Supplemental Information for

Neolithic *Yersinia pestis* infections in humans and a dog

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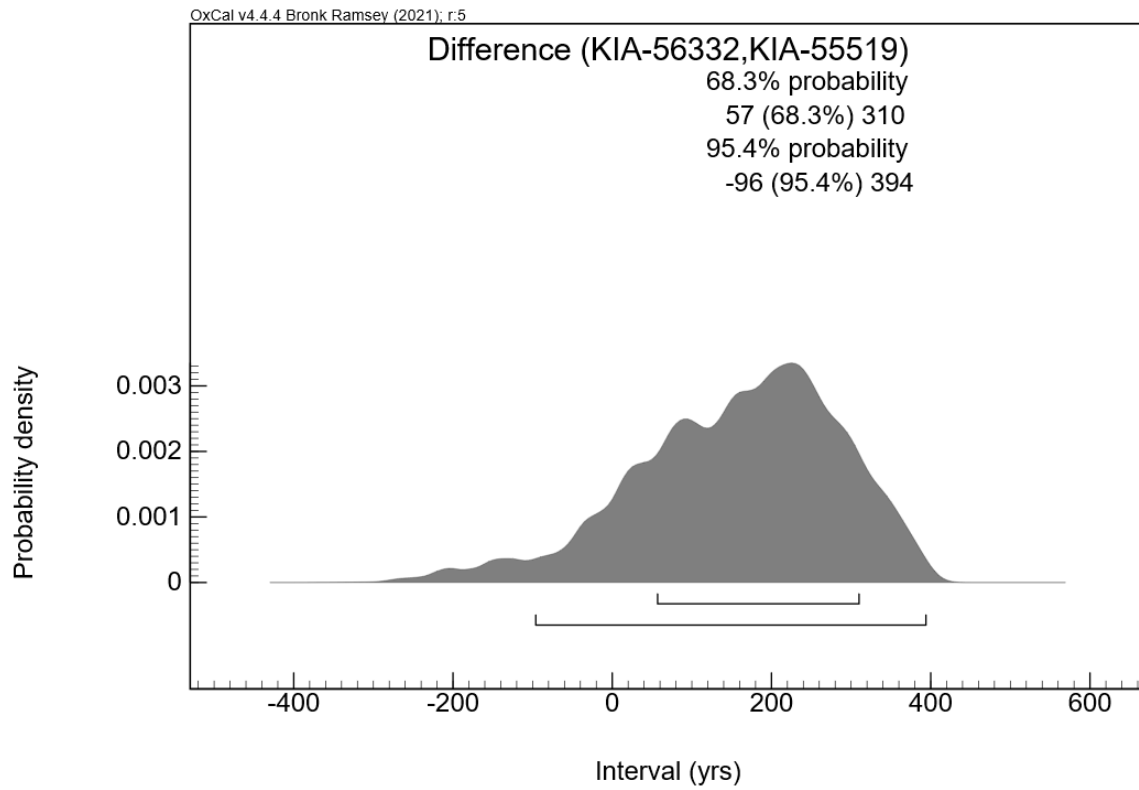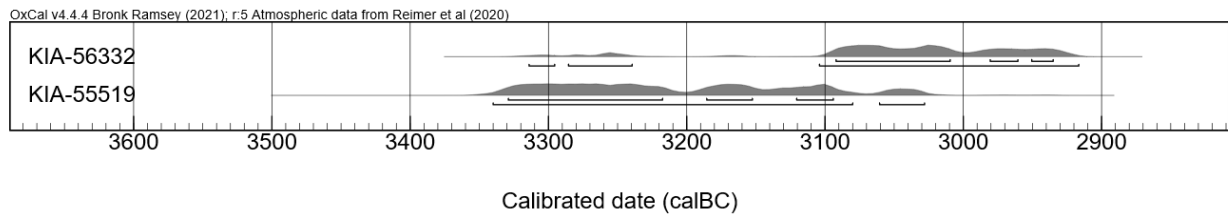
Supplementary Fig. 1. Radiocarbon dating results for Warburg_1 (KIA-55519) and Warburg_2 (KIA-56332), including the calculation of probability distributions for both samples.
