

Table S1. Genes overexpressed 4-fold and higher in *E. coli* L-form colonies versus classical colonies

Fold change	Gene	Product-function
1. INFORMATION STORAGE AND PROCESSING		
DNA replication, recombination and repair		
48.2	<i>recN</i>	recombination and repair protein
46.4	<i>dinD</i>	DNA-damage-inducible protein
44.7	<i>yebG</i>	DNA damage-inducible protein YebG
27.4	<i>recA</i>	DNA strand exchange and recombination protein
26.4	<i>recX</i>	recombination regulator RecX
18.2	<i>ruvB</i>	Holliday junction DNA helicase B
17.2	<i>ruvA</i>	Holliday junction DNA helicase motor protein
17.1	<i>dinI</i>	DNA damage-inducible protein I
16.4	<i>obgE</i>	GTPase ObgE
14.8	<i>yqgF</i>	Holliday junction resolvase-like protein
11.2	<i>umuD</i>	DNA polymerase V subunit UmuD
10.5	<i>lexA</i>	LexA repressor
9.2	<i>mcrA</i>	type IV site-specific deoxyribonuclease/DNA
8.9	<i>iscR</i>	DNA-binding transcriptional regulator
8.3	<i>holD</i>	DNA polymerase III subunit psi
8.3	<i>rdgC</i>	recombination associated protein
7.8	<i>topA</i>	DNA topoisomerase I
7.5	<i>uvrD</i>	DNA-dependent helicase II
7.2	<i>deoR</i>	DNA-binding transcriptional repressor
6.8	<i>yfgE</i>	DNA replication initiation factor
6.8	<i>ligA</i>	NAD-dependent DNA ligase LigA
5.7	<i>seqA</i>	replication initiation regulator SeqA
5.0	<i>holB</i>	DNA polymerase III subunit delta'
4.9	<i>dnaX</i>	DNA polymerase III subunits gamma and tau
Translation, ribosomal structure and metabolism		
32.2	<i>rplW</i>	50S ribosomal protein L23
31.5	<i>infB</i>	translation initiation factor IF-2
29.5	<i>isrB</i>	small RNA
27.3	<i>truB</i>	tRNA pseudouridine synthase B
24.1	<i>rplI</i>	50S ribosomal protein L9
18.6	<i>rplD</i>	50S ribosomal protein L4
14.1	<i>yhdG</i>	tRNA-dihydrouridine synthase B
14.1	<i>alaS</i>	subunit of alanyl-tRNA synthase
12.9	<i>yhbC</i>	ribosomal maturation protein
12.8	<i>rbfA</i>	ribosome-binding factor A
11.2	<i>hisS</i>	histidyl-tRNA synthetase
10.3	<i>ycbY</i>	23S rRNA m ² G2445 methyltransferase
9.8	<i>ykgM</i>	50S ribosomal protein L31 type B
9.8	<i>leuS</i>	leucyl-tRNA synthetase
9.2	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl enzyme
8.4	<i>rplY</i>	50S ribosomal protein L25
7.6	<i>rsuA</i>	16S rRNA pseudouridylate synthase A
7.3	<i>engA</i>	50s ribosomal subunit stability factor
6.9	<i>glyQ</i>	glycyl-tRNA synthetase subunit alpha
6.9	<i>glnS</i>	glutaminyl-tRNA synthetase

6.5	<i>yjbN</i>	tRNA-dihydrouridine synthase A
6.4	<i>gltX</i>	glutamyl-tRNA synthetase
6.3	<i>lysS</i>	lysyl-tRNA synthetase
6.1	<i>prfB</i>	peptide release factor RF-2
5.9	<i>selD</i>	selenide, water dikinase
5.7	<i>serS</i>	seryl-tRNA synthetase

