E. coli genotypes

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Nomenclature & Abbreviations

A listed gene name means that gene carries a loss of function mutation, a Δ preceding a gene name means the gene is deleted. If a gene is not listed, it is not known to be mutated. Prophages present in wt K-12 strains (F, λ, e14, rac) are listed only if absent. E. coli B strains are naturally lon- and dcm-.

- **F-** = Does not carry the F plasmid
- **F+** = Carries the F plasmid. The cell is able to mate with F- through conjugation.
- **F'[ ]** = Carries an F plasmid that has host chromosomal genes on it from a previous recombination event. This cell can also mate with F- through conjugation. Chromosomal genes carried in the F plasmid are listed in brackets.
- $\mathbf{r}_{\mathbf{B/K}}^{+/-}$ = The (B/K) defines the strain lineage. The +/- indicates whether the strain has or hasn't got the restriction system.
- $\mathbf{m}_{\mathbf{B/K}}^{+/-}$ = The (B/K) defines the strain lineage. The +/- indicates whether the strain has or hasn't got the modification (methylation) system.
- **hsdS** = Both restriction and methylation of certain sequences is deleted from the strain. If you transform DNA from such a strain into a wild type strain, it will be degraded.
- **hsdR** = For efficient transformation of cloned unmethylated DNA from PCR amplifications
- **INV( )** = chromosomal inversion between locations indicated
- **ahpC** = mutation to alkyl hydroperoxide reductase conferring disulfide reductase activity
- **ara-14** = cannot metabolize arabinose
- **araD** = mutation in L-ribulose-phosphate 4-epimerase blocks arabinose metabolism
- **cycA** = mutation in alanine transporter; cannot use alanine as a carbon source
- **dapD** = mutation in succinyl diaminopimelate aminotransferase leads to succinate or (lysine + methionine) requirement
- Δ( )≠ chromosomal deletion of genes between the listed genes (may include unlisted genes!)
- **dam** = adenine methylation at GATC sequences exist; high recombination efficiency; DNA repair turned on

- **dcm** = cytosine methylation at second C of CCWGG sites exist. dam & dcm are the default properties and always elided, while dam- or dcm- should be declare explicitly
- **DE3** = Lysogen that encodes T7 RNA polymerase. Used to induce expression in T7-driven expression systems
- **deoR** = regulatory gene that allows constitutive expression of deoxyribose synthesis genes; permits uptake of large plasmids. See Hanahan D, US Patent 4,851,348. ***This has been called into question, as the DH10B genome sequence revealed that it is deoR+. See Durfee08, PMID 18245285.
- **dnaJ** = one of the chaparonins inactivated; stabilizes some mutant proteins
- **dut1** = dUTPase activity abolished, leading to increased dUTP concentrations, allowing uracil instead of thymine incorporation in DNA. Stable U incorporation requires ung gene mutation as well.
- **endA1** = For cleaner preparations of DNA and better results in downstream applications due to the elimination of non-specific digestion by Endonuclease I
- **(e14)** = excisable prophage like element containing mcrA gene; present in K-12 but missing in many other strains
- **galE** = mutations are associated with high competence, increased resistance to phage P1 infection, and 2-deoxygalactose resistance. galE mutations block the production of UDP-galactose, resulting in truncation of LPS glycans to the minimal, "inner core". The exceptional competence of DH10B/TOP10 is thought to be a result of a reduced interference from LPS in the binding and/or uptake of transforming DNA. galE15 is a point mutation resulting in a Ser123 -> Phe conversion near the enzyme's active site. See van Die, et al. PMID 6373734, Hanahan, et al. PMID 1943786, and EcoSal ISBN 1555811647. --Dcekiert 16:56, ~~23 January 20~~08 (CST)
- **galk** ~~= mutants cannot~~ metabolize ~~galactose and are~~ resistant to 2-deoxygalactose. galK16 is an IS2 insertion ~170bp downstream of the galK start codon. See EcoSal ISBN 1555811647. --Dcekiert 16:56, 23 January 2008 (CST)
- **galU** = mutants cannot metabolize galactose
- **gor** = mutation in glutathione reductase; enhances disulphide bond formation
- **glnV** = suppression of amber (UAG) stop codons by insertion of glutamine; required for some phage growth
- **gyrA96** = mutation in DNA gyrase; conveys nalidixic acid resistance
- **gyrA462** = mutation in DNA gyrase; conveys resistance to ccdB colicin gene product
- **hflA150** = protease mutation stabilizing phage cII protein; high frequency of lysogenization by λ

