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Supplemental Information for:

From rivers to ocean basins: the role of ocean barriers and philopatry in the genetic structuring of a cosmopolitan marine predator

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Contents

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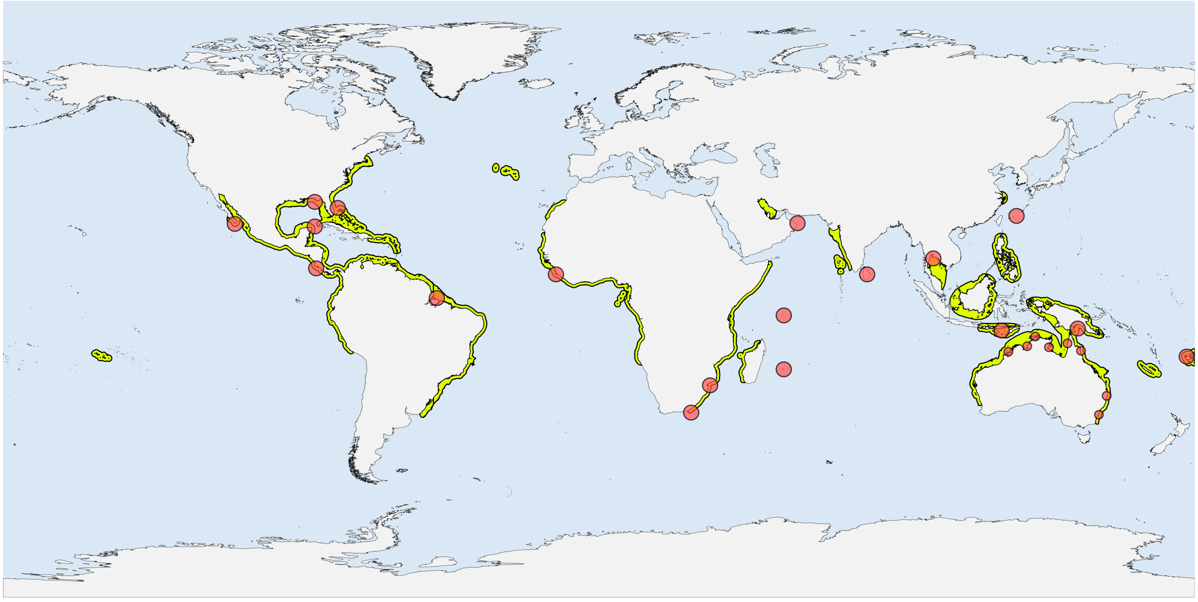
1 Background

This Rmarkdown document described the data-filtering and analysis steps for assessing the population structure of the Bull Shark (*Carcharhinus leucas*) in Devloo-Delva et al. Basically, we followed a step-wise procedure to analyse the data at different hierarchies and with different subsets. Each time the data was sub-sampled, we re-filtered the data:

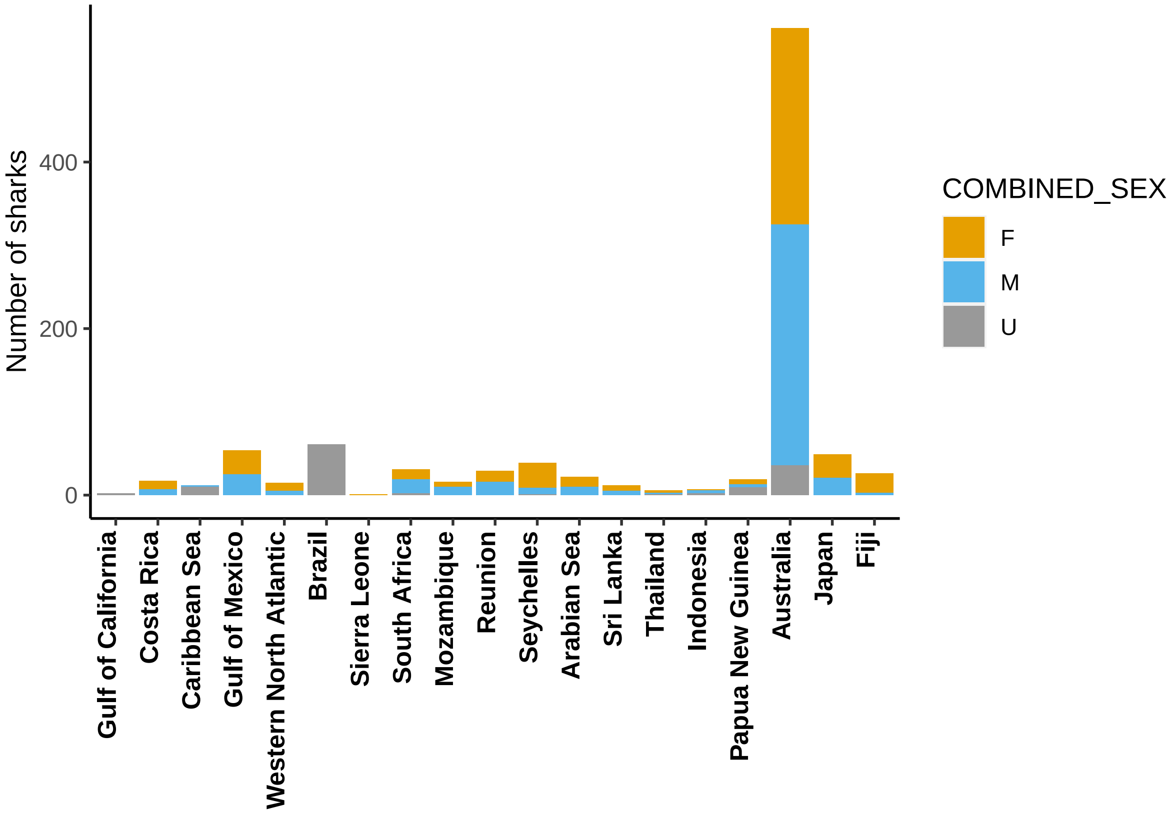
1. Hundred-eighty-eight sharks, with 32 technical replicates, were sequenced and genotyped according to the DArTseq protocol (see Feutry et al. 2017) to yield 250,950 single nucleotide polymorphisms (SNPs).
    - The raw DArTseq data was investigated to find putative sex-linked markers (i.e. markers located on the sex chromosomes), as these markers can assign the genetic sex and could potentially bias the population structure analyses (see Benestan et al. 2017).
    - The data was loosely filtered to identify incorrect species in our data using a simple principal component analysis.
    - The data with only confirmed Bull Sharks was used to select approximately 3400 SNPs to design targeted capture probes for DArTcap genotyping (see Feutry et al. 2020).
    - We also investigated population structure and genetic diversity within Australia, where sample sizes were largest.
2. We analysed the resulting DArTcap SNPs for 940 individuals and an additional 74 technical replicates.
    - The raw DArTcap data was again tested to identify sex-linked markers.
    - We applied a loose data quality filtering to identify incorrect species.
    - The data with only Bull Sharks was analysed for genetic diversity and population structure
3. Subsequently, we randomly subsampled 60 individuals from Australia to reduce the bias that was caused by extreme unequal sample sizes (see Puechmaille 2016; Foster et al. 2018).
4. Within the West-Atlantic population, we looked for signals of (sub)structure that could have been hidden due to the extreme differentiation from other populations.
5. Within the Indo-West Pacific (IWP) population, we looked for signals of (sub)structure that could have been hidden due to the extreme differentiation from other populations. In addition, we looked for close-kin relations within the IWP, given the large sample size.
6. Within Australia, we investigated the potential that rivers or regions form fine-scale structure.
7. Lastly, we amplified the full mitochondrial genome (mitogenome) of 361 Bull Sharks from the eastern Atlantic and Indo-Pacific regions.
    - Genetic diversity
    - Haplotype networks
    - Genetic differentiation

2 Sampling map and metadata

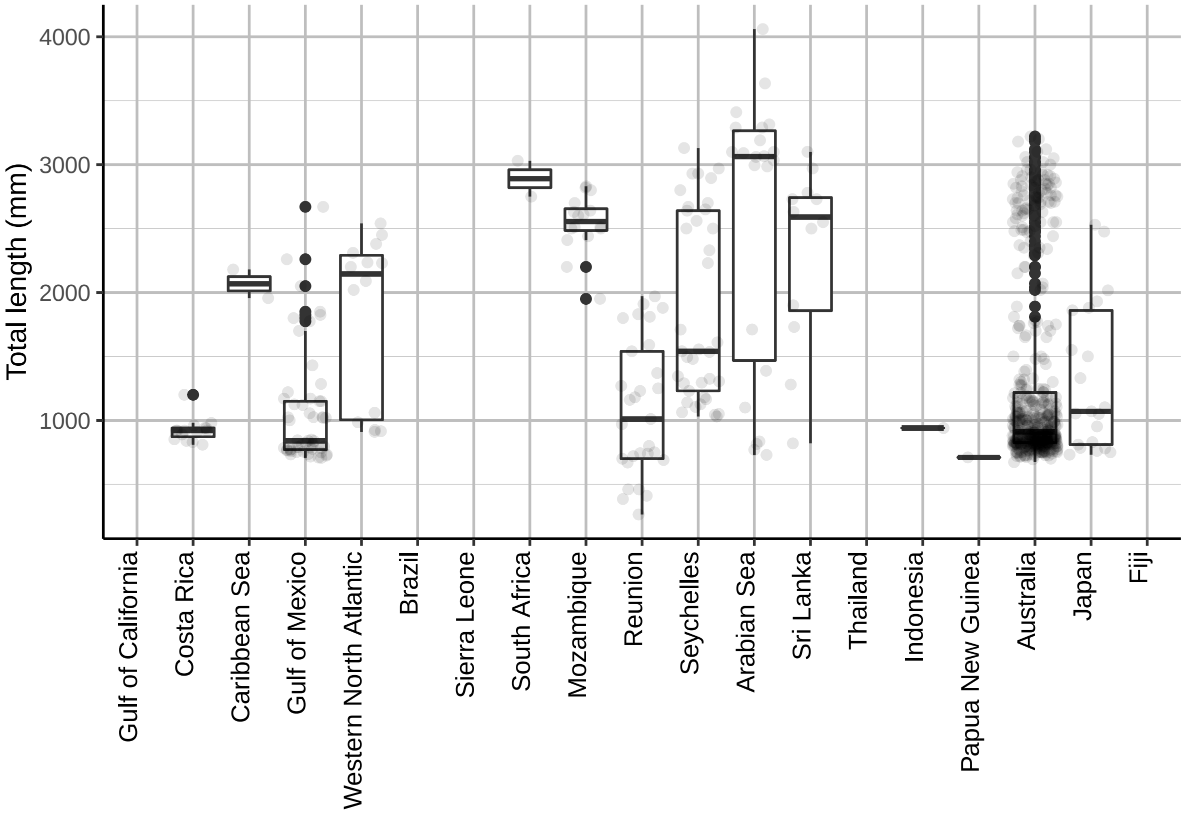


2.1 Visual sex ID

```
metafile <- "1.BullShark_AllSamples_metadata.csv"
meta <- readr::read_csv(metafile) %>%
  dplyr::filter(SpeciesID_genetic == "Carcharhinus leucas")
pop.levels <- c("Gulf of California", "Costa Rica" , "Caribbean Sea",
                "Gulf of Mexico", "Western North Atlantic", "Brazil",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion" ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand",
                "Indonesia", "Papua New Guinea" , "Australia", "Japan", "Fiji")
meta$Site <- factor(meta$Site, levels = pop.levels)
meta$Date_sampled <- as.Date(meta$Date_sampled, "%d/%m/%Y")
```



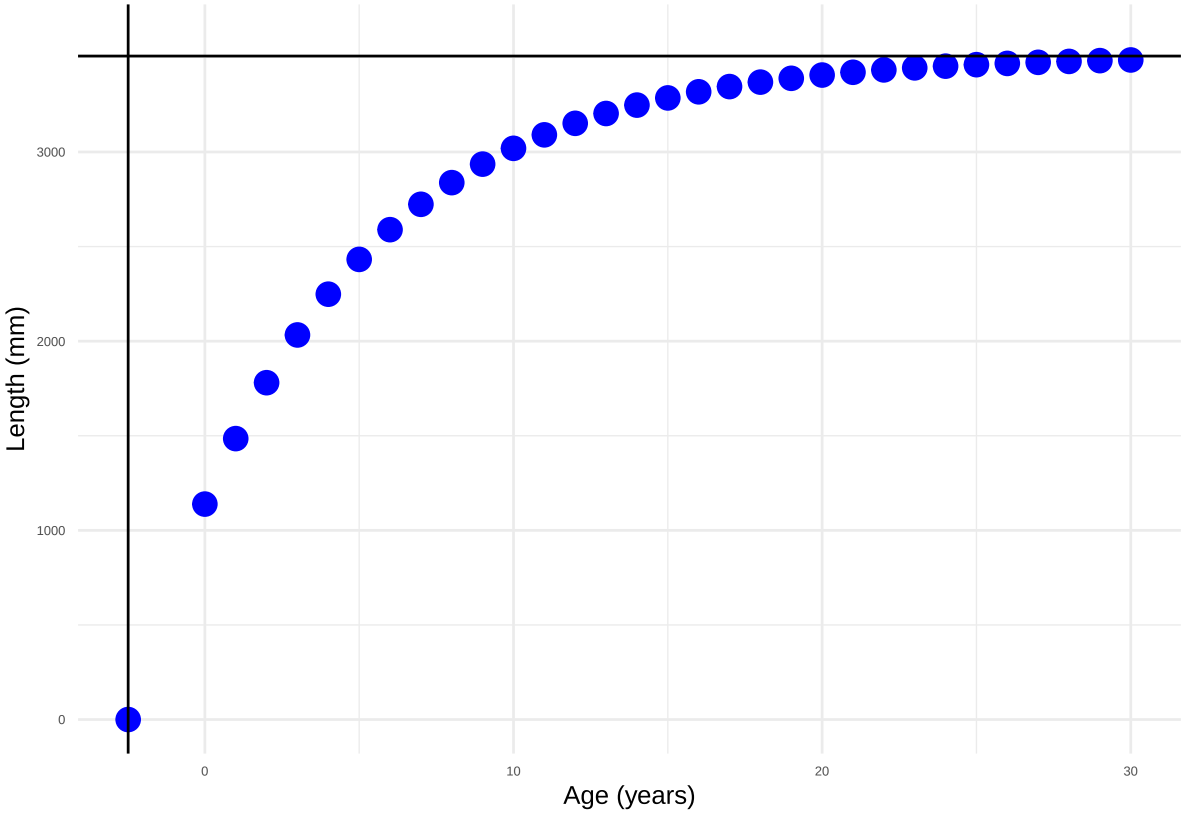
2.2 Total lengths



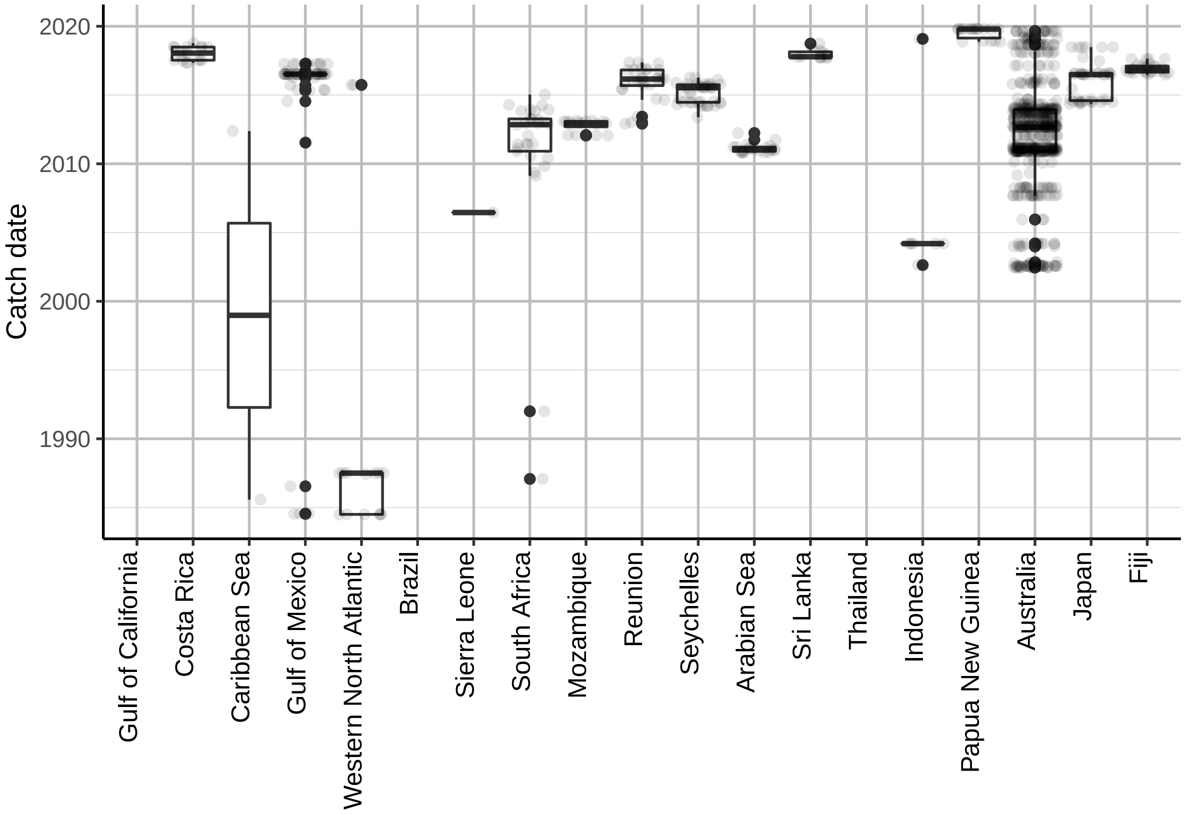
2.3 Aproximate Length-at-age

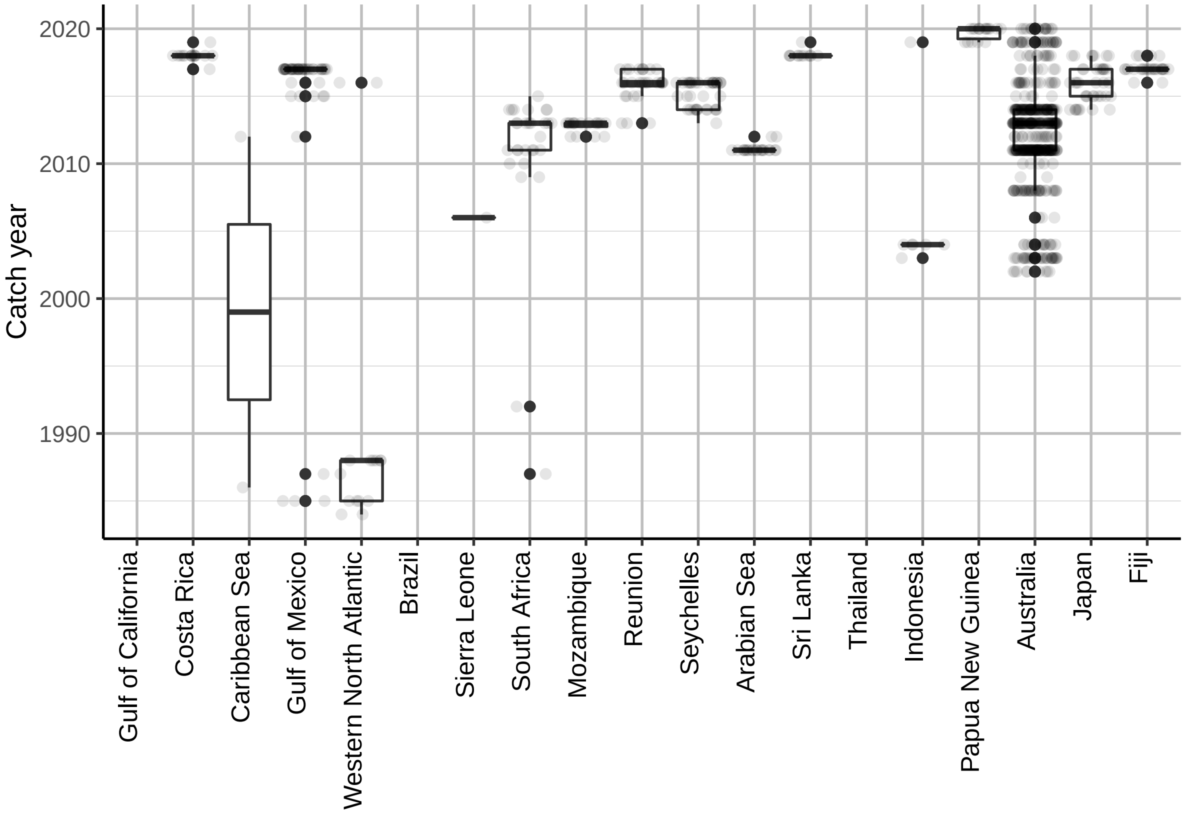
Based on length-at-age function from Tillet et al. (2011).

“Model-averaged growth parameters for these length-at-age data are theoretical asymptotic length (Linf) (s.e.) = 3119 (9.803)mm and a growth coefficient (k) = 0.158 year-1 respectively. Age at maturity was 9.5 years and like pig-eye sharks, bull sharks are long-lived with a predicted longevity of >27 years (Table 2). Juvenile growth rate was 186 mm/year for the first five years and then slowed to 45 mm/year post-maturity.”

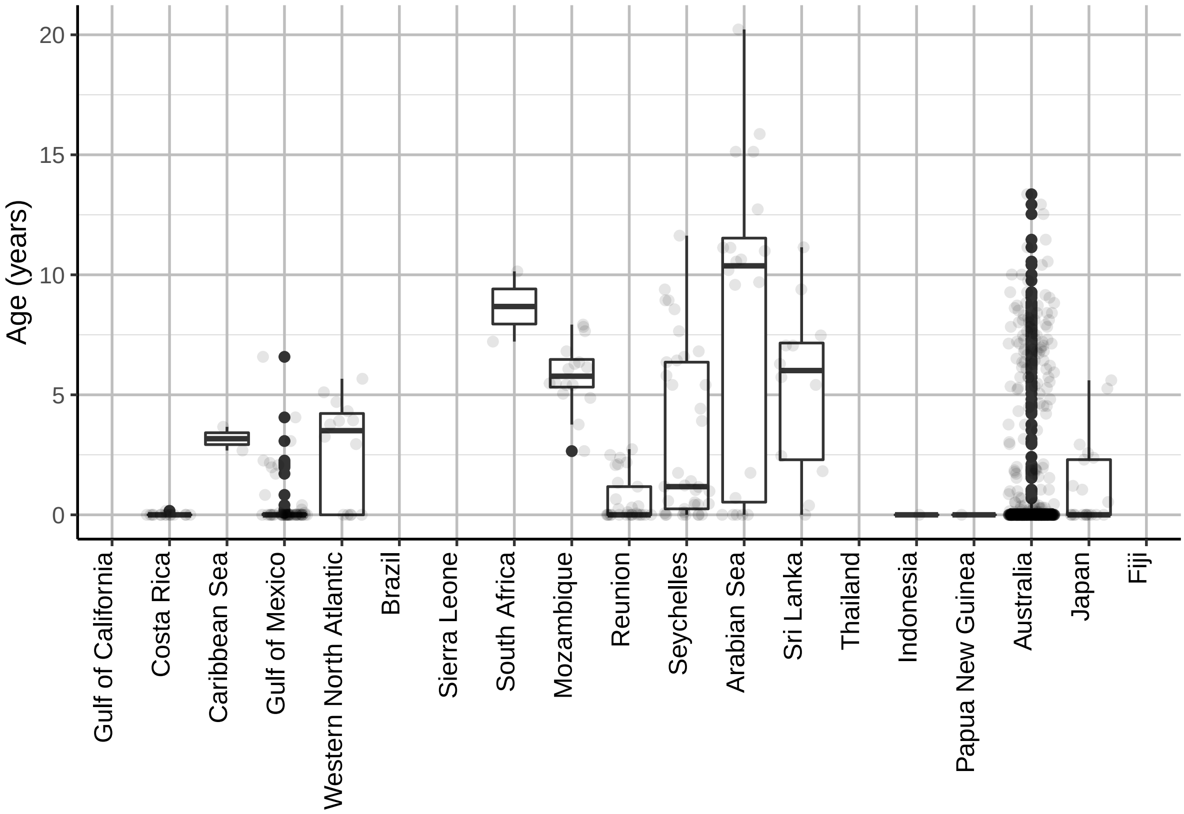


2.3.1 Catch date



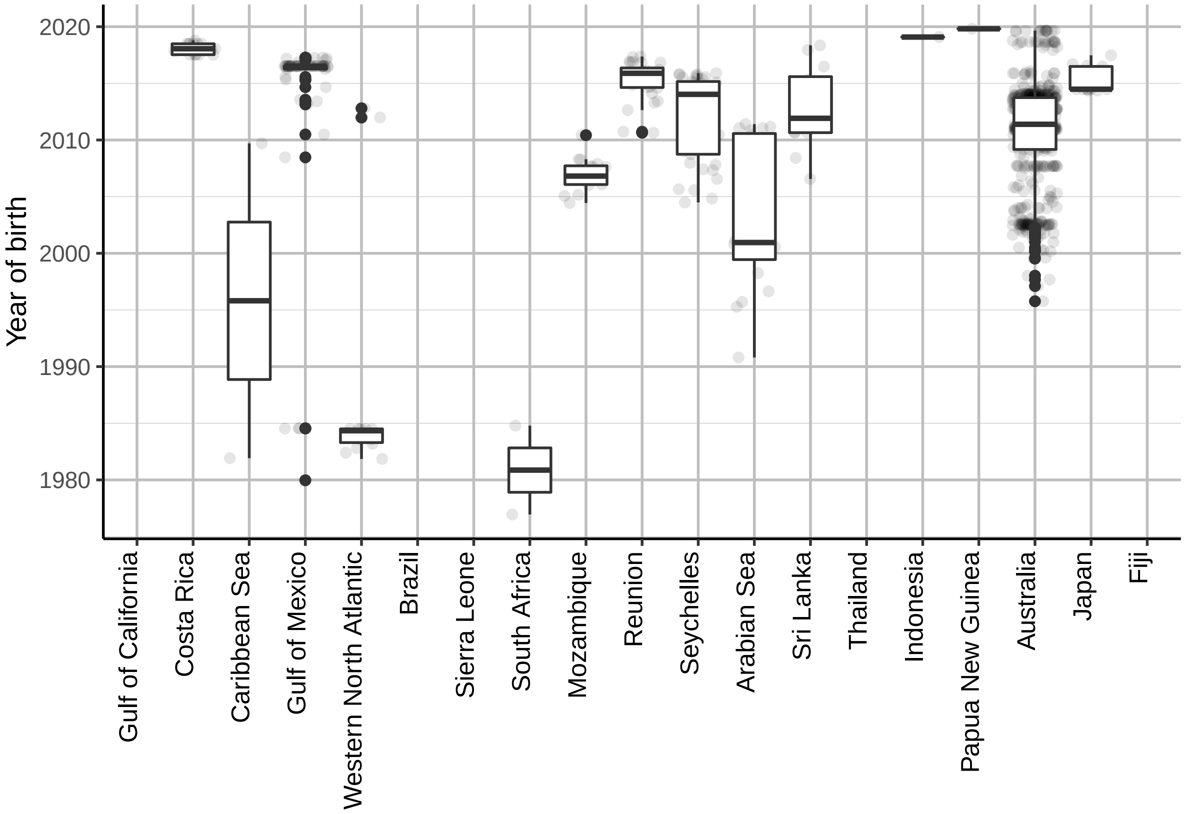


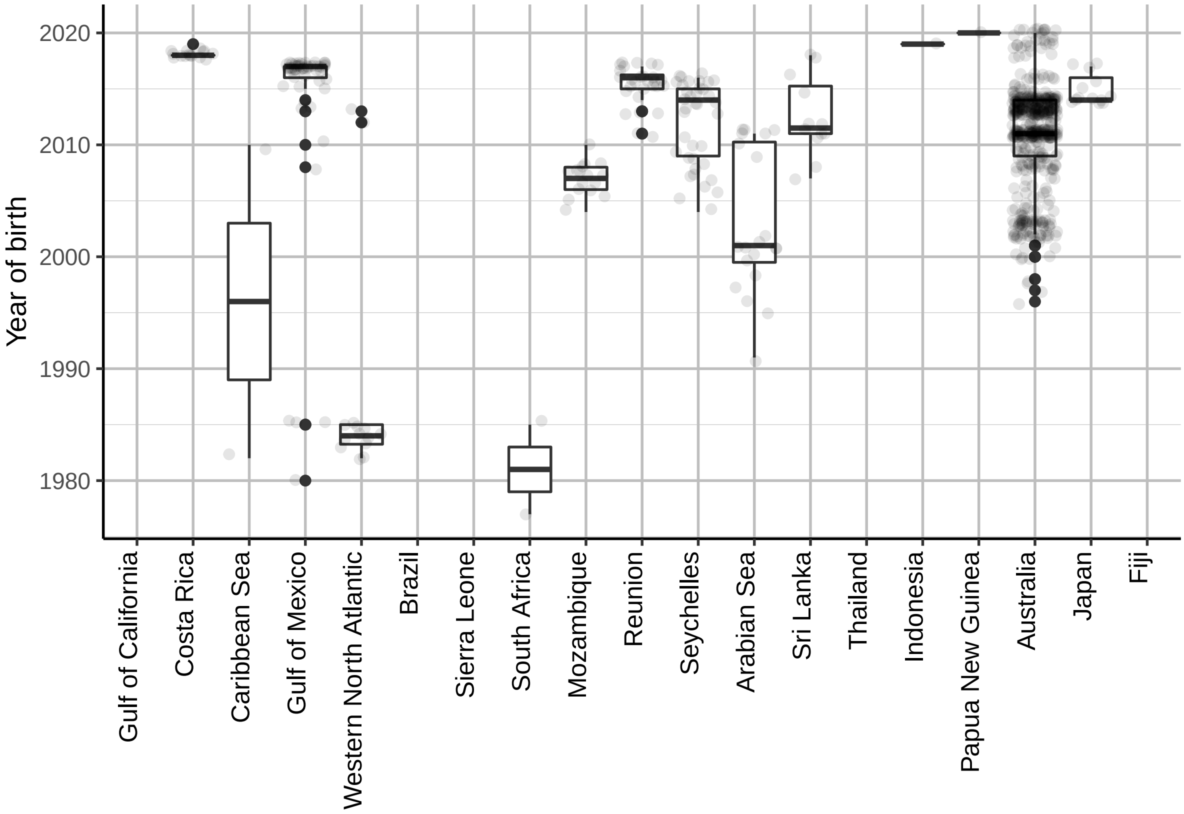
2.3.2 Age



```
## [1] 4060
## [1] 2
```

2.3.3 Cohort


Year of birth
2020
2010
2000
1990
1980
Gulf of California
Costa Rica
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Brazil
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


Year of birth
2020
2010
2000
1990
1980
Gulf of California
Costa Rica
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Brazil
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji

3 Load packages

```r
library(radiator)
library(ggplot2)
library(dplyr)
library(tidyverse)
library(ade4)
library(adegenet)
library(ape)
library(apex)
library(assigner)
library(assignPOP)
library(dartR)
library(fossil)
library(haplotypes)
library(data.table)
library(ggplot2)
library(grid)
library(gridExtra)
library(gtools)
# library(HWxtest)
library(kableExtra)
library(knitr)
library(marmap)
library(magrittr)
library(mvbutils)
library(OutFLANK)
library(pegas)
library(qvalue)
library(rubias)
library(strataG)
library(vegan)
source("Filtering funtions.R")


#set colours

colours.prior <- adegenet::funky(10)

colours.4 <- adegenet::funky(4)
names(colours.4) <- c("Brazil","Caribbean Sea","Gulf of Mexico",
                      "Western North Atlantic")

colours.6 <- adegenet::funky(6)
names(colours.6) <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")

colours.8 <- adegenet::funky(8)
names(colours.8) <- c("E-PAC","E-ATL", "W-IO",  "N-IO", "E-IO",  "W-PAC",
                      "Japan", "Fiji")

colours.10 <- adegenet::funky(10)
names(colours.10) <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                       "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                       "Papua New Guinea" , "Australia")

colours.14 <- adegenet::funky(14)
names(colours.14) <- c("Gulf of California","Costa Rica", "Sierra Leone",
                       "South Africa","Reunion","Seychelles","Arabian Sea",
```

```r
                       "Sri Lanka","Thailand","Indonesia","Papua New Guinea",
                       "Australia","Japan","Fiji")

colours.18 <- adegenet::funky(18)
names(colours.18) <- c("Costa Rica","Brazil", "Caribbean Sea", "Gulf of Mexico",
                       "Western North Atlantic",  "Sierra Leone", "South Africa",
                       "Mozambique", "Reunion","Seychelles","Arabian Sea",
                       "Sri Lanka","Thailand","Indonesia","Papua New Guinea",
                       "Australia","Japan","Fiji")

colours.13 <- adegenet::funky(13)
names(colours.13) <- c("Fitzroy River","Victoria River","Daly River","Adelaide River",
                       "South Alligator River","East Alligator River","Blue mud Bay",
                       "Roper River","Towns River", "Wenlock River","Trinity inlet",
                       "Clarence River","Sydney Harbour")


colours.26 <- adegenet::funky(26)
names(colours.26) <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                       "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                       "Papua New Guinea" , "Fitzroy River", "Daly River",
                       "Adelaide River","Darwin Coastal",  "South Alligator River",
                       "East Alligator River","Blue mud Bay", "Roper River",
                       "Towns River","Unknown","Wenlock River","Trinity inlet",
                       "Clarence River", "Sydney Harbour","Okinawa", "Urauchi River",
                       "Fiji")

colours.27 <- adegenet::funky(27)
names(colours.27) <- c("Gulf of California","Costa Rica", "Sierra Leone",
                       "South Africa","Reunion","Seychelles","Arabian Sea",
                       "Sri Lanka","Thailand","Indonesia","Papua New Guinea",
                       "Fitzroy River", "Victoria River","Daly River",
                       "Adelaide River","South Alligator River", "East Alligator River",
                       "Blue mud Bay", "Roper River","Towns River",
                       "Wenlock River","Trinity inlet","Clarence River",
                       "Sydney Harbour","Okinawa", "Urauchi River", "Fiji")

colours.29 <- adegenet::funky(29)
names(colours.29) <- c("Brazil","Caribbean Sea","Gulf of Mexico",
                       "Western North Atlantic", "Sierra Leone", "South Africa",
                       "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                       "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                       "Fitzroy River", "Daly River", "Adelaide River",
                       "South Alligator River", "East Alligator River","Blue mud Bay",
                       "Roper River","Towns River","Wenlock River","Trinity inlet",
                       "Clarence River", "Sydney Harbour","Okinawa", "Urauchi River",
                       "Fiji")

colours.32 <- adegenet::funky(32)
names(colours.32) <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                       "Western North Atlantic", "Sierra Leone", "South Africa",
                       "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                       "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                       "Fitzroy River", "Daly River", "Adelaide River","Darwin Coastal",
                       "South Alligator River", "East Alligator River","Blue mud Bay",
                       "Roper River","Towns River","Unknown","Wenlock River",
                       "Trinity inlet","Clarence River", "Sydney Harbour", "Okinawa",
                       "Urauchi River", "Fiji")
```

4 DArTseq - All data

We sequenced 188 putative Bull Shark samples with the DArTseq protocol (according to Feutry et al. 2017). Thirty-two sample replicates were included to test the reproducibility of the genotyping.

These DArTseq samples were used to identify sex-linked markers, species and population structure, and subsequently select ~35000 markers for capture probe design.

4.1 Set strata

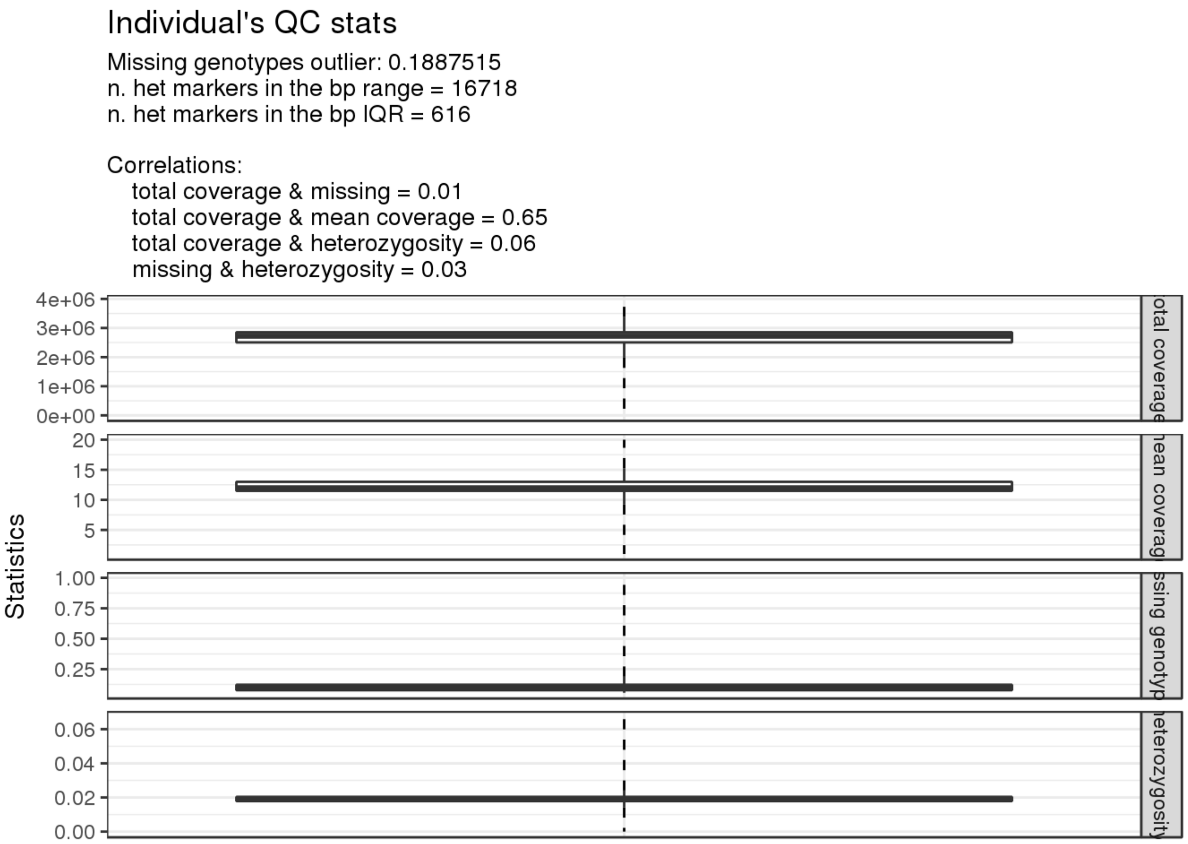
One sample failed library construction

```
data.file.snp <- "DArTseq_SNP_OrderAppendix_2_DCarcha19-4454.csv"
targetid <- readr::read_tsv("DArTseq_target.id.tsv")

strata <- readr::read_csv(metafile) %>%
  dplyr::left_join(targetid, by = "INDIVIDUALS") %>%
  dplyr::filter(!is.na(TARGET_ID)) %>%
  dplyr::mutate(STRATA = Site2)
strata$INDIVIDUALS <- with(strata, make.unique(as.character(INDIVIDUALS)))
# readr::write_tsv(strata, path = "Bull_shark_DArTseq_strata.tsv")
```

4.2 Find sex-linked markers

Sex markers are identified as per Devloo-Delva et al. (2022 preprint).

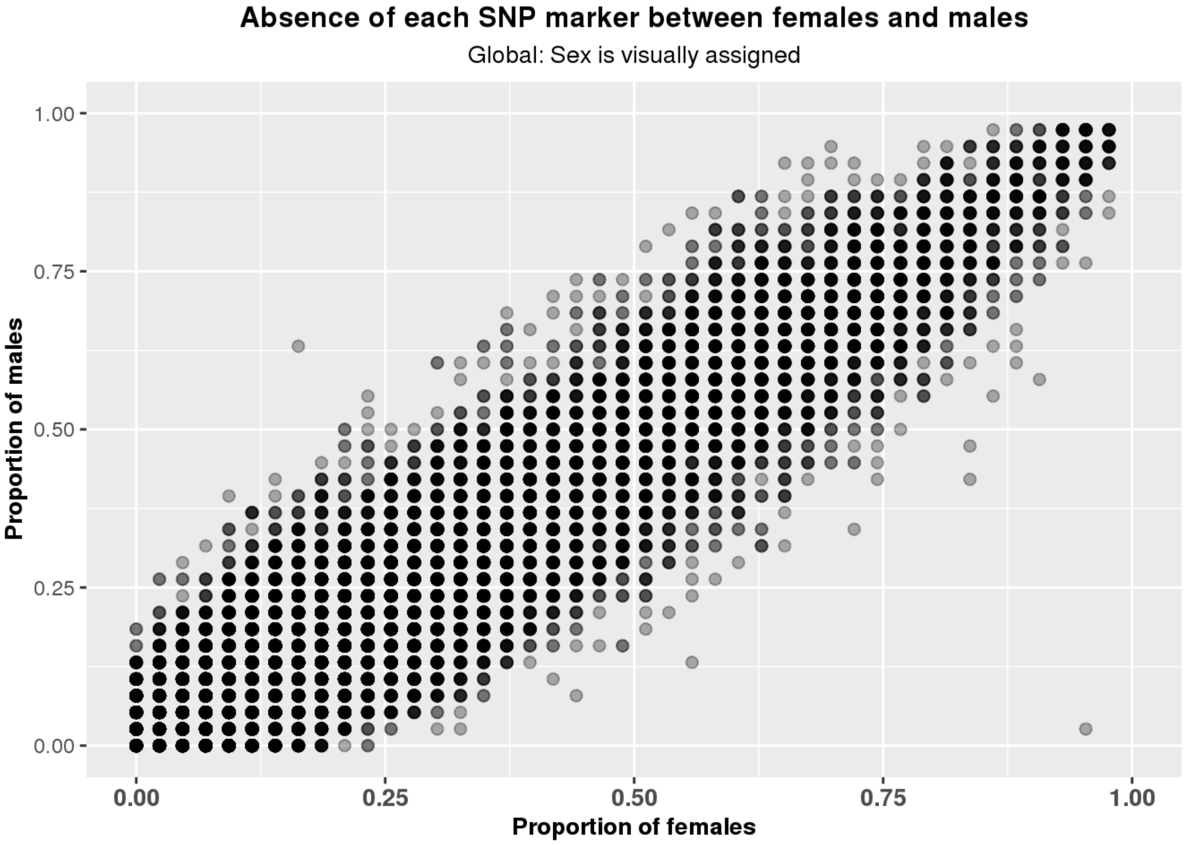
```
data <- "DArTseq_SNP_OrderAppendix_2_DCarcha19-4454.csv"
silicodata <- "DArTseq_SILICO_OrderAppendix_1_DCarcha19-4454.csv"
strata <- radiator::read_strata("Bull_shark_DArTseq_strata.tsv",
                                keep.two = FALSE)$strata
strata %<>% dplyr::rename(POP = "STRATA") %>%
  dplyr::rename(STRATA = "Sex")

bull_shark <- radiator::sexy_markers(
  data = data,
  silicodata = silicodata,
  strata = strata,
  interactive.filter = TRUE)
save(bull_shark, file = "Sex_results.Rdata")
```



Individual's QC stats

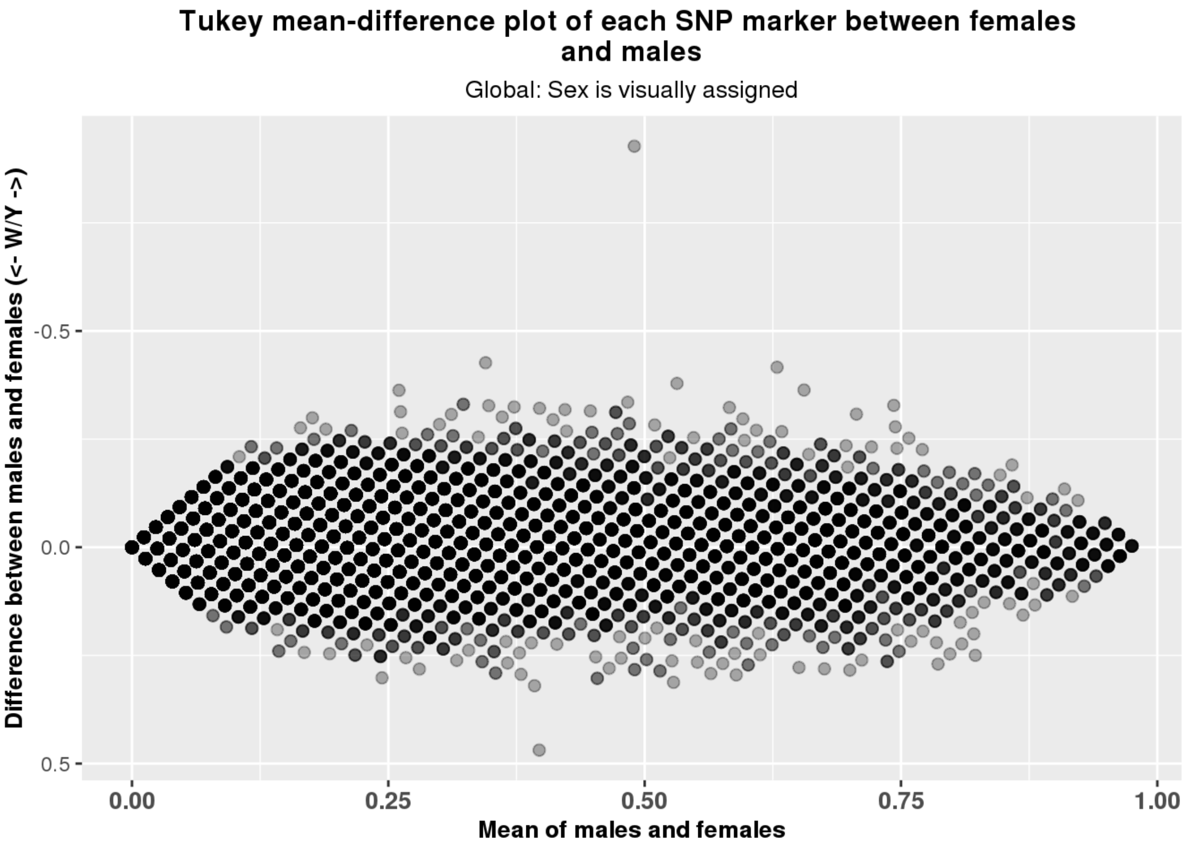
Missing genotypes outlier: 0.1887515
n. het markers in the bp range = 16718
n. het markers in the bp IQR = 616

Correlations:
total coverage & missing = 0.01
total coverage & mean coverage = 0.65
total coverage & heterozygosity = 0.06
missing & heterozygosity = 0.03

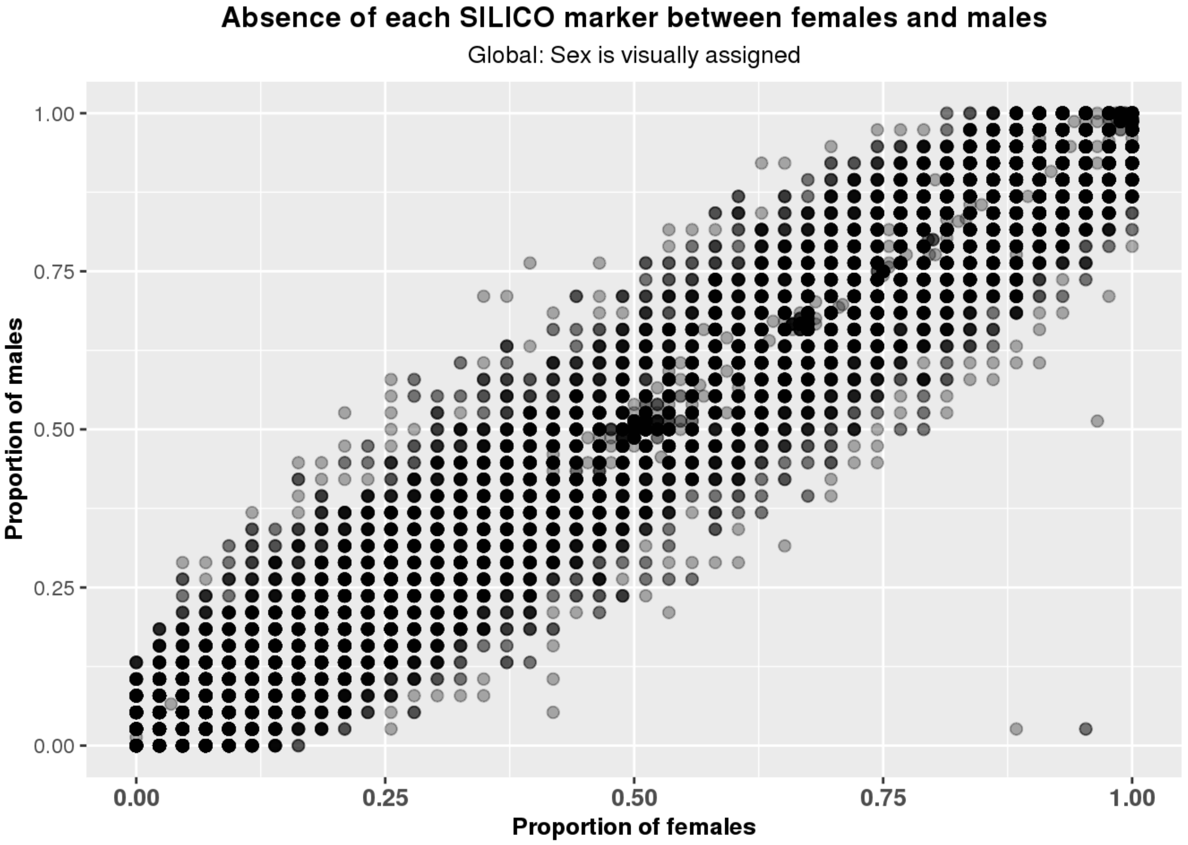


Absence of each SNP marker between females and males

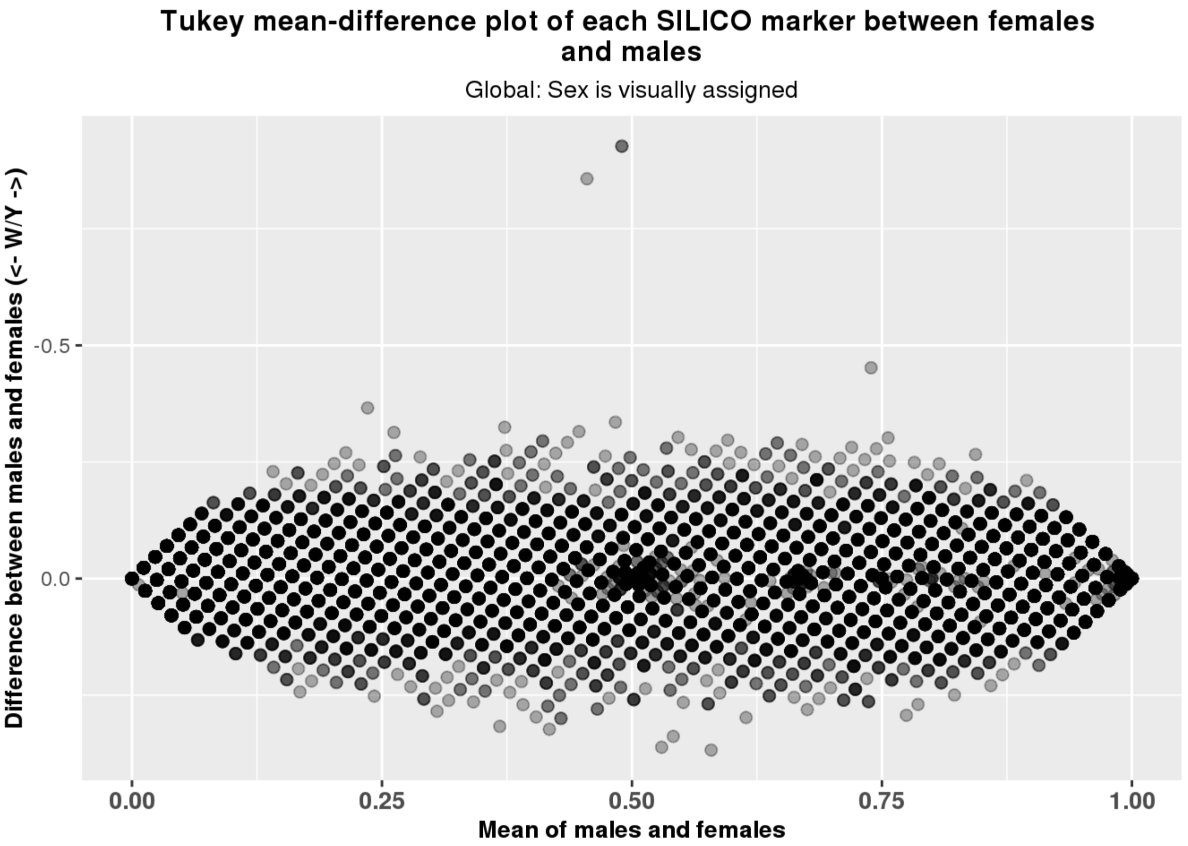
Global: Sex is visually assigned

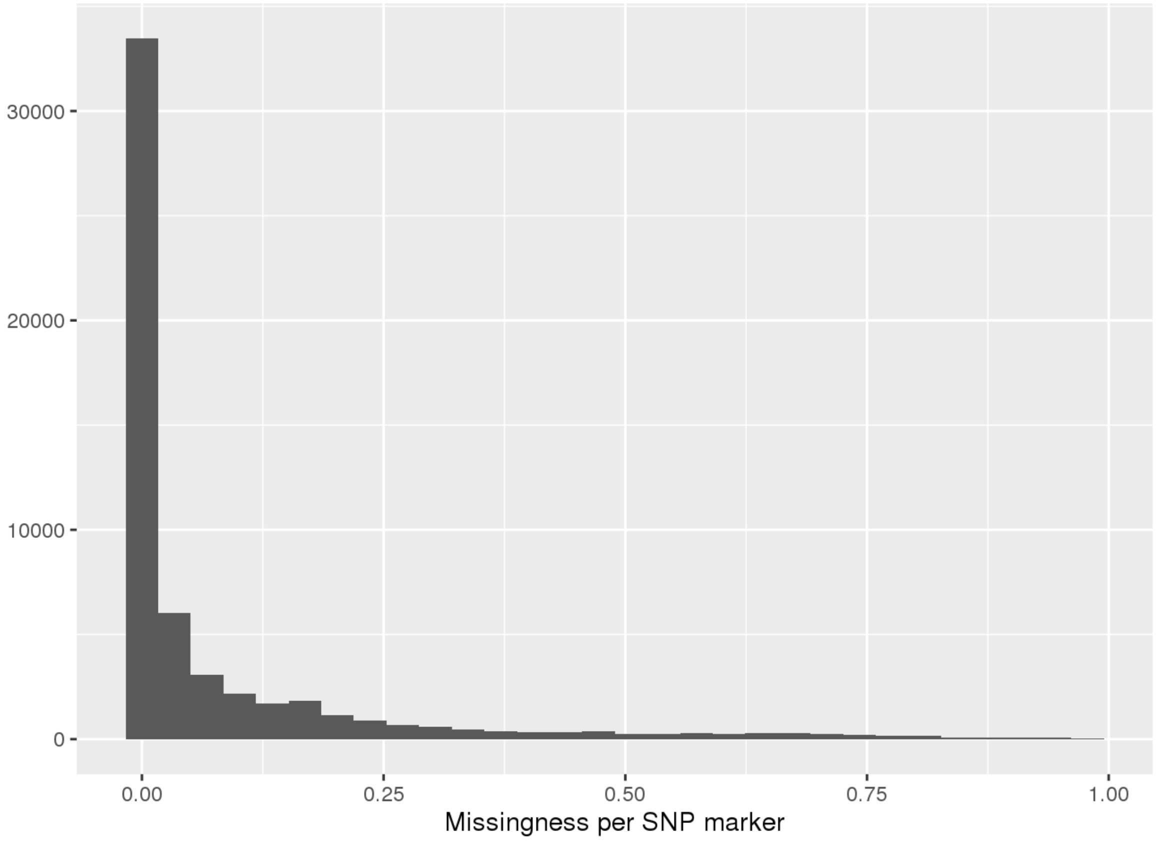

Tukey mean-difference plot of each SNP marker between females and males

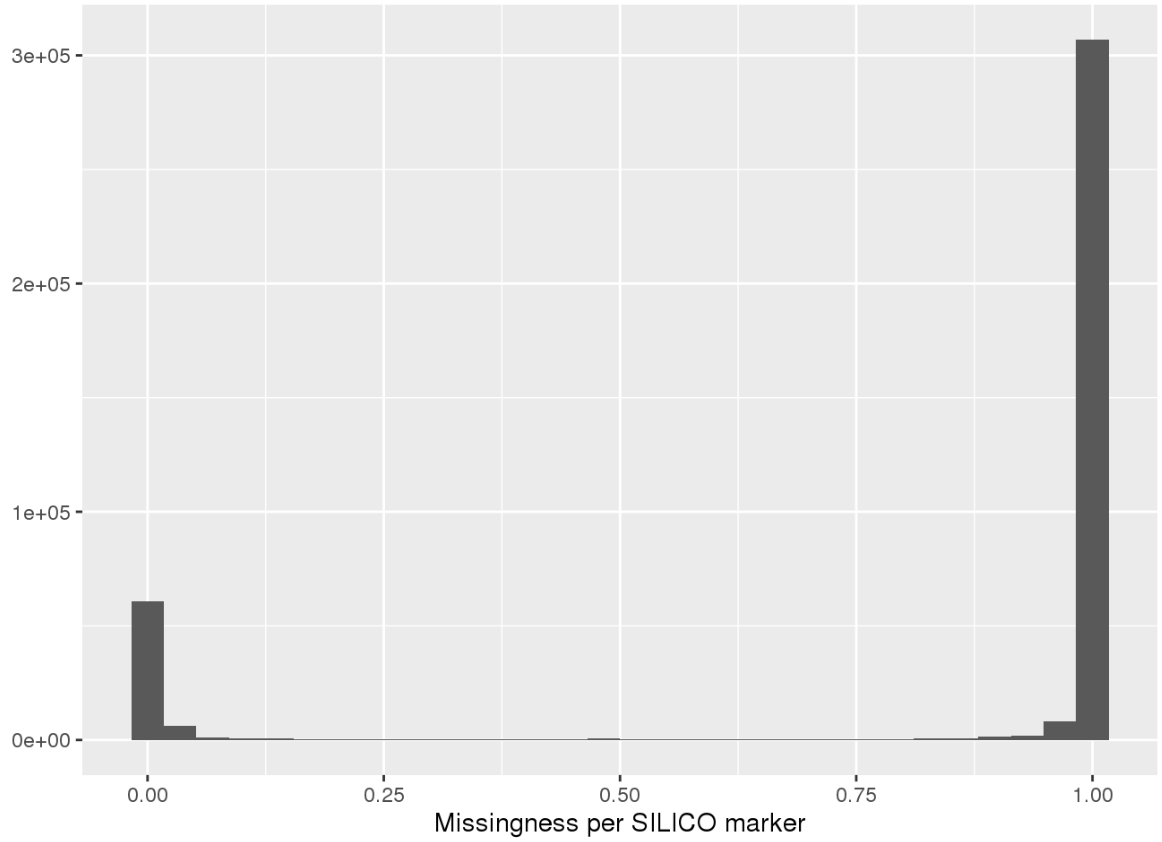
Global: Sex is visually assigned

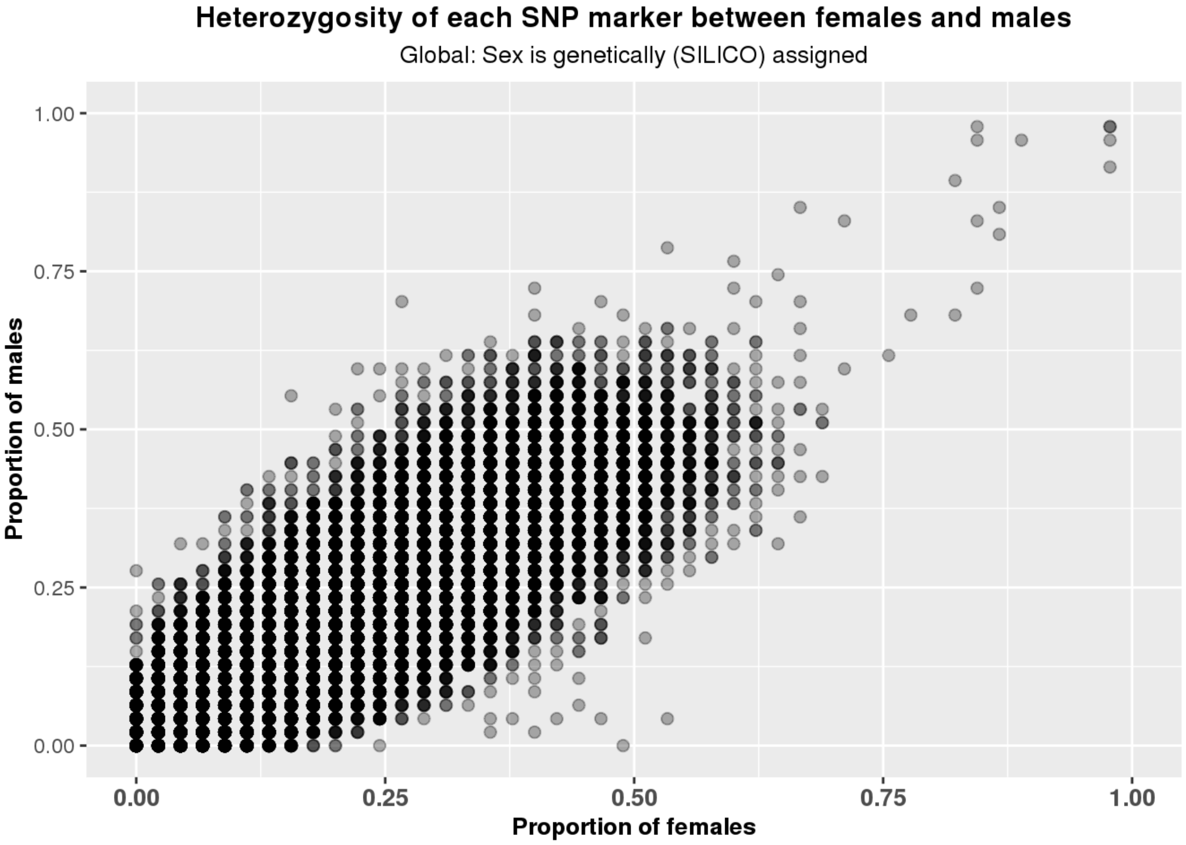

Absence of each SILICO marker between females and males

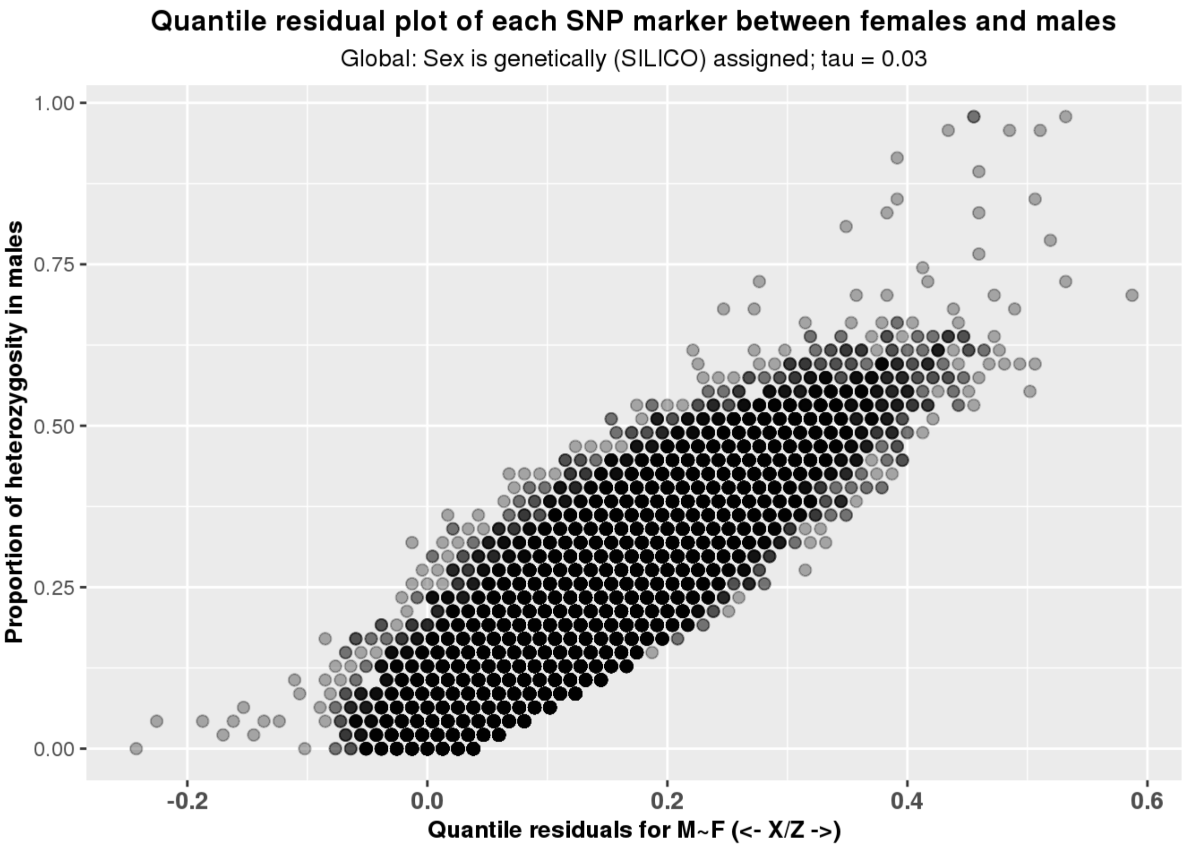
Global: Sex is visually assigned

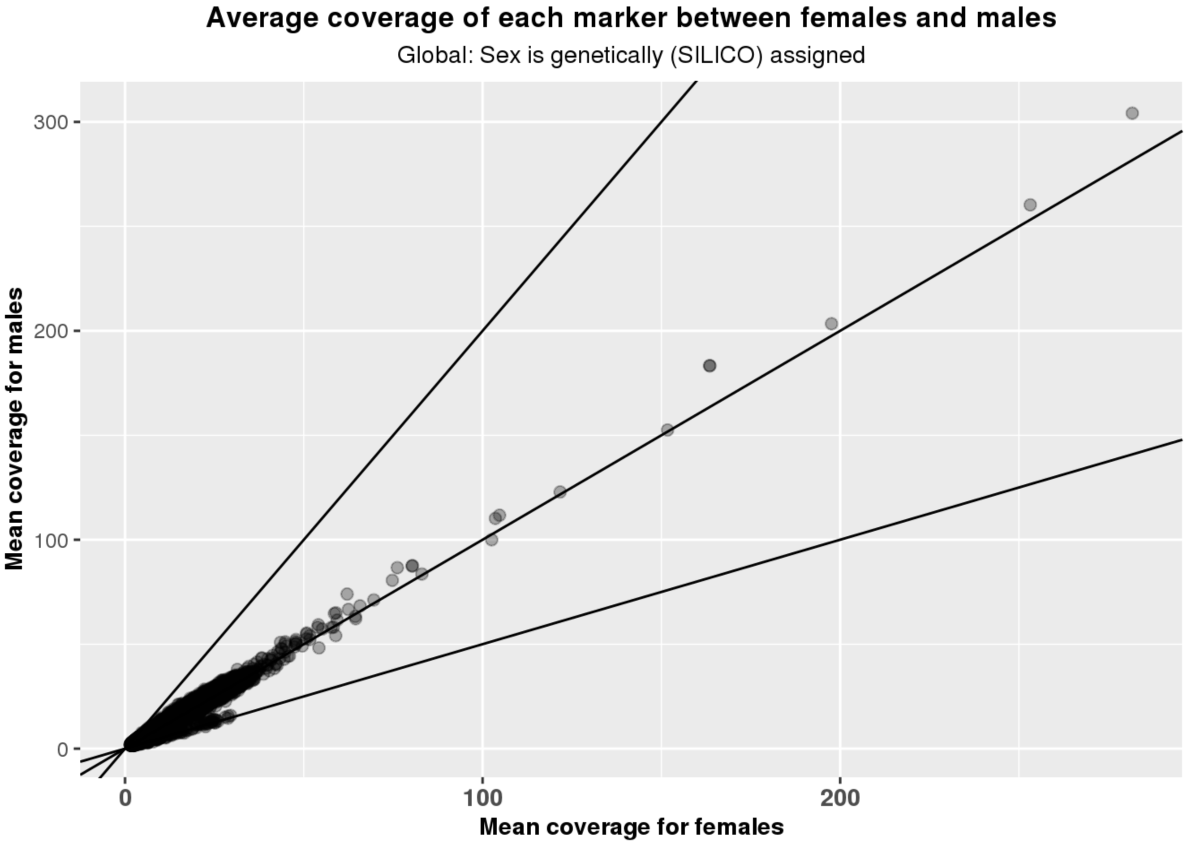

Tukey mean-difference plot of each SILICO marker between females and males
Global: Sex is visually assigned
Difference between males and females (<- W/Y ->)
-0.5
0.0
0.00
0.25
0.50
0.75
1.00
Mean of males and females

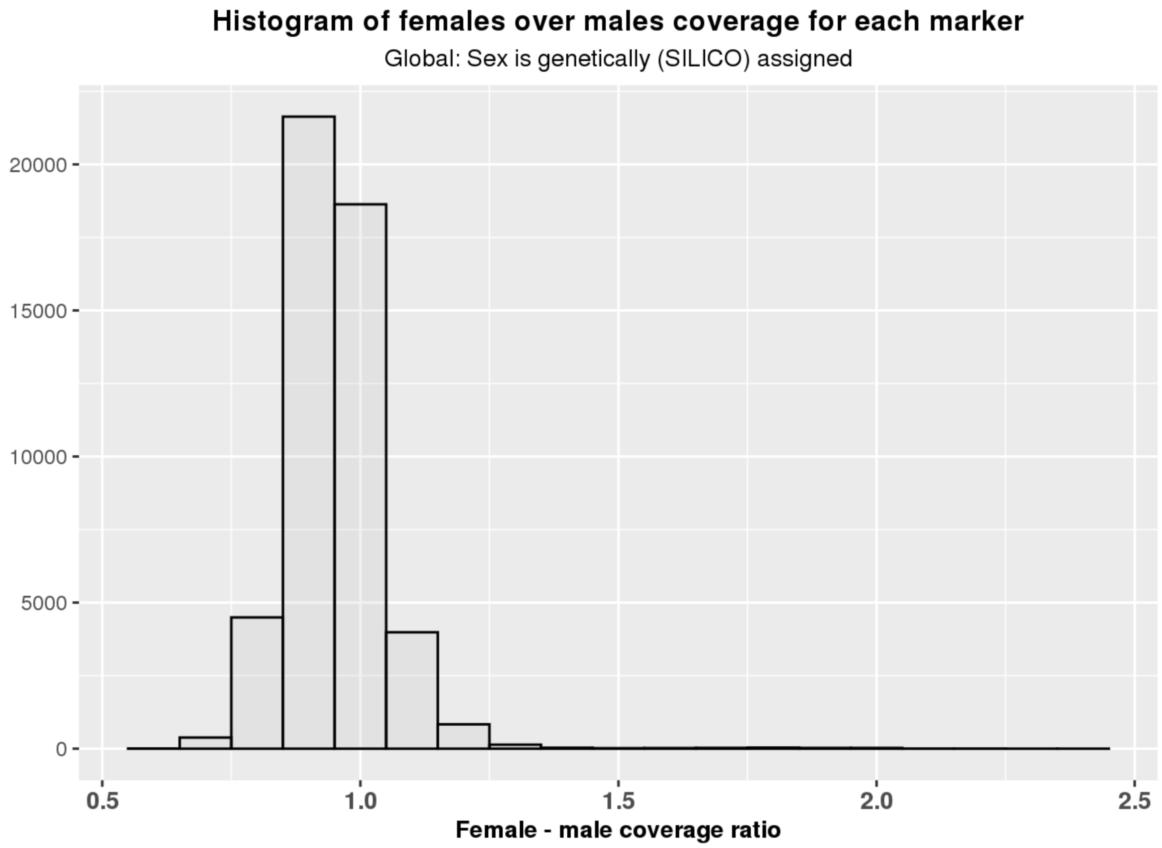

30000
20000
10000
0
0.00
0.25
0.50
0.75
1.00
Missingness per SNP marker

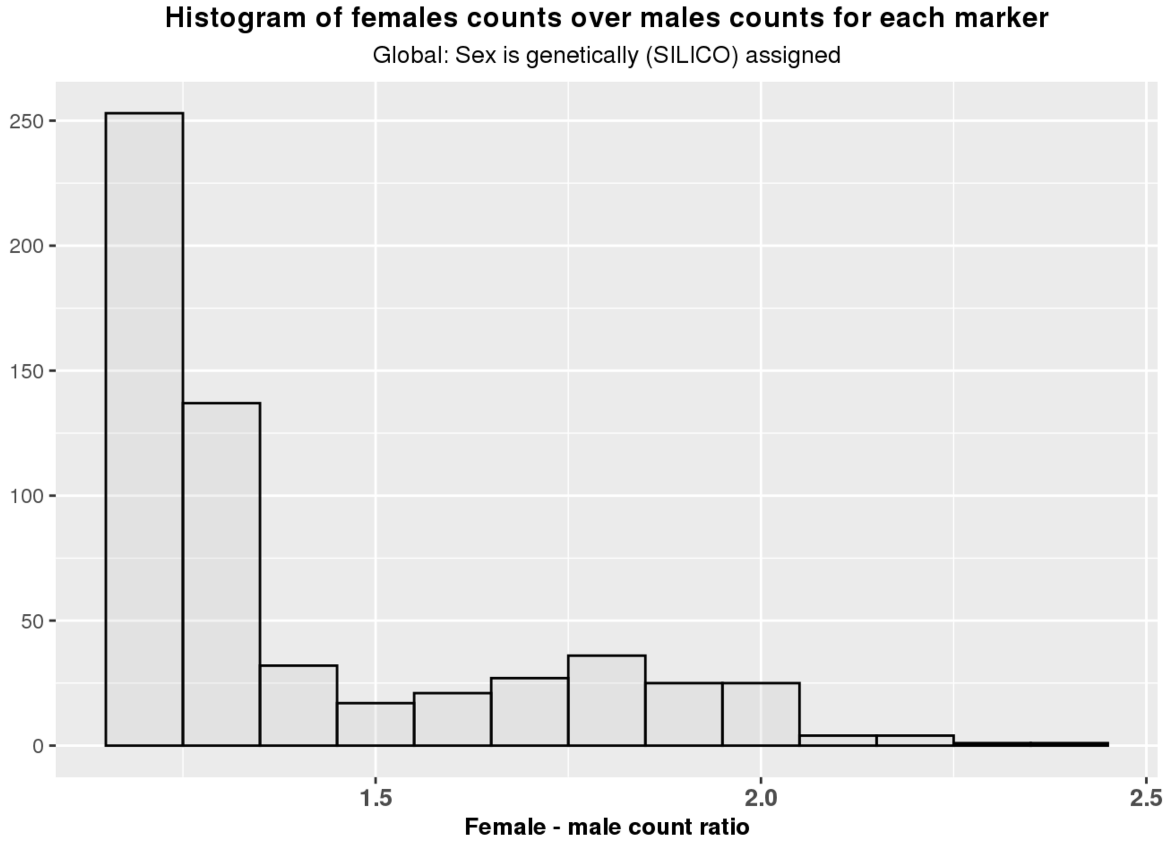

3e+05
2e+05
1e+05
0e+00
0.00
0.25
0.50
0.75
1.00
Missingness per SILICO marker

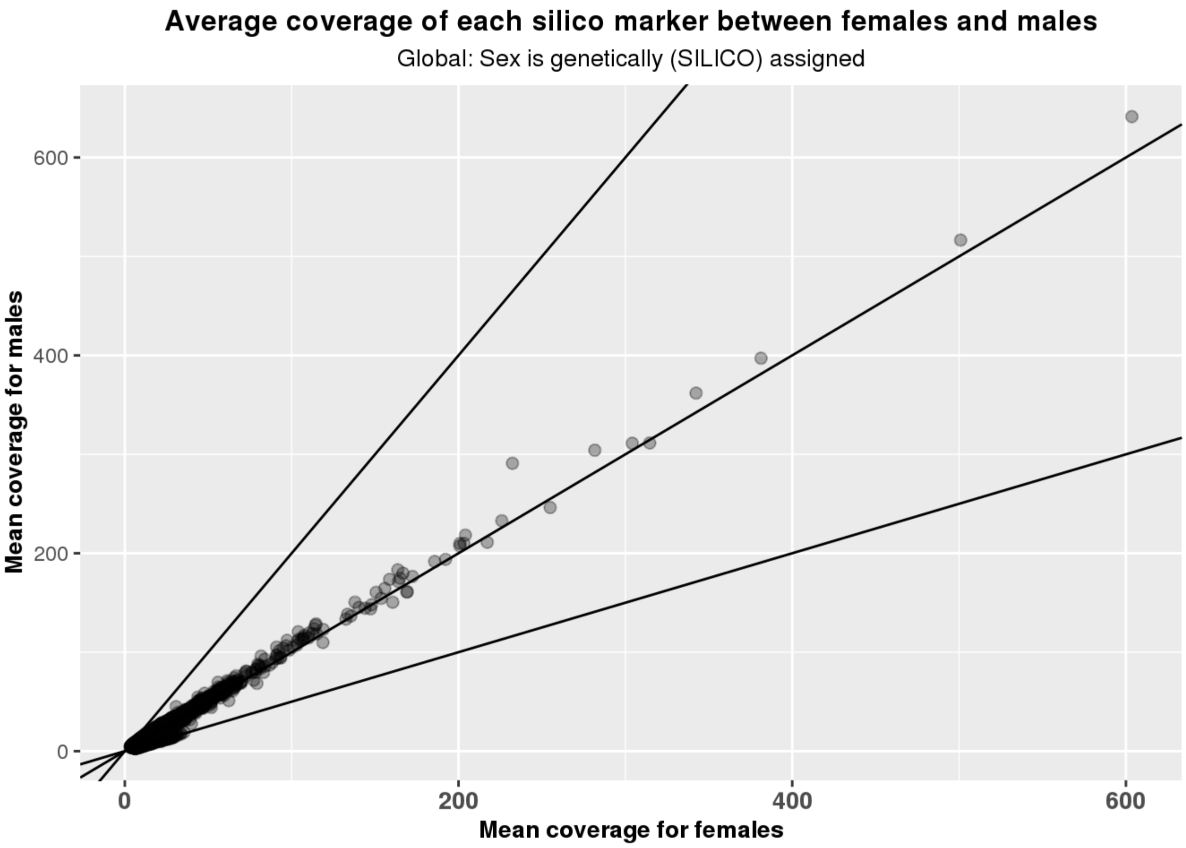

Heterozygosity of each SNP marker between females and males
Global: Sex is genetically (SILICO) assigned
1.00
0.75
0.50
0.25
0.00
Proportion of males
0.00
0.25
0.50
0.75
1.00
Proportion of females

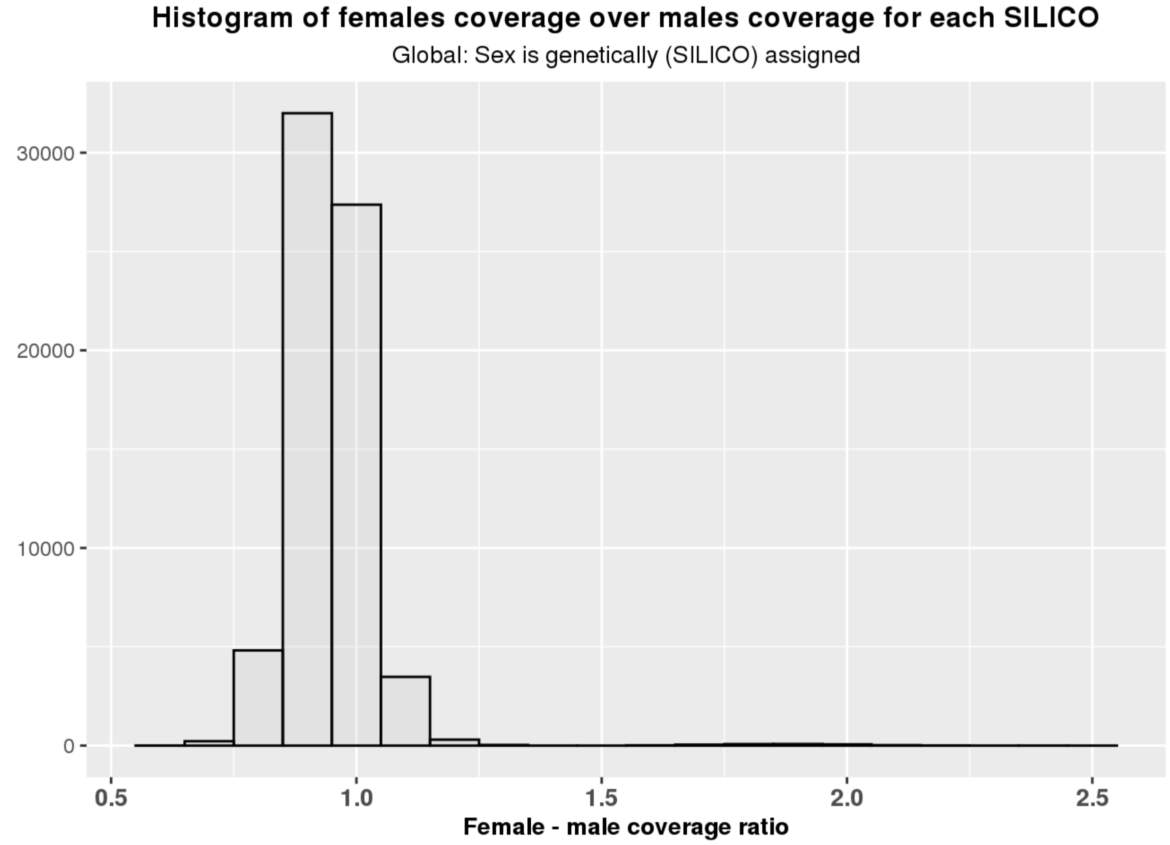

Quantile residual plot of each SNP marker between females and males
Global: Sex is genetically (SILICO) assigned; tau = 0.03
Proportion of heterozygosity in males
1.00
0.75
0.50
0.25
0.00
-0.2
0.0
0.2
0.4
0.6
Quantile residuals for M~F (<- X/Z ->)

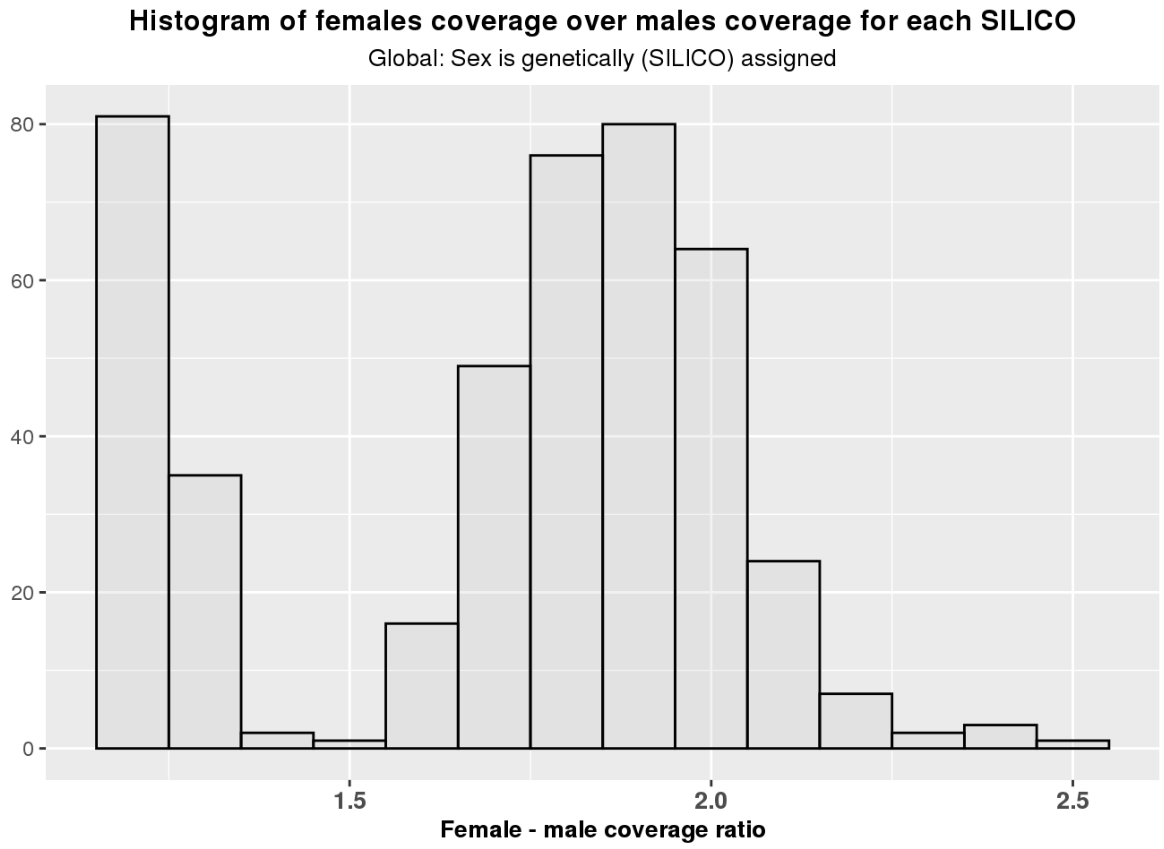

Average coverage of each marker between females and males
Global: Sex is genetically (SILICO) assigned
Mean coverage for males
300
200
100
0
0
100
200
Mean coverage for females

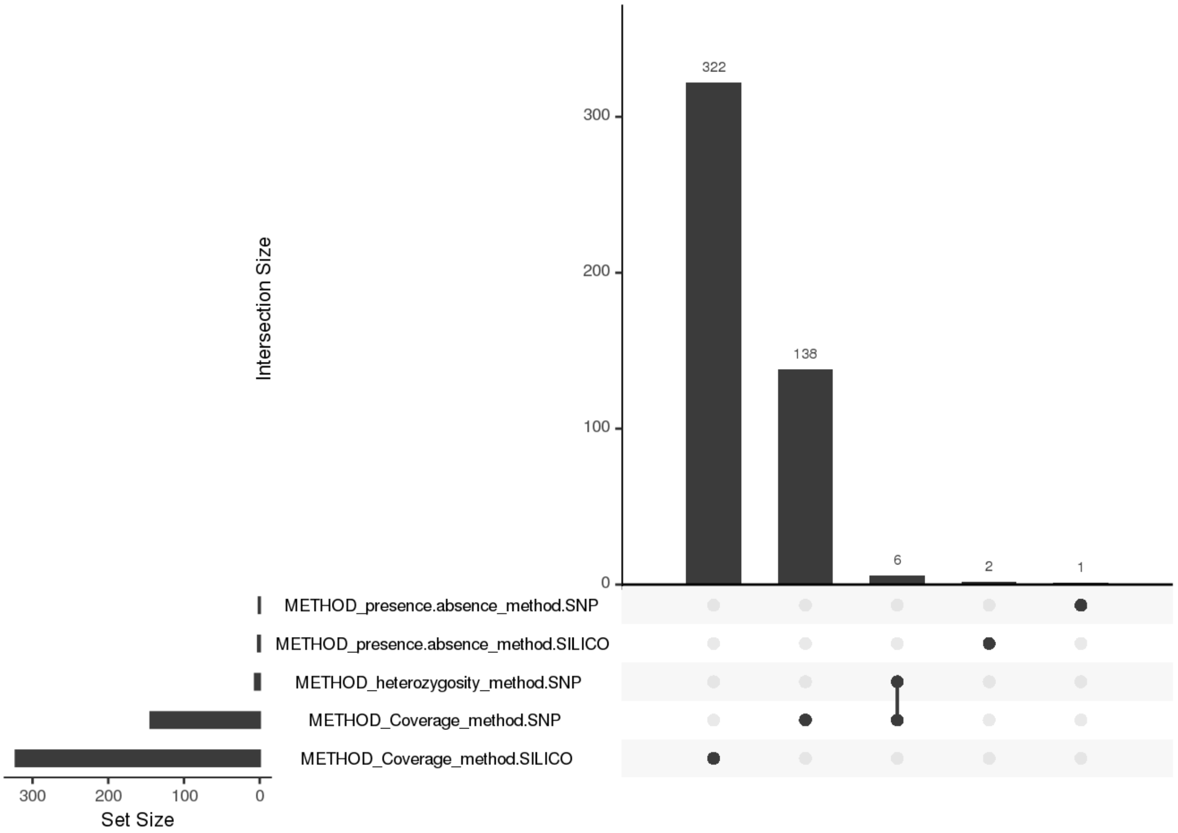

Histogram of females over males coverage for each marker
Global: Sex is genetically (SILICO) assigned
20000
15000
10000
5000
0
0.5
1.0
1.5
2.0
2.5
Female - male coverage ratio


Histogram of females counts over males counts for each marker
Global: Sex is genetically (SILICO) assigned
250
200
150
100
50
0
1.5
2.0
2.5
Female - male count ratio


Average coverage of each silico marker between females and males
Global: Sex is genetically (SILICO) assigned
Mean coverage for males
Mean coverage for females
0
200
400
600
0
200
400
600


Histogram of females coverage over males coverage for each SILICO
Global: Sex is genetically (SILICO) assigned
0
10000
20000
30000
0.5
1.0
1.5
2.0
2.5
Female - male coverage ratio





4.3 Filter data

First we filter all data with a soft filter (SF) to allow for species identification.

1. Marker Reproducibility: 0.98
2. Individual missingness: n
3. Individual Het - low: n
4. Individual Het - high: n
5. Individual total coverage - low: 7,000
6. Individual total coverage - high: 10,000,000
7. Marker MAC - low: 14
8. Marker coverage - low: 5
9. Marker coverage - high:39
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 3 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: n
16. Individual Het - high: n
17. Duplicated individuals: n
18. no filter on HWE

```r
dartseq.data <- "DArTseq_SNP_OrderAppendix_2_DCarcha19-4454.csv"
strata <- "Bull_shark_DArTseq_strata.tsv"
BSsnp <- radiator::filter_rad(dartseq.data, strata,
                               parallel.core = 1)
BS.dartseq.SF.gds <- BSsnp$gds
BS.dartseq.SF.tidy <- BSsnp$output$tidy.data
print(BS.dartseq.SF.gds, expand=TRUE, all=TRUE, attribute=TRUE,
      attribute.trim=FALSE)
save(BS.dartseq.SF.tidy, file = "DArTseq_ALL_SF_objects.Rdata")
```

Table 1:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	219 / 18 / 1 / 168810 / 250945	0 / 0 / 0 / 9754 / 19242
Filter monomorphic markers	NA	219 / 18 / 1 / 159056 / 231703	0 / 0 / 0 / 0 / 0
Filter markers in common	NA	219 / 18 / 1 / 159056 / 231703	0 / 0 / 0 / 70113 / 110685
Filter individuals based on total coverage	7000 1e+07	219 / 18 / 1 / 88943 / 121018	1 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	218 / 18 / 1 / 88943 / 121018	0 / 0 / 0 / 5 / 11
Filter MAC	14	218 / 18 / 1 / 88938 / 121007	0 / 0 / 0 / 34884 / 61921
Filter coverage min / max	5-39	218 / 18 / 1 / 54054 / 59086	0 / 0 / 0 / 14506 / 14976
Filter genotyping	0.1	218 / 18 / 1 / 39548 / 44110	0 / 0 / 0 / 11105 / 13720
Filter SNPs position on the read	all	218 / 18 / 1 / 28443 / 30390	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	218 / 18 / 1 / 28443 / 30390	0 / 0 / 0 / 25 / 123
Filter short ld	mac	218 / 18 / 1 / 28418 / 30267	0 / 0 / 0 / 0 / 1849
detect mixed genomes	0 1	218 / 18 / 1 / 28418 / 28418	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0	218 / 18 / 1 / 28418 / 28418	0 / 0 / 0 / 0 / 0
Filter HWE	NA	218 / 18 / 1 / 28418 / 28418	0 / 0 / 0 / 0 / 0

4.4 Save data

```r
BSconvert <- radiator::genomic_converter(BS.dartseq.SF.gds,output = "genlight")
BS.dartseq.SF.gl <- BSconvert$genlight


markers.meta <- radiator::extract_markers_metadata(BS.dartseq.SF.gds, whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartseq.SF.gds, whitelist = TRUE)
BS.dartseq.SF.gl$other$ind.metrics <- individuals.meta
BS.dartseq.SF.gl$other$loc.metrics <- markers.meta

pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "King Sound","Fitzroy River", "Durack River", "Daly River",
```

```
                "Adelaide River",   "South Alligator River", "East Alligator River",
                "Blue mud Bay", "Roper River","Towns River", "Skardon River",
                "Wenlock River","Trinity inlet","Clarence River", "Sydney Harbour",
                "Japan", "Fiji")
BS.dartseq.SF.gl$pop <- factor(BS.dartseq.SF.gl$other$ind.metrics$pop,
                               levels = pop.levels)

save(BS.dartseq.SF.tidy, BS.dartseq.SF.gl, file = "DArTseq_ALL_SF_objects.Rdata")
```

4.5 Load data

```
load("DArTseq_ALL_SF_objects.Rdata")
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")
BS.dartseq.SF.gl$pop <- factor(BS.dartseq.SF.gl$other$ind.metrics$Site)
BS.dartseq.SF.gl <- BS.dartseq.SF.gl[order(BS.dartseq.SF.gl$pop,
                                           BS.dartseq.SF.gl$ind.names)]

adegenet::nInd(BS.dartseq.SF.gl) # 218
adegenet::nLoc(BS.dartseq.SF.gl) # 28418
summary(BS.dartseq.SF.gl$pop)
sum(duplicated(stringr::str_match(pattern = "-\\s*(.*?)\\s*-",
                                  string =  BS.dartseq.SF.gl$ind.names)[,2])) # 32 replicate left
```

```
## [1] 218
## [1] 28418
##            Arabian Sea              Australia                 Brazil
##                     13                     62                     13
##          Caribbean Sea             Costa Rica                   Fiji
##                      2                     10                     11
##         Gulf of Mexico              Indonesia                  Japan
##                     13                      6                     14
##             Mozambique       Papua New Guinea                Reunion
##                      9                      6                     11
##             Seychelles           Sierra Leone           South Africa
##                     10                      2                     10
##              Sri Lanka               Thailand Western North Atlantic
##                     10                      8                      8
## [1] 32
```

4.6 Remove sex-linked markers

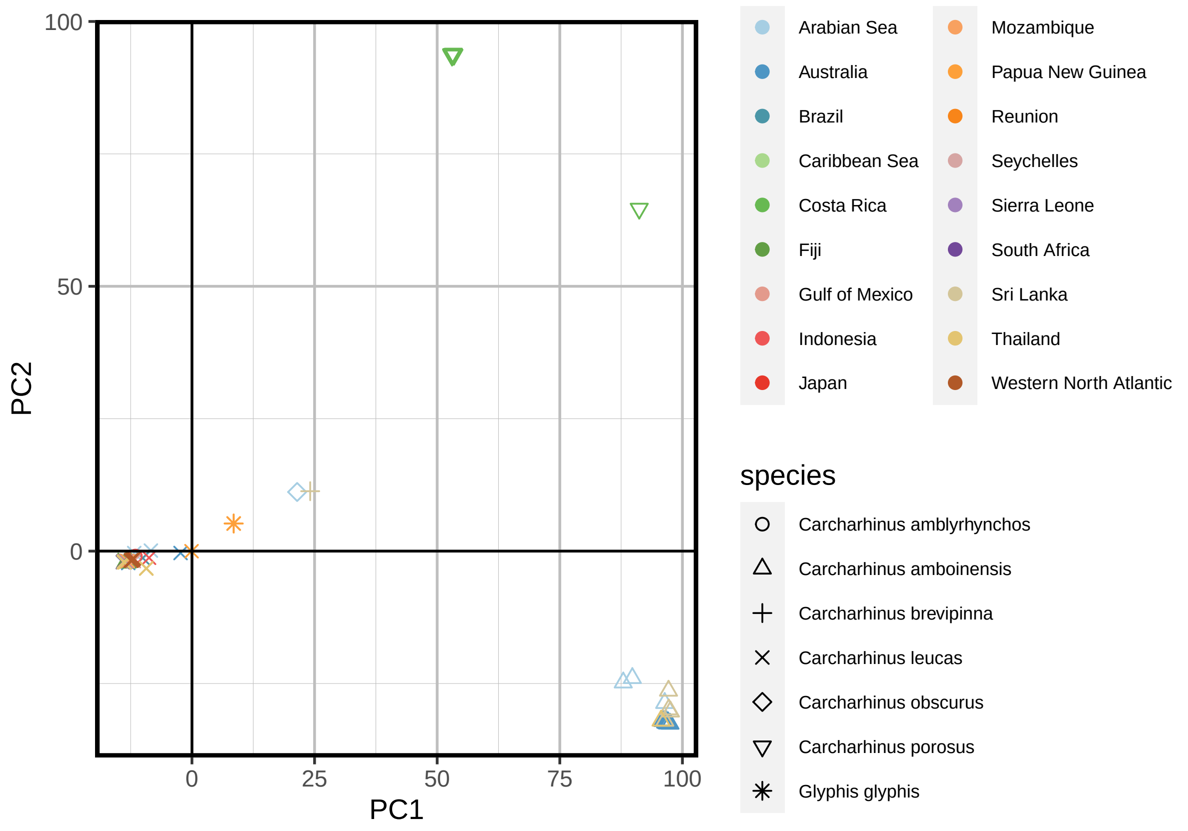
```
load("Sex_results.Rdata")
sum(BS.dartseq.SF.gl$loc.names %in% bull_shark$sexy.summary$CLONE_ID ) #84
sex.markers <- bull_shark$sexy.summary$CLONE_ID

locnames <- BS.dartseq.SF.gl$loc.names
BS.dartseq.SF.gl <- BS.dartseq.SF.gl[,!locnames %in% sex.markers]
BS.dartseq.SF.gl$other$loc.metrics <- BS.dartseq.SF.gl$other$loc.metrics[!locnames %in%
                                                                          sex.markers,]

sum(sex.markers %in% unique(BS.dartseq.SF.tidy$LOCUS)) # 84
BS.dartseq.SF.tidy <- BS.dartseq.SF.tidy[!BS.dartseq.SF.tidy$LOCUS %in%
                                           sex.markers,]
```

```
## [1] 84
## [1] 112
```

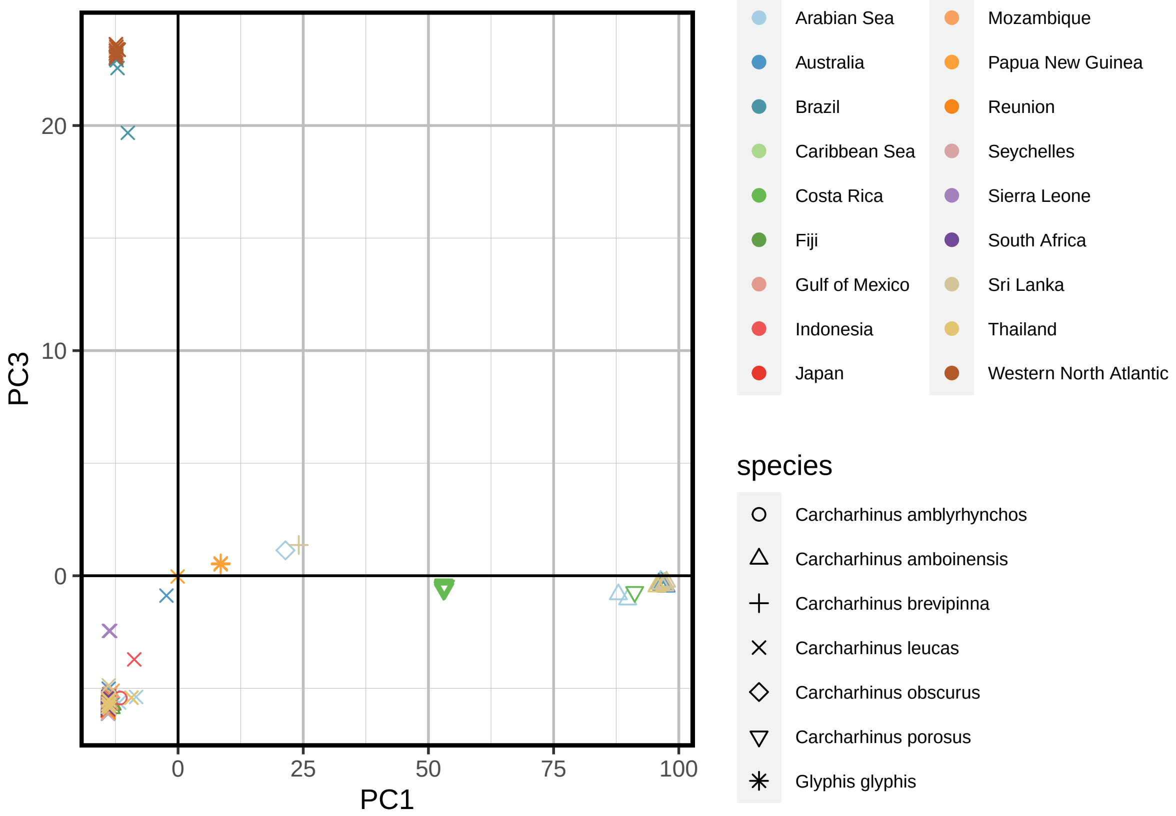
4.7 PCA to identify species

```
pca1 <- adegenet::glPca(BS.dartseq.SF.gl, nf = 4, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTseq_SF_speciesID_PCA.Rdata")
```

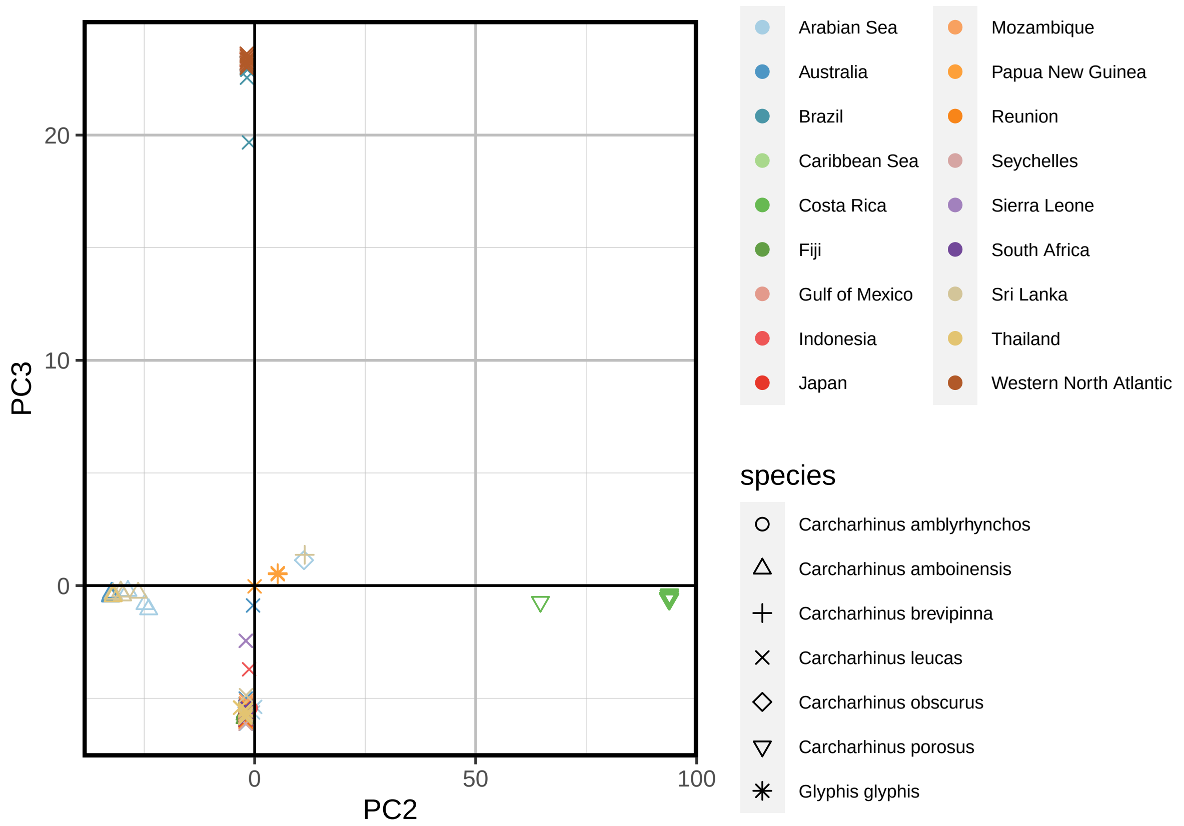
```
load("DArTseq_SF_speciesID_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- adegenet::pop(BS.dartseq.SF.gl)
BS.pca.scores$species <- BS.dartseq.SF.gl$other$ind.metrics$SpeciesID_genetic
cols <- adegenet::funky(adegenet::nPop(BS.dartseq.SF.gl))


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop,
                                                 group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                             fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 1),
                  col = ggplot2::guide_legend(ncol = 2),
                  override.aes = list(size = 0.5))
p
```



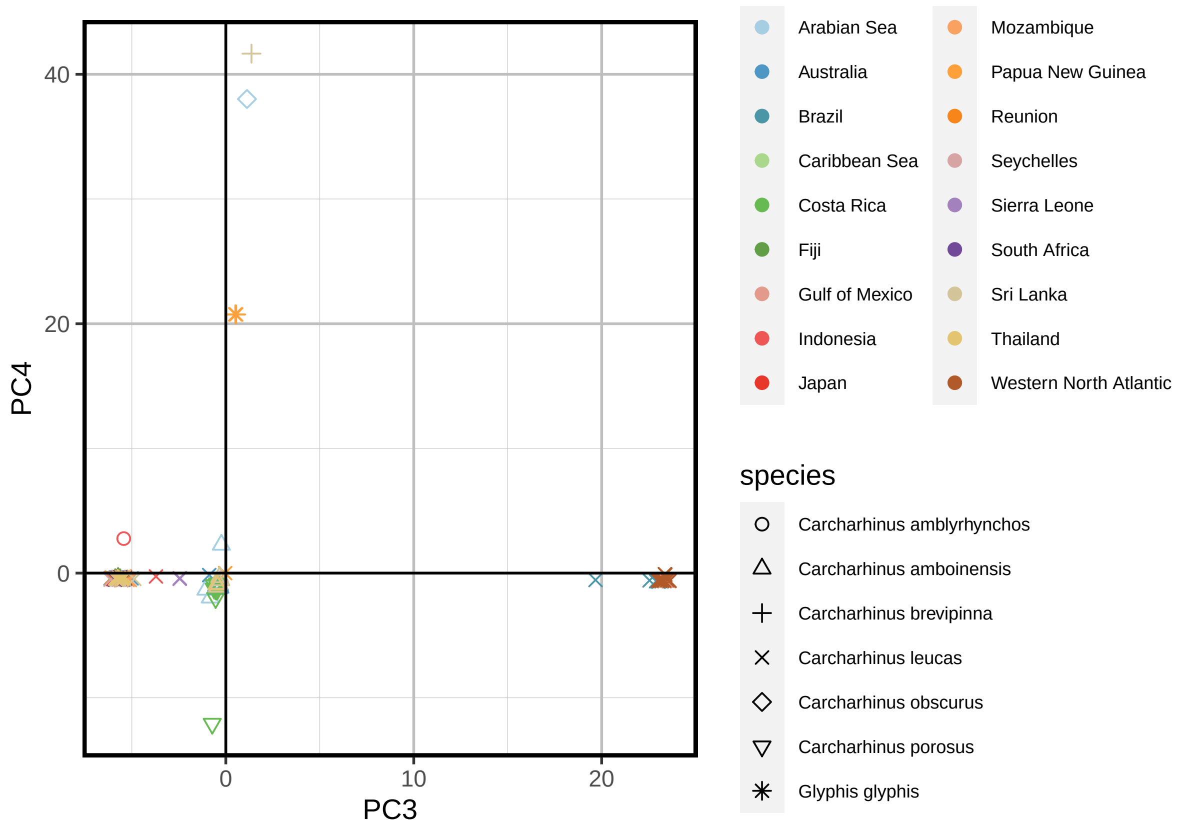
```
ggplot2::ggsave(p, filename = "DArTseq_SF_SpeciesID_PCA1.png",
                width = 30, height = 15,units = "cm")


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop,
                                                 group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA,
                                             size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 1),
                  col = ggplot2::guide_legend(ncol = 2),
                  override.aes = list(size = 0.5))
p
```



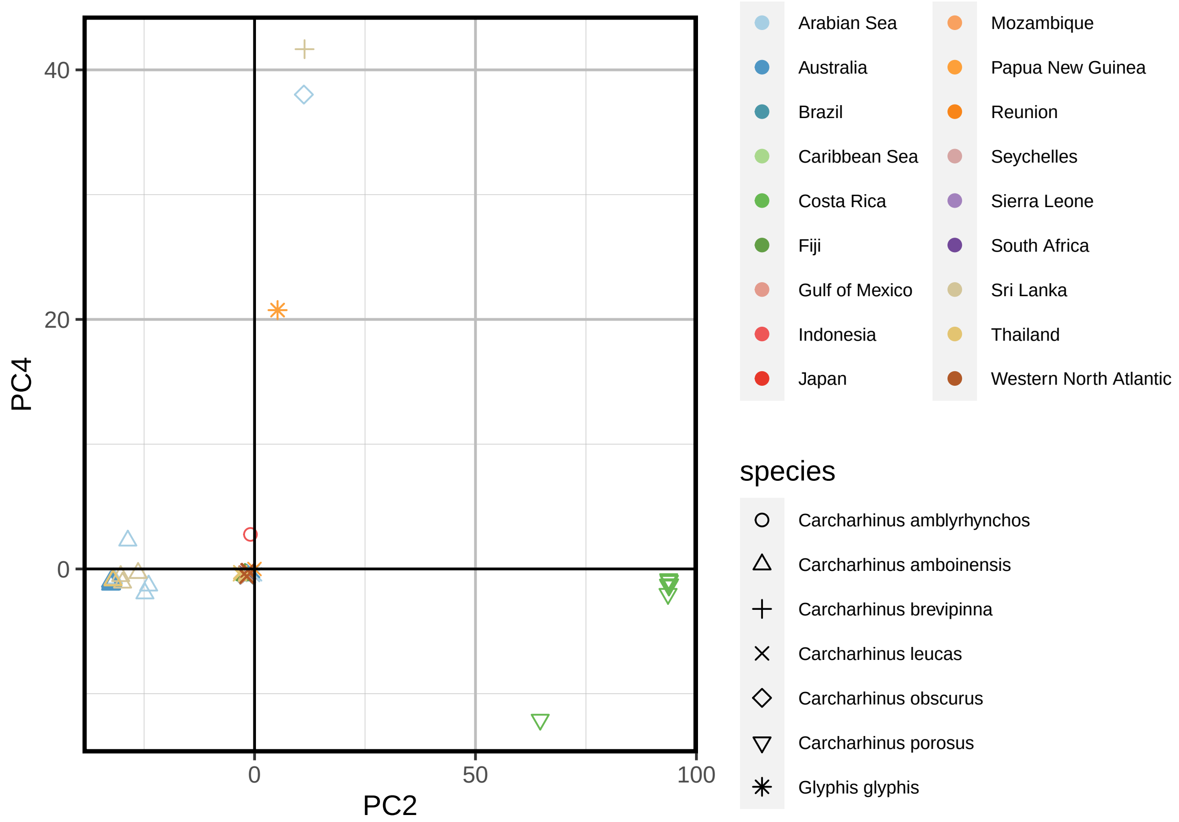
```
ggplot2::ggsave(p, filename = "DArTseq_SF_SpeciesID_PCA2.png", width = 30,
                height = 15,units = "cm")

p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop,
                                                 group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                             fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 1),
                  col = ggplot2::guide_legend(ncol = 2),
                  override.aes = list(size = 0.5))
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_SF_SpeciesID_PCA3.png",
                width = 30, height = 15,units = "cm")


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop,
                                                 group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                             fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 1),
                  col = ggplot2::guide_legend(ncol = 2),
                  override.aes = list(size = 0.5))
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_SF_SpeciesID_PCA4.png",
                width = 30, height = 15,units = "cm")

p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC4, colour = pop,
                                 group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                  colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                  linetype = 'solid',
                                                  colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                  linetype = 'solid',
                                                  colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                      fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 1),
                  col = ggplot2::guide_legend(ncol = 2),
                  override.aes = list(size = 0.5))
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_SF_SpeciesID_PCA4.png",
                width = 30, height = 15,units = "cm")
```

---

5 DArTseq - Only Bull Shark

5.1 Set strata

```r
strata <- radiator::read_strata("Bull_shark_DArTseq_strata.tsv",
                                keep.two = FALSE)$strata %>%
  dplyr:: filter(SpeciesID_genetic == "Carcharhinus leucas")
# readr::write_tsv(strata, path = "Bull_shark_DArTseq_strata2.tsv")
```

5.2 Filter data

1. Marker Reproducibility: 0.98
2. Individual missingness: 0.2
3. Individual Het - low: 0
4. Individual Het - high: 0.1
5. Individual total coverage - low: 7,000
6. Individual total coverage - high: 10,000,000
7. Marker MAC - low: 4
8. Marker coverage - low: 5
9. Marker coverage - high:39
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 3 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: 0
16. Individual Het - high: 0.132
17. Duplicated individuals: 0.1
18. Filter on HWE: 2 pop, 0.01

```r
dartseq.data <- "DArTseq_SNP_OrderAppendix_2_DCarcha19-4454.csv"
strata <- "Bull_shark_DArTseq_strata2.tsv"
BSsnp <- radiator::filter_rad(dartseq.data, strata,
                              parallel.core = 1)
BS.dartseq.gds <- BSsnp$gds
BS.dartseq.tidy <- BSsnp$output$tidy.data
print(BS.dartseq.gds, expand=TRUE, all=TRUE, attribute=TRUE,
      attribute.trim=FALSE)
save(BS.dartseq.tidy, file = "DArTseq_ALL_objects2.Rdata")
```

Table 2:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	182 / 29 / 1 / 168810 / 250945	0 / 0 / 0 / 9754 / 19242
Filter monomorphic markers	NA	182 / 29 / 1 / 159056 / 231703	0 / 0 / 0 / 97626 / 156667
Filter markers in common	NA	182 / 29 / 1 / 61430 / 75036	0 / 0 / 0 / 12699 / 15156
Filter individuals based on missingness	0.2	182 / 29 / 1 / 48731 / 59880	4 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.1	178 / 29 / 1 / 48731 / 59880	1 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	7000 1e+07	177 / 29 / 1 / 48731 / 59880	0 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	177 / 29 / 1 / 48731 / 59880	0 / 0 / 0 / 2510 / 3417
Filter MAC	4	177 / 29 / 1 / 46221 / 56463	0 / 0 / 0 / 25024 / 33343
Filter coverage min / max	5-39	177 / 29 / 1 / 21197 / 23120	0 / 0 / 0 / 2311 / 2382
Filter genotyping	0.1	177 / 29 / 1 / 18886 / 20738	0 / 0 / 0 / 266 / 393
Filter SNPs position on the read	all	177 / 29 / 1 / 18620 / 20345	0 / 0 / 0 / 0 / 0
Filter markers snp number	1	177 / 29 / 1 / 18620 / 20345	0 / 0 / 0 / 1590 / 3315
Filter short ld	not filtering	177 / 29 / 1 / 17030 / 17030	0 / 0 / 0 / 0 / 0
detect mixed genomes	0 0.132	177 / 29 / 1 / 17030 / 17030	5 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	172 / 29 / 1 / 17030 / 17030	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0.1	172 / 29 / 1 / 17030 / 17030	23 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	149 / 29 / 1 / 17030 / 17030	0 / 0 / 0 / 0 / 0
Filter HWE	20.01	149 / 29 / 1 / 17030 / 17030	0 / 0 / 0 / 1 / 1

5.3 Save data

```
BSconvert <- radiator::genomic_converter(BS.dartseq.gds,
                                         output = c("genlight", "stockr",
                                                    "pcadapt", "gtypes"))

BS.dartseq.gl <- BSconvert$genlight
BS.dartseq.stkr <- BSconvert$stockr
BS.dartseq.pc <- BSconvert$pcadapt
BS.dartseq.gt <- BSconvert$gtypes

markers.meta <- radiator::extract_markers_metadata(BS.dartseq.gds, whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartseq.gds,
                                                           whitelist = TRUE)
BS.dartseq.gl$other$ind.metrics <- individuals.meta
BS.dartseq.gl$other$loc.metrics <- markers.meta
BS.dartseq.gt@schemes <- individuals.meta

pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion"  ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea"  , "Fitzroy River", "Daly River", "Adelaide River",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Wenlock River","Trinity inlet","Clarence River",
                "Sydney Harbour","Okinawa", "Urauchi River", "Fiji")
BS.dartseq.gl$pop <- factor(stringr::str_replace_all(
  string = BS.dartseq.gl$other$ind.metrics$STRATA,
  pattern = "_", replacement = " "))
BS.dartseq.gl$pop <- factor(BS.dartseq.gl$pop, levels = pop.levels)


BS.dartseq.gl <- BS.dartseq.gl[order(BS.dartseq.gl$pop, BS.dartseq.gl$ind.names),]

pop.levels1 <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                 "Sierra Leone", "South Africa", "Mozambique", "Reunion"  , "Seychelles",
                 "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea"  ,
                 "Australia", "Japan", "Fiji")
BS.dartseq.tidy$POP_ID <- factor(BS.dartseq.tidy$Site, levels = pop.levels1)
BS.dartseq.tidy <- BS.dartseq.tidy[order(BS.dartseq.tidy$POP_ID,
                                         BS.dartseq.tidy$INDIVIDUALS),]

save(BS.dartseq.tidy, BS.dartseq.gl, BS.dartseq.stkr, BS.dartseq.pc,BS.dartseq.gt,
     markers.meta, individuals.meta, file = "DArTseq_ALL_objects2.Rdata")
# save(BS.dartseq.gl, BS.dartseq.stkr, BS.dartseq.pc,BS.dartseq.gt,
# markers.meta, individuals.meta, file = "DArTseq_ALL_objects3.Rdata")
# save(BS.dartseq.tidy,
#      file = "DArTseq_ALL_objects4.Rdata")
# object.size(BS.dartseq.tidy)  #2,033,649,160 bytes
```

5.4 Load data

```
# load("DArTseq_ALL_objects2.Rdata")
load("DArTseq_ALL_objects3.Rdata")
adegenet::nInd(BS.dartseq.gl) # 149
adegenet::nLoc(BS.dartseq.gl) # 16989
summary(BS.dartseq.gl$pop)
sum(duplicated(stringr::str_match(pattern = "-\\s*(.*?)\\s*-",
                                  string =  BS.dartseq.gl$ind.names)[,2])) # 0 replicate left
```

```
## [1] 149
## [1] 16989
##                Brazil          Caribbean Sea        Gulf of Mexico
##                    11                      2                    11
## Western North Atlantic          Sierra Leone          South Africa
##                     8                      1                     9
##            Mozambique                Reunion            Seychelles
##                     8                      9                    10
##           Arabian Sea              Sri Lanka              Thailand
##                     6                      4                     6
##             Indonesia       Papua New Guinea             Australia
##                     4                      3                    37
##                 Japan                   Fiji
##                    12                      8
## [1] 0
```

5.5 Remove sex-linked markers

```
load("Sex_results.Rdata")
sum(BS.dartseq.gl$loc.names %in% bull_shark$sexy.summary$CLONE_ID ) #24
sex.markers <- bull_shark$sexy.summary$CLONE_ID

locnames <- BS.dartseq.gl$loc.names
BS.dartseq.gl <- BS.dartseq.gl[,!locnames %in% bull_shark$sexy.summary$CLONE_ID]
BS.dartseq.gl$other$loc.metrics <-
  BS.dartseq.gl$other$loc.metrics[!locnames %in%
                                    bull_shark$sexy.summary$CLONE_ID,]

sum(sex.markers %in% unique(BS.dartseq.tidy$LOCUS)) # 24
BS.dartseq.tidy <- BS.dartseq.tidy[!BS.dartseq.tidy$LOCUS %in% sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartseq.gt@data$locus)[,2]
BS.dartseq.gt <- BS.dartseq.gt[,!locus.gt %in% sex.markers, , drop = TRUE]
```

5.6 Genetic diversity

```
set.seed(124)
gl <- BS.dartseq.gl
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "South Africa", "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names)]

gl2gpop(gl, filename = "BS_dartseq_all_genepop2.txt")
bastat <- diveRsity::basicStats(infile = "BS_dartseq_all_genepop2.txt",
                                 outfile = "BS_dartseq_all_BasicStat_output.txt",
                                fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                                ar_boots = 1000,mc_reps = 1000,
                                rarefaction = FALSE, ar_alpha = 0.05, fis_alpha = 0.05)
length(bastat$main_tab) #16
gendiv <- data.frame(
  "Brazil" = bastat$main_tab[[1]]$overall,
  "Caribbean Sea" = bastat$main_tab[[2]]$overall,
```

```
  "Gulf of Mexico" = bastat$main_tab[[3]]$overall,
  "Western North Atlantic" = bastat$main_tab[[4]]$overall,
  "South Africa" = bastat$main_tab[[5]]$overall,
  "Mozambique" = bastat$main_tab[[6]]$overall,
  "Reunion" = bastat$main_tab[[7]]$overall,
  "Seychelles" = bastat$main_tab[[8]]$overall,
  "Arabian Sea" = bastat$main_tab[[9]]$overall,
  "Sri Lanka" = bastat$main_tab[[10]]$overall,
  "Thailand" = bastat$main_tab[[11]]$overall,
  "Indonesia" = bastat$main_tab[[12]]$overall,
  "Papua New Guinea" = bastat$main_tab[[13]]$overall,
  "Australia" = bastat$main_tab[[14]]$overall,
  "Japan" = bastat$main_tab[[15]]$overall,
  "Fiji" = bastat$main_tab[[16]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, file = "DArTseq_ALL_gendiv2.txt")
save(gendiv, file = "DArTseq_ALL_gendiv2.Rdata")
```

```
load("DArTseq_ALL_gendiv2.Rdata")
shortnames <- c("BRZ", "CAR", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(gendiv, col.names = shortnames,caption = "", digits = 4) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

Table 3:

	BRZ	CAR	GOM	WNA	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
ar	1.1500	1.1150	1.1440	1.1430	1.1890	1.1810	1.1880	1.1910	1.1830	1.1810	1.1890	1.1660	1.1750	1.1970	1.1880	1.1810
size	10.9420	1.9890	10.9430	7.9550	8.9680	7.8580	8.9650	9.9550	5.9610	3.9880	5.9790	3.9840	2.9920	36.8550	11.9630	7.9390
obs_het	0.0840	0.0800	0.0810	0.0820	0.1060	0.1020	0.1050	0.1070	0.1050	0.1060	0.1120	0.1060	0.1160	0.1050	0.1080	0.1020
exp_het	0.0840	0.0620	0.0810	0.0800	0.1050	0.1040	0.1040	0.1050	0.1010	0.0960	0.1010	0.0890	0.0930	0.1090	0.1010	0.1010
uexp_het	0.0880	0.0830	0.0840	0.0850	0.1110	0.1110	0.1100	0.1110	0.1110	0.1100	0.1100	0.1020	0.1120	0.1100	0.1050	0.1080
fis	-0.0120	-0.2960	-0.0160	-0.0340	-0.0230	-0.0030	-0.0290	-0.0240	-0.0460	-0.1140	-0.1000	-0.1840	-0.2310	0.0270	-0.0600	-0.0220
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0870	-1.0000	-0.0910	-0.1340	-0.1220	-0.1180	-0.1250	-0.1080	-0.2000	-0.3520	-0.3050	-0.5580	-1.0000	0.0080	-0.1390	-0.1480
fis_hi	-0.0240	-0.2960	-0.0280	-0.0460	-0.0350	-0.0120	-0.0400	-0.0360	-0.0590	-0.1140	-0.1080	-0.1840	-0.2310	0.0200	-0.0670	-0.0350
ar_lo	1.0770	1.0710	1.0750	1.0740	1.1000	1.0680	1.0990	1.1020	1.0990	1.0970	1.1000	1.0970	1.1020	1.1070	1.1010	1.0900
ar_hi	1.1610	1.1530	1.1560	1.1590	1.2060	1.2060	1.2050	1.2070	1.2070	1.2050	1.2190	1.2040	1.2150	1.2130	1.2100	1.2020
fis.hierfstat	0.0326	-0.0480	0.0283	0.0277	0.0312	0.0576	0.0261	0.0246	0.0360	0.0111	-0.0176	-0.0627	-0.0662	0.0399	-0.0190	0.0388
fis.CI.low	0.0359	0.0230	0.0293	0.0315	0.0379	0.0755	0.0340	0.0270	0.0468	0.0264	-0.0295	-0.0660	-0.0571	0.0432	-0.0378	0.0523
fis.CI.high	0.0552	0.0754	0.0501	0.0572	0.0571	0.0963	0.0526	0.0450	0.0711	0.0551	-0.0072	-0.0334	-0.0233	0.0529	-0.0203	0.0720

5.6.1 Number of monomorphic markers per population

```r
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico", "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea",
                "Australia", "Japan", "Fiji")
BS.dartseq.gl$pop <- factor(BS.dartseq.gl$other$ind.metrics$Site, levels = pop.levels)
BS.dartseq.gl <- BS.dartseq.gl[order(BS.dartseq.gl$pop, BS.dartseq.gl$ind.names)]

monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartseq.gl[BS.dartseq.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("BRZ", "CAR", "GOM", "WNA","SIL", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

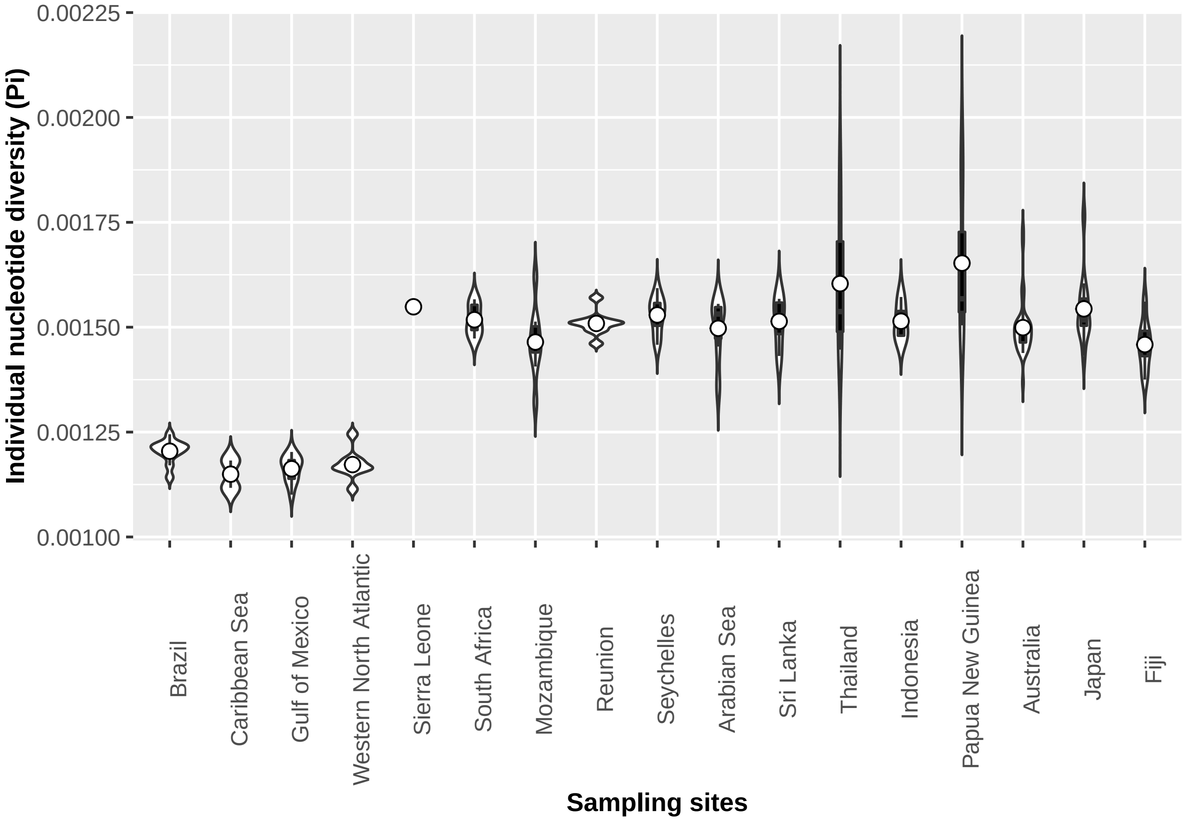
Table 4:

BRZ	CAR	GOM	WNA	SIL	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
9909	12609	10058	10432	16440	9502	9943	9712	9348	10818	11947	10945	12709	12884	5415	9821	10483

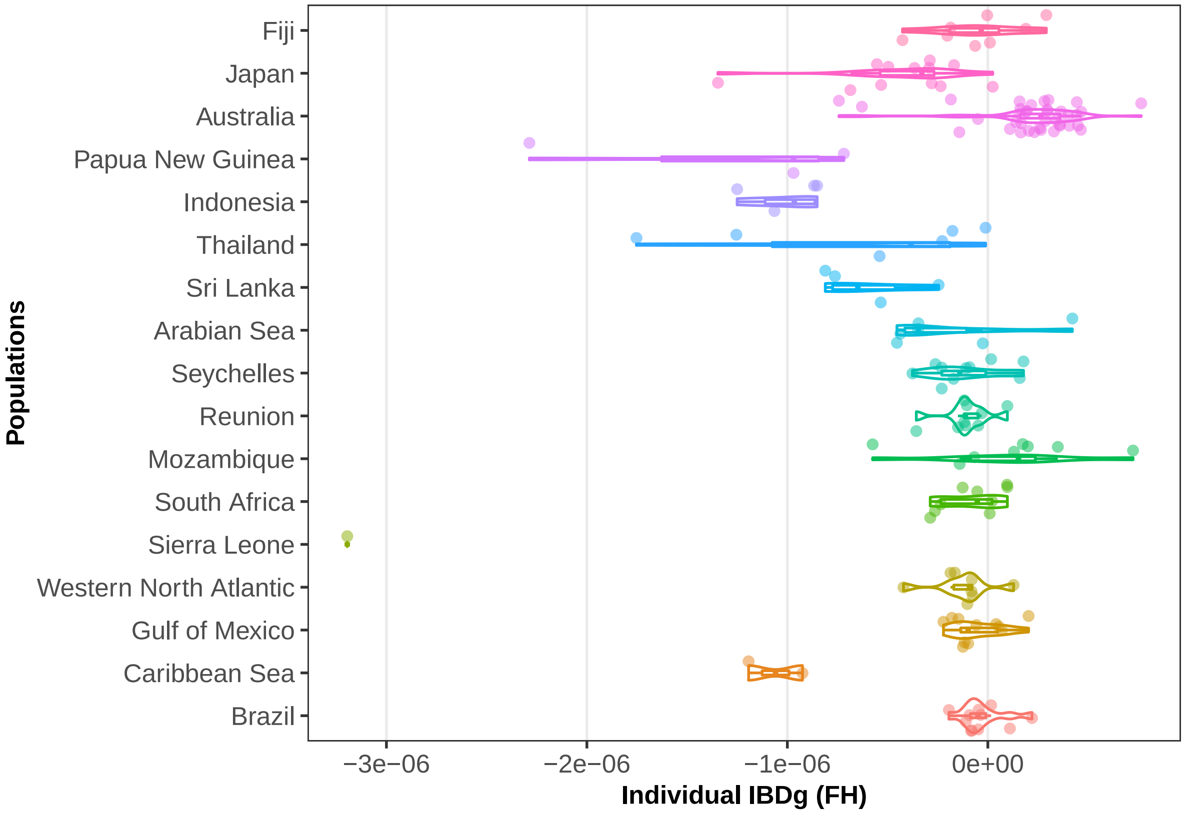
5.6.2 Nucleotide diversity and inbreeding

```r
pi.sum <- radiator::pi(
  data = BS.dartseq.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartseq.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTseq_ALL_pi_FIS_Sites2.Rdata")
# boxplot.pi <- pi.sum$boxplot.pi
# fh.box.plot <- FIS.sum$fh.box.plot
# save(boxplot.pi, fh.box.plot, file = "DArTseq_ALL_pi_FIS_Sites3.Rdata")
```

```r
load("DArTseq_ALL_pi_FIS_Sites3.Rdata")
boxplot.pi
```



```
fh.box.plot
```



```
# pi.sum$boxplot.pi
# FIS.sum$fh.box.plot
```

5.7 Genetic differentiation

```r
Fst.gt <- strataG::popStructTest(
    BS.dartseq.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTseq_ALL_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTseq_ALL_FST.txt")
```

```r
load("DArTseq_ALL_FST.Rdata")
kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                              decreasing = TRUE),
                                        -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 16989 DArTseq loci between the all sites",
  longtable = TRUE, booktabs = T) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

Table 5: Pairwise Fst for 16989 DArTseq loci between the all sites

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Gulf_of_Mexico (11) v. Papua_New_Guinea (2)	77033.084	0.0120	0.1109	0.0120	-5.2515	1.0000	0.6747	0.0451	0.7753	0.0451	0.6907	0.0622	0.8012	0.0622	0.8824	0.0622
Gulf_of_Mexico (11) v. Indonesia (4)	93596.844	0.0010	0.1191	0.0010	-2.7267	1.0000	0.6733	0.0011	0.7762	0.0011	0.5738	0.0011	0.7147	0.0011	0.8187	0.0011
Papua_New_Guinea (2) v. Western_North_Atlantic (8)	61638.548	0.0240	0.1104	0.0240	-6.3798	1.0000	0.6713	0.0745	0.7803	0.0745	0.7239	0.0811	0.8241	0.0811	0.8980	0.0811
Indonesia (4) v. Western_North_Atlantic (8)	76570.194	0.0030	0.1185	0.0030	-3.0371	1.0000	0.6695	0.0033	0.7780	0.0033	0.5893	0.0033	0.7263	0.0033	0.8278	0.0033
Gulf_of_Mexico (11) v. Thailand (4)	92623.543	0.0010	0.1141	0.0010	-2.1662	1.0000	0.6642	0.0011	0.7678	0.0011	0.5473	0.0011	0.6931	0.0011	0.8016	0.0011
Gulf_of_Mexico (11) v. Sri_Lanka (4)	92859.069	0.0020	0.1144	0.0020	-2.0099	1.0000	0.6614	0.0023	0.7655	0.0023	0.5382	0.0023	0.6865	0.0023	0.7962	0.0023
Brazil (11) v. Indonesia (4)	90951.536	0.0010	0.1171	0.0010	-2.4811	1.0000	0.6608	0.0012	0.7656	0.0012	0.5577	0.0012	0.7010	0.0012	0.8080	0.0012
Brazil (11) v. Papua_New_Guinea (2)	74133.916	0.0130	0.1090	0.0130	-4.5918	1.0000	0.6606	0.0491	0.7636	0.0491	0.6659	0.0522	0.7829	0.0522	0.8697	0.0522
Thailand (4) v. Western_North_Atlantic (8)	75824.367	0.0030	0.1136	0.0030	-2.4040	1.0000	0.6593	0.0033	0.7691	0.0033	0.5607	0.0033	0.7036	0.0033	0.8101	0.0033
Fiji (8) v. Gulf_of_Mexico (11)	121032.342	0.0010	0.1201	0.0010	-1.3537	1.0000	0.6562	0.0010	0.7674	0.0010	0.5119	0.0010	0.6660	0.0010	0.7791	0.0010
Sri_Lanka (4) v. Western_North_Atlantic (8)	75994.828	0.0030	0.1139	0.0030	-2.2407	1.0000	0.6560	0.0032	0.7668	0.0032	0.5515	0.0032	0.6970	0.0032	0.8047	0.0032
Gulf_of_Mexico (11) v. Japan (11)	140297.363	0.0010	0.1201	0.0010	-1.0983	1.0000	0.6528	0.0010	0.7624	0.0010	0.5043	0.0010	0.6594	0.0010	0.7736	0.0010
Brazil (11) v. Thailand (4)	89962.341	0.0020	0.1121	0.0020	-2.0210	1.0000	0.6518	0.0023	0.7573	0.0023	0.5335	0.0024	0.6810	0.0024	0.7920	0.0024
Arabian_Sea (6) v. Gulf_of_Mexico (11)	106824.672	0.0010	0.1146	0.0010	-1.2937	1.0000	0.6515	0.0010	0.7631	0.0010	0.5039	0.0010	0.6587	0.0010	0.7730	0.0010
Fiji (8) v. Western_North_Atlantic (8)	102162.153	0.0010	0.1194	0.0010	-1.4973	1.0000	0.6503	0.0010	0.7624	0.0010	0.5195	0.0010	0.6720	0.0010	0.7842	0.0010
Brazil (11) v. Sri_Lanka (4)	90297.515	0.0020	0.1126	0.0020	-1.8575	1.0000	0.6491	0.0023	0.7552	0.0023	0.5243	0.0023	0.6743	0.0023	0.7864	0.0023
Japan (11) v. Western_North_Atlantic (8)	120651.330	0.0010	0.1196	0.0010	-1.1916	1.0000	0.6476	0.0010	0.7597	0.0010	0.5099	0.0010	0.6638	0.0010	0.7773	0.0010
Gulf_of_Mexico (11) v. Mozambique (8)	119009.537	0.0010	0.1159	0.0010	-1.0355	1.0000	0.6474	0.0010	0.7648	0.0010	0.4962	0.0010	0.6520	0.0010	0.7674	0.0010
Caribbean_Sea (2) v. Indonesia (4)	39028.741	0.0779	0.1119	0.0779	-19.5630	1.0000	0.6471	0.1615	0.7609	0.1898	0.8856	0.2274	0.9300	0.2274	0.9629	0.2274
Gulf_of_Mexico (11) v. Reunion (9)	126641.833	0.0010	0.1167	0.0010	-0.9377	1.0000	0.6467	0.0010	0.7573	0.0010	0.4936	0.0010	0.6504	0.0010	0.7659	0.0010
Brazil (11) v. Fiji (8)	118513.284	0.0010	0.1180	0.0010	-1.2409	1.0000	0.6458	0.0010	0.7584	0.0010	0.4996	0.0010	0.6548	0.0010	0.7698	0.0010
Gulf_of_Mexico (11) v. South_Africa (9)	126189.816	0.0010	0.1156	0.0010	-0.8796	1.0000	0.6448	0.0010	0.7550	0.0010	0.4904	0.0010	0.6471	0.0010	0.7632	0.0010
Arabian_Sea (6) v. Western_North_Atlantic (8)	88918.136	0.0010	0.1141	0.0010	-1.4101	1.0000	0.6447	0.0010	0.7573	0.0010	0.5112	0.0010	0.6645	0.0010	0.7780	0.0010
Caribbean_Sea (2) v. Sierra_Leone (1)	18745.883	0.3227	0.0679	0.3227	NA	NA	0.6446	0.3227	0.7406	0.3227	NA	NA	NA	NA	NA	NA
Brazil (11) v. Japan (11)	137727.301	0.0010	0.1183	0.0010	-1.0138	1.0000	0.6435	0.0010	0.7541	0.0010	0.4928	0.0010	0.6488	0.0010	0.7647	0.0010
Gulf_of_Mexico (11) v. Seychelles (10)	132727.138	0.0010	0.1168	0.0010	-0.7989	1.0000	0.6419	0.0010	0.7543	0.0010	0.4868	0.0010	0.6449	0.0010	0.7612	0.0010
Mozambique (8) v. Western_North_Atlantic (8)	100386.634	0.0010	0.1152	0.0010	-1.1268	1.0000	0.6406	0.0010	0.7538	0.0010	0.5017	0.0010	0.6564	0.0010	0.7712	0.0010
Arabian_Sea (6) v. Brazil (11)	104258.428	0.0030	0.1126	0.0030	-1.1959	1.0000	0.6403	0.0030	0.7529	0.0030	0.4915	0.0030	0.6473	0.0030	0.7635	0.0030
Reunion (9) v. Western_North_Atlantic (8)	107588.086	0.0010	0.1161	0.0010	-1.0175	1.0000	0.6400	0.0010	0.7536	0.0010	0.4985	0.0010	0.6542	0.0010	0.7692	0.0010
South_Africa (9) v. Western_North_Atlantic (8)	107195.063	0.0010	0.1149	0.0010	-0.9684	1.0000	0.6380	0.0010	0.7515	0.0010	0.4952	0.0010	0.6510	0.0010	0.7666	0.0010
Caribbean_Sea (2) v. Papua_New_Guinea (2)	27164.723	0.3656	0.1045	0.3656	NA	NA	0.6374	0.3656	0.7505	0.3656	NA	NA	NA	NA	NA	NA
Brazil (11) v. Mozambique (8)	116483.030	0.0010	0.1139	0.0010	-0.9406	1.0000	0.6370	0.0010	0.7556	0.0010	0.4841	0.0010	0.6408	0.0010	0.7580	0.0010
Brazil (11) v. Reunion (9)	124081.652	0.0010	0.1148	0.0010	-0.8638	1.0000	0.6367	0.0010	0.7485	0.0010	0.4822	0.0010	0.6397	0.0010	0.7569	0.0010
Seychelles (10) v. Western_North_Atlantic (8)	113326.862	0.0010	0.1161	0.0010	-0.8798	1.0000	0.6350	0.0010	0.7495	0.0010	0.4911	0.0010	0.6482	0.0010	0.7641	0.0010
Brazil (11) v. South_Africa (9)	123642.988	0.0010	0.1137	0.0010	-0.8041	1.0000	0.6348	0.0010	0.7461	0.0010	0.4788	0.0010	0.6363	0.0010	0.7541	0.0010
Brazil (11) v. Seychelles (10)	130161.195	0.0010	0.1149	0.0010	-0.7239	1.0000	0.6322	0.0010	0.7456	0.0010	0.4754	0.0010	0.6341	0.0010	0.7520	0.0010
Caribbean_Sea (2) v. Japan (11)	76592.764	0.0100	0.1129	0.0100	-2.8319	1.0000	0.6276	0.0450	0.7462	0.0465	0.6239	0.0529	0.7528	0.0529	0.8478	0.0529
Caribbean_Sea (2) v. Thailand (4)	38513.630	0.0749	0.1072	0.0749	-10.0183	1.0000	0.6272	0.1638	0.7437	0.1638	0.8095	0.1638	0.8810	0.1638	0.9342	0.1638
Caribbean_Sea (2) v. Fiji (8)	60456.741	0.0290	0.1127	0.0290	-3.6470	1.0000	0.6238	0.2071	0.7489	0.2071	0.6573	0.2071	0.7774	0.2071	0.8657	0.2071
Australia (34) v. Gulf_of_Mexico (11)	266279.436	0.0010	0.1163	0.0010	-0.2294	1.0000	0.6203	0.0010	0.7371	0.0010	0.4736	0.0010	0.6329	0.0010	0.7509	0.0010
Caribbean_Sea (2) v. Sri_Lanka (4)	38450.471	0.0719	0.1072	0.0719	-8.2881	1.0000	0.6193	0.1319	0.7368	0.1319	0.7833	0.1319	0.8640	0.1319	0.9237	0.1319
Australia (34) v. Western_North_Atlantic (8)	242136.802	0.0010	0.1157	0.0010	-0.2818	1.0000	0.6158	0.0010	0.7332	0.0010	0.4751	0.0010	0.6340	0.0010	0.7518	0.0010
Australia (34) v. Brazil (11)	262424.982	0.0010	0.1144	0.0010	-0.1938	1.0000	0.6134	0.0010	0.7302	0.0010	0.4632	0.0010	0.6228	0.0010	0.7422	0.0010
Caribbean_Sea (2) v. Reunion (9)	65164.107	0.0160	0.1093	0.0160	-2.4310	1.0000	0.6119	0.0645	0.7340	0.0684	0.6031	0.0684	0.7370	0.0684	0.8359	0.0684
Caribbean_Sea (2) v. Mozambique (8)	59068.619	0.0260	0.1086	0.0260	-2.7066	1.0000	0.6098	0.3171	0.7470	0.3171	0.6169	0.3171	0.7469	0.3171	0.8435	0.3171
Arabian_Sea (6) v. Caribbean_Sea (2)	49216.891	0.0559	0.1075	0.0559	-3.6443	1.0000	0.6094	0.1842	0.7275	0.1842	0.6560	0.2036	0.7760	0.2036	0.8647	0.2036
Caribbean_Sea (2) v. South_Africa (9)	64987.779	0.0170	0.1082	0.0170	-2.2823	1.0000	0.6094	0.0592	0.7309	0.0592	0.5952	0.0632	0.7306	0.0632	0.8311	0.0632
Caribbean_Sea (2) v. Seychelles (10)	70039.173	0.0110	0.1096	0.0110	-2.0491	1.0000	0.6071	0.0466	0.7311	0.0466	0.5816	0.0514	0.7208	0.0514	0.8235	0.0514
Australia (34) v. Caribbean_Sea (2)	184513.747	0.0010	0.1092	0.0010	-0.8685	1.0000	0.6017	0.0050	0.7207	0.0050	0.5161	0.0052	0.6683	0.0052	0.7812	0.0052
Papua_New_Guinea (2) v. Sierra_Leone (1)	6416.767	0.3227	0.0042	0.3227	NA	NA	0.0929	0.3227	0.1126	0.3227	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Japan (11)	11178.826	0.0010	0.0025	0.0010	-3.8365	0.9918	0.0750	0.0010	0.0897	0.0010	0.1905	0.0041	0.2406	0.0041	0.3621	0.0041
Fiji (8) v. Indonesia (4)	10448.990	0.0020	0.0029	0.0020	-4.2258	1.0000	0.0732	0.0020	0.0875	0.0020	0.2201	0.0021	0.2747	0.0021	0.4055	0.0021
Fiji (8) v. Japan (11)	13523.753	0.0010	0.0024	0.0010	-2.7437	1.0000	0.0679	0.0010	0.0814	0.0010	0.1088	0.0010	0.1440	0.0010	0.2279	0.0010

Table 5: Pairwise Fst for 16989 DArTseq loci between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Indonesia (4) v. Papua_New_Guinea (2)	6781.410	0.2028	0.0023	0.2028	NA	NA	0.0480	0.0972	0.0573	0.0972	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Thailand (4)	7570.074	0.0320	0.0019	0.0320	-6.8647	1.0000	0.0461	0.0331	0.0552	0.0331	0.3524	0.0342	0.4141	0.0342	0.5668	0.0342
Japan (11) v. Thailand (4)	9733.776	0.0030	0.0018	0.0120	-3.5281	0.8671	0.0440	0.0111	0.0526	0.0111	0.1636	0.0184	0.2091	0.0153	0.3203	0.0164
Indonesia (4) v. Sri_Lanka (4)	7684.223	0.0240	0.0019	0.1029	-6.2934	1.0000	0.0437	0.0247	0.0525	0.0247	0.3330	0.0254	0.3951	0.0254	0.5462	0.0254
Indonesia (4) v. Reunion (9)	9002.416	0.0020	0.0018	0.0020	-3.6602	1.0000	0.0421	0.0020	0.0507	0.0021	0.1785	0.0021	0.2266	0.0021	0.3437	0.0021
Japan (11) v. Reunion (9)	11453.845	0.0010	0.0015	0.0010	-2.5427	1.0000	0.0405	0.0010	0.0487	0.0010	0.0847	0.0010	0.1133	0.0010	0.1826	0.0010
Indonesia (4) v. Seychelles (10)	9067.995	0.0030	0.0018	0.0030	-3.4077	1.0000	0.0404	0.0030	0.0489	0.0030	0.1642	0.0030	0.2102	0.0030	0.3215	0.0030
Japan (11) v. Sri_Lanka (4)	9650.543	0.0010	0.0016	0.0220	-3.4005	0.6767	0.0403	0.0112	0.0482	0.0112	0.1570	0.0300	0.2018	0.0248	0.3101	0.0248
Japan (11) v. Papua_New_Guinea (2)	8561.875	0.0330	0.0021	0.1568	-6.5902	0.8100	0.0403	0.0538	0.0481	0.0538	0.3820	0.3300	0.4454	0.3300	0.5987	0.3300
Japan (11) v. Seychelles (10)	11592.099	0.0010	0.0015	0.0010	-2.4653	1.0000	0.0389	0.0010	0.0468	0.0010	0.0786	0.0010	0.1057	0.0010	0.1708	0.0010
Indonesia (4) v. South_Africa (9)	8789.531	0.0050	0.0017	0.0050	-3.6000	1.0000	0.0381	0.0050	0.0459	0.0050	0.1744	0.0050	0.2217	0.0050	0.3373	0.0050
Fiji (8) v. Reunion (9)	10665.486	0.0010	0.0015	0.0010	-2.6226	1.0000	0.0379	0.0010	0.0457	0.0010	0.0980	0.0010	0.1303	0.0010	0.2080	0.0010
Arabian_Sea (6) v. Japan (11)	10309.704	0.0010	0.0015	0.0050	-2.8363	0.8881	0.0376	0.0040	0.0452	0.0040	0.1087	0.0080	0.1436	0.0060	0.2276	0.0060
Fiji (8) v. Thailand (4)	8865.162	0.0050	0.0018	0.0050	-3.8772	1.0000	0.0374	0.0051	0.0448	0.0051	0.1897	0.0052	0.2396	0.0052	0.3608	0.0052
Fiji (8) v. Seychelles (10)	10839.719	0.0010	0.0016	0.0010	-2.5154	1.0000	0.0372	0.0010	0.0450	0.0010	0.0911	0.0010	0.1219	0.0010	0.1952	0.0010
Japan (11) v. Mozambique (8)	10712.336	0.0010	0.0014	0.0010	-2.6315	0.9960	0.0361	0.0010	0.0439	0.0010	0.0903	0.0010	0.1203	0.0010	0.1932	0.0010
Fiji (8) v. Sri_Lanka (4)	9100.450	0.0010	0.0018	0.0010	-3.6561	0.9713	0.0359	0.0010	0.0431	0.0010	0.1808	0.0010	0.2301	0.0010	0.3480	0.0010
Fiji (8) v. Mozambique (8)	10160.898	0.0010	0.0015	0.0010	-2.7350	1.0000	0.0358	0.0010	0.0437	0.0010	0.1063	0.0010	0.1407	0.0010	0.2232	0.0010
Arabian_Sea (6) v. Indonesia (4)	8113.920	0.0050	0.0018	0.0090	-4.4368	1.0000	0.0358	0.0051	0.0431	0.0051	0.2269	0.0052	0.2815	0.0052	0.4144	0.0052
Indonesia (4) v. Mozambique (8)	8461.219	0.0030	0.0017	0.0030	-3.8955	1.0000	0.0352	0.0030	0.0432	0.0033	0.1914	0.0033	0.2412	0.0033	0.3631	0.0033
Japan (11) v. South_Africa (9)	10864.284	0.0010	0.0014	0.0010	-2.5325	0.9980	0.0351	0.0010	0.0421	0.0010	0.0816	0.0010	0.1092	0.0010	0.1764	0.0010
Fiji (8) v. Papua_New_Guinea (2)	8199.940	0.0340	0.0024	0.0340	-8.0103	1.0000	0.0347	0.1288	0.0416	0.1288	0.4471	0.4416	0.5107	0.4416	0.6619	0.4416
Fiji (8) v. South_Africa (9)	10212.562	0.0010	0.0014	0.0010	-2.6095	1.0000	0.0338	0.0010	0.0407	0.0010	0.0955	0.0010	0.1271	0.0010	0.2033	0.0010
Arabian_Sea (6) v. Fiji (8)	9533.093	0.0010	0.0015	0.0010	-3.0109	1.0000	0.0332	0.0010	0.0403	0.0010	0.1263	0.0010	0.1655	0.0010	0.2591	0.0010
Australia (34) v. Indonesia (4)	10470.950	0.0010	0.0015	0.0010	-2.3894	1.0000	0.0329	0.0010	0.0396	0.0010	0.1031	0.0010	0.1361	0.0010	0.2169	0.0010
Australia (34) v. Fiji (8)	13038.738	0.0010	0.0013	0.0010	-1.9589	1.0000	0.0327	0.0010	0.0395	0.0010	0.0566	0.0010	0.0771	0.0010	0.1265	0.0010
Australia (34) v. Japan (11)	13998.770	0.0010	0.0012	0.0010	-1.9736	1.0000	0.0319	0.0010	0.0384	0.0010	0.0471	0.0010	0.0644	0.0010	0.1065	0.0010
Reunion (9) v. Thailand (4)	7436.247	0.0989	0.0011	0.0869	-3.3835	0.9254	0.0082	0.0935	0.0099	0.0935	0.1514	0.0867	0.1944	0.0887	0.3003	0.0887
Reunion (9) v. Seychelles (10)	8193.729	0.0020	0.0007	0.0080	-2.3873	0.9960	0.0081	0.0060	0.0098	0.0060	0.0682	0.0060	0.0922	0.0060	0.1502	0.0060
Australia (34) v. Reunion (9)	9163.755	0.0010	0.0005	0.0010	-1.9225	0.9990	0.0075	0.0010	0.0090	0.0010	0.0389	0.0010	0.0534	0.0010	0.0888	0.0010
Reunion (9) v. Sri_Lanka (4)	7667.716	0.0969	0.0011	0.1089	-3.1964	0.6727	0.0072	0.1330	0.0087	0.1340	0.1439	0.1692	0.1860	0.1601	0.2884	0.1672
Mozambique (8) v. Reunion (9)	8036.435	0.0040	0.0008	0.0020	-2.5285	0.9880	0.0072	0.0050	0.0087	0.0050	0.0809	0.0040	0.1083	0.0040	0.1750	0.0040
Brazil (11) v. Western_North_Atlantic (8)	5969.634	0.0010	0.0003	0.0010	-5.7343	1.0000	0.0069	0.0010	0.0079	0.0010	0.1470	0.0010	0.1769	0.0010	0.2824	0.0010
Reunion (9) v. South_Africa (9)	7939.288	0.0170	0.0007	0.0080	-2.4433	0.9930	0.0065	0.0110	0.0079	0.0110	0.0724	0.0110	0.0974	0.0110	0.1584	0.0110
Seychelles (10) v. Thailand (4)	7243.604	0.1888	0.0010	0.1059	-3.2235	0.9239	0.0059	0.1131	0.0071	0.1131	0.1400	0.0891	0.1810	0.0911	0.2816	0.0891
Seychelles (10) v. South_Africa (9)	7830.997	0.0150	0.0006	0.0060	-2.3823	0.9910	0.0054	0.0090	0.0065	0.0090	0.0667	0.0080	0.0902	0.0080	0.1471	0.0080
Arabian_Sea (6) v. Reunion (9)	7743.722	0.0699	0.0008	0.1429	-2.7339	0.6593	0.0049	0.1948	0.0060	0.1948	0.0981	0.2168	0.1301	0.2098	0.2078	0.2118
Caribbean_Sea (2) v. Western_North_Atlantic (8)	4466.898	0.2947	0.0009	0.0460	28.5591	1.0000	0.0043	0.4340	0.0050	1.0000	1.5682	1.0000	1.4871	1.0000	1.1897	1.0000
Brazil (11) v. Gulf_of_Mexico (11)	6086.428	0.0010	0.0002	0.0170	-5.1049	0.9960	0.0041	0.0050	0.0047	0.0050	0.1126	0.0050	0.1373	0.0050	0.2246	0.0050
Papua_New_Guinea (2) v. Reunion (9)	7257.257	0.1179	0.0017	0.4466	-5.9832	0.2185	0.0039	0.4290	0.0047	0.4408	0.3588	0.6975	0.4221	0.5798	0.5747	0.5798
Australia (34) v. Seychelles (10)	8496.485	0.0010	0.0004	0.0020	-1.8963	0.7323	0.0035	0.0060	0.0043	0.0060	0.0336	0.0050	0.0463	0.0050	0.0773	0.0050
South_Africa (9) v. Sri_Lanka (4)	7270.440	0.0220	0.0010	0.0460	-3.1960	0.5207	0.0034	0.0535	0.0041	0.0535	0.1420	0.1312	0.1837	0.1140	0.2852	0.1241
Mozambique (8) v. Seychelles (10)	7676.401	0.1708	0.0006	0.1039	-2.4553	0.7952	0.0033	0.1898	0.0040	0.1918	0.0733	0.1279	0.0986	0.1319	0.1601	0.1299
Seychelles (10) v. Sri_Lanka (4)	7383.298	0.1638	0.0010	0.2408	-3.0516	0.6100	0.0031	0.2910	0.0038	0.2910	0.1322	0.3280	0.1721	0.3320	0.2688	0.3320
Papua_New_Guinea (2) v. Thailand (4)	6091.084	0.1299	0.0017	0.4565	NA	NA	0.0024	0.2379	0.0029	0.3265	NA	NA	NA	NA	NA	NA
Australia (34) v. Mozambique (8)	8236.530	0.0010	0.0004	0.0180	-1.9434	0.1419	0.0023	0.0020	0.0028	0.0020	0.0411	0.0020	0.0563	0.0020	0.0935	0.0020
Sri_Lanka (4) v. Thailand (4)	6497.360	0.1149	0.0011	0.2398	-5.5253	0.7436	0.0022	0.2587	0.0027	0.2413	0.2885	0.2925	0.3478	0.2925	0.4938	0.2925
Australia (34) v. South_Africa (9)	8263.583	0.0010	0.0004	0.0040	-1.9207	0.6953	0.0022	0.0040	0.0027	0.0040	0.0361	0.0060	0.0497	0.0060	0.0828	0.0060
Australia (34) v. Thailand (4)	7765.556	0.1978	0.0008	0.1538	-2.2952	1.0000	0.0020	0.1064	0.0024	0.1074	0.0832	0.0171	0.1108	0.0211	0.1791	0.0211
Australia (34) v. Sri_Lanka (4)	8208.993	0.0180	0.0008	0.1698	-2.1999	0.1518	0.0019	0.1052	0.0023	0.1052	0.0797	0.3578	0.1068	0.2905	0.1727	0.3146
Arabian_Sea (6) v. Seychelles (10)	7435.985	0.3037	0.0007	0.4146	-2.6269	0.4625	0.0018	0.3686	0.0022	0.3686	0.0894	0.3746	0.1193	0.3736	0.1915	0.3736
Mozambique (8) v. South_Africa (9)	7504.197	0.0529	0.0007	0.0140	-2.5352	0.8931	0.0017	0.0709	0.0021	0.0719	0.0784	0.0410	0.1049	0.0410	0.1700	0.0410
South_Africa (9) v. Thailand (4)	7002.891	0.3307	0.0009	0.1758	-3.3554	0.9898	0.0017	0.2444	0.0020	0.2444	0.1472	0.0530	0.1892	0.0591	0.2933	0.0591

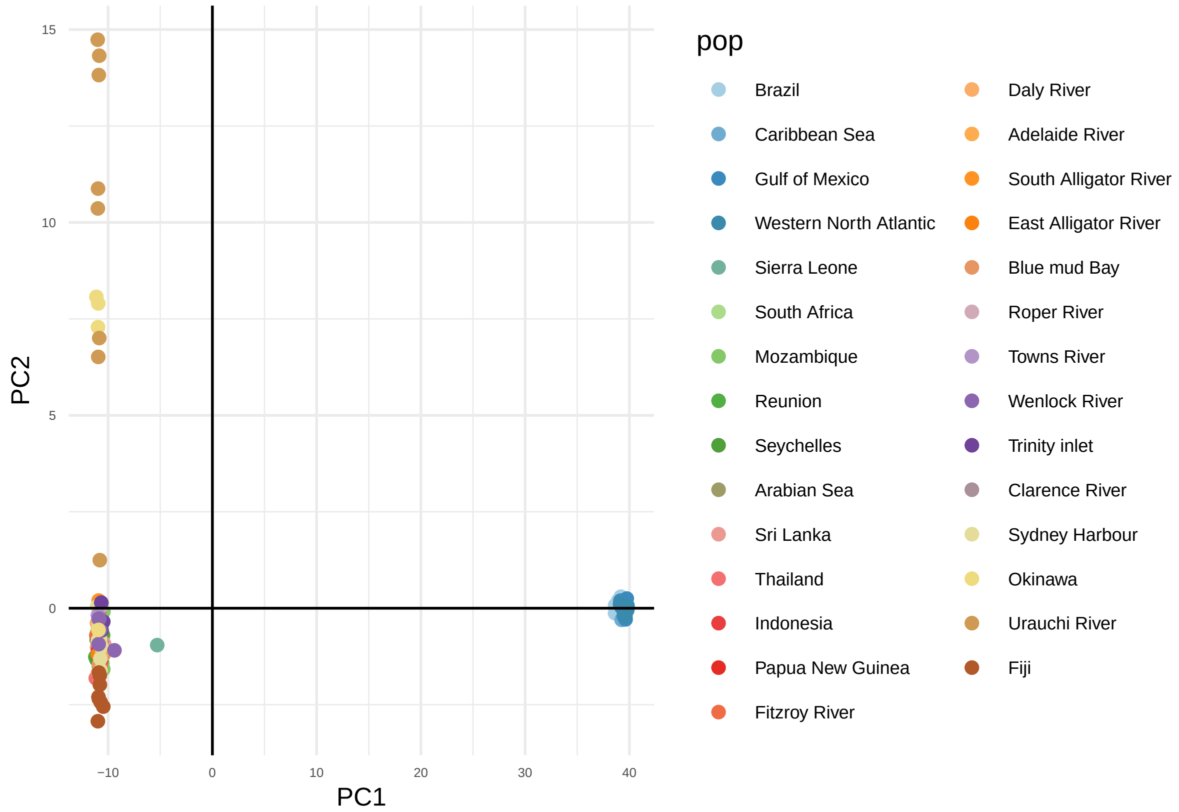
Table 5: Pairwise Fst for 16989 DArTseq loci between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Caribbean_Sea (2) v. Gulf_of_Mexico (11)	4659.761	0.5754	0.0008	0.2348	95.8315	1.0000	0.0011	1.0000	0.0013	1.0000	1.1312	1.0000	1.1146	1.0000	1.0538	1.0000
Papua_New_Guinea (2) v. Sri_Lanka (4)	6164.749	0.3277	0.0017	0.8621	-26.8706	0.3073	0.0007	0.4283	0.0008	0.3458	0.7616	1.0000	0.7981	1.0000	0.8854	1.0000
Gulf_of_Mexico (11) v. Western_North_Atlantic (8)	5176.118	0.4765	0.0002	0.3506	-6.4515	0.6280	0.0003	0.4400	0.0003	0.4400	0.1584	0.4280	0.1888	0.4270	0.2997	0.4260
Brazil (11) v. Caribbean_Sea (2)	4866.404	0.7882	0.0009	0.2078	-211.9907	1.0000	0.0002	1.0000	0.0003	1.0000	0.9505	1.0000	0.9564	1.0000	0.9777	1.0000
Mozambique (8) v. Thailand (4)	6935.491	0.5385	0.0009	0.5554	-3.6041	0.6087	0.0002	0.4400	0.0003	0.4400	0.1636	0.7027	0.2084	0.7224	0.3197	0.7169
Mozambique (8) v. Sri_Lanka (4)	7159.624	0.2448	0.0010	0.3407	-3.3991	0.1049	0.0002	0.4591	0.0003	0.4591	0.1557	0.8559	0.2000	0.8485	0.3078	0.8485
Arabian_Sea (6) v. Australia (34)	7994.027	0.0180	0.0005	0.1898	-2.0228	0.0030	0.0002	0.4585	0.0002	0.4585	0.0515	0.7403	0.0703	0.6853	0.1158	0.7153
Papua_New_Guinea (2) v. Seychelles (10)	7000.832	0.3327	0.0016	0.6054	-5.3888	0.2640	0.0001	0.4757	0.0001	0.6190	0.3286	0.8080	0.3913	0.8080	0.5418	0.8080
Papua_New_Guinea (2) v. South_Africa (9)	6953.554	0.1668	0.0016	0.7572	-5.8186	0.1702	-0.0004	0.6738	-0.0005	0.6935	0.3509	1.0000	0.4139	1.0000	0.5661	1.0000
Arabian_Sea (6) v. South_Africa (9)	7177.547	0.6054	0.0007	0.3876	-2.7254	0.0450	-0.0008	0.7333	-0.0010	0.7333	0.0950	0.8052	0.1261	0.7922	0.2019	0.7982
Arabian_Sea (6) v. Sri_Lanka (4)	6876.948	0.3447	0.0011	0.1269	-3.8635	0.4256	-0.0009	0.6264	-0.0011	0.6264	0.1880	0.6730	0.2380	0.6730	0.3586	0.6730
Arabian_Sea (6) v. Thailand (4)	6678.836	0.6434	0.0010	0.4326	-4.0768	0.9396	-0.0011	0.6703	-0.0013	0.6703	0.1961	0.3857	0.2464	0.4179	0.3700	0.4068
Arabian_Sea (6) v. Mozambique (8)	7148.821	0.8262	0.0007	0.7922	-2.8570	0.0160	-0.0022	0.9451	-0.0028	0.9461	0.1051	0.9820	0.1387	0.9780	0.2206	0.9790
Australia (34) v. Papua_New_Guinea (2)	7672.289	0.4126	0.0015	0.9291	-3.1099	0.0230	-0.0036	0.8812	-0.0043	0.8812	0.1955	1.0000	0.2463	1.0000	0.3695	1.0000
Mozambique (8) v. Papua_New_Guinea (2)	6753.842	0.7932	0.0016	1.0000	-6.7316	0.6102	-0.0077	1.0000	-0.0094	1.0000	0.3916	1.0000	0.4548	1.0000	0.6082	1.0000
Arabian_Sea (6) v. Papua_New_Guinea (2)	6374.787	0.8841	0.0016	1.0000	-9.1102	0.3263	-0.0081	1.0000	-0.0098	1.0000	0.4828	1.0000	0.5444	1.0000	0.6928	1.0000
Arabian_Sea (6) v. Sierra_Leone (1)	9707.152	0.1518	0.0051	0.1518	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Sierra_Leone (1)	24824.983	0.0340	0.0053	0.0340	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. Sierra_Leone (1)	55309.051	0.0819	0.0714	0.0819	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (8) v. Sierra_Leone (1)	12245.299	0.1279	0.0061	0.1279	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Gulf_of_Mexico (11) v. Sierra_Leone (1)	58236.780	0.0789	0.0724	0.0789	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Sierra_Leone (1)	9125.677	0.2088	0.0061	0.2088	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Japan (11) v. Sierra_Leone (1)	14485.463	0.0839	0.0060	0.0839	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Sierra_Leone (1)	11045.550	0.1279	0.0051	0.1279	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Reunion (9) v. Sierra_Leone (1)	12026.058	0.1059	0.0053	0.1059	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Seychelles (10) v. Sierra_Leone (1)	12316.464	0.0819	0.0053	0.0819	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra_Leone (1) v. South_Africa (9)	11819.383	0.1129	0.0051	0.1129	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra_Leone (1) v. Sri_Lanka (4)	8331.470	0.2088	0.0050	0.2088	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra_Leone (1) v. Thailand (4)	8268.943	0.2218	0.0047	0.2218	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra_Leone (1) v. Western_North_Atlantic (8)	46417.112	0.1239	0.0722	0.1239	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

5.8 PCA

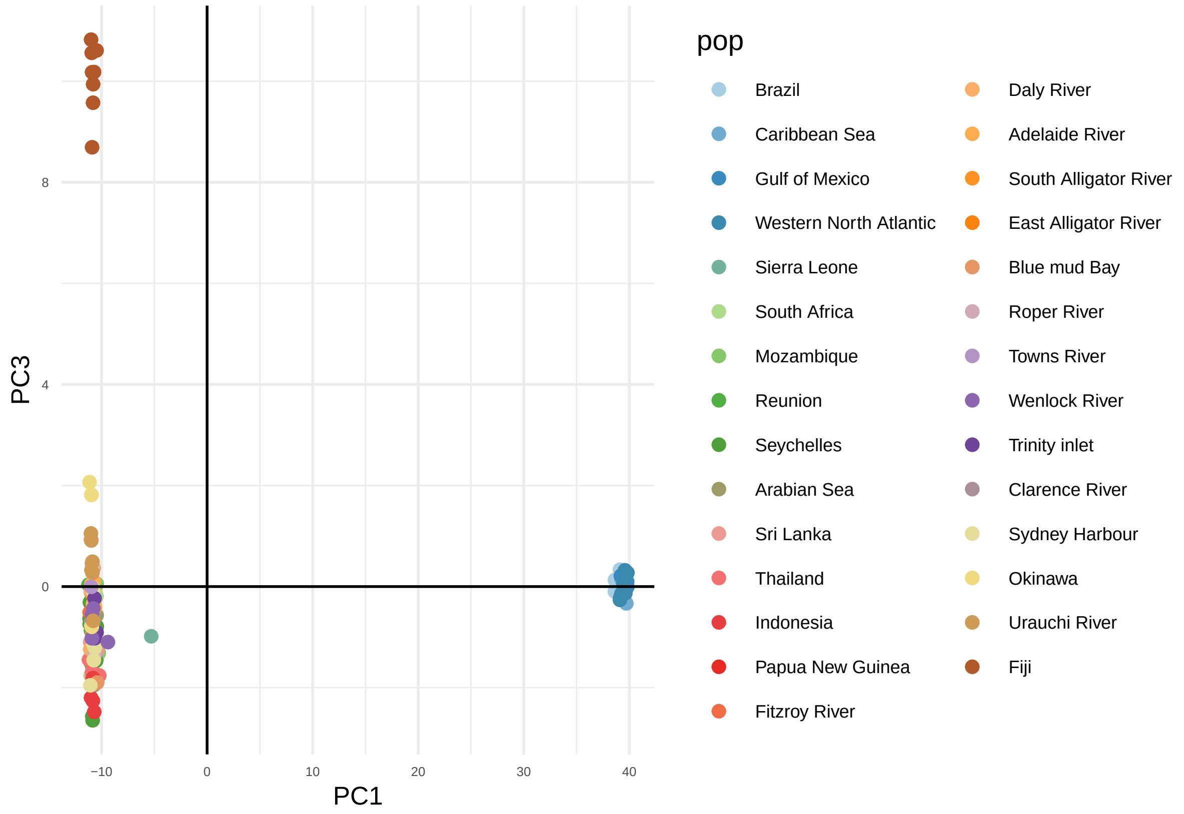
```r
pca1 <- adegenet::glPca(BS.dartseq.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTseq_ALL_PCA2.Rdata")
```

```r
load("DArTseq_ALL_PCA2.Rdata")
load("DArTseq_ALL_objects3.Rdata")

pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion"  ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Fitzroy River", "Daly River", "Adelaide River",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Wenlock River","Trinity inlet","Clarence River",
                "Sydney Harbour", "Okinawa", "Urauchi River", "Fiji")
BS.dartseq.gl$pop <- factor(BS.dartseq.gl$other$ind.metrics$Site2,
                            levels = pop.levels)

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- adegenet::pop(BS.dartseq.gl)
cols <- adegenet::funky(nPop(BS.dartseq.gl))


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

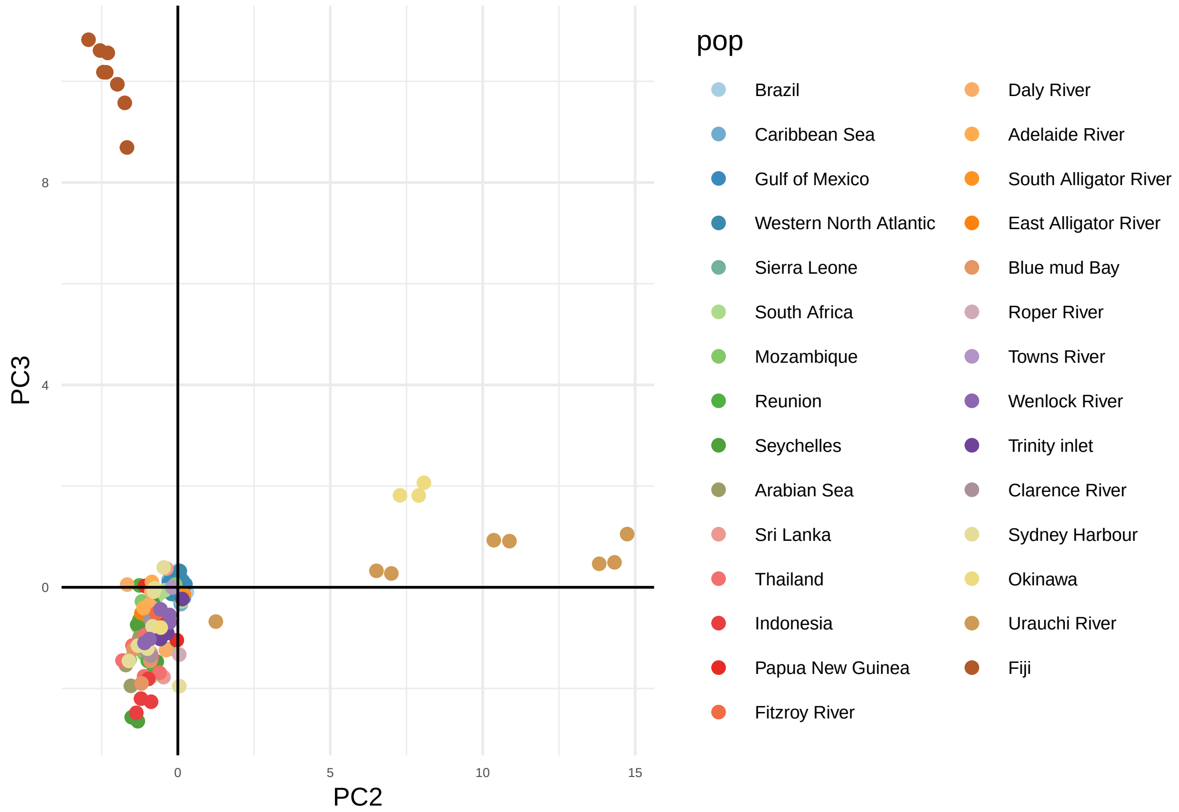


```
ggplot2::ggsave(p, filename = "DArTseq_ALL_PCA1.png", width = 30,
                height = 15,units = "cm")
```

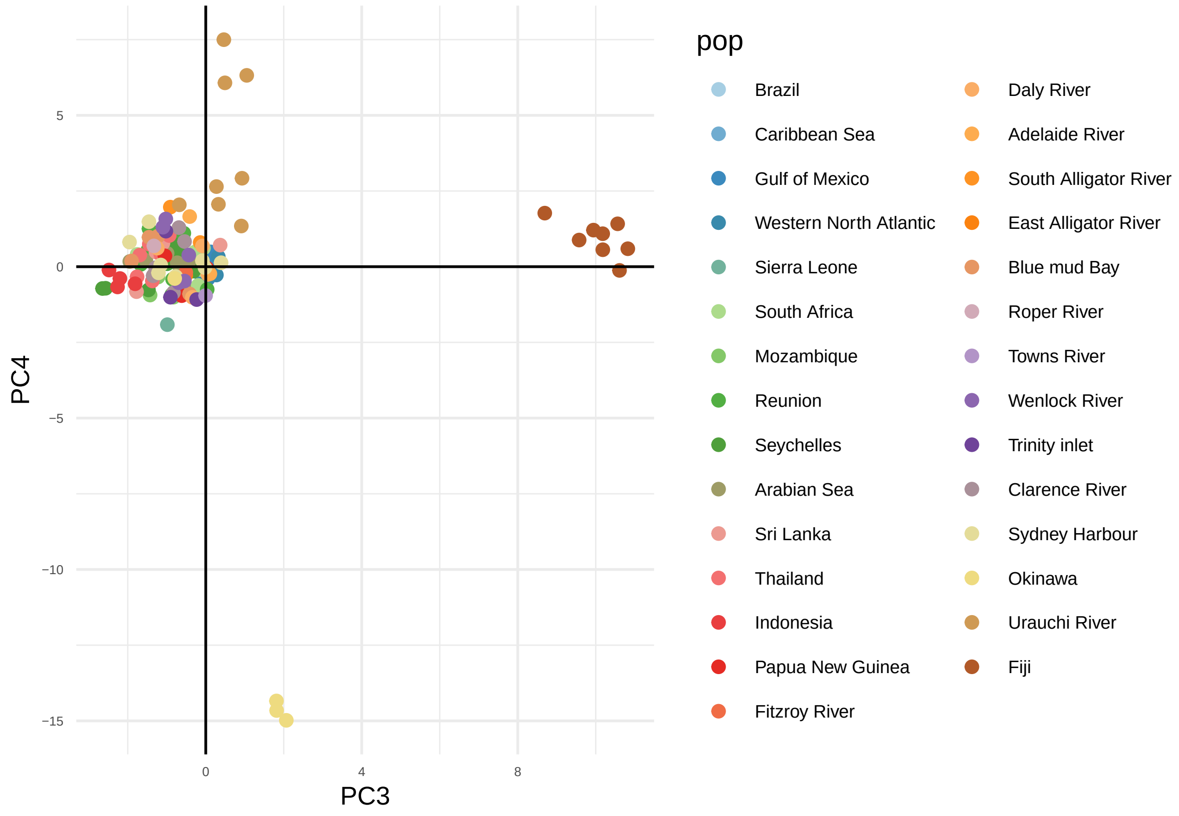
```
p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



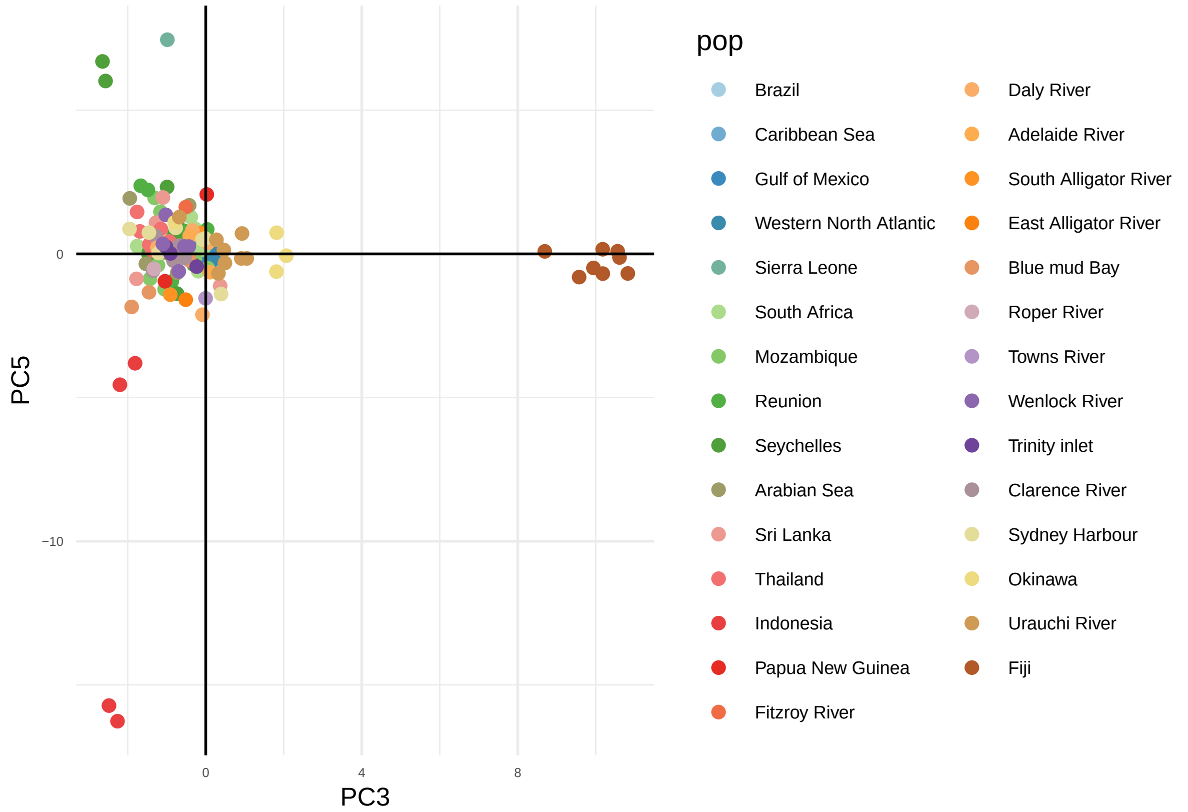
```
ggplot2::ggsave(p, filename = "DArTseq_ALL_PCA2.png", width = 30, height = 15,
                units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_ALL_PCA3.png", width = 30, height = 15,
                units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_ALL_PCA4.png", width = 30, height = 15,
                units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```r
ggplot2::ggsave(p, filename = "DArTseq_ALL_PCA5.png", width = 30, height = 15,
                units = "cm")
```

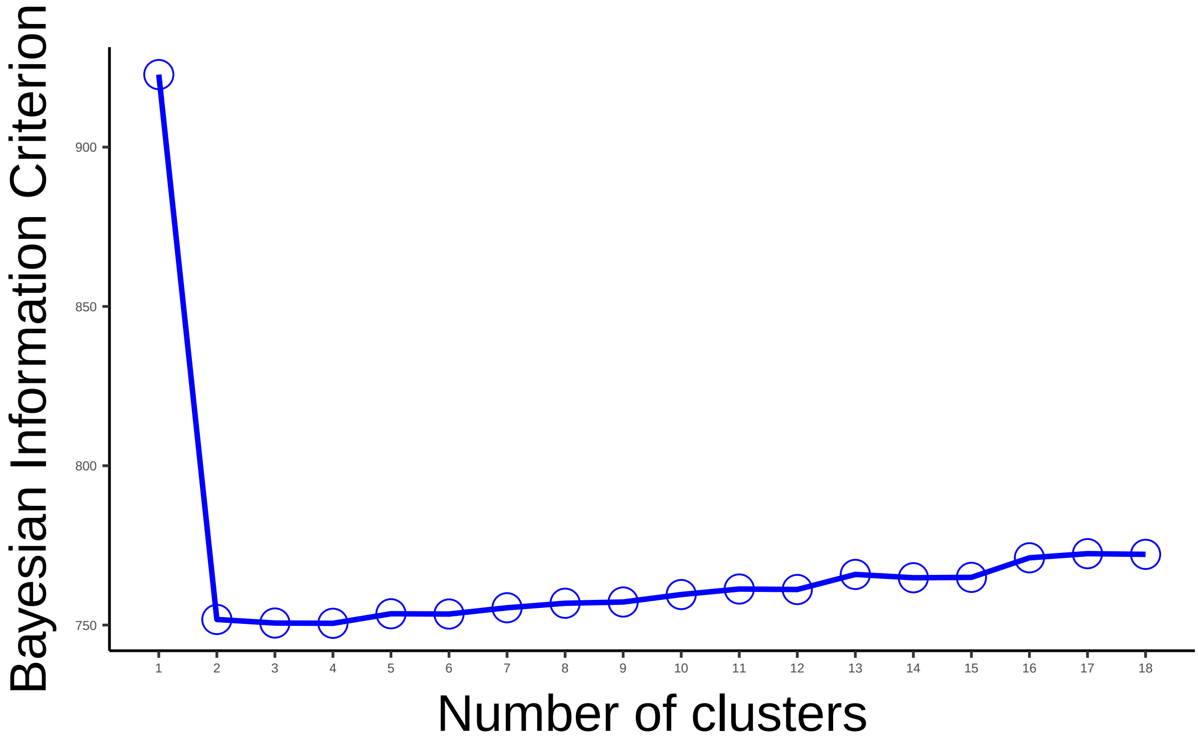
5.9 DAPC

5.9.1 Optimal number of clusters with neutral markers

```r
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartseq.gl,
    max.n.clust = 18,
    n.pca = adegenet::nInd(BS.dartseq.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTseq_ALL_grp_.Rdata")
```

```r
load("DArTseq_ALL_grp_.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:18
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartseq.gl) - 1, by = 1)) +
```

```
  ggplot2::labs(subtitle = "",
                y = "Bayesian Information Criterion",
                x = "Number of clusters",
                title = "",
                caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTseq_ALL_grp.png", width = 30, height = 15,
                units = "cm")
```

5.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartseq.gl
x <- x[x$pop != "Sierra Leone",]
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea",
                "Australia", "Japan", "Fiji")
x$pop <- factor(x$other$ind.metrics$Site, levels = pop.levels)
x <- x[x$pop != "Sierra Leone"] #only 1 sample


xval <-
  adegenet::xvalDapc(
```

```
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 20),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
  scale = FALSE,
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTseq_ALL_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTseq_ALL_xval.rdata")
```

```
load("DArTseq_ALL_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

```
## $`Median and Confidence Interval for Random Chance`
##       2.5%        50%      97.5% 
## 0.03180112 0.06023563 0.10943031 
## 
## $`Mean Successful Assignment by Number of PCs of PCA`
##         6         7         8         9        10        11        12        13 
## 0.3334479 0.3421860 0.3338213 0.3383668 0.3321606 0.3407525 0.3438592 0.3456094 
##        14        15        16        17        18        19        20        21 
## 0.3487801 0.3492491 0.3410468 0.3400176 0.3382993 0.3396637 0.3410831 0.3390233 
##        22        23        24        25        26        27        28        29 
## 0.3431461 0.3447303 0.3461724 0.3434242 0.3417871 0.3413665 0.3411261 0.3391184 
##        30        31        32        33        34        35        36 
## 0.3435539 0.3440634 0.3433089 0.3476013 0.3457444 0.3356826 0.3372854 
## 
## $`Number of PCs Achieving Highest Mean Success`
## [1] "15"
## 
## $`Root Mean Squared Error by Number of PCs of PCA`
##         6         7         8         9        10        11        12        13 
## 0.6675354 0.6591730 0.6674186 0.6629926 0.6691257 0.6606877 0.6575962 0.6558610 
##        14        15        16        17        18        19        20        21 
## 0.6527248 0.6521758 0.6603002 0.6613992 0.6631257 0.6618169 0.6602382 0.6624344 
##        22        23        24        25        26        27        28        29
```

```
## 0.6582304 0.6566346 0.6554321 0.6580812 0.6597661 0.6600890 0.6603060 0.6625241
##        30        31        32        33        34        35        36
## 0.6581730 0.6575802 0.6584071 0.6542000 0.6559334 0.6660468 0.6644172
##
## $`Number of PCs Achieving Lowest MSE`
## [1] "15"
```

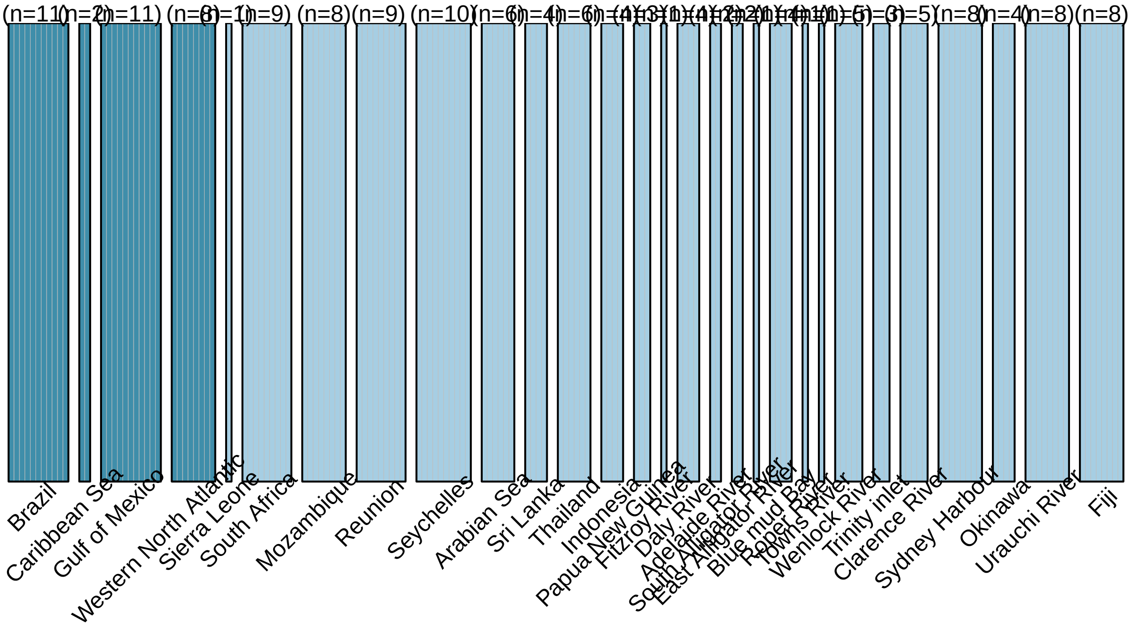
```
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartseq.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartseq.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                             paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTseq_ALL_DAPC2.Rdata")
```

5.9.3 DAPC barplot

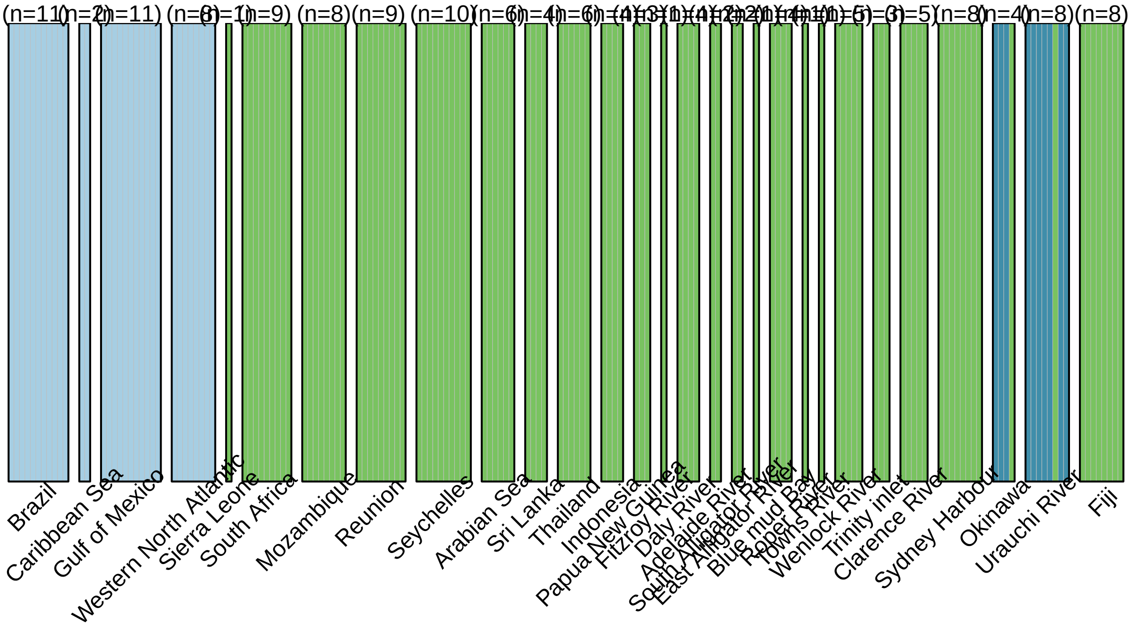
Group individuals according to DAPC posterior membership.

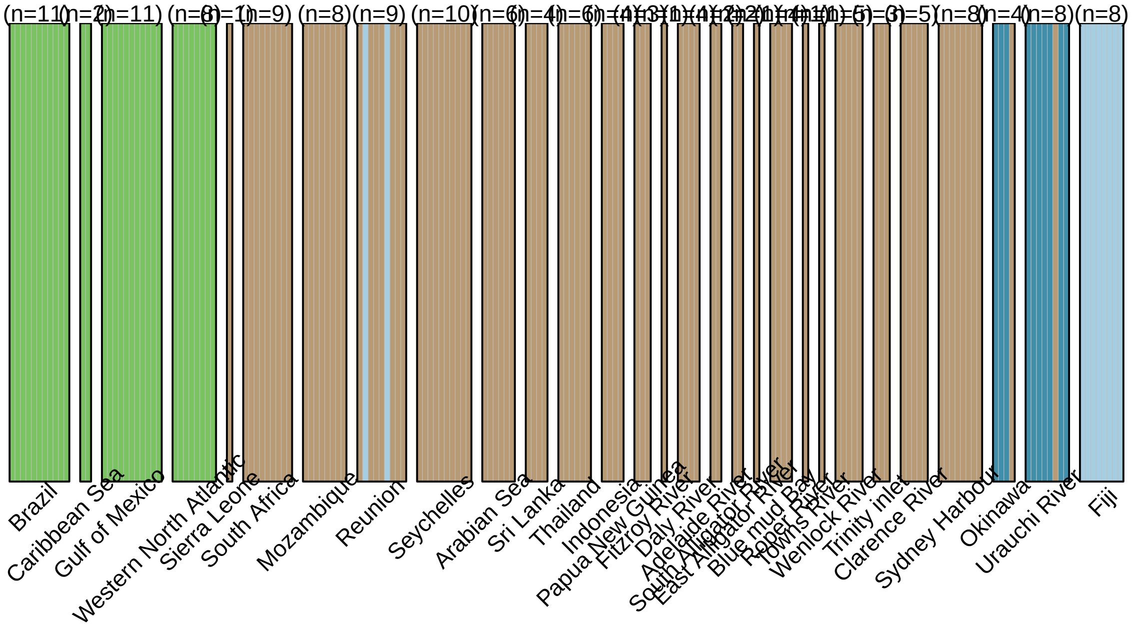
```
load("DArTseq_ALL_DAPC2.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartseq.gl$pop

  plot.dapc.FDD(x = post,
              locations = locations,
              colour = colour,
              region.lwd = 1,
              plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTseq_ALL_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```

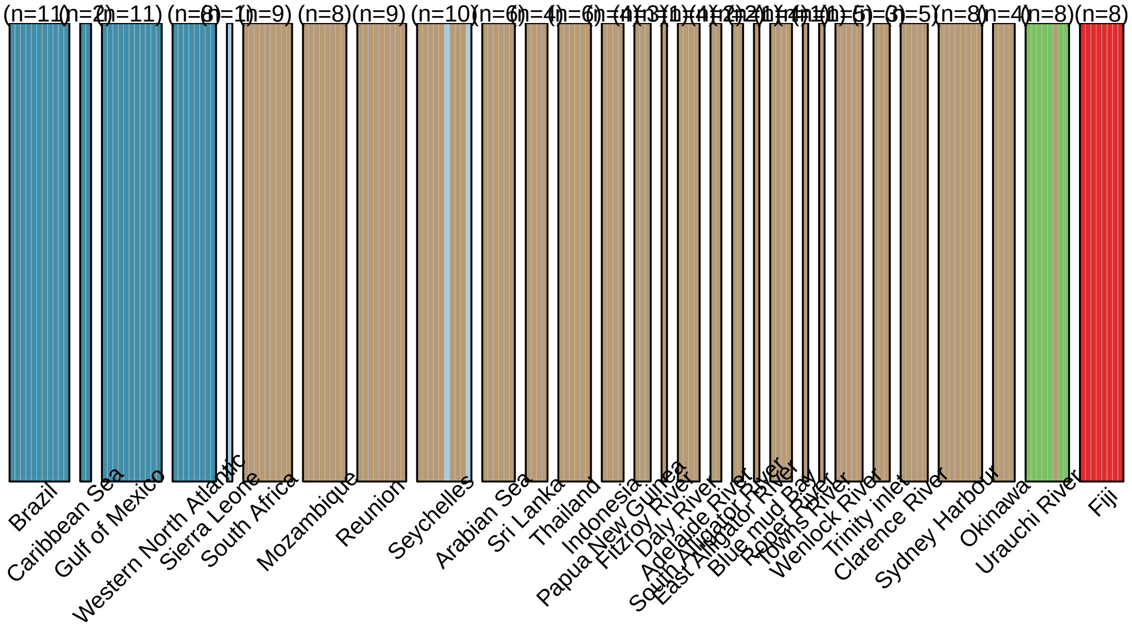
DAPC: all Bull Sharks − subset Australia
for K=2 & PC=15



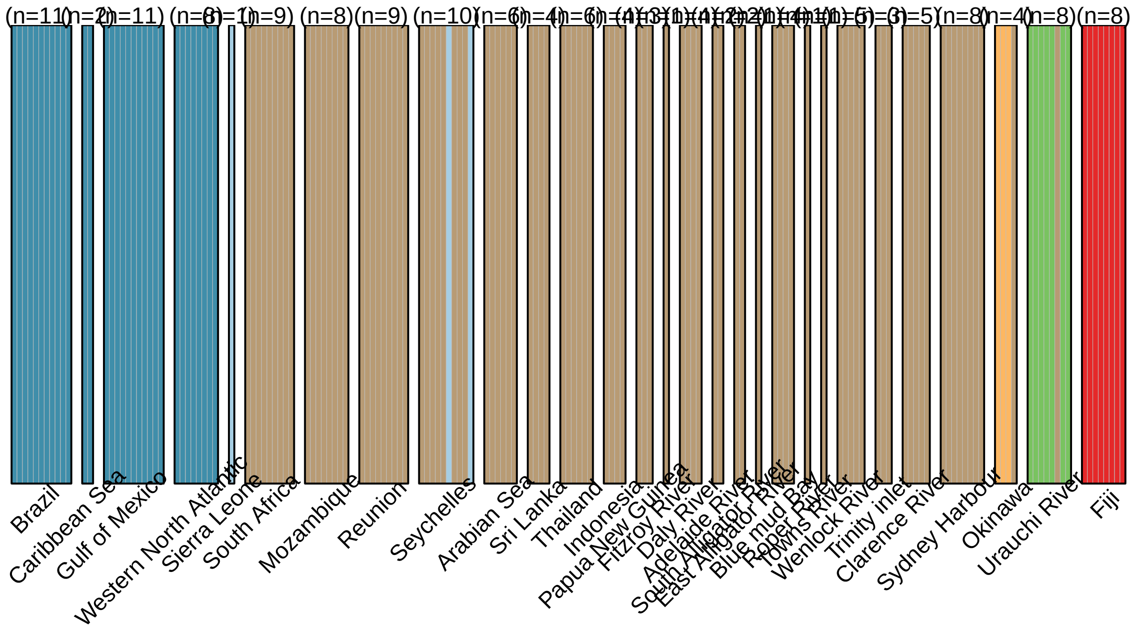
DAPC: all Bull Sharks − subset Australia
for K=3 & PC=15



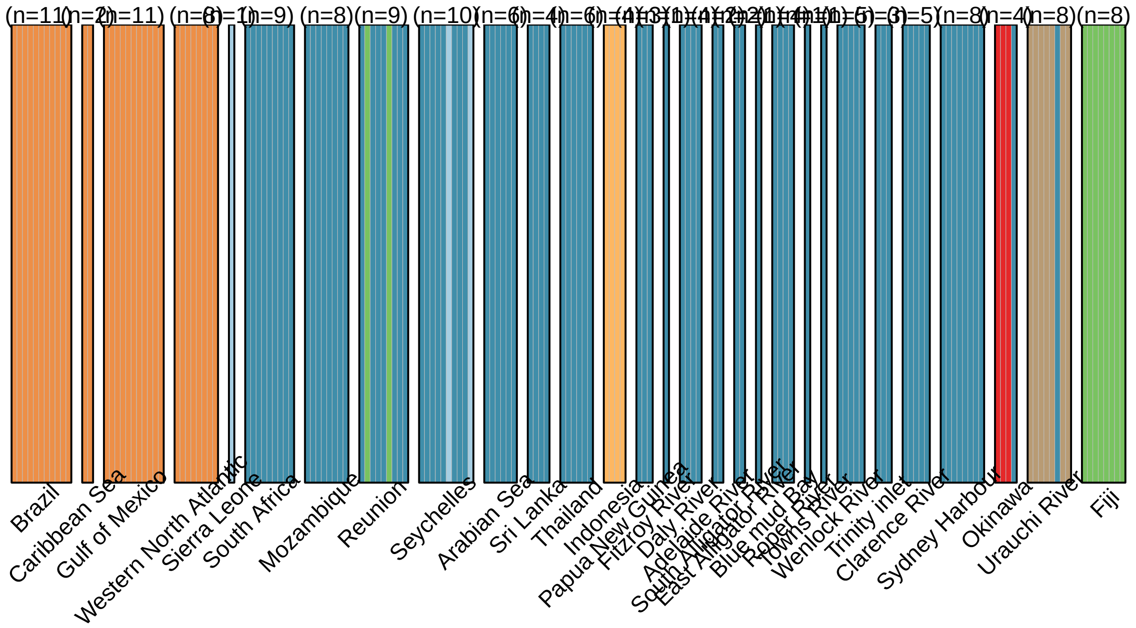

DAPC: all Bull Sharks − subset Australia
for K=4 & PC=15


DAPC: all Bull Sharks − subset Australia
for K=5 & PC=15

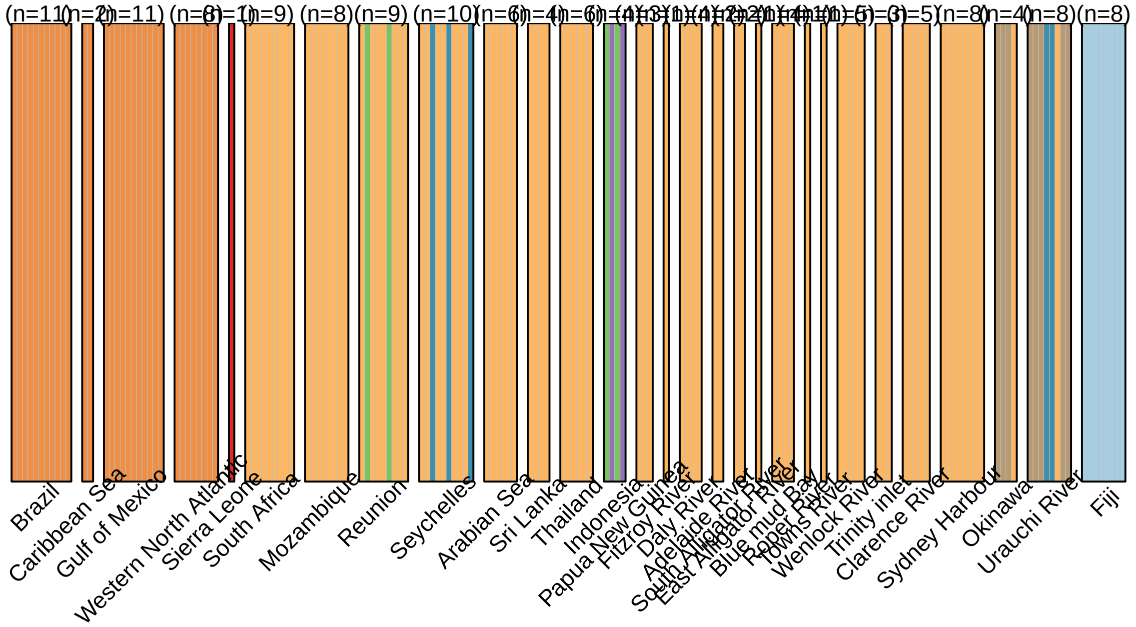
DAPC: all Bull Sharks − subset Australia
for K=6 & PC=15



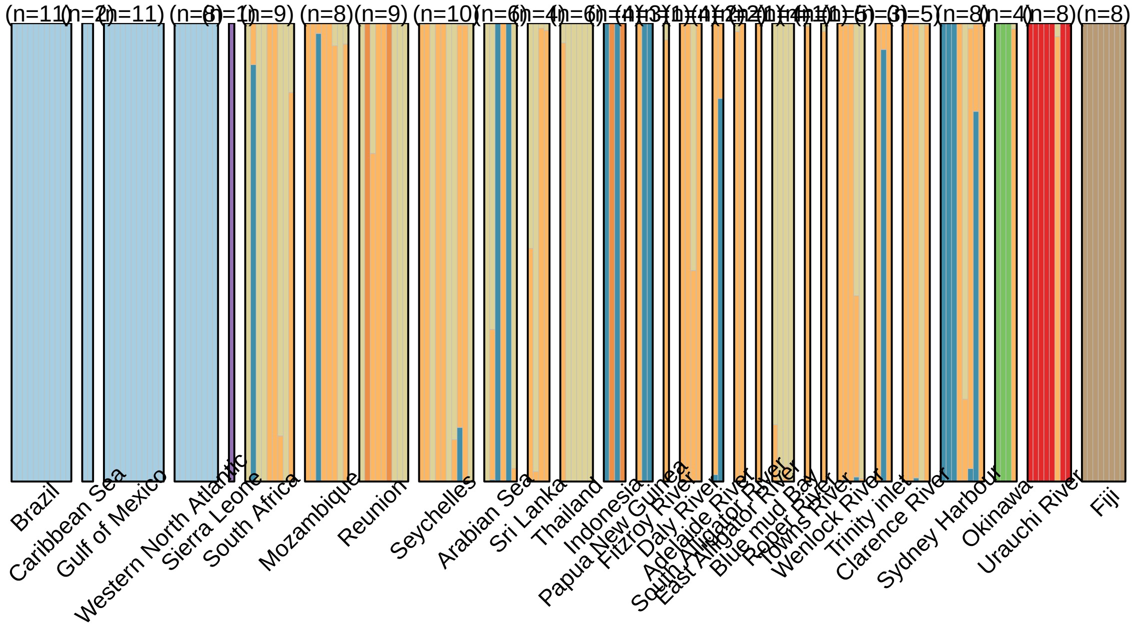
DAPC: all Bull Sharks − subset Australia
for K=7 & PC=15

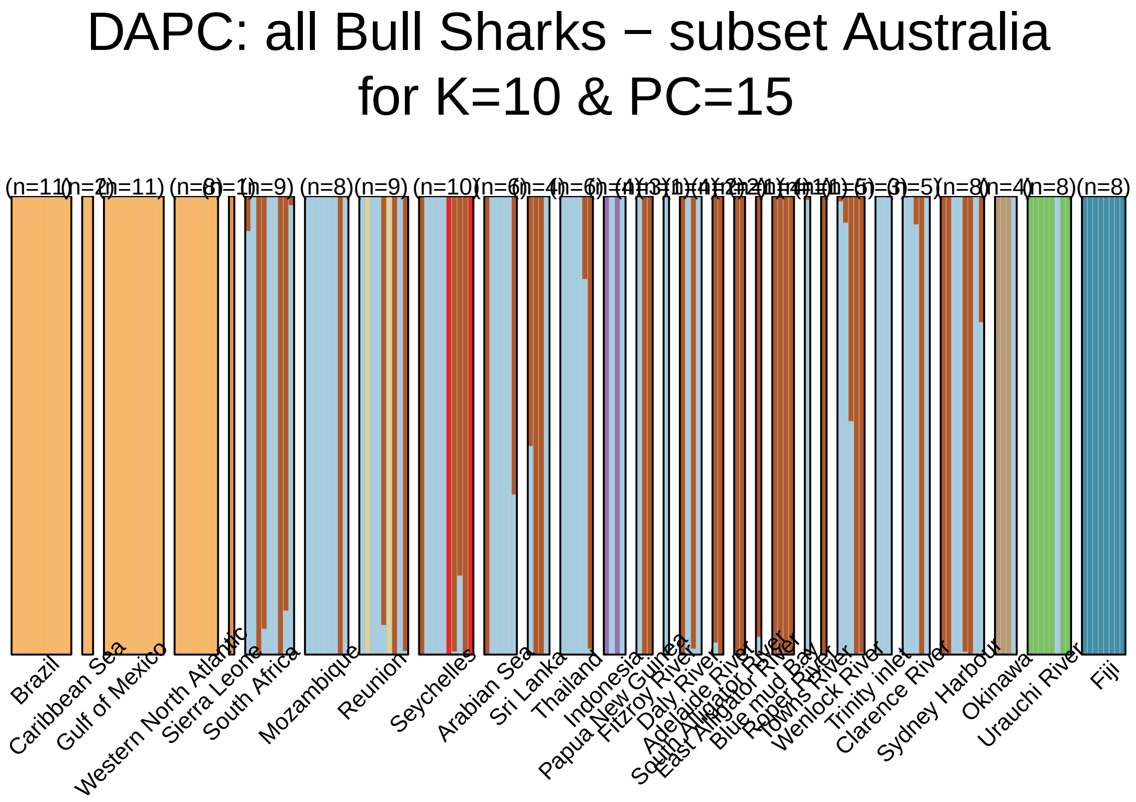


DAPC: all Bull Sharks − subset Australia
for K=8 & PC=15



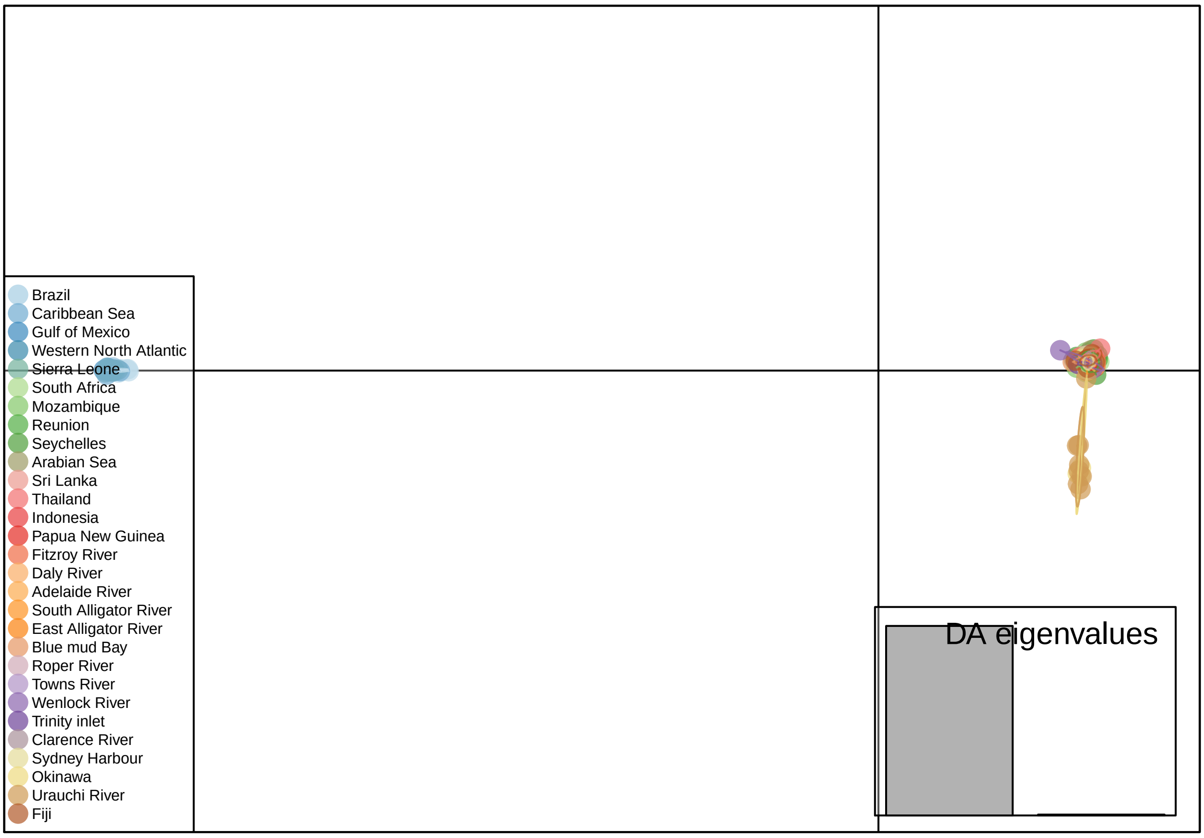
DAPC: all Bull Sharks − subset Australia
for K=9 & PC=15

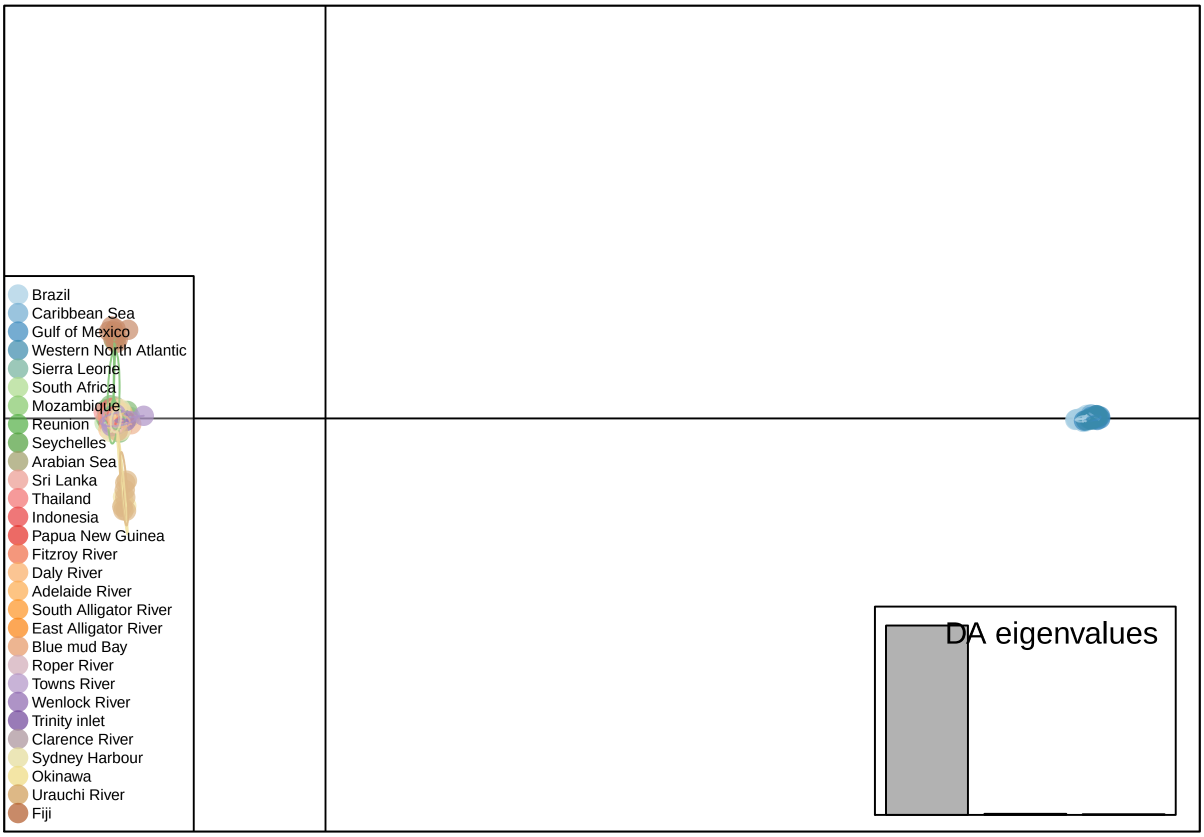


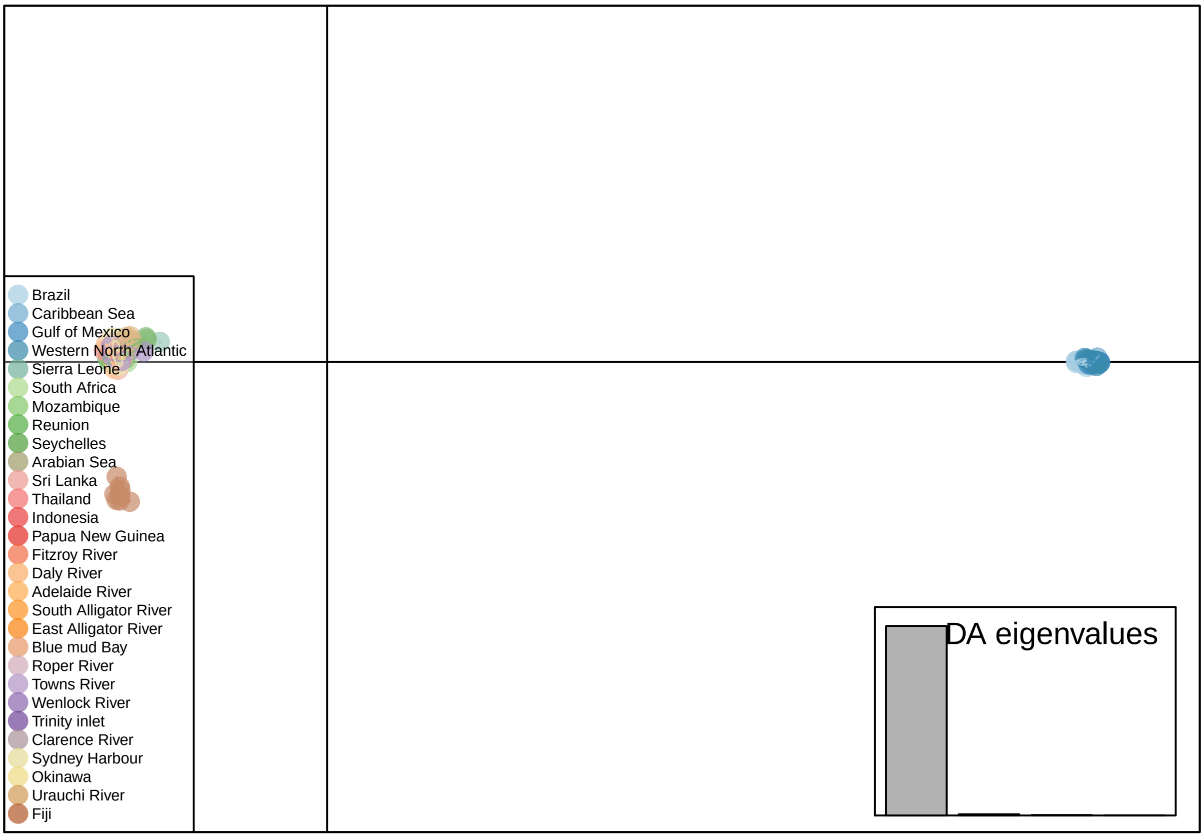


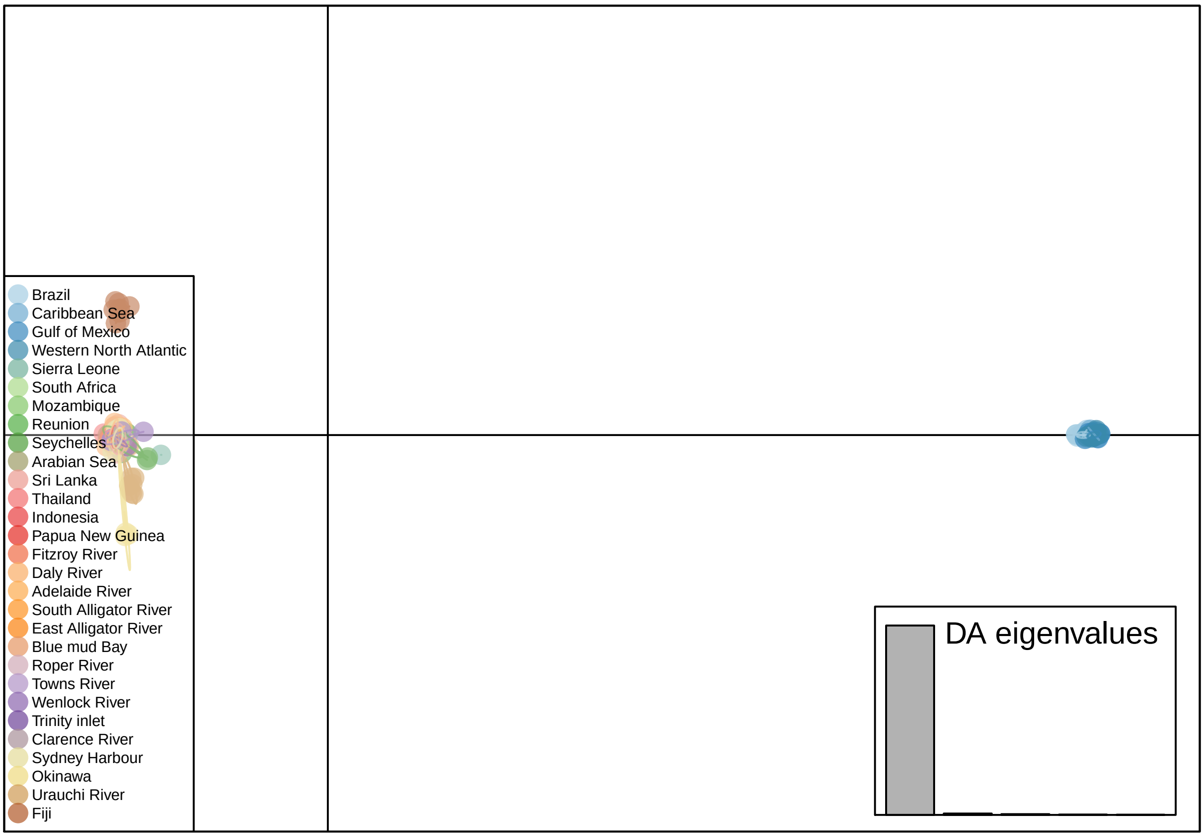
5.9.4 DAPC scatterplot

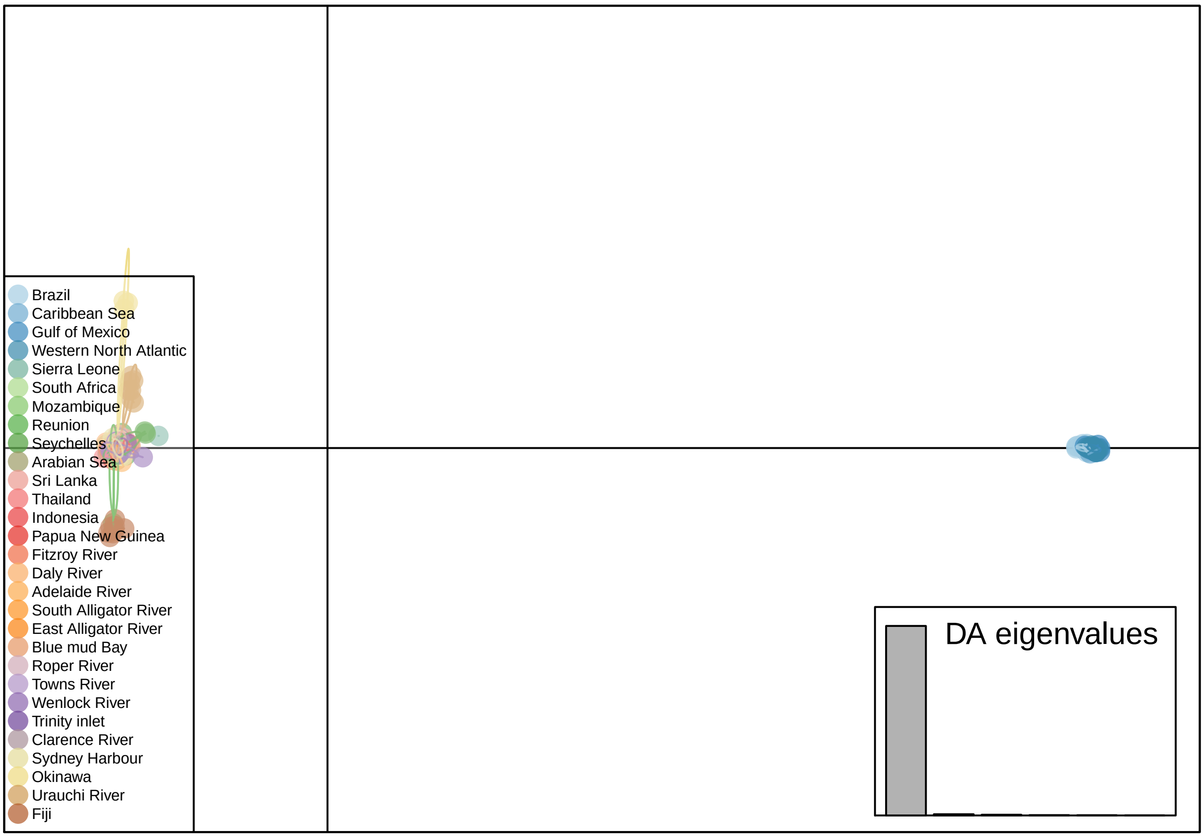
```
load("DArTseq_ALL_DAPC2.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartseq.gl), cex = 2,
                             legend = TRUE, col = colours.29,clabel = FALSE,
                             posi.leg = posi.leg, scree.pca = FALSE,
                             posi.pca = "topleft", cleg = 0.5, xax = 1,
                             yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTseq_ALL_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

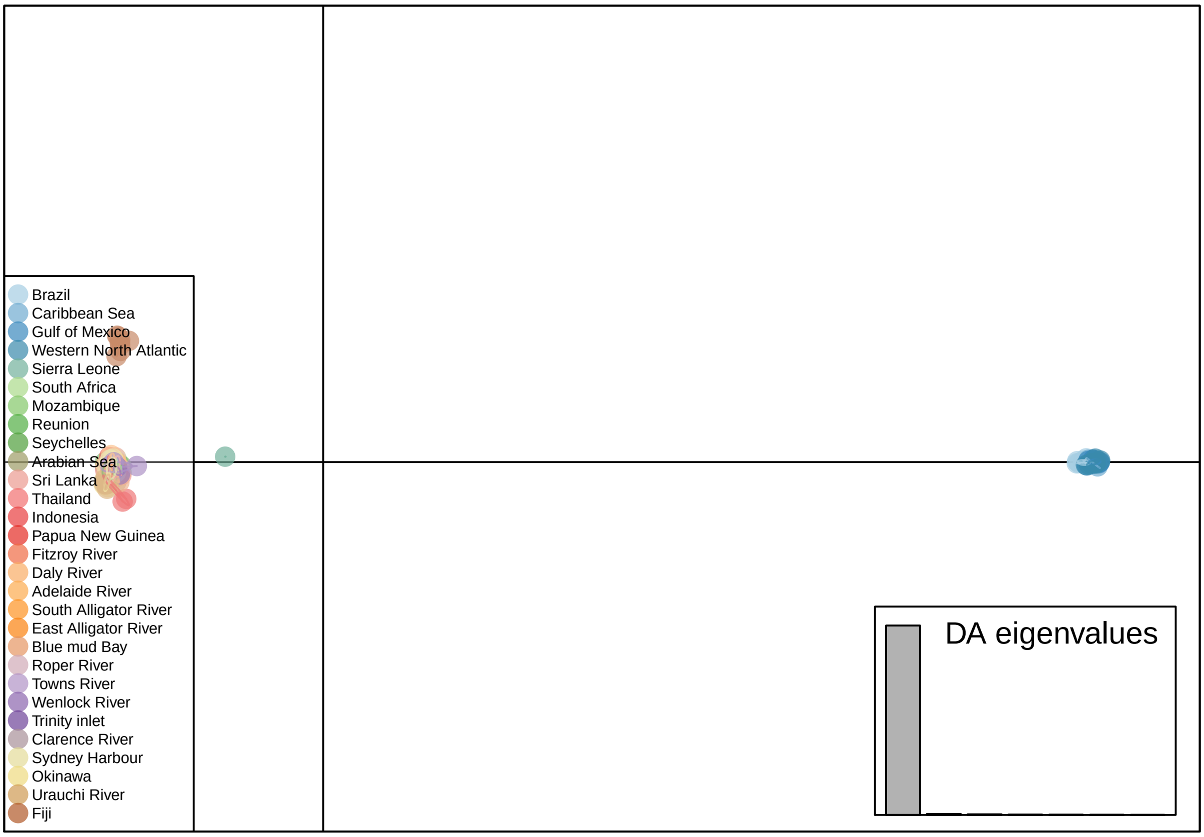

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

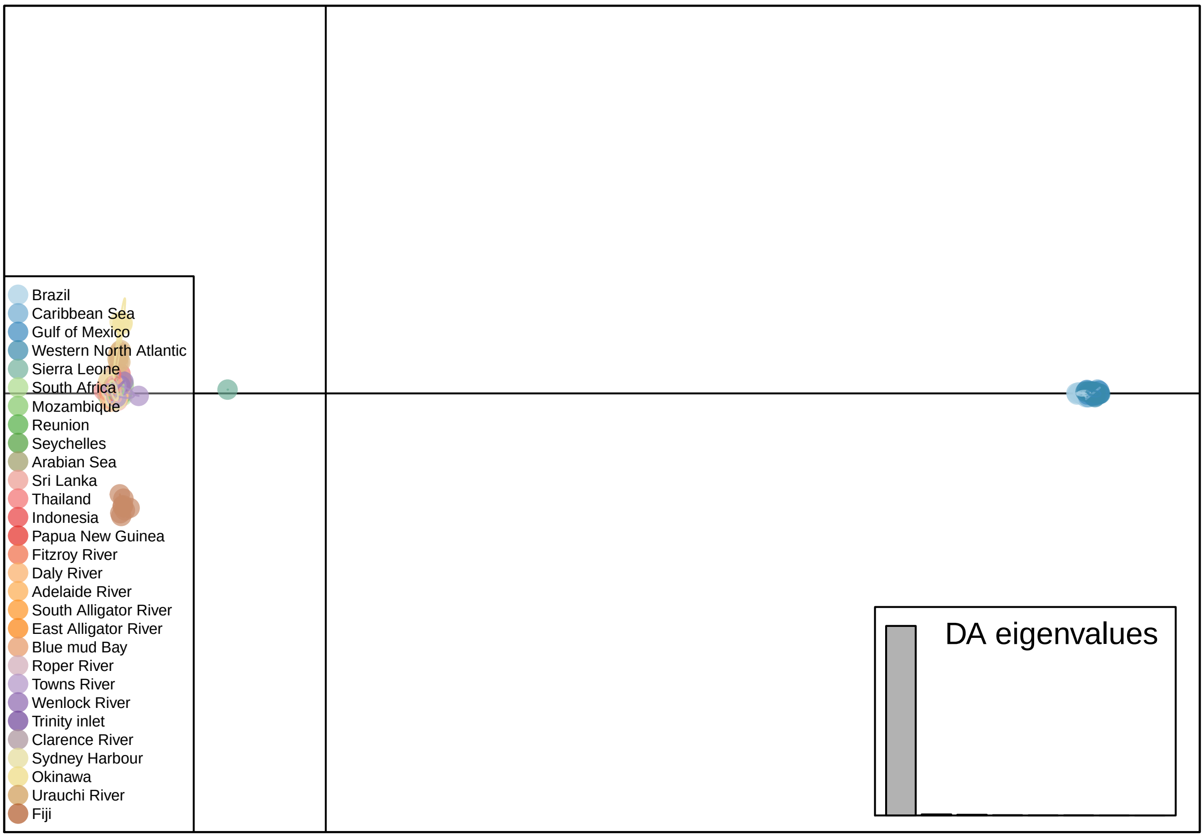

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

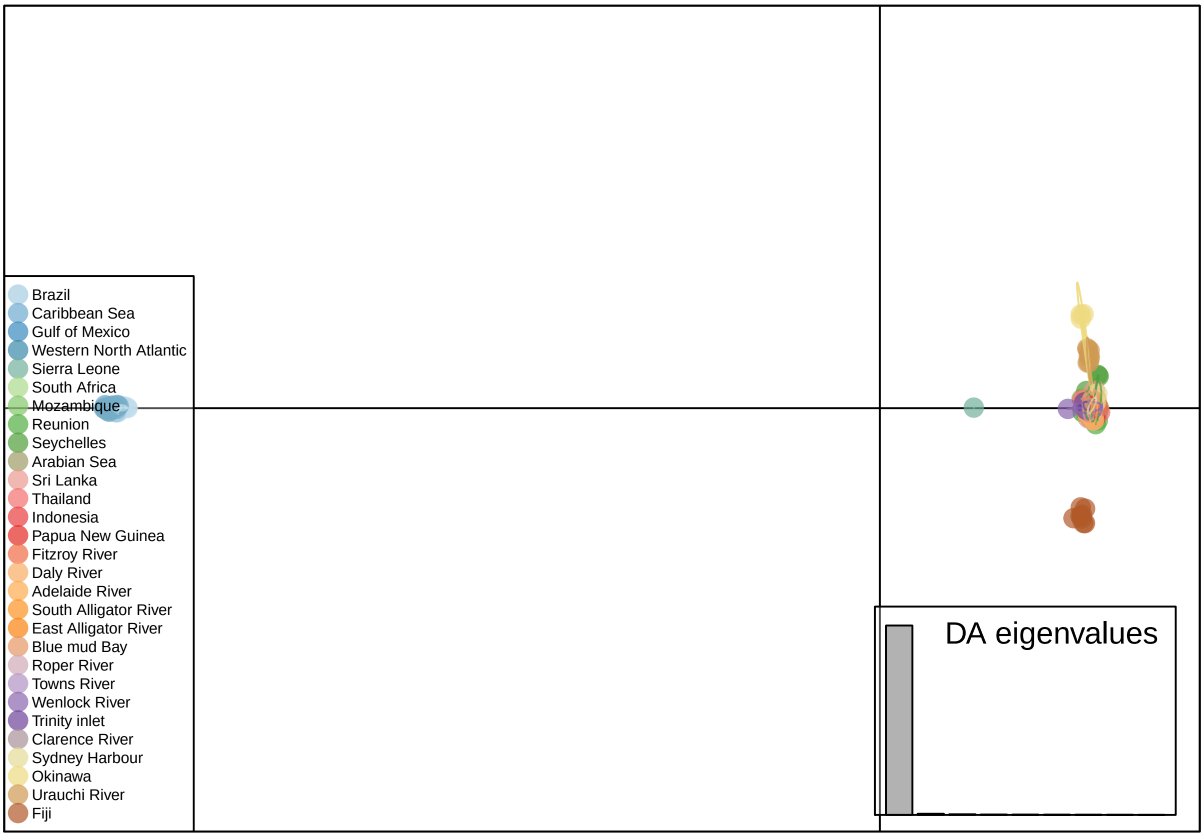

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues


Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues


Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

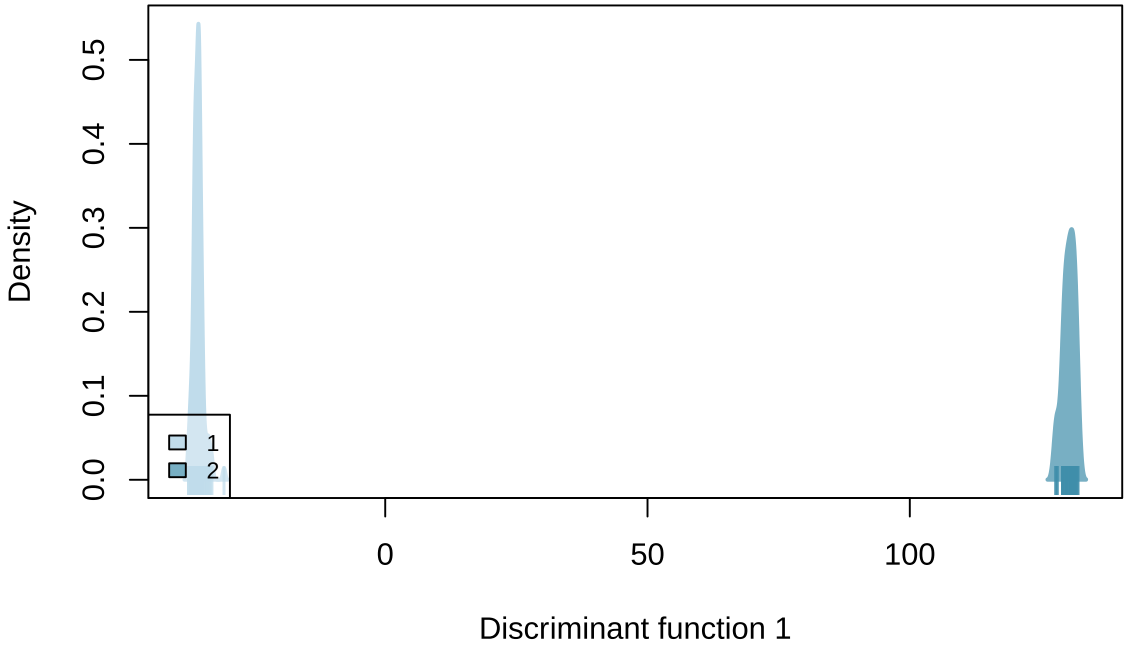

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

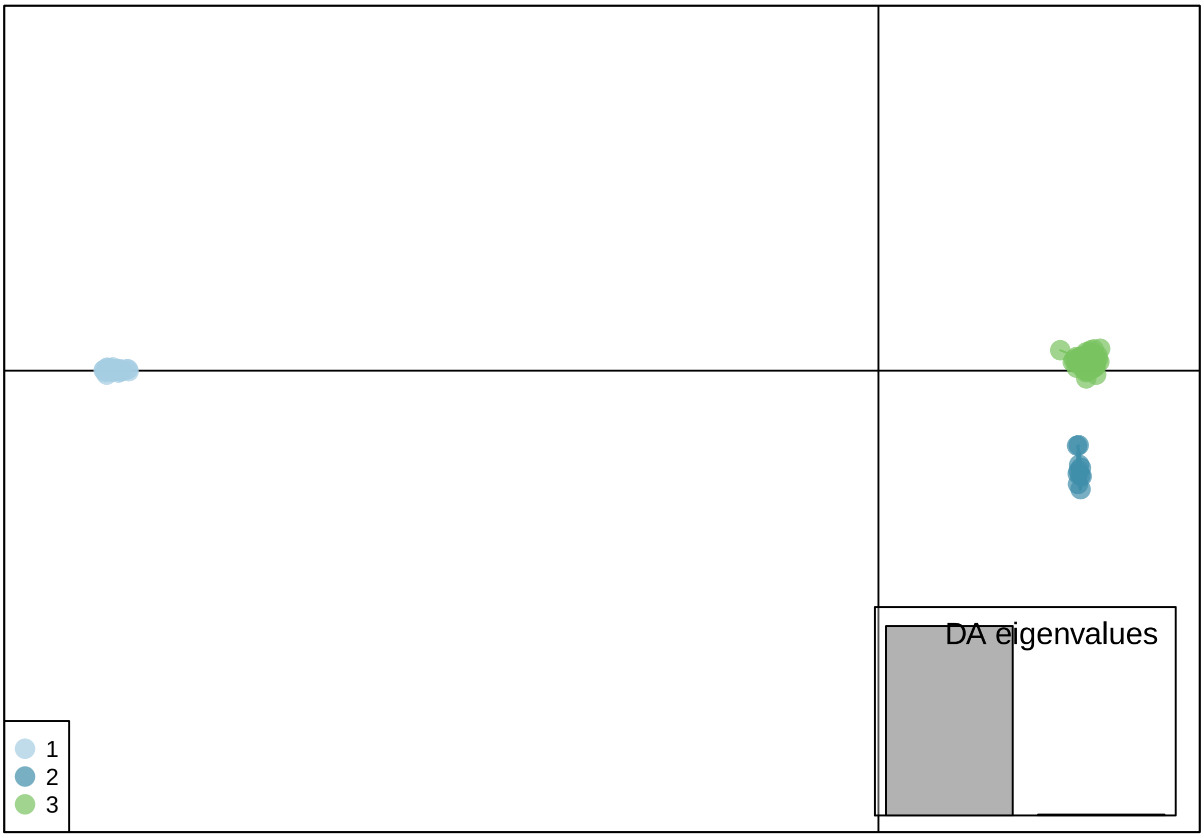


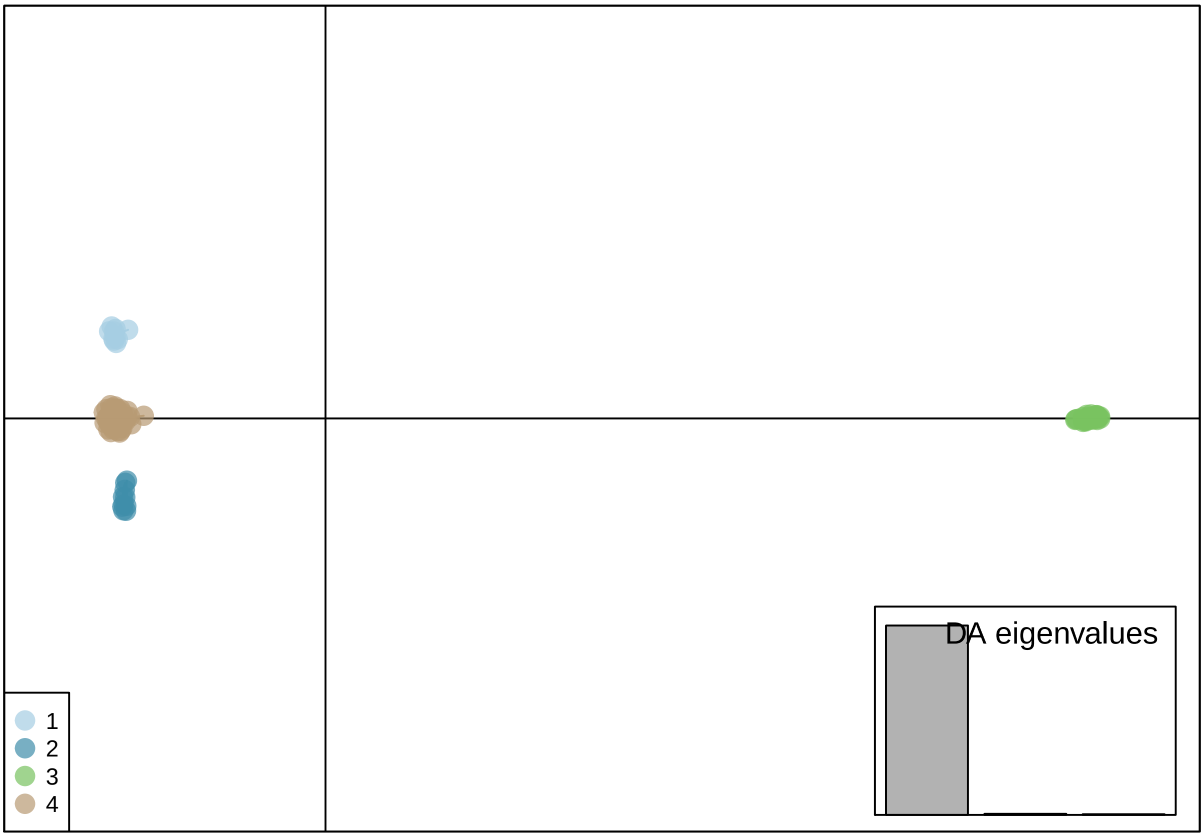


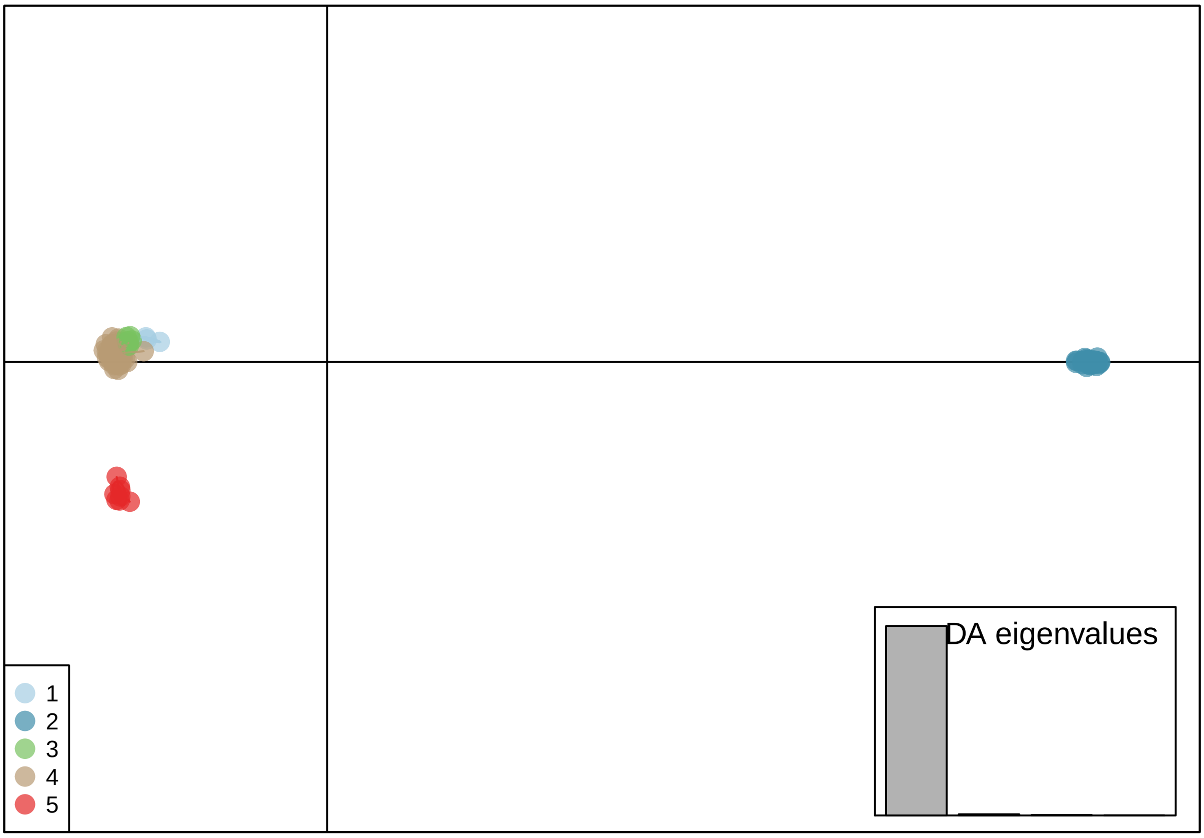
```r
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                             clabel = FALSE, posi.leg = "bottomleft",
```

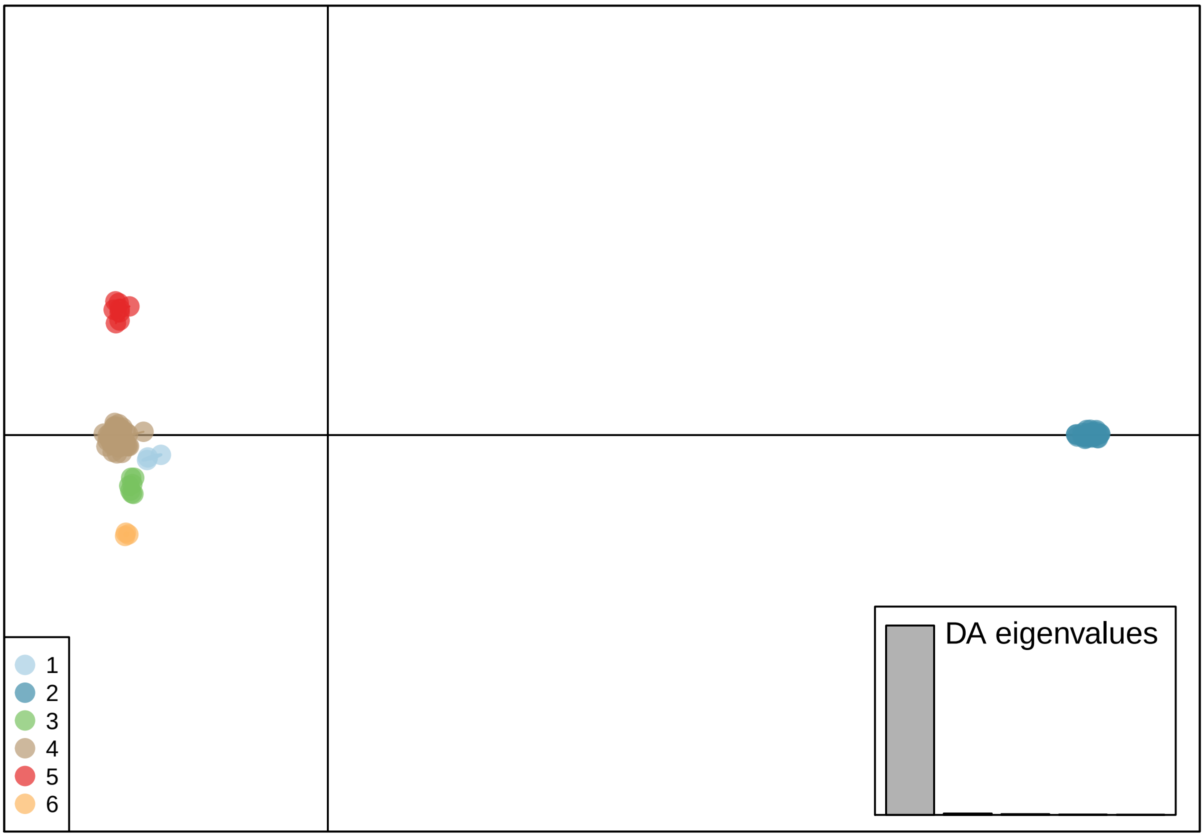
```
                                 scree.pca = FALSE, posi.pca = "topleft",
                                 cleg = 0.75, xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTseq_ALL_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

