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Supporting Online Material for

Emergent Properties of Reduced-Genome *Escherichia coli*

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SUPPORTING ONLINE MATERIAL

1. MATERIALS and METHODS

Plasmids and growth media

Plasmids pCTX and pCTXVP60 were constructed by G. M. K. and pT-ITR-IL2 was obtained from J. Rossi. MT minimal medium (S*1*), MOPS Minimal Medium (S*2*), Rich Defined Medium (S*2*), and LB (S*3*) were described elsewhere. Growth curves were determined as follows: 50 ml of prewarmed medium was used in a 250 ml baffled flasks shaking at 175 rpm in an orbital water bath maintained +/- 0.2°C of set temperature. Overnight cultures were diluted into fresh medium to OD_{600} of 0.05. OD was measured every 14 minutes for 18 hours and the final at 24 hours.

Deletion construction

Typically, deletions were constructed by lambda Red-mediated recombination of linear fragments into the genome, followed by removal of exogenous sequences by double strand break (DSB)-stimulated recombination (S*4*). Single deletions marked by a drug resistance cassette were first constructed in MG1655, and were then accumulated in a MDS by serial application of P1 transduction and DSB-stimulated recombination. Deletion of *tonA* and *endA*, as well as removal of IS*1* from *crl* and IS*5* from the *oppA* region, were carried out by an alternative, suicide plasmid-based deletion method (S*5*). Removal of unpredicted copies of IS*1* from *ais* and IS*2* from *yddA* in MDS40 was accomplished by P1 transduction of the homologous MG1655 genomic regions lacking the ISs into the MDS strain. Specifically, MG1655 genomic segments marked by inserted fragments for MD23 and MD32 deletions were transduced to restore IS-free *ais* and *yddA*, respectively. A modification of deletion MD1 (S*4*), removing exogenous plasmid sequences and extending the deletion into the flanking region, was carried out using suicide plasmid pSG76-CMB (S*5*).

Genome Comparisons

Genomic comparisons were made using precurser versions of the genome aligner Mauve (S*6*). The complete genome sequences of *E. coli* CFT073, EDL933, RS218 and *Shigella flexneri* 2457T were each aligned with MG1655. The comparison for the incomplete genomic contigs of DH10B was based on BLASTN results from searching against an MG1655 database. Results were verified by manual checks on alignment end-points, and combined for display by GenVision (DNASTAR) in a large-scale format for identification of K-islands (i.e. unique to MG1655). More recent versions of Mauve support multi-genome alignments in a single operation allowing new comparisons to be made as new genome sequences become available.

Genome tiling DNA microarray

A NimbleGen microarray was used that contained the complete MG1655 genome, plus all sequences in the IS database (S*7*), bacteriophages P1, lambda, φ80, φX174, M13mp18 and plasmids pBR322, pUC19, pACYC177, pBeloBAC11, pB171, pBin19. Genomic DNA was prepared, labelled and hybridized to the microarrays as described (S*8*).

Analysis of Deletion Strains

Individual deletions were were confirmed by sequencing across the new junctions. After they were accumulated into MDS39, further analysis was performed by hybridization to a DNA microarray. The hybridization results were converted to a histogram and added to the genome alignment data to visualize correspondence between the planned deletions and lack of hybridization signal (Fig. 1). Unexpected elements detected by hybridization were IS*1* (three copies, located in the *crl*, *yeaJ*, and *ais* genes), IS*2* and IS*5* (one of each, in *oppA* and *yddA* respectively). Four were removed by individual small, precise deletions. The last element, the IS*1* in *yeaJ*, was deleted along with flanking sequences to produce MDS40. MDS41 was produced by deleting *fhuACDB* (the *tonA* locus) to provide resistance to phage T1. In MDS42 *endA* is deleted to facilitate plasmid preparation. In MDS43 a 45 kb deletion included the *lac* operon. The MDS genomes were again characterized by DNA microarray hybridization, confirming that they corresponded perfectly to plan (MDS43 in Fig. 1), and no IS, unexpected plasmids or phage were detected.

Fermentations

Fermentations were conducted in a Bioflo 110 fermenter (2-L, New Brunswick Scientific, Edison, NJ) in a modified minimal medium containing 5 g/l glucose, 8 g/l KH_2PO_4, 0.4 g/l $MgSO_4$ and 100 μg/ml ampicillin (S*9*). The fed-batch feed medium contained 480 g/l glucose, 4 g/l $MgSO_4$, 40 mg/l Fe^{III} citrate, and 1.5 X trace metals (S*9*). Starter cultures (200 ml) were grown to 0.75 OD_{600} in batch medium with 20 g/l glucose and used to inoculate 1.5 l of batch medium. The batch phase of the fermentations was 9.5 hours, at which time the glucose in the batch medium was completely consumed. The fed-batch phases used exponential feed rates to control the growth rates (S*10,* S*11*). Fermentations were maintained at pH 6.75 and 37°C. Air was sparged at a constant rate and the dissolved oxygen maintained at 30% saturation by varying the agitation rate. Specific CAT activity was measured colorimetrically (S*12*). CAT expression was induced by IPTG via the *trc* promoter on the pProEX HT-CAT plasmid.

Measurement of electroporation efficiency

Electrocompetent cells were prepared by the method of Dower, et al. (S*13*) with modifications and stored as frozen aliquots in 15% glycerol at final OD_{600} of 200. Electroporation in an Eppendorf model 2510 instrument was at 18kv/cm using 0.1 pg pUC19 or 50 pg pCC145 DNA added to 0.1 ml of competent cells. The median of five electroporations is presented, each with a different batch of competent cells. For commercial DH10B competent cells the five determinations were from different tubes of the same batch. With 20kv/cm as recommended by their manufacturer, the commercial cells gave slightly higher values of 82.3×10^8 for pUC19 and 6.1×10^6 for pCC145 DNA. Assessed by a t-test ($p = 0.002$), the transformation efficiency of MDS42 is significantly improved over MG1655 for electroporation with both large and small plasmid DNAs.

Analysis of mutation rates

To detect mutations caused primarily by IS transposition, adaptation to salicin-minimal medium was measured as described (S*1*), selecting on minimal agar with salicin as the sole carbon source. Carbon-starved wild-type cells remain viable but do not form visible

colonies on the plates. Over several days new colonies of mutant salicin-metabolizing bacteria emerged on the plates and numbers were recorded daily. In a second protocol, designed to detect a range of spontaneous mutation types, cells resistant to D-cycloserine (S*14*, S*15*) were selected. In a fluctuation assay, 20 tubes of 1 ml glucose-MT were inoculated with 10^4 cells each, and cultures were grown to early stationary phase. 50µl aliquots from each tube were then spread on minimal plates containing D-cycloserine (0.04 mM). The estimated number of mutations per tube (m) was calculated from the number of colonies using the Ma-Sandri-Sarkar maximum-likelihood (MSS-MLL) method (S*16*). Equation 41 of Stewart, et al. (S*17*) was used to extrapolate the obtained m value - valid for 50µl - to 1ml. We only made statistical comparison of m values when the difference in total cell number was negligible (<3%, $p \geq 0.6$ with a two tailed, unpaired t-test). The total number of cells in a tube was calculated by spreading dilutions from 4 tubes onto non-selective plates. Dividing the number of mutations per tube by the average total number of cells in a tube gives the mutational rate (mutation/cell/generation). To measure the effect of protein overexpression on the mutation rate, MG1655 carrying pProEX HT-CAT was assayed both in the presence and absence of IPTG inducer in 20-tube fluctuation tests. IPTG (to 0.6 mM) was added to induce the cultures at $A_{590} = 0.7$, and cells were grown to saturation at 37°C. D-cycloserine resistant colonies were selected and analyzed as described above. Mutation rate measurement experiments were performed minimally in triplicate, except for those involving MDS42-(pCTX) and MDS42-(pCTXVP60) which were made in duplicate. The results are described as mean ± SD.

Analysis of mutation types

To analyze the mutational spectrum of the *cycA* gene, a 1877-bp genomic segment encompassing the entire gene was amplified from mutant cells using the primer pair cycA1/cycA2. A representative sample was obtained by analyzing 20 colonies from each parallel plate, yielding a total of 400 samples per experiment. The amplified fragments were resolved on an agarose gel and compared to a fragment generated from the wild-type template. Identical size indicated a mutation affecting only one or a few nucleotides, a decrease in size or failure of amplification indicated a deletion, and an increase in size indicated an IS insertion. The ratios of mutation types found on the growth plates of parallel experiments were compared using two-tailed, unpaired t-tests. The mutational spectrum of the *bglR* region was analyzed in a similar way using primers bglR1 and bglR2. In all cases, where further analysis of the insertion mutants was desired, the identity of the ISs was determined by PCR using combinations of oppositely oriented IS-specific primers and primers flanking *cycA* (cycA1, cycA2) or *bglR* (bglR1, bglR2).

Sequencing pT-ITR

DNA sequencing was performed directly on plasmid templates using Prism BigDye (ABI) reagents, modified to read through the GC-rich ITRs by addition of the betaine, DMSO and dGTP mix in the following proportions: 2 µl BigDye mix, 1 µl dGTP BigDye mix, 4 µl 5M betaine, 1 µl DMSO, 3 µl dilution buffer (ABI), 10 µl plasmid DNA (about 500 ng). Thermal cycling employed steps of 98°C for 15 sec, 50°C for 5 sec, 60°C for 4 min, with 35 cycles. Unused dye was removed by Sephadex G-50 spin-columns and samples analysed on an ABI3700 instrument. Although peak height was lower through the ITR region, most chromatograms were readable.

Plasmids and phage growth on MDS42

MDS42 supports growth of bacteriophages lambda, phi80, P1, and also production and construction of a large range of plasmids including F-based BAC vectors with a secondary inducible multiple copy number origin; also the widely used pUC19, RK2, R6K and derivatives, pGEM series, pTOPO, pACYC184, p15A-ori based vectors and pET expression systems. These plasmids employed Cam, Kan, Amp, and Tet selectable markers, and various expression regimens have been tested, including induction of plasmid-encoded genes driven by the lac promoter, tetracycline promoter, promoters for arabinose and other sugars, T7 system, and temperature shift as well as the plasmids and methods already mentioned in the main text.

Requesting MDS strains

The MDS strains will be made freely available under MTA for academic research use. To request strains, please use the form on our website at www.scarabgenomics.com. Commercial research and production licenses are also available from Scarab Genomics. Other strains developed in this series will also be made available from time to time, and researchers interested in deletions or other modifications of their own design should also contact Scarab Genomics.

2. SUPPORTING TEXT

IS elements in *E. coli*

Laboratory strains in common use have IS-induced genome alterations that are not widely recognized, and others may remain undetected. Most differences between the two sequenced K-12 strains, which have been separated for five decades from a common laboratory ancestor, are due to IS transposition (S*18*). IS transposition from genome to plasmid has also been reported (S*19*) and observed; approximately 0.1% of eukaryotic sequences in the public databases are contaminated with bacterial IS elements. Though direct in vivo transfer of IS from enteric bacteria to to human cells has not yet been ruled out conclusively in all these cases, the preponderance of IS*10* in these data is consistent with the frequent use of strain DH10B for propagation of plasmids in *E. coli* for sequencing (S*20*-S*23*)

IS elements may also be introduced into strains inadvertently by laboratory manipulations. The popular *E. coli* K-12 derivatives DH10B and DH5α carry an IS*10* not present in the ancestral K-12 genome. This was retained when Tn*10* was used as a genetic marker (S*24*). Despite a report that residual IS*10* elements do not transpose in *recA* strains such as DH10B and DH5a (S*25*), the IS*10* contaminants in the eukaryotic databases indicate this is still an issue. An otherwise unpublished GenBank entry (Accession AY319289) described a case in which an 11,131 bp segment of the *E. coli* genome flanked by IS*10* elements was found in a mouse BAC propagated in DH10B. Examination of the partial genome sequence of DH10B (S*26*) shows this precise configuration of IS*10* elements and intervening DNA, demonstrating the accidental creation of a transposon in DH10B in which IS10 has mobilized other genes. Another case of this type may underlie the plasmid contamination by the *Eco*47 gene we report

below. Bioinformatic removal of IS elements would obscure IS-mediated DNA transfer, leaving behind unmarked bacterial DNA. In an industrial environment, IS transpositions have mutated genes in important production hosts, necessitating the re-creation of key strains (S*27*). Such events were long suspected of induction by stress (S*28*), and this is now confirmed by accumulating evidence: UV irradiation was shown to induce IS*10* transposition (S*29*); transposase transcription was shown to be induced by heat shock (S*30*) and by protein overexpression (S*31*); transpositions of some IS elements are induced by nutritional stress (S*32*). We show here genetic evidence that the induction of insertion mutations by stress is due to activation of generalized IS transposition.