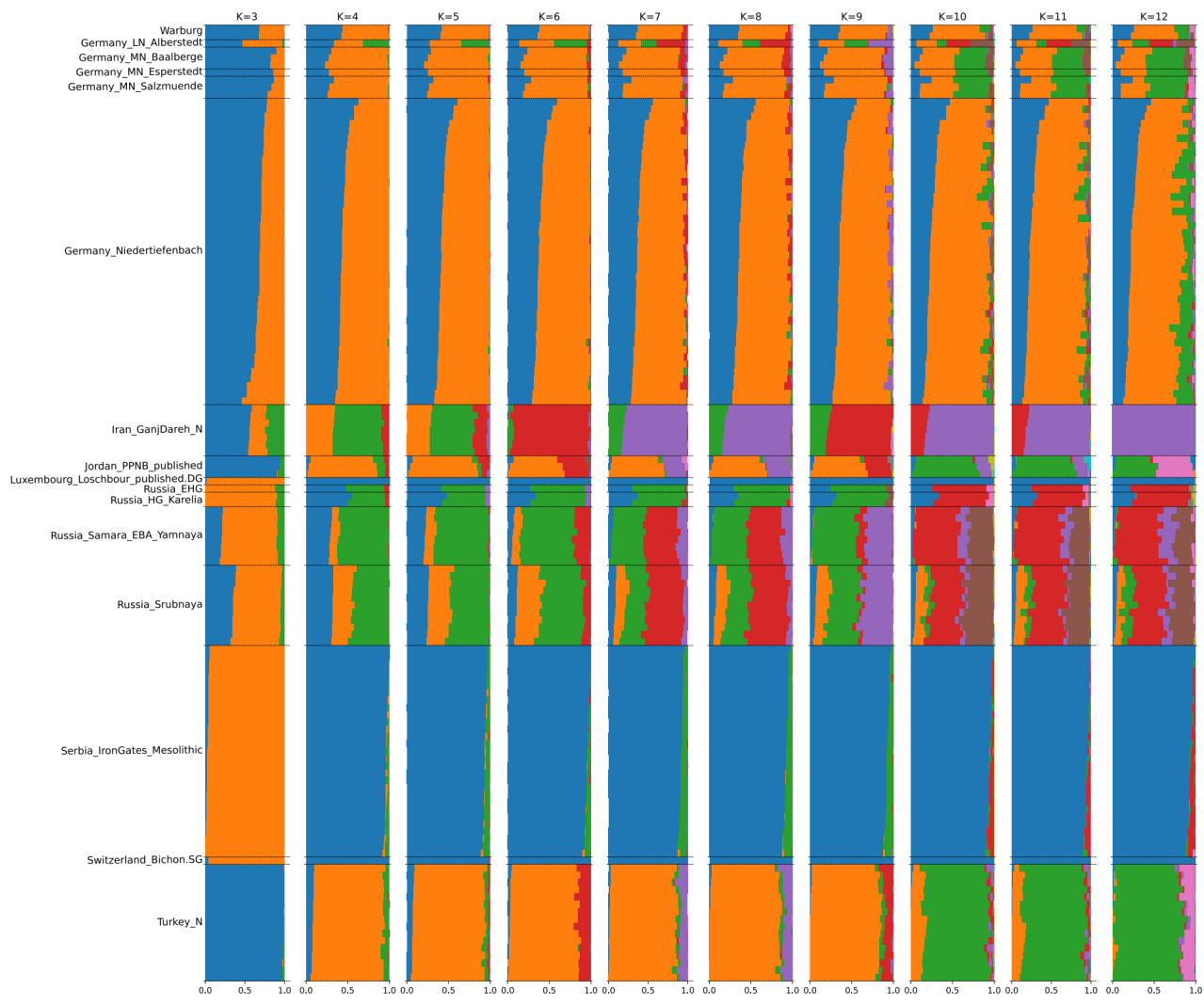
Supplementary Fig. 2. Genomic ancestry components using unsupervised ADMIXTURE. For the two Warburg individuals (red), most models indicate two major genetic components: one maximized in Western hunter-gatherers (i.e., Luxembourg_Loschbour) and the other in Anatolian farmers (i.e., Turkey_N).