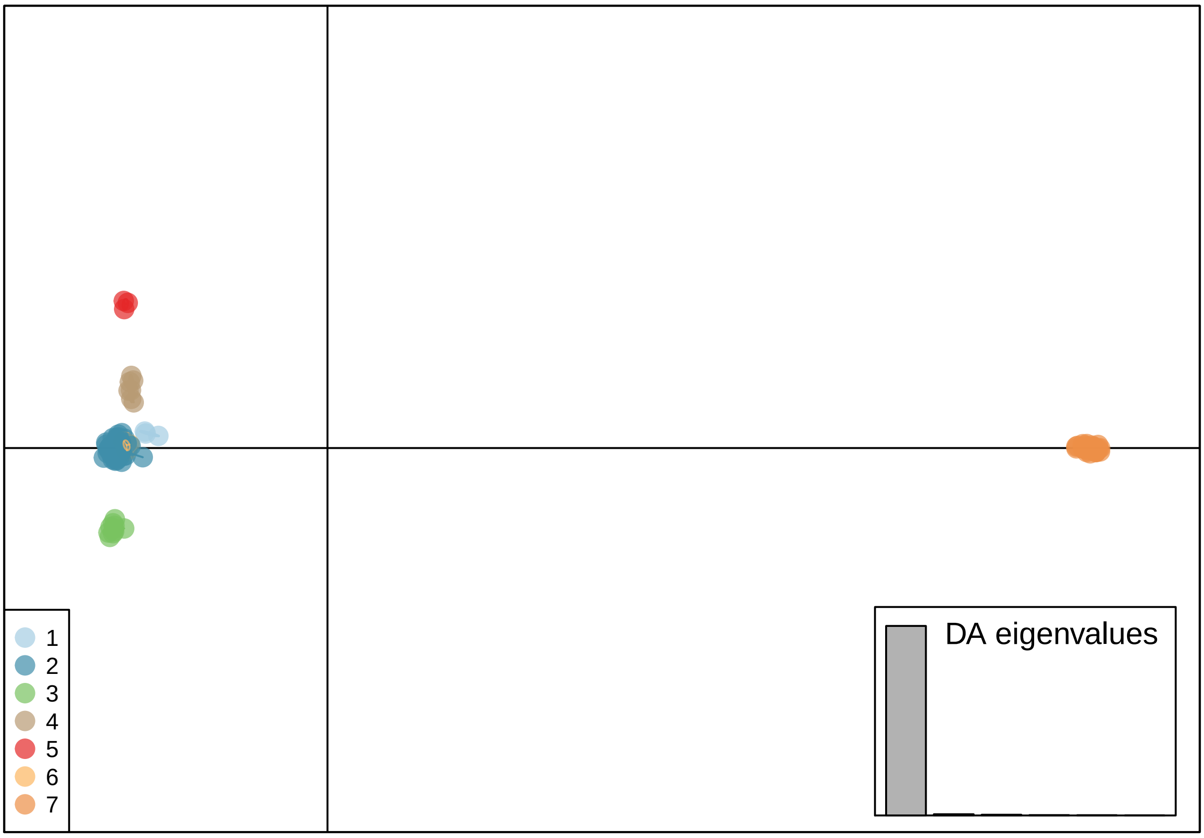


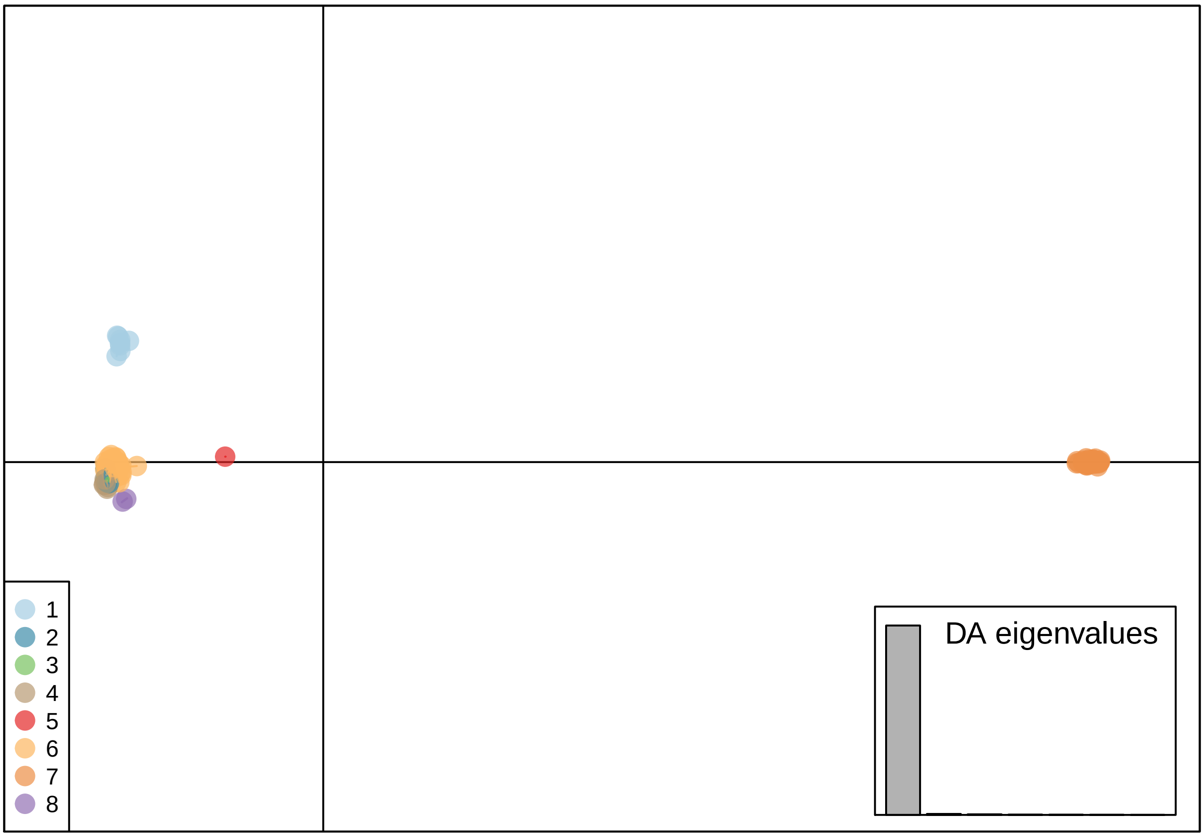

DA eigenvalues
1
2
3

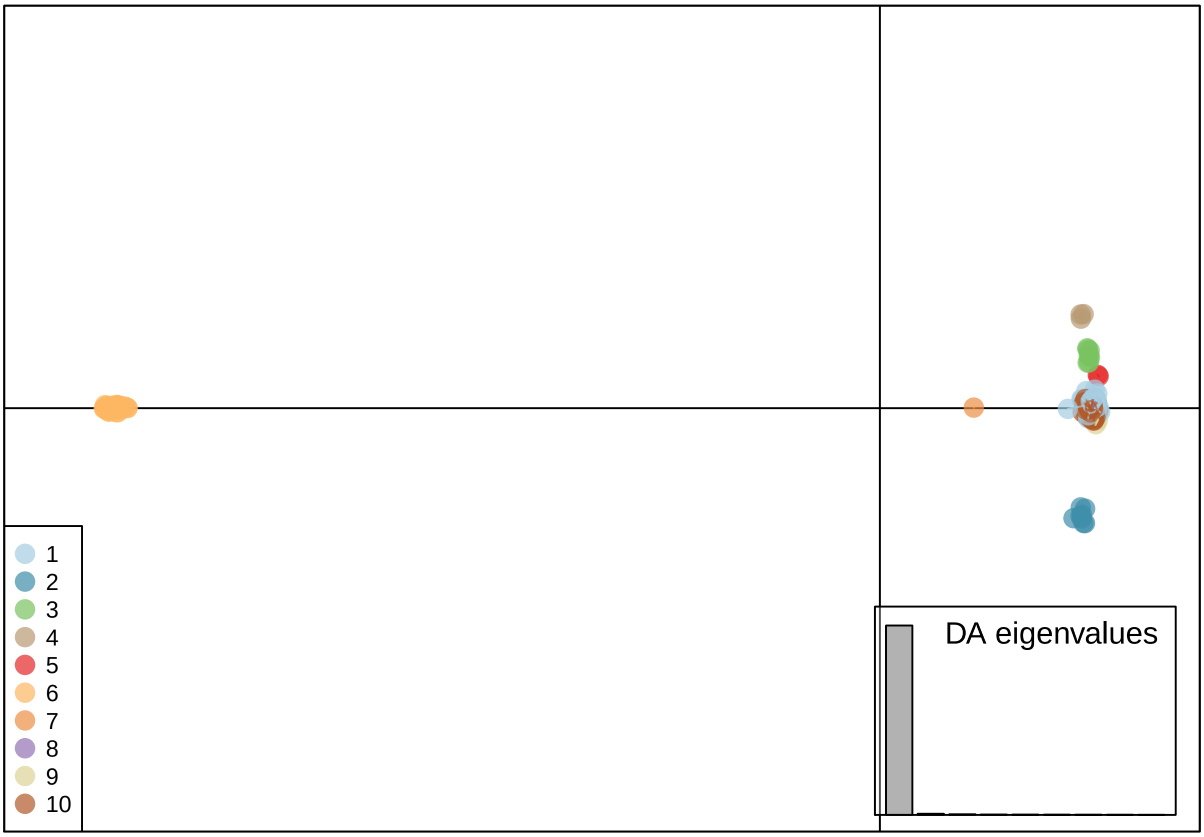

DA eigenvalues
1
2
3
4


DA eigenvalues
1
2
3
4
5


DA eigenvalues
1
2
3
4
5
6


1
2
3
4
5
6
7
DA eigenvalues

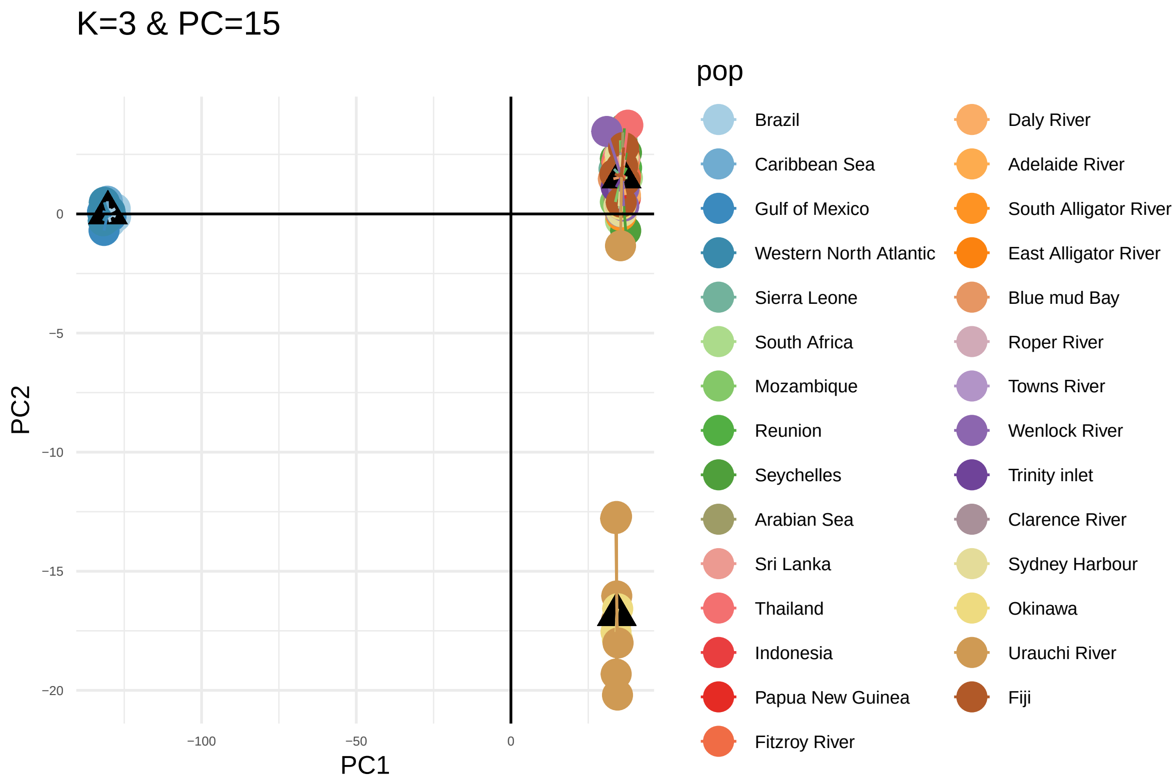

1
2
3
4
5
6
7
8
DA eigenvalues

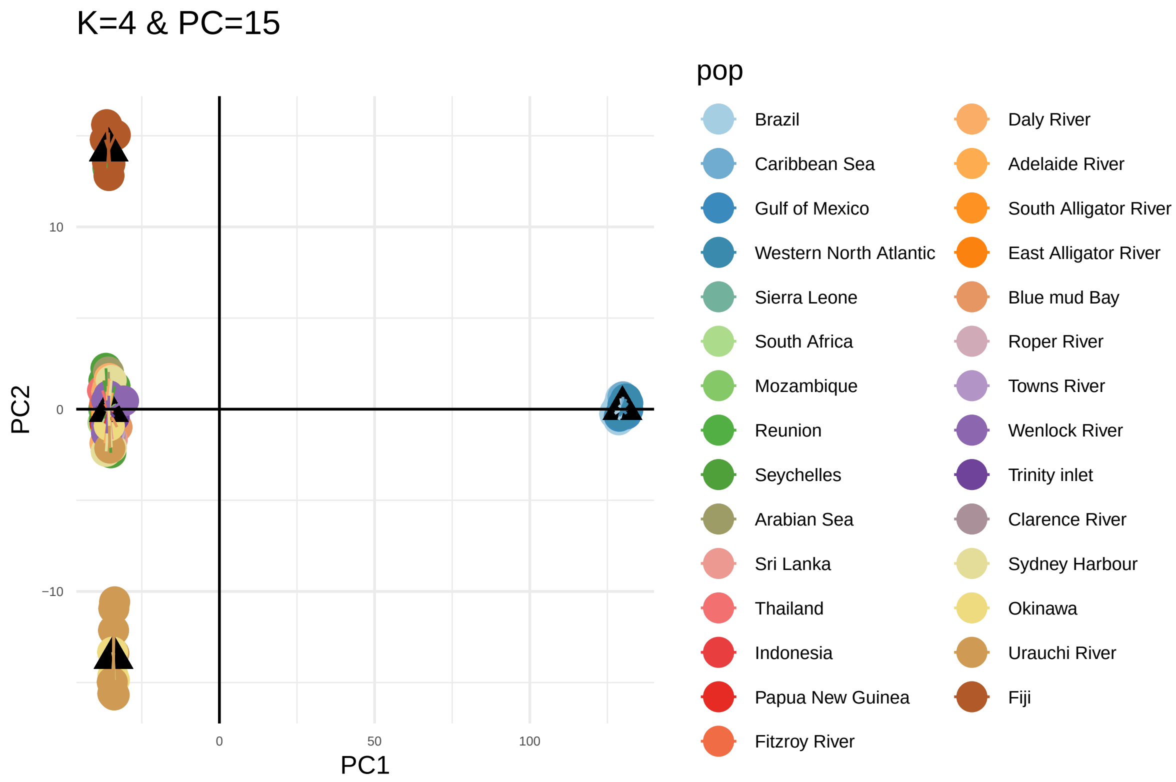


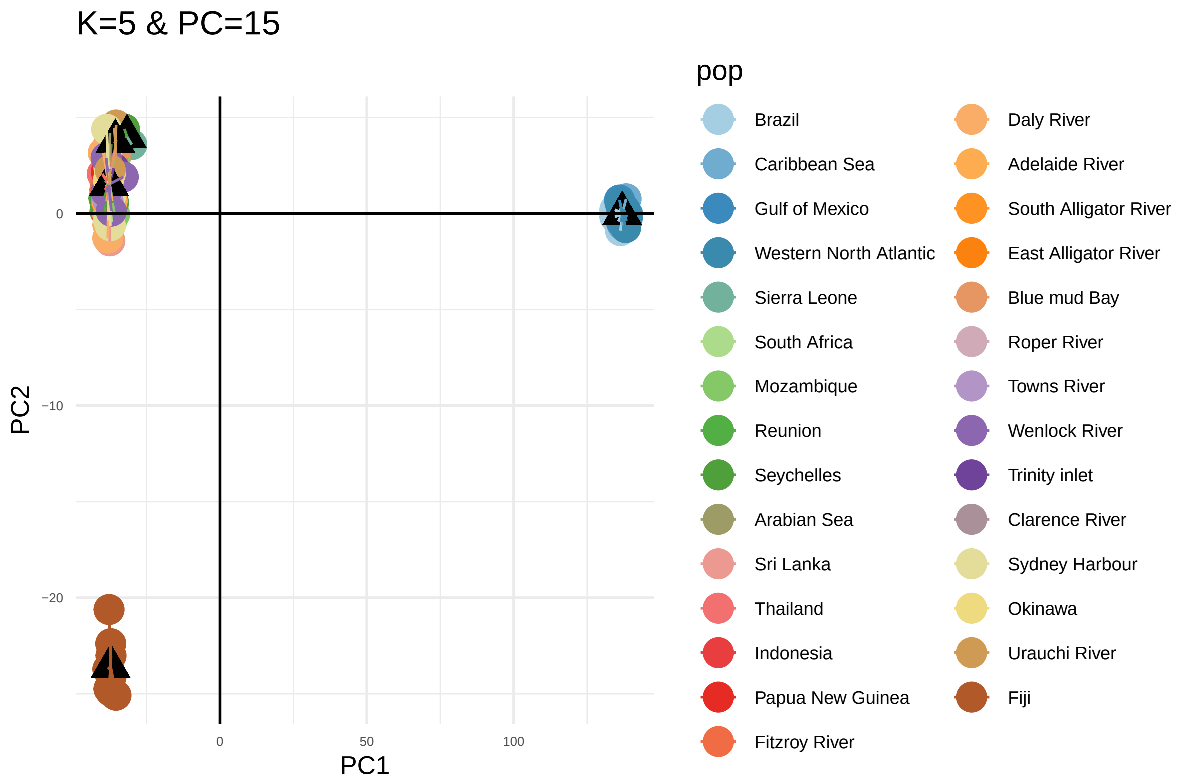
5.9.5 DAPC scatterplot - FLO

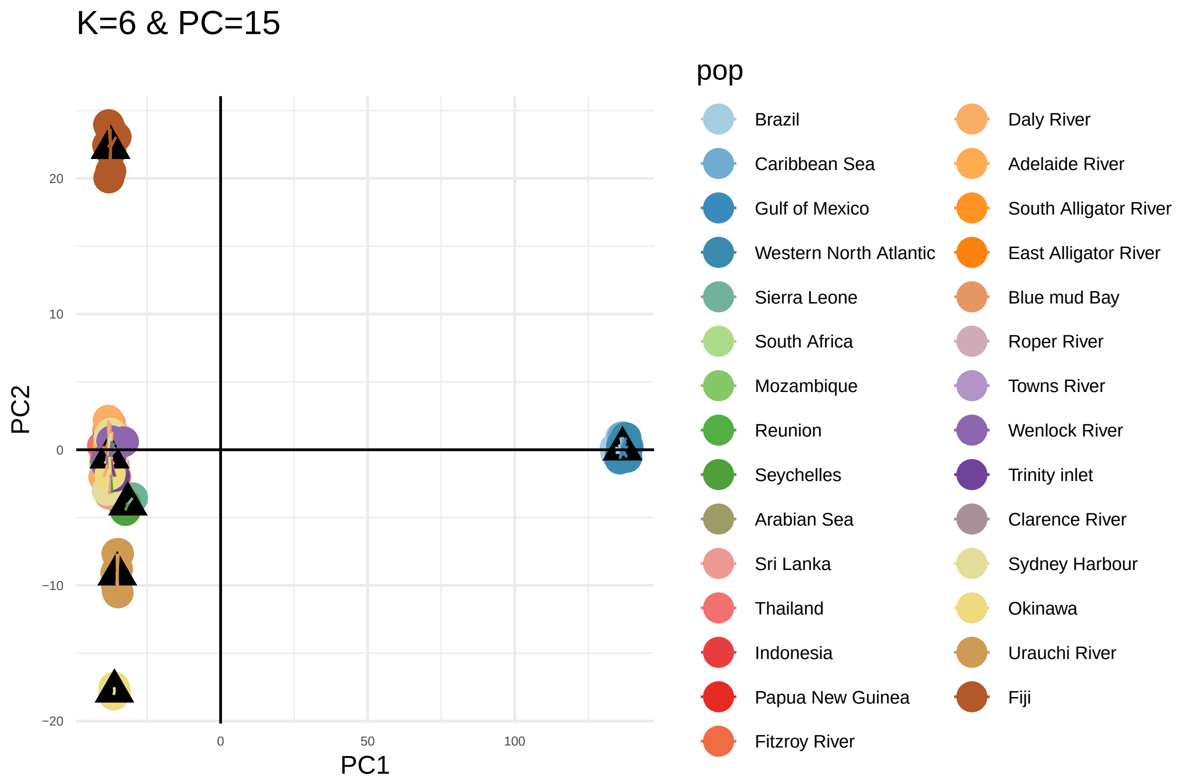
This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

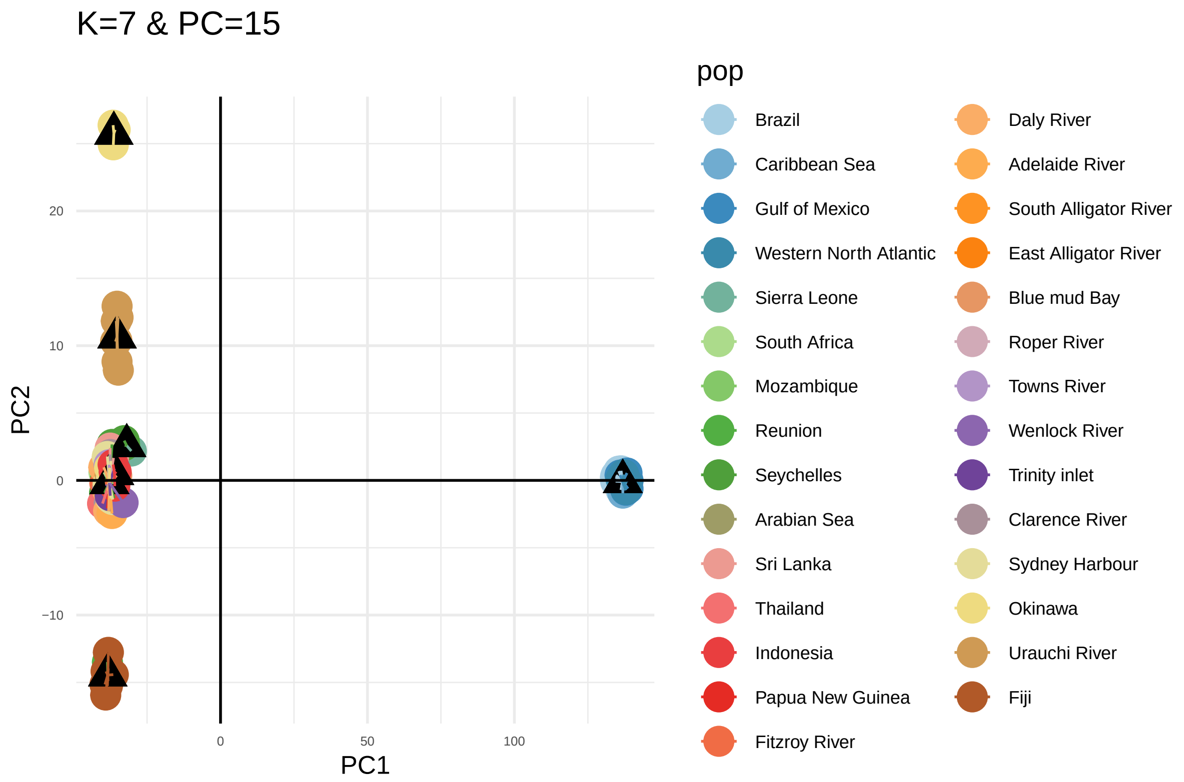
```
for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartseq.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x,mean.y = y)~group,df,mean),
              by = "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x, y = mean.y),size = 5, shape = 17,
                        color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y, xend = x, yend = y)) +
    ggplot2::scale_colour_manual(values = colours.29) +
    ggplot2::scale_fill_manual(values = colours.29) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
        y = "PC2",
        x = "PC1",
        title = paste0("K=",K," & PC=",PC, sep = ""),
        caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot, filename = paste0("DArTseq_ALL_DAPC_scatterplot2_K", K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```

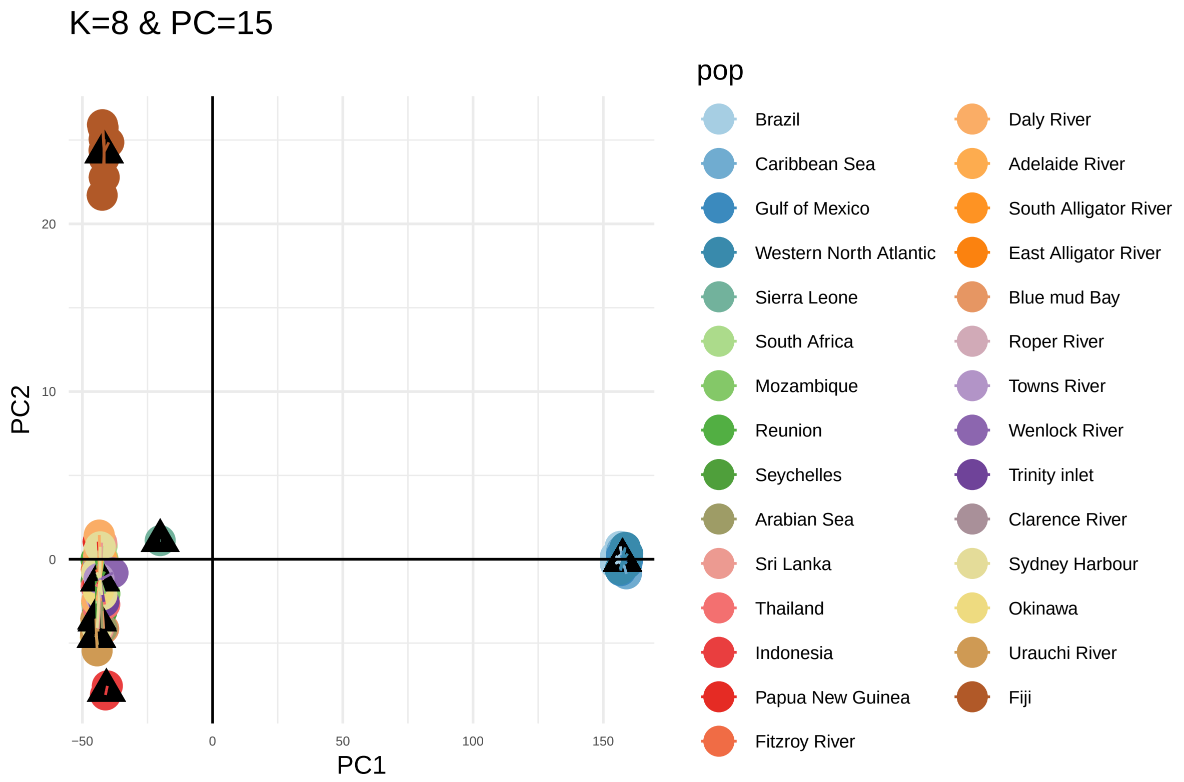

K=3 & PC=15
PC2
0
−5
−10
−15
−20
−100
−50
0
PC1
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji

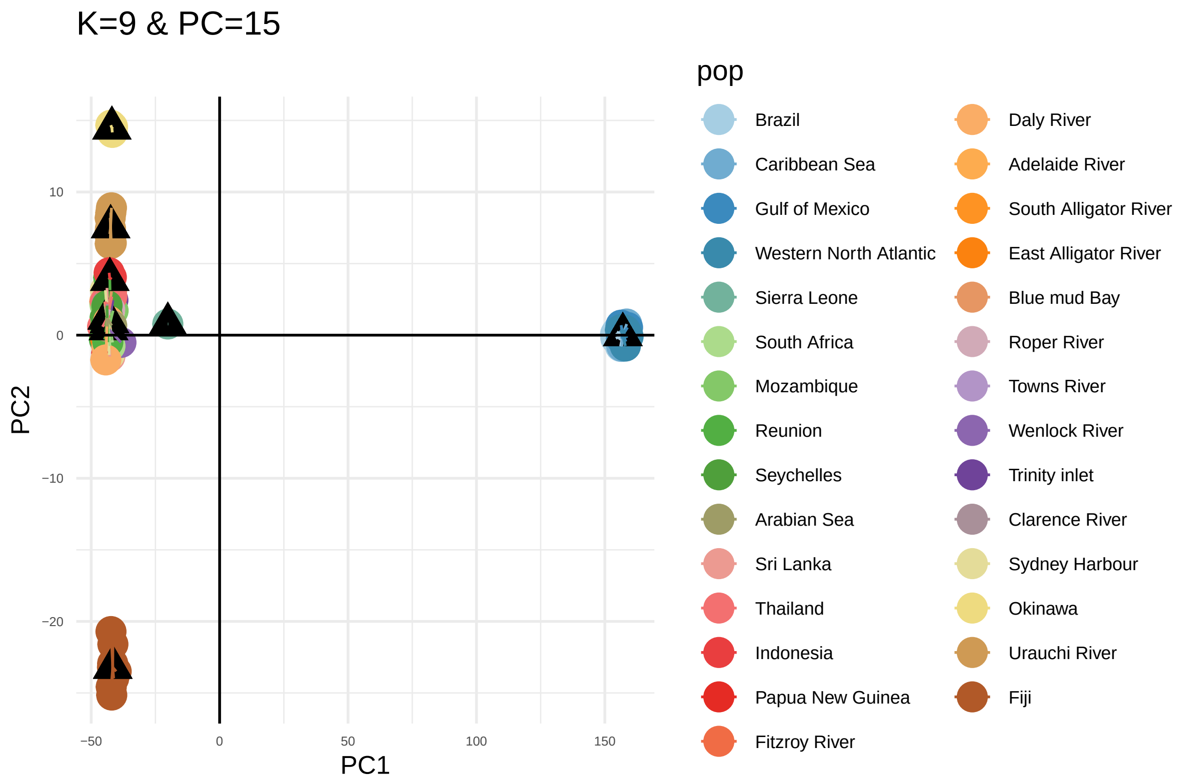

K=4 & PC=15
PC2
10
0
−10
0
50
100
PC1
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji

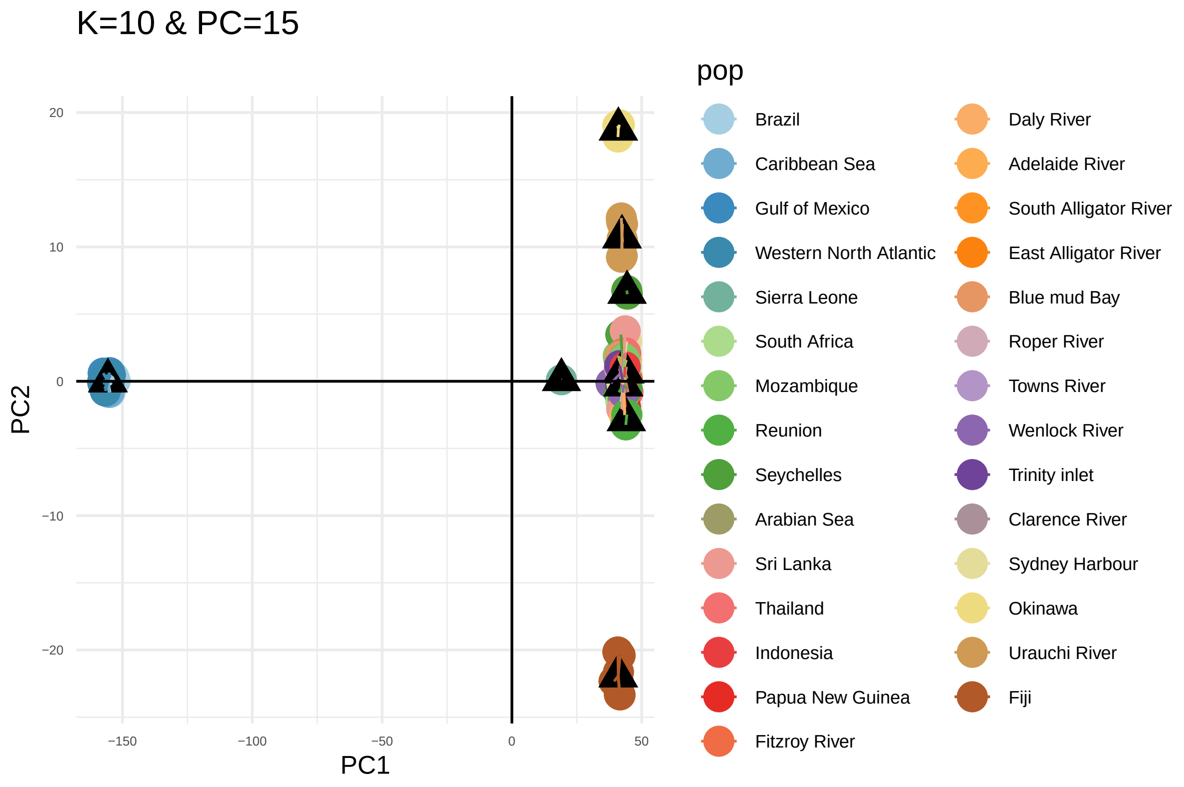

K=5 & PC=15


K=6 & PC=15


K=7 & PC=15


K=8 & PC=15


K=9 & PC=15
PC2
PC1
10
0
−10
−20
−50
0
50
100
150
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji


K=10 & PC=15
PC2
PC1
20
10
0
−10
−20
−150
−100
−50
0
50
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji

6 DArTseq - marker selection

6.1 Sex-linked markers

```
load("Sex_results.Rdata")
bull_shark_sex.markers <- bull_shark$sexy.summary[bull_shark$sexy.summary$METHOD %in%
                          c("presence/absence_method-SNP",
                            "presence/absence_method-SILICO",
                            "heterozygosity_method-SNP",
                            "Coverage_method-SNP"),]
dim(bull_shark_sex.markers) #210 SLMs

knitr::kable(
  bull_shark_sex.markers[c(20:25),],
  caption = "210 sex-linked markers with a SNP from DArTseq data for bait design.") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("hold_position"))

sex.markers <- bull_shark_sex.markers$CLONE_ID
```

```
## [1] 172   5
```

Table 6: 210 sex-linked markers with a SNP from DArTseq data for bait design.

SEX_MARKERS	CLONE_ID	METHOD	MARKER_TYPE	SEQUENCE
CHROM_1___100203043___49	100203043	Coverage_method-SNP	Homogametic_sex-marker	TGCAGCTTCCCCCCCAGTTGCATTTGCAGGGTGTGCAGCT
CHROM_1___100203980___10	100203980	Coverage_method-SNP	Homogametic_sex-marker	TGCAGGAATTYTAAATCCAAAATAATTGCTTTCAGGTGGA
CHROM_1___100204589___28	100204589	Coverage_method-SNP	Homogametic_sex-marker	TGCAGGAGTCACTTTTGCCTCGTGATCARAAACAGTTTGG
CHROM_1___100204774___22	100204774	Coverage_method-SNP	Homogametic_sex-marker	TGCAGGATCACAACTGTGTGCAYGTGCCTGTGTGTGTGCG
CHROM_1___100204975___7	100204975	Coverage_method-SNP	Homogametic_sex-marker	TGCAGGAYTCATGCAGCCACTGCAACAGAGGTCCGAAGTT
CHROM_1___100205908___20	100205908	Coverage_method-SNP	Homogametic_sex-marker	TGCAGGCTGGGTTTGTAACTSATGCACAAGGACTGAGGTC

6.2 Popgen markers

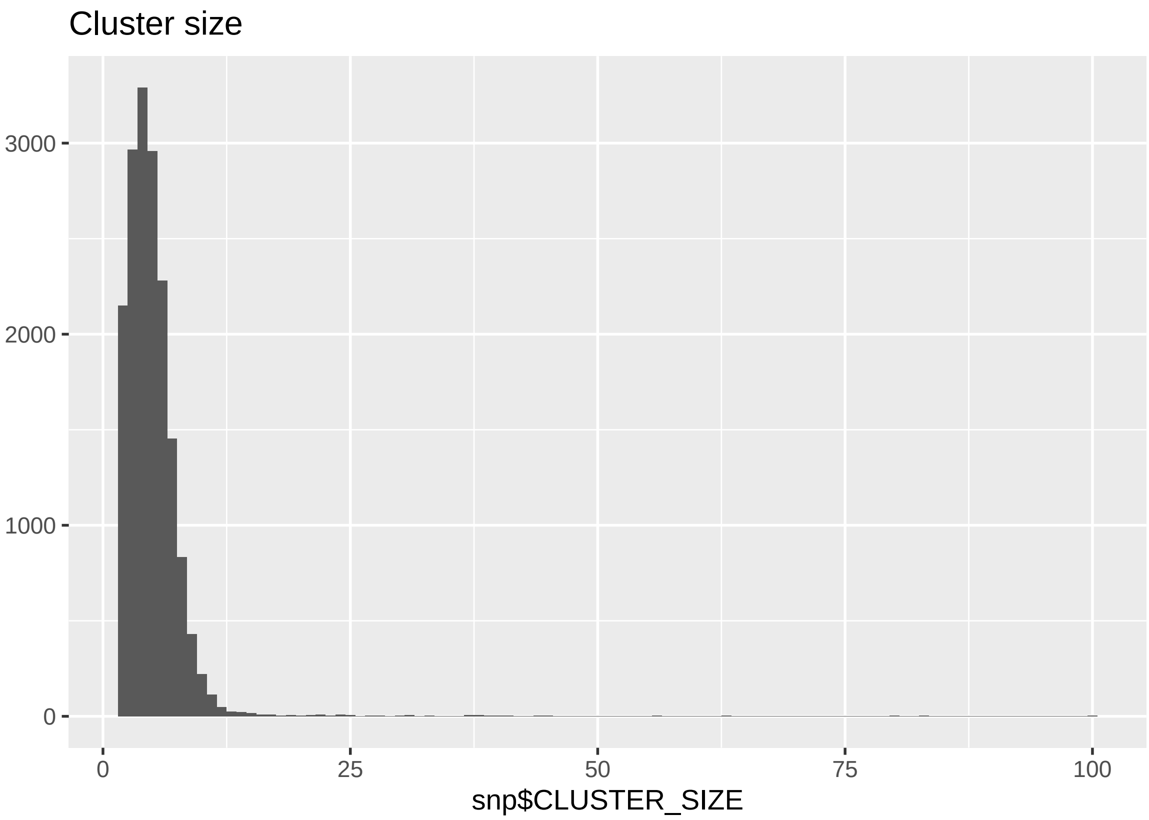
6.2.1 Load data

```
load("DArTseq_ALL_objects3.Rdata")
nInd(BS.dartseq.gl) # 149
nLoc(BS.dartseq.gl) # 16989
```

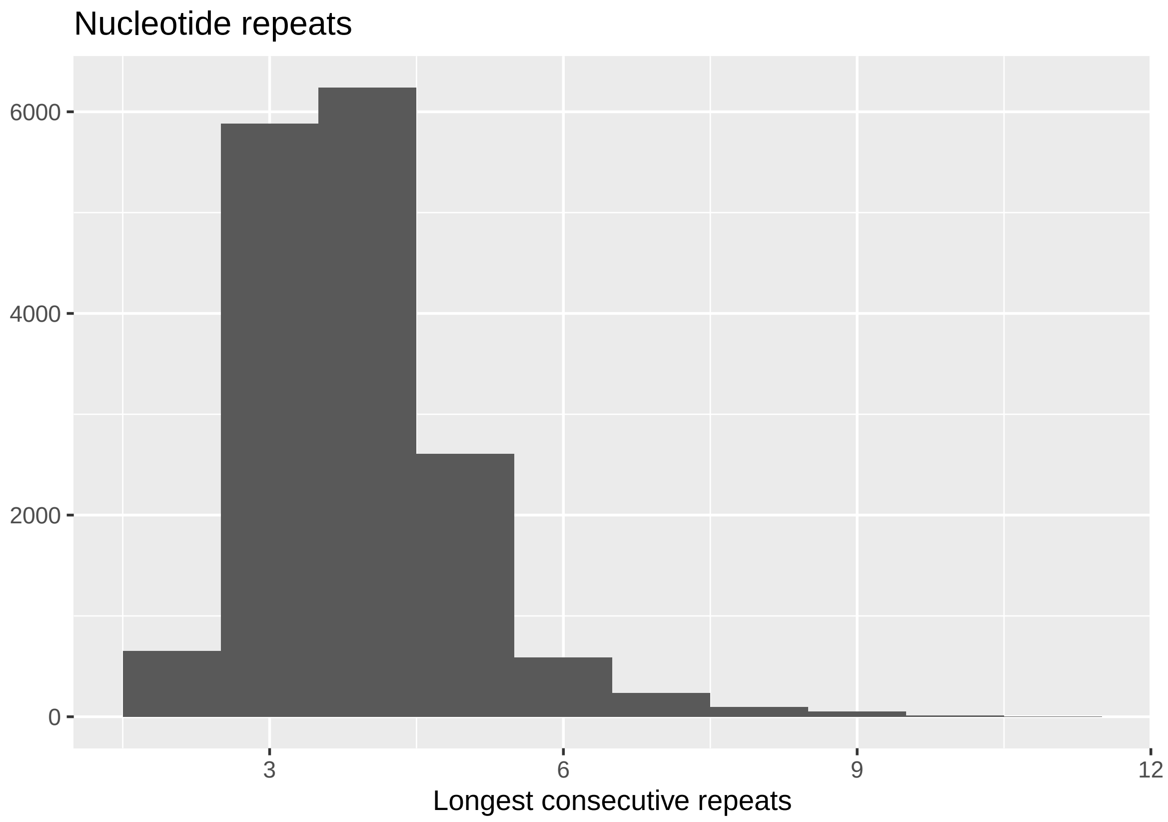
```
## [1] 149
## [1] 16989
```

6.2.2 Extra filters

```
snp <- BS.dartseq.gl$other$loc.metrics

# CLUSTER SIZE
ggplot2::qplot(x = snp$CLUSTER_SIZE, binwidth = 1, main = "Cluster size")
```



```
snp <- dplyr::filter(snp, CLUSTER_SIZE < 10)

# SEQUENCE LENGTH
seq.length <- sapply(X = snp$SEQUENCE, nchar, simplify = TRUE)
summary(seq.length)
snp <- dplyr::filter(snp, seq.length > 60)

# LOW-COMPLEXITY
res <- c()
for (i in 1:length(snp$SEQUENCE)) {
  seqsVector <- snp$SEQUENCE[i]
  lC_nucl <- c()
  for (nucl in c("A", "T", "G", "C")) {
    lC_nucl = c(lC_nucl,
                Biostrings::longestConsecutive(seqsVector, nucl))
  }
  res <- c(res, max(lC_nucl))
}
ggplot2::qplot(x = res, binwidth = 1, main = "Nucleotide repeats",
               xlab = "Longest consecutive repeats")
```



```r
snp <- dplyr::filter(snp, res < 6)

snp <- dplyr::distinct(snp, LOCUS, .keep_all = TRUE) %>%
  dplyr::rename(CLONE_ID = LOCUS, AlleleSequence = SEQUENCE)
dim(snp)
snp <- snp[snp$MARKERS %in% sample(snp$MARKERS, 3200,replace = FALSE),]
snp %<>% dplyr::select(c("CLONE_ID", "AlleleSequence"))
head(snp)
# readr::write_tsv(snp, "Selected_sex-markers_for_baits.tsv")
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      69      69      69      69      69      69
## [1] 15381    36
## # A tibble: 6 x 2
##   CLONE_ID  AlleleSequence
##   <chr>     <chr>
## 1 100190323 TGCAGAGTGCCTCAGAGAGATTCACACTGAAACTCAGTGGGCAGAGCCTATTCCTGCTGAAGAGGCT~
## 2 100190357 TGCAGTGAAGTTATTGTGAAAATCCCCTAGTTGCCACACACTGGTGTCTGTTCAGGTACATGAGGGA~
## 3 100190483 TGCAGAAAAGCAGACATTTAAGACAAGATTTGAACTGGCGGGTGCATGAGCGGTTCAGCAGGAATGC~
## 4 100190716 TGCAGAAAGAATGGATTGCAAGGACATAGCTACAAGTATTGCTTGGGTTAAAGAGAAAATTAGCCAC~
## 5 100190719 TGCAGAAAGACAGTTTAAACAACAAGGTCGAATGCAACATTTCACAGTTGCATGAGCGGTTCAGCAG~
## 6 100190991 TGCAGAAATTCGTGTGTTAGACCTGCCGGGAGACAGCAAACCGAAAGGGTCGGGATTAAACAGGCAG~
```

6.3 Test selected markers

```r
baits <- readr::read_tsv("Total_selected_markers.tsv")

dartseq.data <- "DArTseq_SNP_OrderAppendix_2_DCarcha19-4454.csv"
strata <- "Bull_shark_DArTseq_strata.tsv"
BSsnp <- radiator::read_dart(dartseq.data, strata,tidy.dart = FALSE,
                              parallel.core = 1)
```

```
markers.meta <- radiator::extract_markers_metadata(BSsnp, whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BSsnp, whitelist = TRUE)
BSconvert <- radiator::genomic_converter(BSsnp ,output = "tidy")
BS.dartseq.raw.tidy <- BSconvert$tidy.data
save(BS.dartseq.raw.tidy,markers.meta, individuals.meta,
     file = "DArTseq_Raw_tidy.Rdata")
load("DArTseq_Raw_tidy.Rdata")

length(unique(BS.dartseq.raw.tidy$INDIVIDUALS)) #219
length(unique(BS.dartseq.raw.tidy$MARKERS)) #250945

BS.dartseq.baits.tidy <- BS.dartseq.raw.tidy[BS.dartseq.raw.tidy$MARKERS %in%
                                              baits$AlelleID &
                                              BS.dartseq.raw.tidy$INDIVIDUALS %in%
                                              BS.dartseq.gl$ind.names,]
length(unique(BS.dartseq.baits.tidy$INDIVIDUALS)) #142
length(unique(BS.dartseq.baits.tidy$MARKERS)) #3409

Convert <- radiator::genomic_converter(BS.dartseq.baits.tidy,
                                       output = c("genlight","gtypes"))
BS.dartseq.baits.gl <- Convert$genlight
BS.dartseq.baits.gt <- Convert$gtypes

save(BS.dartseq.baits.tidy,BS.dartseq.baits.gl, BS.dartseq.baits.gt,
     individuals.meta, markers.meta, file = "DArTseq_baits.Rdata")
```

6.3.1 Load data

```
baits <- readr::read_tsv("Total_selected_markers.tsv")
load("DArTseq_baits.Rdata")
pop.levels <- c("Brazil", "Caribbean Sea", "Gulf of Mexico", "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea",
                "Australia", "Japan", "Fiji")
BS.dartseq.baits.gl$pop <- factor(BS.dartseq.baits.gl$other$ind.metrics$Site,
                                  levels = pop.levels)
BS.dartseq.baits.gl <- BS.dartseq.baits.gl[order(BS.dartseq.baits.gl$pop,
                                                 BS.dartseq.baits.gl$ind.names),]

BS.dartseq.baits.tidy$POP_ID <- factor(BS.dartseq.baits.tidy$Site, levels = pop.levels)
BS.dartseq.baits.tidy <- BS.dartseq.baits.tidy[order(
  BS.dartseq.baits.tidy$POP_ID, BS.dartseq.baits.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartseq.baits.gl) # 142
adegenet::nLoc(BS.dartseq.baits.gl) # 3409
summary(BS.dartseq.baits.gl$pop)
sum(duplicated(BS.dartseq.baits.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartseq.baits.gl$other$loc.metrics$LOCUS) #3409
```

```
## [1] 142
## [1] 3409
##                 Brazil          Caribbean Sea         Gulf of Mexico
##                     11                      2                     11
## Western North Atlantic           Sierra Leone           South Africa
##                      8                      1                      9
##             Mozambique                Reunion             Seychelles
##                      8                      9                     10
```

```
##            Arabian Sea              Sri Lanka               Thailand
##                      6                      4                      4
##              Indonesia       Papua New Guinea              Australia
##                      4                      2                     34
##                  Japan                   Fiji
##                     11                      8
## [1] 0
## [1] 3409
```

6.3.2 Genetic diversity

```
set.seed(124)
gl <- BS.dartseq.baits.gl
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "South Africa", "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names)]

gl2gpop(gl, filename = "BS_dartseq_all_baits_genepop.txt")
bastat <- diveRsity::basicStats(infile = "BS_dartseq_all_baits_genepop.txt",
                                outfile = "BS_dartseq_all_baits_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)
length(bastat$main_tab) #16
gendiv <- data.frame(
  "Brazil" = bastat$main_tab[[1]]$overall,
  "Caribbean Sea" = bastat$main_tab[[2]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[3]]$overall,
  "Western North Atlantic" = bastat$main_tab[[4]]$overall,
  "South Africa" = bastat$main_tab[[5]]$overall,
  "Mozambique" = bastat$main_tab[[6]]$overall,
  "Reunion" = bastat$main_tab[[7]]$overall,
  "Seychelles" = bastat$main_tab[[8]]$overall,
  "Arabian Sea" = bastat$main_tab[[9]]$overall,
  "Sri Lanka" = bastat$main_tab[[10]]$overall,
  "Thailand" = bastat$main_tab[[11]]$overall,
  "Indonesia" = bastat$main_tab[[12]]$overall,
  "Papua New Guinea" = bastat$main_tab[[13]]$overall,
  "Australia" = bastat$main_tab[[14]]$overall,
  "Japan" = bastat$main_tab[[15]]$overall,
  "Fiji" = bastat$main_tab[[16]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
```

```
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTseq_ALL_baits_gendiv.txt")
save(gendiv, file = "DArTseq_ALL_baits_gendiv.Rdata")
```

```
load("DArTseq_ALL_baits_gendiv.Rdata")
shortnames <- c("BRZ", "CAR", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(gendiv, col.names = shortnames, digits = 4,caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

Table 7:

	BRZ	CAR	GOM	WNA	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
ar	1.0740	1.0440	1.0700	1.0710	1.1120	1.0690	1.1100	1.1110	1.1040	1.1020	1.0970	1.0930	1.0720	1.1160	1.1070	1.0990
size	10.7760	1.9490	10.7670	7.8190	8.8250	7.2800	8.7800	9.8020	5.8420	3.9550	3.9320	3.9270	1.9720	33.2310	10.8050	7.6950
obs_het	0.0420	0.0380	0.0400	0.0420	0.0620	0.0570	0.0620	0.0610	0.0600	0.0620	0.0590	0.0590	0.0600	0.0610	0.0600	0.0610
exp_het	0.0480	0.0350	0.0460	0.0460	0.0670	0.0650	0.0670	0.0650	0.0630	0.0590	0.0580	0.0560	0.0440	0.0690	0.0630	0.0660
uexp_het	0.0490	0.0440	0.0470	0.0480	0.0710	0.0700	0.0710	0.0680	0.0690	0.0670	0.0670	0.0630	0.0560	0.0700	0.0660	0.0710
fis	0.0500	-0.1950	0.0540	0.0210	0.0390	0.0620	0.0370	0.0280	0.0170	-0.0780	-0.0560	-0.0840	-0.4200	0.0800	0.0210	0.0370
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0220	-1.0000	-0.0150	-0.0940	-0.0790	-0.0660	-0.0600	-0.0510	-0.1690	-0.3350	-0.3090	-0.4580	-1.0000	0.0580	-0.0710	-0.0810
fis_hi	0.0450	-0.1950	0.0490	0.0150	0.0310	0.0570	0.0290	0.0170	0.0130	-0.0780	-0.0560	-0.0840	-0.4200	0.0820	0.0200	0.0260
ar_lo	1.0170	0.9970	1.0130	1.0160	1.0370	0.9010	1.0320	1.0370	0.9570	1.0450	1.0350	1.0350	1.0380	1.0530	1.0380	0.9280
ar_hi	1.0850	1.0770	1.0800	1.0870	1.1310	1.1230	1.1250	1.1240	1.1270	1.1230	1.1210	1.1260	1.0970	1.1290	1.1230	1.1230
fis.hierfstat	0.0936	0.0449	0.0984	0.0818	0.0920	0.1246	0.0907	0.0761	0.0977	0.0439	0.0655	0.0356	-0.2143	0.0939	0.0653	0.0983
fis.CI.low	0.1159	0.0766	0.1240	0.0964	0.1003	0.1669	0.1049	0.0844	0.1185	0.0455	0.0812	0.0359	-0.2006	0.1174	0.0673	0.1138
fis.CI.high	0.1781	0.2514	0.1894	0.1719	0.1583	0.2337	0.1634	0.1433	0.1907	0.1377	0.1707	0.1338	-0.0408	0.1517	0.1230	0.1763

```r
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic",
                "Sierra Leone", "South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea",
                "Australia", "Japan", "Fiji")
BS.dartseq.baits.gl$pop <- factor(BS.dartseq.baits.gl$other$ind.metrics$Site,
                                  levels = pop.levels)
BS.dartseq.baits.gl <- BS.dartseq.baits.gl[order(BS.dartseq.baits.gl$pop,
                                                 BS.dartseq.baits.gl$ind.names)]

monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartseq.baits.gl[BS.dartseq.baits.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("BRZ", "CAR", "GOM", "WNA","SIL", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

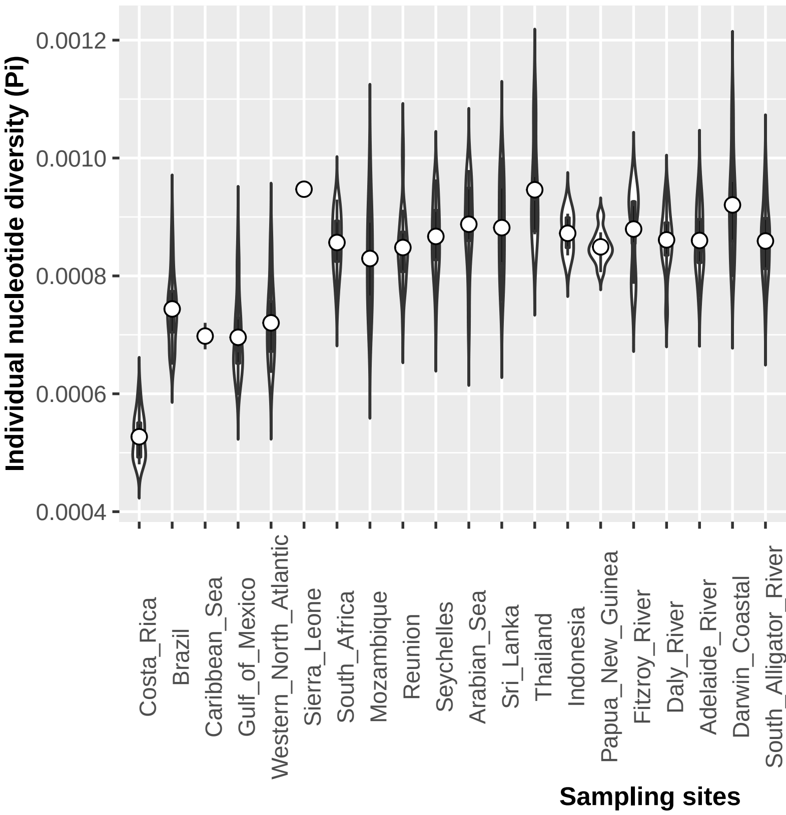
Table 8:

BRZ	CAR	GOM	WNA	SIL	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
2531	2966	2546	2610	3343	2426	2526	2458	2425	2616	2797	2798	2856	3143	1742	2429	2521

6.3.2.1 Number of monomorphic markers per population

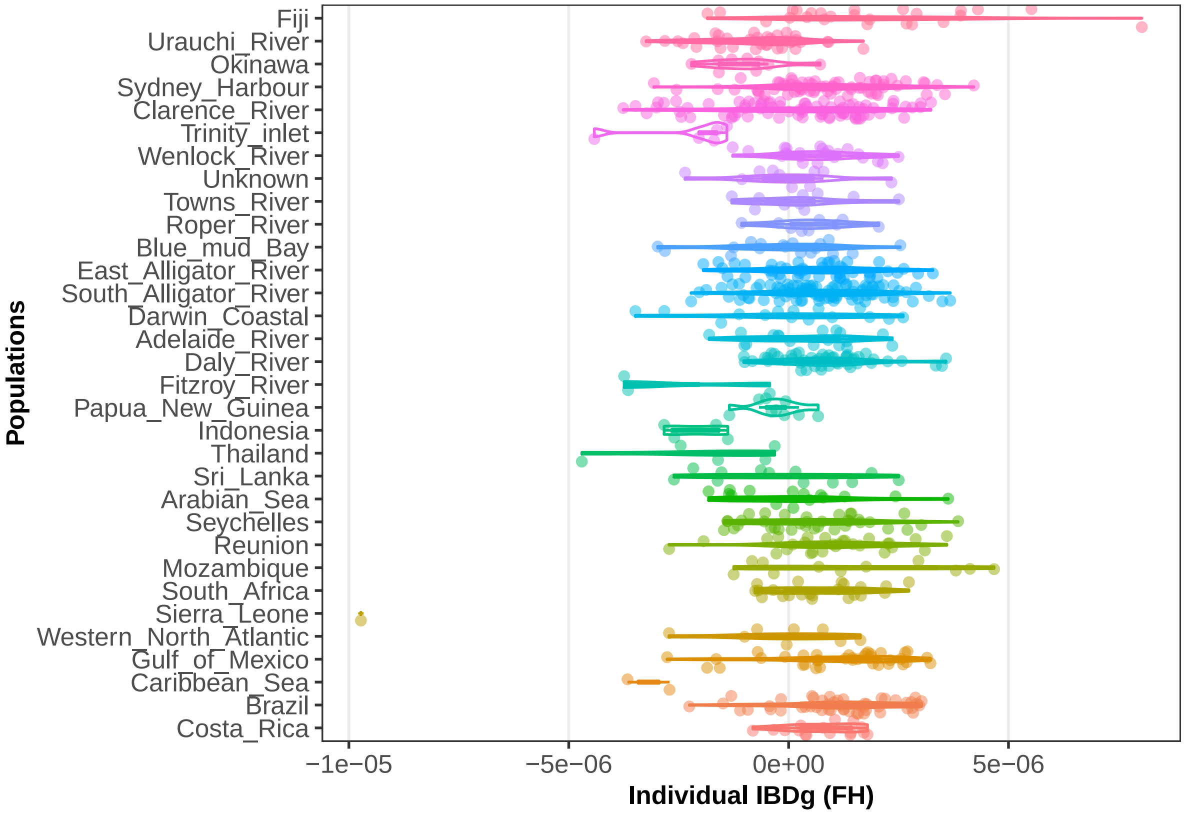
```r
pi.sum <- radiator::pi(
  data = BS.dartseq.baits.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartseq.baits.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTcap_ALL_baits_pi_FIS_Sites2.Rdata")
```

```r
load("DArTcap_ALL_pi_FIS_Sites2.Rdata")
pi.sum$boxplot.pi
```



6.3.2.2 Nucleotide diversity and inbreeding

```
FIS.sum$fh.box.plot
```



6.3.3 Genetic differentiation

```r
strata <- as.character(BS.dartseq.baits.gt@schemes$Site)
names(strata) <- BS.dartseq.baits.gt@schemes$id
strataG::setStrata(BS.dartseq.baits.gt) <- strata

Fst.gt <- strataG::popStructTest(
    BS.dartseq.baits.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTseq_ALL_baits_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTseq_ALL_baits_FST.txt")
```

```r
load("DArTseq_ALL_baits_FST.Rdata")
kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                               decreasing = TRUE),
                                          -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 3409 DArTseq baits between the all sites",
  longtable = TRUE, booktabs = T) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

Table 9: Pairwise Fst for 3409 DArTseq baits between the all sites

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Gulf of Mexico (11) v. Papua New Guinea (2)	8102.5340	0.0100	0.0101	0.0100	NA	NA	0.6089	0.2041	0.6433	0.2041	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Western North Atlantic (8)	6372.1345	0.0230	0.0103	0.0230	NA	NA	0.5985	0.1917	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Indonesia (4)	9532.0578	0.0030	0.0103	0.0030	NA	NA	0.5965	0.0043	0.6344	0.0043	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Thailand (4)	9686.5999	0.0020	0.0104	0.0020	NA	NA	0.5960	0.0026	0.6339	0.0026	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Sri Lanka (4)	9509.0294	0.0040	0.0100	0.0040	NA	NA	0.5872	0.0059	0.6231	0.0059	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Western North Atlantic (8)	7763.2194	0.0030	0.0104	0.0030	NA	NA	0.5870	0.0041	0.6357	0.0041	NA	NA	NA	NA	NA	NA
Brazil (11) v. Indonesia (4)	9236.5349	0.0020	0.0101	0.0020	NA	NA	0.5842	0.0023	0.6223	0.0023	NA	NA	NA	NA	NA	NA
Thailand (4) v. Western North Atlantic (8)	7829.6372	0.0060	0.0104	0.0060	NA	NA	0.5842	0.0078	0.6334	0.0083	NA	NA	NA	NA	NA	NA
Brazil (11) v. Thailand (4)	9378.6255	0.0010	0.0101	0.0010	NA	NA	0.5828	0.0012	0.6208	0.0012	NA	NA	NA	NA	NA	NA
Japan (11) v. Western North Atlantic (8)	12623.2524	0.0010	0.0116	0.0010	NA	NA	0.5824	0.0010	0.6272	0.0010	NA	NA	NA	NA	NA	NA
Brazil (11) v. Japan (11)	14386.7049	0.0010	0.0112	0.0010	NA	NA	0.5807	0.0010	0.6242	0.0010	NA	NA	NA	NA	NA	NA
Sri Lanka (4) v. Western North Atlantic (8)	7713.8626	0.0030	0.0100	0.0030	NA	NA	0.5763	0.0047	0.6248	0.0053	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Gulf of Mexico (11)	10961.0694	0.0010	0.0101	0.0010	NA	NA	0.5759	0.0010	0.6230	0.0011	NA	NA	NA	NA	NA	NA
Fiji (8) v. Gulf of Mexico (11)	12403.9837	0.0010	0.0107	0.0010	NA	NA	0.5750	0.0010	0.6222	0.0010	NA	NA	NA	NA	NA	NA
Brazil (11) v. Sri Lanka (4)	9218.8942	0.0010	0.0098	0.0010	NA	NA	0.5739	0.0014	0.6099	0.0014	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Reunion (9)	13151.6388	0.0010	0.0108	0.0010	NA	NA	0.5708	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Seychelles (10)	13436.3933	0.0010	0.0104	0.0010	NA	NA	0.5684	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Mozambique (8)	11723.3601	0.0010	0.0103	0.0010	NA	NA	0.5680	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. Fiji (8)	12117.7180	0.0010	0.0105	0.0010	NA	NA	0.5640	0.0010	0.6163	0.0010	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Brazil (11)	10647.2547	0.0010	0.0098	0.0010	NA	NA	0.5639	0.0010	0.6109	0.0011	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Western North Atlantic (8)	9079.0498	0.0010	0.0102	0.0010	NA	NA	0.5639	0.0011	0.6112	0.0011	NA	NA	NA	NA	NA	NA
Fiji (8) v. Western North Atlantic (8)	10387.0276	0.0020	0.0108	0.0020	NA	NA	0.5629	0.0025	0.6101	0.0025	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Papua New Guinea (2)	2790.0714	0.3467	0.0099	0.3467	NA	NA	0.5614	0.3467	0.6059	0.3467	NA	NA	NA	NA	NA	NA
Brazil (11) v. Reunion (9)	12855.1300	0.0010	0.0106	0.0010	NA	NA	0.5601	0.0010	0.6077	0.0010	NA	NA	NA	NA	NA	NA
Reunion (9) v. Western North Atlantic (8)	11106.9875	0.0010	0.0109	0.0010	NA	NA	0.5593	0.0010	0.6058	0.0010	NA	NA	NA	NA	NA	NA
Brazil (11) v. Seychelles (10)	13186.7411	0.0010	0.0102	0.0010	NA	NA	0.5580	0.0010	0.6036	0.0010	NA	NA	NA	NA	NA	NA
Seychelles (10) v. Western North Atlantic (8)	11468.7198	0.0010	0.0105	0.0010	NA	NA	0.5580	0.0010	0.6030	0.0010	NA	NA	NA	NA	NA	NA
Brazil (11) v. Mozambique (8)	11470.4265	0.0010	0.0101	0.0010	NA	NA	0.5572	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. South Africa (9)	12589.1098	0.0010	0.0099	0.0010	NA	NA	0.5559	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Western North Atlantic (8)	9811.4527	0.0030	0.0104	0.0030	NA	NA	0.5557	0.0031	0.6040	0.0031	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Indonesia (4)	3907.0225	0.0609	0.0102	0.0609	NA	NA	0.5553	1.0000	NA	NA	NA	NA	NA	NA	NA	NA
South Africa (9) v. Western North Atlantic (8)	10865.6475	0.0010	0.0101	0.0010	NA	NA	0.5550	0.0010	0.6007	0.0010	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Thailand (4)	3880.0798	0.0689	0.0101	0.0689	NA	NA	0.5384	0.3670	0.5877	0.5433	NA	NA	NA	NA	NA	NA
Australia (34) v. Gulf of Mexico (11)	26372.2394	0.0010	0.0104	0.0010	NA	NA	0.5380	0.0010	0.5800	0.0010	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Sri Lanka (4)	3833.6746	0.0749	0.0097	0.0749	NA	NA	0.5343	0.1820	0.5785	0.5474	NA	NA	NA	NA	NA	NA
Australia (34) v. Western North Atlantic (8)	24019.0389	0.0010	0.0105	0.0010	NA	NA	0.5321	0.0011	0.5738	0.0011	NA	NA	NA	NA	NA	NA
Australia (34) v. Brazil (11)	25908.7124	0.0010	0.0102	0.0010	NA	NA	0.5298	0.0010	0.5714	0.0010	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Seychelles (10)	6931.6802	0.0120	0.0101	0.0120	NA	NA	0.5239	0.1121	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Fiji (8)	5943.5605	0.0230	0.0105	0.0230	NA	NA	0.5210	0.2771	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Caribbean Sea (2)	4912.1344	0.0390	0.0098	0.0390	NA	NA	0.5185	0.1418	0.5600	0.1418	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Reunion (9)	6511.0696	0.0170	0.0105	0.0170	NA	NA	0.5178	0.4146	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Mozambique (8)	5511.7323	0.0170	0.0101	0.0170	NA	NA	0.5124	1.0000	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Caribbean Sea (2)	17826.7556	0.0030	0.0102	0.0030	NA	NA	0.5097	0.2727	0.5486	0.2727	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Sierra Leone (1)	869.8667	0.3327	0.0008	0.3327	NA	NA	0.1103	0.3327	0.1184	0.3327	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Japan (11)	1900.8212	0.0010	0.0004	0.0010	NA	NA	0.0777	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (8) v. Japan (11)	2290.7442	0.0010	0.0003	0.0010	-23.8431	1.0000	0.0641	0.0010	0.0698	0.0011	0.4458	0.0012	0.4713	0.0012	0.6343	0.0012
Fiji (8) v. Indonesia (4)	1659.3082	0.0020	0.0004	0.0020	NA	NA	0.0595	0.0021	0.0647	0.0021	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Papua New Guinea (2)	1051.8778	0.2108	0.0005	0.2108	NA	NA	0.0537	0.1734	0.0579	0.1734	NA	NA	NA	NA	NA	NA
Japan (11) v. Sri Lanka (4)	1678.9484	0.0010	0.0003	0.0140	NA	NA	0.0492	0.0050	0.0529	0.0053	NA	NA	NA	NA	NA	NA
Japan (11) v. Thailand (4)	1683.9072	0.0030	0.0003	0.0080	NA	NA	0.0468	0.0150	0.0504	0.0164	NA	NA	NA	NA	NA	NA
Japan (11) v. Mozambique (8)	1958.8523	0.0010	0.0003	0.0010	NA	NA	0.0462	0.0010	0.0523	0.0012	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Thailand (4)	1197.2271	0.0559	0.0003	0.1469	13.5058	0.9760	0.0458	0.0559	0.0498	0.0559	29.4957	0.0345	25.9063	0.0345	1.8167	0.0345
Japan (11) v. Papua New Guinea (2)	1417.8562	0.0430	0.0004	0.0659	NA	NA	0.0432	0.0994	0.0464	0.0994	NA	NA	NA	NA	NA	NA

Table 9: Pairwise Fst for 3409 DArTseq baits between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Japan (11) v. South Africa (9)	2001.5867	0.0010	0.0002	0.0010	NA	NA	0.0405	0.0010	0.0442	0.0019	NA	NA	NA	NA	NA	NA
Fiji (8) v. Seychelles (10)	2046.0674	0.0020	0.0002	0.0030	-21.7300	1.0000	0.0395	0.0021	0.0434	0.0021	0.4257	0.0021	0.4515	0.0021	0.6152	0.0021
Arabian Sea (6) v. Japan (11)	1790.6767	0.0010	0.0002	0.0010	NA	NA	0.0381	0.0010	0.0415	0.0019	NA	NA	NA	NA	NA	NA
Japan (11) v. Reunion (9)	2005.6853	0.0010	0.0003	0.0010	-20.2818	0.9955	0.0374	0.0011	0.0409	0.0011	0.3750	0.0022	0.3999	0.0022	0.5636	0.0022
Japan (11) v. Seychelles (10)	2009.7485	0.0010	0.0002	0.0010	NA	NA	0.0360	0.0010	0.0393	0.0012	NA	NA	NA	NA	NA	NA
Fiji (8) v. Mozambique (8)	1891.5201	0.0010	0.0003	0.0010	-34.8132	0.9978	0.0358	0.0010	0.0413	0.0011	0.5894	0.0011	0.6124	0.0011	0.7561	0.0011
Indonesia (4) v. Mozambique (8)	1451.4379	0.0270	0.0003	0.0509	NA	NA	0.0344	0.0183	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (8) v. Thailand (4)	1527.9697	0.0070	0.0003	0.0090	NA	NA	0.0336	0.0078	0.0365	0.0079	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Seychelles (10)	1509.6262	0.0150	0.0003	0.0170	NA	NA	0.0333	0.0101	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Fiji (8)	3012.8187	0.0010	0.0002	0.0010	-9.1806	0.9909	0.0328	0.0013	0.0357	0.0013	0.1827	0.0013	0.2022	0.0013	0.3254	0.0013
Fiji (8) v. Sri Lanka (4)	1519.3088	0.0060	0.0003	0.0060	NA	NA	0.0325	0.0063	0.0352	0.0069	NA	NA	NA	NA	NA	NA
Australia (34) v. Japan (11)	2806.5855	0.0010	0.0002	0.0010	-9.1646	1.0000	0.0324	0.0010	0.0350	0.0010	0.1477	0.0015	0.1638	0.0015	0.2714	0.0015
Fiji (8) v. South Africa (9)	1921.1801	0.0010	0.0002	0.0010	NA	NA	0.0307	0.0010	0.0338	0.0011	NA	NA	NA	NA	NA	NA
Fiji (8) v. Reunion (9)	1952.9401	0.0010	0.0002	0.0010	-22.7665	1.0000	0.0306	0.0010	0.0338	0.0010	0.4456	0.0010	0.4716	0.0010	0.6345	0.0010
Indonesia (4) v. Sri Lanka (4)	1130.9851	0.1888	0.0002	0.1588	NA	NA	0.0294	0.1588	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Indonesia (4)	2314.2974	0.0010	0.0002	0.0010	NA	NA	0.0280	0.0011	0.0302	0.0011	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Indonesia (4)	1292.8201	0.0839	0.0003	0.0859	NA	NA	0.0262	0.0967	0.0285	0.1067	NA	NA	NA	NA	NA	NA
Indonesia (4) v. South Africa (9)	1474.5715	0.0270	0.0002	0.1409	81.9077	0.9967	0.0260	0.0142	0.0288	0.0153	1.2958	0.0077	1.2727	0.0077	1.1188	0.0077
Arabian Sea (6) v. Fiji (8)	1629.1213	0.0020	0.0002	0.0040	-57.6854	0.9706	0.0217	0.0020	0.0243	0.0025	0.7147	0.0240	0.7322	0.0240	0.8438	0.0240
Sri Lanka (4) v. Thailand (4)	1107.5346	0.0210	0.0002	0.0849	NA	NA	0.0124	0.0839	0.0135	0.0591	NA	NA	NA	NA	NA	NA
Australia (34) v. Mozambique (8)	2276.3729	0.0060	0.0001	0.5115	-10.0857	1.0000	0.0120	0.0018	0.0132	0.0018	0.2040	0.0018	0.2242	0.0018	0.3556	0.0018
Mozambique (8) v. South Africa (9)	1594.8721	0.0260	0.0002	0.0150	NA	NA	0.0086	0.0270	0.0095	0.0227	NA	NA	NA	NA	NA	NA
Australia (34) v. Sri Lanka (4)	2030.6818	0.1818	0.0001	0.6024	-18.2684	0.7222	0.0078	0.0812	0.0084	0.0812	0.4224	0.3137	0.4472	0.3235	0.6114	0.3235
South Africa (9) v. Sri Lanka (4)	1397.1209	0.1329	0.0002	0.0100	NA	NA	0.0076	0.1418	NA	NA	NA	NA	NA	NA	NA	NA
Seychelles (10) v. Sri Lanka (4)	1374.9997	0.1209	0.0002	0.2158	NA	NA	0.0071	0.1636	0.0076	0.1604	NA	NA	NA	NA	NA	NA
Reunion (9) v. Seychelles (10)	1565.7084	0.0759	0.0001	0.0220	-19.6474	0.7569	0.0067	0.0921	0.0074	0.0921	0.3668	0.1410	0.3917	0.1398	0.5550	0.1398
Caribbean Sea (2) v. Gulf of Mexico (11)	981.1163	0.0869	0.0001	0.3277	NA	NA	0.0062	0.2432	NA	NA	NA	NA	NA	NA	NA	NA
Seychelles (10) v. South Africa (9)	1590.4783	0.0929	0.0001	0.0040	NA	NA	0.0056	0.1139	0.0061	0.1196	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Sri Lanka (4)	1294.3686	0.3127	0.0002	0.1419	NA	NA	0.0056	0.2304	0.0060	0.2382	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Seychelles (10)	1553.9683	0.1269	0.0001	0.4156	NA	NA	0.0042	0.1998	0.0046	0.2159	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Thailand (4)	1279.2778	0.4456	0.0002	0.2358	NA	NA	0.0039	0.2745	0.0043	0.2714	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Western North Atlantic (8)	1150.4714	0.1019	0.0000	0.1349	NA	NA	0.0039	0.1556	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Reunion (9)	2090.7826	0.1758	0.0001	0.2268	-8.9360	0.1864	0.0036	0.0833	0.0040	0.0833	0.1479	0.3111	0.1644	0.2853	0.2721	0.2995
Seychelles (10) v. Thailand (4)	1308.7435	0.3596	0.0002	0.1928	NA	NA	0.0036	0.2876	0.0039	0.3096	NA	NA	NA	NA	NA	NA
Brazil (11) v. Western North Atlantic (8)	1174.3975	0.1608	0.0000	0.3377	NA	NA	0.0027	0.2397	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. South Africa (9)	2305.7262	0.0030	0.0001	0.0849	NA	NA	0.0025	0.1309	0.0027	0.1310	NA	NA	NA	NA	NA	NA
Australia (34) v. Seychelles (10)	2176.7156	0.0420	0.0001	0.0350	-8.6955	0.9422	0.0020	0.1359	0.0022	0.1361	0.1355	0.0766	0.1507	0.0797	0.2521	0.0797
Reunion (9) v. Sri Lanka (4)	1309.9356	0.3127	0.0002	0.1638	123.7838	0.6395	0.0016	0.3636	0.0018	0.3636	1.1848	0.3416	1.1707	0.3416	1.0781	0.3416
Australia (34) v. Thailand (4)	1935.2647	0.4885	0.0001	0.6274	NA	NA	0.0008	0.3957	0.0009	0.3951	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Reunion (9)	1478.8841	0.3816	0.0001	0.2977	-29.0749	1.0000	0.0005	0.4842	0.0005	0.4842	0.5147	0.0011	0.5388	0.0011	0.6955	0.0011
Brazil (11) v. Gulf of Mexico (11)	1208.1742	0.2987	0.0000	0.1798	NA	NA	0.0004	0.4380	0.0004	0.4758	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Australia (34)	2043.3687	0.2957	0.0000	0.9960	-11.2122	0.5175	0.0003	0.4555	0.0003	0.4577	0.2357	0.4330	0.2572	0.4412	0.3989	0.4371
Arabian Sea (6) v. South Africa (9)	1424.3239	0.5145	0.0001	0.3057	NA	NA	0.0002	0.4975	0.0003	0.5249	NA	NA	NA	NA	NA	NA
South Africa (9) v. Thailand (4)	1269.4545	0.8352	0.0002	0.4356	106.7048	0.4233	-0.0012	0.5501	-0.0013	0.5501	1.2200	0.5300	1.2033	0.5276	1.0916	0.5264
Caribbean Sea (2) v. Western North Atlantic (8)	805.3188	0.7173	0.0001	0.3816	NA	NA	-0.0015	0.5933	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Sri Lanka (4)	1145.9785	0.8292	0.0002	0.3387	NA	NA	-0.0047	0.7815	-0.0051	0.7753	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Seychelles (10)	1400.2838	0.5425	0.0001	0.9261	NA	NA	-0.0049	0.8142	-0.0054	0.8054	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Reunion (9)	1333.2114	0.6194	0.0001	0.5774	-41.6492	0.3902	-0.0057	0.7993	-0.0063	0.7975	0.6194	0.6545	0.6404	0.6590	0.7779	0.6579
Arabian Sea (6) v. Thailand (4)	1115.7016	0.9660	0.0001	0.9451	NA	NA	-0.0062	0.8847	-0.0067	0.8951	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Mozambique (8)	1279.5434	0.9840	0.0001	0.9720	NA	NA	-0.0107	0.9736	-0.0124	0.9853	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Papua New Guinea (2)	1029.1868	0.8621	0.0003	0.7962	NA	NA	-0.0137	0.9339	-0.0148	0.9339	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Papua New Guinea (2)	1064.4045	0.8751	0.0003	0.6214	NA	NA	-0.0199	1.0000	-0.0216	1.0000	NA	NA	NA	NA	NA	NA
Arabian Sea (6) v. Sierra Leone (1)	1366.8318	0.1439	0.0008	0.3047	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

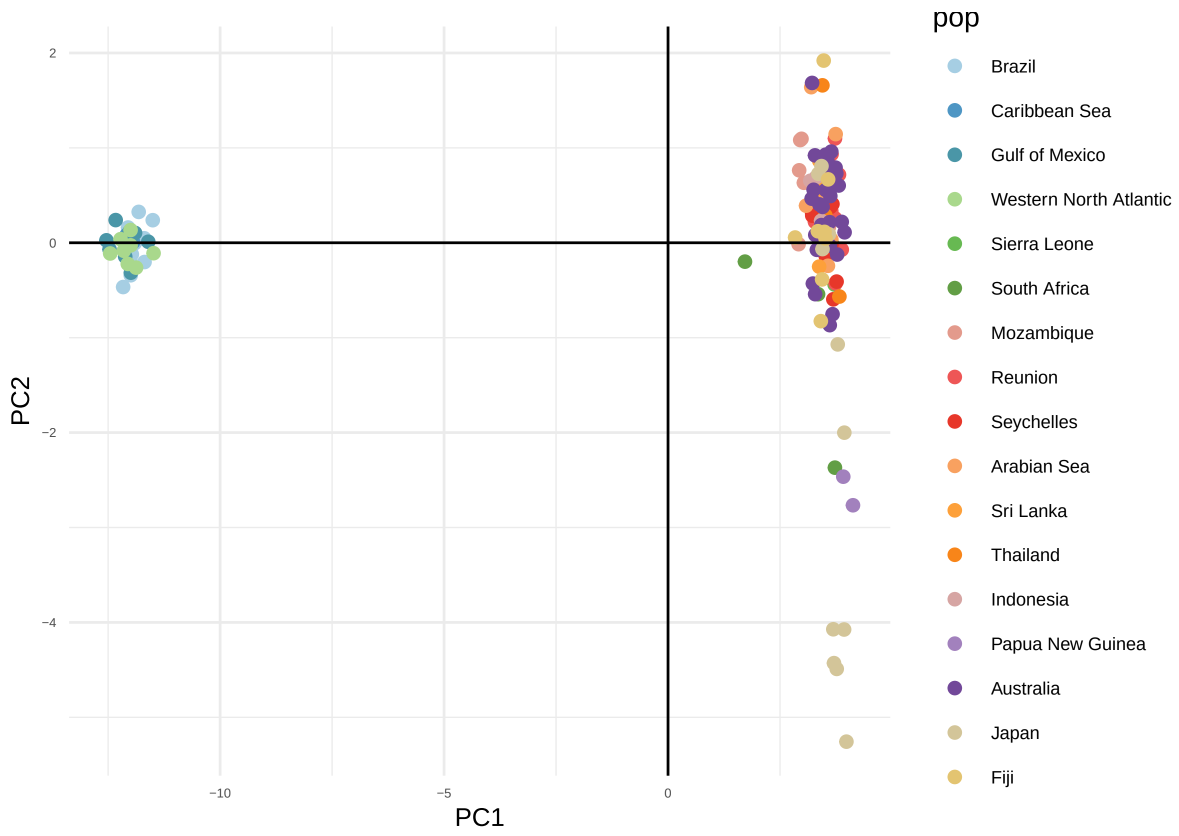
Table 9: Pairwise Fst for 3409 DArTseq baits between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.val
Australia (34) v. Papua New Guinea (2)	1696.0948	0.9181	0.0002	0.7053	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Australia (34) v. Sierra Leone (1)	3623.3691	0.0290	0.0008	0.0290	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. Caribbean Sea (2)	875.3034	0.8432	0.0001	0.4276	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. Papua New Guinea (2)	7747.9949	0.0130	0.0099	0.0130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Brazil (11) v. Sierra Leone (1)	6002.3001	0.0919	0.0065	0.0919	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Japan (11)	7843.8015	0.0110	0.0112	0.0110	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Sierra Leone (1)	1968.9750	0.3516	0.0064	0.3516	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. South Africa (9)	6487.9082	0.0130	0.0099	0.0130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (8) v. Papua New Guinea (2)	1236.9172	0.2418	0.0004	0.0709	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (8) v. Sierra Leone (1)	1668.9862	0.0879	0.0010	0.0879	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Japan (11)	14700.8676	0.0010	0.0114	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. Sierra Leone (1)	6326.3966	0.0769	0.0065	0.0769	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Gulf of Mexico (11) v. South Africa (9)	12895.7845	0.0010	0.0101	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Reunion (9)	1491.6003	0.0280	0.0003	0.0230	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Sierra Leone (1)	1182.9341	0.2208	0.0008	0.2208	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Japan (11) v. Sierra Leone (1)	2129.3009	0.0879	0.0010	0.0879	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Mozambique (8) v. Sierra Leone (1)	1552.4615	0.1139	0.0009	0.1139	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Reunion (9)	1132.4893	0.8432	0.0003	0.4246	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Seychelles (10)	1233.2102	0.4236	0.0003	0.4216	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. South Africa (9)	1088.8191	0.9790	0.0002	0.9031	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Sri Lanka (4)	906.5828	0.4565	0.0003	0.3187	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Papua New Guinea (2) v. Thailand (4)	899.6582	0.8062	0.0003	0.4665	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Reunion (9) v. Sierra Leone (1)	1677.6190	0.0969	0.0009	0.0969	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Reunion (9) v. South Africa (9)	1586.2125	0.0799	0.0001	0.0160	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Reunion (9) v. Thailand (4)	1307.6413	0.3137	0.0002	0.2308	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Seychelles (10) v. Sierra Leone (1)	1803.8697	0.0859	0.0008	0.0859	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra Leone (1) v. South Africa (9)	1691.0264	0.0929	0.0008	0.0929	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra Leone (1) v. Sri Lanka (4)	1113.7442	0.2068	0.0008	0.2068	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra Leone (1) v. Thailand (4)	1135.4761	0.2068	0.0008	0.2068	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Sierra Leone (1) v. Western North Atlantic (8)	4968.4411	0.1059	0.0066	0.1059	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

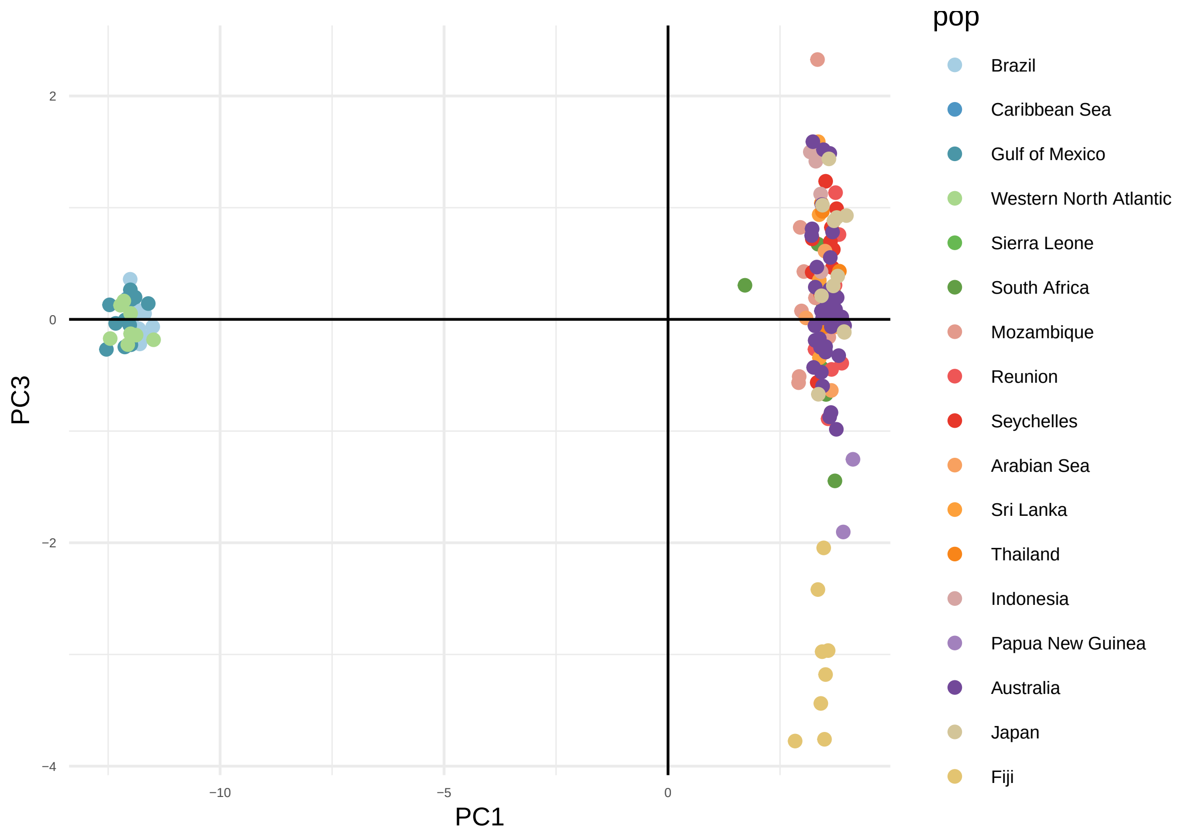
6.3.4 PCA

```r
pca1 <- adegenet::glPca(BS.dartseq.baits.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTseq_ALL_baits_PCA.Rdata")
```

```r
load("DArTseq_ALL_baits_PCA.Rdata")
pop.levels <- c("Costa Rica", "Brazil", "Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")
BS.dartseq.baits.gl$pop <- factor(BS.dartseq.baits.gl$other$ind.metrics$Site,
                                  levels = pop.levels)

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartseq.baits.gl)
cols <- adegenet::funky(nPop(BS.dartseq.baits.gl))


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

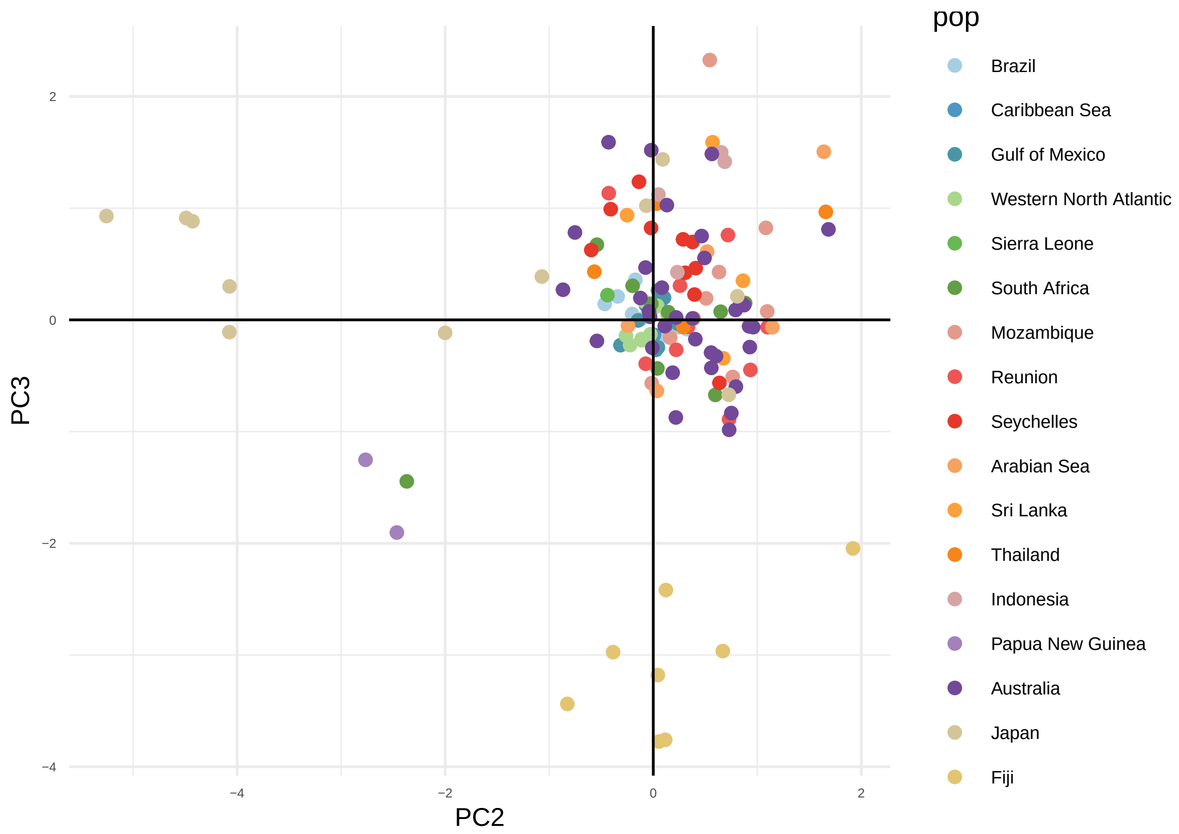


```
ggplot2::ggsave(p, filename = "DArTseq_ALL_baits_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

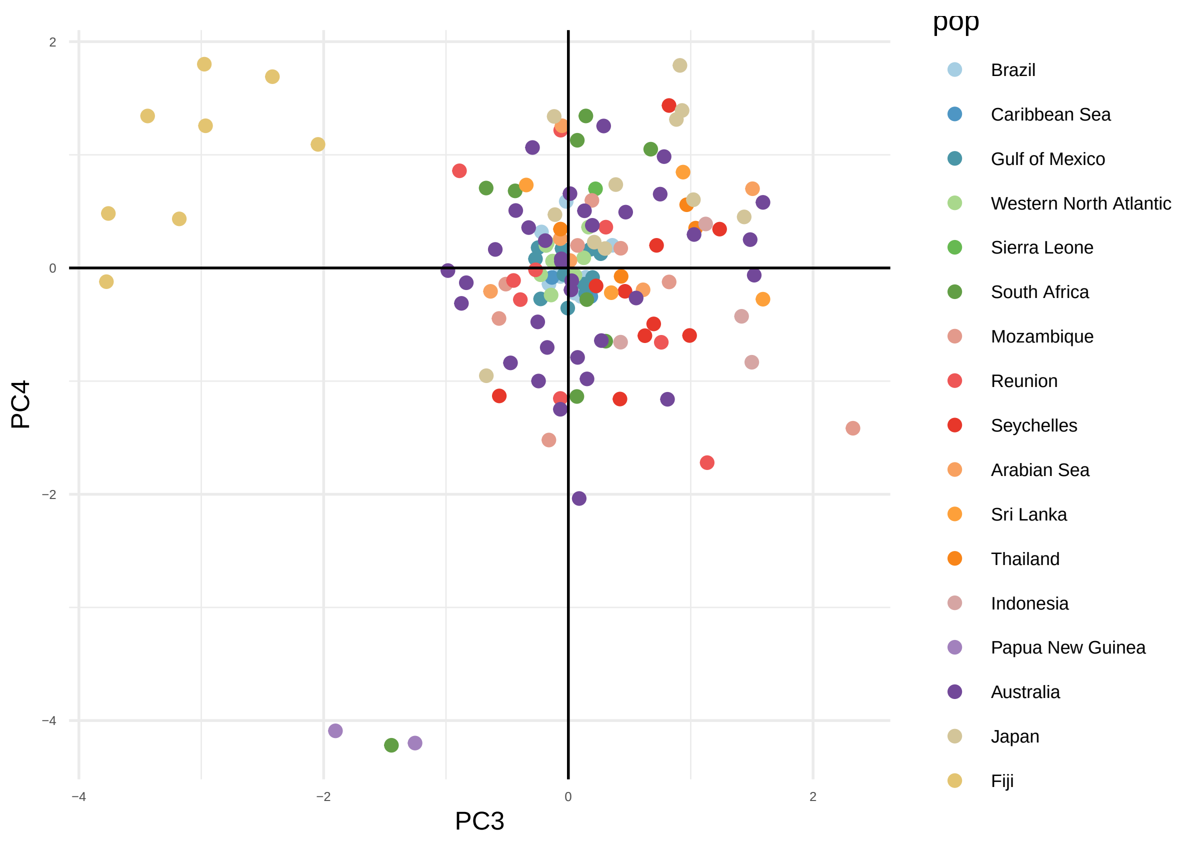


```
ggplot2::ggsave(p, filename = "DArTseq_ALL_baits_PCA2.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
```

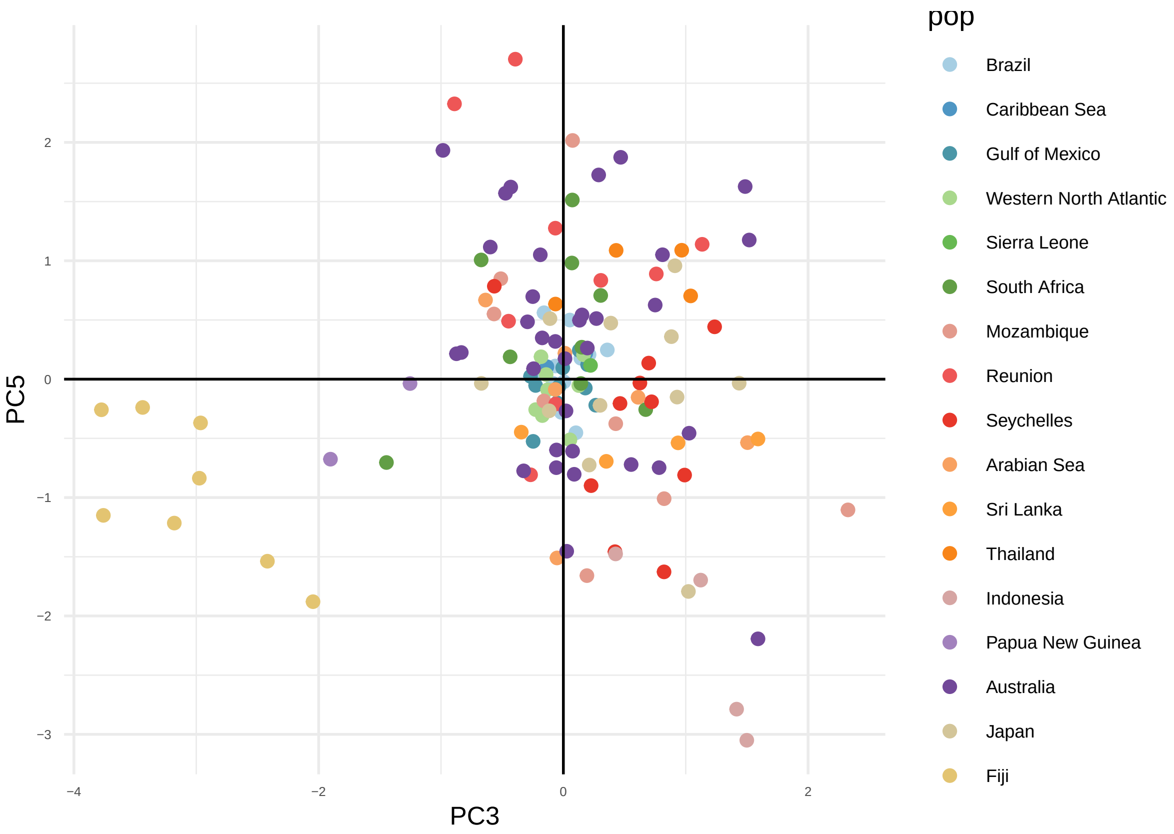
```
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_ALL_baits_PCA3.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_ALL_baits_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTseq_ALL_baits_PCA5.png", width = 30,
                height = 15,units = "cm")
```

---

7 DATA1: DArTcap - All data

5 samples failed library construction

7.1 Set strata

```
targetid <- readr::read_tsv("DArTcap_target_id.tsv")

strata <- readr::read_csv(metafile) %>%
  dplyr::left_join(targetid, by = "INDIVIDUALS") %>%
  dplyr::filter(!is.na(TARGET_ID)) %>%
  dplyr::mutate(STRATA = Site2)
strata$INDIVIDUALS <- with(strata, make.unique(as.character(INDIVIDUALS)))
# readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata.tsv")
```

7.2 Test baiting success

```
baits <- readr::read_tsv("Total_selected_markers.tsv")
```

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata.tsv"
BSsnp <- radiator::read_dart(data = dartcap.data, strata = strata,tidy.dart = TRUE,
                             parallel.core = parallel::detectCores() - 1)
BS.dartcap.raw.tidy <- BSsnp$tidy.data
length(unique(BS.dartcap.raw.tidy$INDIVIDUALS)) #942
length(unique(BS.dartcap.raw.tidy$MARKERS)) #19549
save(BSsnp, file = "DArTcap_Raw_tidy.Rdata")
sum(unique(baits$CloneID) %in% unique(BS.dartcap.raw.tidy$LOCUS)) #453
```

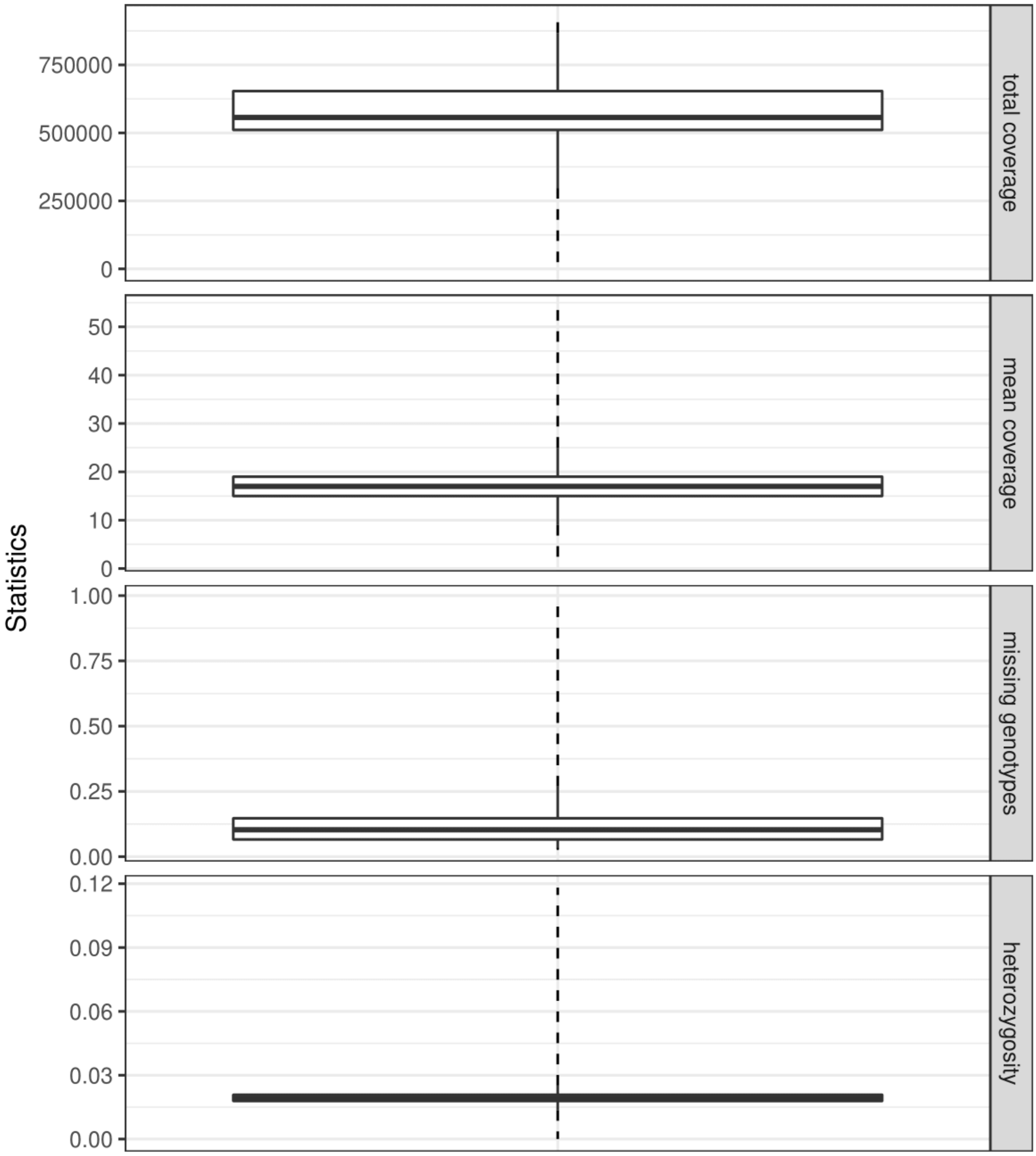
7.3 Find sex-linked markers

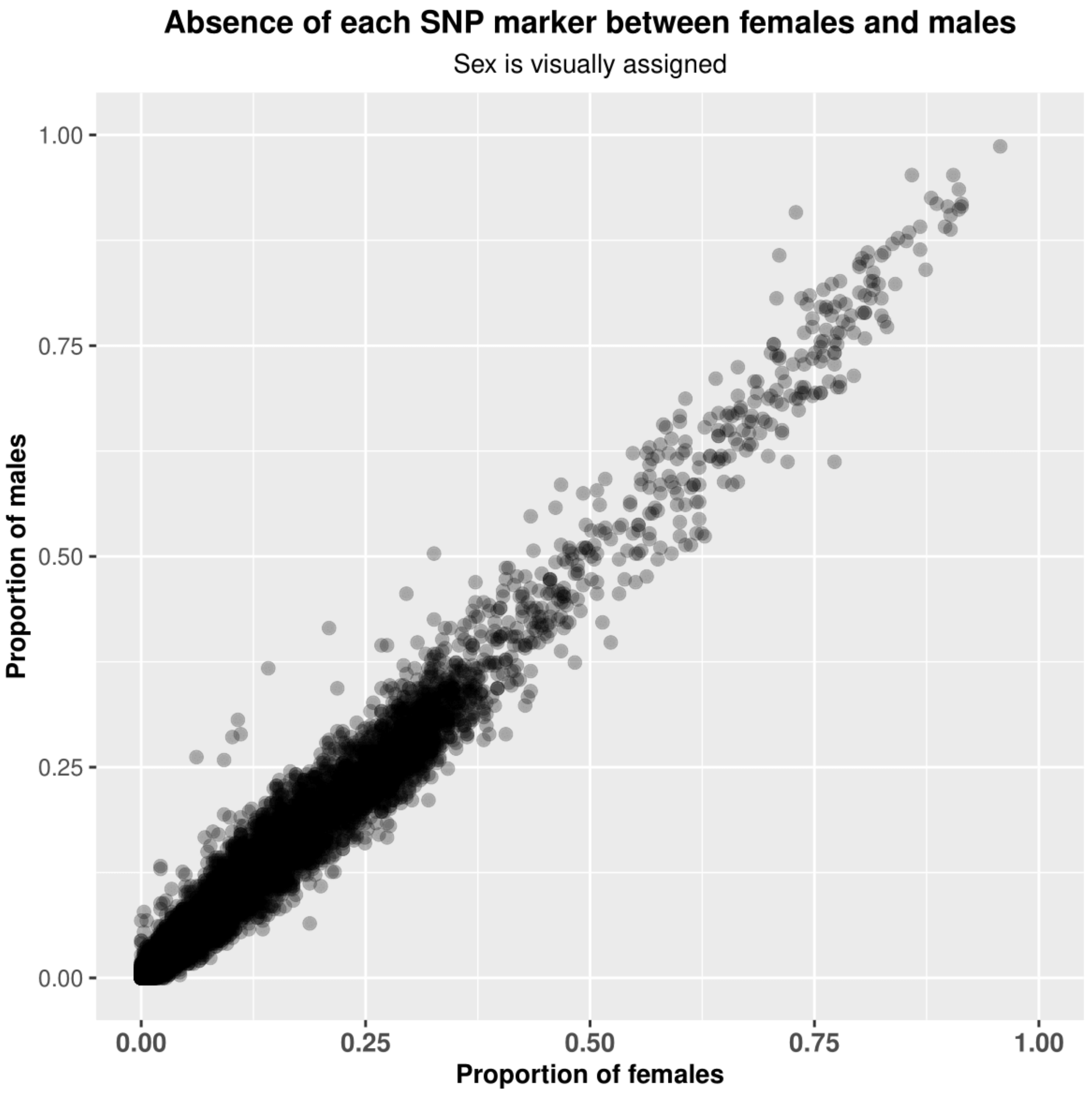
```
data <- "SEQ_SNPs_counts_0_Target_merge.csv"
silicodata <- NULL
strata <- radiator::read_strata("Bull_shark_DArTcap_strata.tsv",
                                keep.two = FALSE)$strata
strata %<>% dplyr::rename(POP = "STRATA") %>%
  dplyr::rename(STRATA = "Sex")

sex.results <- radiator::sexy_markers(
  data = data,
  silicodata = silicodata,
  strata = strata,
  interactive.filter = TRUE)
```

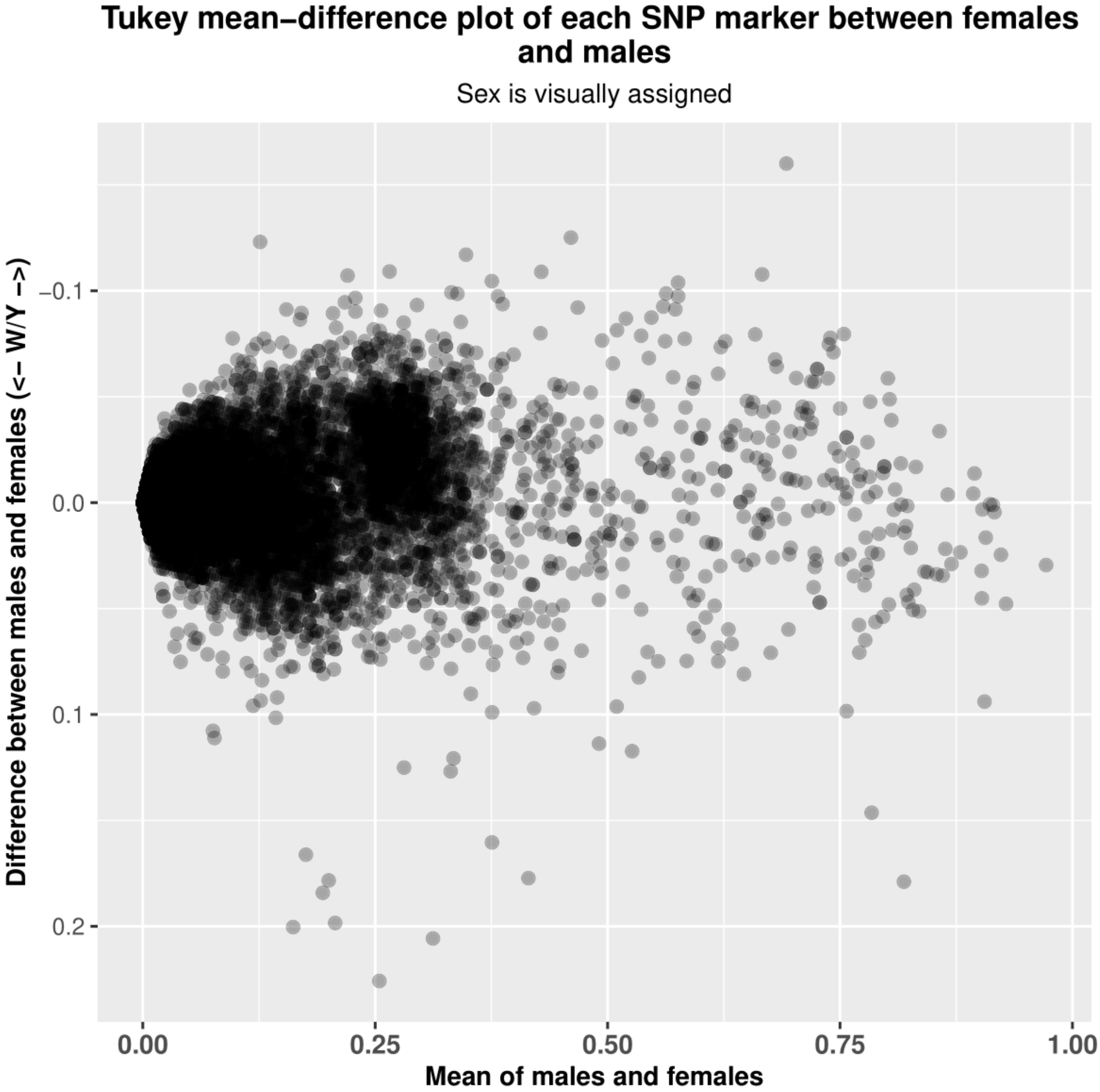
Individual's QC stats

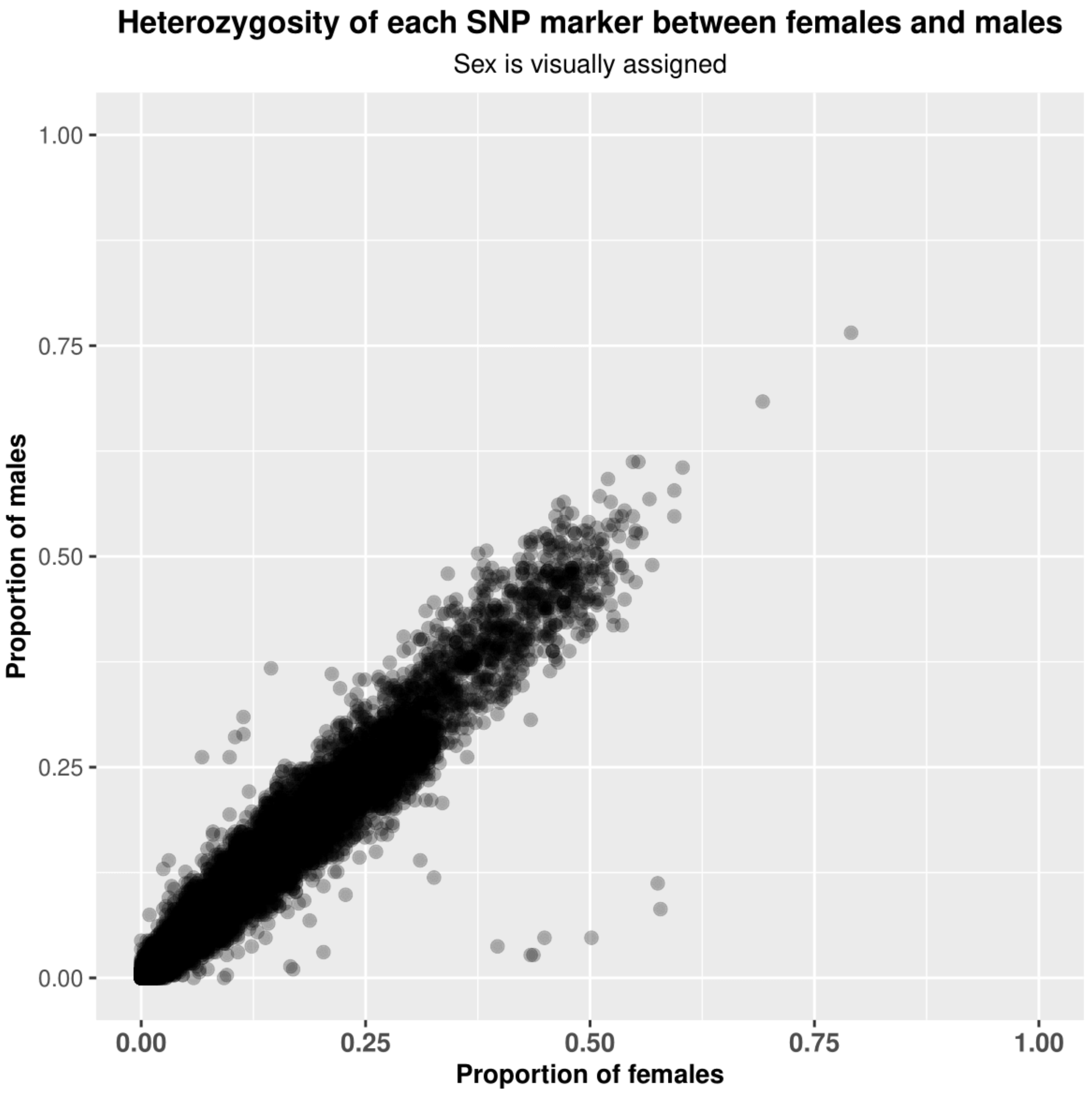
Missing genotypes outlier: 0.26892325
n. het markers in the bp range = 4435
n. het markers in the bp IQR = 109

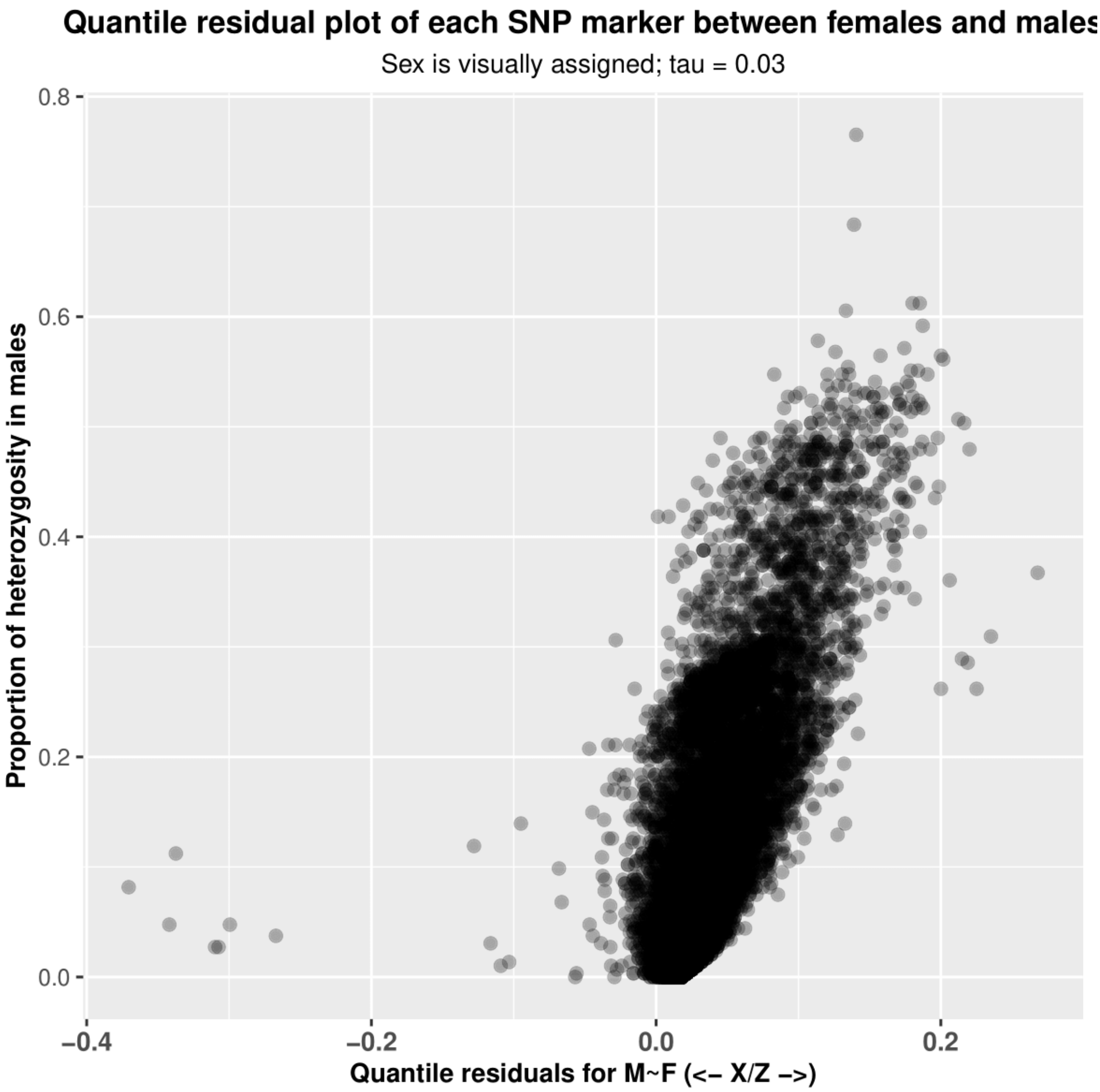
Correlations:
total coverage & missing = −0.02
total coverage & mean coverage = 0.82
total coverage & heterozygosity = 0.03
missing & heterozygosity = −0.14

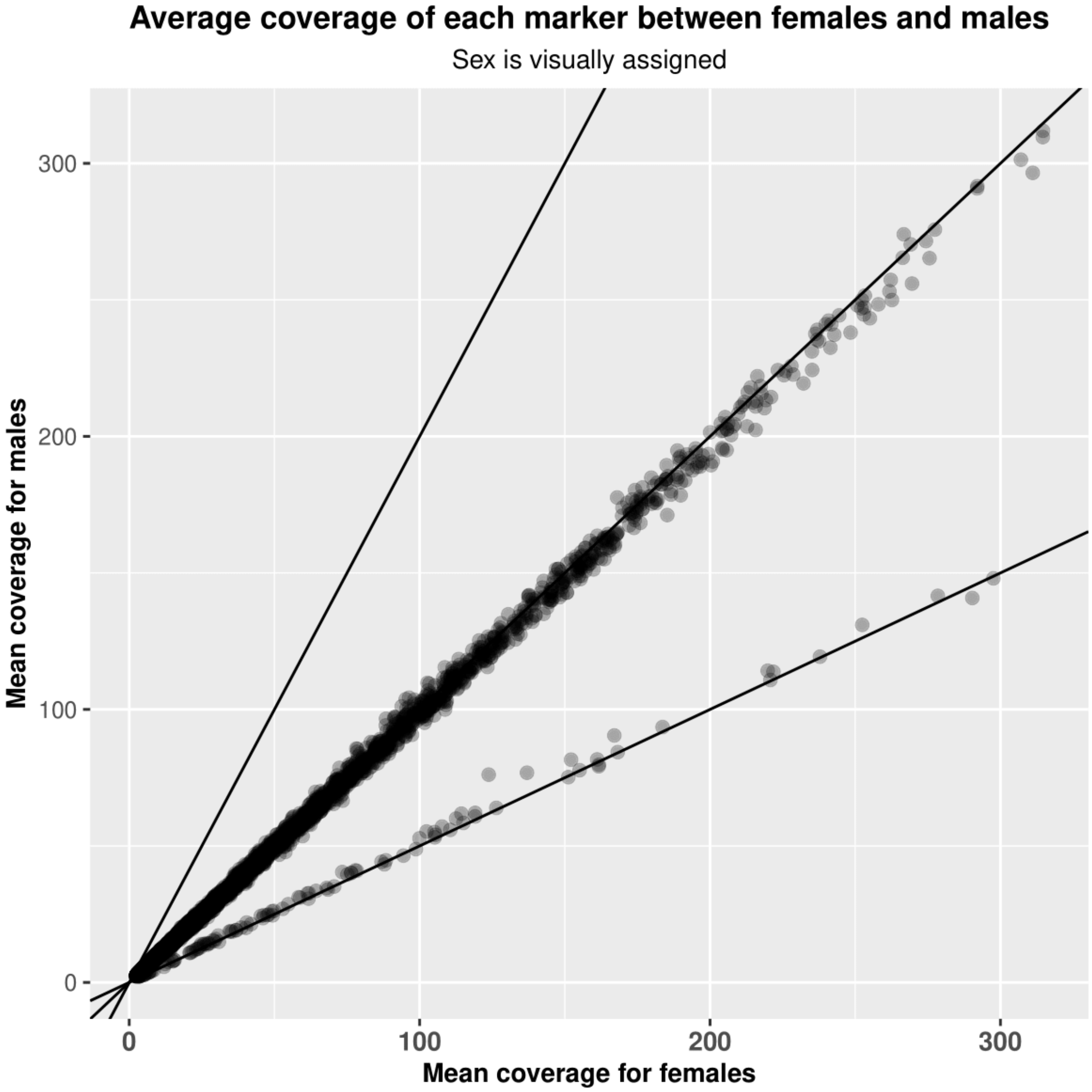


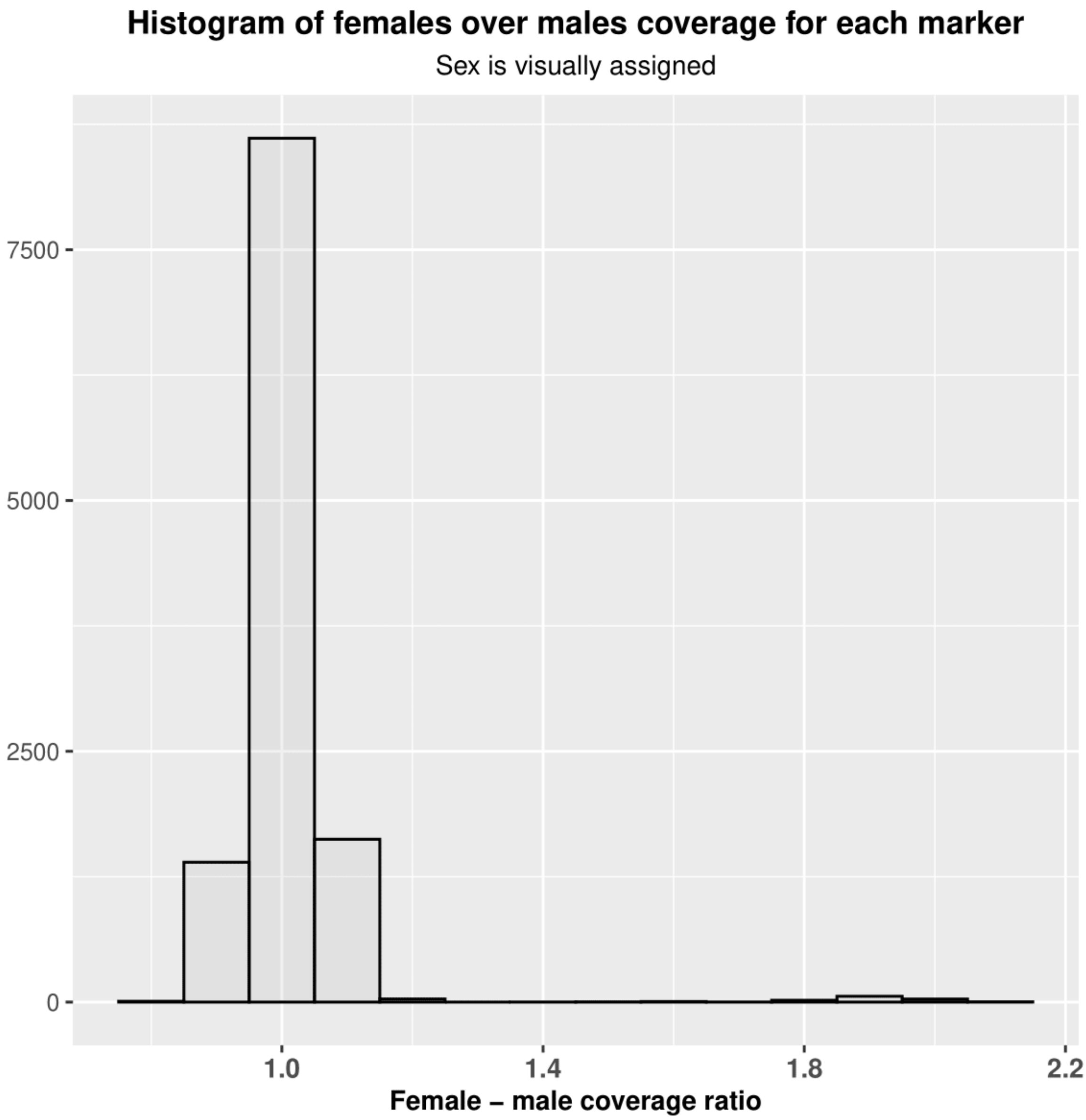

Absence of each SNP marker between females and males
Sex is visually assigned
Proportion of males
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
Proportion of females

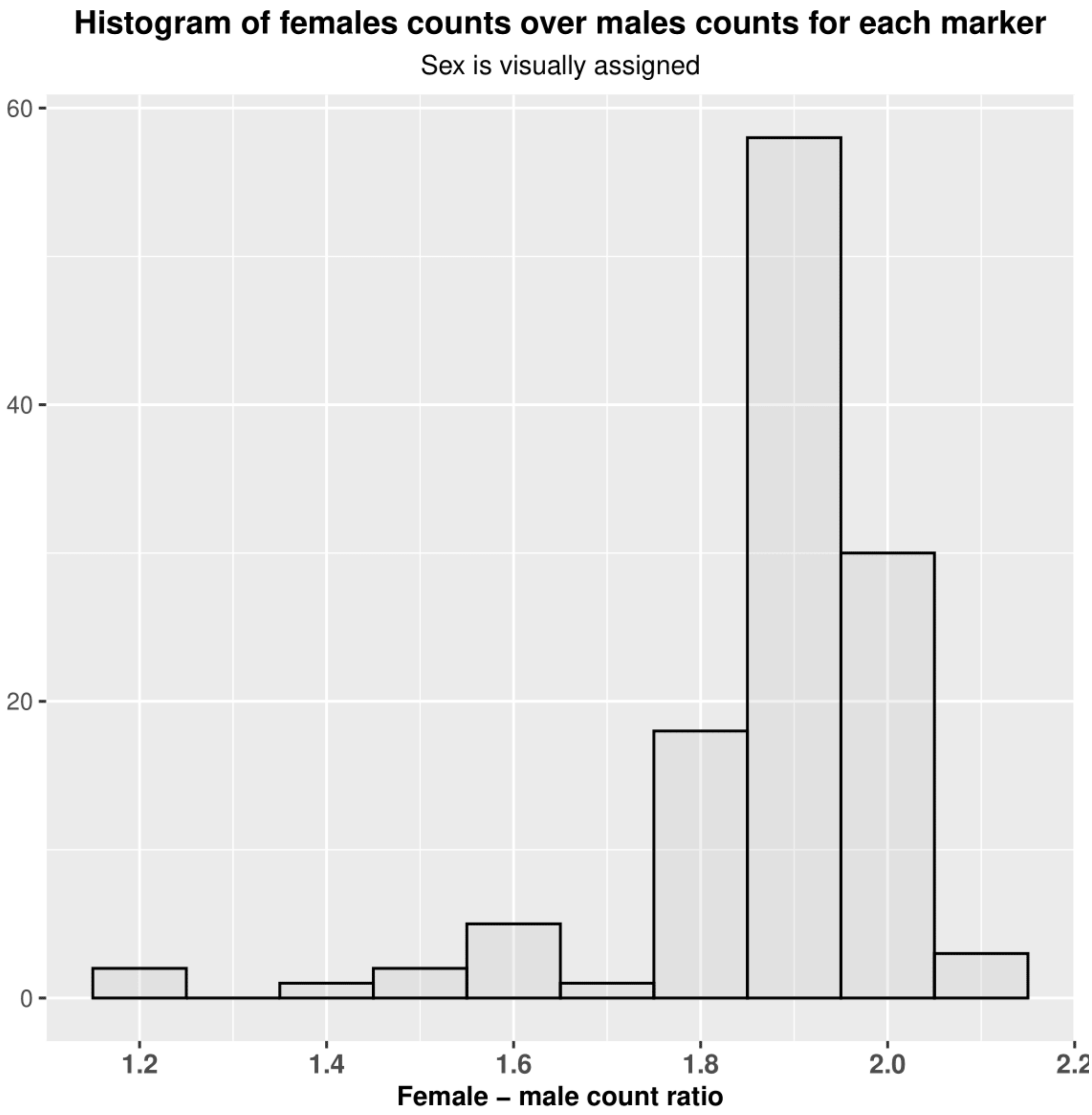

Tukey mean−difference plot of each SNP marker between females and males
Sex is visually assigned
Difference between males and females (<− W/Y −>)
−0.1
0.0
0.1
0.2
0.00
0.25
0.50
0.75
1.00
Mean of males and females

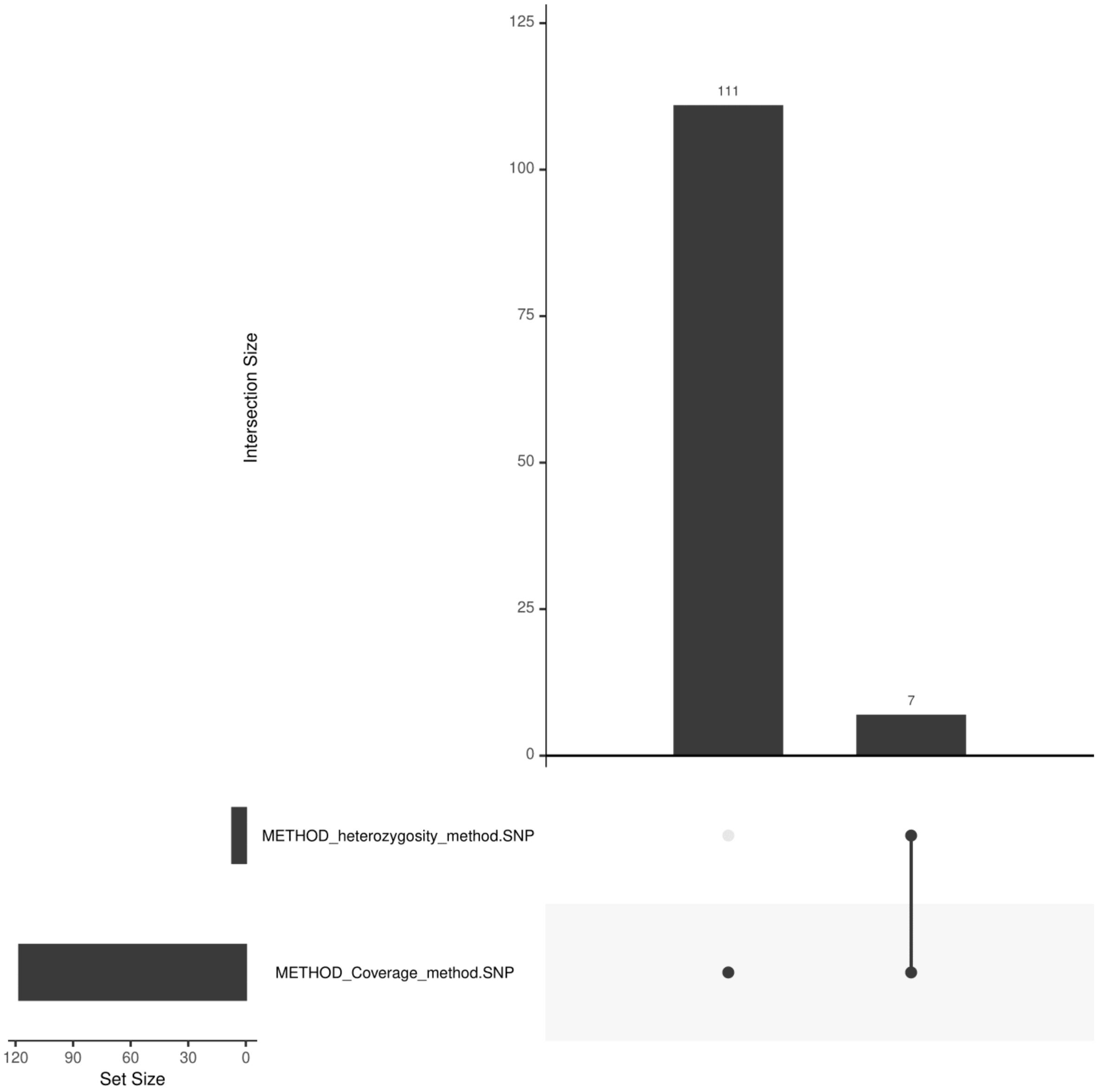

Heterozygosity of each SNP marker between females and males
Sex is visually assigned
Proportion of males
1.00
0.75
0.50
0.25
0.00
0.00
0.25
0.50
0.75
1.00
Proportion of females


Quantile residual plot of each SNP marker between females and males
Sex is visually assigned; tau = 0.03
Proportion of heterozygosity in males
0.8
0.6
0.4
0.2
0.0
−0.4
−0.2
0.0
0.2
Quantile residuals for M~F (<− X/Z −>)


Average coverage of each marker between females and males
Sex is visually assigned
Mean coverage for males
Mean coverage for females
0
100
200
300
0
100
200
300


Histogram of females over males coverage for each marker
Sex is visually assigned
7500
5000
2500
0
1.0
1.4
1.8
2.2
Female – male coverage ratio


Histogram of females counts over males counts for each marker
Sex is visually assigned
60
40
20
0
1.2
1.4
1.6
1.8
2.0
2.2
Female – male count ratio



7.4 Filter data

1. `Marker Reproducibility: 0.98`
2. `Individual missingness: 0.75•`
3. `Individual Het - low: n`
4. `Individual Het - high: n`
5. `Individual total coverage - low: 10,000`
6. `Individual total coverage - high: 1,000,000`
7. `Marker MAC - low: 4`
8. `Marker coverage - low: 4`
9. `Marker coverage - high:33`
10. `Marker maximum missing proportion: 0.1`
11. `Marker snp position on locus: n`
12. `Max 3 SNPs per locus`
13. `1 SNP per locus according to mac`
14. `no LD filter`
15. `Individual Het - low: n`
16. `Individual Het - high: n`
17. `Duplicated individuals: n`

18. No filter on HWE

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = parallel::detectCores() - 1)

BS.dartcap.SF.gds <- BSsnp$gds
BS.dartcap.SF.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.SF.gds, expand = TRUE, all = TRUE, attribute = TRUE,
      attribute.trim = FALSE)
```

Table 10:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	1014 / 34 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	1014 / 34 / 1 / 25292 / 35287	0 / 0 / 0 / 0 / 0
Filter markers in common	NA	1014 / 34 / 1 / 25292 / 35287	0 / 0 / 0 / 10291 / 17213
Filter individuals based on missingness	0.75	1014 / 34 / 1 / 15001 / 18074	8 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+06	1006 / 34 / 1 / 15001 / 18074	5 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	1001 / 34 / 1 / 15001 / 18074	0 / 0 / 0 / 1306 / 1879
Filter MAC	4	1001 / 34 / 1 / 13695 / 16195	0 / 0 / 0 / 2050 / 3069
Filter coverage min / max	4-33	1001 / 34 / 1 / 11645 / 13126	0 / 0 / 0 / 5384 / 5816
Filter genotyping	0.1	1001 / 34 / 1 / 6261 / 7310	0 / 0 / 0 / 1166 / 1285
Filter SNPs position on the read	all	1001 / 34 / 1 / 5095 / 6025	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	1001 / 34 / 1 / 5095 / 6025	0 / 0 / 0 / 33 / 143
Filter short ld	mac	1001 / 34 / 1 / 5062 / 5882	0 / 0 / 0 / 0 / 820
detect mixed genomes	0 1	1001 / 34 / 1 / 5062 / 5062	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0	1001 / 34 / 1 / 5062 / 5062	0 / 0 / 0 / 0 / 0
Filter HWE	NA	1001 / 34 / 1 / 5062 / 5062	0 / 0 / 0 / 0 / 0

7.5 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.SF.gds,
                                       output = c("genlight", "stockr",
                                                  "pcadapt", "gtypes"))
BS.dartcap.SF.gl <- Convert$genlight
BS.dartcap.SF.stkr <- Convert$stockr
BS.dartcap.SF.pc <- Convert$pcadapt
BS.dartcap.SF.gt <- Convert$gtypes


markers.meta <- radiator::extract_markers_metadata(BS.dartcap.SF.gds, whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.SF.gds, whitelist = TRUE)
BS.dartcap.SF.gl$other$ind.metrics <- individuals.meta
BS.dartcap.SF.gl$other$loc.metrics <- markers.meta
BS.dartcap.SF.gt@schemes <- individuals.meta

pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Fitzroy River",
                "Durack River", "Daly River", "Adelaide River","Darwin Coastal",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour", "Okinawa", "Urauchi River", "Fiji")
BS.dartcap.SF.gl$pop <- factor(BS.dartcap.SF.gl$other$ind.metrics$Site2,
                               levels = pop.levels)
BS.dartcap.SF.gl <- BS.dartcap.SF.gl[order(BS.dartcap.SF.gl$pop,
                                           BS.dartcap.SF.gl$ind.names)]

save(BS.dartcap.SF.tidy, BS.dartcap.SF.gl, BS.dartcap.SF.stkr,
     BS.dartcap.SF.pc,BS.dartcap.SF.gt, markers.meta, individuals.meta,
     file = "DArTcap_ALL_SF_objects.Rdata")
```

7.6 Load data

```
load("DArTcap_ALL_SF_objects.Rdata")
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Fitzroy River",
                "Durack River", "Daly River", "Adelaide River","Darwin Coastal",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour", "Okinawa", "Urauchi River", "Fiji")

BS.dartcap.SF.gl$pop <- factor(BS.dartcap.SF.gl$other$ind.metrics$Site2,
                               levels = pop.levels)
BS.dartcap.SF.gl <- BS.dartcap.SF.gl[order(BS.dartcap.SF.gl$pop,
                                           BS.dartcap.SF.gl$ind.names)]

adegenet::nInd(BS.dartcap.SF.gl) # 1001
adegenet::nLoc(BS.dartcap.SF.gl) # 5065
summary(BS.dartcap.SF.gl$pop)
sum(duplicated(stringr::str_replace_all(pattern = "\\.1", replacement = "",
                                  string =  BS.dartcap.SF.gl$ind.names))) # 79 replicate left
sum(baits$CloneID %in% BS.dartcap.SF.gl$other$loc.metrics$LOCUS) #60
```

```
## [1] 1001
## [1] 5062
##             Costa Rica                 Brazil          Caribbean Sea
##                     34                     60                      2
##         Gulf of Mexico Western North Atlantic           Sierra Leone
##                     52                      9                      1
##           South Africa             Mozambique                Reunion
##                     31                     14                     29
##             Seychelles            Arabian Sea              Sri Lanka
##                     42                     43                     23
##               Thailand              Indonesia       Papua New Guinea
##                      8                      8                     17
##          Fitzroy River           Durack River             Daly River
##                      7                      4                     52
##         Adelaide River         Darwin Coastal  South Alligator River
##                     23                     18                     95
##   East Alligator River           Blue mud Bay            Roper River
##                     55                     18                      9
##            Towns River                Unknown          Wenlock River
##                     13                     12                     32
##          Trinity inlet         Clarence River         Sydney Harbour
##                      5                    123                     78
##                Okinawa          Urauchi River                   Fiji
##                     10                     42                     32
## [1] 79
## [1] 60
```

7.7 Remove sex-linked markers

```
load("Sex_results.Rdata")
sum(BS.dartcap.SF.gl$loc.names %in% bull_shark$sexy.summary$CLONE_ID ) #12
sex.markers <-  bull_shark$sexy.summary$CLONE_ID

locnames <- BS.dartcap.SF.gl$loc.names
```

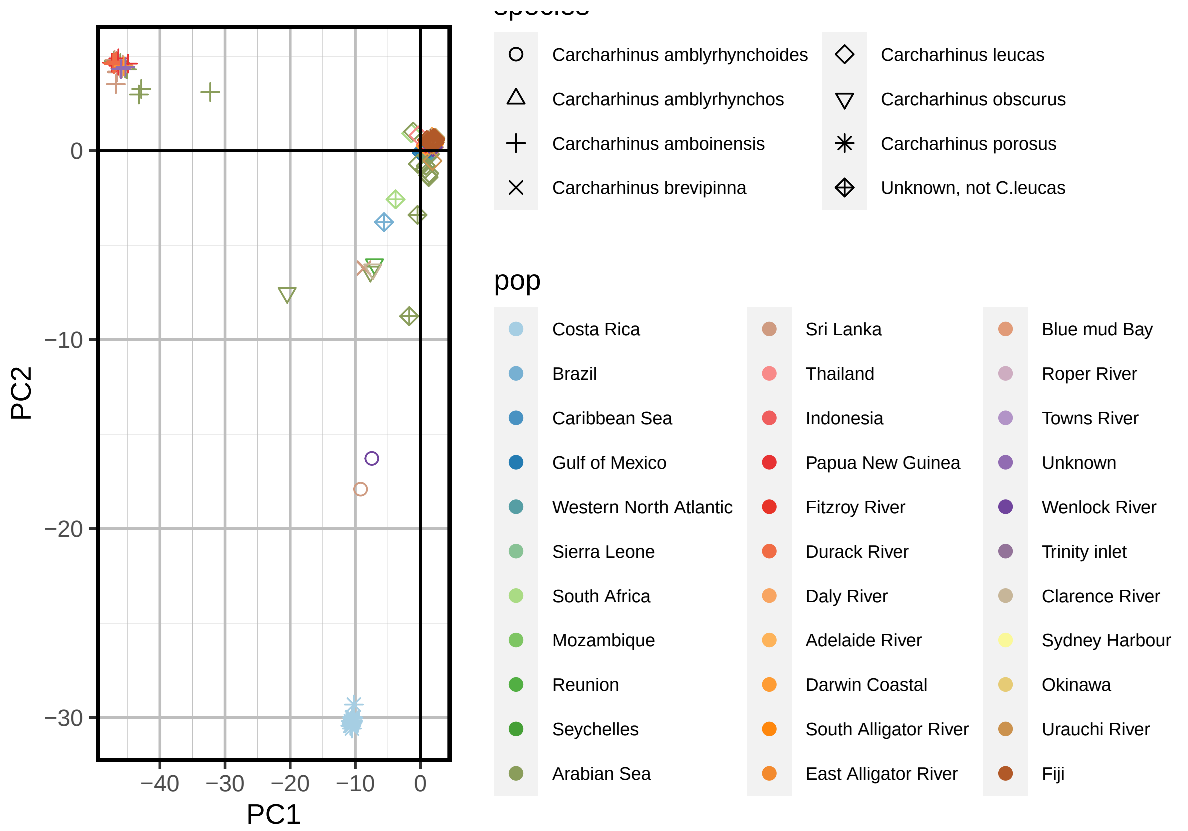
```
BS.dartcap.SF.gl <- BS.dartcap.SF.gl[,!locnames %in% sex.markers]
BS.dartcap.SF.gl$other$loc.metrics <- BS.dartcap.SF.gl$other$loc.metrics[!locnames %in%
                                                                          sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.SF.tidy$LOCUS)) # 12
BS.dartcap.SF.tidy <- BS.dartcap.SF.tidy[!BS.dartcap.SF.tidy$LOCUS %in%
                                           sex.markers,]
```

```
## [1] 12
## [1] 18
```

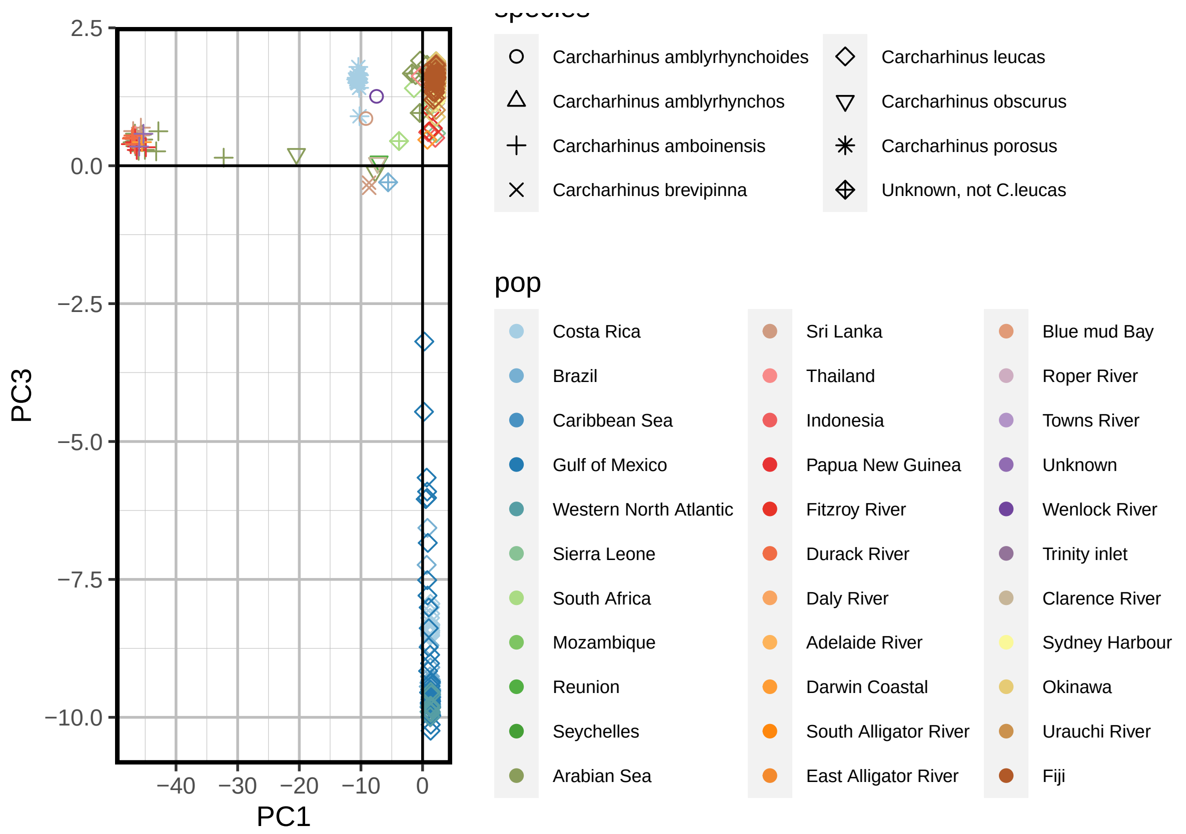
7.8 PCA to identify species

```
pca1 <- adegenet::glPca(BS.dartcap.SF.gl, nf = 8, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_SF_SpeciesID_PCA.Rdata")
```

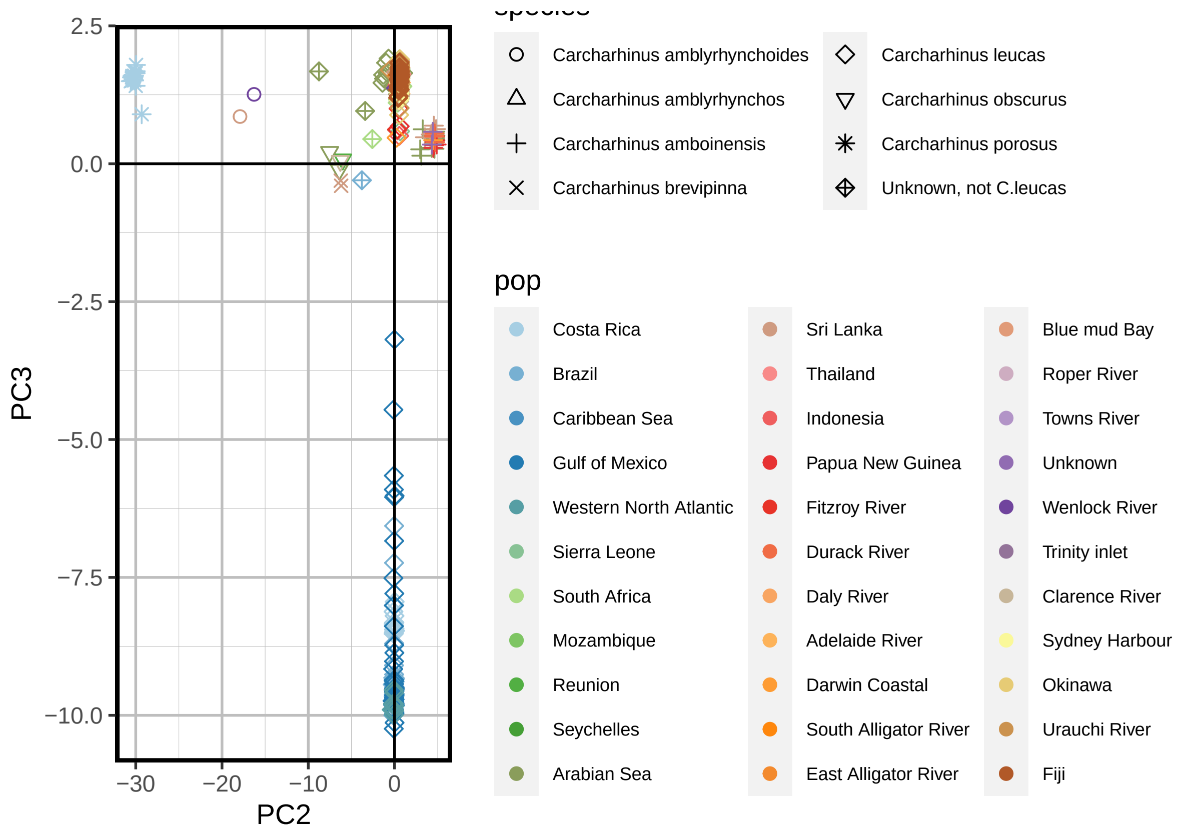
```
load("DArTcap_SF_SpeciesID_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.SF.gl)
BS.pca.scores$species <- BS.dartcap.SF.gl$other$ind.metrics$SpeciesID_genetic
cols <- adegenet::funky(nPop(BS.dartcap.SF.gl))


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop,
                                                  group = species)) +
  ggplot2::geom_point(aes(shape = species), size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA,
                                             size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



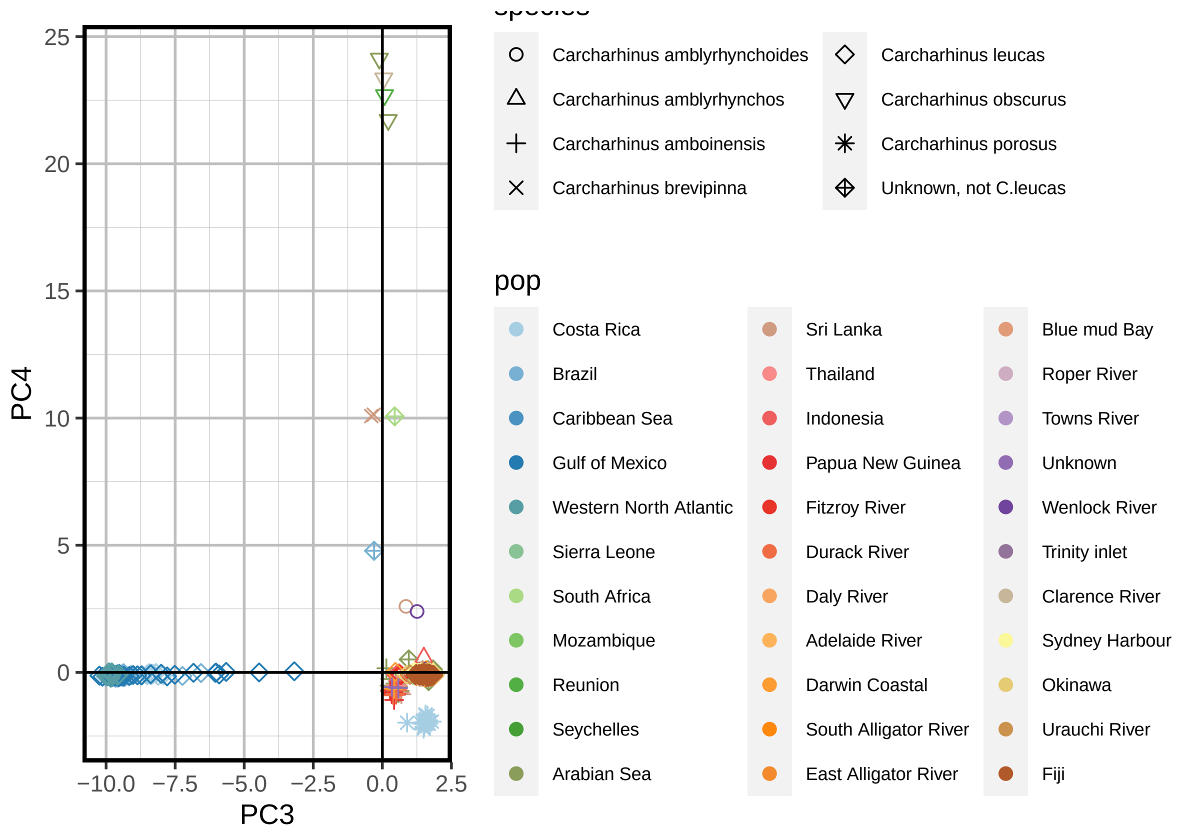
```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA1.png",
                width = 30, height = 15,units = "cm")


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                             fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



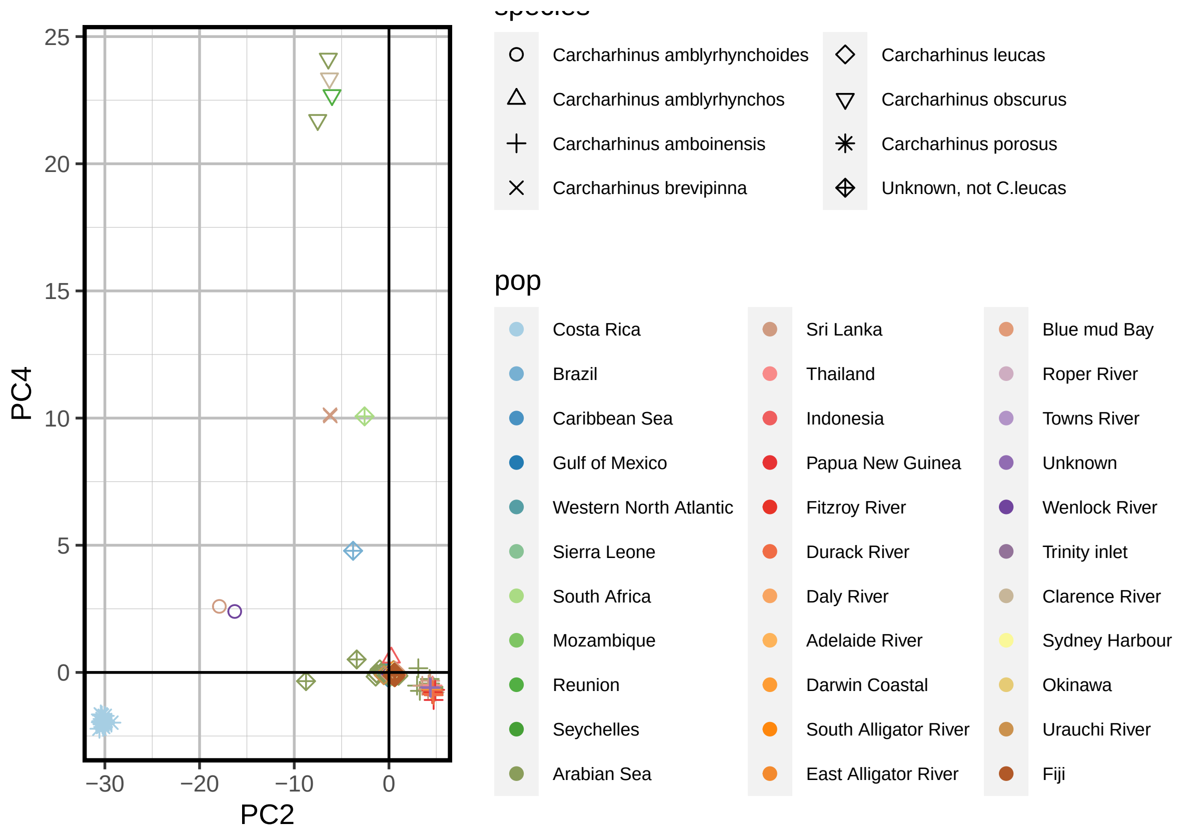
```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA2.png",
                width = 30, height = 15,units = "cm")

p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



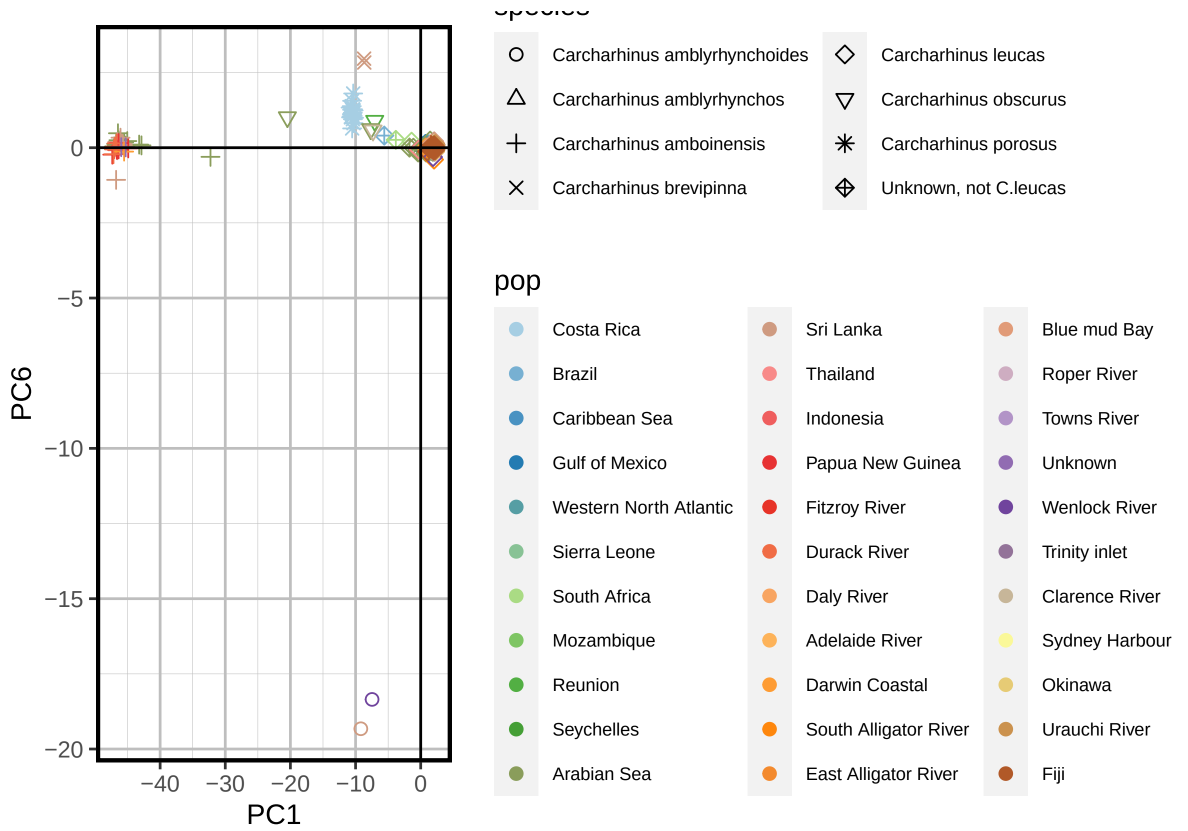
```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA3.png",
                width = 30, height = 15,units = "cm")


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



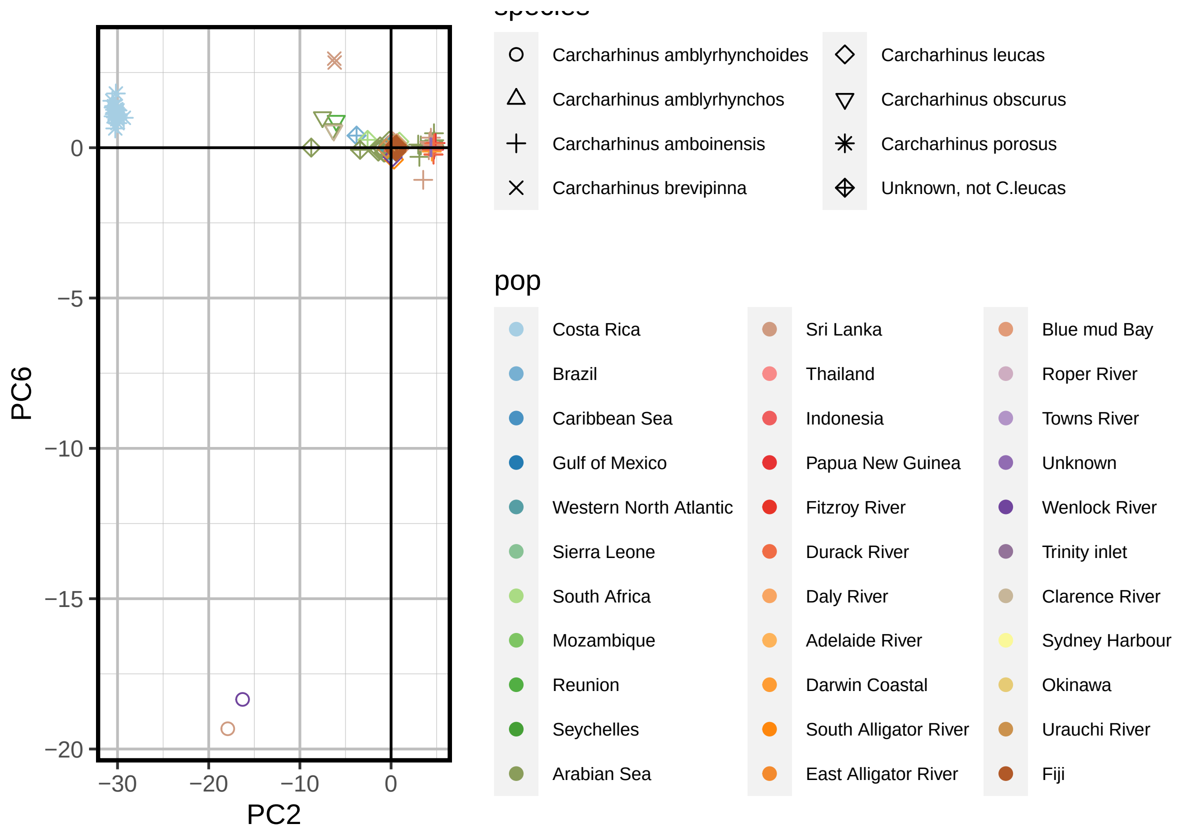
```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA4.png",
                width = 30, height = 15,units = "cm")

p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC4, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA,
                                             size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA5.png",
                width = 30, height = 15,units = "cm")


p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC6, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black", fill = NA,
                                             size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



```r
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA6.png",
                width = 30, height = 15,units = "cm")

p <- ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC6, colour = pop)) +
  ggplot2::geom_point(aes(shape = species),size = 2) +
  ggplot2::scale_color_manual(values = cols) +
  ggplot2::scale_shape_manual(values = c(1,2,3,4,5,6,8,9)) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme(panel.background = ggplot2::element_rect(fill = "white",
                                                          colour = "white"),
                 panel.grid.major = ggplot2::element_line(size = 0.5,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 panel.grid.minor = ggplot2::element_line(size = 0.1,
                                                          linetype = 'solid',
                                                          colour = "grey"),
                 legend.text = ggplot2::element_text(size = 7),
                 legend.position = "right",
                 panel.border = element_rect(colour = "black",
                                             fill = NA, size = 1.5)) +
  ggplot2::guides(shape = ggplot2::guide_legend(ncol = 2),
                  col = ggplot2::guide_legend(ncol = 3),
                  override.aes = list(size = 0.5))
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_SF_SpeciesID_PCA7.png",
                width = 30, height = 15,units = "cm")
```

---

8 DATA2: DArTcap - Only Bull Shark

8.1 Set strata

```
strata <- radiator::read_strata("Bull_shark_DArTcap_strata.tsv",
                                keep.two = FALSE)$strata %>%
  dplyr:: filter(SpeciesID_genetic == "Carcharhinus leucas")
readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata2.tsv")
```

1. Marker Reproducibility: 0.98
2. Individual missingness: 0.35
3. Individual Het - low: 0
4. Individual Het - high: 0.05
5. Individual total coverage - low: 10,000
6. Individual total coverage - high: 1,000,000
7. Marker MAC - low: 4
8. Marker coverage - low: 4
9. Marker coverage - high:60
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 3 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: 0.031
16. Individual Het - high: 0.08
17. Duplicated individuals: n
18. Filter on HWE: 4 pop, 0.001

8.2 Filter data

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata2.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = 1)
BS.dartcap.gds <- BSsnp$gds
BS.dartcap.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.gds, expand=TRUE, all = TRUE, attribute=TRUE,
      attribute.trim = FALSE)

save(BS.dartcap.tidy, file = "DArTcap_ALL_objects.Rdata")
```

Table 11:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	942 / 32 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	942 / 32 / 1 / 25292 / 35287	0 / 0 / 0 / 10550 / 17988
Filter markers in common	NA	942 / 32 / 1 / 14742 / 17299	0 / 0 / 0 / 1710 / 2139
Filter individuals based on missingness	0.35	942 / 32 / 1 / 13032 / 15160	20 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.05	922 / 32 / 1 / 13032 / 15160	10 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+06	912 / 32 / 1 / 13032 / 15160	4 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	908 / 32 / 1 / 13032 / 15160	0 / 0 / 0 / 2115 / 2820
Filter MAC	4	908 / 32 / 1 / 10917 / 12340	0 / 0 / 0 / 5725 / 6709
Filter coverage min / max	4-60	908 / 32 / 1 / 5192 / 5631	0 / 0 / 0 / 1367 / 1436
Filter genotyping	0.1	908 / 32 / 1 / 3825 / 4195	0 / 0 / 0 / 367 / 407
Filter SNPs position on the read	all	908 / 32 / 1 / 3458 / 3788	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	908 / 32 / 1 / 3458 / 3788	0 / 0 / 0 / 4 / 17
Filter short ld	mac	908 / 32 / 1 / 3454 / 3771	0 / 0 / 0 / 0 / 317
detect mixed genomes	0.031 0.08	908 / 32 / 1 / 3454 / 3454	44 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	864 / 32 / 1 / 3454 / 3454	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0.1	864 / 32 / 1 / 3454 / 3454	83 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	781 / 32 / 1 / 3454 / 3454	0 / 0 / 0 / 0 / 0
Filter HWE	40.001	781 / 32 / 1 / 3454 / 3454	0 / 0 / 0 / 11 / 11

8.2.1 Remove extra low and high heterozygous individuals

Because the average heterozygosity per sampling location is not even, certain individuals cannot be excluded without removing ‘good’ individuals.

```
rm <-  c("CL-ARS021-F","CL-GOM025-F.1","CL-GOM012-F","CL-SAF014-M","CL-SAF002-F",
         "CL-BRZ038-U","CLF003-F","CL-GOM011-F","CL-SAF015-F","CL-SAF003-M",
         "CL-PNG005-U","CLCR056-M","CLCR047.1","CLCR055-M","CLCR066-M")

BS.dartcap.tidy <- BS.dartcap.tidy[!BS.dartcap.tidy$INDIVIDUALS %in% rm,]
length(unique(BS.dartcap.tidy$INDIVIDUALS)) # 769
```

8.3 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.tidy,
                                       output = c("genlight", "stockr", "pcadapt", "gtypes", "rubias
BS.dartcap.gl <- Convert$genlight
BS.dartcap.stkr <- Convert$stockr
BS.dartcap.pc <- Convert$pcadapt
BS.dartcap.gt <- Convert$gtypes
BS.dartcap.rubias <- Convert$rubias



markers.meta <- radiator::extract_markers_metadata(BS.dartcap.gds, whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.gds, whitelist = TRUE)
individuals.meta <- individuals.meta[individuals.meta$INDIVIDUALS %in%
                                       BS.dartcap.gl$ind.names,]
BS.dartcap.gl$other$ind.metrics <- individuals.meta
BS.dartcap.gl$other$loc.metrics <- markers.meta
BS.dartcap.gt@schemes <- individuals.meta

pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Fitzroy River", "Daly River", "Adelaide River","Darwin Coastal",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour", "Okinawa", "Urauchi River", "Fiji")
BS.dartcap.gl$pop <- factor(BS.dartcap.gl$other$ind.metrics$Site2, levels = pop.levels)
BS.dartcap.gl <- BS.dartcap.gl[order(BS.dartcap.gl$pop, BS.dartcap.gl$ind.names)]
BS.dartcap.rubias$repunit <- factor(BS.dartcap.rubias$repunit, levels = pop.levels)

save(BS.dartcap.tidy, BS.dartcap.gl, BS.dartcap.stkr, BS.dartcap.pc,BS.dartcap.gt,
     BS.dartcap.rubias,
     markers.meta, individuals.meta, file = "DArTcap_ALL_objects.Rdata")
```

8.4 Load data

```
load("DArTcap_ALL_objects.Rdata")
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Fitzroy River",
                "Daly River", "Adelaide River","Darwin Coastal",  "South Alligator River",
                "East Alligator River","Blue mud Bay", "Roper River","Towns River",
                "Unknown","Wenlock River","Trinity inlet","Clarence River",
```

```
                "Sydney Harbour", "Okinawa", "Urauchi River", "Fiji")


BS.dartcap.gl$pop <- factor(BS.dartcap.gl$other$ind.metrics$Site2,
                            levels = pop.levels)
BS.dartcap.gl <- BS.dartcap.gl[order(BS.dartcap.gl$pop, BS.dartcap.gl$ind.names)]

pop.levels1 <- stringr::str_replace_all(pop.levels, " ", "_")
BS.dartcap.tidy$POP_ID <- factor(BS.dartcap.tidy$POP_ID, levels = pop.levels1)
BS.dartcap.tidy <- BS.dartcap.tidy[order(BS.dartcap.tidy$POP_ID,
                                         BS.dartcap.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartcap.gl) # 769
adegenet::nLoc(BS.dartcap.gl) # 3443
summary(BS.dartcap.gl$pop)
sum(duplicated(BS.dartcap.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartcap.gl$other$loc.metrics$LOCUS) #78
```

```
## [1] 769
## [1] 3443
##             Costa Rica                 Brazil          Caribbean Sea
##                     16                     50                      2
##         Gulf of Mexico Western North Atlantic           Sierra Leone
##                     37                      8                      1
##           South Africa             Mozambique                Reunion
##                     22                     11                     28
##             Seychelles            Arabian Sea              Sri Lanka
##                     36                     15                     12
##               Thailand              Indonesia       Papua New Guinea
##                      5                      4                      9
##          Fitzroy River             Daly River         Adelaide River
##                      3                     49                     18
##         Darwin Coastal  South Alligator River   East Alligator River
##                     15                     88                     47
##           Blue mud Bay            Roper River            Towns River
##                     18                      9                     10
##                Unknown          Wenlock River          Trinity inlet
##                     10                     24                      5
##         Clarence River         Sydney Harbour                Okinawa
##                     83                     65                      9
##          Urauchi River                   Fiji
##                     35                     25
## [1] 0
## [1] 78
```

8.5 Remove sex-linked markers

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sum(bull_shark$sexy.summary$CLONE_ID %in% SLM$sexy.summary$CLONE_ID) #33
sum(SLM$sexy.summary$CLONE_ID %in% bull_shark$sexy.summary$CLONE_ID) #23
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID, SLM$sexy.summary$CLONE_ID))

sum(BS.dartcap.gl$loc.names %in% sex.markers) #34
locnames <- BS.dartcap.gl$loc.names
BS.dartcap.gl <- BS.dartcap.gl[,!locnames %in% sex.markers]
BS.dartcap.gl$other$loc.metrics <- BS.dartcap.gl$other$loc.metrics[!locnames %in%
```

```
                                                                    sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.tidy$LOCUS)) # 34
BS.dartcap.tidy <- BS.dartcap.tidy[!BS.dartcap.tidy$LOCUS %in% sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartcap.gt@data$locus)[,2]
BS.dartcap.gt <- BS.dartcap.gt[,!locus.gt %in% sex.markers, , drop = TRUE]

locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                   string =  colnames(BS.dartcap.rubias))[,2]
BS.dartcap.rubias <- BS.dartcap.rubias[,!locus.rubias %in% sex.markers]
```

```
## [1] 33
## [1] 23
## [1] 34
## [1] 34
```

8.6 Genetic diversity

```
set.seed(124)
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "South Africa", "Mozambique", "Reunion" ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand",
                "Indonesia", "Papua New Guinea" , "Fitzroy River", "Daly River",
                "Adelaide River","Darwin Coastal",  "South Alligator River",
                "East Alligator River","Blue mud Bay", "Roper River","Towns River",
                "Unknown","Wenlock River","Trinity inlet","Clarence River",
                "Sydney Harbour", "Urauchi River","Okinawa", "Fiji")

gl <- BS.dartcap.gl
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site2, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_genepop.txt",
                               outfile = "BS_dartcap_all_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#31
gendiv <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Brazil" = bastat$main_tab[[2]]$overall,
  "Caribbean Sea" = bastat$main_tab[[3]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[4]]$overall,
  "Western North Atlantic" = bastat$main_tab[[5]]$overall,
  "South Africa" = bastat$main_tab[[6]]$overall,
  "Mozambique" = bastat$main_tab[[7]]$overall,
  "Reunion" = bastat$main_tab[[8]]$overall,
  "Seychelles" = bastat$main_tab[[9]]$overall,
  "Arabian Sea" = bastat$main_tab[[10]]$overall,
  "Sri Lanka" = bastat$main_tab[[11]]$overall,
  "Thailand" = bastat$main_tab[[12]]$overall,
```

```
  "Indonesia" = bastat$main_tab[[13]]$overall,
  "Papua New Guinea" = bastat$main_tab[[14]]$overall,
  "Fitzroy River" = bastat$main_tab[[15]]$overall,
  "Daly River" = bastat$main_tab[[16]]$overall,
  "Adelaide River" = bastat$main_tab[[17]]$overall,
  "Darwin Coastal" = bastat$main_tab[[18]]$overall,
  "South Alligator River" = bastat$main_tab[[19]]$overall,
  "East Alligator River" = bastat$main_tab[[20]]$overall,
  "Blue mud Bay" = bastat$main_tab[[21]]$overall,
  "Roper River" = bastat$main_tab[[22]]$overall,
  "Towns River" = bastat$main_tab[[23]]$overall,
  "Unknown" = bastat$main_tab[[24]]$overall,
  "Wenlock River" = bastat$main_tab[[25]]$overall,
  "Trinity inlet" = bastat$main_tab[[26]]$overall,
  "Clarence River" = bastat$main_tab[[27]]$overall,
  "Sydney Harbour" = bastat$main_tab[[28]]$overall,
  "Urauchi River" = bastat$main_tab[[29]]$overall,
  "Okinawa" = bastat$main_tab[[30]]$overall,
  "Fiji" = bastat$main_tab[[31]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTcap_ALL_gendiv.txt")
save(gendiv, file = "DArTcap_ALL_gendiv.Rdata")


pop.levels <- c("Costa Rica" , "Brazil", "Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "South Africa", "Mozambique", "Reunion" ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Australia", "Japan", "Fiji")
gl <- BS.dartcap.gl
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_Sites_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_Sites_genepop.txt",
                               outfile = "BS_dartcap_all_Sites_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)
```

```
length(bastat$main_tab)#17
gendiv <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Brazil" = bastat$main_tab[[2]]$overall,
  "Caribbean Sea" = bastat$main_tab[[3]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[4]]$overall,
  "Western North Atlantic" = bastat$main_tab[[5]]$overall,
  "South Africa" = bastat$main_tab[[6]]$overall,
  "Mozambique" = bastat$main_tab[[7]]$overall,
  "Reunion" = bastat$main_tab[[8]]$overall,
  "Seychelles" = bastat$main_tab[[9]]$overall,
  "Arabian Sea" = bastat$main_tab[[10]]$overall,
  "Sri Lanka" = bastat$main_tab[[11]]$overall,
  "Thailand" = bastat$main_tab[[12]]$overall,
  "Indonesia" = bastat$main_tab[[13]]$overall,
  "Papua New Guinea" = bastat$main_tab[[14]]$overall,
  "Australia" = bastat$main_tab[[15]]$overall,
  "Japan" = bastat$main_tab[[16]]$overall,
  "Fiji" = bastat$main_tab[[17]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)
readr::write_tsv(gendiv, path = "DArTcap_ALL_Sites_gendiv.txt")
save(gendiv, file = "DArTcap_ALL_Sites_gendiv.Rdata")


gl <- BS.dartcap.gl
gl <- gl[!gl$other$ind.metrics$Region == "E-ATL",] #only 1 sample
gl$other$ind.metrics$Region[gl$other$ind.metrics$Region %in%
                              c("W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC")] <- "IWP"
pop.levels <- c("E-PAC","W-ATL","IWP", "Japan","Fiji")
gl$pop <- factor(gl$other$ind.metrics$Region, levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_Regions_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_Regions_genepop.txt",
                               outfile = "BS_dartcap_all_Regions_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#5
gendiv <- data.frame(
```

```
  "E-PAC" = bastat$main_tab[[1]]$overall,
  "W-ATL" = bastat$main_tab[[2]]$overall,
  "IWP" = bastat$main_tab[[3]]$overall,
  "Japan" = bastat$main_tab[[4]]$overall,
  "Fiji" = bastat$main_tab[[5]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)
readr::write_tsv(gendiv, path = "DArTcap_ALL_Regions_gendiv.txt")
save(gendiv, file = "DArTcap_ALL_Regions_gendiv.Rdata")
```

```
load("DArTcap_ALL_gendiv.Rdata")

shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "FZR", "DAR")
knitr::kable(gendiv[,1:16], col.names = shortnames, digits = 4,
             caption = "Table1A") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()

shortnames <- c("ADR","DWC","SAR", "EAR","BMB", "ROR","TOR","UNK","WER","TRI",
                "CLR", "SYH", "URR","OKI", "FIJ")
knitr::kable(gendiv[,17:31], col.names = shortnames, digits = 4,
             caption = "Table1B") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()


load("DArTcap_ALL_Sites_gendiv.Rdata")
shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(gendiv, col.names = shortnames, digits = 4,
             caption = "Table2") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()

load("DArTcap_ALL_Regions_gendiv.Rdata")
shortnames <- c("E-PAC","W-ATL","IWP", "Japan","Fiji")
knitr::kable(gendiv, col.names = shortnames, digits = 4,
             caption = "Table3") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

Table 12: Table1A

	COR	BRZ	CAR	GOM	WNA	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	DAR
ar	1.0620	1.0950	1.0650	1.0870	1.0840	1.1120	1.0860	1.1080	1.1120	1.1140	1.1100	1.1090	1.0970	1.1050	1.0830	1.1140
size	15.6540	49.0870	1.9750	36.0400	7.8830	21.7470	10.2580	27.3810	35.4700	14.8430	11.8850	4.9650	3.9590	8.9060	2.9130	48.5170
obs_het	0.0360	0.0520	0.0490	0.0480	0.0500	0.0600	0.0560	0.0590	0.0600	0.0620	0.0610	0.0660	0.0610	0.0590	0.0600	0.0600
exp_het	0.0390	0.0560	0.0380	0.0530	0.0500	0.0620	0.0600	0.0620	0.0620	0.0630	0.0610	0.0590	0.0540	0.0580	0.0520	0.0630
uexp_het	0.0410	0.0570	0.0510	0.0530	0.0540	0.0630	0.0640	0.0630	0.0630	0.0650	0.0640	0.0660	0.0610	0.0620	0.0620	0.0630
fis	0.0450	0.0480	-0.2930	0.0500	-0.0250	0.0240	0.0520	0.0400	0.0260	0.0040	-0.0050	-0.1080	-0.1360	-0.0270	-0.1750	0.0370
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0030	0.0340	-1.0000	0.0310	-0.1350	-0.0100	-0.0410	0.0110	0.0030	-0.0490	-0.0770	-0.3690	-0.5470	-0.1240	-1.0000	0.0200
fis_hi	0.0430	0.0520	-0.2930	0.0540	-0.0360	0.0190	0.0440	0.0370	0.0250	-0.0030	-0.0150	-0.1080	-0.1360	-0.0370	-0.1750	0.0370
ar_lo	1.0150	1.0850	1.0330	1.0660	1.0290	1.0530	0.9640	1.0490	1.0600	1.0520	1.0490	1.0520	1.0470	1.0450	1.0060	1.1010
ar_hi	1.0720	1.1060	1.0920	1.0990	1.1020	1.1230	1.1190	1.1220	1.1220	1.1280	1.1300	1.1290	1.1190	1.1180	1.1180	1.1240
fis.hierfstat	0.0750	0.0576	-0.0481	0.0638	0.0369	0.0465	0.0959	0.0572	0.0398	0.0370	0.0356	-0.0069	-0.0098	0.0285	-0.0006	0.0470
fis.CI.low	0.0787	0.0694	-0.0306	0.0724	0.0327	0.0467	0.0985	0.0528	0.0312	0.0273	0.0126	-0.0320	-0.0293	0.0192	-0.0016	0.0448
fis.CI.high	0.1376	0.1060	0.1257	0.1165	0.0984	0.0811	0.1568	0.0893	0.0606	0.0668	0.0614	0.0378	0.0551	0.0703	0.0940	0.0704

Table 13: Table1B

	ADR	DWC	SAR	EAR	BMB	ROR	TOR	UNK	WER	TRI	CLR	SYH	URR	OKI	FIJ
ar	1.1120	1.1160	1.1130	1.1110	1.1160	1.1000	1.1060	1.1080	1.1120	1.1110	1.1200	1.1130	1.1090	1.1020	1.0960
size	17.8180	14.8180	87.0540	46.5490	17.7220	8.6150	9.8140	9.8220	23.6920	4.9410	81.9800	64.0920	34.5690	8.9080	23.5170
obs_het	0.0600	0.0640	0.0600	0.0590	0.0650	0.0590	0.0590	0.0610	0.0600	0.0690	0.0650	0.0600	0.0620	0.0590	0.0570
exp_het	0.0610	0.0640	0.0620	0.0610	0.0640	0.0610	0.0600	0.0610	0.0620	0.0610	0.0650	0.0630	0.0590	0.0560	0.0630
uexp_het	0.0630	0.0670	0.0630	0.0620	0.0660	0.0650	0.0630	0.0640	0.0640	0.0680	0.0660	0.0630	0.0600	0.0600	0.0640
fis	0.0120	-0.0060	0.0350	0.0280	-0.0060	0.0090	-0.0060	-0.0150	0.0250	-0.1150	0.0240	0.0370	-0.0130	-0.0570	0.0610
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0310	-0.0580	0.0260	0.0110	-0.0540	-0.0960	-0.0920	-0.0980	-0.0090	-0.3880	0.0110	0.0240	-0.0400	-0.1890	0.0260
fis_hi	0.0050	-0.0110	0.0360	0.0260	-0.0110	0.0020	-0.0140	-0.0240	0.0220	-0.1150	0.0250	0.0380	-0.0180	-0.0620	0.0650
ar_lo	1.0510	1.0470	1.1040	1.1000	1.0530	1.0310	1.0470	1.0430	1.0500	1.0510	1.1090	1.1010	1.0850	1.0450	1.0220
ar_hi	1.1240	1.1330	1.1240	1.1220	1.1340	1.1200	1.1220	1.1210	1.1220	1.1330	1.1310	1.1250	1.1210	1.1220	1.1190
fis.hierfstat	0.0392	0.0275	0.0409	0.0383	0.0212	0.0648	0.0434	0.0342	0.0456	-0.0145	0.0301	0.0448	0.0006	-0.0026	0.0809
fis.CI.low	0.0338	0.0190	0.0370	0.0333	0.0034	0.0614	0.0449	0.0270	0.0441	-0.0430	0.0062	0.0431	-0.0440	-0.0273	0.0954
fis.CI.high	0.0695	0.0588	0.0596	0.0591	0.0410	0.1174	0.0948	0.0768	0.0744	0.0249	0.0296	0.0676	-0.0057	0.0315	0.1351

Table 14: Table2

	COR	BRZ	CAR	GOM	WNA	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
ar	1.0610	1.0950	1.0640	1.0860	1.0850	1.1120	1.0870	1.1090	1.1120	1.1140	1.1110	1.1100	1.0960	1.1050	1.1160	1.1100	1.0960
size	15.6540	49.0870	1.9750	36.0400	7.8830	21.7470	10.2580	27.3810	35.4700	14.8430	11.8850	4.9650	3.9590	8.9060	438.3460	43.4770	23.5170
obs__het	0.0360	0.0520	0.0490	0.0480	0.0500	0.0600	0.0560	0.0590	0.0600	0.0620	0.0610	0.0660	0.0610	0.0590	0.0610	0.0610	0.0570
exp__het	0.0390	0.0560	0.0380	0.0530	0.0500	0.0620	0.0600	0.0620	0.0620	0.0630	0.0610	0.0590	0.0540	0.0580	0.0640	0.0610	0.0630
uexp__het	0.0410	0.0570	0.0510	0.0530	0.0540	0.0630	0.0640	0.0630	0.0630	0.0650	0.0640	0.0660	0.0610	0.0620	0.0640	0.0610	0.0640
fis	0.0450	0.0480	-0.2930	0.0500	-0.0250	0.0240	0.0520	0.0400	0.0260	0.0040	-0.0050	-0.1080	-0.1360	-0.0270	0.0430	0.0040	0.0610
hwe__glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0000	1.0000	1.0000
hwe__hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe__het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0000	1.0000	1.0000
fis__lo	-0.0090	0.0330	-1.0000	0.0310	-0.1450	-0.0090	-0.0350	0.0100	0.0020	-0.0480	-0.0770	-0.3680	-0.5470	-0.1260	0.0370	-0.0170	0.0260
fis__hi	0.0440	0.0520	-0.2930	0.0530	-0.0340	0.0180	0.0450	0.0370	0.0250	-0.0030	-0.0150	-0.1080	-0.1360	-0.0370	0.0430	0.0020	0.0640
ar__lo	1.0130	1.0850	1.0330	1.0360	1.0290	1.0510	0.9460	1.0460	1.0600	1.0480	1.0490	1.0520	1.0470	1.0430	1.1050	1.0550	1.0220
ar__hi	1.0710	1.1070	1.0920	1.0990	1.1020	1.1220	1.1190	1.1210	1.1210	1.1280	1.1280	1.1290	1.1190	1.1180	1.1270	1.1220	1.1190
fis.hierfstat	0.0750	0.0576	-0.0481	0.0638	0.0369	0.0465	0.0959	0.0572	0.0398	0.0370	0.0356	-0.0069	-0.0098	0.0285	0.0440	0.0155	0.0809
fis.CI.low	0.0785	0.0687	-0.0302	0.0736	0.0321	0.0454	0.1015	0.0530	0.0328	0.0261	0.0130	-0.0302	-0.0282	0.0165	0.0387	-0.0142	0.0969
fis.CI.high	0.1389	0.1058	0.1227	0.1164	0.0998	0.0787	0.1564	0.0888	0.0611	0.0675	0.0610	0.0374	0.0545	0.0702	0.0544	0.0171	0.1351

Table 15: Table3

	E-PAC	W-ATL	IWP	Japan	Fiji
ar	1.1540	1.2580	1.3450	1.2800	1.2820
size	15.6540	94.9850	577.7590	43.4770	23.5170
obs_het	0.0360	0.0500	0.0610	0.0610	0.0570
exp_het	0.0390	0.0550	0.0640	0.0610	0.0630
uexp_het	0.0410	0.0550	0.0640	0.0610	0.0640
fis	0.0450	0.0490	0.0460	0.0040	0.0610
hwe_glb	1.0000	1.0000	0.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	0.0000	1.0000	1.0000
fis_lo	-0.0070	0.0410	0.0400	-0.0180	0.0270
fis_hi	0.0440	0.0530	0.0460	0.0030	0.0630
ar_lo	1.1380	1.2350	1.3290	1.2540	1.2520
ar_hi	1.1690	1.2790	1.3600	1.3030	1.3090
fis.hierfstat	0.0750	0.0536	0.0472	0.0155	0.0809
fis.CI.low	0.0781	0.0748	0.0421	-0.0151	0.0955
fis.CI.high	0.1401	0.1082	0.0579	0.0170	0.1358

8.6.1 Number of monomorphic markers per population

```
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Fitzroy River", "Daly River", "Adelaide River","Darwin Coastal",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour","Okinawa", "Urauchi River", "Fiji")
BS.dartcap.gl$pop <- factor(BS.dartcap.gl$other$ind.metrics$Site2, levels = pop.levels)
monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.gl[BS.dartcap.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA", "SIL","SAF", "MOZ", "RUN" ,
                "SEY", "ARS", "SRL", "TAI", "IND", "PNG" , "FZR", "DAR", "ADR",
                "DWC",  "SAR", "EAR","BMB", "ROR","TOR","UNK","WER","TRI","CLR",
                "SYH", "URR","OKI", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

```
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia", "Japan",
                "Fiji")
BS.dartcap.gl$pop <- factor(BS.dartcap.gl$other$ind.metrics$Site, levels = pop.levels)
monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.gl[BS.dartcap.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
```

```
shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA","SIL", "SAF", "MOZ", "RUN" ,
                "SEY", "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))



pop.levels <- c("E-PAC","W-ATL","E-ATL","W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC",
                "Japan","Fiji")
strata <- BS.dartcap.gl$other$ind.metrics$Region
strata[strata %in% c("W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC")] <- "IWP"
pop.levels <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")
BS.dartcap.gl$pop <- factor(strata, levels = pop.levels)
monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.gl[BS.dartcap.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

Table 16:

COR	BRZ	CAR	GOM	WNA	SIL	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	DAR	ADR	DWC	SA
2562	1771	2811	2075	2512	3340	2081	2443	2010	1914	2195	2353	2699	2835	2512	2914	1727	2178	2204	136

Table 17:

COR	BRZ	CAR	GOM	WNA	SIL	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
2562	1771	2811	2075	2512	3340	2081	2443	2010	1914	2195	2353	2699	2835	2512	395	1969	2114

Table 18:

E-PAC	W-ATL	E-ATL	IWP	Japan	Fiji
2562	1370	3340	301	1969	2114

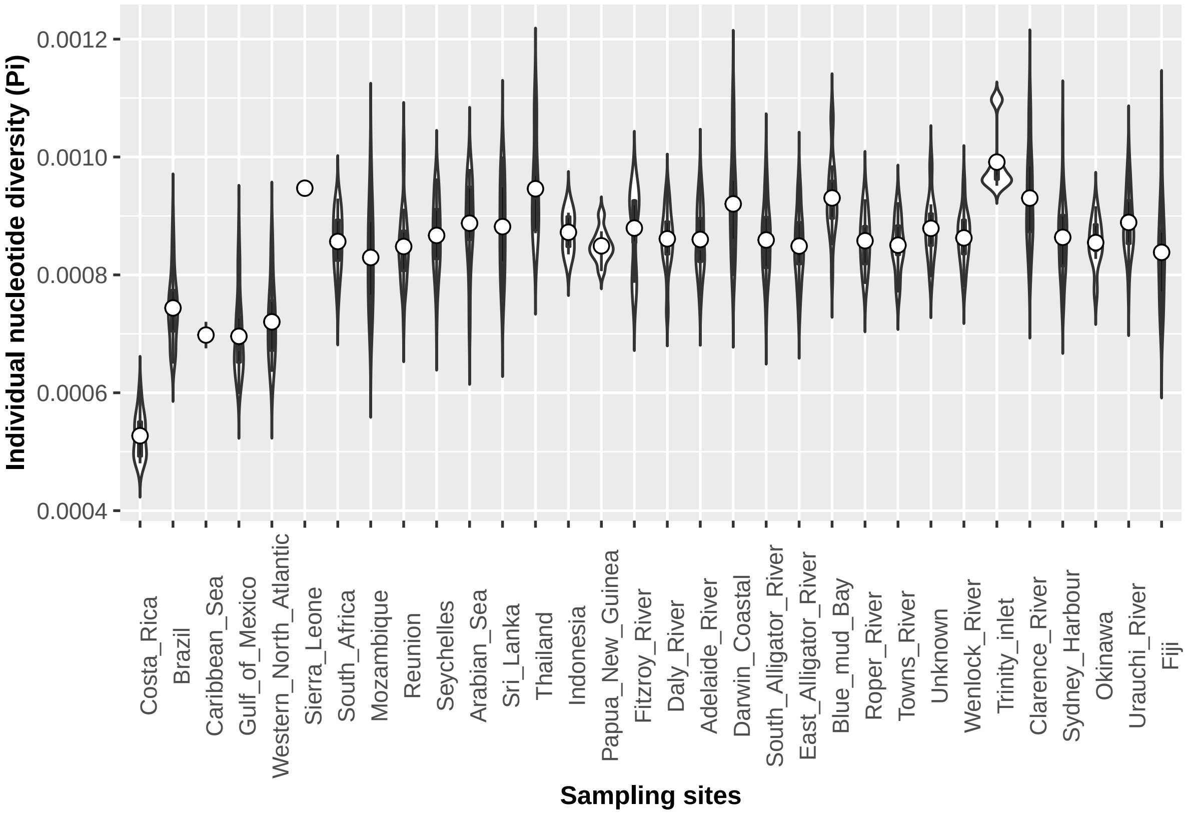
8.6.2 Nucleotide diversity and inbreeding

```
pi.sum <- radiator::pi(
  data = BS.dartcap.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)


BS.dartcap.tidy2 <- BS.dartcap.tidy
BS.dartcap.tidy2$POP_ID <- as.character(BS.dartcap.tidy2$POP_ID)
unique(BS.dartcap.tidy2$POP_ID)
```

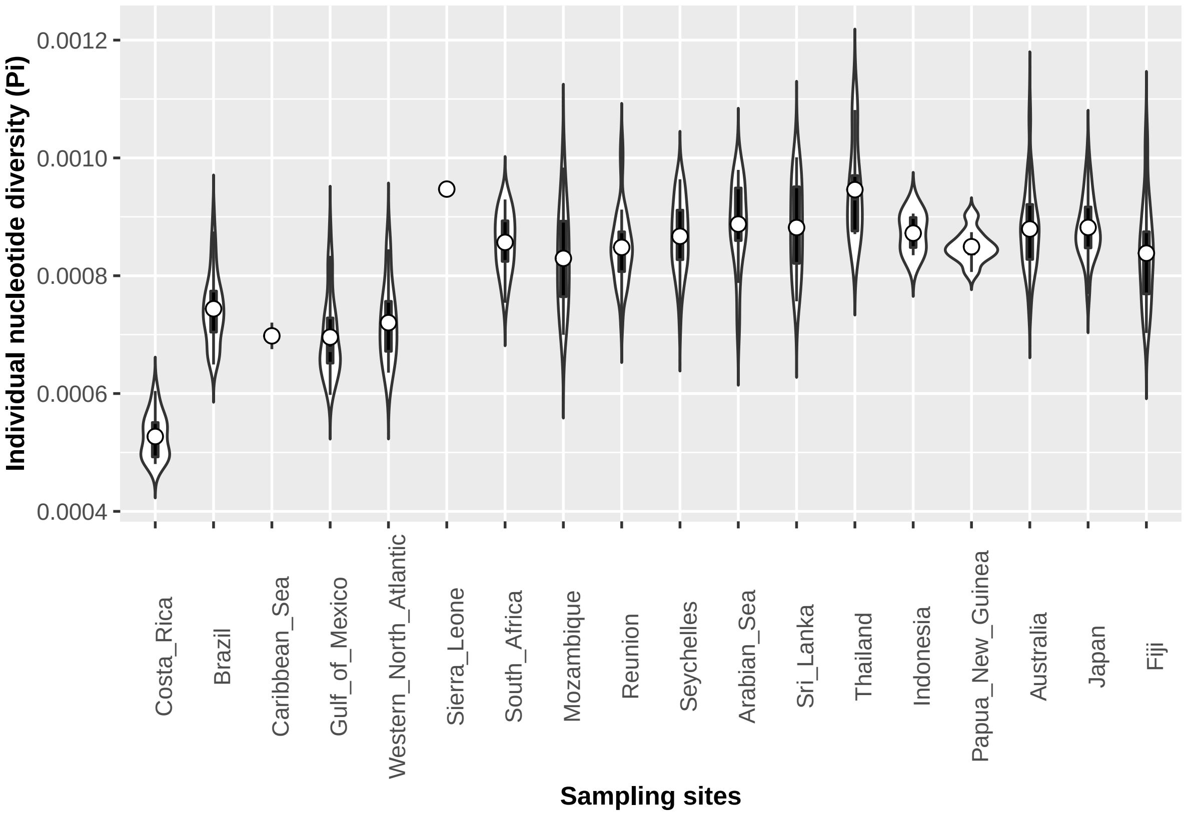
```
BS.dartcap.tidy2$POP_ID[BS.dartcap.tidy2$POP_ID %in% c("Fitzroy_River",
                                                       "Daly_River", "Adelaide_River",
                                                       "Darwin_Coastal",
                                                       "South_Alligator_River",
                                                       "East_Alligator_River",
                                                       "Blue_mud_Bay", "Roper_River",
                                                       "Towns_River","Unknown",
                                                       "Wenlock_River","Trinity_inlet",
                                                       "Clarence_River",
                                                       "Sydney_Harbour")] <- "Australia"
BS.dartcap.tidy2$POP_ID[BS.dartcap.tidy2$POP_ID %in% c("Okinawa",
                                                       "Urauchi_River")] <- "Japan"

pop.levels <- c("Costa_Rica" , "Brazil","Caribbean_Sea", "Gulf_of_Mexico",
                "Western_North_Atlantic", "Sierra_Leone", "South_Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian_Sea",
                "Sri_Lanka", "Thailand", "Indonesia", "Papua_New_Guinea" ,
                "Australia", "Japan", "Fiji")
BS.dartcap.tidy2$POP_ID <- factor(BS.dartcap.tidy2$POP_ID, levels = pop.levels)
BS.dartcap.tidy2 <- BS.dartcap.tidy2[order(BS.dartcap.tidy2$POP_ID,
                                           BS.dartcap.tidy2$INDIVIDUALS),]

pi.sum.site <- radiator::pi(
  data = BS.dartcap.tidy2,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)


BS.dartcap.tidy3 <- BS.dartcap.tidy2
BS.dartcap.tidy3$POP_ID <- as.character(BS.dartcap.tidy3$POP_ID)
BS.dartcap.tidy3$POP_ID[BS.dartcap.tidy3$POP_ID %in% c("Costa_Rica")] <- "E-PAC"
BS.dartcap.tidy3$POP_ID[BS.dartcap.tidy3$POP_ID %in% c("Brazil","Caribbean_Sea",
                                                       "Gulf_of_Mexico",
                                                       "Western_North_Atlantic")] <- "W-ATL"
BS.dartcap.tidy3$POP_ID[BS.dartcap.tidy3$POP_ID %in% c("Sierra_Leone")] <- "E-ATL"
BS.dartcap.tidy3$POP_ID[BS.dartcap.tidy3$POP_ID %in% c("South_Africa", "Mozambique",
                                                       "Reunion" , "Seychelles",
                                                       "Arabian_Sea", "Sri_Lanka",
                                                       "Thailand", "Indonesia",
                                                       "Papua_New_Guinea" ,
                                                       "Australia")] <- "IWP"
BS.dartcap.tidy3$POP_ID[BS.dartcap.tidy3$POP_ID %in% c("Okinawa",
                                                       "Urauchi_River")] <- "Japan"
pop.levels <- c("E-PAC", "W-ATL", "E-ATL", "IWP", "Japan", "Fiji")
BS.dartcap.tidy3$POP_ID <- factor(BS.dartcap.tidy3$POP_ID, levels = pop.levels)
BS.dartcap.tidy3 <- BS.dartcap.tidy3[order(BS.dartcap.tidy3$POP_ID,
                                           BS.dartcap.tidy3$INDIVIDUALS),]

pi.sum.Region <- radiator::pi(
  data = BS.dartcap.tidy3,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
```

```
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartcap.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum,pi.sum.site,pi.sum.Region, FIS.sum,
     file = "DArTcap_ALL_pi_FIS_Sites2.Rdata")
```

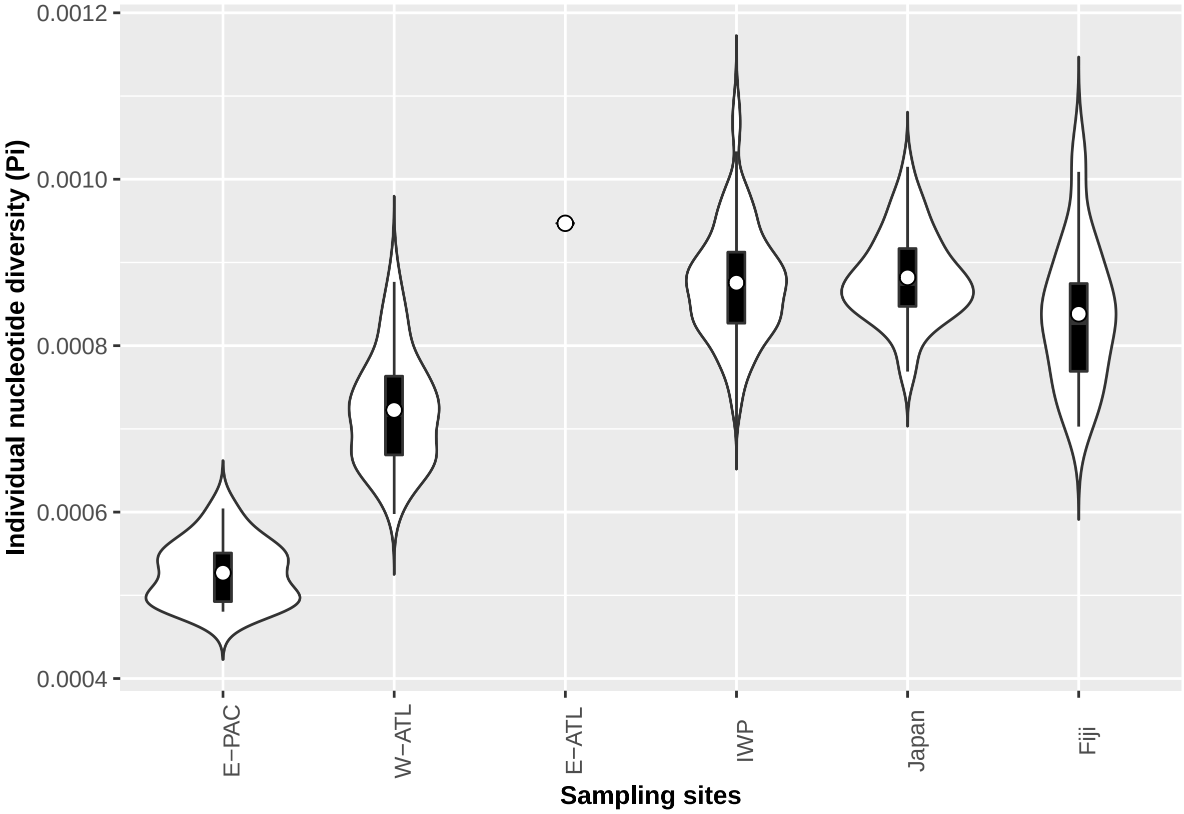
```
load("DArTcap_ALL_pi_FIS_Sites2.Rdata")
pi.sum$boxplot.pi
```



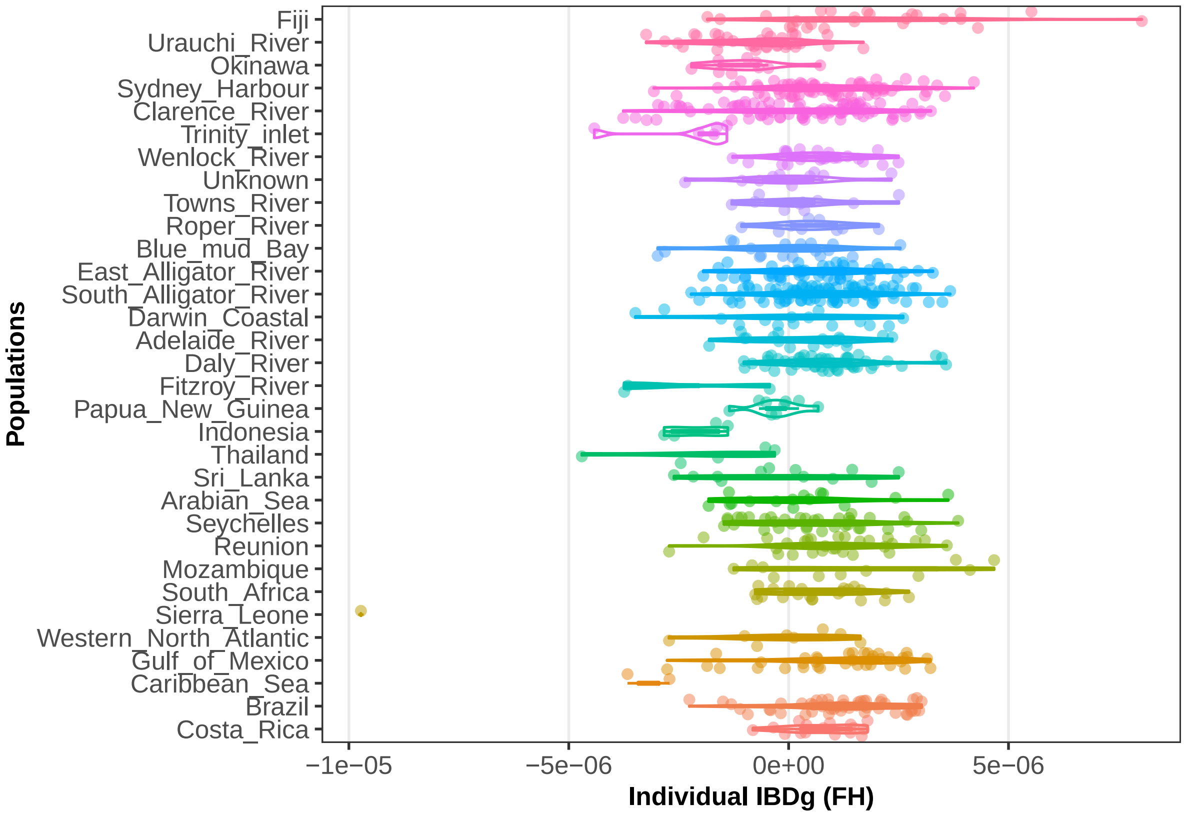
```
pi.sum.site$boxplot.pi
```



```
pi.sum.Region$boxplot.pi
```



```
FIS.sum$fh.box.plot
```



8.7 Genetic differentiation

8.7.1 Fst per location

```
Fst.gt <- strataG::popStructTest(
    BS.dartcap.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_ALL_FST_Sites2.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_ALL_FST_Sites2.txt")
```

```
load("DArTcap_ALL_FST_Sites2.Rdata")
kableExtra::kbl(
  Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                             decreasing = TRUE),
                                       -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 3443 DArTcap loci between the all locations",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                          latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()

pop.levels1 <- c("Costa_Rica","Brazil","Caribbean_Sea","Gulf_of_Mexico",
                 "Western_North_Atlantic","Sierra_Leone","South_Africa",
                 "Mozambique","Reunion","Seychelles","Arabian_Sea", "Sri_Lanka",
```

```
                 "Thailand", "Indonesia", "Papua_New_Guinea" , "Fitzroy_River",
                 "Daly_River", "Adelaide_River","Darwin_Coastal",
                 "South_Alligator_River","East_Alligator_River","Blue_mud_Bay",
                 "Roper_River","Towns_River","Unknown","Wenlock_River",
                 "Trinity_inlet","Clarence_River","Sydney_Harbour","Okinawa",
                 "Urauchi_River","Fiji")

m2 <- Fst.gt$pairwise$result[order(match(
  Fst.gt$pairwise$result$strata.1,pop.levels1)),c(1,2,11)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.1 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst", type = 'lower')

m2 <- Fst.gt$pairwise$result[order(match(
  Fst.gt$pairwise$result$strata.1,pop.levels1)),c(1,2,12)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.2 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst.p.val", type = 'lower')
m2$Fst.p.adj <- p.adjust(m2$Fst.p.val, "bonferroni")
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.3 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst.p.adj", type = 'lower')

write.csv(m2.1, file = "DArTcap_ALL_FST_Sites2.csv")
write.csv(m2.2, file = "DArTcap_ALL_FST_Pval_Sites2.csv")
write.csv(m2.3, file = "DArTcap_ALL_FST_Pval_bonferroni_Sites2.csv")
```

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Costa_Rica (16) v. Fitzroy_River (3)	15244.4823	0.0010	0.0170	0.0010	NA	NA	0.7109	0.0094	0.7494	0.0094	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Indonesia (4)	16273.1465	0.0010	0.0174	0.0010	NA	NA	0.7066	0.0016	0.7426	0.0016	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Sierra_Leone (1)	11158.8583	0.0629	0.0114	0.0629	NA	NA	0.7013	1.0000	0.7320	1.0000	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Okinawa (9)	21164.4339	0.0010	0.0181	0.0010	-31.4871	1.0000	0.6968	0.0010	0.7370	0.0010	0.7755	0.0010	0.8074	0.0010	0.8915	0
Costa_Rica (16) v. Trinity_inlet (5)	17650.9703	0.0010	0.0177	0.0010	-108.5163	1.0000	0.6964	0.0013	0.7348	0.0013	0.9277	0.0013	0.9390	0.0013	0.9684	0
Costa_Rica (16) v. Thailand (5)	17395.3981	0.0010	0.0171	0.0010	-128.4526	1.0000	0.6957	0.0013	0.7321	0.0013	0.9375	0.0013	0.9472	0.0013	0.9728	0
Costa_Rica (16) v. Papua_New_Guinea (9)	20872.6332	0.0010	0.0172	0.0010	-25.9715	1.0000	0.6888	0.0010	0.7293	0.0010	0.7465	0.0010	0.7815	0.0010	0.8749	0
Costa_Rica (16) v. Roper_River (9)	20692.4019	0.0010	0.0174	0.0010	-25.5909	1.0000	0.6838	0.0010	0.7415	0.0010	0.7435	0.0010	0.7791	0.0010	0.8733	0
Costa_Rica (16) v. Towns_River (10)	21787.7844	0.0010	0.0173	0.0010	-22.4141	1.0000	0.6835	0.0010	0.7295	0.0010	0.7190	0.0010	0.7573	0.0010	0.8588	0
Costa_Rica (16) v. Unknown (10)	21738.0344	0.0010	0.0172	0.0010	-21.6159	1.0000	0.6812	0.0010	0.7267	0.0010	0.7125	0.0010	0.7515	0.0010	0.8549	0
Gulf_of_Mexico (37) v. Okinawa (9)	37928.8235	0.0010	0.0212	0.0010	-13.0773	1.0000	0.6797	0.0010	0.7218	0.0010	0.6376	0.0010	0.6881	0.0010	0.8095	0
Gulf_of_Mexico (37) v. Indonesia (4)	30354.5133	0.0010	0.0206	0.0010	NA	NA	0.6790	0.0019	0.7194	0.0019	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Mozambique (11)	21911.2511	0.0010	0.0171	0.0010	-21.4465	1.0000	0.6766	0.0010	0.7455	0.0010	0.7102	0.0010	0.7492	0.0010	0.8533	0
Costa_Rica (16) v. Sri_Lanka (12)	23381.6592	0.0010	0.0171	0.0010	-18.2470	1.0000	0.6765	0.0010	0.7186	0.0010	0.6784	0.0010	0.7208	0.0010	0.8336	0
Gulf_of_Mexico (37) v. Trinity_inlet (5)	32845.5244	0.0010	0.0208	0.0010	-18.3811	1.0000	0.6758	0.0013	0.7174	0.0013	0.7219	0.0013	0.7640	0.0013	0.8629	0
Gulf_of_Mexico (37) v. Papua_New_Guinea (9)	37442.1062	0.0010	0.0202	0.0010	-11.4281	1.0000	0.6735	0.0010	0.7158	0.0010	0.6173	0.0010	0.6692	0.0010	0.7955	0
Gulf_of_Mexico (37) v. Thailand (5)	32159.8344	0.0010	0.0201	0.0010	-19.0984	1.0000	0.6734	0.0013	0.7138	0.0013	0.7257	0.0014	0.7666	0.0014	0.8648	0
Gulf_of_Mexico (37) v. Urauchi_River (35)	64776.6129	0.0010	0.0216	0.0010	-7.4585	1.0000	0.6733	0.0010	0.7220	0.0010	0.5440	0.0010	0.6027	0.0010	0.7427	0
Gulf_of_Mexico (37) v. Towns_River (10)	38728.3190	0.0010	0.0203	0.0010	-10.8329	1.0000	0.6721	0.0010	0.7175	0.0010	0.6035	0.0010	0.6570	0.0010	0.7861	0
Gulf_of_Mexico (37) v. Roper_River (9)	37383.6943	0.0010	0.0205	0.0010	-11.3633	1.0000	0.6713	0.0010	0.7232	0.0010	0.6151	0.0010	0.6677	0.0010	0.7942	0
Gulf_of_Mexico (37) v. Unknown (10)	38750.4443	0.0010	0.0203	0.0010	-10.4049	1.0000	0.6707	0.0010	0.7158	0.0010	0.5978	0.0010	0.6518	0.0010	0.7821	0
Arabian_Sea (15) v. Costa_Rica (16)	25971.5113	0.0010	0.0172	0.0010	-14.4992	1.0000	0.6703	0.0010	0.7190	0.0010	0.6412	0.0010	0.6874	0.0010	0.8095	0
Okinawa (9) v. Western_North_Atlantic (8)	15535.9050	0.0010	0.0207	0.0010	-39.0563	1.0000	0.6700	0.0010	0.7181	0.0010	0.8290	0.0010	0.8561	0.0010	0.9213	0
Fitzroy_River (3) v. Western_North_Atlantic (8)	9762.9230	0.0110	0.0199	0.0110	NA	NA	0.6699	0.0171	0.7229	0.0183	NA	NA	NA	NA	NA	
Indonesia (4) v. Western_North_Atlantic (8)	10796.1481	0.0010	0.0201	0.0010	NA	NA	0.6695	0.0011	0.7210	0.0011	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Urauchi_River (35)	42234.0313	0.0010	0.0184	0.0010	-12.5734	1.0000	0.6693	0.0010	0.7189	0.0010	0.6113	0.0010	0.6604	0.0010	0.7892	0
Gulf_of_Mexico (37) v. Sri_Lanka (12)	40959.6725	0.0010	0.0201	0.0010	-9.3431	1.0000	0.6690	0.0010	0.7122	0.0010	0.5772	0.0010	0.6327	0.0010	0.7671	0
Adelaide_River (18) v. Costa_Rica (16)	28352.4697	0.0010	0.0172	0.0010	-13.8701	1.0000	0.6689	0.0010	0.7167	0.0010	0.6302	0.0010	0.6772	0.0010	0.8020	0
Gulf_of_Mexico (37) v. Mozambique (11)	38936.2039	0.0010	0.0202	0.0010	-10.5682	1.0000	0.6678	0.0010	0.7265	0.0010	0.5984	0.0010	0.6521	0.0010	0.7823	0
Arabian_Sea (15) v. Gulf_of_Mexico (37)	44493.1758	0.0010	0.0203	0.0010	-7.9916	1.0000	0.6674	0.0010	0.7306	0.0010	0.5559	0.0010	0.6134	0.0010	0.7515	0
Adelaide_River (18) v. Gulf_of_Mexico (37)	47395.8479	0.0010	0.0203	0.0010	-7.7838	1.0000	0.6671	0.0010	0.7290	0.0010	0.5500	0.0010	0.6076	0.0010	0.7469	0
Gulf_of_Mexico (37) v. South_Africa (22)	51302.5655	0.0010	0.0203	0.0010	-7.0620	1.0000	0.6645	0.0010	0.7110	0.0010	0.5385	0.0010	0.5969	0.0010	0.7380	0
Gulf_of_Mexico (37) v. Wenlock_River (24)	53455.4440	0.0010	0.0205	0.0010	-6.8025	1.0000	0.6643	0.0010	0.7121	0.0010	0.5356	0.0010	0.5944	0.0010	0.7358	0
Caribbean_Sea (2) v. Okinawa (9)	9746.0586	0.0180	0.0200	0.0180	8.3392	1.0000	0.6641	0.0249	0.7174	0.0353	3.6652	0.4674	3.0121	0.4674	1.4313	0
Urauchi_River (35) v. Western_North_Atlantic (8)	37504.7555	0.0010	0.0212	0.0010	-12.9267	1.0000	0.6640	0.0010	0.7085	0.0010	0.6469	0.0010	0.6969	0.0010	0.8159	0
Costa_Rica (16) v. Darwin_Coastal (15)	25781.4259	0.0010	0.0171	0.0010	-14.2060	1.0000	0.6638	0.0010	0.7095	0.0010	0.6325	0.0010	0.6794	0.0010	0.8036	0
Fiji (25) v. Gulf_of_Mexico (37)	53347.0294	0.0010	0.0208	0.0010	-7.6557	1.0000	0.6636	0.0010	0.7246	0.0010	0.5421	0.0010	0.6007	0.0010	0.7411	0
Blue_mud_Bay (18) v. Gulf_of_Mexico (37)	47552.7908	0.0010	0.0204	0.0010	-7.3318	1.0000	0.6635	0.0010	0.7259	0.0010	0.5416	0.0010	0.6003	0.0010	0.7407	0
Brazil (50) v. Okinawa (9)	44575.3713	0.0010	0.0207	0.0010	-9.8829	1.0000	0.6634	0.0010	0.7060	0.0010	0.5961	0.0010	0.6501	0.0010	0.7808	0
Gulf_of_Mexico (37) v. Reunion (28)	56931.1754	0.0010	0.0205	0.0010	-6.6372	1.0000	0.6632	0.0010	0.7172	0.0010	0.5320	0.0010	0.5909	0.0010	0.7330	0
Darwin_Coastal (15) v. Gulf_of_Mexico (37)	44211.4873	0.0010	0.0201	0.0010	-7.8714	1.0000	0.6626	0.0010	0.7259	0.0010	0.5488	0.0010	0.6067	0.0010	0.7461	0
Blue_mud_Bay (18) v. Costa_Rica (16)	28324.6037	0.0010	0.0174	0.0010	-12.6979	1.0000	0.6623	0.0010	0.7108	0.0010	0.6165	0.0010	0.6650	0.0010	0.7928	0
Costa_Rica (16) v. South_Africa (22)	31374.4245	0.0010	0.0172	0.0010	-12.3324	1.0000	0.6623	0.0010	0.7094	0.0010	0.6108	0.0010	0.6594	0.0010	0.7885	0
Brazil (50) v. Urauchi_River (35)	74289.2054	0.0010	0.0211	0.0010	-5.9170	1.0000	0.6621	0.0010	0.7099	0.0010	0.5202	0.0010	0.5801	0.0010	0.7238	0
Brazil (50) v. Fitzroy_River (3)	32393.5060	0.0010	0.0200	0.0010	NA	NA	0.6615	0.0036	0.7040	0.0036	NA	NA	NA	NA	NA	
Brazil (50) v. Indonesia (4)	34978.7881	0.0010	0.0201	0.0010	NA	NA	0.6610	0.0016	0.7023	0.0016	NA	NA	NA	NA	NA	
Gulf_of_Mexico (37) v. Seychelles (36)	64246.2659	0.0010	0.0204	0.0010	-6.2762	1.0000	0.6609	0.0010	0.7120	0.0010	0.5254	0.0010	0.5846	0.0010	0.7277	0
Costa_Rica (16) v. Wenlock_River (24)	33052.2118	0.0010	0.0174	0.0010	-11.5217	1.0000	0.6609	0.0010	0.7097	0.0010	0.6018	0.0010	0.6513	0.0010	0.7823	0
Papua_New_Guinea (9) v. Western_North_Atlantic (8)	15342.6408	0.0010	0.0198	0.0010	-29.9304	1.0000	0.6609	0.0010	0.7091	0.0010	0.7937	0.0010	0.8255	0.0010	0.9027	0
East_Alligator_River (47) v. Gulf_of_Mexico (37)	73857.5801	0.0010	0.0201	0.0010	-5.6121	1.0000	0.6602	0.0010	0.7153	0.0010	0.5204	0.0010	0.5796	0.0010	0.7235	0
Caribbean_Sea (2) v. Urauchi_River (35)	29663.0390	0.0020	0.0203	0.0020	14.4289	0.6792	0.6599	0.0080	0.7175	0.0174	1.6674	0.6792	1.5296	0.6792	1.1986	0
Costa_Rica (16) v. Fiji (25)	32838.2436	0.0010	0.0177	0.0010	-12.8862	1.0000	0.6594	0.0010	0.7427	0.0010	0.6143	0.0010	0.6629	0.0010	0.7912	0
Caribbean_Sea (2) v. Indonesia (4)	5575.3583	0.0589	0.0193	0.0589	NA	NA	0.6592	0.0741	0.7108	0.1300	NA	NA	NA	NA	NA	

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st
Brazil (50) v. Trinity_inlet (5)	38191.2400	0.0010	0.0203	0.0010	-12.3803	1.0000	0.6591	0.0012	0.7013	0.0012	0.6589	0.0013	0.7079	0.0013	0.8239	0
Trinity_inlet (5) v. Western_North_Atlantic (8)	11938.2254	0.0020	0.0205	0.0020	-509.0860	1.0000	0.6586	0.0020	0.7105	0.0020	0.9854	0.0020	0.9880	0.0020	0.9939	0
Thailand (5) v. Western_North_Atlantic (8)	11762.3727	0.0010	0.0196	0.0010	-1708.8139	1.0000	0.6580	0.0010	0.7092	0.0010	0.9956	0.0010	0.9963	0.0010	0.9982	0
Costa_Rica (16) v. Reunion (28)	35822.7035	0.0010	0.0173	0.0010	-11.2181	1.0000	0.6579	0.0010	0.7153	0.0010	0.5972	0.0010	0.6469	0.0010	0.7790	0
Brazil (50) v. Papua_New_Guinea (9)	43914.5156	0.0010	0.0197	0.0010	-8.8114	1.0000	0.6576	0.0010	0.7002	0.0010	0.5789	0.0010	0.6338	0.0010	0.7681	0
Towns_River (10) v. Western_North_Atlantic (8)	16205.3138	0.0010	0.0199	0.0010	-25.5219	1.0000	0.6571	0.0010	0.7056	0.0010	0.7668	0.0010	0.8024	0.0010	0.8882	0
Daly_River (49) v. Gulf_of_Mexico (37)	75823.0284	0.0010	0.0203	0.0010	-5.3530	1.0000	0.6571	0.0010	0.7122	0.0010	0.5163	0.0010	0.5760	0.0010	0.7204	0
Brazil (50) v. Towns_River (10)	45629.7634	0.0010	0.0198	0.0010	-8.2103	1.0000	0.6568	0.0010	0.7019	0.0010	0.5654	0.0010	0.6217	0.0010	0.7584	0
Brazil (50) v. Thailand (5)	37344.9627	0.0010	0.0195	0.0010	-12.8491	1.0000	0.6564	0.0012	0.6977	0.0012	0.6624	0.0013	0.7103	0.0013	0.8257	0
Brazil (50) v. Roper_River (9)	43908.8353	0.0010	0.0200	0.0010	-8.6219	1.0000	0.6556	0.0010	0.7057	0.0010	0.5747	0.0010	0.6304	0.0010	0.7653	0
Brazil (50) v. Unknown (10)	45557.7229	0.0010	0.0198	0.0010	-8.0175	1.0000	0.6555	0.0010	0.7003	0.0010	0.5615	0.0010	0.6181	0.0010	0.7554	0
Brazil (50) v. Sri_Lanka (12)	48090.5646	0.0010	0.0196	0.0010	-7.4193	1.0000	0.6543	0.0010	0.6976	0.0010	0.5455	0.0010	0.6030	0.0010	0.7431	0
Gulf_of_Mexico (37) v. Sydney_Harbour (65)	89170.2545	0.0010	0.0203	0.0010	-4.4543	1.0000	0.6543	0.0010	0.7080	0.0010	0.5102	0.0010	0.5703	0.0010	0.7154	0
Caribbean_Sea (2) v. Fitzroy_River (3)	4693.6426	0.1159	0.0192	0.1159	NA	NA	0.6543	0.2442	0.7213	1.0000	NA	NA	NA	NA	NA	
Unknown (10) v. Western_North_Atlantic (8)	16181.0705	0.0010	0.0198	0.0010	-24.0526	1.0000	0.6543	0.0010	0.7029	0.0010	0.7576	0.0010	0.7944	0.0010	0.8830	0
Roper_River (9) v. Western_North_Atlantic (8)	15145.0152	0.0010	0.0201	0.0010	-28.9918	1.0000	0.6542	0.0010	0.7035	0.0010	0.7892	0.0010	0.8219	0.0010	0.9005	0
Gulf_of_Mexico (37) v. South_Alligator_River (88)	108650.5315	0.0010	0.0201	0.0010	-3.7651	1.0000	0.6539	0.0010	0.7057	0.0010	0.5076	0.0010	0.5676	0.0010	0.7132	0
Adelaide_River (18) v. Brazil (50)	55498.2702	0.0010	0.0198	0.0010	-6.1093	1.0000	0.6539	0.0010	0.7104	0.0010	0.5225	0.0010	0.5816	0.0010	0.7252	0
Arabian_Sea (15) v. Brazil (50)	52205.7665	0.0010	0.0198	0.0010	-6.3824	1.0000	0.6538	0.0010	0.7111	0.0010	0.5278	0.0010	0.5868	0.0010	0.7296	0
Costa_Rica (16) v. Seychelles (36)	41929.4198	0.0010	0.0172	0.0010	-10.2066	1.0000	0.6532	0.0010	0.7059	0.0010	0.5844	0.0010	0.6350	0.0010	0.7696	0
Brazil (50) v. Mozambique (11)	45890.2124	0.0010	0.0197	0.0010	-8.0143	1.0000	0.6532	0.0010	0.7086	0.0010	0.5607	0.0010	0.6171	0.0010	0.7546	0
Sri_Lanka (12) v. Western_North_Atlantic (8)	17932.6616	0.0010	0.0197	0.0010	-19.3031	1.0000	0.6531	0.0010	0.7009	0.0010	0.7186	0.0010	0.7601	0.0010	0.8604	0
Brazil (50) v. Wenlock_River (24)	62086.1831	0.0010	0.0200	0.0010	-5.4436	1.0000	0.6525	0.0010	0.6994	0.0010	0.5114	0.0010	0.5713	0.0010	0.7163	0
Brazil (50) v. South_Africa (22)	59708.1807	0.0010	0.0198	0.0010	-5.6168	1.0000	0.6522	0.0010	0.6981	0.0010	0.5134	0.0010	0.5730	0.0010	0.7178	0
Brazil (50) v. Fiji (25)	62085.9734	0.0010	0.0203	0.0010	-6.1466	1.0000	0.6521	0.0010	0.7183	0.0010	0.5169	0.0010	0.5767	0.0010	0.7209	0
Brazil (50) v. Reunion (28)	65838.2138	0.0010	0.0199	0.0010	-5.1468	1.0000	0.6518	0.0010	0.7038	0.0010	0.5076	0.0010	0.5676	0.0010	0.7132	0
Adelaide_River (18) v. Western_North_Atlantic (8)	23060.0428	0.0010	0.0198	0.0010	-13.9178	1.0000	0.6515	0.0010	0.6982	0.0010	0.6626	0.0010	0.7104	0.0010	0.8258	0
Costa_Rica (16) v. East_Alligator_River (47)	50018.0707	0.0010	0.0171	0.0010	-9.3118	1.0000	0.6514	0.0010	0.7000	0.0010	0.5760	0.0010	0.6269	0.0010	0.7633	0
Blue_mud_Bay (18) v. Brazil (50)	55679.1565	0.0010	0.0199	0.0010	-5.7981	1.0000	0.6509	0.0010	0.7078	0.0010	0.5151	0.0010	0.5750	0.0010	0.7195	0
Mozambique (11) v. Western_North_Atlantic (8)	16446.4730	0.0010	0.0198	0.0010	-23.8312	1.0000	0.6505	0.0010	0.6993	0.0010	0.7559	0.0010	0.7928	0.0010	0.8820	0
Brazil (50) v. Seychelles (36)	73511.3689	0.0010	0.0198	0.0010	-4.9091	1.0000	0.6504	0.0010	0.7001	0.0010	0.5026	0.0010	0.5628	0.0010	0.7090	0
Caribbean_Sea (2) v. Papua_New_Guinea (9)	9592.1001	0.0280	0.0191	0.0280	8.7392	1.0000	0.6504	0.0426	0.7048	0.0592	3.1407	0.5225	2.6339	0.5225	1.3946	0
Brazil (50) v. East_Alligator_River (47)	83389.1059	0.0010	0.0196	0.0010	-4.4497	1.0000	0.6503	0.0010	0.6977	0.0010	0.4993	0.0010	0.5593	0.0010	0.7061	0
East_Alligator_River (47) v. Western_North_Atlantic (8)	46048.2345	0.0010	0.0197	0.0010	-8.9520	1.0000	0.6495	0.0010	0.6938	0.0010	0.5991	0.0010	0.6526	0.0010	0.7828	0
Brazil (50) v. Darwin_Coastal (15)	51918.8432	0.0010	0.0196	0.0010	-6.1940	1.0000	0.6495	0.0010	0.6944	0.0010	0.5202	0.0010	0.5796	0.0010	0.7235	0
Arabian_Sea (15) v. Western_North_Atlantic (8)	20524.2457	0.0010	0.0199	0.0010	-14.8171	1.0000	0.6495	0.0010	0.6971	0.0010	0.6748	0.0010	0.7215	0.0010	0.8337	0
South_Africa (22) v. Western_North_Atlantic (8)	26233.0639	0.0010	0.0199	0.0010	-12.2867	1.0000	0.6488	0.0010	0.6951	0.0010	0.6416	0.0010	0.6916	0.0010	0.8121	0
Wenlock_River (24) v. Western_North_Atlantic (8)	27981.0891	0.0010	0.0201	0.0010	-11.5652	1.0000	0.6487	0.0010	0.6949	0.0010	0.6333	0.0010	0.6842	0.0010	0.8066	0
Reunion (28) v. Western_North_Atlantic (8)	30966.6961	0.0010	0.0200	0.0010	-11.2130	1.0000	0.6485	0.0010	0.6943	0.0010	0.6274	0.0010	0.6788	0.0010	0.8026	0
Brazil (50) v. Daly_River (49)	85531.1342	0.0010	0.0198	0.0010	-4.1581	1.0000	0.6478	0.0010	0.6959	0.0010	0.4953	0.0010	0.5558	0.0010	0.7030	0
Fiji (25) v. Western_North_Atlantic (8)	27619.8196	0.0010	0.0203	0.0010	-13.2118	1.0000	0.6477	0.0010	0.6944	0.0010	0.6488	0.0010	0.6984	0.0010	0.8171	0
Seychelles (36) v. Western_North_Atlantic (8)	37388.1295	0.0010	0.0199	0.0010	-10.1738	1.0000	0.6475	0.0010	0.6927	0.0010	0.6128	0.0010	0.6654	0.0010	0.7925	0
Costa_Rica (16) v. Daly_River (49)	51564.8265	0.0010	0.0172	0.0010	-8.6238	1.0000	0.6466	0.0010	0.6962	0.0010	0.5682	0.0010	0.6200	0.0010	0.7577	0
Brazil (50) v. South_Alligator_River (88)	118954.5484	0.0010	0.0196	0.0010	-2.9357	1.0000	0.6460	0.0010	0.6968	0.0010	0.4895	0.0010	0.5500	0.0010	0.6979	0
Brazil (50) v. Sydney_Harbour (65)	99187.7704	0.0010	0.0198	0.0010	-3.4957	1.0000	0.6458	0.0010	0.6981	0.0010	0.4910	0.0010	0.5517	0.0010	0.6993	0
Clarence_River (83) v. Gulf_of_Mexico (37)	104026.9077	0.0010	0.0203	0.0010	-3.6088	1.0000	0.6458	0.0010	0.6984	0.0010	0.5003	0.0010	0.5612	0.0010	0.7075	0
South_Alligator_River (88) v. Western_North_Atlantic (8)	77018.9057	0.0010	0.0197	0.0010	-5.6641	1.0000	0.6456	0.0010	0.6895	0.0010	0.5607	0.0010	0.6174	0.0010	0.7548	0
Gulf_of_Mexico (37) v. Sierra_Leone (1)	18859.1589	0.0170	0.0130	0.0170	3.5388	1.0000	0.6452	1.0000	0.6819	1.0000	-4.0811	1.0000	-2.4174	1.0000	2.1091	1
Daly_River (49) v. Western_North_Atlantic (8)	47643.4225	0.0010	0.0198	0.0010	-8.2111	1.0000	0.6447	0.0010	0.6896	0.0010	0.5890	0.0010	0.6437	0.0010	0.7758	0
Caribbean_Sea (2) v. East_Alligator_River (47)	37280.7916	0.0020	0.0189	0.0020	23.9100	0.8542	0.6442	0.0042	0.6989	0.0076	1.2825	0.0167	1.2298	0.0208	1.1007	0
Blue_mud_Bay (18) v. Western_North_Atlantic (8)	22958.2348	0.0010	0.0200	0.0010	-12.7907	1.0000	0.6441	0.0010	0.6917	0.0010	0.6485	0.0010	0.6981	0.0010	0.8169	0
Caribbean_Sea (2) v. Towns_River (10)	10301.4960	0.0210	0.0192	0.0210	9.2722	1.0000	0.6441	0.0358	0.7094	0.0488	2.8210	0.6443	2.3965	0.6443	1.3655	0
Sydney_Harbour (65) v. Western_North_Atlantic (8)	59441.3916	0.0010	0.0198	0.0010	-6.8854	1.0000	0.6437	0.0010	0.6883	0.0010	0.5736	0.0010	0.6295	0.0010	0.7646	0

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Costa_Rica (16) v. Sydney_Harbour (65)	62651.9638	0.0010	0.0172	0.0010	-7.4666	1.0000	0.6424	0.0010	0.6973	0.0010	0.5579	0.0010	0.6104	0.0010	0.7499	0
Darwin_Coastal (15) v. Western_North_Atlantic (8)	20353.8472	0.0010	0.0197	0.0010	-14.4365	1.0000	0.6424	0.0010	0.6904	0.0010	0.6666	0.0010	0.7141	0.0010	0.8285	0
Adelaide_River (18) v. Caribbean_Sea (2)	16478.8830	0.0050	0.0191	0.0050	12.7618	0.6869	0.6417	0.0082	0.6854	0.0082	1.8326	0.5410	1.6578	0.6353	1.2322	0
Caribbean_Sea (2) v. South_Alligator_River (88)	65205.6279	0.0010	0.0190	0.0010	-279.1614	1.0000	0.6413	0.0025	0.6978	0.0041	0.9847	0.0042	0.9873	0.0042	0.9936	0
Caribbean_Sea (2) v. Unknown (10)	10304.5492	0.0180	0.0191	0.0180	9.3650	1.0000	0.6410	0.0441	0.7051	0.0723	2.7377	0.6810	2.3348	0.6810	1.3571	0
Caribbean_Sea (2) v. Seychelles (36)	29492.5761	0.0050	0.0191	0.0050	18.4682	0.8259	0.6409	0.0107	0.7027	0.0204	1.4205	0.1473	1.3387	0.3661	1.1399	0
Costa_Rica (16) v. South_Alligator_River (88)	78976.1339	0.0010	0.0170	0.0010	-6.1985	1.0000	0.6409	0.0010	0.6929	0.0010	0.5482	0.0010	0.6011	0.0010	0.7423	0
Caribbean_Sea (2) v. Sri_Lanka (12)	11881.2980	0.0090	0.0189	0.0090	10.4803	1.0000	0.6407	0.0120	0.6951	0.0142	2.3070	0.6416	2.0162	0.7832	1.3073	0
Caribbean_Sea (2) v. Reunion (28)	23726.1873	0.0030	0.0191	0.0030	16.1387	0.7800	0.6401	0.0080	0.7109	0.0145	1.5290	0.2750	1.4236	0.5850	1.1675	0
Sierra_Leone (1) v. Western_North_Atlantic (8)	6383.0393	0.1049	0.0128	0.1049	NA	NA	0.6399	1.0000	0.6928	1.0000	NA	NA	NA	NA	NA	
Caribbean_Sea (2) v. Thailand (5)	6365.8728	0.0659	0.0190	0.0659	6.5399	1.0000	0.6397	0.0876	0.6900	0.1204	7.7722	0.1447	5.9532	0.1447	1.5646	0
Caribbean_Sea (2) v. Wenlock_River (24)	20891.2023	0.0030	0.0192	0.0030	15.4454	0.8462	0.6397	0.0062	0.6990	0.0096	1.5702	0.1748	1.4554	0.4441	1.1772	0
Caribbean_Sea (2) v. South_Africa (22)	19348.6504	0.0060	0.0191	0.0060	14.6472	0.7519	0.6396	0.0123	0.6969	0.0189	1.6357	0.3722	1.5064	0.6692	1.1921	0
Caribbean_Sea (2) v. Roper_River (9)	9355.1430	0.0170	0.0194	0.0170	8.7860	1.0000	0.6390	0.0375	0.7344	0.0688	3.0794	0.4113	2.5844	0.5455	1.3884	0
Caribbean_Sea (2) v. Fiji (25)	20234.6055	0.0040	0.0196	0.0040	13.8263	0.4231	0.6389	0.0606	0.7519	0.1538	1.7211	0.4231	1.5712	0.4231	1.2099	0
Brazil (50) v. Clarence_River (83)	114423.6165	0.0010	0.0198	0.0010	-2.8508	1.0000	0.6385	0.0010	0.6913	0.0010	0.4825	0.0010	0.5439	0.0010	0.6923	0
Caribbean_Sea (2) v. Daly_River (49)	38671.9822	0.0010	0.0191	0.0010	26.5220	0.6644	0.6385	0.0018	0.6942	0.0033	1.2399	0.0034	1.1954	0.0034	1.0873	0
Caribbean_Sea (2) v. Sydney_Harbour (65)	49538.2031	0.0010	0.0191	0.0010	49.8580	0.0079	0.6383	0.0024	0.6994	0.0039	1.1054	0.0039	1.0867	0.0039	1.0412	0
Caribbean_Sea (2) v. Trinity_inlet (5)	6416.0571	0.0569	0.0196	0.0569	6.5884	1.0000	0.6378	0.0945	0.6940	0.1652	7.0198	0.3540	5.3956	0.3540	1.5481	0
Arabian_Sea (15) v. Caribbean_Sea (2)	14193.4109	0.0080	0.0192	0.0080	12.1323	0.6689	0.6376	0.0150	0.6820	0.0150	1.9032	0.0912	1.7105	0.2736	1.2447	0
Caribbean_Sea (2) v. Mozambique (11)	10554.8552	0.0150	0.0190	0.0150	9.3888	1.0000	0.6367	0.0620	0.7509	0.3571	2.7335	1.0000	2.3336	1.0000	1.3572	1
Caribbean_Sea (2) v. Sierra_Leone (1)	2577.9083	0.3516	0.0123	0.3516	NA	NA	0.6360	0.3516	0.6736	0.3516	NA	NA	NA	NA	NA	
Clarence_River (83) v. Western_North_Atlantic (8)	72357.7473	0.0010	0.0198	0.0010	-5.3436	1.0000	0.6348	0.0010	0.6800	0.0010	0.5509	0.0010	0.6087	0.0010	0.7477	0
Blue_mud_Bay (18) v. Caribbean_Sea (2)	16396.9017	0.0100	0.0192	0.0100	13.7335	0.5577	0.6321	0.0262	0.6769	0.0262	1.7098	0.0481	1.5626	0.0769	1.2076	0
Clarence_River (83) v. Costa_Rica (16)	74936.1797	0.0010	0.0172	0.0010	-5.7062	1.0000	0.6312	0.0010	0.6761	0.0010	0.5381	0.0010	0.5921	0.0010	0.7348	0
Caribbean_Sea (2) v. Clarence_River (83)	60776.8282	0.0010	0.0191	0.0010	-85.2037	1.0000	0.6295	0.0027	0.6892	0.0043	0.9522	0.0043	0.9602	0.0043	0.9796	0
Caribbean_Sea (2) v. Darwin_Coastal (15)	14031.3420	0.0060	0.0190	0.0060	12.4059	0.7853	0.6286	0.0136	0.6871	0.0251	1.8825	0.0368	1.6952	0.3804	1.2412	0
Brazil (50) v. Sierra_Leone (1)	19357.2075	0.0220	0.0128	0.0220	3.7736	1.0000	0.6231	1.0000	0.6609	1.0000	-7.2591	1.0000	-4.7985	1.0000	1.9264	1
Caribbean_Sea (2) v. Costa_Rica (16)	4585.3922	0.0140	0.0023	0.0140	NA	NA	0.4287	0.1186	0.4607	0.8235	NA	NA	NA	NA	NA	
Costa_Rica (16) v. Western_North_Atlantic (8)	6703.9713	0.0010	0.0025	0.0010	-71.9795	1.0000	0.3964	0.0011	0.4187	0.0011	0.7688	0.0013	0.7844	0.0013	0.8781	0
Costa_Rica (16) v. Gulf_of_Mexico (37)	12724.5435	0.0010	0.0025	0.0010	-17.2299	1.0000	0.3692	0.0010	0.4010	0.0010	0.3948	0.0010	0.4218	0.0010	0.5855	0
Brazil (50) v. Costa_Rica (16)	14591.9962	0.0010	0.0024	0.0010	-12.5174	1.0000	0.3484	0.0010	0.3709	0.0010	0.3396	0.0010	0.3666	0.0010	0.5272	0
Sierra_Leone (1) v. Urauchi_River (35)	5368.2307	0.0280	0.0010	0.0280	3.5735	1.0000	0.2262	1.0000	0.2464	1.0000	-1.8664	1.0000	-1.0969	1.0000	3.4203	1
Okinawa (9) v. Sierra_Leone (1)	2105.6689	0.1139	0.0008	0.1139	2.9851	1.0000	0.2052	1.0000	0.2182	1.0000	-1.4594	1.0000	-0.6146	1.0000	4.5143	1
Indonesia (4) v. Sierra_Leone (1)	1287.3999	0.2338	0.0007	0.2338	NA	NA	0.1862	1.0000	0.1985	1.0000	NA	NA	NA	NA	NA	
Papua_New_Guinea (9) v. Sierra_Leone (1)	1927.2893	0.1149	0.0007	0.1149	3.0179	1.0000	0.1688	1.0000	0.1799	1.0000	-1.4903	1.0000	-0.6634	1.0000	4.3923	1
East_Alligator_River (47) v. Sierra_Leone (1)	5739.1351	0.0140	0.0007	0.0140	3.8286	1.0000	0.1680	1.0000	0.1790	1.0000	-2.2140	1.0000	-1.4735	1.0000	3.0375	1
Sierra_Leone (1) v. South_Alligator_River (88)	8806.2537	0.0170	0.0007	0.0170	4.3486	1.0000	0.1642	1.0000	0.1789	1.0000	-3.6247	1.0000	-2.7669	1.0000	2.4351	1
Seychelles (36) v. Sierra_Leone (1)	4675.7140	0.0260	0.0007	0.0260	3.7128	1.0000	0.1641	1.0000	0.1751	1.0000	-2.0433	1.0000	-1.2968	1.0000	3.2014	1
Sierra_Leone (1) v. Trinity_inlet (5)	1409.0407	0.1628	0.0009	0.1628	2.6294	1.0000	0.1619	1.0000	0.1777	1.0000	-1.3772	1.0000	-0.4524	1.0000	4.8499	1
Fiji (25) v. Sierra_Leone (1)	3717.0341	0.0360	0.0008	0.0779	3.5244	1.0000	0.1610	1.0000	0.1720	1.0000	-1.8479	1.0000	-1.0793	1.0000	3.4522	1
Adelaide_River (18) v. Sierra_Leone (1)	2963.9168	0.0410	0.0007	0.0410	3.4155	1.0000	0.1605	1.0000	0.1713	1.0000	-1.7438	1.0000	-0.9761	1.0000	3.6569	1
Sierra_Leone (1) v. Wenlock_River (24)	3561.8064	0.0470	0.0007	0.0470	3.5641	1.0000	0.1603	0.5465	0.1756	1.0000	-1.8914	1.0000	-1.1349	1.0000	3.3951	1
Reunion (28) v. Sierra_Leone (1)	3958.4759	0.0350	0.0007	0.0350	3.6090	1.0000	0.1589	1.0000	0.1697	1.0000	-1.9249	1.0000	-1.1728	1.0000	3.3492	1
Arabian_Sea (15) v. Sierra_Leone (1)	2671.9413	0.0729	0.0007	0.0729	3.3559	1.0000	0.1582	1.0000	0.1691	1.0000	-1.7251	1.0000	-0.9462	1.0000	3.6842	1
Sierra_Leone (1) v. Sydney_Harbour (65)	7160.6347	0.0200	0.0007	0.0200	4.0946	1.0000	0.1580	1.0000	0.1735	1.0000	-2.7843	1.0000	-2.0067	1.0000	2.6851	1
Daly_River (49) v. Sierra_Leone (1)	5861.0233	0.0190	0.0007	0.0190	3.8962	1.0000	0.1579	1.0000	0.1686	1.0000	-2.3404	1.0000	-1.5903	1.0000	2.9324	1
Blue_mud_Bay (18) v. Sierra_Leone (1)	3043.0477	0.0579	0.0008	0.0579	3.4601	1.0000	0.1578	1.0000	0.1690	1.0000	-1.8161	1.0000	-1.0423	1.0000	3.5024	1
Sierra_Leone (1) v. Towns_River (10)	2074.2417	0.0919	0.0007	0.0919	3.0823	1.0000	0.1578	1.0000	0.1750	1.0000	-1.5258	1.0000	-0.7056	1.0000	4.2441	1
Sierra_Leone (1) v. Unknown (10)	2031.8897	0.0899	0.0007	0.0899	3.0918	1.0000	0.1556	1.0000	0.1722	1.0000	-1.5357	1.0000	-0.7168	1.0000	4.2047	1
Sierra_Leone (1) v. Sri_Lanka (12)	2281.1615	0.0999	0.0007	0.0999	3.2091	1.0000	0.1553	1.0000	0.1691	1.0000	-1.5995	1.0000	-0.8048	1.0000	4.0102	1
Fitzroy_River (3) v. Sierra_Leone (1)	1083.3937	0.2557	0.0006	0.2557	NA	NA	0.1551	1.0000	0.1657	1.0000	NA	NA	NA	NA	NA	
Sierra_Leone (1) v. Thailand (5)	1375.9116	0.1518	0.0007	0.1518	2.6272	1.0000	0.1549	1.0000	0.1682	1.0000	-1.3621	1.0000	-0.4434	1.0000	4.9860	1

