**Figure S7**



**Distribution of orthologous virulent factors in GJ0703, CT18 and strain 14028S.** The Venn diagram shows the identified virulence factor relationship amongst strains GJ0703, 14028S and CT18. Virulence factors were characterized by using BLASTp against the VFDB database with cut-offs identities >75%. Based on this scenario *tcf*A-D was identified as shared genes for strain CT18 and absent in strain 14028S.