

Summary of the analysis
pipeline until now

&

Introduction of
Pundamilia cichlids

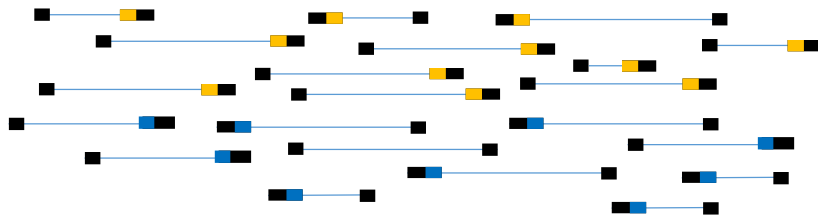
Whole-genome short-read sequencing

DNA

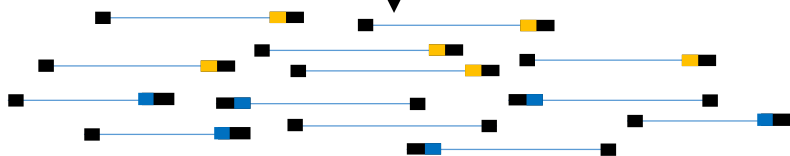
↓ Random shearing



↓ Illumina adapter ligation
incl. individual index



↓ Size selection



paired-end sequencing

Up to 20 billion read pairs

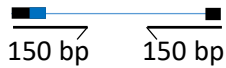


1. Quality check and trimming raw reads

paired-end Illumina sequencing



Up to 20 billion
read pairs



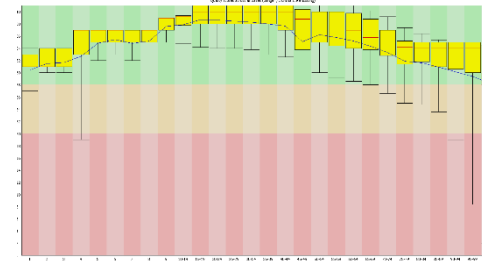
Forward
reads



Reverse
reads

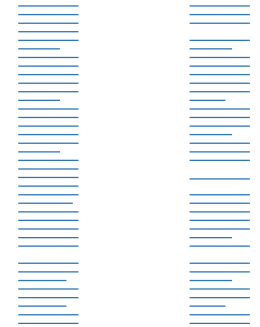


Fastqc quality plots



fastp

Trimmed and filtered
reads of good quality



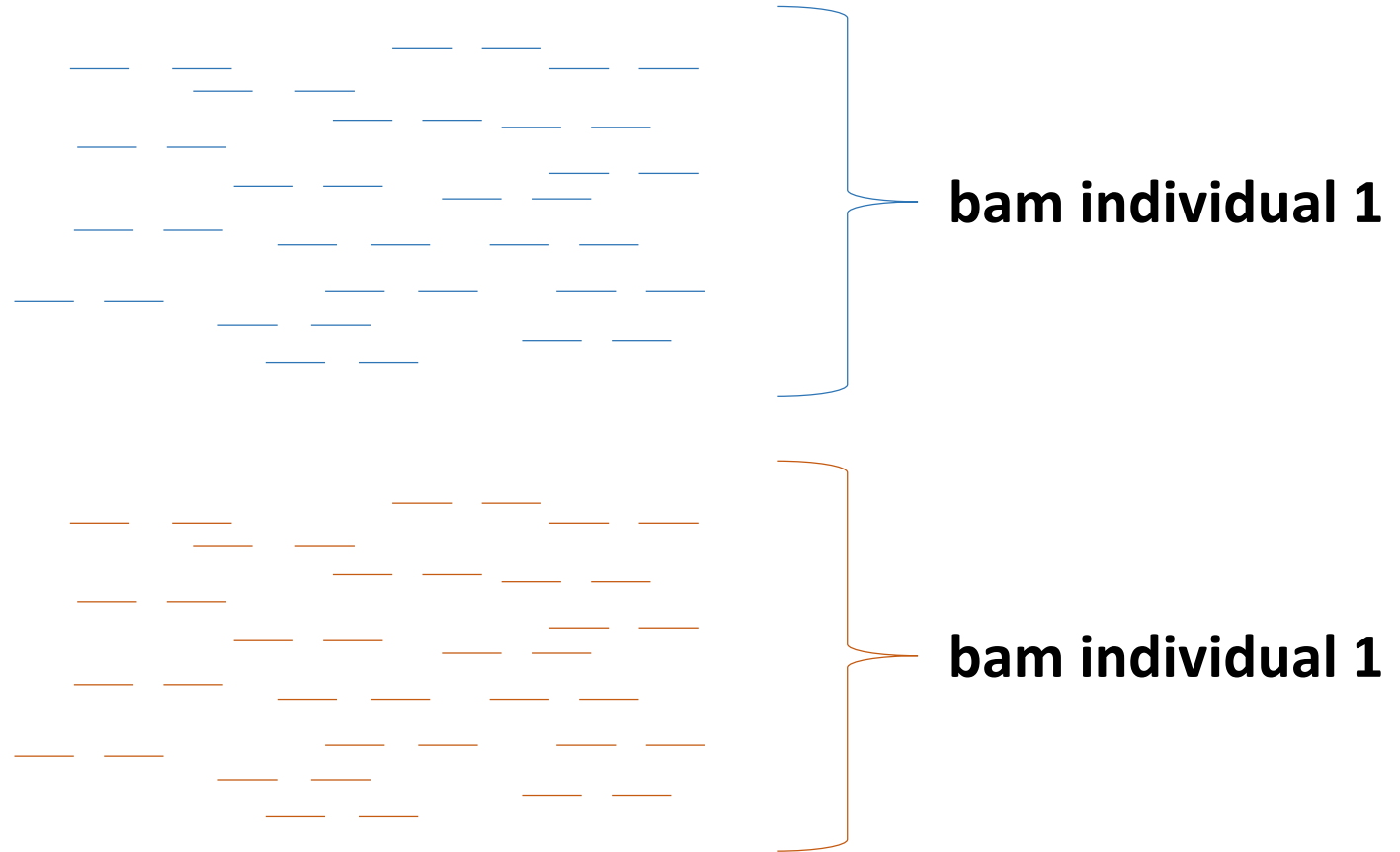
Fastq file of reads

```
@HWUSI-EAS611:34:6669YAAXX:1:1:5069:1159 1:N:0:
TCGATAATACCGTTTTTTTCCGTTTGATGTTGATACCAT
+
IIHHIIHHIIIIIIIIIIIIIIIIIIIIIIIIIIHHIIIIHHIIII
```