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Clarence_River (83) v. Sierra_Leone (1)	8224.2496	0.0130	0.0007	0.0130	4.4698	1.0000	0.1546	1.0000	0.1655	1.0000	-4.1486	1.0000	-3.2123	1.0000	2.3378	1
Sierra_Leone (1) v. South_Africa (22)	3261.7230	0.0490	0.0007	0.0490	3.5162	1.0000	0.1491	1.0000	0.1629	1.0000	-1.8238	1.0000	-1.0701	1.0000	3.5128	1
Darwin_Coastal (15) v. Sierra_Leone (1)	2529.3983	0.0739	0.0007	0.0739	3.3638	1.0000	0.1447	1.0000	0.1550	1.0000	-1.7256	1.0000	-0.9436	1.0000	3.6787	1
Roper_River (9) v. Sierra_Leone (1)	1871.8274	0.0989	0.0007	0.0989	3.0101	1.0000	0.1441	1.0000	0.1541	1.0000	-1.4987	1.0000	-0.6637	1.0000	4.3363	1
Mozambique (11) v. Sierra_Leone (1)	2129.2277	0.0939	0.0007	0.0939	3.0960	1.0000	0.1391	1.0000	0.1486	1.0000	-1.5408	1.0000	-0.7256	1.0000	4.1909	1
Fiji (25) v. Urauchi_River (35)	5569.2779	0.0010	0.0004	0.0010	-9.0775	1.0000	0.0732	0.0010	0.0791	0.0010	0.1153	0.0010	0.1282	0.0010	0.2183	0
Okinawa (9) v. Urauchi_River (35)	3040.3882	0.0010	0.0003	0.0010	-16.0695	0.9990	0.0568	0.0010	0.0616	0.0010	0.2555	0.0010	0.2754	0.0010	0.4229	0
Fiji (25) v. Okinawa (9)	2932.9282	0.0010	0.0003	0.0010	-15.4252	0.9930	0.0555	0.0010	0.0596	0.0010	0.2679	0.0010	0.2889	0.0010	0.4392	0
Blue_mud_Bay (18) v. Urauchi_River (35)	4255.5358	0.0010	0.0003	0.0010	-9.7147	0.9960	0.0532	0.0010	0.0576	0.0010	0.1226	0.0010	0.1360	0.0010	0.2303	0
Towns_River (10) v. Urauchi_River (35)	3360.0904	0.0010	0.0003	0.0010	-13.7006	0.8601	0.0532	0.0010	0.0576	0.0010	0.2149	0.0010	0.2336	0.0010	0.3692	0
Trinity_inlet (5) v. Urauchi_River (35)	3094.1430	0.0010	0.0002	0.0030	-24.2266	0.0161	0.0511	0.0010	0.0556	0.0010	0.4476	0.5246	0.4710	0.4543	0.6346	0
Thailand (5) v. Urauchi_River (35)	2925.5157	0.0010	0.0003	0.0030	-24.7532	0.0473	0.0505	0.0020	0.0549	0.0020	0.4511	0.4728	0.4742	0.4215	0.6376	0
Papua_New_Guinea (9) v. Urauchi_River (35)	2922.8611	0.0010	0.0002	0.0010	-15.0803	0.8791	0.0478	0.0010	0.0519	0.0010	0.2398	0.0020	0.2593	0.0020	0.4026	0
Roper_River (9) v. Urauchi_River (35)	3147.8105	0.0010	0.0002	0.0010	-14.6169	0.6523	0.0478	0.0010	0.0518	0.0010	0.2402	0.0020	0.2601	0.0020	0.4034	0
Reunion (28) v. Urauchi_River (35)	4472.7684	0.0010	0.0002	0.0010	-9.0169	1.0000	0.0470	0.0010	0.0508	0.0010	0.0941	0.0010	0.1048	0.0010	0.1818	0
Mozambique (11) v. Urauchi_River (35)	3233.5745	0.0010	0.0002	0.0010	-13.4797	0.9970	0.0460	0.0010	0.0498	0.0010	0.2086	0.0010	0.2270	0.0010	0.3604	0
Indonesia (4) v. Okinawa (9)	1435.8764	0.0170	0.0002	0.0659	NA	NA	0.0448	0.0382	0.0484	0.0382	NA	NA	NA	NA	NA	
South_Africa (22) v. Urauchi_River (35)	3911.9240	0.0010	0.0002	0.0010	-9.6010	1.0000	0.0446	0.0010	0.0482	0.0010	0.1068	0.0010	0.1185	0.0010	0.2036	0
Sri_Lanka (12) v. Urauchi_River (35)	3300.0097	0.0010	0.0002	0.0010	-12.1349	0.7233	0.0445	0.0010	0.0482	0.0010	0.1722	0.0010	0.1886	0.0010	0.3078	0
Darwin_Coastal (15) v. Urauchi_River (35)	3612.6149	0.0010	0.0002	0.0010	-10.4961	0.5185	0.0441	0.0010	0.0478	0.0010	0.1368	0.0010	0.1512	0.0010	0.2533	0
Daly_River (49) v. Urauchi_River (35)	5212.7936	0.0010	0.0002	0.0010	-7.6065	1.0000	0.0436	0.0010	0.0469	0.0010	0.0682	0.0010	0.0763	0.0010	0.1353	0
Unknown (10) v. Urauchi_River (35)	3167.4032	0.0010	0.0002	0.0010	-13.5824	0.5175	0.0430	0.0010	0.0467	0.0010	0.2082	0.0020	0.2266	0.0020	0.3599	0
Adelaide_River (18) v. Urauchi_River (35)	3676.8947	0.0010	0.0002	0.0010	-10.3731	0.9980	0.0430	0.0010	0.0465	0.0010	0.1231	0.0010	0.1361	0.0010	0.2308	0
Blue_mud_Bay (18) v. Fiji (25)	3568.1928	0.0010	0.0002	0.0010	-9.3354	1.0000	0.0424	0.0010	0.0482	0.0010	0.1297	0.0010	0.1439	0.0010	0.2422	0
Sydney_Harbour (65) v. Urauchi_River (35)	5618.9744	0.0010	0.0002	0.0010	-6.8548	1.0000	0.0424	0.0010	0.0456	0.0010	0.0593	0.0010	0.0665	0.0010	0.1188	0
Arabian_Sea (15) v. Urauchi_River (35)	3558.2360	0.0010	0.0002	0.0010	-10.6566	0.7892	0.0422	0.0010	0.0457	0.0010	0.1373	0.0010	0.1515	0.0010	0.2540	0
East_Alligator_River (47) v. Urauchi_River (35)	4841.2665	0.0010	0.0002	0.0010	-7.9822	1.0000	0.0405	0.0010	0.0436	0.0010	0.0695	0.0010	0.0776	0.0010	0.1375	0
Clarence_River (83) v. Urauchi_River (35)	6104.6689	0.0010	0.0002	0.0010	-5.7870	1.0000	0.0402	0.0010	0.0433	0.0010	0.0503	0.0010	0.0567	0.0010	0.1019	0
Okinawa (9) v. Trinity_inlet (5)	1588.4833	0.0050	0.0002	0.0190	432.3277	0.6034	0.0402	0.0170	0.0433	0.0170	1.0546	0.4296	1.0509	0.4296	1.0248	0
Seychelles (36) v. Urauchi_River (35)	4418.9082	0.0010	0.0002	0.0010	-8.5682	1.0000	0.0402	0.0010	0.0433	0.0010	0.0793	0.0010	0.0884	0.0010	0.1554	0
Urauchi_River (35) v. Wenlock_River (24)	3973.5146	0.0010	0.0002	0.0010	-9.2619	1.0000	0.0401	0.0010	0.0432	0.0010	0.0980	0.0010	0.1089	0.0010	0.1885	0
South_Alligator_River (88) v. Urauchi_River (35)	6136.5114	0.0010	0.0002	0.0010	-6.0025	1.0000	0.0400	0.0010	0.0429	0.0010	0.0506	0.0010	0.0568	0.0010	0.1022	0
Okinawa (9) v. Towns_River (10)	1837.8829	0.0010	0.0002	0.0040	-31.9259	0.9980	0.0395	0.0030	0.0429	0.0020	0.4923	0.0030	0.5141	0.0030	0.6744	0
Fiji (25) v. Trinity_inlet (5)	2589.6902	0.0010	0.0002	0.0010	-23.3960	0.0232	0.0382	0.0010	0.0410	0.0010	0.4534	0.8894	0.4774	0.8805	0.6405	0
Fiji (25) v. Towns_River (10)	2733.0114	0.0010	0.0002	0.0010	-13.2810	0.8402	0.0361	0.0010	0.0390	0.0010	0.2211	0.0110	0.2405	0.0100	0.3780	0
Okinawa (9) v. Thailand (5)	1494.7350	0.0180	0.0002	0.0380	269.9769	0.6104	0.0352	0.0360	0.0377	0.0360	1.0915	0.4336	1.0854	0.4346	1.0408	0
Blue_mud_Bay (18) v. Okinawa (9)	2145.4923	0.0040	0.0002	0.0030	-16.6868	1.0000	0.0345	0.0010	0.0371	0.0010	0.2869	0.0010	0.3083	0.0010	0.4625	0
Fitzroy_River (3) v. Okinawa (9)	1304.4243	0.0340	0.0002	0.1339	NA	NA	0.0342	0.1151	NA	NA	NA	NA	NA	NA	NA	
Okinawa (9) v. Papua_New_Guinea (9)	1634.3227	0.0050	0.0002	0.0100	-39.8064	0.9920	0.0337	0.0100	0.0363	0.0100	0.5557	0.0100	0.5759	0.0100	0.7274	0
Mozambique (11) v. Okinawa (9)	1820.9916	0.0020	0.0002	0.0020	-30.2588	0.9970	0.0335	0.0020	0.0360	0.0020	0.4771	0.0040	0.4991	0.0040	0.6609	0
Fiji (25) v. Wenlock_River (24)	3435.2732	0.0010	0.0002	0.0010	-8.9297	1.0000	0.0334	0.0010	0.0361	0.0010	0.1074	0.0010	0.1195	0.0010	0.2049	0
Fiji (25) v. Mozambique (11)	2767.8705	0.0010	0.0002	0.0010	-13.0854	0.9810	0.0333	0.0010	0.0370	0.0010	0.2182	0.0010	0.2374	0.0010	0.3740	0
Fiji (25) v. Reunion (28)	3650.3859	0.0010	0.0002	0.0010	-8.6350	1.0000	0.0331	0.0010	0.0363	0.0010	0.0993	0.0010	0.1106	0.0010	0.1909	0
Fiji (25) v. South_Alligator_River (88)	5517.0646	0.0010	0.0002	0.0010	-5.5039	0.9780	0.0322	0.0010	0.0350	0.0010	0.0539	0.0010	0.0606	0.0010	0.1086	0
Fiji (25) v. Sydney_Harbour (65)	4910.5200	0.0010	0.0001	0.0010	-6.2706	1.0000	0.0321	0.0010	0.0350	0.0010	0.0621	0.0010	0.0697	0.0010	0.1241	0
Adelaide_River (18) v. Fiji (25)	3161.2909	0.0010	0.0002	0.0010	-9.8244	1.0000	0.0319	0.0010	0.0362	0.0010	0.1291	0.0010	0.1428	0.0010	0.2408	0
Okinawa (9) v. Roper_River (9)	1672.2631	0.0060	0.0002	0.0170	-38.0541	0.9870	0.0318	0.0150	0.0354	0.0140	0.5499	0.0140	0.5707	0.0140	0.7230	0
Fiji (25) v. Sri_Lanka (12)	2847.4077	0.0010	0.0002	0.0010	-11.4689	0.9241	0.0318	0.0010	0.0342	0.0010	0.1768	0.0010	0.1938	0.0010	0.3149	0
Okinawa (9) v. Wenlock_River (24)	2233.4560	0.0010	0.0002	0.0010	-15.0648	1.0000	0.0318	0.0010	0.0345	0.0010	0.2499	0.0010	0.2697	0.0010	0.4158	0
Fiji (25) v. Seychelles (36)	3917.7856	0.0010	0.0002	0.0010	-8.1055	1.0000	0.0318	0.0010	0.0346	0.0010	0.0861	0.0010	0.0962	0.0010	0.1678	0
Daly_River (49) v. Fiji (25)	4361.5812	0.0010	0.0002	0.0010	-7.0577	1.0000	0.0317	0.0010	0.0351	0.0010	0.0714	0.0010	0.0800	0.0010	0.1413	0
Darwin_Coastal (15) v. Fiji (25)	3056.3905	0.0010	0.0002	0.0010	-10.0134	0.9780	0.0315	0.0010	0.0360	0.0010	0.1424	0.0010	0.1575	0.0010	0.2626	0
Fiji (25) v. Papua_New_Guinea (9)	2504.3831	0.0010	0.0002	0.0010	-14.3600	0.7732	0.0313	0.0010	0.0336	0.0010	0.2433	0.0729	0.2633	0.0709	0.4074	0

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Fiji (25) v. South_Africa (22)	3220.1518	0.0010	0.0002	0.0010	-9.2524	1.0000	0.0304	0.0010	0.0328	0.0010	0.1125	0.0010	0.1250	0.0010	0.2135	0
Okinawa (9) v. Reunion (28)	2342.4528	0.0010	0.0002	0.0010	-14.5997	0.9990	0.0302	0.0010	0.0333	0.0010	0.2369	0.0010	0.2562	0.0010	0.3987	0
East_Alligator_River (47) v. Fiji (25)	4262.6123	0.0010	0.0001	0.0010	-7.4029	1.0000	0.0302	0.0010	0.0334	0.0010	0.0738	0.0010	0.0825	0.0010	0.1455	0
Clarence_River (83) v. Fiji (25)	5278.9751	0.0010	0.0002	0.0010	-5.1588	1.0000	0.0296	0.0010	0.0325	0.0010	0.0509	0.0010	0.0575	0.0010	0.1031	0
Okinawa (9) v. Unknown (10)	1695.2462	0.0020	0.0002	0.0050	-31.4185	0.9960	0.0293	0.0040	0.0318	0.0030	0.4842	0.0050	0.5060	0.0050	0.6672	0
Arabian_Sea (15) v. Okinawa (9)	1897.2786	0.0010	0.0002	0.0010	-19.2703	1.0000	0.0290	0.0010	0.0312	0.0010	0.3270	0.0010	0.3489	0.0010	0.5093	0
Fiji (25) v. Unknown (10)	2586.6470	0.0010	0.0002	0.0010	-13.0877	0.6224	0.0287	0.0010	0.0310	0.0010	0.2147	0.0350	0.2338	0.0320	0.3692	0
Adelaide_River (18) v. Okinawa (9)	1983.6289	0.0010	0.0001	0.0020	-18.2479	0.9990	0.0287	0.0020	0.0308	0.0020	0.3016	0.0020	0.3228	0.0020	0.4797	0
Fiji (25) v. Roper_River (9)	2499.6078	0.0010	0.0002	0.0010	-14.2578	0.5634	0.0284	0.0010	0.0310	0.0010	0.2464	0.1089	0.2669	0.0959	0.4119	0
Clarence_River (83) v. Okinawa (9)	3140.4000	0.0010	0.0001	0.0010	-7.6006	1.0000	0.0278	0.0010	0.0298	0.0010	0.1247	0.0010	0.1379	0.0010	0.2335	0
Okinawa (9) v. South_Alligator_River (88)	3154.2653	0.0010	0.0001	0.0010	-8.1770	1.0000	0.0277	0.0010	0.0301	0.0010	0.1312	0.0010	0.1445	0.0010	0.2437	0
Okinawa (9) v. Sri_Lanka (12)	1785.6135	0.0010	0.0002	0.0020	-24.4796	0.9980	0.0277	0.0040	0.0299	0.0040	0.4009	0.0030	0.4232	0.0030	0.5882	0
Darwin_Coastal (15) v. Okinawa (9)	1908.6859	0.0010	0.0002	0.0010	-18.8205	1.0000	0.0277	0.0020	0.0298	0.0020	0.3216	0.0020	0.3437	0.0020	0.5034	0
Arabian_Sea (15) v. Fiji (25)	2979.1597	0.0010	0.0001	0.0010	-9.9954	0.9920	0.0273	0.0010	0.0311	0.0010	0.1401	0.0010	0.1548	0.0010	0.2587	0
East_Alligator_River (47) v. Okinawa (9)	2583.0886	0.0010	0.0001	0.0010	-11.9573	1.0000	0.0270	0.0010	0.0289	0.0010	0.1865	0.0010	0.2032	0.0010	0.3284	0
Daly_River (49) v. Okinawa (9)	2684.5962	0.0010	0.0001	0.0010	-11.1712	1.0000	0.0265	0.0010	0.0284	0.0010	0.1763	0.0010	0.1926	0.0010	0.3136	0
Okinawa (9) v. Sydney_Harbour (65)	2828.3738	0.0010	0.0002	0.0010	-9.6236	1.0000	0.0263	0.0010	0.0287	0.0010	0.1523	0.0010	0.1671	0.0010	0.2772	0
Okinawa (9) v. Seychelles (36)	2346.3625	0.0010	0.0001	0.0010	-13.3959	0.9990	0.0259	0.0010	0.0283	0.0010	0.2107	0.0010	0.2287	0.0010	0.3630	0
Fiji (25) v. Thailand (5)	2350.1840	0.0010	0.0002	0.0020	-23.9823	0.0165	0.0255	0.0040	0.0273	0.0040	0.4525	0.9428	0.4759	0.9351	0.6392	0
Okinawa (9) v. South_Africa (22)	1993.2978	0.0010	0.0001	0.0020	-16.1321	0.9980	0.0241	0.0010	0.0261	0.0010	0.2630	0.0020	0.2831	0.0020	0.4324	0
Indonesia (4) v. Towns_River (10)	1393.0214	0.0430	0.0002	0.0929	NA	NA	0.0233	0.0651	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Indonesia (4)	974.2003	0.3427	0.0002	0.4116	NA	NA	0.0225	0.3427	0.0243	0.3218	NA	NA	NA	NA	NA	
Indonesia (4) v. Thailand (5)	1117.0939	0.1449	0.0002	0.1968	NA	NA	0.0190	0.1918	0.0204	0.1918	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Towns_River (10)	2008.0221	0.0090	0.0001	0.0050	-14.4111	0.9980	0.0187	0.0050	0.0202	0.0050	0.2402	0.0050	0.2604	0.0050	0.4036	0
Fiji (25) v. Fitzroy_River (3)	2109.6916	0.0090	0.0002	0.0200	NA	NA	0.0183	0.0248	0.0196	0.0248	NA	NA	NA	NA	NA	
Papua_New_Guinea (9) v. Trinity_inlet (5)	1396.6217	0.0020	0.0001	0.0769	-448.5102	0.2630	0.0177	0.0020	0.0191	0.0020	0.9516	0.7090	0.9547	0.7070	0.9768	0
Indonesia (4) v. Papua_New_Guinea (9)	1247.3907	0.0909	0.0002	0.1099	NA	NA	0.0171	0.1049	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Trinity_inlet (5)	1125.2542	0.1708	0.0002	0.1808	NA	NA	0.0170	0.2008	NA	NA	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Trinity_inlet (5)	1809.8972	0.0290	0.0001	0.1209	-26.1771	0.3327	0.0165	0.0509	0.0178	0.0509	0.4839	0.4046	0.5074	0.3846	0.6680	0
Reunion (28) v. Trinity_inlet (5)	2038.0213	0.0020	0.0001	0.0539	-21.6200	0.0200	0.0159	0.0060	0.0170	0.0060	0.4168	0.8457	0.4404	0.8246	0.6050	0
Blue_mud_Bay (18) v. Reunion (28)	2571.1409	0.0010	0.0001	0.0010	-9.3099	0.9171	0.0151	0.0010	0.0165	0.0010	0.1083	0.0010	0.1204	0.0010	0.2063	0
Indonesia (4) v. Seychelles (36)	1963.5232	0.0120	0.0001	0.0320	NA	NA	0.0147	0.0150	NA	NA	NA	NA	NA	NA	NA	
Reunion (28) v. Towns_River (10)	2132.1053	0.0010	0.0001	0.0010	-13.0433	0.8661	0.0140	0.0010	0.0150	0.0010	0.1990	0.0090	0.2167	0.0070	0.3467	0
East_Alligator_River (47) v. Indonesia (4)	2176.4787	0.0040	0.0001	0.0280	NA	NA	0.0135	0.0140	0.0144	0.0140	NA	NA	NA	NA	NA	
Towns_River (10) v. Trinity_inlet (5)	1426.5350	0.0160	0.0001	0.1688	-135.4519	0.2408	0.0134	0.0709	0.0144	0.0709	0.8513	0.7213	0.8604	0.7173	0.9246	0
Blue_mud_Bay (18) v. Darwin_Coastal (15)	2097.6601	0.0020	0.0001	0.0010	-10.8646	0.9940	0.0132	0.0010	0.0143	0.0010	0.1556	0.0010	0.1716	0.0010	0.2831	0
Blue_mud_Bay (18) v. South_Africa (22)	2309.9438	0.0010	0.0001	0.0020	-9.8722	0.9960	0.0129	0.0010	0.0140	0.0010	0.1223	0.0010	0.1355	0.0010	0.2297	0
Sri_Lanka (12) v. Trinity_inlet (5)	1520.3449	0.0030	0.0001	0.0549	-55.7394	0.2857	0.0129	0.0050	0.0139	0.0040	0.6880	0.6014	0.7052	0.5814	0.8253	0
Indonesia (4) v. Wenlock_River (24)	1690.0306	0.1089	0.0001	0.0779	NA	NA	0.0128	0.0251	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Reunion (28)	1788.1551	0.0360	0.0001	0.0649	NA	NA	0.0125	0.0504	NA	NA	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Fitzroy_River (3)	1513.8502	0.3317	0.0002	0.1608	NA	NA	0.0124	0.1176	0.0134	0.1176	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. East_Alligator_River (47)	2837.0933	0.0010	0.0001	0.0010	-8.2119	0.0240	0.0124	0.0010	0.0134	0.0010	0.0822	0.0010	0.0917	0.0010	0.1607	0
Arabian_Sea (15) v. Indonesia (4)	1509.7166	0.1628	0.0001	0.0509	NA	NA	0.0124	0.0381	0.0133	0.0381	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Seychelles (36)	2612.4077	0.0010	0.0001	0.0010	-8.8431	0.3766	0.0124	0.0010	0.0135	0.0010	0.0941	0.0010	0.1049	0.0010	0.1819	0
Arabian_Sea (15) v. Blue_mud_Bay (18)	2101.7710	0.0080	0.0001	0.0020	-10.9137	0.9910	0.0122	0.0090	0.0133	0.0090	0.1557	0.0090	0.1714	0.0090	0.2831	0
Indonesia (4) v. Unknown (10)	1306.7498	0.0639	0.0001	0.1359	NA	NA	0.0121	0.0749	NA	NA	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Mozambique (11)	1857.3962	0.0360	0.0001	0.0170	-14.2198	0.9990	0.0119	0.0190	0.0133	0.0170	0.2346	0.0020	0.2544	0.0020	0.3961	0
Blue_mud_Bay (18) v. South_Alligator_River (88)	3529.1418	0.0010	0.0001	0.0010	-6.1041	0.0130	0.0118	0.0010	0.0128	0.0010	0.0563	0.0010	0.0633	0.0010	0.1132	0
Blue_mud_Bay (18) v. Wenlock_River (24)	2283.2736	0.0010	0.0001	0.0040	-9.6120	0.9820	0.0117	0.0010	0.0127	0.0010	0.1152	0.0010	0.1278	0.0010	0.2180	0
Blue_mud_Bay (18) v. Roper_River (9)	1832.6707	0.0420	0.0001	0.0150	-15.2951	0.9920	0.0116	0.0350	0.0128	0.0350	0.2653	0.0080	0.2864	0.0080	0.4360	0
Blue_mud_Bay (18) v. Clarence_River (83)	3400.7508	0.0010	0.0001	0.0010	-5.6968	0.7393	0.0115	0.0010	0.0126	0.0010	0.0536	0.0010	0.0605	0.0010	0.1083	0
Roper_River (9) v. Towns_River (10)	1532.6049	0.0010	0.0001	0.0110	-28.1377	0.9800	0.0115	0.0080	0.0125	0.0090	0.4569	0.0120	0.4794	0.0110	0.6427	0
Indonesia (4) v. Mozambique (11)	1304.4937	0.1818	0.0001	0.1069	NA	NA	0.0115	0.0898	NA	NA	NA	NA	NA	NA	NA	

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
South_Africa (22) v. Trinity_inlet (5)	1810.5807	0.0020	0.0001	0.1209	-25.1053	0.0280	0.0114	0.0040	0.0122	0.0040	0.4614	0.8450	0.4846	0.8270	0.6473	0
Blue_mud_Bay (18) v. Daly_River (49)	2894.5614	0.0010	0.0001	0.0010	-7.7813	0.2418	0.0113	0.0010	0.0123	0.0010	0.0774	0.0010	0.0865	0.0010	0.1521	0
Indonesia (4) v. Roper_River (9)	1252.4752	0.1439	0.0002	0.1518	NA	NA	0.0112	0.1329	0.0127	0.1299	NA	NA	NA	NA	NA	
Arabian_Sea (15) v. Trinity_inlet (5)	1626.7233	0.0040	0.0001	0.1708	-33.4915	0.2218	0.0111	0.0080	0.0120	0.0080	0.5542	0.5804	0.5759	0.5584	0.7271	0
Mozambique (11) v. Papua_New_Guinea (9)	1470.3666	0.0160	0.0001	0.1189	-28.1255	0.8681	0.0111	0.0030	0.0120	0.0030	0.4506	0.0859	0.4728	0.0829	0.6365	0
Blue_mud_Bay (18) v. Papua_New_Guinea (9)	1730.8418	0.0639	0.0001	0.0400	-15.8859	0.9990	0.0109	0.0370	0.0117	0.0370	0.2662	0.0120	0.2868	0.0130	0.4368	0
Blue_mud_Bay (18) v. Thailand (5)	1674.5510	0.0859	0.0001	0.0280	-27.7177	0.4420	0.0109	0.1160	0.0117	0.1160	0.4946	0.4370	0.5175	0.4300	0.6772	0
Indonesia (4) v. Sri_Lanka (12)	1349.5519	0.1868	0.0001	0.0809	NA	NA	0.0108	0.0839	NA	NA	NA	NA	NA	NA	NA	
Adelaide_River (18) v. Trinity_inlet (5)	1700.6529	0.0020	0.0001	0.2308	-30.6847	0.0380	0.0108	0.0100	0.0116	0.0100	0.5209	0.8681	0.5431	0.8601	0.6996	0
Blue_mud_Bay (18) v. Sydney_Harbour (65)	3170.9773	0.0010	0.0001	0.0010	-6.8309	0.0869	0.0106	0.0010	0.0116	0.0010	0.0649	0.0010	0.0728	0.0010	0.1293	0
Thailand (5) v. Towns_River (10)	1415.4509	0.0160	0.0001	0.1099	-145.7607	0.1968	0.0106	0.1059	0.0116	0.1059	0.8593	0.7762	0.8678	0.7742	0.9289	0
Adelaide_River (18) v. Towns_River (10)	1741.0276	0.0050	0.0001	0.0020	-15.8939	0.9730	0.0103	0.0020	0.0111	0.0020	0.2537	0.0010	0.2737	0.0010	0.4206	0
South_Alligator_River (88) v. Trinity_inlet (5)	2945.0540	0.0010	0.0001	0.4036	-9.6837	0.0030	0.0102	0.0090	0.0109	0.0090	0.2217	0.9060	0.2411	0.8610	0.3788	0
Mozambique (11) v. Towns_River (10)	1546.0188	0.0140	0.0001	0.0150	-24.4358	0.9670	0.0100	0.0170	0.0109	0.0170	0.4042	0.0310	0.4268	0.0310	0.5918	0
South_Alligator_River (88) v. Towns_River (10)	2806.4763	0.0010	0.0001	0.0010	-7.5273	0.4925	0.0099	0.0010	0.0106	0.0010	0.1054	0.0020	0.1168	0.0020	0.2010	0
Blue_mud_Bay (18) v. Unknown (10)	1823.9971	0.0310	0.0001	0.0120	-14.2432	0.9840	0.0095	0.0400	0.0103	0.0400	0.2334	0.0250	0.2532	0.0260	0.3945	0
Daly_River (49) v. Towns_River (10)	2310.0903	0.0010	0.0001	0.0030	-10.1573	0.8462	0.0095	0.0010	0.0102	0.0010	0.1450	0.0010	0.1595	0.0010	0.2659	0
Papua_New_Guinea (9) v. Unknown (10)	1404.1215	0.0120	0.0001	0.0080	-28.7742	0.9940	0.0095	0.0030	0.0103	0.0020	0.4552	0.0070	0.4773	0.0070	0.6408	0
Adelaide_River (18) v. Blue_mud_Bay (18)	2068.4350	0.0080	0.0001	0.0190	-10.7243	0.9890	0.0093	0.0090	0.0101	0.0090	0.1401	0.0090	0.1545	0.0090	0.2584	0
Papua_New_Guinea (9) v. Towns_River (10)	1433.7072	0.0440	0.0001	0.0929	-29.2832	0.9540	0.0092	0.0529	0.0100	0.0529	0.4596	0.0519	0.4815	0.0529	0.6447	0
Towns_River (10) v. Wenlock_River (24)	1916.3447	0.0020	0.0001	0.1199	-13.3737	0.9590	0.0091	0.0060	0.0099	0.0060	0.2069	0.0030	0.2250	0.0030	0.3579	0
Mozambique (11) v. Wenlock_River (24)	1929.1416	0.0010	0.0001	0.0020	-13.1429	1.0000	0.0090	0.0010	0.0097	0.0010	0.2042	0.0010	0.2222	0.0010	0.3541	0
Sydney_Harbour (65) v. Trinity_inlet (5)	2520.8663	0.0010	0.0001	0.2008	-11.9718	0.0030	0.0089	0.0060	0.0095	0.0060	0.2629	0.9370	0.2840	0.9150	0.4331	0
East_Alligator_River (47) v. Towns_River (10)	2244.5381	0.0010	0.0001	0.0100	-10.8554	0.4186	0.0087	0.0010	0.0094	0.0010	0.1533	0.0040	0.1682	0.0020	0.2788	0
Arabian_Sea (15) v. Towns_River (10)	1732.2218	0.0050	0.0001	0.0270	-16.0678	0.9910	0.0085	0.0060	0.0093	0.0050	0.2686	0.0020	0.2893	0.0020	0.4398	0
Seychelles (36) v. Trinity_inlet (5)	2158.9166	0.0010	0.0001	0.0849	-18.3290	0.0040	0.0084	0.0180	0.0090	0.0180	0.3652	0.9720	0.3883	0.9650	0.5519	0
Clarence_River (83) v. Towns_River (10)	2567.2184	0.0060	0.0001	0.0020	-7.1376	0.9940	0.0084	0.0010	0.0090	0.0010	0.1007	0.0010	0.1119	0.0010	0.1932	0
Seychelles (36) v. Towns_River (10)	2094.2492	0.0010	0.0001	0.0020	-11.9077	0.7522	0.0082	0.0030	0.0088	0.0030	0.1729	0.0080	0.1891	0.0050	0.3086	0
Blue_mud_Bay (18) v. Sri_Lanka (12)	1869.4295	0.0470	0.0001	0.0190	-12.6550	0.9720	0.0082	0.0470	0.0088	0.0470	0.1926	0.0460	0.2104	0.0470	0.3380	0
South_Africa (22) v. Towns_River (10)	1826.0931	0.0020	0.0001	0.0060	-14.1714	0.9580	0.0081	0.0030	0.0087	0.0030	0.2203	0.0030	0.2390	0.0030	0.3764	0
Fitzroy_River (3) v. Thailand (5)	1023.9241	0.1439	0.0002	0.0380	NA	NA	0.0080	0.1648	0.0086	0.1709	NA	NA	NA	NA	NA	
Sydney_Harbour (65) v. Towns_River (10)	2386.4289	0.0010	0.0001	0.0020	-8.8242	0.7662	0.0079	0.0010	0.0085	0.0010	0.1237	0.0040	0.1366	0.0030	0.2317	0
Reunion (28) v. Roper_River (9)	1942.5524	0.0010	0.0001	0.0010	-13.6369	0.7123	0.0077	0.0110	0.0084	0.0100	0.2203	0.0579	0.2392	0.0519	0.3765	0
Thailand (5) v. Trinity_inlet (5)	1145.6720	0.0320	0.0001	0.1928	35.0389	0.9291	0.0076	0.1049	0.0083	0.1039	2.0068	0.0859	1.9180	0.0859	1.3053	0
Darwin_Coastal (15) v. Indonesia (4)	1422.5570	0.2637	0.0002	0.0300	NA	NA	0.0075	0.0969	0.0081	0.0969	NA	NA	NA	NA	NA	
Darwin_Coastal (15) v. Reunion (28)	2156.7119	0.0010	0.0001	0.0120	-10.1157	0.0759	0.0075	0.0010	0.0083	0.0010	0.1239	0.0270	0.1372	0.0150	0.2324	0
Mozambique (11) v. Trinity_inlet (5)	1405.6092	0.0200	0.0001	0.3017	-112.9994	0.1235	0.0075	0.0556	0.0081	0.0596	0.8264	0.9837	0.8369	0.9837	0.9107	0
Sri_Lanka (12) v. Towns_River (10)	1545.9168	0.0240	0.0001	0.0290	-20.3100	0.9880	0.0075	0.0280	0.0081	0.0280	0.3372	0.0130	0.3592	0.0120	0.5208	0
East_Alligator_River (47) v. Trinity_inlet (5)	2350.5556	0.0010	0.0001	0.5954	-15.8290	0.0010	0.0074	0.0220	0.0079	0.0220	0.3249	0.9800	0.3473	0.9780	0.5073	0
Towns_River (10) v. Unknown (10)	1479.3415	0.0180	0.0001	0.0110	-24.5615	0.9660	0.0071	0.0380	0.0077	0.0380	0.4036	0.0360	0.4262	0.0370	0.5912	0
Trinity_inlet (5) v. Wenlock_River (24)	1866.8551	0.0040	0.0001	0.4885	-22.7634	0.0180	0.0071	0.0370	0.0077	0.0370	0.4318	0.9131	0.4551	0.9021	0.6195	0
Daly_River (49) v. Trinity_inlet (5)	2304.8616	0.0010	0.0001	0.5225	-14.6805	0.0080	0.0070	0.0200	0.0075	0.0200	0.3082	0.9261	0.3306	0.9061	0.4883	0
Reunion (28) v. South_Alligator_River (88)	2998.5133	0.0010	0.0000	0.0010	-5.9769	0.4116	0.0069	0.0010	0.0075	0.0010	0.0390	0.0010	0.0439	0.0010	0.0798	0
Arabian_Sea (15) v. Papua_New_Guinea (9)	1609.9884	0.0430	0.0001	0.0310	-17.7297	0.9960	0.0067	0.0070	0.0072	0.0070	0.2995	0.0040	0.3207	0.0040	0.4772	0
Clarence_River (83) v. Trinity_inlet (5)	2665.7839	0.0040	0.0001	0.4266	-9.0782	0.1132	0.0065	0.0381	0.0070	0.0381	0.2099	0.5762	0.2291	0.5311	0.3628	0
Trinity_inlet (5) v. Unknown (10)	1318.5721	0.0140	0.0001	0.2118	-123.0090	0.0410	0.0059	0.0749	0.0065	0.0750	0.8374	0.9480	0.8473	0.9440	0.9169	0
Papua_New_Guinea (9) v. Reunion (28)	1803.8110	0.0320	0.0001	0.0130	-14.0484	0.8382	0.0058	0.0430	0.0064	0.0430	0.2185	0.1768	0.2368	0.1798	0.3736	0
East_Alligator_River (47) v. Reunion (28)	2508.8505	0.0010	0.0000	0.0010	-7.8039	0.5375	0.0058	0.0010	0.0062	0.0010	0.0579	0.0010	0.0647	0.0010	0.1159	0
Reunion (28) v. Sydney_Harbour (65)	2703.5379	0.0010	0.0000	0.0010	-6.6783	0.9201	0.0058	0.0010	0.0063	0.0010	0.0458	0.0010	0.0514	0.0010	0.0929	0
Arabian_Sea (15) v. Darwin_Coastal (15)	1855.7191	0.0010	0.0000	0.3477	-11.8217	0.9980	0.0057	0.0020	0.0062	0.0020	0.1752	0.0020	0.1921	0.0020	0.3126	0
Mozambique (11) v. South_Alligator_River (88)	2543.3445	0.0080	0.0000	0.0220	-7.4473	0.8442	0.0057	0.0010	0.0062	0.0010	0.1019	0.0010	0.1129	0.0010	0.1949	0
Reunion (28) v. Unknown (10)	1878.0032	0.0030	0.0001	0.0070	-12.9993	0.4915	0.0057	0.0280	0.0061	0.0280	0.1940	0.1818	0.2115	0.1718	0.3396	0
East_Alligator_River (47) v. Mozambique (11)	2122.9034	0.0010	0.0000	0.0380	-10.6939	0.9491	0.0055	0.0030	0.0060	0.0010	0.1497	0.0010	0.1644	0.0010	0.2732	0

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Fitzroy_River (3) v. Trinity_inlet (5)	979.7552	0.3616	0.0002	0.2987	NA	NA	0.0055	0.2348	0.0060	0.2524	NA	NA	NA	NA	NA	
Clarence_River (83) v. Reunion (28)	2845.1394	0.0010	0.0000	0.0010	-5.6161	1.0000	0.0054	0.0010	0.0058	0.0010	0.0367	0.0010	0.0414	0.0010	0.0753	0
Mozambique (11) v. Reunion (28)	1869.1632	0.0150	0.0001	0.0470	-12.9534	0.9810	0.0054	0.0250	0.0059	0.0280	0.1939	0.0020	0.2114	0.0020	0.3395	0
Reunion (28) v. Wenlock_River (24)	2157.5084	0.0010	0.0000	0.0010	-9.1405	0.9860	0.0053	0.0010	0.0057	0.0010	0.0879	0.0030	0.0978	0.0030	0.1706	0
Mozambique (11) v. Seychelles (36)	1974.2569	0.0010	0.0001	0.0070	-11.9120	0.9930	0.0051	0.0050	0.0056	0.0050	0.1714	0.0010	0.1876	0.0010	0.3065	0
Darwin_Coastal (15) v. Mozambique (11)	1637.7308	0.0440	0.0001	0.0110	-15.8054	1.0000	0.0051	0.0180	0.0057	0.0170	0.2637	0.0010	0.2846	0.0010	0.4339	0
Darwin_Coastal (15) v. Towns_River (10)	1651.9702	0.0240	0.0001	0.2438	-16.0045	0.9940	0.0050	0.0669	0.0054	0.0659	0.2663	0.0130	0.2872	0.0140	0.4371	0
Darwin_Coastal (15) v. Trinity_inlet (5)	1525.4953	0.0769	0.0001	0.1588	-32.9632	0.3367	0.0050	0.1179	0.0054	0.1179	0.5483	0.5624	0.5704	0.5465	0.7225	0
Brazil (50) v. Gulf_of_Mexico (37)	2325.3566	0.0010	0.0000	0.0250	-8.6882	1.0000	0.0049	0.0010	0.0053	0.0010	0.0536	0.0010	0.0593	0.0010	0.1071	0
Reunion (28) v. Seychelles (36)	2239.8359	0.0010	0.0000	0.0010	-8.4873	0.9870	0.0048	0.0010	0.0052	0.0010	0.0685	0.0010	0.0766	0.0010	0.1358	0
Fitzroy_River (3) v. Sri_Lanka (12)	1298.4252	0.3377	0.0001	0.3936	NA	NA	0.0046	0.2299	0.0050	0.2397	NA	NA	NA	NA	NA	
Seychelles (36) v. Thailand (5)	1919.1018	0.0010	0.0001	0.0579	-19.2828	0.0230	0.0046	0.1209	0.0049	0.1209	0.3739	0.9630	0.3967	0.9600	0.5609	0
Daly_River (49) v. Mozambique (11)	2181.4988	0.0030	0.0000	0.0549	-10.0095	0.9910	0.0046	0.0050	0.0050	0.0030	0.1408	0.0010	0.1550	0.0010	0.2593	0
Adelaide_River (18) v. Reunion (28)	2014.6971	0.0010	0.0000	0.0050	-10.1316	0.8472	0.0046	0.0070	0.0050	0.0070	0.1108	0.0200	0.1226	0.0200	0.2101	0
Clarence_River (83) v. Roper_River (9)	2381.9697	0.1499	0.0001	0.0030	-7.3091	0.9540	0.0045	0.0170	0.0049	0.0170	0.1125	0.0010	0.1248	0.0010	0.2133	0
Clarence_River (83) v. Mozambique (11)	2435.0830	0.0669	0.0001	0.0040	-6.9857	1.0000	0.0045	0.0070	0.0049	0.0070	0.0965	0.0010	0.1074	0.0010	0.1859	0
Papua_New_Guinea (9) v. Thailand (5)	1272.2324	0.0290	0.0001	0.2647	-944.1888	0.3596	0.0044	0.1948	0.0047	0.1948	0.9760	0.9630	0.9775	0.9630	0.9886	0
Papua_New_Guinea (9) v. Sri_Lanka (12)	1411.8786	0.2338	0.0001	0.1928	-22.9494	0.9371	0.0042	0.0999	0.0045	0.0989	0.3760	0.0529	0.3980	0.0519	0.5625	0
Papua_New_Guinea (9) v. Seychelles (36)	1790.9361	0.0689	0.0001	0.0160	-13.0189	0.8691	0.0042	0.0360	0.0046	0.0360	0.1953	0.0829	0.2125	0.0799	0.3412	0
Adelaide_River (18) v. Papua_New_Guinea (9)	1536.5630	0.2018	0.0001	0.0100	-17.4849	0.9441	0.0041	0.0589	0.0044	0.0589	0.2816	0.0230	0.3021	0.0260	0.4554	0
Roper_River (9) v. South_Alligator_River (88)	2529.3531	0.0120	0.0001	0.0040	-7.7443	0.2088	0.0041	0.0310	0.0045	0.0310	0.1173	0.0150	0.1297	0.0120	0.2210	0
Darwin_Coastal (15) v. Fitzroy_River (3)	1353.1972	0.5704	0.0002	0.1429	NA	NA	0.0041	0.2203	0.0044	0.2203	NA	NA	NA	NA	NA	
Papua_New_Guinea (9) v. Roper_River (9)	1336.7463	0.1469	0.0001	0.2557	-33.7010	0.8492	0.0041	0.1439	0.0045	0.1409	0.5104	0.1359	0.5318	0.1359	0.6900	0
Arabian_Sea (15) v. Mozambique (11)	1666.5157	0.0759	0.0001	0.2867	-15.7147	1.0000	0.0041	0.0290	0.0045	0.0270	0.2620	0.0010	0.2825	0.0010	0.4315	0
East_Alligator_River (47) v. Fitzroy_River (3)	1932.3884	0.0559	0.0001	0.3397	NA	NA	0.0040	0.1998	0.0043	0.1998	NA	NA	NA	NA	NA	
Adelaide_River (18) v. Darwin_Coastal (15)	1799.5237	0.0110	0.0000	0.0999	-11.7234	0.5345	0.0040	0.0120	0.0043	0.0120	0.1607	0.0250	0.1766	0.0220	0.2906	0
Daly_River (49) v. Reunion (28)	2408.6412	0.0010	0.0000	0.0010	-7.5142	0.9081	0.0040	0.0010	0.0043	0.0010	0.0544	0.0010	0.0609	0.0010	0.1094	0
Adelaide_River (18) v. Roper_River (9)	1640.8032	0.0310	0.0001	0.0829	-16.7916	0.8651	0.0039	0.0769	0.0043	0.0729	0.2794	0.0270	0.3003	0.0230	0.4531	0
Sydney_Harbour (65) v. Wenlock_River (24)	2459.1597	0.0010	0.0000	0.0010	-6.8722	0.5624	0.0039	0.0010	0.0042	0.0010	0.0506	0.0010	0.0568	0.0010	0.1023	0
Fitzroy_River (3) v. Papua_New_Guinea (9)	1145.2011	0.2438	0.0001	0.5994	NA	NA	0.0039	0.3239	NA	NA	NA	NA	NA	NA	NA	
Clarence_River (83) v. Papua_New_Guinea (9)	2129.1521	0.7203	0.0001	0.0060	-7.5970	0.9990	0.0038	0.0310	0.0041	0.0310	0.1121	0.0020	0.1241	0.0020	0.2124	0
Darwin_Coastal (15) v. Thailand (5)	1533.7705	0.0519	0.0001	0.0799	-33.2654	0.4525	0.0038	0.1658	0.0041	0.1658	0.5486	0.5335	0.5704	0.5325	0.7226	0
Thailand (5) v. Wenlock_River (24)	1753.5950	0.0230	0.0001	0.2757	-23.3907	0.0529	0.0038	0.1319	0.0041	0.1319	0.4350	0.9421	0.4579	0.9391	0.6222	0
Brazil (50) v. Western_North_Atlantic (8)	1764.9563	0.5994	0.0000	0.3846	-14.8037	0.9937	0.0037	0.0943	0.0040	0.0943	0.2265	0.0053	0.2430	0.0063	0.3828	0
Roper_River (9) v. Sri_Lanka (12)	1491.0231	0.0380	0.0001	0.0460	-22.0378	0.9461	0.0037	0.0689	0.0040	0.0729	0.3726	0.0200	0.3951	0.0180	0.5593	0
East_Alligator_River (47) v. Thailand (5)	2084.7688	0.0010	0.0001	0.2088	-16.4398	0.0110	0.0036	0.1470	0.0039	0.1470	0.3295	0.9860	0.3515	0.9850	0.5123	0
East_Alligator_River (47) v. Roper_River (9)	2050.7647	0.0070	0.0001	0.0959	-11.3029	0.2727	0.0036	0.0480	0.0039	0.0480	0.1720	0.0410	0.1881	0.0280	0.3073	0
Darwin_Coastal (15) v. East_Alligator_River (47)	2350.3973	0.0010	0.0000	0.0230	-8.6418	0.0010	0.0036	0.0040	0.0039	0.0040	0.0920	0.4486	0.1024	0.3516	0.1780	0
Arabian_Sea (15) v. South_Alligator_River (88)	2963.9767	0.0010	0.0000	0.0140	-6.3203	0.0340	0.0034	0.0100	0.0037	0.0100	0.0621	0.1149	0.0695	0.0919	0.1239	0
Reunion (28) v. South_Africa (22)	2046.1101	0.0040	0.0000	0.0020	-9.3965	0.8302	0.0033	0.0110	0.0036	0.0110	0.0929	0.0220	0.1032	0.0230	0.1794	0
Mozambique (11) v. Roper_River (9)	1470.9006	0.0679	0.0001	0.0529	-26.9897	0.4066	0.0033	0.1339	0.0037	0.1369	0.4442	0.4925	0.4667	0.4875	0.6308	0
Mozambique (11) v. Sri_Lanka (12)	1510.9759	0.1199	0.0001	0.1958	-19.8424	0.9980	0.0033	0.0869	0.0036	0.0909	0.3304	0.0020	0.3523	0.0020	0.5132	0
Mozambique (11) v. Sydney_Harbour (65)	2275.9873	0.0120	0.0000	0.0330	-8.6917	0.9810	0.0033	0.0200	0.0036	0.0210	0.1192	0.0010	0.1318	0.0010	0.2243	0
Roper_River (9) v. Wenlock_River (24)	1711.3405	0.1499	0.0001	0.1159	-14.2935	0.8621	0.0033	0.0839	0.0036	0.0839	0.2327	0.0340	0.2521	0.0310	0.3933	0
Reunion (28) v. Sri_Lanka (12)	1944.4230	0.0050	0.0000	0.1419	-11.5330	0.3806	0.0032	0.1039	0.0034	0.1059	0.1553	0.3856	0.1704	0.3756	0.2819	0
Daly_River (49) v. Thailand (5)	2220.9839	0.0020	0.0001	0.0490	-14.8688	0.0470	0.0030	0.1788	0.0032	0.1788	0.3076	0.9409	0.3295	0.9369	0.4872	0
Reunion (28) v. Thailand (5)	1867.7590	0.0160	0.0001	0.0659	-21.9852	0.0220	0.0030	0.2480	0.0032	0.2490	0.4139	0.9700	0.4368	0.9690	0.6017	0
Daly_River (49) v. Unknown (10)	2011.9401	0.0569	0.0001	0.0020	-10.2255	0.5774	0.0029	0.0629	0.0032	0.0629	0.1423	0.0390	0.1566	0.0330	0.2616	0
Unknown (10) v. Wenlock_River (24)	1713.7439	0.1299	0.0001	0.0200	-13.4525	0.7023	0.0029	0.0859	0.0032	0.0859	0.2045	0.0869	0.2225	0.0819	0.3545	0
East_Alligator_River (47) v. Papua_New_Guinea (9)	1885.6818	0.1578	0.0000	0.1209	-11.6441	0.6424	0.0029	0.0909	0.0031	0.0909	0.1706	0.1309	0.1862	0.1249	0.3048	0
Darwin_Coastal (15) v. Unknown (10)	1578.8748	0.0839	0.0001	0.0290	-15.8374	0.9940	0.0029	0.1029	0.0032	0.1019	0.2629	0.0130	0.2838	0.0130	0.4329	0
Seychelles (36) v. Wenlock_River (24)	2182.4773	0.0010	0.0000	0.0050	-8.5257	0.6114	0.0029	0.0050	0.0031	0.0050	0.0733	0.0070	0.0818	0.0070	0.1445	0
Seychelles (36) v. Unknown (10)	1848.6789	0.0220	0.0001	0.0280	-12.0359	0.3127	0.0029	0.0729	0.0031	0.0729	0.1714	0.2897	0.1875	0.2667	0.3064	0

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Clarence_River (83) v. Seychelles (36)	2706.1889	0.0010	0.0000	0.0020	-5.3984	1.0000	0.0029	0.0010	0.0031	0.0010	0.0286	0.0010	0.0323	0.0010	0.0592	0
Daly_River (49) v. Roper_River (9)	2049.4392	0.0380	0.0001	0.0140	-10.6572	0.6933	0.0028	0.0969	0.0030	0.0959	0.1627	0.0120	0.1784	0.0120	0.2934	0
Darwin_Coastal (15) v. Papua_New_Guinea (9)	1476.9374	0.4565	0.0001	0.4825	-17.8863	0.9990	0.0028	0.1499	0.0030	0.1499	0.2995	0.0080	0.3210	0.0100	0.4775	0
Papua_New_Guinea (9) v. Wenlock_River (24)	1640.5390	0.3477	0.0001	0.2098	-14.6334	0.9481	0.0027	0.1139	0.0030	0.1149	0.2307	0.0330	0.2495	0.0350	0.3902	0
Mozambique (11) v. Unknown (10)	1475.8046	0.0350	0.0001	0.0340	-23.7327	0.8282	0.0027	0.1439	0.0030	0.1489	0.3939	0.1169	0.4164	0.1159	0.5813	0
Daly_River (49) v. Darwin_Coastal (15)	2314.4070	0.0010	0.0000	0.0739	-8.3279	0.0080	0.0027	0.0250	0.0029	0.0250	0.0880	0.3297	0.0981	0.2667	0.1710	0
Seychelles (36) v. Sydney_Harbour (65)	2529.7314	0.0010	0.0000	0.0010	-6.5067	0.9491	0.0027	0.0010	0.0030	0.0010	0.0367	0.0010	0.0412	0.0010	0.0751	0
Thailand (5) v. Unknown (10)	1296.8852	0.0280	0.0001	0.3027	-134.9568	0.0521	0.0027	0.2520	0.0030	0.2490	0.8485	0.9409	0.8576	0.9409	0.9230	0
Roper_River (9) v. Sydney_Harbour (65)	2216.4061	0.0549	0.0001	0.0110	-9.0859	0.4675	0.0027	0.0619	0.0030	0.0639	0.1378	0.0300	0.1519	0.0300	0.2546	0
Arabian_Sea (15) v. Roper_River (9)	1581.0131	0.1199	0.0001	0.1868	-17.5233	0.9550	0.0026	0.1518	0.0029	0.1489	0.3012	0.0200	0.3229	0.0190	0.4796	0
Darwin_Coastal (15) v. Seychelles (36)	2141.2217	0.0010	0.0000	0.4835	-9.3549	0.0020	0.0026	0.0400	0.0028	0.0400	0.1051	0.5654	0.1167	0.5165	0.2007	0
Arabian_Sea (15) v. East_Alligator_River (47)	2317.3558	0.0010	0.0000	0.4845	-8.6769	0.0170	0.0026	0.0220	0.0028	0.0220	0.0918	0.4456	0.1020	0.3766	0.1774	0
Adelaide_River (18) v. Wenlock_River (24)	1885.7208	0.0250	0.0000	0.0200	-10.3480	0.9051	0.0026	0.0350	0.0028	0.0350	0.1179	0.0390	0.1303	0.0380	0.2220	0
Roper_River (9) v. Trinity_inlet (5)	1319.8432	0.0380	0.0001	0.7762	-352.3404	0.3508	0.0026	0.2857	0.0028	0.2897	0.9395	0.9678	0.9434	0.9678	0.9708	0
Darwin_Coastal (15) v. Sydney_Harbour (65)	2436.6114	0.0010	0.0000	0.2787	-7.3777	0.0020	0.0026	0.0180	0.0028	0.0180	0.0746	0.5445	0.0835	0.4775	0.1471	0
Roper_River (9) v. Seychelles (36)	1888.0352	0.0140	0.0001	0.1119	-12.5960	0.5574	0.0026	0.1449	0.0028	0.1469	0.1949	0.0769	0.2124	0.0739	0.3408	0
Adelaide_River (18) v. Thailand (5)	1531.3836	0.0839	0.0001	0.3177	-32.3194	0.0661	0.0026	0.2408	0.0027	0.2448	0.5294	0.9299	0.5509	0.9299	0.7064	0
Papua_New_Guinea (9) v. Sydney_Harbour (65)	1927.3047	0.8122	0.0001	0.0160	-9.5687	0.9481	0.0026	0.0849	0.0028	0.0849	0.1395	0.0919	0.1533	0.0969	0.2570	0
South_Africa (22) v. Unknown (10)	1621.6366	0.2817	0.0001	0.1409	-14.1565	0.6803	0.0026	0.1049	0.0028	0.1049	0.2172	0.0879	0.2357	0.0809	0.3721	0
South_Alligator_River (88) v. Thailand (5)	2699.5695	0.0030	0.0001	0.1439	-9.8722	0.0100	0.0025	0.2008	0.0026	0.2008	0.2195	0.9940	0.2384	0.9930	0.3755	0
Darwin_Coastal (15) v. Sri_Lanka (12)	1666.1141	0.0539	0.0000	0.3317	-13.7594	0.9660	0.0025	0.1029	0.0027	0.1029	0.2160	0.0529	0.2350	0.0569	0.3709	0
Roper_River (9) v. South_Africa (22)	1695.4656	0.0450	0.0001	0.2008	-15.0514	0.8751	0.0025	0.1429	0.0027	0.1459	0.2460	0.0300	0.2658	0.0270	0.4107	0
Papua_New_Guinea (9) v. South_Alligator_River (88)	2230.0794	0.3826	0.0000	0.0699	-8.0400	0.8332	0.0023	0.0979	0.0025	0.0979	0.1164	0.0689	0.1284	0.0709	0.2193	0
Roper_River (9) v. Unknown (10)	1411.8743	0.0340	0.0001	0.0010	-27.3583	0.8242	0.0023	0.2128	0.0025	0.2188	0.4461	0.1409	0.4686	0.1409	0.6325	0
Fitzroy_River (3) v. Roper_River (9)	1188.4235	0.2308	0.0002	0.3167	NA	NA	0.0022	0.3477	0.0026	0.3579	NA	NA	NA	NA	NA	
Darwin_Coastal (15) v. South_Alligator_River (88)	2811.3993	0.0010	0.0000	0.0440	-6.3245	0.0010	0.0022	0.0420	0.0024	0.0420	0.0615	0.7173	0.0690	0.6134	0.1229	0
Seychelles (36) v. South_Alligator_River (88)	2659.6655	0.0010	0.0000	0.0010	-5.7037	0.4446	0.0022	0.0010	0.0024	0.0010	0.0293	0.0010	0.0329	0.0010	0.0604	0
Daly_River (49) v. Sri_Lanka (12)	2096.2572	0.0250	0.0000	0.1279	-9.3957	0.5435	0.0022	0.0809	0.0023	0.0809	0.1144	0.1698	0.1266	0.1548	0.2163	0
Daly_River (49) v. Wenlock_River (24)	2245.9005	0.0010	0.0000	0.0839	-7.6746	0.5864	0.0021	0.0090	0.0023	0.0090	0.0595	0.0070	0.0666	0.0070	0.1190	0
Adelaide_River (18) v. Seychelles (36)	2019.8115	0.0010	0.0000	0.0260	-9.5143	0.5165	0.0021	0.0490	0.0023	0.0490	0.0949	0.1269	0.1054	0.1219	0.1830	0
Darwin_Coastal (15) v. Roper_River (9)	1556.4537	0.1279	0.0001	0.0360	-17.3274	0.9920	0.0021	0.1818	0.0023	0.1788	0.2989	0.0080	0.3209	0.0100	0.4771	0
Adelaide_River (18) v. Unknown (10)	1516.7211	0.4146	0.0001	0.1069	-15.8870	0.6054	0.0021	0.1698	0.0023	0.1678	0.2495	0.1449	0.2693	0.1429	0.4152	0
South_Alligator_River (88) v. Wenlock_River (24)	2616.8520	0.0010	0.0000	0.0430	-5.9995	0.1049	0.0021	0.0110	0.0022	0.0110	0.0408	0.0340	0.0458	0.0280	0.0832	0
Arabian_Sea (15) v. Daly_River (49)	2363.0448	0.0010	0.0000	0.1908	-8.2842	0.2118	0.0021	0.0569	0.0022	0.0569	0.0872	0.1948	0.0971	0.1668	0.1695	0
Clarence_River (83) v. South_Africa (22)	2487.0747	0.0320	0.0000	0.0100	-5.8620	0.9870	0.0020	0.0130	0.0022	0.0130	0.0430	0.0030	0.0484	0.0040	0.0876	0
Papua_New_Guinea (9) v. South_Africa (22)	1596.4856	0.3616	0.0001	0.0300	-15.4042	0.9540	0.0020	0.1948	0.0022	0.1948	0.2440	0.0559	0.2633	0.0579	0.4078	0
Arabian_Sea (15) v. South_Africa (22)	1883.4848	0.0110	0.0000	0.1698	-10.8150	0.3796	0.0020	0.0819	0.0022	0.0819	0.1385	0.1658	0.1526	0.1538	0.2557	0
Arabian_Sea (15) v. Sydney_Harbour (65)	2612.4950	0.0010	0.0000	0.0480	-7.2564	0.1379	0.0019	0.0539	0.0021	0.0529	0.0732	0.3766	0.0818	0.3447	0.1444	0
South_Africa (22) v. Wenlock_River (24)	1930.3594	0.0150	0.0000	0.0030	-9.6337	0.9151	0.0019	0.0529	0.0021	0.0529	0.1001	0.0529	0.1111	0.0529	0.1919	0
Arabian_Sea (15) v. Reunion (28)	2088.8182	0.0010	0.0000	0.0829	-9.9971	0.1678	0.0019	0.1309	0.0021	0.1299	0.1199	0.4376	0.1326	0.4216	0.2255	0
Adelaide_River (18) v. South_Africa (22)	1788.5555	0.1339	0.0000	0.0330	-10.8447	0.8671	0.0019	0.1089	0.0021	0.1089	0.1266	0.1049	0.1396	0.1059	0.2363	0
Adelaide_River (18) v. Mozambique (11)	1617.9908	0.2258	0.0001	0.3187	-15.5226	0.9970	0.0019	0.2038	0.0021	0.1998	0.2453	0.0010	0.2649	0.0010	0.4097	0
Sri_Lanka (12) v. Wenlock_River (24)	1782.1350	0.1189	0.0000	0.4985	-11.9012	0.5964	0.0019	0.1379	0.0020	0.1379	0.1650	0.2527	0.1808	0.2468	0.2968	0
Clarence_River (83) v. Wenlock_River (24)	2559.1166	0.0210	0.0000	0.0010	-5.6874	0.9810	0.0018	0.0140	0.0020	0.0140	0.0392	0.0020	0.0441	0.0030	0.0802	0
Arabian_Sea (15) v. Clarence_River (83)	2778.3609	0.0010	0.0000	0.3666	-6.0034	0.7872	0.0018	0.0669	0.0020	0.0669	0.0589	0.0619	0.0662	0.0659	0.1182	0
South_Alligator_River (88) v. Sydney_Harbour (65)	2824.9691	0.0010	0.0000	0.0010	-4.8796	0.4725	0.0017	0.0010	0.0018	0.0010	0.0175	0.0010	0.0197	0.0010	0.0366	0
Sri_Lanka (12) v. Sydney_Harbour (65)	2223.8596	0.0729	0.0000	0.0579	-8.1772	0.4206	0.0017	0.1109	0.0019	0.1109	0.0966	0.4046	0.1073	0.3876	0.1859	0
East_Alligator_River (47) v. Wenlock_River (24)	2175.7310	0.0040	0.0000	0.0699	-8.0475	0.0529	0.0017	0.0350	0.0018	0.0350	0.0627	0.0959	0.0700	0.0819	0.1248	0
Clarence_River (83) v. Sri_Lanka (12)	2403.9630	0.1399	0.0000	0.1089	-6.6491	0.9471	0.0016	0.1299	0.0018	0.1299	0.0775	0.0450	0.0866	0.0500	0.1522	0
Clarence_River (83) v. Darwin_Coastal (15)	2579.6377	0.0030	0.0000	0.1658	-6.0741	0.1758	0.0016	0.0879	0.0018	0.0879	0.0594	0.2817	0.0668	0.2697	0.1192	0
Adelaide_River (18) v. Arabian_Sea (15)	1758.1951	0.1139	0.0000	0.5405	-11.7334	0.4486	0.0016	0.1668	0.0017	0.1668	0.1596	0.2448	0.1751	0.2338	0.2887	0
Brazil (50) v. Caribbean_Sea (2)	1530.3572	0.8342	0.0002	0.3127	14.5573	0.3333	0.0016	0.8000	0.0017	0.8000	7.5662	1.0000	6.9471	1.0000	1.6942	1
Daly_River (49) v. Seychelles (36)	2284.1794	0.0020	0.0000	0.0010	-7.2509	0.9351	0.0016	0.0210	0.0017	0.0210	0.0442	0.0170	0.0496	0.0170	0.0899	0

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
South_Alligator_River (88) v. Unknown (10)	2280.8820	0.2557	0.0000	0.0509	-7.6226	0.1648	0.0015	0.1838	0.0017	0.1838	0.1021	0.2837	0.1132	0.2557	0.1954	0
Daly_River (49) v. Fitzroy_River (3)	1956.9130	0.1688	0.0001	0.5514	NA	NA	0.0015	0.3833	0.0016	0.3833	NA	NA	NA	NA	NA	
Adelaide_River (18) v. East_Alligator_River (47)	2058.7551	0.0180	0.0000	0.1349	-8.8501	0.1588	0.0015	0.0899	0.0016	0.0899	0.0820	0.2897	0.0912	0.2647	0.1600	0
South_Africa (22) v. Sydney_Harbour (65)	2300.0743	0.0160	0.0000	0.0150	-7.0445	0.4625	0.0014	0.0430	0.0016	0.0430	0.0536	0.1059	0.0601	0.1039	0.1080	0
Clarence_River (83) v. South_Alligator_River (88)	3075.1132	0.0010	0.0000	0.0020	-4.1410	0.7872	0.0014	0.0010	0.0015	0.0010	0.0131	0.0010	0.0148	0.0010	0.0275	0
Arabian_Sea (15) v. Unknown (10)	1582.6427	0.1898	0.0001	0.1329	-15.9197	0.8631	0.0014	0.2468	0.0015	0.2448	0.2630	0.0989	0.2835	0.0989	0.4327	0
Clarence_River (83) v. Thailand (5)	2585.1670	0.0330	0.0001	0.4276	-9.0719	0.2478	0.0014	0.2937	0.0015	0.2937	0.2057	0.8012	0.2244	0.7972	0.3568	0
Daly_River (49) v. South_Alligator_River (88)	2618.6747	0.0020	0.0000	0.0100	-5.3747	0.1499	0.0013	0.0080	0.0014	0.0080	0.0222	0.0110	0.0251	0.0110	0.0462	0
Fitzroy_River (3) v. South_Alligator_River (88)	2115.2748	0.5614	0.0001	0.4705	NA	NA	0.0012	0.3760	NA	NA	NA	NA	NA	NA	NA	
Mozambique (11) v. South_Africa (22)	1659.7194	0.3926	0.0000	0.6713	-13.9204	0.9970	0.0012	0.2418	0.0013	0.2458	0.2138	0.0010	0.2321	0.0010	0.3674	0
Adelaide_River (18) v. Clarence_River (83)	2285.3918	0.4885	0.0000	0.0070	-6.2226	0.9940	0.0012	0.1159	0.0013	0.1159	0.0525	0.0170	0.0590	0.0210	0.1059	0
Clarence_River (83) v. Unknown (10)	2258.3642	0.3906	0.0000	0.1169	-7.0606	0.9421	0.0012	0.2188	0.0012	0.2188	0.0958	0.0290	0.1066	0.0330	0.1847	0
Arabian_Sea (15) v. Wenlock_River (24)	1896.2451	0.0320	0.0000	0.3606	-10.3971	0.3157	0.0011	0.2398	0.0012	0.2378	0.1295	0.4026	0.1430	0.3896	0.2413	0
Adelaide_River (18) v. South_Alligator_River (88)	2406.1195	0.0759	0.0000	0.3576	-6.5125	0.2697	0.0011	0.1249	0.0012	0.1249	0.0542	0.2737	0.0607	0.2607	0.1090	0
Arabian_Sea (15) v. Seychelles (36)	2112.8080	0.0020	0.0000	0.2308	-9.4415	0.0819	0.0011	0.2278	0.0012	0.2278	0.1051	0.6354	0.1166	0.6084	0.2006	0
Clarence_River (83) v. Sydney_Harbour (65)	2740.9833	0.0010	0.0000	0.0480	-4.6643	1.0000	0.0011	0.0030	0.0012	0.0030	0.0169	0.0010	0.0191	0.0010	0.0354	0
Sri_Lanka (12) v. Unknown (10)	1483.9574	0.0979	0.0001	0.0290	-19.6900	0.7862	0.0011	0.3207	0.0012	0.3187	0.3272	0.2028	0.3491	0.2048	0.5096	0
Clarence_River (83) v. Daly_River (49)	2573.0517	0.0270	0.0000	0.0090	-5.0794	0.9990	0.0011	0.0140	0.0012	0.0150	0.0214	0.0070	0.0242	0.0070	0.0446	0
Daly_River (49) v. Sydney_Harbour (65)	2417.0567	0.0230	0.0000	0.0030	-5.9562	0.7493	0.0011	0.0230	0.0012	0.0230	0.0274	0.0270	0.0309	0.0260	0.0568	0
Darwin_Coastal (15) v. South_Africa (22)	1818.1321	0.0509	0.0000	0.6623	-10.7661	0.0490	0.0010	0.2458	0.0011	0.2468	0.1376	0.5215	0.1519	0.4805	0.2545	0
East_Alligator_River (47) v. Unknown (10)	1939.9793	0.0440	0.0000	0.2158	-10.8538	0.0929	0.0010	0.2398	0.0011	0.2398	0.1494	0.4875	0.1640	0.4416	0.2726	0
East_Alligator_River (47) v. South_Africa (22)	2166.9004	0.0020	0.0000	0.1179	-8.1874	0.0350	0.0010	0.1479	0.0011	0.1479	0.0668	0.3836	0.0745	0.3626	0.1325	0
Adelaide_River (18) v. Sri_Lanka (12)	1604.2655	0.3477	0.0000	0.4745	-13.8605	0.4775	0.0010	0.3057	0.0011	0.3057	0.2032	0.3606	0.2210	0.3606	0.3526	0
Clarence_River (83) v. East_Alligator_River (47)	2548.0510	0.0290	0.0000	0.0020	-5.2370	1.0000	0.0010	0.0180	0.0011	0.0180	0.0225	0.0030	0.0254	0.0040	0.0469	0
Adelaide_River (18) v. Daly_River (49)	2055.9520	0.1179	0.0000	0.0789	-8.4300	0.6474	0.0009	0.2228	0.0009	0.2228	0.0775	0.2118	0.0863	0.2148	0.1520	0
East_Alligator_River (47) v. Seychelles (36)	2180.9182	0.0070	0.0000	0.1029	-7.5575	0.2078	0.0008	0.1079	0.0009	0.1079	0.0463	0.1239	0.0519	0.1189	0.0939	0
Darwin_Coastal (15) v. Wenlock_River (24)	1847.5847	0.0789	0.0000	0.0539	-10.3647	0.0410	0.0008	0.2807	0.0009	0.2807	0.1291	0.6503	0.1428	0.6194	0.2408	0
South_Africa (22) v. South_Alligator_River (88)	2453.2447	0.0380	0.0000	0.1209	-6.1889	0.1149	0.0008	0.1668	0.0009	0.1668	0.0441	0.3666	0.0495	0.3506	0.0897	0
Daly_River (49) v. Papua_New_Guinea (9)	1879.0255	0.4426	0.0001	0.0150	-10.9855	0.9421	0.0008	0.3267	0.0008	0.3267	0.1610	0.0579	0.1763	0.0639	0.2905	0
Sydney_Harbour (65) v. Unknown (10)	2020.8112	0.5445	0.0000	0.0470	-8.9242	0.3716	0.0008	0.2967	0.0008	0.2967	0.1210	0.3347	0.1337	0.3157	0.2273	0
Sydney_Harbour (65) v. Thailand (5)	2291.4812	0.0100	0.0001	0.3696	-12.1927	0.0210	0.0006	0.3956	0.0007	0.3956	0.2615	0.9930	0.2821	0.9920	0.4309	0
South_Alligator_River (88) v. Sri_Lanka (12)	2449.3820	0.0639	0.0000	0.2527	-7.0459	0.1858	0.0006	0.3267	0.0007	0.3267	0.0806	0.6513	0.0898	0.6214	0.1577	0
South_Africa (22) v. Sri_Lanka (12)	1719.7177	0.1688	0.0000	0.4236	-12.4584	0.5305	0.0005	0.3736	0.0006	0.3736	0.1750	0.4306	0.1913	0.4296	0.3118	0
Seychelles (36) v. South_Africa (22)	1996.9972	0.0420	0.0000	0.4086	-8.8703	0.2827	0.0005	0.3387	0.0005	0.3387	0.0784	0.4625	0.0874	0.4565	0.1538	0
East_Alligator_River (47) v. Sri_Lanka (12)	2050.8942	0.0280	0.0000	0.5185	-9.8506	0.1019	0.0004	0.4016	0.0005	0.4016	0.1190	0.8142	0.1313	0.8002	0.2237	0
East_Alligator_River (47) v. Sydney_Harbour (65)	2296.2695	0.3347	0.0000	0.3077	-6.2028	0.9910	0.0003	0.3017	0.0003	0.3017	0.0287	0.2507	0.0324	0.2567	0.0594	0
Adelaide_River (18) v. Sydney_Harbour (65)	2180.1795	0.2088	0.0000	0.7872	-7.4356	0.6014	0.0003	0.3686	0.0003	0.3686	0.0645	0.4785	0.0721	0.4815	0.1283	0
Daly_River (49) v. East_Alligator_River (47)	2217.7409	0.1718	0.0000	0.0789	-6.7907	0.8801	0.0002	0.3467	0.0002	0.3467	0.0354	0.3337	0.0398	0.3357	0.0726	0
East_Alligator_River (47) v. South_Alligator_River (88)	2387.1555	0.4336	0.0000	0.3187	-5.6194	0.8691	0.0002	0.3017	0.0002	0.3017	0.0232	0.2667	0.0262	0.2757	0.0483	0
Seychelles (36) v. Sri_Lanka (12)	1903.3093	0.0450	0.0000	0.1439	-10.7907	0.2647	0.0002	0.4366	0.0002	0.4366	0.1362	0.7532	0.1499	0.7483	0.2518	0
Fitzroy_River (3) v. Sydney_Harbour (65)	2085.3225	0.2398	0.0001	0.5155	NA	NA	0.0002	0.4706	NA	NA	NA	NA	NA	NA	NA	
Clarence_River (83) v. Fitzroy_River (3)	2110.5316	0.6603	0.0001	0.1938	NA	NA	0.0001	0.5064	0.0001	0.5064	NA	NA	NA	NA	NA	
Gulf_of_Mexico (37) v. Western_North_Atlantic (8)	1571.2543	0.2028	0.0000	0.5015	-21.7644	0.2311	-0.0002	0.5258	-0.0002	0.5258	0.3086	0.7866	0.3267	0.7877	0.4855	0
Daly_River (49) v. South_Africa (22)	2121.9984	0.0609	0.0000	0.5634	-7.9159	0.4376	-0.0003	0.6014	-0.0003	0.6014	0.0635	0.5874	0.0710	0.5894	0.1264	0
Roper_River (9) v. Thailand (5)	1285.4966	0.0989	0.0001	0.1638	-474.6881	0.3828	-0.0003	0.5305	-0.0003	0.5305	0.9540	0.9689	0.9569	0.9689	0.9780	0
Sri_Lanka (12) v. Thailand (5)	1360.2400	0.1798	0.0001	0.7243	-60.7430	0.1210	-0.0005	0.5774	-0.0006	0.5774	0.7015	0.8930	0.7177	0.8930	0.8341	0
Arabian_Sea (15) v. Fitzroy_River (3)	1346.0295	0.7073	0.0001	0.3237	NA	NA	-0.0007	0.5527	-0.0008	0.5527	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. South_Africa (22)	1516.0474	0.3716	0.0001	0.6913	NA	NA	-0.0009	0.5625	NA	NA	NA	NA	NA	NA	NA	
Arabian_Sea (15) v. Sri_Lanka (12)	1614.4357	0.5485	0.0000	0.5265	-13.9062	0.4665	-0.0014	0.7892	-0.0015	0.7892	0.2158	0.7333	0.2344	0.7383	0.3703	0
South_Africa (22) v. Thailand (5)	1618.4549	0.1039	0.0001	0.3107	-25.7692	0.0260	-0.0017	0.6883	-0.0018	0.6873	0.4611	0.9830	0.4836	0.9820	0.6466	0
Arabian_Sea (15) v. Thailand (5)	1441.9783	0.4915	0.0001	0.5814	-35.0742	0.1658	-0.0019	0.7053	-0.0020	0.7043	0.5595	0.8791	0.5805	0.8801	0.7310	0
Caribbean_Sea (2) v. Gulf_of_Mexico (37)	1323.0750	0.5325	0.0001	0.4585	11.3906	1.0000	-0.0020	0.6667	-0.0022	1.0000	-9.8053	1.0000	-8.6016	1.0000	2.0904	1
Fitzroy_River (3) v. Reunion (28)	1610.4646	0.3157	0.0001	0.7043	NA	NA	-0.0022	0.5819	NA	NA	NA	NA	NA	NA	NA	

Table 19: Pairwise Fst for 3443 DArTcap loci between the all locations *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Mozambique (11) v. Thailand (5)	1270.4968	0.5125	0.0001	0.5764	-134.4816	0.1924	-0.0027	0.7163	-0.0029	0.7133	0.8477	0.9946	0.8568	0.9946	0.9225	0
Fitzroy_River (3) v. Wenlock_River (24)	1443.6321	0.7393	0.0001	0.4186	NA	NA	-0.0034	0.7015	NA	NA	NA	NA	NA	NA	NA	
Adelaide_River (18) v. Fitzroy_River (3)	1339.0776	0.7542	0.0001	0.5734	NA	NA	-0.0045	0.7262	-0.0048	0.7262	NA	NA	NA	NA	NA	
Caribbean_Sea (2) v. Western_North_Atlantic (8)	794.9991	0.6713	0.0001	0.4815	NA	NA	-0.0077	1.0000	-0.0083	1.0000	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Mozambique (11)	1190.3368	0.7253	0.0001	0.9980	NA	NA	-0.0093	0.8500	NA	NA	NA	NA	NA	NA	NA	
Adelaide_River (18) v. Indonesia (4)	1529.8090	0.0579	0.0001	0.0200	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Blue_mud_Bay (18) v. Indonesia (4)	1605.8387	0.1548	0.0001	0.1039	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Clarence_River (83) v. Indonesia (4)	2448.1851	0.0969	0.0001	0.0100	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Daly_River (49) v. Indonesia (4)	2154.7460	0.0120	0.0001	0.0160	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fiji (25) v. Indonesia (4)	2319.4034	0.0010	0.0002	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Gulf_of_Mexico (37)	28427.3648	0.0010	0.0204	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Seychelles (36)	1759.9167	0.1069	0.0001	0.3027	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Towns_River (10)	1212.9971	0.1738	0.0001	0.3506	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Unknown (10)	1163.6953	0.2967	0.0001	0.3666	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fitzroy_River (3) v. Urauchi_River (35)	2762.4915	0.0010	0.0003	0.0110	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. South_Africa (22)	1619.1846	0.0649	0.0001	0.0430	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. South_Alligator_River (88)	2672.4750	0.0050	0.0001	0.0180	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Sydney_Harbour (65)	2370.0346	0.0040	0.0001	0.0050	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Urauchi_River (35)	2861.7966	0.0010	0.0003	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	

8.7.2 Fst per Site

```
strata <- BS.dartcap.gt@schemes$Site
names(strata) <- BS.dartcap.gt@schemes$INDIVIDUALS
strataG::setStrata(BS.dartcap.gt) <- strata

Fst.gt <- strataG::popStructTest(
    BS.dartcap.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_ALL_FST_Sites.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_ALL_FST_Sites.txt")
```

```
load("DArTcap_ALL_FST_Sites.Rdata")
kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                       decreasing = TRUE),
                                 -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 3443 DArTcap loci between the all sites",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()

pop.levels1 <- c("Costa_Rica" , "Brazil","Caribbean_Sea", "Gulf_of_Mexico",
                 "Western_North_Atlantic", "Sierra_Leone", "South_Africa",
                 "Mozambique", "Reunion" , "Seychelles", "Arabian_Sea",
                 "Sri_Lanka", "Thailand", "Indonesia", "Papua_New_Guinea" ,
                 "Australia", "Japan", "Fiji")
m2 <- Fst.gt$pairwise$result[order(match(Fst.gt$pairwise$result$strata.1,
                                         pop.levels1)),c(1,2,11)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.1 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst", type = 'lower')

m2 <- Fst.gt$pairwise$result[order(match(Fst.gt$pairwise$result$strata.1,
                                         pop.levels1)),c(1,2,12)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.2 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst.p.val", type = 'lower')
m2$Fst.p.adj <- p.adjust(m2$Fst.p.val, "bonferroni")
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.3 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "Fst.p.adj", type = 'lower')

write.csv(m2.1, file = "DArTcap_ALL_FST_Sites.csv")
write.csv(m2.2, file = "DArTcap_ALL_FST_Pval_Sites.csv")
write.csv(m2.3, file = "DArTcap_ALL_FST_Pval_bonferroni_Sites.csv")
```

Table 20: Pairwise Fst for 3443 DArTcap loci between the all sites

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Costa Rica (16) v. Indonesia (4)	16273.1465	0.0010	0.0174	0.0010	NA	NA	0.7066	0.0016	0.7426	0.0016	NA	NA	NA	NA	NA	NA
Costa Rica (16) v. Sierra Leone (1)	11158.8583	0.0649	0.0114	0.0649	NA	NA	0.7013	1.0000	0.7320	1.0000	NA	NA	NA	NA	NA	NA
Costa Rica (16) v. Thailand (5)	17395.3981	0.0010	0.0171	0.0010	-128.4526	1.0000	0.6957	0.0012	0.7321	0.0012	0.9375	0.0013	0.9472	0.0013	0.9728	0.0013
Costa Rica (16) v. Papua New Guinea (9)	20872.6332	0.0010	0.0172	0.0010	-25.9715	1.0000	0.6888	0.0010	0.7293	0.0010	0.7465	0.0010	0.7815	0.0010	0.8749	0.0010
Gulf of Mexico (37) v. Indonesia (4)	30354.5133	0.0010	0.0206	0.0010	NA	NA	0.6790	0.0018	0.7194	0.0018	NA	NA	NA	NA	NA	NA
Costa Rica (16) v. Mozambique (11)	21911.2511	0.0010	0.0171	0.0010	-21.4465	1.0000	0.6766	0.0010	0.7455	0.0010	0.7102	0.0010	0.7492	0.0010	0.8533	0.0010
Costa Rica (16) v. Sri Lanka (12)	23381.6592	0.0010	0.0171	0.0010	-18.2470	1.0000	0.6765	0.0010	0.7186	0.0010	0.6784	0.0010	0.7208	0.0010	0.8336	0.0010
Gulf of Mexico (37) v. Papua New Guinea (9)	37442.1062	0.0010	0.0202	0.0010	-11.4281	1.0000	0.6735	0.0010	0.7158	0.0010	0.6173	0.0010	0.6692	0.0010	0.7955	0.0010
Gulf of Mexico (37) v. Thailand (5)	32159.8344	0.0010	0.0201	0.0010	-19.0984	1.0000	0.6734	0.0013	0.7138	0.0013	0.7257	0.0014	0.7666	0.0014	0.8648	0.0014
Arabian Sea (15) v. Costa Rica (16)	25971.5113	0.0010	0.0172	0.0010	-14.4992	1.0000	0.6703	0.0010	0.7190	0.0010	0.6412	0.0010	0.6874	0.0010	0.8095	0.0010
Indonesia (4) v. Western North Atlantic (8)	10796.1481	0.0050	0.0201	0.0050	NA	NA	0.6695	0.0057	0.7210	0.0057	NA	NA	NA	NA	NA	NA
Gulf of Mexico (37) v. Sri Lanka (12)	40959.6725	0.0010	0.0201	0.0010	-9.3431	1.0000	0.6690	0.0010	0.7122	0.0010	0.5772	0.0010	0.6327	0.0010	0.7671	0.0010
Gulf of Mexico (37) v. Japan (44)	72645.9399	0.0010	0.0213	0.0010	-6.5832	1.0000	0.6682	0.0010	0.7179	0.0010	0.5329	0.0010	0.5922	0.0010	0.7340	0.0010
Gulf of Mexico (37) v. Mozambique (11)	38936.2039	0.0010	0.0202	0.0010	-10.5682	1.0000	0.6678	0.0010	0.7265	0.0010	0.5984	0.0010	0.6521	0.0010	0.7823	0.0010
Arabian Sea (15) v. Gulf of Mexico (37)	44493.1758	0.0010	0.0203	0.0010	-7.9916	1.0000	0.6674	0.0010	0.7306	0.0010	0.5559	0.0010	0.6134	0.0010	0.7515	0.0010
Gulf of Mexico (37) v. South Africa (22)	51302.5655	0.0010	0.0203	0.0010	-7.0620	1.0000	0.6645	0.0010	0.7110	0.0010	0.5385	0.0010	0.5969	0.0010	0.7380	0.0010
Fiji (25) v. Gulf of Mexico (37)	53347.0294	0.0010	0.0208	0.0010	-7.6557	1.0000	0.6636	0.0010	0.7246	0.0010	0.5421	0.0010	0.6007	0.0010	0.7411	0.0010
Gulf of Mexico (37) v. Reunion (28)	56931.1754	0.0010	0.0205	0.0010	-6.6372	1.0000	0.6632	0.0010	0.7172	0.0010	0.5320	0.0010	0.5909	0.0010	0.7330	0.0010
Costa Rica (16) v. South Africa (22)	31374.4245	0.0010	0.0172	0.0010	-12.3324	1.0000	0.6623	0.0010	0.7094	0.0010	0.6108	0.0010	0.6594	0.0010	0.7885	0.0010
Brazil (50) v. Indonesia (4)	34978.7881	0.0010	0.0201	0.0010	NA	NA	0.6610	0.0016	0.7023	0.0016	NA	NA	NA	NA	NA	NA
Costa Rica (16) v. Japan (44)	48791.2085	0.0010	0.0182	0.0010	-10.8638	1.0000	0.6609	0.0010	0.7115	0.0010	0.5930	0.0010	0.6435	0.0010	0.7762	0.0010
Gulf of Mexico (37) v. Seychelles (36)	64246.2659	0.0010	0.0204	0.0010	-6.2762	1.0000	0.6609	0.0010	0.7120	0.0010	0.5254	0.0010	0.5846	0.0010	0.7277	0.0010
Papua New Guinea (9) v. Western North Atlantic (8)	15342.6408	0.0010	0.0198	0.0010	-29.9304	1.0000	0.6609	0.0010	0.7091	0.0010	0.7937	0.0010	0.8255	0.0010	0.9027	0.0010
Costa Rica (16) v. Fiji (25)	32838.2436	0.0010	0.0177	0.0010	-12.8862	1.0000	0.6594	0.0010	0.7427	0.0010	0.6143	0.0010	0.6629	0.0010	0.7912	0.0010
Caribbean Sea (2) v. Indonesia (4)	5575.3583	0.0619	0.0193	0.0619	NA	NA	0.6592	0.0772	0.7108	0.1330	NA	NA	NA	NA	NA	NA
Japan (44) v. Western North Atlantic (8)	44459.5258	0.0010	0.0209	0.0010	-10.8838	1.0000	0.6581	0.0010	0.7026	0.0010	0.6233	0.0010	0.6755	0.0010	0.8001	0.0010
Brazil (50) v. Japan (44)	82414.0333	0.0010	0.0208	0.0010	-5.2352	1.0000	0.6580	0.0010	0.7067	0.0010	0.5108	0.0010	0.5711	0.0010	0.7161	0.0010
Thailand (5) v. Western North Atlantic (8)	11762.3727	0.0030	0.0196	0.0030	-1708.8139	1.0000	0.6580	0.0030	0.7092	0.0030	0.9956	0.0030	0.9963	0.0030	0.9982	0.0030
Costa Rica (16) v. Reunion (28)	35822.7035	0.0010	0.0173	0.0010	-11.2181	1.0000	0.6579	0.0010	0.7153	0.0010	0.5972	0.0010	0.6469	0.0010	0.7790	0.0010
Brazil (50) v. Papua New Guinea (9)	43914.5156	0.0010	0.0197	0.0010	-8.8114	1.0000	0.6576	0.0010	0.7002	0.0010	0.5789	0.0010	0.6338	0.0010	0.7681	0.0010
Brazil (50) v. Thailand (5)	37344.9627	0.0010	0.0195	0.0010	-12.8491	1.0000	0.6564	0.0012	0.6977	0.0012	0.6624	0.0013	0.7103	0.0013	0.8257	0.0013
Brazil (50) v. Sri Lanka (12)	48090.5646	0.0010	0.0196	0.0010	-7.4193	1.0000	0.6543	0.0010	0.6976	0.0010	0.5455	0.0010	0.6030	0.0010	0.7431	0.0010
Arabian Sea (15) v. Brazil (50)	52205.7665	0.0010	0.0198	0.0010	-6.3824	1.0000	0.6538	0.0010	0.7111	0.0010	0.5278	0.0010	0.5868	0.0010	0.7296	0.0010
Caribbean Sea (2) v. Japan (44)	35935.8757	0.0030	0.0201	0.0030	17.3479	0.6953	0.6537	0.0110	0.7112	0.0204	1.4705	0.6562	1.3773	0.6953	1.1527	0.6953
Costa Rica (16) v. Seychelles (36)	41929.4198	0.0010	0.0172	0.0010	-10.2066	1.0000	0.6532	0.0010	0.7059	0.0010	0.5844	0.0010	0.6350	0.0010	0.7696	0.0010
Brazil (50) v. Mozambique (11)	45890.2124	0.0010	0.0197	0.0010	-8.0143	1.0000	0.6532	0.0010	0.7086	0.0010	0.5607	0.0010	0.6171	0.0010	0.7546	0.0010
Sri Lanka (12) v. Western North Atlantic (8)	17932.6616	0.0010	0.0197	0.0010	-19.3031	1.0000	0.6531	0.0010	0.7009	0.0010	0.7186	0.0010	0.7601	0.0010	0.8604	0.0010
Brazil (50) v. South Africa (22)	59708.1807	0.0010	0.0198	0.0010	-5.6168	1.0000	0.6522	0.0010	0.6981	0.0010	0.5134	0.0010	0.5730	0.0010	0.7178	0.0010
Brazil (50) v. Fiji (25)	62085.9734	0.0010	0.0203	0.0010	-6.1466	1.0000	0.6521	0.0010	0.7183	0.0010	0.5169	0.0010	0.5767	0.0010	0.7209	0.0010
Brazil (50) v. Reunion (28)	65838.2138	0.0010	0.0199	0.0010	-5.1468	1.0000	0.6518	0.0010	0.7038	0.0010	0.5076	0.0010	0.5676	0.0010	0.7132	0.0010
Mozambique (11) v. Western North Atlantic (8)	16446.4730	0.0010	0.0198	0.0010	-23.8312	1.0000	0.6505	0.0010	0.6993	0.0010	0.7559	0.0010	0.7928	0.0010	0.8820	0.0010
Brazil (50) v. Seychelles (36)	73511.3689	0.0010	0.0198	0.0010	-4.9091	1.0000	0.6504	0.0010	0.7001	0.0010	0.5026	0.0010	0.5628	0.0010	0.7090	0.0010
Caribbean Sea (2) v. Papua New Guinea (9)	9592.1001	0.0140	0.0191	0.0140	8.7392	1.0000	0.6504	0.0216	0.7048	0.0308	3.1407	0.4835	2.6339	0.4835	1.3946	0.4835
Arabian Sea (15) v. Western North Atlantic (8)	20524.2457	0.0010	0.0199	0.0010	-14.8171	1.0000	0.6495	0.0010	0.6971	0.0010	0.6748	0.0010	0.7215	0.0010	0.8337	0.0010
South Africa (22) v. Western North Atlantic (8)	26233.0639	0.0010	0.0199	0.0010	-12.2867	1.0000	0.6488	0.0010	0.6951	0.0010	0.6416	0.0010	0.6916	0.0010	0.8121	0.0010
Reunion (28) v. Western North Atlantic (8)	30966.6961	0.0010	0.0200	0.0010	-11.2130	1.0000	0.6485	0.0010	0.6943	0.0010	0.6274	0.0010	0.6788	0.0010	0.8026	0.0010
Fiji (25) v. Western North Atlantic (8)	27619.8196	0.0010	0.0203	0.0010	-13.2118	1.0000	0.6477	0.0010	0.6944	0.0010	0.6488	0.0010	0.6984	0.0010	0.8171	0.0010
Seychelles (36) v. Western North Atlantic (8)	37388.1295	0.0010	0.0199	0.0010	-10.1738	1.0000	0.6475	0.0010	0.6927	0.0010	0.6128	0.0010	0.6654	0.0010	0.7925	0.0010
Gulf of Mexico (37) v. Sierra Leone (1)	18859.1589	0.0240	0.0130	0.0240	3.5388	1.0000	0.6452	1.0000	0.6819	1.0000	-4.0811	1.0000	-2.4174	1.0000	2.1091	1.0000
Australia (444) v. Gulf of Mexico (37)	374538.5986	0.0010	0.0203	0.0010	-0.5217	1.0000	0.6416	0.0010	0.6878	0.0010	0.4921	0.0010	0.5531	0.0010	0.7005	0.0010
Caribbean Sea (2) v. Seychelles (36)	29492.5761	0.0020	0.0191	0.0020	18.4682	0.8525	0.6409	0.0046	0.7027	0.0087	1.4205	0.1982	1.3387	0.4240	1.1399	0.4608
Caribbean Sea (2) v. Sri Lanka (12)	11881.2980	0.0140	0.0189	0.0140	10.4803	1.0000	0.6407	0.0192	0.6951	0.0223	2.3070	0.6608	2.0162	0.7517	1.3073	0.7517
Caribbean Sea (2) v. Reunion (28)	23726.1873	0.0030	0.0191	0.0030	16.1387	0.8138	0.6401	0.0079	0.7109	0.0150	1.5290	0.2340	1.4236	0.5957	1.1675	0.7234

Table 20: Pairwise Fst for 3443 DArTcap loci between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Sierra Leone (1) v. Western North Atlantic (8)	6383.0393	0.1079	0.0128	0.1079	NA	NA	0.6399	1.0000	0.6928	1.0000	NA	NA	NA	NA	NA	NA
Caribbean Sea (2) v. Thailand (5)	6365.8728	0.0460	0.0190	0.0460	6.5399	1.0000	0.6397	0.0605	0.6900	0.0891	7.7722	0.1077	5.9532	0.1077	1.5646	0.4356
Caribbean Sea (2) v. South Africa (22)	19348.6504	0.0040	0.0191	0.0040	14.6472	0.8108	0.6396	0.0086	0.6969	0.0130	1.6357	0.3668	1.5064	0.7104	1.1921	0.7336
Caribbean Sea (2) v. Fiji (25)	20234.6055	0.0030	0.0196	0.0030	13.8263	0.5143	0.6389	0.0341	0.7519	0.0857	1.7211	0.5143	1.5712	0.5143	1.2099	0.5143
Australia (444) v. Western North Atlantic (8)	306261.9566	0.0010	0.0198	0.0010	-0.8403	1.0000	0.6385	0.0010	0.6824	0.0010	0.5002	0.0010	0.5609	0.0010	0.7073	0.0010
Arabian Sea (15) v. Caribbean Sea (2)	14193.4109	0.0090	0.0192	0.0090	12.1323	0.6987	0.6376	0.0166	0.6820	0.0166	1.9032	0.1026	1.7105	0.3046	1.2447	0.4437
Caribbean Sea (2) v. Mozambique (11)	10554.8552	0.0110	0.0190	0.0110	9.3888	1.0000	0.6367	0.0445	0.7509	0.3056	2.7335	1.0000	2.3336	1.0000	1.3572	1.0000
Caribbean Sea (2) v. Sierra Leone (1)	2577.9083	0.3417	0.0123	0.3417	NA	NA	0.6360	0.3417	0.6736	0.3417	NA	NA	NA	NA	NA	NA
Australia (444) v. Brazil (50)	388501.9802	0.0010	0.0197	0.0010	-0.3701	1.0000	0.6359	0.0010	0.6813	0.0010	0.4782	0.0010	0.5395	0.0010	0.6885	0.0010
Australia (444) v. Caribbean Sea (2)	253047.0846	0.0010	0.0191	0.0010	-1.7172	1.0000	0.6353	0.0040	0.6787	0.0040	0.5730	0.0042	0.6287	0.0042	0.7639	0.0042
Australia (444) v. Costa Rica (16)	299205.7214	0.0010	0.0172	0.0010	-1.1032	1.0000	0.6264	0.0010	0.6694	0.0010	0.5104	0.0010	0.5657	0.0010	0.7124	0.0010
Brazil (50) v. Sierra Leone (1)	19357.2075	0.0210	0.0128	0.0210	3.7736	1.0000	0.6231	1.0000	0.6609	1.0000	-7.2591	1.0000	-4.7985	1.0000	1.9264	1.0000
Caribbean Sea (2) v. Costa Rica (16)	4585.3922	0.0120	0.0023	0.0120	NA	NA	0.4287	0.0845	0.4607	0.7059	NA	NA	NA	NA	NA	NA
Costa Rica (16) v. Western North Atlantic (8)	6703.9713	0.0010	0.0025	0.0010	-71.9795	1.0000	0.3964	0.0011	0.4187	0.0011	0.7688	0.0012	0.7844	0.0012	0.8781	0.0012
Costa Rica (16) v. Gulf of Mexico (37)	12724.5435	0.0010	0.0025	0.0010	-17.2299	1.0000	0.3692	0.0010	0.4010	0.0010	0.3948	0.0010	0.4218	0.0010	0.5855	0.0010
Brazil (50) v. Costa Rica (16)	14591.9962	0.0010	0.0024	0.0010	-12.5174	1.0000	0.3484	0.0010	0.3709	0.0010	0.3396	0.0010	0.3666	0.0010	0.5272	0.0010
Japan (44) v. Sierra Leone (1)	6184.4210	0.0190	0.0009	0.0190	3.6975	1.0000	0.2067	1.0000	0.2202	1.0000	-2.0230	1.0000	-1.2649	1.0000	3.2141	1.0000
Indonesia (4) v. Sierra Leone (1)	1287.3999	0.1898	0.0007	0.1898	NA	NA	0.1862	1.0000	0.1985	1.0000	NA	NA	NA	NA	NA	NA
Papua New Guinea (9) v. Sierra Leone (1)	1927.2893	0.1109	0.0007	0.1109	3.0179	1.0000	0.1688	1.0000	0.1799	1.0000	-1.4903	1.0000	-0.6634	1.0000	4.3923	1.0000
Seychelles (36) v. Sierra Leone (1)	4675.7140	0.0190	0.0007	0.0190	3.7128	1.0000	0.1641	1.0000	0.1751	1.0000	-2.0433	1.0000	-1.2968	1.0000	3.2014	1.0000
Fiji (25) v. Sierra Leone (1)	3717.0341	0.0400	0.0008	0.0789	3.5244	1.0000	0.1610	1.0000	0.1720	1.0000	-1.8479	1.0000	-1.0793	1.0000	3.4522	1.0000
Reunion (28) v. Sierra Leone (1)	3958.4759	0.0290	0.0007	0.0290	3.6090	1.0000	0.1589	1.0000	0.1697	1.0000	-1.9249	1.0000	-1.1728	1.0000	3.3492	1.0000
Arabian Sea (15) v. Sierra Leone (1)	2671.9413	0.0519	0.0007	0.0519	3.3559	1.0000	0.1582	1.0000	0.1691	1.0000	-1.7251	1.0000	-0.9462	1.0000	3.6842	1.0000
Australia (444) v. Sierra Leone (1)	27946.7116	0.0020	0.0007	0.0020	-16.0712	1.0000	0.1572	1.0000	0.1679	1.0000	0.7680	1.0000	0.7836	1.0000	0.8776	1.0000
Sierra Leone (1) v. Sri Lanka (12)	2281.1615	0.0789	0.0007	0.0789	3.2091	1.0000	0.1553	1.0000	0.1691	1.0000	-1.5995	1.0000	-0.8048	1.0000	4.0102	1.0000
Sierra Leone (1) v. Thailand (5)	1375.9116	0.1708	0.0007	0.1708	2.6272	1.0000	0.1549	1.0000	0.1682	1.0000	-1.3621	1.0000	-0.4434	1.0000	4.9860	1.0000
Sierra Leone (1) v. South Africa (22)	3261.7230	0.0450	0.0007	0.0450	3.5162	1.0000	0.1491	1.0000	0.1629	1.0000	-1.8238	1.0000	-1.0701	1.0000	3.5128	1.0000
Mozambique (11) v. Sierra Leone (1)	2129.2277	0.0879	0.0007	0.0879	3.0960	1.0000	0.1391	1.0000	0.1486	1.0000	-1.5408	1.0000	-0.7256	1.0000	4.1909	1.0000
Fiji (25) v. Japan (44)	5695.6380	0.0010	0.0003	0.0010	-8.2308	1.0000	0.0617	0.0010	0.0668	0.0010	0.0972	0.0010	0.1084	0.0010	0.1873	0.0010
Japan (44) v. Thailand (5)	2959.4339	0.0010	0.0002	0.0030	-19.8728	0.0260	0.0369	0.0040	0.0394	0.0040	0.3877	0.4770	0.4109	0.4300	0.5755	0.4420
Japan (44) v. Reunion (28)	4298.1505	0.0010	0.0002	0.0010	-8.2811	1.0000	0.0352	0.0010	0.0381	0.0010	0.0771	0.0010	0.0861	0.0010	0.1515	0.0010
Japan (44) v. Papua New Guinea (9)	2849.1844	0.0010	0.0002	0.0010	-13.2332	0.8062	0.0350	0.0010	0.0375	0.0010	0.2059	0.0030	0.2239	0.0020	0.3564	0.0030
Japan (44) v. Mozambique (11)	3221.7881	0.0010	0.0002	0.0010	-11.8248	0.9930	0.0345	0.0010	0.0376	0.0010	0.1777	0.0010	0.1944	0.0010	0.3160	0.0010
Fiji (25) v. Mozambique (11)	2767.8705	0.0010	0.0002	0.0010	-13.0854	0.9810	0.0333	0.0010	0.0370	0.0010	0.2182	0.0020	0.2374	0.0020	0.3740	0.0020
Fiji (25) v. Reunion (28)	3650.3859	0.0010	0.0002	0.0010	-8.6350	1.0000	0.0331	0.0010	0.0363	0.0010	0.0993	0.0010	0.1106	0.0010	0.1909	0.0010
Fiji (25) v. Sri Lanka (12)	2847.4077	0.0010	0.0002	0.0010	-11.4689	0.9331	0.0318	0.0010	0.0342	0.0010	0.1768	0.0010	0.1938	0.0010	0.3149	0.0010
Japan (44) v. South Africa (22)	3710.1260	0.0010	0.0002	0.0010	-8.7590	0.9970	0.0318	0.0010	0.0342	0.0010	0.0877	0.0010	0.0977	0.0010	0.1705	0.0010
Fiji (25) v. Seychelles (36)	3917.7856	0.0010	0.0002	0.0010	-8.1055	1.0000	0.0318	0.0010	0.0346	0.0010	0.0861	0.0010	0.0962	0.0010	0.1678	0.0010
Japan (44) v. Sri Lanka (12)	3216.3450	0.0010	0.0002	0.0010	-10.8310	0.4715	0.0318	0.0010	0.0340	0.0010	0.1458	0.0010	0.1605	0.0010	0.2674	0.0010
Fiji (25) v. Papua New Guinea (9)	2504.3831	0.0010	0.0002	0.0010	-14.3600	0.7592	0.0313	0.0010	0.0336	0.0010	0.2433	0.0969	0.2633	0.0899	0.4074	0.0919
Australia (444) v. Fiji (25)	9451.6632	0.0010	0.0002	0.0010	-1.4442	0.0410	0.0310	0.0010	0.0334	0.0010	0.0244	0.0010	0.0277	0.0010	0.0508	0.0010
Arabian Sea (15) v. Japan (44)	3464.5033	0.0010	0.0001	0.0010	-9.6648	0.4216	0.0306	0.0010	0.0332	0.0010	0.1160	0.0010	0.1285	0.0010	0.2191	0.0010
Fiji (25) v. South Africa (22)	3220.1518	0.0010	0.0002	0.0010	-9.2524	1.0000	0.0304	0.0010	0.0328	0.0010	0.1125	0.0010	0.1250	0.0010	0.2135	0.0010
Australia (444) v. Japan (44)	9334.2816	0.0010	0.0002	0.0010	-1.7096	1.0000	0.0287	0.0010	0.0307	0.0010	0.0204	0.0010	0.0231	0.0010	0.0427	0.0010
Japan (44) v. Seychelles (36)	4153.7717	0.0010	0.0001	0.0010	-7.9267	1.0000	0.0287	0.0010	0.0310	0.0010	0.0637	0.0010	0.0713	0.0010	0.1269	0.0010
Arabian Sea (15) v. Fiji (25)	2979.1597	0.0010	0.0001	0.0010	-9.9954	0.9830	0.0273	0.0010	0.0311	0.0010	0.1401	0.0010	0.1548	0.0010	0.2587	0.0010
Fiji (25) v. Thailand (5)	2350.1840	0.0010	0.0002	0.0020	-23.9823	0.0222	0.0255	0.0072	0.0273	0.0072	0.4525	0.9344	0.4759	0.9288	0.6392	0.9288
Indonesia (4) v. Thailand (5)	1117.0939	0.1229	0.0002	0.1958	NA	NA	0.0190	0.1798	0.0204	0.1798	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Papua New Guinea (9)	1247.3907	0.0819	0.0002	0.1059	NA	NA	0.0171	0.1032	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Seychelles (36)	1963.5232	0.0070	0.0001	0.0320	NA	NA	0.0147	0.0100	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Reunion (28)	1788.1551	0.0270	0.0001	0.0759	NA	NA	0.0125	0.0556	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea (15) v. Indonesia (4)	1509.7166	0.1508	0.0001	0.0320	NA	NA	0.0124	0.0241	0.0133	0.0241	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Mozambique (11)	1304.4937	0.1918	0.0001	0.1499	NA	NA	0.0115	0.1110	NA	NA	NA	NA	NA	NA	NA	NA

Table 20: Pairwise Fst for 3443 DArTcap loci between the all sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.val
Mozambique (11) v. Papua New Guinea (9)	1470.3666	0.0100	0.0001	0.1289	-28.1255	0.8661	0.0111	0.0030	0.0120	0.0030	0.4506	0.0849	0.4728	0.0819	0.6365	0.0819
Indonesia (4) v. Sri Lanka (12)	1349.5519	0.1608	0.0001	0.0909	NA	NA	0.0108	0.0829	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea (15) v. Papua New Guinea (9)	1609.9884	0.0529	0.0001	0.0220	-17.7297	0.9990	0.0067	0.0060	0.0072	0.0060	0.2995	0.0010	0.3207	0.0010	0.4772	0.0010
Papua New Guinea (9) v. Reunion (28)	1803.8110	0.0240	0.0001	0.0100	-14.0484	0.8282	0.0058	0.0260	0.0064	0.0260	0.2185	0.1838	0.2368	0.1858	0.3736	0.1858
Mozambique (11) v. Reunion (28)	1869.1632	0.0150	0.0001	0.0360	-12.9534	0.9880	0.0054	0.0280	0.0059	0.0290	0.1939	0.0040	0.2114	0.0040	0.3395	0.0040
Australia (444) v. Reunion (28)	4038.8765	0.0010	0.0000	0.0010	-1.7006	0.4815	0.0052	0.0010	0.0056	0.0010	0.0112	0.0010	0.0127	0.0010	0.0236	0.0010
Mozambique (11) v. Seychelles (36)	1974.2569	0.0010	0.0001	0.0100	-11.9120	0.9870	0.0051	0.0040	0.0056	0.0040	0.1714	0.0010	0.1876	0.0010	0.3065	0.0010
Brazil (50) v. Gulf of Mexico (37)	2325.3566	0.0010	0.0000	0.0190	-8.6882	1.0000	0.0049	0.0010	0.0053	0.0010	0.0536	0.0010	0.0593	0.0010	0.1071	0.0010
Reunion (28) v. Seychelles (36)	2239.8359	0.0010	0.0000	0.0040	-8.4873	0.9930	0.0048	0.0010	0.0052	0.0010	0.0685	0.0010	0.0766	0.0010	0.1358	0.0010
Seychelles (36) v. Thailand (5)	1919.1018	0.0030	0.0001	0.0749	-19.2828	0.0160	0.0046	0.1049	0.0049	0.1059	0.3739	0.9790	0.3967	0.9790	0.5609	0.9790
Australia (444) v. Mozambique (11)	3639.2817	0.0579	0.0000	0.0210	-1.8496	0.1159	0.0044	0.0010	0.0047	0.0010	0.0271	0.0010	0.0306	0.0010	0.0561	0.0010
Papua New Guinea (9) v. Thailand (5)	1272.2324	0.0410	0.0001	0.2567	-944.1888	0.3776	0.0044	0.1998	0.0047	0.1998	0.9760	0.9560	0.9775	0.9560	0.9886	0.9560
Papua New Guinea (9) v. Sri Lanka (12)	1411.8786	0.2368	0.0001	0.1768	-22.9494	0.9411	0.0042	0.0849	0.0045	0.0849	0.3760	0.0480	0.3980	0.0470	0.5625	0.0470
Papua New Guinea (9) v. Seychelles (36)	1790.9361	0.0749	0.0001	0.0150	-13.0189	0.8761	0.0042	0.0340	0.0046	0.0340	0.1953	0.0649	0.2125	0.0699	0.3412	0.0679
Arabian Sea (15) v. Mozambique (11)	1666.5157	0.0699	0.0001	0.2727	-15.7147	1.0000	0.0041	0.0380	0.0045	0.0360	0.2620	0.0010	0.2825	0.0010	0.4315	0.0010
Brazil (50) v. Western North Atlantic (8)	1764.9563	0.6284	0.0000	0.3706	-14.8037	0.9958	0.0037	0.0884	0.0040	0.0884	0.2265	0.0063	0.2430	0.0073	0.3828	0.0063
Reunion (28) v. South Africa (22)	2046.1101	0.0040	0.0000	0.0020	-9.3965	0.8252	0.0033	0.0230	0.0036	0.0230	0.0929	0.0420	0.1032	0.0400	0.1794	0.0420
Mozambique (11) v. Sri Lanka (12)	1510.9759	0.1429	0.0001	0.1918	-19.8424	0.9980	0.0033	0.0889	0.0036	0.0919	0.3304	0.0020	0.3523	0.0020	0.5132	0.0020
Reunion (28) v. Sri Lanka (12)	1944.4230	0.0060	0.0000	0.1459	-11.5330	0.3926	0.0032	0.0809	0.0034	0.0819	0.1553	0.3966	0.1704	0.3886	0.2819	0.3896
Reunion (28) v. Thailand (5)	1867.7590	0.0110	0.0001	0.0679	-21.9852	0.0190	0.0030	0.2380	0.0032	0.2420	0.4139	0.9790	0.4368	0.9770	0.6017	0.9780
Papua New Guinea (9) v. South Africa (22)	1596.4856	0.3367	0.0001	0.0320	-15.4042	0.9610	0.0020	0.2168	0.0022	0.2168	0.2440	0.0559	0.2633	0.0579	0.4078	0.0569
Arabian Sea (15) v. South Africa (22)	1883.4848	0.0050	0.0000	0.1908	-10.8150	0.3726	0.0020	0.0909	0.0022	0.0909	0.1385	0.1888	0.1526	0.1708	0.2557	0.1788
Arabian Sea (15) v. Reunion (28)	2088.8182	0.0010	0.0000	0.0879	-9.9971	0.1678	0.0019	0.1419	0.0021	0.1409	0.1199	0.4795	0.1326	0.4595	0.2255	0.4665
Australia (444) v. Papua New Guinea (9)	2714.5893	0.9471	0.0001	0.0200	-1.9646	0.9720	0.0018	0.1179	0.0020	0.1179	0.0301	0.0340	0.0339	0.0360	0.0621	0.0350
Arabian Sea (15) v. Australia (444)	4448.0192	0.0010	0.0000	0.2068	-1.7288	0.2877	0.0018	0.0220	0.0020	0.0220	0.0164	0.0679	0.0186	0.0629	0.0345	0.0659
Brazil (50) v. Caribbean Sea (2)	1530.3572	0.8222	0.0002	0.2847	14.5573	1.0000	0.0016	0.6250	0.0017	0.6250	7.5662	0.7500	6.9471	0.7500	1.6942	0.7500
Australia (444) v. Seychelles (36)	3423.0674	0.0629	0.0000	0.0030	-1.6820	0.9201	0.0015	0.0010	0.0016	0.0010	0.0074	0.0010	0.0084	0.0010	0.0157	0.0010
Australia (444) v. Thailand (5)	3817.6280	0.0689	0.0001	0.2008	-2.0420	0.2420	0.0014	0.3150	0.0015	0.3150	0.0537	0.6390	0.0603	0.6140	0.1082	0.6280
Mozambique (11) v. South Africa (22)	1659.7194	0.4166	0.0000	0.6663	-13.9204	0.9950	0.0012	0.2757	0.0013	0.2817	0.2138	0.0010	0.2321	0.0010	0.3674	0.0010
Arabian Sea (15) v. Seychelles (36)	2112.8080	0.0010	0.0000	0.2068	-9.4415	0.0899	0.0011	0.1848	0.0012	0.1848	0.1051	0.6304	0.1166	0.6114	0.2006	0.6184
Australia (444) v. South Africa (22)	3405.3277	0.1139	0.0000	0.1588	-1.7372	0.4146	0.0008	0.1209	0.0008	0.1209	0.0112	0.1239	0.0127	0.1259	0.0237	0.1239
Australia (444) v. Sri Lanka (12)	3481.5843	0.1319	0.0000	0.3037	-1.8199	0.7053	0.0005	0.3127	0.0006	0.3127	0.0206	0.2967	0.0232	0.2947	0.0429	0.2967
South Africa (22) v. Sri Lanka (12)	1719.7177	0.1728	0.0000	0.4416	-12.4584	0.4905	0.0005	0.3646	0.0006	0.3656	0.1750	0.4675	0.1913	0.4615	0.3118	0.4625
Seychelles (36) v. South Africa (22)	1996.9972	0.0390	0.0000	0.3746	-8.8703	0.2807	0.0005	0.3297	0.0005	0.3297	0.0784	0.4765	0.0874	0.4695	0.1538	0.4735
Seychelles (36) v. Sri Lanka (12)	1903.3093	0.0210	0.0000	0.1598	-10.7907	0.2507	0.0002	0.4555	0.0002	0.4555	0.1362	0.7572	0.1499	0.7542	0.2518	0.7542
Gulf of Mexico (37) v. Western North Atlantic (8)	1571.2543	0.1748	0.0000	0.4486	-21.7644	0.2218	-0.0002	0.4883	-0.0002	0.4883	0.3086	0.7946	0.3267	0.7923	0.4855	0.7934
Sri Lanka (12) v. Thailand (5)	1360.2400	0.1818	0.0001	0.7233	-60.7430	0.1041	-0.0005	0.5654	-0.0006	0.5654	0.7015	0.9009	0.7177	0.9009	0.8341	0.9009
Arabian Sea (15) v. Sri Lanka (12)	1614.4357	0.5245	0.0000	0.4935	-13.9062	0.4885	-0.0014	0.7622	-0.0015	0.7622	0.2158	0.7113	0.2344	0.7153	0.3703	0.7143
South Africa (22) v. Thailand (5)	1618.4549	0.0999	0.0001	0.3077	-25.7692	0.0280	-0.0017	0.6863	-0.0018	0.6863	0.4611	0.9820	0.4836	0.9830	0.6466	0.9830
Arabian Sea (15) v. Thailand (5)	1441.9783	0.4725	0.0001	0.5614	-35.0742	0.1528	-0.0019	0.7233	-0.0020	0.7233	0.5595	0.8841	0.5805	0.8851	0.7310	0.8841
Caribbean Sea (2) v. Gulf of Mexico (37)	1323.0750	0.5604	0.0001	0.4815	11.3906	1.0000	-0.0020	0.5714	-0.0022	1.0000	-9.8053	1.0000	-8.6016	1.0000	2.0904	1.0000
Mozambique (11) v. Thailand (5)	1270.4968	0.5355	0.0001	0.5844	-134.4816	0.2073	-0.0027	0.7239	-0.0029	0.7159	0.8477	0.9925	0.8568	0.9925	0.9225	0.9925
Caribbean Sea (2) v. Western North Atlantic (8)	794.9991	0.6404	0.0001	0.4745	NA	NA	-0.0077	1.0000	-0.0083	1.0000	NA	NA	NA	NA	NA	NA
Australia (444) v. Indonesia (4)	4132.4024	0.0240	0.0001	0.0110	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (25) v. Indonesia (4)	2319.4034	0.0010	0.0002	0.0020	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Japan (44)	2889.8901	0.0010	0.0003	0.0020	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Indonesia (4) v. South Africa (22)	1619.1846	0.0679	0.0001	0.0390	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

8.7.3 Fst per Region

```
strata <- BS.dartcap.gt@schemes$Region
strata[strata %in% c("E-IO","W-PAC")] <- "E-IO/W-PAC"
names(strata) <- BS.dartcap.gt@schemes$INDIVIDUALS
strataG::setStrata(BS.dartcap.gt) <- strata

Fst.gt <- strataG::popStructTest(
    BS.dartcap.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_ALL_FST_Regions.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_ALL_FST_Regions.txt")
```

```
load("DArTcap_ALL_FST_Regions.Rdata")
kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                       decreasing = TRUE),
                                  -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 3443 DArTcap loci between the all regions",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                       latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()

pop.levels1 <- c("E-PAC", "W-ATL", "E-ATL", "W-IO", "N-IO", "E-IO/W-PAC",
                 "Japan" , "Fiji")

m2 <- Fst.gt$pairwise$result[order(match(Fst.gt$pairwise$result$strata.1,
                                        pop.levels1)),c(1,2,11)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.1 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                   attr = "Fst", type = 'lower')

m2 <- Fst.gt$pairwise$result[order(match(Fst.gt$pairwise$result$strata.1,
                                        pop.levels1)),c(1,2,12)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.2 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                   attr = "Fst.p.val", type = 'lower')
m2$Fst.p.adj <- p.adjust(m2$Fst.p.val, "bonferroni")
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.3 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                   attr = "Fst.p.adj", type = 'lower')

write.csv(m2.1, file = "DArTcap_ALL_FST_Regions.csv")
write.csv(m2.2, file = "DArTcap_ALL_FST_Pval_Regions.csv")
write.csv(m2.3, file = "DArTcap_ALL_FST_Pval_bonferroni_Regions.csv")
```

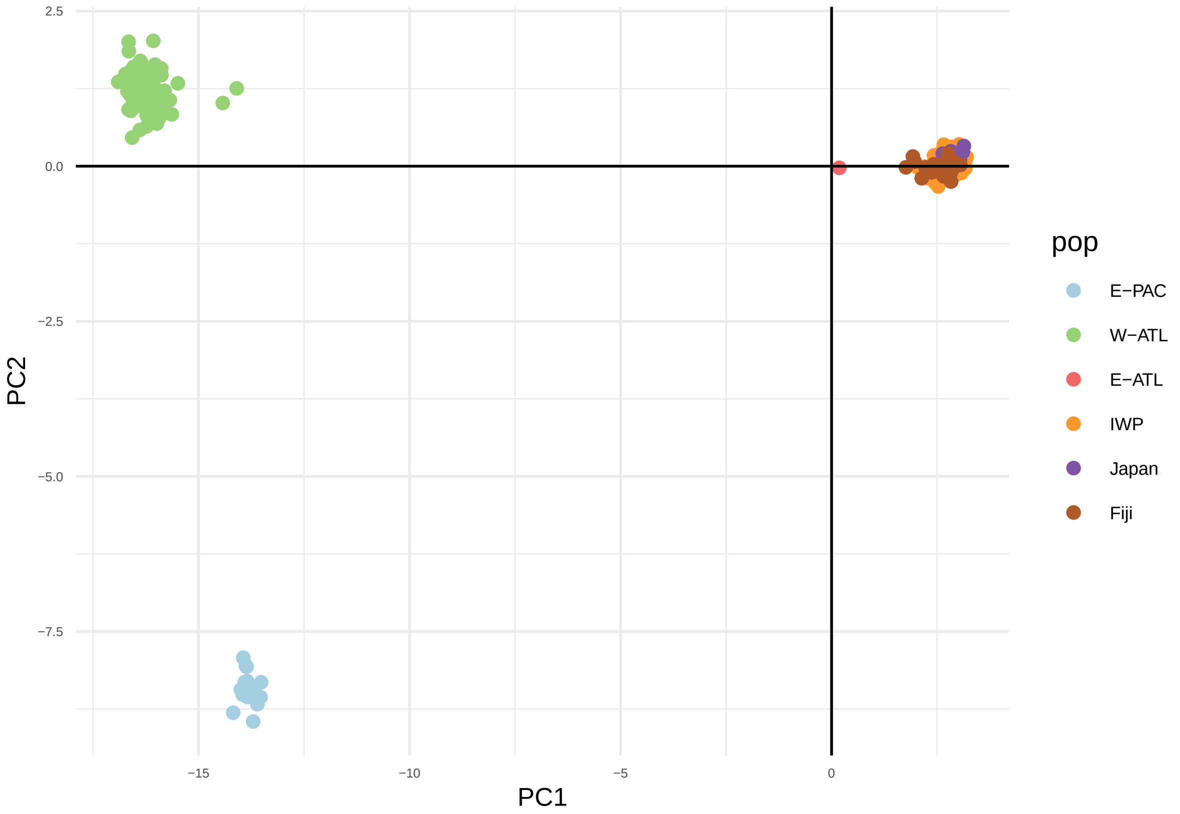
Table 21: Pairwise Fst for 3443 DArTcap loci between the all regions

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.val
E-ATL (1) v. E-PAC (16)	11158.858	0.0559	0.0114	0.0559	NA	NA	0.7013	1.000	0.7555	1.000	NA	NA	NA	NA	NA	NA
Japan (44) v. W-ATL (97)	120117.283	0.0010	0.0211	0.0010	-4.0027	1.0000	0.6667	0.001	0.7245	0.001	0.5080	0.0010	0.5686	0.0010	0.7139	0.0010
Fiji (25) v. W-ATL (97)	95752.021	0.0010	0.0206	0.0010	-4.6818	1.0000	0.6629	0.001	0.7235	0.001	0.5102	0.0010	0.5706	0.0010	0.7157	0.0010
E-PAC (16) v. Japan (44)	48791.209	0.0010	0.0182	0.0010	-10.8638	1.0000	0.6609	0.001	0.7115	0.001	0.5930	0.0010	0.6435	0.0010	0.7762	0.0010
N-IO (32) v. W-ATL (97)	104843.972	0.0010	0.0200	0.0010	-3.4887	1.0000	0.6595	0.001	0.7187	0.001	0.4966	0.0010	0.5574	0.0010	0.7042	0.0010
E-PAC (16) v. Fiji (25)	32838.244	0.0010	0.0177	0.0010	-12.8862	1.0000	0.6594	0.001	0.7427	0.001	0.6143	0.0010	0.6629	0.0010	0.7912	0.0010
W-ATL (97) v. W-IO (97)	167080.101	0.0010	0.0201	0.0010	-2.1320	1.0000	0.6526	0.001	0.7090	0.001	0.4891	0.0010	0.5500	0.0010	0.6978	0.0010
E-PAC (16) v. N-IO (32)	39020.274	0.0010	0.0172	0.0010	-9.3166	1.0000	0.6516	0.001	0.6994	0.001	0.5776	0.0010	0.6289	0.0010	0.7648	0.0010
E-IO/W-PAC (457) v. W-ATL (97)	457028.313	0.0010	0.0200	0.0010	-0.2794	1.0000	0.6413	0.001	0.6887	0.001	0.4836	0.0010	0.5448	0.0010	0.6932	0.0010
E-PAC (16) v. W-IO (97)	83951.675	0.0010	0.0172	0.0010	-5.7967	1.0000	0.6372	0.001	0.7023	0.001	0.5446	0.0010	0.5979	0.0010	0.7397	0.0010
E-ATL (1) v. W-ATL (97)	27769.816	0.0090	0.0129	0.0090	4.1821	1.0000	0.6331	1.000	0.6949	1.000	22.5515	1.0000	16.9504	1.0000	1.6773	1.0000
E-IO/W-PAC (457) v. E-PAC (16)	306720.921	0.0010	0.0172	0.0010	-1.0829	1.0000	0.6265	0.001	0.6694	0.001	0.5104	0.0010	0.5657	0.0010	0.7124	0.0010
E-PAC (16) v. W-ATL (97)	21245.739	0.0010	0.0025	0.0010	-8.8181	1.0000	0.3490	0.001	0.3798	0.001	0.3044	0.0010	0.3305	0.0010	0.4868	0.0010
E-ATL (1) v. Japan (44)	6184.421	0.0210	0.0009	0.0210	3.6975	1.0000	0.2067	1.000	0.2253	1.000	-2.0230	1.0000	-1.2649	1.0000	3.2141	1.0000
E-ATL (1) v. Fiji (25)	3717.034	0.0370	0.0008	0.0719	3.5244	1.0000	0.1610	1.000	0.1913	1.000	-1.8479	1.0000	-1.0793	1.0000	3.4522	1.0000
E-ATL (1) v. E-IO/W-PAC (457)	28506.972	0.0040	0.0007	0.0040	-14.8084	1.0000	0.1574	1.000	0.1724	1.000	0.7535	1.0000	0.7700	1.0000	0.8688	1.0000
E-ATL (1) v. N-IO (32)	4376.922	0.0360	0.0007	0.0360	3.7775	1.0000	0.1573	1.000	0.1714	1.000	-2.1933	1.0000	-1.4427	1.0000	3.0470	1.0000
E-ATL (1) v. W-IO (97)	9473.367	0.0130	0.0007	0.0130	4.4781	1.0000	0.1552	1.000	0.1731	1.000	-4.1996	1.0000	-3.2707	1.0000	2.3348	1.0000
Fiji (25) v. Japan (44)	5695.638	0.0010	0.0003	0.0010	-8.2308	1.0000	0.0617	0.001	0.0668	0.001	0.0972	0.0010	0.1084	0.0010	0.1873	0.0010
Fiji (25) v. W-IO (97)	5603.824	0.0010	0.0002	0.0010	-5.2621	0.9990	0.0313	0.001	0.0346	0.001	0.0517	0.0010	0.0581	0.0010	0.1044	0.0010
E-IO/W-PAC (457) v. Fiji (25)	9554.750	0.0010	0.0002	0.0010	-1.4206	0.0460	0.0310	0.001	0.0334	0.001	0.0243	0.0010	0.0275	0.0010	0.0505	0.0010
Japan (44) v. N-IO (32)	4233.906	0.0010	0.0002	0.0010	-7.4254	1.0000	0.0307	0.001	0.0331	0.001	0.0646	0.0010	0.0724	0.0010	0.1286	0.0010
Fiji (25) v. N-IO (32)	3818.756	0.0010	0.0002	0.0010	-7.3585	1.0000	0.0301	0.001	0.0325	0.001	0.0821	0.0010	0.0918	0.0010	0.1607	0.0010
Japan (44) v. W-IO (97)	6003.192	0.0010	0.0002	0.0010	-5.2873	1.0000	0.0295	0.001	0.0324	0.001	0.0373	0.0010	0.0420	0.0010	0.0764	0.0010
E-IO/W-PAC (457) v. Japan (44)	9393.609	0.0010	0.0002	0.0010	-1.6860	1.0000	0.0287	0.001	0.0308	0.001	0.0204	0.0010	0.0230	0.0010	0.0425	0.0010
E-IO/W-PAC (457) v. N-IO (32)	4130.868	0.0010	0.0000	0.0100	-1.5974	0.4575	0.0017	0.001	0.0019	0.001	0.0078	0.0010	0.0089	0.0010	0.0166	0.0010
E-IO/W-PAC (457) v. W-IO (97)	3975.773	0.0010	0.0000	0.0010	-1.4588	0.2657	0.0014	0.001	0.0015	0.001	0.0031	0.0010	0.0036	0.0010	0.0067	0.0010
N-IO (32) v. W-IO (97)	2893.453	0.0010	0.0000	0.0080	-5.0487	0.1868	0.0010	0.037	0.0011	0.036	0.0271	0.2897	0.0306	0.2747	0.0562	0.2817

8.8 PCA

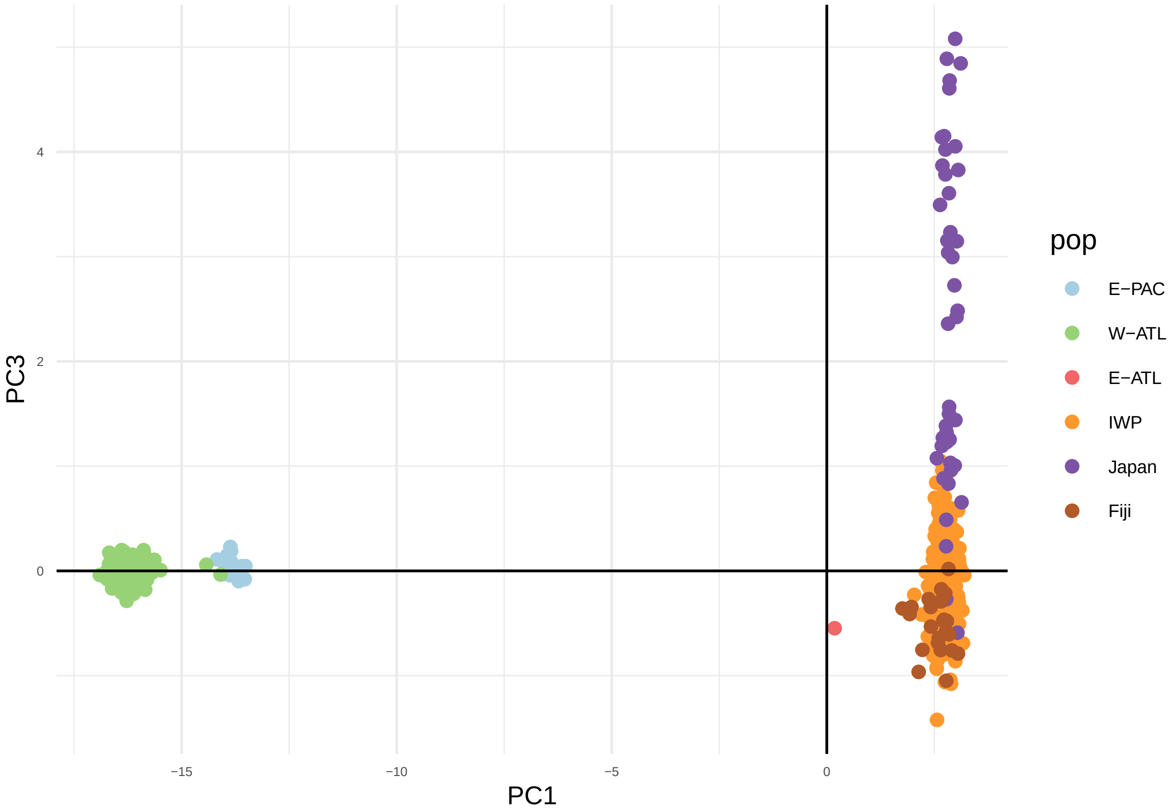
```
pca1 <- adegenet::glPca(BS.dartcap.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_ALL_PCA.Rdata")
```

```
load("DArTcap_ALL_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.gl)
cols <- adegenet::funky(nPop(BS.dartcap.gl))

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

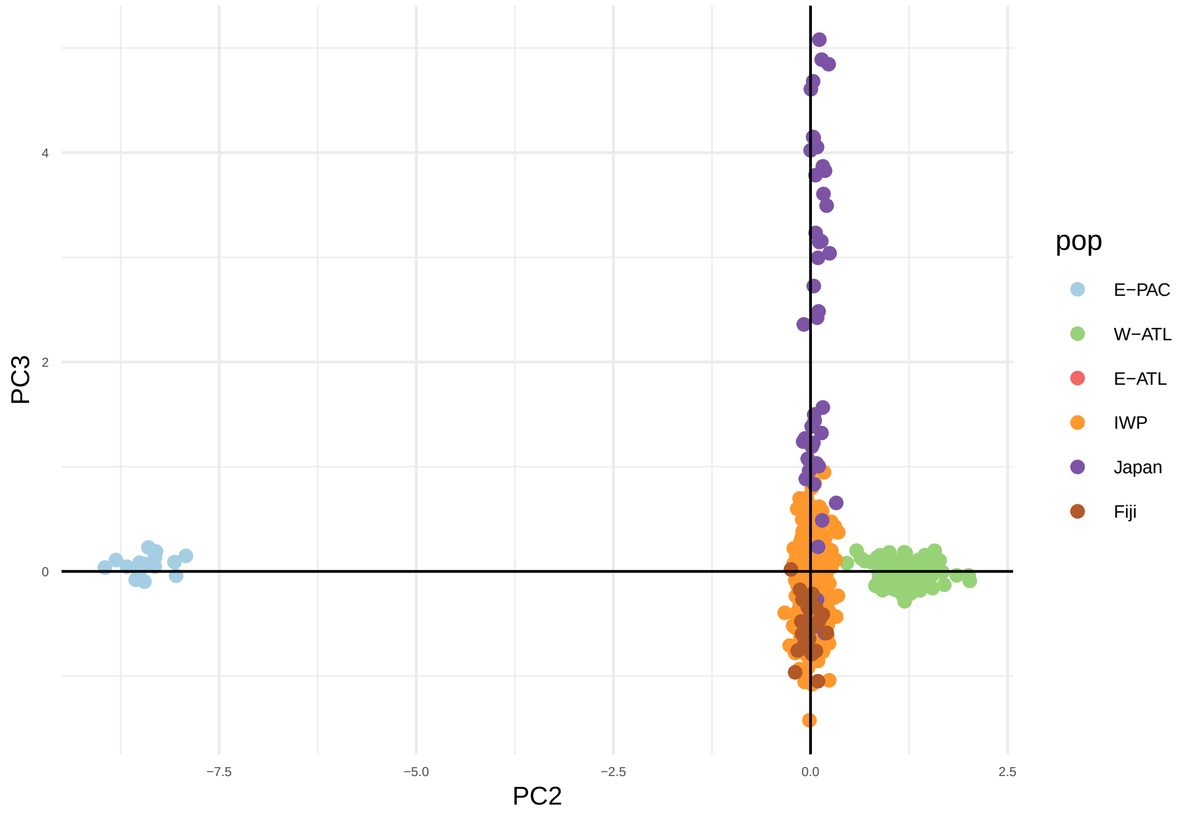


```
ggplot2::ggsave(p, filename = "DArTcap_ALL_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
```

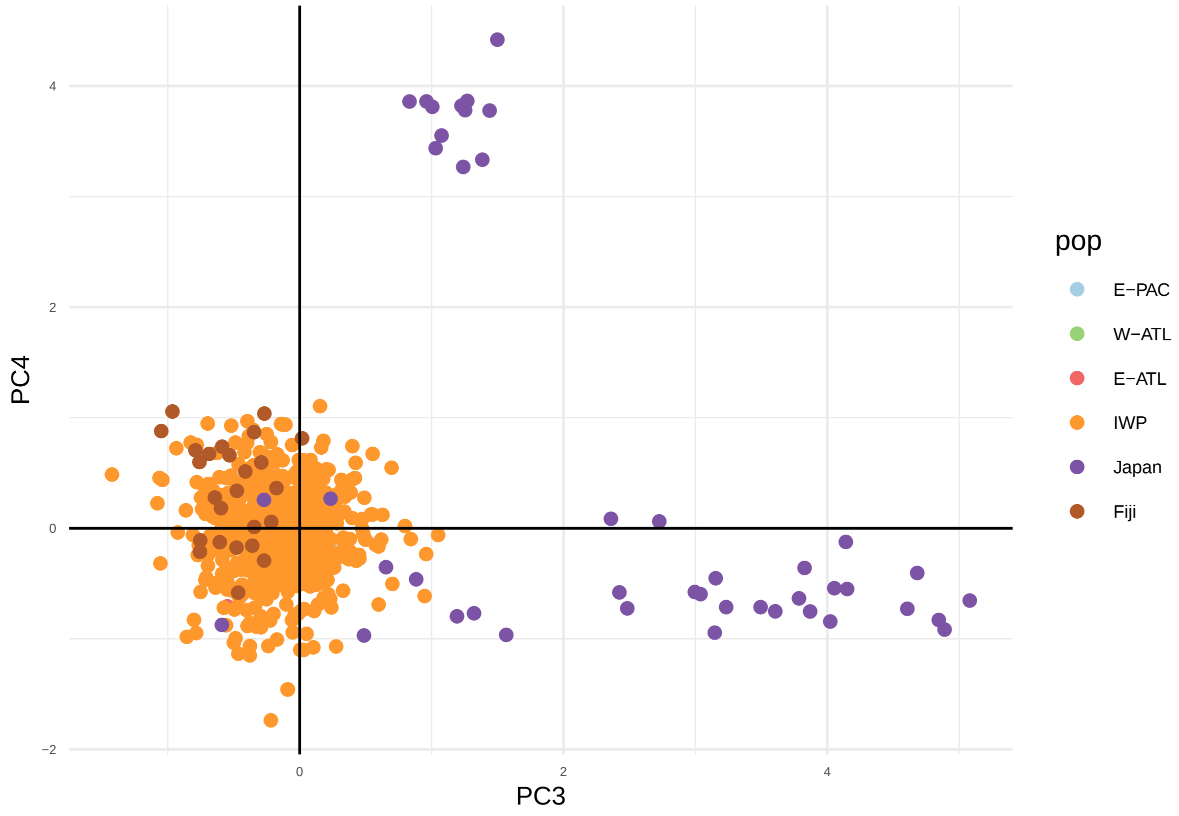
```
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



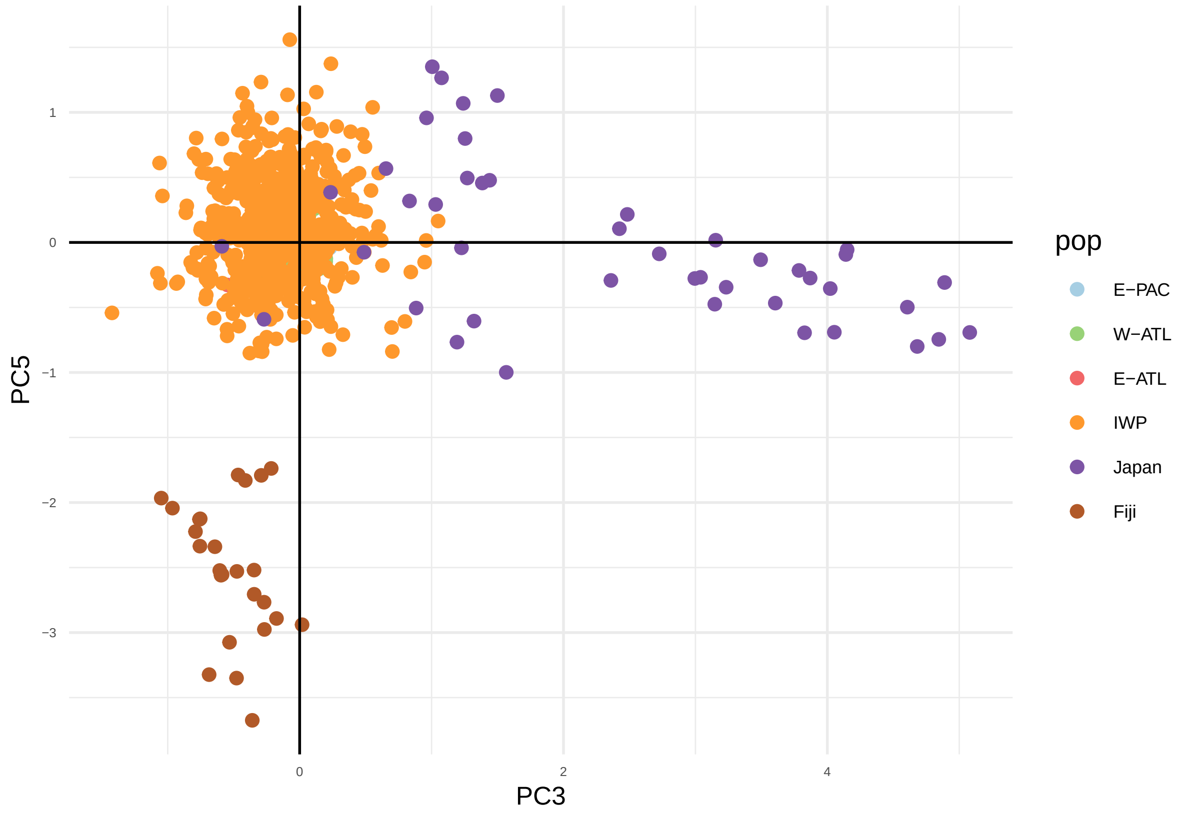
```
ggplot2::ggsave(p, filename = "DArTcap_ALL_PCA2.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_ALL_PCA3.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_ALL_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```r
ggplot2::ggsave(p, filename = "DArTcap_ALL_PCA5.png", width = 30,
                height = 15,units = "cm")
```

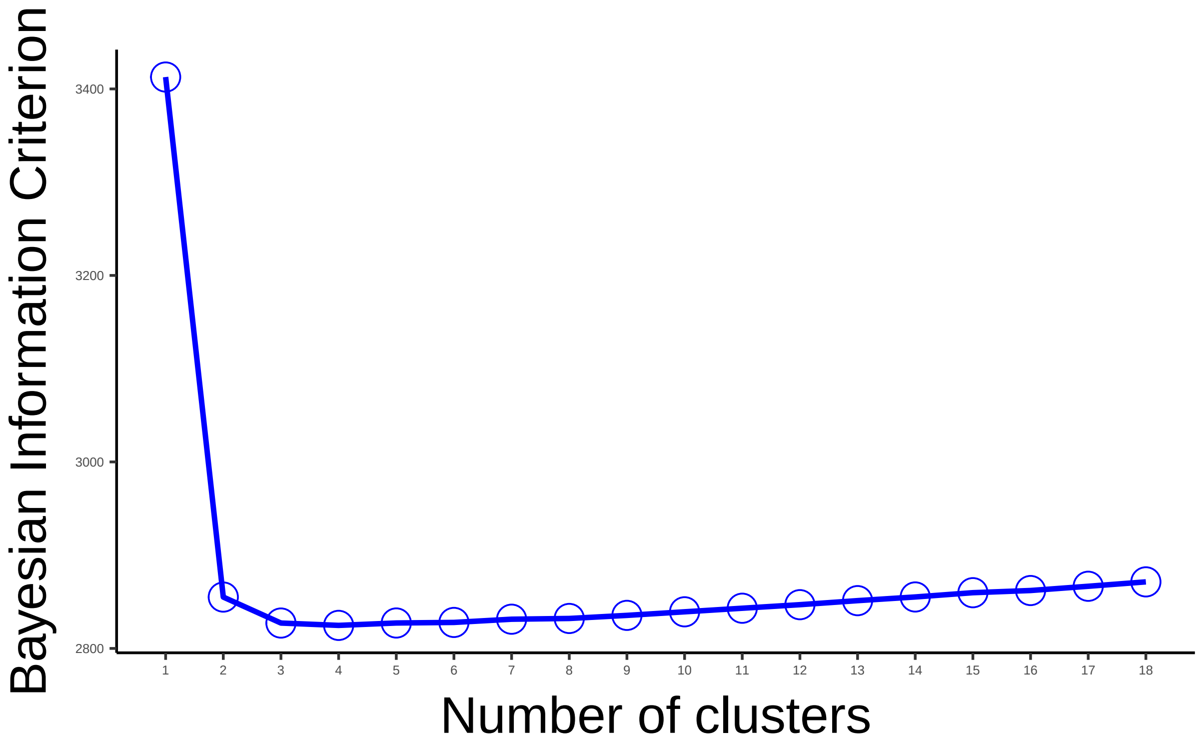
8.9 DAPC

8.9.1 Optimal number of clusters with neutral markers

```r
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartcap.gl,
    max.n.clust = 18,
    n.pca = adegenet::nInd(BS.dartcap.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTcap_ALL_grp_.Rdata")
```

```r
load("DArTcap_ALL_grp_.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:18
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartcap.gl) - 1, by = 1)) +
```

```
  ggplot2::labs(subtitle = "",
                y = "Bayesian Information Criterion",
                x = "Number of clusters",
                title = "",
                caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_ALL_grp.png", width = 30,
                height = 15,units = "cm")
```

8.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartcap.gl
x <- x[x$pop != "Sierra Leone",] #only1 sample

xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 50),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
  scale = FALSE,
```

```r
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTcap_ALL_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTcap_ALL_xval.rdata")
```

```r
load("DArTcap_ALL_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

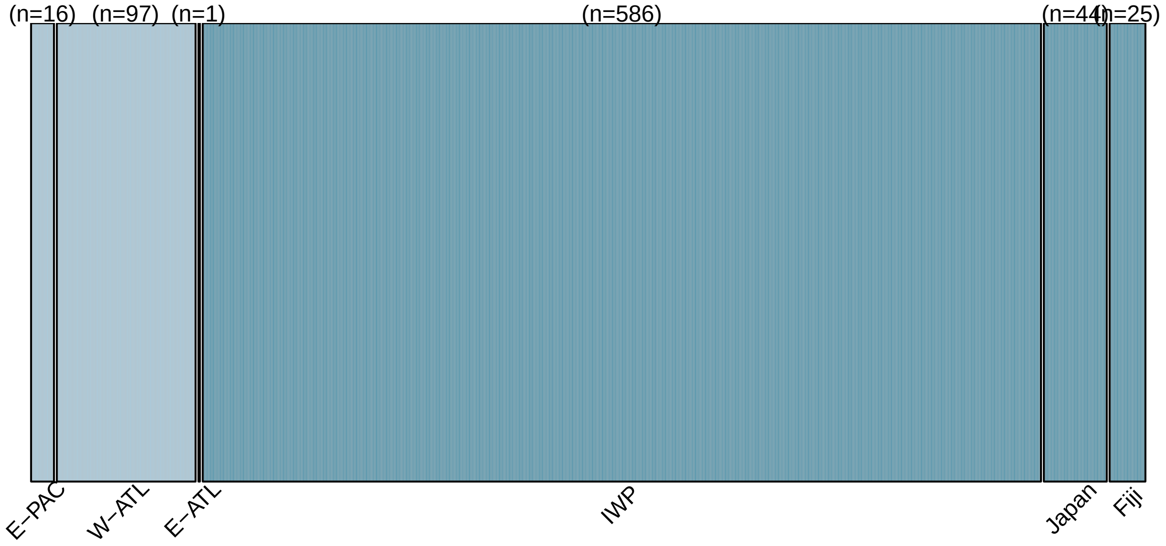
```
## $`Median and Confidence Interval for Random Chance`
##       2.5%        50%      97.5%
## 0.02065971 0.03214135 0.04492563
##
## $`Mean Successful Assignment by Number of PCs of PCA`
##       186       187       188       189       190       191       192       193
## 0.2470927 0.2462834 0.2473624 0.2470312 0.2477719 0.2475748 0.2482662 0.2481249
##       194       195       196       197       198       199       200       201
## 0.2495385 0.2485589 0.2488955 0.2482662 0.2479600 0.2490014 0.2492077 0.2488088
##       202       203       204       205       206       207       208       209
## 0.2495266 0.2486349 0.2480373 0.2491746 0.2475283 0.2507537 0.2510989 0.2529229
##       210       211       212       213       214       215       216
## 0.2517774 0.2515806 0.2515262 0.2518021 0.2508993 0.2504337 0.2498401
##
## $`Number of PCs Achieving Highest Mean Success`
## [1] "209"
##
## $`Root Mean Squared Error by Number of PCs of PCA`
##       186       187       188       189       190       191       192       193
## 0.7530993 0.7539175 0.7528239 0.7531685 0.7524294 0.7526268 0.7519474 0.7520711
##       194       195       196       197       198       199       200       201
## 0.7506672 0.7516384 0.7513023 0.7519209 0.7522335 0.7512127 0.7509966 0.7513961
##       202       203       204       205       206       207       208       209
## 0.7506742 0.7515642 0.7521607 0.7510212 0.7526754 0.7494574 0.7491003 0.7472907
##       210       211       212       213       214       215       216
## 0.7484201 0.7486261 0.7486684 0.7483942 0.7493148 0.7497796 0.7503830
##
## $`Number of PCs Achieving Lowest MSE`
## [1] "209"
```

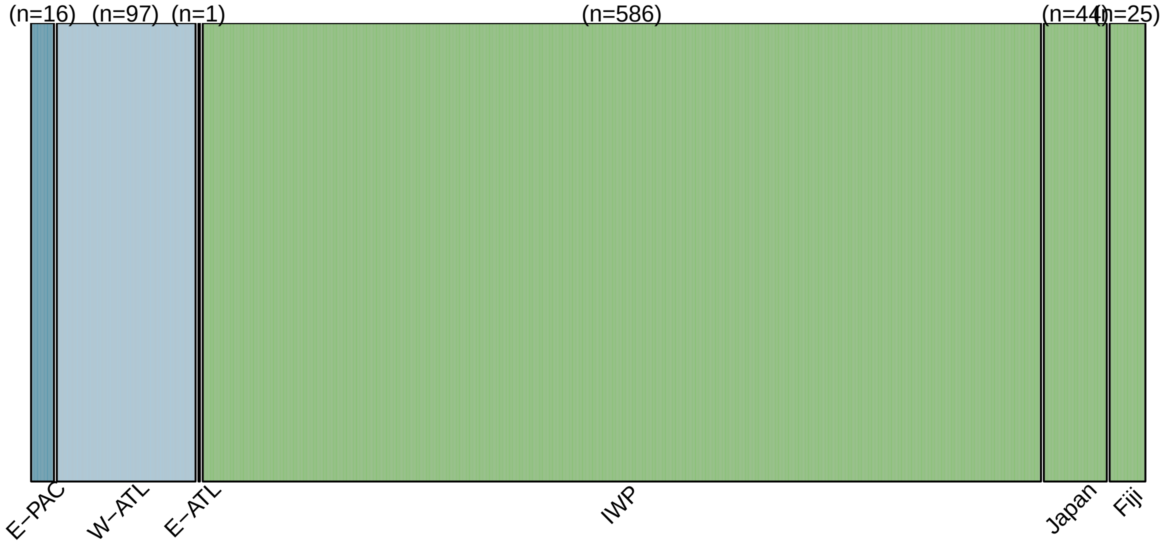
```r
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartcap.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartcap.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                                     paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTcap_ALL_DAPC.Rdata")
```

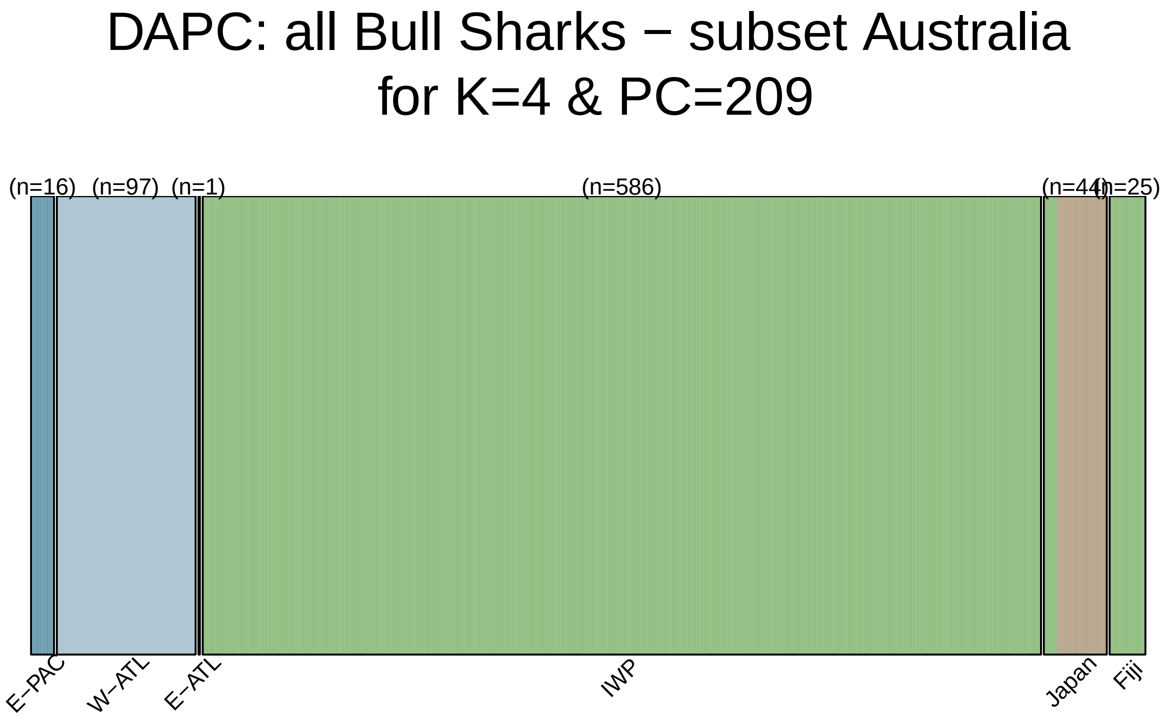
8.9.3 DAPC barplot

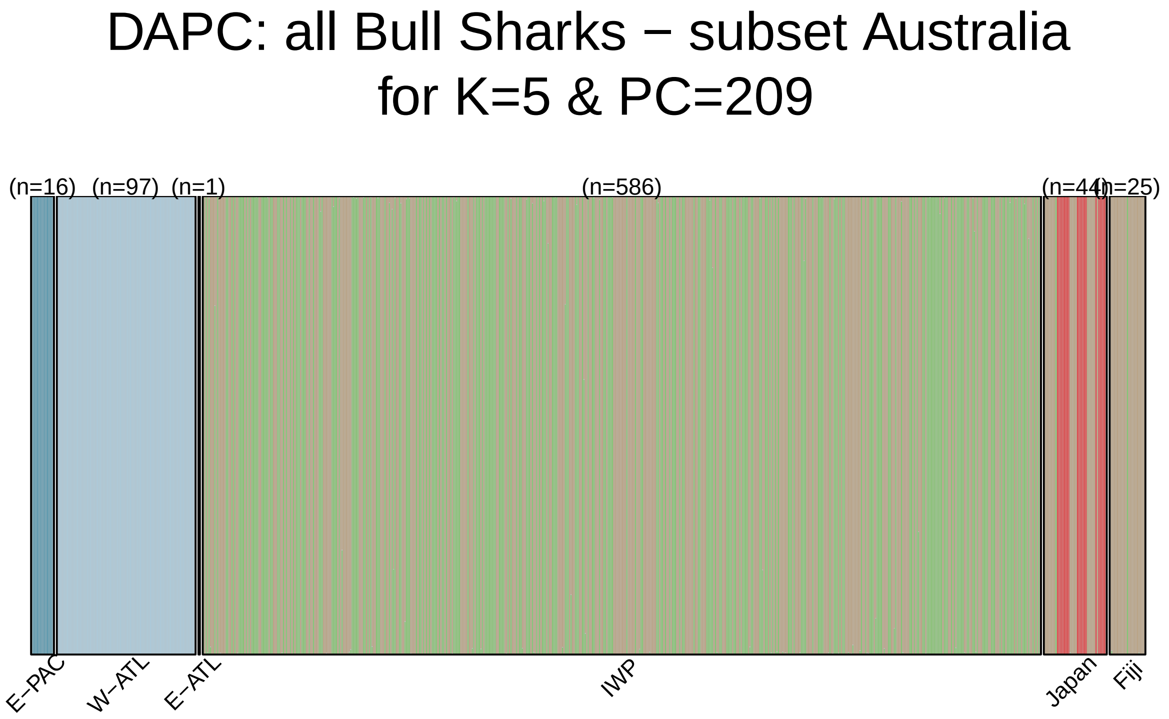
Group individuals according to DAPC posterior membership.

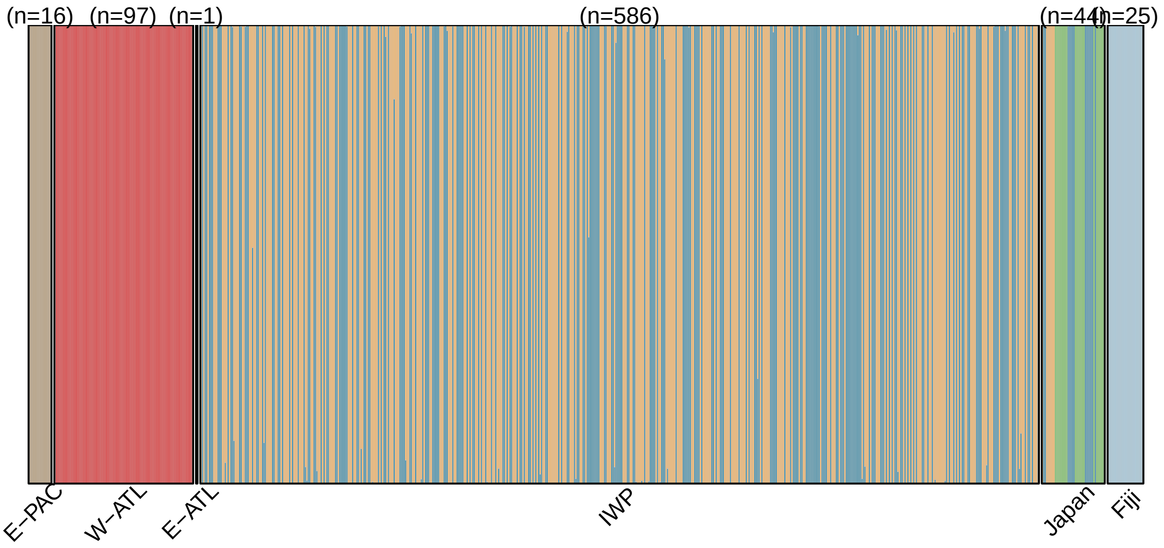
```r
load("DArTcap_ALL_DAPC.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartcap.gl$pop

  plot.dapc.FDD(x = post,
                locations = locations,
                colour = colour,
                region.lwd = 1,
                plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                   K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTcap_ALL_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```


DAPC: all Bull Sharks − subset Australia for K=2 & PC=209

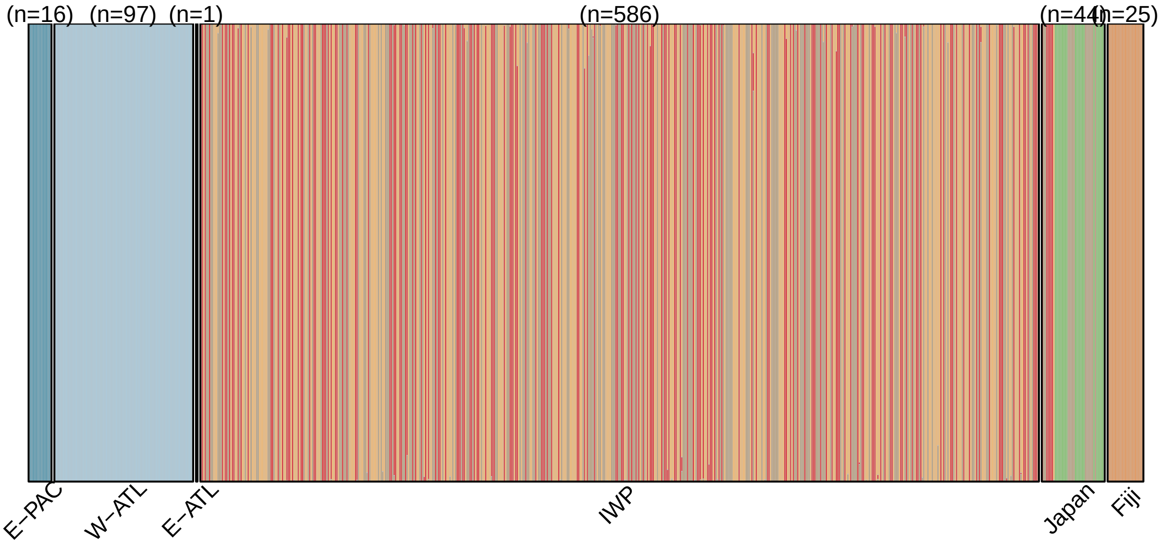

DAPC: all Bull Sharks − subset Australia for K=3 & PC=209


DAPC: all Bull Sharks − subset Australia
for K=4 & PC=209


DAPC: all Bull Sharks − subset Australia
for K=5 & PC=209

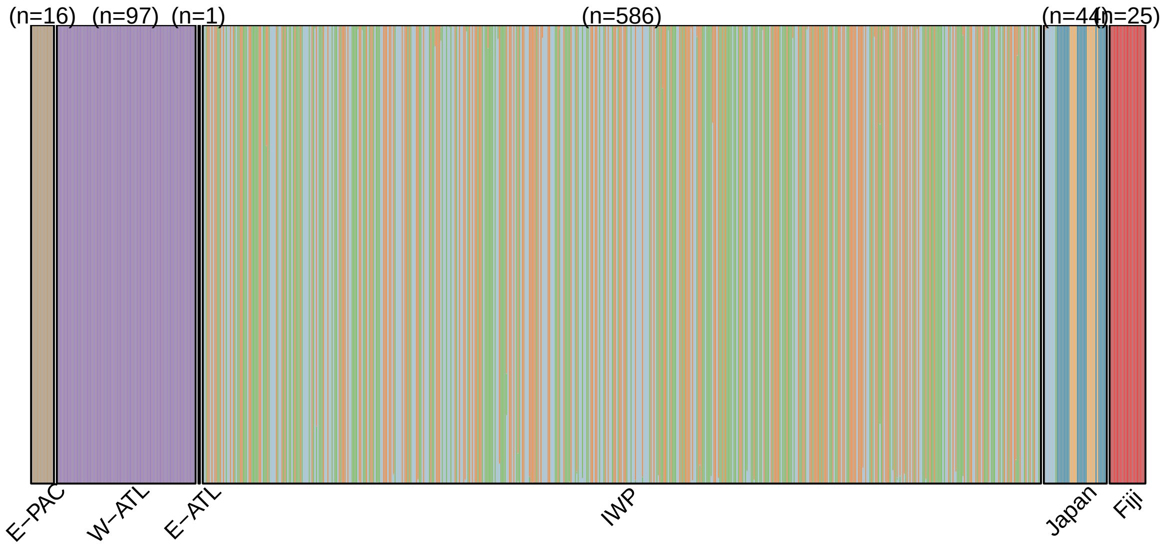


DAPC: all Bull Sharks − subset Australia
for K=6 & PC=209

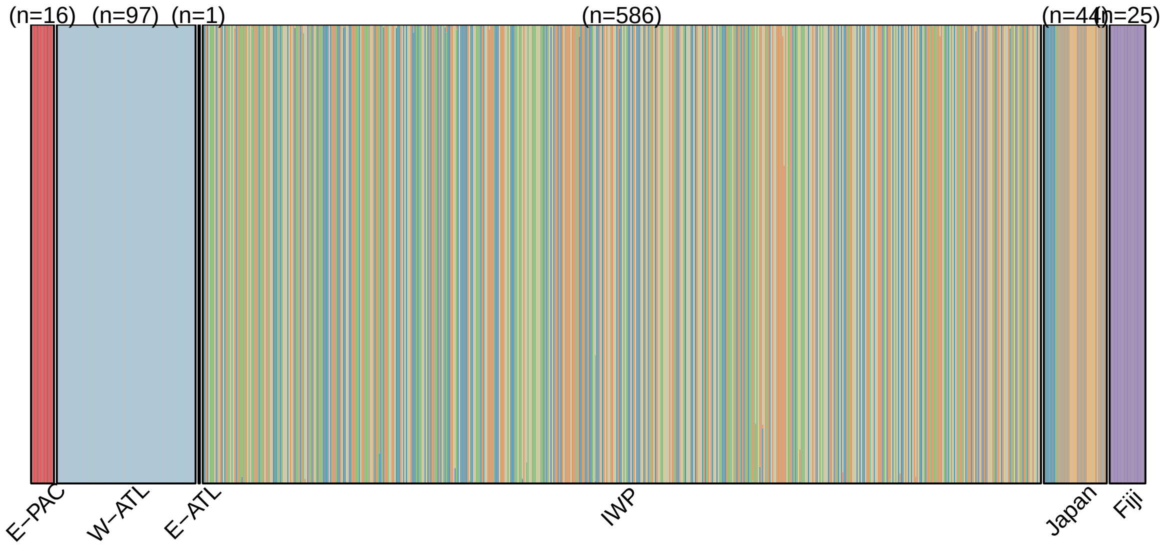


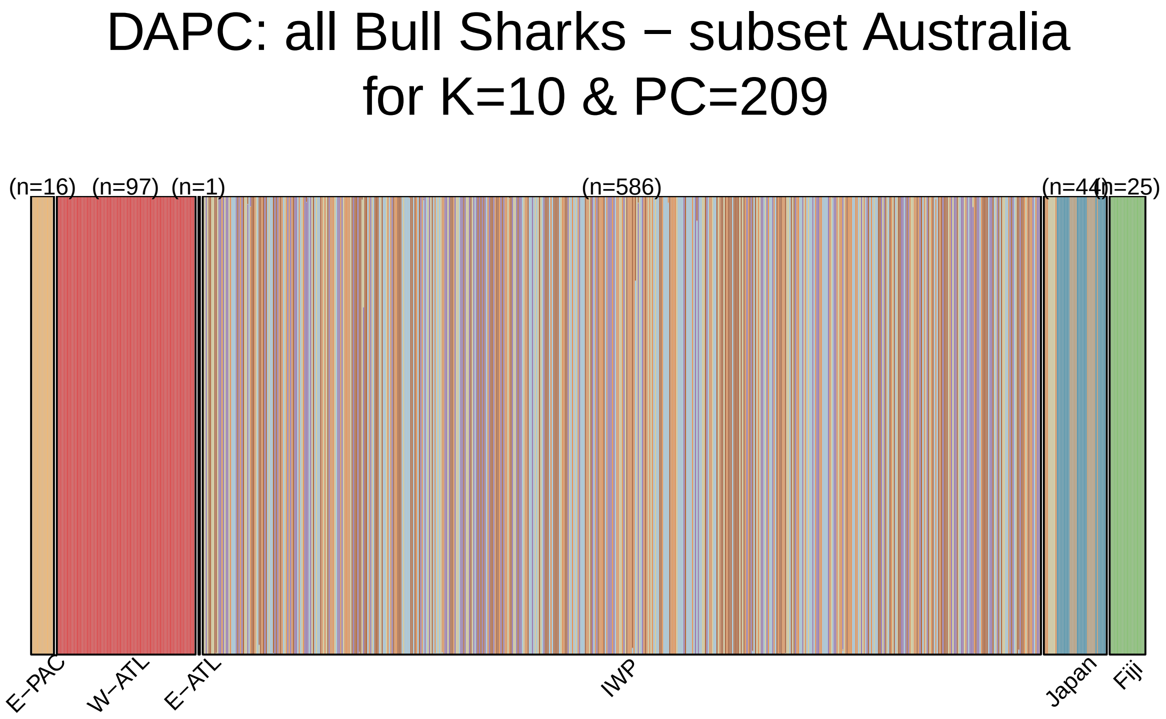
DAPC: all Bull Sharks − subset Australia
for K=7 & PC=209

DAPC: all Bull Sharks − subset Australia
for K=8 & PC=209



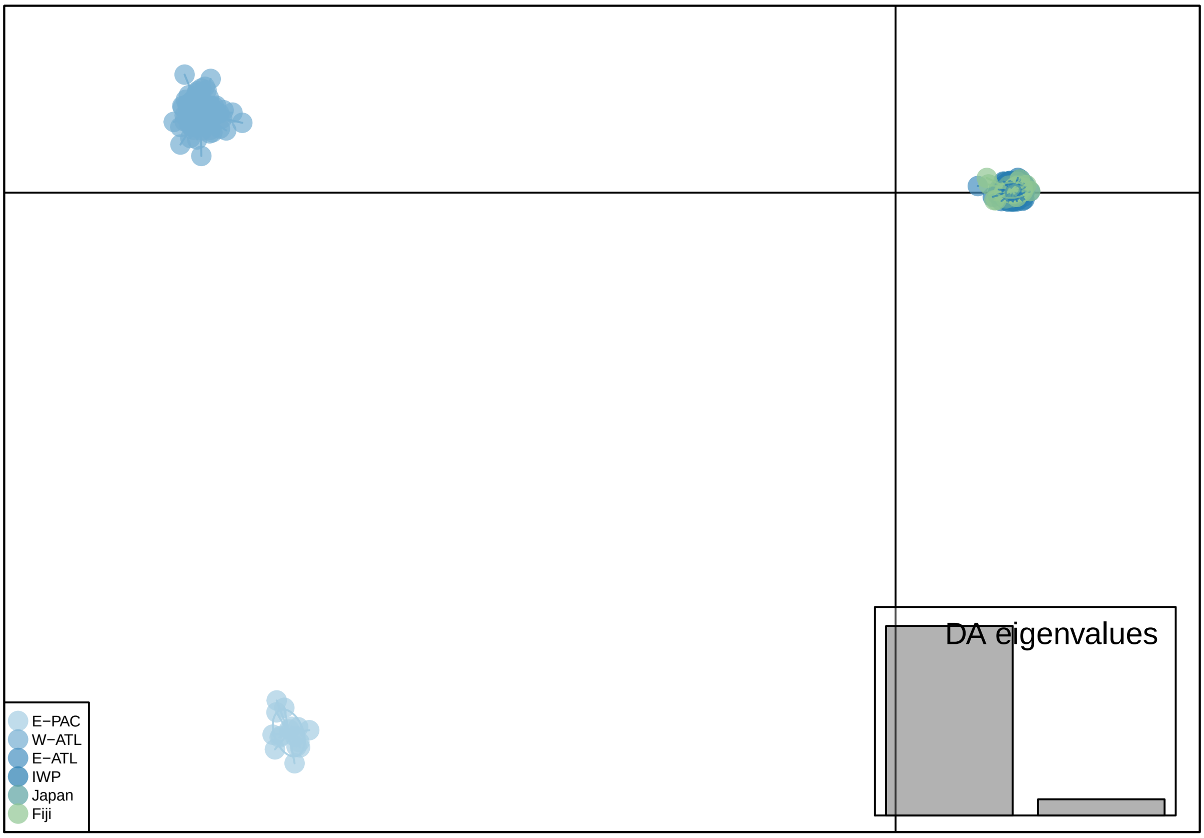
DAPC: all Bull Sharks − subset Australia
for K=9 & PC=209

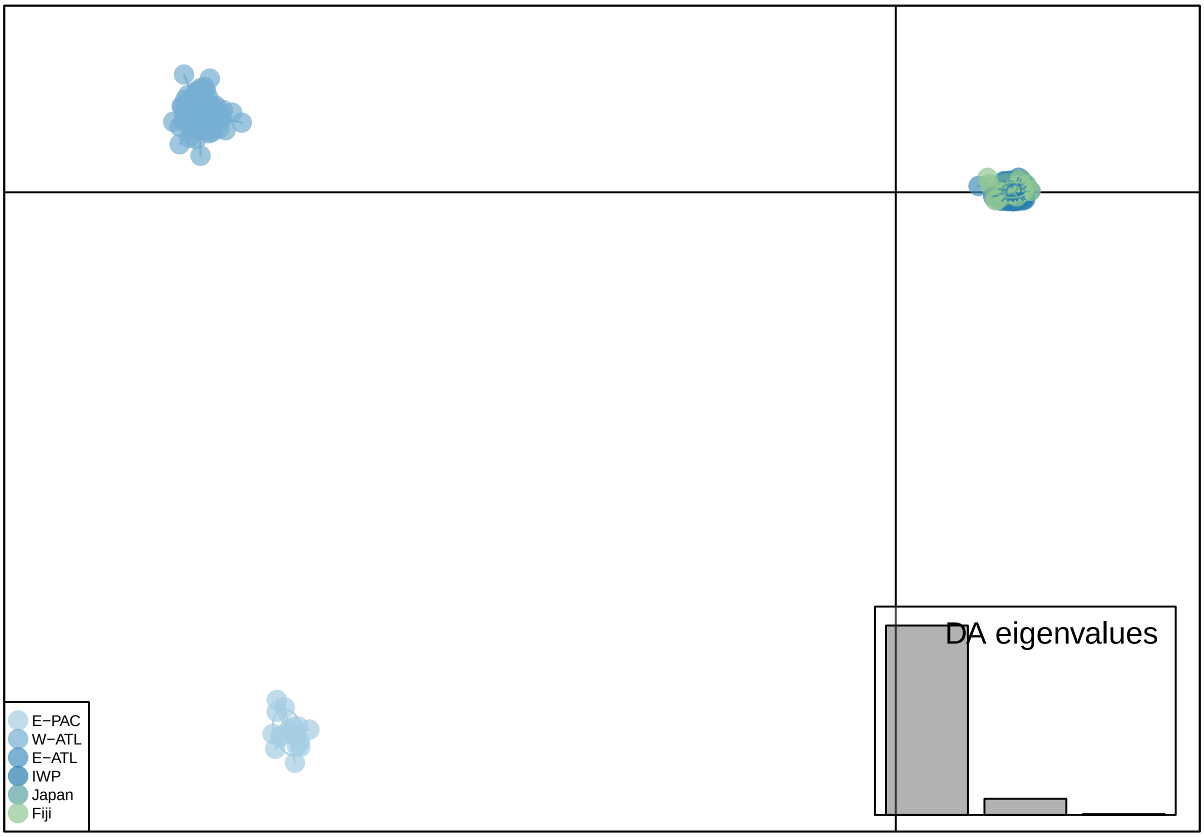


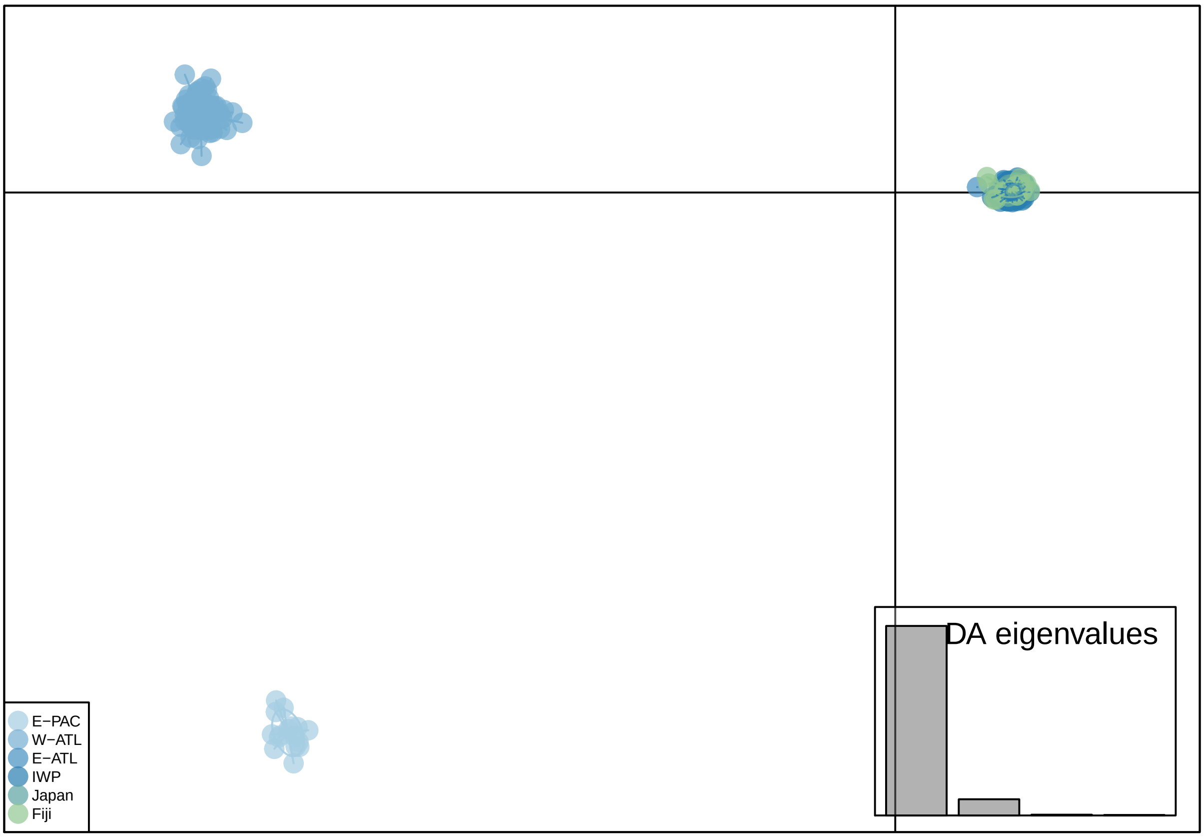


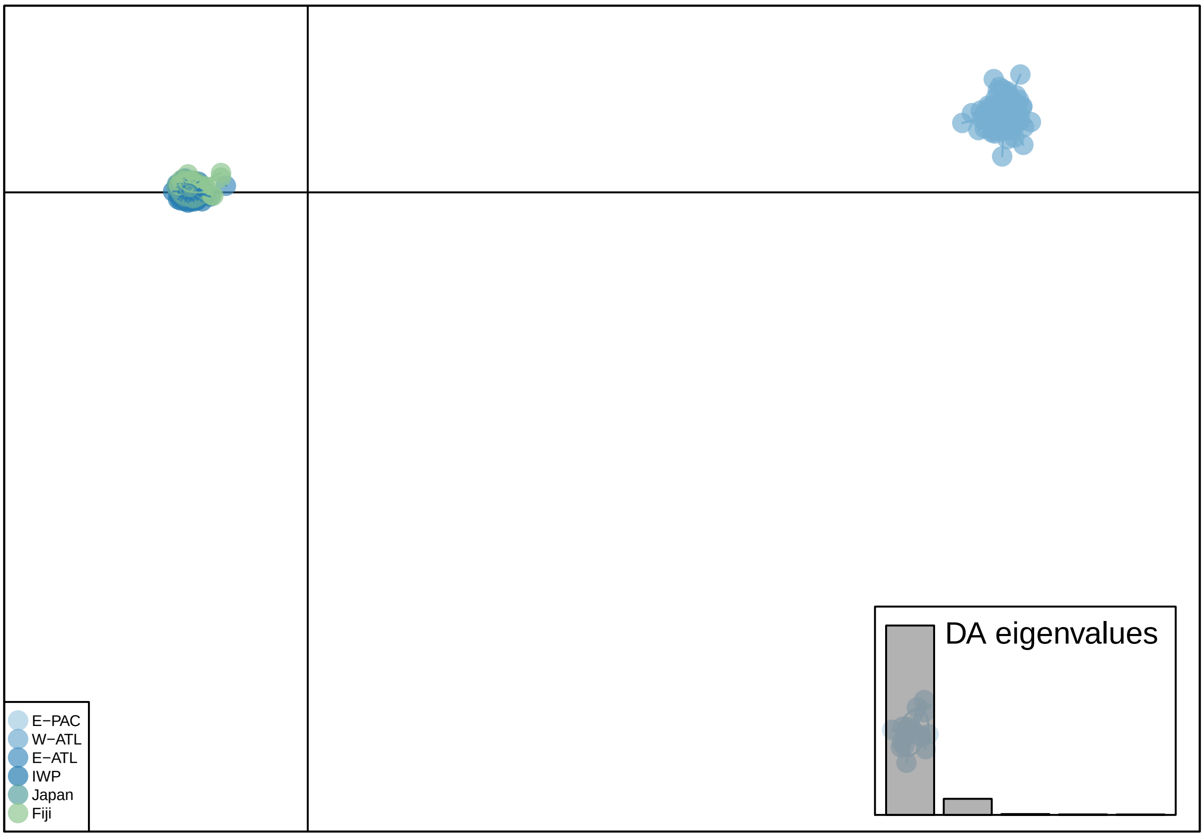
8.9.4 DAPC scatterplot

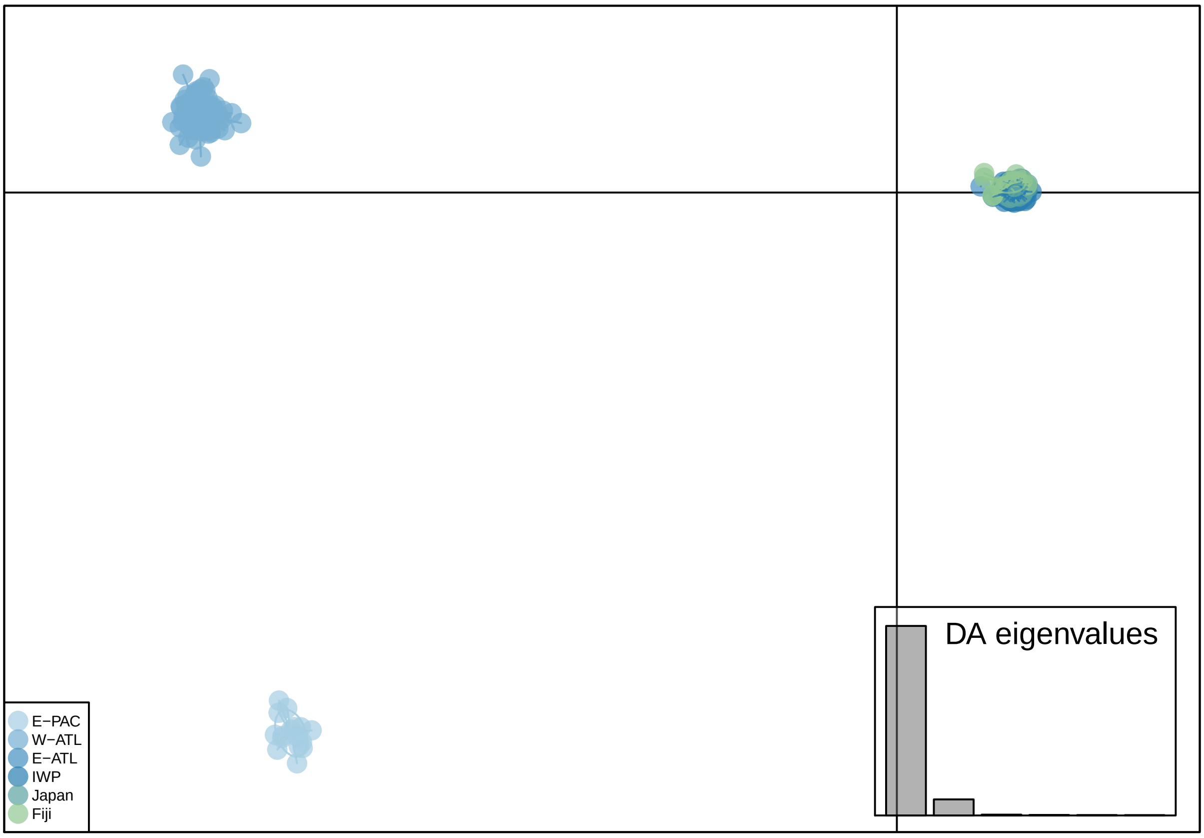
```
load("DArTcap_ALL_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartcap.gl), cex = 2, legend = TRUE,
                             col = colours.32,clabel = FALSE, posi.leg = posi.leg,
                             scree.pca = FALSE,posi.pca = "topleft", cleg = 0.5,
                             xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_ALL_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

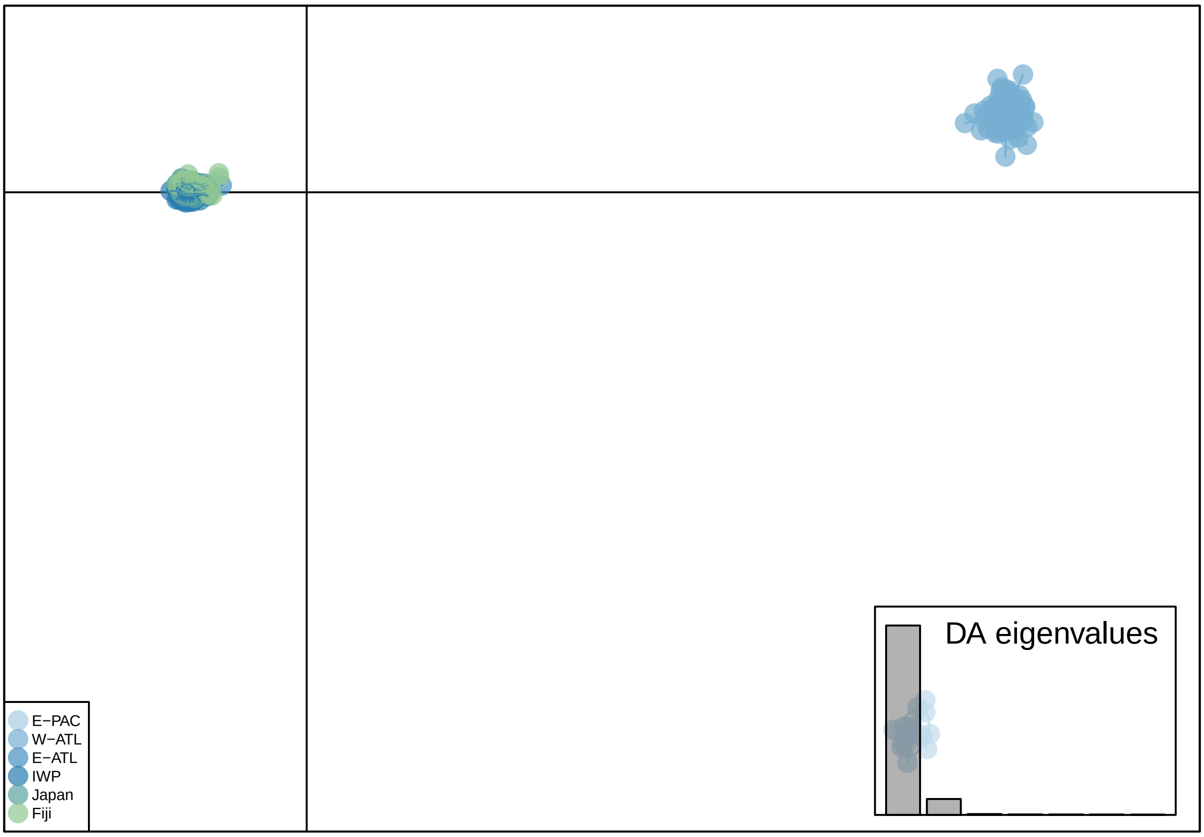

DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji

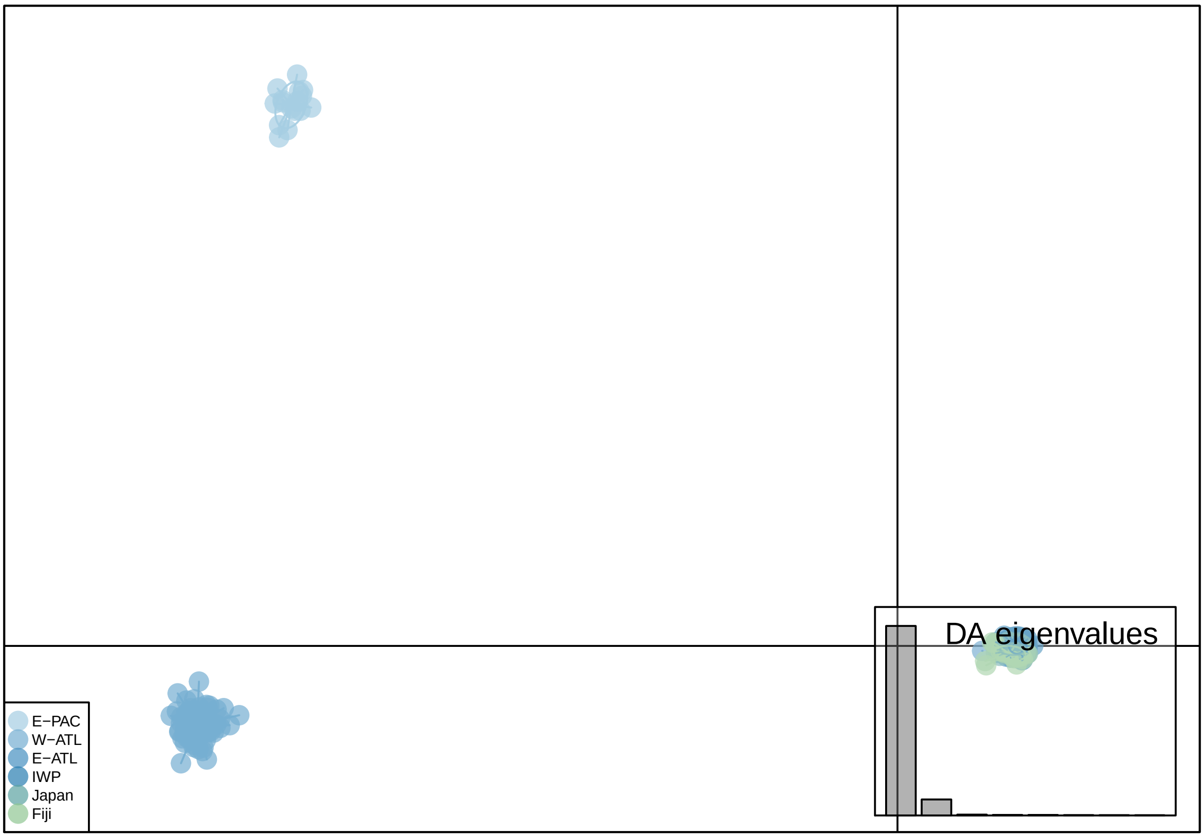

DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji

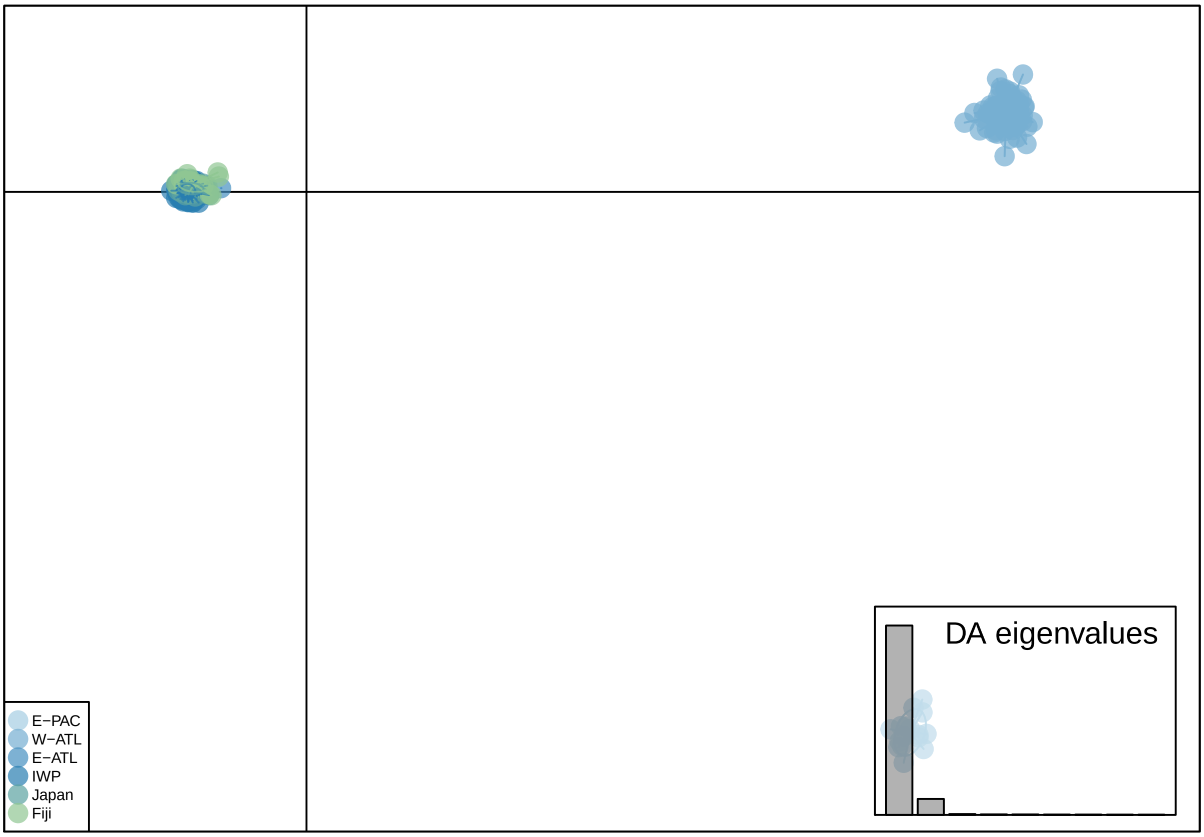

DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji


DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji


DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji

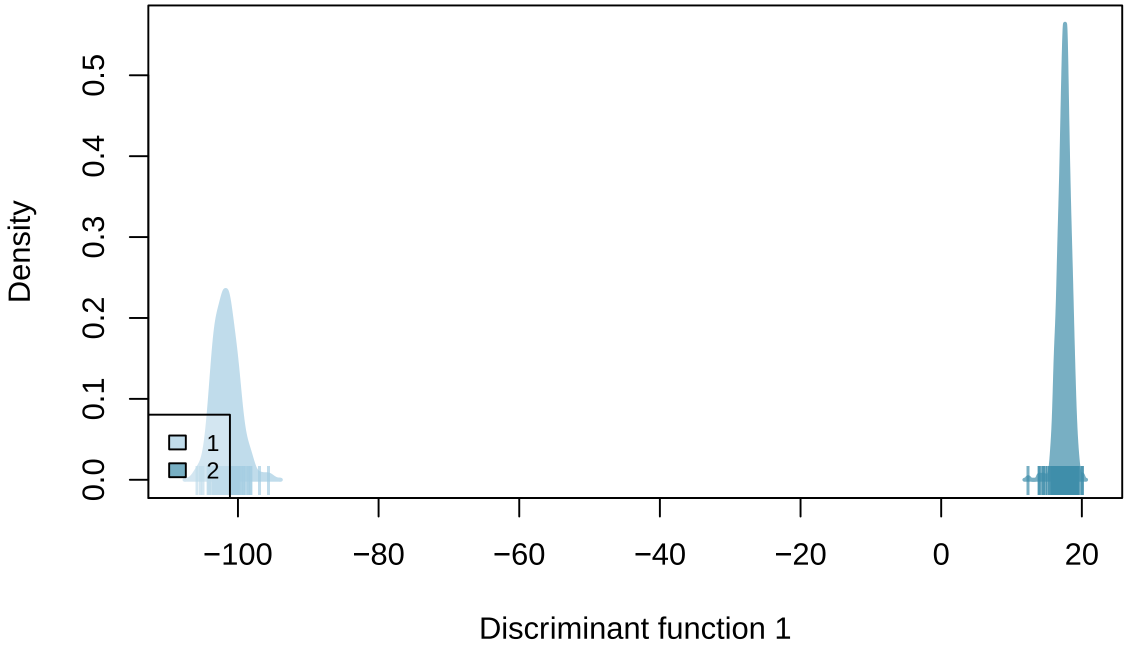

DA eigenvalues
E−PAC
W−ATL
E−ATL
IWP
Japan
Fiji

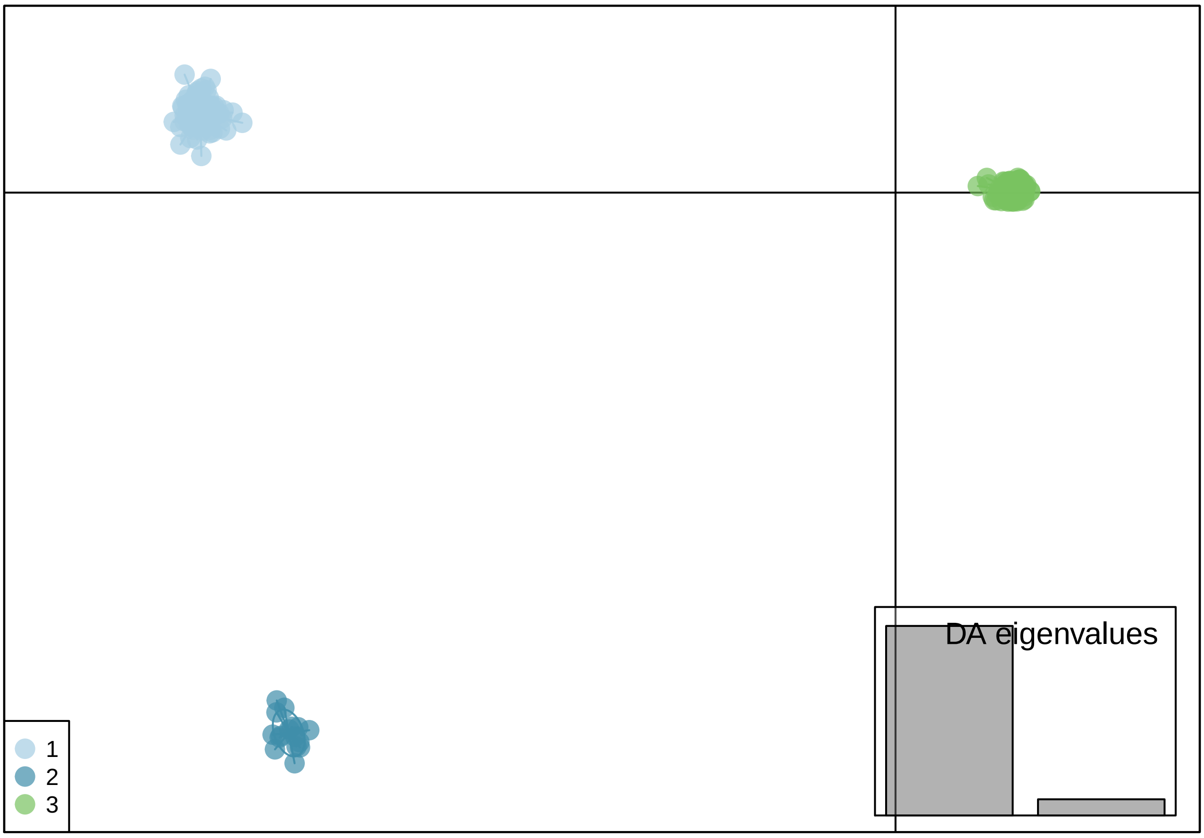


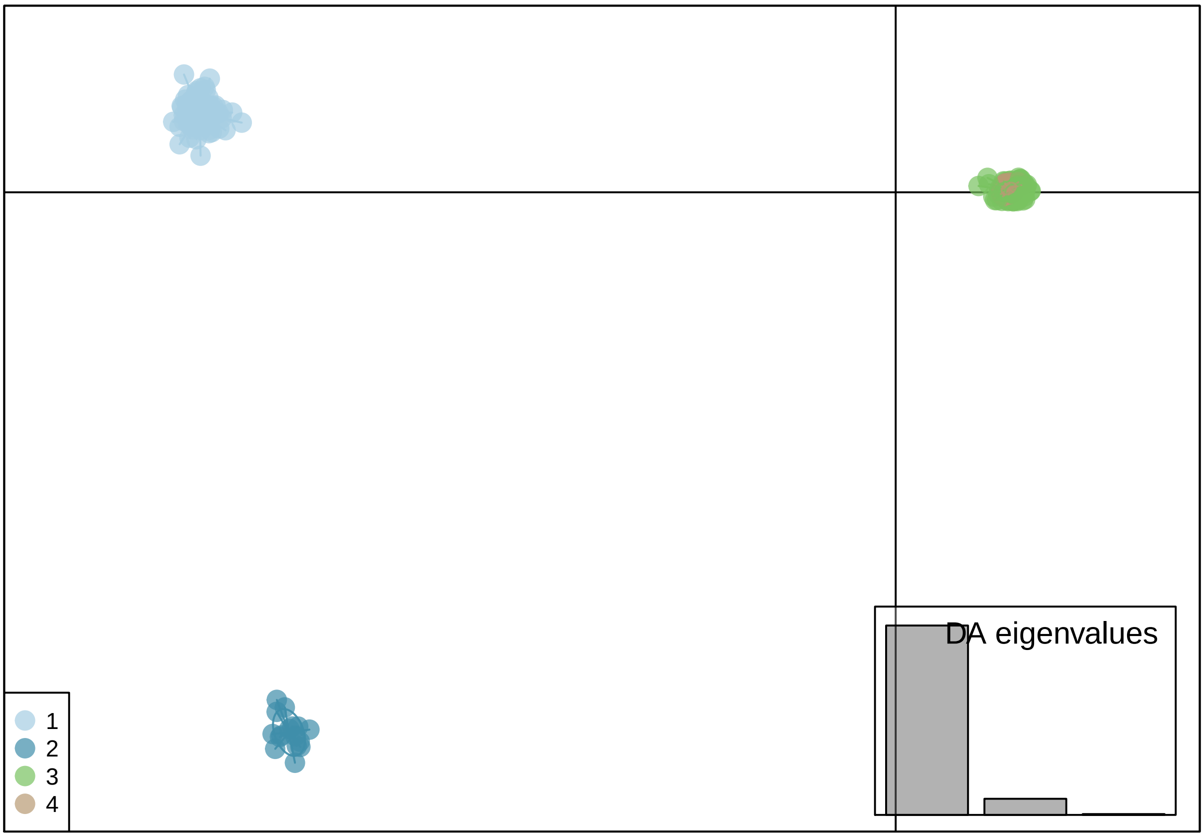


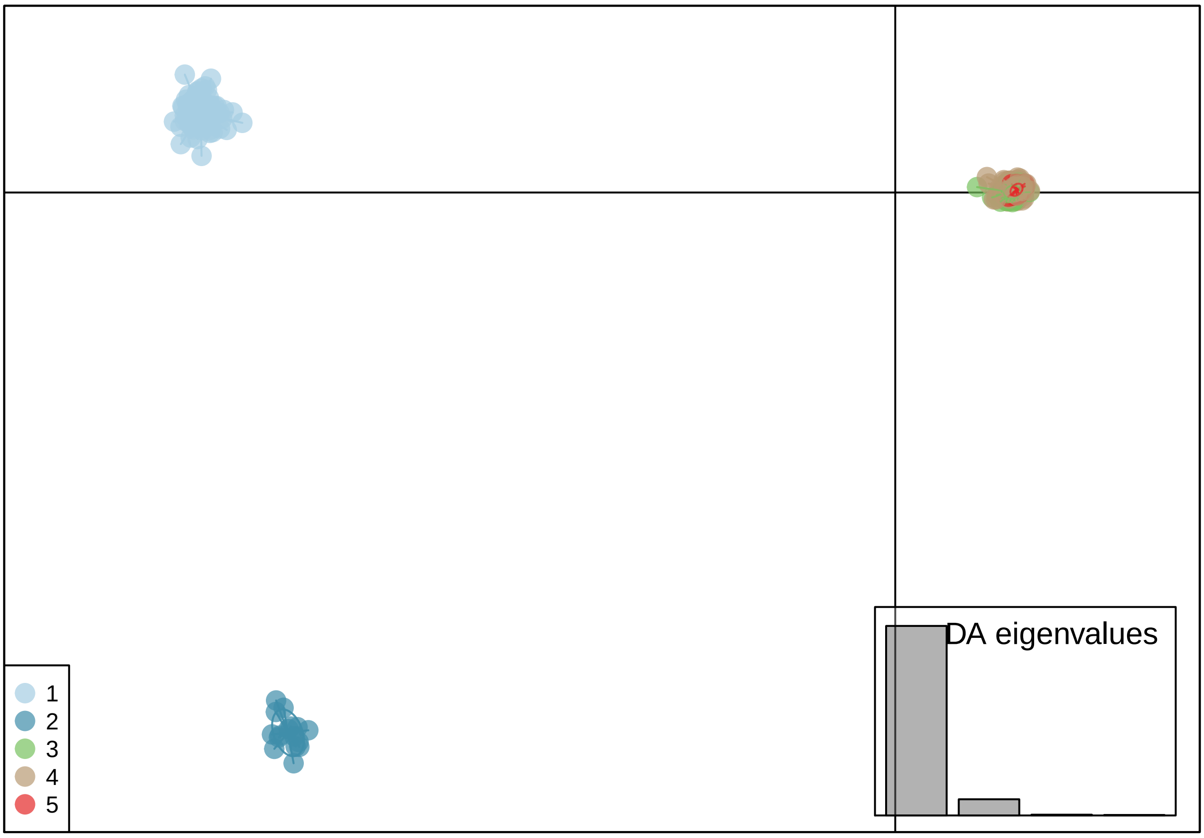
```
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                             clabel = FALSE, posi.leg = "bottomleft",
```

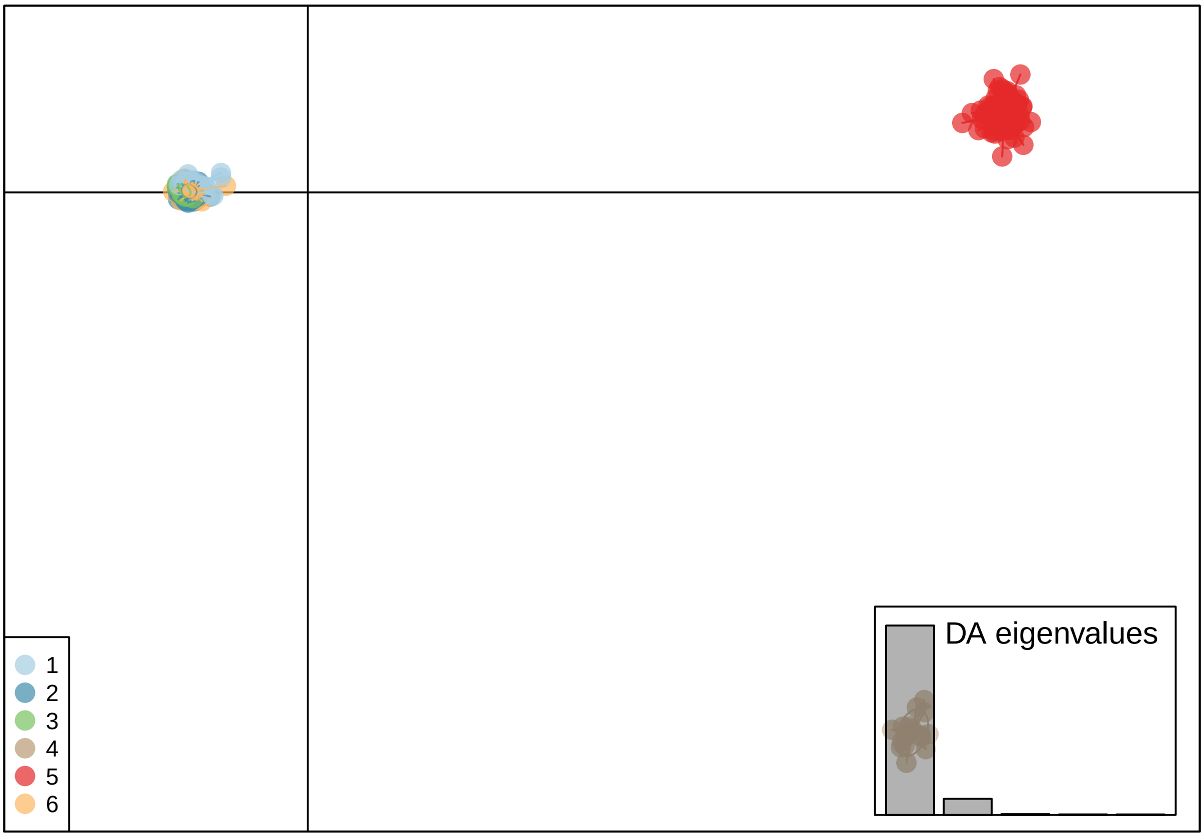
```
                              scree.pca = FALSE,  posi.pca = "topleft",
                              cleg = 0.75, xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_ALL_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

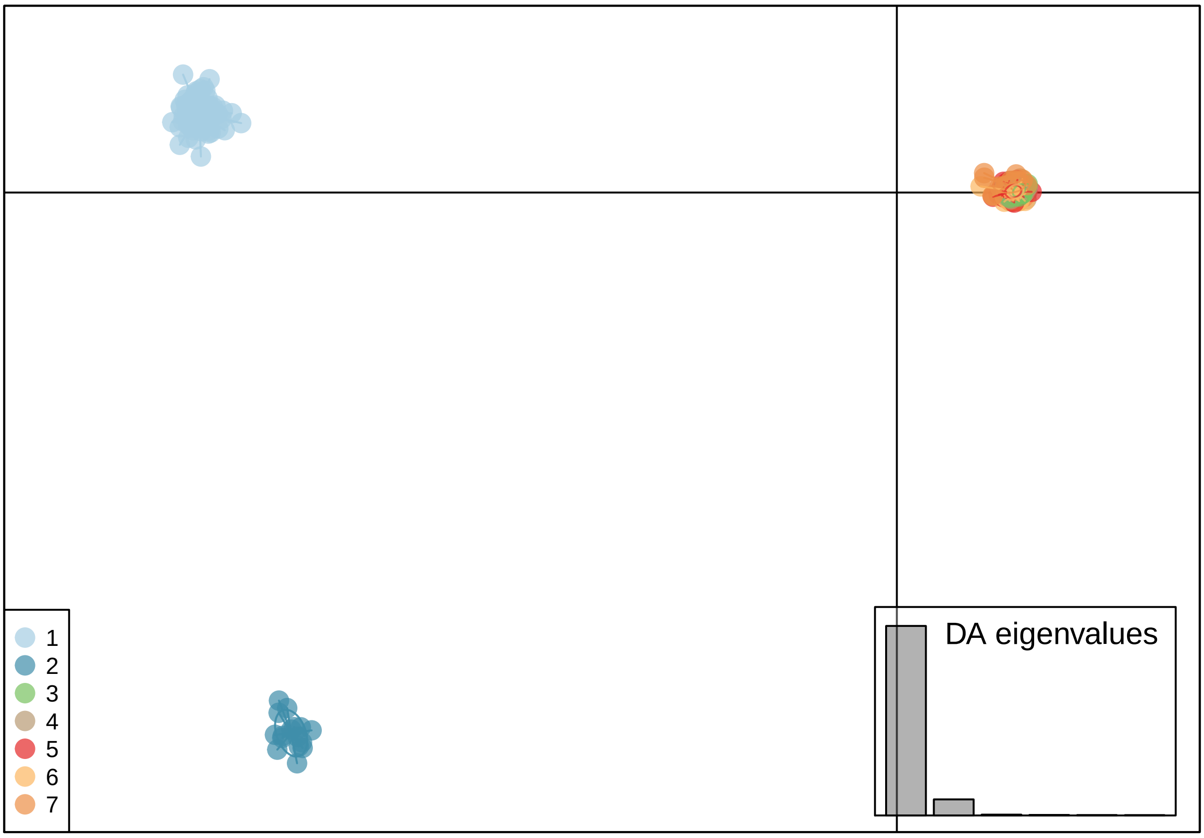



DA eigenvalues
1
2
3

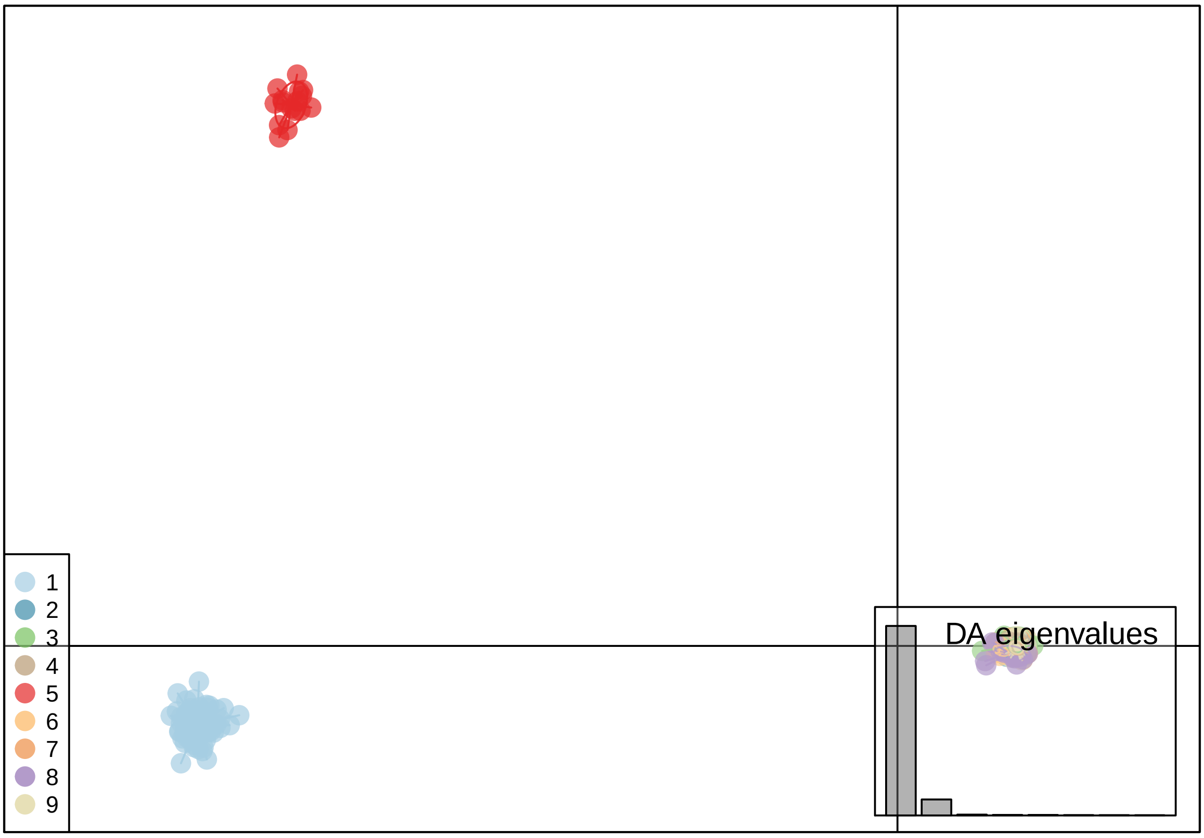

DA eigenvalues
1
2
3
4

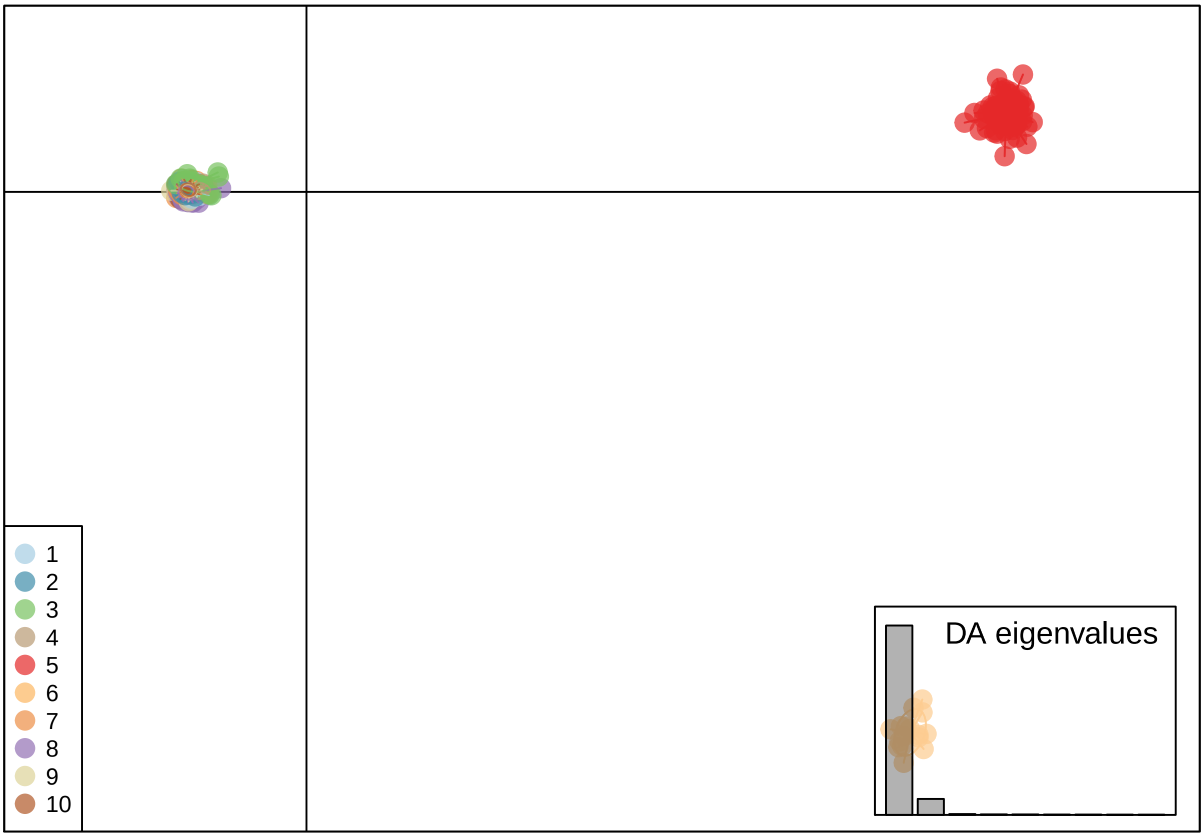

1
2
3
4
5
DA eigenvalues


1
2
3
4
5
6
DA eigenvalues


1
2
3
4
5
6
7
DA eigenvalues


1
2
3
4
5
6
7
8
DA eigenvalues

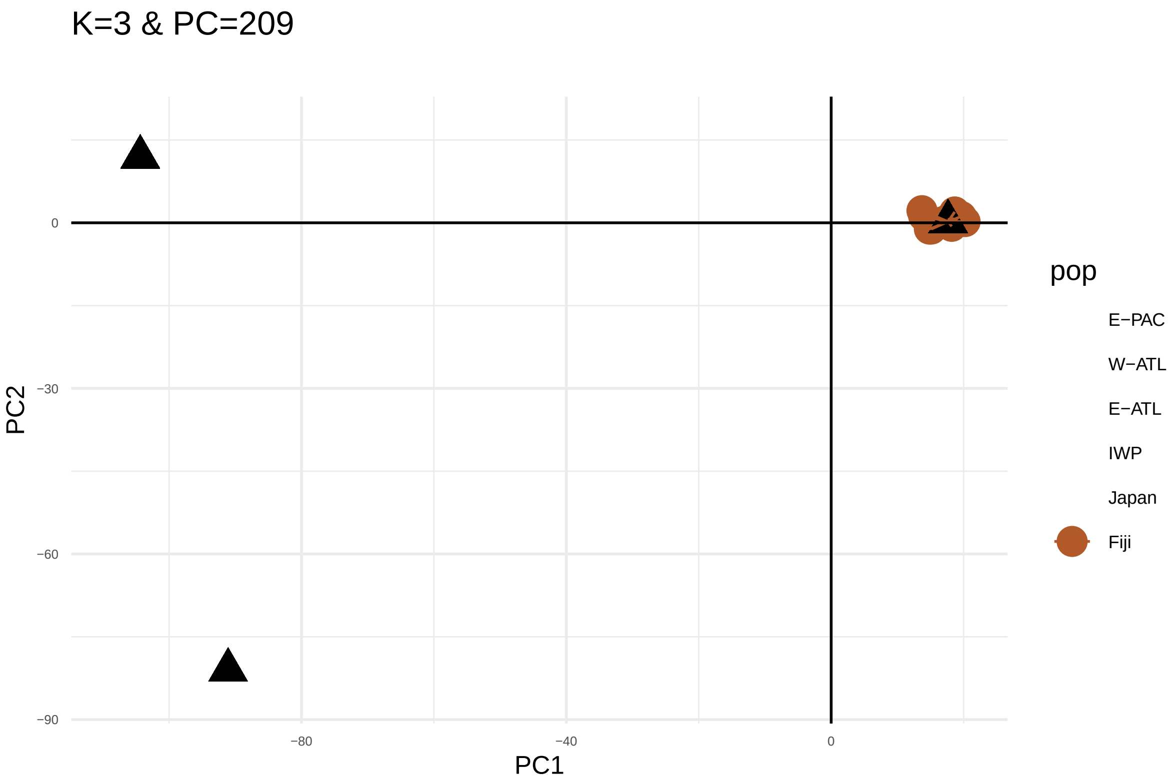


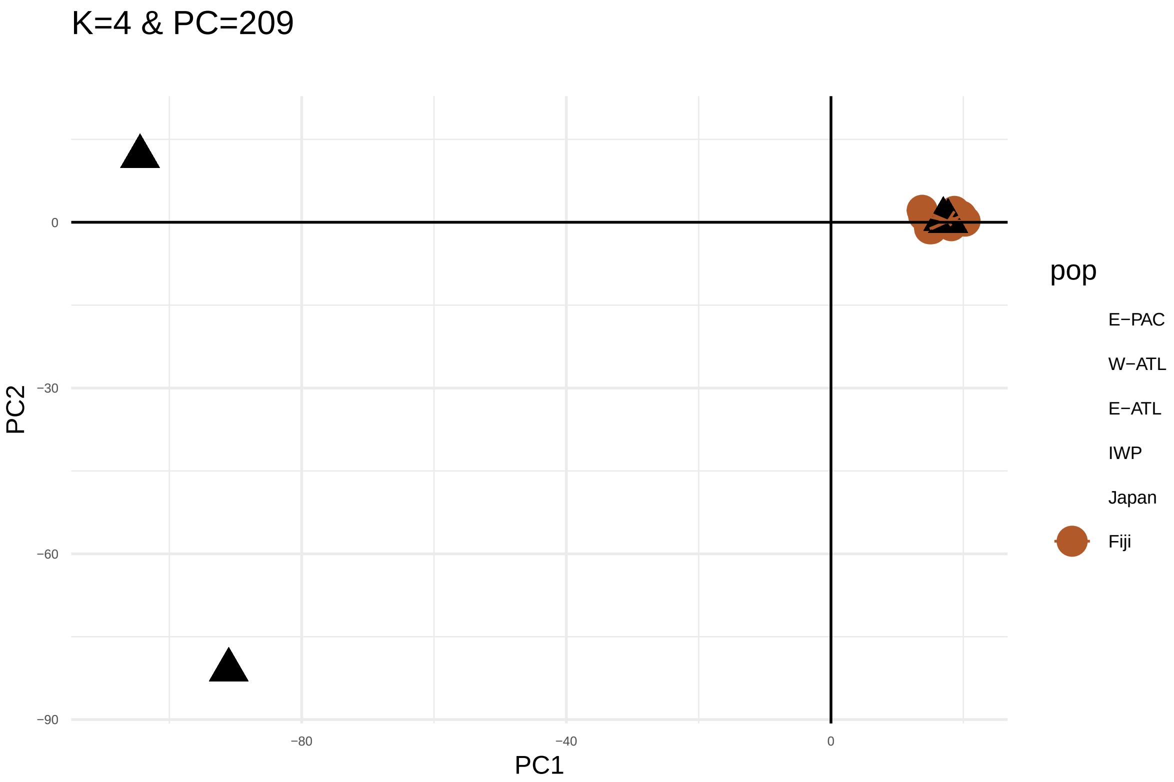


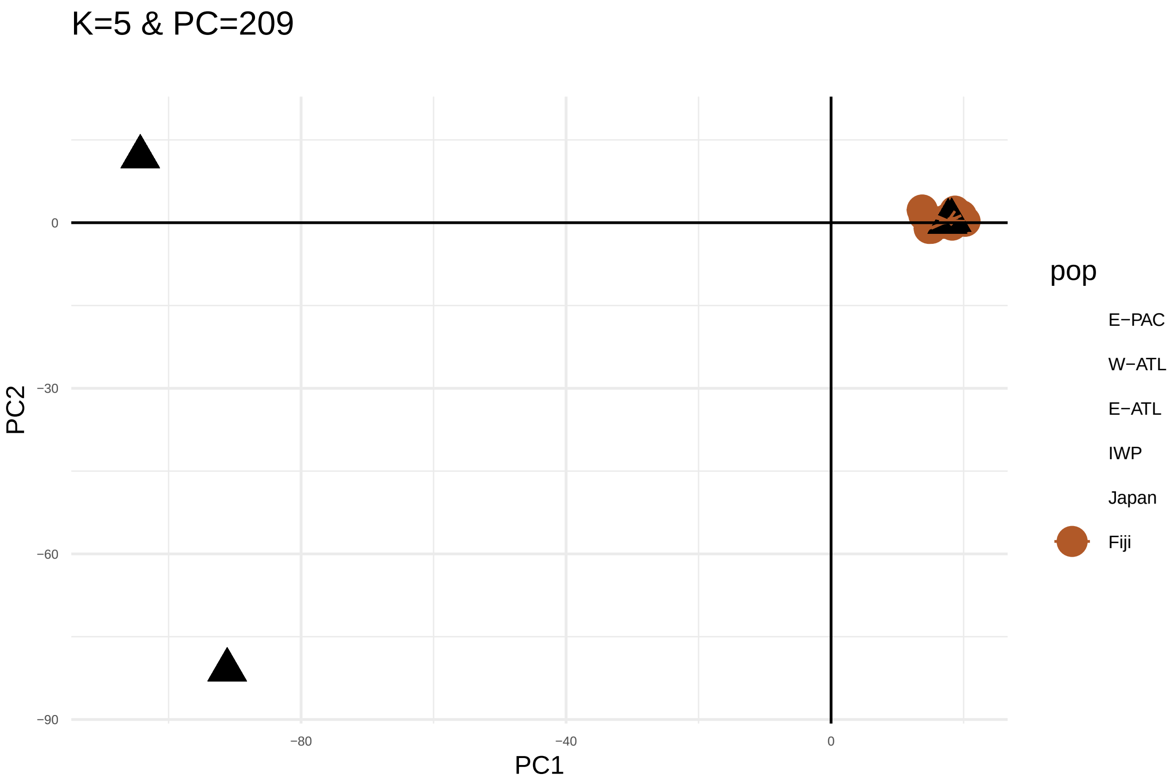
8.9.5 DAPC scatterplot - FLO

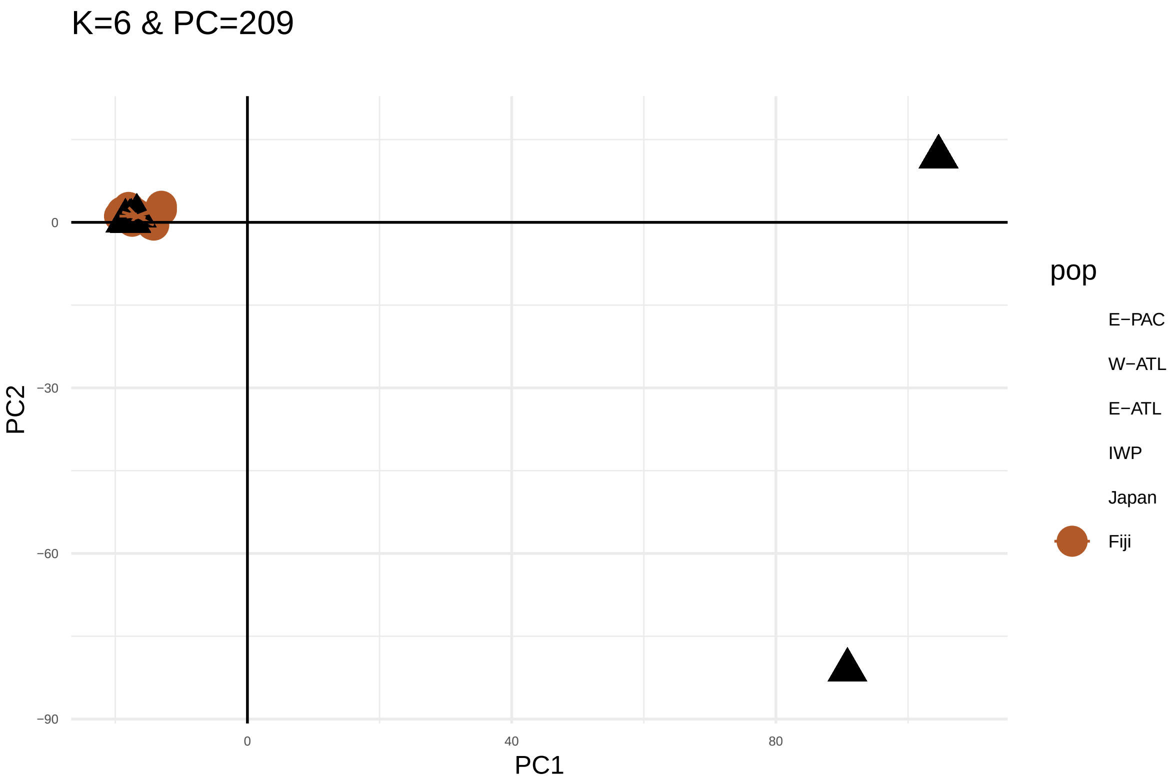
This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

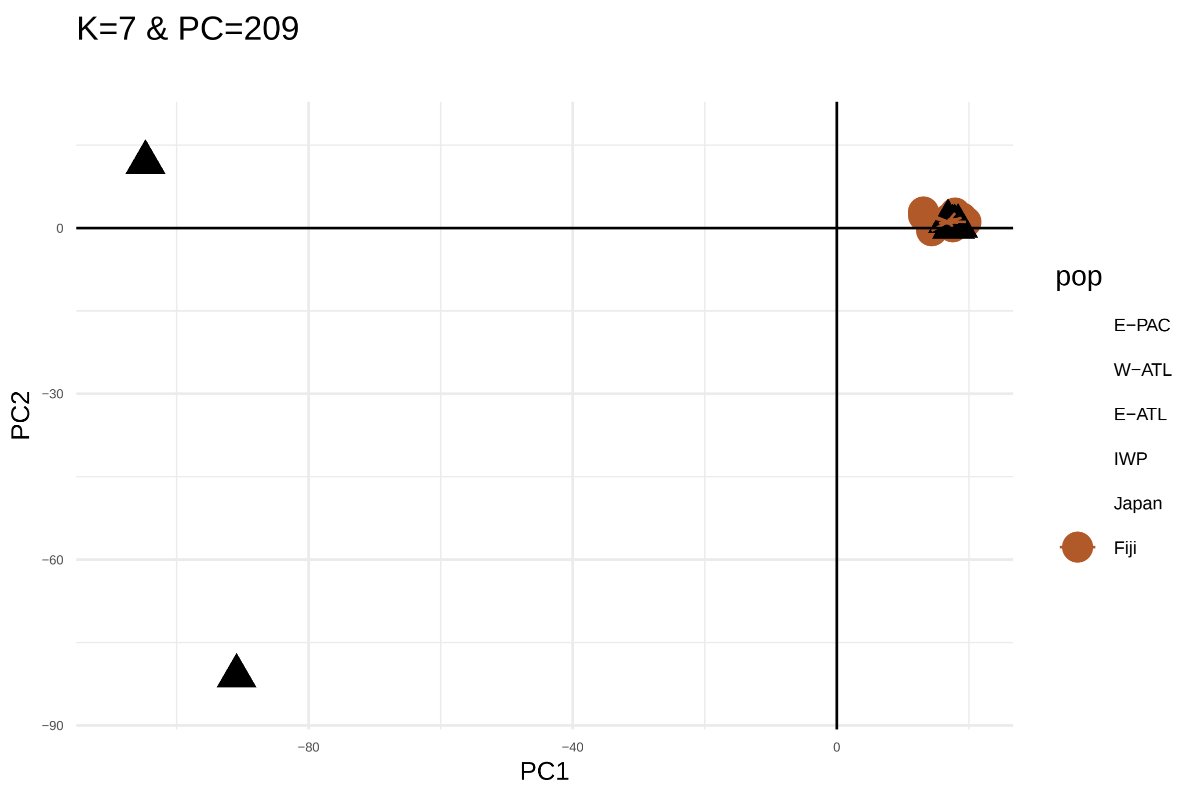
```r
load("DArTcap_ALL_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartcap.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x,mean.y = y)~group, df, mean),
              by = "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x, y = mean.y),size = 5,
                        shape = 17, color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y, xend = x,
                                       yend = y)) +
    ggplot2::scale_colour_manual(values = colours.32) +
    ggplot2::scale_fill_manual(values = colours.32) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
         y = "PC2",
         x = "PC1",
         title = paste0("K=",K," & PC=",PC, sep = ""),
         caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot, filename = paste0("DArTcap_ALL_DAPC_scatterplot2_K", K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```

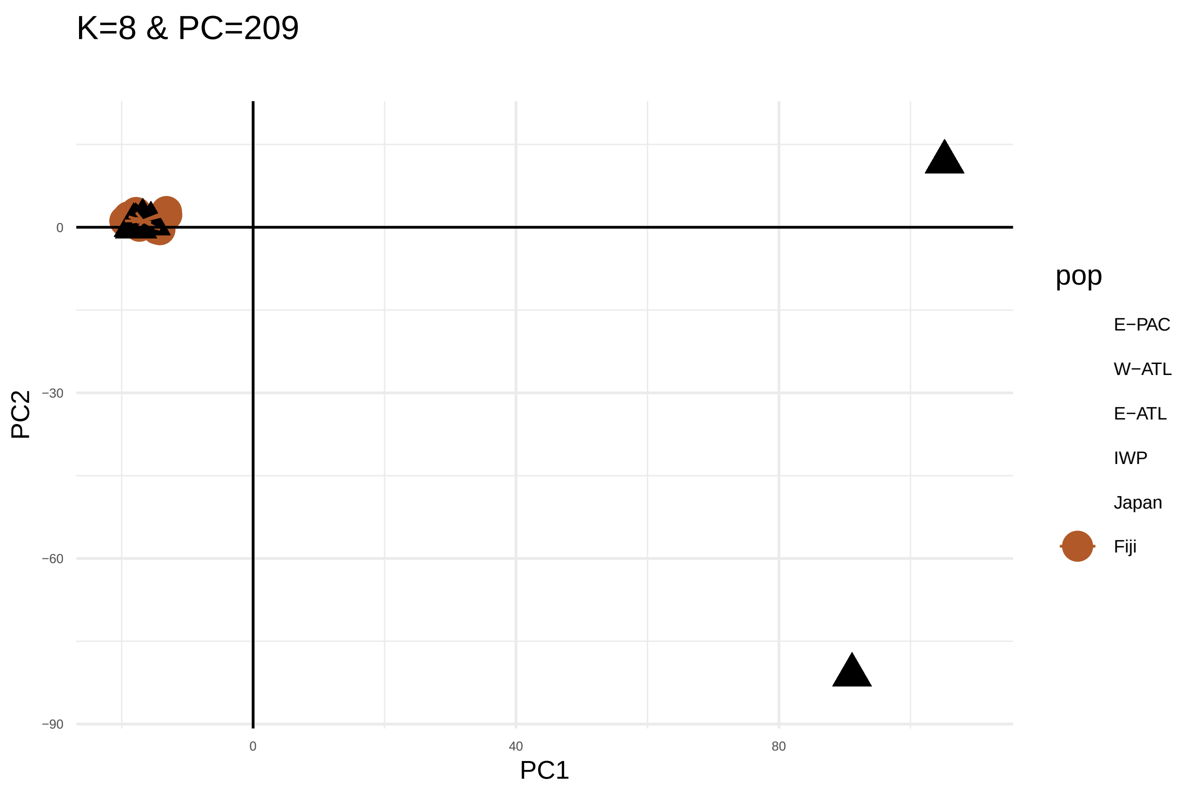

K=3 & PC=209
PC2
0
−30
−60
−90
PC1
−80
−40
0
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji

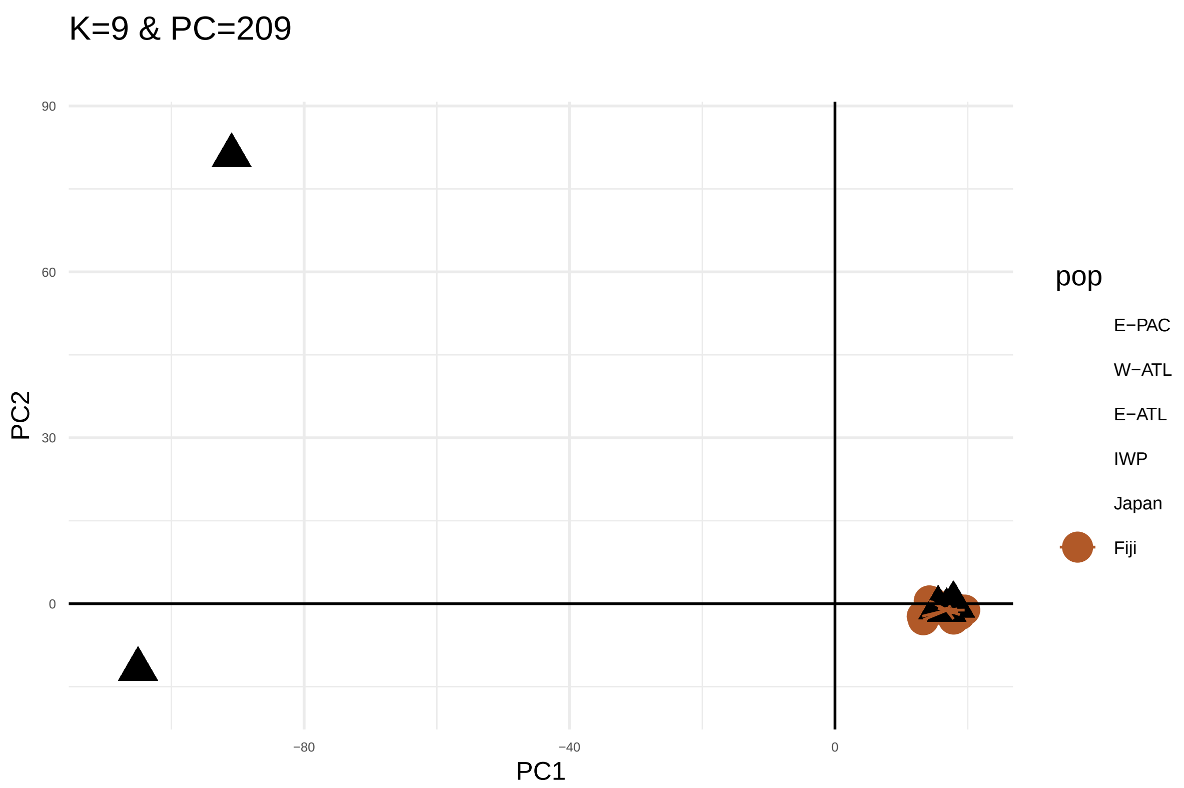

K=4 & PC=209
PC2
0
−30
−60
−90
PC1
−80
−40
0
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji

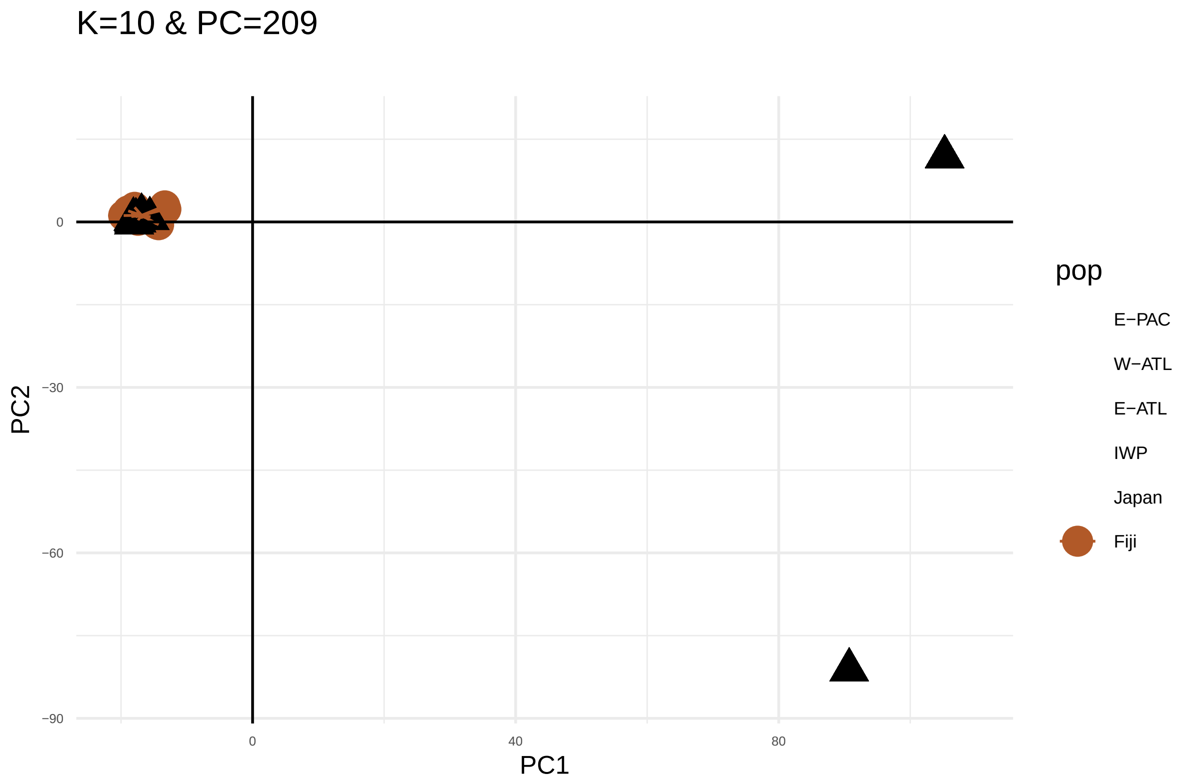

K=5 & PC=209
PC2
0
−30
−60
−90
−80
−40
0
PC1
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji


K=6 & PC=209
PC2
0
−30
−60
−90
0
40
80
PC1
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji


K=7 & PC=209
PC2
0
−30
−60
−90
PC1
−80
−40
0
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji


K=8 & PC=209
PC2
0
−30
−60
−90
PC1
0
40
80
pop
E−PAC
W−ATL
E−ATL
IWP
Japan
● Fiji





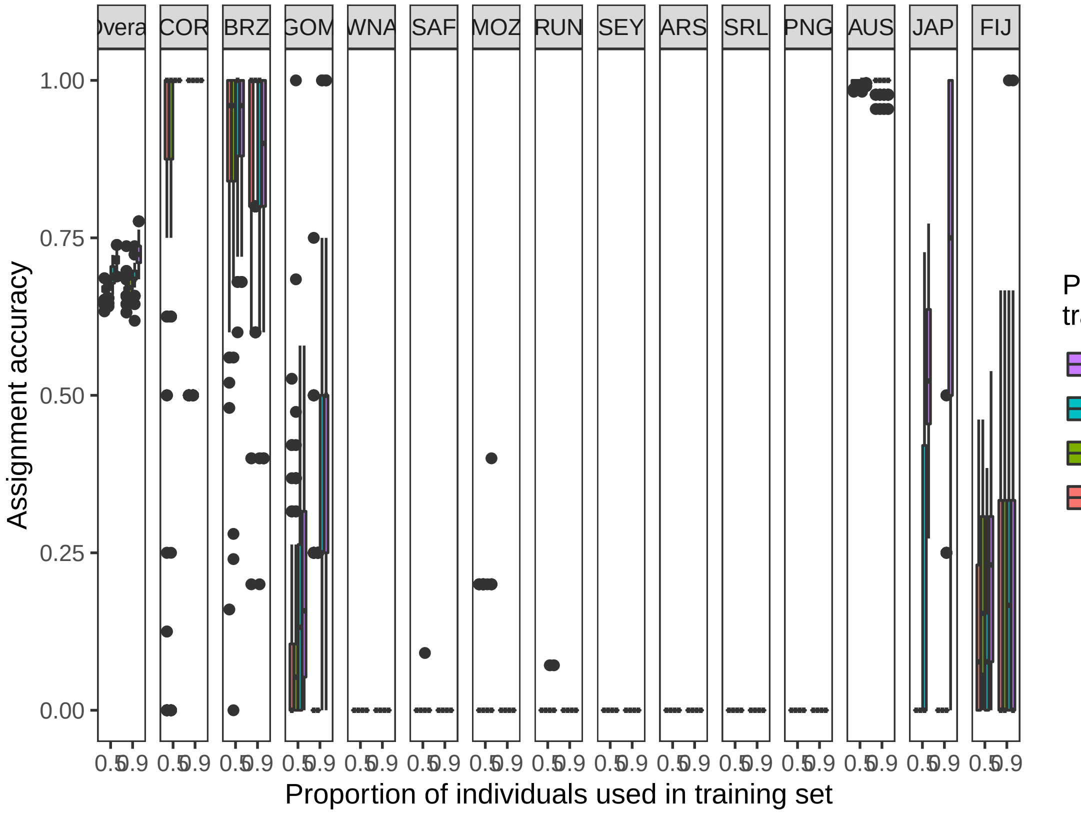
8.10 Provenance assignment

Using the package assignPOP to estimate the assignment success of the DArTcap data

8.10.1 Per Site

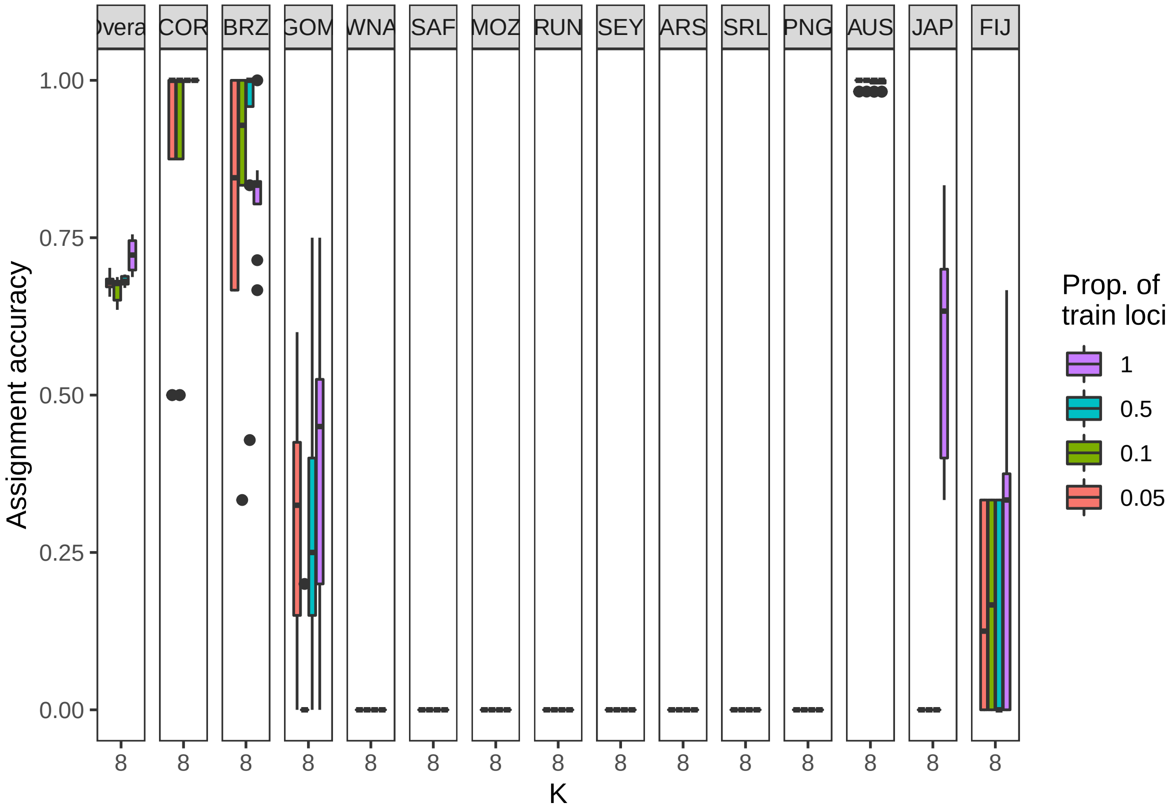
```r
pop.levels <- c("Costa Rica" , "Brazil", "Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Australia", "Japan", "Fiji")
BS.dartcap.gl$pop <- factor(BS.dartcap.gl$other$ind.metrics$Site,
                            levels = pop.levels)

gl2gpop(BS.dartcap.gl[!BS.dartcap.gl$pop %in% c("Caribbean Sea","Sierra Leone",
                                                "Indonesia", "Thailand"),],
        filename = "DArTcap_ALL_assign_Site_genepop.txt") #too few individuals

shortnames <- c("COR","BRZ", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "PNG" , "AUS", "JAP", "FIJ")
gpop <- assignPOP::read.Genepop('DArTcap_ALL_assign_Site_genepop.txt',
  pop.names = shortnames, haploid = FALSE,  pos = 1)

assignPOP::assign.MC(
  x = gpop, train.inds = c(0.5, 0.9),train.loci = c(0.05, 0.1, 0.5, 1),
  loci.sample = 'fst',iterations = 1000, dir = 'AssignPOP_MC_Sites/', scaled = FALSE,
  pca.method = 'mixed', pca.PCs = 'kaiser-guttman',pca.loadings = F,
  model = 'svm', svm.kernel = 'linear',svm.cost = 1, ntree = 50,
  multiprocess = TRUE, processors = 3, skipQ = FALSE)

assignPOP::assign.kfold(
  x = gpop, k.fold = 8, train.loci = c(0.05, 0.1, 0.5, 1),loci.sample = 'fst',
  dir = 'AssignPOP_Kfold_Sites/', scaled = FALSE, pca.method = 'mixed',
  pca.PCs = 'kaiser-guttman', pca.loadings = F, model = 'svm',
  svm.kernel = 'linear',svm.cost = 1, ntree = 50, multiprocess = TRUE, processors = 3,
  skipQ =FALSE)
```

```r
shortnames <- c("COR","BRZ", "GOM", "WNA", "SAF", "MOZ", "RUN" , "SEY",
                "ARS", "SRL", "PNG" , "AUS", "JAP", "FIJ")
df1 <- assignPOP::accuracy.MC(dir = "AssignPOP_MC_Sites/")
MC.assign <- assignPOP::accuracy.plot(df1, pop = c("all",shortnames))
print(MC.assign)
```

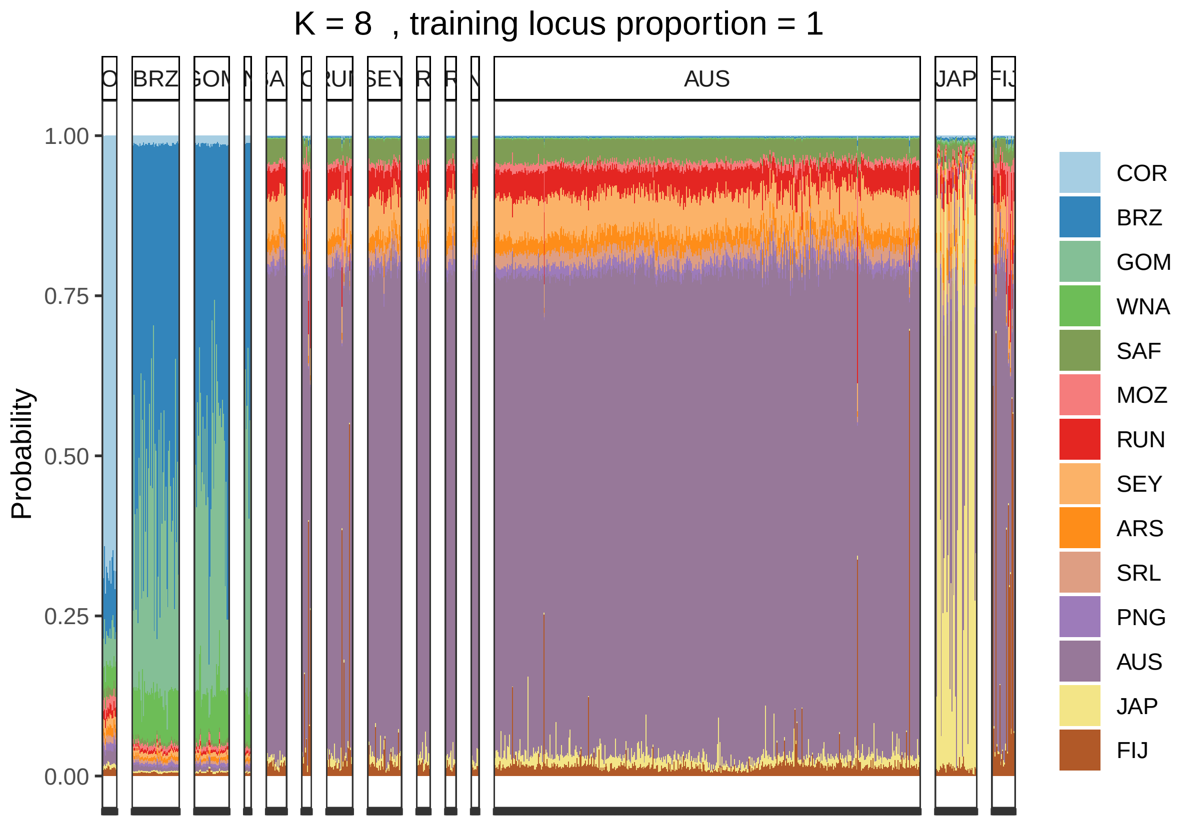


8.10.1.1 AssignPOP

```
ggplot2::ggsave(MC.assign, filename = "DArTcap_ALL_assignPOP_MC_Sites.png",
                width = 30, height = 15,units = "cm")

df2 <- assignPOP::accuracy.kfold(dir = "AssignPOP_Kfold_Sites/")
kfold.assign <- assignPOP::accuracy.plot(df2, pop = c("all",shortnames))
print(kfold.assign)
```



```
ggplot2::ggsave(kfold.assign, filename = "DArTcap_ALL_assignPOP_Kfold_Sites.png",
                width = 30, height = 15,units = "cm")


names(colours.14) <- shortnames
# memb.plot <- assignPOP::membership.plot(dir = "AssignPOP_Kfold_Sites/",
#                              style = 1,
#                              non.genetic = TRUE)
# #choose proportion training loci = 1
# save(memb.plot, file = "memb.plot1.Rdata")
load("memb.plot1.Rdata")
memb.plot$data$origin.pop <- factor(memb.plot$data$origin.pop,
                                    levels = shortnames)
memb.plot + ggplot2::scale_fill_manual(values = colours.14) +
  ggplot2::theme(axis.text.x = ggplot2::element_blank())
```



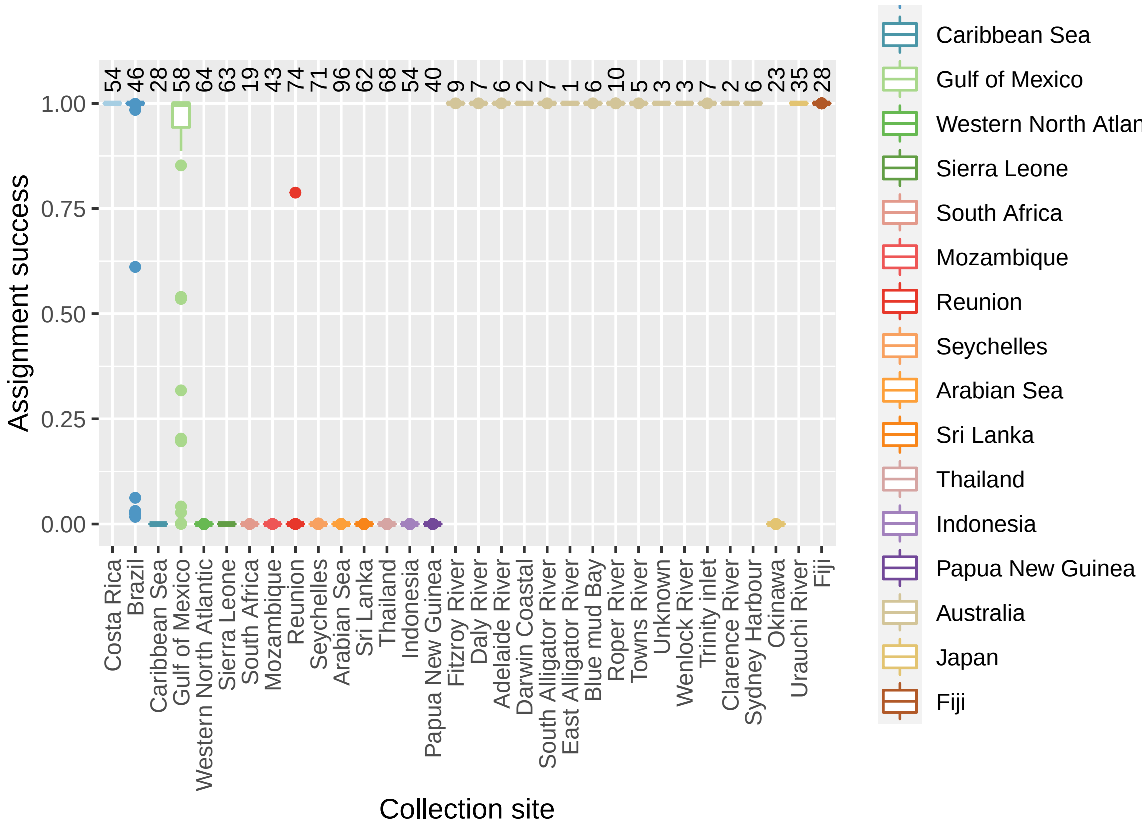
```
ggplot2::ggsave(memb.plot,
                filename = "DArTcap_ALL_assignPOP_Kfold_membership_Sites.png",
                width = 30, height = 15,units = "cm")


df <- data.frame(
 ind = as.character(memb.plot$data$Ind.ID)[
    as.character(memb.plot$data$fold_n) == "fold_8"],
  pop = as.character(memb.plot$data$origin.pop)[
    as.character(memb.plot$data$fold_n) == "fold_8"],
  memb = as.character(memb.plot$data$pred.pop)[
    as.character(memb.plot$data$fold_n) == "fold_8"], stringsAsFactors = FALSE)

summary(df$pop[df$pop != df$memb]) # not a great assignment success
```

```
##
##   Correct assignment rates were estimated!!
##   A total of 800 assignment tests for 14 pops.
##   Results were also saved in a 'Rate_of_800_tests_14_pops.txt' file in the directory.
##   Correct assignment rates were estimated!!
##   A total of 32 assignment tests for 14 pops.
##   Results were also saved in a 'Rate_of_32_tests_14_pops.txt' file in the directory.   the 10 mos
## GOM RUN SEY SAF ARS FIJ JAP AUS BRZ MOZ
##  70  56  56  42  28  28  28  14  14  14
```

```
pop.levels1 <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                 "Western North Atlantic", "Sierra Leone", "South Africa",
                 "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                 "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                 "Fitzroy River", "Daly River", "Adelaide River","Darwin Coastal",
```

