

Supplementary Materials:

Supplementary Figure Legends

Figure S1. Effect of relaxase mutations on retrotransposition.

(A) Results of retrotransposition assays using mutants of D-pLtrB. The mutation in the catalytic tyrosine (likely Y21 in LtrB; GenBank: AAB06502), results in a 4-fold reduction in RTP frequency with alanine (strain Y21A) or phenylalanine (Y21F) substitutions in comparison with wild-type LtrB relaxase (Figure 2C). Other mutants have a more subtle phenotype.

(B) Multiple sequence alignment of relaxases. Amino acid sequences of the three most conserved and catalytically important motifs (Motifs I-III) are shown. Amino acid sequences of relaxases were obtained from NCBI GenBank Protein Database (<http://www.ncbi.nlm.nih.gov/protein>); the accession number for each sequence is indicated in square brackets. The conserved amino acids are shown with different background shading within alignment; the invariable amino acids are white on black background. The sequence logo for each motif shown at the top was built using WebLogo [49]. The putative catalytic tyrosine is highlighted in blue, it corresponds to Y21 in LtrB relaxase from pRS01 conjugative plasmid (GenBank:U50902).

Figure S2. Donor plasmid copy number and mapping of retrotransposition events.

(A) Copy number of donor plasmid. We estimated the relative copy number of donor plasmid pLNRK-RIG among strains after using standard protocols for DNA-DNA hybridization of DNA isolated as described in Materials and Methods. The 5'-labeled [³²P]-ATP-oligonucleotide primer (MB14td 5'-TGTCACCATGCAGAGCAGAC-3') complementary to the group I intron in RIG of pLNRK-RIG was used to detect the donor plasmid.

(B) Retrotransposition events into pLNRK-RIG. We performed mapping of the reads using pLNRK-RIG as a reference sequence with Bowtie software under custom settings [43] (see Materials and Methods). The most prevalent sequence fragment generated from the D-C library appeared to be the 3' region flanking the LI.LtrB intron derived from the pLNRK-RIG vector itself (position 5782; shown by grey arrow) indicating the high level of the background amplification. The distribution of the RTP events in the pLNRK-RIG plasmid varied between libraries but supports the previous observation concerning cold-spots for intron invasion in the

essential replication region of *repD*, *repE*, and pAM β *ori* [22]. Hot-spots for RTP events were scattered throughout the intron sequence but not in the RIG cassette (*kan*^R and group I intron).

Figure S3. Purification of LtrB relaxase and its activity with dsDNA targets.

(A) LtrB-HIS6 protein purification (see Materials and Methods). Abbreviations: M, marker; incl. bodies, inclusion bodies; FT, flow through; W, wash.

(B) DNA target fragment. The pRS01 *oriT* (96 bp fragment; dark blue) from the conjugative element was cloned into pGEM-T vector (Promega) to create pONoriT1. High quality primarily supercoiled plasmid was isolated from fresh *E. coli* DH5 α overnight culture and was used for relaxase activity assays.

(C) LtrB relaxase from pRS01 cannot nick its cognate *oriT* in dsDNA. Plasmid pONoriT1 (dsDNA) was incubated with 20 ng of either LtrB-HIS6 (Lane 1) or LtrB(Y21A)-HIS6 (Lane 2) or left untreated (Lane 3) for 1 h at 37°C in reaction (50 μ l) containing relaxase reaction buffer (50 mM Tris-HCl pH 7.9, 100 mM NaCl, 10 mM MgCl₂, 1mM dithiothreitol) and 100 μ g/ml bovine serum albumin (BSA). Half of the reaction mixture was treated with 0.5 μ l of proteinase K (NEB) for an additional 30 min at 37°C. Untreated and treated samples were analyzed on a 0.7% agarose gel after staining with ethidium bromide. Supercoiled plasmid, nicked circles and plasmid-relaxase complexes are shown.

Figure S4. Mapping of off-target relaxase cleavage.

(A) Cloning of the *glnP* locus for ssDNA preparation. The genomic *glnP* locus was chosen for further tests of LtrB relaxase activity on non-cognate substrate. Plasmid pONLL*glnP*-R was constructed for ssDNA preparation. pONLL*glnP*-R carried the fragment in direct orientation relative to the phage f1 *ori*.

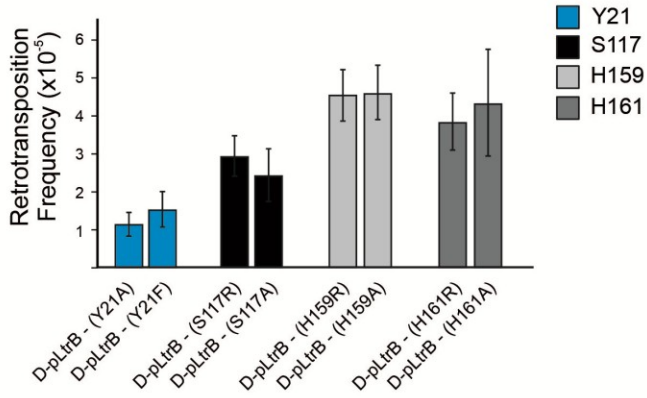
(B) Schematic representation of the cloned fragment of *glnP* gene and mapping strategy. The positions of cloned fragment (grey box) and six intron insertion sites (blue arrows) are shown. The positions of primers used in the primer extension reactions are shown on the top by black arrows with oligonucleotide number. Cleavages (designated as 1 and 2) were observed within the cloned fragment and the location of the cleavage sites was established (vertical arrows).

(C) LtrB relaxase has off-target activity. Primer extension products were analyzed on denaturing PAGE gels. Some subtle additional bands were observed in several reactions (black spheres, and

boxed on gel) with LtrB-HIS6-treated samples (Lane 1), but not LtrB(Y21A)-HIS6-treated DNA (Lane 2) or the negative control (Lane 3). Results are shown for pON*LLglnP*-R. The position of the cleavage is shown schematically at the top of each gel, and the primer used in the reaction is indicated at the bottom of the gel.

Supplementary Figures

A



B

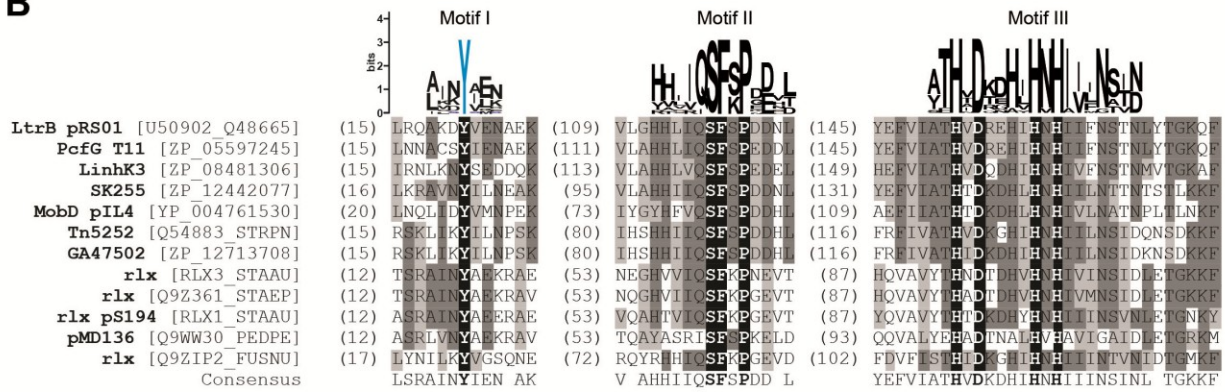


Figure S1. Effect of relaxase mutations on retrotransposition

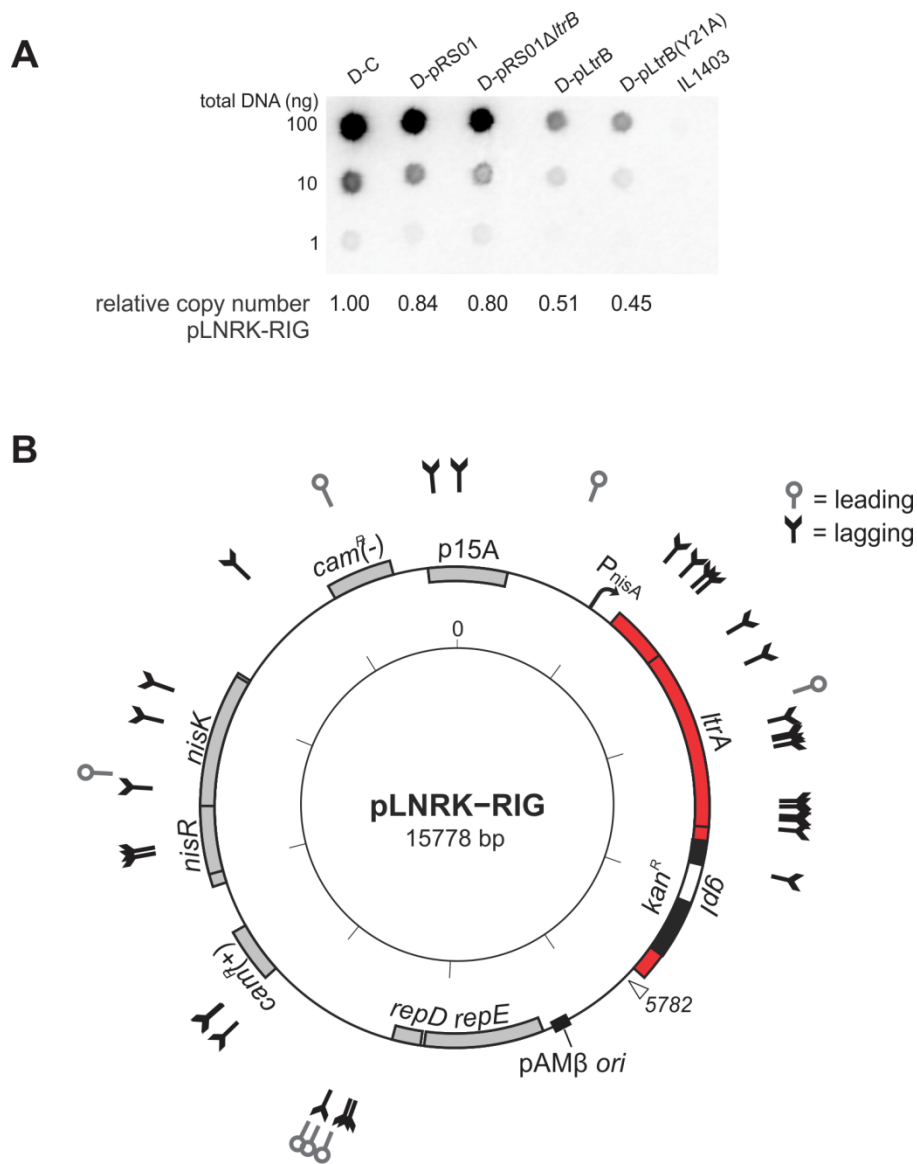


Figure S2. The relative copy number of donor plasmid between strains and mapping of the retrotransposition events onto the donor plasmid

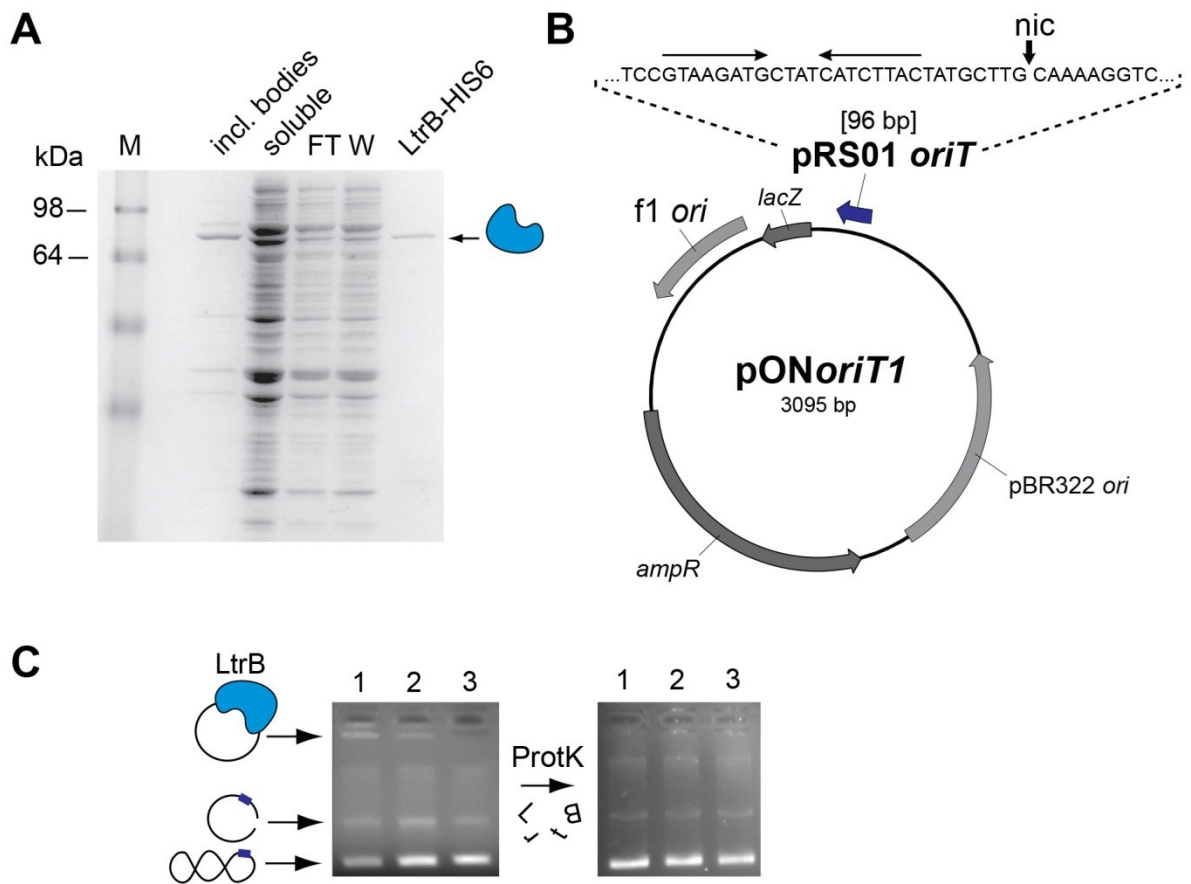


Figure S3. Purification of LtrB relaxase and its effect on dsDNA target

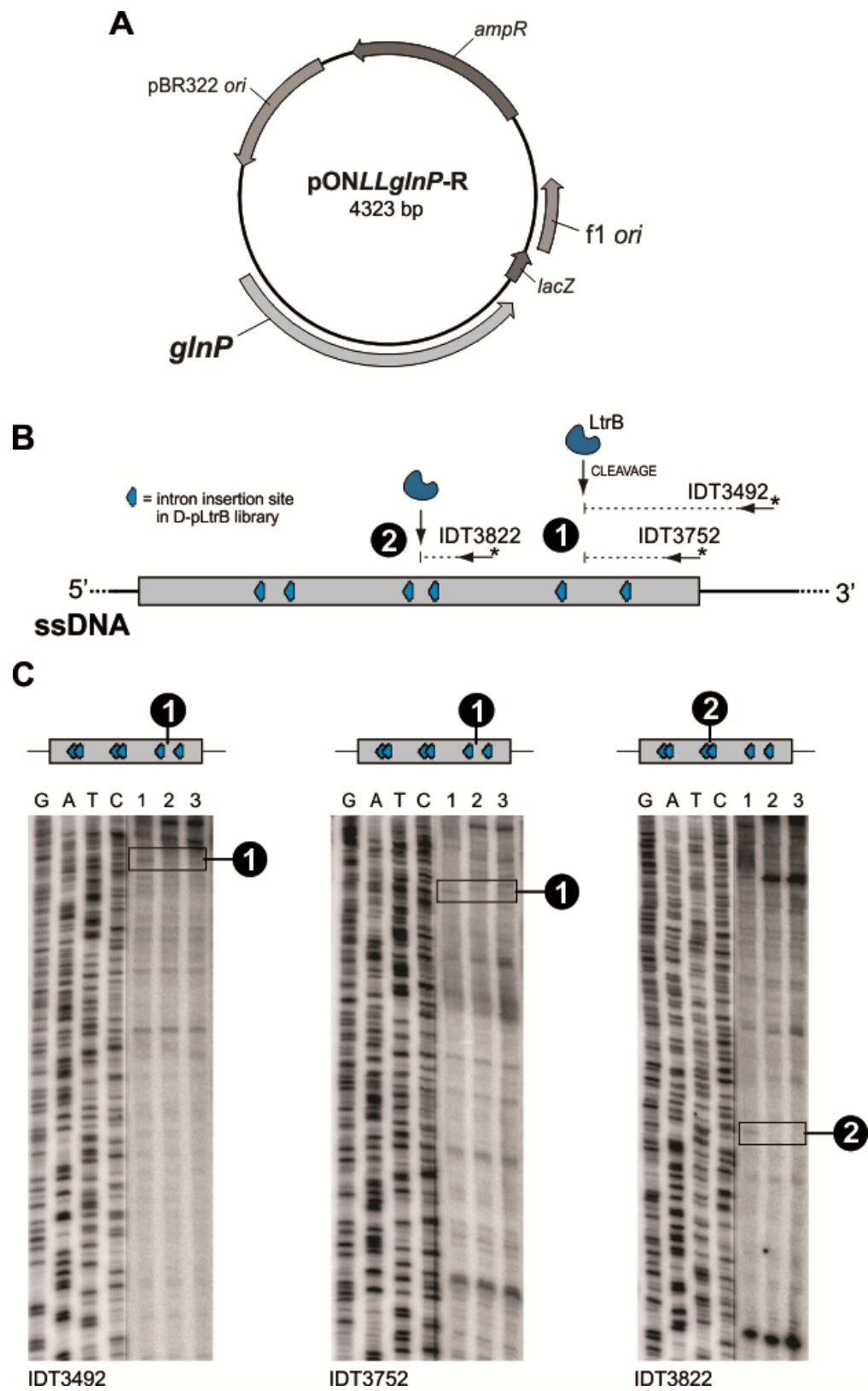


Figure S4. Mapping of off-target relaxase cleavage

Table S2. Multiple alignment of the chromosomal insertion sites of LI.LtrB intron in the absence of the relaxase (D-C strain). Names of the genes and relative frequencies are given in which insertions of LI.LtrB were detected; the orientation of the insertions relative to the direction of the replication (leading strand, lead; lagging strand, lag) and transcription (sense, S; antisense, AS) as well as genomic coordinates are indicated on the right. The sequence of the homing site and location of the insertion are shown on the top. T+5 is highlighted in red.

homing_site	insertion							
	IBS2	IBS1						
citE (104.7E-3)	CGTCGATCGTGAACACATCCATAAC	CATA	CATT	TTTTAATCTA	lead	AS	1208563	1208578
malG (90.6E-3)	CAGGATAAGACTTGGTTTTCATGTC	CACCGGG	TAC	CCCTAACCA	lag	AS	1742504	1742519
yafC (63.5E-3)	CATTGACGTAACAATTTTCGATAAC	TATCAATAAGAA	TG	AAATA	lead	AS	55665	55680
citF (57.5E-3)	ACAACTTCAGCCTCATTAACATAAC	CATG	TC	GGACCACTAAA	lead	AS	1209659	1209674
ywfG (49.4E-3)	GATFACCGACCCGATCAATCTRAAC	CACC	TAC	CGACTGGCGT	lead	AS	2258691	2258706
ysjA (48.7E-3)	TCCTGCAATCGTATTTCCTTGT	CATCCACA	TAAT	TGCAAT	lag	S	1890475	1890490
arcA (37.0E-3)	AACTCGCAATTTATGCCACTTCAC	GCTCACTCTAAT	TC	CGCGAT	lag	S	2115042	2115057
pi134 (36.8E-3)	ACCCATACCAATAGCCACTTCAC	ACGTGACCCACA	GC	CTTCA	lag	S	464964	464979
ytiA (36.3E-3)	AAATGATATGCTCACAACATAAC	TTAT	T	AATTAATAGAGGT	lag	S	1986494	1986509
ybeH (17.4E-3)	TTTAGAGAAAACCTCTATGCCCTAC	CATG	AT	TATGCTGGAAAT	lag	AS	143096	143111
ydiA (16.6E-3)	GATGATATACCTTCGGTCAATAAT	CATA	AA	AAGCTCAAGCA	lag	S	381887	381902
llrB (15.3E-3)	GAGAAGTCTATGATGTTTCAAAAT	TCATATCATATTT	T	AAAAAG	lag	AS	1458230	1458245
yljJ (14.0E-3)	TCGATACAATATTACTTCTTAAAT	CAT	T	GGCAAATAATA	lead	AS	1200004	1200019
xynB (13.3E-3)	AAAGTTTATCTCTAAAGCTCTT	AAAG	T	TATGACAGCTCA	lag	S	1544533	1544548
purA (13.1E-3)	ATGGACAGCCCTATAGTCTAAT	GCCT	T	GGCTTACCCCT	lead	AS	2029172	2029187
malG (12.7E-3)	GTTCCATATCAGTTCCTACTTCAC	GCCT	T	GGCTTACCCCT	lag	AS	1742154	1742169
repB (11.4E-3)	AACACGTAGAAACCTATCCAGAC	CACC	AC	ATAGACCAGTGC	lead	AS	1592521	1592536
ysdA (10.0E-3)	ATTCACAGCAGTCAACAATCAAAAT	CGTA	T	AGAAAGGCGG	lead	AS	4716	4731
ydpA (9.5E-3)	ATTTCCGATTTTTCAATCTGCTAA	TAA	AT	TAACAAACTCC	lead	AS	1834288	1834303
intergenic (9.5E-3)	GTCGATGATCCGACATACCTGAT	CAT	CA	ATGAAATTAAT	lag	AS	1530265	1530280
oppA (9.4E-3)	CGCTTAGATTTGCTAAATCGTCAAT	CATGGG	AC	CACTTGGCA	lag	.	2064332	2064347
yxdC (9.3E-3)	TATCCAAATATAAGTTTTCCTAC	CA	AG	ATACCTTTCA	lag	S	1906589	1906604
ymgK (9.1E-3)	GTGGCAAATGGTCTCTTCTTAC	CAC	AG	TCAATTAATAT	lag	AS	2335310	2335325
ybhB (8.9E-3)	TTCCGATAATGGCTTTTCTGCG	CATA	T	TCTACCGTAA	lag	AS	1268130	1268145
intergenic (8.9E-3)	GCCTCTCAACTGCTCTTGGCTAT	CATA	AT	TAGTATGCTAAC	lead	AS	173543	173558
murC (8.2E-3)	ACATTTAATAAACATGCGCCAC	CA	AT	ATGGAAATGAGTGC	lead	.	1880376	1880391
ycjH (8.1E-3)	GGCTGATTAAGCACAATTTTCAATTT	CAT	T	AGGACGATTTAT	lead	AS	2118446	2118461
intergenic (7.5E-3)	GTAATTTCAACAATGGTCACTTCAC	GTCC	G	ACCGTAAATG	lag	AS	295716	295731
yudI (7.4E-3)	CCTAAATAATGCCGCTTCTCCAG	CA	AT	TAACTAAATAG	lead	.	1891667	1891682
ykjI (7.2E-3)	CTTGTATCTACGCTATTTGAAATA	CA	AA	CTTCCACAA	lag	AS	2036117	2036132
ykpA (7.2E-3)	GCTTCAACAATATCTCACTTCAC	CCCCAA	AA	ATTTGCAATCA	lead	AS	1098929	1098944
ypcA (7.2E-3)	GTGACGTCCCTTTTTCATGAT	TAT	T	TCTCAATTAAGTT	lead	AS	1521196	1521211
ldhX (7.0E-3)	TCTGATAAAGGTCAAAATCATAAT	CA	AA	CAACTTTGCTACCGG	lead	AS	1143058	1143073
rpsI (7.0E-3)	ATAAAGATAACCACTCACTTCAC	GAT	T	CTTACCGTAA	lead	AS	2346610	2346625
celB (6.0E-3)	TCTGATATAGCTTTCTCACTTCAC	GTCC	GT	TAACTGAT	lag	S	178859	178874
pi242 (6.0E-3)	GTGACCGCTCCCTTTTTCATGAT	CAT	GG	TAAACACCAATATGT	lead	AS	1061365	1061380
ymeA (5.8E-3)	GCCCTCGGTTGGCCTACTTCTCCG	TT	AA	AGGCACGATATGT	lead	S	1242476	1242491
lcnC (5.3E-3)	CCCTGACGGTCTTTTATCTCAAC	T	AA	ATGCTCACATTTCAA	lag	S	84331	84346
sigX (5.3E-3)	TTAGCGCTAGTGAAGCACTTCAC	AA	AG	AGCACTTTTAGAGC	lag	AS	2242934	2242949
als (5.2E-3)	GATFAGACGACCCACTGGTCAAAAC	CAC	C	TTCACCTCTT	lead	AS	1201917	1201932
gltD (5.1E-3)	ATGCTTAGCAATATTTAGCAAT	CA	CA	TAGCCAAATCAAC	lag	S	1315536	1315551
yehH (5.0E-3)	TTAGCAGGACTTCGGTTCCTCAAT	TA	CA	ATCAACACAGATTT	lag	S	279638	279653
uvrB (5.0E-3)	TGAGCCAGCACTAATTTCTGAC	C	TA	ATTTGGGGATA	lead	AS	556835	556850
yljE (4.9E-3)	AAAATTCGCAATGGTCACTTCAC	CT	AA	CACTTTCGGCTCAA	lead	AS	1194711	1194726
yidC (4.8E-3)	TCGACGGACAACATATTTGGCAAC	CA	CT	TTCCTTCT	lead	AS	833054	833069
apu (4.6E-3)	TTTGGAAACGATACATATTCATATT	CAT	T	CTTCAATAGATCT	lead	AS	703842	703857
L200119 (4.6E-3)	TATTTTCGATTCCTCGGGTCTTTCG	CACC	G	CAATCTCCTGCTC	lead	AS	2340666	2340681
yyaL (4.5E-3)	CAAGCCGGTGTGTTACCACTTCAC	CACA	C	CGCCATTAATGAA	lead	AS	11386	11401
yrjC (4.5E-3)	ACGTCAATGATGGCTCACTTCAC	G	AT	TGGCAACAAATTT	lead	AS	1787588	1787603
cysD (4.2E-3)	CGAAGCTACGCTCTATTCGAAAT	GAT	T	TAAACCGTAAAC	lag	AS	76567	76582
yoaB (4.0E-3)	TCAGGAAATTAACAATTTGCCCAAT	CA	AG	TTCCGCCCACTCAAC	lead	AS	1403668	1403683
ysaA (4.0E-3)	TGAATGAGTCAACCCAGCCACGAC	CA	AA	CAAGACAAATCCG	lead	AS	1806395	1806410
L200143 (3.9E-3)	CGAAGCTGATTTTTCGCACTTCAC	T	CA	AGGAGGAAGCGGGA	lead	AS	542137	542152
yfcI (3.8E-3)	AGCGCTATCCCTTCTCACTTCAC	TAT	C	AGCCCTGCTCCTGG	lead	S	529084	529099
mend (3.8E-3)	TATGCCCTGACGATTTCACTTCAC	AT	CT	ATTTTTCCTGG	lag	AS	737583	737598
codY (3.7E-3)	AAGGGAATGATTTTGCACAGGAC	CC	CA	AAGGGGGAATAGC	lead	AS	164615	164630
yqgG (3.7E-3)	GAAGCGATAACATGCTCTTTCAC	CAT	CA	AGGCTTCTTATGAT	lag	AS	1664217	1664232
noxD (3.4E-3)	GAAGGATCAACATGACATCCATGAG	T	CT	GATGATTTCCCAATA	lag	S	2195930	2195945
yrjB (3.2E-3)	GGCGGGTCAAAATCTGCTTAAAT	CA	AT	CTGTAATTTCTTGGG	lag	S	1786760	1786775
dnaA (3.0E-3)	CTGAAGCAGTGTGCTGCTTAAAT	GATA	C	ATGAAATCGGCT	lead	AS	1668	1683
icaC (2.7E-3)	TGCTCTCGATCTCTTTTGAACATC	CA	AT	TATTTTCACTTA	lead	AS	684217	684232
ptnC (2.7E-3)	GTGAGAAAGCCCTCATCCGTTGC	CC	CT	TGAATTAATCGATA	lag	AS	1763895	1763910
gatB (2.5E-3)	AGGAAGAAATGGCCATATTCAC	G	AT	GACCAAGGTTGAT	lead	AS	168782	168797
pfl (2.5E-3)	CFATTCAAATATTCGCCATTCAC	CT	TC	CAACCAATTTGAC	lag	S	659540	659555
hemH (2.4E-3)	TTCAAATTCCTGCTGATACTTCAC	ACC	GG	TGCTTCAATAT	lag	S	1608898	1608913
yreB (2.4E-3)	TGCAATTTCTTGAACATTTAAT	GAT	T	AGAAATCAAAATA	lag	AS	1744102	1744117
	CATTCCTACTTCATTAACGAAAT	CATA	T	TTTTAATTTGCA	lag	AS		

