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 [^{32}P]-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 Ll.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 pAMβ *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 pON*oriT1*. High quality primarily supercoiled plasmid was isolated from fresh *E. coli* DH5α overnight culture and was used for relaxase activity assays.
(**C**) LtrB relaxase from pRS01 cannot nick its cognate *oriT* in dsDNA. Plasmid pON*oriT1* (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 µl) containing relaxase reaction buffer (50 mM Tris-HCl pH 7.9, 100 mM NaCl, 10 mM $MgCl_2$, 1mM dithiothreitol) and 100 µg/ml bovine serum albumin (BSA). Half of the reaction mixture was treated with 0.5 µl 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 pON*LLglnP*-R was constructed for ssDNA preparation. pON*LLglnP*-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

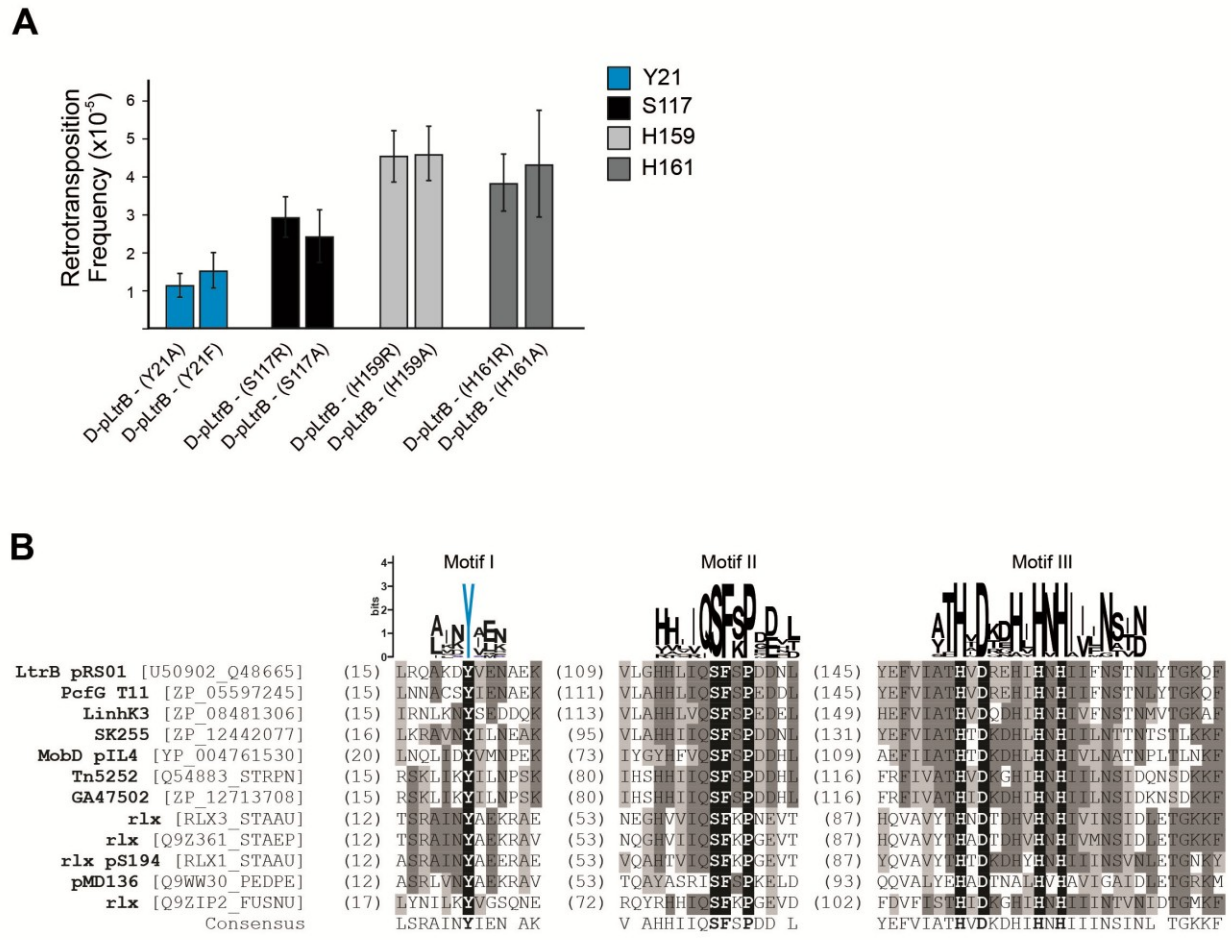


Figure S1. Effect of relaxase mutations on retrotransposition

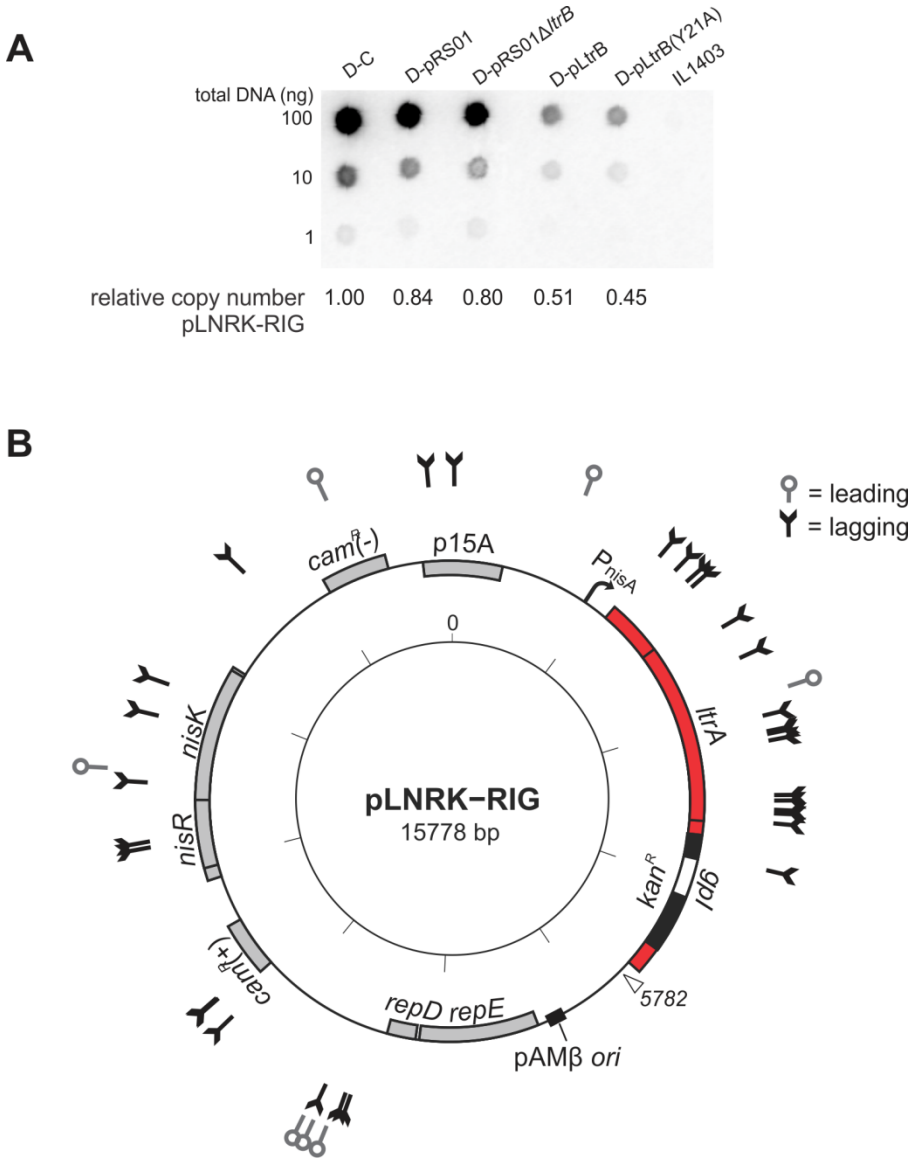


Figure S2. The relative copy number of donor plasmid between strains and mapping of the retrotransposition events onto the donor plasmid

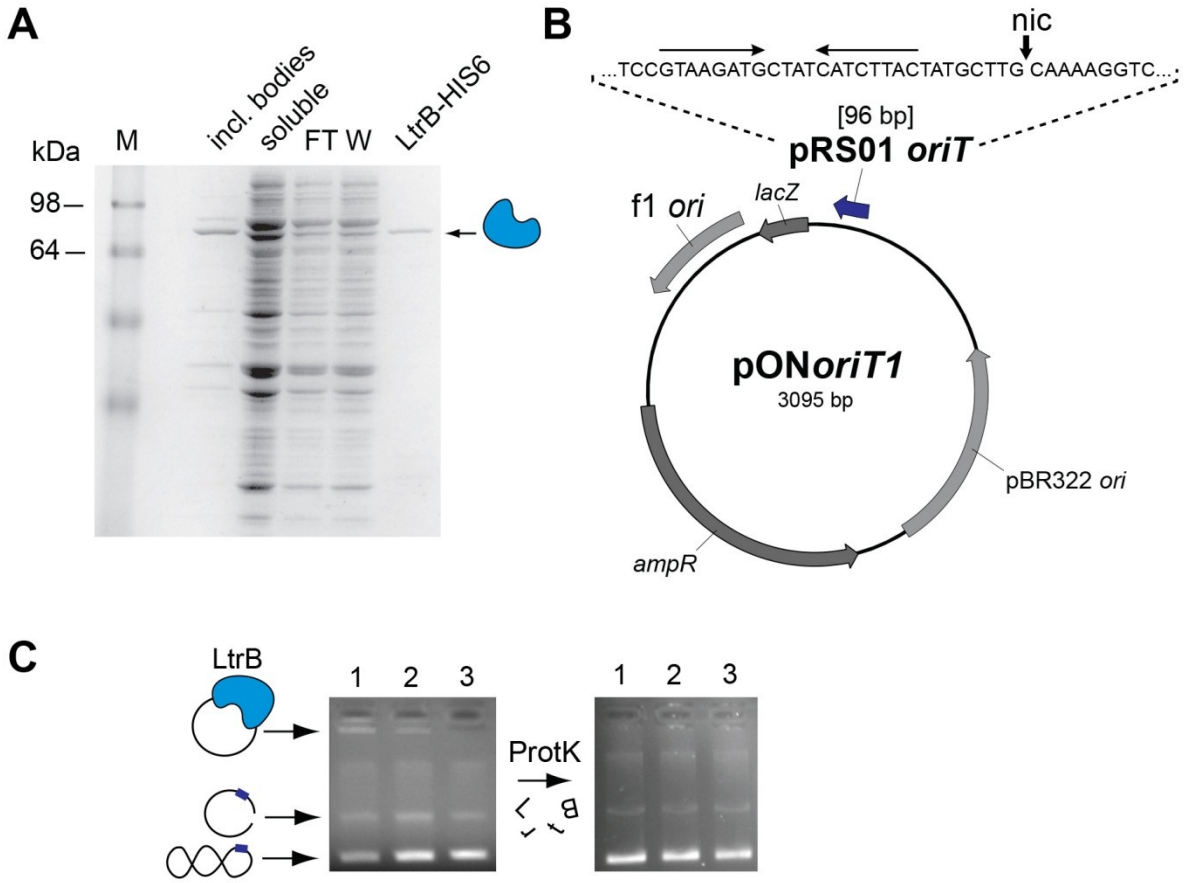


Figure S3. Purification of LtrB relaxase and its effect on dsDNA target

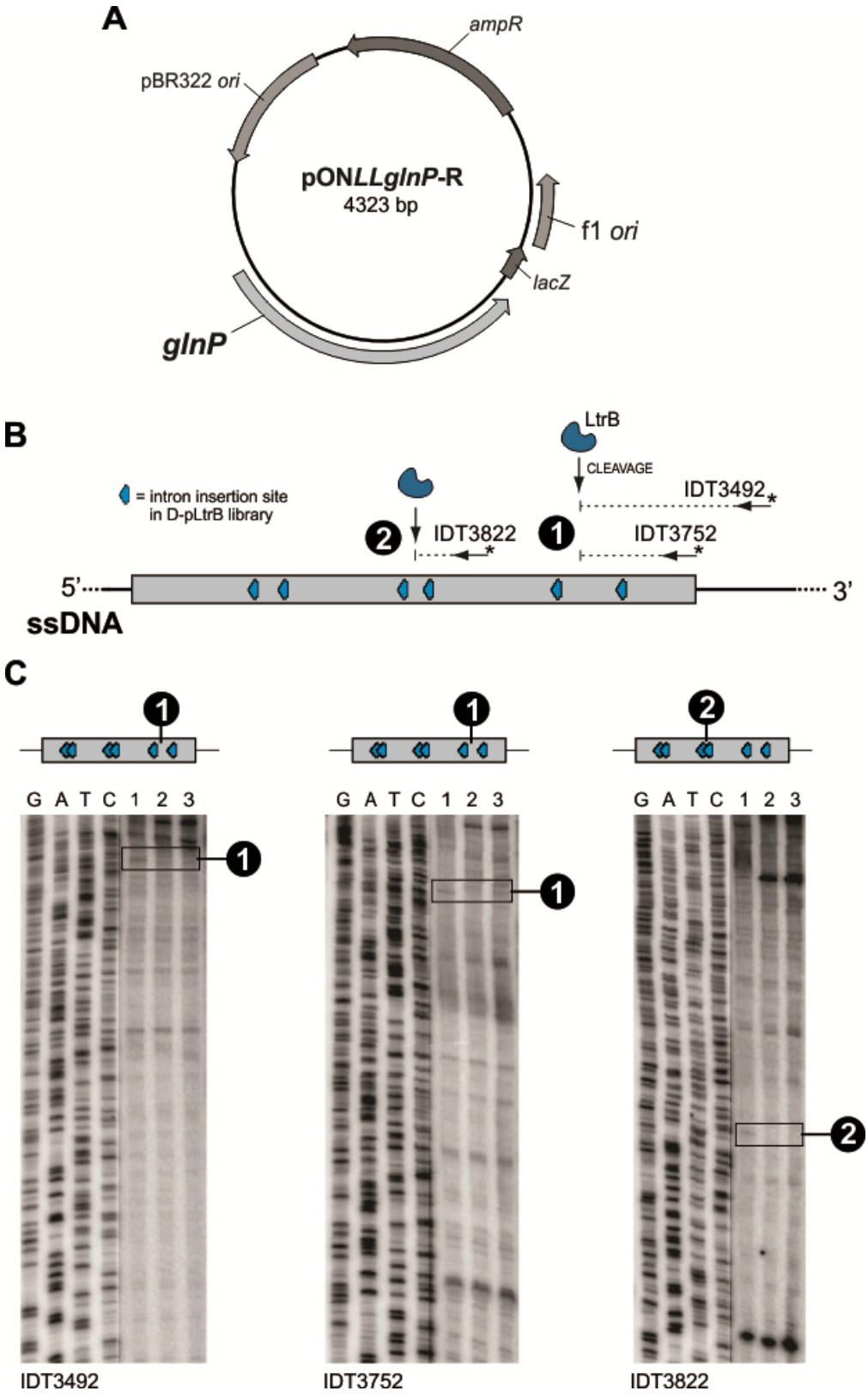
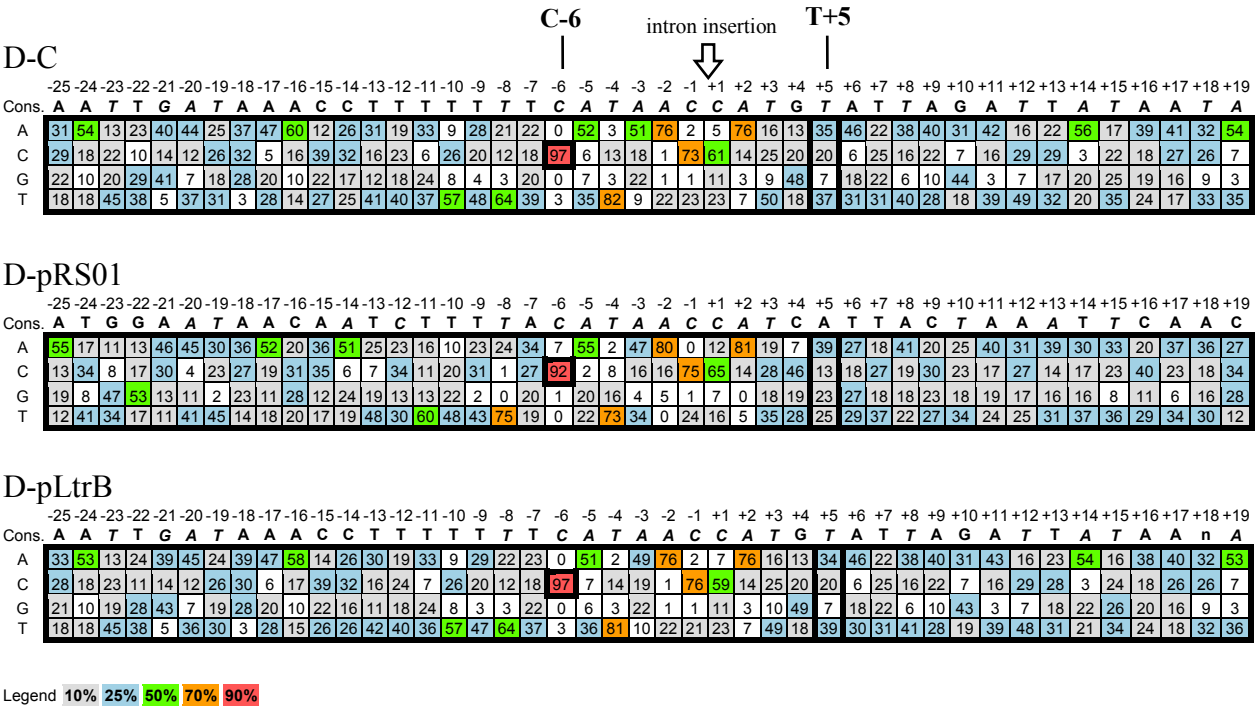


Figure S4. Mapping of off-target relaxase cleavage

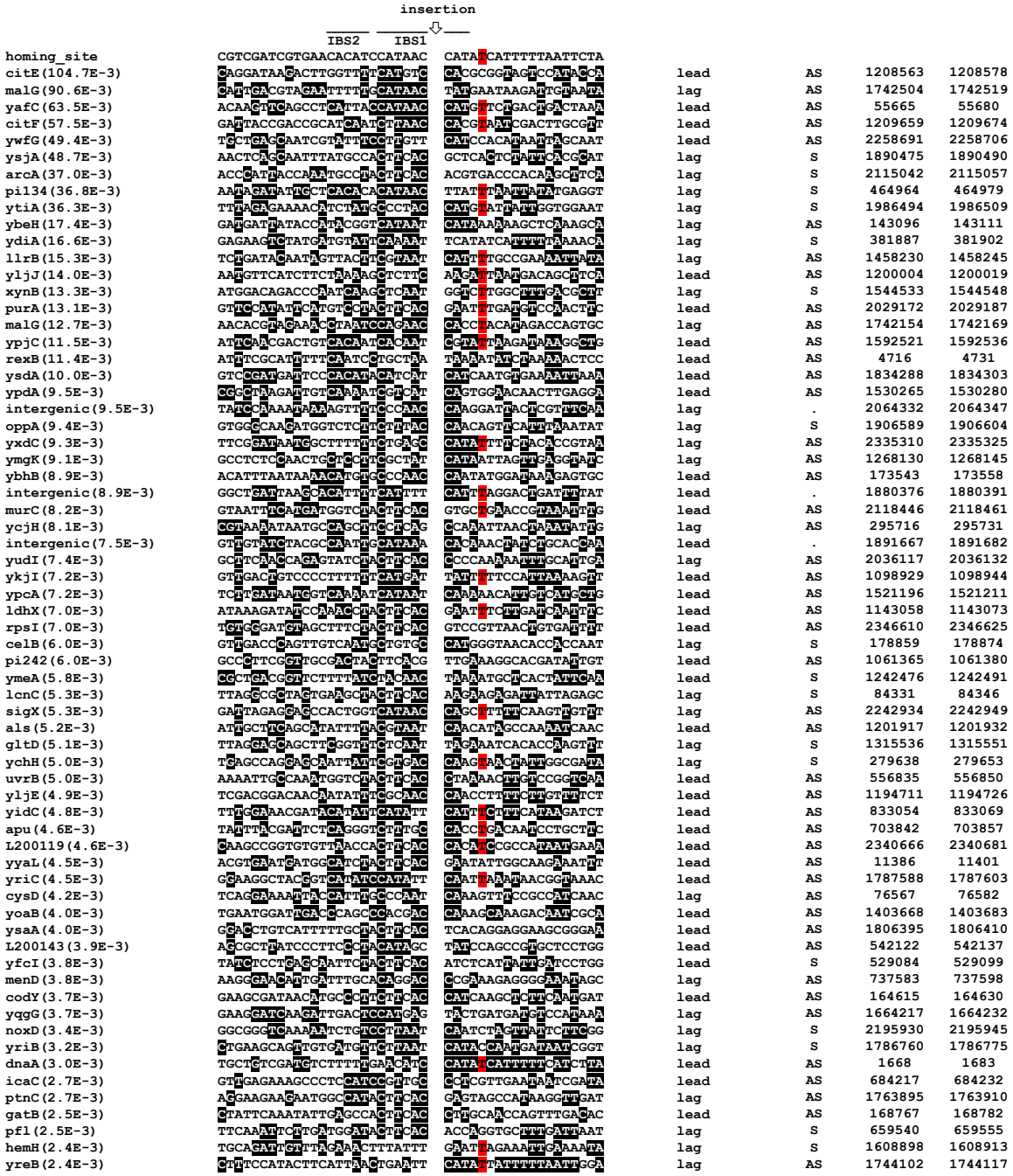
Supplementary Tables

Table S1. Grid profiles based on the multiple sequence alignments of the chromosomal insertion sites.



Integration sites of the Ll.LtrB intron were mapped in the absence/presence of the relaxase. Each cell represents the score of a particular nucleotide (A, C, G, or T) in the corresponding position shown as a percentage (%), color-coded according to the key at the bottom, from the total number of the sequences in the alignment. The nucleotides in consensus sequences that are identical to the nucleotides of the homing site in the corresponding position are highlighted with *italics*. The most conserved position C-6 and position T+5, important for endonuclease activity, are shown on the top. The intron insertion site is indicated by arrow.

Table S2. Multiple alignment of the chromosomal insertion sites of Ll.LtrB intron in the absence of the relaxase (D-C strain). Names of the genes and relative frequencies are given in which insertions of Ll.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.