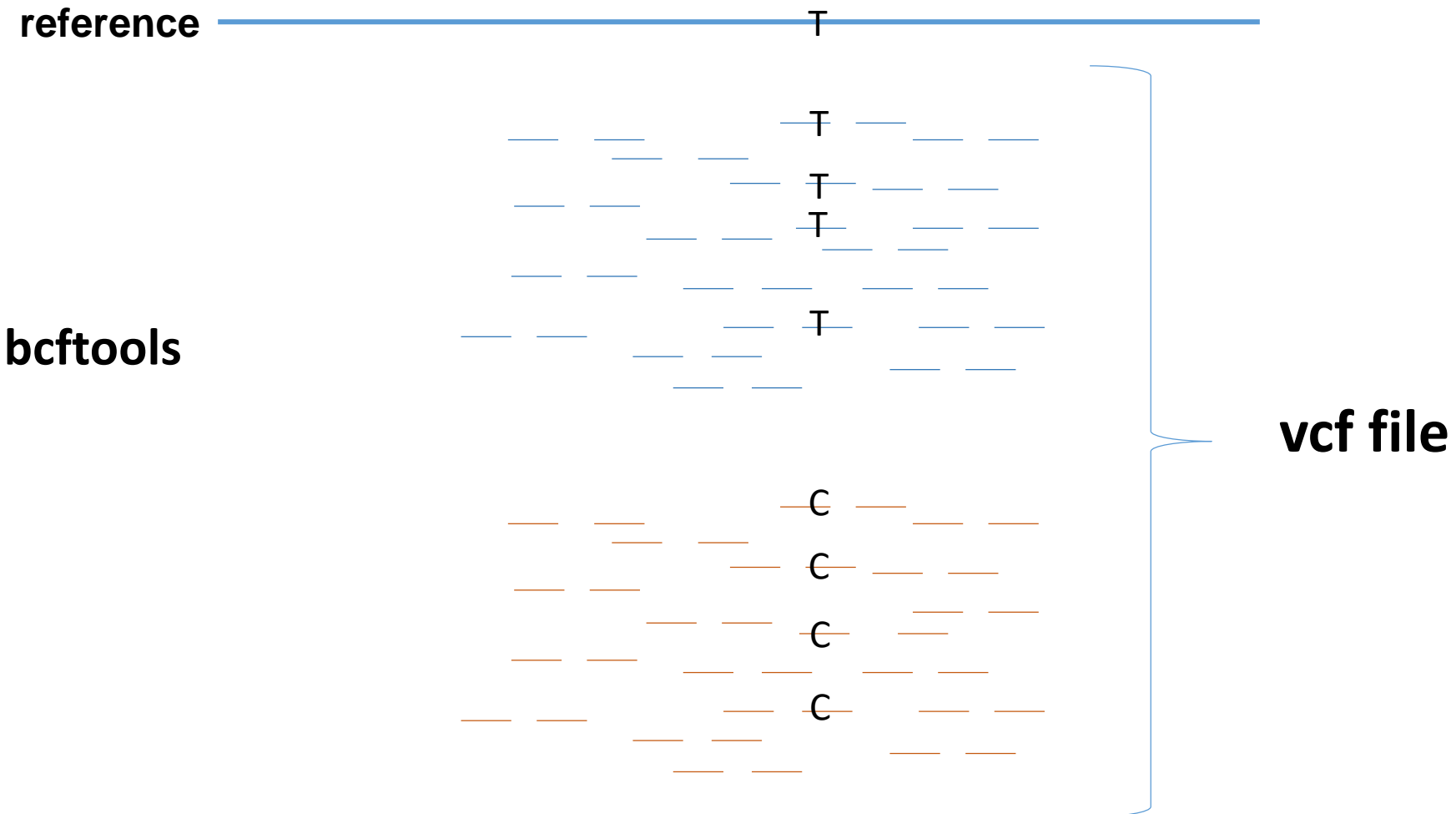
2. Alignment to the reference genome with bwa

reference

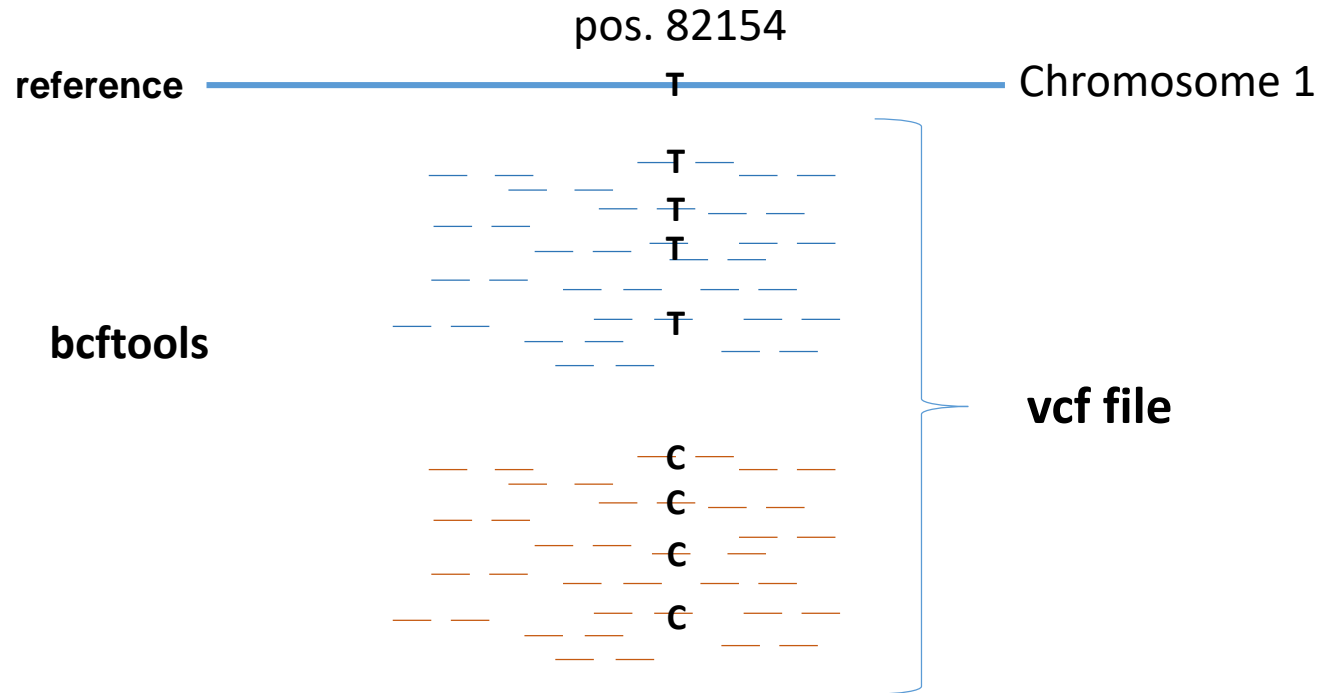
bwa



3. Variant and genotype calling with bcftools



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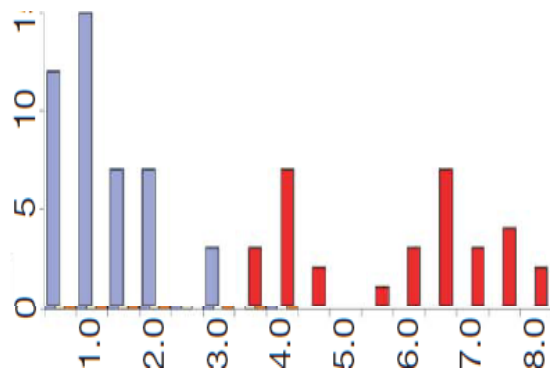
vcf file: Genotypes for each individual at genomic sites

```
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype"
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT GEN
chr1 82154 . T C . GT 0/0 1/1 0/0 1/1 0/0 1/1
chr1 752566 . T . . GT 0/0 0/0 0/0 0/0 0/0 0/0
chr1 752721 . T C . GT 1/1 1/1 1/1 1/1 1/1 1/1
chr1 752721 . A . . GT ./.
```

