

main

September 15, 2021

1 Examine sample make-up

```
[1]: suppressMessages({library(SummarizedExperiment)
                        library(tidyverse)
                        library(ggpubr)})
```

1.1 Samples after quality control

```
[2]: save_ggplots <- function(p, fn, w, h){
      for(ext in c('.pdf', '.png', '.svg')){
        ggsave(paste0(fn, ext), plot=p, width=w, height=h)
      }
    }
```

1.1.1 Load Caudate data

```
[3]: # Load counts and phenotype R variable
load("../input/counts/_m/caudate_brainseq_phase3_hg38_rseGene_merged_n464.
      ↪rda")
### Subset and recode
keepIndex = which((rse_gene$Dx %in% c('Control', 'Schizo')) &
                  rse_gene$Race %in% c('CAUC', 'AA'))
rse_gene = rse_gene[, keepIndex]
### Extract phenotypes
pheno_C <- colData(rse_gene) %>% as.data.frame
```

1.1.2 Load DLPFC data

```
[4]: # Load counts and phenotype R variable
load("../input/counts/_m/
      ↪dlpfc_ribozero_brainseq_phase2_hg38_rseGene_merged_n453.rda")
### Subset and recode
keepIndex = which((rse_gene$Dx %in% c('Control', 'Schizo')) &
                  rse_gene$Race %in% c('CAUC', 'AA'))
rse_gene = rse_gene[, keepIndex]
### Extract phenotypes
pheno_D <- colData(rse_gene) %>% as.data.frame
```

1.1.3 Load Hippocampus data

```
[5]: # Load counts and phenotype R variable
load("../input/counts/_m/hippo_brainseq_phase2_hg38_rseGene_merged_n447.rda")
### Subset and recode
keepIndex = which((rse_gene$Dx %in% c('Control', 'Schizo')) &
                  rse_gene$Race %in% c('CAUC', 'AA'))
rse_gene = rse_gene[, keepIndex]
### Extract phenotypes
pheno_H <- colData(rse_gene) %>% as.data.frame
```

1.1.4 Load DG data

```
[6]: # Load counts and phenotype R variable
load("../input/counts/_m/astellas_dg_hg38_rseGene_n263.rda")
### Subset and recode
keepIndex = which((rse_gene$Dx %in% c('Control', 'Schizo')) &
                  rse_gene$Race %in% c('CAUC', 'AA'))
rse_gene = rse_gene[, keepIndex]
### Extract phenotypes
pheno_dg <- colData(rse_gene) %>% as.data.frame
```

1.1.5 Merge data

```
[7]: allCols <- intersect(intersect(intersect(colnames(pheno_C), colnames(pheno_D)),
                                     colnames(pheno_H)),
                          colnames(pheno_dg))
pheno = rbind(pheno_C[, allCols], pheno_D[, allCols],
              pheno_H[, allCols], pheno_dg[, allCols]) %>%
  filter(Age > 13) %>% mutate(Race=gsub("CAUC", "EA", Race))
```

1.2 STRUCTURE analysis

```
[8]: ancestry = data.table::fread("../input/ancestry_structure/structure.
  ↳out_ancestry_proportion_raceDemo_compare")
ancestry %>% head()
```

A data.table: 6 × 4

| id | Afr | Eur | group |
|--------|-------|-------|-------|
| <chr> | <dbl> | <dbl> | <chr> |
| Br2374 | 0.007 | 0.993 | CAUC |
| Br1857 | 0.001 | 0.999 | CAUC |
| Br1306 | 0.759 | 0.241 | AA |
| Br2605 | 0.644 | 0.356 | AA |
| Br1802 | 0.840 | 0.160 | AA |
| Br2565 | 0.005 | 0.995 | CAUC |

