Supplementary material for Zhu *et al*. (August 7, 2001) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.171579898.

Table 4. *topB* deletion strains containing gyrase compensatory mutations are viable

Strains	Relevant genotype	P1 transduction frequency ($\times 10^{-8}$)*
MG1655	*gyr*$^{+}$	2.14 ± 0.14
QZ116	*gyrA224*	1.99 ± 0.06** (*P* = 0.989)
QZ119	*gyrB225*	2.06 ± 0.11** (*P* = 0.985)

Bacterial strains MG1655, MG1655 *gyrA224*, and MG1655 *gyrB225* were transduced to Δ*topB*::*aphA*. Bacterial strains DM750 and DM800 contain a chromosomal deletion that encompasses *cysB* and *topA*; therefore, a true isogenic parent strain was unavailable. Strain MG1655, a prototype wild-type strain of *E. coli*, was transduced to *gyrA224* and *gyrB225* as described by Miller (1). The cells exhibited a normal growth rate and morphology (data not shown).

*The frequency of P1 Δ*topB*::*aphA* transductants was determined by calculating the total colony numbers of transduced cells per total cell number. The values are presented as mean ± SD ($n = 5$). A hypothesis test was used to compare the numbers of individual mutants to that of wild-type strain. $P < 0.05$ was considered statistically significant.

**, $P > 0.05$ indicates no significant differences vs. wild-type control groups.

Reference:

1. Miller, J. H. (1992) *A Short Course in Bacterial Genetics* (Cold Spring Harbor Lab. Press, Plainview, NY).