- **Δ(lac)X74** = Deletion of the entire *lac* operon as well as some flanking DNA (complete deletion is Δcod-mhpF; see Mol.Micro., 6:1335, and J.Bact., 179:2573)
- **lacI^{q}** or **lacI^{Q}** = overproduction of the lac repressor protein; -35 site in promoter upstream of *lacI* is mutated from GCGCAA to GTGCAA
- **lacI^{Q1}** = overproduction of the lac repressor protein; contains a 15 bp deletion to create optimal -35 site in promoter upstream of *lacI*
- **lacY** = deficient in lactose transport; deletion of lactose permease (M protein)
- **lacZΔM15** = partial deletion of the lacZ gene that allows α complementation of the β-galactosidase gene; required for blue/white selection on XGal plates. Deletes the amino portion of lacZ (aa 11-41).
- **LAM-** or **λ-** = lambda lysogen deletion; approximate map location: 17.40; information from CGSC *__---Karmella__ **13:02, 21 October 2012 (EDT)**:
- **LamR** = mutation in malT1 conferring lambda resistance; synonym malT1(LamR) [1] *__---Karmella__ **13:35, 21 October 2012 (EDT)**:
- **leuB** = requires leucine
- **Δlon** = deletion of the lon protease
- **malA** = cannot metabolize maltose
- **mcrA** = Mutation eliminating restriction of DNA methylated at the sequence C$_{m}$CGG (possibly $_{m}$CG). Carried on the e14 prophage (q.v.)
- **mcrB** = Mutation eliminating restriction of DNA methylated at the sequence R$_{m}$C
- **metB** = requires methionine
- **metC** = requires methionine
- **mrr** = Mutation eliminating restriction of DNA methylated at the sequence C$_{m}$AG or G$_{m}$AC
- **mtlA** = cannot metabilize mannitol
- **(Mu)** = Mu prophage present. Muδ means the phage is defective.
- **mutS** - mutation inhibits DNA repair of mismatches in unmethylated newly synthesized strands
- **nupG** = same as deoR
- **ompT** = mutation in outer membrane protein protease VII, reducing proteolysis of expressed proteins
- **(P1)** = Cell carries a P1 prophage. Cells express the P1 restriction system.
- **(P2)** = Cell carries a P2 prophage. Allows selection against Red+ Gam+ λ
- **(φ80)** = Cell carries the lambdoid prophage φ80. A defective version of this phage carrying lacZM15 deletion (as well as wild-type lacI, lacYA, and flanking sequences) is present in some strains. The φ80 attachment site is just adjacent to tonB.
- **pLysS** = contains pLysS plasmid carrying chloramphenicol resistance and phage T7 lysozyme, effective at attenuating activity of T7 RNA

polymerase, for better inhibition of expression under non-induced conditions. The sequence can be found here.

- **proA/B** = requires proline
- **recA1** = For reduced occurrence of unwanted recombination in cloned DNA; cells UV sensitive, deficient in DNA repair
- **recA13** = as for recA1, but inserts less stable.
- **recBCD** = Exonuclease V; mutation in RecB or RecC reduces general recombination by a factor of 100; impaired DNA repair; UV sensitive, easier propagation of inverted repeats
- **recJ** Exonuclease involved in alternate recombination
- **relA** = relaxed phenotype; permits RNA synthesis in absence of protein synthesis
- **rha** = blocked rhamose metabolism
- **rnc** = encodes RnaseIII (rnc-14 is a common null mutant)
- **rne** = encodes RnaseE (rne-3071 is a common temperature sensitive mutant)
- **rpsL** = mutation in ribosomal protein S12 conveying streptomycin resistance; also called strA, rpsL135(strR), strA135 [2] *---**Karmella 13:27, 21 October 2012 (EDT)**:
- **sbcBC** = ExoI activity abolished; usually present in recBC strains; recombination proficient, stable inverted repeats
- **sr1** = cannot metabolize sorbitol
- **supE** = glnV
- **supF** = tyrT
- **thi** = requires thiamine
- **thyA** = requires thymidine
- **Tn10** = transposon normally carrying Tetracycline resistance
- **Tn5** = transposon normally carrying Kanamycin resistance
- **tonA** = Mutation in outer membrane protein conveying resistance to phage T1 and phage T5
- **traD** = Mutation eliminating transfer factor; prevents transfer of F plasmid
- **trxB** = mutation in thioredoxin reductase; enhances disulphide bond formation in the cytoplasm
- **tsx** = outer membrane protein mutation conveying resistance to phage T6 and colicin K
- **tyrT** = suppression of amber (UAG) stop codons by insertion of tyrosine; needed for some phage infection such as λgt11.
- **ung1** = allows uracil to exist in plasmid DNA
- **xyl-5** = blocked xylose metabolism