clpE (2.3E-3)	ACA	CGTT	TAATTT	CTTCAT	CACGCC	CAATCAC	GGG	CAAT	TTC	lead	AS	550771	550786
yidC (2.3E-3)	TTGGAT	GT	TTTTA	TGAG	CATAAT	CTTTAT	TTGGC	CA	GGGT	lag	S	833363	833378
yedJ (2.1E-3)	ATATA	TTCC	CC	CAAT	TATTAAC	CAATGGCA	AAAT	TAAG	CTGT	lead	AS	239415	239430
intergenic (2.0E-3)	TCGT	CTAGT	TT	TTAC	CACTT	TTCT	ATTC	AAAT	GAAT	lead	.	1299735	1299750
yj3C (1.9E-3)	GAAC	CTCT	CC	CAAT	CTCC	TT	CA	CC	CCAGC	lead	AS	893748	893763
glpD (1.8E-3)	ACCT	TGATAG	CT	CTAC	CCCT	CA	CC	CA	AGAT	lead	AS	1270237	1270252
mgtA (1.8E-3)	TG	CTCAAGCA	TT	CAATA	CATCAC	TACTGT	TAAAA	TT	TCCGAT	lead	AS	1285837	1285852
yx6A (1.8E-3)	TTGGT	GTATAAA	TT	AAAT	TAGC	CA	TAAT	GAAG	TTC	lead	S	2348003	2348018
glgD (1.6E-3)	TGAT	CCAA	TATGGT	CA	TGCTCC	CA	CCCAAA	TTTT	CCCTCC	lag	S	697924	697939
pspA (1.6E-3)	TC	AAAGAG	TACC	ATTGG	CCAT	TAC	TAT	CT	TTT	lag	AS	2304139	2304154
pspA (1.6E-3)	CC	ATTATA	ATAATG	CC	CACTT	CA	AGCC	TGA	TAA	lag	AS	2304622	2304637
intergenic (1.5E-3)	TAT	ATAAGT	CCCTGG	CC	CACTT	CA	TT	TGGT	TAA	lead	.	133760	133760
L200091 (1.5E-3)	GC	AGGC	CA	TGTTACCA	CT	CA	TC	CG	CC	lead	AS	424310	424325
pi234 (1.5E-3)	TT	CATCC	ATAAT	TTC	CTCC	TT	CA	TAT	CA	lead	AS	1058576	1058591
yr3C (1.5E-3)	GG	ATAATCG	AA	CCAT	TAAG	CAT	GT	CA	CC	lag	AS	1792740	1792755
yfbJ (1.4E-3)	AA	TA	CTTA	ATAAT	TCC	CA	TT	CA	ATAA	lag	S	515575	515590
ysgC (1.4E-3)	AA	TG	ATA	TAGCG	CC	CA	TT	CA	CC	lead	AS	1870118	1870133
intergenic (1.3E-3)	CG	AAAT	CC	CTTA	CCG	CA	AC	CG	CT	lag	.	235061	235076
yedJ (1.3E-3)	TT	AGG	CA	ATT	CA	CA	TT	CA	CA	lag	S	237900	237915
ydiB (1.3E-3)	TT	GG	TAG	CC	CTT	CA	CTT	CA	CA	lag	S	383788	383803
yueS (1.3E-3)	GT	TT	CT	CT	CA	CA	TT	CA	CA	lag	S	2009589	2009604
yhdK (1.3E-3)	TC	AG	TT	CT	GA	TAGG	CT	CT	CA	lead	AS	2038474	2038489
preA (1.2E-3)	GC	AA	TCCG	TT	CA	TT	CA	TT	CA	lead	AS	187014	187029
nrdf (1.2E-3)	TC	AT	CG	AC	AT	GG	CT	CC	CA	lag	AS	1001348	1001363
intergenic (1.2E-3)	AAA	A	CT	CT	TT	AA	AT	T	CA	lead	.	1677069	1677084
L200065 (1.2E-3)	T	CA	AA	ATAAA	CC	T	CA	AA	CT	lead	AS	1745995	1746010
recO (1.1E-3)	AT	AT	TT	TT	TA	AA	T	AG	CA	lead	AS	58059	58074
citB (1.1E-3)	C	T	G	A	A	A	T	C	G	lead	AS	669535	669550
yrjD (1.0E-3)	TT	CT	T	T	CA	CA	TT	CA	CA	lag	AS	1793542	1793557
fbaA (1.0E-3)	TC	AC	CT	CA	AT	TG	AA	CC	AA	lead	AS	1979895	1979910
hpt (996.6E-6)	AC	AT	CT	AG	CA	T	AT	T	CA	lead	AS	25358	25373
L200159 (988.4E-6)	TT	T	AC	G	A	T	C	C	A	lead	AS	2364671	2364686
rpoC (980.2E-6)	GA	A	CG	T	A	AG	T	T	T	lead	AS	1857655	1857670
noxB (963.8E-6)	AA	CT	TT	A	T	C	T	G	G	lag	S	842595	842610
hrcA (951.5E-6)	AT	AA	AT	CA	AT	T	G	T	T	lead	AS	977222	977237
yx6D (951.5E-6)	GC	AG	CT	AC	CT	T	G	T	C	lag	S	2319277	2319292
rpsH (918.7E-6)	T	A	C	A	G	T	A	G	T	lead	AS	2162238	2162253
scrK (881.8E-6)	GC	GG	A	A	T	C	A	T	G	lag	S	1518450	1518465
thrA (849.0E-6)	AC	TT	T	C	G	C	A	T	C	lag	AS	747685	747700
yfhL (832.6E-6)	C	C	T	C	T	C	T	T	C	lag	AS	579452	579467
hemH (803.9E-6)	A	C	T	C	A	T	T	C	A	lead	AS	1608810	1608825
gidB (791.5E-6)	C	T	C	C	A	A	A	T	G	lead	S	1381124	1381139
relA (787.4E-6)	T	T	T	T	G	C	T	C	T	lead	AS	108865	108880
yabA (779.2E-6)	TC	AG	CG	AA	CA	AG	CG	AA	CA	lag	AS	10402	10417
ssbB (754.6E-6)	GA	AG	TT	C	CG	CT	CC	A	T	lead	AS	2274356	2274371
asnB (746.4E-6)	GT	TC	TA	CA	AA	T	CG	CA	CT	lead	AS	356847	356862
yeaC (746.4E-6)	T	G	A	T	C	A	T	T	C	lead	AS	405707	405722
intergenic (746.4E-6)	T	G	T	C	T	A	A	T	C	lead	.	1260552	1260567
fbaA (742.3E-6)	ACA	CA	AT	GT	CC	AT	CC	CA	CT	lag	S	1979644	1979659
llrG (725.9E-6)	AT	TT	TT	TC	CT	GG	T	CA	CC	lead	AS	1805025	1805040
yveC (725.9E-6)	A	A	G	T	A	C	G	A	C	lag	AS	2143762	2143777
intergenic (701.3E-6)	C	C	C	T	C	T	G	G	T	lag	.	2016727	2016742
ps105 (693.1E-6)	A	A	G	C	T	C	A	T	C	lag	AS	37893	37908
zitP (680.8E-6)	A	G	A	G	T	T	A	A	T	lag	S	2182929	2182944
ptnC (668.5E-6)	GA	AG	A	T	C	G	A	T	C	lag	AS	1764021	1764036
ptsI (643.9E-6)	G	T	A	G	A	T	C	A	T	lead	AS	121312	121327
yjiB (639.8E-6)	T	C	A	A	T	A	C	A	T	lag	S	982384	982399
purA (635.7E-6)	G	C	T	T	G	T	A	A	G	lag	S	2029214	2029229
ydgC (627.5E-6)	C	A	G	G	C	T	C	A	G	lead	S	362514	362529
L200142 (623.4E-6)	T	A	C	G	T	T	C	G	A	lead	AS	539039	539054
fabD (607.0E-6)	GC	AT	A	A	T	C	A	A	T	lead	AS	783367	783382
alaS (598.8E-6)	T	T	A	G	C	T	C	A	T	lead	AS	1778652	1778667
intergenic (594.7E-6)	T	C	A	T	T	A	A	T	C	lag	.	767701	767716
yqbK (590.6E-6)	T	T	A	G	A	T	T	C	A	lag	S	1619709	1619724
uppP (582.4E-6)	A	A	G	G	T	A	A	T	C	lead	AS	2275479	2275494
ymeA (578.3E-6)	A	T	T	C	A	T	C	C	A	lead	S	1242654	1242669
def (570.1E-6)	A	A	G	G	T	A	A	T	C	lag	AS	555416	555431
asnB (561.9E-6)	G	T	T	C	T	A	A	G	T	lead	AS	356922	356937
rp1M (553.7E-6)	AG	A	T	A	T	A	C	T	C	lag	S	2346912	2346927
nrdd (549.6E-6)	TC	AT	AG	TT	CG	T	C	C	A	lead	AS	271457	271472
ilvD (549.6E-6)	TC	GA	T	G	C	T	C	A	T	lead	AS	1246083	1246098
pi301 (541.4E-6)	TT	CT	CA	GA	CA	CT	CA	TT	CA	lag	S	1414528	1414543
ysjD (541.4E-6)	TT	TT	T	T	A	C	T	T	C	lag	AS	1893720	1893735
comFA (537.3E-6)	TC	AA	CT	TT	CA	CC	AA	CT	CA	lead	S	1097125	1097140
pstC (529.1E-6)	TC	AC	T	TC	G	A	C	T	T	lag	S	1773284	1773299
rqpA (520.9E-6)	C	A	G	G	A	T	C	C	A	lead	AS	202268	202283
ybcH (512.7E-6)	AA	T	G	A	C	T	T	C	C	lag	S	123666	123681
intergenic (512.7E-6)	AT	A	C	G	G	T	A	C	C	lead	.	1781130	1781145
L200142 (508.6E-6)	C	T	T	C	G	G	T	A	C	lead	AS	538980	538995
gyrA (496.3E-6)	A	A	G	C	G	C	A	A	T	lag	S	1123616	1123631
ycfD (492.2E-6)	A	A	G	C	C	G	C	A	A	lead	AS	252972	252987
yujG (475.7E-6)	A	A	C	A	T	A	C	T	T	lead	AS	2099884	2099899
yfjF (471.6E-6)	C	T	T	C	A	G	T	A	C	lead	S	599610	599625
ymcd (471.6E-6)	GT	AT	CG	TT	AG	CC	AT	CC	AG	lead	AS	1221884	1221899
ponA (426.5E-6)	AA	T	C	A	T	A	C	T	C	lead	AS	530491	530506
leuA (418.3E-6)	AT	T	C	A	T	G	C	C	A	lag	S	1240133	1240148
intergenic (410.1E-6)	T	C	A	A	A	T	C	C	C	lead	.	426554	426569
clpC (410.1E-6)	ACA	CT	CT	T	T	T	AG	C	T	lag	S	630146	630161

Table S3. Multiple alignment of the chromosomal insertion sites of LI.LtrB intron in the presence of the relaxase (D-pRS01 strain). Names of the genes and relative frequencies are given in which insertions of LI.LtrB were detected; the orientation of the insertions relative to the direction of the replication (leading strand, lead; lagging strand, lag) and transcription (sense, S; antisense, AS) as well as genomic coordinates are indicated on the right. The sequence of the homing site and location of the insertion are shown on the top. T+5 is highlighted in red.

	insertion						
	IBS2	IBS1					
L200140 (43.5E-3)	CGTCGATCGTGAACACATCCATAAC	CATA	CATTTTAAATCTA	lag	AS	126580	126595
menB (42.1E-3)	ACGGATTCGAGTCCGTCATAC	CACTC	GGCAGCCAC	lag	AS	734626	734641
als (41.8E-3)	ATGGATCAACAGTATTTACCATTC	CACTC	CAATGCTTC	lag	AS	1201917	1201932
citE (37.1E-3)	ATTCGCTCAGCATTATTTACCTAAT	CAACAT	TGCCAATAAC	lead	AS	1208563	1208578
ycpB (34.0E-3)	AGGATAGACTTGGTTTCATGTCC	ACCGG	TACCCATAC	lag	AS	220464	220479
arcA (28.6E-3)	GTGGATAATACATTTTTCGCTAC	TATCAGT	TAAATAAAG	lag	S	2115042	2115057
malG (25.1E-3)	ACCATTACCAATTCGCACTTCAC	ACGTG	ACCACACACCTTCA	lag	AS	1742504	1742519
clpP (20.4E-3)	CAATCGATCAATTTTTCGCAAAC	TATGAATA	AGATTCATATA	lag	AS	672765	672780
ycgP (16.5E-3)	ATGGCAGACCCGACATACACCAAC	CACCAGG	TCATACCGTA	lag	AS	263794	263809
ydgC (14.3E-3)	GCCTGATCAATTAAGCTCAACATAAT	CACCAGC	AACCGTTGGAAT	lag	AS	362156	362171
hrcA (14.2E-3)	GCATAGAACTAAAGCAACATAAT	CAT	TGTAAGGCCAACACA	lead	AS	977477	977492
purA (13.5E-3)	TCCTGAGATTTGCTCACTTCATAAT	CAAG	CATATTTGCGCC	lead	AS	2029172	2029187
intergenic (11.4E-3)	GTTCATATTCATGTCTTACTTCAC	CAAT	TGATGCTCCACTC	lag	AS	492183	492198
yljE (9.9E-3)	TTGCTTAACTCTTTTCCCAACAC	TAC	CGCTTGAATAAGATAT	lead	AS	1194711	1194726
L200158 (9.6E-3)	TCGACGGACAACATATTCGCAAC	CAACCTT	TCTTGTATTTCT	lead	AS	2360508	2360523
ponA (9.5E-3)	CAGCCCTTAACTCTTCTCATATAG	CTATC	CAAGCCCTGCTCCTG	lag	AS	529213	529228
ypaE (9.3E-3)	GATTCGCTTATTTGTTGACCAAC	TATC	CTTTTAAACAGAGC	lag	S	1505183	1505198
ysfA (9.0E-3)	CTGGAGCGCTTTGCTATCTCAAC	CAAT	TCTTAAATCCCTAA	lead	AS	1850611	1850626
murC (8.6E-3)	ACGGACCACTCACTGTTCCATTTAT	CA	CCAATCAATCCGCGAGC	lead	AS	2118446	2118461
tgt (7.9E-3)	GTAAATTCATGATGGTCTTACTTCAC	GTGC	TGATCTTCTTGTATTTG	lag	AS	155934	155949
yveC (7.7E-3)	GATTCGACCTTAAATCTTCAAAAC	CAGC	CTTGAACAAATCC	lag	AS	2143762	2143777
ldhX (6.7E-3)	AAATTCGACCTTCTGTAACAGCAC	CA	AAACGTAATCCAGC	lead	AS	1143058	1143073
yljG (6.5E-3)	ATAAAGATACCCATCTACTTCAC	CAAT	TCTTGAATCAATTC	lead	AS	1197156	1197171
rps1 (6.4E-3)	AAGTCTTCAGATTTCTTTCCTAAT	CAT	GAGTCTTTTATGCGAT	lead	AS	2346620	2346635
menF (6.3E-3)	TGCCTGATCTAGCTTTCTTACTTCAC	GTCCG	TAACTTACTACTTCT	lag	AS	738249	738264
proC (5.8E-3)	AACGATAAAGTTTCTTGCCTCAAT	CAT	CGCGAAGCAATCCG	lag	AS	1953085	1953100
ygdA (5.6E-3)	TCCTCAATCTGTAACATAAGCCAAAT	CAT	CAACAAATTTATTTT	lead	AS	632471	632486
intergenic (5.5E-3)	TTAACTAACTCTGTTACTTCAATAC	CAAT	TAAAGATTAATAGA	lag	AS	74462	74477
yahC (5.5E-3)	ATAATCTCTCTCTTACTTCAATAC	CA	CCCATTTCCGCCAATTC	lead	AS	962423	962438
yjgC (5.4E-3)	GCAGCCCTCAGCTTCCGCTTCATAAC	CCG	TAAATTTCCCTGACT	lag	AS	2036117	2036132
yudI (5.3E-3)	GCAACCAACCTCAATATCTGTAAC	CGC	TAAATTTCCCTGACT	lag	AS	1061365	1061380
pi242 (5.3E-3)	GCTTCACCAAGTATCTTACTTCAC	CCCA	AAATTTCCCTGACT	lag	AS	1208134	1208149
citE (5.3E-3)	CGCCTTCCGCTTCCACTTACTTCAC	GT	TGAAATGGCAGCAATTC	lead	AS	1458230	1458245
llrB (5.2E-3)	CTCTCAAAAATCCCTGATCCATTAAT	CAT	GGCTGGGTTATTCCT	lag	AS	2101484	2101499
glk (5.1E-3)	TCGATACAATAGTACTTCTTAAAT	CAT	TGCGAATAATATA	lag	AS	1617701	1617716
queA (5.1E-3)	AAATCTCCAGCAGCAAAACCCAC	CCCG	TAAATTTCCCTGACT	lag	AS	1742154	1742169
malG (5.0E-3)	TAAGCCCTCAACCAAGTATCTTACTTCAC	CCCA	AAATTTCCCTGACT	lag	AS	1208167	1208182
citE (4.9E-3)	ARCACCTAACAACCTTAAATCCACAC	CA	CAACGATCAGCCAGTCC	lag	AS	1710778	1710793
yrbA (4.8E-3)	CTGCATCTTCCAGTCAACATAAT	CGAG	CAAGCCCTCAAAATTC	lag	AS	369301	369316
ppiA (4.7E-3)	TCCTGATAGCTCAAGATTCCTCAAT	CAT	TAAATTTCCCTGACT	lag	AS	2306115	2306130
pspB (4.6E-3)	TTGTATTAATTTTATTTCTTCAAT	CTC	CAAGCCAGTCAAAAG	lead	AS	309995	310010
ydaG (4.6E-3)	CAATGACCTGCTTCTTCTTCTTCAAT	CAAT	AACTCAATGATCTA	lead	AS	840783	840798
noxA (4.3E-3)	TCATGATTTCTTCCCAATCGCTTC	CAAT	TAAATTTCCCTGACT	lag	AS	1728090	1728105
rliA (4.3E-3)	TTAAAGACAAGACATCATCCATAAC	TAC	AGAGCTTCTTCAATTC	lead	AS	551043	551058
clpE (4.2E-3)	CAAGATTTTCATCATTAACATAAT	CA	CAATTCAGTTCCTG	lag	AS	529831	529846
ponA (4.2E-3)	ACAGCATCTAAAGTATTTCTTCAAT	CAT	TAAACAAATTTCCNAGA	lead	AS	2340666	2340681
L200119 (4.2E-3)	ACAGCATCTAAAGTATTTCTTCAAT	CA	CAATTCAGTTCCTG	lag	AS	962933	962948
yjgC (4.1E-3)	ACAGCATCTAAAGTATTTCTTCAAT	CA	CAATTCAGTTCCTG	lag	AS	364642	364657
ydgF (4.0E-3)	TTGCTCTAATGCAGCAAGCCCAAT	CA	CAATTCAGTTCCTG	lag	AS	2101115	2101130
glk (4.0E-3)	TCACTGAAAGCCTTAAATTCGCGCAC	CA	CAATTCAGTTCCTG	lag	AS	622901	622916
apt (3.9E-3)	GTAGCCGCAAGTATTTAGCCATTTT	CA	CAATTCAGTTCCTG	lag	AS	228492	228507
yccJ (3.9E-3)	TTAAAGCTGCTCCCGTTTCATCAAGTC	CA	CAATTCAGTTCCTG	lag	AS	295716	295731
ycjH (3.9E-3)	GTAAAATAATCCAGTTCCTTCAAT	CA	CAATTCAGTTCCTG	lag	AS	2271599	2271614
gntR (3.8E-3)	GAATTGAAGCCCTCCGTCACATTC	CA	CAATTCAGTTCCTG	lag	AS	1201755	1201770
als (3.8E-3)	CCCTGTGAAAACCAAGCTCCCATCAC	CA	CAATTCAGTTCCTG	lag	AS	1195835	1195850
yljF (3.7E-3)	AAAGCCGCAAACTTCCCTCCGGCAC	CA	CAATTCAGTTCCTG	lag	AS	2117884	2117899
argR (3.7E-3)	CAATCCGCAACCATCGGCTCCAC	CA	CAATTCAGTTCCTG	lag	AS	541048	541063
L200143 (3.6E-3)	ATCACCTGAGCTACTCCGCTCCAC	CA	CAATTCAGTTCCTG	lag	AS	552211	552226
clpE (3.6E-3)	TTAGTTCGTCCTCCAGGAGCGCAC	CA	CAATTCAGTTCCTG	lag	AS	624031	624046
rpoE (3.6E-3)	ATGTCATCTCTTCTTCAATCATTTAT	CA	CAATTCAGTTCCTG	lag	AS	540835	540850
L200143 (3.6E-3)	GCCTACCGGCTCCCTCATCCATCAT	CA	CAATTCAGTTCCTG	lag	AS	2349720	2349735
rnhA (3.6E-3)	ACAAAATTCAGTITTTCTTCACTGA	CA	CAATTCAGTTCCTG	lag	AS	2093418	2093433
typA (3.5E-3)	ATTCACAACTGCTATTCACCCACAC	CA	CAATTCAGTTCCTG	lag	AS	1806395	1806410
ysaA (3.5E-3)	CGACTGTCTATTTCGCTTACTTCAC	CA	CAATTCAGTTCCTG	lag	AS	2132319	2132334
yvdB (3.5E-3)	AACCGATCTTTTTCGCTTCACTGCG	CA	CAATTCAGTTCCTG	lag	AS	1992330	1992345
upp (3.3E-3)	GATTCACCTGCTTAAATTCCTGAAC	CA	CAATTCAGTTCCTG	lag	AS	2316615	2316630
yxhC (3.2E-3)	TCACGATGAACTGCTTTTCTTCTGAT	CA	CAATTCAGTTCCTG	lag	AS	1204442	1204457
mae (3.2E-3)	AATCTACGCTGCTGAACATTCGCACT	CA	CAATTCAGTTCCTG	lag	AS		

feoB (3.1E-3)	GCCCTTCAAATCGATGGTCATAAT	CTAAGTCTGACTTTCAGG	lag	AS	191636	191651
yhfb (3.1E-3)	TCATATATTATCAAGTCAGTACG	CATATCAATTTTAAATAA	lead	AS	752675	752690
uvrB (3.0E-3)	AAARTTGCCAAATGGTCTACCTGAC	CTAARACTTGTCCCGGTGAA	lead	AS	556835	556850
xerD (3.0E-3)	CAATGAACTCAGGAAATTCCTAAT	CATGGATGATACATTTGA	lead	AS	1310409	1310424
intergenic (2.9E-3)	AAATAAAGCCCTGAAATCAGGGC	CTTTAAGATTTTACATCAAT	lag	.	672356	672371
pflA (2.9E-3)	TCATCATATTTTGGTACATAAT	CTACAGTCAAATATGGTTG	lead	AS	1880878	1880893
yjcC (2.9E-3)	AAATCGATACTGAACACCTTCTCGGT	TAATCTCAAGTCTCAAGTCC	lead	AS	292573	292588
citD (2.9E-3)	GCTTACCARACTGTTTTTCTCATC	TGAAATCAAATCTATCGAA	lead	AS	1207881	1207896
murA1 (2.8E-3)	GTTCGACGAGCCCTAATATCAAC	CAACAGGCAAGCCCTACTGT	lead	AS	313400	313415
pepXP (2.8E-3)	CCAGGCAACCCGACAGACCCATTTT	CAAGATTCGAATTTATACCA	lag	AS	2135812	2135827
citF (2.8E-3)	GCACCTTACACTCACGGCTCAAT	CAACAGGTCCTTTGCTTCCG	lead	AS	1209068	1209083
ydgF (2.8E-3)	TATGCCCTAGATATCATTCCTGTC	TATATGCAAGCAAGCCCAAT	lag	AS	364624	364639
ybcB (2.8E-3)	ATAGCCGAAGTGTATAGGCATTTT	CATTCCTCCCTTCCAAATA	lead	AS	212015	212030
ycbB (2.8E-3)	ATAGCCGAAGTGTATAGGCATTTT	CATTCCTCCCTTCCAAATA	lead	AS	212015	212030
yffD (2.7E-3)	ACCTTCTGCGAAGCCCTCAGCTCATC	CACTCTGCTCGTTTACCTA	lead	AS	555725	555740
citR (2.7E-3)	TTAGATAAATTCACATTTCACTCC	CCAGCAATCATTTGCACCTT	lead	S	1206297	1206312
noxD (2.7E-3)	AAACTATCTCTTTATTAAGTCTTTC	CACTCAATCTACCTTTTCAT	lead	AS	2194773	2194788
yvjA (2.7E-3)	AAACTATCTCTTTATTAAGTCTTTC	CACTCAATCTACCTTTTCAT	lead	AS	2194773	2194788
uvrA (2.6E-3)	CAATCAACCAACCAACCAACATAAC	CATCTTTTGGATTCGGTC	lead	AS	1887923	1887938
yoaB (2.6E-3)	AAAGTTGTAAGGCCATAGCCCAAC	CCATTTCCAGGTCGAATTTT	lead	AS	1403419	1403434
hslO (2.6E-3)	TCAGCTGTAATTAATCAACTTCAC	CACTATAGGTTTGTATTAAG	lag	AS	2034682	2034697
intergenic (2.6E-3)	CCAGCTAGAGCAAGTTCGCAACATAAC	CTATCAACTTCAGTCCGAAAGC	lag	.	492284	492299
yngF (2.6E-3)	AAATCCCTAARACCAACCAACCAAC	CAACAGGCGCACCCGGAC	lag	AS	1367812	1367827
intergenic (2.6E-3)	CAAAGATAAGCGCATATCTGCT	CCAGAGTTCAGGCTCGGA	lag	.	492237	492252
yahC (2.6E-3)	TTTGTCAATACAAATTCAGCGCAAC	CCATCAAGAAATGATTCAC	lag	AS	73624	73639
citE (2.5E-3)	CTTCGATACCCTTTCACCATGGC	CCGCAATCTTTTTCGCAAA	lead	AS	1208323	1208338
ysjA (2.5E-3)	GCCTGTGAATGACTTTTCCCAAC	CTAATAATAGTCCGTAACC	lead	AS	1891336	1891351
mutS (2.5E-3)	CTGCCCAAGTTCATCAARCAAGC	CAACTTCTTTTCTCCCT	lead	AS	1692844	1692859
rgxB (2.5E-3)	TTGGTGATATTTGTTTTCACATTT	CAACTTCAATTTGGGCGCT	lead	AS	1461344	1461359
L200146 (2.4E-3)	CTCTCCAGCACCAGCCAGCCCTCAC	CCCTATACAGTCCGTTGTC	lead	AS	1982423	1982438
citC (2.4E-3)	ATGGATTAACATTCATGACCACTTC	CCGATATTTTTTTCGCAAA	lead	AS	1207184	1207199
yrbB (2.4E-3)	TCGTGCTAATGCTATTAAGCCCAT	CCCTAGCAGAAATAGCCGAC	lead	AS	1711588	1711603
clpE (2.4E-3)	ACAATTTAAAGCAATTTCTCTGTC	TCATAGCAGAGATTCAT	lead	AS	552319	552334
citD (2.4E-3)	CTACCCCAATCGCTCTGGCCTAAT	CAACCAATCCAAAGCCCT	lead	AS	1207998	1208013
citF (2.4E-3)	TCACATCAAGCAACAGTTCGCAAT	CCGCTCCGCGCACCAAGGT	lead	AS	1210229	1210244
ypbD (2.3E-3)	CACTGCTAAATCAATGCTCAAAAC	CATATAGGAAAGCAGGCG	lead	AS	1514931	1514946
yogD (2.3E-3)	GGTTCGCAATTCGTTTAAATCAAT	ATTTCTCCCTTCTTCAGC	lag	AS	264608	264623
nrdG (2.3E-3)	AGTGAGCAAGCCAGCCCTTCCATCT	CAACCAATTTGAGGGTTC	lead	AS	272739	272754
gidC (2.3E-3)	CCAGATCCAGCTGATTCATACATAC	CCCTTACTCCCTGTCATTC	lead	AS	1257813	1257828
citR (2.3E-3)	CGACACCTTTTTCATATGCGCTAAC	CAATATCATTCATTTGACA	lead	AS	1209302	1209317
pfl (2.2E-3)	GGCCGCAAGCAAGCAATTCATCAC	CATCATATCTTTTCAGTTC	lead	AS	657523	657538
pepDB (2.2E-3)	CGTAATCAACCAATAATCATAAT	TGCTATCACCAGCAACGC	lead	AS	1600812	1600827
yneH (2.2E-3)	TCAGCAATATCTCTTTTCACAAT	GAACCTTGGAAATGAGAA	lead	AS	1346280	1346295
yfcI (2.2E-3)	AGTGCTGACGATTCATTCGCGAT	CAATAATGAGATGGAAGT	lead	S	529084	529099
potA (2.2E-3)	GTTCGATGAATGACCATTCGTTT	TAAATTCACCTCCAGGCTAC	lead	AS	1176621	1176636
lenc (2.2E-3)	TTAGCCGCTAGTGAAGCACTTCAC	ATGCAAGCAATATATAGGC	lag	S	84331	84346
sdaB (2.2E-3)	CAACGATTTAAATTCAGTTCAGGT	CATGTTCGAAATCCCTTTT	lead	AS	843781	843796
yjhd (2.2E-3)	ATTCGATTAATCAATTTTCATGAC	CTTTTGAAGCCTTTTTC	lead	AS	973074	973089
ygdA (2.2E-3)	GGTAGAATCATGTCCAACATATC	CATCTGACACTGCTTCT	lead	AS	632818	632833
intergenic (2.1E-3)	GCAACAATAAAGCCGGCCATCTC	CCCGATAAAGCAATTTAA	lag	.	506679	506694
yyal (2.1E-3)	ACGTGATATGCTCATCTCACTCAC	CAATATTTGGCAAGAAATTT	lead	AS	11386	11401
hflX (2.1E-3)	TTGACCAAGCACTTTTTCCTAAT	TCAGGTTCAGTATGCTGCTT	lead	AS	225887	225902
citF (2.1E-3)	GCCGCAAGATGACCGTCCGAAC	CAACATAACGTTACCGTT	lead	AS	1210134	1210149
glnQ (2.1E-3)	TTTTTCATAACGGTAGAAGCTCAC	CAACCATTTTCAGGCTCAAG	lag	AS	1819568	1819583
yoaD (2.1E-3)	TGTGCTTTAGCCCGAATAATCATC	CCCATTCGCAATTTGCGATA	lead	AS	1406099	1406114
ywiA (2.0E-3)	TCCTCCGCAAAATTCAGCAATCTCC	CAATATTCCTGCTTATAC	lead	AS	2280342	2280357
pepO (2.0E-3)	AACTAATGAAGGAGTATATGCAAT	CAATTTTTCAAATGGCTTTT	lag	AS	1867511	1867526
citC (2.0E-3)	GTCGCTGAAATGCTTCTTTCATTTT	CATCAGCTTTTTCGCTC	lead	AS	1207623	1207638
potB (2.0E-3)	AAAATGATTCGCTTAAATAGCATGGC	CAATGGGAGCAATCAAAAG	lead	AS	1177014	1177029
ylhB (2.0E-3)	CAATAATAATTTAGCCGGCATAAT	CATGGGATTCATTTTTCOA	lead	AS	1173553	1173568
intergenic (2.0E-3)	TAGTAAATAAATAACAGGCTTGCT	CATATATTCGCAAAATAAT	lag	.	494197	494212
pnpA (2.0E-3)	AGCGCTCCGCTGACCAATTTCCAC	GTTCCAGGTCGCCCCAACG	lead	AS	1923022	1923037
ylhB (1.9E-3)	TCAGCATGTTCTTTAGGACATAAC	CAACCCAGCTTCATTACAGG	lead	AS	1173752	1173767
intergenic (1.9E-3)	TACTGATTAATTCATAAACAATAAC	TATTTTAAATAAGTAAATA	lag	.	2316411	2316426
yncB (1.9E-3)	GTAGGAAATCATGATTCCTCACTAT	CATATACACAGTTCCCCAGC	lead	AS	1311522	1311537
intergenic (1.9E-3)	TTGCGAATAAACAATCTTCTCCAC	TTTCAATTCAGCCCATTCG	lead	.	1501790	1501805
ytgG (1.9E-3)	TTAATCATCAATTAATGTAATCCAT	CATATAATGCTTCTTTAA	lead	AS	1969437	1969452
tra904E (1.9E-3)	CCARAGAAAGCCATTTAATCTAAC	CCGGAATAATCGACCTTTT	lead	S	626963	626978
citF (1.9E-3)	TAAGCCGAATTCAGATAACATCAT	TACCATAGAGGCAATTTT	lead	AS	1209756	1209771
yoaB (1.9E-3)	CTCGTTTACTTTCAGCAAGCCGCAAC	CACTGATTAATTAATCAAA	lead	AS	1405483	1405498
ygcI (1.9E-3)	ACTTGTGAAATGGATTAATCATTTT	CACTAGCTGGGACGGTTCG	lag	AS	653935	653950
pacF (1.8E-3)	GATCCCTCTAATCATAACTCATTT	AAATAATTCGCAATATGAAGT	lead	AS	677838	677853
pepDA (1.8E-3)	AGACGATGACGCAATATCAATAAC	CCCTGTCGGGATTCGAAT	lag	AS	249255	249270
ydiA (1.8E-3)	GAGAAGCTATGATGATTTCAAAAT	TCATATCAATTTTAAACA	lag	S	381887	381902
yrfE (1.8E-3)	GTTFATACTTTTTCATTCATTTG	CATATTTAATATCAAGT	lead	AS	1760358	1760373
potA (1.8E-3)	CTCAATGCTTCATTTTTCAGCAATC	CCACCATTCGACAGGCTCA	lead	AS	1176465	1176480
yahA (1.8E-3)	AAGAACCAGCTTATTCAAACATTTT	CAATCATTCATTTTGGTCA	lag	AS	72409	72424
glnP (1.8E-3)	CGGACATTCATGGGAGTTCATTTG	TAAATCTCCCTTTGTTTC	lag	AS	1817470	1817485
ptnC (1.8E-3)	GAAGATGAGTACATTTCCCAAC	CAACAGACTTTGGAGGTTC	lag	AS	1764021	1764036
malG (1.8E-3)	TAGATTAAGAAATGAAATACATTCG	CATCATTCCTTCAATTCCT	lag	AS	1742084	1742099
yudI (1.8E-3)	CCGACGACCTCTGTTTCATCAAT	CATCGGTTCCGCTTCTCA	lag	AS	2036542	2036557
yljG (1.8E-3)	GCCAAAGATTTTCATTAGCAAAAC	CAACATCCAAAGATCTTGA	lead	AS	1197310	1197325
pepQ (1.8E-3)	TTACCTGAGCCGATGCGCAAAAC	CAATTCAAACCTTTGCTC	lag	AS	1697596	1697611
frdC (1.7E-3)	ACCAATAAACCCTCAACTGCTGAC	CATCATGTCGGTGGTGGAGT	lead	AS	1138403	1138418
pepQ (1.7E-3)	AAAGACAGTCTTCATATCCGCAAC	TACTTTCACGAGATATATA	lag	AS	1698129	1698144
yqjD (1.7E-3)	TTGCTCTCAAACTCATTAGCATTAC	TACTTGTGCGGCAATTTGT	lead	AS	1698715	1698730
ywcC (1.7E-3)	GTTGTCAAAGAAATCAGTCCACCTT	TGAGATTAAGGAGGAAATTT	lag	AS	2229240	2229255
clsB (1.7E-3)	CTTATTAAGCCCTTATTAACAGAC	CATTTAATAATTCGGAATA	lead	AS	1188583	1188598
deoB (1.7E-3)	AAATGCTGACAAAGCATATGTCAC	GTCCATCAGCCGTTCAAA	lead	AS	955858	955873
dexA (1.7E-3)	CTTTCGAAATCTCAACACCATCAC	CATTAGCAATTCATAAAG	lead	AS	1736621	1736636