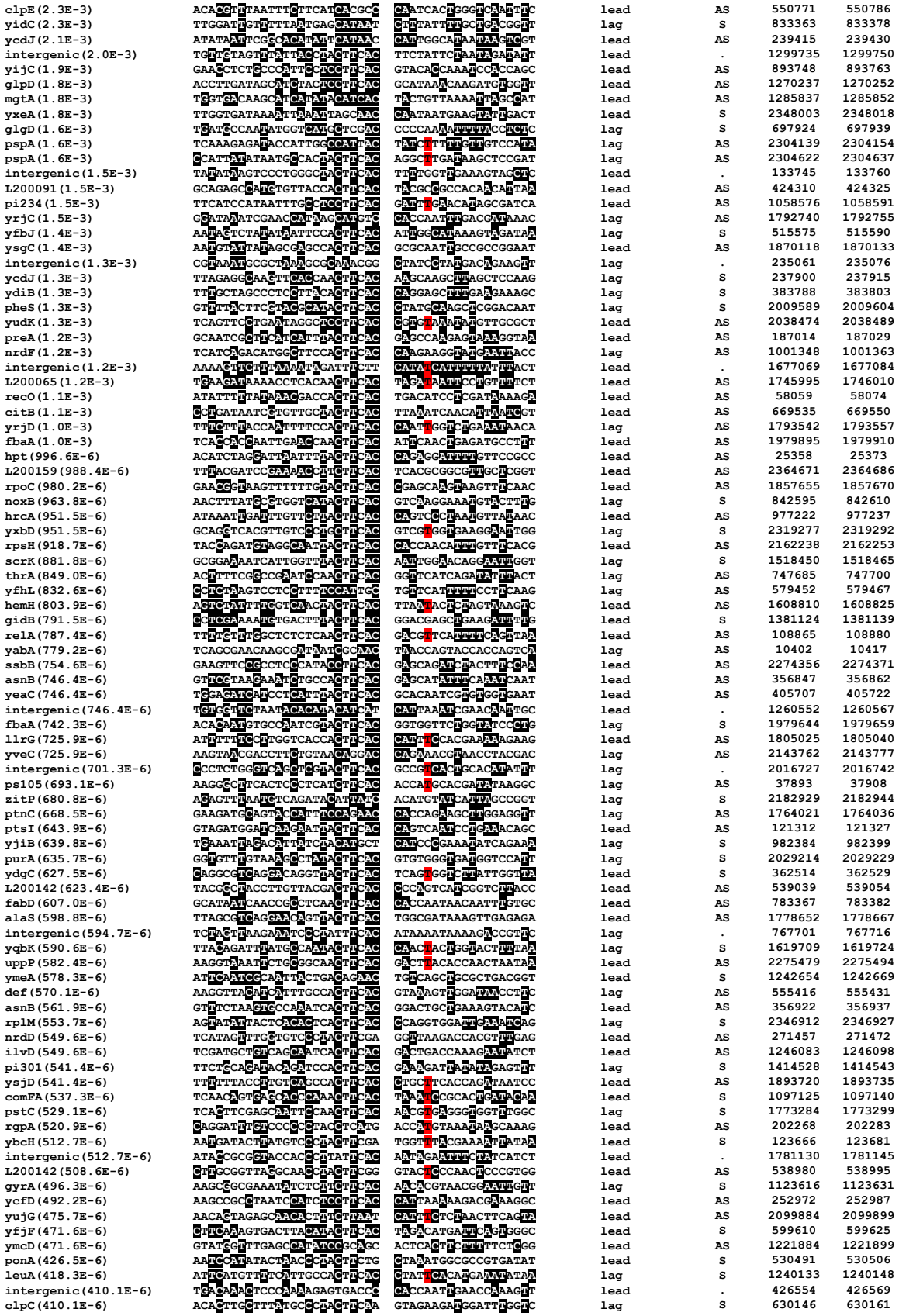
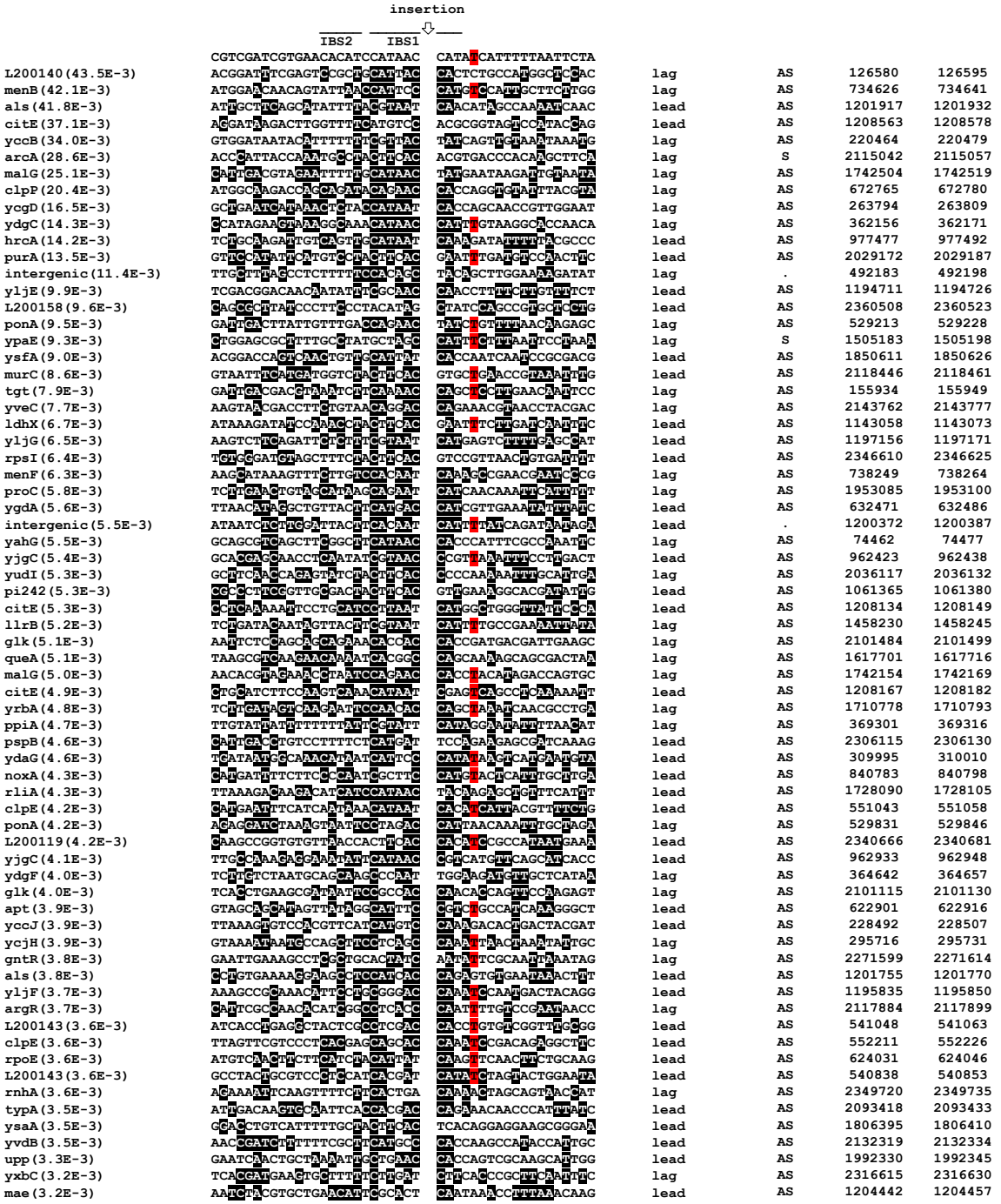
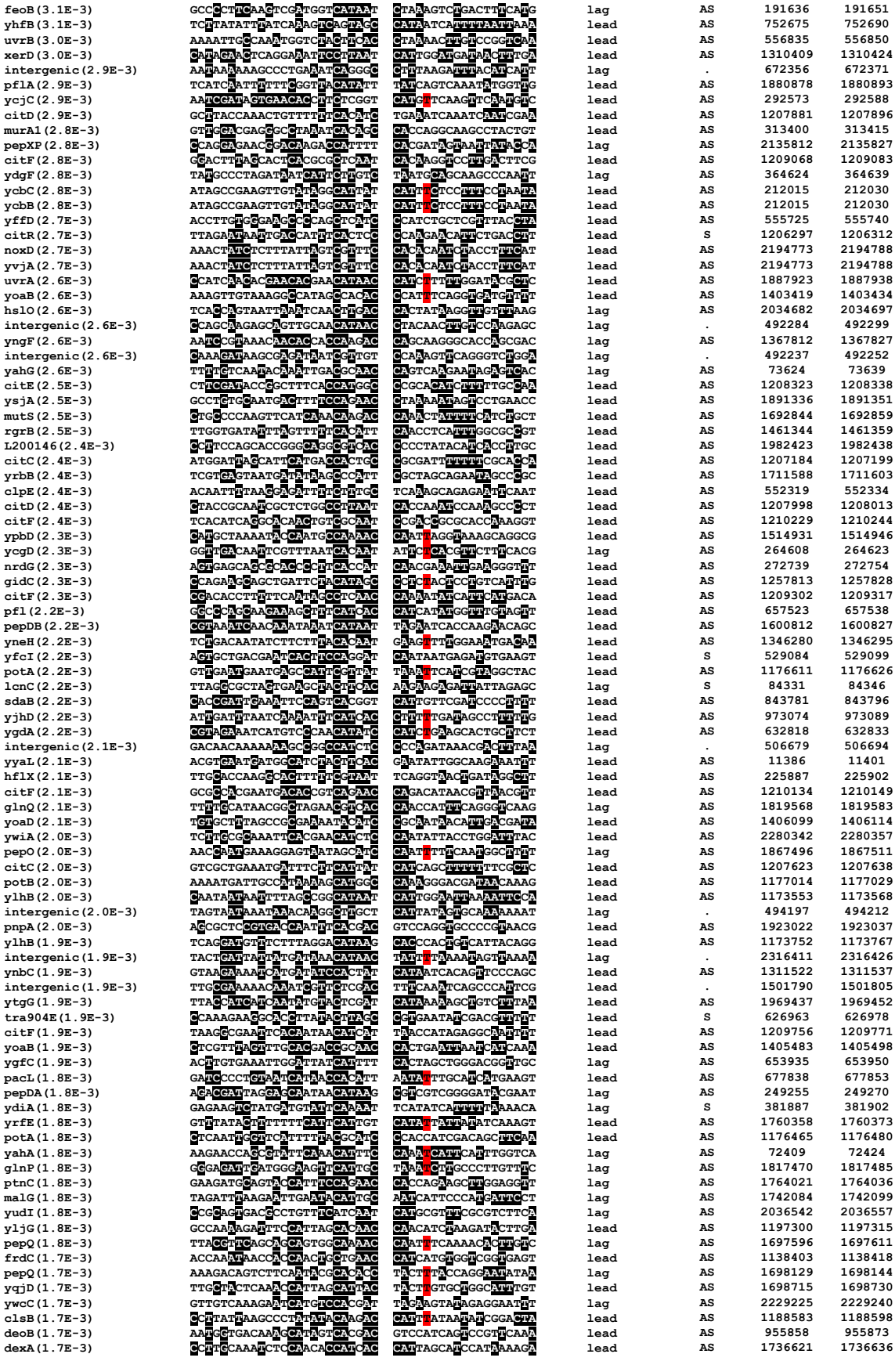
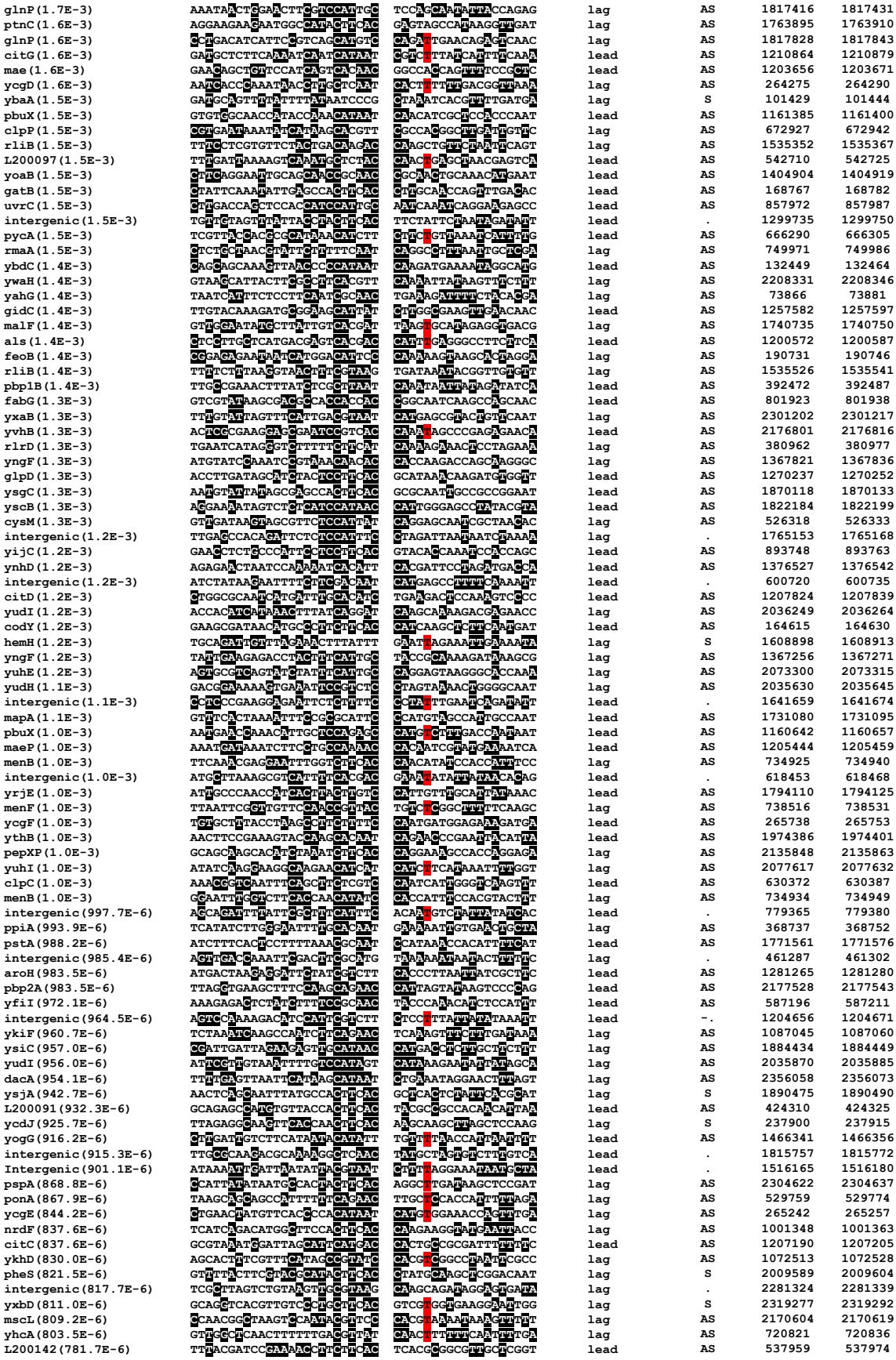
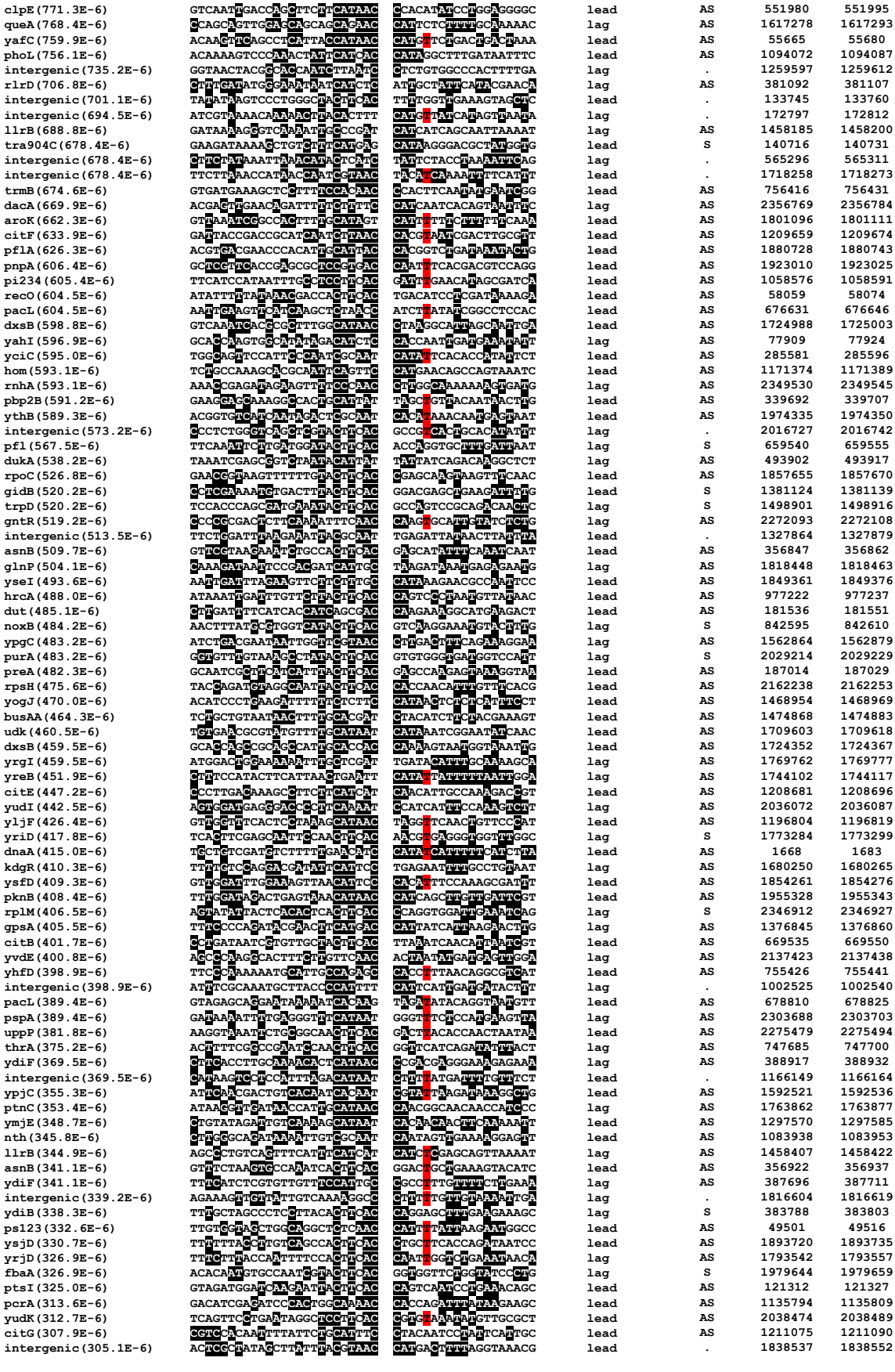

clpE(2.3E-3) lead AS 550771 550786
yidC(2.3E-3) lag S 833363 833378
ycdJ(2.1E-3) lead AS 239415 239430
intergenic(2.0E-3) lead . 1299735 1299750
yijC(1.9E-3) lead AS 893748 893763
glpD(1.8E-3) lead AS 1270237 1270252
mgtA(1.8E-3) lead AS 1285837 1285852
yxeA(1.8E-3) lead S 2348003 2348018
glgD(1.6E-3) lag S 697924 697939
pspA(1.6E-3) lag AS 2304139 2304154
pspA(1.6E-3) lag AS 2304622 2304637
intergenic(1.5E-3) lead . 133745 133760
L200091(1.5E-3) lead AS 424310 424325
pi234(1.5E-3) lead AS 1058576 1058591
yrjC(1.5E-3) lag AS 1792740 1792755
yfbJ(1.4E-3) lag S 515575 515590
ysgC(1.4E-3) lead AS 1870118 1870133
intergenic(1.3E-3) lag . 235061 235076
ycdJ(1.3E-3) lag S 237900 237915
ydiB(1.3E-3) lag S 383788 383803
pheS(1.3E-3) lag S 2009589 2009604
yudK(1.3E-3) lead AS 2038474 2038489
preA(1.2E-3) lead AS 187014 187029
nrdF(1.2E-3) lag AS 1001348 1001363
intergenic(1.2E-3) lead . 1677069 1677084
L200065(1.2E-3) lead AS 1745995 1746010
recO(1.1E-3) lead AS 58059 58074
citB(1.1E-3) lead AS 669535 669550
yrjD(1.0E-3) lag AS 1793542 1793557
fbaA(1.0E-3) lead AS 1979895 1979910
hpt(996.6E-6) lead AS 25358 25373
L200159(988.4E-6) lead AS 2364671 2364686
rpoC(980.2E-6) lead AS 1857655 1857670
noxB(963.8E-6) lag S 842595 842610
hrcA(951.5E-6) lead AS 977222 977237
yxbD(951.5E-6) lag S 2319277 2319292
rpsH(918.7E-6) lead AS 2162238 2162253
scrK(881.8E-6) lag S 1518450 1518465
thrA(849.0E-6) lag AS 747685 747700
yfhL(832.6E-6) lag AS 579452 579467
hemH(803.9E-6) lead AS 1608810 1608825
gidB(791.5E-6) lead S 1381124 1381139
relA(787.4E-6) lead AS 108865 108880
yabA(779.2E-6) lag AS 10402 10417
ssbB(754.6E-6) lead AS 2274356 2274371
asnB(746.4E-6) lead AS 356847 356862
yeaC(746.4E-6) lead AS 405707 405722
intergenic(746.4E-6) lead . 1260552 1260567
fbaA(742.3E-6) lag S 1979644 1979659
llrG(725.9E-6) lead AS 1805025 1805040
yveC(725.9E-6) lag AS 2143762 2143777
intergenic(701.3E-6) lag . 2016727 2016742
ps105(693.1E-6) lag AS 37893 37908
zitP(680.8E-6) lag S 2182929 2182944
ptnC(668.5E-6) lag AS 1764021 1764036
ptsI(643.9E-6) lead AS 121312 121327
yjiB(639.8E-6) lag S 982384 982399
purA(635.7E-6) lag S 2029214 2029229
ydgC(627.5E-6) lead S 362514 362529
L200142(623.4E-6) lead AS 539039 539054
fabD(607.0E-6) lead AS 783367 783382
alaS(598.8E-6) lead AS 1778652 1778667
intergenic(594.7E-6) lag . 767701 767716
yqbK(590.6E-6) lag S 1619709 1619724
uppP(582.4E-6) lead AS 2275479 2275494
ymeA(578.3E-6) lead S 1242654 1242669
def(570.1E-6) lag AS 555416 555431
asnB(561.9E-6) lead AS 356922 356937
rplM(553.7E-6) lag S 2346912 2346927
nrdD(549.6E-6) lead AS 271457 271472
ilvD(549.6E-6) lead AS 1246083 1246098
pi301(541.4E-6) lag S 1414528 1414543
ysjD(541.4E-6) lead AS 1893720 1893735
comFA(537.3E-6) lead S 1097125 1097140
pstC(529.1E-6) lag S 1773284 1773299
rgpA(520.9E-6) lead AS 202268 202283
ybcH(512.7E-6) lead S 123666 123681
intergenic(512.7E-6) lead . 1781130 1781145
L200142(508.6E-6) lead AS 538980 538995
gyrA(496.3E-6) lag S 1123616 1123631
ycfD(492.2E-6) lead AS 252972 252987
yujG(475.7E-6) lead AS 2099884 2099899
yfjF(471.6E-6) lead S 599610 599625
ymcD(471.6E-6) lead AS 1221884 1221899
ponA(426.5E-6) lead S 530491 530506
leuA(418.3E-6) lag S 1240133 1240148
intergenic(410.1E-6) lead . 426554 426569
clpC(410.1E-6) lag S 630146 630161

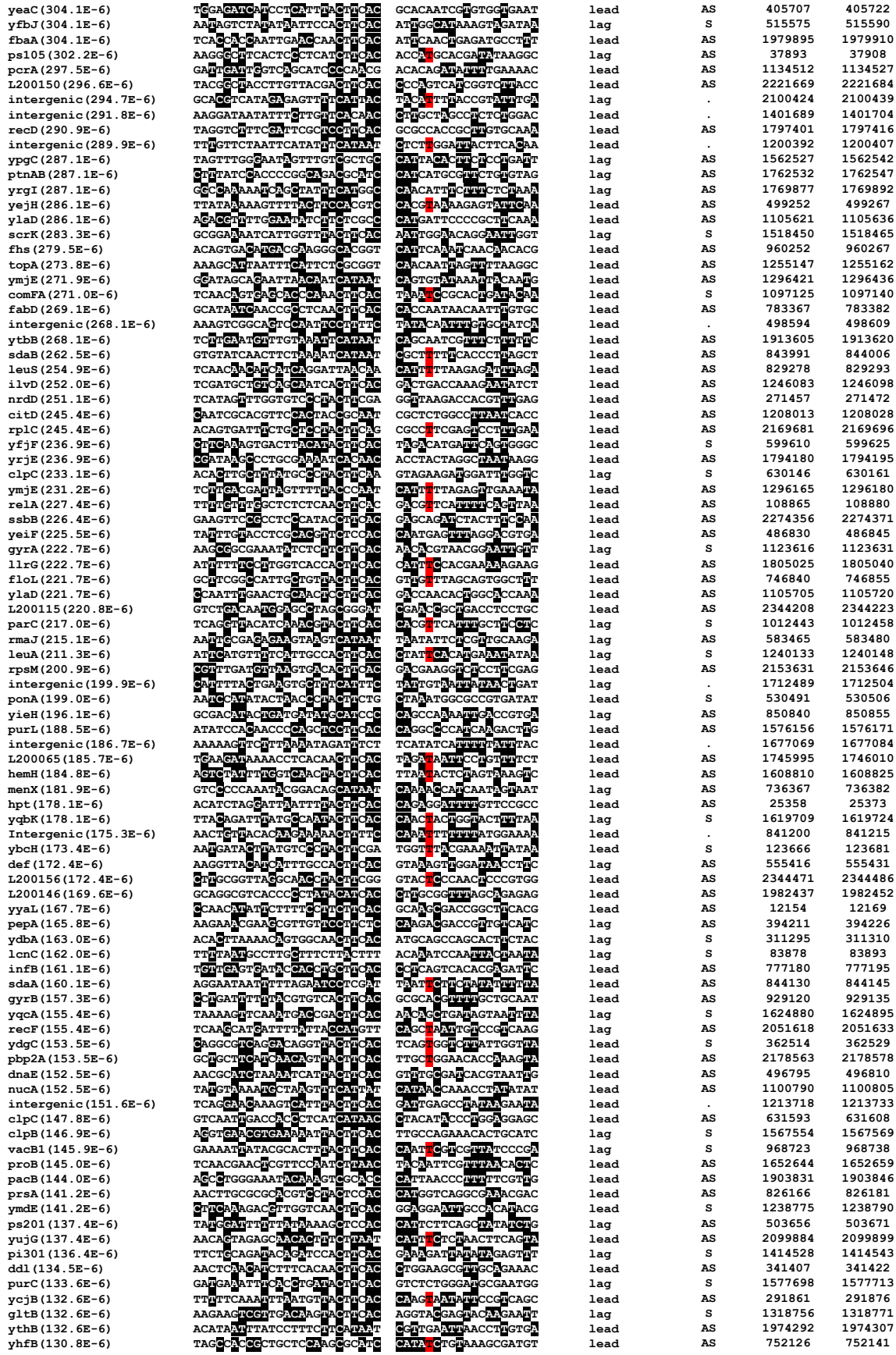
Table S3. Multiple alignment of the chromosomal insertion sites of Ll.LtrB intron in the presence of the relaxase (D-pRS01 strain). Names of the genes and relative frequencies are given in which insertions of Ll.LtrB were detected; the orientation of the insertions relative to the direction of the replication (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.




