A Rapid, High-throughput Melt-based Optimization of OLA to Detect MDR-TB

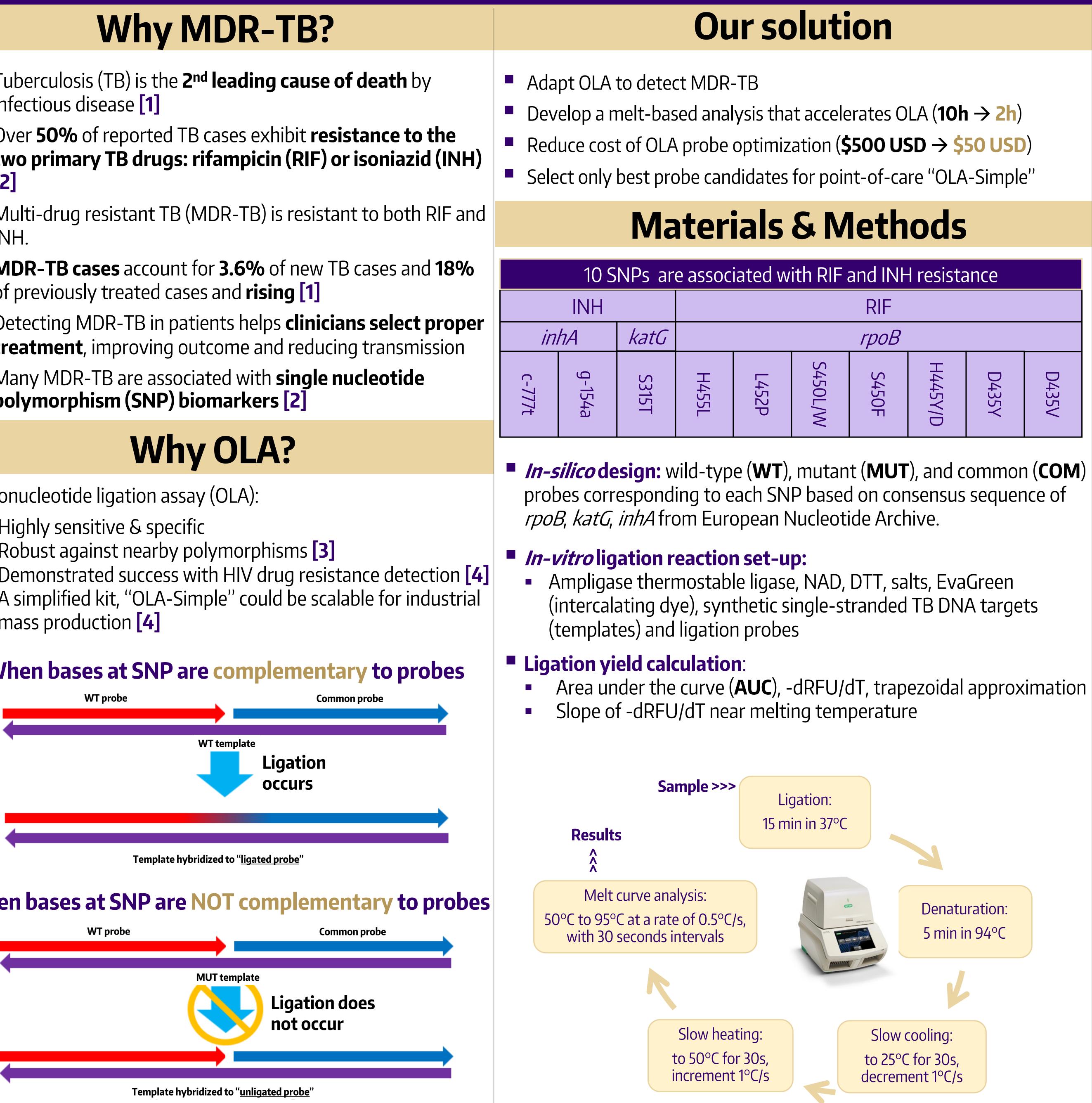
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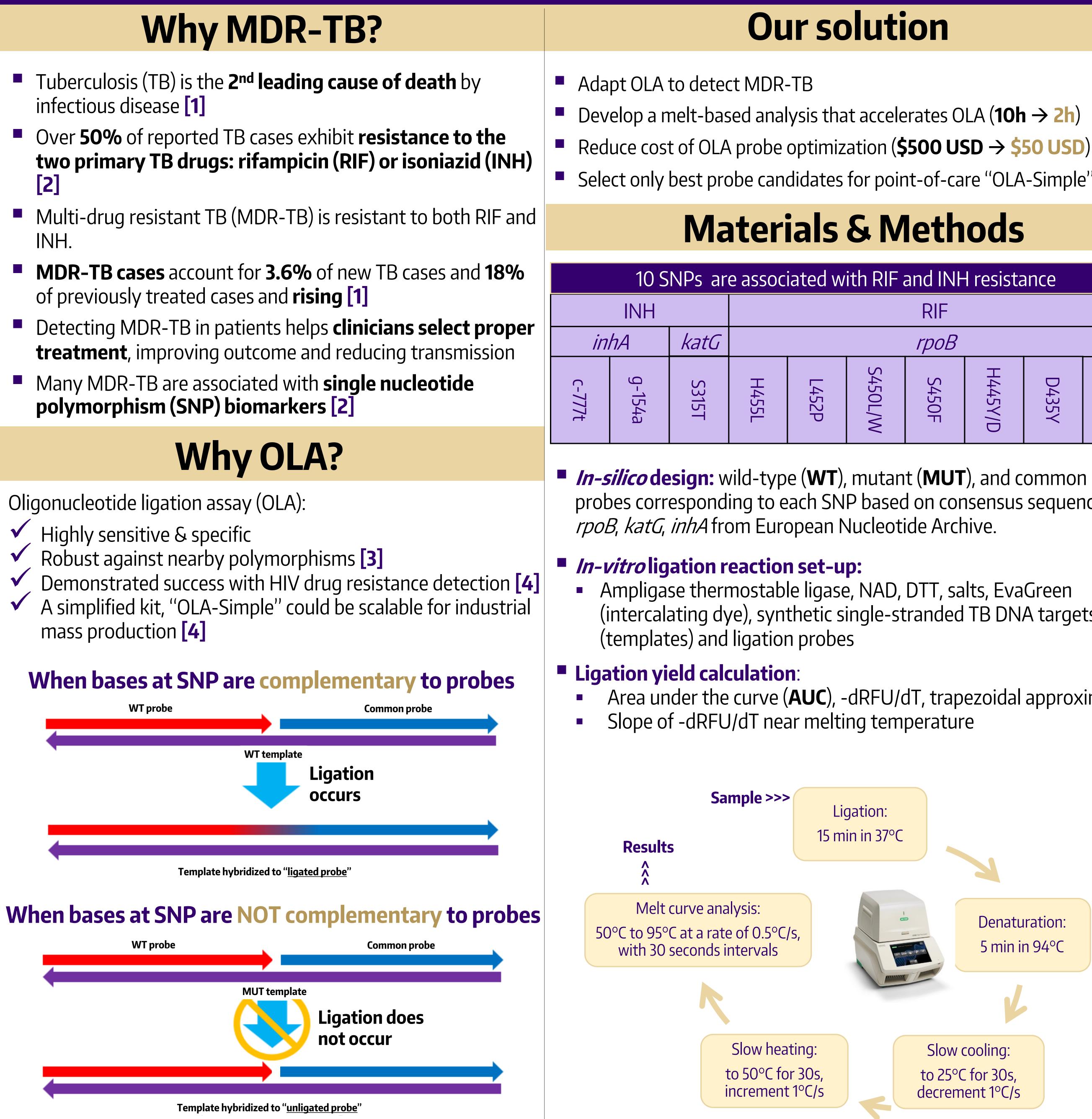
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- Tuberculosis (TB) is the 2nd leading cause of death by infectious disease [1]
- Over **50%** of reported TB cases exhibit **resistance to the** [2]
- INH.
- of previously treated cases and **rising** [1]
- Many MDR-TB are associated with single nucleotide polymorphism (SNP) biomarkers [2]

