

# Targeted nanopore sequencing using hybridisation probes reveals immune escape polymorphisms in malaria vaccine candidates


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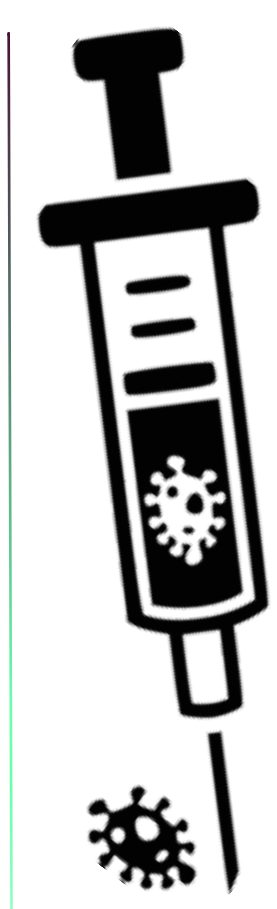
## BACKGROUND

### MALARIA



- Caused by eukaryotic parasites (*Plasmodium* spp.)
- Transmitted by anopheline mosquitoes
- Major cause, and effect of, poverty worldwide
- Increasing resistance to interventions

### MALARIA VACCINE DEVELOPMENT




- Only one candidate has passed Phase 2 trials (RTS,S based on Circumsporozoite Protein, CSP)
- Partial and short-lived efficacy in infants after 4 doses<sup>1</sup>
- Evidence of immune escape<sup>2</sup>

### PROBLEM:

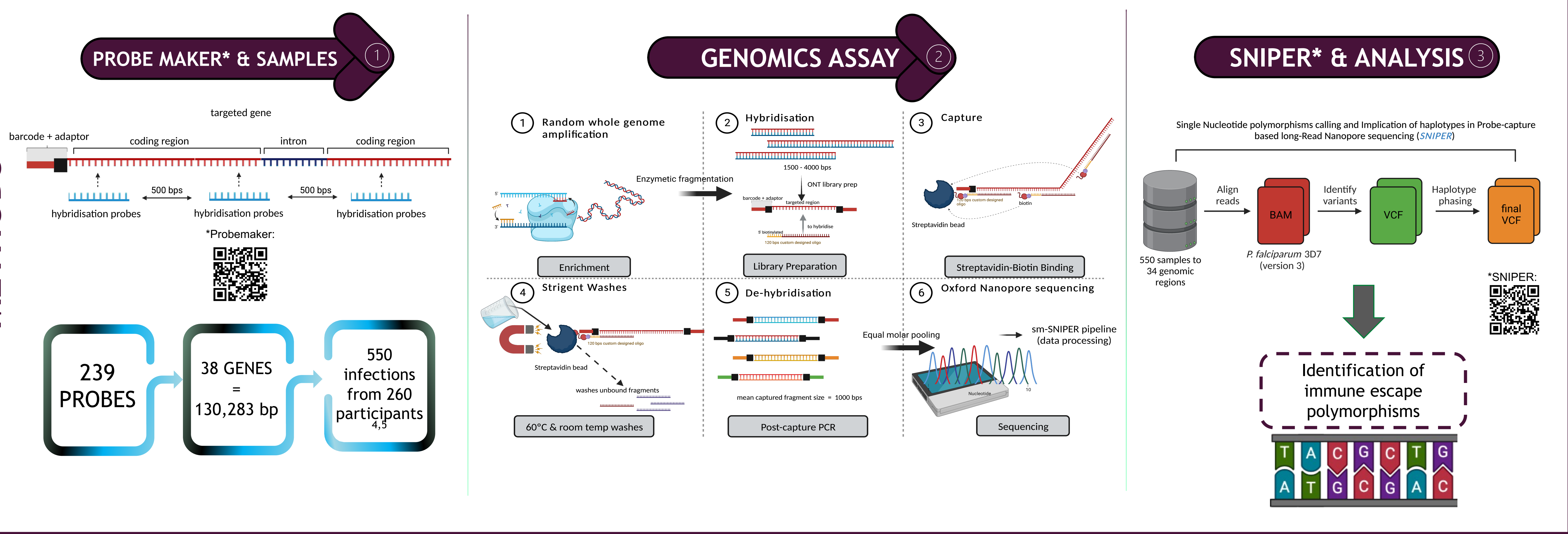
- Diverse antigens
- Immune escape
- Which polymorphisms?

