**Table S2 Resistant gene primers used in this study**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Target  Gene | Sequence(5’ -3’) | Amplicon length (bp) | Annealing Temperature (℃) | Reference |
| 16s rRNA | 27F: YMAGAGTTTGATYMTGGCTCAG  1492R: TACCTTGTTACGACTT | 1492 | 50 | / |
| *blaNDM-1* | F: GGTTTGGCGATCTGGTTTTC  R: CGGAATGGCTCATCACGATC | 621 | 56 | 1 |
| *blaKPC* | F: GTATCGCCGTCTAGTTCTGC  R: GGTCGTGTTTCCCTTTAGCC | 638 | 56 | 2 |
| *blaSME* | F: GAGGAAGACTTTGATGGGAGGAT  R: TCCCCTCAGGACCGCCAAG | 334 | 52 | 3 |
| *blaIMP* | F: GGAATAGAGTGGCTTAAYTCTC  R: uAAAACAACCACC | 232 | 56 | 4 |
| *blaOXA-23* | F: GATCGGATTGGAGAACCAGA  R: ATTTCTGACCGCATTTCCAT | 501 | 56 | 5 |
| *blaCTX-M* | F: ATGTGCAGYACCAGTAARGT  R: TGGGTRAARTARGTSACCAGA | 593 | 52 | 6 |
| *blaTEM* | F: CATTTCCGTGTCGCCCTTATTC  R: CGTTCATCCATAGTTGCCTGAC | 800 | 52 | 7 |
| *blaSHV* | F: AGCCGCTTGAGCAAATTAAAC  R: ATCCCGCAGATAAATCACCAC | 713 | 52 |
| *blaOXA-1 group* | F: GGCACCAGATTCAACTTTCAAG  R: GACCCCAAGTTTCCTGTAAGTG | 564 | 52 |
| *qnrA* | F:CAGCAAGAGGATTTCTCACG  R:AATCCGGCAGCACTATTACTC | 630 | 57 | 8 |
| *qnrB* | F:GGCTGTCAGTTCTATGATCG  R:SAKCAACGATGCCTGGTAG | 488 | 57 |
| *qnrC* | F:GCAGAATTCAGGGGTGTGAT  R:AACTGCTCCAAAAGCTGCTC | 118 | 57 |
| *qnrD* | F:CGAGATCAATTTACGGGGAATA  R:AACAAGCTGAAGCGCCTG | 581 | 57 |
| *qnrS* | F:GCAAGTTCATTGAACAGGGT  R:TCTAAACCGTCGAGTTCGGCG | 428 | 57 |
| *qnrVC* | F:GGATAAAACAGACCAGTTATATGTACAAG  R:AGATTTGCGCCAATCCATCTATT | 444 | 57 |
| *oqxAB* | F:CCGCACCGATAAATTAGTCC  R:GGCGAGGTTTTGATAGTGGA | 313 | 57 |
| *qeqA* | F:GCAGGTCCAGCAGCGGGTAG  R:CTTCCTGCCCGAGTATCGTG | 218 | 57 |
| *mph(A)* | F:GTGAGGAGGAGCTTCGCGAG  R:TGCCGCAGGACTCGGAGGTC | 403 | 56 | 9 |
| *mph(B)* | F:GATATTAAACAAGTAATCAGAATAG  R:GCTCTTACTGCATCCATACG | 494 | 56 |
| *mph(D)* | F:AGCCAATTGCTACATGCGCTCT  R:GGGTTTACGAGCCAAGCAAGAA | 756 | 56 |
| *mph(E)* | F:ATGCCCAGCATATAAATCGC  R:ATATGGACAAAGATAGCCCG | 271 | 56 |
| *erm(A)* | F:TCTAAAAAGCATGTAAAAGAAA  R:CGATACTTTTTGTAGTCCTTC | 533 | 56 |
| *erm(B)* | F:GAAAAAGTACTCAACCAAATA  R:AATTTAAGTACCGTTACT | 639 | 45 |
| *erm(C)* | F:TCAAAACATAATATAGATAAA  R:GCTAATATTGTTTAAATCGTCAAT | 642 | 45 |
| *tetA* | F:GCTACATCCTGCTTGCCTTC  R:CATAGATCGCCGTGAAGAGG | 210 | 50 | 10 |
| *tetB* | F:TTGGTTAGGGGCAAGTTTTG  R:GTAATGGGCCAATAACACCG | 659 | 50 |
