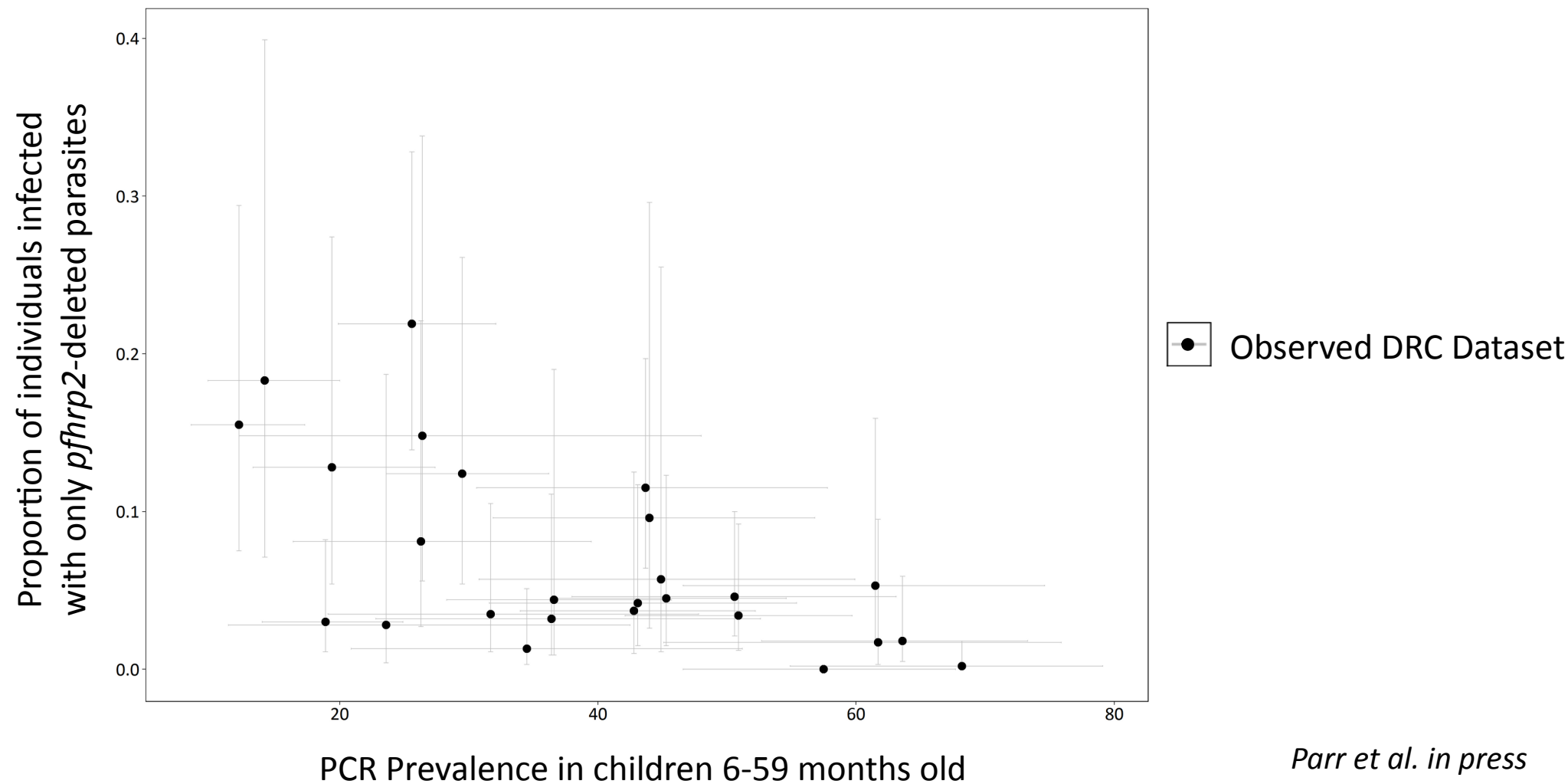


Oliver Watson

Modelling the spread of *pfhrp2* deletion concern in Africa

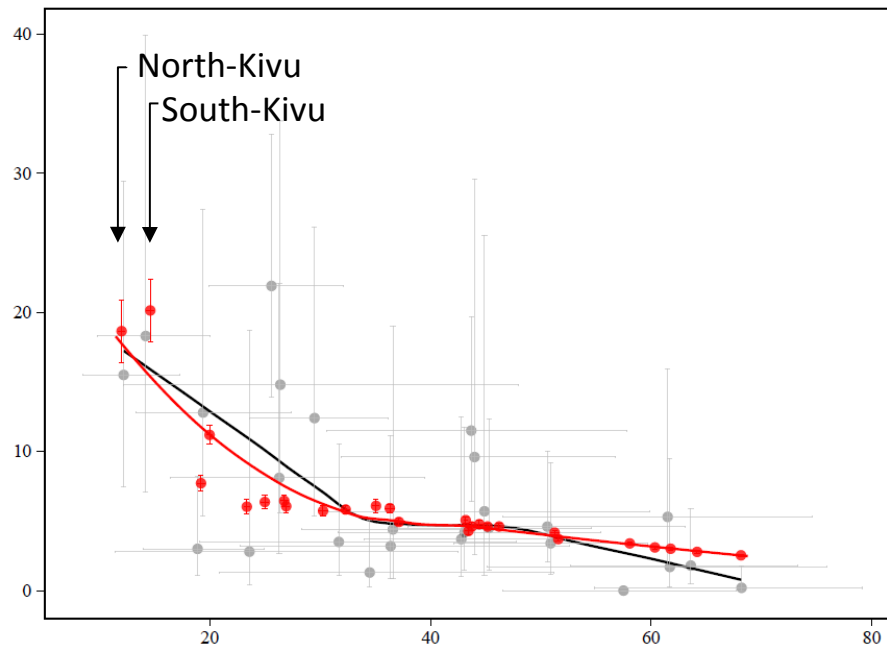


