Reviewer’s report

Title: Genomic characterization of MDR/XDR-TB in Kazakhstan by a combination of high-throughput methods predominantly shows the ongoing transmission of the L2/Beijing 94-32 Central Asian/Russian clusters.

Version: 1 Date: 10 Apr 2019

Reviewer: Igor Mokrousov

Reviewer’s report:

I have only one terminological comment:

"94-32 Central Asian Outbreak (CAO) Cluster" does not exist, you have confused/merged two entities.

sigE mutation is a marker of a large 94-32 (Central Asian/Russian) sublineage inside Beijing.

Central Asian Outbreak (CAO) strain is not synonyme of Beijing 94-32 (Central Asian/Russian) sublineage.

Instead CAO is part of Beijing 94-32 (Central Asian/Russian) sublineage.

But it has the same VNTR 94-32 profile, and the same mutation sigE.

Thus sigE snp analaysis permitted you to identify not CAO, but the larger Beijing 94-32 (Central Asian/Russian) sublineage.

Keep in mind, that this Beijing 94-32 (Central Asian/Russian) sublineage may be MDR in Kazakhstan but it is less MDR than Beijing B0/W148 in Russia (see Pasechnik et al. Tuberc. 2018).

Please revise your article accordingly throughout.

Are the methods appropriate and well described?

If not, please specify what is required in your comments to the authors.

Yes

Does the work include the necessary controls?

If not, please specify which controls are required in your comments to the authors.

Yes

Are the conclusions drawn adequately supported by the data shown?
If not, please explain in your comments to the authors.

Yes

**Are you able to assess any statistics in the manuscript or would you recommend an additional statistical review?**
If an additional statistical review is recommended, please specify what aspects require further assessment in your comments to the editors.

I am able to assess the statistics

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Please indicate the quality of language in the manuscript:

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