glnP (1.7E-3)	AAATACTGSACTTCTCCATTGC	TCCGCAAAATCCAGAG	lag	AS	1817416	1817431
ptnC (1.6E-3)	AGGAAGAAATGGCCATACTCAC	GTAGCCAAAGGTTGAT	lag	AS	1763895	1763910
glnP (1.6E-3)	CTGACATCATTCCTCAGCAWSTC	CGCTTGAACAGGCTCAAC	lag	AS	1817828	1817843
citG (1.6E-3)	GATGCTCTCAAAATCAATCATAAAT	CGCTTTATCAATTTCAAA	lead	AS	1210864	1210879
maeI (1.6E-3)	GAAAGCTCTCCATCAGTCAAC	GGCCACAGTTTTCCGCTC	lead	AS	1203656	1203671
ycgP (1.6E-3)	AACTCCCAAAATACCTTCTCAAT	CACTTTTTCAGCGGTTAAA	lag	AS	264275	264290
ybaA (1.5E-3)	GAGCGCTTTTATTTTAAATCCCG	CTAATCACTCGTTTTGATGA	lag	S	101429	101444
pbuX (1.5E-3)	GTGTGCAACCTTACCBAACATAAT	CTACATCCGCTCCCCCAAT	lead	AS	1161385	1161400
clpP (1.5E-3)	CGTGATAAAATCATAGCAAGT	CGCCACGGGCTGATTTGTC	lag	AS	672927	672942
rliB (1.5E-3)	TTTCCTCGTGTCTACTGACAAAC	CAAGCTCTTCTAATTCAGT	lag	AS	1535352	1535367
L200097 (1.5E-3)	TTTGATAAAAGTCAAACTCTCAC	CAAGCTGCGCAACGAGTCA	lead	AS	542710	542725
yoaB (1.5E-3)	CTTCAGGAATTCGAGCAACCGCAAC	CGCCAACTGCAAACTGAAT	lead	AS	1404904	1404919
gatB (1.5E-3)	CTATTCAAATTTGCGCCACTGAC	CTTGCACCCAGTTTGAAC	lead	AS	168767	168782
uvrC (1.5E-3)	CTTGACCACTCCACCATCCATGCG	AAACAAATCAGGAGAGCC	lead	AS	857972	857987
intergenic (1.5E-3)	TGTTGTAGTTTATTACTTACTCAC	TTCTATTCTCAATGATTAAT	lead	.	1299735	1299750
pcaA (1.5E-3)	TCGTTACCAACCGCAAAACATCTT	CTTCTGTAAAATCTATTG	lead	AS	666290	666305
rmaA (1.5E-3)	CTCTCGTAACCTTCTTTTCAAT	CAAGCCCTTAAATCTCTCA	lag	AS	749971	749986
ybdC (1.4E-3)	CAGSAGCAAATTTACCCCAATAAT	CAAGATGAAAATGGCAAG	lead	AS	132449	132464
ywaH (1.4E-3)	GTAACTATTACTCTGCTTCAAGT	CAAAATTAAGTTTCTT	lag	AS	2208331	2208346
yahC (1.4E-3)	TAATCATTTCTCCCTCAATCGCAAC	TGAAAGATTTTCTCAAG	lag	AS	73866	73881
gidC (1.4E-3)	TTGTACAAGATGCGCAAGCATTTAT	CTTGGCGAAGTTTCAACAC	lead	AS	1257582	1257597
malF (1.4E-3)	TTTCCGATATCTTTTATTGTCCGAT	TGACGTGCAAGAGGAGCG	lag	AS	1740735	1740750
als (1.4E-3)	CTCCTTGTCTATGACCGTCAACG	CAATGGCCCTCTCTCA	lead	AS	1200572	1200587
feoB (1.4E-3)	CGGACGAAATATCATGGACATCC	CAAAAGTAAGCAACAGGA	lag	AS	190731	190746
rliB (1.4E-3)	TTTCTTTAAAGTAACTTCTTAAG	TGATAATACCGGTTGCTT	lag	AS	1535526	1535541
pbp1B (1.4E-3)	TTTCGAAACTTTATCTCCGTAAT	CAAAATTAATTAAGTATCA	lead	AS	392472	392487
fabG (1.3E-3)	TTTCGATTAAGCGACGCAACCAAC	CGCCAACTCAAGCCCAAC	lead	AS	801923	801938
yxhB (1.3E-3)	TTTCTATTAGTTTCTTTGACCTAAT	CAATGAGCCGACCTTCAAT	lag	AS	2301202	2301217
yyvB (1.3E-3)	ACTCCGGAAGGAGCAATCCGTAC	CAAAAGCCCGAGGAACA	lead	AS	2176801	2176816
lrg (1.3E-3)	TGAATCATAGCTCTTTTCTTCAAT	CAAAAGCAACCTTAGAAA	lag	AS	380962	380977
ynfP (1.3E-3)	ATGTATCAAACTCTTAAACCAAC	CAACAAGCCAGGAGGGC	lag	AS	1367821	1367836
glpD (1.3E-3)	ACCTTGATAGCATTTACTCTCTCAC	GCATAAAACAAGTGGCT	lead	AS	1270237	1270252
ysgC (1.3E-3)	AAATGATTAAGCGGCCACTGAC	GCGCAATGCCCGCGAAT	lead	AS	1870118	1870133
yscB (1.3E-3)	AGGAAATATAGTCTCTCATCCATAAC	CAATGGGAGCCCTTACGTA	lead	AS	1822184	1822199
cysM (1.3E-3)	GTGTATAAGTAGCGTCTCCATTTAT	CAGGAGCAATCGCTAACAC	lag	AS	526318	526333
intergenic (1.2E-3)	TTGACCCCACTATCTCTCCATTTTC	CTAGATTAATAATCAAAA	lag	.	1765153	1765168
yijC (1.2E-3)	GAACTCTCTCCCTTCTCTCTCAC	GTACACCAAACTCCACAGC	lead	AS	893748	893763
ynhD (1.2E-3)	AGAGACTAATCCAAATATCAAT	CTCGATTCCTAGTGAACA	lead	AS	1376527	1376542
intergenic (1.2E-3)	ATCTATAAATATTTTCTGCAAAAT	CAATGAGCCCTTTTCAAAAT	lead	.	600720	600735
cidD (1.2E-3)	CTGGCCCAATCTGATTTCCACATC	TGAAAGACCTAAGGCTCC	lead	AS	1207824	1207839
yudI (1.2E-3)	ACCACATCAAAAGTTTATCAGGAT	CAGCAAAAGACCGCAACC	lag	AS	2036249	2036264
codY (1.2E-3)	GAAGCGATAACATGCCCTTCTCAC	CAATCAAGCTCTTCTAAGAT	lead	AS	164615	164630
hemH (1.2E-3)	TGCACTATCTTAACTTCTTTTATTT	CAATAGAAAATGAAAAT	lag	S	1608898	1608913
ynfP (1.2E-3)	TATTCGAGAGACCTACTTCAATGCG	CTCCGCAAAAGATTAAGCG	lag	AS	1367256	1367271
yuhE (1.2E-3)	AGTCCCTCAGTATCTATTTCAATGCG	CAGAGTAAGGGGCCCCAA	lag	AS	2073300	2073315
yudH (1.1E-3)	GACGCAAAAATGAAATCTCCCTCTC	CTAGTAATCAACGGGGCAAT	lag	AS	2035630	2035645
intergenic (1.1E-3)	CTCCCGAAGCAAGATTTCTCTTTTC	CTATTTTGAATGAAATTT	lead	.	1641659	1641674
mapA (1.1E-3)	GTCTCTCTAAATTTTCCGSCATTC	CTCTGTGCCCATGCCCAAT	lead	AS	1731080	1731095
pbuX (1.0E-3)	AAATGACCAAACTTTCCTCCAGCG	CAATCTGTTGACCTAATAAT	lead	AS	1160642	1160657
maeP (1.0E-3)	AAATGATAAACTTCTTCCCAAAAC	CACTCTGTTCAAGTAATCA	lead	AS	1205444	1205459
menB (1.0E-3)	TTCAAACGAGAAATTTGGTCTTCAAC	CAACATAACCCACTATCC	lag	AS	734925	734940
intergenic (1.0E-3)	ATGCTTAAAGCGTCAATTTCAACGAC	CAATTTTGAATTAATCAAG	lead	.	618453	618468
yrjE (1.0E-3)	ATGSCCAACCTTCACTTACTGTC	CAATCTTGCATTTAARAC	lead	AS	1794110	1794125
menF (1.0E-3)	TTAATTCGCTGTTTCAACCGTTAC	TGCTTGGCTTTTCAAGC	lag	AS	738516	738531
ycgP (1.0E-3)	TGTGCTTTTACCTAAGCTTCTTTTC	CAAGATGAGGAGAAATGA	lead	AS	265738	265753
ythB (1.0E-3)	AACTTCCGAAGTACCAAGCAAAAT	CAGCAACCGCAATTCATTA	lead	AS	1974386	1974401
pepXP (1.0E-3)	GCAGCGAGCACATTAATCTTCTCAC	CTAGAAATGCCACCAGAGA	lag	AS	2135848	2135863
yuhI (1.0E-3)	ATATCAGGAGGCAAGCAATCTGCT	CAATCTCAAAATTTTGGT	lag	AS	2077617	2077632
clpC (1.0E-3)	AAACGGCAATTTGAGCTTCTGCTC	CAATCATTTGGCTGAGTGT	lead	AS	630372	630387
menB (1.0E-3)	GGAAATTTGCTCTTCCCAACATAAC	CACTCATTTCCACGTACTTT	lag	AS	734934	734949
intergenic (997.7E-6)	AGCACATTTTATTCTCTTCAATTTTC	ACAACTGTCATTAATATCAC	lead	.	779365	779380
ppiA (993.9E-6)	TCATATCTTTCGAAATTTCCAAAT	CAAAATTTGTGAATGCTA	lag	AS	368737	368752
pstA (988.2E-6)	ATCTTTTCCACTTTTAAAGCAAT	CAATAAACCCACTTTGAT	lead	AS	1771561	1771576
intergenic (985.4E-6)	AGTTGACCAAAATTTGACTTGGCATG	TAATAAATAACTTTTCTC	lag	.	461287	461302
aroH (983.5E-6)	ATGACTAAAGCAATTTCTATCTCTCT	CAACCCCTTAATATGCTCTC	lead	AS	1281265	1281280
pbp2A (983.5E-6)	TTAGCTGAAGCTTTCAGCAAAAC	CAATTAGTAATAGTCCGAG	lead	AS	2177528	2177543
yfiI (972.1E-6)	AAAGAGACTCTATTTTCCGCAAC	TCCCAATCCATCCCATTT	lead	AS	587196	587211
intergenic (964.5E-6)	AGTGCBAAGACTTCCATTTCTCTT	CTCCCTTAAATTAATAAT	lead	.	1204656	1204671
ykiF (960.7E-6)	TCTAAATCAAGCCAACTTCCAGAAC	TCAATAGTTCTTTGATAAA	lag	AS	1087045	1087060
ysic (957.0E-6)	CGATTGATTAAGCAAGTTCATAAAC	CATGACCTTCTTCTCTTT	lag	AS	1884434	1884449
yudI (956.0E-6)	ATTCGATGTAATTTTGTCCATAGT	CATAAAGAAATTTATAGCA	lag	AS	2035870	2035885
dacA (954.1E-6)	TTTTCGTTAATTCATAAGCATAAT	CTGAAATGAGGAATTTAGT	lag	AS	2356058	2356073
ysjA (942.7E-6)	AACTCCCAATTTATGCCACTTCCAC	GCACACTCAATTTCCGAT	lag	S	1890475	1890490
L200091 (932.3E-6)	GCAGAGCCAACTGTTACCACTTCCAC	TTCGCCGCCCAACATTA	lead	AS	424310	424325
ycdI (925.7E-6)	TTAGAGGCAATTTCCCAACTTCCAC	AAAGCAAGCTTAGCTCCAAG	lag	S	237900	237915
yogG (916.2E-6)	CTTGATTTGCTCTATAAATCATAAT	TGTTTACCAATTTAATTT	lead	AS	1466341	1466356
intergenic (915.3E-6)	TTGCGCAACAGCAAAAGGCTCAAC	TTTCTCTGCTTGTGTC	lead	.	1815777	1815792
Intergenic (901.1E-6)	ATARAATTCATTAATATTAAGCAAT	CTTTAGGAAAATAAGCTA	lead	.	1516165	1516180
pspA (868.8E-6)	CAATTAATAAATGCACTAATCTCAC	AGGCTGTAAGAGCTCCGAT	lag	AS	2304622	2304637
ponA (867.9E-6)	TAAGCTCCAGCCATTTTTCAGAAC	TTGCTCCACCAATTTTAA	lag	AS	529759	529774
ycgE (844.2E-6)	CTGAACTATGTTCCACCCACATAAT	CAATGGAAACCCACTTGA	lag	AS	265242	265257
nrdR (837.6E-6)	TCATCCACATGCTTCCACTTCCAC	CAAGAAGGTAATCAATACC	lag	AS	1001348	1001363
citC (837.6E-6)	GCGTAAATGSAATTAGCAATCAWAG	CACTGCCGCGATTTTCTC	lead	AS	1207190	1207205
ykhD (830.0E-6)	AGCACTTTCGTTTCAATAGCCATAC	CACTTGGCCCTAATTTGCC	lag	AS	1072513	1072528
pheS (821.5E-6)	CTTCTTCTTCCAGCATACTTCTCAC	CAATGCAAGCTCGGCAAA	lag	S	2009589	2009604
intergenic (817.7E-6)	TCGCTTAGTCTGTAGTCTTCCATAG	CAGCAGAAAGGCTGATA	lag	.	2281324	2281339
yxhD (811.0E-6)	GCAGCTCACGTTGTCCTTCTTCCAC	GTCCTGGTGAAGGAAATGG	lag	S	2319277	2319292
mscL (809.2E-6)	CCAAACGGTAAAGTCAATAGCTTCC	CACTTAATAAATCAATTT	lag	AS	2170604	2170619
yhcA (803.5E-6)	GTTCGCTCAACTTTTGTAGCTTAT	CAACCTTTTCAATTTTGA	lag	AS	720821	720836
L200142 (781.7E-6)	TTTACCATCCCAAACTTCTCTCAC	TCAAGCGGGTTCCTCGGT	lead	AS	537959	537974

clpE (771.3E-6)	GTCAATGACCAGCTTTCATCAAC	CCACATTCCTCCGGGGGGC	lead	AS	551980	551995
queA (768.4E-6)	CCAGCGTTTGAGCAGCAGCAAC	CATTCCTTTTCCGAAAAC	lag	AS	1617278	1617293
yafC (759.9E-6)	ACAACTGAGCCTATTACCAAC	CATCTCAGCTGACAAA	lead	AS	55665	55680
phoC (756.1E-6)	ACAAAAGTCCCACTATTCATAC	CATAGGCTTTGATAAATTC	lead	AS	1094072	1094087
intergenic (735.2E-6)	GGTAACTACCGCAGCAATCTAATC	CTCTGTGGCCGCAATTTGA	lag	.	1259597	1259612
rIxD (706.8E-6)	CTTCATATGCGAAATATCATCTC	ATTCGCTATTCATCGAAC	lag	AS	381092	381107
intergenic (701.1E-6)	TAAATAGTCCCTGGCTAATC	TTTGGTGAAGAATGATC	lead	.	133760	133775
intergenic (694.5E-6)	ATCGTAAACAAACCTTACCTTT	CATCTTACAGTAAADA	lag	.	172797	172812
llrB (688.8E-6)	GATAAAGGCTCAATTCCTCCGAT	CATCAGCAATTAATAAT	lag	AS	1458185	1458200
tra904C (678.4E-6)	GAAGATAAAACTGCTCTTCATGAG	CATAGGGACCGCATGGTG	lead	S	140716	140731
intergenic (678.4E-6)	CTTCATAAATTAACATACTCAAC	TATCTACCAAAATTCAG	lag	.	565296	565311
intergenic (678.4E-6)	TTCTTAACCATTAACAACTAAC	TCATCAAAATTTCAATTT	lead	.	1718258	1718273
trmB (674.6E-6)	GTGATGAAGCTCTTTTCCACAC	CCACTCAATTAAGATCGG	lead	AS	756416	756431
dacA (669.9E-6)	ACGAGTGAACGATTTTCATTTTC	CATCAATCAGTAAATTC	lag	AS	2356769	2356784
aroK (662.3E-6)	GTAAATCGGCCACTTTTCATATTC	CATCTTTCTTTCTTTCAAA	lead	AS	1801096	1801111
citF (633.9E-6)	GATACCCAGCCCATCAATCTAAC	CACCTAATCGACTTGGCTT	lead	AS	1209659	1209674
pflA (626.3E-6)	ACGTGCGAACCACATTCATTAAC	CCGGTCTCAAAATGATG	lead	AS	1880728	1880743
pnpA (606.4E-6)	GCTCGTACCCGACCGCTCCGAC	CAATTCACAGCTCCAGG	lead	AS	1923010	1923025
pi234 (605.4E-6)	TTCATCCATAATTTGCTCTCTCAC	GATTTGAACAFAGGGATCA	lead	AS	1058576	1058591
reco (604.5E-6)	ATATTTTATAAAGACCACTCAC	TGACATCCCGCATAAAGA	lead	AS	58059	58074
pacL (604.5E-6)	AAATGAGTTCATCAAGCTTAAAC	ATCTTATAACGGCTCCAC	lead	AS	676631	676646
dxs (598.8E-6)	GTCAATCACCGCTTTGGCATAAC	CTAGCGTCAAAATGATG	lead	AS	1724988	1725003
yahI (596.9E-6)	GCACTAAGTGCCTTTGACATCTC	CCCAATGATGAAATTAAT	lag	AS	77909	77924
yciC (595.0E-6)	TGGGATTCCTATTCCTCAATGCAAT	CATATTCACCCATTAATCT	lead	AS	285581	285596
hom (593.1E-6)	TCGCCAAAGCCAGCAATTCAGTTT	CATCAACACCGCAATAATC	lead	AS	1171374	1171389
rnhA (593.1E-6)	AAACCGAGATGAGAGTTTCCCAAC	CTGGCAAAAATGCAATG	lag	AS	2349530	2349545
pbp2B (591.2E-6)	GAAGGCGAAGGACACCTCATTT	TCGCTGTAAACAATCTTG	lead	AS	339692	339707
ythB (589.3E-6)	ACGGTCTCACTCAATTCCTCAAT	CCCAACAAATGATTAAT	lead	AS	1974335	1974350
intergenic (573.2E-6)	CCCTCTGGCTCAGTCTCAATCTAC	GCCGTCAGCCACATATTT	lag	.	2016727	2016742
pfl (567.5E-6)	TTCAAAATTCCTGATGGATACCTCAC	ACCGGCTGATTTGATTAAT	lag	S	659540	659555
duka (538.2E-6)	TAAATCGAGCGCTTAATACATTT	TATTAATCAGACAAAGGCTCT	lag	AS	493902	493917
rpoC (526.8E-6)	GAAAGGTAAGTTTGTGATCTCAC	CCGACCAATTTGATTTCAAC	lead	AS	1857655	1857670
gidB (520.2E-6)	CTCGAATTCGACTTACCTCAC	GGACGAGCTGAGATTTTG	lead	S	1381124	1381139
trpD (520.2E-6)	TCCACCCAGCGATGAAATACCTCAC	GCCCTCCGACAGCAATCTC	lag	S	1498901	1498916
gntR (519.2E-6)	CCCGGACTCTTCAAAATTTCAAC	CATCTCCGATTTGATTTCAAC	lag	AS	2272093	2272108
intergenic (513.5E-6)	TTCTGATTTAAAGATTAACGCAAT	TGAGATTAACACTTAATTA	lead	.	1327864	1327879
asnB (509.7E-6)	GTTCGTAACAAATTTGCCAATCAC	GCGCATTTTCAATCAAT	lead	AS	356827	356842
glnP (504.1E-6)	CAATGATTAATCCGACATCAATGC	TAAGATTAATGAGCAATG	lag	AS	1818448	1818463
yseI (493.6E-6)	AAATGATTTAAGATTTCTTCTTTC	CATAAAGAACCCCAATCC	lead	AS	1849361	1849376
hrca (488.0E-6)	ATAAATGATTTGTTCTTCTACCTCAC	CATCTCCGATTTGATTAAC	lead	AS	977222	977237
dut (485.1E-6)	CTTGATTTTCATCACCATCAGCCAC	CAGAAAGCGCATGAGACT	lead	AS	181536	181551
noxB (484.2E-6)	AACTTTATCTCTGGTCAATCTCAC	GTCAAGGAAATGATCTTG	lag	S	842595	842610
ypgC (483.2E-6)	ATCTCGAATTAATGTTGTTCTAAC	CTGAGCTTTCAGTGGAA	lag	AS	1562864	1562879
purA (483.2E-6)	GGTGTGTAAGCTCTAATACCTCAC	GTGTTGGGAGTGGTCCAT	lag	S	2029214	2029229
preA (482.3E-6)	GCAATCGCTCTCAATTAATCTCAC	CAAGCTGAGTAAAGGTAAT	lead	AS	187014	187029
rpsH (475.6E-6)	TACAGATTCAGGCAATTAATCTCAC	CCCAACATTTGTTTCCG	lead	AS	2162238	2162253
yogY (470.0E-6)	ACATCCCTCAAGTCTTTTCTCTTC	CATTAATCTCAATCTCT	lead	AS	1468954	1468969
busAA (464.3E-6)	TCTCCTGTAATTAATTTGCGGAT	CTACACTCTCAACGAAGT	lead	AS	1474868	1474883
udk (460.5E-6)	TGTGATCGCGTATGTTTGCATAAT	CATAAATCGGAATTAAC	lead	AS	1709603	1709618
dxsB (459.5E-6)	GCACTCGCGCGACCTATTCACAC	CATBAGTAATGTTAAATG	lead	AS	1724362	1724377
yrqI (459.5E-6)	ATGGAGCGAAAATTTCTCCGAT	TGATACATTTGCAAAAGCA	lag	AS	1769762	1769777
yreB (451.9E-6)	CTTCCATACTCATTAATGATTT	CATAATTTTAAATGGA	lag	AS	1744117	1744132
citE (447.2E-6)	CCCTTGAACAAAGCTTCTTCACTCT	CAACATTCGCAATGAGCT	lead	AS	1208681	1208696
yudI (442.5E-6)	AGTGGATGAGTCACTCTTCAAAAT	CCATCTTTCCAAAGCTCT	lag	AS	2036072	2036087
yljF (426.4E-6)	GTTCGATTCCTCTCAATAGCATAAC	TAGCTTCAACTGTTCCCAT	lead	AS	1196804	1196819
yrjD (417.8E-6)	TCAATTCGAGCAATTCACATCTCAC	AACCTCAAGGGTGGTGGC	lag	S	1773284	1773299
dnaA (415.0E-6)	TGCTGTCGATCTCTTTTGAATCAC	CATCACTTTTCTTCTTTA	lead	AS	1668	1683
kdgR (410.3E-6)	TTTTCCTCAGGACCGATTAATCTTC	TGGAATTTTGCCTGTAAT	lag	AS	1680250	1680265
ysfD (409.3E-6)	GTTCGATTTGAAAGTAAACATTC	CATCTTTCCAAAGCGGATTT	lead	AS	1854261	1854276
pknB (408.4E-6)	TTTCGATGACTGAGTAAACATAAC	CATCAGCTTTGTTACTCTG	lead	AS	1955328	1955343
rplM (406.5E-6)	ACTATATTAACACACATCACTCAC	CCAGGTGGATTAAGTACAG	lag	S	2346912	2346927
gpsA (405.5E-6)	TTTCGCCAATAACGACTTCACTCAC	CATATATCAATTAAGACTTG	lag	AS	1376845	1376860
citB (401.7E-6)	CCGATAATCTGTTGCTAATCTCAC	TTAATCAACATTAATGCT	lead	AS	669535	669550
yvdE (400.8E-6)	AGCCCAAGCACTTTCTTCTTCAAC	ACTAATTAAGTAAATGGA	lag	AS	2137423	2137438
yhfD (398.9E-6)	TTCCGAAAAAATGATTCGCAAC	CACCTTTAACAGGGCTCAT	lead	AS	755426	755441
intergenic (398.9E-6)	ATTCGCAAAATGCTTACCCTATTT	CATCACTTCAATTAATCT	lag	.	1002525	1002540
pacL (389.4E-6)	GTAGAGCACTAATAAATCAACAG	TGATATACAGGTAATGTT	lead	AS	678810	678825
pspA (389.4E-6)	GATTAATTTGCGGTTTCAATTAAT	GGGTCTCCCAATGAGTAA	lag	AS	2303688	2303703
uppP (381.8E-6)	AAGGTAAATCTGCGCAACTCTCAC	GCCTTACACCAACTAATAA	lead	AS	2275479	2275494
thra (375.2E-6)	ACTTTTCGCGCAATCAACTCTCAC	GGTTCATCAGATTAATTAAT	lag	AS	747685	747700
ydiF (369.5E-6)	CTTCACCTTGCAATCAACTCATAAC	CCGCTCGGGAAGAAGAA	lag	AS	388917	388932
intergenic (369.5E-6)	GATAAGTCTCCCTTTAAGCATAAT	CTTATGATTTTTTCTTCT	lead	.	1166149	1166164
ypjC (355.3E-6)	ATTCAGGACTGTCACATCTCAAT	CTTATGATTAATGCGTG	lead	AS	1592521	1592536
ptnC (353.4E-6)	ATAAGCTTCAATCAATTCATAAC	CACGGCAACCAACTCC	lag	AS	1763862	1763877
ymjE (348.7E-6)	CTGTATAGATTTGCAABAGCATAAT	CACTCAACTTCAAAATTT	lead	AS	1297580	1297595
nth (345.8E-6)	CTTCGGCACTAATAATTTGCGCAAT	CAATAGTTGAAAGGAGTT	lead	AS	1083938	1083953
llrB (344.9E-6)	AGCTCTGTCATTTTCATTTCACT	CATCTCAGCCAGTAAATAT	lead	AS	1458407	1458422
asnB (341.1E-6)	GTTCCTAAGTCCCAATCACTCAC	GGACGCTGAAGTACATC	lead	AS	356922	356937
ydiF (341.1E-6)	TTTCATCTCGTGTGTTTCCATTC	CCCTTTGTTTTTCTGAA	lag	AS	387696	387711
intergenic (339.2E-6)	AGAAACTTCTTATTGTCAAAAGGCC	CTTATGATTTGAAATTTGA	lag	.	1816604	1816619
ydiB (338.3E-6)	TTTCGTAAGCTGCTTACATCTCAC	CCGAGGCTTTGAAAGAA	lag	S	383788	383803
ps123 (332.6E-6)	TTTGTGTAAGCTGCGGCTCTCAC	CATTTTAAAGATTTGGCC	lead	AS	49516	49531
ysjD (330.7E-6)	TTTATTACCTTGTGAGCCACTCAC	CTGCTCACCAGATRAATC	lead	AS	1893720	1893735
yrjD (326.9E-6)	TTTCCTTACCAATTTTCCAATCTCAC	CATTTGCTGAAATTAAC	lag	AS	1793542	1793557
fbak (326.9E-6)	ACACATGTGCCAATCTTACTCTCAC	GGTGGTTCTGCAATCCCTG	lag	S	1979644	1979659
ptsI (325.0E-6)	GTAGATGGATCAATTAATCTCAC	CATCACTCTGCAACAGC	lead	AS	121312	121327
porA (313.6E-6)	GACATCGAATCCACTGGCAAAAC	CCACAGTTTAAAGCAAGC	lead	AS	1135794	1135809
yudK (312.7E-6)	TCAGTCTGATAGGCTGCTCAC	CCCTTAATTTGTTGGCT	lead	AS	2038474	2038489
citG (307.9E-6)	ACTCCCAATTTTATCTCAATTT	CTAACAATCTCAATTTG	lead	AS	1211075	1211090
intergenic (305.1E-6)	CTCGCTATACTTTTACCTAAC	CATGACTTTTAGGTAACG	lead	.	1838537	1838552

