

**Supplementary data**

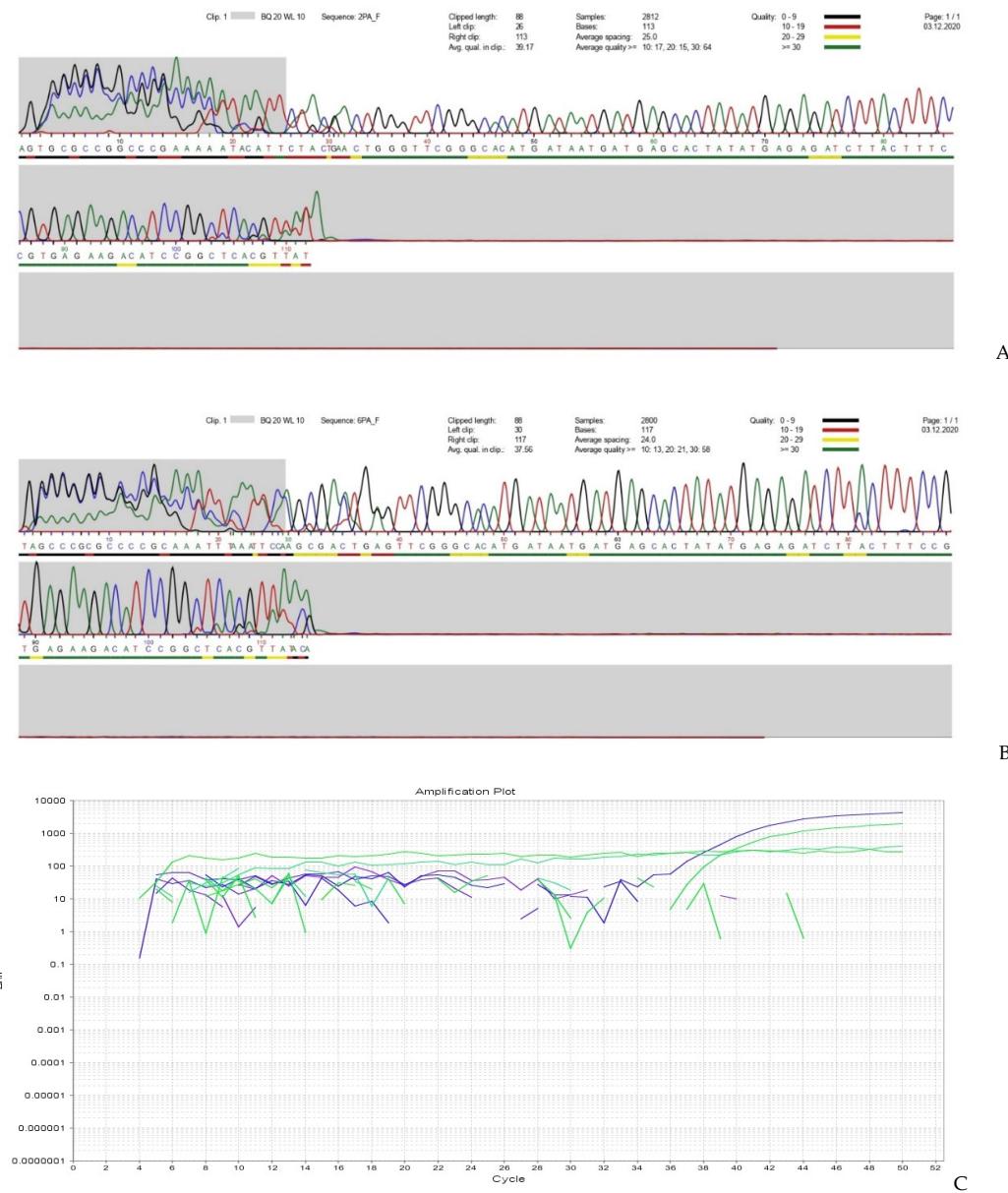


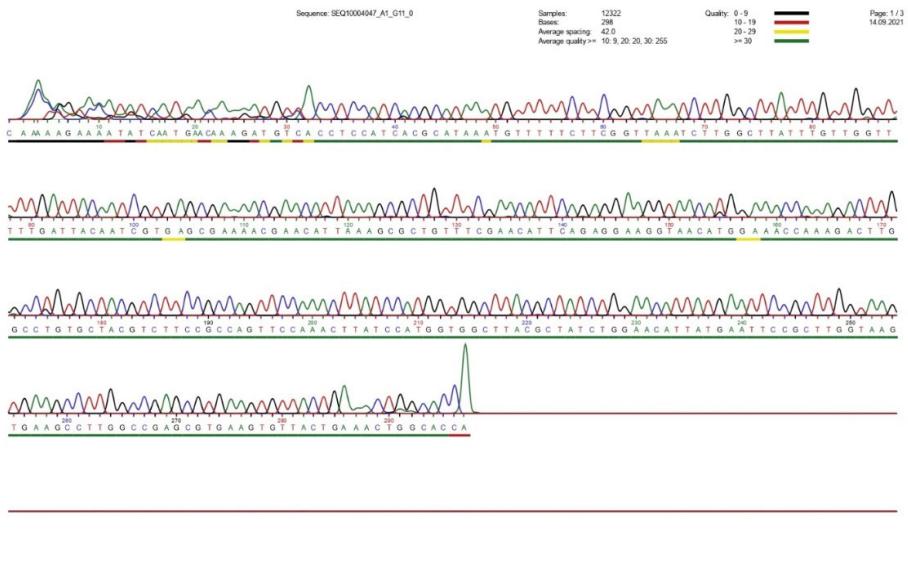
**Figure S1.**

Figure S1: Map of participating labs: 1: LB1 in Manfredonia (FG); 2,3: Detail of Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata in Foggia with locations of laboratories included in this project or discarded because potentially unsuitable caused high risk of cross contamination (Red star: Headquarters; Yellow spot: S.S. Ricerca e Sviluppo (LB2); DNA extraction; Blue spot: S.S. Virologia (LB3); DNA amplification; Black spot: Biotecnologia e Vaccini (this lab was discarded and it was not included in this project