- **Sm^R** = Streptomycin resistance

Methylation Issues in E. coli

- Type I methylation systems:
  - *E. coli* K-12 restricts DNA which is **not** protected by adenine methylation at sites AA*C[N_6]GTGC or GCA*C[N_6]GTT, encoded by the hsdRMS genes(EcoKI). Deletions in these genes removes either the restriction or methylation or both of these functions.
  - *E. coli* B derivative strains contain an hsdRMS system (EcoBI) restricting and protectiing the sequence TGA*[N_8]TGCT or AGCA*[N_8]TCA.
- The **mcrA** gene (carried on the e14 prophage) restricts DNA which **is** methylated in C$_m$CWGG or $_m$CG sequences (methylation by the **dcm** gene product).
- The **mcrBC** genes restrict R$_m$C sequences.
- The **mrr** gene product restricts adenine methylated sequences at CAG or GAC sites.
- E. coli methylates the adenine in GATC (and the corresponding A on the opposite strand) with the **dam** gene product.
- M.EcoKII methylates the first A at the palindromic site ATGCAT (as well as the corresponding A on the opposite strand), see (Kossykh VG (2004) J. Bact 186: 2061-2067 PMID 15028690) Note that this article has been retracted; the retraction appears to center on textual plagarism, not experimental results. The homology to AvaIII is real. I think I believe it. tk 20:28, 9 December 2005 (EST). Rich Roberts reports: "We have tried ourselves to detect activity with this gene product and cannot detect any methyltransferase activity. In our case we used antibodies able to detect N6-methyladenine or N4 methylcytosine in DNA. The ones we have are very sensitive and should have been able to detect 5 methyl groups in the whole E. coli chromosome. Nothing was detected in an over expressing strain."
- For additional information see E. coli restriction-modification system and the NEB technical information on methylation.

Commonly used strains

AG1

endA1 recA1 gyrA96 thi-1 relA1 glnV44 hsdR17(r_{K^-} m_{K^+})

AB1157

thr-1, araC14, leuB6(Am), Δ(gpt-proA)62, lacY1, tsx-33, qsr'-0, glnV44(AS), galK2(Oc), LAM-, Rac-0, hisG4(Oc), rfbC1, mgl-51, rpoS396(Am), rpsL31(strR), kdgK51, xylA5, mtl-1, argE3(Oc), thi-1

- Bachmann BJ: Derivation and genotypes of some mutant derivatives of Escherichia coli K-12.

Escherichia coli and Salmonella typhimurium. Cellular and Molecular Biology (Edited by: F C Neidhardt J L Ingraham KB Low B Magasanik M Schaechter H E Umbarger). Washington, D.C., American Society for Microbiology 1987, 2:1190-1219.
See CGSC#1157

B2155

thrB1004 pro thi strA hsdsS lacZD M15 (F`lacZD M15 $lacI^q$ traD36 $proA^+$ $proB^+$) D dapA::erm (Erm^r) pir::RP4 [::kan (Km^r) from SM10]

An *E. coli* strain carrying the *pir* sequence required for maintenance of plasmids containing R6K ori. Also, this strain is auxotrophic for DAP (diaminopimelic acid - a lysine precursor). The auxotrophy helps in removal of this strain from a bi-parental mating setup after conjugation.

