

Table S6. Additional class-specific MIC changes (non-aminoglycosides).

Genotype	Relative Susceptibility ^a / Change in Enrichment ^b						
	DOX	TET	LOM	NAL	BLM	SLF	TRM
<i>lon::kan</i>	1 / ↑	1 / ↑	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔
<i>ppk::kan</i>	1 / ↑	1 / ↑	-1 / ↔	1 / ↑	ND / ↔	ND / ↔	ND / ↔
<i>rseB::kan</i>	-1 / ↓	0 / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔
<i>qseB::kan</i>	<-2 / ↓	0 / ↔	-1 / ↔	-2 / ↓	ND / ↔	ND / ↔	ND / ↔
<i>ompR::kan</i>	0 / ↔	1 / ↑	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔
<i>sbmA::kan</i>	ND / ↔	ND / ↔	ND / ↔	ND / ↔	2 / ↑	ND / ↔	ND / ↔
<i>prlC::kan</i>	ND / ↔	ND / ↔	ND / ↔	ND / ↔	-1 / ND	ND / ↔	ND / ↔
<i>folM::kan</i>	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔	4 / ↑	0 / ↑
<i>folX::kan</i>	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔	2 / ↔	0 / ↑
<i>yafD::kan</i>	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔	ND / ↔	1 / ↑

^a Relative susceptibility is expressed as $\log_{1.5}(\text{MIC mutant})/(\text{MIC wild-type})$, where MIC is the minimal inhibitory concentration for the given antibiotic.

^b A “↑” (“↓”) indicates that mutants with transposons in or near the locus were significantly enriched (depleted) during growth in the indicated antibiotic; “↔” indicates that no significant change occurred. ND: no data