yeaC (304.1E-6)	TGGACATCACTTCACTTAC	GCACAATCGGTGGTGAAT	lead	AS	405707	405722
yfbF (304.1E-6)	AAATAGTCTAATATTCACCT	ATGGGCTAAAGTGCATAA	lag	S	515575	515590
fbaA (304.1E-6)	TCAACCCCAATTGACCAACT	ATCAACGAGATGCCTTT	lead	AS	1979895	1979910
psl05 (302.2E-6)	AAGGGCTTCACTCCTCATOT	ACCCAGCAGATTAAGGC	lag	AS	37893	37908
pcrA (297.5E-6)	GATGATTCGTACGATCCCA	ACACAGATATTTTGAACA	lead	AS	1134512	1134527
L200150 (296.6E-6)	TACGGTACCTTGTACGACT	CCCTGACCGGTCTACC	lead	AS	2221669	2221684
intergenic (294.7E-6)	GCAAGTCATAGAGATTTCA	TCCATTTTCTGTTTGA	lag	.	2100424	2100439
intergenic (291.8E-6)	AAGGATAATATTTTGTGTC	CTTGCTGSCCTCTCGGAC	lead	.	1401689	1401704
recD (290.9E-6)	TAGGCTTTTCATTTCGCTC	GCGCCACCCGTTTGGCAA	lead	AS	1797401	1797416
intergenic (289.9E-6)	TTTCTTAAATTCATATTTCA	CTCTGGATTACTTCAAAA	lead	.	1200392	1200407
ypgC (287.1E-6)	TAGTTTGGCAATGTTTGTG	CATTAACACTTCCCGAAT	lag	AS	1562527	1562542
ptnAB (287.1E-6)	CTTTATCCACCCGGCAGAG	CATCATGCTTCTGTAG	lag	AS	1762532	1762547
yrgI (287.1E-6)	GCCCAAAACAGGATTTCA	CAACATTTCTTCTCTAAA	lag	AS	1769877	1769892
yejH (286.1E-6)	TTATAAAAGTTTACTTCCA	CACCATAAGAGTATTCAA	lead	AS	499252	499267
ylad (286.1E-6)	AGCGGTTTGGAAATCTTTC	CATGTTCCCGCTTCAAA	lead	AS	1105621	1105636
scrK (283.3E-6)	GCGGAATCATTGGTTTACT	AATGGACAGGAAATGGT	lag	S	1518450	1518465
fhs (279.5E-6)	ACAGTGAATACAGCAGGCA	CTCTCAAAACAACACAG	lead	AS	960252	960267
topA (273.8E-6)	AAAGCATTAATTTCTTCTC	CAACAAATAGTTTAAAGC	lead	AS	1255147	1255162
ymjE (271.9E-6)	GCAATGCAATTAACAATATA	CAGTGTAAATAATCAAG	lead	AS	1296421	1296436
comFA (271.0E-6)	TCAACGTGACACCAAACTC	TAAATTCGGCAGATCAAA	lead	S	1097125	1097140
fabd (269.1E-6)	GCATAATCAACCCCTCAAC	CAACAATAACAATTTGTG	lead	AS	783367	783382
intergenic (268.1E-6)	AAAGTCGGCACTCAATTC	TATCAATTTTCTGTACA	lead	.	498594	498609
ytbB (268.1E-6)	TCCTGAAATGTTGTAAATC	CAACAATCTGTTCTTTTC	lead	AS	1913605	1913620
sdaB (262.5E-6)	GTGTATCAACTTCTAATAT	CGCTTTTTCACCCCTAGC	lead	AS	843991	844006
leus (254.9E-6)	TCAACATCACTCAGGATTA	CATGTTTAAAGTATTAGA	lead	AS	829278	829293
ilvD (252.0E-6)	TCCATGCTCTCAATCACTC	CGCTGACCAAAAGATATC	lead	AS	1246083	1246098
nrdD (251.1E-6)	TCCATGTTTGGTGTCTACT	GCTTAAAGCAACGTTTGG	lead	AS	271457	271472
citD (245.4E-6)	CAATCGCACGTTCACTAC	CGCTCTGGCCTTAACTACC	lead	AS	1208013	1208028
rplC (245.4E-6)	ACAGTGATTTCTGCTCACT	CGCCCTCGAGTCCCTTGA	lead	AS	2169681	2169696
yfjF (236.9E-6)	CTTCATGACTTACATACCT	TAGCATGATTTCCGTTGG	lead	S	599610	599625
yrfJ (236.9E-6)	CGATAACCCCTGGCAAACT	ACCTACTAGCAATTAAGC	lead	AS	1794180	1794195
clpC (233.1E-6)	ACAATTGCTTATGCTCTACT	GTAGAAGATGATTTGGTC	lag	S	630146	630161
ymjE (231.2E-6)	TCCTGCGAATGTTTTACCA	CATTTTAGAGTTGAARDA	lead	AS	1296165	1296180
relA (227.4E-6)	TTTGTCTGCTCTCAACTC	GACCTCAATTTTCTGTAA	lead	AS	108865	108880
ssbB (226.4E-6)	GAACTCCGCTCCATACCTC	GAGCAATCTACTCTCAAA	lead	AS	2274356	2274371
yieF (225.5E-6)	TATTTGACCTCCGACTTCTC	CAATGAGTTTAGGCGTGA	lead	AS	486830	486845
gyrA (222.7E-6)	AAGGGCGAAATTTCTCTT	AACTCGTAAAGGATTTCT	lag	S	1123631	1123646
llrG (222.7E-6)	ATTTTTCTCTGGTCACCACT	CAATCTCACGAARGAAG	lead	AS	1805025	1805040
flol (221.7E-6)	GCTTCGGCCATTCGTACTC	GTCTTTAGCAGTGGCTTT	lead	AS	746840	746855
ylad (221.7E-6)	CCAAATGAACTGCAACTCC	GATCAACACGGCCCAAA	lead	AS	1105720	1105735
L200115 (220.8E-6)	GTCCTCAATCGCCCTACGG	CGACTCCGACCTCTCTGC	lead	AS	2344208	2344223
parC (217.0E-6)	TCAGGTTACATCAAGTACT	CACCTCTCAATTTGCTCT	lag	S	1012443	1012458
rmaJ (215.1E-6)	AAATCGGACATGATAGTCA	TBATATTCCTGTCAGA	lag	AS	583465	583480
leuA (211.3E-6)	ATTCATGTTTCAATGCACT	CTATTCACATGAATATA	lag	S	1240133	1240148
rpsM (200.9E-6)	GGTTGATCTAATGCACTCT	GACGAAGGCTCCCTGGAG	lead	AS	2153631	2153646
intergenic (199.9E-6)	CAATTTACGAAATGCTTCA	TATGTTTAAATTAAGGAT	lag	.	1712489	1712504
ponA (199.0E-6)	AAATCATACTTACCTACTCT	CTAATGCGCCGCGATAT	lead	S	530491	530506
yieH (196.1E-6)	GCACTACTGATGATGCTACT	CAACCAATTTCCCGTGA	lag	AS	850840	850855
purI (188.5E-6)	ATATCCCAACCCGAGCTCC	CAGCCCCCAACAGACTTG	lead	AS	1576156	1576171
intergenic (186.7E-6)	AAAACTTCTTTAATAGATT	TCAATCACTTTTATTTAC	lead	.	1677069	1677084
L200065 (185.7E-6)	TCAAGTAAACCTCAACACT	TAGCAATTCAGTCTTCT	lead	AS	1745995	1746010
hemf (184.8E-6)	AGTCTATTTTGTCTCACTC	TBAATCTCTHGTAAAGTC	lead	AS	1608825	1608840
menX (181.9E-6)	GTCGCCAATTCGGACAGTA	CAATACATCAATCTAAT	lag	AS	736367	736382
hpt (178.1E-6)	ACATCTAGATTAATTTAORT	CAGAGGATTTGTTCCCGCC	lead	AS	25358	25373
yqbK (178.1E-6)	TTAGAGATTATGCCAATAC	CAAGCACTGGGATTTTAA	lag	S	1619709	1619724
Intergenic (175.3E-6)	AACTCTACACAGAAACATTT	CAAAATTTTATATGAAAA	lead	.	841200	841215
ybhC (173.4E-6)	AAAGATACTTATGTCTACT	TGGTTTGGAAATATAA	lead	S	123666	123681
def (172.4E-6)	AAGGTTACACTTTGCCACTC	GTAAAGTTGGAAATCTTC	lag	AS	555416	555431
L200156 (172.4E-6)	CTTGGGTTAGCAACTAORT	GTACTCCAACTCCCGTGG	lead	AS	2344471	2344486
L200146 (169.6E-6)	GCAGGGTCAACCCCTTACT	CTACCGGTTTAGCGAGAG	lead	AS	1982437	1982452
yyaI (167.7E-6)	CCAACTATTTCTTTCTTCT	GCAACTGACCCGGTCCAGC	lead	AS	12154	12169
pepA (165.8E-6)	AAGAAACGAAACGTTGTT	GCAGACACCGCTTCACTC	lag	AS	394211	394226
ydbA (163.0E-6)	ACAATTAARACGTTGCARCT	ATCGAGCCAGCACTCTAC	lag	S	311295	311310
lncC (162.0E-6)	TTTAAATGCCCTGTTTCTT	ACAAATCCAAATTAACAAT	lag	S	83878	83893
yfjB (161.1E-6)	TGTTGAGTCAATCCAGCTC	CTCCAGTCAACAGGATTC	lead	AS	777180	777195
sdaA (160.1E-6)	AGGAATAATTTTAGAATCC	TBAATCTCTCAATTTTAA	lead	AS	844130	844145
gyrB (157.3E-6)	CTGATTTTTCAGTGTCACT	GCGGACGTTTTCCTGCAAT	lead	AS	929120	929135
yqcA (155.4E-6)	TAAACCTCAATGACCGACT	AACTCCGCTAGTAAATTA	lag	S	1624880	1624895
recF (155.4E-6)	TCAACCATGATTTTATCCAT	CAGCAATTTGTCCTCAAG	lag	AS	2051618	2051633
ydgC (153.5E-6)	GAGGCTCAGACAGGTACTC	CTACAGGCTTATTTGGTTA	lead	S	362514	362529
pbp2A (153.5E-6)	GCTGCTCAATCAAGTACTC	TGTGCGGAACACCAAGTA	lead	AS	2178563	2178578
dnaE (152.5E-6)	AACGCTCTAATATCATTTAC	GTCTGCAACAGTAAATTC	lead	AS	496795	496810
nucA (152.5E-6)	TATGTAARAATCTAATTTCA	CAATACCAACCTTATAT	lead	AS	1100790	1100805
intergenic (151.6E-6)	TCAGGAAAGAAATTAORTC	CATGAGCCCAATAAGAAAT	lead	.	1213718	1213733
clpC (147.8E-6)	GTCAAATGACCCCTCATCAT	CTACATTTCCCGGAGGAGC	lead	AS	631593	631608
clpB (146.9E-6)	AGGTGACCTGAAATTAATCT	TTCGCAAGAAACACTGCATC	lag	S	1567554	1567569
vacB1 (145.9E-6)	GAAATATACGCACTTAACT	CAATCTCTGTTTACCCGA	lag	S	968723	968738
proB (145.0E-6)	TCAACGAAACGTTCCATCT	TBAATTTCTGTTTAACTC	lead	AS	1652644	1652659
pacB (144.0E-6)	AGCTGGGAAATACAAATG	CATTAACCTTTTCTGTTG	lead	AS	1903831	1903846
prsA (141.2E-6)	AACTTGGCCGACGCTCTACT	CATGGTCAAGGCAAGCAGC	lead	AS	826166	826181
ymd (141.2E-6)	CTTCAAGACCTTGGTCAACT	GGAGGAATTTGCCAATACG	lead	S	1238775	1238790
ps201 (137.4E-6)	TATGATTTTAAAGGCTCCAC	CATCTTTCAGCTAATCTG	lag	AS	503656	503671
yujG (137.4E-6)	AACAGTAGAGCAGACTTTCT	CAATCTTCACTTCAGTA	lead	AS	2099884	2099899
pl301 (136.4E-6)	TTCTGAGATACATCCACTC	GAAAGATTTAATGAGTTT	lag	S	1414528	1414543
ddl (134.5E-6)	AACTCAATCTTCTCACACTC	CTGGAAGCTTCCGGAACAC	lead	AS	341407	341422
purC (133.6E-6)	GATGAAATTTCACTCAACTC	GTCCTGCGGATCCGATGG	lag	S	1577698	1577713
yojB (132.6E-6)	TTTTCAAATTTATGTTACTC	CAATCAATTTTCCGACGC	lead	AS	291861	291876
glbB (132.6E-6)	AAGAATCGTTCAGACTCTC	AGGTACGACACTCAATTT	lag	S	1318756	1318771
ythB (132.6E-6)	ACATATTTTACCTTCTTCA	CTTGAATTTACCTTTGTA	lead	AS	1974292	1974307
yhbB (130.8E-6)	TAGCCACCCCTGCTCAAGCC	CATATCTGTAAGCGATGT	lead	AS	752126	752141

ptnC (130.8E-6)	CATTGCTCAACCAATACCTTCAAGAC	CAGCAAGGAAGGCACCAAC	lag	AS	1763328	1763343
potB (127.9E-6)	TCATGCAAGCAACATGGCTACATAC	TAAATACACAGCAATGGTT	lead	AS	1177686	1177701
y1fD (126.0E-6)	TGCTGTTATAGGCATATGTTCTC	CATCCTTGCTTCTGAAAT	lead	AS	1154773	1154788
yrdB (124.1E-6)	GTGACGAGATAGGGTTTCATATT	CATAAGGGCAACTCCTTC	lag	AS	1748651	1748666

Table S4. Multiple alignment of the chromosomal insertion sites of LI.LtrB intron in the presence of the relaxase (D-pLtrB strain) arranged by the frequency of the event. Names of the genes and relative frequencies are given in which insertions of LI.LtrB were detected; the orientation of the insertions relative to the direction of the replication (leading strand, lead; lagging strand, lag) and transcription (sense, S; antisense, AS) as well as genomic coordinates are indicated on the right. The sequence of the homing site and location of the insertion are shown on the top. T+5 is highlighted in red.

	IBS2	IBS1	insertion ↓					
homing_site	CGTCGATCGTGAACACATCCATAAC	CATATCATT	TTTTAATTCTA					
citE (60.5E-3)	CAGGATAACACTTGGTTTTCATGTC	CGCGCGGAGGCCATGCA	CGCGCGGAGGCCATGCA	lead	AS	1208563	1208578	
arca (51.2E-3)	ACCATATACCAATGCGACTTCAC	ACGTGAGCCACAAAGCTCA	ACGTGAGCCACAAAGCTCA	lag	S	2115042	2115057	
L200140 (35.8E-3)	ACGGATTCGAGTCCGCTGCAATAG	CACTCTGCCAATGGCTCAC	CACTCTGCCAATGGCTCAC	lag	AS	126580	126595	
purA (26.5E-3)	GTTCATATTCGTCTCACTTCAC	GAATTTGAGTGCCTACTTC	GAATTTGAGTGCCTACTTC	lead	AS	2029172	2029187	
als (25.7E-3)	ATTCCTTCAGCTATTTTACCAAT	CAACATAGCCAAATCAAC	CAACATAGCCAAATCAAC	lead	AS	1201917	1201932	
menB (22.9E-3)	ATGGACCAACAGTATTACCATTC	CATCTCATTGCTTCCTGC	CATCTCATTGCTTCCTGC	lag	AS	734626	734641	
ycgP (17.2E-3)	ACTCAATCATTAACCTCCATTA	TCACCAGCAACCGTGGAA	TCACCAGCAACCGTGGAA	lag	AS	263794	263809	
murC (16.9E-3)	GTAATTCATGATGGTCTACTTCAC	GTGCCGACCCGTTAATTTG	GTGCCGACCCGTTAATTTG	lead	AS	2118466	2118481	
rpsI (15.3E-3)	TGTCGGATCAAGCTTTCCTACTTCAC	GTCCGTTAACCTGTGATTT	GTCCGTTAACCTGTGATTT	lead	AS	2346610	2346625	
ycbB (14.8E-3)	TGTCGGATAATACATTTTTCGTTA	GTATCAGTCTGATATAAAT	GTATCAGTCTGATATAAAT	lag	AS	220464	220479	
ldhX (13.5E-3)	ATAAAGATAATCCAAACCTACTTCAC	GTATTCCTGCAATCAATTC	GTATTCCTGCAATCAATTC	lead	AS	1143058	1143073	
malG (12.4E-3)	CATTCACCTGATAATTTTTCATAAC	TATGAATAAGATTCGAATA	TATGAATAAGATTCGAATA	lag	AS	1742504	1742519	
malG (12.2E-3)	AACACCTCAAACTATTCCTGAGC	CACTACCAATAGACCAGTCC	CACTACCAATAGACCAGTCC	lag	AS	1742154	1742169	
yudI (12.2E-3)	GCTTCAACCAAGTATCTACTTCAC	CCCAAATAATTCGATGGA	CCCAAATAATTCGATGGA	lag	AS	2036117	2036132	
pi242 (11.5E-3)	CGGCTTCCGCTTGCACACTTCAC	GTGAAAGGCAGCATATGG	GTGAAAGGCAGCATATGG	lead	AS	1061365	1061380	
yafC (11.3E-3)	ACAACTTCAGCCTCATTACCAATC	CATCTTCGACACCTCAAA	CATCTTCGACACCTCAAA	lead	AS	55665	55680	
L200119 (10.8E-3)	CAAGCCGGTGTGTTACCACTTCAC	CACATCGCCCAATGAAA	CACATCGCCCAATGAAA	lead	AS	2340666	2340681	
citC (10.1E-3)	ATGGATTCACATTCATGACCTCTGC	CCCGATTTTTCGCAACA	CCCGATTTTTCGCAACA	lead	AS	1207184	1207199	
yvdD (9.9E-3)	ATTAACCAAACTCATAAAGCCCAAC	CAATAATCAATCCAAATATG	CAATAATCAATCCAAATATG	lead	AS	2134373	2134388	
llrB (9.4E-3)	TCTGATAAATGTTACTTCCTAAT	CATTTCCCGCAAAATATA	CATTTCCCGCAAAATATA	lag	AS	1458230	1458245	
clpP (9.4E-3)	ATGGCCAGACCCGCAATACCAAAC	CACCAAGTTCCTTACGTA	CACCAAGTTCCTTACGTA	lag	AS	672765	672780	
citD (9.1E-3)	CATTCGCAATCGCTTCGGCTTAAT	CACCAATCCAAAGCCCT	CACCAATCCAAAGCCCT	lead	AS	1207998	1208013	
yljG (8.7E-3)	AAGTCTTCAGATTCTCTTGGAAAT	GATGAGTCTTTCAGGCAT	GATGAGTCTTTCAGGCAT	lead	AS	1197156	1197171	
yahG (8.1E-3)	GCAGCGTAGCTTGGCTTCATAAC	CACCCATTTCGCCAAATTC	CACCCATTTCGCCAAATTC	lag	AS	74462	74477	
citC (7.8E-3)	GTCGCTGAAATGATTTCTCATTTT	CATCAGCTTTTTCGCTTC	CATCAGCTTTTTCGCTTC	lead	AS	1207623	1207638	
ysaA (7.5E-3)	GGACTGTCAATTTTTCCTACTTCAC	TCACAGGAGGAAGCGGGAA	TCACAGGAGGAAGCGGGAA	lead	AS	1806395	1806410	
yxhC (7.3E-3)	TCACGATGAACTGCTTTTCTCTAT	CTTCAACCCGCTTCAATTC	CTTCAACCCGCTTCAATTC	lag	AS	2316615	2316630	
uvrB (6.9E-3)	AAAATTGCCAATTCGCTCTACTTCAC	GTAAAGGCAATTCGCGTAA	GTAAAGGCAATTCGCGTAA	lead	AS	556835	556850	
yljE (6.4E-3)	TCGACGGACAACATATTTTCGAAAC	CAACCTTTCCTTGTCTTCT	CAACCTTTCCTTGTCTTCT	lead	AS	1194711	1194726	
yuhE (6.1E-3)	AGTTCGCAATTTGCTTTTCTCTAT	CACTGAGCTTTCGCAAAAGC	CACTGAGCTTTCGCAAAAGC	lag	AS	2073393	2073408	
gntR (6.0E-3)	TGAATGAAAACCTTCGCTCACTAT	CAATATTCGCAATTAATA	CAATATTCGCAATTAATA	lag	AS	2271599	2271614	
lcnC (5.9E-3)	TTAGCCGTATCGAAGCTACTTCAC	AACGAGCAATTTATAGAGC	AACGAGCAATTTATAGAGC	lag	S	84331	84346	
citF (5.7E-3)	GATTCGCGACCGCATCAATCTAAT	CACCTTTCATCTTCGCTT	CACCTTTCATCTTCGCTT	lead	AS	1209659	1209674	
citE (5.5E-3)	CCTCAAAAATTCCTGCATCTTAAT	CATGGCTGGGTTATTCGCA	CATGGCTGGGTTATTCGCA	lead	AS	1208134	1208149	
queA (5.4E-3)	GCATCAAACTTTCATCTCAATAC	CAGGTTTAAAGAAATCTC	CAGGTTTAAAGAAATCTC	lag	AS	1617614	1617629	
yyaI (5.1E-3)	ACGTCAATCATGGCATCTACTTCAC	GAATATTCGCAATTAATA	GAATATTCGCAATTAATA	lead	AS	11386	11401	
citE (5.0E-3)	CGCGGATTTCCGCGCATCTCATC	GCCAGCCGAGACTCAAGT	GCCAGCCGAGACTCAAGT	lead	AS	1208482	1208497	
L200150 (5.0E-3)	TGCTTCAAGCCCGGAAAGCTAAT	CCCGCGGCTGCTGATCC	CCCGCGGCTGCTGATCC	lead	AS	2221784	2221799	
intergenic (4.5E-3)	TGTTCTAGTATTTTACCTACTTCAC	TTCTATTCCAAAGATAT	TTCTATTCCAAAGATAT	.		1299735	1299750	
menB (4.0E-3)	GCGGCAAGTAAACCAAGCCATAAC	CAAGCATCAAAGCAACAAC	CAAGCATCAAAGCAACAAC	lag	AS	734727	734742	
ptnC (3.9E-3)	AGGAAGAAATGCGCCATACTTCAC	GTAGTACCAAAAGGATGAT	GTAGTACCAAAAGGATGAT	lag	AS	1763895	1763910	
typA (3.9E-3)	TTGATGTTCCTCGGAATAACCGTC	CAATACCAATAGCTCCAAC	CAATACCAATAGCTCCAAC	lead	AS	2093826	2093841	
ywaB (3.9E-3)	AAAGTCAAATCCAGCCTTCAAT	CATCTCAATCTTCTCTT	CATCTCAATCTTCTCTT	lead	AS	2201396	2201411	
codY (3.8E-3)	GAAGCGATAACTGCTCTTCTTCAC	CATCAAGCTCTTCAATGAT	CATCAAGCTCTTCAATGAT	lead	AS	164615	164630	
plsX (3.8E-3)	GTGACTCTTGCTTATTTCTCTTAAC	CAAAAGTAAGCCGGCGT	CAAAAGTAAGCCGGCGT	lag	AS	71836	71851	
yljJ (3.5E-3)	TCATACAAAGCCGCGCTTCAAT	CATTTCCAAAGCTTTATG	CATTTCCAAAGCTTTATG	lag	AS	1200077	1200092	
ysiC (3.4E-3)	CGATTGATGACAGTTCGATAAC	CATGACTTCTGCTTCTT	CATGACTTCTGCTTCTT	lag	AS	1884434	1884449	
gatB (3.3E-3)	GTATTCAAATATTCAGCCACTTCAC	GTGCAACCCAGCTTTGAC	GTGCAACCCAGCTTTGAC	lead	AS	168767	168782	
yijC (3.3E-3)	GAACTCTTCCCTTCTCTCTTCAC	GTACACCAAATCCACCAGC	GTACACCAAATCCACCAGC	lead	AS	893748	893763	
acmA (3.3E-3)	ATTCGATTCAGGGAAGCAACATAAT	TGGGTCACTTGCATATTC	TGGGTCACTTGCATATTC	lag	AS	269483	269498	
clpC (3.2E-3)	GTCAATGACCTCCTCATATAAC	CTACATCCCGGGAGGAGC	CTACATCCCGGGAGGAGC	lead	AS	631593	631608	
apt (3.2E-3)	TGCATTAGAATTTTATCTCAAT	CTCCGATTTTTCCGCGACC	CTCCGATTTTTCCGCGACC	lead	AS	623294	623309	
proc (3.1E-3)	TCTCTAATGCTGCTTACGCTAAT	CTACACCAAATCTCAATTT	CTACACCAAATCTCAATTT	lag	AS	1953085	1953100	
aroc (3.1E-3)	AGCTTGGCAAAATACACTTCAC	GAATAGAAATTCGAATAG	GAATAGAAATTCGAATAG	lag	S	1810915	1810930	
citD (3.1E-3)	TAGCTTCAATCGCACCTTCCAATAC	CGCAATCGCTTGGCCATA	CGCAATCGCTTGGCCATA	lead	AS	1280819	1280834	
ysgC (3.1E-3)	AATGTATTAAGCCAGCCACTTCAC	GCGCAATTCGCGCGGAAT	GCGCAATTCGCGCGGAAT	lead	AS	1870118	1870133	
yijC (3.1E-3)	TTGCTAAACAGCAATTTTCATAAC	CGTCATCTTCCAGCATCACC	CGTCATCTTCCAGCATCACC	lead	AS	962933	962948	
citF (3.0E-3)	GCGCTCAAGATGACCGCTCAAGAC	CAATCATAACCTTACGCT	CAATCATAACCTTACGCT	lead	AS	1210134	1210149	
ycgE (3.0E-3)	CTGAACATATGTTCCACCCACATAAT	CATTTGGAAACCTGTTGA	CATTTGGAAACCTGTTGA	lag	AS	265242	265257	
yvdF (3.0E-3)	TTATTTCGCGCAATTTGCTCAAGAC	CACTCGTCAAAGCGCTAA	CACTCGTCAAAGCGCTAA	lag	AS	2138104	2138119	
als (2.9E-3)	CCAAATCAACGGCTGCTGAGCGAC	CATATTTCAATTTCTCTG	CATATTTCAATTTCTCTG	lead	AS	1201884	1201899	
ycjC (2.9E-3)	AATCGATCTGACACCTTCTCGGT	CATCTTCAAGTCTCAATTC	CATCTTCAAGTCTCAATTC	lead	AS	292573	292588	
glnQ (2.8E-3)	TTTTCATACCGCTGAGAACCTAC	CAACCATTTGAGGCTCRAAG	CAACCATTTGAGGCTCRAAG	lag	AS	1819568	1819583	
feoB (2.7E-3)	CGGACAATAATCATGGACATTC	CAAAAGTAAGCAAGGAA	CAAAAGTAAGCAAGGAA	lag	AS	190731	190746	

