```
ereA2      TAACCTGCCAATCCACCG--GACGGTT-------------------------------------TTC-----------------------------------------------AACCGCCGGTGATCAGCGCGTTA
oxa2       TAACCCGGC-AGTCAACTCGGACGCTGCGCG---------------------------------ATAAAAC-----------------------------------------CGCGCAGCGCCGGTTACT-TCAACGTTA
aadA5      TAACTCGGC-GTTCAAG-CGGACGGGC-------------------------------------TGC-----------------------------------------------GCCCGCCGCTCAAC-TATGCGTTA
oxa9       TAACCCTGC-GCTCGAG-CGGACCTCGCGC----------------------------------ATAAAGCC-----------------------------------------GCGCGAGTCCGCTCACCTTGAACGTTA
dfrB1      TAACTTGTC-GCTCCAG-CGGACGGC--------------------------------------TTC-----------------------------------------------GCCGCCCGCTGAGCTAATTCGTTA
dfrB3      TAACTGGTC-GCTCCAG-CGGACGGC--------------------------------------TTC-----------------------------------------------GCCGCCCGCTGAGCTAGAGCGTTA
aacA-IIb   TAACTTTTCGCTCCAA--CGGACGCTTGACCCGTCGGCCCGGCCGC------------------TGCC---------------------------GCAGCCGGACCGCCGCGTCAACCGCCGCTGACCTCCGGAGTTA
dfrA15     TAACAAGTGGCAGCAA--CTGACCGCCAAAAGTGTCACTTGTTTTGCC----------------AAAAAGCC-----------------------GGCAAAACAAGCGCCAATTTTGTCGGCAGCTGTG-CCAGGCGTTA
dfrA16     TAACAAGCGCCTGCAA-TCTGACCTCCGGTTACTGTCACCTTTTTTTGCGG-------------TGGAG-------------------------CTGCAAAAAAGGCGCCATTAACCTCCGGCAGTTGAGGCGGGCGTTA
dfrA1      TAACAAGTGGCAGCAA--CGGATTCGCAAA-CCTGTCACGCCTTTT------------------GTGCC----------------------------AAAAGCCGCGCCAGGTTTGCGATCCGCTGTG-CCAGGCGTTA
blaP1      TAACAAGGC-CATCAAGTTG-ACGGCTTTT-CC-GTCGCTTGTTTTGTGGT-------------TTAACGCT-------------------ACGCTACCACAAAACAATCAACTCCAAAGCCGCAACTTATGGCGGCGTTA
blaP2      TAACAAGGC-CATCAAGTTG-ACGGCTTTT-CC-GTCGCTTGTTTTGTGG----------CTTAACGCTACGCTA--------------------CCACAAAACAATCAACTACAAAGCCGCAACTTATGGCGGCGTTA
aadA6      TAACAATTC-ATTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAATTCAGGCGTTA
catB3      TAACAATTC-AATCAAGCCG-ATGCCGC------------------------------------TTC-----------------------------------------------GCGGCACGGCTTATTTCAGGCGTTA
catB5      TAACAATTC-ATTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCACGGCTTAATTCTGGCGTTA
qacF       TAACAATTC-ATTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAATTCAGGCGTTA
aadA7      TAACAATTC-ATTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAATTCAAGCGTTA
aacA-IIa   TAACAACTC-ATTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAATTCAGGCGTTA
sat        TAACAATTC-ATTCAAGCCG-ACACCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAATTCAGGAGTTA
aadA1a     TAACAATTC-GTTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAACTCAAGCGTTA
aadB       TAACAATTC-GTCCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAACTCAGGTGTTA
aadA1b     TAACAATTC-GTTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTACCTTGGCCGTTA
aadA3      TAACAATTC-GTTCAAGCCG-ACGCCGC------------------------------------TTC-----------------------------------------------GCGGCGCGGCTTAACTCAAGCGTTA
arr2       TAACAAAGC-CATCAAACCGGACGCCAGAGATTCCGCGCCTGTTGCGCATGGC------------TTC---------------------GCATATGCGCAATAGGCG-CGCCACCCTGTCGCCGTTTATGGCGGCGTTA
aacA-Iq    TAACAACCG-CTTCAAC-CTGAC-TCAGGGCGCTGTCACGATTTCTGCAGG--------------TAAT--------------------TCTGGACGCAGAAATCGCGCCAACGCCCTTCGCAGGTTAAGCGAAGTGTTA
