

Admixture Analysis

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```
setwd("./")
```

```
#Admixture Analyses
```

```
Ran admixture with admixture_wrapper with 10 repetitions from K=1-10
```

```
library(sfsmisc)
library(ggplot2)
library(ggpubr)
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:sfsmisc':
```

```
##
```

```
## last
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
## filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
## intersect, setdiff, setequal, union
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v forcats 1.0.0 v stringr 1.5.0
```

```
## v lubridate 1.9.2 v tibble 3.2.1
```

```
## v purrr 1.0.1 v tidyr 1.3.0
```

```
## v readr 2.1.4
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag() masks stats::lag()
```

```
## x dplyr::last() masks sfsmisc::last()
```

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(tibble)
library(plyr)
```

```
## -----
## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)
## -----
##
## Attaching package: 'plyr'
##
## The following object is masked from 'package:purrr':
##
##   compact
##
## The following objects are masked from 'package:dplyr':
##
##   arrange, count, desc, failwith, id, mutate, rename, summarise,
##   summarize
##
## The following object is masked from 'package:ggpubr':
##
##   mutate
```

```
library(patchwork)
#####
#Plots for Admixture cross-validation results

****Change path below to correct file
Cresults <- read.delim("./Complete_9794_no_scaffold_noX_recode.CV_Avg.txt", header = TRUE, sep = "\t")
Cresults
```

```
##      K CV_Avg CV_Stdev
## 1    1 0.5807  0.0002
## 2    2 0.4650  0.0002
## 3    3 0.4528  0.0027
## 4    4 0.4449  0.0005
## 5    5 0.4509  0.0015
## 6    6 0.4710  0.0123
## 7    7 0.4906  0.0123
## 8    8 0.5149  0.0129
## 9    9 0.5402  0.0108
## 10  10 0.5623  0.0121
## 11  11 0.5909  0.0155
## 12  12 0.6191  0.0172
## 13  13 0.6441  0.0160
## 14  14 0.6707  0.0143
## 15  15 0.7016  0.0173
## 16  16 0.7310  0.0169
## 17  17 0.7607  0.0133
## 18  18 0.7928  0.0146
## 19  19 0.8261  0.0150
## 20  20 0.8507  0.0150
```

```
ls(Cresults)
```

```
## [1] "CV_Avg" "CV_Stdev" "K"
```

```
# Headers = "K" "CV_Avg" "CV_Stdev"
```

```
Nresults <- read.delim("./Neutral_8958.CV_Avg.txt", header = TRUE, sep = "\t")  
Nresults
```

```
##      K CV_Avg CV_Stdev  
## 1    1 0.5614 0.0002  
## 2    2 0.4757 0.0002  
## 3    3 0.4655 0.0031  
## 4    4 0.4592 0.0009  
## 5    5 0.4675 0.0027  
## 6    6 0.4907 0.0123  
## 7    7 0.5086 0.0137  
## 8    8 0.5320 0.0118  
## 9    9 0.5590 0.0108  
## 10 10 0.5847 0.0119  
## 11 11 0.6114 0.0151  
## 12 12 0.6428 0.0162  
## 13 13 0.6708 0.0159  
## 14 14 0.7004 0.0159  
## 15 15 0.7352 0.0157  
## 16 16 0.7660 0.0181  
## 17 17 0.7969 0.0175  
## 18 18 0.8305 0.0182  
## 19 19 0.8642 0.0206  
## 20 20 0.8965 0.0164
```

```
ls(Nresults)
```

```
## [1] "CV_Avg" "CV_Stdev" "K"
```

```
GNresults <- read.delim("./GB75_Neutral_8958.CV_Avg.txt", header = TRUE, sep = "\t")  
GNresults
```

```
##      K CV_Avg CV_Stdev  
## 1    1 0.5188 0.0005  
## 2    2 0.5330 0.0009  
## 3    3 0.5848 0.0030  
## 4    4 0.6387 0.0052  
## 5    5 0.6948 0.0067  
## 6    6 0.7543 0.0076  
## 7    7 0.8154 0.0131  
## 8    8 0.8779 0.0107  
## 9    9 0.9471 0.0122  
## 10 10 1.0171 0.0151  
## 11 11 1.0843 0.0150  
## 12 12 1.1586 0.0163  
## 13 13 1.2272 0.0175
```

```
## 14 14 1.2997    0.0203
## 15 15 1.3638    0.0252
## 16 16 1.4292    0.0312
## 17 17 1.4822    0.0359
## 18 18 1.5199    0.0562
## 19 19 1.5592    0.0422
## 20 20 1.5774    0.0814
```

```
ls(GNresults)
```

```
## [1] "CV_Avg"    "CV_Stdev" "K"
```

```
GCresults <- read.delim("./GB75_Complete_9794.CV_Avg.txt", header = TRUE, sep = "\t")
GCresults
```

```
##      K CV_Avg CV_Stdev
## 1     1 0.4980  0.0005
## 2     2 0.5119  0.0004
## 3     3 0.5618  0.0043
## 4     4 0.6124  0.0050
## 5     5 0.6672  0.0063
## 6     6 0.7233  0.0075
## 7     7 0.7817  0.0099
## 8     8 0.8441  0.0109
## 9     9 0.9079  0.0128
## 10    10 0.9773  0.0156
## 11    11 1.0462  0.0170
## 12    12 1.1097  0.0156
## 13    13 1.1776  0.0175
## 14    14 1.2413  0.0169
## 15    15 1.3064  0.0233
## 16    16 1.3595  0.0249
## 17    17 1.4084  0.0328
## 18    18 1.4571  0.0378
## 19    19 1.5033  0.0538
## 20    20 1.5289  0.0586
```

```
ls(GCresults)
```

```
## [1] "CV_Avg"    "CV_Stdev" "K"
```

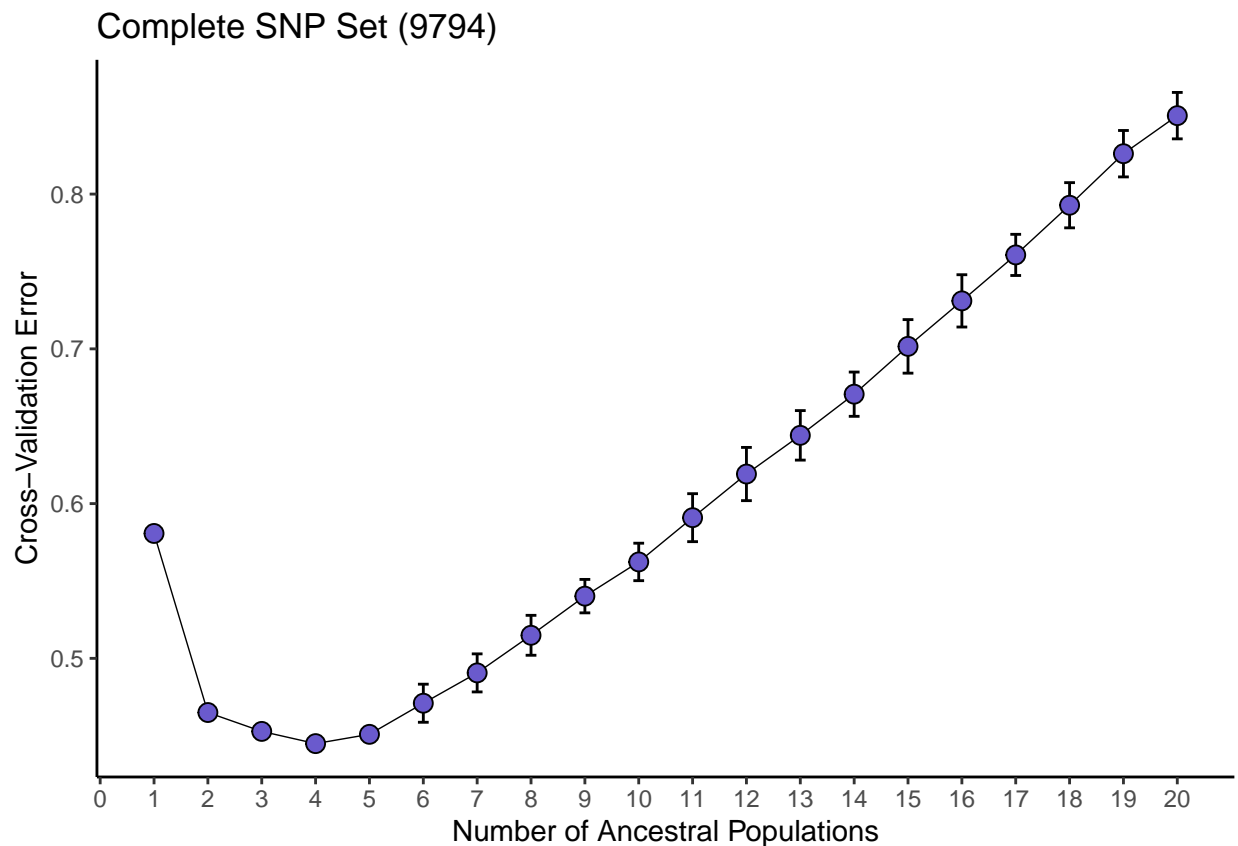
```
#Pop info
pops=read.table("./PopMap4.txt", header = TRUE)
meta<-read.csv("~/Desktop/PYRA/Publications/Genomics_Data/DATA/FINAL/geofile2.csv", header = TRUE)
metaGB<-read.csv("geofile_GB.csv", header = TRUE)
popsGB=read.table("PopMap_GB.txt",header = TRUE)
```

```
#Plot average cross-validation error against K value
```

```
Admix.C.CV=ggplot(Cresults, aes(x = K, y = CV_Avg)) +
  geom_line(color = "black", size = 0.25 ) +
  geom_errorbar(aes(ymin = CV_Avg-CV_Stdev, ymax = CV_Avg+CV_Stdev),width=.2,
    position=position_dodge(0.05)) +
  geom_point(shape = 21, size = 3, color = "black", fill = "slateblue") +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  labs(x = "Number of Ancestral Populations", y = "Cross-Validation Error") +
  theme_classic()+
  ggtitle("Complete SNP Set (9794)")
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

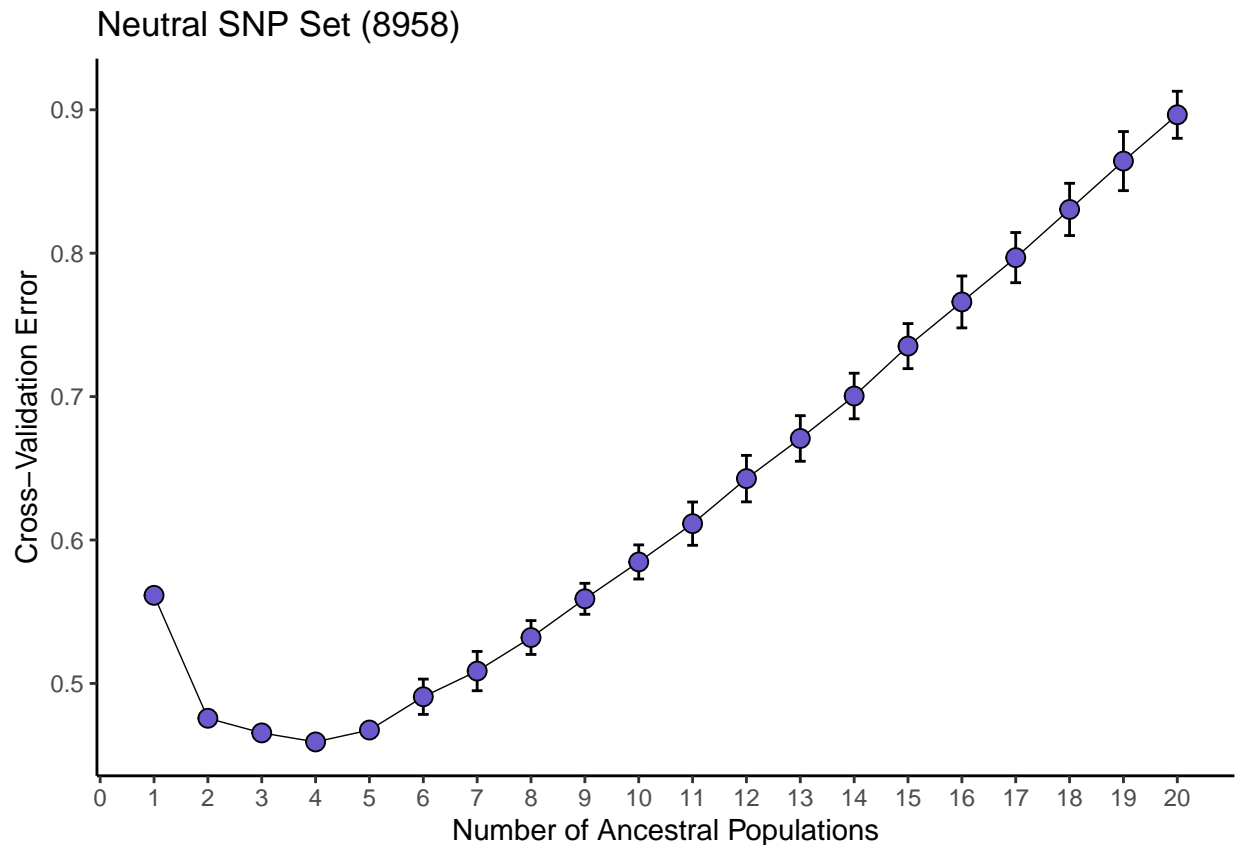
```
Admix.C.CV
```



