RAD
Applications

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24 June 2020

Genetic Diversity Centre (GDC)
Bioinformatics
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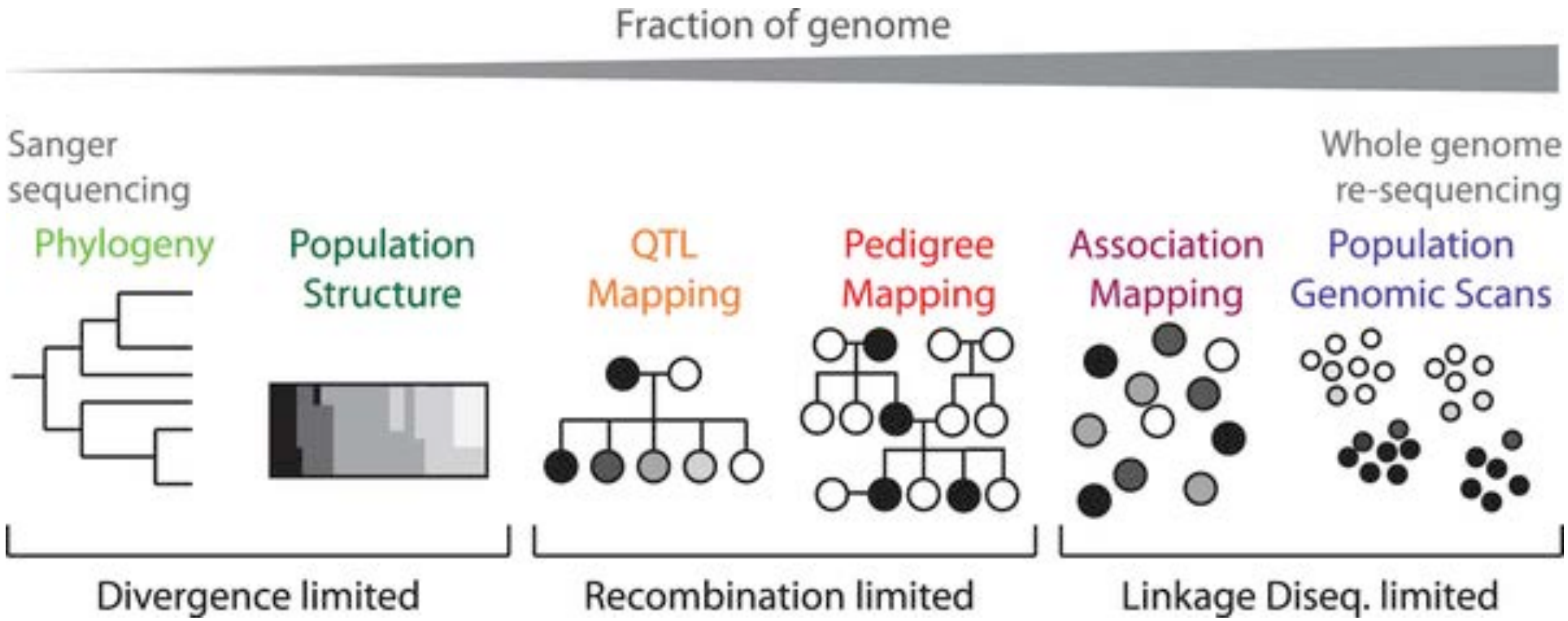
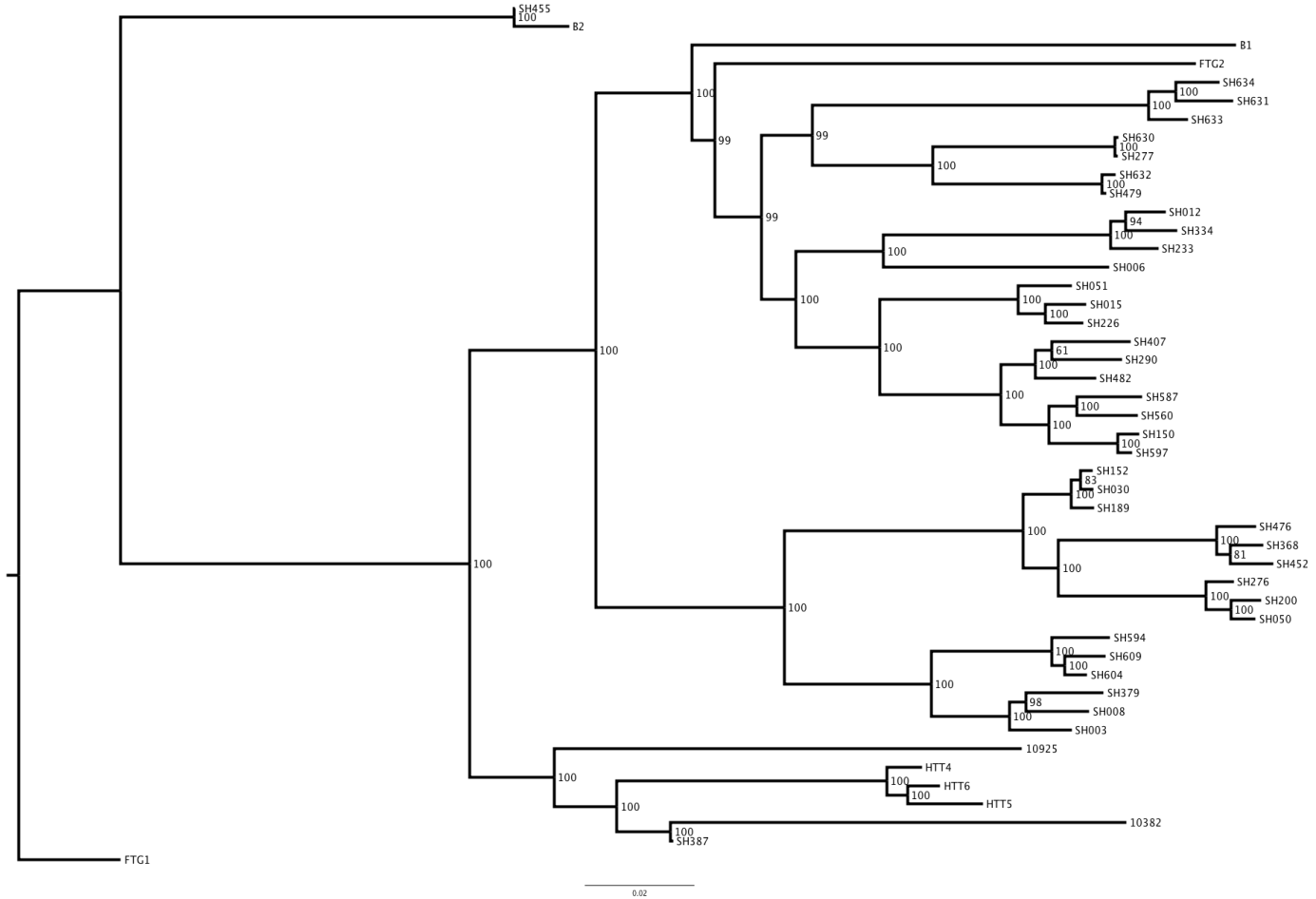
What is it good for?



