

# Next-Generation Sequencing of *Mycobacterium tuberculosis*

## Technical Appendix



**Technical Appendix Figure.** Whole-genome, short-sequencing reads of *Mycobacterium tuberculosis* strain 4542 mapped to complete genome of reference strain H37Rv (NC\_00962.3) by using Geneious 9.0 package: genome locus of spacers 7–9 in DR/CRISPR locus. Spacer numbers are given according to 43-spoligotyping (1). DR/CRISPR locus in *M. tuberculosis* is located on complementary strand, whereas spacers are consecutively numbered within the locus, not genome. Such a situation (IS6110 asymmetrically inserted in the direct repeat unit immediately adjacent to a spacer) was discovered by Filliol et al. (2).

## References

1. Kamerbeek J, Schouls L, Kolk A, van Agterveld M, van Soolingen D, Kuijper S, et al. Simultaneous detection and strain differentiation of *Mycobacterium tuberculosis* for diagnosis and epidemiology. *J Clin Microbiol.* 1997;35:907–14. [PubMed](#)
2. Filliol I, Sola C, Rastogi N. Detection of a previously unamplified spacer within the DR locus of *Mycobacterium tuberculosis*: epidemiological implications. *J Clin Microbiol.* 2000;38:1231–4. [PubMed](#)