IS contamination of isolated plasmid DNA

Yields of plasmids pBR322 or pUC19 propagated in MDS, DH5α or DH10B were similar. Starting with a commercial preparation of pBR322 DNA introduced by electroporation, plasmid samples were then isolated from DH10B and MDS hosts. To assay for IS contamination, PCR was performed with two sets of primers (outward and inward) specific for IS*1*, IS*2*, IS*3*, IS*5*, IS*10* and IS*186* (Fig. S1). Amplification with the outward primers (oriented back-to-back) detects only circular structures, whereas the inward primers detect both linear and circular IS forms. Results from DH10B were the same for both purchased or laboratory strains. Positive controls were constructed by cloning each IS type into pBR322 (minus about 20 bp from its ends to prevent mobilization). Both sets of primers amplified IS elements in the DH10B-grown sample but plasmids grown in MDS42 were IS-free (Fig. S1). The circular forms in the DH10B samples included sizes expected for a simple insertion of the IS into the plasmid, or were consistent with a circular form of the element itself.

Amplimers from outward primers were examined by cloning and sequencing. After growth in DH10B, IS*2*, IS*5* and IS*10* (but not IS*3* or IS*186*) were found as simple insertions in pBR322. Outward primed PCR products smaller than expected were gel purified and sequenced with the same primers, confirming the presence of mini-circles for IS*2*, IS*3* and IS*10*R. Primers for IS*1* revealed a complex arrangement in which both the *tet*^{R} and the copy control locus (*rop*) of pBR322 were replaced by an IS*1,* flanked on both sides by DNA that is not present in DH10B (Fig. S1(G) lane 1). The DNA yield of the IS*1* plasmid was higher than others, as expected with the loss of *rop*. The rogue sequence on one side of IS*1* was composed of a copy of the *lac* promoter upstream of the carboxyl part of the gene for restriction endonuclease Eco47I. On the other side was a 56 bp segment with no match in the sequence databases. Our data suggest accidental contamination of the purchased plasmid DNA with an Eco47 expression plasmid (never used in our laboratories) in which an IS*1*-mediated rearrangement had occured.

Growth rates of MDS42

At 37°C, doubling times of MDS42 were 65 min in MOPS Minimal Medium, 26 min in Rich Defined Medium, and 30 minutes in LB. At 30°C, the doubling times were 92 min, 46 min and 35 min, respectively. These rates are not significantly different (by t-test) from those of MG1655 growing under the same conditions.

Stability of pT-ITR in *E. coli*

Plasmid pT-ITR was electroporated into MDS42 and plasmid samples isolated from seven resulting colonies. One of the seven showed the predicted NotI digestion pattern, and was used for the experiment. This DNA was chemically transformed into MG1655 and MDS42 and plasmid was re-isolated from six transformants for NotI, KpnI and MscI digestion. Triplicate inoculations of correct clones from both hosts were made in LB and grown for 24 hr at 37°C with selection. Culture samples were withdrawn for plasmid analysis and one correct culture of each set used to start a serial passage, by dilutions of 10^{-6} – 10^{-7} in fresh identical medium. Four more similar serial passages were made, and plasmid DNA isolated from each stage for restriction and agarose gel analysis (Fig. S3B). In each case, the digestion patterns from MDS42 plasmids did not change with the serial passages whereas in MG1655 progressive changes are seen that are consistent with loss of the hammerhead region. KpnI linearizes the plasmid; accumulation of a smaller linear fragment shows in MG1655. NotI cuts outside each of the hammerheads to release a 1.6 kb fragment which is gradually lost in MG1655. MscI cuts at the 5′ end of the stem to release 1.2 kb fragment from between the hammerheads. This is also progressively lost in MG1655 passages, but remains stable in MDS42. In the wild-type viral sequence (Fig. S3A) an MscI site is present at both the 5′ and 3′ stem base, so the stem can be cut in the folded form. The 3′-site was replaced by a BglII sequence in pT-ITR.

Bystander mutagenesis due to pCTXVP60

Electroporation outgrowth cultures were examined for acquisition of cycloserine resistance and salicin adaptation. For the latter test, MG1655 cells were electroporated with either pCTX or pCTXVP60 and after growth to saturation, the cultures were spread on salicin/minimal agar. After incubation, we observed a 400% higher mutation rate in the pCTXVP60 strain compared with pCTX (Fig. S4B). The *bgl* mutants of MG1655(pCTXVP600) were found to carry insertions in the plasmid as well. The influence of the plasmids on the *cycA* mutation rates and spectrum in MG1655 and MDS42 hosts were then investigated in fluctuation assays (Fig.S4C). To minimize the effect of potential selection of clones with mutant plasmids, host cells were electroporated with plasmids prepared from MDS42, and the cultures were directly grown to saturation in glucose/minimal medium. D-cycloserine resistant mutants were then selected, and *cycA* disruptions were characterized by PCR. Those with IS in *cycA* were further analyzed for potential IS insertions in the plasmid as well.

Compared with MG1655(pCTX), MG1655(pCTXVP60) cells exhibited a higher mutation rate (5.7×10^{-8} and 1.19×10^{-7}, respectively), due primarily to a 4-fold higher rate of IS transpositions. An IS-specific PCR scan demonstrated that at least four different types of IS element (IS*1*, IS*2*, IS*5*, IS*150*) contributed to the higher mutation rate of *cycA*. Thirty two percent of the IS mutants of *cycA* also carried IS in pCTXVP60. The high proportion of these double mutants is not explained by independent single transposition events at the rate observed. Selection combined with IS transposition could provide the explanation. As expected, MDS42(pCTX) and MDS42(pCTXVP60) cells were IS-free. Point mutation rates were not significantly different from those in MG1655 (Fig. S4C).

Although *bgl* activation is most commonly caused by IS elements (usually IS1 or IS5) inserting into *bglR* (S*33*), it can also be a result of the deletion of the sequence upstream of the CAP binding site (S*34*, S*35*), or two base substitutions within the CAP binding site (S*34*). Rarely, mutations in *gyrA*, *gyrB* (S*36*), *hns* (S*37*) or in *bglJ* can also activate the *bgl* operon in trans (S*38*). Other cryptic elements that can be activated to turn the phenotype of *E. coli* to Bgl^+ are the *cel* (S*39*) and *asc* operons (S*40*) and the *arbT* transporter gene (S*41*). Despite all the possibilities listed, 98% of the Bgl^+ mutants obtained during growth arise from the insertion of an IS element into the *bglR* region (S*42*) In the absence of growth, only 79% of the Bgl^+ mutants are the results of insertions. The rest are mostly caused by mutations in *hns* (S*1*). These non-IS mutations were shown to occur in MDS at the same rate as in MG1655 (Fig. S4A).

We investigated the effect of protein overexpression itself on IS transposition. Cultures of MG1655 carrying an expression plasmid for CAT were compared with and without induction of expression. Using fluctuation tests, we found the number of transpositions into *cycA* was 236% higher in expression-induced cells. Insertions of IS*1*, IS*2*, IS*5* and IS*150* were detected, while point mutation rates were not significantly changed (Fig. S5). A mock induction did not change the mutation rate in MG1655 without the plasmid. We conclude that overexpression of even a well-tolerated protein leads to IS transposition.

3. SUPPORTING FIGURES

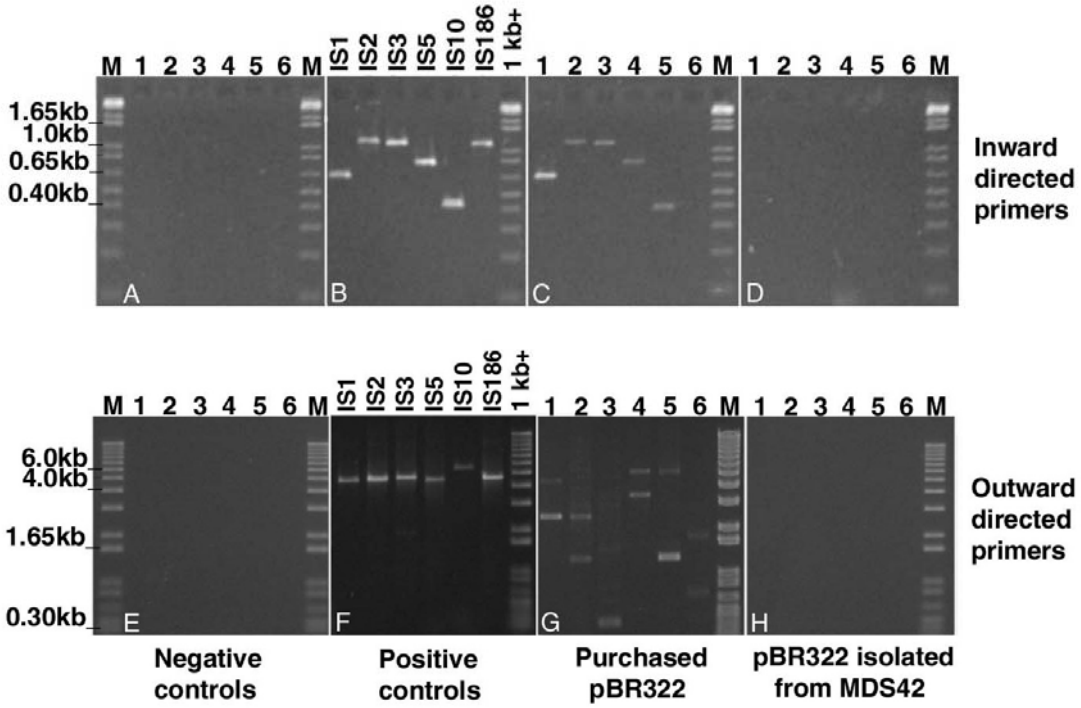

Fig. S1 Detection of IS contamination in a commercial plasmid preparation of pBR322. Inward primers (a-d) or outward primers (E-H) specific for IS*1*, IS*2*, IS*3*, IS*5*, IS*10* and IS*186* were used (lanes 1-6, respectively; M, 1 kb-plus size standard). (A, E) negative controls (no DNA); (B, F) positive controls are the individual IS elements cloned into pBR322. (C, G) purchased pBR322; (D, H) pBR322 isolated from MDS42. PCR amplimers generated with outward primers specific for IS*1*, IS*2*, IS*3*, IS*5*, IS*10* and IS*186* were ligated, cloned with selection for tetracycline or ampicillin resistance, and sequenced (data not shown). These data are qualitative and were not designed to estimate levels of contamination.

