

Control of bacterial phenotype and chromosomal gene expression by single plasmids of *Lactococcus lactis* IL594

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Supplementary Materials

Table S1. Differentially expressed genes within plasmid-containing *L. lactis* strains and plasmid-free derivative IL1403. A gene was identified as differentially expressed between compared *L. lactis* strains if the level of its transcript differed by $|\text{Log2Ratio}| \geq 1.5$ with the statistical significance, $p < 0.05$. Differentially expressed genes were grouped based on putative functions of the encoded proteins into COG categories. In comparative transcriptomic analysis, a range of 42 to 189 changes in chromosomal genes expression caused by single-plasmid presence were detected, representing from 2% to 9% of all annotated chromosomal genes in the *L. lactis* IL1403 genome. The total number of identified unique genes reached 435.

Gene	NCBI	COG	Gene upregulation or downregulation								Protein function
	GeneID		<i>L. lactis</i> strain								
			IL1618	IL1421	IL2661	IL1619	IL1420	IL1530	IL1392	IL594	
Plasmid / plasmids		pIL1	pIL3	pIL4	pIL5	pIL6	pIL7	pIL1 pIL2 pIL3 pIL5	pIL1- pIL7		
Energy production and conversion											
<i>adhE</i>	WP_129881180.1	C			3.2		1.7	2.1	2.2	bifunctional acetaldehyde-CoA	
<i>agl</i>	CP009472.1	C							4.8	alpha-glucosidase	
<i>citB</i>	AY268077.1	C		1.8		2.0		2.3	2.5	acetate-SH-citrate lyase	
<i>citC</i>	AY268077.1	C							2.3	acetate-SH-citrate lyase	

<i>citD</i>	AY268077.1	C				3.0		citrate lyase subunit gamma
<i>gltA</i>	NC_002662.1	C		2.1	1.6			citrate synthase
<i>gltP</i>	NC_009004.1	C	1.8	1.5	3.0	2.1		glutamate ABC transporter permease
<i>gltQ</i>	NC_002662.1	C			2.9	1.8	1.9	glutamate ABC transporter ATP-binding protein
<i>gltS</i>	NC_017486.1	C	1.9	2.3	3.2	3.0		glutamate or arginine ABC transporter substrate binding protein
<i>ipd</i>	NC_017486.1	C		1.6				indole-3-pyruvate decarboxylase
<i>maa</i>	NC_020450.1	C				4.6		maltose O-acetyltransferase
<i>mleP</i>	NC_020450.1	C	3.0			3.2		malate transporter
<i>mleS</i>	AAK04998.1	C	3.0			2.9		malate dehydrogenase
<i>msmK</i>	NC_017486.1	C					-2.6	multiple sugar ABC transporter ATP-binding protein
<i>pdhB</i>	NC_020450.1	C				2.1		PDH E1 component subunit beta
<i>pydA</i>	NC_002662.1	C		1.8				dihydroorotate dehydrogenase 1A
<i>pyrZ</i>	AAK05445.1	C		-2.0		-2.4		dihydroorotate dehydrogenase electron transfer subunit
<i>trxA</i>	NZ_CP059048.1	C	2.6					thioredoxin
<i>trxB1</i>	NZ_CP059048.1	C	1.8					thioredoxin reductase
<i>tyrS</i>	WP_058204081.1	C	-1.7		-2.5			tyrosyl-tRNA synthetase
<i>ybiE</i>	GFO78088.1	C	1.9			3.3		oxidoreductase
<i>yddB</i>	AAK04431.1	C				2.0		oxidoreductase
<i>yfdE</i>	NP_389061.1	C	-1.8					hypothetical protein similar to myo-inositol monophosphatases
<i>yfhC</i>	AAK04676.1	C	2.6	1.5	3.7			hypothetical protein
<i>ygaJ</i>	NP_388758.2	C	2.0					putative peptidase
<i>yiaD</i>	AAK04894.1	C	3.4	1.9		2.1		NADH-flavin reductase
<i>yjcA</i>	YP_026228.1	C	1.7					ABC transporter ATP-binding protein
<i>yjgC</i>	NP_389098.1	C					-1.5	amino acid ABC transporter substrate binding protein
<i>ylbA</i>	NP_459521.1	C	1.6					ABC transporter ATP-binding protein
<i>ymgG</i>	NZ_CM001513.1	C	1.7					hypothetical protein

<i>ymgH</i>	NZ_CM001513.1	C	1.6		1.5		hypothetical protein	
<i>ymgK</i>	YP_009518766.1	C	1.5		2.4		oxidoreductase	
<i>yobA</i>	NP_416355.1	C	1.9		1.7		hypothetical protein	
<i>yogA</i>	NP_389725.1	C			-1.7		hypothetical protein	
<i>yphC</i>	NP_417040.2	C			-3.9		oxidoreductase	
<i>yqcA</i>	NP_417270.1	C			1.7		oxidoreductase	
<i>yrjA</i>	NZ_CP059048.1	C	-1.5				hypothetical protein	
<i>yrjB</i>	AAK05831.1	C	1.6	1.5	2.0	1.9	oxidoreductase	
<i>yrjC</i>	NZ_CP059048.1	C			1.7		iron-binding oxidase subunit	
<i>yugB</i>	NP_268143.1	C			2.3		oxidoreductase	
<i>ywdA</i>	NP_268313.1	C			1.8		hypothetical protein	
<i>ywdC</i>	NP_268315.1	C	1.7		1.7		hypothetical protein	
<i>ywiD</i>	AAK06296.1	C	2.9				hypothetical protein	
<i>ywiH</i>	AAK06302.1	C	2.8	2.2	1.6	3.3	ABC transporter permease	
<i>ywjF</i>	NP_268372.1	C	1.6				3-hydroxyisobutyrate dehydrogenase	
Cell cycle control, cell division, chromosome partitioning								
<i>ezrA</i>	NC_022369.1	D	2.4		1.8		septation ring formation regulator EzrA	
<i>scpA</i>	NP_267433.1	D			-1.6		segregation and condensation protein A	
<i>yihA</i>	NP_267005.1	D	1.8		1.8		hypothetical protein	
<i>yihB</i>	NP_267006.1	D	1.7		1.6		hypothetical protein	
Amino acid transport and metabolism								
<i>arcA</i>	WP_004254504.1	E	1.8		3.0	2.8	2.5	arginine deiminase
<i>arcB</i>	AJ001103.1	E	1.7		2.8	2.2	2.3	ornithine carbamoyltransferase
<i>arcC1</i>	AAK06131.1	E			2.7			carbamate kinase
<i>arcC2</i>	AAK06131.1	E	2.6	1.7	2.6			carbamate kinase
<i>arcD1</i>	U81991.1	E	1.8		3.2	1.9	2.1	arginine/ornithine antiporter
<i>argF</i>	NC_022369.1	E	1.7				1.7	ornithine carbamoyltransferase

<i>aroH</i>	NC_000913.3	E			-2.0				phospho-2-dehydro-3-deoxyheptonate aldolase
<i>asd</i>	NC_000913.3	E					2.3		aspartate-semialdehyde dehydrogenase
<i>bmpA</i>	AE005176.1	E					-2.2		basic membrane protein A
<i>ceo</i>	U23376.1	E			1.7				N5-carboxyethyl-ornithine synthase
<i>cysD</i>	AAK04171.1	E					-2.2		O-acetylhomoserine sulfhydrylase
<i>cysK</i>	QOK50869.1	E		-2.5	-2.6	-1.6	-2.7		cysteine synthase serine family
<i>cysM</i>	NC_049805.1	E		-3.0	-2.9	-1.7	-2.4		cysteine synthase
<i>glnB</i>	AAK05689.1	E				2.1			nitrogen regulatory protein P-II
<i>glnQ</i>	SPS12229.1	E						-1.9	glutamine ABC transporter ATP-binding protein
<i>hisA</i>	NC_022369.1	E				1.5			1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase
<i>ilvD</i>	SPS12837.1	E					2.2		dihydroxy-acid dehydratase
<i>leuC</i>	NC_022369.1	E				1.5			isopropylmalate isomerase large subunit dehydratase component
<i>lysP</i>	NC_020450.1	E		2.0			2.3		lysine specific permease
<i>mapA</i>	NC_002662.1	E	2.8				5.2		maltose phosphorylase
<i>metB1</i>	NC_017486.1	E	-1.5						cystathionine gamma-synthase
<i>metB2</i>	NC_020450.1	E		-2.8	-1.6	-2.4	-1.6	-3.2	cystathionine gamma-synthase
<i>oppA</i>	QQF01346.1	E		1.8			2.4		oligopeptide ABC transporter substrate binding protein
<i>oppB</i>	QQF01347.1	E		3.2	7.6		3.8	6.4	oligopeptide ABC transporter permease
<i>oppC</i>	QQF01348.1	E			7.9	2.0	2.0	6.3	oligopeptide ABC transporter permease
<i>oppD</i>	QQF01345.1	E			5.9			5.0	oligopeptide ABC transporter ATP binding protein
<i>oppF</i>	QQE99754.1	E		1.5	6.9		1.8	5.7	oligopeptide ABC transporter ATP binding protein
<i>optS</i>	NC_002662.1	E		1.8		2.3	1.5	2.2	oligopeptide ABC transporter substrate binding protein
<i>pepDB</i>	NC_002662.1	E	1.7						dipeptidase
<i>pepF</i>	CAA83534.1	E					2.0	1.6	oligoendopeptidase F
<i>potA</i>	NC_000913.3	E					-1.8		spermidine/putrescine ABC transporter ATP-binding protein

