**Table S1 PCR detection of carbapenemase and extended-spectrum ß-lactamase (ESBL) genes**

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| --- | --- |
| **ß-lactamase** | **PCR detection** |
| **Ambler****class** | **Type** | **Subtype** | **Gene** | **Primers** | **AL** | **AT** | **Reference** |
| **Carbapenemases** |
| A | GES | GES-2, GES-4 to GES-6, GES-11, GES-14, GES-18 | *bla*GES | GES-F: GCTTCATTCACGCACTATTGES-R: CGATGCTAGAAACCGCTC | 323 | 52 | [[1](#_ENREF_1)] |
| KPC | KPC-1 to KPC-15 | *bla*KPC | KPC-F: GTATCGCCGTCTAGTTCTGCKPC-R: GGTCGTGTTTCCCTTTAGCC | 638 | 56 | [[1](#_ENREF_1)] |
| SME | SME-1 to SME-3 | *bla*SME | SME-F1: GAGGAAGACTTTGATGGGAGGATSME-R1: TCCCCTCAGGACCGCCAAG | 334 | 52 | [[1](#_ENREF_1)] |
| IMI(NMC-A) | IMI-1 to IMI-3 | *bla*IMI | IMI-F: TGCGGTCGATTGGAGATAAAIMI-R: CGATTCTTGAAGCTTCTGCG | 399 | 52 | [[1](#_ENREF_1)] |
| BIC | BIC-1 | *bla*BIC | BIC-F: TATGCAGCTCCTTTAAGGGCBIC-R: TCATTGGCGGTGCCGTACAC | 537 | 52 | [[2](#_ENREF_2)] |
| B1 | IMP | IMP-1 to IMP-44 | *bla*IMP | IMP-F: GGAATAGAGTGGCTTAAYTCTCIMP-R: GGTTTAAYAAAACAACCACC | 232 | 56 | [[2](#_ENREF_2)] |
| VIM | VIM-1 to VIM-37 | *bla*VIM | VIM-F: GATGGTGTTTGGTCGCATAVIM-R: CGAATGCGCAGCACCAG | 390 | 52 | [[2](#_ENREF_2)] |
| NDM | NDM-1 to NDM-8 | *bla*NDM | NDM-F: GGTTTGGCGATCTGGTTTTCNDM-R: CGGAATGGCTCATCACGATC | 621 | 56 | [[2](#_ENREF_2)] |
| TMB | TMB-1 to TMB-2 | *bla*TMB | TMB-F: CAAGGAGCTCATTCAAAGGTMB-R: TTCTAGCGGATTGTGGCCAC |  | 52 | [[3](#_ENREF_3)] |
| FIM | FIM-1 | *bla*FIM | FIM-F: GAAGCACATGGAAAACTGGGFIM-R: GATGGGCGAATGAGACAGC |  | 52 | [[4](#_ENREF_4)] |
| SPM | SPM-1 | *bla*SPM | SPM-F: AAAATCTGGGTACGCAAACGSPM-R: ACATTATCCGCTGGAACAGG | 271 | 52 | [[2](#_ENREF_2)] |
| DIM | DIM-1 | *bla*DIM | DIM-F: GCTTGTCTTCGCTTGCTAACGDIM-R: CGTTCGGCTGGATTGATTTG | 699 | 52 | [[2](#_ENREF_2)] |
| GIM | GIM-1 | *bla*GIM | GIM-F: TCGACACACCTTGGTCTGAAGIM-R: AACTTCCAACTTTGCCATGC | 477 | 52 | [[2](#_ENREF_2)] |
| SIM | SIM-1 | *bla*SIM | SIM-F: TACAAGGGATTCGGCATCGSIM-R: TAATGGCCTGTTCCCATGTG | 570 | 52 | [[2](#_ENREF_2)] |
| B3 | AIM | AIM-1 | *bla*AIM | AIM-F: CTGAAGGTGTACGGAAACACAIM-R: GTTCGGCCACCTCGAATTG | 322 | 52 | [[2](#_ENREF_2)] |
| SMB | SMB-1 | *bla*SMB | SMB-F: CAGCAGCCATTCACCATCTASMB-R: GAAGACCACGTCCTTGCACT | 492 | 52 | [[5](#_ENREF_5)] |
| D | OXA | OXA-23-like | *bla*OXA-23-like | OXA-23-F: GATCGGATTGGAGAACCAGAOXA-23-R: ATTTCTGACCGCATTTCCAT | 501 | 56 | [[6](#_ENREF_6)] |
| OXA-24-like | *bla*OXA-24-like | OXA-24-F: GGTTAGTTGGCCCCCTTAAAOXA-24-R: AGTTGAGCGAAAAGGGGATT | 246 | 52 | [[6](#_ENREF_6)] |
