TABLE S1 Distribution of isolates showing a conflict between their phenotypic DST data and mutation analysis in different categories.[a]

Mutated codon[b]	No. of isolates (% in each category)		ID of mixed infections (ID with the secondary peak)	
(No. of isolates)	R^R	S^R	R^R	S^R
None (74)	8 (10.81)	66 (89.19)	SSCM034, SC262, SSC0407, SC187	SSC0617, SSC0619 SC240, (SC023)
Single (177)	165 (93.22)	10 (5.65)	SC107, SSC0620, (SC187, SC262)	SSC0588, SC023
146 (4)	4 (100)	0 (0)		
511 (7)	5 (71.43)	2 (28.57)		SC023
513 (3)[c]	2 (66.67)	0 (0)		
516 (11)	10 (90.91)	1 (0.09)		
526 (27)	25 (92.59)	2 (7.41)		
531 (117)[d]	112 (95.73)	4 (3.42)		SSC0588
533 (5)	5 (100)	0 (0)		
572 (1)	1 (100)	0 (0)		
626 (1)	1 (100)	0 (0)		
657 (1)	0 (0)	1 (100)		
Multiple (41)	39 (95.12)	2 (4.88)	SC081	
144, 526 (1)	1 (100)	0 (0)		
146, 402 (1)	1 (100)	0 (0)		
149, 516 (1)	1 (100)	0 (0)		
195, 531 (1)	1 (100)	0 (0)		
381, 531 (1)	1 (100)	0 (0)		
481, 531 (2)	2 (100)	0 (0)		
505, 511 (1)	0 (0)	1 (100)		
511, 513 (1)	1 (100)	0 (0)		
511, 516 (5)	5 (100)	0 (0)	SC081	
511, 572 (1)	0 (0)	1 (100)		
511, 574 (3)	3 (100)	0 (0)		
513, 574 (1)	1 (100)	0 (0)		
513, 564 (1)	1 (100)	0 (0)		
513, 633 (1)	1 (100)	0 (0)		
516, 572 (2)	2 (100)	0 (0)		
516, 518 (1)	1 (100)	0 (0)		
516, 522 (1)	1 (100)	0 (0)		
518, 533 (1)	1 (100)	0 (0)		
526, 572 (3)	3 (100)	0 (0)		
526, 574 (1)	1 (100)	0 (0)		
526, 531 (1)	1 (100)	0 (0)		
526, 626 (2)	2 (100)	0 (0)		
526, 541 (1)	1 (100)	0 (0)		
530, 531 (3)	3 (100)	0 (0)		
531, 604 (2)	2 (100)	0 (0)		
531, 616 (1)	1 (100)	0 (0)		

511, 572, 643 (1)	1 (100)	0 (0)

[a] A total of 292 isolates that were sequenced on *rpoB* gene were included in this statistical analysis. Two clinical information-lost isolates had a single mutation. The isolates of patients whose ID showed in parentheses were RIF hetero-resistant. R^R = resistant to RIF, S^R = susceptible to RIF.

[b] Escherichia coli numbering system for the *rpoB* gene.

[c] Isolate of SC100 had a single mutation at codon 513.

[d] Isolate of SC099 had a single mutation at codon 531.

Supplemental material legend:

TABLE S1 Distribution of isolates showing a conflict between their phenotypic DST data and mutation analysis in different categories.