```
ggsave("./Figures/Complete_9794_123ind_CV.pdf")
```

```
## Saving 6.5 x 4.5 in image
```

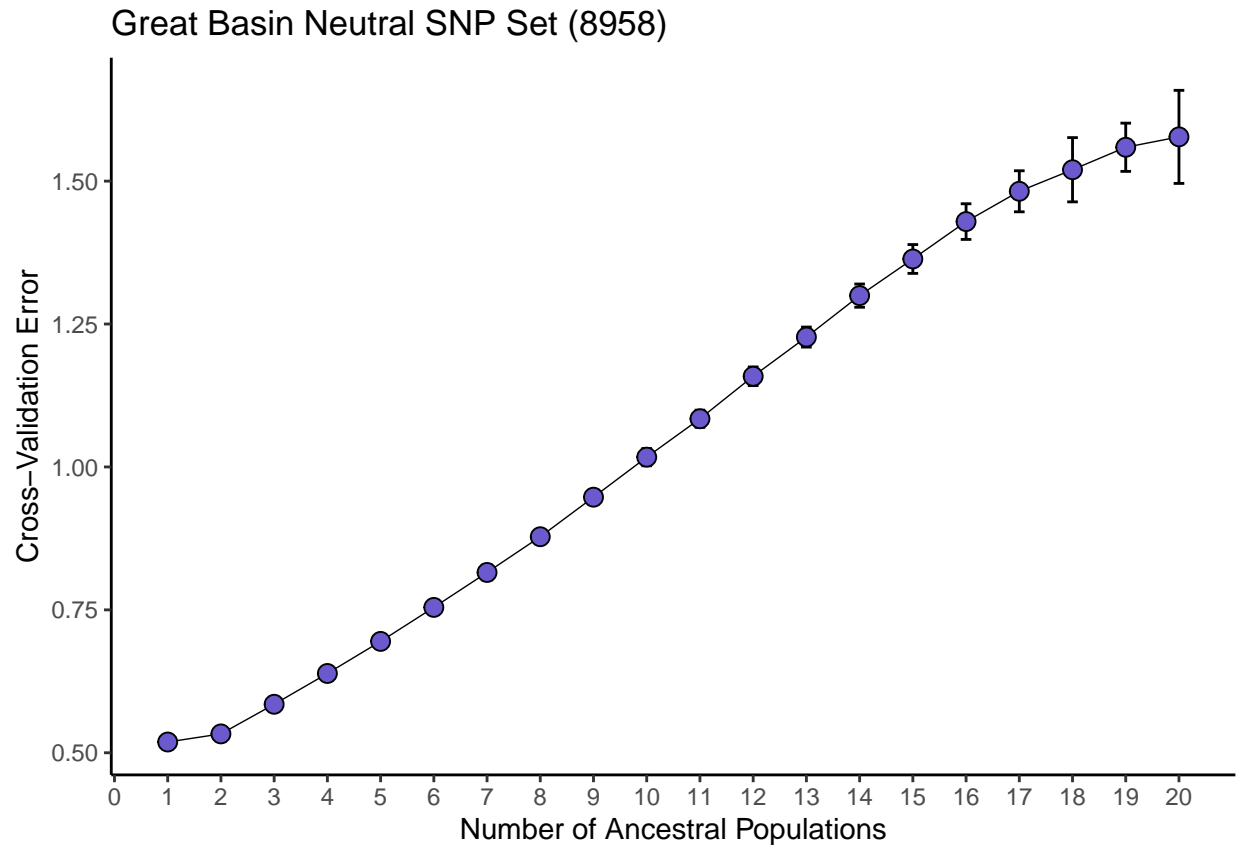
```
Admix.N.CV=ggplot(Nresults, aes(x = K, y = CV_Avg)) +
  geom_line(color = "black", size = 0.25 ) +
  geom_errorbar(aes(ymin = CV_Avg-CV_Stdev, ymax = CV_Avg+CV_Stdev),width=.2,
    position=position_dodge(0.05)) +
  geom_point(shape = 21, size = 3, color = "black", fill = "slateblue") +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  labs(x = "Number of Ancestral Populations", y = "Cross-Validation Error") +
  theme_classic()+
  ggtitle("Neutral SNP Set (8958)")
Admix.N.CV
```



```
ggsave("./Figures/Neutral_8958_123ind_CV.pdf")
```

Saving 6.5 x 4.5 in image

```
Admix.GB.N.CV=ggplot(GNresults, aes(x = K, y = CV_Avg)) +
  geom_line(color = "black", size = 0.25 ) +
  geom_errorbar(aes(ymin = CV_Avg-CV_Stdev, ymax = CV_Avg+CV_Stdev),width=.2,
    position=position_dodge(0.05)) +
  geom_point(shape = 21, size = 3, color = "black", fill = "slateblue") +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  labs(x = "Number of Ancestral Populations", y = "Cross-Validation Error") +
  theme_classic()+
  ggtitle("Great Basin Neutral SNP Set (8958)")
Admix.GB.N.CV
```

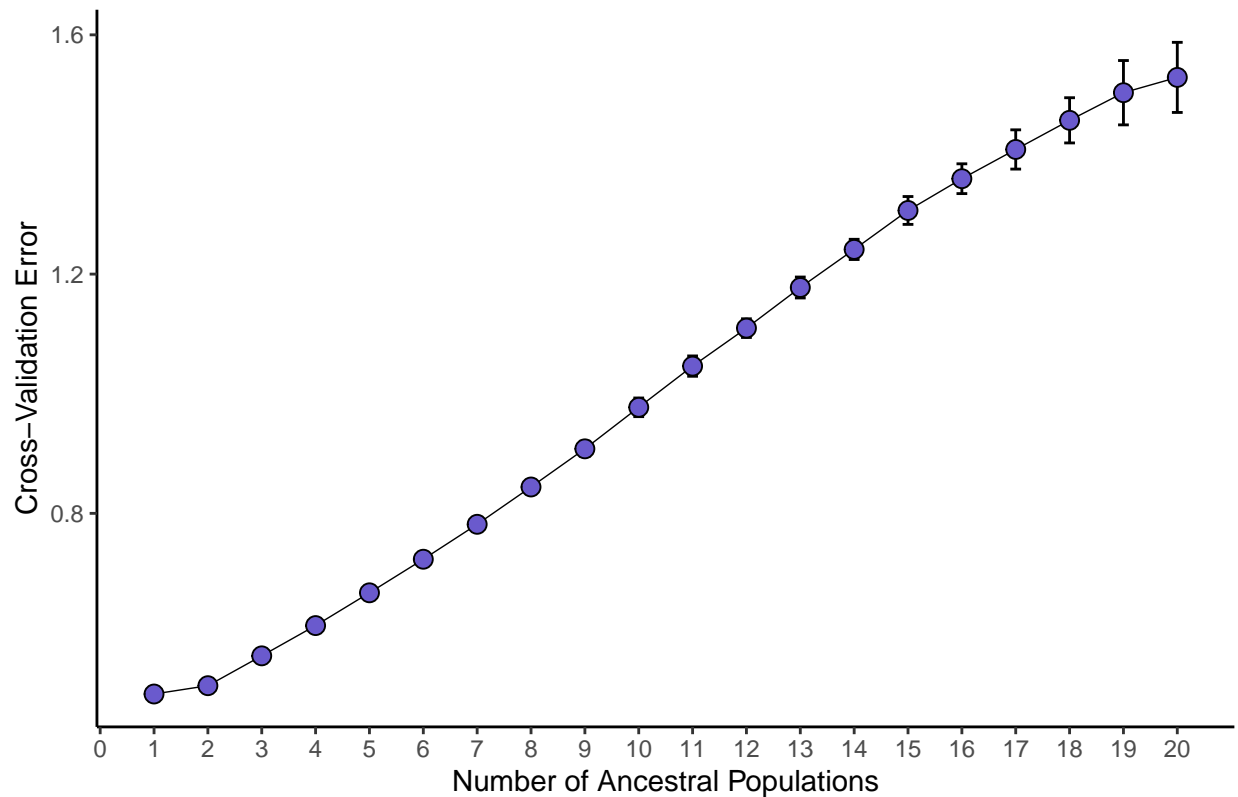


```
ggsave("./Figures/GB_Neutral_8958_75ind_CV.pdf")
```

```
## Saving 6.5 x 4.5 in image
```

```
Admix.GB.C.CV=ggplot(GCresults, aes(x = K, y = CV_Avg)) +
  geom_line(color = "black", size = 0.25 ) +
  geom_errorbar(aes(ymin = CV_Avg-CV_Stdev, ymax = CV_Avg+CV_Stdev),width=.2,
    position=position_dodge(0.05)) +
  geom_point(shape = 21, size = 3, color = "black", fill = "slateblue") +
  scale_x_continuous(breaks = seq(0, 20, by = 1)) +
  labs(x = "Number of Ancestral Populations", y = "Cross-Validation Error") +
  theme_classic()+
  ggtitle("Great Basin Complete SNP Set (9794)")
Admix.GB.C.CV
```

Great Basin Complete SNP Set (9794)



```
ggsave("./Figures/GB_Complete_9794_75ind_CV.pdf")
```

```
## Saving 6.5 x 4.5 in image
```

```
#Read in Admixture data
```

```
Cad2=read.table("./Complete_9794_no_scaffold_noX_recode.2.44.Q")
Cad3=read.table("./Complete_9794_no_scaffold_noX_recode.3.30.Q")
Cad4=read.table("./Complete_9794_no_scaffold_noX_recode.4.48.Q")
Cad5=read.table("./Complete_9794_no_scaffold_noX_recode.5.23.Q")
Cad6=read.table("./Complete_9794_no_scaffold_noX_recode.6.6.Q")
Nad2=read.table("./Neutral_8958.2.41.Q")
Nad3=read.table("./Neutral_8958.3.50.Q")
Nad4=read.table("./Neutral_8958.4.36.Q")
Nad5=read.table("./Neutral_8958.5.20.Q")
Nad6=read.table("./Neutral_8958.6.7.Q")
CGad2=read.table("./GB75_Complete_9794.2.34.Q")
CGad3=read.table("./GB75_Complete_9794.3.40.Q")
CGad4=read.table("./GB75_Complete_9794.4.36.Q")
NGad2=read.table("./GB75_Neutral_8958.2.50.Q")
NGad3=read.table("./GB75_Neutral_8958.3.15.Q")
NGad4=read.table("./GB75_Neutral_8958.4.33.Q")

colnames(Cad2) <- paste0("P", 1:2)
colnames(Cad3) <- paste0("P", 1:3)
```



```

colnames(Cad4) <- paste0("P", 1:4)
colnames(Cad5) <- paste0("P", 1:5)
colnames(Cad6) <- paste0("P", 1:6)

colnames(Nad2) <- paste0("P", 1:2)
colnames(Nad3) <- paste0("P", 1:3)
colnames(Nad4) <- paste0("P", 1:4)
colnames(Nad5) <- paste0("P", 1:5)
colnames(Nad6) <- paste0("P", 1:6)

colnames(CGad2) <- paste0("P", 1:2)
colnames(CGad3) <- paste0("P", 1:3)
colnames(CGad4) <- paste0("P", 1:4)

colnames(NGad2) <- paste0("P", 1:2)
colnames(NGad3) <- paste0("P", 1:3)
colnames(NGad4) <- paste0("P", 1:4)

```

#K2-Admixture Data

```

Cad2_df <- Cad2 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Cad2_df

```

```

## # A tibble: 123 x 9
##       P1      P2 individual region order  lat  long site      region2
##   <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>
## 1 0.981 0.0191 KCLA-B01    CA      1  37.7 -119. MonoBsn CA
## 2 1.00 0.00001 KCLA-B03    CA      2  37.7 -119. MonoBsn CA
## 3 0.987 0.0126 KCLA-B04    CA      3  37.7 -119. MonoBsn CA
## 4 0.979 0.0214 KCLA-B16    CA      4  37.7 -119. MonoBsn CA
## 5 0.00001 1.00  ARANEA     WA     107  47.5 -120. ColumbBsn WA
## 6 0.00001 1.00  BASIL      WA     119  47.5 -120. ColumbBsn WA
## 7 0.00001 1.00  BESS       WA     123  47.5 -120. ColumbBsn WA
## 8 0.00001 1.00  BRYN       WA     110  47.5 -120. ColumbBsn WA
## 9 0.00001 1.00  CHAEN      WA     115  47.5 -120. ColumbBsn WA
## 10 0.00001 1.00  CHIVE      WA     117  47.5 -120. ColumbBsn WA
## # i 113 more rows

```

```

Nad2_df <- Nad2 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,

```

```

order = pops$Order,
lat=meta$Lat,
long=meta$Long,
site=meta$Site,
region2=pops$Region2)

```

Nad2_df

```

## # A tibble: 123 x 9
##       P1      P2 individual region order  lat  long site      region2
##       <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>
## 1 0.968 0.0325 KCLA-B01  CA      1  37.7 -119. MonoBsn  CA
## 2 0.983 0.0170 KCLA-B03  CA      2  37.7 -119. MonoBsn  CA
## 3 0.975 0.0252 KCLA-B04  CA      3  37.7 -119. MonoBsn  CA
## 4 0.952 0.0481 KCLA-B16  CA      4  37.7 -119. MonoBsn  CA
## 5 0.00001 1.00  ARANEA    WA     107  47.5 -120. ColumbBsn WA
## 6 0.00001 1.00  BASIL     WA     119  47.5 -120. ColumbBsn WA
## 7 0.00001 1.00  BESS      WA     123  47.5 -120. ColumbBsn WA
## 8 0.00001 1.00  BRYN      WA     110  47.5 -120. ColumbBsn WA
## 9 0.00001 1.00  CHAEN     WA     115  47.5 -120. ColumbBsn WA
## 10 0.00001 1.00  CHIVE     WA     117  47.5 -120. ColumbBsn WA
## # i 113 more rows

```

#K3-Admixture Data