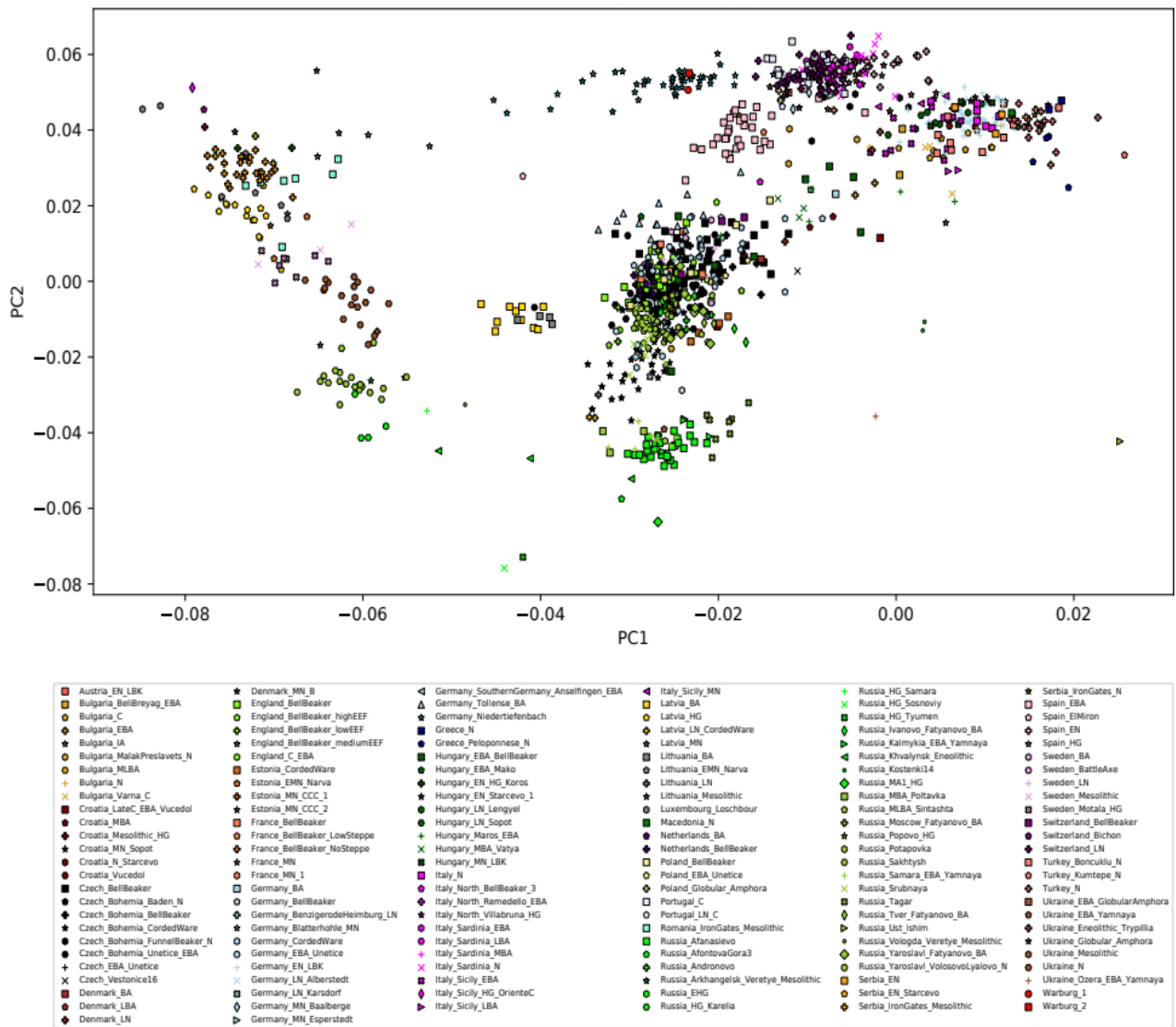
Supplementary Fig. 3. Principal component analysis of the individuals Warburg_1 and Warburg_2 buried in the WBC gallery graves of Warburg (red) in the context of 150 prehistoric populations, including individuals from the WBC gallery grave of Niedertiefenbach (blue stars).
