

# SABETI LAB



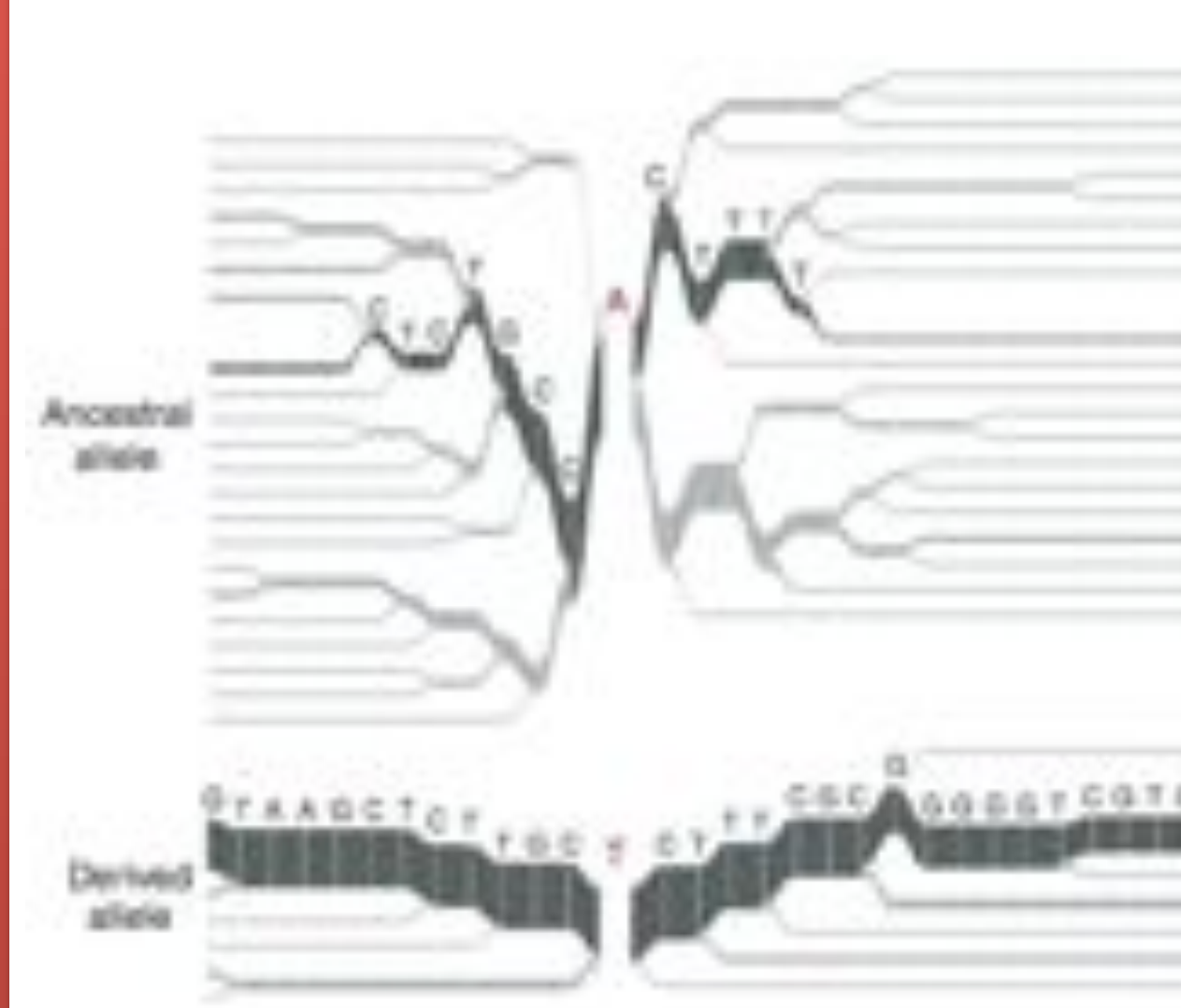
The Sabeti Lab develops and uses computational methods to scan the genome of humans and pathogens for signals of natural selection. We apply these methods to investigate the history and biological function of adaptive alleles.

