

## Description of Additional Supplementary Files

**Supplementary Data 1.** Background information of 2,336 newly sequenced *Y. pestis* strains.

**Supplementary Data 2.** Background information of publicly available *Y. pestis* genomes.

**Supplementary Data 3.** Statistics of 45 identified hot regions.

**Supplementary Data 4.** Statistics of HR and non-HR SNPs and indels identified in 3,318 *Y. pestis* strains.

**Supplementary Data 5.** Statistics of 1,336 mutations located in hot regions.

**Supplementary Data 6.** The variance of relative abundance for mutation sites throughout distinct phylogroups for each HR.

**Supplementary Data 7.** High-confidence HR-associated gene interactions identified in STRING analysis.

**Supplementary Data 8.** Inferred recombination parameters for *Y. pestis* and *Y. pseudotuberculosis* using different methods across different dataset sizes.

**Supplementary Data 9.** 31 groups of physically linked variations.

**Supplementary Data 10.** Genes with  $dN/dS > 1$  or a significantly high number of nonsynonymous SNPs.

**Supplementary Data 11.** 138 identified homoplastic SNP sites.

**Supplementary Data 12.** *Y. pestis* strains used for streptomycin susceptibility testing.

**Supplementary Data 13.** Identification of hot regions in 100 simulated genomic sequences under neutral evolution.