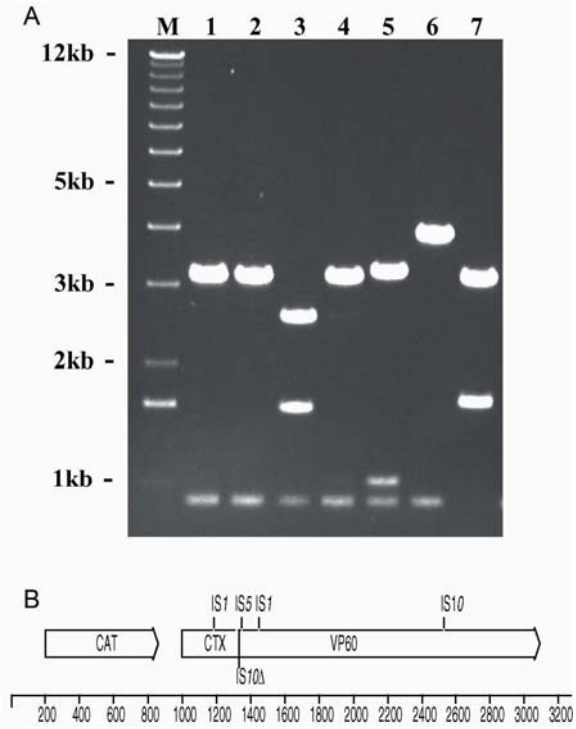

Fig. S2**.** Representative restriction patterns of pCTXVP60. (A) Plasmid DNA from MDS42 was transformed and propagated in the indicated host, then digested with NcoI and EcoRI. A representative of each restriction pattern was purified and sequenced. M, molecular weight marker, 1 kbp ladder; 1, MDS41, no insertion; 2, MDS42, no insertion; 3, DH10B, IS*10* insertion; 4, DH10B, IS*10* insertion/deletion; 5, C600, IS*5* insertion; 6, C600, IS*1* insertion; 7, C600, IS*1* insertion. (B) Relative position of the IS element insertion sites in the CTXVP60 reading frame determined for the five examples presented above. Scale in bp.

A

B

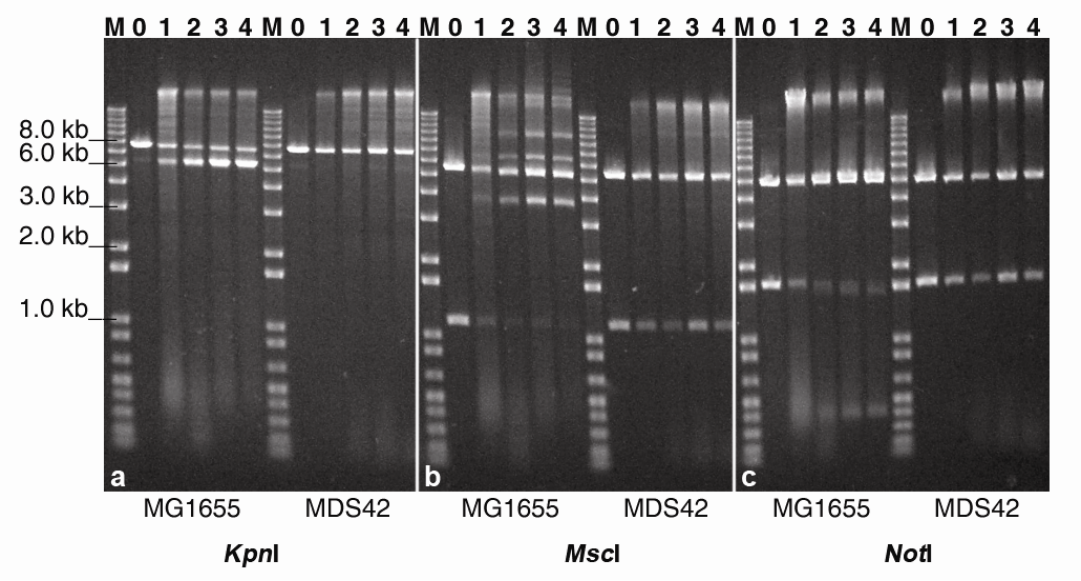

Fig. S3 A: DNA sequence and folding of the ITR (viral ends) of AAV. The MscI restriction site is underlined B: Plasmid pT-ITR stability in MDS42 and MG1655, monitored by changes in restriction patterns on agarose gels. Plasmid DNAs isolated from MDS42 and MG1655 serial cultures, were digested with (a) KpnI, (b) MscI, (c) NotI. Lanes 0, primary cultures from freshly transformed bacteria; lanes 1-4, subcultures 1-4. Fragment sizes in lanes 0 are consistent with predictions from the pT-ITR sequence (KpnI and NotI sites are outside the ITR). The gel was loaded with sample amounts that compensate for the slight decrease in yield all strains, to normalize band intensities, and to ensure that no smaller bands appeared in later subcultures.

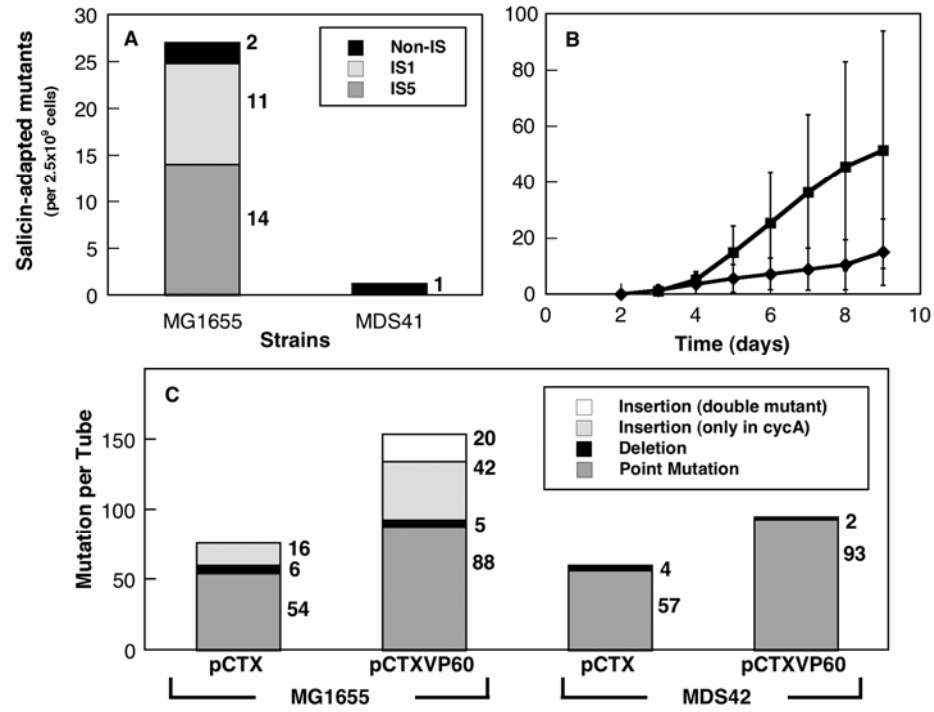

Fig S4 Analysis of mutation rates and spectrum in MDS and MG1655 cells. (A) Spectrum of mutations in the *bglR* region of MG1655 and MDS41 cells adapted to salicin/minimal medium on day 9. (B) Adaptation of MG1655 carrying the plasmids pCTX and pCTXVP60 to salicin/minimal medium. All salicin-adapted mutant numbers are normalized to 2.5 x 10^9 total cells. (C) Effect of the plasmids on the mutational spectrum of the *cycA* gene in MG1655 and MDS42. Total cell numbers and SD values are in Table S2.

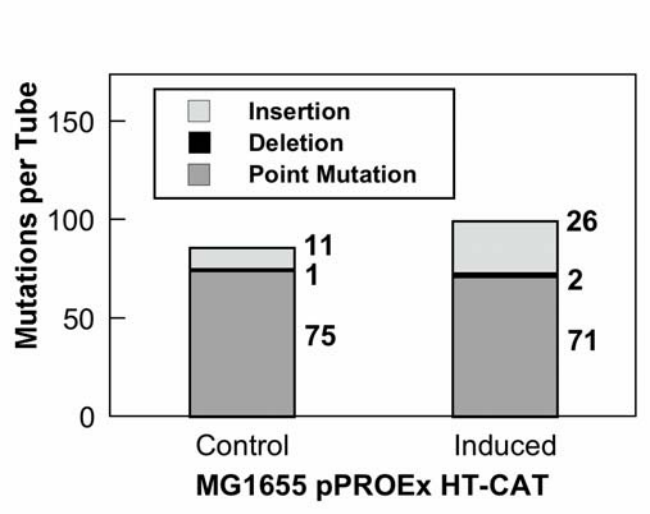

Fig. S5 Effect of CAT overexpression on the mutational spectrum of the *cycA* gene in MG1655.

4. SUPPORTING TABLES

TABLE S1. Individual deleted segments in MDS41, 42 and 43; coordinates refer to the updated MG1655 sequence (U00096.2) deposited in June 2004. Strain MDS 41 contains deletions del-MD1* through del-MD41, MDS42 also contains del-MD42, and MDS43 also contains del-MD43.

Deletion	Coordinates
del-MD13	15388..20562
del-MD41	167484..173447
del-MD1*****	262738..324634
del-MD43†	331590..376540
del-MD16	379334..387870
del-MD17	389122..399029
del-MD30	522062..529349
del-MD12	564278..585331
del-MD14	602688..608572
del-MD20	687083..688267
del-MD31	728588..738185
del-MD35	1041254..1049768
del-MD36	1085330..1096545
del-MD26	1128620..1140210
del-MD11	1196360..1222299
del-MD21	1386912..1396645
del-MD2	1398350..1480279
del-MD32	1525916..1531650
del-MD8	1625542..1650785
del-MD40	1870053..1871489
del-MD27	1960590..1977353
del-MD28	1995136..2021702

Deletion	Coordinates
del-MD5	2064329..2078615
del-MD22	2099420..2135740
del-MD37	2163175..2175232
del-MD23	2284423..2288202
del-MD7	2464567..2474200
del-MD15	2507653..2515971
del-MD3	2556713..2563502
del-MD4	2754181..2789271
del-MD18	2993014..2996890
del-MD42‡	3088369..3089076
del-MD10	3108702..3134399
del-MD19	3182803..3189718
del-MD24	3360184..3365664
del-MD6	3451950..3467875
del-MD38	3579161..3583065
del-MD33	3617014..3623701
del-MD25	3649314..3651735
del-MD39	3718657..3720098
del-MD34	3760016..3768265
del-MD9	4494698..4547733
del-MD29	4553513..4595035

***** an FRT site adjacent to the original MD1 was removed by extending the deletion
† MDS43
‡ MDS42 and MDS43

TABLE S2 Numbers of bacteria and mutations in fluctuation tests

A. (Fig. 3B)	MG1655	MDS41
mean total cell number	1.06×10^9	1.04×10^9
compared to MG1655 by t-test		$p = 0.92$
mutations/tube	69.3	54.6
SD_1	5.2	4.4
SD_2	4.8	4.1
compared to MG1655 by t-test		$p \leq 0.0001$

B. (Fig. S4C)	MG1655 (pCTX)	MG1655 (pCTXVP60)	MDS42 (pCTX)	MDS42 (pCTXVP60)
mean total cell number	1.34×10^9	1.30×10^9	1.36×10^9	1.33×10^9
compared to MG1655(pCTX) by t-test		$p = 0.69$	$p = 0.82$	$p = 0.72$
mutations/tube	76.4	154.0	60.2	95.3
SD_1	5.5	8.9	8.3	7.6
SD_2	5.2	8.4	7.8	7.1
compared to MG1655(pCTX) by t-test		$p \leq 0.0001$	$p \leq 0.0001$	$p \leq 0.0001$

C. (Fig. S5)	uninduced	induced
mean total cell number	7.58×10^8	7.75×10^8
compared to uninduced by t-test		$p = 0.86$
mutations/tube	84.5	99.9
SD_1	5.9	6.6
SD_2	5.5	6.2
compared to uninduced by t-test		$p \leq 0.0001$

TABLE S3 Primer sequences

(A) Primers for PCR-detection of IS contamination in plasmid DNA (Fig S1)