Oligonucleotide ligation assay (OLA):

- mass production [4]





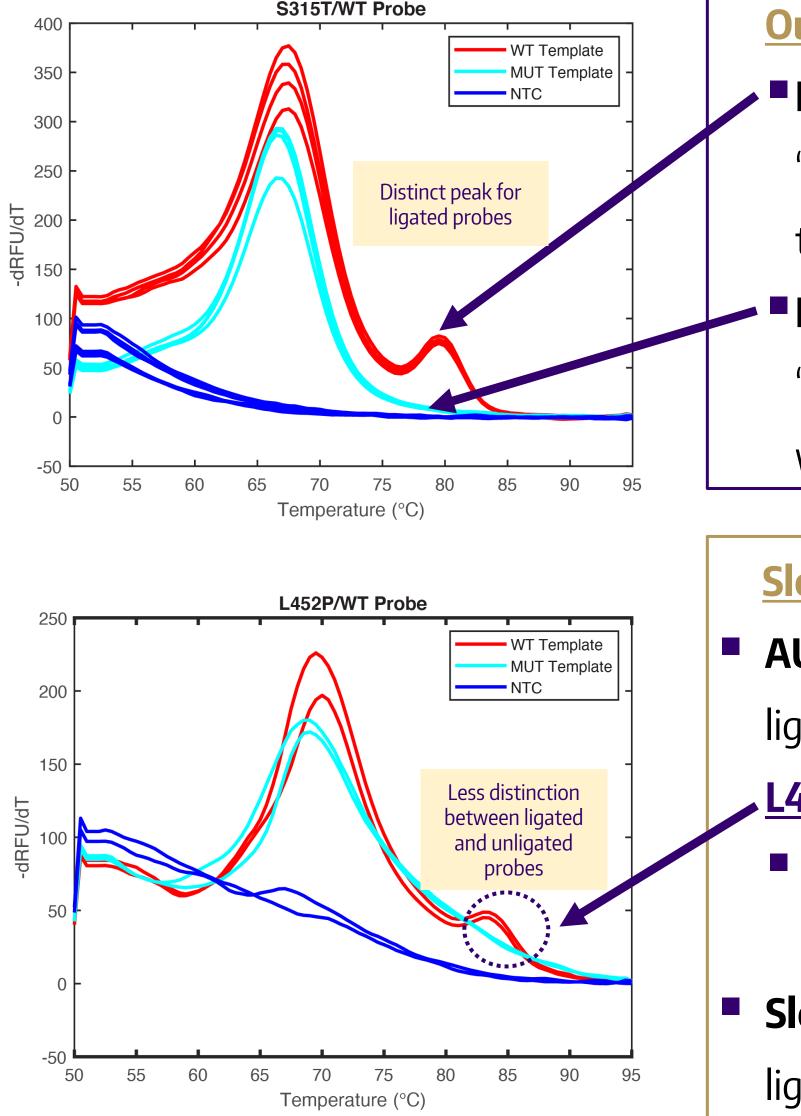
Visit the website using the QR code on the top right corner to download poster after the BMES conference ends.

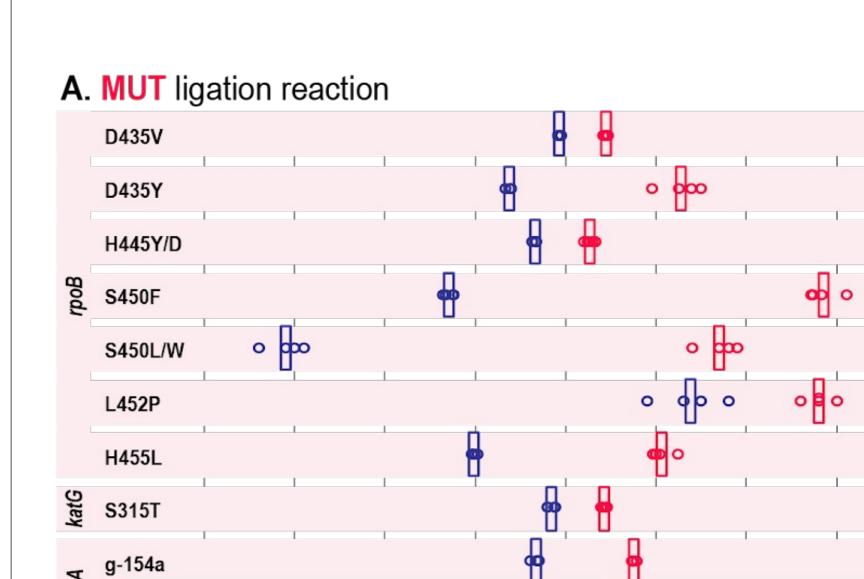
Oligonucleotide Ligation Assay



Results, Discussion, Conclusion

D435V





Slope (d(-d(RFU)/d(T))/d(T

O MUT DNA ○ WT DNA ▷ MUT DNA ▷ WT DNA

Acknowledgements

Collaborators:

