



Supplementary Figure S2. Pangenome analysis. Genes were classified according to their presence in the 114 genomes analysed as: *Core* if present in $\geq 99\%$ of samples, *Soft-core* between 95 and 99%, *Shell* between 15 and 95% and *Cloud* at $<15\%$. Doughnut charts show the distribution fractions of core, shell, and cloud genes by ST, by CC and the total gene pool, with the total number of isolates of each group in the centre of the chart and the total number of genes below each chart.