SUPPLEMENTARY TABLE 1. Table of large differences between MG1655 and NCM3722 $\,$

Position	MG1655	NCM3722	Genes Affected
278387-279154 289858-290625	IS1 IS1	IS1 11 kb deletion 279155-290625	Deletion of 11 genes of cryptic prophage CP4-6 by apparent recombination of IS1 elements
573810-575013	IS5	No insert	Outer membrane porin gene <i>nmpC</i> of DLP12 prophage interrupted by IS5 in MG1655 is intact in NCM3722
687070-688272	IS5	No insert	IS5 upstream of <i>gltIJKL</i> operon (glutamate/aspartate transport) in MG1655 is not present in NCM3722
806552-806565	No insert	Lambda	NCM3722 is a lambda lysogen. Lambda phage has wild type lambda sequence
916093-916101	No insert	IS1	IS1 interrupts <i>ybjD</i> gene. YbjD is a putative ATP-dependent endonuclease of OLD family
1876598-1876594	No insert	IS5	IS5 interrupts <i>yeaP</i> gene. YeaP is a putative diguanylate cyclase
1976527-1977294 1977312-1977316	IS1	Tn1000	Insert sites for IS1 and Tn1000 are separated by 9 base pairs. Both are upstream of the <i>flhDC</i> operon and disrupt the regulatory region in potentially different ways. FlhDC is the principal regulator of flagellar sysnthesis and swarming
2099769-2100970	IS5	No insert	Lipopolysaccharide biosynthesis gene <i>wbbL</i> interrupted by IS5 in MG1655 is intact in NCM3722

2108321-2126617	No insert	IS1 and 18 kb deletion	Genes deleted are rfbA, rfbD, rfbB, galF, wcaM, wcaL, wcaK, wzxC, wcaJ, cpsG, cpsB, wcaI, fcl, gmd, wcaF. All are related to lipopolysaccharide and capsule formation.
2168198-2169452	IS3	No insert	Repressor of galactitol utilization operon <i>gatR</i> interrupted in MG1655 is intact in NCM3722
2481860-2481868	No insert	IS1	IS1 interrupts <i>evgA</i> gene. EvgA is a transcriptional activator that interacts with sensor histidine kinase EvgS to regulate acid and drug resistance
2773185-2773189	No insert	IS2	IS2 inserted between pseudogenes <i>yfjW</i> and <i>ypjI</i> , remnants of CP4-57 cryptic prophage
3128165-3129367	IS5	2 IS5 elements 7 kb sequence not in MG1655	7 kb sequence includes genes like those of <i>E.coli</i> strain BL21(DE3) at this location. The six genes code for a conserved protein, an acyl CoA synthetase, 2 permeases, an epimerase, and an oxomonoate synthase. Appears that sequence was deleted in MG1655
3363724-3364740	IS5	No insert	The <i>yceF</i> gene interrupted in MG1655 is intact in NCM3722. It lies in a cluster of genes of unknown function
3936750-3936758	No insert	IS5	IS5 inserted into <i>rbsR</i> , transcriptional repressor for ribose metabolism operon <i>rbsDACBKR</i> .
4478833-4478826	No insert	IS1	IS1 inserted in <i>yjgN</i> , which encodes an inner membrane protein of unknown function
4496204-4497534	IS2	No insert	IS2 element located between pseudogenes in KpLE2 phage

F plasmid

In addition to the above large differences, NCM3722 carries an F plasmid of 67 kb. The F plasmid is identical to the 99159 bp plasmid annotated in Genbank (AP00198) except in two regions. The *finO* gene is intact in the NCM3722 F plasmid because the IS3 element at 1-1258 is not present. (Disruption of *finO*, which codes for the transacting fertility inhibition factor, results in constitutive *tra* expression.) The 37 kb region between 4191-41089 is absent from the F plasmid in NCM3722 and is replaced with a 6.4 kb region. The 37 kb region that is missing consists of 22 genes including the *repB* gene, which codes for the RepFIB replication protein of plasmid P307. The 6.4 kb region that replaces it carries an intact *repA* gene, which codes for the RepFIC protein. (This gene is disrupted by Tn1000 in the missing 37 kb region.) It also contains 2.7 kb that codes for a PHP N-terminal protein, a putative phosphoesterase, and 1.3 kb without similarity to any sequence in the database.