

Locus	Gene	Protein Description	alleles	Growth condition			Conserved association?
				Ciprofloxacin	Naladixic acid	Trimethoprim	
FTN_0122	<i>recA</i>	Recombinase	3 of 3	■	■		+
FTN_0189	<i>priA</i>	Primase	3 of 3	■	■	■	
FTN_0399	<i>radA</i>	DNA repair	3 of 3	■			+
FTN_0412	<i>recN</i>	DNA repair	4 of 4	■	■		+
FTN_0632	<i>dgt</i>	dGTP triphosphatase	3 of 5	■		■	+
FTN_0787	<i>rep</i>	Helicase	5 of 5	■	■		
FTN_0891	<i>ruvB</i>	Helicase	4 of 4	■	■		
FTN_1025	<i>ruvA</i>	Helicase	2 of 2	■	■		+
FTN_1027*	<i>ruvC</i>	DNase	2 of 2	■			+
FTN_1168*	<i>xseA</i>	Exonuclease	3 of 3	■	■		+
FTN_1177*	<i>sbcB</i>	Exonuclease	4 of 4	■	■		
FTN_1356	<i>recD</i>	Exonuclease	3 of 3	■	■	■	
FTN_1357	<i>recB</i>	Exonuclease	5 of 5	■	■	■	+
FTN_1359*	<i>recC</i>	Exonuclease	3 of 3	■	■	■	+
FTN_1513	<i>xerC</i>	Recombinase	3 of 3	■	■		+
FTN_1558	<i>xerD</i>	Recombinase	3 of 3	■	■		+

log₂ growth: -8.0  0  ≥0

Figure S4. Quinolone antibiotic hypersensitive mutants. Mutations leading to increased ciprofloxacin and/or naladixic acid sensitivity are shown. Shadings reflect average growth of the two alleles with the strongest defects for each gene. Nutritional phenotypes are not shown. Asterisks indicate cases in which polar effects on expression of downstream genes could contribute to phenotypes. Several genes with strong mutant phenotypes that could be explained by polarity were not included in the table (FTN_0120, FTN_0121, FTN_0188, FTN_400, and FTN_401). The number of mutant alleles for each gene leading to increased sensitivity is provided. Functions associated with quinolone intrinsic resistance in *E. coli* are indicated.