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## Background

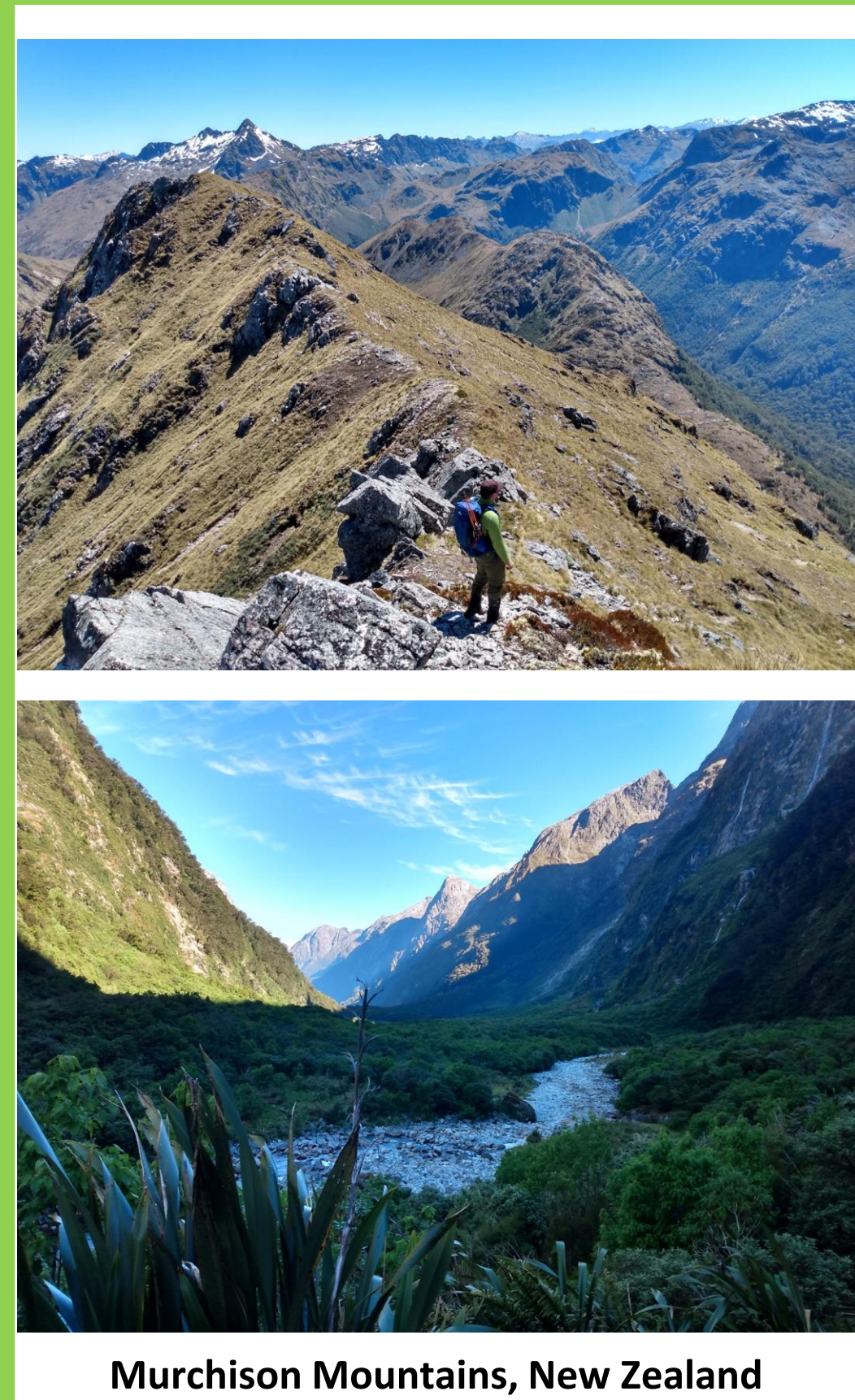


- Critically endangered flightless rail endemic to New Zealand
- One single wild population was rediscovered in 1948 in the Murchison Mountains
- Recently bottlenecked population (~120 individuals in 1980)
- Currently ~500 individuals
- Monitoring of genomic diversity, inbreeding and population structure will guide conservation management
- Population-wide genomic data enables non-invasive real-time *in situ* genomic monitoring