feoB(3.1E-3) GCCCCTTCAAGTCGATGGTCATAAT CTAAAGTCTGACTTTCATG lag AS 191636 191651
yhfB(3.1E-3) TCTTATATTTATCAAAGTCAGTAGC CATAATCATTTTAATTAAA lead AS 752675 752690
uvrB(3.0E-3) AAAATTGCCAATGGTCTACTTCAC GTAAAACTTGTCCGGTCAA lead AS 556835 556850
xerD(3.0E-3) CATAGAACTCAGGAAATCCTTAAT CATTGGATGATAACTTTGA lead AS 1310409 1310424
intergenic(2.9E-3) AATAAAAAAGCCCTGAAATCAGGCC CTTTAAGATTTACATCATT lag . 672356 672371
pflA(2.9E-3) TCATCAATTTTTCGGTTACATATT TATCAGTCAAATATGGTTG lead AS 1880878 1880893
ycjC(2.9E-3) AATCGATATGTGAACACCTTCTCGGT CATGTTCAAGTTCAATGTC lead AS 292573 292588
citD(2.9E-3) GCTTACCAAACTGTTTTTTCCATC TGAAATCAAATCAATCGAA lead AS 1207881 1207896
murA1(2.8E-3) GTTGGACGAGGCCTAAATCACAGC CACCAGGCAAGCCTACTGT lead AS 313400 313415
pepXP(2.8E-3) CCAGGAGAACGCACAAGACATTTT CACGATAGTAATTATACCA lag AS 2135812 2135827
citF(2.8E-3) GCACTTTAGCACTCACGCGCTCAAT CACAAGGTCCTTGACTTCG lead AS 1209068 1209083
ydgF(2.8E-3) TATGCCCTAGATAATCATTCTTGTC TAATGCAGCAAGCCCAATT lag AS 364624 364639
ycbC(2.8E-3) ATAGCCGAAGTTGTTTAAGGCATTAT CATTTTCTCCTTTCCTAATA lead AS 212015 212030
ycbB(2.8E-3) ATAGCCGAAGTTGTTTAAGGCATTAT CATTTTCTCCTTTCCTAATA lead AS 212015 212030
yffD(2.7E-3) ACCTTGTGGAAGCCGCAGCTCATC CCATCTGCTCGTTTACCTA lead AS 555725 555740
citR(2.7E-3) TTAGAATAATTGACCATTTCACTCC CCAAGAACATTCTGACCTT lead S 1206297 1206312
noxD(2.7E-3) AAACTATCTCTTTATTAGTCGTTTC CACACAATCCACCTTTCAT lead AS 2194773 2194788
yvjA(2.7E-3) AAACTATCTCTTTATTAGTCGTTTC CACACAATCCACCTTTCAT lead AS 2194773 2194788
uvrA(2.6E-3) CCATCAACACGAACACGAACATAAC CATCTTTTTGGATACGCTC lead AS 1887923 1887938
yoaB(2.6E-3) AAAGTTGTAAAGGCATAGCCACAC CCATTTCAGGTGATGTTTT lead AS 1403419 1403434
hslO(2.6E-3) TCACCAGTAATTAAATCAACTTGCAC CACTATAAGGTTGTTTAAG lag AS 2034682 2034697
intergenic(2.6E-3) CCAGCAAGAGCAGTTGCAACATAAC CTACAACTTGTCCAAGAGC lag . 492284 492299
yngF(2.6E-3) AATCCTAAACAACACCACCAGAC CAGCAAGGGCACCAGCGAC lag AS 1367812 1367827
intergenic(2.6E-3) CAAAGATAAGCGAGTTATCGTTGT CCAAAGTTCAGGGTCTGGA lag . 492237 492252
yahG(2.6E-3) TTTTTCTCAATACAATTTGACGCAAC CAGTCAAGAAAGAGTCAC lag AS 73624 73639
citE(2.5E-3) CTTCGATACCGCTTTCACCATGGC CCGCACATCTTTTTGCCAA lead AS 1208323 1208338
ysjA(2.5E-3) GCCTCTGCAATGACTTTTCCAGAAC CTAAAATAGTCCTGAACC lead AS 1891336 1891351
mutS(2.5E-3) CTGCCCCAAGTTCATCAAACAAGAC CAAACTATTTTCATCTGCT lead AS 1692844 1692859
rgrB(2.5E-3) TTGGTGATATTTAGTTTTTCCACATT CAACCTCATTTTGGCGCCGT lead AS 1461344 1461359
L200146(2.4E-3) CCTTCCAGCACCGGGCAGGCGCAC CCCCTATACACCCTTGC lead AS 1982423 1982438
citC(2.4E-3) ATGGATTACCATTCATGACCATCGC CGCGATTTTTTTCGCACCA lead AS 1207184 1207199
yrbB(2.4E-3) TCGTGACGTAATGATTTTAGCCCATT CGCTAGCAGAATTAGCCCGC lead AS 1711588 1711603
clpE(2.4E-3) ACAATTTGTAAGGAGATTTTCTTTGC TCAAAGCAGAGATTTCAAT lead AS 552319 552334
citD(2.4E-3) CTACCGCAATCGCTCTGGCGTTAAT CACCAAATCCAAAGCCCCT lead AS 1207998 1208013
citF(2.4E-3) TCACATCACGCACAACTGTCGCAAT CCGACCGCGCACCAAAGGT lead AS 1210229 1210244
ypbD(2.3E-3) CATGCTAAAATACCAATGCCAAAAC CAATTAGGTAAAGCAGGCG lead AS 1514931 1514946
ycgD(2.3E-3) GGTTGACAATTCGTTTAATCACAAT ATTCTCACGTTCTTCACG lag AS 264608 264623
nrdG(2.3E-3) AGTGAGCACGCACCCCTTCACCAT CAACGAAATTGAAGGGTTT lead AS 272739 272754
gidC(2.3E-3) CCAGAAGCAGCTGATTCAACATAGC CCTCTACTCCTGTCATTTG lead AS 1257813 1257828
citF(2.3E-3) CGACACCTTTTTCAATAGCGTCAAG CAAAATATCAATTCATGACA lead AS 1209302 1209317
pfl(2.2E-3) GCCCCAGCAAGAAAGTTTCATCAC CATCATATGGTTTGTAGTT lead AS 657523 657538
pepDB(2.2E-3) CGTAATATCAACAAATATATCATAAT TAGAATCACCAAGAACAGC lead AS 1600812 1600827
yneH(2.2E-3) TCTGACAATATCTTCTTTACACCAAT GAAGTTTTGGAAATGAGAA lead AS 1346280 1346295
yfcI(2.2E-3) AGTGCTGACGATTCAGTTCCAGGAT CAATAATGAGATGTGAAGT lead S 529084 529099
potA(2.2E-3) GTTGAATGAATCAGCCATTCGTTAT TAAATTCATCGTAGGCTAC lead AS 1176611 1176626
lcnC(2.2E-3) TTAGCGCCTAGTGAGCCTACTTCAC AAGAAGAGATTATTAGAGC lag S 84331 84346
sdaB(2.2E-3) CACCGATTCAATTTCCAGTCACGGT CATTGTTCGATCCCCTTTT lead AS 843781 843796
yjhD(2.2E-3) ATTGATTTAATCAAATTTCATCAC CTTTTTGATAGCCTTTTTG lead AS 973074 973089
ygdA(2.2E-3) CGTAGAAATCATGTCCCAACATATC CATCTGAGCACTGCTTCT lead AS 632818 632833
intergenic(2.1E-3) GACAACAAAAAAAGCGGGCCATCTC CCCAGATAAACGACTTTAA lag . 506679 506694
yyaL(2.1E-3) ACGTGAATCATGCCTCTACTTCAC GAATATTGGCAAGAATTT lead AS 11386 11401
hflX(2.1E-3) TTGCACCAAGGCACTTTTTCGTAAT TCAGGTTACTGATAGCTT lead AS 225887 225902
citF(2.1E-3) GCGCCACGAATGCACACGTCAGAAC CAGACATAACGTTACGTT lead AS 1210134 1210149
glnQ(2.1E-3) TTTTTCATAACGGCTAGAACCGCAC CAACCATTTCAGGGTCAAG lag AS 1819568 1819583
yoaD(2.1E-3) TGTGCTTTAGCCGCGAAAATACATC CGCAATACACATTGACGATA lead AS 1406099 1406114
ywiA(2.0E-3) TCTTCGCGCAAATTCACGAACATCTC CAATATTACCTGGATTTAC lead AS 2280342 2280357
pepO(2.0E-3) AACCAATGAAAGGAGTAATAGCATC CAATTTTTCAATGGCTTTT lag AS 1867496 1867511
citC(2.0E-3) GTCGCTGAAATCATTTCTTCATTAT CATCAGCTTTTTTCGCTC lead AS 1207623 1207638
potB(2.0E-3) AAAATGATTCCCATTAAAGCATGCG CAAAGGGACGATAACAAAG lead AS 1177014 1177029
ylhB(2.0E-3) CAATATAATTTTTAGCCGCCATAAT CATTGGAATTAAAATTGCA lead AS 1173553 1173568
intergenic(2.0E-3) TAGTATAAAATAAACAAGGCTTGCT CATTATAGTGCAAAAAAT lag . 494197 494212
pnpA(2.0E-3) AGCGCTCCGTGACCATATTCACGAG GTCCAGGTGCCCCGTAACG lead AS 1923022 1923037
ylhB(1.9E-3) TCAGGATGTTTCTTTAGGACATAAG CAGCCACTGTCATTACAGG lead AS 1173752 1173767
intergenic(1.9E-3) TACTGATTATTTTTGTATAACATAAC TATTTTTAAAATAGTTAAAA lag . 2316411 2316426
ynbC(1.9E-3) GTAAGAAAATCTGTATCCACTAT CATAATCACAGTTCCCAGC lead AS 1311522 1311537
intergenic(1.9E-3) TTGCGAAAAACAAATGGTTCTCGAC TTGCAATCAGCCCATTCG lead . 1501790 1501805
ytgG(1.9E-3) TTACCATCATCAATTGTTACTCGAT CATAAAAAGCTGTCTTTAA lead AS 1969437 1969452
tra904E(1.9E-3) CCAAAGAAGCACCTTATACTTAGC CGTGAATATCGACGTTTTT lead S 626963 626978
citF(1.9E-3) TAAGCGAATTCACATATAACATCAT TAACCATAGAGGCAATTTT lead AS 1209756 1209771
yoaB(1.9E-3) CTCGTTTACTTTGCACGACCGCAAG CACTGATATTAATCATCAAA lead AS 1405483 1405498
ygfC(1.9E-3) ACTTGTGAAATTGGTTTATCATTTT CACTAGCTGGGACGGTTGC lag AS 653935 653950
pacL(1.8E-3) GATCCCCTGTAATCATTAACCACATT AATATTTGCATCATGAAGT lead AS 677838 677853
pepDA(1.8E-3) AGACGATTAGGAGCAATAACATAAG CGTCGTCGGGGATACGAAT lag AS 249255 249270
ydiA(1.8E-3) GAGAAGTCTATGATGTATTCAAAAT TCATATCATTTTTAAACA lag S 381887 381902
yrfE(1.8E-3) GTTTATACTTTTTTTCATTCATTGT CATATTTATTATATCAAAGT lead AS 1760358 1760373
potA(1.8E-3) CTCAATTGGTTCATTTTTACGCATC CCACCATCGACAGCTTCAA lead AS 1176465 1176480
yahA(1.8E-3) AAGAACCACGCTATTTCAAACATTTC CAAATCATTCATTGGTCA lag AS 72409 72424
glnP(1.8E-3) GGGAGATTCATGGGAAGTTCATTGC TAAATCTTGCCCTTGTTTC lag AS 1817470 1817485
ptnC(1.8E-3) GAAGATGCAGTACCATTTCCAGAAC CACCAGAAGCTTGGAGGTT lag AS 1764021 1764036
malG(1.8E-3) TAGATTAAGAATTGAATACATTGC AATCATTCCCATGATTCCT lag AS 1742084 1742099
yudI(1.8E-3) CCGCAGTGACGCCTGTTCATCAAT CATGCGTTTCGCGTCTTCA lag AS 2036542 2036557
yljG(1.8E-3) GCCAAAAGATTTCCATTAGCAGAAC CAACATCAAAGATACTTGA lead AS 1197300 1197315
pepQ(1.8E-3) TTACGTTCAGCAGCAGTGGCAAAAG CAATTTCAAAACACTTGTC lag AS 1697596 1697611
frdC(1.7E-3) ACCAATAACCACCAACTGCTGAAC CATCATGTGGTCGGTGAGT lead AS 1138403 1138418
pepQ(1.7E-3) AAAGACAGTCTTCAATACGCAGACC TACTTTACCAGGAATATAA lag AS 1698129 1698144
yqjD(1.7E-3) TTGCTTACTCAAAACCATTAGCATTAG TACTTTGTGCTGGCATTTGT lead AS 1698715 1698730
ywcC(1.7E-3) GTTGTCAAAGAATCATGTCCACGAT TAGAAGTATAGAGGAATTT lag AS 2229225 2229240
clsB(1.7E-3) GCTTATTAAGCCCTTATATACAAGAC CATTTTATAATATCGGACTA lead AS 1188583 1188598
deoB(1.7E-3) AATGGTGACAAAGCATAGTCACGAC GTCCATCAGTCCGTTCAAA lead AS 955858 955873
dexA(1.7E-3) CCTTGCAAATCTCCAACACCATCAC CATTAGCATCCATTAAAGA lead AS 1736621 1736636


glnP(1.7E-3) lag AS 1817416 1817431
ptnC(1.6E-3) lag AS 1763895 1763910
glnP(1.6E-3) lag AS 1817828 1817843
citG(1.6E-3) lead AS 1210864 1210879
mae(1.6E-3) lead AS 1203656 1203671
ycgD(1.6E-3) lag AS 264275 264290
ybaA(1.5E-3) lag S 101429 101444
pbuX(1.5E-3) lead AS 1161385 1161400
clpP(1.5E-3) lag AS 672927 672942
rliB(1.5E-3) lag AS 1535352 1535367
L200097(1.5E-3) lead AS 542710 542725
yoaB(1.5E-3) lead AS 1404904 1404919
gatB(1.5E-3) lead AS 168767 168782
uvrC(1.5E-3) lead AS 857972 857987
intergenic(1.5E-3) lead . 1299735 1299750
pycA(1.5E-3) lead AS 666290 666305
rmaA(1.5E-3) lag AS 749971 749986
ybdC(1.4E-3) lead AS 132449 132464
ywaH(1.4E-3) lag AS 2208331 2208346
yahG(1.4E-3) lag AS 73866 73881
gidC(1.4E-3) lead AS 1257582 1257597
malF(1.4E-3) lag AS 1740735 1740750
als(1.4E-3) lead AS 1200572 1200587
feoB(1.4E-3) lag AS 190731 190746
rliB(1.4E-3) lag AS 1535526 1535541
pbp1B(1.4E-3) lead AS 392472 392487
fabG(1.3E-3) lead AS 801923 801938
yxaB(1.3E-3) lag AS 2301202 2301217
yvhB(1.3E-3) lead AS 2176801 2176816
rlrD(1.3E-3) lag AS 380962 380977
yngF(1.3E-3) lag AS 1367821 1367836
glpD(1.3E-3) lead AS 1270237 1270252
ysgC(1.3E-3) lead AS 1870118 1870133
yscB(1.3E-3) lead AS 1822184 1822199
cysM(1.3E-3) lag AS 526318 526333
intergenic(1.2E-3) lag . 1765153 1765168
yijC(1.2E-3) lead AS 893748 893763
ynhD(1.2E-3) lead AS 1376527 1376542
intergenic(1.2E-3) lead . 600720 600735
citD(1.2E-3) lead AS 1207824 1207839
yudI(1.2E-3) lag AS 2036249 2036264
codY(1.2E-3) lead AS 164615 164630
hemH(1.2E-3) lag S 1608898 1608913
yngF(1.2E-3) lag AS 1367256 1367271
yuhE(1.2E-3) lag AS 2073300 2073315
yudH(1.1E-3) lag AS 2035630 2035645
intergenic(1.1E-3) lead . 1641659 1641674
mapA(1.1E-3) lead AS 1731080 1731095
pbuX(1.0E-3) lead AS 1160642 1160657
maeP(1.0E-3) lead AS 1205444 1205459
menB(1.0E-3) lag AS 734925 734940
intergenic(1.0E-3) lead . 618453 618468
yrjE(1.0E-3) lead AS 1794110 1794125
menF(1.0E-3) lag AS 738516 738531
ycgF(1.0E-3) lead AS 265738 265753
ythB(1.0E-3) lead AS 1974386 1974401
pepXP(1.0E-3) lag AS 2135848 2135863
yuhI(1.0E-3) lag AS 2077617 2077632
clpC(1.0E-3) lead AS 630372 630387
menB(1.0E-3) lag AS 734934 734949
intergenic(997.7E-6) lead . 779365 779380
ppiA(993.9E-6) lag AS 368737 368752
pstA(988.2E-6) lead AS 1771561 1771576
intergenic(985.4E-6) lag . 461287 461302
aroH(983.5E-6) lead AS 1281265 1281280
pbp2A(983.5E-6) lead AS 2177528 2177543
yfiI(972.1E-6) lead AS 587196 587211
intergenic(964.5E-6) lead -. 1204656 1204671
ykiF(960.7E-6) lag AS 1087045 1087060
ysiC(957.0E-6) lag AS 1884434 1884449
yudI(956.0E-6) lag AS 2035870 2035885
dacA(954.1E-6) lag AS 2356058 2356073
ysjA(942.7E-6) lag S 1890475 1890490
L200091(932.3E-6) lead AS 424310 424325
ycdJ(925.7E-6) lag S 237900 237915
yogG(916.2E-6) lead AS 1466341 1466356
intergenic(915.3E-6) lead . 1815757 1815772
Intergenic(901.1E-6) lead . 1516165 1516180
pspA(868.8E-6) lag AS 2304622 2304637
ponA(867.9E-6) lag AS 529759 529774
ycgE(844.2E-6) lag AS 265242 265257
nrdF(837.6E-6) lag AS 1001348 1001363
citC(837.6E-6) lead AS 1207190 1207205
ykhD(830.0E-6) lag AS 1072513 1072528
pheS(821.5E-6) lag S 2009589 2009604
intergenic(817.7E-6) lag . 2281324 2281339
yxbD(811.0E-6) lag S 2319277 2319292
mscL(809.2E-6) lag AS 2170604 2170619
yhcA(803.5E-6) lag AS 720821 720836
L200142(781.7E-6) lead AS 537959 537974


clpE(771.3E-6) lead AS 551980 551995
queA(768.4E-6) lag AS 1617278 1617293
yafC(759.9E-6) lead AS 55665 55680
phoL(756.1E-6) lead AS 1094072 1094087
intergenic(735.2E-6) lag . 1259597 1259612
rlrD(706.8E-6) lag AS 381092 381107
intergenic(701.1E-6) lead . 133745 133760
intergenic(694.5E-6) lag . 172797 172812
llrB(688.8E-6) lag AS 1458185 1458200
tra904C(678.4E-6) lead S 140716 140731
intergenic(678.4E-6) lag . 565296 565311
intergenic(678.4E-6) lead . 1718258 1718273
trmB(674.6E-6) lead AS 756416 756431
dacA(669.9E-6) lag AS 2356769 2356784
aroK(662.3E-6) lead AS 1801096 1801111
citF(633.9E-6) lead AS 1209659 1209674
pflA(626.3E-6) lead AS 1880728 1880743
pnpA(606.4E-6) lead AS 1923010 1923025
pi234(605.4E-6) lead AS 1058576 1058591
recO(604.5E-6) lead AS 58059 58074
pacL(604.5E-6) lead AS 676631 676646
dxsB(598.8E-6) lead AS 1724988 1725003
yahI(596.9E-6) lag AS 77909 77924
yciC(595.0E-6) lead AS 285581 285596
hom(593.1E-6) lead AS 1171374 1171389
rnhA(593.1E-6) lag AS 2349530 2349545
pbp2B(591.2E-6) lead AS 339692 339707
ythB(589.3E-6) lead AS 1974335 1974350
intergenic(573.2E-6) lag . 2016727 2016742
pfl(567.5E-6) lag S 659540 659555
dukA(538.2E-6) lag AS 493902 493917
rpoC(526.8E-6) lead AS 1857655 1857670
gidB(520.2E-6) lead S 1381124 1381139
trpD(520.2E-6) lag S 1498901 1498916
gntR(519.2E-6) lag AS 2272093 2272108
intergenic(513.5E-6) lead . 1327864 1327879
asnB(509.7E-6) lead AS 356847 356862
glnP(504.1E-6) lag AS 1818448 1818463
yseI(493.6E-6) lead AS 1849361 1849376
hrcA(488.0E-6) lead AS 977222 977237
dut(485.1E-6) lead AS 181536 181551
noxB(484.2E-6) lag S 842595 842610
ypgC(483.2E-6) lag AS 1562864 1562879
purA(483.2E-6) lag S 2029214 2029229
preA(482.3E-6) lead AS 187014 187029
rpsH(475.6E-6) lead AS 2162238 2162253
yogJ(470.0E-6) lead AS 1468954 1468969
busAA(464.3E-6) lead AS 1474868 1474883
udk(460.5E-6) lead AS 1709603 1709618
dxsB(459.5E-6) lead AS 1724352 1724367
yrgI(459.5E-6) lag AS 1769762 1769777
yreB(451.9E-6) lag AS 1744102 1744117
citE(447.2E-6) lead AS 1208681 1208696
yudI(442.5E-6) lag AS 2036072 2036087
yljF(426.4E-6) lead AS 1196804 1196819
yriD(417.8E-6) lag S 1773284 1773299
dnaA(415.0E-6) lead AS 1668 1683
kdgR(410.3E-6) lag AS 1680250 1680265
ysfD(409.3E-6) lead AS 1854261 1854276
pknB(408.4E-6) lead AS 1955328 1955343
rplM(406.5E-6) lag S 2346912 2346927
gpsA(405.5E-6) lag AS 1376845 1376860
citB(401.7E-6) lead AS 669535 669550
yvdE(400.8E-6) lag AS 2137423 2137438
yhfD(398.9E-6) lead AS 755426 755441
intergenic(398.9E-6) lag . 1002525 1002540
pacL(389.4E-6) lead AS 678810 678825
pspA(389.4E-6) lag AS 2303688 2303703
uppP(381.8E-6) lead AS 2275479 2275494
thrA(375.2E-6) lag AS 747685 747700
ydiF(369.5E-6) lag AS 388917 388932
intergenic(369.5E-6) lead . 1166149 1166164
ypjC(355.3E-6) lead AS 1592521 1592536
ptnC(353.4E-6) lag AS 1763862 1763877
ymjE(348.7E-6) lead AS 1297570 1297585
nth(345.8E-6) lead AS 1083938 1083953
llrB(344.9E-6) lag AS 1458407 1458422
asnB(341.1E-6) lead AS 356922 356937
ydiF(341.1E-6) lag AS 387696 387711
intergenic(339.2E-6) lag . 1816604 1816619
ydiB(338.3E-6) lag S 383788 383803
ps123(332.6E-6) lead AS 49501 49516
ysjD(330.7E-6) lead AS 1893720 1893735
yrjD(326.9E-6) lag AS 1793542 1793557
fbaA(326.9E-6) lag S 1979644 1979659
ptsI(325.0E-6) lead AS 121312 121327
pcrA(313.6E-6) lead AS 1135794 1135809
yudK(312.7E-6) lead AS 2038474 2038489
citG(307.9E-6) lead AS 1211075 1211090
intergenic(305.1E-6) lead . 1838537 1838552


yeaC(304.1E-6) lead AS 405707 405722
yfbJ(304.1E-6) lag S 515575 515590
fbaA(304.1E-6) lead AS 1979895 1979910
ps105(302.2E-6) lag AS 37893 37908
pcrA(297.5E-6) lead AS 1134512 1134527
L200150(296.6E-6) lead AS 2221669 2221684
intergenic(294.7E-6) lag . 2100424 2100439
intergenic(291.8E-6) lead . 1401689 1401704
recD(290.9E-6) lead AS 1797401 1797416
intergenic(289.9E-6) lead . 1200392 1200407
ypgC(287.1E-6) lag AS 1562527 1562542
ptnAB(287.1E-6) lag AS 1762532 1762547
yrgI(287.1E-6) lag AS 1769877 1769892
yejH(286.1E-6) lead AS 499252 499267
ylaD(286.1E-6) lead AS 1105621 1105636
scrK(283.3E-6) lag S 1518450 1518465
fhs(279.5E-6) lead AS 960252 960267
topA(273.8E-6) lead AS 1255147 1255162
ymjE(271.9E-6) lead AS 1296421 1296436
comFA(271.0E-6) lead S 1097125 1097140
fabD(269.1E-6) lead AS 783367 783382
intergenic(268.1E-6) lead . 498594 498609
ytbB(268.1E-6) lead AS 1913605 1913620
sdaB(262.5E-6) lead AS 843991 844006
leuS(254.9E-6) lead AS 829278 829293
ilvD(252.0E-6) lead AS 1246083 1246098
nrdD(251.1E-6) lead AS 271457 271472
citD(245.4E-6) lead AS 1208013 1208028
rplC(245.4E-6) lead AS 2169681 2169696
yfjF(236.9E-6) lead S 599610 599625
yrjE(236.9E-6) lead AS 1794180 1794195
clpC(233.1E-6) lag S 630146 630161
ymjE(231.2E-6) lead AS 1296165 1296180
relA(227.4E-6) lead AS 108865 108880
ssbB(226.4E-6) lead AS 2274356 2274371
yeiF(225.5E-6) lead AS 486830 486845
gyrA(222.7E-6) lag S 1123616 1123631
llrG(222.7E-6) lead AS 1805025 1805040
floL(221.7E-6) lead AS 746840 746855
ylaD(221.7E-6) lead AS 1105705 1105720
L200115(220.8E-6) lead AS 2344208 2344223
parC(217.0E-6) lag S 1012443 1012458
rmaJ(215.1E-6) lag AS 583465 583480
leuA(211.3E-6) lag S 1240133 1240148
rpsM(200.9E-6) lead AS 2153631 2153646
intergenic(199.9E-6) lag . 1712489 1712504
ponA(199.0E-6) lead S 530491 530506
yieH(196.1E-6) lag AS 850840 850855
purL(188.5E-6) lead AS 1576156 1576171
intergenic(186.7E-6) lead . 1677069 1677084
L200065(185.7E-6) lead AS 1745995 1746010
hemH(184.8E-6) lead AS 1608810 1608825
menX(181.9E-6) lag AS 736367 736382
hpt(178.1E-6) lead AS 25358 25373
yqbK(178.1E-6) lag S 1619709 1619724
Intergenic(175.3E-6) lead . 841200 841215
ybcH(173.4E-6) lead S 123666 123681
def(172.4E-6) lag AS 555416 555431
L200156(172.4E-6) lead AS 2344471 2344486
L200146(169.6E-6) lead AS 1982437 1982452
yyaL(167.7E-6) lead AS 12154 12169
pepA(165.8E-6) lag AS 394211 394226
ydbA(163.0E-6) lag S 311295 311310
lcnC(162.0E-6) lag S 83878 83893
infB(161.1E-6) lead AS 777180 777195
sdaA(160.1E-6) lead AS 844130 844145
gyrB(157.3E-6) lead AS 929120 929135
yqcA(155.4E-6) lag S 1624880 1624895
recF(155.4E-6) lag AS 2051618 2051633
ydgC(153.5E-6) lead S 362514 362529
pbp2A(153.5E-6) lead AS 2178563 2178578
dnaE(152.5E-6) lead AS 496795 496810
nucA(152.5E-6) lead AS 1100790 1100805
intergenic(151.6E-6) lead . 1213718 1213733
clpC(147.8E-6) lead AS 631593 631608
clpB(146.9E-6) lag S 1567554 1567569
vacB1(145.9E-6) lag S 968723 968738
proB(145.0E-6) lead AS 1652644 1652659
pacB(144.0E-6) lead AS 1903831 1903846
prsA(141.2E-6) lead AS 826166 826181
ymdE(141.2E-6) lead S 1238775 1238790
ps201(137.4E-6) lag AS 503656 503671
yujG(137.4E-6) lead AS 2099884 2099899
pi301(136.4E-6) lag S 1414528 1414543
ddl(134.5E-6) lead AS 341407 341422
purC(133.6E-6) lag S 1577698 1577713
ycjB(132.6E-6) lead AS 291861 291876
gltB(132.6E-6) lag S 1318756 1318771
ythB(132.6E-6) lead AS 1974292 1974307
yhfB(130.8E-6) lead AS 752126 752141