Ref: Maintenance of broad-host-range incompatibility group P and group Q plasmids and transposition of Tn5 in Bartonella henselae following conjugal plasmid transfer from Escherichia coli
Dehio, C. & Meyer, M. (1997) J. Bacteriol. 179, 538–540

BL21

E. coli B F- *dcm ompT hsdS*(r_B- m_B-) gal $[malB^+]_{K-12}(\lambda^S)$

- The "malB region" was transduced in from the K-12 strain W3110 to make the strain $Mal^+\lambda^S$. See Studier et al. (2009) J. Mol. Biol. 394(4), 653 for a discussion of the extent of the transfer.
- Stratagene E. coli Genotype Strains

BL21(AI)

F– ompT gal dcm lon $hsdS_B(r_B$- m_B-) araB::T7RNAP-tetA

- an *E. coli* B strain carrying the T7 RNA polymerase gene in the *araB* locus of the *araBAD* $operon^q$.
- Transformed plasmids containing T7 promoter driven expression are repressed until L-arabinose induction of T7 RNA polymerase.

    - Maximal expression is lower than that of BL21(DE3)(customer support 10/2012)
- Derived from BL21.
- See the product page for more information.
- Brian Caliendo (Voigt lab) reported trouble getting the Datsenko and Wanner (2000) plasmid pCP20 to transform into this strain, when other strains transformed fine. Cause is unknown.

BL21(DE3)

F– ompT gal dcm lon hsdS_B(r_B- m_B-) λ(DE3 [lacI lacUV5-T7 gene 1 ind1 sam7 nin5])

- an E. coli B strain with DE3, a λ prophage carrying the T7 RNA polymerase gene and $lacI^q$
- Transformed plasmids containing T7 promoter driven expression are repressed until IPTG induction of T7 RNA polymerase from a lac promoter.
- Derived from B834 (Wood, 1966) by transducing to Met^+.
- See the original Studier paper or the summary in Methods in Enzymology for more details.
- Whole genome sequence available [3]

BL21 (DE3) pLysS

F- ompT gal dcm lon hsdS_B(r_B- m_B-) λ(DE3) pLysS(cm^R)

- pLysS plasmid chloramphenicol resistant; grow with chloramphenicol to retain plasmid
- Chloramphenicol resistant
- The pLysS plasmid encodes T7 phage lysozyme, an inhibitor for T7 polymerase which reduces and almost eliminates expression from transformed T7 promoter containing plasmids when not induced.
- see Moffatt87 for details of pLysS and pLysE plasmids

BNN93

F- tonA21 thi-1 thr-1 leuB6 lacY1 glnV44 rfbC1 fhuA1 mcrB e14-(mcrA-) hsdR(r_K-m_K+) λ-

- Some C600 strains are really BNN93

BNN97

- BNN93 (λgt11)

- A λgt11 lysogen producing phage at 42C

BW26434, CGSC Strain # 7658

Δ(araD-araB)567, Δ(lacA-lacZ)514(::kan), lacIp-4000($lacI^q$), λ-, rpoS396(Am)?, rph-1, Δ(rhaD-rhaB)568, hsdR514

- This information is from a printout sent by the *E. coli* Genetic Stock Center with the strain.
- B.L. Wanner strain
- rph-1 is a 1bp deletion that results in a frameshift over last 15 codons and has a polar effect on pyrE leading to suboptimal pyrimidine levels on minimal medium. (Jensen 1993 J Bact. 175:3401)
- Δ(araD-araB)567 was formerly called $\Delta araBAD_{AH33}$ by Datsenko and Wanner
- Am = amber(UAG) mutation
- Reference: Datsenko and Wanner, 2000, PNAS, 97:6640

NOTE:

- This promoter driving the expression of lacI was sequenced in this strain using a primer in mhpR (upstream of lacI) and a primer in the opposite orientation in lacI. The lac promoter was found to be identical to wildtype. Thus, the -35 sequence was GCGCAA not GTGCAA as expected with $lacI^q$. Therefore this strain (or at least the version obtained from the *E. coli* Genetic Stock Center) does NOT appear to be $lacI^q$. According to Barry Wanner, this is an unexpected result. -Reshma 13:19, 5 May 2005 (EDT)
- "We have now confirmed that BW25113, BW25141, and BW26434 are all $lacI^+$, and not $lacI^q$. We thank you for alerting us to the error with respect to BW26434. Apparently, the lacI region was restored to wild-type in a predecessor of BW25113." (from Barry Wanner November 18, 2005)
- The genotype has been corrected at the CGSC

C600

F- tonA21 thi-1 thr-1 leuB6 lacY1 glnV44 rfbC1 fhuA1 λ-

- There are strains circulating with both e14+($mcrA^+$) and e14-($mcrA^-$)
- General purpose host
- See CGSC#3004
- References: Appleyard, R.K. (1954) Genetics 39, 440; Hanahan, D. (1983) J. Mol. Biol. 166, 577.

