**S 4 Table: Correlation between the genomic content of antibiotic resistance genes (ARG) and observed phenotypic resistance**

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| --- | --- | --- | --- |
| Antibiotics families  | Phenotypically resistant isolates n (%)  | Isolates carrying acquired ARG  n (%)  | Phenotypically susceptible isolates carrying ARG  n (%) |
| Carbapenems | 78 (100) | 73 (94) | 0 (0) |
| Monobactams  | 62 (79) | 62 (79) | 0 (0) |
| Aminoglycosides  | 24 (31) | 22 (28) | 1(1) |
| Sulfonamides/Trimethoprim | 73 (94) | 73 (94) | 2 (3) |
| Quinolones  | 77 (99) | 17 (22) | 1 (1) |
| Polymyxins  | 1 (1) | 1 (1) | 0 (0) |

 n= number of isolates %= Percentage

For carbapenems, the ARG considered to confer resistance to carbapenems were *bla*NDM-1, *bla*NDM-5, *bla*NDM-7, *bla*NDM,(variant not specified), *bla*OXA-181 and *bla*OXA-232. For monobactams, the ARG were *bla*CTX-M-15, *bla*CTX-M-139, and different *bla*CMY variants. For aminoglycosides (amikacin and gentamicin), aminoglycoside modifying enzymes (AME) – encoding genes such as *aac(3)-IIa* and 16S rRNA methylases such as a*rmA, rmtB1, and rmtF1* were detected. For sulfonamides/trimethoprim, the ARG were *sul* (dihydropteroate synthase) and *dfr* (dihydrofolate reductase). For quinolones, the ARG were *qnrS1, qepA4, qepA9, qnrB4*. For polymyxins, the gene was *mcr-1*.