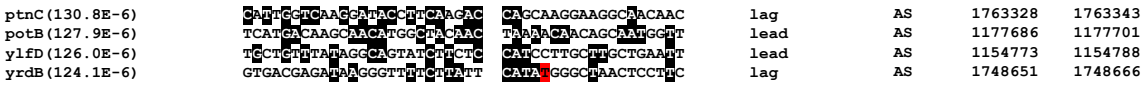
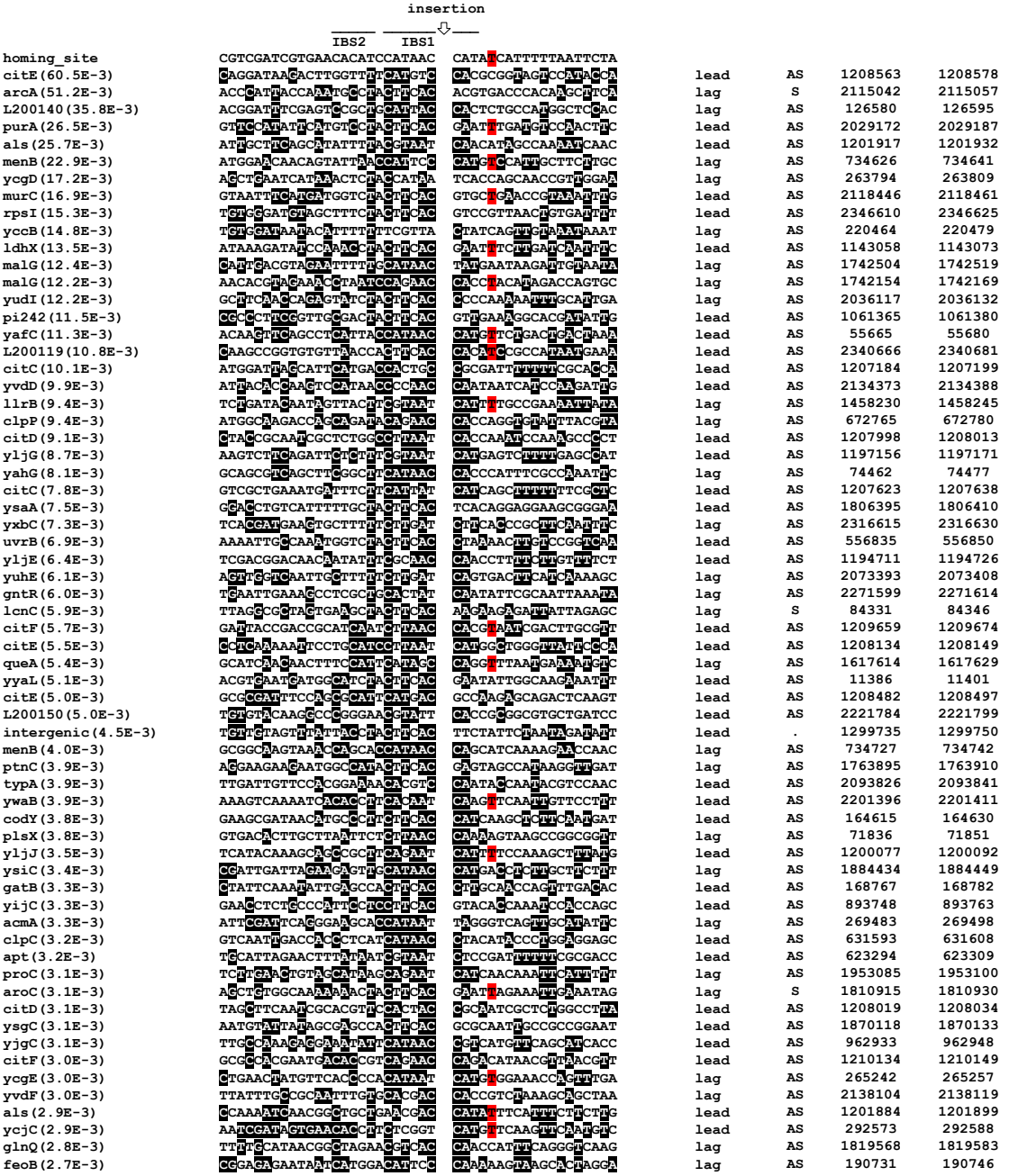
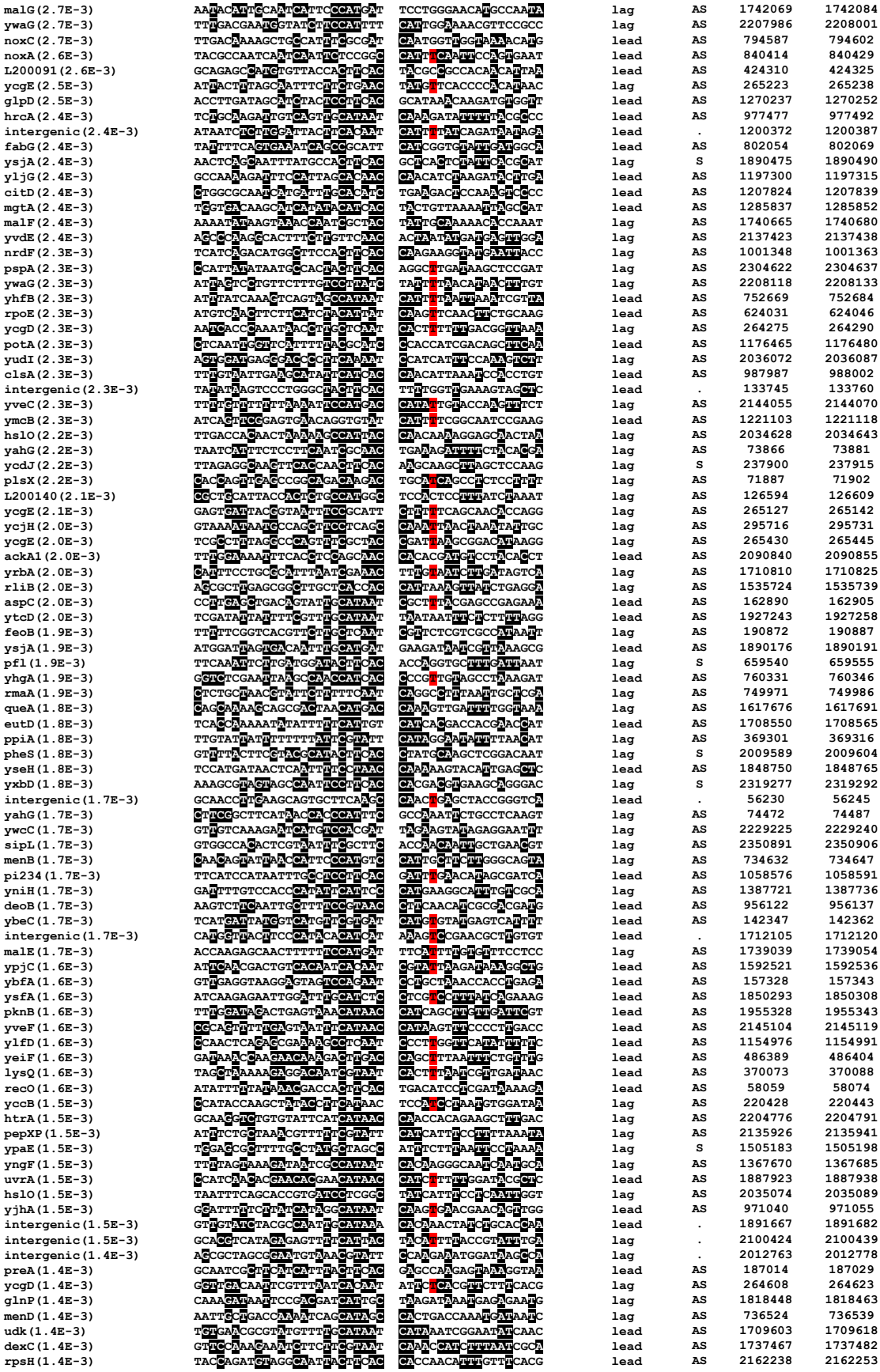
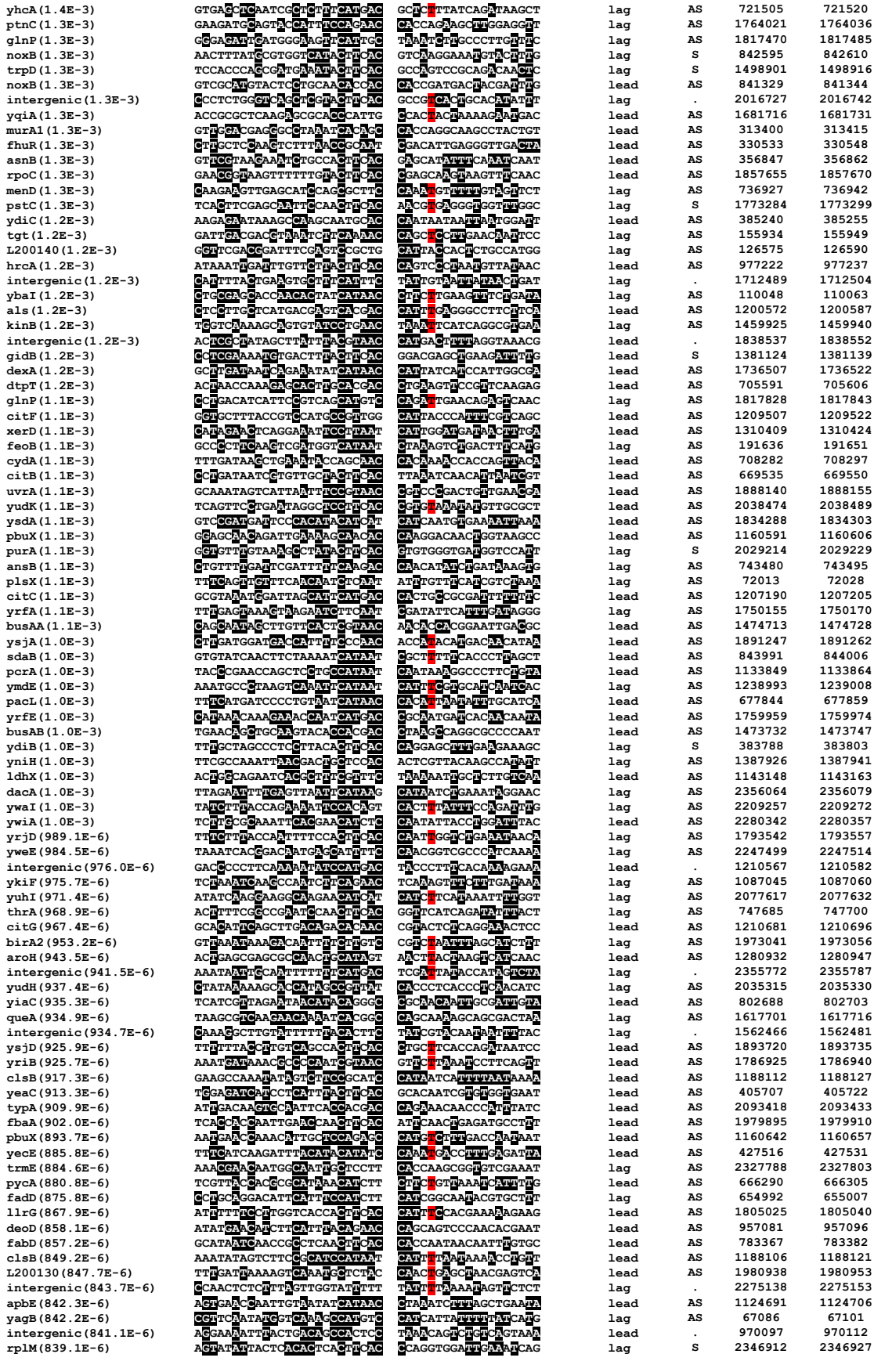
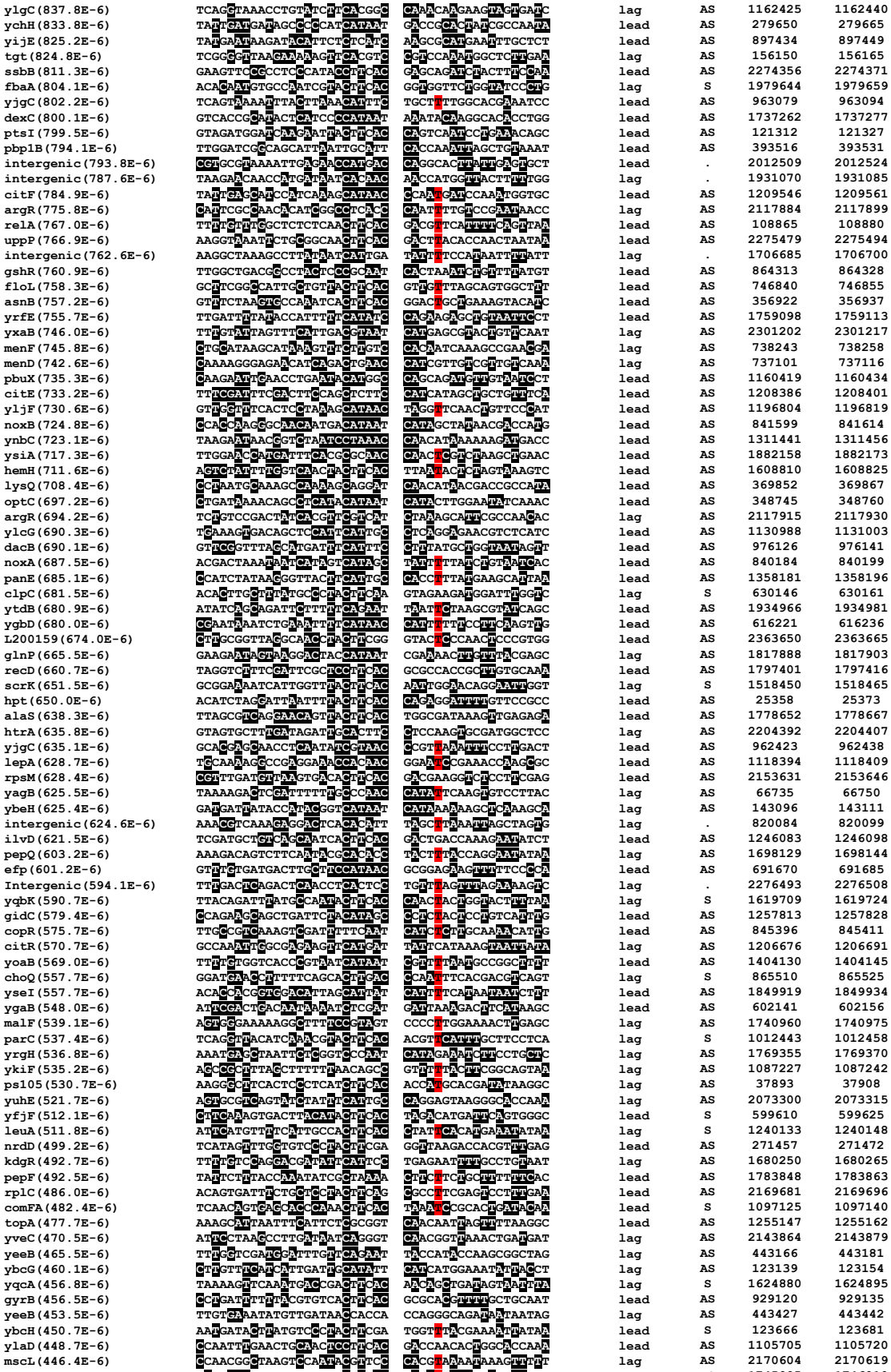

ptnC(130.8E-6) CATTGCTCAAGCATACCTTCAAGAC CAGCAAGGAAGGCAACAAC lag AS 1763328 1763343
potB(127.9E-6) TCATGACAAGCAACATGGCTACAAC TAAAACAACAGCAATGGTT lead AS 1177686 1177701
ylfD(126.0E-6) TGCTGTTTATAGGCAGTATCTTCTC CATCCTTGCTTGCTGAATT lead AS 1154773 1154788
yrdB(124.1E-6) GTGACGAGATAAGGGTTTTCTTATT CATATGGGCTAACTCCTTC lag AS 1748651 1748666

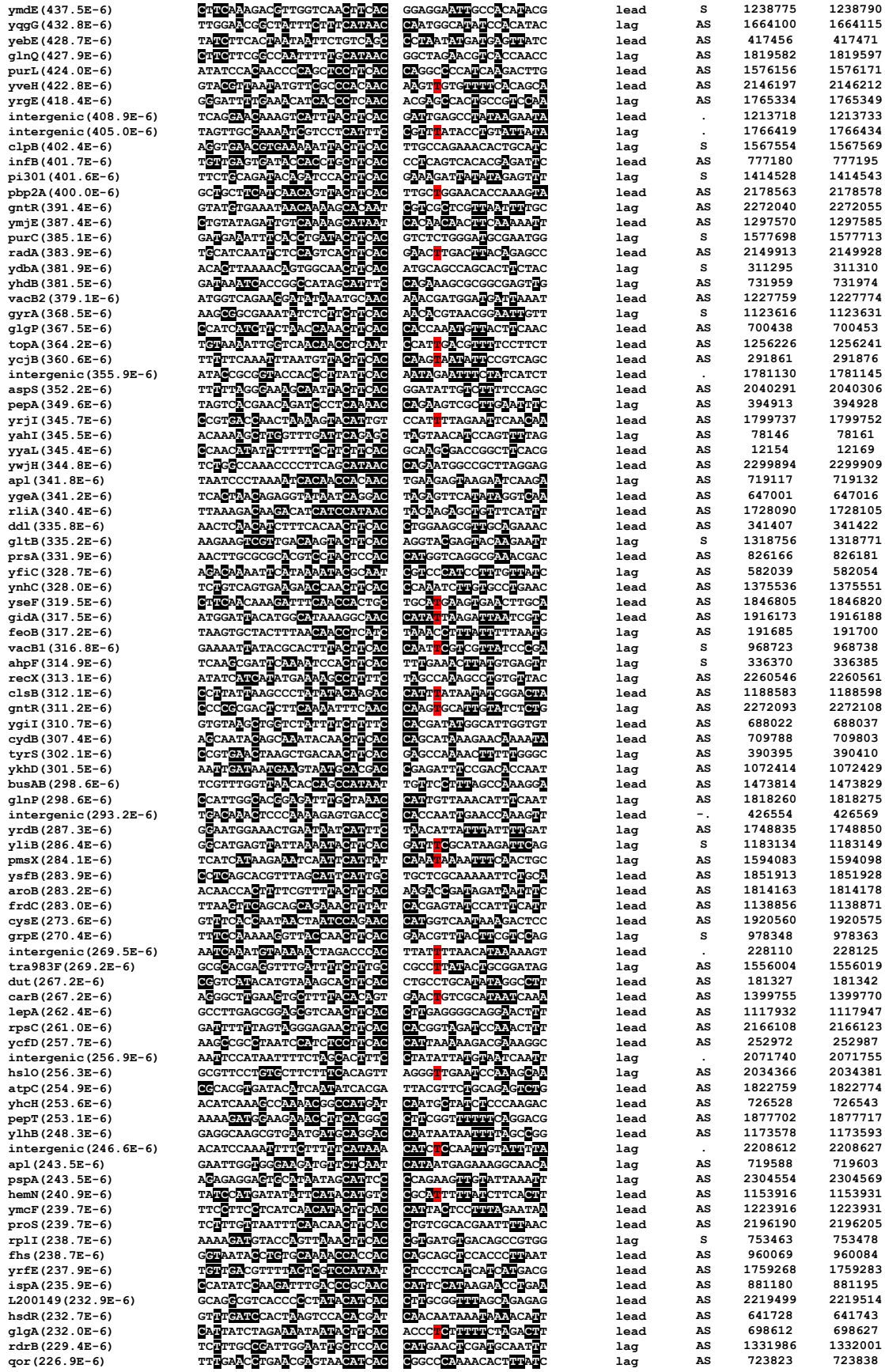
Table S4. Multiple alignment of the chromosomal insertion sites of Ll.LtrB intron in the presence of the relaxase (D-pLtrB strain) arranged by the frequency of the event. Names of the genes and relative frequencies are given in which insertions of Ll.LtrB were detected; the orientation of the insertions 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.

