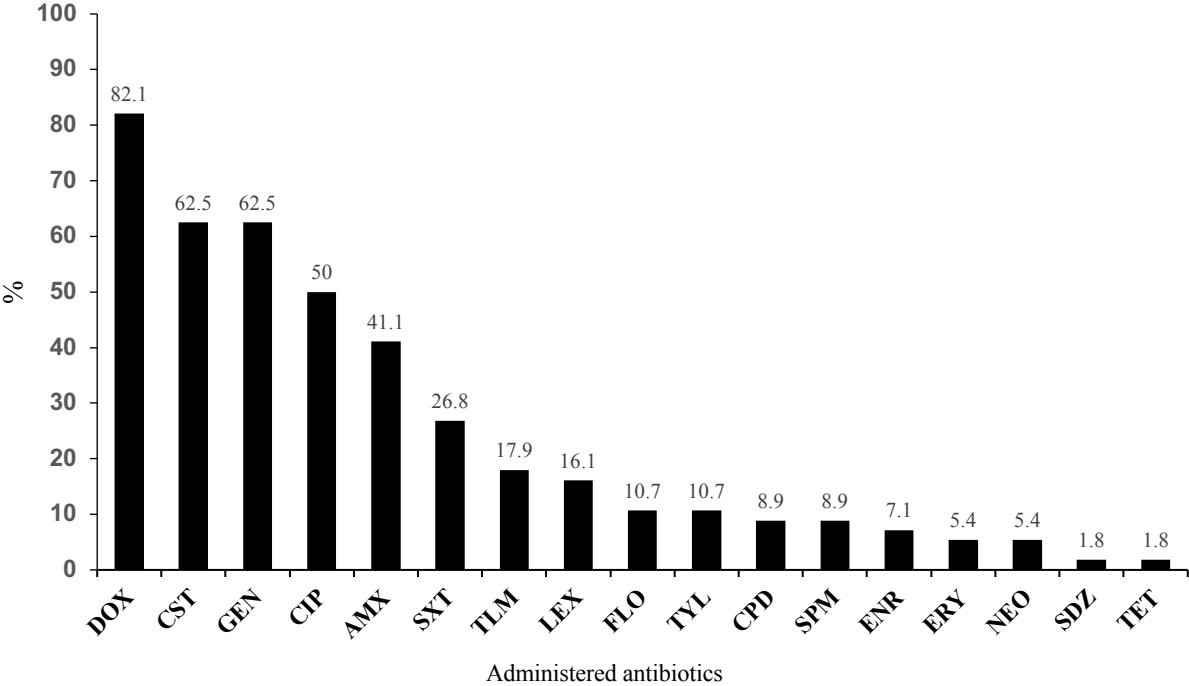
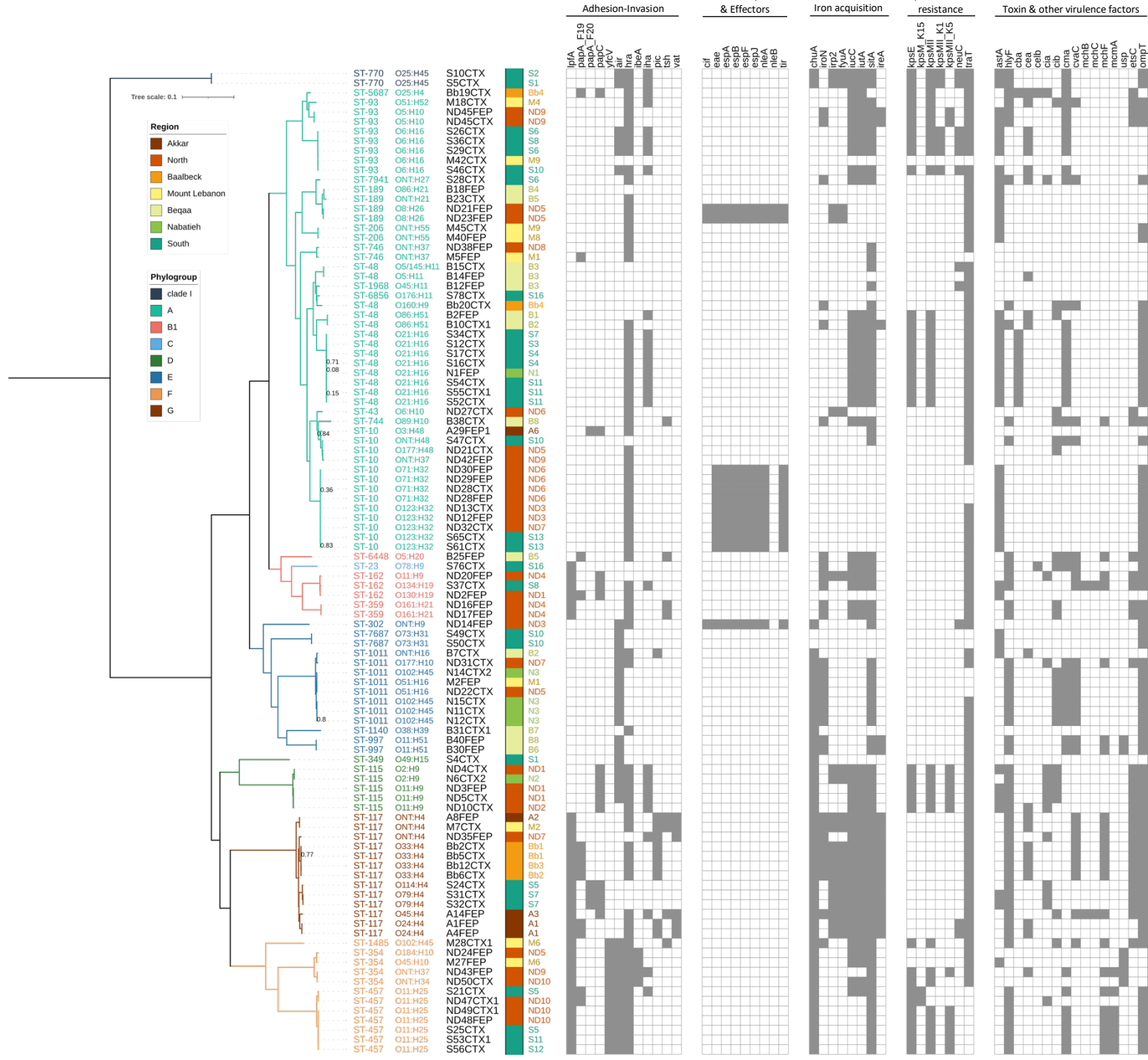