Target	Primer name	Note	Product	Sequence
IS*1*	IS1-fwd	∗	640 bp	5′-TGAGAACGACAGCGA-3′
	IS1-rev			5′-CTCCAGTGGCTTCTGTT-3′
IS*2*	IS2whole1		1185 bp	5′-ATTGGAGAACAGATGATTGA-3′
	IS2-whole2			5′-ATTCCCGTGGCGAGCGATAA-3′
IS*3*	IS3-whole1		1173 bp	5′-ACGCGGCTAAGTGAGTAAA-3′
	IS3-whole2			5′-GGACTGAGGCCGCCACAC-3′
IS*5*	IS5-fwd		827 bp	5′-GCCGAACTGTCGCTTGA-3′
	IS5-rev			5′-TCAGCAGTAAGCGCCGT-3′
IS*10*	IS10L_IN-F1		429 bp	5′-TGCGAGCTTCAGTCGCACTACACG-3′
	IS10L-IN-R1			5′-ACGGGTGGTGACAATGAGTCCGTG-3′
IS*186*	IS186-whole1		1159 bp	5′-ATTGGTAAGCCCGAAGAACTGGAT-3′
	IS186-whole2			5′-AATTGCGTTTTGTAGGCTGTCAGG-3
IS*1*	IS1-invPCR-R1	†	311 bp	5′-AGTTGCCATGTTTTACGGCAGTG-3′
	IS1-invPCR-F1			5′-ACCTGAATCTGAGGCAGCACCTG-3′
IS*2*	IS2-out2		1327 bp	5′-GCCCATACCCGACGATAACCA-3′
	IS2-out1			5′-CTTCGCAGACAGGCAGAACTTGAT-3′
IS*3*	IS3-invPCR-R1		392 bp	5′-AGTAACACCGATGCGTTCAGC-3′
	IS3-invPCR-F1			5′-TGCTACGATAATGCCTGCGTGG-3′
IS*5*	IS5-out2		1195 bp	5′-GCGTGGATGCTGTTTCAAGGTTCT-3′
	IS5-out1			5′-AAGAACAAAACGGCCATCAACATC-3′
IS*10*	IS10L-out1		1329 bp	5′-GACTCGCTGTATACCGTTGGCA-3′
	IS10L-out2			5′-GCTCTTTGTGGAGGTGACGATTA-3′
IS*186*	IS186-out2		1336 bp	5′-GGTCCAGCCGTTCAGCGTCTC-3′
	IS186-out1			5′-GCGCAAACGGCAGACGAGATAC-3′

∗ Inward oriented, PCR detects all IS forms.

† Outward oriented, PCR detects IS mini-circles

TABLE S3B Primers for PCR analysis of mutations (Fig. 3B, S4A, S4C)

Target	Primer name	Type	Sequence
pCTXVP60	T7: 5′	Normal	5′-TAATACGACTCACTATAGGG-3′
	CVek3		5′-GCCTGGTTGTACGCCTGAA-3′
cycA	cycA1		5′-CTGATGCCGGTAGGTTCT-3′
	cycA2		5′-GCGCCATCCAGCATGATA-3′
bglR	bglR1		5`-GTGGCGATGAGCTGGAT-3′
	bglR2		5`-CCGACTTCACCAGTATTC-3′
IS*1*	IS1/1	Inward	5′-TGAGAACGACAGCGAC-3′
	IS1/2	oriented, PCR	5′-CTCCAGTGGCTTCTGTT-3′
IS*2*	IS2/1	detects all IS	5′-TTGATGGTATGCCTGCGA-3′
	IS2/2	forms	5′-TGCCGTTAACCCGTCTG-3′
IS*5*	IS5be1		5′-GCCGAACTGTCGCTTGA-3
	IS5be2		5′-TCAGCAGTAAGCGCCGT-3′
IS*1*	IS1A1	Outward	5′-TCGCTGTCGTTCTCA-3′
	IS1A2	oriented, PCR	5′-AAGCCACTGGAGCAC-3′
IS*2*	UK1R	detects IS	5′-TCGCAGGCATACCATCAA-3′
	UK2R	mini-circles	5′-CAGACGGGTTAACGGCA-3′
IS*5*	IS5ki3		5′-ATAGGCTGATTCAAGGCA-3′
	IS5ki2		5′-GCTCGATGACTTCCACCA-3′
IS*150*	IS150ki1		5′-ACGTGCCGAGATGATCCT-3′
	IS150ki2		5′-CAGACCTATATGCCTCGT-3′

TABLE S4 Genes removed by each MD deletion. Names and locus_tags (b-numbers) are from the recent annotation update (S*43*) and subsequent refinements as entered in the ASAP database (S*44*). In the case of annotated multi-part pseudogenes their substituent pseudogene fragments (25 total) are not separately counted; e.g., *gatR* is counted but not *gatR_1* or *gatR_2*

