Fig S1. Histogram of the hit lengths (represented as its $\log_{10}$ here) when ancient contigs are aligned to the ancestral genome of *Yersinia pestis*. The bimodality of the distribution is explained by the enrichment in insertion sequences and small repetitions of the *Yersinias* genomes, producing a large number of small hits, and led to the threshold of $10^{2.5}$ to exclude such hits.