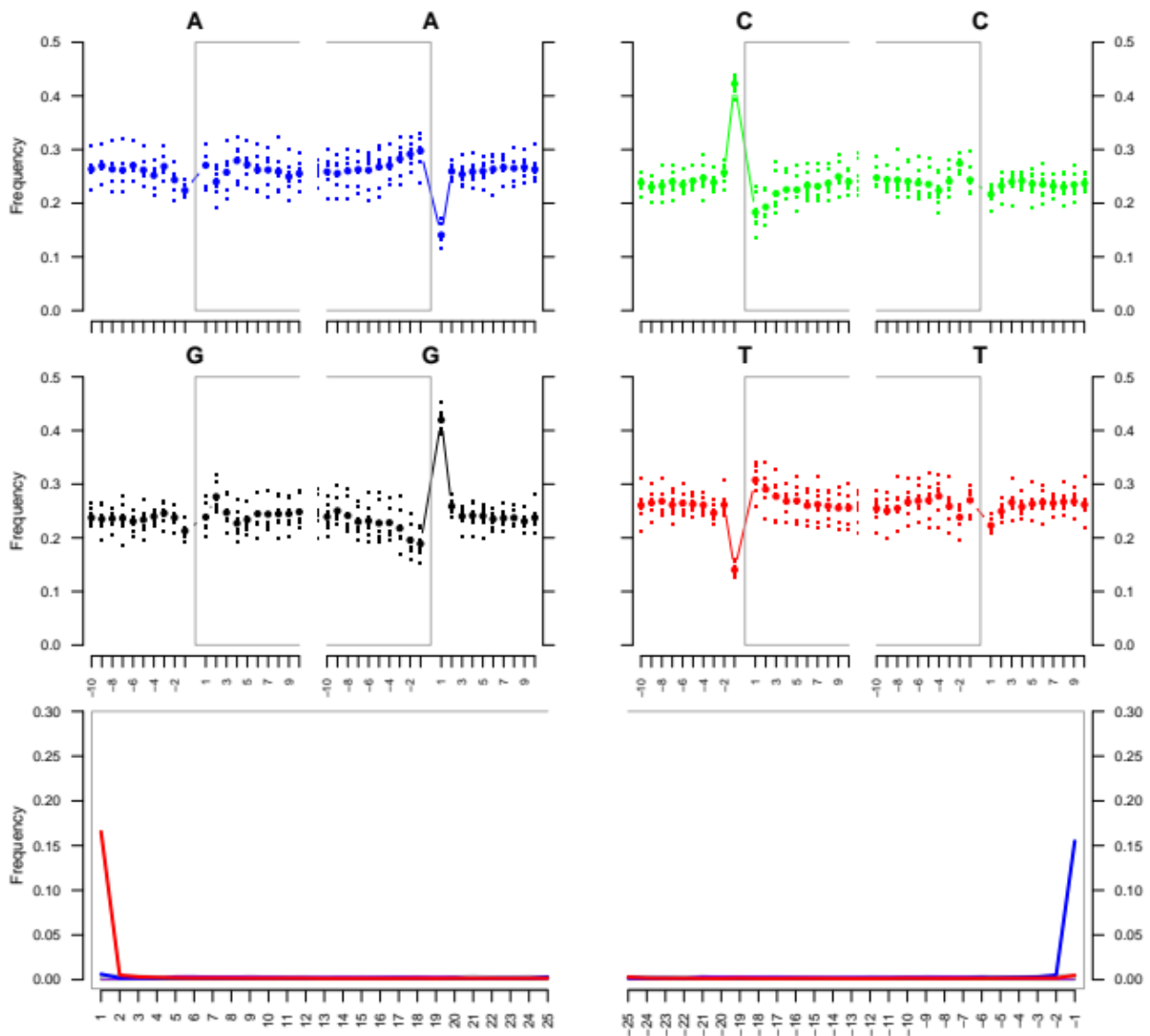
Supplementary Fig. 4. Damage plots supporting the ancient origin of *Y. pestis* reads for Warburg_1.
