Fig. 2. M. tb. genomic sequencing data exclusion criteria.

*Specimens demonstrating polyclonal infections were already excluded (n = 386), leaving a full dataset of 1,834 M. tb isolates.

Exclusions made to the genomic sequencing drug susceptibility testing dataset are shown along with the number of observations. This dataset of pretreatment isolates is described elsewhere [1,2]. The presence of a mutation conferring resistance to rifampicin was assumed to convey full resistance, and vice versa.

The dataset with exclusion criteria applied is available at

https://github.com/lyndonpjames/BPaLM_Moldova/blob/main/tbl_WGS_allRR.csv while original publicly available datasets can be found at

https://www.ncbi.nlm.nih.gov/biosample?Db=biosample&DbFrom=bioproject&Cmd=Link&LinkName=
TB – tuberculosis

REFERENCES

These references are provided here for convenience. They are also cited within the main manuscript file in the legend for S2 Fig.