## Computational Biology

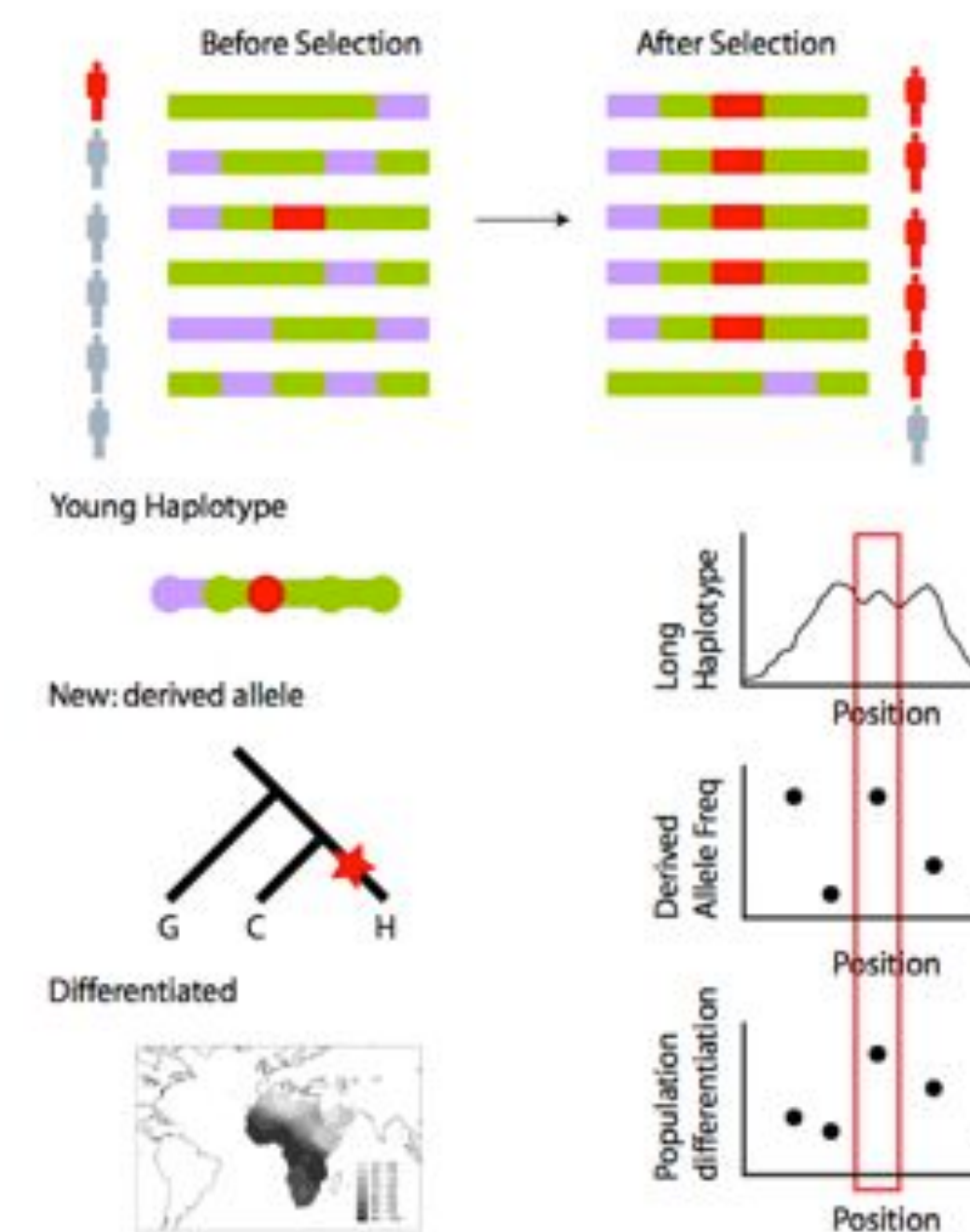
Our lab's computational focus involves the development of population genetic algorithms and bioinformatic software.

We use these methods primarily to detect signals of natural selection in the genome, but also to visualize the spread of infectious disease, and mine large-scale datasets.

