### Table S1. Genes with most resistance to antimicrobials and hierarchical clustering.

| States | Antimicrobial-resistance genes |
|--------|--------------------------------|
| PA     | aadA, aph(3’’), aph(3’’)-Ib, aph(6)-I, aph(6)-Id, bla, blaCMY, sul2, tet, and tet(A) |
| NY     | aadA, aph(3’’), aph(3’’)-Ib, aph(6)-I, aph(6)-Id, blaCMY, blaCMY-2, blaTEM, blaTEM-1, bla, sul2, tet, and tet(A) |
| MD     | aadA, aph(3’’), aph(3’’)-Ib, aph(6)-I, aph(6)-Id, blaCMY, sul2, tet, and tet(A) |
| NM     | aadA, aph(3’’), aph(3’’)-Ib, aph(6)-I, aph(6)-Id, aac(3), aadA1, aph(3’’), aph(3’’)-Ia, blaCMY, and blaCMY-2, blaTEM, blaTEM-1, fos, fosA, qac, qacEdelta1, sul1, sul2, tet(A), and tet(B) |
| MN     | aadA, aadA1, aph(3’’), aph(3’’)-I, aph(3’’)-Ib, aph(6)-I, aph(6)-Id, bla, and blaCMY, blaCMY-2, blaTEM, blaTEM-1, fosA, sul2, tet, tet(A), and tet(B) |
| CA     | aadA, aph(3’’), aph(3’’)-Ib, aph(6)-I, aph(6)-Id, bla, fos, fosA, and qoxB |

### Table S2. Metabolic functions of the most common antimicrobial-resistance genes.

| Genes | Metabolic Functions |
|-------|---------------------|
| aadA  | • Aminoglycoside resistance  
|       | • Integration of the plastome-specific aadA cassette into the nuclear genome for a fraction of the resistant cell lines |
| aph(3’’) | • Aminoglycoside resistance  
|       | • Catalysis of the addition of phosphate from ATP to the 3’-hydroxyl group of a 4,6-disubstituted aminoglycoside |
| aph(3’’)-Ia | • Origination from enzymes from the metabolic pathway for aminoglycosides and development in order to counteract the toxic effects of these antibiotics in the host bacterial cell  
|       | • Transferase |
| aph(3’’)-Ib | • Aminoglycoside resistance  
|       | • A transposon-encoded aminoglycoside phosphotransferase |
|       | • Conference of resistance to kanamycin and neomycin |
| aph(6)-I | • Aminoglycoside resistance  
|       | • Catalysis of ATP-dependent phosphorylation of a hydroxyl group |
| aph(6)-Id | • Aminoglycoside phosphotransferase encoding by plasmids, transposons, integrative conjugative elements, and chromosomes in Enterobacteriaceae and Pseudomonas spp  
|       | • Phosphotransferase activity, alcohol group as an acceptor |
| bla   | • Hydrolysis of the beta-lactam bond in susceptible beta-lactam antibiotics, thus conferring resistance to penicillin and cephalosporin |
| Gene     | Description                                                                 |
|----------|-----------------------------------------------------------------------------|
| **blaCMY**<br>• Beta-lactamase<br>• Hydrolysis of the beta-lactam bond in susceptible beta-lactam antibiotics<br>• ampC-related bla gene | |
| **blaCMY-2**<br>• Hydrolysis of beta-lactam bond<br>• Beta-lactamase | |
| **blaTEM, blaTEM-1**<br>• Responsibility of amino acid substitutions for the extended-spectrum beta lactamase (ESBL) phenotype cluster around the active site of the enzyme and change its configuration, allowing access to oxyimino-beta-lactam substrates. | |
| **tet, tet(A), tet(B)**<br>• Tetracycline-resistant protein<br>• Active tetracycline efflux<br>• Decrease of the accumulation of the antibiotic in whole cells<br>• Metal-tetracycline/H+ antiporter | |
| **fos, fos(A)**<br>• Fosfomycin-resistant genes<br>• Inactivation of fosfomycin by addition of a glutathione residue | |
| **oqxB**<br>• Efflux pump membrane transporter<br>• Component of RND-type multidrug efflux pump that confers resistance to olaquindox | |
| **sul2**<br>• Dihydropteroate synthase activity<br>• High-affinity sulfate permease<br>• Sulfate transmembrane transporter activity | |