yhcA (1.4E-3)	GTGACGCAATCGCTCTTCATGAC	GCTTTATCAGATAAGCT	lag	AS	721505	721520
ptnC (1.3E-3)	GAAGATGAGTCCATTTCCAGAAC	CAACAGAGCTTGGAGGCT	lag	AS	1764021	1764036
glnP (1.3E-3)	GGGACATTCATGGGAGTTCATTCG	TAAATCTGGCCCTTGTTTC	lag	AS	1817470	1817485
noxB (1.3E-3)	AACTTTATCCGTGGTCAATCTTCAC	GTCGAGGAAATGTCCTTTC	lag	S	842595	842610
trpD (1.3E-3)	TCCACCCACCGTTCATATCACTTCAC	GCCGTCCCGCAGCAACCTC	lag	S	1498901	1498916
noxB (1.3E-3)	GTCGCAATGCTACTGCAACACCCAC	CAACCGATGACACCAATTCG	lead	AS	841329	841344
intergenic (1.3E-3)	CCCTCTGGCTCCGCTGCACTTCAC	GCCGCACTGCACATATTTT	lag	.	2016727	2016742
yqiA (1.3E-3)	ACCGCGCTCAAGCCGGCACCCATTC	GCACACAAAAGAAAGAC	lead	AS	1681716	1681731
murA1 (1.3E-3)	GTTCCGACGAGCCCTAATCAACCCG	CAACGAGCAAGCCCTACTGT	lead	AS	313400	313415
fhuR (1.3E-3)	CTTCTCCAACTCTTTAACCAGAT	CGCATTTGAGGGTTCAGTA	lead	AS	330533	330548
asnB (1.3E-3)	GTTCCGTAACAAATTCGCCACTTCAC	GGCATATTTTCAATCAAT	lead	AS	356847	356862
rpoC (1.3E-3)	GAAACGAAAGTTTTTTGACTTCAC	CGAGCACTCAAGTTTCAAC	lead	AS	1857655	1857670
menD (1.3E-3)	CAAGAACTTGAGCATCCACCCCTTC	CAAACTTTTTTTCTACTCT	lag	AS	736927	736942
pstC (1.3E-3)	TCAGTTTCGAGCAATTCACACTTCAC	AACGAGGGGGTTCCTGGC	lag	S	1773284	1773299
ydiC (1.2E-3)	AAGAAGATAAAGCCAGCAATGCAC	CAATAATAATTCATTTGGATT	lead	AS	385240	385255
tgt (1.2E-3)	GATTCACGACCTAATCTTCACAAAC	CAGCTCTGCAACCAATTC	lag	AS	155934	155949
L200140 (1.2E-3)	GTTTCGACCGAATTCGACTTCGCTG	CATTAATCCCTTTCGCCATGG	lag	AS	126575	126590
hrcA (1.2E-3)	ATAAATGCAATTTGTTCTTACTTCAC	CACTCCCAAACTTATAAAC	lead	AS	977222	977237
intergenic (1.2E-3)	CAATTTAATGATGCTTTCATTTTC	TATTTGTTAATTAATCACTGAT	lag	.	1712489	1712504
ybaI (1.2E-3)	CTCGGACCACTACACATACATAAC	CTTTTGAAGTTCAGGATA	lag	AS	110048	110063
als (1.2E-3)	CTCTTTCGCTCATGACCACTCAAC	CATTTGCGGGCTTCCTCA	lead	AS	1200572	1200587
kinB (1.2E-3)	TGCTCAAAAGCTGTGTTCTCTGAC	TAAATCATCAGCGCGGAA	lag	AS	1459925	1459940
intergenic (1.2E-3)	ACTCCGATAGCTTTTTCACCTAAC	CATGACTTTTGGTAAAGG	lead	.	1838537	1838552
gidB (1.2E-3)	CCCTCGAAAGTTCGCTTTCATTCAC	GGAGGAGCTGAAGATTTTC	lead	S	1381124	1381139
dexA (1.2E-3)	GCTTGATAAATCAGAAATATCATAAC	CATTAATAATCCATTTGGCGA	lead	AS	1736522	1736537
dtpP (1.2E-3)	ACTAACCAAAAGCACCTTCACCGAC	CTCGAGTCCCGTCAAGAG	lead	AS	705591	705606
glnP (1.1E-3)	CCGACATCATTCCTCAGCATGTC	CAGACTGAACACAGCTCAAC	lag	AS	1817828	1817843
citF (1.1E-3)	GCTGCTTTACCGTCCATGCCCTTGG	CATTTACCCATTTCCGTCAGC	lead	AS	1209507	1209522
xerD (1.1E-3)	CATACAACTCAGGAAATTCCTTAAT	CATTTGGATGATTAATTTGA	lead	AS	1310409	1310424
feoB (1.1E-3)	GCCCTTCGAACTTCGATGGTCATAAT	CTAAGCTCCCATTTCCATG	lag	AS	191636	191651
cydA (1.1E-3)	TTTGATAAAGCTGAAATTCAGCAAC	CACAAAACCAACAGTTACA	lead	AS	708282	708297
citB (1.1E-3)	CCGATAATCTGTTGCTTACTTCAC	TTAATCAACATTTATCTGT	lead	AS	669535	669550
uvrA (1.1E-3)	GCAATAGTCATTAATTCCTCCAAC	CCCTCCGACTGTGAACTGA	lead	AS	1888140	1888155
yudR (1.1E-3)	TCAGTTCTGATAGGCTCCTTCAC	CTTTAATAATTTGCGCT	lead	AS	2038474	2038489
ysdA (1.1E-3)	CTCGCATGATTCGCACATACATTC	CTCAATGCTGAABATTAATA	lead	AS	1834288	1834303
pbuX (1.1E-3)	CGAGCAACAGATTCACAAACACAC	CAAGGACAACTGGTAAGCC	lead	AS	1160591	1160606
purA (1.1E-3)	GCTGTTCTGAAAGCTTACTTCAC	CTGCGGTGAACTGGCCAT	lag	S	2029214	2029229
ansB (1.1E-3)	CTGTTTTCGATTCGATTTTTCAGAC	CAACATATTCGATTAACG	lag	AS	743480	743495
plsX (1.1E-3)	TTTTCAGTCTTTCACCAATCTCAAT	ATTTGTTTCAACCTGCTAATA	lag	AS	72013	72028
citC (1.1E-3)	GCCTAATCTGATTAGCATTCATGAC	CACTCGCGCGGATTTTTC	lag	AS	1207190	1207205
yrfA (1.1E-3)	TTTGACATAAATCAGAAATCTTCAAT	CGATATTCATTTATAGGG	lag	AS	1750155	1750170
busAA (1.1E-3)	CAGCAATACCTTCTTCACTCCAAC	AATCAACCGGAATTTGAC	lead	AS	1474728	1474743
ysjA (1.0E-3)	CTTGATGGATGACATTTTCCACAC	ACCAACACGACAAACATA	lead	AS	1891247	1891262
sdaB (1.0E-3)	GTGTATCAACTTCTAAATACATAAC	CGCTTTTCCACCTTAGCT	lead	AS	843991	844006
pcrA (1.0E-3)	TACCGCAACCAAGCTCCGCGATAAT	CAATAAGTCCCGCTTCTGTA	lead	AS	1133849	1133864
ymdE (1.0E-3)	AAATGCCCTAAGTCAATTCATAAT	CATTTCTGCGCATTCATCAC	lag	AS	1238993	1239008
pacI (1.0E-3)	TTTGATGATCCCTGTTAATCATAAC	CACATTCGCGGATTCGATCA	lead	AS	677844	677859
yrfE (1.0E-3)	CAATAACCAAGCAACCAATCATGAC	CCCATGATACCAACCAATA	lead	AS	1759959	1759974
busAB (1.0E-3)	TGAACAGCTGCACTACACCCGAC	CTAAGCCAGGCCCCCAAT	lead	AS	1473732	1473747
ydiB (1.0E-3)	TTTGCTAGCCCTCTTACACTTCAC	CGAGAGCTTTGAGAAAGC	lag	S	383788	383803
yniH (1.0E-3)	TTCGCCAATTTACGACCTCTTCC	ACTCGTACCAAGCCCAAT	lag	AS	1387926	1387941
ldhX (1.0E-3)	ACTGCGCAGAATCAGCTTCTCTTC	TAAATAATTCGCTTCTGTA	lag	AS	1143148	1143163
dacA (1.0E-3)	TTAGAAATTTGACTAATTCATAG	CATATCTGAAATTCGAAAC	lag	AS	2356064	2356079
ywaI (1.0E-3)	TATCTTTACCAAGAAATTCCTCAAT	CACTTTATTTCCGATTTTC	lag	AS	2209257	2209272
ywiA (1.0E-3)	TCPTGCGCAATTCAGCAACTCTCT	CAATATTTACCCGGATTTAC	lead	AS	2280352	2280367
yrjD (989.1E-6)	TTTCTTTACCAATTTTCCACTTCAC	CATTTGGTTCGAAATTAACA	lag	AS	1793542	1793557
yweE (984.5E-6)	TAAATCACGACATGCTCATTTTC	CAACGGTCCGCCATTCAAAA	lag	AS	2247499	2247514
intergenic (976.0E-6)	GACCCCTTCADAAATTCCTATGAC	TCCCTTTCCACAAAGAAA	lead	.	1210567	1210582
ykiF (975.7E-6)	TCTAATACAAACCAATCTTCAGAAC	TCAAGTTCCTTGTGATAAA	lag	AS	1087045	1087060
yuhY (971.4E-6)	ATATCCAGCAAGGCAGAAACATTC	CATTTCTCAAAATTTTGGT	lag	AS	2077632	2077647
thrA (968.9E-6)	ACTTTTCGCGGATTCACACTTCAC	GGTCTCACTGAAATTTACT	lag	AS	747685	747700
citG (967.4E-6)	GCAATTCAGCTTCACAGACAAC	CGTACTCTCAGGAACCTCC	lead	AS	1210681	1210696
birA2 (953.2E-6)	GTAAATTAAGCAATTTCTCTCTG	CGTCTAATTTAGCATCTTT	lag	AS	1973041	1973056
aroH (943.5E-6)	ACTGAGCGAGCCCACTTCATAGT	ACTTACAGAACTCATCAAC	lead	AS	1280932	1280947
intergenic (941.5E-6)	AAATAATTCATTTTTCATTCAC	TCTGATTTAACCATGCTCA	lag	.	2355772	2355787
yudH (937.4E-6)	CTATAAAAGCCATATGCCCTTTC	CCCTCACCCTCCACATCT	lag	AS	2035315	2035330
yiaC (935.3E-6)	TCATCGTTAGATTAACATACAGGC	CGCAATCTTGGCATTTGTA	lead	AS	802688	802703
queA (934.9E-6)	TAAGCCGCAAAACCAATTCACCGC	CGCAAAAGCAGCGACTTA	lag	AS	1617701	1617716
intergenic (934.7E-6)	CAAAAGCTTGTATTTTTCACCTTC	TATCGTCAAAATTTTAC	lag	.	1562466	1562481
ysjD (925.9E-6)	TTTATTACCTTGTGACGCCACTTCAC	CTGCTTACCAACGATAATCC	lead	AS	1893720	1893735
yriB (925.7E-6)	AAATCATAAACCCCAATCCGATC	GTTCTTAAATCTTCAGTT	lead	AS	1786925	1786940
clsB (917.3E-6)	GAAGCCAAATATCTCTCCGCAATC	CATATCATTTTATATAAA	lead	AS	1188127	1188142
yeaC (913.3E-6)	TGCAATGACCTCATTTACTTCAC	GCACATCTCTCTCGAAT	lead	AS	405707	405722
typA (909.9E-6)	ATTTGACAACTGCAATTCACACGAC	CAACAAACCACTTTATC	lead	AS	2093418	2093433
fbxA (902.0E-6)	TCACCCCAATGACCAACTTCAC	ATTCACAGGAGATGCCCTT	lead	AS	1979895	1979910
pbuX (893.7E-6)	AAATGACCAAACTTCTGCTCCAGCC	CATCTCTTCCACCAATTAAT	lead	AS	1160642	1160657
yecE (885.8E-6)	TTTCAATCAAGATTTACATACATAAC	CAAACTCTCTTTCGATTA	lead	AS	427531	427546
trmE (884.6E-6)	AAAACCAAAATGCGAATTCCTCTT	CAACCAAGGGTCTCGAAT	lag	AS	2327788	2327803
pycA (880.8E-6)	TCGTTTACACCGCATTAACATCTT	CTTCTGTTAAACTCATTTTC	lead	AS	666290	666305
fadh (875.8E-6)	CCGCGGGACATTCATTCCTATCT	CATCGGCAACAGCTGCTT	lag	AS	654992	655007
llrC (867.9E-6)	ATTTTTCCTTGGTCCACCACTTCAC	CATTTCCAGCAAAAGAAAG	lead	AS	1805025	1805040
deoD (858.1E-6)	ATATGACAACTCTCATTTACACAAAC	CAACAGTCCCAACAGAAAT	lead	AS	957096	957111
fabD (857.2E-6)	GCATATTCACCCCTCAACTTCAC	CCCAATACATTTCTGTC	lead	AS	783367	783382
clsB (849.2E-6)	AAATATAGTCTTCCATCCATAAT	CATTTTAAATAAACCCTT	lead	AS	1188106	1188121
L200130 (847.7E-6)	TTTGATTAAGATCAAACTCTCTTC	CCACCTGCAACAGAGTCA	lead	AS	1980938	1980953
intergenic (843.7E-6)	CCAACTCTCTTCTGTTGTTATTTT	TATTTTAAATAGTTCTCT	lag	.	2275138	2275153
apbE (842.3E-6)	ACTGACCAATTTGTAATATCATAAC	CTAATCTTTTACTGCTGAATA	lead	AS	1124691	1124706
yagB (842.2E-6)	CGTTCATATGCTCAACCCATGTC	CATTCATTAATTTTATCAG	lag	AS	67086	67101
intergenic (841.1E-6)	AGGAAATTTACTCAGCCACTTCAC	TAAACAGTCTGCTGATAA	lead	S	970097	970112
rplM (839.1E-6)	AGTATATTACTCAGCCACTTCAC	CCAGTGGATTCGAAATCAG	lag	.	2346912	2346927

ylgC (837.8E-6)	TCAGCTAAACCTGTATCTCAAGCC	CAAAACAAGTACGGATC	lag	AS	1162425	1162440
yehI (833.8E-6)	TATTCATGATAGCCCTCATCATAT	GCCGCACTAAGCCCAATA	lead	AS	279650	279665
yijE (825.2E-6)	TATGATAAGATACATTTCTCTC	AGCGCATGAAATTTGCTCT	lead	AS	897434	897449
tgt (824.8E-6)	TCCGCTTAAGARAGTTCACGTC	CCATCAATGGCTCTGAA	lag	AS	156150	156165
ssbB (811.3E-6)	GAAGTCCCTCCATACCTTTCAC	GCCGAGATCTACTTCCGA	lead	AS	2274356	2274371
fbaA (804.1E-6)	ACAATATGTCCATCGTACTTCAC	GGGGTTCGGTATCCCTCG	lag	S	1979644	1979659
yjgC (802.2E-6)	TCAGTAAATTTATTTAAACATTT	TGCTTTGGCCAGCAATCC	lead	AS	963079	963094
dexC (800.1E-6)	GTCACCGTAATCTCTCCCATAT	AAATACAGGCACCTCTGG	lead	AS	1737262	1737277
ptsI (799.5E-6)	GTAGATGGATCAATATTTTCAC	CACTCAATCCCTCAACAGC	lead	AS	121312	121327
pbp1B (794.1E-6)	TTGGATCGCAGCATTTATTGCAT	CCCAATTAAGCTGAAAT	lead	AS	393516	393531
intergenic (793.8E-6)	CCGCGCAAAATTCACCAATGAC	CAAGCATTATTCAGTCTG	lead	.	2012509	2012524
intergenic (787.6E-6)	TAAGAACCAACTTCATATCAAAC	AACCATGGTACTTTTGG	lag	.	1931070	1931085
citF (784.9E-6)	TATTCAGTCCCTCAATACATAAG	CCAACTCAATTTGGTGC	lead	AS	1209546	1209561
argR (775.8E-6)	CAATTCGGCAACCATGGCTCAAC	CAATTTGTCGCAATAACC	lag	AS	2117884	2117899
relA (767.0E-6)	TTTGTGTTCCCTCTCAACTTCAC	GCCGATCTACTTCCGTA	lead	AS	108880	108895
uppF (766.9E-6)	AAGGTAAATCTGGCAACTTCAC	GCTTACCAACCAATAATA	lead	AS	2275479	2275494
intergenic (762.6E-6)	AAGGCTAAAGCCTTATATCATGCA	TATTTCCAAATTTTATT	lag	.	1706685	1706700
gshR (760.9E-6)	TTGGCTGACCGCCTTCTCCGCAAT	CACTAAATCTCTTTATGT	lead	AS	864313	864328
flolI (758.3E-6)	GCTTCGGCCATTGCTGTACTTCAC	GTATTTAGCAGTGGCTTT	lead	AS	746840	746855
asnB (757.2E-6)	GTATCTAACTGCCATATCACTTCAC	GGACTGCAAAAGTACATC	lead	AS	356922	356937
yrfE (755.7E-6)	TTGATTTTAAACCATTTTTCATACT	CAAGAGGCTGTAATTTCT	lead	AS	1759098	1759113
yxas (746.0E-6)	TTTGTATTAGTTTCAATGACCAAT	CATGATGGTACTTTCAT	lag	AS	2301202	2301217
menF (745.8E-6)	CTGCATAAGCATTAATTTCTTTCTC	CAATCAAAAGCCGAAACA	lag	AS	738243	738258
menD (742.6E-6)	CAAAAGGGAGATCATCGACTGAC	CATGTTGTCGTTCTCAAA	lag	AS	737101	737116
pbuX (735.3E-6)	CAAGAATTCAACTGATATCATGGC	CAGCAGATTAAGCTTAATCT	lead	AS	1160419	1160434
citE (733.2E-6)	TTTCCATTTTCACTTCAGCTCTTC	CATCATAGCTGCTGTTCA	lead	AS	1208386	1208401
yljF (730.6E-6)	GTTCGTTTCACTCTAATAGCATAAC	TGCTTCAACACTTCCCAT	lead	AS	1196804	1196819
noxB (724.8E-6)	CCAGCTAGGCTCAATGACATAAT	CAATGCTAATACCCCAATG	lead	AS	841599	841614
ynbC (723.1E-6)	TAAGATAAAGCTCAATCCATAAC	CAACATTAATAAAGTAAACC	lead	AS	1311441	1311456
ysiaI (717.3E-6)	TTGGACCCATGATTTCACTCCCAAC	CATCTGCTTAAGCTGAAC	lead	AS	1882158	1882173
hemI (711.6E-6)	AGTCAATTTTCTGCTCACTACTTCAC	TTATAGCTCAAGTAAGTC	lead	AS	1608810	1608825
lysO (708.4E-6)	CCAAATGCAAAAGCCAAAGCAGGT	CAACATCAAGCCGCCATA	lead	AS	369852	369867
optC (697.2E-6)	CTGATTAACACAGCTCAATCAATAT	CAATCTTGGAAATCAAAC	lead	AS	348745	348760
argT (694.2E-6)	TCGTCCGACTTCACTGTTCTGCT	CTAAGCACTTCCGCAAC	lag	AS	2117915	2117930
ylcC (690.3E-6)	TGAAAGTGACAGCTCATCTCATTCG	CTCAGGCTAACCTCTCATC	lead	AS	1130988	1131003
dacB (690.1E-6)	GTTCGGTTTACCTGATTTCACTTC	CTTATCTGCTGTAATAGCT	lead	AS	976126	976141
noxA (687.5E-6)	ACGACTAAATATCAATCTCATACTC	TATTTTATCTTATCTAC	lead	AS	840184	840199
panE (685.1E-6)	CCATCTATAAGCGTTACTTCATTCG	CACTTTAAGGCAATTA	lead	AS	1358181	1358196
clpC (681.5E-6)	ACAATTTGCTTTTCCCTCACTTCA	GTAGAAGATGGATTTGGTC	lag	S	630146	630161
ytdB (680.9E-6)	ATATCTAGCAGATTTCTTTTCAGAT	TATTTCTAAGCTATCCAGC	lead	AS	1934966	1934981
yqdB (680.0E-6)	CGAATTAATCTGATTTTTCATAACT	CATTTTCTCTTCAAGTGG	lead	AS	616221	616236
L200159 (674.0E-6)	CTTGGCGTTACCAACCTACTTCGG	CTCTGCCAAGCCCGTGG	lead	AS	2363650	2363665
glnP (665.5E-6)	GAAGATTAATGAGCACTACCAATAT	CGAAACTTCTTTCGAGC	lag	AS	1817888	1817903
recD (660.7E-6)	TAGGCTCTTCCATTCGCTCCCTTC	GGCCACCCGTTGTGCATA	lead	AS	1797401	1797416
scrR (651.5E-6)	GCGGAATATCATTGGTTTACTTCAC	AATGGCTCAGAGCAATGGT	lag	S	1518450	1518465
hpt (650.0E-6)	ACATCTAGCATTTATTTTACTTCAC	CACTGGATTTGCTCCGCC	lead	AS	25358	25373
alaS (638.3E-6)	TTAGCTTCAGCAACATTTACTTCAC	TGGCGATTAAGTGTAGAGA	lead	AS	1778652	1778667
htraA (635.8E-6)	GTAGTGCTTTGATAGATTCCTTTTC	CTCCAAGCTGCGATGGCTCC	lag	AS	2204392	2204407
yjgC (635.1E-6)	GCACTAGCAACCTCAATACCTTCAC	CCGTTAATTTCTTGACT	lead	AS	962423	962438
lepA (628.7E-6)	TGCAAAAGCCCGAGGAACAACAAC	GGATTCGAAACCAAGGCC	lead	AS	1118394	1118409
rpsM (628.4E-6)	CGTTTGATCTTATGTCGACTTCAC	GCCGAAGGCTCTTCCGAG	lead	AS	2153631	2153646
yagB (625.5E-6)	TAAAGAATCTGATTTTTCCTCAAC	CATACTCAAGTCTCTTAC	lag	AS	66735	66750
ybeH (625.4E-6)	GATGATTAATCCCTTCCGTCATAT	CAATTAATAGCTCAAGCA	lag	AS	143096	143111
intergenic (624.6E-6)	AAAAGCTCAAAAGGAGCACTCACT	TAGCTTAATTAGCTAGTG	lag	.	820084	820099
ilvD (621.5E-6)	TCGATGCTCTGCACTCACTTCAC	GCTGACCAAGCAATATCT	lead	AS	1246083	1246098
pepQ (603.2E-6)	AAAGACAGTCTTCAATCCCAACCC	TCTTCCAGGATATAATA	lag	AS	1698129	1698144
efp (601.2E-6)	GTTTGATGACTTCTTCCATAAC	GCGGAGCACTCTTCCCA	lead	AS	691670	691685
Intergenic (594.1E-6)	TTTGACTGAGACTCACTCTCTCC	TCTTACTTTCAATCAAGCT	lag	.	2276493	2276508
yqbr (590.7E-6)	TTACAGATTTATGCAATCACTTCAC	CACTACCTGGTACTTTTAA	lead	S	1619709	1619724
gidC (579.4E-6)	CCAGAGCCAGCTGATTCATCACTG	CCCTTTCATGCTCAATGG	lead	AS	1257813	1257828
copR (575.7E-6)	TTGCTCCCAAGTCAATTTTCAAT	CATCTTCCGAAACAATGG	lead	AS	845396	845411
citR (570.7E-6)	GCCAAATTCGCGCAAGTTCATCTC	TATTCATAAAGTAATATA	lead	AS	1206676	1206691
yoaB (569.0E-6)	TTTCTGGTCAACCCTTATCAATAT	CCCTTAAAGCCGGCTTT	lead	AS	1404130	1404145
choQ (557.7E-6)	GGATCAACCTTTTCAGCACTTTTAC	CCATTTCAACGACCTCAGT	lag	S	865510	865525
yseI (557.7E-6)	ACAACCCGCTGACCAATTACATTTAT	CATTTTCAAAATATCTTT	lead	AS	1849919	1849934
ygaB (548.0E-6)	ATTTCCACTCAATTAATATCTCGAT	GATTAACCACTTCATAAGC	lead	AS	602141	602156
malF (539.1E-6)	AGTGGAAAAGGCTTTTCCGATAT	CCCCGGAAACTTGAGC	lag	AS	1740960	1740975
parC (537.4E-6)	TCAGCTACATCAACCGTACTTCAC	ACGTTCAATTTGCTTCTCA	lag	S	1012443	1012458
yrgH (536.8E-6)	AAATGAGCTAATTTCTGGTCCCAAT	CAATGATTAATCTTCTGTC	lag	AS	1769355	1769370
ykiF (535.2E-6)	AGCCGCTTTAGCTTTTAAACAGGC	GTATTTCTTCTTCCGAGTAA	lag	AS	1087227	1087242
ps105 (530.7E-6)	AAGGCTCTCACTCTCTCATCTTCAC	ACCTTCCAGCAATAAAGGC	lag	AS	37893	37908
yuhE (521.7E-6)	AGTCCCTCAGTCTTATTTTCACTTC	CAAGGATTAAGGCTCCAA	lag	AS	2073300	2073315
yfjF (512.1E-6)	CTTCAAGTCACTTCAATCTTCAC	TGCAATGATTTCTGGGC	lead	S	599610	599625
leuA (511.8E-6)	ATTTGATGTTTCTTTGCCACTTCAC	CTATTCAGAGAAATATA	lag	S	1240133	1240148
nrdD (499.2E-6)	TCATAGTTTGTGCTCCCTACTTCGA	GCTTAAGACCACCTTTGAG	lead	AS	271457	271472
kdgR (492.7E-6)	TTTCTTCCAGGACCAATTTCACTTC	TGAAATTTTCCCTGTAAT	lag	AS	1680250	1680265
pepF (492.5E-6)	TATTTCTTACCAATAATCCGTAATA	CTTCTTCTGCTTTTTCAC	lead	AS	1783848	1783863
rplC (486.0E-6)	ACAGTGATTTCTGCTCTTACTTCAC	CCCTTCTGAGTCTTTCGA	lead	AS	2169681	2169696
comFA (482.4E-6)	TCAACCTGTCAGCCCAAACTTCAC	TAAAGCCGCACTCAATAAA	lead	S	1097125	1097140
topA (477.7E-6)	AAAGCATTAATTTCACTCTCCGCTG	CAACAATTAAGTTTAAGGC	lead	AS	1255147	1255162
yveC (470.5E-6)	ATTTCTAAACCTTCAATCAAGGGT	CAAGGTTAAACTGATGAT	lag	AS	2143864	2143879
yeeB (465.5E-6)	TTTCTTCGATCAATTTTCTCAAT	TACCATCTCAAGCGCTAG	lag	AS	443161	443176
ybcG (460.1E-6)	CTTGTTCATCTTTCATTTCCATTT	CAATCATGAAATTTTACT	lag	AS	123139	123154
yqcA (456.8E-6)	TAAAGCTCAATTCAGCGACTTCAC	AACGCTGATAGTAAATTA	lag	S	1624880	1624895
gyrB (456.5E-6)	CCGATTTTTCAGTGTCACTTCAC	GCGCACCTGCTGCAAT	lead	AS	929120	929135
yeeE (453.5E-6)	TTGTCAATATGTTGATAACCAACA	CCAGGGCAGAAATAATAG	lag	AS	443427	443442
ybcH (450.7E-6)	AAAGATATGATGTCCTCACTTCGA	TGGTTTCCGAAATTAATA	lead	S	123666	123681
ylaD (448.7E-6)	CCAAATTTGAAGTCACTCTTCAC	GCCCAACCTGGCCCAAA	lead	AS	1105705	1105720
mscL (446.4E-6)	CCAAAGGCTAAGTCAATCACTTCAC	CACTTAATAAAGCTTTAT	lag	AS	2170604	2170619
L200065 (444.5E-6)	TGAAGATAAAACCTCAACAATTCAC	TGAAATTTCCGCTTTCT	lead	AS	1745995	1746010