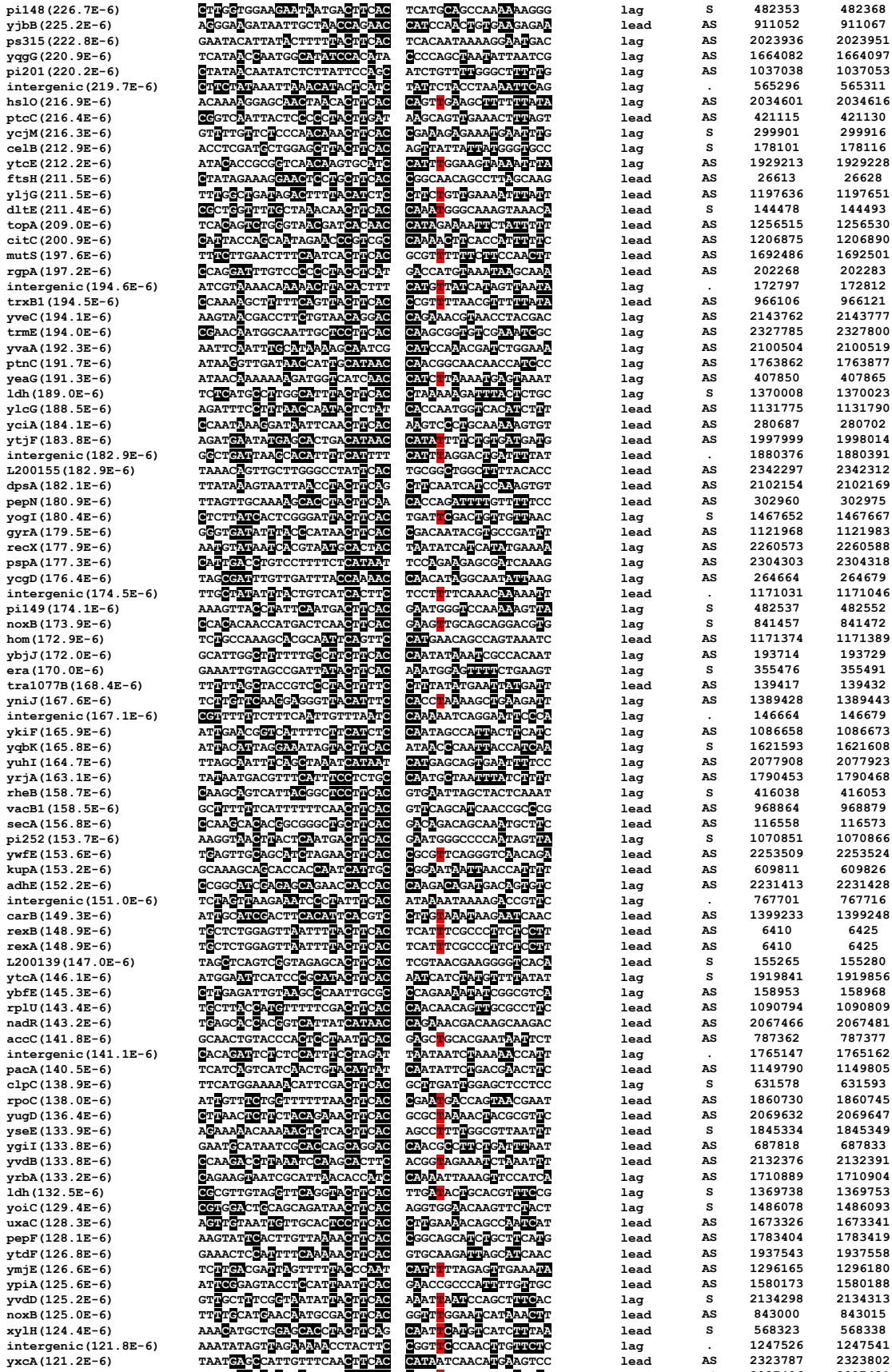


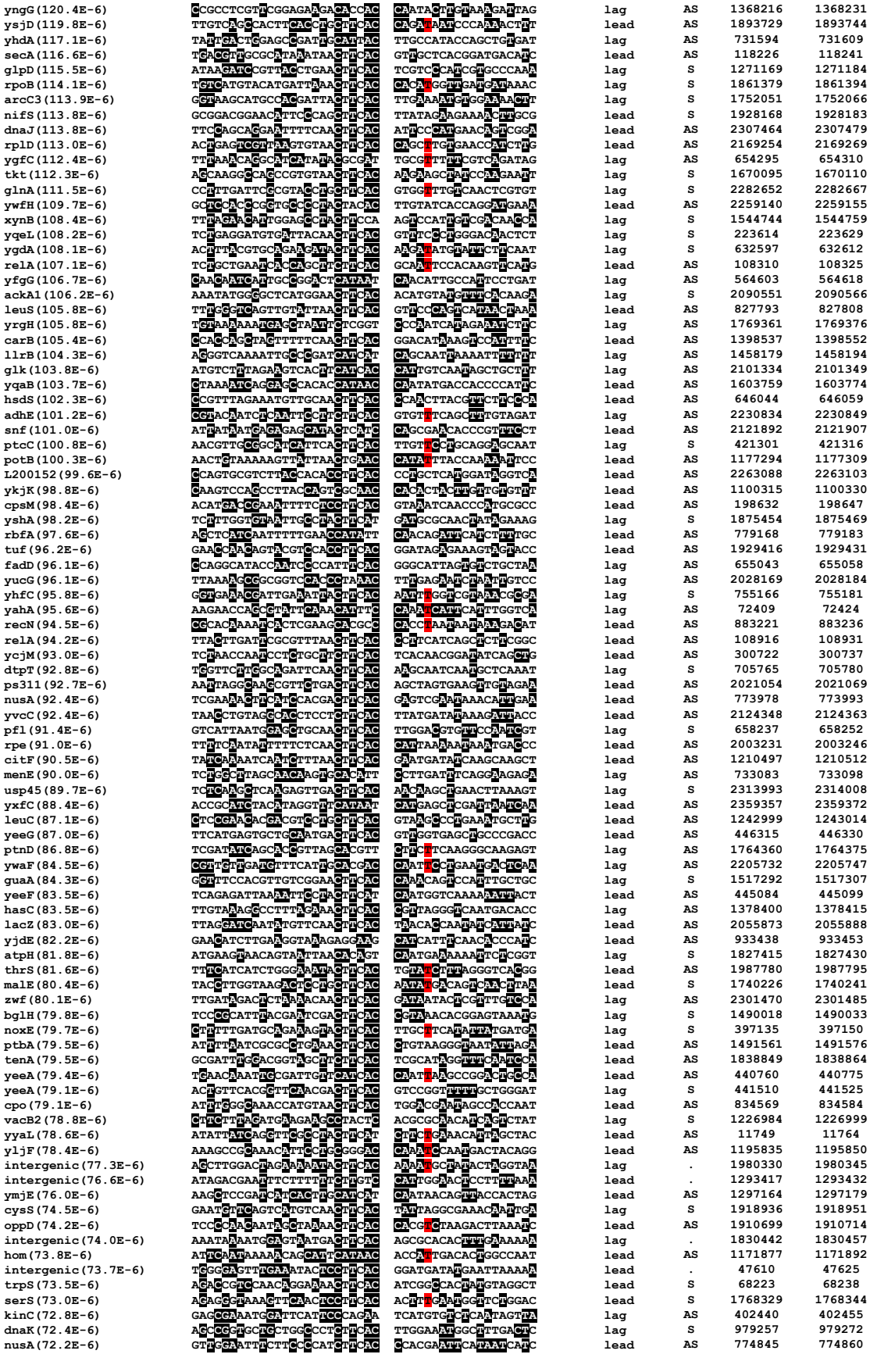

malG(2.7E-3) lag AS 1742069 1742084
ywaG(2.7E-3) lag AS 2207986 2208001
noxC(2.7E-3) lead AS 794587 794602
noxA(2.6E-3) lead AS 840414 840429
L200091(2.6E-3) lead AS 424310 424325
ycgE(2.5E-3) lag AS 265223 265238
glpD(2.5E-3) lead AS 1270237 1270252
hrcA(2.4E-3) lead AS 977477 977492
intergenic(2.4E-3) lead . 1200372 1200387
fabG(2.4E-3) lead AS 802054 802069
ysjA(2.4E-3) lag S 1890475 1890490
yljG(2.4E-3) lead AS 1197300 1197315
citD(2.4E-3) lead AS 1207824 1207839
mgtA(2.4E-3) lead AS 1285837 1285852
malF(2.4E-3) lag AS 1740665 1740680
yvdE(2.4E-3) lag AS 2137423 2137438
nrdF(2.3E-3) lag AS 1001348 1001363
pspA(2.3E-3) lag AS 2304622 2304637
ywaG(2.3E-3) lag AS 2208118 2208133
yhfB(2.3E-3) lead AS 752669 752684
rpoE(2.3E-3) lead AS 624031 624046
ycgD(2.3E-3) lag AS 264275 264290
potA(2.3E-3) lead AS 1176465 1176480
yudI(2.3E-3) lag AS 2036072 2036087
clsA(2.3E-3) lead AS 987987 988002
intergenic(2.3E-3) lead . 133745 133760
yveC(2.3E-3) lag AS 2144055 2144070
ymcB(2.3E-3) lead AS 1221103 1221118
hslO(2.2E-3) lag AS 2034628 2034643
yahG(2.2E-3) lag AS 73866 73881
ycdJ(2.2E-3) lag S 237900 237915
plsX(2.2E-3) lag AS 71887 71902
L200140(2.1E-3) lag AS 126594 126609
ycgE(2.1E-3) lag AS 265127 265142
ycjH(2.0E-3) lag AS 295716 295731
ycgE(2.0E-3) lag AS 265430 265445
ackA1(2.0E-3) lead AS 2090840 2090855
yrbA(2.0E-3) lag AS 1710810 1710825
rliB(2.0E-3) lag AS 1535724 1535739
aspC(2.0E-3) lead AS 162890 162905
ytcD(2.0E-3) lead AS 1927243 1927258
feoB(1.9E-3) lag AS 190872 190887
ysjA(1.9E-3) lead AS 1890176 1890191
pfl(1.9E-3) lag S 659540 659555
yhgA(1.9E-3) lead AS 760331 760346
rmaA(1.9E-3) lag AS 749971 749986
queA(1.8E-3) lag AS 1617676 1617691
eutD(1.8E-3) lead AS 1708550 1708565
ppiA(1.8E-3) lag AS 369301 369316
pheS(1.8E-3) lag S 2009589 2009604
yseH(1.8E-3) lead AS 1848750 1848765
yxbD(1.8E-3) lag S 2319277 2319292
intergenic(1.7E-3) lead . 56230 56245
yahG(1.7E-3) lag AS 74472 74487
ywcC(1.7E-3) lag AS 2229225 2229240
sipL(1.7E-3) lag AS 2350891 2350906
menB(1.7E-3) lag AS 734632 734647
pi234(1.7E-3) lead AS 1058576 1058591
yniH(1.7E-3) lag AS 1387721 1387736
deoB(1.7E-3) lead AS 956122 956137
ybeC(1.7E-3) lead AS 142347 142362
intergenic(1.7E-3) lead . 1712105 1712120
malE(1.7E-3) lag AS 1739039 1739054
ypjC(1.6E-3) lead AS 1592521 1592536
ybfA(1.6E-3) lead AS 157328 157343
ysfA(1.6E-3) lead AS 1850293 1850308
pknB(1.6E-3) lead AS 1955328 1955343
yveF(1.6E-3) lead AS 2145104 2145119
ylfD(1.6E-3) lead AS 1154976 1154991
yeiF(1.6E-3) lead AS 486389 486404
lysQ(1.6E-3) lead AS 370073 370088
recO(1.6E-3) lead AS 58059 58074
yccB(1.5E-3) lag AS 220428 220443
htrA(1.5E-3) lag AS 2204776 2204791
pepXP(1.5E-3) lag AS 2135926 2135941
ypaE(1.5E-3) lag S 1505183 1505198
yngF(1.5E-3) lag AS 1367670 1367685
uvrA(1.5E-3) lead AS 1887923 1887938
hslO(1.5E-3) lag AS 2035074 2035089
yjhA(1.5E-3) lead AS 971040 971055
intergenic(1.5E-3) lead . 1891667 1891682
intergenic(1.5E-3) lag . 2100424 2100439
intergenic(1.4E-3) lag . 2012763 2012778
preA(1.4E-3) lead AS 187014 187029
ycgD(1.4E-3) lag AS 264608 264623
glnP(1.4E-3) lag AS 1818448 1818463
menD(1.4E-3) lag AS 736524 736539
udk(1.4E-3) lead AS 1709603 1709618
dexC(1.4E-3) lead AS 1737467 1737482
rpsH(1.4E-3) lead AS 2162238 2162253

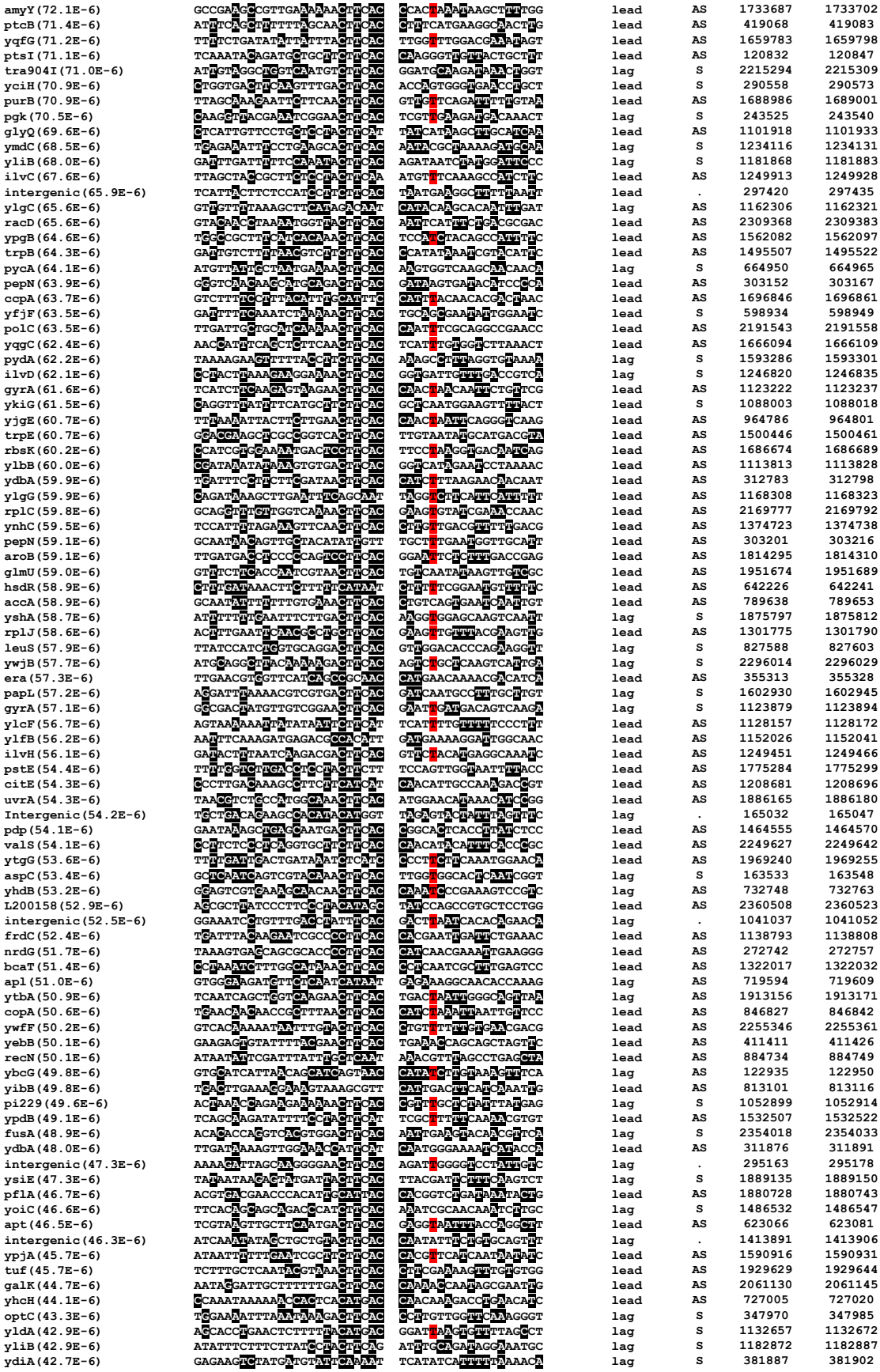

yhcA(1.4E-3) GTGAGCTCAATCGCTCTTCATGAC GCTCTTATCAGATAAGCT lag AS 721505 721520
ptnC(1.3E-3) GAAGATGCAGTACCATTTCCAGAAC CACCAGAAGCTTGGAGGTT lag AS 1764021 1764036
glnP(1.3E-3) GGGACATTCATGGGAAGTTCATTGC TAATTCTGCCCTTGTTTC lag AS 1817470 1817485
noxB(1.3E-3) AACTTTATCGTGGTCATAGTTCAC GTCAAGGAAATGTACTTTG lag S 842595 842610
trpD(1.3E-3) TCCACCCAGCGATGAATAGTTCAC GCCAGTCCGCAGACAACTC lag S 1498901 1498916
noxB(1.3E-3) GTCGCATGTACTCCTGCAACACCAC CACCGATGACTACGATTTG lead AS 841329 841344
intergenic(1.3E-3) CCCTCTGGGTCACGTGTAGTTCAC GCCGTCACTGCACATATATT lag . 2016727 2016742
yqiA(1.3E-3) ACCGCGCTCAAGAGCGCACCCATTG GCACTACTAAAAGAATGAC lead AS 1681716 1681731
murA1(1.3E-3) GTTGCACGAGGGCCTAAATCACAGC CACCAGGCAAGCCTACTGT lead AS 313400 313415
fhuR(1.3E-3) CTTGCTCCAAGTCTTTAACCGCAAT CGACATTGAGGGTTGACTA lead AS 330533 330548
asnB(1.3E-3) GTTCGTAACAAATCTGCCAGTTCAC GAGCATATTTCAAATCAAT lead AS 356847 356862
rpoC(1.3E-3) GAACGGTAAGTTTTTTGTACTTCAC CGAGCAACTAAGTTTCAAC lead AS 1857655 1857670
menD(1.3E-3) CAAGAAGTTGAGCATCCACGCGCTTC CAAATGTTTTTGTACTTCT lag AS 736927 736942
pstC(1.3E-3) TCACTTCGAGCAATTCCAAGTTCAC AACGTGAGGGTGGTTTGGC lag S 1773284 1773299
ydiC(1.2E-3) AAGACTATAAAGCCAAGCAATGCAC CAATAATAATTAATGGATT lead AS 385240 385255
tgt(1.2E-3) GATTCACGACGTTAATCTTCAAAAG CAGCTCCTTGAACTAATCC lag AS 155934 155949
L200140(1.2E-3) GCTTCGACGGATTTCGAGTCCGCTG CATTACCACTCTGCCATGG lag AS 126575 126590
hrcA(1.2E-3) ATAAATTGATTTGTTCTTACTTCAC CAGTCCCTAAAGTTATAAC lead AS 977222 977237
intergenic(1.2E-3) CATTTTACTGAAGTGCTTTCATTTC TATTGTAATTATAACTGAT lag . 1712489 1712504
ybaI(1.2E-3) CTCGGAGCACCAACAGTATCATAAC CTTCTTGAAGTTTCTGATA lag AS 110048 110063
als(1.2E-3) CTCCTTGCTCATGACGAGTCACGAC CATTTGAGGGCCTTCCTCA lead AS 1200572 1200587
kinB(1.2E-3) TGGTCAAAAGCAGTGTATCCTGAAC TAAATTCATCAGGCGTGAA lag AS 1459925 1459940
intergenic(1.2E-3) ACTCGCTATAGCTTATTTACGTAAC CATGACGTTTTAGGTAAACG lead . 1838537 1838552
gidB(1.2E-3) CCTCGAAAAGTGACTTTACGTCAC GGACGAGCTGAAGATTTTG lead S 1381124 1381139
dexA(1.2E-3) GCTTGATAACCAGAATATCATAAC CATTATCATCCATTGGCGA lead AS 1736507 1736522
dtpT(1.2E-3) ACTAACCAAAGACGACTTGCACGAC CTGAAGTTCCGTTCAAGAG lead AS 705591 705606
glnP(1.1E-3) CCTGACATCATTCGTCAGCAATGTC CAGATTGAACAGAGTCAAC lag AS 1817828 1817843
citF(1.1E-3) GGTGCTTTACCGTCCATGCCGTTGG CATTACCCATTTCGTCAGC lead AS 1209507 1209522
xerD(1.1E-3) CATAGAACTCAGGAAATTCCTTAAT CATTGGATGATAACTTTGA lead AS 1310409 1310424
feoB(1.1E-3) GCCCTTCAAGTCGATGGTCATAAT CTAAAGTCTGACTTTCATG lag AS 191636 191651
cydA(1.1E-3) TTTGATAAGCTGAATACCAGCAAC CACTAAACCACCAGTTACA lead AS 708282 708297
citB(1.1E-3) CCTGATAATCGTGTTGCTACTTCAC TTAAATCAACATTTATTCGT lead AS 669535 669550
uvrA(1.1E-3) GCAAAATAGTCATTATTTCCGTAAC CGTCCCGACTGTTGAACGA lead AS 1888140 1888155
yudK(1.1E-3) TCAGTTCCTGAATAGGCTCCTTCAC CGTGTAAATAAGTTGCGCT lead AS 2038474 2038489
ysdA(1.1E-3) GTCCGATGATTCCCACATACATCAT CATCAATGTGAAAATTAAA lead AS 1834288 1834303
pbuX(1.1E-3) GGAGCAACAGATTGAAAGCAACAC CAAGGACAACTGGTAAGCC lead AS 1160591 1160606
purA(1.1E-3) GGTGTTTGTAAAGCCTATACTTCAC GTGTGGGTGATGGTCCATT lag S 2029214 2029229
ansB(1.1E-3) CTGTTTTGAATCGATTTTTCAAGAC CAACATATCTGATTAAGTG lag AS 743480 743495
plsX(1.1E-3) TTTCAGTTGTTTCACAATGTCAAT ATTTGTTTCATCGTCTAAA lag AS 72013 72028
citC(1.1E-3) GCGTAAATGGATTAGCATTCATGAC CACTGCCGCGATTTTTTC lead AS 1207190 1207205
yrfA(1.1E-3) TTTGAGTAAAGTTAGATGTTCAAT CGATATTCATTTGATAGGG lag AS 1750155 1750170
busAA(1.1E-3) CAGCAATAAGCTTGTTCACTGGTAAC AACACCACGGAATTGAGGC lead AS 1474713 1474728
ysjA(1.0E-3) CTTGATGGATCACCATTTTCCCAAC ACCATACATGACAACATAA lead AS 1891247 1891262
sdaB(1.0E-3) GTGTATCAACTTCTAAAATCATAAT CGCTTTTTCACCCTTAGCT lead AS 843991 844006
pcrA(1.0E-3) TACCCGAACCAGCTCTGCCATAAT CATATAAGGCCCTTCTGTA lead AS 1133849 1133864
ymdE(1.0E-3) AAATGCCCTAAGTCAAATTCATAAT CATTTCGTGCATCTATCAC lag AS 1238993 1239008
pacL(1.0E-3) TTTCATGATCCCCTGTAATCATAAC CACATTATATTTGCATCA lead AS 677844 677859
yrfE(1.0E-3) CATAAACAAACAACAATCATGAC CGCTATGATCACAACAATA lead AS 1759959 1759974
busAB(1.0E-3) TGAACTGCTGCAATGTACACCACGAC CTATGCCAGGCGCCCCAAT lead AS 1473732 1473747
ydiB(1.0E-3) TTTGCTAGCCCTCCTTACATTCCAC CAGGAGCTTTGAAGAAAGC lag S 383788 383803
yniH(1.0E-3) TTCGCCAAATTAACGACTCGTCCAG ACTCGTTACAAGCCATATT lag AS 1387926 1387941
ldhX(1.0E-3) ACTGCCAGAATCACGTTTCGTTC TAAAATTGCTCTTGTCAA lead AS 1143148 1143163
dacA(1.0E-3) TTAGAATTTTGATGTTAATTCATAAG CATTATCTGAAATAGGAAC lag AS 2356064 2356079
ywaI(1.0E-3) TATCTTTACCAGAAATTCCACAGT CACTTTATTTCCAGATTTG lag AS 2209257 2209272
ywiA(1.0E-3) TCTTGCGCAAATTCAGGAACATCTC CAATATTACCTGGATTTAC lead AS 2280342 2280357
yrjD(989.1E-6) TTTCTTTACCATTTTCCAGTTCAC CAATTGGTCTGAAATAACA lag AS 1793542 1793557
yweE(984.5E-6) TAAATCACGGACTATGAGCATTTTC CAACGGTCGCCCATCAAAA lag AS 2247499 2247514
intergenic(976.0E-6) GACGCCCTTCAAAATATCCATGAC TACCCTTTCACAAAAGAAA lead . 1210567 1210582
ykiF(975.7E-6) TCTAAATCAACCCATCTTCAGAAC TCATAGTTTCTTTGATAAA lag AS 1087045 1087060
yuhI(971.4E-6) ATATCTAGCAAGCCAAGAACATCAT CATCTTCATAAATTTTGGT lag AS 2077617 2077632
thrA(968.9E-6) ACTTTTCGCCGCAATCCAACTTCAC GGTTCATCAGATATTTACT lag AS 747685 747700
citG(967.4E-6) GCACATTCAGCTTGACAGACAACAAC CGTACTCTCAGGAAACTCC lead AS 1210681 1210696
birA2(953.2E-6) GTTAAATAAACACACATTTTCTTGTC CGTCTAATTTAGCATCTTT lag AS 1973041 1973056
aroH(943.5E-6) ACTGAGCGAGCGCCAACTCCATAGT AACTTACTAAGTCATCAAC lead AS 1280932 1280947
intergenic(941.5E-6) AAATAATTGCATTTTTTTTCATGAC TCGATTATAACCATTAGTCTA lag . 2355772 2355787
yudH(937.4E-6) CTATAAAAGCACCATAGCCGTTAT CACCCTCACCCTCACATC lag AS 2035315 2035330
yiaC(935.3E-6) TCATCGTTAGATTAACATTCAGGGC GCCAACAATTGCGATTGTA lead AS 802688 802703
queA(934.9E-6) TAAGCGTCAACAACAATCACGGC CAGCAAAGCAGCGACTAA lag AS 1617701 1617716
intergenic(934.7E-6) CAAAGGCTTGTATTTTTTACACTTC TATCGTACAATAATTTTAC lag . 1562466 1562481
ysjD(925.9E-6) TTTTTTACCTTGTCAGCCATTCAC CTGCTTCACCAGATAATCC lead AS 1893720 1893735
yriB(925.7E-6) AAATGATAAACGCCCAATGGTAAC GTTCTTAAATCCTTCAGTT lead AS 1786925 1786940
clsB(917.3E-6) GAAGCCAAATATGTGTTCCGCATC CATTATCATTTTAATAAAA lead AS 1188112 1188127
yeaC(913.3E-6) TGGACATCAACCTCATTTACTTCAC GCACAATCGTCTGGTGAAT lead AS 405707 405722
typA(909.9E-6) ATGACAATGTGCATTCACCACGAC CAGAACAACCCATTTATC lead AS 2093418 2093433
fbaA(902.0E-6) TCACCACAATTGAAGCAACTTCAC ATTCAACTGAGATGCCTTT lead AS 1979895 1979910
pbuX(893.7E-6) AATGAACCAAACATTGCTCCAGAGC CATGTCTTTGACCTATAAT lead AS 1160642 1160657
yecE(885.8E-6) TTTCATCAAGATTTACATCATATC CAAATGACCTTTGAGATTA lead AS 427516 427531
trmE(884.6E-6) AAACGCACAATGGCAATTCGTCCTT CACCAAGCGGTGTCGAAAT lag AS 2327788 2327803
pycA(880.8E-6) TCGTTACCACGCCCATAAACATCTT CTTCTGTTAAATTCATTTG lead AS 666290 666305
fadD(875.8E-6) CCTGCAGGACATTCATTTCCATCTT CATCGGCAATACGTGCTTT lag AS 654992 655007
llrG(867.9E-6) ATGTTTTCCTTGGTCACCATTCAC CATTTCCACGAAAAAGAAG lead AS 1805025 1805040
deoD(858.1E-6) ATATGAACAACTTCATTTACAGAAC CAGCAGTCCCAACACGAAT lead AS 957081 957096
fabD(857.2E-6) GCATAATCAACCGCCTCAACTTCAC CACCAATAACAATTTGTGC lead AS 783367 783382
clsB(849.2E-6) AAATATAGTCTTCCGCATCCATAAT CATTTTTAATAAACCTGTT lead AS 1188106 1188121
L200130(847.7E-6) TTTGATTAAAAGTCAAATGGTCTAC CAACTGAGCTAACGAGTCA lead AS 1980938 1980953
intergenic(843.7E-6) CCAACTCTCTTTTAGTTGGTATTTTT TATTTTTAAAATAGTTCTCT lag . 2275138 2275153
apbE(842.3E-6) AGTGAACCAATTGTATATCATAAC CTATATCTTTAGCTGAATA lead AS 1124691 1124706
yagB(842.2E-6) CGTTCTATATGGTCAAAGCCATGTC CATCATTATTTTTATCATG lag AS 67086 67101
intergenic(841.1E-6) AGGAAAATTTACTGACAGCCACTCC TAAACAGTCTTTCAGTAAA lead . 970097 970112
rplM(839.1E-6) AGTATATTACTCACACTCATGTCAC CCAGGTGGATTGAAATCAG lag S 2346912 2346927

