

Additional file 1. Primers used in this study.

Goal	Name	Sequence (5' to 3')	Amplicon size (bp)	Elongation time in PCR (min)
<i>metQ</i> gene detection	metQ_Fw	TACCAAACCTGGCTCATCCAT	705	0.5
	metQ_Rev	GCCGTTGGGATAAAGTTCAA		
Generation of <i>metQ</i> mutant or complemented strain: downstream flanking segment amplification	metQ_L-Fw	GCGCGCGCGCAGATCTGAACCTGATCGTAAATGCCT	932	0.5
	metQ_L-Rev	AGTCAGTTCGATCACAAC TATGCGCAAA TAGGTTGAGGACTGGGC		
Generation of <i>metQ</i> mutant: upstream flanking segment amplification	metQ_R-Fw	AGTCTACGTACATAGTCAGTTAAAGCA GCCGTTGCCAAAC	988	0.5
	metQ_R-Rev	GCGCGCGCGCGCGCGGATATCATATTTTT TATCAAGCCATA		
Generation of <i>metQ</i> complemented strain: upstream flanking segment amplification	metQ_R_Fw_c	AGTCTACGTACATAGTCAGTTTACCAA ACTGGCTC	1799	1
	metQ_R-Rev	GCGCGCGCGCGCGCGGATATCATATTTTT TATCAAGCCATA		
Spectinomycin-resistance cassette amplification	SPECT_Fw	ATAGTTGTGATCGACTGACTGCAGGTC GATTTTCGTTTCGTG	1199	1
	SPECT_Rev	ACTGACTATGTACGTAGACTATGCAAG GGTTTATTGTTTTCTAAAA		
Chloramphenicol-resistance cassette amplification	CAM-Fw	ATAGTTGTGATCGACTGACTAAGGGAT CCGGCACCTATCT	1196	1
	CAM-Rev	ACTGACTATGTACGTAGACTTGCCCGG GGATCCTCCGATA		
Amplification of hlpA-GFP-Tet ^R construct	GFP-Fw	TCCACTAATAGGGAACAGCT	4799	3
	GFP-Rev	ATGAACAGAGACAAGCTGTC		
Confirmation of (1) wild type, (2) <i>metQ</i> mutant or (3) complemented strains.	metQ_L-Fw	GCGCGCGCGCAGATCTGAACCTGATCGTAAATGCCT	(1) 2695 (2) 3079 (3) 3887	2.5
	metQ_R-Rev	GCGCGCGCGCGCGCGGATATCATATTTTT TATCAAGCCATA		