Transcription

26.5	<i>emrR</i>	transcriptional repressor MprA
26.2	<i>cspA</i>	transcriptional activator cold shock protein
22.8	<i>stpA</i>	DNA binding protein, nucleoid-associated
22.1	<i>pdhR</i>	transcriptional regulator PdhR
18.2	<i>ilvY</i>	DNA-binding transcriptional regulator
16.2	<i>rpoD</i>	sigma D factor
15.6	<i>marA</i>	DNA-binding transcriptional activator MarA
14.2	<i>deaD</i>	ATP-dependent RNA helicase DeaD
13.9	<i>cbl</i>	transcriptional regulator Cbl
13.8	<i>narP</i>	DNA-binding response regulator
13.6	<i>soxS</i>	DNA-binding transcriptional dual regulator
12.4	<i>gcvA</i>	DNA-binding transcriptional activator GcvA
12.4	<i>evgA</i>	DNA-binding response regulator in two-component
12.4	<i>rfaH</i>	transcriptional activator RfaH
12.1	<i>rcsB</i>	DNA-binding response regulator in two-component
12.1	<i>ycjC</i>	DNA-binding transcriptional repressor
11.1	<i>nusB</i>	transcription antitermination protein NusB
10.3	<i>mngR</i>	DNA-binding transcriptional dual regulator, fatty-acyl-binding
10.2	<i>yhiX</i>	DNA-binding transcriptional dual regulator
10.0	<i>bglJ</i>	DNA-binding transcriptional activator BglJ
9.9	<i>phoB</i>	DNA-binding response regulator in two-component
9.4	<i>xapR</i>	DNA-binding transcriptional activator
9.4	<i>rho</i>	transcription termination factor Rho
9.3	<i>yaiN</i>	regulator protein FrmR
9.0	<i>greA</i>	transcription elongation factor GreA
8.3	<i>zntR</i>	zinc-responsive transcriptional regulator
8.1	<i>pspC</i>	DNA-binding transcriptional activator
8.0	<i>glnG</i>	nitrogen regulation protein NR(I)
7.9	<i>sdiA</i>	DNA-binding transcriptional activator
7.7	<i>marR</i>	DNA-binding transcriptional repressor MarR
7.5	<i>fimZ</i>	transcriptional regulator FimZ
6.7	<i>yohL</i>	RcnR transcriptional repressor
6.4	<i>yciT</i>	transcriptional regulator
5.7	<i>bglG</i>	transcriptional antiterminator BglG
5.6	<i>fimB</i>	tyrosine recombinase/inversion of on/off regulator of fimA
5.6	<i>nhaR</i>	transcriptional activator NhaR

2. CELLULAR PROCESSES

Adaptation, defense and survival

59.7	<i>pspB</i>	phage shock protein B
53.4	<i>rcaA</i>	colanic acid capsular biosynthesis activation protein A
51.4	<i>pspG</i>	phage shock protein G
41.1	<i>pspA</i>	phage shock protein A

33.9	<i>wza</i>	capsular polysaccharide transport
32.0	<i>wcaF</i>	putative colanic acid biosynthesis acetyltransferase WcaF
29.8	<i>wcaH</i>	GDP-mannose mannosyl hydrolase
28.7	<i>gmd</i>	GDP-mannose 4,6-dehydratase
21.6	<i>ycfR</i>	stress resistance/biofilm formation
20.9	<i>cspG</i>	cold-shock
19.8	<i>wcaD</i>	putative colanic acid polymerase
17.9	<i>ugd</i>	UDP-glucose 6-dehydrogenase
17.5	<i>pspD</i>	peripheral inner membrane phage-shock protein
17.1	<i>chpA</i>	toxin ChpA
15.9	<i>wzb</i>	tyrosine phosphatase/colanic acid
15.2	<i>ykfE</i>	vertebrate C-lysozyme inhibitor
14.6	<i>marB</i>	multiple antibiotic resistance protein
12.1	<i>chpR</i>	antitoxin MazE
10.0	<i>acrB</i>	RND-permease/drug efflux
9.5	<i>acrA</i>	membrane fusion protein/drug efflux system
9.4	<i>cpsB</i>	mannose-1-phosphate guanylyltransferase
8.9	<i>yaiM</i>	serine hydrolase
8.4	<i>yfiD</i>	autonomous glycyl radical cofactor GrcA
7.9	<i>osmB</i>	lipoprotein
7.4	<i>mazG</i>	nucleoside triphosphate pyrophosphohydrolase
6.6	<i>ybaU</i>	peptidyl-prolyl cis-trans isomerase (rotamase D)
5.5	<i>manA</i>	mannose-6-phosphate isomerase
5.0	<i>cpsG</i>	Phosphomannomutase
4.8	<i>galU</i>	UTP--glucose-1-phosphate uridylyltransferase subunit GalU
4.7	<i>chpS</i>	antitoxin

