophage bIL310 protein 07
<u>ps109</u>	X			2.6	4.2			prophage bIL310 protein 09
<u>ps115</u>	X					-2.2		prophage bIL310 protein 15 transcription regulator
<u>ps116</u>	X			-3.5	-3.0		-2.3	prophage bIL310 protein 16
<u>ps210</u>	X					2.6		prophage bIL312 protein 10
<u>ps211</u>	X				2.3			prophage bIL312 protein 11
<u>ps216</u>	X			2.1				prophage bIL312 protein 16
<u>ps303</u>	X	3.2	2.4					prophage bIL311 protein 03
<u>ps304</u>	X	2.4	2.4					prophage bIL311 protein 04
<u>ps305</u>	X	2.2						prophage bIL311 protein 05
<u>ps306</u>	X		2.5	3.7		2.0		prophage bIL311 protein 06
<u>ps311</u>	X					-4.0		prophage bIL311 protein 11
<u>ps315</u>	X				-2.5	-2.5		prophage bIL311 protein 15

GCF\_000838045.1