Significantly higher proportion of deleted samples in low transmission areas

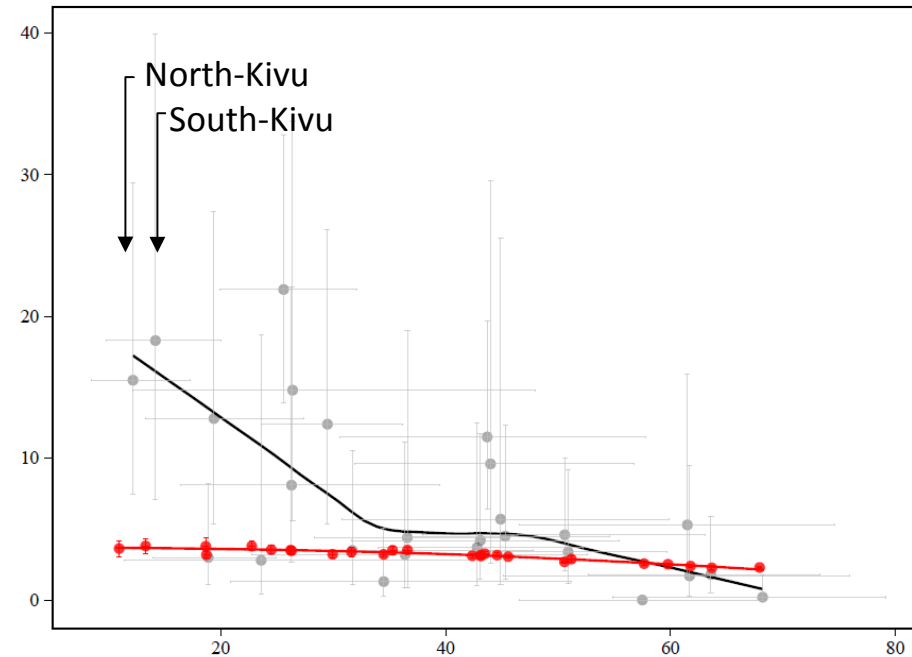
- Can only be explained by selection through RDT-guided treatment decisions