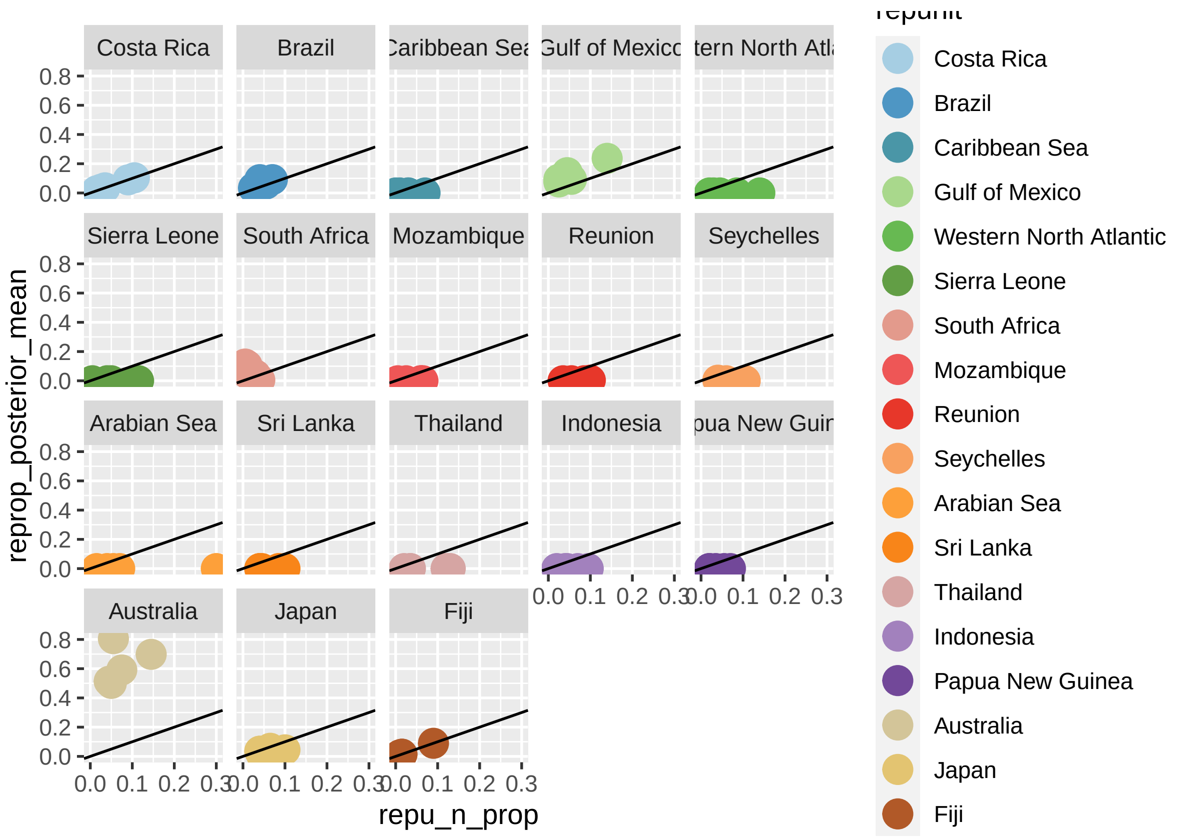
```r
                 "South Alligator River", "East Alligator River","Blue mud Bay",
                 "Roper River","Towns River","Unknown","Wenlock River",
                 "Trinity inlet","Clarence River", "Sydney Harbour", "Okinawa",
                 "Urauchi River", "Fiji")
pop.levels2 <- c("Costa Rica" , "Brazil","Caribbean Sea", "Gulf of Mexico",
                 "Western North Atlantic", "Sierra Leone", "South Africa",
                 "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                 "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                 "Japan", "Fiji")

BS.dartcap.rubias2 <- BS.dartcap.rubias
# BS.dartcap.rubias2$indiv == BS.dartcap.gt@schemes$INDIVIDUALS

BS.dartcap.rubias2$collection <- factor(BS.dartcap.gt@schemes$Site2,
                                        levels = pop.levels1)
BS.dartcap.rubias2$repunit <- factor(BS.dartcap.gt@schemes$Site,
                                     levels = pop.levels2)
BS.dartcap.rubias2 <- BS.dartcap.rubias2[order(BS.dartcap.rubias2$repunit,
                                               BS.dartcap.rubias2$collection),]


BS.dartcap.rubias2 %<>%
  dplyr::mutate_all(as.character)

BS_sims <- rubias::assess_reference_loo(reference = BS.dartcap.rubias2,
                     gen_start_col = 5,
                     reps = 5,
                     mixsize = 200,
                     return_indiv_posteriors = TRUE,
                     resampling_unit = "gene_copies")

repu_pofzs <- BS_sims$indiv_posteriors %>%
  dplyr::filter(repunit == simulated_repunit) %>%
  dplyr::group_by(iter, indiv, simulated_collection, repunit) %>%
  dplyr::summarise(repu_PofZ = sum(PofZ)) %>%
  dplyr::ungroup() %>%
  dplyr::arrange(repunit, simulated_collection) %>%
  dplyr::mutate(simulated_collection = factor(simulated_collection,
                                              levels = unique(simulated_collection)))

num_simmed <- BS_sims$indiv_posteriors %>%
  dplyr::group_by(iter, indiv) %>%
  dplyr::slice(1) %>%
  dplyr::ungroup() %>%
  dplyr::count(simulated_collection)

num_simmed <- num_simmed[order(factor(num_simmed$simulated_collection,
                                      levels = pop.levels1)),]
repu_pofzs$repunit <- factor(repu_pofzs$repunit, levels = pop.levels2)
repu_pofzs$simulated_collection <- factor(repu_pofzs$simulated_collection,
                                          levels = pop.levels1)
repu_pofzs <- repu_pofzs[order(repu_pofzs$repunit, repu_pofzs$simulated_collection),]

plot <- ggplot2::ggplot(repu_pofzs, ggplot2::aes(x = simulated_collection,
                                                 y = repu_PofZ)) +
  ggplot2::geom_boxplot(ggplot2::aes(colour = repunit)) +
  ggplot2::scale_color_manual(values = colours.18) +
  ggplot2::geom_text(data = num_simmed, mapping = aes(y = 1.025, label = n),
```

```
                     angle = 90, hjust = 0, vjust = 0.5, size = 3) +
  ggplot2::labs(subtitle = "",
         y = "Assignment success",
         x = "Collection site") +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 90, hjust = 1,
                                                     size = 9, vjust = 0.5)) +
  ggplot2::ylim(c(NA, 1.05))
print(plot)
```



8.10.1.2 Rubias

```
ggplot2::ggsave(plot,
                filename = "DArTcap_ALL_Assign_Rubias_Sites_Assignment_success.png",
                width = 30, height = 15,units = "cm")

repunit_BS <- unique(BS.dartcap.rubias2$repunit)
BS_corr <- BS_sims$mixing_proportions %>%
  dplyr::mutate(repunit = ifelse(repunit %in% repunit_BS, repunit, "OTHER")) %>%
  dplyr::group_by(iter, repunit) %>%
  dplyr::summarise(true_repprop = sum(true_pi),
            reprop_posterior_mean = sum(post_mean_pi),
            repu_n = sum(n)) %>%
  dplyr::mutate(repu_n_prop = repu_n / sum(repu_n))

BS_corr$repunit <- factor(BS_corr$repunit, levels = pop.levels2)
plot <- ggplot2::ggplot(BS_corr, ggplot2::aes(x = repu_n_prop,
                                              y = reprop_posterior_mean,
                                              colour = repunit)) +
  ggplot2::geom_point(size = 5) +
  ggplot2::scale_color_manual(values = colours.18) +
  ggplot2::geom_abline(intercept = 0, slope = 1) +
  ggplot2::facet_wrap(~ repunit)
print(plot)
```



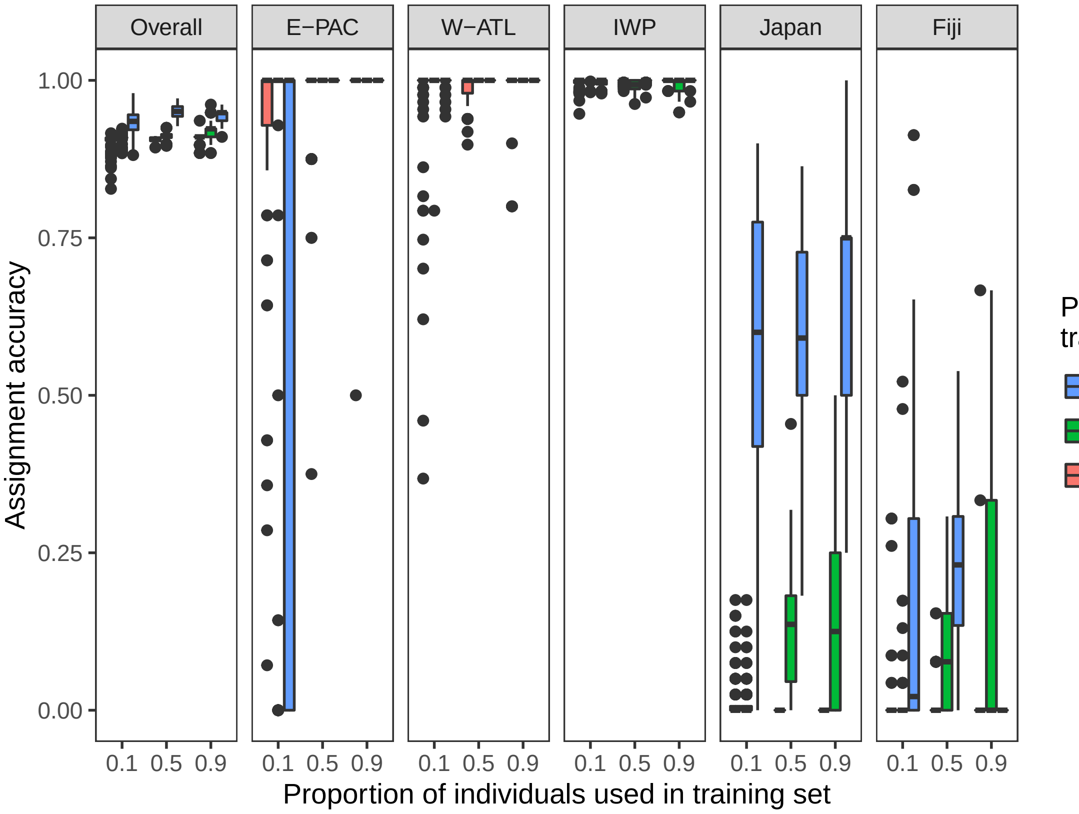
```
ggplot2::ggsave(plot, filename = "DArTcap_ALL_Assign_Rubias_Sites_correlation.png",
                width = 30, height = 15,units = "cm")
```

8.10.2 Per region

```
strata <- BS.dartcap.gl$other$ind.metrics$Region
strata[strata %in% c("W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC")] <- "IWP"
pop.levels <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")
BS.dartcap.gl$pop <- factor(strata, levels = pop.levels)
BS.dartcap.gl <- BS.dartcap.gl[order(BS.dartcap.gl$pop, BS.dartcap.gl$ind.names)]

gl2gpop(BS.dartcap.gl[BS.dartcap.gl$pop != "E-ATL",],
        filename = "DArTcap_ALL_assign_Region_genepop.txt") #too few individuals
shortnames <- c("E-PAC","W-ATL","IWP", "Japan","Fiji")
gpop <- assignPOP::read.Genepop(
  'DArTcap_ALL_assign_Region_genepop.txt',
  pop.names = shortnames,
  haploid = FALSE,
  pos = 1
  )

assignPOP::assign.MC(
  x = gpop, train.inds = c(0.1, 0.5, 0.9),train.loci = c(0.05, 0.1, 0.5, 1),
  loci.sample = 'fst',iterations = 1000, dir = 'AssignPOP_MC_Regions/', scaled = FALSE,
  pca.method = 'mixed', pca.PCs = 'kaiser-guttman',pca.loadings = F,
  model = 'svm', svm.kernel = 'linear',svm.cost = 1, ntree = 50,
  multiprocess = TRUE, processors = 3, skipQ = FALSE)

assignPOP::assign.kfold(
  x = gpop, k.fold = 10, train.loci =  c(0.1, 0.5, 1), loci.sample = 'fst',
```

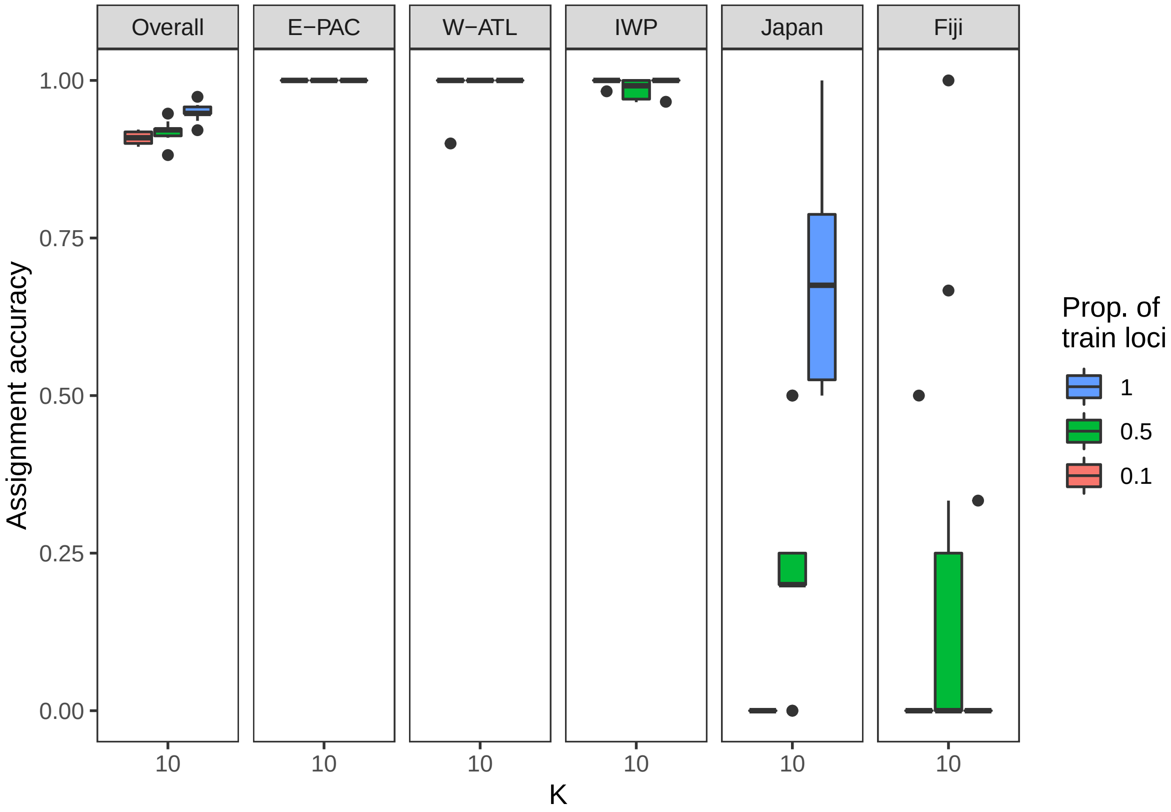
```
  dir = 'AssignPOP_Kfold_Region/', scaled = FALSE, pca.method = 'mixed',
  pca.PCs = 'kaiser-guttman', pca.loadings = F, model = 'svm',
  svm.kernel = 'linear',svm.cost = 1, ntree = 50, multiprocess = TRUE, processors = 3,
  skipQ =FALSE)
```

```
shortnames <- c("E-PAC","W-ATL","IWP", "Japan","Fiji")
df1 <- assignPOP::accuracy.MC(dir = "AssignPOP_MC_Regions/")
MC.assign <- assignPOP::accuracy.plot(df1, pop = c("all",shortnames))
print(MC.assign)
```

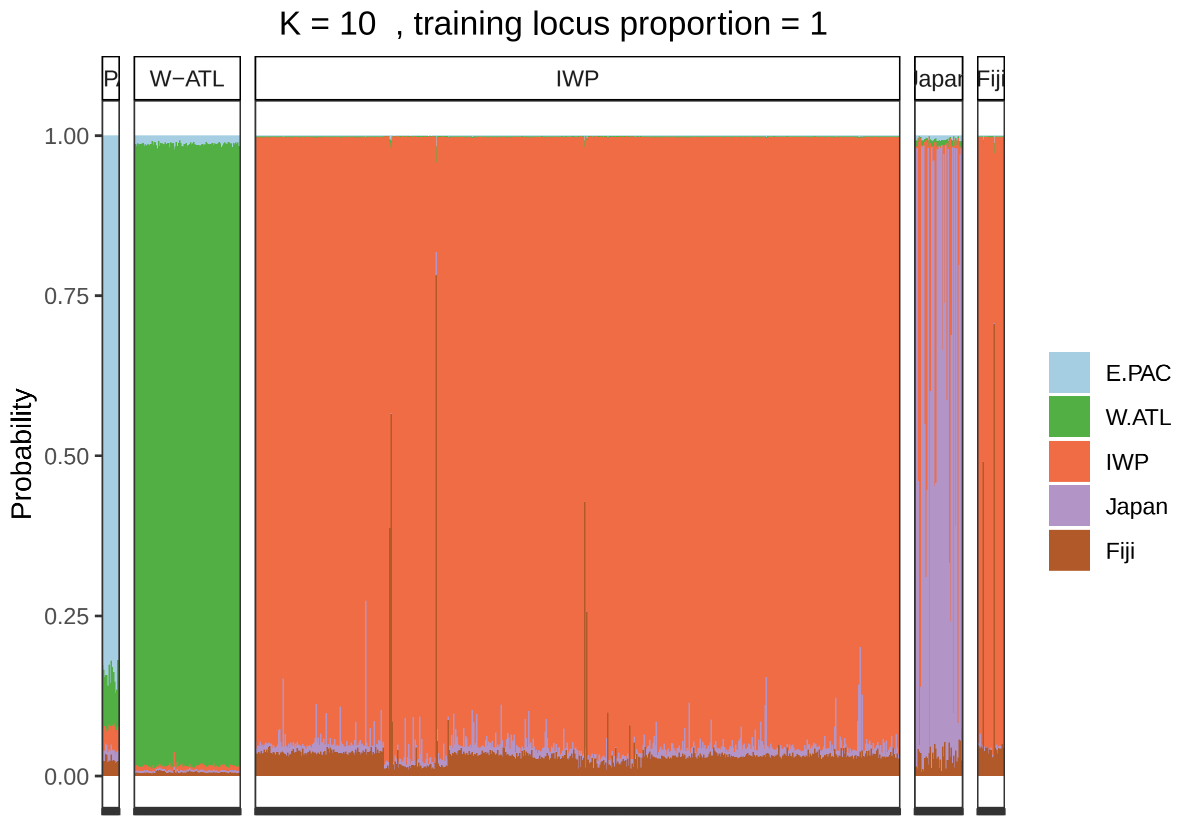


8.10.2.1 AssignPOP

```
ggplot2::ggsave(MC.assign, filename = "DArTcap_ALL_assignPOP_MC_Regions.png",
                width = 30, height = 15,units = "cm")

df2 <- assignPOP::accuracy.kfold(dir = "AssignPOP_Kfold_Region/")
kfold.assign <- assignPOP::accuracy.plot(df2, pop = c("all",shortnames))
print(kfold.assign)
```



```r
ggplot2::ggsave(kfold.assign, filename = "DArTcap_ALL_assignPOP_Kfold_Regions.png",
                width = 30, height = 15,units = "cm")

shortnames1 <- c("E.PAC","W.ATL","IWP", "Japan","Fiji")
colours.5 <- adegenet::funky(5)
names(colours.5) <- shortnames1
# memb.plot <- assignPOP::membership.plot(dir = "AssignPOP_Kfold_Region/",
#                              style = 1,
#                              non.genetic = TRUE)
# # choose proportion training loci = 1
# save(memb.plot, file = "memb.plot2.Rdata")
load("memb.plot2.Rdata")
memb.plot$data$origin.pop <- factor(memb.plot$data$origin.pop,
                                    levels = shortnames)
memb.plot + ggplot2::scale_fill_manual(values = colours.5) +
  ggplot2::theme(axis.text.x = ggplot2::element_blank())
```



```
ggplot2::ggsave(memb.plot,
                filename = "DArTcap_ALL_assignPOP_Kfold_membership_Regions.png",
                width = 30, height = 15,units = "cm")


df <- data.frame(
  ind = as.character(memb.plot$data$Ind.ID)[
    as.character(memb.plot$data$fold_n) == "fold_10"],
  pop = as.character(memb.plot$data$origin.pop)[
    as.character(memb.plot$data$fold_n) == "fold_10"],
  memb = as.character(memb.plot$data$pred.pop)[
    as.character(memb.plot$data$fold_n) == "fold_10"], stringsAsFactors = FALSE)

summary(df$pop[df$pop != df$memb]) #still some difficulties to differentiate Japan and Fiji
```

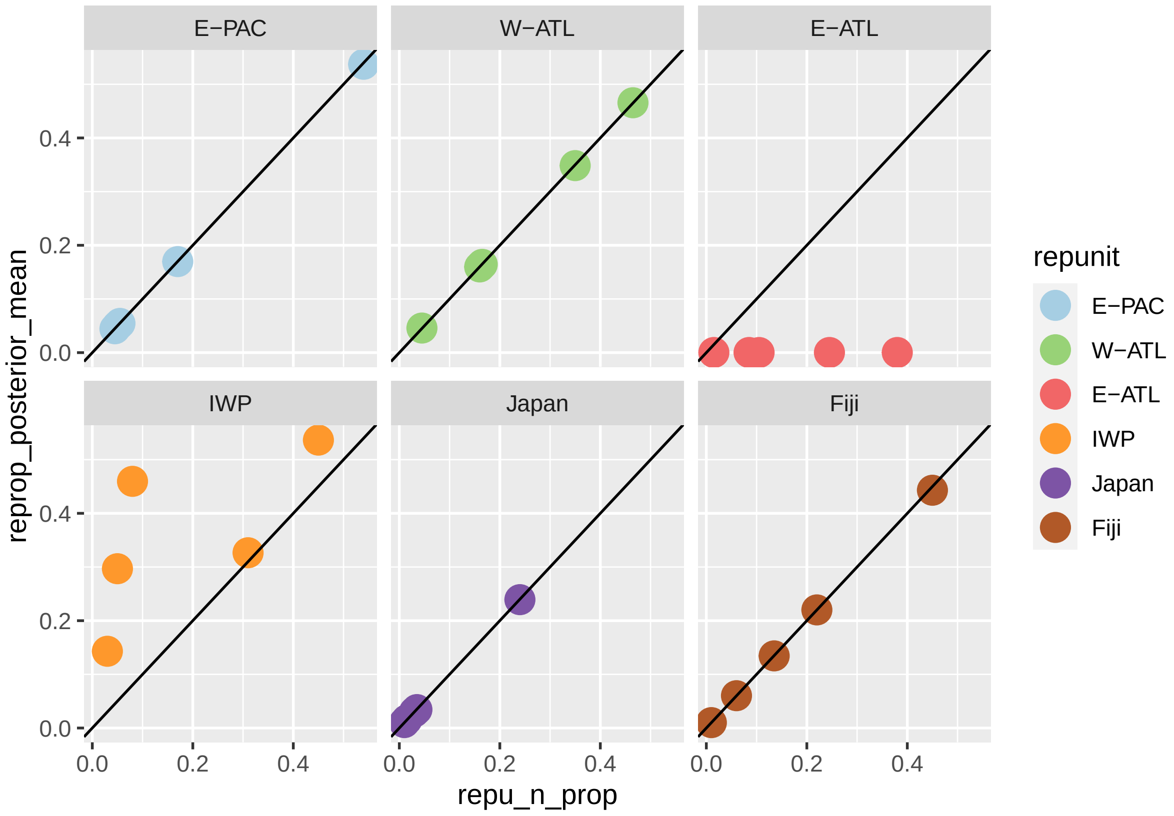
```
##
##   Correct assignment rates were estimated!!
##   A total of 900 assignment tests for 5 pops.
##   Results were also saved in a 'Rate_of_900_tests_5_pops.txt' file in the directory.
##   Correct assignment rates were estimated!!
##   A total of 30 assignment tests for 5 pops.
##   Results were also saved in a 'Rate_of_30_tests_5_pops.txt' file in the directory. Fiji Japan
##    10     5
```

```
pop.levels1 <- c("Costa Rica" , "Brazil","Caribbean Sea", "Gulf of Mexico",
                 "Western North Atlantic", "Sierra Leone", "South Africa",
                 "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                 "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                 "Japan", "Fiji")
pop.levels2 <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")
```

```
BS.dartcap.rubias2 <- BS.dartcap.rubias
# BS.dartcap.rubias2$indiv == BS.dartcap.gt@schemes$INDIVIDUALS

strata <- BS.dartcap.gt@schemes$Region
strata[strata %in% c("W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC")] <- "IWP"
BS.dartcap.rubias2$collection <- factor(BS.dartcap.gt@schemes$Site,
                                        levels = pop.levels1)
BS.dartcap.rubias2$repunit <- factor(strata, levels = pop.levels2)
BS.dartcap.rubias2 <- BS.dartcap.rubias2[order(BS.dartcap.rubias2$repunit,
                                               BS.dartcap.rubias2$collection),]

BS.dartcap.rubias2 %<>%
  dplyr::mutate_all(as.character)

BS_sims <- rubias::assess_reference_loo(reference = BS.dartcap.rubias2,
                     gen_start_col = 5,
                     reps = 5,
                     mixsize = 200,
                     return_indiv_posteriors = TRUE,
                     resampling_unit = "gene_copies")

repu_pofzs <- BS_sims$indiv_posteriors %>%
  dplyr::filter(repunit == simulated_repunit) %>%
  dplyr::group_by(iter, indiv, simulated_collection, repunit) %>%
  dplyr::summarise(repu_PofZ = sum(PofZ)) %>%
  dplyr::ungroup() %>%
  dplyr::arrange(repunit, simulated_collection) %>%
  dplyr::mutate(simulated_collection = factor(simulated_collection,
                                              levels = unique(simulated_collection)))

num_simmed <- BS_sims$indiv_posteriors %>%
  dplyr::group_by(iter, indiv) %>%
  dplyr::slice(1) %>%
  dplyr::ungroup() %>%
  dplyr::count(simulated_collection)

num_simmed <- num_simmed[order(factor(num_simmed$simulated_collection,
                                      levels = pop.levels1)),]
repu_pofzs$repunit <- factor(repu_pofzs$repunit, levels = pop.levels2)
repu_pofzs$simulated_collection <- factor(repu_pofzs$simulated_collection,
                                          levels = pop.levels1)
repu_pofzs <- repu_pofzs[order(repu_pofzs$repunit, repu_pofzs$simulated_collection),]

plot <- ggplot2::ggplot(repu_pofzs, ggplot2::aes(x = simulated_collection,
                                                 y = repu_PofZ)) +
  ggplot2::geom_boxplot(ggplot2::aes(colour = repunit)) +
  ggplot2::scale_color_manual(values = colours.6) +
  ggplot2::geom_text(data = num_simmed, mapping = aes(y = 1.025, label = n),
                     angle = 90, hjust = 0, vjust = 0.5, size = 3) +
  ggplot2::labs(subtitle = "",
         y = "Assignment success",
         x = "Collection site") +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 90, hjust = 1,
                                                     size = 9, vjust = 0.5)) +
  ggplot2::ylim(c(NA, 1.05))
print(plot)
```

8.10.2.2 Rubias

```
ggplot2::ggsave(plot,
                filename = "DArTcap_ALL_Assign_Rubias_Regions_Assignment_success.png",
                width = 30, height = 15,units = "cm")

repunit_BS <- unique(BS.dartcap.rubias2$repunit)
BS_corr <- BS_sims$mixing_proportions %>%
  dplyr::mutate(repunit = ifelse(repunit %in% repunit_BS, repunit, "OTHER")) %>%
  dplyr::group_by(iter, repunit) %>%
  dplyr::summarise(true_repprop = sum(true_pi),
            reprop_posterior_mean = sum(post_mean_pi),
            repu_n = sum(n)) %>%
  dplyr::mutate(repu_n_prop = repu_n / sum(repu_n))

BS_corr$repunit <- factor(BS_corr$repunit, levels = pop.levels2)
plot <- ggplot2::ggplot(BS_corr, ggplot2::aes(x = repu_n_prop,
                                              y = reprop_posterior_mean,
                                              colour = repunit)) +
  ggplot2::geom_point(size = 5) +
  ggplot2::scale_color_manual(values = colours.6) +
  ggplot2::geom_abline(intercept = 0, slope = 1) +
  ggplot2::facet_wrap(~ repunit)
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_ALL_Assign_Rubias_Regions_correlation.png",
                width = 30, height = 15,units = "cm")
```

8.10.3 Test number of informative markers chosen by DAPC contribution

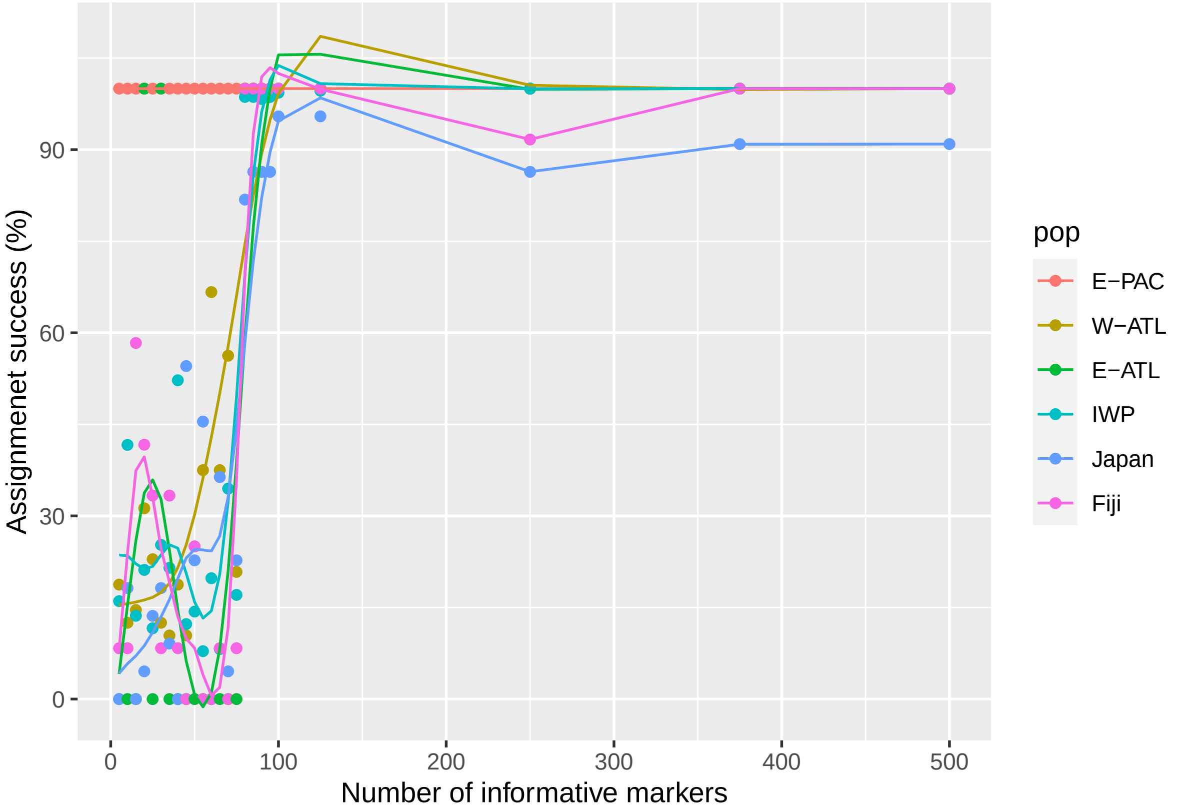
Using a 50% training dataset and validate the assignment success on a 50% hold-out dataset.

```
region.levels <- c("E-PAC","W-ATL","E-ATL", "IWP", "Japan","Fiji")
BS.dartcap.gl1 <- BS.dartcap.gl
region <- BS.dartcap.gl$other$ind.metrics$Region
region[region %in% c("W-IO","N-IO", "E-IO", "E-IO/W-PAC", "W-PAC")] <- "IWP"
BS.dartcap.gl1$pop <- factor(region, levels = region.levels)

subset.names <- c()
for (i in levels(BS.dartcap.gl1$pop)) {
  gl <- BS.dartcap.gl1[BS.dartcap.gl1$pop == i,]
  subset.names <- c(subset.names,sample(gl$ind.names,
                                        size = ceiling(adegenet::nInd(gl)/2)))
}
BS.dartcap.gl2 <- BS.dartcap.gl1[BS.dartcap.gl1$ind.names %in% subset.names,]
BS.dartcap.gl3 <- BS.dartcap.gl1[!BS.dartcap.gl1$ind.names %in%
                                   subset.names[subset.names != "CL-SIL001-F"],] #only 1 sample


dapc1 <- adegenet::dapc(BS.dartcap.gl2, n.da = 5, n.pca = 76)
assign.success <- summary(dapc1)$assign.per.pop*100

plot.data <- data.frame(dapc1$ind.coord, pop = BS.dartcap.gl2$pop)
ggplot(plot.data, aes(x = LD1, y = LD2, col = pop)) + ggplot2::geom_point() +
  ggplot2::scale_color_manual(values = adegenet::funky(6))
ggplot(plot.data, aes(x = LD3, y = LD5, col = pop)) + ggplot2::geom_point() +
  ggplot2::scale_color_manual(values = adegenet::funky(6))
```

```
ggplot(plot.data, aes(x = LD3, y = LD4, col = pop)) + ggplot2::geom_point() +
  ggplot2::scale_color_manual(values = adegenet::funky(6))
ggplot(plot.data, aes(x = LD4, y = LD5, col = pop)) + ggplot2::geom_point() +
  ggplot2::scale_color_manual(values = adegenet::funky(6))

marker.sample <- c(seq(5,100, by = 5), 125, 250, 375, 500)
loc.number <- list()
loc.names <- list()
assign.success <- data.frame(Pop =  levels(BS.dartcap.gl2$pop))
for (i in 1:length(marker.sample)) {
  loc.number[[i]] <- c(
    rownames(dapc1$var.contr %>%
        as.data.frame() %>%
        dplyr::slice_max(n = marker.sample[i] / 5, with_ties  = FALSE,
                         order_by = LD1)
    ),
    rownames(dapc1$var.contr %>%
        as.data.frame() %>%
        dplyr::slice_max(n = marker.sample[i] / 5, with_ties  = FALSE,
                         order_by = LD2)
    ),
    rownames(dapc1$var.contr %>%
        as.data.frame() %>%
        dplyr::slice_max(n = marker.sample[i] / 5, with_ties  = FALSE,
                         order_by = LD3)
    ),
    rownames(dapc1$var.contr %>%
        as.data.frame() %>%
        dplyr::slice_max(n = marker.sample[i] / 5, with_ties  = FALSE,
                         order_by = LD4)
    ),
    rownames(dapc1$var.contr %>%
        as.data.frame() %>%
        dplyr::slice_max(n = marker.sample[i] / 5, with_ties  = FALSE,
                         order_by = LD5)
    ))
  loc.names[[i]] <- BS.dartcap.gl2$loc.names[as.integer(loc.number[[i]])]
  BS.dartcap.gl4 <- BS.dartcap.gl3[, as.integer(loc.number[[i]])]
  dapc2 <- adegenet::dapc(BS.dartcap.gl4,n.da = 5, n.pca = 76) # DAPC on hold-out data
  assign.success[[i + 1]] <- as.double(summary(dapc2)$assign.per.pop*100)
}
colnames(assign.success) <- c("pop", as.character(marker.sample))
save(assign.success,marker.sample, loc.number,loc.names, subset.names,
     file = "DArTcap_ALL_Informative_DAPC_markers.Rdata")

loc.names2 <- unlist(loc.names)
provenance.markers <- BS.dartcap.gl$other$loc.metrics[
  BS.dartcap.gl$other$loc.metrics$LOCUS %in% loc.names2,]
readr::write_tsv(provenance.markers,
                 file = "500_DArTcap_markers_for_Bull_Shark_provenance.tsv")
```

```
load("DArTcap_ALL_Informative_DAPC_markers.Rdata")
mean.assign.success <- colMeans(assign.success[,-1])

region.levels <- c("E-PAC", "W-ATL", "E-ATL", "IWP","Japan", "Fiji")

plot.data <- gather(assign.success, Markers, Assignment, 2:ncol(assign.success))
plot.data$Markers <- as.integer(plot.data$Markers)
```

```
plot.data$pop <- factor(plot.data$pop, levels = region.levels)
plot.data <- plot.data[order(as.integer(plot.data$Markers), plot.data$pop),]
assign.plot <- ggplot2::ggplot(plot.data,
                               aes(x = Markers,
                                   y = Assignment,
                                   col = pop,
                                   group = 1)) +
  ylab("Assignmenet success (%)") +
  xlab("Number of informative markers") +
  ggplot2::geom_point() +
  ggformula::geom_spline(aes(group = pop))

print(assign.plot)
```



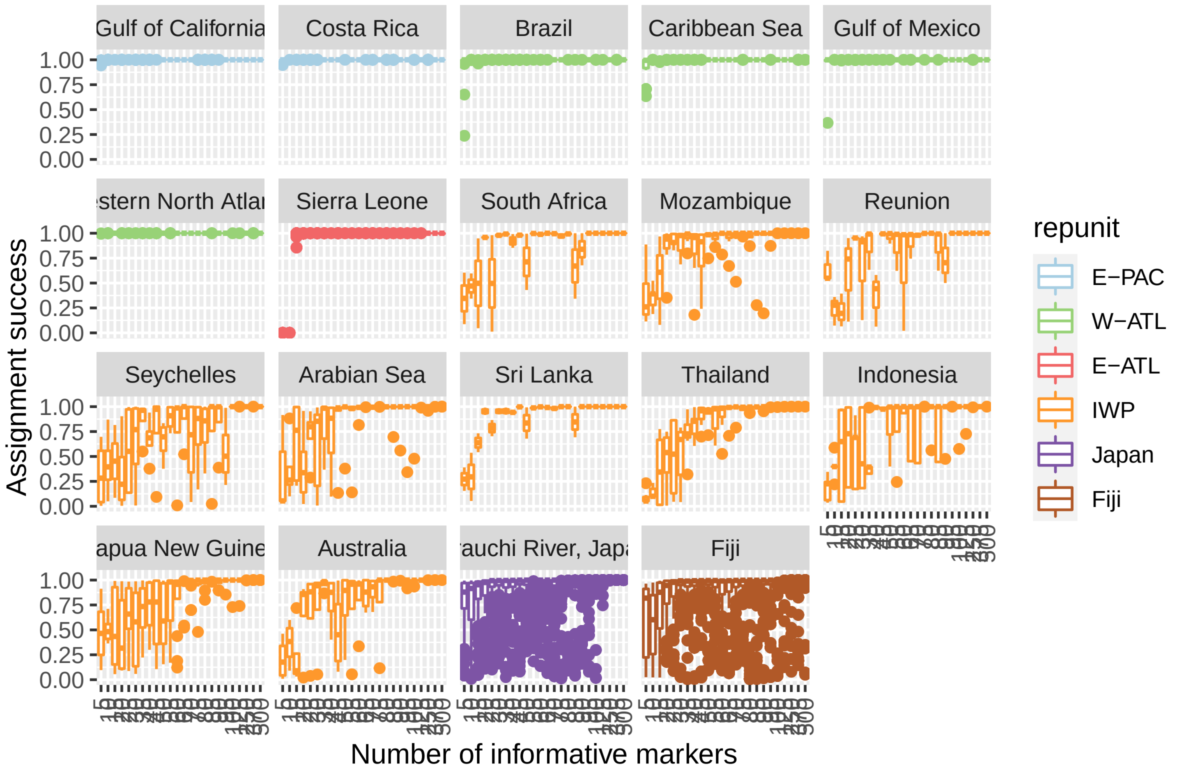
```
ggplot2::ggsave(assign.plot,
                filename = "DArTcap_ALL_Assign_DAPC.png",
                width = 30, height = 15, units = "cm")
```

Test rubias assignment success, based on 5-500 markers with highest loading contributions. Note that only samples from wild populations were use here (i.e. not the Okinawa aquarium, Japan).

```
load("DArTcap_ALL_Informative_DAPC_markers.Rdata")

pop.levels1 <- c("Costa Rica" , "Brazil","Caribbean Sea", "Gulf of Mexico",
                 "Western North Atlantic", "Sierra Leone", "South Africa",
                 "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                 "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                 "Australia", "Urauchi River, Japan", "Fiji")
pop.levels2 <- c("E-PAC","W-ATL","E-ATL","IWP", "Japan","Fiji")

colnames(BS.dartcap.rubias2)
BS.dartcap.rubias2 <- BS.dartcap.rubias
```

```
# BS.dartcap.rubias2$indiv == BS.dartcap.gt@schemes$INDIVIDUALS

strata <- BS.dartcap.gt@schemes$Region
strata[strata %in% c("W-IO","N-IO","E-IO","W-PAC","E-IO/W-PAC")] <- "IWP"
BS.dartcap.rubias2$collection <- factor(BS.dartcap.gt@schemes$Site,
                                        levels = pop.levels1)
BS.dartcap.rubias2$repunit <- factor(strata, levels = pop.levels2)
BS.dartcap.rubias2 <- BS.dartcap.rubias2[order(BS.dartcap.rubias2$repunit,
                                               BS.dartcap.rubias2$collection),]

BS.dartcap.rubias2 %<>%
  dplyr::mutate_all(as.character)

res <- data.frame(iter = integer(), indiv = integer(),
                  simulated_collection = factor(),
                  repunit = factor(), repu_PofZ = double(), Nmarkers = double())
for (i in 1:length(marker.sample)) {
  locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                     string =  colnames(BS.dartcap.rubias2))[,2]
  locus.rubias <- c("sample_type","repunit","collection","indiv",
                    locus.rubias[-c(1:4)])
  BS.dartcap.rubias3 <- BS.dartcap.rubias2[,locus.rubias %in%
                                             c("sample_type","repunit",
                                               "collection","indiv",
                                               loc.names[[i]])]
  BS_sims <- rubias::assess_reference_loo(reference = BS.dartcap.rubias3,
                     gen_start_col = 5,
                     reps = 5,
                     mixsize = 200,
                     return_indiv_posteriors = TRUE)
  repu_pofzs <- BS_sims$indiv_posteriors %>%
    dplyr::filter(repunit == simulated_repunit) %>%
    dplyr::group_by(iter, indiv, simulated_collection, repunit) %>%
    dplyr::summarise(repu_PofZ = sum(PofZ)) %>%
    dplyr::ungroup() %>%
    dplyr::arrange(repunit, simulated_collection) %>%
    dplyr::mutate(simulated_collection = factor(simulated_collection,
                                                levels = unique(simulated_collection)))

  num_simmed <- BS_sims$indiv_posteriors %>%
    dplyr::group_by(iter, indiv) %>%
    dplyr::slice(1) %>%
    dplyr::ungroup() %>%
    dplyr::count(simulated_collection)

  num_simmed <- num_simmed[order(factor(num_simmed$simulated_collection,
                                        levels = pop.levels1)),]
  repu_pofzs$repunit <- factor(repu_pofzs$repunit, levels = pop.levels2)
  repu_pofzs$simulated_collection <- factor(repu_pofzs$simulated_collection,
                                            levels = pop.levels1)
  repu_pofzs <- repu_pofzs[order(repu_pofzs$repunit,
                                 repu_pofzs$simulated_collection),]
  repu_pofzs$Nmarkers <- marker.sample[[i]]
  res <- rbind(res,repu_pofzs)
}
save(res, file = "DArTcap_ALL_Informative_DAPC_markers_rubias assignment2.Rdata")
```

```
load("DArTcap_ALL_Informative_DAPC_markers_rubias_assignment2.Rdata")
plot <- ggplot2::ggplot(res, ggplot2::aes(x = as.factor(Nmarkers),
                                          y = repu_PofZ)) +
  ggplot2::geom_boxplot(ggplot2::aes(colour = repunit)) +
  ggplot2::scale_color_manual(values = colours.6) +
  ggplot2::facet_wrap(~simulated_collection) +
  ggplot2::labs(subtitle = "",
        y = "Assignment success",
        x = "Number of informative markers") +
  ggplot2::theme(axis.text.x = ggplot2::element_text(angle = 90,
                                                     hjust = 1, size = 9,
                                                     vjust = 0.5)) +
  ggplot2::ylim(c(NA, 1.05))
print(plot)
```



```
ggplot2::ggsave(plot,
                filename = "DArTcap_ALL_Informative_DAPC_markers_rubias assignment2.png",
                width = 30, height = 15,units = "cm")
```

8.11 Sex-specific connectivity

8.11.1 Sex-linked markers

```
load("DArTcap_Raw_tidy.Rdata")
BS.dartcap.raw.tidy <- BSsnp$tidy.data
length(unique(BS.dartcap.raw.tidy$INDIVIDUALS)) #942
length(unique(BS.dartcap.raw.tidy$MARKERS)) #19549

load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
x.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID[
```

```
  bull_shark$sexy.summary$MARKER_TYPE == "Homogametic_sex-marker"],
                      SLM$sexy.summary$CLONE_ID[
                        SLM$sexy.summary$MARKER_TYPE == "Homogametic_sex-marker"]))
y.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID[
  bull_shark$sexy.summary$MARKER_TYPE == "Heterogametic_sex-marker"],
                      SLM$sexy.summary$CLONE_ID[
                        SLM$sexy.summary$MARKER_TYPE == "Heterogametic_sex-marker"]))

sum(unique(BS.dartcap.raw.tidy$LOCUS) %in% x.markers) ##121
BS.dartcap.x.tidy <- BS.dartcap.raw.tidy[BS.dartcap.raw.tidy$LOCUS %in% x.markers, ]

sum(unique(BS.dartcap.raw.tidy$LOCUS) %in% y.markers) ##0

Convert <- radiator::genomic_converter(BS.dartcap.x.tidy,
                                       output = c("genlight","gtypes"))
BS.dartcap.gl.x <- Convert$genlight
BS.dartcap.gt.x <- Convert$gtypes

pop.levels <- c("Costa Rica", "Brazil", "Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Australia", "Japan", "Fiji")
BS.dartcap.gl.x$pop <- factor(BS.dartcap.gl.x$other$ind.metrics$Site,
                              levels = pop.levels)
BS.dartcap.gl.x <- BS.dartcap.gl.x[order(BS.dartcap.gl.x$pop,
                                         BS.dartcap.gl.x$ind.names),]

pop.levels <- c("Costa_Rica", "Brazil", "Caribbean_Sea", "Gulf_of_Mexico",
                "Western_North_Atlantic", "Sierra_Leone", "South_Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian_Sea", "Sri_Lanka",
                "Thailand", "Indonesia", "Papua_New_Guinea" , "Australia",
                "Japan", "Fiji")
BS.dartcap.gt.x@data$stratum <- factor(BS.dartcap.gt.x@data$stratum,
                                       levels = pop.levels)
BS.dartcap.gt.x <- BS.dartcap.gt.x[order(BS.dartcap.gt.x@data$id),]
BS.dartcap.gt.x@data <- BS.dartcap.gt.x@data[order(BS.dartcap.gt.x@data$id),]
BS.dartcap.gt.x@schemes <- BS.dartcap.gt.x@schemes[order(BS.dartcap.gt.x@schemes$id),]

save(BS.dartcap.x.tidy, BS.dartcap.gl.x,BS.dartcap.gt.x,
     file = "DArTcap_X_SLM.Rdata")
```

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID, SLM$sexy.summary$CLONE_ID))

load("DArTcap_X_SLM.Rdata")
sum(BS.dartcap.gl.x$other$loc.metrics$CloneID %in% sex.markers) #148


pop.levels <- c("Costa Rica" , "Brazil", "Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic",   "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Australia", "Japan", "Fiji")
BS.dartcap.gl.x$pop <- factor(BS.dartcap.gl.x$other$ind.metrics$Site,
                              levels = pop.levels)
```

```r
gl.x.F.filtered <- BS.dartcap.gl.x[
  BS.dartcap.gl.x@other$ind.metrics$COMBINED_SEX == "F" &
    BS.dartcap.gl.x$ind.names %in% BS.dartcap.gl$ind.names,]
gl.x.M.filtered <- BS.dartcap.gl.x[
  BS.dartcap.gl.x@other$ind.metrics$COMBINED_SEX == "M" &
    BS.dartcap.gl.x$ind.names %in% BS.dartcap.gl$ind.names,]

gt.x.F.filtered <- BS.dartcap.gt.x[
  BS.dartcap.gt.x@schemes$COMBINED_SEX == "F" &
    getIndNames(BS.dartcap.gt.x) %in% getIndNames(BS.dartcap.gt),,drop = TRUE]
gt.x.M.filtered <- BS.dartcap.gt.x[
  BS.dartcap.gt.x@schemes$COMBINED_SEX == "M" &
    BS.dartcap.gt.x@schemes$id %in% BS.dartcap.gt@schemes$id,,drop = TRUE]
gt.x.F.filtered@schemes <- BS.dartcap.gt.x@schemes[
  BS.dartcap.gt.x@schemes$COMBINED_SEX == "F" &
    BS.dartcap.gt.x@schemes$id %in% BS.dartcap.gt@schemes$id,]
gt.x.M.filtered@schemes <- BS.dartcap.gt.x@schemes[
  BS.dartcap.gt.x@schemes$COMBINED_SEX == "M" &
    BS.dartcap.gt.x@schemes$id %in% BS.dartcap.gt@schemes$id,]

adegenet::nInd(gl.x.F.filtered) #353
summary(gl.x.F.filtered$pop)
adegenet::nInd(gl.x.M.filtered) #338
summary(gl.x.M.filtered$pop)
adegenet::nLoc(gl.x.F.filtered) #148
sum(as.data.frame(gl.x.M.filtered) == 1, na.rm = TRUE) #351
sum(as.data.frame(gl.x.F.filtered) == 1, na.rm = TRUE) #2156
```

```
## [1] 148
## [1] 353
##             Costa Rica         Gulf of Mexico Western North Atlantic
##                      9                     18                      6
##           Sierra Leone           South Africa             Mozambique
##                      1                      9                      5
##                Reunion             Seychelles            Arabian Sea
##                     13                     28                      9
##              Sri Lanka               Thailand              Indonesia
##                      7                      3                      1
##       Papua New Guinea              Australia                  Japan
##                      4                    193                     25
##                   Fiji
##                     22
## [1] 338
##             Costa Rica          Caribbean Sea         Gulf of Mexico
##                      7                      2                     19
## Western North Atlantic           South Africa             Mozambique
##                      2                     12                      6
##                Reunion             Seychelles            Arabian Sea
##                     15                      8                      6
##              Sri Lanka               Thailand              Indonesia
##                      5                      2                      3
##       Papua New Guinea              Australia                  Japan
##                      4                    225                     19
##                   Fiji
##                      3
## [1] 148
## [1] 351
```

```
## [1] 2156
```

```
pop.levels <- c("Costa Rica" , "Brazil", "Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "South Africa", "Mozambique",
                "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand",
                "Indonesia", "Papua New Guinea" , "Australia", "Japan", "Fiji")

gl <- BS.dartcap.gl
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_Sites_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_Sites_genepop.txt",
                               outfile = "BS_dartcap_all_Sites_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#17
gendiv <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Brazil" = bastat$main_tab[[2]]$overall,
  "Caribbean Sea" = bastat$main_tab[[3]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[4]]$overall,
  "Western North Atlantic" = bastat$main_tab[[5]]$overall,
  "South Africa" = bastat$main_tab[[6]]$overall,
  "Mozambique" = bastat$main_tab[[7]]$overall,
  "Reunion" = bastat$main_tab[[8]]$overall,
  "Seychelles" = bastat$main_tab[[9]]$overall,
  "Arabian Sea" = bastat$main_tab[[10]]$overall,
  "Sri Lanka" = bastat$main_tab[[11]]$overall,
  "Thailand" = bastat$main_tab[[12]]$overall,
  "Indonesia" = bastat$main_tab[[13]]$overall,
  "Papua New Guinea" = bastat$main_tab[[14]]$overall,
  "Australia" = bastat$main_tab[[15]]$overall,
  "Japan" = bastat$main_tab[[16]]$overall,
  "Fiji" = bastat$main_tab[[17]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)
readr::write_tsv(gendiv, path = "DArTcap_ALL_Sites_gendiv.txt")
save(gendiv, file = "DArTcap_ALL_Sites_gendiv.Rdata")
```

```
gl <- gl.x.F.filtered
gl <- gl[!gl$pop %in% c("Sierra Leone", "Indonesia")] #only 1 sample
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_X_F_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_X_F_genepop.txt",
                               outfile = "BS_dartcap_all_X_F_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#14
gendiv.x.F <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[2]]$overall,
  "Western North Atlantic" = bastat$main_tab[[3]]$overall,
  "South Africa" = bastat$main_tab[[4]]$overall,
  "Mozambique" = bastat$main_tab[[5]]$overall,
  "Reunion" = bastat$main_tab[[6]]$overall,
  "Seychelles" = bastat$main_tab[[7]]$overall,
  "Arabian Sea" = bastat$main_tab[[8]]$overall,
  "Sri Lanka" = bastat$main_tab[[9]]$overall,
  "Thailand" = bastat$main_tab[[10]]$overall,
  "Papua New Guinea" = bastat$main_tab[[11]]$overall,
  "Australia" = bastat$main_tab[[12]]$overall,
  "Japan" = bastat$main_tab[[13]]$overall,
  "Fiji" = bastat$main_tab[[14]]$overall,
  check.names = FALSE)
row.names(gendiv.x.F) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv.x.F <- rbind(gendiv.x.F, df)

readr::write_tsv(gendiv.x.F, path = "DArTcap_ALL_gendiv_X_F.txt")
save(gendiv.x.F, file = "DArTcap_ALL_gendiv_X_perSites.Rdata")


gl <- gl.x.M.filtered
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_all_X_M_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_all_X_M_genepop.txt",
                               outfile = "BS_dartcap_all_X_M_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
```

```
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#16
gendiv.x.M <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Caribbean Sea" = bastat$main_tab[[2]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[3]]$overall,
  "Western North Atlantic" = bastat$main_tab[[4]]$overall,
  "South Africa" = bastat$main_tab[[5]]$overall,
  "Mozambique" = bastat$main_tab[[6]]$overall,
  "Reunion" = bastat$main_tab[[7]]$overall,
  "Seychelles" = bastat$main_tab[[8]]$overall,
  "Arabian Sea" = bastat$main_tab[[9]]$overall,
  "Sri Lanka" = bastat$main_tab[[10]]$overall,
  "Thailand" = bastat$main_tab[[11]]$overall,
  "Indonesia" = bastat$main_tab[[12]]$overall,
  "Papua New Guinea" = bastat$main_tab[[13]]$overall,
  "Australia" = bastat$main_tab[[14]]$overall,
  "Japan" = bastat$main_tab[[15]]$overall,
  "Fiji" = bastat$main_tab[[16]]$overall,
  check.names = FALSE)
row.names(gendiv.x.M) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv.x.M <- rbind(gendiv.x.M, df)

readr::write_tsv(gendiv.x.M, path = "DArTcap_ALL_gendiv_X_M.txt")
save(gendiv.x.F,gendiv.x.M,
     file = "DArTcap_ALL_gendiv_X_perSites.Rdata")
```

```
load("DArTcap_ALL_Sites_gendiv.Rdata")
load("DArTcap_ALL_gendiv_X_perSites.Rdata")
knitr::kable(gendiv, digits = 4,
             caption = "Genetic diversity for all loci") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
knitr::kable(gendiv.x.F, digits = 4,
             caption = "Genetic diversity for all X-linked loci: Only females") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
knitr::kable(gendiv.x.M, digits = 4,
             caption = "Genetic diversity for all X-linked loci: Only males") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
```

```
                                latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

8.11.1.1 Genetic diversity

Table 22: Genetic diversity for all loci

	Costa.Rica	Brazil	Caribbean.Sea	Gulf.of.Mexico	Western.North.Atlantic	South.Africa	Mozambique	Reunion	Seychelles	Arabian.Sea	Sri.Lanka	Thailand	Indonesia	Papua.New.Guinea	Australia
ar	1.0610	1.0950	1.0640	1.0860	1.0850	1.1120	1.0870	1.1090	1.1120	1.1140	1.1110	1.1100	1.0960	1.1050	1.1160
size	15.6540	49.0870	1.9750	36.0400	7.8830	21.7470	10.2580	27.3810	35.4700	14.8430	11.8850	4.9650	3.9590	8.9060	438.3460
obs__het	0.0360	0.0520	0.0490	0.0480	0.0500	0.0600	0.0560	0.0590	0.0600	0.0620	0.0610	0.0660	0.0610	0.0590	0.0610
exp__het	0.0390	0.0560	0.0380	0.0530	0.0500	0.0620	0.0600	0.0620	0.0620	0.0630	0.0610	0.0590	0.0540	0.0580	0.0640
uexp__het	0.0410	0.0570	0.0510	0.0530	0.0540	0.0630	0.0640	0.0630	0.0630	0.0650	0.0640	0.0660	0.0610	0.0620	0.0640
fis	0.0450	0.0480	-0.2930	0.0500	-0.0250	0.0240	0.0520	0.0400	0.0260	0.0040	-0.0050	-0.1080	-0.1360	-0.0270	0.0430
hwe__glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0000
hwe__hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe__het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.0000
fis__lo	-0.0090	0.0330	-1.0000	0.0310	-0.1450	-0.0090	-0.0350	0.0100	0.0020	-0.0480	-0.0770	-0.3680	-0.5470	-0.1260	0.0370
fis__hi	0.0440	0.0520	-0.2930	0.0530	-0.0340	0.0180	0.0450	0.0370	0.0250	-0.0030	-0.0150	-0.1080	-0.1360	-0.0370	0.0430
ar__lo	1.0130	1.0850	1.0330	1.0360	1.0290	1.0510	0.9460	1.0460	1.0600	1.0480	1.0490	1.0520	1.0470	1.0430	1.1050
ar__hi	1.0710	1.1070	1.0920	1.0990	1.1020	1.1220	1.1190	1.1210	1.1210	1.1280	1.1280	1.1290	1.1190	1.1180	1.1270
fis.hierfstat	0.0750	0.0576	-0.0481	0.0638	0.0369	0.0465	0.0959	0.0572	0.0398	0.0370	0.0356	-0.0069	-0.0098	0.0285	0.0440
fis.CI.low	0.0785	0.0687	-0.0302	0.0736	0.0321	0.0454	0.1015	0.0530	0.0328	0.0261	0.0130	-0.0302	-0.0282	0.0165	0.0387
fis.CI.high	0.1389	0.1058	0.1227	0.1164	0.0998	0.0787	0.1564	0.0888	0.0611	0.0675	0.0610	0.0374	0.0545	0.0702	0.0544

Table 23: Genetic diversity for all X-linked loci: Only females

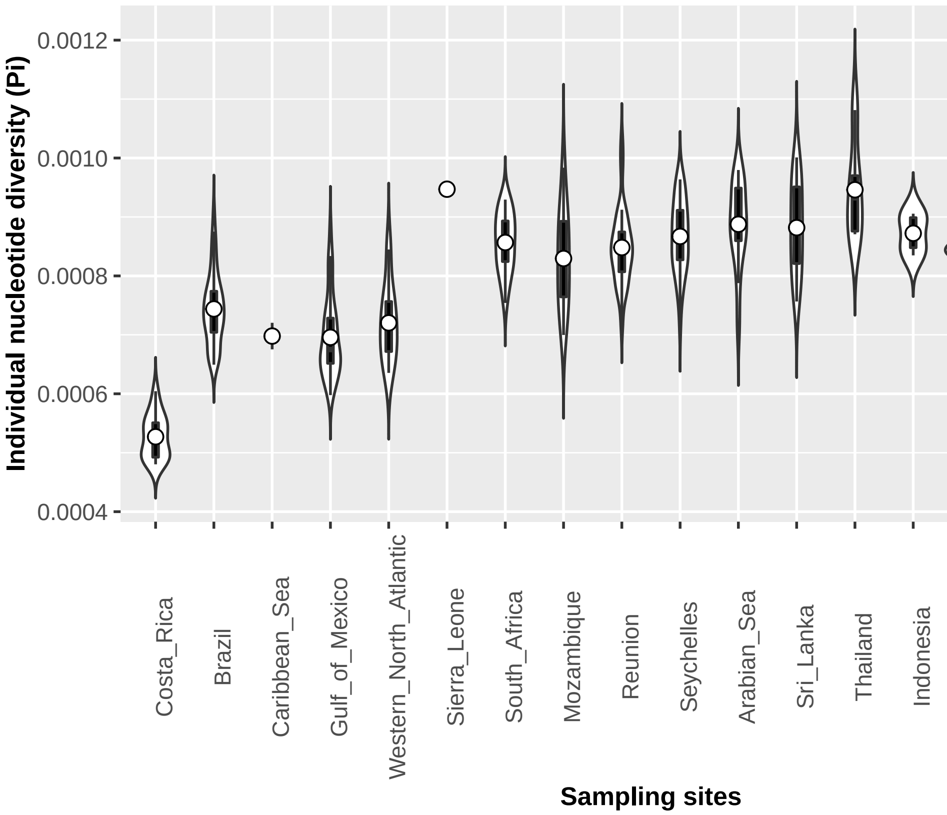
	Costa.Rica	Gulf.of.Mexico	Western.North.Atlantic	South.Africa	Mozambique	Reunion	Seychelles	Arabian.Sea	Sri.Lanka	Thailand	Papua.New.Guinea	Australia	Japan	Fiji
ar	1.0190	1.0530	1.0470	1.0920	1.0920	1.0980	1.0980	1.0990	1.0910	1.0990	1.0780	1.1000	1.0920	1.0850
size	8.8450	17.7360	5.9120	8.9730	4.9590	12.8650	27.7160	8.8920	6.9320	2.9930	3.9860	191.2500	24.7090	21.3650
obs_het	0.0110	0.0220	0.0250	0.0410	0.0490	0.0470	0.0460	0.0420	0.0400	0.0560	0.0470	0.0440	0.0440	0.0420
exp_het	0.0180	0.0220	0.0210	0.0410	0.0390	0.0420	0.0450	0.0450	0.0410	0.0460	0.0340	0.0450	0.0420	0.0390
uexp_het	0.0120	0.0220	0.0230	0.0440	0.0440	0.0440	0.0460	0.0480	0.0450	0.0550	0.0390	0.0450	0.0430	0.0400
fis	-0.0400	-0.0280	-0.1550	-0.0050	-0.2070	-0.0870	-0.0200	-0.0120	-0.0170	-0.2090	-0.3050	0.0110	-0.0100	-0.0470
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.3150	-0.0970	-0.5200	-0.2080	-0.5220	-0.2140	-0.0810	-0.1710	-0.3110	-1.0000	-0.7940	-0.0030	-0.0820	-0.1150
fis_hi	0.1040	-0.0040	-0.0930	0.0640	-0.1650	-0.0430	0.0130	0.0650	0.1780	-0.1810	-0.2820	0.0250	0.0130	-0.0200
ar_lo	1.0000	1.0200	1.0200	1.0470	1.0470	1.0610	1.0610	1.0470	1.0470	1.0340	1.0470	1.0680	1.0540	1.0410
ar_hi	1.0470	1.0880	1.0810	1.1350	1.1150	1.1280	1.1280	1.1420	1.1220	1.1220	1.1010	1.1420	1.1220	1.1280
fis.hierfstat	0.0188	0.0004	-0.0666	0.0478	-0.1052	-0.0476	-0.0022	0.0447	0.0573	-0.0648	-0.1848	0.0137	0.0087	-0.0229
fis.CI.low	-0.0323	-0.1037	-0.2234	-0.1210	-0.3056	-0.1582	-0.1452	-0.0241	-0.0408	-0.3333	-0.5000	-0.0411	-0.1585	-0.1671
fis.CI.high	0.1157	0.1489	0.0141	0.2515	0.0690	0.0071	0.1465	0.2382	0.2372	0.2882	-0.0485	0.1247	0.1417	0.0873

Table 24: Genetic diversity for all X-linked loci: Only males

	Costa.Rica	Caribbean.Sea	Gulf.of.Mexico	Western.North.Atlantic	South.Africa	Mozambique	Reunion	Seychelles	Arabian.Sea	Sri.Lanka	Thailand	Indonesia	Papua.New.Guinea	Australia	Japan
ar	0.994	0.999	1.0130	1.0440	1.0370	0.9950	1.0280	1.0360	1.0460	1.0130	1.002	1.0230	1.0330	1.0380	1.0180
size	6.696	1.932	18.3450	1.9530	11.6350	5.5340	14.5680	7.7500	5.8510	4.7970	1.946	2.9530	3.9460	218.2910	18.3110
obs__het	0.001	0.003	0.0070	0.0340	0.0100	0.0050	0.0030	0.0090	0.0190	0.0010	0.003	0.0050	0.0120	0.0080	0.0030
exp__het	0.009	0.013	0.0170	0.0490	0.0390	0.0450	0.0330	0.0400	0.0380	0.0290	0.023	0.0250	0.0280	0.0410	0.0270
uexp__het	0.010	0.017	0.0180	0.0470	0.0410	0.0420	0.0340	0.0430	0.0420	0.0320	0.021	0.0300	0.0320	0.0410	0.0280
fis	0.731	0.667	0.2970	-0.0260	0.4100	0.7590	0.7650	0.6730	0.4300	0.9070	0.733	0.7330	0.4700	0.3660	0.8670
hwe__glb	1.000	1.000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.000	1.0000	1.0000	0.0000	1.0000
hwe__hom	1.000	1.000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.000	1.0000	1.0000	1.0000	1.0000
hwe__het	1.000	1.000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.000	1.0000	1.0000	0.0000	1.0000
fis__lo	0.576	-1.000	0.1470	-1.0000	0.3640	0.5660	0.6990	0.5300	-0.0180	0.7620	-1.000	-1.0000	-0.4290	0.3680	0.6780
fis__hi	1.000	0.667	0.7460	-0.0260	0.6110	1.0000	0.9090	0.8110	0.6300	1.0000	0.733	1.0000	1.0000	0.4670	0.9740
ar__lo	0.953	0.959	0.9530	0.9800	0.9660	0.9110	0.9730	0.9590	0.9800	0.9390	0.973	0.9860	0.9800	1.0070	0.9660
ar__hi	1.014	1.027	1.0680	1.0740	1.0680	1.0410	1.0540	1.0740	1.0880	1.0340	1.027	1.0540	1.0680	1.0740	1.0610
fis.hierfstat	0.750	0.750	0.3168	0.2308	0.4352	0.7804	0.7737	0.6971	0.4820	0.9167	0.800	0.7778	0.5403	0.3672	0.8728
fis.CI.low	0.000	0.000	0.3169	0.0000	0.5675	0.7849	0.8262	0.6609	0.3721	0.8571	0.500	0.6250	0.3334	0.7566	0.7840
fis.CI.high	1.000	1.000	0.7737	0.6667	0.8695	0.9802	0.9635	0.9264	0.7569	1.0000	1.000	1.0000	0.8800	0.8590	0.9707

```
BS.dartcap.x.F.tidy <- BS.dartcap.x.tidy[BS.dartcap.x.tidy$INDIVIDUALS %in%
                                           gl.x.F.filtered$ind.names,]
BS.dartcap.x.F.tidy <- BS.dartcap.x.F.tidy[!BS.dartcap.x.F.tidy$POP_ID %in%
                                             c("Indonesia"), ]
BS.dartcap.x.F.tidy$POP_ID <- factor(BS.dartcap.x.F.tidy$POP_ID)
pi.sum.X.F <- radiator::pi(
  data = BS.dartcap.x.F.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

BS.dartcap.x.M.tidy <- BS.dartcap.x.tidy[BS.dartcap.x.tidy$INDIVIDUALS %in%
                                           gl.x.M.filtered$ind.names,]
BS.dartcap.x.M.tidy <- BS.dartcap.x.M.tidy[!BS.dartcap.x.M.tidy$POP_ID %in%
                                             c("Indonesia"), ]
BS.dartcap.x.M.tidy$POP_ID <- factor(BS.dartcap.x.M.tidy$POP_ID)

pi.sum.X.M <- radiator::pi(
  data = BS.dartcap.x.M.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

save(pi.sum.X.F, pi.sum.X.M, file = "DArTcap_ALL_pi_Sites_X_FM.Rdata")
```

```
load("DArTcap_ALL_pi_FIS_Sites2.Rdata")
load("DArTcap_ALL_pi_Sites_X_FM.Rdata")
pi.sum.site$boxplot.pi
```



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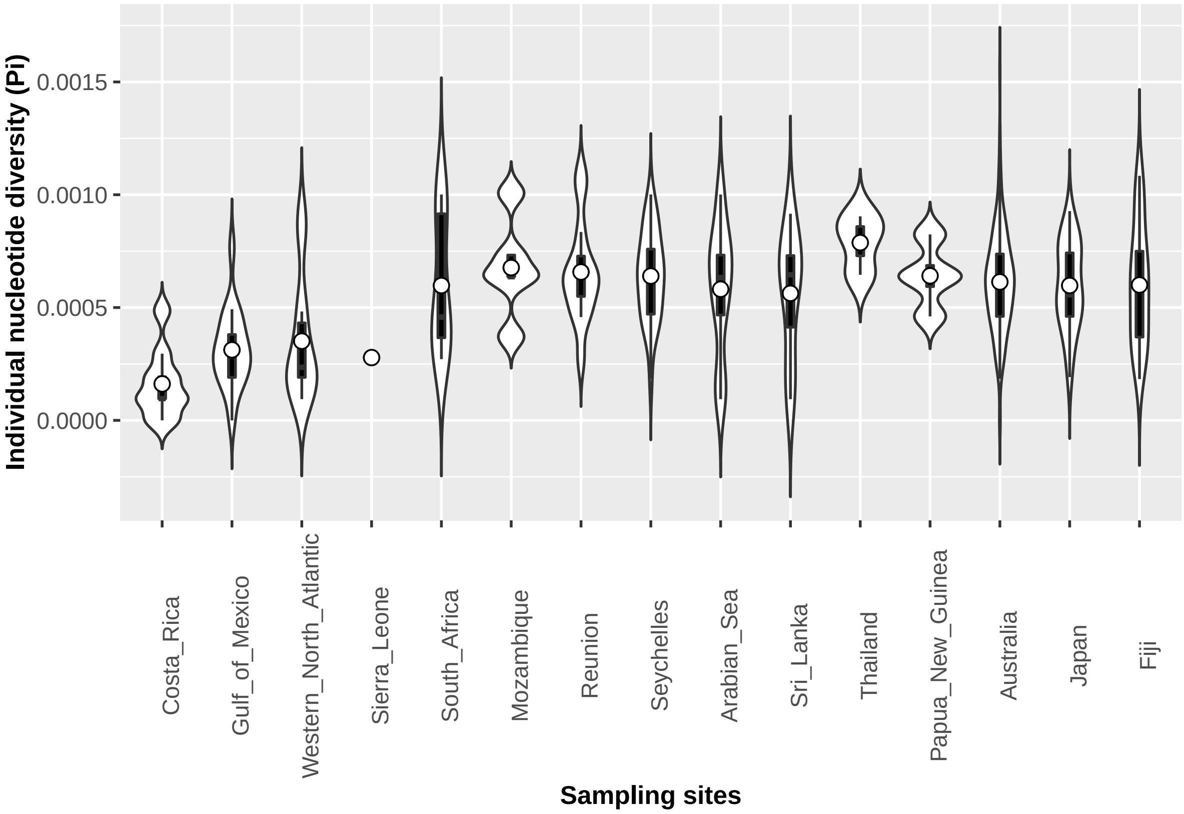
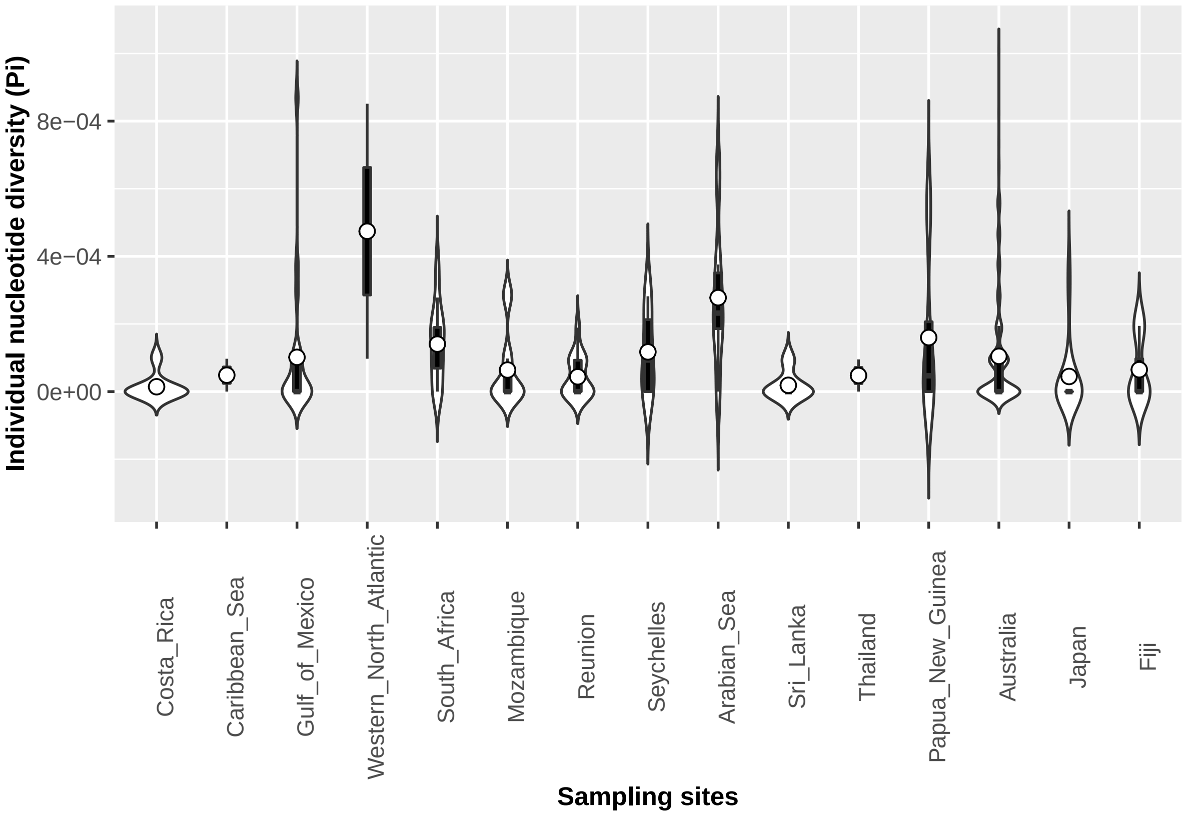
```
pi.sum.X.F$boxplot.pi
```



```
pi.sum.X.M$boxplot.pi
```



```r
Fst.gt <-
  strataG::popStructTest(
    gt.all.neutral,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )

strata <- gt.x.F.filtered@schemes$Site
names(strata) <- gt.x.F.filtered@schemes$id
strataG::setStrata(gt.x.F.filtered) <- strata

Fst.x.F.filtered <-
  strataG::popStructTest(
    gt.x.F.filtered,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )

strata <- gt.x.M.filtered@schemes$Site
names(strata) <- gt.x.M.filtered@schemes$id
```

```
strataG::setStrata(gt.x.M.filtered) <- strata

Fst.x.M.filtered <-
  strataG::popStructTest(
    gt.x.M.filtered,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.x.F.filtered, Fst.x.M.filtered,
     file = "DArTcap_ALL_FST_X_Sites.Rdata")
```

```
load("DArTcap_ALL_FST_Sites.Rdata")
load("DArTcap_ALL_FST_X_Sites.Rdata")

names.1 <- paste0(Fst.gt$pairwise$result$strata.1,"_",
                  Fst.gt$pairwise$result$strata.2)
names.2 <- paste0(Fst.x.F.filtered$pairwise$result$strata.1,"_",
                  Fst.x.F.filtered$pairwise$result$strata.2)
names.3 <- paste0(Fst.x.M.filtered$pairwise$result$strata.1,"_",
                  Fst.x.M.filtered$pairwise$result$strata.2)

result.1 <- Fst.gt$pairwise$result
result.1$names.comb <- names.1
result.2 <- Fst.x.F.filtered$pairwise$result
result.2$names.comb <- names.2
result.3 <- Fst.x.M.filtered$pairwise$result
result.3$names.comb <- names.3

data <- left_join(result.1,result.2, by = "names.comb" ) %>%
  left_join(., result.3, by = "names.comb")


pwFst <- data[,c(1:4,11:12, 24:25,32:33, 44:45,52:53)]
colnames(pwFst) <- c("strata.1", "strata.2", "n.auDNA.1", "n.auDNA.2",
                     "Fst.auDNA", "Fst.auDNA.Pval",
                     "n.xDNA.F.1", "n.xDNA.F.2", "Fst.xDNA.F", "Fst.xDNA.F.Pval",
                     "n.xDNA.M.1", "n.xDNA.M.2", "Fst.xDNA.M", "Fst.xDNA.M.Pval")

kableExtra::kbl(pwFst, digits = 4,
  caption = "Pairwise Fst for autosomal and X-linked markers in females and males",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                          latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

8.11.1.2 nuFst - xFst

Table 25: Pairwise Fst for autosomal and X-linked markers in females and males

strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fst.auDNA	Fst.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fst.xDNA.F	Fst.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fst.xDNA.M	Fst.xDNA.M.Pval
Arabian Sea	Australia	15	444	0.0018	0.0220	9	193	-0.0076	0.7230	6	225	0.0028	0.4074
Arabian Sea	Brazil	15	50	0.6538	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea	Caribbean Sea	15	2	0.6376	0.0166	NA	NA	NA	NA	6	2	0.6899	0.0350
Arabian Sea	Costa Rica	15	16	0.6703	0.0010	9	9	0.7611	0.0010	6	7	0.7948	0.0020
Arabian Sea	Fiji	15	25	0.0273	0.0010	9	22	0.0588	0.0010	6	3	NA	NA
Arabian Sea	Gulf of Mexico	15	37	0.6674	0.0010	9	18	0.7427	0.0010	6	19	0.8008	0.0010
Arabian Sea	Indonesia	15	4	0.0124	0.0241	9	1	-0.0347	0.6893	6	3	0.0257	0.3027
Arabian Sea	Japan	15	44	0.0306	0.0010	9	25	0.0545	0.0120	6	19	0.1678	0.0010
Arabian Sea	Mozambique	15	11	0.0041	0.0380	9	5	0.0132	0.2368	6	6	-0.0377	0.7423
Arabian Sea	Papua New Guinea	15	9	0.0067	0.0060	9	4	0.0284	0.1588	6	4	-0.0878	0.9590
Arabian Sea	Reunion	15	28	0.0019	0.1419	9	13	-0.0053	0.6134	6	15	0.0362	0.1653
Arabian Sea	Seychelles	15	36	0.0011	0.1848	9	28	0.0026	0.3776	6	8	-0.0040	0.4775
Arabian Sea	Sierra Leone	15	1	0.1582	1.0000	9	1	0.1749	0.2306	NA	NA	NA	NA
Arabian Sea	South Africa	15	22	0.0020	0.0909	9	9	-0.0312	0.9760	6	12	-0.0313	0.7960
Arabian Sea	Sri Lanka	15	12	-0.0014	0.7622	9	7	-0.0359	0.9610	6	5	0.0532	0.1291
Arabian Sea	Thailand	15	5	-0.0019	0.7233	9	3	-0.0366	0.8412	6	2	NA	NA
Arabian Sea	Western North Atlantic	15	8	0.6495	0.0010	9	6	0.7067	0.0010	6	2	0.6518	0.0390
Australia	Brazil	444	50	0.6359	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Australia	Caribbean Sea	444	2	0.6353	0.0040	NA	NA	NA	NA	225	2	0.6879	0.0021
Australia	Costa Rica	444	16	0.6264	0.0010	193	9	0.6928	0.0010	225	7	0.7135	0.0010
Australia	Fiji	444	25	0.0310	0.0010	193	22	0.0599	0.0010	225	3	NA	NA
Australia	Gulf of Mexico	444	37	0.6416	0.0010	193	18	0.6812	0.0010	225	19	0.7075	0.0010
Australia	Indonesia	444	4	NA	NA	193	1	NA	NA	225	3	0.0539	0.1994
Australia	Japan	444	44	0.0287	0.0010	193	25	0.0304	0.0010	225	19	0.1152	0.0010
Australia	Mozambique	444	11	0.0044	0.0010	193	5	0.0286	0.0682	225	6	0.0261	0.1758
Australia	Papua New Guinea	444	9	0.0018	0.1179	193	4	0.0298	0.1280	225	4	-0.0225	0.6108
Australia	Reunion	444	28	0.0052	0.0010	193	13	0.0137	0.0440	225	15	0.0293	0.0280
Australia	Seychelles	444	36	0.0015	0.0010	193	28	0.0012	0.3197	225	8	0.0341	0.0785
Australia	Sierra Leone	444	1	0.1572	1.0000	193	1	0.1869	0.0107	NA	NA	NA	NA
Australia	South Africa	444	22	0.0008	0.1209	193	9	-0.0152	0.9510	225	12	0.0176	0.1251
Australia	Sri Lanka	444	12	0.0005	0.3127	193	7	-0.0118	0.7946	225	5	0.0363	0.1721
Australia	Thailand	444	5	0.0014	0.3150	193	3	-0.0028	0.4341	225	2	NA	NA
Australia	Western North Atlantic	444	8	0.6385	0.0010	193	6	0.6809	0.0010	225	2	0.6803	0.0021
Brazil	Caribbean Sea	50	2	0.0016	0.6250	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Costa Rica	50	16	0.3484	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Fiji	50	25	0.6521	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Gulf of Mexico	50	37	0.0049	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Indonesia	50	4	0.6610	0.0016	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Japan	50	44	0.6580	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Mozambique	50	11	0.6532	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Papua New Guinea	50	9	0.6576	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Reunion	50	28	0.6518	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Seychelles	50	36	0.6504	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Sierra Leone	50	1	0.6231	1.0000	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	South Africa	50	22	0.6522	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Sri Lanka	50	12	0.6543	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Thailand	50	5	0.6564	0.0012	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Western North Atlantic	50	8	0.0037	0.0884	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea	Costa Rica	2	16	0.4287	0.0845	NA	NA	NA	NA	2	7	0.6704	0.0380
Caribbean Sea	Fiji	2	25	0.6389	0.0341	NA	NA	NA	NA	2	3	0.7248	0.0939
Caribbean Sea	Gulf of Mexico	2	37	-0.0020	0.5714	NA	NA	NA	NA	2	19	-0.1106	0.7202
Caribbean Sea	Indonesia	2	4	0.6592	0.0772	NA	NA	NA	NA	2	3	0.7086	0.1089
Caribbean Sea	Japan	2	44	0.6537	0.0110	NA	NA	NA	NA	2	19	0.7804	0.0100

Table 25: Pairwise Fst for autosomal and X-linked markers in females and males *(continued)*

strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fst.auDNA	Fst.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fst.xDNA.F	Fst.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fst.xDNA.M	Fst.xDNA.M.Pval
Caribbean Sea	Mozambique	2	11	0.6367	0.0445	NA	NA	NA	NA	2	6	0.6568	0.0815
Caribbean Sea	Papua New Guinea	2	9	0.6504	0.0216	NA	NA	NA	NA	2	4	0.7336	0.0679
Caribbean Sea	Reunion	2	28	0.6401	0.0079	NA	NA	NA	NA	2	15	0.7245	0.0061
Caribbean Sea	Seychelles	2	36	0.6409	0.0046	NA	NA	NA	NA	2	8	0.6816	0.0161
Caribbean Sea	Sierra Leone	2	1	0.6360	0.3417	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea	South Africa	2	22	0.6396	0.0086	NA	NA	NA	NA	2	12	0.6793	0.0061
Caribbean Sea	Sri Lanka	2	12	0.6407	0.0192	NA	NA	NA	NA	2	5	0.7267	0.0529
Caribbean Sea	Thailand	2	5	0.6397	0.0605	NA	NA	NA	NA	2	2	0.7647	0.3187
Caribbean Sea	Western North Atlantic	2	8	-0.0077	1.0000	NA	NA	NA	NA	2	2	-0.1220	1.0000
Costa Rica	Fiji	16	25	0.6594	0.0010	9	22	0.7623	0.0010	7	3	0.8562	0.0063
Costa Rica	Gulf of Mexico	16	37	0.3692	0.0010	9	18	0.5201	0.0010	7	19	0.6018	0.0010
Costa Rica	Indonesia	16	4	0.7066	0.0016	9	1	0.9021	0.1250	7	3	0.8386	0.0091
Costa Rica	Japan	16	44	0.6609	0.0010	9	25	0.7547	0.0010	7	19	0.8228	0.0010
Costa Rica	Mozambique	16	11	0.6766	0.0010	9	5	0.8143	0.0010	7	6	0.7916	0.0021
Costa Rica	Papua New Guinea	16	9	0.6888	0.0010	9	4	0.8405	0.0020	7	4	0.8378	0.0040
Costa Rica	Reunion	16	28	0.6579	0.0010	9	13	NA	NA	7	15	0.7800	0.0010
Costa Rica	Seychelles	16	36	0.6532	0.0010	9	28	0.7273	0.0010	7	8	0.7817	0.0010
Costa Rica	Sierra Leone	16	1	0.7013	1.0000	9	1	0.8934	0.1354	NA	NA	NA	NA
Costa Rica	South Africa	16	22	0.6623	0.0010	9	9	0.7768	0.0010	7	12	0.7505	0.0010
Costa Rica	Sri Lanka	16	12	0.6765	0.0010	9	7	0.7817	0.0010	7	5	0.8244	0.0010
Costa Rica	Thailand	16	5	0.6957	0.0012	9	3	0.8105	0.0060	7	2	0.8787	0.0326
Costa Rica	Western North Atlantic	16	8	0.3964	0.0011	9	6	0.5826	0.0020	7	2	0.6580	0.0320
Fiji	Gulf of Mexico	25	37	0.6636	0.0010	22	18	0.7498	0.0010	3	19	0.8276	0.0020
Fiji	Indonesia	25	4	NA	NA	22	1	0.0951	0.1054	3	3	0.0982	0.3397
Fiji	Japan	25	44	0.0617	0.0010	22	25	0.1148	0.0010	3	19	NA	NA
Fiji	Mozambique	25	11	0.0333	0.0010	22	5	0.1609	0.0010	3	6	NA	NA
Fiji	Papua New Guinea	25	9	0.0313	0.0010	22	4	0.0848	0.0051	3	4	0.0120	0.4436
Fiji	Reunion	25	28	0.0331	0.0010	22	13	0.0950	0.0010	3	15	0.0166	0.3347
Fiji	Seychelles	25	36	0.0318	0.0010	22	28	0.0723	0.0010	3	8	NA	NA
Fiji	Sierra Leone	25	1	0.1610	1.0000	22	1	0.3115	0.2784	NA	NA	NA	NA
Fiji	South Africa	25	22	0.0304	0.0010	22	9	0.0548	0.0040	3	12	0.0589	0.1608
Fiji	Sri Lanka	25	12	0.0318	0.0010	22	7	0.0654	0.0020	3	5	0.1228	0.0480
Fiji	Thailand	25	5	0.0255	0.0072	22	3	0.0657	0.0342	3	2	-0.2218	0.9171
Fiji	Western North Atlantic	25	8	0.6477	0.0010	22	6	0.7318	0.0010	3	2	0.6637	0.1044
Gulf of Mexico	Indonesia	37	4	0.6790	0.0018	18	1	0.8293	0.0831	19	3	0.8060	0.0020
Gulf of Mexico	Japan	37	44	0.6682	0.0010	18	25	0.7451	0.0010	19	19	0.8170	0.0010
Gulf of Mexico	Mozambique	37	11	0.6678	0.0010	18	5	0.7747	0.0010	19	6	0.7948	0.0010
Gulf of Mexico	Papua New Guinea	37	9	0.6735	0.0010	18	4	0.7929	0.0010	19	4	0.8220	0.0010
Gulf of Mexico	Reunion	37	28	0.6632	0.0010	18	13	0.7422	0.0010	19	15	0.7851	0.0010
Gulf of Mexico	Seychelles	37	36	0.6609	0.0010	18	28	0.7200	0.0010	19	8	0.7963	0.0010
Gulf of Mexico	Sierra Leone	37	1	0.6452	1.0000	18	1	0.8057	0.0661	NA	NA	NA	NA
Gulf of Mexico	South Africa	37	22	0.6645	0.0010	18	9	0.7542	0.0010	19	12	0.7692	0.0010
Gulf of Mexico	Sri Lanka	37	12	0.6690	0.0010	18	7	0.7560	0.0010	19	5	0.8164	0.0010
Gulf of Mexico	Thailand	37	5	0.6734	0.0013	18	3	0.7681	0.0020	19	2	0.8304	0.0074
Gulf of Mexico	Western North Atlantic	37	8	-0.0002	0.4883	18	6	-0.0149	0.7213	19	2	0.3533	0.0604
Indonesia	Japan	4	44	NA	NA	1	25	NA	NA	3	19	0.3125	0.0032
Indonesia	Mozambique	4	11	0.0115	0.1110	1	5	-0.0165	0.6753	3	6	-0.0997	0.7803
Indonesia	Papua New Guinea	4	9	0.0171	0.1032	1	4	0.1621	0.1958	3	4	0.0199	0.4675
Indonesia	Reunion	4	28	0.0125	0.0556	1	13	0.0392	0.3337	3	15	0.0022	0.4426
Indonesia	Seychelles	4	36	0.0147	0.0100	1	28	NA	NA	3	8	0.0430	0.2531
Indonesia	Sierra Leone	4	1	0.1862	1.0000	1	1	NA	NA	NA	NA	NA	NA
Indonesia	South Africa	4	22	NA	NA	1	9	NA	NA	3	12	0.0597	0.1858
Indonesia	Sri Lanka	4	12	0.0108	0.0829	1	7	-0.0706	0.4126	3	5	0.1017	0.1598

Table 25: Pairwise Fst for autosomal and X-linked markers in females and males *(continued)*

strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fst.auDNA	Fst.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fst.xDNA.F	Fst.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fst.xDNA.M	Fst.xDNA.M.Pval
Indonesia	Thailand	4	5	0.0190	0.1798	1	3	-0.0220	0.7762	3	2	-0.0297	0.6044
Indonesia	Western North Atlantic	4	8	0.6695	0.0057	1	6	0.8338	0.1359	3	2	0.6238	0.0989
Japan	Mozambique	44	11	0.0345	0.0010	25	5	0.0767	0.0180	19	6	0.1620	0.0110
Japan	Papua New Guinea	44	9	0.0350	0.0010	25	4	0.0382	0.0769	19	4	0.1177	0.0548
Japan	Reunion	44	28	0.0352	0.0010	25	13	0.0865	0.0010	19	15	0.2451	0.0010
Japan	Seychelles	44	36	0.0287	0.0010	25	28	0.0256	0.0110	19	8	0.1521	0.0010
Japan	Sierra Leone	44	1	0.2067	1.0000	25	1	0.1477	0.0397	NA	NA	NA	NA
Japan	South Africa	44	22	0.0318	0.0010	25	9	0.0298	0.0310	19	12	0.1652	0.0010
Japan	Sri Lanka	44	12	0.0318	0.0010	25	7	0.0201	0.1009	19	5	0.3094	0.0020
Japan	Thailand	44	5	0.0369	0.0040	25	3	0.0730	0.0595	19	2	NA	NA
Japan	Western North Atlantic	44	8	0.6581	0.0010	25	6	0.7255	0.0010	19	2	0.7641	0.0036
Mozambique	Papua New Guinea	11	9	0.0111	0.0030	5	4	0.1287	0.0220	6	4	-0.0214	0.5155
Mozambique	Reunion	11	28	0.0054	0.0280	5	13	0.0043	0.3566	6	15	0.0451	0.1484
Mozambique	Seychelles	11	36	0.0051	0.0040	5	28	0.0232	0.1053	6	8	-0.0520	0.7932
Mozambique	Sierra Leone	11	1	0.1391	1.0000	5	1	0.3089	0.2481	NA	NA	NA	NA
Mozambique	South Africa	11	22	0.0012	0.2757	5	9	0.0099	0.3037	6	12	0.0265	0.2490
Mozambique	Sri Lanka	11	12	0.0033	0.0889	5	7	0.0267	0.1768	6	5	0.0429	0.2588
Mozambique	Thailand	11	5	-0.0027	0.7239	5	3	0.0375	0.1508	6	2	NA	NA
Mozambique	Western North Atlantic	11	8	0.6505	0.0010	5	6	0.7504	0.0030	6	2	0.6036	0.0427
Papua New Guinea	Reunion	9	28	0.0058	0.0260	4	13	0.0691	0.0100	4	15	0.0128	0.3357
Papua New Guinea	Seychelles	9	36	0.0042	0.0340	4	28	0.0434	0.0779	4	8	0.0030	0.3912
Papua New Guinea	Sierra Leone	9	1	0.1688	1.0000	4	1	0.2146	0.2008	NA	NA	NA	NA
Papua New Guinea	South Africa	9	22	0.0020	0.2168	4	9	0.0154	0.2567	4	12	0.0024	0.4486
Papua New Guinea	Sri Lanka	9	12	0.0042	0.0849	4	7	-0.0095	0.5654	4	5	0.1800	0.0350
Papua New Guinea	Thailand	9	5	0.0044	0.1998	4	3	0.0495	0.2018	4	2	0.0656	0.1948
Papua New Guinea	Western North Atlantic	9	8	0.6609	0.0010	4	6	0.7783	0.0060	4	2	0.6814	0.0659
Reunion	Seychelles	28	36	0.0048	0.0010	13	28	0.0176	0.0519	15	8	0.0763	0.0170
Reunion	Sierra Leone	28	1	0.1589	1.0000	13	1	0.2673	0.1113	NA	NA	NA	NA
Reunion	South Africa	28	22	0.0033	0.0230	13	9	-0.0174	0.9251	15	12	0.0469	0.0440
Reunion	Sri Lanka	28	12	0.0032	0.0809	13	7	0.0037	0.3666	15	5	0.1078	0.0190
Reunion	Thailand	28	5	0.0030	0.2380	13	3	0.0052	0.3826	15	2	-0.1061	0.8256
Reunion	Western North Atlantic	28	8	0.6485	0.0010	13	6	0.7150	0.0010	15	2	0.6998	0.0074
Seychelles	Sierra Leone	36	1	0.1641	1.0000	28	1	0.1876	0.0771	NA	NA	NA	NA
Seychelles	South Africa	36	22	0.0005	0.3297	28	9	-0.0155	0.8911	8	12	0.0508	0.0589
Seychelles	Sri Lanka	36	12	0.0002	0.4555	28	7	0.0014	0.3610	8	5	0.0433	0.2150
Seychelles	Thailand	36	5	0.0046	0.1049	28	3	0.0140	0.2630	8	2	NA	NA
Seychelles	Western North Atlantic	36	8	0.6475	0.0010	28	6	0.6982	0.0010	8	2	0.6547	0.0334
Sierra Leone	South Africa	1	22	0.1491	1.0000	1	9	0.1700	0.1172	NA	NA	NA	NA
Sierra Leone	Sri Lanka	1	12	0.1553	1.0000	1	7	0.1404	0.3857	NA	NA	NA	NA
Sierra Leone	Thailand	1	5	0.1549	1.0000	1	3	0.1502	0.3541	NA	NA	NA	NA
Sierra Leone	Western North Atlantic	1	8	0.6399	1.0000	1	6	0.8145	0.1359	NA	NA	NA	NA
South Africa	Sri Lanka	22	12	0.0005	0.3646	9	7	-0.0370	0.9770	12	5	0.0427	0.1808
South Africa	Thailand	22	5	-0.0017	0.6863	9	3	-0.0198	0.6372	12	2	-0.0818	0.8021
South Africa	Western North Atlantic	22	8	0.6488	0.0010	9	6	0.7243	0.0020	12	2	0.6531	0.0196
Sri Lanka	Thailand	12	5	-0.0005	0.5654	7	3	-0.0284	0.7233	5	2	-0.0471	0.6104
Sri Lanka	Western North Atlantic	12	8	0.6531	0.0010	7	6	0.7239	0.0020	5	2	0.6795	0.0525
Thailand	Western North Atlantic	5	8	0.6580	0.0030	3	6	0.7358	0.0080	2	2	0.6492	0.3257

```
pwFis <- data[,c(1:4,11:12, 24:25,32:33, 44:45,52:53)]
colnames(pwFis) <- c("strata.1", "strata.2", "n.auDNA.1", "n.auDNA.2", "Fis.auDNA",
                     "Fis.auDNA.Pval",
                     "n.xDNA.F.1", "n.xDNA.F.2", "Fis.xDNA.F", "Fis.xDNA.F.Pval",
                     "n.xDNA.M.1", "n.xDNA.M.2", "Fis.xDNA.M", "Fis.xDNA.M.Pval")

kableExtra::kbl(pwFis, digits = 4,
  caption = "Pairwise Fis for autosomal and X-linked markers in females and males",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

8.11.1.3 nuFis - xFis

Table 26: Pairwise Fis for autosomal and X-linked markers in females and males

strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fis.auDNA	Fis.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fis.xDNA.F	Fis.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fis.xDNA.M	Fis.xDNA.M.Pval
Arabian Sea	Australia	15	444	0.0018	0.0220	9	193	-0.0076	0.7230	6	225	0.0028	0.4074
Arabian Sea	Brazil	15	50	0.6538	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Arabian Sea	Caribbean Sea	15	2	0.6376	0.0166	NA	NA	NA	NA	6	2	0.6899	0.0350
Arabian Sea	Costa Rica	15	16	0.6703	0.0010	9	9	0.7611	0.0010	6	7	0.7948	0.0020
Arabian Sea	Fiji	15	25	0.0273	0.0010	9	22	0.0588	0.0010	6	3	NA	NA
Arabian Sea	Gulf of Mexico	15	37	0.6674	0.0010	9	18	0.7427	0.0010	6	19	0.8008	0.0010
Arabian Sea	Indonesia	15	4	0.0124	0.0241	9	1	-0.0347	0.6893	6	3	0.0257	0.3027
Arabian Sea	Japan	15	44	0.0306	0.0010	9	25	0.0545	0.0120	6	19	0.1678	0.0010
Arabian Sea	Mozambique	15	11	0.0041	0.0380	9	5	0.0132	0.2368	6	6	-0.0377	0.7423
Arabian Sea	Papua New Guinea	15	9	0.0067	0.0060	9	4	0.0284	0.1588	6	4	-0.0878	0.9590
Arabian Sea	Reunion	15	28	0.0019	0.1419	9	13	-0.0053	0.6134	6	15	0.0362	0.1653
Arabian Sea	Seychelles	15	36	0.0011	0.1848	9	28	0.0026	0.3776	6	8	-0.0040	0.4775
Arabian Sea	Sierra Leone	15	1	0.1582	1.0000	9	1	0.1749	0.2306	NA	NA	NA	NA
Arabian Sea	South Africa	15	22	0.0020	0.0909	9	9	-0.0312	0.9760	6	12	-0.0313	0.7960
Arabian Sea	Sri Lanka	15	12	-0.0014	0.7622	9	7	-0.0359	0.9610	6	5	0.0532	0.1291
Arabian Sea	Thailand	15	5	-0.0019	0.7233	9	3	-0.0366	0.8412	6	2	NA	NA
Arabian Sea	Western North Atlantic	15	8	0.6495	0.0010	9	6	0.7067	0.0010	6	2	0.6518	0.0390
Australia	Brazil	444	50	0.6359	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Australia	Caribbean Sea	444	2	0.6353	0.0040	NA	NA	NA	NA	225	2	0.6879	0.0021
Australia	Costa Rica	444	16	0.6264	0.0010	193	9	0.6928	0.0010	225	7	0.7135	0.0010
Australia	Fiji	444	25	0.0310	0.0010	193	22	0.0599	0.0010	225	3	NA	NA
Australia	Gulf of Mexico	444	37	0.6416	0.0010	193	18	0.6812	0.0010	225	19	0.7075	0.0010
Australia	Indonesia	444	4	NA	NA	193	1	NA	NA	225	3	0.0539	0.1994
Australia	Japan	444	44	0.0287	0.0010	193	25	0.0304	0.0010	225	19	0.1152	0.0010
Australia	Mozambique	444	11	0.0044	0.0010	193	5	0.0286	0.0682	225	6	0.0261	0.1758
Australia	Papua New Guinea	444	9	0.0018	0.1179	193	4	0.0298	0.1280	225	4	-0.0225	0.6108
Australia	Reunion	444	28	0.0052	0.0010	193	13	0.0137	0.0440	225	15	0.0293	0.0280
Australia	Seychelles	444	36	0.0015	0.0010	193	28	0.0012	0.3197	225	8	0.0341	0.0785
Australia	Sierra Leone	444	1	0.1572	1.0000	193	1	0.1869	0.0107	NA	NA	NA	NA
Australia	South Africa	444	22	0.0008	0.1209	193	9	-0.0152	0.9510	225	12	0.0176	0.1251
Australia	Sri Lanka	444	12	0.0005	0.3127	193	7	-0.0118	0.7946	225	5	0.0363	0.1721
Australia	Thailand	444	5	0.0014	0.3150	193	3	-0.0028	0.4341	225	2	NA	NA
Australia	Western North Atlantic	444	8	0.6385	0.0010	193	6	0.6809	0.0010	225	2	0.6803	0.0021
Brazil	Caribbean Sea	50	2	0.0016	0.6250	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Costa Rica	50	16	0.3484	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Fiji	50	25	0.6521	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Gulf of Mexico	50	37	0.0049	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Indonesia	50	4	0.6610	0.0016	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Japan	50	44	0.6580	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Mozambique	50	11	0.6532	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Papua New Guinea	50	9	0.6576	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Reunion	50	28	0.6518	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Seychelles	50	36	0.6504	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Sierra Leone	50	1	0.6231	1.0000	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	South Africa	50	22	0.6522	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Sri Lanka	50	12	0.6543	0.0010	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Thailand	50	5	0.6564	0.0012	NA	NA	NA	NA	NA	NA	NA	NA
Brazil	Western North Atlantic	50	8	0.0037	0.0884	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea	Costa Rica	2	16	0.4287	0.0845	NA	NA	NA	NA	2	7	0.6704	0.0380
Caribbean Sea	Fiji	2	25	0.6389	0.0341	NA	NA	NA	NA	2	3	0.7248	0.0939
Caribbean Sea	Gulf of Mexico	2	37	-0.0020	0.5714	NA	NA	NA	NA	2	19	-0.1106	0.7202
Caribbean Sea	Indonesia	2	4	0.6592	0.0772	NA	NA	NA	NA	2	3	0.7086	0.1089
Caribbean Sea	Japan	2	44	0.6537	0.0110	NA	NA	NA	NA	2	19	0.7804	0.0100

Table 26: Pairwise Fis for autosomal and X-linked markers in females and males *(continued)*

strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fis.auDNA	Fis.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fis.xDNA.F	Fis.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fis.xDNA.M	Fis.xDNA.M.Pval
Caribbean Sea	Mozambique	2	11	0.6367	0.0445	NA	NA	NA	NA	2	6	0.6568	0.0815
Caribbean Sea	Papua New Guinea	2	9	0.6504	0.0216	NA	NA	NA	NA	2	4	0.7336	0.0679
Caribbean Sea	Reunion	2	28	0.6401	0.0079	NA	NA	NA	NA	2	15	0.7245	0.0061
Caribbean Sea	Seychelles	2	36	0.6409	0.0046	NA	NA	NA	NA	2	8	0.6816	0.0161
Caribbean Sea	Sierra Leone	2	1	0.6360	0.3417	NA	NA	NA	NA	NA	NA	NA	NA
Caribbean Sea	South Africa	2	22	0.6396	0.0086	NA	NA	NA	NA	2	12	0.6793	0.0061
Caribbean Sea	Sri Lanka	2	12	0.6407	0.0192	NA	NA	NA	NA	2	5	0.7267	0.0529
Caribbean Sea	Thailand	2	5	0.6397	0.0605	NA	NA	NA	NA	2	2	0.7647	0.3187
Caribbean Sea	Western North Atlantic	2	8	-0.0077	1.0000	NA	NA	NA	NA	2	2	-0.1220	1.0000
Costa Rica	Fiji	16	25	0.6594	0.0010	9	22	0.7623	0.0010	7	3	0.8562	0.0063
Costa Rica	Gulf of Mexico	16	37	0.3692	0.0010	9	18	0.5201	0.0010	7	19	0.6018	0.0010
Costa Rica	Indonesia	16	4	0.7066	0.0016	9	1	0.9021	0.1250	7	3	0.8386	0.0091
Costa Rica	Japan	16	44	0.6609	0.0010	9	25	0.7547	0.0010	7	19	0.8228	0.0010
Costa Rica	Mozambique	16	11	0.6766	0.0010	9	5	0.8143	0.0010	7	6	0.7916	0.0021
Costa Rica	Papua New Guinea	16	9	0.6888	0.0010	9	4	0.8405	0.0020	7	4	0.8378	0.0040
Costa Rica	Reunion	16	28	0.6579	0.0010	9	13	NA	NA	7	15	0.7800	0.0010
Costa Rica	Seychelles	16	36	0.6532	0.0010	9	28	0.7273	0.0010	7	8	0.7817	0.0010
Costa Rica	Sierra Leone	16	1	0.7013	1.0000	9	1	0.8934	0.1354	NA	NA	NA	NA
Costa Rica	South Africa	16	22	0.6623	0.0010	9	9	0.7768	0.0010	7	12	0.7505	0.0010
Costa Rica	Sri Lanka	16	12	0.6765	0.0010	9	7	0.7817	0.0010	7	5	0.8244	0.0010
Costa Rica	Thailand	16	5	0.6957	0.0012	9	3	0.8105	0.0060	7	2	0.8787	0.0326
Costa Rica	Western North Atlantic	16	8	0.3964	0.0011	9	6	0.5826	0.0020	7	2	0.6580	0.0320
Fiji	Gulf of Mexico	25	37	0.6636	0.0010	22	18	0.7498	0.0010	3	19	0.8276	0.0020
Fiji	Indonesia	25	4	NA	NA	22	1	0.0951	0.1054	3	3	0.0982	0.3397
Fiji	Japan	25	44	0.0617	0.0010	22	25	0.1148	0.0010	3	19	NA	NA
Fiji	Mozambique	25	11	0.0333	0.0010	22	5	0.1609	0.0010	3	6	NA	NA
Fiji	Papua New Guinea	25	9	0.0313	0.0010	22	4	0.0848	0.0051	3	4	0.0120	0.4436
Fiji	Reunion	25	28	0.0331	0.0010	22	13	0.0950	0.0010	3	15	0.0166	0.3347
Fiji	Seychelles	25	36	0.0318	0.0010	22	28	0.0723	0.0010	3	8	NA	NA
Fiji	Sierra Leone	25	1	0.1610	1.0000	22	1	0.3115	0.2784	NA	NA	NA	NA
Fiji	South Africa	25	22	0.0304	0.0010	22	9	0.0548	0.0040	3	12	0.0589	0.1608
Fiji	Sri Lanka	25	12	0.0318	0.0010	22	7	0.0654	0.0020	3	5	0.1228	0.0480
Fiji	Thailand	25	5	0.0255	0.0072	22	3	0.0657	0.0342	3	2	-0.2218	0.9171
Fiji	Western North Atlantic	25	8	0.6477	0.0010	22	6	0.7318	0.0010	3	2	0.6637	0.1044
Gulf of Mexico	Indonesia	37	4	0.6790	0.0018	18	1	0.8293	0.0831	19	3	0.8060	0.0020
Gulf of Mexico	Japan	37	44	0.6682	0.0010	18	25	0.7451	0.0010	19	19	0.8170	0.0010
Gulf of Mexico	Mozambique	37	11	0.6678	0.0010	18	5	0.7747	0.0010	19	6	0.7948	0.0010
Gulf of Mexico	Papua New Guinea	37	9	0.6735	0.0010	18	4	0.7929	0.0010	19	4	0.8220	0.0010
Gulf of Mexico	Reunion	37	28	0.6632	0.0010	18	13	0.7422	0.0010	19	15	0.7851	0.0010
Gulf of Mexico	Seychelles	37	36	0.6609	0.0010	18	28	0.7200	0.0010	19	8	0.7963	0.0010
Gulf of Mexico	Sierra Leone	37	1	0.6452	1.0000	18	1	0.8057	0.0661	NA	NA	NA	NA
Gulf of Mexico	South Africa	37	22	0.6645	0.0010	18	9	0.7542	0.0010	19	12	0.7692	0.0010
Gulf of Mexico	Sri Lanka	37	12	0.6690	0.0010	18	7	0.7560	0.0010	19	5	0.8164	0.0010
Gulf of Mexico	Thailand	37	5	0.6734	0.0013	18	3	0.7681	0.0020	19	2	0.8304	0.0074
Gulf of Mexico	Western North Atlantic	37	8	-0.0002	0.4883	18	6	-0.0149	0.7213	19	2	0.3533	0.0604
Indonesia	Japan	4	44	NA	NA	1	25	NA	NA	3	19	0.3125	0.0032
Indonesia	Mozambique	4	11	0.0115	0.1110	1	5	-0.0165	0.6753	3	6	-0.0997	0.7803
Indonesia	Papua New Guinea	4	9	0.0171	0.1032	1	4	0.1621	0.1958	3	4	0.0199	0.4675
Indonesia	Reunion	4	28	0.0125	0.0556	1	13	0.0392	0.3337	3	15	0.0022	0.4426
Indonesia	Seychelles	4	36	0.0147	0.0100	1	28	NA	NA	3	8	0.0430	0.2531
Indonesia	Sierra Leone	4	1	0.1862	1.0000	1	1	NA	NA	NA	NA	NA	NA
Indonesia	South Africa	4	22	NA	NA	1	9	NA	NA	3	12	0.0597	0.1858
Indonesia	Sri Lanka	4	12	0.0108	0.0829	1	7	-0.0706	0.4126	3	5	0.1017	0.1598

Table 26: Pairwise Fis for autosomal and X-linked markers in females and males *(continued)*

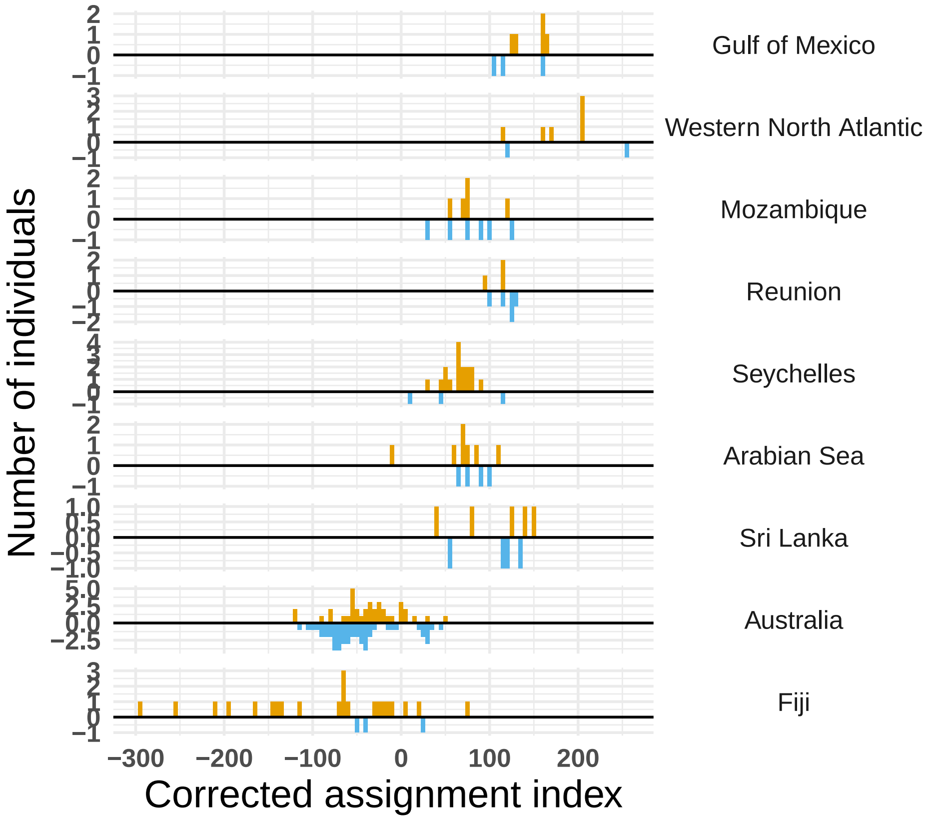
strata.1	strata.2	n.auDNA.1	n.auDNA.2	Fis.auDNA	Fis.auDNA.Pval	n.xDNA.F.1	n.xDNA.F.2	Fis.xDNA.F	Fis.xDNA.F.Pval	n.xDNA.M.1	n.xDNA.M.2	Fis.xDNA.M	Fis.xDNA.M.Pval
Indonesia	Thailand	4	5	0.0190	0.1798	1	3	-0.0220	0.7762	3	2	-0.0297	0.6044
Indonesia	Western North Atlantic	4	8	0.6695	0.0057	1	6	0.8338	0.1359	3	2	0.6238	0.0989
Japan	Mozambique	44	11	0.0345	0.0010	25	5	0.0767	0.0180	19	6	0.1620	0.0110
Japan	Papua New Guinea	44	9	0.0350	0.0010	25	4	0.0382	0.0769	19	4	0.1177	0.0548
Japan	Reunion	44	28	0.0352	0.0010	25	13	0.0865	0.0010	19	15	0.2451	0.0010
Japan	Seychelles	44	36	0.0287	0.0010	25	28	0.0256	0.0110	19	8	0.1521	0.0010
Japan	Sierra Leone	44	1	0.2067	1.0000	25	1	0.1477	0.0397	NA	NA	NA	NA
Japan	South Africa	44	22	0.0318	0.0010	25	9	0.0298	0.0310	19	12	0.1652	0.0010
Japan	Sri Lanka	44	12	0.0318	0.0010	25	7	0.0201	0.1009	19	5	0.3094	0.0020
Japan	Thailand	44	5	0.0369	0.0040	25	3	0.0730	0.0595	19	2	NA	NA
Japan	Western North Atlantic	44	8	0.6581	0.0010	25	6	0.7255	0.0010	19	2	0.7641	0.0036
Mozambique	Papua New Guinea	11	9	0.0111	0.0030	5	4	0.1287	0.0220	6	4	-0.0214	0.5155
Mozambique	Reunion	11	28	0.0054	0.0280	5	13	0.0043	0.3566	6	15	0.0451	0.1484
Mozambique	Seychelles	11	36	0.0051	0.0040	5	28	0.0232	0.1053	6	8	-0.0520	0.7932
Mozambique	Sierra Leone	11	1	0.1391	1.0000	5	1	0.3089	0.2481	NA	NA	NA	NA
Mozambique	South Africa	11	22	0.0012	0.2757	5	9	0.0099	0.3037	6	12	0.0265	0.2490
Mozambique	Sri Lanka	11	12	0.0033	0.0889	5	7	0.0267	0.1768	6	5	0.0429	0.2588
Mozambique	Thailand	11	5	-0.0027	0.7239	5	3	0.0375	0.1508	6	2	NA	NA
Mozambique	Western North Atlantic	11	8	0.6505	0.0010	5	6	0.7504	0.0030	6	2	0.6036	0.0427
Papua New Guinea	Reunion	9	28	0.0058	0.0260	4	13	0.0691	0.0100	4	15	0.0128	0.3357
Papua New Guinea	Seychelles	9	36	0.0042	0.0340	4	28	0.0434	0.0779	4	8	0.0030	0.3912
Papua New Guinea	Sierra Leone	9	1	0.1688	1.0000	4	1	0.2146	0.2008	NA	NA	NA	NA
Papua New Guinea	South Africa	9	22	0.0020	0.2168	4	9	0.0154	0.2567	4	12	0.0024	0.4486
Papua New Guinea	Sri Lanka	9	12	0.0042	0.0849	4	7	-0.0095	0.5654	4	5	0.1800	0.0350
Papua New Guinea	Thailand	9	5	0.0044	0.1998	4	3	0.0495	0.2018	4	2	0.0656	0.1948
Papua New Guinea	Western North Atlantic	9	8	0.6609	0.0010	4	6	0.7783	0.0060	4	2	0.6814	0.0659
Reunion	Seychelles	28	36	0.0048	0.0010	13	28	0.0176	0.0519	15	8	0.0763	0.0170
Reunion	Sierra Leone	28	1	0.1589	1.0000	13	1	0.2673	0.1113	NA	NA	NA	NA
Reunion	South Africa	28	22	0.0033	0.0230	13	9	-0.0174	0.9251	15	12	0.0469	0.0440
Reunion	Sri Lanka	28	12	0.0032	0.0809	13	7	0.0037	0.3666	15	5	0.1078	0.0190
Reunion	Thailand	28	5	0.0030	0.2380	13	3	0.0052	0.3826	15	2	-0.1061	0.8256
Reunion	Western North Atlantic	28	8	0.6485	0.0010	13	6	0.7150	0.0010	15	2	0.6998	0.0074
Seychelles	Sierra Leone	36	1	0.1641	1.0000	28	1	0.1876	0.0771	NA	NA	NA	NA
Seychelles	South Africa	36	22	0.0005	0.3297	28	9	-0.0155	0.8911	8	12	0.0508	0.0589
Seychelles	Sri Lanka	36	12	0.0002	0.4555	28	7	0.0014	0.3610	8	5	0.0433	0.2150
Seychelles	Thailand	36	5	0.0046	0.1049	28	3	0.0140	0.2630	8	2	NA	NA
Seychelles	Western North Atlantic	36	8	0.6475	0.0010	28	6	0.6982	0.0010	8	2	0.6547	0.0334
Sierra Leone	South Africa	1	22	0.1491	1.0000	1	9	0.1700	0.1172	NA	NA	NA	NA
Sierra Leone	Sri Lanka	1	12	0.1553	1.0000	1	7	0.1404	0.3857	NA	NA	NA	NA
Sierra Leone	Thailand	1	5	0.1549	1.0000	1	3	0.1502	0.3541	NA	NA	NA	NA
Sierra Leone	Western North Atlantic	1	8	0.6399	1.0000	1	6	0.8145	0.1359	NA	NA	NA	NA
South Africa	Sri Lanka	22	12	0.0005	0.3646	9	7	-0.0370	0.9770	12	5	0.0427	0.1808
South Africa	Thailand	22	5	-0.0017	0.6863	9	3	-0.0198	0.6372	12	2	-0.0818	0.8021
South Africa	Western North Atlantic	22	8	0.6488	0.0010	9	6	0.7243	0.0020	12	2	0.6531	0.0196
Sri Lanka	Thailand	12	5	-0.0005	0.5654	7	3	-0.0284	0.7233	5	2	-0.0471	0.6104
Sri Lanka	Western North Atlantic	12	8	0.6531	0.0010	7	6	0.7239	0.0020	5	2	0.6795	0.0525
Thailand	Western North Atlantic	5	8	0.6580	0.0030	3	6	0.7358	0.0080	2	2	0.6492	0.3257

8.11.2 Individual-based tests by Site

```
pop.levels <- c("Costa Rica" ,"Brazil", "Caribbean Sea",  "Gulf of Mexico",
                "Western North Atlantic",  "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")

gl <- BS.dartcap.gl
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names)]

gl$other$ind.metrics$`TL (mm)` <- as.integer(gl$other$ind.metrics$`TL (mm)`)
gl <- gl[(gl$other$ind.metrics$`TL (mm)` > 1500 &
            !is.na(gl$other$ind.metrics$`TL (mm)`)) | gl$pop == "Fiji",] #Because all Fiji samples w
gl <- gl[!gl$other$ind.metrics$Site %in% c("Caribbean Sea", "Sierra Leone",
                                           "Indonesia", "Japan"),] #need at least 2 samples per grou
Pop <- gl$pop

table( gl$other$ind.metrics$Site, gl$other$ind.metrics$COMBINED_SEX)

df <- as.data.frame(gl)
df[df == 0] <- 11
df[df == 1] <- 12
df[df == 2] <- 22
dat <- data.frame(as.character(Pop) , df)
sex <- gl$other$ind.metrics$Sex
dat <- dat[sex != "U",]
sex <- sex[sex != "U"]

FST <- hierfstat::sexbias.test(dat, sex, nperm = 100,
                               test = "FST",alternative = "two.sided")
#for mean you need at least 2 individuals per group
FIS <- hierfstat::sexbias.test(dat, sex, nperm = 100,
                               test = "FIS",alternative = "two.sided")
#for mean you need at least 2 individuals per group
mAIc <- hierfstat::sexbias.test(dat, sex, nperm = 100,
                                test = "mAIc",alternative = "two.sided")
#for mean you need at least 2 individuals per group
vAIc <- hierfstat::sexbias.test(dat, sex, nperm = 100,
                                test = "vAIc",alternative = "two.sided")
#for mean you need at least 2 individuals per group

aic <- hierfstat::AIc(dat)
plot.data <- data.frame(sex, aic)
rownames(plot.data) <- rownames(dat)

save(FST, FIS, mAIc, vAIc, aic, plot.data,
     file = "DArTcap_ALL_Aic_sex_Sites_OnlyAdults.Rdata")
```

```
load("DArTcap_ALL_Aic_sex_Sites_OnlyAdults.Rdata")

print(FST)
print(FIS)
print(mAIc)
print(vAIc)
```

```r
sex <- plot.data$sex
aic.F <- aic[sex == "F"]
aic.M <- aic[sex == "M"]

maic.F <- mean(aic.F, na.rm = TRUE)
maic.M <- mean(aic.M, na.rm = TRUE)
vaic.F <- var(aic.F, na.rm = TRUE)
vaic.M <- var(aic.M, na.rm = TRUE)


df <- data.frame(INDIVIDUALS = BS.dartcap.gl$ind.names,
                 pop = BS.dartcap.gl$other$ind.metrics$Site)
test.data <- data.frame(INDIVIDUALS = rownames(plot.data),plot.data,
                        stringsAsFactors = FALSE)

test.data %<>% dplyr::left_join(df, by = "INDIVIDUALS")
plot.data <- test.data
pop.levels <- c("Gulf of Mexico", "Western North Atlantic","Mozambique",
                "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Australia", "Fiji")
plot.data$pop <- factor(plot.data$pop, levels = pop.levels)

aic.plot <- ggplot2::ggplot() +
  ggplot2::geom_histogram(data = subset(plot.data, sex == "F"),
                          ggplot2::aes(aic, fill = "F", y = ..count..),
                          binwidth = 5) +
  ggplot2::geom_histogram(data = subset(plot.data, sex == "M"),
                          ggplot2::aes(aic, fill = "M", y = -..count..),
                          binwidth = 5) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::scale_fill_manual(values = c("#E69F00", "#56B4E9"),
                             labels = c("Female", "Male")) +
  ggplot2::labs(x = "Corrected assignment index",
                y = "Number of individuals",
                fill = "") +
  ggplot2::facet_grid(pop~., scales = "free_y") +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text.x = ggplot2::element_text(size = 10, angle = 0, face = "bold"),
    axis.text.y = ggplot2::element_text(size = 10, angle = 0, face = "bold"),
    axis.title = ggplot2::element_text(size = 15),
    legend.text = ggplot2::element_text(hjust = 0, size = 15),
    legend.title = ggplot2::element_text(hjust = 0, size = 15),
    strip.text.y = element_text(angle = 0,size = 10)
  )
print(aic.plot)
```



8.11.2.1 Individual assignment

```
ggplot2::ggsave(plot = aic.plot,
                filename = "DArTcap_ALL_Aic_sex_Sites_OnlyAdults3.png",
       width = 30, height = 20, units = "cm")

res <- plot.data[(plot.data$pop == "Arabian Sea" & plot.data$aic < 0 &
                    !is.na(plot.data$aic)) |
                 (plot.data$pop == "Australia" & plot.data$aic < (-106) &
                    !is.na(plot.data$aic)) |
                 (plot.data$pop == "Fiji" & plot.data$aic < (-100) &
                    !is.na(plot.data$aic)), ]

knitr::kable(res, digits = 4,
             caption = "Individuals with low population assignment indices") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 9,
                            latex_options = c( "hold_position"))
```

```
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "FST",
##     alternative = "two.sided")
##
## $statistic
## [1] 0.02967566
##
## $p.value
## [1] 1
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "FIS",
##     alternative = "two.sided")
##
## $statistic
```

```
## [1] 0.01131135
##
## $p.value
## [1] 0.63
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "mAIc",
##     alternative = "two.sided")
##
## $statistic
## [1] 0.5283601
##
## $p.value
## [1] 0.48
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "vAIc",
##     alternative = "two.sided")
##
## $statistic
## [1] 1.386015
##
## $p.value
## [1] 0.12
```

Table 27: Individuals with low population assignment indices

	INDIVIDUALS	sex	aic	pop
58	CL-ARS012-F	F	-9.2111	Arabian Sea
147	CLSH047-F	F	-118.9014	Australia
153	CLSH055-M	M	-116.2028	Australia
157	CLSH059-F	F	-119.5633	Australia
173	CL-FIJ005-F.1	F	-146.8808	Fiji
186	CL-FIJ021-F	F	-253.5579	Fiji
187	CL-FIJ022-F	F	-292.7706	Fiji
188	CL-FIJ023-F	F	-138.5194	Fiji
189	CL-FIJ024-F	F	-116.8141	Fiji
190	CL-FIJ026-F	F	-162.5851	Fiji
191	CL-FIJ027-F	F	-132.5392	Fiji
192	CL-FIJ029-F	F	-195.0195	Fiji
193	CL-FIJ031-F	F	-208.0313	Fiji

```
strata <- BS.dartcap.gt@schemes$Site
names(strata) <- BS.dartcap.gt@schemes$INDIVIDUALS
strataG::setStrata(BS.dartcap.gt) <- strata

BS.dartcap.gt@schemes$`TL (mm)` <- as.integer(BS.dartcap.gt@schemes$`TL (mm)`)
gt.all.F <- BS.dartcap.gt[BS.dartcap.gt@schemes$COMBINED_SEX == "F" &
                                     (BS.dartcap.gt@schemes$`TL (mm)` > 1500 &
                                     !is.na(BS.dartcap.gt@schemes$`TL (mm)`)|
                                       BS.dartcap.gt@schemes$Site == "Fiji"),]
gt.all.M <- BS.dartcap.gt[BS.dartcap.gt@schemes$COMBINED_SEX == "M" &
                                     BS.dartcap.gt@schemes$ `TL (mm)` > 1500 &
                                     (!is.na(BS.dartcap.gt@schemes$`TL (mm)`)|
                                        BS.dartcap.gt@schemes$Site == "Fiji"),]

Fst.all.pop.F <-
```

```
  strataG::popStructTest(
    gt.all.F,
    nrep = 1000,
    stats = c("fst", "fis"),
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )
Fst.all.pop.M <-
  strataG::popStructTest(
    gt.all.M,
    nrep = 1000,
    stats = c("fst", "fis"),
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.all.pop.F, Fst.all.pop.M, file = "DArTcap_ALL_Fst_sex_Site2.Rdata")
```

```
load("DArTcap_ALL_Fst_sex_Site2.Rdata")
dim(Fst.all.pop.F$pairwise$result) #91  8
dim(Fst.all.pop.M$pairwise$result) #66  8

names.1 <- paste0(Fst.all.pop.F$pairwise$result$strata.1,"_",
                  Fst.all.pop.F$pairwise$result$strata.2)
names.2 <- paste0(Fst.all.pop.M$pairwise$result$strata.1,"_",
                  Fst.all.pop.M$pairwise$result$strata.2)

result.1 <- Fst.all.pop.F$pairwise$result
result.1$names.comb <- names.1
result.2 <- Fst.all.pop.M$pairwise$result
result.2$names.comb <- names.2

data <- left_join(result.1,result.2, by = "names.comb" )

pwFst.FM <- data[,c(1:6, 12:15)]
colnames(pwFst.FM) <- c("strata.1", "strata.2", "n.auDNA.F.1", "n.auDNA.F.2",
                        "Fst.auDNA.F", "Fst.auDNA.F.Pval",
                     "n.auDNA.M.1", "n.auDNA.M.2", "Fst.auDNA.M",
                     "Fst.auDNA.M.Pval")
knitr::kable(pwFst.FM, digits = 4,
             caption = "Pairwise Fst between females and males for autosomal markers") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

8.11.2.2 Fst test

```
## [1] 36  8
## [1] 21  8
```

Table 28: Pairwise Fst between females and males for autosomal markers

strata.1	strata.2	n.auDNA.F.1	n.auDNA.F.2	Fst.auDNA.F	Fst.auDNA.F.Pval	n.auDNA.M.1	n.auDNA.M.2	Fst.auDNA.M	Fst.auDNA.M.Pval
Arabian Sea	Australia	12	48	0.0016	0.1199	NA	NA	NA	NA
Arabian Sea	Brazil	12	29	0.6526	0.0010	NA	NA	NA	NA
Arabian Sea	Fiji	12	5	0.0288	0.0010	NA	NA	NA	NA
Arabian Sea	Japan	12	2	NA	NA	NA	NA	NA	NA
Arabian Sea	Mozambique	12	3	NA	NA	NA	NA	NA	NA
Arabian Sea	Reunion	12	1	NA	NA	NA	NA	NA	NA
Arabian Sea	Seychelles	12	4	-0.0050	0.8452	NA	NA	NA	NA
Arabian Sea	South Africa	12	11	0.0033	0.0699	NA	NA	NA	NA
Australia	Brazil	48	29	0.6449	0.0010	62	10	0.6375	0.0010
Australia	Fiji	48	5	0.0292	0.0010	62	4	NA	NA
Australia	Japan	48	2	NA	NA	NA	NA	NA	NA
Australia	Mozambique	48	3	NA	NA	62	1	NA	NA
Australia	Reunion	48	1	NA	NA	NA	NA	NA	NA
Australia	Seychelles	48	4	-0.0020	0.6863	62	3	0.0085	0.0570
Australia	South Africa	48	11	0.0047	0.0020	62	2	NA	NA
Brazil	Fiji	29	5	0.6589	0.0011	10	4	0.6483	0.0034
Brazil	Japan	29	2	0.6688	0.0444	NA	NA	NA	NA
Brazil	Mozambique	29	3	0.6553	0.0055	10	1	NA	NA
Brazil	Reunion	29	1	NA	NA	NA	NA	NA	NA
Brazil	Seychelles	29	4	0.6572	0.0014	10	3	0.6580	0.0079
Brazil	South Africa	29	11	0.6546	0.0010	10	2	0.6600	0.0755
Fiji	Japan	5	2	NA	NA	NA	NA	NA	NA
Fiji	Mozambique	5	3	0.0214	0.0334	4	1	NA	NA
Fiji	Reunion	5	1	NA	NA	NA	NA	NA	NA
Fiji	Seychelles	5	4	0.0150	0.0300	4	3	0.0318	0.0545
Fiji	South Africa	5	11	0.0240	0.0030	4	2	0.0306	0.2331
Japan	Mozambique	2	3	0.0687	0.1755	NA	NA	NA	NA
Japan	Reunion	2	1	0.2182	0.3297	NA	NA	NA	NA
Japan	Seychelles	2	4	0.0917	0.0904	NA	NA	NA	NA
Japan	South Africa	2	11	NA	NA	NA	NA	NA	NA
Mozambique	Reunion	3	1	NA	NA	NA	NA	NA	NA
Mozambique	Seychelles	3	4	NA	NA	1	3	NA	NA
Mozambique	South Africa	3	11	NA	NA	1	2	0.0748	0.3377
Reunion	Seychelles	1	4	NA	NA	NA	NA	NA	NA
Reunion	South Africa	1	11	NA	NA	NA	NA	NA	NA
Seychelles	South Africa	4	11	-0.0088	0.9590	3	2	0.0418	0.1094

```
pwFis.FM <- data[,c(1:4,7:8, 12:13,16:17)]
colnames(pwFis.FM) <- c("strata.1", "strata.2", "n.auDNA.F.1", "n.auDNA.F.2",
                        "Fis.auDNA.F", "Fis.auDNA.F.Pval",
                     "n.auDNA.M.1", "n.auDNA.M.2", "Fis.auDNA.M",
                     "Fis.auDNA.M.Pval")
knitr::kable(pwFis.FM, digits = 4,
             caption = "Pairwise Fis between females and males for autosomal markers") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

8.11.2.3 Fis test

Table 29: Pairwise Fis between females and males for autosomal markers

strata.1	strata.2	n.auDNA.F.1	n.auDNA.F.2	Fis.auDNA.F	Fis.auDNA.F.Pval	n.auDNA.M.1	n.auDNA.M.2	Fis.auDNA.M	Fis.auDNA.M.Pval
Arabian Sea	Australia	12	48	-9.0058	0.1858	NA	NA	NA	NA
Arabian Sea	Brazil	12	29	-9.0370	1.0000	NA	NA	NA	NA
Arabian Sea	Fiji	12	5	-125.9573	1.0000	NA	NA	NA	NA
Arabian Sea	Japan	12	2	NA	NA	NA	NA	NA	NA
Arabian Sea	Mozambique	12	3	NA	NA	NA	NA	NA	NA
Arabian Sea	Reunion	12	1	NA	NA	NA	NA	NA	NA
Arabian Sea	Seychelles	12	4	367.8651	0.6845	NA	NA	NA	NA
Arabian Sea	South Africa	12	11	-17.2164	0.9111	NA	NA	NA	NA
Australia	Brazil	48	29	-5.1005	1.0000	62	10	-6.2749	1.0000
Australia	Fiji	48	5	-17.6149	1.0000	62	4	NA	NA
Australia	Japan	48	2	NA	NA	NA	NA	NA	NA
Australia	Mozambique	48	3	NA	NA	62	1	NA	NA
Australia	Reunion	48	1	NA	NA	NA	NA	NA	NA
Australia	Seychelles	48	4	-22.5505	0.6372	62	3	-43.3537	0.9922
Australia	South Africa	48	11	-9.6001	0.3437	62	2	NA	NA
Brazil	Fiji	29	5	-25.5253	1.0000	10	4	NA	NA
Brazil	Japan	29	2	NA	NA	NA	NA	NA	NA
Brazil	Mozambique	29	3	NA	NA	10	1	NA	NA
Brazil	Reunion	29	1	NA	NA	NA	NA	NA	NA
Brazil	Seychelles	29	4	-36.1107	1.0000	10	3	20.0861	0.1136
Brazil	South Africa	29	11	-9.8749	1.0000	10	2	NA	NA
Fiji	Japan	5	2	NA	NA	NA	NA	NA	NA
Fiji	Mozambique	5	3	NA	NA	4	1	NA	NA
Fiji	Reunion	5	1	NA	NA	NA	NA	NA	NA
Fiji	Seychelles	5	4	15.6026	0.4627	4	3	NA	NA
Fiji	South Africa	5	11	-662.8514	0.9960	4	2	NA	NA
Japan	Mozambique	2	3	NA	NA	NA	NA	NA	NA
Japan	Reunion	2	1	NA	NA	NA	NA	NA	NA
Japan	Seychelles	2	4	NA	NA	NA	NA	NA	NA
Japan	South Africa	2	11	NA	NA	NA	NA	NA	NA
Mozambique	Reunion	3	1	NA	NA	NA	NA	NA	NA
Mozambique	Seychelles	3	4	NA	NA	1	3	NA	NA
Mozambique	South Africa	3	11	NA	NA	1	2	NA	NA
Reunion	Seychelles	1	4	NA	NA	NA	NA	NA	NA
Reunion	South Africa	1	11	NA	NA	NA	NA	NA	NA
Seychelles	South Africa	4	11	106.2843	0.6607	3	2	NA	NA

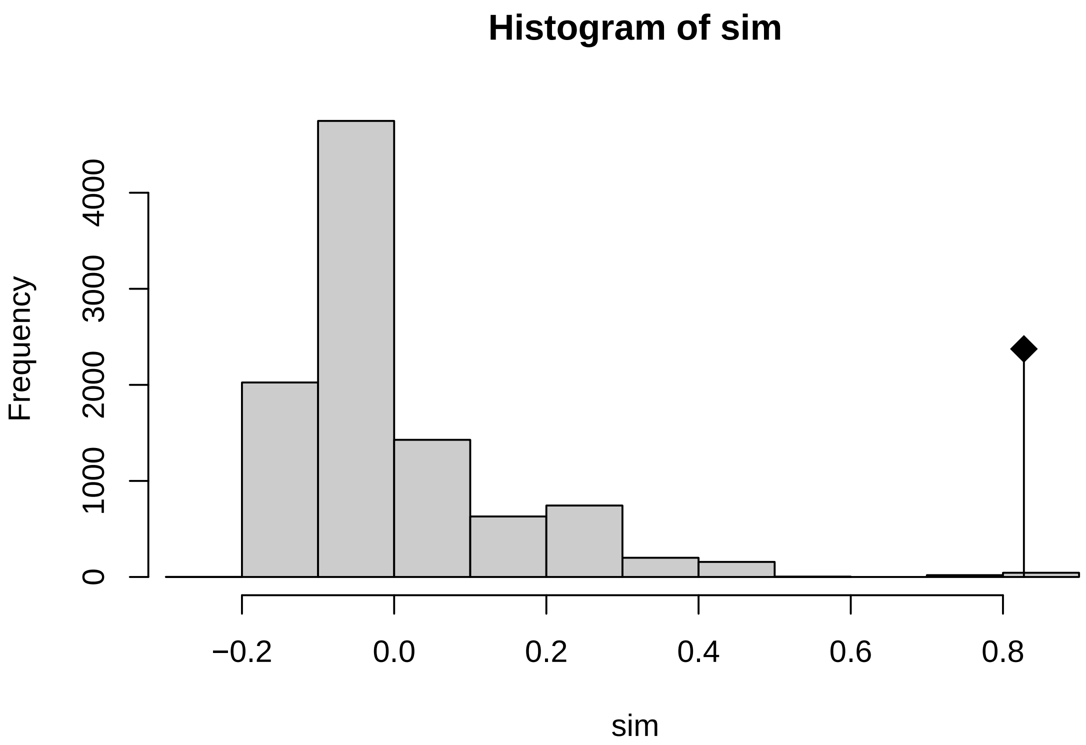
8.11.2.4 Spatial correlation

Test the correlation between the genetic and geographic distance between the sampling sites. The genetic distance is calculated based on Fst and Euclidean distance.

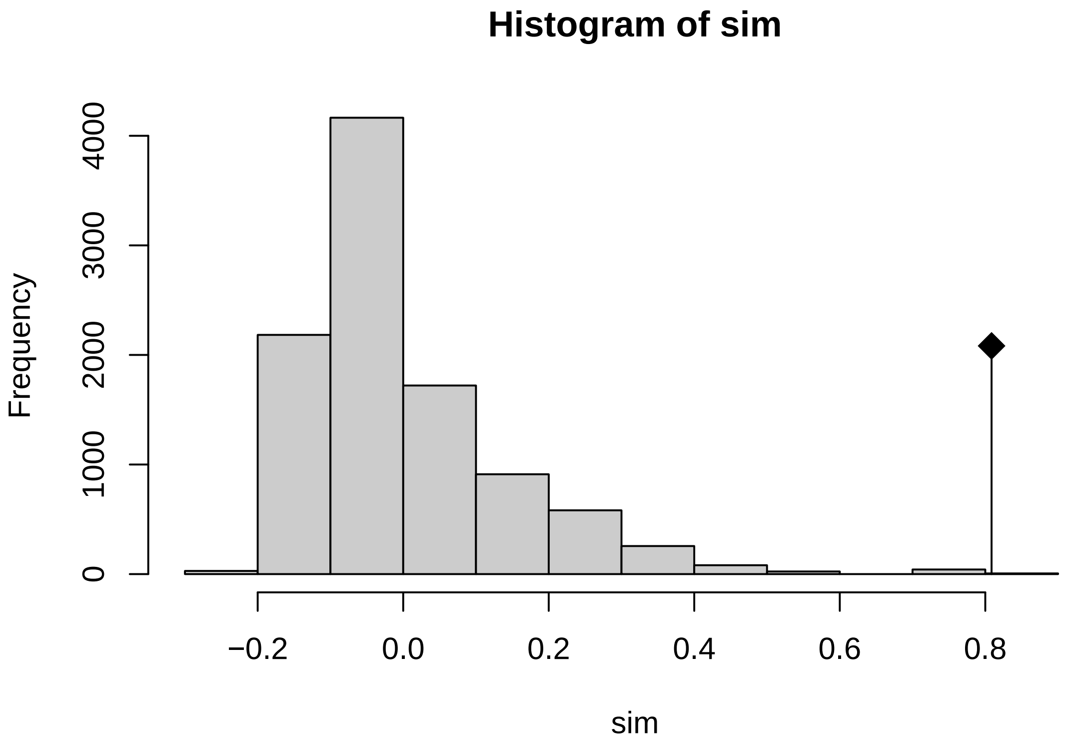
```
# geographic file that contain coordinates of the 8 sampling locations
coord.sites <- readr::read_csv(file = "Least_cost_distance_Sites.csv")
coord.sites <- coord.sites[!coord.sites$Site %in% c("Costa.Rica", "Brazil",
                                                    "Caribbean.Sea", "Sierra.Leone",
                                                    "South.Africa", "Thailand",
                                                    "Indonesia", "Papua.New.Guinea",
                                                    "Japan"),]

world <- marmap::getNOAA.bathy(lon1 = -180, lon2 = 180, lat1 = -90, lat2 = 90,
                               resolution = 10) #Res 10 good for calculating a least cost path

dist.sites <- round(fossil::earth.dist(as.matrix(coord.sites[,-1])), 0)
trans1 <- marmap::trans.mat(world)
lc.dist.sites1 <- round(marmap::lc.dist(trans1, as.matrix(coord.sites[,-1]),
                                        res = "dist"), 0)
trans2 <- marmap::trans.mat(world,min.depth=-1, max.depth=-200)
lc.dist.sites2 <- round(marmap::lc.dist(trans2, as.matrix(coord.sites[,-1]),
                                        res = "dist"), 0)



pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea",  "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")
gl <- BS.dartcap.gl
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl$other$ind.metrics$`TL (mm)` <- as.integer(gl$other$ind.metrics$`TL (mm)`)
gl <- gl[(gl$other$ind.metrics$`TL (mm)` > 1500 &
            !is.na(gl$other$ind.metrics$`TL (mm)`)) | gl$pop == "Fiji",] #Because all Fiji samples w
gl <- gl[!gl$other$ind.metrics$Site %in% c("Caribbean Sea", "Sierra Leone",
                                           "Indonesia", "Japan"),] #need at least 2 samples per grou
table(gl$pop, gl$other$ind.metrics$COMBINED_SEX)
gl.F <- gl[gl@other$ind.metrics$COMBINED_SEX == "F",]
gl.M <- gl[gl@other$ind.metrics$COMBINED_SEX == "M",]

gi.F <- gl2gi_mvb(gl.F)
gi.M <- gl2gi_mvb(gl.M)
gpop <- adegenet::genind2genpop(gi.F)
Eucl.D.F <- adegenet::dist.genpop(gpop,method = 2) #method 2 Euclidean = Angular distance
gpop <- adegenet::genind2genpop(gi.M)
Eucl.D.M <- adegenet::dist.genpop(gpop,method = 2) #method 2 Euclidean = Angular distance

save(world, dist.sites, lc.dist.sites1, lc.dist.sites2, Eucl.D.F,
     Eucl.D.M, file = "DArTcap_ALL_autocorr_by_sex_Sites2.Rdata")
```

```
load("DArTcap_ALL_autocorr_by_sex_Sites2.Rdata")
load("DArTcap_ALL_autocorr_by_sex_Sites.Rdata")

Dgeo <- lc.dist.sites1
Dgen.F <- Eucl.D.F
Dgen.M <- Eucl.D.M
```

```
fst.test.F <- ade4::mantel.randtest(Dgen.F, Dgeo, nrepet = 10000)
plot(fst.test.F)
```

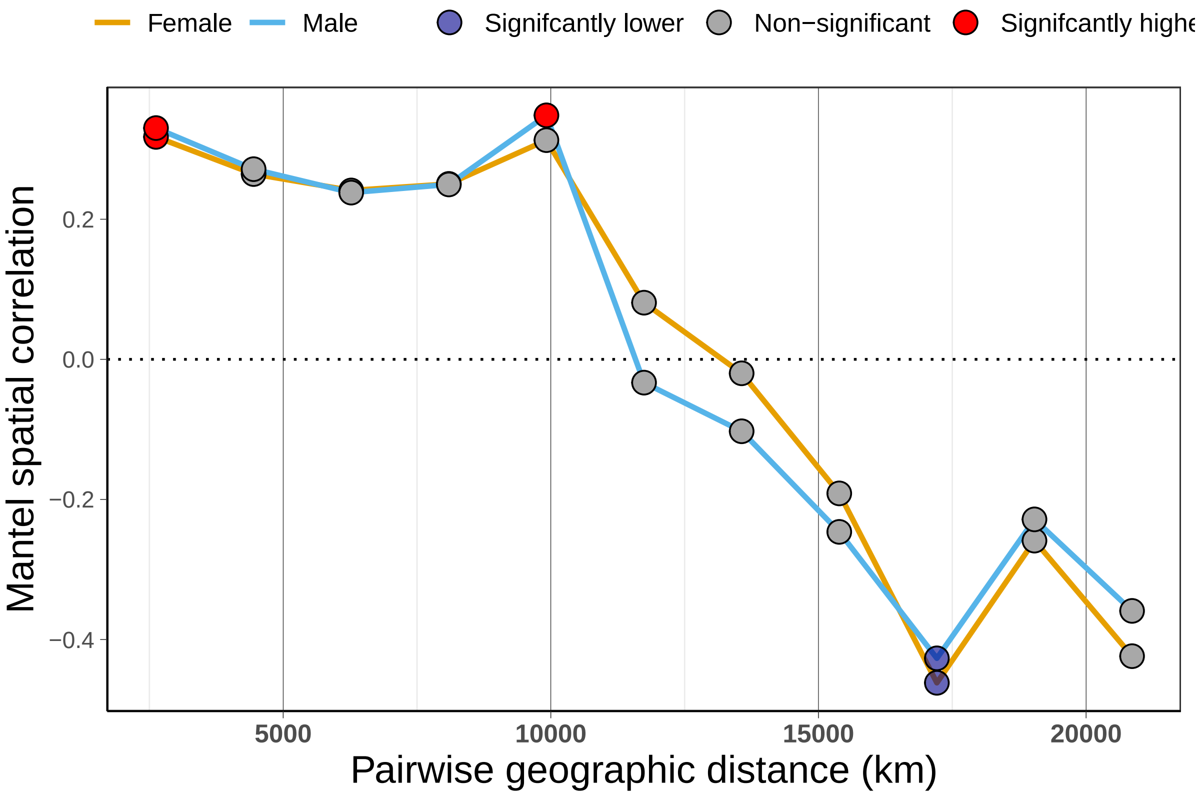


```
fst.test.F
fst.test.M <- ade4::mantel.randtest(Dgen.M, Dgeo, nrepet = 10000)
plot(fst.test.M)
```



```
fst.test.M

corr.test.F <- vegan::mantel.correlog(
  Dgen.F, D.geo = Dgeo, XY = NULL, n.class = 11, break.pts = NULL,
  cutoff = FALSE, r.type = "pearson", nperm = 10000, mult = "holm",
  progressive = TRUE)
corr.test.F.data <- as.data.frame(corr.test.F$mantel.res)
corr.test.F.data$Sex <- "Female"

corr.test.M <- vegan::mantel.correlog(
  Dgen.M, D.geo = Dgeo, XY = NULL, n.class = 11, break.pts = NULL,
  cutoff = FALSE, r.type = "pearson", nperm = 10000, mult = "holm",
  progressive = TRUE)
corr.test.M.data <- as.data.frame(corr.test.M$mantel.res)
corr.test.M.data$Sex <- "Male"


plot.data <- rbind(corr.test.F.data, corr.test.M.data)

sig <- ifelse(plot.data$Pr.corrected. <= 0.05, "sig", "non-sig")
# sig <- ifelse(plot.data$Pr.Mantel. <= 0.05, "sig", "non-sig")
sig_cat <- sig
sig_cat[sig_cat == "sig" & plot.data$Mantel.cor < 0] <- "Lower"
sig_cat[sig_cat == "sig" & plot.data$Mantel.cor > 0] <- "Higher"
sig_cat[sig_cat == "non-sig"] <- "Neutral"
plot.data$sig <- factor(sig, levels = c("sig", "non-sig"))
plot.data$sig_cat <- factor(sig_cat, levels = c("Lower", "Neutral", "Higher"))


plot <- ggplot2::ggplot(plot.data, ggplot2::aes(x = class.index,
                                                y = Mantel.cor)) +
```

```
  ggplot2::geom_hline(yintercept = 0,
             linetype = "dotted",
             size = 0.5) +
  ggplot2::geom_line(ggplot2::aes(group = Sex, color = Sex),
                     size = 1) +
  ggplot2::geom_point(ggplot2::aes(fill = sig_cat), size = 4,
                      shape = 21) +
  ggplot2::scale_fill_manual(values = c(alpha("darkblue", 0.6),
                                        gray.colors(12)[6], "red"),
                             labels = c("Signifcantly lower",
                                        "Non-significant",
                                        "Signifcantly higher")) +
  ggplot2::scale_color_manual(values = c("#E69F00", "#56B4E9")) +
  ggplot2::theme_bw() +
  ggplot2::theme(
    panel.background = ggplot2::element_rect(color = "white", fill = "white"),
    panel.grid.major.x = ggplot2::element_line(size = 0.1, color = "black"),
    axis.line = ggplot2::element_line(color = "black", size = 0.35),
    axis.text.x = ggplot2::element_text(size = 10, angle = 0, face = "bold"),
    axis.title = ggplot2::element_text(size = 15),
    axis.ticks = ggplot2::element_line(size = 0.15),
    legend.text = ggplot2::element_text(hjust = 0, size = 10),
    legend.title = ggplot2::element_text(hjust = 0, size = 10),
    panel.grid.major.y = ggplot2::element_blank(),
    panel.grid.minor.y = ggplot2::element_blank(),
    legend.position = "top",
    strip.text = ggplot2::element_text(size = 10)
  ) +
  # ggplot2::labs(title = "Euclidean distance") +
  ggplot2::xlab("Pairwise geographic distance (km)") +
  ylab("Mantel spatial correlation") +
  ggplot2::guides(
    fill = ggplot2::guide_legend(title = ""),
    color = ggplot2::guide_legend(title = "")
  )
print(plot)
```



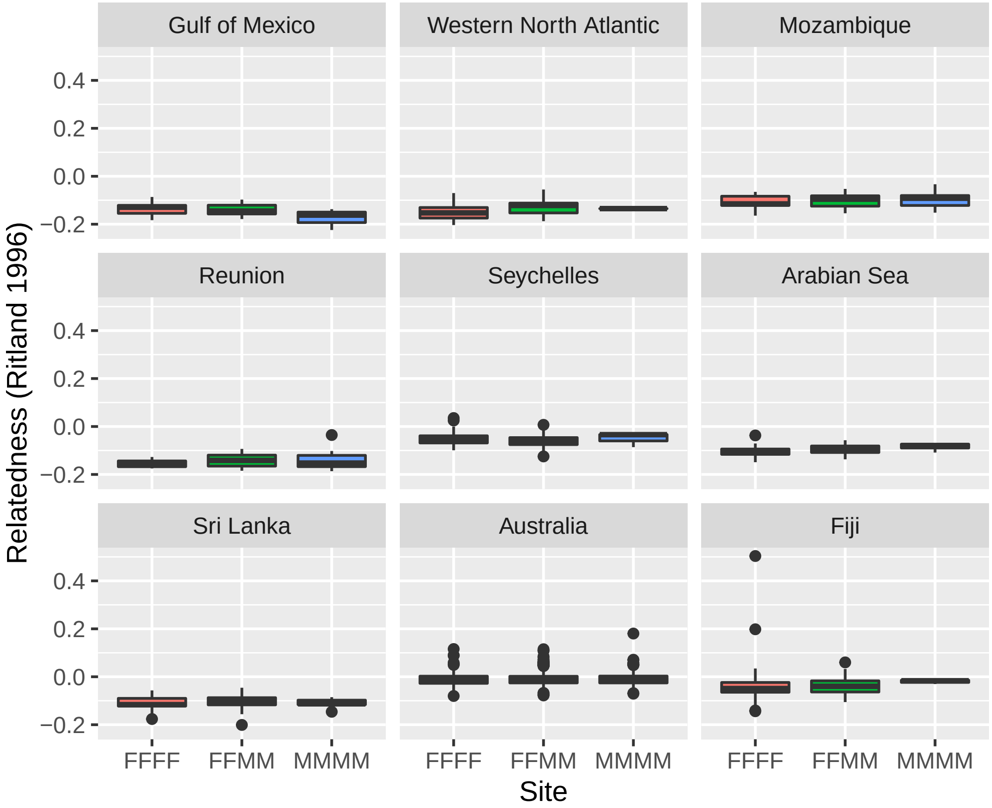
```
ggplot2::ggsave(plot = plot,
                filename = "DArTcap_ALL_autocorr_by_sex_Sites_EUCL_FM3.png",
       width = 30, height = 15, units = "cm")
```

```
## Monte-Carlo test
## Call: ade4::mantel.randtest(m1 = Dgen.F, m2 = Dgeo, nrepet = 10000)
##
## Observation: 0.827511
##
## Based on 10000 replicates
## Simulated p-value: 0.00019998
## Alternative hypothesis: greater
##
##       Std.Obs   Expectation      Variance
##  5.700761e+00 -7.302451e-05  2.107456e-02
## Monte-Carlo test
## Call: ade4::mantel.randtest(m1 = Dgen.M, m2 = Dgeo, nrepet = 10000)
##
## Observation: 0.8086319
##
## Based on 10000 replicates
## Simulated p-value: 0.00039996
## Alternative hypothesis: greater
##
##       Std.Obs   Expectation      Variance
##  5.7551025251 -0.0002985323  0.0197567815
```

```
gl <- BS.dartcap.gl
pop.levels <- c("Costa Rica" ,"Brazil", "Caribbean Sea",  "Gulf of Mexico",
                "Western North Atlantic",  "Sierra Leone", "South Africa",
```

```
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Australia", "Japan", "Fiji")
gl <- BS.dartcap.gl
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names)]
gl$other$ind.metrics$`TL (mm)` <- as.integer(gl$other$ind.metrics$`TL (mm)`)
gl <- gl[(gl$other$ind.metrics$`TL (mm)` > 1500 &
            !is.na(gl$other$ind.metrics$`TL (mm)`)) | gl$pop == "Fiji",] #Because all Fiji samples w
gl <- gl[!gl$other$ind.metrics$Site %in% c("Caribbean Sea", "Sierra Leone", "Indonesia",
                                           "Japan"),] #need at least 2 samples per group
gl$other$loc.metrics.flags$monomorphs <- FALSE
gl$other$loc.metrics.flags$CallRate  <- FALSE


gl2rel <- function(gl, filename = "relate"){
  group.name <- paste(gl$other$ind.metrics$COMBINED_SEX,
                      gl$other$ind.metrics$COMBINED_SEX, "_",
                      gl$ind.names, sep = "")
  glmat <- as.matrix(gl)
  glmat[glmat==0] <- '2 2'
  glmat[glmat==1] <- '1 2'
  glmat[glmat==2] <- '1 1'
  glmat[is.na(glmat)] <- '0 0'
  df <- cbind(group.name, glmat)
  write.table(df, file = paste0(filename,".txt", sep = ""), quote = FALSE,
              sep = " ", row.names = FALSE, col.names = FALSE)
}


res.rel <- list()
summ.rel <- data.frame(sex.group = c("FF", "FM", "MM"))
plot.data <- data.frame(pair.no = NA,ind1.id = NA,ind2.id = NA, group = NA,
                        condition = NA, measurement = NA,Site = NA)
for (i in 1:nlevels(gl$pop)) {
  print(i)
  gl.tmp <- gl[gl$pop == levels(gl$pop)[i],]
  gl.tmp <- dartR::gl.filter.callrate(gl.tmp, method = 'loc', threshold = 1,
                                      mono.rm = TRUE, plot = FALSE, verbose = 0)

  gl2rel(gl.tmp, filename = "relate")
  data <- related::readgenotypedata("relate.txt")
  outfile <- related::coancestry (data$gdata , lynchli = 1, lynchrd = 1,
                                  quellergt = 1, wang = 1, ritland = 1)
  res <- outfile$relatedness[!outfile$relatedness$group %in%
                               c("FFUU","UUUU","MMUU","UUFF", "UUMM"),]
  res$group[res$group == "MMFF"] <- "FFMM"
  data_long <- gather(res, condition, measurement, 5:11, factor_key=TRUE)
  data_long$Site <- levels(gl$pop)[i]
  plot.data <- rbind(plot.data, data_long)
  summ <- dplyr::group_by(res, group) %>%
    dplyr::summarise(mean(ritland))
  colnames(summ) <- c("sex.group", levels(gl$pop)[i])
  summ.rel <- cbind(summ.rel, summ[,2])
  res.rel[[i]] <- res
}
plot.data <- plot.data[-1,]
save(res.rel,summ.rel,plot.data, file = "DArTcap_ALL_relatedness_sex_Site2.Rdata")
```

```
load("DArTcap_ALL_relatedness_sex_Site2.Rdata")
pop.levels <- c("Gulf of Mexico", "Western North Atlantic",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Australia", "Fiji")
plot.data$Site <- factor(plot.data$Site, levels = pop.levels)
plot.data <- plot.data[plot.data$condition == "ritland",]
plot <- ggplot2::ggplot(plot.data, ggplot2::aes(x = group,
                                                y = measurement,
                                                fill = group)) +
  ggplot2::geom_boxplot() +
  ggplot2::facet_wrap(Site~.) +
  ggplot2::labs(x = "Site", y = "Relatedness (Ritland 1996)")
print(plot)
```



8.11.2.5 Relatedness test

```
knitr::kable(summ.rel, digits = 4,
             caption = "Relatedness between female and males according to Ritland (1996)") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

Table 30: Relatedness between female and males according to Ritland (1996)

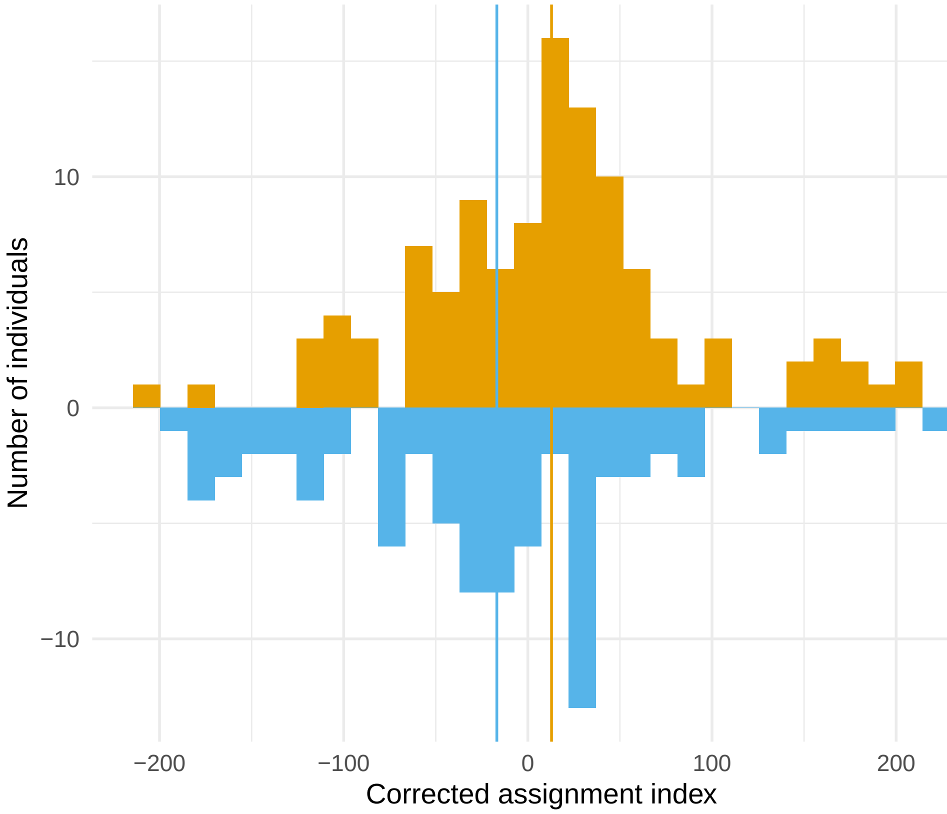
sex.group	Gulf of Mexico	Western North Atlantic	Mozambique	Reunion	Seychelles	Arabian Sea	Sri Lanka	Australia	Fiji
FF	-0.1345	-0.1476	-0.1071	-0.1541	-0.0536	-0.1026	-0.1118	-0.0115	-0.0428
FM	-0.1397	-0.1266	-0.1030	-0.1414	-0.0612	-0.0968	-0.1053	-0.0108	-0.0410
MM	-0.1745	-0.1349	-0.0963	-0.1383	-0.0510	-0.0838	-0.1111	-0.0107	-0.0197

8.11.3 Individual-based tests by Region

```
gl <- BS.dartcap.gl

pop.levels <- c("E-PAC","W-ATL","E-ATL","W-IO","N-IO","E-IO","W-PAC",
                "E-IO/W-PAC", "Japan","Fiji")
gl$pop <- factor(gl$other$ind.metrics$Region, levels = pop.levels)
gl$pop[gl$pop %in% c("E-IO","W-PAC")] <- "E-IO/W-PAC"
pop.levels <- c("E-PAC","W-ATL","E-ATL","W-IO","N-IO","E-IO/W-PAC",
                "Japan","Fiji")
gl$pop <- factor(gl$pop , levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names),]

gl$other$ind.metrics$`TL (mm)` <- as.integer(gl$other$ind.metrics$`TL (mm)`)
gl <- gl[(gl$other$ind.metrics$`TL (mm)` > 1500 &
            !is.na(gl$other$ind.metrics$`TL (mm)`)) | gl$pop == "Fiji",] #Because all Fiji samples w
gl <- gl[!gl$other$ind.metrics$Site %in% c("E-ATL", "Japan"),]
Pop <- gl$pop

table(gl$pop, gl$other$ind.metrics$COMBINED_SEX)

df <- as.data.frame(gl)
df[df == 0] <- 11
df[df == 1] <- 12
df[df == 2] <- 22
dat <- data.frame(as.character(Pop) , df)
sex <- gl$other$ind.metrics$Sex
dat <- dat[sex != "U",]
sex <- sex[sex != "U"]
FST <- hierfstat::sexbias.test(dat, sex, nperm = 100,test = "FST",
                               alternative = "two.sided")
#for mean you need at least 2 individuals per group
FIS <- hierfstat::sexbias.test(dat, sex, nperm = 100,test = "FIS",
                               alternative = "two.sided")
#for mean you need at least 2 individuals per group
mAIc <- hierfstat::sexbias.test(dat, sex, nperm = 100,test = "mAIc",
                                alternative = "two.sided")
#for mean you need at least 2 individuals per group
vAIc <- hierfstat::sexbias.test(dat, sex, nperm = 100,test = "vAIc",
                                alternative = "two.sided")
#for mean you need at least 3 individuals per group

aic <- hierfstat::AIc(dat)
plot.data <- data.frame(sex, aic)
rownames(plot.data) <- rownames(dat)

save(FST, FIS, mAIc, vAIc, aic, plot.data,
     file = "DArTcap_ALL_Aic_sex_Regions_OnlyAdults.Rdata")
```

```
load("DArTcap_ALL_Aic_sex_Regions_OnlyAdults.Rdata")

print(FST)
print(FIS)
print(mAIc)
print(vAIc)

sex <- plot.data$sex
aic.F <- aic[sex == "F"]
aic.M <- aic[sex == "M"]
```

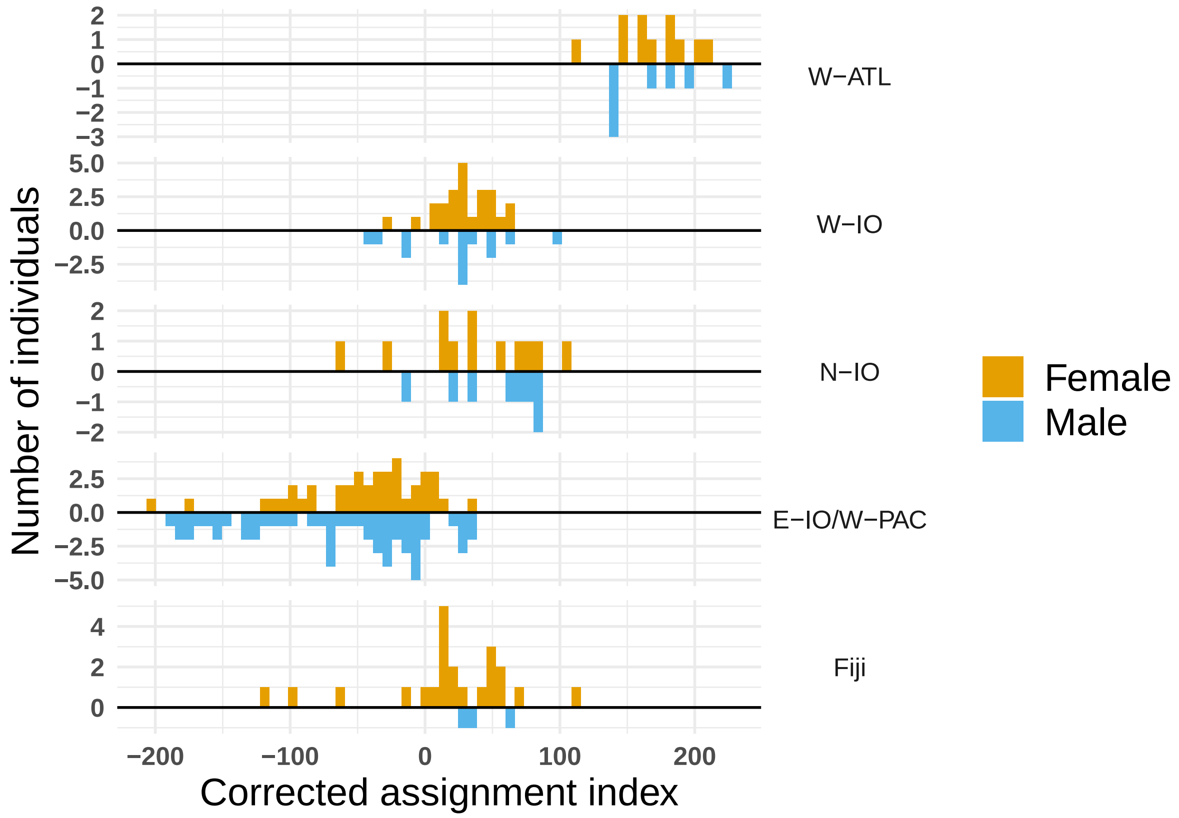
```
maic.F <- mean(aic.F, na.rm = TRUE)
maic.M <- mean(aic.M, na.rm = TRUE)
vaic.F <- var(aic.F, na.rm = TRUE)
vaic.M <- var(aic.M, na.rm = TRUE)

aic.plot <- ggplot2::ggplot() +
  ggplot2::geom_histogram(data = subset(plot.data, sex == "F"),
                          ggplot2::aes(aic, fill = "F", y =  ..count..)) +
  ggplot2::geom_histogram(data = subset(plot.data, sex == "M"),
                          ggplot2::aes(aic, fill = "M", y =  -..count..)) +
  ggplot2::geom_vline(ggplot2::aes(xintercept = maic.F), colour = "#E69F00") +
  ggplot2::geom_vline(ggplot2::aes(xintercept = maic.M), colour = "#56B4E9") +
  ggplot2::scale_fill_manual(values = c("#E69F00", "#56B4E9"),
                             labels = c("Female", "Male")) +
  ggplot2::labs(x = "Corrected assignment index",
                y = "Number of individuals",
                fill = "Sex") +
  ggplot2::theme_minimal()
print(aic.plot)
```



8.11.3.1 Individual assignment

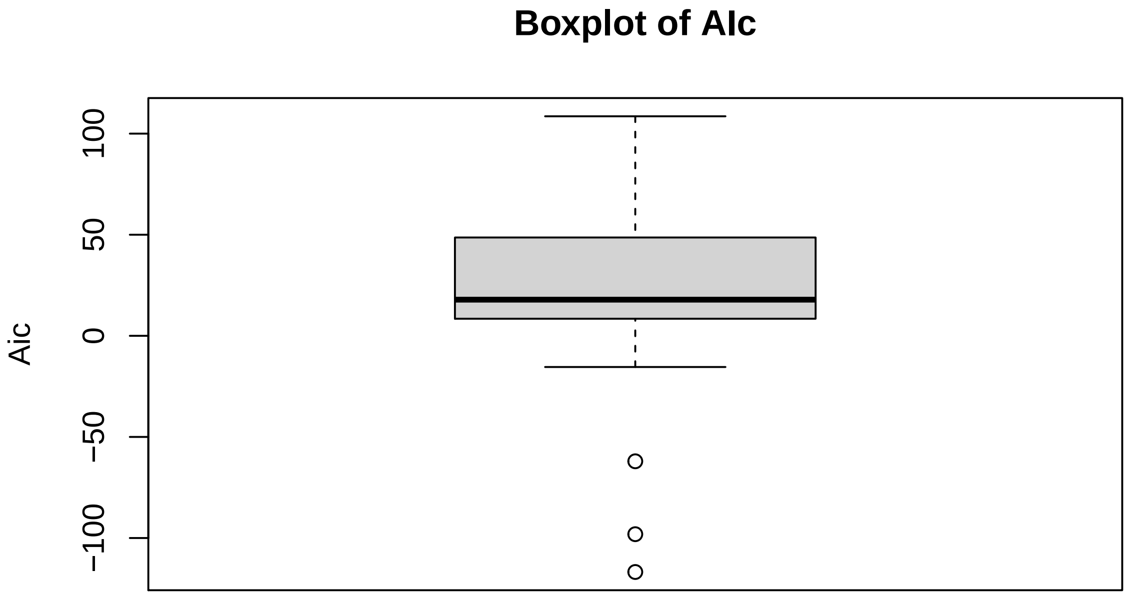
```
region <- BS.dartcap.gl$other$ind.metrics$Region
region[region %in% c("E-IO","W-PAC")] <- "E-IO/W-PAC"
df <- data.frame(INDIVIDUALS = BS.dartcap.gl$ind.names, pop = region)
test.data <- data.frame(INDIVIDUALS = rownames(plot.data),plot.data,
                        stringsAsFactors = FALSE)
test.data %<>% dplyr::left_join(df, by = "INDIVIDUALS")
plot.data <- test.data
pop.levels <- c("W-ATL","W-IO","N-IO","E-IO/W-PAC","Fiji")
plot.data$pop <- factor(plot.data$pop, levels = pop.levels)

aic.plot <- ggplot2::ggplot() +
```

```
  ggplot2::geom_histogram(data = subset(plot.data, sex == "F"),
                          ggplot2::aes(aic, fill = "F", y = ..count..),
                          binwidth = 7) +
  ggplot2::geom_histogram(data = subset(plot.data, sex == "M"),
                          ggplot2::aes(aic, fill = "M", y = -..count..),
                          binwidth = 7) +
  ggplot2::geom_hline(yintercept = 0) +
  ggplot2::scale_fill_manual(values = c("#E69F00", "#56B4E9"),
                             labels = c("Female", "Male")) +
  ggplot2::labs(x = "Corrected assignment index",
                y = "Number of individuals",
                fill = "") +
  ggplot2::facet_grid(pop~., scales = "free_y") +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text.x = ggplot2::element_text(size = 10, angle = 0, face = "bold"),
    axis.text.y = ggplot2::element_text(size = 10, angle = 0, face = "bold"),
    axis.title = ggplot2::element_text(size = 15),
    legend.text = ggplot2::element_text(hjust = 0, size = 15),
    legend.title = ggplot2::element_text(hjust = 0, size = 15),
    strip.text.y = element_text(angle = 0,size = 10)
  )
print(aic.plot)
```



```
ggplot2::ggsave(plot = aic.plot, filename = "DArTcap_ALL_Aic_sex_Regions_OnlyAdults.png",
       width = 30, height = 15, units = "cm")

res <- plot.data[(plot.data$pop == "N-IO" & plot.data$aic < (-50) &
                    !is.na(plot.data$aic)) |
                 (plot.data$pop == "E-IO/W-PAC" & plot.data$aic < (-200) &
                    !is.na(plot.data$aic)) |
```

```
                  (plot.data$pop == "Fiji" & plot.data$aic < (-50) &
                     !is.na(plot.data$aic)), ]
knitr::kable(res, digits = 4,
             caption = "Individuals with low population assignment indices") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 9,
                            latex_options = c( "hold_position")
)


dat <- plot.data$aic[plot.data$sex=="F" & plot.data$pop=="Fiji"]
quantile(dat, 0.025)
boxplot(dat,
  ylab = "Aic",
  main = "Boxplot of AIc"
)
```



```
out <- boxplot.stats(dat)$out
```

```
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "FST",
##     alternative = "two.sided")
##
## $statistic
## [1] -0.02210322
##
## $p.value
## [1] 1
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "FIS",
##     alternative = "two.sided")
```

```
##
## $statistic
## [1] 0.01046105
##
## $p.value
## [1] 0.17
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "mAIc",
##     alternative = "two.sided")
##
## $statistic
## [1] 2.432244
##
## $p.value
## [1] 0.58
##
## $call
## hierfstat::sexbias.test(dat = dat, sex = sex, nperm = 100, test = "vAIc",
##     alternative = "two.sided")
##
## $statistic
## [1] 0.6944592
##
## $p.value
## [1] 0.05
```

Table 31: Individuals with low population assignment indices

	INDIVIDUALS	sex	aic	pop
60	CL-ARS012-F	F	-64.7406	N-IO
149	CLSH047-F	F	-204.4526	E-IO/W-PAC
175	CL-FIJ005-F.1	F	-116.7981	Fiji
188	CL-FIJ021-F	F	-62.0468	Fiji
189	CL-FIJ022-F	F	-98.1071	Fiji

```
##      2.5%
## -106.9853
```

```
strata <- BS.dartcap.gt@schemes$Region
strata[strata %in% c("E-IO","W-PAC")] <- "E-IO/W-PAC"
names(strata) <- BS.dartcap.gt@schemes$INDIVIDUALS
strataG::setStrata(BS.dartcap.gt) <- strata
BS.dartcap.gt@schemes$`TL (mm)` <- as.integer(BS.dartcap.gt@schemes$`TL (mm)`)
gt.all.F <- BS.dartcap.gt[BS.dartcap.gt@schemes$COMBINED_SEX == "F" &
                                     (BS.dartcap.gt@schemes$`TL (mm)` > 1500 &
                                     !is.na(BS.dartcap.gt@schemes$`TL (mm)`)|
                                       BS.dartcap.gt@schemes$Site == "Fiji"),]
gt.all.M <- BS.dartcap.gt[BS.dartcap.gt@schemes$COMBINED_SEX == "M" &
                                     BS.dartcap.gt@schemes$ `TL (mm)` > 1500 &
                                     (!is.na(BS.dartcap.gt@schemes$`TL (mm)`)|
                                        BS.dartcap.gt@schemes$Site == "Fiji"),]

Fst.all.region.F <-
  strataG::popStructTest(
    gt.all.F,
    nrep = 1000,
```

```
    stats = c("fst", "fis"),
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.all.region.F, file = "DArTcap_ALL_Fst_sex_Region.Rdata")
Fst.all.region.M <-
  strataG::popStructTest(
    gt.all.M,
    nrep = 1000,
    stats = c("fst", "fis"),
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.all.region.F, Fst.all.region.M,
     file = "DArTcap_ALL_Fst_sex_Region.Rdata")
```

```
load("DArTcap_ALL_Fst_sex_Region.Rdata")
dim(Fst.all.region.F$pairwise$result) #91  8
dim(Fst.all.region.M$pairwise$result) #66  8

names.1 <- paste0(Fst.all.region.F$pairwise$result$strata.1,"_",
                  Fst.all.region.F$pairwise$result$strata.2)
names.2 <- paste0(Fst.all.region.M$pairwise$result$strata.1,"_",
                  Fst.all.region.M$pairwise$result$strata.2)

result.1 <- Fst.all.region.F$pairwise$result
result.1$names.comb <- names.1
result.2 <- Fst.all.region.M$pairwise$result
result.2$names.comb <- names.2

data <- left_join(result.1,result.2, by = "names.comb" )

pwFst.FM <- data[,c(1:6, 12:15)]
colnames(pwFst.FM) <- c("strata.1", "strata.2", "n.auDNA.F.1", "n.auDNA.F.2",
                        "Fst.auDNA.F", "Fst.auDNA.F.Pval",
                     "n.auDNA.M.1", "n.auDNA.M.2", "Fst.auDNA.M", "Fst.auDNA.M.Pval")
knitr::kable(pwFst.FM, digits = 4,
             caption = "Pairwise Fst between females and males for autosomal markers") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

8.11.3.2 Fst test

```
## [1] 21  8
## [1] 21  8
```

Table 32: Pairwise Fst between females and males for autosomal markers

strata.1	strata.2	n.auDNA.F.1	n.auDNA.F.2	Fst.auDNA.F	Fst.auDNA.F.Pval	n.auDNA.M.1	n.auDNA.M.2	Fst.auDNA.M	Fst.auDNA.M.Pval
E-IO/W-PAC	E-PAC	165	6	NA	NA	176	10	NA	NA
E-IO/W-PAC	Fiji	165	11	0.0288	0.0010	176	7	0.0306	0.0010
E-IO/W-PAC	Japan	165	2	NA	NA	176	2	NA	NA
E-IO/W-PAC	N-IO	165	19	0.0005	0.2517	176	8	0.0020	0.1279
E-IO/W-PAC	W-ATL	165	41	0.6392	0.0010	176	21	0.6365	0.0010
E-IO/W-PAC	W-IO	165	31	0.0018	0.0010	176	13	0.0006	0.2807
E-PAC	Fiji	6	11	NA	NA	10	7	0.6720	0.0010
E-PAC	Japan	6	2	0.7197	0.0796	10	2	NA	NA
E-PAC	N-IO	6	19	NA	NA	10	8	NA	NA
E-PAC	W-ATL	6	41	NA	NA	10	21	NA	NA
E-PAC	W-IO	6	31	NA	NA	10	13	NA	NA
Fiji	Japan	11	2	NA	NA	7	2	NA	NA
Fiji	N-IO	11	19	0.0267	0.0010	7	8	0.0269	0.0010
Fiji	W-ATL	11	41	0.6604	0.0010	7	21	0.6535	0.0010
Fiji	W-IO	11	31	0.0276	0.0010	7	13	0.0258	0.0010
Japan	N-IO	2	19	NA	NA	2	8	0.0447	0.0320
Japan	W-ATL	2	41	0.6704	0.0492	2	21	NA	NA
Japan	W-IO	2	31	NA	NA	2	13	0.0363	0.0177
N-IO	W-ATL	19	41	0.6538	0.0010	8	21	0.6540	0.0010
N-IO	W-IO	19	31	0.0007	0.2827	8	13	0.0011	0.3407
W-ATL	W-IO	41	31	0.6499	0.0010	21	13	0.6549	0.0010

```
pwFis.FM <- data[,c(1:4,7:8, 12:13,16:17)]
colnames(pwFis.FM) <- c("strata.1", "strata.2", "n.auDNA.F.1", "n.auDNA.F.2",
                        "Fis.auDNA.F", "Fis.auDNA.F.Pval",
                     "n.auDNA.M.1", "n.auDNA.M.2", "Fis.auDNA.M", "Fis.auDNA.M.Pval")
knitr::kable(pwFis.FM, digits = 4,
             caption = "Pairwise Fis between females and males for autosomal markers") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

8.11.3.3 Fis test

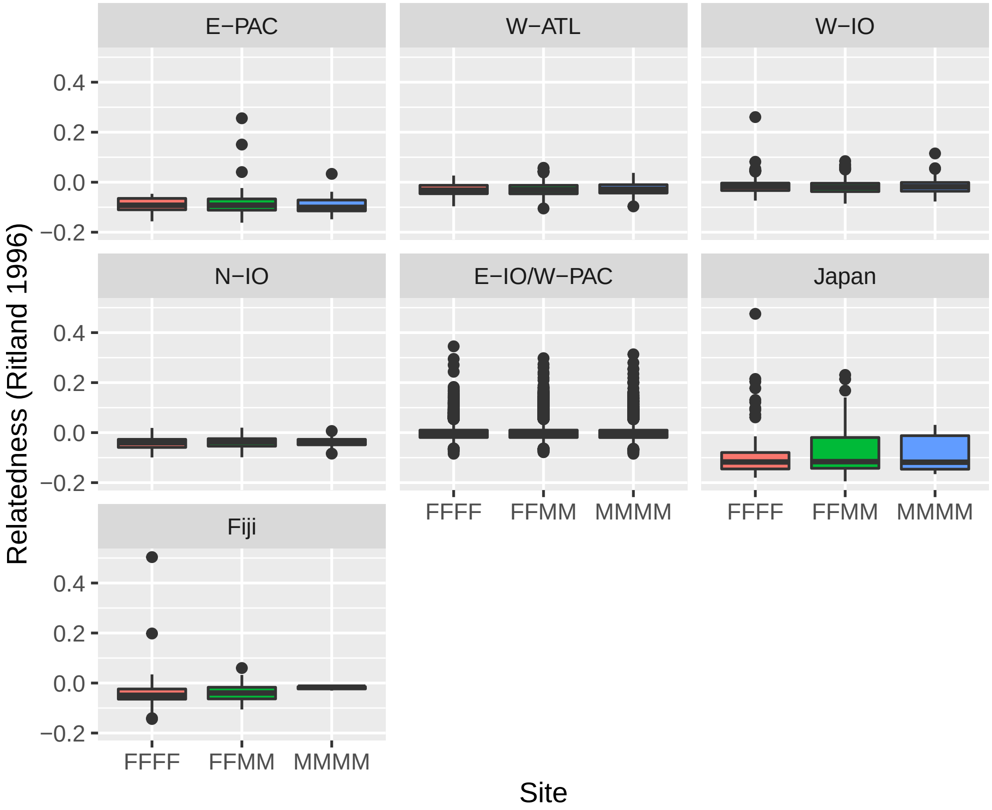
Table 33: Pairwise Fis between females and males for autosomal markers

strata.1	strata.2	n.auDNA.F.1	n.auDNA.F.2	Fis.auDNA.F	Fis.auDNA.F.Pval	n.auDNA.M.1	n.auDNA.M.2	Fis.auDNA.M	Fis.auDNA.M.Pval
E-IO/W-PAC	E-PAC	165	6	NA	NA	176	10	NA	NA
E-IO/W-PAC	Fiji	165	11	-4.3618	0.9411	176	7	-4.3394	0.5145
E-IO/W-PAC	Japan	165	2	NA	NA	176	2	NA	NA
E-IO/W-PAC	N-IO	165	19	-3.9486	0.5804	176	8	-4.4266	0.1439
E-IO/W-PAC	W-ATL	165	41	-1.8571	1.0000	176	21	-2.2058	1.0000
E-IO/W-PAC	W-IO	165	31	-3.8246	0.4925	176	13	-4.2056	0.8771
E-PAC	Fiji	6	11	NA	NA	10	7	NA	NA
E-PAC	Japan	6	2	NA	NA	10	2	NA	NA
E-PAC	N-IO	6	19	NA	NA	10	8	NA	NA
E-PAC	W-ATL	6	41	NA	NA	10	21	NA	NA
E-PAC	W-IO	6	31	NA	NA	10	13	NA	NA
Fiji	Japan	11	2	NA	NA	7	2	NA	NA
Fiji	N-IO	11	19	-13.4680	1.0000	7	8	-59.0989	1.0000
Fiji	W-ATL	11	41	-9.5707	1.0000	7	21	-18.4592	1.0000
Fiji	W-IO	11	31	-11.5127	1.0000	7	13	-30.2224	0.9910
Japan	N-IO	2	19	NA	NA	2	8	NA	NA
Japan	W-ATL	2	41	NA	NA	2	21	NA	NA
Japan	W-IO	2	31	NA	NA	2	13	NA	NA
N-IO	W-ATL	19	41	-6.4767	1.0000	8	21	-13.9027	1.0000
N-IO	W-IO	19	31	-9.0011	0.4845	8	13	-22.6698	0.0420
W-ATL	W-IO	41	31	-5.5483	1.0000	21	13	-10.8381	1.0000

```r
gl <- BS.dartcap.gl
pop.levels <- c("E-PAC","W-ATL","E-ATL","W-IO","N-IO","E-IO","W-PAC",
                "E-IO/W-PAC", "Japan","Fiji")
gl$pop <- factor(gl$other$ind.metrics$Region, levels = pop.levels)
gl$pop[gl$pop %in% c("E-IO","W-PAC")] <- "E-IO/W-PAC"
pop.levels <- c("E-PAC","W-ATL","E-ATL","W-IO","N-IO","E-IO/W-PAC",
                "Japan","Fiji")
gl$pop <- factor(gl$pop , levels = pop.levels)
gl <- gl[order(gl$pop, gl$ind.names),]

gl$other$ind.metrics$`TL (mm)` <- as.integer(gl$other$ind.metrics$`TL (mm)`)
gl <- gl[(gl$other$ind.metrics$`TL (mm)` > 1500 &
            !is.na(gl$other$ind.metrics$`TL (mm)`)) | gl$pop == "Fiji",] #Because all Fiji samples w
gl <- gl[!gl$other$ind.metrics$Site == "E-ATL",] #only 1 sample
gl$other$loc.metrics.flags$monomorphs <- FALSE
gl$other$loc.metrics.flags$CallRate  <- FALSE


gl2rel <- function(gl, filename = "relate"){
  group.name <- paste(gl$other$ind.metrics$COMBINED_SEX,
                      gl$other$ind.metrics$COMBINED_SEX, "_",
                      gl$ind.names, sep = "")
  glmat <- as.matrix(gl)
  glmat[glmat==0] <- '2 2'
  glmat[glmat==1] <- '1 2'
  glmat[glmat==2] <- '1 1'
  glmat[is.na(glmat)] <- '0 0'
  df <- cbind(group.name, glmat)
  write.table(df, file = paste0(filename,".txt", sep = ""), quote = FALSE,
              sep = " ", row.names = FALSE, col.names = FALSE)
}


res.rel <- list()
summ.rel <- data.frame(sex.group = c("FF", "FM", "MM"))
plot.data <- data.frame(pair.no = NA,ind1.id = NA,ind2.id = NA, group = NA,
                        condition = NA, measurement = NA,Site = NA)
for (i in 1:nlevels(gl$pop)) {
  print(i)
  gl.tmp <- gl[gl$pop == levels(gl$pop)[i],]
  gl.tmp <- dartR::gl.filter.callrate(gl.tmp, method = 'loc', threshold = 1,
                                      mono.rm = TRUE, plot = FALSE, verbose = 0)

  gl2rel(gl.tmp, filename = "relate")
  data <- related::readgenotypedata("relate.txt")
  outfile <- related::coancestry (data$gdata , lynchli = 1, lynchrd = 1,
                                  quellergt = 1, wang = 1, ritland = 1)
  res <- outfile$relatedness[!outfile$relatedness$group %in%
                               c("FFUU","UUUU","MMUU","UUFF", "UUMM"),]
  res$group[res$group == "MMFF"] <- "FFMM"
  data_long <- gather(res, condition, measurement, 5:11, factor_key=TRUE)
  data_long$Site <- levels(gl$pop)[i]
  plot.data <- rbind(plot.data, data_long)
  summ <- dplyr::group_by(res, group) %>%
    dplyr::summarise(mean(ritland))
  colnames(summ) <- c("sex.group", levels(gl$pop)[i])
  summ.rel <- cbind(summ.rel, summ[,2])
```

```
  res.rel[[i]] <- res
}
plot.data <- plot.data[-1,]
save(res.rel,summ.rel,plot.data,
     file = "DArTcap_ALL_relatedness_sex_Region.Rdata")
```

```
load("DArTcap_ALL_relatedness_sex_Region.Rdata")
pop.levels <- c("E-PAC","W-ATL","W-IO","N-IO","E-IO/W-PAC", "Japan","Fiji")
plot.data$Site <- factor(plot.data$Site, levels = pop.levels)
plot.data <- plot.data[plot.data$condition == "ritland",]
plot <- ggplot2::ggplot(plot.data, ggplot2::aes(x = group, y = measurement,
                                               fill = group)) +
  ggplot2::geom_boxplot() +
  ggplot2::facet_wrap(Site~.) +
  ggplot2::labs(x = "Site", y = "Relatedness (Ritland 1996)")
print(plot)
```



8.11.3.4 Relatedness test

```
knitr::kable(summ.rel, digits = 2,
             caption = "Relatedness between female and males according to Ritland (1996)") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

Table 34: Relatedness between female and males according to Ritland (1996)

sex.group	E-PAC	W-ATL	W-IO	N-IO	E-IO/W-PAC	Japan	Fiji
FF	-0.09	-0.03	-0.02	-0.04	0	-0.07	-0.04
FM	-0.08	-0.03	-0.02	-0.04	0	-0.06	-0.04
MM	-0.09	-0.03	-0.02	-0.04	0	-0.08	-0.02

9 DATA3: DArTcap - All data, subset Australia

9.1 Set strata

```
strata <- radiator::read_strata("Bull_shark_DArTcap_strata.tsv",
                                keep.two = FALSE)$strata %>%
  dplyr:: filter(SpeciesID_genetic == "Carcharhinus leucas")
id.sub <- c(strata$INDIVIDUALS[strata$Site != "Australia"],
            sample(strata$INDIVIDUALS[strata$Site == "Australia"], size = 60))
strata <- strata[strata$INDIVIDUALS %in% id.sub,]
readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata3_AUS_subset.tsv")
```

9.2 Filter data

1. `Marker Reproducibility: 0.98`
2. `Individual missingness: 0.35`
3. `Individual Het - low: 0`
4. `Individual Het - high: 0.08`
5. `Individual total coverage - low: 10,000`
6. `Individual total coverage - high: 1,000,000`
7. `Marker MAC - low: 4`
8. `Marker coverage - low: 5`
9. `Marker coverage - high:90`
10. `Marker maximum missing proportion: 0.1`
11. `Marker snp position on locus: n`
12. `Max 3 SNPs per locus`
13. `1 SNP per locus according to mac`
14. `no LD filter`
15. `Individual Het - low: 0.037`
16. `Individual Het - high: 0.1165`
17. `Duplicated individuals: 0.1`
18. `Filter on HWE: 2 pops, 0.001`

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata3_AUS_subset.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = 1)
BS.dartcap.sub.gds <- BSsnp$gds
BS.dartcap.sub.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.sub.gds, expand = TRUE, all = TRUE, attribute = TRUE,
      attribute.trim = FALSE)

save(BS.dartcap.sub.tidy, file = "DArTcap_ALL_AUS_subset.Rdata")
```

Table 35:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	465 / 30 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	465 / 30 / 1 / 25292 / 35287	0 / 0 / 0 / 12443 / 20404
Filter markers in common	NA	465 / 30 / 1 / 12849 / 14883	0 / 0 / 0 / 5477 / 6377
Filter individuals based on missingness	0.35	465 / 30 / 1 / 7372 / 8506	10 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.05	455 / 30 / 1 / 7372 / 8506	14 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+06	441 / 30 / 1 / 7372 / 8506	2 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	439 / 30 / 1 / 7372 / 8506	0 / 0 / 0 / 1571 / 2036
Filter MAC	4	439 / 30 / 1 / 5801 / 6470	0 / 0 / 0 / 3211 / 3699
Filter coverage min / max	5-90	439 / 30 / 1 / 2590 / 2771	0 / 0 / 0 / 611 / 633
Filter genotyping	0.1	439 / 30 / 1 / 1979 / 2138	0 / 0 / 0 / 94 / 107
Filter SNPs position on the read	all	439 / 30 / 1 / 1885 / 2031	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	439 / 30 / 1 / 1885 / 2031	0 / 0 / 0 / 0 / 0
Filter short ld	mac	439 / 30 / 1 / 1885 / 2031	0 / 0 / 0 / 0 / 146
detect mixed genomes	0.037 0.1165	439 / 30 / 1 / 1885 / 1885	11 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	428 / 30 / 1 / 1885 / 1885	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0.1	428 / 30 / 1 / 1885 / 1885	40 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	388 / 30 / 1 / 1885 / 1885	0 / 0 / 0 / 0 / 0
Filter HWE	20.001	388 / 30 / 1 / 1885 / 1885	0 / 0 / 0 / 7 / 7

9.2.1 Remove extra low and high heterozygous individuals

Because the average heterozygosity per sampling location is not even, certain individuals cannot be excluded without removing ‘good’ individuals.

```
rm <-  c("CL-ARS021-F","CL-GOM025-F.1","CL-GOM012-F","CL-SAF014-M","CL-SAF002-F",
         "CL-BRZ038-U","CLF003-F","CL-GOM011-F","CL-SAF015-F","CL-SAF003-M",
         "CL-PNG005-U","CLCR056-M","CLCR047.1","CLCR055-M","CLCR066-M")

BS.dartcap.sub.tidy <- BS.dartcap.sub.tidy[!BS.dartcap.sub.tidy$INDIVIDUALS %in% rm,]
length(unique(BS.dartcap.sub.tidy$INDIVIDUALS)) # 382
```

‘

9.3 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.sub.tidy,
                                       output = c("genlight", "stockr",
                                                  "pcadapt", "gtypes", "rubias"))
BS.dartcap.sub.gl <- Convert$genlight
BS.dartcap.sub.stkr <- Convert$stockr
BS.dartcap.sub.pc <- Convert$pcadapt
BS.dartcap.sub.gt <- Convert$gtypes
BS.dartcap.sub.rubias <- Convert$rubias

markers.meta <- radiator::extract_markers_metadata(BS.dartcap.sub.gds,
                                                   whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.sub.gds,
                                                           whitelist = TRUE)
individuals.meta <- individuals.meta[individuals.meta$INDIVIDUALS %in%
                                       BS.dartcap.sub.gl$ind.names,]
BS.dartcap.sub.gl$other$ind.metrics <- individuals.meta
BS.dartcap.sub.gl$other$loc.metrics <- markers.meta
BS.dartcap.sub.gt@schemes <- individuals.meta

pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Fitzroy River", "Daly River", "Adelaide River","Darwin Coastal",
                "South Alligator River", "East Alligator River","Blue mud Bay",
                "Roper River","Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour", "Okinawa", "Urauchi River",
                "Fiji")
BS.dartcap.sub.gl$pop <- factor(BS.dartcap.sub.gl$other$ind.metrics$Site2,
                                levels = pop.levels)
BS.dartcap.sub.gl <- BS.dartcap.sub.gl[order(BS.dartcap.sub.gl$pop,
                                             BS.dartcap.sub.gl$ind.names),]
BS.dartcap.sub.gl <- BS.dartcap.sub.gl[order(BS.dartcap.sub.gl$pop,
                                             BS.dartcap.gl$ind.names)]
BS.dartcap.sub.rubias$repunit <- factor(BS.dartcap.sub.rubias$repunit,
                                        levels = pop.levels)

save(BS.dartcap.sub.tidy, BS.dartcap.sub.gl, BS.dartcap.sub.stkr, BS.dartcap.sub.pc,
     BS.dartcap.sub.gt,BS.dartcap.sub.rubias,
     markers.meta, individuals.meta, file = "DArTcap_ALL_AUS_subset.Rdata")
```

9.4 Load data

```
load("DArTcap_ALL_AUS_subset.Rdata")

pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea", "Gulf of Mexico",
                "Western North Atlantic", "Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea", "Sri Lanka",
                "Thailand", "Indonesia", "Papua New Guinea" , "Australia",
                "Japan", "Fiji")

BS.dartcap.sub.gl$pop <- factor(BS.dartcap.sub.gl$other$ind.metrics$Site,
                                levels = pop.levels)
BS.dartcap.sub.gl <- BS.dartcap.sub.gl[order(BS.dartcap.sub.gl$pop,
                                             BS.dartcap.sub.gl$ind.names)]

unique(BS.dartcap.sub.tidy$POP_ID)
AUS <- c( "Daly_River","Wenlock_River","Sydney_Harbour","Clarence_River",
          "Adelaide_River","South_Alligator_River","Trinity_inlet",
          "East_Alligator_River","Towns_River","Darwin_Coastal","Unknown")
JAP <- c( "Urauchi_River", "Okinawa")
POP_ID <- as.character(BS.dartcap.sub.tidy$POP_ID)
POP_ID[POP_ID %in% AUS] <- "Australia"
POP_ID[POP_ID %in% JAP] <- "Japan"
pop.levels1 <- stringr::str_replace_all(pop.levels, " ", "_")
BS.dartcap.sub.tidy$POP_ID <- factor(POP_ID, levels = pop.levels1)
BS.dartcap.sub.tidy <- BS.dartcap.sub.tidy[order(BS.dartcap.sub.tidy$POP_ID,
                                                 BS.dartcap.sub.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartcap.sub.gl) # 382
adegenet::nLoc(BS.dartcap.sub.gl) # 1878
summary(BS.dartcap.sub.gl$pop)
sum(duplicated(BS.dartcap.sub.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartcap.sub.gl$other$loc.metrics$LOCUS) #88
```

```
##  [1] Fiji                   Arabian_Sea            Sri_Lanka
##  [4] Western_North_Atlantic Costa_Rica             Thailand
##  [7] Mozambique             Gulf_of_Mexico         Reunion
## [10] Urauchi_River          South_Africa           Papua_New_Guinea
## [13] Sierra_Leone           Okinawa                Brazil
## [16] Seychelles             Caribbean_Sea          Indonesia
## [19] Daly_River             Wenlock_River          Sydney_Harbour
## [22] Clarence_River         Adelaide_River         South_Alligator_River
## [25] Trinity_inlet          East_Alligator_River   Towns_River
## [28] Darwin_Coastal         Unknown
## 30 Levels: Fiji Arabian_Sea Sri_Lanka Western_North_Atlantic ... Unknown
## [1] 382
## [1] 1878
##             Costa Rica                 Brazil          Caribbean Sea
##                     15                     52                      2
##         Gulf of Mexico Western North Atlantic           Sierra Leone
##                     40                      8                      1
##           South Africa             Mozambique                Reunion
##                     23                     11                     28
##             Seychelles            Arabian Sea              Sri Lanka
##                     36                     15                     12
##               Thailand              Indonesia       Papua New Guinea
##                      5                      4                      8
##              Australia                  Japan                   Fiji
```

```
##                      54                     44                     24
## [1] 0
## [1] 88
```

9.5 Remove sex-linked markers

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sum(bull_shark$sexy.summary$CLONE_ID %in% SLM$sexy.summary$CLONE_ID) #33
sum(SLM$sexy.summary$CLONE_ID %in% bull_shark$sexy.summary$CLONE_ID) #23
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID,
                        SLM$sexy.summary$CLONE_ID))

sum(BS.dartcap.sub.gl$loc.names %in% sex.markers) #29
locnames <- BS.dartcap.sub.gl$loc.names
BS.dartcap.sub.gl <- BS.dartcap.sub.gl[,!locnames %in% sex.markers]
BS.dartcap.sub.gl$other$loc.metrics <- BS.dartcap.sub.gl$other$loc.metrics[
  !locnames %in% sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.sub.tidy$LOCUS)) # 29
BS.dartcap.sub.tidy <- BS.dartcap.sub.tidy[!BS.dartcap.sub.tidy$LOCUS %in%
                                             sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartcap.sub.gt@data$locus)[,2]
BS.dartcap.sub.gt <- BS.dartcap.sub.gt[,!locus.gt %in% sex.markers, ,
                                       drop = TRUE]

locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                   string =  colnames(BS.dartcap.sub.rubias))[,2]
BS.dartcap.sub.rubias <- BS.dartcap.sub.rubias[,!locus.rubias %in% sex.markers]
```

```
## [1] 33
## [1] 23
## [1] 29
## [1] 29
```

9.6 Genetic diversity

```
set.seed(124)
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic", "South Africa", "Mozambique", "Reunion" ,
                "Seychelles", "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Australia", "Japan", "Fiji")

gl <- BS.dartcap.sub.gl
gl <- gl[gl$pop != "Sierra Leone"] #only 1 sample
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_aus_subset_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_aus_subset_genepop.txt",
                               outfile = "BS_dartcap_aus_subset_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)
length(bastat$main_tab) #17
```

```
gendiv <- data.frame(
  "Costa Rica" = bastat$main_tab[[1]]$overall,
  "Brazil" = bastat$main_tab[[2]]$overall,
  "Caribbean Sea" = bastat$main_tab[[3]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[4]]$overall,
  "Western North Atlantic" = bastat$main_tab[[5]]$overall,
  "South Africa" = bastat$main_tab[[6]]$overall,
  "Mozambique" = bastat$main_tab[[7]]$overall,
  "Reunion" = bastat$main_tab[[8]]$overall,
  "Seychelles" = bastat$main_tab[[9]]$overall,
  "Arabian Sea" = bastat$main_tab[[10]]$overall,
  "Sri Lanka" = bastat$main_tab[[11]]$overall,
  "Thailand" = bastat$main_tab[[12]]$overall,
  "Indonesia" = bastat$main_tab[[13]]$overall,
  "Papua New Guinea" = bastat$main_tab[[14]]$overall,
  "Australia" = bastat$main_tab[[15]]$overall,
  "Japan" = bastat$main_tab[[16]]$overall,
  "Fiji" = bastat$main_tab[[17]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTcap_aus_subset_gendiv.txt")
save(gendiv, file = "DArTcap_aus_subset_gendiv.Rdata")
```

```
load("DArTcap_aus_subset_gendiv.Rdata")
shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA", "SAF", "MOZ", "RUN" ,
                "SEY", "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(gendiv, col.names = shortnames, digits = 4,caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

Table 36:

	COR	BRZ	CAR	GOM	WNA	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
ar	1.0770	1.1230	1.0880	1.1140	1.1120	1.1640	1.1570	1.1670	1.1710	1.1690	1.1680	1.1690	1.1440	1.1620	1.1720	1.1700	1.1600
size	14.8250	51.5410	1.9920	39.1040	7.9670	22.6290	10.7600	27.7700	35.7970	14.9280	11.9440	4.9830	3.9750	7.9570	53.7240	43.7640	23.4910
obs_het	0.0440	0.0670	0.0630	0.0640	0.0640	0.0890	0.0870	0.0900	0.0920	0.0920	0.0950	0.1010	0.0890	0.0910	0.0910	0.0950	0.0870
exp_het	0.0450	0.0680	0.0470	0.0650	0.0610	0.0930	0.0910	0.0930	0.0930	0.0920	0.0910	0.0890	0.0790	0.0880	0.0950	0.0930	0.0910
uexp_het	0.0470	0.0690	0.0630	0.0660	0.0650	0.0950	0.0960	0.0940	0.0950	0.0960	0.0950	0.0990	0.0890	0.0940	0.0960	0.0940	0.0940
fis	0.0090	0.0250	-0.3240	0.0220	-0.0520	0.0240	0.0240	0.0200	0.0150	-0.0030	-0.0270	-0.1230	-0.1440	-0.0420	0.0250	-0.0030	0.0290
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0470	0.0040	-1.0000	-0.0050	-0.1620	-0.0100	-0.0590	-0.0110	-0.0110	-0.0580	-0.0980	-0.3820	-0.5790	-0.1600	0.0080	-0.0270	-0.0060
fis_hi	0.0050	0.0260	-0.3240	0.0250	-0.0600	0.0210	0.0160	0.0190	0.0140	-0.0090	-0.0370	-0.1230	-0.1440	-0.0540	0.0280	-0.0030	0.0300
ar_lo	1.0330	1.1090	1.0580	1.0880	1.0570	1.0820	1.0490	1.0870	1.1570	1.0840	1.0840	1.0900	1.0730	1.0740	1.1530	1.1250	1.0800
ar_hi	1.0890	1.1360	1.1160	1.1330	1.1270	1.1810	1.1830	1.1880	1.1880	1.1940	1.1980	1.1960	1.1800	1.1880	1.1920	1.1890	1.1840
fis.hierfstat	0.0418	0.0343	-0.0841	0.0340	0.0101	0.0450	0.0681	0.0378	0.0282	0.0293	0.0139	-0.0229	-0.0180	0.0194	0.0344	0.0086	0.0500
fis.CI.low	0.0200	0.0188	-0.0760	0.0135	-0.0139	0.0430	0.0631	0.0277	0.0175	0.0141	-0.0234	-0.0551	-0.0484	0.0013	0.0304	-0.0282	0.0526
fis.CI.high	0.0898	0.0506	0.1036	0.0565	0.0637	0.0815	0.1264	0.0643	0.0486	0.0604	0.0306	0.0183	0.0466	0.0645	0.0588	0.0074	0.0929

9.6.1 Number of monomorphic markers per population

```
pop.levels <- c("Costa Rica" , "Brazil","Caribbean Sea","Gulf of Mexico",
                "Western North Atlantic","Sierra Leone", "South Africa",
                "Mozambique", "Reunion" , "Seychelles", "Arabian Sea",
                "Sri Lanka", "Thailand", "Indonesia", "Papua New Guinea" ,
                "Australia", "Japan", "Fiji")

monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.sub.gl[BS.dartcap.sub.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("COR","BRZ", "CAR", "GOM", "WNA","SIL", "SAF", "MOZ", "RUN" ,
                "SEY", "ARS", "SRL", "TAI", "IND", "PNG" , "AUS", "JAP", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

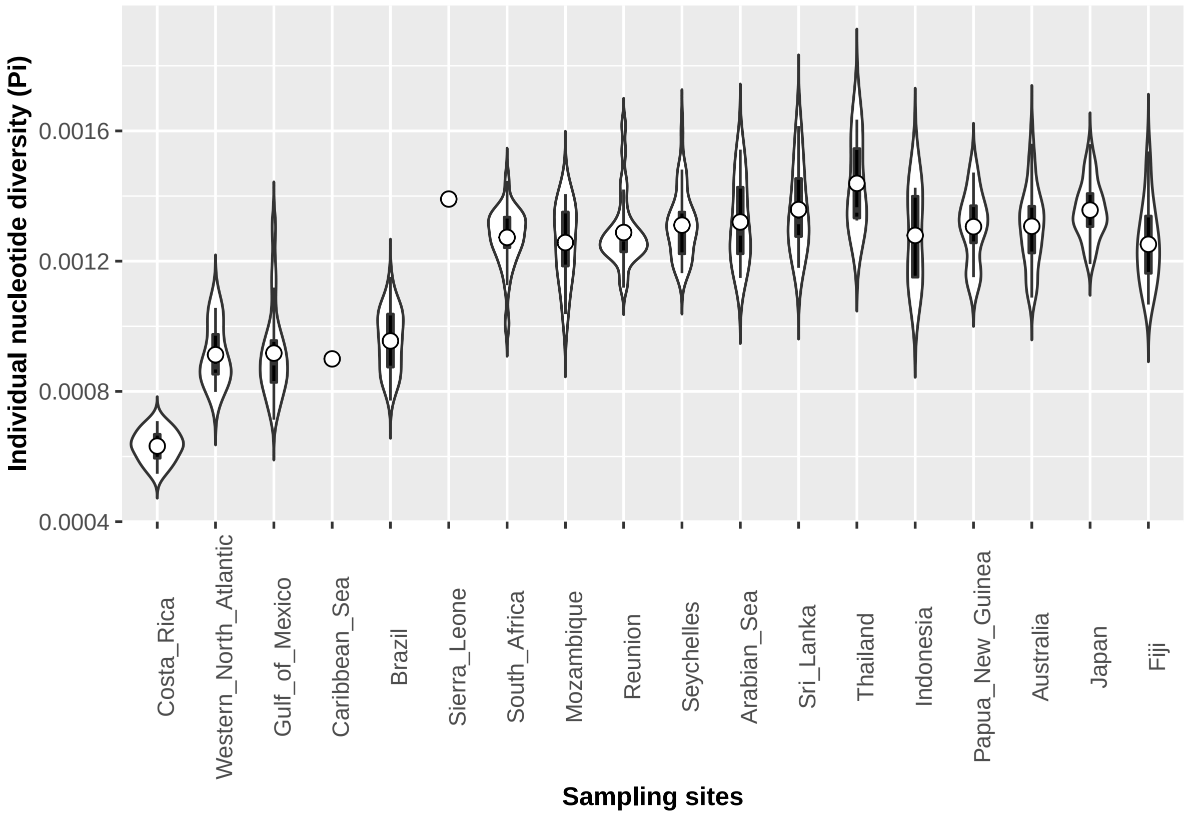
Table 37:

COR	BRZ	CAR	GOM	WNA	SIL	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
1335	812	1476	973	1270	1791	845	1082	813	741	969	1040	1294	1398	1175	627	831	929

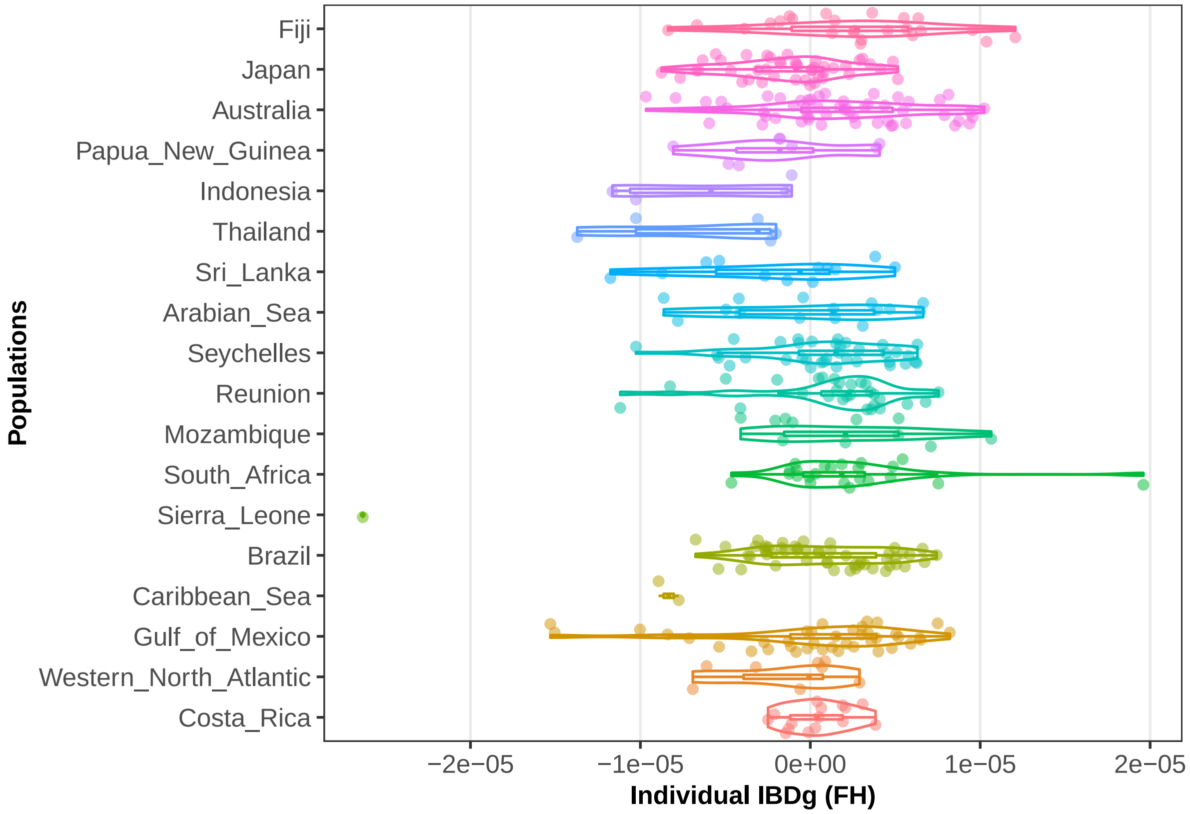
9.6.2 Nucleotide diversity and inbreeding

```
pi.sum <- radiator::pi(
  data = BS.dartcap.sub.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartcap.sub.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTcap_aus_subset_pi_FIS_Sites.Rdata")
```

```
load("DArTcap_aus_subset_pi_FIS_Sites.Rdata")
pi.sum$boxplot.pi
```



```
FIS.sum$fh.box.plot
```



9.7 Genetic differentiation

```
Fst.gt <- strataG::popStructTest(
    BS.dartcap.sub.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_aus_subset_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_aus_subset_FST.txt")
```

```
load("DArTcap_aus_subset_FST.Rdata")

kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                        decreasing = TRUE),
                                  -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australi
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st
Costa_Rica (15) v. Trinity_inlet (1)	8283.4461	0.0619	0.0204	0.0619	3.2680	1.0000	0.7414	1.0000	0.7793	1.0000	-3.9814	1.0000	-2.0069	1.0000	2.0086	1
Costa_Rica (15) v. Towns_River (2)	9222.5207	0.0060	0.0252	0.0060	11.5056	1.0000	0.7261	0.0240	0.7667	0.0240	2.0202	0.0423	1.7680	0.0423	1.2543	0
Costa_Rica (15) v. Sierra_Leone (1)	7661.4419	0.0579	0.0166	0.0579	3.2672	1.0000	0.7221	1.0000	0.7592	1.0000	-3.4660	1.0000	-1.7230	1.0000	2.1042	1
Costa_Rica (15) v. Darwin_Coastal (2)	9257.6375	0.0050	0.0249	0.0050	12.5054	1.0000	0.7219	0.0133	0.7619	0.0133	1.8793	0.0219	1.6654	0.0219	1.2311	0
Costa_Rica (15) v. Unknown (2)	9189.7795	0.0090	0.0247	0.0090	12.3599	1.0000	0.7207	0.0256	0.7606	0.0256	1.9014	0.0435	1.6832	0.0435	1.2355	0
Adelaide_River (4) v. Costa_Rica (15)	10908.0732	0.0010	0.0266	0.0010	-44.1032	1.0000	0.7088	0.0011	0.7613	0.0013	0.8711	0.0013	0.8955	0.0013	0.9441	0
Costa_Rica (15) v. Daly_River (3)	10225.9312	0.0020	0.0261	0.0020	381.6588	0.0040	0.7084	0.0028	0.7505	0.0028	1.0169	0.0040	1.0135	0.0040	1.0067	0
Costa_Rica (15) v. Indonesia (4)	10792.2218	0.0010	0.0264	0.0010	NA	NA	0.7064	0.0011	0.7496	0.0011	NA	NA	NA	NA	NA	
Costa_Rica (15) v. Wenlock_River (4)	11032.6671	0.0010	0.0266	0.0010	-27.0705	1.0000	0.6990	0.0011	0.7429	0.0011	0.8096	0.0013	0.8450	0.0013	0.9143	0
Costa_Rica (15) v. Thailand (5)	11727.2773	0.0010	0.0272	0.0010	-17.0550	1.0000	0.6913	0.0010	0.7365	0.0010	0.7263	0.0011	0.7748	0.0011	0.8696	0
Costa_Rica (15) v. East_Alligator_River (7)	12626.4320	0.0010	0.0259	0.0010	-12.3826	1.0000	0.6815	0.0010	0.7280	0.0010	0.6599	0.0010	0.7160	0.0010	0.8289	0
Costa_Rica (15) v. Okinawa (9)	13962.7470	0.0010	0.0280	0.0010	-11.8202	1.0000	0.6776	0.0010	0.7260	0.0010	0.6408	0.0010	0.6999	0.0010	0.8171	0
Gulf_of_Mexico (40) v. Trinity_inlet (1)	16001.1132	0.0250	0.0239	0.0250	4.0949	1.0000	0.6769	1.0000	0.7254	1.0000	13.4579	1.0000	9.2853	1.0000	1.5731	1
Costa_Rica (15) v. Papua_New_Guinea (8)	13298.5700	0.0010	0.0267	0.0010	-10.6383	1.0000	0.6758	0.0010	0.7241	0.0010	0.6319	0.0010	0.6918	0.0010	0.8112	0
Costa_Rica (15) v. Sydney_Harbour (8)	13439.5029	0.0010	0.0274	0.0010	-10.4232	1.0000	0.6744	0.0010	0.7239	0.0010	0.6278	0.0010	0.6889	0.0010	0.8089	0
Trinity_inlet (1) v. Western_North_Atlantic (8)	5008.5600	0.1189	0.0234	0.1189	3.1212	1.0000	0.6741	0.5409	0.7283	1.0000	-4.3408	1.0000	-2.1394	1.0000	1.9397	1
Gulf_of_Mexico (40) v. Towns_River (2)	18358.0969	0.0030	0.0286	0.0030	58.2252	0.2747	0.6713	0.0067	0.7206	0.0067	1.0919	0.7963	1.0718	0.7963	1.0343	0
Caribbean_Sea (2) v. Trinity_inlet (1)	1969.5667	0.3467	0.0234	0.3467	NA	NA	0.6711	0.3467	0.7214	0.3467	NA	NA	NA	NA	NA	
Adelaide_River (4) v. Gulf_of_Mexico (40)	22033.4331	0.0010	0.0306	0.0010	-9.6500	0.9812	0.6703	0.0010	0.7479	0.0010	0.6557	0.0010	0.7170	0.0010	0.8291	0
Darwin_Coastal (2) v. Gulf_of_Mexico (40)	18729.0359	0.0010	0.0286	0.0010	137.1104	0.0030	0.6698	0.0023	0.7484	0.0030	1.0368	0.7508	1.0289	0.7508	1.0142	0
Gulf_of_Mexico (40) v. Unknown (2)	18394.7831	0.0010	0.0289	0.0010	102.7843	0.0032	0.6693	0.0024	0.7182	0.0024	1.0502	0.7331	1.0393	0.7331	1.0192	0
Gulf_of_Mexico (40) v. Indonesia (4)	21967.7890	0.0010	0.0305	0.0010	NA	NA	0.6687	0.0010	0.7187	0.0010	NA	NA	NA	NA	NA	
Daly_River (3) v. Gulf_of_Mexico (40)	20742.6390	0.0010	0.0303	0.0010	-12.9215	0.2460	0.6678	0.0012	0.7462	0.0012	0.7187	0.0012	0.7716	0.0012	0.8671	0
Costa_Rica (15) v. South_Alligator_River (10)	14341.6767	0.0010	0.0265	0.0010	-9.4239	1.0000	0.6671	0.0010	0.7161	0.0010	0.6054	0.0010	0.6679	0.0010	0.7931	0
Gulf_of_Mexico (40) v. Wenlock_River (4)	22399.0465	0.0010	0.0303	0.0010	-7.9557	0.4767	0.6655	0.0010	0.7159	0.0010	0.6189	0.0010	0.6859	0.0010	0.8060	0
Gulf_of_Mexico (40) v. Thailand (5)	23758.0033	0.0010	0.0308	0.0010	-6.5729	0.9990	0.6639	0.0010	0.7148	0.0010	0.5763	0.0010	0.6484	0.0010	0.7769	0
Gulf_of_Mexico (40) v. Okinawa (9)	27391.1075	0.0010	0.0320	0.0010	-5.5230	1.0000	0.6622	0.0010	0.7142	0.0010	0.5356	0.0010	0.6107	0.0010	0.7465	0
Towns_River (2) v. Western_North_Atlantic (8)	5814.0950	0.0290	0.0280	0.0290	11.2684	0.7018	0.6622	0.0420	0.7164	0.0588	1.8961	0.4077	1.6634	0.4077	1.2291	0
Brazil (52) v. Trinity_inlet (1)	16194.6308	0.0180	0.0234	0.0180	4.6021	1.0000	0.6606	0.4615	0.7103	0.4615	4.5555	1.0000	3.4695	1.0000	1.4445	1
East_Alligator_River (7) v. Gulf_of_Mexico (40)	25167.0866	0.0010	0.0300	0.0010	-5.5072	1.0000	0.6604	0.0010	0.7363	0.0010	0.5436	0.0010	0.6171	0.0010	0.7520	0
Gulf_of_Mexico (40) v. Sydney_Harbour (8)	26569.0852	0.0010	0.0312	0.0010	-4.9426	1.0000	0.6593	0.0010	0.7118	0.0010	0.5261	0.0010	0.6025	0.0010	0.7395	0
Gulf_of_Mexico (40) v. Papua_New_Guinea (8)	26294.0411	0.0010	0.0305	0.0010	-4.7993	1.0000	0.6589	0.0010	0.7107	0.0010	0.5264	0.0010	0.6018	0.0010	0.7391	0
Darwin_Coastal (2) v. Western_North_Atlantic (8)	5822.3231	0.0310	0.0278	0.0310	12.2432	0.3403	0.6580	0.0471	0.7125	0.0541	1.7761	0.3403	1.5768	0.3403	1.2078	0
Unknown (2) v. Western_North_Atlantic (8)	5787.2291	0.0170	0.0280	0.0170	11.9544	0.4007	0.6578	0.0231	0.7122	0.0304	1.8144	0.3596	1.6053	0.3596	1.2151	0
Costa_Rica (15) v. Mozambique (11)	14811.2507	0.0010	0.0265	0.0010	-8.0933	1.0000	0.6574	0.0010	0.7168	0.0010	0.5824	0.0010	0.6474	0.0010	0.7772	0
Adelaide_River (4) v. Brazil (52)	24872.8512	0.0010	0.0298	0.0010	-6.8222	0.9886	0.6572	0.0010	0.7183	0.0010	0.6052	0.0010	0.6723	0.0010	0.7958	0
Brazil (52) v. Towns_River (2)	19897.1581	0.0010	0.0279	0.0010	-54.6719	0.3446	0.6568	0.0020	0.7070	0.0020	0.9245	0.0026	0.9399	0.0026	0.9688	0
Gulf_of_Mexico (40) v. South_Alligator_River (10)	27892.8176	0.0010	0.0306	0.0010	-4.5377	1.0000	0.6560	0.0010	0.7080	0.0010	0.5142	0.0010	0.5904	0.0010	0.7295	0
Brazil (52) v. Indonesia (4)	24789.4679	0.0010	0.0297	0.0010	NA	NA	0.6554	0.0010	0.7061	0.0010	NA	NA	NA	NA	NA	
Clarence_River (11) v. Costa_Rica (15)	15107.8708	0.0010	0.0272	0.0010	-7.4903	1.0000	0.6553	0.0010	0.7111	0.0010	0.5719	0.0010	0.6390	0.0010	0.7703	0
Costa_Rica (15) v. Sri_Lanka (12)	15422.5073	0.0010	0.0268	0.0010	-7.7350	1.0000	0.6551	0.0010	0.7061	0.0010	0.5741	0.0010	0.6400	0.0010	0.7713	0
Brazil (52) v. Darwin_Coastal (2)	20142.8088	0.0020	0.0278	0.0020	-35.8236	0.1843	0.6549	0.0040	0.7049	0.0040	0.8898	0.0051	0.9120	0.0051	0.9534	0
Brazil (52) v. Unknown (2)	19725.1591	0.0020	0.0281	0.0020	-44.9478	0.1772	0.6545	0.0041	0.7045	0.0041	0.9093	0.0079	0.9277	0.0079	0.9621	0
Brazil (52) v. Daly_River (3)	22999.2758	0.0010	0.0295	0.0010	-8.4252	0.1928	0.6544	0.0011	0.7050	0.0011	0.6515	0.0012	0.7136	0.0012	0.8266	0
Brazil (52) v. Wenlock_River (4)	25237.7951	0.0010	0.0295	0.0010	-5.8267	0.2828	0.6529	0.0010	0.7039	0.0010	0.5741	0.0010	0.6456	0.0010	0.7749	0
Brazil (52) v. Thailand (5)	27112.0193	0.0010	0.0301	0.0010	-4.9947	0.9910	0.6522	0.0010	0.7037	0.0010	0.5410	0.0010	0.6159	0.0010	0.7508	0
Brazil (52) v. Okinawa (9)	31644.5308	0.0010	0.0312	0.0010	-4.4824	1.0000	0.6517	0.0010	0.7039	0.0010	0.5122	0.0010	0.5886	0.0010	0.7279	0
Adelaide_River (4) v. Western_North_Atlantic (8)	7323.2616	0.0050	0.0299	0.0050	-35.6066	1.0000	0.6517	0.0050	0.7071	0.0050	0.8587	0.0050	0.8872	0.0050	0.9393	0
Gulf_of_Mexico (40) v. Mozambique (11)	28536.3039	0.0010	0.0305	0.0010	-4.1008	1.0000	0.6515	0.0010	0.7092	0.0010	0.5020	0.0010	0.5793	0.0010	0.7199	0
Clarence_River (11) v. Gulf_of_Mexico (40)	29041.3696	0.0010	0.0310	0.0010	-3.7833	1.0000	0.6506	0.0010	0.7260	0.0010	0.4939	0.0010	0.5729	0.0010	0.7141	0
Gulf_of_Mexico (40) v. Sri_Lanka (12)	29374.9490	0.0010	0.0305	0.0010	-3.8221	1.0000	0.6502	0.0010	0.7032	0.0010	0.4957	0.0010	0.5734	0.0010	0.7148	0
Indonesia (4) v. Western_North_Atlantic (8)	7265.3114	0.0040	0.0296	0.0040	NA	NA	0.6500	0.0040	0.7052	0.0040	NA	NA	NA	NA	NA	
Brazil (52) v. East_Alligator_River (7)	28932.2700	0.0010	0.0292	0.0010	-4.3123	1.0000	0.6491	0.0010	0.7005	0.0010	0.5162	0.0010	0.5915	0.0010	0.7306	0

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Brazil (52) v. Sydney_Harbour (8)	30704.2647	0.0010	0.0304	0.0010	-3.8210	1.0000	0.6489	0.0010	0.7016	0.0010	0.5006	0.0010	0.5783	0.0010	0.7190	0
Brazil (52) v. Papua_New_Guinea (8)	30294.1036	0.0010	0.0297	0.0010	-3.8839	1.0000	0.6482	0.0010	0.7003	0.0010	0.5033	0.0010	0.5800	0.0010	0.7206	0
Gulf_of_Mexico (40) v. Sierra_Leone (1)	14355.5370	0.0200	0.0186	0.0200	4.0852	1.0000	0.6474	1.0000	0.6939	1.0000	42.8681	1.0000	29.3232	1.0000	1.6456	1
Arabian_Sea (15) v. Gulf_of_Mexico (40)	31767.5391	0.0010	0.0307	0.0010	-3.2755	1.0000	0.6469	0.0010	0.7208	0.0010	0.4856	0.0010	0.5644	0.0010	0.7068	0
Daly_River (3) v. Western_North_Atlantic (8)	6679.0770	0.0050	0.0295	0.0050	-685.1037	1.0000	0.6468	0.0051	0.7028	0.0053	0.9917	0.0053	0.9935	0.0053	0.9967	0
Brazil (52) v. South_Alligator_River (10)	32317.7661	0.0010	0.0297	0.0010	-3.5437	1.0000	0.6461	0.0010	0.6983	0.0010	0.4919	0.0010	0.5691	0.0010	0.7112	0
Gulf_of_Mexico (40) v. Urauchi_River (35)	45733.6541	0.0010	0.0335	0.0010	-3.2182	1.0000	0.6458	0.0010	0.7037	0.0010	0.4911	0.0010	0.5709	0.0010	0.7122	0
Arabian_Sea (15) v. Costa_Rica (15)	17106.4638	0.0010	0.0269	0.0010	-6.3976	1.0000	0.6456	0.0010	0.7014	0.0010	0.5518	0.0010	0.6201	0.0010	0.7552	0
Fiji (24) v. Gulf_of_Mexico (40)	37844.7634	0.0010	0.0320	0.0010	-3.4626	1.0000	0.6451	0.0010	0.7173	0.0010	0.4884	0.0010	0.5674	0.0010	0.7094	0
Sierra_Leone (1) v. Western_North_Atlantic (8)	4475.4535	0.1109	0.0179	0.1109	3.1210	1.0000	0.6427	0.5337	0.6945	1.0000	-3.6139	1.0000	-1.7595	1.0000	2.0557	1
Brazil (52) v. Mozambique (11)	33120.9672	0.0010	0.0297	0.0010	-3.2204	1.0000	0.6425	0.0010	0.6992	0.0010	0.4814	0.0010	0.5596	0.0010	0.7027	0
Brazil (52) v. Clarence_River (11)	33703.3157	0.0010	0.0301	0.0010	-2.9623	1.0000	0.6418	0.0010	0.6951	0.0010	0.4739	0.0010	0.5535	0.0010	0.6971	0
Brazil (52) v. Sri_Lanka (12)	33981.3894	0.0010	0.0297	0.0010	-3.1417	1.0000	0.6412	0.0010	0.6942	0.0010	0.4774	0.0010	0.5557	0.0010	0.6993	0
Brazil (52) v. Urauchi_River (35)	52029.7382	0.0010	0.0326	0.0010	-2.5235	1.0000	0.6405	0.0010	0.6977	0.0010	0.4762	0.0010	0.5564	0.0010	0.6995	0
Caribbean_Sea (2) v. Sierra_Leone (1)	1784.8167	0.3397	0.0178	0.3397	NA	NA	0.6403	0.3397	0.6886	0.3397	NA	NA	NA	NA	NA	
Caribbean_Sea (2) v. Towns_River (2)	2563.0048	0.3457	0.0281	0.3457	NA	NA	0.6394	0.3457	0.7010	0.1698	NA	NA	NA	NA	NA	
Arabian_Sea (15) v. Brazil (52)	36760.3836	0.0010	0.0299	0.0010	-2.6437	1.0000	0.6391	0.0010	0.7002	0.0010	0.4686	0.0010	0.5479	0.0010	0.6921	0
Wenlock_River (4) v. Western_North_Atlantic (8)	7366.7088	0.0040	0.0296	0.0040	-22.6825	1.0000	0.6389	0.0040	0.6957	0.0040	0.7985	0.0040	0.8384	0.0040	0.9101	0
Brazil (52) v. Fiji (24)	43520.2780	0.0010	0.0312	0.0010	-2.7987	1.0000	0.6386	0.0010	0.7006	0.0010	0.4726	0.0010	0.5520	0.0010	0.6958	0
Gulf_of_Mexico (40) v. South_Africa (23)	36690.5573	0.0010	0.0306	0.0010	-2.5036	1.0000	0.6384	0.0010	0.7000	0.0010	0.4741	0.0010	0.5531	0.0010	0.6968	0
Costa_Rica (15) v. Fiji (24)	21613.7417	0.0010	0.0280	0.0010	-6.1858	1.0000	0.6369	0.0010	0.7048	0.0010	0.5462	0.0010	0.6151	0.0010	0.7511	0
Gulf_of_Mexico (40) v. Reunion (28)	40078.5966	0.0010	0.0308	0.0010	-2.4030	1.0000	0.6365	0.0010	0.6949	0.0010	0.4737	0.0010	0.5530	0.0010	0.6967	0
Thailand (5) v. Western_North_Atlantic (8)	8033.0419	0.0030	0.0301	0.0030	-14.7546	1.0000	0.6351	0.0030	0.6924	0.0030	0.7200	0.0030	0.7731	0.0030	0.8681	0
Costa_Rica (15) v. Urauchi_River (35)	27662.1809	0.0010	0.0291	0.0010	-6.0830	1.0000	0.6343	0.0010	0.6924	0.0010	0.5466	0.0010	0.6163	0.0010	0.7519	0
Okinawa (9) v. Western_North_Atlantic (8)	10363.4737	0.0010	0.0312	0.0010	-10.3435	1.0000	0.6338	0.0010	0.6907	0.0010	0.6395	0.0010	0.7033	0.0010	0.8190	0
East_Alligator_River (7) v. Western_North_Atlantic (8)	9094.2573	0.0010	0.0293	0.0010	-10.6806	1.0000	0.6329	0.0010	0.6893	0.0010	0.6553	0.0010	0.7164	0.0010	0.8287	0
Brazil (52) v. South_Africa (23)	42160.0679	0.0010	0.0297	0.0010	-2.0854	1.0000	0.6321	0.0010	0.6922	0.0010	0.4600	0.0010	0.5392	0.0010	0.6844	0
Brazil (52) v. Reunion (28)	45869.0575	0.0010	0.0300	0.0010	-1.8295	1.0000	0.6308	0.0010	0.6883	0.0010	0.4592	0.0010	0.5386	0.0010	0.6838	0
Brazil (52) v. Sierra_Leone (1)	14333.3910	0.0180	0.0181	0.0180	4.5739	1.0000	0.6300	1.0000	0.6775	1.0000	6.0027	1.0000	4.5323	1.0000	1.5044	1
Gulf_of_Mexico (40) v. Seychelles (36)	44912.0898	0.0010	0.0309	0.0010	-2.1106	1.0000	0.6300	0.0010	0.6884	0.0010	0.4691	0.0010	0.5488	0.0010	0.6928	0
Caribbean_Sea (2) v. Unknown (2)	2542.7000	0.3526	0.0277	0.3526	3.7075	1.0000	0.6299	0.3526	0.6878	0.1858	-7.0754	0.3526	-3.9645	0.3526	1.8171	0
Costa_Rica (15) v. South_Africa (23)	20816.9559	0.0010	0.0266	0.0010	-5.1465	1.0000	0.6295	0.0010	0.6943	0.0010	0.5297	0.0010	0.5993	0.0010	0.7381	0
Papua_New_Guinea (8) v. Western_North_Atlantic (8)	9706.4549	0.0010	0.0298	0.0010	-9.0767	1.0000	0.6284	0.0010	0.6854	0.0010	0.6257	0.0010	0.6910	0.0010	0.8099	0
Caribbean_Sea (2) v. Darwin_Coastal (2)	2559.0238	0.3157	0.0278	0.3157	3.7461	1.0000	0.6267	0.3157	0.6847	0.1499	-7.7041	1.0000	-4.3619	1.0000	1.7998	0
Sydney_Harbour (8) v. Western_North_Atlantic (8)	9780.1098	0.0010	0.0305	0.0010	-9.0582	1.0000	0.6264	0.0010	0.6842	0.0010	0.6239	0.0010	0.6901	0.0010	0.8092	0
Brazil (52) v. Seychelles (36)	50969.9405	0.0010	0.0300	0.0010	-1.5817	1.0000	0.6254	0.0010	0.6828	0.0010	0.4554	0.0010	0.5352	0.0010	0.6806	0
Costa_Rica (15) v. Reunion (28)	23454.2807	0.0010	0.0269	0.0010	-4.7007	1.0000	0.6251	0.0010	0.6845	0.0010	0.5245	0.0010	0.5947	0.0010	0.7341	0
South_Alligator_River (10) v. Western_North_Atlantic (8)	10838.2134	0.0010	0.0298	0.0010	-8.1197	1.0000	0.6247	0.0010	0.6819	0.0010	0.6019	0.0010	0.6698	0.0010	0.7939	0
Caribbean_Sea (2) v. Indonesia (4)	3700.8168	0.0699	0.0295	0.0699	NA	NA	0.6214	0.0745	0.6826	0.1163	NA	NA	NA	NA	NA	
Urauchi_River (35) v. Western_North_Atlantic (8)	24604.6728	0.0010	0.0327	0.0010	-5.1041	1.0000	0.6198	0.0010	0.6790	0.0010	0.5422	0.0010	0.6179	0.0010	0.7522	0
Adelaide_River (4) v. Caribbean_Sea (2)	3718.3094	0.0749	0.0296	0.0749	7.2692	1.0000	0.6189	0.0851	0.6763	0.0851	3.0806	0.0995	2.4719	0.0995	1.3607	0
Mozambique (11) v. Western_North_Atlantic (8)	11263.4552	0.0010	0.0297	0.0010	-6.9854	1.0000	0.6164	0.0010	0.6744	0.0010	0.5790	0.0010	0.6495	0.0010	0.7780	0
Sri_Lanka (12) v. Western_North_Atlantic (8)	11868.0788	0.0010	0.0298	0.0010	-6.5049	1.0000	0.6160	0.0010	0.6740	0.0010	0.5679	0.0010	0.6395	0.0010	0.7701	0
Costa_Rica (15) v. Seychelles (36)	27353.9216	0.0010	0.0269	0.0010	-4.0224	1.0000	0.6158	0.0010	0.6746	0.0010	0.5142	0.0010	0.5852	0.0010	0.7261	0
Fiji (24) v. Western_North_Atlantic (8)	18191.8114	0.0010	0.0311	0.0010	-5.3489	1.0000	0.6135	0.0010	0.6724	0.0010	0.5429	0.0010	0.6176	0.0010	0.7521	0
Clarence_River (11) v. Western_North_Atlantic (8)	11446.3472	0.0010	0.0302	0.0010	-6.4380	1.0000	0.6127	0.0010	0.6717	0.0010	0.5666	0.0010	0.6393	0.0010	0.7698	0
Arabian_Sea (15) v. Western_North_Atlantic (8)	13534.4065	0.0010	0.0299	0.0010	-5.4304	1.0000	0.6107	0.0010	0.6694	0.0010	0.5454	0.0010	0.6195	0.0010	0.7538	0
Caribbean_Sea (2) v. Okinawa (9)	6348.1732	0.0180	0.0310	0.0180	15.4804	0.0216	0.6097	0.0212	0.6726	0.0212	1.4948	0.0216	1.3717	0.0216	1.1490	0
Caribbean_Sea (2) v. Urauchi_River (35)	19161.2817	0.0010	0.0324	0.0010	-55.0393	1.0000	0.6090	0.0014	0.6750	0.0018	0.9271	0.0019	0.9427	0.0019	0.9703	0
South_Africa (23) v. Western_North_Atlantic (8)	17466.8199	0.0010	0.0298	0.0010	-4.1921	1.0000	0.6047	0.0010	0.6636	0.0010	0.5205	0.0010	0.5964	0.0010	0.7345	0
Reunion (28) v. Western_North_Atlantic (8)	20237.7524	0.0010	0.0301	0.0010	-3.8775	1.0000	0.6046	0.0010	0.6637	0.0010	0.5155	0.0010	0.5919	0.0010	0.7308	0
Caribbean_Sea (2) v. East_Alligator_River (7)	5259.9809	0.0260	0.0293	0.0260	13.8073	0.0327	0.6029	0.0285	0.6651	0.0327	1.5621	0.0327	1.4218	0.0327	1.1646	0

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Caribbean_Sea (2) v. Daly_River (3)	3149.1187	0.1209	0.0294	0.1209	5.8210	1.0000	0.6020	0.1209	0.6626	0.1209	5.2198	0.1315	3.8800	0.1315	1.4630	0
Seychelles (36) v. Western_North_Atlantic (8)	24232.9745	0.0010	0.0301	0.0010	-3.3147	1.0000	0.5999	0.0010	0.6595	0.0010	0.5041	0.0010	0.5815	0.0010	0.7218	0
Caribbean_Sea (2) v. Papua_New_Guinea (8)	5760.8634	0.0260	0.0296	0.0260	17.1768	0.0308	0.5982	0.0295	0.6625	0.0295	1.4017	0.0308	1.3042	0.0308	1.1266	0
Caribbean_Sea (2) v. South_Alligator_River (10)	6781.6840	0.0160	0.0297	0.0160	22.4176	0.0210	0.5979	0.0183	0.6609	0.0194	1.2800	0.0210	1.2140	0.0210	1.0939	0
Caribbean_Sea (2) v. Fiji (24)	13143.0515	0.0050	0.0311	0.0050	-91.8125	1.0000	0.5970	0.0100	0.6805	0.0133	0.9541	0.0135	0.9639	0.0135	0.9815	0
Caribbean_Sea (2) v. Thailand (5)	4251.8777	0.0529	0.0302	0.0529	10.0058	0.5177	0.5966	0.0555	0.6593	0.0555	1.9743	0.0646	1.7099	0.0646	1.2387	0
Caribbean_Sea (2) v. Wenlock_River (4)	3714.4194	0.0679	0.0295	0.0679	7.9460	0.3622	0.5952	0.0726	0.6574	0.0726	2.5621	0.0784	2.1141	0.0784	1.3128	0
Caribbean_Sea (2) v. Sydney_Harbour (8)	5786.2777	0.0220	0.0302	0.0220	17.8923	0.0285	0.5929	0.0269	0.6595	0.0269	1.3780	0.0285	1.2858	0.0285	1.1202	0
Caribbean_Sea (2) v. Sri_Lanka (12)	7665.6193	0.0200	0.0294	0.0200	53.9606	0.0251	0.5901	0.0234	0.6545	0.0242	1.0951	0.0251	1.0739	0.0251	1.0353	0
Caribbean_Sea (2) v. Reunion (28)	15203.0711	0.0020	0.0297	0.0020	-17.6781	1.0000	0.5883	0.0030	0.6575	0.0031	0.8191	0.0032	0.8550	0.0032	0.9203	0
Arabian_Sea (15) v. Caribbean_Sea (2)	9164.2691	0.0070	0.0298	0.0070	-220.7442	1.0000	0.5868	0.0080	0.6471	0.0080	0.9803	0.0085	0.9846	0.0085	0.9922	0
Caribbean_Sea (2) v. Mozambique (11)	7144.3222	0.0120	0.0295	0.0120	35.0583	0.0319	0.5863	0.0244	0.6684	0.0284	1.1574	0.0319	1.1215	0.0319	1.0563	0
Caribbean_Sea (2) v. Seychelles (36)	18801.7891	0.0030	0.0299	0.0030	-11.6595	1.0000	0.5863	0.0040	0.6530	0.0043	0.7643	0.0044	0.8099	0.0044	0.8923	0
Caribbean_Sea (2) v. South_Africa (23)	12645.9916	0.0040	0.0296	0.0040	-23.8798	1.0000	0.5858	0.0054	0.6649	0.0059	0.8548	0.0060	0.8841	0.0060	0.9375	0
Caribbean_Sea (2) v. Clarence_River (11)	7257.9437	0.0090	0.0300	0.0090	47.1972	0.0120	0.5831	0.0110	0.6491	0.0110	1.1102	0.0120	1.0851	0.0120	1.0403	0
Caribbean_Sea (2) v. Costa_Rica (15)	2893.6819	0.0060	0.0032	0.0060	9.3903	1.0000	0.4308	0.0192	0.4601	0.0341	-52.5077	1.0000	-43.5363	1.0000	1.8647	1
Costa_Rica (15) v. Western_North_Atlantic (8)	4105.2733	0.0010	0.0032	0.0010	-30.8133	1.0000	0.3832	0.0010	0.4057	0.0010	0.6068	0.0010	0.6338	0.0010	0.7721	0
Costa_Rica (15) v. Gulf_of_Mexico (40)	8142.6036	0.0010	0.0034	0.0010	-11.1297	1.0000	0.3526	0.0010	0.3869	0.0010	0.3368	0.0010	0.3682	0.0010	0.5274	0
Brazil (52) v. Costa_Rica (15)	9169.3636	0.0010	0.0032	0.0010	-8.1577	1.0000	0.3323	0.0010	0.3565	0.0010	0.2953	0.0010	0.3258	0.0010	0.4795	0
Sierra_Leone (1) v. Urauchi_River (35)	3537.3346	0.0270	0.0019	0.0270	4.5406	1.0000	0.1875	1.0000	0.2084	1.0000	-5.5054	1.0000	-3.9614	1.0000	2.1012	1
Okinawa (9) v. Sierra_Leone (1)	1449.3241	0.1129	0.0016	0.1129	3.3895	1.0000	0.1572	1.0000	0.1730	1.0000	-2.1137	1.0000	-1.1208	1.0000	2.9042	1
Indonesia (4) v. Sierra_Leone (1)	935.4608	0.2348	0.0013	0.2348	NA	NA	0.1556	0.5622	0.1711	0.5622	NA	NA	NA	NA	NA	
Fiji (24) v. Sierra_Leone (1)	2413.7037	0.0430	0.0016	0.0430	4.4327	1.0000	0.1373	1.0000	0.1514	1.0000	-4.8777	1.0000	-3.4768	1.0000	2.1545	1
Adelaide_River (4) v. Sierra_Leone (1)	910.9826	0.2028	0.0014	0.2028	2.5969	1.0000	0.1325	1.0000	0.1460	1.0000	-1.5533	1.0000	-0.5169	1.0000	3.7415	1
Sierra_Leone (1) v. Towns_River (2)	662.4667	0.3536	0.0012	0.3536	NA	NA	0.1288	0.3536	0.1453	0.3536	NA	NA	NA	NA	NA	
East_Alligator_River (7) v. Sierra_Leone (1)	1156.7100	0.1359	0.0014	0.1359	3.2295	1.0000	0.1265	1.0000	0.1396	1.0000	-2.0160	1.0000	-1.0346	1.0000	3.0026	1
Reunion (28) v. Sierra_Leone (1)	2602.7451	0.0360	0.0014	0.0360	4.9788	1.0000	0.1248	0.5538	0.1379	0.5538	-12.5774	1.0000	-9.7044	1.0000	1.9246	1
Arabian_Sea (15) v. Sierra_Leone (1)	1781.1143	0.0639	0.0014	0.0639	4.1711	1.0000	0.1233	1.0000	0.1365	1.0000	-3.9437	1.0000	-2.7023	1.0000	2.2577	1
Seychelles (36) v. Sierra_Leone (1)	3018.7283	0.0270	0.0014	0.0270	5.5605	1.0000	0.1219	1.0000	0.1347	1.0000	36.3786	1.0000	29.5263	1.0000	1.7632	1
Sierra_Leone (1) v. Sydney_Harbour (8)	1283.9870	0.1209	0.0015	0.1209	3.4030	1.0000	0.1211	1.0000	0.1359	1.0000	-2.2485	1.0000	-1.2355	1.0000	2.7906	1
Papua_New_Guinea (8) v. Sierra_Leone (1)	1248.3091	0.1189	0.0013	0.1189	3.3834	1.0000	0.1199	0.5219	0.1325	0.5219	-2.1846	1.0000	-1.1957	1.0000	2.8535	1
Sierra_Leone (1) v. Sri_Lanka (12)	1556.1057	0.0719	0.0013	0.0719	3.8713	1.0000	0.1178	0.4444	0.1314	1.0000	-2.9790	1.0000	-1.9075	1.0000	2.4692	1
Sierra_Leone (1) v. Thailand (5)	978.5387	0.1698	0.0015	0.1698	2.9111	1.0000	0.1168	1.0000	0.1305	1.0000	-1.7844	1.0000	-0.7697	1.0000	3.2560	1
Clarence_River (11) v. Sierra_Leone (1)	1453.4856	0.0879	0.0015	0.0879	3.8156	1.0000	0.1139	0.5146	0.1265	0.5146	-2.9214	1.0000	-1.8332	1.0000	2.4746	1
Sierra_Leone (1) v. South_Alligator_River (10)	1400.4489	0.0839	0.0013	0.0839	3.5773	1.0000	0.1138	0.3294	0.1266	0.5091	-2.3774	1.0000	-1.3837	1.0000	2.7306	1
Darwin_Coastal (2) v. Sierra_Leone (1)	659.5417	0.3267	0.0011	0.3267	NA	NA	0.1104	0.3267	0.1220	0.3267	NA	NA	NA	NA	NA	
Sierra_Leone (1) v. South_Africa (23)	2193.7608	0.0430	0.0013	0.0799	4.7410	1.0000	0.1085	1.0000	0.1239	1.0000	-7.5959	1.0000	-5.7079	1.0000	2.0170	1
Mozambique (11) v. Sierra_Leone (1)	1497.0249	0.0939	0.0014	0.0939	3.7329	1.0000	0.1052	1.0000	0.1165	1.0000	-2.7257	1.0000	-1.6785	1.0000	2.5521	1
Sierra_Leone (1) v. Wenlock_River (4)	897.8710	0.2128	0.0016	0.2128	2.6582	1.0000	0.1021	0.5285	0.1144	1.0000	-1.6367	1.0000	-0.5907	1.0000	3.4985	1
Sierra_Leone (1) v. Unknown (2)	634.6667	0.3347	0.0010	0.3347	NA	NA	0.0965	0.3347	0.1079	0.3347	NA	NA	NA	NA	NA	
Daly_River (3) v. Sierra_Leone (1)	777.5623	0.2657	0.0014	0.2657	2.3085	1.0000	0.0859	1.0000	0.0956	1.0000	-1.4345	1.0000	-0.3314	1.0000	4.0639	1
Fiji (24) v. Urauchi_River (35)	4024.2388	0.0010	0.0009	0.0010	-4.3109	1.0000	0.0717	0.0010	0.0794	0.0010	0.0750	0.0010	0.0889	0.0010	0.1525	0
Trinity_inlet (1) v. Urauchi_River (35)	1666.6853	0.0260	0.0011	0.0260	4.4311	1.0000	0.0649	0.5000	0.0722	1.0000	-3.5925	1.0000	-2.5347	1.0000	2.3634	1
Okinawa (9) v. Trinity_inlet (1)	950.1565	0.0839	0.0011	0.2008	3.3500	1.0000	0.0639	1.0000	0.0703	1.0000	-1.8885	1.0000	-0.9747	1.0000	3.2226	1
Okinawa (9) v. Urauchi_River (35)	2432.4996	0.0010	0.0007	0.0010	-6.4012	0.9920	0.0633	0.0010	0.0702	0.0010	0.1362	0.0010	0.1579	0.0010	0.2588	0
Darwin_Coastal (2) v. Urauchi_River (35)	1785.5963	0.0030	0.0007	0.0320	-148.9762	0.4298	0.0568	0.0115	0.0631	0.0129	0.9236	0.6125	0.9308	0.6080	0.9640	0
Fiji (24) v. Okinawa (9)	2148.5829	0.0010	0.0006	0.0010	-6.0998	1.0000	0.0550	0.0010	0.0607	0.0010	0.1382	0.0010	0.1602	0.0010	0.2622	0
Indonesia (4) v. Okinawa (9)	1136.2430	0.0150	0.0006	0.0370	NA	NA	0.0508	0.0210	0.0562	0.0230	NA	NA	NA	NA	NA	
Daly_River (3) v. Urauchi_River (35)	1910.5521	0.0010	0.0006	0.0050	-12.7465	0.0509	0.0500	0.0022	0.0555	0.0022	0.4084	0.3905	0.4439	0.3319	0.6051	0
Adelaide_River (4) v. Urauchi_River (35)	1905.4973	0.0010	0.0006	0.0040	-9.6565	0.7655	0.0498	0.0041	0.0553	0.0041	0.2903	0.0194	0.3223	0.0194	0.4748	0
Darwin_Coastal (2) v. Okinawa (9)	1025.9434	0.0400	0.0007	0.1648	15.7435	0.8638	0.0493	0.1257	0.0547	0.0805	3.0311	0.4817	2.7481	0.4817	1.4336	0
Sydney_Harbour (8) v. Urauchi_River (35)	2307.4937	0.0010	0.0006	0.0010	-6.0692	0.3447	0.0487	0.0010	0.0541	0.0010	0.1324	0.0020	0.1540	0.0010	0.2529	0

