

Supplementary data

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Article title: Expanded roles of Lrp in transcription regulation of the *Escherichia coli* genome: Genomic SELEX screening of the regulation targets

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This article has 3 supplemental tables.

**Supplemental Table S1. Lrp-binding sites on the *E. coli* genome.** Genomic SELEX screening of Lrp-binding sequences were identified in a total of 314 sites on the *E. coli* genome (see Table 1). When Lrp-binding sites are located within spacer regions, only the flanking genes are indicated. The direction of transcription is shown by arrows. The genes shown in parentheses carry the Lrp-binding sites on the open reading frames. These Lrp-binding sites are classified into four groups: Type-A spacer; type-B spacer; type-C spacer; and inside open reading frames. Type-A and type-B spacers and their flanking genes are listed in this table.

**Supplemental Table S2. Amino acids and peptides affecting the growth of *lrp* mutant.** Compounds affecting the growth retardation are listed in (1). Compounds affecting the growth enhancement are listed in (2). The growth curves are shown in Figure 2.

**Supplemental Table S3. The concentration of metabolites in wild-type strain and the *lrp* mutant.** The intracellular levels of metabolites in *E. coli* wild-type BW25113 and its *lrp* mutant JW0872 were determined by TOF/MS analysis. Details of these determinations are described in this table. The results of major metabolites are shown in Figures 3 and 4.