ymdE (437.5E-6)	CTTCAGAGACCTTGGTCAACCTTCAC	GGAGGATGTCGCCACATACCG	lead	S	1238775	1238790
yqg (432.8E-6)	TTGGACCGCTTTTCTTTCATAAC	CAATGGCATAATCCCATAC	lag	AS	1664100	1664115
yebE (428.7E-6)	TATCTTCACCAATTAATTCRGTCC	CTAATATGATGACGTTATC	lead	AS	417456	417471
glnQ (427.9E-6)	CTTCTTCGCCCAATTTTTCATAAC	GGCTAGACAGGTGACCAACC	lag	AS	1819582	1819597
purI (424.0E-6)	ATATCCAACACCCCGCTCCCTTCAC	CAAGCCCAATCAAGACTTG	lead	AS	1576156	1576171
yveH (422.8E-6)	GTACCTTAATATGTTCCGCCCAAC	AGGTGTGTTTTCACAGCA	lead	AS	2146197	2146212
yrge (418.4E-6)	GGATTTTCAAACATCACCTCCAC	ACGGCCATCCGCCCTCCAA	lag	AS	1765349	1765364
intergenic (408.9E-6)	TCACCAAAAAGTCAATTAATTCAC	GAATGAGCCATTAAGAAATA	lead	.	1213718	1213733
intergenic (405.0E-6)	TAGTTGCCAAAATCTCTCCATTTTC	CTTTATACCTGATTAATA	lag	.	1766419	1766434
clpB (402.4E-6)	AGGTGAACGTGAAATTAATTAATTC	TTGCCAGAACACTGCATC	lag	S	1567554	1567569
infB (401.7E-6)	TCTTCACTGATCCACCTCCCTTCAC	CCGAGTACACCGGATTC	lead	AS	777180	777195
pi301 (401.6E-6)	TTCTGCAGATACATCCCACTTCAC	GAAGATTAATAAGATTT	lag	S	1414528	1414543
pbp2A (400.0E-6)	GCCTGTCATCCACAGTTCCTTCAC	TTGCAGAACCAAACTTA	lead	AS	2178563	2178578
gntR (391.4E-6)	GTATCTGAAATTAACAAAGCAAT	CTTCGCTCCGTAATTTTGC	lag	AS	2272040	2272055
ymjE (387.4E-6)	CTGTATAGATTGTCARAGCATAT	CACAGCAATCTCAAAAAT	lead	AS	1297570	1297585
purC (385.1E-6)	GATGAAATTTCCCTGATTAATTCAC	GTCTCTGGAGCCGAATGG	lag	S	1577698	1577713
radA (383.9E-6)	TGCATCAATCTCCAGTCCATTCAC	CTAACCTGACCTTACGAGCC	lead	AS	2149928	2149943
ydbA (381.9E-6)	ACAATTAAACCTGTGGCAACTTCAC	ATGCAGCCAGCACTCTAC	lag	S	311295	311310
yhdB (381.5E-6)	GATTAATCCACCCGCATAGCAATTC	CACAAAGCCGGCGAGTNG	lead	AS	731959	731974
vacB2 (379.1E-6)	ATGGTCAGAACTGATTAATGCAAC	AATAGCAGTGAATTAATAA	lag	AS	1227759	1227774
gyrA (368.5E-6)	AAGCGCGAAATCTCTCTCTTCAC	AACCGTAAACCGAATTTGT	lag	S	1123616	1123631
glgR (367.5E-6)	CCATCATCTCTTACCAAACTTCAC	CACCAATCTTACTTCAAC	lead	AS	700438	700453
topA (364.2E-6)	TCTAAATTTGCTCAAGCACTTCAC	CCATGACCTTCTCTTCT	lead	AS	1256226	1256241
ycjB (360.6E-6)	TTTTCCAAATTAATGTTACTTCAC	CACGATTAATCCGTCAGC	lead	AS	291861	291876
intergenic (355.9E-6)	ATAACCGCTACCCACCTTATTCAC	AATAGCATTTTCTCATCT	lead	.	1781130	1781145
aspS (352.2E-6)	TTTTCGGAAAGCAATTAATTCAC	GGATATTCCTTTCCAGC	lead	AS	2040291	2040306
pepA (349.6E-6)	TAGTCCGAAACGATCCCTCAAAAC	CACAGTCCGCTTCAATTC	lag	AS	394928	394943
yrjI (345.7E-6)	CCGTCAACAACTTAAGTCAATTC	CCATTTAGAAATCAACAA	lead	AS	1799737	1799752
yahI (345.5E-6)	ACAARAAGCTGCTTTCATTCAGAGC	TAGTAACATCCAGTTTAG	lag	AS	78146	78161
yyal (345.4E-6)	CCAACTATATCTTTTCTCTTCAC	GCAGCGACCCGCTCCAGC	lead	AS	12154	12169
ywjI (344.8E-6)	TCTCCCAAAACCCCTTCACATAAC	CACATAGCCCGCTTAGGAG	lead	AS	2299894	2299909
apl (341.8E-6)	TAATCCCTAAATCACAACTTCAC	TGAGAGCTAAGAAATCAAGA	lag	AS	719117	719132
ygeA (341.2E-6)	TCACTTAACAGAGGTTTATCAAGAC	TCCGTTCAATTAAGTCAA	lead	AS	647001	647016
rliA (340.4E-6)	TTAAAGAAGACATCATCCATAAC	TCCAGAGCCGCTTTCATTT	lead	AS	1728090	1728105
ddl (335.8E-6)	AACCTAACATCTTTCACAACTTCAC	CTGGAAAGCCCTCGAAGAC	lead	AS	341407	341422
gltB (335.2E-6)	AAGAAGCCGTTGACAGTACTTCAC	AGGTAACAGCAAGAAAT	lag	S	1318756	1318771
prsa (331.9E-6)	AACTTGCAGCGCTCTCTTTCAC	CATGGTCAAGCCGACACGAC	lead	AS	826166	826181
yfic (328.7E-6)	AGCAAAATCTTAATAATCCGATTC	CTCCCAATCCCTTCTTTC	lag	AS	582039	582054
yhnc (328.0E-6)	TCTGTCAGTGAAGCAACTTCAC	CCATATCTTTCGCCGAAC	lead	AS	1375536	1375551
yseF (319.5E-6)	CTTCAACAAAGATTTCAACCACTCC	TGCTTGAAGGACTTTCGA	lead	AS	1846805	1846820
gidA (317.5E-6)	ATGGATTAACATGGCATAAAGGCAC	CATATTTAGATTAATTCGCT	lead	AS	1916173	1916188
foeB (317.2E-6)	TAAGTGCTACTTTAAACAACCTTCAC	TAACTCTTAAATTTTAAAG	lag	AS	191685	191700
vacB1 (316.8E-6)	GAAAATTAATCCGCACTTTCATTCAC	CAATCTCCGCTTATCCGCA	lag	S	968723	968738
ahpP (314.9E-6)	TCAAACGATTCATAATCCACTTCAC	TTTGAATCTTAAAGTGAAT	lag	S	336370	336385
reox (313.1E-6)	ATATCATCATATGAAATGCTTTCAC	TGCGCAAGCCGCTGTGTAC	lag	AS	2260546	2260561
clsB (312.1E-6)	CCATTAATAGCCCTTATTAACAGAC	CATTTATAAATCCGGAATA	lead	AS	1188583	1188598
gntR (311.2E-6)	CCCGCGGACTCTTCAAAATTCAC	CCGCTCAAGCTTATCTCTG	lag	AS	2272093	2272108
ygiI (310.7E-6)	GTGTAACTGCTCTTTCATTCAC	CACGATTAAGCCATGGTGT	lead	AS	688022	688037
cydB (307.4E-6)	AGCAATAAGCAATACAACTTCAC	CAGCATTAAGAACAAAATA	lead	AS	709788	709803
tyrS (302.1E-6)	CCGTGAACCTAAGCTGACAACTTCAC	AGCCAACTTATTTGGGC	lag	AS	390395	390410
ykhD (301.5E-6)	AAATCAATAAGCAATAATCCAGAC	CGAGATTCGCAACCAAT	lag	AS	1072414	1072429
busAB (298.6E-6)	TCCGTTGGTTTACACCAAGCCATAAT	TCTTCTTAAAGCCAAAGGA	lead	AS	1473829	1473844
glnP (298.6E-6)	CCATTGGACCGCAATTCCTAAGC	CAATGTTAAACATTTCAAT	lag	AS	1818260	1818275
intergenic (293.2E-6)	TCAAGAACTCCCAAAAGAGTGACCC	CACCAATTAAGAACAAAGT	lead	.	426554	426569
yrdB (287.3E-6)	GGAATGGAAACTGATTAATCAATTC	TACATTAATTAATTTGAT	lag	AS	1748835	1748850
yljB (286.4E-6)	GGCATGAGTATTAATAATCAATTCAC	GATTTCCATAAGATTCAG	lag	S	1183134	1183149
pmsX (284.1E-6)	TCATCATAAAGAAATCAATTCATTC	CAAAATTAAGCAATTCACTGC	lag	AS	1594083	1594098
ysfB (283.9E-6)	CCCTGACGACGTTTACCAATTCATTC	TGCTCGCAAAAATTCGCA	lead	AS	1851913	1851928
aroB (283.2E-6)	ACAACCACTTTTCGTTTACTTCAC	ATCCCGAATGATTAATTC	lead	AS	1814163	1814178
frdC (283.0E-6)	TTAAGTTCAGCAGCAGAACTTCAC	CCAGATTAACCATTCATTC	lead	AS	1138856	1138871
cysE (273.6E-6)	GTHTCCCAATTAATAATCCAGAC	CATGGTCAAAATTAAGACTCC	lead	AS	1920560	1920575
grpE (270.4E-6)	TTTCCAAAACGCTTACCAACTTCAC	CGAGCTTACTCTCTCTGAG	lag	S	978363	978378
intergenic (269.5E-6)	AAATCAATTAATAACTAGACCCAG	TTATTTAACAATAAAGT	lead	.	228110	228125
tra983F (269.2E-6)	GCGACGAGCTTTCATTTCTTCAC	CGCCCTTAACTCCGGATAG	lag	AS	1556004	1556019
dut (267.2E-6)	CGGTCAATACATGTAAGCACTTCAC	CTGCCCTCAATTAAGCCCTT	lead	AS	181327	181342
carB (267.2E-6)	AGSGCTTGAACGCTTTTACCACTTC	GAACCTGCCAATAATCAAA	lead	AS	1399755	1399770
lepA (262.4E-6)	GCCTTGAAGCGGCTGTCCAACTTCAC	CTTGAGGGCGAGGACTTTC	lead	AS	1117932	1117947
rpcC (261.0E-6)	GATTTTGTAGTGGGAGAACTTCAC	CACGGTGAATCCACTTTC	lead	AS	2166108	2166123
ycfD (257.7E-6)	AAGCGCTAATCATCTCCCTTCAC	CATTAATAAGACGAAAGGC	lead	AS	252972	252987
intergenic (256.9E-6)	AAATCCATAAATTTCTTACACTTC	CTATATTAATGATTAATAAT	lag	.	2071740	2071755
hslO (256.3E-6)	CGGTCCCTCTCTCTTTCACAGTTC	AGGCTGAATCCCAAGGAA	lag	AS	2034366	2034381
atp (254.9E-6)	CGCACCTGATACATCAATATCAGGA	TTACGTTTCCAGACCTTCG	lead	AS	1822759	1822774
yhch (253.6E-6)	ACATCAAACTCCAAACGCTCATTC	CAATGTTTCTCCCAAGAC	lead	AS	726528	726543
pepT (253.1E-6)	AAAACATGCAAGAAAGCTTCCAGGC	CTTCGGTTTTTCTCGGACG	lead	AS	1877702	1877717
ylhB (248.3E-6)	GAGCAAGCGGTGATGATCCAGGAC	CAATAATAATTAATTCGGG	lead	AS	1173578	1173593
intergenic (246.6E-6)	ACATCCAAATTTTCTTTCATAAAA	CATCTCCAAATTTATTTAA	lag	.	2208612	2208627
apl (243.5E-6)	GAAATGGTGGGAACTATGCTCAAT	CATTAATGAGAAAGGCAACA	lag	AS	719582	719603
pspA (243.5E-6)	AGAGAGGACTGCTTATACCAATTC	CCAGAACCTGATTAATAAT	lag	AS	2304554	2304569
hemN (240.9E-6)	TATCCATGATATATTCATACATTC	CGCTTTTAAATCTCACTTC	lead	AS	1153916	1153931
ymcF (239.7E-6)	TTCTTCCTCATCAATCACTTCAC	CATTAATTCCTTATGAAATA	lead	AS	1223916	1223931
proS (239.7E-6)	TCTTTCATTAATTCACAACTTCAC	CTGTCGCAAGATTTAAC	lead	AS	2196190	2196205
rplL (238.7E-6)	AAAAGATGTACCACTTAACTTCAC	CTGATCTGACAGCCGTTGG	lag	S	753478	753493
fhs (238.7E-6)	GCTAATACTCTGCTAATAACCCAGC	CGGACGCTCCACCCCTAAT	lead	AS	960069	960084
yrfE (237.9E-6)	TCTTGAAGTTTACTGCTCCATAAT	CTCCCTCATCATGAGC	lead	AS	1759268	1759283
ispA (235.9E-6)	CCATATCCAAAGATTTGACCCGAC	CATTCCTAAGAAACCCGAA	lead	AS	881180	881195
L200149 (232.9E-6)	CGACCGCTCACCCCTTACATTCAC	CTTCCGGTTTTACGAGAG	lead	AS	2219499	2219514
hsdR (232.7E-6)	GTHTGATCACTAAGTCCACACTTC	CATCAATAAATAAATAACAT	lead	AS	641728	641743
glgA (232.0E-6)	CAATATCTAGAAATTAATTCATTC	ACCCCTTTTTTCTGACTTC	lead	AS	698612	698627
rdrB (229.4E-6)	TCTTTGCCAATTTGCAATTCCTCC	CATGAAGCTGAAAGCAATTC	lag	AS	1331986	1332001
yqr (226.9E-6)	TTTGAACTGAACTCAATCACTTC	CGGCCAAACACTTATTC	lag	AS	723823	723838

pi148 (226.7E-6)	CTTCCTGGAACTAATGACTTCAC	TCATGCGCCAAATAAGGG	lag	S	482353	482368
yjbb (225.2E-6)	AGGGAGATAAATGCTAACCGAACA	CATCCACCTGCGAAGAGA	lead	AS	911052	911067
ps315 (222.8E-6)	GAATACATTATCTTTTACTTCAC	TCACAATAAAGGAAAGAC	lag	AS	2023936	2023951
yqgg (220.9E-6)	TCATACCAATGGCATATCCACATA	CCCGAGCAAAATTAATCG	lag	AS	1664082	1664097
pi201 (220.2E-6)	CTATACCAATATCTCTTATTCGAC	ATCTGTTCTGGGCTTTTGG	lag	AS	1037038	1037053
intergenic (219.7E-6)	CTTCTATAAATTAACCACTACTCAC	TATCTCTCTAATAATTCAG	lag	.	565296	565311
hsl0 (216.9E-6)	ACAAAACGAGCACTACACTTCAC	CAGTCTGAGCTTTTATATA	lag	AS	2034601	2034616
ptcc (216.4E-6)	CGCTCAATTACTCTCCCTACTTCAT	AGCCAGTGGAACTTTTACT	lead	AS	421115	421130
ycjM (216.3E-6)	GTATTCTGCTCCCAACAACTTCAC	CGAAGAGAAATCAATTTGG	lag	S	299901	299916
celB (212.9E-6)	ACCTCGATCTGAGCTTACTTCAC	AGTATATTATTTGGGTCGCC	lag	S	178101	178116
ytce (212.2E-6)	ATACACCCGCTTCAACAGTGCATC	CATTTGGAAAGAAATTTTA	lag	AS	1929213	1929228
ftsH (211.5E-6)	CTATAGAAAGGACTCTCTCTTCAC	CGGCAACAGCCCTTCCAAG	lead	AS	26613	26628
yljG (211.5E-6)	TTTCCCTGATAGACTTTTACTTCAC	CTTCTGTGAAATTTTAT	lead	AS	1197636	1197651
dlte (211.4E-6)	CGCTCGTTTGTGCTAACAACTTCAC	CATAGGGGCAAGTAAACA	lead	S	144478	144493
topA (209.0E-6)	TCAAGCTCTGGTAACTCATCAAC	CATAGAATACTTATTTT	lag	AS	1256515	1256530
citC (200.9E-6)	CATATCCCACTAATAGAACCCCTCC	CATAGCACTTACCATTTTTC	lead	AS	1206875	1206890
mutS (197.6E-6)	TTTCTTGAACCTTCAATCACTTCAC	CGCTTTTCTTCCAACTT	lag	AS	1692486	1692501
rgpA (197.2E-6)	CCACCAATTGTCCTCCCTACTTCAC	GCATCTCAAAATTAACCA	lead	AS	202268	202283
intergenic (194.6E-6)	ATCGTAAACAAATCACTACTTTT	CATCTTATCAAGTAAATA	lag	.	172797	172812
trxB1 (194.5E-6)	CCAAAACCTTTTCTACTTCAC	CGCTTTTAAACCTTTTATA	lag	AS	966106	966121
yveC (194.1E-6)	AAGTACCGACCTTGTAAACAGGAC	CACAAACGTAACCTACGAC	lag	AS	2143762	2143777
trmE (194.0E-6)	CGAACATGGCAATTCCTCTTCAC	CAGCGCTTCCGCAATCTCC	lag	AS	2327785	2327800
yvaA (192.3E-6)	AATTCAATTGCTCTTAACTTCAC	CATCCAAACGACTCTGGAA	lag	AS	2100504	2100519
ptnc (191.7E-6)	ATAAGGTTGATACCATTCATTAAC	CACGGGCAACAACCATCC	lag	AS	1763862	1763877
yeac (191.3E-6)	ATAACAAAAAGATGGTCACTAAC	CATCTTAAACGTAATAAT	lag	AS	407850	407865
ldh (189.0E-6)	TCTCATGCTTGGCATTTACTTCAC	CTAAATAACATTTAATCTCC	lag	S	1370008	1370023
ylcG (188.5E-6)	AGATTTCCTTCACTCACTTCAC	CCCAATGCTCCGCAATCTT	lead	AS	1131775	1131790
yciA (184.1E-6)	CCAAATAAAGATATTCACTTCAC	AGTCCCTSCAAATAGTCT	lead	AS	280687	280702
ytjF (183.8E-6)	AGATGATATAGCACTGACATAAC	CATCTTTCTGCGATGATG	lead	AS	1997999	1998014
intergenic (182.9E-6)	GGCTGATTAAGCACTTTCATTTT	CATTTAGGCACTTTCAT	lead	.	1880376	1880391
L200155 (182.9E-6)	TAAACGTTGCTGGGCTTATTCAC	TCCGCTGGCTTTTACACC	lead	AS	2342297	2342312
dpsA (182.1E-6)	TTATAGTAATTAACCTACTTCAC	CTAAATCACTTCCGCAATG	lead	AS	2102154	2102169
pepN (180.9E-6)	TTAGTTGCAAAACCACTACTTCAC	CAACGATTTTCTTTTCC	lead	AS	302960	302975
yogI (180.4E-6)	CTCTTACTACTCGGGATTCCTTCAC	TGATCTGACCTTCTGTTAAC	lag	S	1467652	1467667
gyrA (179.5E-6)	GGTGTATATTTACTCATAACTTCAC	CGACAATACGTCGGGATTT	lead	AS	1121968	1121983
recX (177.9E-6)	AATGTATAAATCGTAACTTCAC	TATATCACTCATATGAAA	lag	AS	2260573	2260588
pspA (177.3E-6)	CATGCACTGCTTCTCTATAAT	TCCGCAAGAGCCATCAAG	lag	AS	2304308	2304323
ycgD (176.4E-6)	TAGCCATTTGTTGATTAACCAAC	CAACATGGCAATTTAAG	lag	AS	264664	264679
intergenic (174.5E-6)	TTGCTATATTTCTGTCACTTCAC	TCCTTTCAAACTAAAT	lead	.	1171031	1171046
pi149 (174.1E-6)	AAAGTACCTTATCATGACTTCAC	GTATGCTCCAAAGTAA	lag	S	482537	482552
noxB (173.9E-6)	CCACACAACCTGACTCAACTTCAC	GACCTGACAGGACCGG	lag	S	841457	841472
hom (172.9E-6)	TCTGCCAAGCCGCAATTCATTC	CATGAACAGCCGTAATAC	lead	AS	1171374	1171389
ybjJ (172.0E-6)	GCATTGGCTTTTTCCTCTTCAC	CAATATTAACGCCACAAT	lag	AS	193714	193729
era (170.0E-6)	GAAATGTAGCCGATTTACTTCAC	AAATGGCTTCTGTAAGT	lag	S	355476	355491
tral077B (168.4E-6)	TTTCTTACTACCGCTCTACTTCAC	CTTATCTGAAATATGAT	lead	AS	139417	139432
yniD (167.6E-6)	TCTTCTCAAGCGGTTCACTTCAC	CCCTTAAAGCTCAGAT	lag	AS	1389428	1389443
intergenic (167.1E-6)	CGTTTCTTCTCAATTTGTTAATC	CATTAATCAGGCAATTC	lag	.	146664	146679
ykiF (165.9E-6)	ATGCAACGGCTTTTCTCTACTTC	CAATAGCCATTTACTTCA	lag	AS	1086658	1086673
yqbr (165.8E-6)	ATTACATTTAGGATATAGTACTTC	ATACCTCAATACCATCA	lag	S	1621593	1621608
yuhI (164.7E-6)	TTAGCAATTTCACTAATATCAAT	CATGAGGCACTCAATTTCC	lag	AS	2077908	2077923
yrjA (163.1E-6)	TAAATGACGTTTCACTTCCCTCC	CATGCTAAATTTATCTT	lag	AS	1790453	1790468
rheB (158.7E-6)	CAAGCTCATTTAGGGCTCTTCAC	GTCACTGACTCAAAAT	lag	S	416038	416053
vacB1 (158.5E-6)	GCPTTTTTCATTTTTTCACTTCAC	GTCTAGCACTAACCCGCG	lead	AS	968864	968879
secA (156.8E-6)	CCAAACCAACCGCGGCTCTTCAC	GACTGACAGCAATGCTTC	lead	AS	116558	116573
pi252 (153.7E-6)	AAGGTAACTTACTCAATGACTTCAC	GTATGGCCCTCAATAGTAA	lag	S	1070851	1070866
ywfe (153.6E-6)	TGAGTTGCGAGCTTGAAGACTTCAC	CGCTCTCAGGGTCAACAGA	lead	AS	2253509	2253524
kupa (153.2E-6)	GCAAAGCAACCAACCAATCTTC	GGTAAATTAACCAATTT	lead	AS	609826	609841
adhE (152.2E-6)	CCGGCACTGAGCAAGCACTTCAC	CAAGCAAGGACTCTTC	lag	AS	2231413	2231428
intergenic (151.0E-6)	TCTACTTAAAGATCTCTATTTCAC	ATATAATAAAGCCGTTTC	lag	.	767701	767716
carB (149.3E-6)	ATTGCTATCCACTTCACTTCAC	CTTATTAAGAGCAATCAAC	lead	AS	1399233	1399248
rexB (148.9E-6)	TGCTCTGGAGTTTATTTACTTCAC	TCATCTCGCCCTCTCTTC	lead	AS	6410	6425
rexA (148.9E-6)	TGCTCTGGAGTTTATTTACTTCAC	TCATCTCGCCCTCTCTTC	lead	AS	6410	6425
L200139 (147.0E-6)	TAGCTCAGTCTGTAGACCACTTCAC	TCGTAACGAAGGGCTCACA	lead	S	155265	155280
ytca (146.1E-6)	ATGGAAATTCATCCCTCATTTTCAC	AAATCATCTAATTTTATAT	lag	S	1919841	1919856
ybfE (145.3E-6)	CTTGGAGATTGTAGCCCAATTCGCG	CCAGAAATAAGCCGCGTCA	lag	AS	158953	158968
rplU (143.4E-6)	TGCTTCCCAATTTTTCGACTTCAC	CAACAACAGTCCGCCCTTC	lead	AS	1090794	1090809
nadr (143.2E-6)	TGAGCACTACCTCATTTACTTCAC	CAACAAGCAAGCAAGAC	lead	AS	2067466	2067481
accC (141.8E-6)	GCAACTGTACCACTCTCAATTCAC	GAGCTGCAGATTAATCT	lead	AS	787362	787377
intergenic (141.1E-6)	CACACATTTCTCTCATTTCTAGAT	TATAAATCAAAACCAAT	lag	.	1765147	1765162
pacA (140.5E-6)	TCATCTACTCATCTACTGTACTTC	CAATATCTGACGCCACTTC	lead	AS	1149790	1149805
clpC (138.9E-6)	TTCATGGAAAACTTCTCGACTTCAC	GCCTGATTTGGGCTCCTTC	lag	S	631578	631593
ropC (138.0E-6)	ATTTCTTCTGCTTTTAACTTCAC	CGAATGCTCAGTAACGAAT	lead	AS	1860730	1860745
yugD (136.4E-6)	CTTAACTCTTCTCACTTAACTTCAC	CGCTTAACTTCCGCTTC	lead	AS	2069632	2069647
yseE (133.9E-6)	AGAAAACAAAATCTCTCACTTCAC	AGCCCTTTGGCTTAAAT	lead	S	1845334	1845349
ygiI (133.8E-6)	GAATGCATAATCGCACCAAGGAC	CAAGCCCTTTCTTAAAT	lead	AS	687818	687833
yvdB (133.8E-6)	CCAACTCTTAAATCCACCACTTC	ACGGTAAAGCTTAAAT	lead	AS	2132376	2132391
yrbA (133.2E-6)	CAGAAGTAATCGCATTTACACCACT	CAATAATAAAGTCCATCA	lag	AS	1710889	1710904
ldh (132.5E-6)	CGCGTTGTAGCTTCAAGTACTTCAC	TTGCACTGCACGTTTCCG	lag	S	1369738	1369753
yoiC (129.4E-6)	CGTGGATCTCAGCAGATACTTCAC	AGGTGGTACAAGTCTACT	lag	S	1486078	1486093
uxac (128.3E-6)	AGTTGTAATGTTGCACTCTTCAC	CTTGAATCAGACCCATCT	lead	AS	1673326	1673341
pepF (128.1E-6)	AAGTATCTACTTGTAAACTTCAC	CGGACAGCACTCTTCAAG	lead	AS	1783404	1783419
ytdF (126.8E-6)	GAAACTCTCTTTTCAAACTTCAC	GTGCAAGTAATACCATCAAC	lead	AS	1937543	1937558
ymjE (126.6E-6)	TCTTCACTGATTTTCTTTCAC	CATTTTAGAGTTGAAATA	lead	AS	1296165	1296180
ypiA (125.6E-6)	ATTCTGGAGTACCTCATTAATTCAC	GAACCGCCATTTTGTTCG	lead	AS	1580173	1580188
yvdD (125.2E-6)	GTCTCTTCTGCTTATATACTTCAC	AAATATCTGACCCCTTTCAC	lag	S	2134298	2134313
noxB (125.0E-6)	TTTCTCATCACTATGCGACTTCAC	GCCTTGGAAATTAACCTT	lead	AS	843000	843015
xylH (124.4E-6)	AAAATGCTCTGACCACTTACTTCAC	CATCTCACTCTTAA	lead	S	568328	568343
intergenic (121.8E-6)	AAATATAGTATGAAAACCTACTTC	CGGTCCCAACTCTTCTTC	lag	.	1247526	1247541
yxca (121.2E-6)	TAATCACTCATTTTCACTTCAC	CATATCAACCTAGTCC	lead	AS	2323787	2323802
chiA (121.1E-6)	ACGGCATTTCTGCTTTTCACTAAC	CTGTCTCCACAGCCGCAAT	lag	AS	2027406	2027421

