NextGenerationSequencing

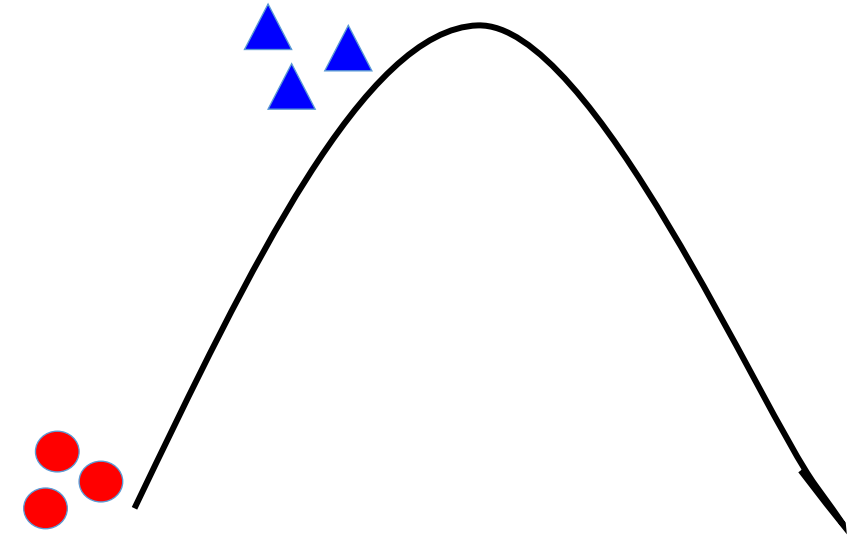## Genomics

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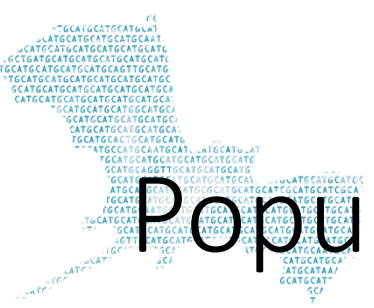ETH Zurich

Which genes genes are responsible for altitudinal adaptation in Carnation?

Re-sequencing of population pools

Fior, unpublished

Population genomics in a non model organism

1) **Genome assembly**: short paired-end reads at 100 X, different mate-pair libraries from **one individual**

   Option 1: Long reads only PacBio/Nanopore reads at 80 X coverage and for polishing short Illumina reads, Optical mapping/10X/Hi-C

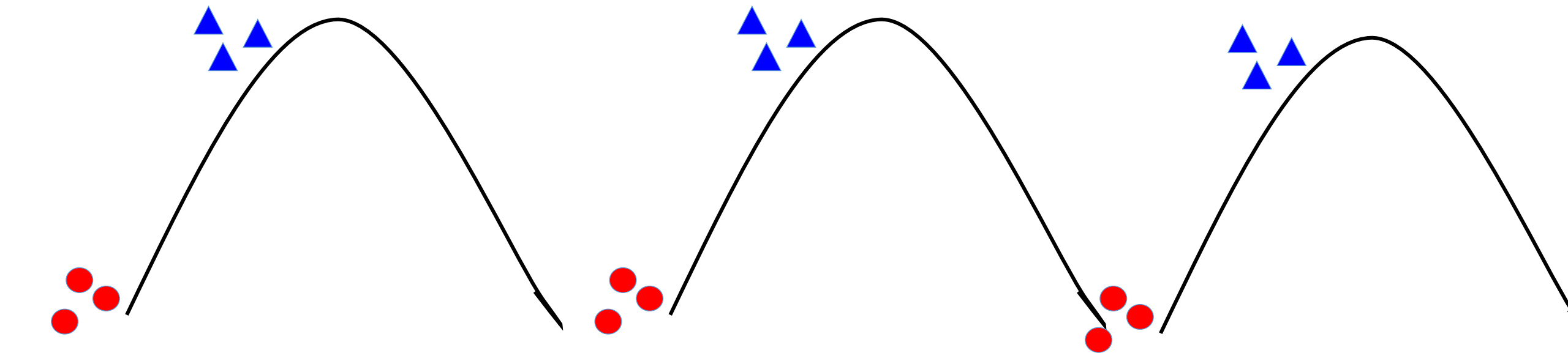   Option 2: PacBio/Nanopore read at 10 X plus Illumina at 50X

   Option 3: llumina paired-end reads (100X)

   RNAseq data for the genome annotation (Illumina or ONT)