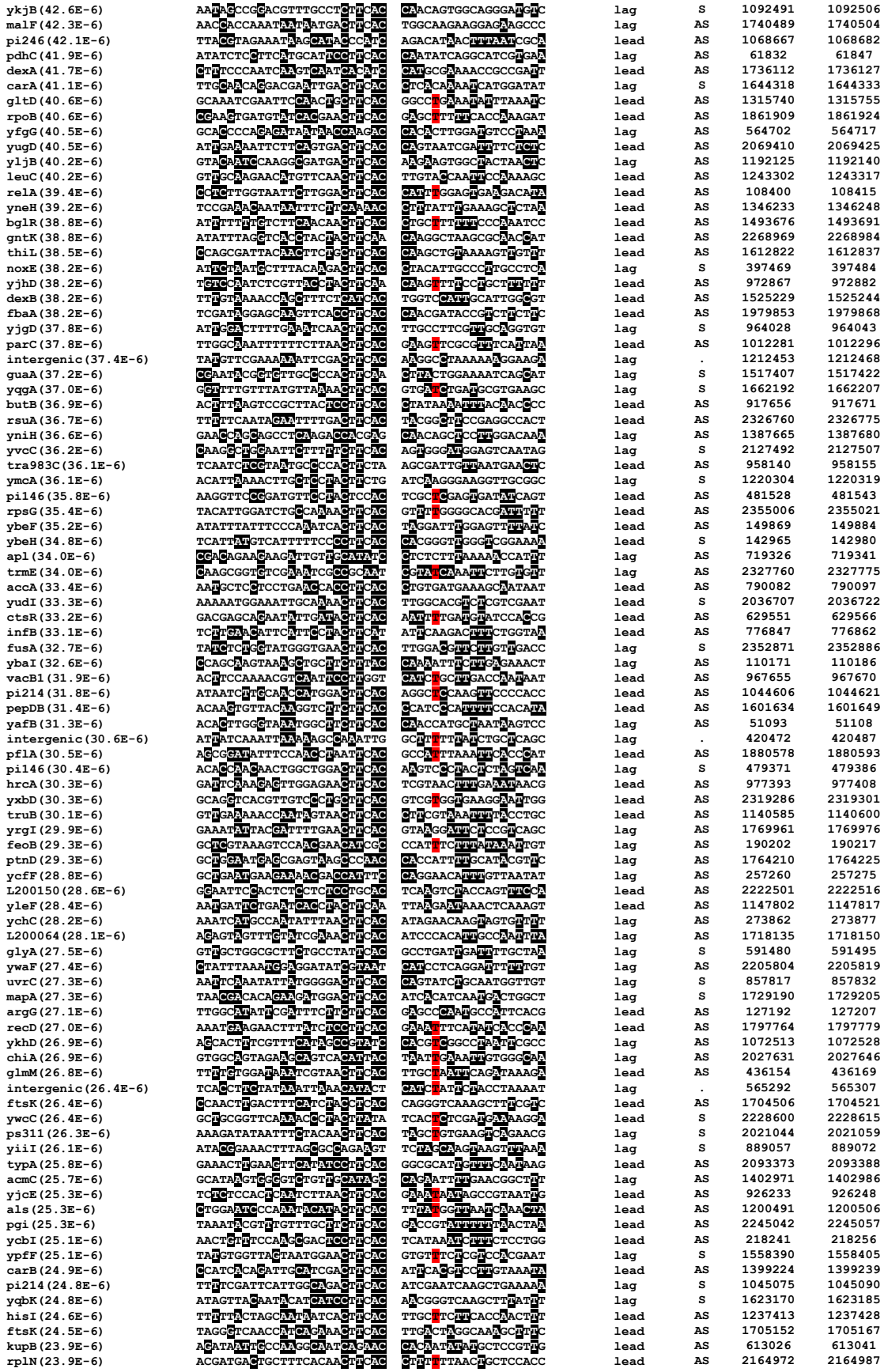

ylgC(837.8E-6) lag AS 1162425 1162440
ychH(833.8E-6) lead AS 279650 279665
yijE(825.2E-6) lead AS 897434 897449
tgt(824.8E-6) lag AS 156150 156165
ssbB(811.3E-6) lead AS 2274356 2274371
fbaA(804.1E-6) lag S 1979644 1979659
yjgC(802.2E-6) lead AS 963079 963094
dexC(800.1E-6) lead AS 1737262 1737277
ptsI(799.5E-6) lead AS 121312 121327
pbp1B(794.1E-6) lead AS 393516 393531
intergenic(793.8E-6) lead . 2012509 2012524
intergenic(787.6E-6) lag . 1931070 1931085
citF(784.9E-6) lead AS 1209546 1209561
argR(775.8E-6) lag AS 2117884 2117899
relA(767.0E-6) lead AS 108865 108880
uppP(766.9E-6) lead AS 2275479 2275494
intergenic(762.6E-6) lag . 1706685 1706700
gshR(760.9E-6) lead AS 864313 864328
floL(758.3E-6) lead AS 746840 746855
asnB(757.2E-6) lead AS 356922 356937
yrfE(755.7E-6) lead AS 1759098 1759113
yxaB(746.0E-6) lag AS 2301202 2301217
menF(745.8E-6) lag AS 738243 738258
menD(742.6E-6) lag AS 737101 737116
pbuX(735.3E-6) lead AS 1160419 1160434
citE(733.2E-6) lead AS 1208386 1208401
yljF(730.6E-6) lead AS 1196804 1196819
noxB(724.8E-6) lead AS 841599 841614
ynbC(723.1E-6) lead AS 1311441 1311456
ysiA(717.3E-6) lead AS 1882158 1882173
hemH(711.6E-6) lead AS 1608810 1608825
lysQ(708.4E-6) lead AS 369852 369867
optC(697.2E-6) lead AS 348745 348760
argR(694.2E-6) lag AS 2117915 2117930
ylcG(690.3E-6) lead AS 1130988 1131003
dacB(690.1E-6) lead AS 976126 976141
noxA(687.5E-6) lead AS 840184 840199
panE(685.1E-6) lead AS 1358181 1358196
clpC(681.5E-6) lag S 630146 630161
ytdB(680.9E-6) lead AS 1934966 1934981
ygbD(680.0E-6) lead AS 616221 616236
L200159(674.0E-6) lead AS 2363650 2363665
glnP(665.5E-6) lag AS 1817888 1817903
recD(660.7E-6) lead AS 1797401 1797416
scrK(651.5E-6) lag S 1518450 1518465
hpt(650.0E-6) lead AS 25358 25373
alaS(638.3E-6) lead AS 1778652 1778667
htrA(635.8E-6) lag AS 2204392 2204407
yjgC(635.1E-6) lead AS 962423 962438
lepA(628.7E-6) lead AS 1118394 1118409
rpsM(628.4E-6) lead AS 2153631 2153646
yagB(625.5E-6) lag AS 66735 66750
ybeH(625.4E-6) lag AS 143096 143111
intergenic(624.6E-6) lag . 820084 820099
ilvD(621.5E-6) lead AS 1246083 1246098
pepQ(603.2E-6) lag AS 1698129 1698144
efp(601.2E-6) lead AS 691670 691685
Intergenic(594.1E-6) lag . 2276493 2276508
yqbK(590.7E-6) lag S 1619709 1619724
gidC(579.4E-6) lead AS 1257813 1257828
copR(575.7E-6) lead AS 845396 845411
citR(570.7E-6) lag AS 1206676 1206691
yoaB(569.0E-6) lead AS 1404130 1404145
choQ(557.7E-6) lag S 865510 865525
yseI(557.7E-6) lead AS 1849919 1849934
ygaB(548.0E-6) lead AS 602141 602156
malF(539.1E-6) lag AS 1740960 1740975
parC(537.4E-6) lag S 1012443 1012458
yrgH(536.8E-6) lag AS 1769355 1769370
ykiF(535.2E-6) lag AS 1087227 1087242
ps105(530.7E-6) lag AS 37893 37908
yuhE(521.7E-6) lag AS 2073300 2073315
yfjF(512.1E-6) lead S 599610 599625
leuA(511.8E-6) lag S 1240133 1240148
nrdD(499.2E-6) lead AS 271457 271472
kdgR(492.7E-6) lag AS 1680250 1680265
pepF(492.5E-6) lead AS 1783848 1783863
rplC(486.0E-6) lead AS 2169681 2169696
comFA(482.4E-6) lead S 1097125 1097140
topA(477.7E-6) lead AS 1255147 1255162
yveC(470.5E-6) lag AS 2143864 2143879
yeeB(465.5E-6) lag AS 443166 443181
ybcG(460.1E-6) lag AS 123139 123154
yqcA(456.8E-6) lag S 1624880 1624895
gyrB(456.5E-6) lead AS 929120 929135
yeeB(453.5E-6) lag AS 443427 443442
ybcH(450.7E-6) lead S 123666 123681
ylaD(448.7E-6) lead AS 1105705 1105720
mscL(446.4E-6) lag AS 2170604 2170619
L200065(444.5E-6) lead AS 1745995 1746010

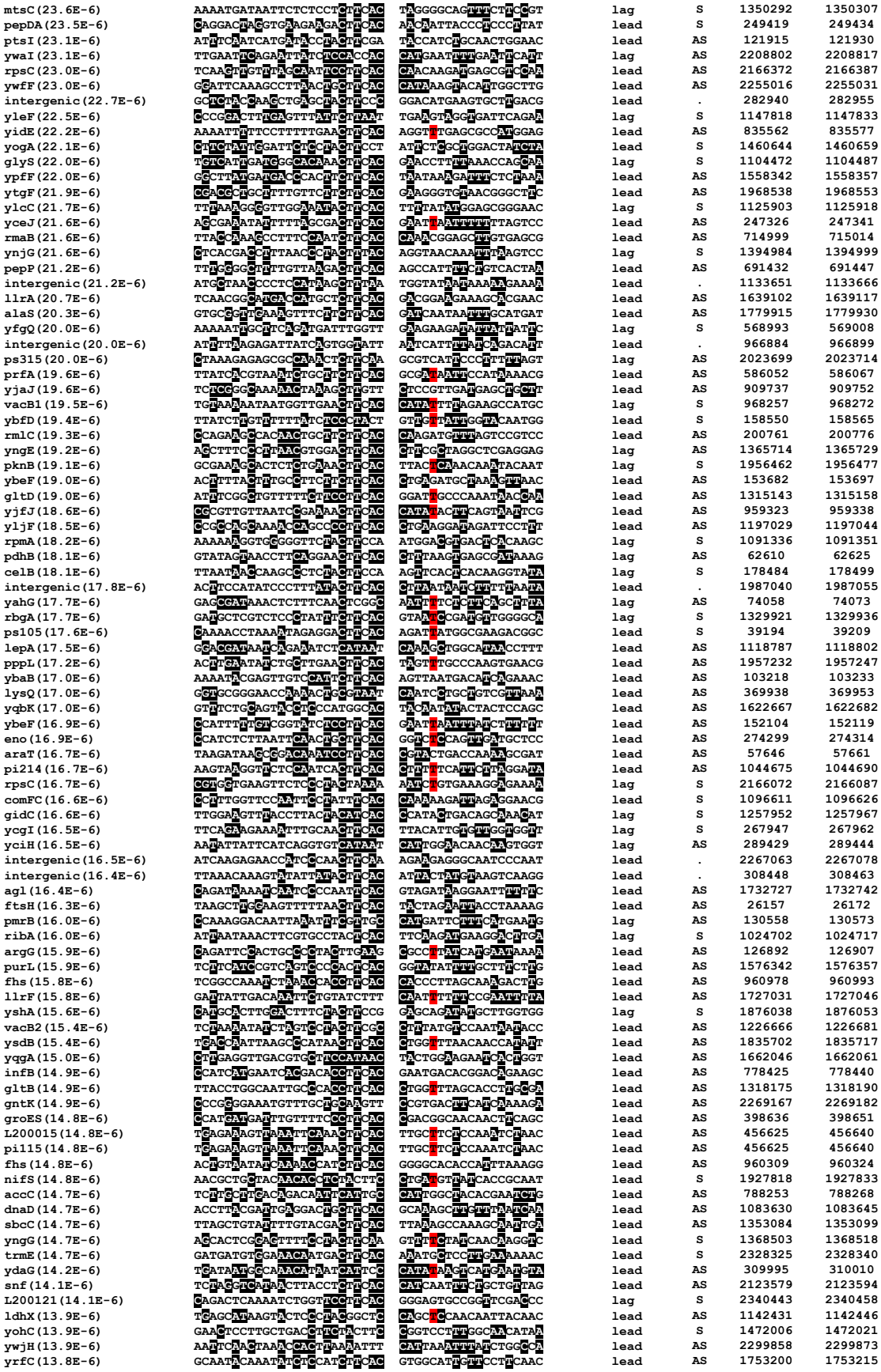

ymdE(437.5E-6) lead S 1238775 1238790
yqgG(432.8E-6) lag AS 1664100 1664115
yebE(428.7E-6) lead AS 417456 417471
glnQ(427.9E-6) lag AS 1819582 1819597
purL(424.0E-6) lead AS 1576156 1576171
yveH(422.8E-6) lead AS 2146197 2146212
yrgE(418.4E-6) lag AS 1765334 1765349
intergenic(408.9E-6) lead . 1213718 1213733
intergenic(405.0E-6) lag . 1766419 1766434
clpB(402.4E-6) lag S 1567554 1567569
infB(401.7E-6) lead AS 777180 777195
pi301(401.6E-6) lag S 1414528 1414543
pbp2A(400.0E-6) lead AS 2178563 2178578
gntR(391.4E-6) lag AS 2272040 2272055
ymjE(387.4E-6) lead AS 1297570 1297585
purC(385.1E-6) lag S 1577698 1577713
radA(383.9E-6) lead AS 2149913 2149928
ydbA(381.9E-6) lag S 311295 311310
yhdB(381.5E-6) lag AS 731959 731974
vacB2(379.1E-6) lead AS 1227759 1227774
gyrA(368.5E-6) lag S 1123616 1123631
glgP(367.5E-6) lead AS 700438 700453
topA(364.2E-6) lead AS 1256226 1256241
ycjB(360.6E-6) lead AS 291861 291876
intergenic(355.9E-6) lead . 1781130 1781145
aspS(352.2E-6) lag AS 2040291 2040306
pepA(349.6E-6) lag AS 394913 394928
yrjI(345.7E-6) lead AS 1799737 1799752
yahI(345.5E-6) lag AS 78146 78161
yyaL(345.4E-6) lead AS 12154 12169
ywjH(344.8E-6) lead AS 2299894 2299909
apl(341.8E-6) lag AS 719117 719132
ygeA(341.2E-6) lead AS 647001 647016
rliA(340.4E-6) lead AS 1728090 1728105
ddl(335.8E-6) lead AS 341407 341422
gltB(335.2E-6) lag S 1318756 1318771
prsA(331.9E-6) lead AS 826166 826181
yfiC(328.7E-6) lag AS 582039 582054
ynhC(328.0E-6) lead AS 1375536 1375551
yseF(319.5E-6) lead AS 1846805 1846820
gidA(317.5E-6) lead AS 1916173 1916188
feoB(317.2E-6) lag AS 191685 191700
vacB1(316.8E-6) lag S 968723 968738
ahpF(314.9E-6) lag S 336370 336385
recX(313.1E-6) lag AS 2260546 2260561
clsB(312.1E-6) lead AS 1188583 1188598
gntR(311.2E-6) lag AS 2272093 2272108
ygiI(310.7E-6) lead AS 688022 688037
cydB(307.4E-6) lead AS 709788 709803
tyrS(302.1E-6) lag AS 390395 390410
ykhD(301.5E-6) lag AS 1072414 1072429
busAB(298.6E-6) lead AS 1473814 1473829
glnP(298.6E-6) lag AS 1818260 1818275
intergenic(293.2E-6) lead -. 426554 426569
yrdB(287.3E-6) lag AS 1748835 1748850
yliB(286.4E-6) lag S 1183134 1183149
pmsX(284.1E-6) lag AS 1594083 1594098
ysfB(283.9E-6) lead AS 1851913 1851928
aroB(283.2E-6) lead AS 1814163 1814178
frdC(283.0E-6) lead AS 1138856 1138871
cysE(273.6E-6) lead AS 1920560 1920575
grpE(270.4E-6) lag S 978348 978363
intergenic(269.5E-6) lead . 228110 228125
tra983F(269.2E-6) lag AS 1556004 1556019
dut(267.2E-6) lead AS 181327 181342
carB(267.2E-6) lead AS 1399755 1399770
lepA(262.4E-6) lead AS 1117932 1117947
rpsC(261.0E-6) lead AS 2166108 2166123
ycfD(257.7E-6) lead AS 252972 252987
intergenic(256.9E-6) lag . 2071740 2071755
hslO(256.3E-6) lag AS 2034366 2034381
atpC(254.9E-6) lead AS 1822759 1822774
yhcH(253.6E-6) lead AS 726528 726543
pepT(253.1E-6) lead AS 1877702 1877717
ylhB(248.3E-6) lead AS 1173578 1173593
intergenic(246.6E-6) lag . 2208612 2208627
apl(243.5E-6) lag AS 719588 719603
pspA(243.5E-6) lag AS 2304554 2304569
hemN(240.9E-6) lead AS 1153916 1153931
ymcF(239.7E-6) lead AS 1223916 1223931
proS(239.7E-6) lead AS 2196190 2196205
rplI(238.7E-6) lag S 753463 753478
fhs(238.7E-6) lead AS 960069 960084
yrfE(237.9E-6) lead AS 1759268 1759283
ispA(235.9E-6) lead AS 881180 881195
L200149(232.9E-6) lead AS 2219499 2219514
hsdR(232.7E-6) lead AS 641728 641743
glgA(232.0E-6) lead AS 698612 698627
rdrB(229.4E-6) lag AS 1331986 1332001
qor(226.9E-6) lag AS 723823 723838

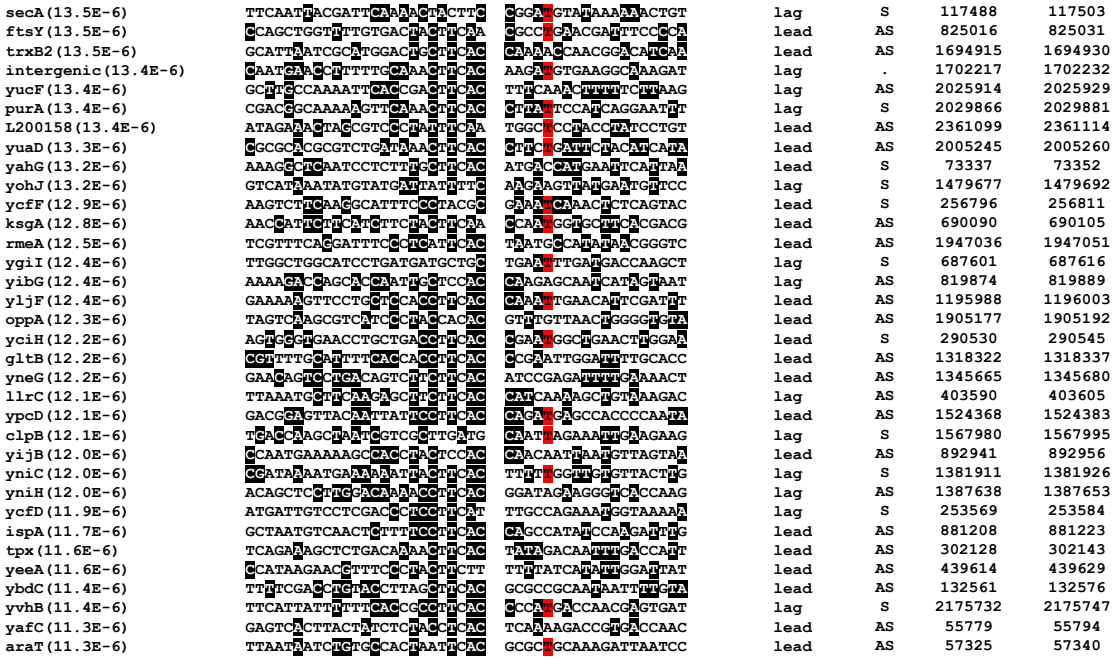

pi148(226.7E-6) lag S 482353 482368
yjbB(225.2E-6) lead AS 911052 911067
ps315(222.8E-6) lag AS 2023936 2023951
yqgG(220.9E-6) lag AS 1664082 1664097
pi201(220.2E-6) lag AS 1037038 1037053
intergenic(219.7E-6) lag . 565296 565311
hslO(216.9E-6) lag AS 2034601 2034616
ptcC(216.4E-6) lead AS 421115 421130
ycjM(216.3E-6) lag S 299901 299916
celB(212.9E-6) lag S 178101 178116
ytcE(212.2E-6) lag AS 1929213 1929228
ftsH(211.5E-6) lead AS 26613 26628
yljG(211.5E-6) lead AS 1197636 1197651
dltE(211.4E-6) lead S 144478 144493
topA(209.0E-6) lead AS 1256515 1256530
citC(200.9E-6) lead AS 1206875 1206890
mutS(197.6E-6) lead AS 1692486 1692501
rgpA(197.2E-6) lead AS 202268 202283
intergenic(194.6E-6) lag . 172797 172812
trxB1(194.5E-6) lead AS 966106 966121
yveC(194.1E-6) lag AS 2143762 2143777
trmE(194.0E-6) lag AS 2327785 2327800
yvaA(192.3E-6) lag AS 2100504 2100519
ptnC(191.7E-6) lag AS 1763862 1763877
yeaG(191.3E-6) lag AS 407850 407865
ldh(189.0E-6) lag S 1370008 1370023
ylcG(188.5E-6) lead AS 1131775 1131790
yciA(184.1E-6) lead AS 280687 280702
ytjF(183.8E-6) lead AS 1997999 1998014
intergenic(182.9E-6) lead . 1880376 1880391
L200155(182.9E-6) lead AS 2342297 2342312
dpsA(182.1E-6) lead AS 2102154 2102169
pepN(180.9E-6) lead AS 302960 302975
yogI(180.4E-6) lag S 1467652 1467667
gyrA(179.5E-6) lead AS 1121968 1121983
recX(177.9E-6) lag AS 2260573 2260588
pspA(177.3E-6) lag AS 2304303 2304318
ycgD(176.4E-6) lag AS 264664 264679
intergenic(174.5E-6) lead . 1171031 1171046
pi149(174.1E-6) lag S 482537 482552
noxB(173.9E-6) lag S 841457 841472
hom(172.9E-6) lead AS 1171374 1171389
ybjJ(172.0E-6) lag AS 193714 193729
era(170.0E-6) lag S 355476 355491
tra1077B(168.4E-6) lead AS 139417 139432
yniJ(167.6E-6) lag AS 1389428 1389443
intergenic(167.1E-6) lag . 146664 146679
ykiF(165.9E-6) lag AS 1086658 1086673
yqbK(165.8E-6) lag S 1621593 1621608
yuhI(164.7E-6) lag AS 2077908 2077923
yrjA(163.1E-6) lag AS 1790453 1790468
rheB(158.7E-6) lag S 416038 416053
vacB1(158.5E-6) lead AS 968864 968879
secA(156.8E-6) lead AS 116558 116573
pi252(153.7E-6) lag S 1070851 1070866
ywfE(153.6E-6) lead AS 2253509 2253524
kupA(153.2E-6) lead AS 609811 609826
adhE(152.2E-6) lag AS 2231413 2231428
intergenic(151.0E-6) lag . 767701 767716
carB(149.3E-6) lead AS 1399233 1399248
rexB(148.9E-6) lead AS 6410 6425
rexA(148.9E-6) lead AS 6410 6425
L200139(147.0E-6) lead S 155265 155280
ytcA(146.1E-6) lag S 1919841 1919856
ybfE(145.3E-6) lag AS 158953 158968
rplU(143.4E-6) lead AS 1090794 1090809
nadR(143.2E-6) lead AS 2067466 2067481
accC(141.8E-6) lead AS 787362 787377
intergenic(141.1E-6) lag . 1765147 1765162
pacA(140.5E-6) lead AS 1149790 1149805
clpC(138.9E-6) lead S 631578 631593
rpoC(138.0E-6) lead AS 1860730 1860745
yugD(136.4E-6) lead AS 2069632 2069647
yseE(133.9E-6) lead S 1845334 1845349
ygiI(133.8E-6) lead AS 687818 687833
yvdB(133.8E-6) lead AS 2132376 2132391
yrbA(133.2E-6) lag AS 1710889 1710904
ldh(132.5E-6) lag S 1369738 1369753
yoiC(129.4E-6) lag S 1486078 1486093
uxaC(128.3E-6) lead AS 1673326 1673341
pepF(128.1E-6) lead AS 1783404 1783419
ytdF(126.8E-6) lead AS 1937543 1937558
ymjE(126.6E-6) lead AS 1296165 1296180
ypiA(125.6E-6) lead AS 1580173 1580188
yvdD(125.2E-6) lag S 2134298 2134313
noxB(125.0E-6) lead AS 843000 843015
xylH(124.4E-6) lead S 568323 568338
intergenic(121.8E-6) lag . 1247526 1247541
yxcA(121.2E-6) lead AS 2323787 2323802
chiA(121.1E-6) lag AS 2027406 2027421