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Thailand (5) v. Urauchi_River (35)	2122.4778	0.0010	0.0006	0.0020	-7.4291	0.0821	0.0470	0.0010	0.0522	0.0010	0.2054	0.0320	0.2342	0.0280	0.3647	0
Urauchi_River (35) v. Wenlock_River (4)	2035.7053	0.0010	0.0005	0.0110	-8.6894	0.0416	0.0469	0.0101	0.0517	0.0101	0.2666	0.1653	0.2991	0.1278	0.4466	0
East_Alligator_River (7) v. Urauchi_River (35)	2125.4060	0.0010	0.0005	0.0010	-6.5674	0.7413	0.0469	0.0010	0.0521	0.0010	0.1517	0.0010	0.1748	0.0010	0.2835	0
Reunion (28) v. Urauchi_River (35)	3314.2143	0.0010	0.0005	0.0010	-3.9530	1.0000	0.0468	0.0010	0.0519	0.0010	0.0554	0.0010	0.0660	0.0010	0.1151	0
Towns_River (2) v. Urauchi_River (35)	1574.6857	0.0030	0.0008	0.0230	321.1123	0.2485	0.0468	0.0112	0.0520	0.0134	1.0394	0.0676	1.0357	0.0676	1.0175	0
South_Alligator_River (10) v. Urauchi_River (35)	2278.7697	0.0010	0.0004	0.0010	-5.7953	0.8681	0.0459	0.0010	0.0509	0.0010	0.1110	0.0010	0.1296	0.0010	0.2166	0
Mozambique (11) v. Urauchi_River (35)	2368.2467	0.0010	0.0004	0.0010	-5.4065	0.6653	0.0444	0.0010	0.0493	0.0010	0.1008	0.0010	0.1183	0.0010	0.1990	0
South_Africa (23) v. Urauchi_River (35)	2934.1943	0.0010	0.0005	0.0010	-4.1179	1.0000	0.0440	0.0010	0.0488	0.0010	0.0593	0.0010	0.0705	0.0010	0.1226	0
Sri_Lanka (12) v. Urauchi_River (35)	2425.6881	0.0010	0.0005	0.0010	-5.1672	0.8611	0.0439	0.0010	0.0488	0.0010	0.0912	0.0010	0.1073	0.0010	0.1819	0
Papua_New_Guinea (8) v. Urauchi_River (35)	2065.3361	0.0010	0.0005	0.0010	-6.2555	0.6294	0.0431	0.0010	0.0478	0.0010	0.1327	0.0020	0.1539	0.0020	0.2531	0
Clarence_River (11) v. Urauchi_River (35)	2409.3563	0.0010	0.0004	0.0010	-5.2721	0.2388	0.0428	0.0010	0.0476	0.0010	0.0960	0.0010	0.1131	0.0010	0.1908	0
Arabian_Sea (15) v. Urauchi_River (35)	2605.1108	0.0010	0.0005	0.0010	-4.7753	0.9401	0.0425	0.0010	0.0472	0.0010	0.0765	0.0010	0.0905	0.0010	0.1551	0
Daly_River (3) v. Fiji (24)	1731.2166	0.0010	0.0006	0.0010	-12.0407	0.0737	0.0402	0.0011	0.0459	0.0012	0.4043	0.7450	0.4401	0.7181	0.6013	0
Okinawa (9) v. Thailand (5)	1196.3141	0.0070	0.0005	0.0320	-15.0077	0.7992	0.0401	0.0240	0.0444	0.0240	0.4052	0.0609	0.4407	0.0599	0.6020	0
Unknown (2) v. Urauchi_River (35)	1644.1489	0.0070	0.0006	0.0549	-270.8899	0.6652	0.0396	0.0137	0.0439	0.0084	0.9559	0.4700	0.9600	0.4700	0.9796	0
Mozambique (11) v. Okinawa (9)	1445.0771	0.0010	0.0004	0.0020	-8.1618	1.0000	0.0392	0.0010	0.0434	0.0010	0.2018	0.0010	0.2298	0.0010	0.3591	0
Okinawa (9) v. Towns_River (2)	910.1759	0.0759	0.0007	0.0999	13.5855	0.9769	0.0382	0.1535	0.0421	0.1535	4.2907	0.0373	3.8174	0.0373	1.5325	0
Seychelles (36) v. Urauchi_River (35)	3210.9643	0.0010	0.0004	0.0010	-3.6732	1.0000	0.0380	0.0010	0.0421	0.0010	0.0451	0.0010	0.0538	0.0010	0.0947	0
Fiji (24) v. Mozambique (11)	2051.6416	0.0010	0.0003	0.0010	-5.1843	0.9930	0.0374	0.0010	0.0418	0.0010	0.1043	0.0010	0.1224	0.0010	0.2053	0
East_Alligator_River (7) v. Okinawa (9)	1188.0786	0.0110	0.0004	0.0240	-11.7379	0.9840	0.0367	0.0130	0.0407	0.0130	0.3034	0.0130	0.3360	0.0130	0.4906	0
Okinawa (9) v. South_Alligator_River (10)	1350.8773	0.0010	0.0005	0.0010	-9.2828	1.0000	0.0364	0.0010	0.0403	0.0010	0.2249	0.0010	0.2539	0.0010	0.3909	0
Okinawa (9) v. Reunion (28)	1846.5327	0.0010	0.0004	0.0010	-5.3551	1.0000	0.0363	0.0010	0.0405	0.0010	0.1125	0.0010	0.1313	0.0010	0.2192	0
Fiji (24) v. Sri_Lanka (12)	2069.2960	0.0010	0.0004	0.0010	-4.8808	0.9990	0.0361	0.0010	0.0400	0.0010	0.0928	0.0010	0.1092	0.0010	0.1848	0
Arabian_Sea (15) v. Okinawa (9)	1483.1431	0.0010	0.0004	0.0010	-6.9062	1.0000	0.0355	0.0010	0.0394	0.0010	0.1577	0.0010	0.1817	0.0010	0.2932	0
Okinawa (9) v. Sydney_Harbour (8)	1279.3208	0.0020	0.0005	0.0030	-10.0700	0.9900	0.0351	0.0060	0.0390	0.0060	0.2587	0.0080	0.2902	0.0080	0.4361	0
Adelaide_River (4) v. Okinawa (9)	1057.1778	0.0300	0.0004	0.0709	-28.1316	0.9276	0.0350	0.0509	0.0387	0.0493	0.5974	0.0674	0.6264	0.0674	0.7661	0
Fiji (24) v. Wenlock_River (4)	1686.2553	0.0010	0.0005	0.0010	-8.5160	0.0590	0.0348	0.0010	0.0385	0.0010	0.2708	0.4669	0.3037	0.4059	0.4521	0
Adelaide_River (4) v. Fiji (24)	1520.2940	0.0010	0.0005	0.0010	-9.6552	0.6875	0.0347	0.0010	0.0396	0.0010	0.2972	0.1076	0.3295	0.0984	0.4832	0
Fiji (24) v. Reunion (28)	2589.1311	0.0010	0.0003	0.0010	-3.7079	1.0000	0.0345	0.0010	0.0384	0.0010	0.0542	0.0010	0.0645	0.0010	0.1126	0
Okinawa (9) v. Sri_Lanka (12)	1415.0744	0.0010	0.0004	0.0010	-7.7167	1.0000	0.0344	0.0010	0.0382	0.0010	0.1828	0.0010	0.2090	0.0010	0.3312	0
Okinawa (9) v. Wenlock_River (4)	1075.3271	0.0150	0.0004	0.1019	-22.5017	0.5000	0.0344	0.0549	0.0381	0.0549	0.5419	0.2798	0.5746	0.2525	0.7241	0
Clarence_River (11) v. Okinawa (9)	1373.5403	0.0020	0.0004	0.0020	-7.8838	0.9980	0.0344	0.0030	0.0382	0.0030	0.1914	0.0030	0.2190	0.0030	0.3445	0
Fiji (24) v. South_Alligator_River (10)	1944.1067	0.0010	0.0003	0.0010	-5.5174	0.9960	0.0341	0.0010	0.0377	0.0010	0.1115	0.0010	0.1301	0.0010	0.2174	0
Daly_River (3) v. Okinawa (9)	1055.9473	0.0380	0.0005	0.1888	-101.0515	0.4168	0.0332	0.0960	0.0369	0.0960	0.8683	0.5081	0.8803	0.5081	0.9360	0
Fiji (24) v. Seychelles (36)	2711.5330	0.0010	0.0003	0.0010	-3.4246	1.0000	0.0327	0.0010	0.0364	0.0010	0.0471	0.0010	0.0562	0.0010	0.0987	0
Fiji (24) v. Sydney_Harbour (8)	1799.8069	0.0010	0.0004	0.0010	-5.8538	0.6304	0.0326	0.0010	0.0362	0.0010	0.1317	0.0010	0.1531	0.0010	0.2516	0
Fiji (24) v. South_Africa (23)	2316.0134	0.0010	0.0004	0.0010	-3.9623	1.0000	0.0324	0.0010	0.0364	0.0010	0.0595	0.0010	0.0708	0.0010	0.1230	0
Okinawa (9) v. Unknown (2)	938.6960	0.0689	0.0006	0.2288	15.0048	0.9129	0.0321	0.1044	0.0354	0.1044	3.4339	0.3076	3.0945	0.3076	1.4724	0
Okinawa (9) v. Papua_New_Guinea (8)	1208.1026	0.0070	0.0004	0.0120	-10.3885	0.9840	0.0318	0.0140	0.0352	0.0140	0.2627	0.0160	0.2938	0.0150	0.4407	0
Clarence_River (11) v. Fiji (24)	1992.4897	0.0010	0.0003	0.0010	-4.9915	0.8262	0.0316	0.0010	0.0358	0.0010	0.0962	0.0010	0.1134	0.0010	0.1912	0
Okinawa (9) v. Seychelles (36)	1808.3408	0.0010	0.0004	0.0010	-4.9176	1.0000	0.0308	0.0010	0.0343	0.0010	0.0983	0.0010	0.1151	0.0010	0.1943	0
Indonesia (4) v. Trinity_inlet (1)	667.8216	0.1808	0.0006	0.3876	NA	NA	0.0304	0.6424	0.0334	0.6424	NA	NA	NA	NA	NA	
East_Alligator_River (7) v. Fiji (24)	1671.9338	0.0010	0.0004	0.0010	-6.4000	0.8521	0.0303	0.0010	0.0344	0.0010	0.1519	0.0010	0.1749	0.0010	0.2837	0
Darwin_Coastal (2) v. Indonesia (4)	702.5932	0.3277	0.0006	0.2028	NA	NA	0.0301	0.3501	0.0334	0.4926	NA	NA	NA	NA	NA	
Fiji (24) v. Thailand (5)	1694.0464	0.0010	0.0004	0.0010	-7.3051	0.1212	0.0300	0.0010	0.0332	0.0010	0.2070	0.2094	0.2359	0.1633	0.3670	0
Fiji (24) v. Papua_New_Guinea (8)	1699.2647	0.0010	0.0004	0.0010	-6.0110	0.8472	0.0289	0.0010	0.0320	0.0010	0.1326	0.0010	0.1537	0.0010	0.2528	0
Darwin_Coastal (2) v. Fiji (24)	1471.1495	0.0090	0.0006	0.0250	-141.3704	0.5160	0.0289	0.0085	0.0331	0.0115	0.9211	0.8484	0.9285	0.8484	0.9628	0
Arabian_Sea (15) v. Fiji (24)	2078.4294	0.0010	0.0003	0.0010	-4.4720	0.9990	0.0288	0.0010	0.0325	0.0010	0.0747	0.0010	0.0884	0.0010	0.1518	0
Okinawa (9) v. South_Africa (23)	1575.4970	0.0010	0.0003	0.0010	-5.7127	1.0000	0.0285	0.0010	0.0322	0.0010	0.1195	0.0010	0.1391	0.0010	0.2310	0
Indonesia (4) v. Sydney_Harbour (8)	971.3347	0.0529	0.0005	0.0190	NA	NA	0.0230	0.0320	0.0257	0.0320	NA	NA	NA	NA	NA	
Clarence_River (11) v. Indonesia (4)	1039.7297	0.0719	0.0004	0.0270	NA	NA	0.0226	0.0270	0.0251	0.0270	NA	NA	NA	NA	NA	
East_Alligator_River (7) v. Indonesia (4)	902.0496	0.0709	0.0004	0.1009	NA	NA	0.0222	0.0430	0.0246	0.0430	NA	NA	NA	NA	NA	

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Indonesia (4) v. South_Alligator_River (10)	1014.3479	0.0290	0.0004	0.0629	NA	NA	0.0217	0.0250	NA	NA	NA	NA	NA	NA	NA	
Towns_River (2) v. Trinity_inlet (1)	514.2333	0.3367	0.0005	0.6633	NA	NA	0.0208	0.3367	0.0229	0.3367	NA	NA	NA	NA	NA	
Fiji (24) v. Trinity_inlet (1)	1235.3158	0.1319	0.0009	0.6324	4.3398	1.0000	0.0188	1.0000	0.0207	1.0000	-3.4436	1.0000	-2.4129	1.0000	2.3967	1
Daly_River (3) v. East_Alligator_River (7)	892.7082	0.0320	0.0004	0.0370	-516.5499	0.5186	0.0185	0.0292	0.0206	0.0292	0.9730	0.7704	0.9756	0.7674	0.9876	0
Indonesia (4) v. Towns_River (2)	677.8618	0.3946	0.0006	0.2687	NA	NA	0.0183	0.3357	0.0202	0.3357	NA	NA	NA	NA	NA	
Darwin_Coastal (2) v. Thailand (5)	769.5439	0.0589	0.0005	0.1578	10.2804	1.0000	0.0181	0.0615	0.0202	0.0615	9.2098	0.0723	7.8492	0.0723	1.6708	0
Adelaide_River (4) v. Indonesia (4)	779.0209	0.3726	0.0004	0.3686	NA	NA	0.0176	0.3726	0.0195	0.3626	NA	NA	NA	NA	NA	
Indonesia (4) v. Thailand (5)	843.8398	0.1399	0.0004	0.2048	NA	NA	0.0174	0.2008	0.0193	0.2008	NA	NA	NA	NA	NA	
Fiji (24) v. Towns_River (2)	1248.1029	0.0599	0.0006	0.0070	174.3806	0.4225	0.0173	0.0365	0.0191	0.0365	1.0735	0.3526	1.0664	0.3526	1.0320	0
Indonesia (4) v. Mozambique (11)	1008.3876	0.0889	0.0004	0.0729	NA	NA	0.0173	0.0412	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Reunion (28)	1297.9224	0.0320	0.0003	0.0340	NA	NA	0.0170	0.0171	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Seychelles (36)	1356.4138	0.0160	0.0003	0.0210	NA	NA	0.0157	0.0070	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Papua_New_Guinea (8)	917.6883	0.1169	0.0003	0.1638	NA	NA	0.0157	0.1139	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Wenlock_River (4)	811.3902	0.3497	0.0004	0.3227	NA	NA	0.0154	0.3497	0.0170	0.3497	NA	NA	NA	NA	NA	
Fiji (24) v. Unknown (2)	1339.3128	0.0220	0.0006	0.0370	-617.4173	0.8660	0.0147	0.0660	0.0163	0.0698	0.9807	0.6340	0.9825	0.6340	0.9912	0
Indonesia (4) v. Sri_Lanka (12)	982.6080	0.2048	0.0003	0.0480	NA	NA	0.0139	0.0430	NA	NA	NA	NA	NA	NA	NA	
Papua_New_Guinea (8) v. Trinity_inlet (1)	825.1671	0.2278	0.0007	0.6613	3.3463	1.0000	0.0133	0.5312	0.0147	0.5312	-1.9354	1.0000	-1.0364	1.0000	3.1770	1
Arabian_Sea (15) v. Indonesia (4)	1094.2521	0.1029	0.0003	0.0350	NA	NA	0.0132	0.0370	0.0146	0.0370	NA	NA	NA	NA	NA	
East_Alligator_River (7) v. Wenlock_River (4)	922.8167	0.0240	0.0003	0.1538	-25.4102	0.2238	0.0111	0.0470	0.0123	0.0470	0.5873	0.6334	0.6178	0.6104	0.7592	0
Adelaide_River (4) v. South_Alligator_River (10)	941.5904	0.0380	0.0003	0.3856	-20.2887	0.9076	0.0099	0.0300	0.0109	0.0301	0.5020	0.0502	0.5339	0.0502	0.6897	0
Adelaide_River (4) v. Daly_River (3)	770.7919	0.0899	0.0004	0.5734	18.8076	0.4316	0.0096	0.2048	0.0106	0.2048	2.5450	0.8242	2.3400	0.8242	1.3780	0
Sydney_Harbour (8) v. Wenlock_River (4)	962.0491	0.0220	0.0003	0.0819	-18.8519	0.3387	0.0094	0.0390	0.0104	0.0390	0.5013	0.4864	0.5355	0.4734	0.6906	0
Reunion (28) v. South_Alligator_River (10)	1364.2555	0.0040	0.0002	0.0070	-5.1789	0.9091	0.0094	0.0040	0.0104	0.0040	0.0895	0.0060	0.1049	0.0060	0.1785	0
Adelaide_River (4) v. Reunion (28)	1222.1808	0.1469	0.0003	0.1459	-7.8471	0.8586	0.0089	0.0803	0.0100	0.0808	0.2403	0.0939	0.2695	0.0960	0.4110	0
Clarence_River (11) v. Reunion (28)	1454.0720	0.0020	0.0001	0.0300	-4.6313	0.1269	0.0087	0.0060	0.0097	0.0060	0.0756	0.0300	0.0895	0.0240	0.1535	0
East_Alligator_River (7) v. Thailand (5)	902.3264	0.0270	0.0003	0.0500	-17.0205	0.3666	0.0086	0.0490	0.0095	0.0490	0.4489	0.2987	0.4833	0.2667	0.6434	0
Adelaide_River (4) v. Sri_Lanka (12)	988.2344	0.2757	0.0003	0.0879	-13.8484	0.9530	0.0085	0.0629	0.0095	0.0629	0.3944	0.0090	0.4279	0.0080	0.5897	0
Daly_River (3) v. Papua_New_Guinea (8)	874.8755	0.1678	0.0003	0.5355	-75.9501	0.1439	0.0085	0.1738	0.0095	0.1718	0.8341	0.8611	0.8490	0.8611	0.9177	0
East_Alligator_River (7) v. Reunion (28)	1286.8956	0.0689	0.0002	0.0230	-5.6705	0.8591	0.0084	0.0330	0.0094	0.0330	0.1232	0.0370	0.1428	0.0350	0.2368	0
Sri_Lanka (12) v. Sydney_Harbour (8)	1099.1365	0.0140	0.0001	0.3746	-7.5142	0.7592	0.0080	0.0070	0.0089	0.0070	0.1768	0.0090	0.2025	0.0090	0.3223	0
Daly_River (3) v. Seychelles (36)	1335.6156	0.0440	0.0003	0.2308	-7.8035	0.0631	0.0079	0.1247	0.0088	0.1250	0.2857	0.7872	0.3186	0.7597	0.4700	0
East_Alligator_River (7) v. Towns_River (2)	760.0716	0.4406	0.0005	0.0669	12.0980	0.9713	0.0079	0.1856	0.0088	0.1856	5.6343	0.0276	4.9526	0.0276	1.5958	0
Indonesia (4) v. Unknown (2)	667.3588	0.4715	0.0004	0.3916	NA	NA	0.0075	0.4715	0.0082	0.4715	NA	NA	NA	NA	NA	
Adelaide_River (4) v. East_Alligator_River (7)	856.8397	0.1708	0.0003	0.1449	-35.7227	0.8791	0.0074	0.1239	0.0082	0.1279	0.6665	0.0929	0.6916	0.0929	0.8149	0
Mozambique (11) v. Papua_New_Guinea (8)	1043.5265	0.1369	0.0001	0.7403	-8.2953	0.8332	0.0073	0.0330	0.0081	0.0340	0.2000	0.0709	0.2273	0.0679	0.3561	0
Arabian_Sea (15) v. East_Alligator_River (7)	1104.7522	0.1259	0.0002	0.0440	-7.2099	0.9500	0.0073	0.0090	0.0081	0.0090	0.1720	0.0020	0.1968	0.0020	0.3147	0
Seychelles (36) v. Sydney_Harbour (8)	1400.0457	0.0020	0.0002	0.0140	-4.7432	0.2977	0.0071	0.0110	0.0079	0.0110	0.0909	0.0350	0.1068	0.0280	0.1812	0
Reunion (28) v. Thailand (5)	1346.7053	0.0150	0.0002	0.1489	-6.2375	0.0980	0.0065	0.1089	0.0072	0.1099	0.1680	0.5850	0.1931	0.5440	0.3092	0
Reunion (28) v. Wenlock_River (4)	1346.2016	0.0140	0.0002	0.4995	-7.0671	0.0424	0.0065	0.1512	0.0072	0.1512	0.2193	0.8184	0.2486	0.7871	0.3837	0
South_Alligator_River (10) v. Sydney_Harbour (8)	1018.1389	0.0360	0.0001	0.6803	-8.9427	0.7003	0.0063	0.0330	0.0070	0.0330	0.2163	0.0689	0.2447	0.0619	0.3790	0
Arabian_Sea (15) v. Clarence_River (11)	1207.4258	0.0200	0.0001	0.4695	-5.5931	0.7213	0.0063	0.0130	0.0070	0.0130	0.1071	0.0230	0.1256	0.0220	0.2102	0
Clarence_River (11) v. Sri_Lanka (12)	1163.7924	0.0220	0.0002	0.0280	-6.2141	0.9191	0.0063	0.0420	0.0070	0.0420	0.1280	0.0470	0.1490	0.0460	0.2456	0
East_Alligator_River (7) v. South_Alligator_River (10)	975.5935	0.0999	0.0002	0.3696	-10.1834	0.8392	0.0062	0.0629	0.0069	0.0629	0.2532	0.0759	0.2831	0.0759	0.4280	0
Sri_Lanka (12) v. Thailand (5)	1037.7147	0.0609	0.0002	0.4406	-9.7728	0.2797	0.0060	0.0709	0.0066	0.0709	0.2751	0.4695	0.3076	0.4246	0.4569	0
Mozambique (11) v. Wenlock_River (4)	1031.0080	0.1069	0.0003	0.3397	-13.2967	0.0834	0.0060	0.1541	0.0066	0.1572	0.3917	0.8642	0.4271	0.8588	0.5883	0
Sri_Lanka (12) v. Towns_River (2)	859.1948	0.6703	0.0005	0.2198	26.6100	0.9777	0.0059	0.2900	0.0065	0.2900	1.7219	0.0432	1.6385	0.0432	1.2346	0
East_Alligator_River (7) v. Sydney_Harbour (8)	932.6645	0.1908	0.0002	0.3337	-11.1195	0.9461	0.0057	0.0609	0.0064	0.0609	0.2909	0.0589	0.3231	0.0599	0.4757	0
Arabian_Sea (15) v. Mozambique (11)	1207.9446	0.0180	0.0001	0.1768	-5.8082	0.9371	0.0057	0.0110	0.0064	0.0110	0.1127	0.0050	0.1315	0.0060	0.2195	0
South_Africa (23) v. Towns_River (2)	1027.9503	0.7682	0.0005	0.1199	-118.5844	0.9803	0.0055	0.1743	0.0061	0.1743	0.9082	0.0319	0.9165	0.0319	0.9562	0
Mozambique (11) v. Reunion (28)	1367.2751	0.0080	0.0001	0.2677	-4.8361	0.4216	0.0054	0.0320	0.0061	0.0330	0.0789	0.0210	0.0929	0.0180	0.1592	0
Caribbean_Sea (2) v. Gulf_of_Mexico (40)	911.5208	0.3417	0.0002	0.4266	19.0179	0.4043	0.0053	0.2949	0.0059	0.2943	3.1415	0.6170	2.9350	0.6099	1.4672	0
Reunion (28) v. Sydney_Harbour (8)	1294.5729	0.0430	0.0001	0.1399	-5.3241	0.2318	0.0053	0.0609	0.0059	0.0609	0.1046	0.1968	0.1222	0.1798	0.2053	0

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Adelaide_River (4) v. Clarence_River (11)	941.4020	0.4066	0.0003	0.0939	-14.6119	0.9790	0.0052	0.2657	0.0058	0.2657	0.4116	0.0310	0.4458	0.0320	0.6074	0
Brazil (52) v. Western_North_Atlantic (8)	1078.0912	0.6563	0.0000	0.5255	-8.6921	0.9870	0.0052	0.0410	0.0056	0.0410	0.1440	0.0190	0.1594	0.0190	0.2652	0
East_Alligator_River (7) v. Mozambique (11)	1030.0325	0.1499	0.0002	0.2228	-8.9136	0.7942	0.0052	0.0649	0.0058	0.0639	0.2245	0.1758	0.2532	0.1798	0.3901	0
Reunion (28) v. Sri_Lanka (12)	1390.3773	0.0070	0.0001	0.0939	-4.5725	0.6923	0.0051	0.0170	0.0057	0.0170	0.0691	0.0340	0.0817	0.0320	0.1410	0
Reunion (28) v. Seychelles (36)	1571.8855	0.0010	0.0001	0.0050	-3.5600	0.9990	0.0051	0.0010	0.0056	0.0010	0.0310	0.0010	0.0371	0.0010	0.0661	0
Clarence_River (11) v. East_Alligator_River (7)	996.9789	0.2727	0.0002	0.2438	-8.5864	0.9820	0.0050	0.1778	0.0055	0.1788	0.2148	0.0639	0.2434	0.0729	0.3771	0
Clarence_River (11) v. South_Africa (23)	1250.3632	0.0400	0.0001	0.1469	-4.9951	0.1229	0.0048	0.0270	0.0055	0.0270	0.0838	0.1728	0.0989	0.1518	0.1686	0
South_Alligator_River (10) v. Wenlock_River (4)	969.7762	0.0599	0.0002	0.8402	-16.3397	0.0671	0.0048	0.1852	0.0053	0.1852	0.4447	0.8519	0.4792	0.8448	0.6395	0
South_Africa (23) v. South_Alligator_River (10)	1209.3466	0.1548	0.0001	0.2957	-5.4308	0.9191	0.0047	0.0410	0.0052	0.0420	0.0962	0.0959	0.1125	0.0959	0.1904	0
Daly_River (3) v. Sri_Lanka (12)	961.0287	0.3117	0.0003	0.5015	-21.5636	0.1465	0.0045	0.2503	0.0050	0.2503	0.5599	0.8535	0.5916	0.8555	0.7382	0
Papua_New_Guinea (8) v. Reunion (28)	1210.6043	0.2228	0.0001	0.2677	-5.5034	0.6444	0.0045	0.1039	0.0050	0.1039	0.1073	0.1359	0.1250	0.1319	0.2098	0
Darwin_Coastal (2) v. Reunion (28)	1230.3032	0.1578	0.0004	0.7063	-33.5158	0.3099	0.0044	0.2821	0.0050	0.2559	0.7277	0.6901	0.7499	0.6901	0.8553	0
Mozambique (11) v. Towns_River (2)	895.5756	0.5105	0.0006	0.0959	22.5004	0.6591	0.0044	0.2655	0.0049	0.2655	1.9386	0.3788	1.8244	0.3788	1.2805	0
Reunion (28) v. Towns_River (2)	1183.6801	0.2657	0.0005	0.1289	-54.0274	0.9062	0.0044	0.3009	0.0049	0.3009	0.8160	0.0973	0.8315	0.0973	0.9072	0
Adelaide_River (4) v. Seychelles (36)	1216.3055	0.3546	0.0002	0.3706	-6.6652	0.9221	0.0043	0.1878	0.0048	0.1878	0.2046	0.0699	0.2315	0.0769	0.3621	0
Reunion (28) v. South_Africa (23)	1472.1707	0.0050	0.0001	0.0020	-3.8544	0.9640	0.0043	0.0080	0.0049	0.0080	0.0408	0.0080	0.0486	0.0080	0.0859	0
Clarence_River (11) v. Daly_River (3)	930.0515	0.3766	0.0003	0.4905	-22.8094	0.4525	0.0043	0.3463	0.0048	0.3463	0.5795	0.5325	0.6112	0.5325	0.7538	0
Arabian_Sea (15) v. Papua_New_Guinea (8)	1089.1414	0.1978	0.0001	0.4316	-6.8242	0.8721	0.0042	0.0589	0.0047	0.0589	0.1507	0.0360	0.1736	0.0350	0.2819	0
South_Africa (23) v. Sydney_Harbour (8)	1180.4263	0.2168	0.0002	0.0629	-5.7041	0.2408	0.0042	0.0639	0.0047	0.0639	0.1160	0.3387	0.1351	0.3197	0.2250	0
Mozambique (11) v. Sri_Lanka (12)	1130.5400	0.0819	0.0002	0.0869	-6.5048	0.8641	0.0041	0.0809	0.0046	0.0829	0.1345	0.0719	0.1558	0.0699	0.2559	0
Mozambique (11) v. Seychelles (36)	1390.0386	0.0140	0.0001	0.1888	-4.3710	0.3556	0.0041	0.0300	0.0046	0.0300	0.0671	0.0150	0.0794	0.0120	0.1372	0
Seychelles (36) v. South_Alligator_River (10)	1305.5406	0.0609	0.0001	0.0949	-4.6829	0.8661	0.0041	0.0340	0.0045	0.0340	0.0749	0.0260	0.0881	0.0260	0.1517	0
South_Alligator_River (10) v. Thailand (5)	983.2481	0.0150	0.0003	0.0919	-12.3873	0.0929	0.0040	0.1738	0.0045	0.1748	0.3381	0.6873	0.3721	0.6573	0.5308	0
Daly_River (3) v. Thailand (5)	763.8674	0.2288	0.0003	0.5375	46.6455	0.5788	0.0039	0.3835	0.0043	0.3835	1.3796	0.4751	1.3362	0.4629	1.1413	0
Clarence_River (11) v. Seychelles (36)	1411.9116	0.0040	0.0001	0.1169	-4.2002	0.0639	0.0038	0.0480	0.0043	0.0480	0.0629	0.1948	0.0747	0.1578	0.1295	0
Clarence_River (11) v. Mozambique (11)	1124.7493	0.1159	0.0001	0.4705	-6.5442	0.8362	0.0038	0.1479	0.0043	0.1469	0.1404	0.1329	0.1628	0.1329	0.2659	0
Brazil (52) v. Gulf_of_Mexico (40)	1437.4854	0.0010	0.0000	0.1738	-5.5718	1.0000	0.0038	0.0010	0.0041	0.0010	0.0328	0.0010	0.0373	0.0010	0.0679	0
Adelaide_River (4) v. Papua_New_Guinea (8)	850.1131	0.4146	0.0003	0.1578	-26.3131	0.8939	0.0037	0.2727	0.0041	0.2727	0.5825	0.1231	0.6117	0.1221	0.7546	0
Mozambique (11) v. South_Africa (23)	1238.8978	0.1728	0.0001	0.5335	-5.0399	0.4366	0.0037	0.0569	0.0041	0.0589	0.0860	0.0699	0.1011	0.0669	0.1722	0
Seychelles (36) v. Thailand (5)	1283.7125	0.0829	0.0002	0.0679	-5.5690	0.0919	0.0036	0.1808	0.0040	0.1818	0.1468	0.6863	0.1698	0.6284	0.2761	0
Arabian_Sea (15) v. Sydney_Harbour (8)	1135.0700	0.0909	0.0001	0.5415	-6.5343	0.5744	0.0036	0.0939	0.0040	0.0939	0.1451	0.1239	0.1677	0.1139	0.2732	0
Arabian_Sea (15) v. South_Africa (23)	1320.0624	0.0220	0.0001	0.2258	-4.4496	0.6823	0.0035	0.0230	0.0039	0.0230	0.0624	0.0480	0.0740	0.0490	0.1284	0
Arabian_Sea (15) v. South_Alligator_River (10)	1115.0126	0.1938	0.0001	0.0989	-6.3538	0.9441	0.0034	0.0909	0.0038	0.0909	0.1248	0.0569	0.1447	0.0589	0.2396	0
Adelaide_River (4) v. Arabian_Sea (15)	993.5807	0.6264	0.0002	0.6264	-11.2483	0.9449	0.0034	0.2593	0.0038	0.2595	0.3324	0.0541	0.3652	0.0571	0.5236	0
Adelaide_River (4) v. Thailand (5)	781.4286	0.2188	0.0004	0.0220	-195.7076	0.9401	0.0033	0.3377	0.0037	0.3377	0.9266	0.0719	0.9334	0.0719	0.9654	0
East_Alligator_River (7) v. Seychelles (36)	1195.8916	0.5554	0.0001	0.3237	-5.1411	0.8711	0.0032	0.1279	0.0035	0.1279	0.1061	0.0669	0.1236	0.0689	0.2077	0
South_Africa (23) v. Sri_Lanka (12)	1252.2227	0.0989	0.0001	0.1938	-4.8724	0.7183	0.0032	0.0589	0.0035	0.0599	0.0770	0.1229	0.0908	0.1179	0.1558	0
Clarence_River (11) v. Sydney_Harbour (8)	1006.3243	0.3387	0.0002	0.0400	-7.7431	0.8202	0.0031	0.2587	0.0035	0.2587	0.1845	0.1978	0.2113	0.2028	0.3341	0
Adelaide_River (4) v. Mozambique (11)	946.6996	0.4605	0.0003	0.1898	-16.2080	0.5687	0.0030	0.3086	0.0035	0.3001	0.4403	0.5100	0.4737	0.5268	0.6346	0
Seychelles (36) v. Wenlock_River (4)	1327.9458	0.0400	0.0002	0.8771	-6.1447	0.0170	0.0030	0.2657	0.0033	0.2657	0.1896	0.9221	0.2166	0.9031	0.3414	0
Arabian_Sea (15) v. Reunion (28)	1444.5863	0.0050	0.0001	0.1469	-4.1460	0.3976	0.0030	0.0799	0.0033	0.0799	0.0541	0.1309	0.0642	0.1249	0.1122	0
Papua_New_Guinea (8) v. Thailand (5)	910.1297	0.1439	0.0002	0.7672	-14.2907	0.1918	0.0029	0.3267	0.0032	0.3277	0.3904	0.6573	0.4252	0.6364	0.5866	0
Sydney_Harbour (8) v. Thailand (5)	925.8270	0.0949	0.0002	0.4525	-13.6220	0.3506	0.0027	0.2807	0.0030	0.2807	0.3795	0.5225	0.4147	0.5065	0.5758	0
Arabian_Sea (15) v. Darwin_Coastal (2)	1005.1362	0.3586	0.0004	0.5405	111.3996	0.6475	0.0026	0.3474	0.0029	0.3474	1.1179	0.3391	1.1060	0.3391	1.0501	0
East_Alligator_River (7) v. Trinity_inlet (1)	720.2502	0.2248	0.0007	0.6064	3.1924	1.0000	0.0026	1.0000	0.0029	1.0000	-1.7843	1.0000	-0.8893	1.0000	3.4089	1
Adelaide_River (4) v. Trinity_inlet (1)	666.6240	0.1878	0.0006	1.0000	2.5850	1.0000	0.0026	0.5040	0.0028	0.5040	-1.4523	1.0000	-0.4728	1.0000	4.2563	1
Clarence_River (11) v. South_Alligator_River (10)	1061.2904	0.1259	0.0001	0.4026	-7.2648	0.8482	0.0025	0.2378	0.0028	0.2378	0.1570	0.2118	0.1807	0.2158	0.2919	0
Mozambique (11) v. South_Alligator_River (10)	1064.2663	0.2298	0.0001	0.4675	-7.4770	0.7512	0.0024	0.2148	0.0027	0.2168	0.1636	0.2248	0.1875	0.2248	0.3017	0
South_Africa (23) v. Thailand (5)	1203.2235	0.0519	0.0002	0.7353	-6.7062	0.0669	0.0024	0.2478	0.0027	0.2478	0.1820	0.8142	0.2083	0.7652	0.3302	0
Daly_River (3) v. Mozambique (11)	949.4926	0.3996	0.0003	0.7712	-26.0216	0.0914	0.0023	0.3981	0.0026	0.4020	0.6137	0.9173	0.6433	0.9173	0.7789	0
Darwin_Coastal (2) v. Towns_River (2)	576.4500	0.6364	0.0004	0.6364	NA	NA	0.0022	0.6364	0.0024	0.4835	NA	NA	NA	NA	NA	
Sri_Lanka (12) v. Trinity_inlet (1)	913.8882	0.3706	0.0007	0.5095	3.8034	1.0000	0.0020	0.6017	0.0022	0.6017	-2.4250	1.0000	-1.5183	1.0000	2.7672	1

Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
East_Alligator_River (7) v. Sri_Lanka (12)	976.7977	0.5315	0.0002	0.2258	-8.4117	0.7602	0.0019	0.2897	0.0021	0.2897	0.2040	0.2008	0.2311	0.2008	0.3614	0
Seychelles (36) v. Sri_Lanka (12)	1345.7969	0.0480	0.0001	0.0559	-4.2228	0.6104	0.0019	0.1508	0.0021	0.1508	0.0587	0.1558	0.0695	0.1489	0.1211	0
Darwin_Coastal (2) v. South_Alligator_River (10)	878.4396	0.1818	0.0004	0.6284	20.5747	0.5574	0.0018	0.4458	0.0020	0.4639	2.1530	0.4962	2.0093	0.5100	1.3201	0
Papua_New_Guinea (8) v. Sydney_Harbour (8)	931.5514	0.4366	0.0002	0.3616	-9.9910	0.6553	0.0018	0.3097	0.0020	0.3087	0.2538	0.3237	0.2844	0.3227	0.4292	0
Papua_New_Guinea (8) v. Sri_Lanka (12)	989.6342	0.6074	0.0001	0.7303	-7.7814	0.6913	0.0017	0.2957	0.0019	0.2957	0.1787	0.2677	0.2040	0.2717	0.3247	0
Papua_New_Guinea (8) v. Seychelles (36)	1161.5383	0.7343	0.0001	0.5824	-4.9730	0.7103	0.0017	0.2577	0.0019	0.2577	0.0921	0.2268	0.1079	0.2218	0.1832	0
Mozambique (11) v. Sydney_Harbour (8)	1026.9265	0.3387	0.0002	0.5954	-8.0200	0.3706	0.0015	0.3407	0.0016	0.3437	0.1920	0.4975	0.2189	0.4935	0.3448	0
Daly_River (3) v. Sydney_Harbour (8)	864.6303	0.2947	0.0003	0.7153	-62.0937	0.1833	0.0014	0.4328	0.0015	0.4257	0.8033	0.8452	0.8208	0.8452	0.9006	0
Darwin_Coastal (2) v. Seychelles (36)	1268.7705	0.1409	0.0003	0.9061	-19.4939	0.5145	0.0014	0.4030	0.0015	0.4075	0.6036	0.4882	0.6327	0.4910	0.7710	0
Gulf_of_Mexico (40) v. Western_North_Atlantic (8)	1031.9298	0.1209	0.0000	0.4056	-11.8541	0.3487	0.0013	0.3317	0.0014	0.3357	0.1902	0.7433	0.2081	0.7433	0.3347	0
Daly_River (3) v. South_Africa (23)	1101.0772	0.5564	0.0002	0.9381	-10.7395	0.0394	0.0012	0.3963	0.0014	0.3977	0.3634	0.9565	0.3980	0.9534	0.5585	0
Arabian_Sea (15) v. Seychelles (36)	1397.9962	0.0220	0.0001	0.1948	-3.9018	0.3017	0.0012	0.2338	0.0013	0.2338	0.0463	0.2897	0.0552	0.2807	0.0970	0
Daly_River (3) v. Reunion (28)	1221.9850	0.1578	0.0002	0.8132	-9.4452	0.0557	0.0012	0.3774	0.0013	0.3715	0.3277	0.9474	0.3615	0.9443	0.5191	0
South_Alligator_River (10) v. Sri_Lanka (12)	1038.7596	0.3407	0.0001	0.2278	-7.1773	0.7373	0.0012	0.3287	0.0013	0.3287	0.1492	0.2927	0.1716	0.3017	0.2791	0
Sydney_Harbour (8) v. Towns_River (2)	805.0978	0.5055	0.0005	0.2977	14.8429	0.9618	0.0011	0.4925	0.0013	0.4925	3.2821	0.0688	2.9674	0.1116	1.4594	0
Clarence_River (11) v. Thailand (5)	986.7409	0.2378	0.0002	0.3736	-9.8864	0.5285	0.0010	0.4545	0.0011	0.4545	0.2813	0.4745	0.3147	0.4665	0.4651	0
Arabian_Sea (15) v. Daly_River (3)	1027.3070	0.3107	0.0003	0.7193	-15.4736	0.1748	0.0009	0.4188	0.0010	0.4188	0.4663	0.8425	0.5007	0.8445	0.6595	0
Arabian_Sea (15) v. Wenlock_River (4)	1051.2558	0.3437	0.0002	0.7922	-9.8805	0.1189	0.0009	0.4316	0.0010	0.4316	0.3017	0.8511	0.3352	0.8452	0.4893	0
Brazil (52) v. Caribbean_Sea (2)	1012.4079	0.6693	0.0002	0.6314	43.6705	0.8585	0.0008	0.3664	0.0009	0.3664	1.4301	0.1538	1.3964	0.1538	1.1631	0
Clarence_River (11) v. Papua_New_Guinea (8)	974.7991	0.4995	0.0002	0.3876	-7.9186	0.8941	0.0008	0.4016	0.0009	0.4016	0.1865	0.2697	0.2131	0.2857	0.3368	0
Seychelles (36) v. South_Africa (23)	1344.5068	0.3107	0.0001	0.4236	-3.5881	0.4885	0.0005	0.3117	0.0006	0.3107	0.0327	0.2697	0.0391	0.2707	0.0695	0
South_Africa (23) v. Wenlock_River (4)	1186.3131	0.1848	0.0002	0.7163	-7.5866	0.0190	0.0005	0.4314	0.0005	0.4314	0.2349	0.9520	0.2651	0.9439	0.4049	0
Darwin_Coastal (2) v. Sydney_Harbour (8)	827.2518	0.3566	0.0004	0.9550	16.9535	0.5166	0.0005	0.4439	0.0005	0.3963	2.6332	0.4983	2.4143	0.4983	1.3893	0
East_Alligator_River (7) v. South_Africa (23)	1086.5319	0.8432	0.0001	0.6893	-6.0880	0.7692	0.0003	0.4246	0.0004	0.4236	0.1323	0.4176	0.1529	0.4256	0.2519	0
Clarence_River (11) v. Towns_River (2)	826.5694	0.6853	0.0005	0.2717	24.3432	1.0000	0.0003	0.4728	0.0003	0.4728	1.8187	0.0108	1.7205	0.0108	1.2556	0
Papua_New_Guinea (8) v. South_Alligator_River (10)	943.7299	0.4645	0.0002	0.5524	-9.3035	0.3846	0.0002	0.4625	0.0002	0.4625	0.2199	0.5105	0.2479	0.5045	0.3835	0
Papua_New_Guinea (8) v. South_Africa (23)	1107.5972	0.7433	0.0001	0.3776	-5.8132	0.5964	0.0002	0.4525	0.0002	0.4525	0.1159	0.5025	0.1347	0.5105	0.2246	0
Seychelles (36) v. Towns_River (2)	1124.2415	0.6953	0.0005	0.1658	-24.8041	0.9673	0.0000	0.4602	0.0000	0.4602	0.6643	0.0327	0.6898	0.0299	0.8136	0
Clarence_River (11) v. Darwin_Coastal (2)	880.5217	0.4296	0.0004	0.5175	33.2906	0.9103	0.0000	0.4833	0.0000	0.4833	1.5119	0.1539	1.4529	0.1539	1.1803	0
Arabian_Sea (15) v. Thailand (5)	1028.5982	0.4076	0.0002	0.4545	-8.3948	0.1960	0.0000	0.4860	0.0000	0.4860	0.2323	0.7830	0.2625	0.7750	0.4015	0
Clarence_River (11) v. Wenlock_River (4)	977.8491	0.3636	0.0002	0.8032	-12.0893	0.3556	0.0000	0.4935	-0.0001	0.4935	0.3630	0.6204	0.3985	0.6214	0.5587	0
Adelaide_River (4) v. South_Africa (23)	1029.3770	0.9431	0.0002	0.6813	-8.6341	0.8164	-0.0003	0.5045	-0.0003	0.5045	0.2601	0.2247	0.2901	0.2317	0.4367	0
Darwin_Coastal (2) v. Papua_New_Guinea (8)	789.9184	0.4545	0.0003	0.8871	16.0588	0.5132	-0.0003	0.4844	-0.0003	0.4844	2.9094	0.5921	2.6527	0.5921	1.4227	0
Thailand (5) v. Wenlock_River (4)	790.7350	0.4256	0.0004	0.1079	-63.2605	0.5215	-0.0003	0.4895	-0.0003	0.4895	0.8020	0.4915	0.8198	0.4915	0.9000	0
Mozambique (11) v. Thailand (5)	954.9798	0.4545	0.0002	0.7103	-10.8081	0.0796	-0.0003	0.5030	-0.0004	0.5020	0.3024	0.9113	0.3359	0.9083	0.4901	0
Arabian_Sea (15) v. Sri_Lanka (12)	1114.7194	0.6723	0.0001	0.3257	-5.5370	0.5694	-0.0003	0.5654	-0.0004	0.5654	0.0983	0.5395	0.1151	0.5365	0.1943	0
Thailand (5) v. Towns_River (2)	699.8974	0.5435	0.0005	0.1499	9.4260	1.0000	-0.0005	0.5367	-0.0005	0.5367	29.2654	0.0672	24.4901	0.0672	1.7761	0
Sri_Lanka (12) v. Wenlock_River (4)	949.1637	0.5405	0.0002	0.6673	-12.2126	0.1040	-0.0011	0.5460	-0.0012	0.5460	0.3586	0.9060	0.3932	0.9090	0.5534	0
Daly_River (3) v. Towns_River (2)	635.9042	0.4865	0.0006	0.3966	5.6817	0.8871	-0.0015	0.4865	-0.0017	0.4865	-3.5528	0.1009	-2.5127	0.1009	2.3760	0
East_Alligator_River (7) v. Papua_New_Guinea (8)	891.1094	0.7732	0.0001	0.9291	-11.1798	0.3916	-0.0017	0.6653	-0.0018	0.6653	0.2883	0.6454	0.3197	0.6454	0.4719	0
Reunion (28) v. Trinity_inlet (1)	1235.6088	0.1958	0.0007	0.7193	4.8126	1.0000	-0.0018	0.5333	-0.0020	0.5333	-5.4582	1.0000	-4.1318	1.0000	2.1511	1
South_Alligator_River (10) v. Trinity_inlet (1)	827.4026	0.2567	0.0007	0.7193	3.5281	1.0000	-0.0019	1.0000	-0.0021	1.0000	-2.0482	1.0000	-1.1634	1.0000	3.0639	1
Adelaide_River (4) v. Wenlock_River (4)	756.8356	0.5884	0.0003	0.8541	60.9724	0.3724	-0.0023	0.6134	-0.0026	0.6004	1.2906	0.6556	1.2598	0.6556	1.1134	0
South_Alligator_River (10) v. Towns_River (2)	823.2817	0.4036	0.0004	0.4276	17.2796	0.8650	-0.0026	0.5903	-0.0028	0.5903	2.6859	0.0802	2.4692	0.0802	1.3986	0
Darwin_Coastal (2) v. South_Africa (23)	1088.5364	0.5954	0.0003	0.9730	-47.5421	0.3403	-0.0030	0.5766	-0.0034	0.5846	0.7928	0.6758	0.8104	0.6758	0.8943	0
Adelaide_River (4) v. Sydney_Harbour (8)	834.4309	0.7363	0.0002	0.8082	-24.8980	0.8938	-0.0031	0.6613	-0.0034	0.6572	0.5674	0.1800	0.5975	0.1891	0.7432	0
Papua_New_Guinea (8) v. Wenlock_River (4)	857.8924	0.6174	0.0002	0.6943	-20.1621	0.0290	-0.0032	0.6803	-0.0036	0.6803	0.5130	0.9590	0.5459	0.9580	0.6999	0
Papua_New_Guinea (8) v. Towns_River (2)	750.3967	0.7173	0.0004	0.4026	14.0403	0.9477	-0.0033	0.5678	-0.0036	0.5678	3.7850	0.0753	3.3999	0.0753	1.5016	0
Seychelles (36) v. Trinity_inlet (1)	1222.1414	0.2717	0.0007	0.6384	5.2967	1.0000	-0.0034	1.0000	-0.0037	1.0000	-11.2934	1.0000	-8.9809	1.0000	1.9696	1
Adelaide_River (4) v. Unknown (2)	680.5192	0.3257	0.0004	0.8032	7.4697	0.3084	-0.0034	0.5786	-0.0038	0.5786	-7.6348	0.8000	-6.0014	0.8000	2.0553	0
Arabian_Sea (15) v. Towns_River (2)	935.7404	0.6953	0.0005	0.1998	53.6252	0.9933	-0.0036	0.5948	-0.0039	0.5948	1.2749	0.0189	1.2464	0.0189	1.1083	0
Darwin_Coastal (2) v. Sri_Lanka (12)	879.6630	0.5954	0.0003	0.7383	37.5049	0.3973	-0.0037	0.6048	-0.0042	0.6048	1.4461	0.5728	1.3969	0.5605	1.1623	0

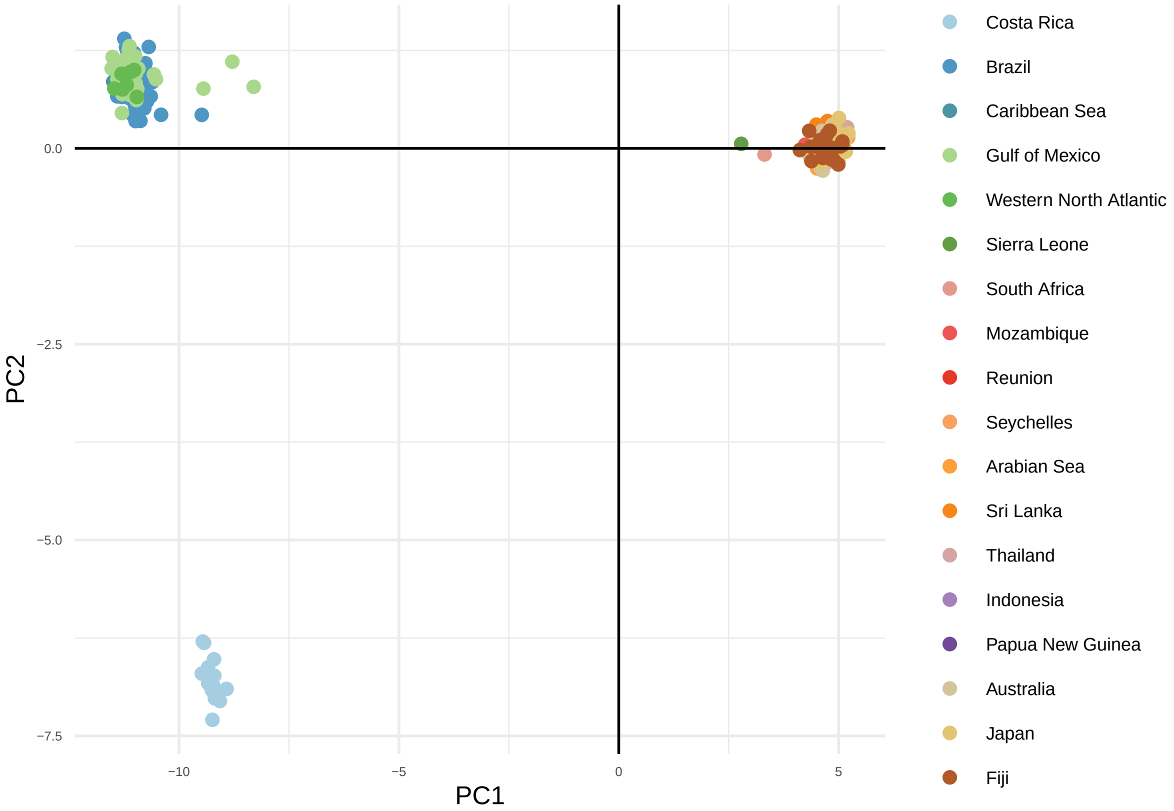
Table 38: Pairwise Fst for 1849 DArTcap loci between the all sites, but with a subset of Australia
(continued)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st
Adelaide_River (4) v. Towns_River (2)	628.5349	0.7313	0.0004	0.7483	6.9651	1.0000	-0.0044	0.5927	-0.0048	0.5927	-5.2701	0.1431	-4.0376	0.1431	2.1798	0
Darwin_Coastal (2) v. East_Alligator_River (7)	750.0513	0.5764	0.0003	0.7832	13.5712	0.5058	-0.0046	0.6767	-0.0051	0.6923	4.0794	0.6773	3.6425	0.6773	1.5202	0
Adelaide_River (4) v. Darwin_Coastal (2)	673.5342	0.2727	0.0003	1.0000	7.5064	0.2357	-0.0047	0.4874	-0.0052	0.4874	-7.8941	0.8750	-6.2094	0.8750	2.0457	1
Caribbean_Sea (2) v. Western_North_Atlantic (8)	508.1961	0.7443	0.0002	0.7502	8.5480	0.7754	-0.0053	0.7561	-0.0058	0.6254	-4.1316	0.3832	-3.3410	0.3832	2.3862	0
Darwin_Coastal (2) v. Trinity_inlet (1)	521.3750	0.6643	0.0005	0.6643	NA	NA	-0.0058	1.0000	-0.0064	0.6643	NA	NA	NA	NA	NA	
Daly_River (3) v. South_Alligator_River (10)	874.9653	0.3796	0.0002	0.9760	-40.4013	0.0626	-0.0059	0.7916	-0.0066	0.7916	0.7121	0.9507	0.7354	0.9507	0.8455	0
Daly_River (3) v. Wenlock_River (4)	740.3896	0.7672	0.0004	0.7213	23.1691	0.2727	-0.0065	0.7672	-0.0072	0.7672	1.9954	0.5854	1.8670	0.5854	1.2894	0
Darwin_Coastal (2) v. Unknown (2)	559.5262	1.0000	0.0004	1.0000	3.8406	0.3287	-0.0065	1.0000	-0.0072	1.0000	-1.9410	0.3287	-1.0623	0.3287	3.1916	0
Arabian_Sea (15) v. Trinity_inlet (1)	914.4754	0.6993	0.0007	0.4915	4.0808	1.0000	-0.0066	1.0000	-0.0073	1.0000	-2.9064	1.0000	-1.9490	1.0000	2.5469	1
Towns_River (2) v. Unknown (2)	544.1417	0.6583	0.0005	0.3127	NA	NA	-0.0067	1.0000	-0.0074	0.8292	NA	NA	NA	NA	NA	
Darwin_Coastal (2) v. Mozambique (11)	858.6603	0.7612	0.0004	0.8432	27.7003	0.3692	-0.0079	0.6713	-0.0090	0.6307	1.6825	0.6774	1.6025	0.6774	1.2246	0
Daly_River (3) v. Darwin_Coastal (2)	645.8198	0.6154	0.0005	0.6154	6.0191	0.6508	-0.0080	0.7133	-0.0089	0.7133	-4.2394	0.5359	-3.0819	0.4420	2.2601	0
Clarence_River (11) v. Trinity_inlet (1)	840.8295	0.3896	0.0008	0.4855	3.7561	1.0000	-0.0086	0.4824	-0.0095	0.4824	-2.3866	1.0000	-1.4671	1.0000	2.7792	1
Thailand (5) v. Unknown (2)	670.2214	0.7942	0.0005	0.1928	9.9531	1.0000	-0.0094	0.8402	-0.0104	0.8402	14.8594	0.0499	12.5654	0.0499	1.7292	0
East_Alligator_River (7) v. Unknown (2)	735.2443	0.6653	0.0003	0.8791	13.2841	0.5807	-0.0095	0.7922	-0.0105	0.7922	4.3775	0.5143	3.8981	0.5143	1.5389	0
South_Africa (23) v. Trinity_inlet (1)	1010.1417	0.7982	0.0007	0.8332	4.5868	1.0000	-0.0096	1.0000	-0.0107	1.0000	-4.3532	1.0000	-3.2004	1.0000	2.2527	1
Clarence_River (11) v. Unknown (2)	806.1261	0.8252	0.0004	0.4955	29.8404	0.9452	-0.0102	0.7260	-0.0113	0.7260	1.6118	0.0635	1.5409	0.0635	1.2071	0
Papua_New_Guinea (8) v. Unknown (2)	769.2311	0.7203	0.0003	0.8791	15.8789	0.4786	-0.0103	0.8567	-0.0114	0.8567	3.0248	0.5577	2.7542	0.5577	1.4359	0
Darwin_Coastal (2) v. Wenlock_River (4)	667.6609	1.0000	0.0004	0.8751	8.0633	0.7143	-0.0114	0.9259	-0.0127	0.9259	-19.5609	0.1925	-15.7431	0.1925	1.9021	0
Reunion (28) v. Unknown (2)	1051.9413	0.7143	0.0003	0.8791	-37.6713	0.4035	-0.0115	0.8006	-0.0127	0.8006	0.7465	0.6316	0.7670	0.6368	0.8666	0
Sri_Lanka (12) v. Unknown (2)	887.2710	0.5205	0.0003	0.7552	34.4005	0.6362	-0.0118	0.8682	-0.0130	0.8682	1.5064	0.3441	1.4506	0.3441	1.1798	0
Thailand (5) v. Trinity_inlet (1)	642.0085	0.6623	0.0007	0.8362	2.8892	1.0000	-0.0124	1.0000	-0.0137	1.0000	-1.6216	1.0000	-0.6815	1.0000	3.7051	1
Sydney_Harbour (8) v. Trinity_inlet (1)	757.5779	0.5604	0.0007	0.8941	3.3631	1.0000	-0.0135	1.0000	-0.0150	1.0000	-1.9376	1.0000	-1.0397	1.0000	3.1755	1
Seychelles (36) v. Unknown (2)	1050.5379	0.9121	0.0003	0.9431	-21.9235	0.6319	-0.0137	0.9383	-0.0152	0.9383	0.6280	0.4087	0.6553	0.4174	0.7883	0
Towns_River (2) v. Wenlock_River (4)	658.9220	0.9411	0.0005	0.3586	7.6012	0.8929	-0.0140	0.8537	-0.0157	0.8308	-10.1449	0.2273	-8.0333	0.2273	1.9878	0
Arabian_Sea (15) v. Unknown (2)	890.8158	0.8871	0.0003	0.9860	81.3743	0.6275	-0.0148	0.9607	-0.0164	0.9607	1.1720	0.3686	1.1546	0.3686	1.0712	0
Sydney_Harbour (8) v. Unknown (2)	761.5227	0.7922	0.0004	0.8521	16.1916	0.5161	-0.0151	0.9387	-0.0168	0.9387	2.8872	0.3986	2.6344	0.3986	1.4205	0
South_Africa (23) v. Unknown (2)	1001.7286	0.8781	0.0003	0.9790	-58.1887	0.4757	-0.0153	0.9590	-0.0169	0.9590	0.8227	0.5604	0.8378	0.5604	0.9110	0
Unknown (2) v. Wenlock_River (4)	644.6439	1.0000	0.0004	1.0000	8.0260	0.5532	-0.0187	1.0000	-0.0209	1.0000	-16.1912	0.1790	-13.0059	0.1790	1.9220	0
South_Alligator_River (10) v. Unknown (2)	761.8605	0.9600	0.0003	0.9750	19.7495	0.5007	-0.0207	1.0000	-0.0229	1.0000	2.3162	0.3737	2.1534	0.3737	1.3478	0
Trinity_inlet (1) v. Wenlock_River (4)	631.1450	1.0000	0.0008	1.0000	2.6428	1.0000	-0.0262	1.0000	-0.0294	1.0000	-1.5163	1.0000	-0.5327	1.0000	3.9687	1
Daly_River (3) v. Unknown (2)	597.6625	1.0000	0.0004	1.0000	5.9453	0.5563	-0.0278	1.0000	-0.0309	1.0000	-3.8841	0.1192	-2.8042	0.2373	2.3190	0
Mozambique (11) v. Trinity_inlet (1)	817.3900	0.7413	0.0007	0.8132	3.6731	1.0000	-0.0288	1.0000	-0.0319	1.0000	-2.2404	1.0000	-1.3475	1.0000	2.8926	1
Mozambique (11) v. Unknown (2)	815.7891	0.9011	0.0003	1.0000	26.7065	0.3398	-0.0297	0.9757	-0.0329	0.9757	1.7470	0.6988	1.6607	0.6988	1.2405	0
Trinity_inlet (1) v. Unknown (2)	467.2917	1.0000	0.0004	1.0000	NA	NA	-0.0360	1.0000	-0.0402	1.0000	NA	NA	NA	NA	NA	
Daly_River (3) v. Trinity_inlet (1)	566.7849	1.0000	0.0007	1.0000	2.2976	1.0000	-0.0465	1.0000	-0.0517	1.0000	-1.3569	1.0000	-0.2993	1.0000	4.6405	1
Daly_River (3) v. Indonesia (4)	788.6998	0.2787	0.0005	0.3636	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Fiji (24) v. Indonesia (4)	1624.5788	0.0010	0.0005	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. South_Africa (23)	1195.6827	0.0829	0.0003	0.0559	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Indonesia (4) v. Urauchi_River (35)	2021.5069	0.0010	0.0008	0.0010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Sierra_Leone (1) v. Trinity_inlet (1)	566.6667	1.0000	0.0009	1.0000	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	

9.8 PCA

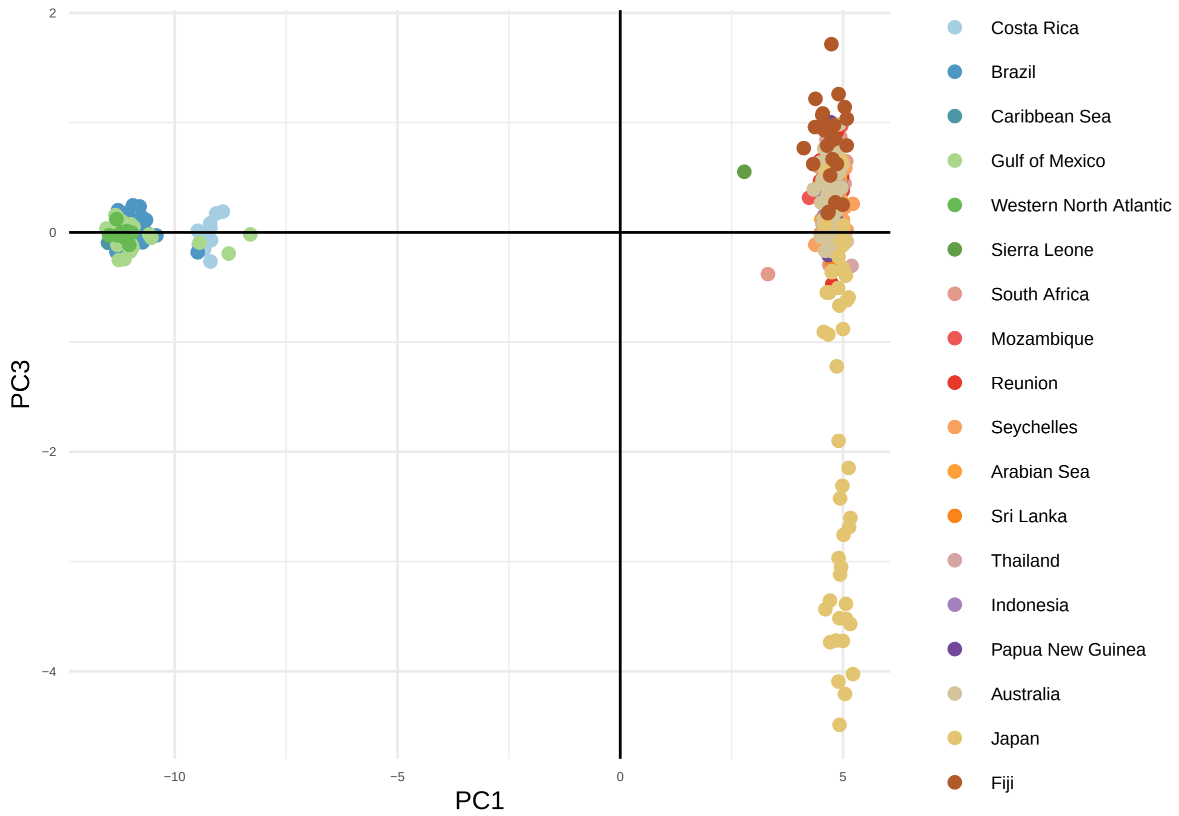
```
pca1 <- adegenet::glPca(BS.dartcap.sub.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_AUS_subset_PCA.Rdata")
```

```
load("DArTcap_AUS_subset_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.sub.gl)
cols <- adegenet::funky(nPop(BS.dartcap.sub.gl))


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

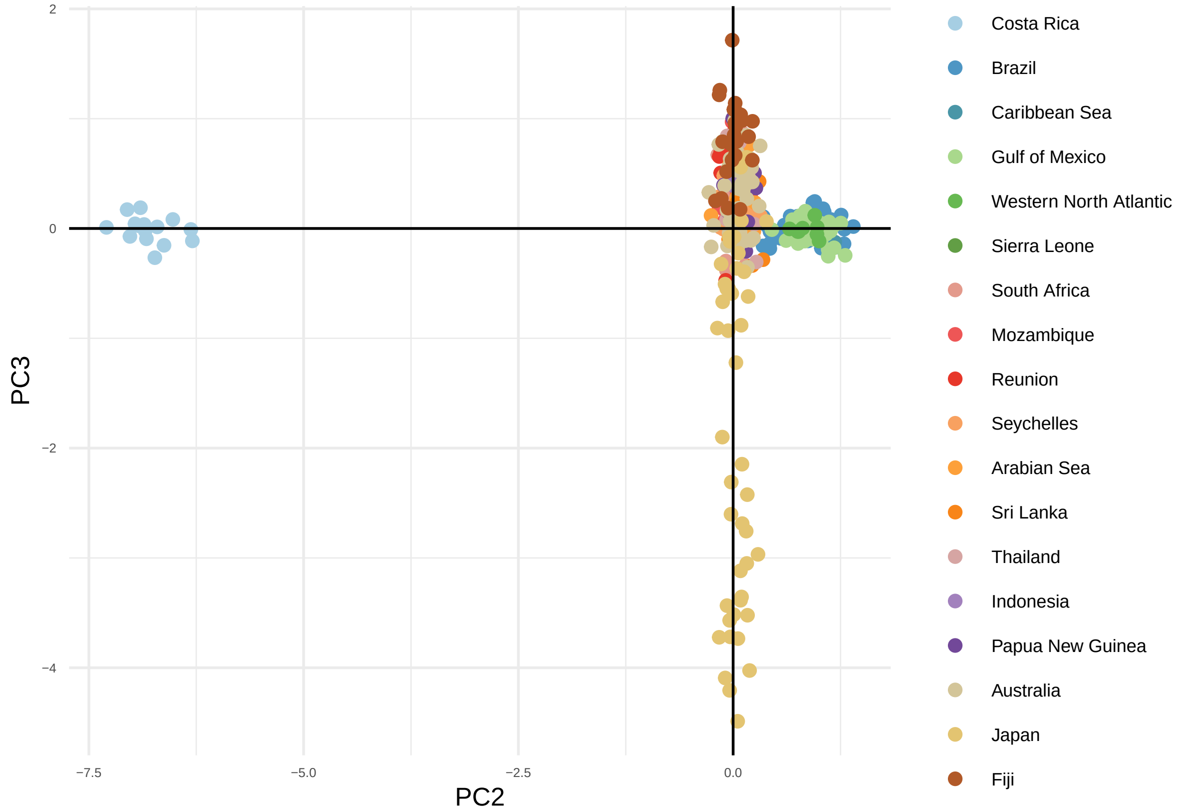


```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
```

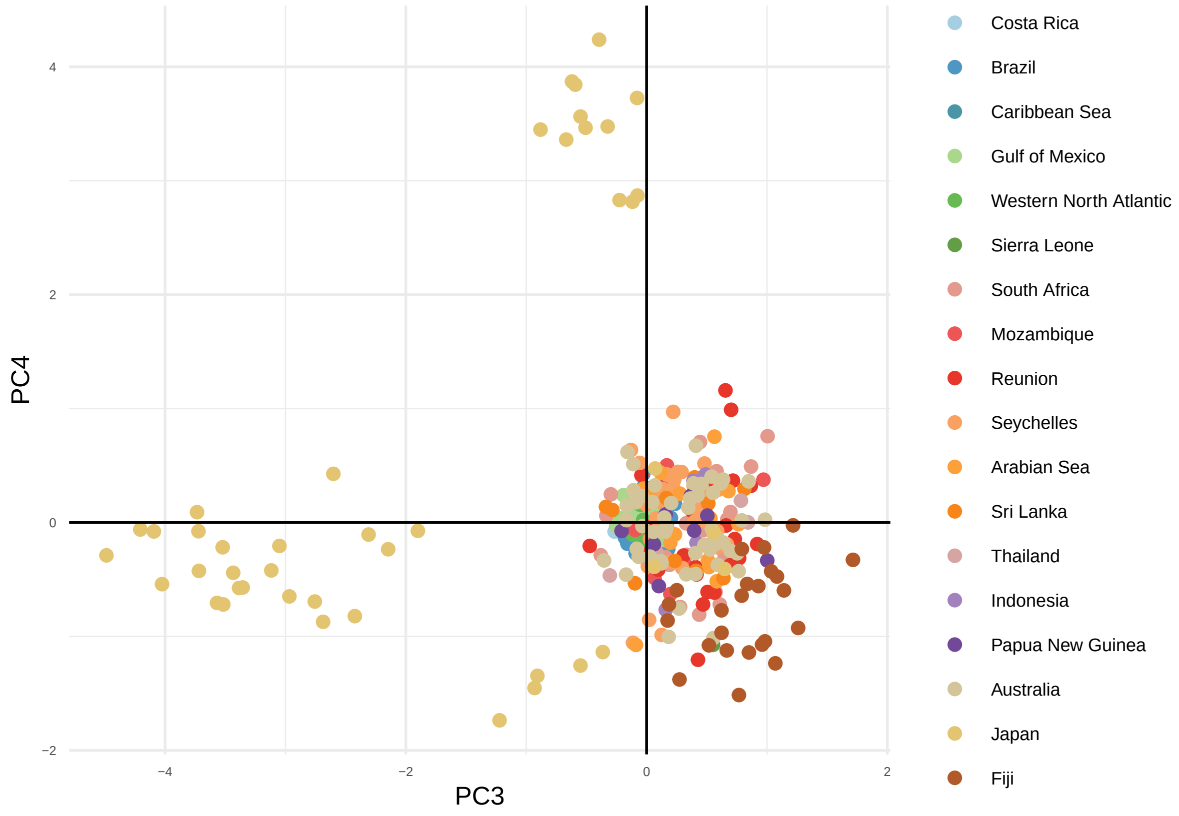
```
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



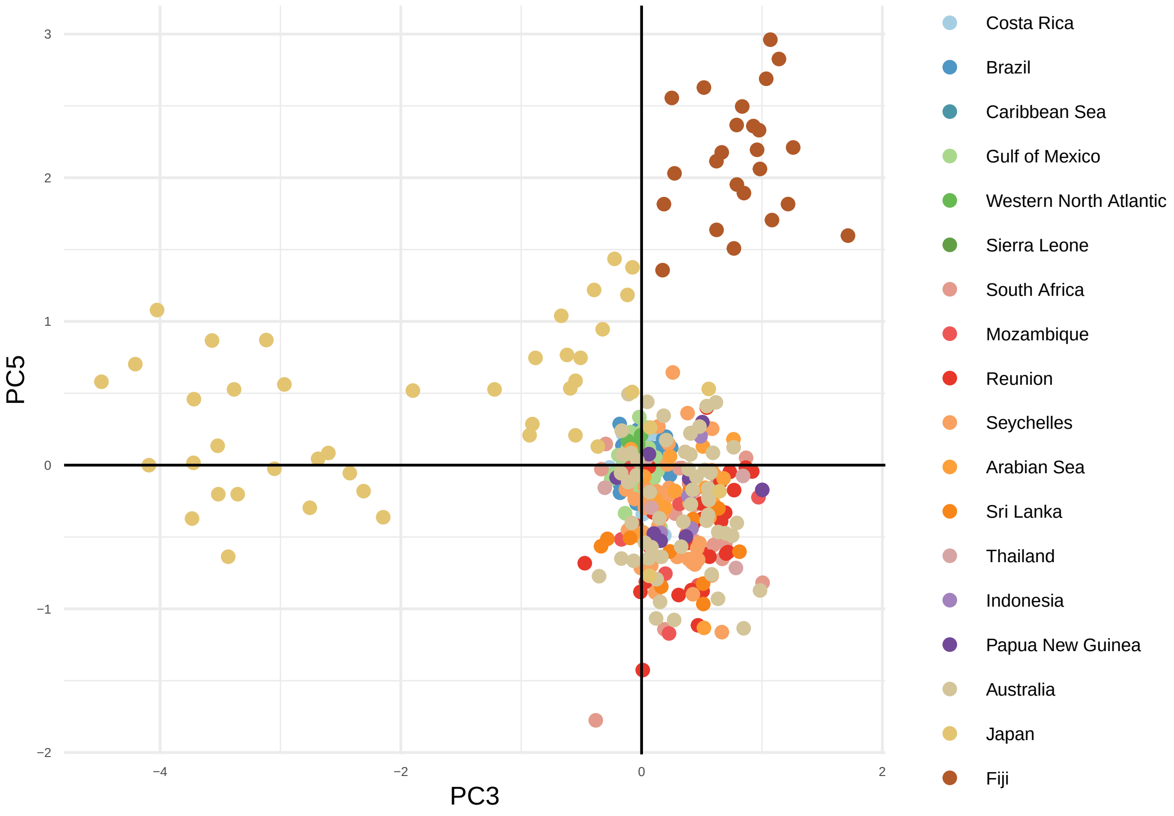
```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA2.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



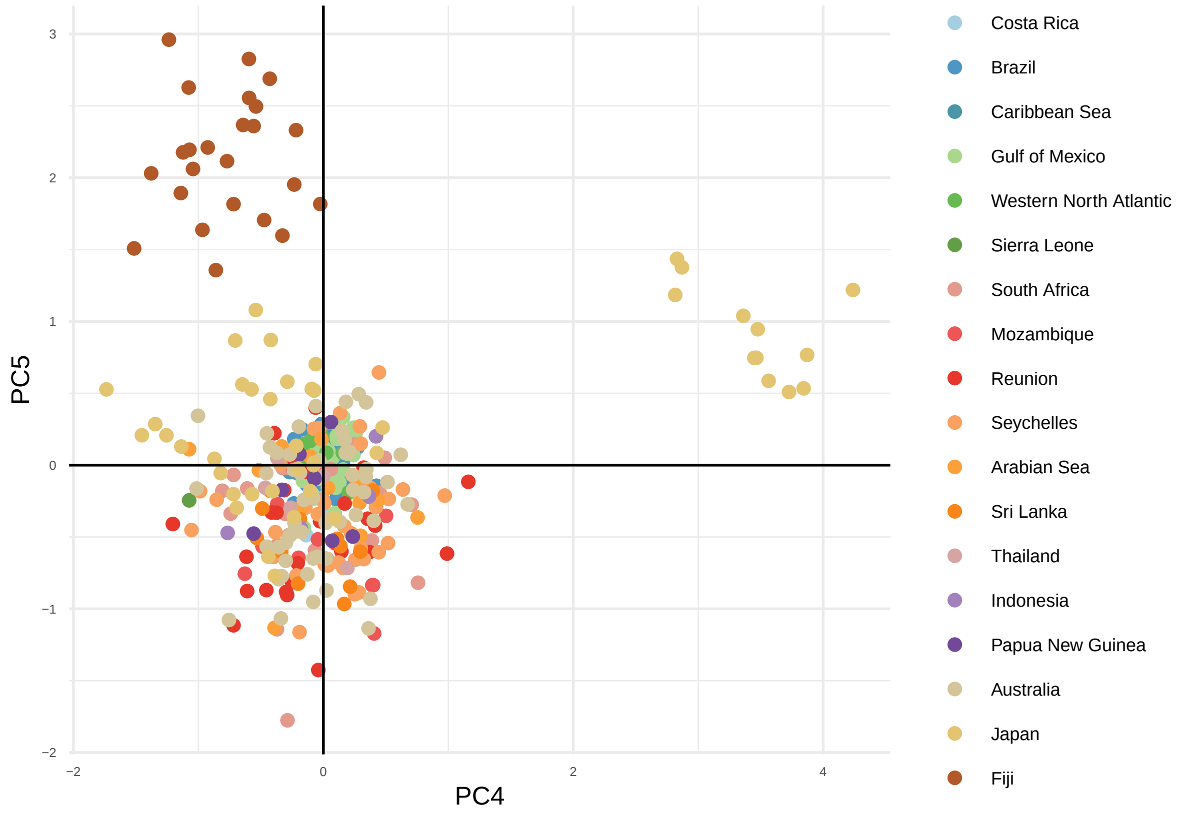
```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA3.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA5.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC4, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_AUS_subset_PCA6.png", width = 30,
                height = 15,units = "cm")
```

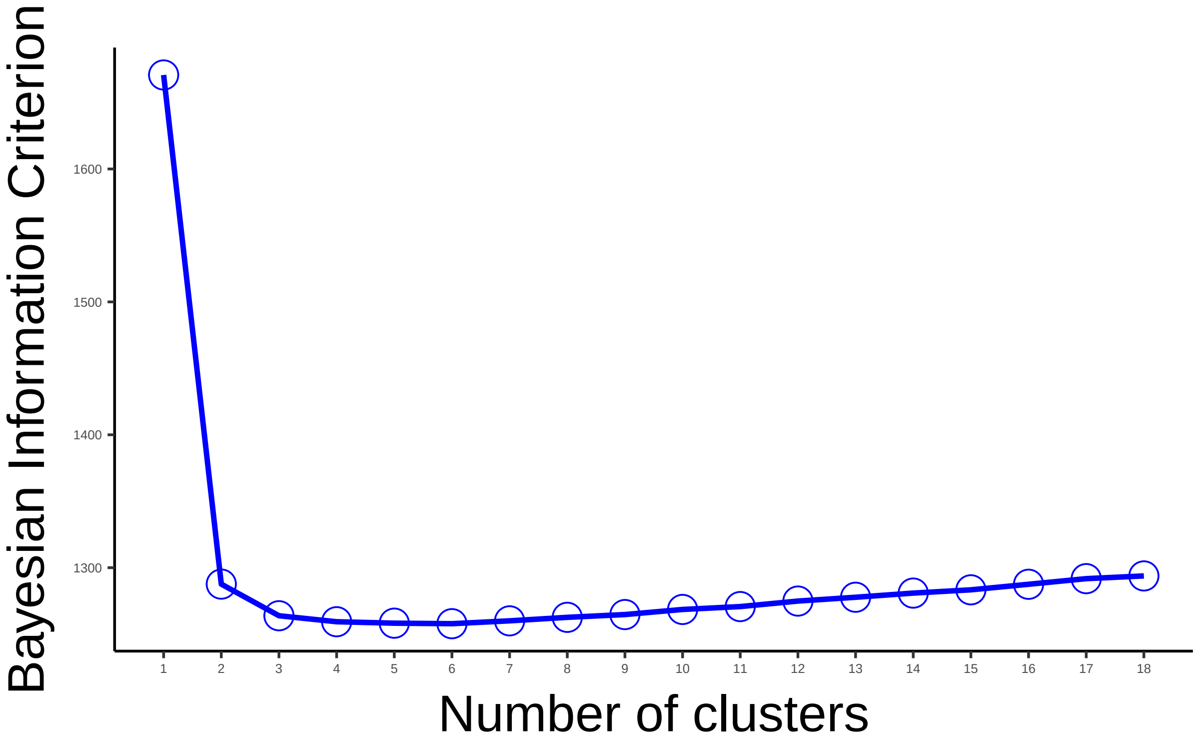
9.9 DAPC

9.9.1 Optimal number of clusters with neutral markers

```
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartcap.sub.gl,
    max.n.clust = 18,
    n.pca = adegenet::nInd(BS.dartcap.sub.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTcap_AUS_subset_grp_.Rdata")
```

```
load("DArTcap_AUS_subset_grp_.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:18
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartcap.sub.gl) - 1,
```

```
                                                   by = 1)) +
  ggplot2::labs(subtitle = "",
                y = "Bayesian Information Criterion",
                x = "Number of clusters",
                title = "",
                caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_AUS_subset_grp.png", width = 30,
                height = 15,units = "cm")
```

9.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartcap.sub.gl
x <- x[x$pop != "Sierra Leone",]

xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 50),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
```

```
  scale = FALSE,
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTcap_AUS_subset_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTcap_AUS_subset_xval.rdata")
```

```
load("DArTcap_AUS_subset_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

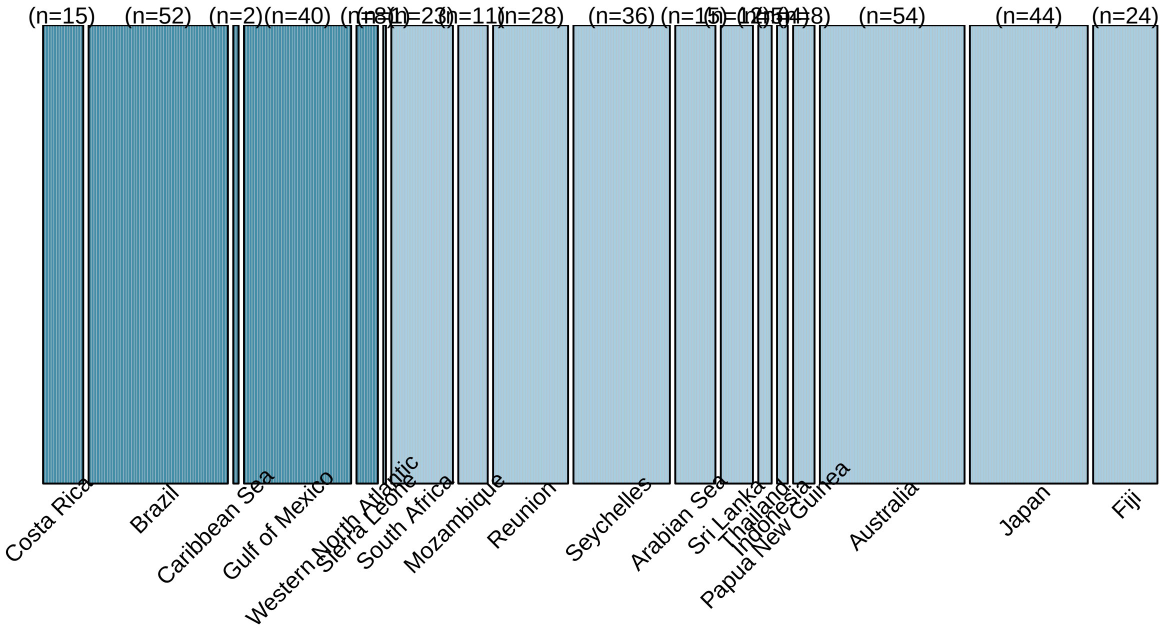
```
## $`Median and Confidence Interval for Random Chance`
##       2.5%        50%      97.5%
## 0.03861550 0.05695908 0.08868781
##
## $`Mean Successful Assignment by Number of PCs of PCA`
##        36        37        38        39        40        41        42        43
## 0.3338533 0.3343388 0.3376489 0.3371772 0.3356450 0.3439839 0.3454886 0.3482663
##        44        45        46        47        48        49        50        51
## 0.3494908 0.3464274 0.3467327 0.3502776 0.3493193 0.3541947 0.3556213 0.3585058
##        52        53        54        55        56        57        58        59
## 0.3548909 0.3550931 0.3545634 0.3529064 0.3560120 0.3526906 0.3537629 0.3516880
##        60        61        62        63        64        65        66
## 0.3503346 0.3497025 0.3500120 0.3511077 0.3515862 0.3513141 0.3521010
##
## $`Number of PCs Achieving Highest Mean Success`
## [1] "51"
##
## $`Root Mean Squared Error by Number of PCs of PCA`
##        36        37        38        39        40        41        42        43
## 0.6665824 0.6660893 0.6627735 0.6632440 0.6647774 0.6564674 0.6550179 0.6522013
##        44        45        46        47        48        49        50        51
## 0.6509811 0.6540736 0.6537285 0.6502198 0.6511483 0.6462868 0.6448894 0.6419722
##        52        53        54        55        56        57        58        59
## 0.6456393 0.6453911 0.6459184 0.6475422 0.6444630 0.6478024 0.6467376 0.6487830
##        60        61        62        63        64        65        66
## 0.6501345 0.6507866 0.6504542 0.6494049 0.6489529 0.6491762 0.6484199
##
## $`Number of PCs Achieving Lowest MSE`
## [1] "51"
```

```
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartcap.sub.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartcap.sub.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                                     paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTcap_AUS_subset_DAPC.Rdata")
```

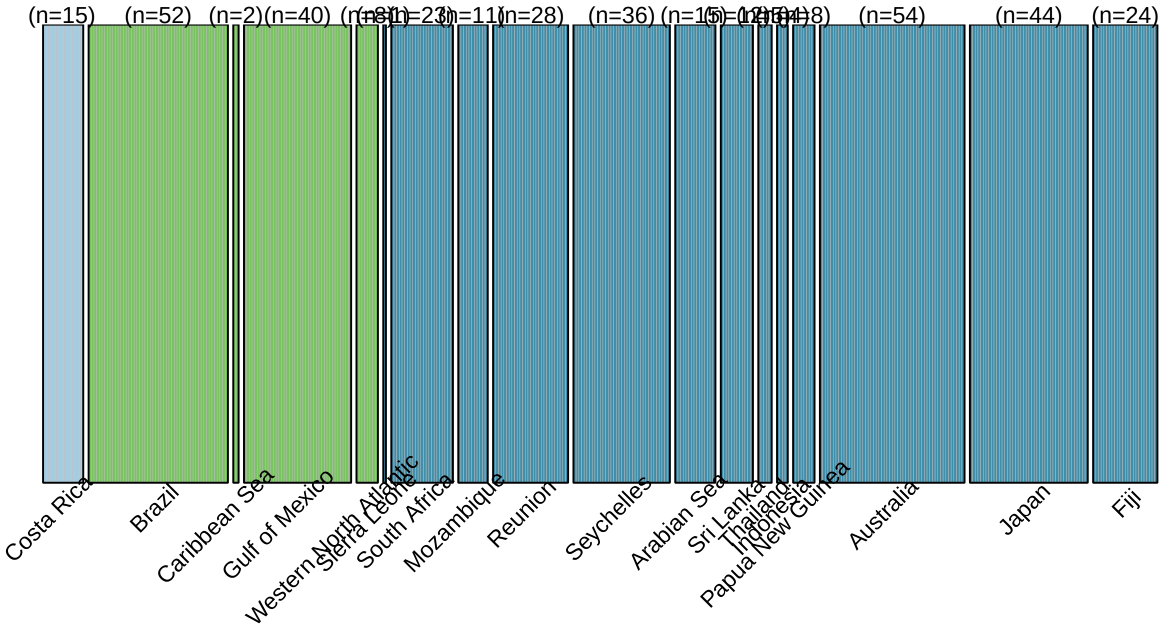
9.9.3 DAPC barplot

Group individuals according to DAPC posterior membership.

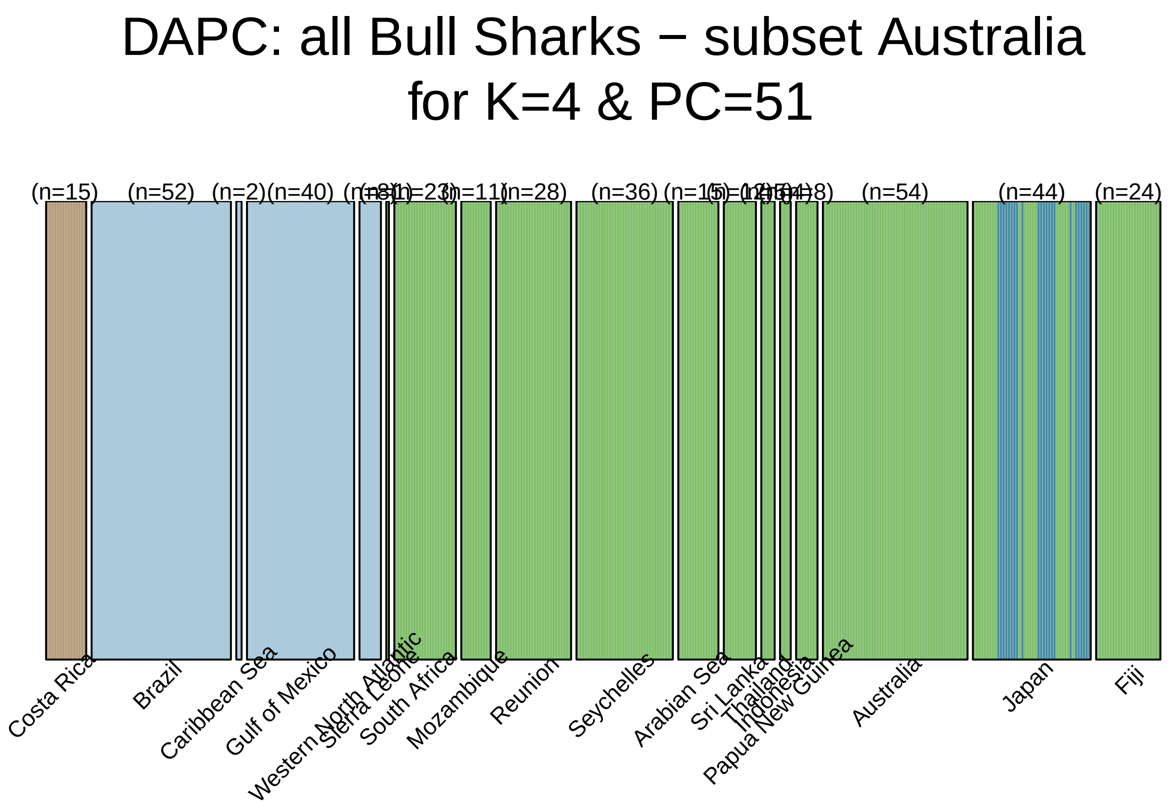
```
load("DArTcap_AUS_subset_DAPC.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartcap.sub.gl$pop

  plot.dapc.FDD(x = post,
              locations = locations,
              colour = colour,
              region.lwd = 1,
              plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTcap_AUS_subset_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```

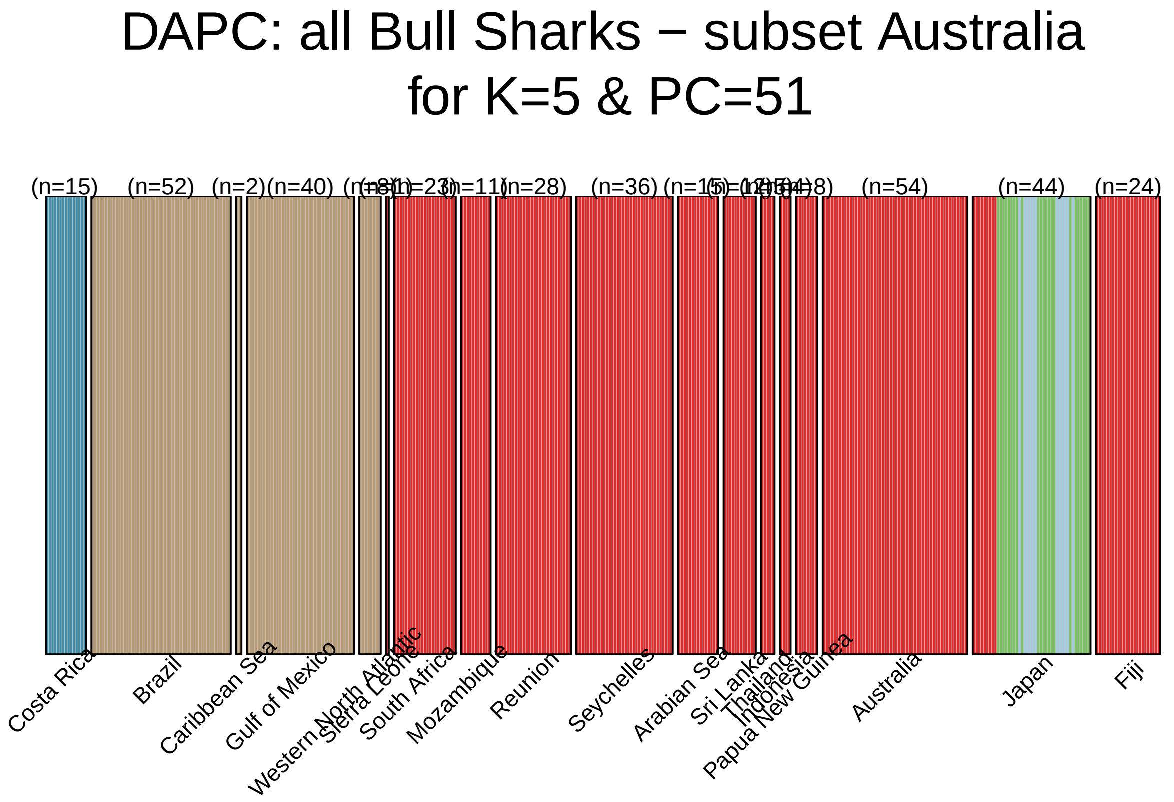


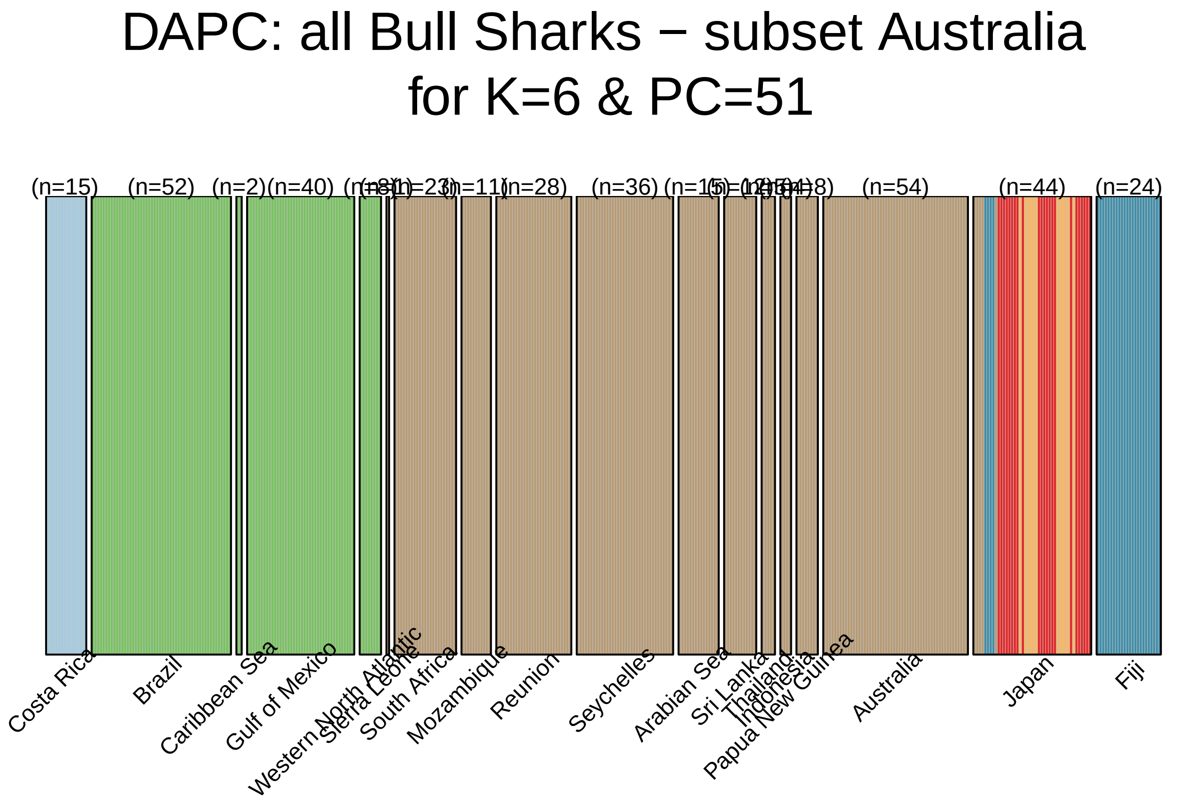
DAPC: all Bull Sharks − subset Australia
for K=2 & PC=51

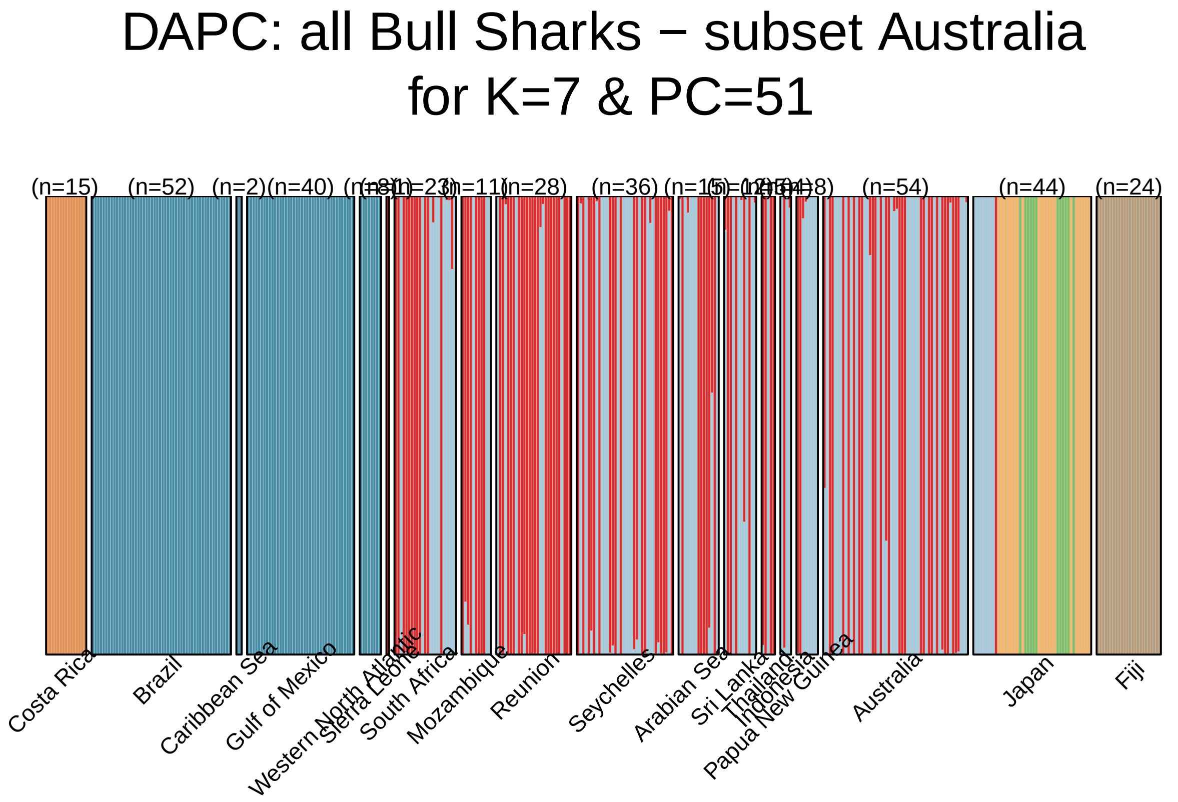


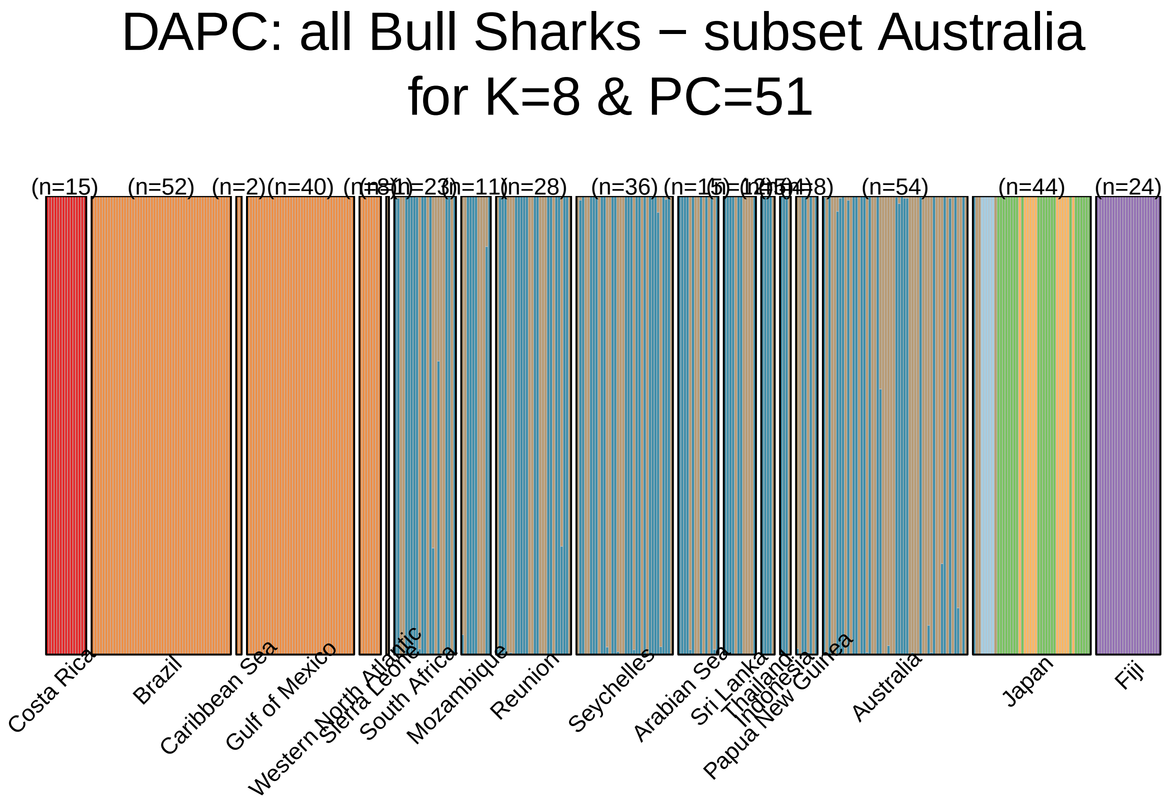
DAPC: all Bull Sharks − subset Australia
for K=3 & PC=51


DAPC: all Bull Sharks − subset Australia
for K=4 & PC=51

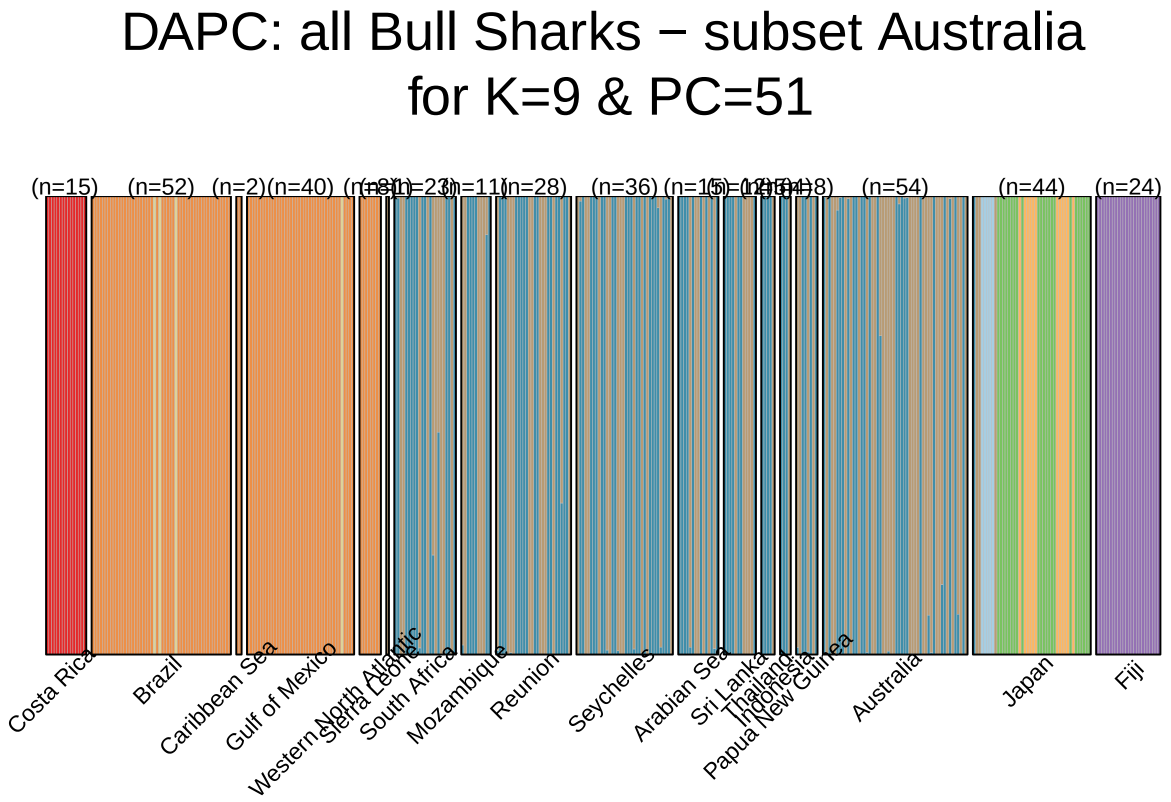

DAPC: all Bull Sharks − subset Australia
for K=5 & PC=51


DAPC: all Bull Sharks − subset Australia
for K=6 & PC=51

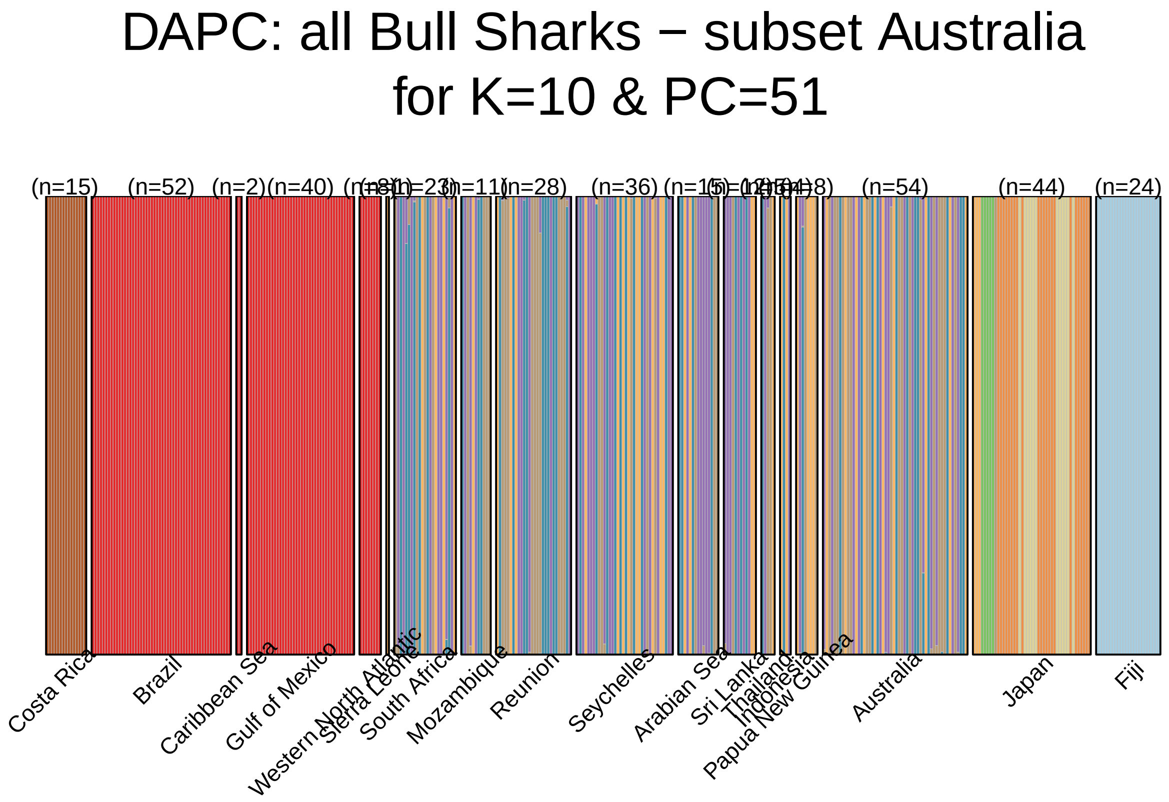

DAPC: all Bull Sharks − subset Australia
for K=7 & PC=51



DAPC: all Bull Sharks − subset Australia for K=8 & PC=51

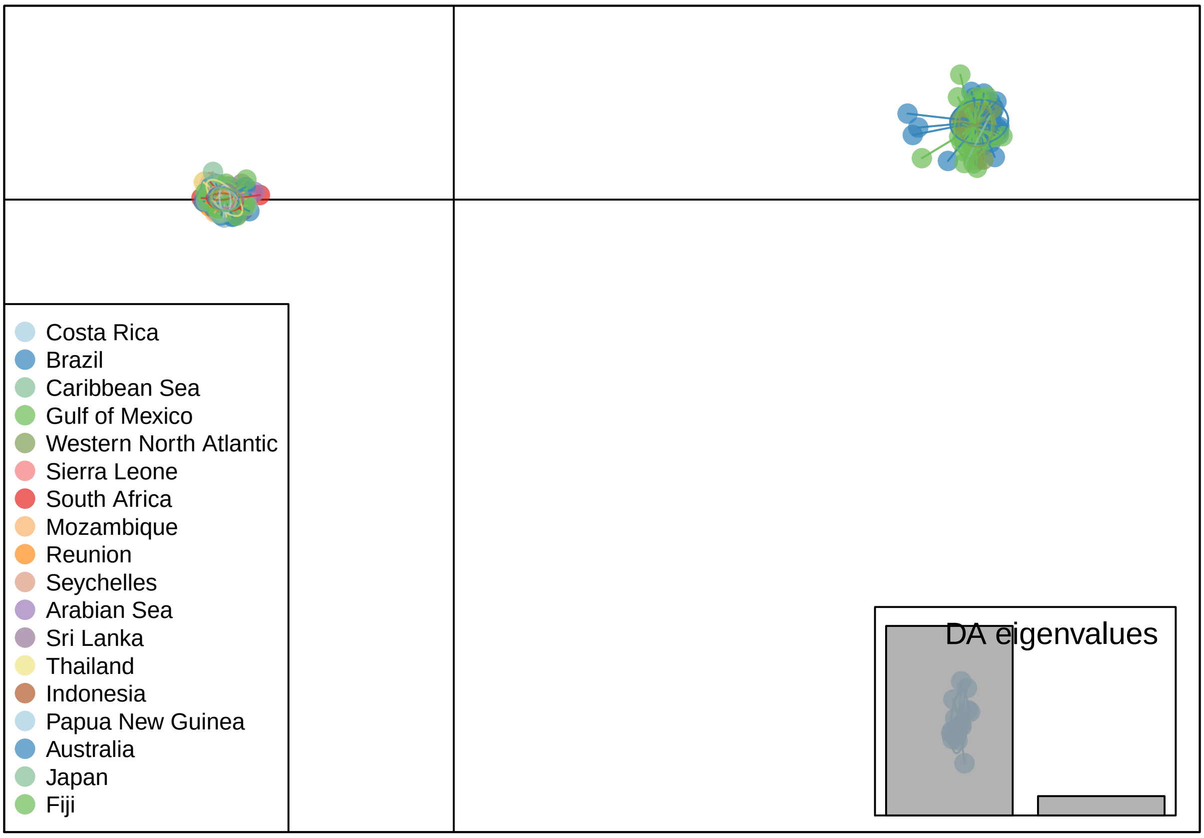


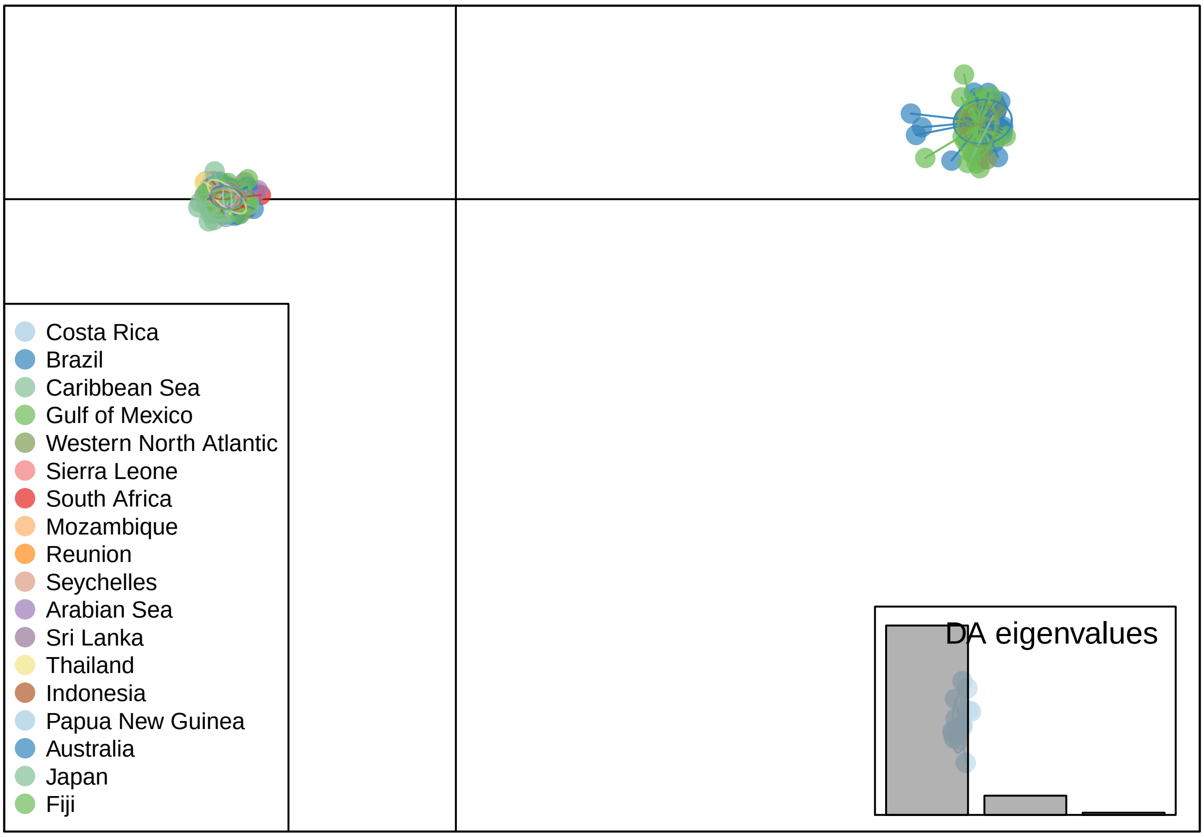
DAPC: all Bull Sharks − subset Australia for K=9 & PC=51

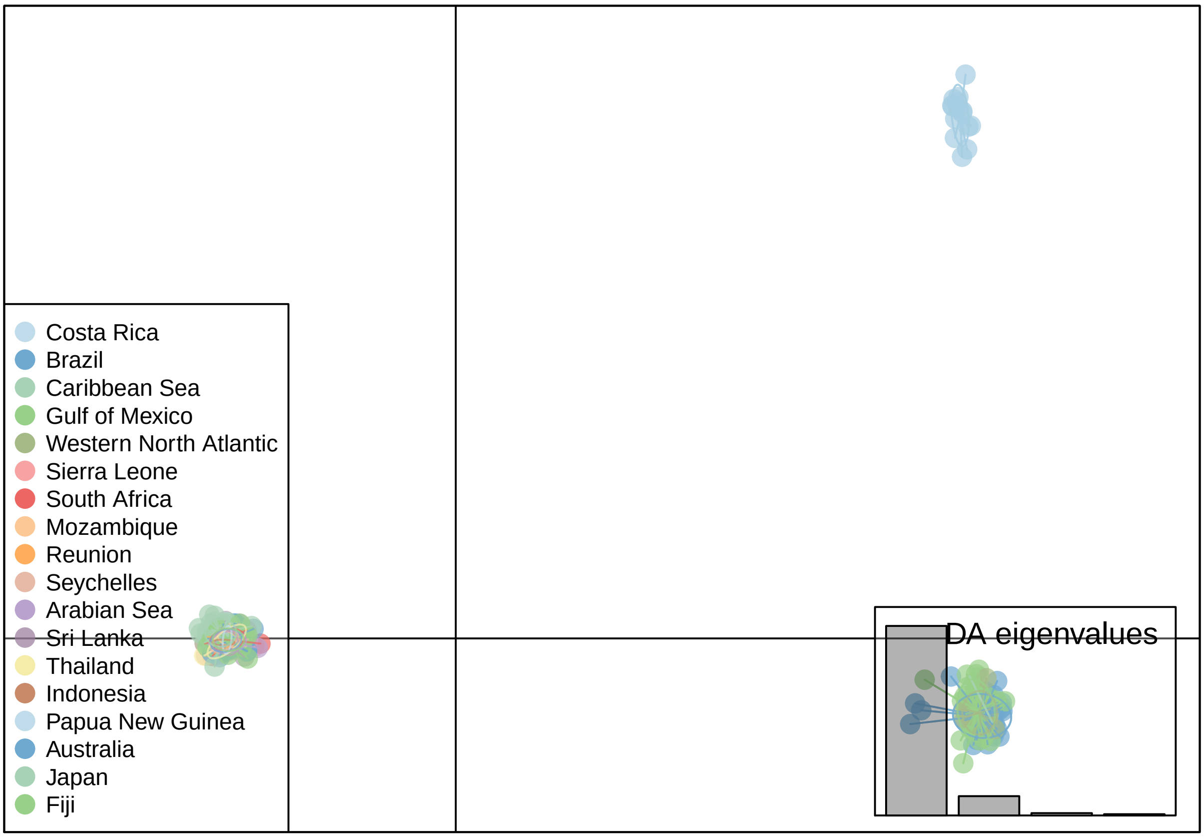


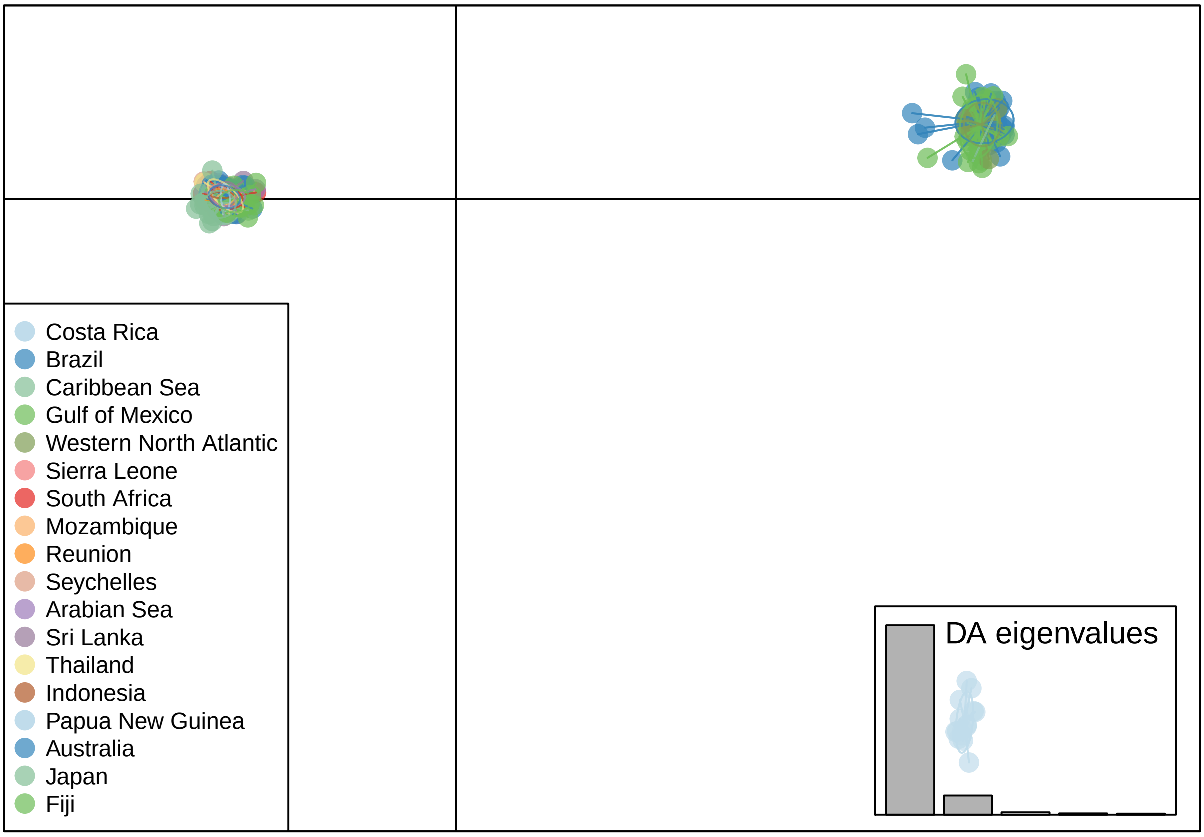
9.9.4 DAPC scatterplot

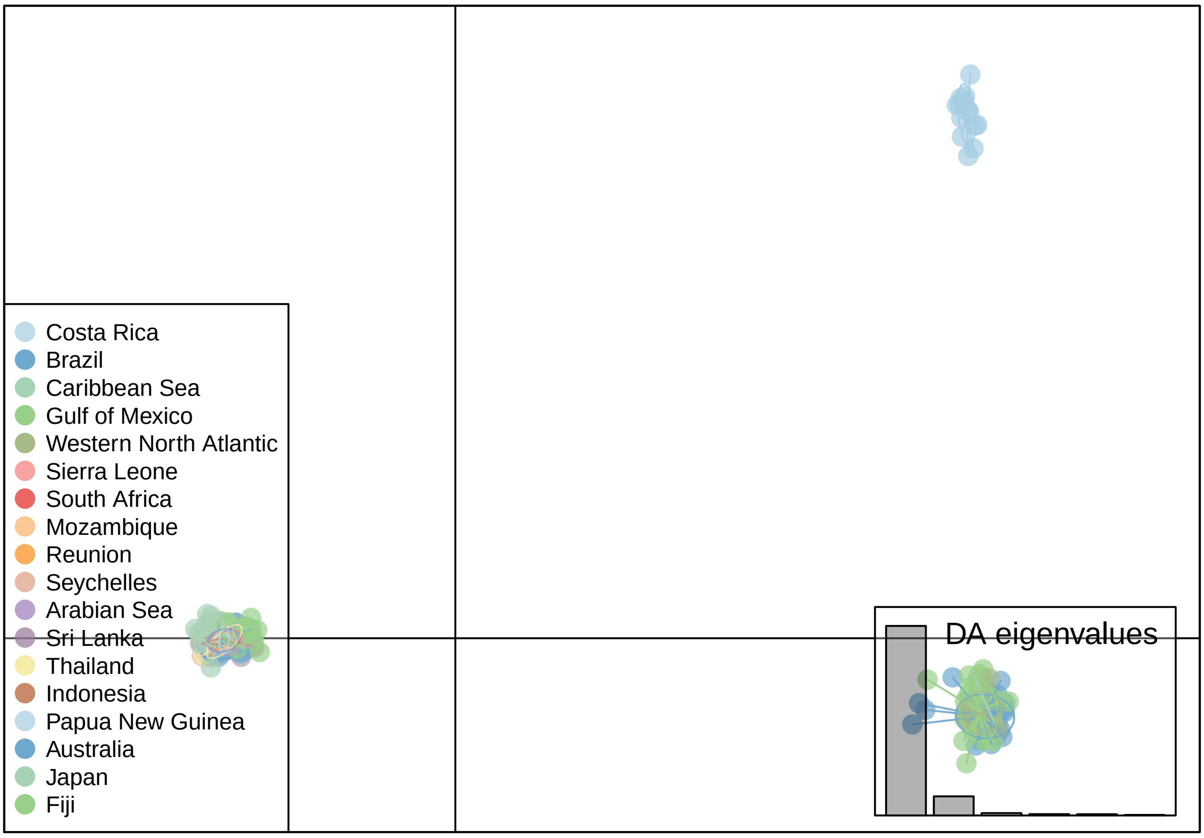
```
load("DArTcap_AUS_subset_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartcap.sub.gl), cex = 2,
                             legend = TRUE, col = colours.14,clabel = FALSE,
                             posi.leg = posi.leg, scree.pca = FALSE,
                             posi.pca = "topleft", cleg = 0.75, xax = 1,
                             yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_AUS_subset_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

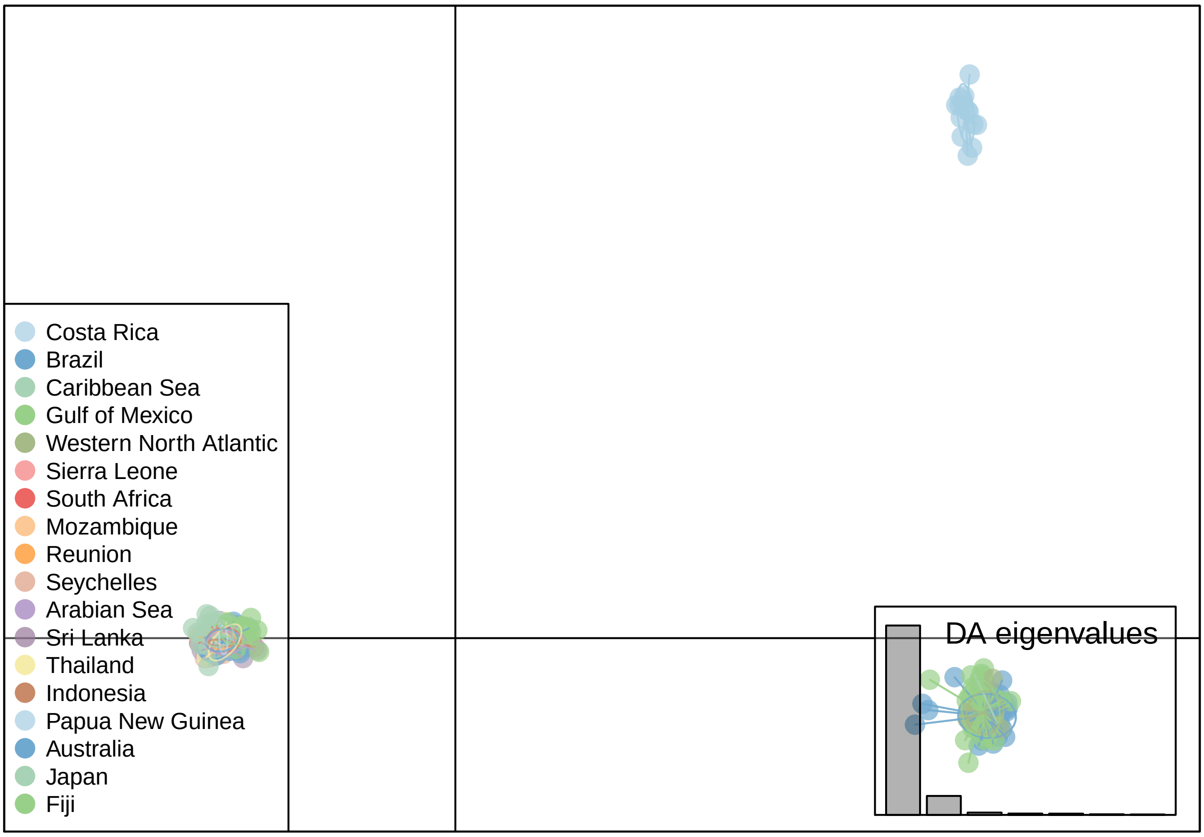

Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues

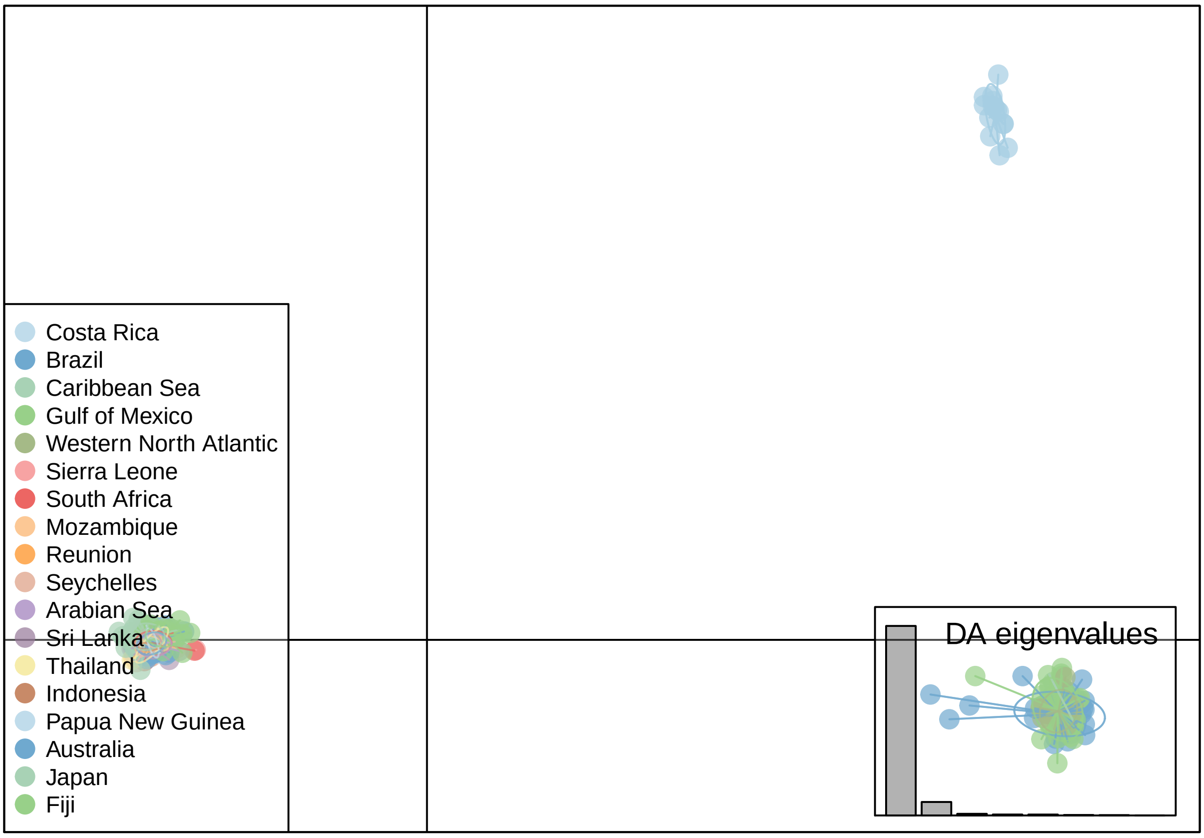

Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues

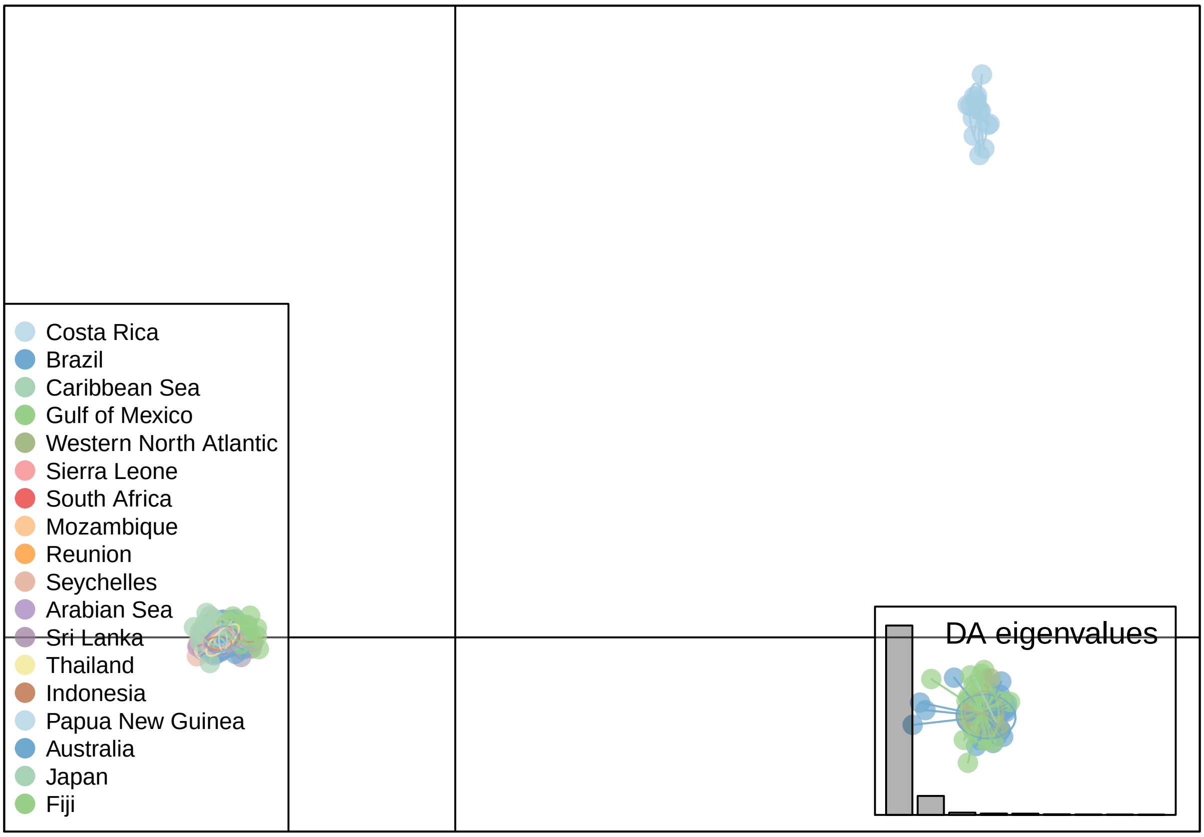

Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues


Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues


Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues

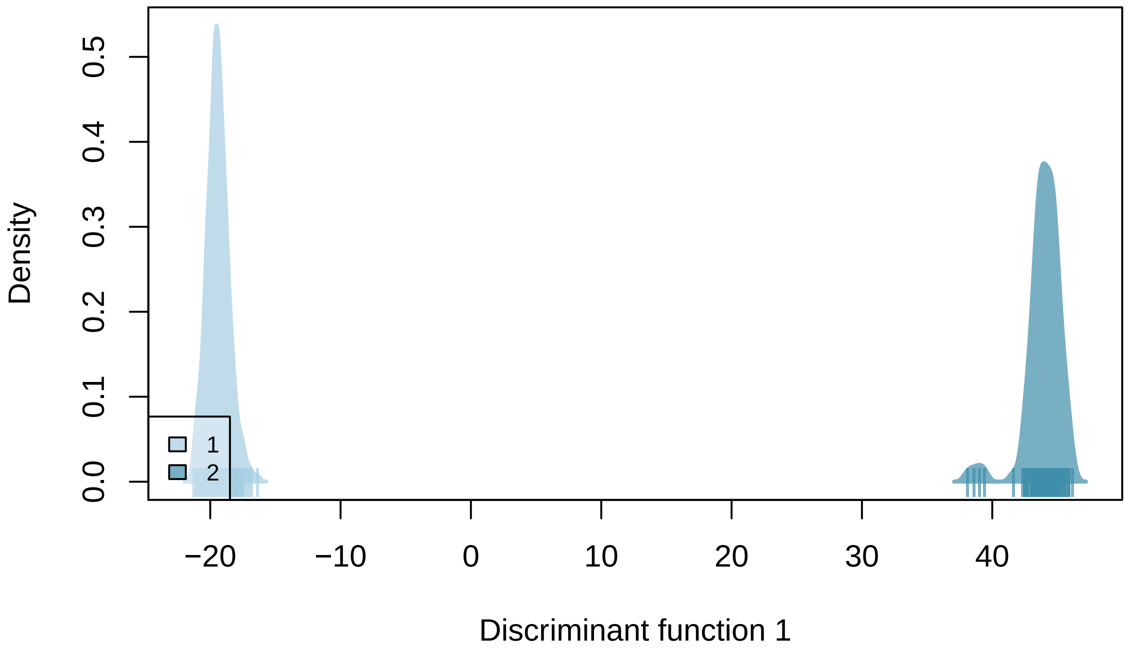

Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji
DA eigenvalues

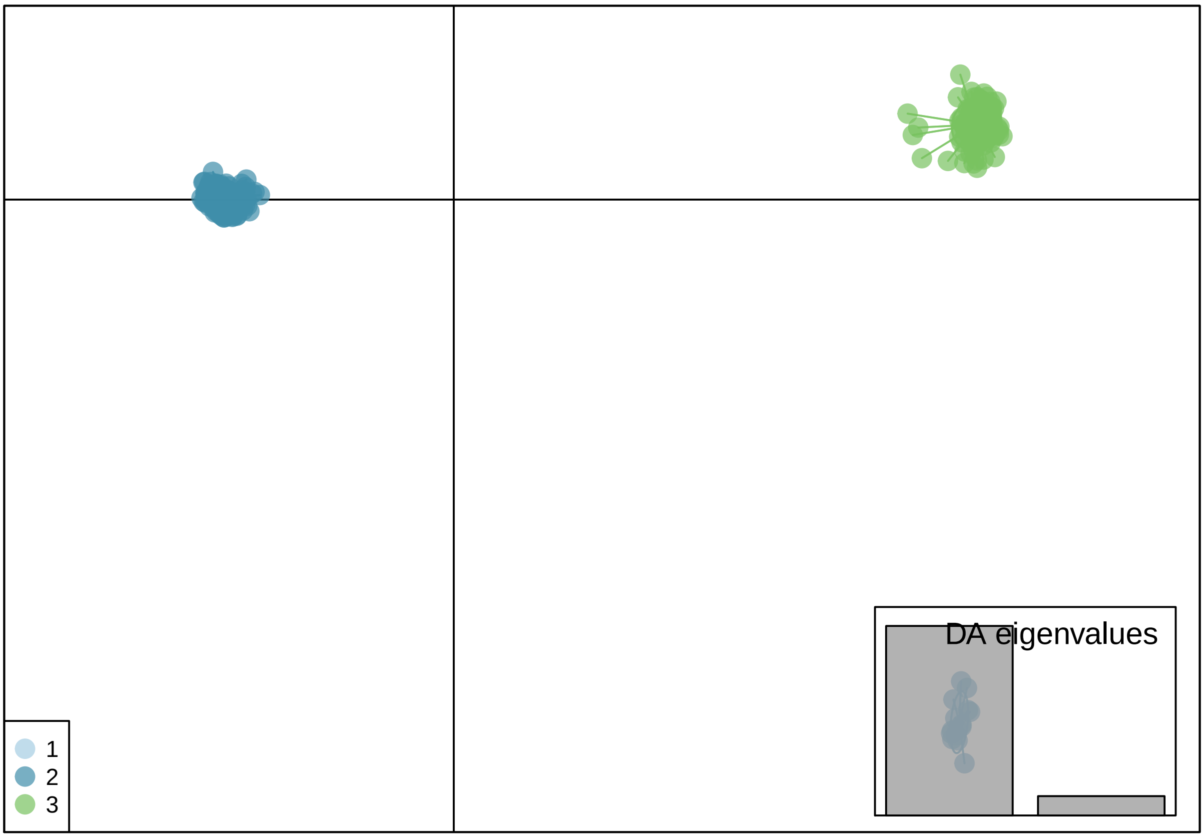


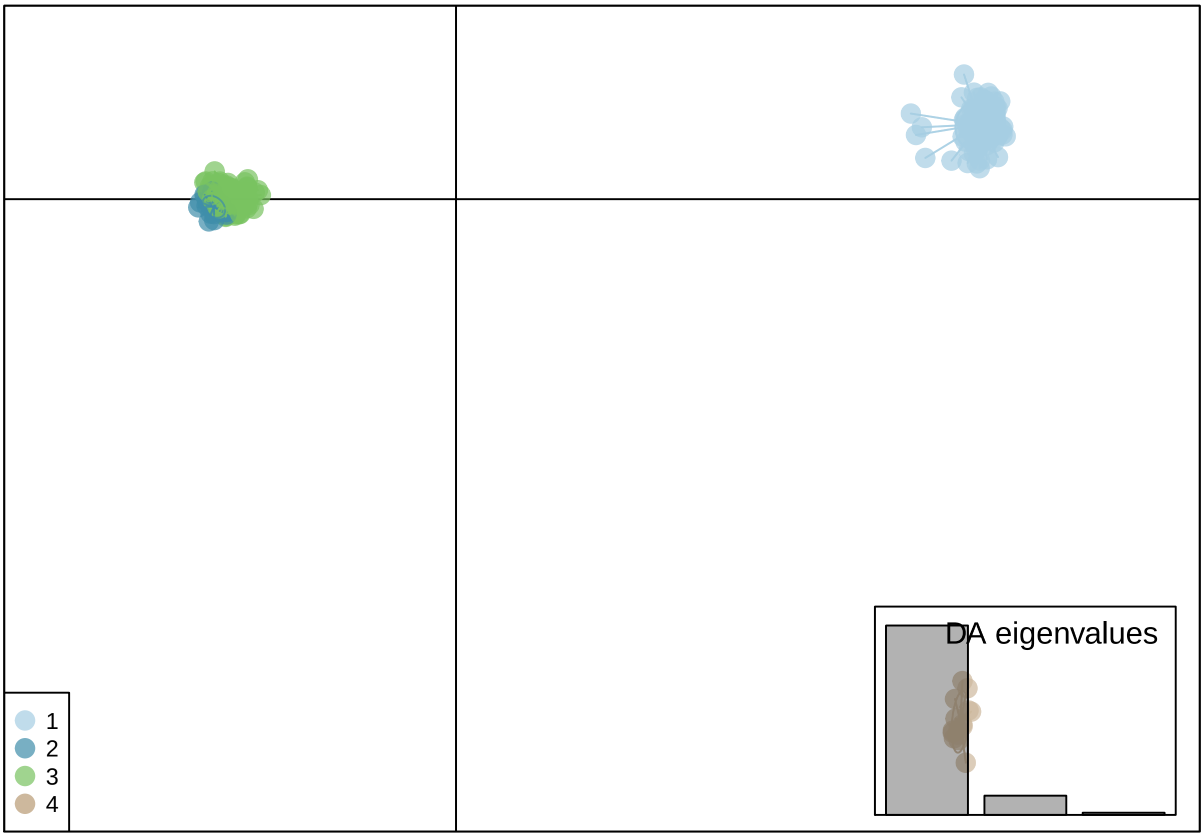


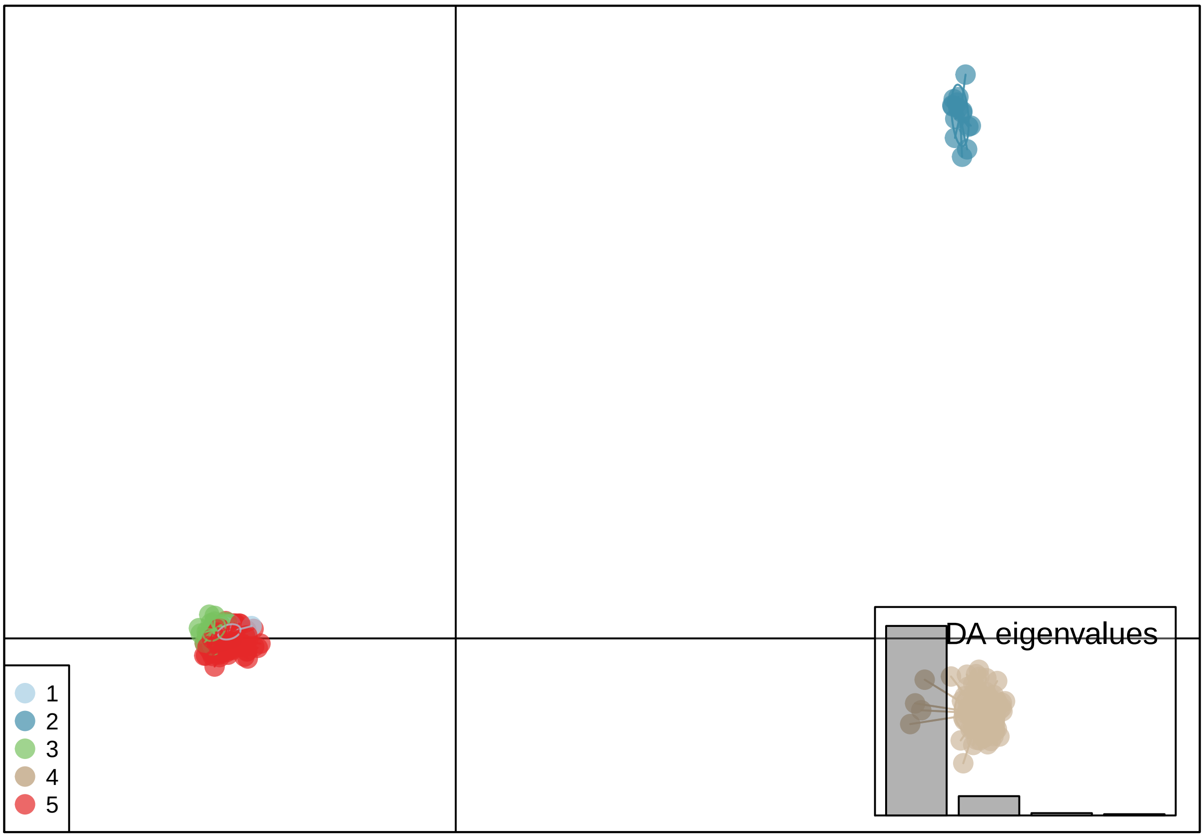
```
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                                       clabel = FALSE, posi.leg = "bottomleft",
```

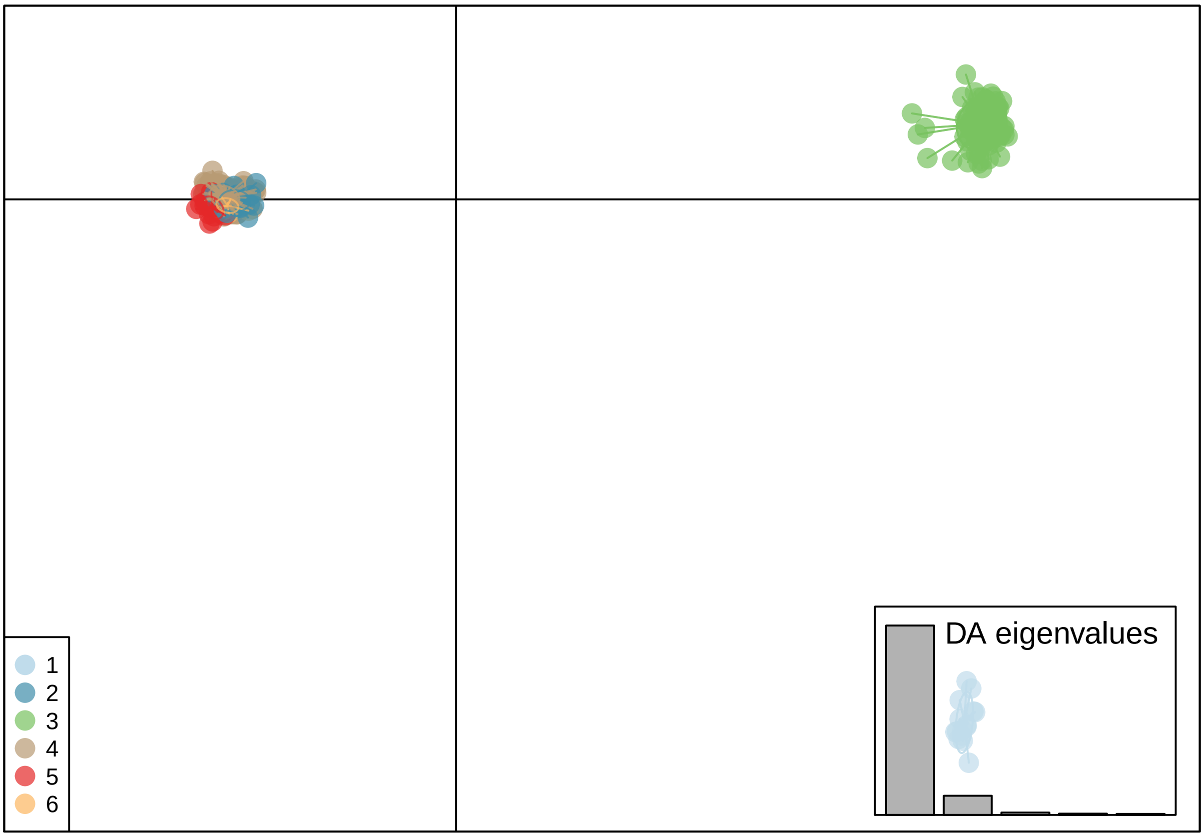
```
                             scree.pca = FALSE,
                                     posi.pca = "topleft", cleg = 0.75,
                             xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_AUS_subset_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

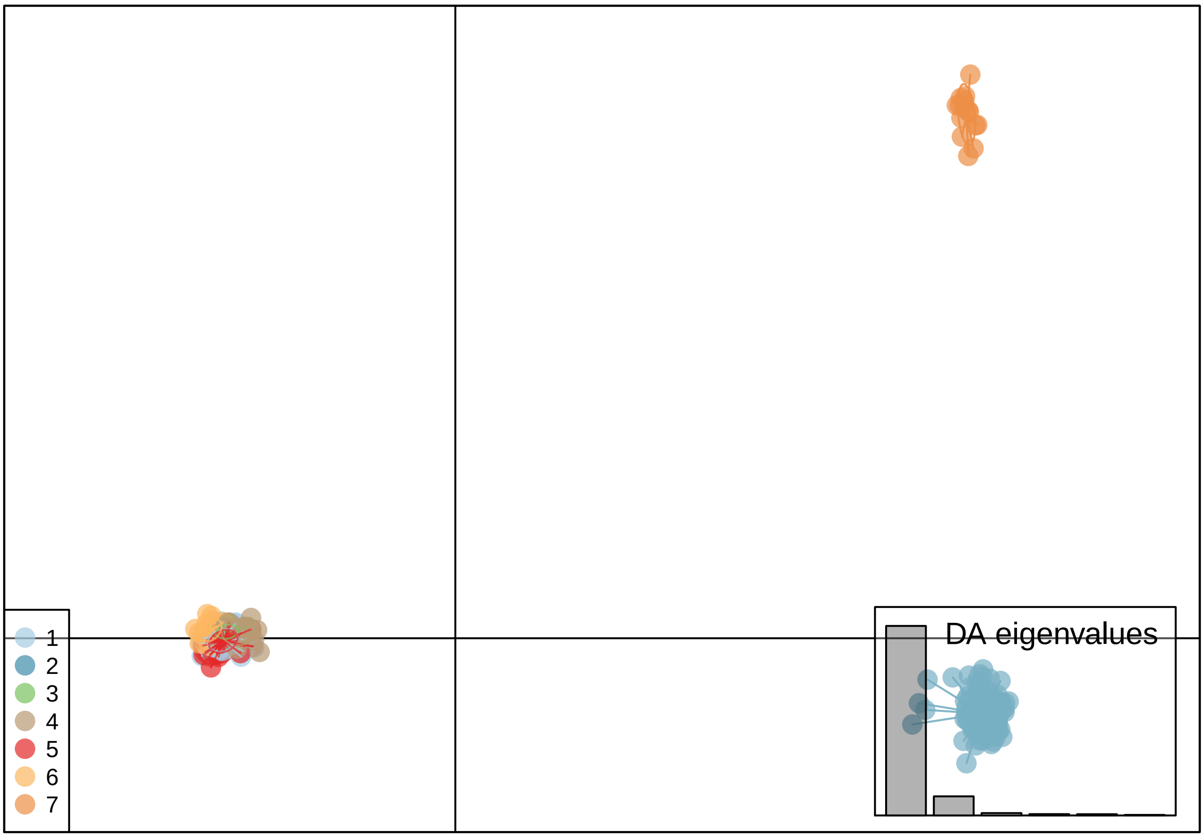


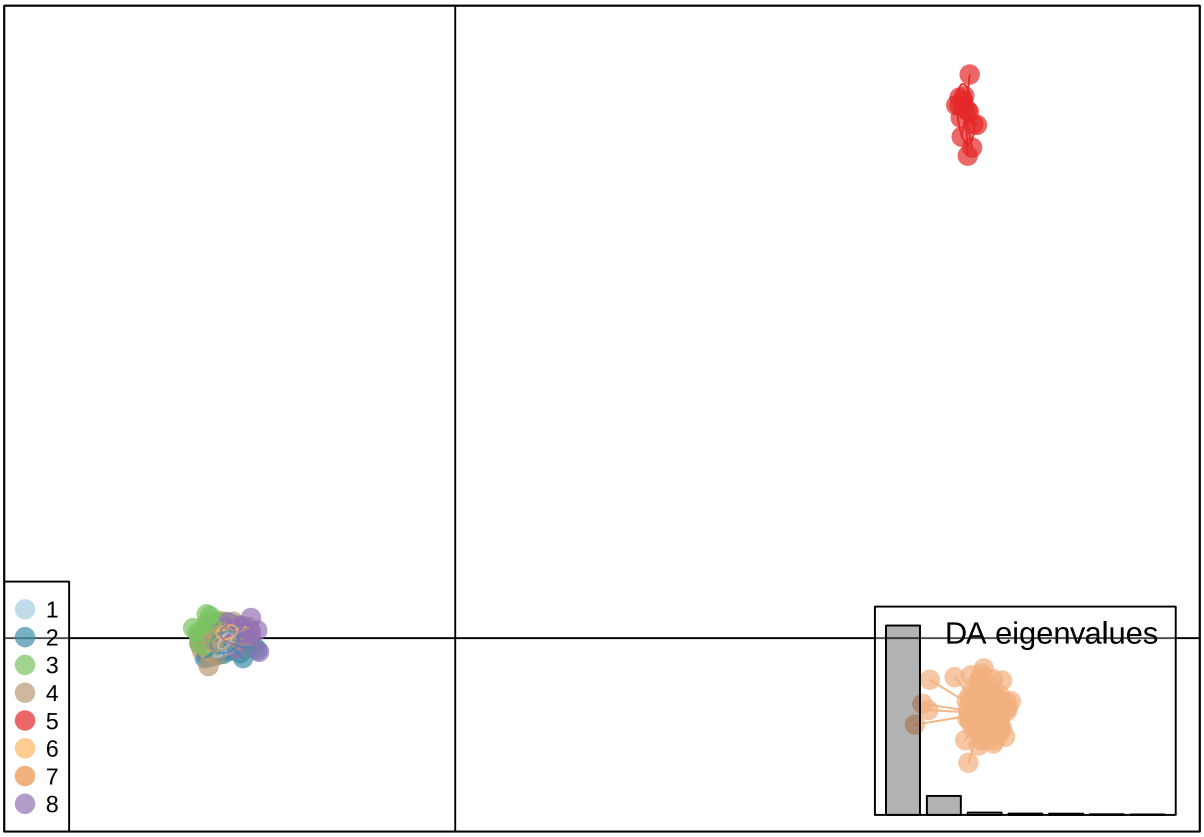

DA eigenvalues
1
2
3

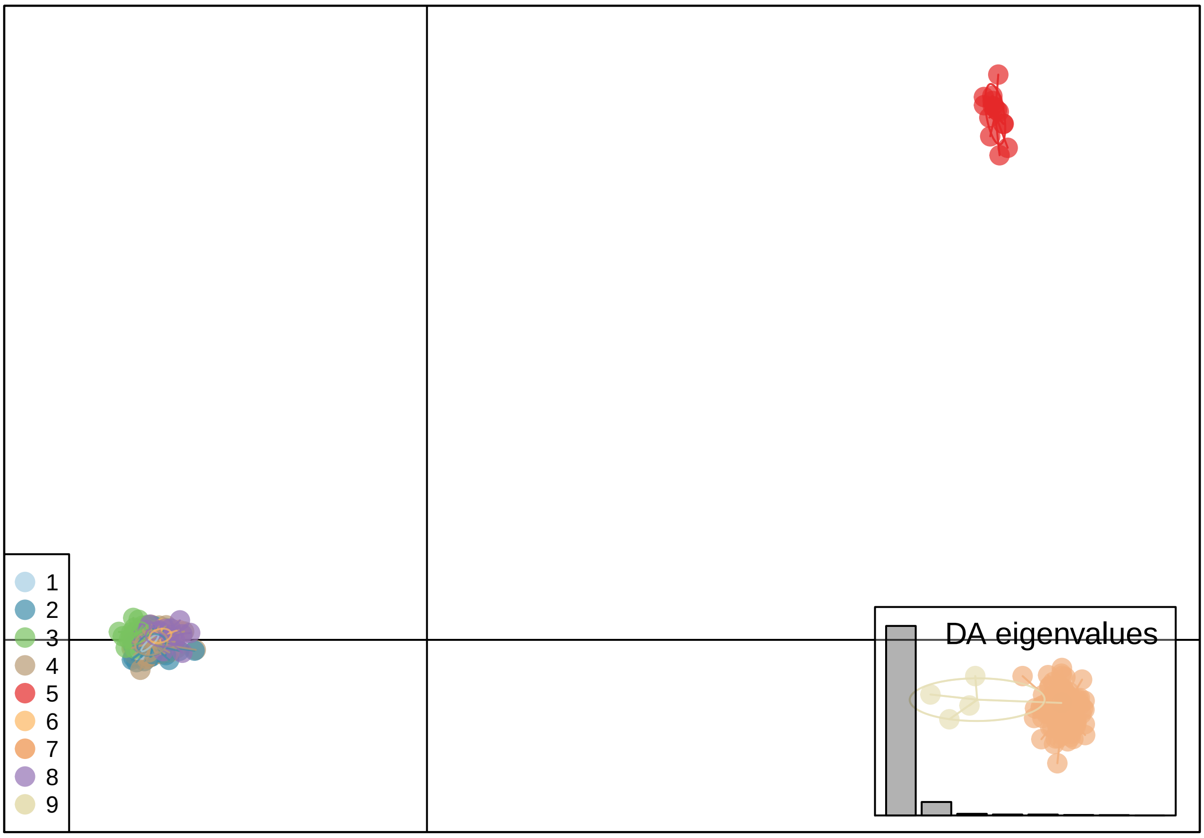

DA eigenvalues
1
2
3
4

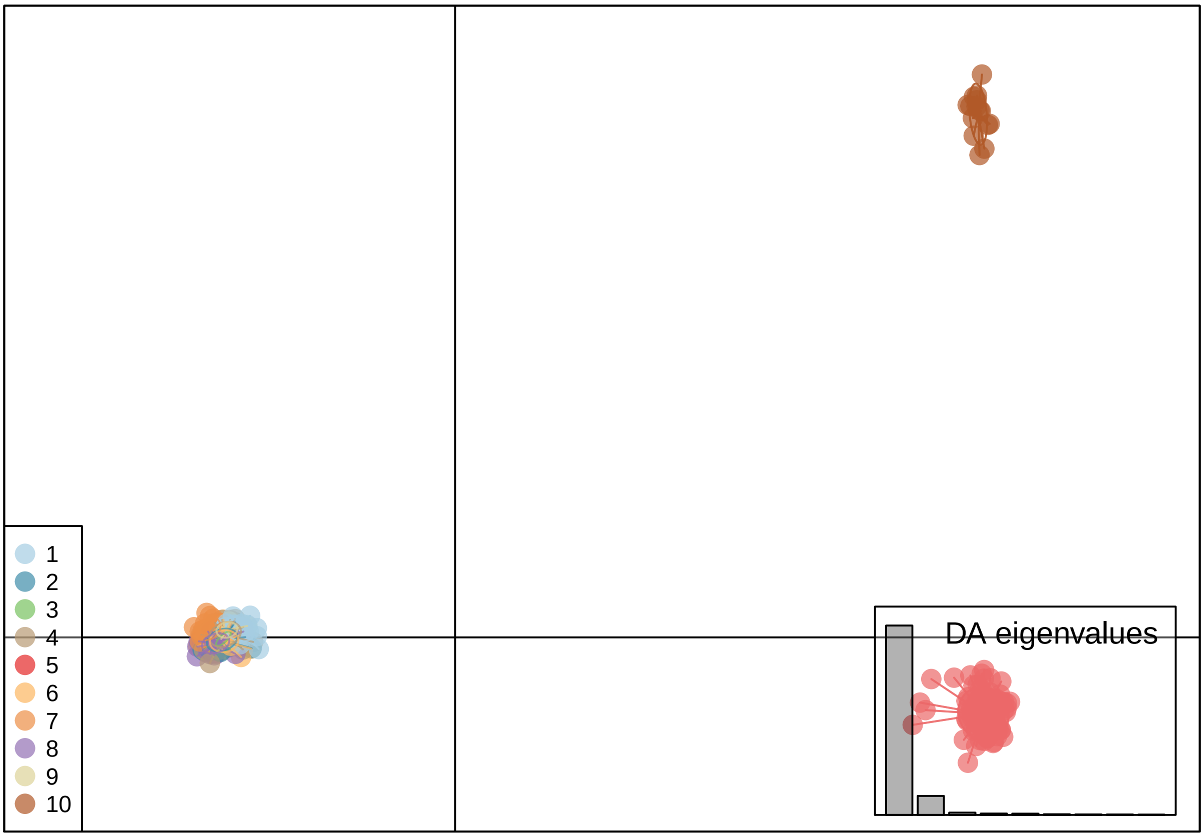

1
2
3
4
5
DA eigenvalues


1
2
3
4
5
6
DA eigenvalues


1
2
3
4
5
6
7
DA eigenvalues


1
2
3
4
5
6
7
8
DA eigenvalues

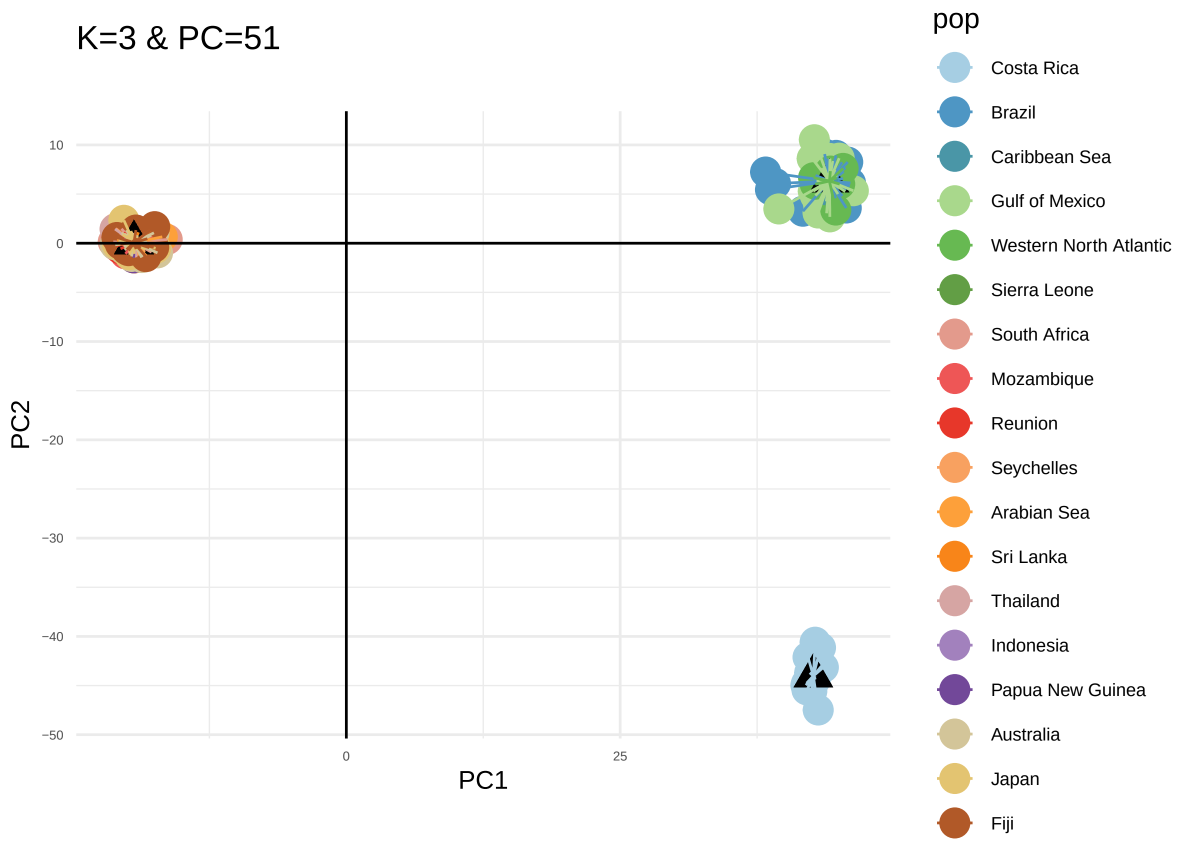




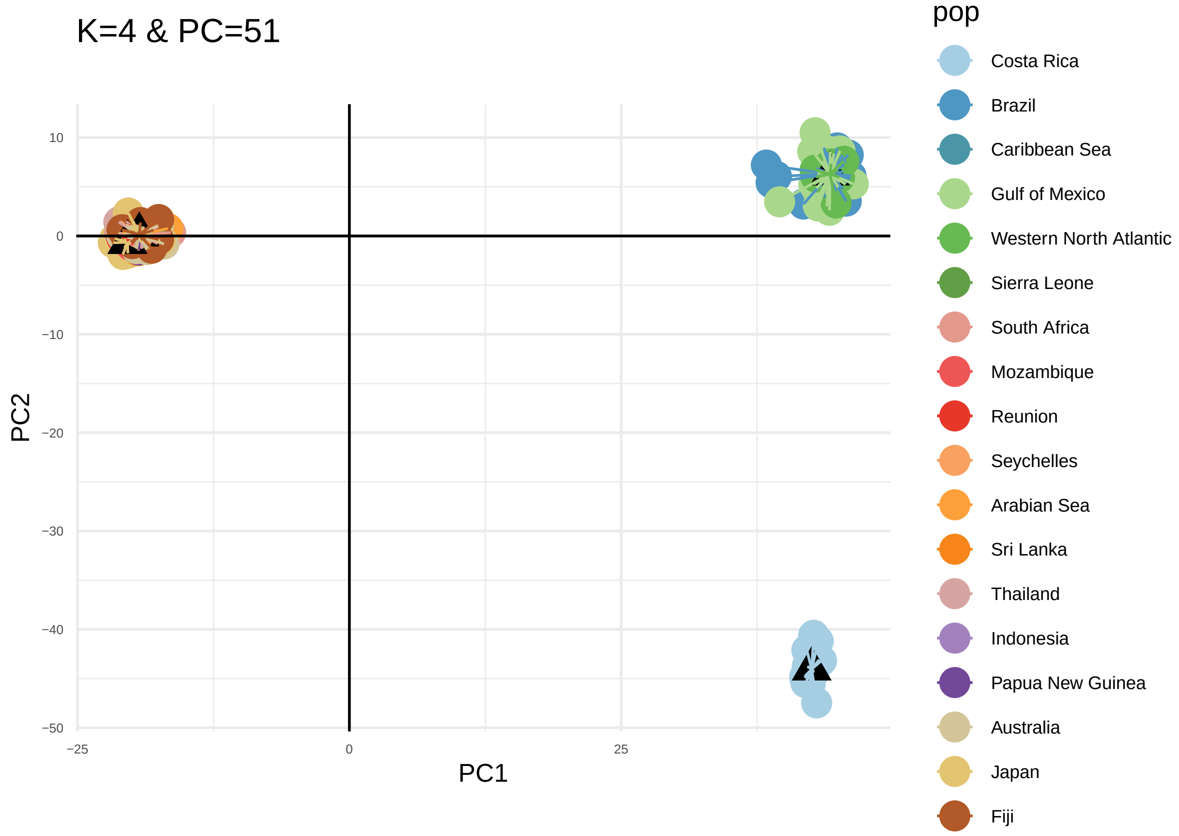
9.9.5 DAPC scatterplot - FLO

This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

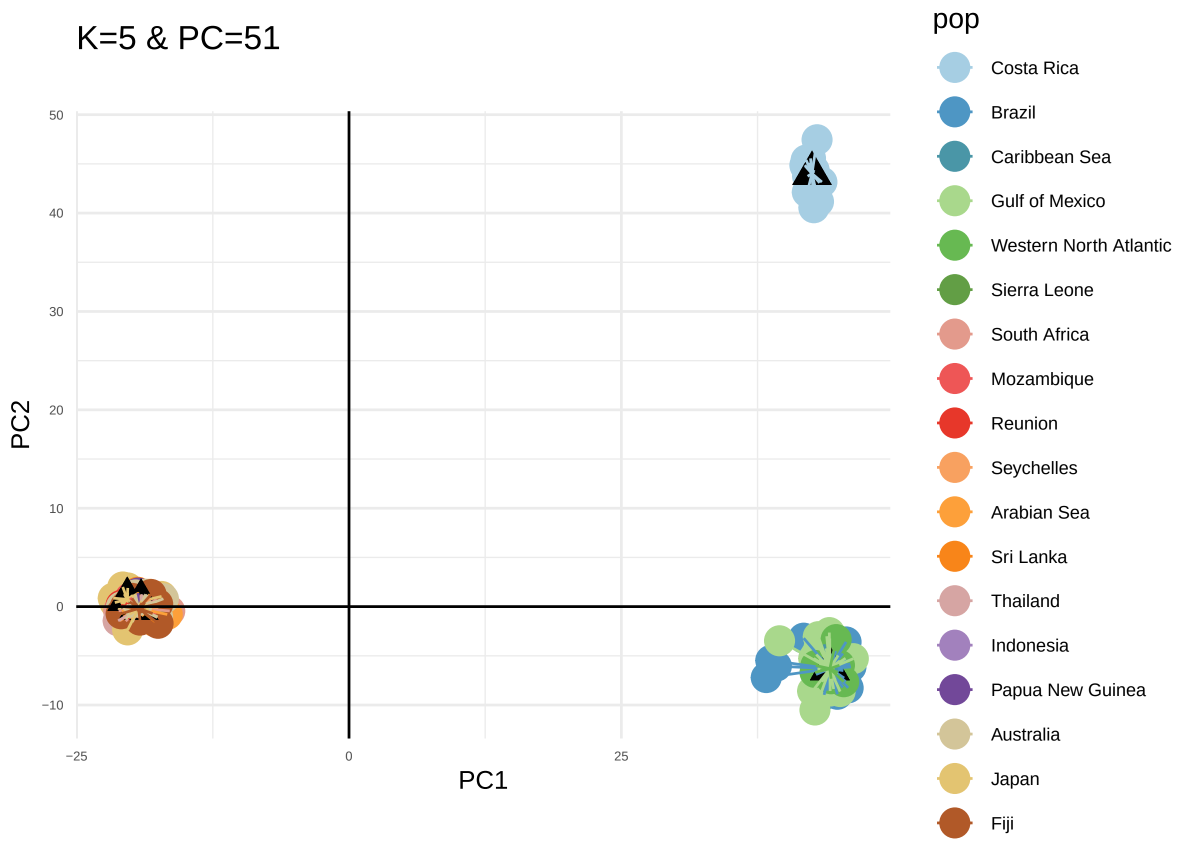
```
for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartcap.sub.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x, mean.y = y)~group, df, mean),
              by = "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x, y = mean.y), size = 5,
                        shape = 17, color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y, xend = x,
                                       yend = y)) +
    ggplot2::scale_colour_manual(values = colours.18) +
    ggplot2::scale_fill_manual(values = colours.18) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
        y = "PC2",
        x = "PC1",
        title = paste0("K=",K," & PC=",PC, sep = ""),
        caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot,
                  filename = paste0("DArTcap_AUS_subset_DAPC_scatterplot2_K", K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```

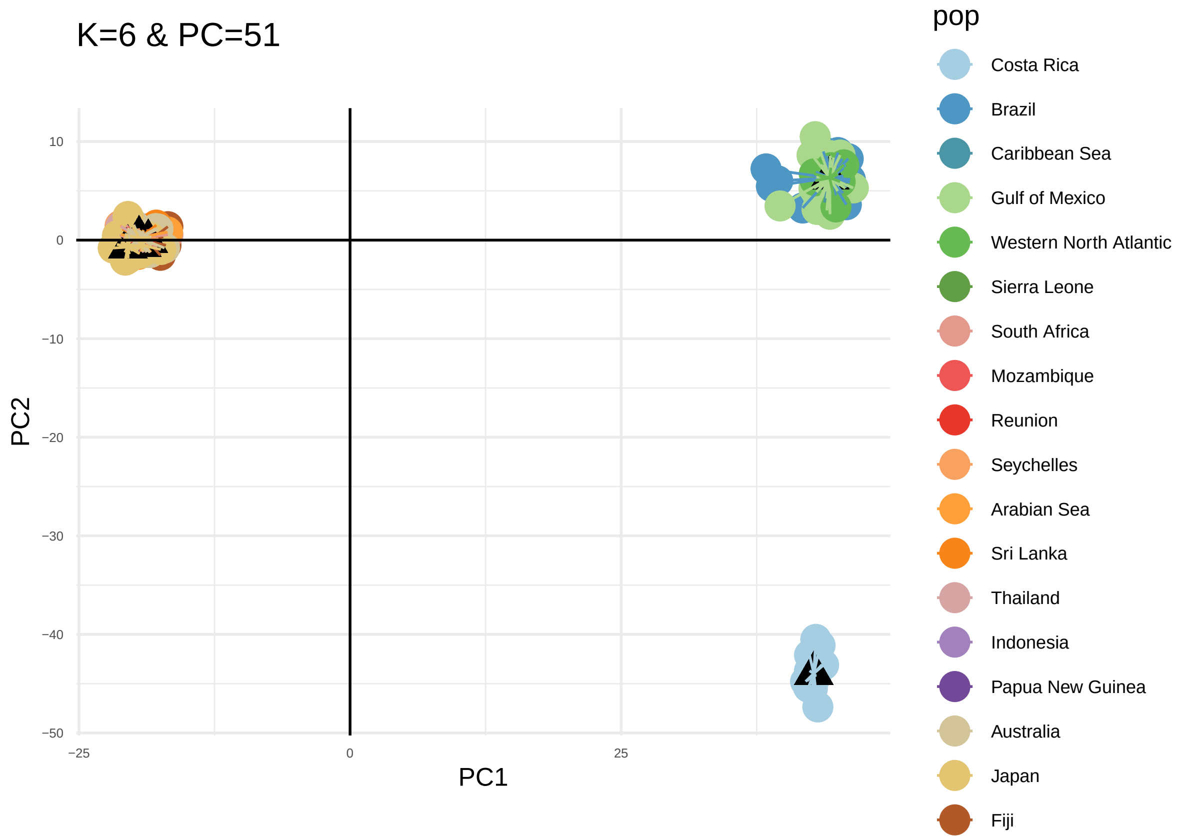


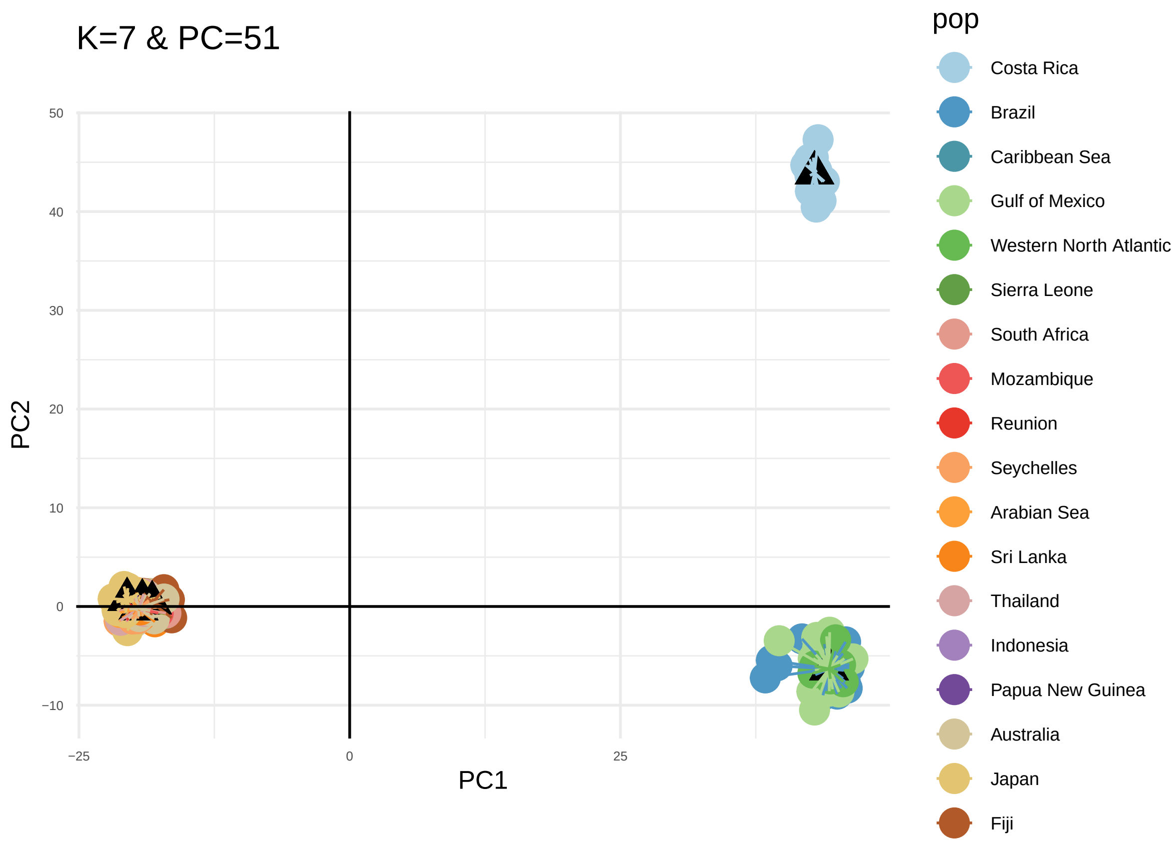
K=3 & PC=51

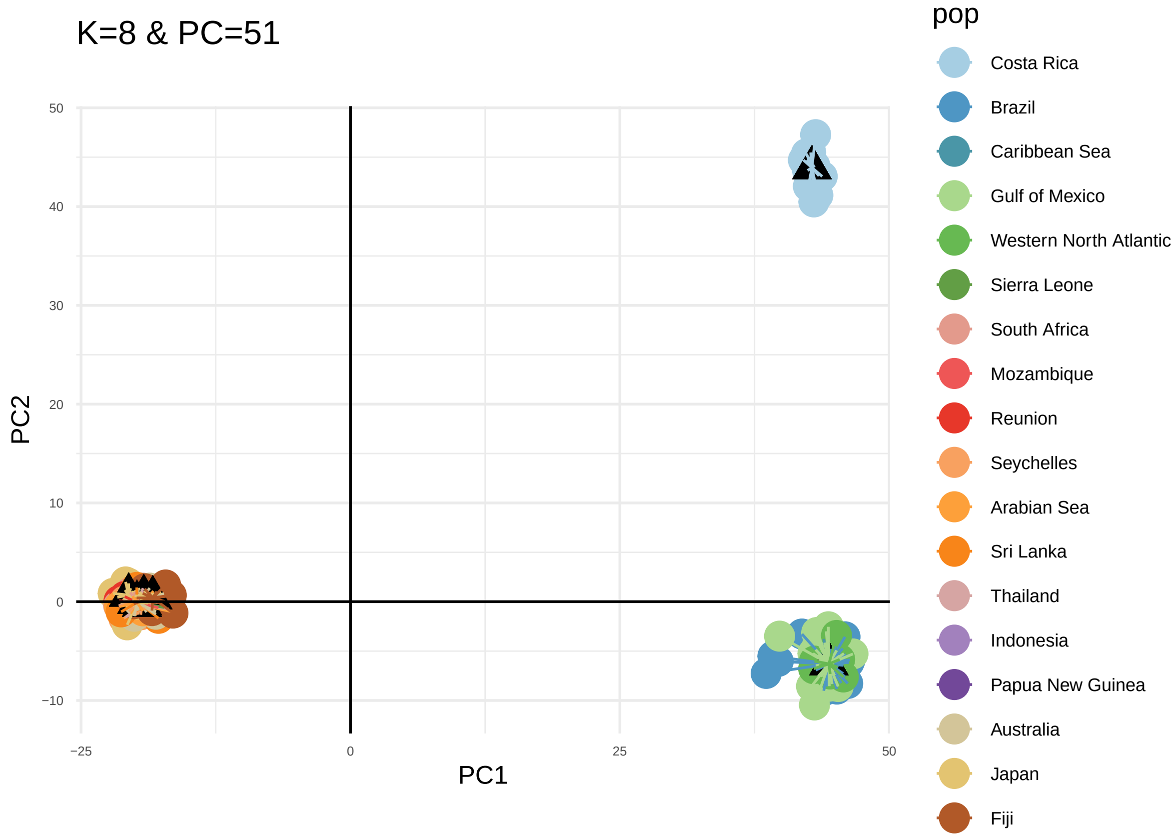


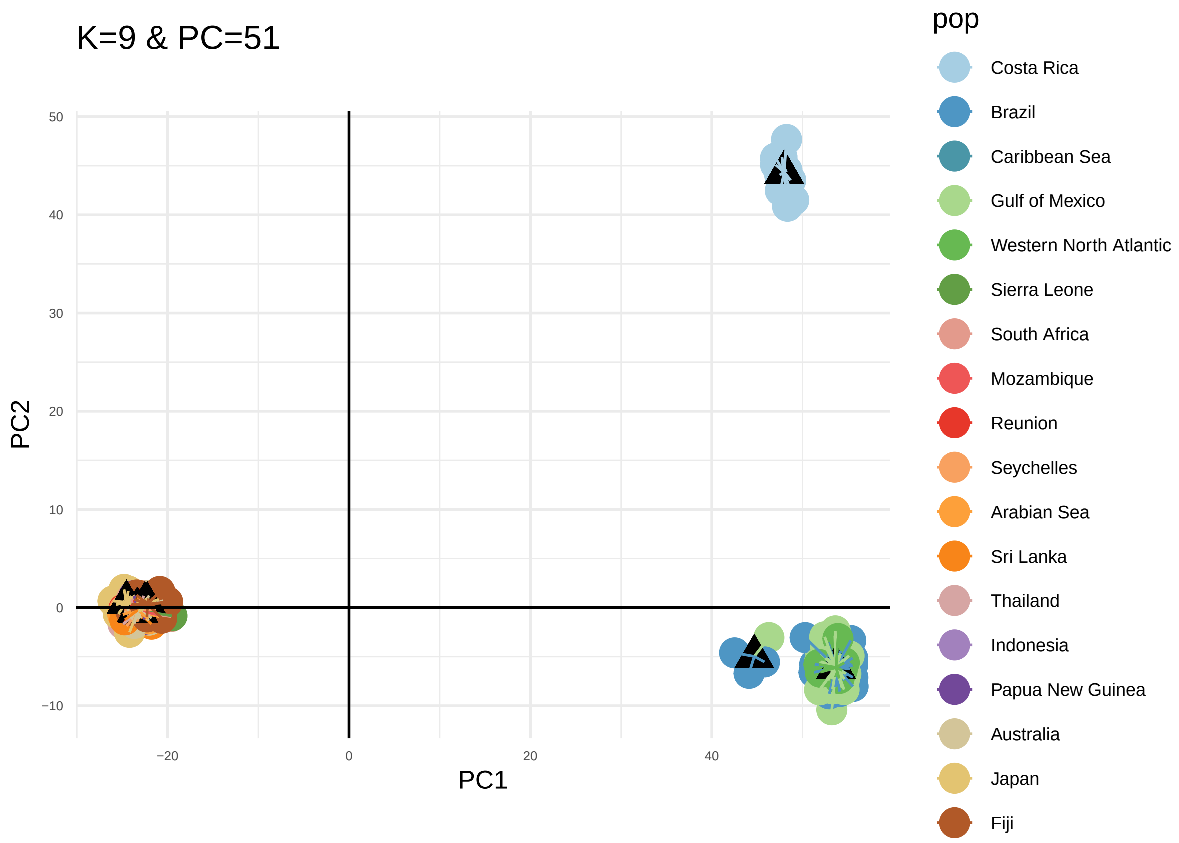
K=4 & PC=51

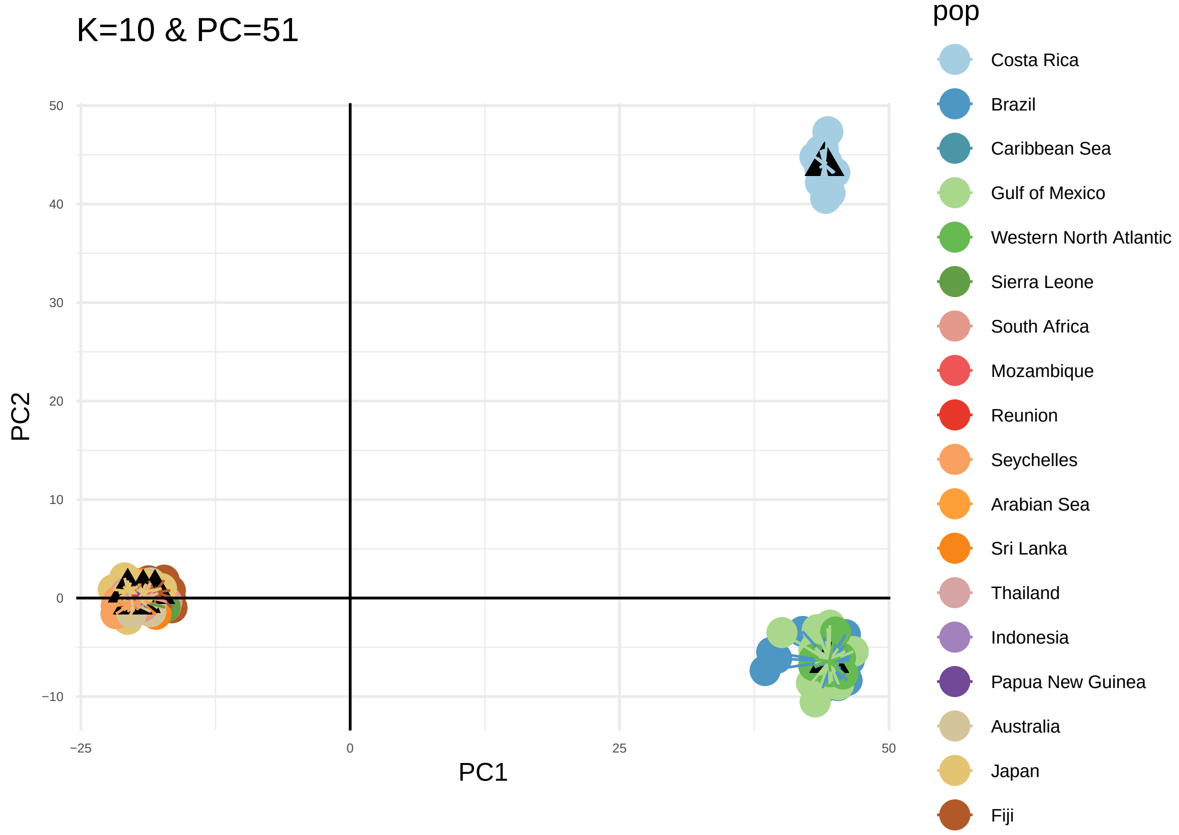

K=5 & PC=51
PC2
PC1
50
40
30
20
10
0
−10
−25
0
25
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


K=6 & PC=51
PC2
PC1
10
0
−10
−20
−30
−40
−50
−25
0
25
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


K=7 & PC=51
PC2
50
40
30
20
10
0
−10
−25
0
25
PC1
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


K=8 & PC=51
PC2
50
40
30
20
10
0
−10
−25
0
25
50
PC1
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


K=9 & PC=51
PC2
50
40
30
20
10
0
−10
−20
0
20
40
PC1
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji


K=10 & PC=51
PC2
50
40
30
20
10
0
−10
−25
0
25
50
PC1
pop
Costa Rica
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
Sierra Leone
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
Japan
Fiji

10 DATA4: DArTcap - West-Atlantic

10.1 Set strata

```
strata <- radiator::read_strata("Bull_shark_DArTcap_strata.tsv",
                                keep.two = FALSE)$strata %>%
  dplyr:: filter(SpeciesID_genetic == "Carcharhinus leucas") %>%
  dplyr:: filter(Region == "W-ATL")
readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata4_WATL.tsv")
```

10.2 Filter data

1. Marker Reproducibility: 0.98
2. Individual missingness: 0.35
3. Individual Het - low: 0
4. Individual Het - high: 0.07
5. Individual total coverage - low: 10,000
6. Individual total coverage - high: 1,000,000
7. Marker MAC - low: 3
8. Marker coverage - low: 5
9. Marker coverage - high:65
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 2 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: 0.141
16. Individual Het - high: 0.200
17. Duplicated individuals: 0.35
18. No filter on HWE

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata4_WATL.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = 1)
BS.dartcap.WATL.gds <- BSsnp$gds
BS.dartcap.WATL.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.WATL.gds, expand = TRUE, all = TRUE, attribute = TRUE,
      attribute.trim = FALSE)

save(BS.dartcap.WATL.tidy, file = "DArTcap_WATL.Rdata")
```

Table 39:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	125 / 4 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	125 / 4 / 1 / 25292 / 35287	0 / 0 / 0 / 19147 / 28615
Filter markers in common	NA	125 / 4 / 1 / 6145 / 6672	0 / 0 / 0 / 384 / 506
Filter individuals based on missingness	0.35	125 / 4 / 1 / 5761 / 6166	12 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.08	113 / 4 / 1 / 5761 / 6166	0 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+06	113 / 4 / 1 / 5761 / 6166	3 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	110 / 4 / 1 / 5761 / 6166	0 / 0 / 0 / 1074 / 1201
Filter MAC	3	110 / 4 / 1 / 4687 / 4965	0 / 0 / 0 / 3182 / 3402
Filter coverage min / max	5-65	110 / 4 / 1 / 1505 / 1563	0 / 0 / 0 / 486 / 507
Filter genotyping	0.1	110 / 4 / 1 / 1019 / 1056	0 / 0 / 0 / 74 / 100
Filter SNPs position on the read	all	110 / 4 / 1 / 945 / 956	0 / 0 / 0 / 0 / 0
Filter markers snp number	2	110 / 4 / 1 / 945 / 956	0 / 0 / 0 / 0 / 0
Filter short ld	mac	110 / 4 / 1 / 945 / 956	0 / 0 / 0 / 0 / 11
detect mixed genomes	0.141 0.2	110 / 4 / 1 / 945 / 945	8 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	102 / 4 / 1 / 945 / 945	0 / 0 / 0 / 0 / 0
detect duplicate genomes	0.35	102 / 4 / 1 / 945 / 945	11 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	91 / 4 / 1 / 945 / 945	0 / 0 / 0 / 3 / 3
Filter HWE	NA	91 / 4 / 1 / 942 / 942	0 / 0 / 0 / 0 / 0

10.2.1 Remove extra low and high heterozygous individuals

Because the average heterozygosity per sampling location is not even, certain individuals cannot be excluded without removing 'good' individuals.

```
rm <-  c("CL-ARS021-F","CL-GOM025-F.1","CL-GOM012-F","CL-SAF014-M","CL-SAF002-F",
         "CL-BRZ038-U","CLF003-F","CL-GOM011-F","CL-SAF015-F","CL-SAF003-M",
         "CL-PNG005-U","CLCR056-M","CLCR047.1","CLCR055-M","CLCR066-M")

BS.dartcap.WATL.tidy <- BS.dartcap.WATL.tidy[
  !BS.dartcap.WATL.tidy$INDIVIDUALS %in% rm,]
length(unique(BS.dartcap.WATL.tidy$INDIVIDUALS)) # 91
```

‘

10.3 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.WATL.tidy,
                                       output = c("genlight", "stockr",
                                                  "pcadapt", "gtypes", "rubias"))
BS.dartcap.WATL.gl <- Convert$genlight
BS.dartcap.WATL.stkr <- Convert$stockr
BS.dartcap.WATL.pc <- Convert$pcadapt
BS.dartcap.WATL.gt <- Convert$gtypes
BS.dartcap.WATL.rubias <- Convert$rubias


markers.meta <- radiator::extract_markers_metadata(BS.dartcap.WATL.gds,
                                                   whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.WATL.gds,
                                                           whitelist = TRUE)
individuals.meta <- individuals.meta[individuals.meta$INDIVIDUALS %in%
                                       BS.dartcap.WATL.gl$ind.names,]
BS.dartcap.WATL.gl$other$ind.metrics <- individuals.meta
BS.dartcap.WATL.gl$other$loc.metrics <- markers.meta
BS.dartcap.WATL.gt@schemes <- individuals.meta

pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic")
BS.dartcap.WATL.gl$pop <- factor(BS.dartcap.WATL.gl$other$ind.metrics$Site2,
                                 levels = pop.levels)
BS.dartcap.WATL.gl <- BS.dartcap.WATL.gl[order(BS.dartcap.WATL.gl$pop,
                                               BS.dartcap.WATL.gl$ind.names),]
BS.dartcap.WATL.gl <- BS.dartcap.WATL.gl[order(BS.dartcap.WATL.gl$pop,
                                               BS.dartcap.WATL.gl$ind.names)]
BS.dartcap.WATL.rubias$repunit <- factor(BS.dartcap.WATL.rubias$repunit,
                                         levels = pop.levels)

save(BS.dartcap.WATL.tidy, BS.dartcap.WATL.gl, BS.dartcap.WATL.stkr,
     BS.dartcap.WATL.pc,BS.dartcap.WATL.gt,BS.dartcap.WATL.rubias,
     markers.meta, individuals.meta, file = "DArTcap_WATL.Rdata")
```

10.4 Load data

```
load("DArTcap_WATL.Rdata")
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico",  "Western North Atlantic")

BS.dartcap.WATL.gl$pop <- factor(BS.dartcap.WATL.gl$other$ind.metrics$Site,
                                 levels = pop.levels)
```

```
BS.dartcap.WATL.gl <- BS.dartcap.WATL.gl[order(BS.dartcap.WATL.gl$pop,
                                               BS.dartcap.WATL.gl$ind.names)]

pop.levels1 <- stringr::str_replace_all(pop.levels, " ", "_")
BS.dartcap.WATL.tidy$POP_ID <- factor(BS.dartcap.WATL.tidy$POP_ID,
                                      levels = pop.levels1)
BS.dartcap.WATL.tidy <- BS.dartcap.WATL.tidy[order(BS.dartcap.WATL.tidy$POP_ID,
                                                   BS.dartcap.WATL.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartcap.WATL.gl) # 91
adegenet::nLoc(BS.dartcap.WATL.gl) # 942
summary(BS.dartcap.WATL.gl$pop)
sum(duplicated(BS.dartcap.WATL.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartcap.WATL.gl$other$loc.metrics$LOCUS) #24
```

```
## [1] 91
## [1] 942
##                  Brazil          Caribbean Sea         Gulf of Mexico
##                      47                      2                     34
## Western North Atlantic
##                       8
## [1] 0
## [1] 24
```

10.5 Remove sex-linked markers

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sum(bull_shark$sexy.summary$CLONE_ID %in% SLM$sexy.summary$CLONE_ID) #33
sum(SLM$sexy.summary$CLONE_ID %in% bull_shark$sexy.summary$CLONE_ID) #23
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID, SLM$sexy.summary$CLONE_ID))

sum(BS.dartcap.WATL.gl$loc.names %in% sex.markers) #11
locnames <- BS.dartcap.WATL.gl$loc.names
BS.dartcap.WATL.gl <- BS.dartcap.WATL.gl[,!locnames %in% sex.markers]
BS.dartcap.WATL.gl$other$loc.metrics <- BS.dartcap.WATL.gl$other$loc.metrics[
  !locnames %in% sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.WATL.tidy$LOCUS)) # 11
BS.dartcap.WATL.tidy <- BS.dartcap.WATL.tidy[!BS.dartcap.WATL.tidy$LOCUS %in%
                                               sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartcap.WATL.gt@data$locus)[,2]
BS.dartcap.WATL.gt <- BS.dartcap.WATL.gt[,!locus.gt %in% sex.markers, ,
                                         drop = TRUE]

locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                   string =  colnames(BS.dartcap.WATL.rubias))[,2]
BS.dartcap.WATL.rubias <- BS.dartcap.WATL.rubias[,!locus.rubias %in% sex.markers]
```

```
## [1] 33
## [1] 23
## [1] 11
## [1] 11
```

10.6 Genetic diversity

```
set.seed(124)
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico", "Western North Atlantic")

gl <- BS.dartcap.WATL.gl
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]


gl2gpop(gl, filename = "BS_dartcap_WATL_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_WATL_genepop.txt",
                               outfile = "BS_dartcap_WATL_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#4
gendiv <- data.frame(
  "Brazil" = bastat$main_tab[[1]]$overall,
  "Caribbean Sea" = bastat$main_tab[[2]]$overall,
  "Gulf of Mexico" = bastat$main_tab[[3]]$overall,
  "Western North Atlantic" = bastat$main_tab[[4]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTcap_WATL_gendiv.txt")
save(gendiv, file = "DArTcap_WATL_gendiv.Rdata")
```

```
load("DArTcap_WATL_gendiv.Rdata")
shortnames <- c("BRZ", "CAR", "GOM", "WNA")
knitr::kable(gendiv, col.names = shortnames, digits = 4,caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

10.6.1 Number of monomorphic markers per population

```
pop.levels <- c("Brazil","Caribbean Sea","Gulf of Mexico", "Western North Atlantic")

monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.WATL.gl[BS.dartcap.WATL.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
```

Table 40:

	BRZ	CAR	GOM	WNA
ar	1.3270	1.2470	1.3070	1.2960
size	46.7390	1.9940	33.7090	7.9720
obs_het	0.1770	0.1780	0.1680	0.1700
exp_het	0.1820	0.1340	0.1720	0.1640
uexp_het	0.1840	0.1790	0.1750	0.1750
fis	0.0300	-0.3290	0.0290	-0.0390
hwe_glb	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000
fis_lo	0.0080	-1.0000	0.0000	-0.1530
fis_hi	0.0300	-0.3290	0.0300	-0.0490
ar_lo	1.3010	1.1680	1.1880	1.1570
ar_hi	1.3500	1.3230	1.3320	1.3400
fis.hierfstat	0.0401	-0.0997	0.0430	0.0214
fis.CI.low	0.0192	-0.0784	0.0208	-0.0031
fis.CI.high	0.0538	0.0811	0.0658	0.0719

```
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("BRZ", "CAR", "GOM", "WNA")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

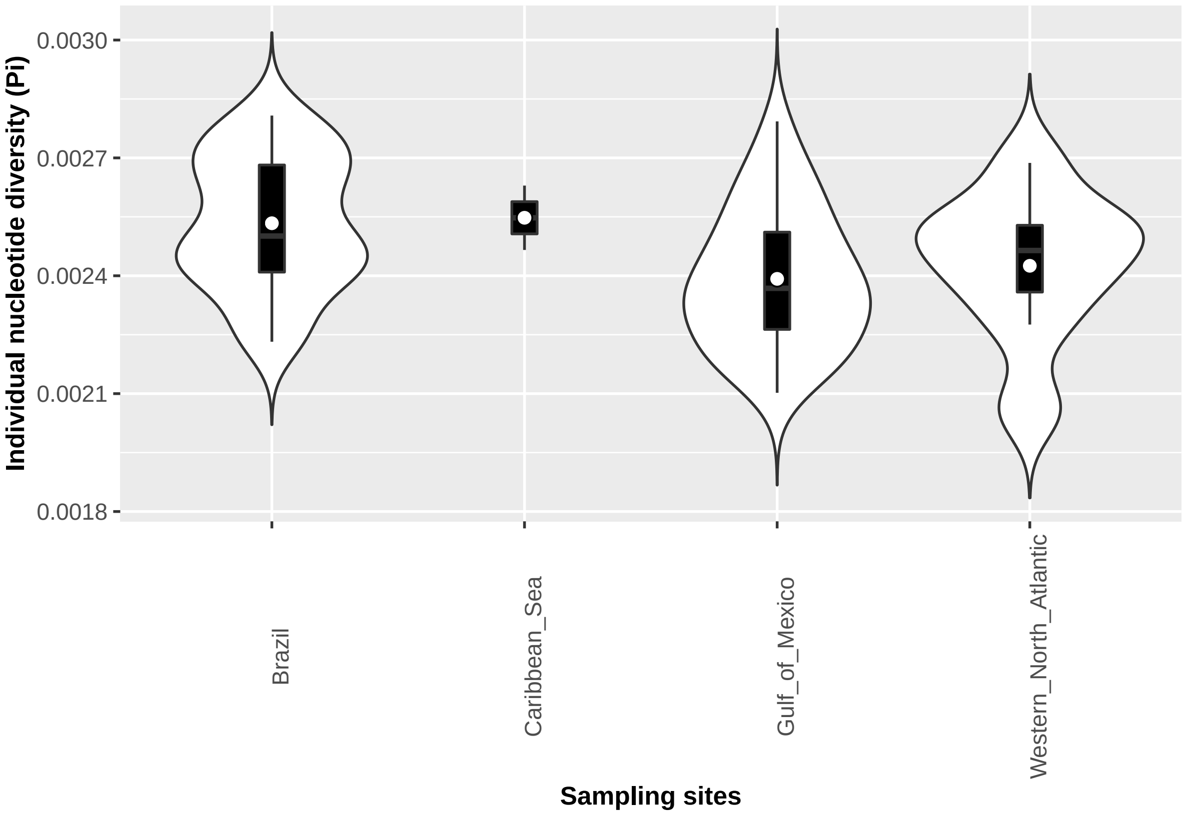
Table 41:

BRZ	CAR	GOM	WNA
36	682	144	385

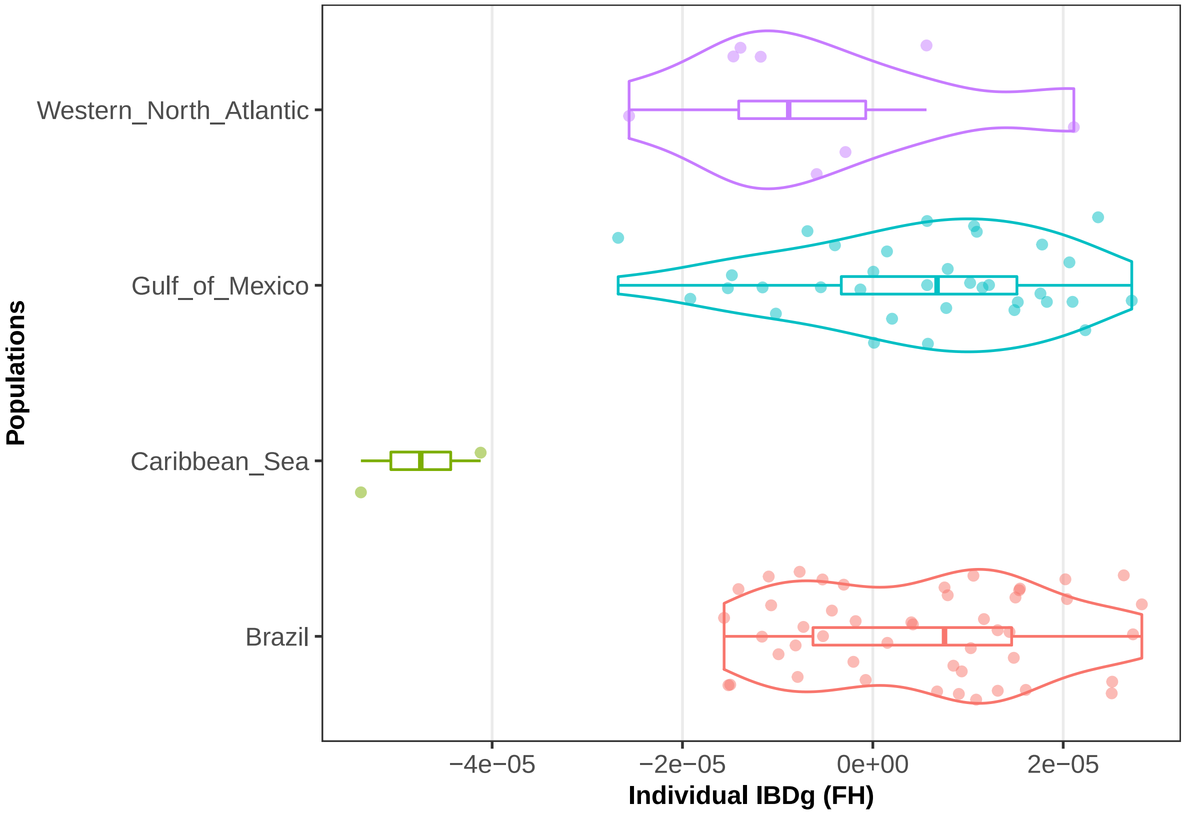
10.6.2 Nucleotide diversity and inbreeding

```
pi.sum <- radiator::pi(
  data = BS.dartcap.WATL.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartcap.WATL.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTcap_WATL_pi_FIS_Sites.Rdata")
```

```
load("DArTcap_WATL_pi_FIS_Sites.Rdata")
pi.sum$boxplot.pi
```



```
FIS.sum$fh.box.plot
```



10.7 Genetic differentiation

```
Fst.gt <-
  strataG::popStructTest(
    BS.dartcap.WATL.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_WATL_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_WATL_FST.txt")
```

```
load("DArTcap_WATL_FST.Rdata")
knitr::kable(
  Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                        decreasing = TRUE),
                                  -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 931 loci between the West Atlantic sites") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

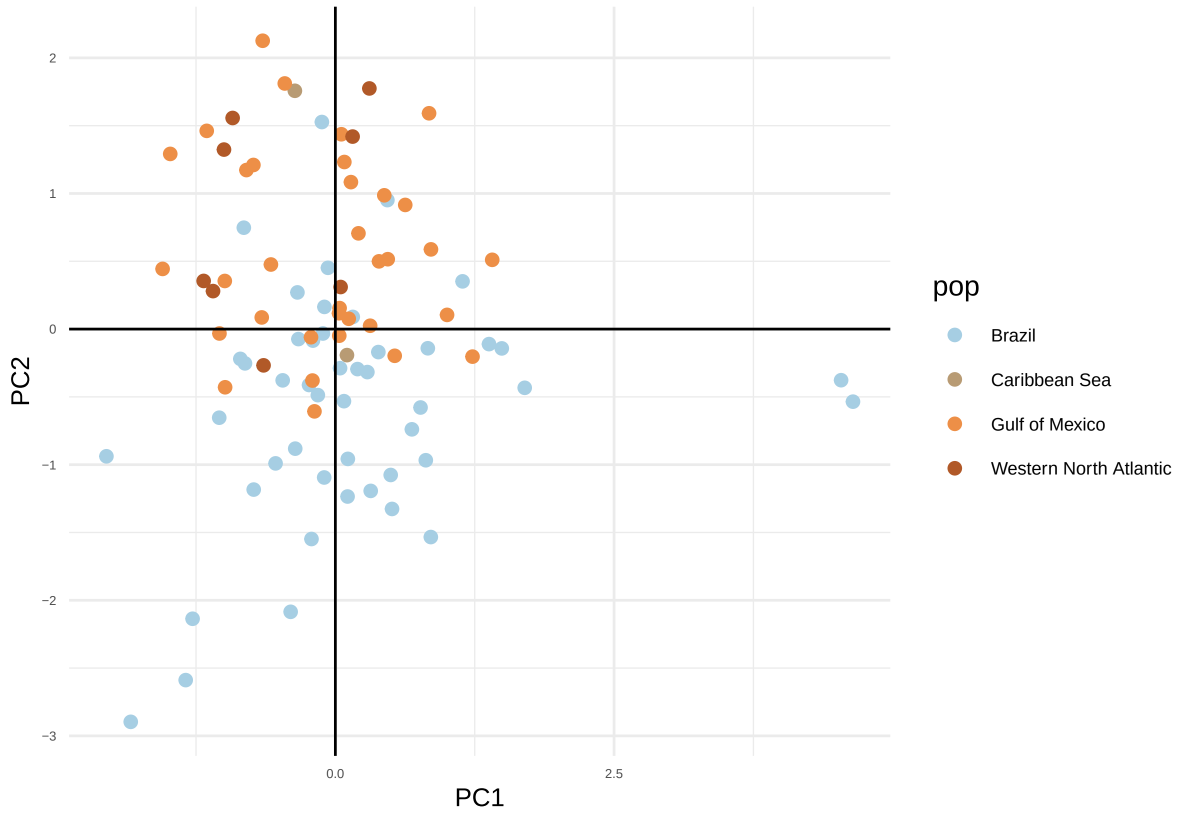
Table 42: Pairwise Fst for 931 loci between the West Atlantic sites

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Brazil (47) v. Western_North_Atlantic (8)	976.2829	0.3686	0.0005	0.2098	-0.1240	0.8032	0.0067	0.0160	0.0082	0.0160	0.0069	0.0120	0.0099	0.0120	0.0167	0.0120
Brazil (47) v. Gulf_of_Mexico (34)	1267.0889	0.0010	0.0002	0.0220	0.0271	0.9920	0.0061	0.0010	0.0075	0.0010	0.0032	0.0010	0.0046	0.0010	0.0079	0.0010
Gulf_of_Mexico (34) v. Western_North_Atlantic (8)	948.0094	0.0739	0.0004	0.2627	-0.6087	0.7113	0.0027	0.1479	0.0033	0.1479	0.0144	0.1558	0.0203	0.1518	0.0341	0.1538
Brazil (47) v. Caribbean_Sea (2)	997.6150	0.3347	0.0016	0.6563	-0.1850	0.6014	0.0012	0.4338	0.0015	0.4338	0.0177	0.4113	0.0253	0.4113	0.0423	0.4113
Caribbean_Sea (2) v. Gulf_of_Mexico (34)	982.2654	0.0599	0.0014	0.7093	-1.0572	0.3402	-0.0008	0.5051	-0.0010	0.5051	0.0777	0.6655	0.1054	0.6199	0.1698	0.6324
Caribbean_Sea (2) v. Western_North_Atlantic (8)	657.8576	0.4326	0.0015	0.4366	-4.6634	0.3099	-0.0023	0.5425	-0.0028	0.5425	0.3066	0.6501	0.3701	0.6706	0.5180	0.6706

10.8 PCA

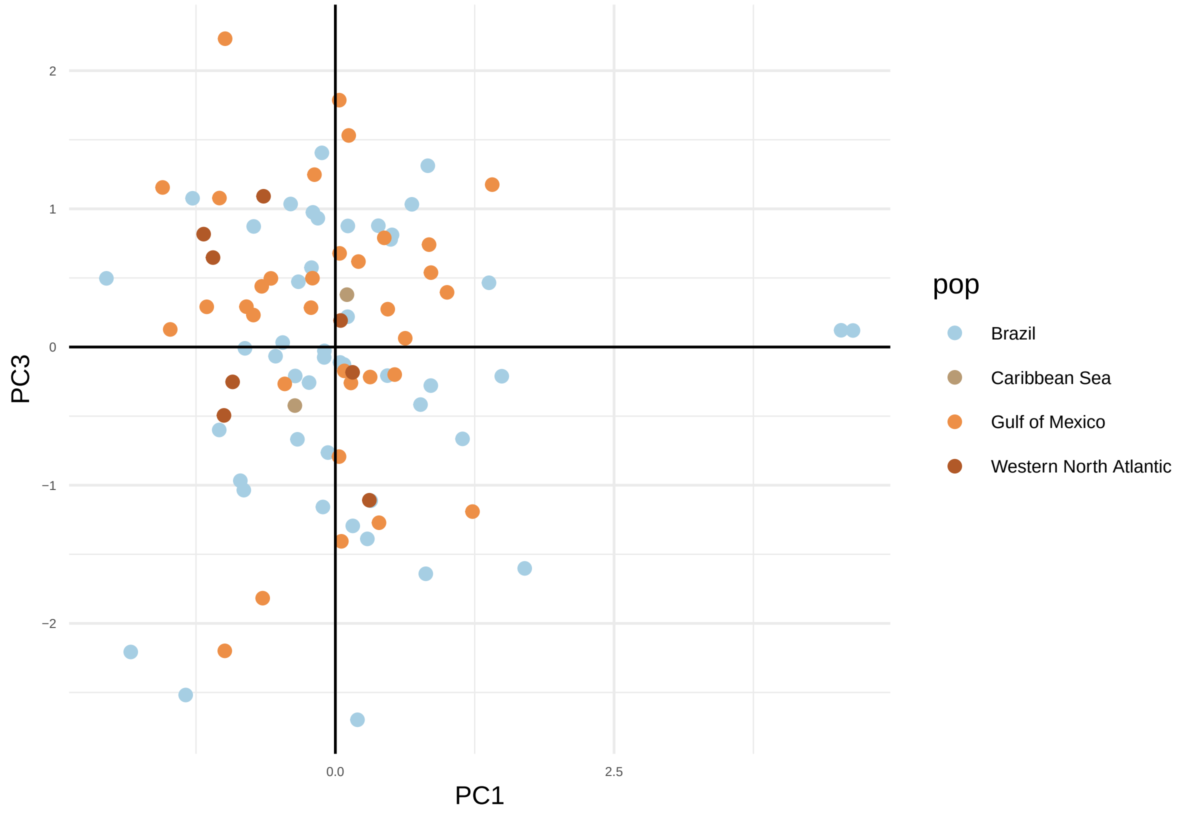
```r
pca1 <- adegenet::glPca(BS.dartcap.WATL.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_WATL_PCA.Rdata")
```

```r
load("DArTcap_WATL_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.WATL.gl)
cols <- adegenet::funky(nPop(BS.dartcap.WATL.gl))


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

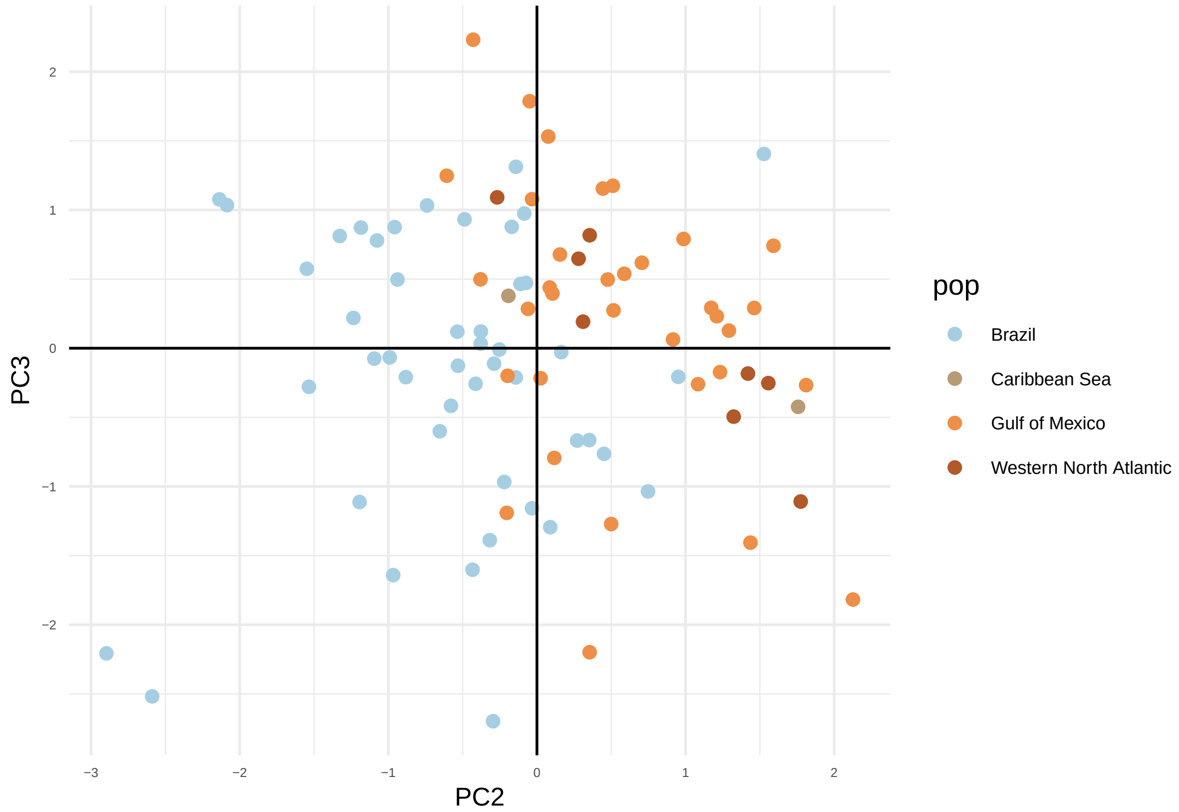


```r
ggplot2::ggsave(p, filename = "DArTcap_WATL_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
```

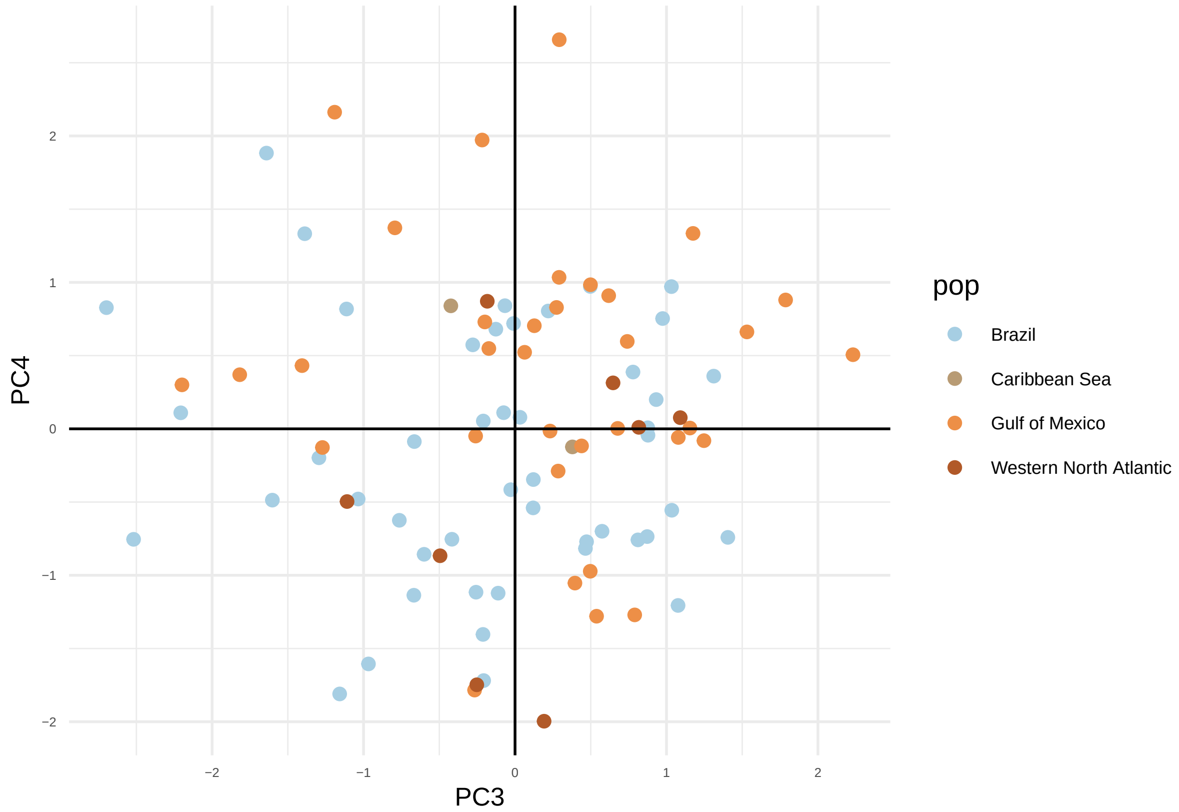
```
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



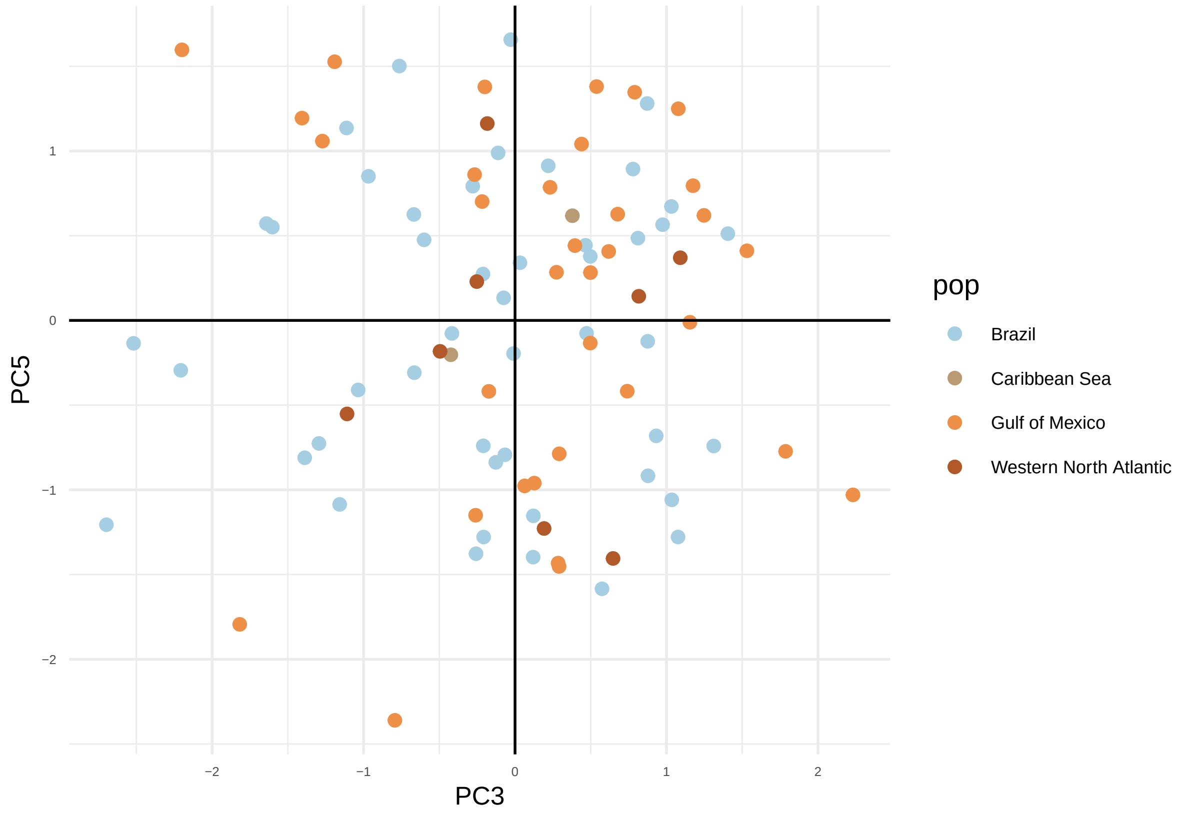
```
ggplot2::ggsave(p, filename = "DArTcap_WATL_PCA2.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_WATL_PCA3.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_WATL_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_WATL_PCA5.png", width = 30,
                height = 15,units = "cm")
```

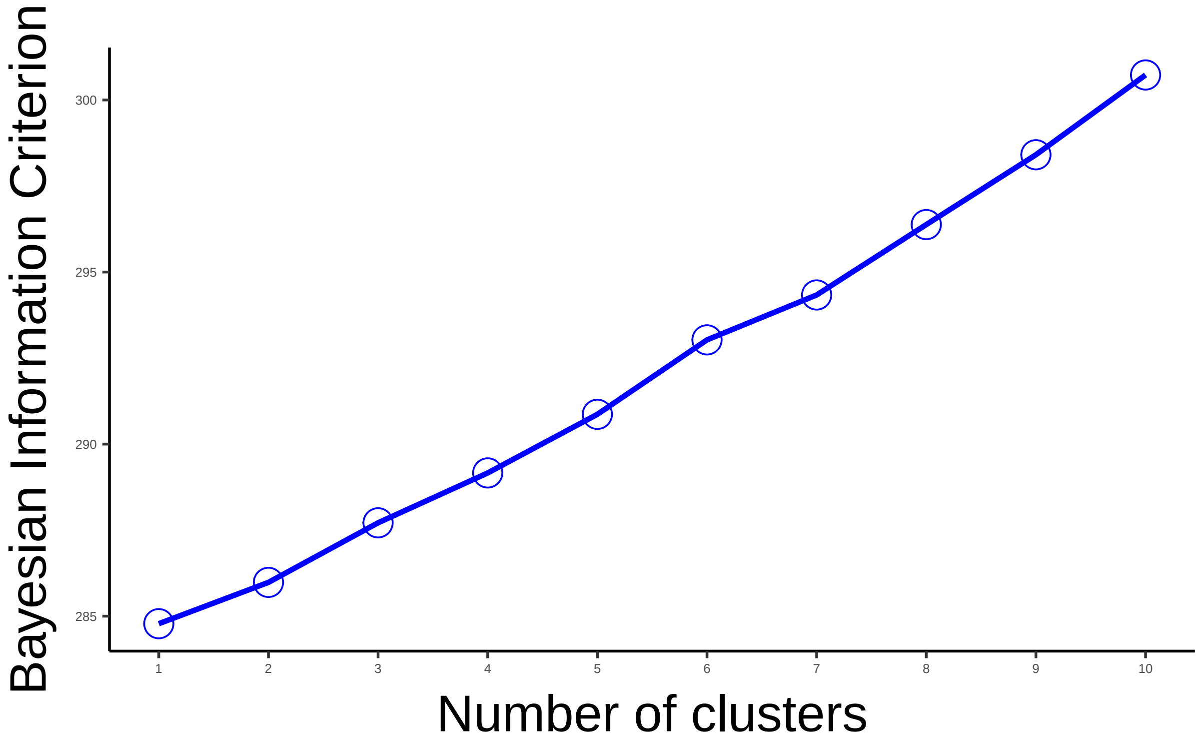
10.9 DAPC

10.9.1 Optimal number of clusters with neutral markers

```
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartcap.WATL.gl,
    max.n.clust = 10,
    n.pca = adegenet::nInd(BS.dartcap.WATL.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTcap_WATL_grp.Rdata")
```

```
load("DArTcap_WATL_grp.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:10
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartcap.WATL.gl) - 1,
```

```
                                              by = 1)) +
  ggplot2::labs(subtitle = "",
                y = "Bayesian Information Criterion",
                x = "Number of clusters",
                title = "",
                caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_WATL_grp.png", width = 30,
                height = 15,units = "cm")
```

10.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartcap.WATL.gl

xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 10),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
  scale = FALSE,
```

```
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTcap_WATL_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTcap_WATL_xval.rdata")
```

```
load("DArTcap_WATL_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

```
## $`Median and Confidence Interval for Random Chance`
##      2.5%       50%     97.5% 
## 0.1799124 0.2468515 0.3532883 
## 
## $`Mean Successful Assignment by Number of PCs of PCA`
##         6         7         8         9        10        11        12        13 
## 0.4011797 0.3993416 0.3917924 0.3895222 0.3781002 0.3818176 0.3772300 0.3763163 
##        14        15        16        17        18        19        20        21 
## 0.3724941 0.3787820 0.3765043 0.3744480 0.3960404 0.3886894 0.4241026 0.4147128 
##        22        23        24        25        26        27        28        29 
## 0.4074313 0.4047105 0.3907887 0.3772498 0.3712890 0.3764682 0.3709447 0.3634170 
##        30        31        32        33        34        35        36 
## 0.3573215 0.3559965 0.3442917 0.3289377 0.3282196 0.3141950 0.3014086 
## 
## $`Number of PCs Achieving Highest Mean Success`
## [1] "20"
## 
## $`Root Mean Squared Error by Number of PCs of PCA`
##         6         7         8         9        10        11        12        13 
## 0.6005609 0.6023505 0.6100747 0.6124445 0.6237366 0.6201820 0.6245583 0.6256715 
##        14        15        16        17        18        19        20        21 
## 0.6291852 0.6230769 0.6254401 0.6279443 0.6068985 0.6146509 0.5811306 0.5905123 
##        22        23        24        25        26        27        28        29 
## 0.5966892 0.5991244 0.6128676 0.6264447 0.6323786 0.6272664 0.6330625 0.6403656 
##        30        31        32        33        34        35        36 
## 0.6464854 0.6481012 0.6597074 0.6747974 0.6761027 0.6901762 0.7027381 
## 
## $`Number of PCs Achieving Lowest MSE`
## [1] "20"
```

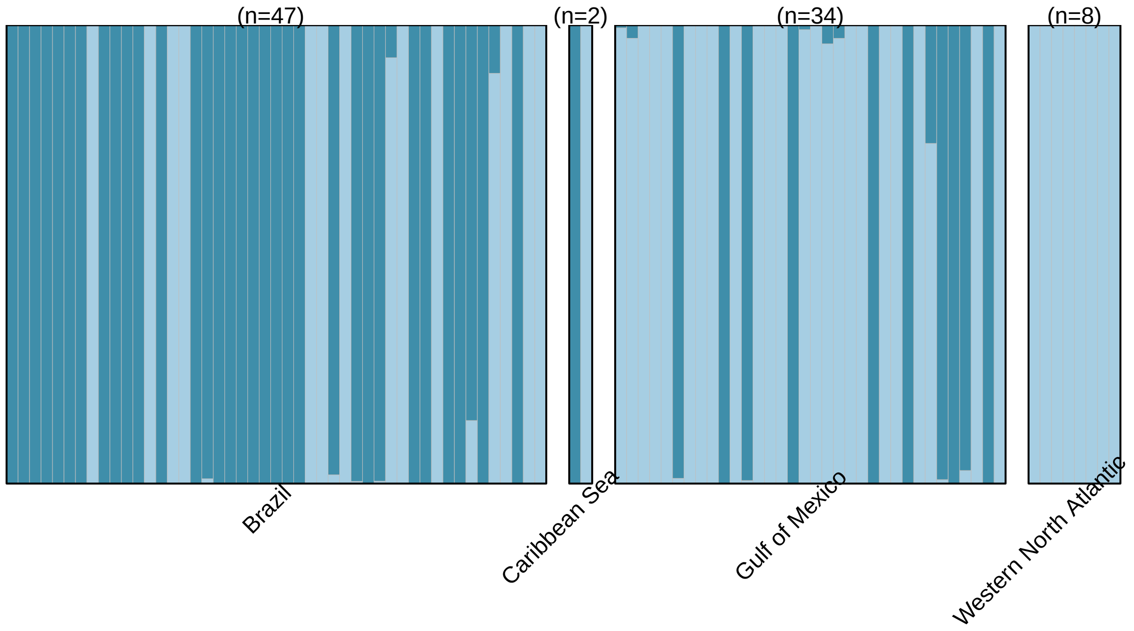
```r
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartcap.WATL.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartcap.WATL.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                                     paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTcap_WATL_DAPC.Rdata")
```

10.9.3 DAPC barplot

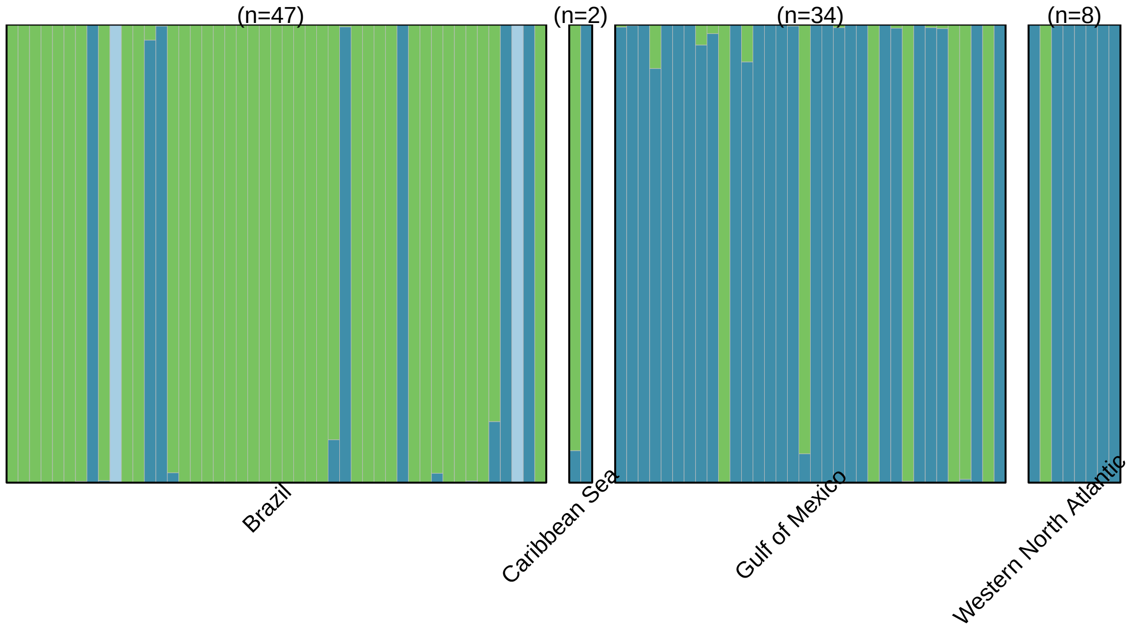
Group individuals according to DAPC posterior membership.