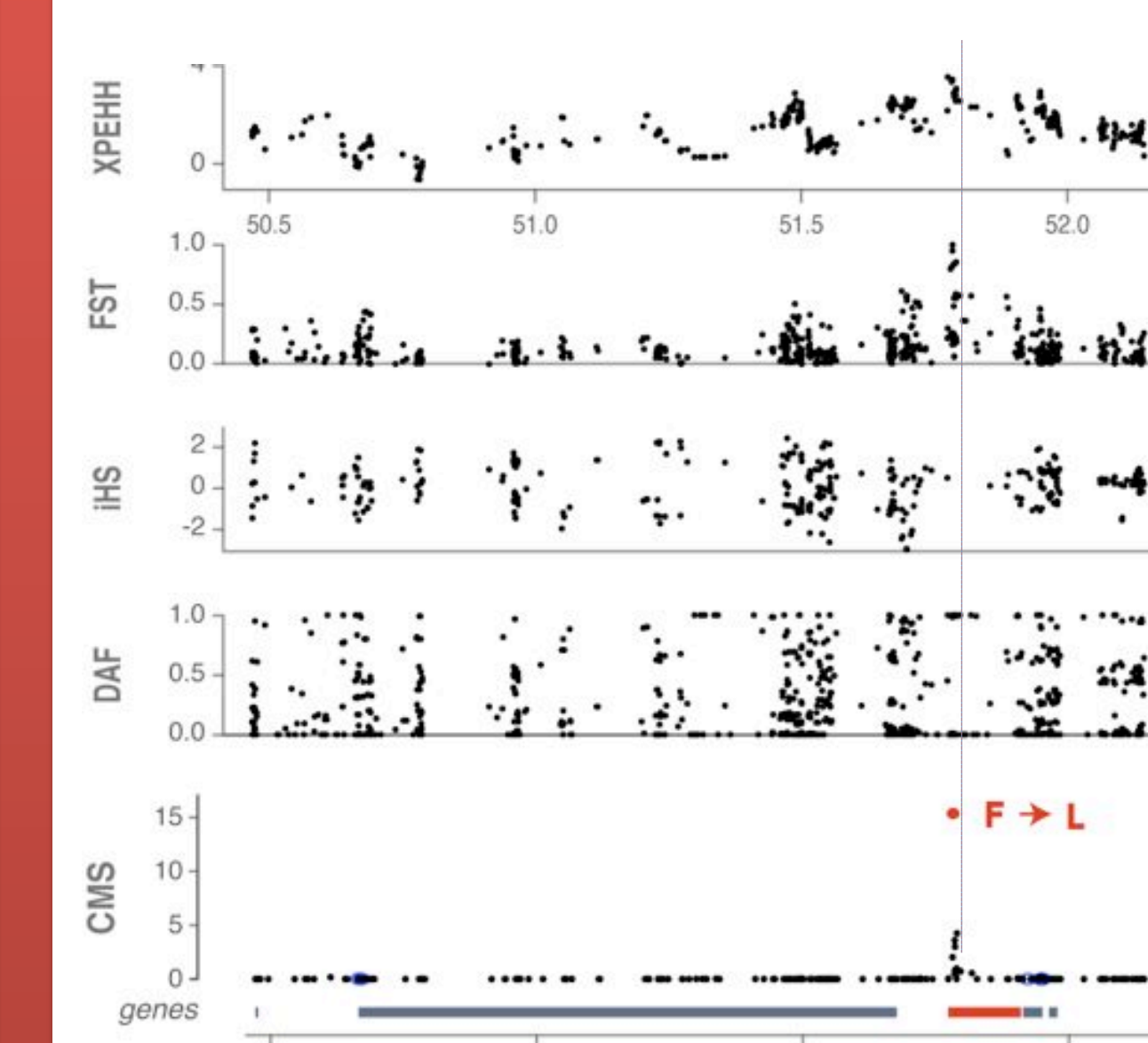
### Visualizing the Genome



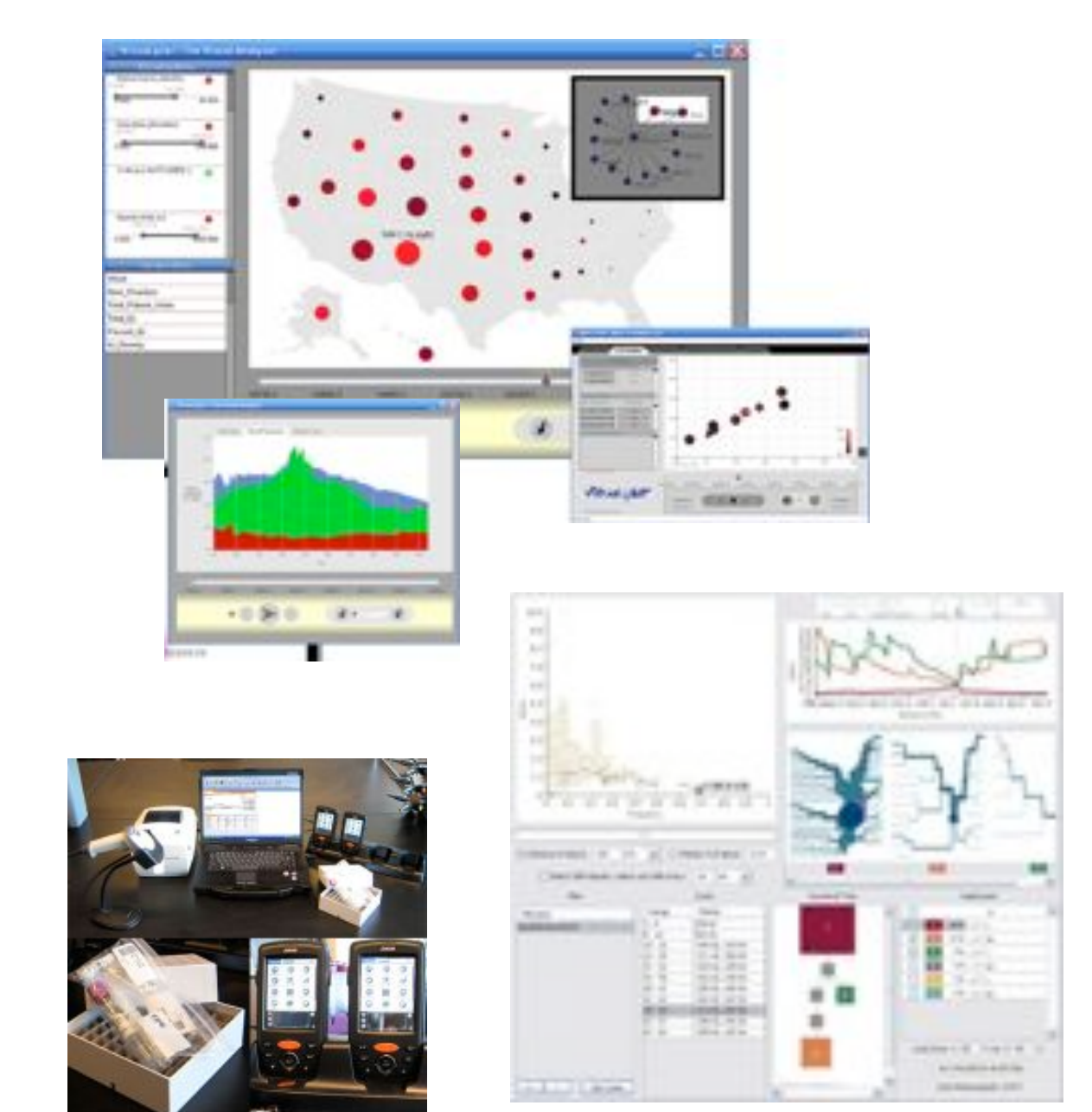
### Signals of Selection



### Composite of Signals

