

CSP project POP2021-06: Fur seal population estimate and bycatch analysis, Cook Strait

Genetic analyses of bycatch



Professor Bruce Robertson, Dr Ludovic Dutoit

Department of Zoology, University of Otago, Dunedin, NEW
ZEALAND

CSP project POP2021-06

- Collaborative project between Cawthron, DOC and the University of Otago

Project Objectives:

1. To identify New Zealand fur seal colonies and / or haul outs within the Cook Strait which could overlap with fisheries.
2. To increase the understanding of interactions between New Zealand fur seals and the commercial hoki fishery within this area.

Pavanato et al. CSP draft report No.3854:

- It will include genetic analysis of bycaught animals to confirm locations most impacted by the fishery, building on work from Stovall 2016.

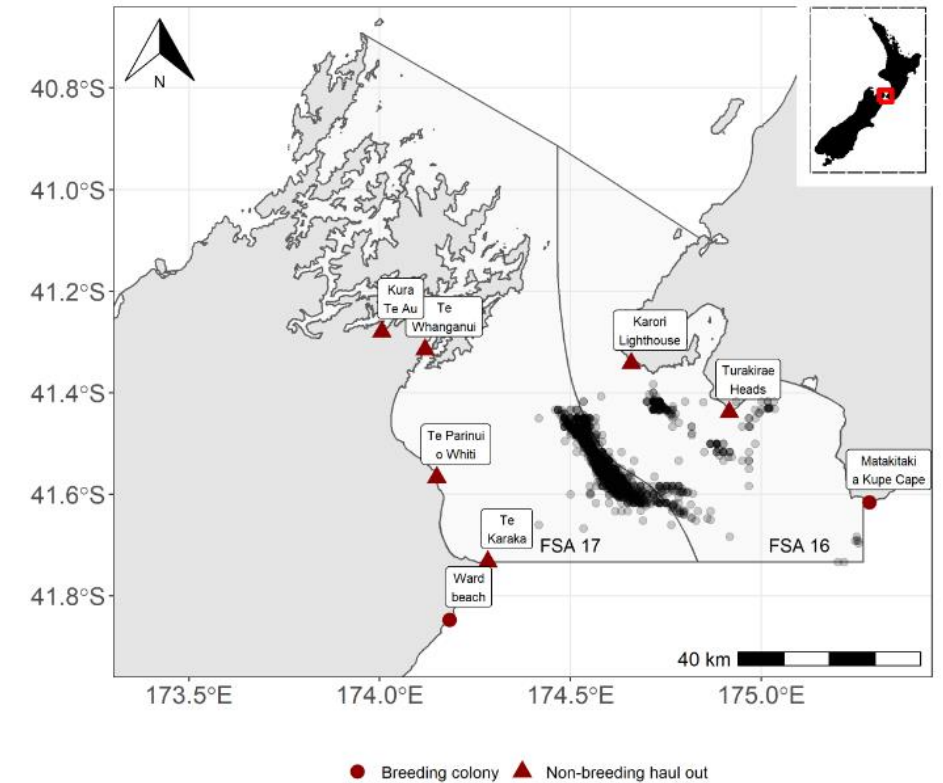
Stovall 2016 = Dussex et al. 2018

POP2021-06: Genomic analyses

1. Assess genetic population structure with the aim of assigning NZFS bycatch to colonies of origin
2. Determine genetic sexes of bycatch individuals
3. Trial blood as a source of DNA for genomic analyses