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD13	*insL-1*	b0016	CDS	15445	16557	+
del-MD13	*hokC*	b4412	CDS	16751	16903	-
del-MD13	*mokC*	b0018	CDS	16751	16960	-
del-MD13	*sokC*	b4413	misc_RNA	16952	17006	+
del-MD13	*nhaA*	b0019	CDS	17489	18655	+
del-MD13	*nhaR*	b0020	CDS	18715	19620	+
del-MD13	*insB-1*	b0021	CDS	19811	20314	-
del-MD13	*insA-1*	b0022	CDS	20233	20508	-
del-MD41	*fhuA*	b0150	CDS	167484	169727	+
del-MD41	*fhuC*	b0151	CDS	169778	170575	+
del-MD41	*fhuD*	b0152	CDS	170575	171465	+
del-MD41	*fhuB*	b0153	CDS	171462	173444	+
del-MD1	*ykfI*	b0245	CDS	262552	262893	-
del-MD1	*yafW*	b0246	CDS	262914	263231	-
del-MD1	*ykfH*	b4504	CDS	263250	263471	-
del-MD1	*ykfG*	b0247	CDS	263480	263956	-
del-MD1	*yafX*	b0248	CDS	263972	264430	-
del-MD1	*ykfF*	b0249	CDS	264528	264767	-
del-MD1	*ykfB*	b0250	CDS	264844	265311	-
del-MD1	*yafY*	b0251	CDS	265334	266191	-
del-MD1	*yafZ*	b0252	CDS	266408	267229	-
del-MD1	*ykfA*	b0253	CDS	267321	268184	-
del-MD1	*perR*	b0254	CDS	268513	269406	-
del-MD1	*insN-1*	b0255	CDS	269466	269870	+
del-MD1	*insI-1*	b0256	CDS	269827	270978	+
del-MD1	*insO-1*	b0257	CDS	271054	271479	+
del-MD1	*ykfC*	b0258	CDS	272071	273216	+
del-MD1	*insH-1*	b0259	CDS	273325	274341	-
del-MD1	*mmuP*	b0260	CDS	274549	275952	+
del-MD1	*mmuM*	b0261	CDS	275939	276871	+
del-MD1	*afuC*	b0262	CDS	276980	278026	-
del-MD1	*afuB*	b0263	CDS	278038	278400	-
del-MD1	*insB-2*	b0264	CDS	278402	278905	-
del-MD1	*insA-2*	b0265	CDS	278824	279099	-
del-MD1	*ykgN*	b4505	CDS	279248	279586	-
del-MD1	*yagB*	b0266	CDS	279609	279959	-
del-MD1	*yagA*	b0267	CDS	280053	281207	-
del-MD1	*yagE*	b0268	CDS	281481	282410	+
del-MD1	*yagF*	b0269	CDS	282425	284392	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD1	*yagG*	b0270	CDS	284619	286001	+
del-MD1	*yagH*	b0271	CDS	286013	287623	+
del-MD1	*yagI*	b0272	CDS	287628	288386	-
del-MD1	*argF*	b0273	CDS	288525	289529	-
del-MD1	*insB-3*	b0274	CDS	289873	290376	-
del-MD1	*insA-3*	b0275	CDS	290295	290570	-
del-MD1	*yagJ*	b0276	CDS	290724	291455	+
del-MD1	*yagK*	b0277	CDS	291546	292172	-
del-MD1	*yagL*	b0278	CDS	292444	293142	-
del-MD1	*yagM*	b0279	CDS	293169	294023	-
del-MD1	*yagN*	b0280	CDS	294363	294803	-
del-MD1	*intF*	b0281	CDS	294920	296320	-
del-MD1	*yagP*	b0282	CDS	296605	297015	-
del-MD1	*yagQ*	b0283	CDS	296994	297950	-
del-MD1	*yagR*	b0284	CDS	297960	300158	-
del-MD1	*yagS*	b0285	CDS	300155	301111	-
del-MD1	*yagT*	b0286	CDS	301108	301797	-
del-MD1	*yagU*	b0287	CDS	302215	302829	+
del-MD1	*ykgJ*	b0288	CDS	303077	303406	-
del-MD1	*yagV*	b0289	CDS	303719	304429	-
del-MD1	*yagW*	b0290	CDS	304398	306041	-
del-MD1	*yagX*	b0291	CDS	306031	308556	-
del-MD1	*yagY*	b0292	CDS	308582	309250	-
del-MD1	*yagZ*	b0293	CDS	309308	309895	-
del-MD1	*ykgK*	b0294	CDS	309970	310560	-
del-MD1	*ykgL*	b0295	CDS	311336	311563	+
del-MD1	*ykgO*	b4506	CDS	311598	311738	-
del-MD1	*ykgM*	b0296	CDS	311738	312001	-
del-MD1	*eaeH*	b0297	CDS	313581	314468	+
del-MD1	*insE-1*	b0298	CDS	314506	314814	+
del-MD1	*insF-1*	b0299	CDS	314811	315677	+
del-MD1	*ykgA*	b0300	CDS	315674	316360	-
del-MD1	*ykgB*	b0301	CDS	316950	317543	-
del-MD1	*ykgI*	b0303	CDS	317555	317791	-
del-MD1	*ykgC*	b0304	CDS	317900	319225	-
del-MD1	*ykgD*	b0305	CDS	319451	320305	+
del-MD1	*ykgE*	b0306	CDS	320832	321551	+
del-MD1	*ykgF*	b0307	CDS	321562	322989	+
del-MD1	*ykgG*	b0308	CDS	322982	323677	+
del-MD1	*ykgH*	b0310	CDS	323920	324588	-
del-MD43	*yahA*	b0315	CDS	331595	332683	+
del-MD43	*yahB*	b0316	CDS	332725	333657	-
del-MD43	*yahC*	b0317	CDS	333749	334246	-
del-MD43	*yahD*	b0318	CDS	334504	335109	+
del-MD43	*yahE*	b0319	CDS	335149	336012	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD43	*yahF*	b0320	CDS	336002	337549	+
del-MD43	*yahG*	b0321	CDS	337549	338967	+
del-MD43	*yahH*	b0322	CDS	339017	339313	+
del-MD43	*yahI*	b0323	CDS	339389	340339	+
del-MD43	*yahJ*	b0324	CDS	340349	341731	+
del-MD43	*yahK*	b0325	CDS	342108	343157	+
del-MD43	*yahL*	b0326	CDS	343400	344215	+
del-MD43	*yahM*	b0327	CDS	344628	344873	+
del-MD43	*yahN*	b0328	CDS	344890	345561	-
del-MD43	*yahO*	b0329	CDS	345708	345983	+
del-MD43	*prpR*	b0330	CDS	346081	347667	-
del-MD43	*prpB*	b0331	CDS	347906	348796	+
del-MD43	*prpC*	b0333	CDS	349236	350405	+
del-MD43	*prpD*	b0334	CDS	350439	351890	+
del-MD43	*prpE*	b0335	CDS	351930	353816	+
del-MD43	*codB*	b0336	CDS	354146	355405	+
del-MD43	*codA*	b0337	CDS	355395	356678	+
del-MD43	*cynR*	b0338	CDS	357015	357914	-
del-MD43	*cynT*	b0339	CDS	358023	358682	+
del-MD43	*cynS*	b0340	CDS	358713	359183	+
del-MD43	*cynX*	b0341	CDS	359216	360370	+
del-MD43	*lacA*	b0342	CDS	360473	361084	-
del-MD43	*lacY*	b0343	CDS	361150	362403	-
del-MD43	*lacZ*	b0344	CDS	362455	365529	-
del-MD43	*lacI*	b0345	CDS	365652	366734	-
del-MD43	*mhpR*	b0346	CDS	366811	367758	-
del-MD43	*mhpA*	b0347	CDS	367835	369499	+
del-MD43	*mhpB*	b0348	CDS	369501	370445	+
del-MD43	*mhpC*	b0349	CDS	370448	371329	+
del-MD43	*mhpD*	b0350	CDS	371339	372148	+
del-MD43	*mhpF*	b0351	CDS	372145	373095	+
del-MD43	*mhpE*	b0352	CDS	373092	374105	+
del-MD43	*mhpT*	b0353	CDS	374683	375894	+
del-MD43	*yaiL*	b0354	CDS	375996	376535	+
del-MD16	*yaiO*	b0358	CDS	379293	380066	-
del-MD16	*yaiX*	b4579	pseudogene	380068	382096	-
del-MD16	*insC-1*	b0360	CDS	380530	380940	+
del-MD16	*insD-1*	b0361	CDS	380898	381803	+
del-MD16	*yaiP*	b0363	CDS	381963	383159	-
del-MD16	*yaiS*	b0364	CDS	383283	383840	-
del-MD16	*tauA*	b0365	CDS	384456	385418	+
del-MD16	*tauB*	b0366	CDS	385431	386198	+
del-MD16	*tauC*	b0367	CDS	386195	387022	+
del-MD16	*tauD*	b0368	CDS	387019	387870	+
del-MD17	*ykiB*	b0370	CDS	389121	389339	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD17	*yaiT*	b4580	pseudogene	389475	393642	
del-MD17	*insF-2*	b0372	CDS	390963	391829	-
del-MD17	*insE-2*	b0373	CDS	391826	392134	-
del-MD17	*yaiV*	b0375	CDS	393685	394353	+
del-MD17	*ampH*	b0376	CDS	394354	395511	-
del-MD17	*sbmA*	b0377	CDS	395863	397083	+
del-MD17	*yaiW*	b0378	CDS	397096	398190	+
del-MD17	*yaiY*	b0379	CDS	398249	398557	-
del-MD17	*yaiZ*	b0380	CDS	398817	399029	+
del-MD30	*rhsD*	b0497	CDS	522485	526765	+
del-MD30	*ybbC*	b0498	CDS	526805	527173	+
del-MD30	*ylbH*	b0499	CDS	527173	527883	+
del-MD30	*ybbD*	b0500	CDS	527864	528124	+
del-MD30	*ylbG*	b0502	CDS	528869	529240	-
del-MD12	*intD*	b0537	CDS	564038	565201	-
del-MD12	*ybcC*	b0539	CDS	565321	565584	-
del-MD12	*ybcD*	b4508	pseudogene	565674	565910	+
del-MD12	*insE-3*	b0540	CDS	566056	566364	+
del-MD12	*insF-3*	b0541	CDS	566361	567227	+
del-MD12	*renD*	b0542	CDS	567285	567470	+
del-MD12	*emrE*	b0543	CDS	567538	567870	+
del-MD12	*ybcK*	b0544	CDS	568125	569651	+
del-MD12	*ybcL*	b0545	CDS	570116	570667	+
del-MD12	*ybcM*	b0546	CDS	570677	571474	+
del-MD12	*ybcN*	b0547	CDS	571689	572144	+
del-MD12	*ninE*	b0548	CDS	572144	572314	+
del-MD12	*ybcO*	b0549	CDS	572307	572597	+
del-MD12	*rusA*	b0550	CDS	572594	572956	+
del-MD12	*ylcG*	b4509	CDS	572953	573093	+
del-MD12	*ybcQ*	b0551	CDS	573179	573562	+
del-MD12	*insH-2*	b0552	CDS	573960	574976	-
del-MD12	*nmpC*	b0553	pseudogene	574981	576108	-
del-MD12	*essD*	b0554	CDS	576621	576836	+
del-MD12	*ybcS*	b0555	CDS	576836	577333	+
del-MD12	*rzpD*	b0556	CDS	577330	577791	+
del-MD12	*rzoD*	b4510	CDS	577550	577732	+
del-MD12	*borD*	b0557	CDS	577823	578116	-
del-MD12	*ybcV*	b0558	CDS	578407	578817	-
del-MD12	*ybcW*	b0559	CDS	579103	579309	+
del-MD12	*nohB*	b0560	CDS	580057	580602	+
del-MD12	*tfaD*	b0561	pseudogene	580757	581320	+
del-MD12	*ybcY*	b0562	CDS	581375	581959	-
del-MD12	*ylcE*	b0563	CDS	582098	582283	+
del-MD12	*appY*	b0564	CDS	582904	583653	+
del-MD12	*ompT*	b0565	CDS	583903	584856	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD14	*ybdG*	b0577	CDS	602639	603886	-
del-MD14	*nfnB*	b0578	CDS	603994	604647	-
del-MD14	*ybdF*	b0579	CDS	604741	605109	-
del-MD14	*ybdJ*	b0580	CDS	605174	605422	-
del-MD14	*ybdK*	b0581	CDS	605488	606606	-
del-MD14	*hokE*	b4415	CDS	607059	607211	+
del-MD14	*insL-2*	b0582	CDS	607288	608400	+
del-MD20	*insH-3*	b0656	CDS	687220	688236	-
del-MD31	*rhsC*	b0700	CDS	728806	732999	+
del-MD31	*ybfB*	b0702	CDS	732999	733325	+
del-MD31	*ybfO*	b0703	CDS	733443	734876	+
del-MD31	*ybfC*	b0704	CDS	734873	735442	+
del-MD31	*ybfQ*	b4514	CDS	735668	735922	+
del-MD31	*ybfL*	b0705	pseudogene	736123	737184	+
del-MD31	*ybfD*	b0706	CDS	737315	738076	+
del-MD35	*yccC*	b0981	CDS	1041253	1043433	-
del-MD35	*etp*	b0982	CDS	1043453	1043899	-
del-MD35	*yccZ*	b0983	CDS	1043887	1045026	-
del-MD35	*ymcA*	b0984	CDS	1045072	1047168	-
del-MD35	*ymcB*	b0985	CDS	1047168	1047914	-
del-MD35	*ymcC*	b0986	CDS	1047911	1048555	-
del-MD35	*ymcD*	b0987	CDS	1048662	1048967	-
del-MD35	*insA-4*	b4516	CDS	1049056	1049331	+
del-MD35	*insB-4*	b0988	CDS	1049250	1049753	+
del-MD36	*ycdP*	b1021	CDS	1085329	1085742	-
del-MD36	*ycdQ*	b1022	CDS	1085744	1087069	-
del-MD36	*ycdR*	b1023	CDS	1087062	1089080	-
del-MD36	*ycdS*	b1024	CDS	1089089	1091512	-
del-MD36	*ycdT*	b1025	CDS	1092099	1093457	+
del-MD36	*insF-4*	b1026	CDS	1093498	1094364	-
del-MD36	*insE-4*	b1027	CDS	1094361	1094669	-
del-MD36	*ymdE*	b1028	pseudogene	1094767	1095069	+
del-MD36	*ycdU*	b1029	CDS	1095066	1096052	+
del-MD26	*flgN*	b1070	CDS	1128637	1129053	-
del-MD26	*flgM*	b1071	CDS	1129058	1129351	-
del-MD26	*flgA*	b1072	CDS	1129427	1130086	-
del-MD26	*flgB*	b1073	CDS	1130241	1130657	+
del-MD26	*flgC*	b1074	CDS	1130661	1131065	+
del-MD26	*flgD*	b1075	CDS	1131077	1131772	+
del-MD26	*flgE*	b1076	CDS	1131797	1133005	+
del-MD26	*flgF*	b1077	CDS	1133025	1133780	+
del-MD26	*flgG*	b1078	CDS	1133952	1134734	+
del-MD26	*flgH*	b1079	CDS	1134787	1135485	+
del-MD26	*flgI*	b1080	CDS	1135497	1136594	+
del-MD26	*flgJ*	b1081	CDS	1136594	1137535	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD26	*flgK*	b1082	CDS	1137601	1139244	+
del-MD26	*flgL*	b1083	CDS	1139256	1140209	+
del-MD11	*ymfD*	b1137	CDS	1196090	1196755	-
del-MD11	*ymfE*	b1138	CDS	1196756	1197460	-
del-MD11	*lit*	b1139	CDS	1197918	1198811	+
del-MD11	*intE*	b1140	CDS	1198902	1200029	-
del-MD11	*ymfG*	b1141	CDS	1200010	1200255	-
del-MD11	*ymfH*	b1142	CDS	1200292	1200603	-
del-MD11	*ymfI*	b1143	CDS	1200720	1201061	+
del-MD11	*ymfJ*	b1144	CDS	1200999	1201307	-
del-MD11	*ymfK*	b1145	CDS	1201482	1202156	-
del-MD11	*ymfT*	b1146	CDS	1202247	1202447	+
del-MD11	*ymfL*	b1147	CDS	1202479	1203048	+
del-MD11	*ymfM*	b1148	CDS	1203045	1203383	+
del-MD11	*ymfN*	b1149	CDS	1203393	1204760	+
del-MD11	*ymfR*	b1150	CDS	1204772	1204954	+
del-MD11	*ymfO*	b1151	CDS	1204954	1205427	+
del-MD11	*ymfP*	b1152	CDS	1205483	1206145	+
del-MD11	*ymfQ*	b1153	CDS	1206136	1206720	+
del-MD11	*ycfK*	b1154	CDS	1206724	1207353	+
del-MD11	*ymfS*	b1155	CDS	1207355	1207768	+
del-MD11	*tfaE*	b1156	CDS	1207740	1208342	-
del-MD11	*stfE*	b1157	pseudogene	1208342	1208878	-
del-MD11	*pin*	b1158	CDS	1208908	1209462	+
del-MD11	*mcrA*	b1159	CDS	1209569	1210402	+
del-MD11	*icdC*	b4519	pseudogene	1210648	1210800	+
del-MD11	*elbA*	b1160	CDS	1210903	1211226	-
del-MD11	*ycgX*	b1161	CDS	1211926	1212330	-
del-MD11	*ycgE*	b1162	CDS	1212551	1213282	-
del-MD11	*ycgF*	b1163	CDS	1213487	1214698	-
del-MD11	*ycgZ*	b1164	CDS	1215012	1215248	+
del-MD11	*ymgA*	b1165	CDS	1215291	1215563	+
del-MD11	*ymgB*	b1166	CDS	1215592	1215858	+
del-MD11	*ymgC*	b1167	CDS	1215971	1216219	+
del-MD11	*ycgG*	b1168	CDS	1216551	1218074	+
del-MD11	*ymgF*	b4520	CDS	1218206	1218424	+
del-MD11	*ycgH*	b4491	pseudogene	1218824	1221445	+
del-MD11	*ymgD*	b1171	CDS	1221528	1221857	-
del-MD11	*ymgG*	b1172	CDS	1221867	1222142	-
del-MD21	*ycjG*	b1325	CDS	1386954	1387919	+
del-MD21	*mpaA*	b1326	CDS	1387894	1388682	-
del-MD21	*ymjC*	b4525	CDS	1388704	1388886	-
del-MD21	*ycjY*	b1327	CDS	1388957	1389889	-
del-MD21	*ycjZ*	b1328	CDS	1390015	1390914	+
del-MD21	*mppA*	b1329	CDS	1391251	1392864	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD21	*ynaI*	b1330	CDS	1392915	1393946	-
del-MD21	*insH-4*	b1331	CDS	1394100	1395116	+
del-MD21	*ynaJ*	b1332	CDS	1395389	1395646	+
del-MD21	*uspE*	b1333	CDS	1395696	1396646	-
del-MD2	*abgT*	b1336	CDS	1398271	1399797	-
del-MD2	*abgB*	b1337	CDS	1399834	1401279	-
del-MD2	*abgA*	b1338	CDS	1401279	1402589	-
del-MD2	*abgR*	b1339	CDS	1402765	1403673	+
del-MD2	*isrA*	b4426	misc_RNA	1403676	1403833	-
del-MD2	*ydaL*	b1340	CDS	1404003	1404566	+
del-MD2	*ydaM*	b1341	CDS	1404587	1405819	-
del-MD2	*ydaN*	b1342	CDS	1406074	1407057	+
del-MD2	*dbpA*	b1343	CDS	1407535	1408908	+
del-MD2	*ydaO*	b1344	CDS	1409037	1409972	-
del-MD2	*intR*	b1345	CDS	1410024	1411259	-
del-MD2	*ydaQ*	b1346	CDS	1411261	1411476	-
del-MD2	*ydaC*	b1347	CDS	1411555	1411764	-
del-MD2	*lar*	b1348	CDS	1411757	1411951	-
del-MD2	*recT*	b1349	CDS	1412008	1412817	-
del-MD2	*recE*	b1350	CDS	1412810	1415410	-
del-MD2	*racC*	b1351	CDS	1415512	1415787	-
del-MD2	*ydaE*	b4526	CDS	1415862	1416032	-
del-MD2	*kil*	b1352	CDS	1416032	1416253	-
del-MD2	*sieB*	b1353	CDS	1416695	1417183	+
del-MD2	*ydaF*	b4527	CDS	1417180	1417335	-
del-MD2	*ydaG*	b1355	CDS	1417346	1417480	-
del-MD2	*racR*	b1356	CDS	1417789	1418265	-
del-MD2	*ydaS*	b1357	CDS	1418389	1418685	+
del-MD2	*ydaT*	b1358	CDS	1418708	1419130	+
del-MD2	*ydaU*	b1359	CDS	1419143	1420000	+
del-MD2	*ydaV*	b1360	CDS	1420007	1420753	+
del-MD2	*ydaW*	b1361	CDS	1420776	1421336	+
del-MD2	*rzpR*	b1362	CDS	1421369	1421668	+
del-MD2	*rzoR*	b4528	CDS	1421424	1421609	+
del-MD2	*trkG*	b1363	CDS	1421806	1423263	+
del-MD2	*ynaK*	b1365	CDS	1423401	1423664	+
del-MD2	*ydaY*	b1366	CDS	1423645	1424004	+
del-MD2	*ynaA*	b1368	CDS	1424478	1425506	+
del-MD2	*lomR*	b4570	pseudogene	1425419	1427008	+
del-MD2	*insH-5*	b1370	CDS	1425770	1426750	-
del-MD2	*stfR*	b1372	CDS	1427073	1430435	+
del-MD2	*tfaR*	b1373	CDS	1430435	1431010	+
del-MD2	*pinR*	b1374	CDS	1431108	1431698	-
del-MD2	*ynaE*	b1375	CDS	1432015	1432281	-
del-MD2	*uspF*	b1376	CDS	1433209	1433643	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD2	*ompN*	b1377	CDS	1433784	1434917	-
del-MD2	*micC*	b4427	misc_RNA	1435145	1435253	+
del-MD2	*ydbK*	b1378	CDS	1435284	1438808	-
del-MD2	*ydbJ*	b4529	CDS	1439082	1439348	+
del-MD2	*hslJ*	b1379	CDS	1439345	1439767	-
del-MD2	*ldhA*	b1380	CDS	1439878	1440867	-