because it currently works on the molecular detection of Bioterrorism agents); 4: LB4, Vibrione Milano (Sequencing Center).

**Figure S2.**

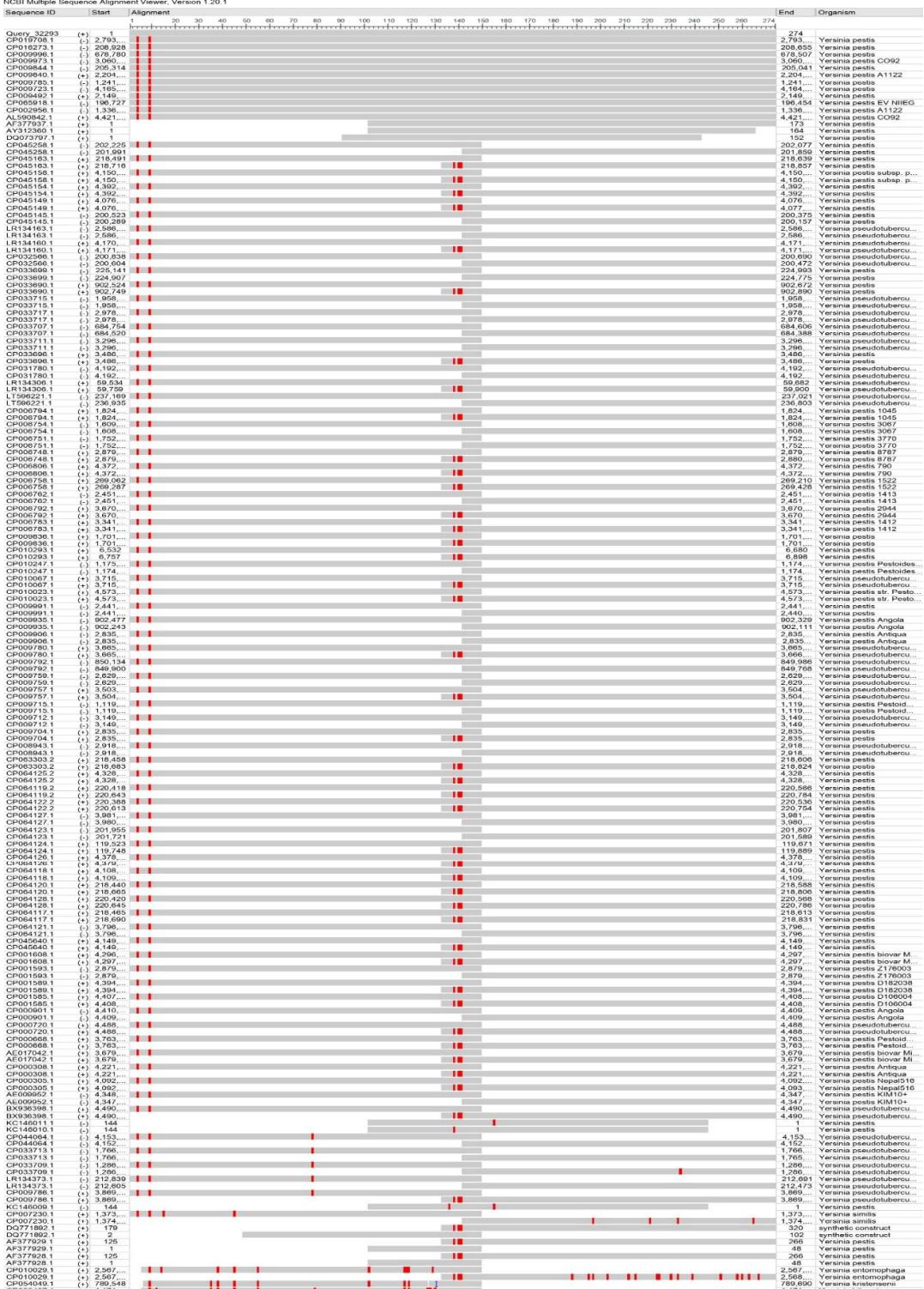
A four-colour chromatogram showing the results of Sanger sequencing of *pla* gene detected in T.6 (A) e T.2 (B); Amplification plot of *pla* gene of *Yersinia pestis* using a FAM-dye revelation running on the StepOne Realtime PCR instrument (Applied Biosystem, ThermoFischer scientific, MA, USA); Nucleotide chromatogram of *Y.pestis* *glpD* gene sequenced from T.6 (D) and sequence alignment (E).





D

## NCBI Multiple Sequence Alignment Viewer, Version 1.20.1



E