aacA-Ip    TAACAATCG-CTTCAAC-CTGAC-TCAGGGCGCCGTCACGATTTCTGCTAGTT-----------ATCCTGG----------------------GACGCAGAAATCGCGCCAACGCCCTTCGCAGGTTAAGCGAAGTGTTA
aacA4b     TAACCCTTC-CATCGAGGGGGACGTCCAAGG---------------------------------GCTGGCG-----------------------------------------CCTTGGCCG-CCCTCATGTCAAACGTTA
aacA4a     TAACCCTTC-CATCGAGGGGGACGTCCAAGGGC-------------------------------TGGC-----------------------------------------GCCCTTGGCCGCCCCTCATGTCAAACGTTA
orfB       TAACCCTTC-CATCGAG-GGGATGCCCAAAAGGC------------------------------TGC-------------------------------------GCCTTCTGTGCACCCCTCATGTCAAACGTTA
dfrA12     TAACCATTC-CGTCAAC-GGGACGCCAAAATGC-------------------------------TGC---------------------------------GCATTTTGGTTCCCTCCGCTGCGCTCCGGC-TCTCGTTA
aacC1      TAACAATTC-GTTCAAGCCG-AGATCGGCTTCCCGGCCGCGGAGTTGTTCGG-------------TAAA---------------------TTGTCACAACGCCGCGGCCGCAAAGCGCTCCGGCTTAACTCAGGCGTTA
aadA2      TAACAATTC-GTTCAAGCCG-ACCGCGC------------------------------------TAC-----------------------------------------------GCGCGGCGGCTTAACTCCGGCGTTA
aacA7      TAACAATTC-GTTCAAGCCGAACTTGCTTCGTTACACCAAAGCCATGGCAG-------------AAAGAGC--------------------TTGCCATGGCTTTGGCTCCACTACGCAAGTCGGCTTAACTCAGGCGTTA
orfD       TAACATTTC-GGTCAAGCCG-ACCCGCA------------------------------------TTC-----------------------------------------------TGCG-GTCGGCTTACCTCGCCCGTTA
blaVIM2    TAACATGAAGTTGCA-GCCG-ACCATCACTCCGC------------------------------TGC-------------------------------------GCTCCGTTCTGGCGGCTGAACTTCGGCGTTA
dfrB2      TAACAATTCGCTCCA-G-CGGACGGC--------------------------------------TTC-----------------------------------------------GCCGCCCGCTGAGCTTTATCGTTA
oxa7       TAACAATTCGCTGCAGGCGCGACGGCCC------------------------------------TGAC----------------------------------------GGGCCGCGGCCTGAGCTCAAACGGTTA
cmlA       TAACAAATCGCTGCA-GCCG-ACCCAAAACCGC-------------------------------TAC-----------------------------------------GCGGTTTCGGTCGGCTGAGCTCAGGCGTTA
cmlA2      TAACAAATCGCTGCA-GCCG-ACCCAAAACCGC-------------------------------TAC-----------------------------------------GCGGTTTCGGTCGGCTGAGCTCAAGCGTTA
cmlA4      TAACAAATCGCTGCA-GCCG-ACCCAAAACCGC-------------------------------TAC-----------------------------------------GCGGTTTCGGTCGGCTGAGCTCAGGCGTTA
dfrA14     TAACAAAGCTATGCAAT-CG-ACGGCAAAAAGCTTCGTTCGC----------------------TTC-------------------------------GCGCACTACGCT-TTTT-CCGC-GATTGATAGCGACGTTA
dfrA5      TAACAAAGCTATGCAATTG--ACGGTAAAAAGCTTCGTTCGC----------------------TTC-------------------------------GCTTGCTACGCT-TCTTACCGC-AATTGATAACGGCGTTA
blaP3      TAACAAAGCATTT-AAGAGGGACAGCCAACGCGTGGCACTTTTATTAT-------------GCGTTGGTTTTT----GTGGTTACGGTGTTATGCGGTAAGTTGGTAGTAGCGTTGGCTGCCCCTTAAT-GCGGCGTTA
VCR2/1     TAACAAAC-GCCTCAAGAGGGACTGTCAACGCGTGGCGTTTCCAGTCCCATTGAGCCGCGGTGGTTGCTGTTG-----------TTGTGTT-TGAGTTTAG-TGGTAGT-GCGTTGTCAGCCCCTTAGG-CGGGCGTTA
blaVIM1    TAACAAATCGTTGGAGC-GGGACTTTTGCTACGCAGGC--------------------------TGC-------------------------------------GCCTACTCCGCAAAAGCCCCTCAACTCAGGCGTTA
```

R” L” L’ R’

- **Figure S1** -
Sequence alignment of the top strand of various attC sites. The inverted repeats L‘, L‘‘, R’ and R‘’ are boxed