**Supplemental Table S1**  
**Lrp-binding sites on the *E. coli* genome (SELEX screening)**

**Type-A spacers**

Position	Function	Operon	Gene	D	Lrp	D	Gene	Operon	Function
42168	predicted transporter	<i>cai</i> TABCDE	<i>cai</i> T	<		>	<i>fixA</i>	<i>fix</i> ABCX	electron transfer flavoprotein
83830	<i>leu</i> operon leader peptide	<i>leu</i> LABCD	<i>leu</i> L	<		>	<i>leu</i> O	<i>leu</i> O	transcription factor
255832	aminoacyl-histidine dipeptidase	<i>pep</i> D	<i>pep</i> D	<		>	<i>gpt</i>	<i>gpt</i>	guanine-xanthine phosphoribosyltransferase
310970	transcription factor	<i>mat</i> A	<i>mat</i> A	<		>	<i>ykg</i> L	<i>ykg</i> L	predicted protein
400468	D-alanine-D-alanine ligase A	<i>ddl</i> A	<i>ddl</i> A	<		>	<i>ira</i> P	<i>ira</i> P	predicted protein
584962	DLP12 prophage OM protease VII	<i>omp</i> T	<i>omp</i> T	<		>	<i>pau</i> D	<i>pau</i> D	Xaa tRNA
632754	predicted oxidoreductase	<i>ydb</i> H- <i>ydb</i> E- <i>ydb</i> L	<i>ydb</i> H	<		>	<i>ybd</i> L	<i>ybd</i> L	methionine aminotransferase
651072	citrate lyase synthetase	<i>cit</i> CDEFXG	<i>cit</i> C	<		>	<i>dpi</i> B	<i>dpi</i> BA	CitAB TCS sensor kinase
655436	anaerobic C4-dicarboxylate transport	<i>dcu</i> C	<i>dcu</i> C	<		>	<i>pag</i> P	<i>pag</i> P	palmitoyl transferase for Lipid A
675858	conserved protein	<i>ybe</i> Q	<i>ybe</i> Q	<		>	<i>ybe</i> R	<i>ybe</i> R- <i>djl</i> B	predicted protein
784656	conserved protein	<i>ybg</i> S	<i>ybg</i> S	<		>	<i>aro</i> G	<i>aro</i> G	2-dehydro-3-deoxyphosphoheptonate aldolase
815960	NAD(P)-binding Rossmann-fold	<i>ybh</i> K	<i>ybh</i> K	<		>	<i>moa</i> A	<i>moa</i> ABCDE	molybdopterin biosynthesis protein A
823832	predicted DNase	<i>ybh</i> PON	<i>ybh</i> P	<		>	<i>ybh</i> Q	<i>ybh</i> Q	predicted IM protein
865772	molybdopterin biosynthesis protein	<i>moe</i> AB	<i>moe</i> A	<		>	<i>iaa</i> A	<i>iaa</i> A- <i>qsi</i> ABCD	L-asparaginase
915432	aquaporin	<i>agp</i> Z	<i>agp</i> Z	<		>	<i>ybj</i> D	<i>ybj</i> D	nucleoside triphosphate hydrolase
931532	thioredoxin reductase	<i>trx</i> B	<i>trx</i> B	<		>	<i>lrp</i>	<i>lrp</i>	transcription factor
1E+06	predicted OM protein	<i>pga</i> ABCD	<i>pga</i> A	<		>	<i>ycd</i> T	<i>ycd</i> T	predicted diguanylate cyclase
1E+06	e14 prophage IM protein	<i>ymf</i> ED	<i>ymf</i> E	<		>	<i>lit</i>	<i>lit</i>	e14 prophage cell death peptidase
1E+06	conserved protein	<i>ycq</i> B	<i>ycq</i> B	<		>	<i>dad</i> A	<i>dad</i> AX	D-amino acid dehydrogenase
1E+06	calcium/sodium:proton antiporter	<i>cha</i> A	<i>cha</i> A	<		>	<i>cha</i> B	<i>cha</i> BC	predicted cation regulator
1E+06	aldehyde-alcohol dehydrogenase	<i>adh</i> E	<i>adh</i> E	<		>	<i>yche</i> E	<i>yche</i> E	predicted IM protein
1E+06	predicted protein	<i>yci</i> N	<i>yci</i> N	<		>	<i>top</i> A	<i>top</i> A	DNA topoisomerase I
1E+06	GGDEF diguanylate cyclase	<i>yda</i> M	<i>yda</i> M	<		>	<i>yda</i> N	<i>yda</i> N	predicted Zn(II) transporter
2E+06	biofilm-dependent modulation protein	<i>bdm</i> - <i>sra</i>	<i>bdm</i>	<		>	<i>osm</i> C	<i>osm</i> C	osmotically inducible membrane
2E+06	pyridine nucleotide transhydrogenase	<i>pnt</i> AB	<i>pnt</i> A	<		>	<i>ydg</i> H	<i>ydg</i> H	predicted protein
2E+06	transcription factor	<i>sly</i> A	<i>sly</i> A	<		>	<i>ydh</i> I	<i>ydh</i> IJK	predicted IM protein
2E+06	conserved protein	<i>grxD</i>	<i>grxD</i>	<		>	<i>ydh</i> O	<i>ydh</i> O	predicted lipoprotein
2E+06	conserved protein	<i>ydh</i> Q	<i>ydh</i> Q	<		>	<i>val</i> V	<i>val</i> VW	Val tRNA
2E+06	phosphoenolpyruvate synthase	<i>pps</i> A	<i>pps</i> A	<		>	<i>pps</i> R	<i>pps</i> R	PEP synthetase regulatory protein
2E+06	succinylornithine transaminase	<i>ast</i> CADBE	<i>ast</i> C	<		>	<i>xth</i> A	<i>xth</i> A	exonuclease III
2E+06	KpLE2 IS1 repressor InsA	<i>ins</i> A	<i>ins</i> A	<		>	<i>usp</i> C	<i>usp</i> C	universal stress protein
2E+06	L-arabinose transporter	<i>ara</i> FGH	<i>ara</i> F	<		>	<i>ftn</i> B	<i>ftn</i> B	predicted ferritin-like protein
2E+06	predicted protein	<i>yec</i> H	<i>yec</i> H	<		>	<i>tyr</i> P	<i>tyr</i> P	tyrosine transporter
2E+06	YedVW TCS response regulator	<i>yed</i> WV	<i>yed</i> W	<		>	<i>yed</i> X	<i>yed</i> X	conserved protein
2E+06	IS5 transposase and trans-activator	<i>ins</i> H	<i>ins</i> H	<		>	<i>yoe</i> A	<i>yoe</i> A	CP4-44 hemin or colicin receptor
2E+06	predicted protein	<i>yeg</i> RZ	<i>yeg</i> R	<		>	<i>yeg</i> S	<i>yeg</i> S	phosphatidylglycerol kinase
2E+06	beta-D-glucoside glucohydrolase	<i>bgl</i> X	<i>bgl</i> X	<		>	<i>dld</i>	<i>dld</i>	D-lactate dehydrogenase
2E+06	ferredoxin-type protein	<i>nap</i> FDAGHB C- <i>ccm</i> ABCDEF	<i>nap</i> F	<		>	<i>yoj</i> O	<i>yoj</i> O	hypothetical protein
2E+06	conserved protein	<i>ais</i>	<i>ais</i>	<		>	<i>arn</i> B	<i>arn</i> BCADTEF	UDP-Ara4O aminotransferase
2E+06	transcription factor	<i>lrh</i> A	<i>lrh</i> A	<		>	<i>ala</i> A	<i>ala</i> A	glutamate-pyruvate aminotransferase
2E+06	conserved protein	<i>yfc</i> Z	<i>yfc</i> Z	<		>	<i>fad</i> L	<i>fad</i> L	long-chain fatty acid OM transporter
3E+06	purine nucleoside phosphorylase II	<i>xap</i> AB	<i>xap</i> A	<		>	<i>yfe</i> N	<i>yfe</i> N	conserved OM protein
3E+06	predicted oxidoreductase	<i>aeg</i> A	<i>aeg</i> A	<		>	<i>nar</i> Q	<i>nar</i> Q	NarQP(L) TCS sensor kinase
3E+06	ile tRNA	<i>ile</i> Y	<i>ile</i> Y	<		>	<i>yqa</i> Q	<i>yqa</i> Q	predicted protein
3E+06	nucleoid-associated transcription factor	<i>stp</i> A	<i>stp</i> A	<		>	<i>yga</i> W	<i>yga</i> W	predicted IM protein
3E+06	HD nuclease-DEAD box helicase	<i>cas</i> 3	<i>cas</i> 3	<		>	<i>sok</i> X	<i>sok</i> X	sok-related sRNA
3E+06	N-acetylmuramoyl-L-alanine amidase	<i>ami</i> C	<i>ami</i> C	<		>	<i>arg</i> A	<i>arg</i> A	N-acetylglutamate synthase
3E+06	predicted acyltransferase	<i>yqe</i> F	<i>yqe</i> F	<		>	<i>yqe</i> G	<i>yqe</i> G	predicted transporter
3E+06	predicted protein	<i>yqe</i> K	<i>yqe</i> K	<		>	<i>yqe</i> G	<i>yqe</i> G	predicted chaperone
3E+06	predicted IM protein	<i>yqq</i> D	<i>yqq</i> D	<		>	<i>met</i> K	<i>met</i> K	methionine adenosyltransferase 1
3E+06	conserved protein	<i>yqi</i> W	<i>yqi</i> W	<		>	<i>qse</i> B	<i>qse</i> BC	QseBC TCS response regulator
3E+06	methyl-accepting aerotaxis sensor	<i>aer</i>	<i>aer</i>	<		>	<i>pat</i> A	<i>pat</i> A	putrescine aminotransferase
3E+06	transcription factor	<i>tdc</i> ABCDEFG	<i>tdc</i> A	<		>	<i>tdc</i> R	<i>tdc</i> R	transcription factor
3E+06	predicted Fe-S oxidoreductase	<i>yhc</i> C	<i>yhc</i> C	<		>	<i>glt</i> B	<i>glt</i> BDF	glutamate synthase
3E+06	transcription factor	<i>nan</i> R	<i>nan</i> R	<		>	<i>dcu</i> D	<i>dcu</i> D	predicted transporter
3E+06	transcription factor	<i>env</i> R	<i>env</i> R	<		>	<i>acr</i> E	<i>acr</i> EF	cytoplasmic membrane lipoprotein
3E+06	peptidyl-prolyl cis-trans isomerase	<i>fkp</i> A	<i>fkp</i> A	<		>	<i>sly</i> X	<i>sly</i> X	conserved protein
4E+06	predicted inner membrane protein	<i>yhg</i> E	<i>yhg</i> E	<		>	<i>pck</i>	<i>pck</i>	phosphoenolpyruvate carboxykinase
4E+06	leucine transporter	<i>liv</i> KHMGF	<i>liv</i> K	<		>	<i>yhh</i> K	<i>yhh</i> K	conserved protein
4E+06	predicted protein	<i>yhi</i> L	<i>yhi</i> L	<		>	<i>yhi</i> M	<i>yhi</i> M	conserved IM protein
4E+06	IS5 transposase and trans-activator	<i>ins</i> H	<i>ins</i> H	<		>	<i>slp</i>	<i>slp</i> - <i>dct</i> R	OM lipoprotein
4E+06	<i>qed</i> VW TCS response regulator	<i>gad</i> W	<i>gad</i> W	<		>	<i>gad</i> Y	<i>gad</i> Y	ncRNA
4E+06	conserved protein	<i>yhi</i> R	<i>yhi</i> R	<		>	<i>bcs</i> E	<i>bcs</i> EFG	conserved protein
4E+06	D-xylose isomerase	<i>xyl</i> AB	<i>xyl</i> A	<		>	<i>xyl</i> F	<i>xyl</i> FGHR	D-xylose transporter
4E+06	conserved protein	<i>bax</i>	<i>bax</i>	<		>	<i>mal</i> S	<i>mal</i> S	alpha-amylase
4E+06	glutamate transporter	<i>glt</i> S	<i>glt</i> S	<		>	<i>xan</i> P	<i>xan</i> P	xanthine NCS2 transporter
4E+06	predicted transcription factor	<i>yie</i> P- <i>hsr</i> A	<i>yie</i> P	<		>	<i>rrs</i> C	<i>rrs</i> C- <i>glt</i> U- <i>rrl</i> C- <i>rrf</i> C	16S rRNA
4E+06	predicted endonuclease	<i>yih</i> G	<i>yih</i> G	<		>	<i>pol</i> A	<i>pol</i> A	DNA polymerase I
4E+06	GTP-binding protein	<i>yih</i> A	<i>yih</i> A	<		>	<i>csr</i> C	<i>csr</i> C	ncRNA
4E+06	pyridine nucleotide transhydrogenase	<i>sth</i> A	<i>sth</i> A	<		>	<i>fab</i> R	<i>fab</i> R- <i>yij</i> D	transcription factor
4E+06	hypothetical protein	<i>yib</i> S	<i>yib</i> S	<		>	<i>aph</i> A	<i>aph</i> A	acid phosphatase/phosphotransferase
4E+06	aspartate ammonia-lyase	<i>asp</i> A- <i>dcu</i> A	<i>asp</i> A	<		>	<i>fxs</i> A	<i>fxs</i> A	IM protein
4E+06	anaerobic fumarate reductase	<i>frd</i> ABCD	<i>frd</i> A	<		>	<i>pox</i> A	<i>pox</i> A	predicted lysyl-tRNA synthetase
4E+06	predicted transcriptional factor	<i>ytf</i> J	<i>ytf</i> J	<		>	<i>ytf</i> K	<i>ytf</i> K	conserved protein
4E+06	methionine sulfoxide reductase A	<i>msr</i> A	<i>msr</i> A	<		>	<i>ytf</i> M	<i>ytf</i> MNP	OM protein surface antigen
5E+06	KpLE2 IS4 transposase	<i>ins</i> G	<i>ins</i> G	<		>	<i>yjh</i> B	<i>yjh</i> BC	KpLE2 phage transporter
5E+06	predicted protein	<i>yji</i> C	<i>yji</i> C	<		>	<i>ira</i> D	<i>ira</i> D	RpoS proteolysis inhibitor
5E+06	nucleoid-associated transcription factor	<i>rob</i>	<i>rob</i>	<		>	<i>cre</i> A	<i>cre</i> ABCD	conserved protein