<i>poxL</i>	NC_009004.1	E	2.8	1.7	1.8	2.7	2.3	pyruvate oxidase	
<i>serB</i>	NP_266761.1	E			1.6			phosphoserine phosphatase	
<i>ybeC</i>	NP_266300.1	E	1.9				1.6	hypothetical protein	
<i>yceJ</i>	NP_266406.1	E				1.6		hypothetical protein	
<i>ycjI</i>	WP_226319220.1	E					-1.9	hypothetical protein	
<i>yddA</i>	NP_266488.1	E		2.4	2.6		3.0	transporter transport and binding protein	
<i>ydgC</i>	NP_266512.1	E					1.8	amino acid permease	
<i>yibG</i>	AAK04907.1	E				-1.6		amino acid permease transport and binding protein	
<i>ylcC</i>	NP_267269.1	E	2.0					hypothetical protein	
<i>ylcF</i>	NP_267272.1	E		2.0			1.6	hypothetical protein	
<i>yneH</i>	NP_267469.2	E			2.5			hypothetical protein	
<i>yrfB</i>	NP_267851.1	E					1.8	NADH-dependent oxidoreductase	
<i>yrfD</i>	AAK05797.1	E					1.8	amino acid antiporter	
<i>ysaB</i>	NP_267905.1	E	3.7			3.0	2.2	ABC transporter permease and substrate binding protein	
<i>ysaC</i>	NP_267906.1	E	3.0			2.8	2.1	ABC transporter ATP-binding protein	
<i>ysaD</i>	NP_267907.1	E	2.8			2.9	1.6	hypothetical protein	
<i>yshA</i>	AAK05907.1	E				-2.1	-1.6	glutamate antiporter	
<i>ysjA</i>	NP_267979.1	E					-2.2	-1.6	amino acid permease transport and binding protein
Nucleotide transport and metabolism									
<i>apt</i>	AE005176.1	F	-2.5						adenine phosphoribosyltransferase
<i>carA</i>	NC_022369.1	F			-2.3		-1.7		carbamoyl phosphate synthase small subunit
<i>carB</i>	AJ000109.1	F			-1.9		-2.3		carbamoyl phosphate synthase large subunit
<i>coaA</i>	AB863013.1	F			1.6		-3.2		pantothenate kinase
<i>dukA</i>	GEB08937.1	F		-1.7	-1.8		-2.2		deoxynucleoside kinase nucleotide and nucleoside interconversions
<i>gmk</i>	NC_022369.1	F	-2.0						guanylate kinase
<i>nrdE</i>	NZ_CP094882.1	F	-2.1				-1.5		ribonucleotide-diphosphate reductase subunit alpha
<i>nrdG</i>	NC_020450.1	F	-1.6						anaerobic ribonucleoside-triphosphate reductase

<i>pbuX</i>	NC_000964.3	F	-1.8							xanthine/uracil permease	
<i>purR</i>	NP_268416.1	F	1.9		1.7					<i>pur</i> operon repressor general regulatory function	
<i>pydB</i>	NP_267502.1	F		-2.5	-1.5	-2.4				dihydroorotate transferase	
<i>pyrB</i>	NP_267758.1	F		-2.1						aspartate carbamoyltransferase catalytic subunit	
<i>pyrC</i>	NP_267225.1	F		-2.2		-1.8				dihydroorotase	
<i>pyrE</i>	NP_267224.1	F		-2.7	-2.0	-2.2		-1.9		orotate phosphoribosyltransferase	
<i>pyrF</i>	NP_267501.1	F		-1.9		-1.8				orotidine 5'-phosphate decarboxylase type 1 subfamily	
<i>pyrP</i>	NP_267759.1	F		-2.6		-2.1				uracil permease	
<i>pyrR</i>	SPS10181.1	F				-2.4				bifunctional pyrimidine regulatory protein PyrR	
<i>xpt</i>	AAK05244.1	F	-2.8							xanthine phosphoribosyltransferase	
<i>yfiC</i>	NP_266745.1	F		-1.6						hypothetical protein	
<i>yfiG</i>	NP_266749.1	F	-2.0							thymidine kinase	
<i>ygcC</i>	NP_266791.1	F	-1.7							hypothetical protein	
<i>yriD</i>	NP_267887.1	F	-1.7							xanthine/uracil/vitamin C permease	
Carbohydrate transport and metabolism											
<i>agl</i>	NP_267834.1	G					4.8			alpha-glucosidase degradation of polysaccharides	
<i>amyL</i>	AE005176.1	G			1.7					alpha-amylase	
<i>amyY</i>	AE005176.1	G					5.1			alpha-amylase	
<i>dexA</i>	AE005176.1	G					4.7			oligo—alpha-1,6-glucosidase	
<i>dexC</i>	GFO79576.1	G					5.1			neopullulanase	
<i>dhaL</i>	NC_022369.1	G			1.6			1.9		dihydroxyacetone kinase	
<i>dhaM</i>	NC_022369.1	G			1.5			1.6		dihydroxyacetone kinase	
<i>eno</i>	NC_022369.1	G			2.3		3.9			phosphopyruvate hydratase enolase	
<i>fruA</i>	AAK05057.1	G	2.0		1.8					PTS system fructose-specific transporter subunit IIABC	
<i>fruC</i>	NC_015902.1	G	2.1		1.7	2.2				1-phosphofructokinase	
<i>galE</i>	WP_058218180.1	G		-1.9			-1.9			UDP-glucose 4-epimerase	
<i>galK</i>	NC_002662.1	G		-3.4	-3.7		-3.6	-2.9	-2.4	-3.2	galactokinase

<i>galM</i>	NC_020450.1	G	-3.4	-3.5	-3.7	-2.9	-2.3	-2.9	aldose 1-epimerase
<i>galT</i>	NC_022369.1	G	-3.6	-3.9	-3.3	-3.2	-3.0	-2.6	galactose-1-phosphate uridylyltransferase
<i>galP</i>	WP_004254704.1	G	-3.7	-4.0	-3.0	-3.0	-2.4	-2.5	glycoside-pentoside-hexuronide (GHP): cation symporter
<i>thgA</i>	NP_268138.1	G	-2.9	-3.0	-3.0	-2.4	-2.0	-2.4	thiogalactoside acetyltransferase
<i>lacZ</i>	NC_002662.1	G	-3.1	-3.5	-3.4	-2.8	-2.4	-3.1	beta-D-galactosidase
<i>gapA</i>	NC_020450.1	G	2.6						glyceraldehyde 3-phosphate dehydrogenase
<i>glpF1</i>	NC_009004.1	G	1.7		1.7				glycerol uptake facilitator
<i>glpT</i>	NC_009004.1	G					1.5		glycerol-3-phosphatase transporter
<i>kdgA</i>	NC_002662.1	G	2.1	1.8			2.4		keto-hydroxyglutarate-aldolase
<i>malE</i>	AAK05781.1	G						-5.4	maltose ABC transporter substrate binding protein
<i>malF</i>	AAK05782.1	G						-5.3	maltose ABC transporter permease
<i>malG</i>	AAK05783.1	G						-4.5	maltose ABC transporter permease
<i>malQ</i>	NC_002662.1	G			1.6				4-alpha-glucanotransferase
<i>mtlF</i>	NC_020450.1	G					1.6		PTS system mannitol-specific transporter subunit IIA
<i>nagA</i>	NZ_CP094882.1	G	-1.5						N-acetylglucosamine-6-phosphate deacetylase
<i>ptbA</i>	NP_267616.1	G						-1.6	PTS system beta-glucoside-specific transporter subunit IIABC
<i>rpiA</i>	NP_268390.1	G	2.0		1.7			2.1	ribose-5-phosphate isomerase A
<i>tagH</i>	NP_267071.1	G	1.6	1.6			1.9		teichoic acid ABC transporter ATP binding protein
<i>xylA</i>	NP_267665.1	G			2.0				xylose isomerase
<i>xylH</i>	NP_266730.1	G			-1.6				4-oxalocrotonate tautomerase
<i>xylT</i>	AAK05601.1	G	2.1	2.1			2.4		D-xylose proton-symporter
<i>xynB</i>	NP_267664.1	G					1.6		beta-1,4-xylosidase
<i>xynT</i>	AAK05604.1	G		1.6			2.1		xyloside transporter
<i>ycgC</i>	NP_266420.1	G	1.5						hypothetical protein
<i>yeeB</i>	AAK04528.1	G	2.1						hydrolase
<i>yfbG</i>	NP_266680.1	G		-5.4					hypothetical protein
<i>yhgD</i>	NP_266913.1	G	2.7	2.6			3.2		hypothetical protein

<i>yhgE</i>	AAK04856.1	G	4.1	3.7	2.3	4.0	hypothetical protein		
<i>yoiC</i>	NP_267614.1	G				1.6	hypothetical protein		
<i>ypcA</i>	NP_267645.1	G		2.3		2.4	P-beta-glucosidase		
<i>ypcC</i>	NP_267647.1	G		-1.6			hypothetical protein		
<i>ypcD</i>	NP_267648.1	G		-1.6			endo-beta-N-acetylglucosaminidase		
<i>ypjA</i>	NP_267705.1	G	1.9	1.5	1.7	2.4	dehydrogenase		
<i>yqgE</i>	NP_267779.1	G		1.8			transporter		
<i>yqhA</i>	AAK05727.1	G		-1.7			hypothetical protein aldose-1-epimerase		
<i>yvdD</i>	NP_268205.1	G		1.5			transporter		
<i>yxdE</i>	NP_268407.1	G	1.6				oxidoreductase		
<i>yxdG</i>	NP_268409.1	G	2.6	2.7	2.7	1.9	2.0	3.3	transporter
<i>yxfA</i>	NP_268421.1	G				-1.7	transporter		
Coenzyme transport and metabolism									
<i>apbE</i>	AE005176.1	H				-2.3	thiamine biosynthesis lipoprotein		
<i>hemH</i>	NC_022369.1	H			-1.7		ferrochelatase protoheme ferro-lyase		
<i>nadE</i>	NC_022369.1	H	3.2		1.9		NAD synthetase		
<i>pabA</i>	NC_000913.3	H			-2.2		-2.4	para-aminobenzoate synthase component II folic acid	
<i>pabB</i>	NC_000913.3	H			-2.5		-2.4	-1.7	para-aminobenzoate synthase component I folic acid
<i>preA</i>	NC_013656.1	H	1.5	1.5	1.9		prenyl transferase		
<i>ribG</i>	NP_267149.1	H		1.6	1.9		riboflavin-specific deaminase riboflavin and cobalamin		
Lipid transport and metabolism									
<i>accB</i>	WP_012897457.1	I				2.4	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit		
<i>accC</i>	WP_012897458.1	I				1.7	acetyl-CoA carboxylase biotin carboxylase subunit		
<i>accD</i>	SPS12911.1	I				1.6	acetyl-CoA carboxylase subunit beta		
<i>acpD</i>	CP009472.1	I		-1.9			ACP phosphodiesterase		
<i>butA</i>	NC_020450.1	I		1.5			acetoin reductase fermentation		
<i>fabD</i>	NC_022369.1	I				2.3	ACP S-malonyltransferase		