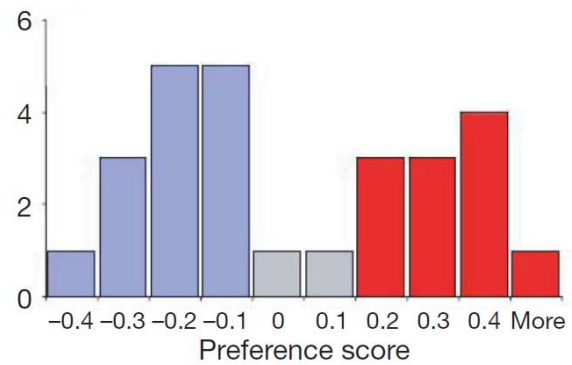

Pundamilia species complex



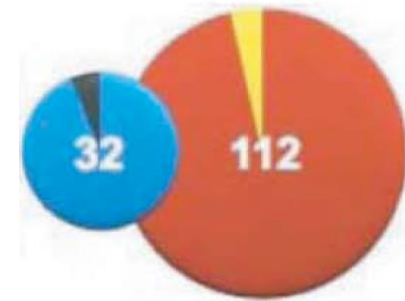
Water depth distribution



Female preference

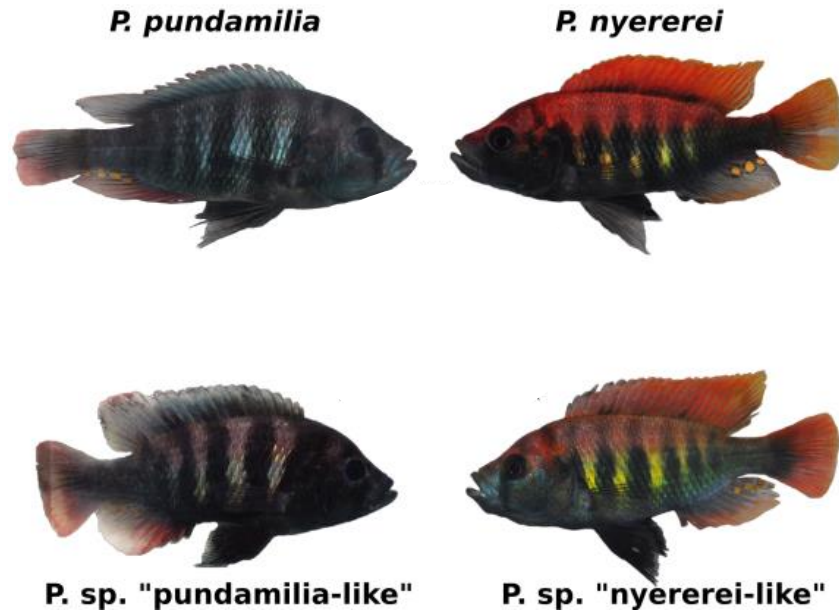


LWS opsin alleles

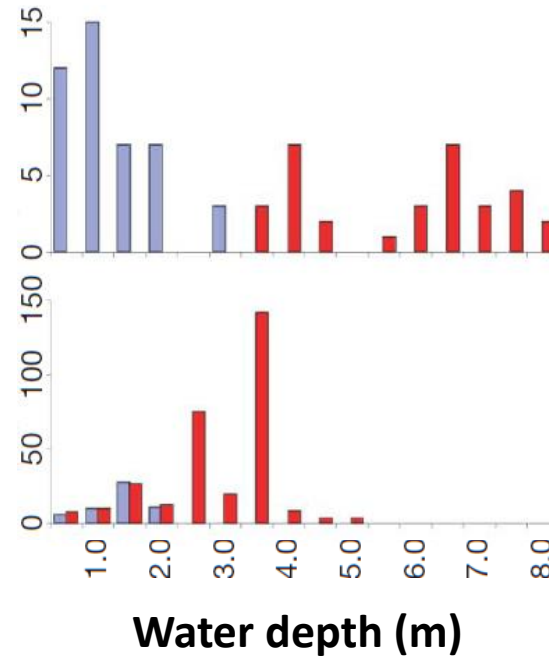