c-777t

Drs. Lisa Frenkel, Grace John-Stewart, and Bhavna Chohan at the University of Washington; Dr. Diana Marangu at the University of Nairobi; and Preston Omondi and Dr. Steve Wandiga at Kenya Medical Research Institute; and Ronald Odero at AMREF Africa.

Funds:

SEATRAC NIA Panpradist). Inyoung Seo thanks 2023 l Ugrad Confer Travel Award

Multi-Drug Resistant TuBerculosis

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Our assay specifically detected MDR-TB SNPs.

Melt peaks of ligated probes observed in reactions with "Matched" probes and templates (e.g., WT probe with WT template)

No melt peaks of ligated probes observed in

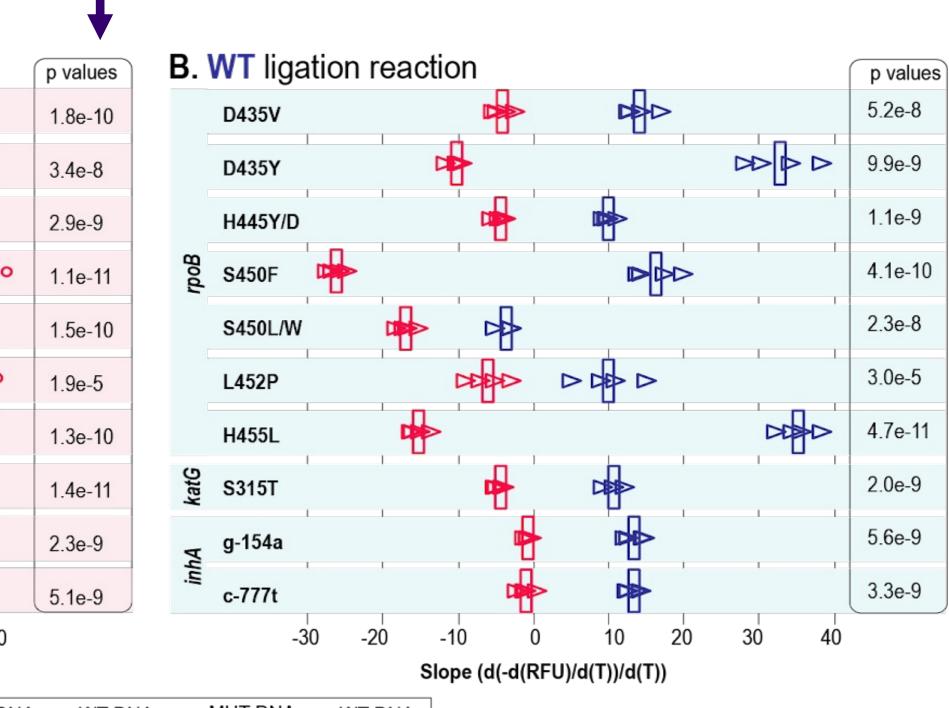
"Mismatched" probes and templates (e.g., MUT probe with WT template)

Slope-based approach yielded a better distinction.

• **AUC approach**: successfully distinguished melt peaks of ligated probes from unligated probes for all SNPs **except** <u>L452P</u>

We observed unusually high baseline in WT probe + MUT template reaction

Slope-based approach differentiated melt peaks between ligated and unligated probes for all SNPs.



S	References
A (PI:	[1] WHO. (2023, April 21) Tuberculosis Fact Sheet. www. who.int /teams/ global-tuberculosis-programme/tb- reports
UW rence d	[2] WHO. (2021, June 25) Catalogue of mutations in Mycobacterium tuberculosis complex and their association with drug resistance.
	[3] IA Beck et. al. (2002). Journal of Clinical Microbiology.
	[4] N Panpradist et. al. (2019). Lancet Ebiomedicine.