Peterson et al. 2012

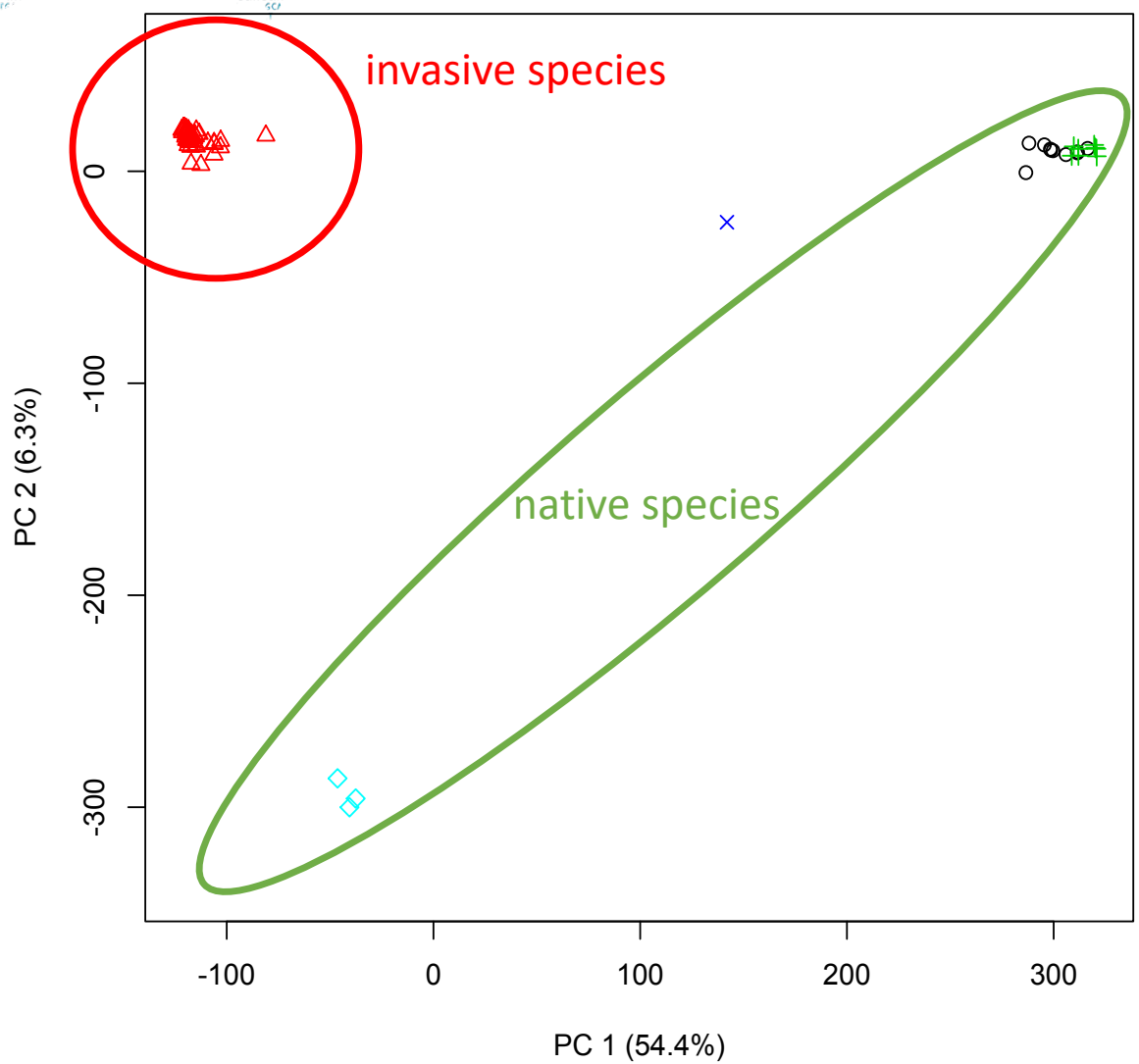
Phylogeny of rosewood species from Madagascar