With selection

Proportion of individuals infected
with only *pfhrp2*-deleted parasites

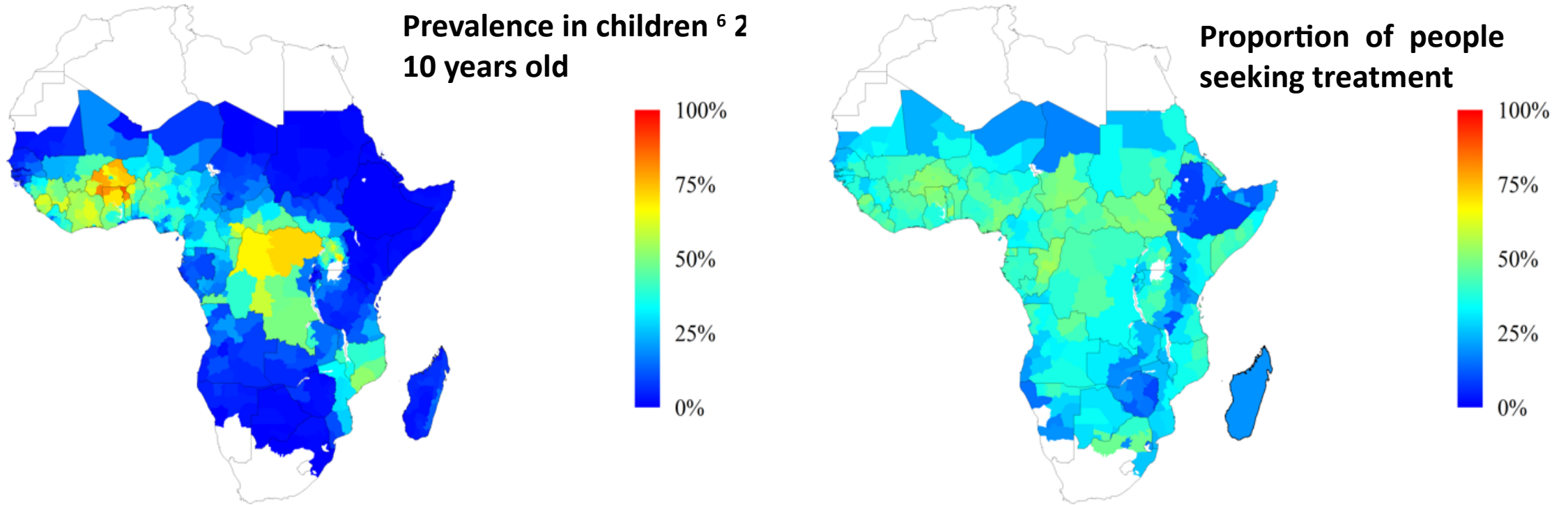