Post-translational modification, protein turnover and chaperones

43.5	<i>fhuF</i>	ferric iron reductase involved in ferric hydroximate transport
41.3	<i>yjiD</i>	inhibitor of sigma factor s proteolysis
27.2	<i>lspA</i>	lipoprotein signal peptidase
16.7	<i>ompT</i>	outer membrane protease
15.9	<i>hslJ</i>	heat-inducible protein
15.9	<i>ytfE</i>	repair of damaged iron-sulfur clusters
13.7	<i>ppiC</i>	peptidyl-prolyl cis-trans isomerase C
12.6	<i>yrfH</i>	ribosome-associated heat shock protein Hsp15
12.5	<i>iscU</i>	scaffold protein
10.9	<i>dsbA</i>	periplasmic protein disulfide isomerase I
10.5	<i>pepB</i>	aminopeptidase B
10.4	<i>groEL</i>	chaperonin GroEL
9.7	<i>hflC</i>	FtsH protease regulator HflC
8.8	<i>hslV</i>	ATP-dependent protease peptidase subunit
8.7	<i>ibpB</i>	heat shock chaperone IbpB
7.8	<i>iap</i>	aminopeptidase in alkaline phosphatase isozyme conversion
7.7	<i>fkpA</i>	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
7.0	<i>hscB</i>	co-chaperone HscB
7.0	<i>pphB</i>	serine/threonine-specific protein phosphatase 2
6.7	<i>dsbC</i>	thiol:disulfide interchange protein DsbC
6.2	<i>ffh</i>	signal recognition particle protein
5.9	<i>ybbN</i>	chaperone and protein oxidoreductase
4.9	<i>dcp</i>	dipeptidyl carboxypeptidase II

4.8	<i>dnaJ</i>	chaperone protein DnaJ
4.3	<i>htpG</i>	heat shock protein 90

Cell envelope biogenesis

27.1	<i>cld</i>	regulator of length of O-antigen component
21.7	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase subunit,
17.2	<i>yidC</i>	putative inner membrane protein translocase component
15.1	<i>rfbB</i>	dTDP-glucose 4,6 dehydratase, NAD(P)-binding
14.2	<i>nlpA</i>	cytoplasmic membrane lipoprotein-28
14.0	<i>amiC</i>	N-acetylmuramoyl-L-alanine amidase <i>amiC</i> precursor
13.2	<i>ispH</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
9.9	<i>rfbA</i>	glucose-1-phosphate thymidyltransferase
9.1	<i>yaeS</i>	undecaprenyl pyrophosphate synthase
8.9	<i>ddg</i>	lipid A biosynthesis palmitoleoyl acyltransferase
8.5	<i>kdsA</i>	2-dehydro-3-deoxyphosphooctonate aldolase
8.3	<i>rfaP</i>	kinase that phosphorylates core heptose of lipopolysaccharide
8.0	<i>rfaD</i>	ADP-L-glycero-D-mannoheptose-6-epimerase
7.1	<i>wecB</i>	UDP-N-acetylglucosamine 2-epimerase
7.0	<i>rfaG</i>	glucosyltransferase I
6.3	<i>mreC</i>	cell wall structural complex MreBCD
6.0	<i>wbbI</i>	β -1,6-galactofuranosyltransferase
5.6	<i>rfaJ</i>	(galactosyl)lipopolysaccharide glucosyltransferase
5.5	<i>rfaQ</i>	lipopolysaccharide core biosynthesis protein
5.2	<i>murI</i>	glutamate racemase
4.8	<i>yrbI</i>	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase

Transport

39.2	<i>sbp</i>	sulfate transporter subunit
21.5	<i>cysP</i>	thiosulfate transporter subunit
21.1	<i>pstS</i>	phosphate transporter subunit
18.7	<i>efeU</i>	putative cytochrome
13.7	<i>exbD</i>	biopolymer transport protein ExbD
11.9	<i>emrA</i>	multidrug resistance protein A
11.3	<i>phoU</i>	transcriptional regulator PhoU
11.2	<i>kgtP</i>	alpha-ketoglutarate transporter
10.5	<i>oppA</i>	periplasmic oligopeptide-binding protein precursor
8.6	<i>pstB</i>	phosphate transporter subunit
8.6	<i>proV</i>	glycine betaine transporter ATP-binding subunit
8.3	<i>secE</i>	preprotein translocase subunit SecE
8.1	<i>lolA</i>	outer-membrane lipoprotein carrier protein
8.0	<i>proX</i>	glycine betaine transporter periplasmic subunit
7.5	<i>fliY</i>	cystine transporter subunit
6.3	<i>tatE</i>	twin arginine translocase protein E
5.6	<i>cysW</i>	sulfate/thiosulfate transporter permease subunit