| *tetC* | F:CTTGAGAGCCTTCAACCCAG  R:ATGGTCGTCATCTACCTGCC | 418 | 49 |
| *tetD* | F:AAACCATTACGGCATTCTGC  R:GACCGGATACACCATCCATC | 787 | 48 |
| *catA1* | F:GGGTGAGTTTCACCAGTTTTGATT  R: CACCTTGTCGCCTTGCGTATA | 952 | 52 | 11 |
| *catA2* | F: GCACTCGATGCCTTCCAAAA  R: AGAGCCGATCCAAACGTCAT | 482 | 56 |
| *catA3* | F:AGGAAGCATCGGAACGTTGA  R:ACAGACCGAGCACGACTGTTG | 358 | 52 |
| *floR* | F:ATTGTCTTCACGGTGTCCGTTA  R:CCGCGATGTCGTCGAACT | 962 | 52 |
| *cmlA* | F:TAGGAAGCATCGGAACGTTGAT  R:CAGACCGAGCACGACTGTTG | 665 | 56 |
| *fosA3* | F:ATTCCCCACATGCAGCTCCAGCTTATGGCC  R:AAACGCCCCCTCAGGAAAGCGACTATACCC | 182 | 53 | 12 |
| *fosB* | F:TCACTGTAACTAATGAAGCATTAGACCAT  R:CCATCTGGATCTGTAAAGTAAAGAGATC | 271 | 60 |
| *fosX* | F:GATTAAGCCATATCACTTTAATTGTGAAAG  R:TCTCCTTCCATAATGCAAATCCA | 217 | 50 |
| *aphA6* | F: ATACAGAGACCACCATACAGT  R: GGACAATCAATAATAGCAAT | 235 | 55 | 13 |
| *aacC* | F:CGTCACTTATTCGATGCCCTTAC  R:GTCGGGCGCGGCATA | 465 | 57 |
| *aadA2* | F:ACGGCTCCGCAGTGGAT  R:GGCCACAGTAACCAACAAATCA | 265 | 56 |
| *aac(6')-Ib-cr* | F:TTGGAAGCGGGGACGGAM  R:ACACGGCTGGACCATA | 260 | 57 |
| *sul1* | F:TCATCTGCCAAACTCGTCGTTA  R:GTCAAAGAACGCCGCAATGT | 105 | 56 | 14 |
| *sul2* | F:CAGCGCTATGCGCTCAAG  R:ATCCCGCTGCGCTGAGT | 129 | 56 |
| *folp1* | F:CAGGCTCGTAAATTGATAGCAGAAG  R:CTTTCCTTGCGAATCGCTTT | 140 | 55 |
| *folp2* | F:GCGATTCGCAAGGAAAGTGA  R:CACATGGGCCATTTTTTCATC | 138 | 54 |
| *folp3* | F:CACGGCTTCGGCTCATGT  R:TGCCATCCTGTGACTAGCTACGT | 288 | 58 |
| *mcr-1* | F:CGGTCAGTCCGTTTGTTC  R:CTTGGTCGGTCTGTAGGG | 309 | 56 | 15 |
| *mcr-2* | F:TGTTGCTTGTGCCGATTGGA  R:CAGCAACCAACAATACCATCT | 567 | 60 | 16 |
| *mcr-3* | F:AGTTTGGTTTCGCCATTTCATTAC  R:ATATCACTGCGTGGACAGTCAGG | 1084 | 58 |
| *mcr-4* | F:TTACAGCCAGAATCATTATCA  R:ATTGGGATAGTCGCCTTTTT | 488 | 58 |
| *intI1* | F:GGCTTCGTGATGCCTGCTT  R:CATTCCTGGCCGTGGTTCT | 149 |  | 17 |
| *intI2* | intI2L:CACGGATATGCGACAAAAAGGT  Int2R:GTAGCAAACGAGTGACGAAATG | 789 |  | 18 |
| *intI3* | int3L:GCCTCCGGCAGCGACTTTCAG  Int3R:ACGGATCTGCCAAACCTGACT | 980 |  |
| Cassette arrays in class 1 integrons | hep58:TCATGGCTTGTTATGACTGT  hep59:GTAGGGCTTATTATGCACGC | class 1 integron variable region |  | 19 |
| Cassette arrays in class 2 integrons | hep51: GATGCCATCGCAAGTACGAG  hep74: CGGGATCCCGGACGGCATGCACGATTTGTA | class 2 integron variable region |  |

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