del-MD2	*ydbH*	b1381	CDS	1441075	1443714	+
del-MD2	*ynbE*	b1382	CDS	1443711	1443896	+
del-MD2	*ydbL*	b1383	CDS	1443904	1444230	+
del-MD2	*feaR*	b1384	CDS	1444402	1445307	-
del-MD2	*feaB*	b1385	CDS	1445543	1447042	+
del-MD2	*tynA*	b1386	CDS	1447100	1449373	-
del-MD2	*maoC*	b1387	CDS	1449621	1451666	-
del-MD2	*paaA*	b1388	CDS	1451951	1452880	+
del-MD2	*paaB*	b1389	CDS	1452892	1453179	+
del-MD2	*paaC*	b1390	CDS	1453188	1453934	+
del-MD2	*paaD*	b1391	CDS	1453949	1454446	+
del-MD2	*paaE*	b1392	CDS	1454454	1455524	+
del-MD2	*paaF*	b1393	CDS	1455521	1456288	+
del-MD2	*paaG*	b1394	CDS	1456288	1457076	+
del-MD2	*paaH*	b1395	CDS	1457078	1458505	+
del-MD2	*paaI*	b1396	CDS	1458495	1458917	+
del-MD2	*paaJ*	b1397	CDS	1458917	1460122	+
del-MD2	*paaK*	b1398	CDS	1460149	1461462	+
del-MD2	*paaX*	b1399	CDS	1461563	1462513	+
del-MD2	*paaY*	b1400	CDS	1462495	1463085	+
del-MD2	*ydbA*	b4492	pseudogene	1463416	1472037	+
del-MD2	*insD-2*	b1402	CDS	1465945	1466850	-
del-MD2	*insC-2*	b1403	CDS	1466808	1467218	-
del-MD2	*insI-2*	b1404	CDS	1467382	1468533	+
del-MD2	*ydbC*	b1406	CDS	1472245	1473105	+
del-MD2	*ydbD*	b1407	CDS	1473168	1475474	+
del-MD2	*ynbA*	b1408	CDS	1475645	1476250	+
del-MD2	*ynbB*	b1409	CDS	1476250	1477146	+
del-MD2	*ynbC*	b1410	CDS	1477162	1478919	+
del-MD2	*ynbD*	b1411	CDS	1478933	1480225	+
del-MD32	*rhsE*	b1456	CDS	1525914	1527962	+
del-MD32	*ydcD*	b1457	CDS	1527946	1528428	+
del-MD32	*yncI*	b1458	CDS	1528610	1529356	+
del-MD32	*yncM*	b1459	CDS	1529400	1529600	+
del-MD32	*ydcC*	b1460	CDS	1529840	1530976	+
del-MD32	*ydcE*	b1461	CDS	1531076	1531309	+
del-MD32	*yddH*	b1462	CDS	1531306	1531875	-
del-MD8	*ydfG*	b1539	CDS	1625541	1626287	+
del-MD8	*ydfH*	b1540	CDS	1626376	1627062	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD8	*ydfZ*	b1541	CDS	1627239	1627442	+
del-MD8	*ydfI*	b1542	CDS	1627477	1628937	-
del-MD8	*ydfJ*	b1543	CDS	1629026	1630309	-
del-MD8	*ydfK*	b1544	CDS	1631063	1631329	+
del-MD8	*pinQ*	b1545	CDS	1631646	1632236	+
del-MD8	*tfaQ*	b1546	CDS	1632334	1632909	-
del-MD8	*stfQ*	b1547	CDS	1632909	1633871	-
del-MD8	*nohA*	b1548	CDS	1633822	1634391	-
del-MD8	*ynfO*	b4533	CDS	1634780	1635013	+
del-MD8	*ydfO*	b1549	CDS	1635071	1635481	+
del-MD8	*gnsB*	b1550	CDS	1635633	1635806	-
del-MD8	*ynfN*	b1551	CDS	1635978	1636133	-
del-MD8	*cspI*	b1552	CDS	1636479	1636691	-
del-MD8	*ydfP*	b1553	CDS	1637054	1637551	-
del-MD8	*ydfQ*	b1554	CDS	1637548	1638081	-
del-MD8	*ydfR*	b1555	CDS	1638078	1638389	-
del-MD8	*essQ*	b1556	CDS	1638394	1638609	-
del-MD8	*cspB*	b1557	CDS	1639363	1639578	-
del-MD8	*cspF*	b1558	CDS	1639879	1640091	+
del-MD8	*ydfT*	b1559	CDS	1640513	1641265	-
del-MD8	*ydfU*	b1560	CDS	1641279	1642328	-
del-MD8	*rem*	b1561	CDS	1642675	1642926	-
del-MD8	*hokD*	b1562	CDS	1643143	1643298	-
del-MD8	*relE*	b1563	CDS	1643370	1643657	-
del-MD8	*relB*	b1564	CDS	1643657	1643896	-
del-MD8	*ydfV*	b1565	CDS	1643921	1644226	+
del-MD8	*flxA*	b1566	CDS	1644429	1644761	+
del-MD8	*ydfW*	b1567	CDS	1645198	1645347	-
del-MD8	*ydfX*	b1568	CDS	1645370	1645660	-
del-MD8	*dicC*	b1569	CDS	1645644	1645874	-
del-MD8	*dicA*	b1570	CDS	1645958	1646365	+
del-MD8	*ydfA*	b1571	CDS	1646532	1646687	+
del-MD8	*ydfB*	b1572	CDS	1646689	1646817	+
del-MD8	*ydfC*	b1573	CDS	1646847	1647065	+
del-MD8	*dicF*	b1574	misc_RNA	1647406	1647458	+
del-MD8	*dicB*	b1575	CDS	1647633	1647821	+
del-MD8	*ydfD*	b1576	CDS	1647818	1648009	+
del-MD8	*ydfE*	b1577	CDS	1648102	1649022	+
del-MD8	*insD-7*	b1578	CDS	1648905	1649561	+
del-MD8	*intQ*	b1579	CDS	1649536	1650732	+
del-MD8	*ynfP*	b4534	pseudogene	1650752	1650862	-
del-MD40	*yeaJ*	b1786	CDS	1870065	1871555	+
del-MD27	*flhE*	b1878	CDS	1960604	1960996	-
del-MD27	*flhA*	b1879	CDS	1960996	1963074	-
del-MD27	*flhB*	b1880	CDS	1963067	1964215	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD27	*cheZ*	b1881	CDS	1964417	1965061	-
del-MD27	*cheY*	b1882	CDS	1965072	1965461	-
del-MD27	*cheB*	b1883	CDS	1965476	1966525	-
del-MD27	*cheR*	b1884	CDS	1966528	1967388	-
del-MD27	*tap*	b1885	CDS	1967407	1969008	-
del-MD27	*tar*	b1886	CDS	1969054	1970715	-
del-MD27	*cheW*	b1887	CDS	1970860	1971363	-
del-MD27	*cheA*	b1888	CDS	1971384	1973348	-
del-MD27	*motB*	b1889	CDS	1973353	1974279	-
del-MD27	*motA*	b1890	CDS	1974276	1975163	-
del-MD27	*flhC*	b1891	CDS	1975290	1975868	-
del-MD27	*flhD*	b1892	CDS	1975871	1976230	-
del-MD27	*insB-5*	b1893	CDS	1976542	1977045	-
del-MD27	*insA-5*	b1894	CDS	1976964	1977239	-
del-MD28	*yecC*	b1917	CDS	1995086	1995838	-
del-MD28	*yecS*	b1918	CDS	1995835	1996503	-
del-MD28	*yedO*	b1919	CDS	1996518	1997504	-
del-MD28	*fliY*	b1920	CDS	1997609	1998409	-
del-MD28	*fliZ*	b1921	CDS	1998497	1999048	-
del-MD28	*fliA*	b1922	CDS	1999094	1999813	-
del-MD28	*fliC*	b1923	CDS	2000134	2001630	-
del-MD28	*fliD*	b1924	CDS	2001896	2003302	+
del-MD28	*fliS*	b1925	CDS	2003327	2003737	+
del-MD28	*fliT*	b1926	CDS	2003737	2004102	+
del-MD28	*amyA*	b1927	CDS	2004180	2005667	+
del-MD28	*yedD*	b1928	CDS	2005701	2006114	-
del-MD28	*yedE*	b1929	CDS	2006301	2007506	+
del-MD28	*yedF*	b1930	CDS	2007503	2007736	+
del-MD28	*yedK*	b1931	CDS	2007845	2008513	+
del-MD28	*yedL*	b1932	CDS	2008624	2009103	+
del-MD28	*yedN*	b4495	pseudogene	2009372	2009893	-
del-MD28	*yedM*	b1935	CDS	2010025	2010375	-
del-MD28	*intG*	b1936	pseudogene	2010526	2010804	+
del-MD28	*fliE*	b1937	CDS	2010724	2011038	-
del-MD28	*fliF*	b1938	CDS	2011253	2012911	+
del-MD28	*fliG*	b1939	CDS	2012904	2013899	+
del-MD28	*fliH*	b1940	CDS	2013892	2014578	+
del-MD28	*fliI*	b1941	CDS	2014578	2015951	+
del-MD28	*fliJ*	b1942	CDS	2015970	2016413	+
del-MD28	*fliK*	b1943	CDS	2016410	2017537	+
del-MD28	*fliL*	b1944	CDS	2017642	2018106	+
del-MD28	*fliM*	b1945	CDS	2018111	2019115	+
del-MD28	*fliN*	b1946	CDS	2019112	2019525	+
del-MD28	*fliO*	b1947	CDS	2019528	2019893	+
del-MD28	*fliP*	b1948	CDS	2019893	2020630	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD28	*fliQ*	b1949	CDS	2020640	2020909	+
del-MD28	*fliR*	b1950	CDS	2020917	2021702	+
del-MD5	*insH-6*	b1994	CDS	2064329	2065345	-
del-MD5	*yoeA*	b4582	pseudogene	2066659	2068498	+
del-MD5	*insD-3*	b1996	CDS	2066976	2067881	-
del-MD5	*insC-3*	b1997	CDS	2067839	2068249	-
del-MD5	*yeeP*	b1999	pseudogene	2068810	2069235	+
del-MD5	*isrC*	b4435	misc_RNA	2069339	2069542	+
del-MD5	*flu*	b2000	CDS	2069563	2072682	+
del-MD5	*yeeR*	b2001	CDS	2072803	2074335	+
del-MD5	*yeeS*	b2002	CDS	2074332	2074778	+
del-MD5	*yeeT*	b2003	CDS	2074841	2075062	+
del-MD5	*yeeU*	b2004	CDS	2075136	2075504	+
del-MD5	*yeeV*	b2005	CDS	2075593	2075967	+
del-MD5	*yeeW*	b2006	CDS	2075964	2076158	+
del-MD5	*yoeF*	b4538	CDS	2076599	2076955	+
del-MD5	*yeeX*	b2007	CDS	2077056	2077451	-
del-MD5	*yeeA*	b2008	CDS	2077557	2078615	-
del-MD22	*wbbL*	b4571	pseudogene	2099420	2101413	-
del-MD22	*insH-7*	b2030	CDS	2099919	2100935	-
del-MD22	*wbbK*	b2032	CDS	2101415	2102533	-
del-MD22	*wbbJ*	b2033	CDS	2102518	2103108	-
del-MD22	*wbbI*	b2034	CDS	2103089	2104081	-
del-MD22	*wbbH*	b2035	CDS	2104084	2105250	-
del-MD22	*glf*	b2036	CDS	2105250	2106353	-
del-MD22	*rfbX*	b2037	CDS	2106361	2107608	-
del-MD22	*rfbC*	b2038	CDS	2107605	2108162	-
del-MD22	*rfbA*	b2039	CDS	2108162	2109043	-
del-MD22	*rfbD*	b2040	CDS	2109101	2110000	-
del-MD22	*rfbB*	b2041	CDS	2110000	2111085	-
del-MD22	*galF*	b2042	CDS	2111458	2112351	-
del-MD22	*wcaM*	b2043	CDS	2112526	2113920	-
del-MD22	*wcaL*	b2044	CDS	2113931	2115151	-
del-MD22	*wcaK*	b2045	CDS	2115148	2116428	-
del-MD22	*wzxC*	b2046	CDS	2116704	2118182	-
del-MD22	*wcaJ*	b2047	CDS	2118184	2119578	-
del-MD22	*cpsG*	b2048	CDS	2119633	2121003	-
del-MD22	*cpsB*	b2049	CDS	2121108	2122544	-
del-MD22	*wcaI*	b2050	CDS	2122547	2123770	-
del-MD22	*nudD*	b2051	CDS	2123767	2124246	-
del-MD22	*fcl*	b2052	CDS	2124249	2125214	-
del-MD22	*gmd*	b2053	CDS	2125217	2126338	-
del-MD22	*wcaF*	b2054	CDS	2126364	2126912	-
del-MD22	*wcaE*	b2055	CDS	2126928	2127674	-
del-MD22	*wcaD*	b2056	CDS	2127685	2128902	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD22	*wcaC*	b2057	CDS	2128877	2130094	-
del-MD22	*wcaB*	b2058	CDS	2130091	2130579	-
del-MD22	*wcaA*	b2059	CDS	2130582	2131421	-
del-MD22	*wzc*	b2060	CDS	2131514	2133676	-
del-MD22	*wzb*	b2061	CDS	2133679	2134122	-
del-MD22	*wza*	b2062	CDS	2134128	2135267	-
del-MD37	*yegP*	b2080	CDS	2163213	2163545	+
del-MD37	*yegQ*	b2081	CDS	2163692	2165053	+
del-MD37	*ryeE*	b4438	misc_RNA	2165136	2165221	+
del-MD37	*ogrK*	b2082	CDS	2165326	2165544	-
del-MD37	*yegZ*	b2083	pseudogene	2165626	2165844	-
del-MD37	*yegR*	b2085	CDS	2166013	2166330	-
del-MD37	*yegS*	b2086	CDS	2166736	2167635	+
del-MD37	*gatR*	b4498	pseudogene	2167717	2169757	-
del-MD37	*insE-5*	b2088	CDS	2168251	2168559	+
del-MD37	*insF-5*	b2089	CDS	2168556	2169422	+
del-MD37	*gatD*	b2091	CDS	2169857	2170897	-
del-MD37	*gatC*	b2092	CDS	2170945	2172300	-
del-MD37	*gatB*	b2093	CDS	2172304	2172588	-
del-MD37	*gatA*	b2094	CDS	2172619	2173071	-
del-MD37	*gatZ*	b2095	CDS	2173081	2174343	-
del-MD37	*gatY*	b2096	CDS	2174372	2175226	-
del-MD23	*yejO*	b2190	CDS	2284412	2286922	-
del-MD23	*insH-8*	b2192	CDS	2287087	2288103	-
del-MD7	*intS*	b2349	CDS	2464567	2465724	+
del-MD7	*yfdG*	b2350	CDS	2465877	2466239	+
del-MD7	*yfdH*	b2351	CDS	2466236	2467156	+
del-MD7	*yfdI*	b2352	CDS	2467153	2468484	+
del-MD7	*tfaS*	b2353	pseudogene	2468825	2469127	+
del-MD7	*yfdK*	b2354	CDS	2469099	2469539	-
del-MD7	*yfdL*	b2355	CDS	2469566	2470084	-
del-MD7	*yfdM*	b2356	CDS	2470134	2470409	-
del-MD7	*yfdN*	b2357	CDS	2470409	2470903	-
del-MD7	*yfdO*	b2358	CDS	2470900	2471268	-
del-MD7	*yfdP*	b2359	CDS	2471542	2471988	+
del-MD7	*yfdQ*	b2360	CDS	2472054	2472878	+
del-MD7	*yfdR*	b2361	CDS	2473006	2473542	+
del-MD7	*yfdS*	b2362	CDS	2473533	2473895	+
del-MD7	*yfdT*	b2363	CDS	2473895	2474200	+
del-MD7	*ypdJ*	b4545	CDS	2474116	2474256	+
del-MD15	*yfeO*	b2389	CDS	2507652	2508908	+
del-MD15	*ypeC*	b2390	CDS	2509023	2509349	+
del-MD15	*mntH*	b2392	CDS	2509490	2510728	-
del-MD15	*nupC*	b2393	CDS	2511064	2512266	+
del-MD15	*insL-3*	b2394	CDS	2512353	2513465	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD15	*yfeA*	b2395	CDS	2513665	2515854	-
del-MD3	*intZ*	b2442	CDS	2556793	2558088	+
del-MD3	*yffL*	b2443	CDS	2558279	2558920	+
del-MD3	*yffM*	b2444	CDS	2559390	2559635	+
del-MD3	*yffN*	b2445	CDS	2559632	2560015	+
del-MD3	*yffO*	b2446	CDS	2560133	2560549	+
del-MD3	*yffP*	b2447	CDS	2560546	2561139	+
del-MD3	*yffQ*	b2448	CDS	2561599	2561991	+
del-MD3	*yffR*	b2449	CDS	2562002	2562394	+
del-MD3	*yffS*	b2450	CDS	2562515	2563354	+
del-MD4	*intA*	b2622	CDS	2754181	2755422	+
del-MD4	*yfjH*	b2623	CDS	2755666	2756622	-
del-MD4	*alpA*	b2624	CDS	2756666	2756878	+
del-MD4	*yfjI*	b2625	CDS	2757007	2758416	+
del-MD4	*yfjJ*	b2626	CDS	2758569	2759195	+
del-MD4	*yfjK*	b2627	CDS	2759373	2761562	-
del-MD4	*yfjL*	b2628	CDS	2761559	2763175	-
del-MD4	*yfjM*	b2629	CDS	2763535	2763798	-
del-MD4	*yfjN*	b2630	CDS	2763940	2765013	+
del-MD4	*yfjO*	b2631	CDS	2765006	2765377	+
del-MD4	*yfjP*	b2632	CDS	2765732	2766595	+
del-MD4	*yfjQ*	b2633	CDS	2766687	2767508	+
del-MD4	*yfjR*	b2634	CDS	2767725	2768426	+
del-MD4	*ypjK*	b2635	CDS	2768467	2768703	+
del-MD4	*yfjS*	b2636	CDS	2768703	2769146	+
del-MD4	*yfjT*	b2637	CDS	2769170	2769637	+
del-MD4	*yfjU*	b2638	CDS	2769862	2770176	-
del-MD4	*ypjL*	b2639	CDS	2770189	2770707	-
del-MD4	*yfjV*	b2640	CDS	2770858	2771058	-
del-MD4	*ypjM*	b2641	pseudogene	2770998	2771180	-
del-MD4	*yfjW*	b2642	CDS	2771340	2773043	+
del-MD4	*yfjX*	b2643	CDS	2773941	2774399	+
del-MD4	*yfjY*	b2644	CDS	2774408	2774890	+
del-MD4	*ypjJ*	b4548	CDS	2774899	2775099	+
del-MD4	*yfjZ*	b2645	CDS	2775137	2775454	+
del-MD4	*ypjF*	b2646	CDS	2775475	2775804	+
del-MD4	*ypjA*	b2647	CDS	2776168	2780748	-
del-MD4	*pinH*	b2648	pseudogene	2781087	2781230	-
del-MD4	*ypjB*	b2649	CDS	2781660	2782451	-
del-MD4	*ypjC*	b2650	CDS	2782551	2783033	-
del-MD4	*ileY*	b2652	tRNA	2783784	2783859	-
del-MD4	*ygaQ*	b2654	CDS	2784419	2784751	+
del-MD4	*ygaR*	b4462	CDS	2784770	2785456	+
del-MD4	*yqaC*	b2657	pseudogene	2785664	2786260	+
del-MD4	*yqaD*	b2658	CDS	2786399	2786671	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD4	*ygaT*	b2659	CDS	2787007	2787984	+
del-MD4	*ygaF*	b2660	CDS	2788004	2789272	+
del-MD18	*ygeL*	b2856	CDS	2992959	2993114	-
del-MD18	*ygeM*	b2857	CDS	2993336	2993767	-
del-MD18	*ygeN*	b2858	pseudogene	2993770	2994042	-
del-MD18	*ygeO*	b2859	CDS	2993984	2994409	-
del-MD18	*insD-4*	b2860	CDS	2994394	2995299	-
del-MD18	*insC-4*	b2861	CDS	2995257	2995667	-
del-MD18	*ygeP*	b2862	CDS	2995711	2996010	-
del-MD18	*ygeQ*	b2863	CDS	2996056	2996850	-
del-MD42	*endA*	b2945	CDS	3088369	3089076	+
del-MD10	*yghD*	b2968	CDS	3108612	3109148	-
del-MD10	*yghE*	b2969	pseudogene	3109150	3110010	-
del-MD10	*yghF*	b2970	CDS	3110076	3110942	-
del-MD10	*yghG*	b2971	CDS	3111089	3111499	-
del-MD10	*pppA*	b2972	CDS	3111565	3112374	-
del-MD10	*yghJ*	b4466	CDS	3112572	3117134	-
del-MD10	*glcA*	b2975	CDS	3117619	3119301	-
del-MD10	*glcB*	b2976	CDS	3119656	3121827	-
del-MD10	*glcG*	b2977	CDS	3121849	3122253	-
del-MD10	*glcF*	b4467	CDS	3122258	3123481	-
del-MD10	*glcE*	b4468	CDS	3123492	3124544	-
del-MD10	*glcD*	b2979	CDS	3124544	3126043	-
del-MD10	*glcC*	b2980	CDS	3126294	3127058	+
del-MD10	*yghO*	b2981	CDS	3127065	3128237	-
del-MD10	*insH-9*	b2982	CDS	3128200	3129216	+
del-MD10	*yghQ*	b2983	CDS	3129363	3130430	-
del-MD10	*yghR*	b2984	CDS	3130476	3131234	-
del-MD10	*yghS*	b2985	CDS	3131266	3131979	-
del-MD10	*yghT*	b2986	CDS	3132153	3132845	+
del-MD10	*pitB*	b2987	CDS	3132894	3134393	-
del-MD19	*yqiC*	b3042	CDS	3182862	3183152	+
del-MD19	*ygiL*	b3043	CDS	3183436	3183987	+
del-MD19	*insC-5*	b3044	CDS	3184164	3184574	+
del-MD19	*insD-5*	b3045	CDS	3184532	3185437	+
del-MD19	*yqiG*	b3046	CDS	3185422	3187887	+
del-MD19	*yqiH*	b3047	CDS	3187903	3188652	+
del-MD19	*yqiI*	b3048	CDS	3188654	3189718	+
del-MD24	*yhcA*	b3215	CDS	3360134	3360808	+
del-MD24	*yhcD*	b3216	CDS	3360829	3363210	+
del-MD24	*yhcE*	b4569	pseudogene	3363207	3364951	+
del-MD24	*insH-10*	b3218	CDS	3363724	3364740	-
del-MD24	*yhcF*	b3219	CDS	3364948	3365664	+
del-MD6	*gspA*	b3323	CDS	3451951	3453420	-
del-MD6	*gspC*	b3324	CDS	3453600	3454415	+