| OXA-48-like | *bla*OXA-48-like | OXA-48-F: TTGGTGGCATCGATTATCGGOXA-48-R: GAGCACTTCTTTTGTGATGGC | 744 | 52 | [[7](#_ENREF_7)] |
| OXA-58-like | *bla*OXA-58-like | OXA-58-F: AAGTATTGGGGCTTGTGCTGOXA-58-R: CCCCTCTGCGCTCTACATAC | 599 | 56 | [[6](#_ENREF_6)] |
| OXA-143-like | *bla*OXA-143-like | OXA-143-F: TGGCACTTTCAGCAGTTCCTOXA-143-R: TAATCTTGAGGGGGCCAACC | 149 | 52 | [[8](#_ENREF_8)] |
| OXA-235-like | *bla*OXA-235-like | OXA-235-F: TTGTTGCCTTTACTTAGTTGCOXA-235-R: CAAAATTTTAAGACGGATCG | 768 | 52 | [[9](#_ENREF_9)] |
| OXA-114 | *bla*OXA-114 | OXA-114-F: CGCATCCTGTTCCAGCAOXA-114-R: GTGCCGGTCTTGCCATAC | 509 | 52 | [[10](#_ENREF_10)] |
| **ESBLs** |
| A | CTX-M | CTX-M universal | *bla*CTX-M universal | CTX-M-UF: ATGTGCAGYACCAGTAARGTCTX-M-UR: TGGGTRAARTARGTSACCAGA | 593 | 52 | [[11](#_ENREF_11)] |
| CTX-M-1 group | *bla*CTX-M-1 group | CTX-M-1GF: AAAAATCACTGCGCCAGTTCCTX-M-1GR: AGCTTATTCATCGCCACGTT | 415 | 52 | [[12](#_ENREF_12)] |
| CTX-M-2 group | *bla*CTX-M-2 group | CTX-M-2GF: CGACGCTACCCCTGCTATTCTX-M-2GR: CCAGCGTCAGATTTTTCAGG | 552 | 52 | [[12](#_ENREF_12)] |
| CTX-M-8 group | *bla*CTX-M-8 group | CTX-M-8GF: TCGCGTTAAGCGGATGATGCCTX-M-8GR: AACCCACGATGTGGGTAGC | 666 | 52 | [[12](#_ENREF_12)] |
| CTX-M-9 group | *bla*CTX-M-9 group | CTX-M-9GF: ATGGTGACAAAGAGAGTGCACTX-M-9GR: CCCTTCGGCGATGATTCTC | 869 | 52 | [[13](#_ENREF_13)] |
| CTX-M-25 group | *bla*CTX-M-25 group | CTX-M-25GF: GCACGATGACATTCGGGCTX-M-25GR: AACCCACGATGTGGGTAGC | 327 | 52 | [[12](#_ENREF_12)] |
| TEM |  | *bla*TEM | TEM-F: CATTTCCGTGTCGCCCTTATTCTEM-R: CGTTCATCCATAGTTGCCTGAC | 800 | 52 | [[14](#_ENREF_14)] |
| SHV |  | *bla*SHV | SHV-F: AGCCGCTTGAGCAAATTAAACSHV-R: ATCCCGCAGATAAATCACCAC | 713 | 52 | [[14](#_ENREF_14)] |
| GES |  | *bla*GES | GES-ESBL-F: AGTCGGCTAGACCGGAAAGGES-ESBL-R: TTTGTCCGTGCTCAGGAT | 399 | 52 | [[14](#_ENREF_14)] |
| PER |  | *bla*PER | PER-F: GCTCCGATAATGAAAGCGTPER-R: TTCGGCTTGACTCGGCTGA | 520 | 52 | [[14](#_ENREF_14)] |
| VEB |  | *bla*VEB | VEB-F: CATTTCCCGATGCAAAGCGTVEB-R: CGAAGTTTCTTTGGACTCTG | 648 | 52 | [[14](#_ENREF_14)] |
| D | OXA | OXA-1 group | *bla*OXA-1 group | OXA-1-F: GGCACCAGATTCAACTTTCAAGOXA-1-R: GACCCCAAGTTTCCTGTAAGTG | 564 | 52 | [[14](#_ENREF_14)] |
| OXA-2 group | *bla*OXA-2 group | OXA-2-F: GACCAAGATTTGCGATCAGCAATGCGOXA-2-R: CYTTGACCAAGCGCTGATGTTCYACC | 256 | 52 | [[14](#_ENREF_14)] |
| OXA-10 group | *bla*OXA-10 group | OXA-10-F: CGCCAGAGAAGTTGGCGAAGTAAGOXA-10-R: GAAACTCCACTTGATTAACTGCGG | 138 | 52 | [[14](#_ENREF_14)] |

AL: amplicon length (bp); AT: annealing temperature (°C)

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