**Supplementary Table 1.** List of primers used in this study

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Target gene** | **Primer name** | **Sequence (5’ 🡪 3’)** | **Product size (bp)** | **Reference** |
| **ESBL primers** | *blaCTX-M-1* | M13-upper | GGTTAAAAAATCACTGCGTC | 866 | (36) |
| M13-lower | TTGGTGACGATTTTAGCCGC |
| *blaCTX-M-2* | M25-upper | ATGATGACTCAGAGCATTCG | 866 |
| M25-lower | TGGGTT ACGATTTTCGCCGC |
| *blaCTX-M-8* | CTXM8 -F | TCGCGTTAAGCGGATGATGC | 688 | (37) |
| CTXM8-R | AACCCACGATGTGGGTAGC |
| *blaCTX-M-9* | M9-upper | ATGGTGACAAAGAGAGTGCA | 870 | (36) |
| M9-lower | CCCTTCGGCGATGATTCTC |
| *blaCTX-M-15* | CTX-M-15-SF | CACACGTGGAATTTAGGGACT | 996 | (38) |
| CTX-M-15-SR | GCCGTCTAAGGCGATAAACA |
| *blaCTX-M-25* | CTX-M-25-F | CACACGAATTGAATGTTCAG | 924 | (39) |
| CTX-M-25-R | TCACTCCACATGGTGAGT |
| *blaSHV* | SHV-F | CACTCAAGGATGTATTGTG | 885 | (41)  |
| SHV-R | TTAGCGTTGCCAGTGCTCG |
| *blaTEM* | TEM-F | TCGGGGAAATGTGCGCG | 850 | (40) |
| TEM-R | TGCTTAATCAGTGAGGACCC |
| **Intestinal pathogenic primers** | *estA* | ST-F | GCTAAACCAGTAGAGGTCTTCAAAA | 147 | (99) |
| ST-R | CCCGGTACAGAGCAGGATTACAACA |
| *eltB* | LT-F | CACACGGAGCTCCTCAGT C | 508 | (40) |
| LT-R | CCCCCAGCCTAGCTTAGTTT |
| *bfpA* | bfpA-F | GGAAGTCAAATTCATGGGGG | 300 | (40) |
| bfpA-R | GGAATCAGACGCAGACTGGT |
| *eae* | eae-F | CCCGAATTCGGCACAAGCATAAGC | 881 | (100) |
| eae-R | CCCGGATCCGTCTCGCCAGTATTCG |
| *aaiC* | aaiC-F | ATTGTCCTCAGGCATTTCAC | 215 | (40) |
| aaiC-R | ACGACACCCCTGATAAACAA |
| *aat* | pcvd432-F | CTGGCGAAAGACTGTATCAT | 650 | (101) |
| pcvd432-R | CAATGTATAGAAATCCGCTGTT |
| *iaa* | ial upper | CTGGATGGTATGGTGAGG | 320 | (102) |
| ial lower | GGAGGCCAACAATTATTTCC |
| *ipaH* | Shig-1 | TGGAAAAACTCAGTGCCTCT | 424 | (103) |
| Shig-2 | CCAGTCCGTAAATTCATTCT |
| *stx1* | stx1F | CACAATCAGGCGTCGCCAGCGCACTTGCT | 606 | (48) |
| stx1R | TGTTGCAGGGATCAGTGGTACGGGGATGC |
| *stx2* | stx2F | CCACATCGGTGTCTGTTATTAACCACACC | 372 | (47) |
| stx2R | GCAGAACTGCTCTGGATGCATCTCTGGTC |
| **ExPEC primers** | *focG* | focG\_106F | CGTACCTGTACCATTGGTAATGGAGG | 366 | (51) |
| focG\_471R | TGAATTAATACTTCCCGCACCAGC |
| *kpsMII* | kpsMII\_121F | GCGCATTTGCTGATACTGTTG | 452 |
| kpsMII\_572 | GGGAACATGATGCAGGAGATG |
| *papA* | papA\_67F | ATGGCAGTGGTGTCTTTTGGTG | 717 |
| papA\_+202R | CGTCCCACCATACGTGCTCTTC |
| *sfaS* | sfaS\_210F | GTCTCTCACCGGATGCCAGAATAT | 138 |
| sfaS\_347R | GCATTACTTCCATCCCTGTCCTG |
| *afa* | afa F | GGCAGAGGGCCGGCAACAGGC | 594 |
| afa R | CCCGTAACGCGCCAGCATCTC |
| *hlyD* | hlyD\_92F | CTCCGGTACGTGAAAAGGAC | 904 |
| hlyD\_995R | GCCCTGATTACTGAAGCCTG |
| *iutA* | iutA\_674F | ATCGGCTGGACATCATGGGAAC | 314 |
| iutA\_987R | CGCATTTACCGTCGGGAACGG |