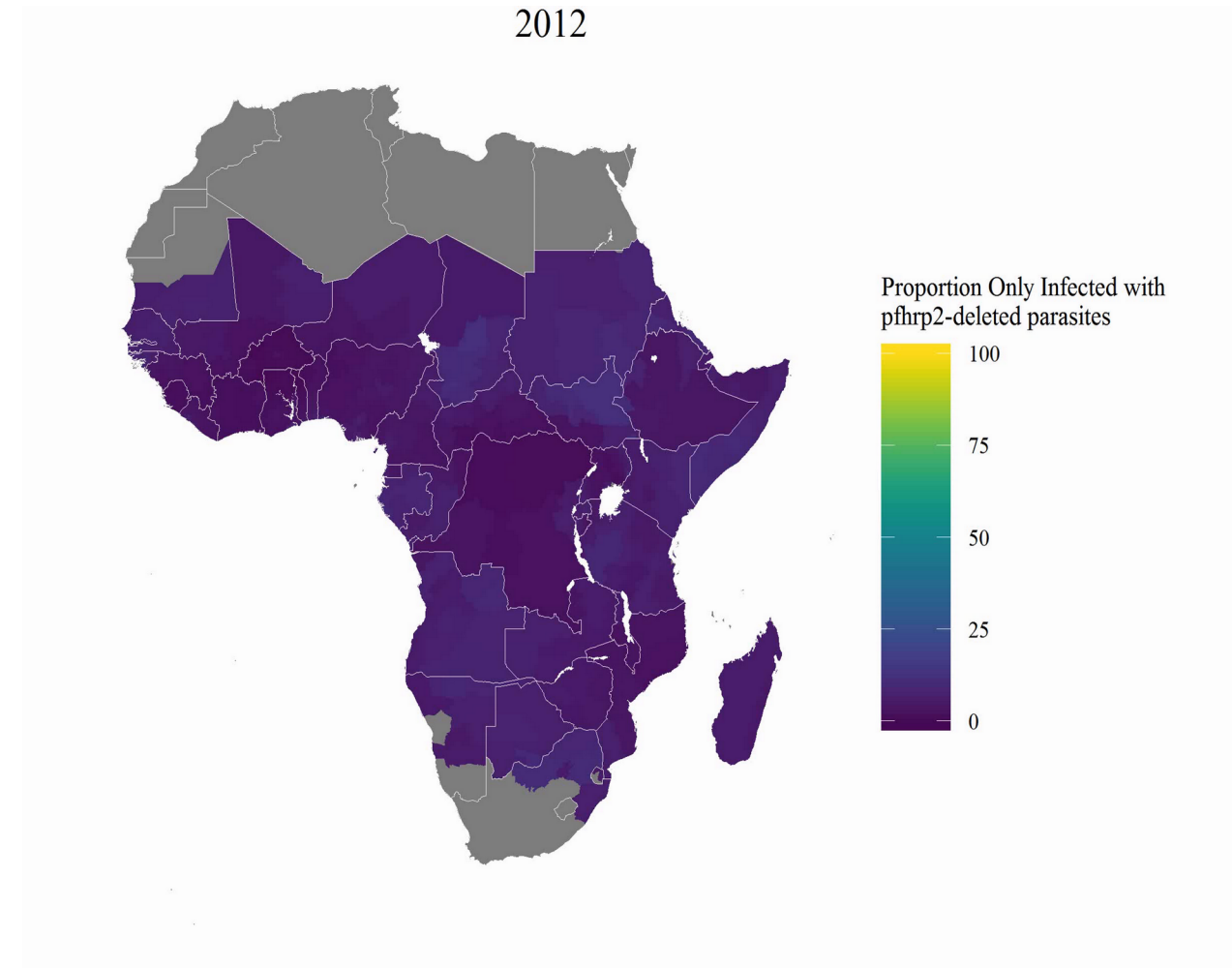
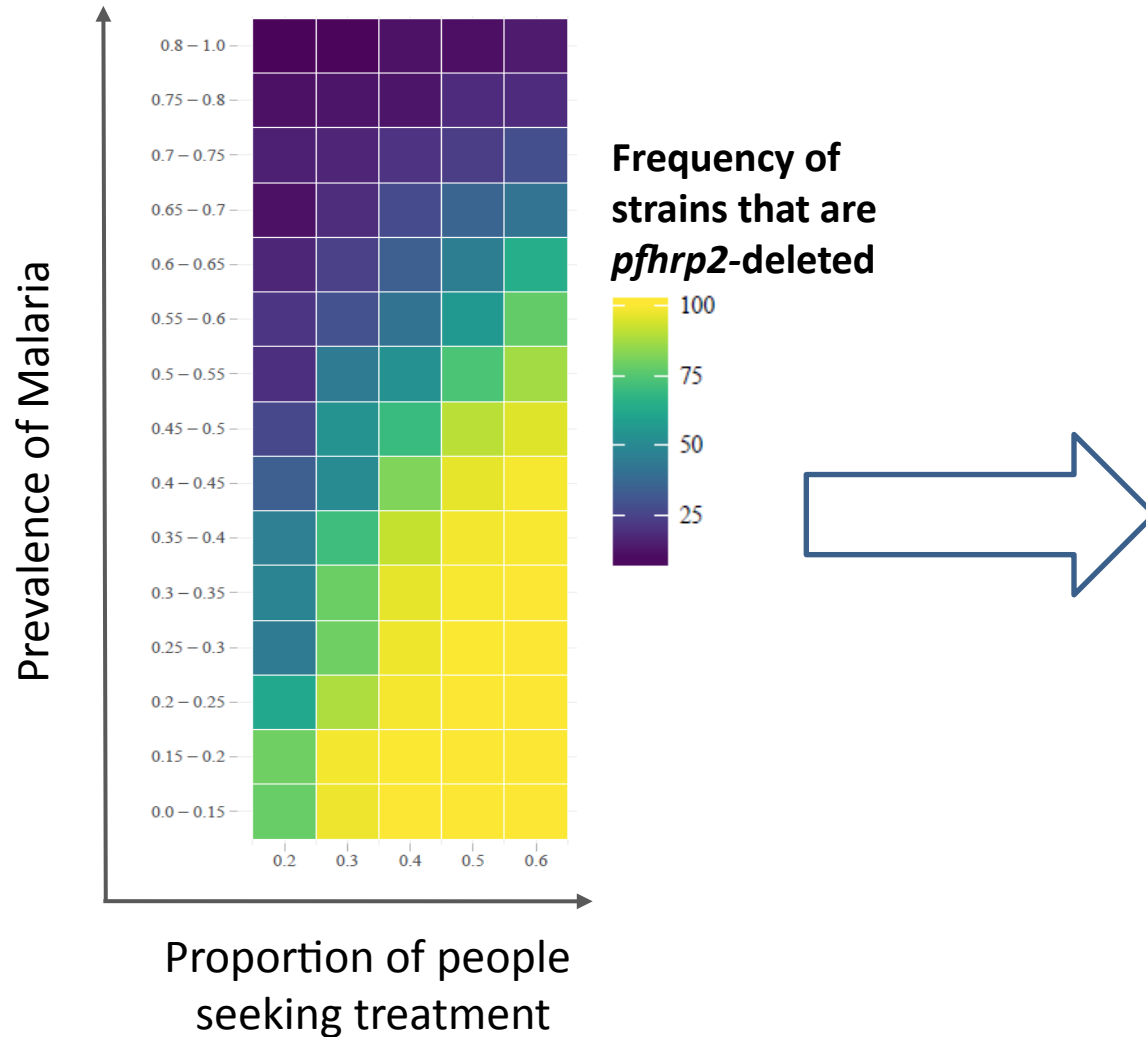
Without selection



