Table S1. Main MS/MS parameters set for the detection of SMX, ENR and CIP. RT means retention time; ESI mode means positive (+) ionization mode; DP means declustering potential; CE means collision energy.

Compound	RT (min)	ESI Mode	Precursor ion (m/z)	Product ion (m/z)	DP (V)	CE (eV)
SMX	6.4	+	254.1	92.0	40	39.0
				108.1		39.4
				156.0		22.8
ENR	13.8	+	360.2	342.1	40	21.0
				316.1		35.0
CIP	14.5	+	332.2	245.2	40	33.6
				288.2		26.5

Table S2. List of primers used for ARGs quantification

Primer name	Target gene	Primer sequence (5'->3')	Reference
Sul1 fw	*sul1*	CGCACCGGAAACATCGCTGCAC	[67]
Sul1 rv		TGAAGTTCCGCCGCAAGGCTCG	
Sul2 fw	*sul2*	GCGCTCAAGGCAGATGGCATT	[68]
Sul2 rv		GCGTTTGATACCGGCACCCGT	
IntI1 fw	*intI1*	TCGTGCGTCGCCATACA	[69]
IntI1 rv		GCTTGTTCTACGGCCGTTTGA	
16S fw	*16S rRNA*	CGGTGAATACGTTCYCGG	[70]
16S rv		TACCTTGTTACGACTT	
qnrS fw	*qnrS*	GACGTGCTAACTTGCGTGAT	[71]
qnrS rv		TGGCATTGTTGGAAACTT	
qepA fw	*qepA*	GCAGGTCCAGCAGCGGGTAG	[72]
qepA rv		CTTCCTGCCCGAGTATCGTG	
Aac-(6′)-Ib cr fw	*aac-(6′)-Ib-cr*	TGCATCACAACTGGGCAAAGGCT	[73]
Aac-(6′)-Ib cr rv		ACACGGCTGGACCATATGGGGT	