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD6	*gspD*	b3325	CDS	3454399	3456351	+
del-MD6	*gspE*	b3326	CDS	3456361	3457842	+
del-MD6	*gspF*	b3327	CDS	3457839	3459035	+
del-MD6	*gspG*	b3328	CDS	3459045	3459482	+
del-MD6	*gspH*	b3329	CDS	3459490	3459999	+
del-MD6	*gspI*	b3330	CDS	3459996	3460373	+
del-MD6	*gspJ*	b3331	CDS	3460366	3460953	+
del-MD6	*gspK*	b3332	CDS	3460946	3461929	+
del-MD6	*gspL*	b3333	CDS	3461944	3463107	+
del-MD6	*gspM*	b3334	CDS	3463104	3463565	+
del-MD6	*gspO*	b3335	CDS	3463565	3464242	+
del-MD6	*bfr*	b3336	CDS	3464271	3464747	-
del-MD6	*bfd*	b3337	CDS	3464819	3465013	-
del-MD6	*chiA*	b3338	CDS	3465182	3467875	-
del-MD38	*yhhY*	b3441	CDS	3579161	3579649	+
del-MD38	*yhhZ*	b3442	CDS	3579886	3581064	+
del-MD38	*yrhA*	b3443	CDS	3581064	3581477	+
del-MD38	*insA-6*	b3444	CDS	3581506	3581781	+
del-MD38	*insB-6*	b3445	CDS	3581700	3582203	+
del-MD38	*yrhB*	b3446	CDS	3582782	3583066	+
del-MD33	*rhsB*	b3482	CDS	3617215	3621450	+
del-MD33	*yhhH*	b3483	CDS	3621422	3621805	+
del-MD33	*yrhC*	b4552	pseudogene	3621910	3622155	+
del-MD33	*yhhI*	b3484	CDS	3622401	3623537	+
del-MD25	*yhiS*	b3504	CDS	3649314	3650096	+
del-MD25	*insH-11*	b3505	CDS	3650205	3651221	-
del-MD39	*insJ*	b3557	CDS	3718703	3719224	+
del-MD39	*insK*	b3558	CDS	3719221	3720072	+
del-MD34	*rhsA*	b3593	CDS	3760206	3764339	+
del-MD34	*yibA*	b3594	CDS	3764360	3765202	+
del-MD34	*yibJ*	b3595	CDS	3765244	3765945	+
del-MD34	*yibG*	b3596	CDS	3766200	3766661	+
del-MD9	*intB*	b4271	CDS	4494773	4495963	+
del-MD9	*insC-6*	b4272	CDS	4496250	4496660	+
del-MD9	*insD-6*	b4273	CDS	4496618	4497523	+
del-MD9	*yjgW*	b4274	CDS	4497622	4497957	+
del-MD9	*yjgX*	b4575	pseudogene	4497700	4498814	-
del-MD9	*yjgZ*	b4277	CDS	4499283	4499612	+
del-MD9	*insG*	b4278	CDS	4500126	4501454	-
del-MD9	*yjhB*	b4279	CDS	4502081	4503298	+
del-MD9	*yjhC*	b4280	CDS	4503310	4504428	+
del-MD9	*yjhD*	b4281	pseudogene	4504649	4504879	-
del-MD9	*yjhE*	b4282	pseudogene	4504884	4505132	+
del-MD9	*insN-2*	b4283	CDS	4505220	4505486	+
del-MD9	*insI-3*	b4284	CDS	4505489	4506640	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD9	*insM*	b4561	pseudogene	4506597	4506965	-
del-MD9	*insO-2*	b4285	pseudogene	4506981	4507577	+
del-MD9	*yjhW*	b4562	pseudogene	4507574	4507816	+
del-MD9	*yjhV*	b4286	CDS	4507743	4508156	+
del-MD9	*fecE*	b4287	CDS	4508713	4509480	-
del-MD9	*fecD*	b4288	CDS	4509481	4510437	-
del-MD9	*fecC*	b4289	CDS	4510434	4511432	-
del-MD9	*fecB*	b4290	CDS	4511429	4512331	-
del-MD9	*fecA*	b4291	CDS	4512376	4514700	-
del-MD9	*fecR*	b4292	CDS	4514787	4515740	-
del-MD9	*fecI*	b4293	CDS	4515737	4516258	-
del-MD9	*insA-7*	b4294	CDS	4516550	4516825	+
del-MD9	*insB-7*	b4576	pseudogene	4516744	4517247	+
del-MD9	*yjhU*	b4295	CDS	4517361	4518347	-
del-MD9	*yjhF*	b4296	CDS	4518694	4520043	-
del-MD9	*yjhG*	b4297	CDS	4520150	4522117	-
del-MD9	*yjhH*	b4298	CDS	4522128	4523033	-
del-MD9	*yjhI*	b4299	CDS	4523038	4523826	-
del-MD9	*sgcR*	b4300	CDS	4524129	4524911	-
del-MD9	*sgcE*	b4301	CDS	4524928	4525560	-
del-MD9	*sgcA*	b4302	CDS	4525572	4526003	-
del-MD9	*sgcQ*	b4303	CDS	4526134	4526940	-
del-MD9	*sgcC*	b4304	CDS	4526953	4528266	-
del-MD9	*sgcB*	b4565	CDS	4528278	4528556	-
del-MD9	*sgcX*	b4305	CDS	4528553	4529674	-
del-MD9	*yjhP*	b4306	CDS	4530460	4531206	-
del-MD9	*yjhQ*	b4307	CDS	4531262	4531807	-
del-MD9	*yjhX*	b4566	CDS	4531819	4532076	-
del-MD9	*yjhR*	b4308	CDS	4533038	4534054	+
del-MD9	*yjhS*	b4309	CDS	4534637	4535617	-
del-MD9	*yjhT*	b4310	CDS	4535682	4536788	-
del-MD9	*yjhA*	b4311	CDS	4536808	4537524	-
del-MD9	*fimB*	b4312	CDS	4538980	4539582	+
del-MD9	*fimE*	b4313	CDS	4540060	4540656	+
del-MD9	*fimA*	b4314	CDS	4541138	4541686	+
del-MD9	*fimI*	b4315	CDS	4541751	4542290	+
del-MD9	*fimC*	b4316	CDS	4542327	4543052	+
del-MD9	*fimD*	b4317	CDS	4543119	4545755	+
del-MD9	*fimF*	b4318	CDS	4545765	4546295	+
del-MD9	*fimG*	b4319	CDS	4546308	4546811	+
del-MD9	*fimH*	b4320	CDS	4546831	4547733	+
del-MD29	*yjiC*	b4325	CDS	4553513	4554343	-
del-MD29	*yjiD*	b4326	CDS	4555016	4555408	+
del-MD29	*yjiE*	b4327	CDS	4555401	4556312	-
del-MD29	*iadA*	b4328	CDS	4556377	4557549	-

