

**Q3: why genetic diversity might be low in a genomic region**

low  $N_e$  (-> genome-wide low diversity)

high  $\mu$  (-> genome-wide low diversity)

linked selection (generally)

background selection (specific type of linked selection)

positive selection / sweep (specific type of linked selection)

low recombination (leading to high linked selection)

high density of non-neutral sites

**Q4: doodle summary statistics around selected site**

low  $\pi$  in 1, 2 at selected site

same dip in  $\pi$  in  $p_1$  and  $p_2$  at selected site

negative  $t_{ajD}$  in 1, 2 at selected site

high LD at selected site in 1,2,3

wider peaks for all statistics in pop2

lower baseline  $\pi$  in pop2

higher baseline LD in pop2

high  $\pi$  in 3

high  $T_{ajD}$  in 3

**Q5: why in GWAS half of genome might appear associated with trait?**

pop structure unaccounted for

genome-wide introgression (remember admixture mapping)

poly/omnigenic trait

omnigenic explanation is likely with huge sample size

maybe LD clumping was not performed

must correct for multiple comparisons