Total, 78 peaks (target operons, 156)

**Type-B spacers**

Position	Function	Operon	Gene	D	Lrp	D	Gene	Operon	Function
9262	transaldolase B		<i>tal</i> B	>		>	<i>mog</i>	<i>mog</i>	predicted molybdochelatase

85536	transcriptional factor		<b>leuO</b>	>	>	<b>ilvI</b>	<i>ilvIH</i>	acetolactate synthase III
152844	predicted fimbrial-like adhesin protein	<i>yadMLKC</i>	<b>yadM</b>	<	<	<b>htrE</b>		predicted OM usher protein
155442	predicted OM usher protein	<i>htrE</i>	<b>htrE</b>	<	<	<b>ecpD</b>		predicted periplasmic pilin chaperone
236848	DNA polymerase III		<b>dnaQ</b>	>	>	<b>aspV</b>		Asp tRNA
251970	DNA polymerase IV		<b>dinB</b>	>	>	<b>yafN</b>	<i>yafNOP</i>	YafO-YafN toxin-antitoxin
317836	predicted protein	<i>ykgIB</i>	<b>ykgI</b>	<	<	<b>ykgC</b>		predicted oxidoreductase
320346	transcription factor		<b>ykgD</b>	>	>	<b>ykgE</b>	<i>ykgEFG</i>	predicted oxidoreductase
389160	porphobilinogen synthase	<i>hemB</i>	<b>hemB</b>	<	<	<b>insF</b>		IS3 element protein InsF
418534	PhoBR TCS sensor kinase		<b>phoR</b>	>	>	<b>brnQ</b>	<i>brnQ-proY</i>	branched amino acid transporter
433872	diaminohydroxyphosphoribosylaminopyrimidine deaminase-amino-(5-phosphoribosylamino)uracil reductase		<b>ribD</b>	>	>	<b>ribE</b>	<i>ribE-nusB-thiL-pgpA</i>	riboflavin synthase beta chain
467530	thiamin pyrimidine pyrophosphate hydrolase		<b>cof</b>	>	>	<b>ybaO</b>	<i>ybaO</i>	predicted transcription factor
479234	maltose O-acetyltransferase	<i>maa</i>	<b>maa</b>	<	<	<b>hha</b>		H-NS regulator
530448	tRNA 2-selenouridine synthase	<i>ybbB</i>	<b>ybbB</b>	<	<	<b>allS</b>		transcription factor
536860	tartronate semialdehyde reductase		<b>glxR</b>	>	>	<b>ybbW</b>	<i>ybbW-allB-ybbY-glxK</i>	predicted allantoin transporter
567532	IS3 element protein InsF		<b>insF</b>	>	>	<b>emrE</b>	<i>emrE</i>	DLP12 multidrug resistance protein
569664	DLP12 prophage recombinase		<b>ybcK</b>	>	>	<b>ybcL</b>	<i>ybcLM</i>	DLP12 kinase inhibitor
603938	mechanosensitive channel	<i>mscM</i>	<b>mscM</b>	<	<	<b>nfsB</b>		dihydropteridine reductase
659532	lipate synthase	<i>lipA</i>	<b>lipA</b>	<	<	<b>ybeF</b>		predicted transcription factor
696540	Met tRNA	<i>metT-leuW-glnUW-metU-glnVX</i>	<b>metT</b>	<	<	<b>asnB</b>		asparagine synthetase B
735642	predicted protein		<b>ybfC</b>	>	>	<b>ybfQ</b>	<i>ybfQ</i>	predicted transposase
736068	predicted transposase		<b>ybfQ</b>	>	>	<b>ybfL</b>	<i>ybfL</i>	predicted transposase
802538	predicted transporter		<b>ybhI</b>	>	>	<b>ybhJ</b>	<i>ybhJ</i>	predicted hydratase
837438	predicted protein	<i>ybiJ</i>	<b>ybiJ</b>	<	<	<b>ybil</b>		conserved protein
892742	predicted oxidoreductase		<b>ybiN</b>	>	>	<b>potF</b>	<i>potFGHI</i>	putrescine transporter
903170	arginine transporter	<i>artPIQM</i>	<b>artP</b>	<	<	<b>ybiP</b>		predicted lipoprotein
936430	chromosome resolution and recombination protein		<b>ftsK</b>	>	>	<b>lolA</b>	<i>lolA-rarA</i>	chaperone for lipoproteins
938542	recombination protein		<b>rarA</b>	>	>	<b>serS</b>	<i>serS</i>	seryl-tRNA synthetase
946370	predicted transporter		<b>ycaD</b>	>	>	<b>ycaM</b>	<i>ycaM</i>	predicted transporter
956734	conserved inner membrane protein		<b>ycaP</b>	>	>	<b>serC</b>	<i>serC-aroA</i>	phosphohydroxythreonine aminotransferase
985134	aspartate aminotransferase	<i>aspC</i>	<b>aspC</b>	<	<	<b>ompF</b>		OM porin 1a
986550	OM porin 1a	<i>ompF</i>	<b>ompF</b>	<	<	<b>asnS</b>		asparaginyl tRNA synthetase
1E+06	DNA-binding protein	<i>hspQ</i>	<b>hspQ</b>	<	<	<b>yccW</b>		predicted methyltransferase
1E+06	conserved protein		<b>efeB</b>	>	>	<b>phoH</b>	<i>phoH</i>	nucleoside triphosphate hydrolase
1E+06	predicted protein	<i>bssS</i>	<b>bssS</b>	<	<	<b>dinI</b>		DNA damage-inducible protein I
1E+06	predicted lipoprotein	<i>yceB</i>	<b>yceB</b>	<	<	<b>grxB</b>		glutaredoxin 2
1E+06	e14 prophage methyltransferase	<i>ymlD</i>	<b>ymlD</b>	<	<	<b>ymlE</b>		e14 prophage IM protein
1E+06	RpoS proteolysis inhibitor	<i>iraM</i>	<b>iraM</b>	<	<	<b>ycgX</b>		predicted protein
1E+06	predicted transcription factor	<i>ycaE</i>	<b>ycgE</b>	<	<	<b>ycqF</b>		FAD-binding phosphodiesterase
1E+06	conserved IM protein		<b>ycgG</b>	>	>	<b>ymgF</b>	<i>ymgF</i>	predicted protein
1E+06	predicted adhesin	<i>ycqV</i>	<b>ycqV</b>	<	<	<b>ychF</b>		predicted GTP-binding protein
1E+06	predicted transcription factor		<b>ycaA</b>	>	>	<b>kdsA</b>	<i>kdsA</i>	D-manno-octulosonate 8-phosphate synthase
1E+06	nitrate/nitrite transporter		<b>narK</b>	>	>	<b>narG</b>	<i>narGHJ</i>	nitrate reductase 1
1E+06	predicted IM protein		<b>ychE</b>	>	>	<b>oppA</b>	<i>oppABCDF</i>	oligopeptide transporter
1E+06	predicted IM protein		<b>yciQ</b>	>	>	<b>rluB</b>	<i>rluB</i>	23S rRNA pseudouridylate synthase
1E+06	DNA topoisomerase II		<b>topA</b>	>	>	<b>cysB</b>	<i>cysB</i>	transcription factor
1E+06	transcription factor		<b>cysB</b>	>	>	<b>ymlA</b>	<i>ymlA-yciX</i>	hypothetical protein
1E+06	hypothetical protein	<i>yciZT</i>	<b>yciZ</b>	<	<	<b>gmr</b>		RNase II modulator
1E+06	RNase II stability modulator	<i>gmr</i>	<b>gmr</b>	<	<	<b>rrb</b>		ribonuclease II
1E+06	conserved IM protein		<b>yciF</b>	>	>	<b>tyrR</b>	<i>tyrR</i>	transcription factor
1E+06	Rac prophage site-specific	<i>pinR</i>	<b>pinR</b>	<	<	<b>ynaE</b>		Rac transcription factor
2E+06	SAM-dependent methyltransferase		<b>tehB</b>	>	>	<b>ydcL</b>	<i>ydcL</i>	predicted lipoprotein
2E+06	nitrate/nitrite transporter	<i>narU</i>	<b>narU</b>	<	<	<b>yddJ</b>		predicted protein
2E+06	predicted protein	<i>yddJ</i>	<b>yddJ</b>	<	<	<b>yddG</b>		methyl viologen efflux pump
2E+06	diguanylate cyclase	<i>dosCP</i>	<b>dosC</b>	<	<	<b>yddW</b>		predicted lipoprotein
2E+06	glutamate decarboxylase B	<i>gadBC</i>	<b>gadB</b>	<	<	<b>pqqL</b>		predicted peptidase
2E+06	conserved protein	<i>ydeN</i>	<b>ydeN</b>	<	<	<b>ydeO</b>		transcription factor
2E+06	predicted lipoprotein	<i>ydeK</i>	<b>ydeK</b>	<	<	<b>IsrK</b>		autoinducer-2 (AI-2) kinase
2E+06	predicted diguanylate cyclase	<i>yneF</i>	<b>yneF</b>	<	<	<b>yneG</b>		conserved protein
2E+06	conserved protein	<i>ydeH</i>	<b>ydeH</b>	<	<	<b>ydel</b>		conserved protein
2E+06	Qin prophage transcription factor		<b>ydkK</b>	>	>	<b>pinQ</b>	<i>pinQ</i>	Qin site-specific recombinase
2E+06	predicted protein		<b>vdqH</b>	>	>	<b>ydqI</b>	<i>vdqI-foIM</i>	arginine/ornithine antiporter transporter
2E+06	DNA glycosylase-endonuclease III		<b>nth</b>	>	>	<b>tpdB</b>	<i>tpdB</i>	predicted transporter
2E+06	conserved protein	<i>ydiV</i>	<b>ydiV</b>	<	<	<b>nlpC</b>		predicted lipoprotein
2E+06	predicted diguanylate cyclase		<b>yeal</b>	>	>	<b>yeaJ</b>	<i>yeaJ</i>	predicted diguanylate cyclase
2E+06	neutral amino-acid efflux system	<i>leuE</i>	<b>leuE</b>	<	<	<b>yeaT</b>		transcription factor
2E+06	predicted NUDIX hydrolase		<b>nudL</b>	>	>	<b>sdaA</b>	<i>sdaA</i>	L-serine deaminase I
2E+06	ncRNA		<b>rseX</b>	>	>	<b>hchA</b>	<i>hchA</i>	Hsp31 molecular chaperone
2E+06	AMP nucleosidase		<b>amn</b>	>	>	<b>yeeN</b>	<i>yeeN</i>	conserved protein
2E+06	cobinamide kinase	<i>cobUST</i>	<b>cobU</b>	<	<	<b>insH</b>		IS5 transposase and trans-activator
2E+06	predicted IM protein	<i>yeeED</i>	<b>yeeE</b>	<	<	<b>yeeF</b>		predicted amino-acid transporter
2E+06	predicted peptidase		<b>yegQ</b>	>	>	<b>cyaR</b>	<i>cyaR</i>	ncRNA
2E+06	galactitol-specific PTS IIA	<i>gatABCD</i>	<b>gatA</b>	<	<	<b>gatZ</b>		D-tagatose 1,6-bisphosphate aldolase
2E+06	predicted protein		<b>yehK</b>	>	>	<b>yehL</b>	<i>yehLMPQ</i>	predicted transporter subunit
2E+06	conserved protein	<i>yehS</i>	<b>yehS</b>	<	<	<b>yehT</b>		YehUT TCS response regulator
2E+06	predicted IM protein		<b>yehS</b>	>	>	<b>yehT</b>		YehUT TCS response regulator
2E+06	predicted IM protein		<b>yehS</b>	>	>	<b>yehT</b>		YehUT TCS response regulator
2E+06	endonuclease IV		<b>nfo</b>	>	>	<b>yehI</b>	<i>yehI</i>	Dihydropyrimidine dehydrogenase
2E+06	undecaprenyl pyrophosphate		<b>lpxT</b>	>	>	<b>spr</b>	<i>spr</i>	predicted peptidase
2E+06	hypothetical protein		<b>yoiO</b>	>	>	<b>eco</b>	<i>eco</i>	serine protease inhibitor ecptin
2E+06	ncRNA		<b>micF</b>	>	>	<b>rcsD</b>	<i>rcsDB</i>	RcsBC TCS phospho transfer
2E+06	predicted protein	<i>yfaQP</i>	<b>yfaQ</b>	<	<	<b>yfaT</b>		predicted protein
2E+06	NADH:ubiquinone oxidoreductase	<i>nuoABCEFGHIJKLMN</i>	<b>nuoA</b>	<	<	<b>lrhA</b>		transcription factor
2E+06	phosphate acetyltransferase		<b>pta</b>	>	>	<b>yfcC</b>	<i>yfcC</i>	predicted IM protein
3E+06	predicted peptidase		<b>yfhR</b>	>	>	<b>csiE</b>	<i>csiE</i>	stationary phase inducible protein
3E+06	16S rRNA	<i>rrsG-gltW-rrlG-rrfG</i>	<b>rrsG</b>	<	<	<b>clpB</b>		protein disaggregation chaperone
3E+06	cold shock protein		<b>raiA</b>	>	>	<b>pheL</b>	<i>pheLA</i>	<i>pheA</i> gene leader peptide