Parallel differences in phenotype, water depth, color vision

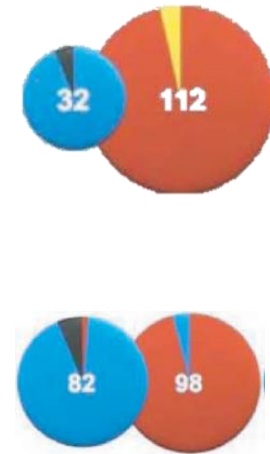
Male nuptial coloration



Water depth distribution

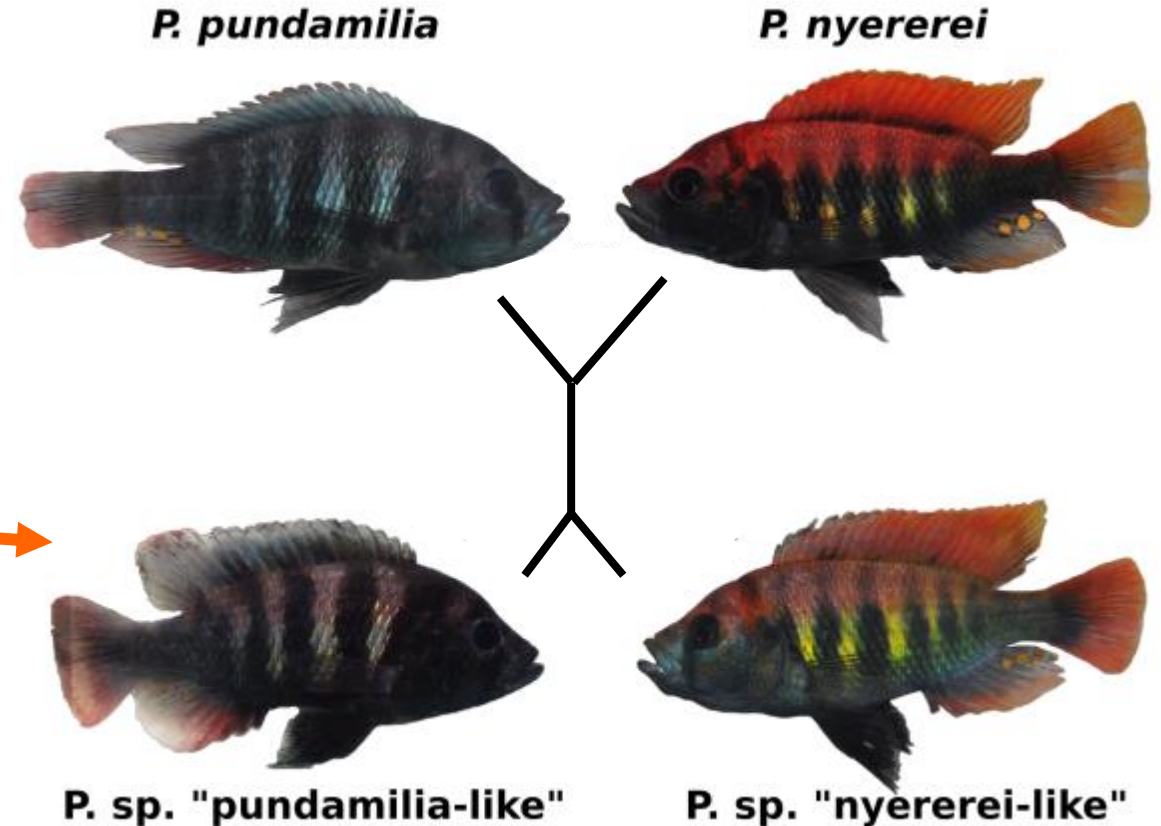
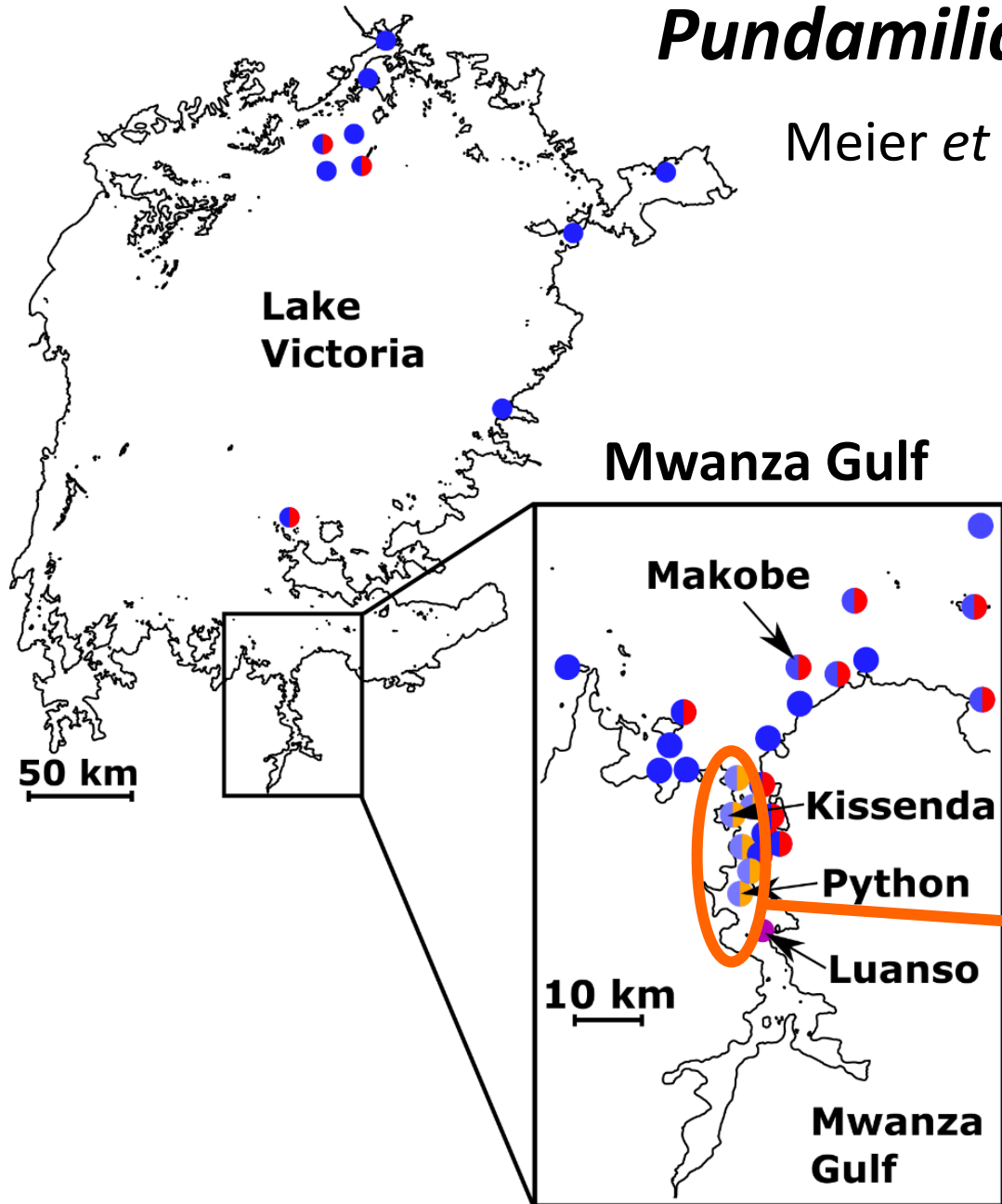


