**S5 Table. Antimicrobial resistance (AMR) phenotypes of *S.* Typhimurium isolates, and their corresponding AMR genotypes, as predicted based on their hybrid, MinION, and MiSeq assemblies.a**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Isolate | 45 | 46 | 53 | 56 | 90 | 101 | 106 | 113 |
| ARGs | *β*-lactam | Phenotype | AMPb |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AMC |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| EFT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CEP |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CRO |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| FOX |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *blaCMY* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaCMY-2* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaCTX-M* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaCTX-M-55* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaOXA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaOXA-1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaTEM* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *blaTEM-1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Phenicol | Phenotype | CHL |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *catA1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *catA2* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *catB3* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *cmlA1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *floR* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Phenicol/Quinolone | Genotype | *oqxA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *oqxB* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Quinolone | Phenotype | NAL |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| CIP |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| LVX |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| OFX |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *qepA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *qepA1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *qnrS* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *qnrS1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Aminoglycoside/Quinolone | Genotype | *aac(6')-Ib-cr* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(6')-Ib-cr5* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Aminoglycoside | Phenotype | AMK |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| GEN |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| KAN |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| STR |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *aac(3)-IV* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(3)-Iva* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(3)-II* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(3)-IIa* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(3)-IId* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aac(6')-Il* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aadA1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aadA2* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aadA22* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aph(3')-Ia* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aph(3'')-Ib*  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aph(3')-IIa* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aph(4)-Ia* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *aph(6)-Id* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *rmtB1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Tetracycline | Phenotype | TET |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *tet(A)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *tet(B)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *tet(M)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Sulfonamide | Phenotype | SUL |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *sul1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *sul2* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *sul3* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Trimethoprim | Phenotype | SXT |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *dfrA12* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Rifamycin | Genotype | *arr-3* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Colistin | Genotype | *mcr-3* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *mcr-3.1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Bleomycin | Genotype | *ble* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *bleO* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Macrolide | Genotype | *erm(B)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *erm(42)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *mph(A)* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Quaternary ammonium compound | Genotype | *qacE* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *qacEdelta1* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| *qacL* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Point mutations | Quinolone | Genotype | *gyrA* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Genotype | *parC* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Colistin | Genotype | *pmrB* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

aGreen, phenotypically positive; dark orange, genotypically positive as predicted based on the hybrid assemblies; cross, genotypically positive as predicted based on the MinION assemblies; light orange, genotypically positive as predicted based on the MiSeq assemblies.

bAMP, ampicillin; AMC, amoxicillin/clavulanic acid; EFT, ceftiofur; CEP, cefalexin; CRO, ceftriaxone; FOX, cefoxitin; CHL, chloramphenicol; NAL, nalidixic acid; CIP, ciprofloxacin; LVX, levofloxacin; OFX, ofloxacin; AMK, amikacin; GEN, gentamicin; KAN, kanamycin; STR, streptomycin; TET, tetracycline; SUL, sulfafurazole; SXT, trimethoprim/sulfamethoxazole.