



Figure S4. Multilocus sequence based maximum-likelihood tree based on concatenated nucleotide sequences showing the phylogenetic variety of *E. coli* isolates. All isolated from output samples are marked in bolt. Sequence types, CTX-M-groups and phylogenetic *E. coli* assignments are given in brackets. ST types were determined using the *E. coli* MLST database (<http://mlst.warwick.ac.uk/mlst/dbs/Ecoli>). Bar: 0.001 Nucleotide substitutions per sequence positions.