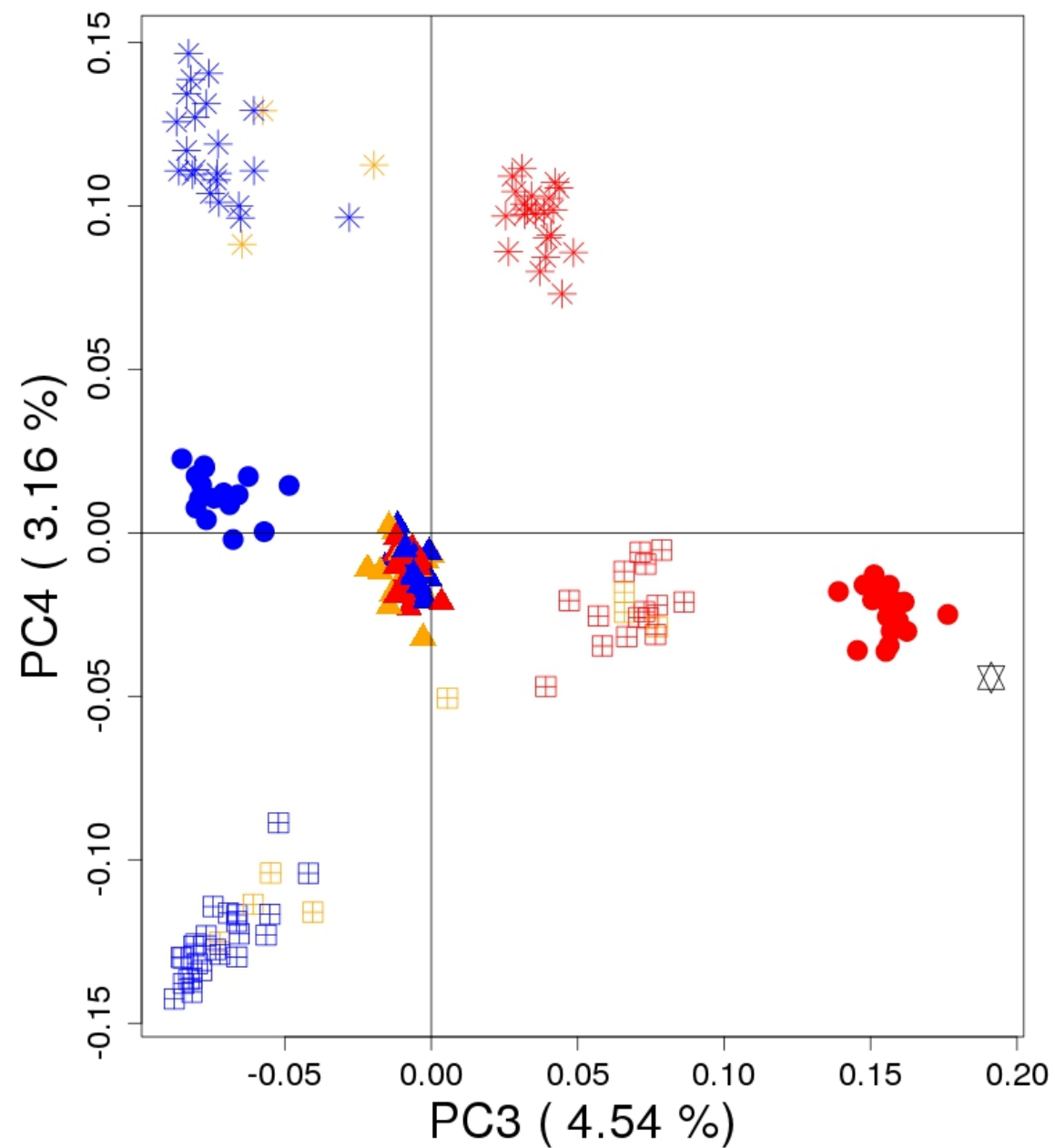
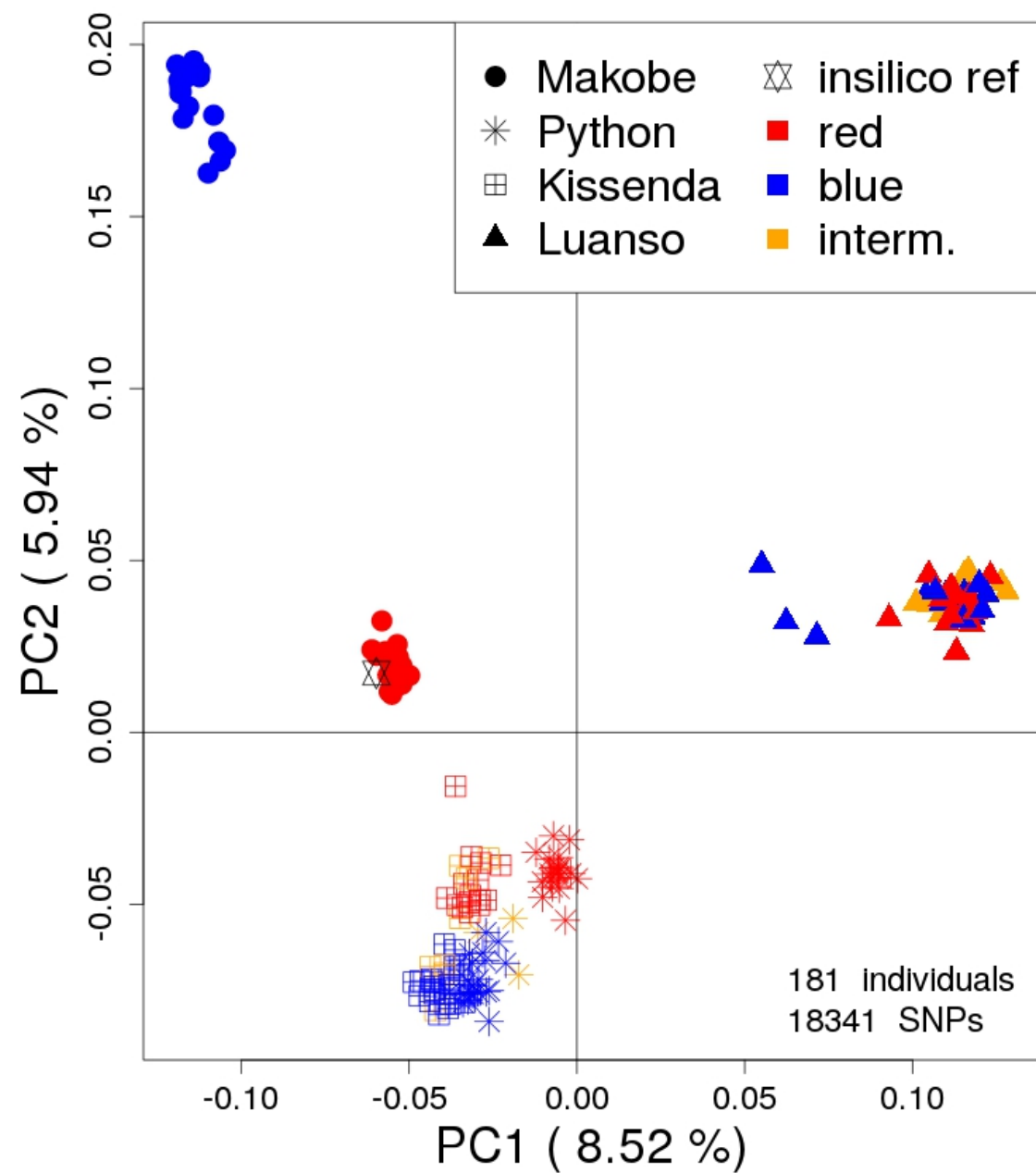
LWS opsin haplotypes