### SOLUTION:

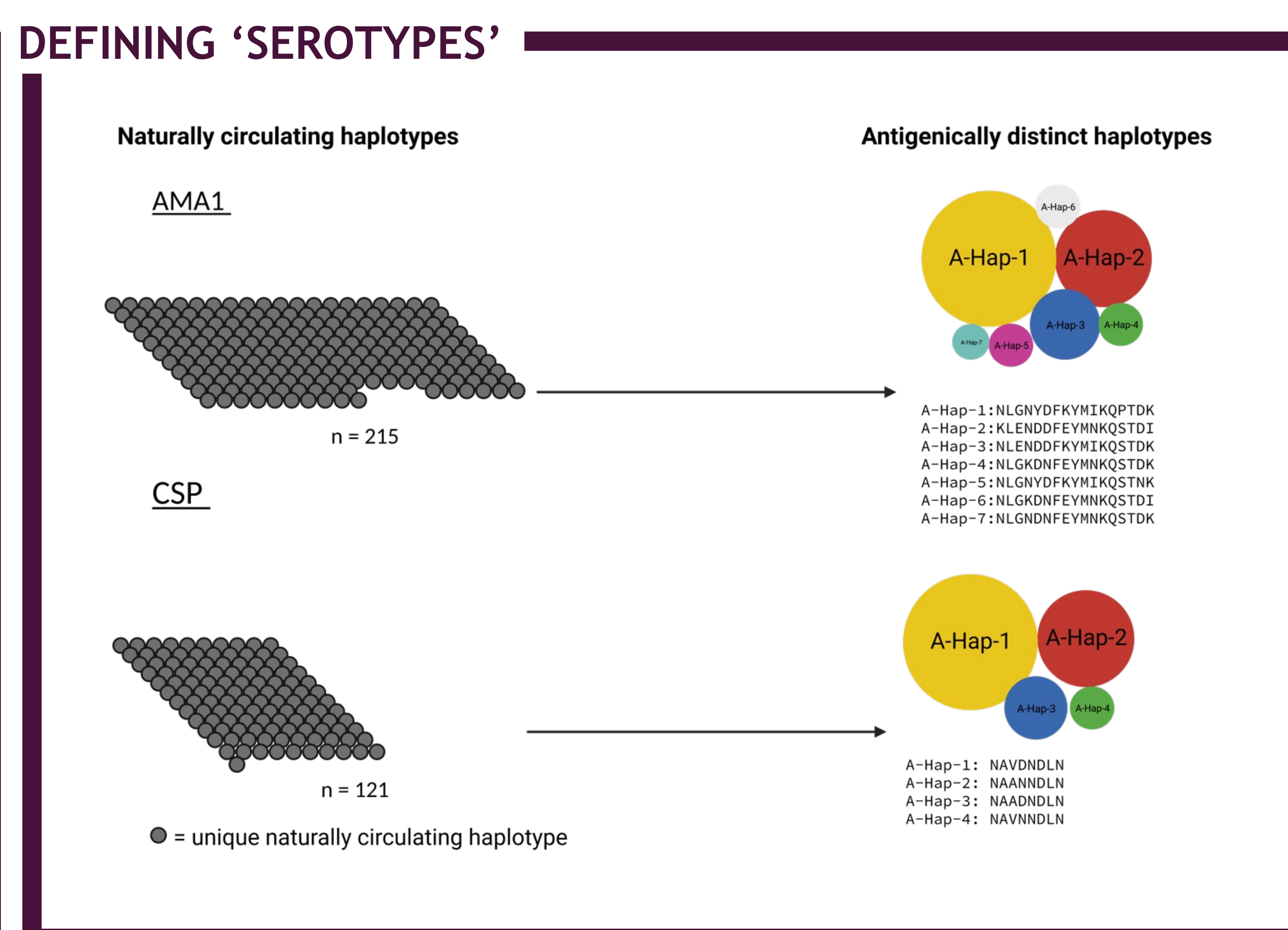
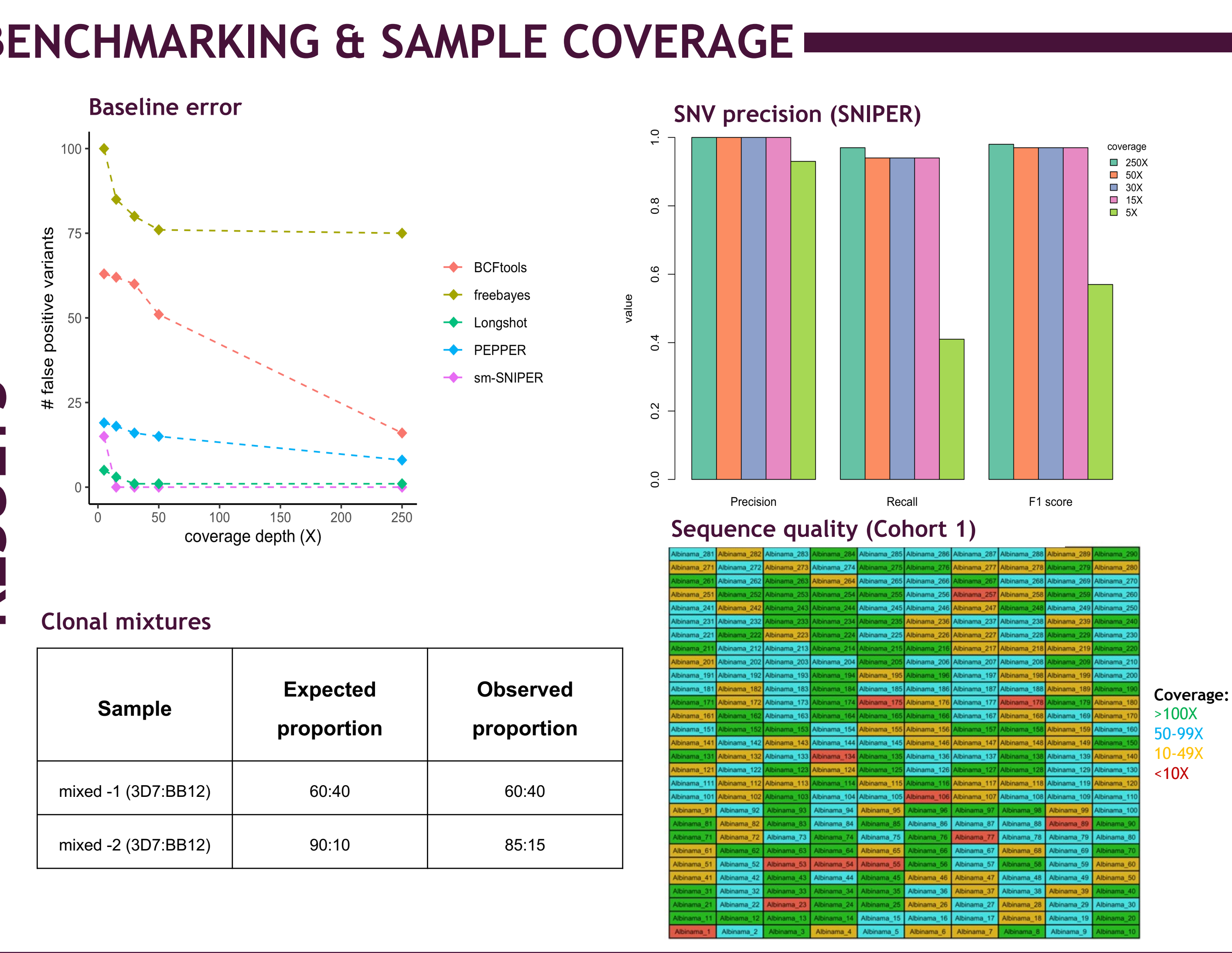
- Discover polymorphisms associated with immune escape<sup>3</sup>
- Targeted sequencing using Nanopore
- Samples from longitudinal cohorts from Papua New Guinea<sup>4,5</sup>



## METHODS



## RESULTS



## CONCLUSIONS

- Our novel targeted Nanopore sequencing assay sequences 38 malaria vaccine antigen genes in parallel
- SNIPER has more accurate variant calling (>15X) and haplotype phasing for multiple infections
- Applied to samples from a longitudinal cohort to identify immune escape polymorphisms
- Framework for improving understanding of infection dynamics, immune escape, and malaria vaccine design