```

Cad3_df <- Cad3 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)

```

Cad3_df

```

## # A tibble: 123 x 10
##       P1      P2      P3 individual region order  lat  long site      region2
##       <dbl> <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>
## 1 0.0151 0.0402 0.945  KCLA-B01  CA      1  37.7 -119. MonoBsn  CA
## 2 0.00001 0.0434 0.957  KCLA-B03  CA      2  37.7 -119. MonoBsn  CA
## 3 0.00001 0.0405 0.959  KCLA-B04  CA      3  37.7 -119. MonoBsn  CA
## 4 0.0127 0.0577 0.930  KCLA-B16  CA      4  37.7 -119. MonoBsn  CA
## 5 1.00 0.00001 0.00001 ARANEA    WA     107  47.5 -120. ColumbBsn WA
## 6 1.00 0.00001 0.00001 BASIL     WA     119  47.5 -120. ColumbBsn WA
## 7 1.00 0.00001 0.00001 BESS      WA     123  47.5 -120. ColumbBsn WA
## 8 1.00 0.00001 0.00001 BRYN      WA     110  47.5 -120. ColumbBsn WA
## 9 1.00 0.00001 0.00001 CHAEN     WA     115  47.5 -120. ColumbBsn WA
## 10 1.00 0.00001 0.00001 CHIVE     WA     117  47.5 -120. ColumbBsn WA
## # i 113 more rows

```

```
Nad3_df <- Nad3 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Nad3_df
```

```
## # A tibble: 123 x 10
##       P1      P2      P3 individual region order  lat  long site    region2
##       <dbl> <dbl> <dbl> <chr>    <chr>  <int> <dbl> <dbl> <chr>    <chr>
## 1 0.942  0.0209 0.0366 KCLA-B01  CA      1  37.7 -119. MonoBsn  CA
## 2 0.954  0.00129 0.0448 KCLA-B03  CA      2  37.7 -119. MonoBsn  CA
## 3 0.947  0.0101 0.0427 KCLA-B04  CA      3  37.7 -119. MonoBsn  CA
## 4 0.913  0.0334 0.0540 KCLA-B16  CA      4  37.7 -119. MonoBsn  CA
## 5 0.00001 1.00    0.00001 ARANEA    WA     107  47.5 -120. ColumBsn WA
## 6 0.00001 1.00    0.00001 BASIL     WA     119  47.5 -120. ColumBsn WA
## 7 0.00001 1.00    0.00001 BESS     WA     123  47.5 -120. ColumBsn WA
## 8 0.00001 1.00    0.00001 BRYN     WA     110  47.5 -120. ColumBsn WA
## 9 0.00001 1.00    0.00001 CHAEN    WA     115  47.5 -120. ColumBsn WA
## 10 0.00001 1.00    0.00001 CHIVE    WA     117  47.5 -120. ColumBsn WA
## # i 113 more rows
```

#K4-Admixture Data

```
Cad4_df <- Cad4 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Cad4_df
```

```
## # A tibble: 123 x 11
##       P1      P2      P3      P4 individual region order  lat  long site    region2
##       <dbl> <dbl> <dbl> <dbl> <chr>    <chr>  <int> <dbl> <dbl> <chr>    <chr>
## 1 0.717  0.0146 0.230  0.0389 KCLA-B01  CA      1  37.7 -119. MonoBsn
## 2 0.766  0.00001 0.203  0.0303 KCLA-B03  CA      2  37.7 -119. MonoBsn
## 3 0.732  0.00001 0.235  0.0334 KCLA-B04  CA      3  37.7 -119. MonoBsn
## 4 0.704  0.0131 0.231  0.0525 KCLA-B16  CA      4  37.7 -119. MonoBsn
## 5 0.000019 1.00    0.00001 0.00001 ARANEA    WA     107  47.5 -120. ColumB~
## 6 0.00001 1.00    0.00001 0.00001 BASIL     WA     119  47.5 -120. ColumB~
## 7 0.00001 1.00    0.00001 0.00001 BESS     WA     123  47.5 -120. ColumB~
## 8 0.00001 1.00    0.00001 0.00001 BRYN     WA     110  47.5 -120. ColumB~
```

```
## 9 0.00001 1.00 0.00001 0.00001 CHAEN WA 115 47.5 -120. ColumB~
## 10 0.00001 1.00 0.00001 0.00001 CHIVE WA 117 47.5 -120. ColumB~
## # i 113 more rows
## # i 1 more variable: region2 <chr>
```

```
Nad4_df <- Nad4 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Nad4_df
```

```
## # A tibble: 123 x 11
##       P1      P2      P3      P4 individual region order  lat  long site
##       <dbl> <dbl> <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>
## 1 0.0109 0.449 0.515 0.0251 KCLA-B01 CA      1 37.7 -119. MonoBsn
## 2 0.00001 0.435 0.532 0.0331 KCLA-B03 CA      2 37.7 -119. MonoBsn
## 3 0.00110 0.460 0.506 0.0332 KCLA-B04 CA      3 37.7 -119. MonoBsn
## 4 0.0169 0.479 0.466 0.0380 KCLA-B16 CA      4 37.7 -119. MonoBsn
## 5 1.00 0.00001 0.00001 0.00001 ARANEA WA     107 47.5 -120. ColumBsn
## 6 1.00 0.00001 0.00001 0.00001 BASIL WA     119 47.5 -120. ColumBsn
## 7 1.00 0.00001 0.00001 0.00001 BESS WA     123 47.5 -120. ColumBsn
## 8 1.00 0.00001 0.00001 0.00001 BRYN WA     110 47.5 -120. ColumBsn
## 9 1.00 0.00001 0.00001 0.00001 CHAEN WA     115 47.5 -120. ColumBsn
## 10 1.00 0.00001 0.00001 0.00001 CHIVE WA     117 47.5 -120. ColumBsn
## # i 113 more rows
## # i 1 more variable: region2 <chr>
```

#K5-Admixture Data

```
Cad5_df <- Cad5 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Cad5_df
```

```
## # A tibble: 123 x 12
##       P1      P2      P3      P4      P5 individual region order  lat  long
##       <dbl> <dbl> <dbl> <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl>
## 1 0.0389 0.0140 0.228 0.00001 0.720 KCLA-B01 CA      1 37.7 -119.
## 2 0.0305 0.000012 0.202 0.00001 0.768 KCLA-B03 CA      2 37.7 -119.
## 3 0.0339 0.00001 0.232 0.00166 0.732 KCLA-B04 CA      3 37.7 -119.
```

```
## 4 0.0529 0.00001 0.225 0.0159 0.706 KCLA-B16 CA 4 37.7 -119.
## 5 0.000013 0.542 0.00001 0.458 0.00001 ARANEA WA 107 47.5 -120.
## 6 0.000014 1.00 0.00001 0.00001 0.00001 BASIL WA 119 47.5 -120.
## 7 0.000011 0.00001 0.00001 1.00 0.00001 BESS WA 123 47.5 -120.
## 8 0.000015 0.154 0.00001 0.846 0.00001 BRYN WA 110 47.5 -120.
## 9 0.00001 1.00 0.00001 0.00001 0.00001 CHAEN WA 115 47.5 -120.
## 10 0.00001 1.00 0.00001 0.00001 0.00001 CHIVE WA 117 47.5 -120.
## # i 113 more rows
## # i 2 more variables: site <chr>, region2 <chr>
```

```
Nad5_df <- Nad5 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Nad5_df
```

```
## # A tibble: 123 x 12
##       P1      P2      P3      P4      P5 individual region order  lat  long
##   <dbl> <dbl> <dbl> <dbl> <dbl> <chr>    <chr> <int> <dbl> <dbl>
## 1 0.0265 0.443 0.514 0.00001 0.0162 KCLA-B01 CA      1 37.7 -119.
## 2 0.0339 0.431 0.532 0.00001 0.00326 KCLA-B03 CA      2 37.7 -119.
## 3 0.0340 0.455 0.506 0.00447 0.00001 KCLA-B04 CA      3 37.7 -119.
## 4 0.0391 0.472 0.467 0.0222 0.00001 KCLA-B16 CA      4 37.7 -119.
## 5 0.00001 0.00001 0.00001 0.527 0.473 ARANEA WA    107 47.5 -120.
## 6 0.00002 0.00001 0.00001 0.00001 1.00 BASIL WA    119 47.5 -120.
## 7 0.00001 0.00001 0.00001 1.00 0.00001 BESS WA    123 47.5 -120.
## 8 0.00001 0.00001 0.00001 0.908 0.0919 BRYN WA    110 47.5 -120.
## 9 0.00001 0.00001 0.00001 0.131 0.869 CHAEN WA    115 47.5 -120.
## 10 0.00001 0.00001 0.00001 0.00001 1.00 CHIVE WA    117 47.5 -120.
## # i 113 more rows
## # i 2 more variables: site <chr>, region2 <chr>
```

#K6-Admixture Data

```
Cad6_df <- Cad6 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Cad6_df
```

```
## # A tibble: 123 x 13
```

```
##          P1          P2          P3          P4          P5          P6 individual region order  lat
##          <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl> <chr>      <chr>  <int> <dbl>
##  1 1.00          0.00001 0.00001 0.00001 0.00001 1e-5 KCLA-B01  CA        1  37.7
##  2 1.00          0.00001 0.00001 0.00001 0.00001 1e-5 KCLA-B03  CA        2  37.7
##  3 1.00          0.00001 0.00001 0.00001 0.00001 1e-5 KCLA-B04  CA        3  37.7
##  4 1.00          0.00001 0.00001 0.00001 0.00001 1e-5 KCLA-B16  CA        4  37.7
##  5 0.000014 0.00001 0.538  0.462  0.00001 1e-5 ARANEA  WA       107  47.5
##  6 0.00001 0.00001 1.00  0.00001 0.00001 1e-5 BASIL   WA       119  47.5
##  7 0.00001 0.00001 0.00001 1.00  0.00001 1e-5 BESS    WA       123  47.5
##  8 0.00001 0.000016 0.148  0.852  0.00001 1e-5 BRYN    WA       110  47.5
##  9 0.00001 0.00001 1.00  0.00001 0.00001 1e-5 CHAEN    WA       115  47.5
## 10 0.00001 0.00001 1.00  0.00001 0.00001 1e-5 CHIVE     WA       117  47.5
## # i 113 more rows
## # i 3 more variables: long <dbl>, site <chr>, region2 <chr>
```

```
Nad6_df <- Nad6 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = pops$INDIVIDUALS,
         region = pops$Region,
         order = pops$Order,
         lat=meta$Lat,
         long=meta$Long,
         site=meta$Site,
         region2=pops$Region2)
Nad6_df
```

```
## # A tibble: 123 x 13
##          P1          P2          P3          P4          P5          P6 individual region order  lat  long
##          <dbl>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl> <chr>      <chr>  <int> <dbl> <dbl>
##  1 1e-5 1.00e+0 1e-5 1e-5 0.00001 0.00001 KCLA-B01  CA        1  37.7 -119.
##  2 1e-5 1.00e+0 1e-5 1e-5 0.00001 0.00001 KCLA-B03  CA        2  37.7 -119.
##  3 1e-5 1.00e+0 1e-5 1e-5 0.00001 0.00001 KCLA-B04  CA        3  37.7 -119.
##  4 1e-5 1.00e+0 1e-5 1e-5 0.00001 0.00001 KCLA-B16  CA        4  37.7 -119.
##  5 1e-5 1.9 e-5 1e-5 1e-5 0.471  0.529  ARANEA  WA       107  47.5 -120.
##  6 1e-5 1 e-5 1e-5 1e-5 1.00  0.00001 BASIL   WA       119  47.5 -120.
##  7 1e-5 1 e-5 1e-5 1e-5 0.00001 1.00  BESS    WA       123  47.5 -120.
##  8 1e-5 1 e-5 1e-5 1e-5 0.0855 0.914  BRYN    WA       110  47.5 -120.
##  9 1e-5 1 e-5 1e-5 1e-5 0.866 0.134  CHAEN    WA       115  47.5 -120.
## 10 1e-5 1 e-5 1e-5 1e-5 1.00  0.00001 CHIVE     WA       117  47.5 -120.
## # i 113 more rows
## # i 2 more variables: site <chr>, region2 <chr>
```

#K2-GB Admixture Data

```
CGad2_df <- CGad2 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,
         region = popsGB$Region,
         order = popsGB$Order,
         lat=metaGB$Lat,
         long=metaGB$Long,
```

```

    site=metaGB$Site,
    region2=popsGB$Region2)
CGad2_df

```

```

## # A tibble: 75 x 9
##       P1      P2 individual region order  lat  long site      region2
##       <dbl>   <dbl> <chr>      <chr>   <int> <dbl> <dbl> <chr>      <chr>
##  1 1.00    0.00001 KCLA-B01    CA         1  37.7 -119. MonoBsn    CA
##  2 1.00    0.00001 KCLA-B03    CA         2  37.7 -119. MonoBsn    CA
##  3 1.00    0.00001 KCLA-B04    CA         3  37.7 -119. MonoBsn    CA
##  4 1.00    0.00001 KCLA-B16    CA         4  37.7 -119. MonoBsn    CA
##  5 0.235    0.765   8M1        ID        43  44.2 -113. IDNLemhi  IDN
##  6 0.221    0.779   8M7        ID        44  44.2 -113. IDNLemhi  IDN
##  7 0.00001  1.00    ALLIE_ID    ID        46  43.5 -112. IDNINL    IDN
##  8 1.00    0.00001 ALLIE_NV    NV        20  40.0 -115. NVParisCk  NV
##  9 1.00    0.00001 ALLISON    NV        12  39.7 -115. NVOven    NV
## 10 0.727    0.273   CAS2        ID        26  42.2 -114. IDSCas    IDS
## # i 65 more rows

```