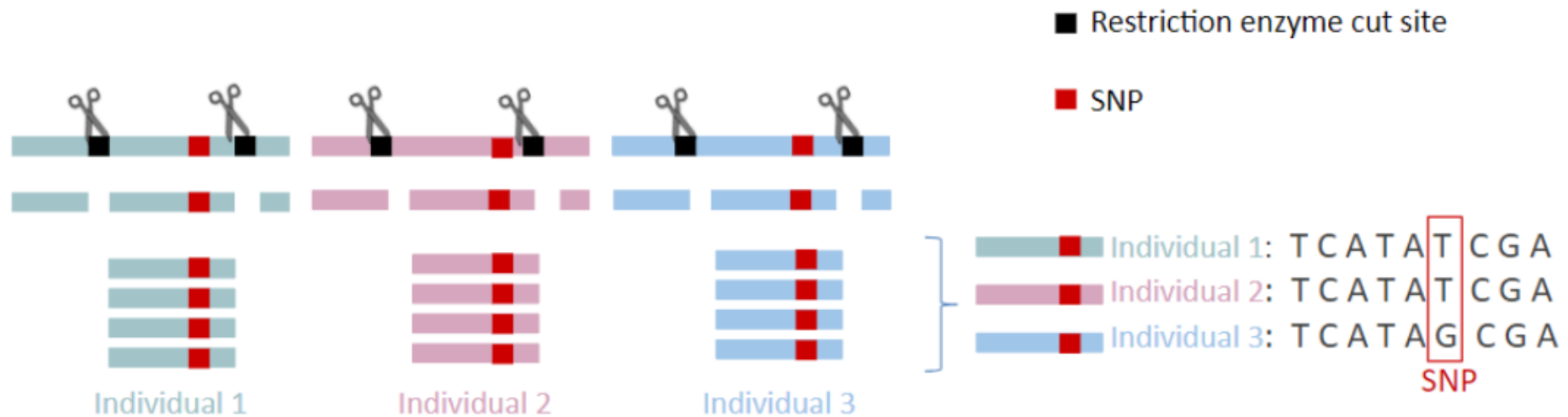
Sampling

- Only two breeding colonies in Cook Strait = “broaden sampling area”
- Skin samples (104 live pups)
 - Cape Palliser (20)
 - Taumaka Island (20)
 - Wekakura Point (20)
 - North Kaikōura (20) – old Ohau Point Lookout
 - South Kaikōura (20) – Barney’s Rock
 - Needles Point (4)
- Blood samples (7 live pups): Needles (2) & Cape Palliser (5)



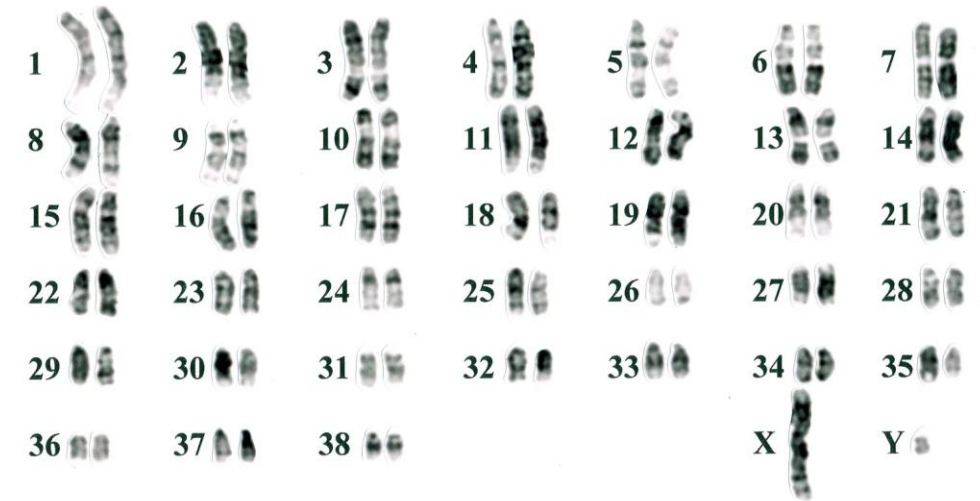
Genotyping-by-Sequencing (GBS)

- Reduced representational genome sequencing
- Targets 1-5% whole genome
- Detects 1000s of single nucleotide polymorphisms (SNPs) – 150,000 for seal SNPs



