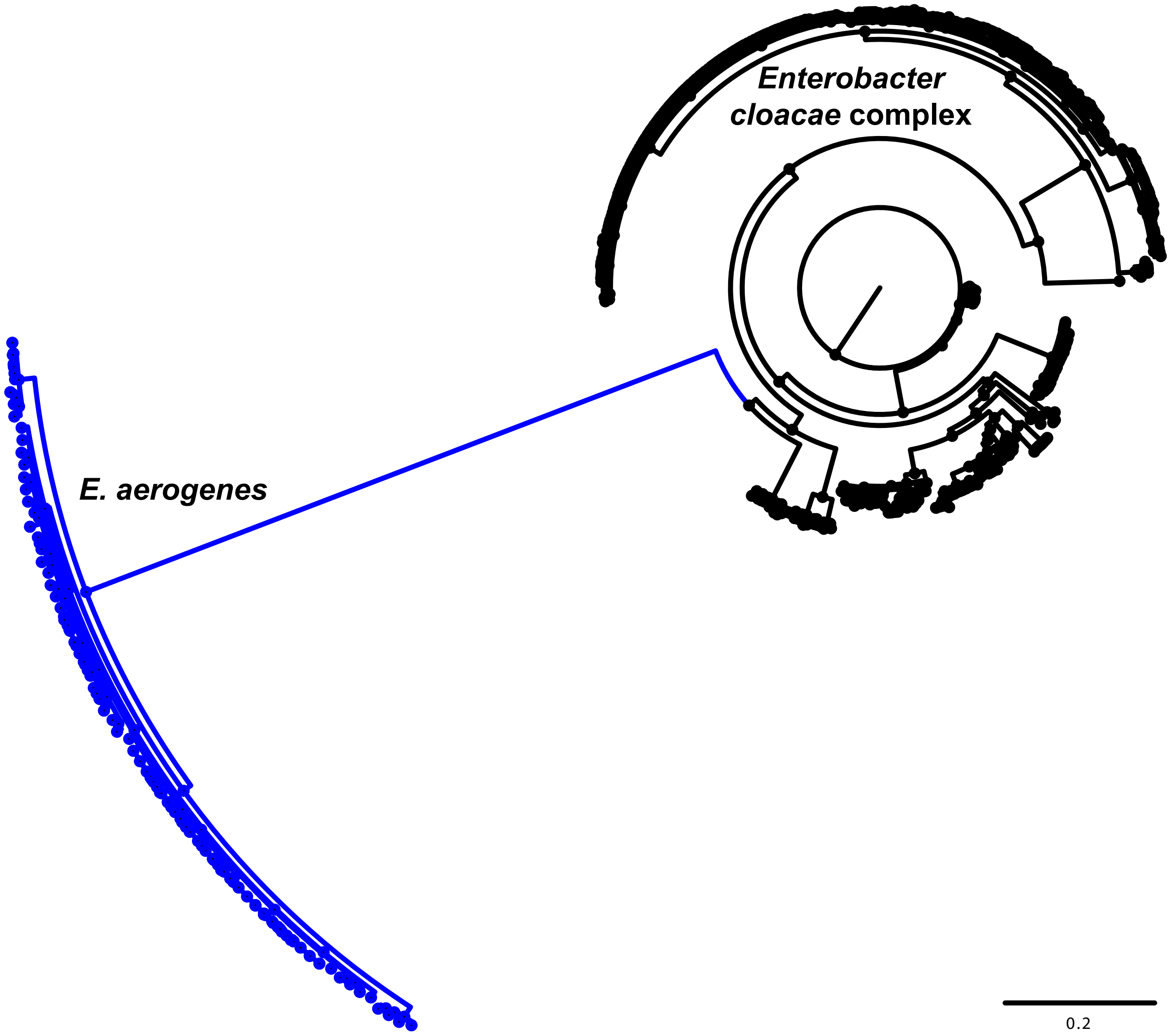

Figure S4. Phylogenetic SNP tree of *Enterobacter* genomes.
A whole genome core SNP tree was constructed for 447 *Enterobacter* spp. genomes using kSNP (30) and RaXML (31) (see Methods). The dendrogram was generated using FigTree v1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/). This dataset included genomes within the 379 *E. cloacae* complex (black) and 68 *E. aerogenes* (blue). The scale bar indicates the number of nucleotide substitutions.