Cell division and chromosomal partitioning

29.5	<i>sulA</i>	SOS cell division inhibitor
13.6	<i>hflK</i>	FtsH protease regulator HflK
10.1	<i>ftsY</i>	cell division protein FtsY
6.9	<i>tig</i>	trigger factor
6.8	<i>xerC</i>	site-specific tyrosine recombinase XerC

6.7	<i>ftsN</i>	essential cell division protein
5.4	<i>yhjQ</i>	cell division protein

Inorganic ion transport and metabolism

16.6	<i>cirA</i>	ferric iron-catecholate outer membrane transporter
10.4	<i>corA</i>	magnesium/nickel/cobalt transporter CorA
9.3	<i>copA</i>	copper transporter
8.7	<i>znuA</i>	high-affinity zinc transporter periplasmic component
8.5	<i>znuC</i>	high-affinity zinc transporter ATPase
5.3	<i>fepB</i>	iron-enterobactin transporter periplasmic binding protein

Signal transduction mechanism

8.7	<i>phoR</i>	phosphate regulon sensor protein
7.3	<i>rscC</i>	hybrid sensory kinase in two-component

Protein assembly

12.8	<i>iscA</i>	iron-sulfur cluster assembly protein
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Motility and chemotaxis

20.2	<i>ycdT</i>	diguanylate cyclase
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3. METABOLISM

Amino acid transport and metabolism

34.3	<i>cysK</i>	cysteine synthase A
17.7	<i>tyrA</i>	bifunctional chorismate mutase/prephenate dehydrogenase
16.4	<i>gltP</i>	glutamate/aspartate:proton symporter
11.7	<i>ilvG</i>	acetolactate synthase 2 catalytic subunit
11.7	<i>metQ</i>	DL-methionine transporter substrate-binding subunit
10.7	<i>avtA</i>	valine--pyruvate transaminase
10.3	<i>aroB</i>	3-dehydroquinate synthase
8.8	<i>iscS</i>	cysteine desulfurase
8.7	<i>argG</i>	argininosuccinate synthase
8.3	<i>glnA</i>	glutamine synthetase
7.9	<i>proB</i>	gamma-glutamyl kinase
6.5	<i>yedO</i>	D-cysteine desulfhydrase
6.0	<i>thrC</i>	threonine synthase
5.7	<i>metK</i>	methionine adenosyltransferase
5.6	<i>ybiK</i>	L-asparaginase

Carbohydrate transport and metabolism

14.6	<i>ybiV</i>	sugar phosphatase
14.6	<i>lpdA</i>	dihydrolipoamide dehydrogenase
11.8	<i>yadF</i>	carbonic anhydrase
10.0	<i>glpD</i>	glycerol-3-phosphate dehydrogenase
9.8	<i>gnd</i>	6-phosphogluconate dehydrogenase
7.4	<i>ppsA</i>	phosphoenolpyruvate synthase
6.3	<i>adhC</i>	Alcohol dehydrogenase class III
6.3	<i>eda</i>	keto-hydroxyglutarate-aldolase
5.5	<i>fruB</i>	fructose-specific PTS IIA/HPr components
5.2	<i>yfbT</i>	sugar phosphatase
4.9	<i>zwf</i>	glucose-6-phosphate 1-dehydrogenase

4.5 *ackA* acetate kinase

Energy production and conversion

25.4 *acnB* bifunctional aconitate hydratase 2/2-methylisocitrate
19.6 *aceE* pyruvate dehydrogenase subunit E1
19.1 *nudE* ADP-ribose diphosphatase NudE
16.7 *aceF* dihydrolipoamide acetyltransferase
16.6 *cysJ* sulfite reductase subunit alpha
15.0 *cysC* adenylsulfate kinase
14.6 *cysM* cysteine synthase B
14.1 *csdA* cysteine sulfinatase desulfinate
14.0 *cysH* phosphoadenosine phosphosulfate reductase
11.3 *yeckK* Cytochrome c-type protein torY
11.0 *fdx* Ferredoxin, 2Fe-2S
9.5 *yjhT* N-acetylneuraminatase mutarotase
9.4 *ldhA* D-lactate dehydrogenase
8.8 *ubiE* ubiquinone/menaquinone biosynthesis methyltransferase
8.4 *glpE* thiosulfate sulfurtransferase
6.2 *ahpF* Alkyl hydroperoxide reductase subunit F
6.0 *ndh* respiratory NADH dehydrogenase
5.9 *yojH* malate:quinone oxidoreductase
5.4 *cysN* sulfate adenyltransferase, subunit 1