Better resolution with ddRAD compared to traditional barcoding markers

Crameri S, unpublished

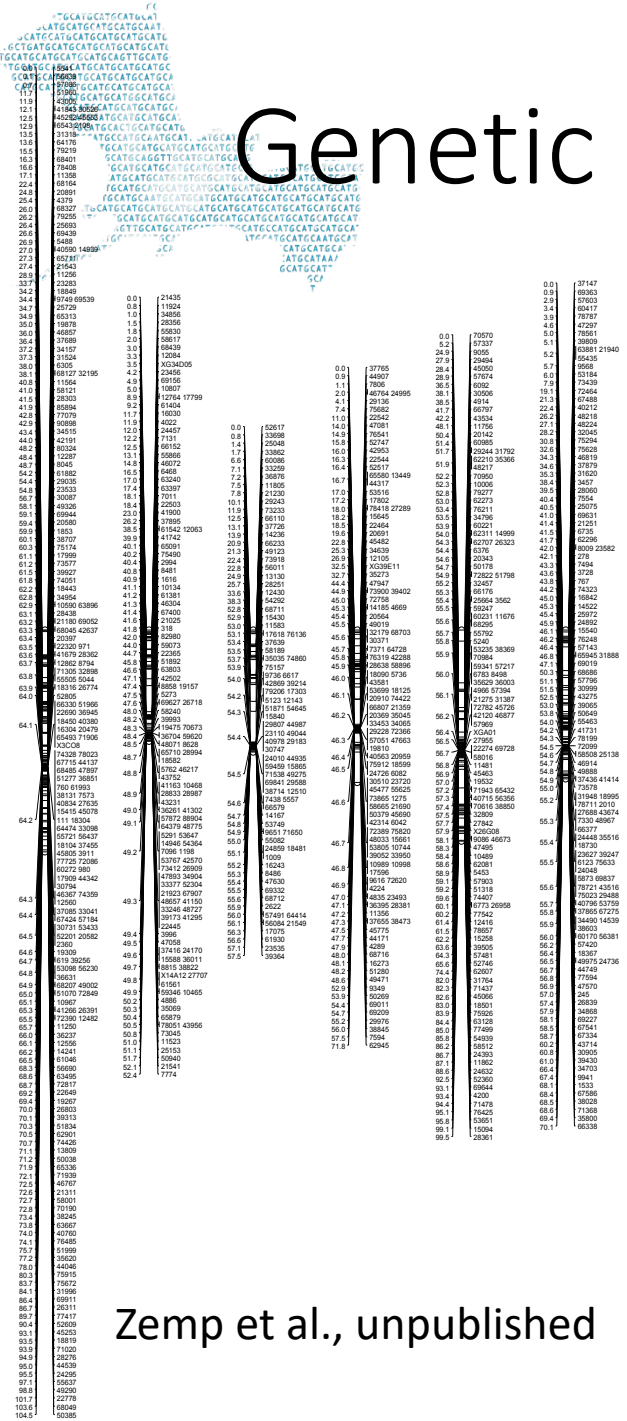
Population structure



Widmer and Zemp, unpublished

No hybridization between invasive and native groundsel species

Genetic linkage mapping



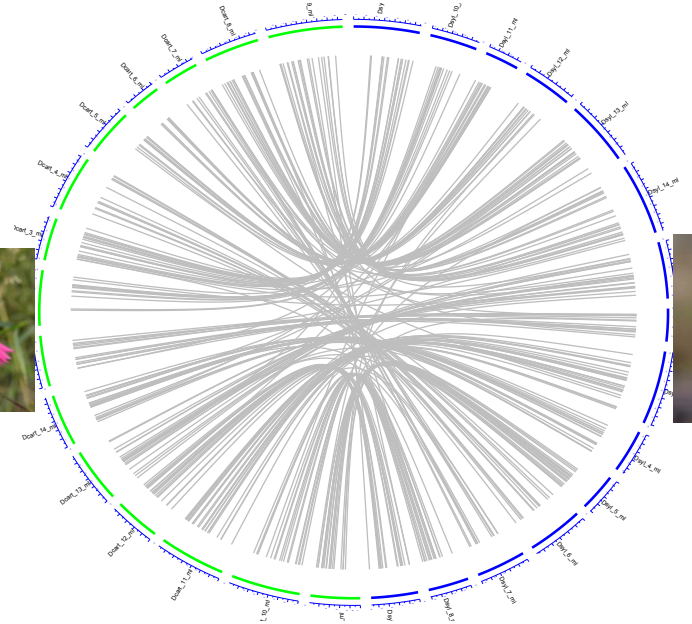
Zemp et al., unpublished

A

B

C

More recombination events between A and C than A and B

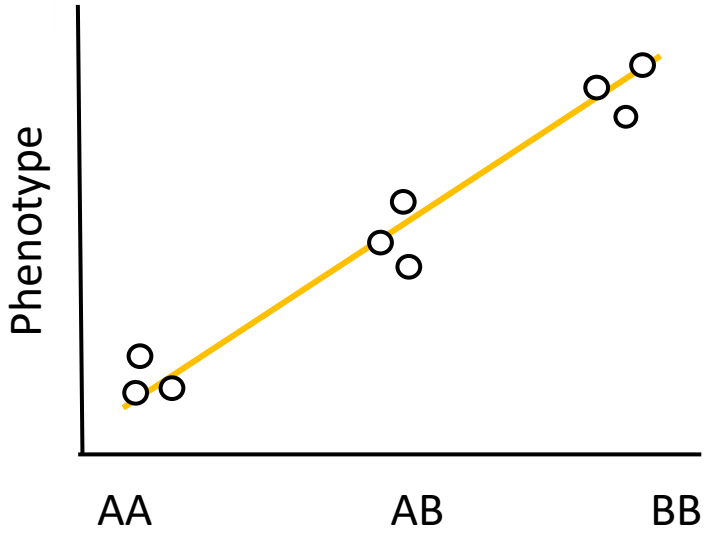


Fior et al., unpublished

Ordering the fragments using recombination rates in the offspring

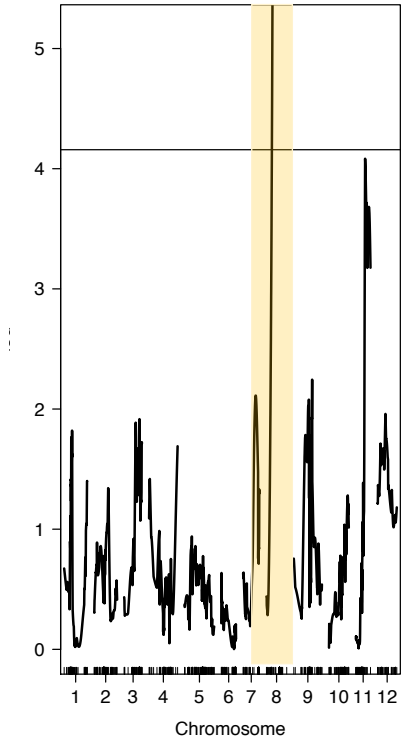
- Distribution of fragments across the genome
- Scaffolding and comparative analyses of draft genomes
- Estimate recombination rate across the genome

Correlations between phenotype and genotype (QTL, GWAS)