yngG (120.4E-6)	CGCCCTCGTCCGGAGAGCACCC	CAATACCTGCAAAAGATTAG	lag	AS	1368216	1368231
ysjD (119.8E-6)	TTGTCCGCACTTCACTGCTTAC	CAGAAATCCCAAAACTT	lead	AS	1893729	1893744
yhdA (117.1E-6)	TATTSACTCGAGCCGATTCGATAC	TTGCCATACCAGCTGGAT	lag	AS	731594	731609
secA (116.6E-6)	TGACGTTGCGCTAATATAACTTAC	GTTCCTCAGGATGACATC	lead	AS	118226	118241
glpB (115.5E-6)	ATAAGATCCGTTACTGAACTTAC	TCGTCCCACTCCGCCCAAA	lag	S	1271169	1271184
rpoB (114.1E-6)	TGTCATGTACATGATTAACCTTAC	CACTCGGTTGATGATAAAC	lag	S	1861379	1861394
arcC (113.9E-6)	GTTAAGCATGCCAGATTTACTTAC	TTGCAATCGGCAAAACTT	lag	S	1752051	1752066
nifs (113.8E-6)	GCCGACGGAACTTCCACCTTAC	TTATAGAGAAAATTCGG	lead	S	1928168	1928183
dnaJ (113.8E-6)	TTCCAGCAAGATTTTCAACTTAC	ATTCCTAGAAAGCTCCGGA	lead	AS	2307464	2307479
rplD (113.0E-6)	ACCGAGTCGTTAGGTAACTTAC	CGCTCTCGAACCACTCTTG	lead	AS	2169254	2169269
ygfC (112.4E-6)	TTTAAACAGCCATATAACGCGGT	TGCCCTTTTCGGTCGATAG	lag	AS	654295	654310
tkk (112.3E-6)	AGCAAGGCACCCGTTAACTTAC	AGCAGGCTAGCCAAAGAT	lag	S	1670095	1670110
glnA (111.5E-6)	CCCTTGATTCGGTACCCCTTAC	GTGCCTTGCACACTCGTGT	lag	S	2282652	2282667
ywfH (109.7E-6)	GCTCCACCCGTTCCCTACTAC	TTGTATCACCAGGATGAAA	lead	AS	2259140	2259155
xynB (109.4E-6)	TTTAAAGACATGGAGCCACTTAC	AGTCCATTCGCGCAACCA	lag	S	1544759	1544774
yqeL (108.2E-6)	TCCGAGGATGTGTTCAACCTTAC	GTTCCTCCGGGCACTCT	lag	S	223614	223629
ygdA (108.1E-6)	ACTTTTCGTGCAGAACTTACTAC	AGCAATGTAATGCTTCAAT	lag	S	632597	632612
relA (107.1E-6)	TCCCTGAATCCACCTTCTTAC	GCACTCCACAGTTCATAG	lead	AS	108310	108325
yfgG (106.7E-6)	CAAGATATATGCCGGCTCAATAT	CAACATTCGCACTCTCTGAT	lag	AS	564603	564618
ackA1 (106.2E-6)	AAATATGGCGCTCATGGAACCTTAC	ACATGTCCTGCTTCAAGA	lag	S	2090551	2090566
leus (105.8E-6)	TTTCCGCTAGTGTATTAACCTTAC	GTTCCTCCCTAATACAAA	lead	AS	827793	827808
yrgH (105.8E-6)	TCTAAAGAAATGAGCTAATTTCCG	CCCATCATAGAAATCTTTC	lag	AS	1769316	1769331
carB (105.4E-6)	CCACCGAGTATTTTTCACCTTAC	GGACATTAAGCCATTTTC	lead	AS	1398537	1398552
llrB (104.3E-6)	AGSGTCAAAATTTCCGATCATO	CAAGCAATAAAATTTT	lag	AS	1458179	1458194
glk (103.8E-6)	ATGCTTTTAGAATGCACCTTAC	CATGTCCTAATGCTGCTT	lag	AS	2101334	2101349
yqab (103.7E-6)	CTAAATATCAGGACACACACATA	CAATATGACCCCCCATTC	lead	AS	1603759	1603774
hds (102.3E-6)	CCGTTTAGAAATGTGCAACTTAC	CCACTACGTTCTTCCCA	lead	AS	646049	646064
adhE (101.2E-6)	CCCTACATCTCCCTTCTTAC	GTGCTTCAGCTTTGTAGAT	lag	AS	2230834	2230849
snf (101.0E-6)	ATTATATATCAGAGCATACTACTC	CAGCGAACCACCGTTCCT	lead	AS	2121892	2121907
ptcC (100.8E-6)	AACGTTGCCGCTTATTCTACTTAC	TTGCTTCCGACGAGCAAT	lag	S	421301	421316
ptcB (100.3E-6)	AACCTTAAAGATTTAATCACTGAC	CATACTTACCAAAATTC	lead	AS	1177294	1177309
L200152 (99.6E-6)	CCAGTCGCTTACTCACACCTTAC	CCGCTCATAGGATCGTCA	lead	AS	2263088	2263103
ykjK (98.8E-6)	CAAGTCCAACCTTACTACTCCAC	CAACTCTTCTTCTGCTT	lead	AS	1100315	1100330
cpmB (98.4E-6)	ACATCAACCAATTTTCTCCTTAC	GTATATCAACCCATGCGCC	lead	AS	198632	198647
yshA (98.2E-6)	TCTTTGGTGTATTTGCTACTTAC	AATTCGCTCAACATGAAAG	lag	S	1875454	1875469
rbfA (97.6E-6)	AGCTCATCAATTTTGAACCATAT	CAACAGATCACTTTCG	lead	AS	779168	779183
tuf (96.2E-6)	GAACTCAAGTTCGTCCACTTAC	GGATAGCAAGATTCAC	lead	AS	1929416	1929431
fadD (96.1E-6)	CCAGGCATACCCATCCCATTTAC	GGCCATTAGCTCTGCTA	lag	AS	655043	655058
yucC (96.1E-6)	TTAAAGCCGCGGTCACCTTAC	TTTGAAGATCAATTTTCC	lag	AS	2028169	2028184
yhfC (95.8E-6)	GGTGAAACGATTGAAATTAATTAC	AATTCGCTCAACATGAAAG	lag	S	755166	755181
yahA (95.6E-6)	AAGAACCACCTTCTCAACATTTAC	CATACTTCACTTGGTCA	lag	AS	72409	72424
recM (94.5E-6)	CCGACAAATCTCCGAAGCACGCC	CACCATAAATAAAGACAT	lead	AS	883236	883251
relA (94.2E-6)	TTACTTGATTCGGTTTAACTTAC	CTTCATCAGCTCTCGGC	lead	AS	108916	108931
ycjM (93.0E-6)	TCTAACCAATCCTTGGCTTCTTAC	TCACAACGGATATCAGCTG	lead	AS	300722	300737
dtpT (92.8E-6)	TGGTTCTTGGCAAGATTCACCTTAC	AAGCAACAGGCTCAAAAT	lag	S	705765	705780
ps311 (92.7E-6)	AAATAGGCAGCGCTTCTGACTTAC	AGCTAGTGAAGTCTGAGAA	lead	AS	2021054	2021069
nusA (92.4E-6)	TCGAAATCTTCTTCCACGACTTAC	CGTCCGATTAACCAATGAA	lag	AS	773993	773993
yvcC (92.4E-6)	TAACTGTAGCCACTCCTTCTTAC	TTATGATAAAGATTTACC	lead	AS	2124348	2124363
pfl (91.4E-6)	GTCATTAATGAGCTGCAACTTAC	TTGAGCTGCTCCATGCT	lag	S	658237	658252
rpe (91.0E-6)	TTTTCATATTTTCTCAACTTAC	CATTAAGCAACATATGACC	lead	AS	2003231	2003246
citF (90.5E-6)	TATCBAATCAATTTTAACTTAC	GATGATTAACAGCAAGCT	lead	AS	1210497	1210512
menE (90.0E-6)	TCCGCTTAGCCACAGGCTCAAT	CTGTGATTTCCAGGAGAGA	lag	AS	733083	733098
usp45 (89.7E-6)	TCTGACCTCAGAGTTCATTTAC	AGCAGGCTGAACCTTAAAGT	lag	S	2313993	2314008
yxfC (88.4E-6)	ACCGCATCTACTAGGTTTCAATAT	CATGAGGCTGATTAATGAA	lead	AS	2359357	2359372
leucC (87.1E-6)	CTCCGAACACAGCTCTCTTCTTAC	GTACGCTCAACCTGCTTGG	lead	AS	1242999	1243014
yeeC (87.0E-6)	TTCATGAGTCTGCAATGACTTAC	GTGGTGAAGCCCGCCACC	lead	AS	446315	446330
ptnD (86.8E-6)	TCGATATCAGCCCTGTTAGCACT	CTTCTCAAGGGCAAGAGT	lag	AS	1764360	1764375
ywaF (84.5E-6)	CGTTCTTGAATTTTCATTCGAC	CAATCTCGAAGCTCAAT	lag	AS	2205732	2205747
guaA (84.3E-6)	GGTTCCACGTTGTCCGAACTTAC	CAACAGGCTCAATTTGCTGC	lead	S	1517292	1517307
yeeF (83.5E-6)	TCAGAGATTAATTTCTTACTTAC	CATGGCTCAAAAATTAAT	lag	AS	445089	445099
hacC (83.5E-6)	TTGTAAAGCCCTTTAATCACTTAC	CTTAGGCTCAATGACACC	lag	AS	1378400	1378415
lacZ (83.0E-6)	TTAGGATCAATTTGTCAACTTAC	TAAACAACAAATTAATATC	lead	AS	2055873	2055888
yjdB (82.2E-6)	GAAATCTTGAATGTAAGAGGAA	CAATCTTCAACCTCCATC	lead	AS	933438	933453
atpH (81.8E-6)	ATGAAGCAACAGTAAATTAACAGT	CAATGAAAAAATCTCGGT	lag	S	1827415	1827430
thrs (81.6E-6)	TTTCATCATCTGGGAAATTAATTAC	TCTACTTAAAGGGTCAAGG	lead	AS	1987780	1987795
malE (80.4E-6)	TACCTTGGTAAGACTCTCTCTTAC	AATACTGACAGCTCAATTA	lead	S	1740226	1740241
zwf (80.1E-6)	TTGATTCGACTTAACAACACTTAC	GATTAATCTGCTTCTTCA	lag	AS	2301470	2301485
bgIH (79.8E-6)	TCCGCAATTTACGATTCGACTTAC	CTTAAACAGGAGTAAAG	lag	S	1490018	1490033
noxE (79.7E-6)	CTTTTGTATGCCAAGTACTTAC	TTGCTCAAAATTTGATGA	lag	S	397135	397150
ptbA (79.5E-6)	ATPTTAAATCGCGCTGAAACTTAC	CTGTAAAGGCAAAATATAGA	lead	AS	1491561	1491576
tenA (79.5E-6)	GCGATTTGACGGTACCTTCTTAC	TCCGATTCGCTTCAATCCA	lead	AS	1838849	1838864
yeeA (79.4E-6)	TGAACAAATTCGATTTGCTTAC	CGATCAACCCGCACTGCA	lag	AS	440775	440790
yeeA (79.1E-6)	ACTTTTCCAGCTTCAACGACTTAC	GTCCGCTTTTCTGTTGGAT	lag	S	441510	441525
cpo (79.1E-6)	ATTTGGGAAACCATGTAACCTTAC	TGGCCGTAAGCCCAAT	lead	AS	834569	834584
vacB2 (78.8E-6)	CTTCTTAAATGAGAGAGCCCTACTC	ACCGGCTACACCTGCTTAT	lag	S	1226984	1226999
yyaL (78.6E-6)	ATATTATCAGCTTCCCTACTTAC	CTTCTGAAACATGCTTAC	lead	AS	11749	11764
yljF (78.4E-6)	AAAGCCGCAACACTTCCGCGGGT	CAACCAATGACTACAGG	lead	AS	1195850	1195865
intergenic (77.3E-6)	AGCTTGGACTAGAAATTAATCTTAC	AAATGCTTACTCGTAA	lag	.	1980330	1980345
intergenic (76.6E-6)	ATAGACGAATTTCTTTTCTTCTTAC	CATTTGGTACCTCTTTTAA	lead	.	1293417	1293432
ymjE (76.0E-6)	AAGTCCGATCTTCACTTCCATCTTAC	CAATAACAGTACCACCTAG	lead	AS	1297164	1297179
cysS (74.5E-6)	GAATCTTACGCTGTTCAACTTAC	TTTATAGCCCAAAATTCGA	lag	S	1918936	1918951
oppD (74.2E-6)	TCCCTCAATTCCTAATTAATCTTAC	CACTCTAAGACTTAAATC	lead	AS	1910699	1910714
intergenic (74.0E-6)	AAATTAATGCAATATGACTTCTTAC	AGCGCACACTTCAAAA	lag	.	1830442	1830457
hom (73.8E-6)	ATTTCATAAAACAGCATTCATAT	ACCTTGCACCTGGCCAAAT	lead	AS	1173717	1173732
intergenic (73.7E-6)	TGGGACTTTGAAATACTCTTCTTAC	GGATGATAAATTAATAA	lag	.	47610	47625
trpS (73.5E-6)	AGACCGCTCAACAGGAACCTTAC	ATCCGCTCACTGATAGGCT	lead	S	68223	68238
serS (73.0E-6)	AGAGCTAAAATTCACCTCTTAC	ACTTCTAATGCTTCCGGAC	lead	S	1768329	1768344
kinC (72.8E-6)	GAGCGAATGCTTTCATTCGCA	TCAATGCTCTCAATAGTAA	lag	AS	402440	402455
dnaK (72.4E-6)	AGCCGCTGCTGGCCCTTCTTAC	TTGGAAATGGCTTCACTC	lag	S	979257	979272
nusA (72.2E-6)	GTTCGATTTCTTCCCATCTTAC	CCACGATTCATAATCATC	lead	AS	774845	774860

amyY (72.1E-6)	GCCGAGGCGCTTGA	CCACAA	AS	1733687	1733702
ptcB (71.4E-6)	ATTTTCGCTTTT	CTTTCATGAAGG	AS	419068	419083
yqfG (71.2E-6)	TTTCTGATATTT	TTGGTTGGAGC	AS	1659783	1659798
pts1 (71.1E-6)	TCAAAATAGATG	CAAGGTTGTTAC	AS	120832	120847
tra904I (71.0E-6)	ATTTGTTGGCTG	GGATGCGAGATA	S	2215294	2215309
yciB (70.9E-6)	TTGGTGAATTC	ACCGTGGCGG	S	290558	290573
purB (70.9E-6)	TTAGCAACAAT	CTTCCAGATT	AS	1688986	1689001
pgk (70.5E-6)	CAAGCTTACGAA	TCGGTGGAGAT	S	243525	243540
glyQ (69.6E-6)	CTCATTTGTTCC	TATCATAGCTT	AS	1101918	1101933
ymdC (68.5E-6)	TCAGAAATTTCC	AATCCGTAACA	S	1234116	1234131
yliB (68.0E-6)	GATTTGATTTTC	AGATAATCAAG	S	1181868	1181883
ilvC (67.6E-6)	TTAGTACCGCT	ATGTTCAAGGCC	AS	1249913	1249928
intergenic (65.9E-6)	TCATTTCTTCC	TTATGATGGCT	.	297420	297435
ylgC (65.6E-6)	GTGTTTAAAGCT	CATACAGGCAC	AS	1162306	1162321
racD (65.6E-6)	GTAGAACCTAA	AATTCATTTCC	AS	2309368	2309383
ypb (64.6E-6)	TTGGCGCTTCA	TCCATACAGCC	AS	1562082	1562097
trpB (64.3E-6)	GATTTGCTTTP	CCATATGAACT	AS	1495502	1495517
pycA (64.1E-6)	ATGTTATCTCT	AGCTGGTCAAG	S	664950	664965
pepM (63.9E-6)	GGTTCATAAAG	GATAGTGAATC	AS	303152	303167
ccpA (63.7E-6)	GTCCTTTCCT	CATTTCAACAC	AS	1696846	1696861
yfjB (63.5E-6)	GATTTTCAAA	TGCAGGAAAT	S	598934	598949
polC (63.5E-6)	TTGATTCGCT	CATTCAGCGCA	AS	2191543	2191558
yqgC (62.4E-6)	AACGATTCAC	TCATTCGGCTT	AS	1666094	1666109
pydA (62.2E-6)	TAAAGAACTTT	AAGCTTAAAGT	S	1593286	1593301
ilvD (62.1E-6)	CCACTTAAAG	GGATGTTTCC	S	1246820	1246835
gyrA (61.6E-6)	TCATCTTCAAG	CTAAGAACTG	AS	1123222	1123237
ykiG (61.5E-6)	CAAGTTCAT	TTTCATGCTT	S	1088003	1088018
yjgE (60.7E-6)	TTTAAATTA	CTTGAACCT	AS	964786	964801
trpE (60.7E-6)	GGACGAGCT	CGGTCACCT	AS	1500446	1500461
rbsR (60.2E-6)	CCATCCGCG	GAATGACTC	AS	1686674	1686689
ylbB (60.0E-6)	CGATATATATA	GTGTGACTC	AS	1113813	1113828
ydbA (59.9E-6)	TGATTTCTCT	CTTGATAACT	AS	312783	312798
ylgG (59.9E-6)	CAGATTAAG	CTTGAATTT	AS	1168308	1168323
rplC (59.8E-6)	GCAGCTTTT	TTGGTCAAA	AS	2169777	2169792
ynhC (59.5E-6)	TCCATTTTAG	AGTTCAACT	AS	1374723	1374738
pepN (59.1E-6)	GCAATTAAC	AGTTGACAT	AS	303201	303216
aroB (59.1E-6)	TTGATGAC	CTCCCGAGT	AS	1814295	1814310
glmU (59.0E-6)	GTTRCTTCR	CCCTCGTAA	AS	1951674	1951689
hsdR (58.9E-6)	CTTTGATAA	AACTTTTTC	AS	642226	642241
acca (58.9E-6)	GCAATATTT	TTTGTGAAC	AS	789638	789653
yshA (58.7E-6)	ATTTTTHCA	ATTTCTTGA	S	1875797	1875812
rplL (58.6E-6)	ACTTTGAAT	CAAGCCCTC	AS	1301775	1301790
leuS (57.9E-6)	TTATCCATC	CTGTCAGGA	S	827588	827603
ywjB (57.7E-6)	ATGAGGCTT	CAAAAGACT	S	2296014	2296029
era (57.3E-6)	TTGAACGCT	CTTCCATCA	AS	355313	355328
papL (57.2E-6)	AGGATTTAA	AAACGTCGT	S	1602930	1602945
gyrA (57.1E-6)	GCCGACATG	TTTGTCCGA	AS	1123879	1123894
ylcF (56.7E-6)	AGTAAATAA	TTTATATTC	AS	1128157	1128172
ylfB (56.2E-6)	AAATTCAA	AGATGACCG	AS	1152026	1152041
ilvH (56.1E-6)	GATTAATTT	TAATCAGAC	AS	1249451	1249466
pstE (54.4E-6)	TTTTCGCTC	CTGCTGCTC	AS	1775284	1775299
citE (54.3E-6)	CCCTTGA	CAAAAGCT	AS	1208696	1208711
uvrA (54.3E-6)	TAACTCTC	CCCTGGCA	AS	1886165	1886180
Intergenic (54.2E-6)	TGCTGAC	CAAGCCAC	AS	165032	165047
pdp (54.1E-6)	GAATAAAG	CTGAGCAAT	AS	1464552	1464567
valS (54.1E-6)	CCCTCTC	CCCTGCTC	AS	2249627	2249642
ytgG (53.6E-6)	TTTGTGAT	CTACTGATA	AS	1969240	1969255
aspC (53.4E-6)	GCTCAATC	AGTCTGTA	S	163533	163548
yhdB (53.2E-6)	GGAGTCGT	CAAAACA	AS	732748	732763
L200158 (52.9E-6)	AGCGCTT	ATCCCTCC	AS	2360508	2360523
intergenic (52.5E-6)	GGAAATC	CTGTTGCT	AS	1041037	1041052
frdC (52.4E-6)	TGATTTA	CAAGATCC	AS	1138793	1138808
nrdG (51.7E-6)	TAAAGTGA	CCAGCCACC	AS	272742	272757
bcat (51.4E-6)	CCATAAT	CTTTGGCAT	AS	1322017	1322032
apl (51.0E-6)	GTGGAGAG	ATCTTCAAT	AS	719594	719609
ytbA (50.9E-6)	TCAATCAG	CTGTCAGAA	AS	1913156	1913171
copA (50.6E-6)	TGAACAA	CAACCCCT	AS	846827	846842
ywff (50.2E-6)	GTCACAAA	ATAATTTG	AS	2255346	2255361
yebB (50.1E-6)	GAAGAGT	TATTTAG	AS	411411	411426
recN (50.1E-6)	ATAATAT	TCGATTTAT	AS	884734	884749
ybcC (49.8E-6)	GTGCATCAT	TAAACAGCAT	AS	122935	122950
yibB (49.8E-6)	TGACTTGAA	AGCAAGTAA	AS	813101	813116
pi229 (49.6E-6)	ACTAAAC	AGAGAAATA	S	1052899	1052914
ypdB (49.1E-6)	TCAGCAG	ATATTTT	AS	1532502	1532517
fusa (48.9E-6)	ACAACCA	CTCAGCTGG	AS	2354018	2354033
ydbA (48.0E-6)	TTGATTA	AAAGTTG	AS	311876	311891
intergenic (47.3E-6)	AAAACNT	TAGCAAGG	.	295167	295182
ysiE (47.3E-6)	TAAATAA	CACTTGTAT	S	1889135	1889150
pflA (46.7E-6)	ACGTCAG	AACCCACAT	AS	1880728	1880743
yoic (46.6E-6)	TTCACAG	AGCCAGAC	S	1486532	1486547
apt (46.5E-6)	TCGTATG	TGCTTCAAT	AS	623066	623081
intergenic (46.3E-6)	ATCAAAT	ATACTGCTG	.	1413891	1413906
ypjA (45.7E-6)	ATAATTT	TTTTGAT	AS	1590916	1590931
tuf (45.7E-6)	TCTTTGCT	CAATGCT	AS	1929629	1929644
galK (44.7E-6)	AATAAG	ATGCTTTT	AS	2061130	2061145
yhcH (44.1E-6)	CCAAATA	AAAAAC	AS	727005	727020
ohtC (43.3E-6)	TGGAAT	TTTAAATA	S	347900	347915
yldA (42.9E-6)	AGCACC	CGAACTCT	S	1132657	1132672
yliB (42.9E-6)	ATATTTCT	TCTTATCT	S	1182872	1182887
ydiA (42.7E-6)	GAGAAG	CTATGATG	S	381887	381902
lead	AS	1733687	1733702		
lead	AS	419068	419083		
lead	AS	1659783	1659798		
lead	AS	120832	120847		
lead	S	2215294	2215309		
lead	S	290558	290573		
lead	AS	1688986	1689001		
lag	S	243525	243540		
lead	AS	1101918	1101933		
lag	S	1234116	1234131		
lag	S	1181868	1181883		
lead	AS	1249913	1249928		
lead	.	297420	297435		
lag	AS	1162306	1162321		
lag	AS	2309368	2309383		
lead	AS	1562082	1562097		
lead	AS	1495502	1495517		
lag	S	664950	664965		
lead	AS	303152	303167		
lead	AS	1696846	1696861		
lead	S	598934	598949		
lead	AS	2191543	2191558		
lead	AS	1666094	1666109		
lag	S	1593286	1593301		
lag	S	1246820	1246835		
lead	AS	1123222	1123237		
lead	S	1088003	1088018		
lead	AS	964786	964801		
lead	AS	1500446	1500461		
lead	AS	1686674	1686689		
lead	AS	1113813	1113828		
lead	AS	312783	312798		
lead	AS	1168308	1168323		
lead	AS	2169777	2169792		
lead	AS	1374723	1374738		
lead	AS	303201	303216		
lead	AS	1814295	1814310		
lead	AS	1951674	1951689		
lead	AS	642226	642241		
lag	S	789638	789653		
lag	S	1875797	1875812		
lead	AS	1301775	1301790		
lag	S	827588	827603		
lag	S	2296014	2296029		
lead	AS	355313	355328		
lag	S	1602930	1602945		
lag	S	1123879	1123894		
lead	AS	1128157	1128172		
lead	AS	1152026	1152041		
lead	AS	1249451	1249466		
lead	AS	1775284	1775299		
lead	AS	1208696	1208711		
lead	AS	1886165	1886180		
lag	.	165032	165047		
lead	AS	1464552	1464567		
lead	AS	2249627	2249642		
lead	AS	1969240	1969255		
lag	S	163533	163548		
lag	AS	732748	732763		
lead	AS	2360508	2360523		
lag	.	1041037	1041052		
lead	AS	1138793	1138808		
lead	AS	272742	272757		
lead	AS	1322017	1322032		
lag	AS	719594	719609		
lag	AS	1913156	1913171		
lead	AS	846827	846842		
lead	AS	2255346	2255361		
lead	AS	411411	411426		
lead	AS	884734	884749		
lag	AS	122935	122950		
lag	AS	813101	813116		
lag	S	1052899	1052914		
lead	AS	1532502	1532517		
lead	AS	2354018	2354033		
lead	AS	311876	311891		
lag	.	295167	295182		
lag	S	1889135	1889150		
lead	AS	1880728	1880743		
lag	S	1486532	1486547		
lead	AS	623066	623081		
lag	.	1413891	1413906		
lead	AS	1590916	1590931		
lead	AS	1929629	1929644		
lead	AS	2061130	2061145		
lead	AS	727005	727020		
lag	S	347900	347915		
lag	S	1132657	1132672		
lag	S	1182872	1182887		
lag	S	381887	381902		

