Figure S1. Whole-genome SNP phylogeny of all 78 strains containing non-synonymous dnaA mutations and their neareast, non-mutant phylogenetic neighbor. The tree is rooted using *Mycobacterium canettii* as an outgroup. The inner ring depicts strains with non-synonymous *dnaA* mutations while each successive ring shows isolates containing a mutation shared by multiple strains. Mutations that were constructed into H37Rv are shown as stars.