```

NGad2_df <- NGad2 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,
    region = popsGB$Region,
    order = popsGB$Order,
    lat=metaGB$Lat,
    long=metaGB$Long,
    site=metaGB$Site,
    region2=popsGB$Region2)
NGad2_df

```

```

## # A tibble: 75 x 9
##       P1      P2 individual region order  lat  long site      region2
##       <dbl>   <dbl> <chr>      <chr>   <int> <dbl> <dbl> <chr>      <chr>
##  1 0.00001  1.00    KCLA-B01    CA         1  37.7 -119. MonoBsn    CA
##  2 0.00001  1.00    KCLA-B03    CA         2  37.7 -119. MonoBsn    CA
##  3 0.00001  1.00    KCLA-B04    CA         3  37.7 -119. MonoBsn    CA
##  4 0.00001  1.00    KCLA-B16    CA         4  37.7 -119. MonoBsn    CA
##  5 0.730    0.270   8M1        ID        43  44.2 -113. IDNLemhi  IDN
##  6 0.766    0.234   8M7        ID        44  44.2 -113. IDNLemhi  IDN
##  7 1.00    0.00001 ALLIE_ID    ID        46  43.5 -112. IDNINL    IDN
##  8 0.00001  1.00    ALLIE_NV    NV        20  40.0 -115. NVParisCk  NV
##  9 0.00001  1.00    ALLISON    NV        12  39.7 -115. NVOven    NV
## 10 0.262    0.738   CAS2        ID        26  42.2 -114. IDSCas    IDS
## # i 65 more rows

```

#K3-GB Admixture Data

```

CGad3_df <- CGad3 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,

```

```

    region = popsGB$Region,
    order = popsGB$Order,
    lat=metaGB$Lat,
    long=metaGB$Long,
    site=metaGB$Site,
    region2=popsGB$Region2)
CGad3_df

```

```

## # A tibble: 75 x 10
##       P1      P2      P3 individual region order  lat  long site    region2
##       <dbl> <dbl> <dbl> <chr>    <chr>  <int> <dbl> <dbl> <chr>    <chr>
##  1 0.00001 1.00    0.00001 KCLA-B01  CA      1  37.7 -119. MonoBsn  CA
##  2 0.00001 1.00    0.00001 KCLA-B03  CA      2  37.7 -119. MonoBsn  CA
##  3 0.00001 1.00    0.00001 KCLA-B04  CA      3  37.7 -119. MonoBsn  CA
##  4 0.00001 1.00    0.00001 KCLA-B16  CA      4  37.7 -119. MonoBsn  CA
##  5 0.452    0.0519  0.496    8M1      ID     43  44.2 -113. IDNLemhi  IDN
##  6 0.510    0.0817  0.408    8M7      ID     44  44.2 -113. IDNLemhi  IDN
##  7 1.00     0.00001  0.00001 ALLIE_ID  ID     46  43.5 -112. IDNINL   IDN
##  8 0.00001 1.00    0.00001 ALLIE_NV  NV     20  40.0 -115. NVParisCk  NV
##  9 0.00001 1.00    0.00001 ALLISON   NV     12  39.7 -115. NVOven    NV
## 10 0.129    0.628   0.244    CAS2      ID     26  42.2 -114. IDSCas   IDS
## # i 65 more rows

```

```

NGad3_df <- NGad3 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,
    region = popsGB$Region,
    order = popsGB$Order,
    lat=metaGB$Lat,
    long=metaGB$Long,
    site=metaGB$Site,
    region2=popsGB$Region2)
NGad3_df

```

```

## # A tibble: 75 x 10
##       P1      P2      P3 individual region order  lat  long site    region2
##       <dbl> <dbl> <dbl> <chr>    <chr>  <int> <dbl> <dbl> <chr>    <chr>
##  1 1.00     0.00001 0.00001 KCLA-B01  CA      1  37.7 -119. MonoBsn  CA
##  2 1.00     0.00001 0.00001 KCLA-B03  CA      2  37.7 -119. MonoBsn  CA
##  3 1.00     0.00001 0.00001 KCLA-B04  CA      3  37.7 -119. MonoBsn  CA
##  4 1.00     0.00001 0.00001 KCLA-B16  CA      4  37.7 -119. MonoBsn  CA
##  5 0.115    0.367   0.518    8M1      ID     43  44.2 -113. IDNLemhi  IDN
##  6 0.173    0.553   0.273    8M7      ID     44  44.2 -113. IDNLemhi  IDN
##  7 0.00001 0.798   0.202    ALLIE_ID  ID     46  43.5 -112. IDNINL   IDN
##  8 1.00     0.00001 0.00001 ALLIE_NV  NV     20  40.0 -115. NVParisCk  NV
##  9 0.893    0.00001 0.107    ALLISON   NV     12  39.7 -115. NVOven    NV
## 10 0.704    0.214   0.0818   CAS2      ID     26  42.2 -114. IDSCas   IDS
## # i 65 more rows

```

#K4-GB Admixture Data


```
CGad4_df <- CGad4 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,
         region = popsGB$Region,
         order = popsGB$Order,
         lat=metaGB$Lat,
         long=metaGB$Long,
         site=metaGB$Site,
         region2=popsGB$Region2)
CGad4_df
```

```
## # A tibble: 75 x 11
##       P1      P2      P3      P4 individual region order  lat  long site
##       <dbl> <dbl> <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>
##  1 1.00    0.00001 0.00001 0.00001 KCLA-B01    CA      1  37.7 -119. MonoBsn
##  2 1.00    0.00001 0.00001 0.00001 KCLA-B03    CA      2  37.7 -119. MonoBsn
##  3 1.00    0.00001 0.00001 0.00001 KCLA-B04    CA      3  37.7 -119. MonoBsn
##  4 1.00    0.00001 0.00001 0.00001 KCLA-B16    CA      4  37.7 -119. MonoBsn
##  5 0.407    0.422    0.171    0.00001 8M1        ID     43  44.2 -113. IDNLemhi
##  6 0.00001 0.542    0.245    0.212    8M7        ID     44  44.2 -113. IDNLemhi
##  7 0.00001 0.894    0.106    0.00001 ALLIE_ID    ID     46  43.5 -112. IDNINL
##  8 0.0376   0.00001 0.00001 0.962    ALLIE_NV    NV     20  40.0 -115. NVParisCk
##  9 0.521    0.00001 0.00001 0.479    ALLISON     NV     12  39.7 -115. NVOven
## 10 0.162    0.0358   0.269    0.534    CAS2        ID     26  42.2 -114. IDSCas
## # i 65 more rows
## # i 1 more variable: region2 <chr>
```

```
NGad4_df <- NGad4 %>%
  as_tibble() %>%
  # add the pops data for plotting
  mutate(individual = popsGB$INDIVIDUALS,
         region = popsGB$Region,
         order = popsGB$Order,
         lat=metaGB$Lat,
         long=metaGB$Long,
         site=metaGB$Site,
         region2=popsGB$Region2)
NGad4_df
```

```
## # A tibble: 75 x 11
##       P1      P2      P3      P4 individual region order  lat  long site
##       <dbl> <dbl> <dbl> <dbl> <chr>      <chr> <int> <dbl> <dbl> <chr>
##  1 0.00001 0.00001 0.00001 1.00    KCLA-B01    CA      1  37.7 -119. MonoBsn
##  2 0.00001 0.00001 0.00001 1.00    KCLA-B03    CA      2  37.7 -119. MonoBsn
##  3 0.00001 0.00001 0.00001 1.00    KCLA-B04    CA      3  37.7 -119. MonoBsn
##  4 0.00001 0.00001 0.00001 1.00    KCLA-B16    CA      4  37.7 -119. MonoBsn
##  5 0.458    0.00001 0.134    0.408    8M1        ID     43  44.2 -113. IDNLemhi
##  6 0.613    0.228    0.159    0.00001 8M7        ID     44  44.2 -113. IDNLemhi
##  7 0.863    0.00001 0.0805   0.0561   ALLIE_ID    ID     46  43.5 -112. IDNINL
##  8 0.00001 0.891    0.00001 0.109    ALLIE_NV    NV     20  40.0 -115. NVParisCk
##  9 0.00001 0.459    0.00001 0.541    ALLISON     NV     12  39.7 -115. NVOven
## 10 0.162    0.553    0.124    0.160    CAS2        ID     26  42.2 -114. IDSCas
```

```
## # i 65 more rows
## # i 1 more variable: region2 <chr>
```

#Long Format of Admixture Data

```
Cad2_df_long <- Cad2_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Cad2_df_long
```

```
## # A tibble: 246 x 9
##   individual region order  lat  long site      region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn  CA      P1    0.981
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn  CA      P2    0.0191
## 3 KCLA-B03   CA      2  37.7 -119. MonoBsn  CA      P1    1.00
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn  CA      P2    0.00001
## 5 KCLA-B04   CA      3  37.7 -119. MonoBsn  CA      P1    0.987
## 6 KCLA-B04   CA      3  37.7 -119. MonoBsn  CA      P2    0.0126
## 7 KCLA-B16   CA      4  37.7 -119. MonoBsn  CA      P1    0.979
## 8 KCLA-B16   CA      4  37.7 -119. MonoBsn  CA      P2    0.0214
## 9 ARANEA     WA     107  47.5 -120. ColumbBsn WA      P1    0.00001
## 10 ARANEA     WA     107  47.5 -120. ColumbBsn WA      P2    1.00
## # i 236 more rows
```

```
Nad2_df_long <- Nad2_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Nad2_df_long
```

```
## # A tibble: 246 x 9
##   individual region order  lat  long site      region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn  CA      P1    0.968
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn  CA      P2    0.0325
## 3 KCLA-B03   CA      2  37.7 -119. MonoBsn  CA      P1    0.983
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn  CA      P2    0.0170
## 5 KCLA-B04   CA      3  37.7 -119. MonoBsn  CA      P1    0.975
## 6 KCLA-B04   CA      3  37.7 -119. MonoBsn  CA      P2    0.0252
## 7 KCLA-B16   CA      4  37.7 -119. MonoBsn  CA      P1    0.952
## 8 KCLA-B16   CA      4  37.7 -119. MonoBsn  CA      P2    0.0481
## 9 ARANEA     WA     107  47.5 -120. ColumbBsn WA      P1    0.00001
## 10 ARANEA     WA     107  47.5 -120. ColumbBsn WA      P2    1.00
## # i 236 more rows
```

```
Cad3_df_long <- Cad3_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Cad3_df_long
```

```
## # A tibble: 369 x 9
##   individual region order  lat  long site      region2 pop      q
```

```
##      <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>      <chr>      <dbl>
## 1 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P1      0.0151
## 2 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P2      0.0402
## 3 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P3      0.945
## 4 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P1      0.00001
## 5 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P2      0.0434
## 6 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P3      0.957
## 7 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P1      0.00001
## 8 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P2      0.0405
## 9 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P3      0.959
## 10 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1      0.0127
## # i 359 more rows
```

```
Nad3_df_long <- Nad3_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Nad3_df_long
```

```
## # A tibble: 369 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>      <chr>      <dbl>
## 1 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P1      0.942
## 2 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P2      0.0209
## 3 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P3      0.0366
## 4 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P1      0.954
## 5 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P2      0.00129
## 6 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P3      0.0448
## 7 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P1      0.947
## 8 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P2      0.0101
## 9 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P3      0.0427
## 10 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1      0.913
## # i 359 more rows
```

```
Cad4_df_long <- Cad4_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Cad4_df_long
```

```
## # A tibble: 492 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr>      <chr>      <dbl>
## 1 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P1      0.717
## 2 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P2      0.0146
## 3 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P3      0.230
## 4 KCLA-B01    CA      1  37.7 -119. MonoBsn CA      P4      0.0389
## 5 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P1      0.766
## 6 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P2      0.00001
## 7 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P3      0.203
## 8 KCLA-B03    CA      2  37.7 -119. MonoBsn CA      P4      0.0303
## 9 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P1      0.732
## 10 KCLA-B04    CA      3  37.7 -119. MonoBsn CA      P2      0.00001
## # i 482 more rows
```

```
Nad4_df_long <- Nad4_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Nad4_df_long
```

```
## # A tibble: 492 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr> <chr>    <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1     0.0109
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2     0.449
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3     0.515
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4     0.0251
## 5 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1     0.00001
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2     0.435
## 7 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3     0.532
## 8 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P4     0.0331
## 9 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1     0.00110
## 10 KCLA-B04  CA      3  37.7 -119. MonoBsn CA      P2     0.460
## # i 482 more rows
```

```
Cad5_df_long <- Cad5_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Cad5_df_long
```

```
## # A tibble: 615 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr> <chr>    <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1     0.0389
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2     0.0140
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3     0.228
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4     0.00001
## 5 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P5     0.720
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1     0.0305
## 7 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2     0.000012
## 8 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3     0.202
## 9 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P4     0.00001
## 10 KCLA-B03  CA      2  37.7 -119. MonoBsn CA      P5     0.768
## # i 605 more rows
```

```
Nad5_df_long <- Nad5_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Nad5_df_long
```

```
## # A tibble: 615 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr> <chr>    <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1     0.0265
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2     0.443
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3     0.514
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4     0.00001
```