ykjB (42.6E-6)	AAATCCCGACGTTTGCCCTCTTCAC	CAACAGTGGCCAGGGAGGCTC	lag	S	1092491	1092506
malF (42.3E-6)	AACACCAAAATATATGATGATTCAC	TGGCAAGAGGAGGAGGCC	lag	AS	1740489	1740504
pi246 (42.1E-6)	TTACTAGAAATAGCATACCCCTAC	AGACATACCTTTAAATCGCA	lead	AS	1068667	1068682
pdhC (41.9E-6)	ATATCTCCCTTCATGCAATCCCTTAC	CAATATCAGGCATCGTGAA	lag	AS	61832	61847
dexA (41.7E-6)	CTTTCCCAATCAATGCAATCACTAC	CATCCGTAACACCGCCGAT	lead	AS	1736112	1736127
carA (41.1E-6)	TTGCATCAGCAGCAATTTGACTTCAC	CTCCAAATACATGGATAT	lag	S	1644318	1644333
gltd (40.6E-6)	GCAAAATCGAATTCACATGCTTCAC	GGCCGTAATTTAAATC	lead	AS	1315740	1315755
rpoB (40.6E-6)	CGAATGTAGTGTTCACGAACTTCAC	GGCTTTTTCACCAAGAT	lead	AS	1861909	1861924
yfgG (40.5E-6)	GCAACCCACAGATATTCACAGAC	CACCTTGGATCTCCATAA	lag	AS	564702	564717
yugD (40.5E-6)	ATTTGAAATCTCTCAGTGACTTCAC	CAGTAATCCGATTTCTCTCC	lead	AS	2069410	2069425
yljB (40.2E-6)	GTAATATCCAGGCGATGACTTCAC	ATCCAGTGGCTACTAACTC	lag	AS	1192125	1192140
leuC (40.2E-6)	GTTCGTAAGAACCTGTTCACACTTCAC	TTGTAACAAATCCAAAGC	lead	AS	1243302	1243317
relA (39.4E-6)	CCCTTTGGTAATCTTGGACTTCAC	CATTTGGAGGATGACADA	lead	AS	108400	108415
yneH (39.2E-6)	TCCGAAACAAATTTCTTCAAAAC	CTTTATTTGAAAGCTATA	lead	AS	1346233	1346248
bgIR (38.8E-6)	ATTTTCTCTCTTCAACAACCTTCAC	CTGCCTTTTCCCAATCC	lead	AS	1493676	1493691
gntC (38.8E-6)	ATATTTAGCTCCCTACTACTTCAC	CAAGCTTAAGCCACATAC	lead	AS	2268969	2268984
thiI (38.5E-6)	CCAGCGATTACACTTTCCTTCAC	CAAGCTTAAAGTGTGT	lead	AS	1612822	1612837
noxE (38.2E-6)	ATTTCTATCTTTTACAACTTCAC	CTACATTCGCCCTGCCCTA	lag	S	397469	397484
yjhd (38.2E-6)	TCTCCATCTCGTTCATCACTTCAC	CACCTTTTCCGCTTTT	lead	AS	972867	972882
dexB (38.2E-6)	TTTGTAAACCTGCTTCTCATTCAC	TGGTCCATGGATTCGGCT	lead	AS	1525229	1525244
fbxA (38.2E-6)	TCGATGGAGCACTTCACTTCAC	CAACGATCCCGCTCTTTC	lead	AS	1979853	1979868
yjgD (37.8E-6)	ATTTGCACTTTTGAATTCACACTTCAC	TTGCTTCCCTTCCGCTGT	lag	S	964023	964038
parC (37.8E-6)	TTGGCAATTTTTCTTAACTTCAC	GAACCTCGCTTTCATTA	lead	AS	1012281	1012296
intergenic (37.4E-6)	TATTTTCGAAATTCGACTTCAC	ATGGCTTAAAAAGGAAGA	lag	S	1212453	1212468
guaA (37.2E-6)	CGAATCCGCTTTCGCCCACTTCAC	CTTACTGGAAATCAGAT	lag	S	1517407	1517422
yqgA (37.0E-6)	GGTTTGTGTTATGTTAAACTTCAC	GTCTCTGATGCGTGAAGC	lag	S	1662192	1662207
butB (36.9E-6)	ACTTTAGTCCGCTTACCTTCAC	CTATAATTAATCCACCC	lead	AS	917656	917671
rsuA (36.7E-6)	TTTTCATACTTTTTCGACTTCAC	TCGGCTTCCGAGGCCACT	lead	AS	2326760	2326775
yniH (36.6E-6)	GAACTCCGAGCTCAGACCCCTGAG	CAACAGCTTCTTGGACATA	lag	AS	1387665	1387680
yvcC (36.2E-6)	CAAGCCGCAATTTCTTTCCTTCAC	ATGGGATGGAGCTCAATAG	lag	S	2127492	2127507
tra983C (36.1E-6)	TCAATCCCTTATGCCCCACTTCAC	AGCATTGTTTAAATGAACTC	lead	AS	958140	958155
ymcA (36.1E-6)	ACATTAACACTTCTCTACTTCAC	ATCAAGGGAATGTCGGCC	lag	S	1220304	1220319
pil46 (35.8E-6)	AAGTTCCGCGATGTTCTTCTTCAC	TCGCTCGAGGATATCAGT	lead	AS	481528	481543
rpsG (35.4E-6)	TACATTTGGATCTGCAAACTTCAC	GTTTGGGGCAGCATTT	lead	AS	2355006	2355021
yber (35.2E-6)	ATATTTATTTCCCAATCACTTCAC	TGGATTTGGAGTATTATC	lead	AS	149884	149899
ybeH (34.8E-6)	TCATTTATTCATTTTCCCTTCAC	CCGGGTGGGGCGGAAA	lag	S	142965	142980
apl (34.0E-6)	CGAAGAAACAAGATTTGTCATTCAC	CTCTCTTAAATCCATTT	lag	AS	719326	719341
trmE (34.0E-6)	CAAGCGGTCTCGAATCCGCSCTT	CTTACAAATTTCTGCT	lag	AS	2327760	2327775
acca (33.4E-6)	AAATGCTCTCCCTGAACCACTTCAC	CTGTGATGAAGCAATAAT	lead	AS	790082	790097
yudI (33.3E-6)	AAAAATGGAAATTCRAAACTTCAC	TTGGCAGCTCCCTCGAAT	lead	S	2036722	2036737
ctsR (33.2E-6)	GACGAGCAAAATTCGACTTCAC	AATTTGAGGATTCACCG	lead	AS	629551	629566
infB (33.1E-6)	TCTTGAACATTCATCTCTACTTCAC	ATCAAGCACTTCTGGTA	lead	AS	776862	776877
fusa (32.7E-6)	TATCTCTCTATGGGTGAACCTTCAC	TTGGACCTTCTGTTGACC	lag	S	2352871	2352886
ybat (32.6E-6)	CCAGCTAGTAAATGCTCTTCCTTCAC	CAATATTTCTGAGAACT	lag	AS	110171	110186
vacB1 (31.9E-6)	ACTTCCAAAACGCTCAATTCCTTGGT	CATCTGCTTACCATAAAT	lead	AS	967655	967670
pi214 (31.8E-6)	ATAATCTCTCAACTGATGGACTTCAC	AGGCTCCCAAGTCCACC	lead	AS	1044606	1044621
pepD (31.4E-6)	ACAAGTGTACAGGTTCTTCCTTCAC	CCATCTGATTTTCCACATA	lead	AS	1601649	1601664
yafB (31.3E-6)	ACAATTGCTAATGGCTTCTTCAC	CAACCATGCTAATGAGTCC	lag	AS	51093	51108
intergenic (30.6E-6)	ATTTATCAAAATTAAGAGCAATTTG	GCCTTTTATCTGCTCAGC	lag	.	420472	420487
pf1A (30.5E-6)	AGCGGATATTTCCCACTCAATTCAC	GCCTTTTAAATCTCCCAT	lead	AS	1880578	1880593
pi146 (30.4E-6)	ACAACCAAACTGGCTGGACTTCAC	ATGCTCCACTCTGCTCA	lag	S	479371	479386
hrcA (30.3E-6)	GATTTCAACACTTTGGAGAACTTCAC	TCGTAATTTGAAATAACG	lead	AS	977408	977423
yxbD (30.3E-6)	GCAGCTCAGCTTCTCTCTTCAC	GTCCCTGCGAAGCAATGG	lead	AS	2319286	2319301
truB (30.1E-6)	GTTCGAAACCAATGTAACCTTCAC	CTTCGTAAATTTTCCCTGC	lead	AS	1140585	1140600
yrjG (29.9E-6)	GAAATATTACGATTTTGAACCTTCAC	GTAGGATTTCCCTGAGC	lag	AS	1769976	1769991
feoB (29.3E-6)	GCTCTGTAAGTCCAACTCAACTTCAC	CCATCTCTTTTAAATTTGT	lag	AS	190202	190217
ptnD (29.3E-6)	GCCTCATCACTCGAGTTCAGCCAACT	CCCATTTTTCATTCCTGCTC	lag	AS	1764210	1764225
ycfF (28.8E-6)	GCCTGATGAAACCACTCAACTTCAC	CAAGAACCTTTGTTAATAT	lag	AS	257260	257275
L200150 (28.6E-6)	GGAAATTCCTACTCTCTCTTCCTTC	TCAGTCTACACAGTTCCTCA	lead	AS	2222501	2222516
yleF (28.4E-6)	AAATGATCTGAACTCACCTACTTCAC	TTATGATATAACTCAAAGT	lag	AS	1147802	1147817
y2hC (28.2E-6)	AAATCATGCCAAATTTAACTTCAC	ATAGCAACAAGTAGTGT	lag	AS	273862	273877
L200064 (28.1E-6)	AGAGTCTTTCTATCCGAACTTCAC	ATCCCACTTCCCAATTTA	lag	AS	1718135	1718150
glyA (27.5E-6)	GTTCCTGGCGCTTTGCTTATTCAC	GCCTGATGAAATTTGCTTA	lag	S	591480	591495
ywaF (27.4E-6)	CTATTTAAATGAGGATATCTGAAAT	CATCTCAGGATTTTGT	lag	AS	2205804	2205819
uvrC (27.3E-6)	AAATCCAAATATTTGGGGACTTCAC	CAGTATCTGCAATGGTGT	lag	S	857817	857832
mapA (27.3E-6)	TAAACCAACAGCACTGGACTTCAC	ATCCATCAAACTCTGGCT	lag	S	1729190	1729205
argG (27.1E-6)	TTGGCATATTCGATTTCTTCCTTCAC	CGCCCATTTGCCATTCAG	lead	AS	127192	127207
recD (27.0E-6)	AAATGAGAACCTTTCTCTCTTCAC	GAATTTTCANATCCCA	lead	AS	1797764	1797779
ykhD (26.9E-6)	AGCACTTCTGTTCTATGCTCTTCAC	CACCTGGCCATTTCTGCC	lag	AS	1072513	1072528
chiA (26.9E-6)	GTGGCTGTAGAGCACTCACTTCAC	TATTTGTAATTTGGGGAA	lag	AS	2027631	2027646
glmM (26.8E-6)	TTTCTGGTAATACTGTAACCTTCAC	TTGCAATTTCACTAAAGA	lead	AS	436154	436169
intergenic (26.4E-6)	TCACTTCTATTAATTAACATACT	CATCTATTTTACCATAAAT	lag	.	565292	565307
ftsK (26.4E-6)	CCAACTTGACTTTCTCTCTTCAC	CAGGCTCAAAGCTTTCTGC	lead	AS	1704506	1704521
ywcC (26.4E-6)	GCCTGGTTCAAACTCTACTTATA	TCACTCTGCAATAAAGGA	lead	S	2228600	2228615
ps311 (26.3E-6)	AAAGATATAAATTTCTACAACTTCAC	TTCCTGTGAAGCTCAAGC	lag	S	2021044	2021059
yjiI (26.1E-6)	ATAACGAACTTTAGCCGAGAGT	TCTCCACAGCAAGTTTAA	lag	S	889057	889072
typA (25.8E-6)	GAAACTTGAACCTCATTTCTTCAC	GGCCGATTTCTTCAATAG	lead	AS	2093373	2093388
acmC (25.7E-6)	GCATATGTCGGCTCTGTTCCTTCAC	CAATATTTTGAACGCTTT	lag	AS	1402971	1402986
yjce (25.3E-6)	TCTCTCCACTCACTTAACTTCAC	GAATATTTAGCCGTAATGG	lead	AS	926233	926248
als (25.3E-6)	CTGGAACTCCAAATTCATCTTCAC	TTATTTGTAATTTGAACTA	lead	AS	1200491	1200506
pgi (25.3E-6)	TAAATCCGTTGTTGCTTTCCTTCAC	GCCTGATTTTCTACTA	lead	AS	2245042	2245057
yobI (25.1E-6)	AACTGTTTCCAACTGACCTTCAC	TCAATAATTTCTCTCTGG	lead	AS	218254	218269
ypfF (25.1E-6)	TATTTGGTTAATAAAGGAACTTCAC	GTGTTCTCTGCTCCGAAAT	lag	S	1558390	1558405
carB (24.9E-6)	CCATCACTAATTCGACTTCAC	ATTCACCTCACTTAAATA	lead	AS	1399224	1399239
pi214 (24.8E-6)	TTTTCGATTCATTTGGCAGACTTCAC	ATCCAACTCAAGTGAATA	lag	S	1045075	1045090
yqbr (24.8E-6)	ATAGTTAACAATCATCATCTTCAC	ATCCGGTCAAGCTTATTT	lag	S	1623170	1623185
hisT (24.6E-6)	TTTCTCTAGCAATAATCACTTCAC	TTGCTTTTCTTCCACTTT	lead	AS	1237413	1237428
ftsK (24.5E-6)	TAGCTCAACCTTCACTAACTTCAC	TTGCTTTGGCAAGCTTTC	lead	AS	1705152	1705167
kupB (23.9E-6)	AGATATTTCCAAAGCAATCACTTCAC	CACATTAATGCTCCGTTG	lead	AS	613026	613041
rplN (23.9E-6)	ACGATGACTGCTTTTCAAACTTCAC	CTTTTTCACCTCCCTCAC	lead	AS	2164972	2164987

mtsC (23.6E-6)	AAAATGATAATTCTCTCCCTCCTC	TGGGGCAGCTTTCTCCTCCT	lag	S	1350292	1350307
pepDA (23.5E-6)	CAGGACACGCTGAGAGGACCTCAC	AACATATTACCCCTCCCTAT	lead	S	249419	249434
ptsI (23.1E-6)	ATATCATCATGATCCCTACCTCGA	TCCATCAGCACTGGGAAC	lead	AS	121915	121930
ywaI (23.1E-6)	TTGAATTCAGATTTATCTCCACCC	CATGAATTTGAAATTCATT	lag	AS	2208802	2208817
rpsc (23.0E-6)	TCAAAGTGTATGCAATTCCTTCAC	CAACAAGTAGGAGCCGCGAA	lead	AS	2166372	2166387
ywff (23.0E-6)	GGATTCAAAGCCTTAACTCCTTCAC	CATAAAGTACATGGCTTGG	lead	AS	2255016	2255031
intergenic (22.7E-6)	GCTCTCAAACTCAAGCTACCTCCG	GGACATGAAGTCTTGACG	lead	.	282945	282955
yleF (22.5E-6)	CCCCGATTTCGATTTTATCTTAAAT	TGAGCTGGGATTTCAGAA	lag	S	1147818	1147833
yidE (22.2E-6)	AAAATTTTCCCTTTTGAACCTTCAC	AGGTGTGAGCGCCATGGAG	lead	AS	835562	835577
yogA (22.1E-6)	CTTCTATTGCAATTCCTACCTTCCT	ATCTCCGCGGACTATCTA	lead	S	1460644	1460659
glyS (22.0E-6)	TGTCATTTGATGGCACAACCTTCAC	GCACCTTTAAACACCGAA	lag	S	1104472	1104487
ypfF (22.0E-6)	GCCTTATGATGACCCACTTCCTCAC	TAATAAGCAATTTCTCAAA	lead	AS	1558342	1558357
ytgF (21.9E-6)	CGACCCGCTTTTGTCTCTCTTCAC	GAAGGGTGAACGGGCTTC	lead	AS	1968538	1968553
ylcC (21.7E-6)	TTTAAAGGGCTTGGCAATTCCTTCAC	TTTATATGGGAGCGGGAAC	lag	S	1125903	1125918
yceE (21.6E-6)	AGCGAATAATTTTACCGCACTTCAC	GAATATATTTTATAGTCC	lead	AS	247324	247341
rnaB (21.6E-6)	TTACAAAACCTTTCCATCTTCCTCAC	CAACCGGAGCTTTGAGGCG	lead	AS	714999	715014
ynjG (21.6E-6)	CTCACGACCTTAAACCTACCTTCAC	AGGTAACAATTTAGTCC	lag	S	1394984	1394999
pepP (21.2E-6)	TTTCCGGCTTTGTTAAGACTTCAC	AGCCATTTCTCCTACTAA	lead	AS	691432	691447
intergenic (21.2E-6)	ATGCTAAACCCCTCATAGCTTTTAA	TGGTATTAATAAAGAAAA	lead	.	1133651	1133666
llrA (20.7E-6)	TCAACGGCAATGACATGCTCTTCAC	GTCCGAGAAACCTCGAAC	lead	AS	1639102	1639117
alas (20.3E-6)	GTGCCTTCAAAGTTCCTTCCTTCAC	GATCAATAATTTGCATGAT	lead	AS	1779915	1779930
yfgG (20.0E-6)	AAAAATGGCTTCAATGATTGGTATT	GCAAGAAGCAATTTATATTC	lag	S	568993	569008
intergenic (20.0E-6)	ATTTTAAAGAGATTATCGTGGGATT	ATTCATTTAAACGACAT	lead	.	966884	966899
ps315 (20.0E-6)	CTAAAGAGAGCGCCCAACTCTTCAC	GGTTCATTCCTCTTTTAGT	lag	AS	2023699	2023714
prfA (19.6E-6)	TTATCCGTAATTTCTGCTCTTCAC	GCGTATTCCTCAAAACG	lead	AS	586052	586067
yjaJ (19.6E-6)	TCTCCGGGAAAACATAAGCTTGT	CTCCGTGTAAGAGCCGCT	lead	AS	909737	909752
vacB1 (19.5E-6)	TGTAATAATAATGGTTGAACCTCAC	CATAATTTAGAGCCATGC	lag	S	968272	968287
ybfd (19.4E-6)	TTATCTCTTTTTCCTCCCTACT	GTTCATTTGGTCAATGG	lead	S	158550	158565
rmlC (19.3E-6)	CCAGAGGCGCACACTGCTCTTCAC	CAAGATGTTAGTCCGCTCC	lead	AS	200761	200776
ynpE (19.2E-6)	AGCTTTCCTTTACGTGGACTTCAC	GTCCGAGAAACCTCGAGG	lag	AS	1365714	1365729
pknB (19.1E-6)	GCGAAGGCACTCTCTGAACTTCAC	TTACCAACAATATCAAT	lag	S	1956462	1956477
ybeF (19.0E-6)	ACTTTTACTTTGCTTCTCTTCCTCAC	CTGCAATGCAATAAAGTAAAC	lead	AS	153682	153697
gltD (19.0E-6)	ATTCGGGCTGTTTTCTCTCTTCAC	GGATGCCCAATTAACAA	lead	AS	1315143	1315158
yjfJ (18.6E-6)	CGCGTGTTAATCGAATACTTCAC	CATAAGCTTCAGTAAATCG	lead	AS	959323	959338
yljF (18.5E-6)	CCGCGGCAAAAACGAGCCCTTCAC	CTGTAGAGAGATTCCTT	lead	AS	1197029	1197044
rpmA (18.2E-6)	AAAAAAGGTCGGGTCTCACTTCCA	ATGGAAGGCACTCAAGC	lag	S	1091336	1091351
pdbB (18.1E-6)	GTATAGAACCTTACGGAACCTCAC	CTTAAAGTGGCCGATAAAG	lag	AS	62610	62625
celB (18.1E-6)	TTAATTAACAAGCCCTCTCACTTCCA	ACTCACCCACAAAGGTA	lag	S	178484	178499
intergenic (17.8E-6)	ACTTCCATATCCCTTTTACTTCAC	CTTAAATTAATCTTAAATA	lead	.	1987040	1987055
yahC (17.7E-6)	GAGCGATAAACTCTTCAAACCTCGCG	AATTTCTCTCTCAAGCTTAA	lag	S	74058	74073
rbgA (17.7E-6)	GATGCTCGTCTCCCTATTTCTTCAC	GTAACTCGAATCTGGGGCA	lag	S	1329921	1329936
ps105 (17.6E-6)	CAAAACCTAAATAGAGGACTTCAC	AGATATGGCGAAGACGGC	lead	S	39194	39209
lepA (17.5E-6)	CGACCAATAATCGAATCTCAATAT	CAACCTGGCAATTAACCTTT	lead	AS	1118787	1118802
pppI (17.2E-6)	ACTTCAATATCTGCTTGAACCTTCAC	TAGTGTGCCAAGTGAAC	lead	AS	1957232	1957247
ybaB (17.0E-6)	AAAAATCGAGTTGTCATCTTCCTCAC	AGTAAATGACACTCGAACC	lead	AS	103218	103233
lysC (17.0E-6)	GCTCCGGGAACCAAACTCTCAATAT	CAATCCGCGCTCTCTTAA	lead	AS	369938	369953
yqkR (17.0E-6)	GTTCCTGAGTACCTCCACTGGGAC	TACTAATTAAGTACTCCAGC	lead	AS	1622667	1622682
ybeF (16.9E-6)	CCATTTTCTCGGATCTCCCTTCAC	GAATTAATTAATCTTAT	lead	AS	152104	152119
eno (16.9E-6)	CCATCTCTTAATCAACTCTTCCTCAC	GGTCTCCAGTGTATGCTCC	lead	AS	274299	274314
arat (16.7E-6)	TAAGATAACCGGACAAATCTTCCTCAC	CGTACGACCAAAACGGAT	lead	AS	57646	57661
pi214 (16.7E-6)	AAGTAAAGTCTCACTCACTTCCTCAC	CTTTCTCAATCTTGGATA	lead	AS	1044675	1044690
rpsC (16.7E-6)	CGTGGTGAAGTCTCTCTCACTTCAA	AATCTTGGAAAGCGAAAA	lag	S	2166072	2166087
comFC (16.6E-6)	CCPTTGGTTCCTTCTCTATTCCTCAC	CAABAAGATAAGGGAACG	lead	S	1096611	1096626
gidC (16.6E-6)	TTGGAGTTCACCTTACTTCACTCAC	CCATATGACAGCAAAAT	lag	S	1257952	1257967
ycgI (16.5E-6)	TTCAAGAGAAATTTTGCACACTTCAC	TTACATGCTTCTGGGCT	lag	S	267947	267962
yciH (16.5E-6)	AAATATATTCATCAGGTGTCAATAT	CAATGGGCAACAATGTGT	lag	AS	289429	289444
intergenic (16.5E-6)	ATCAAGAGAACCCTCCAACTTCAA	AGAGGGCCCAATCCCAAT	lead	.	2267063	2267078
intergenic (16.4E-6)	TTAAACAAAGTTATTTACTTCCTCAC	ATTAATTAATTAAGTCAAGG	lead	.	308448	308463
agl (16.4E-6)	CAGATTAATACTCACTCCCAATTCAC	GTAGATTAAGGAATTTTTC	lead	AS	1732727	1732742
ftsB (16.3E-6)	TAAGCTTGAAGTTTAACTTCCTCAC	TCTAGATTAAGCTTAAAG	lead	AS	26157	26172
pnrB (16.0E-6)	CCAAAGGCAATTAATTTCTCTCTCAC	CATGATTTCTTCTGAAAG	lag	AS	130558	130573
riba (16.0E-6)	ATTAATAAAGTCTCTGCTTCTCAC	TTCAGATTAAGGACTTGA	lag	S	1024702	1024717
argG (15.9E-6)	CAGATTCGACTGCCCTTCTTCCTCAC	CCCTTCACTCAATTAATA	lead	AS	126892	126907
purI (15.9E-6)	TCTTCAATCGCTGCTCCCACTTCAC	GGTATATTTGCTCTCTG	lead	AS	1576342	1576357
fhs (15.8E-6)	TCCGCCAAATCTTAACTCACTTCCTCAC	CACTCCCTTACCAAGACTTG	lead	AS	960993	960999
llrF (15.8E-6)	GATTTATGACAAATCTGTATCTTCT	CAATTTCTTCCGAATTTAA	lead	AS	1727031	1727046
yshA (15.6E-6)	CAAGCCTCTGCACTTCTCACTTCCTCAC	GCAGACTTAAGCTTGGTGG	lag	S	1876038	1876053
vacB2 (15.4E-6)	TCPAATAATCTCTCTCACTTCCTCAC	CTTATCTCCAATTAATCC	lead	AS	1226666	1226681
ydsB (15.4E-6)	TGACCAATTAAGCCATAACTTCCTCAC	CTGGCTTAACAACCAATAT	lead	AS	1835702	1835717
yqgA (15.0E-6)	CTTGAAGTTGACGCTCTTCCATAAC	TACTGGTAGAAATCTCTGGT	lead	AS	1662046	1662061
infB (14.9E-6)	CCATCATTAATCAACCACTTCCTCAC	GAATGACCGGACGAAGC	lead	AS	778425	778440
gltB (14.9E-6)	TTACCTGGCAATTCGCTCACTTCCTCAC	CTGCTTAGCACTTCCGA	lead	AS	1318175	1318190
gntK (14.9E-6)	CCCCGGAAATGTTTGCCTCACTTCCTCAC	CCGTGACTTCACTTAAAG	lead	AS	2269167	2269182
groES (14.8E-6)	CCATGATGATTTGTTTCTCTTCCTCAC	CGACGGCAACAACCTTCAGC	lead	AS	398636	398651
L200015 (14.8E-6)	TGAGAAAGTAAATTAATCAAACTTCAC	TTGCTTCTTCCAACTTCAAC	lead	AS	456625	456640
pi115 (14.8E-6)	TGAGAAAGTAAATTAATCAAACTTCAC	TTGCTTCTTCCAAATCAAC	lead	AS	456625	456640
fhs (14.8E-6)	ACGCTAATACTCAAACTATCTTCAC	GGGGCAGACCACTTAAAG	lead	AS	960324	960324
nifs (14.8E-6)	AACGCTGTACACAGCTCTCTCTCAC	CTGAATTAATCAACCCGAAT	lead	S	1927818	1927833
accC (14.7E-6)	TCTTCTCTTACAGCAATTCATTCAC	CATTTGGTACAGCAATCTG	lead	AS	788253	788268
dnad (14.7E-6)	ACCTTTCGATTTGAGGACTCTTCCTCAC	GCAAGGCTTCTTAAATCA	lead	AS	1083630	1083645
sbcC (14.7E-6)	TTAGCTGTATTTGTACGACTTCCTCAC	TTAAGCCAAAGCAATTCGA	lead	AS	1353084	1353099
ynpG (14.7E-6)	AGCACTCCGATTTTCTCACTTCCTCAC	GTTCCTTCAACAGGCTC	lead	S	1368503	1368518
trmE (14.7E-6)	GATGATGTGGAACAATGACTTCCTCAC	AAATGCTCCCTTCAAAAC	lead	S	2328325	2328340
ydaG (14.2E-6)	TGATAATGCGCAATTAATCAATTCAC	CATAAATCTCAAGTAAAT	lead	AS	309995	310010
snf (14.1E-6)	TCTAAGCTCAATCTTACCTTCCTCAC	CATCAATTTCTCTGTAG	lead	AS	2123594	2123594
L200121 (14.1E-6)	CAGACTCAAAATCTGGTTCCTTCCTCAC	GGGAGTCCCGGTCGACCC	lag	S	2340443	2340458
ldhX (13.9E-6)	TGAGCAATAAGTCTCTCACTTCCTCAC	CACTTCAACAACTTCAAC	lag	AS	1142441	1142456
yohC (13.9E-6)	GAACTCTTGTCTGACCTCTCTCTCAC	GGTCCCTTGGCAATCA	lead	S	1472006	1472021
ywjH (13.9E-6)	AAATCAATTAACCACTTAAATATTC	CATTAATTTTCTGGGCA	lead	AS	2299858	2299873
yrfC (13.8E-6)	GCAATCAAAATCTCTCACTTCCTCAC	GTGCGACTTCTCTTCAAC	lead	AS	1753200	1753215

secA (13.5E-6)	TTCAATACGATTCAAAACCTCTC	CGCAAGTAAATAAACTGT	lag	S	117488	117503
ftsY (13.5E-6)	CCAGCTGGTTTGTGACACTTCA	CGCCGACGATTTCCCA	lead	AS	825016	825031
trxB2 (13.5E-6)	GCATTATCGCTGGACCTTAC	CAAAACAACCGGCACTCA	lead	AS	1694915	1694930
intergenic (13.4E-6)	CAATCAACCTTTTGCAAAACCTAC	AAGAAGTGAAGGCAAGAT	lag	.	1702217	1702232
yucF (13.4E-6)	GCTTCCAAAATTCAACGACTTAC	TTTCAAACCTTTTCTTAAG	lag	AS	2025914	2025929
purA (13.4E-6)	CGACGCAAAAGTTCAAACTTAC	CTTAATCCATCAGGAATTT	lag	S	2029866	2029881
L200158 (13.4E-6)	ATAGAAATACCGTCCCTATTCA	TGGCCCTTACCATTCCCTGT	lead	AS	2361099	2361114
yuaD (13.3E-6)	CGCCGACGCGTCTCTTAACTTAC	CTTGGTTCACACTTATA	lead	AS	2005245	2005260
yahG (13.2E-6)	AAAGCTCAATCCTTTTCTTAC	ATGACCAATGAAATCAATTA	lead	S	73337	73352
yohG (13.2E-6)	GTCATAAATATGTATGATTAATTT	AAGGAGTAAAGATGATTC	lag	S	1479677	1479692
ycfF (12.9E-6)	AAGTCTTCAAGCATTTCTTACCG	GATAACAACCTCAGTAC	lead	S	256796	256811
ksgA (12.8E-6)	AACATTTCTTCTTTTCACTTCA	CCAAAGCTTCTCCGACG	lead	AS	690090	690105
rmeA (12.5E-6)	TCGTTCAAGATTTCTTCAATTAC	TGATGCCAATAAAGGGGTC	lead	AS	1947036	1947051
ygiI (12.4E-6)	TTGGCTGGCATCCTGATGATGCTG	TGAAATTGAAAGACCAAGCT	lag	S	687601	687616
yibG (12.4E-6)	AAAAGACAGCTCCATTCCTCCAC	CAAGAGCAATCATAGTAAT	lag	AS	819874	819889
yljF (12.4E-6)	GAAAAGTTTCTCTGCTCACTTAC	CAAAATGAACATCGATTT	lead	AS	1195988	1196003
oppA (12.3E-6)	TAGTCAAGGCTATCTCCACACAC	GTTTGTAAACGGGGCTTA	lead	AS	1905177	1905192
yciH (12.2E-6)	AGTCCGAAACCTGCTGACTTAC	CGAAAGGCAACTTGGAA	lead	S	290530	290545
glbB (12.2E-6)	CGTTTTGAATTTTCAACCTTAC	CCGAAATGGATTTTGCACC	lead	AS	1318322	1318337
yneG (12.2E-6)	GAAAGCTCTGACAGTCTTCTTAC	ATCCGAGATTTTGAAGTAA	lead	AS	1345665	1345680
llrC (12.1E-6)	TTAAATGCTTCAACGCTTCTTAC	CATCAAAAGCTTAAGAC	lag	AS	403590	403605
ypcD (12.1E-6)	GACGGAATTACATTAATCTTAC	CACAAGGCCACCCCAATA	lead	AS	1524368	1524383
clpB (12.1E-6)	TGACCAAGCTAATCTCCGTTGATG	CAATAGAAAATCAGAAAG	lag	S	1567980	1567995
yiiB (12.0E-6)	CCAATGAAAAGCCACCTACTCCAC	CAACAATTAATGTAGTAA	lead	AS	892941	892956
yniC (12.0E-6)	CGATAAATGAAATTAATTAATAC	TTTTTGGTCTGTACTTGG	lag	S	1381911	1381926
yniH (12.0E-6)	ACAGCTCTTCCGACAAACCTTAC	GGATAGAGGGGCTCCAAG	lag	AS	1387638	1387653
ycfD (11.9E-6)	ATGATTGCTCCGACCTCCCTTACT	TTGCCAGAAAAGGTAAAAA	lag	S	253569	253584
ispA (11.7E-6)	GCTAATGTCAACTCTTTTCCCTTAC	CGCCATAACCAAGATTGG	lead	AS	881208	881223
tpx (11.6E-6)	TCAGAAAGCTCTGACAAAACCTTAC	TATAAGACAATTTGCCAAT	lead	AS	302128	302143
yeeA (11.6E-6)	CCATAAGAACCTTTCCTTACTTCTT	TTTTATCAATTTGGATAT	lead	AS	439614	439629
ybdC (11.4E-6)	TTTTCGACCTTCACTTACTTCTTAC	GCCCGCAAAATTTTCTTA	lead	AS	132561	132576
yvhB (11.4E-6)	TTTCATATTCTTCTCACCGCTTAC	CCCAAGCCAACGCTGAT	lag	S	2175732	2175747
yafC (11.3E-6)	GAGTCACTTACTTCTCTTACTTCTAC	TCAAAGACCGCTTCCAAC	lead	AS	55779	55794
araT (11.3E-6)	TTAATATCTGTCACATAATTAC	GCGCTGCAAGATTAATCC	lead	AS	57325	57340