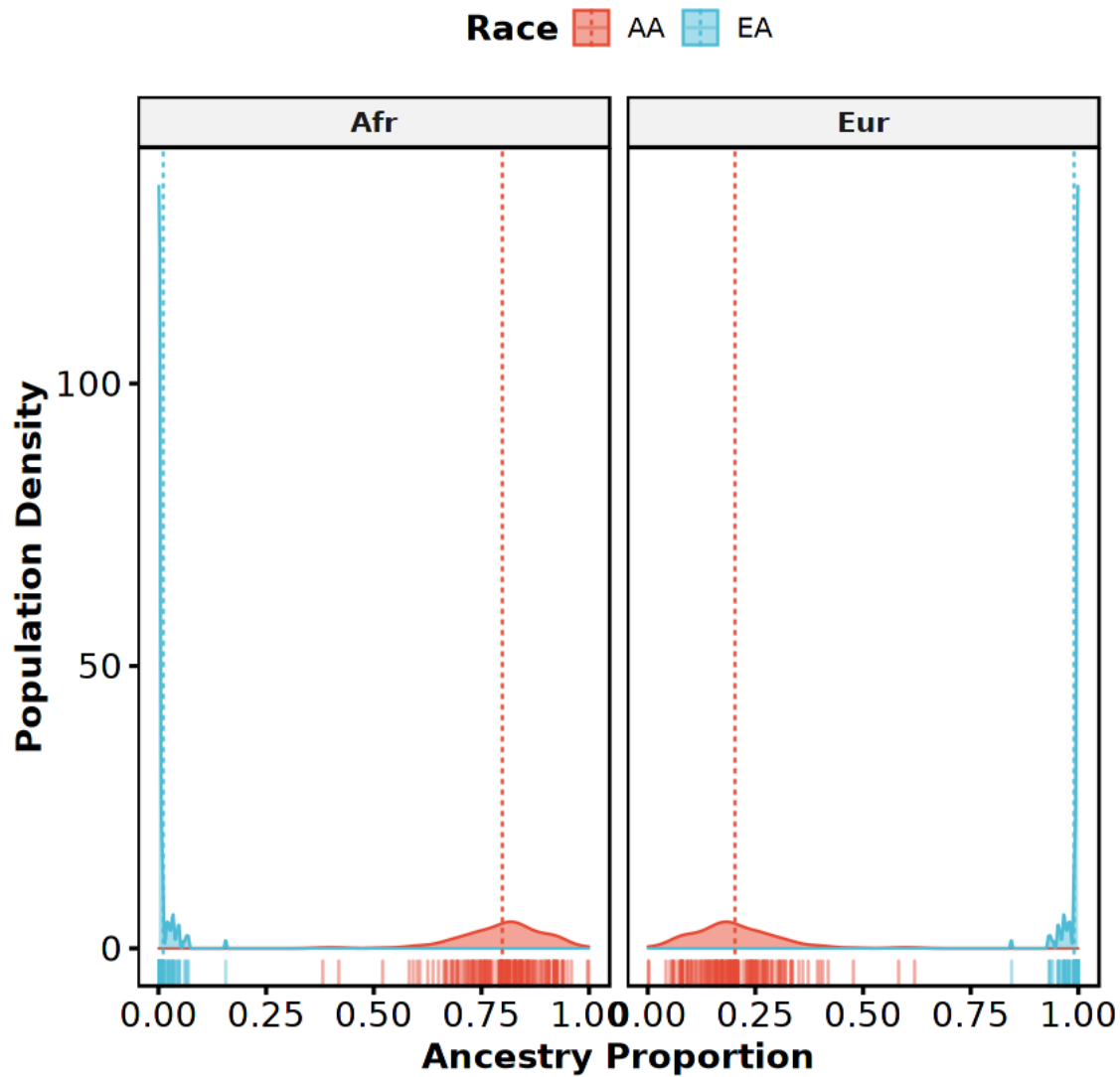
```
[9]: ancestry %>% mutate_if(is.character, as.factor) %>%
  group_by(group) %>% summarize(AA=mean(Afr), EA=mean(Eur))
```