3E+06	ribonucleoside-diphosphate reductase		<i>nrdF</i>	>	>	<i>proV</i>	<i>proVWX</i>	glycine betaine transporter
3E+06	cascade subunit A	<i>casABCDE12</i>	<i>casA</i>	<	<	<i>cas3</i>		HD nuclease-DEAD box helicase
3E+06	predicted D-glucarate transporter	<i>gudPXD</i>	<i>gudP</i>	<	<	<i>yqcA</i>		predicted flavoprotein
3E+06	conserved protein		<i>ygdH</i>	>	>	<i>sdaC</i>	<i>sdaCB</i>	predicted serine transporter
3E+06	predicted chaperone		<i>ygeG</i>	>	>	<i>ygeH</i>	<i>ygeH</i>	transcription factor
3E+06	predicted transporter		<i>ygfO</i>	>	>	<i>quaD</i>	<i>quaD-ygfQ</i>	guanine deaminase
3E+06	aminomethyltransferase	<i>gcvTHP</i>	<i>gcvT</i>	<	<	<i>visC</i>		predicted oxidoreductase
3E+06	D-3-phosphoglycerate dehydrogenase	<i>serA</i>	<i>serA</i>	<	<	<i>rpiA</i>		ribose 5-phosphate isomerase
3E+06	periplasmic L-asparaginase II	<i>ansB</i>	<i>ansB</i>	<	<	<i>yggN</i>		predicted protein
3E+06	predicted IM lipoprotein	<i>yghJ</i>	<i>yghJ</i>	<	<	<i>glcA</i>		glycolate transporter
3E+06	glycolate transporter	<i>glcA</i>	<i>glcA</i>	<	<	<i>glcB</i>		malate synthase G
3E+06	phosphate transporter	<i>pitB</i>	<i>pitB</i>	<	<	<i>gsp</i>		glutathionylspermidine synthetase
3E+06	conserved protein		<i>yqiC</i>	>	>	<i>yqiL</i>	<i>yqiL</i>	predicted fimbrial-like adhesin
3E+06	transcription factor		<i>tdcR</i>	>	>	<i>yhaB</i>	<i>yhaBC</i>	predicted protein
3E+06	glutamate synthase, 4Fe-4S protein		<i>gltD</i>	>	>	<i>gltF</i>	<i>gltF</i>	periplasmic protein
3E+06	transcription factor		<i>argR</i>	>	>	<i>yhcN</i>	<i>yhcN</i>	conserved protein
3E+06	predicted OM protein		<i>yhdV</i>	>	>	<i>yhdW</i>	<i>yhdWXYZ</i>	YhdW
3E+06	conserved protein	<i>yhdN-zntR</i>	<i>yhdN</i>	<	<	<i>rplQ</i>		50S ribosomal subunit protein L17
3E+06	50S ribosome protein L6	<i>rplFR-rpsE-rpmD-rplO-secY-rpmJ</i>	<i>rplF</i>	<	<	<i>rpsH</i>		30S ribosomal subunit protein S8
4E+06	conserved protein		<i>yhhZ</i>	>	>	<i>yrhA</i>	<i>yrhA-insA-6AB-6B-6</i>	conserved protein
4E+06	leucine/isoleucine/valine transporter	<i>livJ</i>	<i>livJ</i>	<	<	<i>rpoH</i>		RNA polymerase RpoH sigma
4E+06	predicted protein		<i>yhhH</i>	>	>	<i>yhhI</i>	<i>yhhI</i>	predicted transposase
4E+06	universal stress protein		<i>uspA</i>	>	>	<i>dtpB</i>	<i>dtpB</i>	predicted transporter
4E+06	arsenate reductase		<i>arsC</i>	>	>	<i>yhiS</i>	<i>yhiS</i>	predicted protein
4E+06	conserved IM protein		<i>yhiD</i>	>	>	<i>yhiE</i>	<i>yhiE</i>	predicted transporter
4E+06	predicted OM biogenesis protein	<i>yhiG</i>	<i>yhiG</i>	<	<	<i>yhiH</i>		flagellar function EAL regulator
4E+06	dipeptide transporter	<i>dppABCDF</i>	<i>dppA</i>	<	<	<i>proK</i>		Pro tRNA
4E+06	alpha-amylase		<i>malS</i>	>	>	<i>avtA</i>	<i>avtA</i>	valine-pyruvate aminotransferase
4E+06	conserved IM protein	<i>yiaWV</i>	<i>yiaW</i>	<	<	<i>aldB</i>		aldehyde dehydrogenase B
4E+06	Fe-containing alcohol dehydrogenase	<i>viaY</i>	<i>viaY</i>	<	<	<i>selB</i>		selecnOCys-tRNA translation factor
4E+06	glycine C-acetyltransferase	<i>kbl-tdh</i>	<i>kbl</i>	>	>	<i>htrL</i>		predicted protein
4E+06	LPS heptosyl transferase I		<i>rfaC</i>	>	>	<i>rfaL</i>	<i>rfaL</i>	O-antigen ligase
4E+06	lexA-regulated toxic peptide		<i>tisB</i>	>	>	<i>emrD</i>	<i>emrD</i>	multidrug efflux system protein
4E+06	GTPase		<i>mnmE</i>	>	>	<i>tnaC</i>	<i>tnaCAB</i>	tryptophanase leader peptide
4E+06	tryptophanase leader peptide		<i>tnaC</i>	>	>	<i>tnaA</i>	<i>tnaAB</i>	tryptophanase/cysteine desulfhydrase
4E+06	glucosamine-1-phosphate acetyl transferase	<i>glmUS</i>	<i>glmU</i>	<	<	<i>atpC</i>		F1 membrane-bound ATP synthase
4E+06	disulfide isomerase I		<i>dsbA</i>	>	>	<i>yihF</i>	<i>yihF</i>	conserved protein
4E+06	predicted acetyltransferase		<i>yiiD</i>	>	>	<i>yiiE</i>	<i>yiiE</i>	predicted transcriptional regulator
4E+06	homoserine O-transsuccinylase		<i>metA</i>	>	>	<i>aceB</i>	<i>aceBAK</i>	malate synthase A
4E+06	ankyrin repeat protein	<i>arpA</i>	<i>arpA</i>	<	<	<i>iclR</i>		DNA-binding transcriptional repressor
4E+06	SOS response protein		<i>dinF</i>	>	>	<i>yjbJ</i>	<i>yjbJ</i>	predicted stress response protein
4E+06	heme lyase		<i>nrfG</i>	>	>	<i>gltP</i>	<i>gltP</i>	glutamate/aspartate:proton symporter
4E+06	predicted alkyl sulfatase	<i>yicS</i>	<i>yicS</i>	<	<	<i>alsK</i>		D-allose kinase
4E+06	transcription factor	<i>adiY</i>	<i>adiY</i>	<	<	<i>adiA</i>		biodegradative arginine decarboxylase
4E+06	C4-dicarboxylate antiporter	<i>dcuB-fumB</i>	<i>dcuB</i>	<	<	<i>dcuR</i>		DcuSR TCS response regulator
4E+06	lysine tRNA synthetase, inducible	<i>lysU</i>	<i>lysU</i>	<	<	<i>yjdL</i>		predicted transporter
4E+06	predicted lysine/cadaverine transporter	<i>cadBA</i>	<i>cadB</i>	<	<	<i>cadC</i>		DNA-binding transcriptional activator
4E+06	predicted lysyl-tRNA synthetase		<i>poxA</i>	>	>	<i>yjeM</i>	<i>yjeM</i>	predicted transporter
4E+06	conserved protein		<i>yjiM</i>	>	>	<i>yifC</i>	<i>yifC</i>	predicted synthetase/amidase
4E+06	peptidyl-prolyl cis-trans isomerase		<i>fkfB</i>	>	>	<i>cycA</i>	<i>cycA</i>	D-alanine/D-serine/glycine transporter
4E+06	KpLE2 IS2 insertion transposase		<i>insD</i>	>	>	<i>yiqW</i>	<i>yiqW</i>	KpLE2 phage-like element
5E+06	KpLE2 transcription factor	<i>yjhIHG</i>	<i>yjhI</i>	<	<	<i>sgcR</i>		KpLE2 transcription factor
5E+06	<i>fimA</i> switch tyrosine recombinase		<i>fimE</i>	>	>	<i>fimA</i>	<i>fimAICDFGH</i>	major type 1 subunit fimbria (pilin)
5E+06	peptide chain release factor RF-3		<i>prfC</i>	>	>	<i>osmY</i>	<i>osmY</i>	periplasmic protein