Nucleotide transport, conversions and metabolism

33.0 *yahA* c-di-GMP
12.7 *gpt* xanthine-guanine phosphoribosyltransferase
9.6 *adk* adenylate kinase
8.8 *gmk* guanylate kinase
8.3 *pyrG* CTP synthase
7.5 *nrdI* ribonucleotide reductase stimulatory protein
7.1 *tmk* thymidylate kinase
5.9 *deoB* phosphopentomutase
5.8 *tdk* thymidine kinase
4.6 *nrdE* ribonucleotide-diphosphate reductase subunit alpha
13.6 *cyaA* adenylate cyclase
7.7 *purU* formyltetrahydrofolate deformylase
5.7 *yjjG* nucleotidase
5.6 *yfbR* dCMP phosphohydrolase

Cofactor and coenzyme metabolism

12.4 *cobT* nicotinate-nucleotide- phosphoribosyltransferase
9.4 *mioC* flavodoxin
11.4 *hemA* glutamyl-tRNA reductase
8.1 *ribH* riboflavin synthase subunit beta
7.9 *yaeM* 1-deoxy-D-xylulose 5-phosphate reductoisomerase
7.0 *ribB* 3,4-dihydroxy-2-butanone 4-phosphate synthase
5.9 *ribF* bifunctional riboflavin kinase/FMN adenyltransferase
5.8 *pncB* nicotinate phosphoribosyltransferase
5.0 *pabC* 4-amino-4-deoxychorismate lyase

Lipid metabolism

18.1	<i>cdh</i>	CDP-diacylglycerol pyrophosphatase
6.2	<i>accC</i>	acetyl-CoA carboxylase biotin carboxylase subunit
5.7	<i>accB</i>	acetyl-CoA carboxylase biotin carboxyl carrier subunit

Phosphate metabolism

11.5	<i>phoA</i>	bacterial alkaline phosphatase
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4. EXTRACHROMOSOMAL

Phage, phage-like element, transposon

138.4	<i>ymfJ</i>	e14 prophage; predicted protein
48.3	<i>xisE</i>	e14 prophage; predicted excisionase
31.8	<i>intE</i>	e14 prophage; predicted integrase
27.3	<i>pal</i>	peptidoglycan-associated outer membrane lipoprotein
21.5	<i>ymfT</i>	e14 prophage; predicted DNA-binding transcriptional regulator
19.0	<i>intG</i>	hypothetical protein
18.7	<i>insK</i>	IS150 conserved protein InsB
16.4	<i>insJ</i>	IS150 protein InsA
16.3	<i>ybcY</i>	hypothetical protein
16.2	<i>ymfM</i>	e14 prophage; predicted protein
14.3	<i>yagK</i>	CP4-6 prophage; conserved protein
13.3	<i>ymfD</i>	e14 prophage; predicted SAM-dependent methyltransferase
10.2	<i>yjhC</i>	KpLE2 phage-like element; predicted oxidoreductase
9.7	<i>ymfL</i>	e14 prophage; predicted DNA-binding transcriptional regulator
8.9	<i>yfdI</i>	CPS-53 (KpLE1) prophage; predicted inner membrane protein
8.2	<i>insN-2</i>	KpLE2 phage-like element
7.7	<i>ybcW</i>	prophage
6.9	<i>ybcM</i>	DLP12 prophage DNA-binding transcriptional regulator
6.3	<i>yfdH</i>	CPS-53 (KpLE1) prophage; bactoprenol glucosyl transferase
6.1	<i>insB-7</i>	IS1 protein InsB
5.6	<i>yjhI</i>	KpLE2 phage-like element
5.4	<i>yfjO</i>	CP4-57 prophage; predicted protein