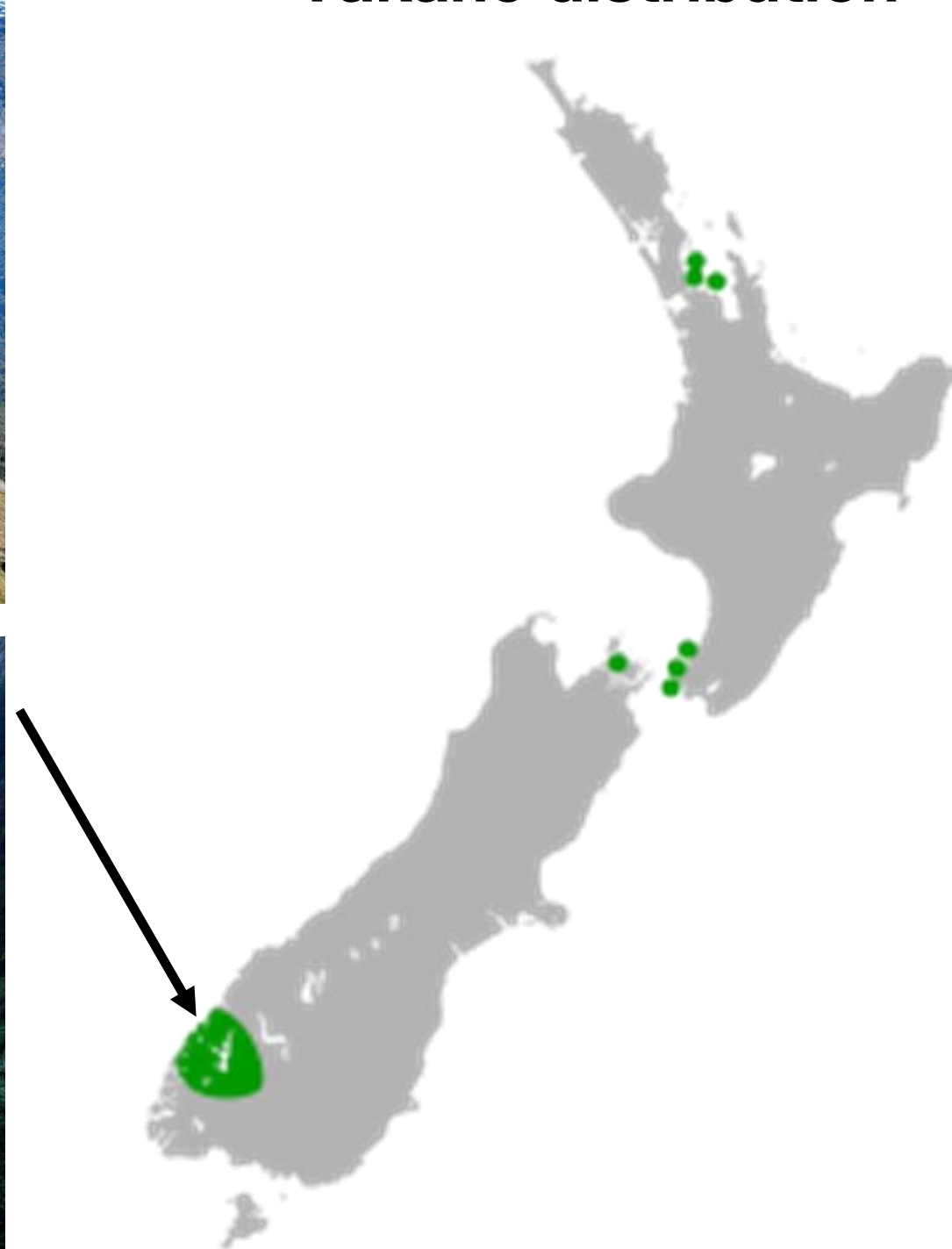
## Objectives

1. Population genetic assessment with low coverage whole genome sequencing data
2. Identification of individuals and sex using noninvasive sampling and portable sequencing

