

# The malaria vector selection atlas



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## How has vector control in sub-Saharan Africa shaped the genomes of malaria vectors?

We built a web resource displaying signals of positive selection in wild mosquitoes from phase 3 of the *Anopheles* 1000 genomes project. The selection atlas is powered by an automated snakemake workflow - allowing us to repeat the analysis as WGS samples pass through the Vector Observatory pipeline. This continually updated resource will enable the community to track emerging resistance mechanisms and inform vector control strategies.

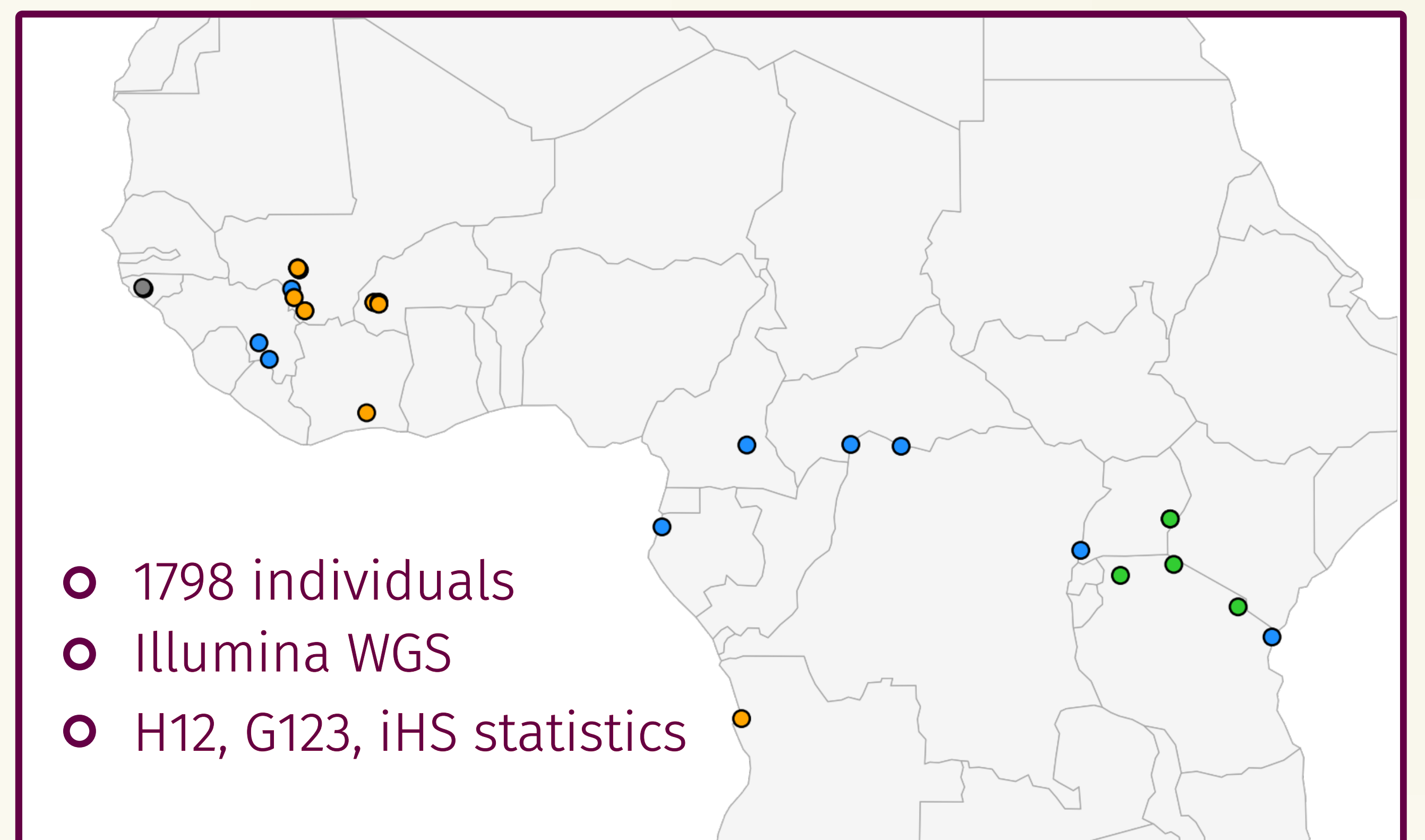


Fig 1. A map of collection sites for Ag1000G phase 3 cohorts with more than 20 individuals.