DNA sexing

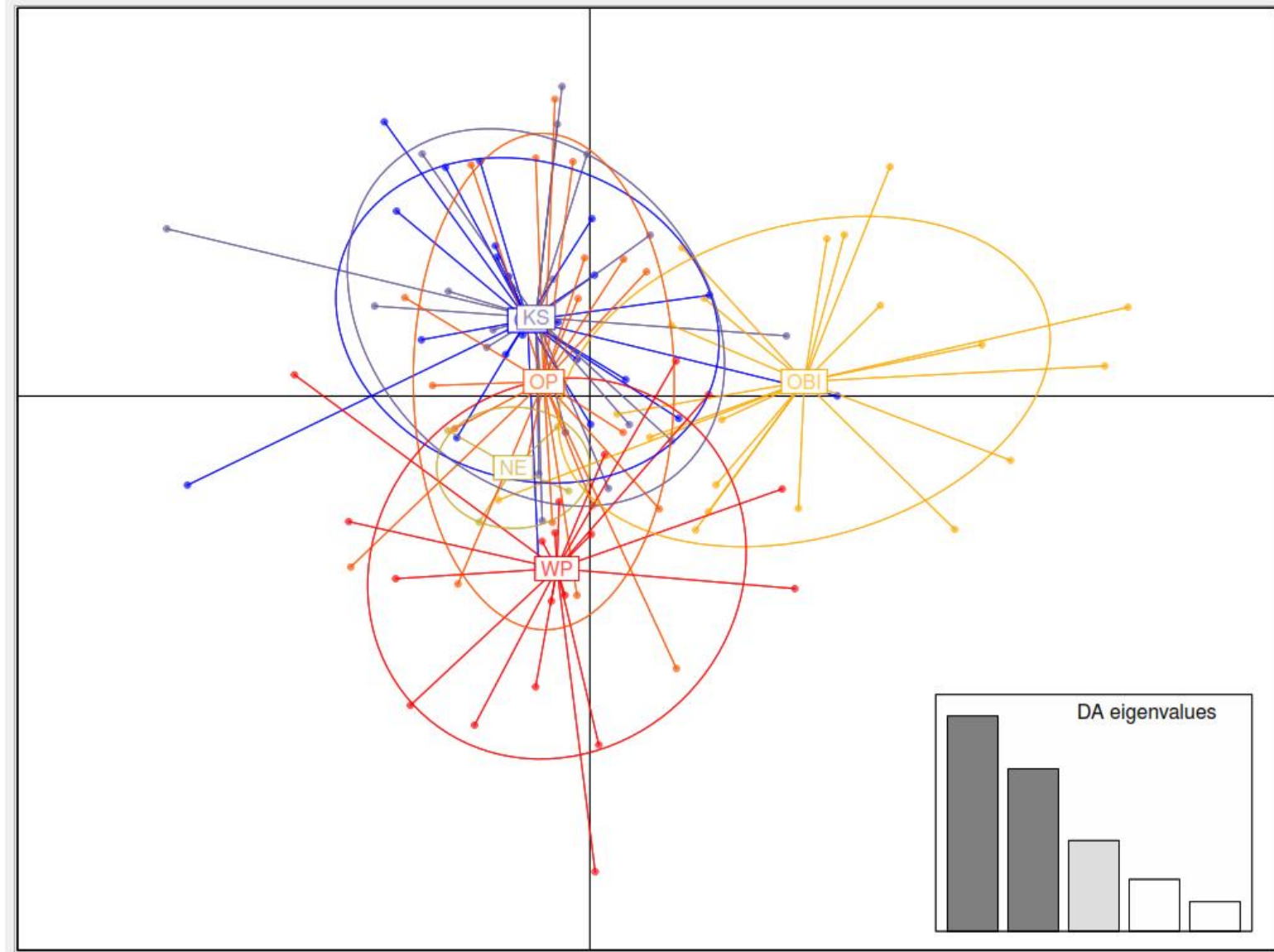
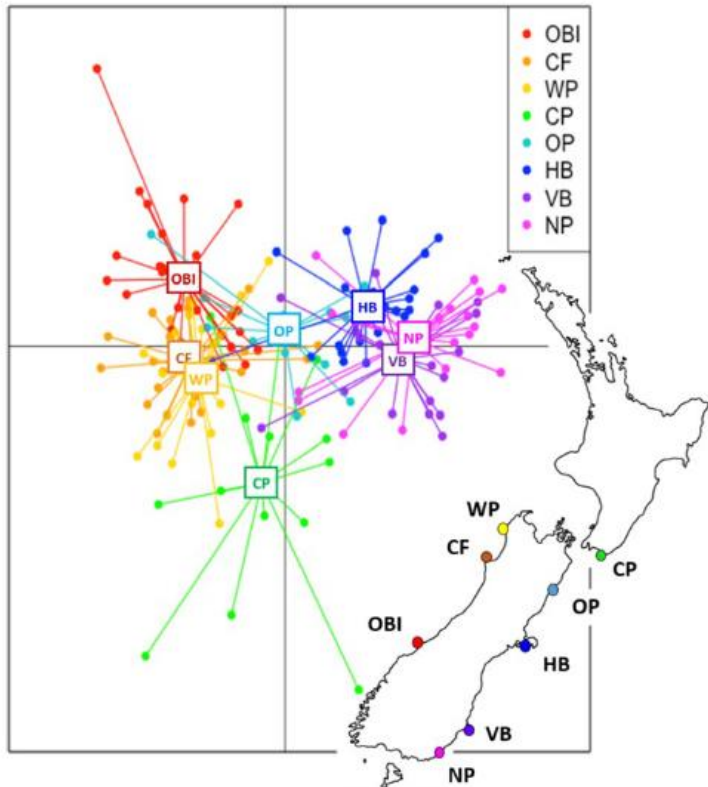
- Dog reference genome = find X chromosome in fur seal genome
- Coverage for SNPs on X vs coverage for SNPs on other non-sex chromosomes (autosomes)
- Males (XY) and Females (XX)
 - Expect 1:2 ratio of coverage in males
 - Expect 2:2 (1:1) ratio of coverage in females
- Verified using “known-sex” individuals – 104 pups