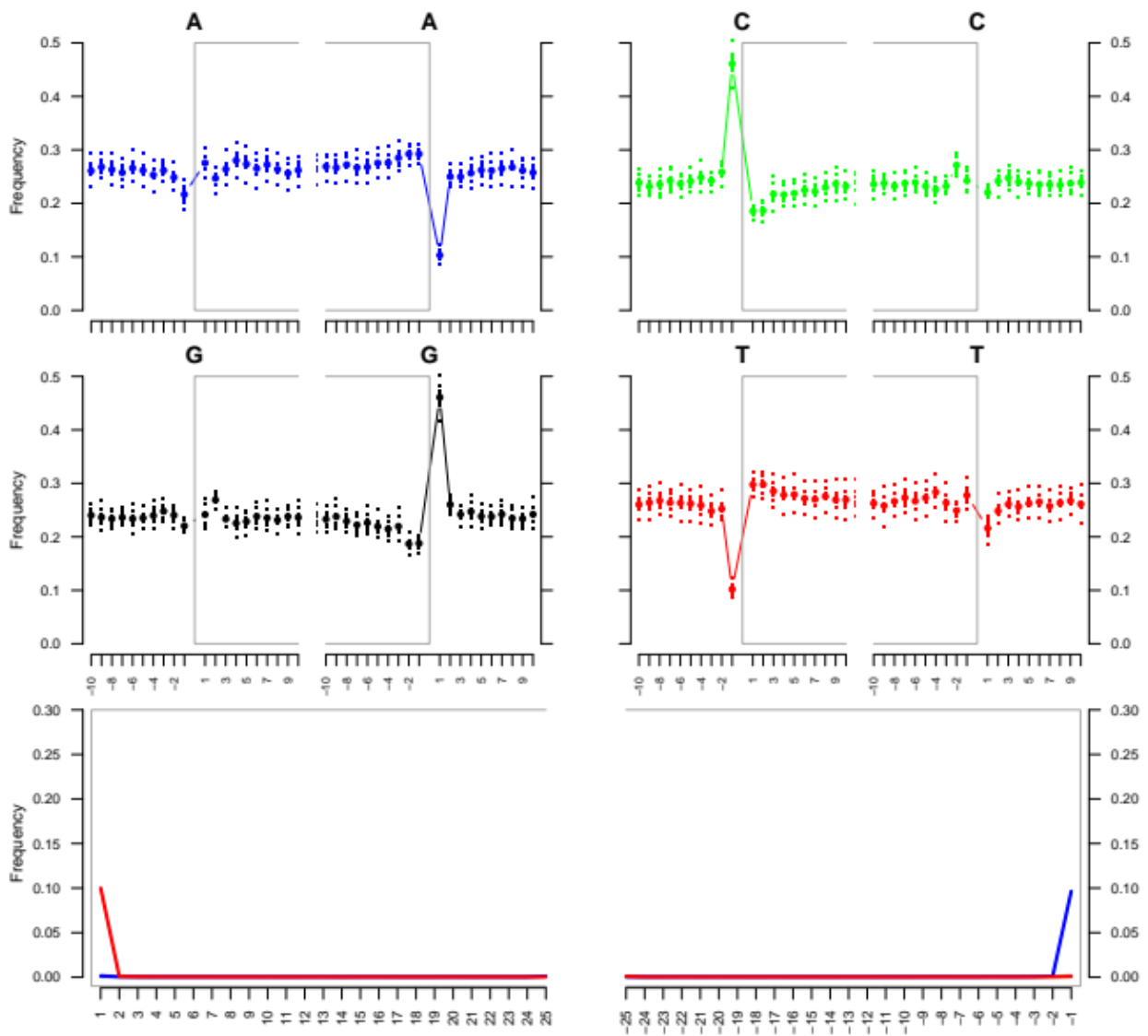
Supplementary Fig. 5. Damage plots supporting the ancient origin of *Y. pestis* reads for Warburg_2.