<i>fabI</i>	NC_022369.1	I	1.7				enoyl-ACP reductase
<i>fabZ</i>	NC_022369.1	I	1.6			2.2	(3R)-hydroxymyristoyl-ACP dehydratase
<i>fadD</i>	AE005176.1	I		-5.9		2.1	long-chain acyl-CoA synthetase
<i>yfbB</i>	NP_461239.3	I		-7.2	-1.8	-2.4	hypothetical protein
<i>ygbB</i>	NP_266781.1	I	1.7	2.2	1.7	1.5	hypothetical protein
<i>yqaG</i>	NP_267722.1	I		-2.7	-1.5		hypothetical protein
<i>yveB</i>	NP_268212.1	I				1.6	hypothetical protein
<i>yveH</i>	NP_268218.1	I		4.0		1.6	hypothetical protein
Translation, ribosomal structure and biogenesis							
<i>aldR</i>	JXKB01000001.1	J	1.5				AldR regulatory protein
<i>rluC</i>	NP_267508.1	J				1.7	pseudouridine synthase
<i>truB</i>	NP_267282.1	J				-1.6	tRNA pseudouridine synthase B
<i>yabC</i>	NP_266164.1	J	1.8				hypothetical protein
<i>ybiD</i>	NP_266335.1	J			1.5		ribosomal RNA large subunit methyltransferase
<i>ygdA</i>	NP_266799.1	J		1.6	1.9	1.7	hypothetical protein
<i>ynjI</i>	AAK05309.1	J	1.9		1.7	1.6	hypothetical protein
<i>ynjJ</i>	NP_267518.1	J	2.3		1.6		hypothetical protein
<i>ywfF</i>	NP_268336.1	J	-1.7				hypothetical protein
<i>ywfG</i>	NP_268337.1	J	2.4		2.5		hypothetical protein
Transcription							
<i>adaA</i>	WP_129881369.1	K				1.9	methylphosphotriester-DNA alkyltransferase
<i>cspD</i>	AE005176.1	K		-6.1			cold shock protein D
<i>cspE</i>	Y17217.1	K		1.6			cold shock protein E
<i>dhaK</i>	NP_266402.2	K			2.0	2.3	<i>dhaKLM</i> operon coactivator, dihydroxyacetone utilization pathway
<i>fur</i>	NC_002662.1	K	2.2				ferric uptake regulator
<i>gadR</i>	NZ_CP017194.1	K		-2.2		-1.9	positive regulator
<i>hrcA</i>	NC_022369.1	K	1.6				heat-inducible transcription repressor

<i>fruR</i>	NC_017478.1	K						1.6	DeoR family transcription regulator of fructose utilization pathway
<i>nadR</i>	NC_020450.1	K	2.1					1.7	NadR family transcription regulator, NAD cellular biosynthesis pathway
<i>phoU</i>	NC_022369.1	K	2.1						phosphate transport system regulator
<i>rcfB</i>	NP_268391.1	K						1.8	CRP/FNR family transcription regulator involved in pH homeostasis
<i>rliA</i>	NP_267832.1	K	2.8	1.6				1.9	transcriptional regulator LacI-family regulators, putative regulatory function
<i>rliDB</i>	NP_268306.1	K		3.0	2.3	3.2	2.1	3.3	transcriptional regulator LacI-family regulators, putative regulatory function
<i>rlrA</i>	NP_267392.1	K						-1.6	LysR-family transcription regulator, putative regulatory function
<i>rmaA</i>	NP_266898.1	K		-1.6				-1.6	MarR family transcriptional regulator of fatty acid biosynthesis pathway
<i>rmaG</i>	NP_266926.1	K		-2.1					MarR family transcriptional regulator of fatty acid biosynthesis pathway
<i>rmaJ</i>	NP_266747.1	K	-1.6						MarR-family transcriptional regulator of hyaluronan biosynthesis pathway
<i>rpoD</i>	NP_266709.1	K	1.8						RNA polymerase sigma factor RpoD
<i>sigX</i>	NP_268323.1	K						1.6	RNA polymerase ECF sigma factor
<i>tagR</i>	NP_267067.1	K						1.9	transcriptional regulator similar to EpsR, possibly involved in exopolysaccharides biosynthesis
<i>ybaI</i>	NP_266263.1	K	-1.8						glycosyl transferase glycosyltransferase family 2
<i>ybeF</i>	NP_266307.1	K		1.7	2.0	1.9		2.3	hypothetical protein
<i>yfeA</i>	NP_266710.1	K		1.6		2.1			RpiR family of transcription regulator, putative regulatory function
<i>ygfC</i>	NP_266817.1	K		-2.9				-4.8	TetR/AcrR family transcription regulator of heme homeostasis processes
<i>yjaB</i>	NP_267035.1	K	2.5						transcriptional regulator, LytR family, putative regulatory function

<i>yjaJ</i>	AAK04985.1	K	1.6			transcriptional regulator, LytR family, putative regulatory function	
<i>ykhD</i>	NP_267216.1	K		1.8		redox-sensing transcriptional repressor Rex	
<i>yliA</i>	NP_267323.1	K	2.0			positive transcription regulator	
<i>ynaA</i>	NP_267426.1	K	2.2			transcriptional regulator, heat and DNA damage induction	
<i>ynaB</i>	AAK05369.1	K	2.2		1.5	transcriptional regulator, putative regulatory function	
<i>ynaE</i>	NP_267430.2	K		1.6		hypothetical protein, putative regulatory function	
<i>yogM</i>	NP_267604.1	K	1.6	1.6		hypothetical protein	
<i>yohC</i>	AAK05547.1	K			1.6	TetR/AcrR family transcription regulator, putative regulatory function	
<i>yqfA</i>	NP_266815.1	K		-1.7		hypothetical protein	
<i>yrfA</i>	NP_267850.1	K	1.5			ArsR family transcription regulator, putative regulatory function	
<i>yrfE</i>	NP_267858.1	K		-1.6		LytR family transcriptional regulator , putative regulatory function	
<i>glaR</i>	NP_268142.1	K		-1.8	-1.7	RpiR family transcription regulator of galactose utilization Leloir pathway	
<i>ywjD</i>	NP_268370.1	K		-1.7	-1.7	-1.8	PBSX(XRE) family transcription regulator, putative regulatory function
<i>yxbF</i>	NP_268394.1	K		-2.2	2.4		hypothetical protein
Replication, recombination and repair							
<i>comEA</i>	NC_002662.1	L	1.6				hypothetical protein competence protein
<i>dinG</i>	NC_022369.1	L			-1.5		DinG ATP-dependent helicase
<i>dinP</i>	NC_000962.3	L				1.7	DNA polymerase IV
<i>hslB</i>	NC_002662.1	L	2.5			2.3	HU-like DNA-binding protein
<i>recJ</i>	SPS10369.1	L	-1.6				ssDNA-specific exonuclease RecJ
<i>recX</i>	NP_268339.1	L	1.7				recombination regulator RecX
<i>ssbA</i>	NP_266548.1	L			3.1	1.6	single-stranded DNA-binding protein
<i>xerD</i>	NP_266801.1	L	1.5				integrase-recombinase

Posttranslational modification, protein turnover, chaperones									
<i>clpE</i>	AF023421.1	O	2.4						ATP-dependent protease
<i>gpo</i>	NC_020450.1	O	1.8						glutathione peroxidase thioredoxin, glutaredoxin, and glutathione
<i>groES</i>	NC_022369.1	O	2.8						co-chaperonin GroES 10 kDa chaperonin
<i>osmC</i>	PLW60135.1	O	2.5						osmotically inducible protein
<i>pmsX</i>	NC_020450.1	O	2.0						peptide methionine sulfoxide reductase t
<i>sugE</i>	NP_266278.1	O		1.8	2.3	2.2			SugE protein chaperones
<i>ybjA</i>	NP_266345.1	O	1.9						methionine sulfoxide reductase B
<i>yfcF</i>	NP_266694.1	O		2.0	1.5	2.0		1.9	hypothetical protein
<i>ynhC</i>	NP_267492.1	O	1.5						hypothetical protein
<i>ynhD</i>	NP_267493.1	O			1.7				hypothetical protein
Inorganic ion transport and metabolism									
<i>amtB</i>	AAK05690.1	P				-1.7		1.9	-1.7 -2.2 ammonium transporter
<i>busAB</i>	AF393650.1	P					1.8		betaine ABC transporter permease and substrate binding protein
<i>cadA</i>	U78967.1	P	2.3			3.7		2.4	cadmium efflux ATPase transort and binding protein
<i>cbiO</i>	AE005176.1	P				2.3		3.9	cobalt transporter ATP-binding subunit
<i>feoA</i>	NC_022369.1	P						1.5	ferrous ion transport protein A
<i>mtsA</i>	AAK05414.1	P				-3.2		-3.7 -3.6	manganese ABC importer
<i>mtsB</i>	AAK05416.1	P				-2.0		-2.7	manganese ABC importer
<i>mtsC</i>	AAK05415.1	P				-2.0		-2.6 -3.8	manganese ABC importer permease
<i>pacL</i>	AAK04776.1	P				2.3		2.4	magnesium-transporting ATPase
<i>pstF</i>	NC_022369.1	P	1.5						phosphate ABC transporter substrate-binding protein
<i>yafB</i>	AAK04148.1	P		2.1	1.6	2.7		2.6	sulfate permease, MFS superfamily
<i>ybcC</i>	NP_266275.1	P		1.8		1.7		1.7	MATE family efflux transporter
<i>yceA</i>	NP_266398.1	P		1.6				1.6	hypothetical protein
<i>ydiF</i>	NP_266539.1	P					1.7		Na ⁺ /H ⁺ antiporter transort and binding protein, cations
<i>ygfE</i>	AAK04761.1	P			1.8	-5.7		-1.9 -2.7 2.0	magnesium importer and exporter