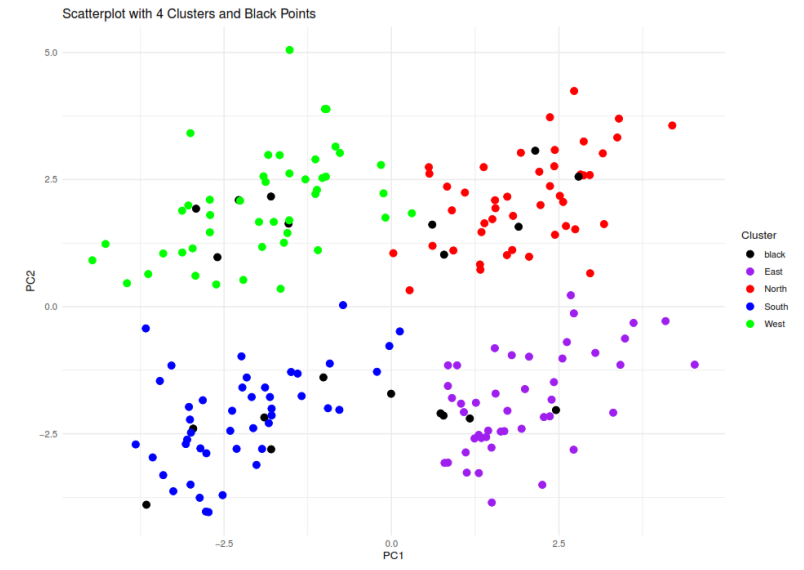
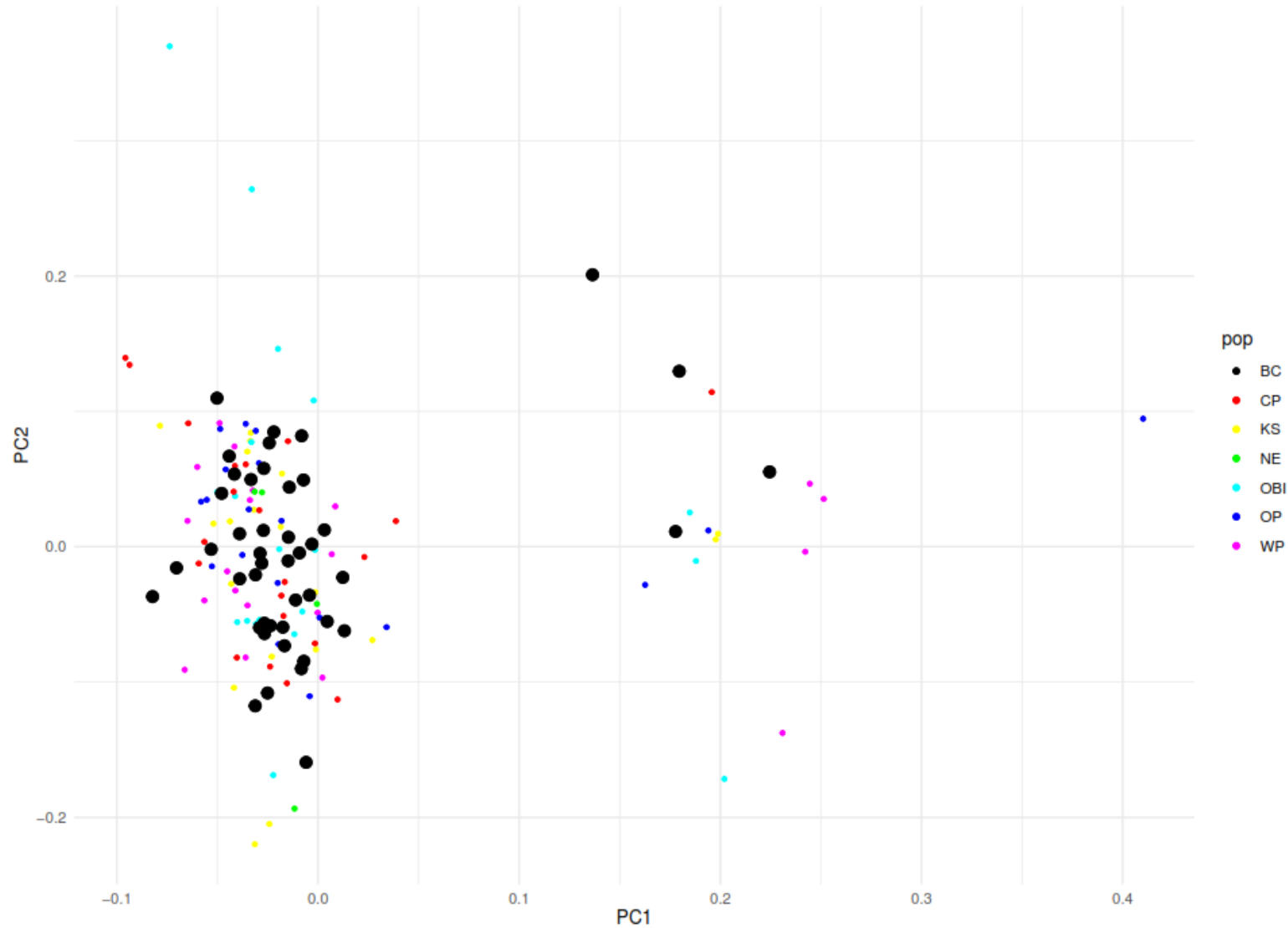
Dog karyotype (American Kennel Club)

