Figure S1. *F. tularensis mediasiatica* genetic diversity reflected by wgSNP analysis. Fifty-three strains were included (28 from this project and 25 from public repositories). The maximum parsimony tree was based upon 330 core-genome SNPs, tree size is 330 (no homoplasia). Branch lengths above five are indicated. Nodes are colored according to clade (M.II, M.III) or subclade (within M.I).