<i>yjdJ</i>	NP_266539.1	P	1.7	2.1	1.8	potassium channel protein transort and binding protein, cations	
<i>ymgF</i>	NP_267394.1	P	1.9	1.6		hypothetical protein	
<i>ynjC</i>	NP_267510.1	P			1.6	hypothetical protein	
<i>ynjE</i>	NP_267512.1	P	1.9	1.5	1.6	hypothetical protein	
<i>ynjF</i>	NP_267513.1	P			1.6	hypothetical protein	
<i>yphB</i>	NP_267639.1	P	1.8	2.0	2.1	magnesium transporter transport and binding protein	
<i>ytgB</i>	NP_268049.1	P	2.3	2.0		cesium ABC transporter substrate binding protein	
<i>yuhE</i>	AAK06092.1	P	2.5	1.5	1.8	copper homeostasis protein	
<i>yvfA</i>	NP_268222.1	P	1.5			metal ABC transporter substrate binding protein	
Secondary metabolites biosynthesis, transport and catabolism							
<i>aldC</i>	NC_000962.3	Q		2.0		alpha-acetolactate decarboxylase fermentation	
<i>dltA</i>	WP_058205708.1	Q	3.0	2.1		D-alanine-poly(phosphoribitol) ligase subunit 1	
<i>dltC</i>	QQE99144.1	Q	-1.9	2.2	-1.8	-2.2	D-alanine-poly(phosphoribitol) ligase subunit 2
<i>fabG2</i>	AE005176.1	Q	2.1	1.9	2.1	1.6	3-oxoacyl-ACP reductase
<i>yoaI</i>	NP_267527.1	Q		1.6			hypothetical protein
<i>yrbC</i>	NP_267819.1	Q			1.8		1,4-dihydroxy-2-naphthoate octaprenyltransferase
<i>yrbE</i>	NP_267821.1	Q		1.6	2.0		hypothetical protein
General function prediction							
<i>comEC</i>	AAK05870.1	R	1.9	1.9	2.4		hypothetical protein competence protein
<i>yhhD</i>	AAK04860.1	R	2.0	1.7	1.5	2.6	hypothetical protein
<i>ysbA</i>	AAK05851.1	R	1.6			1.6	hypothetical protein
<i>ysbD</i>	NP_267914.1	R	-2.2		-1.8		hypothetical protein
<i>ythC</i>	AAK06004.1	R		2.4			hypothetical protein
Function unknown							
<i>L20006</i> <i>5</i>	YP_005869326.1	S			2.3	1.7	hypothetical protein
<i>yafJ</i>	NP_266211.1	S	1.6		2.0		hypothetical protein
<i>yaiB</i>	NP_266234.1	S	1.7	1.7	2.0		hypothetical protein

<i>yaiH</i>	NP_266241.1	S		1.7	1.6	1.7	hypothetical protein
<i>yaiI</i>	NP_266239.1	S	2.4	2.0		2.4	hypothetical protein
<i>yaiJ</i>	BAL52160.1	S	2.6	2.2	1.8	3.2	hypothetical protein
<i>ybeH</i>	NP_266301.1	S			2.3	1.9	hypothetical protein
<i>ybfC</i>	NP_266313.1	S		2.0			hypothetical protein
<i>ybgA</i>	NP_266314.1	S	1.6	1.8			hypothetical protein
<i>ycdA</i>	NP_266387.1	S		1.6			hypothetical protein
<i>yciF</i>	NP_266444.1	S	1.5				hypothetical protein
<i>yciG</i>	NP_266445.1	S	1.8		2.1	2.3	hypothetical protein
<i>ydbD</i>	AAK04412.1	S				1.5	hypothetical protein
<i>yeiD</i>	NP_266641.1	S	2.2		-2.3		hypothetical protein
<i>yfbK</i>	NP_266684.1	S		-3.5	-2.1		hypothetical protein
<i>yfiH</i>	AAK04692.1	S	-1.8				hypothetical protein
<i>yfiI</i>	AAK04694.1	S	-2.0				hypothetical protein
<i>ygaD</i>	AAK04713.1	S	-1.8				hypothetical protein
<i>ygeB</i>	NP_266810.1	S			-1.6	-2.1	hypothetical protein
<i>ygeC</i>	NP_266811.1	S	-2.1				hypothetical protein
<i>yghB</i>	NP_266830.1	S				1.5	hypothetical protein
<i>yhhA</i>	NP_266915.1	S	1.8			2.3	hypothetical protein
<i>yhhB</i>	NP_266916.1	S				1.7	hypothetical protein
<i>yhhC</i>	NP_266917.1	S			2.6		hypothetical protein
<i>yhjA</i>	AAK04881.1	S	4.3	2.1	1.9	2.5	hypothetical protein
<i>yhjE</i>	NP_266943.1	S				-1.7	hypothetical protein
<i>yiaC</i>	NP_266951.1	S	-1.8				hypothetical protein
<i>yiiD</i>	NP_267017.1	S			2.1		hypothetical protein
<i>yjdl</i>	NP_267069.1	S	2.0			1.8	hypothetical protein
<i>yjff</i>	NP_267090.1	S	1.6				hypothetical protein
<i>ykbC</i>	AAK05084.1	S	1.8			2.2	hypothetical protein
<i>ykbD</i>	NP_267143.1	S	1.9	1.5		1.9	hypothetical protein

<i>ykbE</i>	NP_267144.1	S			1.6					hypothetical protein
<i>ykcE</i>	NP_267155.1	S	2.0							hypothetical protein
<i>ykJI</i>	NP_267241.1	S		-2.0				-2.3		hypothetical protein
<i>ylhB</i>	NP_267317.1	S			2.5					hypothetical protein
<i>yliD</i>	AAK05268.1	S		2.5	1.9			2.6		hypothetical protein
<i>ymbC</i>	NP_267348.1	S			1.7	2.0	1.9	1.9		hypothetical protein
<i>ymbD</i>	NP_267349.1	S		2.3	2.0	2.1		2.6		hypothetical protein
<i>ymbH</i>	NP_835314.1	S		1.7				1.8		hypothetical protein, putative protease
<i>ymcA</i>	NP_267355.1	S		1.6				2.1		hypothetical protein
<i>ymcB</i>	NP_267356.1	S		2.0				2.0		hypothetical protein
<i>ymcC</i>	NP_267357.1	S		2.2				1.6		hypothetical protein
<i>ymeA</i>	AAK05317.1	S		2.6	2.5		1.8	3.2		hypothetical protein
<i>ymhG</i>	YP_007508531.1	S						1.8		hypothetical protein
<i>yndE</i>	NP_267456.1	S		1.7						hypothetical protein
<i>yneC</i>	NP_267464.1	S	4.0		2.4	3.1				hypothetical protein
<i>yneG</i>	NP_267468.1	S			2.6					hypothetical protein
<i>ynfH</i>	NP_267481.1	S		2.4		2.7	2.9	1.9	2.1	hypothetical protein
<i>ynhA</i>	NP_267490.1	S							-2.8	hypothetical protein
<i>yniC</i>	NP_267500.1	S					-1.6			hypothetical protein
<i>yniJ</i>	NP_267507.1	S		1.7		1.7		2.1		hypothetical protein
<i>yofM</i>	NP_267590.1	S		-2.0				-1.8		DNA-binding protein
<i>yohD</i>	NP_267606.1	S	1.7							hypothetical protein
<i>ypaG</i>	NP_267633.1	S			1.6					hypothetical protein
<i>ypiH</i>	AAK05645.1	S						1.7		hypothetical protein
<i>ypiJ</i>	NP_267702.1	S						1.8		hypothetical protein
<i>ypiL</i>	NP_267704.1	S			1.5					hypothetical protein
<i>yqbl</i>	YP_007508825.1	S			1.6			2.0		hypothetical protein
<i>yraE</i>	NP_267813.1	S					1.6			hypothetical protein
<i>yrbB</i>	AAK05760.1	S				-1.7				hypothetical protein

<i>yrbH</i>	AAK05766.1	S	1.8	1.6	2.6	hypothetical protein
<i>yreB</i>	NP_267843.1	S	-1.6			hypothetical protein
<i>yreD</i>	AAK05787.1	S	3.7		3.9 3.8	hypothetical protein
<i>yseD</i>	AAK05883.1	S	2.0	2.0	2.3	hypothetical protein
<i>ysjF</i>	AAK05925.1	S	1.8	2.0	2.6	hypothetical protein
<i>ytbD</i>	NP_268007.1	S	3.3			hypothetical protein
<i>ytcD</i>	NP_268015.1	S	2.3			hypothetical protein
<i>yuaE</i>	NP_268084.2	S			-2.1 -1.9	hypothetical protein
<i>yueC</i>	NP_268082.1	S	1.8	2.0	1.8 2.0	hypothetical protein
<i>yuhC</i>	NP_268149.1	S	1.5			hypothetical protein
<i>yujF</i>	NP_268177.1	S	2.4	1.9	2.3	hypothetical protein
<i>yviI</i>	NP_268276.1	S	2.0	1.8	2.9	hypothetical protein
<i>yxcD</i>	NP_268398.1	S		1.9	1.5	hypothetical protein
Signal transduction mechanisms						
<i>floL</i>	NC_002662.1	T	1.6			flotillin-like protein
<i>kinA</i>	NC_002662.1	T			-1.7	sensor protein kinase
<i>kinB</i>	NC_002662.1	T	1.7			sensor protein kinase
<i>llrA</i>	NC_019435.1	T	1.7			two-component system regulator
<i>ybdC</i>	NP_266285.1	T	-2.1		-1.5	hypothetical protein
<i>yfgF</i>	NP_266724.1	T			2.0	ABC transporter permease
<i>yjjE</i>	NP_267123.1	T	2.6			hypothetical protein
<i>ythA</i>	AAK06002.1	T	1.9	3.3		hypothetical protein
<i>ythB</i>	AAK06003.1	T		2.8		hypothetical protein
<i>yudH</i>	NP_268117.1	T	-1.7			hypothetical protein dihydrofolate reductase
Intracellular trafficking, secretion, and vesicular transport						
<i>comC</i>	NC_002662.1	U			2.0	type 4 prepilin-like protein specific leader peptidase transformation
<i>comGA</i>	AAK06221.1	U	2.6	2.6	2.8	protein ComGA competence protein
<i>comGB</i>	NC_000964.3	U	2.5	1.8	2.6	protein ComGB competence protein