Total 140 peaks (target operons, 140)

#### Type-C spacers

Position	Function	Operon	Gene	D	Lrp	D	Gene	Operon	Function
238230	predicted aminopeptidase		<i>yafT</i>	>	<	<	<i>ykfM</i>		hypothetical protein
583650	DLP12 transcriptional activator		<i>appY</i>	>	<	<	<i>ompT</i>		DLP12 OM protease VII
1E+06	cation transport regulator		<i>chaC</i>	>	<	<	<i>ychn</i>		conserved protein
1E+06	IM phosphatase		<i>yhbD</i>	>	<	<	<i>azoR</i>		NADH-azoreductase
3E+06	RNA-binding protein		<i>yhbY</i>	>	<	<	<i>greA</i>		transcription elongation factor
4E+06	sn-glycerol-3-phosphate		<i>glpD</i>	>	<	<	<i>glgP</i>		glycogen phosphorylase
4E+06	IM protein		<i>yhiM</i>	>	<	<	<i>yhiN</i>		oxidoreductase
4E+06	Trp tRNA		<i>trpT</i>	>	<	<	<i>hdfR</i>		transcription factor
4E+06	heat shock protein		<i>yjaZ</i>	>	<	<	<i>sroH</i>		SroH small RNA
5E+06	ncRNA		<i>symR</i>	>	<	<	<i>hdsS</i>		HsdM and HsdR regulator