```
## 5 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P5 0.0162
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.0339
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.431
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.532
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P5 0.00326
## # i 605 more rows
```

```
Cad6_df_long <- Cad6_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Cad6_df_long
```

```
## # A tibble: 738 x 9
##   individual region order lat long site region2 pop q
##   <chr> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 1.00
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.00001
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 0.00001
## 5 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P5 0.00001
## 6 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P6 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 1.00
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## # i 728 more rows
```

```
Nad6_df_long <- Nad6_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
Nad6_df_long
```

```
## # A tibble: 738 x 9
##   individual region order lat long site region2 pop q
##   <chr> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.00001
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 1.00
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 0.00001
## 5 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P5 0.00001
## 6 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P6 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 1.00
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## # i 728 more rows
```

```
CGad2_df_long <- CGad2_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
CGad2_df_long
```

```
## # A tibble: 150 x 9
##   individual region order  lat  long site      region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1      1.00
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2      0.00001
## 3 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1      1.00
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2      0.00001
## 5 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1      1.00
## 6 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P2      0.00001
## 7 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1      1.00
## 8 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P2      0.00001
## 9 8M1        ID     43  44.2 -113. IDNLemhi IDN     P1      0.235
## 10 8M1        ID     43  44.2 -113. IDNLemhi IDN     P2      0.765
## # i 140 more rows
```

```
NGad2_df_long <- NGad2_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
NGad2_df_long
```

```
## # A tibble: 150 x 9
##   individual region order  lat  long site      region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1      0.00001
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2      1.00
## 3 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1      0.00001
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2      1.00
## 5 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1      0.00001
## 6 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P2      1.00
## 7 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1      0.00001
## 8 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P2      1.00
## 9 8M1        ID     43  44.2 -113. IDNLemhi IDN     P1      0.730
## 10 8M1        ID     43  44.2 -113. IDNLemhi IDN     P2      0.270
## # i 140 more rows
```

```
CGad3_df_long <- CGad3_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
CGad3_df_long
```

```
## # A tibble: 225 x 9
##   individual region order  lat  long site      region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>      <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1      0.00001
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2      1.00
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3      0.00001
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1      0.00001
## 5 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2      1.00
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3      0.00001
## 7 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1      0.00001
## 8 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P2      1.00
## 9 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P3      0.00001
## 10 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1      0.00001
## # i 215 more rows
```

```

NGad3_df_long <- NGad3_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
NGad3_df_long

```

```

## # A tibble: 225 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>
## 1 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P1    1.00
## 2 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P2    0.00001
## 3 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P3    0.00001
## 4 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P1    1.00
## 5 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P2    0.00001
## 6 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P3    0.00001
## 7 KCLA-B04  CA        3  37.7 -119. MonoBsn CA      P1    1.00
## 8 KCLA-B04  CA        3  37.7 -119. MonoBsn CA      P2    0.00001
## 9 KCLA-B04  CA        3  37.7 -119. MonoBsn CA      P3    0.00001
## 10 KCLA-B16 CA        4  37.7 -119. MonoBsn CA      P1    1.00
## # i 215 more rows

```

```

CGad4_df_long <- CGad4_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
CGad4_df_long

```

```

## # A tibble: 300 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>
## 1 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P1    1.00
## 2 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P2    0.00001
## 3 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P3    0.00001
## 4 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P4    0.00001
## 5 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P1    1.00
## 6 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P2    0.00001
## 7 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P3    0.00001
## 8 KCLA-B03  CA        2  37.7 -119. MonoBsn CA      P4    0.00001
## 9 KCLA-B04  CA        3  37.7 -119. MonoBsn CA      P1    1.00
## 10 KCLA-B04 CA        3  37.7 -119. MonoBsn CA      P2    0.00001
## # i 290 more rows

```

```

NGad4_df_long <- NGad4_df %>%
  # transform the data to a "long" format so proportions can be plotted
  pivot_longer(cols = starts_with("P"), names_to = "pop", values_to = "q")
NGad4_df_long

```

```

## # A tibble: 300 x 9
##   individual region order  lat  long site    region2 pop      q
##   <chr>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>
## 1 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P1    0.00001
## 2 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P2    0.00001
## 3 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P3    0.00001
## 4 KCLA-B01  CA        1  37.7 -119. MonoBsn CA      P4    1.00

```

```
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 1.00
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.00001
## 10 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.00001
## # i 290 more rows
```

#Time to plot Admixture Results

#Order Admixture Data by Order Number

```
Cad2_df_long_SN <- Cad2_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Cad2_df_long_SN
```

```
## # A tibble: 246 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.981
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.0191
## 3 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 1.00
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 5 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.987
## 6 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.0126
## 7 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.979
## 8 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P2 0.0214
## 9 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P1 0.960
## 10 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P2 0.0399
## # i 236 more rows
```

```
Nad2_df_long_SN <- Nad2_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Nad2_df_long_SN
```

```
## # A tibble: 246 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.968
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.0325
## 3 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.983
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.0170
## 5 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.975
## 6 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.0252
## 7 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.952
## 8 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P2 0.0481
## 9 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P1 0.931
```



```
## 10 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P2 0.0692
## # i 236 more rows
```

```
Cad3_df_long_SN <- Cad3_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Cad3_df_long_SN
```

```
## # A tibble: 369 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.0151
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.0402
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.945
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.0434
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.957
## 7 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.00001
## 8 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.0405
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P3 0.959
## 10 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.0127
## # i 359 more rows
```

```
Nad3_df_long_SN <- Nad3_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Nad3_df_long_SN
```

```
## # A tibble: 369 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.942
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.0209
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.0366
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.954
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00129
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.0448
## 7 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.947
## 8 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.0101
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P3 0.0427
## 10 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.913
## # i 359 more rows
```

```
Cad4_df_long_SN <- Cad4_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Cad4_df_long_SN
```

```
## # A tibble: 492 x 9
##   individual region order  lat  long site  region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1    0.717
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2    0.0146
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3    0.230
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4    0.0389
## 5 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1    0.766
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2    0.00001
## 7 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3    0.203
## 8 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P4    0.0303
## 9 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1    0.732
## 10 KCLA-B04  CA      3  37.7 -119. MonoBsn CA      P2    0.00001
## # i 482 more rows
```

```
Nad4_df_long_SN <- Nad4_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Nad4_df_long_SN
```

```
## # A tibble: 492 x 9
##   individual region order  lat  long site  region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1    0.0109
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2    0.449
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3    0.515
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4    0.0251
## 5 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1    0.00001
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2    0.435
## 7 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3    0.532
## 8 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P4    0.0331
## 9 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1    0.00110
## 10 KCLA-B04  CA      3  37.7 -119. MonoBsn CA      P2    0.460
## # i 482 more rows
```

```
Cad5_df_long_SN <- Cad5_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Cad5_df_long_SN
```

```
## # A tibble: 615 x 9
##   individual region order  lat  long site  region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1    0.0389
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2    0.0140
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3    0.228
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4    0.00001
## 5 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P5    0.720
## 6 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1    0.0305
```

```
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.000012
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.202
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P5 0.768
## # i 605 more rows
```

```
Nad5_df_long_SN <- Nad5_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Nad5_df_long_SN
```

```
## # A tibble: 615 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.0265
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.443
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.514
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 0.00001
## 5 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P5 0.0162
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.0339
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.431
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.532
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P5 0.00326
## # i 605 more rows
```

```
Cad6_df_long_SN <- Cad6_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
Cad6_df_long_SN
```

```
## # A tibble: 738 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 1.00
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.00001
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 0.00001
## 5 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P5 0.00001
## 6 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P6 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 1.00
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 9 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 10 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## # i 728 more rows
```

```
Nad6_df_long_SN <- Nad6_df_long %>%
  # arrange the data set by the plot order
```

```

arrange(order) %>%
# this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
mutate(individual = forcats::fct_inorder(factor(individual)))
Nad6_df_long_SN

```

```

## # A tibble: 738 x 9
##   individual region order  lat  long site    region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1    0.00001
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2    1.00
## 3 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P3    0.00001
## 4 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P4    0.00001
## 5 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P5    0.00001
## 6 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P6    0.00001
## 7 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1    0.00001
## 8 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2    1.00
## 9 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P3    0.00001
## 10 KCLA-B03  CA      2  37.7 -119. MonoBsn CA      P4    0.00001
## # i 728 more rows

```

```

CGad2_df_long_SN <- CGad2_df_long %>%
# arrange the data set by the plot order
arrange(order) %>%
# this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
mutate(individual = forcats::fct_inorder(factor(individual)))
CGad2_df_long_SN

```

```

## # A tibble: 150 x 9
##   individual region order  lat  long site    region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>
## 1 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P1    1.00
## 2 KCLA-B01   CA      1  37.7 -119. MonoBsn CA      P2    0.00001
## 3 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P1    1.00
## 4 KCLA-B03   CA      2  37.7 -119. MonoBsn CA      P2    0.00001
## 5 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P1    1.00
## 6 KCLA-B04   CA      3  37.7 -119. MonoBsn CA      P2    0.00001
## 7 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P1    1.00
## 8 KCLA-B16   CA      4  37.7 -119. MonoBsn CA      P2    0.00001
## 9 KWGA-B64   NV      5  38.0 -114. NVWGulch NV      P1    0.870
## 10 KWGA-B64  NV      5  38.0 -114. NVWGulch NV      P2    0.130
## # i 140 more rows

```

```

NGad2_df_long_SN <- NGad2_df_long %>%
# arrange the data set by the plot order
arrange(order) %>%
# this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
mutate(individual = forcats::fct_inorder(factor(individual)))
NGad2_df_long_SN

```

```

## # A tibble: 150 x 9
##   individual region order  lat  long site    region2 pop      q
##   <fct>      <chr> <int> <dbl> <dbl> <chr>    <chr>  <chr>  <dbl>

```

```
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.00001
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 1.00
## 3 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 1.00
## 5 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.00001
## 6 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 1.00
## 7 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.00001
## 8 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P2 1.00
## 9 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P1 0.136
## 10 KWGA-B64 NV 5 38.0 -114. NVWGulch NV P2 0.864
## # i 140 more rows
```

```
CGad3_df_long_SN <- CGad3_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
CGad3_df_long_SN
```

```
## # A tibble: 225 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.00001
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 1.00
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 1.00
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 7 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.00001
## 8 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 1.00
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P3 0.00001
## 10 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 0.00001
## # i 215 more rows
```

```
NGad3_df_long_SN <- NGad3_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
NGad3_df_long_SN
```

```
## # A tibble: 225 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 1.00
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.00001
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 1.00
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 7 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 1.00
## 8 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.00001
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P3 0.00001
```

```
## 10 KCLA-B16 CA 4 37.7 -119. MonoBsn CA P1 1.00
## # i 215 more rows
```

```
CGad4_df_long_SN <- CGad4_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
CGad4_df_long_SN
```

```
## # A tibble: 300 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 1.00
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.00001
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 0.00001
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 1.00
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 0.00001
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 1.00
## 10 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.00001
## # i 290 more rows
```

```
NGad4_df_long_SN <- NGad4_df_long %>%
  # arrange the data set by the plot order
  arrange(order) %>%
  # this ensures that the factor levels for the individuals follow the ordering we just did. This is ne
  mutate(individual = forcats::fct_inorder(factor(individual)))
NGad4_df_long_SN
```

```
## # A tibble: 300 x 9
##   individual region order lat long site region2 pop q
##   <fct> <chr> <int> <dbl> <dbl> <chr> <chr> <chr> <dbl>
## 1 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P1 0.00001
## 2 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P2 0.00001
## 3 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P3 0.00001
## 4 KCLA-B01 CA 1 37.7 -119. MonoBsn CA P4 1.00
## 5 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P1 0.00001
## 6 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P2 0.00001
## 7 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P3 0.00001
## 8 KCLA-B03 CA 2 37.7 -119. MonoBsn CA P4 1.00
## 9 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P1 0.00001
## 10 KCLA-B04 CA 3 37.7 -119. MonoBsn CA P2 0.00001
## # i 290 more rows
```

#K2-Admixture Plot

```
mycolors2C=c("P1"= "slateblue",
             "P2"="cadetblue2",
             "P3"="salmon",
```

```

      "P4"="hotpink",
      "P5"="cornflowerblue",
      "P6"="turquoise4")
mycolors2=c("P1"= "slateblue",
            "P3"="cadetblue2",
            "P2"="salmon",
            "P4"="hotpink",
            "P5"="cornflowerblue",
            "P6"="turquoise4")
k2CAAd <-
  ggplot(Cad2_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Complete SNP Set K=2", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors2)+
  theme(legend.position="none")

```

```

## Warning: 'expand_scale()' was deprecated in ggplot2 3.3.0.
## i Please use 'expansion()' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