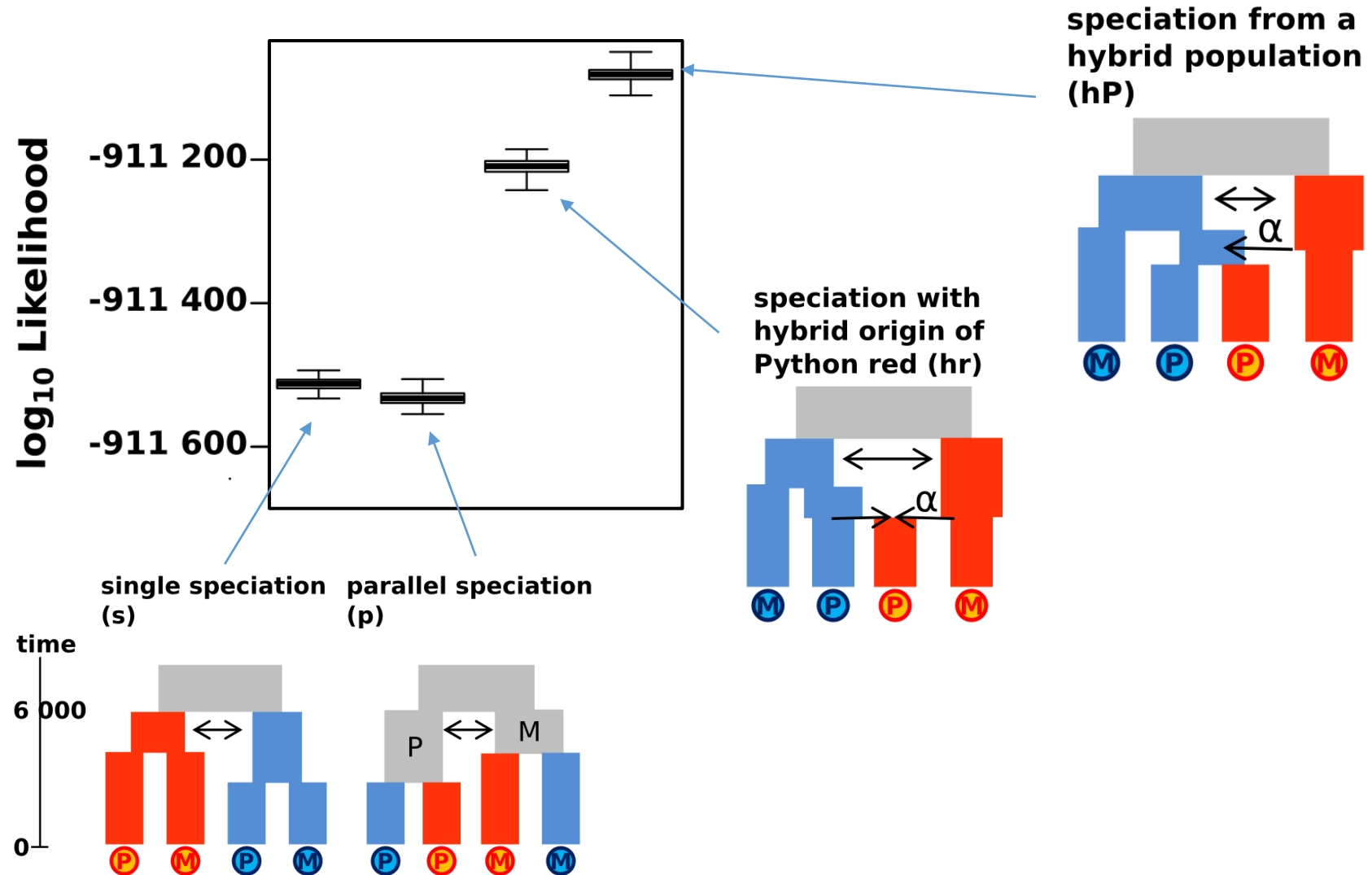
Pundamilia species complex

Meier *et al.* (2017) *MolEcol*

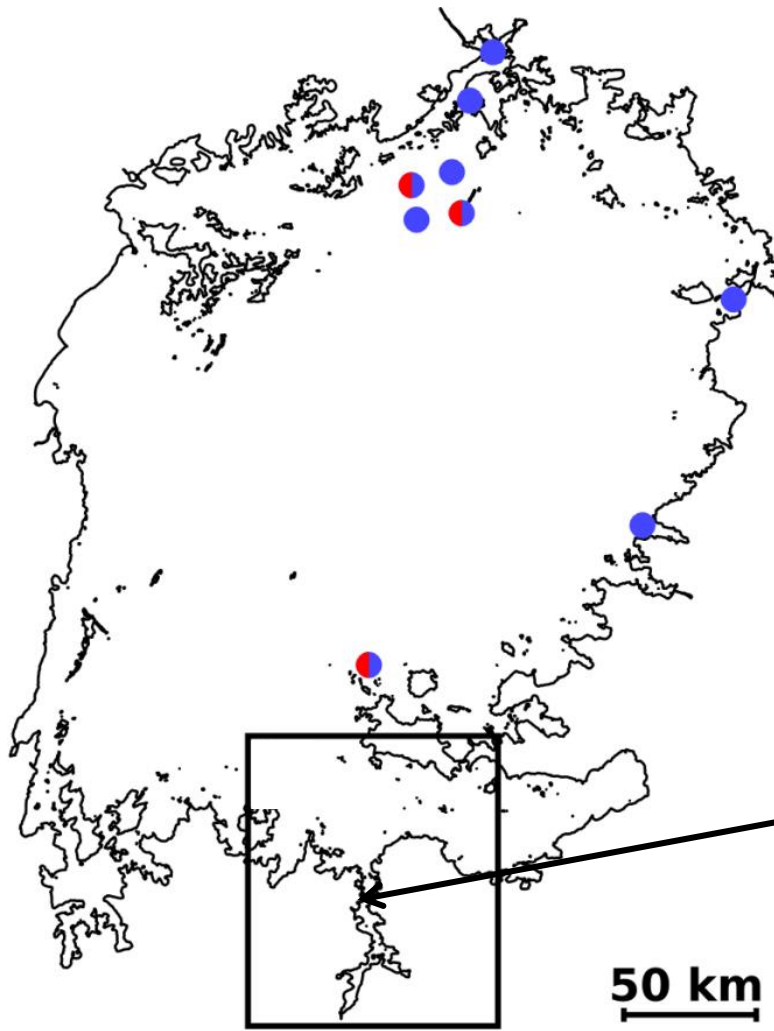




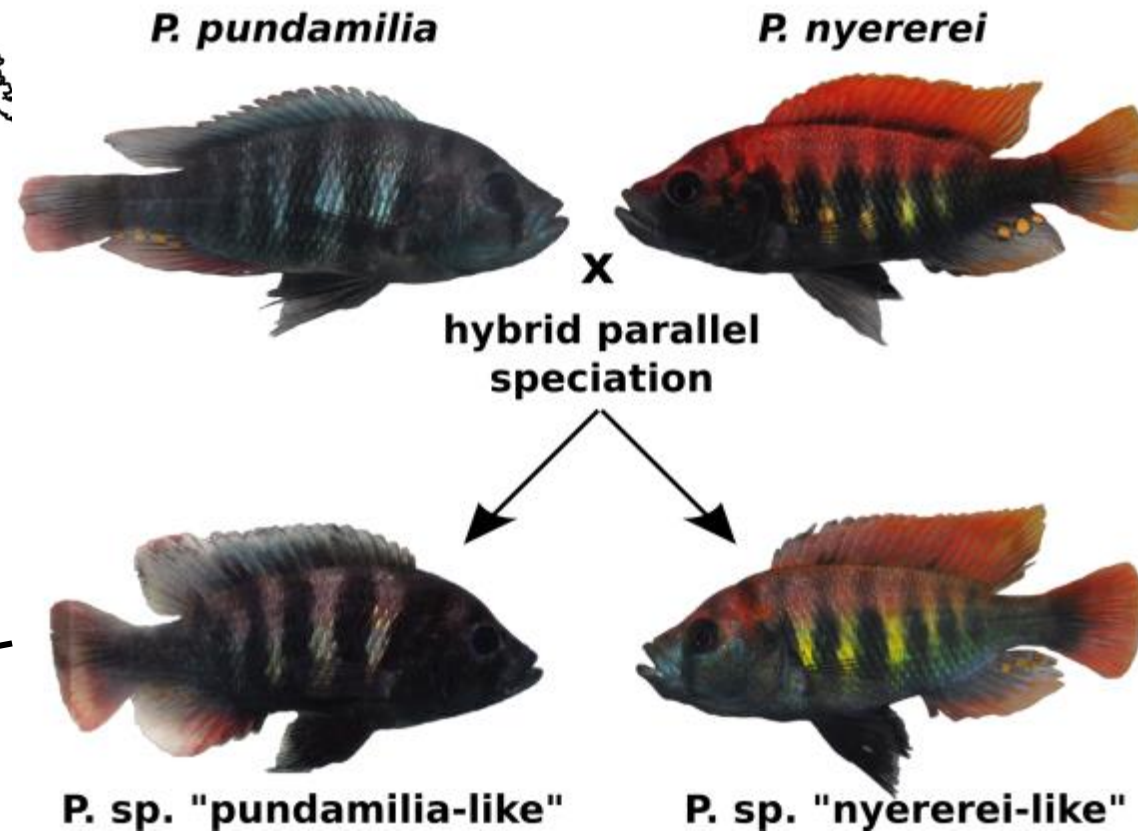
Demographic modeling of whole genomes reveals speciation from a hybrid population in the Mwanza Gulf species pair