Population structure

- low population structure
= Dussex et al. 2018



Poor signal for “colony of origin” assignment



Similar conclusion to Dussex et al. 2018

Bycatch sexes

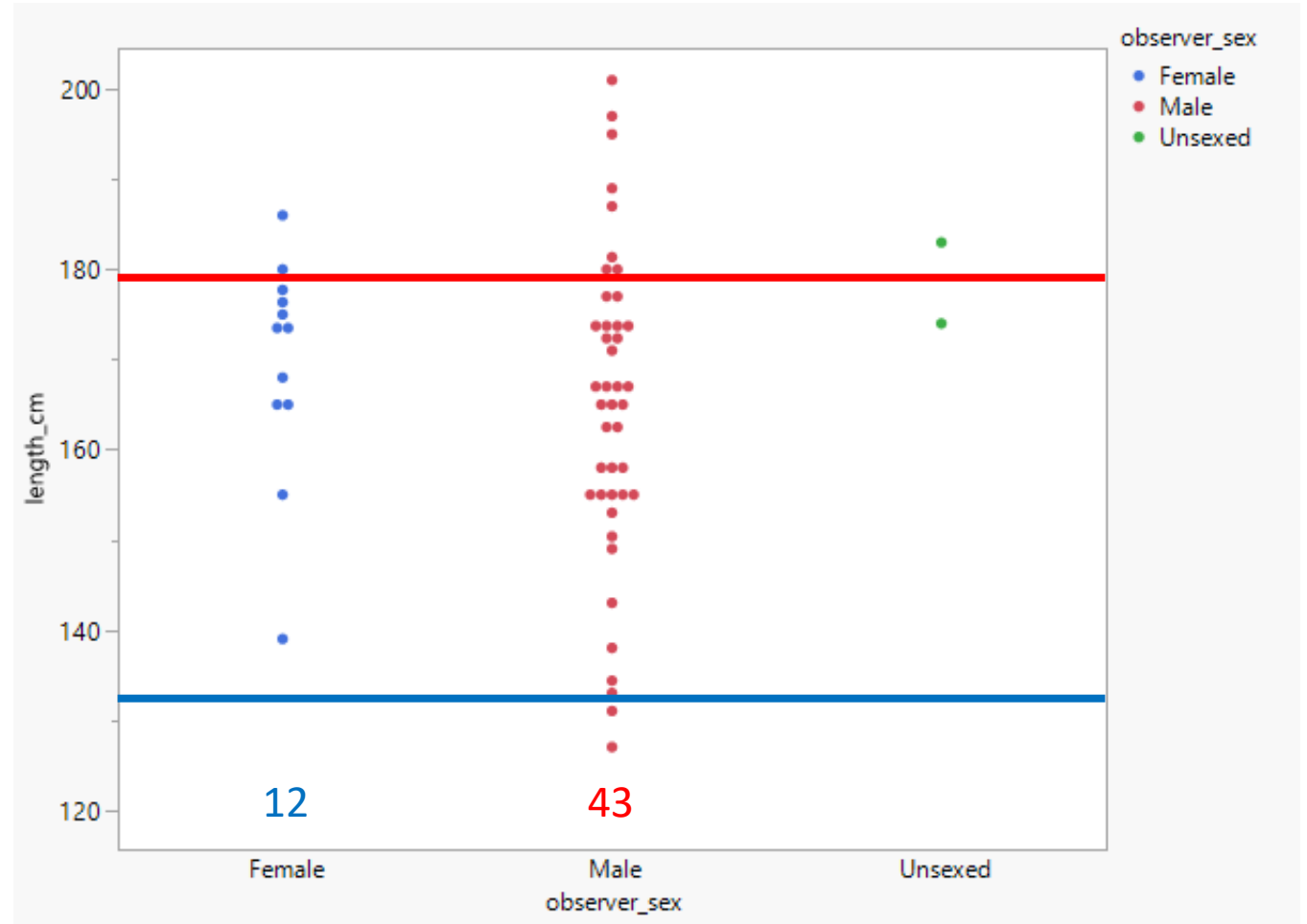


Female

Male