Looking for loci that are highly correlated with a certain phenotype

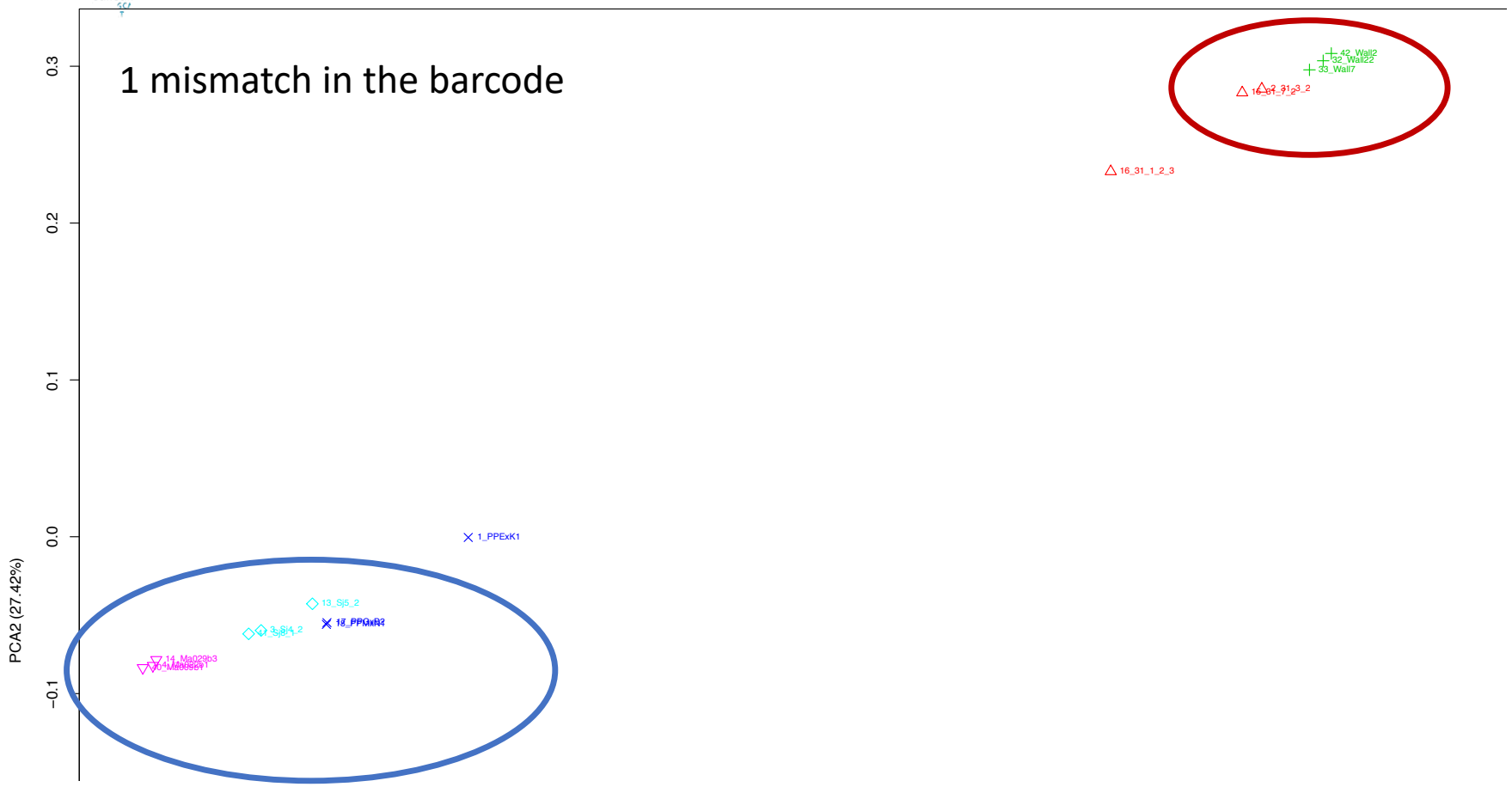
Plant height



Crameri, Nenadic and Zemp, unpublished

ddRAD data from single individuals

1 mismatch in the barcode