**Figure S1.** Proportion of broiler farms using each antibiotic.

DOX: Doxycycline, CST: Colistin, GEN: Gentamicin, CIP: Cirpofloxacin, AMX: Amoxicillin, SXT: Trimethoprim+Sulfamethoxazole, TLM: Tilmicosin, LEX: Cefalexin, FLO: Florfenicol, TYL: Tylosin, CPD: Cefpodoxime, SPM: Spyramicin, ENR: Enrofloxacin, ERY: Erythromycin, NEO: Neomycin, SDZ: Sulfadiazin, TET: Tetracycline.

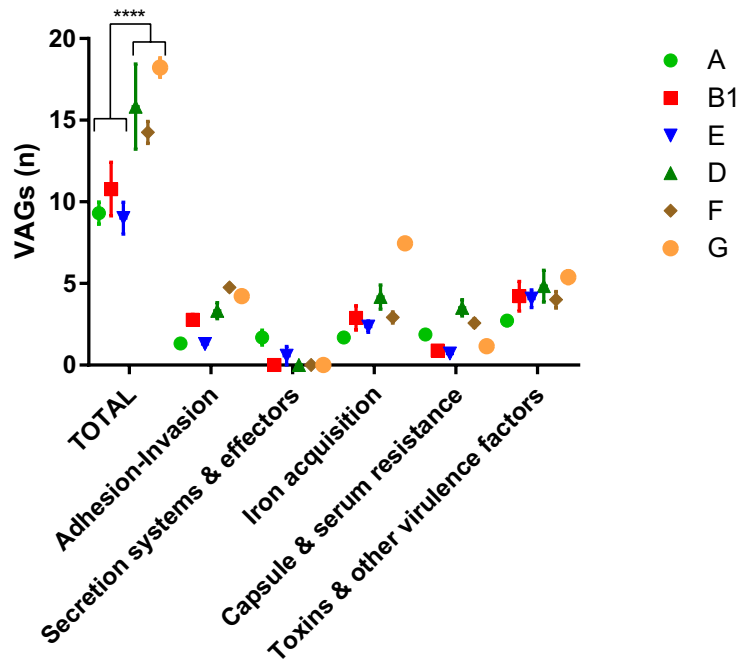


**Figure S2.** Phylogenetic relationships between the 102 sequenced ESC-resistant *E. coli* strains. The tree was inferred from the 176,818 SNPs present in genomic regions shared by all isolates. Local branching support values are based on the Shimodaira-Hasegawa test. Values of 1, indicating maximum support, are not displayed. The tree was rooted according to the known relationships between *E. coli* phylogroups. For each strain, the sequence type, serotype, identifier, region and farm of origin are indicated in columns 1-5 on the right side of the tree. Presence of virulence-associated genes detected using VirulenceFinder 2.0 are indicated with a filled box.



**Figure S3.** Virulence-associated genes by *E. coli* phylogroup (A) or main STs (B). Means and SD are represented (two-way ANOVA test, statistical significance is indicated as follow: \*\*\*\*,  $P < 0.0001$ ; \*\*\*,  $P < 0.001$ ).

A.



B.