```r
load("DArTcap_WATL_DAPC.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartcap.WATL.gl$pop

  plot.dapc.FDD(x = post,
                locations = locations,
                colour = colour,
                region.lwd = 1,
                plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                   K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTcap_WATL_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```

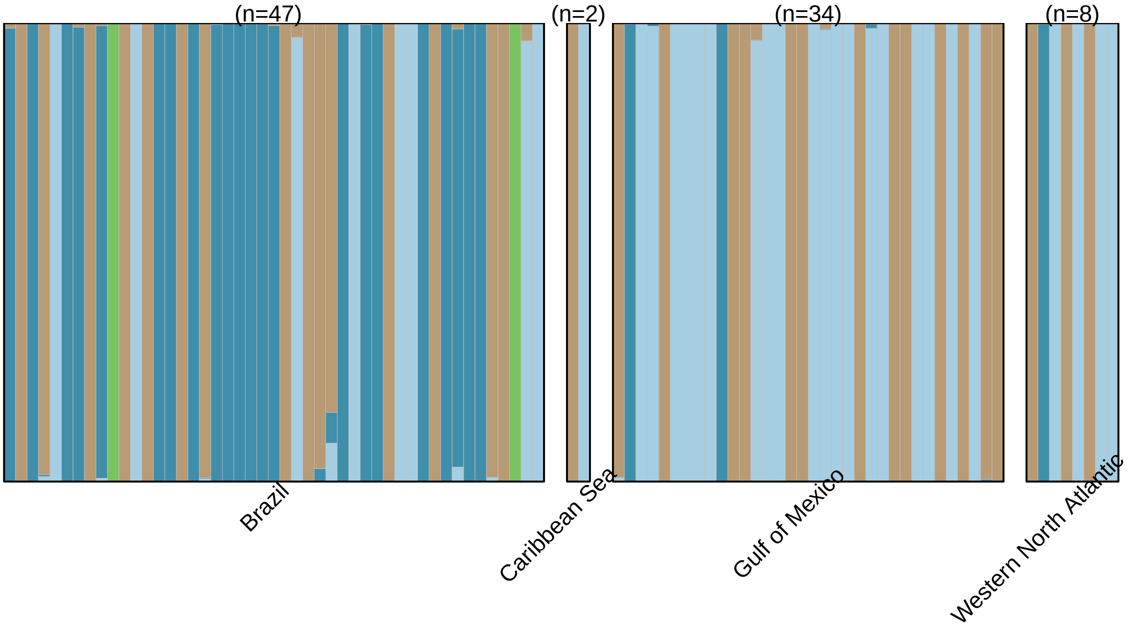
DAPC: all Bull Sharks − subset Australia
for K=2 & PC=20



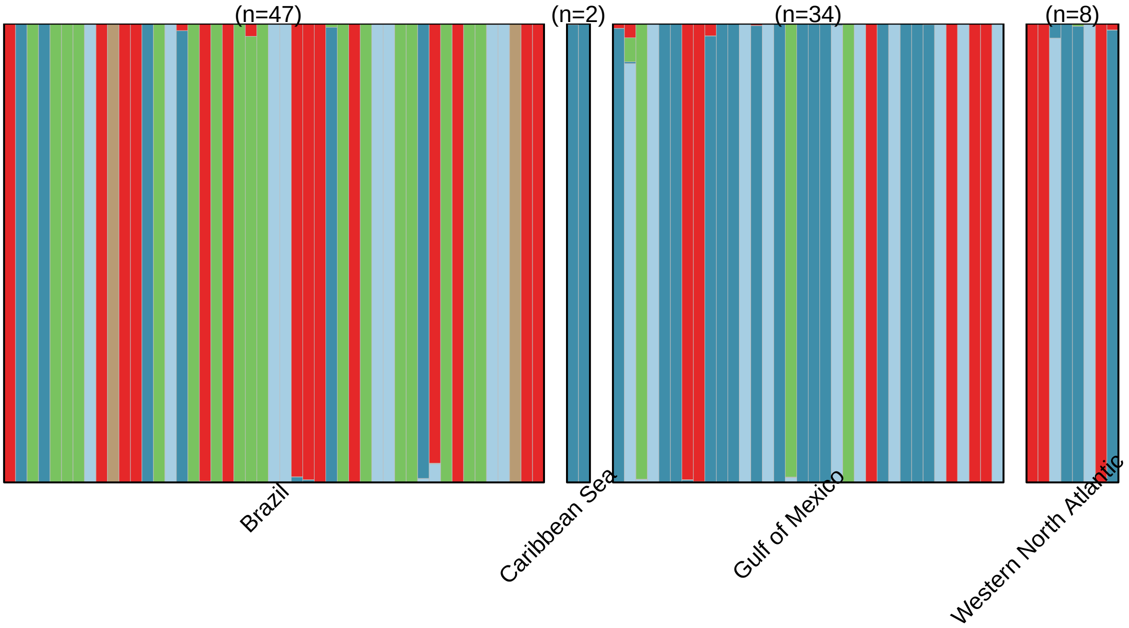
DAPC: all Bull Sharks − subset Australia
for K=3 & PC=20



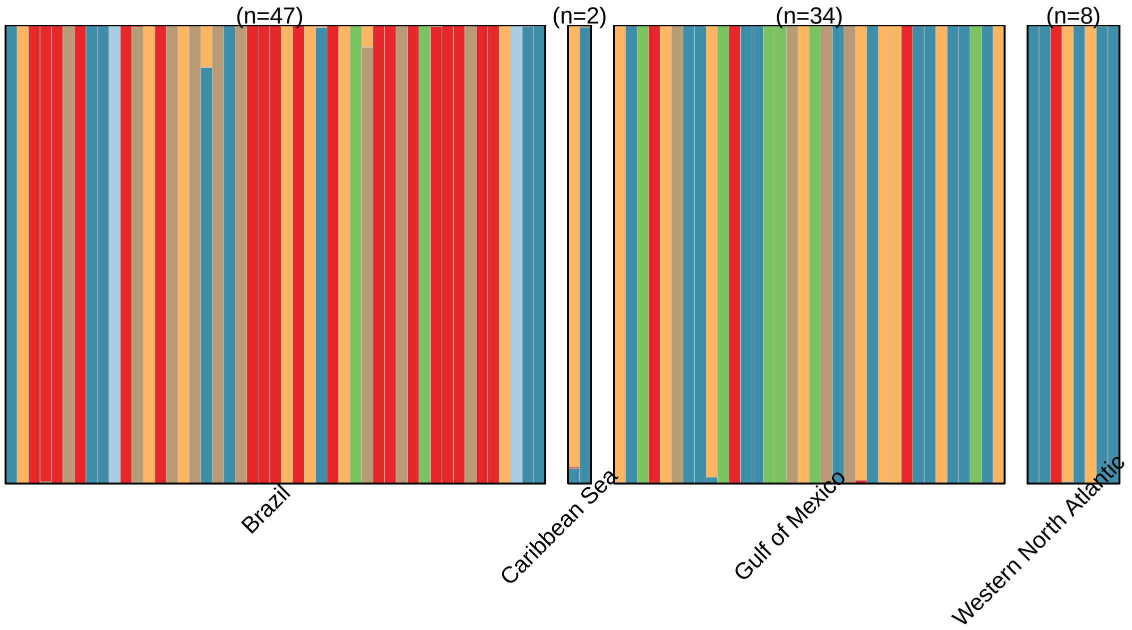
DAPC: all Bull Sharks − subset Australia
for K=4 & PC=20



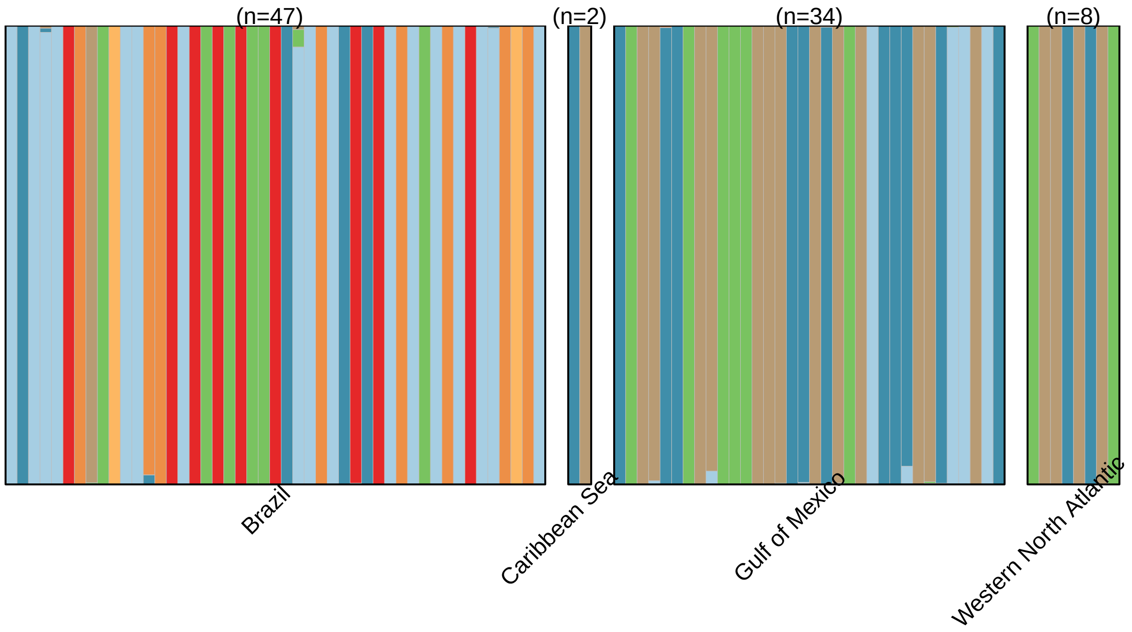
DAPC: all Bull Sharks − subset Australia
for K=5 & PC=20

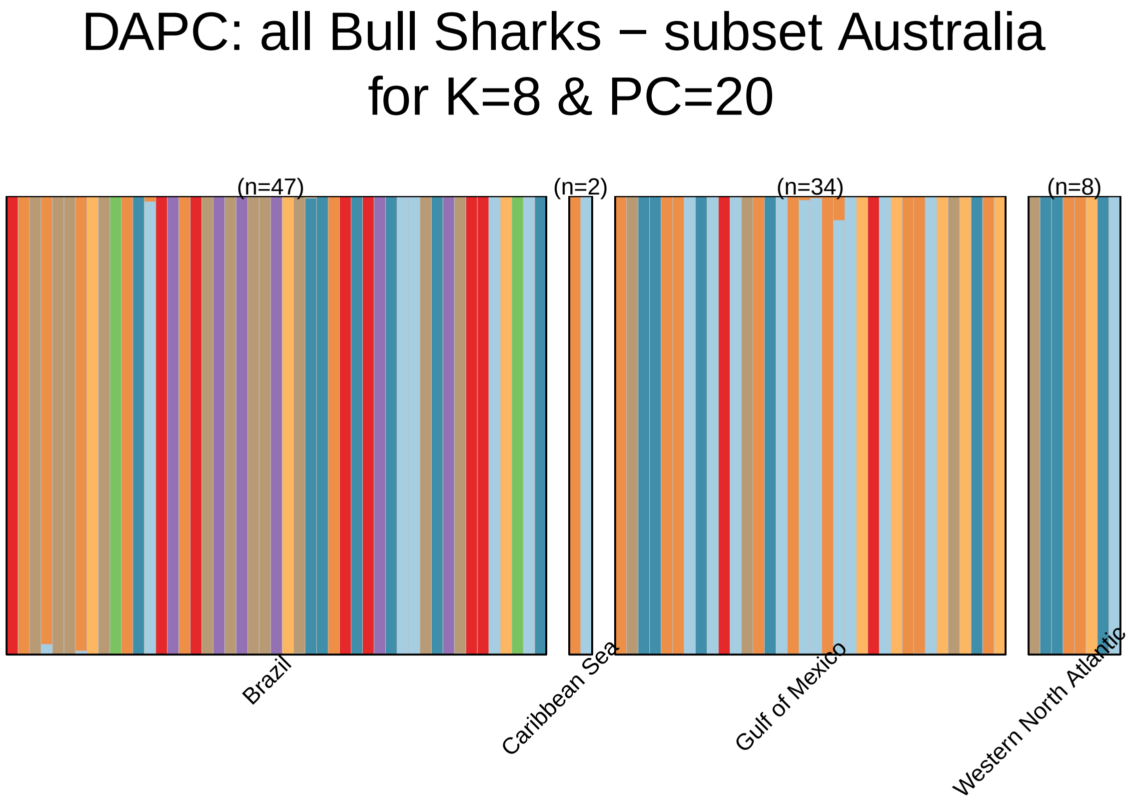


DAPC: all Bull Sharks − subset Australia
for K=6 & PC=20

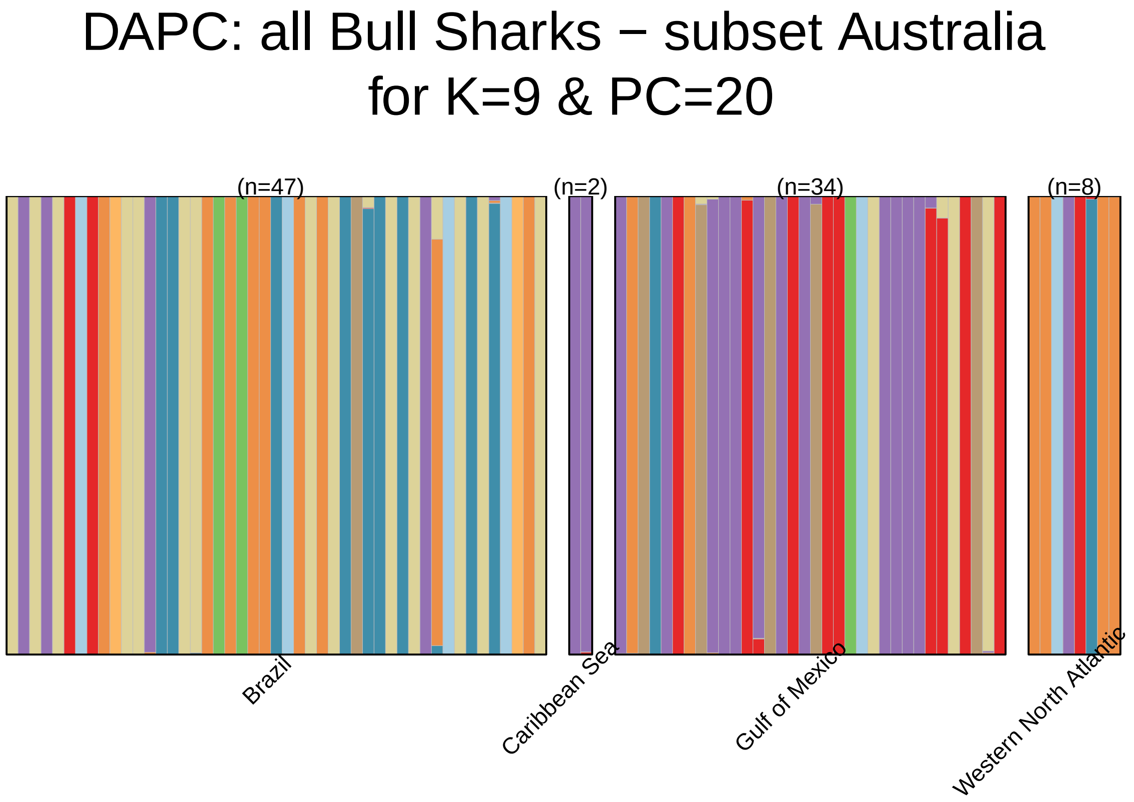


DAPC: all Bull Sharks − subset Australia
for K=7 & PC=20

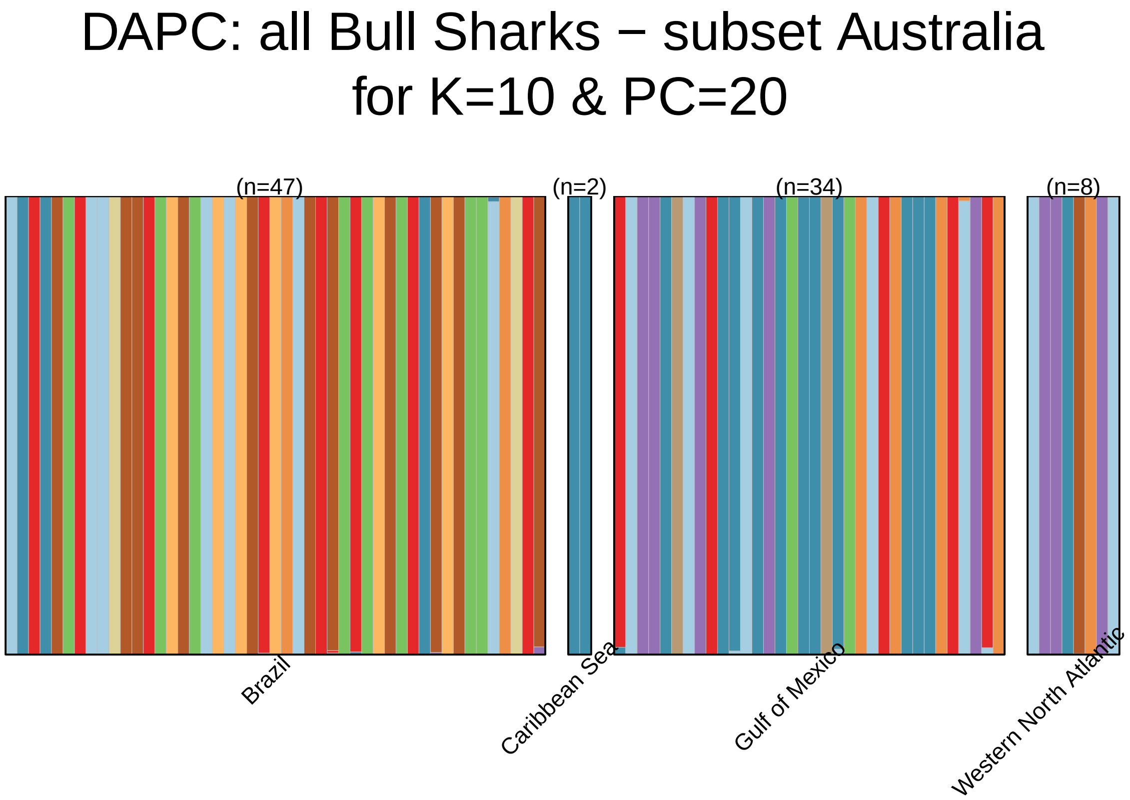




DAPC: all Bull Sharks − subset Australia
for K=8 & PC=20

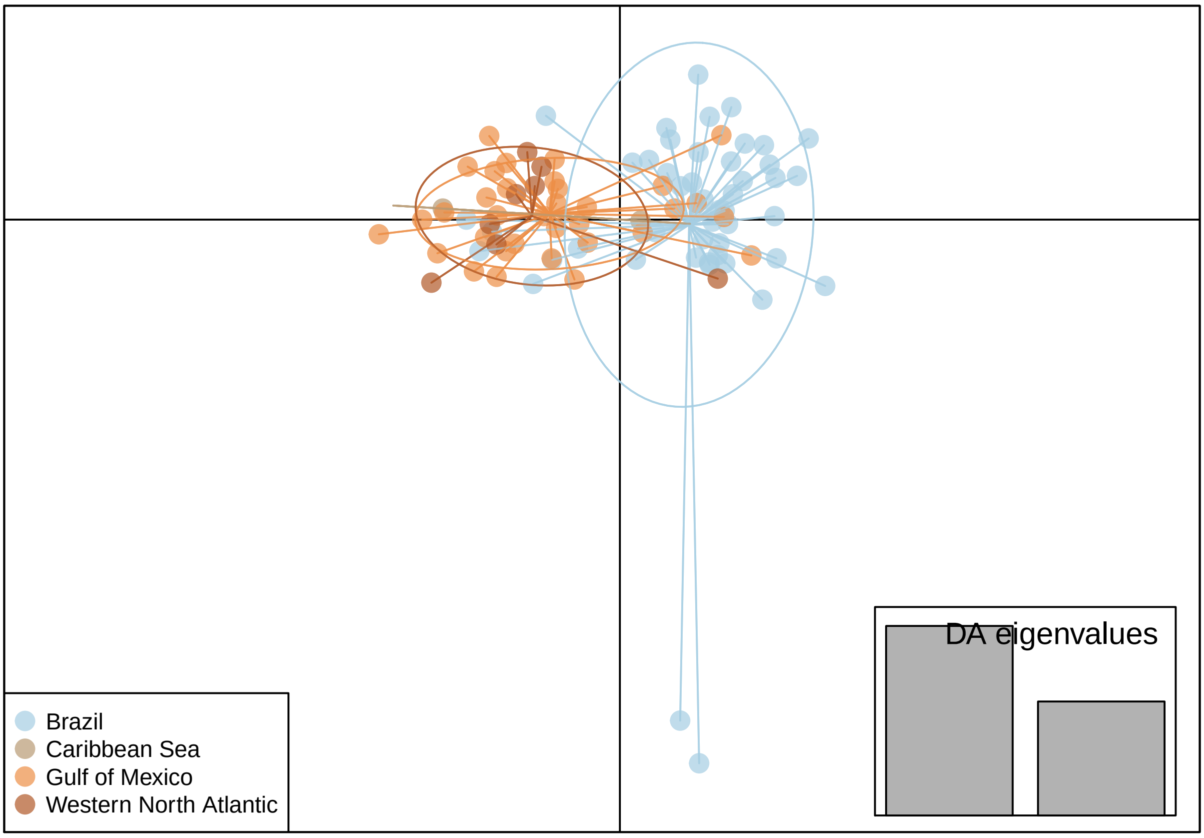


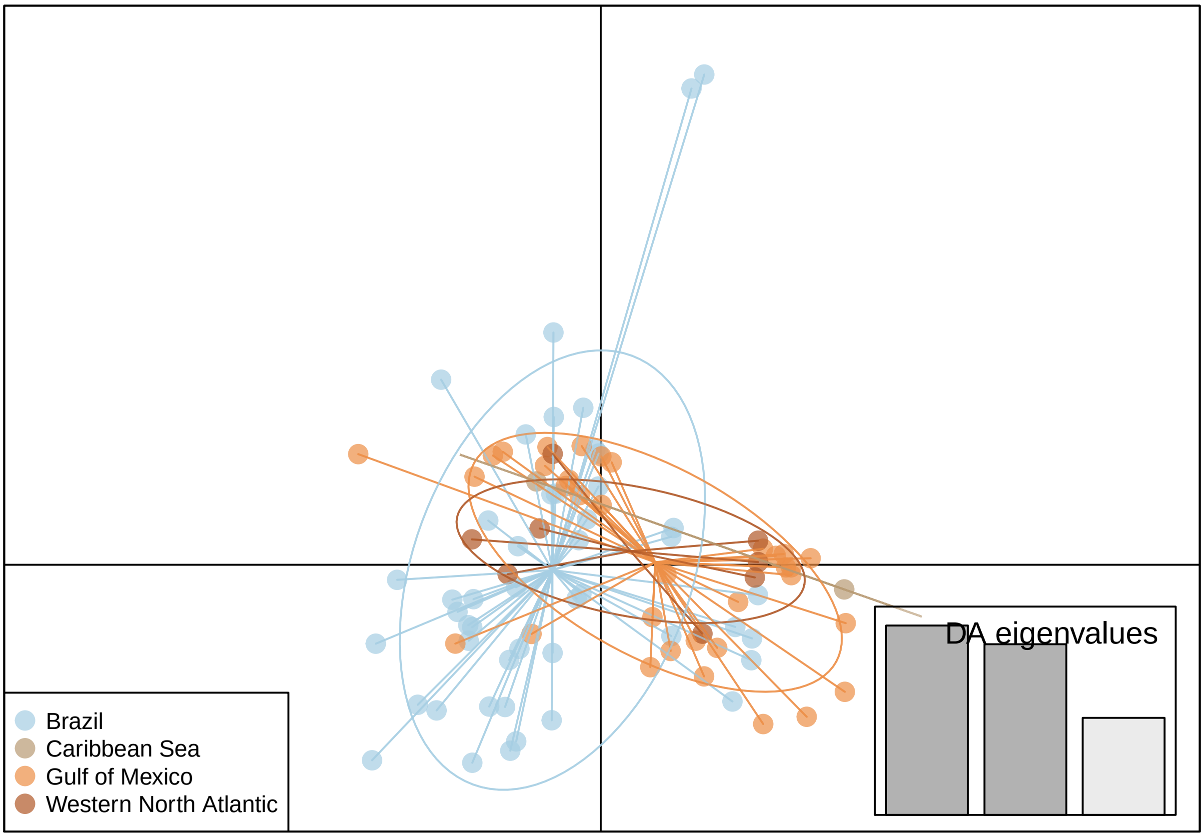
DAPC: all Bull Sharks − subset Australia
for K=9 & PC=20

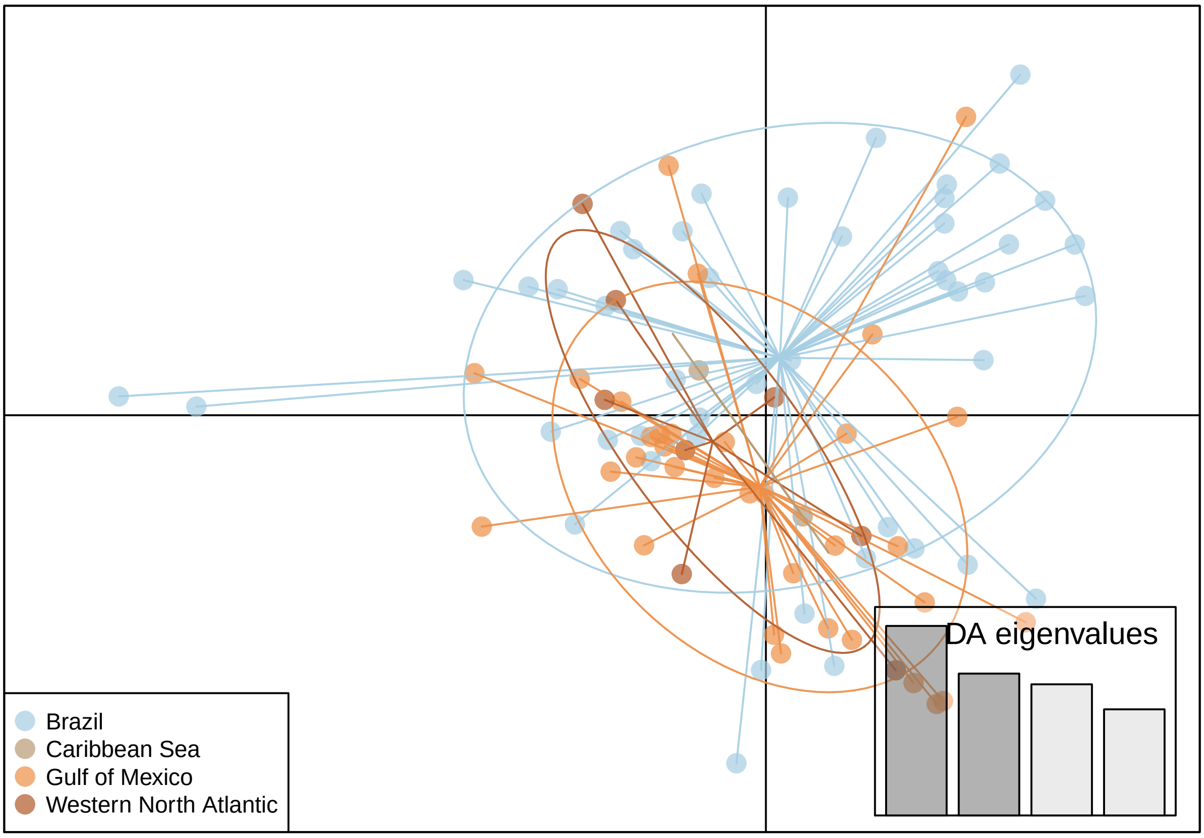


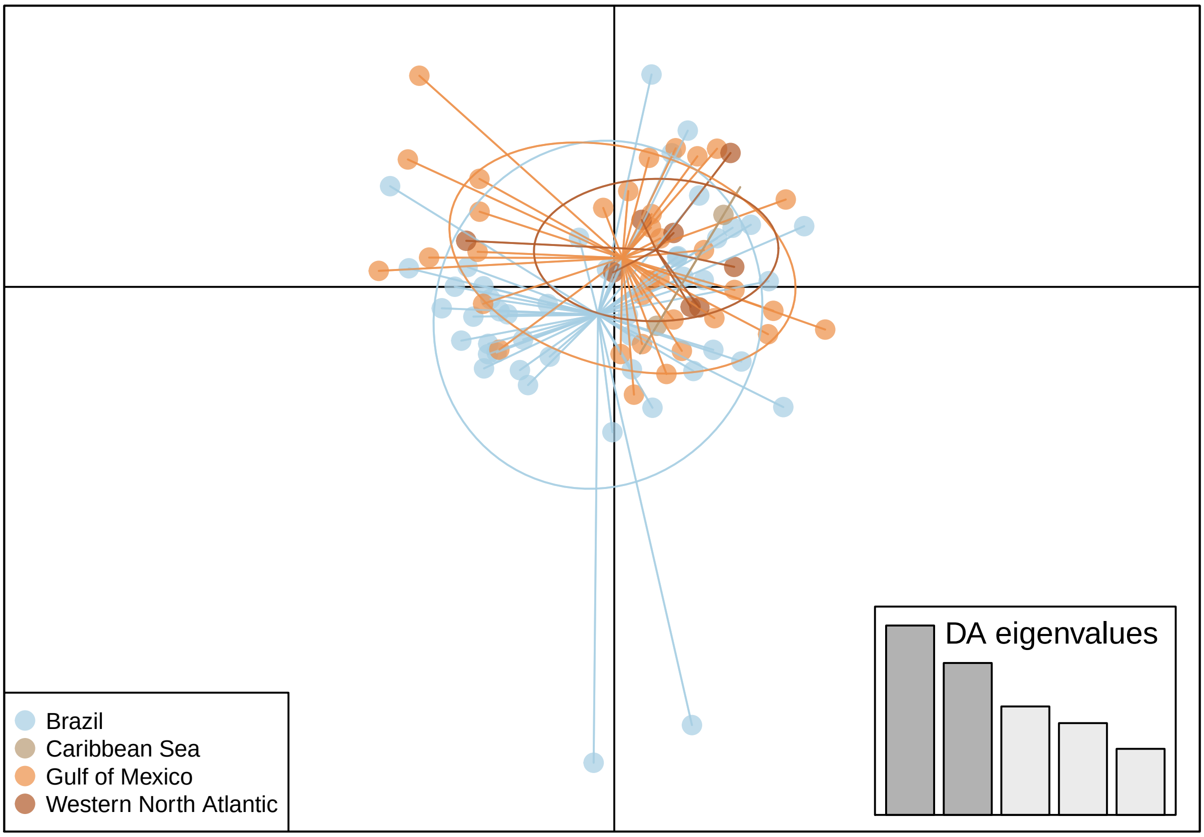
10.9.4 DAPC scatterplot

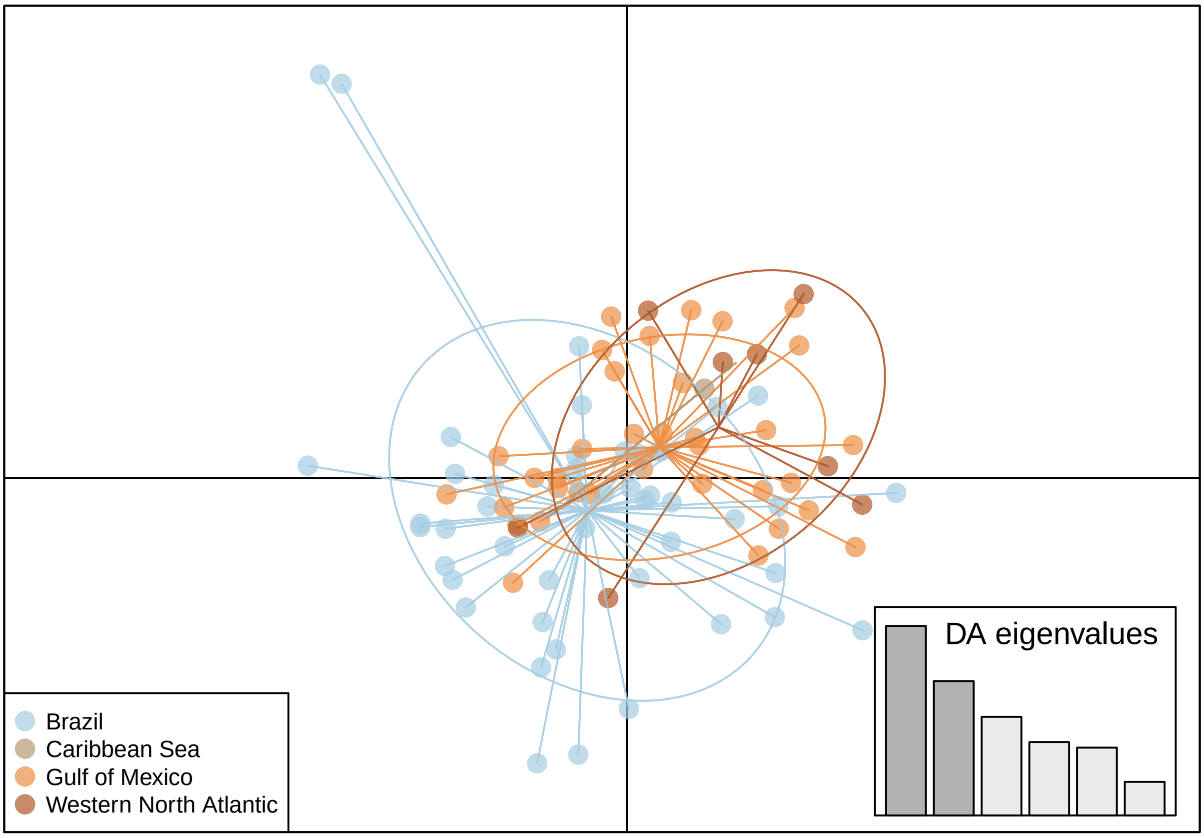
```r
load("DArTcap_WATL_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartcap.WATL.gl), cex = 2,
                             legend = TRUE, col = colours.4,clabel = FALSE,
                             posi.leg = posi.leg, scree.pca = FALSE,
                             posi.pca = "topleft", cleg = 0.75, xax = 1,
                             yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_WATL_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

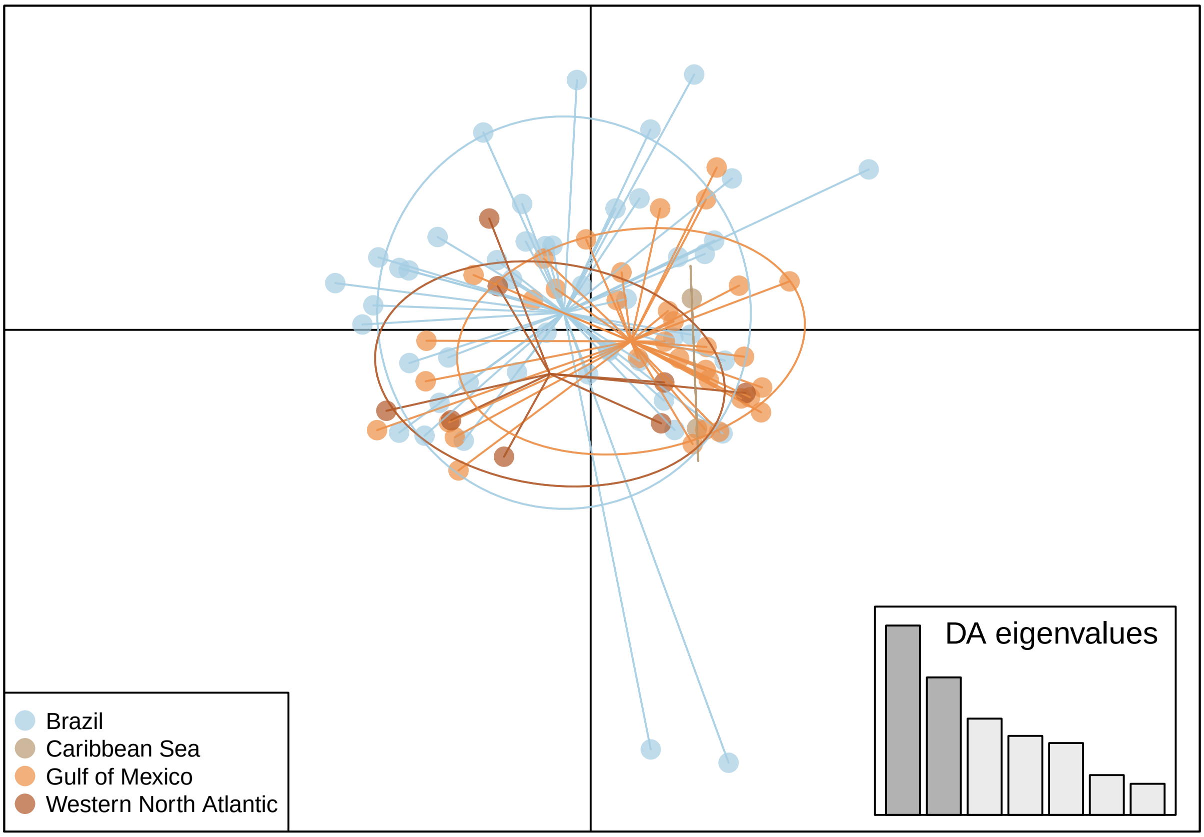

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
DA eigenvalues

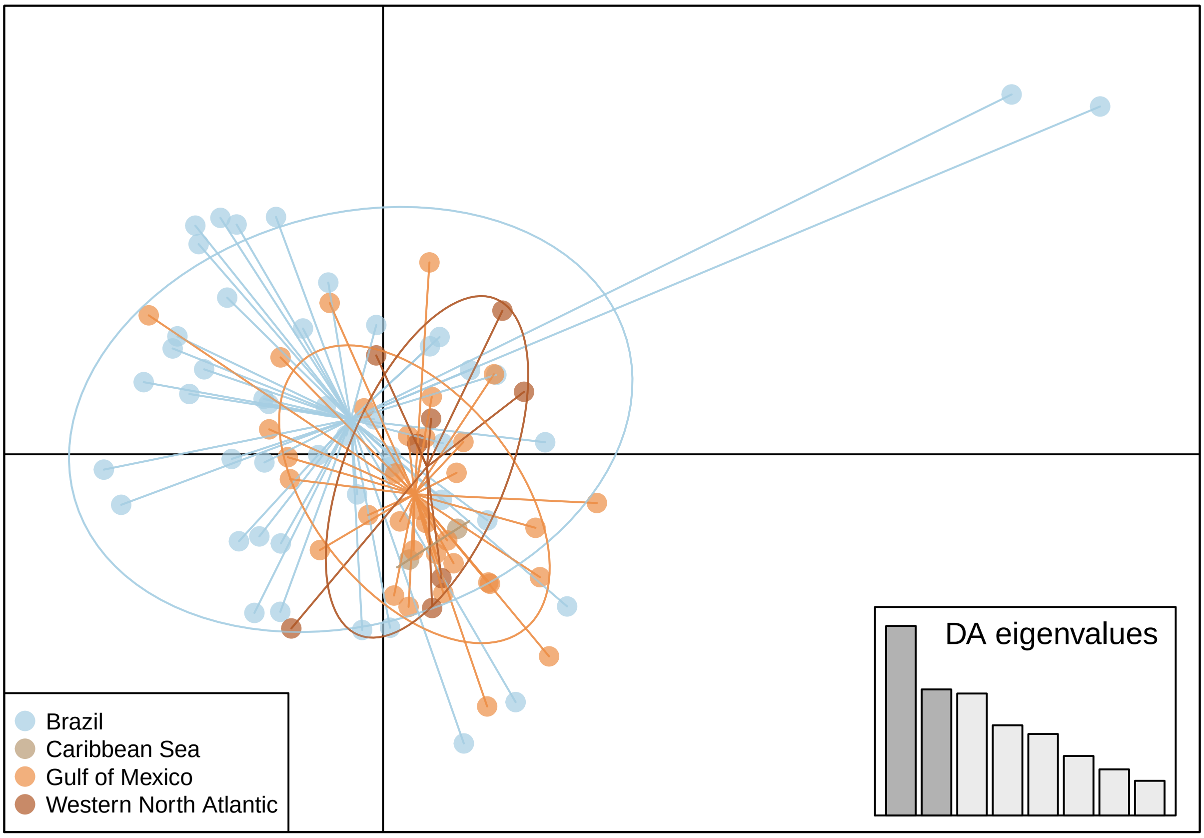

Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic
DA eigenvalues

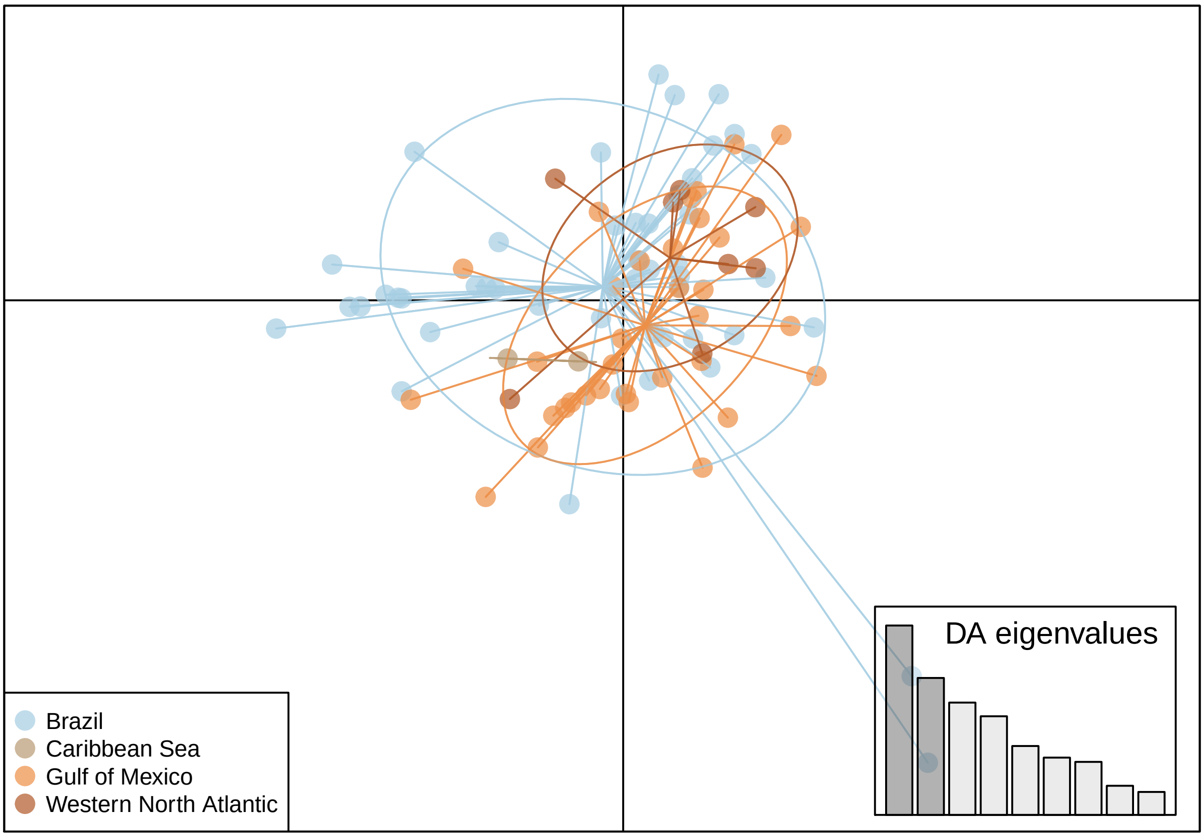

DA eigenvalues
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic


DA eigenvalues
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic


DA eigenvalues
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic

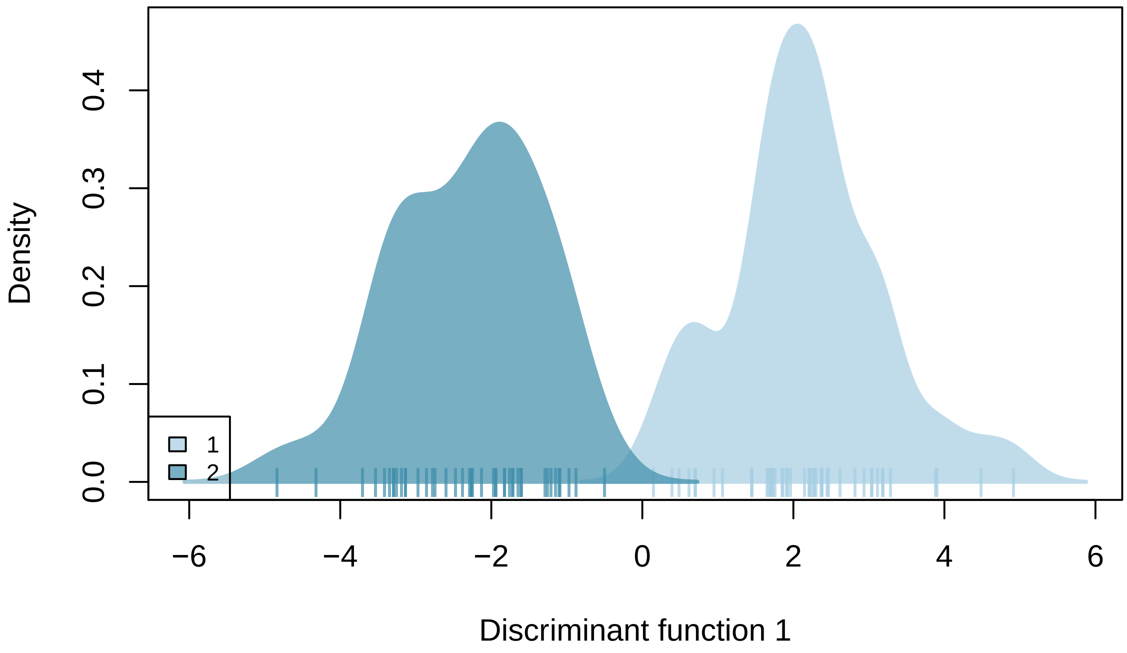

DA eigenvalues
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic

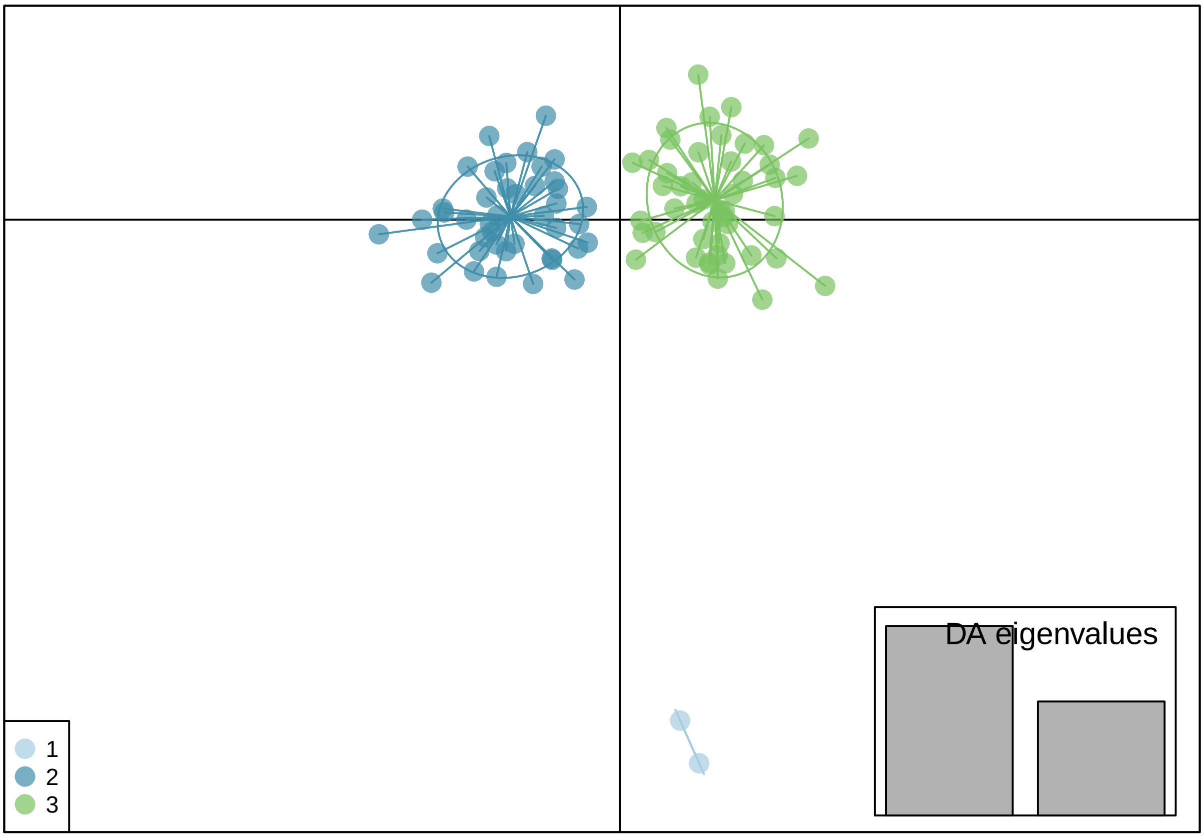


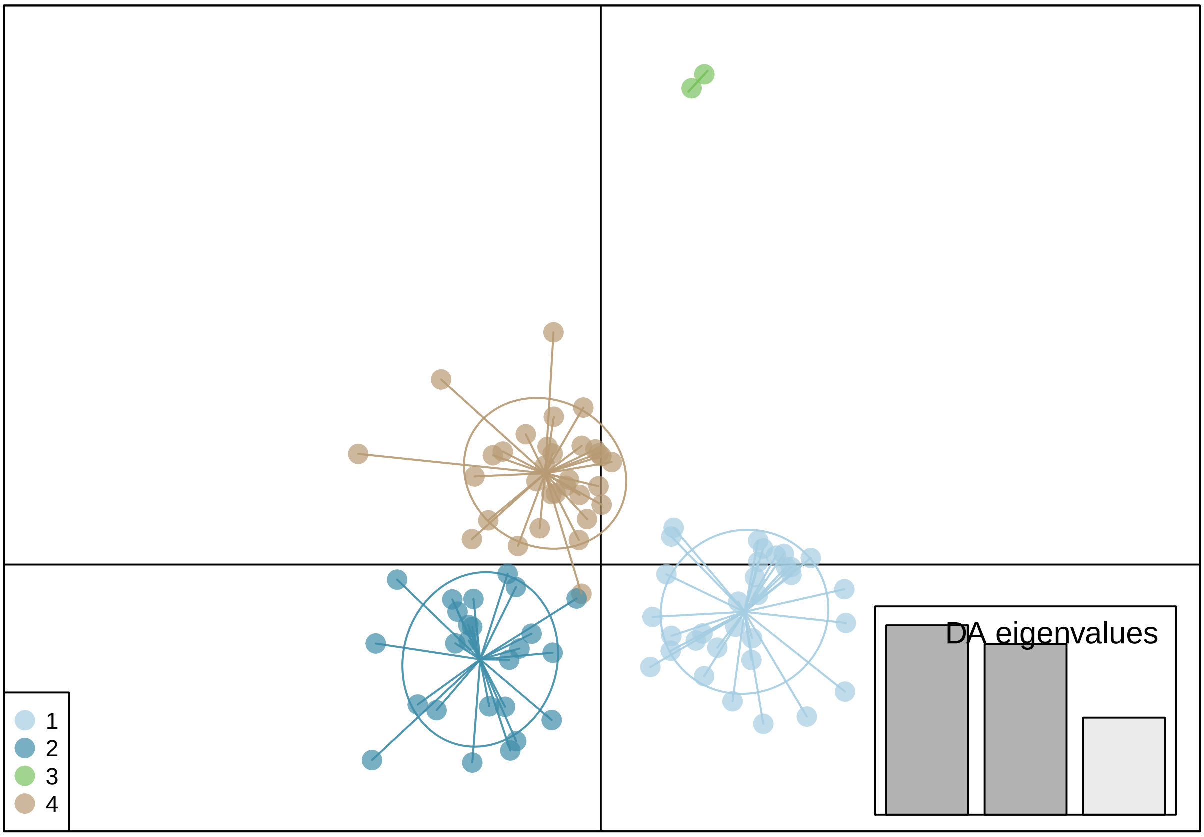


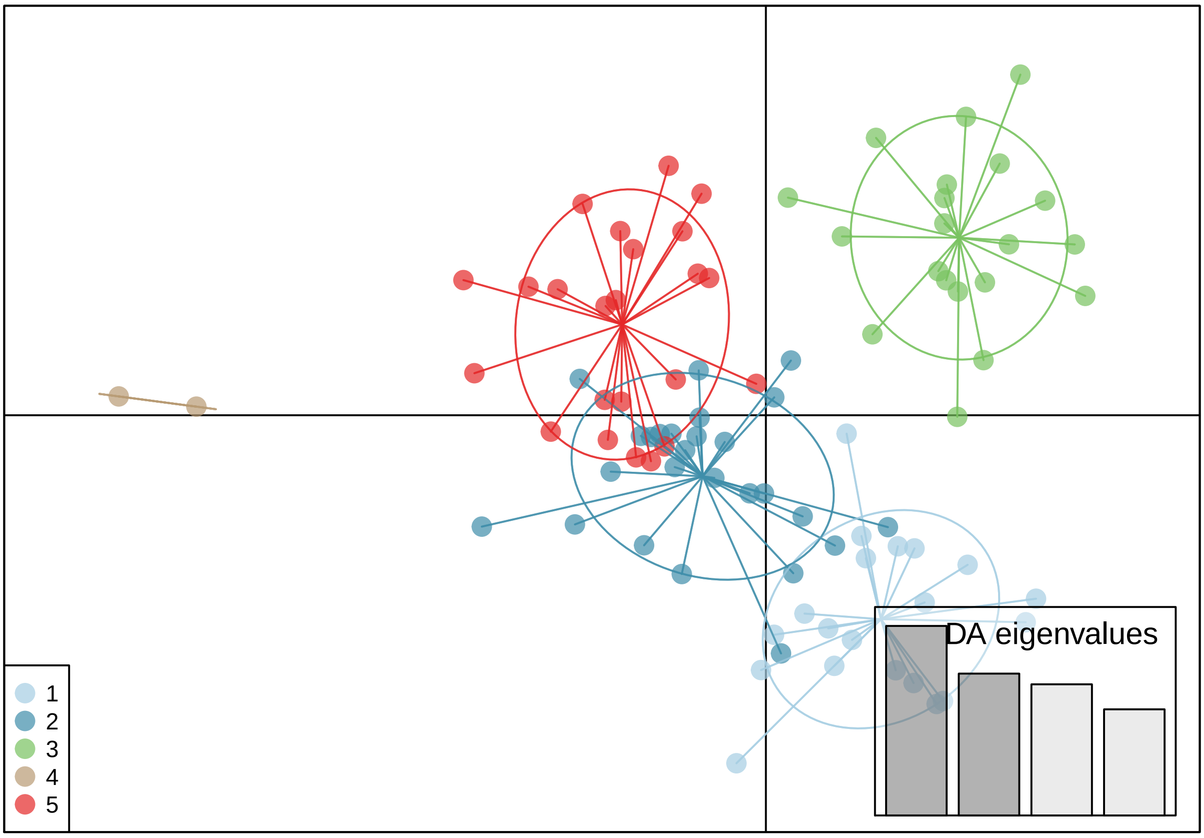
```r
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                             clabel = FALSE, posi.leg = "bottomleft",
```

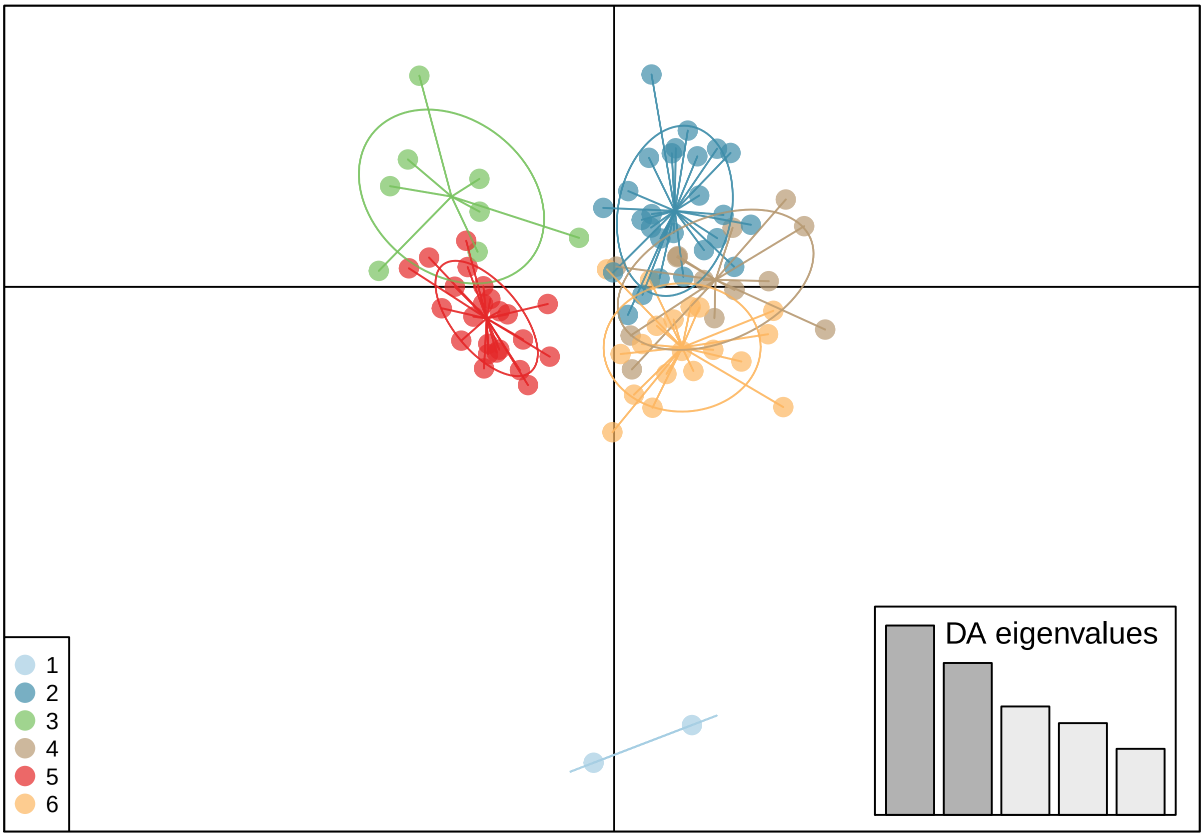
```
                             scree.pca = FALSE,  posi.pca = "topleft",
                             cleg = 0.75, xax = 1, yax = 2,
                             inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_WATL_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

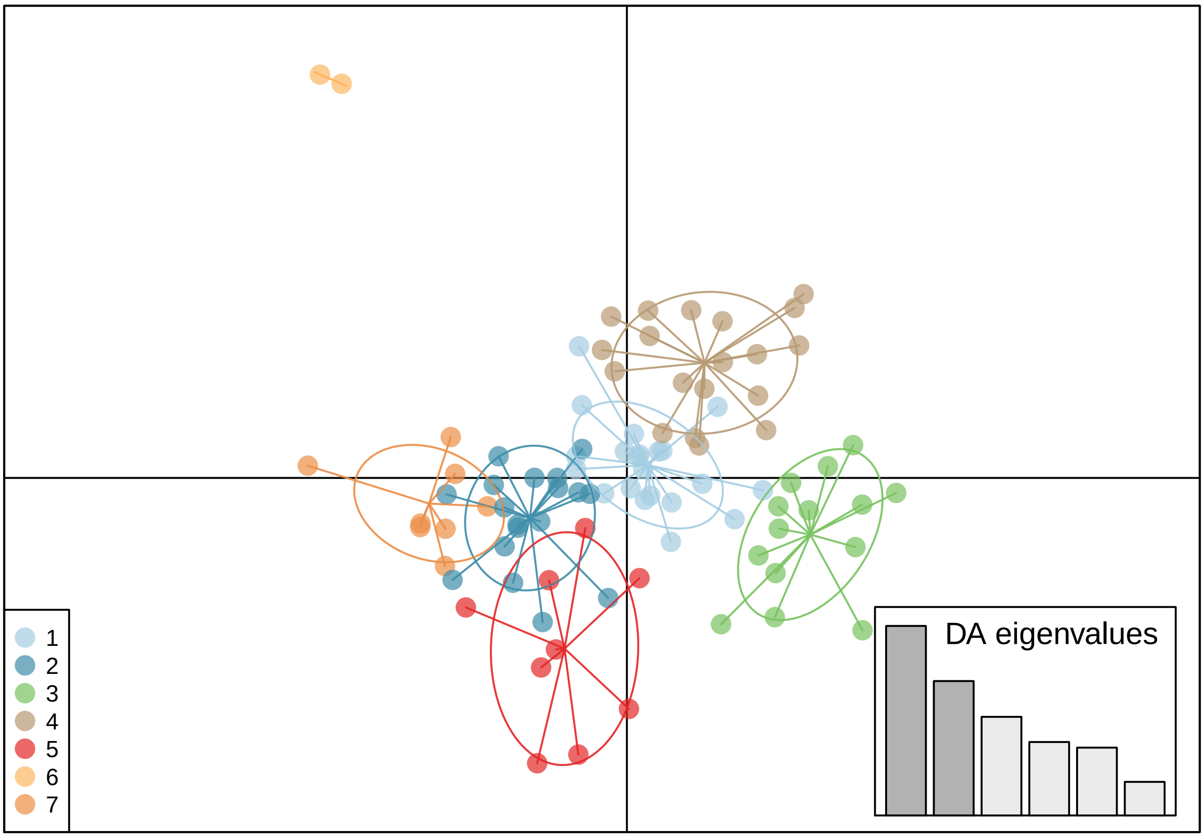


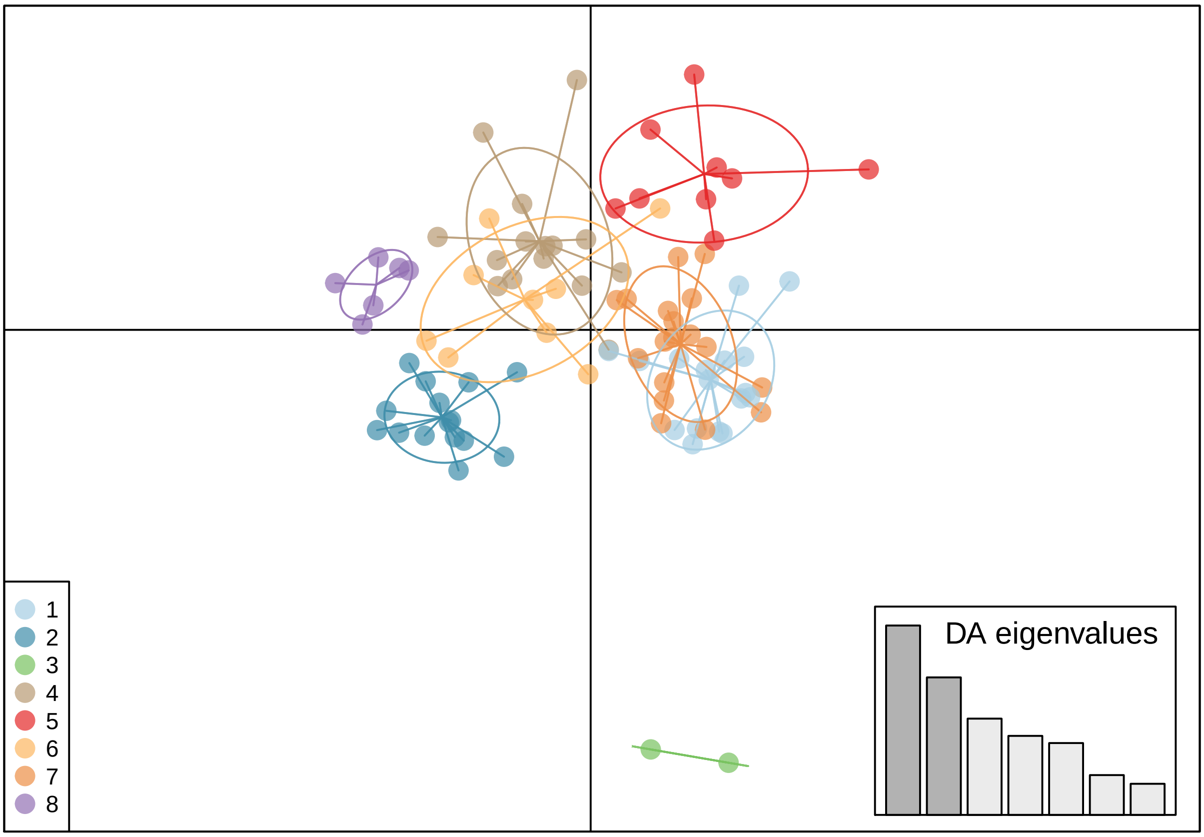

DA eigenvalues
1
2
3

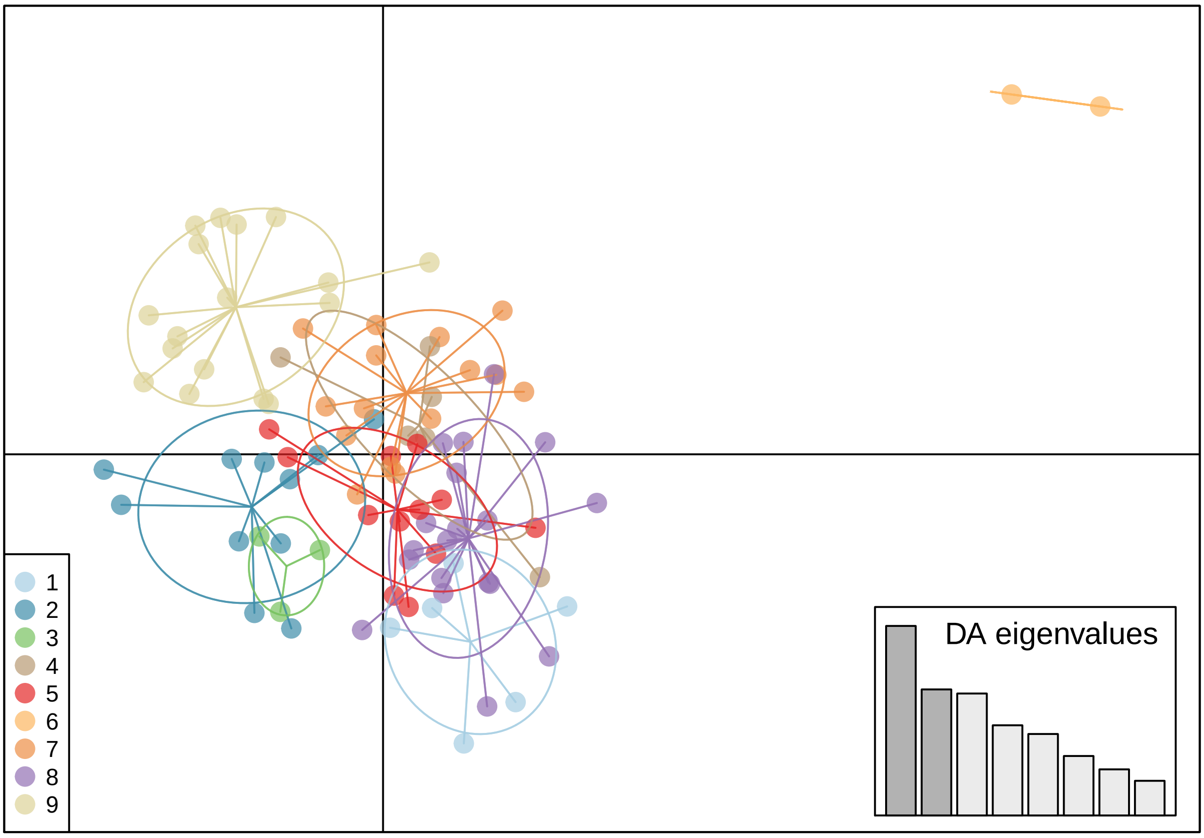

DA eigenvalues
1
2
3
4

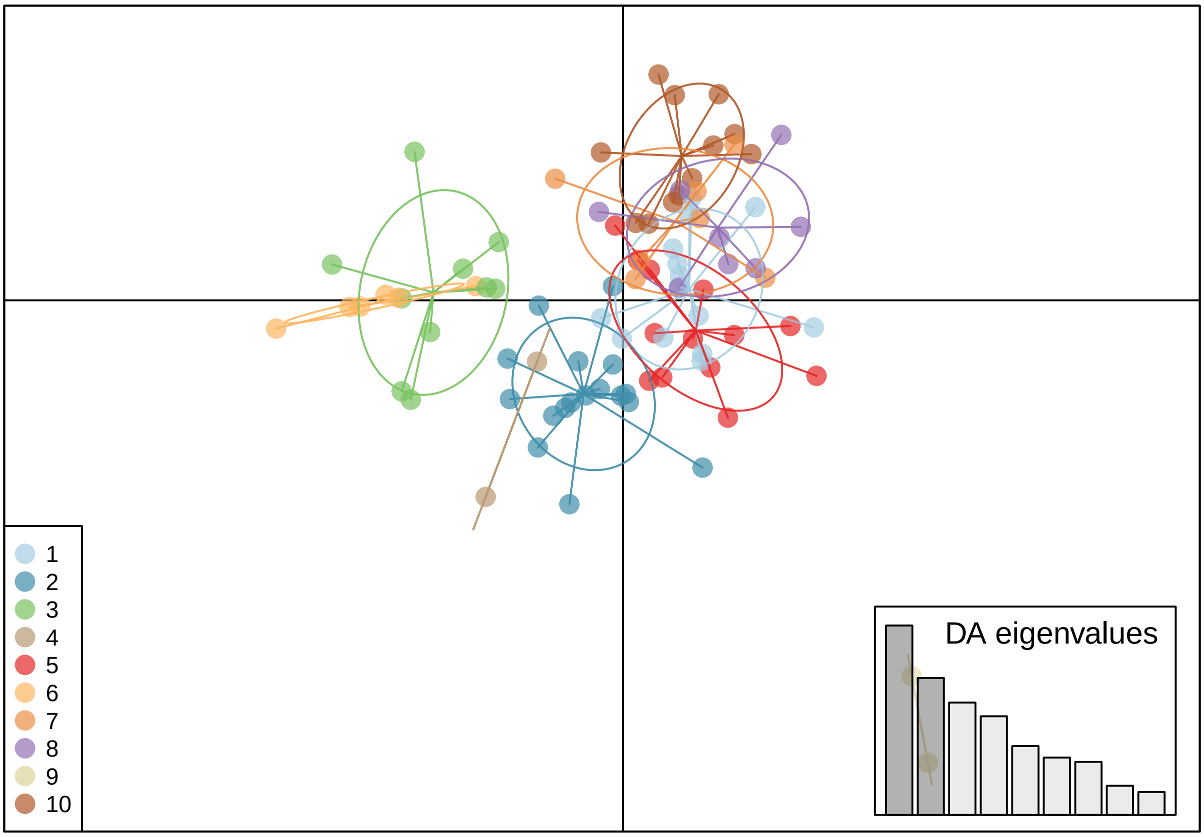

DA eigenvalues
1
2
3
4
5


DA eigenvalues
1
2
3
4
5
6


1
2
3
4
5
6
7
DA eigenvalues


1
2
3
4
5
6
7
8
DA eigenvalues

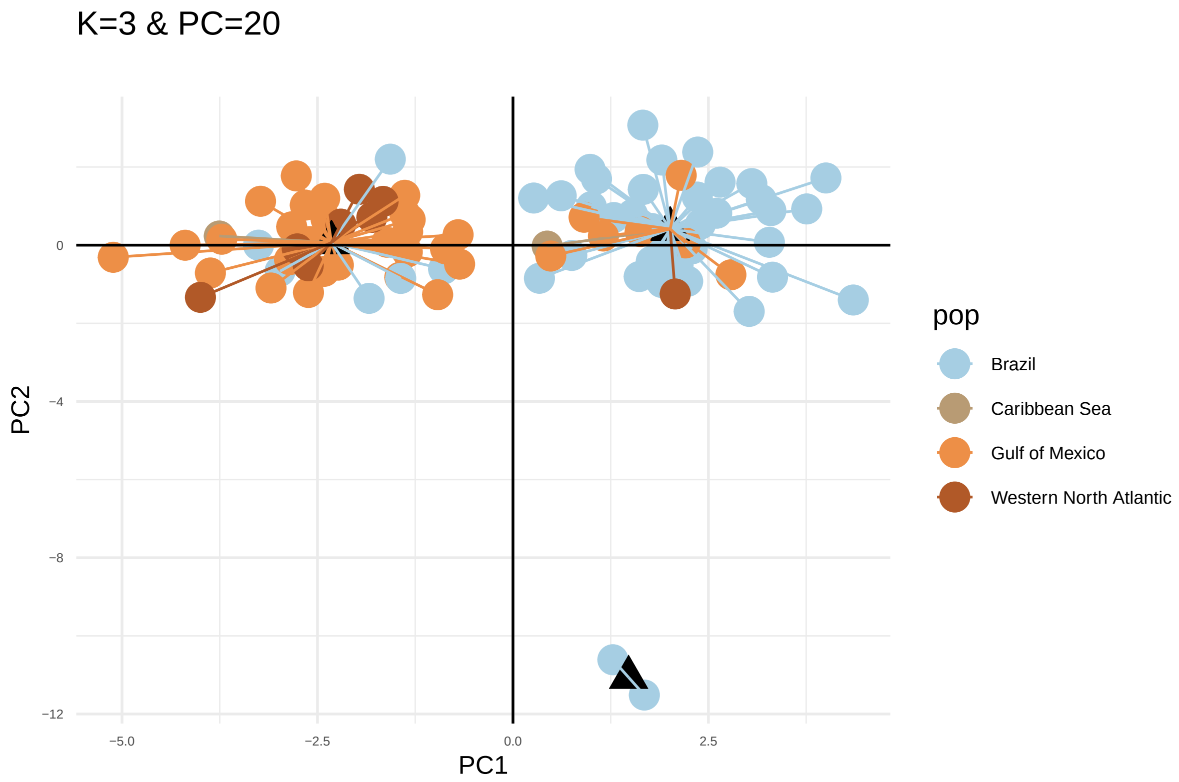


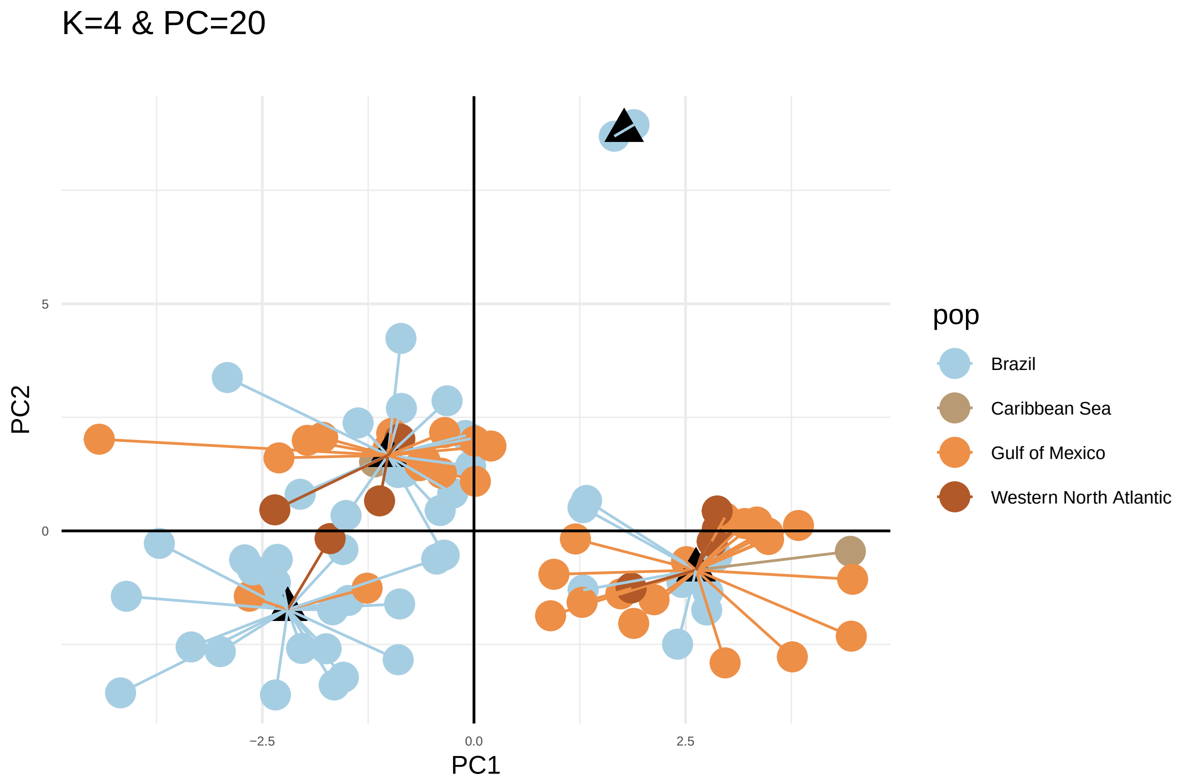


10.9.5 DAPC scatterplot - FLO

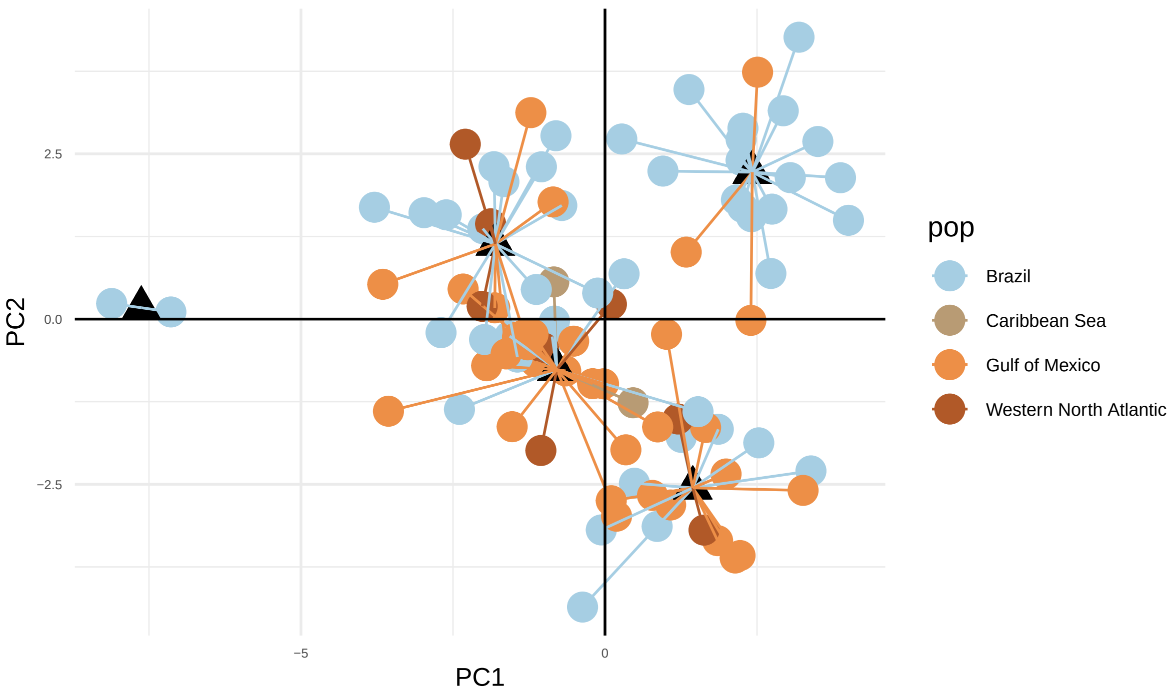
This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

```
for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartcap.WATL.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x,mean.y = y)~group,df,mean),
              by  =  "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x,y = mean.y),size = 5, shape = 17,
                        color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y, xend = x,
                                       yend = y)) +
    ggplot2::scale_colour_manual(values = colours.4) +
    ggplot2::scale_fill_manual(values = colours.4) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
         y = "PC2",
         x = "PC1",
         title = paste0("K=",K," & PC=",PC, sep = ""),
         caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot, filename = paste0("DArTcap_WATL_DAPC_scatterplot2_K",
                                          K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```

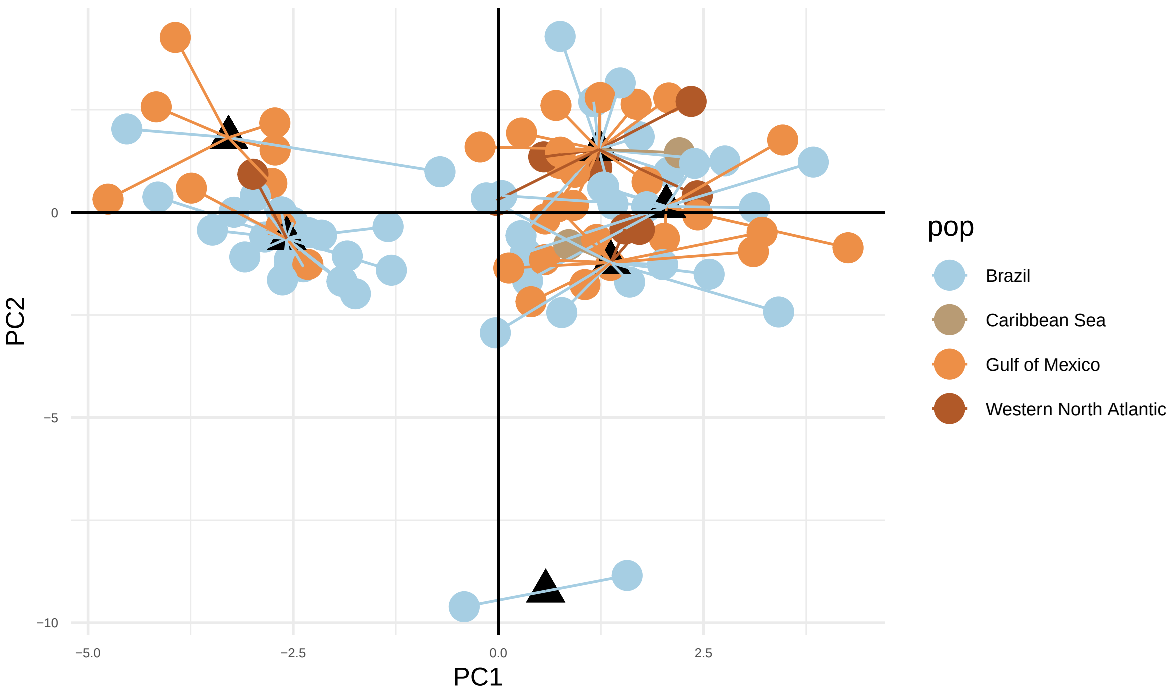

K=3 & PC=20

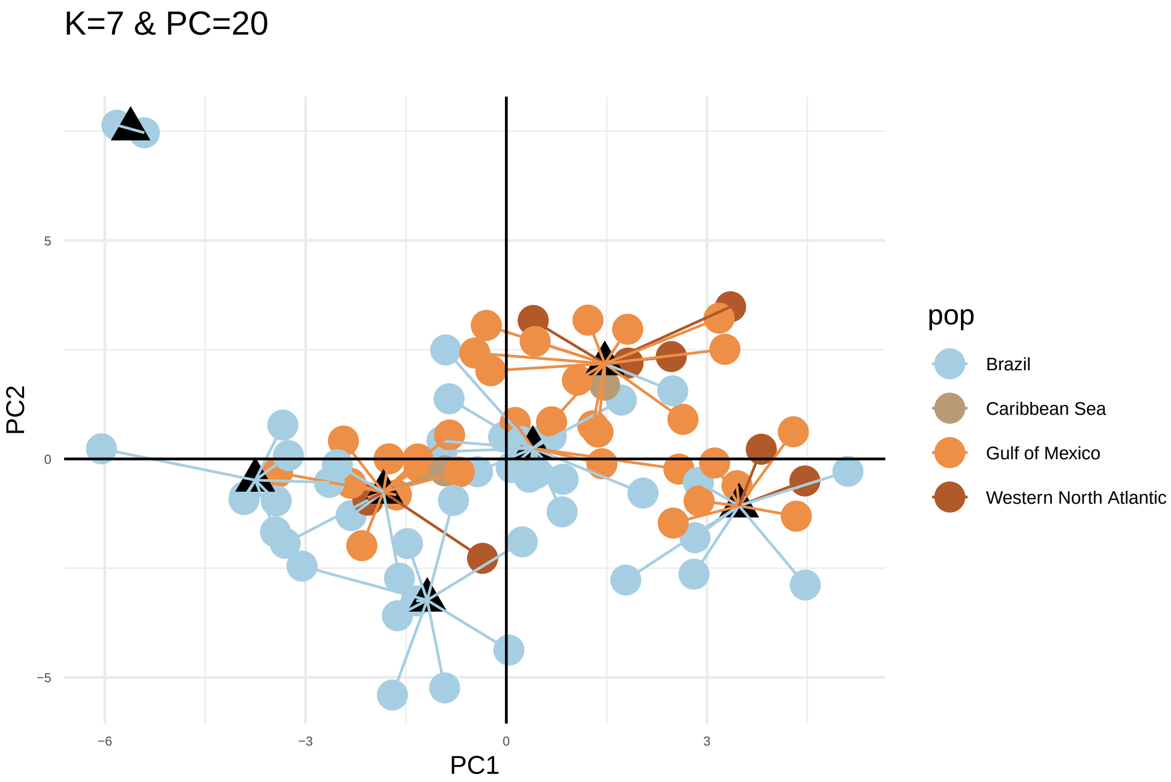

K=4 & PC=20

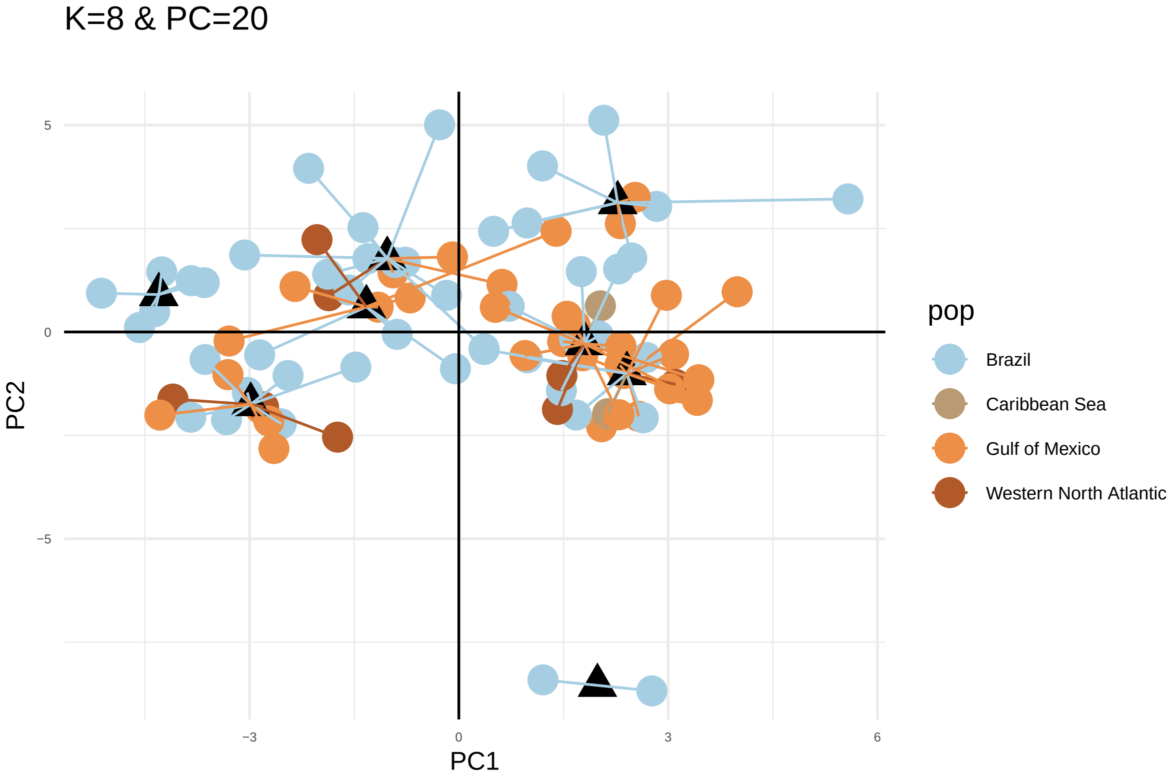
K=5 & PC=20

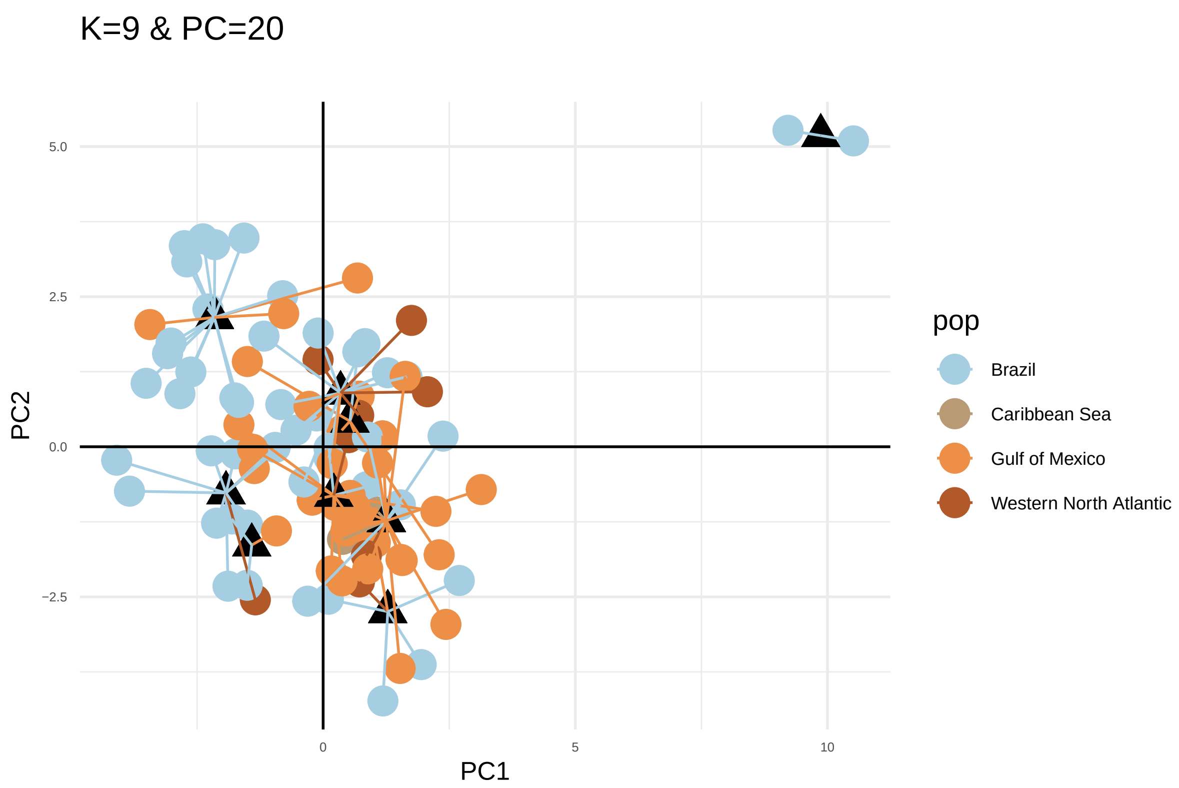


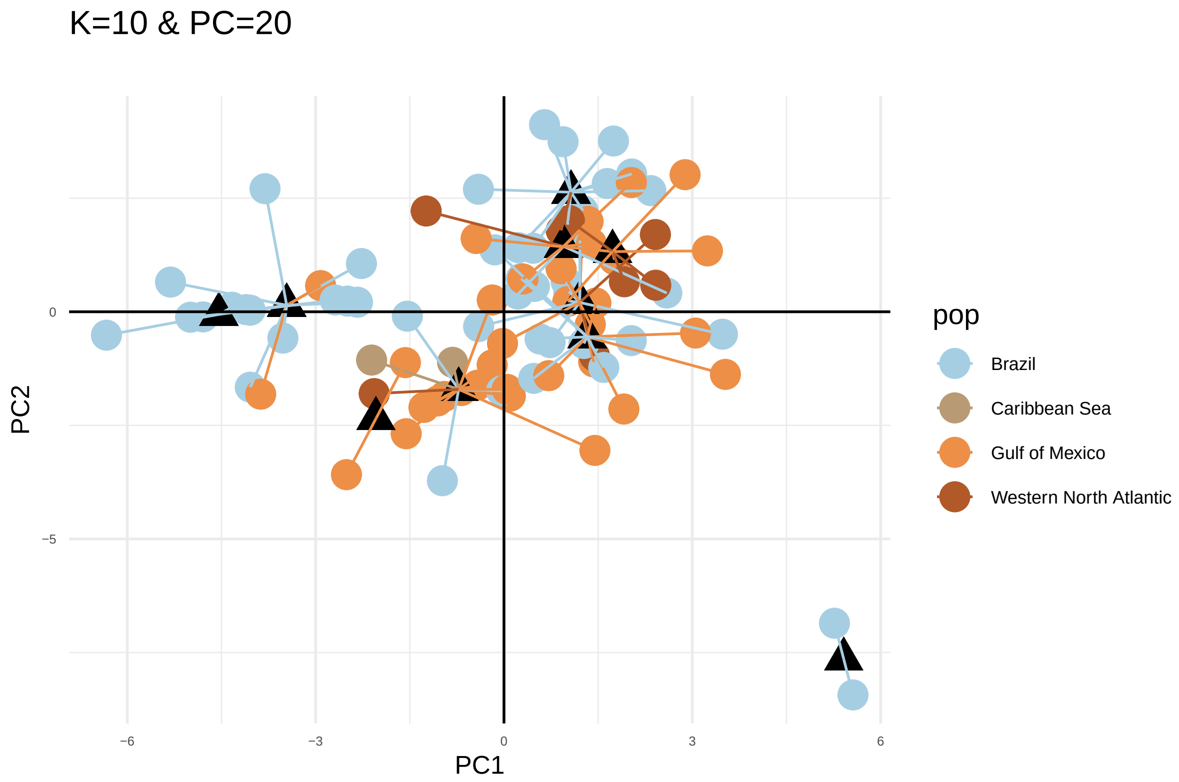
K=6 & PC=20




K=7 & PC=20
5
0
−5
−6
−3
0
3
PC1
PC2
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic


K=8 & PC=20
5
0
−5
−3
0
3
6
PC1
PC2
pop
Brazil
Caribbean Sea
Gulf of Mexico
Western North Atlantic


K=9 & PC=20


K=10 & PC=20

11 DATA5: DArTcap - Indo - West Pacific

11.1 Set strata

```
strata <- radiator::read_strata("Bull_shark_DArTcap_strata.tsv",
                                keep.two = FALSE)$strata %>%
  dplyr:: filter(SpeciesID_genetic == "Carcharhinus leucas") %>%
  dplyr:: filter(Region %in% c("W-IO","N-IO", "E-IO","E-IO/W-PAC","W-PAC",
                               "Japan", "Fiji"))

readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata5_IWP.tsv")
```

11.2 Filter data

1. Marker Reproducibility: 0.98
2. Individual missingness: 0.25
3. Individual Het - low: 0
4. Individual Het - high: 0.07
5. Individual total coverage - low: 10,000
6. Individual total coverage - high: 1,000,000
7. Marker MAC - low: 3
8. Marker coverage - low: 4
9. Marker coverage - high:60
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 2 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: 0.051
16. Individual Het - high: 0.076
17. Duplicated individuals: 0.2
18. Filter on HWE: 4 pops, 0.001

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata5_IWP.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = 1)
BS.dartcap.IWP.gds <- BSsnp$gds
BS.dartcap.IWP.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.IWP.gds, expand = TRUE, all = TRUE, attribute = TRUE,
      attribute.trim = FALSE)

save(BS.dartcap.IWP.tidy, file = "DArTcap_IWP.Rdata")
```

Table 43:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	798 / 26 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	798 / 26 / 1 / 25292 / 35287	0 / 0 / 0 / 11939 / 19900
Filter markers in common	NA	798 / 26 / 1 / 13353 / 15387	0 / 0 / 0 / 187 / 224
Filter individuals based on missingness	0.25	798 / 26 / 1 / 13166 / 15163	12 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.07	786 / 26 / 1 / 13166 / 15163	9 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+07	777 / 26 / 1 / 13166 / 15163	2 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	775 / 26 / 1 / 13166 / 15163	0 / 0 / 0 / 2030 / 2633
Filter MAC	3	775 / 26 / 1 / 11136 / 12530	0 / 0 / 0 / 5456 / 6385
Filter coverage min / max	4-60	775 / 26 / 1 / 5680 / 6145	0 / 0 / 0 / 1612 / 1695
Filter genotyping	0.1	775 / 26 / 1 / 4068 / 4450	0 / 0 / 0 / 591 / 640
Filter SNPs position on the read	all	775 / 26 / 1 / 3477 / 3810	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	775 / 26 / 1 / 3477 / 3810	0 / 0 / 0 / 5 / 21
Filter short ld	mac	775 / 26 / 1 / 3472 / 3789	0 / 0 / 0 / 0 / 317
detect mixed genomes	0.051 0.076	775 / 26 / 1 / 3472 / 3472	71 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	704 / 26 / 1 / 3472 / 3472	0 / 0 / 0 / 9 / 9
detect duplicate genomes	0.2	704 / 26 / 1 / 3463 / 3463	68 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	636 / 26 / 1 / 3463 / 3463	0 / 0 / 0 / 3 / 3
Filter HWE	40.001	636 / 26 / 1 / 3460 / 3460	0 / 0 / 0 / 9 / 9

11.2.1 Remove extra low and high heterozygous individuals

Because the average heterozygosity per sampling location is not even, certain individuals cannot be excluded without removing ‘good’ individuals.

```
rm <-  c("CL-ARS021-F","CL-GOM025-F.1","CL-GOM012-F","CL-SAF014-M","CL-SAF002-F",
         "CL-BRZ038-U","CLF003-F","CL-GOM011-F","CL-SAF015-F","CL-SAF003-M",
         "CL-PNG005-U","CLCR056-M","CLCR047.1","CLCR055-M","CLCR066-M")

BS.dartcap.IWP.tidy <- BS.dartcap.IWP.tidy[!BS.dartcap.IWP.tidy$INDIVIDUALS %in% rm,]
length(unique(BS.dartcap.IWP.tidy$INDIVIDUALS)) # 635
```

‘

11.3 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.IWP.tidy,
                                       output = c("genlight", "stockr",
                                                  "pcadapt", "gtypes", "rubias"))
BS.dartcap.IWP.gl <- Convert$genlight
BS.dartcap.IWP.stkr <- Convert$stockr
BS.dartcap.IWP.pc <- Convert$pcadapt
BS.dartcap.IWP.gt <- Convert$gtypes
BS.dartcap.IWP.rubias <- Convert$rubias


markers.meta <- radiator::extract_markers_metadata(BS.dartcap.IWP.gds,
                                                   whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.IWP.gds,
                                                           whitelist = TRUE)
individuals.meta <- individuals.meta[individuals.meta$INDIVIDUALS %in%
                                       BS.dartcap.IWP.gl$ind.names,]
BS.dartcap.IWP.gl$other$ind.metrics <- individuals.meta
BS.dartcap.IWP.gl$other$loc.metrics <- markers.meta
BS.dartcap.IWP.gt@schemes <- individuals.meta

pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Fitzroy River", "Daly River",
                "Adelaide River","Darwin Coastal",  "South Alligator River",
                "East Alligator River","Blue mud Bay", "Roper River",
                "Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour", "Okinawa", "Urauchi River",
                "Fiji")
BS.dartcap.IWP.gl$pop <- factor(BS.dartcap.IWP.gl$other$ind.metrics$Site2,
                                levels = pop.levels)
BS.dartcap.IWP.gl <- BS.dartcap.IWP.gl[order(BS.dartcap.IWP.gl$pop,
                                             BS.dartcap.IWP.gl$ind.names),]
BS.dartcap.IWP.gl <- BS.dartcap.IWP.gl[order(BS.dartcap.IWP.gl$pop,
                                             BS.dartcap.IWP.gl$ind.names)]
BS.dartcap.IWP.rubias$repunit <- factor(BS.dartcap.IWP.rubias$repunit,
                                        levels = pop.levels)

save(BS.dartcap.IWP.tidy, BS.dartcap.IWP.gl, BS.dartcap.IWP.stkr,
     BS.dartcap.IWP.pc,BS.dartcap.IWP.gt,BS.dartcap.IWP.rubias,
     markers.meta, individuals.meta, file = "DArTcap_IWP.Rdata")
```

11.4 Load data

```
load("DArTcap_IWP.Rdata")
pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Fitzroy River", "Daly River",
                "Adelaide River","Darwin Coastal",  "South Alligator River",
                "East Alligator River","Blue mud Bay", "Roper River",
                "Towns River","Unknown","Wenlock River","Trinity inlet",
                "Clarence River", "Sydney Harbour","Okinawa", "Urauchi River",
                "Fiji")
BS.dartcap.IWP.gl$pop <- factor(BS.dartcap.IWP.gl$pop, levels = pop.levels)
BS.dartcap.IWP.gl <- BS.dartcap.IWP.gl[order(BS.dartcap.IWP.gl$pop,
                                             BS.dartcap.IWP.gl$ind.names),]

pop.levels1 <- stringr::str_replace_all(pop.levels, " ", "_")
BS.dartcap.IWP.tidy$POP_ID <- factor(BS.dartcap.IWP.tidy$POP_ID,
                                     levels = pop.levels1)
BS.dartcap.IWP.tidy <- BS.dartcap.IWP.tidy[order(BS.dartcap.IWP.tidy$POP_ID,
                                                 BS.dartcap.IWP.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartcap.IWP.gl) # 635
adegenet::nLoc(BS.dartcap.IWP.gl) # 3451
summary(BS.dartcap.IWP.gl$pop)
sum(duplicated(BS.dartcap.IWP.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartcap.IWP.gl$other$loc.metrics$LOCUS) #74
```

```
## [1] 635
## [1] 3451
##          South Africa            Mozambique               Reunion
##                    21                    11                    28
##            Seychelles           Arabian Sea             Sri Lanka
##                    36                    15                    12
##              Thailand             Indonesia      Papua New Guinea
##                     4                     4                     9
##         Fitzroy River            Daly River        Adelaide River
##                     3                    49                    18
##        Darwin Coastal South Alligator River  East Alligator River
##                    13                    88                    47
##          Blue mud Bay           Roper River           Towns River
##                    17                     9                    10
##               Unknown         Wenlock River         Trinity inlet
##                    10                    24                     4
##        Clarence River        Sydney Harbour               Okinawa
##                    74                    65                     9
##         Urauchi River                  Fiji
##                    35                    20
## [1] 0
## [1] 74
```

11.5 Remove sex-linked markers

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sum(bull_shark$sexy.summary$CLONE_ID %in% SLM$sexy.summary$CLONE_ID) #33
sum(SLM$sexy.summary$CLONE_ID %in% bull_shark$sexy.summary$CLONE_ID) #23
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID,
                        SLM$sexy.summary$CLONE_ID))
```

```
sum(BS.dartcap.IWP.gl$loc.names %in% sex.markers) #35
locnames <- BS.dartcap.IWP.gl$loc.names
BS.dartcap.IWP.gl <- BS.dartcap.IWP.gl[,!locnames %in% sex.markers]
BS.dartcap.IWP.gl$other$loc.metrics <- BS.dartcap.IWP.gl$other$loc.metrics[
  !locnames %in% sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.IWP.tidy$LOCUS)) # 35
BS.dartcap.IWP.tidy <- BS.dartcap.IWP.tidy[!BS.dartcap.IWP.tidy$LOCUS %in%
                                             sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartcap.IWP.gt@data$locus)[,2]
BS.dartcap.IWP.gt <- BS.dartcap.IWP.gt[,!locus.gt %in% sex.markers, ,
                                       drop = TRUE]

locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                   string =  colnames(BS.dartcap.IWP.rubias))[,2]
BS.dartcap.IWP.rubias <- BS.dartcap.IWP.rubias[,!locus.rubias %in% sex.markers]
```

```
## [1] 33
## [1] 23
## [1] 35
## [1] 35
```

11.6 Genetic diversity

```
set.seed(124)
pop.levels <- c( "South Africa", "Mozambique", "Reunion", "Seychelles",
                 "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                 "Papua New Guinea" , "Fitzroy River", "Daly River", "Adelaide River",
                 "Darwin Coastal",  "South Alligator River", "East Alligator River",
                 "Blue mud Bay", "Roper River", "Towns River", "Unknown",
                 "Wenlock River", "Trinity inlet", "Clarence River", "Sydney Harbour",
                 "Okinawa", "Urauchi River", "Fiji")

gl <- BS.dartcap.IWP.gl
gl$pop <- factor(gl$other$ind.metrics$Site2, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]


gl2gpop(gl, filename = "BS_dartcap_IWP_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_IWP_genepop.txt",
                               outfile = "BS_dartcap_IWP_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)


length(bastat$main_tab) #26
gendiv <- data.frame(
  "South Africa" = bastat$main_tab[[1]]$overall,
  "Mozambique" = bastat$main_tab[[2]]$overall,
  "Reunion" = bastat$main_tab[[3]]$overall,
  "Seychelles" = bastat$main_tab[[4]]$overall,
  "Arabian Sea" = bastat$main_tab[[5]]$overall,
  "Sri Lanka" = bastat$main_tab[[6]]$overall,
```

```
  "Thailand" = bastat$main_tab[[7]]$overall,
  "Indonesia" = bastat$main_tab[[8]]$overall,
  "Papua New Guinea" = bastat$main_tab[[9]]$overall,
  "Fitzroy River" = bastat$main_tab[[10]]$overall,
  "Daly River" = bastat$main_tab[[11]]$overall,
  "Adelaide River" = bastat$main_tab[[12]]$overall,
  "Darwin Coastal" = bastat$main_tab[[13]]$overall,
  "South Alligator River" = bastat$main_tab[[14]]$overall,
  "East Alligator River" = bastat$main_tab[[15]]$overall,
  "Blue mud Bay" = bastat$main_tab[[16]]$overall,
  "Roper River" = bastat$main_tab[[17]]$overall,
  "Towns River" = bastat$main_tab[[18]]$overall,
  "Unknown" = bastat$main_tab[[19]]$overall,
  "Wenlock River" = bastat$main_tab[[20]]$overall,
  "Trinity inlet" = bastat$main_tab[[21]]$overall,
  "Clarence River" = bastat$main_tab[[22]]$overall,
  "Sydney Harbour" = bastat$main_tab[[23]]$overall,
  "Urauchi River" = bastat$main_tab[[24]]$overall,
  "Okinawa" = bastat$main_tab[[25]]$overall,
  "Fiji" = bastat$main_tab[[26]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTcap_IWP_gendiv.txt")
save(gendiv, file = "DArTcap_IWP_gendiv.Rdata")
```

```
load("DArTcap_IWP_gendiv.Rdata")
shortnames <- c("SAF", "MOZ", "RUN" , "SEY", "ARS", "SRL", "TAI", "IND", "PNG" ,
                "FZR", "DAR", "ADR","DWC",  "SAR", "EAR","BMB", "ROR","TOR","UNK",
                "WER","TRI","CLR", "SYH", "URR","OKI", "FIJ")
knitr::kable(gendiv, col.names = shortnames, digits = 4,caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position")) %>%
  kableExtra::landscape()
```

Table 44:

	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	DAR	ADR	DWC	SAR	EAR	BMB	ROR	TOR	UNK	WER	TRI
ar	1.1500	1.1290	1.1480	1.1500	1.1540	1.1480	1.1340	1.1230	1.1420	1.1120	1.1540	1.1490	1.1530	1.1530	1.1500	1.1550	1.1390	1.1410	1.1450	1.1530	1.1360
size	20.7310	10.2200	27.3360	35.4140	14.8220	11.8720	3.9710	3.9530	8.8880	2.9070	48.4430	17.7910	12.8110	86.9180	46.4840	16.7170	8.5940	9.8000	9.7930	23.6650	3.9430
obs_het	0.0610	0.0570	0.0600	0.0610	0.0640	0.0630	0.0660	0.0620	0.0610	0.0610	0.0610	0.0620	0.0640	0.0610	0.0610	0.0660	0.0600	0.0600	0.0630	0.0620	0.0680
exp_het	0.0640	0.0620	0.0640	0.0640	0.0650	0.0630	0.0590	0.0550	0.0600	0.0530	0.0650	0.0630	0.0650	0.0640	0.0630	0.0660	0.0630	0.0610	0.0630	0.0650	0.0610
uexp_het	0.0660	0.0660	0.0650	0.0650	0.0670	0.0660	0.0670	0.0630	0.0640	0.0630	0.0650	0.0650	0.0680	0.0650	0.0640	0.0680	0.0670	0.0640	0.0660	0.0660	0.0700
fis	0.0320	0.0540	0.0470	0.0300	0.0100	-0.0020	-0.1320	-0.1330	-0.0200	-0.1720	0.0390	0.0120	-0.0010	0.0360	0.0320	-0.0010	0.0180	-0.0020	-0.0160	0.0290	-0.1280
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	-0.0010	-0.0350	0.0140	0.0070	-0.0430	-0.0750	-0.3760	-0.5440	-0.1190	-1.0000	0.0220	-0.0290	-0.0590	0.0270	0.0140	-0.0450	-0.0940	-0.0840	-0.0970	-0.0060	-0.3810
fis_hi	0.0270	0.0470	0.0440	0.0290	0.0020	-0.0120	-0.1320	-0.1330	-0.0290	-0.1720	0.0380	0.0060	-0.0100	0.0370	0.0300	-0.0080	0.0110	-0.0100	-0.0230	0.0260	-0.1280
ar_lo	1.1130	1.0440	1.1110	1.1140	1.1150	1.1120	1.0590	1.0470	1.1120	1.0040	1.1190	1.1120	1.1150	1.1220	1.1140	1.1180	1.0920	1.1040	1.1100	1.1150	1.0520
ar_hi	1.1630	1.1580	1.1600	1.1620	1.1730	1.1720	1.1630	1.1590	1.1590	1.1500	1.1650	1.1640	1.1730	1.1640	1.1620	1.1760	1.1620	1.1610	1.1630	1.1680	1.1680
fis.hierfstat	0.0554	0.0983	0.0641	0.0433	0.0429	0.0388	-0.0044	-0.0062	0.0349	0.0007	0.0485	0.0394	0.0368	0.0418	0.0423	0.0283	0.0727	0.0475	0.0338	0.0490	-0.0008
fis.CI.low	0.0563	0.1030	0.0615	0.0396	0.0329	0.0192	-0.0185	-0.0232	0.0306	-0.0037	0.0487	0.0359	0.0324	0.0410	0.0394	0.0184	0.0741	0.0480	0.0311	0.0496	-0.0147
fis.CI.high	0.0928	0.1607	0.0973	0.0672	0.0731	0.0668	0.0560	0.0587	0.0789	0.0915	0.0735	0.0718	0.0753	0.0626	0.0669	0.0581	0.1286	0.0990	0.0783	0.0796	0.0589

11.6.1 Number of monomorphic markers per population

```r
pop.levels <- c( "South Africa", "Mozambique", "Reunion", "Seychelles",
                 "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                 "Papua New Guinea" , "Fitzroy River", "Daly River", "Adelaide River",
                 "Darwin Coastal",  "South Alligator River", "East Alligator River",
                 "Blue mud Bay", "Roper River", "Towns River", "Unknown",
                 "Wenlock River", "Trinity inlet", "Clarence River", "Sydney Harbour",
                 "Urauchi River", "Okinawa", "Fiji")
monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.IWP.gl[BS.dartcap.IWP.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("SAF", "MOZ", "RUN" , "SEY", "ARS", "SRL", "TAI", "IND", "PNG" ,
                "FZR", "DAR", "ADR","DWC",  "SAR", "EAR","BMB", "ROR","TOR","UNK",
                "WER","TRI","CLR", "SYH", "URR","OKI", "FIJ")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

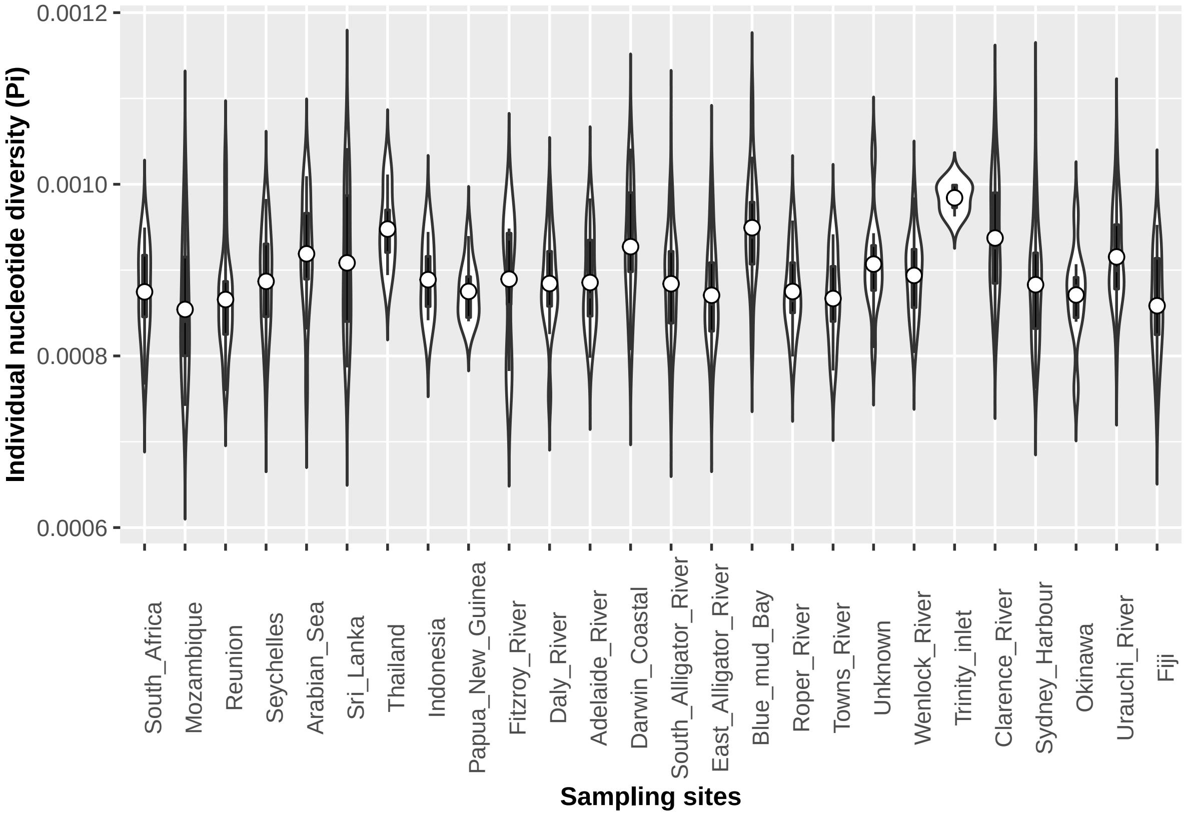
Table 45:

SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	DAR	ADR	DWC	SAR	EAR	BMB	ROR	TOR	UNK	WE
2050	2406	1947	1837	2119	2306	2773	2825	2469	2919	1624	2134	2231	1235	1690	2087	2489	2452	2415	195

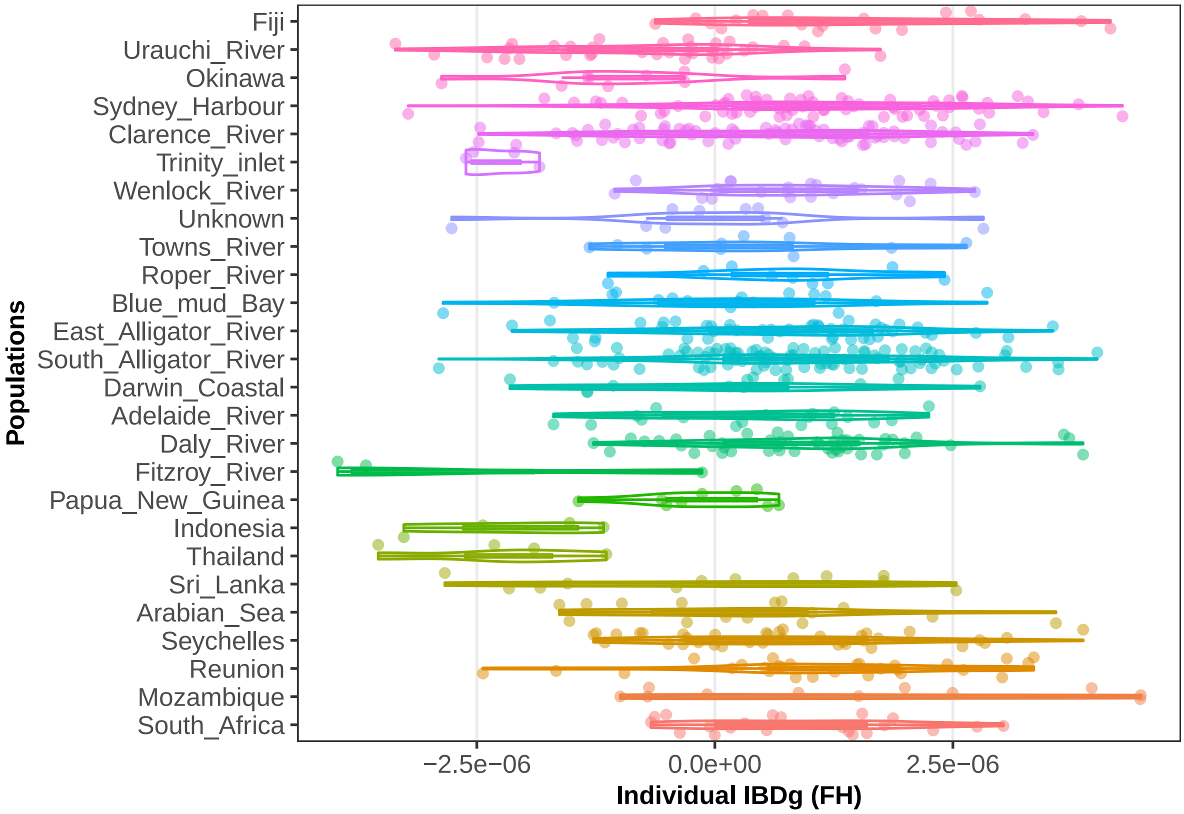
11.6.2 Nucleotide diversity and inbreeding

```r
pi.sum <- radiator::pi(
  data = BS.dartcap.IWP.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartcap.IWP.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTcap_IWP_pi_FIS_Sites2.Rdata")
```

```r
load("DArTcap_IWP_pi_FIS_Sites2.Rdata")
pi.sum$boxplot.pi
```



```
FIS.sum$fh.box.plot
```



11.7 Genetic differentiation

```r
Fst.gt <- strataG::popStructTest(
    BS.dartcap.IWP.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_IWP_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_IWP_FST.txt")
```

```r
load("DArTcap_IWP_FST.Rdata")

kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                        decreasing = TRUE),
                                  -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 3416 DArTcap loci between the IWP sites",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
Fiji (20) v. Urauchi_River (35)	5388.4074	0.0010	4e-04	0.0010	-9.0446	1.0000	0.0760	0.0010	0.0825	0.0010	0.1261	0.0010	0.1402	0.0010	0.2364	0.0010
Indonesia (4) v. Urauchi_River (35)	2993.2512	0.0010	4e-04	0.0010	-41.5699	0.5787	0.0637	0.0020	0.0695	0.0021	0.6333	0.1502	0.6525	0.1439	0.7872	0.1439
Fiji (20) v. Okinawa (9)	2794.0827	0.0010	3e-04	0.0010	-16.3836	0.9990	0.0586	0.0010	0.0631	0.0010	0.2921	0.0010	0.3143	0.0010	0.4694	0.0010
Okinawa (9) v. Urauchi_River (35)	3217.6843	0.0010	3e-04	0.0010	-14.4384	0.9920	0.0586	0.0010	0.0638	0.0010	0.2391	0.0010	0.2590	0.0010	0.4020	0.0010
Towns_River (10) v. Urauchi_River (35)	3526.7775	0.0010	3e-04	0.0010	-12.3740	0.9271	0.0543	0.0010	0.0591	0.0010	0.2009	0.0010	0.2195	0.0010	0.3501	0.0010
Trinity_inlet (4) v. Urauchi_River (35)	3102.3571	0.0010	3e-04	0.0060	-34.4901	0.0312	0.0535	0.0041	0.0585	0.0042	0.5876	0.7031	0.6090	0.6562	0.7537	0.6667
Blue_mud_Bay (17) v. Urauchi_River (35)	4357.8966	0.0010	3e-04	0.0010	-8.8342	0.9530	0.0520	0.0010	0.0566	0.0010	0.1175	0.0010	0.1309	0.0010	0.2223	0.0010
Thailand (4) v. Urauchi_River (35)	2896.9249	0.0010	3e-04	0.0030	-34.7092	0.0402	0.0510	0.0020	0.0557	0.0011	0.5847	0.7799	0.6057	0.7619	0.7512	0.7672
Roper_River (9) v. Urauchi_River (35)	3338.2073	0.0010	3e-04	0.0010	-13.0815	0.6304	0.0496	0.0010	0.0541	0.0010	0.2235	0.0010	0.2434	0.0010	0.3816	0.0010
Reunion (28) v. Urauchi_River (35)	4762.2518	0.0010	3e-04	0.0010	-8.1018	1.0000	0.0494	0.0010	0.0536	0.0010	0.0890	0.0010	0.0995	0.0010	0.1731	0.0010
Papua_New_Guinea (9) v. Urauchi_River (35)	3112.8556	0.0010	2e-04	0.0010	-13.3160	0.8492	0.0490	0.0010	0.0534	0.0010	0.2208	0.0010	0.2402	0.0010	0.3776	0.0010
Mozambique (11) v. Urauchi_River (35)	3474.1127	0.0010	2e-04	0.0010	-12.0236	0.9980	0.0490	0.0010	0.0533	0.0010	0.1941	0.0010	0.2124	0.0010	0.3404	0.0010
Darwin_Coastal (13) v. Urauchi_River (35)	3713.8639	0.0010	2e-04	0.0010	-10.0498	0.3896	0.0467	0.0010	0.0508	0.0010	0.1448	0.0010	0.1603	0.0010	0.2666	0.0010
South_Africa (21) v. Urauchi_River (35)	4127.6671	0.0010	3e-04	0.0010	-8.7052	1.0000	0.0463	0.0010	0.0502	0.0010	0.1027	0.0010	0.1145	0.0010	0.1970	0.0010
Sri_Lanka (12) v. Urauchi_River (35)	3514.0811	0.0010	2e-04	0.0010	-10.8402	0.6384	0.0456	0.0010	0.0496	0.0010	0.1592	0.0020	0.1754	0.0010	0.2887	0.0010
Adelaide_River (18) v. Urauchi_River (35)	3899.2966	0.0010	2e-04	0.0010	-9.3785	1.0000	0.0449	0.0010	0.0488	0.0010	0.1156	0.0010	0.1285	0.0010	0.2188	0.0010
Unknown (10) v. Urauchi_River (35)	3357.2812	0.0010	2e-04	0.0010	-12.1235	0.5524	0.0442	0.0010	0.0481	0.0010	0.1929	0.0020	0.2111	0.0020	0.3387	0.0020
Daly_River (49) v. Urauchi_River (35)	5465.3608	0.0010	2e-04	0.0010	-6.6411	1.0000	0.0440	0.0010	0.0476	0.0010	0.0631	0.0010	0.0710	0.0010	0.1261	0.0010
Sydney_Harbour (65) v. Urauchi_River (35)	5957.1169	0.0010	2e-04	0.0010	-5.9518	1.0000	0.0433	0.0010	0.0467	0.0010	0.0552	0.0010	0.0622	0.0010	0.1112	0.0010
Arabian_Sea (15) v. Urauchi_River (35)	3856.4156	0.0010	2e-04	0.0010	-9.3106	0.6993	0.0431	0.0010	0.0469	0.0010	0.1249	0.0010	0.1387	0.0010	0.2344	0.0010
Indonesia (4) v. Okinawa (9)	1478.2974	0.0120	2e-04	0.0639	43.3210	0.7992	0.0431	0.0291	0.0467	0.0293	1.7858	0.3486	1.7220	0.3649	1.2592	0.3670
Blue_mud_Bay (17) v. Fiji (20)	3330.6963	0.0010	2e-04	0.0010	-9.5476	1.0000	0.0426	0.0010	0.0477	0.0010	0.1449	0.0010	0.1608	0.0010	0.2670	0.0010
Clarence_River (74) v. Urauchi_River (35)	6255.5369	0.0010	2e-04	0.0010	-4.9884	1.0000	0.0418	0.0010	0.0452	0.0010	0.0482	0.0010	0.0545	0.0010	0.0980	0.0010
Seychelles (36) v. Urauchi_River (35)	4708.7080	0.0010	2e-04	0.0010	-7.6307	1.0000	0.0417	0.0010	0.0452	0.0010	0.0742	0.0010	0.0832	0.0010	0.1465	0.0010
East_Alligator_River (47) v. Urauchi_River (35)	5161.3271	0.0010	2e-04	0.0010	-6.9864	1.0000	0.0416	0.0010	0.0450	0.0010	0.0644	0.0010	0.0723	0.0010	0.1284	0.0010
Urauchi_River (35) v. Wenlock_River (24)	4244.2007	0.0010	2e-04	0.0010	-8.1753	1.0000	0.0410	0.0010	0.0443	0.0010	0.0902	0.0010	0.1008	0.0010	0.1753	0.0010
South_Alligator_River (88) v. Urauchi_River (35)	6536.0386	0.0010	2e-04	0.0010	-4.9996	1.0000	0.0408	0.0010	0.0439	0.0010	0.0463	0.0010	0.0522	0.0010	0.0942	0.0010
Okinawa (9) v. Towns_River (10)	1928.3144	0.0010	2e-04	0.0020	-28.1073	1.0000	0.0407	0.0010	0.0443	0.0010	0.4626	0.0010	0.4853	0.0010	0.6481	0.0010
Okinawa (9) v. Trinity_inlet (4)	1562.9446	0.0130	2e-04	0.0470	54.7396	0.5153	0.0394	0.0291	0.0424	0.0291	1.5314	0.7249	1.4886	0.7372	1.1930	0.7382
Fiji (20) v. Trinity_inlet (4)	2323.4592	0.0010	3e-04	0.0050	-52.4566	0.0322	0.0384	0.0073	0.0412	0.0073	0.7000	0.9236	0.7174	0.9236	0.8338	0.9236
Okinawa (9) v. Thailand (4)	1509.6999	0.0180	2e-04	0.0639	53.8887	0.4297	0.0381	0.0330	0.0408	0.0330	1.5562	0.7745	1.5120	0.7867	1.2003	0.7887
Fiji (20) v. Towns_River (10)	2620.1691	0.0010	2e-04	0.0010	-13.9361	0.9830	0.0374	0.0010	0.0406	0.0010	0.2406	0.0010	0.2612	0.0010	0.4045	0.0010
Fiji (20) v. Indonesia (4)	2161.3683	0.0010	2e-04	0.0080	-71.6720	0.2780	0.0374	0.0042	0.0401	0.0052	0.7598	0.6916	0.7737	0.6857	0.8714	0.6857
Fitzroy_River (3) v. Okinawa (9)	1350.3746	0.0440	2e-04	0.0879	NA	NA	0.0367	0.0832	NA	NA	NA	NA	NA	NA	NA	NA
Fiji (20) v. Papua_New_Guinea (9)	2482.7329	0.0010	2e-04	0.0010	-14.8453	0.9580	0.0360	0.0010	0.0387	0.0010	0.2628	0.0020	0.2841	0.0020	0.4331	0.0020
Fiji (20) v. Mozambique (11)	2692.3627	0.0010	2e-04	0.0010	-13.5223	0.9980	0.0357	0.0010	0.0399	0.0010	0.2359	0.0010	0.2565	0.0010	0.3984	0.0010
Okinawa (9) v. Papua_New_Guinea (9)	1733.6778	0.0050	2e-04	0.0110	-33.1632	0.9940	0.0352	0.0090	0.0380	0.0090	0.5126	0.0090	0.5344	0.0090	0.6922	0.0090
Fiji (20) v. Wenlock_River (24)	3382.0143	0.0010	2e-04	0.0010	-8.7077	1.0000	0.0352	0.0010	0.0383	0.0010	0.1156	0.0010	0.1287	0.0010	0.2190	0.0010
Fiji (20) v. Reunion (28)	3540.6320	0.0010	2e-04	0.0010	-8.6755	1.0000	0.0350	0.0010	0.0385	0.0010	0.1099	0.0010	0.1224	0.0010	0.2093	0.0010
Fiji (20) v. Sri_Lanka (12)	2768.2168	0.0010	2e-04	0.0010	-11.6935	0.9970	0.0340	0.0010	0.0367	0.0010	0.1909	0.0010	0.2092	0.0010	0.3360	0.0010
Blue_mud_Bay (17) v. Okinawa (9)	2200.2988	0.0010	2e-04	0.0010	-15.2999	1.0000	0.0339	0.0010	0.0365	0.0010	0.2746	0.0010	0.2964	0.0010	0.4480	0.0010
Mozambique (11) v. Okinawa (9)	1914.0960	0.0020	2e-04	0.0020	-26.0982	0.9960	0.0336	0.0020	0.0363	0.0020	0.4425	0.0030	0.4655	0.0030	0.6294	0.0030
Fiji (20) v. South_Alligator_River (88)	5324.9691	0.0010	2e-04	0.0010	-4.9823	0.9980	0.0336	0.0010	0.0366	0.0010	0.0572	0.0010	0.0644	0.0010	0.1150	0.0010
Adelaide_River (18) v. Fiji (20)	3045.6429	0.0010	2e-04	0.0010	-9.9690	1.0000	0.0333	0.0010	0.0372	0.0010	0.1412	0.0010	0.1562	0.0010	0.2606	0.0010
Fiji (20) v. Unknown (10)	2556.4398	0.0010	2e-04	0.0010	-13.5310	0.9291	0.0329	0.0010	0.0357	0.0010	0.2335	0.0010	0.2539	0.0010	0.3952	0.0010
Daly_River (49) v. Fiji (20)	4192.4120	0.0010	2e-04	0.0010	-6.7568	1.0000	0.0328	0.0010	0.0359	0.0010	0.0775	0.0010	0.0869	0.0010	0.1526	0.0010
Fiji (20) v. South_Africa (21)	3137.9922	0.0010	2e-04	0.0010	-9.3698	1.0000	0.0328	0.0010	0.0355	0.0010	0.1267	0.0010	0.1407	0.0010	0.2373	0.0010
Fiji (20) v. Sydney_Harbour (65)	4716.2588	0.0010	1e-04	0.0010	-5.9569	1.0000	0.0327	0.0010	0.0358	0.0010	0.0672	0.0010	0.0755	0.0010	0.1337	0.0010
Fiji (20) v. Seychelles (36)	3775.7483	0.0010	2e-04	0.0010	-7.9274	1.0000	0.0327	0.0010	0.0357	0.0010	0.0939	0.0010	0.1050	0.0010	0.1818	0.0010
Darwin_Coastal (13) v. Fiji (20)	2818.4246	0.0010	2e-04	0.0010	-10.9110	0.9920	0.0324	0.0010	0.0365	0.0010	0.1742	0.0010	0.1918	0.0010	0.3117	0.0010
East_Alligator_River (47) v. Fiji (20)	4146.6801	0.0010	2e-04	0.0010	-7.1477	1.0000	0.0317	0.0010	0.0347	0.0010	0.0806	0.0010	0.0902	0.0010	0.1581	0.0010
Okinawa (9) v. Wenlock_River (24)	2354.3461	0.0010	2e-04	0.0010	-13.1658	1.0000	0.0311	0.0010	0.0340	0.0010	0.2274	0.0010	0.2470	0.0010	0.3865	0.0010
Clarence_River (74) v. Fiji (20)	4865.4235	0.0010	2e-04	0.0010	-4.8476	1.0000	0.0303	0.0010	0.0331	0.0010	0.0560	0.0010	0.0633	0.0010	0.1130	0.0010

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
Okinawa (9) v. Reunion (28)	2426.4054	0.0010	2e-04	0.0010	-13.1817	0.9990	0.0301	0.0010	0.0333	0.0010	0.2207	0.0010	0.2398	0.0010	0.3772	0.0010
Okinawa (9) v. Roper__River (9)	1739.1946	0.0050	2e-04	0.0110	-32.2964	0.9940	0.0301	0.0090	0.0337	0.0070	0.5102	0.0060	0.5324	0.0070	0.6904	0.0070
Fiji (20) v. Roper__River (9)	2421.4187	0.0010	2e-04	0.0010	-14.8553	0.7992	0.0296	0.0010	0.0326	0.0010	0.2658	0.0100	0.2875	0.0080	0.4371	0.0090
Okinawa (9) v. Unknown (10)	1764.3354	0.0010	2e-04	0.0040	-27.2677	0.9970	0.0290	0.0040	0.0316	0.0040	0.4507	0.0040	0.4735	0.0040	0.6371	0.0040
Adelaide__River (18) v. Okinawa (9)	2070.0534	0.0010	1e-04	0.0010	-16.4720	0.9990	0.0290	0.0010	0.0312	0.0010	0.2821	0.0010	0.3034	0.0010	0.4567	0.0010
Clarence__River (74) v. Okinawa (9)	3208.9096	0.0010	2e-04	0.0010	-6.6401	1.0000	0.0280	0.0010	0.0301	0.0010	0.1141	0.0010	0.1268	0.0010	0.2162	0.0010
Arabian__Sea (15) v. Fiji (20)	2920.1431	0.0010	2e-04	0.0010	-9.7938	1.0000	0.0280	0.0010	0.0314	0.0010	0.1479	0.0010	0.1636	0.0010	0.2713	0.0010
Arabian__Sea (15) v. Okinawa (9)	1982.5267	0.0010	2e-04	0.0010	-16.6438	1.0000	0.0278	0.0010	0.0300	0.0010	0.2970	0.0010	0.3191	0.0010	0.4750	0.0010
Okinawa (9) v. Sri__Lanka (12)	1865.0523	0.0020	2e-04	0.0050	-21.3791	0.9990	0.0278	0.0040	0.0300	0.0040	0.3704	0.0030	0.3933	0.0030	0.5573	0.0030
Okinawa (9) v. South__Alligator__River (88)	3295.2727	0.0010	2e-04	0.0010	-6.8669	1.0000	0.0272	0.0010	0.0297	0.0010	0.1149	0.0010	0.1274	0.0010	0.2173	0.0010
East__Alligator__River (47) v. Okinawa (9)	2729.5616	0.0010	1e-04	0.0010	-10.4814	1.0000	0.0271	0.0010	0.0290	0.0010	0.1693	0.0010	0.1855	0.0010	0.3034	0.0010
Daly__River (49) v. Okinawa (9)	2787.1429	0.0010	1e-04	0.0010	-9.7344	1.0000	0.0263	0.0010	0.0283	0.0010	0.1591	0.0010	0.1749	0.0010	0.2881	0.0010
Okinawa (9) v. Sydney__Harbour (65)	2961.6580	0.0010	2e-04	0.0010	-8.4520	1.0000	0.0261	0.0010	0.0287	0.0010	0.1383	0.0010	0.1526	0.0010	0.2555	0.0010
Okinawa (9) v. Seychelles (36)	2430.2545	0.0010	2e-04	0.0010	-11.9599	1.0000	0.0257	0.0010	0.0281	0.0010	0.1942	0.0010	0.2119	0.0010	0.3400	0.0010
Darwin__Coastal (13) v. Okinawa (9)	1888.3229	0.0020	2e-04	0.0040	-18.9395	1.0000	0.0255	0.0030	0.0276	0.0030	0.3355	0.0010	0.3584	0.0010	0.5196	0.0010
Fiji (20) v. Thailand (4)	2116.3784	0.0010	2e-04	0.0130	-52.7453	0.0182	0.0243	0.0187	0.0261	0.0187	0.6943	0.9720	0.7114	0.9708	0.8297	0.9708
Fitzroy__River (3) v. Indonesia (4)	1013.2851	0.2817	2e-04	0.3157	NA	NA	0.0242	0.2817	0.0262	0.3047	NA	NA	NA	NA	NA	NA
Okinawa (9) v. South__Africa (21)	2060.9975	0.0010	1e-04	0.0010	-14.8221	1.0000	0.0240	0.0010	0.0261	0.0010	0.2509	0.0010	0.2712	0.0010	0.4173	0.0010
Fiji (20) v. Fitzroy__River (3)	1990.0145	0.0060	2e-04	0.0160	NA	NA	0.0235	0.0134	0.0253	0.0134	NA	NA	NA	NA	NA	NA
Indonesia (4) v. Towns__River (10)	1433.2349	0.0549	2e-04	0.1019	78.7206	0.6112	0.0219	0.0680	0.0241	0.0680	1.3369	0.4028	1.3120	0.4028	1.1335	0.4028
Papua__New__Guinea (9) v. Trinity__inlet (4)	1435.1476	0.0020	1e-04	0.0509	81.0946	0.2884	0.0189	0.0040	0.0204	0.0040	1.3103	0.8281	1.2867	0.8342	1.1241	0.8342
Blue__mud__Bay (17) v. Towns__River (10)	1991.2789	0.0120	1e-04	0.0110	-13.2927	0.9990	0.0151	0.0090	0.0165	0.0090	0.2290	0.0020	0.2492	0.0020	0.3891	0.0020
Blue__mud__Bay (17) v. Indonesia (4)	1621.5721	0.2178	1e-04	0.0899	-53.8364	0.9329	0.0149	0.0661	0.0161	0.0661	0.7026	0.0855	0.7192	0.0865	0.8351	0.0865
Indonesia (4) v. Papua__New__Guinea (9)	1301.8746	0.1199	2e-04	0.1149	56.8305	0.8128	0.0146	0.1269	0.0159	0.1269	1.5187	0.2212	1.4790	0.2232	1.1902	0.2232
Adelaide__River (18) v. Indonesia (4)	1593.1398	0.0619	1e-04	0.0300	-73.8098	0.8877	0.0146	0.0300	0.0157	0.0300	0.7615	0.0772	0.7750	0.0752	0.8723	0.0752
Indonesia (4) v. Thailand (4)	1073.1255	0.3027	2e-04	0.3347	14.2870	0.6334	0.0136	0.3926	0.0147	0.3926	21.5582	0.3387	19.1145	0.3387	1.8030	0.3786
Mozambique (11) v. Papua__New__Guinea (9)	1581.5293	0.0040	1e-04	0.1429	-23.7994	0.9151	0.0135	0.0010	0.0146	0.0010	0.4123	0.0509	0.4355	0.0480	0.6003	0.0470
Blue__mud__Bay (17) v. Reunion (28)	2620.0231	0.0010	1e-04	0.0010	-8.5001	0.5764	0.0132	0.0010	0.0146	0.0010	0.1029	0.0010	0.1149	0.0010	0.1975	0.0010
Reunion (28) v. Towns__River (10)	2203.4878	0.0010	1e-04	0.0010	-11.8453	0.9011	0.0129	0.0010	0.0139	0.0010	0.1845	0.0070	0.2019	0.0060	0.3262	0.0060
Reunion (28) v. Trinity__inlet (4)	2044.6432	0.0040	1e-04	0.0390	-29.1164	0.0226	0.0121	0.0462	0.0130	0.0462	0.5424	0.9126	0.5647	0.9074	0.7178	0.9074
Indonesia (4) v. Seychelles (36)	2027.1014	0.0180	1e-04	0.0559	-26.0019	0.7127	0.0119	0.0250	0.0131	0.0252	0.5045	0.2550	0.5265	0.2540	0.6853	0.2540
Indonesia (4) v. South__Alligator__River (88)	2787.3675	0.0190	1e-04	0.0340	-10.2014	0.7748	0.0119	0.0142	0.0130	0.0143	0.2747	0.0931	0.2957	0.0839	0.4474	0.0870
Indonesia (4) v. Trinity__inlet (4)	1088.9811	0.3497	2e-04	0.3457	14.3096	0.6786	0.0112	0.4336	0.0122	0.4116	17.6351	0.2784	15.6467	0.2784	1.7860	0.2559
Blue__mud__Bay (17) v. Trinity__inlet (4)	1739.6500	0.0659	1e-04	0.1359	-41.9806	0.4728	0.0112	0.0782	0.0121	0.0782	0.6485	0.4441	0.6681	0.4338	0.7987	0.4379
Indonesia (4) v. Mozambique (11)	1359.9089	0.2288	2e-04	0.1798	94.6150	0.1131	0.0110	0.1058	0.0128	0.0996	1.2671	0.8907	1.2477	0.8907	1.1093	0.8907
Towns__River (10) v. Trinity__inlet (4)	1434.7344	0.0290	1e-04	0.2717	123.4753	0.1840	0.0109	0.1280	0.0118	0.1280	1.1923	0.8643	1.1783	0.8684	1.0813	0.8695
Indonesia (4) v. Unknown (10)	1361.0802	0.0679	1e-04	0.1339	94.2569	0.6197	0.0108	0.0759	0.0119	0.0760	1.2697	0.3823	1.2502	0.3793	1.1102	0.3793
Indonesia (4) v. Sydney__Harbour (65)	2470.6889	0.0050	1e-04	0.0160	-13.9163	0.7865	0.0107	0.0070	0.0118	0.0070	0.3433	0.1813	0.3659	0.1843	0.5280	0.1823
Blue__mud__Bay (17) v. South__Africa (21)	2344.0332	0.0010	1e-04	0.0060	-9.0482	0.9880	0.0107	0.0010	0.0117	0.0010	0.1183	0.0010	0.1317	0.0010	0.2235	0.0010
Daly__River (49) v. Indonesia (4)	2246.8295	0.0110	1e-04	0.0210	-17.8710	0.8645	0.0107	0.0240	0.0114	0.0240	0.4048	0.0954	0.4277	0.0894	0.5926	0.0934
Papua__New__Guinea (9) v. Towns__River (10)	1505.8548	0.0350	1e-04	0.1039	-25.4511	0.9730	0.0106	0.0190	0.0116	0.0190	0.4267	0.0270	0.4495	0.0270	0.6142	0.0270
Blue__mud__Bay (17) v. Seychelles (36)	2642.0241	0.0010	1e-04	0.0010	-7.9749	0.1808	0.0105	0.0010	0.0114	0.0010	0.0885	0.0020	0.0991	0.0020	0.1723	0.0020
Indonesia (4) v. Wenlock__River (24)	1748.9899	0.2168	1e-04	0.1329	-35.4065	0.9284	0.0103	0.0300	0.0113	0.0302	0.5933	0.0736	0.6135	0.0736	0.7574	0.0736
Blue__mud__Bay (17) v. Mozambique (11)	1905.0446	0.0629	1e-04	0.0270	-12.8792	1.0000	0.0101	0.0320	0.0114	0.0320	0.2216	0.0010	0.2416	0.0010	0.3792	0.0010
Roper__River (9) v. Towns__River (10)	1592.7288	0.0020	1e-04	0.0090	-24.7724	0.9371	0.0101	0.0190	0.0111	0.0220	0.4263	0.0270	0.4496	0.0250	0.6141	0.0250
Papua__New__Guinea (9) v. Unknown (10)	1495.8544	0.0160	1e-04	0.0100	-24.3306	0.9920	0.0101	0.0050	0.0110	0.0050	0.4159	0.0070	0.4390	0.0070	0.6038	0.0070
Arabian__Sea (15) v. Blue__mud__Bay (17)	2173.1892	0.0080	1e-04	0.0010	-9.6558	0.9930	0.0100	0.0100	0.0109	0.0100	0.1434	0.0090	0.1590	0.0090	0.2644	0.0090
East__Alligator__River (47) v. Indonesia (4)	2259.8999	0.0060	1e-04	0.0589	-20.2203	0.7319	0.0100	0.0231	0.0107	0.0231	0.4354	0.1472	0.4579	0.1381	0.6223	0.1421
Blue__mud__Bay (17) v. East__Alligator__River (47)	2861.5864	0.0010	1e-04	0.0010	-7.3078	0.0100	0.0099	0.0010	0.0108	0.0010	0.0762	0.0010	0.0854	0.0010	0.1502	0.0010
Blue__mud__Bay (17) v. Roper__River (9)	1851.5513	0.0529	1e-04	0.0130	-14.0082	0.9910	0.0096	0.0300	0.0107	0.0290	0.2526	0.0100	0.2741	0.0100	0.4205	0.0090
Adelaide__River (18) v. Trinity__inlet (4)	1751.2904	0.0040	1e-04	0.2178	-51.7056	0.1121	0.0096	0.0440	0.0103	0.0440	0.6912	0.8218	0.7085	0.8178	0.8276	0.8178
Indonesia (4) v. Reunion (28)	1850.3730	0.0500	1e-04	0.1768	-34.5664	0.5329	0.0095	0.0675	0.0105	0.0688	0.5819	0.4579	0.6022	0.4559	0.7485	0.4579
Blue__mud__Bay (17) v. South__Alligator__River (88)	3600.8806	0.0010	1e-04	0.0010	-5.0876	0.0070	0.0094	0.0010	0.0102	0.0010	0.0493	0.0010	0.0557	0.0010	0.1001	0.0010

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
Adelaide_River (18) v. Towns_River (10)	1812.9247	0.0020	1e-04	0.0010	-14.4419	0.9780	0.0094	0.0030	0.0102	0.0030	0.2364	0.0020	0.2562	0.0020	0.3984	0.0020
Blue_mud_Bay (17) v. Clarence_River (74)	3350.6386	0.0010	1e-04	0.0010	-4.8805	0.4286	0.0093	0.0010	0.0102	0.0010	0.0491	0.0010	0.0556	0.0010	0.0998	0.0010
Blue_mud_Bay (17) v. Fitzroy_River (3)	1504.2709	0.5175	2e-04	0.1578	NA	NA	0.0093	0.1775	0.0100	0.1775	NA	NA	NA	NA	NA	NA
Blue_mud_Bay (17) v. Darwin_Coastal (13)	2023.6360	0.0210	1e-04	0.0030	-10.6158	0.9620	0.0092	0.0170	0.0100	0.0160	0.1655	0.0190	0.1827	0.0190	0.2987	0.0190
Indonesia (4) v. Roper_River (9)	1302.7152	0.1858	2e-04	0.2138	57.8007	0.4702	0.0091	0.1888	0.0104	0.1798	1.4946	0.5348	1.4562	0.5318	1.1829	0.5318
Clarence_River (74) v. Indonesia (4)	2487.5808	0.1479	1e-04	0.0180	-9.9007	0.9869	0.0090	0.0291	0.0097	0.0291	0.2703	0.0172	0.2916	0.0182	0.4423	0.0172
Arabian_Sea (15) v. Indonesia (4)	1560.3991	0.3427	1e-04	0.1019	-71.6146	0.9710	0.0090	0.0689	0.0097	0.0689	0.7619	0.0270	0.7756	0.0270	0.8726	0.0270
Blue_mud_Bay (17) v. Daly_River (49)	2911.0649	0.0010	1e-04	0.0010	-6.8504	0.1069	0.0090	0.0010	0.0098	0.0010	0.0711	0.0010	0.0799	0.0010	0.1410	0.0010
Indonesia (4) v. Sri_Lanka (12)	1402.8136	0.2088	1e-04	0.0749	1084.9211	0.1946	0.0089	0.0649	0.0097	0.0651	1.0200	0.0802	1.0187	0.0802	1.0092	0.0802
Blue_mud_Bay (17) v. Sydney_Harbour (65)	3254.5310	0.0010	1e-04	0.0010	-5.9744	0.0370	0.0089	0.0010	0.0097	0.0010	0.0596	0.0010	0.0671	0.0010	0.1196	0.0010
Mozambique (11) v. Wenlock_River (24)	2038.9295	0.0010	1e-04	0.0020	-11.4864	1.0000	0.0088	0.0010	0.0096	0.0010	0.1847	0.0010	0.2024	0.0010	0.3267	0.0010
Blue_mud_Bay (17) v. Wenlock_River (24)	2318.9034	0.0020	1e-04	0.0030	-8.5499	0.9041	0.0088	0.0020	0.0096	0.0020	0.1064	0.0030	0.1187	0.0030	0.2035	0.0030
Blue_mud_Bay (17) v. Papua_New_Guinea (9)	1764.8423	0.1229	1e-04	0.0290	-14.2905	0.9980	0.0088	0.0529	0.0095	0.0529	0.2500	0.0110	0.2709	0.0130	0.4167	0.0130
South_Alligator_River (88) v. Towns_River (10)	2897.7702	0.0010	1e-04	0.0020	-6.3324	0.6973	0.0086	0.0020	0.0092	0.0020	0.0906	0.0030	0.1010	0.0030	0.1758	0.0030
Daly_River (49) v. Towns_River (10)	2404.8295	0.0010	1e-04	0.0060	-8.9135	0.9510	0.0086	0.0010	0.0092	0.0010	0.1301	0.0010	0.1439	0.0010	0.2424	0.0010
South_Alligator_River (88) v. Trinity_inlet (4)	2956.3054	0.0100	1e-04	0.1369	-9.5168	0.0429	0.0085	0.0182	0.0091	0.0182	0.2619	0.7357	0.2834	0.6765	0.4321	0.6980
Mozambique (11) v. Towns_River (10)	1597.6281	0.0230	1e-04	0.0370	-21.6602	0.9560	0.0083	0.0240	0.0091	0.0250	0.3762	0.0360	0.3993	0.0360	0.5635	0.0360
Towns_River (10) v. Wenlock_River (24)	2004.3581	0.0040	1e-04	0.1269	-11.8097	0.9920	0.0082	0.0060	0.0089	0.0060	0.1877	0.0030	0.2054	0.0030	0.3310	0.0030
South_Africa (21) v. Trinity_inlet (4)	1798.3932	0.0050	1e-04	0.1029	-38.5483	0.0937	0.0081	0.0391	0.0087	0.0391	0.6192	0.8056	0.6393	0.7946	0.7772	0.7946
Arabian_Sea (15) v. Towns_River (10)	1835.2962	0.0070	1e-04	0.0380	-14.0075	1.0000	0.0080	0.0040	0.0088	0.0040	0.2433	0.0010	0.2638	0.0010	0.4079	0.0010
Adelaide_River (18) v. Blue_mud_Bay (17)	2114.9291	0.0090	1e-04	0.0110	-9.8243	0.9780	0.0077	0.0160	0.0084	0.0160	0.1332	0.0160	0.1476	0.0160	0.2478	0.0160
South_Africa (21) v. Towns_River (10)	1892.1145	0.0010	1e-04	0.0050	-12.9725	0.9950	0.0076	0.0020	0.0082	0.0020	0.2085	0.0010	0.2272	0.0010	0.3605	0.0010
Sydney_Harbour (65) v. Trinity_inlet (4)	2594.0254	0.0010	1e-04	0.0559	-12.7534	0.0130	0.0075	0.0330	0.0080	0.0330	0.3228	0.8967	0.3460	0.8746	0.5056	0.8816
Fitzroy_River (3) v. Thailand (4)	989.0411	0.1029	2e-04	0.1109	NA	NA	0.0074	0.1219	0.0080	0.1219	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Papua_New_Guinea (9)	1197.1304	0.2627	1e-04	0.3566	NA	NA	0.0074	0.1320	NA	NA	NA	NA	NA	NA	NA	NA
Clarence_River (74) v. Towns_River (10)	2623.8601	0.0220	1e-04	0.0020	-6.2361	1.0000	0.0074	0.0030	0.0080	0.0030	0.0906	0.0010	0.1012	0.0010	0.1759	0.0010
Papua_New_Guinea (9) v. Reunion (28)	1927.2220	0.0240	1e-04	0.0200	-12.5260	0.7762	0.0073	0.0210	0.0080	0.0190	0.2013	0.1499	0.2194	0.1419	0.3502	0.1429
Sri_Lanka (12) v. Trinity_inlet (4)	1503.1102	0.0330	1e-04	0.0569	-227.3737	0.4076	0.0072	0.0589	0.0078	0.0589	0.9149	0.5793	0.9205	0.5783	0.9585	0.5783
Darwin_Coastal (13) v. Reunion (28)	2217.5237	0.0010	1e-04	0.0160	-9.6755	0.0689	0.0072	0.0040	0.0080	0.0040	0.1301	0.0779	0.1443	0.0579	0.2428	0.0619
East_Alligator_River (47) v. Towns_River (10)	2304.7931	0.0010	1e-04	0.0230	-9.6023	0.5854	0.0071	0.0020	0.0077	0.0020	0.1381	0.0020	0.1523	0.0020	0.2551	0.0020
Blue_mud_Bay (17) v. Unknown (10)	1823.4100	0.0709	1e-04	0.0180	-13.0600	0.9890	0.0071	0.0599	0.0077	0.0599	0.2220	0.0200	0.2420	0.0200	0.3797	0.0200
Indonesia (4) v. South_Africa (21)	1655.1729	0.1439	1e-04	0.0789	-47.8486	0.9358	0.0070	0.0671	0.0076	0.0672	0.6669	0.0602	0.6844	0.0602	0.8107	0.0602
Reunion (28) v. Roper_River (9)	2017.2914	0.0090	1e-04	0.0040	-12.2881	0.5055	0.0069	0.0210	0.0076	0.0210	0.2037	0.0779	0.2224	0.0739	0.3540	0.0759
Reunion (28) v. South_Alligator_River (88)	3161.5912	0.0010	0e+00	0.0010	-5.0515	0.6953	0.0069	0.0010	0.0075	0.0010	0.0339	0.0010	0.0383	0.0010	0.0699	0.0010
Darwin_Coastal (13) v. Indonesia (4)	1425.2385	0.3616	2e-04	0.0310	-193.2944	0.9609	0.0069	0.1139	0.0075	0.1149	0.8993	0.0431	0.9056	0.0431	0.9503	0.0431
Sydney_Harbour (65) v. Towns_River (10)	2467.2546	0.0010	1e-04	0.0010	-7.8019	0.8841	0.0069	0.0010	0.0074	0.0010	0.1114	0.0020	0.1237	0.0020	0.2115	0.0020
Seychelles (36) v. Towns_River (10)	2141.3092	0.0010	1e-04	0.0030	-10.6753	0.8951	0.0068	0.0040	0.0073	0.0040	0.1580	0.0070	0.1737	0.0070	0.2864	0.0070
East_Alligator_River (47) v. Trinity_inlet (4)	2454.4429	0.0010	1e-04	0.2258	-18.1408	0.0161	0.0067	0.0440	0.0072	0.0440	0.4090	0.9335	0.4326	0.9215	0.5973	0.9245
Arabian_Sea (15) v. Papua_New_Guinea (9)	1716.2144	0.0999	1e-04	0.0739	-15.0745	1.0000	0.0066	0.0080	0.0072	0.0080	0.2678	0.0030	0.2890	0.0030	0.4392	0.0030
Daly_River (49) v. Trinity_inlet (4)	2351.4533	0.0020	1e-04	0.0829	-16.3546	0.0817	0.0066	0.0480	0.0070	0.0480	0.3846	0.7399	0.4085	0.7177	0.5728	0.7228
Mozambique (11) v. Reunion (28)	2001.5428	0.0100	1e-04	0.0330	-11.6557	0.9820	0.0063	0.0140	0.0069	0.0140	0.1798	0.0020	0.1970	0.0020	0.3194	0.0020
East_Alligator_River (47) v. Mozambique (11)	2275.8266	0.0020	1e-04	0.0200	-9.3675	0.8931	0.0062	0.0040	0.0068	0.0040	0.1348	0.0010	0.1489	0.0010	0.2500	0.0010
Arabian_Sea (15) v. Trinity_inlet (4)	1632.4740	0.0859	1e-04	0.3227	-53.2932	0.4764	0.0061	0.0739	0.0066	0.0739	0.7051	0.4462	0.7221	0.4352	0.8370	0.4372
Reunion (28) v. Sydney_Harbour (65)	2891.3000	0.0010	0e+00	0.0010	-5.8632	0.9770	0.0060	0.0010	0.0066	0.0010	0.0411	0.0010	0.0464	0.0010	0.0840	0.0010
Sri_Lanka (12) v. Towns_River (10)	1608.1513	0.0539	1e-04	0.0669	-17.9931	0.9940	0.0060	0.0519	0.0066	0.0519	0.3108	0.0140	0.3330	0.0150	0.4911	0.0140
Mozambique (11) v. South_Alligator_River (88)	2752.7983	0.0040	1e-04	0.0170	-6.2009	0.7053	0.0060	0.0020	0.0066	0.0020	0.0874	0.0010	0.0976	0.0010	0.1702	0.0010
Seychelles (36) v. Trinity_inlet (4)	2212.2961	0.0020	1e-04	0.1578	-22.2859	0.0101	0.0060	0.0991	0.0064	0.0991	0.4651	0.9576	0.4886	0.9485	0.6510	0.9505
East_Alligator_River (47) v. Reunion (28)	2652.4144	0.0010	0e+00	0.0010	-6.8905	0.7512	0.0058	0.0010	0.0063	0.0010	0.0520	0.0010	0.0584	0.0010	0.1050	0.0010
Clarence_River (74) v. Reunion (28)	2970.7179	0.0010	0e+00	0.0010	-4.8433	1.0000	0.0058	0.0010	0.0063	0.0010	0.0335	0.0010	0.0379	0.0010	0.0690	0.0010
Blue_mud_Bay (17) v. Sri_Lanka (12)	1915.8700	0.0649	1e-04	0.0150	-11.3891	0.9590	0.0057	0.0729	0.0062	0.0749	0.1798	0.0629	0.1975	0.0649	0.3198	0.0639
Towns_River (10) v. Unknown (10)	1526.0653	0.0480	1e-04	0.0190	-21.7538	0.9261	0.0056	0.0989	0.0061	0.0969	0.3753	0.0939	0.3984	0.0959	0.5625	0.0959
Trinity_inlet (4) v. Wenlock_River (24)	1904.5321	0.0280	1e-04	0.3397	-29.6457	0.1071	0.0055	0.1031	0.0060	0.1048	0.5499	0.7970	0.5722	0.7788	0.7240	0.7848
Papua_New_Guinea (9) v. Sri_Lanka (12)	1525.0491	0.1588	1e-04	0.2418	-19.5709	0.9830	0.0055	0.0340	0.0059	0.0340	0.3410	0.0120	0.3636	0.0120	0.5255	0.0120

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
East_Alligator_River (47) v. Fitzroy_River (3)	1989.2696	0.1598	1e-04	0.1119	NA	NA	0.0054	0.1721	0.0058	0.1711	NA	NA	NA	NA	NA	NA
Reunion (28) v. Unknown (10)	1995.5362	0.0070	1e-04	0.0110	-11.6580	0.3177	0.0054	0.0350	0.0059	0.0370	0.1785	0.2308	0.1956	0.2098	0.3175	0.2158
Reunion (28) v. Wenlock_River (24)	2317.4735	0.0010	1e-04	0.0010	-8.0692	0.9760	0.0053	0.0010	0.0058	0.0010	0.0790	0.0010	0.0884	0.0010	0.1552	0.0010
Papua_New_Guinea (9) v. Seychelles (36)	1930.8100	0.0450	1e-04	0.1219	-11.4056	0.8921	0.0053	0.0140	0.0059	0.0140	0.1769	0.0310	0.1937	0.0320	0.3149	0.0320
Clarence_River (74) v. Papua_New_Guinea (9)	2326.9965	0.5385	1e-04	0.0170	-6.5637	0.9980	0.0052	0.0110	0.0056	0.0110	0.1010	0.0010	0.1125	0.0010	0.1940	0.0010
Thailand (4) v. Towns_River (10)	1371.3016	0.0480	1e-04	0.3187	123.5569	0.0511	0.0052	0.2523	0.0058	0.2523	1.1964	0.9559	1.1823	0.9559	1.0830	0.9559
Clarence_River (74) v. Mozambique (11)	2553.2382	0.0629	1e-04	0.0090	-6.0722	1.0000	0.0052	0.0040	0.0057	0.0040	0.0872	0.0010	0.0975	0.0010	0.1699	0.0010
Arabian_Sea (15) v. Darwin_Coastal (13)	1910.4886	0.0050	0e+00	0.5145	-11.1126	0.9780	0.0052	0.0050	0.0056	0.0050	0.1778	0.0060	0.1955	0.0050	0.3169	0.0050
Mozambique (11) v. Seychelles (36)	2100.4591	0.0010	1e-04	0.0010	-10.5278	0.9920	0.0051	0.0030	0.0056	0.0030	0.1556	0.0010	0.1713	0.0010	0.2829	0.0010
Adelaide_River (18) v. Papua_New_Guinea (9)	1633.3815	0.1299	1e-04	0.0210	-15.5144	0.9151	0.0051	0.0320	0.0055	0.0320	0.2595	0.0290	0.2800	0.0280	0.4283	0.0280
Darwin_Coastal (13) v. Mozambique (11)	1670.2078	0.0739	1e-04	0.0330	-15.5169	0.9990	0.0050	0.0320	0.0057	0.0300	0.2737	0.0010	0.2955	0.0010	0.4469	0.0010
Daly_River (49) v. Mozambique (11)	2340.9063	0.0010	1e-04	0.0300	-8.6633	0.9960	0.0049	0.0010	0.0054	0.0010	0.1254	0.0010	0.1389	0.0010	0.2348	0.0010
Adelaide_River (18) v. Reunion (28)	2121.8280	0.0020	0e+00	0.0080	-9.2177	0.7982	0.0049	0.0040	0.0054	0.0040	0.1025	0.0220	0.1140	0.0200	0.1964	0.0200
Darwin_Coastal (13) v. Fitzroy_River (3)	1348.0815	0.6484	2e-04	0.1099	NA	NA	0.0047	0.2063	0.0051	0.2063	NA	NA	NA	NA	NA	NA
Trinity_inlet (4) v. Unknown (10)	1339.6359	0.0210	1e-04	0.3457	161.3117	0.0524	0.0045	0.1497	0.0049	0.1503	1.1420	0.9568	1.1318	0.9568	1.0615	0.9568
Reunion (28) v. Seychelles (36)	2332.0104	0.0010	0e+00	0.0080	-7.5897	0.9970	0.0045	0.0010	0.0049	0.0010	0.0621	0.0010	0.0697	0.0010	0.1240	0.0010
Fitzroy_River (3) v. Sri_Lanka (12)	1355.5475	0.3746	1e-04	0.2877	NA	NA	0.0044	0.2205	0.0048	0.2247	NA	NA	NA	NA	NA	NA
Clarence_River (74) v. Trinity_inlet (4)	2669.1115	0.0260	1e-04	0.2018	-9.2359	0.2214	0.0043	0.1263	0.0046	0.1273	0.2559	0.4541	0.2776	0.4255	0.4248	0.4378
Clarence_River (74) v. Roper_River (9)	2508.0552	0.1179	1e-04	0.0050	-6.3572	0.8791	0.0042	0.0320	0.0045	0.0320	0.1012	0.0020	0.1130	0.0020	0.1945	0.0020
Arabian_Sea (15) v. Mozambique (11)	1795.4018	0.0869	1e-04	0.2717	-13.4631	1.0000	0.0041	0.0290	0.0047	0.0250	0.2345	0.0010	0.2548	0.0010	0.3964	0.0010
Daly_River (49) v. Reunion (28)	2558.8318	0.0010	0e+00	0.0010	-6.5805	0.9890	0.0040	0.0010	0.0044	0.0010	0.0485	0.0010	0.0546	0.0010	0.0983	0.0010
Adelaide_River (18) v. Darwin_Coastal (13)	1862.0462	0.0120	1e-04	0.1179	-11.3164	0.3497	0.0040	0.0240	0.0044	0.0240	0.1680	0.0659	0.1847	0.0619	0.3020	0.0639
Darwin_Coastal (13) v. Papua_New_Guinea (9)	1550.2356	0.3237	1e-04	0.5195	-17.3639	0.9980	0.0040	0.0729	0.0044	0.0729	0.3074	0.0100	0.3297	0.0120	0.4873	0.0110
Roper_River (9) v. South_Alligator_River (88)	2717.7623	0.0140	1e-04	0.0040	-6.4670	0.1588	0.0039	0.0400	0.0043	0.0400	0.1007	0.0120	0.1122	0.0090	0.1934	0.0100
Sydney_Harbour (65) v. Wenlock_River (24)	2707.1511	0.0010	0e+00	0.0010	-5.8688	0.3287	0.0039	0.0010	0.0042	0.0010	0.0440	0.0010	0.0497	0.0010	0.0898	0.0010
Blue_mud_Bay (17) v. Thailand (4)	1612.2558	0.2567	1e-04	0.1259	-43.0209	0.3513	0.0037	0.3029	0.0039	0.3039	0.6487	0.6487	0.6678	0.6487	0.7985	0.6477
Arabian_Sea (15) v. South_Alligator_River (88)	3346.1117	0.0010	0e+00	0.0110	-5.1203	0.0120	0.0037	0.0020	0.0040	0.0020	0.0516	0.0779	0.0581	0.0579	0.1043	0.0679
Adelaide_River (18) v. Roper_River (9)	1736.7142	0.0190	1e-04	0.1049	-15.0451	0.7932	0.0037	0.0779	0.0040	0.0769	0.2589	0.0330	0.2798	0.0290	0.4279	0.0290
Reunion (28) v. Sri_Lanka (12)	2078.6819	0.0060	1e-04	0.1169	-10.3263	0.1908	0.0036	0.0729	0.0039	0.0729	0.1420	0.4575	0.1568	0.4416	0.2617	0.4525
Reunion (28) v. South_Africa (21)	2165.2760	0.0050	0e+00	0.0030	-8.5336	0.7033	0.0036	0.0170	0.0039	0.0180	0.0878	0.0310	0.0980	0.0280	0.1708	0.0300
East_Alligator_River (47) v. Papua_New_Guinea (9)	2053.2167	0.0889	1e-04	0.0719	-10.1188	0.5854	0.0036	0.0480	0.0039	0.0480	0.1528	0.0839	0.1679	0.0779	0.2782	0.0809
Darwin_Coastal (13) v. East_Alligator_River (47)	2477.1204	0.0010	0e+00	0.0799	-7.9754	0.0020	0.0036	0.0080	0.0039	0.0080	0.0952	0.4356	0.1062	0.3427	0.1838	0.3846
Papua_New_Guinea (9) v. Sydney_Harbour (65)	2113.4285	0.5914	1e-04	0.0579	-8.3339	0.9191	0.0036	0.0280	0.0039	0.0290	0.1251	0.0330	0.1383	0.0330	0.2341	0.0330
Mozambique (11) v. Sydney_Harbour (65)	2433.8819	0.0030	1e-04	0.0260	-7.5988	0.9481	0.0035	0.0150	0.0038	0.0150	0.1068	0.0010	0.1187	0.0010	0.2037	0.0010
Mozambique (11) v. Roper_River (9)	1555.3710	0.0460	1e-04	0.0490	-23.2409	0.4456	0.0035	0.1279	0.0039	0.1309	0.4092	0.4595	0.4327	0.4486	0.5974	0.4515
Darwin_Coastal (13) v. Towns_River (10)	1645.6191	0.0939	1e-04	0.3626	-15.9843	0.9850	0.0035	0.1658	0.0038	0.1658	0.2784	0.0410	0.3001	0.0450	0.4525	0.0430
East_Alligator_River (47) v. Roper_River (9)	2200.2523	0.0040	1e-04	0.0739	-9.9052	0.1708	0.0034	0.0539	0.0037	0.0519	0.1549	0.0430	0.1705	0.0340	0.2817	0.0380
Daly_River (49) v. Unknown (10)	2182.7564	0.0220	1e-04	0.0020	-8.8620	0.5774	0.0033	0.0270	0.0036	0.0270	0.1269	0.0160	0.1405	0.0150	0.2373	0.0160
Mozambique (11) v. Sri_Lanka (12)	1608.2682	0.1489	1e-04	0.1938	-17.2515	0.9970	0.0033	0.1189	0.0036	0.1219	0.3013	0.0030	0.3235	0.0030	0.4802	0.0030
Mozambique (11) v. Unknown (10)	1573.3394	0.0240	1e-04	0.0160	-20.5176	0.8462	0.0033	0.1129	0.0036	0.1179	0.3614	0.0909	0.3846	0.0889	0.5479	0.0899
Fitzroy_River (3) v. Trinity_inlet (4)	957.9348	0.5135	2e-04	0.1219	NA	NA	0.0031	0.4070	0.0034	0.4070	NA	NA	NA	NA	NA	NA
Darwin_Coastal (13) v. Unknown (10)	1631.5012	0.0659	1e-04	0.0280	-15.4535	0.9820	0.0030	0.0879	0.0033	0.0859	0.2715	0.0190	0.2932	0.0200	0.4442	0.0190
Mozambique (11) v. Trinity_inlet (4)	1410.4190	0.0619	2e-04	0.1439	174.0446	0.0260	0.0030	0.2226	0.0032	0.2270	1.1295	0.9812	1.1202	0.9812	1.0564	0.9812
Papua_New_Guinea (9) v. South_Alligator_River (88)	2486.1042	0.1788	0e+00	0.1938	-6.6420	0.8042	0.0030	0.0759	0.0032	0.0759	0.0993	0.0589	0.1103	0.0569	0.1906	0.0569
Seychelles (36) v. Unknown (10)	1986.4551	0.0110	1e-04	0.0340	-10.6108	0.3626	0.0029	0.0659	0.0032	0.0659	0.1552	0.1548	0.1709	0.1479	0.2823	0.1508
Roper_River (9) v. Wenlock_River (24)	1824.1022	0.1688	1e-04	0.1548	-12.4579	0.8861	0.0029	0.1069	0.0031	0.1089	0.2101	0.0270	0.2292	0.0270	0.3630	0.0260
Clarence_River (74) v. Seychelles (36)	2842.1582	0.0010	0e+00	0.0010	-4.5702	1.0000	0.0028	0.0010	0.0031	0.0010	0.0255	0.0010	0.0290	0.0010	0.0532	0.0010
Daly_River (49) v. Roper_River (9)	2196.8381	0.0170	1e-04	0.0140	-9.2527	0.5425	0.0028	0.0739	0.0030	0.0729	0.1453	0.0250	0.1604	0.0250	0.2669	0.0240
Darwin_Coastal (13) v. Trinity_inlet (4)	1482.6685	0.1758	1e-04	0.2757	-97.0409	0.3746	0.0027	0.2527	0.0029	0.2527	0.8177	0.6042	0.8291	0.6012	0.9060	0.6012
Roper_River (9) v. Unknown (10)	1497.2012	0.0210	1e-04	0.0030	-23.5918	0.7962	0.0027	0.1618	0.0029	0.1638	0.4115	0.1628	0.4350	0.1618	0.5997	0.1618
Roper_River (9) v. Sri_Lanka (12)	1577.5046	0.0509	1e-04	0.0899	-19.0935	0.9311	0.0027	0.1439	0.0029	0.1499	0.3405	0.0330	0.3635	0.0330	0.5252	0.0330
Papua_New_Guinea (9) v. Wenlock_River (24)	1756.5815	0.4076	1e-04	0.1928	-12.6433	0.9850	0.0026	0.1479	0.0029	0.1479	0.2068	0.0200	0.2253	0.0220	0.3580	0.0200
Papua_New_Guinea (9) v. Roper_River (9)	1390.0644	0.2827	1e-04	0.4116	-28.3085	0.7512	0.0026	0.2358	0.0029	0.2308	0.4677	0.2198	0.4904	0.2178	0.6528	0.2178

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.va
Seychelles (36) v. Wenlock_River (24)	2314.3078	0.0010	0e+00	0.0140	-7.4752	0.3876	0.0026	0.0080	0.0028	0.0080	0.0651	0.0210	0.0731	0.0200	0.1298	0.0200
Unknown (10) v. Wenlock_River (24)	1812.7937	0.1528	1e-04	0.0270	-11.7854	0.8362	0.0026	0.0779	0.0028	0.0799	0.1848	0.0280	0.2024	0.0280	0.3268	0.0290
Seychelles (36) v. Sydney_Harbour (65)	2677.3422	0.0010	0e+00	0.0020	-5.6200	0.9151	0.0026	0.0010	0.0028	0.0010	0.0321	0.0010	0.0363	0.0010	0.0662	0.0010
Arabian_Sea (15) v. East_Alligator_River (47)	2544.4612	0.0010	0e+00	0.4655	-7.4604	0.0070	0.0025	0.0240	0.0027	0.0240	0.0803	0.4735	0.0898	0.3936	0.1575	0.4276
South_Africa (21) v. Unknown (10)	1709.9569	0.2907	1e-04	0.2188	-12.8478	0.7812	0.0024	0.1079	0.0026	0.1079	0.2046	0.0509	0.2232	0.0480	0.3551	0.0500
Thailand (4) v. Trinity_inlet (4)	1056.3377	0.2228	1e-04	0.4955	15.2219	0.7152	0.0024	0.3327	0.0026	0.3157	9.5347	0.2690	8.5308	0.2690	1.7149	0.2384
Darwin_Coastal (13) v. Sydney_Harbour (65)	2601.2776	0.0010	0e+00	0.3257	-6.6880	0.0050	0.0023	0.0350	0.0025	0.0350	0.0765	0.5445	0.0858	0.4835	0.1508	0.5005
Darwin_Coastal (13) v. Sri_Lanka (12)	1708.2605	0.1049	1e-04	0.1808	-13.3115	0.8821	0.0023	0.1578	0.0025	0.1578	0.2228	0.1499	0.2427	0.1499	0.3807	0.1499
Adelaide_River (18) v. Unknown (10)	1608.8782	0.3317	1e-04	0.0500	-14.2537	0.6294	0.0023	0.1399	0.0025	0.1389	0.2308	0.1019	0.2506	0.0909	0.3911	0.0929
Daly_River (49) v. Darwin_Coastal (13)	2432.8262	0.0010	0e+00	0.3187	-7.5514	0.0400	0.0023	0.0509	0.0024	0.0509	0.0895	0.3886	0.1001	0.3447	0.1741	0.3636
Darwin_Coastal (13) v. South_Alligator_River (88)	3020.1834	0.0010	0e+00	0.0689	-5.4505	0.0070	0.0022	0.0460	0.0024	0.0460	0.0608	0.5495	0.0683	0.4705	0.1217	0.5005
Darwin_Coastal (13) v. Seychelles (36)	2232.0110	0.0010	0e+00	0.1778	-8.7589	0.0220	0.0022	0.0719	0.0024	0.0709	0.1092	0.6114	0.1215	0.5495	0.2080	0.5774
Papua_New_Guinea (9) v. South_Africa (21)	1692.4121	0.3646	1e-04	0.0959	-13.8424	0.9720	0.0022	0.1778	0.0024	0.1778	0.2283	0.0410	0.2477	0.0400	0.3876	0.0400
Clarence_River (74) v. South_Africa (21)	2637.0514	0.0330	0e+00	0.0140	-5.0636	0.9491	0.0022	0.0110	0.0024	0.0110	0.0401	0.0050	0.0453	0.0050	0.0821	0.0050
Roper_River (9) v. Sydney_Harbour (65)	2381.0609	0.0120	1e-04	0.0270	-7.9318	0.3576	0.0021	0.1239	0.0023	0.1259	0.1231	0.0420	0.1365	0.0370	0.2312	0.0380
Clarence_River (74) v. Sri_Lanka (12)	2584.2490	0.0599	0e+00	0.0509	-5.7213	0.8621	0.0021	0.0769	0.0023	0.0769	0.0690	0.0759	0.0776	0.0819	0.1372	0.0799
Arabian_Sea (15) v. Sydney_Harbour (65)	2905.2078	0.0010	0e+00	0.0320	-6.1908	0.0470	0.0021	0.0350	0.0023	0.0350	0.0636	0.3806	0.0715	0.3407	0.1271	0.3616
Adelaide_River (18) v. Wenlock_River (24)	1976.3190	0.0609	0e+00	0.0370	-9.2034	0.9471	0.0021	0.0689	0.0023	0.0689	0.1065	0.0480	0.1184	0.0480	0.2033	0.0490
Fitzroy_River (3) v. South_Alligator_River (88)	2156.0229	0.7113	1e-04	0.2857	NA	NA	0.0021	0.3323	NA	NA	NA	NA	NA	NA	NA	NA
Daly_River (49) v. Sri_Lanka (12)	2290.0326	0.0070	0e+00	0.1129	-8.0934	0.4046	0.0021	0.0879	0.0022	0.0879	0.1006	0.2408	0.1120	0.2218	0.1931	0.2288
Arabian_Sea (15) v. Reunion (28)	2269.4690	0.0010	0e+00	0.0789	-8.7636	0.0380	0.0020	0.1409	0.0022	0.1389	0.1073	0.5714	0.1194	0.5365	0.2047	0.5524
Arabian_Sea (15) v. Clarence_River (74)	3038.3218	0.0010	0e+00	0.4965	-5.0190	0.4326	0.0020	0.0569	0.0022	0.0569	0.0511	0.1099	0.0578	0.1059	0.1036	0.1079
Seychelles (36) v. South_Alligator_River (88)	2819.2585	0.0010	0e+00	0.0010	-4.7139	0.4575	0.0020	0.0010	0.0022	0.0010	0.0245	0.0010	0.0278	0.0010	0.0511	0.0010
Roper_River (9) v. South_Africa (21)	1789.5620	0.0400	1e-04	0.2418	-13.6047	0.8551	0.0019	0.1958	0.0021	0.1998	0.2309	0.0490	0.2508	0.0480	0.3913	0.0480
South_Africa (21) v. Wenlock_River (24)	2050.3229	0.0330	0e+00	0.0370	-8.5770	0.9201	0.0019	0.0679	0.0021	0.0679	0.0926	0.0659	0.1033	0.0659	0.1793	0.0659
Arabian_Sea (15) v. Daly_River (49)	2622.2411	0.0010	0e+00	0.2547	-6.9893	0.0769	0.0019	0.0699	0.0020	0.0699	0.0749	0.3407	0.0840	0.2857	0.1478	0.3027
Adelaide_River (18) v. Mozambique (11)	1707.2964	0.1618	1e-04	0.3506	-13.9099	0.9970	0.0018	0.2008	0.0021	0.1948	0.2267	0.0010	0.2462	0.0010	0.3855	0.0010
Roper_River (9) v. Seychelles (36)	1987.1160	0.0260	1e-04	0.2118	-11.1310	0.4176	0.0018	0.2278	0.0020	0.2298	0.1767	0.1189	0.1938	0.1149	0.3149	0.1159
Clarence_River (74) v. Wenlock_River (24)	2748.2030	0.0090	0e+00	0.0060	-4.7666	0.8991	0.0018	0.0160	0.0020	0.0160	0.0342	0.0080	0.0388	0.0080	0.0706	0.0080
Daly_River (49) v. Fitzroy_River (3)	2019.8560	0.2847	1e-04	0.3556	NA	NA	0.0018	0.3371	0.0019	0.3371	NA	NA	NA	NA	NA	NA
Daly_River (49) v. Wenlock_River (24)	2405.4276	0.0030	0e+00	0.1479	-6.5842	0.3816	0.0018	0.0230	0.0020	0.0230	0.0517	0.0300	0.0582	0.0300	0.1045	0.0290
Adelaide_River (18) v. Seychelles (36)	2109.7935	0.0110	0e+00	0.0440	-8.5416	0.5664	0.0018	0.0679	0.0020	0.0679	0.0864	0.1379	0.0964	0.1359	0.1682	0.1389
South_Alligator_River (88) v. Wenlock_River (24)	2854.0892	0.0010	0e+00	0.0559	-4.9225	0.0430	0.0018	0.0190	0.0019	0.0190	0.0339	0.0649	0.0384	0.0539	0.0699	0.0589
Arabian_Sea (15) v. Unknown (10)	1714.4087	0.1798	1e-04	0.0659	-13.6519	0.9341	0.0018	0.1808	0.0019	0.1808	0.2356	0.0450	0.2559	0.0450	0.3978	0.0450
Adelaide_River (18) v. Arabian_Sea (15)	1898.0038	0.0500	0e+00	0.4765	-10.3121	0.3177	0.0017	0.1489	0.0019	0.1479	0.1437	0.2378	0.1586	0.2238	0.2643	0.2328
Sri_Lanka (12) v. Sydney_Harbour (65)	2404.9826	0.0320	0e+00	0.0679	-7.1263	0.2767	0.0017	0.1159	0.0019	0.1159	0.0856	0.5035	0.0957	0.4865	0.1670	0.4975
Arabian_Sea (15) v. Roper_River (9)	1686.4100	0.2348	1e-04	0.2547	-14.9567	0.9491	0.0017	0.2398	0.0019	0.2368	0.2697	0.0330	0.2914	0.0300	0.4419	0.0310
South_Alligator_River (88) v. Sydney_Harbour (65)	3078.4199	0.0010	0e+00	0.0020	-3.8867	0.6064	0.0017	0.0010	0.0018	0.0010	0.0142	0.0010	0.0162	0.0010	0.0300	0.0010
Clarence_River (74) v. Darwin_Coastal (13)	2647.7639	0.0190	0e+00	0.1628	-5.4426	0.2697	0.0017	0.1129	0.0018	0.1129	0.0618	0.2298	0.0697	0.2188	0.1238	0.2228
East_Alligator_River (47) v. Wenlock_River (24)	2346.9028	0.0020	0e+00	0.0879	-6.9942	0.0120	0.0017	0.0260	0.0018	0.0260	0.0552	0.1109	0.0620	0.0979	0.1111	0.1069
Daly_River (49) v. Papua_New_Guinea (9)	2036.7218	0.3197	1e-04	0.1908	-9.4690	0.9291	0.0016	0.2008	0.0017	0.1998	0.1432	0.0549	0.1578	0.0559	0.2633	0.0559
Adelaide_River (18) v. South_Africa (21)	1879.9233	0.1029	0e+00	0.1249	-9.9455	0.8831	0.0016	0.1359	0.0017	0.1359	0.1199	0.1239	0.1329	0.1229	0.2257	0.1229
Clarence_River (74) v. South_Alligator_River (88)	3314.7268	0.0010	0e+00	0.0010	-3.1910	0.0969	0.0016	0.0010	0.0017	0.0010	0.0110	0.0010	0.0125	0.0010	0.0233	0.0010
Sri_Lanka (12) v. Wenlock_River (24)	1903.0051	0.1628	0e+00	0.5215	-10.3649	0.6304	0.0015	0.1858	0.0017	0.1858	0.1472	0.2777	0.1624	0.2717	0.2699	0.2727
South_Africa (21) v. Sydney_Harbour (65)	2507.1685	0.0040	0e+00	0.0699	-6.1389	0.3097	0.0015	0.0519	0.0016	0.0519	0.0490	0.1399	0.0552	0.1349	0.0994	0.1369
Sri_Lanka (12) v. Unknown (10)	1585.8206	0.0509	1e-04	0.0260	-17.1253	0.9001	0.0015	0.2248	0.0016	0.2238	0.2984	0.0959	0.3205	0.0969	0.4767	0.0959
Mozambique (11) v. South_Africa (21)	1765.9109	0.2607	0e+00	0.6713	-12.6116	0.9980	0.0015	0.1968	0.0016	0.2028	0.2012	0.0010	0.2197	0.0010	0.3504	0.0010
South_Alligator_River (88) v. Unknown (10)	2469.8689	0.1908	1e-04	0.0190	-6.3938	0.2088	0.0014	0.1758	0.0015	0.1758	0.0879	0.1908	0.0981	0.1708	0.1710	0.1798
Arabian_Sea (15) v. South_Africa (21)	2004.8732	0.0100	0e+00	0.3047	-9.5733	0.2667	0.0013	0.1838	0.0014	0.1828	0.1269	0.3077	0.1407	0.2937	0.2375	0.2987
Daly_River (49) v. Seychelles (36)	2423.7529	0.0030	0e+00	0.0010	-6.2612	0.9261	0.0013	0.0300	0.0014	0.0300	0.0386	0.0210	0.0435	0.0220	0.0791	0.0220
Darwin_Coastal (13) v. Wenlock_River (24)	1943.7442	0.1039	1e-04	0.0380	-9.6767	0.1798	0.0013	0.1978	0.0014	0.1978	0.1328	0.4356	0.1472	0.4166	0.2472	0.4236
Clarence_River (74) v. Unknown (10)	2399.8405	0.3956	0e+00	0.1109	-6.1173	0.9371	0.0013	0.2008	0.0014	0.2008	0.0860	0.0280	0.0962	0.0280	0.1678	0.0280
Clarence_River (74) v. Daly_River (49)	2752.4200	0.0260	0e+00	0.0150	-4.1806	1.0000	0.0012	0.0130	0.0012	0.0130	0.0187	0.0090	0.0213	0.0090	0.0392	0.0090

Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
Daly_River (49) v. South_Alligator_River (88)	2810.8610	0.0030	0e+00	0.0150	-4.3444	0.1948	0.0011	0.0110	0.0012	0.0110	0.0182	0.0160	0.0206	0.0140	0.0382	0.0140
Clarence_River (74) v. Sydney_Harbour (65)	2878.2925	0.0060	0e+00	0.3536	-3.8645	1.0000	0.0011	0.0080	0.0012	0.0080	0.0149	0.0070	0.0170	0.0070	0.0315	0.0070
East_Alligator_River (47) v. Seychelles (36)	2325.5770	0.0100	0e+00	0.1009	-6.6050	0.2208	0.0011	0.0529	0.0012	0.0529	0.0411	0.0569	0.0463	0.0549	0.0839	0.0559
East_Alligator_River (47) v. South_Africa (21)	2308.1099	0.0040	0e+00	0.3487	-7.2438	0.0230	0.0011	0.1039	0.0012	0.1039	0.0617	0.3816	0.0692	0.3467	0.1233	0.3596
Adelaide_River (18) v. Clarence_River (74)	2394.5540	0.5914	0e+00	0.0160	-5.3691	0.9880	0.0011	0.1379	0.0012	0.1379	0.0469	0.0430	0.0529	0.0509	0.0953	0.0460
Adelaide_River (18) v. East_Alligator_River (47)	2166.7993	0.0450	0e+00	0.1788	-7.8315	0.1748	0.0011	0.1558	0.0012	0.1558	0.0734	0.3257	0.0821	0.2977	0.1449	0.3107
Adelaide_River (18) v. South_Alligator_River (88)	2539.1492	0.1459	0e+00	0.3786	-5.5005	0.3846	0.0010	0.1718	0.0011	0.1718	0.0465	0.2607	0.0523	0.2498	0.0945	0.2527
Clarence_River (74) v. East_Alligator_River (47)	2713.2285	0.0330	0e+00	0.0010	-4.3753	1.0000	0.0010	0.0310	0.0010	0.0310	0.0199	0.0150	0.0226	0.0150	0.0416	0.0150
Daly_River (49) v. Sydney_Harbour (65)	2589.7394	0.0160	0e+00	0.0050	-5.0120	0.7043	0.0010	0.0240	0.0010	0.0230	0.0234	0.0320	0.0265	0.0320	0.0487	0.0320
Fitzroy_River (3) v. Reunion (28)	1669.1039	0.4336	1e-04	0.4366	NA	NA	0.0008	0.4078	NA	NA	NA	NA	NA	NA	NA	NA
Seychelles (36) v. Thailand (4)	1904.6806	0.0559	1e-04	0.1548	-23.3446	0.0151	0.0008	0.4270	0.0009	0.4270	0.4708	0.9899	0.4938	0.9899	0.6558	0.9899
South_Alligator_River (88) v. Sri_Lanka (12)	2671.5402	0.0400	0e+00	0.2158	-5.8582	0.1209	0.0008	0.2877	0.0008	0.2877	0.0684	0.6833	0.0766	0.6553	0.1357	0.6713
Arabian_Sea (15) v. Seychelles (36)	2295.8547	0.0010	0e+00	0.2717	-8.1978	0.0330	0.0008	0.2747	0.0008	0.2747	0.0928	0.7572	0.1036	0.7303	0.1797	0.7393
Fitzroy_River (3) v. Sydney_Harbour (65)	2180.2845	0.2917	1e-04	0.2547	NA	NA	0.0007	0.4063	NA	NA	NA	NA	NA	NA	NA	NA
Adelaide_River (18) v. Sri_Lanka (12)	1703.5383	0.2807	0e+00	0.5115	-12.3870	0.2967	0.0007	0.3576	0.0008	0.3576	0.1860	0.5215	0.2035	0.5065	0.3284	0.5115
South_Africa (21) v. South_Alligator_River (88)	2690.1292	0.0190	0e+00	0.3367	-5.1108	0.0839	0.0007	0.2008	0.0008	0.2008	0.0383	0.4106	0.0432	0.3956	0.0785	0.4016
Sydney_Harbour (65) v. Unknown (10)	2210.5736	0.2937	1e-04	0.0370	-7.7849	0.4006	0.0007	0.3347	0.0008	0.3347	0.1081	0.2498	0.1202	0.2328	0.2061	0.2388
Adelaide_River (18) v. Daly_River (49)	2167.7013	0.2138	0e+00	0.0709	-7.3999	0.6933	0.0006	0.2767	0.0007	0.2767	0.0689	0.2448	0.0772	0.2488	0.1367	0.2448
East_Alligator_River (47) v. Sri_Lanka (12)	2203.9336	0.0120	0e+00	0.5085	-8.6225	0.0440	0.0006	0.3556	0.0006	0.3556	0.1061	0.8601	0.1179	0.8422	0.2025	0.8511
Arabian_Sea (15) v. Wenlock_River (24)	2056.0306	0.0190	0e+00	0.2647	-8.9214	0.2517	0.0005	0.3576	0.0005	0.3576	0.1134	0.5295	0.1261	0.5185	0.2151	0.5235
Seychelles (36) v. South_Africa (21)	2113.0760	0.0360	0e+00	0.5465	-7.9629	0.2048	0.0004	0.3117	0.0004	0.3117	0.0733	0.5175	0.0820	0.5085	0.1447	0.5125
Darwin_Coastal (13) v. South_Africa (21)	1878.9222	0.0829	0e+00	0.8452	-10.3985	0.0739	0.0004	0.4026	0.0004	0.4026	0.1469	0.6294	0.1623	0.6024	0.2696	0.6144
East_Alligator_River (47) v. Unknown (10)	2062.6184	0.0599	0e+00	0.3197	-9.5133	0.1039	0.0003	0.4056	0.0003	0.4046	0.1337	0.4905	0.1477	0.4525	0.2482	0.4705
East_Alligator_River (47) v. Sydney_Harbour (65)	2454.4485	0.2647	0e+00	0.3347	-5.3022	0.9960	0.0001	0.3616	0.0002	0.3616	0.0248	0.3117	0.0280	0.3177	0.0515	0.3157
Papua_New_Guinea (9) v. Thailand (4)	1281.3563	0.1409	1e-04	0.2687	80.2821	0.0180	0.0001	0.4555	0.0001	0.4555	1.3270	0.9860	1.3028	0.9860	1.1301	0.9860
Thailand (4) v. Unknown (10)	1305.2689	0.1069	1e-04	0.2857	160.1180	0.0415	0.0000	0.4577	0.0000	0.4577	1.1458	0.9615	1.1355	0.9615	1.0631	0.9615
Seychelles (36) v. Sri_Lanka (12)	2037.9513	0.0330	0e+00	0.1768	-9.4906	0.1908	0.0000	0.5165	0.0000	0.5165	0.1221	0.8322	0.1352	0.8222	0.2293	0.8282
Daly_River (49) v. East_Alligator_River (47)	2356.7982	0.2807	0e+00	0.1838	-5.8189	0.8212	0.0000	0.4835	0.0000	0.4835	0.0305	0.4685	0.0345	0.4705	0.0631	0.4695
Adelaide_River (18) v. Sydney_Harbour (65)	2302.3892	0.2438	0e+00	0.8442	-6.5338	0.6104	0.0000	0.4945	0.0000	0.4945	0.0573	0.5644	0.0644	0.5704	0.1151	0.5694
Darwin_Coastal (13) v. Roper_River (9)	1574.5441	0.2408	1e-04	0.1938	-17.1266	0.9411	0.0000	0.5075	0.0000	0.5075	0.3088	0.0819	0.3316	0.0829	0.4893	0.0829
East_Alligator_River (47) v. South_Alligator_River (88)	2557.4033	0.4945	0e+00	0.4216	-4.5998	0.8761	-0.0001	0.5544	-0.0001	0.5544	0.0191	0.5105	0.0216	0.5245	0.0399	0.5155
Clarence_River (74) v. Fitzroy_River (3)	2109.1963	0.8302	2e-04	0.0809	NA	NA	-0.0001	0.4757	-0.0001	0.4757	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Roper_River (9)	1221.3031	0.3287	2e-04	0.4076	NA	NA	-0.0002	0.4633	-0.0002	0.4501	NA	NA	NA	NA	NA	NA
Darwin_Coastal (13) v. Thailand (4)	1455.0609	0.3127	1e-04	0.1688	-93.7242	0.2302	-0.0002	0.4900	-0.0002	0.4900	0.8097	0.8070	0.8213	0.8080	0.9013	0.8080
Daly_River (49) v. South_Africa (21)	2295.0260	0.0380	0e+00	0.5534	-6.8820	0.3167	-0.0002	0.5684	-0.0002	0.5684	0.0577	0.6154	0.0648	0.6104	0.1158	0.6134
South_Africa (21) v. Sri_Lanka (12)	1795.5717	0.2657	0e+00	0.5445	-11.2577	0.4076	-0.0003	0.5365	-0.0003	0.5365	0.1632	0.6114	0.1795	0.6054	0.2946	0.6064
East_Alligator_River (47) v. Thailand (4)	2065.5141	0.0679	1e-04	0.5784	-18.6980	0.0181	-0.0007	0.5707	-0.0007	0.5707	0.4088	0.9879	0.4319	0.9879	0.5967	0.9879
Fitzroy_River (3) v. South_Africa (21)	1557.7934	0.4975	1e-04	0.5664	NA	NA	-0.0016	0.6127	NA	NA	NA	NA	NA	NA	NA	NA
Arabian_Sea (15) v. Sri_Lanka (12)	1725.5932	0.6693	0e+00	0.5984	-12.0014	0.4735	-0.0017	0.8382	-0.0019	0.8382	0.1923	0.7862	0.2104	0.7922	0.3378	0.7902
Adelaide_River (18) v. Thailand (4)	1511.7822	0.3177	1e-04	0.7493	-54.5834	0.0431	-0.0018	0.6240	-0.0019	0.6240	0.6965	0.9709	0.7131	0.9709	0.8309	0.9709
Arabian_Sea (15) v. Fitzroy_River (3)	1390.8797	0.8531	1e-04	0.2388	NA	NA	-0.0021	0.6133	-0.0023	0.6133	NA	NA	NA	NA	NA	NA
South_Alligator_River (88) v. Thailand (4)	2650.8199	0.0519	1e-04	0.7502	-9.5226	0.0245	-0.0023	0.6957	-0.0024	0.6957	0.2525	0.9949	0.2732	0.9949	0.4197	0.9949
Roper_River (9) v. Trinity_inlet (4)	1320.9973	0.1029	1e-04	0.8222	80.2456	0.0721	-0.0023	0.6373	-0.0025	0.6333	1.3145	0.9540	1.2904	0.9540	1.1255	0.9540
Clarence_River (74) v. Thailand (4)	2461.8605	0.1998	1e-04	0.6374	-9.2000	0.2889	-0.0023	0.6767	-0.0025	0.6767	0.2478	0.9030	0.2688	0.9111	0.4140	0.9061
Daly_River (49) v. Thailand (4)	2171.0507	0.0320	1e-04	0.5914	-16.2078	0.0374	-0.0023	0.7180	-0.0025	0.7180	0.3737	0.9838	0.3970	0.9848	0.5610	0.9838
Thailand (4) v. Wenlock_River (24)	1746.8600	0.2418	1e-04	0.4366	-29.7036	0.0594	-0.0024	0.6727	-0.0026	0.6754	0.5430	0.9638	0.5648	0.9658	0.7180	0.9658
Fitzroy_River (3) v. Wenlock_River (24)	1498.1683	0.8242	1e-04	0.2368	NA	NA	-0.0031	0.6519	NA	NA	NA	NA	NA	NA	NA	NA
Reunion (28) v. Thailand (4)	1844.1871	0.0529	1e-04	0.4715	-28.9871	0.0062	-0.0032	0.6958	-0.0034	0.6948	0.5317	0.9969	0.5535	0.9969	0.7085	0.9969
Sydney_Harbour (65) v. Thailand (4)	2327.3946	0.0579	1e-04	0.8611	-12.8716	0.0262	-0.0041	0.8739	-0.0044	0.8739	0.3168	0.9939	0.3392	0.9960	0.4982	0.9960
Adelaide_River (18) v. Fitzroy_River (3)	1369.5109	0.8232	1e-04	0.5584	NA	NA	-0.0047	0.7308	-0.0051	0.7318	NA	NA	NA	NA	NA	NA
Sri_Lanka (12) v. Thailand (4)	1356.9701	0.5075	1e-04	0.8801	-256.1097	0.1510	-0.0050	0.8621	-0.0054	0.8621	0.9218	0.8620	0.9268	0.8630	0.9619	0.8630
South_Africa (21) v. Thailand (4)	1572.0260	0.5405	1e-04	0.5285	-38.5533	0.0212	-0.0072	0.9679	-0.0078	0.9679	0.6106	0.9889	0.6304	0.9909	0.7705	0.9889
Roper_River (9) v. Thailand (4)	1261.5201	0.4156	1e-04	0.7303	81.4655	0.0153	-0.0074	0.8831	-0.0080	0.8831	1.3158	0.9878	1.2921	0.9878	1.1261	0.9878

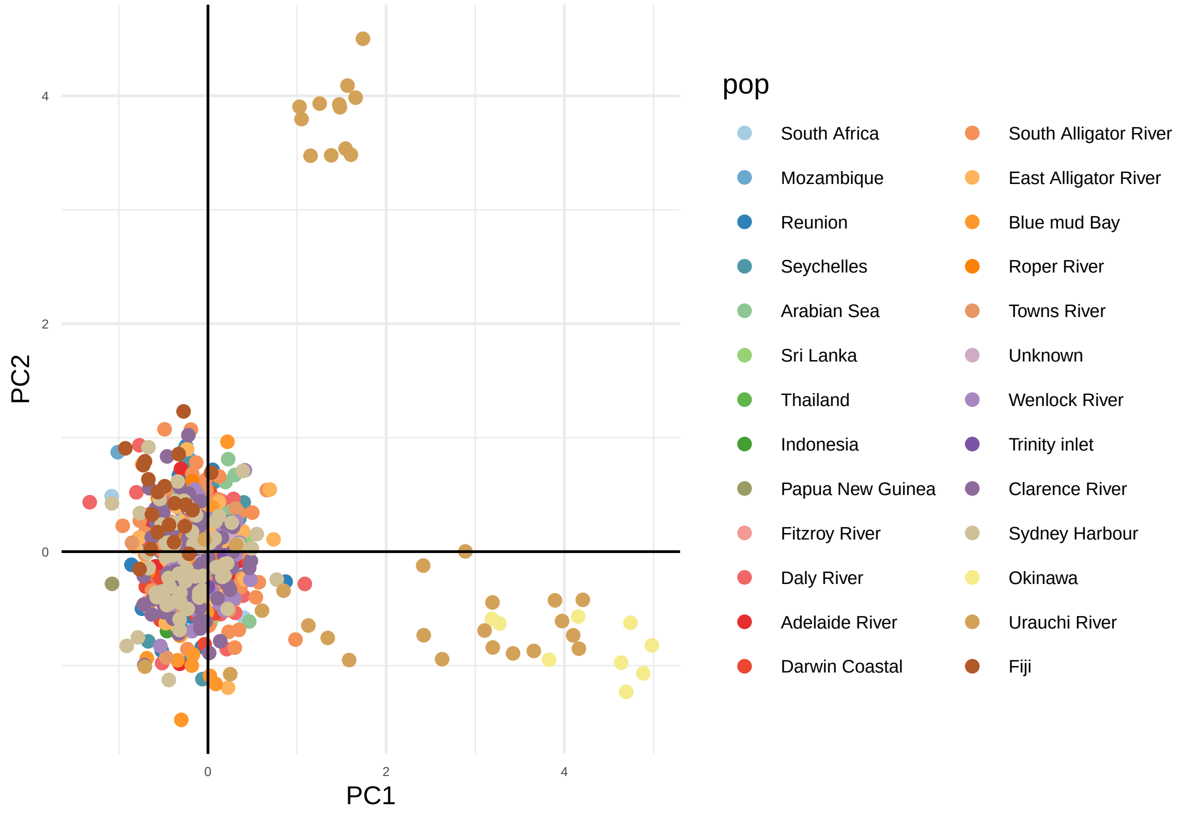
Table 46: Pairwise Fst for 3416 DArTcap loci between the IWP sites *(continued)*

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F’st	F’st.p.val	Gst	Gst.p.val	G’st	G’st.p.val	G”st	G”st.p.va
Arabian_Sea (15) v. Thailand (4)	1433.1283	0.9071	1e-04	0.7912	-54.8151	0.1910	-0.0079	0.9750	-0.0085	0.9750	0.7041	0.8640	0.7207	0.8670	0.8361	0.8660
Mozambique (11) v. Thailand (4)	1247.1550	0.8891	1e-04	0.9630	157.8144	0.0075	-0.0084	0.9346	-0.0091	0.9281	1.1490	0.9938	1.1385	0.9938	1.0645	0.9938
Fitzroy_River (3) v. Mozambique (11)	1230.1591	0.7792	1e-04	0.9800	NA	NA	-0.0097	0.8419	NA	NA	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Seychelles (36)	1808.8073	0.1868	1e-04	0.1908	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Towns_River (10)	1249.3455	0.2168	2e-04	0.2737	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Unknown (10)	1211.0390	0.4166	2e-04	0.2687	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Fitzroy_River (3) v. Urauchi_River (35)	2817.7795	0.0010	3e-04	0.0060	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

11.8 PCA

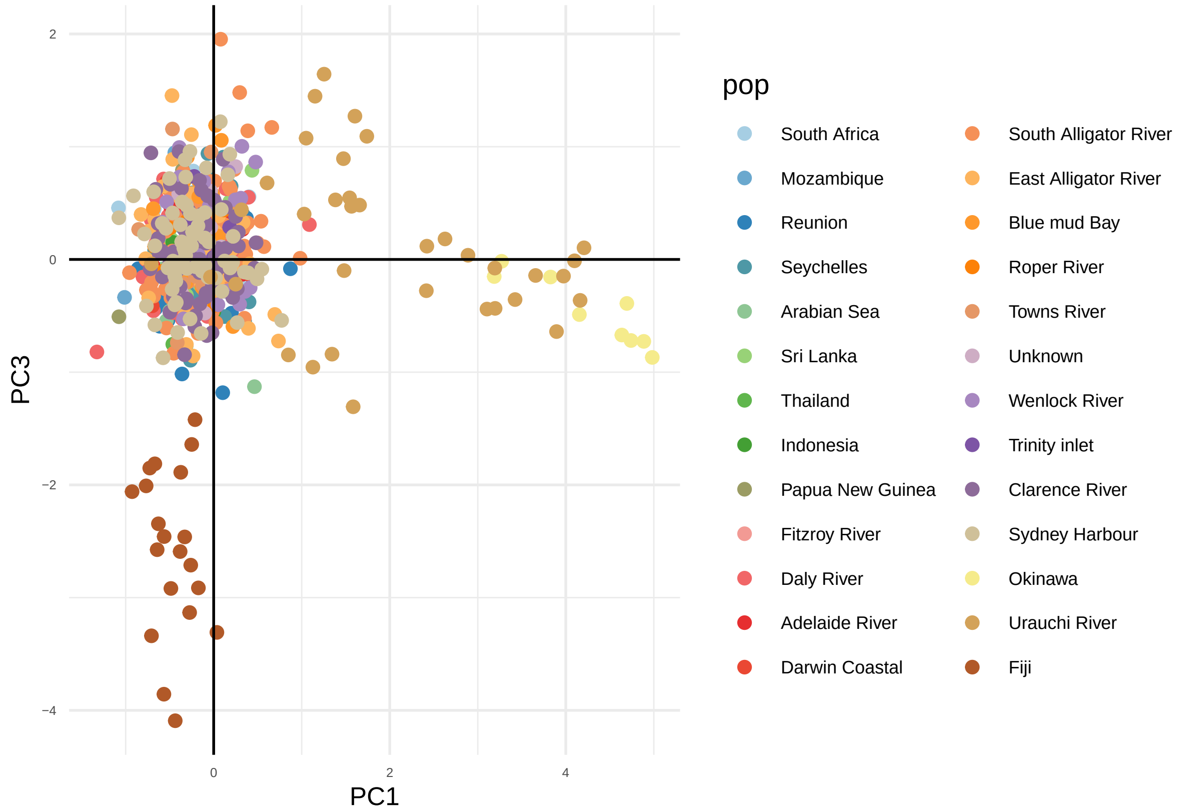
```
pca1 <- adegenet::glPca(BS.dartcap.IWP.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_IWP_PCA.Rdata")
```

```
load("DArTcap_IWP_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.IWP.gl)
cols <- adegenet::funky(nPop(BS.dartcap.IWP.gl))


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

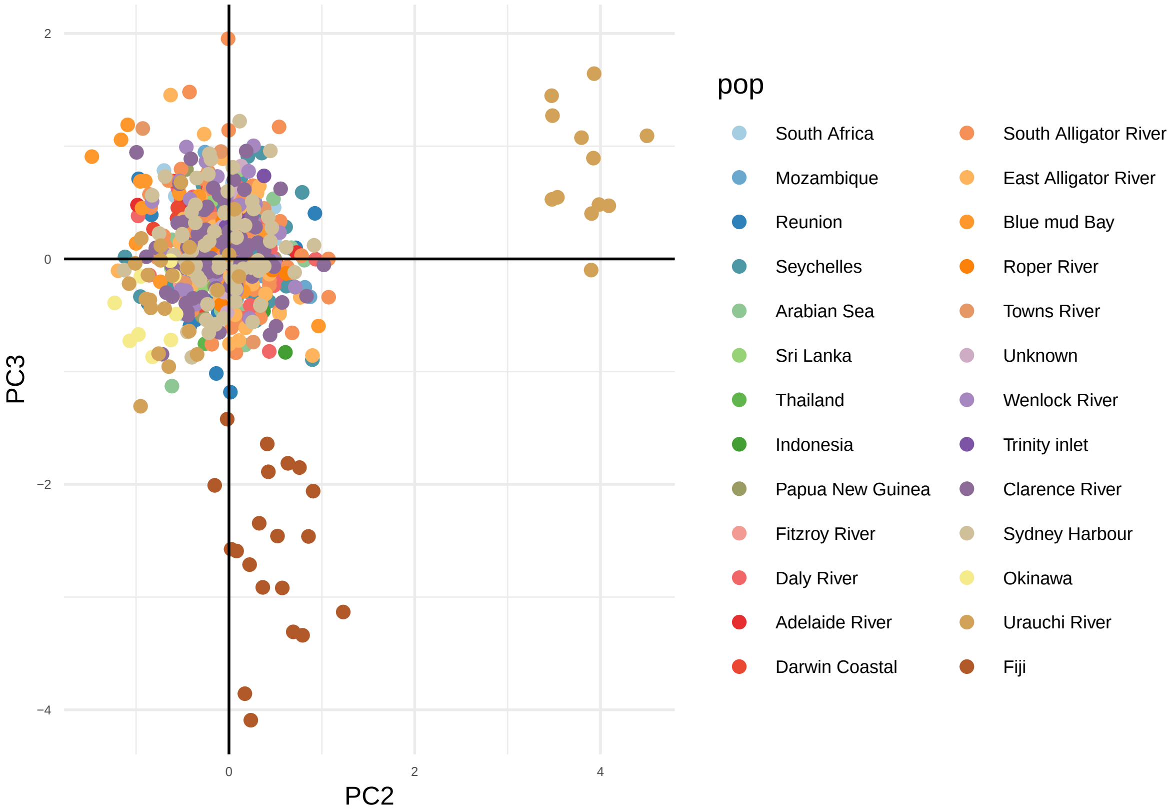


```
ggplot2::ggsave(p, filename = "DArTcap_IWP_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
```

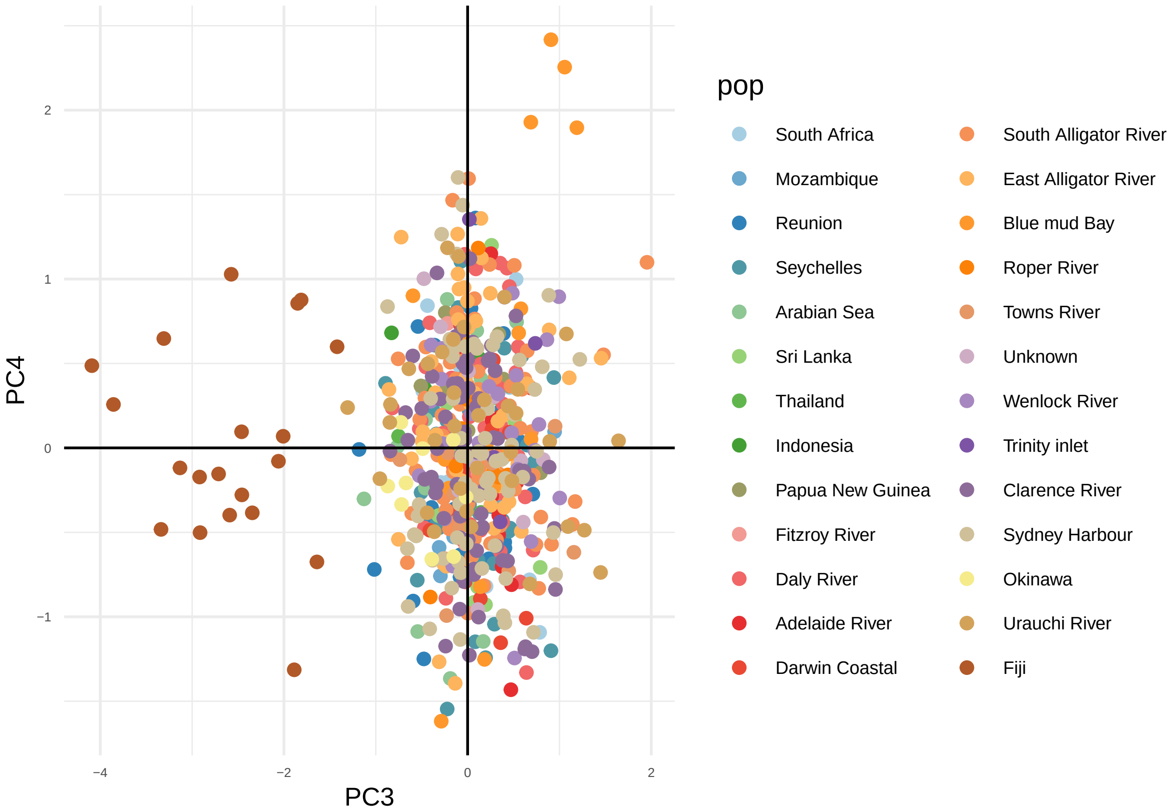
```
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



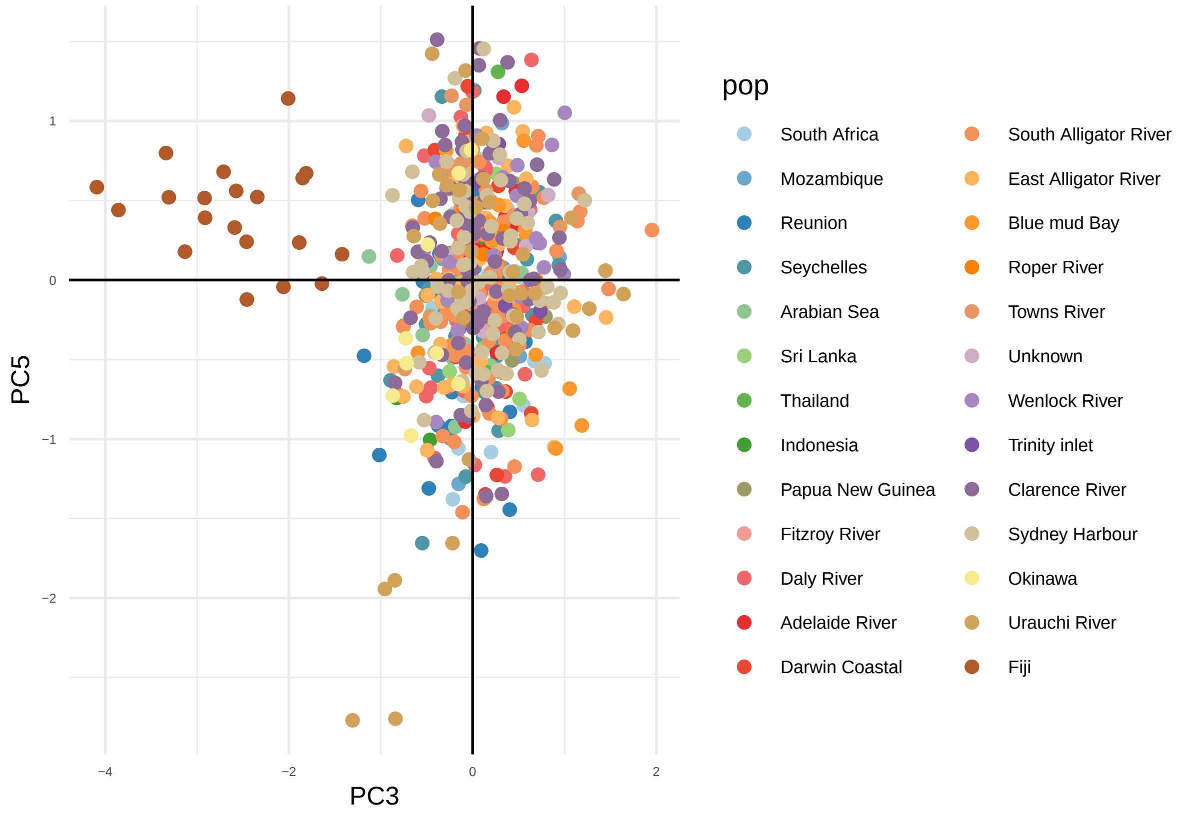
```
ggplot2::ggsave(p, filename = "DArTcap_IWP_PCA2.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_IWP_PCA3.png", width = 30,
        height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_IWP_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_IWP_PCA5.png", width = 30,
                height = 15,units = "cm")
```

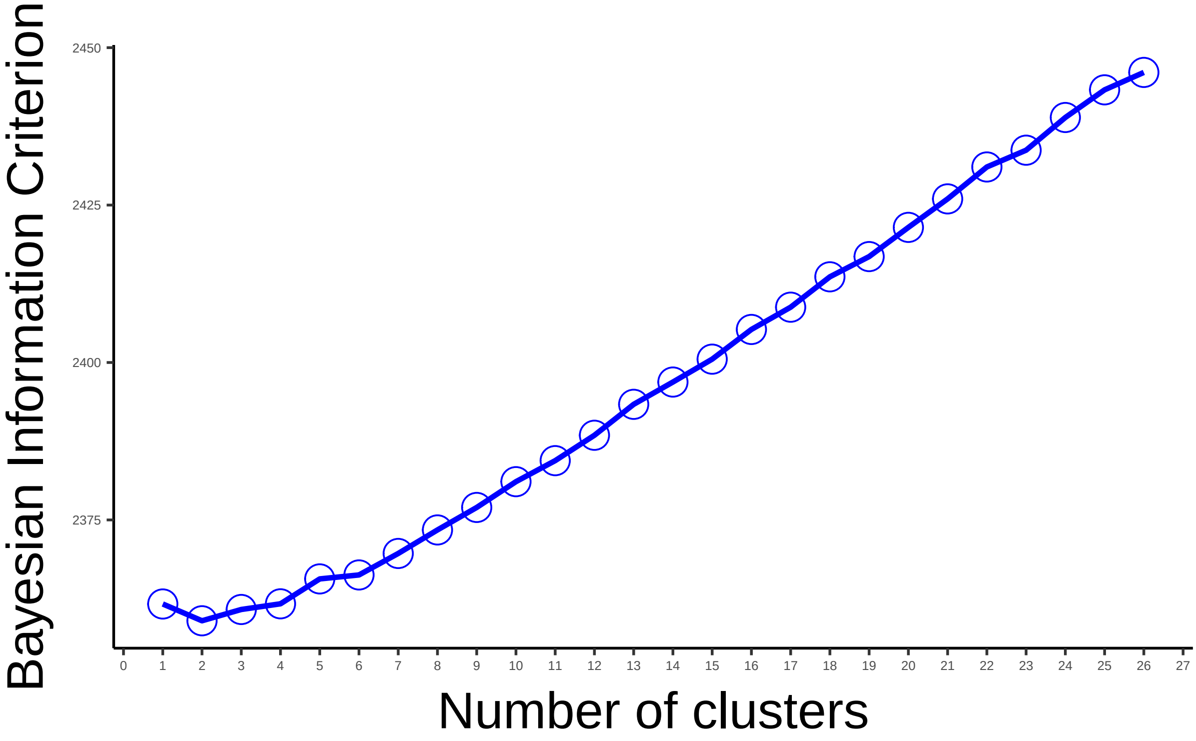
11.9 DAPC

11.9.1 Optimal number of clusters with neutral markers

```
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartcap.IWP.gl,
    max.n.clust = 26,
    n.pca = adegenet::nInd(BS.dartcap.IWP.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTcap_IWP_grp.Rdata")
```

```
load("DArTcap_IWP_grp.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:26
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartcap.IWP.gl) - 1,
```

```
                                               by = 1)) +
  ggplot2::labs(subtitle = "",
              y = "Bayesian Information Criterion",
              x = "Number of clusters",
              title = "",
              caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_IWP_grp.png", width = 30,
                height = 15,units = "cm")
```

11.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartcap.IWP.gl

xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 50),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
  scale = FALSE,
```

```
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTcap_IWP_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTcap_IWP_xval.rdata")
```

```
load("DArTcap_IWP_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

```
## $`Median and Confidence Interval for Random Chance`
##       2.5%        50%      97.5%
## 0.02438735 0.03734027 0.05508623
##
## $`Mean Successful Assignment by Number of PCs of PCA`
##       186       187       188       189       190       191       192       193
## 0.2324804 0.2306034 0.2321176 0.2329844 0.2300221 0.2284677 0.2318179 0.2328035
##       194       195       196       197       198       199       200       201
## 0.2288689 0.2310550 0.2324531 0.2295151 0.2295611 0.2286921 0.2269646 0.2322773
##       202       203       204       205       206       207       208       209
## 0.2295792 0.2298527 0.2290045 0.2298239 0.2280632 0.2260452 0.2277085 0.2286509
##       210       211       212       213       214       215       216
## 0.2277546 0.2264222 0.2281876 0.2280022 0.2292683 0.2289469 0.2295428
##
## $`Number of PCs Achieving Highest Mean Success`
## [1] "189"
##
## $`Root Mean Squared Error by Number of PCs of PCA`
##       186       187       188       189       190       191       192       193
## 0.7680637 0.7699528 0.7684520 0.7675715 0.7705111 0.7721376 0.7687126 0.7677602
##       194       195       196       197       198       199       200       201
## 0.7716703 0.7695454 0.7680836 0.7710186 0.7710227 0.7718648 0.7735771 0.7682334
##       202       203       204       205       206       207       208       209
## 0.7709948 0.7707494 0.7715608 0.7706960 0.7724861 0.7745113 0.7728612 0.7719175
##       210       211       212       213       214       215       216
## 0.7728060 0.7741488 0.7723893 0.7725922 0.7712791 0.7716179 0.7710302
##
## $`Number of PCs Achieving Lowest MSE`
## [1] "189"
```

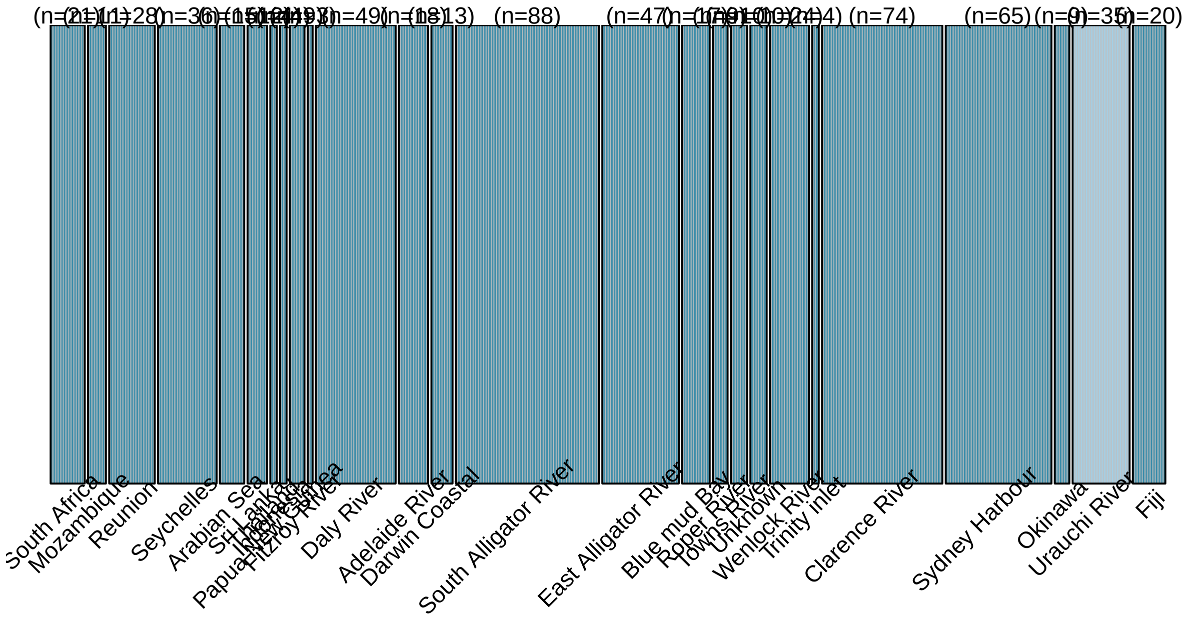
```
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartcap.IWP.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartcap.IWP.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                                     paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTcap_IWP_DAPC.Rdata")
```

11.9.3 DAPC barplot

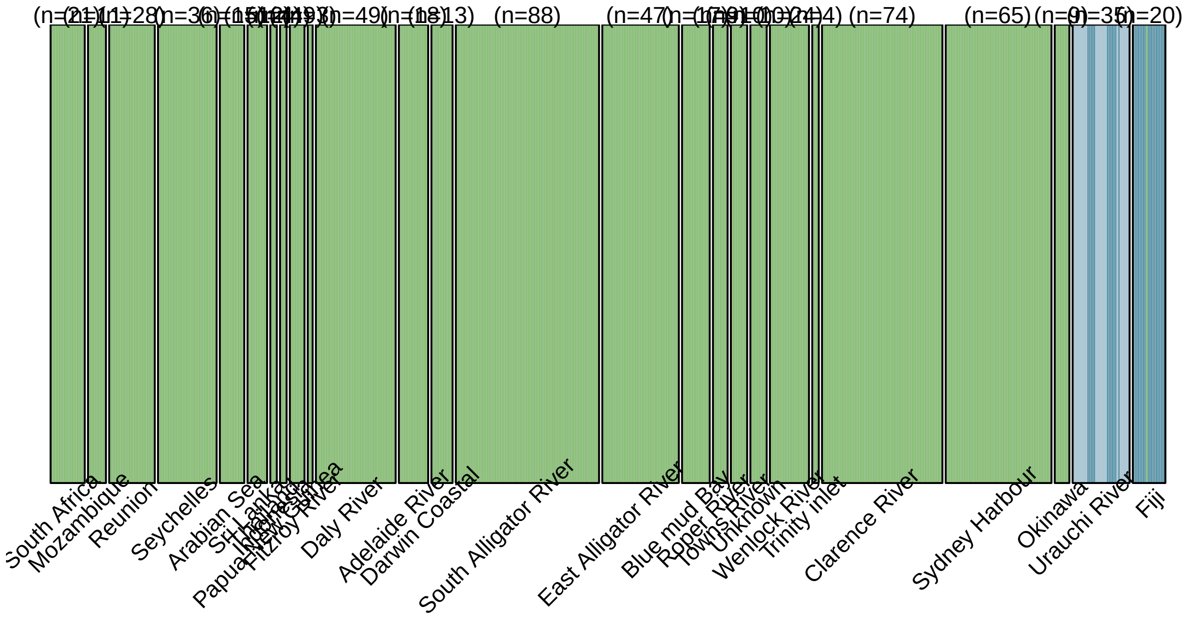
Group individuals according to DAPC posterior membership.

```
load("DArTcap_IWP_DAPC.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartcap.IWP.gl$pop

  plot.dapc.FDD(x = post,
              locations = locations,
              colour = colour,
              region.lwd = 1,
              plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                  K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```

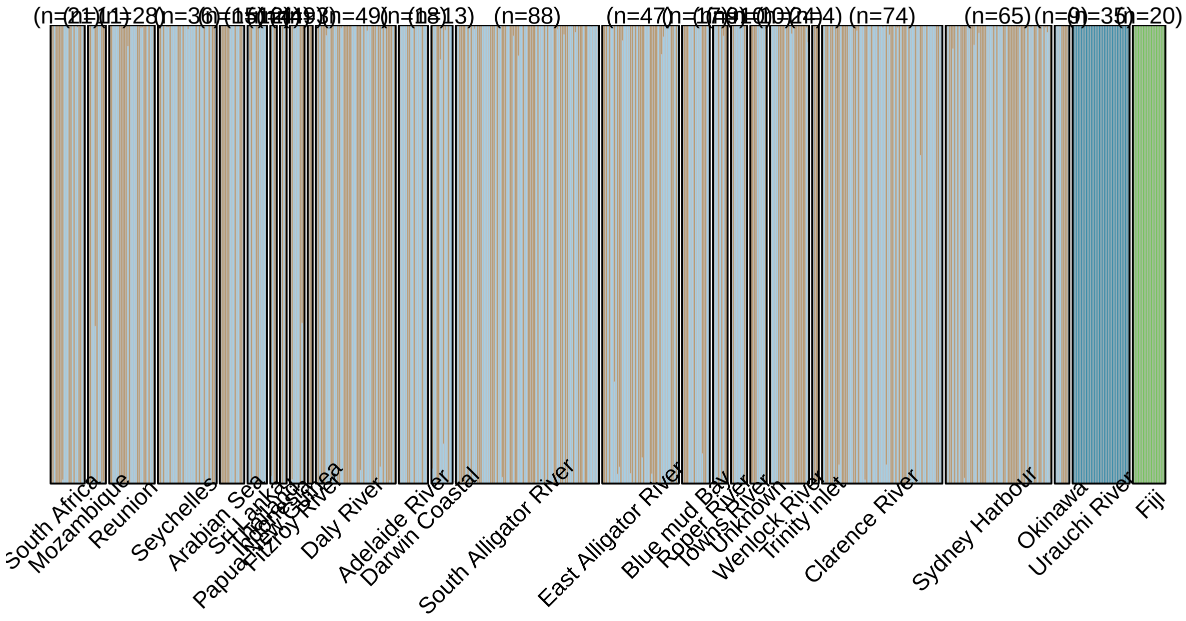
DAPC: all Bull Sharks − subset Australia
for K=2 & PC=189



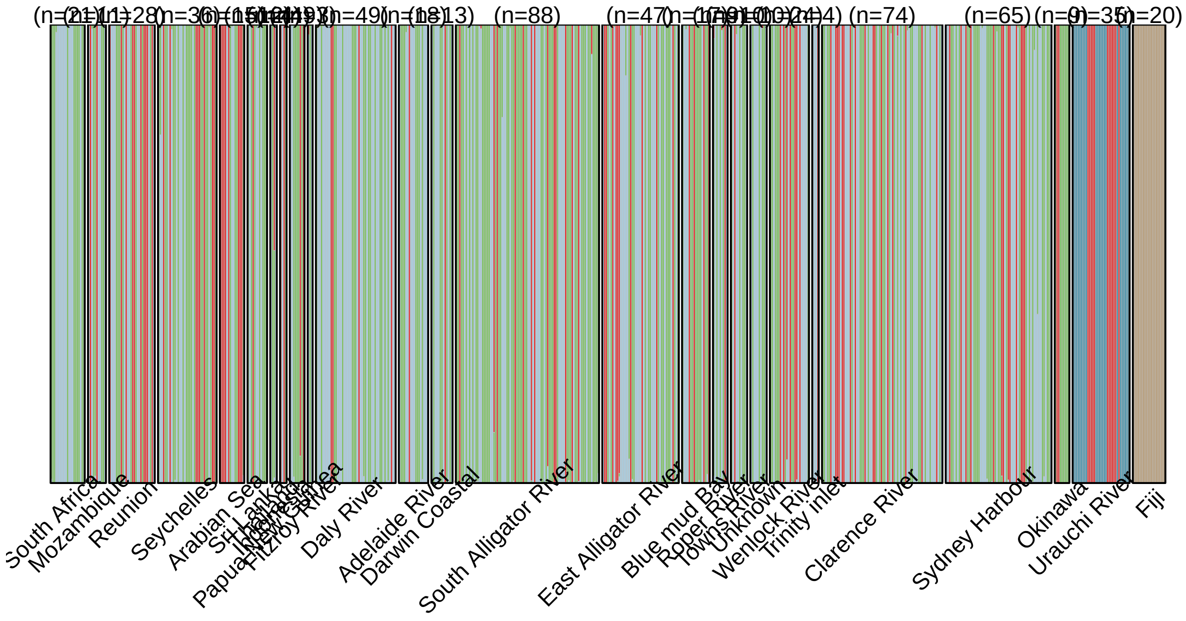
DAPC: all Bull Sharks − subset Australia
for K=3 & PC=189



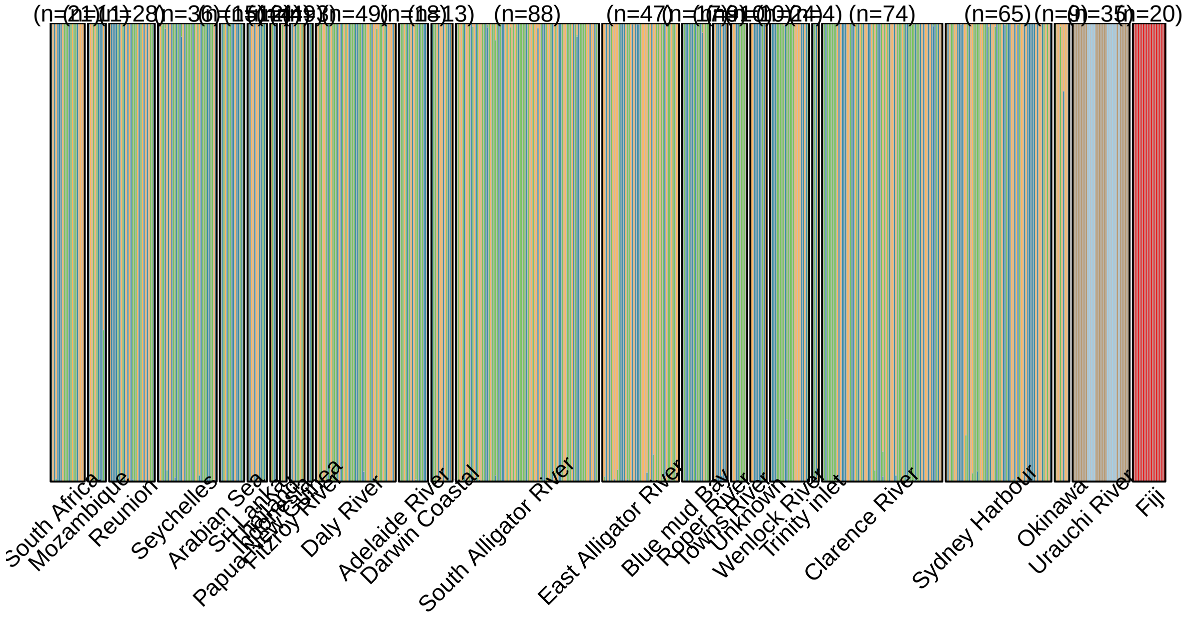
DAPC: all Bull Sharks − subset Australia
for K=4 & PC=189



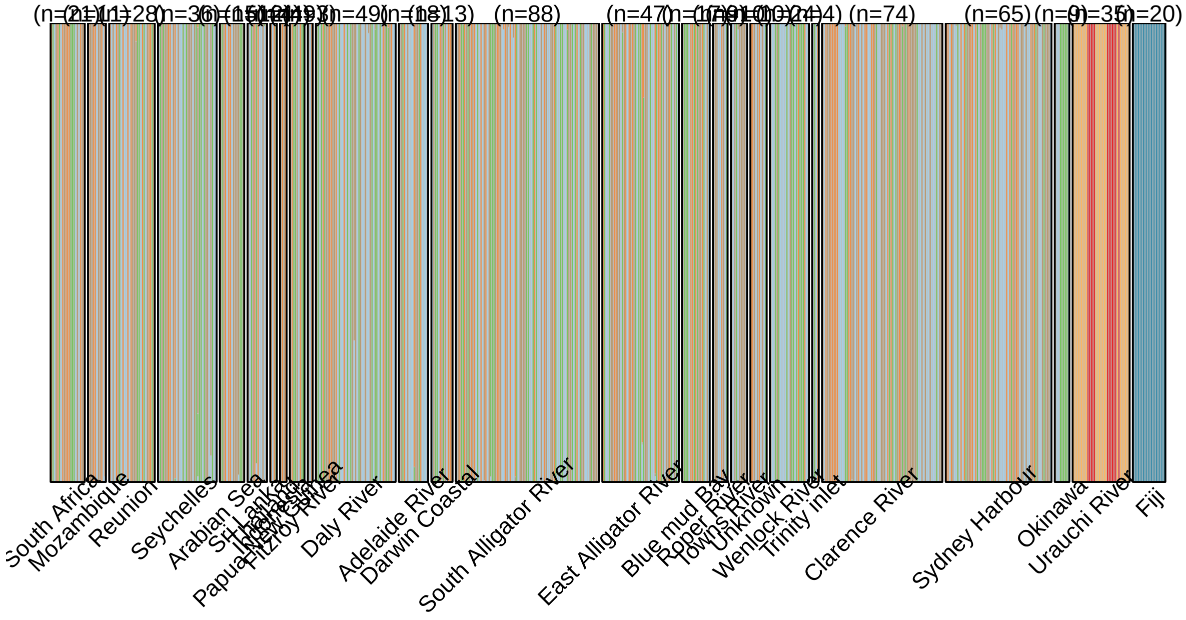
DAPC: all Bull Sharks − subset Australia
for K=5 & PC=189

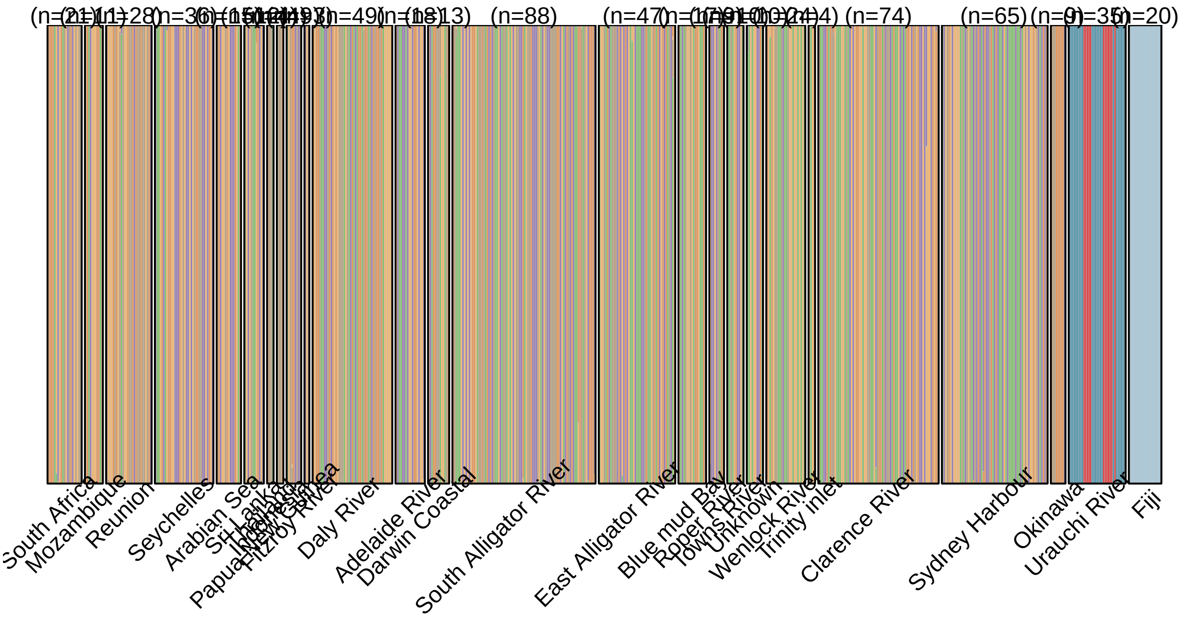


DAPC: all Bull Sharks − subset Australia
for K=6 & PC=189

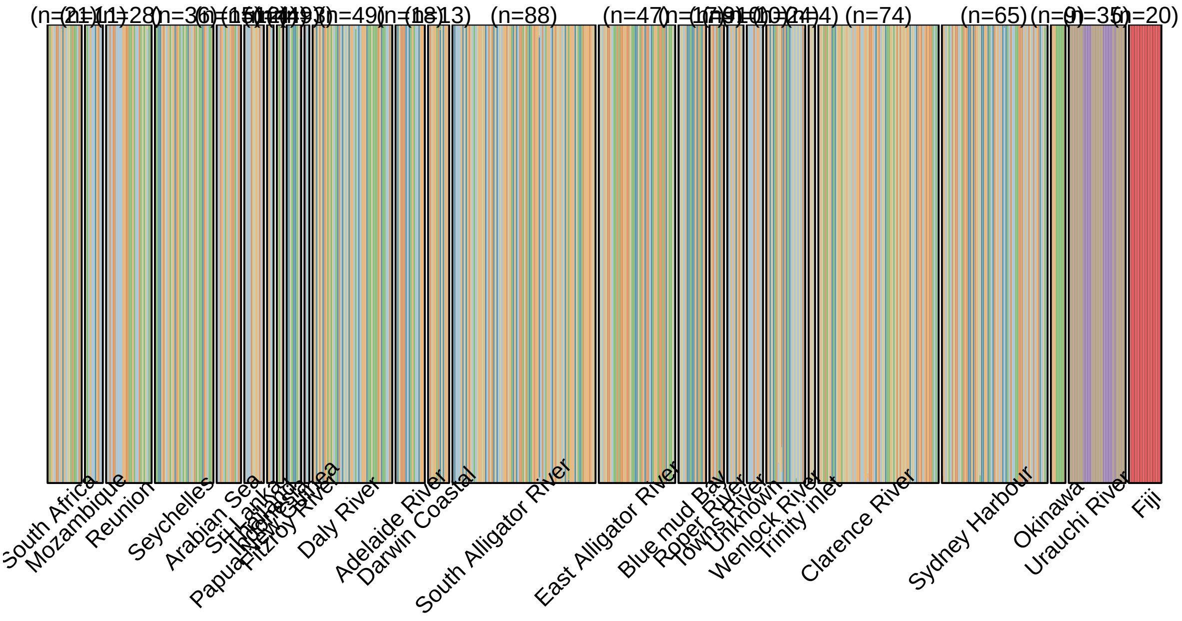


DAPC: all Bull Sharks − subset Australia
for K=7 & PC=189

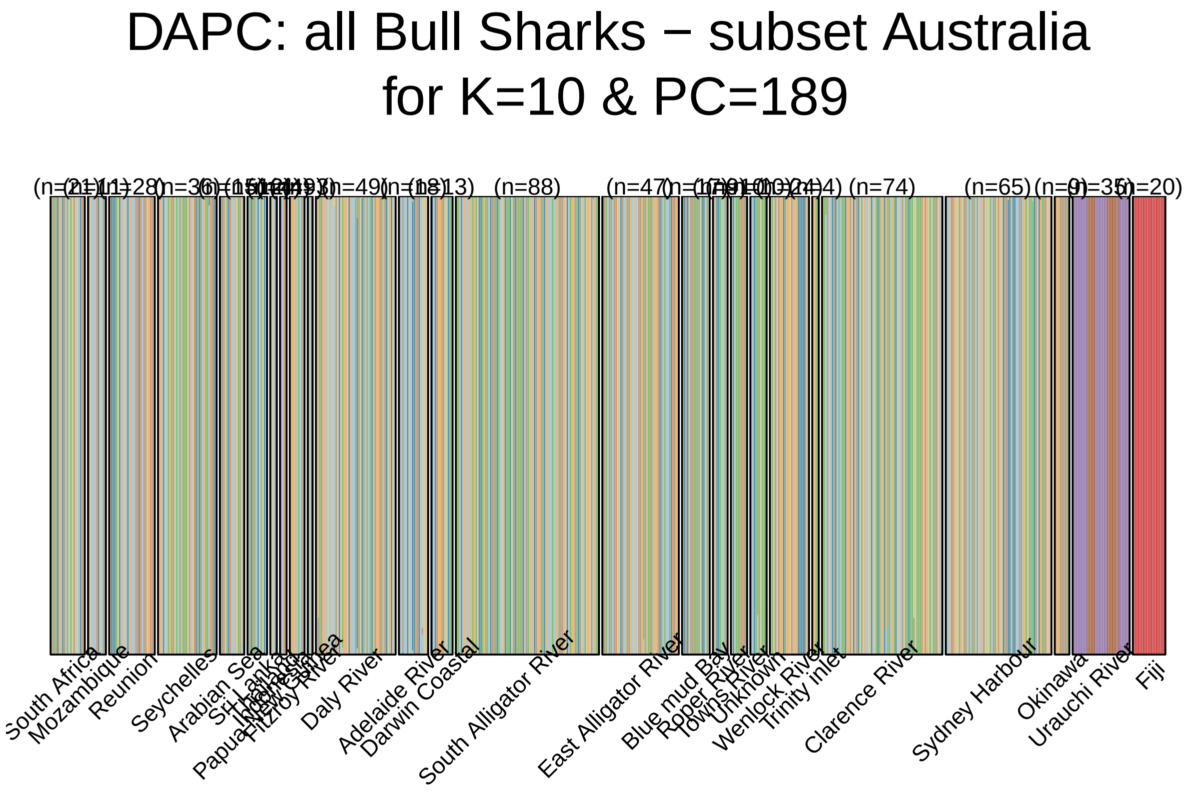




DAPC: all Bull Sharks − subset Australia for K=8 & PC=189

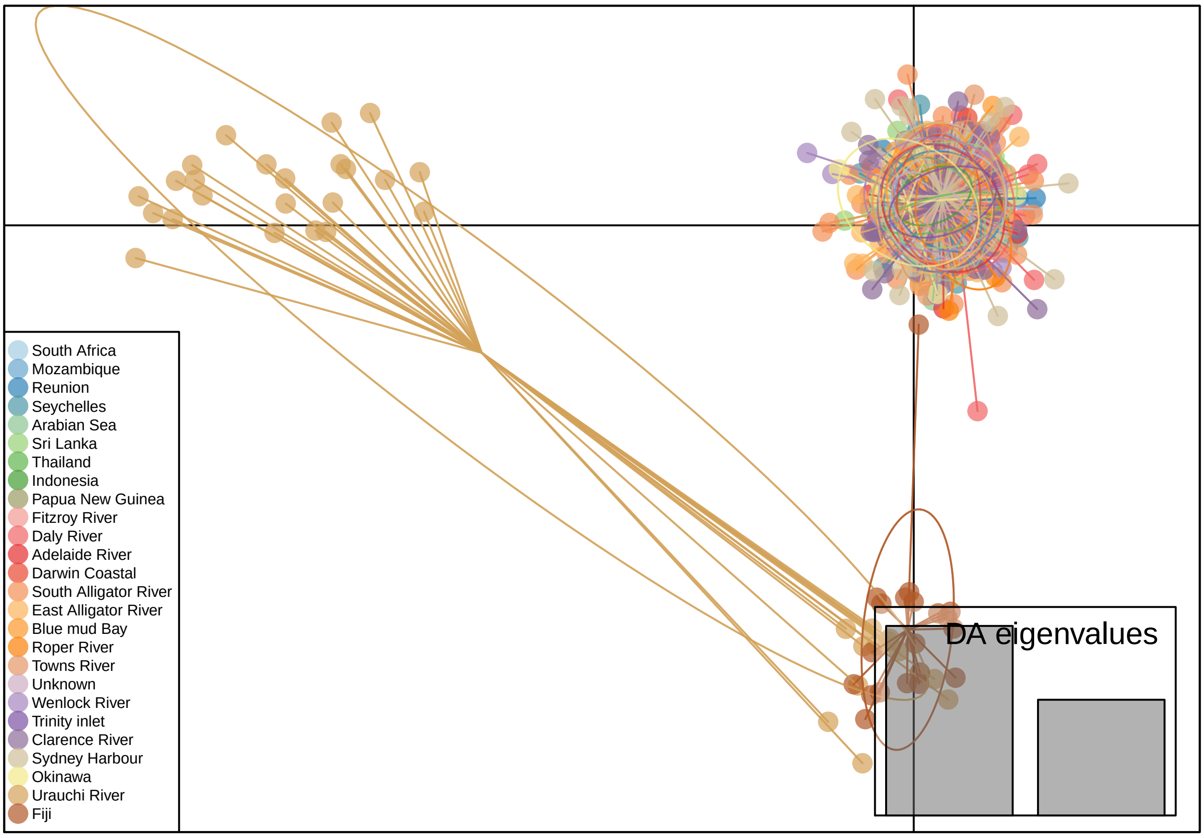


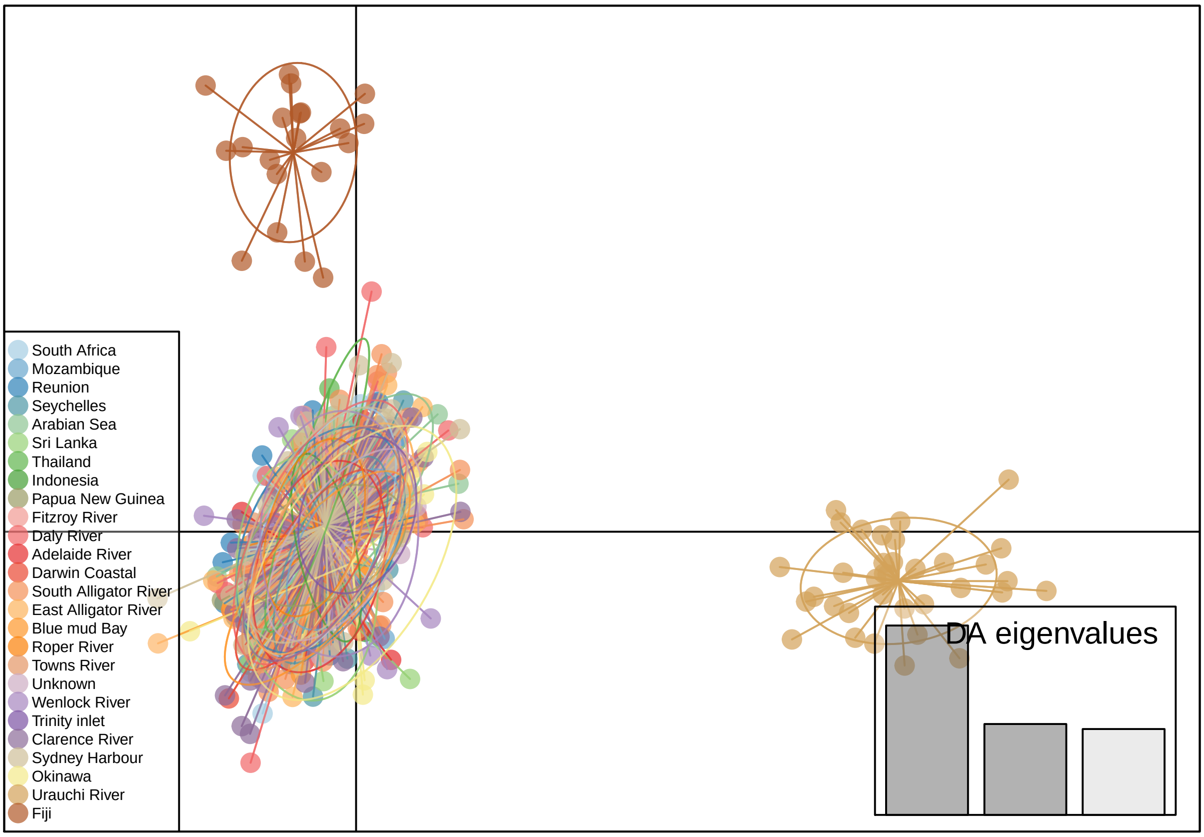
DAPC: all Bull Sharks − subset Australia for K=9 & PC=189

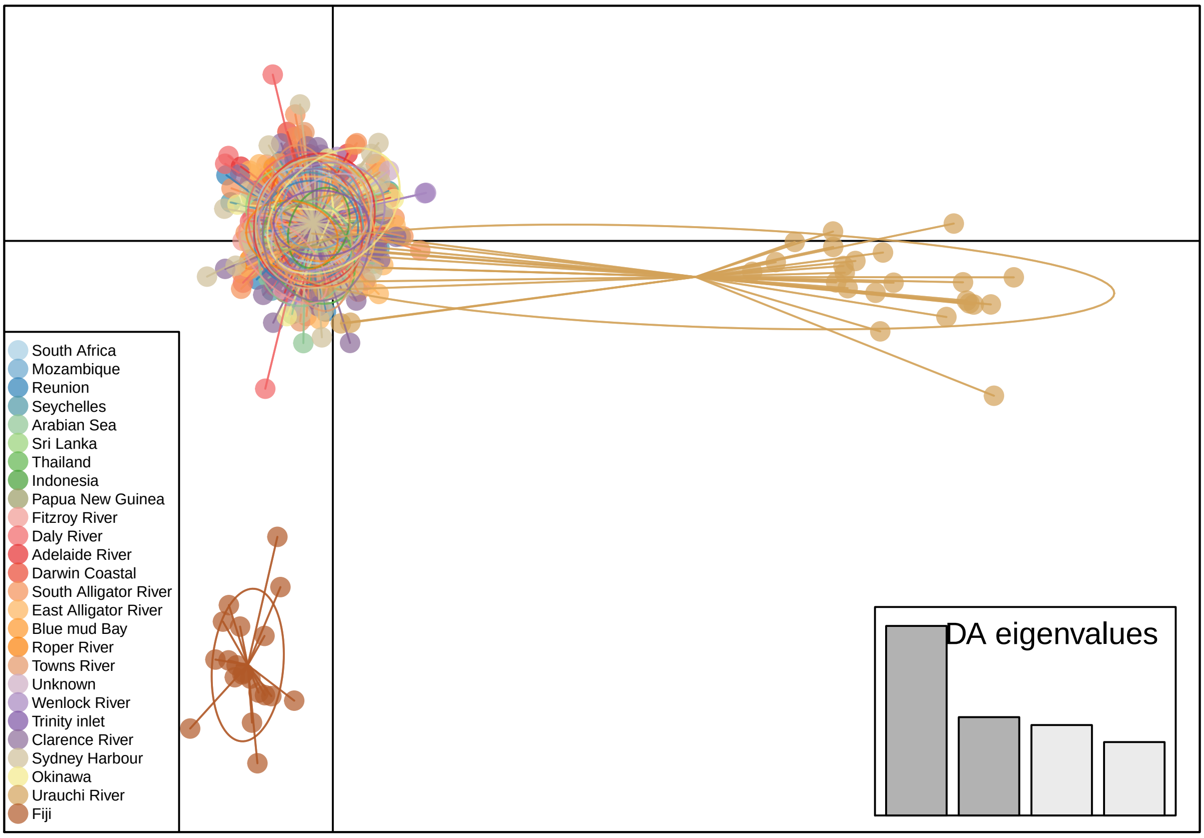


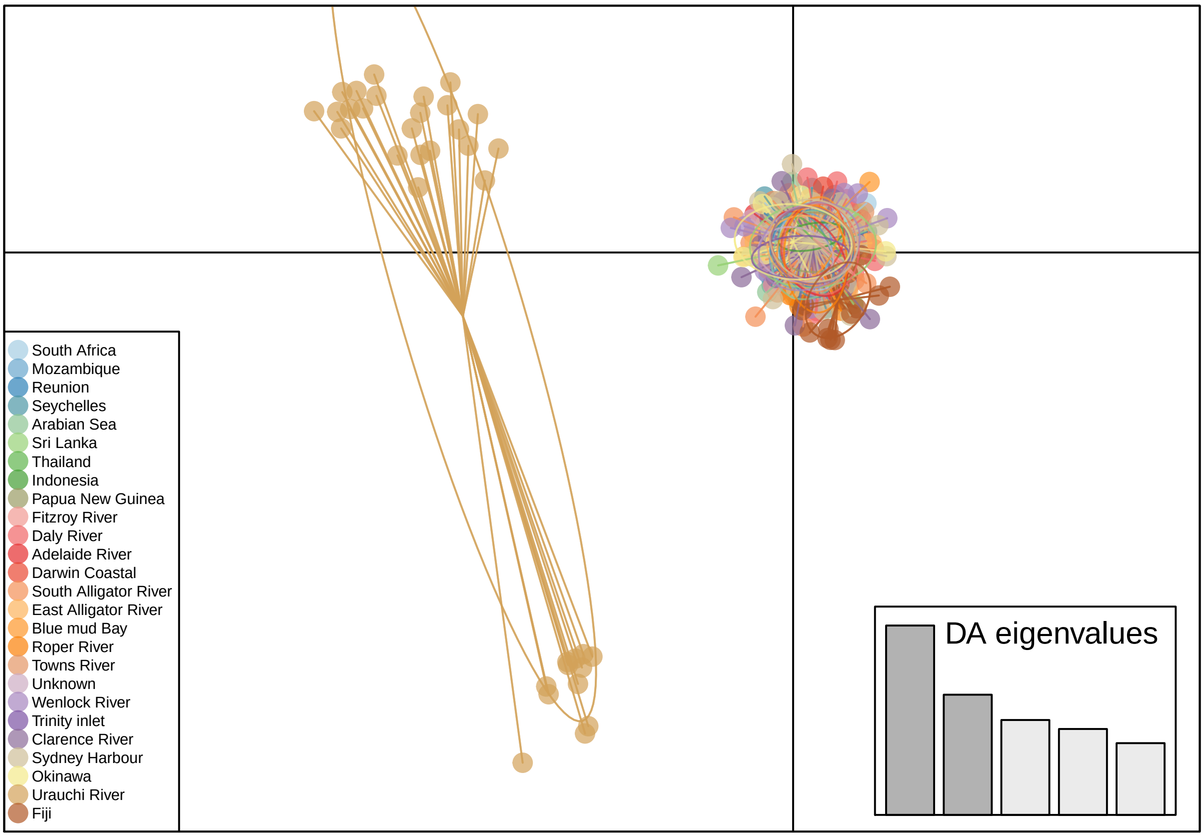
11.9.4 DAPC scatterplot

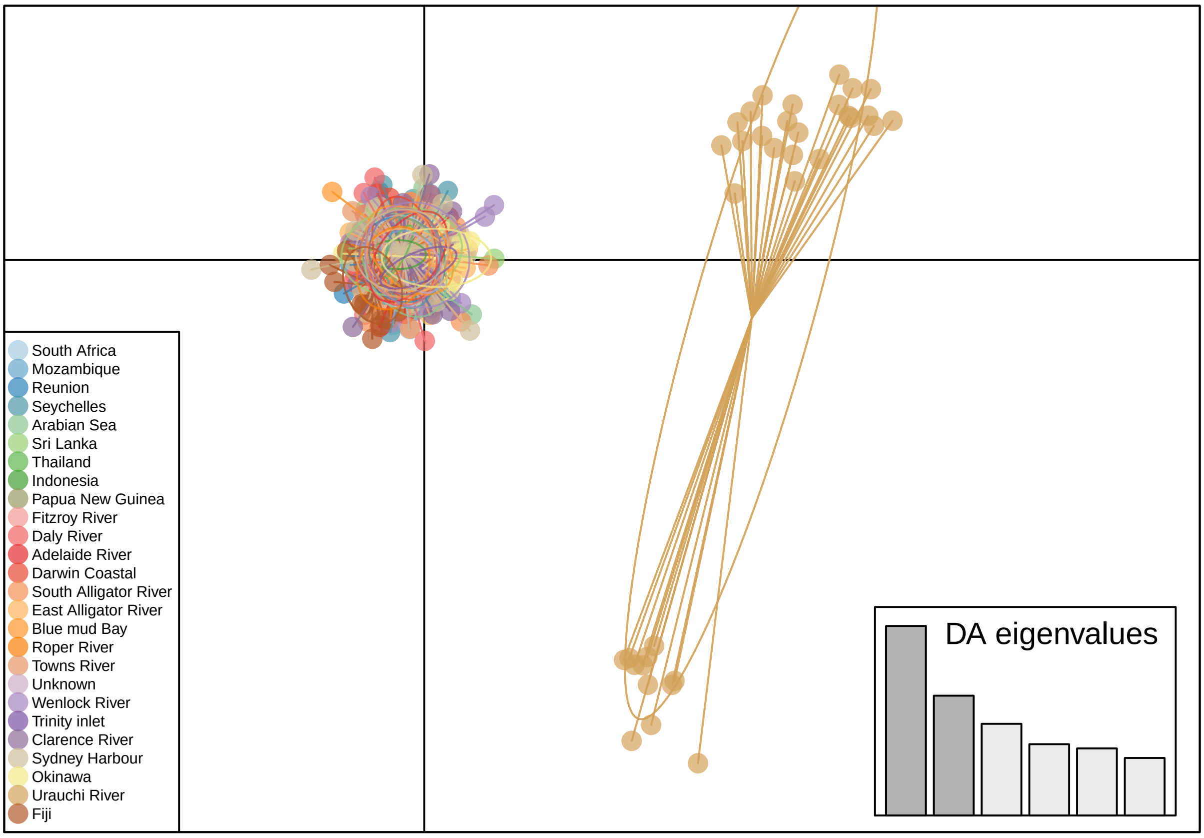
```
load("DArTcap_IWP_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartcap.IWP.gl), cex = 2,
                             legend = TRUE, col = colours.26,clabel = FALSE,
                             posi.leg = posi.leg, scree.pca = FALSE,
                             posi.pca = "topleft", cleg = 0.5, xax = 1,
                             yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