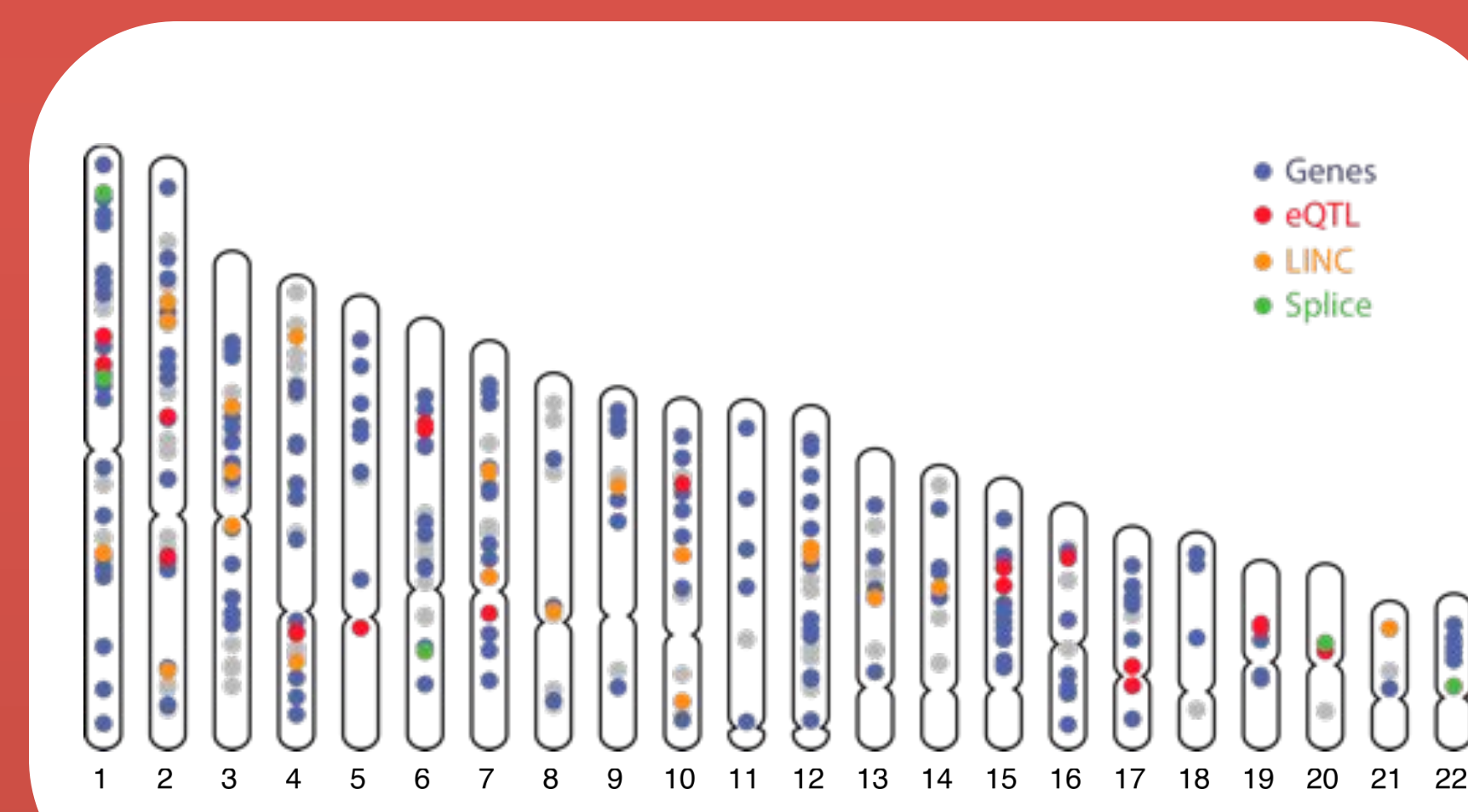


### Computational Tools



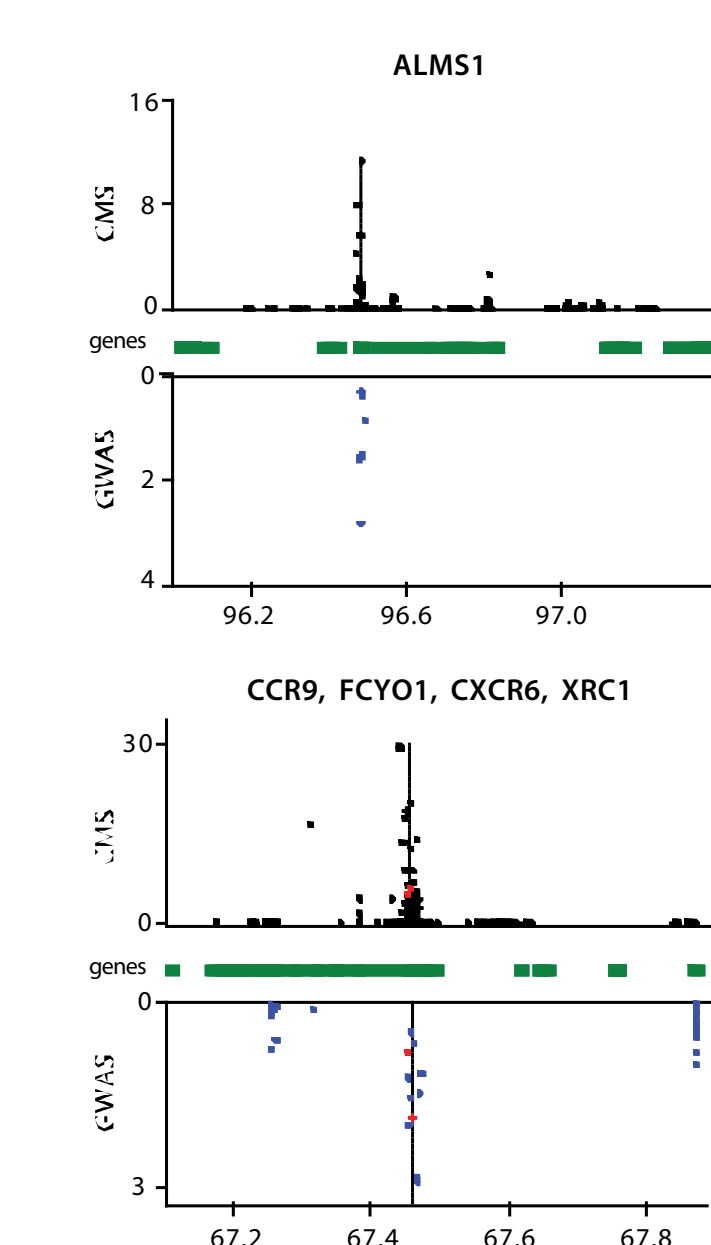
## Investigating Adaptive Evolution

Our computational methods allow us to identify