Deletion	Gene	Locus_Tag	Gene_Type	Left End	Right End	Strand
del-MD29	*yjiG*	b4329	CDS	4557562	4558023	-
del-MD29	*yjiH*	b4330	CDS	4558020	4558703	-
del-MD29	*kptA*	b4331	CDS	4558953	4559507	+
del-MD29	*yjiJ*	b4332	CDS	4559520	4560698	-
del-MD29	*yjiK*	b4333	CDS	4560766	4561734	-
del-MD29	*yjiL*	b4334	CDS	4561945	4562712	-
del-MD29	*yjiM*	b4335	CDS	4562722	4563873	-
del-MD29	*yjiN*	b4336	CDS	4563989	4565269	-
del-MD29	*yjiO*	b4337	CDS	4565310	4566542	-
del-MD29	*yjiP*	b4338	pseudogene	4567021	4567332	+
del-MD29	*yjiQ*	b4339	CDS	4567381	4567941	+
del-MD29	*yjiR*	b4340	CDS	4568185	4569597	-
del-MD29	*yjiS*	b4341	CDS	4569774	4569938	+
del-MD29	*yjiT*	b4342	CDS	4570437	4571954	+
del-MD29	*yjiV*	b4486	pseudogene	4572158	4574878	+
del-MD29	*mcrC*	b4345	CDS	4574935	4575981	-
del-MD29	*mcrB*	b4346	CDS	4575981	4577360	-
del-MD29	*yjiW*	b4347	CDS	4577522	4577920	-
del-MD29	*hsdS*	b4348	CDS	4578091	4579485	-
del-MD29	*hsdM*	b4349	CDS	4579482	4581071	-
del-MD29	*hsdR*	b4350	CDS	4581272	4584838	-
del-MD29	*mrr*	b4351	CDS	4584972	4585886	+
del-MD29	*yjiA*	b4352	CDS	4585932	4586888	-
del-MD29	*yjiX*	b4353	CDS	4586899	4587102	-
del-MD29	*yjiY*	b4354	CDS	4587152	4589302	-
del-MD29	*tsr*	b4355	CDS	4589680	4591335	+
del-MD29	*yjiZ*	b4356	CDS	4591384	4592745	-
del-MD29	*yjjM*	b4357	CDS	4592960	4593874	-
del-MD29	*yjjN*	b4358	CDS	4594013	4595035	+

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