## Study area

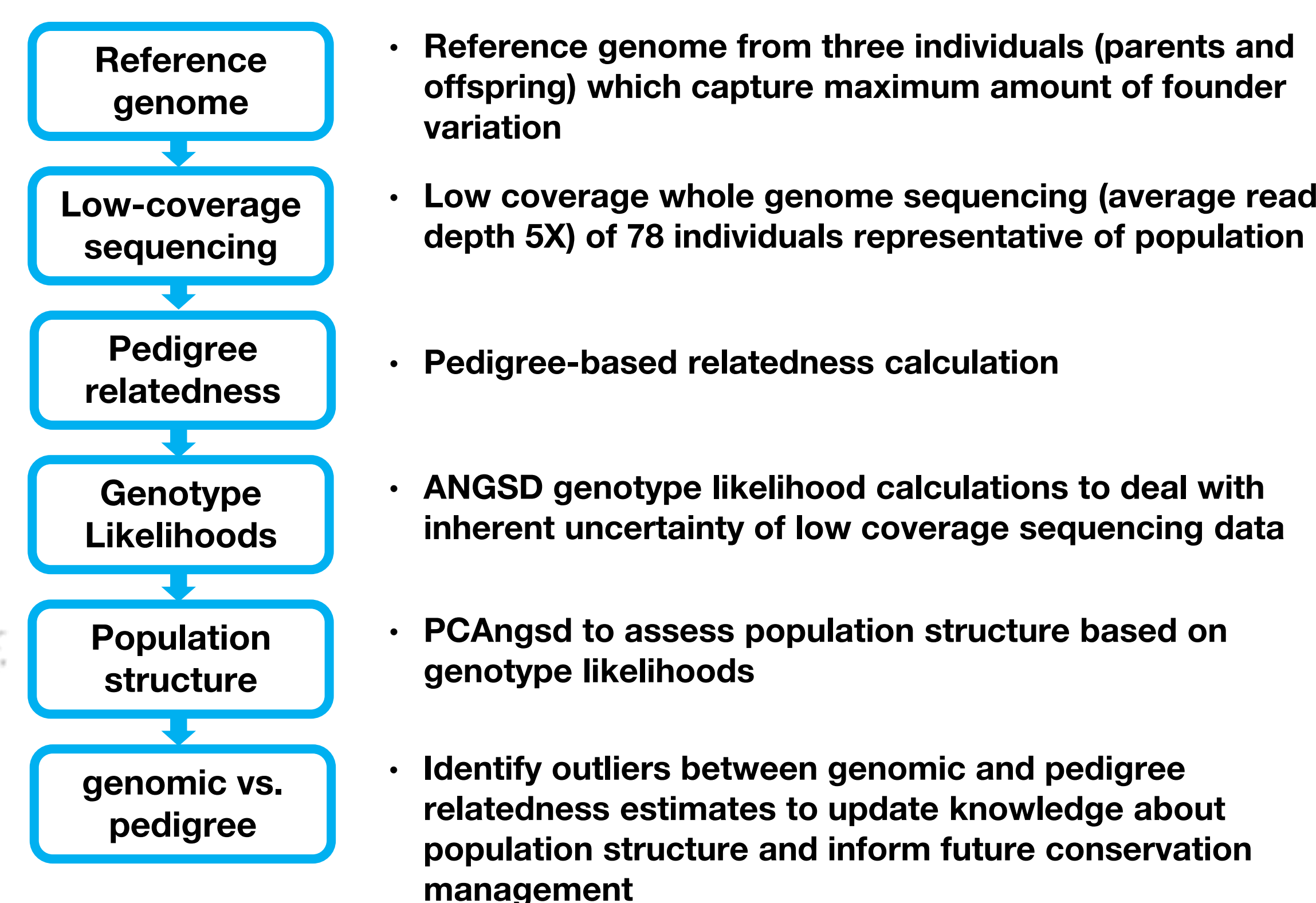


Takahē distribution

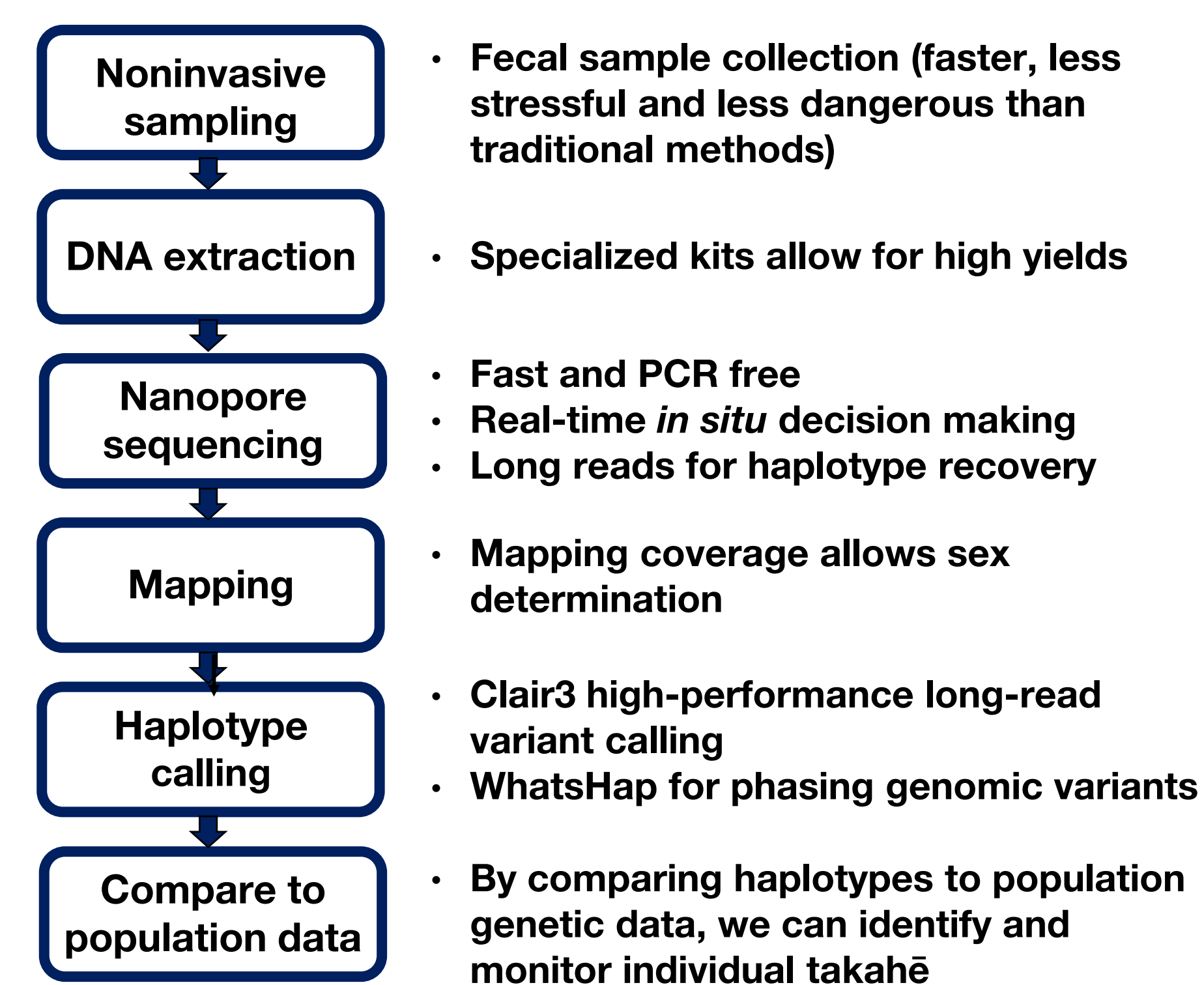


Murchison Mountains, New Zealand

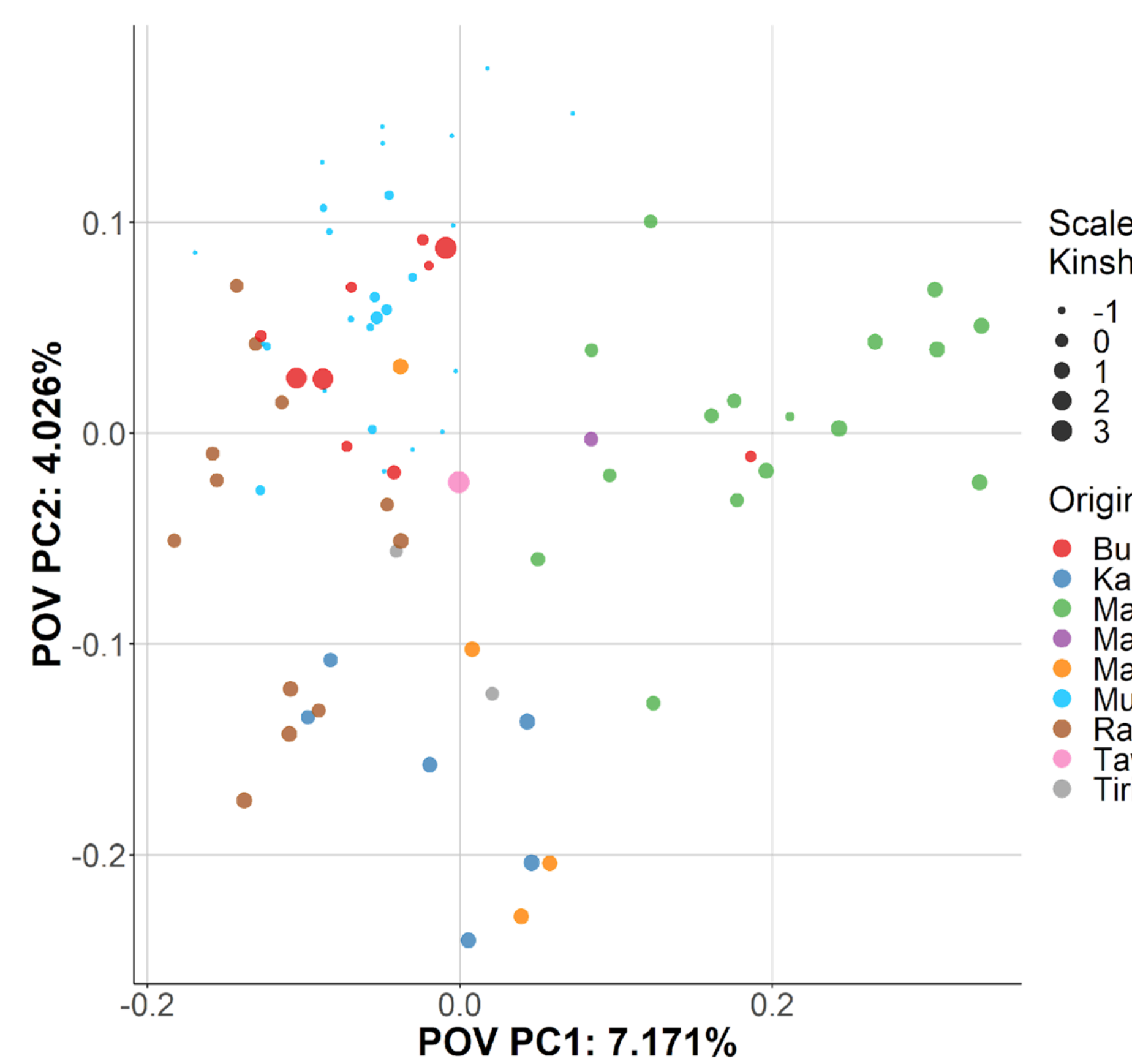