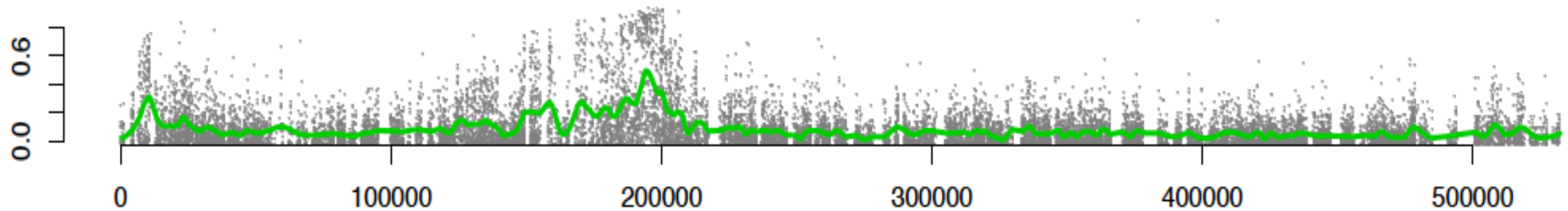2) **Resequencing** (80X, short paired-end reads) of multiple populations (Pool-seq)

   Option: ultra low coverage sequencing (0.5-2X)

Sampling design

3 low-high altitudinal population pairs in three valleys
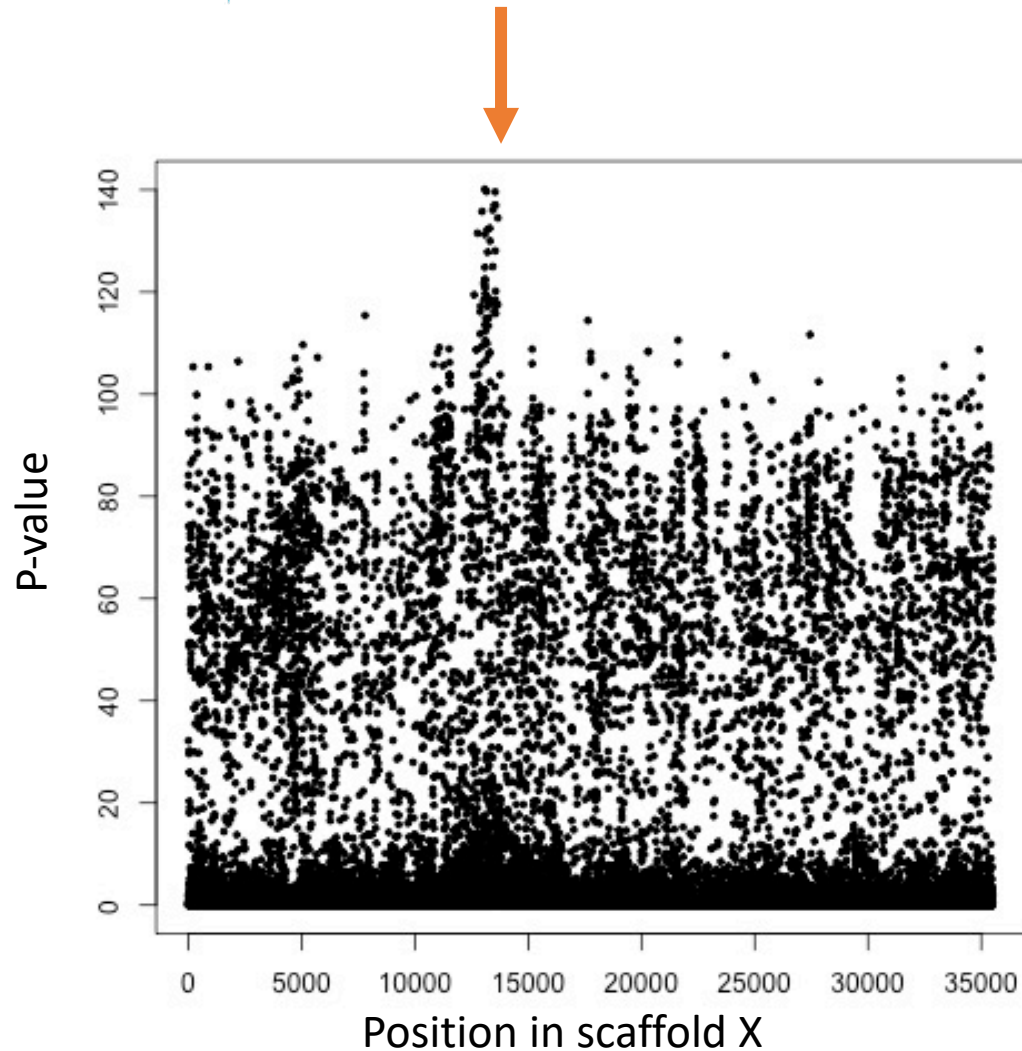
Method: Genome Scan
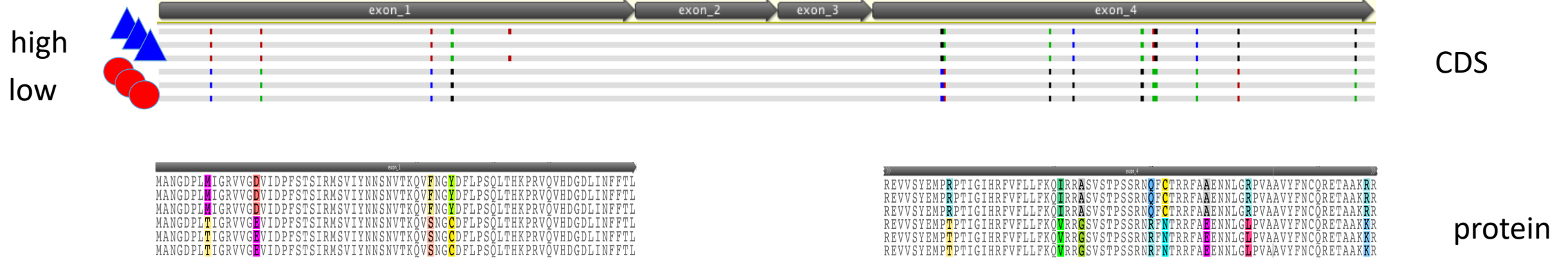