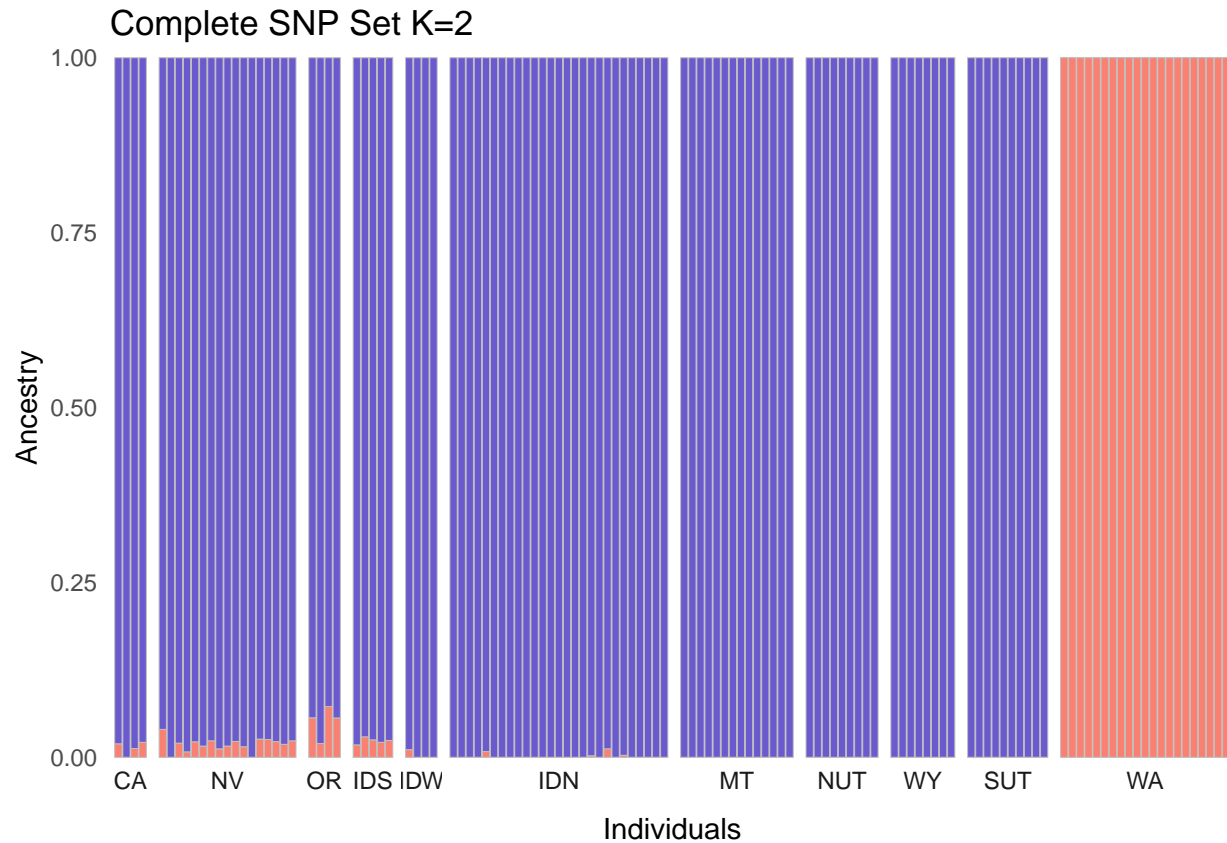
```

```

#scale_fill_gdocs(guide = FALSE)+

k2CAAd

```

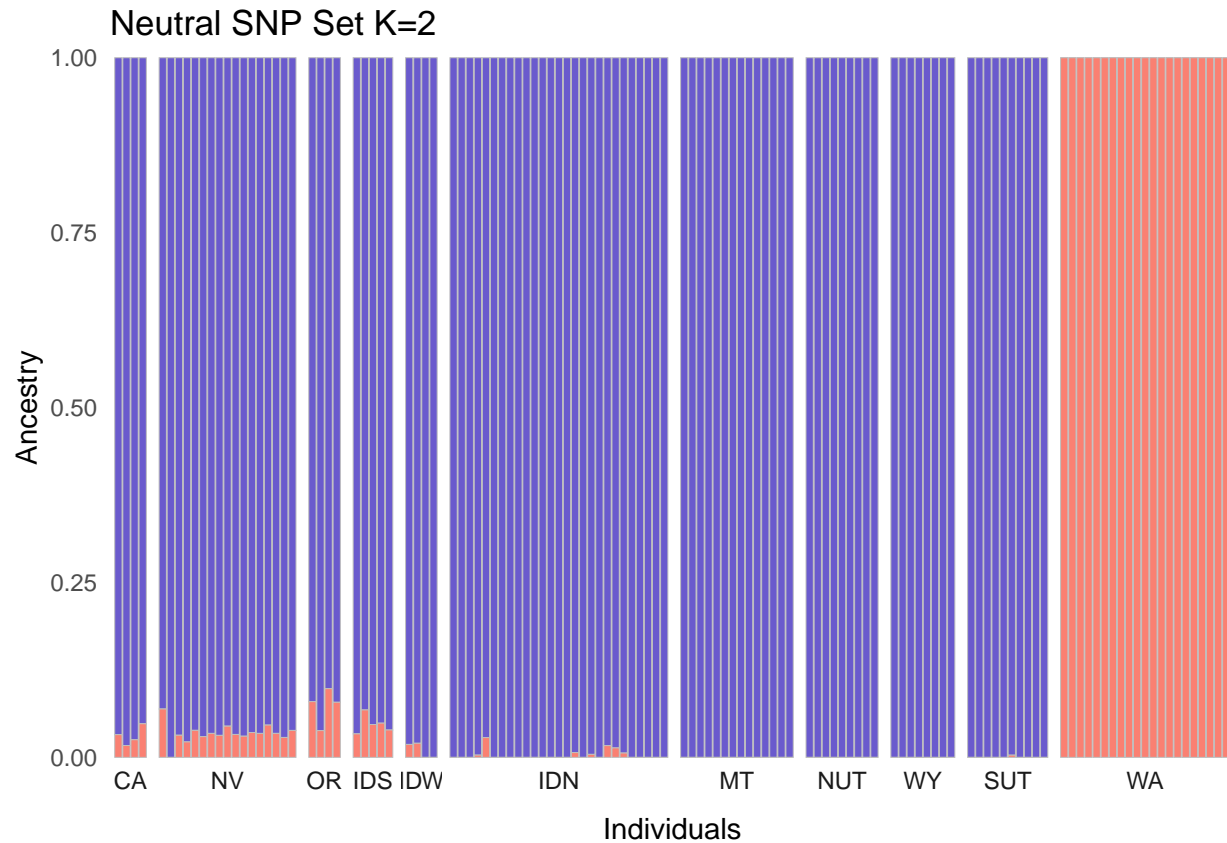


```
mycolors2N=c("P3"= "cadetblue2",
             "P1"="slateblue",
             "P2"="salmon",
             "P4"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k2NAd <-
  ggplot(Nad2_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Neutral SNP Set K=2", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors2N)+
  theme(legend.position="none")
  #scale_fill_gdocs(guide = FALSE)+

k2NAd
```

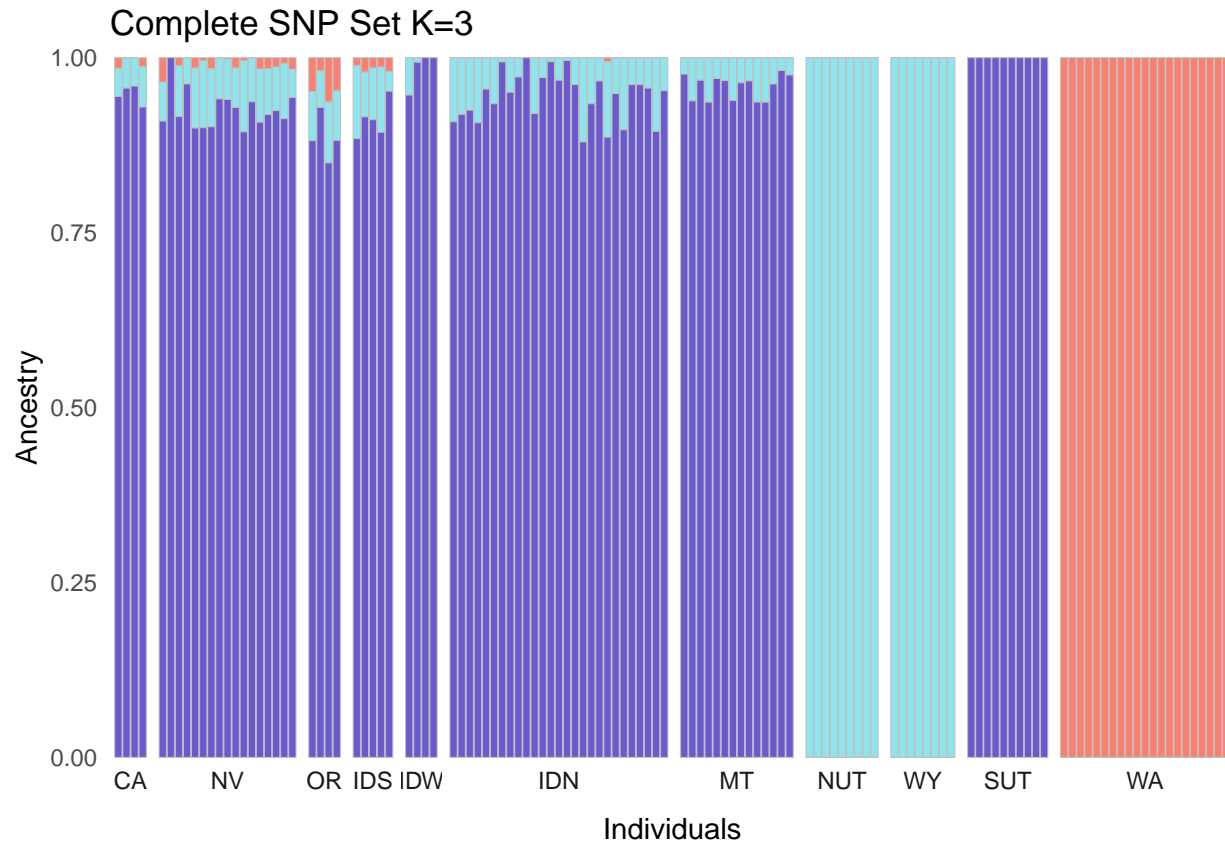
#K3-Admixture Plot

```
mycolors3C=c("P3"= "slateblue",
             "P2"="cadetblue2",
             "P1"="salmon",
             "P4"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k3CAd <-
  ggplot(Cad3_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Complete SNP Set K=3", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors3C)+
  theme(legend.position="none")
  #scale_fill_gdocs(guide = FALSE)+

k3CAd
```

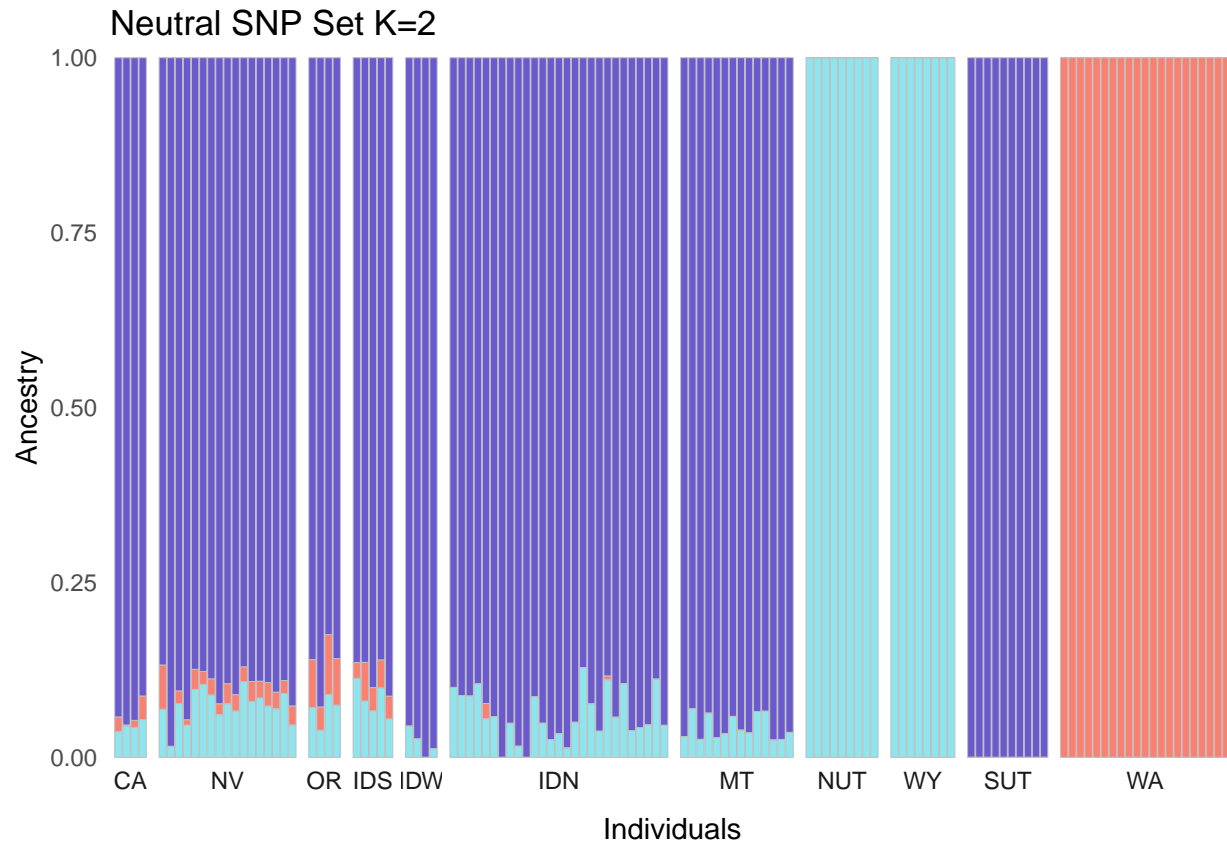


```
mycolors3N=c("P3"= "cadetblue2",
             "P1"="slateblue",
             "P2"="salmon",
             "P4"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k3NAd <-
  ggplot(Nad3_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Neutral SNP Set K=2", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors3N)+
  theme(legend.position="none")
  #scale_fill_gdocs(guide = FALSE)+

