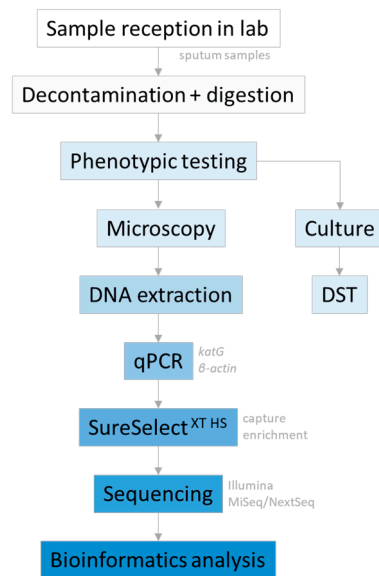


**Figure S1.** Core-genome phylogenetic analysis of 37 *M. tuberculosis* samples with (near) complete genome sequences. The minimum spanning tree was constructed based on a core-genome SNP-based alignment involving a total 3441 variant sites. Each circle (node) represents a unique SNP profile. Potential clusters (SNP distance below 12 SNPs) are highlighted by red colored circles. Data visualization was adapted from GrapeTree dashboard [see methods], with the colored nodes referring to the same-patient samples. Only samples yielding  $\geq 90\%$  horizontal coverage and at least 10-fold depth of coverage were included in the phylogenetic analysis.



**Figure S2.** Procedure workflow for the capture and enrichment of *Mycobacterium tuberculosis* genomes directly from clinical samples. DST: drug susceptibility testing; RT-PCR: real time PCR.