Recent hybrid parallel speciation



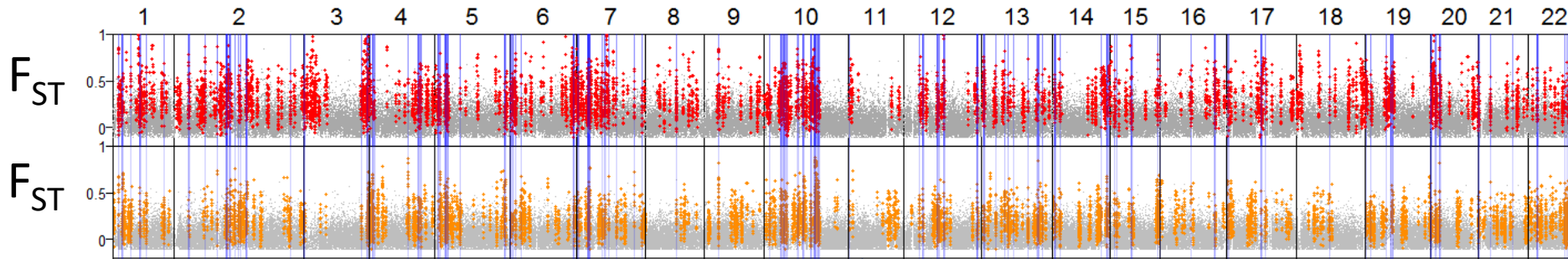
Mwanza Gulf



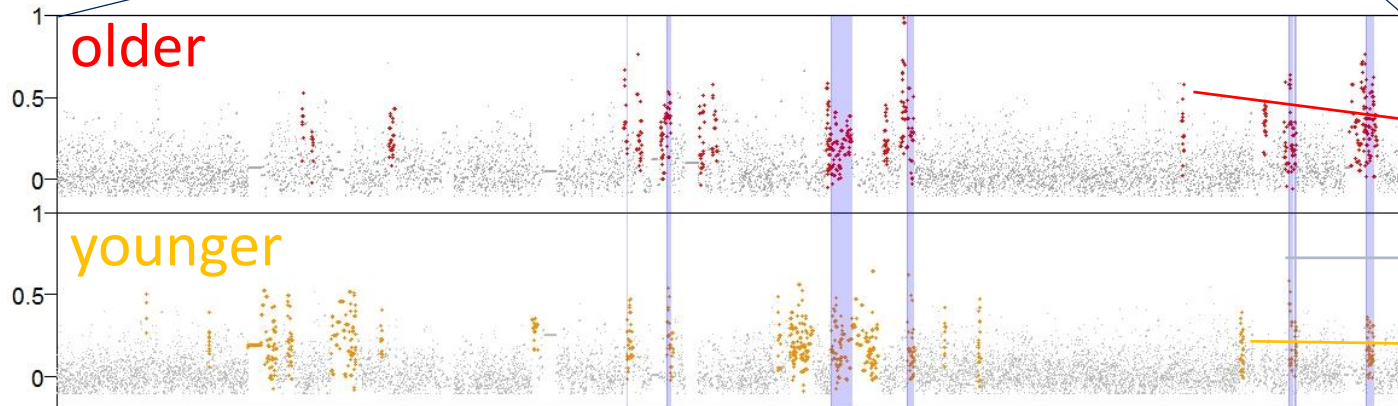
older original
species pair

younger
species pair of
hybrid origin

Many regions are highly differentiated between the species



1/3 of the highly differentiated regions are shared between the species pairs



226

highly differentiated regions in the older species pair

120

shared

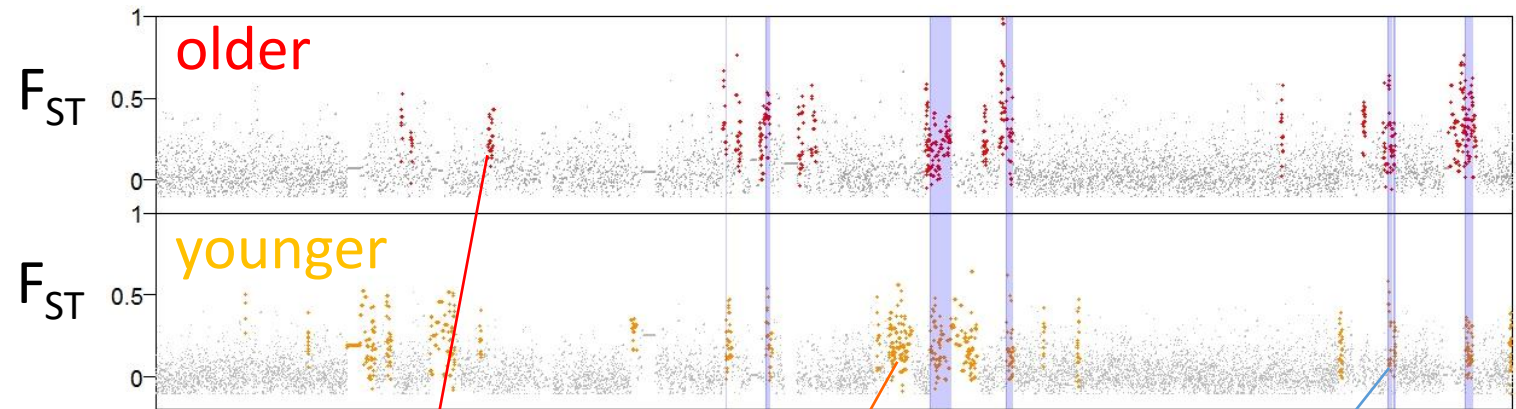
245

highly differentiated regions in the younger species pair

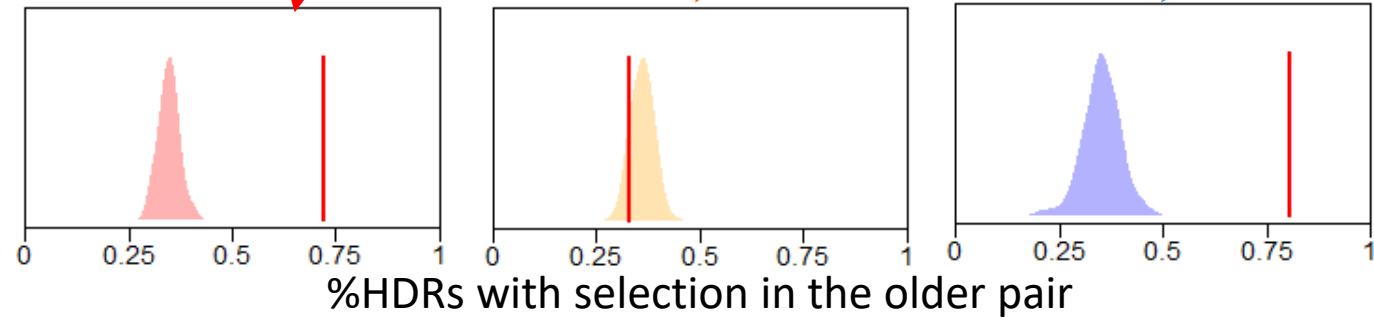
Enrichment of selection statistics support the action of selection