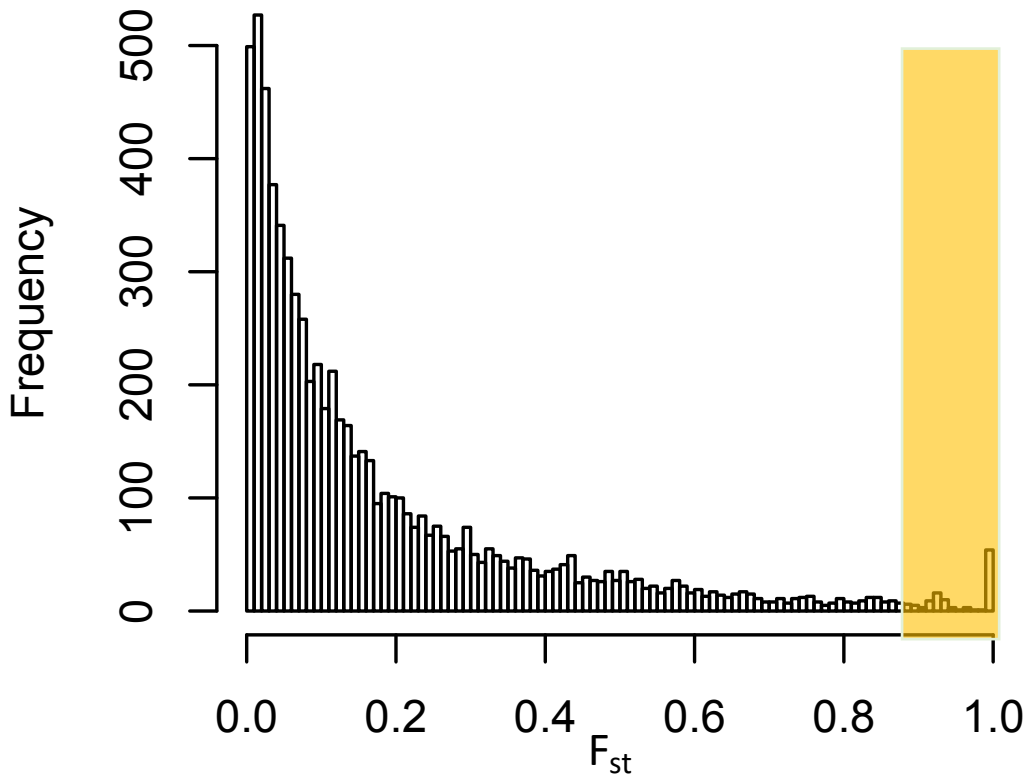


Species A

Species B

Fischer MC, unpublished

Genome scans

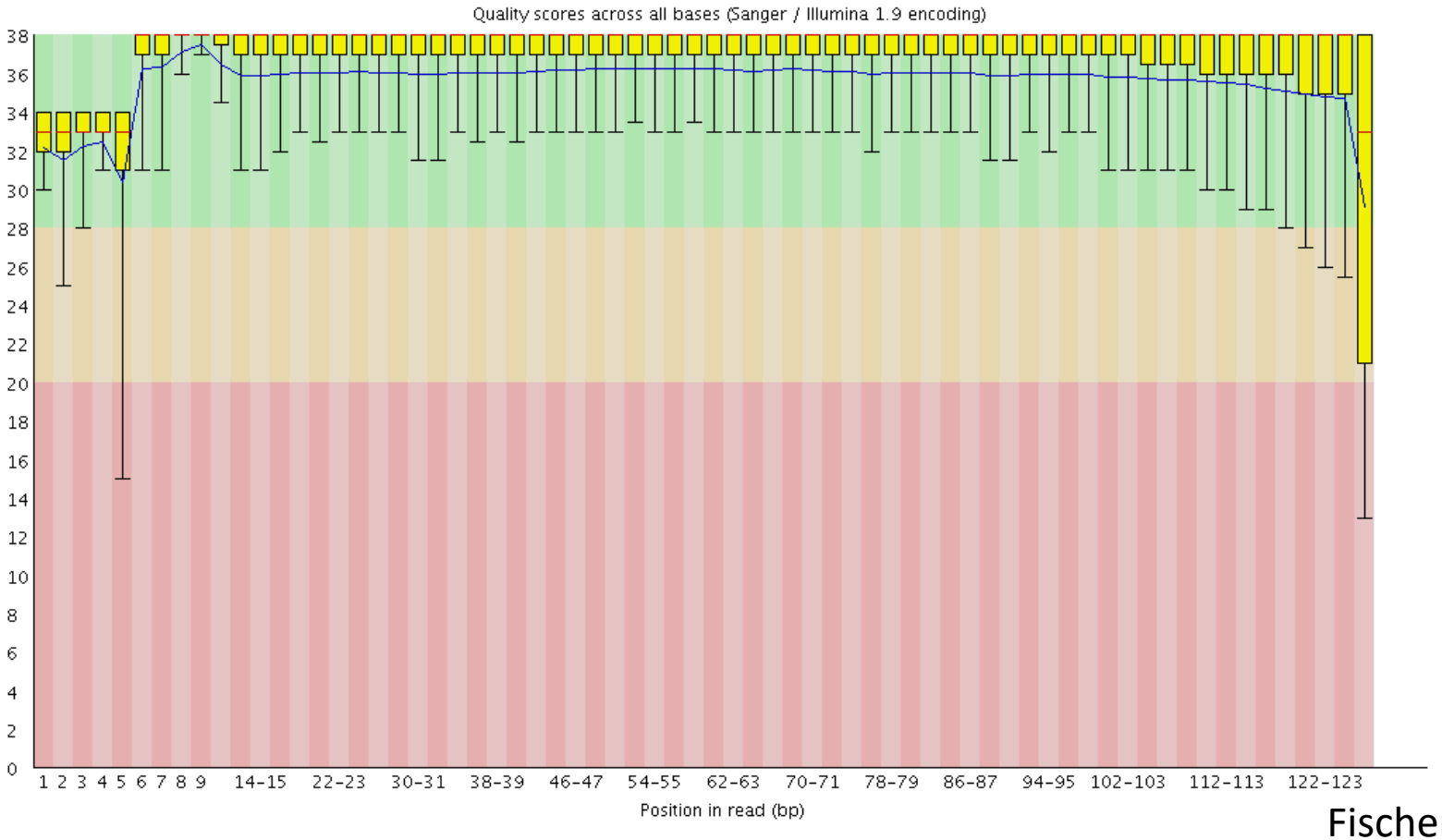


no differentiation → complete differentiation