● DRC
● Simulation

PCR Prevalence in children 6-59 months old





* Model assumes no change in prevalence and treatment coverage – spread therefore conservative

Fitted model identifies areas of concern for potential selection-driven spread in Africa

- Highest concern: Low prevalence plus high RDT-guided treatment

Proportion of infected population
possessing only *pfhrp2*-deleted mutants

HRP2 Concern

>20% by 2016

>20% by 2022

>20% by 2030

<20% by 2030

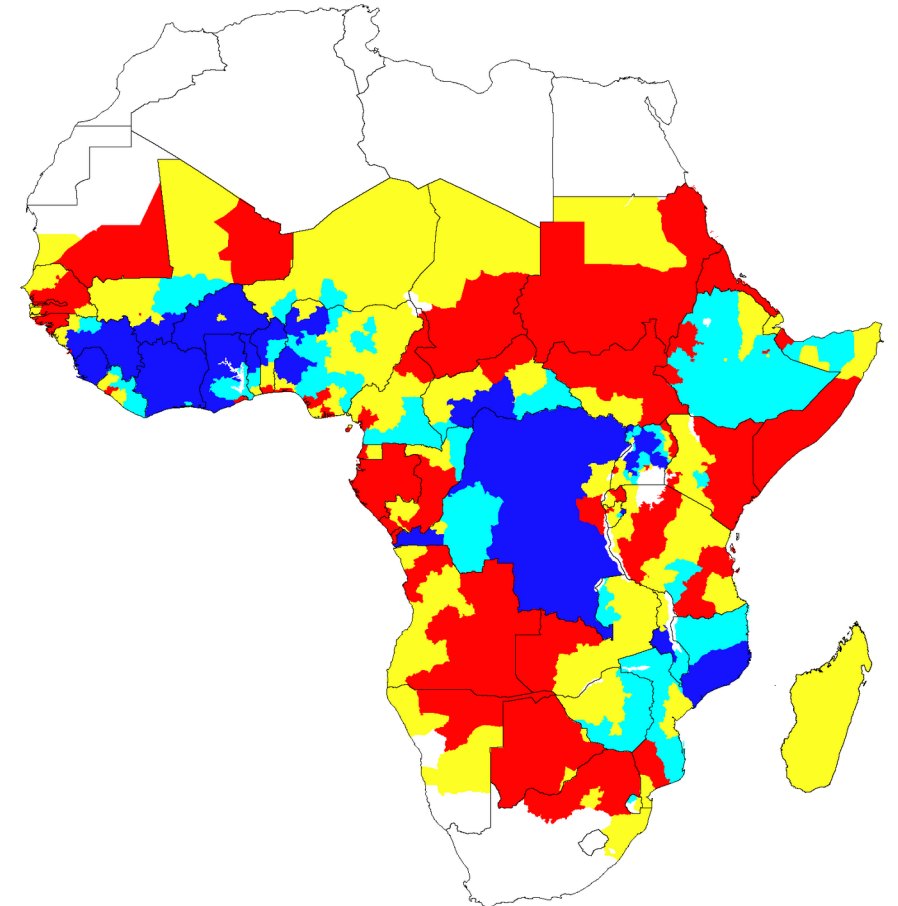


High

Moderate

Slight

Marginal



1. An increased emergence of *pfhrp2*-deleted mutants can be explained by the introduction of testing by PfHRP2-based RDTs in the last 10 years.
2. The use of these RDTs will result in the greatest selection pressure in regions that have low malaria transmission and a high frequency of people seeking treatment.
3. Need for further genetic investigations in the regions identified as having a high HRP2 concern.

1. Imperial College London:

- A. C. Ghani
- H. C. Slater
- R. Verity
- Malaria Modelling Group

2. University of North Carolina:

- S. R. Meshnick
- J. B. Parr

3. University of Kinshasa:

- M. K. Mwandagalirwa
- A. Tshefu

4. Wellcome Trust & MRC Centre for Outbreak Analysis and Modelling

Thank you for listening

Email: o.watson15@imperial.ac.uk