<i>comGC</i>	NC_022369.1	U	2.2	2.6	2.6	protein ComGC competence protein
<i>comGD</i>	NZ_CP059048.1	U	2.7	1.7	1.5 1.9 1.6	protein ComGD competence protein
<i>ftsY</i>	NC_022369.1	U	1.7	1.7		hypothetical protein
Defence mechanisms						
<i>lmrP</i>	QQF00039.1	V	-1.9	2.5	1.5 1.8	multidrug efflux MFS transporter
<i>ybdI</i>	NP_266290.1	V			1.6 1.7	hypothetical protein
<i>ybfD</i>	NP_266310.1	V	1.6	2.4	1.9	transporter transport and binding protein
<i>yffF</i>	NP_266765.1	V		2.7	1.9	membrane transport protein transport and binding protein
<i>ygfA</i>	NP_266815.1	V		-2.8		ABC transporter ATP-binding protein
<i>ygfB</i>	NP_266816.1	V		-4.8		ABC transporter permease
<i>yhcA</i>	NP_266870.1	V		1.5		ABC transporter ATP-binding protein/permease
<i>yhcC</i>	NP_266871.1	V		2.0		hypothetical protein
<i>yhcE</i>	NP_266874.1	V	-2.1		-1.7	hypothetical protein
<i>ykJJ</i>	NP_267248.1	V		1.5	1.8	hypothetical protein
<i>ymdC</i>	AAK05309.1	V			1.8	kanamycin kinase
<i>ypbC</i>	AAK05582.1	V	2.2	1.9	2.8	MATE family efflux transporter
<i>ypfE</i>	NP_267672.1	V	1.8	1.9	2.0	transporter transport and binding protein
<i>ypgD</i>	AAK05620.1	V	-1.7			multidrug resistance ABC transporter ATP-binding protein
<i>yvhA</i>	AAK06200.1	V	1.7	1.6		MATE family efflux transporter
<i>yweA</i>	NP_268321.1	V	1.7		2.0	membrane protein
<i>yweE</i>	NP_268328.1	V	2.1	1.5		hypothetical protein
<i>yweF</i>	NP_268329.1	V	1.8			hypothetical protein
<i>ywiG</i>	AAK06301.1	V	2.5	1.8	2.8	ABC-type multidrug transport system, ATPase component
<i>yxbD</i>	NP_268392.1	V		3.9	3.1 -3.0	multidrug transporter transport and binding protein
<i>yxbE</i>	NP_268393.1	V	-2.2	2.2	-2.1	hypothetical protein
<i>yxeA</i>	NP_268412.1	V	1.6	1.9		hypothetical protein

Table S2. Transcriptomic data set with relaxed Log2Ratio thresholds. A gene was identified as differentially expressed between the *L. lactis* strains if its transcript level differed by $|\text{Log2Ratio}| \geq 1.5$ with statistical significance, $p < 0.05$. Bold and italic font shows chromosomal genes differentially expressed in the presence of plasmids with transcript levels 20% below the applied significance threshold ($|\text{Log2Ratio}| \geq 1.2$) with statistical significance, $p < 0.05$.

[illegible]

<i>tyrS</i>	-1.7		-2.5				tyrosyl-tRNA synthetase
<i>ybiE</i>	1.9				3.3		oxidoreductase
<i>yddB</i>		1.3			2.0		oxidoreductase
<i>yfdE</i>	-1.8						hypothetical protein similar to myo-inositol monophosphatases
<i>yfhC</i>	2.6		1.5	3.7			hypothetical protein
<i>ygaJ</i>	2.0		1.2				putative peptidase
<i>yiaD</i>	3.4		1.9	1.4		2.1	NADH-flavin reductase
<i>yjcA</i>		1.7	-1.2				ABC transporter ATP-binding protein
<i>yjgC</i>		-1.4				-1.5	amino acid ABC transporter substrate binding protein
<i>ylbA</i>	1.6						ABC transporter ATP-binding protein
<i>ymgG</i>	1.4	1.7		1.5	1.4		hypothetical protein
<i>ymgH</i>		1.6			1.4	1.5	hypothetical protein
<i>ymgK</i>	1.5					2.4	oxidoreductase
<i>yobA</i>	1.9		1.4	1.7			hypothetical protein
<i>yogA</i>					-1.7		hypothetical protein
<i>yphC</i>					-3.9		oxidoreductase
<i>yqcA</i>		1.2				1.7	oxidoreductase
<i>yrjA</i>	-1.5						hypothetical protein
<i>yrjB</i>	1.4	1.6	1.5		2.0	1.9	oxidoreductase
<i>yrjC</i>					1.7		iron-binding oxidase subunit
<i>yugB</i>				1.5		2.3	oxidoreductase
<i>ywdA</i>		1.3				1.8	hypothetical protein
<i>ywdC</i>		1.7				1.7	hypothetical protein
<i>ywiD</i>	2.9						hypothetical protein
<i>ywiH</i>		2.8	2.2		1.6	3.3	ABC transporter permease
<i>ywjF</i>				1.6		1.4	3-hydroxyisobutyrate dehydrogenase
<i>ezrA</i>	2.4			1.8			septation ring formation regulator EzrA
<i>scpA</i>						-1.6	segregation and condensation protein A
<i>yihA</i>		1.8	1.8			1.8	hypothetical protein

<i>yihB</i>		1.7	1.6		1.5		hypothetical protein
<i>arcA</i>	1.8			3.0	2.8	2.5	arginine deiminase
<i>arcB</i>	1.4	1.7		2.8	2.2	2.3	ornithine carbamoyltransferase
<i>arcC1</i>				2.7			carbamate kinase
<i>arcC2</i>	2.6	1.7		2.6		1.4	carbamate kinase
<i>arcD1</i>		1.8		3.2	1.9	2.1	arginine/ornithine antiporter
<i>argF</i>	1.3	1.7		1.3		1.7	ornithine carbamoyltransferase
<i>aroH</i>			-2.0				phospho-2-dehydro-3-deoxyheptonate aldolase
<i>asd</i>						2.3	aspartate-semialdehyde dehydrogenase
<i>bmpA</i>						-2.2	basic membrane protein A
<i>ceo</i>				1.7			N5-carboxyethyl-ornithine synthase
<i>cysD</i>						-2.2	O-acetylhomoserine sulfhydrylase
<i>cysK</i>		-2.5	-1.4	-2.6	-1.6	-2.7	cysteine synthase serine family
<i>cysM</i>		-3.0		-2.9	-1.7	-2.4	cysteine synthase
<i>glnB</i>					2.1		nitrogen regulatory protein P-II
<i>glnQ</i>			-1.4			-1.9	glutamine ABC transporter ATP-binding protein
<i>hisA</i>					1.5		1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase
<i>ilvD</i>		1.5	1.3			2.2	dihydroxy-acid dehydratase
<i>leuC</i>					1.5	1.4	isopropylmalate isomerase large subunit dehydratase component
<i>lysP</i>		2.0	1.2	1.3		2.3	lysine specific permease
<i>mapA</i>	2.8					5.2	maltose phosphorylase
<i>metB1</i>	-1.5	-1.5	-1.3				cystathionine gamma-synthase
<i>metB2</i>		-2.8	-1.6	-2.4	-1.6	-3.2	cystathionine gamma-synthase
<i>oppA</i>		1.8	1.4			2.4	oligopeptide ABC transporter substrate binding protein
<i>oppB</i>		3.2	7.6	1.5		3.8	6.4 oligopeptide ABC transporter permease
<i>oppC</i>		1.5	7.9	2.0		2.0	6.3 oligopeptide ABC transporter permease
<i>oppD</i>			5.9				5.0 oligopeptide ABC transporter ATP binding protein
<i>oppF</i>		1.5	6.9			1.8	5.7 oligopeptide ABC transporter ATP binding protein

<i>optS</i>		1.8	1.3	2.3	1.5	1.5	2.2	oligopeptide ABC transporter substrate binding protein
<i>pepDB</i>	1.7							dipeptidase
<i>pepF</i>							2.0 1.6	oligoendopeptidase F
<i>potA</i>		-1.3	-1.3				-1.8	spermidine/putrescine ABC transporter ATP-binding protein
<i>poxL</i>	2.8	1.7	1.8	2.7			2.3	pyruvate oxidase
<i>serB</i>			1.6					phosphoserine phosphatase
<i>ybeC</i>	1.9		1.3				1.6	hypothetical protein
<i>yceJ</i>				1.6			1.5	hypothetical protein
<i>ycjI</i>			-1.3				-1.9	hypothetical protein
<i>yddA</i>		2.4	2.6				3.0	transporter transport and binding protein
<i>ydgC</i>							1.8	amino acid permease
<i>yibG</i>				-1.6				amino acid permease transport and binding protein
<i>ylcC</i>	2.0							hypothetical protein
<i>ylcF</i>		2.0	1.4				1.6	hypothetical protein
<i>yneH</i>			2.5					hypothetical protein
<i>yrfB</i>			1.4				1.8	NADH-dependent oxidoreductase
<i>yrfD</i>							1.8	amino acid antiporter
<i>ysaB</i>	3.7			3.0			2.2	ABC transporter permease and substrate binding protein
<i>ysaC</i>	3.0			2.8			2.1	ABC transporter ATP-binding protein
<i>ysaD</i>	2.8			2.9			1.6	hypothetical protein
<i>yshA</i>	-1.4			-2.1		-1.6		glutamate antiporter
<i>ysjA</i>							-2.2 -1.6	amino acid permease transport and binding protein
<i>apt</i>	-2.5							adenine phosphoribosyltransferase
<i>carA</i>			-2.3		-1.7			carbamoyl phosphate synthase small subunit
<i>carB</i>			-1.9		-2.3			carbamoyl phosphate synthase large subunit
<i>coaA</i>			1.6	1.4	-3.2			pantothenate kinase
<i>dukA</i>		-1.7	-1.8		-2.2			deoxynucleoside kinase nucleotide and nucleoside interconversions
<i>gmK</i>	-2.0							guanylate kinase
<i>nrdE</i>	-2.1					-1.5		ribonucleotide-diphosphate reductase subunit alpha