k3NAd
```



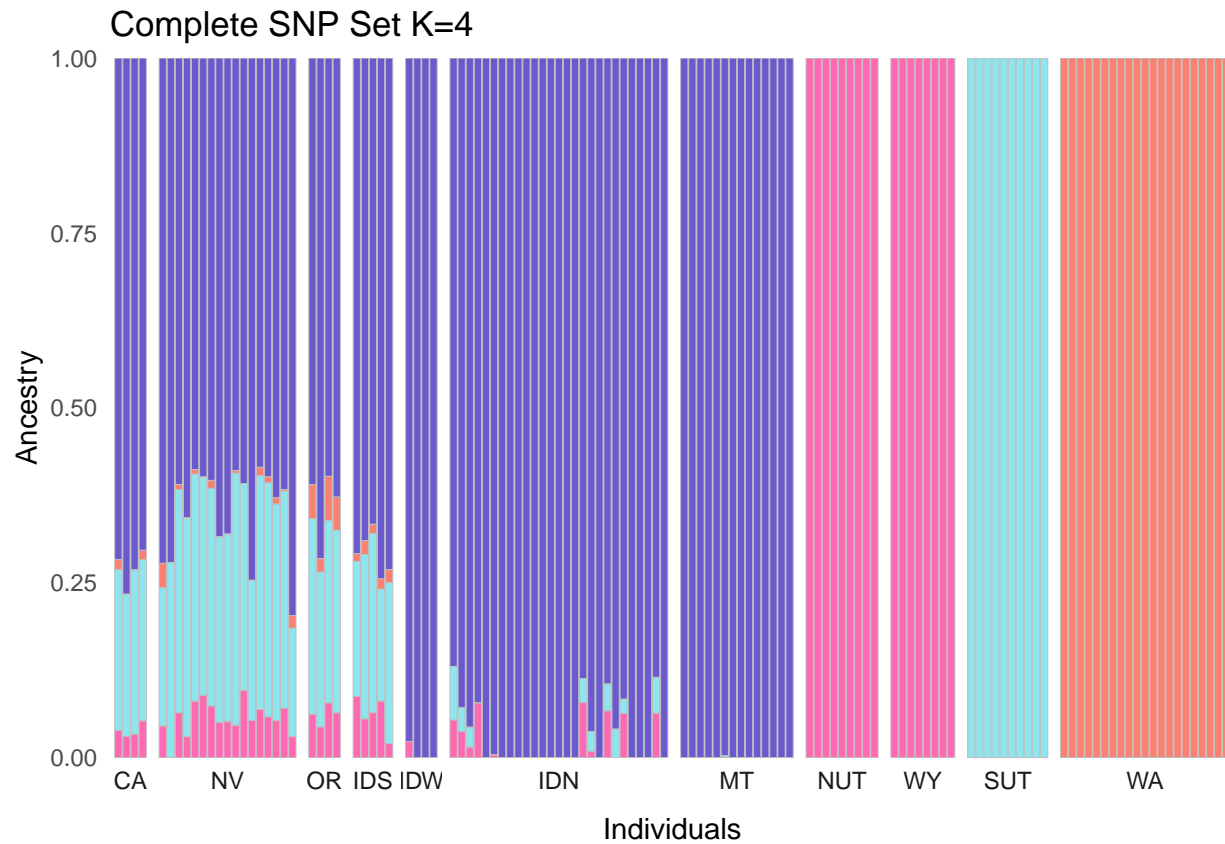
#K4-Admixture Plot

```
mycolors4C=c("P1"= "slateblue",
             "P3"="cadetblue2",
             "P2"="salmon",
             "P4"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k4Cad <-
  ggplot(Cad4_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Complete SNP Set K=4", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors4C)+
  theme(legend.position="none")
#scale_fill_gdocs(guide = FALSE)+
```

k4CAAd

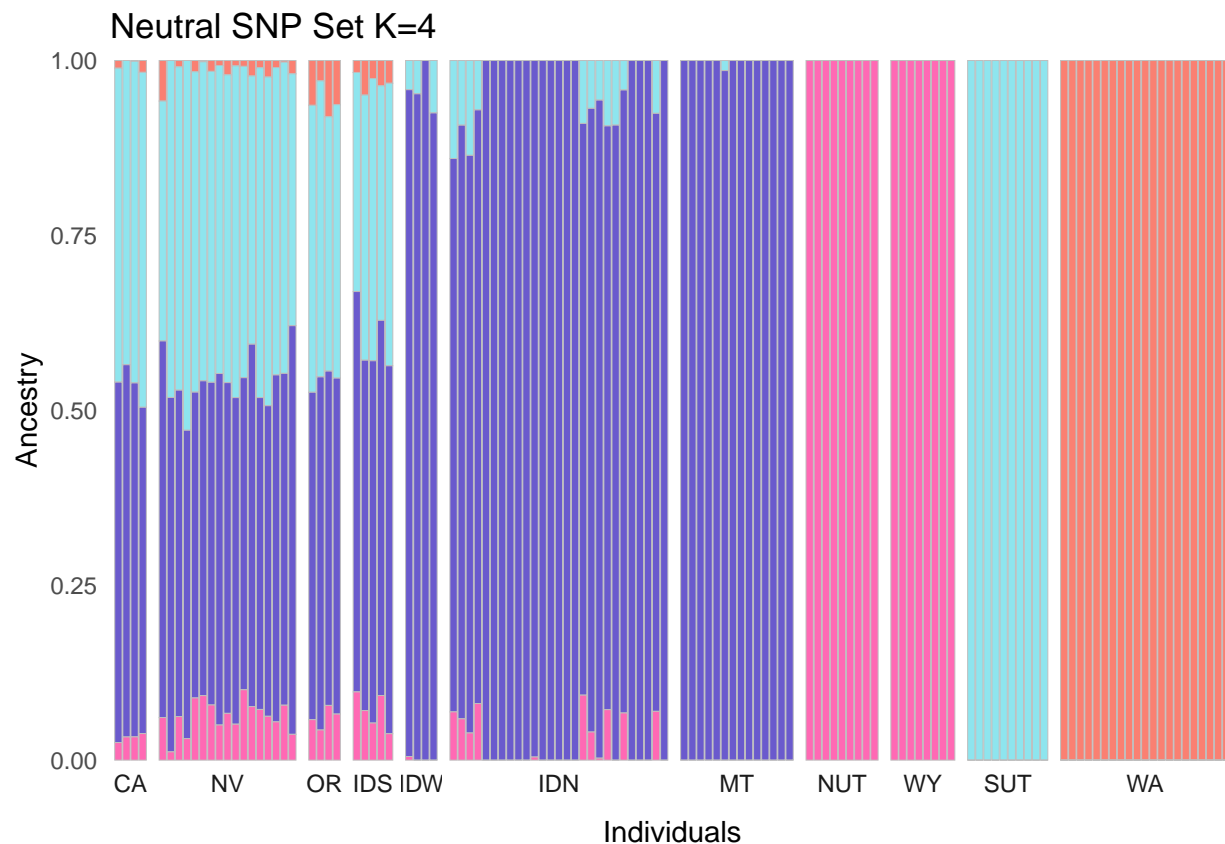


```
mycolors4N=c("P2"= "cadetblue2",
             "P3"="slateblue",
             "P1"="salmon",
             "P4"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k4NAd <-
  ggplot(Nad4_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Neutral SNP Set K=4", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors4N)+
  theme(legend.position="none")
#scale_fill_gdocs(guide = FALSE)+
```

k4NAd



#K5-Admixture Plot

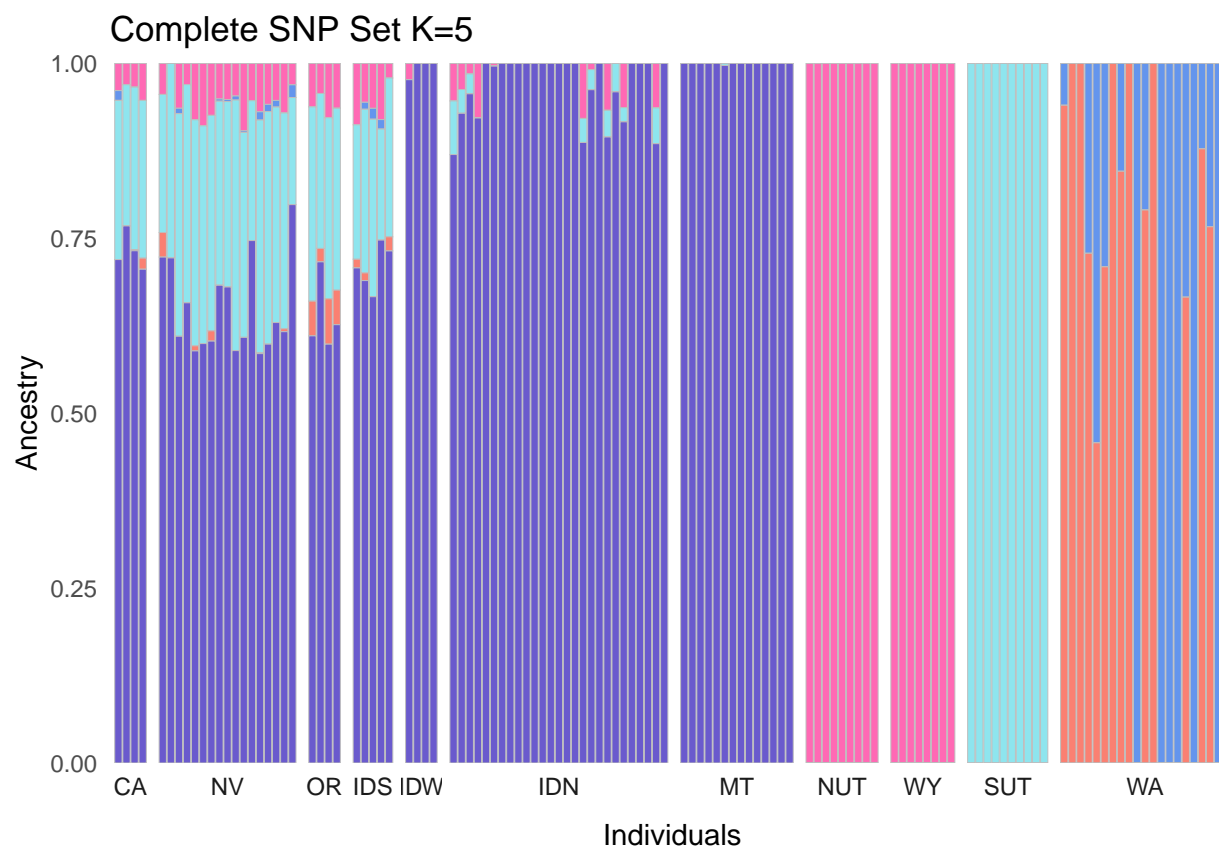
```
mycolors5C=c("P5"= "slateblue",
             "P3"="cadetblue2",
             "P4"="salmon",
             "P1"="hotpink",
             "P2"="cornflowerblue",
             "P6"="turquoise4")

k5CAAd <-
  ggplot(Cad5_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Complete SNP Set K=5", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors5C)+
  theme(legend.position="none")
```

```
#scale_fill_gdocs(guide = FALSE)+
```

k5CAAd



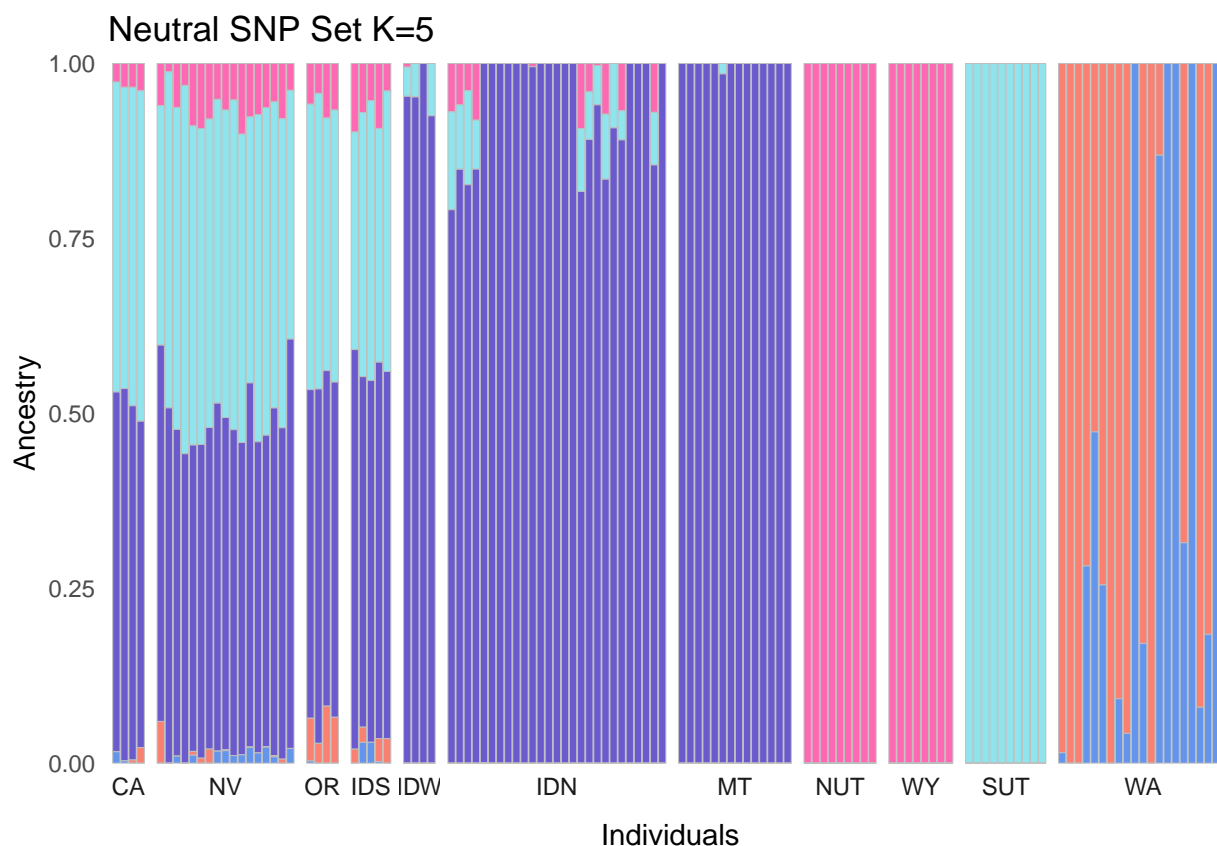
```
mycolors5N=c("P2"= "cadetblue2",
             "P3"="slateblue",
             "P4"="salmon",
             "P1"="hotpink",
             "P5"="cornflowerblue",
             "P6"="turquoise4")