Total, 10 peaks

#### Inside ORF

Position	Function	Operon	Gene	D	Lrp	D	Gene	Operon	Function
168	predicted protein		<i>yjiY</i>	>	<i>yjtD</i>	>	<i>thrL</i>	<i>thrLABC</i>	<i>thr</i> operon leader peptide
102758	UDP-N-acetylmuramate:alanine ligase		<i>murC</i>	>	<i>ddlB</i>	>	<i>ftsQ</i>	<i>ftsQAZ-lpxC</i>	cell division septum protein
223368	DL-methionine transporter	<i>metNIQ</i>	<i>metN</i>	<	<i>gmhB</i>	>	<i>rrsH</i>	<i>rrsH-ileV-alaV-rrfH</i>	16S rRNA
296170	CP4-6 prophage protein	<i>yagN</i>	<i>yagN</i>	<	<i>intF</i>	<	<i>yagP</i>		predicted transcriptional regulator
302552	predicted xanthine dehydrogenase	<i>yagTSRQ</i>	<i>yagT</i>	<	<i>yagU</i>	<	<i>ykgJ</i>		predicted ferredoxin
360530	predicted cyanate transporter		<i>cynX</i>	>	<i>lacA</i>	<	<i>lacY</i>		lactose/galactose transporter
515656	membrane-associated protease	<i>qmcA-ybbJ</i>	<i>qmcA</i>	<	<i>ybbL</i>	>	<i>ybbM</i>	<i>ybbM</i>	predicted IM protein
526956	rhd element protein		<i>rhdS</i>	>	<i>ybbC</i>	>	<i>ybbH</i>	<i>ybbH-ybbD</i>	conserved protein
568958	DLP12 MD resistance protein		<i>emrE</i>	>	<i>ybcK</i>	>	<i>ybcL</i>	<i>ybcLM</i>	DLP12 prophage kinase inhibitor
578634	DLP12 prophage lipoprotein	<i>borD</i>	<i>borD</i>	<	<i>ybcV</i>	>	<i>ybcW</i>	<i>ybcW</i>	DLP12 prophage protein
636446	conserved protein	<i>ybdN</i>	<i>ybdN</i>	<	<i>ybdO</i>	<	<i>dsbG</i>		disulfide isomerase
677132	predicted protein		<i>ybeR</i>	>	<i>djIB</i>	<	<i>ybeT</i>		conserved OM protein
737356	predicted transposase		<i>ybfQ</i>	>	<i>ybfD</i>	>	<i>ybgA</i>	<i>ybgA-phr</i>	conserved protein
776330	ToIAQR complex protein		<i>tolR</i>	>	<i>tolA</i>	>	<i>tolB</i>	<i>tolB-pal-ybgF</i>	periplasmic protein
811762	biotin synthesis methyltransferase		<i>bioC</i>	>	<i>bioD</i>	<	<i>ybhU</i>		hypothetical protein
906136	NAD(P)H-binding oxidoreductase		<i>ybjS</i>	<	<i>ybjT</i>	<	<i>ltaE</i>		L-allo-threonine aldolase
909154	L-allo-threonine aldolase	<i>ltaE-ybjT</i>	<i>ltaE</i>	<	<i>poxB</i>	<	<i>hcr</i>		HCP oxidoreductase
921444	macrolide transporter		<i>macA</i>	>	<i>macB</i>	<	<i>cspD</i>		cold shock protein homolog
988572	asparaginyl tRNA synthetase	<i>asnS</i>	<i>asnS</i>	<	<i>pncB</i>	>	<i>pepN</i>	<i>pepN</i>	aminopeptidase N