<i>nrdG</i>	-1.6				-1.3			anaerobic ribonucleoside-triphosphate reductase
<i>pbuX</i>	-1.8							xanthine/uracil permease
<i>purR</i>	1.9		1.7			1.4		pur operon repressor general regulatory function
<i>pydB</i>		-2.5	-1.5	-2.4		-1.3		dihydroorotate transferase
<i>pyrB</i>		-2.1						aspartate carbamoyltransferase catalytic subunit
<i>pyrC</i>		-2.2		-1.8		-1.3		dihydroorotase
<i>pyrE</i>		-2.7	-2.0	-2.2		-1.9		orotate phosphoribosyltransferase
<i>pyrF</i>		-1.9		-1.8				orotidine 5'-phosphate decarboxylase type 1 subfamily
<i>pyrP</i>		-2.6		-2.1		-1.2		uracil permease
<i>pyrR</i>		-1.2		-2.4				bifunctional pyrimidine regulatory protein PyrR
<i>xpt</i>	-2.8							xanthine phosphoribosyltransferase
<i>yfiC</i>		-1.6			-1.4			hypothetical protein
<i>yfiG</i>	-2.0			-1.3				thymidine kinase
<i>ygcC</i>	-1.7			-1.3				hypothetical protein
<i>yriD</i>	-1.7							xanthine/uracil/vitamin C permease
<i>agl</i>						4.8		alpha-glucosidase degradation of polysaccharides
<i>amyL</i>			1.7		1.4			alpha-amylase
<i>amyY</i>						5.1		alpha-amylase
<i>dexA</i>						4.7		oligo-alpha-1,6-glucosidase
<i>dexC</i>						5.1		neopullulanase
<i>dhaL</i>			1.6				1.9	dihydroxyacetone kinase subunit
<i>dhaM</i>			1.5				1.6	dihydroxyacetone kinase
<i>eno</i>			2.3			3.9		phosphopyruvate hydratase enolase
<i>fruC</i>	2.1		1.7	2.2				1-phosphofructokinase
<i>fruA</i>	2.0		1.8					PTS system fructose-specific transporter subunit IIBC
<i>galE</i>		-1.9	-1.2		-1.9	-1.2		UDP-glucose 4-epimerase
<i>galK</i>		-3.4	-3.7	1.3	-3.6	-2.9	-2.4	galactokinase
<i>galM</i>		-3.4	-3.5	1.4	-3.7	-2.9	-2.3	aldose 1-epimerase
<i>galT</i>		-3.6	-3.9		-3.3	-3.2	-3.0	galactose-1-phosphate uridylyltransferase

<i>gapA</i>	2.6							glyceraldehyde 3-phosphate dehydrogenase
<i>glpF1</i>	1.7		1.7					glycerol uptake facilitator
<i>glpT</i>	1.3	1.4			1.5			glycerol-3-phosphatase transporter
<i>kdgA</i>	2.1	1.8			2.4			keto-hydroxyglutarate-aldolase
<i>galP</i>	-3.7	-4.0		-3.0	-3.0	-2.4	-2.5	glycoside-pentoside-hexuronide (GPH):cation symporter
<i>lacZ</i>	-3.1	-3.5		-3.4	-2.8	-2.4	-3.1	beta-D-galactosidase
<i>malE</i>							-5.4	maltose ABC transporter substrate binding protein
<i>malF</i>							-5.3	maltose ABC transporter permease
<i>malG</i>							-4.5	maltose ABC transporter permease
<i>malQ</i>			1.6		1.3			4-alpha-glucanotransferase
<i>mtlF</i>	1.4				1.6			PTS system mannitol-specific transporter subunit IIA
<i>nagA</i>	-1.5							N-acetylglucosamine-6-phosphate deacetylase
<i>ptbA</i>							-1.6	PTS system beta-glucoside-specific transporter subunit IIAABC
<i>rpiA</i>	2.0		1.7				2.1	ribose-5-phosphate isomerase A
<i>tagH</i>	1.6	1.6			1.9			teichoic acid ABC transporter ATP binding protein
<i>thgA</i>	-2.9	-3.0		-3.0	-2.4	-2.0	-2.4	thiogalactoside acetyltransferase
<i>xylA</i>			2.0					xylose isomerase
<i>xylH</i>	-1.4			-1.6				4-oxalocrotonate tautomerase
<i>xylT</i>	2.1	2.1		1.3		2.4		D-xylose proton-symporter
<i>xynB</i>	1.4	1.2				1.6		beta-1,4-xylosidase
<i>xynT</i>		1.6				2.1		xyloside transporter
<i>ycgC</i>	1.5							hypothetical protein
<i>yeeB</i>	2.1							hydrolase
<i>yfbG</i>		-5.4						hypothetical protein
<i>yhgD</i>	2.7	2.6		1.4		3.2		hypothetical protein
<i>yhgE</i>	4.1	3.7		2.3		4.0		hypothetical protein
<i>yoiC</i>	1.4					1.6		hypothetical protein
<i>ypcA</i>		2.3				2.4		P-beta-glucosidase
<i>ypcC</i>		-1.6						hypothetical protein

<i>ypcD</i>			-1.6					endo-beta-N-acetylglucosaminidase
<i>ypjA</i>	1.9	1.5	1.7	2.4		1.4		dehydrogenase
<i>yqgE</i>	1.4	1.4	1.8	1.5				transporter
<i>yqhA</i>			-1.7	-1.2				hypothetical protein aldose-1-epimerase
<i>yvdD</i>			1.5					transporter
<i>yxdE</i>		1.6						oxidoreductase
<i>yxdG</i>		2.6	2.7	2.7	1.9	2.0	3.3	transporter
<i>yxfA</i>							-1.7	transporter
<i>apbE</i>							-2.3	thiamine biosynthesis lipoprotein
<i>hemH</i>				-1.7				ferrochelatase protoheme ferro-lyase
<i>nadE</i>	3.2			1.9				NAD synthetase
<i>pabA</i>				-2.2			-2.4	para-aminobenzoate synthase component II folic acid
<i>pabB</i>				-2.5			-2.4	para-aminobenzoate synthase component I folic acid
<i>preA</i>		1.5	1.5		1.9			prenyl transferase
<i>ribG</i>			1.6		1.9			riboflavin-specific deaminase riboflavin and cobalamin
<i>accB</i>			-1.2				2.4	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
<i>accC</i>							1.7	acetyl-CoA carboxylase biotin carboxylase subunit
<i>accD</i>							1.6	acetyl-CoA carboxylase subunit beta
<i>acpD</i>		-1.5	-1.9					ACP phosphodiesterase
<i>butA</i>	1.3			1.5				acetoin reductase fermentation
<i>fabD</i>							2.3	ACP S-malonyltransferase
<i>fabI</i>			1.7					enoyl-ACP reductase
<i>fabZ</i>							2.2	(3R)-hydroxymyristoyl-ACP dehydratase
<i>fadD</i>				-5.9			2.1	long-chain acyl-CoA synthetase
<i>yfbB</i>			-7.2		-1.8		-2.4	hypothetical protein
<i>ygbB</i>		1.7	2.2	1.7	1.5			hypothetical protein
<i>yqaG</i>		-1.2	-2.7	-1.5				hypothetical protein
<i>yveB</i>		1.4					1.6	hypothetical protein
<i>yveH</i>		1.4	4.0				1.6	hypothetical protein

<i>aldR</i>	1.5						AldR regulatory protein
<i>rluC</i>						1.7	pseudouridine synthase
<i>truB</i>			-1.4		-1.6		tRNA pseudouridine synthase B
<i>yabC</i>	1.8						hypothetical protein
<i>ybiD</i>	1.3		1.5				ribosomal RNA large subunit methyltransferase
<i>ygdA</i>		1.6	1.9		1.2	1.7	hypothetical protein
<i>ynjI</i>	1.9			1.7	1.6		hypothetical protein
<i>ynjJ</i>	2.3	1.4	1.4	1.6	1.5		hypothetical protein
<i>ywfF</i>	-1.7						hypothetical protein
<i>ywfG</i>	2.4	1.2	2.5		1.3		hypothetical protein
<i>adaA</i>					1.9		methylphosphotriester-DNA alkyltransferase
<i>cspD</i>			-6.1				cold shock protein D
<i>cspE</i>			1.6				cold shock protein E
<i>dhaK</i>			2.0		2.3	1.9	dhaKLM operon coactivator, dihydroxyacetone utilization pathway
<i>fur</i>	2.2						ferric uptake regulator
<i>gadR</i>		-2.2			-1.9		positive regulator
<i>hrcA</i>	1.6						heat-inducible transcription repressor
<i>fruR</i>			1.641				DeoR family transcription regulator of fructose utilization pathway
<i>nadR</i>	2.1	1.5	1.7				NadR family transcription regulator, NAD cellular biosynthesis pathway
<i>phoU</i>	2.1		1.3				phosphate transport system regulator
<i>rcfB</i>			1.8				CRP/FNR family transcription regulator involved in pH homeostasis
<i>rliA</i>		1.6				1.9	transcriptional regulator LacI-family regulators, putative regulatory function
<i>rliDB</i>		3.0	2.3	3.2	2.1	3.3	transcriptional regulator LacI-family regulators, putative regulatory function
<i>rlrA</i>						-1.6	LysR-family transcription regulator, putative regulatory function
<i>rmaA</i>		-1.6	-1.2	-1.6			MarR family transcriptional regulator of fatty acid biosynthesis pathway
<i>rmaG</i>		-2.1					MarR family transcriptional regulator of fatty acid biosynthesis pathway
<i>rmaJ</i>	-1.6						MarR-family transcriptional regulator of hyaluronan biosynthesis pathway