yngG(120.4E-6) CCGCCTCGTTCGGAGAAGACACCAC CAATACTTGTAAAGATTAG lag AS 1368216 1368231
ysjD(119.8E-6) TTGTCAGCACTTCACCTGCTTCAC CAGATAATCCCAAAACTTT lead AS 1893729 1893744
yhdA(117.1E-6) TATTCACTGGAGCCGATTCCATTAC TTGCCATACCAGCTGTGAT lag AS 731594 731609
secA(116.6E-6) TGACGTTGCGCATAATAATGTCAC GTTGCTCACGGATGACATC lead AS 118226 118241
glpD(115.5E-6) ATAAGATCCGTTACCTGAACTTCAC TCGTCCCATCCGTGCCCAAA lag S 1271169 1271184
rpoB(114.1E-6) TGTCATGTACATGATTAAGTTCAC CACATGGTTGATGATAAAC lag S 1861379 1861394
arcC3(113.9E-6) GGTAAGCATGCCCAGGATTAGTTCAC TTGAAAATGTGGAAAACTT lag S 1752051 1752066
nifS(113.8E-6) GCGGACGGAACATTCCCAGCTTCAC TTATAGAAGAAACTTGCG lead S 1928168 1928183
dnaJ(113.8E-6) TTCGAGCAGGATTTTCAAGTTCAC ATTCCCATGAACAGTCGGA lead AS 2307464 2307479
rplD(113.0E-6) ACTGAGTCGTTAAGTGTAACTTCAC CAGCTTGTGTGAACCATCTTG lead AS 2169254 2169269
ygfC(112.4E-6) TTTAAACAGCGCTTCATATAGGCGAT TGCGTTTTTCGTCAGATAG lag AS 654295 654310
tkt(112.3E-6) AGCAAGGCCAGCCGTGTAAGTTCAC AAGAAGCTATCCAAGAATT lag S 1670095 1670110
glnA(111.5E-6) CCTTTGATTCCGCTAGCTTCTTCAC GTGGTTTGTCAACTCGTGT lag S 2282652 2282667
ywfH(109.7E-6) GCTGCACCCGGTGCCCTTAGTACAC TTGTATCACCAGGATGAAA lead AS 2259140 2259155
xynB(108.4E-6) TTTACAACATTGGAGCCTAGTTCCA AGTCCATTGTCGACAACCA lag S 1544744 1544759
yqeL(108.2E-6) TCTGAGGATGTGATTACAAGTTCAC GTTTCCCTGGGACTACTCT lag S 223614 223629
ygdA(108.1E-6) ACTTTACGTGCAGAGCATAGTTCAC AAGATATGTATTCTTCAAT lag S 632597 632612
relA(107.1E-6) TCTGCTGAATCACCAGCGTTCTCAC GCAATTCCACAAGTTCATG lead AS 108310 108325
yfgG(106.7E-6) CAACAATCAATGCCGGACTCATAAAT CAACATTGCCATTCCTGAT lag AS 564603 564618
ackA1(106.2E-6) AAATATGGCGCTCATGGAAGTTCAC ACATGTATGTTTCACAAGA lag S 2090551 2090566
leuS(105.8E-6) TTTGCGTCAGTTGTATTAACTTCAC GTTCCCAGTCATAACTAAA lead AS 827793 827808
yrgH(105.8E-6) TGTAATAAAAGACGTAATTGTCGGT CCCAATCATAGAAATCTTC lag AS 1769361 1769376
carB(105.4E-6) CCACGCAGCTAGTTTTTCAAGTTCAC GGACATAAAGTCCATTTGC lead AS 1398537 1398552
llrB(104.3E-6) AGGGTCAAAATTGCCGCGATCATCAT CACCAATTAAAATTTTTTT lag AS 1458179 1458194
glk(103.8E-6) ATGTCTTTAGAGTCACTTCATCAC CATTGTCAATAGCTGCTTT lag AS 2101334 2101349
yqaB(103.7E-6) CTAAAATCAGGACGCCACACCATAAC CAATATGACCACCCCATTC lead AS 1603759 1603774
hsdS(102.3E-6) CCGTTTAGAAATGTTGCAAGTTCAC CCACTTACGTTCTTCCCA lead AS 646044 646059
adhE(101.2E-6) CGTACAATCTCCAATTTCCTTCTTCAC GTGTTTCAGCTTTGTAGAT lag AS 2230834 2230849
snf(101.0E-6) ATTATTATCACAGAGCATATCTCATC CAGCGAACACCCGTTTCCT lead AS 2121892 2121907
ptcC(100.8E-6) AACGTTGCGCGTTCATTCAGTTCAC TTGTTCCCGCAGGACGCAAT lag S 421301 421316
potB(100.3E-6) AACTGTAAAAAGTTATTAATGTGAAC CATATTTACCAAAAATTCC lead AS 1177294 1177309
L200152(99.6E-6) CCAGTGCGTCTTACACACCTTCCAC CCTGCTCATGGATAGGTCA lead AS 2263088 2263103
ykjK(98.8E-6) CAAGTCCAGCCTTACCAGTCGCAAC CACCTCTCTTGTTGTTGTT lead AS 1100315 1100330
cpsM(98.4E-6) ACATCACCGAAATTTTCTCCTTCAC GTAAATCAACCCATGCGCC lead AS 198632 198647
yshA(98.2E-6) TCTTTGGTGTAATTGCCTACTTCAT GATGCGCAACTATAGAAAG lag S 1875454 1875469
rbfA(97.6E-6) AGCTCTATCAATTTTGAACCATATT CACACAGATTCATCTTTTGC lead AS 779168 779183
tuf(96.2E-6) GAACCTACAGTACGTCCACCTTCAC GGATAGAGAAAGTAGTACC lead AS 1929416 1929431
fadD(96.1E-6) CCAGGCATACCAATCCCCATTTCAC GGGCATTAGTTCTGCTAA lag AS 655043 655058
yucG(96.1E-6) TTAAAACCGCGGTCCACCGTAAAC TTTGAGAATCTAATTGTCC lag AS 2028169 2028184
yhfC(95.8E-6) GGTGAACGCATTGAATATTCTTCAC AATTTCGGTCGTAAACGCGA lag S 755166 755181
yahA(95.6E-6) AAGAACCAGCGTTTTCAAACATTTC CAAATCATTCATTTGGTCA lag AS 72409 72424
recN(94.5E-6) CGCACTAAAACACTCGAAGCACGCC CACCTAATAATAAAGACAT lead AS 883221 883236
relA(94.2E-6) TTACTTGATTCGCGTTTAGTTCAC CCTTCATCAGCTCTTCGGC lead AS 108916 108931
ycjM(93.0E-6) TCTAACCAACCCTGTGCTTCTTCAC TCACAACGGATATCAGCTG lead AS 300722 300737
dtpT(92.8E-6) TGGTTCTTGCAGATTCAACTTCAC AAGCAATCAATGCTCAAAT lag S 705765 705780
ps311(92.7E-6) AATAGGCAACGCGTTCTGACTTCAC AGCTAGTGAAGTTGTAGAA lead AS 2021054 2021069
nusA(92.4E-6) TCGAATACTTCTTCACGACTTCAC GAGTCGTAATAAACATTGAA lead AS 773978 773993
yvcC(92.4E-6) TAACCTGTAGCCACCTCCTTCTCAC TTATGATATAAAGATTACC lead AS 2124348 2124363
pfl(91.4E-6) GTCATTAATGCACGTGCAACTTCAC TTGGACGTGTTCCCAATCGT lag S 658237 658252
rpe(91.0E-6) TTTTCTATATTTTTCTCAACTTCAC CATTAAAAATAAATGACCC lead AS 2003231 2003246
citF(90.5E-6) TATCAAAATCATCTTTAATTCAC GAATGATATCAAGCAAGCT lead AS 1210497 1210512
menE(90.0E-6) TCTGCTTAGCAACAAGTCACATT CCTTGATTTCAGGAAGAGA lag AS 733083 733098
usp45(89.7E-6) TCTCAACGTCAAGAGTTGACTTCAC AACTAGCTGAACTTAAAGT lag S 2313993 2314008
yxfC(88.4E-6) ACCGCATCTACATAGGTTCCATAAAT CATGAGCTCGATTTAATCAA lead AS 2359357 2359372
leuC(87.1E-6) CTCCGCAACACGACGTCCTCGTTCAC GTAAGCCCTGAAATGCTTG lead AS 1242999 1243014
yeeG(87.0E-6) TTCATGAGTGCTGCAATGACTTCAC GTTGGTGAGCTGCCCGACC lead AS 446315 446330
ptnD(86.8E-6) TCGATATCAGCACCGTTACCACGTT CTTCTTCAAGGGCAAGAGT lag AS 1764360 1764375
ywaF(84.5E-6) CGTTGTTGAAGTTTCATTCGACGAC CAATTCCTGAATGACTCAA lag AS 2205732 2205747
guaA(84.3E-6) GGTTTCCACGTTGTCGGAACTTCAC CAACACGTCCATTTGCTGC lag S 1517292 1517307
yeeF(83.5E-6) TCAGAGATTAAAATTCCTACTTCAT CAATGGTCAAAAAATTACT lead AS 445084 445099
hasC(83.5E-6) TTGTAAAGCCCTTTAGAAACTTCAC CGTTAGGGTCAATGACACC lag AS 1378400 1378415
lacZ(83.0E-6) TTAGGATCAATATGTTCAAGTTCAC TAACACAATATCATTATC lead AS 2055873 2055888
yjdE(82.2E-6) GAACATCTTGAAGGTAAGAGGAAG CATCATTTCAACACCCAAC lead AS 933438 933453
atpH(81.8E-6) ATGAAGTAACAGTAATTAACAAGT CAATGAAAAATTCTCGGT lag S 1827415 1827430
thrS(81.6E-6) TTTCATCATCTGGGAATACTTCAC TGTATCTTTAGGGTCACGG lead AS 1987780 1987795
malE(80.4E-6) TACGTTGGTAAGAGTCCTCGTTCAC AATATGACAGTCAACTTAA lead S 1740226 1740241
zwf(80.1E-6) TTGATAGACTCTTAAACAATTCAC GATAATACTCCGTTGTCCA lag AS 2301470 2301485
bglH(79.8E-6) TCCCGCATTTACGATCGATTCAC CCTAAACACGGAGTAAATG lag S 1490018 1490033
noxE(79.7E-6) CTTTTTGATGCAGAAGTACTTCAC TTGCTTCATATTATGATGA lag S 397135 397150
ptbA(79.5E-6) ATTTTAATCGCGCCTGAACTTCAC CTGTAAGGGTAATATTAGA lead AS 1491561 1491576
tenA(79.5E-6) GCGATTTGCACGGTACGCTTCTTCAC TCGCATAGGTTTCAATCCA lead AS 1838849 1838864
yeeA(79.4E-6) TCAACAAATTGCGATTGTTCATCAC CAATTAAGCCGGACTGCCA lead AS 440760 440775
yeeA(79.1E-6) ACTGTTCACGCTTCAACGACTTCAC GTCCGGTTTTTGCTGGGAT lag S 441510 441525
cpo(79.1E-6) ATTTGGGCAAACCATGTAAGTTCAC TGGACGAATAGCCACCAAT lead AS 834569 834584
vacB2(78.8E-6) CTTGTTTACATGTAGAAGCCTACTC ACGCGCAACATCAGTCTAT lag S 1226984 1226999
yyaL(78.6E-6) ATATTATCAGCTTCGCCTAGTTCAT CTTCTGAAACATTAGCTAC lead AS 11749 11764
yljF(78.4E-6) AAAGCCGCAAACTTCCTCGGGGAC CAAATCCAATGACTACAGG lead AS 1195835 1195850
intergenic(77.3E-6) AGCTTGGACTAGAAAATCGTTCAC AAATTGCTATACTAGGTAA lag . 1980330 1980345
intergenic(76.6E-6) ATAGACGAATTTCTTTTTTCTTGTC CATTGGAACTCCTTTTAAA lead . 1293417 1293432
ymjE(76.0E-6) AAGCTCCGATCTCAGTTGCATCAT CAATAACAGTTACCACTAG lead AS 1297164 1297179
cysS(74.5E-6) GAATGTCAGTCATGTCAACTTCAC TATTAGGCGAAACAATTGA lag S 1918936 1918951
oppD(74.2E-6) TCCCCACAATAGCTAAAGTTCAC CACGGTAAGACTTAAATC lead AS 1910699 1910714
intergenic(74.0E-6) AAATAAAATGCAGTATGACTTCAC AGCGCACACTTTGAAAAA lag . 1830442 1830457
hom(73.8E-6) ATTGAATAAAACAGCATTCATAAC ACCATTGACACTGGCCAAT lead AS 1171877 1171892
intergenic(73.7E-6) TGGGGATGTTCAATATACTCCTTCAC GGATGATATGAATTAAAAA lead . 47610 47625
trpS(73.5E-6) ACACCGTCCAACAGGAAAGTTCAC ATCGGCCACTATTGTAGGCT lead S 68223 68238
serS(73.0E-6) AGAGGTAAAGTTCAACTCCTTCAC ACTTTGAATGGTTCTGGAC lead S 1768329 1768344
kinC(72.8E-6) GAGCGAAATGGATTCATCCCAGAA TCATGTGTCTCAATAGTTA lag AS 402440 402455
dnaK(72.4E-6) AGCCGCGTGCTGCTGGCCTGTTCAC TTGGAAATGGCTTTGACTC lag S 979257 979272
nusA(72.2E-6) GTTGGAATTTCTTCCCATGTTCAC CCACGAATTCATAATCATC lead AS 774845 774860


amyY(72.1E-6) GCCGAGCCGTTGAAAAAGTTCAC CCACTAATAAGCTTTTGG lead AS 1733687 1733702
ptcB(71.4E-6) ATTTCAGTTTTTTAGCAACTTCAC CTTTCATGAAGGCAACTTG lead AS 419068 419083
yqfG(71.2E-6) TTTTCTGATATTTTATTTTCAC TTGGTTGGACGAAATAGT lead AS 1659783 1659798
ptsI(71.1E-6) TCAAATACAGATGCTGCTTCAC CAAGGGTTGTTACTGCTTT lead AS 120832 120847
tra904I(71.0E-6) ATTGTAGGCTGGTCAATGTCAC GGATCCAAGATAAACTGGT lag S 2215294 2215309
yciH(70.9E-6) CTGGTGACTTCAAGTTTGACTCAC ACCAGTGGGTGAACCTGCT lead S 290558 290573
purB(70.9E-6) TTAGCAAACAATTCTTCAACTCAC GTTGTTCAGATTTTTGTAA lead AS 1688986 1689001
pgk(70.5E-6) CAAGCTTACGAAATCGGAACTCAC TCGTTGAGAAGCACAACT lag S 243525 243540
glyQ(69.6E-6) CTCATTGTTCCTGCTCCTACTCAT TATCATAAGCTTGCATCAA lead AS 1101918 1101933
ymdC(68.5E-6) TGAGAAATTTCCTGAAGCACTCAC AATACGCTAAAAGATGCAA lag S 1234116 1234131
yliB(68.0E-6) GATTTGATTTTCCAAATACTCAC AGATAATCTAAGGATTGCC lag S 1181868 1181883
ilvC(67.6E-6) TTAGCTACCGCTTGTCCTACTCAA ATGTTTCAAAGCCATCTTC lead AS 1249913 1249928
intergenic(65.9E-6) TCATTACTTCTCCATCCTTCTCAC TAATGAAGGCTTTTTAAAT lead . 297420 297435
ylgC(65.6E-6) GTTGTTTAAAGCTTCATAGACAAT CATACAAGCACAATTTGAT lag AS 1162306 1162321
racD(65.6E-6) GTACAACCTAAAATGGTACTCAC AATTCATTTCTGACGCGAC lead AS 2309368 2309383
ypgB(64.6E-6) TGCCGCTTTCCTCACAAACTCAC TCCATCTACAGCCATTTTC lead AS 1562082 1562097
trpB(64.3E-6) GATTGTCTTTAACGTCTTCTCAC CATATAAATCGTACATTC lead AS 1495507 1495522
pycA(64.1E-6) ATGTTATTGCTAATGAAACTCAC AAGTGGTCAAGCAACAACA lag S 664950 664965
pepN(63.9E-6) GGGTCAACAAGCATGCAGACTCAC GATAAGTGATACATCCCCA lead AS 303152 303167
ccpA(63.7E-6) GTCTTTTGCTTTACATTTGCATTTC CATTTACAACACGACTAAC lead AS 1696846 1696861
yfjF(63.5E-6) GATTTTTGAAATCTAAAACTCAC TGCAGCGAATATTGGAATC lead S 598934 598949
polC(63.5E-6) TTGATTGCTGCTCAAAAACTCAC CAATTTCGCAGGCCGAACC lead AS 2191543 2191558
yqgC(62.4E-6) AACGATTCAGCTGTTCAACTCAC TCATTTGTGGGCTTAAACT lead AS 1666094 1666109
pydA(62.2E-6) TAAAAGAAGTTTTTAGCTTCTCAC AAAGCGTTTAGGTGTAAAA lag S 1593286 1593301
ilvD(62.1E-6) CCTACTTAAAGAAGGAAAACTCAC GGTGATTGTTTGACCGTCA lag S 1246820 1246835
gyrA(61.6E-6) TCATCTTCAAGATGTAGAACTCAC CAACTAACAATTCTGTTCG lead AS 1123222 1123237
ykiG(61.5E-6) CAGGTTTATTTTCATGCTTCTCAC GCTCAATGGAAGTTTTACT lead S 1088003 1088018
yjgE(60.7E-6) TTTAAAATTACTTCTTGAACTCAC CAACTAATTCAGGGTCAAG lead AS 964786 964801
trpE(60.7E-6) GGACGGAGCTCGCGGGTCACTCAC TTGTAATATGCATGACGTA lead AS 1500446 1500461
rbsK(60.2E-6) CCATCGTGGAAAATGACTCCTCAC TTCCTAAGGTGACAATCAG lead AS 1686674 1686689
ylbB(60.0E-6) CGATAAATATAAAGTGTGACTCAC GGTCATAGAAGCCTAAAAC lead AS 1113813 1113828
ydbA(59.9E-6) TGATTTCCTTCTTCGATAACTCAC CATCTTTAAGAACAACAAT lead AS 312783 312798
ylgG(59.9E-6) CAGATAAAGCTTGATTTCAGCAAT TAGGTCTCATTCATTTTT lead AS 1168308 1168323
rplC(59.8E-6) GCAGCTTTGTTGGTCAAAACTCAC GAAGTGTATCGAAACCAAC lead AS 2169777 2169792
ynhC(59.5E-6) TCCATTTTAGAAGTTCAACTCAC CTTGTTGACGTTTTTGACG lead AS 1374723 1374738
pepN(59.1E-6) GCAATAACAGTTGCTACATATTGTT TGCTTTGAATGGTTGCAAT lead AS 303201 303216
aroB(59.1E-6) TTGATGACCTCCCGCAGTCCTCAC GGAATTCTCTTTGACCGAG lead AS 1814295 1814310
glmU(59.0E-6) GTTTCTCCACCAATCGTAACTCAC TGTCAATATAAGTTGTGGC lead AS 1951674 1951689
hsdR(58.9E-6) CTTTGATAAACTTCTTTTCATAAT CTTTTTCGGAATGTTTTTC lead AS 642226 642241
accA(58.9E-6) GCAATATTTTTTTGTGAAACTCAC CTGTCAGTGAATCAATGT lead AS 789638 789653
yshA(58.7E-6) ATTTTTTTCAATTTCTTGACTCAC AAGGTGGAGCAAGTCAATT lag S 1875797 1875812
rplJ(58.6E-6) ACTTTGAATCCAAGGCTCGTCAC GAAGTTGTTTACGAAGTTG lead AS 1301775 1301790
leuS(57.9E-6) TTATCCATCTGGTGCAGGACTCAC GTTGGACACCCAGAAGCTT lag S 827588 827603
ywjB(57.7E-6) ATCGAGGCTTACTAAAAGACTCAC AGTCTGCTCAAGTCATTGA lag S 2296014 2296029
era(57.3E-6) TTGAACGTGTTCATCAGCCGCAAC CATGAACAAAACGACATCA lead AS 355313 355328
papL(57.2E-6) AGGATTTAAAACGTCGTGACTCAC GATCAATGCCTTTGCTTGT lag S 1602930 1602945
gyrA(57.1E-6) GGCGACTATGTTGTCGGAACTCAC GAATTGATGACAGTCAAGA lag S 1123879 1123894
ylcF(56.7E-6) AGTAAAAAATTTATATAATCTCAT TCATTTTTGTTTTTCCCTTT lead AS 1128157 1128172
ylfB(56.2E-6) AATTTCAAAGATGAGACGCCACATT GATGAAAAGGATTGGCAAC lead AS 1152026 1152041
ilvH(56.1E-6) GATACTTTAATCAAGACGACTCAC GTTCTACATGAGGCAAATC lead AS 1249451 1249466
pstE(54.4E-6) TTTTGGTCTTCATCTCCTACTCTT TCCAGTTGGTAATTTTACC lead AS 1775284 1775299
citE(54.3E-6) CCCTTGACAAAGCTTCTTCATCAT CAACATTGCCAAAGACCGT lead AS 1208681 1208696
uvrA(54.3E-6) TAACGTCTCCCATGGCAAACTCAC ATGGAACATAAACATCCGG lead AS 1886165 1886180
Intergenic(54.2E-6) TGCTGACACAAGCCACATACAAGGT TAGAGTACTATTTTGTTTC lag . 165032 165047
pdp(54.1E-6) GAATAAAGCTGACAATGACTCAC CGGCACTCACCTTATCTCC lead AS 1464555 1464570
valS(54.1E-6) CCTTCTCCCTCAGGTGCTCTCAC CAACATACATTTCACCGC lead AS 2249627 2249642
ytgG(53.6E-6) TTTTGATTCACTGATAAATCTCAT CCCTTCTCAAATGGAACA lead AS 1969240 1969255
aspC(53.4E-6) GCTCAATCAGTCGTACAAACTCAC TTGGTGGCACTCAATCGGT lag S 163533 163548
yhdB(53.2E-6) GCAGTCGTCAAACCAACAACTCAC CAAATCCCGAAAGTCCGTC lag AS 732748 732763
L200158(52.9E-6) AGCGCTTATCCCTTCCCTACATAGC TATCCAGCCGTGCTCCTGG lead AS 2360508 2360523
intergenic(52.5E-6) GGAAATCTGTTTGAGCTATTTCAC GACTTAATCACACAGAACA lag . 1041037 1041052
frdC(52.4E-6) TCATTTACAACAATCGCCCTTCAC CACGAATTGATTCTGAAAC lead AS 1138793 1138808
nrdG(51.7E-6) TAAAGTGACCAGCGCACCCCTTCAC CATCAACGAAATTGAAGGG lead AS 272742 272757
bcaT(51.4E-6) CCTAAATCTTTGGCATAAACTTCAC CCTCAATCGCTTTGAGTCC lead AS 1322017 1322032
apl(51.0E-6) GTGGCAAGATGTTCTCAATCATAAT GAGAAGGCAACACCAAAG lag AS 719594 719609
ytbA(50.9E-6) TCAATCAGCTGGTCAAGAACTCAC TGACTAATTGGGCAGTTAA lag AS 1913156 1913171
copA(50.6E-6) TGAACAACAACCCTTTAACTCAC CATCTAATTTAATTGTTCC lead AS 846827 846842
ywfF(50.2E-6) GTCACAAAAATATTTGTACTCAC CTGTTTTTTGCAACGACG lead AS 2255346 2255361
yebB(50.1E-6) GAAGAGTGTATTTTAGGAACTCAC TGAAACCAGCAGCTAGTTC lead AS 411411 411426
recN(50.1E-6) ATAATTATTCGATTTATTTCCTCAAT AAACGTTAAGCCTGAGCTA lead AS 884734 884749
ybcG(49.8E-6) GTCGATCATTACAGCATCAGTAAC CATATCTTGTAAAGTTTCA lag AS 122935 122950
yibB(49.8E-6) TGACTTGAAACGAAAGTAAAGCGTT CATTGACTTCATCAAATTG lead AS 813101 813116
pi229(49.6E-6) ACTAACCAGAAGAAAAACTCAC CCTTTGCTCTATTTATGAG lag S 1052899 1052914
ypdB(49.1E-6) TCAGCAAGATATTTTCTACTCAT TCGCTTTTTCAAAACGTGT lead AS 1532507 1532522
fusA(48.9E-6) ACACACCACGTCACGTGGACTCAC AATTGAACTACAACGTCA lag S 2354018 2354033
ydbA(48.0E-6) TTGATAAAGTTGGAAACCATCAT CAATGGGAAAATCAATACCA lead AS 311876 311891
intergenic(47.3E-6) AAAACATTAGCAAGGGAACTCAC AGATTGGGGTCCTAATTGC lag . 295163 295178
ysiE(47.3E-6) TATAATAACACTTGATTACTCAC TTACGATTCTTTCAAGTCT lag S 1889135 1889150
pflA(46.7E-6) ACGTGACGAACCCACATTCCATTAC CACGGTCTGATAAATACTG lead AS 1880728 1880743
yoiC(46.6E-6) TTCACAGCAGCAGACGCATTCAC AAATCGCAACAATCTTGC lag S 1486532 1486547
apt(46.5E-6) TCGTAGTTGCTTCAATGATCAC GAGGTAATTTACCAGGCTT lead AS 623066 623081
intergenic(46.3E-6) ATCAATATATGCTGCTGTACTCAC CAATATTTCTGTGCAGTTT lag . 1413891 1413906
ypjA(45.7E-6) ATAATTTTTTCAATCGCTTCTCAC CACGTTCATCAATTATATC lead AS 1590916 1590931
tuf(45.7E-6) TCTTTGCTCAATACGTAAACTCAC CTTCGAAAAGTTTGTGTGG lead AS 1929629 1929644
galK(44.7E-6) AATAGGATTGCTTTTTTGACTCAC CAAAACCAATAGCGAATTG lead AS 2061130 2061145
yhcH(44.1E-6) CCAAATAAAAATCCAGTCACAACAC CAACAATGACCTGTACATC lead AS 727005 727020
optC(43.3E-6) TGGAAATATTTAATTAAGACTCAC CCTTGTTGGTTCAAAGGGT lag S 347970 347985
yldA(42.9E-6) AGCACCTGAACTCTTTTTACAATGAC GGATTAAGTGTTTTAGCCT lag S 1132657 1132672
yliB(42.9E-6) ATATTTCTTTCTTATCCTACTCAG ATTTGCAGATAGGAAATGC lag S 1182872 1182887
ydiA(42.7E-6) GAGAAGTCTATGTTGTATTCAAAAT TCATATCATTTTTTAAACA lag S 381887 381902


