Table S1. Primers targeting the regions containing the predicted SNPs designed based on the reference genome of *Escherichia coli* CVM N37067PS.

No.	Target mutation	Sequence 5’-3’	Amplicon size (bp)
SNP1	A530T	F-CCTTGTGCCAGGTAAGTACAGAG R-ATTATCCCTGGCGGCGTTAG	439
SNP2	G664A	F-AAAGTATGGCGAACCGACGC R-TATCTTCCAGGCGTTGCTCCAG	416
SNP3	T364G	F-ACACAGGAGCATCTCGATCG R-AGTTGCCGCGTTGGTGTTG	332
SNP4	A208G	F-TTTATCGACGATGCGATTGAAGC R-GCGGTTCCCAGCAAATTGTG	302
SNP5	T575A	F-ACAGCCAGGTGATACGTCCAC R-ATTTGCACCTGCTGCATCGC	416
SNP6	A248T	F-TTCATTCAGCCACTCGCTCAATG R-TGGCATTTGCCGCTTGACG	387
SNP7	G53T	F-AAACTTCAATGCCACCGGCG R-GTTGAGATGGCCGATCCGATG	402
SNP8	G241T	F-ATGAGCGATATGGCAGAGCG R-TTTCGGCTCCTGCAAAGTGC	436
SNP9	A1541G	F-CCTCATTGCCAACACTAAACAGG R-GCATGACAAATTCACTGCCCTC	357
SNP10	C739T	F-GTCAGGACACCGATGAAGACAG R-ACATAGCTTTCGCCAGCGG	343
SNP11	C605T	F-AACGCAGTACCTGCAACTGTAG R-TGCTGATTATGCGTCTGCTACC	410
SNP12	G374A	F-ACCGTAACATTTCTTGATCCAGC R-ACCGTTGAAATTCCAGTGTGC	397

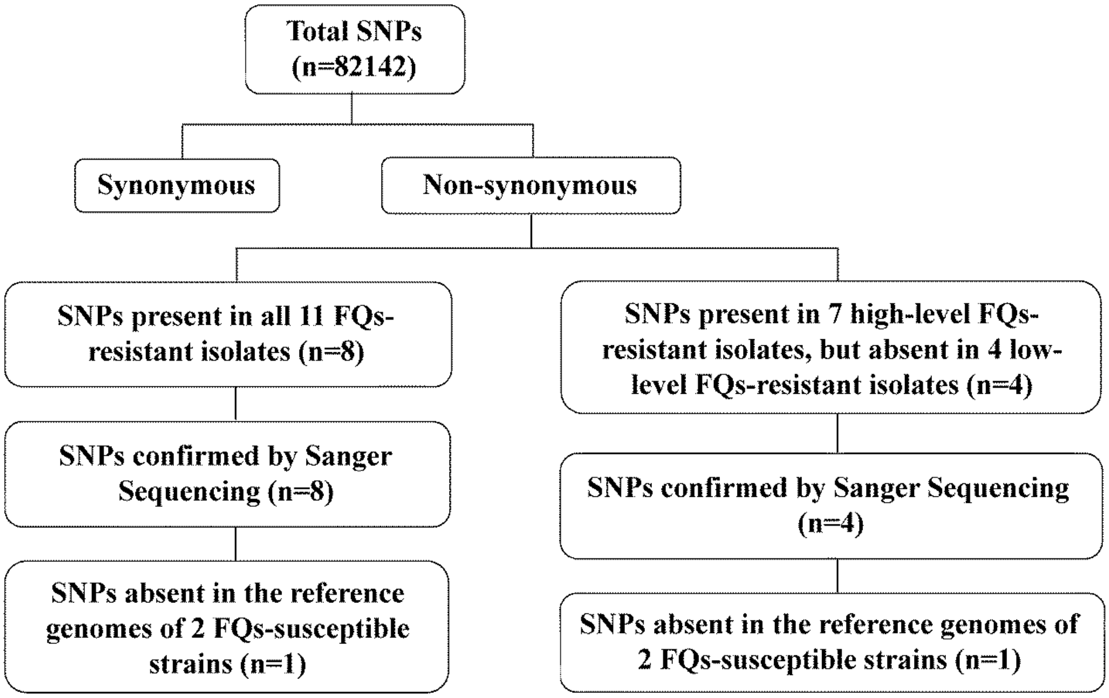

Fig. S1. Screening work flow of key SNPs.

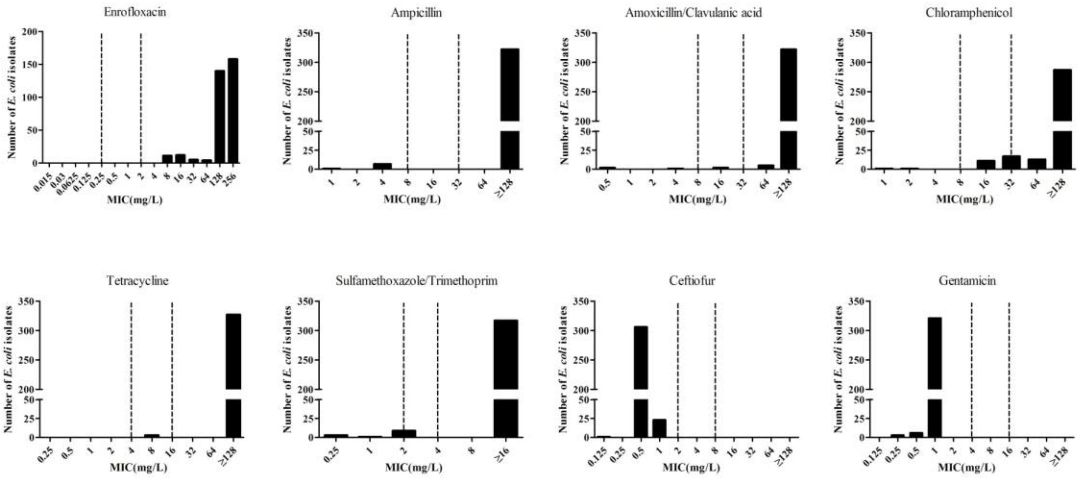

Fig. S2. MIC distributions of the *E. coli* isolates to enrofloxacin, amoxicillin/clavulanic acid, ampicillin, sulfamethoxazole/trimethoprim, gentamicin, tetracycline, chloramphenicol and ceftiofur. The dashed lines indicated the susceptible and resistant breakpoints.