<https://mmapl.ucsc.edu/basic-response/gender-id/pinnipeds>

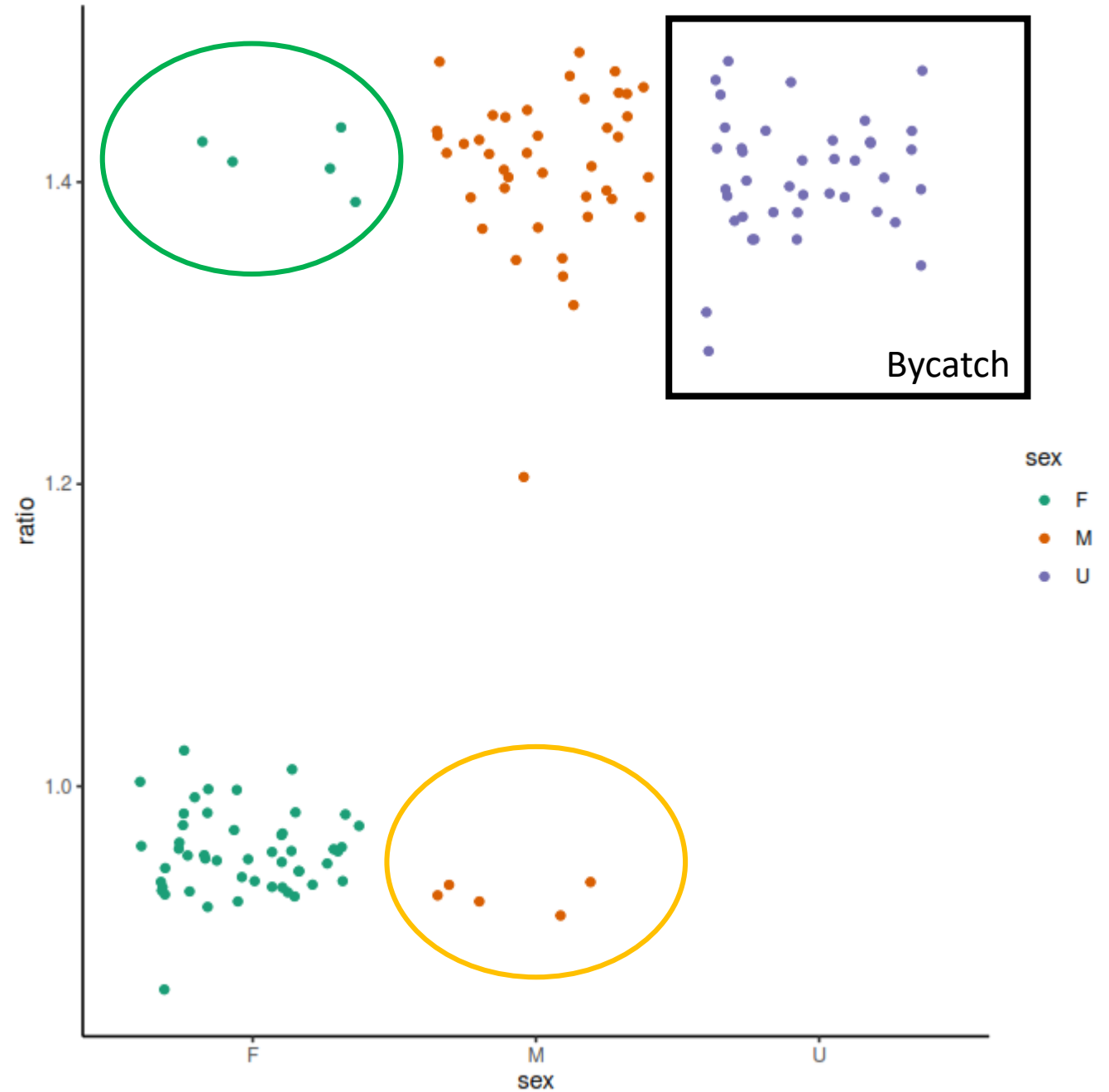
Lines are max lengths: Dickie & Dawson (2006)



Females, 2 separate openings between hind flippers (males, one);
Males, a preputial opening (for the penis); both sexes, an umbilical scar

