



Figure S1. Performance of different primer sets (PS) designed for PCR amplification of formerly-*Enterobacteriaceae* 16S rRNA genes. **A)** Number of 16S rRNA gene sequences recognized by each primer pair using the TestPrime 1.0 software at the SILVA Database. Gray dotted lines represent the total number of sequences of 1) *Enterobacteriaceae* ($n = 67,849$) and 2) *Enterobacteriales* ($n = 95,655$) in the SILVA database. NF: matches not found; Primer sets PS12 - PS16 were unable to match sequences from the SILVA database. Analysis of specificity/coverage for each primer pair at **B)** *Enterobacteriaceae* and **C)** *Enterobacteriales* level. **D)** OTU coverage analysis at the family level for each primer set. The seven families included in the analysis are listed in Figure 3. Because primer sets PS8 - PS16 covered <50% of the genera within each bacterial family, they were not included in panel D. A detailed description of the OUT coverage at the genus and family levels are depicted in **Table S4**.



Figure S2. Analysis of family and genus coverage of different primer sets (PS) targeting 16S rRNA genes. Heat map depicts sequence coverage for each taxon belonging to the *Enterobacteriales* order, using the TestPrime 1.0 software at the SILVA Database