1E+06	predicted hydrolase		<i>ymdC</i>	>	<i>mdo</i>	>	<i>mdoG</i>	<i>mdoGH</i>	glucan biosynthesis protein
1E+06	RpoS proteolysis inhibitor	<i>iraM</i>	<i>iraM</i>	<	<i>ycqX</i>	<	<i>ycqE</i>		predicted transcription factor
1E+06	Tyr tRNA	<i>tyrTV-tp</i>	<i>tyrT</i>	<	<i>purU</i>	<	<i>ychJ</i>		conserved protein
1E+06	aconitate hydratase 1		<i>acrA</i>	>	<i>ribA</i>	>	<i>pqpB</i>	<i>pqpB</i>	phosphatidylglycerophosphatase B
1E+06	conserved IM protein		<i>ycjF</i>	>	<i>tyrR</i>	<	<i>tpx</i>		lipid hydroperoxide peroxidase
1E+06	fermentative D-lactate dehydrogenase	<i>ldhA</i>	<i>ldhA</i>	<	<i>ydbH</i>	>	<i>ynbE</i>	<i>ynbE-ydbL</i>	predicted lipoprotein
1E+06	L7/L12-serine acetyltransferase		<i>rimL</i>	>	<i>ydcK</i>	>	<i>tehA</i>	<i>tehAB</i>	proflavin transporter
2E+06	predicted protein		<i>ydcD</i>	>	<i>ydcC</i>	>	<i>pptA</i>	<i>pptA</i>	4-oxalocrotonate tautomerase
2E+06	predicted peptidase	<i>pqqL</i>	<i>pqqL</i>	<	<i>yddB</i>	<	<i>yddA</i>		ABC-family MD transporter
2E+06	autoinducer-2 (AI-2) kinase	<i>lsrK</i>	<i>lsrK</i>	<	<i>lsrR</i>	>	<i>lsrA</i>	<i>lsrACDBFG-</i>	ABC-family AI2 transporter
2E+06	cysteine acetyl-serine efflux system	<i>eamA</i>	<i>eamA</i>	<	<i>ydeE</i>	>	<i>yneM</i>	<i>yneM</i>	hypothetical protein
2E+06	predicted protein		<i>ynfD</i>	>	<i>ynfE</i>	>	<i>ynfF</i>	<i>ynfFGH-dmsD</i>	oxidoreductase subunit
2E+06	OM porin protein	<i>uidBC</i>	<i>uidB</i>	<	<i>uidA</i>	<	<i>uidR</i>		transcription factor
2E+06	threonyl-tRNA synthetase	<i>thrS-infC-rpmI-rplT-pheMST-ihfA</i>	<i>thrS</i>	<	<i>arpB</i>	>	<i>yniD</i>	<i>yniD</i>	predicted protein
2E+06	predicted acyltransferase		<i>yedN</i>	<	<i>yedN<sub>1</sub></i>	<	<i>yedM</i>		conserved protein
2E+06	IS5 transposase and trans-activator	<i>insH</i>	<i>insH</i>	<	<i>wbbK</i>	<	<i>wbbJ</i>		predicted acyl transferase
2E+06	conserved protein	<i>wbbJJK</i>	<i>wbbJ</i>	<	<i>rfc</i>	<	<i>glf</i>		UDP-galactopyranose mutase
2E+06	O-antigen polymerase		<i>rfc</i>	<	<i>glf</i>	<	<i>rfbX</i>		polisoprenol-linked O-antigen
2E+06	UDP-galactopyranose mutase	<i>glf-rfc</i>	<i>glf</i>	<	<i>rfbX</i>	<	<i>rfbC</i>		dTDP-4-deoxyrihamnose-3,5-
2E+06	predicted subunit with GalU	<i>galF</i>	<i>galF</i>	>	<i>wcaM</i>	<	<i>wcaL</i>		predicted glycosyl transferase
2E+06	IS3 element protein InsF		<i>insF</i>	>	<i>gatR</i>	<	<i>gatD</i>		galactitol-1-phosphate dehydrogenase
2E+06	predicted OM protein	<i>yehBA</i>	<i>yehB</i>	<	<i>yehC</i>	<	<i>yehD</i>		predicted fimbrial-like adhesin protein
2E+06	predicted protein	<i>yfaTS</i>	<i>yfaT</i>	<	<i>yfaA</i>	<	<i>gyrA</i>		DNA gyrase (type II topoisomerase)
2E+06	predicted NUDIX hydrolase		<i>nudI</i>	>	<i>ais</i>	>	<i>arnB</i>	<i>arnBCADTEF</i>	Ur (pentapyranosyl diphosphate) aminotransferase
2E+06	enoyl-CoA hydratase and epimerase	<i>fadJ</i>	<i>fadJ</i>	<	<i>fadI</i>	<	<i>yfcZ</i>		conserved protein
2E+06	predicted CoA-transferase	<i>yfdE</i>	<i>yfdE</i>	<	<i>yfdV</i>	<	<i>oxc</i>		predicted oxalyl-CoA decarboxylase
3E+06	transaldolase A		<i>talA</i>	>	<i>tktB</i>	<	<i>ypfG</i>		predicted protein
3E+06	predicted protein		<i>yfiR</i>	>	<i>yfiN</i>	>	<i>yfiB</i>	<i>yfiB</i>	predicted OM lipoprotein
3E+06	CP4-57 prophage protein	<i>ypjM</i>	<i>ypjM</i>	<	<i>yfjW</i>	>	<i>yfjX</i>	<i>yfjXY-ypjJ-yfjZ-ypjF</i>	CP4-57 antirestriction protein
3E+06	alanyl-tRNA synthetase	<i>alaS</i>	<i>alaS</i>	<	<i>recX</i>	<	<i>recA</i>		recombination protein
3E+06	enolase	<i>eno</i>	<i>eno</i>	<	<i>pyrG</i>	<	<i>mazG</i>		NTP pyrophosphohydrolase
3E+06	L-fucose-1-phosphate aldolase	<i>fucAO</i>	<i>fucA</i>	<	<i>fucP</i>	>	<i>fucI</i>	<i>fucIKUR</i>	L-fucose isomerase
3E+06	predicted chaperone		<i>ygeG</i>	>	<i>ygeH</i>	>	<i>ygeI</i>	<i>ygeI</i>	predicted protein
3E+06	conserved protein	<i>ygiQ</i>	<i>ygiQ</i>	<	<i>ftsP</i>	<	<i>plsC</i>		acyl-glycerol-3-phosphate
3E+06	conserved IM protein		<i>ygiH</i>	>	<i>ttdR</i>	>	<i>ttdA</i>	<i>ttdABT</i>	L-tartrate dehydratase
3E+06	conserved IM protein		<i>yqjA</i>	>	<i>yqjB</i>	>	<i>yqjC</i>	<i>yqjCDEK</i>	conserved protein
3E+06	predicted protein		<i>yhaB</i>	>	<i>yhaC</i>	<	<i>rnpB</i>		ncRNA
4E+06	heat shock protein Hsp33		<i>hslO</i>	>	<i>yhgE</i>	>	<i>pck</i>	<i>pck</i>	phosphoenolpyruvate carboxykinase
4E+06	predicted acetyltransferase		<i>yhhY</i>	>	<i>yhhZ</i>	>	<i>yrhA</i>	<i>yrhA-insA-6AB</i>	conserved protein
4E+06	<i>rhsB</i> element core protein RshB		<i>rhsB</i>	>	<i>yhhh</i>	>	<i>yhhl</i>	<i>yhhl</i>	predicted transposase
4E+06	predicted transposase		<i>yhhI</i>	>	<i>yhhJ</i>	<	<i>rbbA</i>		ribosome-associated ATPase
4E+06	predicted HlyD family secretion protein	<i>yhil-rbbA-</i>	<i>yhil</i>	<	<i>yhiJ</i>	<	<i>yhiK</i>		predicted protein
4E+06	MgtC-family IM transporterr	<i>yhiD</i>	<i>yhiD</i>	<	<i>hdeB</i>	<	<i>hdeA</i>		acid-resistance protein
4E+06	multidrug transporter		<i>mdtF</i>	>	<i>gadW</i>	>	<i>gadY</i>	<i>gadY</i>	ncRNA
4E+06	ncRNA		<i>rdiD</i>	>	<i>yhiV</i>	<	<i>dppF</i>		dipeptide transporter
4E+06	predicted transporter	<i>yhiX</i>	<i>yhiX</i>	>	<i>yhiY</i>	>	<i>tag</i>	<i>tag-yiaC</i>	3-methyl-adenine DNA glycosylase I
4E+06	predicted protein	<i>ysaB</i>	<i>ysaB</i>	<	<i>wecH</i>	<	<i>yiaA</i>		conserved IM protein
4E+06	predicted glutathione S-transferase	<i>yibF</i>	<i>yibF</i>	<	<i>rhsA</i>	>	<i>yibA</i>	<i>yibA</i>	lyase containing HEAT-repeat
4E+06	<i>rhsA</i> element core protein		<i>rhsA</i>	>	<i>yibA</i>	>	<i>yibG</i>	<i>yibG</i>	conserved protein
4E+06	LPS core biosynthesis	<i>waaK</i>	<i>waaK</i>	<	<i>rfaZ</i>	<	<i>rfaY</i>		LP core biosynthesis protein
4E+06	UDP-D-galactose galactosyltransferase	<i>waaBIJY-rfaZ-waaK</i>	<i>waaB</i>	<	<i>rfaS</i>	<	<i>rfaP</i>		LP kinase
4E+06	predicted alpha-glucosidase	<i>yicI</i>	<i>yicI</i>	<	<i>yicJ</i>	>	<i>selC</i>	<i>selC</i>	Sec tRNA
4E+06	conserved IM protein	<i>yigF</i>	<i>yigF</i>	<	<i>yigG</i>	<	<i>rarD</i>		chloramphenicol resistance permease
4E+06	OM porin protein	<i>ompL</i>	<i>ompL</i>	<	<i>yihO</i>	<	<i>yihP</i>		predicted transporter
4E+06	isocitrate dehydrogenase kinase		<i>aceK</i>	>	<i>arpA</i>	<	<i>iclR</i>		transcription factor
4E+06	predicted cation/proton antiporter		<i>yjcE</i>	>	<i>yjcF</i>	<	<i>actP</i>		acetate transporter
4E+06	formate-dependent nitrite reductase		<i>nrFD</i>	>	<i>nrFE</i>	>	<i>nrFF</i>	<i>nrFFG</i>	heme lyase (NrfEFG)
4E+06	transcription factor	<i>melR</i>	<i>melR</i>	>	<i>melA</i>	>	<i>melB</i>	<i>melB</i>	melibiose:sodium symporter
4E+06	predicted protein		<i>yjdO</i>	>	<i>lysU</i>	<	<i>yjdL</i>		predicted transporter
4E+06	predicted lysyl-tRNA synthetase		<i>poxA</i>	>	<i>yjeM</i>	>	<i>yjeN</i>	<i>yjeNO</i>	predicted protein
4E+06	cell envelope opacity protein	<i>ytfB</i>	<i>ytfB</i>	<	<i>fkIB</i>	>	<i>cycA</i>	<i>cycA</i>	D-alanine/D-serine/glycine transporter
4E+06	predicted IM protein	<i>ytfF</i>	<i>ytfF</i>	<	<i>ytfG</i>	>	<i>ytfH</i>	<i>ytfH</i>	transcription factor
4E+06	ABC-family sugar transporter y		<i>yjff</i>	>	<i>fbp</i>	>	<i>mpl</i>	<i>mpl</i>	UDP-N-acetylmuramate ligase
5E+06	KpLE2 transposase	<i>insG</i>	<i>insG</i>	<	<i>yjhb</i>	>	<i>yjhc</i>	<i>yjhc</i>	KpLE2 phage oxidoreductase
5E+06	KpLE2 phage transporter		<i>yjhb</i>	>	<i>yjhc</i>	>	<i>ytha</i>	<i>ytha</i>	small predicted membrane protein
5E+06	ncRNA		<i>symR</i>	>	<i>hsdS</i>	<	<i>hsdM</i>		DNA methylase M
5E+06	lipoate-protein ligase A	<i>lplA</i>	<i>lplA</i>	<	<i>ytiB</i>	>	<i>serB</i>	<i>serB-radA-</i>	3-phosphoserine phosphatase