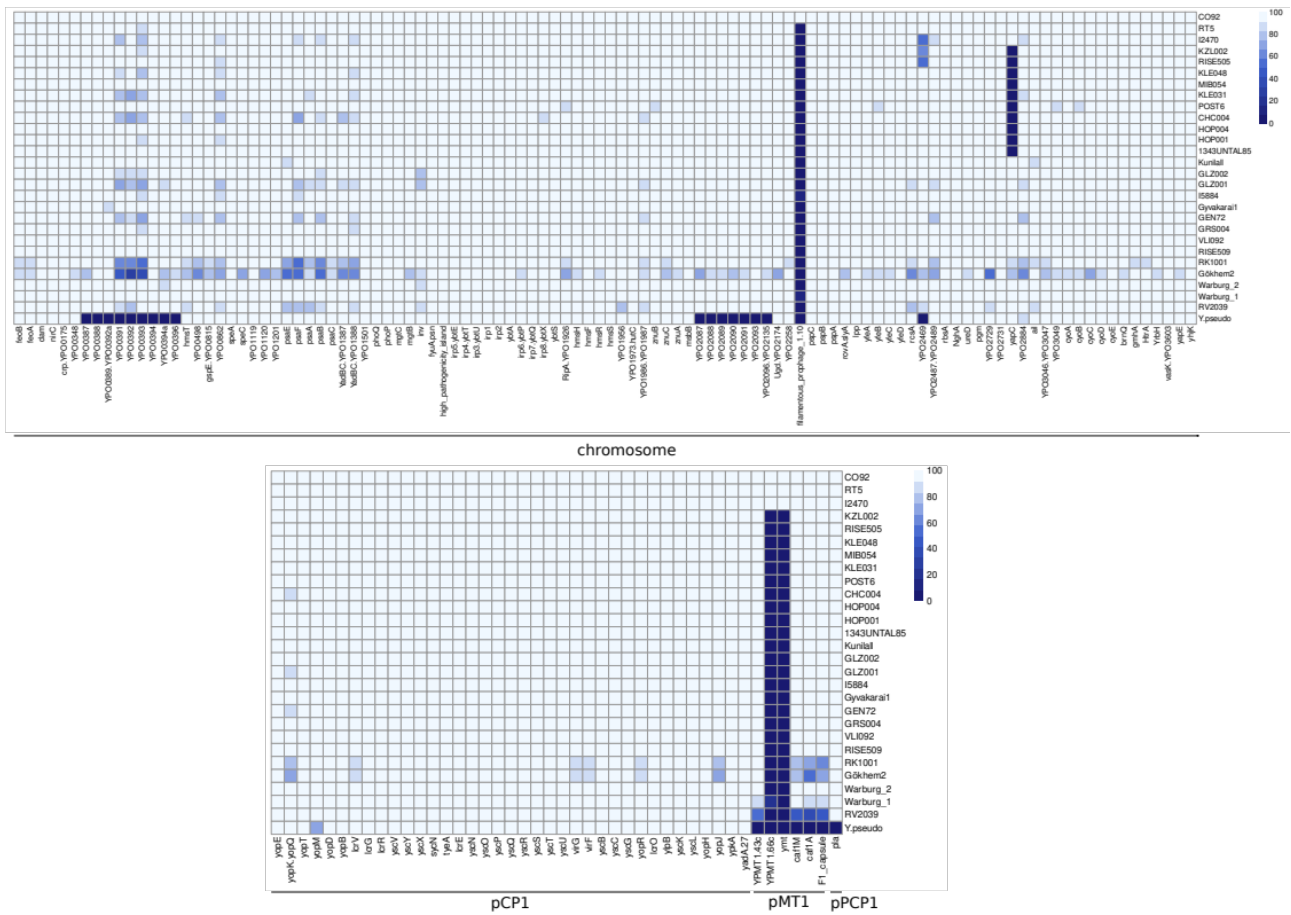
Supplementary Fig. 6. Visualization of virulence factors in ancient *Y. pestis* strains. Heatmap shows the presence or absence of 159 virulence factors on the chromosome (n=115) and the plasmids pCD1 (n=37), pMT1 (n=6) and pPCP1 (n=1). Genomes are sorted according to their placement in the phylogenetic tree (Fig. 2).