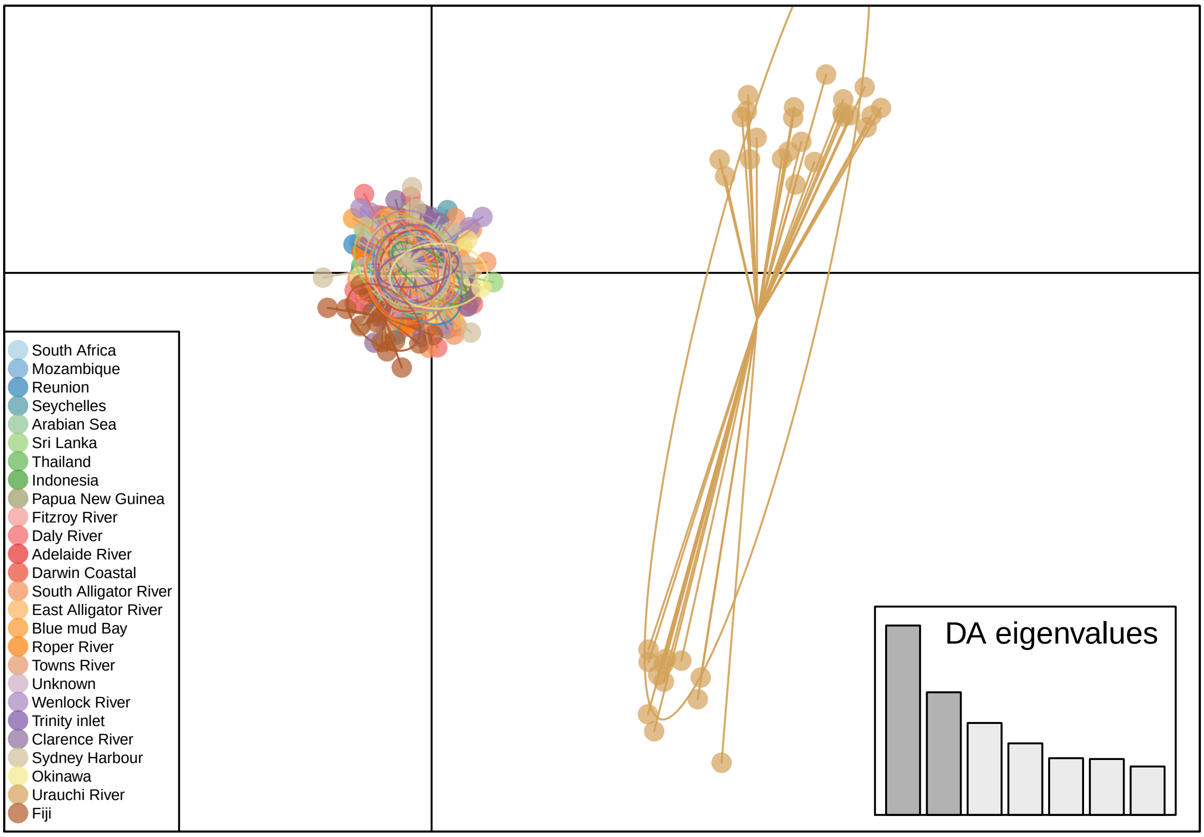

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

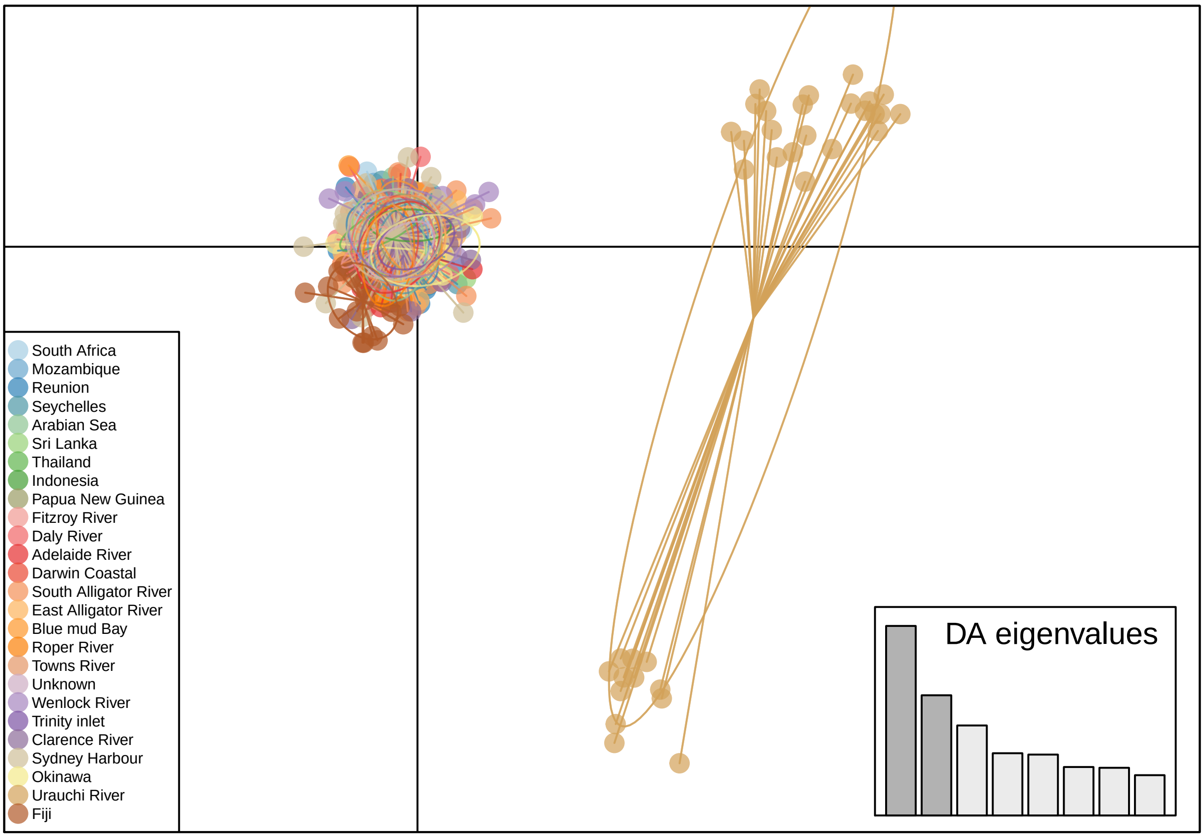

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

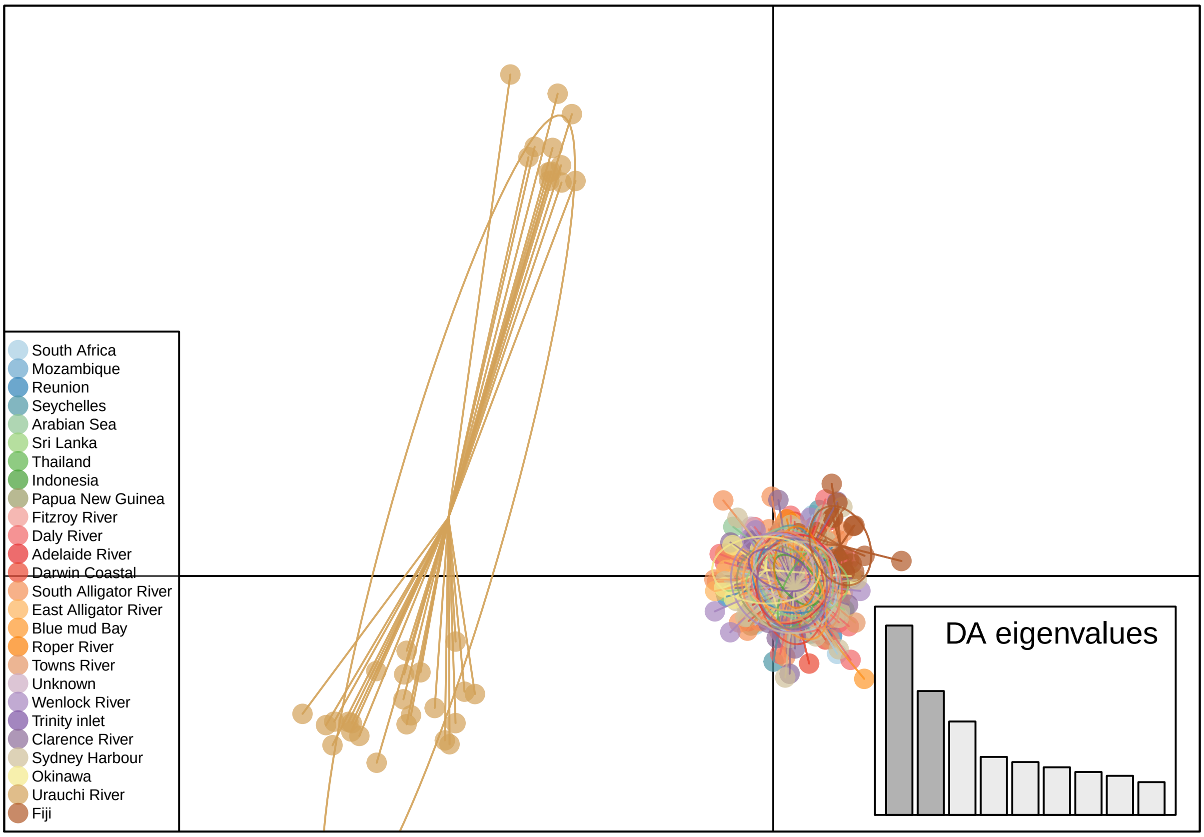

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues


South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues


South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

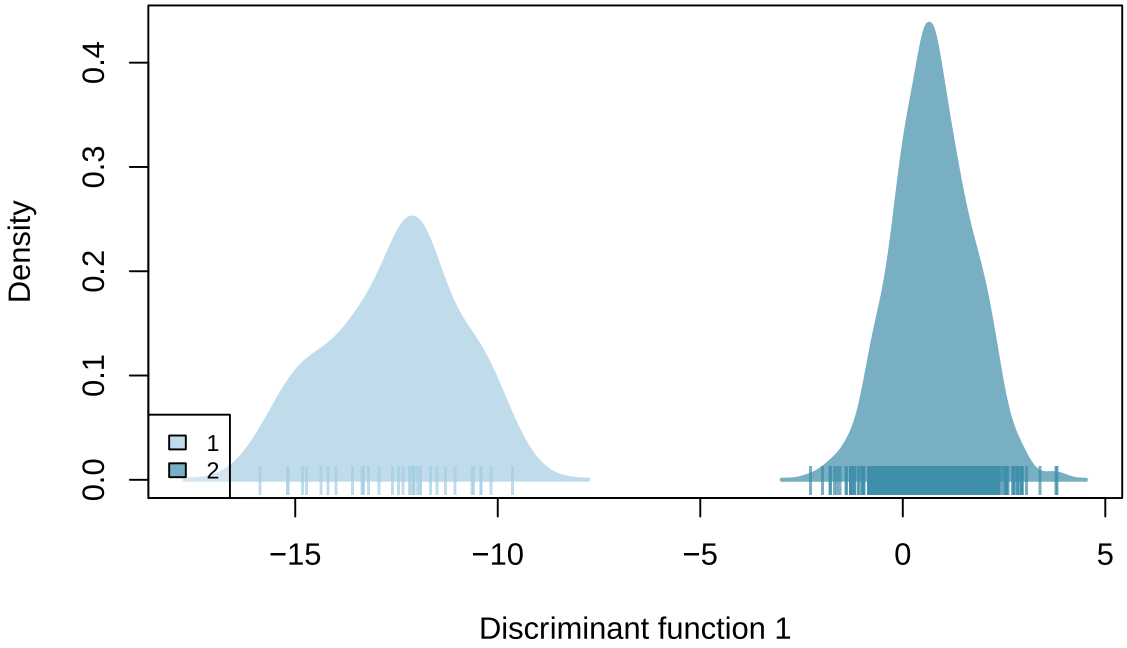

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji
DA eigenvalues

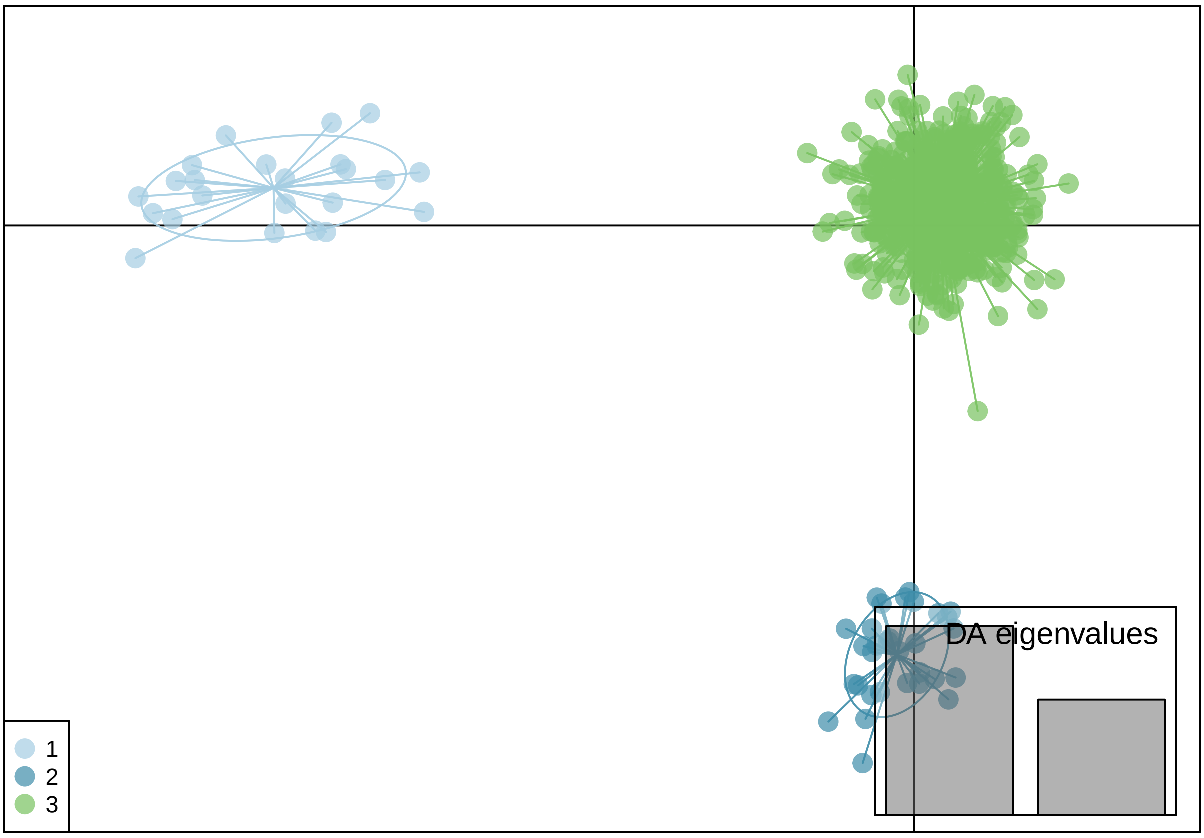


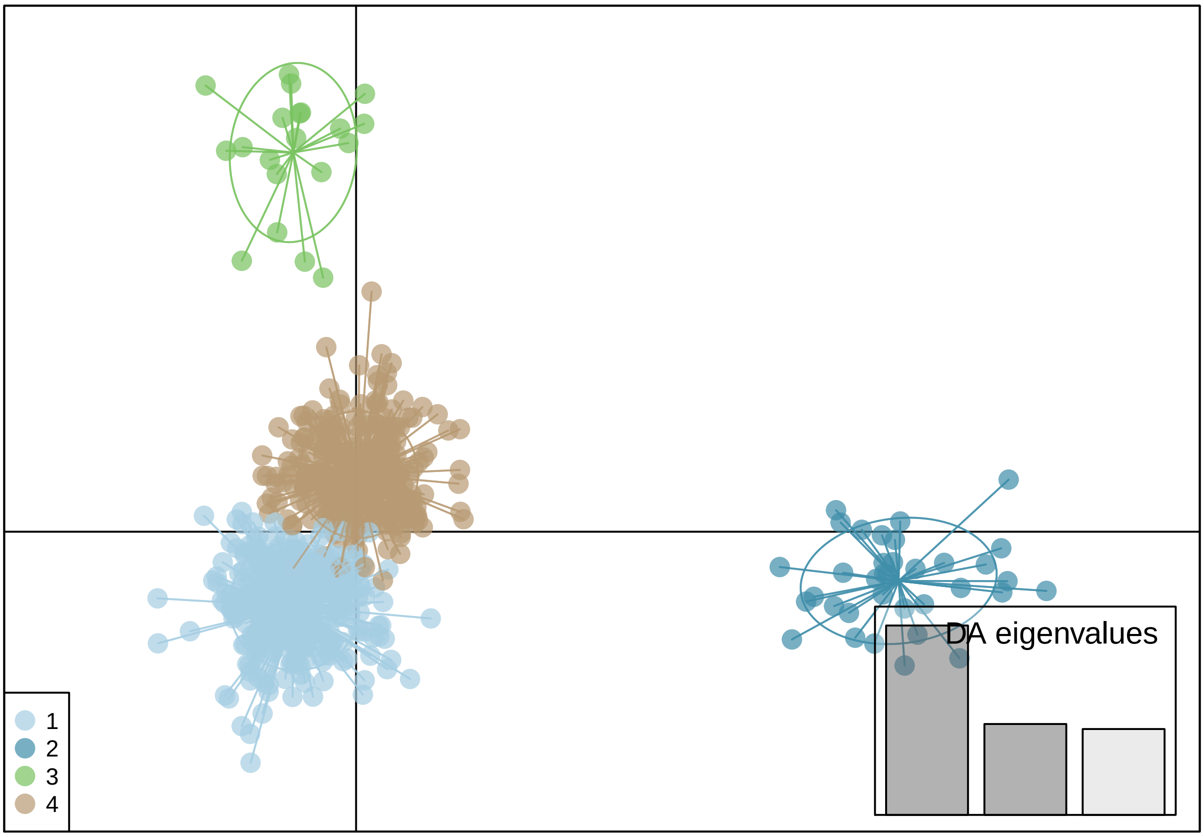


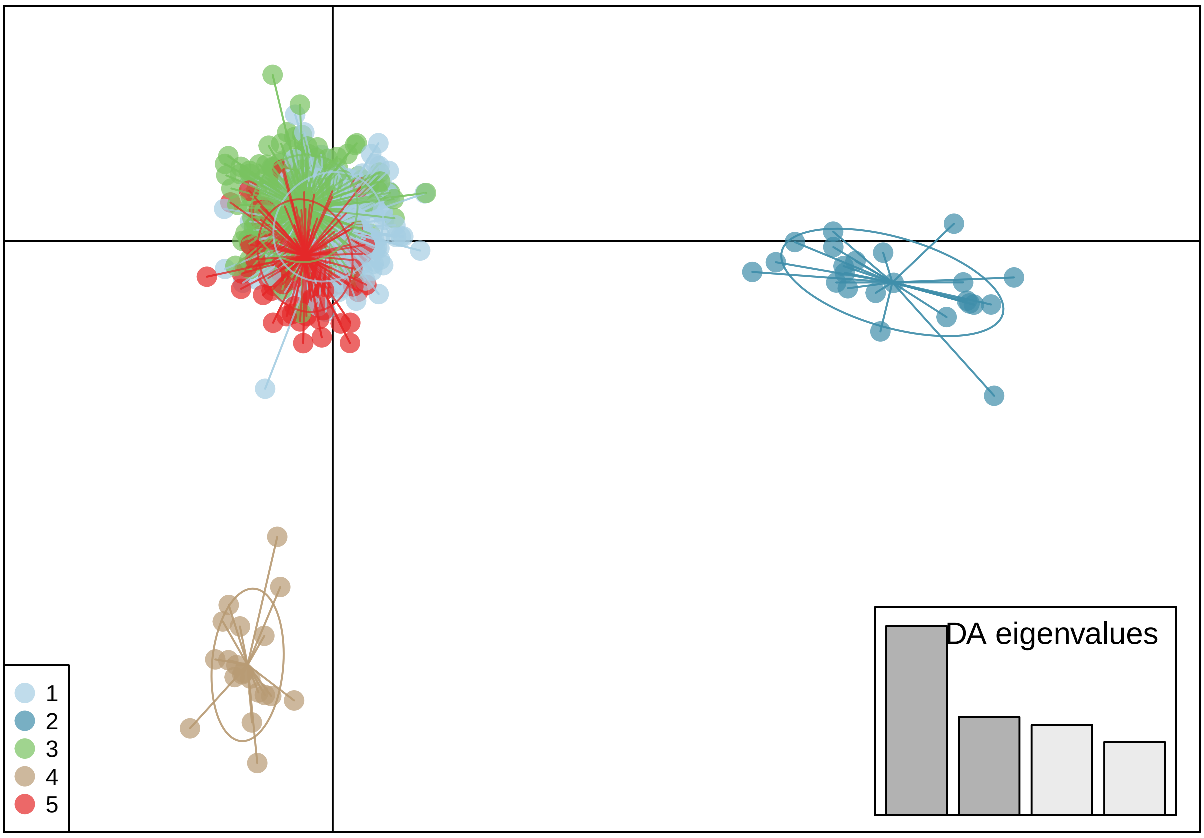
```
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                             clabel = FALSE, posi.leg = "bottomleft",
```

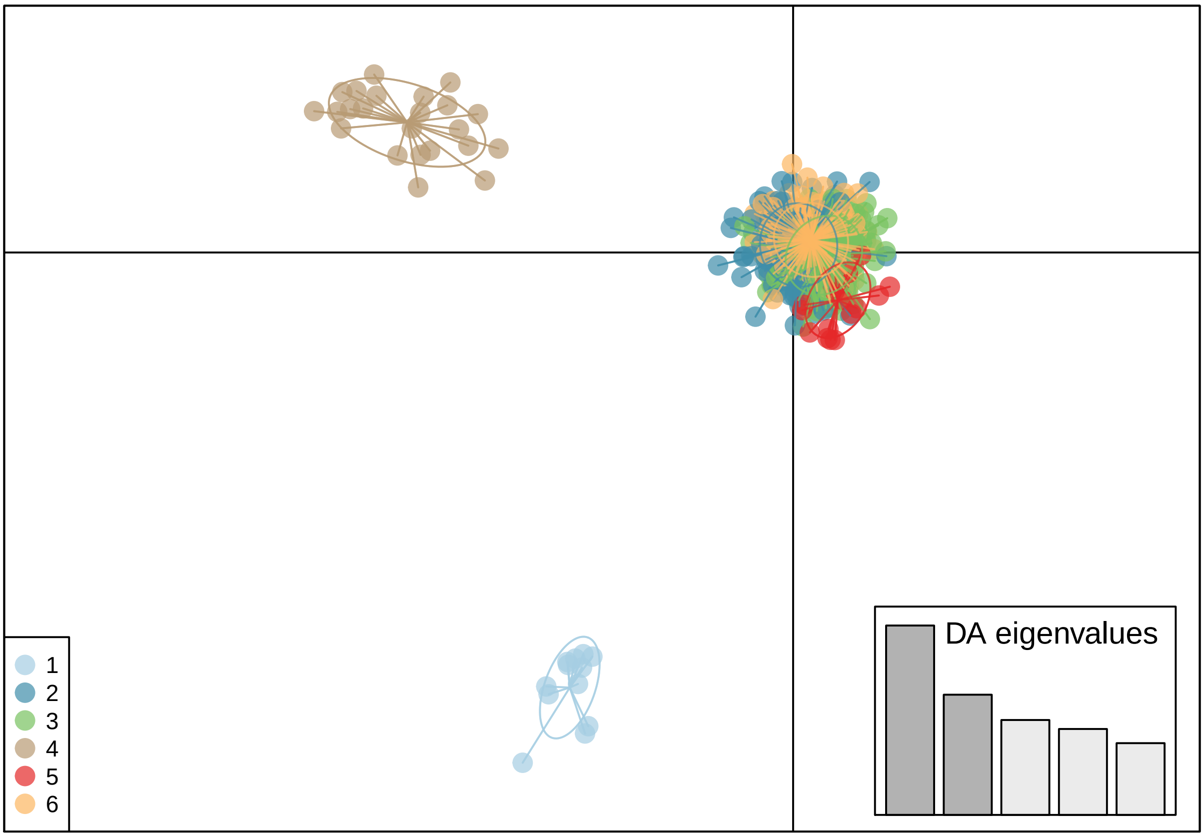
```
                                scree.pca = FALSE, posi.pca = "topleft",
                                cleg = 0.75, xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

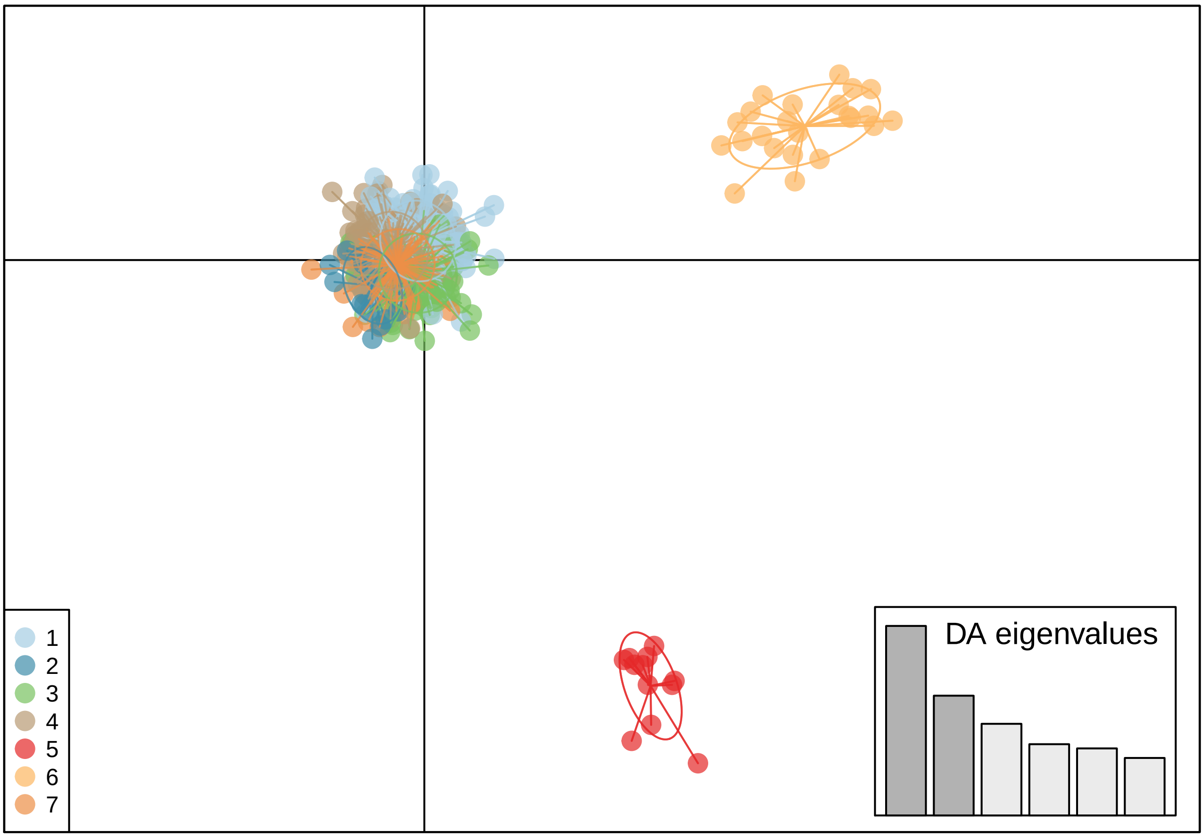


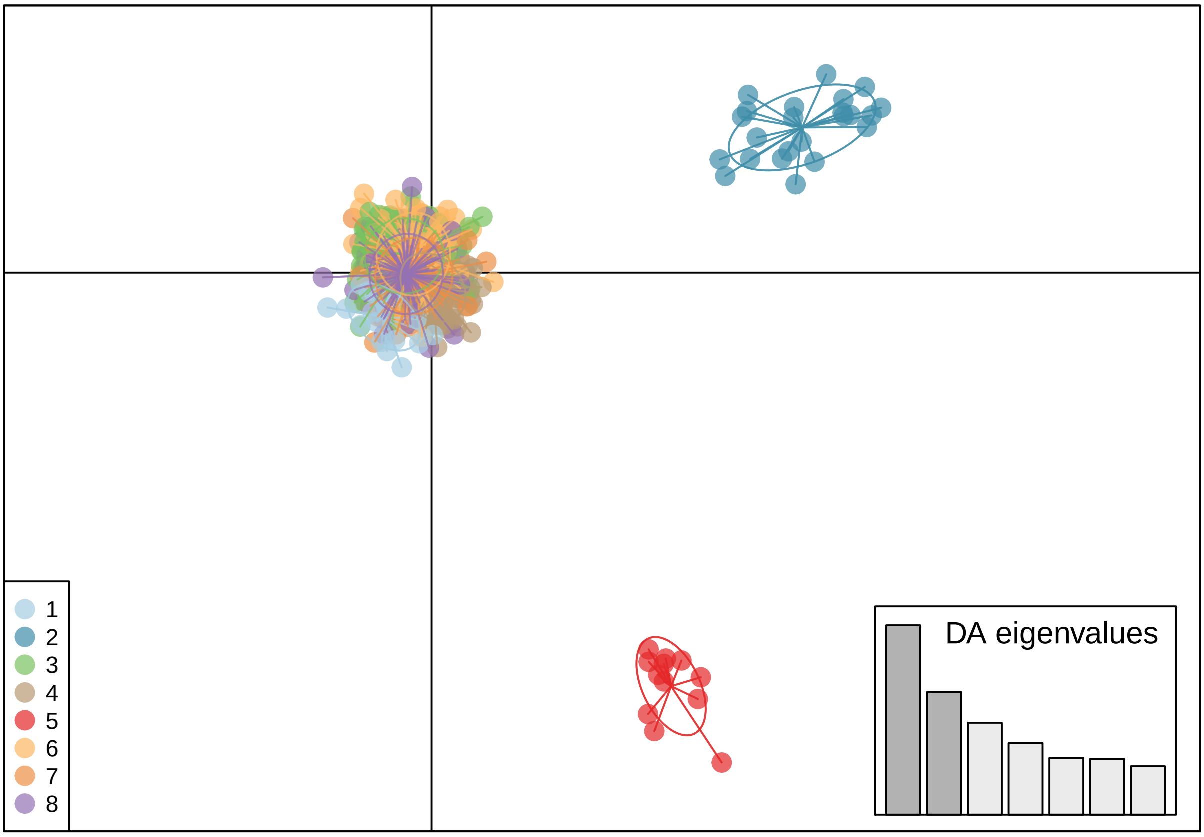

DA eigenvalues
1
2
3

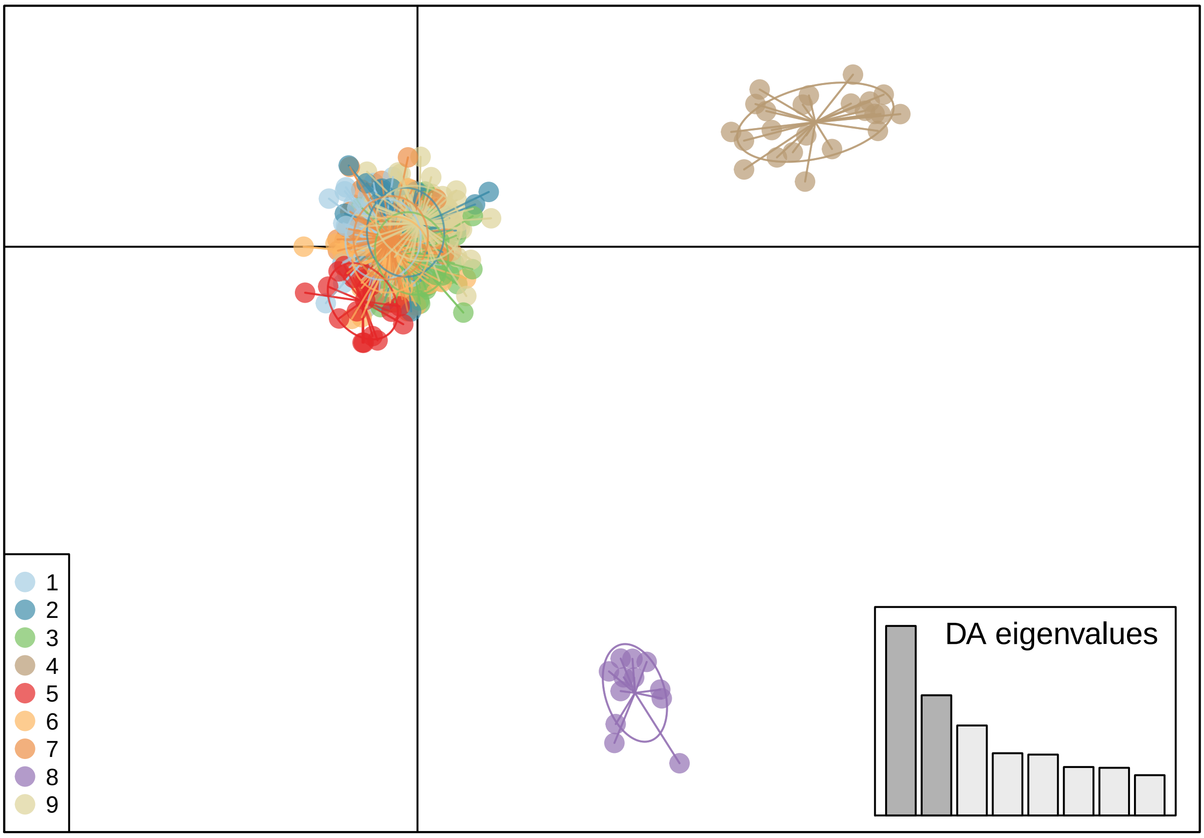

DA eigenvalues
1
2
3
4

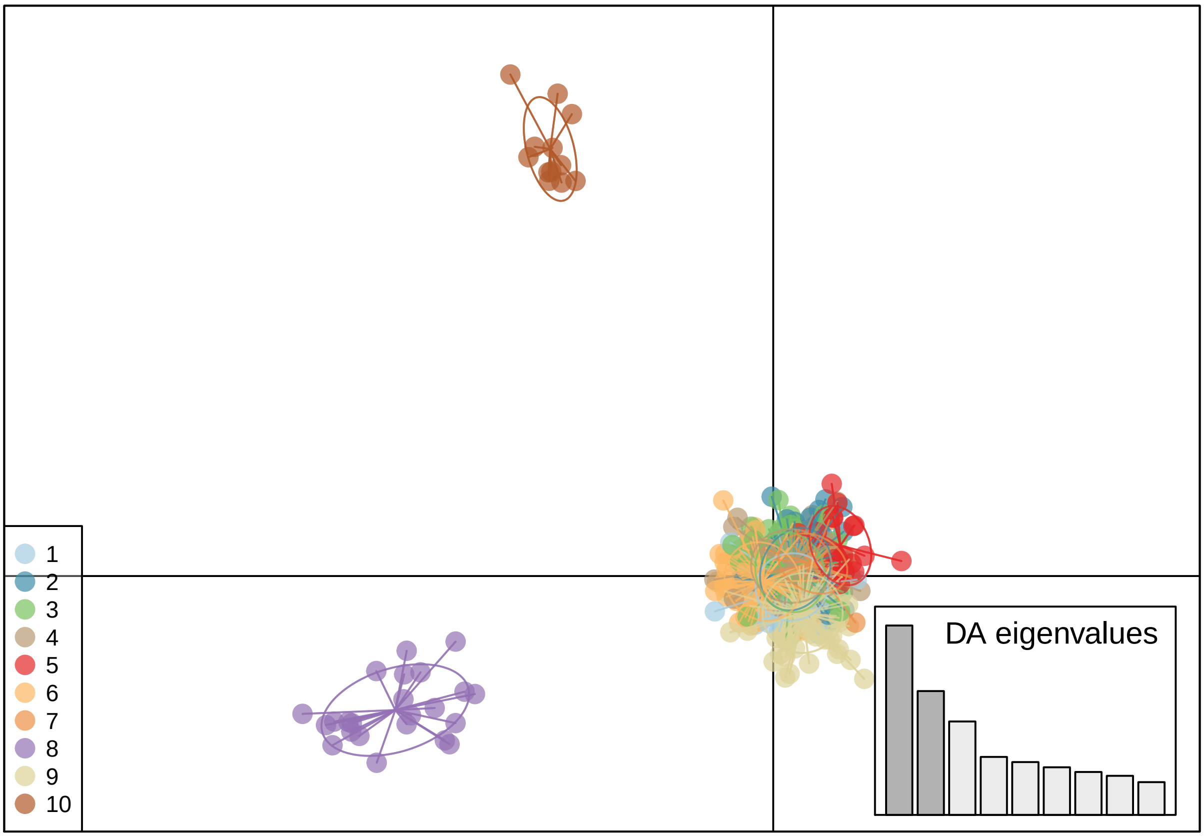

DA eigenvalues
1
2
3
4
5


DA eigenvalues
1
2
3
4
5
6


1
2
3
4
5
6
7
DA eigenvalues


1
2
3
4
5
6
7
8
DA eigenvalues

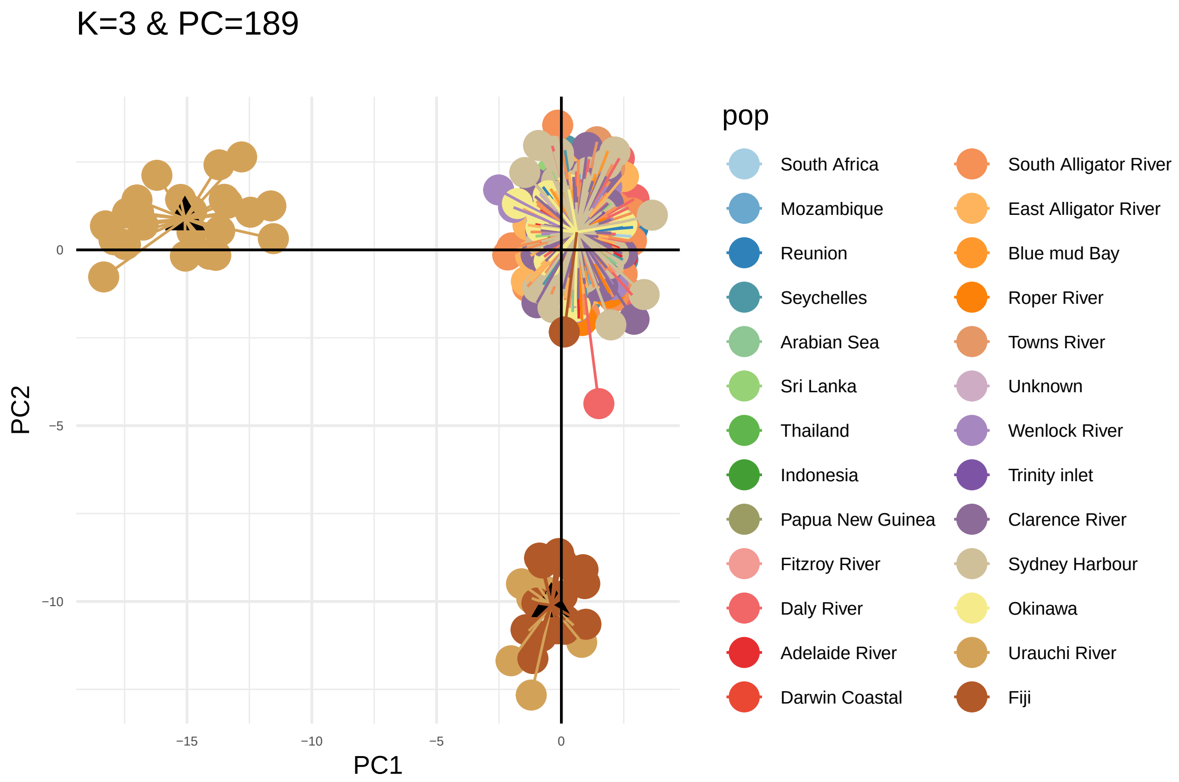




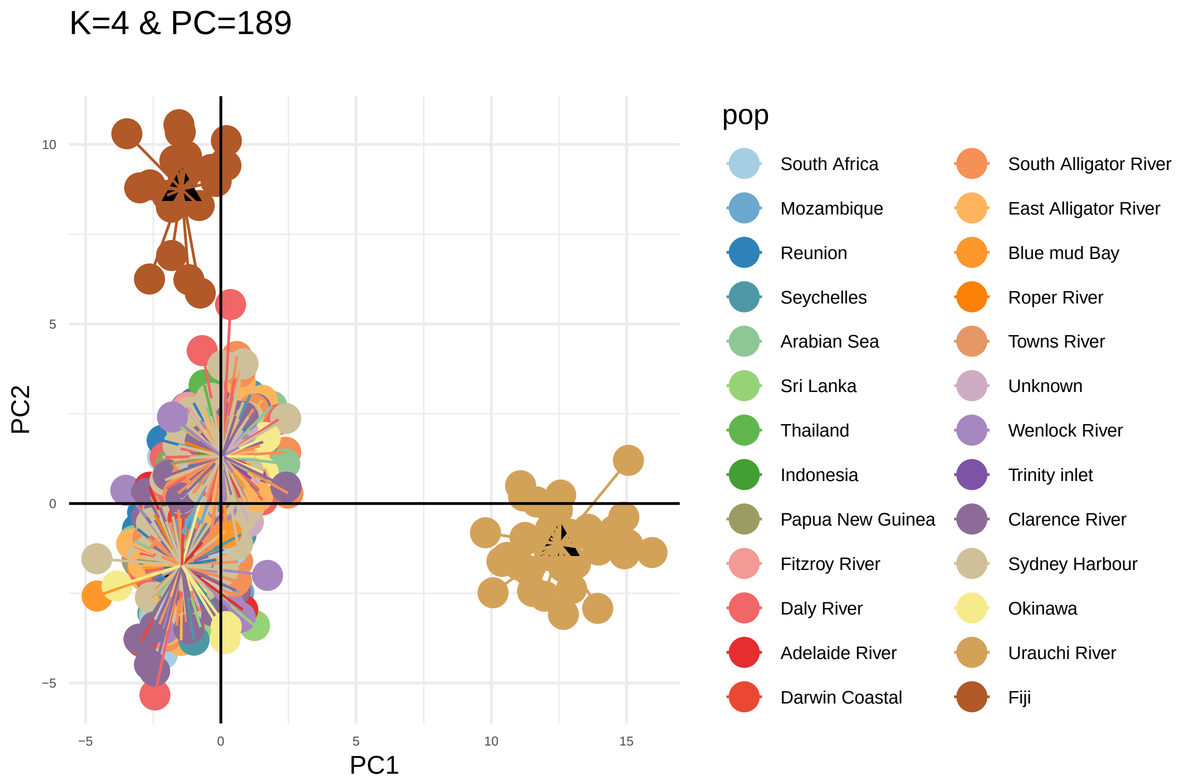
11.9.5 DAPC scatterplot - FLO

This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

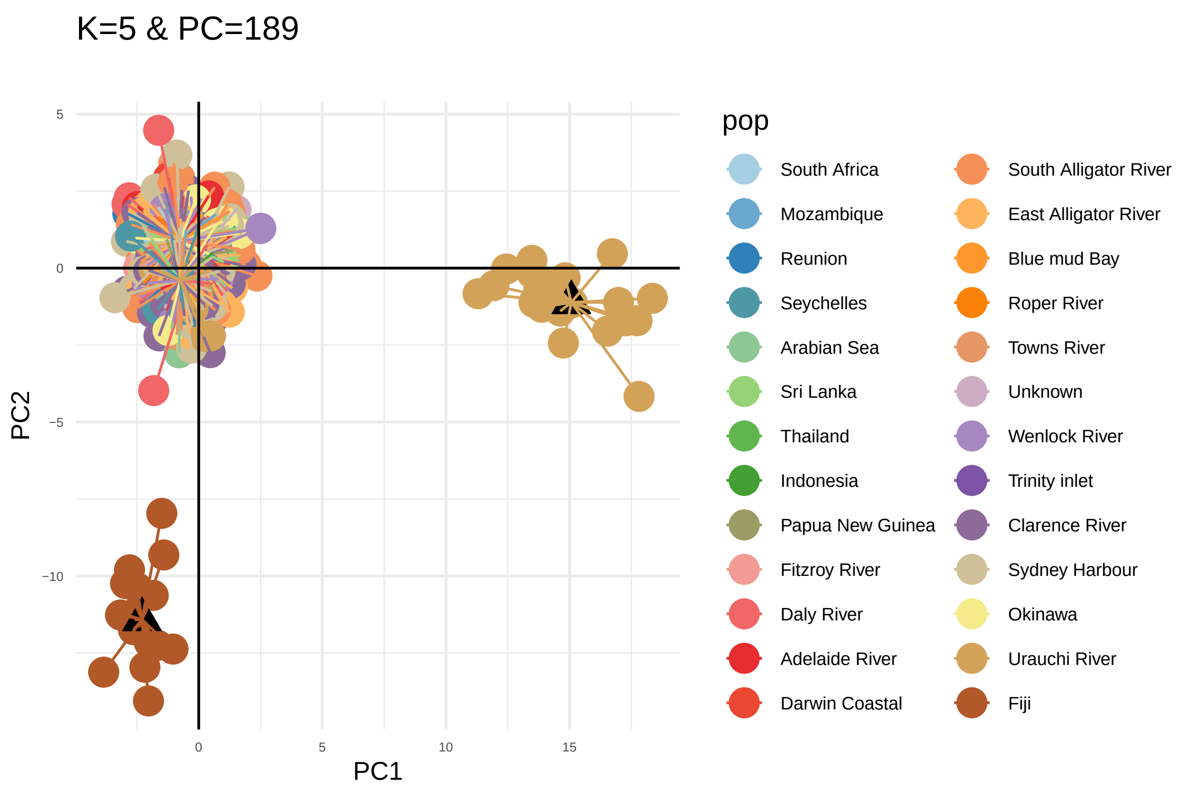
```r
for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartcap.IWP.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x,mean.y = y)~group,df,mean),
              by = "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x,y = mean.y),size = 5,
                        shape = 17, color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y, xend = x,
                                       yend = y)) +
    ggplot2::scale_colour_manual(values = colours.26) +
    ggplot2::scale_fill_manual(values = colours.26) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
         y = "PC2",
         x = "PC1",
         title = paste0("K=",K," & PC=",PC, sep = ""),
         caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot, filename = paste0("DArTcap_IWP_DAPC_scatterplot2_K",
                                          K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```

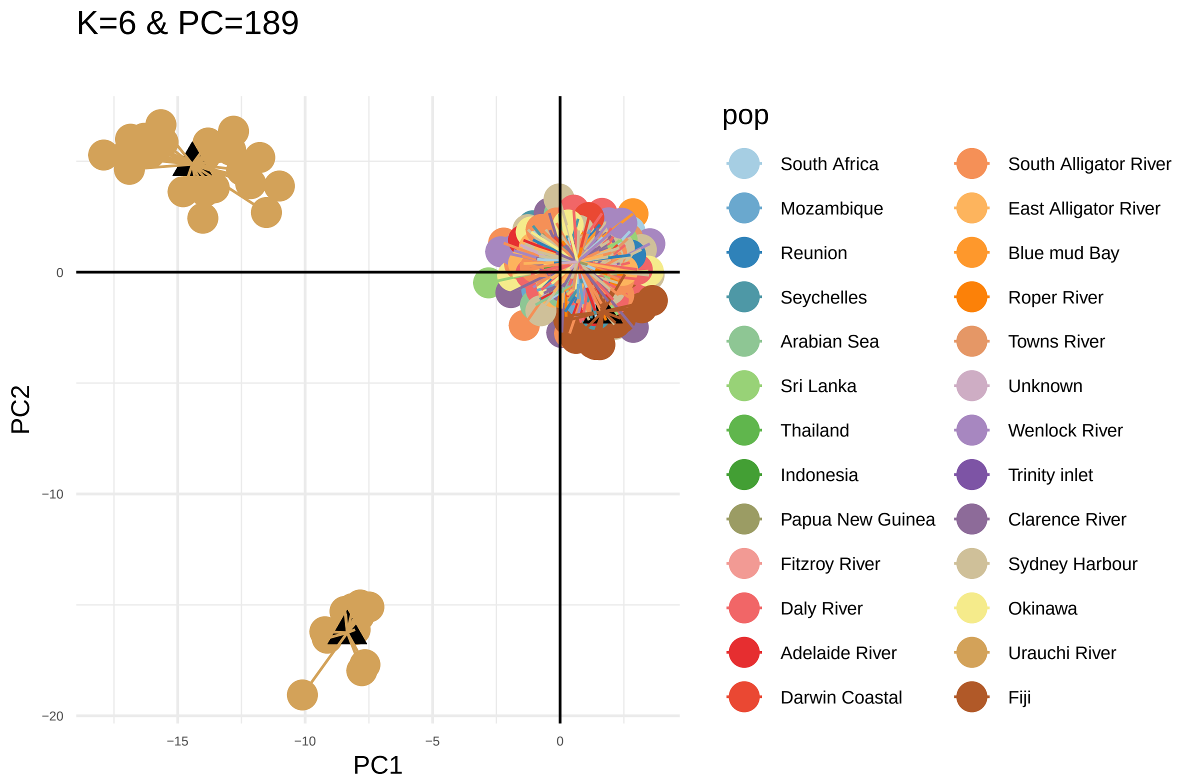


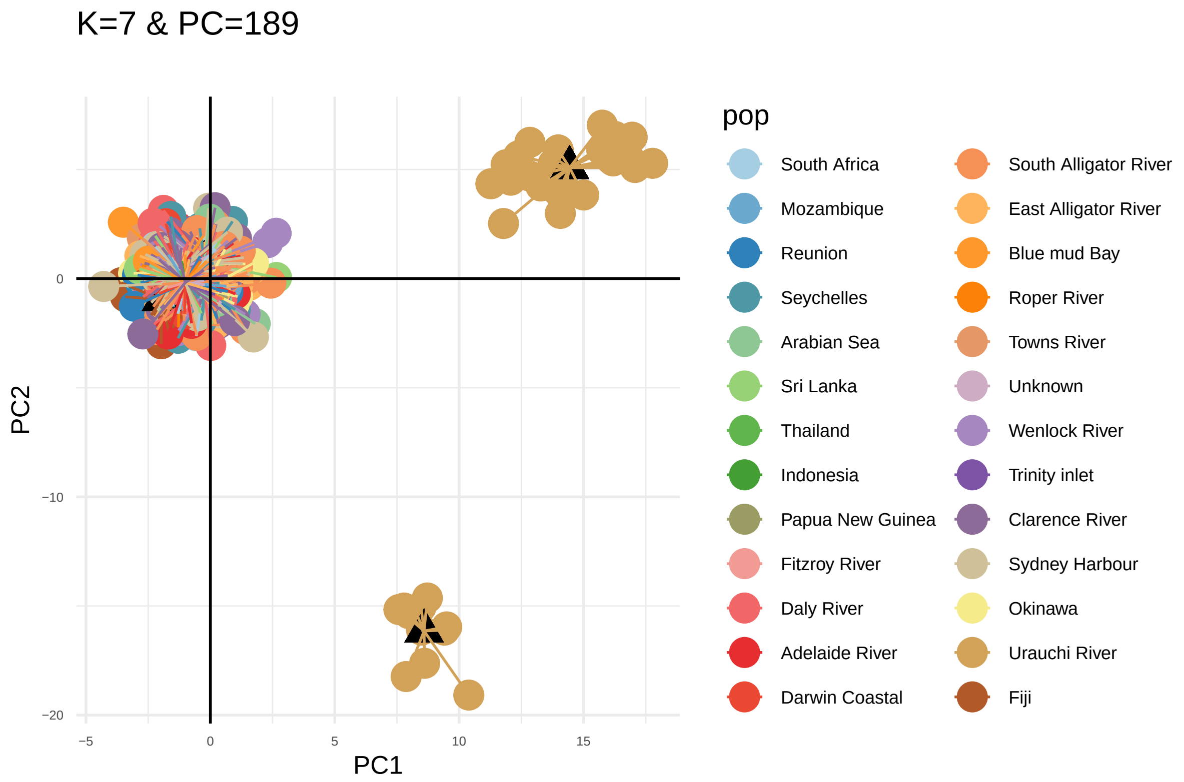
K=3 & PC=189

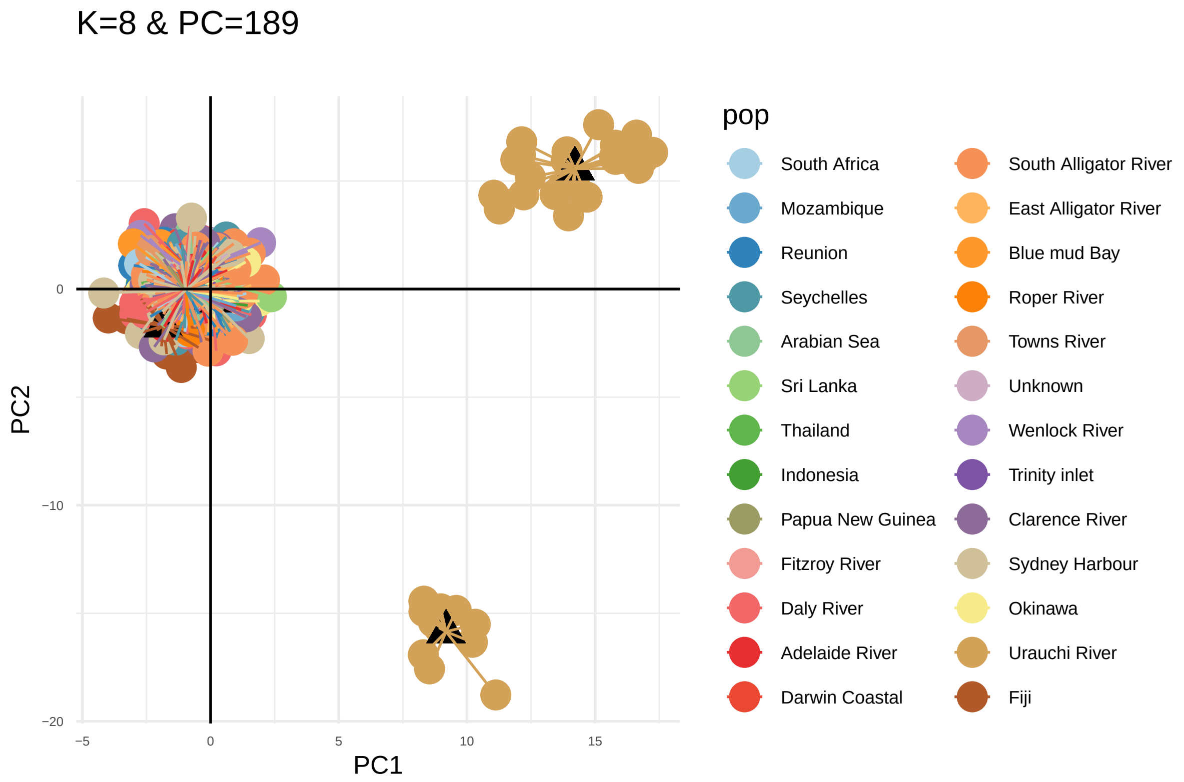


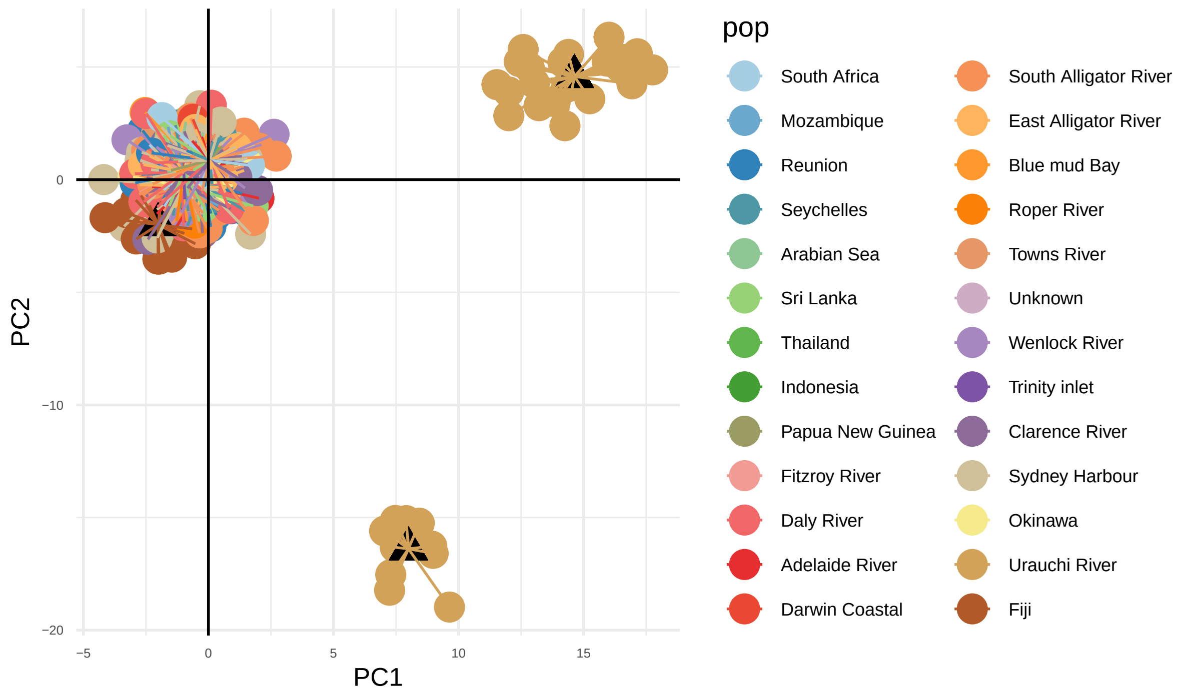
K=4 & PC=189

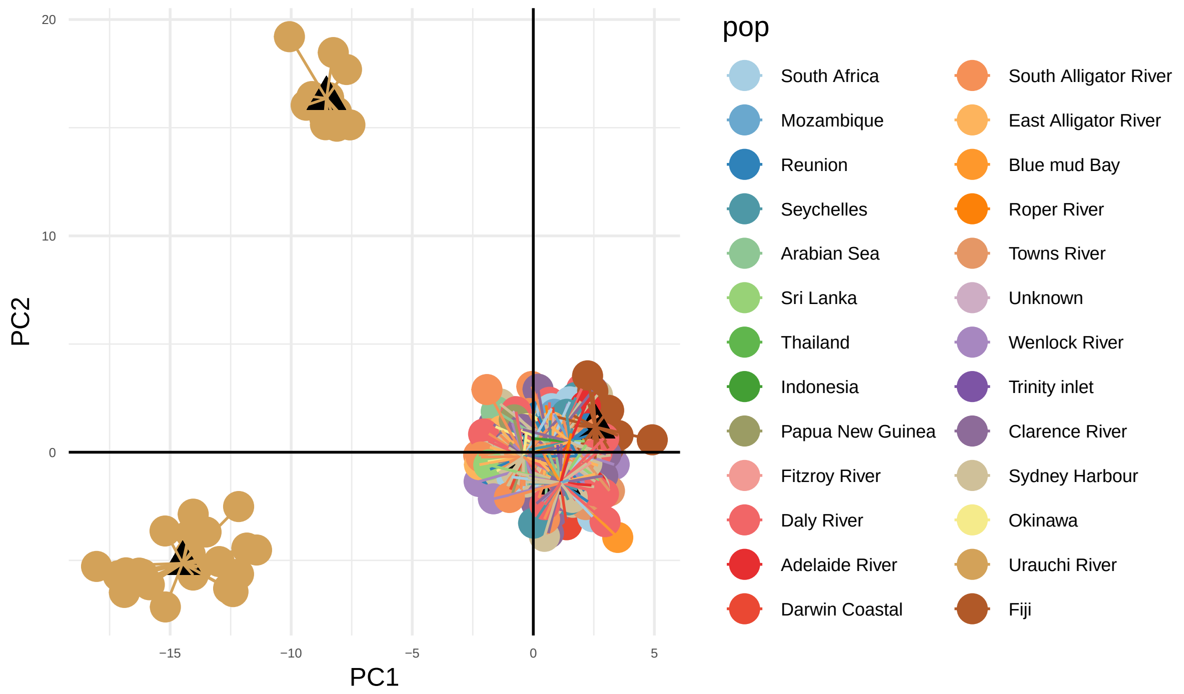

K=5 & PC=189
PC2
PC1
5
0
−5
−10
0
5
10
15
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji


K=6 & PC=189
PC2
PC1
0
−10
−20
−15
−10
−5
0
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji


K=7 & PC=189
PC2
PC1
0
−10
−20
−5
0
5
10
15
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji


K=8 & PC=189
PC2
PC1
0
−10
−20
−5
0
5
10
15
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Fitzroy River
Daly River
Adelaide River
Darwin Coastal
South Alligator River
East Alligator River
Blue mud Bay
Roper River
Towns River
Unknown
Wenlock River
Trinity inlet
Clarence River
Sydney Harbour
Okinawa
Urauchi River
Fiji


K=9 & PC=189


K=10 & PC=189

12 DATA6: DArTcap - Indo - West Pacific: no Japan or Fiji and subset from Australia

12.1 Set strata

```
strata <- radiator::read_strata("Bull_shark_DArTcap_strata5_IWP.tsv",
                                 keep.two = FALSE)$strata %>%
  dplyr:: filter(Region %in% c("W-IO","N-IO", "E-IO","E-IO/W-PAC","W-PAC"))
id.sub <- c(strata$INDIVIDUALS[strata$Site != "Australia"],
            sample(strata$INDIVIDUALS[strata$Site == "Australia"], size = 60))
strata <- strata[strata$INDIVIDUALS %in% id.sub,]
readr::write_tsv(strata, path = "Bull_shark_DArTcap_strata6_IWP2.tsv")
```

12.2 Filter data

1. Marker Reproducibility: 0.98
2. Individual missingness: 0.25
3. Individual Het - low: 0
4. Individual Het - high: 0.07
5. Individual total coverage - low: 10,000
6. Individual total coverage - high: 1,000,000
7. Marker MAC - low: 3
8. Marker coverage - low: 5
9. Marker coverage - high:80
10. Marker maximum missing proportion: 0.1
11. Marker snp position on locus: n
12. Max 2 SNPs per locus
13. 1 SNP per locus according to mac
14. no LD filter
15. Individual Het - low: 0.100
16. Individual Het - high: 0.1337
17. Duplicated individuals: 0.2
18. Filter on HWE: 2 pops, 0.001

```
dartcap.data <- "SEQ_SNPs_counts_0_Target_merge.csv"
strata <- "Bull_shark_DArTcap_strata6_IWP2.tsv"
BSsnp <- radiator::filter_rad(dartcap.data, strata,
                              parallel.core = 1)
BS.dartcap.IWP2.gds <- BSsnp$gds
BS.dartcap.IWP2.tidy <- BSsnp$output$tidy.data
print(BS.dartcap.IWP2.gds, expand = TRUE, all = TRUE, attribute = TRUE,
      attribute.trim = FALSE)

save(BS.dartcap.IWP2.tidy, file = "DArTcap_IWP2.Rdata")
```

Table 47:

FILTERS	VALUES	BEFORE	BLACKLIST
Filter DArT reproducibility	0.98	241 / 21 / 1 / 26335 / 37537	0 / 0 / 0 / 1043 / 2250
Filter monomorphic markers	NA	241 / 21 / 1 / 25292 / 35287	0 / 0 / 0 / 15102 / 23847
Filter markers in common	NA	241 / 21 / 1 / 10190 / 11440	0 / 0 / 0 / 2105 / 2291
Filter individuals based on missingness	0.25	241 / 21 / 1 / 8085 / 9149	4 / 0 / 0 / 0 / 0
Filter individuals based on heterozygosity	0 0.07	237 / 21 / 1 / 8085 / 9149	10 / 0 / 0 / 0 / 0
Filter individuals based on total coverage	10000 1e+06	227 / 21 / 1 / 8085 / 9149	1 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	226 / 21 / 1 / 8085 / 9149	0 / 0 / 0 / 2298 / 2825
Filter MAC	3	226 / 21 / 1 / 5787 / 6324	0 / 0 / 0 / 3358 / 3750
Filter coverage min / max	5-80	226 / 21 / 1 / 2429 / 2574	0 / 0 / 0 / 526 / 537
Filter genotyping	0.1	226 / 21 / 1 / 1903 / 2037	0 / 0 / 0 / 91 / 97
Filter SNPs position on the read	all	226 / 21 / 1 / 1812 / 1940	0 / 0 / 0 / 0 / 0
Filter markers snp number	3	226 / 21 / 1 / 1812 / 1940	0 / 0 / 0 / 0 / 0
detect mixed genomes	0.1 0.1337	226 / 21 / 1 / 1812 / 1940	20 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	206 / 21 / 1 / 1812 / 1940	0 / 0 / 0 / 1 / 1
detect duplicate genomes	0.2	206 / 21 / 1 / 1811 / 1939	17 / 0 / 0 / 0 / 0
Filter monomorphic markers	NA	189 / 21 / 1 / 1811 / 1939	0 / 0 / 0 / 1 / 1
Filter HWE	20.001	189 / 21 / 1 / 1810 / 1938	0 / 0 / 0 / 2 / 2

12.2.1 Remove extra low and high heterozygous individuals

Because the average heterozygosity per sampling location is not even, certain individuals cannot be excluded without removing 'good' individuals.

```
rm <-  c("CL-ARS021-F","CL-GOM025-F.1","CL-GOM012-F","CL-SAF014-M","CL-SAF002-F",
         "CL-BRZ038-U","CLF003-F","CL-GOM011-F","CL-SAF015-F","CL-SAF003-M",
         "CL-PNG005-U","CLCR056-M","CLCR047.1","CLCR055-M","CLCR066-M")

BS.dartcap.IWP2.tidy <- BS.dartcap.IWP2.tidy[
  !BS.dartcap.IWP2.tidy$INDIVIDUALS %in% rm,]
length(unique(BS.dartcap.IWP2.tidy$INDIVIDUALS)) # 189
```

12.3 Save data

```
Convert <- radiator::genomic_converter(BS.dartcap.IWP2.tidy,
                                       output = c("genlight", "stockr",
                                                  "pcadapt", "gtypes", "rubias"))
BS.dartcap.IWP2.gl <- Convert$genlight
BS.dartcap.IWP2.stkr <- Convert$stockr
BS.dartcap.IWP2.pc <- Convert$pcadapt
BS.dartcap.IWP2.gt <- Convert$gtypes
BS.dartcap.IWP2.rubias <- Convert$rubias

markers.meta <- radiator::extract_markers_metadata(BS.dartcap.IWP2.gds,
                                                   whitelist = TRUE)
individuals.meta <- radiator::extract_individuals_metadata(BS.dartcap.IWP2.gds,
                                                           whitelist = TRUE)
individuals.meta <- individuals.meta[individuals.meta$INDIVIDUALS %in%
                                       BS.dartcap.IWP2.gl$ind.names,]
BS.dartcap.IWP2.gl$other$ind.metrics <- individuals.meta
BS.dartcap.IWP2.gl$other$loc.metrics <- markers.meta
BS.dartcap.IWP2.gt@schemes <- individuals.meta

pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Fitzroy River", "Daly River",
                "Adelaide River","Darwin Coastal",  "South Alligator River",
                "East Alligator River","Blue mud Bay", "Roper River",
                "Towns River","Wenlock River", "Trinity inlet","Clarence River",
                "Sydney Harbour")
BS.dartcap.IWP2.gl$pop <- factor(BS.dartcap.IWP2.gl$other$ind.metrics$Site2,
                                 levels = pop.levels)
BS.dartcap.IWP2.gl <- BS.dartcap.IWP2.gl[order(BS.dartcap.IWP2.gl$pop,
                                               BS.dartcap.IWP2.gl$ind.names),]
BS.dartcap.IWP2.gl <- BS.dartcap.IWP2.gl[order(BS.dartcap.IWP2.gl$pop,
                                               BS.dartcap.IWP2.gl$ind.names)]
BS.dartcap.IWP2.rubias$repunit <- factor(BS.dartcap.IWP2.rubias$repunit,
                                         levels = pop.levels)

save(BS.dartcap.IWP2.tidy, BS.dartcap.IWP2.gl, BS.dartcap.IWP2.stkr,
     BS.dartcap.IWP2.pc,BS.dartcap.IWP2.gt,BS.dartcap.IWP2.rubias,
     markers.meta, individuals.meta, file = "DArTcap_IWP2.Rdata")
```

12.4 Load data

```
load("DArTcap_IWP2.Rdata")
```

```
pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Australia")
BS.dartcap.IWP2.gl$pop <- factor(BS.dartcap.IWP2.gl$other$ind.metrics$Site,
                                 levels = pop.levels)
BS.dartcap.IWP2.gl <- BS.dartcap.IWP2.gl[order(BS.dartcap.IWP2.gl$pop,
                                               BS.dartcap.IWP2.gl$ind.names),]


unique(BS.dartcap.IWP2.tidy$POP_ID)
AUS <- c( "Daly_River", "Wenlock_River", "Sydney_Harbour","Clarence_River",
          "Fitzroy_River","Adelaide_River","South_Alligator_River","Trinity_inlet",
          "Blue_mud_Bay","East_Alligator_River","Towns_River","Darwin_Coastal")
POP_ID <- as.character(BS.dartcap.IWP2.tidy$POP_ID)
POP_ID[POP_ID %in% AUS] <- "Australia"
pop.levels1 <- stringr::str_replace_all(pop.levels, " ", "_")
BS.dartcap.IWP2.tidy$POP_ID <- factor(POP_ID, levels = pop.levels1)
BS.dartcap.IWP2.tidy <- BS.dartcap.IWP2.tidy[order(BS.dartcap.IWP2.tidy$POP_ID,
                                                   BS.dartcap.IWP2.tidy$INDIVIDUALS),]

adegenet::nInd(BS.dartcap.IWP2.gl) # 189
adegenet::nLoc(BS.dartcap.IWP2.gl) # 1808
summary(BS.dartcap.IWP2.gl$pop)
sum(duplicated(BS.dartcap.IWP2.gl$other$ind.metrics$`Genetic code`))# 0 replicate left
sum(baits$CloneID %in% BS.dartcap.IWP2.gl$other$loc.metrics$LOCUS) #72
```

```
##  [1] Arabian_Sea           Sri_Lanka             Thailand
##  [4] Mozambique            Reunion               South_Africa
##  [7] Papua_New_Guinea      Seychelles            Indonesia
## [10] Daly_River            Wenlock_River         Sydney_Harbour
## [13] Clarence_River        Fitzroy_River         Adelaide_River
## [16] South_Alligator_River Trinity_inlet         Blue_mud_Bay
## [19] East_Alligator_River  Towns_River           Darwin_Coastal
## 21 Levels: Arabian_Sea Sri_Lanka Thailand Mozambique Reunion ... Darwin_Coastal
## [1] 189
## [1] 1936
##     South Africa       Mozambique          Reunion       Seychelles
##               22                9               26               35
##      Arabian Sea        Sri Lanka         Thailand        Indonesia
##               15               11                4                4
## Papua New Guinea        Australia
##                9               54
## [1] 0
## [1] 72
```

12.5 Remove sex-linked markers

```
load("Sex-linked_marker_DArTcap.Rdata")
load("Sex_results.Rdata")
sum(bull_shark$sexy.summary$CLONE_ID %in% SLM$sexy.summary$CLONE_ID) #33
sum(SLM$sexy.summary$CLONE_ID %in% bull_shark$sexy.summary$CLONE_ID) #23
sex.markers <- unique(c(bull_shark$sexy.summary$CLONE_ID,
                        SLM$sexy.summary$CLONE_ID))

sum(BS.dartcap.IWP2.gl$loc.names %in% sex.markers) #23
locnames <- BS.dartcap.IWP2.gl$loc.names
BS.dartcap.IWP2.gl <- BS.dartcap.IWP2.gl[,!locnames %in% sex.markers]
```

```
BS.dartcap.IWP2.gl$other$loc.metrics <- BS.dartcap.IWP2.gl$other$loc.metrics[
  !locnames %in% sex.markers,]

sum(sex.markers %in% unique(BS.dartcap.IWP2.tidy$LOCUS)) # 22
BS.dartcap.IWP2.tidy <- BS.dartcap.IWP2.tidy[!BS.dartcap.IWP2.tidy$LOCUS %in%
                                               sex.markers,]

locus.gt <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                               string =  BS.dartcap.IWP2.gt@data$locus)[,2]
BS.dartcap.IWP2.gt <- BS.dartcap.IWP2.gt[,!locus.gt %in% sex.markers, ,
                                         drop = TRUE]

locus.rubias <- stringr::str_match(pattern = "__\\s*(.*?)\\s*__",
                                   string =  colnames(BS.dartcap.IWP2.rubias))[,2]
BS.dartcap.IWP2.rubias <- BS.dartcap.IWP2.rubias[,!locus.rubias %in%
                                                   sex.markers]
```

```
## [1] 33
## [1] 23
## [1] 23
## [1] 22
```

12.6 Genetic diversity

```
set.seed(124)

pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Australia")

gl <- BS.dartcap.IWP2.gl
gl$pop <- factor(gl$other$ind.metrics$Site, levels = pop.levels)
gl <- gl[order(gl$pop,gl$ind.names)]

gl2gpop(gl, filename = "BS_dartcap_IWP2_genepop.txt")
bastat <-diveRsity::basicStats(infile = "BS_dartcap_IWP2_genepop.txt",
                               outfile = "BS_dartcap_IWP2_BasicStat_output.txt",
                               fis_ci = TRUE,ar_ci = TRUE, fis_boots = 1000,
                               ar_boots = 1000,mc_reps = 1000,
                               rarefaction = FALSE, ar_alpha = 0.05,
                               fis_alpha = 0.05)

length(bastat$main_tab)#10
gendiv <- data.frame(
  "South Africa" = bastat$main_tab[[1]]$overall,
  "Mozambique" = bastat$main_tab[[2]]$overall,
  "Reunion" = bastat$main_tab[[3]]$overall,
  "Seychelles" = bastat$main_tab[[4]]$overall,
  "Arabian Sea" = bastat$main_tab[[5]]$overall,
  "Sri Lanka" = bastat$main_tab[[6]]$overall,
  "Thailand" = bastat$main_tab[[7]]$overall,
  "Indonesia" = bastat$main_tab[[8]]$overall,
  "Papua New Guinea" = bastat$main_tab[[9]]$overall,
  "Australia" = bastat$main_tab[[10]]$overall,
  check.names = FALSE)
row.names(gendiv) <- rownames(bastat$main_tab[[1]])

df <- as.data.frame(gl)
```

```r
df[df == "0"] <- "11"
df[df == "1"] <- "12"
df[df == "2"] <- "22"
gen.gi <- adegenet::df2genind(df, ploidy = 2,ncode = 2, pop = gl$pop)
ris_basic <- hierfstat::basic.stats(gen.gi)
fis.hierfstat <- apply(ris_basic$Fis, 2, mean, na.rm=T)
fis.CI <- hierfstat::boot.ppfis(gen.gi, nboot = 1000, quant = c(0.025,0.975),
                                diploid = TRUE,dig = 4)
df <- data.frame(fis.hierfstat,fis.CI.low = fis.CI$fis.ci[,1],
                 fis.CI.high = fis.CI$fis.ci[,2])
df <- as.data.frame(t(df))
gendiv <- rbind(gendiv, df)

readr::write_tsv(gendiv, path = "DArTcap_IWP2_gendiv.txt")
save(gendiv, file = "DArTcap_IWP2_gendiv.Rdata")
```

```r
load("DArTcap_IWP2_gendiv.Rdata")
shortnames <- c("SAF", "MOZ", "RUN" , "SEY", "ARS", "SRL", "TAI", "IND",
                "PNG" , "AUS")
knitr::kable(gendiv, col.names = shortnames, digits = 4,caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

Table 48:

	SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS
ar	1.3280	1.3010	1.3220	1.3300	1.3210	1.3080	1.2800	1.2580	1.3050	1.3340
size	21.8700	8.7070	25.6740	34.7520	14.9200	10.9490	3.9810	3.9740	8.9420	53.6900
obs_het	0.1150	0.1140	0.1130	0.1170	0.1160	0.1160	0.1240	0.1150	0.1160	0.1150
exp_het	0.1200	0.1180	0.1190	0.1200	0.1180	0.1150	0.1090	0.1020	0.1140	0.1210
uexp_het	0.1230	0.1250	0.1220	0.1220	0.1220	0.1210	0.1250	0.1170	0.1210	0.1230
fis	0.0350	0.0210	0.0430	0.0270	0.0030	-0.0120	-0.1360	-0.1300	-0.0260	0.0430
hwe_glb	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_hom	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
hwe_het	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
fis_lo	0.0000	-0.0830	0.0080	0.0020	-0.0530	-0.0930	-0.3910	-0.5630	-0.1220	0.0270
fis_hi	0.0280	0.0080	0.0390	0.0250	-0.0040	-0.0210	-0.1360	-0.1300	-0.0360	0.0410
ar_lo	1.2780	1.2020	1.2710	1.2800	1.2290	1.2150	1.2240	1.1690	1.2160	1.2830
ar_hi	1.3570	1.3530	1.3470	1.3520	1.3550	1.3570	1.3500	1.3200	1.3500	1.3590
fis.hierfstat	0.0570	0.0750	0.0613	0.0409	0.0353	0.0326	-0.0083	-0.0052	0.0286	0.0518
fis.CI.low	0.0515	0.0693	0.0585	0.0292	0.0255	0.0109	-0.0232	-0.0178	0.0215	0.0506
fis.CI.high	0.0855	0.1314	0.0937	0.0579	0.0669	0.0606	0.0511	0.0617	0.0716	0.0762

12.6.1 Number of monomorphic markers per population

```r
pop.levels <- c("South Africa", "Mozambique", "Reunion" , "Seychelles",
                "Arabian Sea", "Sri Lanka", "Thailand", "Indonesia",
                "Papua New Guinea" , "Australia")

monomorphics <- c()
for (i in 1:length(pop.levels)) {
  x <- BS.dartcap.IWP2.gl[BS.dartcap.IWP2.gl$pop == pop.levels[i]]
  x2 <- dartR::gl.filter.monomorphs(x, verbose = 0)
  locs <-  adegenet::nLoc(x) - adegenet::nLoc(x2)
  monomorphics[i] <- locs
}
names(monomorphics) <- pop.levels
shortnames <- c("SAF", "MOZ", "RUN" , "SEY", "ARS", "SRL", "TAI", "IND",
                "PNG" , "AUS")
knitr::kable(t(as.table(monomorphics)), col.names = shortnames, digits = 4,
             caption = "") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

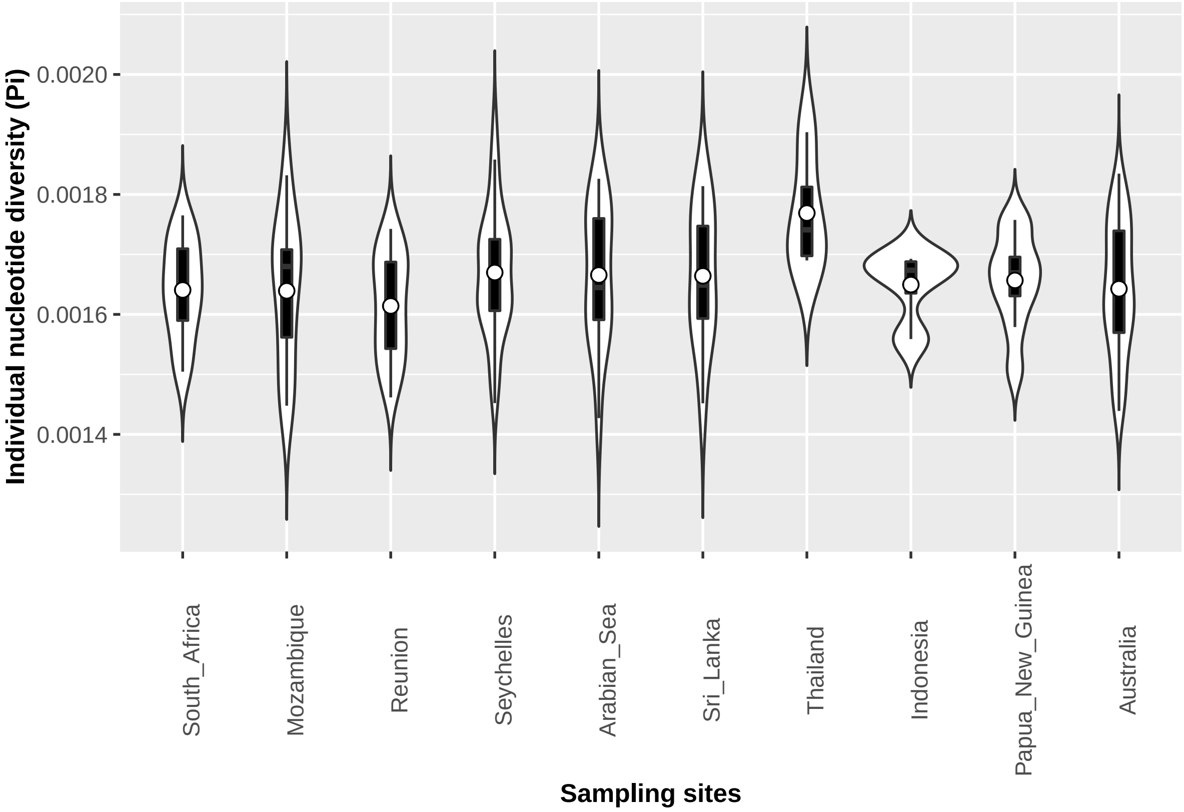
Table 49:

SAF	MOZ	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS
625	1012	627	491	794	928	1299	1356	1010	276

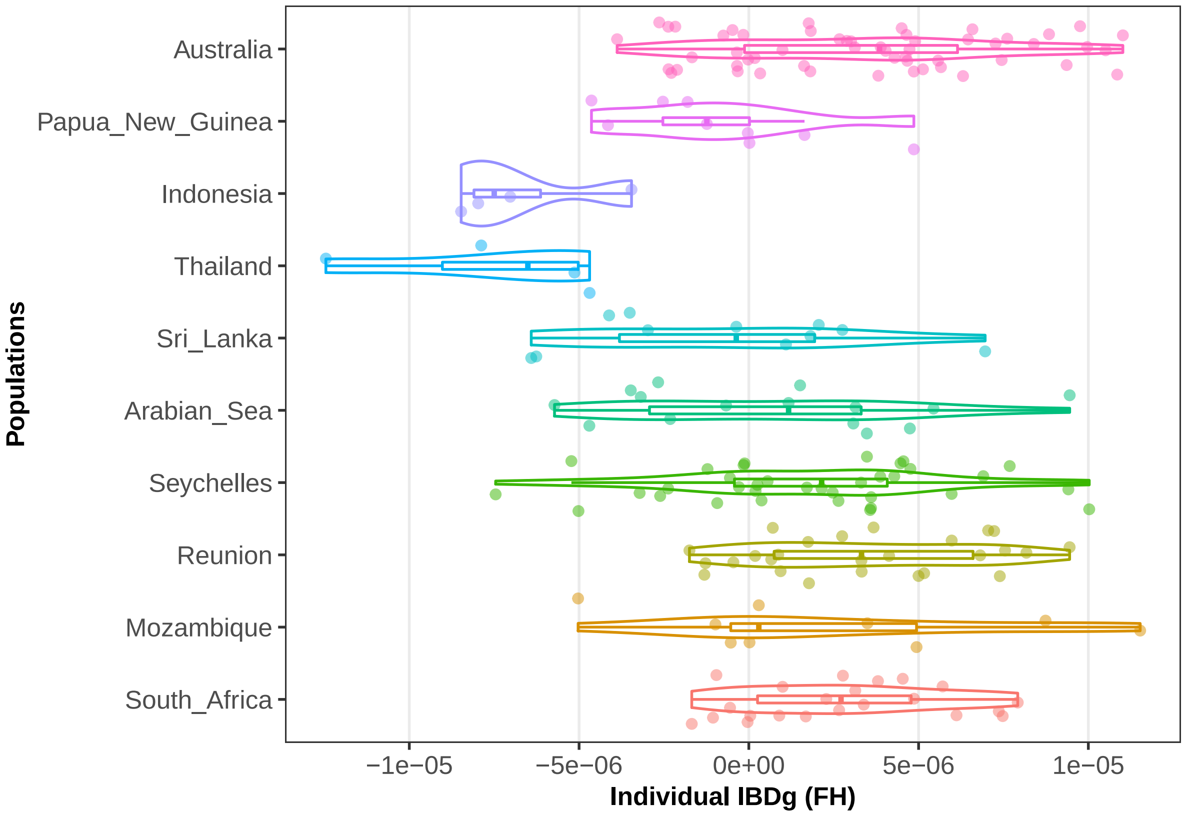
12.6.2 Nucleotide diversity and inbreeding

```
pi.sum <- radiator::pi(
  data = BS.dartcap.IWP2.tidy,
  read.length = 70,
  parallel.core = parallel::detectCores() - 1,
  path.folder = NULL,
  verbose = TRUE
)

FIS.sum<- radiator::ibdg_fh(data = BS.dartcap.IWP2.tidy,
        path.folder = NULL, verbose = TRUE)

save(pi.sum, FIS.sum, file = "DArTcap_IWP2_pi_FIS_Sites.Rdata")
```

```
load("DArTcap_IWP2_pi_FIS_Sites.Rdata")
pi.sum$boxplot.pi
```



```
FIS.sum$fh.box.plot
```



12.7 Genetic differentiation

```
strata <- BS.dartcap.IWP2.gt@schemes$Site
names(strata) <- BS.dartcap.IWP2.gt@schemes$INDIVIDUALS
strataG::setStrata(BS.dartcap.IWP2.gt) <- strata

Fst.gt <- strataG::popStructTest(
    BS.dartcap.IWP2.gt,
    nrep = 1000,
    stats = "all",
    type = "pairwise",
    keep.null = FALSE,
    quietly = TRUE,
    nb.cores =  parallel::detectCores() - 1,
    write.output = FALSE
  )
save(Fst.gt, file = "DArTcap_IWP2_FST.Rdata")
readr::write_tsv(Fst.gt$pairwise$result, path = "DArTcap_IWP2_FST.txt")
```

```
load("DArTcap_IWP2_FST.Rdata")

kableExtra::kbl(Fst.gt$pairwise$result[order(Fst.gt$pairwise$result$Fst,
                                        decreasing = TRUE),
                                  -c(1:4)], digits = 4,
  caption = "Pairwise Fst for 1924 DArTcap loci between the IWP sites (no JAP/FIJ and with subset of
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()
```

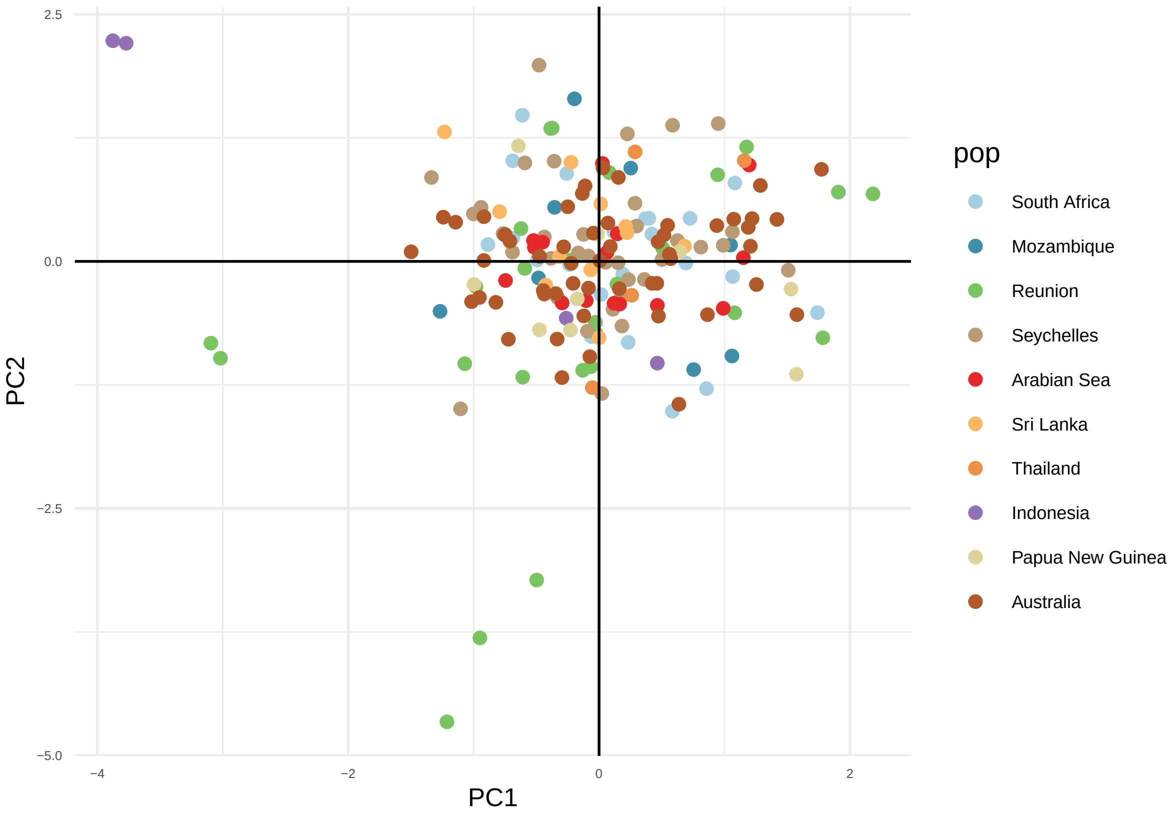
Table 50: Pairwise Fst for 1924 DArTcap loci between the IWP sites (no JAP/FIJ and with subset of AUS)

	Chi2	Chi2.p.val	D	D.p.val	Fis	Fis.p.val	Fst	Fst.p.val	F'st	F'st.p.val	Gst	Gst.p.val	G'st	G'st.p.val	G"st	G"st.p.val
Indonesia (4) v. Papua New Guinea (9)	1334.839	0.0589	7e-04	0.0370	-6.7164	0.9730	0.0218	0.0430	0.0250	0.0430	0.2650	0.0310	0.3054	0.0340	0.4510	0.0330
Indonesia (4) v. Seychelles (35)	1830.180	0.0190	5e-04	0.0220	-2.2181	0.9770	0.0165	0.0120	0.0190	0.0120	0.0884	0.0100	0.1085	0.0110	0.1809	0.0100
Indonesia (4) v. Thailand (4)	1079.938	0.3516	7e-04	0.3237	-18.9626	0.6533	0.0161	0.3776	0.0184	0.3776	0.5845	0.3776	0.6236	0.3776	0.7625	0.3776
Arabian Sea (15) v. Indonesia (4)	1528.321	0.0330	6e-04	0.0290	-4.0712	0.9749	0.0159	0.0291	0.0182	0.0291	0.1610	0.0291	0.1921	0.0301	0.3041	0.0301
Indonesia (4) v. Reunion (26)	1717.534	0.0390	6e-04	0.0480	-3.0000	0.9538	0.0149	0.0392	0.0173	0.0392	0.1165	0.0452	0.1414	0.0472	0.2310	0.0472
Indonesia (4) v. Mozambique (9)	1307.929	0.1868	6e-04	0.0939	-6.3804	0.8108	0.0142	0.0750	0.0169	0.0742	0.2569	0.2358	0.2976	0.2461	0.4411	0.2430
Australia (54) v. Indonesia (4)	1973.169	0.0410	6e-04	0.0020	-1.1134	0.9980	0.0142	0.0030	0.0162	0.0030	0.0495	0.0030	0.0619	0.0030	0.1062	0.0030
Indonesia (4) v. Sri Lanka (11)	1355.726	0.1229	6e-04	0.0559	-5.5080	0.9570	0.0140	0.0639	0.0160	0.0639	0.2153	0.0589	0.2518	0.0589	0.3844	0.0589
Mozambique (9) v. Papua New Guinea (9)	1508.837	0.0030	3e-04	0.1219	-3.6037	0.9990	0.0132	0.0020	0.0152	0.0020	0.1074	0.0020	0.1316	0.0020	0.2159	0.0020
Indonesia (4) v. South Africa (22)	1583.104	0.1738	5e-04	0.0220	-3.0250	0.9930	0.0109	0.0210	0.0125	0.0210	0.1180	0.0120	0.1432	0.0120	0.2337	0.0120
Papua New Guinea (9) v. Reunion (26)	1804.936	0.0130	3e-04	0.0390	-2.0813	0.9381	0.0076	0.0210	0.0088	0.0200	0.0446	0.0200	0.0559	0.0200	0.0961	0.0200
Arabian Sea (15) v. Papua New Guinea (9)	1633.386	0.0010	3e-04	0.0270	-2.6123	0.9560	0.0071	0.0040	0.0081	0.0040	0.0626	0.0040	0.0778	0.0040	0.1321	0.0040
Mozambique (9) v. Reunion (26)	1891.018	0.0020	3e-04	0.0420	-1.9940	0.2917	0.0069	0.0170	0.0080	0.0170	0.0443	0.0120	0.0557	0.0100	0.0957	0.0120
Papua New Guinea (9) v. Sri Lanka (11)	1432.583	0.1319	3e-04	0.2837	-3.3196	0.9500	0.0060	0.0250	0.0069	0.0250	0.0860	0.0240	0.1057	0.0240	0.1765	0.0240
Australia (54) v. Reunion (26)	2304.753	0.0010	2e-04	0.0010	-0.5943	0.8412	0.0056	0.0010	0.0065	0.0010	0.0077	0.0010	0.0098	0.0010	0.0174	0.0010
Mozambique (9) v. Seychelles (35)	1914.374	0.0020	2e-04	0.1319	-1.5864	0.0350	0.0056	0.0130	0.0064	0.0140	0.0330	0.0120	0.0418	0.0110	0.0724	0.0110
Reunion (26) v. Seychelles (35)	2114.155	0.0010	1e-04	0.0020	-1.0778	0.9451	0.0053	0.0010	0.0061	0.0010	0.0124	0.0010	0.0158	0.0010	0.0279	0.0010
Arabian Sea (15) v. Mozambique (9)	1641.319	0.0080	3e-04	0.0709	-2.4872	0.3127	0.0049	0.0260	0.0057	0.0230	0.0605	0.0160	0.0756	0.0150	0.1283	0.0150
Papua New Guinea (9) v. Seychelles (35)	1774.081	0.0230	3e-04	0.0100	-1.7114	0.7393	0.0048	0.0210	0.0055	0.0210	0.0337	0.0190	0.0424	0.0200	0.0736	0.0190
Reunion (26) v. South Africa (22)	1983.382	0.0010	2e-04	0.0010	-1.2610	0.9870	0.0044	0.0050	0.0050	0.0050	0.0165	0.0050	0.0210	0.0050	0.0369	0.0050
Reunion (26) v. Sri Lanka (11)	1814.081	0.0120	2e-04	0.2887	-1.8398	0.9500	0.0044	0.0430	0.0050	0.0430	0.0335	0.0470	0.0421	0.0460	0.0732	0.0470
Arabian Sea (15) v. Reunion (26)	1947.800	0.0010	2e-04	0.0589	-1.5135	0.9421	0.0033	0.0589	0.0038	0.0589	0.0228	0.0619	0.0289	0.0619	0.0505	0.0619
Australia (54) v. Mozambique (9)	1997.119	0.0280	2e-04	0.3057	-0.8019	0.0150	0.0032	0.0400	0.0037	0.0400	0.0165	0.0430	0.0211	0.0380	0.0370	0.0410
Mozambique (9) v. Sri Lanka (11)	1449.012	0.2138	3e-04	0.1209	-3.2057	0.5754	0.0026	0.1628	0.0030	0.1728	0.0842	0.1159	0.1039	0.1129	0.1735	0.1139
Australia (54) v. Papua New Guinea (9)	1827.823	0.3746	2e-04	0.0160	-0.9249	0.9231	0.0020	0.1399	0.0023	0.1399	0.0176	0.0789	0.0224	0.0849	0.0393	0.0809
Papua New Guinea (9) v. South Africa (22)	1614.736	0.2517	3e-04	0.0430	-2.0687	0.9461	0.0019	0.1878	0.0022	0.1878	0.0432	0.1179	0.0541	0.1209	0.0933	0.1209
Mozambique (9) v. South Africa (22)	1631.674	0.3137	2e-04	0.5315	-2.0358	0.2198	0.0017	0.2258	0.0019	0.2278	0.0438	0.1309	0.0552	0.1259	0.0949	0.1269
Arabian Sea (15) v. South Africa (22)	1771.898	0.0190	2e-04	0.2907	-1.5184	0.9520	0.0016	0.1289	0.0018	0.1289	0.0233	0.1089	0.0295	0.1119	0.0516	0.1099
Arabian Sea (15) v. Australia (54)	2068.432	0.0010	1e-04	0.2168	-0.5996	0.9411	0.0010	0.1718	0.0012	0.1718	0.0078	0.1409	0.0099	0.1419	0.0176	0.1419
Arabian Sea (15) v. Seychelles (35)	1886.888	0.0080	1e-04	0.2697	-1.2555	0.5355	0.0010	0.2378	0.0012	0.2378	0.0163	0.2567	0.0207	0.2577	0.0363	0.2577
Australia (54) v. South Africa (22)	1970.053	0.0859	1e-04	0.0549	-0.5473	0.3107	0.0005	0.2587	0.0006	0.2587	0.0053	0.2797	0.0067	0.2787	0.0120	0.2797
Seychelles (35) v. Thailand (4)	1705.603	0.0979	4e-04	0.1618	-2.0796	0.2700	0.0005	0.4290	0.0005	0.4290	0.0742	0.6640	0.0920	0.6410	0.1547	0.6540
Seychelles (35) v. South Africa (22)	1865.330	0.0849	1e-04	0.3716	-1.0063	0.0649	0.0004	0.3417	0.0005	0.3417	0.0102	0.3666	0.0130	0.3616	0.0230	0.3656
Australia (54) v. Sri Lanka (11)	1880.911	0.2897	1e-04	0.4825	-0.7601	0.9740	0.0003	0.4016	0.0003	0.4016	0.0117	0.3017	0.0149	0.3097	0.0263	0.3047
Australia (54) v. Seychelles (35)	2054.899	0.0110	1e-04	0.0300	-0.4074	0.9950	0.0002	0.3856	0.0002	0.3856	0.0029	0.3656	0.0037	0.3666	0.0066	0.3656
South Africa (22) v. Sri Lanka (11)	1612.444	0.5534	2e-04	0.3057	-1.8525	0.9181	-0.0001	0.5205	-0.0001	0.5205	0.0330	0.4336	0.0416	0.4466	0.0722	0.4426
Seychelles (35) v. Sri Lanka (11)	1717.271	0.2478	1e-04	0.5295	-1.5159	0.6593	-0.0002	0.5305	-0.0003	0.5305	0.0236	0.5375	0.0298	0.5375	0.0522	0.5385
Papua New Guinea (9) v. Thailand (4)	1254.400	0.2298	4e-04	0.4356	-5.7035	0.1330	-0.0005	0.4760	-0.0006	0.4760	0.2233	0.7660	0.2613	0.7370	0.3961	0.7440
Arabian Sea (15) v. Sri Lanka (11)	1503.034	0.6863	2e-04	0.8232	-2.3378	0.3007	-0.0021	0.8771	-0.0024	0.8771	0.0460	0.8761	0.0575	0.8731	0.0989	0.8721
Sri Lanka (11) v. Thailand (4)	1276.722	0.4625	3e-04	0.8172	-4.9286	0.0999	-0.0032	0.7582	-0.0036	0.7582	0.1875	0.9051	0.2220	0.8971	0.3448	0.9021
Australia (54) v. Thailand (4)	1796.699	0.4376	3e-04	0.6623	-1.0756	0.6853	-0.0033	0.7922	-0.0038	0.7922	0.0378	0.8242	0.0477	0.8092	0.0824	0.8172
Reunion (26) v. Thailand (4)	1670.672	0.0689	4e-04	0.4106	-2.6801	0.2305	-0.0033	0.6854	-0.0038	0.6854	0.0957	0.8457	0.1175	0.8307	0.1946	0.8357
Arabian Sea (15) v. Thailand (4)	1371.048	0.4426	3e-04	0.6813	-3.7791	0.1171	-0.0052	0.8989	-0.0059	0.8989	0.1395	0.9690	0.1682	0.9620	0.2701	0.9640
South Africa (22) v. Thailand (4)	1491.926	0.5934	4e-04	0.4416	-2.7460	0.3227	-0.0063	0.9451	-0.0072	0.9451	0.0985	0.9650	0.1208	0.9650	0.1996	0.9660
Mozambique (9) v. Thailand (4)	1174.486	0.8771	4e-04	0.8801	-5.8031	0.0738	-0.0078	0.9108	-0.0090	0.9108	0.2277	0.9713	0.2668	0.9682	0.4028	0.9713

12.8 PCA

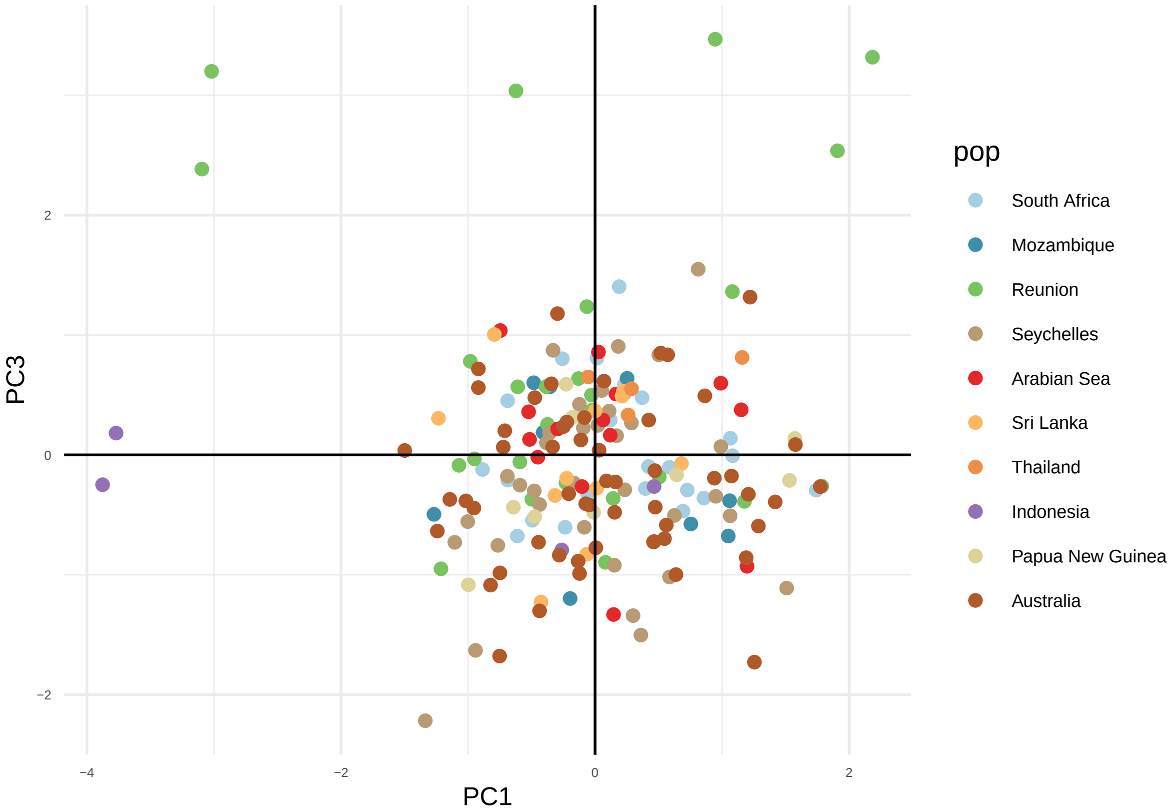
```
pca1 <- adegenet::glPca(BS.dartcap.IWP2.gl, nf = 5, parallel = TRUE,
                        n.cores = parallel::detectCores() - 1)
save(pca1, file = "DArTcap_IWP2_PCA.Rdata")
```

```
load("DArTcap_IWP2_PCA.Rdata")

BS.pca.scores <- as.data.frame(pca1$scores)
BS.pca.scores$pop <- pop(BS.dartcap.IWP2.gl)
cols <- adegenet::funky(nPop(BS.dartcap.IWP2.gl))


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC2, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```

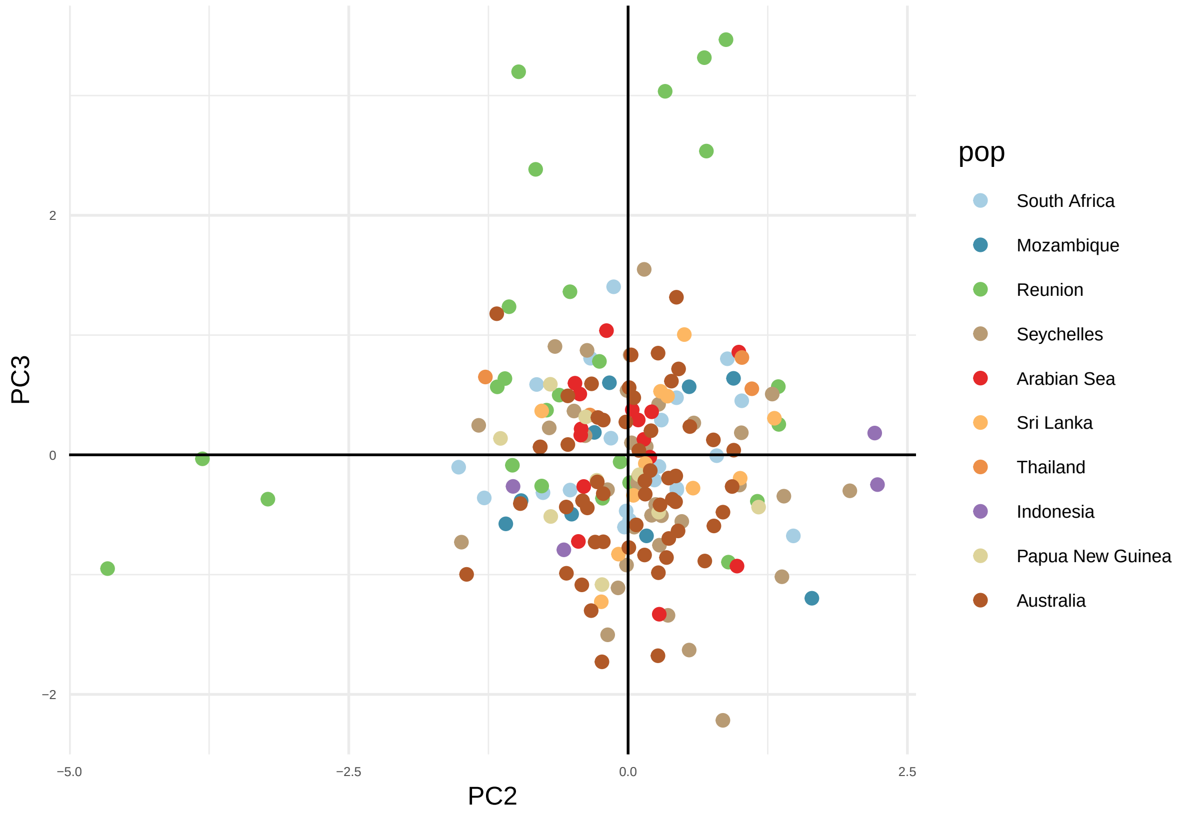


```
ggplot2::ggsave(p, filename = "DArTcap_IWP2_PCA1.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC1, y = PC3, colour = pop)) +
```

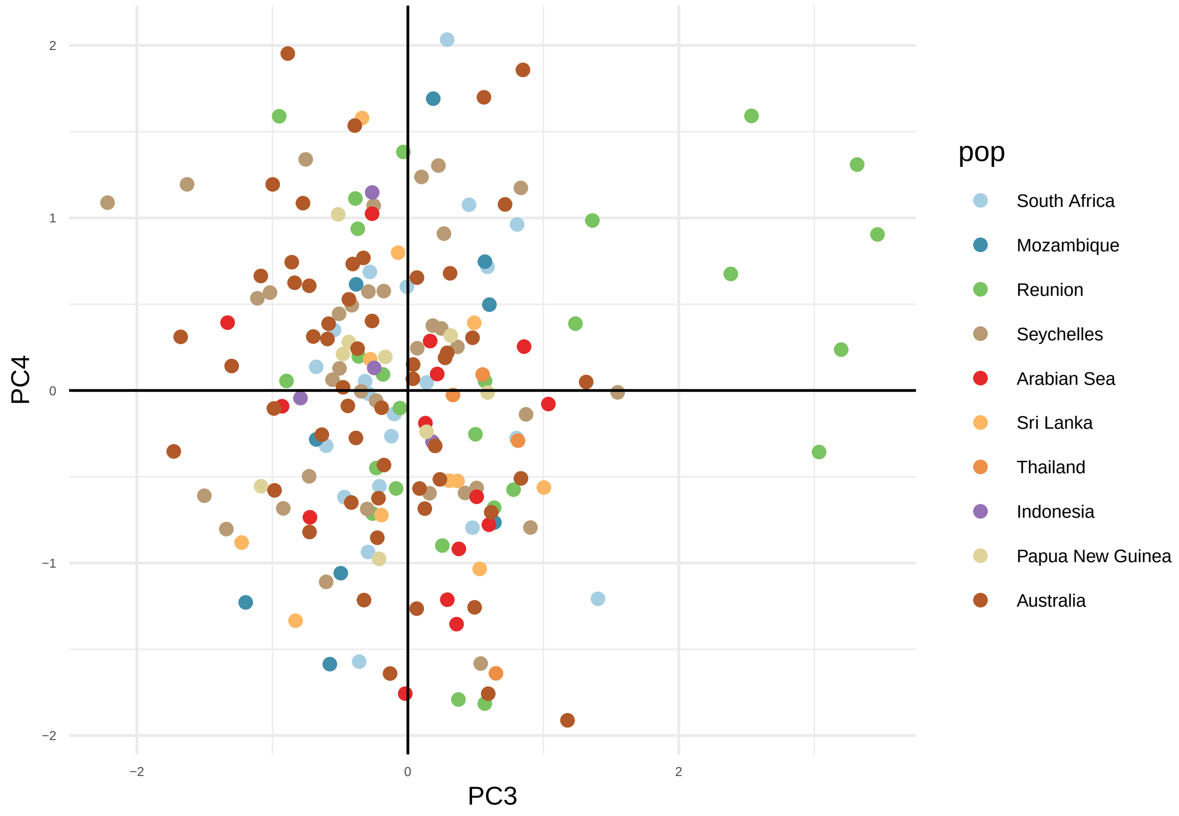
```
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



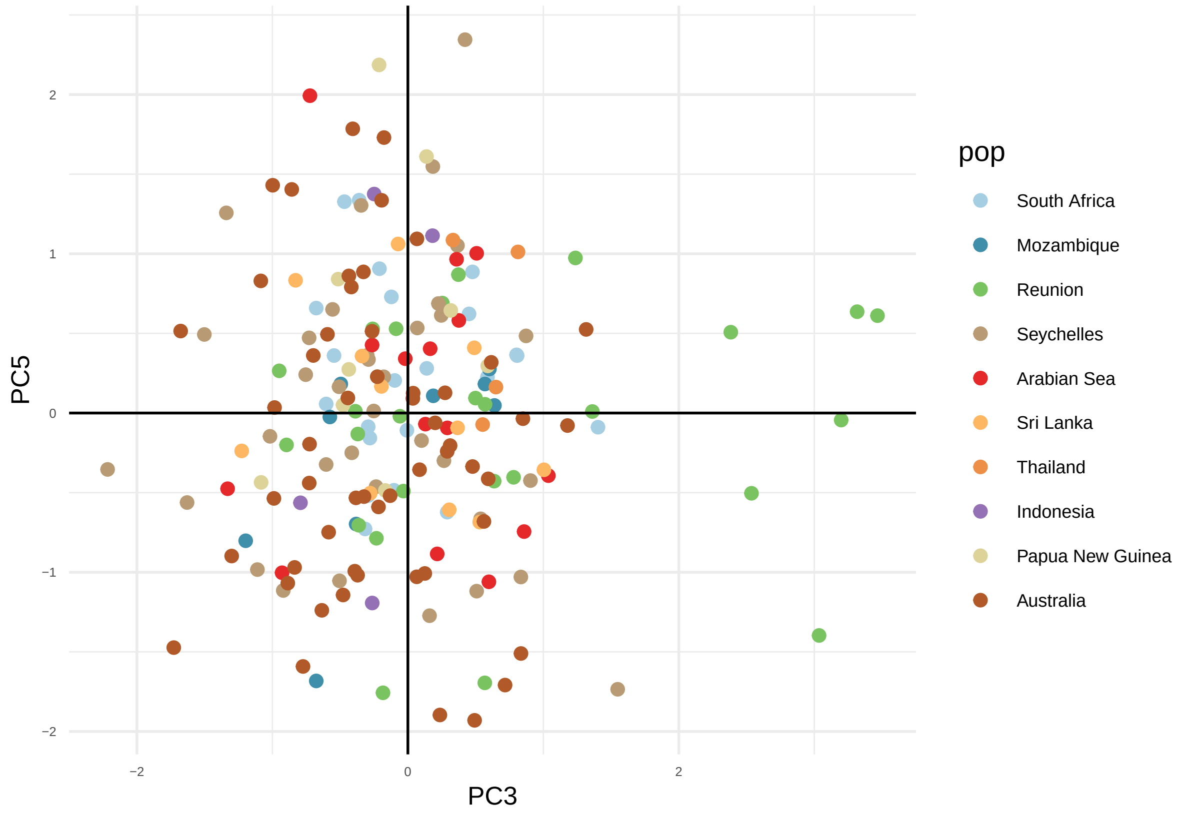
```
ggplot2::ggsave(p, filename = "DArTcap_IWP2_PCA2.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC2, y = PC3, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```r
ggplot2::ggsave(p, filename = "DArTcap_IWP2_PCA3.png", width = 30,
                height = 15,units = "cm")


p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC4, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```
ggplot2::ggsave(p, filename = "DArTcap_IWP2_PCA4.png", width = 30,
                height = 15,units = "cm")

p <-
  ggplot2::ggplot(BS.pca.scores, ggplot2::aes(x = PC3, y = PC5, colour = pop)) +
  ggplot2::geom_point(size = 2) + ggplot2::scale_color_manual(values = cols) +
  ggplot2::geom_hline(yintercept = 0) + ggplot2::geom_vline(xintercept = 0) +
  ggplot2::theme_minimal() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7)
  )
p
```



```r
ggplot2::ggsave(p, filename = "DArTcap_IWP2_PCA5.png", width = 30,
                height = 15,units = "cm")
```

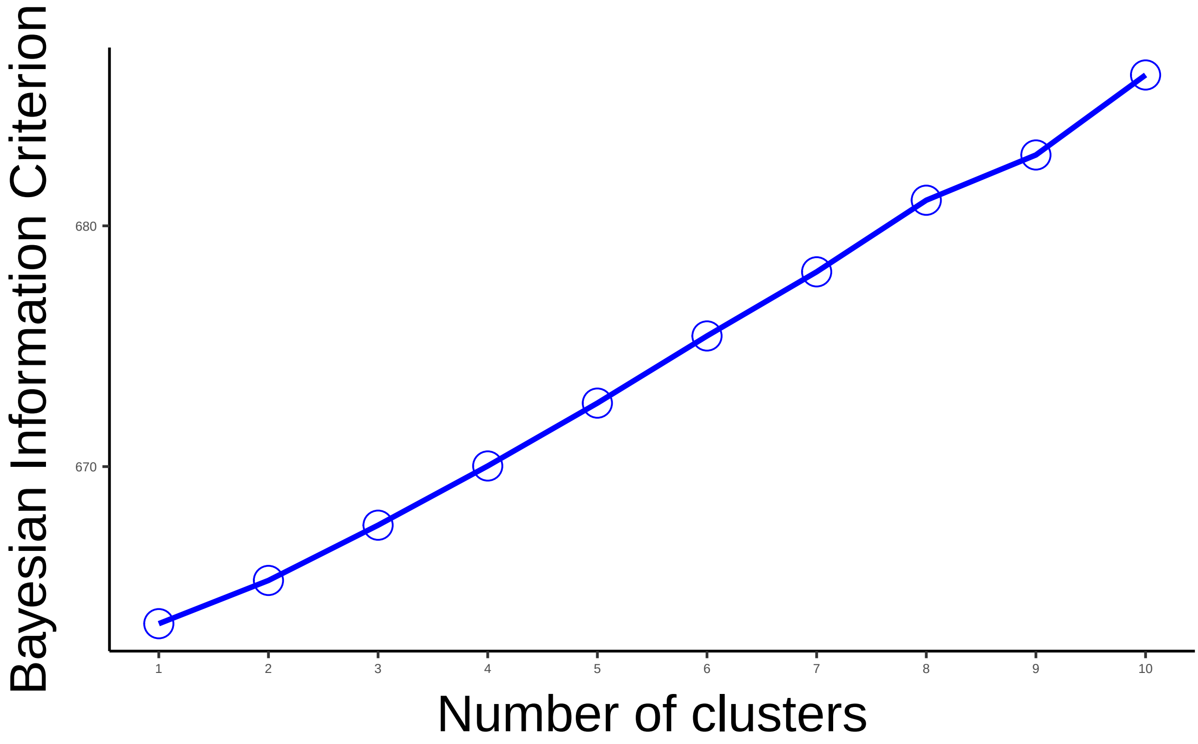
12.9 DAPC

12.9.1 Optimal number of clusters with neutral markers

```r
set.seed(124)
grp <-
  adegenet::find.clusters(
    BS.dartcap.IWP2.gl,
    max.n.clust = 10,
    n.pca = adegenet::nInd(BS.dartcap.IWP2.gl) / 3,
    stat = "BIC",
    parallel = TRUE,
    n.cores = parallel::detectCores() - 1
  )

save(grp, file = "DArTcap_IWP2_grp.Rdata")
```

```r
load("DArTcap_IWP2_grp.Rdata")

y <- as.numeric(grp$Kstat)
x <- 1:10
data <- data.frame(x,y,stringsAsFactors = F)
plot <- ggplot2::ggplot(data, ggplot2::aes(x,y)) +
  ggplot2::geom_point(size = 5, shape = 1, color = "blue") +
  ggplot2::geom_line(size = 1,color = "blue") +
  ggplot2::scale_x_continuous(name = waiver(),
                              breaks = seq(from = 0,
                                           to = nrow(BS.dartcap.IWP2.gl) - 1,
```

```
                                           by = 1)) +
  ggplot2::labs(subtitle = "",
                y = "Bayesian Information Criterion",
                x = "Number of clusters",
                title = "",
                caption = "") +
  ggplot2::theme_classic() +
  ggplot2::theme(
    axis.text = ggplot2::element_text(size = 5),
    axis.title.x = ggplot2::element_text(size = 20,vjust = 0, hjust = 0.5),
    axis.title.y = ggplot2::element_text(size = 20,vjust = 2, hjust = 0.5))
print(plot)
```



```
ggplot2::ggsave(plot, filename = "DArTcap_IWP2_grp.png", width = 30,
                height = 15,units = "cm")
```

12.9.2 Cross-validation to identify the optimal number of PCs

Uses a training - holdout set of individuals to check how reliable individuals can be assigned.

```
set.seed(124)
x <- BS.dartcap.IWP2.gl
x$loc.names <- x$other$loc.metrics$MARKERS

xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = seq(1, adegenet::nInd(x), by = 50),
  training.set = 0.9,
  result = "groupMean",
  center = TRUE,
```

```r
  scale = FALSE,
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)

#refine the analysis
set.seed(124)
png(file="DArTcap_IWP2_xval.png")
xval <-
  adegenet::xvalDapc(
  tab(x, NA.method = "mean"),
  adegenet::pop(x),
  n.pca = (PC - 15):(PC + 15),
  n.rep = 1000,
  parallel = "multicore",
  ncpus = 1,
  xval.plot = TRUE
  )
dev.off()
save(xval, file = "DArTcap_IWP2_xval.rdata")
```

```r
load("DArTcap_IWP2_xval.rdata")
print(xval[2:6])
PC <- as.numeric(xval$`Number of PCs Achieving Lowest MSE`)
```

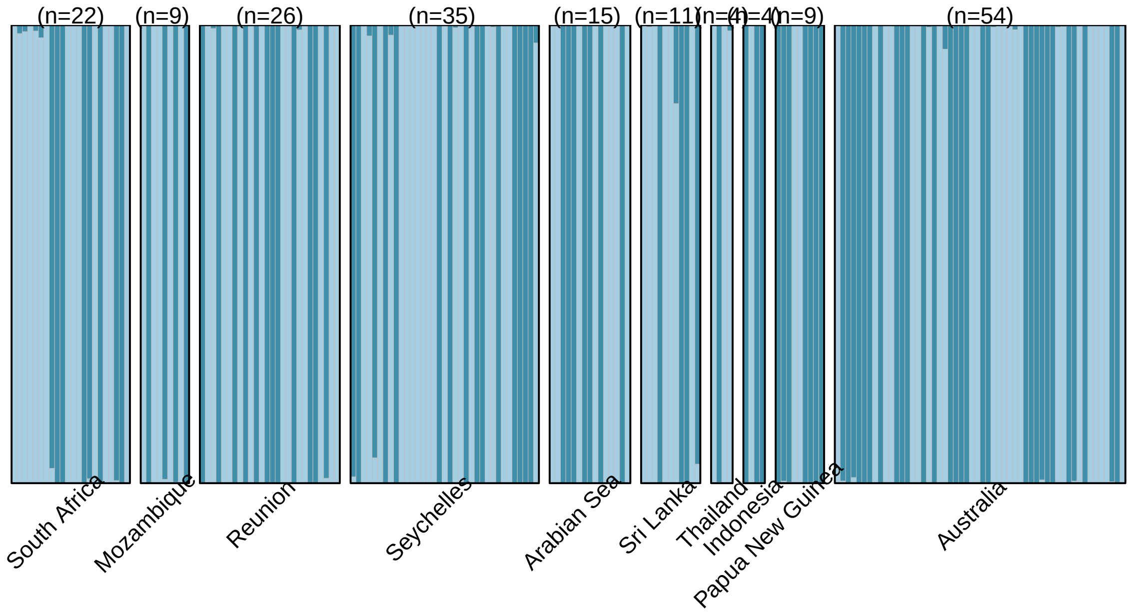
```
## $`Median and Confidence Interval for Random Chance`
##       2.5%        50%      97.5%
## 0.06180334 0.09925630 0.13873901
##
## $`Mean Successful Assignment by Number of PCs of PCA`
##        36        37        38        39        40        41        42        43
## 0.1930960 0.2027357 0.1990421 0.2038611 0.2115881 0.2072631 0.2076766 0.2035103
##        44        45        46        47        48        49        50        51
## 0.2019516 0.2055075 0.2049619 0.2057060 0.2084857 0.2061317 0.2061722 0.2070675
##        52        53        54        55        56        57        58        59
## 0.2073901 0.2032528 0.2099532 0.2065258 0.2039921 0.2058381 0.2079246 0.2048988
##        60        61        62        63        64        65        66
## 0.2099571 0.2044837 0.2062091 0.2048567 0.2004135 0.1984770 0.2010897
##
## $`Number of PCs Achieving Highest Mean Success`
## [1] "40"
##
## $`Root Mean Squared Error by Number of PCs of PCA`
##        36        37        38        39        40        41        42        43
## 0.8095453 0.8002350 0.8037620 0.7990092 0.7914135 0.7955968 0.7953047 0.7994862
##        44        45        46        47        48        49        50        51
## 0.8008700 0.7974081 0.7978982 0.7972406 0.7942725 0.7966445 0.7966600 0.7956200
##        52        53        54        55        56        57        58        59
## 0.7955904 0.7998644 0.7930704 0.7964852 0.7991029 0.7970035 0.7948072 0.7979593
##        60        61        62        63        64        65        66
## 0.7929512 0.7983287 0.7964667 0.7979294 0.8022374 0.8045400 0.8018440
##
## $`Number of PCs Achieving Lowest MSE`
## [1] "40"
```

```
dapc.all.object.names <- c()
for (K in 2:10) {
  set.seed(124)
  grp <- adegenet::find.clusters(BS.dartcap.IWP2.gl, n.clust = K, n.pca = PC)
  set.seed(124)
  dapc.all.neutral <- adegenet::dapc(BS.dartcap.IWP2.gl, grp$grp, n.da = K - 1,
                                     n.pca = PC)
  assign(paste0("dapc.all.", K),value = dapc.all.neutral)
  dapc.all.object.names <- c(dapc.all.object.names,
                                     paste0("dapc.all.", K))
}
save(list = dapc.all.object.names, dapc.all.object.names,
     file = "DArTcap_IWP2_DAPC.Rdata")
```

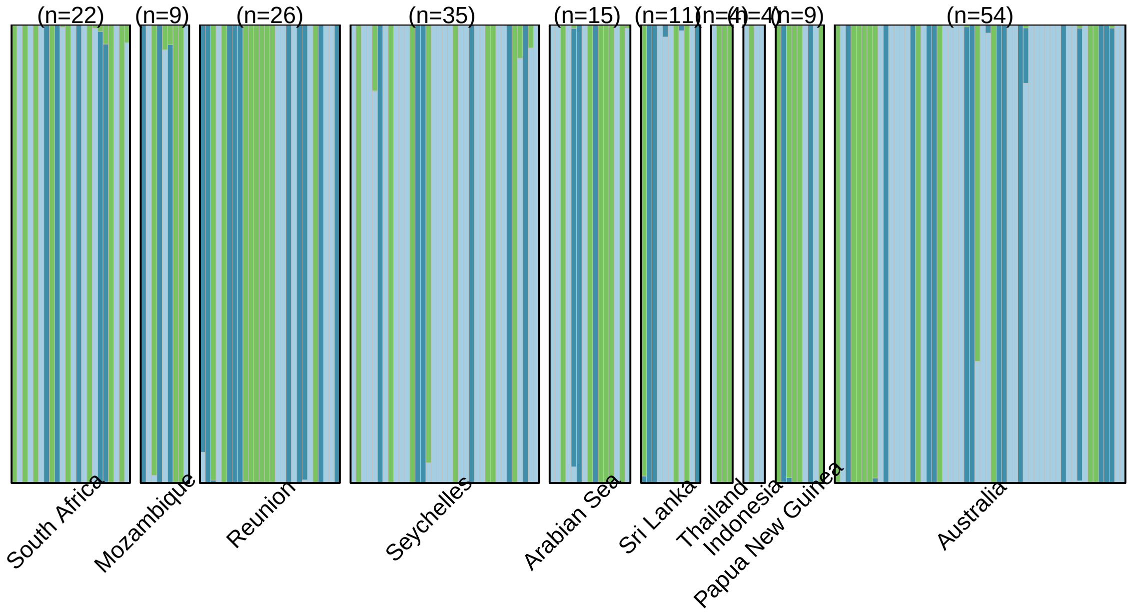
12.9.3 DAPC barplot

Group individuals according to DAPC posterior membership.

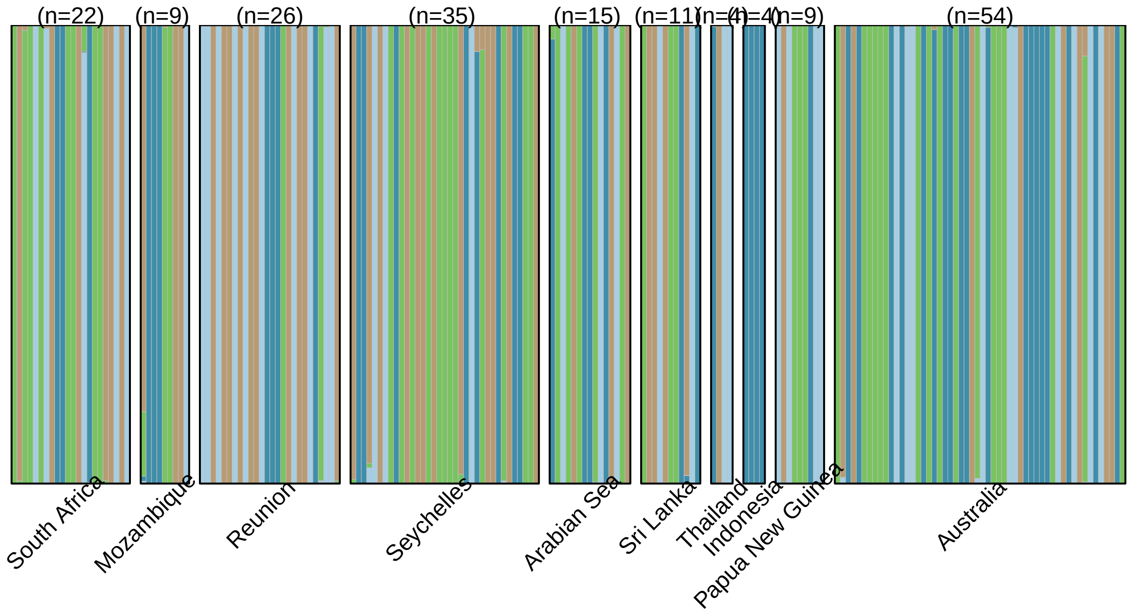
```
load("DArTcap_IWP2_DAPC.Rdata")
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  post <- as.matrix(dapc$posterior)
  colnames(post) <- paste0("Group", 1:nlevels(dapc$grp))
  locations <- BS.dartcap.IWP2.gl$pop

  plot.dapc.FDD(x = post,
                locations = locations,
                colour = colour,
                region.lwd = 1,
                plotTitle = paste0("DAPC: all Bull Sharks - subset Australia\n for K=",
                                   K, " & PC=", PC, sep = ""))
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP2_DAPC_barplot_K", K, ".png"),
    res = 300,
    width = 30,
    height = 15,
    units = "cm")
}
```



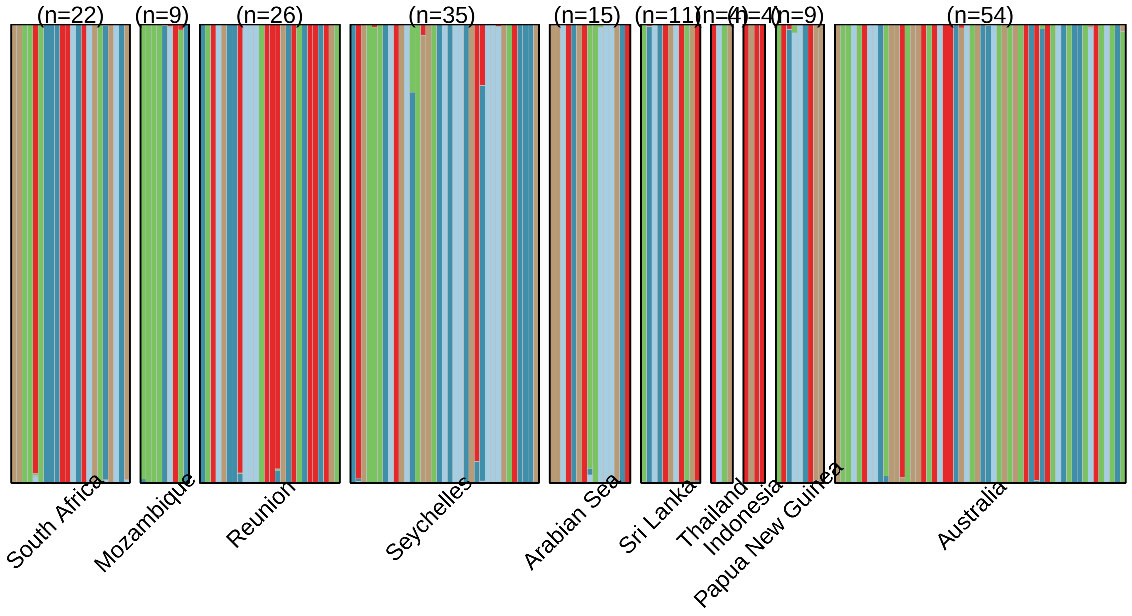
DAPC: all Bull Sharks − subset Australia
for K=2 & PC=40



DAPC: all Bull Sharks − subset Australia
for K=3 & PC=40

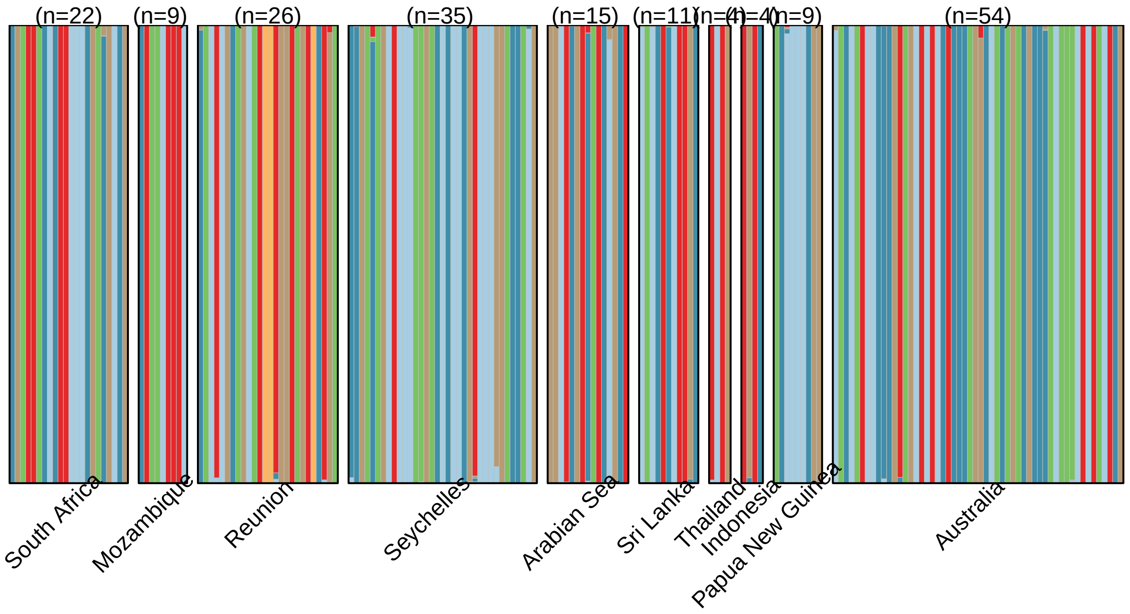


DAPC: all Bull Sharks − subset Australia
for K=4 & PC=40

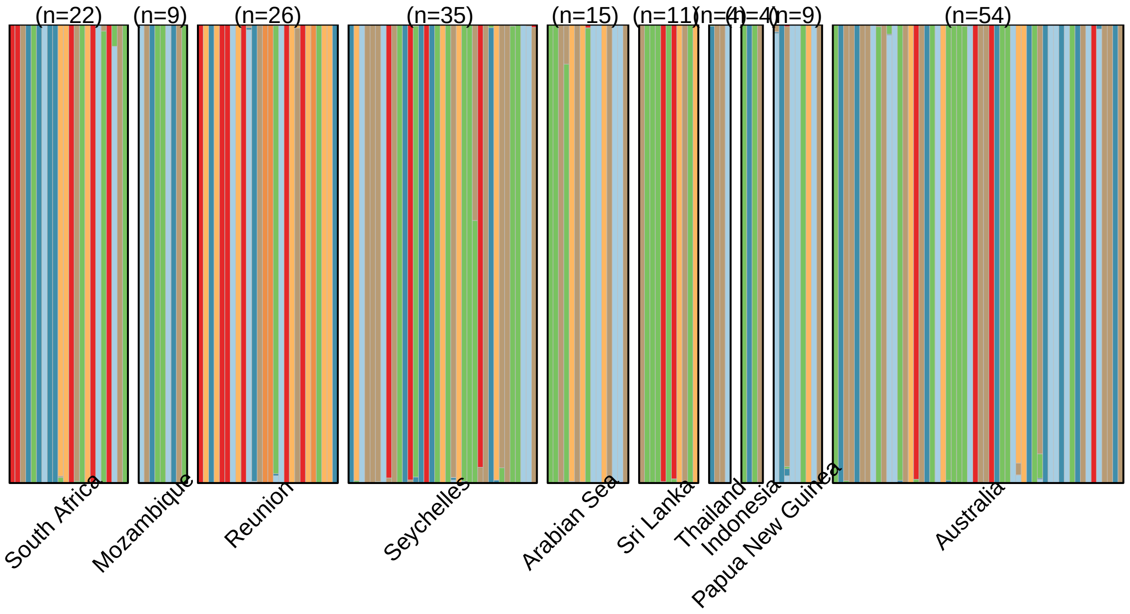


DAPC: all Bull Sharks − subset Australia
for K=5 & PC=40

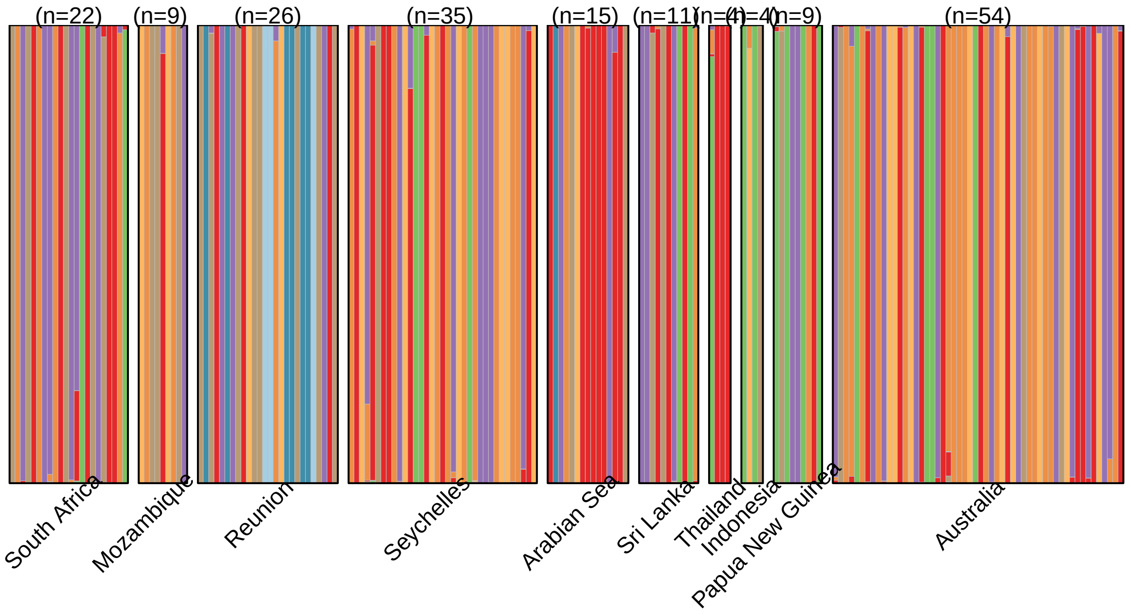
DAPC: all Bull Sharks − subset Australia
for K=6 & PC=40



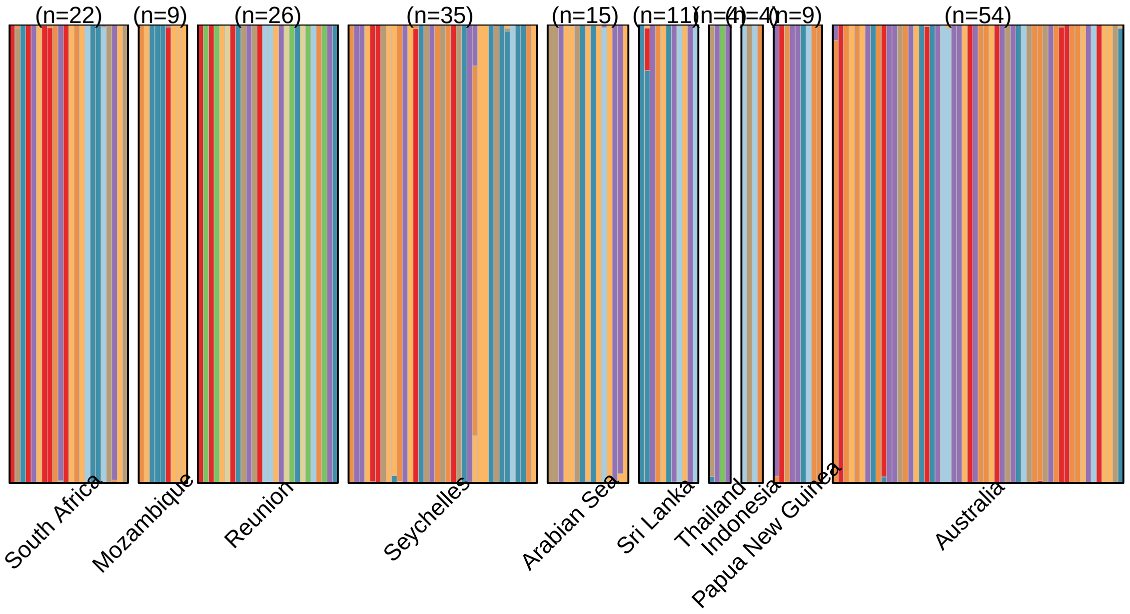
DAPC: all Bull Sharks − subset Australia
for K=7 & PC=40

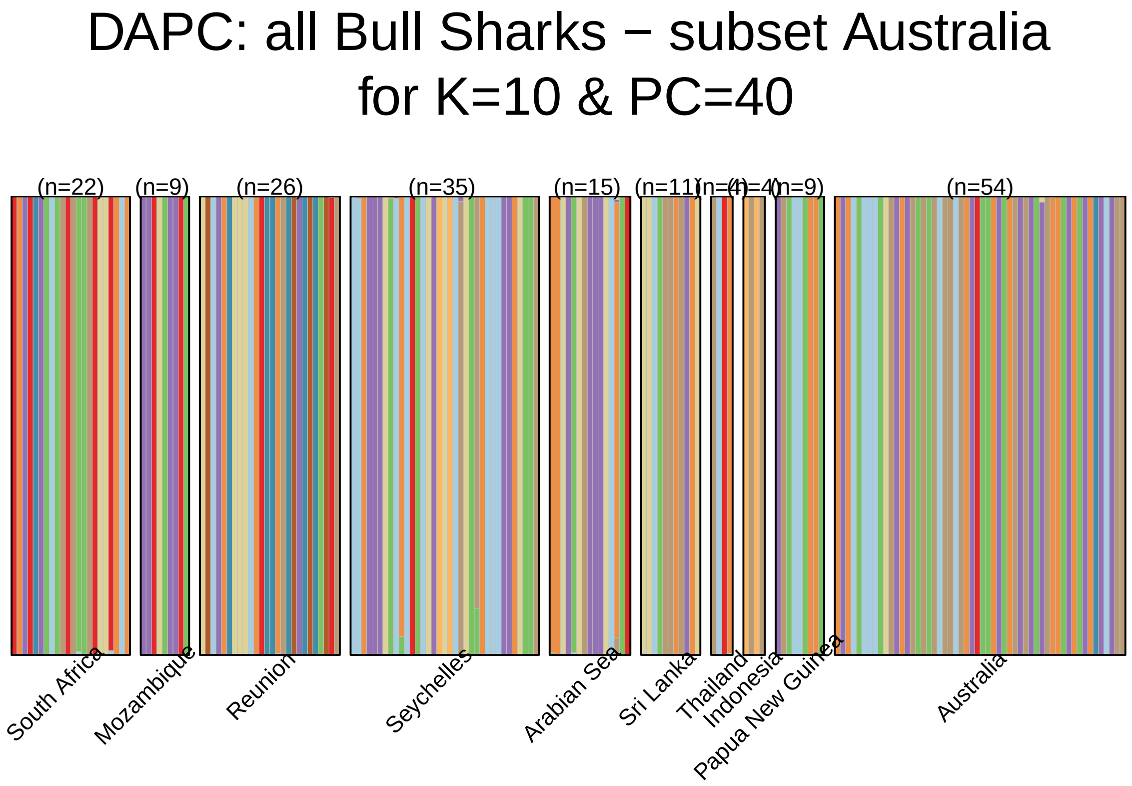


DAPC: all Bull Sharks − subset Australia
for K=8 & PC=40



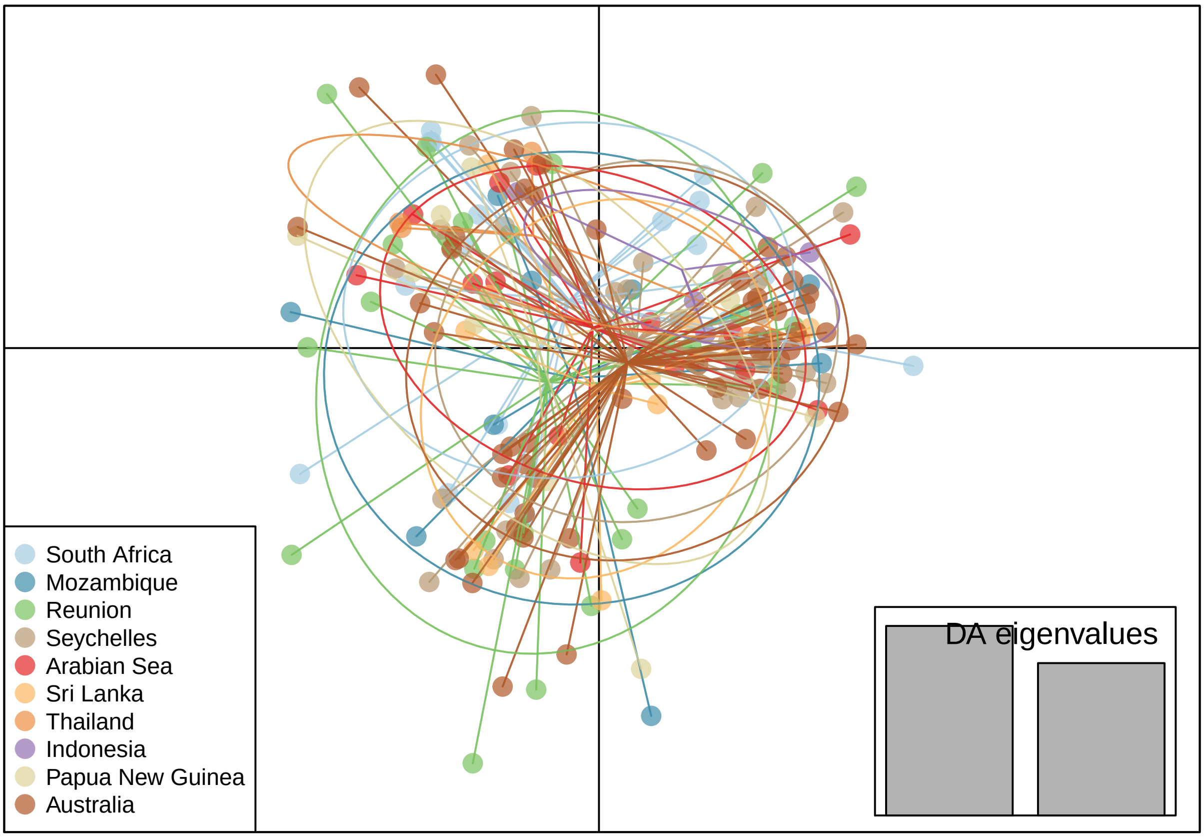
DAPC: all Bull Sharks − subset Australia
for K=9 & PC=40

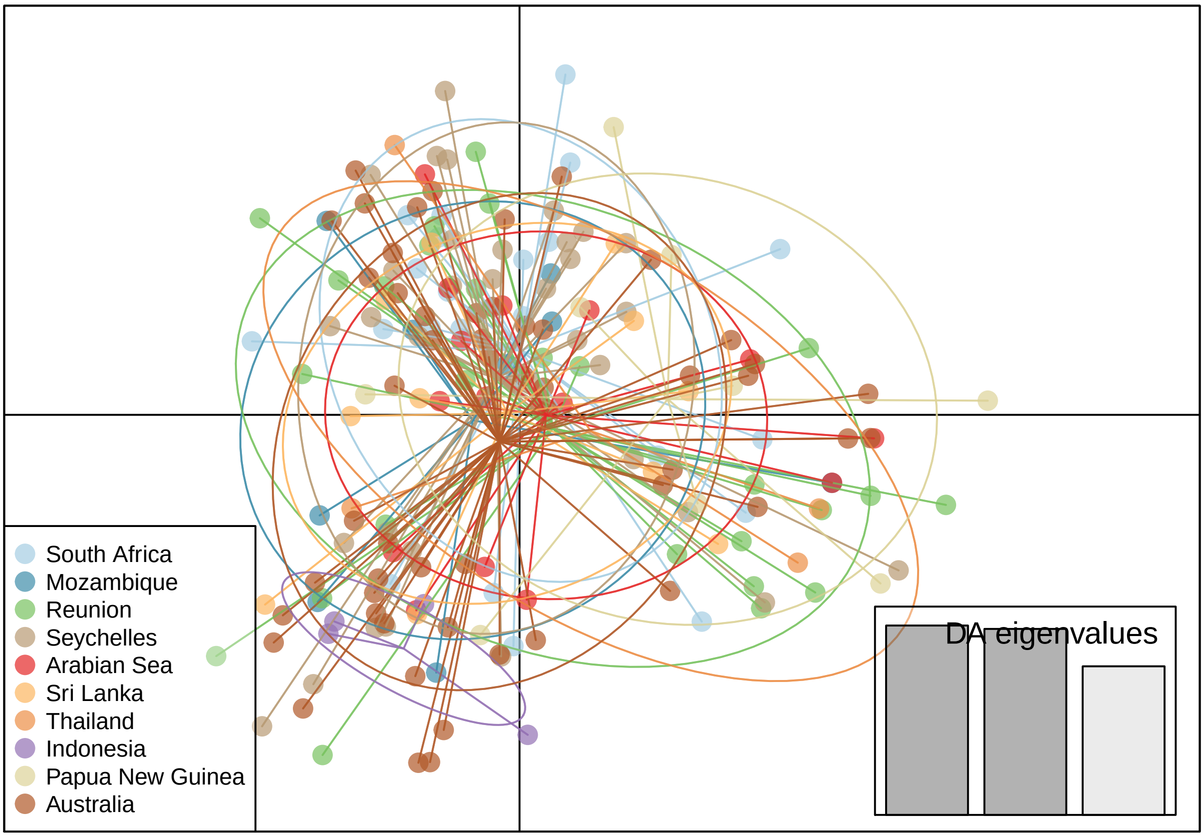


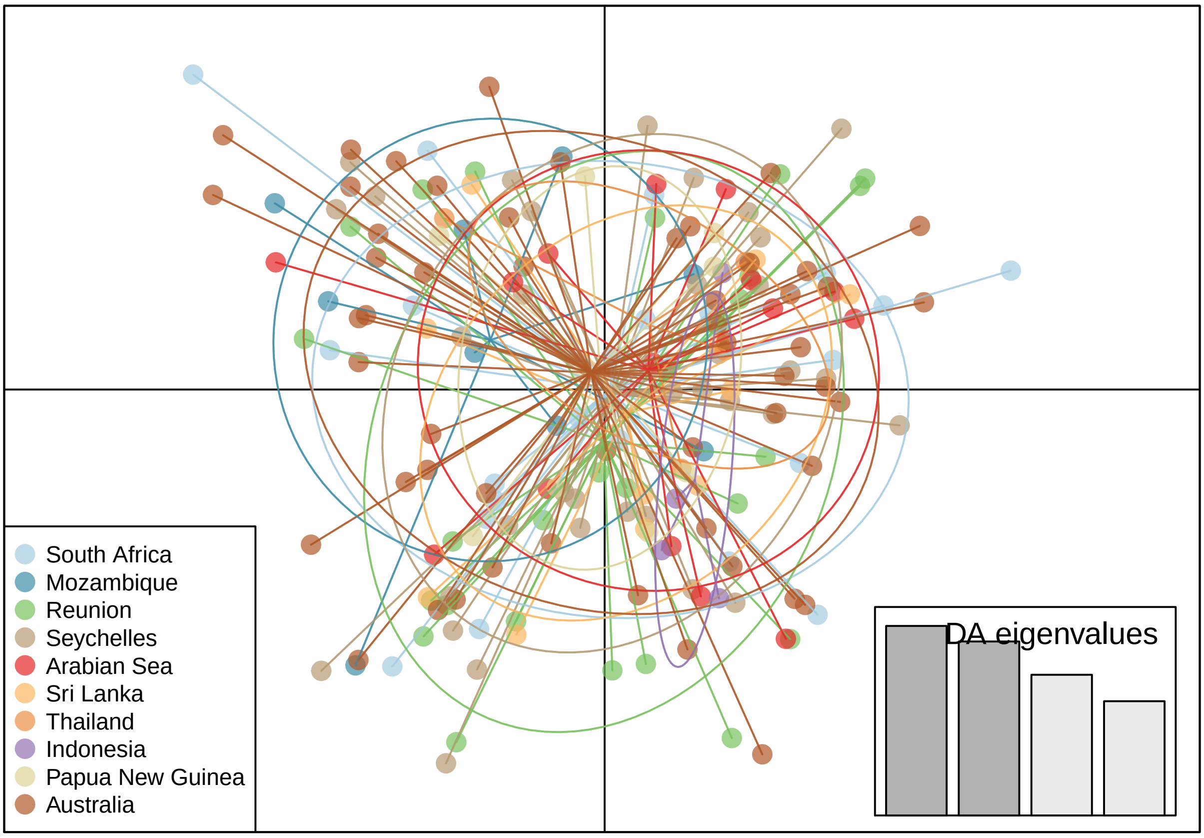


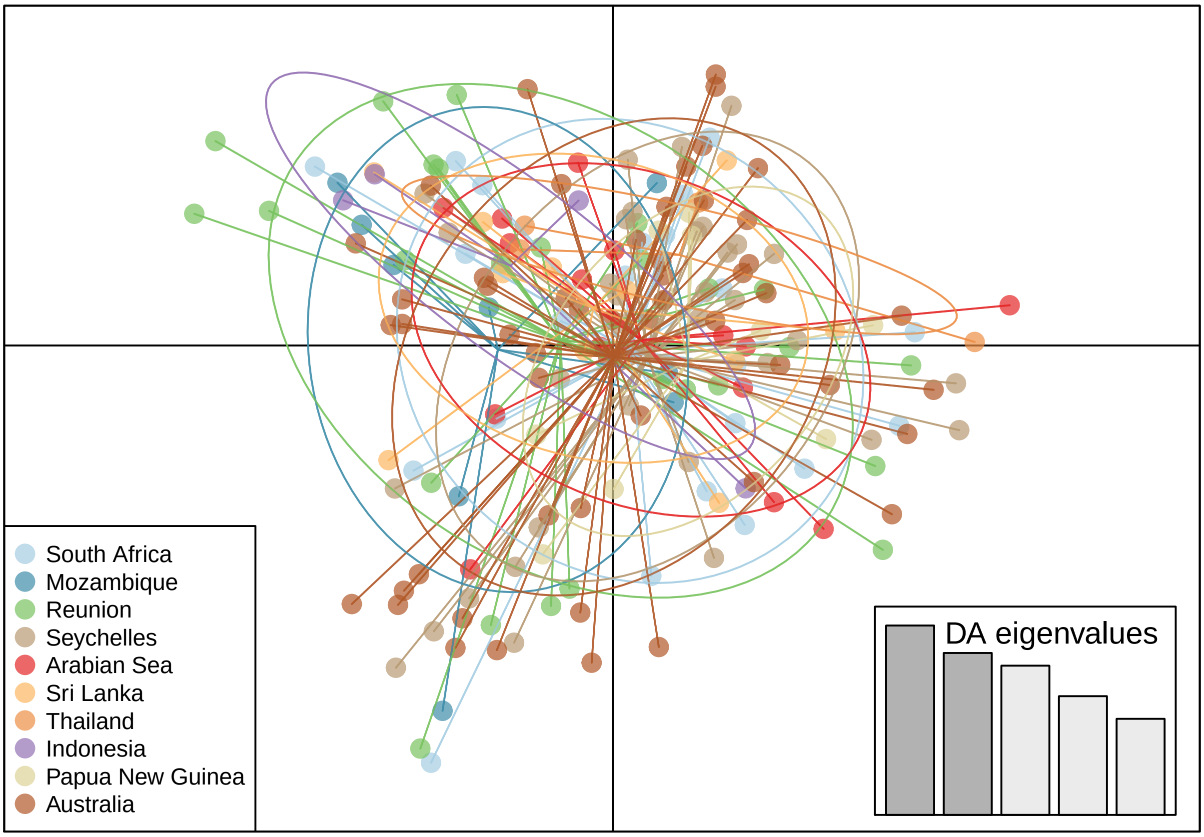
12.9.4 DAPC scatterplot

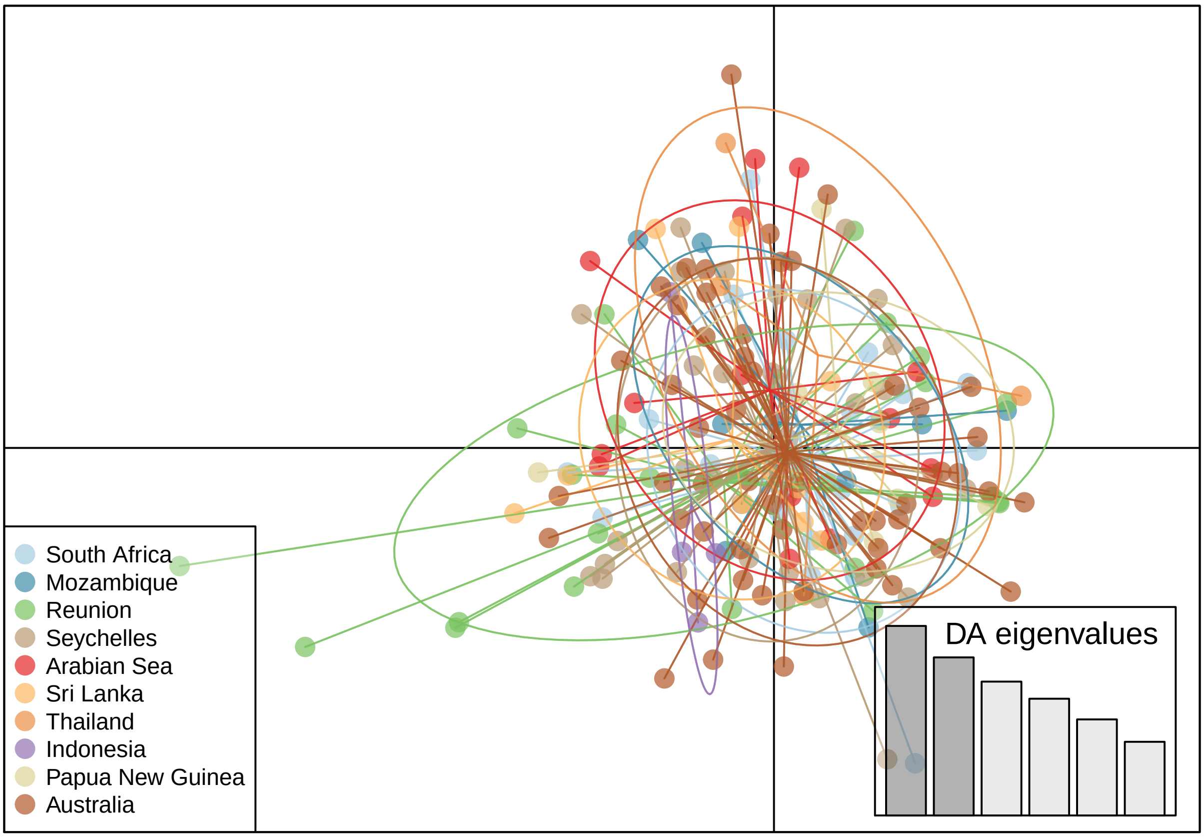
```
load("DArTcap_IWP2_DAPC.Rdata")

for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  if (K == 2) {
    posi.leg <- "bottomright"
  } else {posi.leg <- "bottomleft"}
  dapc.plot <- ade4::scatter(dapc, grp = pop(BS.dartcap.IWP2.gl), cex = 2,
                             legend = TRUE, col = colours.10, clabel = FALSE,
                             posi.leg = posi.leg, scree.pca = FALSE,
                             posi.pca = "topleft", cleg = 0.75, xax = 1,
                             yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP2_DAPC_scatterplot_K", K, ".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

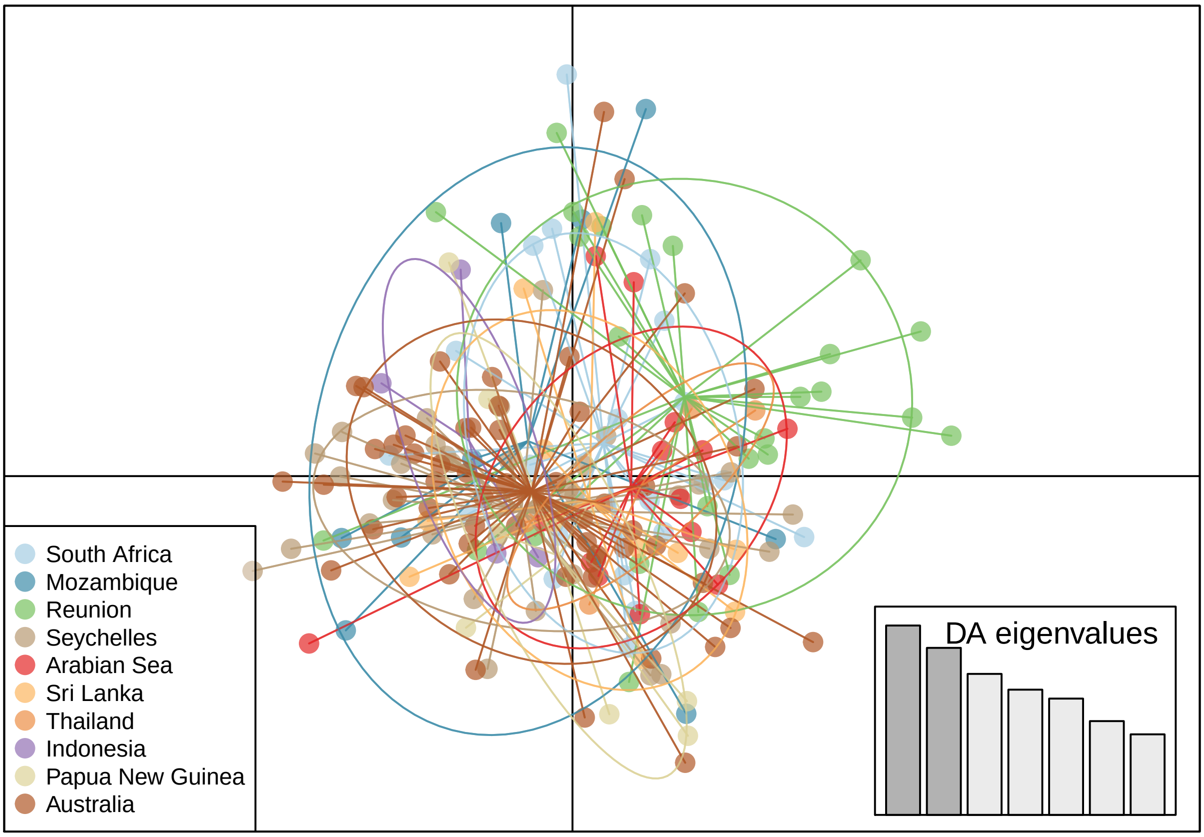

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues

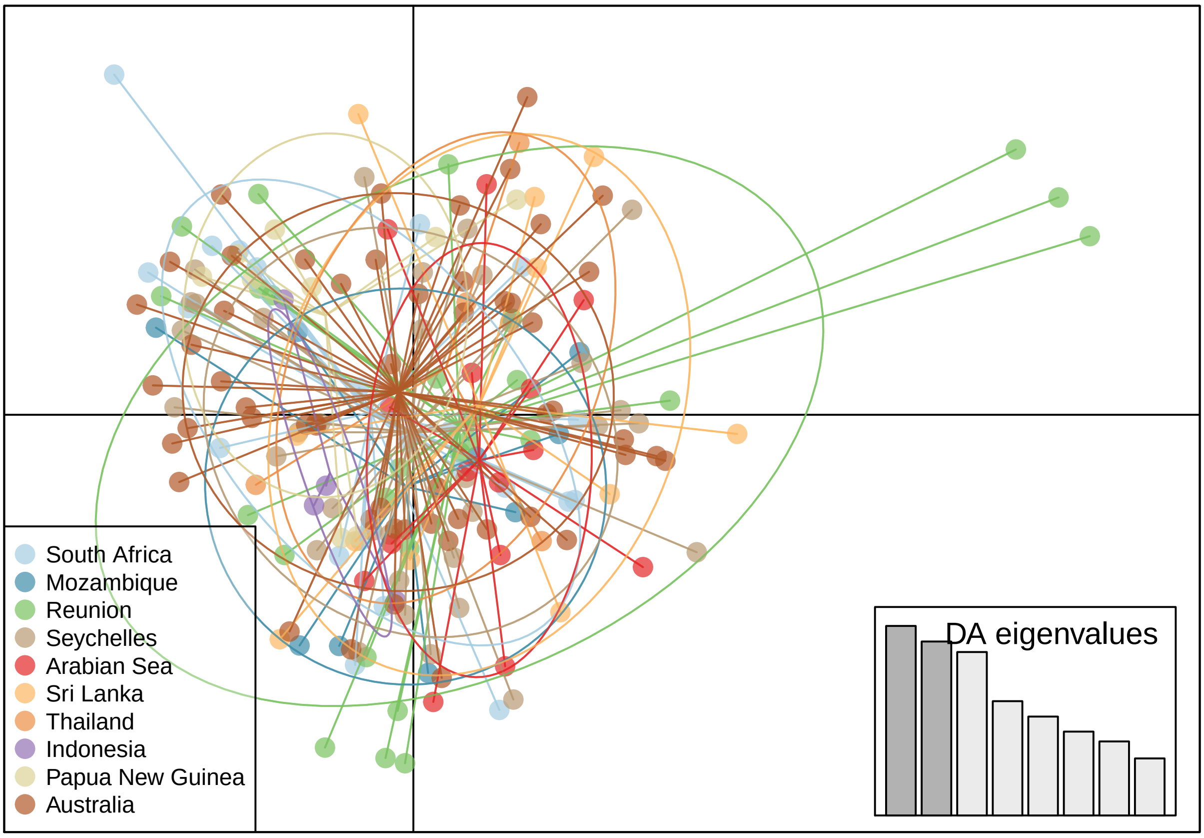

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues

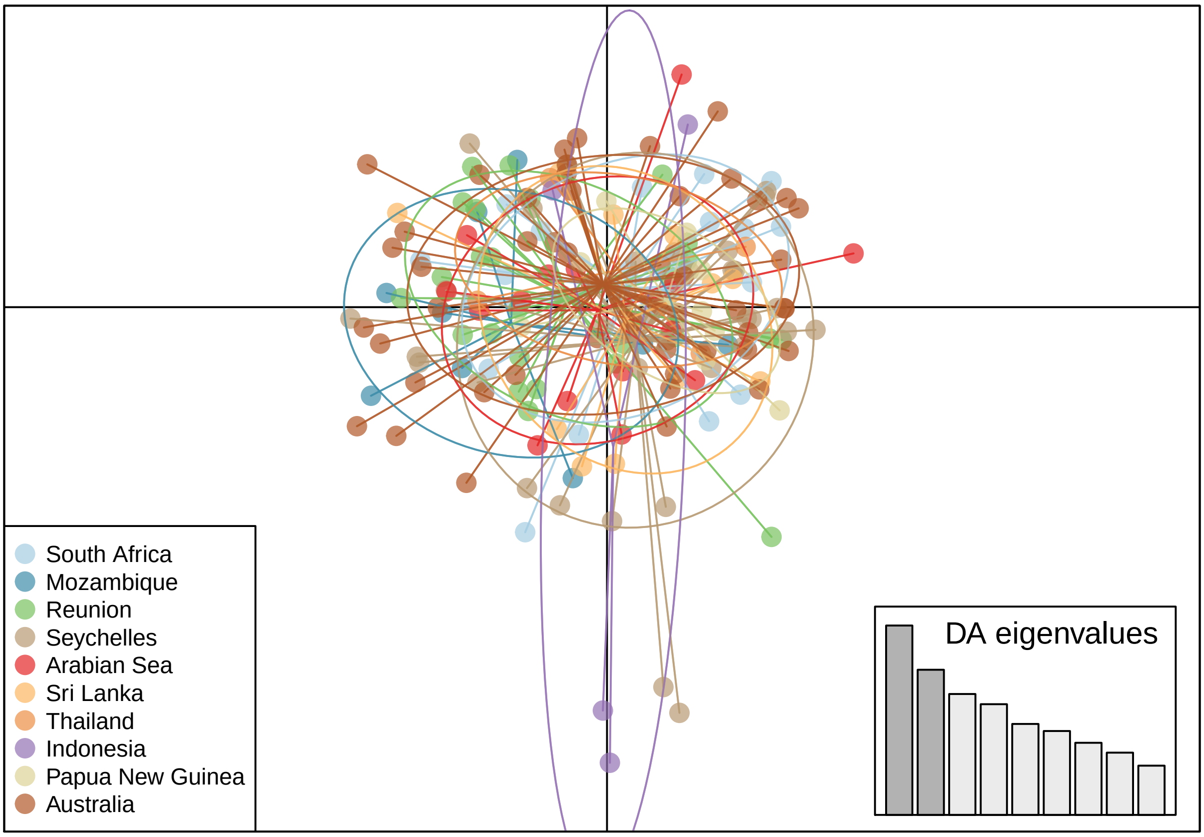

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues


South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues


South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues

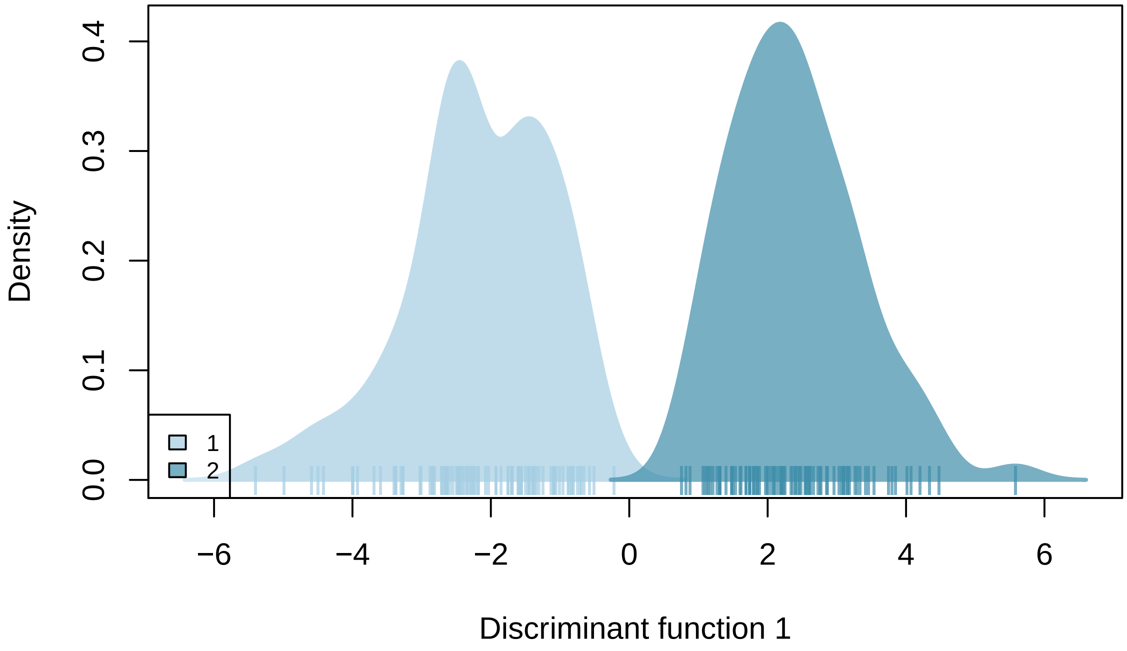

South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia
DA eigenvalues

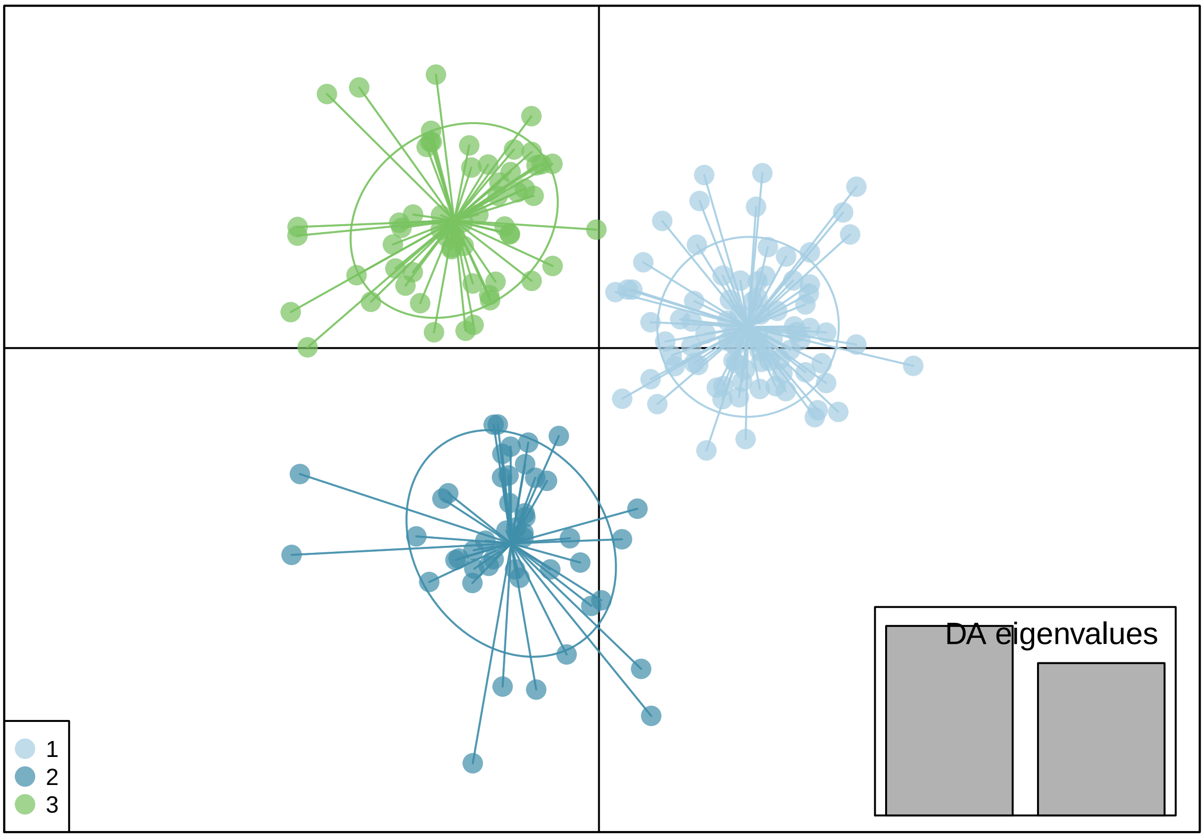


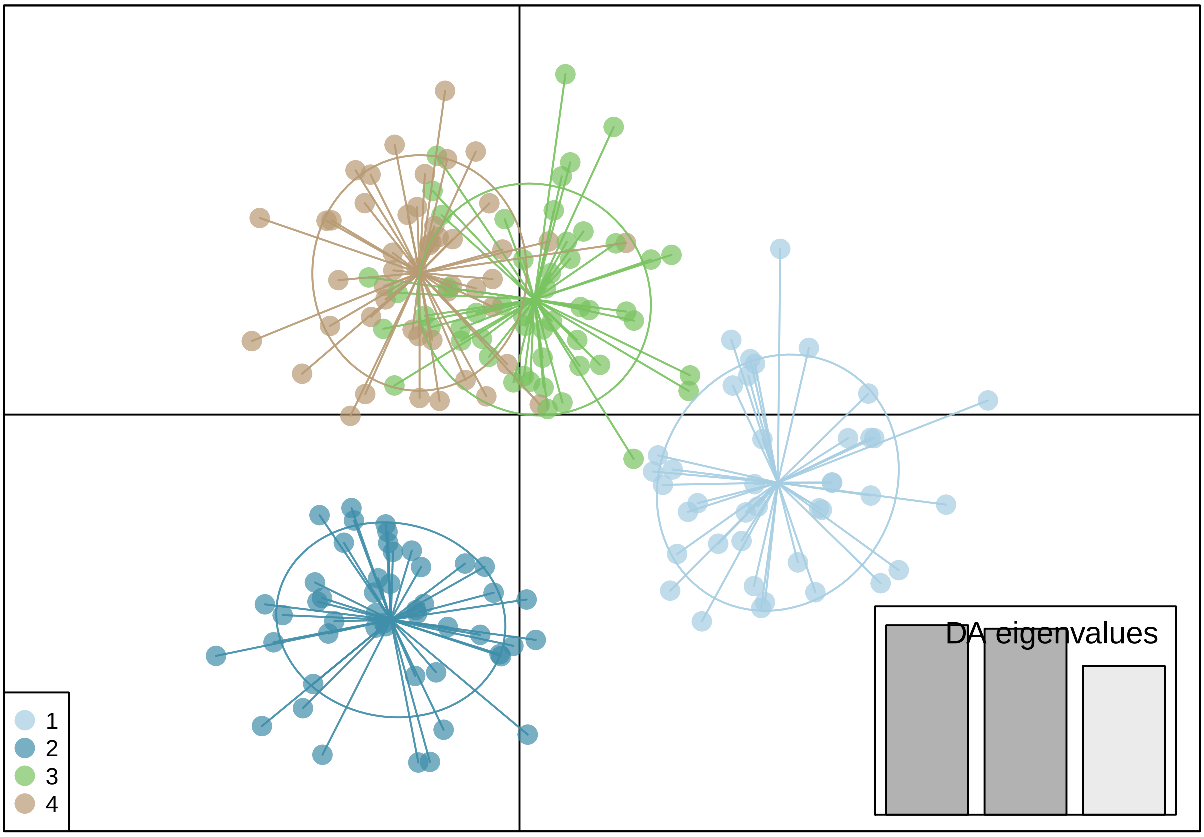


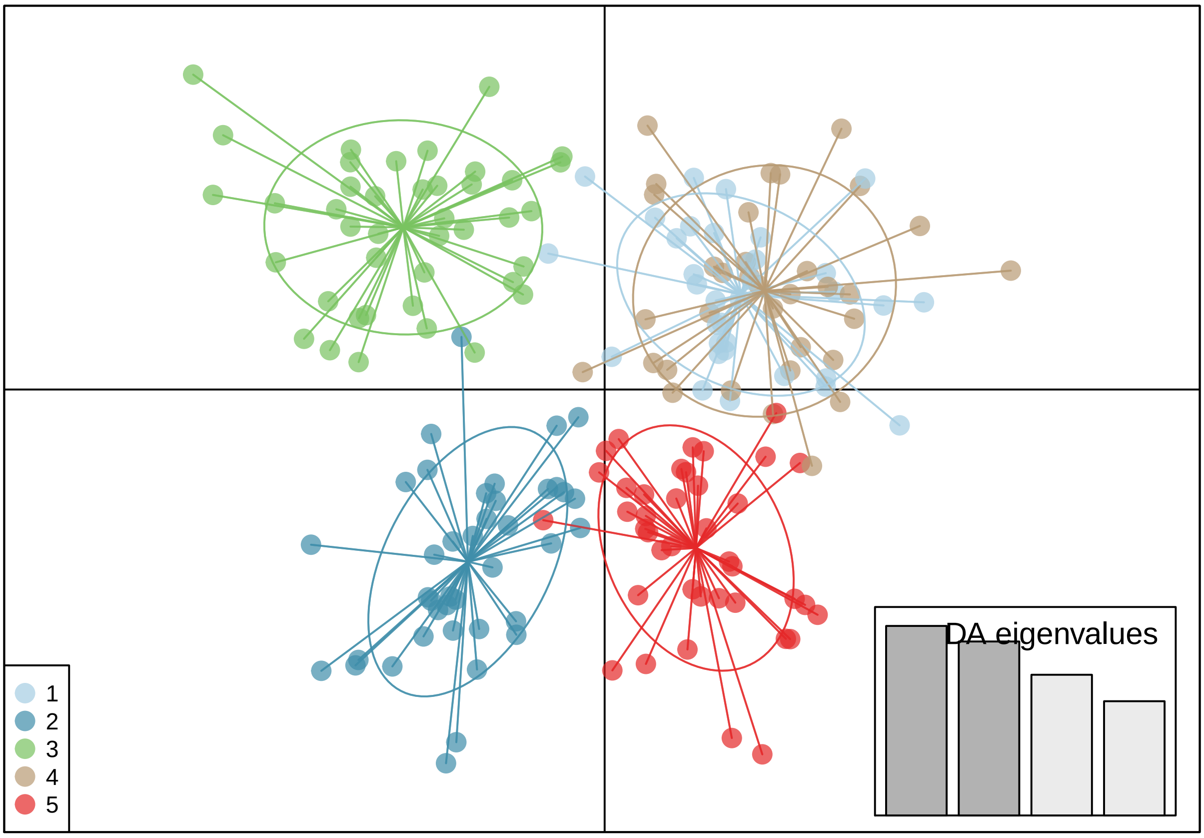
```
for (K in 2:10) {
  colour <- colours.prior[1:K]
  dapc <- get(dapc.all.object.names[K - 1])
  dapc.plot <- ade4::scatter(dapc, cex = 2, legend = TRUE, col = colour,
                             clabel = FALSE, posi.leg = "bottomleft",
```

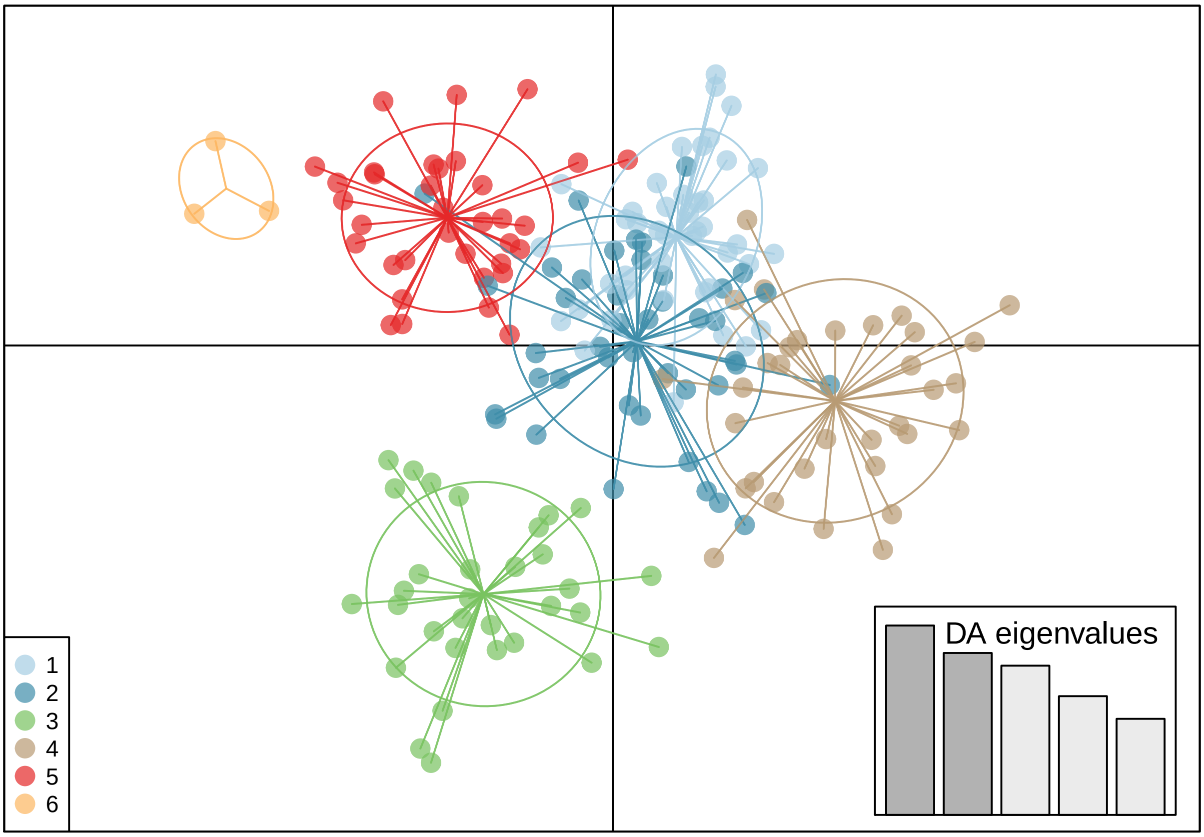
```
                                scree.pca = FALSE,  posi.pca = "topleft",
                                cleg = 0.75, xax = 1, yax = 2, inset.solid = 0.3)
  dev.print(
    device = png,
    file = paste0("DArTcap_IWP2_DAPC_scatterplot_pergroups_K",
                  K,".png"),
    width = 30,
    height = 15,
    units = "cm",
    res = 300
  )
}
```

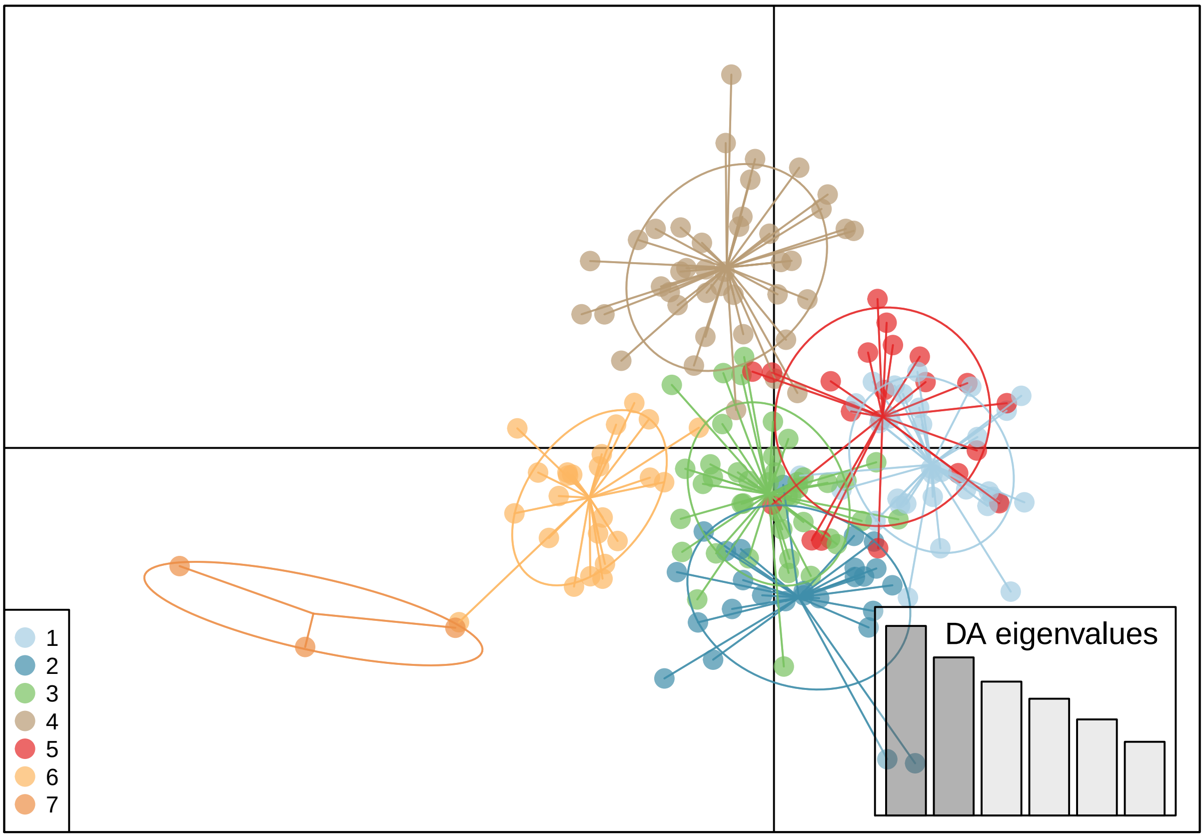


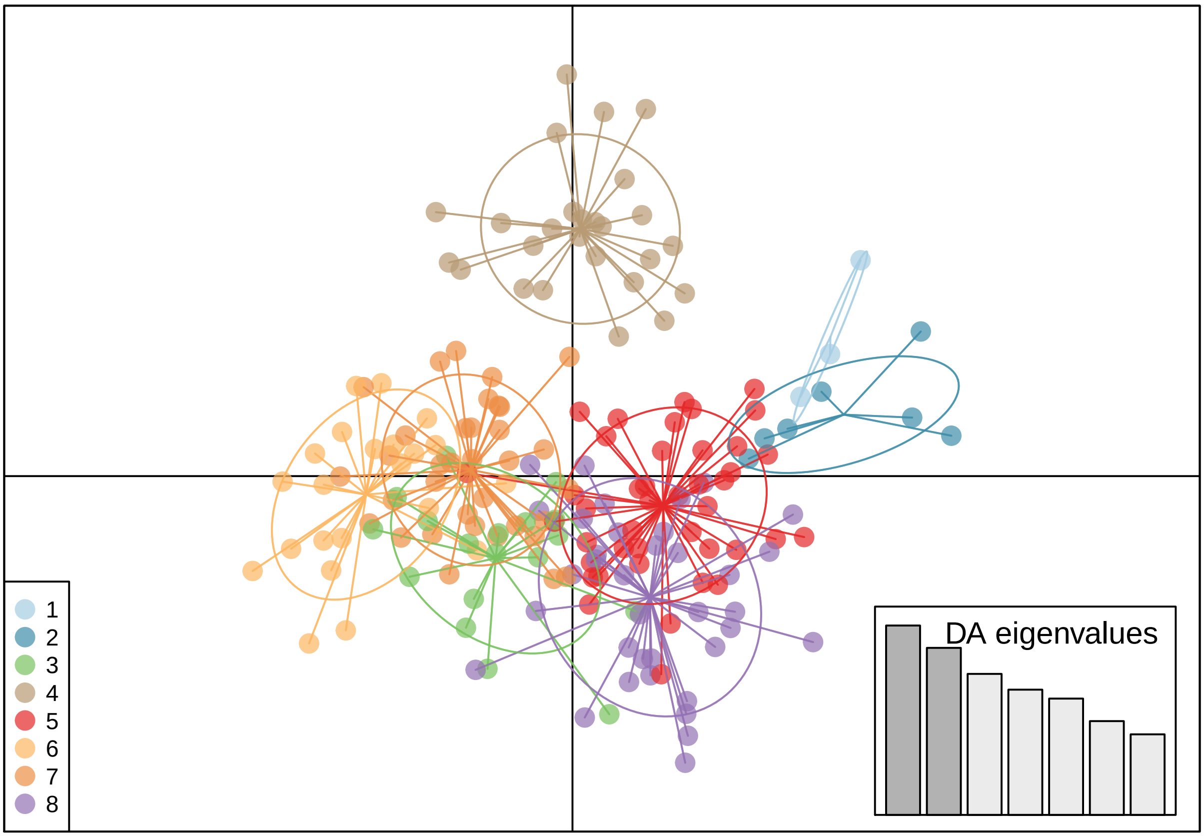

DA eigenvalues
1
2
3

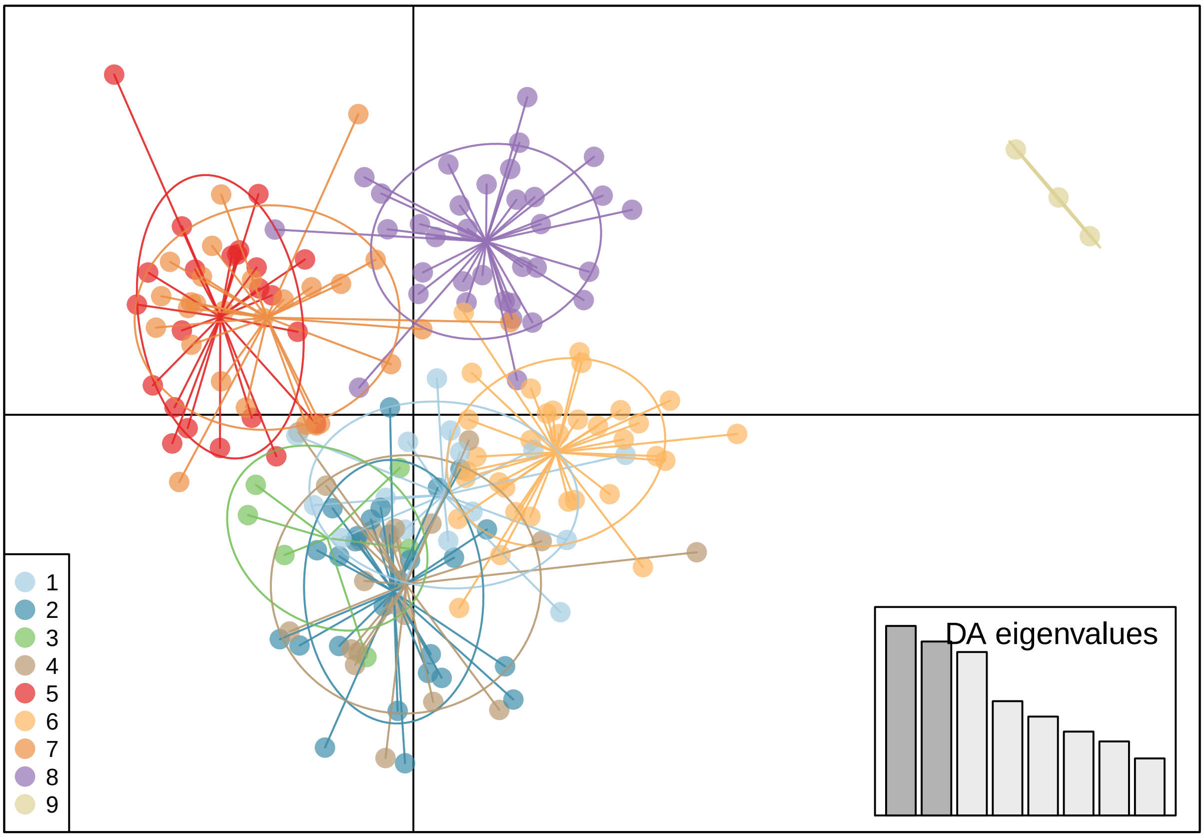

DA eigenvalues
1
2
3
4

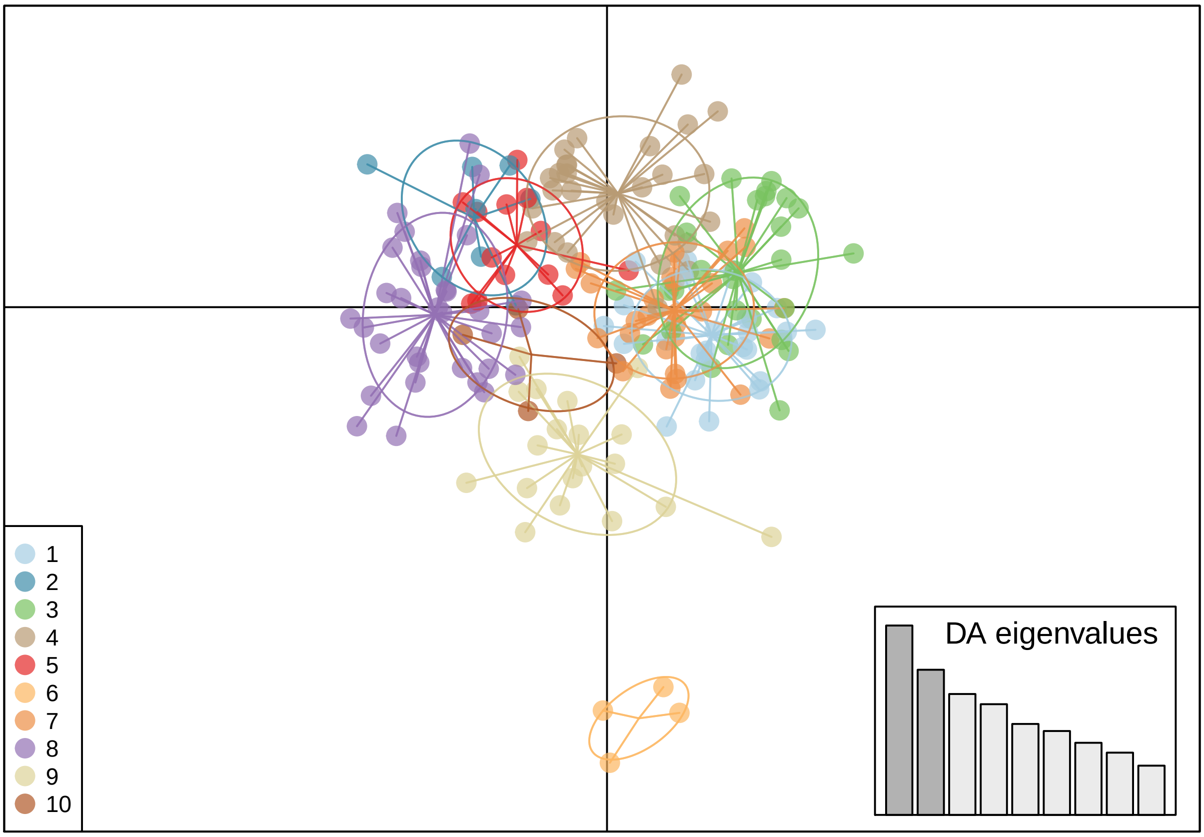

DA eigenvalues
1
2
3
4
5


DA eigenvalues
1
2
3
4
5
6


1
2
3
4
5
6
7
DA eigenvalues


1
2
3
4
5
6
7
8
DA eigenvalues

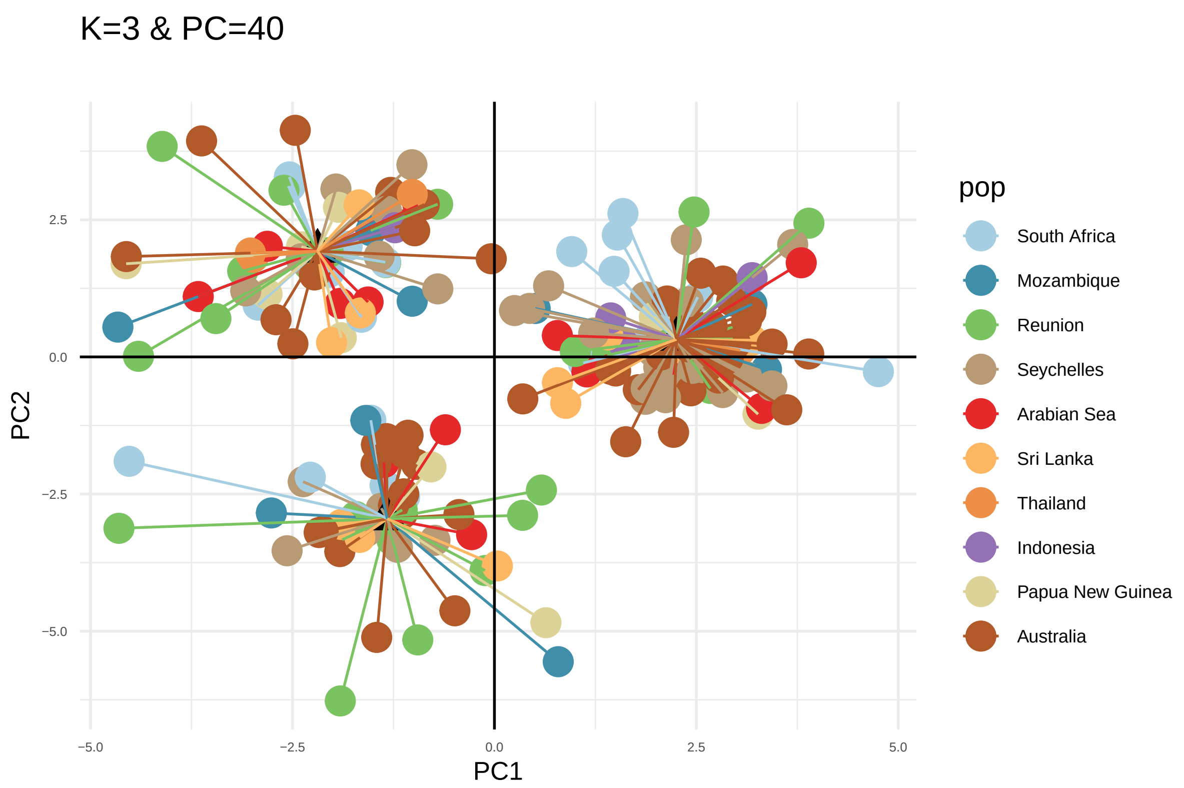




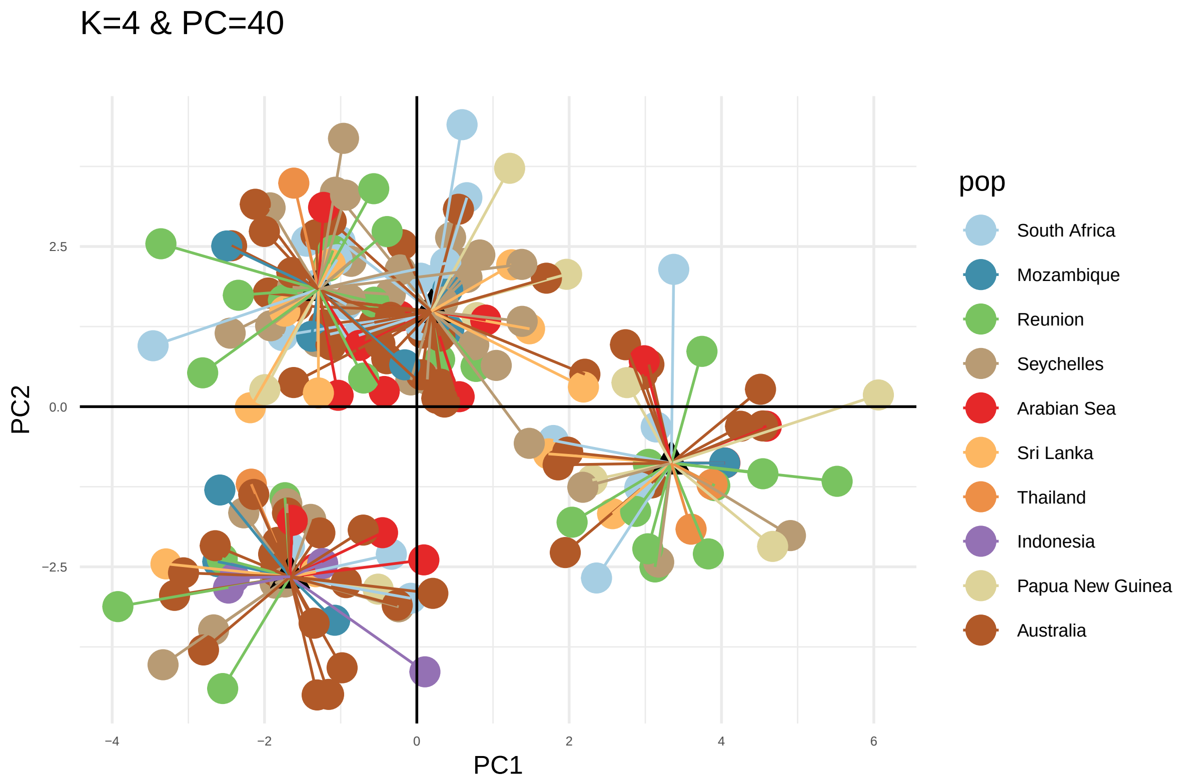
12.9.5 DAPC scatterplot - FLO

This code will *colour* individuals according to *sampling location* and **group** individuals according to DAPC **posterior membership**.

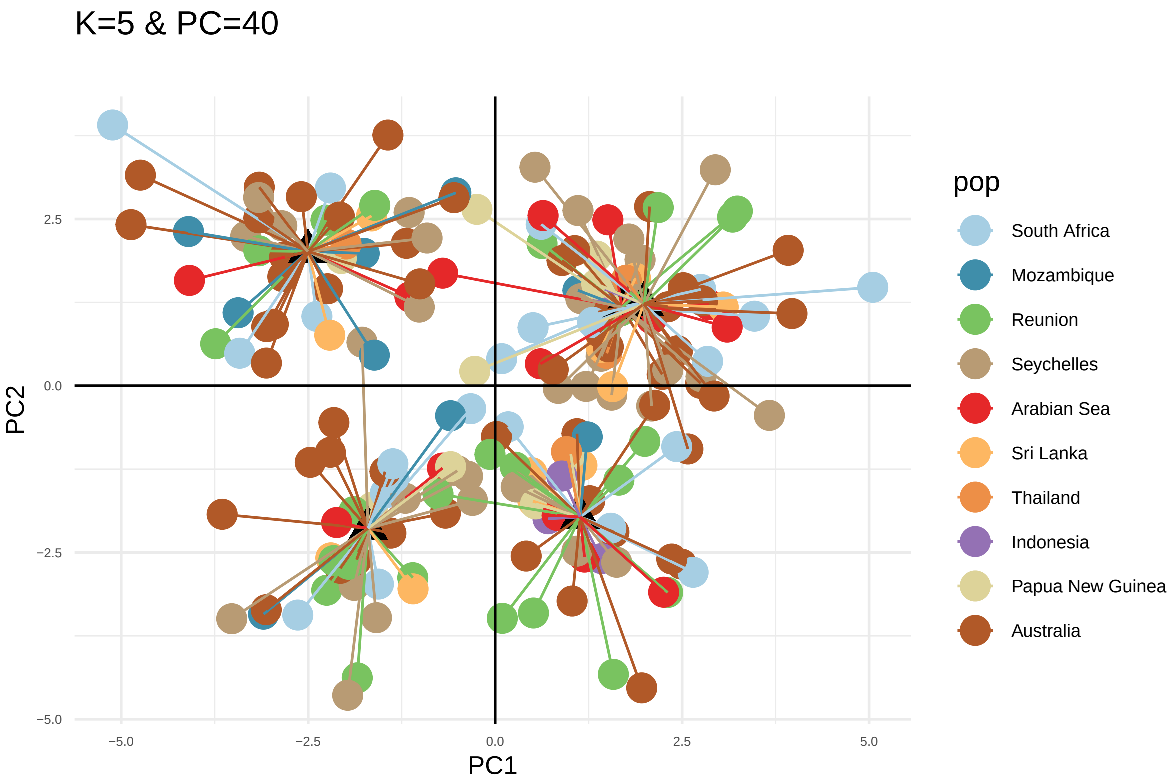
```
for (K in 3:10) {
  dapc <- get(dapc.all.object.names[K - 1])
  x <- dapc$ind.coord[,1]
  y <- dapc$ind.coord[,2]
  group <- paste("Group", as.numeric(dapc$assign))
  pop <- BS.dartcap.IWP2.gl$pop
  df <- data.frame(x, y, group, pop)
  colnames(df) <- c("x","y","group","pop")
  gg <- merge(df,aggregate(cbind(mean.x = x,mean.y = y)~group,df,mean),
              by = "group")

  plot <- ggplot2::ggplot(gg, ggplot2::aes(x,y,color = pop)) +
    ggplot2::geom_point(size = 5) +
    ggplot2::geom_point(ggplot2::aes(x = mean.x,y = mean.y),size = 5,
                        shape = 17, color = "black") +
    ggplot2::geom_segment(ggplot2::aes(x = mean.x, y = mean.y,
                                       xend = x, yend = y)) +
    ggplot2::scale_colour_manual(values = colours.10) +
    ggplot2::scale_fill_manual(values = colours.10) +
    ggplot2::geom_hline(yintercept = 0) +
    ggplot2::geom_vline(xintercept = 0) +
    ggplot2::labs(subtitle = "",
         y = "PC2",
         x = "PC1",
         title = paste0("K=",K," & PC=",PC, sep = ""),
         caption = "") +
    ggplot2::theme_minimal() +
    ggplot2::theme(
      axis.text = ggplot2::element_text(size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
  print(plot)
  ggplot2::ggsave(plot,
                  filename = paste0("DArTcap_IWP2_DAPC_scatterplot2_K", K, ".png"),
                  width = 30, height = 15,units = "cm")
}
```



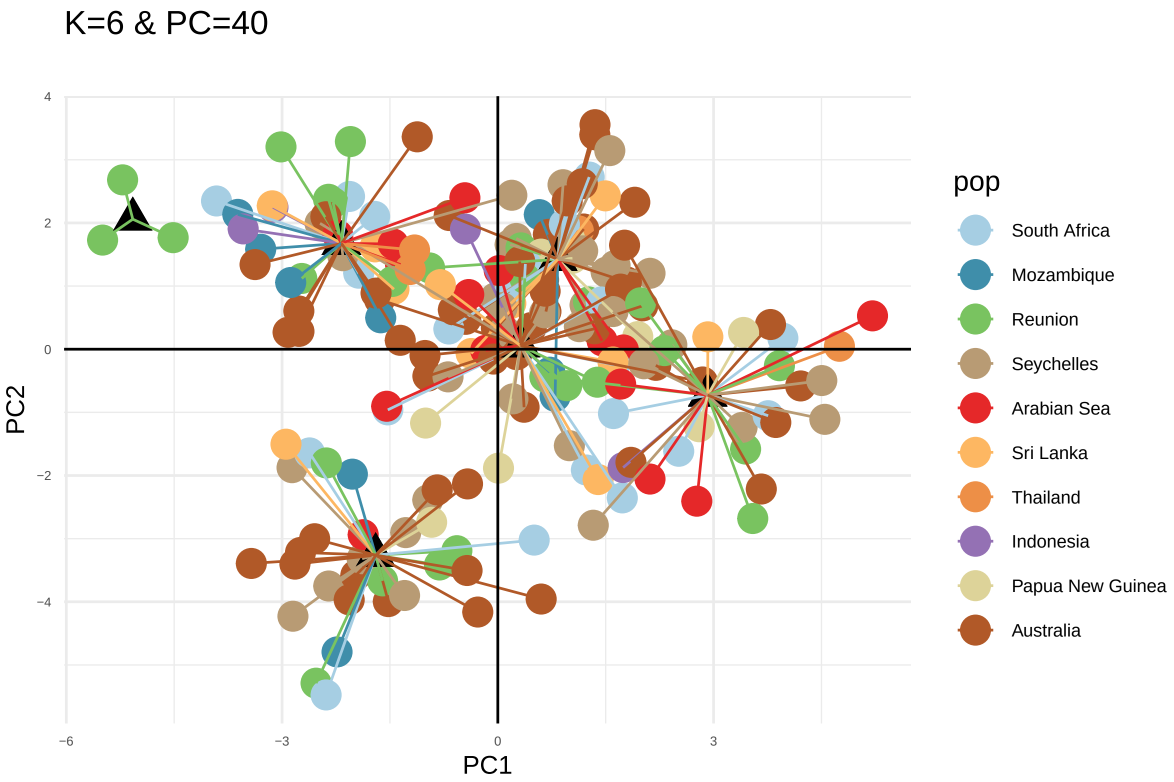
K=3 & PC=40



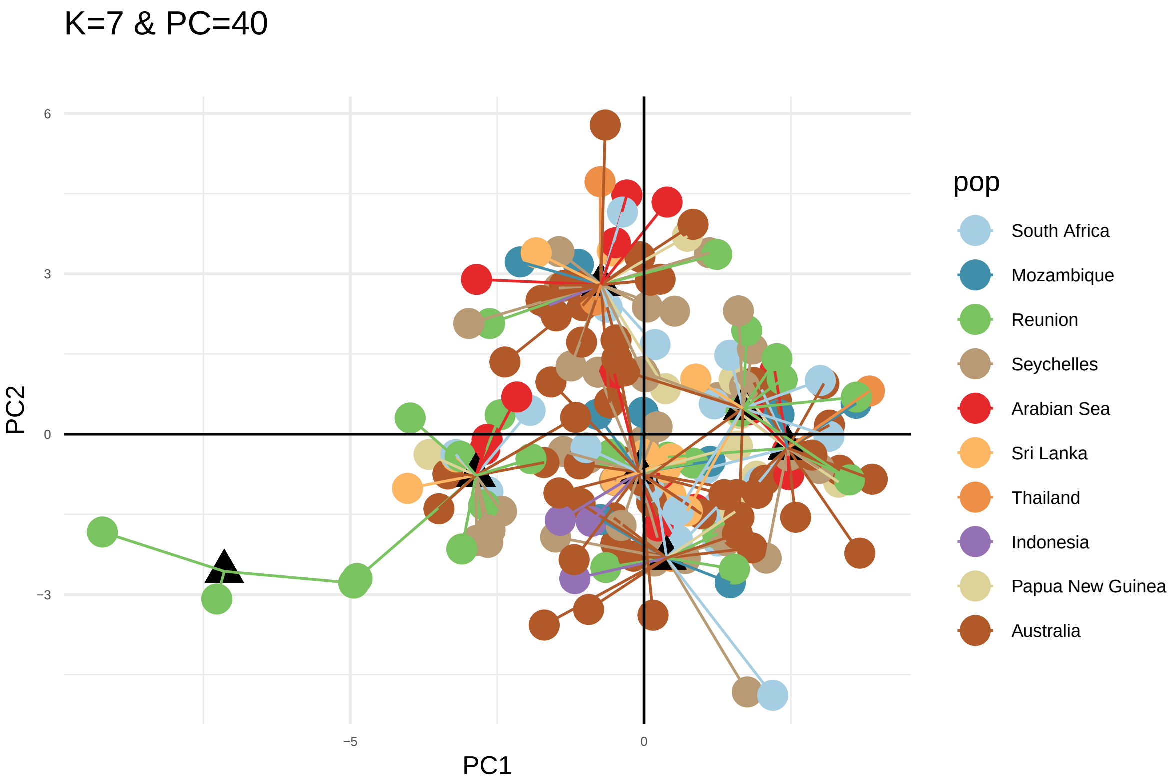
K=4 & PC=40



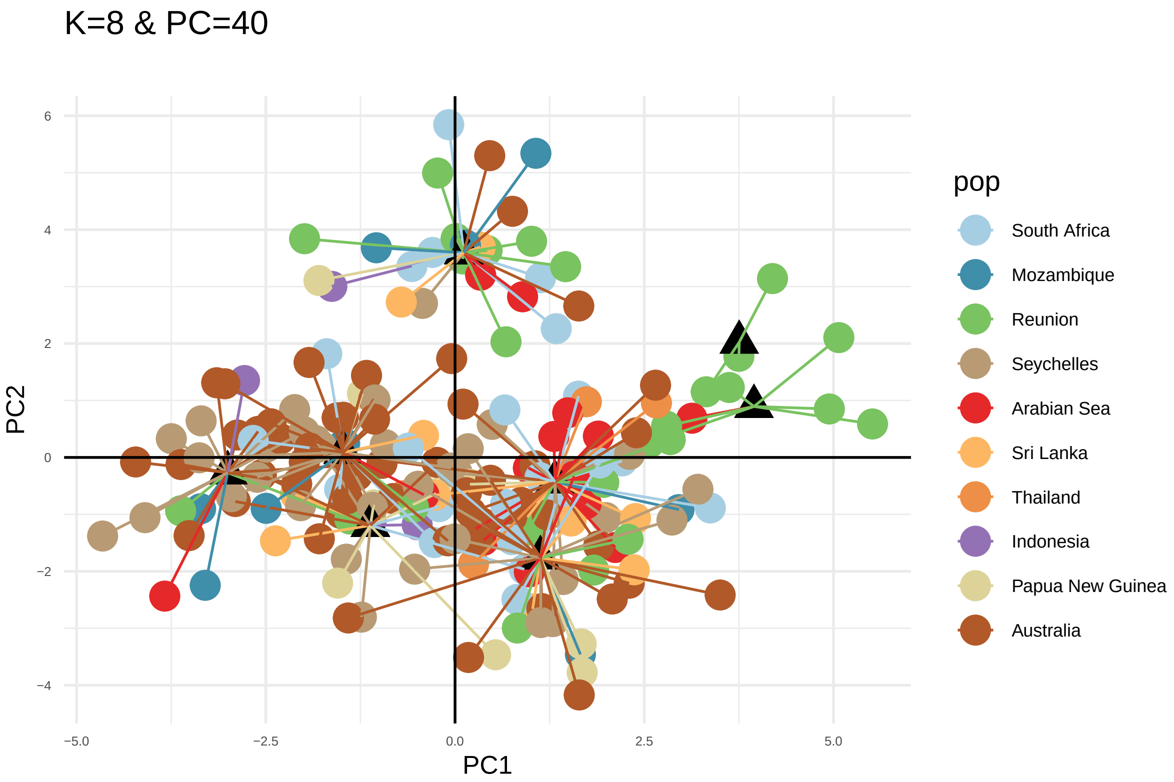
K=5 & PC=40



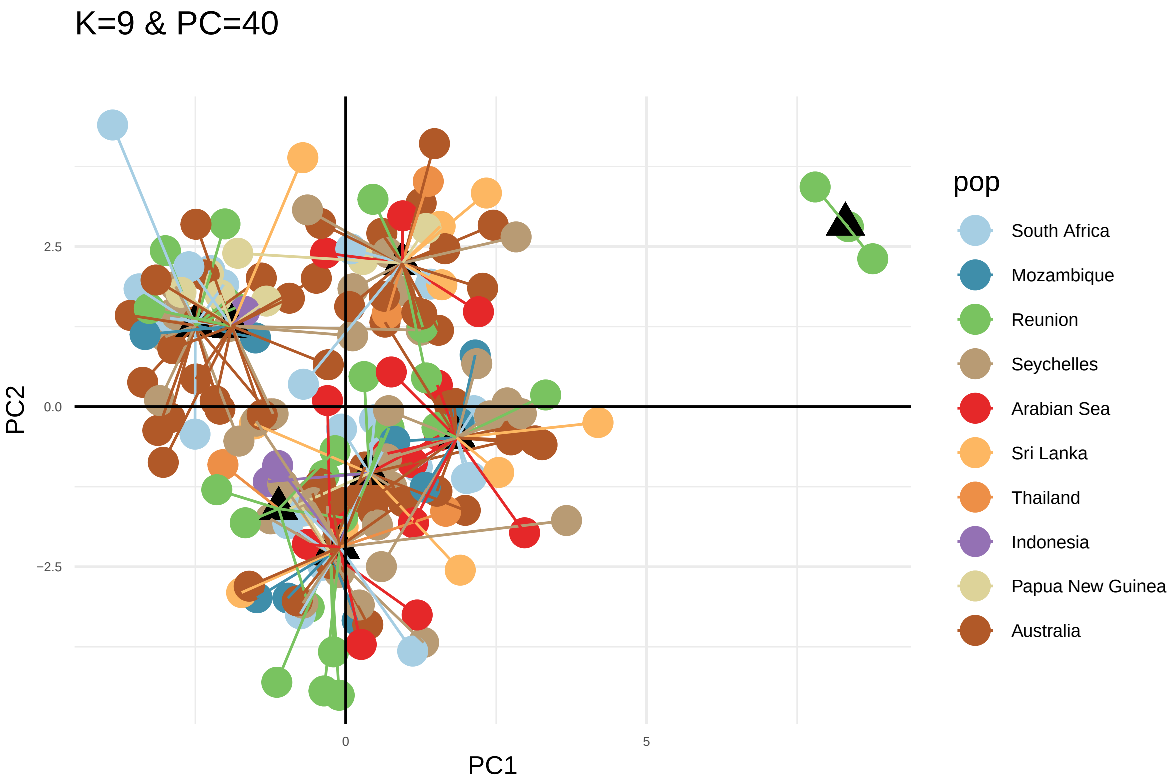
K=6 & PC=40

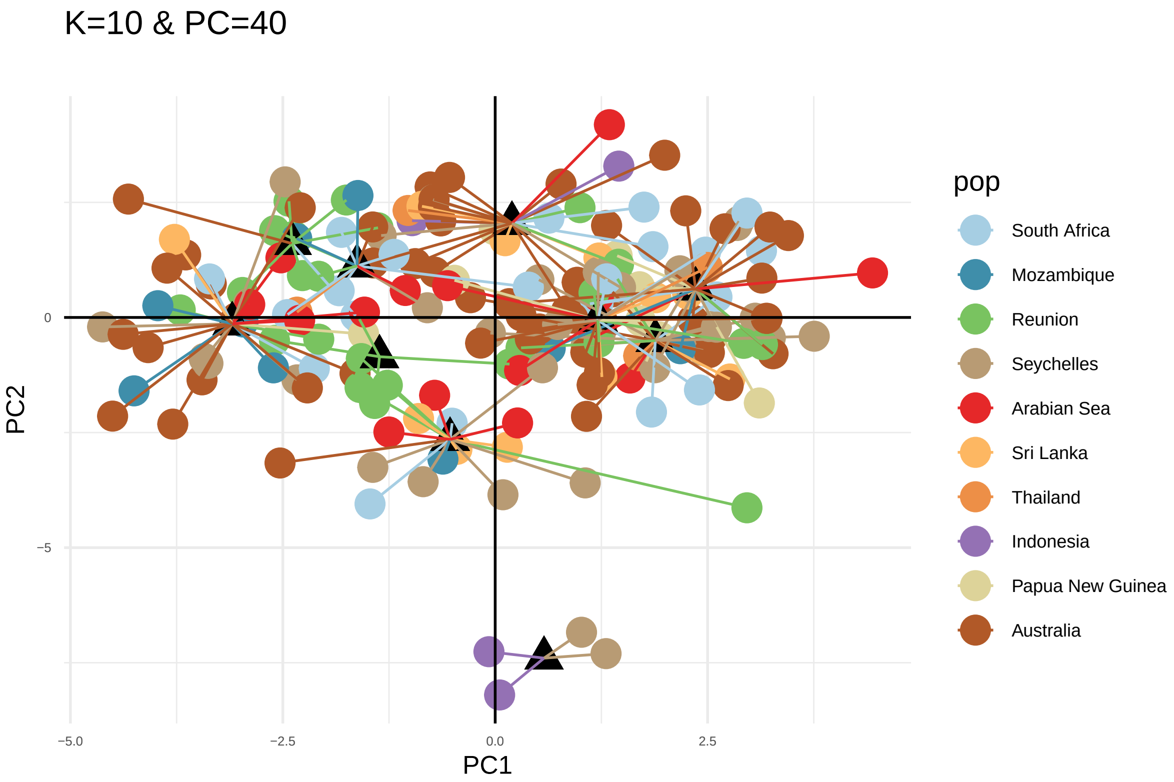


K=7 & PC=40



K=8 & PC=40


K=9 & PC=40
PC2
2.5
0.0
−2.5
0
5
PC1
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia


K=10 & PC=40
PC2
0
−5
−5.0
−2.5
0.0
2.5
PC1
pop
South Africa
Mozambique
Reunion
Seychelles
Arabian Sea
Sri Lanka
Thailand
Indonesia
Papua New Guinea
Australia

13 Mitogenome analyses

13.1 Sequencing primers

Primers were designed to amplify the mitochondrial genome of *C. leucas*. The mitochondrial genomes were amplified with two primer pairs.

Table 51: Primer sequences used for amplifying the two halves of the mitochondrial genome

Mitogenome fragment	Primer name	Primer sequence	Amplicon length (bp)	Ref
A	BSh(1975L_for	5'-AACACAAACTCCGCCTGTTTACCAAAAACATC	9039	Devloo-Delva et al. in prep
A	BSh(10999H_rev	5'-CAACCGGCAATTGGAGCTTCAACGTGGG	9039	Devloo-Delva et al. in prep
B	BSh(9198L_for	5'-GAGCCCATCATAGCTTAATAGAAGGTAAC	9710	Devloo-Delva et al. in prep
B	16s(747-H_rev	5'-GGTGTCTAAAGCTCCATAGGGTCTTCTCGTCT	9710	Devloo-Delva et al. in prep

13.2 Preparing the mitogenome data files

13.2.1 MultiDNA format

```
f.in <- "BS_mitogenome_361_no ambiguous.fasta"
metafile <- "1.BullShark_AllSamples_metadata.csv"
BS.ml <- apex::read.multiFASTA(f.in)
(apex::setLocusNames(BS.ml) <- "Mitogenome")
```

13.2.2 Genind format

```
BS.gi <- apex::multidna2genind(BS.ml, mlst = TRUE)
```

13.2.3 Add metadata

```
meta <- read.csv(metafile)
meta <- meta[meta$mtDNA_ID %in% indNames(BS.gi),]
meta <- meta[order(match(meta$mtDNA_ID, indNames(BS.gi))),]

unique(meta$Location)

pop.levels0 <- c("Gulf of California","Costa Rica","Sierra Leone","South Africa",
                 "Reunion","Seychelles","Abu Dhabi","Dubai","Sri Lanka","Thailand",
                 "South-Indonesia","Jakarta","Omati River","Kikori Delta",
                 "Turama River","Sepik River","Fitzroy River", "Victoria River",
                 "Daly River","Adelaide River",
                 "South Alligator River","East Alligator River","Blue mud Bay",
                 "Roper River",
                 "Towns River","Cape York, QLD","Trinity inlet","Clarence River",
                 "Sydney Harbour",
                 "Okinawa ","Iriomote Island","Fiji")
meta$Location <- factor(x = meta$Location, levels = pop.levels0)

pop.levels1 <- c("Gulf of California","Costa Rica","Sierra Leone", "South Africa",
                 "Reunion","Seychelles","Arabian Sea","Sri Lanka","Thailand",
                 "Indonesia","Papua New Guinea","Australia","Japan","Fiji")
meta$Site <- factor(x = meta$Site, levels = pop.levels1)

pop.levels2 <- c("E-PAC","E-ATL","W-IO","N-IO","E-IO","W-PAC","Japan","Fiji")
meta$Region <- factor(x = meta$Region, levels = pop.levels2)

BS.gi$other$ind.meta <- meta
my_strata <- data.frame(Location = meta$Location,
                        Site = meta$Site ,
```

```
                        regions = meta$Region)
strata(BS.gi) <- my_strata
BS.gi$pop <- as.factor(meta$Site)

BS.gi <- BS.gi[order(BS.gi$other$ind.meta$Region, BS.gi$other$ind.meta$Site,
                     BS.gi$other$ind.meta$Location, indNames(BS.gi)),]
```

```
##  [1] "Kikori Delta"          "Okinawa "              "Iriomote Island"
##  [4] "South Africa"          "Clarence River"        "Sydney Harbour"
##  [7] "Adelaide River"        "Daly River"            "Victoria River"
## [10] "Turama River"          "Omati River"           "Sepik River"
## [13] "Towns River"           "East Alligator River"  "South Alligator River"
## [16] "Cape York, QLD"        "Blue mud Bay"          "Fitzroy River"
## [19] "Roper River"           "Abu Dhabi"             "Thailand"
## [22] "Dubai"                 "South-Indonesia"       "Sri Lanka"
## [25] "Jakarta"               "Fiji"                  "Trinity inlet"
## [28] "Reunion"               "Seychelles"            "Sierra Leone"
## [31] "Costa Rica"            "Gulf of California"
```

13.2.4 Gtypes format

```
Location <-  BS.gi$other$ind.meta$Location[order(match(indNames(BS.gi),
                                                  BS.ml@labels))]
Site <- BS.gi$other$ind.meta$Site[order(match(indNames(BS.gi),
                                         BS.ml@labels))]
Region <- BS.gi$other$ind.meta$Region[order(match(indNames(BS.gi),
                                             BS.ml@labels))]

strata.schemes <- data.frame(Region, Site, Location)
row.names(strata.schemes) <- BS.ml@labels

BS.gt <- strataG::sequence2gtypes(BS.ml, strata = Site, seq.names = NULL,
                                    schemes = strata.schemes,
                                    description = NULL, other = NULL)
```

13.2.5 Haplotype format

13.2.5.1 Haplotypes package This package includes indels: 26 HTs

```
BS.dna <- haplotypes::read.fas(f.in)
BS.hap <- haplotypes::haplotype(BS.dna,indels = "sic")

Location <- BS.gi$other$ind.meta$Location[order(match(indNames(BS.gi),
                                                 BS.dna@seqnames))]
Site <- BS.gi$other$ind.meta$Site[order(match(indNames(BS.gi),
                                         BS.dna@seqnames))]
Region <- BS.gi$other$ind.meta$Region[order(match(indNames(BS.gi),
                                             BS.dna@seqnames))]

BS.hapgroup <- haplotypes::grouping(BS.hap,Site)
```

13.2.5.2 Pegas package This package does not include indels: 165Hts

```
BS.bin <- read.FASTA(f.in, type = "DNA")
HTs <- paste0("HT", sprintf('%0.3d', 1:165))
BS.h <- pegas::haplotype(BS.bin, HTs)
```

13.2.6 Save data

```
save(BS.ml,BS.bin, BS.dna, BS.gi, BS.gt, BS.hap, BS.h,
     file = "6.BS.Rdata")
```

13.2.7 Load data

```
load("6.BS.Rdata")
adegenet::nInd(BS.gi)
summary(BS.gi$pop)
summary(BS.gi$other$ind.meta$Location)
```

```
## [1] 359
## Gulf of California         Costa Rica      Sierra Leone      South Africa
##                  1                 15                 1                 7
##            Reunion         Seychelles       Arabian Sea         Sri Lanka
##                 16                 18                19                12
##           Thailand          Indonesia  Papua New Guinea         Australia
##                  6                  6                15               203
##              Japan               Fiji
##                 31                  9
##    Gulf of California            Costa Rica          Sierra Leone
##                     1                    15                     1
##          South Africa               Reunion            Seychelles
##                     7                    16                    18
##           Arabian Sea             Sri Lanka              Thailand
##                    19                    12                     6
##             Indonesia      Papua New Guinea         Fitzroy River
##                     6                    15                     5
##        Victoria River            Daly River        Adelaide River
##                    21                    25                    18
## South Alligator River  East Alligator River          Blue mud Bay
##                    38                    17                    13
##           Roper River           Towns River         Wenlock River
##                     4                     5                    19
##         Trinity inlet        Clarence River        Sydney Harbour
##                     4                    21                    13
##              Okinawa          Urauchi River                  Fiji
##                    10                    21                     9
```

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata
BS.gt.AUS <- BS.gt[,,"Australia", drop = TRUE]

schemes.AUS <- BS.gt.AUS@schemes[BS.gt.AUS@schemes$Site == "Australia",]
strata <- as.character(schemes.AUS$Location)
names(strata) <- as.character(schemes.AUS$id)
strataG::setStrata(BS.gt.AUS) <- strata
BS.gt.AUS@schemes <- schemes.AUS

ind.names <- names(BS.dna) %in% BS.gt.AUS@data$id
BS.dna.AUS <- as.dna(BS.dna[ind.names, , drop = TRUE])
BS.bin.AUS <- subset(BS.bin, names(BS.bin) %in% BS.gt.AUS@data$id)
BS.gi.aus <- BS.gi[adegenet::indNames(BS.gi) %in% BS.gt.AUS@data$id]
BS.hap.aus <- haplotypes::haplotype(BS.dna.AUS,indels = "sic")
BS.h.aus <- strataG::labelHaplotypes(BS.bin.AUS, prefix = "HT",
```

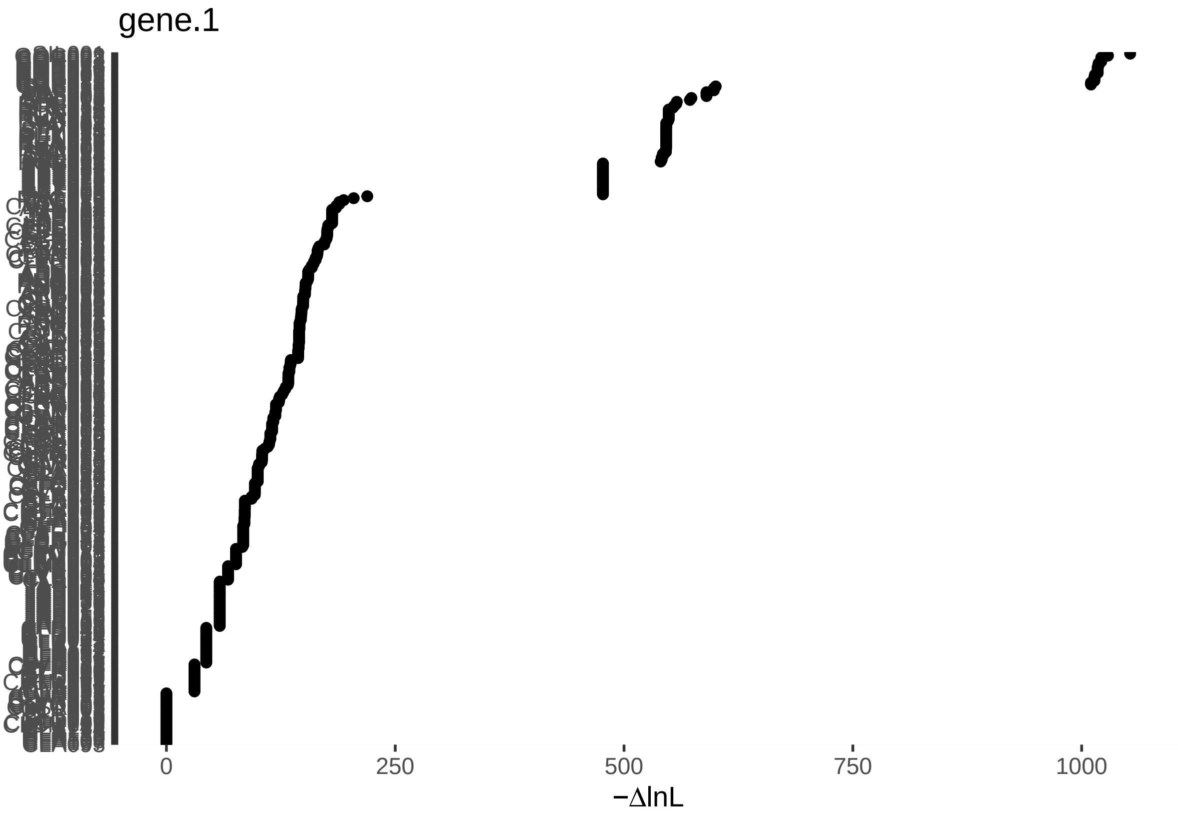
```
                                        use.indels = TRUE)
```

13.2.7.1 Subset Australia

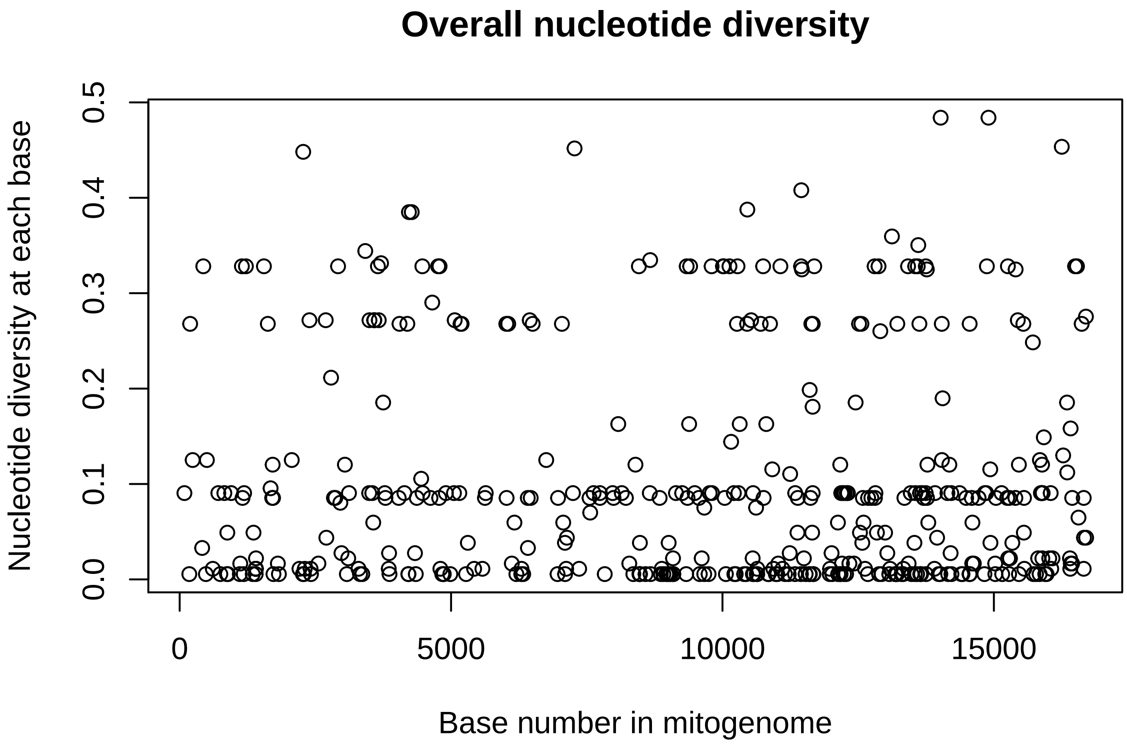
13.3 Genetic diversity

13.3.1 Overall diversity

```
seqLL <- strataG::sequenceLikelihoods(BS.bin, model = "N",
                                      pairwise.deletion = FALSE, n = NULL,
                                      plot = TRUE, simplify = TRUE)
```



```
{bases <- haplotypes::basecomp(BS.dna)
print(paste0("Mitogenome base composition:"))
print(colMeans(bases))}

{pi.gt <- strataG::nucleotideDiversity(BS.gt, bases = c("a", "c", "g", "t"),
                                       simplify = TRUE)
plot(names(pi.gt[pi.gt != 0]),pi.gt[pi.gt != 0],
     xlab = "Base number in mitogenome",
     ylab = "Nucleotide diversity at each base",
     main = "Overall nucleotide diversity")}
```



```
print(paste0("Nucleotide diversity according to strataG = ",mean(pi.gt)))
{print(paste0("Nucleotide diversity and variance according to pegas:"))
pegas::nuc.div(BS.bin, variance = TRUE, pairwise.deletion = FALSE)}
{print(paste0("Haplotype diversity and variance according to pegas:"))
pegas::hap.div(BS.bin, variance = TRUE, method = "Nei")}

varsites <- strataG::variableSites(BS.gt, bases = c("a", "c", "g", "t", "-"),
                                   simplify = TRUE)

kableExtra::kbl(t(varsites$site.freqs),
  caption = "Variable sites in mitogenome for all individuals",
  longtabs = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))
```

```
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146193 0.2430317 0.1311460 0.3112030
## [1] "Nucleotide diversity according to strataG = 0.00263330094093478"
## [1] "Nucleotide diversity and variance according to pegas:"
## [1] 2.634878e-03 1.604305e-06
## [1] "Haplotype diversity and variance according to pegas:"
## [1] 9.886556e-01 2.119587e-06
```

Table 52: Variable sites in mitogenome for all individuals

	a	c	g	t	-
55	0	0	0	295	64
87	342	0	17	0	0
177	0	358	0	1	0
193	57	0	302	0	0
239	0	335	0	24	0
414	353	0	6	0	0
435	0	285	0	74	0
483	1	0	358	0	0
501	0	335	0	24	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

	a	c	g	t	-
610	0	357	0	2	0
712	0	342	0	17	0
749	358	0	0	1	0
806	0	0	0	4	355
823	0	17	0	342	0
870	1	0	358	0	0
878	0	350	0	9	0
889	0	1	0	358	0
948	0	17	0	342	0
1108	1	0	358	0	0
1116	356	0	3	0	0
1146	0	285	0	74	0
1158	0	343	0	16	0
1180	0	358	0	1	0
1187	0	17	0	342	0
1220	74	0	285	0	0
1346	0	358	0	1	0
1360	0	350	0	9	0
1399	2	0	357	0	0
1401	0	358	0	1	0
1402	0	2	0	357	0
1403	357	0	0	2	0
1404	357	0	0	2	0
1406	0	355	0	4	0
1552	0	285	0	74	0
1624	0	57	0	302	0
1675	18	0	341	0	0
1704	0	16	0	343	0
1713	0	336	0	23	0
1720	0	16	0	343	0
1728	0	1	0	358	0
1809	0	3	0	356	0
1828	1	0	358	0	0
2065	0	335	0	24	0
2207	0	2	0	357	0
2270	0	358	0	1	0
2276	0	121	0	238	0
2288	0	358	0	1	0
2304	0	2	0	357	0
2391	0	58	0	301	0
2412	0	2	0	357	0
2419	0	358	0	1	0
2556	0	356	0	3	0
2691	0	301	0	58	0
2702	0	8	0	351	0
2789	0	316	0	43	0
2842	0	343	0	16	0
2868	0	343	0	16	0
2918	0	285	0	74	0
2960	0	344	0	15	0
2981	0	5	0	354	0
3044	0	336	0	23	0
3080	0	358	0	1	0
3105	4	0	355	0	0
3119	17	0	342	0	0
3295	2	0	357	0	0
3323	0	358	0	1	0
3365	0	358	0	1	0
3419	0	280	0	79	0
3491	17	0	342	0	0
3497	0	58	0	301	0
3548	0	342	0	17	0
3566	0	11	0	348	0
3582	0	58	0	301	0
3587	0	301	0	58	0
3652	0	74	0	285	0
3668	0	58	0	301	0
3710	0	75	0	284	0
3749	0	322	0	37	0
3779	0	17	0	342	0
3791	0	16	0	343	0
3852	357	0	2	0	0
3858	5	0	354	0	0
3866	1	0	358	0	0
4035	0	343	0	16	0
4050	0	302	0	57	0
4140	0	17	0	342	0
4194	0	57	0	302	0
4212	0	358	0	1	0
4215	0	1	0	358	0
4224	0	93	0	266	0
4275	0	93	0	266	0
4335	0	354	0	5	0
4350	0	358	0	1	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

	a	c	g	t	-
4368	0	343	0	16	0
4449	0	339	0	20	0
4471	0	285	0	74	0
4476	0	17	0	342	0
4620	0	343	0	16	0
4653	0	296	0	63	0
4761	0	285	0	74	0
4780	0	16	0	343	0
4788	74	0	285	0	0
4803	0	357	0	2	0
4837	0	1	0	358	0
4857	0	358	0	1	0
4866	0	1	0	358	0
4905	0	342	0	17	0
4986	0	358	0	1	0
5053	342	0	0	17	0
5067	0	58	0	301	0
5152	0	17	0	342	0
5175	0	57	0	302	0
5194	57	0	302	0	0
5276	1	0	358	0	0
5309	7	0	352	0	0
5425	2	0	357	0	0
5577	2	0	357	0	0
5624	0	16	0	343	0
5639	0	17	0	342	0
6017	0	57	0	302	0
6023	0	343	0	16	0
6053	0	302	0	57	0
6119	0	356	0	3	0
6167	0	11	0	348	0
6203	0	358	0	1	0
6293	1	0	358	0	0
6297	2	0	357	0	0
6329	0	1	0	358	0
6413	0	16	0	343	0
6416	0	353	0	6	0
6449	301	0	58	0	0
6467	0	16	0	343	0
6503	0	57	0	302	0
6753	0	335	0	24	0
6962	0	358	0	1	0
6971	0	343	0	16	0
7042	0	302	0	57	0
7066	0	348	0	11	0
7098	0	7	0	352	0
7100	0	358	0	1	0
7121	0	357	0	2	0
7134	8	0	351	0	0
7245	0	17	0	342	0
7275	0	236	0	123	0
7360	2	0	357	0	0
7551	0	343	0	16	0
7563	0	346	0	13	0
7626	0	342	0	17	0
7741	342	0	17	0	0
7743	0	343	0	16	0
7831	1	0	358	0	0
7976	0	17	0	342	0
7993	0	343	0	16	0
8080	0	327	0	32	0
8145	0	17	0	342	0
8221	0	343	0	16	0
8283	0	3	0	356	0
8358	0	1	0	358	0
8397	336	0	0	23	0
8460	0	285	0	74	0
8470	0	358	0	1	0
8475	0	358	0	1	0
8479	0	352	0	7	0
8481	0	358	0	1	0
8583	0	1	0	358	0
8661	17	0	342	0	0
8668	0	76	0	283	0
8676	0	1	0	358	0
8842	0	343	0	16	0
8864	1	0	358	0	0
8882	0	357	0	2	0
8911	0	1	0	358	0
8963	0	1	0	358	0
8995	0	358	0	1	0
9009	7	0	352	0	0
9017	0	1	0	358	0
9048	1	0	358	0	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

	a	c	g	t	-
9089	0	355	0	4	0
9092	0	1	0	358	0
9095	0	358	0	1	0
9143	0	342	0	17	0
9257	0	17	0	342	0
9332	1	0	358	0	0
9341	0	285	0	74	0
9356	0	343	0	16	0
9386	0	327	0	32	0
9404	0	285	0	74	0
9488	0	17	0	342	0
9566	16	0	343	0	0
9582	0	1	0	358	0
9617	0	4	0	355	0
9664	0	358	0	1	0
9665	0	345	0	14	0
9744	0	358	0	1	0
9764	0	342	0	17	0
9800	0	74	0	285	0
9807	0	342	0	17	0
10009	285	0	74	0	0
10025	0	74	0	285	0
10040	16	0	343	0	0
10063	0	1	0	358	0
10129	0	285	0	74	0
10159	0	28	0	331	0
10210	0	17	0	342	0
10219	0	358	0	1	0
10244	0	358	0	1	0
10267	0	302	0	57	0
10277	0	74	0	285	0
10294	0	17	0	342	0
10318	0	327	0	32	0
10399	0	358	0	1	0
10437	0	358	0	1	0
10454	0	57	0	302	0
10458	0	94	0	265	0
10528	0	301	0	58	0
10556	4	0	355	0	0
10560	358	0	1	0	0
10564	0	342	0	17	0
10578	0	1	0	358	0
10619	14	0	345	0	0
10632	0	1	0	358	0
10641	0	1	0	358	0
10642	0	357	0	2	0
10704	0	57	0	302	0
10749	74	0	285	0	0
10758	0	16	0	343	0
10807	0	327	0	32	0
10840	0	358	0	1	0
10851	358	0	1	0	0
10876	0	57	0	302	0
10917	337	0	22	0	0
10939	2	0	357	0	0
10983	0	1	0	358	0
11010	0	358	0	1	0
11028	0	3	0	356	0
11067	0	285	0	74	0
11105	0	2	0	357	0
11151	0	0	1	358	0
11220	1	358	0	0	0
11239	5	0	354	0	0
11247	0	21	0	338	0
11337	0	358	0	1	0
11340	0	342	0	17	0
11382	0	350	0	9	0
11388	16	0	343	0	0
11445	0	358	0	1	0
11448	0	74	0	285	0
11452	0	102	0	257	0
11463	0	73	0	286	0
11500	0	355	0	4	0
11532	0	358	0	1	0
11599	358	0	1	0	0
11607	0	40	0	319	0
11610	0	358	0	1	0
11621	0	343	0	16	0
11637	0	57	0	302	0
11652	0	350	0	9	0
11661	0	323	0	36	0
11662	0	342	0	17	0
11664	0	302	0	57	0
11670	0	358	0	1	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

	a	c	g	t	-
11676	0	358	0	1	0
11691	0	74	0	285	0
11976	358	0	1	0	0
11982	2	0	357	0	0
12010	0	354	0	5	0
12023	1	0	358	0	0
12127	0	348	0	11	0
12131	0	358	0	1	0
12167	0	358	0	1	0
12170	0	336	0	23	0
12176	0	358	0	1	0
12188	0	342	0	17	0
12202	0	3	0	356	0
12219	0	342	0	17	0
12239	0	1	0	358	0
12251	0	342	0	17	0
12278	0	358	0	1	0
12290	0	17	0	342	0
12311	0	17	0	342	0
12338	0	356	0	3	0
12423	3	0	356	0	0
12453	37	0	322	0	0
12516	0	302	0	57	0
12533	0	350	0	9	0
12560	0	302	0	57	0
12576	0	352	0	7	0
12587	0	16	0	343	0
12599	0	348	0	11	0
12626	0	357	0	2	0
12678	0	1	0	358	0
12683	0	343	0	16	0
12743	16	0	0	343	0
12803	0	74	0	285	0
12809	0	343	0	16	0
12818	0	342	0	17	0
12846	9	0	350	0	0
12875	74	0	285	0	0
12885	1	0	358	0	0
12908	0	304	0	55	0
12932	0	358	0	1	0
12996	9	0	350	0	0
13037	5	0	0	354	0
13073	0	1	0	358	0
13088	0	2	0	357	0
13122	84	0	275	0	0
13183	0	1	0	358	0
13190	358	0	0	1	0
13200	1	0	358	0	0
13217	0	1	0	358	0
13221	57	0	302	0	0
13301	0	358	0	1	0
13328	0	358	0	1	0
13332	2	0	357	0	0
13352	0	343	0	16	0
13419	285	0	74	0	0
13429	0	356	0	3	0
13469	0	342	0	17	0
13484	0	1	0	358	0
13536	0	7	0	352	0
13544	0	1	0	358	0
13550	285	0	74	0	0
13554	0	17	0	342	0
13586	0	1	0	358	0
13598	0	285	0	74	0
13607	0	81	0	278	0
13628	0	57	0	302	0
13640	0	17	0	342	0
13643	0	358	0	1	0
13659	0	358	0	1	0
13679	0	342	0	17	0
13709	0	16	0	343	0
13710	0	343	0	16	0
13745	0	17	0	342	0
13746	0	74	0	285	0
13750	0	1	0	358	0
13765	0	286	0	73	0
13768	0	16	0	343	0
13776	0	336	0	23	0
13792	0	348	0	11	0
13905	0	357	0	2	0
13916	0	342	0	17	0
13954	0	8	0	351	0
13983	0	1	0	358	0
14014	0	358	0	1	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

	a	c	g	t	-
14020	0	146	0	213	0
14040	0	302	0	57	0
14043	0	24	0	335	0
14056	0	321	0	38	0
14145	17	0	342	0	0
14158	358	0	1	0	0
14180	23	0	336	0	0
14203	5	0	354	0	0
14215	17	0	342	0	0
14219	1	0	358	0	0
14367	0	342	0	17	0
14400	0	358	0	1	0
14422	1	0	358	0	0
14490	0	16	0	343	0
14551	1	0	358	0	0
14554	57	0	302	0	0
14557	0	358	0	1	0
14592	0	16	0	343	0
14601	0	356	0	3	0
14605	11	0	348	0	0
14631	0	356	0	3	0
14718	0	343	0	16	0
14826	1	0	358	0	0
14832	342	0	17	0	0
14859	0	342	0	17	0
14871	0	74	0	285	0
14901	0	213	0	146	0
14933	0	337	0	22	0
14937	0	352	0	7	0
15024	0	356	0	3	0
15027	0	358	0	1	0
15039	0	343	0	16	0
15141	0	17	0	342	0
15153	0	1	0	358	0
15246	0	343	0	16	0
15258	0	285	0	74	0
15262	0	4	0	355	0
15281	0	358	0	1	0
15285	0	343	0	16	0
15297	0	4	0	355	0
15340	7	0	352	0	0
15396	0	343	0	16	0
15401	0	286	0	73	0
15441	0	58	0	301	0
15461	0	336	0	23	0
15462	0	358	0	1	0
15543	0	57	0	302	0
15552	0	350	0	9	0
15555	16	0	343	0	0
15561	0	2	0	357	0
15671	40	0	0	0	319
15718	0	52	0	307	0
15728	0	1	0	358	0
15777	358	0	1	0	0
15805	358	0	0	0	1
15816	4	0	355	0	0
15843	0	358	0	1	0
15848	0	24	0	335	0
15867	0	342	0	17	0
15869	17	0	342	0	0
15888	0	23	0	336	0
15891	342	0	17	0	0
15893	0	4	0	355	0
15899	342	0	17	0	0
15920	29	0	330	0	0
15946	0	358	0	1	0
15971	0	1	0	358	0
16020	0	0	4	355	0
16047	17	0	0	342	0
16057	0	357	0	2	0
16080	355	0	4	0	0
16084	0	0	0	355	4
16251	235	0	124	0	0
16277	0	25	0	334	0
16348	322	0	37	0	0
16352	338	13	0	8	0
16402	0	4	0	355	0
16408	2	0	357	0	0
16414	328	0	31	0	0
16417	0	3	0	356	0
16442	356	0	3	0	0
16443	0	343	0	16	0
16496	0	285	0	74	0
16531	74	285	0	0	0

Table 52: Variable sites in mitogenome for all individuals *(continued)*

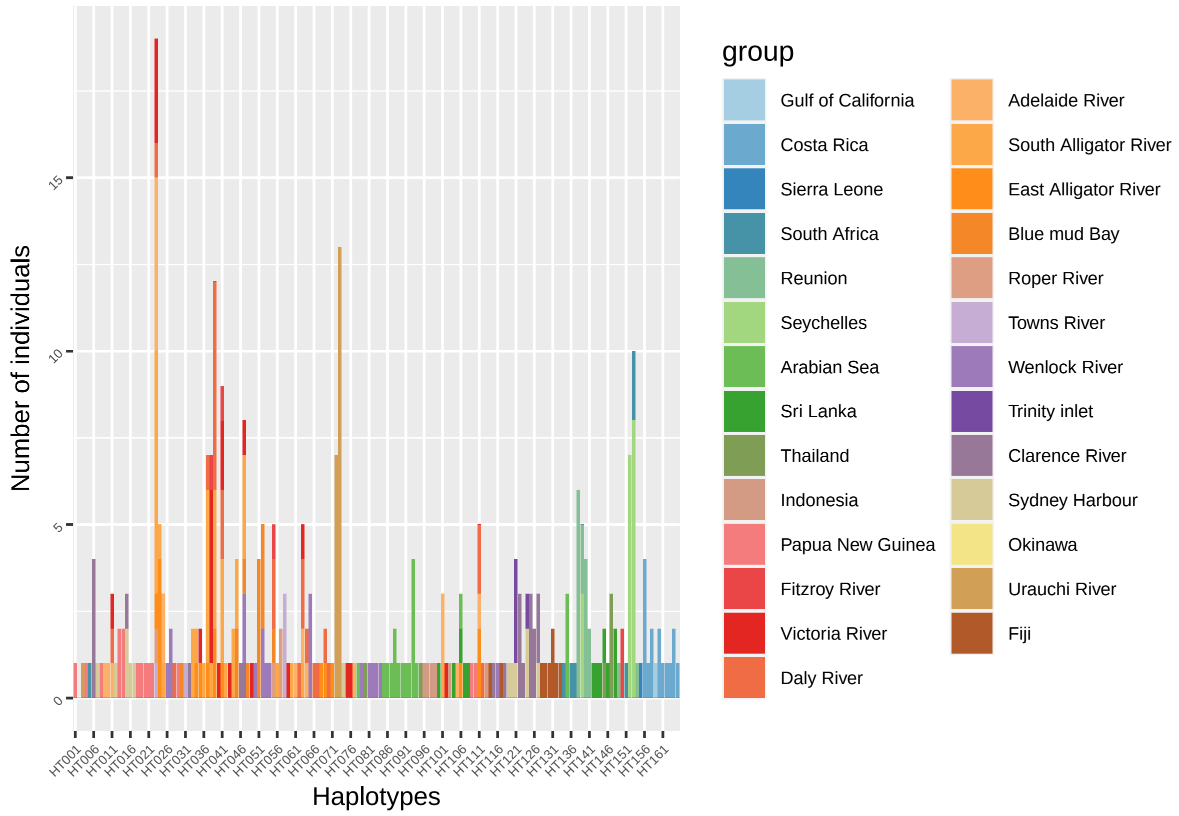
	a	c	g	t	-
16559	0	347	0	12	0
16562	137	0	0	0	222
16618	57	0	302	0	0
16655	0	2	0	357	0
16656	0	16	0	343	0
16660	0	351	0	8	0
16686	0	0	0	56	303
16687	56	0	0	0	303
16696	300	0	59	0	0
16700	351	0	8	0	0
16705	0	0	0	358	1
16706	0	0	358	0	1