Looking for loci with increased differentiation (F_{st}) between species

Zemp et al., unpublished

ddRAD data from single individuals



Fischer MC, unpublished

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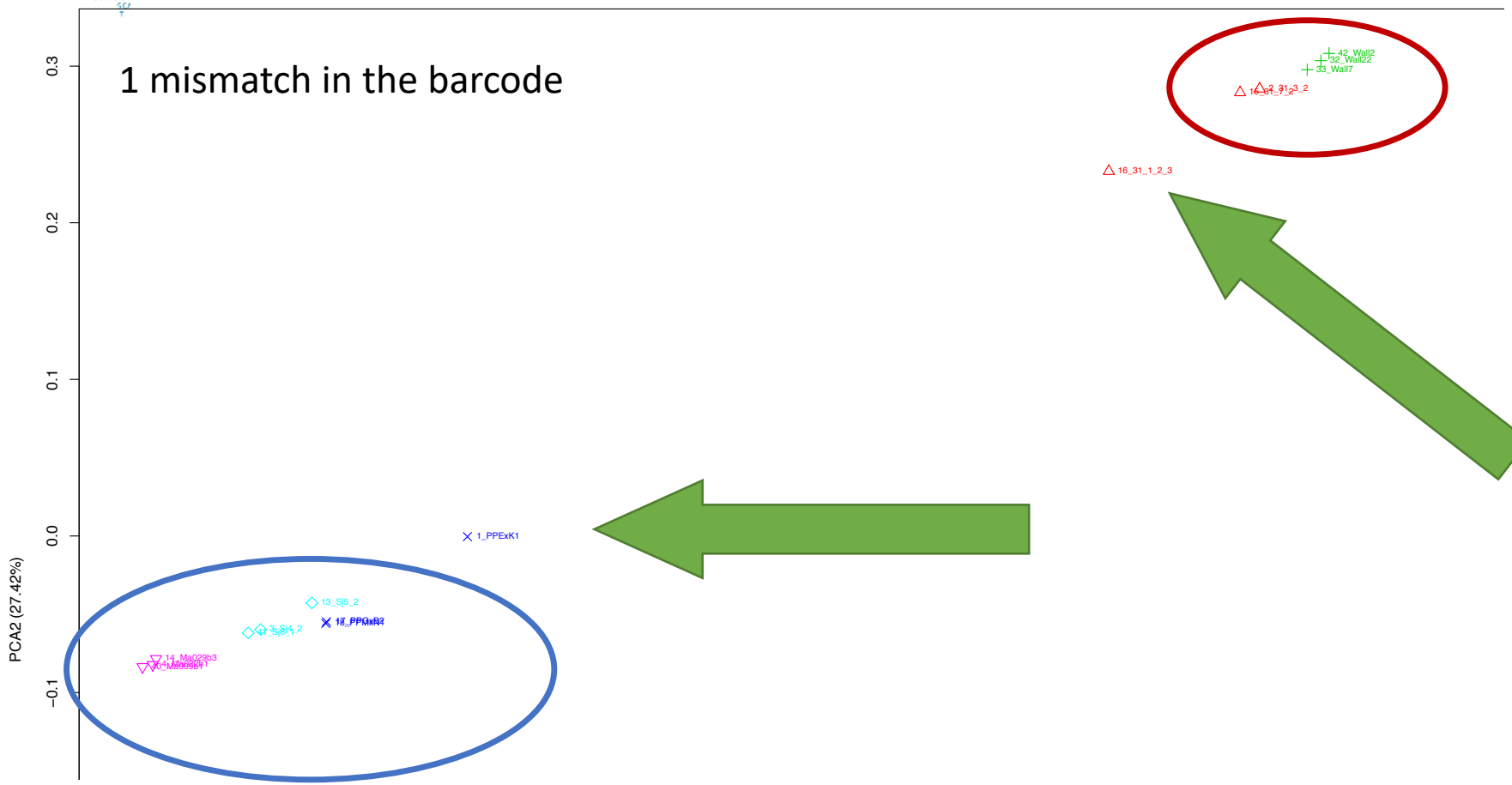