C600 hflA150 (Y1073, BNN102)

F- thi-1 thr-1 leuB6 lacY1 tonA21 glnV44 λ- hflA150(chr::Tn10)

- host for repressing plaques of λgt10 when establishing cDNA libraries
- Reference Young R.A. and Davis, R. (1983) Proc. Natl. Acad. Sci. USA 80, 1194.
- Tetracycline resistance from the Tn10 insertion

CSH50

F- λ- ara Δ(lac-pro) rpsL thi fimE::IS1

- See CGSC#8085
- References: Miller, J.H. 1972. Expts. in Molec. Genetics, CSH 0:14-0; Blomfeld et al., J.Bact. 173: 5298-5307, 1991.

D1210

HB101 $lacI^q$ $lacY^+$

DB3.1

F- gyrA462 endA1 glnV44 Δ(sr1-recA) mcrB mrr hsdS20(r_B^-, m_B^-) ara14 galK2 lacY1 proA2 rpsL20(Sm^r) xyl5 Δleu mtl1

- useful for propagating plasmids containing the ccdB operon.
- gyrA462 enables ccdB containing plasmid propagation
- streptomycin resistant
- appears to NOT contain lacI (based on a colony PCR) --Austin Che 16:16, 18 June 2007 (EDT)

1. Bernard P and Couturier M. . pmid:1324324. PubMed HubMed [Bernard-JMolBiol-1992]
2. Miki T, Park JA, Nagao K, Murayama N, and Horiuchi T. . pmid:1316444. PubMed HubMed [Miki-JMolBiol-1992]

All Medline abstracts: PubMed HubMed

DH1

endA1 recA1 gyrA96 thi-1 glnV44 relA1 hsdR17(r_K^- m_K^+) λ-

- parent of DH5α
- An Hoffman-Berling 1100 strain derivative (Meselson68)

- more efficient at transforming large (40-60Kb) plasmids
- nalidixic acid resistant
- Reference: Meselson M. and Yuan R. (1968) Nature 217:1110 PMID 4868368.

DH5α

F- endA1 glnV44 thi-1 recA1 relA1 gyrA96 deoR nupG Φ80d*lacZ*ΔM15 Δ(*lacZYA-argF*)U169, hsdR17(r_{K^-} m_{K^+}), λ–

- An Hoffman-Berling 1100 strain derivative (Meselson68)
- Promega also lists phoA
- nalidixic acid resistant
- References:
  - FOCUS (1986) 8:2, 9.
  - Hanahan, D. (1985) in DNA Cloning: A Practical Approach (Glover, D.M., ed.), Vol. 1, p. 109, IRL Press, McLean, Virginia.
  - Grant, S.G.N. et al. (1990) Proc. Natl. Acad. Sci. USA 87: 4645-4649 PMID 2162051.
  - Meselson M. and Yuan R. (1968) Nature 217:1110 PMID 4868368.

DH5α Turbo (NEB)

F´ proA+B+ $lacI^q$ Δ lacZ M15/ fhuA2 Δ(lac-proAB) glnV gal R(zgb-210::Tn10)Tet^S endA1 thi-1 Δ(hsdS-mcrB)5

- Also known as NEB Turbo
- T1 phage resistant
- Rapid growth: visible colonies on agar, ~6.5 hours; shaking liquid culture OD 600 = 2.0, ~4 hours
- Expresses the Lac repressor
- References:
  - New England Biolabs, product catalogue number C2984H

DH10B (Invitrogen)

F- endA1 recA1 galE15 galK16 nupG rpsL ΔlacX74 Φ80lacZΔM15 araD139 Δ(ara,leu)7697 mcrA Δ(mrr-hsdRMS-mcrBC) λ-

- suitable for cloning methylated cytosine or adenine containing DNA
- an MC1061 derivative (Casadaban80). Prepare cells for chemical transformation with CCMB80 buffer
- blue/white selection