13.3.2 Diversity per location

```r
strata <- as.character(BS.gt@schemes$Location)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

divers.location <- data.frame(Location = character(), pi.strataG = numeric(),
                           pi.pegas = numeric(), pi.pegas.var = numeric(),
                           HT.richness.strataG = numeric(), h.pegas = numeric(),
                           h.pegas.var = numeric())
for (Location in levels(BS.gt@schemes$Location)) {
  print(Location)
  BS.gt.sub <- BS.gt[,,Location, drop = TRUE]
  BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)
  BS.h.sub <- strataG::labelHaplotypes(BS.bin.sub, prefix = "HT",
                                        use.indels = TRUE)
  BS.dna.sub <- as.dna(BS.dna[names(BS.dna) %in% BS.gt.sub@data$id, ,
                                 drop = TRUE])
  bases <- haplotypes::basecomp(BS.dna.sub)
  print(paste0("Mitogenome base composition:"))
  print(colMeans(bases))

  pi.gt <-
    strataG::nucleotideDiversity(BS.gt.sub,bases = c("a", "c", "g", "t"),
    simplify = TRUE)
  pi.peg <- pegas::nuc.div(BS.bin.sub, variance = TRUE,
                           pairwise.deletion = FALSE)
  h.peg <- pegas::hap.div(BS.bin.sub, variance = TRUE, method = "Nei")
  res <- data.frame(Location, mean(pi.gt), pi.peg[1], pi.peg[2],
                    length(unique(BS.h.sub$haps)),
                    h.peg[1], h.peg[2])
  colnames(res) <- c("Location", "pi.strataG", "pi.pegas", "pi.pegas.var",
                     "HT.richness.strataG", "h.pegas", "h.pegas.var")
  divers.location <- rbind(divers.location, res)
}

knitr::kable(
  divers.location,
  caption = "Nucleotide and haplotype diversity per Location",
  # format = "html",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))
```

```
dA.gt <- strataG::nucleotideDivergence(BS.gt,
                                       probs = c(0, 0.025, 0.5, 0.975, 1),
                                       model = "RAW")
knitr::kable(
  dA.gt$within[order(dA.gt$within$mean, decreasing = TRUE), -1],
  # format = "html",
  caption = "Nucleotide divergence within each Location",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))

kableExtra::kbl(dA.gt$between[order(dA.gt$between$mean, decreasing = TRUE), -1],
  caption = "Nucleotide divergence between each Location",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))

hapcount <- pegas::haploFreq(BS.dna@sequence, fac = BS.gt@schemes$Location,
                             split = NULL, what = 1, haplo = NULL)
row.names(hapcount) <- paste0("HT", sprintf('%0.2d', 1:BS.hap@nhap))
shortnames <- c("GOC", "COR","SIL", "SAF", "RUN", "SEY", "ARS", "SRL", "TAI",
                "IND", "PNG", "FZR", "VIR", "DAR", "ADR","SAR", "EAR","BMB",
                "ROR","TOR","WER","TRI","CLR", "SYH", "URR","OKI", "FIJ")

kableExtra::kbl(hapcount, col.names = shortnames,
  caption = "Haplotype counts per Location according to pegas",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position")) %>%
  kableExtra::landscape()

# group.levels <- levels(BS.gi$other$ind.meta$Location)
group.levels <- c("Gulf of California","Costa Rica","Sierra Leone","South Africa",
                  "Reunion","Seychelles","Arabian Sea","Sri Lanka", "Thailand",
                  "Indonesia","Papua New Guinea","Fitzroy River","Victoria River",
                  "Daly River","Adelaide River","South Alligator River",
                  "East Alligator River","Blue mud Bay","Roper River","Towns River",
                  "Wenlock River","Trinity inlet","Clarence River","Sydney Harbour",
                  "Okinawa","Urauchi River","Fiji")

group.names <- BS.gi$other$ind.meta$Location

HTs <- paste0("HT", sprintf('%0.3d', 1:BS.hap@nhap))
df <- data.frame(group = NULL,nind = NULL, hap = NULL, nhap = NULL,
                 hapfreq = NULL, stringsAsFactors = FALSE)
for (k in 1:length(group.levels)) {
  group.inds <- adegenet::indNames(BS.gi)[group.names == group.levels[k]]
  for (i in 1:BS.hap@nhap) {
    group <- group.levels[k]
    nind <- length(group.inds)
    hap <- HTs[i]
    nhap <- sum(group.inds %in% BS.hap@haplist[[i]])
    hapfreq <- nhap/nind
    df <- plyr::rbind.fill(df, data.frame(group = group, nind = nind, hap = hap,
                                          nhap = nhap, hapfreq = hapfreq,
                                          stringsAsFactors = FALSE))
```

```
  }
}

df$group <- factor(df$group, levels = group.levels)

haplotype.labels <- unique(df$hap)
haplotype.labels2 <- haplotype.labels[seq(1, length(haplotype.labels), by = 5)]

HT.plot <- ggplot2::ggplot(data = df) +
  ggplot2::geom_bar(ggplot2::aes(x = hap, y = nhap, fill = group),
                    stat = "identity",position = "stack") +
  ggplot2::labs(x = "Haplotypes", y = "Number of individuals") +
  ggplot2::scale_fill_manual(values = colours.27) +
  ggplot2::scale_x_discrete(breaks = haplotype.labels2) +
  ggplot2::theme(
      axis.text = ggplot2::element_text(angle = 45, hjust = 1, size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
print(HT.plot)
```



```
ggplot2::ggsave(HT.plot, filename = "HT_barplot_per_Location.png", width = 30,
                height = 15, units = "cm")
```

```
## [1] "Gulf of California"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3151972 0.2423535 0.1307236 0.3117256
## [1] "Costa Rica"
## [1] "Mitogenome base composition:"
##         A         T         G         C
```

```
## 0.3151516 0.2424022 0.1307582 0.3116879
## [1] "Sierra Leone"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145576 0.2423680 0.1312702 0.3118041
## [1] "South Africa"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3148254 0.2429858 0.1309720 0.3112168
## [1] "Reunion"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3148585 0.2431229 0.1309273 0.3110912
## [1] "Seychelles"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3149296 0.2427989 0.1309067 0.3113648
## [1] "Arabian Sea"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146861 0.2433287 0.1310578 0.3109275
## [1] "Sri Lanka"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3147039 0.2430626 0.1310614 0.3111722
## [1] "Thailand"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3147902 0.2430688 0.1310021 0.3111388
## [1] "Indonesia"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145539 0.2432308 0.1311531 0.3110621
## [1] "Papua New Guinea"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145063 0.2429284 0.1312395 0.3113257
## [1] "Fitzroy River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146811 0.2429575 0.1311042 0.3112572
## [1] "Victoria River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144800 0.2431203 0.1312718 0.3111278
## [1] "Daly River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145202 0.2431297 0.1312253 0.3111248
## [1] "Adelaide River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144881 0.2430869 0.1312493 0.3111758
## [1] "South Alligator River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144745 0.2430951 0.1312734 0.3111570
## [1] "East Alligator River"
```

```
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145003 0.2431766 0.1312349 0.3110882
## [1] "Blue mud Bay"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144696 0.2430240 0.1312830 0.3112234
## [1] "Roper River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144773 0.2430786 0.1313041 0.3111400
## [1] "Towns River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3144650 0.2430620 0.1313124 0.3111606
## [1] "Wenlock River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145160 0.2430987 0.1312248 0.3111606
## [1] "Trinity inlet"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146261 0.2429249 0.1311603 0.3112887
## [1] "Clarence River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145786 0.2429470 0.1311568 0.3113176
## [1] "Sydney Harbour"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145503 0.2429270 0.1312004 0.3113223
## [1] "Okinawa "
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3147088 0.2429724 0.1310459 0.3112729
## [1] "Urauchi River"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146495 0.2431236 0.1311374 0.3110895
## [1] "Fiji"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146038 0.2429049 0.1311531 0.3113381
```

Table 55: Nucleotide divergence between each Location

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
297	Sierra Leone	South Africa	0.0081950	0.0091702	0.0089820	0.0089820	0.0092814	0.0092814	0.0092814
206	Gulf of California	South Africa	0.0081779	0.0091531	0.0089820	0.0089820	0.0091617	0.0093832	0.0094012
200	Gulf of California	Okinawa	0.0088263	0.0091138	0.0090419	0.0090419	0.0091617	0.0091617	0.0091617
202	Gulf of California	Reunion	0.0089646	0.0091093	0.0090419	0.0090419	0.0091617	0.0091617	0.0091617
263	Reunion	Sierra Leone	0.0089646	0.0091093	0.0090419	0.0090419	0.0091617	0.0091617	0.0091617
111	Costa Rica	South Africa	0.0079994	0.0091092	0.0088623	0.0088623	0.0091018	0.0094012	0.0094012
34	Arabian Sea	Gulf of California	0.0082085	0.0091049	0.0089222	0.0089760	0.0091018	0.0092545	0.0092814
199	Gulf of California	Indonesia	0.0088583	0.0090818	0.0089820	0.0089970	0.0091018	0.0091018	0.0091018
105	Costa Rica	Okinawa	0.0086478	0.0090699	0.0089222	0.0089222	0.0090419	0.0091617	0.0091617
201	Gulf of California	Papua New Guinea	0.0087505	0.0090659	0.0089222	0.0089222	0.0091018	0.0092006	0.0092216
107	Costa Rica	Reunion	0.0087861	0.0090654	0.0089222	0.0089222	0.0090419	0.0091617	0.0091617
29	Arabian Sea	Costa Rica	0.0080300	0.0090610	0.0088024	0.0088683	0.0090419	0.0092216	0.0092814
213	Gulf of California	Urauchi River	0.0089963	0.0090476	0.0090419	0.0090419	0.0090419	0.0091018	0.0091617
104	Costa Rica	Indonesia	0.0086798	0.0090379	0.0088623	0.0088757	0.0090419	0.0091018	0.0091018
210	Gulf of California	Thailand	0.0075689	0.0090319	0.0089222	0.0089296	0.0090419	0.0091467	0.0091617
41	Arabian Sea	Sierra Leone	0.0081266	0.0090230	0.0088024	0.0088563	0.0089820	0.0092814	0.0092814
9	Adelaide River	Gulf of California	0.0086730	0.0090220	0.0087425	0.0088189	0.0089820	0.0092216	0.0092216
106	Costa Rica	Papua New Guinea	0.0085720	0.0090220	0.0088024	0.0088383	0.0090419	0.0092216	0.0092216
163	Fiji	Gulf of California	0.0083350	0.0090220	0.0089820	0.0089820	0.0090419	0.0090419	0.0090419

Table 55: Nucleotide divergence between each Location *(continued)*

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
204	Gulf of California	Seychelles	0.0088623	0.0090120	0.0089820	0.0089820	0.0089820	0.0091617	0.0091617
208	Gulf of California	Sri Lanka	0.0074932	0.0090120	0.0089222	0.0089222	0.0089820	0.0091452	0.0091617
286	Seychelles	Sierra Leone	0.0088623	0.0090120	0.0089820	0.0089820	0.0089820	0.0091617	0.0091617
124	Daly River	Gulf of California	0.0087076	0.0090084	0.0087425	0.0087425	0.0089820	0.0092216	0.0092216
215	Gulf of California	Wenlock River	0.0086977	0.0090041	0.0088623	0.0088892	0.0089820	0.0091018	0.0091018
118	Costa Rica	Urauchi River	0.0088178	0.0090037	0.0089222	0.0089222	0.0089820	0.0091018	0.0091617
209	Gulf of California	Sydney Harbour	0.0087049	0.0089959	0.0087425	0.0087605	0.0090419	0.0092635	0.0092814
236	Okinawa	Sierra Leone	0.0087066	0.0089940	0.0089222	0.0089222	0.0090419	0.0090419	0.0090419
301	Sierra Leone	Thailand	0.0075289	0.0089920	0.0088024	0.0088249	0.0090419	0.0090419	0.0090419
115	Costa Rica	Thailand	0.0073904	0.0089880	0.0088024	0.0088159	0.0089820	0.0091617	0.0091617
144	East Alligator River	Gulf of California	0.0087240	0.0089785	0.0087425	0.0087425	0.0089820	0.0091617	0.0091617
4	Adelaide River	Costa Rica	0.0084945	0.0089780	0.0086228	0.0086826	0.0089222	0.0092216	0.0092216
101	Costa Rica	Fiji	0.0081565	0.0089780	0.0088623	0.0088623	0.0089820	0.0090419	0.0090419
214	Gulf of California	Victoria River	0.0087542	0.0089763	0.0088623	0.0088623	0.0089222	0.0091617	0.0091617
211	Gulf of California	Towns River	0.0089042	0.0089701	0.0089222	0.0089281	0.0089820	0.0089820	0.0089820
109	Costa Rica	Seychelles	0.0086838	0.0089681	0.0088623	0.0088623	0.0089820	0.0091617	0.0091617
113	Costa Rica	Sri Lanka	0.0073147	0.0089681	0.0088024	0.0088024	0.0089820	0.0091617	0.0091617
99	Costa Rica	Daly River	0.0085291	0.0089645	0.0086228	0.0086826	0.0089820	0.0092216	0.0092216
221	Indonesia	Sierra Leone	0.0087385	0.0089621	0.0088623	0.0088772	0.0089820	0.0089820	0.0089820
299	Sierra Leone	Sri Lanka	0.0074433	0.0089621	0.0088024	0.0088024	0.0089820	0.0091452	0.0091617
120	Costa Rica	Wenlock River	0.0085192	0.0089602	0.0087425	0.0088024	0.0089820	0.0091018	0.0091018
58	Blue mud Bay	Gulf of California	0.0089068	0.0089590	0.0088623	0.0088802	0.0089820	0.0089820	0.0089820
114	Costa Rica	Sydney Harbour	0.0085264	0.0089519	0.0086228	0.0086826	0.0089820	0.0092814	0.0092814
207	Gulf of California	South Alligator River	0.0088432	0.0089474	0.0088623	0.0088623	0.0089222	0.0090509	0.0091617
181	Fitzroy River	Gulf of California	0.0073713	0.0089461	0.0088623	0.0088623	0.0089222	0.0090419	0.0090419
250	Papua New Guinea	Sierra Leone	0.0086307	0.0089461	0.0088024	0.0088024	0.0089820	0.0090808	0.0091018
203	Gulf of California	Roper River	0.0088822	0.0089371	0.0088623	0.0088668	0.0089521	0.0089820	0.0089820
100	Costa Rica	East Alligator River	0.0085455	0.0089346	0.0086228	0.0086826	0.0089222	0.0091617	0.0091617
119	Costa Rica	Victoria River	0.0085746	0.0089313	0.0087425	0.0087425	0.0089222	0.0091617	0.0091617
304	Sierra Leone	Urauchi River	0.0088765	0.0089279	0.0089222	0.0089222	0.0089222	0.0089820	0.0090419
116	Costa Rica	Towns River	0.0087257	0.0089261	0.0088024	0.0088024	0.0089222	0.0089820	0.0089820
53	Blue mud Bay	Costa Rica	0.0087283	0.0089151	0.0087425	0.0088024	0.0089222	0.0089820	0.0089820
112	Costa Rica	South Alligator River	0.0086647	0.0089035	0.0087425	0.0088024	0.0089222	0.0090419	0.0091617
102	Costa Rica	Fitzroy River	0.0071928	0.0089022	0.0087425	0.0087425	0.0088623	0.0090419	0.0090419
170	Fiji	Sierra Leone	0.0082152	0.0089022	0.0088623	0.0088623	0.0089222	0.0089222	0.0089222
108	Costa Rica	Roper River	0.0087037	0.0088932	0.0087425	0.0087425	0.0089222	0.0089820	0.0089820
16	Adelaide River	Sierra Leone	0.0085400	0.0088889	0.0086228	0.0086991	0.0088623	0.0091018	0.0091018
81	Clarence River	Gulf of California	0.0087257	0.0088765	0.0087425	0.0087725	0.0088623	0.0091018	0.0091018
300	Sierra Leone	Sydney Harbour	0.0085851	0.0088761	0.0086228	0.0086407	0.0089222	0.0091437	0.0091617
188	Fitzroy River	Sierra Leone	0.0072994	0.0088743	0.0087425	0.0087425	0.0088024	0.0090419	0.0090419
306	Sierra Leone	Wenlock River	0.0085653	0.0088717	0.0088024	0.0088024	0.0088623	0.0089222	0.0089222
131	Daly River	Sierra Leone	0.0085687	0.0088695	0.0086228	0.0086228	0.0088623	0.0091018	0.0091018
151	East Alligator River	Sierra Leone	0.0086043	0.0088588	0.0086228	0.0086228	0.0088623	0.0090419	0.0090419
305	Sierra Leone	Victoria River	0.0086287	0.0088509	0.0087425	0.0087425	0.0088024	0.0090419	0.0090419
302	Sierra Leone	Towns River	0.0087844	0.0088503	0.0088024	0.0088084	0.0088623	0.0088623	0.0088623
65	Blue mud Bay	Sierra Leone	0.0087870	0.0088392	0.0087425	0.0087605	0.0088623	0.0088623	0.0088623
76	Clarence River	Costa Rica	0.0085472	0.0088326	0.0086228	0.0086826	0.0088024	0.0091018	0.0091018
298	Sierra Leone	South Alligator River	0.0087203	0.0088245	0.0087425	0.0087425	0.0088024	0.0089222	0.0089222
275	Roper River	Sierra Leone	0.0087625	0.0088174	0.0087425	0.0087470	0.0088323	0.0088623	0.0088623
212	Gulf of California	Trinity inlet	0.0088024	0.0088024	0.0088024	0.0088024	0.0088024	0.0088024	0.0088024
88	Clarence River	Sierra Leone	0.0086116	0.0087625	0.0086826	0.0086826	0.0087425	0.0089820	0.0089820
117	Costa Rica	Trinity inlet	0.0086239	0.0087585	0.0086826	0.0086826	0.0087425	0.0088024	0.0088024
303	Sierra Leone	Trinity inlet	0.0086826	0.0086826	0.0086826	0.0086826	0.0086826	0.0086826	0.0086826
205	Gulf of California	Sierra Leone	0.0063473	0.0063473	0.0063473	0.0063473	0.0063473	0.0063473	0.0063473
110	Costa Rica	Sierra Leone	0.0061688	0.0063034	0.0062275	0.0062275	0.0062874	0.0063473	0.0063473
233	Okinawa	Reunion	0.0053298	0.0057620	0.0052695	0.0053862	0.0058683	0.0059880	0.0059880
273	Reunion	Wenlock River	0.0051835	0.0056347	0.0052695	0.0053293	0.0056287	0.0058084	0.0058084
13	Adelaide River	Reunion	0.0051326	0.0056262	0.0050898	0.0052695	0.0056287	0.0059177	0.0059281
128	Daly River	Reunion	0.0051775	0.0056231	0.0050898	0.0052695	0.0056287	0.0059281	0.0059281
148	East Alligator River	Reunion	0.0052036	0.0056028	0.0050898	0.0052695	0.0056287	0.0058683	0.0058683
247	Papua New Guinea	Reunion	0.0051292	0.0055893	0.0052096	0.0053278	0.0055689	0.0059880	0.0059880
272	Reunion	Victoria River	0.0052170	0.0055838	0.0052096	0.0052695	0.0056287	0.0058683	0.0058683
62	Blue mud Bay	Reunion	0.0053863	0.0055833	0.0052096	0.0053293	0.0055689	0.0056886	0.0056886
267	Reunion	Sydney Harbour	0.0051384	0.0055740	0.0050898	0.0052201	0.0055689	0.0059281	0.0059281
265	Reunion	South Alligator River	0.0053227	0.0055716	0.0052096	0.0052695	0.0055689	0.0057485	0.0058683
218	Indonesia	Reunion	0.0051981	0.0055664	0.0052096	0.0052545	0.0055689	0.0058084	0.0058084
271	Reunion	Urauchi River	0.0053675	0.0055635	0.0052695	0.0052695	0.0056287	0.0058683	0.0059880
269	Reunion	Towns River	0.0053164	0.0055269	0.0052695	0.0053293	0.0055689	0.0056886	0.0056886
261	Reunion	Roper River	0.0053056	0.0055052	0.0052096	0.0053039	0.0055389	0.0056287	0.0056287
85	Clarence River	Reunion	0.0052052	0.0055008	0.0051497	0.0052096	0.0055090	0.0056886	0.0058084
235	Okinawa	Seychelles	0.0050579	0.0054950	0.0052096	0.0052096	0.0055689	0.0059880	0.0059880
270	Reunion	Trinity inlet	0.0052819	0.0054266	0.0051497	0.0051497	0.0054491	0.0055090	0.0055090
296	Seychelles	Wenlock River	0.0049116	0.0053677	0.0052096	0.0052096	0.0053293	0.0057769	0.0058084
15	Adelaide River	Seychelles	0.0048607	0.0053593	0.0050299	0.0050299	0.0053293	0.0058638	0.0059281
130	Daly River	Seychelles	0.0049056	0.0053561	0.0050299	0.0050299	0.0052994	0.0058683	0.0059281
249	Papua New Guinea	Seychelles	0.0048743	0.0053393	0.0051497	0.0051497	0.0052695	0.0056886	0.0059880
150	East Alligator River	Seychelles	0.0049316	0.0053358	0.0050299	0.0050299	0.0053293	0.0058084	0.0058683
295	Seychelles	Victoria River	0.0049494	0.0053213	0.0051497	0.0051497	0.0052096	0.0057485	0.0058683
64	Blue mud Bay	Seychelles	0.0051144	0.0053163	0.0051497	0.0051497	0.0052695	0.0056886	0.0056886
292	Seychelles	Towns River	0.0050998	0.0053154	0.0052096	0.0052096	0.0052695	0.0056751	0.0056886
290	Seychelles	Sydney Harbour	0.0048664	0.0053071	0.0050299	0.0050299	0.0052695	0.0057695	0.0059281
288	Seychelles	South Alligator River	0.0050508	0.0053047	0.0051497	0.0051497	0.0052096	0.0056886	0.0058683
220	Indonesia	Seychelles	0.0049261	0.0052994	0.0051497	0.0051497	0.0052695	0.0057275	0.0058084
294	Seychelles	Urauchi River	0.0050955	0.0052965	0.0052096	0.0052096	0.0052096	0.0056287	0.0059880

Table 55: Nucleotide divergence between each Location *(continued)*

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
274	Roper River	Seychelles	0.0050798	0.0052844	0.0051497	0.0051497	0.0052695	0.0056287	0.0056287
87	Clarence River	Seychelles	0.0049333	0.0052338	0.0050898	0.0050898	0.0051497	0.0056287	0.0058084
293	Seychelles	Trinity inlet	0.0050100	0.0051597	0.0050898	0.0050898	0.0050898	0.0055090	0.0055090
237	Okinawa	South Africa	0.0038785	0.0051411	0.0015569	0.0015569	0.0056886	0.0061078	0.0061078
167	Fiji	Reunion	0.0041974	0.0050291	0.0003593	0.0009581	0.0055090	0.0056287	0.0056287
315	South Africa	Wenlock River	0.0037074	0.0049890	0.0011976	0.0012575	0.0053892	0.0059281	0.0059281
132	Daly River	South Africa	0.0036989	0.0049749	0.0009581	0.0011587	0.0055090	0.0060479	0.0060479
17	Adelaide River	South Africa	0.0036450	0.0049691	0.0009581	0.0011976	0.0054491	0.0059880	0.0060479
222	Indonesia	South Africa	0.0037599	0.0049587	0.0014970	0.0016168	0.0053892	0.0059281	0.0059281
152	East Alligator River	South Africa	0.0037233	0.0049530	0.0011377	0.0012545	0.0054491	0.0059880	0.0059880
313	South Africa	Urauchi River	0.0039256	0.0049521	0.0015569	0.0015569	0.0053293	0.0057485	0.0061078
314	South Africa	Victoria River	0.0037316	0.0049289	0.0009581	0.0011976	0.0053892	0.0059880	0.0059880
66	Blue mud Bay	South Africa	0.0038940	0.0049214	0.0011377	0.0011976	0.0053892	0.0058084	0.0058084
307	South Africa	South Alligator River	0.0038322	0.0049115	0.0011377	0.0011976	0.0053293	0.0058683	0.0059880
251	Papua New Guinea	South Africa	0.0036145	0.0049050	0.0006587	0.0007784	0.0053892	0.0060000	0.0061078
309	South Africa	Sydney Harbour	0.0036342	0.0049003	0.0007784	0.0007934	0.0054491	0.0060329	0.0060479
311	South Africa	Towns River	0.0038503	0.0048914	0.0011976	0.0012485	0.0052695	0.0058084	0.0058084
38	Arabian Sea	Reunion	0.0038407	0.0048818	0.0002395	0.0002395	0.0056886	0.0059536	0.0059880
276	Roper River	South Africa	0.0038352	0.0048653	0.0011377	0.0011781	0.0052695	0.0057485	0.0057485
89	Clarence River	South Africa	0.0037373	0.0048633	0.0007784	0.0012754	0.0052695	0.0058084	0.0059281
169	Fiji	Seychelles	0.0039726	0.0048093	0.0002994	0.0002994	0.0053293	0.0056287	0.0056287
312	South Africa	Trinity inlet	0.0038238	0.0047990	0.0013174	0.0013174	0.0052096	0.0056287	0.0056287
40	Arabian Sea	Seychelles	0.0037038	0.0047500	0.0003593	0.0007680	0.0053892	0.0058368	0.0059880
171	Fiji	South Africa	0.0029002	0.0045623	0.0002994	0.0003653	0.0053892	0.0057485	0.0057485
42	Arabian Sea	South Africa	0.0026248	0.0044964	0.0001198	0.0001198	0.0054491	0.0060479	0.0061078
241	Okinawa	Thailand	0.0022315	0.0039820	0.0003593	0.0003593	0.0052695	0.0057485	0.0057485
255	Papua New Guinea	Thailand	0.0021450	0.0039235	0.0002395	0.0003593	0.0053293	0.0057350	0.0057485
337	Thailand	Towns River	0.0023812	0.0039102	0.0007186	0.0007620	0.0053892	0.0054491	0.0054491
70	Blue mud Bay	Thailand	0.0023838	0.0038991	0.0006587	0.0007186	0.0053892	0.0054491	0.0054491
331	Sydney Harbour	Thailand	0.0021267	0.0038807	0.0005389	0.0005988	0.0052695	0.0056287	0.0056287
280	Roper River	Thailand	0.0023593	0.0038772	0.0006587	0.0006931	0.0053293	0.0054491	0.0054491
318	South Alligator River	Thailand	0.0023087	0.0038759	0.0002395	0.0006587	0.0053293	0.0055090	0.0055689
21	Adelaide River	Thailand	0.0020592	0.0038711	0.0001796	0.0002799	0.0053293	0.0055689	0.0056287
340	Thailand	Victoria River	0.0021818	0.0038670	0.0003593	0.0004940	0.0053293	0.0055090	0.0055689
136	Daly River	Thailand	0.0020864	0.0038503	0.0001796	0.0002994	0.0053293	0.0055689	0.0056287
341	Thailand	Wenlock River	0.0020802	0.0038497	0.0001796	0.0002395	0.0053892	0.0055090	0.0055090
156	East Alligator River	Thailand	0.0021271	0.0038447	0.0001796	0.0002710	0.0053293	0.0055090	0.0055689
93	Clarence River	Thailand	0.0022027	0.0038167	0.0005988	0.0005988	0.0052695	0.0055015	0.0055689
226	Indonesia	Thailand	0.0020592	0.0037458	0.0002994	0.0004042	0.0052096	0.0055689	0.0055689
338	Thailand	Trinity inlet	0.0022794	0.0037425	0.0005988	0.0005988	0.0052395	0.0052695	0.0052695
175	Fiji	Thailand	0.0015703	0.0037203	0.0000599	0.0003593	0.0054192	0.0055090	0.0055090
185	Fitzroy River	Reunion	0.0020005	0.0037201	0.0002395	0.0003563	0.0054491	0.0056287	0.0056287
339	Thailand	Urauchi River	0.0021920	0.0037064	0.0003593	0.0003593	0.0052695	0.0056437	0.0057485
46	Arabian Sea	Thailand	0.0012181	0.0035776	0.0001198	0.0001198	0.0053892	0.0057695	0.0058683
239	Okinawa	Sri Lanka	0.0017706	0.0035768	0.0003593	0.0003593	0.0052695	0.0058683	0.0058683
253	Papua New Guinea	Sri Lanka	0.0016908	0.0035250	0.0002395	0.0002994	0.0053293	0.0056886	0.0058683
326	Sri Lanka	Towns River	0.0019163	0.0035010	0.0007186	0.0007470	0.0053892	0.0055090	0.0055090
68	Blue mud Bay	Sri Lanka	0.0019174	0.0034884	0.0006587	0.0007186	0.0053293	0.0055090	0.0055090
324	Sri Lanka	Sydney Harbour	0.0016760	0.0034857	0.0003593	0.0004716	0.0052096	0.0056886	0.0058084
278	Roper River	Sri Lanka	0.0018944	0.0034681	0.0006587	0.0006692	0.0053293	0.0054985	0.0055090
316	South Alligator River	Sri Lanka	0.0018413	0.0034643	0.0000599	0.0006587	0.0053293	0.0055090	0.0057485
329	Sri Lanka	Victoria River	0.0017100	0.0034510	0.0001796	0.0002994	0.0053293	0.0056287	0.0057485
19	Adelaide River	Sri Lanka	0.0015829	0.0034506	0.0000599	0.0000823	0.0053293	0.0056886	0.0058084
134	Daly River	Sri Lanka	0.0016279	0.0034475	0.0001796	0.0002395	0.0052695	0.0056886	0.0058084
330	Sri Lanka	Wenlock River	0.0016216	0.0034468	0.0002395	0.0002994	0.0053293	0.0056287	0.0056886
189	Fitzroy River	South Africa	0.0008871	0.0034371	0.0001796	0.0001796	0.0051497	0.0057485	0.0057485
154	East Alligator River	Sri Lanka	0.0016604	0.0034337	0.0000000	0.0001796	0.0052695	0.0056287	0.0056886
91	Clarence River	Sri Lanka	0.0017402	0.0034098	0.0005988	0.0005988	0.0052096	0.0055090	0.0056886
173	Fiji	Sri Lanka	0.0011952	0.0034010	0.0000599	0.0003398	0.0052695	0.0055090	0.0055090
327	Sri Lanka	Trinity inlet	0.0018146	0.0033333	0.0005988	0.0005988	0.0051796	0.0053892	0.0053892
44	Arabian Sea	Sri Lanka	0.0009149	0.0033302	0.0000000	0.0003593	0.0053293	0.0057485	0.0058084
328	Sri Lanka	Urauchi River	0.0017366	0.0033067	0.0003593	0.0003593	0.0052096	0.0056392	0.0058683
224	Indonesia	Sri Lanka	0.0015436	0.0032859	0.0001198	0.0001662	0.0051796	0.0055823	0.0056886
187	Fitzroy River	Seychelles	0.0015589	0.0032834	0.0001796	0.0001796	0.0051497	0.0056153	0.0056287
193	Fitzroy River	Thailand	0.0000898	0.0031277	0.0004192	0.0004192	0.0052695	0.0053892	0.0053892
191	Fitzroy River	Sri Lanka	-0.0000158	0.0030778	0.0004192	0.0004192	0.0052695	0.0053892	0.0054491
33	Arabian Sea	Fitzroy River	0.0004156	0.0028869	0.0006587	0.0007395	0.0010778	0.0057275	0.0057485
308	South Africa	Sri Lanka	0.0003717	0.0028657	0.0002395	0.0002395	0.0013174	0.0058638	0.0058683
266	Reunion	Sri Lanka	0.0011883	0.0028518	0.0002994	0.0004057	0.0010180	0.0057485	0.0057485
183	Fitzroy River	Okinawa	0.0008970	0.0027593	0.0007784	0.0007784	0.0010778	0.0056287	0.0056287
325	Sri Lanka	Thailand	-0.0002457	0.0027362	0.0000000	0.0000599	0.0009581	0.0055090	0.0055689
162	Fiji	Fitzroy River	0.0004381	0.0026999	0.0004790	0.0005030	0.0008383	0.0053892	0.0053892
182	Fitzroy River	Indonesia	0.0008204	0.0026188	0.0007186	0.0007186	0.0008982	0.0054491	0.0054491
196	Fitzroy River	Urauchi River	0.0009743	0.0026005	0.0007784	0.0007784	0.0008383	0.0052695	0.0056287
310	South Africa	Thailand	0.0001095	0.0025478	0.0002395	0.0002410	0.0011976	0.0058683	0.0058683
289	Seychelles	Sri Lanka	0.0008598	0.0025283	0.0002395	0.0002395	0.0009281	0.0056886	0.0057485
184	Fitzroy River	Papua New Guinea	0.0006311	0.0025214	0.0001796	0.0002305	0.0007186	0.0055778	0.0056287
192	Fitzroy River	Sydney Harbour	0.0006436	0.0025094	0.0005389	0.0005389	0.0007186	0.0055329	0.0055689
268	Reunion	Thailand	0.0008847	0.0024925	0.0002994	0.0003593	0.0010778	0.0057485	0.0057485
8	Adelaide River	Fitzroy River	0.0005114	0.0024351	0.0000599	0.0000599	0.0008982	0.0055090	0.0055689
80	Clarence River	Fitzroy River	0.0006958	0.0024214	0.0000599	0.0000599	0.0006587	0.0053293	0.0054491
198	Fitzroy River	Wenlock River	0.0005329	0.0024141	0.0000599	0.0000599	0.0008383	0.0054491	0.0054491
123	Daly River	Fitzroy River	0.0005244	0.0024000	0.0000000	0.0000000	0.0008982	0.0055689	0.0055689
195	Fitzroy River	Trinity inlet	0.0008204	0.0023952	0.0005389	0.0005389	0.0005988	0.0051497	0.0051497

Table 55: Nucleotide divergence between each Location *(continued)*

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
143	East Alligator River	Fitzroy River	0.0005053	0.0023346	0.0000000	0.0000599	0.0008383	0.0055090	0.0055090
197	Fitzroy River	Victoria River	0.0004836	0.0022806	0.0000000	0.0000000	0.0008383	0.0055090	0.0055090
194	Fitzroy River	Towns River	0.0005629	0.0022036	0.0000599	0.0000599	0.0001796	0.0053293	0.0053293
190	Fitzroy River	South Alligator River	0.0005145	0.0021935	0.0000000	0.0000000	0.0001198	0.0053892	0.0055090
57	Blue mud Bay	Fitzroy River	0.0005655	0.0021925	0.0000000	0.0000359	0.0001796	0.0053293	0.0053293
186	Fitzroy River	Roper River	0.0005409	0.0021707	0.0000000	0.0000000	0.0001497	0.0053293	0.0053293
32	Arabian Sea	Fiji	0.0004830	0.0020664	0.0007186	0.0008383	0.0010180	0.0057485	0.0057485
291	Seychelles	Thailand	0.0004431	0.0020559	0.0002395	0.0002395	0.0002994	0.0056677	0.0057485
37	Arabian Sea	Papua New Guinea	0.0005237	0.0017355	0.0002395	0.0003593	0.0010778	0.0058084	0.0061078
47	Arabian Sea	Towns River	0.0007320	0.0016943	0.0007186	0.0007784	0.0009581	0.0057874	0.0058084
27	Arabian Sea	Blue mud Bay	0.0007450	0.0016936	0.0006587	0.0007784	0.0009581	0.0058084	0.0058084
45	Arabian Sea	Sydney Harbour	0.0005045	0.0016919	0.0003593	0.0006587	0.0010180	0.0058683	0.0059880
36	Arabian Sea	Okinawa	0.0005079	0.0016918	0.0003593	0.0004790	0.0010778	0.0061078	0.0061078
39	Arabian Sea	Roper River	0.0007119	0.0016633	0.0006587	0.0007710	0.0008982	0.0057485	0.0057485
43	Arabian Sea	South Alligator River	0.0006600	0.0016606	0.0000599	0.0005988	0.0008982	0.0058084	0.0059880
50	Arabian Sea	Victoria River	0.0005133	0.0016319	0.0001796	0.0005389	0.0008982	0.0058683	0.0059880
28	Arabian Sea	Clarence River	0.0005690	0.0016163	0.0005988	0.0006587	0.0008383	0.0057485	0.0059281
1	Adelaide River	Arabian Sea	0.0003674	0.0016127	0.0000599	0.0003308	0.0008982	0.0059281	0.0059880
165	Fiji	Okinawa	0.0006025	0.0015768	0.0008383	0.0008383	0.0011377	0.0057485	0.0057485
30	Arabian Sea	Daly River	0.0003677	0.0015650	0.0001796	0.0002994	0.0008383	0.0059880	0.0060479
31	Arabian Sea	East Alligator River	0.0004134	0.0015643	0.0000000	0.0002994	0.0008982	0.0059251	0.0059880
51	Arabian Sea	Wenlock River	0.0003530	0.0015559	0.0002395	0.0002994	0.0008982	0.0058683	0.0059281
48	Arabian Sea	Trinity inlet	0.0006415	0.0015380	0.0005988	0.0005988	0.0007784	0.0056287	0.0056287
166	Fiji	Papua New Guinea	0.0004459	0.0014482	0.0005988	0.0006587	0.0009581	0.0054491	0.0057485
35	Arabian Sea	Indonesia	0.0003155	0.0014355	0.0001198	0.0002395	0.0005988	0.0057305	0.0059281
7	Adelaide River	Fiji	0.0003953	0.0014312	0.0005988	0.0006587	0.0008982	0.0055674	0.0056886
178	Fiji	Urauchi River	0.0006916	0.0014298	0.0008383	0.0008383	0.0009581	0.0053892	0.0057485
164	Fiji	Indonesia	0.0005111	0.0014216	0.0007186	0.0007186	0.0009581	0.0054491	0.0055689
122	Daly River	Fiji	0.0004161	0.0014039	0.0005988	0.0006347	0.0008982	0.0055928	0.0056886
180	Fiji	Wenlock River	0.0003909	0.0013842	0.0004192	0.0004790	0.0008982	0.0055090	0.0055689
49	Arabian Sea	Urauchi River	0.0004341	0.0013819	0.0003593	0.0003593	0.0005389	0.0057485	0.0061078
142	East Alligator River	Fiji	0.0004319	0.0013733	0.0005988	0.0005988	0.0008982	0.0055090	0.0056287
179	Fiji	Victoria River	0.0004640	0.0013731	0.0007186	0.0007186	0.0008383	0.0054491	0.0056287
176	Fiji	Towns River	0.0006191	0.0013719	0.0007784	0.0007784	0.0008982	0.0054491	0.0054491
56	Blue mud Bay	Fiji	0.0006217	0.0013609	0.0007186	0.0007725	0.0008383	0.0054491	0.0054491
172	Fiji	South Alligator River	0.0005574	0.0013485	0.0007186	0.0007186	0.0008383	0.0054491	0.0056287
168	Fiji	Roper River	0.0005971	0.0013390	0.0007186	0.0007186	0.0008383	0.0054491	0.0054491
264	Reunion	South Africa	0.0001344	0.0012543	0.0000599	0.0001527	0.0008982	0.0050299	0.0050299
287	Seychelles	South Africa	0.0000627	0.0011876	0.0000000	0.0000000	0.0010778	0.0046108	0.0050299
174	Fiji	Sydney Harbour	0.0001813	0.0011592	0.0001796	0.0001796	0.0008383	0.0055090	0.0056886
240	Okinawa	Sydney Harbour	0.0004663	0.0010447	0.0006587	0.0006722	0.0010180	0.0014371	0.0014371
242	Okinawa	Towns River	0.0006766	0.0010299	0.0008383	0.0008383	0.0010778	0.0011377	0.0011377
232	Okinawa	Papua New Guinea	0.0004255	0.0010283	0.0003593	0.0003593	0.0010180	0.0013772	0.0013772
60	Blue mud Bay	Okinawa	0.0006793	0.0010189	0.0007784	0.0007919	0.0010778	0.0011377	0.0011377
11	Adelaide River	Okinawa	0.0003657	0.0010020	0.0002994	0.0003593	0.0010778	0.0014970	0.0014970
234	Okinawa	Roper River	0.0006547	0.0009970	0.0007784	0.0007784	0.0010180	0.0011377	0.0011377
238	Okinawa	South Alligator River	0.0006018	0.0009934	0.0003593	0.0007784	0.0010778	0.0011976	0.0011976
245	Okinawa	Victoria River	0.0004822	0.0009917	0.0004790	0.0005988	0.0010778	0.0013832	0.0014371
217	Indonesia	Papua New Guinea	0.0004378	0.0009767	0.0002994	0.0004192	0.0010778	0.0011976	0.0012575
126	Daly River	Okinawa	0.0003747	0.0009629	0.0002994	0.0002994	0.0010180	0.0013174	0.0014371
246	Okinawa	Wenlock River	0.0003655	0.0009593	0.0003593	0.0004192	0.0010778	0.0011976	0.0011976
146	East Alligator River	Okinawa	0.0004091	0.0009510	0.0002994	0.0002994	0.0009581	0.0011976	0.0011976
83	Clarence River	Okinawa	0.0005038	0.0009421	0.0007186	0.0007186	0.0009581	0.0012575	0.0012575
79	Clarence River	Fiji	0.0000972	0.0009350	0.0001796	0.0001796	0.0002994	0.0053473	0.0055689
258	Papua New Guinea	Urauchi River	0.0005602	0.0009269	0.0003593	0.0003593	0.0010180	0.0012066	0.0013772
227	Indonesia	Towns River	0.0006367	0.0009261	0.0007784	0.0008219	0.0009581	0.0009581	0.0009581
59	Blue mud Bay	Indonesia	0.0006393	0.0009151	0.0007186	0.0007784	0.0009581	0.0009581	0.0009581
216	Indonesia	Okinawa	0.0003952	0.0009062	0.0004192	0.0004192	0.0010778	0.0012575	0.0012575
343	Towns River	Urauchi River	0.0007804	0.0008976	0.0008383	0.0008383	0.0008982	0.0011377	0.0011377
334	Sydney Harbour	Urauchi River	0.0005548	0.0008971	0.0006587	0.0006587	0.0008383	0.0011976	0.0014371
225	Indonesia	Sydney Harbour	0.0003822	0.0008967	0.0003593	0.0004790	0.0008982	0.0012575	0.0012575
219	Indonesia	Roper River	0.0006148	0.0008932	0.0007186	0.0007530	0.0008982	0.0009581	0.0009581
73	Blue mud Bay	Urauchi River	0.0007830	0.0008866	0.0007784	0.0007784	0.0008982	0.0011377	0.0011377
223	Indonesia	South Alligator River	0.0005495	0.0008772	0.0000599	0.0006198	0.0008982	0.0010180	0.0011377
283	Roper River	Urauchi River	0.0007585	0.0008647	0.0007784	0.0007784	0.0008982	0.0010734	0.0011377
243	Okinawa	Trinity inlet	0.0005749	0.0008623	0.0007186	0.0007186	0.0009581	0.0009581	0.0009581
321	South Alligator River	Urauchi River	0.0006951	0.0008506	0.0003593	0.0005808	0.0008383	0.0010778	0.0011976
260	Papua New Guinea	Wenlock River	0.0002140	0.0008358	0.0002395	0.0002994	0.0008383	0.0011377	0.0011976
230	Indonesia	Victoria River	0.0003831	0.0008288	0.0000599	0.0001796	0.0008982	0.0012575	0.0012575
349	Urauchi River	Victoria River	0.0005482	0.0008216	0.0004790	0.0004790	0.0008383	0.0011976	0.0014371
127	Daly River	Papua New Guinea	0.0001985	0.0008147	0.0001796	0.0002395	0.0007186	0.0012575	0.0014371
96	Clarence River	Urauchi River	0.0006076	0.0008098	0.0007186	0.0007186	0.0007784	0.0010180	0.0012575
10	Adelaide River	Indonesia	0.0002343	0.0008067	0.0000599	0.0001796	0.0008982	0.0013174	0.0013174
82	Clarence River	Indonesia	0.0004316	0.0008060	0.0005389	0.0005464	0.0008383	0.0010778	0.0010778
125	Daly River	Indonesia	0.0002812	0.0008056	0.0002395	0.0003593	0.0008383	0.0012575	0.0012575
336	Sydney Harbour	Wenlock River	0.0002061	0.0008034	0.0002395	0.0005479	0.0007784	0.0011377	0.0012575
135	Daly River	Sydney Harbour	0.0002082	0.0008000	0.0004192	0.0004251	0.0007784	0.0012575	0.0013772
145	East Alligator River	Indonesia	0.0003186	0.0007966	0.0001198	0.0002395	0.0008982	0.0010464	0.0011377
231	Indonesia	Wenlock River	0.0002663	0.0007963	0.0002994	0.0004087	0.0008982	0.0010284	0.0010778
24	Adelaide River	Urauchi River	0.0003959	0.0007962	0.0002994	0.0002994	0.0008383	0.0012575	0.0014970
84	Clarence River	Papua New Guinea	0.0003227	0.0007889	0.0001198	0.0002395	0.0008383	0.0010778	0.0012575
20	Adelaide River	Sydney Harbour	0.0001480	0.0007879	0.0001198	0.0004192	0.0007186	0.0012081	0.0014371
147	East Alligator River	Papua New Guinea	0.0002163	0.0007862	0.0001796	0.0002395	0.0007784	0.0011976	0.0012575
12	Adelaide River	Papua New Guinea	0.0001208	0.0007851	0.0001796	0.0002395	0.0007784	0.0012740	0.0014970

Table 55: Nucleotide divergence between each Location *(continued)*

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
177	Fiji	Trinity inlet	0.0000915	0.0007784	0.0001796	0.0001796	0.0002395	0.0052695	0.0052695
155	East Alligator River	Sydney Harbour	0.0002243	0.0007698	0.0003593	0.0004192	0.0007186	0.0011377	0.0013174
257	Papua New Guinea	Trinity inlet	0.0004511	0.0007665	0.0005988	0.0005988	0.0007784	0.0009581	0.0009581
159	East Alligator River	Urauchi River	0.0004507	0.0007565	0.0002994	0.0002994	0.0008383	0.0011377	0.0011976
139	Daly River	Urauchi River	0.0003991	0.0007512	0.0002994	0.0002994	0.0007784	0.0011976	0.0014371
259	Papua New Guinea	Victoria River	0.0002109	0.0007484	0.0001796	0.0002395	0.0006587	0.0011467	0.0014371
262	Reunion	Seychelles	0.0004528	0.0007473	0.0000000	0.0000000	0.0008982	0.0010180	0.0010778
3	Adelaide River	Clarence River	0.0002448	0.0007445	0.0000000	0.0001198	0.0007186	0.0011377	0.0013174
350	Urauchi River	Wenlock River	0.0003857	0.0007435	0.0003593	0.0003593	0.0008383	0.0011377	0.0011976
335	Sydney Harbour	Victoria River	0.0002281	0.0007412	0.0000599	0.0005269	0.0006587	0.0011377	0.0013772
332	Sydney Harbour	Towns River	0.0003802	0.0007370	0.0005988	0.0005988	0.0007186	0.0010778	0.0010778
256	Papua New Guinea	Towns River	0.0003533	0.0007345	0.0002395	0.0002994	0.0007186	0.0011377	0.0011377
346	Trinity inlet	Urauchi River	0.0006786	0.0007300	0.0007186	0.0007186	0.0007186	0.0009581	0.0009581
69	Blue mud Bay	Sydney Harbour	0.0003846	0.0007278	0.0005389	0.0005988	0.0007186	0.0010778	0.0010778
77	Clarence River	Daly River	0.0002697	0.0007213	0.0000000	0.0001796	0.0007186	0.0010778	0.0012575
61	Blue mud Bay	Papua New Guinea	0.0003534	0.0007210	0.0001796	0.0002994	0.0007186	0.0011377	0.0011377
317	South Alligator River	Sydney Harbour	0.0003244	0.0007195	0.0002994	0.0005389	0.0006587	0.0010778	0.0013174
23	Adelaide River	Trinity inlet	0.0003697	0.0007186	0.0004192	0.0004192	0.0006587	0.0010180	0.0010180
228	Indonesia	Trinity inlet	0.0004950	0.0007186	0.0005389	0.0005389	0.0007784	0.0007784	0.0007784
252	Papua New Guinea	South Alligator River	0.0002978	0.0007173	0.0001796	0.0002395	0.0007186	0.0011377	0.0012575
279	Roper River	Sydney Harbour	0.0003600	0.0007059	0.0005389	0.0005389	0.0006587	0.0010614	0.0010778
248	Papua New Guinea	Roper River	0.0003313	0.0007016	0.0001796	0.0002680	0.0007186	0.0011093	0.0011377
98	Clarence River	Wenlock River	0.0002388	0.0006961	0.0000000	0.0001198	0.0007186	0.0010180	0.0010778
138	Daly River	Trinity inlet	0.0003890	0.0006898	0.0004192	0.0004192	0.0006587	0.0009581	0.0009581
254	Papua New Guinea	Sydney Harbour	0.0000803	0.0006866	0.0001198	0.0001198	0.0007784	0.0012575	0.0014371
78	Clarence River	East Alligator River	0.0002733	0.0006786	0.0000000	0.0001796	0.0007186	0.0010180	0.0011377
26	Adelaide River	Wenlock River	0.0000118	0.0006671	0.0000000	0.0000000	0.0007784	0.0012575	0.0013174
97	Clarence River	Victoria River	0.0002936	0.0006666	0.0000000	0.0001198	0.0006587	0.0010180	0.0012575
5	Adelaide River	Daly River	0.0000156	0.0006653	0.0000000	0.0000000	0.0007186	0.0013772	0.0014371
348	Trinity inlet	Wenlock River	0.0003554	0.0006618	0.0002395	0.0002395	0.0006587	0.0007784	0.0007784
347	Trinity inlet	Victoria River	0.0004366	0.0006587	0.0005389	0.0005389	0.0005988	0.0009581	0.0009581
158	East Alligator River	Trinity inlet	0.0004007	0.0006552	0.0004192	0.0004192	0.0006587	0.0008383	0.0008383
342	Towns River	Trinity inlet	0.0005808	0.0006467	0.0005988	0.0005988	0.0006587	0.0006587	0.0006587
244	Okinawa	Urauchi River	0.0002977	0.0006364	0.0000000	0.0000000	0.0010778	0.0010778	0.0010778
72	Blue mud Bay	Trinity inlet	0.0005834	0.0006357	0.0005389	0.0005389	0.0006587	0.0006587	0.0006587
94	Clarence River	Towns River	0.0004186	0.0006353	0.0000000	0.0001198	0.0007186	0.0009222	0.0009581
141	Daly River	Wenlock River	0.0000181	0.0006253	0.0000000	0.0000599	0.0006587	0.0011377	0.0012575
320	South Alligator River	Trinity inlet	0.0005198	0.0006240	0.0005389	0.0005389	0.0005988	0.0007455	0.0008383
52	Blue mud Bay	Clarence River	0.0004190	0.0006221	0.0000000	0.0000599	0.0006587	0.0009581	0.0009581
6	Adelaide River	East Alligator River	0.0000179	0.0006213	0.0000000	0.0000000	0.0006587	0.0012799	0.0013772
90	Clarence River	South Alligator River	0.0003648	0.0006198	0.0000000	0.0001198	0.0006587	0.0008982	0.0011377
282	Roper River	Trinity inlet	0.0005589	0.0006138	0.0005389	0.0005389	0.0006287	0.0006587	0.0006587
86	Clarence River	Roper River	0.0003995	0.0006052	0.0000000	0.0000644	0.0006587	0.0008937	0.0009581
25	Adelaide River	Victoria River	0.0000216	0.0005926	0.0000000	0.0000000	0.0007186	0.0013174	0.0013772
161	East Alligator River	Wenlock River	0.0000260	0.0005869	0.0000000	0.0000629	0.0005988	0.0010180	0.0010778
229	Indonesia	Urauchi River	0.0003116	0.0005864	0.0004192	0.0004192	0.0005389	0.0011377	0.0012575
351	Victoria River	Wenlock River	0.0000386	0.0005671	0.0000000	0.0000599	0.0007186	0.0010778	0.0012575
22	Adelaide River	Towns River	0.0001521	0.0005669	0.0000000	0.0000000	0.0006587	0.0010778	0.0010778
140	Daly River	Victoria River	0.0000365	0.0005595	0.0000000	0.0000000	0.0005988	0.0011976	0.0013772
121	Daly River	East Alligator River	0.0000035	0.0005588	0.0000000	0.0000000	0.0005389	0.0011377	0.0013174
18	Adelaide River	South Alligator River	0.0000964	0.0005495	0.0000000	0.0000000	0.0006587	0.0010778	0.0013772
2	Adelaide River	Blue mud Bay	0.0001450	0.0005461	0.0000000	0.0000599	0.0006287	0.0010778	0.0010778
14	Adelaide River	Roper River	0.0001351	0.0005389	0.0000000	0.0000000	0.0006287	0.0010314	0.0010778
137	Daly River	Towns River	0.0001679	0.0005346	0.0000000	0.0000599	0.0004192	0.0010778	0.0010778
92	Clarence River	Sydney Harbour	0.0000899	0.0005317	0.0000000	0.0000000	0.0006587	0.0010778	0.0011976
54	Blue mud Bay	Daly River	0.0001692	0.0005222	0.0000000	0.0000599	0.0004192	0.0010778	0.0010778
345	Towns River	Wenlock River	0.0001484	0.0005206	0.0000000	0.0000599	0.0002994	0.0009581	0.0009581
323	South Alligator River	Wenlock River	0.0000982	0.0005087	0.0000000	0.0000000	0.0003593	0.0009581	0.0010778
129	Daly River	Roper River	0.0001467	0.0005024	0.0000000	0.0000000	0.0003892	0.0010778	0.0010778
133	Daly River	South Alligator River	0.0000915	0.0004964	0.0000000	0.0000000	0.0004192	0.0010778	0.0013174
285	Roper River	Wenlock River	0.0001343	0.0004956	0.0000000	0.0000524	0.0002994	0.0009581	0.0009581
75	Blue mud Bay	Wenlock River	0.0001326	0.0004912	0.0000000	0.0000000	0.0002994	0.0009581	0.0009581
160	East Alligator River	Victoria River	0.0000142	0.0004908	0.0000000	0.0000599	0.0002994	0.0010778	0.0013174
333	Sydney Harbour	Trinity inlet	0.0001604	0.0004514	0.0000000	0.0000000	0.0005988	0.0009581	0.0009581
157	East Alligator River	Towns River	0.0001122	0.0004325	0.0000000	0.0000659	0.0002994	0.0010180	0.0010180
55	Blue mud Bay	East Alligator River	0.0001127	0.0004194	0.0000000	0.0000599	0.0002994	0.0010180	0.0010180
153	East Alligator River	South Alligator River	0.0000469	0.0004055	0.0000000	0.0000000	0.0002395	0.0010180	0.0010778
149	East Alligator River	Roper River	0.0000913	0.0004007	0.0000000	0.0000404	0.0002395	0.0010180	0.0010180
344	Towns River	Victoria River	0.0000559	0.0003439	0.0000000	0.0000000	0.0001796	0.0010180	0.0010180
322	South Alligator River	Victoria River	0.0000103	0.0003366	0.0000000	0.0000000	0.0001198	0.0010180	0.0013174
74	Blue mud Bay	Victoria River	0.0000536	0.0003279	0.0000000	0.0000599	0.0001796	0.0010180	0.0010180
284	Roper River	Victoria River	0.0000388	0.0003158	0.0000000	0.0000000	0.0001796	0.0010180	0.0010180
103	Costa Rica	Gulf of California	0.0001728	0.0003074	0.0002395	0.0002395	0.0002994	0.0004192	0.0004192
319	South Alligator River	Towns River	0.0000417	0.0002118	0.0000000	0.0000000	0.0001796	0.0008278	0.0010180
67	Blue mud Bay	South Alligator River	0.0000342	0.0001906	0.0000000	0.0000000	0.0001796	0.0008593	0.0010180
277	Roper River	South Alligator River	0.0000245	0.0001836	0.0000000	0.0000000	0.0001796	0.0008054	0.0010180
71	Blue mud Bay	Towns River	0.0000533	0.0001713	0.0000000	0.0000599	0.0001796	0.0002395	0.0002395
95	Clarence River	Trinity inlet	0.0000202	0.0001711	0.0000000	0.0000000	0.0000599	0.0007784	0.0007784
63	Blue mud Bay	Roper River	0.0000438	0.0001509	0.0000000	0.0000165	0.0001198	0.0002395	0.0002395
281	Roper River	Towns River	-0.0000220	0.0000988	0.0000000	0.0000000	0.0001198	0.0002395	0.0002395

Table 53: Nucleotide and haplotype diversity per Location

	Location	pi.strataG	pi.pegas	pi.pegas.var	HT.richness.strataG	h.pegas	h.pegas.var
1	Gulf of California	NaN	NaN	NaN	1	NaN	NaN
11	Costa Rica	0.000269	0.000269	0e+00	9	0.914286	0.002208
12	Sierra Leone	NaN	NaN	NaN	1	NaN	NaN
13	South Africa	NaN	0.001950	1e-06	6	0.952381	0.005950
14	Reunion	0.000289	0.000289	0e+00	6	0.808333	0.004289
15	Seychelles	0.000299	0.000299	0e+00	3	0.660131	0.002867
16	Arabian Sea	0.001792	0.001792	1e-06	13	0.941520	0.001170
17	Sri Lanka	0.003036	0.003037	3e-06	11	0.984848	0.000986
18	Thailand	NaN	0.002925	3e-06	4	0.800000	0.025926
19	Indonesia	0.000447	0.000447	0e+00	6	1.000000	0.004630
110	Papua New Guinea	0.000630	0.000631	0e+00	13	0.980952	0.000600
111	Fitzroy River	0.003148	0.003149	4e-06	4	0.900000	0.017760
112	Victoria River	0.000444	0.000444	0e+00	14	0.933333	0.001401
113	Daly River	0.000601	0.000601	0e+00	16	0.936667	0.001178
114	Adelaide River	0.000697	0.000698	0e+00	12	0.921569	0.002350
115	South Alligator River	0.000208	0.000208	0e+00	18	0.934566	0.000394
116	East Alligator River	0.000509	0.000509	0e+00	12	0.941176	0.001566
117	Blue mud Bay	0.000104	0.000104	0e+00	7	0.871795	0.003701
118	Roper River	0.000110	0.000110	0e+00	3	0.833333	0.035156
119	Towns River	NaN	0.000132	0e+00	3	0.700000	0.043040
120	Wenlock River	0.000612	0.000613	0e+00	14	0.964912	0.000549
121	Trinity inlet	0.000000	0.000000	0e+00	2	0.500000	0.066406
122	Clarence River	0.000302	0.000302	0e+00	12	0.933333	0.000784
123	Sydney Harbour	0.000582	0.000582	0e+00	11	0.974359	0.000968
124	Okinawa	0.000575	0.000575	0e+00	3	0.711111	0.005120
125	Urauchi River	0.000103	0.000103	0e+00	3	0.528571	0.005884
126	Fiji	NaN	0.001374	1e-06	8	0.972222	0.002578

Table 54: Nucleotide divergence within each Location

	stratum	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
9	Fitzroy River	0.003150	0	0.0e+00	0.005210	0.005269	0.005269
20	Sri Lanka	0.003038	0	3.7e-05	0.005210	0.005569	0.005629
22	Thailand	0.002926	0	0.0e+00	0.005269	0.005428	0.005449
18	South Africa	0.001950	0	6.0e-05	0.001138	0.005150	0.005150
2	Arabian Sea	0.001793	0	0.0e+00	0.000240	0.006048	0.006108
8	Fiji	0.001374	0	0.0e+00	0.000240	0.005509	0.005509
1	Adelaide River	0.000698	0	0.0e+00	0.000778	0.001377	0.001437
13	Papua New Guinea	0.000631	0	0.0e+00	0.000778	0.001257	0.001377
27	Wenlock River	0.000613	0	0.0e+00	0.000838	0.001018	0.001018
6	Daly River	0.000602	0	0.0e+00	0.000599	0.001257	0.001377
21	Sydney Harbour	0.000582	0	0.0e+00	0.000778	0.001082	0.001257
12	Okinawa	0.000575	0	0.0e+00	0.001078	0.001078	0.001078
7	East Alligator River	0.000509	0	0.0e+00	0.000449	0.001078	0.001078
11	Indonesia	0.000447	0	0.0e+00	0.000240	0.001078	0.001078
26	Victoria River	0.000444	0	0.0e+00	0.000180	0.001018	0.001317
4	Clarence River	0.000302	0	0.0e+00	0.000120	0.000838	0.001078
16	Seychelles	0.000299	0	0.0e+00	0.000000	0.001018	0.001018
14	Reunion	0.000289	0	0.0e+00	0.000120	0.001078	0.001078
5	Costa Rica	0.000269	0	0.0e+00	0.000299	0.000419	0.000419
19	South Alligator River	0.000208	0	0.0e+00	0.000180	0.000958	0.001078
23	Towns River	0.000132	0	0.0e+00	0.000180	0.000240	0.000240
15	Roper River	0.000110	0	7.0e-06	0.000120	0.000180	0.000180
3	Blue mud Bay	0.000104	0	0.0e+00	0.000120	0.000240	0.000240
25	Urauchi River	0.000103	0	0.0e+00	0.000000	0.001078	0.001078
24	Trinity inlet	0.000000	0	0.0e+00	0.000000	0.000000	0.000000
10	Gulf of California	NA	NA	NA	NA	NA	NA
17	Sierra Leone	NA	NA	NA	NA	NA	NA

Table 56: Haplotype counts per Location according to pegas

	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH	URR	OKI	FIJ
HT01	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT02	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT03	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT04	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT05	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT06	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT07	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT08	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT09	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT10	0	0	0	2	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT11	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT12	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT13	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT14	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT15	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT16	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT17	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT18	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT20	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT21	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT22	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0
HT24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0
HT25	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT28	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
HT30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	0	0	0
HT31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0
HT32	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT33	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT34	0	0	0	0	0	0	0	0	0	0	0	1	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0
HT35	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
HT37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
HT38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
HT39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
HT40	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
HT42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
HT43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
HT44	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	1	1	0	0	0	0	0	0	0	0
HT45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0
HT46	0	0	0	0	0	0	0	0	0	0	0	1	2	2	0	3	1	0	0	0	0	0	0	0	0	0	0
HT47	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
HT50	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	4	2	0	0	0	0	0	0	0	0	0	0
HT51	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	5	1	0	0	0	0	0	0	0	0	0	0
HT52	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

Table 56: Haplotype counts per Location according to pegas *(continued)*

	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH	URR	OKI	FIJ
HT54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT55	0	0	0	0	0	0	0	0	0	0	0	0	3	1	5	7	1	0	1	1	0	0	0	0	0	0	0
HT56	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	3	0	1	0	0	2	0	1	0	0	0	0
HT57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT59	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
HT61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT64	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT65	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT67	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
HT69	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT70	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT71	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT72	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT73	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT74	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT75	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT76	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT77	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0
HT78	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT79	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT80	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT81	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT83	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT85	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0
HT86	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
HT87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
HT88	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT90	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT91	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT92	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT93	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0
HT94	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
HT95	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT97	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT98	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HT99	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT102	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0
HT103	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT105	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0
HT106	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0

Table 56: Haplotype counts per Location according to pegas *(continued)*

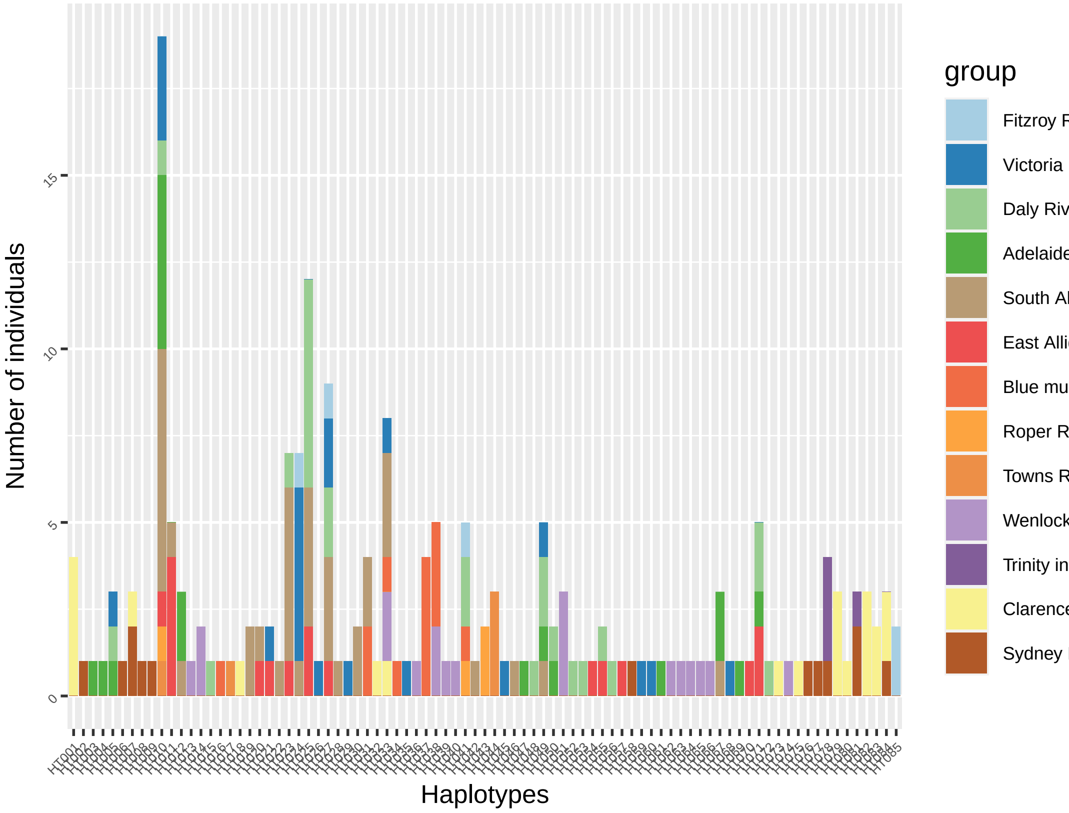
	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH	URR	OKI	FIJ
HT107	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT108	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT110	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT111	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT112	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT113	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT114	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT115	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT116	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT117	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0
HT118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT119	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT120	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT122	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT123	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT124	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	1	0
HT125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
HT127	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	2	0	0	0	0	0	0
HT128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0
HT129	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT130	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT131	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT132	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT133	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT134	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT135	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT136	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0
HT137	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT138	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT139	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT140	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT141	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT142	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT143	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT144	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT145	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT146	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT147	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT148	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT149	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT150	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
HT151	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT152	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	7	0
HT153	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0
HT154	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT155	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT156	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT157	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT158	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT159	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 56: Haplotype counts per Location according to pegas *(continued)*

	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH	URR	OKI	FIJ
HT160	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT161	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT162	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT163	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT164	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HT165	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

```r
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata
BS.gt.AUS <- BS.gt[,,"Australia", drop = TRUE]


schemes.AUS <- BS.gt.AUS@schemes[BS.gt.AUS@schemes$Site == "Australia",]
strata <- as.character(schemes.AUS$Location)
names(strata) <- as.character(schemes.AUS$id)
strataG::setStrata(BS.gt.AUS) <- strata
BS.gt.AUS@schemes <- schemes.AUS

group.levels <- c("Fitzroy River", "Victoria River", "Daly River","Adelaide River",
                 "South Alligator River","East Alligator River","Blue mud Bay",
                 "Roper River","Towns River","Wenlock River","Trinity inlet",
                 "Clarence River","Sydney Harbour")
BS.gt.AUS@schemes$Location <- factor(BS.gt.AUS@schemes$Location,
                                     levels = group.levels)

ind.names <- names(BS.dna) %in% BS.gt.AUS@data$id
BS.dna.AUS <- as.dna(BS.dna[ind.names, , drop = TRUE])
BS.bin.AUS <- subset(BS.bin, names(BS.bin) %in% BS.gt.AUS@data$id)
BS.hap.aus <- strataG::labelHaplotypes(BS.bin.AUS, prefix = "HT",
                                       use.indels = TRUE)
haps <- BS.hap.aus$haps
HTs <- unique(haps[names(haps) %in% names(BS.bin.AUS)])
BS.h.AUS <- pegas::haplotype(BS.bin.AUS, HTs)



hapcount <- pegas::haploFreq(BS.dna.AUS@sequence,
                             fac = BS.gt.AUS@schemes$Location,
                             split = NULL, what = 1, haplo = NULL)
row.names(hapcount) <- paste0("HT", sprintf('%0.3d', 1:85))
shortnames <- c("FZR", "VIR", "DAR", "ADR","SAR", "EAR","BMB", "ROR","TOR",
                "WER","TRI","CLR", "SYH")

kableExtra::kbl(hapcount, col.names = shortnames,
  caption = "Haplotype counts per Site according to pegas",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))

group.names <- BS.gt.AUS@schemes$Location
BS.hap.aus <- haplotypes::haplotype(BS.dna.AUS,indels = "sic")
HTs <- paste0("HT", sprintf('%0.3d', 1:85))
df <- data.frame(group = NULL,nind = NULL, hap = NULL, nhap = NULL,
                 hapfreq = NULL, stringsAsFactors = FALSE)
for (k in 1:length(group.levels)) {
  group.inds <- BS.gt.AUS@schemes$id[group.names == group.levels[k]]
  for (i in 1:85) {
    group <- group.levels[k]
    nind <- length(group.inds)
    hap <- HTs[i]
    nhap <- sum(group.inds %in% BS.hap.aus@haplist[[i]])
    # nhap <- sum(group.inds %in% names(BS.hap.aus$haps)[BS.hap.aus$haps == hap])
    hapfreq <- nhap/nind
```

```
    df <- plyr::rbind.fill(df, data.frame(group = group, nind = nind,
                                          hap = hap,
                                          nhap = nhap, hapfreq = hapfreq,
                                          stringsAsFactors = FALSE))
  }
}

df$group <- factor(df$group, levels = group.levels)

HT.plot <- ggplot2::ggplot(data = df) +
  ggplot2::geom_bar(ggplot2::aes(x = hap, y = nhap, fill = group),
                    stat = "identity",position = "stack") +
  ggplot2::labs(x = "Haplotypes", y = "Number of individuals") +
  ggplot2::scale_fill_manual(values = colours.13) +
  ggplot2::theme(
    axis.text = ggplot2::element_text(angle = 45, hjust = 1, size = 5),
    axis.title.x = ggplot2::element_text(size = 10),
    axis.title.y = ggplot2::element_text(size = 10),
    legend.text = ggplot2::element_text(size = 7))
print(HT.plot)
```



13.3.2.1 Within AUS

```
ggplot2::ggsave(HT.plot, filename = "HT_barplot_per_Location_AUS.png",
                width = 30, height = 15, units = "cm")
```

Table 57: Haplotype counts per Site according to pegas

	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH
HT001	2	0	0	0	0	0	0	0	0	0	0	0	0
HT002	0	0	0	0	0	0	0	0	0	0	1	0	2
HT003	0	0	0	0	0	0	0	0	0	0	3	0	1
HT004	0	0	1	0	0	0	0	0	0	0	0	0	0
HT005	0	0	0	0	0	0	0	0	0	0	0	0	1
HT006	0	0	0	0	0	0	0	0	0	1	0	0	0
HT007	0	0	0	0	2	0	0	0	0	0	0	0	0
HT008	0	0	0	0	1	4	0	0	0	0	0	0	0

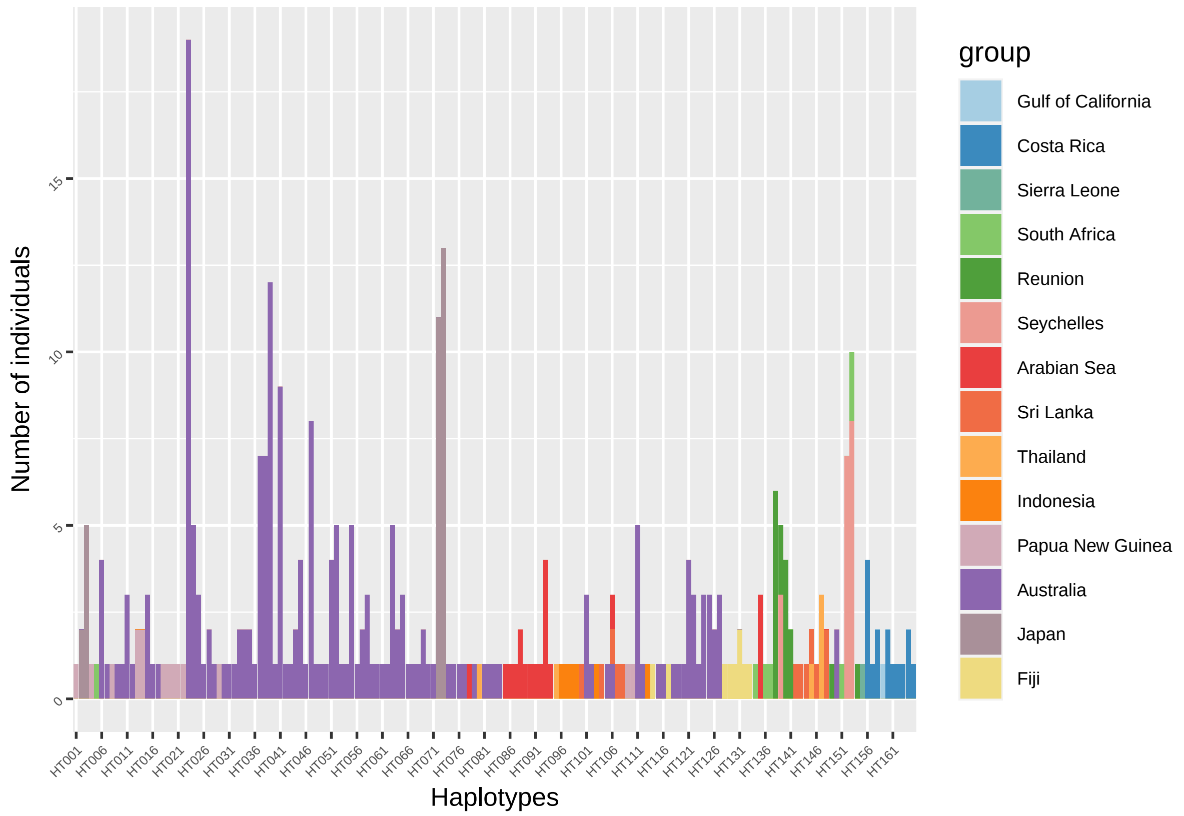
Table 57: Haplotype counts per Site according to pegas *(continued)*

	FZR	VIR	DAR	ADR	SAR	EAR	BMB	ROR	TOR	WER	TRI	CLR	SYH
HT009	0	0	0	2	1	0	0	0	0	0	0	0	0
HT010	0	1	0	0	0	0	0	0	0	0	0	0	0
HT011	1	5	0	0	1	0	0	0	0	0	0	0	0
HT012	0	1	0	0	0	0	0	0	0	0	0	0	0
HT013	0	0	0	0	0	0	0	0	3	0	0	0	0
HT014	0	0	0	0	0	0	0	2	0	0	0	0	0
HT015	0	0	0	0	1	1	0	0	0	0	0	0	0
HT016	0	0	0	0	2	0	0	0	0	0	0	0	0
HT017	0	1	0	0	0	1	0	0	0	0	0	0	0
HT018	0	0	0	0	1	0	0	0	0	0	0	0	0
HT019	0	0	0	0	1	0	0	0	0	0	0	0	0
HT020	0	0	0	0	1	0	0	0	0	0	0	0	0
HT021	1	0	2	0	0	0	1	1	0	0	0	0	0
HT022	0	0	0	0	2	0	2	0	0	0	0	0	0
HT023	1	2	2	0	3	1	0	0	0	0	0	0	0
HT024	0	1	0	0	0	0	0	0	0	0	0	0	0
HT025	0	0	0	1	0	0	0	0	0	0	0	0	0
HT026	0	0	0	0	1	0	0	0	0	0	0	0	0
HT027	0	0	6	0	4	2	0	0	0	0	0	0	0
HT028	0	0	1	0	5	1	0	0	0	0	0	0	0
HT029	0	0	1	0	0	0	0	0	0	0	0	0	0
HT030	0	0	0	0	0	0	1	0	0	0	0	0	0
HT031	0	0	0	0	0	0	0	0	0	1	0	0	0
HT032	0	3	1	5	7	1	0	1	1	0	0	0	0
HT033	0	1	0	0	3	0	1	0	0	2	0	1	0
HT034	0	0	0	0	0	0	0	0	0	1	0	0	0
HT035	0	0	0	0	0	0	0	0	0	1	0	0	0
HT036	0	1	0	0	0	0	0	0	0	0	0	0	0
HT037	0	0	0	0	0	0	0	0	0	2	0	0	0
HT038	0	0	0	0	0	0	0	0	0	1	0	0	0
HT039	0	0	0	0	0	0	0	0	0	1	0	0	0
HT040	0	0	0	0	0	0	0	0	0	1	0	0	0
HT041	0	0	0	0	0	0	0	0	0	1	0	0	0
HT042	0	0	0	0	0	0	0	0	0	3	0	0	0
HT043	0	0	1	0	0	0	0	0	0	0	0	0	0
HT044	0	0	2	1	0	2	0	0	0	0	0	0	0
HT045	0	0	0	0	0	0	0	0	0	1	0	0	0
HT046	0	0	0	0	0	0	0	0	0	1	0	0	0
HT047	0	0	0	0	0	0	0	0	0	0	0	1	0
HT048	0	0	0	0	0	0	0	0	0	0	0	2	1
HT049	0	0	0	0	0	0	0	0	0	0	0	3	0
HT050	0	0	0	0	0	0	0	0	0	0	0	2	0
HT051	0	0	0	0	0	0	0	0	0	0	0	0	1
HT052	0	0	0	0	0	0	0	0	0	0	0	1	0
HT053	0	0	0	0	0	0	0	0	0	0	0	4	0
HT054	0	0	0	0	0	0	0	0	0	0	0	3	0
HT055	0	0	0	0	0	0	0	0	0	0	0	1	0
HT056	0	0	0	0	0	0	0	0	0	0	0	0	1
HT057	0	0	0	0	0	1	0	0	0	0	0	0	0
HT058	0	0	1	0	0	1	0	0	0	0	0	0	0
HT059	0	0	1	0	0	0	0	0	0	0	0	0	0
HT060	0	0	0	0	0	1	0	0	0	0	0	0	0
HT061	0	1	2	1	1	0	0	0	0	0	0	0	0
HT062	0	0	1	1	0	0	0	0	0	0	0	0	0
HT063	0	0	0	0	0	0	0	0	0	0	0	1	0
HT064	0	0	0	0	0	0	0	0	0	0	0	0	1
HT065	0	0	0	0	0	0	0	0	0	0	0	0	1
HT066	0	0	0	0	0	0	0	0	0	0	0	1	2
HT067	0	0	0	0	0	0	0	0	0	0	0	0	1
HT068	0	0	0	0	0	0	0	0	1	0	0	0	0
HT069	0	0	0	0	0	0	0	0	0	0	0	1	0
HT070	0	0	0	0	0	0	1	0	0	0	0	0	0
HT071	0	0	0	0	0	0	3	0	0	2	0	0	0
HT072	0	0	0	0	0	0	4	0	0	0	0	0	0
HT073	0	0	1	0	0	0	0	0	0	0	0	0	0
HT074	0	0	1	0	0	0	0	0	0	0	0	0	0
HT075	0	1	0	0	0	0	0	0	0	0	0	0	0
HT076	0	1	0	0	0	0	0	0	0	0	0	0	0
HT077	0	0	0	2	1	0	0	0	0	0	0	0	0
HT078	0	0	0	0	0	1	0	0	0	0	0	0	0
HT079	0	0	0	1	0	0	0	0	0	0	0	0	0
HT080	0	1	0	0	0	0	0	0	0	0	0	0	0
HT081	0	0	0	1	0	0	0	0	0	0	0	0	0
HT082	0	0	0	0	0	0	0	0	0	0	0	0	1
HT083	0	0	0	1	0	0	0	0	0	0	0	0	0
HT084	0	0	0	1	0	0	0	0	0	0	0	0	0
HT085	0	1	1	1	0	0	0	0	0	0	0	0	0

13.3.3 Diversity per Site

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

divers.Site <- data.frame(Site = character(), pi.strataG = numeric(),
                          pi.pegas = numeric(), pi.pegas.var = numeric(),
                          HT.richness.strataG = numeric(), h.pegas = numeric(),
                          h.pegas.var = numeric())
for (Site in levels(BS.gt@schemes$Site)) {
  print(Site)
  BS.gt.sub <- BS.gt[,,Site, drop = TRUE]
  BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)
  BS.h.sub <- strataG::labelHaplotypes(BS.bin.sub, prefix = "HT",
                                        use.indels = TRUE)
  BS.dna.sub <- as.dna(BS.dna[names(BS.dna) %in% BS.gt.sub@data$id, ,
                                drop = TRUE])
  bases <- haplotypes::basecomp(BS.dna.sub)
  print(paste0("Mitogenome base composition:"))
  print(colMeans(bases))

  pi.gt <-
    strataG::nucleotideDiversity(BS.gt.sub,bases = c("a", "c", "g", "t"),
    simplify = TRUE)
  pi.peg <- pegas::nuc.div(BS.bin.sub, variance = TRUE,
                          pairwise.deletion = FALSE)
  h.peg <- pegas::hap.div(BS.bin.sub, variance = TRUE, method = "Nei")
  res <- data.frame(Site, mean(pi.gt), pi.peg[1], pi.peg[2],
                    length(unique(BS.h.sub$haps)),
                    h.peg[1], h.peg[2])
  colnames(res) <- c("Site", "pi.strataG", "pi.pegas", "pi.pegas.var",
                     "HT.richness.strataG", "h.pegas", "h.pegas.var")
  divers.Site <- rbind(divers.Site, res)
}

knitr::kable(
  divers.Site,
  caption = "Nucleotide and haplotype diversity per Site",
  # format = "html",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c( "hold_position"))


dA.gt <- strataG::nucleotideDivergence(BS.gt,
                                        probs = c(0, 0.025, 0.5, 0.975, 1),
                                        model = "RAW")
knitr::kable(
  dA.gt$within[order(dA.gt$within$mean, decreasing = TRUE), -1],
  # format = "html",
  caption = "Nucleotide divergence within each Site",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
knitr::kable(
  dA.gt$between[order(dA.gt$between$mean, decreasing = TRUE), -1],
```

```
  # format = "html",
  caption = "Nucleotide divergence between each Site",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE, font_size = 5)




hapcount <- pegas::haploFreq(BS.dna@sequence, fac = BS.gt@schemes$Site,
                             split = NULL, what = 1, haplo = NULL)
row.names(hapcount) <- paste0("HT", sprintf('%0.2d', 1:BS.hap@nhap))
shortnames <- c("GOC", "COR","SIL", "SAF", "RUN", "SEY", "ARS", "SRL", "TAI",
                "IND", "PNG", "AUS", "JAP","FIJ")

kableExtra::kbl(hapcount, col.names = shortnames,
  caption = "Haplotype counts per Site according to pegas",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))

group.levels <- levels(BS.gi$other$ind.meta$Site)
group.names <- BS.gi$other$ind.meta$Site

HTs <- paste0("HT", sprintf('%0.3d', 1:BS.hap@nhap))
df <- data.frame(group = NULL,nind = NULL, hap = NULL, nhap = NULL,
                 hapfreq = NULL, stringsAsFactors = FALSE)
for (k in 1:length(group.levels)) {
  group.inds <- adegenet::indNames(BS.gi)[group.names == group.levels[k]]
  for (i in 1:BS.hap@nhap) {
    group <- group.levels[k]
    nind <- length(group.inds)
    hap <- HTs[i]
    nhap <- sum(group.inds %in% BS.hap@haplist[[i]])
    hapfreq <- nhap/nind
    df <- plyr::rbind.fill(df, data.frame(group = group, nind = nind, hap = hap,
                                          nhap = nhap, hapfreq = hapfreq,
                                          stringsAsFactors = FALSE))
  }
}

df$group <- factor(df$group, levels = group.levels)

haplotype.labels <- unique(df$hap)
haplotype.labels2 <- haplotype.labels[seq(1, length(haplotype.labels), by = 5)]

HT.plot <- ggplot2::ggplot(data = df) +
  ggplot2::geom_bar(ggplot2::aes(x = hap, y = nhap, fill = group),
                    stat = "identity",position = "stack") +
  ggplot2::labs(x = "Haplotypes", y = "Number of individuals") +
  ggplot2::scale_fill_manual(values = funky(15)) +
  ggplot2::scale_x_discrete(breaks = haplotype.labels2) +
  ggplot2::theme(
      axis.text = ggplot2::element_text(angle = 45, hjust = 1, size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
print(HT.plot)
```



```
ggplot2::ggsave(HT.plot, filename = "HT_barplot_per_Sites.png", width = 30,
                height = 15, units = "cm")
```

```
## [1] "Gulf of California"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3151972 0.2423535 0.1307236 0.3117256
## [1] "Costa Rica"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3151516 0.2424022 0.1307582 0.3116879
## [1] "Sierra Leone"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145576 0.2423680 0.1312702 0.3118041
## [1] "South Africa"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3148254 0.2429858 0.1309720 0.3112168
## [1] "Reunion"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3148585 0.2431229 0.1309273 0.3110912
## [1] "Seychelles"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3149296 0.2427989 0.1309067 0.3113648
## [1] "Arabian Sea"
## [1] "Mitogenome base composition:"
##         A         T         G         C
```

```
## 0.3146861 0.2433287 0.1310578 0.3109275
## [1] "Sri Lanka"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3147039 0.2430626 0.1310614 0.3111722
## [1] "Thailand"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3147902 0.2430688 0.1310021 0.3111388
## [1] "Indonesia"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145539 0.2432308 0.1311531 0.3110621
## [1] "Papua New Guinea"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145063 0.2429284 0.1312395 0.3113257
## [1] "Australia"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145112 0.2430699 0.1312364 0.3111825
## [1] "Japan"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146686 0.2430748 0.1311079 0.3111486
## [1] "Fiji"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146038 0.2429049 0.1311531 0.3113381
```

Table 58: Nucleotide and haplotype diversity per Site

	Site	pi.strataG	pi.pegas	pi.pegas.var	HT.richness.strataG	h.pegas	h.pegas.var
1	Gulf of California	NaN	NaN	NaN	1	NaN	NaN
11	Costa Rica	0.000269	0.000269	0e+00	9	0.914286	0.002208
12	Sierra Leone	NaN	NaN	NaN	1	NaN	NaN
13	South Africa	NaN	0.001950	1e-06	6	0.952381	0.005950
14	Reunion	0.000289	0.000289	0e+00	6	0.808333	0.004289
15	Seychelles	0.000299	0.000299	0e+00	3	0.660131	0.002867
16	Arabian Sea	0.001792	0.001792	1e-06	13	0.941520	0.001170
17	Sri Lanka	0.003036	0.003037	3e-06	11	0.984848	0.000986
18	Thailand	NaN	0.002925	3e-06	4	0.800000	0.025926
19	Indonesia	0.000447	0.000447	0e+00	6	1.000000	0.004630
110	Papua New Guinea	0.000630	0.000631	0e+00	13	0.980952	0.000600
111	Australia	0.000629	0.000630	0e+00	85	0.977711	0.000014
112	Japan	0.000389	0.000389	0e+00	4	0.690323	0.001877
113	Fiji	NaN	0.001374	1e-06	8	0.972222	0.002578

Table 59: Nucleotide divergence within each Site

	stratum	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
13	Sri Lanka	0.003038	0	3.7e-05	0.005210	0.005569	0.005629
14	Thailand	0.002926	0	0.0e+00	0.005269	0.005428	0.005449
12	South Africa	0.001950	0	6.0e-05	0.001138	0.005150	0.005150
1	Arabian Sea	0.001793	0	0.0e+00	0.000240	0.006048	0.006108
4	Fiji	0.001374	0	0.0e+00	0.000240	0.005509	0.005509
8	Papua New Guinea	0.000631	0	0.0e+00	0.000778	0.001257	0.001377
2	Australia	0.000630	0	0.0e+00	0.000599	0.001257	0.005569
6	Indonesia	0.000447	0	0.0e+00	0.000240	0.001078	0.001078
7	Japan	0.000389	0	0.0e+00	0.000000	0.001078	0.001078
10	Seychelles	0.000299	0	0.0e+00	0.000000	0.001018	0.001018
9	Reunion	0.000289	0	0.0e+00	0.000120	0.001078	0.001078
3	Costa Rica	0.000269	0	0.0e+00	0.000299	0.000419	0.000419
5	Gulf of California	NA	NA	NA	NA	NA	NA
11	Sierra Leone	NA	NA	NA	NA	NA	NA

Table 60: Nucleotide divergence between each Site

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
86	Sierra Leone	South Africa	0.008195	0.009170	0.008982	0.008982	0.009281	0.009281	0.009281
53	Gulf of California	South Africa	0.008178	0.009153	0.008982	0.008982	0.009162	0.009383	0.009401
50	Gulf of California	Reunion	0.008965	0.009109	0.009042	0.009042	0.009162	0.009162	0.009162
78	Reunion	Sierra Leone	0.008965	0.009109	0.009042	0.009042	0.009162	0.009162	0.009162
34	Costa Rica	South Africa	0.007999	0.009109	0.008862	0.008862	0.009102	0.009401	0.009401
4	Arabian Sea	Gulf of California	0.008208	0.009105	0.008922	0.008976	0.009102	0.009254	0.009281
47	Gulf of California	Indonesia	0.008858	0.009082	0.008982	0.008997	0.009102	0.009102	0.009102
48	Gulf of California	Japan	0.008874	0.009069	0.009042	0.009042	0.009042	0.009162	0.009162
49	Gulf of California	Papua New Guinea	0.008750	0.009066	0.008922	0.008922	0.009102	0.009201	0.009222
31	Costa Rica	Reunion	0.008786	0.009065	0.008922	0.008922	0.009042	0.009162	0.009162
2	Arabian Sea	Costa Rica	0.008030	0.009061	0.008802	0.008868	0.009042	0.009222	0.009281
28	Costa Rica	Indonesia	0.008680	0.009038	0.008862	0.008876	0.009042	0.009102	0.009102
55	Gulf of California	Thailand	0.007569	0.009032	0.008922	0.008930	0.009042	0.009147	0.009162
29	Costa Rica	Japan	0.008696	0.009025	0.008922	0.008922	0.009042	0.009162	0.009162
10	Arabian Sea	Sierra Leone	0.008127	0.009023	0.008802	0.008856	0.008982	0.009281	0.009281
30	Costa Rica	Papua New Guinea	0.008572	0.009022	0.008802	0.008838	0.009042	0.009222	0.009222
37	Fiji	Gulf of California	0.008335	0.009022	0.008982	0.008982	0.009042	0.009042	0.009042
51	Gulf of California	Seychelles	0.008862	0.009012	0.008982	0.008982	0.008982	0.009162	0.009162
54	Gulf of California	Sri Lanka	0.007493	0.009012	0.008922	0.008922	0.008982	0.009145	0.009162
82	Seychelles	Sierra Leone	0.008862	0.009012	0.008982	0.008982	0.008982	0.009162	0.009162
88	Sierra Leone	Thailand	0.007529	0.008992	0.008802	0.008825	0.009042	0.009042	0.009042
36	Costa Rica	Thailand	0.007390	0.008988	0.008802	0.008816	0.008982	0.009162	0.009162
26	Costa Rica	Fiji	0.008156	0.008978	0.008862	0.008862	0.008982	0.009042	0.009042
32	Costa Rica	Seychelles	0.008684	0.008968	0.008862	0.008862	0.008982	0.009162	0.009162
35	Costa Rica	Sri Lanka	0.007315	0.008968	0.008802	0.008802	0.008982	0.009162	0.009162
16	Australia	Gulf of California	0.008652	0.008966	0.008743	0.008743	0.008922	0.009222	0.009281
60	Indonesia	Sierra Leone	0.008739	0.008962	0.008862	0.008877	0.008982	0.008982	0.008982
87	Sierra Leone	Sri Lanka	0.007443	0.008962	0.008802	0.008802	0.008982	0.009145	0.009162
67	Japan	Sierra Leone	0.008754	0.008949	0.008922	0.008922	0.008922	0.009042	0.009042
73	Papua New Guinea	Sierra Leone	0.008631	0.008946	0.008802	0.008802	0.008982	0.009081	0.009102
14	Australia	Costa Rica	0.008473	0.008922	0.008623	0.008683	0.008922	0.009162	0.009281
43	Fiji	Sierra Leone	0.008215	0.008902	0.008862	0.008862	0.008922	0.008922	0.008922
22	Australia	Sierra Leone	0.008528	0.008843	0.008623	0.008626	0.008862	0.009102	0.009162
52	Gulf of California	Sierra Leone	0.006347	0.006347	0.006347	0.006347	0.006347	0.006347	0.006347
33	Costa Rica	Sierra Leone	0.006169	0.006303	0.006228	0.006228	0.006287	0.006347	0.006347
65	Japan	Reunion	0.005288	0.005628	0.005269	0.005269	0.005629	0.005988	0.005988
71	Papua New Guinea	Reunion	0.005129	0.005589	0.005210	0.005328	0.005569	0.005988	0.005988
58	Indonesia	Reunion	0.005198	0.005566	0.005210	0.005254	0.005569	0.005808	0.005808
20	Australia	Reunion	0.005076	0.005535	0.000240	0.005210	0.005569	0.005868	0.005928
66	Japan	Seychelles	0.005016	0.005361	0.005210	0.005210	0.005210	0.005988	0.005988
72	Papua New Guinea	Seychelles	0.004874	0.005339	0.005150	0.005150	0.005269	0.005689	0.005988
59	Indonesia	Seychelles	0.004926	0.005299	0.005150	0.005150	0.005269	0.005728	0.005808
21	Australia	Seychelles	0.004802	0.005267	0.000180	0.005030	0.005269	0.005749	0.005928
41	Fiji	Reunion	0.004197	0.005029	0.000359	0.000958	0.005509	0.005629	0.005629
68	Japan	South Africa	0.003843	0.005013	0.001557	0.001557	0.005569	0.006108	0.006108
61	Indonesia	South Africa	0.003760	0.004959	0.001497	0.001617	0.005389	0.005928	0.005928
74	Papua New Guinea	South Africa	0.003614	0.004905	0.000659	0.000778	0.005389	0.006000	0.006108
23	Australia	South Africa	0.003602	0.004892	0.000180	0.001198	0.005389	0.005988	0.006048
8	Arabian Sea	Reunion	0.003841	0.004882	0.000240	0.000240	0.005689	0.005954	0.005988
42	Fiji	Seychelles	0.003973	0.004809	0.000299	0.000299	0.005329	0.005629	0.005629
9	Arabian Sea	Seychelles	0.003704	0.004750	0.000359	0.000768	0.005389	0.005837	0.005988
44	Fiji	South Africa	0.002900	0.004562	0.000299	0.000365	0.005389	0.005749	0.005749
11	Arabian Sea	South Africa	0.002625	0.004496	0.000120	0.000120	0.005449	0.006048	0.006108
76	Papua New Guinea	Thailand	0.002145	0.003923	0.000240	0.000359	0.005329	0.005735	0.005749
25	Australia	Thailand	0.002064	0.003842	0.000180	0.000419	0.005329	0.005569	0.005629
70	Japan	Thailand	0.002138	0.003795	0.000359	0.000359	0.005269	0.005749	0.005749
63	Indonesia	Thailand	0.002059	0.003746	0.000299	0.000404	0.005210	0.005569	0.005569
46	Fiji	Thailand	0.001570	0.003720	0.000060	0.000359	0.005419	0.005509	0.005509
13	Arabian Sea	Thailand	0.001218	0.003578	0.000120	0.000120	0.005389	0.005769	0.005868
75	Papua New Guinea	Sri Lanka	0.001691	0.003525	0.000240	0.000299	0.005329	0.005689	0.005868
24	Australia	Sri Lanka	0.001608	0.003442	0.000000	0.000299	0.005269	0.005629	0.005808
45	Fiji	Sri Lanka	0.001195	0.003401	0.000060	0.000340	0.005269	0.005509	0.005509
69	Japan	Sri Lanka	0.001680	0.003394	0.000359	0.000359	0.005210	0.005808	0.005868
12	Arabian Sea	Sri Lanka	0.000915	0.003330	0.000000	0.000359	0.005329	0.005749	0.005808
62	Indonesia	Sri Lanka	0.001544	0.003286	0.000120	0.000166	0.005180	0.005582	0.005689
89	South Africa	Sri Lanka	0.000372	0.002866	0.000240	0.000240	0.001317	0.005864	0.005868
80	Reunion	Sri Lanka	0.001188	0.002852	0.000299	0.000406	0.001018	0.005749	0.005749
91	Sri Lanka	Thailand	-0.000246	0.002736	0.000000	0.000060	0.000958	0.005509	0.005569
90	South Africa	Thailand	0.000109	0.002548	0.000240	0.000241	0.001198	0.005868	0.005868
84	Seychelles	Sri Lanka	0.000860	0.002528	0.000240	0.000240	0.000928	0.005689	0.005749
81	Reunion	Thailand	0.000885	0.002493	0.000299	0.000359	0.001078	0.005749	0.005749
3	Arabian Sea	Fiji	0.000483	0.002066	0.000719	0.000838	0.001018	0.005749	0.005749
85	Seychelles	Thailand	0.000443	0.002056	0.000240	0.000240	0.000299	0.005668	0.005749
7	Arabian Sea	Papua New Guinea	0.000524	0.001735	0.000240	0.000359	0.001078	0.005808	0.006108
1	Arabian Sea	Australia	0.000441	0.001652	0.000000	0.000359	0.000898	0.005868	0.006048
6	Arabian Sea	Japan	0.000391	0.001482	0.000359	0.000359	0.000539	0.006108	0.006108
39	Fiji	Japan	0.000596	0.001477	0.000838	0.000838	0.000958	0.005407	0.005749
40	Fiji	Papua New Guinea	0.000446	0.001448	0.000599	0.000659	0.000958	0.005449	0.005749
5	Arabian Sea	Indonesia	0.000316	0.001436	0.000120	0.000240	0.000599	0.005731	0.005928
38	Fiji	Indonesia	0.000511	0.001422	0.000719	0.000719	0.000958	0.005449	0.005569
15	Australia	Fiji	0.000337	0.001339	0.000180	0.000240	0.000838	0.005509	0.005689
79	Reunion	South Africa	0.000134	0.001254	0.000060	0.000153	0.000898	0.005030	0.005030
83	Seychelles	South Africa	0.000063	0.001188	0.000000	0.000000	0.001078	0.004611	0.005030
57	Indonesia	Papua New Guinea	0.000438	0.000977	0.000299	0.000419	0.001078	0.001198	0.001257
64	Japan	Papua New Guinea	0.000450	0.000960	0.000359	0.000359	0.001018	0.001257	0.001377
18	Australia	Japan	0.000401	0.000910	0.000299	0.000359	0.000898	0.001257	0.005629
17	Australia	Indonesia	0.000342	0.000880	0.000060	0.000265	0.000898	0.001257	0.005449
19	Australia	Papua New Guinea	0.000176	0.000807	0.000120	0.000240	0.000719	0.001198	0.005629
77	Reunion	Seychelles	0.000453	0.000747	0.000000	0.000000	0.000898	0.001018	0.001078
56	Indonesia	Japan	0.000271	0.000690	0.000419	0.000419	0.000539	0.001257	0.001257
27	Costa Rica	Gulf of California	0.000173	0.000307	0.000240	0.000240	0.000299	0.000419	0.000419

Table 61: Haplotype counts per Site according to pegas

	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
HT01	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT02	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT03	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT04	0	0	0	0	1	0	0	0	0	0	0	0	0	0
HT05	0	0	0	0	0	0	0	0	3	0	0	0	0	0
HT06	0	0	0	0	0	0	0	2	0	0	0	0	0	0
HT07	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT08	0	0	0	0	1	0	0	0	0	0	0	0	0	0
HT09	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT10	0	0	0	2	0	8	0	0	0	0	0	0	0	0
HT11	0	0	0	0	0	7	0	0	0	0	0	0	0	0
HT12	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT13	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT14	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT15	0	0	0	0	6	0	0	0	0	0	0	0	0	0
HT16	0	0	0	0	2	3	0	0	0	0	0	0	0	0
HT17	0	0	0	0	2	0	0	0	0	0	0	0	0	0
HT18	0	0	0	0	4	0	0	0	0	0	0	0	0	0
HT19	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT20	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT21	0	0	0	0	0	0	0	1	1	0	0	0	0	0
HT22	0	0	0	0	0	0	3	0	0	0	0	0	0	0
HT23	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT24	0	0	0	0	0	0	0	0	0	0	0	4	0	0
HT25	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT26	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT27	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT28	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT29	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT30	0	0	0	0	0	0	0	0	0	0	0	5	0	0
HT31	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT32	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT33	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT34	0	0	0	0	0	0	0	0	0	0	0	7	0	0
HT35	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT36	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT37	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT38	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT39	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT40	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT41	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT42	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT43	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT44	0	0	0	0	0	0	0	0	0	0	0	5	0	0
HT45	0	0	0	0	0	0	0	0	0	0	0	4	0	0
HT46	0	0	0	0	0	0	0	0	0	0	0	9	0	0
HT47	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT48	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT49	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT50	0	0	0	0	0	0	0	0	0	0	0	12	0	0
HT51	0	0	0	0	0	0	0	0	0	0	0	7	0	0
HT52	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT53	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT54	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT55	0	0	0	0	0	0	0	0	0	0	0	19	0	0
HT56	0	0	0	0	0	0	0	0	0	0	0	8	0	0
HT57	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT58	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT59	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT60	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT61	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT62	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT63	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT64	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT65	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT66	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT67	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT68	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT69	0	0	0	0	0	0	2	0	0	0	0	0	0	0
HT70	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT71	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT72	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT73	0	0	0	0	0	0	0	0	1	0	0	0	0	0
HT74	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT75	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT76	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT77	0	0	0	0	0	0	0	0	0	0	0	5	0	0
HT78	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT79	0	0	0	0	0	0	4	0	0	0	0	0	0	0
HT80	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT81	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT82	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT83	0	0	0	0	0	0	1	0	0	0	0	0	0	0
HT84	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Table 61: Haplotype counts per Site according to pegas *(continued)*

	GOC	COR	SIL	SAF	RUN	SEY	ARS	SRL	TAI	IND	PNG	AUS	JAP	FIJ
HT85	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT86	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT87	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT88	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT89	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT90	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT91	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT92	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT93	0	0	0	0	0	0	0	0	0	0	0	4	0	0
HT94	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT95	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT96	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT97	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT98	0	0	0	0	0	0	0	0	0	0	0	0	0	2
HT99	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT100	0	0	0	0	0	0	0	0	0	0	0	0	0	1
HT101	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT102	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT103	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT104	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT105	0	0	0	0	0	0	0	0	0	0	0	5	0	0
HT106	0	0	0	0	0	0	0	0	0	0	0	2	0	0
HT107	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT108	0	0	0	1	0	0	0	0	0	0	0	0	0	0
HT109	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT110	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT111	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT112	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT113	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT114	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT115	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HT116	0	0	0	0	0	0	0	0	0	0	2	0	0	0
HT117	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT118	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT119	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT120	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT121	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT122	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT123	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT124	0	0	0	0	0	0	0	0	0	0	0	0	5	0
HT125	0	0	0	0	0	0	0	0	0	0	0	0	2	0
HT126	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT127	0	0	0	0	0	0	0	0	0	0	0	5	0	0
HT128	0	0	0	0	0	0	0	0	0	0	0	4	0	0
HT129	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT130	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT131	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT132	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT133	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT134	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT135	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT136	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT137	0	0	0	0	0	0	1	1	0	0	0	1	0	0
HT138	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT139	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT140	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT141	0	0	0	0	0	0	0	1	0	0	0	0	0	0
HT142	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT143	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT144	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT145	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HT146	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT147	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT148	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT149	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HT150	0	0	0	0	0	0	0	0	0	0	0	3	0	0
HT151	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HT152	0	0	0	0	0	0	0	0	0	0	0	0	11	0
HT153	0	0	0	0	0	0	0	0	0	0	0	0	13	0
HT154	0	0	0	0	0	0	0	0	1	0	0	0	0	0
HT155	0	4	0	0	0	0	0	0	0	0	0	0	0	0
HT156	0	2	0	0	0	0	0	0	0	0	0	0	0	0
HT157	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT158	0	2	0	0	0	0	0	0	0	0	0	0	0	0
HT159	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT160	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT161	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT162	1	0	0	0	0	0	0	0	0	0	0	0	0	0
HT163	0	2	0	0	0	0	0	0	0	0	0	0	0	0
HT164	0	1	0	0	0	0	0	0	0	0	0	0	0	0
HT165	0	0	1	0	0	0	0	0	0	0	0	0	0	0

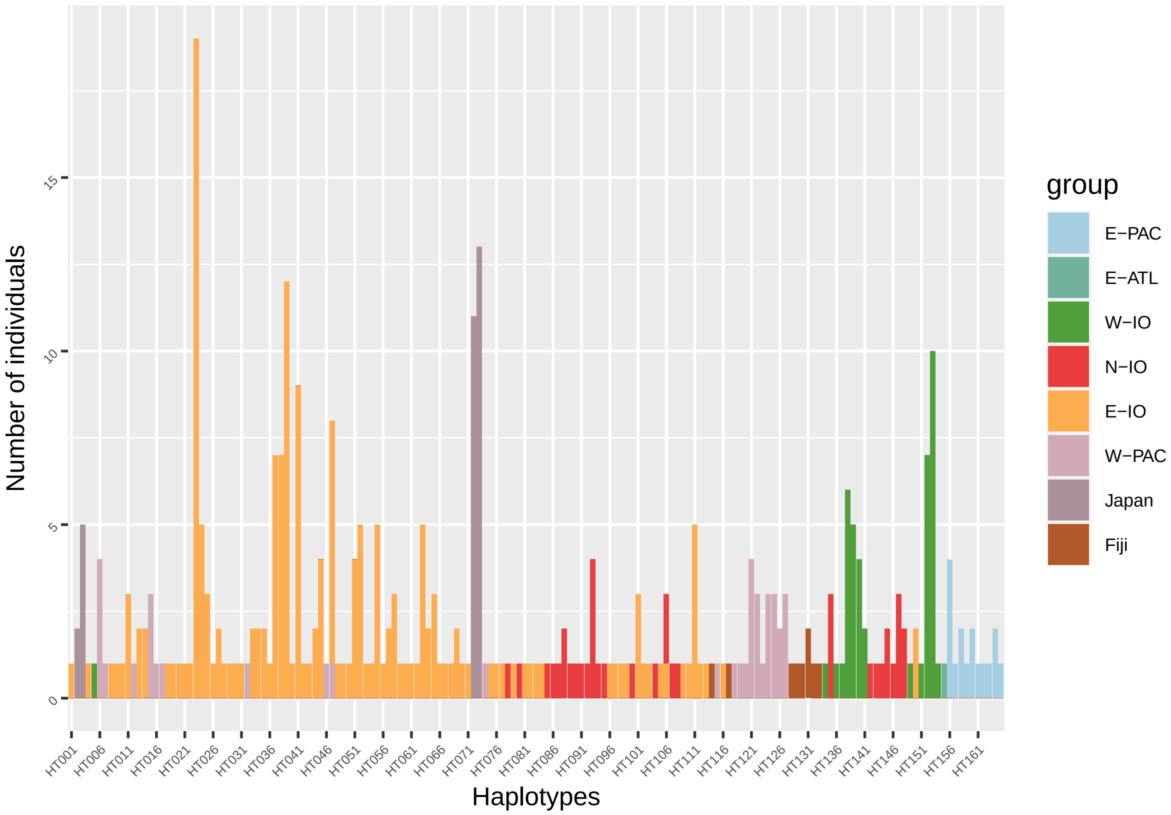
13.3.4 Diversity per region

```r
strata <- as.character(BS.gt@schemes$Region)
strata[strata %in% c("W-IO", "N-IO", "E-IO", "W-PAC")] <- "IWP"
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

divers.region <- data.frame(Region = character(), pi.strataG = numeric(),
                           pi.pegas = numeric(), pi.pegas.var = numeric(),
                           HT.richness.strataG = numeric(), h.pegas = numeric(),
                           h.pegas.var = numeric())
strat.levels <- c("E-PAC", "E-ATL", "IWP","Japan", "Fiji")
for (Region in strat.levels) {
  print(Region)
  BS.gt.sub <- BS.gt[,,Region, drop = TRUE]
  BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)
  BS.h.sub <- strataG::labelHaplotypes(BS.bin.sub, prefix = "HT",
                                         use.indels = TRUE)
  BS.dna.sub <- as.dna(BS.dna[names(BS.dna) %in% BS.gt.sub@data$id, ,
                                  drop = TRUE])

  bases <- haplotypes::basecomp(BS.dna.sub)
  print(paste0("Mitogenome base composition:"))
  print(colMeans(bases))

  pi.gt <- strataG::nucleotideDiversity(BS.gt.sub,
                                        bases = c("a", "c", "g", "t"),
                                        simplify = TRUE)
  pi.peg <- pegas::nuc.div(BS.bin.sub, variance = TRUE,
                           pairwise.deletion = FALSE)
  h.peg <- pegas::hap.div(BS.bin.sub, variance = TRUE, method = "Nei")
  res <- data.frame(Region, mean(pi.gt), pi.peg[1], pi.peg[2],
                    length(unique(BS.h.sub$haps)), h.peg[1], h.peg[2])
  colnames(res) <- c("Region", "pi.strataG", "pi.pegas", "pi.pegas.var",
                     "HT.richness.strataG", "h.pegas", "h.pegas.var")
  divers.region <- rbind(divers.region, res)
}

knitr::kable(
  divers.region,
  caption = "Nucleotide and haplotype diversity per region",
  # format = "html",
  digits = 6
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)


dA.gt <- strataG::nucleotideDivergence(BS.gt,
                                       probs = c(0, 0.025, 0.5, 0.975, 1),
                                       model = "RAW")
knitr::kable(
  dA.gt$within[order(dA.gt$within$mean, decreasing = TRUE), -1],
  # format = "html",
  caption = "Nucleotide divergence within each region"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
knitr::kable(
  dA.gt$between[order(dA.gt$between$mean, decreasing = TRUE), -1],
```

```
  # format = "html",
  caption = "Nucleotide divergence between each region"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE, font_size = 5)



hapcount <- pegas::haploFreq(BS.dna@sequence, fac = BS.gt@schemes$Region,
                             split = NULL, what = 1, haplo = NULL)
row.names(hapcount) <- paste0("HT", sprintf('%0.2d', 1:BS.hap@nhap))

kableExtra::kbl(hapcount,
  caption = "Haplotype counts per region according to pegas",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))

group.levels <- levels(BS.gi$other$ind.meta$Region)
group.names <- BS.gi$other$ind.meta$Region

HTs <- paste0("HT", sprintf('%0.3d', 1:BS.hap@nhap))
df <- data.frame(group = NULL,nind = NULL, hap = NULL, nhap = NULL,
                 hapfreq = NULL, stringsAsFactors = FALSE)
for (k in 1:length(group.levels)) {
  group.inds <- adegenet::indNames(BS.gi)[group.names == group.levels[k]]
  for (i in 1:BS.hap@nhap) {
    group <- group.levels[k]
    nind <- length(group.inds)
    hap <- HTs[i]
    nhap <- sum(group.inds %in% BS.hap@haplist[[i]])
    hapfreq <- nhap/nind
    df <- plyr::rbind.fill(df, data.frame(group = group, nind = nind, hap = hap,
                                          nhap = nhap, hapfreq = hapfreq,
                                          stringsAsFactors = FALSE))
  }
}
df$group <- factor(df$group, levels = group.levels)

haplotype.labels <- unique(df$hap)
haplotype.labels2 <- haplotype.labels[seq(1, length(haplotype.labels), by = 5)]

HT.plot <- ggplot2::ggplot(data = df) +
  ggplot2::geom_bar(ggplot2::aes(x = hap, y = nhap, fill = group),
                    stat = "identity", position = "stack") +
  ggplot2::labs(x = "Haplotypes", y = "Number of individuals") +
  ggplot2::scale_fill_manual(values = colours.8) +
  ggplot2::scale_x_discrete(breaks = haplotype.labels2) +
  ggplot2::theme(
      axis.text = ggplot2::element_text(angle = 45, hjust = 1, size = 5),
      axis.title.x = ggplot2::element_text(size = 10),
      axis.title.y = ggplot2::element_text(size = 10),
      legend.text = ggplot2::element_text(size = 7))
print(HT.plot)
```

Table 62: Nucleotide and haplotype diversity per region

	Region	pi.strataG	pi.pegas	pi.pegas.var	HT.richness.strataG	h.pegas	h.pegas.var
1	E-PAC	0.000274	0.000274	0e+00	10	0.925000	0.001807
11	E-ATL	NaN	NaN	NaN	1	NaN	NaN
12	IWP	0.002089	0.002090	1e-06	142	0.987349	0.000003
13	Japan	0.000389	0.000389	0e+00	4	0.690323	0.001877
14	Fiji	NaN	0.001374	1e-06	8	0.972222	0.002578



```
ggplot2::ggsave(HT.plot, filename = "HT_barplot_per_Region.png", width = 30,
                height = 15, units = "cm")
```

```
## [1] "E-PAC"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3151545 0.2423992 0.1307560 0.3116903
## [1] "E-ATL"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145576 0.2423680 0.1312702 0.3118041
## [1] "IWP"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3145866 0.2430667 0.1311699 0.3111767
## [1] "Japan"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146686 0.2430748 0.1311079 0.3111486
## [1] "Fiji"
## [1] "Mitogenome base composition:"
##         A         T         G         C
## 0.3146038 0.2429049 0.1311531 0.3113381
```

Table 63: Nucleotide divergence within each region

	stratum	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
4	IWP	0.0020900	0	5.99e-05	0.0008982	0.0058084	0.0061078
3	Fiji	0.0013739	0	0.00e+00	0.0002395	0.0055090	0.0055090
5	Japan	0.0003894	0	0.00e+00	0.0000000	0.0010778	0.0010778
2	E-PAC	0.0002740	0	0.00e+00	0.0002994	0.0004192	0.0004192
1	E-ATL	NA	NA	NA	NA	NA	NA

Table 64: Nucleotide divergence between each region

	strata.1	strata.2	dA	mean	q.0	q.0.025	q.0.5	q.0.975	q.1
7	E-PAC	Japan	0.0086961	0.0090278	0.0089222	0.0089222	0.0090419	0.0091617	0.0091617
5	E-PAC	Fiji	0.0081569	0.0089808	0.0088623	0.0088623	0.0089820	0.0090419	0.0090419
6	E-PAC	IWP	0.0077769	0.0089588	0.0086228	0.0087425	0.0089222	0.0092216	0.0094012
4	E-ATL	Japan	0.0087545	0.0089492	0.0089222	0.0089222	0.0089222	0.0090419	0.0090419
2	E-ATL	Fiji	0.0082152	0.0089022	0.0088623	0.0088623	0.0089222	0.0089222	0.0089222
3	E-ATL	IWP	0.0078560	0.0089009	0.0086228	0.0086826	0.0088623	0.0091617	0.0092814
1	E-ATL	E-PAC	0.0061692	0.0063061	0.0062275	0.0062275	0.0063174	0.0063473	0.0063473
8	Fiji	IWP	0.0002662	0.0019981	0.0000599	0.0002395	0.0008982	0.0056287	0.0057485
10	IWP	Japan	0.0004710	0.0017107	0.0002994	0.0003593	0.0008982	0.0057485	0.0061078
9	Fiji	Japan	0.0005956	0.0014773	0.0008383	0.0008383	0.0009581	0.0054072	0.0057485

Table 65: Haplotype counts per region according to pegas

	E-PAC	E-ATL	W-IO	N-IO	E-IO	W-PAC	Japan	Fiji
HT01	0	0	1	0	0	0	0	0
HT02	0	0	1	0	0	0	0	0
HT03	0	0	1	0	0	0	0	0
HT04	0	0	1	0	0	0	0	0
HT05	0	0	0	3	0	0	0	0
HT06	0	0	0	2	0	0	0	0
HT07	0	0	0	1	0	0	0	0
HT08	0	0	1	0	0	0	0	0
HT09	0	0	1	0	0	0	0	0
HT10	0	0	10	0	0	0	0	0
HT11	0	0	7	0	0	0	0	0
HT12	0	0	0	0	2	0	0	0
HT13	0	0	0	1	0	0	0	0
HT14	0	0	0	1	0	0	0	0
HT15	0	0	6	0	0	0	0	0
HT16	0	0	5	0	0	0	0	0
HT17	0	0	2	0	0	0	0	0
HT18	0	0	4	0	0	0	0	0
HT19	0	0	0	0	0	0	0	1
HT20	0	0	0	1	0	0	0	0
HT21	0	0	0	2	0	0	0	0
HT22	0	0	0	3	0	0	0	0
HT23	0	0	0	0	0	3	0	0
HT24	0	0	0	0	0	4	0	0
HT25	0	0	0	0	1	0	0	0
HT26	0	0	0	0	0	1	0	0
HT27	0	0	0	0	1	0	0	0
HT28	0	0	0	0	1	0	0	0
HT29	0	0	0	0	2	0	0	0
HT30	0	0	0	0	5	0	0	0
HT31	0	0	0	0	3	0	0	0
HT32	0	0	0	0	1	0	0	0
HT33	0	0	0	0	1	0	0	0
HT34	0	0	0	0	7	0	0	0
HT35	0	0	0	0	1	0	0	0
HT36	0	0	0	0	3	0	0	0
HT37	0	0	0	0	2	0	0	0
HT38	0	0	0	0	2	0	0	0
HT39	0	0	0	0	2	0	0	0
HT40	0	0	0	0	2	0	0	0
HT41	0	0	0	0	1	0	0	0
HT42	0	0	0	0	1	0	0	0
HT43	0	0	0	0	1	0	0	0
HT44	0	0	0	0	5	0	0	0
HT45	0	0	0	0	4	0	0	0
HT46	0	0	0	0	9	0	0	0
HT47	0	0	0	0	1	0	0	0
HT48	0	0	0	0	1	0	0	0
HT49	0	0	0	0	1	0	0	0
HT50	0	0	0	0	12	0	0	0
HT51	0	0	0	0	7	0	0	0
HT52	0	0	0	0	1	0	0	0
HT53	0	0	0	0	1	0	0	0
HT54	0	0	0	0	1	0	0	0
HT55	0	0	0	0	19	0	0	0
HT56	0	0	0	0	7	1	0	0
HT57	0	0	0	0	1	0	0	0
HT58	0	0	0	0	1	0	0	0

Table 65: Haplotype counts per region according to pegas *(continued)*

	E-PAC	E-ATL	W-IO	N-IO	E-IO	W-PAC	Japan	Fiji
HT59	0	0	0	0	1	0	0	0
HT60	0	0	0	0	2	0	0	0
HT61	0	0	0	0	1	0	0	0
HT62	0	0	0	0	1	0	0	0
HT63	0	0	0	0	1	0	0	0
HT64	0	0	0	1	0	0	0	0
HT65	0	0	0	1	0	0	0	0
HT66	0	0	0	0	1	0	0	0
HT67	0	0	0	1	0	0	0	0
HT68	0	0	0	0	3	0	0	0
HT69	0	0	0	2	0	0	0	0
HT70	0	0	0	1	0	0	0	0
HT71	0	0	0	1	0	0	0	0
HT72	0	0	0	1	0	0	0	0
HT73	0	0	0	1	0	0	0	0
HT74	0	0	0	0	1	0	0	0
HT75	0	0	0	0	1	0	0	0
HT76	0	0	0	0	1	0	0	0
HT77	0	0	0	0	5	0	0	0
HT78	0	0	0	1	0	0	0	0
HT79	0	0	0	4	0	0	0	0
HT80	0	0	0	1	0	0	0	0
HT81	0	0	0	0	1	0	0	0
HT82	0	0	0	0	1	0	0	0
HT83	0	0	0	1	0	0	0	0
HT84	0	0	0	0	0	1	0	0
HT85	0	0	0	0	0	3	0	0
HT86	0	0	0	0	0	3	0	0
HT87	0	0	0	0	0	2	0	0
HT88	0	0	0	0	0	1	0	0
HT89	0	0	0	0	0	0	0	1
HT90	0	0	0	0	0	0	0	1
HT91	0	0	0	0	0	0	0	1
HT92	0	0	0	0	0	1	0	0
HT93	0	0	0	0	0	4	0	0
HT94	0	0	0	0	0	3	0	0
HT95	0	0	0	0	0	1	0	0
HT96	0	0	0	0	0	1	0	0
HT97	0	0	0	0	0	0	0	1
HT98	0	0	0	0	0	0	0	2
HT99	0	0	0	0	0	0	0	1
HT100	0	0	0	0	0	0	0	1
HT101	0	0	0	0	1	0	0	0
HT102	0	0	0	0	2	0	0	0
HT103	0	0	0	0	1	0	0	0
HT104	0	0	0	0	1	0	0	0
HT105	0	0	0	0	5	0	0	0
HT106	0	0	0	0	2	0	0	0
HT107	0	0	0	0	0	1	0	0
HT108	0	0	1	0	0	0	0	0
HT109	0	0	0	0	0	1	0	0
HT110	0	0	0	0	1	0	0	0
HT111	0	0	0	0	1	0	0	0
HT112	0	0	0	0	0	1	0	0
HT113	0	0	0	0	1	0	0	0
HT114	0	0	0	0	1	0	0	0
HT115	0	0	0	0	2	0	0	0
HT116	0	0	0	0	2	0	0	0
HT117	0	0	0	0	0	3	0	0
HT118	0	0	0	0	0	1	0	0
HT119	0	0	0	0	1	0	0	0
HT120	0	0	0	0	1	0	0	0
HT121	0	0	0	0	0	1	0	0
HT122	0	0	0	0	1	0	0	0
HT123	0	0	0	0	1	0	0	0
HT124	0	0	0	0	0	0	5	0
HT125	0	0	0	0	0	0	2	0
HT126	0	0	0	0	1	0	0	0
HT127	0	0	0	0	5	0	0	0
HT128	0	0	0	0	4	0	0	0
HT129	0	0	0	0	1	0	0	0
HT130	0	0	0	0	1	0	0	0
HT131	0	0	0	0	1	0	0	0
HT132	0	0	0	0	1	0	0	0
HT133	0	0	0	1	0	0	0	0
HT134	0	0	0	0	1	0	0	0
HT135	0	0	0	0	1	0	0	0
HT136	0	0	0	0	3	0	0	0
HT137	0	0	0	2	1	0	0	0
HT138	0	0	0	1	0	0	0	0
HT139	0	0	0	0	1	0	0	0
HT140	0	0	0	1	0	0	0	0
HT141	0	0	0	1	0	0	0	0
HT142	0	0	0	0	1	0	0	0

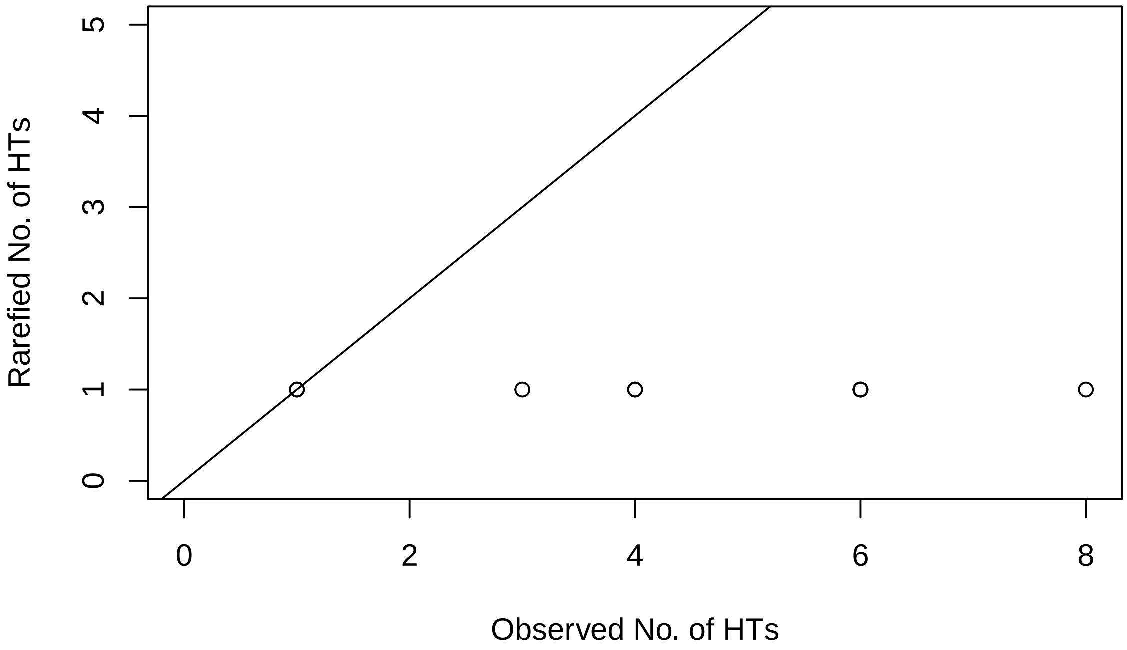
Table 65: Haplotype counts per region according to pegas *(continued)*

	E-PAC	E-ATL	W-IO	N-IO	E-IO	W-PAC	Japan	Fiji
HT143	0	0	0	0	1	0	0	0
HT144	0	0	0	0	1	0	0	0
HT145	0	0	0	0	1	0	0	0
HT146	0	0	0	0	1	0	0	0
HT147	0	0	0	0	0	1	0	0
HT148	0	0	0	0	1	0	0	0
HT149	0	0	0	0	1	0	0	0
HT150	0	0	0	0	3	0	0	0
HT151	0	0	0	0	1	0	0	0
HT152	0	0	0	0	0	0	11	0
HT153	0	0	0	0	0	0	13	0
HT154	0	0	0	1	0	0	0	0
HT155	4	0	0	0	0	0	0	0
HT156	2	0	0	0	0	0	0	0
HT157	1	0	0	0	0	0	0	0
HT158	2	0	0	0	0	0	0	0
HT159	1	0	0	0	0	0	0	0
HT160	1	0	0	0	0	0	0	0
HT161	1	0	0	0	0	0	0	0
HT162	1	0	0	0	0	0	0	0
HT163	2	0	0	0	0	0	0	0
HT164	1	0	0	0	0	0	0	0
HT165	0	1	0	0	0	0	0	0

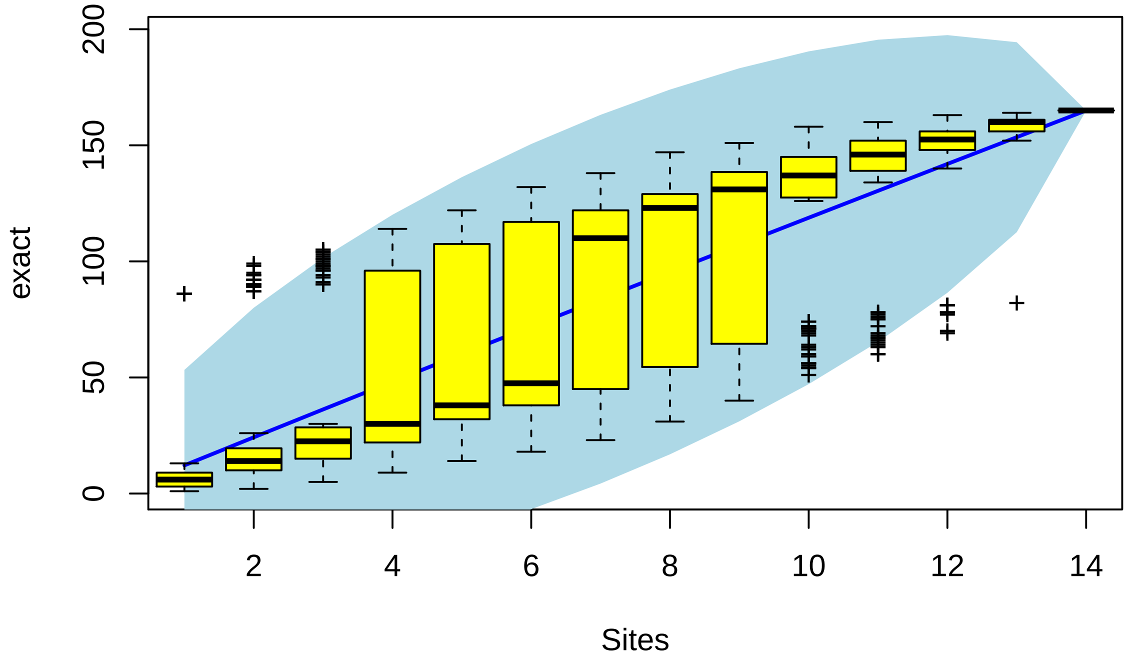
13.4 Haplotype network

13.4.1 Rarefaction

```
hapcount <- pegas::haploFreq(BS.dna@sequence, fac = BS.gt@schemes$Site,
                             split = NULL, what = 1, haplo = NULL)
BCI <- t(hapcount)

S <- vegan::specnumber(BCI) ## observed number of HTs
(raremax <- min(rowSums(BCI)))
Srare <- vegan::rarefy(BCI, raremax, se = FALSE)

plot(S, Srare, xlab = "Observed No. of HTs", ylab = "Rarefied No. of HTs",
     xlim = c(0,8),ylim = c(0,5))
abline(0, 1)
```



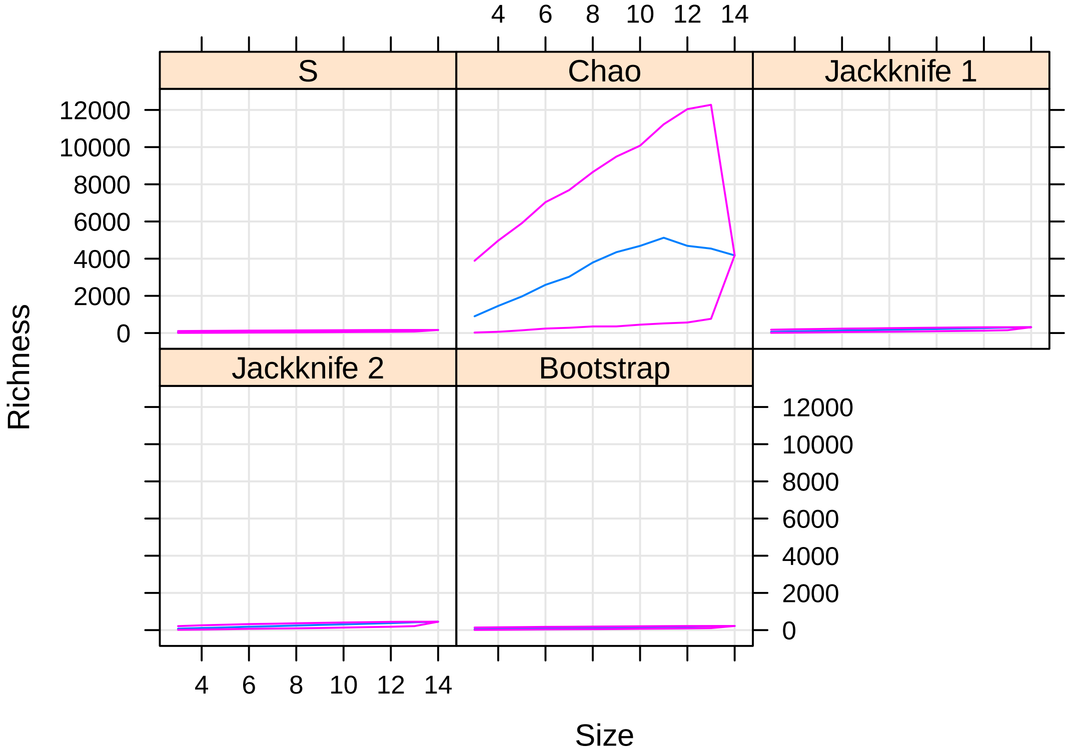
```
# vegan::rarecurve(BCI, step = 5, sample = raremax, col = "blue", cex = 0.6)

## HT accumulation curve based on observed HTs
sp1 <- vegan::specaccum(BCI)
sp2 <- vegan::specaccum(BCI, "random")
plot(sp1, ci.type = "poly", col = "blue", lwd = 2, ci.lty = 0,
     ci.col = "lightblue")
boxplot(sp2, col = "yellow", add = TRUE, pch = "+")
```



```r
## Extrapolated HT richness based on unobserved HTs
pool <- vegan::poolaccum(BCI)
knitr::kable(pool$means,
             # format = "html",
             caption = "Observed and extrapolated HT richness based on resampling") %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
plot(pool)
```

Table 66: Observed and extrapolated HT richness based on resampling

N	S	Chao	Jackknife 1	Jackknife 2	Bootstrap
3	38.53	907.120	64.08333	76.82833	49.89407
4	50.61	1466.492	88.30500	113.32167	66.53387
5	60.89	1987.694	109.14600	145.09950	80.69728
6	74.24	2619.667	135.33167	183.74100	98.86869
7	83.42	3050.469	153.93714	212.07048	111.48729
8	95.70	3860.636	178.16000	248.01714	128.21404
9	107.10	4479.339	200.70000	281.56556	143.74568
10	116.44	4786.255	219.26500	309.37078	156.48238
11	128.68	5240.840	243.35273	345.08545	173.12754
12	140.01	4773.671	265.47417	377.63098	188.48911
13	154.95	4540.759	294.63923	420.50814	208.75565
14	165.00	4176.583	314.50000	450.12637	222.42879



```
## [1] 1
```

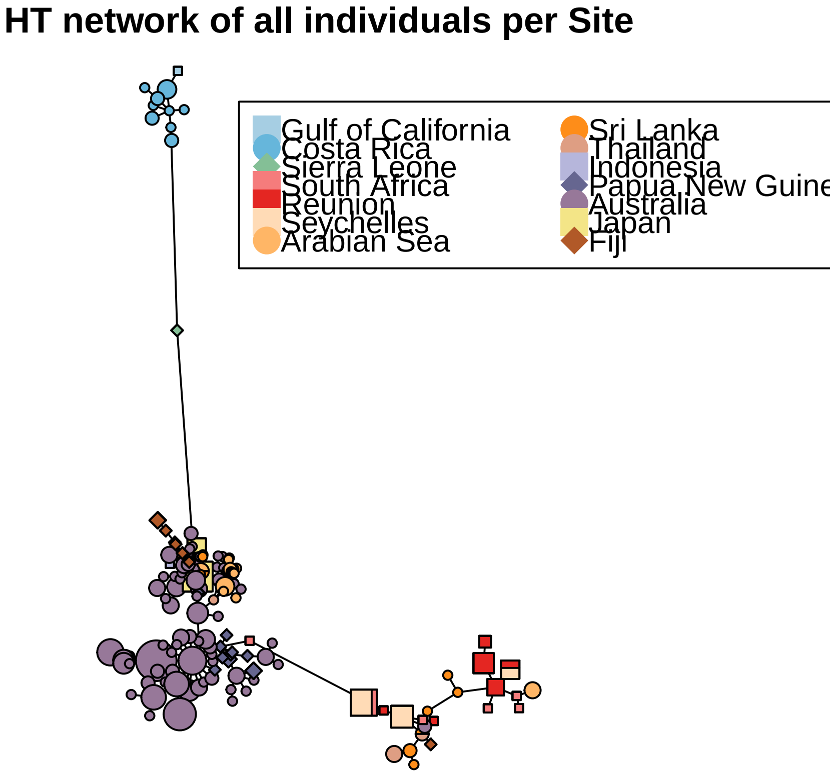
13.4.2 Network

13.4.2.1 Global

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

net <- pegas::haploNet(BS.h)
ind.hap <- with(
    stack(setNames(attr(BS.h, "index"), rownames(BS.h))),
    table(hap = ind, pop = strata[values]))

size.new <- attr(net, "freq")
size.new <- sqrt(size.new)
```

```
# colours.14 <- adegenet::funky(14)
colours.14 <- c("#a6cee3", "#66b6db", "#84bf96", "#f57c7c", "#e42622",  "#ffdbb6",
                "#ffb666", "#fe8d19", "#de9e83", "#b6b6db", "#666690", "#977899",
                "#f3e587", "#b15928")

names(colours.14) <- c("Gulf of California","Costa Rica", "Sierra Leone",
                       "South Africa","Reunion","Seychelles","Arabian Sea",
                       "Sri Lanka","Thailand","Indonesia","Papua New Guinea",
                       "Australia","Japan","Fiji")
colours.14.new <- colours.14[order(names(colours.14))]


#### SHAPES #####
df <- as.data.frame(ind.hap)
df2 <- select(df, hap, pop, Freq) %>%
  reshape(., idvar = "hap", timevar = "pop", direction = "wide")
df.rownames <- df2$hap
row.names(df2) <- df.rownames
df2$hap <- NULL
df2 <- sapply(df2, as.integer)
row.names(df2) <- df.rownames
colnames(df2) <- stringr::str_replace_all(string = colnames(df2),
                                          pattern = "Freq.", replacement = "")
res <- colnames(df2)[max.col(df2)]
res2 <- data.frame(HT = row.names(df2), site = res)
res3 <- res2[order(res2$HT),]
shape <- res3$site

tes <- rowSums(df2 > 0)
tes2 <- df2[tes > 1,]
# tes2[,colSums(as.data.frame(tes2) > 0) > 0]

#       Arabian Sea Australia Reunion Seychelles South Africa Sri Lanka Thailand
# HT106           1         1       0          0            0         1        0
# HT139           0         0       2          3            0         0        0
# HT145           0         0       0          0            0         1        1
# HT153           0         0       0          8            2         0        0

shape[shape == "Gulf of California"] <- "square"
shape[shape == "Costa Rica"] <- "circle"
shape[shape == "Sierra Leone"] <- "diamond"
shape[shape == "South Africa"] <- "square"
shape[shape == "Reunion"] <- "square"
shape[shape == "Seychelles"] <- "square"
shape[shape == "Arabian Sea"] <- "circle"
shape[shape == "Sri Lanka"] <- "circle"
shape[shape == "Thailand"] <- "circle"
shape[shape == "Indonesia"] <- "square"
shape[shape == "Papua New Guinea"] <- "diamond"
shape[shape == "Australia"] <- "circle"
shape[shape == "Japan"] <- "square"
shape[shape == "Fiji"] <- "diamond"

names(shape) <- res3$site
shape.leg <- shape[unique(names(shape))]
shape.leg <- shape.leg[order(match(names(shape.leg), names(colours.14)))]
shape.leg[shape.leg == "circle"] <- 16
```

```
shape.leg[shape.leg == "square"] <- 15
shape.leg[shape.leg == "diamond"] <- 18
shape.leg2 <- shape.leg[order(names(shape.leg))]


par(mar = c(1,1,1,1))
plot(net, size = size.new, scale.ratio = 0.2, pie = ind.hap, labels = FALSE,
     shape = shape,
     show.mutation = 0,threshold = 0,  srt = 1, cex = 0.75, bg = colours.14.new)
# legend(5, 60, names(colours.14), col = colours.14, pch = 19, ncol = 2,
#        x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
legend(5, 60, names(colours.14), col = colours.14, pch = as.numeric(shape.leg),
       ncol = 2, x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
title(paste0("HT network of all individuals per Site"))
```

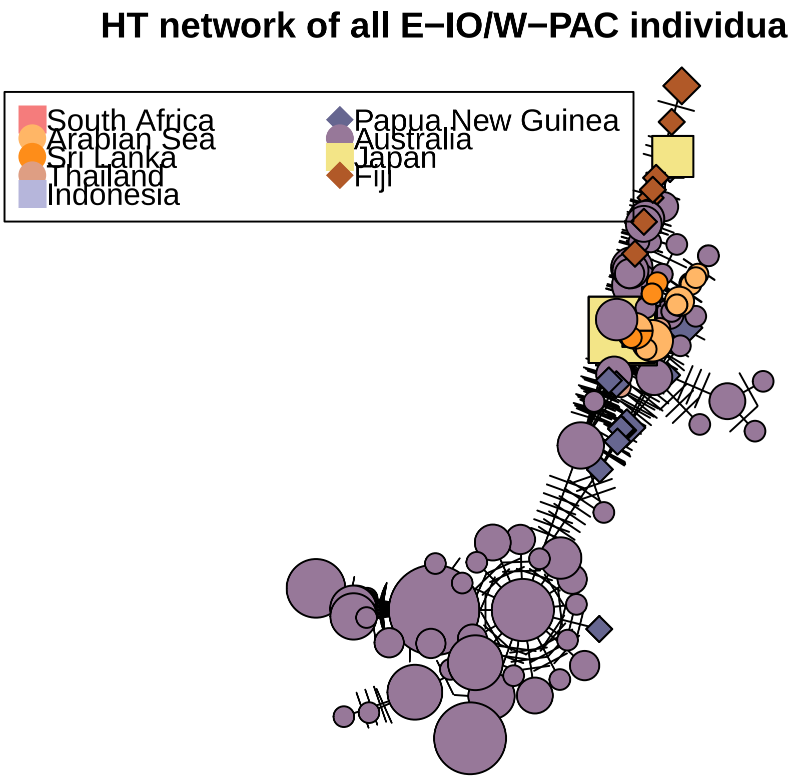


13.4.2.1.1 Per Site

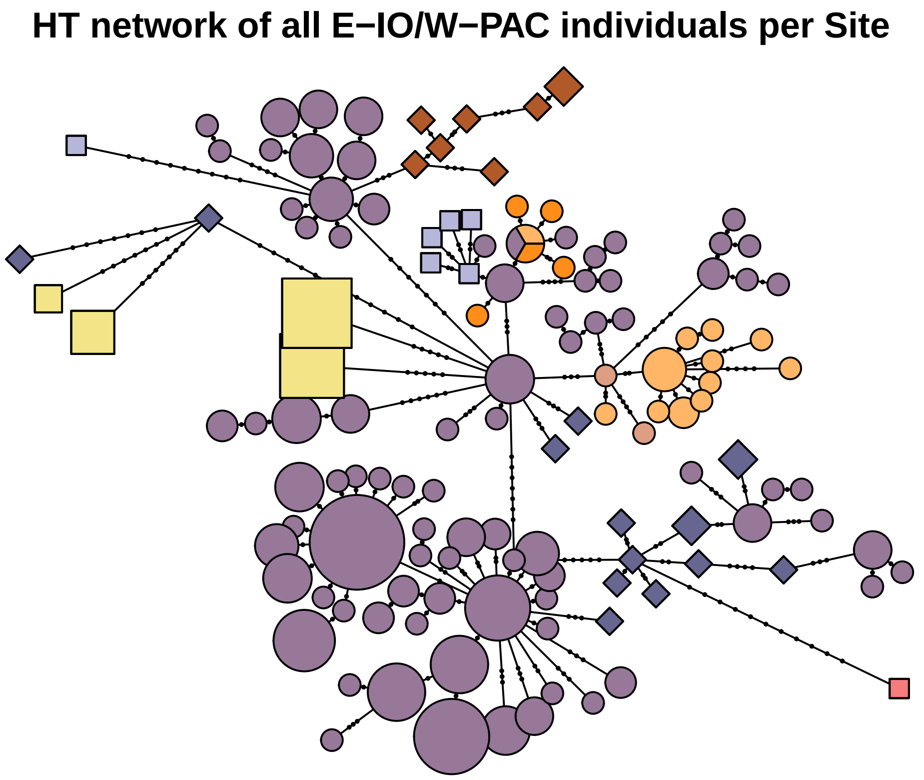
```
dev.print(
device = png,
file = "Global_per_Site_HT_network2.png",
res = 600,
width = 30,
height = 30,
units = "cm")



# xy <- replot()
# plot(net, xy = xy, size = size.new, scale.ratio = 0.2, pie = ind.hap,
#      labels = FALSE,
#      shape = shape,
#      show.mutation = 0,threshold = 0,  srt = 1, cex = 0.75, bg = colours.14.new)
# # legend(5, 60, names(colours.14), col = colours.14, pch = 19, ncol = 2,
```

```
# #        x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
# legend(5, 60, names(colours.14), col = colours.14, pch = as.numeric(shape.leg),
#        ncol = 2, x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
# title(paste0("HT network of all individuals per Site"))
#
#
# dev.print(
# device = png,
# file = "Global_per_Site_HT_network3.png",
# res = 600,
# width = 30,
# height = 30,
# units = "cm")

################################################################
clust.names <- unlist(BS.hap@haplist[1:132])
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata
BS.gt.clust <- BS.gt[clust.names,,, drop = TRUE]

schemes.clust  <- BS.gt.clust@schemes[BS.gt.clust@schemes$id %in% clust.names,]
strata <- as.character(schemes.clust$Site)
names(strata) <- as.character(schemes.clust$id)
strataG::setStrata(BS.gt.clust) <- strata

ind.names <- names(BS.dna) %in% BS.gt.clust@data$id
BS.dna.clust <- as.dna(BS.dna[ind.names, , drop = TRUE])
BS.bin.clust <- subset(BS.bin, names(BS.bin) %in% BS.gt.clust@data$id)
BS.haps <- strataG::labelHaplotypes(BS.bin.clust, prefix = "HT",
                                    use.indels = TRUE)
haps <- BS.haps$haps
BS.hap.clust <- haplotypes::haplotype(BS.dna.clust,indels = "sic")


HTs <- unique(haps[names(haps) %in% names(BS.bin.clust)])
BS.h.clust <- pegas::haplotype(BS.bin.clust, HTs)

net <- pegas::haploNet(BS.h.clust)
ind.hap <- with(
    stack(setNames(attr(BS.h.clust, "index"), rownames(BS.h.clust))),
    table(hap = ind, pop = strata[values]))

size.new <- attr(net, "freq")
size.new <- sqrt(size.new)


colours <- colours.14[-c(1:3,5,6)]
colours.new <- colours[order(names(colours))]


### SHAPES
df <- as.data.frame(ind.hap)
df2 <- select(df, hap, pop, Freq) %>%
  reshape(., idvar = "hap", timevar = "pop", direction = "wide")
df.rownames <- df2$hap
row.names(df2) <- df.rownames
```

```r
df2$hap <- NULL
df2 <- sapply(df2, as.integer)
row.names(df2) <- df.rownames
colnames(df2) <- stringr::str_replace_all(string = colnames(df2),
                                          pattern = "Freq.", replacement = "")
res <- colnames(df2)[max.col(df2)]
res2 <- data.frame(HT = row.names(df2), site = res)
res3 <- res2[order(res2$HT),]
shape <- res2$site

tes <- rowSums(df2 > 0)
tes2 <- df2[tes > 1,]
#       Arabian Sea        Australia         Sri Lanka
#HT026      1                1                1

shape[shape == "South Africa"] <- "square"
shape[shape == "Arabian Sea"] <- "circle"
shape[shape == "Sri Lanka"] <- "circle"
shape[shape == "Thailand"] <- "circle"
shape[shape == "Indonesia"] <- "square"
shape[shape == "Papua New Guinea"] <- "diamond"
shape[shape == "Australia"] <- "circle"
shape[shape == "Japan"] <- "square"
shape[shape == "Fiji"] <- "diamond"


names(shape) <- res2$site
shape.leg <- shape[unique(names(shape))]
shape.leg <- shape.leg[order(match(names(shape.leg), names(colours)))]
shape.leg[shape.leg == "circle"] <- 16
shape.leg[shape.leg == "square"] <- 15
shape.leg[shape.leg == "diamond"] <- 18



par(mar = c(1,1,1,1))
plot(net, size = size.new, scale.ratio = 0.6, pie = ind.hap, labels = FALSE,
     asp = 1, shape = shape,
     show.mutation = 1,threshold = 0,  srt = 1, cex = 0.75, bg = colours.new,
     fast = FALSE)
# legend(-40, 70, names(colours), col = colours, pch = 19, ncol = 2,
#        x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
legend(-25, 25, names(colours), col = colours, pch = as.numeric(shape.leg),
       ncol = 2, x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
title(paste0("HT network of all E-IO/W-PAC individuals per Site"))
```



```r
dev.print(
device = png,
file = "E-IO-W-PAC_cluster_HT_network.png",
res = 600,
width = 30,
height = 30,
units = "cm")


# xy <- replot()
# save(xy, file = "HT_network_replot_by_E-IO_cluster.Rdata")
load("HT_network_replot_by_E-IO_cluster.Rdata")
par(mar = c(1,1,1,1))
plot(net, xy = xy, size = size.new, scale.ratio = 0.2, pie = ind.hap,
     labels = FALSE, asp = 1, shape = shape,
     show.mutation = 2,threshold = 0,  srt = 1, cex = 0.75, bg = colours.new,
     fast = FALSE)
# legend(-40, 70, names(colours), col = colours, pch = 19, ncol = 2,
#        x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
# legend(-20, 35, names(colours), col = colours, pch = as.numeric(shape.leg),
#        ncol = 2, x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
title(paste0("HT network of all E-IO/W-PAC individuals per Site"))
```



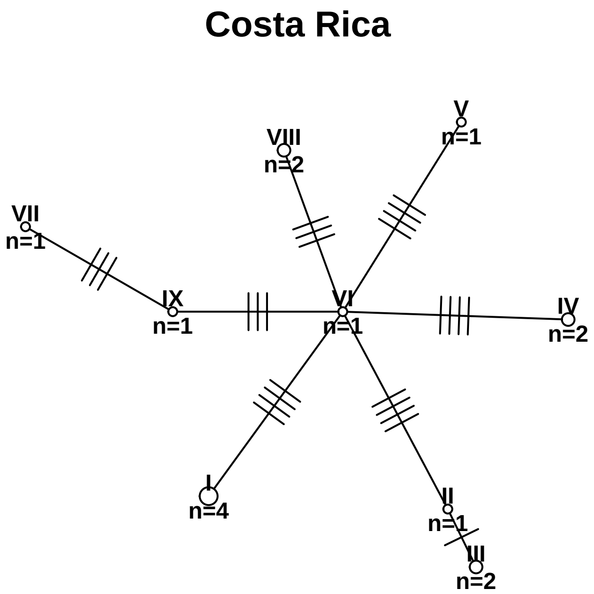
```
dev.print(
device = png,
file = "E-IO-W-PAC_cluster_HT_network3.png",
res = 600,
width = 30,
height = 30,
units = "cm")
```

```
## pdf
##   2
## pdf
##   2
## pdf
##   2
```

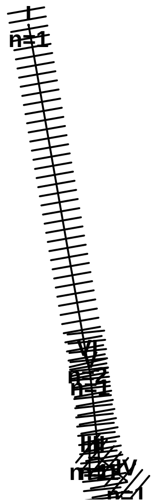
HT network per Site

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

BS.haps <- strataG::labelHaplotypes(BS.bin, prefix = "HT", use.indels = FALSE)
haps <- BS.haps$haps

for (Site in levels(BS.gt@schemes$Site)) {
  BS.gt.sub <- BS.gt[,,Site, drop = TRUE]
  if (length(BS.gt.sub@data$id) > 1) {
    ind.names <- names(BS.dna) %in% BS.gt.sub@data$id
    BS.dna.sub <- as.dna(BS.dna[ind.names, , drop = TRUE])
    BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)

    HTs <- unique(haps[names(haps) %in% names(BS.bin.sub)])
    BS.h.sub <- pegas::haplotype(BS.bin.sub)
```

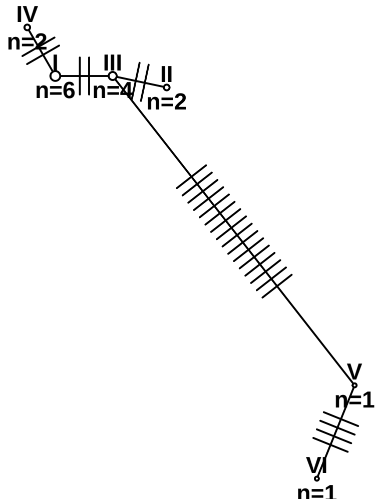
```
    BS.h.sub <- sort(BS.h.sub, what = "label")
    net <- pegas::haploNet(BS.h.sub)
    ind.hap <- with(
      stack(setNames(attr(BS.h.sub, "index"), rownames(BS.h.sub))),
      table(hap = ind, pop = BS.gt.sub@data$stratum[values]))

     size.new <- attr(net, "freq")
     size.new <- sqrt(size.new)

    attr(net, "labels") <- paste0(attr(net, "labels"),"\nn=",
                                  attr(net, "freq"))
    plot(net, size = size.new, scale.ratio = 6, pie = NULL,
      show.mutation = 1,threshold = 0,  srt = 1, cex = 0.75)
    title(paste0(Site))
  }
}
```



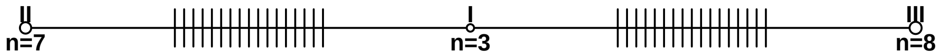
South Africa



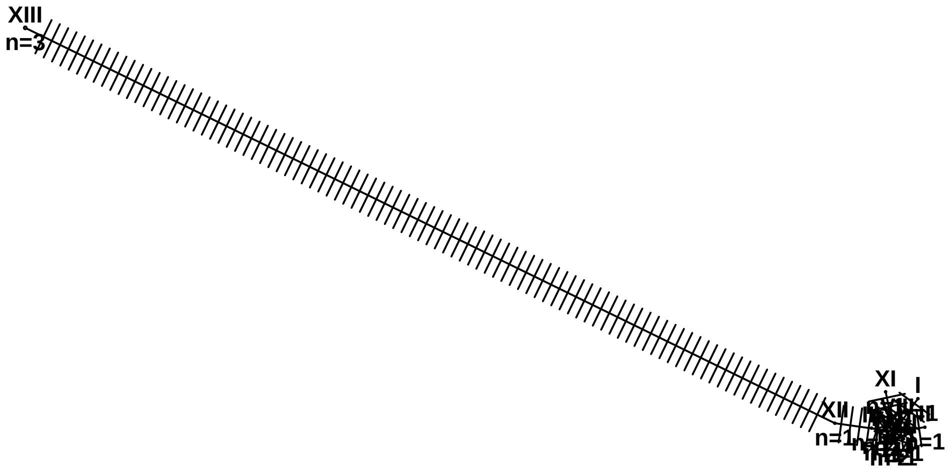
Reunion

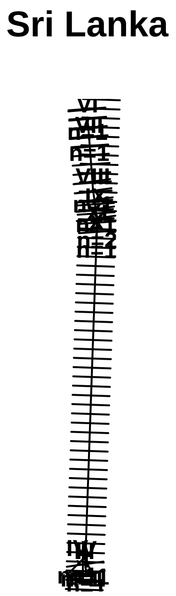


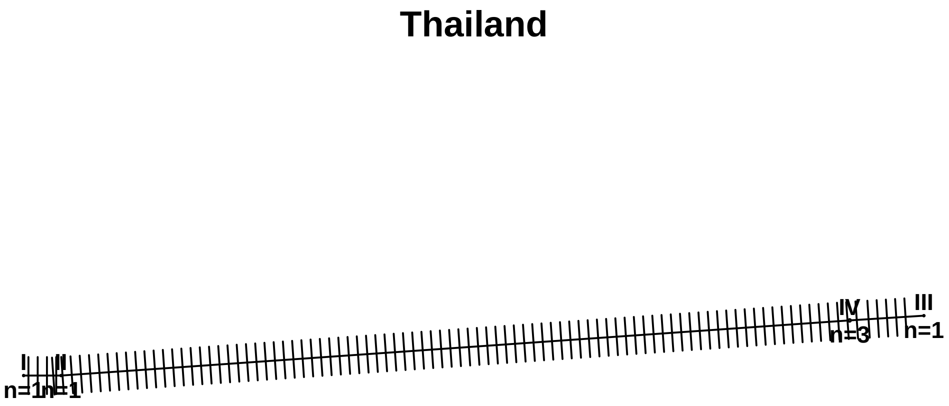
Seychelles



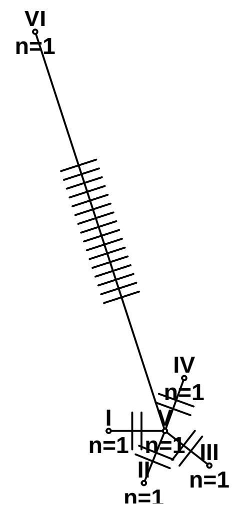
Arabian Sea



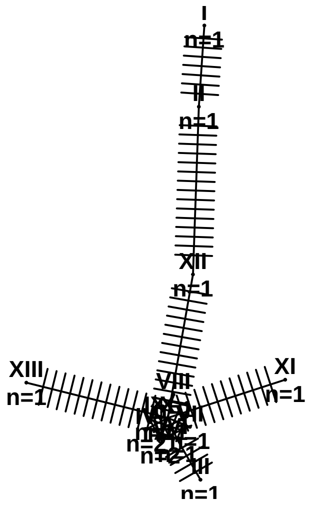

Sri Lanka
VI
VII
n=1
n=1
VIII
IX
n=2
n=1
IV
III


Thailand
I
n=1
II
n=1
IV
n=3
III
n=1

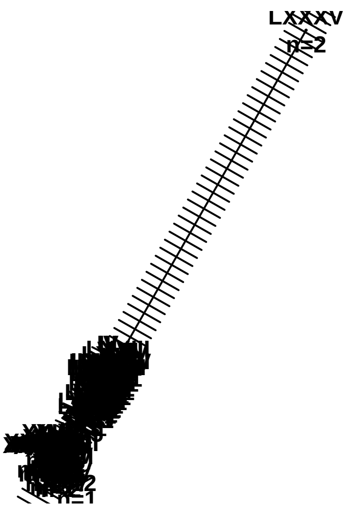
Indonesia



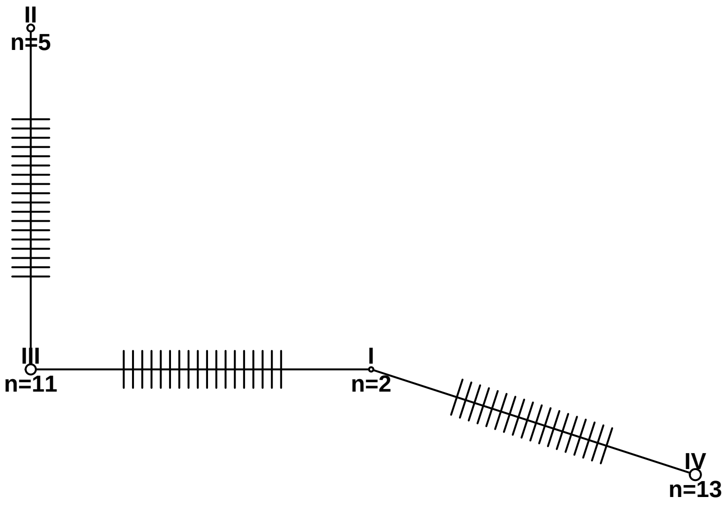
Papua New Guinea

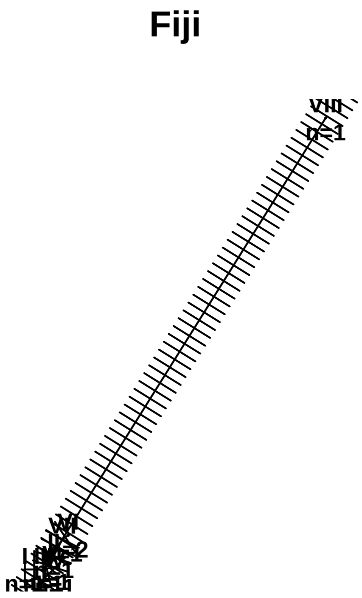


Australia

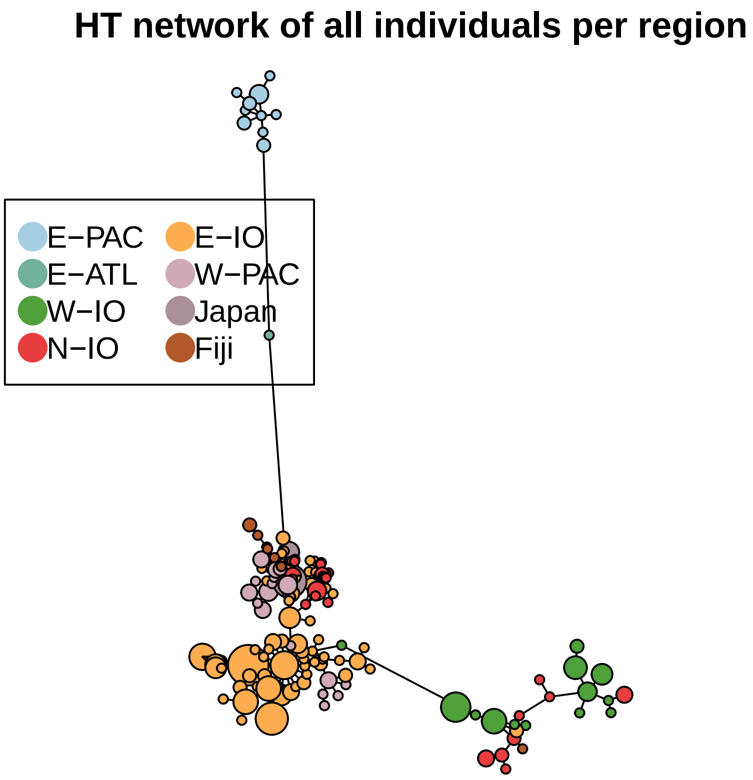


Japan





```
strata <- as.character(BS.gt@schemes$Region)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

net <- pegas::haploNet(BS.h)
ind.hap <- with(
    stack(setNames(attr(BS.h, "index"), rownames(BS.h))),
    table(hap = ind, pop = BS.gt@schemes$Region[values]))

size.new <- attr(net, "freq")
size.new <- sqrt(size.new)
colours.8.new <- colours.8[order(names(colours.8))]
par(mar = c(1,1,1,1))
plot(net, size = size.new, scale.ratio = 0.2, pie = ind.hap, labels = FALSE,
     show.mutation = 0,threshold = 0,  srt = 1, cex = 0.75, bg = colours.8)
legend(-30, 50, names(colours.8), col = colours.8, pch = 19, ncol = 2,
       x.intersp = 0.5, y.intersp = 1, pt.cex = 2)
title(paste0("HT network of all individuals per region"))
```

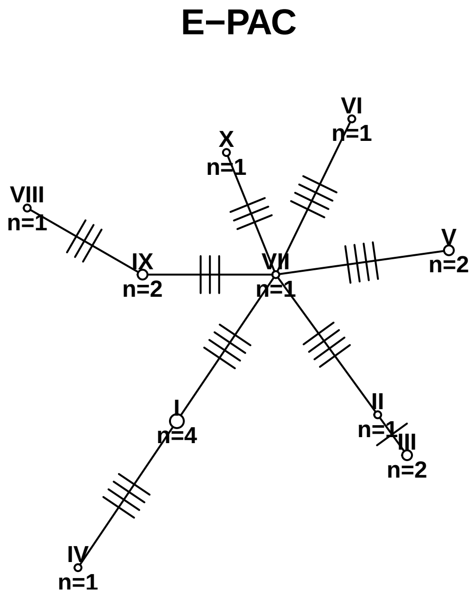


13.4.2.1.2 Per region

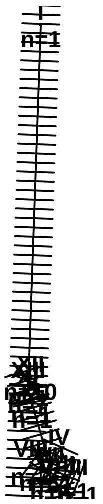
HT network per region

```
strata <- as.character(BS.gt@schemes$Region)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

BS.haps <- strataG::labelHaplotypes(BS.bin, prefix = "HT", use.indels = FALSE)
haps <- BS.haps$haps

for (pop in levels(BS.gt@schemes$Region)) {
  BS.gt.sub <- BS.gt[,,pop, drop = TRUE]
    if (length(BS.gt.sub@data$id) > 1) {
      ind.names <- names(BS.dna) %in% BS.gt.sub@data$id
      BS.dna.sub <- as.dna(BS.dna[ind.names, , drop = TRUE])
      BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)

      HTs <- unique(haps[names(haps) %in% names(BS.bin.sub)])
      # BS.h.sub <- pegas::haplotype(BS.bin.sub, HTs)
      BS.h.sub <- pegas::haplotype(BS.bin.sub)

      BS.h.sub <- sort(BS.h.sub, what = "label")
      net <- pegas::haploNet(BS.h.sub)
      ind.hap <- with(
        stack(setNames(attr(BS.h.sub, "index"), rownames(BS.h.sub))),
        table(hap = ind, pop = BS.gt.sub@data$stratum[values]))

      size.new <- attr(net, "freq")
      size.new <- sqrt(size.new)

      attr(net, "labels") <- paste0(attr(net, "labels"),"\nn=",
                                    attr(net, "freq"))
```

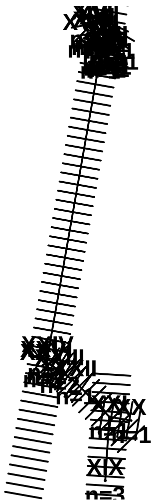
```
      plot(net, size = size.new, scale.ratio = 6, pie = NULL,
        show.mutation = 1,threshold = 0,  srt = 1, cex = 0.75)
      title(paste0(pop))
    }
}
```

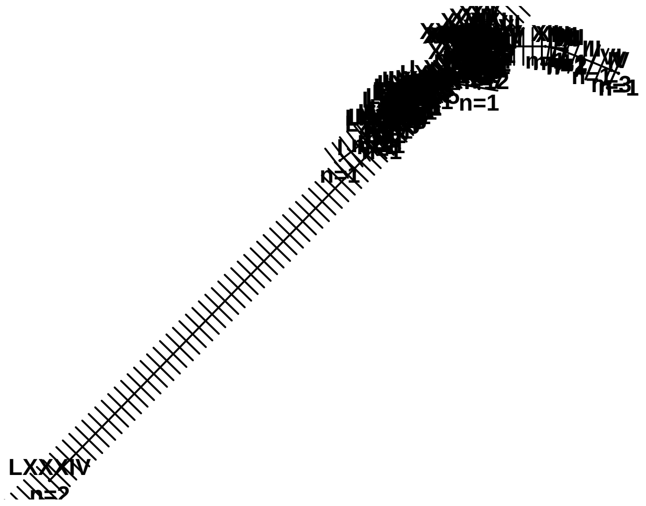


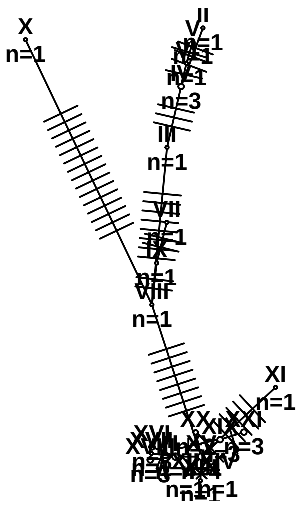
W−IO

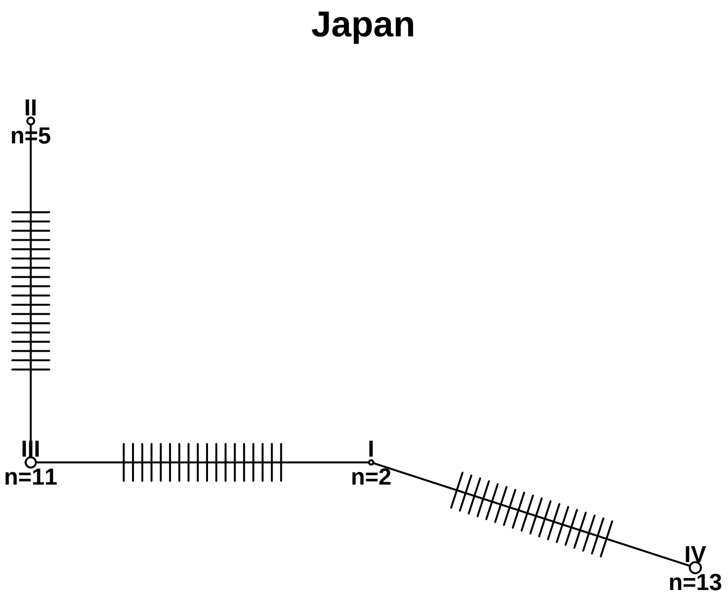


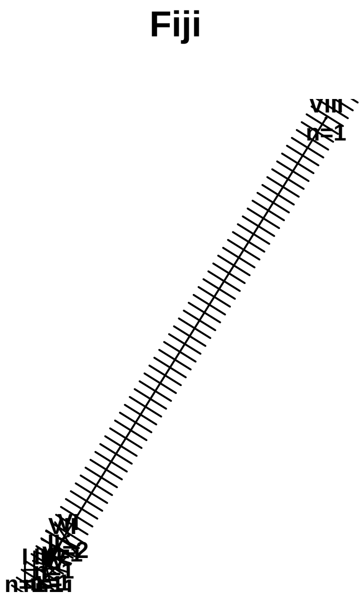
N−IO




E−IO
LXXXIV
n=2
n=1
n=1
n=3
n=1

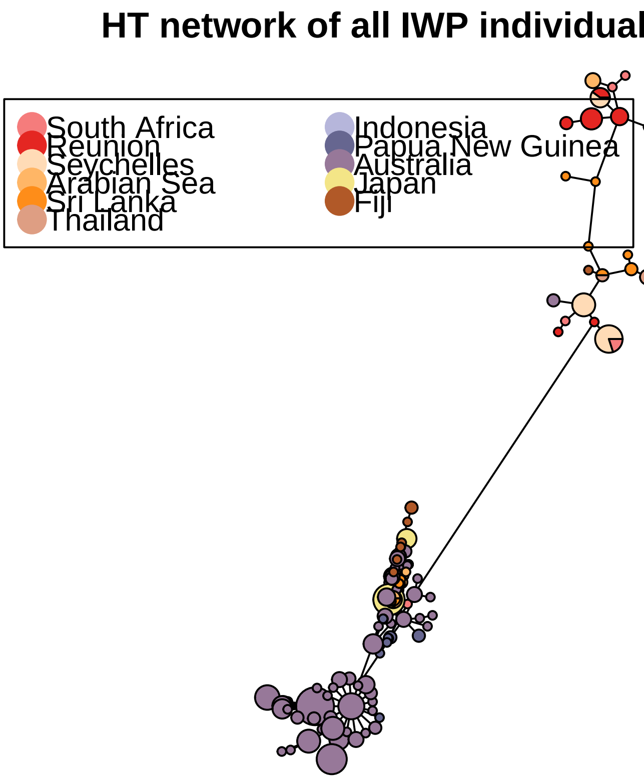

W−PAC
X
n=1
II
V
n=1
n=1
n=3
III
n=1
VII
n=1
IX
n=1
VIII
n=1
XI
n=1
n=3
n=1
n=1





```r
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata
```

```
BS.gt.IO <- BS.gt[BS.gt@schemes$id[!BS.gt@schemes$Site %in%
                                     c("Gulf of California","Costa Rica",
                                       "Sierra Leone")],,, drop = TRUE]


schemes.IO <- BS.gt.IO@schemes[!BS.gt.IO@schemes$Site %in%
                                 c("Gulf of California","Costa Rica", "Sierra Leone"),]
strata <- as.character(schemes.IO$Site)
names(strata) <- as.character(schemes.IO$id)
strataG::setStrata(BS.gt.IO) <- strata

ind.names <- names(BS.dna) %in% BS.gt.IO@data$id
BS.dna.IO <- as.dna(BS.dna[ind.names, , drop = TRUE])
BS.bin.IO <- subset(BS.bin, names(BS.bin) %in% BS.gt.IO@data$id)

BS.haps <- strataG::labelHaplotypes(BS.bin.IO, prefix = "HT", use.indels = TRUE)
haps <- BS.haps$haps

HTs <- unique(haps[names(haps) %in% names(BS.bin.IO)])
BS.h.IO <- pegas::haplotype(BS.bin.IO, HTs)

net <- pegas::haploNet(BS.h.IO)
ind.hap <- with(
    stack(setNames(attr(BS.h.IO, "index"), rownames(BS.h.IO))),
    table(hap = ind, pop = strata[values]))

size.new <- attr(net, "freq")
size.new <- sqrt(size.new)

colours <- colours.14[-c(1:3)]
colours.new <- colours[order(names(colours))]

par(mar = c(1,1,1,1))
plot(net, size = size.new, scale.ratio = 0.5, pie = ind.hap, labels = FALSE, asp = 1,
     show.mutation = 0,threshold = 0,  srt = 1, cex = 0.75, bg = colours.new)
legend(-40, 70, names(colours), col = colours, pch = 19, ncol = 2,
       x.intersp = 0.5, y.intersp = 0.5, pt.cex = 2)
title(paste0("HT network of all IWP individuals per Site"))
```



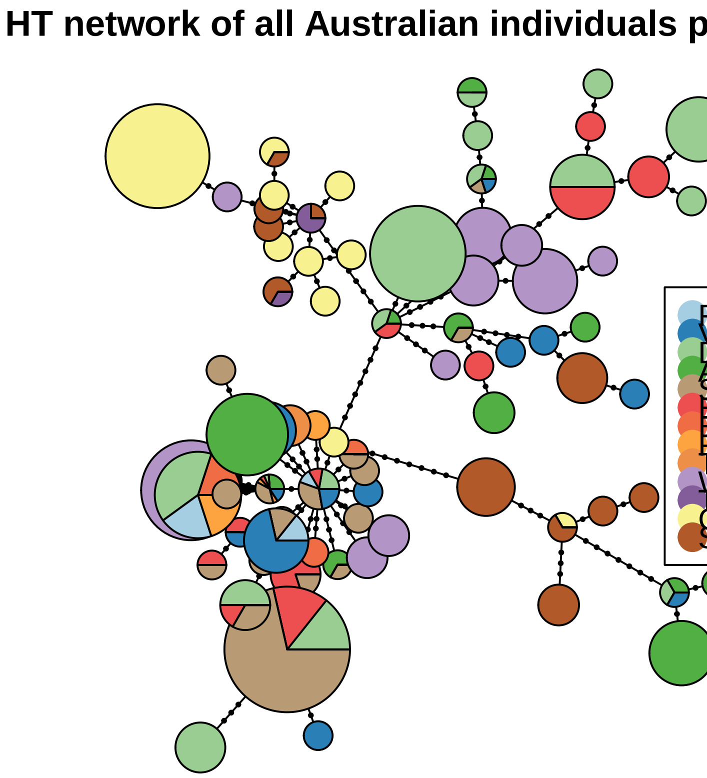
13.4.2.2 Within Indo - West Pacific per Site

```
colours <- colours.27[-c(1:3)]
colours.new <- colours[order(names(colours))]


dev.print(
device = png,
file = "Indian_Ocean_HT_network.png",
res = 600,
width = 30,
height = 30,
units = "cm")
```

```
## pdf
##   2
```

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata
AUS.names <- BS.gt@schemes$id[BS.gt@schemes$Site == "Australia" &
                                !BS.gt@schemes$id %in% c("CLF012",
                                                         "CLF014")] # 2 samples with high divergence
BS.gt.AUS <- BS.gt[AUS.names,,, drop = TRUE]

schemes.AUS <- BS.gt.AUS@schemes[BS.gt.AUS@schemes$id %in% AUS.names,]
strata <- as.character(schemes.AUS$Location)
names(strata) <- as.character(schemes.AUS$id)
strataG::setStrata(BS.gt.AUS) <- strata
BS.gt.AUS@schemes <- schemes.AUS
```

```
ind.names <- names(BS.dna) %in% AUS.names
BS.dna.AUS <- as.dna(BS.dna[ind.names, , drop = TRUE])
BS.bin.AUS <- subset(BS.bin, names(BS.bin) %in% BS.gt.AUS@data$id)
BS.haps <- strataG::labelHaplotypes(BS.bin.AUS, prefix = "HT", use.indels = TRUE)
haps <- BS.haps$haps
HTs <- unique(haps[names(haps) %in% names(BS.bin.AUS)])
BS.h.AUS <- pegas::haplotype(BS.bin.AUS, HTs)

net <- pegas::haploNet(BS.h.AUS)
ind.hap <- with(
    stack(setNames(attr(BS.h.AUS, "index"), rownames(BS.h.AUS))),
    table(hap = ind, pop = strata[values]))

colours.13.new <- colours.13[order(names(colours.13))]

par(mar = c(1,1,1,1))
plot(net, size = size.new, scale.ratio = 0.5, pie = ind.hap, labels = FALSE, asp = 1,
     show.mutation = 2,threshold = 0,  srt = 1, cex = 0.75, bg = colours.13.new)
legend(12, 7, names(colours.13), col = colours.13, pch = 19, ncol = 1,
       x.intersp = 0.2, y.intersp = 0.5, pt.cex = 2)
title(paste0("HT network of all Australian individuals per river"))
```



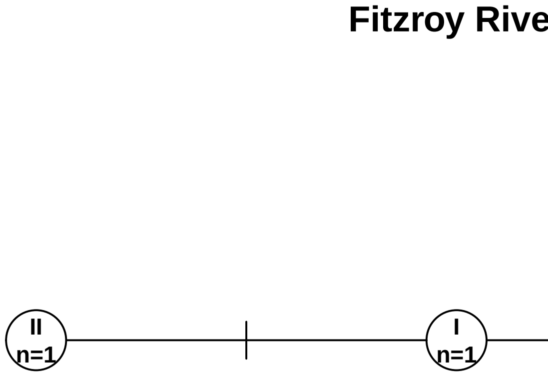
13.4.2.3 Within Australia per River

```
dev.print(
device = png,
file = "Australia_HT_network4.png",
res = 600,
width = 30,
height = 30,
units = "cm")
```

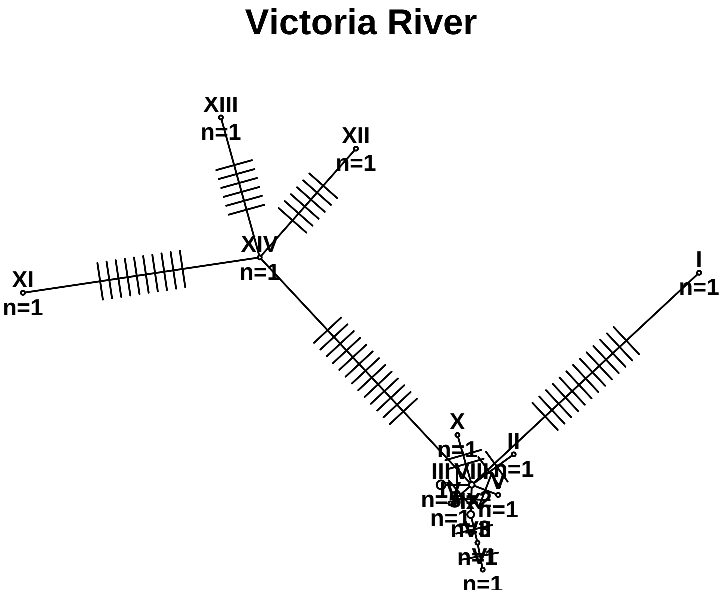
```
## pdf
```

```
##   2
```

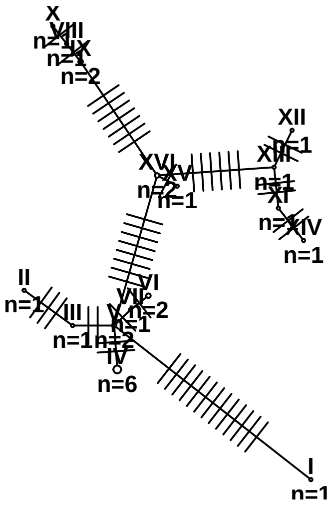
```
strata <- as.character(BS.gt.AUS@schemes$Location)
names(strata) <- as.character(BS.gt.AUS@schemes$id)
strataG::setStrata(BS.gt.AUS) <- strata

pop.levels <- c("Fitzroy River","Victoria River","Daly River",
                "Adelaide River","South Alligator River", "East Alligator River",
                "Blue mud Bay","Roper River","Towns River","Wenlock River",
                "Trinity inlet","Clarence River","Sydney Harbour")
BS.gt.AUS@schemes$Location <- factor(BS.gt.AUS@schemes$Location,
                                     levels = pop.levels)

BS.haps <- strataG::labelHaplotypes(BS.bin.AUS, prefix = "HT",
                                    use.indels = FALSE)
haps <- BS.haps$haps

for (Location in levels(BS.gt.AUS@schemes$Location)) {
  BS.gt.sub <- BS.gt.AUS[,,Location, drop = TRUE]
  if (length(BS.gt.sub@data$id) > 1) {
    ind.names <- names(BS.dna) %in% BS.gt.sub@data$id
    BS.dna.sub <- as.dna(BS.dna[ind.names, , drop = TRUE])
    BS.bin.sub <- subset(BS.bin, names(BS.bin) %in% BS.gt.sub@data$id)

    HTs <- unique(haps[names(haps) %in% names(BS.bin.sub)])
    BS.h.sub <- pegas::haplotype(BS.bin.sub)
     if (length(HTs) > 1) {
       BS.h.sub <- sort(BS.h.sub, what = "label")
       net <- pegas::haploNet(BS.h.sub)
        ind.hap <- with(
          stack(setNames(attr(BS.h.sub, "index"), rownames(BS.h.sub))),
          table(hap = ind, pop = BS.gt.sub@data$stratum[values]))

       size.new <- attr(net, "freq")
       size.new <- sqrt(size.new)

       attr(net, "labels") <- paste0(attr(net, "labels"),"\nn=",
                                     attr(net, "freq"))
       plot(net, size = size.new, scale.ratio = 6, pie = NULL,
            show.mutation = 1,threshold = 0,  srt = 1, cex = 0.75)
       title(paste0(Location))
     }
  }
}
```



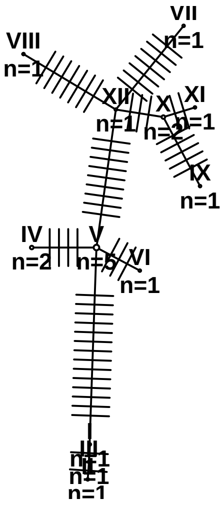
13.4.2.3.1 HT network per Location in Australia



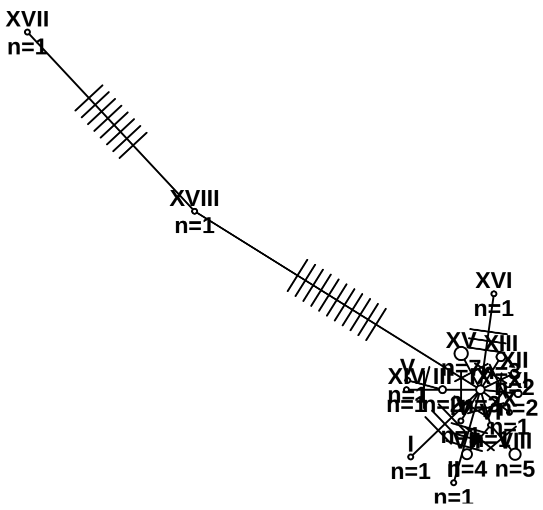
Daly River



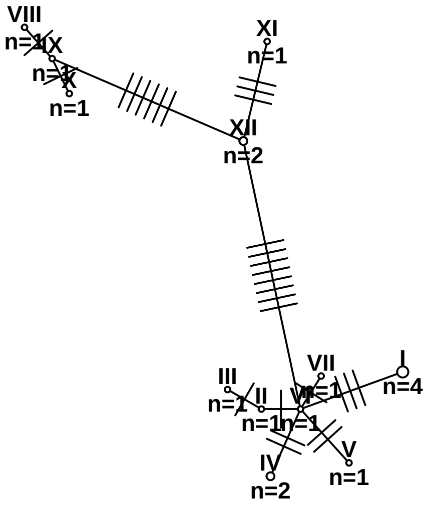
Adelaide River



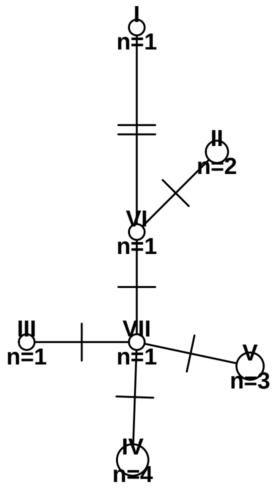
South Alligator River



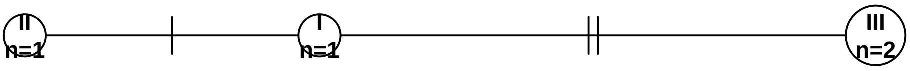
East Alligator River

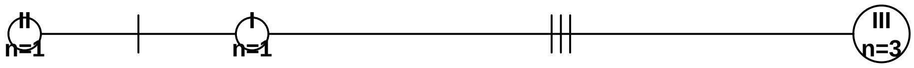


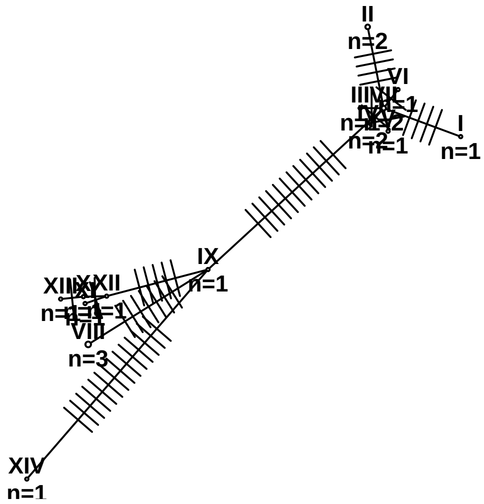
Blue mud Bay



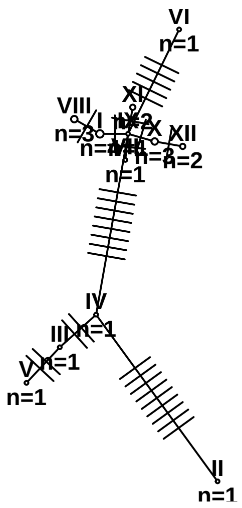
Roper River



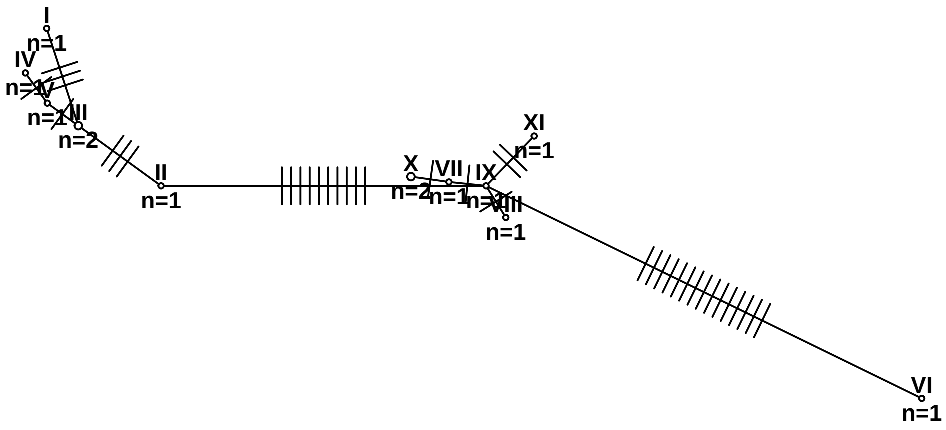

Towns River


Wenlock River

Clarence River



Sydney Harbour



13.5 Genetic differentiation

13.5.1 PHIst per Location

```
strata <- as.character(BS.gt@schemes$Location)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

popstr.mt.Location <-
  strataG::popStructTest(
    BS.gt,
    nrep = 1000,
    stats = "all",
    type = "both",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores()-1,
    write.output = TRUE
  )
save(popstr.mt.Location, file = "Mitogenome_ALL_Locations_phist.Rdata")
readr::write_tsv(popstr.mt.Location$pairwise$result,
                 path = "Mitogenome_ALL_Locations_phist.txt")
```

```
load("Mitogenome_ALL_Locations_phist.Rdata")
knitr::kable(
  popstr.mt.Location$overall$result,
  digits = 4,
  # format = "html",
  caption = "Overall mtDNA differentiation between Sites"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)

kableExtra::kbl(
  popstr.mt.Location$pairwise$result[order(popstr.mt.Location$pairwise$result$PHIst,
                                       decreasing  = TRUE), -c(1:8)],
  caption = "Pairwise mtDNA differentiation between Sites",
  longtable = TRUE, booktabs = TRUE) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5,
                            latex_options = c("repeat_header", "hold_position"))


pop.levels1 <- c("Gulf of California","Costa Rica","Sierra Leone","South Africa",
                 "Reunion","Seychelles","Arabian Sea","Sri Lanka","Thailand",
                 "Indonesia","Papua New Guinea","Fitzroy River","Victoria River",
                 "Daly River","Adelaide River","South Alligator River",
                 "East Alligator River","Blue mud Bay","Roper River","Towns River",
                 "Wenlock River","Trinity inlet","Clarence River","Sydney Harbour",
                 "Okinawa","Urauchi River","Fiji")

m2 <- popstr.mt.Location$pairwise$result[order(match(
  popstr.mt.Location$pairwise$result$strata.1,pop.levels1)),c(1,2,9)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.1 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "PHIst", type = 'upper')

m2 <- popstr.mt.Location$pairwise$result[order(match(
  popstr.mt.Location$pairwise$result$strata.1,pop.levels1)),c(1,2,10)]
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.2 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
```

Table 67: Overall mtDNA differentiation between Sites

	estimate	p.val
Chi2	9334.0000	0.001
Fst	0.0000	1.000
PHIst	0.7537	0.001

```
                                    attr = "PHIst.p.val", type = 'upper')
m2$PHIst.p.adj <- p.adjust(m2$PHIst.p.val, "bonferroni")
Gdf <- igraph::graph.data.frame(m2, directed = FALSE)
m2.3 <- igraph::as_adjacency_matrix(Gdf, names = TRUE, sparse = FALSE,
                                    attr = "PHIst.p.adj", type = 'upper')
write.csv(m2.1, file = "Mitogenome_ALL_phist_Locations.csv")
write.csv(m2.2, file = "Mitogenome_ALL_phist_Pval_Locations.csv")
write.csv(m2.3, file = "Mitogenome_ALL_phist_Pval_Bonferroni_Locations.csv")
```

Table 68: Pairwise mtDNA differentiation between Sites

	PHIst	PHIst.p.val
Gulf of California (1) v. Trinity inlet (4)	1.0000000	0.2047952
Sierra Leone (1) v. Trinity inlet (4)	1.0000000	0.2147852
Gulf of California (1) v. Urauchi River (21)	0.9887413	0.0519481
Sierra Leone (1) v. Urauchi River (21)	0.9885876	0.0439560
Blue mud Bay (13) v. Gulf of California (1)	0.9884460	0.0709291
Blue mud Bay (13) v. Sierra Leone (1)	0.9882860	0.0969031
Gulf of California (1) v. Roper River (4)	0.9878215	0.2077922
Roper River (4) v. Sierra Leone (1)	0.9876525	0.2037962
Gulf of California (1) v. Towns River (5)	0.9854394	0.1518482
Sierra Leone (1) v. Towns River (5)	0.9852380	0.1718282
Costa Rica (15) v. Urauchi River (21)	0.9811117	0.0009990
Blue mud Bay (13) v. Costa Rica (15)	0.9785333	0.0009990
Gulf of California (1) v. South Alligator River (38)	0.9769065	0.0269730
Sierra Leone (1) v. South Alligator River (38)	0.9765779	0.0219780
Costa Rica (15) v. Trinity inlet (4)	0.9750733	0.0009990
Costa Rica (15) v. South Alligator River (38)	0.9748986	0.0009990
Costa Rica (15) v. Towns River (5)	0.9735751	0.0009990
Costa Rica (15) v. Roper River (4)	0.9732309	0.0019980
Costa Rica (15) v. Reunion (16)	0.9694116	0.0009990
Gulf of California (1) v. Reunion (16)	0.9684873	0.0679321
Reunion (16) v. Sierra Leone (1)	0.9684819	0.0529471
Costa Rica (15) v. Seychelles (18)	0.9684040	0.0009990
Clarence River (21) v. Costa Rica (15)	0.9676359	0.0009990
Reunion (16) v. Urauchi River (21)	0.9672442	0.0009990
Gulf of California (1) v. Seychelles (18)	0.9670436	0.0499500
Seychelles (18) v. Sierra Leone (1)	0.9670379	0.0569431
Clarence River (21) v. Gulf of California (1)	0.9662884	0.0499500
Clarence River (21) v. Sierra Leone (1)	0.9658398	0.0399600
Costa Rica (15) v. Indonesia (6)	0.9652015	0.0009990
Seychelles (18) v. Urauchi River (21)	0.9636613	0.0009990
Blue mud Bay (13) v. Reunion (16)	0.9631304	0.0009990
Blue mud Bay (13) v. Seychelles (18)	0.9591600	0.0009990
Costa Rica (15) v. Victoria River (21)	0.9587297	0.0009990
Reunion (16) v. South Alligator River (38)	0.9584980	0.0009990
Costa Rica (15) v. Sierra Leone (1)	0.9575420	0.0629371
Costa Rica (15) v. Okinawa (10)	0.9573514	0.0009990
Reunion (16) v. Trinity inlet (4)	0.9563031	0.0009990
Costa Rica (15) v. East Alligator River (17)	0.9559540	0.0009990
Seychelles (18) v. South Alligator River (38)	0.9553989	0.0009990
Reunion (16) v. Towns River (5)	0.9541431	0.0009990
Costa Rica (15) v. Sydney Harbour (13)	0.9541290	0.0009990
Reunion (16) v. Roper River (4)	0.9534421	0.0009990
Seychelles (18) v. Trinity inlet (4)	0.9515810	0.0009990
Gulf of California (1) v. Indonesia (6)	0.9511629	0.1458541
Gulf of California (1) v. Victoria River (21)	0.9509015	0.0439560
Costa Rica (15) v. Papua New Guinea (15)	0.9505300	0.0009990
Indonesia (6) v. Sierra Leone (1)	0.9504958	0.1268731
Seychelles (18) v. Towns River (5)	0.9502713	0.0009990
Sierra Leone (1) v. Victoria River (21)	0.9501907	0.0499500
Roper River (4) v. Seychelles (18)	0.9494001	0.0009990
Costa Rica (15) v. Wenlock River (19)	0.9489106	0.0009990
Costa Rica (15) v. Daly River (25)	0.9472102	0.0009990
Clarence River (21) v. Reunion (16)	0.9463779	0.0009990
Adelaide River (18) v. Costa Rica (15)	0.9443990	0.0009990
East Alligator River (17) v. Gulf of California (1)	0.9437660	0.0589411
East Alligator River (17) v. Sierra Leone (1)	0.9429891	0.0619381
Clarence River (21) v. Seychelles (18)	0.9428199	0.0009990
Indonesia (6) v. Reunion (16)	0.9408742	0.0009990
Gulf of California (1) v. Okinawa (10)	0.9374170	0.0909091
Indonesia (6) v. Seychelles (18)	0.9370692	0.0009990

Table 68: Pairwise mtDNA differentiation between Sites *(continued)*

	PHIst	PHIst.p.val
Okinawa (10) v. Sierra Leone (1)	0.9365667	0.0829171
Gulf of California (1) v. Sydney Harbour (13)	0.9358266	0.0799201
Sierra Leone (1) v. Sydney Harbour (13)	0.9349417	0.0589411
Daly River (25) v. Gulf of California (1)	0.9337473	0.0419580
Reunion (16) v. Victoria River (21)	0.9327623	0.0009990
Daly River (25) v. Sierra Leone (1)	0.9326885	0.0319680
Gulf of California (1) v. Wenlock River (19)	0.9324838	0.0469530
Sierra Leone (1) v. Wenlock River (19)	0.9314555	0.0559441
Okinawa (10) v. Reunion (16)	0.9311654	0.0009990
Gulf of California (1) v. Papua New Guinea (15)	0.9309788	0.0739261
Papua New Guinea (15) v. Sierra Leone (1)	0.9300344	0.0529471
Seychelles (18) v. Victoria River (21)	0.9294086	0.0009990
East Alligator River (17) v. Reunion (16)	0.9285024	0.0009990
Okinawa (10) v. Seychelles (18)	0.9280175	0.0009990
East Alligator River (17) v. Seychelles (18)	0.9251465	0.0009990
Reunion (16) v. Sydney Harbour (13)	0.9249207	0.0009990
Costa Rica (15) v. Fiji (9)	0.9246048	0.0009990
Adelaide River (18) v. Gulf of California (1)	0.9232640	0.0589411
Adelaide River (18) v. Sierra Leone (1)	0.9220914	0.0579421
Seychelles (18) v. Sydney Harbour (13)	0.9215933	0.0009990
Papua New Guinea (15) v. Reunion (16)	0.9190447	0.0009990
Reunion (16) v. Wenlock River (19)	0.9179158	0.0009990
Papua New Guinea (15) v. Seychelles (18)	0.9160519	0.0009990
Daly River (25) v. Reunion (16)	0.9152573	0.0009990
Seychelles (18) v. Wenlock River (19)	0.9146460	0.0009990
Costa Rica (15) v. South Africa (7)	0.9130404	0.0019980
Daly River (25) v. Seychelles (18)	0.9118562	0.0009990
Roper River (4) v. Trinity inlet (4)	0.9106151	0.0339660
Adelaide River (18) v. Reunion (16)	0.9105991	0.0009990
Adelaide River (18) v. Seychelles (18)	0.9073780	0.0009990
South Africa (7) v. South Alligator River (38)	0.8974237	0.0009990
Costa Rica (15) v. Fitzroy River (5)	0.8910443	0.0009990
Costa Rica (15) v. Thailand (6)	0.8866068	0.0009990
Towns River (5) v. Trinity inlet (4)	0.8846628	0.0039960
South Africa (7) v. Urauchi River (21)	0.8838649	0.0009990
Blue mud Bay (13) v. Urauchi River (21)	0.8834663	0.0009990
Trinity inlet (4) v. Urauchi River (21)	0.8820587	0.0009990
Roper River (4) v. Urauchi River (21)	0.8799386	0.0009990
Towns River (5) v. Urauchi River (21)	0.8792479	0.0009990
Arabian Sea (19) v. Costa Rica (15)	0.8773310	0.0009990
Blue mud Bay (13) v. Trinity inlet (4)	0.8729977	0.0019980
Fiji (9) v. Reunion (16)	0.8639407	0.0009990
Fiji (9) v. Seychelles (18)	0.8618021	0.0009990
Clarence River (21) v. South Africa (7)	0.8488479	0.0009990
Fiji (9) v. Gulf of California (1)	0.8483095	0.0889111
Blue mud Bay (13) v. South Africa (7)	0.8464529	0.0009990
Fiji (9) v. Sierra Leone (1)	0.8462238	0.0929071
Costa Rica (15) v. Sri Lanka (12)	0.8322144	0.0009990
South Africa (7) v. Victoria River (21)	0.8282895	0.0009990
South Alligator River (38) v. Thailand (6)	0.8250337	0.0009990
Daly River (25) v. South Africa (7)	0.8128966	0.0009990
East Alligator River (17) v. South Africa (7)	0.8081566	0.0009990
Arabian Sea (19) v. Gulf of California (1)	0.8037655	0.0559441
South Alligator River (38) v. Urauchi River (21)	0.8021153	0.0009990
Arabian Sea (19) v. Sierra Leone (1)	0.8019334	0.0469530
South Africa (7) v. Wenlock River (19)	0.7998318	0.0009990
Sierra Leone (1) v. South Africa (7)	0.7883953	0.1148851
Gulf of California (1) v. South Africa (7)	0.7880327	0.1358641
Adelaide River (18) v. South Africa (7)	0.7839000	0.0009990
Papua New Guinea (15) v. South Africa (7)	0.7819128	0.0009990
South Africa (7) v. Sydney Harbour (13)	0.7806569	0.0009990
Thailand (6) v. Urauchi River (21)	0.7801245	0.0009990
Okinawa (10) v. South Africa (7)	0.7771304	0.0009990
Arabian Sea (19) v. Seychelles (18)	0.7762695	0.0009990
Arabian Sea (19) v. Reunion (16)	0.7756795	0.0009990
Blue mud Bay (13) v. Indonesia (6)	0.7616878	0.0009990
South Africa (7) v. Towns River (5)	0.7565992	0.0009990
Clarence River (21) v. Urauchi River (21)	0.7503802	0.0009990
Indonesia (6) v. South Africa (7)	0.7474610	0.0019980
Clarence River (21) v. Thailand (6)	0.7412919	0.0009990
South Africa (7) v. Trinity inlet (4)	0.7407161	0.0049950
Roper River (4) v. South Africa (7)	0.7363390	0.0039960
Blue mud Bay (13) v. Thailand (6)	0.7294146	0.0009990
South Alligator River (38) v. Trinity inlet (4)	0.7202121	0.0009990
Thailand (6) v. Victoria River (21)	0.7132750	0.0009990
Fitzroy River (5) v. Reunion (16)	0.7125173	0.0009990
Indonesia (6) v. South Alligator River (38)	0.7053679	0.0009990
South Alligator River (38) v. Sri Lanka (12)	0.6920817	0.0009990
Daly River (25) v. Thailand (6)	0.6913071	0.0009990
Blue mud Bay (13) v. Okinawa (10)	0.6912234	0.0009990
Okinawa (10) v. South Alligator River (38)	0.6873925	0.0009990
Fitzroy River (5) v. Seychelles (18)	0.6784070	0.0049950
Gulf of California (1) v. Thailand (6)	0.6772203	0.1418581
East Alligator River (17) v. Thailand (6)	0.6765307	0.0009990

Table 68: Pairwise mtDNA differentiation between Sites *(continued)*

	PHIst	PHIst.p.val
Sierra Leone (1) v. Thailand (6)	0.6757185	0.1658342
Indonesia (6) v. Towns River (5)	0.6727657	0.0059940
Urauchi River (21) v. Victoria River (21)	0.6671736	0.0009990
Thailand (6) v. Wenlock River (19)	0.6658557	0.0009990
Sydney Harbour (13) v. Urauchi River (21)	0.6656183	0.0009990
Fitzroy River (5) v. Urauchi River (21)	0.6655974	0.0019980
Gulf of California (1) v. Sri Lanka (12)	0.6642238	0.0689311
Sierra Leone (1) v. Sri Lanka (12)	0.6622797	0.0749251
Indonesia (6) v. Urauchi River (21)	0.6598200	0.0009990
Indonesia (6) v. Roper River (4)	0.6513836	0.0079920
Fitzroy River (5) v. Gulf of California (1)	0.6491786	0.1648352
Papua New Guinea (15) v. Thailand (6)	0.6477381	0.0009990
Blue mud Bay (13) v. Clarence River (21)	0.6463417	0.0009990
Fitzroy River (5) v. Sierra Leone (1)	0.6462521	0.1728272
Adelaide River (18) v. Thailand (6)	0.6456381	0.0009990
Fiji (9) v. South Africa (7)	0.6425882	0.0029970
Papua New Guinea (15) v. Urauchi River (21)	0.6385181	0.0009990
Sydney Harbour (13) v. Thailand (6)	0.6381324	0.0009990
Indonesia (6) v. Trinity inlet (4)	0.6291095	0.0049950
Okinawa (10) v. Thailand (6)	0.6211585	0.0009990
East Alligator River (17) v. Urauchi River (21)	0.6152912	0.0009990
Fitzroy River (5) v. South Alligator River (38)	0.6109927	0.0069930
Fiji (9) v. Urauchi River (21)	0.6107598	0.0009990
Sri Lanka (12) v. Urauchi River (21)	0.6102716	0.0009990
Reunion (16) v. Seychelles (18)	0.6057351	0.0009990
Clarence River (21) v. South Alligator River (38)	0.6028123	0.0009990
Okinawa (10) v. Towns River (5)	0.5981897	0.0009990
Clarence River (21) v. Towns River (5)	0.5971462	0.0009990
Fiji (9) v. South Alligator River (38)	0.5935288	0.0009990
Arabian Sea (19) v. South Africa (7)	0.5897958	0.0019980
Clarence River (21) v. Sri Lanka (12)	0.5847829	0.0009990
Thailand (6) v. Towns River (5)	0.5803960	0.0249750
Clarence River (21) v. Roper River (4)	0.5782384	0.0009990
Okinawa (10) v. Roper River (4)	0.5735961	0.0049950
Clarence River (21) v. Indonesia (6)	0.5712502	0.0009990
Clarence River (21) v. Okinawa (10)	0.5695569	0.0009990
Sri Lanka (12) v. Victoria River (21)	0.5633338	0.0009990
Blue mud Bay (13) v. Sri Lanka (12)	0.5611878	0.0009990
Okinawa (10) v. Urauchi River (21)	0.5547461	0.0029970
Daly River (25) v. Sri Lanka (12)	0.5521694	0.0009990
Okinawa (10) v. Trinity inlet (4)	0.5505012	0.0029970
Indonesia (6) v. Thailand (6)	0.5499141	0.0139860
Roper River (4) v. Thailand (6)	0.5435733	0.0069930
Clarence River (21) v. Fitzroy River (5)	0.5430071	0.0009990
Thailand (6) v. Trinity inlet (4)	0.5393582	0.0069930
Urauchi River (21) v. Wenlock River (19)	0.5292057	0.0009990
Blue mud Bay (13) v. Sydney Harbour (13)	0.5284805	0.0009990
South Alligator River (38) v. Sydney Harbour (13)	0.5270156	0.0009990
East Alligator River (17) v. Sri Lanka (12)	0.5241172	0.0009990
Sri Lanka (12) v. Wenlock River (19)	0.5204537	0.0009990
Reunion (16) v. Thailand (6)	0.5202350	0.0009990
Daly River (25) v. Urauchi River (21)	0.5144132	0.0009990
Adelaide River (18) v. Urauchi River (21)	0.5143602	0.0009990
Blue mud Bay (13) v. Fiji (9)	0.5119905	0.0009990
Papua New Guinea (15) v. Sri Lanka (12)	0.5035981	0.0009990
Trinity inlet (4) v. Victoria River (21)	0.5021163	0.0009990
Okinawa (10) v. Victoria River (21)	0.5005285	0.0009990
Adelaide River (18) v. Sri Lanka (12)	0.5004452	0.0009990
Sri Lanka (12) v. Sydney Harbour (13)	0.4898373	0.0009990
Papua New Guinea (15) v. South Alligator River (38)	0.4858569	0.0009990
Arabian Sea (19) v. South Alligator River (38)	0.4830534	0.0009990
Okinawa (10) v. Sri Lanka (12)	0.4758559	0.0009990
Blue mud Bay (13) v. Papua New Guinea (15)	0.4748028	0.0009990
Blue mud Bay (13) v. Fitzroy River (5)	0.4691471	0.0049950
Indonesia (6) v. Victoria River (21)	0.4628799	0.0019980
Reunion (16) v. Sri Lanka (12)	0.4561799	0.0009990
Fiji (9) v. Thailand (6)	0.4506479	0.0019980
East Alligator River (17) v. Trinity inlet (4)	0.4491245	0.0009990
Okinawa (10) v. Sydney Harbour (13)	0.4461679	0.0009990
Clarence River (21) v. Victoria River (21)	0.4404689	0.0009990
Fitzroy River (5) v. Victoria River (21)	0.4389129	0.0269730
East Alligator River (17) v. Okinawa (10)	0.4353099	0.0009990
Sri Lanka (12) v. Towns River (5)	0.4340831	0.0059940
Daly River (25) v. Fitzroy River (5)	0.4331509	0.0079920
Fitzroy River (5) v. Okinawa (10)	0.4312088	0.0009990
Papua New Guinea (15) v. Trinity inlet (4)	0.4287198	0.0009990
Sydney Harbour (13) v. Towns River (5)	0.4276393	0.0019980
Clarence River (21) v. Papua New Guinea (15)	0.4271172	0.0009990
Indonesia (6) v. Okinawa (10)	0.4246671	0.0129870
Indonesia (6) v. Papua New Guinea (15)	0.4237095	0.0009990
Okinawa (10) v. Papua New Guinea (15)	0.4109033	0.0009990
Clarence River (21) v. East Alligator River (17)	0.4107713	0.0009990
Fiji (9) v. Victoria River (21)	0.4101916	0.0009990
Indonesia (6) v. Sydney Harbour (13)	0.4093502	0.0009990

Table 68: Pairwise mtDNA differentiation between Sites *(continued)*

	PHIst	PHIst.p.val
Fitzroy River (5) v. Papua New Guinea (15)	0.4048663	0.0039960
Fitzroy River (5) v. Wenlock River (19)	0.4047859	0.0089910
East Alligator River (17) v. Fitzroy River (5)	0.4039457	0.0289710
Roper River (4) v. Sri Lanka (12)	0.4038690	0.0229770
Seychelles (18) v. Thailand (6)	0.3993580	0.0009990
Fitzroy River (5) v. Sydney Harbour (13)	0.3990371	0.0009990
Seychelles (18) v. Sri Lanka (12)	0.3954333	0.0009990
Roper River (4) v. Sydney Harbour (13)	0.3935885	0.0009990
Sri Lanka (12) v. Trinity inlet (4)	0.3926234	0.0169830
Arabian Sea (19) v. Blue mud Bay (13)	0.3921366	0.0009990
Indonesia (6) v. Sri Lanka (12)	0.3909716	0.0339660
East Alligator River (17) v. Indonesia (6)	0.3893668	0.0009990
Fiji (9) v. Okinawa (10)	0.3891665	0.0009990
Arabian Sea (19) v. Thailand (6)	0.3865570	0.0059940
Daly River (25) v. Okinawa (10)	0.3861823	0.0009990
Papua New Guinea (15) v. Towns River (5)	0.3796237	0.0019980
Okinawa (10) v. Wenlock River (19)	0.3779682	0.0009990
Daly River (25) v. Trinity inlet (4)	0.3768918	0.0009990
Adelaide River (18) v. Fitzroy River (5)	0.3750436	0.0219780
Fiji (9) v. Towns River (5)	0.3671478	0.0009990
Clarence River (21) v. Daly River (25)	0.3659189	0.0009990
East Alligator River (17) v. Fiji (9)	0.3631261	0.0009990
Arabian Sea (19) v. Clarence River (21)	0.3615792	0.0009990
Daly River (25) v. Fiji (9)	0.3583998	0.0009990
Trinity inlet (4) v. Wenlock River (19)	0.3573103	0.0009990
Adelaide River (18) v. Okinawa (10)	0.3564518	0.0009990
Clarence River (21) v. Wenlock River (19)	0.3479436	0.0009990
Fitzroy River (5) v. Indonesia (6)	0.3454361	0.0019980
Papua New Guinea (15) v. Roper River (4)	0.3425044	0.0049950
Fiji (9) v. Papua New Guinea (15)	0.3391077	0.0009990
Adelaide River (18) v. Clarence River (21)	0.3375021	0.0009990
Adelaide River (18) v. Trinity inlet (4)	0.3346570	0.0019980
Fiji (9) v. Sri Lanka (12)	0.3337432	0.0039960
Blue mud Bay (13) v. Towns River (5)	0.3311125	0.0069930
Fiji (9) v. Wenlock River (19)	0.3279948	0.0009990
Fiji (9) v. Roper River (4)	0.3264978	0.0059940
Arabian Sea (19) v. Urauchi River (21)	0.3259254	0.0009990
Arabian Sea (19) v. Victoria River (21)	0.3223922	0.0009990
Fiji (9) v. Indonesia (6)	0.3212353	0.0009990
Daly River (25) v. Indonesia (6)	0.3204187	0.0009990
Sydney Harbour (13) v. Victoria River (21)	0.3169697	0.0009990
Adelaide River (18) v. Fiji (9)	0.3118569	0.0009990
Indonesia (6) v. Wenlock River (19)	0.3078026	0.0009990
Blue mud Bay (13) v. Roper River (4)	0.2955472	0.0169830
East Alligator River (17) v. Sydney Harbour (13)	0.2940437	0.0009990
Arabian Sea (19) v. Sri Lanka (12)	0.2920615	0.0019980
Papua New Guinea (15) v. Victoria River (21)	0.2898890	0.0009990
Fitzroy River (5) v. Trinity inlet (4)	0.2881883	0.1938062
Arabian Sea (19) v. Towns River (5)	0.2872795	0.0189810
Arabian Sea (19) v. Papua New Guinea (15)	0.2857166	0.0009990
East Alligator River (17) v. Papua New Guinea (15)	0.2770597	0.0009990
Fitzroy River (5) v. South Africa (7)	0.2758936	0.0859141
Arabian Sea (19) v. Sydney Harbour (13)	0.2715370	0.0009990
Blue mud Bay (13) v. Daly River (25)	0.2681789	0.0039960
Daly River (25) v. Sydney Harbour (13)	0.2588976	0.0009990
Papua New Guinea (15) v. Wenlock River (19)	0.2565555	0.0009990
Arabian Sea (19) v. Roper River (4)	0.2562320	0.0759241
Arabian Sea (19) v. Okinawa (10)	0.2557410	0.0049950
Arabian Sea (19) v. East Alligator River (17)	0.2555895	0.0009990
Fitzroy River (5) v. Towns River (5)	0.2555059	0.0039960
Adelaide River (18) v. Indonesia (6)	0.2553233	0.0109890
Sydney Harbour (13) v. Wenlock River (19)	0.2551439	0.0009990
Arabian Sea (19) v. Daly River (25)	0.2519896	0.0009990
Daly River (25) v. Papua New Guinea (15)	0.2452140	0.0009990
Blue mud Bay (13) v. East Alligator River (17)	0.2450737	0.0029970
Blue mud Bay (13) v. Wenlock River (19)	0.2355891	0.0029970
Adelaide River (18) v. Blue mud Bay (13)	0.2343158	0.0019980
South Alligator River (38) v. Wenlock River (19)	0.2331459	0.0009990
Arabian Sea (19) v. Trinity inlet (4)	0.2277714	0.0589411
Arabian Sea (19) v. Wenlock River (19)	0.2265136	0.0009990
Adelaide River (18) v. Arabian Sea (19)	0.2244192	0.0009990
Adelaide River (18) v. South Alligator River (38)	0.2225027	0.0009990
Arabian Sea (19) v. Fiji (9)	0.2193626	0.0109890
Reunion (16) v. South Africa (7)	0.2107817	0.0049950
Fiji (9) v. Fitzroy River (5)	0.2099277	0.0299700
Daly River (25) v. South Alligator River (38)	0.2060549	0.0009990
Arabian Sea (19) v. Fitzroy River (5)	0.2025943	0.0419580
Fitzroy River (5) v. Roper River (4)	0.1973826	0.2187812
Daly River (25) v. Towns River (5)	0.1944328	0.0269730
Clarence River (21) v. Sydney Harbour (13)	0.1879409	0.0049950
Sydney Harbour (13) v. Trinity inlet (4)	0.1864946	0.1348651
Adelaide River (18) v. Sydney Harbour (13)	0.1842047	0.0019980
Clarence River (21) v. Fiji (9)	0.1784404	0.0029970
Fiji (9) v. Sydney Harbour (13)	0.1783542	0.0019980

Table 68: Pairwise mtDNA differentiation between Sites *(continued)*

	PHIst	PHIst.p.val
Towns River (5) v. Wenlock River (19)	0.1748255	0.0489510
East Alligator River (17) v. Towns River (5)	0.1626439	0.0699301
Seychelles (18) v. South Africa (7)	0.1586276	0.0279720
Adelaide River (18) v. Towns River (5)	0.1562088	0.0269730
Adelaide River (18) v. Papua New Guinea (15)	0.1528138	0.0069930
South Alligator River (38) v. Towns River (5)	0.1480850	0.0289710
East Alligator River (17) v. South Alligator River (38)	0.1477612	0.0029970
Blue mud Bay (13) v. South Alligator River (38)	0.1468654	0.0019980
Daly River (25) v. Roper River (4)	0.1454959	0.0799201
Arabian Sea (19) v. Indonesia (6)	0.1349157	0.1158841
Blue mud Bay (13) v. Victoria River (21)	0.1326374	0.0089910
Roper River (4) v. Wenlock River (19)	0.1319979	0.1258741
Costa Rica (15) v. Gulf of California (1)	0.1242849	0.1818182
Papua New Guinea (15) v. Sydney Harbour (13)	0.1162714	0.0229770
South Africa (7) v. Sri Lanka (12)	0.1128273	0.1288711
Adelaide River (18) v. Roper River (4)	0.1096056	0.1418581
East Alligator River (17) v. Roper River (4)	0.1027974	0.1088911
Towns River (5) v. Victoria River (21)	0.0734100	0.0749251
Victoria River (21) v. Wenlock River (19)	0.0692990	0.0379620
Daly River (25) v. Victoria River (21)	0.0634446	0.0489510
Roper River (4) v. South Alligator River (38)	0.0616557	0.2297702
South Africa (7) v. Thailand (6)	0.0484505	0.1698302
East Alligator River (17) v. Wenlock River (19)	0.0435785	0.1158841
South Alligator River (38) v. Victoria River (21)	0.0423776	0.0409590
Adelaide River (18) v. Victoria River (21)	0.0387443	0.1238761
Fitzroy River (5) v. Thailand (6)	0.0298249	0.2457542
East Alligator River (17) v. Victoria River (21)	0.0297948	0.1508492
Daly River (25) v. Wenlock River (19)	0.0290248	0.1338661
Adelaide River (18) v. East Alligator River (17)	0.0281864	0.1558442
Adelaide River (18) v. Daly River (25)	0.0249065	0.1658342
Adelaide River (18) v. Wenlock River (19)	0.0178644	0.1848152
Roper River (4) v. Victoria River (21)	0.0085205	0.2727273
Daly River (25) v. East Alligator River (17)	0.0045904	0.2987013
Fitzroy River (5) v. Sri Lanka (12)	-0.0031832	0.2847153
Fiji (9) v. Trinity inlet (4)	-0.0134690	0.3066933
Clarence River (21) v. Trinity inlet (4)	-0.0463369	0.4815185
Sri Lanka (12) v. Thailand (6)	-0.0912389	0.6243756
Roper River (4) v. Towns River (5)	-0.2264393	0.9950050
Gulf of California (1) v. Sierra Leone (1)	NA	NA

13.5.2 PHIst per Site

```
strata <- as.character(BS.gt@schemes$Site)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

fxdiff <- strataG::fixedDifferences(BS.gt, count.indels = TRUE,
                                    consec.indels.as.one = TRUE,
  bases = c("a", "c", "g", "t", "-"))
knitr::kable(
  fxdiff$num.fixed[order(fxdiff$num.fixed$num.fixed, decreasing = TRUE),],
  # format = "html",
  caption = "Fixed mtDNA differences between Sites"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
```

```
popstr.mt.Site <-
  strataG::popStructTest(
    BS.gt,
    nrep = 1000,
    stats = "all",
    type = "both",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores()-1,
    write.output = TRUE
  )
save(popstr.mt.Site, file = "Mitogenome_ALL_sites_phist.Rdata")
```

Table 69: Fixed mtDNA differences between Sites

	strata.1	strata.2	num.fixed
50	Gulf of California	Reunion	146
51	Gulf of California	Seychelles	146
78	Reunion	Sierra Leone	145
82	Seychelles	Sierra Leone	145
47	Gulf of California	Indonesia	144
48	Gulf of California	Japan	143
31	Costa Rica	Reunion	142
32	Costa Rica	Seychelles	142
49	Gulf of California	Papua New Guinea	142
60	Indonesia	Sierra Leone	141
67	Japan	Sierra Leone	141
28	Costa Rica	Indonesia	140
29	Costa Rica	Japan	139
73	Papua New Guinea	Sierra Leone	139
30	Costa Rica	Papua New Guinea	138
53	Gulf of California	South Africa	113
86	Sierra Leone	South Africa	112
34	Costa Rica	South Africa	109
52	Gulf of California	Sierra Leone	107
55	Gulf of California	Thailand	107
37	Fiji	Gulf of California	106
54	Gulf of California	Sri Lanka	106
16	Australia	Gulf of California	105
88	Sierra Leone	Thailand	105
4	Arabian Sea	Gulf of California	104
22	Australia	Sierra Leone	104
87	Sierra Leone	Sri Lanka	104
10	Arabian Sea	Sierra Leone	103
33	Costa Rica	Sierra Leone	103
43	Fiji	Sierra Leone	103
26	Costa Rica	Fiji	102
35	Costa Rica	Sri Lanka	102
36	Costa Rica	Thailand	102
14	Australia	Costa Rica	101
2	Arabian Sea	Costa Rica	100
65	Japan	Reunion	78
66	Japan	Seychelles	78
58	Indonesia	Reunion	76
59	Indonesia	Seychelles	76
71	Papua New Guinea	Reunion	75
72	Papua New Guinea	Seychelles	75
68	Japan	South Africa	12
61	Indonesia	South Africa	11
74	Papua New Guinea	South Africa	10
27	Costa Rica	Gulf of California	2
20	Australia	Reunion	1
21	Australia	Seychelles	1
39	Fiji	Japan	1
1	Arabian Sea	Australia	0
3	Arabian Sea	Fiji	0
5	Arabian Sea	Indonesia	0
6	Arabian Sea	Japan	0
7	Arabian Sea	Papua New Guinea	0
8	Arabian Sea	Reunion	0
9	Arabian Sea	Seychelles	0
11	Arabian Sea	South Africa	0
12	Arabian Sea	Sri Lanka	0
13	Arabian Sea	Thailand	0
15	Australia	Fiji	0
17	Australia	Indonesia	0
18	Australia	Japan	0
19	Australia	Papua New Guinea	0
23	Australia	South Africa	0
24	Australia	Sri Lanka	0
25	Australia	Thailand	0
38	Fiji	Indonesia	0
40	Fiji	Papua New Guinea	0
41	Fiji	Reunion	0
42	Fiji	Seychelles	0
44	Fiji	South Africa	0
45	Fiji	Sri Lanka	0
46	Fiji	Thailand	0
56	Indonesia	Japan	0
57	Indonesia	Papua New Guinea	0
62	Indonesia	Sri Lanka	0
63	Indonesia	Thailand	0
64	Japan	Papua New Guinea	0
69	Japan	Sri Lanka	0
70	Japan	Thailand	0
75	Papua New Guinea	Sri Lanka	0
76	Papua New Guinea	Thailand	0
77	Reunion	Seychelles	0
79	Reunion	South Africa	0
80	Reunion	Sri Lanka	0
81	Reunion	Thailand	0
83	Seychelles	South Africa	0
84	Seychelles	Sri Lanka	0
85	Seychelles	Thailand	0
89	South Africa	Sri Lanka	0
90	South Africa	Thailand	0
91	Sri Lanka	Thailand	0

Table 70: Overall mtDNA differentiation between Sites

	estimate	p.val
Chi2	4667.0000	0.987
Fst	0.0000	1.000
PHIst	0.7858	0.001

```r
readr::write_tsv(popstr.mt.Site$pairwise$result,
                 path = "Mitogenome_ALL_sites_phist.txt")
```

```r
load("Mitogenome_ALL_sites_phist.Rdata")
knitr::kable(
  popstr.mt.Site$overall$result,
  digits = 4,
  # format = "html",
  caption = "Overall mtDNA differentiation between Sites"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
knitr::kable(
  popstr.mt.Site$pairwise$result[order(popstr.mt.Site$pairwise$result$PHIst,
                                       decreasing  = TRUE), -c(1:8)],
  # format = "html",
  digits = 4,
  caption = "Pairwise mtDNA differentiation between Sites"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
```

13.5.3 PHIst per region

```r
strata <- as.character(BS.gt@schemes$Region)
names(strata) <- as.character(BS.gt@schemes$id)
strataG::setStrata(BS.gt) <- strata

fxdiff <- strataG::fixedDifferences(BS.gt, count.indels = TRUE,
                                    consec.indels.as.one = TRUE,
                                    bases = c("a", "c", "g", "t", "-"))
knitr::kable(
  fxdiff$num.fixed[order(fxdiff$num.fixed$num.fixed, decreasing = TRUE), ],
  # format = "html",
  caption = "Fixed mtDNA differences between regions"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
```

```r
popstr.mt.pop <-
  strataG::popStructTest(
    BS.gt,
    nrep = 10000,
    stats = "all",
    type = "both",
    keep.null = FALSE,
    quietly = TRUE,
    max.cores = parallel::detectCores()-1,
    write.output = TRUE
  )
save(popstr.mt.pop, file = "Mitogenome_ALL_region_phist.Rdata")
readr::write_tsv(popstr.mt.Site$pairwise$result,
                 path = "Mitogenome_ALL_region_phist.txt")
```

Table 71: Pairwise mtDNA differentiation between Sites

	PHIst	PHIst.p.val
Costa Rica (15) v. Reunion (16)	0.9694	0.0010
Gulf of California (1) v. Reunion (16)	0.9685	0.0699
Reunion (16) v. Sierra Leone (1)	0.9685	0.0679
Costa Rica (15) v. Seychelles (18)	0.9684	0.0010
Gulf of California (1) v. Seychelles (18)	0.9670	0.0480
Seychelles (18) v. Sierra Leone (1)	0.9670	0.0559
Costa Rica (15) v. Indonesia (6)	0.9652	0.0010
Costa Rica (15) v. Japan (31)	0.9615	0.0010
Costa Rica (15) v. Sierra Leone (1)	0.9575	0.0470
Gulf of California (1) v. Japan (31)	0.9574	0.0310
Japan (31) v. Sierra Leone (1)	0.9568	0.0410
Gulf of California (1) v. Indonesia (6)	0.9512	0.1598
Costa Rica (15) v. Papua New Guinea (15)	0.9505	0.0010
Indonesia (6) v. Sierra Leone (1)	0.9505	0.1449
Indonesia (6) v. Reunion (16)	0.9409	0.0010
Japan (31) v. Reunion (16)	0.9372	0.0010
Indonesia (6) v. Seychelles (18)	0.9371	0.0010
Japan (31) v. Seychelles (18)	0.9339	0.0010
Australia (203) v. Costa Rica (15)	0.9336	0.0010
Gulf of California (1) v. Papua New Guinea (15)	0.9310	0.0689
Australia (203) v. Gulf of California (1)	0.9303	0.0020
Papua New Guinea (15) v. Sierra Leone (1)	0.9300	0.0729
Australia (203) v. Sierra Leone (1)	0.9293	0.0050
Costa Rica (15) v. Fiji (9)	0.9246	0.0010
Papua New Guinea (15) v. Reunion (16)	0.9190	0.0010
Papua New Guinea (15) v. Seychelles (18)	0.9161	0.0010
Costa Rica (15) v. South Africa (7)	0.9130	0.0010
Australia (203) v. Reunion (16)	0.8936	0.0010
Australia (203) v. Seychelles (18)	0.8885	0.0010
Costa Rica (15) v. Thailand (6)	0.8866	0.0010
Arabian Sea (19) v. Costa Rica (15)	0.8773	0.0010
Fiji (9) v. Reunion (16)	0.8639	0.0010
Fiji (9) v. Seychelles (18)	0.8618	0.0010
Japan (31) v. South Africa (7)	0.8587	0.0010
Fiji (9) v. Gulf of California (1)	0.8483	0.1069
Australia (203) v. South Africa (7)	0.8474	0.0010
Fiji (9) v. Sierra Leone (1)	0.8462	0.0969
Costa Rica (15) v. Sri Lanka (12)	0.8322	0.0010
Arabian Sea (19) v. Gulf of California (1)	0.8038	0.0529
Arabian Sea (19) v. Sierra Leone (1)	0.8019	0.0529
Sierra Leone (1) v. South Africa (7)	0.7884	0.1469
Gulf of California (1) v. South Africa (7)	0.7880	0.1349
Papua New Guinea (15) v. South Africa (7)	0.7819	0.0010
Arabian Sea (19) v. Seychelles (18)	0.7763	0.0010
Arabian Sea (19) v. Reunion (16)	0.7757	0.0010
Australia (203) v. Thailand (6)	0.7673	0.0010
Japan (31) v. Thailand (6)	0.7551	0.0010
Indonesia (6) v. South Africa (7)	0.7475	0.0020
Australia (203) v. Sri Lanka (12)	0.6938	0.0010
Gulf of California (1) v. Thailand (6)	0.6772	0.1499
Sierra Leone (1) v. Thailand (6)	0.6757	0.1588
Gulf of California (1) v. Sri Lanka (12)	0.6642	0.0669
Sierra Leone (1) v. Sri Lanka (12)	0.6623	0.0839
Papua New Guinea (15) v. Thailand (6)	0.6477	0.0010
Fiji (9) v. South Africa (7)	0.6426	0.0010
Japan (31) v. Sri Lanka (12)	0.6144	0.0010
Reunion (16) v. Seychelles (18)	0.6057	0.0010
Arabian Sea (19) v. South Africa (7)	0.5898	0.0010
Indonesia (6) v. Thailand (6)	0.5499	0.0220
Reunion (16) v. Thailand (6)	0.5202	0.0010
Fiji (9) v. Japan (31)	0.5153	0.0010
Papua New Guinea (15) v. Sri Lanka (12)	0.5036	0.0010
Japan (31) v. Papua New Guinea (15)	0.4933	0.0010
Reunion (16) v. Sri Lanka (12)	0.4562	0.0010
Fiji (9) v. Thailand (6)	0.4506	0.0030
Indonesia (6) v. Papua New Guinea (15)	0.4237	0.0010
Indonesia (6) v. Japan (31)	0.4090	0.0050
Seychelles (18) v. Thailand (6)	0.3994	0.0020
Australia (203) v. Japan (31)	0.3989	0.0010
Seychelles (18) v. Sri Lanka (12)	0.3954	0.0010
Arabian Sea (19) v. Australia (203)	0.3925	0.0010
Indonesia (6) v. Sri Lanka (12)	0.3910	0.0290
Arabian Sea (19) v. Thailand (6)	0.3866	0.0090
Australia (203) v. Fiji (9)	0.3641	0.0010
Australia (203) v. Indonesia (6)	0.3433	0.0030
Fiji (9) v. Papua New Guinea (15)	0.3391	0.0010
Fiji (9) v. Sri Lanka (12)	0.3337	0.0060
Fiji (9) v. Indonesia (6)	0.3212	0.0020
Arabian Sea (19) v. Japan (31)	0.3063	0.0010
Arabian Sea (19) v. Sri Lanka (12)	0.2921	0.0060
Arabian Sea (19) v. Papua New Guinea (15)	0.2857	0.0010
Arabian Sea (19) v. Fiji (9)	0.2194	0.0090
Australia (203) v. Papua New Guinea (15)	0.2187	0.0010
Reunion (16) v. South Africa (7)	0.2108	0.0060
Seychelles (18) v. South Africa (7)	0.1586	0.0230
Arabian Sea (19) v. Indonesia (6)	0.1349	0.1379
Costa Rica (15) v. Gulf of California (1)	0.1243	0.1588
South Africa (7) v. Sri Lanka (12)	0.1128	0.1209
South Africa (7) v. Thailand (6)	0.0485	0.1928
Sri Lanka (12) v. Thailand (6)	-0.0912	0.6553
Gulf of California (1) v. Sierra Leone (1)	NA	NA

Table 72: Fixed mtDNA differences between regions

	strata.1	strata.2	num.fixed
4	E-ATL	Japan	141
7	E-ATL	W-PAC	140
15	E-PAC	Japan	139
18	E-PAC	W-PAC	138
6	E-ATL	W-IO	112
17	E-PAC	W-IO	109
1	E-ATL	E-IO	103
2	E-ATL	E-PAC	103
3	E-ATL	Fiji	103
5	E-ATL	N-IO	103
14	E-PAC	Fiji	102
8	E-IO	E-PAC	101
16	E-PAC	N-IO	100
24	Japan	W-IO	12
28	W-IO	W-PAC	9
19	Fiji	Japan	1
9	E-IO	Fiji	0
10	E-IO	Japan	0
11	E-IO	N-IO	0
12	E-IO	W-IO	0
13	E-IO	W-PAC	0
20	Fiji	N-IO	0
21	Fiji	W-IO	0
22	Fiji	W-PAC	0
23	Japan	N-IO	0
25	Japan	W-PAC	0
26	N-IO	W-IO	0
27	N-IO	W-PAC	0

Table 73: Overall mtDNA differentiation between regions

	estimate	p.val
Chi2	2513.0000	0.3916
Fst	0.0000	1.0000
PHIst	0.7576	0.0001

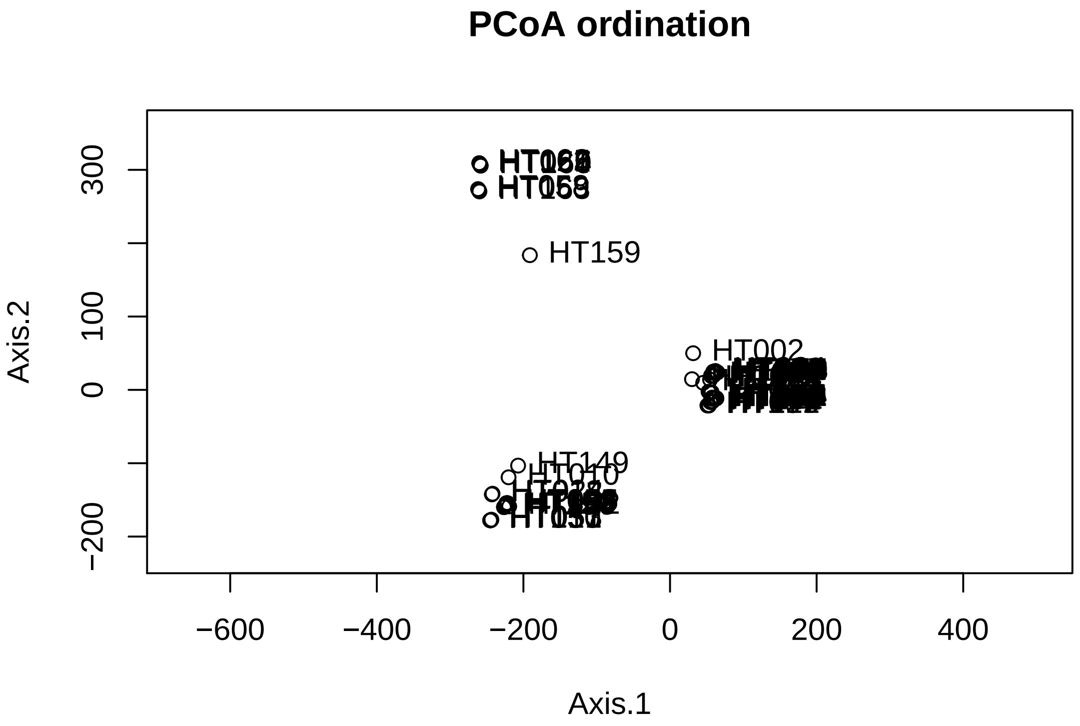
```
load("Mitogenome_ALL_region_phist.Rdata")
knitr::kable(
  popstr.mt.pop$overall$result,
  digits = 4,
  # format = "html",
  caption = "Overall mtDNA differentiation between regions"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
knitr::kable(
  popstr.mt.pop$pairwise$result[order(popstr.mt.pop$pairwise$result$PHIst,
  decreasing = TRUE), -c(1:8)],
  # format = "html",
  digits = 4,
  caption = "Pairwise mtDNA differentiation between regions"
  ) %>%
  kableExtra::kable_styling(full_width = FALSE,font_size = 5)
```

Table 74: Pairwise mtDNA differentiation between regions

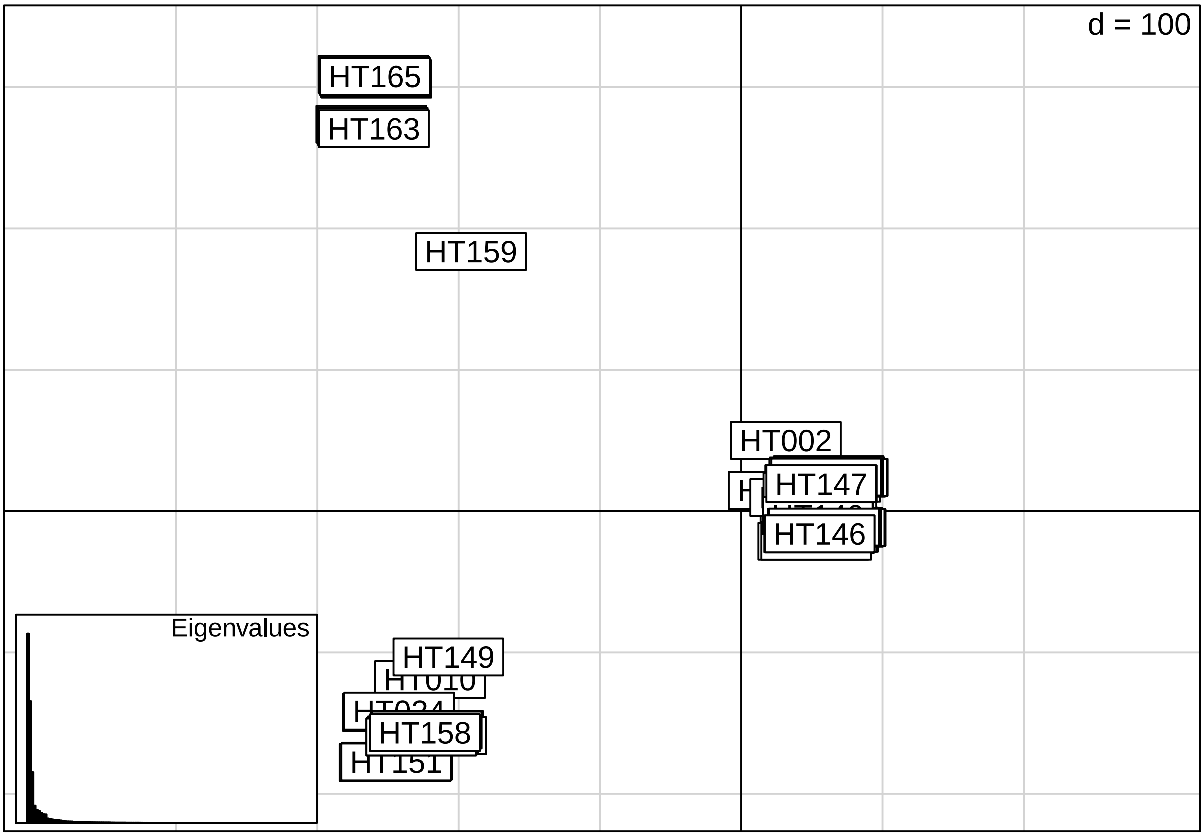
	PHIst	PHIst.p.val
E-PAC (16) v. Japan (31)	0.9615	0.0001
E-PAC (16) v. W-PAC (38)	0.9583	0.0001
E-ATL (1) v. Japan (31)	0.9568	0.0305
E-ATL (1) v. E-PAC (16)	0.9568	0.0582
E-ATL (1) v. W-PAC (38)	0.9532	0.0228
E-IO (186) v. E-PAC (16)	0.9334	0.0001
E-PAC (16) v. W-IO (41)	0.9314	0.0001
E-ATL (1) v. E-IO (186)	0.9286	0.0057
E-PAC (16) v. Fiji (9)	0.9261	0.0001
E-ATL (1) v. W-IO (41)	0.9163	0.0233
Japan (31) v. W-IO (41)	0.8892	0.0001
W-IO (41) v. W-PAC (38)	0.8878	0.0001
E-IO (186) v. W-IO (41)	0.8754	0.0001
E-ATL (1) v. Fiji (9)	0.8462	0.0993
Fiji (9) v. W-IO (41)	0.8153	0.0001
E-PAC (16) v. N-IO (37)	0.7789	0.0001
E-ATL (1) v. N-IO (37)	0.6815	0.0266
Japan (31) v. W-PAC (38)	0.5398	0.0001
N-IO (37) v. W-IO (41)	0.5162	0.0001
Fiji (9) v. Japan (31)	0.5153	0.0001
E-IO (186) v. N-IO (37)	0.4620	0.0001
E-IO (186) v. Fiji (9)	0.4045	0.0002
E-IO (186) v. Japan (31)	0.3972	0.0001
N-IO (37) v. W-PAC (38)	0.3628	0.0001
Japan (31) v. N-IO (37)	0.3244	0.0001
E-IO (186) v. W-PAC (38)	0.2738	0.0001
Fiji (9) v. W-PAC (38)	0.1954	0.0018
Fiji (9) v. N-IO (37)	0.1814	0.0427

13.6 PCA

```r
BS.haps <- strataG::labelHaplotypes(x = BS.bin, prefix = "HT",
                                    use.indels = TRUE)
BS.hapdist <- dist(BS.haps$hap.seqs)
table(BS.haps$haps)
x <- ape::pcoa(BS.hapdist, correction = "none", rn = NULL)
biplot(x, Y = NULL, plot.axes = c(1,2), dir.axis1 = 1,
       dir.axis2 = 1, rn = NULL, main = NULL)
```



```
pco1 <- dudi.pco(BS.hapdist, scannf = FALSE, nf = 2)
scatter(pco1, posi = "bottomleft")
```



```
##
## HT001 HT002 HT003 HT004 HT005 HT006 HT007 HT008 HT009 HT010 HT011 HT012 HT013
##    19    13    12    11    10     9     8     7     7     7     6     5     5
## HT014 HT015 HT016 HT017 HT018 HT019 HT020 HT021 HT022 HT023 HT024 HT025 HT026
##     5     5     5     5     5     4     4     4     4     4     4     4     3
## HT027 HT028 HT029 HT030 HT031 HT032 HT033 HT034 HT035 HT036 HT037 HT038 HT039
##     3     3     3     3     3     3     3     3     3     3     3     3     2
## HT040 HT041 HT042 HT043 HT044 HT045 HT046 HT047 HT048 HT049 HT050 HT051 HT052
##     2     2     2     2     2     2     2     2     2     2     2     2     2
## HT053 HT054 HT055 HT056 HT057 HT058 HT059 HT060 HT061 HT062 HT063 HT064 HT065
##     2     2     2     2     2     2     2     1     1     1     1     1     1
## HT066 HT067 HT068 HT069 HT070 HT071 HT072 HT073 HT074 HT075 HT076 HT077 HT078
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT079 HT080 HT081 HT082 HT083 HT084 HT085 HT086 HT087 HT088 HT089 HT090 HT091
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT092 HT093 HT094 HT095 HT096 HT097 HT098 HT099 HT100 HT101 HT102 HT103 HT104
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT105 HT106 HT107 HT108 HT109 HT110 HT111 HT112 HT113 HT114 HT115 HT116 HT117
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT118 HT119 HT120 HT121 HT122 HT123 HT124 HT125 HT126 HT127 HT128 HT129 HT130
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT131 HT132 HT133 HT134 HT135 HT136 HT137 HT138 HT139 HT140 HT141 HT142 HT143
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT144 HT145 HT146 HT147 HT148 HT149 HT150 HT151 HT152 HT153 HT154 HT155 HT156
##     1     1     1     1     1     1     1     1     1     1     1     1     1
## HT157 HT158 HT159 HT160 HT161 HT162 HT163 HT164 HT165
##     1     1     1     1     1     1     1     1     1
```

14 References

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Puechmaille, S. J. (2016). The program structure does not reliably recover the correct population structure when sampling is uneven: subsampling and new estimators alleviate the problem. Molecular Ecology Resources, 16(3), 608-627.

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Tillett, B. J., Meekan, M. G., Field, I. C., Hua, Q., & Bradshaw, C. J. A. (2011). Similar life history traits in bull (Carcharhinus leucas) and pig-eye (C. amboinensis) sharks. Marine and Freshwater Research, 62(7), 850-860.

15 Citations for packages

```r
packages <- c(
"radiator",
"ggplot2",
"dplyr",
"tidyverse",
"ade4",
"adegenet",
"ape",
"apex",
"assigner",
"assignPOP",
"dartR",
"haplotypes",
"data.table",
"ggplot2",
"grid",
```

```
"gridExtra",
"gtools",
"kableExtra",
"knitr",
"magrittr",
"marmap",
"mvbutils",
"OutFLANK",
"pegas",
"qvalue",
"rubias",
"strataG",
"vegan"
)
for (P in packages) {
p <- utils::citation(P)
print(attr(unclass(p)[[1]], "textVersion"))
}
```

```
## [1] "Gosselin, T. (2020). radiator: RADseq Data Exploration, Manipulation and Visualization using
## [1] "H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016."
## [1] "Hadley Wickham, Romain François, Lionel Henry and Kirill Müller (2021). dplyr: A Grammar of
## [1] "Wickham et al., (2019). Welcome to the tidyverse. Journal of Open Source Software, 4(43), 16
## NULL
## [1] "Jombart, T. (2008) adegenet: a R package for the multivariate analysis of genetic markers. B
## [1] "Paradis E. & Schliep K. 2019. ape 5.0: an environment for modern phylogenetics and evolution
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## [1] "Kuan-Yu Chen, Elizabeth A. Marschall, Michael G. Sovic, Anthony C. Fries, H. Lisle Gibbs and
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## [1] "Yihui Xie (2021). knitr: A General-Purpose Package for Dynamic Report Generation in R. R pac
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## [1] "Eric Pante, Benoit Simon-Bouhet (2013) marmap: A Package for Importing, Plotting and Analyzi
## [1] "Mark V. Bravington (2018). mvbutils: Workspace Organization, Code and Documentation Editing,
## [1] "Michael C. Whitlock and Katie Lotterhos (2014). OutFLANK: Fst outliers with trimming. R pack
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## [1] "Moran, BM and Anderson, EC. 2018. Bayesian inference from the conditional genetic stock iden
## [1] "Archer, F. I., Adams, P. E. and Schneiders, B. B. (2016) strataG: An R package for manipulat
## [1] "Jari Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan M
```

---

16 Session Info

```
sessioninfo::session_info()
```

```
## - Session info ---------------------------------------------------------------
##  setting  value
##  version  R version 4.0.2 (2020-06-22)
##  os       Ubuntu 18.04.1 LTS
##  system   x86_64, linux-gnu
##  ui       X11
##  language (EN)
##  collate  en_AU.UTF-8
##  ctype    en_AU.UTF-8
##  tz       Australia/Canberra
##  date     2022-07-11
##
## - Packages -------------------------------------------------------------------
##  package        * version    date       lib
##  ade4           * 1.7-15     2020-02-13 [2]
##  adegenet       * 2.1.3      2020-05-10 [2]
##  adehabitatMA     0.3.14     2020-01-13 [1]
##  ape            * 5.6-1      2022-01-07 [1]
##  apex           * 1.0.4      2020-04-11 [1]
##  assertthat       0.2.1      2019-03-21 [2]
##  assigner       * 0.5.8      2020-10-30 [1]
##  assignPOP      * 1.2.2      2020-11-17 [1]
##  backports        1.4.1      2021-12-13 [1]
##  bit              4.0.3      2020-07-30 [2]
##  bit64            0.9-7.1    2020-07-15 [2]
##  blob             1.2.1      2020-01-20 [2]
##  boot             1.3-25     2020-04-26 [2]
##  broom            0.7.6      2021-04-05 [1]
##  cachem           1.0.5      2021-05-15 [1]
##  calibrate        1.7.7      2020-06-19 [1]
##  callr            3.7.0      2021-04-20 [1]
##  caret            6.0-86     2020-03-20 [2]
##  cellranger       1.1.0      2016-07-27 [2]
##  class            7.3-17     2020-04-26 [2]
##  classInt         0.4-3      2020-04-07 [2]
##  cli              3.3.0      2022-04-25 [1]
##  cluster          2.1.0      2019-06-19 [2]
##  coda             0.19-4     2020-09-30 [1]
##  codetools        0.2-16     2018-12-24 [2]
##  colorspace       2.0-2      2021-06-24 [1]
##  combinat         0.0-8      2012-10-29 [2]
##  crayon           1.4.2      2021-10-29 [1]
##  dartR          * 1.9.9.1    2022-01-13 [1]
##  data.table     * 1.14.2     2021-09-27 [1]
##  DBI              1.1.2      2021-12-20 [1]
##  dbplyr           2.1.1      2021-04-06 [1]
##  deldir           1.0-6      2021-10-23 [1]
##  DEoptimR         1.0-8      2016-11-19 [2]
##  desc             1.3.0      2021-03-05 [2]
##  devtools         2.4.1      2021-05-05 [1]
##  digest           0.6.27     2020-10-24 [2]
##  dismo            1.3-3      2020-11-17 [1]
##  doParallel       1.0.15     2019-08-02 [2]
##  dplyr          * 1.0.6      2021-05-05 [1]
```

```
## e1071           1.7-9      2021-09-16 [1]
## ellipsis        0.3.2      2021-04-29 [1]
## evaluate        0.14       2019-05-28 [2]
## expm            0.999-6    2021-01-13 [1]
## fansi           1.0.0      2022-01-10 [1]
## farver          2.1.0      2021-02-28 [1]
## fastmap         1.1.0      2021-01-25 [1]
## fastmatch       1.1-0      2017-01-28 [2]
## forcats       * 0.5.1      2021-01-27 [1]
## foreach         1.5.0      2020-03-30 [2]
## foreign       * 0.8-80     2020-05-24 [2]
## formatR       * 1.7        2019-06-11 [2]
## fossil        * 0.4.0      2020-03-23 [1]
## fs              1.5.2      2021-12-08 [1]
## gap             1.2.3-1    2021-04-21 [1]
## gdata           2.18.0     2017-06-06 [2]
## gdistance       1.3-6      2020-06-29 [1]
## gdsfmt          1.26.1     2020-12-22 [1]
## generics        0.1.1      2021-10-25 [1]
## genetics        1.3.8.1.3  2021-03-01 [1]
## GGally          2.0.0      2020-06-06 [2]
## ggplot2       * 3.3.3      2020-12-30 [1]
## glue            1.6.0      2021-12-17 [1]
## gmodels         2.18.1     2018-06-25 [2]
## gower           0.2.2      2020-06-23 [2]
## gridExtra     * 2.3        2017-09-09 [2]
## gtable          0.3.0      2019-03-25 [2]
## gtools        * 3.8.2      2020-03-31 [2]
## haplotypes    * 1.1.2      2020-02-28 [1]
## haven           2.4.1      2021-04-23 [1]
## hierfstat       0.5-10     2021-11-17 [1]
## hms             1.1.0      2021-05-17 [1]
## htmltools       0.5.1.1    2021-01-22 [1]
## httpuv          1.5.4      2020-06-06 [2]
## httr            1.4.2      2020-07-20 [2]
## igraph          1.2.11     2022-01-04 [1]
## ipred           0.9-9      2019-04-28 [2]
## iterators       1.0.12     2019-07-26 [2]
## jsonlite        1.7.2      2020-12-09 [1]
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## KernSmooth      2.23-17    2020-04-26 [2]
## knitr         * 1.33       2021-04-24 [1]
## labeling        0.4.2      2020-10-20 [1]
## later           1.1.0.1    2020-06-05 [2]
## lattice       * 0.20-41    2020-04-02 [2]
## lava            1.6.7      2020-03-05 [2]
## LearnBayes      2.15.1     2018-03-18 [2]
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## lubridate       1.7.10     2021-02-26 [1]
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## maps          * 3.3.0      2018-04-03 [2]
## marmap        * 1.0.5      2020-11-19 [1]
## MASS            7.3-51.6   2020-04-26 [2]
## Matrix          1.2-18     2019-11-27 [2]
## memoise         2.0.0      2021-01-26 [2]
## mgcv            1.8-31     2019-11-09 [2]
## mime            0.12       2021-09-28 [1]
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##  network           1.16.0     2019-12-01 [2]
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##  permute         * 0.9-5      2019-03-12 [2]
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##  pkgconfig         2.0.3      2019-09-22 [2]
##  pkgload           1.2.1      2021-04-06 [2]
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##  plyr              1.8.6      2020-03-03 [2]
##  png               0.1-7      2013-12-03 [2]
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##  prettyunits       1.1.1      2020-01-24 [2]
##  pROC              1.16.2     2020-03-19 [2]
##  processx          3.5.2      2021-04-30 [1]
##  prodlim           2019.11.13 2019-11-17 [2]
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##  qvalue          * 2.20.0     2020-04-27 [2]
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##  R.oo              1.24.0     2020-08-26 [1]
##  R.utils           2.11.0     2021-09-26 [1]
##  R6                2.5.1      2021-08-19 [1]
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##  raster            3.4-10     2021-05-03 [1]
##  RColorBrewer      1.1-2      2014-12-07 [2]
##  Rcpp              1.0.7      2021-07-07 [1]
##  RcppParallel      5.0.2      2020-06-24 [2]
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##  readxl            1.3.1      2019-03-13 [2]
##  recipes           0.1.13     2020-06-23 [2]
##  remotes           2.3.0      2021-04-01 [1]
##  reprex            2.0.0      2021-04-02 [1]
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##  reshape2          1.4.4      2020-04-09 [2]
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##  rlang             0.4.11     2021-04-30 [1]
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##  robustbase        0.93-6     2020-03-23 [2]
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##  rprojroot         2.0.2      2020-11-15 [1]
##  RSQLite           2.2.0      2020-01-07 [2]
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##  seqinr           3.6-1     2019-09-07 [2]
##  sessioninfo      1.1.1     2018-11-05 [2]
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##  shapefiles     * 0.7       2013-01-26 [2]
##  shiny            1.5.0     2020-06-23 [2]
##  sna              2.5       2019-12-10 [2]
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##  spData           0.3.8     2020-07-03 [2]
##  spdep            1.1-5     2020-06-29 [2]
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##  statnet.common   4.3.0     2019-06-02 [2]
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##  stringr        * 1.4.0     2019-02-10 [2]
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##  survival         3.1-12    2020-04-10 [2]
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##  testthat         3.0.2     2021-02-14 [2]
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##  tidyselect       1.1.1     2021-04-30 [1]
##  tidyverse      * 1.3.1     2021-04-15 [1]
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##  tree             1.0-40    2019-04-26 [2]
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##  usethis          2.0.1     2021-02-10 [2]
##  utf8             1.2.1     2021-03-12 [1]
##  vctrs            0.3.8     2021-04-29 [1]
##  vegan          * 2.5-7     2020-11-28 [1]
##  viridisLite      0.4.0     2021-04-13 [1]
##  webshot          0.5.2     2019-11-22 [1]
##  withr            2.4.2     2021-04-18 [1]
##  xfun             0.31      2022-05-10 [1]
##  xml2             1.3.2     2020-04-23 [2]
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##  yaml             2.2.1     2020-02-01 [2]
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##  Github (thierrygosselin/assigner@d39a692)
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## [1] /home/dev093/R/x86_64-pc-linux-gnu-library/4.0
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