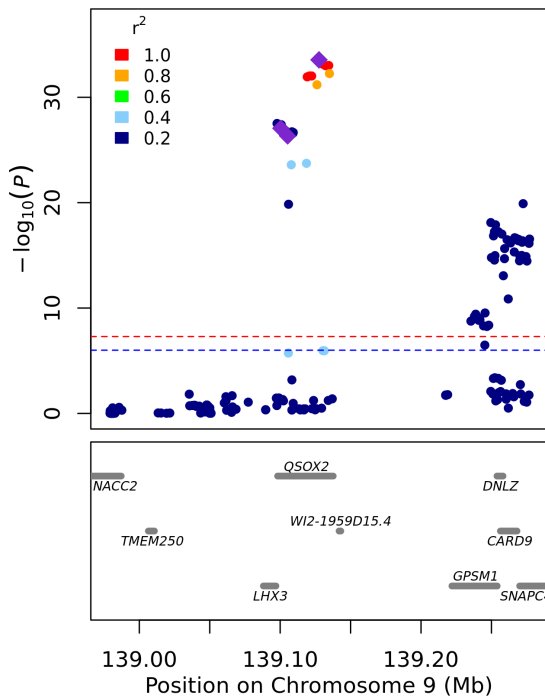


## XMAP

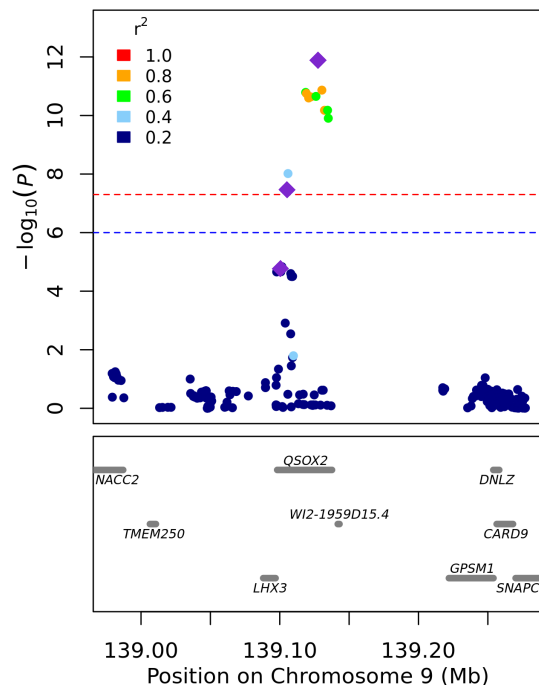
### EUR Population



### LD in EUR Population



### EAS/AFR Population



### LD in EAS/AFR Population



+

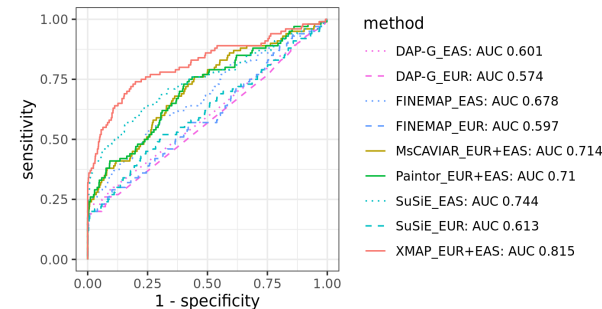
- EUR Population reference genotypes
- GWAS summary statistics from EUR population

## INPUT

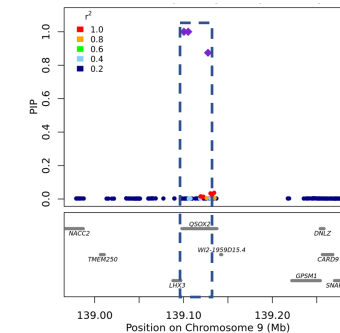
- EAS/AFR Population reference genotypes
- GWAS summary statistics from EAS/AFR population

## OUTPUT

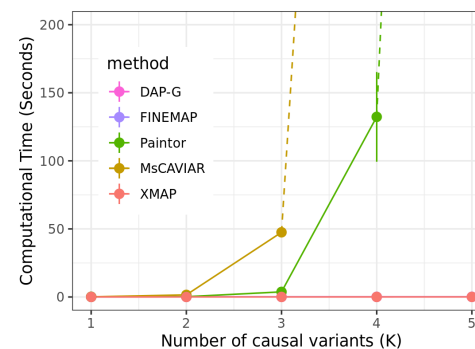
Improve power and reduce false positive by accounting for confounding bias



Detect multiple causal signals



Computationally efficient



Interpret causal variants in their cellular context at single-cell resolution