-> 20 individuals from each population

Genome scan show flowering gene that is under selection between low and high altitudinal population

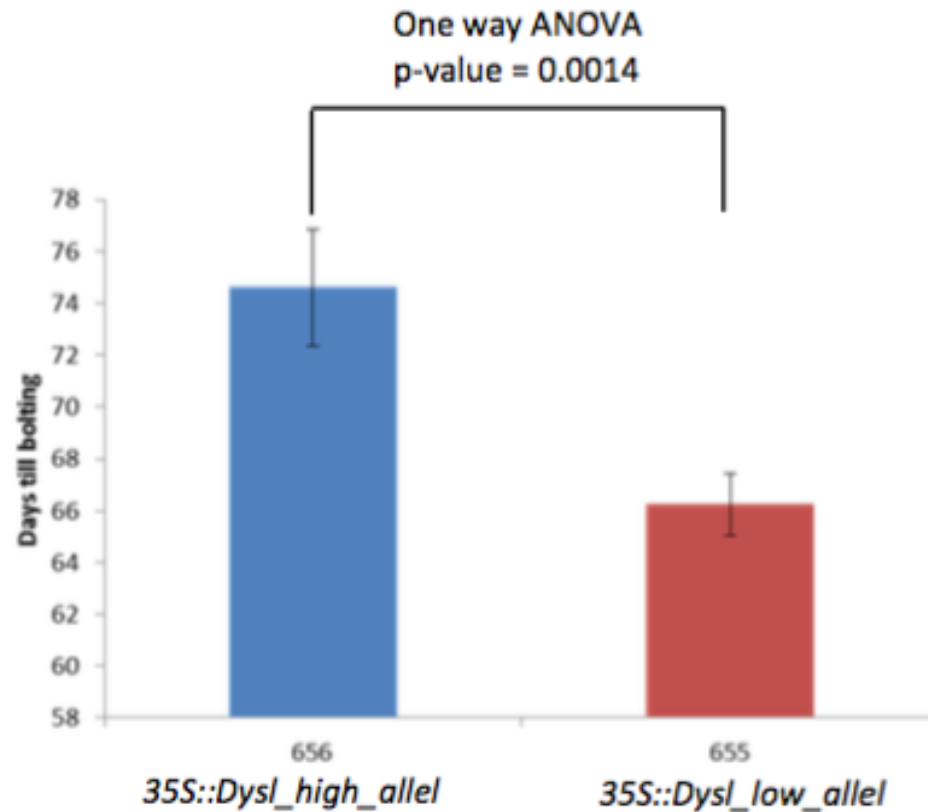# Method: Correlation between phenotype and genotype (GWAS)

Variation in the flowering gene is highly correlated with differences in flowering time.

Method: SNPs in CDS and protein translation

Fixed differences between the low and high altitudinal allele.

Method: Phenotypic effects of the two alleles

The two alleles induce different phenotypes in *A. thaliana*.