## Population genomics



## Non-invasive monitoring

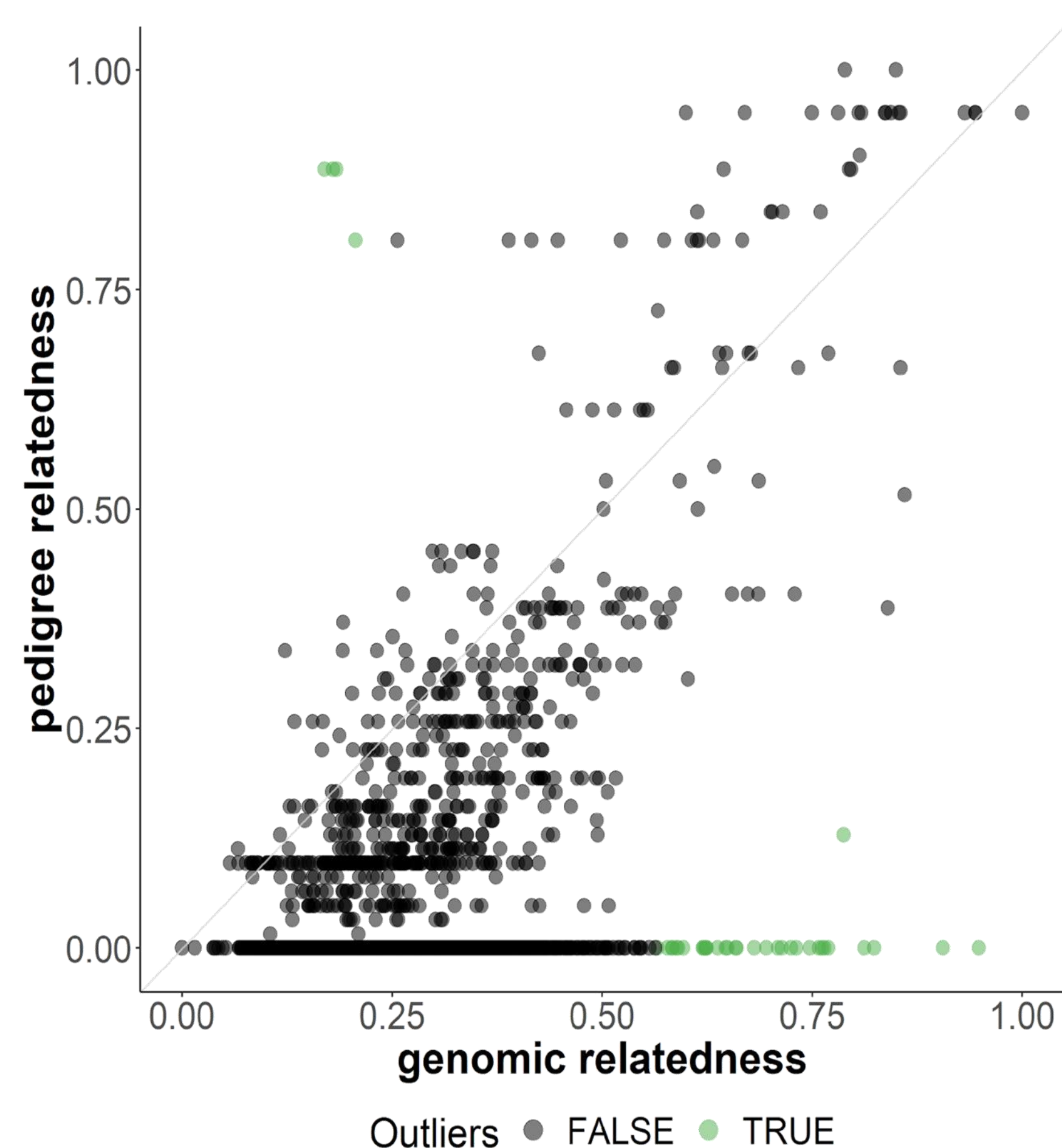


## Genomic population assessments



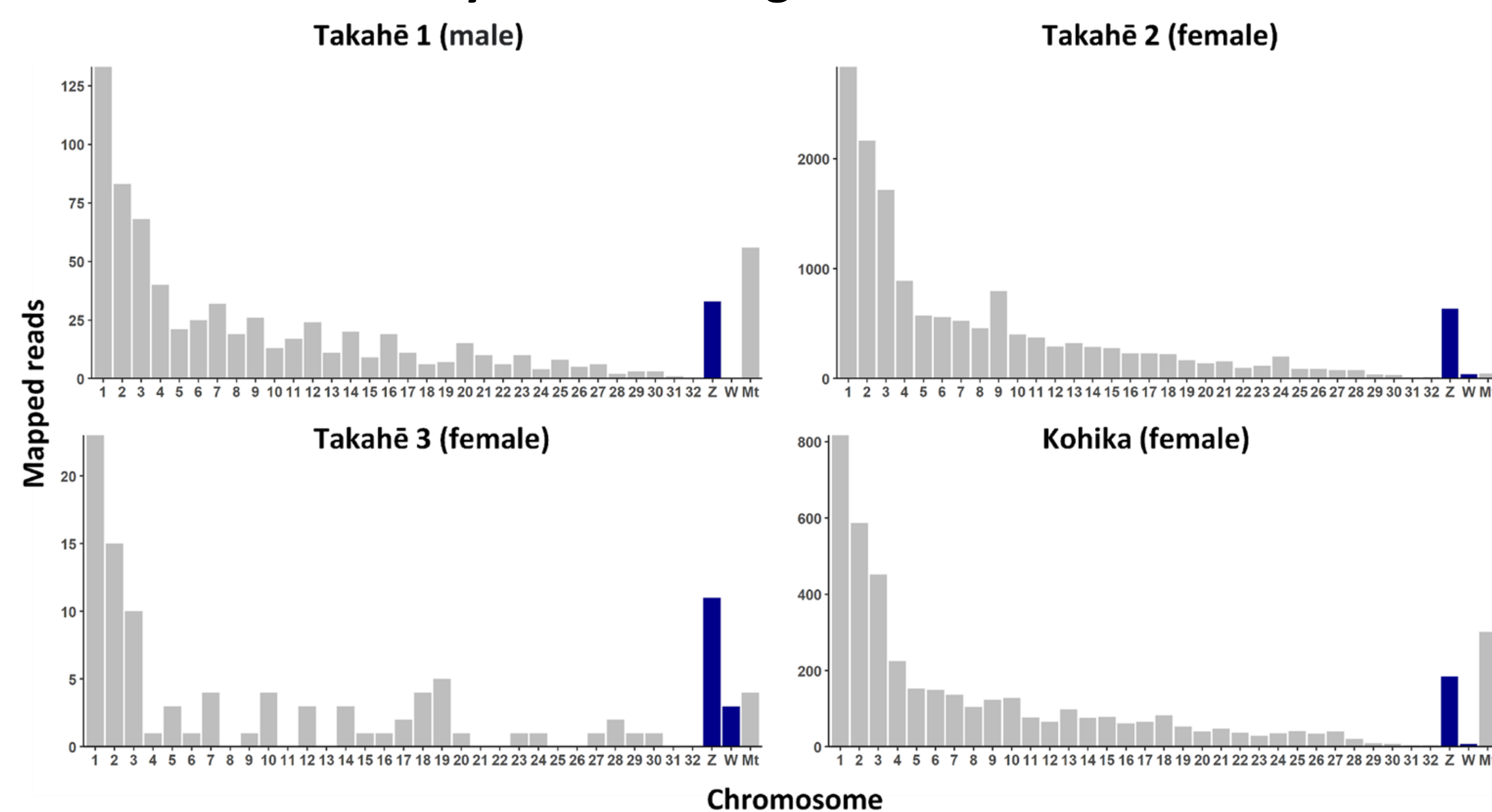
- PCA based on genomic relatedness calculated by **ANGSD** using **genotype likelihoods**
- **Birth Location** is reflected by genomic relatedness
- Mana and Kapiti separations could be due to **founding effects** and **rare allelic variants**
- Burwood population is genetically closest to wild (Murchison) population

- Pedigree-based relationships tend to underestimate relatedness
- No information of pedigree for wild takahē population
- Pairs with **low pedigree relatedness** and **high genomic relatedness** have the potential to inform conservation management
- Conservationists can **better understand inbreeding depression** in supposedly unrelated pairs