- While DH10B has been classically reported to be galU galK, the preliminary genome sequence for DH10B indicates that DH10B (and by their lineage also TOP10 and any other MC1061 derivatives) is actually galE galK galU+. **Dcekiert 16:37, 23 January 2008 (CST)**
- Genome sequence indicates that DH10B is actually deoR+. Presumably TOP10 and MC1061 are also deoR+.
- Streptomycin resistant
- References:
  - Casdaban, M. and Cohen, S. (1980) J Mol Biol 138:179 PMID 6997493.
  - Grant, S.G.N. et al. (1990) Proc. Natl. Acad. Sci. USA 87: 4645-4649 PMID 2162051.
  - E. coli Genetic Stock Center, MC1061 Record
  - DH10B Genome Sequencing Project, Baylor College of Medicine
  - Complete sequence is available, see Durfee08, PMID 18245285.

DH12S (Invitrogen)

mcrA Δ(mrr-hsdRMS-mcrBC) φ80d lacZΔM15 ΔlacX74 recA1 deoR Δ(ara, leu)7697 araD139 galU galK rpsL F' [proAB+ lacIqZΔM15]

- host for phagemid and M13 vectors
- useful for generating genomic libraries containing methylated cytosine or adenine residues
- streptomycin resistant
- References: Lin, J.J., Smith, M., Jessee, J., and Bloom, F. (1991) FOCUS 13, 96.; Lin, J.J., Smith, M., Jessee, J., and Bloom, F. (1992) BioTechniques 12, 718.

DM1 (Invitrogen)

F-dam-13::Tn9(CmR)dcm-mcrB hsdR-M+ gal1 gal2 ara-lac-thr-leu-tonR tsxR Su0

- Host for pBR322 and other non-pUC19 plasmids; useful for generating plasmids that can be cleaved with dam and dcm sensitive enzymes
- Chloramphenicol resistant
- Promega lists as F' not F-
- Reference: Lorow-Murray D and Bloom F (1991) Focus 13:20

E. cloni(r) 5alpha (Lucigen)

fhuA2Δ(argF-lacZ)U169 phoA glnV44 Φ80 Δ(lacZ)M15 gyrA96 recA1 relA1 endA1 thi-1 hsdR17

- Common cloning strain.

E. cloni(r) 10G (Lucigen)

F- *mcrA* Δ(*mrr-hsd*RMS-*mcr*BC) *end*A1 *rec*A1 Φ80*dlac*ZΔM15Δ*lac*X74 *ara*D139 Δ(*ara,leu*)7697 *gal*U *gal*K *rps*L *nup*G λ- *ton*A

- Common cloning strain.
- Resistant to phage T1.

E. cloni(r) 10GF' (Lucigen)

[F´*pro*A+B+*lac*IqZΔM15::Tn10(TetR)]/*mcr*AΔ(*mrr-hsd*RMS-*mcr*BC)*end*A1 *rec*A1 Φ80d*lac*ZΔM15 Δ*lac*X74 *ara*D139 Δ(*ara, leu*)7697 *gal*U *gal*K *rps*L *nup*Gλ *ton*A

- Strain for cloning and single-strand DNA production.

E. coli K12 ER2738 (NEB)

F´proA+B+ lacIq Δ(lacZ)M15 zzf::Tn10(TetR)/ fhuA2 glnV Δ(lac-proAB) thi-1 Δ(hsdS-mcrB)5

- Phage propagation strain
- Also available from Lucigen Corporation.

ER2566 (NEB)

F- λ- fhuA2 [lon] ompT lacZ::T7 gene 1 gal sulA11 Δ(mcrC-mrr)114::IS10 R(mcr-73::miniTn10-TetS)2 R(zgb-210::Tn10)(TetS) endA1 [dcm]

- Host strain for the expression of a target gene cloned in the pTYB vectors.
- Carry a chromosomal copy of the T7 RNA polymerase gene inserted into *lacZ* gene and thus under the control of the lac promoter. In the absence of IPTG induction expression of T7 RNA polymerase is suppressed by the binding of *lac* I repressor to the *lac* promoter.
- Deficient in both *lon* and *ompT* proteases.

ER2267 (NEB)

F´ proA+B+ lacIq Δ(lacZ)M15 zzf::mini-Tn10 (KanR)/ Δ(argF-lacZ)U169 glnV44 e14-(McrA-) rfbD1? recA1 relA1? endA1 spoT1? thi-1 Δ(mcrC-mrr)114::IS10