Visit the  
web resource

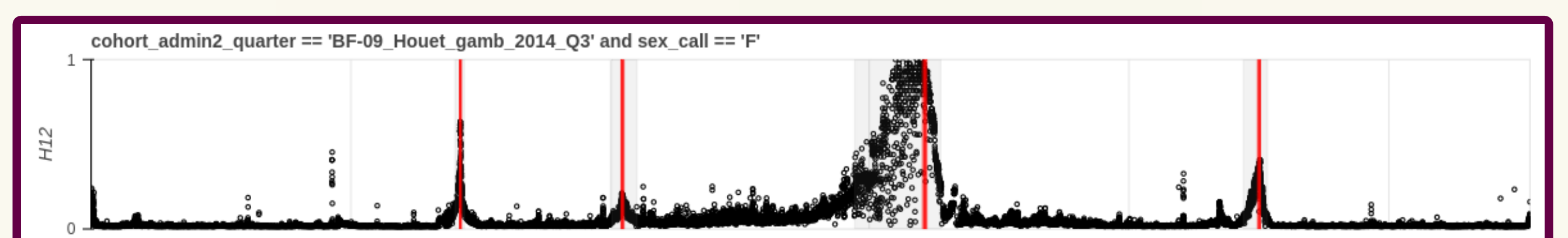
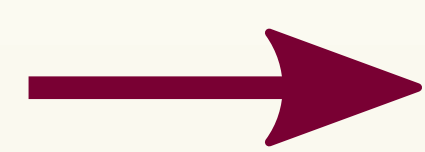


Fig 2. An example H12 genome-wide selection scan with signals called with a custom peak calling algorithm

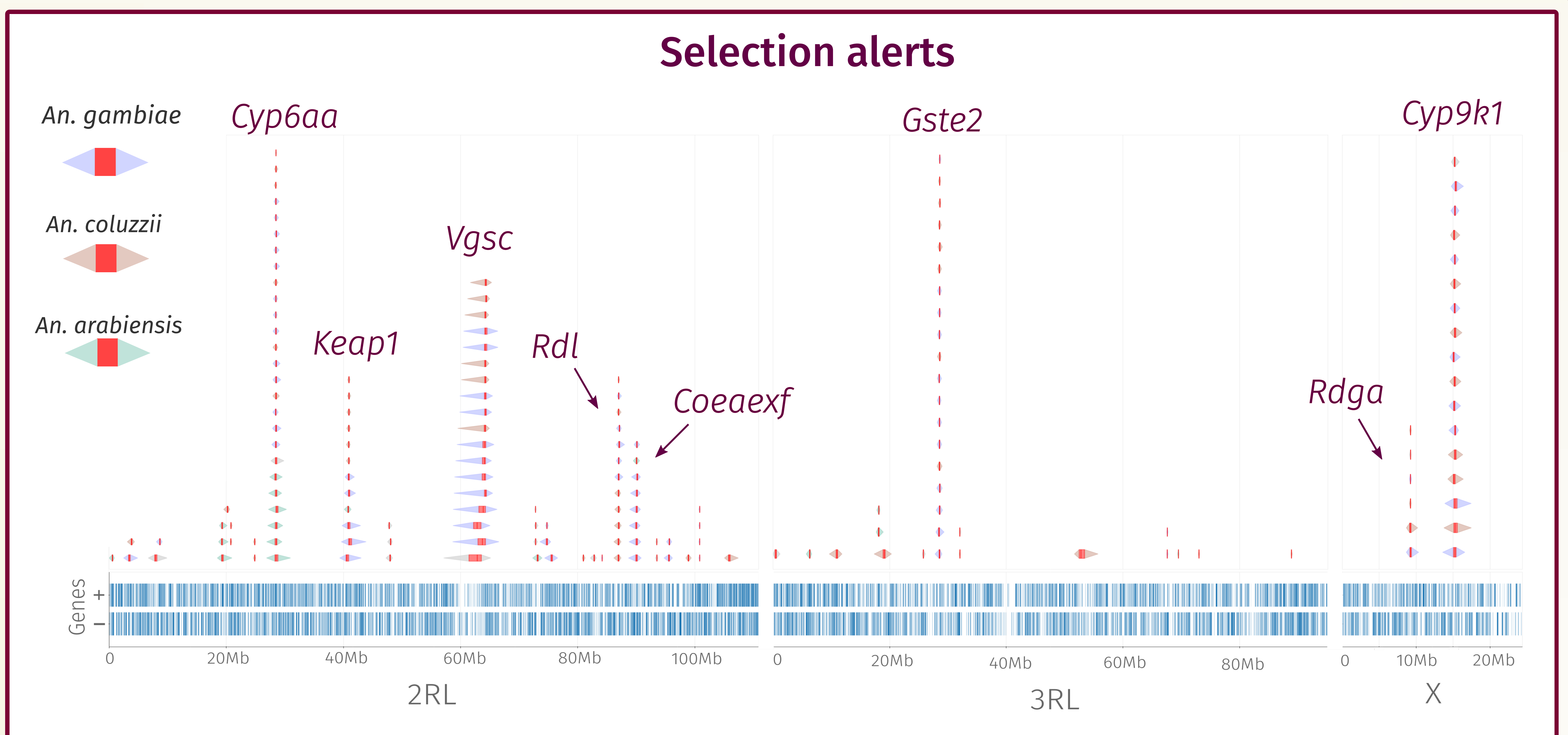


Fig 3. A summary of selection signals in phase 3 of the Ag1000G. Each diamond shape corresponds to a H12 selection signal in a given cohort. The width of the diamond corresponds to the breadth of the selection signal.

Methods



malariagen\_data



GENOMIC EPIDEMIOLOGY NETWORK