<i>rpoD</i>	1.8					RNA polymerase sigma factor RpoD
<i>sigX</i>				1.6		RNA polymerase ECF sigma factor
<i>tagR</i>		1.5		1.9		transcriptional regulator similar to EpsR, possibly involved in exopolysaccharides biosynthesis
<i>yabA</i>						transcriptional regulator belongs to the PBSX(XRE) family of transcription regulators
<i>ybaI</i>	-1.8					glycosyl transferase glycosyltransferase family 2
<i>ybeF</i>		1.7	2.0	1.9	2.3	hypothetical protein
<i>yfeA</i>		1.6	1.5	2.1		RpiR family of transcription regulator, putative regulatory function
<i>ygfC</i>		-2.9		-4.8		TetR/AcrR family transcription regulator of heme homeostasis process
<i>yjaB</i>	2.5					transcriptional regulator, LytR family, putative regulatory function
<i>yjaJ</i>		1.6				transcriptional regulator, LytR family, putative regulatory function
<i>ykhD</i>			1.8			redox-sensing transcriptional repressor Rex
<i>yliA</i>	2.0		1.3		1.4	positive transcription regulator
<i>ynaA</i>	2.2		-1.5			transcriptional regulator, heat and DNA damage induction
<i>ynaB</i>	2.2				1.5	transcriptional regulator, putative regulatory function
<i>ynaE</i>			1.6			hypothetical protein, putative regulatory function
<i>yogM</i>		1.6	1.6		1.4 1.3	hypothetical protein
<i>yohC</i>				1.6		TetR/AcrR family transcription regulator, putative regulatory function
<i>yqfA</i>		-1.4	-1.7		-1.4	hypothetical protein
<i>yrfA</i>	1.5		1.4			ArsR family transcription regulator, putative regulatory function
<i>yrfE</i>		-1.6				LytR family transcriptional regulator, putative regulatory function
<i>glcR</i>		-1.8		-1.7	-1.3	RpiR family transcription regulator of galactose utilization Leloir pathway
<i>ywjD</i>		-1.7		-1.7	-1.4 -1.8	PBSX(XRE) family transcription regulator, putative regulatory function
<i>yxbF</i>		-2.2		2.4		hypothetical protein
<i>comEA</i>		1.6				hypothetical protein competence protein
<i>dinG</i>		-1.3		-1.5	-1.4	DinG ATP-dependent helicase
<i>dinP</i>		1.2		1.6	1.7	DNA polymerase IV
<i>hslB</i>	2.5				2.3	HU-like DNA-binding protein

<i>recJ</i>	-1.6							ssDNA-specific exonuclease RecJ	
<i>recX</i>	1.7		1.4					recombination regulator RecX	
<i>ssbA</i>			3.1		1.6			single-stranded DNA-binding protein	
<i>xerD</i>		1.5			1.4			integrase-recombinase	
<i>yajF</i>		1.4	2.4	1.2		1.7		hypothetical protein	
<i>yjaF</i>	2.4							hypothetical protein	
<i>yneB</i>		1.2	1.3	1.8		1.3		hypothetical protein	
<i>dapA</i>	1.6							dihydrodipicolinate synthase	
<i>dltB</i>	2.8	-1.7		2.1		-1.6	-1.7	-2.4	peptidoglycan biosynthesis protein
<i>dltD</i>	4.1	-1.6		3.6			-1.3		peptidoglycan biosynthesis protein
<i>glmS</i>	1.8				1.4				glucosamine--fructose-6-phosphate aminotransferase
<i>mscL</i>	1.8								large-conductance mechanosensitive channel
<i>murB</i>	1.5		1.9						UDP-N-acetylenolpyruvoylglucosamine reductase
<i>murQ</i>		-1.8	-1.5				-1.6		N-acetylmuramic acid 6-phosphate etherase
<i>plpA</i>	-2.8	-2.2	-1.6	-3.0	-1.8	-1.6	-2.5		outer membrane lipoprotein
<i>plpB</i>		-1.4	-1.2	-2.1	-1.5		-1.7		outer membrane lipoprotein
<i>plpC</i>	-2.2	-1.6	-1.4	-2.4	-1.3		-1.8		outer membrane lipoprotein
<i>ptk</i>	2.7	1.5		1.9					phosphoketolase
<i>tagL</i>		2.0	1.2				1.3		exopolysaccharide biosynthesis protein
<i>ycbH</i>	-1.6								sugar transferase
<i>ycbI</i>	-1.7								sugar transferase
<i>ycbK</i>	-1.7								polysaccharide biosynthesis export protein
<i>yfbI</i>			-7.6						hypothetical protein
<i>yfbJ</i>			-7.2						hypothetical protein
<i>yijB</i>			1.7						hypothetical protein
<i>yijC</i>			1.7						ABC transporter permease transport and binding protein
<i>yijH</i>	1.8								hypothetical protein
<i>ymjE</i>	1.5								glycosyl transferase family protein
<i>yncA</i>			1.3	1.7					acetyltransferase

<i>ynfC</i>	1.5	1.5	1.5				hypothetical protein	
<i>ytbA</i>		1.6	1.3	1.2	2.1		hypothetical protein	
<i>ytjA</i>	1.8		1.2				hypothetical protein	
<i>clpE</i>	2.4	1.2	1.5				ATP-dependent protease	
<i>gpo</i>	1.8						glutathione peroxidase thioredoxin, glutaredoxin, and glutathione	
<i>groES</i>	2.8						co-chaperonin GroES 10 kDa chaperonin	
<i>osmC</i>	2.5		1.5				osmotically inducible protein	
<i>pmsX</i>	2.0						peptide methionine sulfoxide reductase t	
<i>sugE</i>		1.8	2.3	2.2	1.3	1.3	SugE protein chaperones	
<i>ybjA</i>	1.9		1.4				methionine sulfoxide reductase B	
<i>yfcF</i>		2.0	1.5	2.0	1.3	1.9	hypothetical protein	
<i>ynhC</i>	1.5						hypothetical protein	
<i>ynhD</i>		1.7					hypothetical protein	
<i>amtB</i>				1.9	-1.7	-2.2	ammonium transporter	
<i>busAB</i>				1.8			betaine ABC transporter permease and substrate binding protein	
<i>cadA</i>	2.3		3.7		2.4		cadmium efflux ATPase transort and binding protein	
<i>cbiO</i>			2.6		3.2		cobalt transporter ATP-binding subunit	
<i>feoA</i>						1.5	ferrous ion transport protein A	
<i>mtsA</i>			-3.2		-3.7	-3.6	manganese ABC importer	
<i>mtsB</i>			-2.0		-2.7		manganese ABC importer	
<i>mtsC</i>			-2.0		-2.6	-3.8	manganese ABC importer permease	
<i>pacL</i>			2.3		2.4		magnesium-transporting ATPase	
<i>pstF</i>	1.5						phosphate ABC transporter substrate-binding protein	
<i>yafB</i>		2.1	1.6	2.7	2.6		sulfate permease, MFS superfamily	
<i>ybcC</i>		1.8	1.7		1.7		MATE family efflux transporter	
<i>yceA</i>		1.6			1.6		hypothetical protein	
<i>ydiF</i>		1.3		1.7	1.2		Na ⁺ /H ⁺ antiporter transort and binding protein, cations	
<i>ygfE</i>			1.8	-5.7	-1.9	-2.7	2.0	magnesium importer and exporter
<i>yjdJ</i>		1.7	1.5	2.1		1.8		potassium channel protein transort and binding protein, cations

<i>ymgF</i>	1.9			1.6		hypothetical protein
<i>ynjC</i>	1.4				1.6	hypothetical protein
<i>ynjE</i>	1.9	1.5			1.6	hypothetical protein
<i>ynjF</i>				1.3	1.6	hypothetical protein
<i>yphB</i>	1.8	1.3		1.3	2.1	magnesium transporter transport and binding protein
<i>ytgB</i>	2.3			2.0		cesium ABC transporter substrate binding protein
<i>yuhE</i>	2.5			1.5	1.8	copper homeostasis protein
<i>yvfA</i>	1.5				1.5	metal ABC transporter substrate binding protein
<i>aldC</i>		2.0				alpha-acetolactate decarboxylase fermentation
<i>dltA</i>	3.0			2.1	-1.3	D-alanine--poly(phosphoribitol) ligase subunit 1
<i>dltC</i>	-1.9			2.2	-1.8	-2.2 D-alanine--poly(phosphoribitol) ligase subunit 2
<i>fabG2</i>	2.1	1.9	2.1	1.6	2.6	3-oxoacyl-ACP reductase
<i>yoaI</i>				1.6		hypothetical protein
<i>yrbC</i>	1.3				1.8	1,4-dihydroxy-2-naphthoate octaprenyltransferase
<i>yrbE</i>	1.4	1.6			2.0	hypothetical protein
<i>comEC</i>	1.9	1.9			2.4	hypothetical protein competence protein
<i>yhhD</i>	2.0	1.7		1.5	2.6	hypothetical protein
<i>ysbA</i>	-1.2	1.6			1.6	hypothetical protein
<i>ysbD</i>	-2.2			-1.3	-1.3	-1.8 -1.5 hypothetical protein
<i>ythC</i>		2.4				hypothetical protein
<i>L200065</i>	1.2				2.3	1.7 hypothetical protein
<i>yafJ</i>	1.6	1.3			2.0	hypothetical protein
<i>yaiB</i>	1.7			1.7	2.0	hypothetical protein
<i>yaiH</i>		1.7		1.6	1.7	hypothetical protein
<i>yaiI</i>	2.4	2.0		1.2	2.4	hypothetical protein
<i>yaiJ</i>	2.6	2.2		1.8	3.2	hypothetical protein
<i>ybeH</i>				2.3	1.9	hypothetical protein
<i>ybfC</i>	1.4	2.0				hypothetical protein
<i>ybgA</i>	1.6	1.8				hypothetical protein