loci of positive selection in the genome, but further analysis is required to determine what these alleles were selected for.

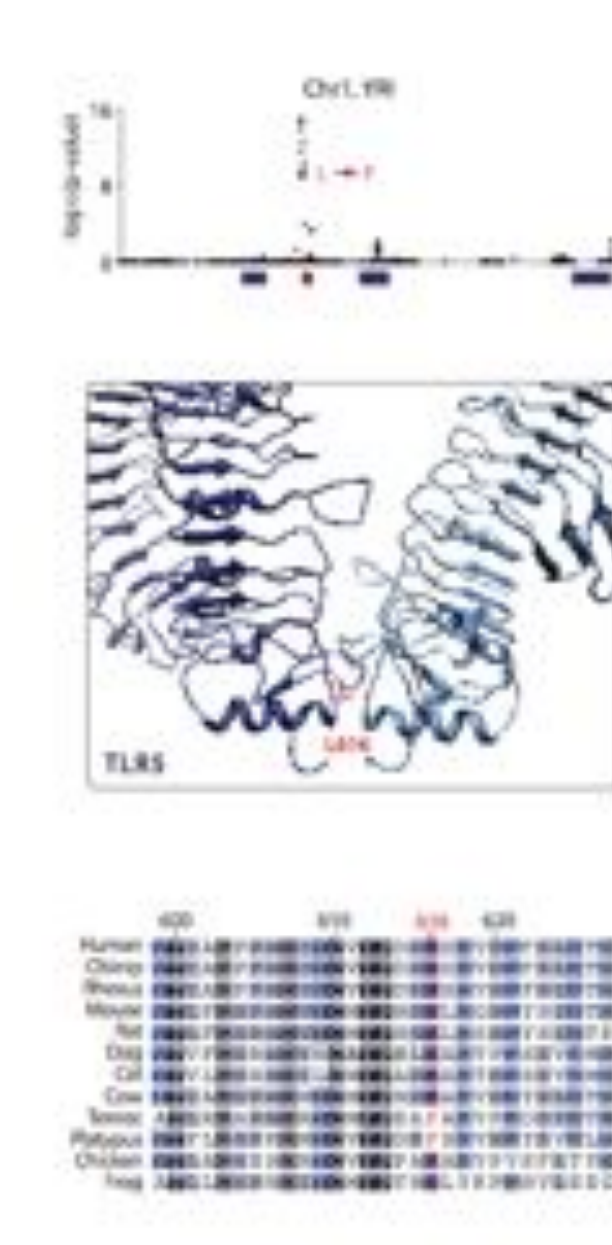


We use a number of methods including Genome-Wide Association Studies (GWAS), transgenics, and cell culture to identify the functional consequences of statistically significant loci.

