Figure S1. A Maximum Likelihood tree based on core genome SNPs that combines the isolates used in the current (highlighted in red) and a previous study (Deng X et al. 2014. Genomics epidemiology of Salmonella enterica serotype Enteritidis based on population structure of prevalent lineages. Emerging infectious diseases 2014 Sep;20(9):1481-9). Previously sequenced isolates with the same PFGE patterns as some the of outbreak isolates analyzed in the current study were highlighted in blue. Braches leading to major lineages defined in the current and previous studies were thickened.