Total, 86 (possible targets, 89)

## Supplemental Table S2

### Amino acids and peptides affecting the growth of *lrp* mutant

#### 1) Compounds affecting the growth retardation

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Amino acids	L-Ala, L-Cys, L-Gly, L-Ser, L-Trp D-Ala, D-Ser
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Peptides	Ala-Gly, Ala-His, Ala-Thr, Gly-Asn, Ala-Ala, Ala-Arg, Ala-Asn, Ala-His, Ala-Ser, Ala-Thr, Arg-Ser, Gln-Gln, Gly-Ala, Gly-Arg, Gly-Gly, Gly-Lys, Gly-Met, Gly-Ser, Gly-Thr, Leu-Ala, Leu-Arg, Leu-Glu, Met-Gly, Phe-Ala, Phe-Gly, Phe-Ser, Ser-Ala, Ser-Gly, Ser-His, Ser-Met, Ser-Phe, Ser-Ser, Thr-Ala, Thr-Gly, Trp-Ala, Trp-Leu, Trp-Ser, Tyr-Ala, Tyr-Gly, Lys-Gly, Met-Thr, Ser-Asn, Ala-Ala-Ala, Gly-Gly-Ile, Gly-Gly-Leu, Gly-Gly-Phe
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#### 2) Compounds affecting the growth enhancement

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Amino acids	None
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Peptides	Pro-Phe, Pro-Pro, Pro-Tyr, Tyr-Glu, His-Glu, Phe-Asp, Phe-Glu, Pro-Glu, Pro-Ile, Pro-Trp
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**Supplemental Table S3**  
**Concentration of major intermediate metabolites in wild-type and lrp mutant**  
**(measured by TOF/MS)**

Annotation Name	Ave m/z	Conc (pmol/OD/ml)		
		WT	lrp mutant	ratio (lrp/wt)
Glyoxylate	72.996	0.0	0.0	–
Glycolate	75.011	0.0	0.0	–
Gly	76.042	319.3	833.1	2.61
Pyruvate	87.009	0.0	0.0	–
Lactate	89.026	4234.6	2227.6	0.53
Putrescine(1,4-Butanediamine)	89.109	282.6	96.0	0.34
beta-Ala	90.057	9.2	3.4	0.38
Ala	90.058	192.6	87.1	0.45
Spermine divalent	102.118	0.0	0.0	–
GABA	104.073	55.8	6.3	0.11
2-Aminobutyrate	104.073	51.4	25.7	0.50
Ser	106.051	121.4	70.5	0.58
Hypotaurine	110.027	0.0	0.0	–
Cytosine	112.051	1.2	1.4	1.12
Uracil	113.035	0.0	0.0	–
Carnosine divalent	114.062	0.0	0.0	–
Fumarate	115.005	197.6	219.0	1.11
2-Oxoisopentanoate	115.042	0.0	0.0	–
Pro	116.071	54.7	32.3	0.59
Succinate	117.020	228.5	195.5	0.86
Val	118.087	162.9	162.2	1.00
Thr	120.066	150.1	73.6	0.49
Homoserine	120.066	36.5	23.0	0.63
Cys	122.028	0.0	0.0	–
Taurine	126.022	0.0	0.0	–
Hydroxyproline	132.066	0.0	0.0	–
Creatine	132.077	0.0	0.0	–
Ile	132.102	11.8	7.5	0.63
Leu	132.102	43.9	47.8	1.09
Malate	133.015	479.3	448.1	0.93
Asn	133.061	81.4	74.5	0.91
Ornithine	133.097	5.9	4.4	0.74
Asp	134.044	244.1	86.9	0.36
Homocysteine	136.042	0.0	0.0	–
Adenine	136.063	94.3	49.1	0.52
Hypoxanthine	137.046	204.5	127.5	0.62
Anthranilate	138.055	0.0	0.0	–
Tyramine	138.092	1.6	1.0	0.59
2-Oxoglutarate	145.015	0.0	0.0	–
Spermidine	146.164	1.4	0.0	0.00
2-Hydroxyglutarate	147.031	0.0	25.7	–
Gln	147.077	339.5	82.1	0.24
Lys	147.113	335.8	407.3	1.21
Glu	148.061	3598.3	753.6	0.21
Met	150.059	24.9	23.9	0.96
Cysteine sulfinic acid	152.004	0.0	0.0	–
Guanine	152.057	29.7	23.5	0.79
His	156.077	30.4	31.3	1.03
Phe	166.086	34.4	52.9	1.54
PEP	166.976	483.3	366.9	0.76
DHAP	168.992	0.0	0.0	–
DHAP	168.992	76.0	16.5	0.22

Glycerophosphate	171.007	337.5	225.6	0.67
cis-Aconitate	173.010	6.2	2.5	0.41
Arg	175.120	143.9	105.3	0.73
Citrulline	176.103	9.1	11.4	1.25
Tyr	182.081	115.9	210.6	1.82
3PG;2PG	184.987	1408.5	1135.0	0.81
2PG	184.987	0.0	0.0	-
Citrate	191.021	38.4	45.5	1.19
Isocitrate	191.022	0.0	0.0	-
S-Adenosylhomocysteine	193.069	2.0	1.7	0.82
Gluconate	195.052	0.0	0.0	-
DOPA	198.076	0.0	0.0	-
S-Adenosylmethionine	200.078	39.9	36.6	0.92
Trp	205.098	1.9	3.7	1.95
Cystathionine	223.074	0.0	0.0	-
R5P	229.013	45.4	30.2	0.67
Ru5P	229.013	76.8	31.6	0.41
gamma-Glu-2-aminobutyrate	233.113	0.0	2.6	-
Cytidine	244.094	0.0	0.8	-
Uridine	245.077	0.0	0.0	-
gamma-Glu-cys	251.071	0.0	0.0	-
G6P	259.023	174.0	108.2	0.62
F6P	259.024	52.7	39.6	0.75
G1P	259.024	76.8	34.9	0.45
2,3-DPG	264.954	34.3	8.5	0.25
Adenosine	268.104	4.9	10.2	2.09
Inosine	269.088	11.0	16.0	1.45
6-Phosphogluconate	275.019	18.6	9.8	0.52
Guanosine	284.100	4.9	6.1	1.23
S7P	289.035	66.1	32.8	0.50
Ophthalmate	290.135	156.5	291.8	1.86
Glutathione(ox)	307.084	1185.5	821.3	0.69
Glutathione(red)	308.092	0.0	0.0	-
dTMP	321.050	70.9	68.2	0.96
CMP	322.046	82.7	35.9	0.43
cAMP	328.046	31.8	31.1	0.98
F1,6P	338.990	129.1	32.5	0.25
cGMP	344.042	0.0	0.0	-
AMP	346.057	175.0	196.2	1.12
IMP	347.041	77.1	202.5	2.63
GMP	362.052	14.5	16.5	1.14
NADPH	371.540	0.0	0.0	-
CoA	382.558	0.0	0.0	-
PRPP	388.947	0.0	0.0	-
dTDP	401.017	54.8	34.5	0.63
CDP	402.012	124.6	54.4	0.44
Acetyl CoA	403.559	20.5	1.0	0.05
Malonyl CoA	425.554	0.0	0.0	-
ADP	426.024	751.1	654.7	0.87
Succinyl CoA	432.563	0.0	0.0	-
GDP	442.018	295.7	211.1	0.71
dCTP	465.984	108.6	66.7	0.61
dTTP	480.984	209.7	94.2	0.45
CTP	481.979	627.1	244.1	0.39
UTP	482.962	1638.6	925.4	0.56
dATP	489.995	209.2	115.2	0.55
ATP	505.990	3894.2	2378.2	0.61



GTP	521.985	1945.9	1020.3	0.52
NAD+	662.103	975.9	580.3	0.59
NADH	664.119	0.0	0.0	-
NADP+	742.070	413.2	218.6	0.53
FAD	784.153	17.7	0.0	0.00

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