S1 Primers used to generate standard amplicons (forward primer=FP, reverse primer=RV). The amplicon size is in number of base pairs (bp)

Primer	Target gene	Base sequence 5’-3’	Amplicon size (bp)	Reference
tet(A)_std_FW *tet*(A)_std_RV	*tet*(A)	GTAATTCTGAGCACTGTCGC CTGTCCTGGACAACATTGCTT	937	(1-3)
tet(B)_std_FW *tet*(B)_std_RV	*tet*(B)	ACTTGTCTCCTGTTTACTCCCCTGAGC GCCTTATCATGCCAGTCTTGCCAACG	1142	This study
tet(C)_std_FW *tet*(C)_std_RV	*tet*(C)	CGCTCATCGTCATCCTCGGCAC CAACCCGTTCCATGTGCTCGC	1091	This study
tet(M)_std_FW *tet*(M)_std_RV	*tet*(M)	GAAGCGTGGACAAAGGTACAACGAGG CGACGGGGCTGGCAAACAGG	1768	This study
tet(O)_std_FW *tet*(O)_std_RV	*tet*(O)	CTGGCTCACGTTGACGCAGGAAAG TATTCGGGCGGCGGGGTTG	1852	This study
tet(W)_std_FW *tet*(W)_std_RV	*tet*(W)	AAAGACGACCTTGACGGAGAGCC TCTCGCCAGTAAAGACAACTTCATCC	1697	This study
*sulI*_std_FW *sulI*_std_RV	*sulI*	ATGGTGACGGTGTTCGGCATTCTG GATCTAACCCTCGGTCTCTGGCGT	832	This study
*sulII*_std_FW *sulII*_std_RV	*sulII*	CGGCATCGTCAACATAACCTCGGAC CGGCTCGTGTGTGCGGATGAAG	730	This study
*ermB*_std_FW *ermB*_std_RV	*ermB*	GGGCATTTAACGACGAAACTGGCT ACTTTGGCGTGTTTCATTGCTTGATG	539	This study
*ermF*_std_FW *ermF*_std_RV	*ermF*	TCGTTTTACGGGTCAGCACTT CAACCAAAGCTGTGTCGTTT	182	(4)
*vanA*_std_FW *vanA*_std_RV	*vanA*	GAAATCAACCATGTTGATGTAGCA TTTGCCGTTTCCTGTATCCGT	572	(5)
CMY-2_std_FW CMY-2_std_RV	*bla*$_{\text{CMY-2}}$	ATGATGAAAAAATCGTTATGC GCTTTTCAAGAATGCGCCAGG	758	(6-8)

FW_SHV_OS5 FW_SHV_OS6	*bla*$_{\text{SHV}}$ family	TTATCTCCCTGTTAGCCACC GATTTGCTGATTTCGCTCGG	854	(6-8)
CTX-M-U1_FW CTXXM-U2nds_RV	*bla*$_{\text{CTX-M-1}}$ group	ATGTGCAGYACCAGTAARGTKATGGC GGGTRAARTARGTSACCAGAAYSAGCGG	593	(6,8)
8FX 1407RX	16S rDNA	AGAGTTTGATCCTGGCTNAG TGACGGGCGGTGTGTACAA	1392	(9)

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