5. UNKNOWN AND POORLY CHARACTERIZED

Conserved proteins

26.3	<i>yafO</i>	putative toxin YafO
24.6	<i>ybjX</i>	hypothetical protein ybjX
22.8	<i>yhhI</i>	hypothetical protein
21.1	<i>yebE</i>	hypothetical protein yebE
20.7	<i>yafK</i>	hypothetical protein yafK precursor
19.2	<i>yhcN</i>	hypothetical protein yhcN precursor
17.1	<i>yeeD</i>	hypothetical protein
16.2	<i>yjaA</i>	hypothetical protein
14.5	<i>yfeS</i>	conserved protein
14.2	<i>ygjN</i>	hypothetical protein
11.9	<i>yqiC</i>	conserved protein
11.1	<i>ygdL</i>	hypothetical protein ygdL
10.8	<i>yibG</i>	hypothetical protein
10.4	<i>ycbK</i>	hypothetical protein ycbK
9.9	<i>yhdN</i>	hypothetical protein
8.9	<i>yabB</i>	hypothetical protein
8.9	<i>ygbE</i>	hypothetical protein

7.7	<i>yjiV</i>	pseudogene
7.5	<i>yjeO</i>	conserved inner membrane protein
6.6	<i>yhgl</i>	hypothetical protein
6.2	<i>matB</i>	hypothetical protein
5.7	<i>aroM</i>	hypothetical protein
5.4	<i>yggE</i>	hypothetical protein
5.3	<i>ybaB</i>	hypothetical protein
5.0	<i>ycaQ</i>	hypothetical protein ycaQ
4.8	<i>yhfY</i>	hypothetical protein yhfY

Predicted function

35.7	<i>iscX</i>	hypothetical protein
23.4	<i>smpA</i>	small membrane protein, lipoprotein
20.9	<i>yedV</i>	putative 2-component sensor protein
16.3	<i>yrfF</i>	putative membrane protein igaA homolog
16.3	<i>yeeE</i>	putative transport system permease protein
16.2	<i>wcaE</i>	predicted glycosyl transferase
16.2	<i>ydjN</i>	hypothetical symporter ydjN
16.1	<i>yibD</i>	predicted glycosyl transferase
16.1	<i>yqeH</i>	hypothetical protein
14.6	<i>yjbF</i>	hypothetical lipoprotein yjbF precursor
13.6	<i>yihK</i>	GTP-binding protein
12.6	<i>yafN</i>	putative antitoxin of the YafO-YafN toxin-antitoxin system
12.4	<i>yhgF</i>	transcriptional accessory protein
12.3	<i>ygjM</i>	hypothetical protein ygjM
11.0	<i>era</i>	GTP-binding protein Era
10.3	<i>ygeV</i>	hypothetical sigma-54-dependent transcriptional regulator
10.2	<i>ygiS</i>	putative binding protein
9.3	<i>ycbL</i>	hypothetical protein ycbL
9.3	<i>rfbX</i>	predicted polysoprenol-linked O-antigen transporter
9.3	<i>yaeR</i>	hypothetical protein
9.2	<i>ybeX</i>	Magnesium and cobalt efflux protein corC
9.0	<i>bdm</i>	biofilm-dependent modulation protein
9.0	<i>ybiS</i>	hypothetical protein
8.5	<i>yjgM</i>	hypothetical protein
8.3	<i>yedW</i>	transcriptional regulatory protein YedW
8.2	<i>yfgL</i>	outer membrane protein assembly complex subunit YfgL
7.8	<i>yajO</i>	putative NAD(P)H-dependent xylose reductase
7.8	<i>eco</i>	ecotin precursor
7.6	<i>yebA</i>	hypothetical protein
7.2	<i>ybdG</i>	hypothetical protein ybdG
7.1	<i>yfjG</i>	hypothetical protein
6.8	<i>yhjX</i>	major facilitator superfamily transporter
6.4	<i>ybgF</i>	hypothetical protein
6.3	<i>yfiO</i>	predicted lipoprotein
6.2	<i>yrbD</i>	hypothetical protein
6.0	<i>vacB</i>	Rnase R
6.0	<i>yrbK</i>	hypothetical protein
6.0	<i>damX</i>	hypothetical protein
6.0	<i>ycfQ</i>	hypothetical transcriptional regulator
5.9	<i>sbmA</i>	transport protein