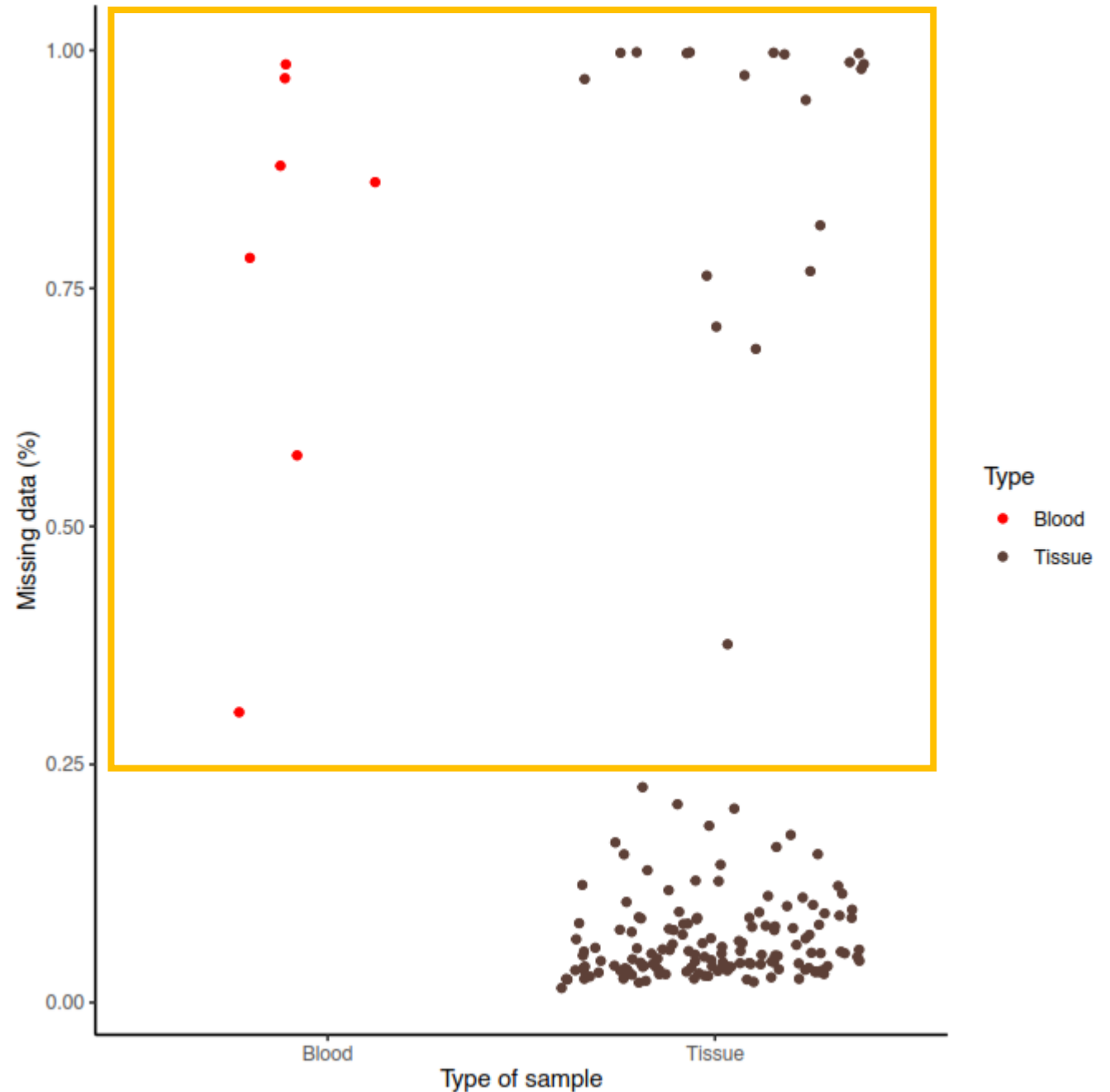
DNA sexing

- Method distinguishes sexes
- Incorrect sexes in “known-sex” pups
- 12 “female” bycatch samples:
 - 6 identified as Male by genomics
 - 6 failed GBS filtering



Blood samples for genomics

- Bloods had a higher level of missing data
- Filtering removes these samples from downstream analyses
- Bloods hard to collect



Summary

- Low levels of population structure detected (as noted by Dussex et al 2018)
- Not sufficient to assign bycatch to colonies of origin
- Fur seals can be sexed using genomics (also done by Stovall et al. 2018)
- Errors in sex identification by observers
- Blood samples are not appropriate for fur seal genomic sampling