<i>ycdA</i>		1.6				hypothetical protein
<i>yciF</i>	1.5					hypothetical protein
<i>yciG</i>	1.8	1.4	2.1		2.3	hypothetical protein
<i>ydbD</i>					1.5	hypothetical protein
<i>yeiD</i>	2.2	-1.3			-2.3	hypothetical protein
<i>yfbK</i>		-1.5	-3.5		-2.1	hypothetical protein
<i>yfiH</i>	-1.8					hypothetical protein
<i>yfiI</i>	-2.0		-1.3			hypothetical protein
<i>ygaD</i>	-1.8					hypothetical protein
<i>ygeB</i>			-1.2	-1.6	-2.1	hypothetical protein
<i>ygeC</i>	-2.1		-1.3		-1.2	hypothetical protein
<i>yghB</i>				1.5		hypothetical protein
<i>yhhA</i>	1.8	1.4			2.3	hypothetical protein
<i>yhhB</i>					1.7	hypothetical protein
<i>yhhC</i>		1.3	2.6		1.5	hypothetical protein
<i>yhjA</i>	4.3		2.1	1.9	2.5	hypothetical protein
<i>yhjE</i>					-1.7	hypothetical protein
<i>yiaC</i>	-1.8					hypothetical protein
<i>yiiD</i>			2.1			hypothetical protein
<i>yjdI</i>	2.0	1.5			1.8	hypothetical protein
<i>yjff</i>	1.6					hypothetical protein
<i>ykbC</i>	1.8	1.4			2.2	hypothetical protein
<i>ykbD</i>	1.9	1.5			1.9	hypothetical protein
<i>ykbE</i>			1.6			hypothetical protein
<i>ykcE</i>	2.0					hypothetical protein
<i>yklI</i>	-2.0				-2.3	hypothetical protein
<i>ylhB</i>		2.5		1.2		hypothetical protein
<i>yliD</i>	2.5	1.9	1.4		2.6	hypothetical protein
<i>ymbC</i>		1.7	2.0	1.9	1.9	hypothetical protein

<i>ymbD</i>	2.3	2.0	2.1		2.6	hypothetical protein	
<i>ymbH</i>	1.7	1.3			1.8	hypothetical protein, putative protease	
<i>ymcA</i>	1.6	1.2			2.1	hypothetical protein	
<i>ymcB</i>	2.0	1.5	1.3		2.0	hypothetical protein	
<i>ymcC</i>	2.2				1.6	hypothetical protein	
<i>ymeA</i>	2.6	2.5	1.8		3.2	hypothetical protein	
<i>ymhG</i>	1.3				1.8	hypothetical protein	
<i>yndE</i>	1.7				1.4	hypothetical protein	
<i>yneC</i>	4.0	2.4	3.1		1.3	hypothetical protein	
<i>yneG</i>		2.6				hypothetical protein	
<i>ynfH</i>	2.4		2.7	2.9	1.9	2.1	hypothetical protein
<i>ynhA</i>				-1.3		-2.8	hypothetical protein
<i>yniC</i>	-1.3			-1.6			hypothetical protein
<i>yniJ</i>	1.7	1.3	1.7			2.1	hypothetical protein
<i>yofM</i>	-2.0					-1.8	DNA-binding protein
<i>yohD</i>	1.7						hypothetical protein
<i>ypaG</i>			1.6				hypothetical protein
<i>ypiH</i>					1.7		hypothetical protein
<i>ypiJ</i>	1.2				1.8		hypothetical protein
<i>ypiL</i>	1.2	1.3	1.5		1.3		hypothetical protein
<i>yqbI</i>	1.5	1.6			2.0		hypothetical protein
<i>yraE</i>			1.3		1.6		hypothetical protein
<i>yrbB</i>				-1.7			hypothetical protein
<i>yrbH</i>	1.8	1.6			2.6		hypothetical protein
<i>yreB</i>	-1.6					-1.2	hypothetical protein
<i>yreD</i>	3.7				3.9	3.8	hypothetical protein
<i>yseD</i>	2.0	1.4	2.0		2.3		hypothetical protein
<i>ysjF</i>	1.8	1.5	2.0		2.6		hypothetical protein
<i>ytdD</i>	3.3	1.4	1.4				hypothetical protein

<i>ytcD</i>	2.3		1.4			1.5	hypothetical protein	
<i>yuaE</i>			-1.3	-1.3	-2.1	-1.9	hypothetical protein	
<i>yueC</i>	1.8	2.0	1.8			2.0	hypothetical protein	
<i>yuhC</i>	1.5		1.3				hypothetical protein	
<i>yujF</i>		2.4	1.9		1.3	2.3	hypothetical protein	
<i>yviJ</i>		2.0	1.8	2.9			hypothetical protein	
<i>ycxD</i>	1.3		1.9	1.4		1.5	hypothetical protein	
<i>floL</i>	1.6		1.3				flotillin-like protein	
<i>kinA</i>		1.4		-1.7			sensor protein kinase	
<i>kinB</i>	1.7		1.4	1.2		1.3	sensor protein kinase	
<i>llrA</i>	1.7						two-component system regulator	
<i>ybdC</i>	-2.1			-1.5			hypothetical protein	
<i>yfgF</i>		1.5	1.3			2.0	ABC transporter permease	
<i>yjjE</i>	2.6						hypothetical protein	
<i>ythA</i>	1.9	1.2	3.3			1.3	hypothetical protein	
<i>ythB</i>			2.8			1.2	hypothetical protein	
<i>yudH</i>		-1.7					hypothetical protein dihydrofolate reductase	
<i>comC</i>		1.4	1.2			2.0	type 4 prepilin-like protein specific leader peptidase transformation	
<i>comGA</i>		2.6	2.6		1.4	2.8	protein ComGA competence protein	
<i>comGB</i>		2.5	1.8			2.6	protein ComGB competence protein	
<i>comGC</i>		2.2		2.6		2.6	protein ComGC competence protein	
<i>comGD</i>		2.7	1.7		1.5	1.9	1.6	protein ComGD competence protein
<i>ftsY</i>	1.7		1.7					hypothetical protein
<i>lmrP</i>	-1.9			2.5	1.5		1.8	multidrug efflux MFS transporter
<i>ybdI</i>					1.6	1.7	1.4	hypothetical protein
<i>ybfD</i>		1.6		2.4			1.9	transporter transport and binding protein
<i>yjfF</i>		1.4	1.5	2.7			1.9	membrane-bound transport protein transport and binding protein
<i>ygfA</i>				-2.8				ABC transporter ATP-binding protein
<i>ygfB</i>				-4.8				ABC transporter permease

<i>L200055</i>	-6.9	-1.7	-2.2		-2.2	-2.4		hypothetical protein
<i>L200056</i>	-2.4	-2.0	-1.8	-1.3	-2.2	-2.2	-1.3	hypothetical protein
<i>L200058</i>	-3.3	-1.5	-2.0	-1.5		-2.5		hypothetical protein
<i>L200071</i>	1.6	1.3						hypothetical protein
<i>L200072</i>	1.9	1.9				1.8		hypothetical protein
<i>L200073</i>	2.4	2.2		1.8		2.7		hypothetical protein
<i>L200074</i>	3.6	3.3		1.9		4.5		hypothetical protein
<i>L200075</i>						2.3		hypothetical protein
<i>L200077</i>	-3.4	-3.7		-3.1	-2.8	-2.7	-2.7	hypothetical protein
<i>L200079</i>			1.7					hypothetical protein
<i>tra1077B</i>	1.7					1.8		IS1077B transposase
<i>tra904A</i>	2.4	1.4				2.9		transposase of IS904A
<i>tra904B</i>	2.2	1.3				2.7	1.9	transposase of IS904B
<i>tra904D</i>	2.2	1.4				2.7		transposase of IS904D
<i>tra904E</i>	1.3				1.2		1.9	transposase of IS904E
<i>tra981A</i>			2.0		1.5	1.5		transposase of IS981A
<i>tra981E</i>			2.0		1.4	1.3		transposase of IS981E
<i>tra981G</i>			1.9		1.3	1.2		transposase of IS981G
<i>yafI</i>	1.5				1.6	1.8	2.1	hypothetical protein transposon related function
<i>yajA</i>	1.7	1.9				1.7		transposase
<i>yajE</i>			1.5				1.3	transposase
<i>yajG</i>			2.2		1.3	1.2	1.4	transposase
<i>ybdL</i>	1.6							hypothetical protein transposon related function
<i>ydhD</i>	1.4	2.8			1.6	1.8	2.1	hypothetical protein transposon related function
<i>ygcE</i>	1.6							hypothetical protein transposon related function
<i>yidF</i>	1.5				1.7	1.8	2.3	hypothetical protein transposon related function
<i>ymbI</i>			1.5				1.4	transposase
<i>ymhB</i>			1.5				1.4	transposase

Table S3. Primers used in this study. 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>)

Strain or primer pair	Genotypic characteristics
p1orf3zF / p1orf3zR	CTTGCTGACGAATTAGGAGTTAG/TCAGCGGTTAATAGCTTCATAC
p1orf6zF / p1orf6zR	CCTTGTTTCGTTGGATTGATTAG/AGAACTCGCTTCTAAATTTGTG
p2citRzF / p2citRzR	AGGAGACAACAACATGAAAGTC/GAGCGTTTGTCTCCAATCTG
p2orf2zF / p2orf2zR	AGCTAAACAGACCGTTCAATAC/GTTTAGGACGATCGAACCAC
p3orf2tF / p3orf2tR	CAACAACAGAACGAAACACAAC/AAGTTCTGTTCTAAGAATACTGACG
p3orf3zF / p3orf3zR	TCTCAGGTGTTTATCTGGTATTTG/GACAACAAGTCCTACTCCAAAG
p4or24zF / p4or24zR	GTTTGATCTTACCTTGCTGTTG/GTTACTGGGAACCGATTACG
p4or49zF / p4or49zR	CCTTACCAATGGTGATGTAATCG/GTCAAAGATACTGGCGGTTTAG
p5cadAzF / p5cadAzR	GCATCGACGGTTGGTATTG/GTTTGGCGGCTAAGTCTAAC
p5cadCzF / p5cadCzR	GTTGATAGTCACAAGGATGGTAAG/AATTTACGCCAAGCTCCATAAG
p6orf6zF / p6orf6zR	TCAGGGAATTCCTTTATTAGGTTCTG/CTTGTTTCATCTACCTTAGTCAAGTATC
p6orf7zF / p6orf7zR	GATATACTGCGACTCCAGTTG/ATTCTAATGCCACATGGTAAGG
p7or11zF / p7or11zR	ATCGAACCGCCAATCAAG/CCGTATTGATCCCAGAAGTAAG
p7orfXzF / p7orfXzR	TGCAGATGAGTTGAGTGTTAC/TGCTACCACTTTCTACTTTACC