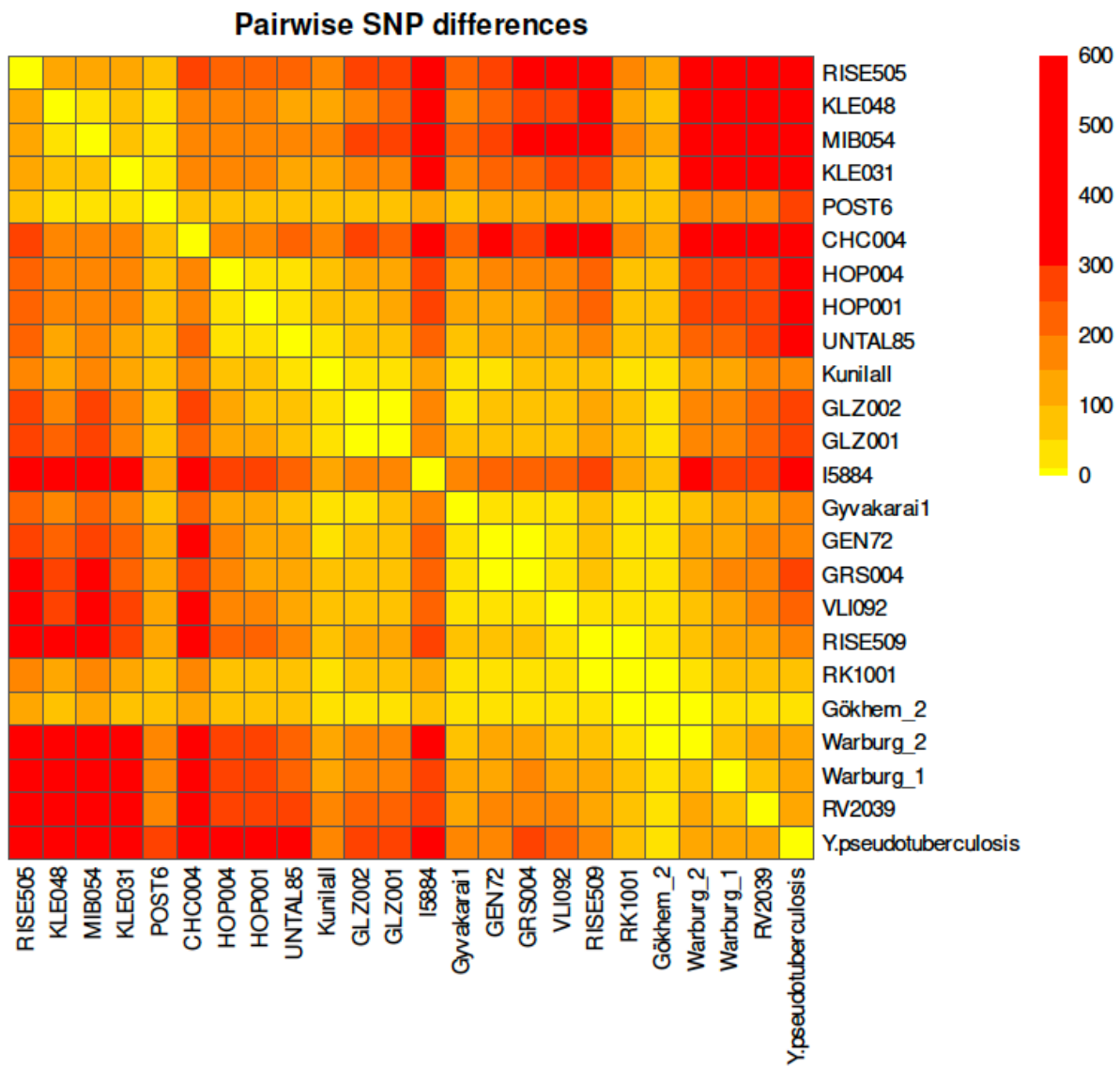
Supplementary Fig. 7. SNP distance matrix of LNBA and LN strains based on the Fasta alignments. Variants are counted if supported by a minimal coverage of 4 x.