



CTX-M-1

CTX-M-25

CTX-M-2

CTX-M-9

**Figure S3 Phylogenetic assignment of CTX-M genes detected in ESBL isolates to main CTX-M groups based on partial amino acid sequence based phylogenetic analysis.** A Neighbor-joining tree was calculated in MEGA5 based on the evolutionary JTT matrix and 100 re-samplings (bootstrap analysis). A total of 183 amino acid sequences were included in the analysis including a total of 4 different CTX-M-gene types. The phylogenetic analysis based on 165 amino acid sequence positions. Bar: 0.01 substitutions per amino acid sequence position.