5.6 *yrbC* protein yrbC precursor

Predicted protein

43.6	<i>ypfG</i>	hypothetical protein ypfG precursor
32.7	<i>yegZ</i>	pseudo
28.4	<i>yqgB</i>	hypothetical protein yqgB
28.1	<i>spy</i>	periplasmic protein, spheroblast
25.5	<i>ypeC</i>	hypothetical protein
25.2	<i>ycfJ</i>	hypothetical protein
24.7	<i>yibA</i>	hypothetical protein
23.0	<i>ygaC</i>	hypothetical protein
21.0	<i>ydhA</i>	hypothetical protein
20.0	<i>yajI</i>	hypothetical protein
18.4	<i>yfdX</i>	hypothetical protein
18.0	<i>htrL</i>	hypothetical protein
17.1	<i>yeeN</i>	hypothetical protein
14.7	<i>yfgM</i>	hypothetical protein yfgM
13.8	<i>ycbW</i>	hypothetical protein ycbW
13.7	<i>ylbH</i>	conserved protein
13.2	<i>yggN</i>	hypothetical protein
12.3	<i>yobH</i>	hypothetical protein
12.2	<i>yjcB</i>	hypothetical protein yjcB
12.1	<i>yibJ</i>	rhsA core protein with extension
12.0	<i>ais</i>	Ais protein
11.8	<i>yjjQ</i>	hypothetical protein yjjQ
11.7	<i>ysaB</i>	hypothetical protein
11.6	<i>yfbP</i>	predicted protein
11.5	<i>yedJ</i>	hypothetical protein
11.3	<i>wbbL</i>	pseudo
11.3	<i>ykiA</i>	hypothetical protein ykiA
11.0	<i>yiiF</i>	conserved protein
11.0	<i>sseB</i>	protein sseB
10.9	<i>matA</i>	hypothetical protein ykgK
10.8	<i>ybeB</i>	hypothetical protein
10.8	<i>yidX</i>	predicted lipoproteinC
10.6	<i>yadM</i>	predicted fimbrial-like adhesin protein
10.3	<i>yjfF</i>	hypothetical protein
10.2	<i>yejK</i>	nucleoid-associated protein NdpA
10.0	<i>yohN</i>	hypothetical protein yohN precursor
9.7	<i>wbbJ</i>	predicted acyl transferase
9.6	<i>ybbC</i>	predicted protein
9.3	<i>yaiY</i>	hypothetical protein yaiY
9.3	<i>nlpB</i>	lipoprotein
9.2	<i>yjeJ</i>	hypothetical protein yjeJ
9.0	<i>wcal</i>	predicted glycosyl transferase
9.0	<i>yfcL</i>	hypothetical protein yfcL
9.0	<i>yncE</i>	hypothetical protein yncE precursor
8.5	<i>yhhX</i>	putative oxidoreductase yhhX
8.4	<i>ygeO</i>	hypothetical protein
8.3	<i>ygeK</i>	hypothetical protein
8.2	<i>yceB</i>	predicted lipoprotein

8.1	<i>syd</i>	SecY interacting protein Syd
7.9	<i>yhhH</i>	predicted protein
7.9	<i>yfiR</i>	hypothetical protein yfiR precursor
7.5	<i>yafE</i>	hypothetical protein yafE
7.4	<i>ygeP</i>	hypothetical protein
7.4	<i>ygck</i>	predicted protein
7.1	<i>yfgJ</i>	hypothetical protein
6.8	<i>yciF</i>	putative structural protein
6.7	<i>yfbN</i>	predicted protein
6.6	<i>yejG</i>	hypothetical protein
6.5	<i>yqeK</i>	hypothetical protein
6.4	<i>yeiS</i>	hypothetical protein
6.4	<i>ybeA</i>	hypothetical protein
6.3	<i>yebY</i>	hypothetical protein yebY precursor
6.1	<i>wcaM</i>	predicted colanic acid biosynthesis protein
5.9	<i>ynjI</i>	hypothetical protein
5.6	<i>yabl</i>	conserved inner membrane protein
5.4	<i>yecT</i>	hypothetical protein
5.0	<i>yebO</i>	hypothetical protein yebO
4.8	<i>yeeY</i>	hypothetical transcriptional regulator yeeY
4.7	<i>ybhK</i>	predicted transferase