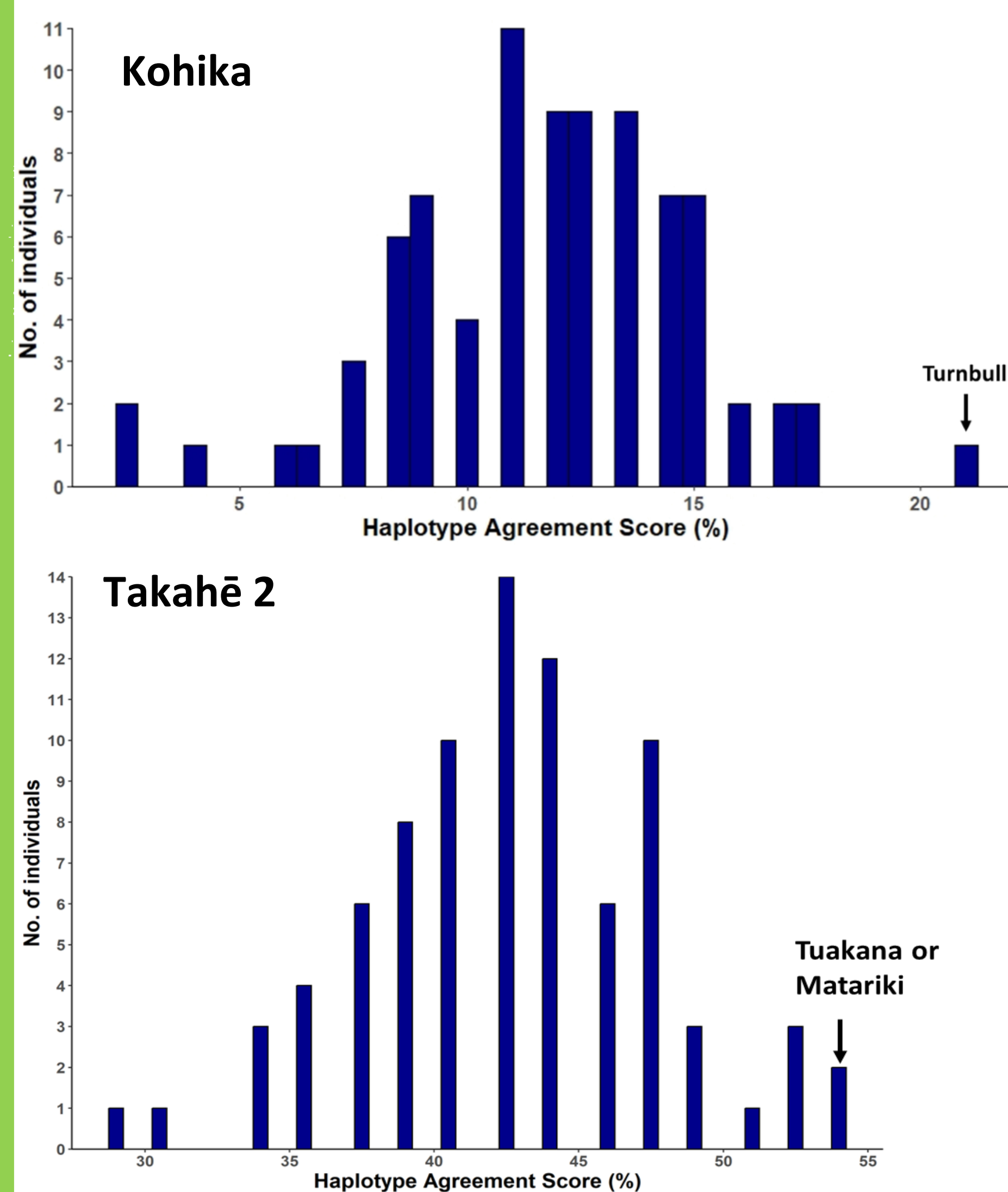


## Non-invasive monitoring

### Sex determination by read coverage



### Individual identification



- We compared the haplotypes recovered from fecal samples to a population wide genetic database to potentially identify the individual
- The sample obtained from a takahē individual named **Kohika** had the highest haplotype overlap (**20%**) with **Turnbull** from the population dataset
- Haplotypes recovered from an unknown takahē overlapped by **~54%** with two individuals from the population dataset named **Tuakana** and **Matariki**

## Bibliography

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