Species A

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Fischer MC, unpublished

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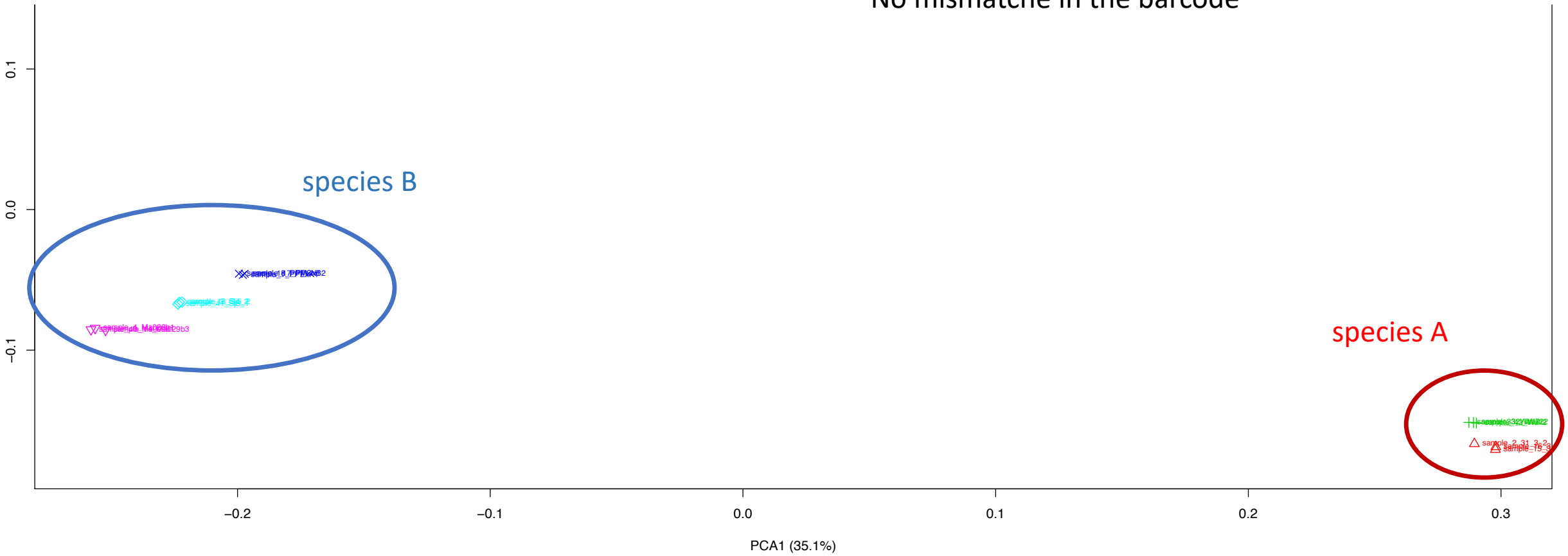
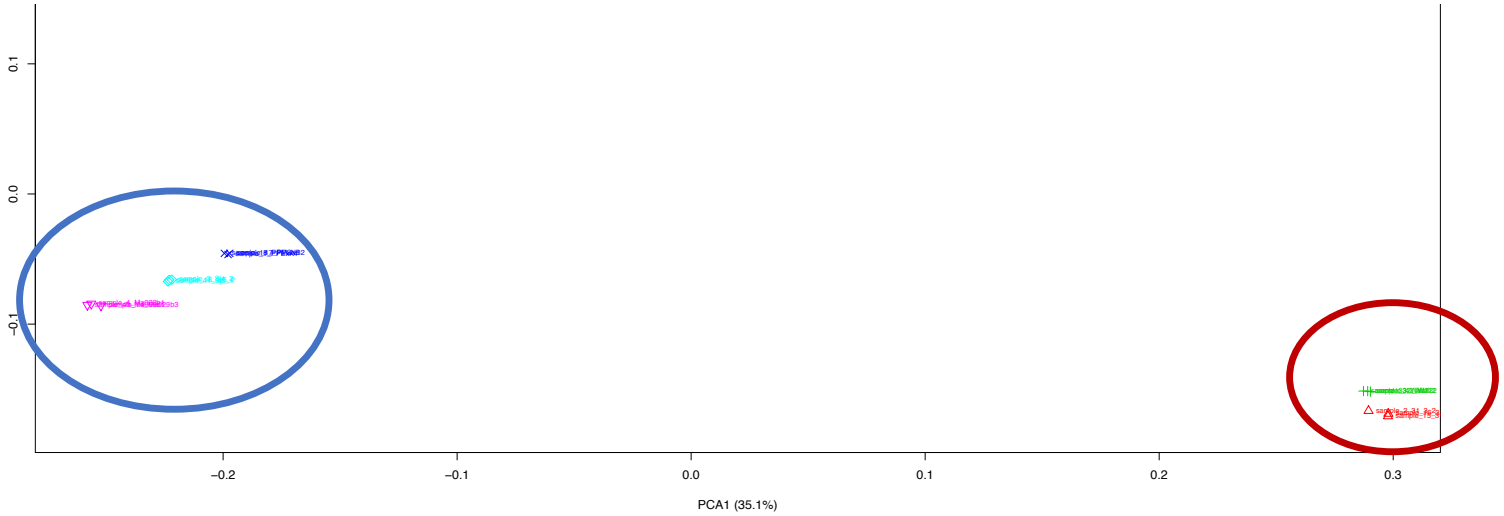