k5NAd <-
  ggplot(Nad5_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Neutral SNP Set K=5", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +

  scale_fill_manual(values=mycolors5N)+
  theme(legend.position="none")
```

```
#scale_fill_gdocs(guide = FALSE)+
```

k5NAd



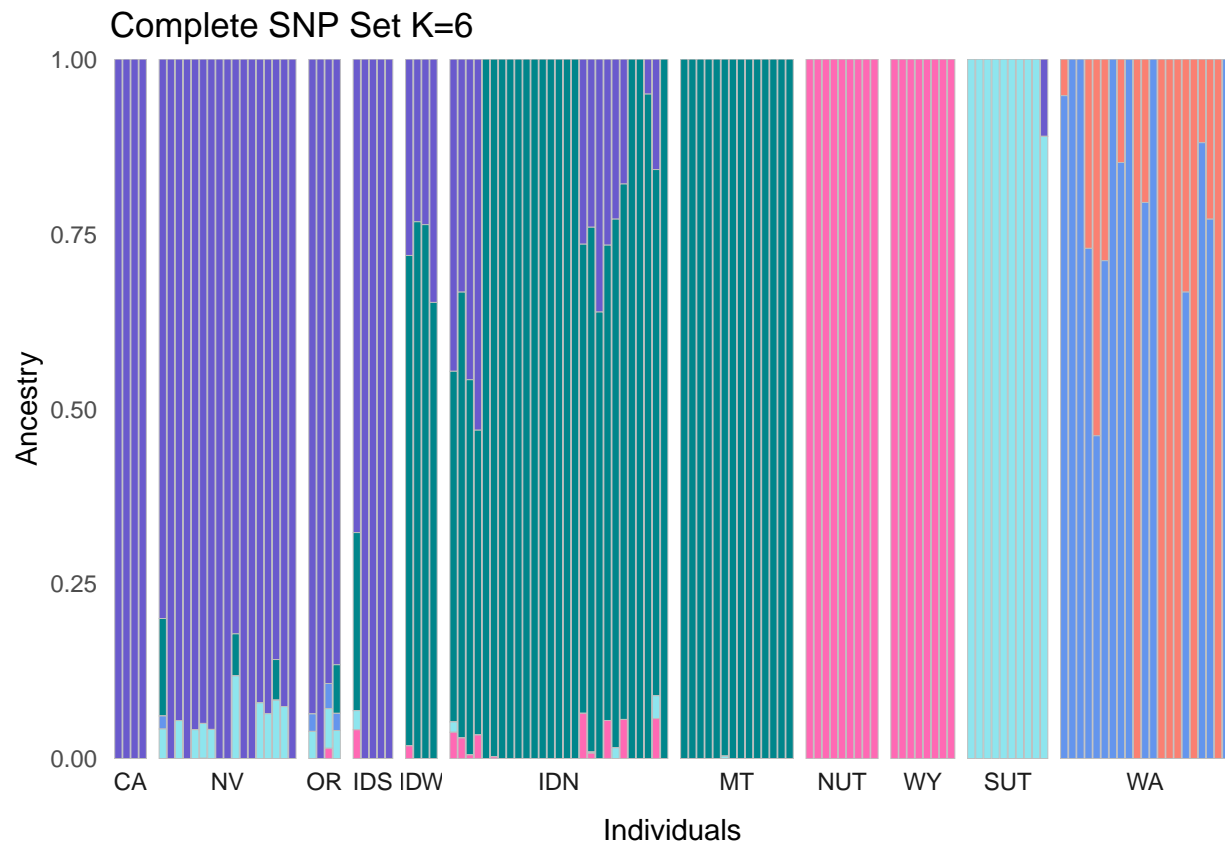
#K6-Admixture Plot

```
mycolors6C=c("P1"= "slateblue",
              "P5"="cadetblue2",
              "P3"="salmon",
              "P6"="hotpink",
              "P4"="cornflowerblue",
              "P2"="turquoise4")

k6CAAd <-
  ggplot(Cad6_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Complete SNP Set K=6", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +
```

```
scale_fill_manual(values=mycolors6C)+
theme(legend.position="none")
#scale_fill_gdocs(guide = FALSE)+
```

k6CAAd



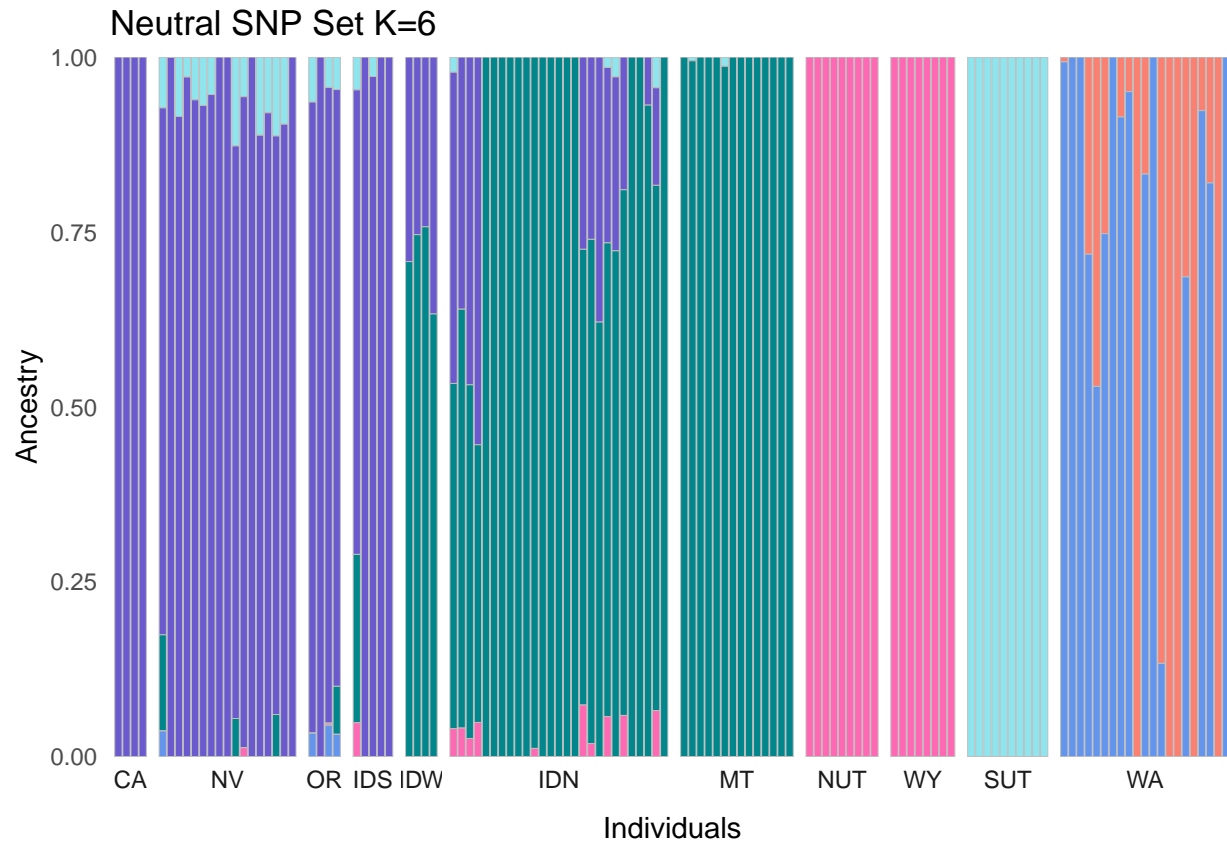
```
mycolors6N=c("P1"= "cadetblue2",
             "P2"="slateblue",
             "P5"="salmon",
             "P4"="hotpink",
             "P6"="cornflowerblue",
             "P3"="turquoise4")

k6NAd <-
  ggplot(Nad6_df_long_SN, aes(factor(individual), y=q, fill = factor(pop))) +
  geom_col(color = "gray", size = 0.1) +
  facet_grid(~fct_inorder(region2), switch = "x", scales = "free", space = "free") +
  theme_minimal() + labs(x = "Individuals", title = "Neutral SNP Set K=6", y = "Ancestry") +
  scale_y_continuous(expand = c(0, 0)) +
  scale_x_discrete(expand = expand_scale(add = 1)) +
  theme(
    panel.spacing.x = unit(0.1, "lines"),
    axis.text.x = element_blank(),
    panel.grid = element_blank()
  ) +
```



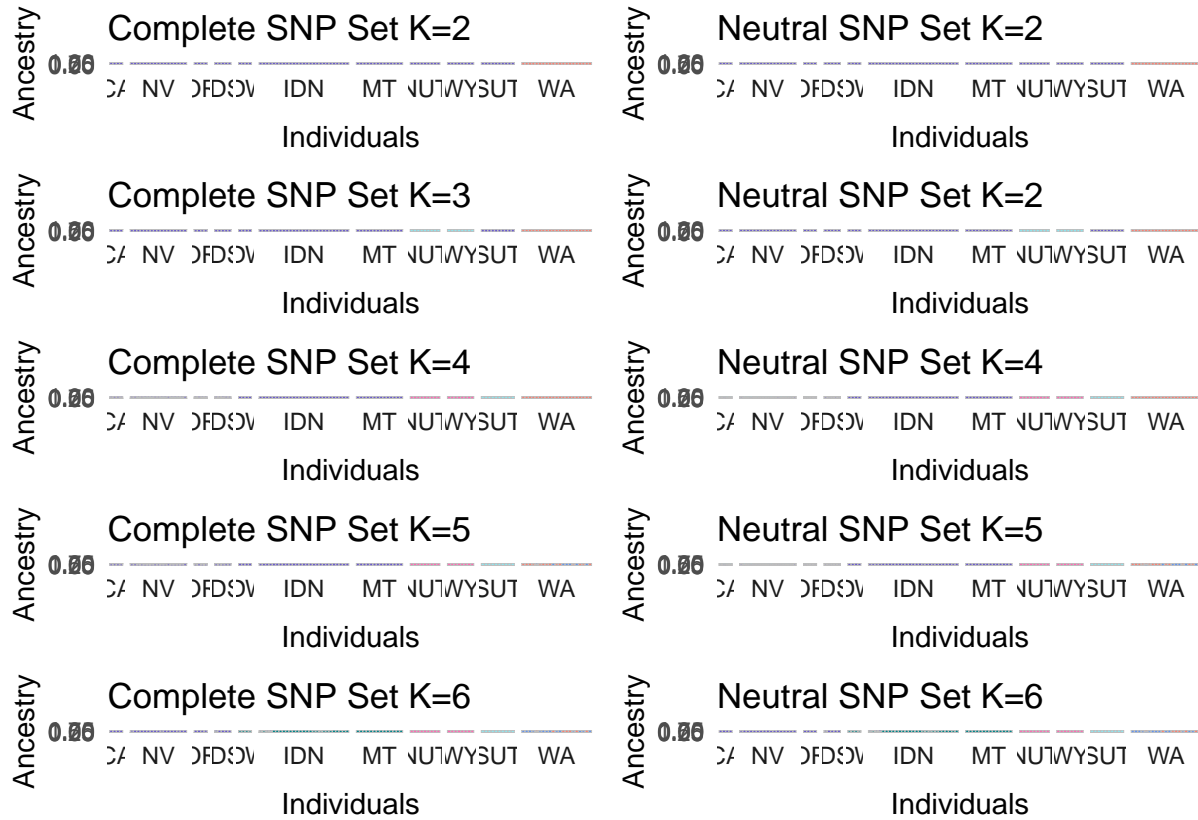
```
scale_fill_manual(values=mycolors6N)+
theme(legend.position="none")
#scale_fill_gdocs(guide = FALSE)+
```

k6NAd



#Plot Side by Side - Admixture

```
K2_k6Ad=k2CAd+k2NAd+k3CAd+k3NAd+k4CAd+k4NAd+k5CAd+k5NAd+k6CAd+k6NAd+plot_layout(ncol = 2)
K2_k6Ad
```



```
ggsave("./Figures/K2_K6_Admixture.pdf", width = 49.95, height = 40)
k2_k4Ad=k2CAd + k2NAd+k3CAd+k3NAd+k4CAd+k4NAd+plot_layout(ncol = 2)
ggsave("./Figures/K2_K4_Admixture.pdf", width = 49.95, height = 40)
k5_k6Ad=k5CAd+k5NAd+k6CAd+k6NAd+plot_layout(ncol = 2)
ggsave("./Figures/K5_K6_Admixture.pdf", width = 49.95, height = 40)
```