Selection statistics:

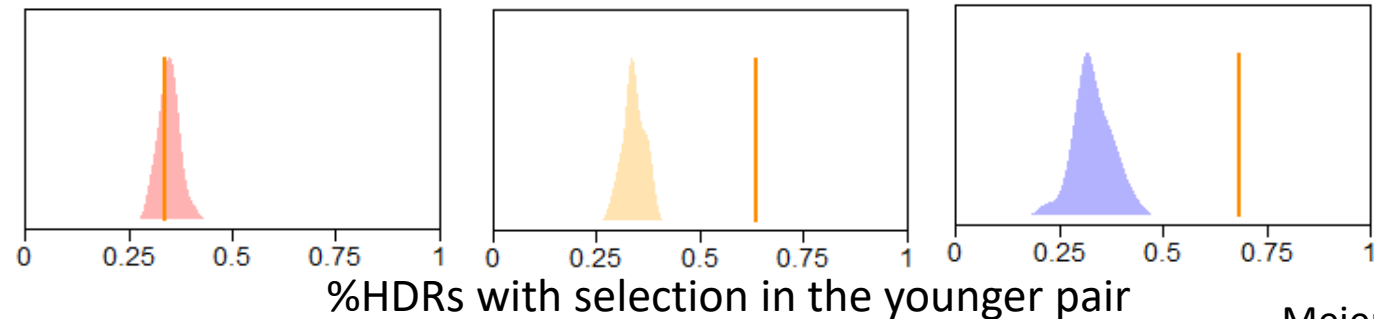
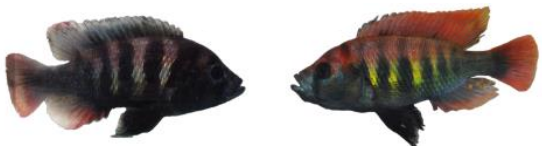
d_{xy}
Tajima's D
 $\Delta\pi$
XP-EHH
iHS



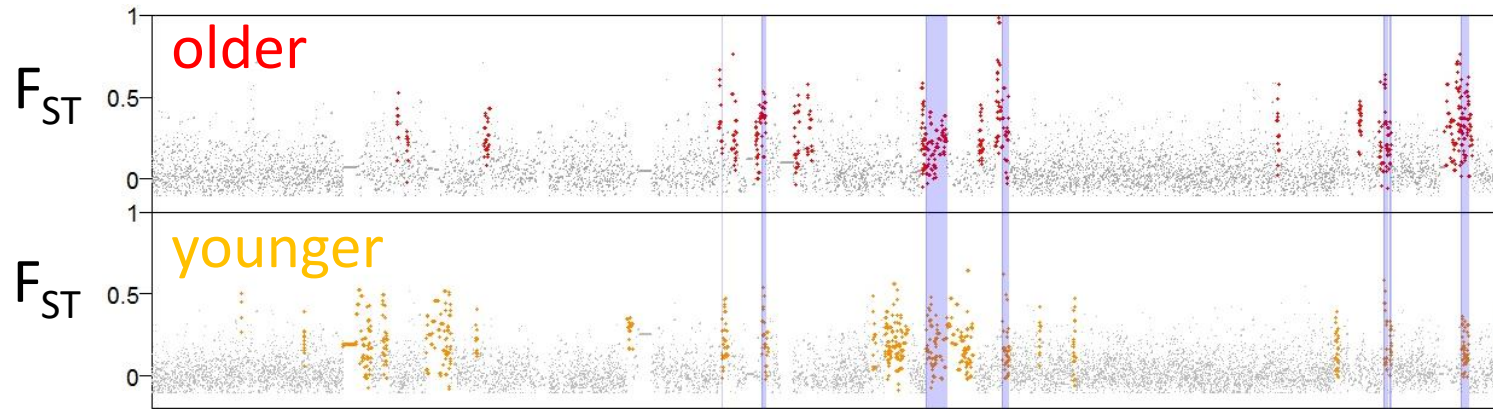
Selection in the older pair



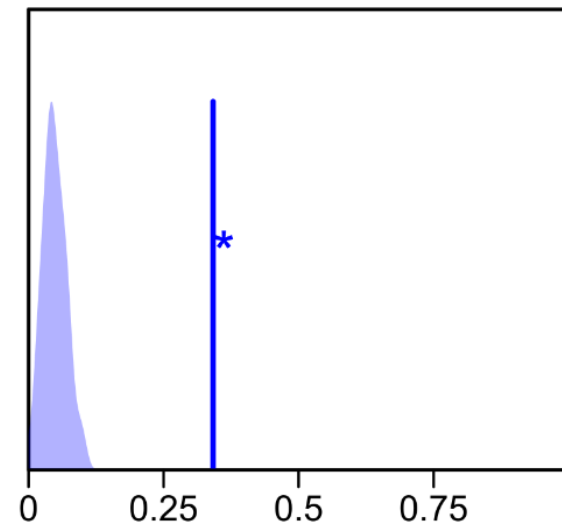
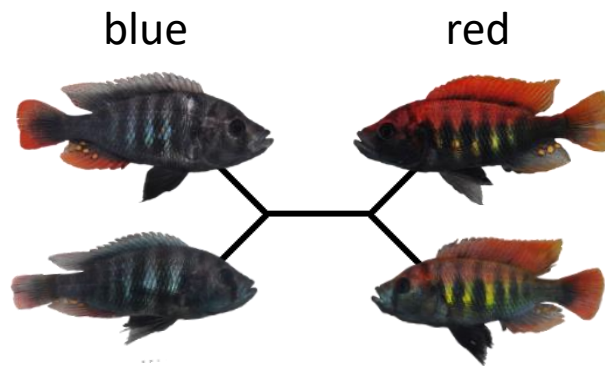
Selection in the younger pair



Highly differentiated regions shared by both species pairs show parallel allele frequency differences



Species group by color



%shared HDRs with color topology

TWISST

(Martin & Van Belleghem, 2017)

Sorting of admixture variation under parallel selection pressures