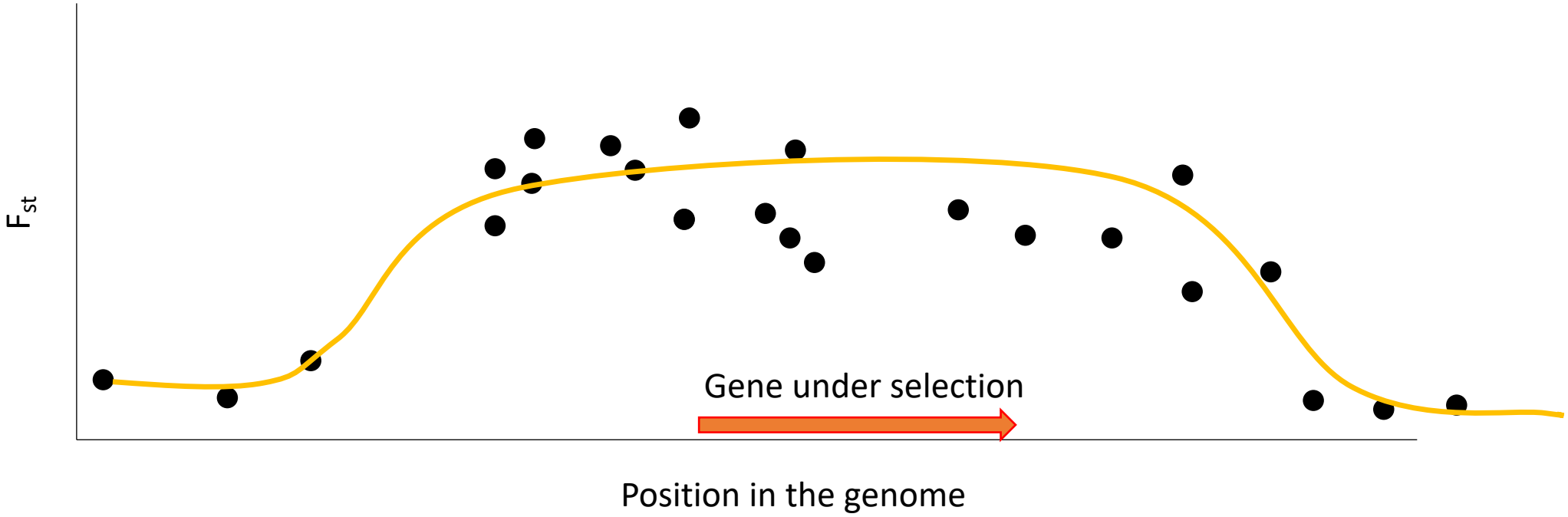
Fischer MC, unpublished

ddRAD data of single individuals

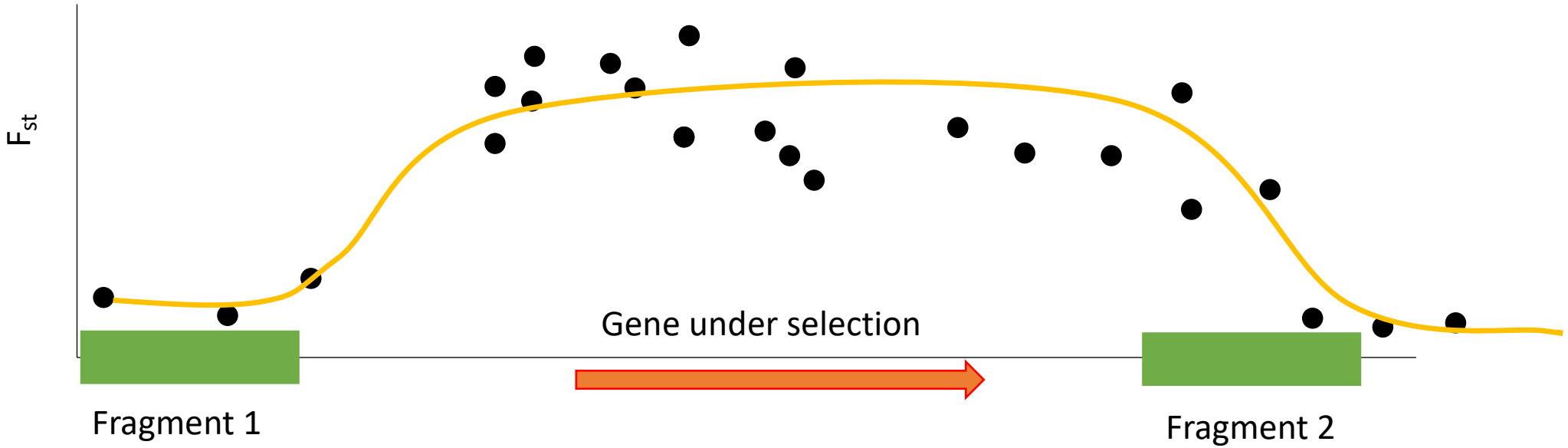


stringent demultiplexing
biological replicates

Can RAD be used to detect genes under selection?



Can RAD detect every genomic signal?



- Linkage decay (LD)
- Fragment density
- Island size

Potential challenges

High stochasticity in read coverage

Consistent library preparation, appropriate filtering

Reconstruction of loci can be difficult because of short single-end reads

Long paired-end reads can improve the de novo assembly

Wrongly inferred SNPs due to PCR duplicates

Modifications of the protocol, few PCR cycles during library preparation

Single individuals

Use replicates or apply stringent demultiplexing

Potential challenges

Allele dropouts

Biased population genetic estimators

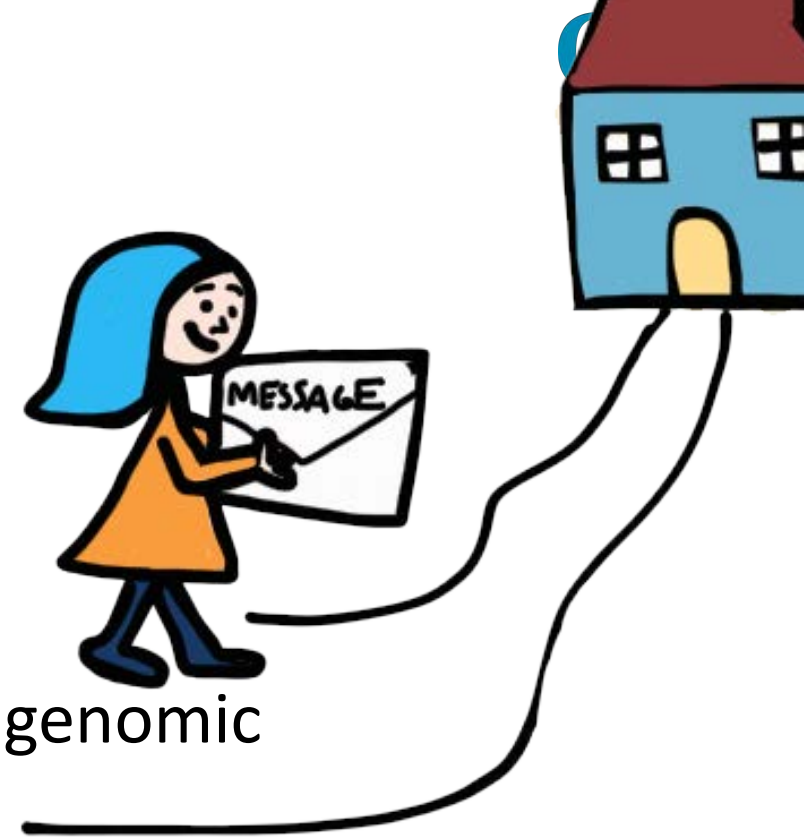
Often not in gene regions

Possible signals could not be detected in genome scans or GWAS

Single loci

The reconstruction of single loci can be challenging even with a genome

Take home message



- Useful and inexpensive approach for a wide range of genomic questions
- There are limitations