### Disease Resistance



### Functional Changes

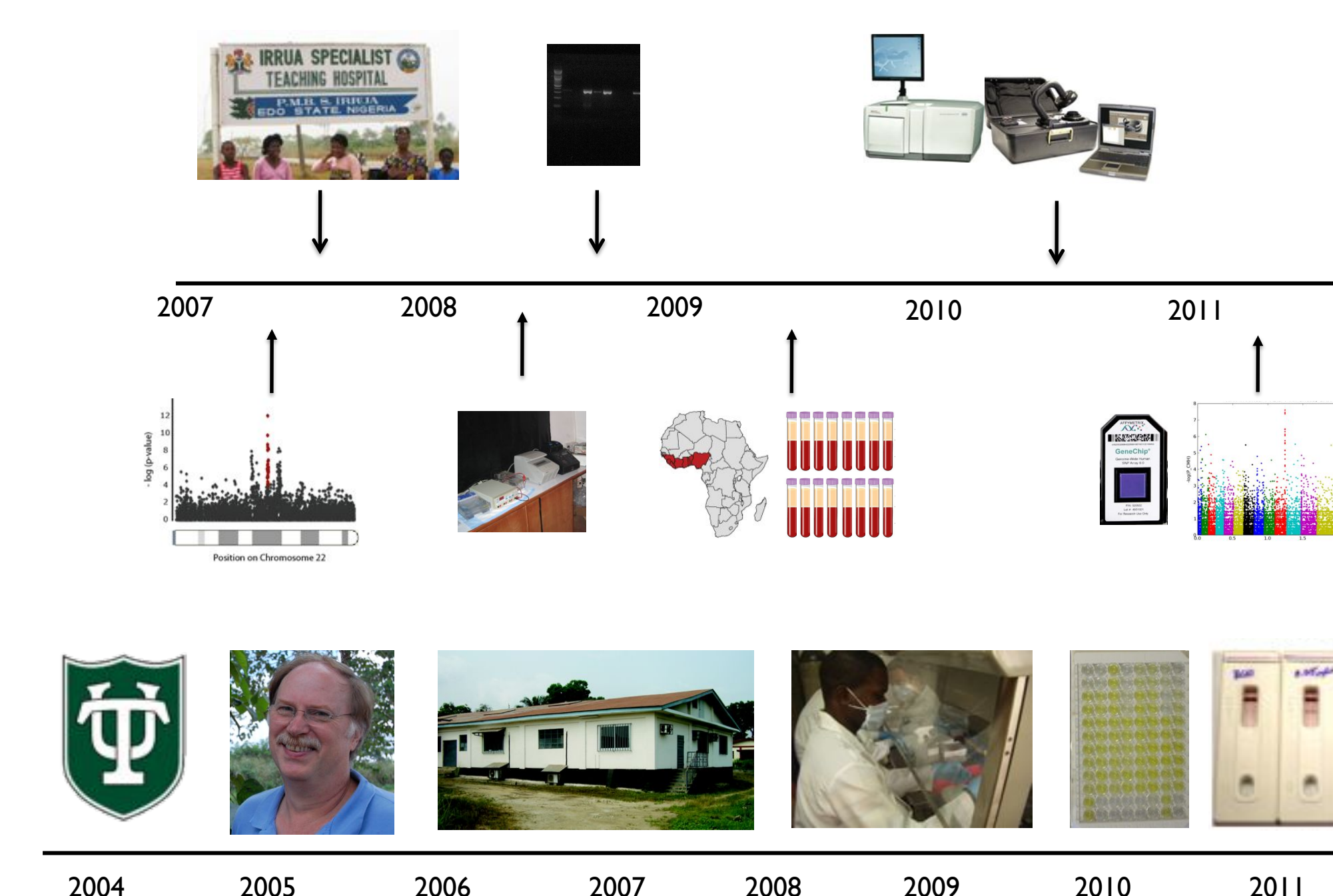


## Infectious Diseases: Malaria, Lassa Fever, and Ebola

Our computational methods are especially useful in the study of infectious diseases. Many pathogens are highly recombinant, and quickly evolve resistance to medicine. Conversely, many human populations over time develop genetic immunity to endemic diseases. Working with our collaborators abroad, we seek to identify genes that confer resistance or susceptibility, which will ultimately inform treatment and prevention strategies.



### Host And Virus Genomics in Lassa Fever



### Malaria Parasite Genomics

