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Accuracy of whole-genome sequencing to determine recent tuberculosis transmission: an 11-year population-based study in Hamburg, Germany

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To the Editor:

Controlling human-to-human tuberculosis (TB) transmission is key for achieving the targets of the End TB Strategy set by the World Health Organization (WHO) [1, 2]. Stopping TB transmission, in large cities especially, is a challenging top priority worldwide [3]. Metropolitan areas have higher TB case notification rates than the rest of a country, as they concentrate high-risk groups, such as homeless people, drug users and migrants often from (other) high TB incidence settings. Opportunities for transmission are amplified by population density and complex social interactions, regularly leading to large, temporally extended transmission networks [3]. Targeted interventions to interrupt transmission require the combination of effective genotyping of TB strains with enhanced epidemiological investigation. While classic IS*6110* DNA fingerprinting and 24-locus MIRU–VNTR (mycobacterial interspersed repetitive units–variable number of tandem repeats) typing provide standardised and easily computable typing results with an online nomenclature system, several studies have now demonstrated that whole-genome sequencing (WGS) has a superior discriminatory power, allowing for an unparalleled resolution of outbreak strains [4–10].

However, predictivity of WGS for detecting transmission in metropolitan areas has not yet been quantified *versus* most deterministic references, *i.e.* tangible epidemiological links identified by *ad hoc* investigation, at extended time and population scales.