ykjB(42.6E-6) lag S 1092491 1092506
malF(42.3E-6) lag AS 1740489 1740504
pi246(42.1E-6) lead AS 1068667 1068682
pdhC(41.9E-6) lag AS 61832 61847
dexA(41.7E-6) lead AS 1736112 1736127
carA(41.1E-6) lag S 1644318 1644333
gltD(40.6E-6) lead AS 1315740 1315755
rpoB(40.6E-6) lead AS 1861909 1861924
yfgG(40.5E-6) lag AS 564702 564717
yugD(40.5E-6) lead AS 2069410 2069425
yljB(40.2E-6) lag AS 1192125 1192140
leuC(40.2E-6) lead AS 1243302 1243317
relA(39.4E-6) lead AS 108400 108415
yneH(39.2E-6) lead AS 1346233 1346248
bglR(38.8E-6) lead AS 1493676 1493691
gntK(38.8E-6) lead AS 2268969 2268984
thiL(38.5E-6) lead AS 1612822 1612837
noxE(38.2E-6) lag S 397469 397484
yjhD(38.2E-6) lead AS 972867 972882
dexB(38.2E-6) lead AS 1525229 1525244
fbaA(38.2E-6) lead AS 1979853 1979868
yjgD(37.8E-6) lag S 964028 964043
parC(37.8E-6) lead AS 1012281 1012296
intergenic(37.4E-6) lag . 1212453 1212468
guaA(37.2E-6) lag S 1517407 1517422
yqgA(37.0E-6) lag S 1662192 1662207
butB(36.9E-6) lead AS 917656 917671
rsuA(36.7E-6) lead AS 2326760 2326775
yniH(36.6E-6) lag AS 1387665 1387680
yvcC(36.2E-6) lag S 2127492 2127507
tra983C(36.1E-6) lead AS 958140 958155
ymcA(36.1E-6) lag S 1220304 1220319
pi146(35.8E-6) lead AS 481528 481543
rpsG(35.4E-6) lead AS 2355006 2355021
ybeF(35.2E-6) lead AS 149869 149884
ybeH(34.8E-6) lead S 142965 142980
apl(34.0E-6) lag AS 719326 719341
trmE(34.0E-6) lag AS 2327760 2327775
accA(33.4E-6) lead AS 790082 790097
yudI(33.3E-6) lead S 2036707 2036722
ctsR(33.2E-6) lead AS 629551 629566
infB(33.1E-6) lead AS 776847 776862
fusA(32.7E-6) lag S 2352871 2352886
ybaI(32.6E-6) lag AS 110171 110186
vacB1(31.9E-6) lead AS 967655 967670
pi214(31.8E-6) lead AS 1044606 1044621
pepDB(31.4E-6) lead AS 1601634 1601649
yafB(31.3E-6) lag AS 51093 51108
intergenic(30.6E-6) lag . 420472 420487
pflA(30.5E-6) lead AS 1880578 1880593
pi146(30.4E-6) lag S 479371 479386
hrcA(30.3E-6) lead AS 977393 977408
yxbD(30.3E-6) lead AS 2319286 2319301
truB(30.1E-6) lead AS 1140585 1140600
yrgI(29.9E-6) lag AS 1769961 1769976
feoB(29.3E-6) lag AS 190202 190217
ptnD(29.3E-6) lag AS 1764210 1764225
ycfF(28.8E-6) lag AS 257260 257275
L200150(28.6E-6) lead AS 2222501 2222516
yleF(28.4E-6) lead AS 1147802 1147817
ychC(28.2E-6) lag AS 273862 273877
L200064(28.1E-6) lag AS 1718135 1718150
glyA(27.5E-6) lag S 591480 591495
ywaF(27.4E-6) lag AS 2205804 2205819
uvrC(27.3E-6) lag S 857817 857832
mapA(27.3E-6) lag S 1729190 1729205
argG(27.1E-6) lead AS 127192 127207
recD(27.0E-6) lead AS 1797764 1797779
ykhD(26.9E-6) lag AS 1072513 1072528
chiA(26.9E-6) lag AS 2027631 2027646
glmM(26.8E-6) lead AS 436154 436169
intergenic(26.4E-6) lag . 565292 565307
ftsK(26.4E-6) lead AS 1704506 1704521
ywcC(26.4E-6) lead S 2228600 2228615
ps311(26.3E-6) lag S 2021044 2021059
yiiI(26.1E-6) lag S 889057 889072
typA(25.8E-6) lead AS 2093373 2093388
acmC(25.7E-6) lag AS 1402971 1402986
yjcE(25.3E-6) lead AS 926233 926248
als(25.3E-6) lead AS 1200491 1200506
pgi(25.3E-6) lead AS 2245042 2245057
ycbI(25.1E-6) lead AS 218241 218256
ypfF(25.1E-6) lag S 1558390 1558405
carB(24.9E-6) lead AS 1399224 1399239
pi214(24.8E-6) lag S 1045075 1045090
yqbK(24.8E-6) lag S 1623170 1623185
hisI(24.6E-6) lead AS 1237413 1237428
ftsK(24.5E-6) lead AS 1705152 1705167
kupB(23.9E-6) lead AS 613026 613041
rplN(23.9E-6) lead AS 2164972 2164987


mtsC(23.6E-6) AAAATGATAATTCTCTCCTCTCTCAC TAGGGGCAGTTTCTTCCGT lag S 1350292 1350307
pepDA(23.5E-6) CAGGACTACGTGTAGAAGACGTTCAC AACTATTACCCTCCCTTAT lead S 249419 249434
ptsI(23.1E-6) ATTTCTATCATCATTACCTACGTTCGA TTCCATCTGCAACTGGAAC lead AS 121915 121930
ywaI(23.1E-6) TTGAATTCAGAATTATCTCCACCAC CATGAATTTTGAATTCATT lag AS 2208802 2208817
rpsC(23.0E-6) TCAACGTTGTTTTCCATTCCTTCAC CAACAAGATGAGCCGTCAA lead AS 2166372 2166387
ywfF(23.0E-6) GCATTCAAAGCCTTTACTCGTTCAC CATTAAAGTACATTGGCTTG lead AS 2255016 2255031
intergenic(22.7E-6) GCTCTACCAAGCTGAGCTAGTCCC GGACATGAAGTGCTTGACG lead . 282940 282955
yleF(22.5E-6) CCCGCACTTTGATGTTTATTCTTAAT TGAAGTAGGTGATTCAGAA lag S 1147818 1147833
yidE(22.2E-6) AAAATTTTTCCTTTTTGAACTTCAC AGGTTTGAGCGCCATGGAG lead AS 835562 835577
yogA(22.1E-6) CTTCTATTCGATTGTCCTACTTCCT ATTCTGGCTGGACTATCTA lead S 1460644 1460659
glyS(22.0E-6) TGTCATTGAAGGGCACAAACTTCAC GAACCTTTAAACCAGCAA lag S 1104472 1104487
ypfF(22.0E-6) GCCTTTATGATGACCCACTTCTTCAC TTATAAAGATTTCTCTAAA lead AS 1558342 1558357
ytgF(21.9E-6) CGACGCTTGCTTTTGTTCTTCTTCAC CAAGGGTCTAACGGGCTTC lead AS 1968538 1968553
ylcC(21.7E-6) TTTAAAGGCGTTGGTGGAATATCTCAC TTTTATATTGGAGCGGGAAC lag S 1125903 1125918
yceJ(21.6E-6) AGCGATATATTTTTAGCGACTTCAC GAATTAATTTTTTTAGTCC lead AS 247326 247341
rmaB(21.6E-6) TTACCTAAGCCTTTCCAATCTTCAC CAAACGGAGCTTGTGAGCG lead AS 714999 715014
ynjG(21.6E-6) CTCACGACCTTTAACCCTACTTTAC AGGTAACAAATTTTAGTCC lag S 1394984 1394999
pepP(21.2E-6) TTTGCGGCGTTTGTTAAGACTTCAC AGCCATTTTCTGTCACTAA lead AS 691432 691447
intergenic(21.2E-6) ATCGTAACCCCTCCATTAGCTTTTA TGGTATTAATAAAAGAAAA lead . 1133651 1133666
llrA(20.7E-6) TCAACGGCAATGACCATGCTTTCAC GACGGAAGAAAGCACGAAC lead AS 1639102 1639117
alaS(20.3E-6) GTGCGTTTCAAAGTTTCTTCTTCAC GATCAATAATTTGCATGAT lead AS 1779915 1779930
yfgQ(20.0E-6) AAAAATTGCTTCTAGTGATTTGGTT GAAGAAGATATTATTATTC lag S 568993 569008
intergenic(20.0E-6) ATTTTAAGAGATTATCAGTGGTATT AATCATTTTAACAGACATT lead . 966884 966899
ps315(20.0E-6) CTAAAGAGAGCGCCAAACTCTTCAA GCGTCATTCCCTTTTTAGT lag AS 2023699 2023714
prfA(19.6E-6) TTATCTACGTAATCTCGCTTCTTCAC GCGATAATTCCATTAAACG lead AS 586052 586067
yjaJ(19.6E-6) TCTCGGGCAAAAACTAAAGTTGTT CTCCGTTGATGAGCTGCTT lead AS 909737 909752
vacB1(19.5E-6) TGTAAAAATAATGGTTGAACTTCAC CATATTTTAGAAGCCATGC lag S 968257 968272
ybfD(19.4E-6) TTATCTTGTTTTTATCTCCCTACT GTTGTTATTGGTTACAATGG lead S 158550 158565
rmlC(19.3E-6) CCAGAACCCACAACTGCTTCTTCAC CAAGATGTTTAGTCCGTCC lead AS 200761 200776
yngE(19.2E-6) AGCTTTCCTTTAACGTGGACTTCAC CTTCGCTAGGCTCGAGGAG lag AS 1365714 1365729
pknB(19.1E-6) GCGAAACGCACTCTGTGAAAGTTCAC TTACTCAAACAAATACAAT lag S 1956462 1956477
ybeF(19.0E-6) ACTTTTAGTTTGCTTCTTCTTCAC CTGAGATGCTAAAGTTAAC lead AS 153682 153697
gltD(19.0E-6) ATTTCGGCGTGTTTTTTCTCCTTCAC GGATTGCCCAAATTACCAA lead AS 1315143 1315158
yjfJ(18.6E-6) CGCGTTGTTAATCCGAAAAGTTCAC CATATTACTTCAGTTATTCG lead AS 959323 959338
yljF(18.5E-6) CCGCCACGCAAAACCAGCCCTTCAC CTGAAGGATAGATTCCTTT lead AS 1197029 1197044
rpmA(18.2E-6) AAAAAAGGTGCGGGTTCTTCTTCCA ATGGAGCTGACTCACAAGC lag S 1091336 1091351
pdhB(18.1E-6) GTATAGTAACCTTCAGGAAGTTCAC CTTTAAGTGAGCGATAAAG lag AS 62610 62625
celB(18.1E-6) TTAATTACGCAAGCCCTCTACTTCCA AGTTCACTCACAAGGTATA lag S 178484 178499
intergenic(17.8E-6) ACTTCCATATCCCTTTATGTTCAC CTTAATATTCTTTTTAATA lead . 1987040 1987055
yahG(17.7E-6) GACGCATAAACTCTTTCAACTCGGC AATTTTCTCTTCAGCTTTA lag AS 74058 74073
rbgA(17.7E-6) GATGCTCGTCTCCCTATTTCTTCAC GTATATCCGATTGTTGGGGCA lag S 1329921 1329936
ps105(17.6E-6) CAAAACCTAAAATAGAGGAGTTCAC AGATTATGGCGAAGACGGC lead S 39194 39209
lepA(17.5E-6) GCACGATAATCAGAAATCTCATAAT CAAAGCTGGCATAACCTTT lead AS 1118787 1118802
pppL(17.2E-6) ACTTGATATACTGCTTGAAGTTCAC TTGTTTGCCCAAGTGAACG lead AS 1957232 1957247
ybaB(17.0E-6) AAAATTCGAGTTGTCCATTTTTCAC AGTTAATGACATCAGAAAC lead AS 103218 103233
lysQ(17.0E-6) GCTGCGGGAACCAAAACTGGGTAAT CAATCCTGCTGTCGTTAAA lead AS 369938 369953
yqbK(17.0E-6) GTTTCTGCAGTACGTCCCATGGCAC TTCTATATACTACTCCAGC lead AS 1622667 1622682
ybeF(16.9E-6) CCATTTTTGTCGGTATCTCCTTCAC GAATTAATTTTATCTTTTT lead AS 152104 152119
eno(16.9E-6) CCATCTCTTAATTCAACTGTCCTCAC GGTCTCCAGTTGATGCTCC lead AS 274299 274314
araT(16.7E-6) TAAGATAAGCGCGACAAATCCTTCAC CGTACTGACCAAAAGCGAT lead AS 57646 57661
pi214(16.7E-6) AAGTAAGGTTCTCCAATCATCTTCAG CTTTTTCATTCTTTCGGATA lead AS 1044675 1044690
rpsC(16.7E-6) CGTGCGTGAAGTTCTCCTTACTATAAA AATCTGTGAAAGGAGAAAA lag S 2166072 2166087
comFC(16.6E-6) CCTTTGGTTCCAATTTCCTATTTCAC CAAAAAGATTAGAGGAACG lead S 1096611 1096626
gidC(16.6E-6) TTGGAAGTTTACCTTACTACAACAC CCATACTGACAGCAAACAT lag S 1257952 1257967
ycgI(16.5E-6) TTCAGAAGAAATTTGCAACTTCAC TTACATTGTGTTGGTGGTT lag S 267947 267962
yciH(16.5E-6) AATATTATTCATCAGGTGTCATAAT CATTGGAACAACAAGTGGT lag AS 289429 289444
intergenic(16.5E-6) ATCAAGAGAACCTTCCAAGTTCAA AGAAGAGGGCAATCCCAAT lead . 2267063 2267078
intergenic(16.4E-6) TTAAACAAAGTATATTATAGTTCAC ATTACTATGTAAGTCAAGG lead . 308448 308463
agl(16.4E-6) CAGATAAAATCAATCCCAATTCAG GTAGATAAGGAATTTTTTC lead AS 1732727 1732742
ftsH(16.3E-6) TAAGCTTGGAAGTTTTTAACTTCAC TACTAGTAATTACCTAAAAG lead AS 26157 26172
pmrB(16.0E-6) CCAAAGGACAATTATATTTGGTTGC CATGATTCTTTCATGAATG lag AS 130558 130573
ribA(16.0E-6) ATTAATAAACTTCGTGCCTACTCAC TTCAAGATGAAGGACTTGA lag S 1024702 1024717
argG(15.9E-6) CAGATTCCACTGCGCCTAGTTGAAG CGCCTTATCATGAATAAAA lead AS 126892 126907
purL(15.9E-6) TCTTCATCCGTCAGTCCCACTTCAC GGTATATTTTGCTTTCTTG lead AS 1576342 1576357
fhs(15.8E-6) TCGGCCAAATCTAAGCACCTTCAC CACCCTTAGCAAAGACTTG lead AS 960978 960993
llrF(15.8E-6) GATTATTGACAATTTGTGTATCTTT CAATTTTTTCCGAATTTTA lead AS 1727031 1727046
yshA(15.6E-6) CATGCACTTCCACTTTCTACTTCCG GAGCAGATATGCTTGGTGG lag S 1876038 1876053
vacB2(15.4E-6) TCTAAATATACTTGTCTACTTCGC CTTTATGTCCAATTATACC lead AS 1226666 1226681
ysdB(15.4E-6) TGACCTATTAAGCCATAAGTTCAC CTGGTTTAACAACCATATT lead AS 1835702 1835717
yqgA(15.0E-6) CTTGAGGTTGACGTGCTTCCATAAC TACTGGAAGAATCACTGGT lead AS 1662046 1662061
infB(14.9E-6) CCATCATGAATCACGACACCTTCAC GAATGACACGGACAGAAGC lead AS 778425 778440
gltB(14.9E-6) TTACCTGGCAATTGCCCACCTTCAC CTGGTTTAGCACCTTGCGA lead AS 1318175 1318190
gntK(14.9E-6) CCCGCGGGAAATGTTTGCTCCAAGTT CCGTGACTTCATCAAAAGA lead AS 2269167 2269182
groES(14.8E-6) CCATCATGATTGTTTTCCGTTCAC CGACGGCAACAACTTCAGC lead AS 398636 398651
L200015(14.8E-6) TGAGAAAGTTAAATTCAAACTTCAC TTGCTTCTCCAATCTAAC lead AS 456625 456640
pi115(14.8E-6) TGAGAAAGTTAAATTCAAACTTCAC TTGCTTCTCCAAATCTAAC lead AS 456625 456640
fhs(14.8E-6) ACTGTTATATCAAAAGCATCTTCAC GGGGCACACCATTTAAAGG lead AS 960309 960324
nifS(14.8E-6) AACGCTGCTACAACAGCTGTTACTTC CTGATGTTATCACCGCAAT lead S 1927818 1927833
accC(14.7E-6) TCTTGCTTCACAGACAATTCATTGC CATTGGCTACACGAATCTG lead AS 788253 788268
dnaD(14.7E-6) ACCTTACGATTGAGGACTGTTCAC GCAAAGCTTGTTTTAATCAA lead AS 1083630 1083645
sbcC(14.7E-6) TTAGCTGTATTTGTACGACTTCAC TTAAAGCCAAAGCAATTGA lead AS 1353084 1353099
yngG(14.7E-6) AGCACTCGCACTTTTCCTAGTTCAA GTTTTCGTATCAACAAGGC lead S 1368503 1368518
trmE(14.7E-6) GATGATGTGCGAAACAATGACTTCAC AAATGCTCCTTGCAAAAAC lead S 2328325 2328340
ydaG(14.2E-6) TGATAATGCAAACATAATCATTCC CATTATAGTCATGAATGTA lead AS 309995 310010
snf(14.1E-6) TCAAGCACAAACTTACCTGTTCAC CATCAATTTCCGCTGTTAG lead AS 2123579 2123594
L200121(14.1E-6) CAGACTCAAAATCTGGTTCCTTCAG GGGAGTGCCGGTTCGAGCC lag S 2340443 2340458
ldhX(13.9E-6) TGAGCATAAGTACTCCTACGGCTC CAGCTCCAACAATTACAAC lead AS 1142431 1142446
yohC(13.9E-6) GAACTCCTTGCTGACGTTGTACTTC CGGTCCTTTGGCAACATAA lead S 1472006 1472021
ywjH(13.9E-6) AATTCAACTAACAGCAGTTAAAATTT CATTAAATTTATCTGGCCA lead AS 2299858 2299873
yrfC(13.8E-6) GCAATACAAATTTCTCCATGTTCAC GTGGCATTGTTCCTTCAAC lead AS 1753200 1753215


secA(13.5E-6) lag S 117488 117503
ftsY(13.5E-6) lead AS 825016 825031
trxB2(13.5E-6) lead AS 1694915 1694930
intergenic(13.4E-6) lag . 1702217 1702232
yucF(13.4E-6) lag AS 2025914 2025929
purA(13.4E-6) lag S 2029866 2029881
L200158(13.4E-6) lead AS 2361099 2361114
yuaD(13.3E-6) lead AS 2005245 2005260
yahG(13.2E-6) lead S 73337 73352
yohJ(13.2E-6) lag S 1479677 1479692
ycfF(12.9E-6) lead S 256796 256811
ksgA(12.8E-6) lead AS 690090 690105
rmeA(12.5E-6) lead AS 1947036 1947051
ygiI(12.4E-6) lag S 687601 687616
yibG(12.4E-6) lag AS 819874 819889
yljF(12.4E-6) lead AS 1195988 1196003
oppA(12.3E-6) lead AS 1905177 1905192
yciH(12.2E-6) lead S 290530 290545
gltB(12.2E-6) lead AS 1318322 1318337
yneG(12.2E-6) lead AS 1345665 1345680
llrC(12.1E-6) lag AS 403590 403605
ypcD(12.1E-6) lead AS 1524368 1524383
clpB(12.1E-6) lag S 1567980 1567995
yijB(12.0E-6) lead AS 892941 892956
yniC(12.0E-6) lag S 1381911 1381926
yniH(12.0E-6) lag AS 1387638 1387653
ycfD(11.9E-6) lag S 253569 253584
ispA(11.7E-6) lead AS 881208 881223
tpx(11.6E-6) lead AS 302128 302143
yeeA(11.6E-6) lead AS 439614 439629
ybdC(11.4E-6) lead AS 132561 132576
yvhB(11.4E-6) lag S 2175732 2175747
yafC(11.3E-6) lead AS 55779 55794
araT(11.3E-6) lead AS 57325 57340