| | group | AA | EA |
|-----------------|-------|-------------|-----------|
| | <fct> | <dbl> | <dbl> |
| A tibble: 2 × 3 | AA | 0.782219451 | 0.2177805 |
| | CAUC | 0.007510536 | 0.9924895 |

```
[10]: ancestry %>% inner_join(pheno, by=c("id"="BrNum")) %>%
  filter(Age > 17, Dx == "Control") %>% select(group, Afr, Eur) %>%
  mutate_if(is.character, as.factor) %>% distinct %>%
  group_by(group) %>%
  summarize(AA_mean=mean(Afr), AA_sd=sd(Afr), AA_max=max(Afr),
  ↪AA_min=min(Afr),
  EA_mean=mean(Eur), EA_sd=sd(Eur), EA_max=max(Eur),
  ↪EA_min=min(Eur))
```

| | group | AA_mean | AA_sd | AA_max | AA_min | EA_mean | EA_sd | EA_max |
|-----------------|-------|------------|------------|--------|--------|-----------|------------|--------|
| | <fct> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> | <dbl> |
| A tibble: 2 × 9 | AA | 0.78962609 | 0.10611682 | 0.999 | 0.381 | 0.2103739 | 0.10611682 | 0.619 |
| | CAUC | 0.03087879 | 0.02997578 | 0.156 | 0.001 | 0.9691212 | 0.02997578 | 0.999 |

```
[11]: bxp = ancestry %>% inner_join(pheno, by=c("id"="BrNum")) %>%
  filter(Age > 17, Dx == "Control") %>% select(id, Race, Afr, Eur) %>%
  mutate_if(is.character, as.factor) %>% distinct %>%
  pivot_longer(-c("Race", "id"), names_to="Ancestry", values_to="Proportion")
  ↪%>%
  ggdensity(x="Proportion", color="Race", fill="Race", facet.by="Ancestry",
  ncol=2, rug=TRUE, add="mean", palette="npg", ylab="Population
  ↪Density",
  xlab="Ancestry Proportion", panel.labs.font=list(face='bold'),
  ggtheme=theme_pubr(base_size=15, border=TRUE)) +
  font("xy.title", face="bold") + font("legend.title", face="bold")
save_ggplots(bxp, "ancestry_structure_distribution", 10, 5)
bxp
```



1.3 eQTL analysis

```
[12]: pheno %>% dim
```

```
1. 1334 2. 21
```

```
[13]: print(paste("There are", unique(pheno$BrNum) %>% length, "unique BrNum."))
```

```
[1] "There are 509 unique BrNum."
```

```
[14]: pheno %>% select(BrNum, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region) %>% count()
```

| A grouped_df: 4 × 2 | Region | n |
|---------------------|--------------|-------|
| | <fct> | <int> |
| | Caudate | 400 |
| | DentateGyrus | 161 |
| | DLPFC | 378 |
| | HIPPO | 395 |

```
[15]: pheno %>% select(BrNum, Race) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Race) %>% count()
```

| A grouped_df: 2 × 2 | Race | n |
|---------------------|-------|-------|
| | <fct> | <int> |
| | AA | 256 |
| | EA | 253 |

```
[16]: pheno %>% select(BrNum, Race, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region, Race) %>% count()
```

| A grouped_df: 8 × 3 | Region | Race | n |
|---------------------|--------------|-------|-------|
| | <fct> | <fct> | <int> |
| | Caudate | AA | 206 |
| | Caudate | EA | 194 |
| | DentateGyrus | AA | 78 |
| | DentateGyrus | EA | 83 |
| | DLPFC | AA | 204 |
| | DLPFC | EA | 174 |
| | HIPPO | AA | 213 |
| | HIPPO | EA | 182 |

```
[17]: pheno %>% select(BrNum, Sex, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region, Sex) %>% count()
```

| A grouped_df: 8 × 3 | Region | Sex | n |
|---------------------|--------------|-------|-------|
| | <fct> | <fct> | <int> |
| | Caudate | F | 126 |
| | Caudate | M | 274 |
| | DentateGyrus | F | 48 |
| | DentateGyrus | M | 113 |
| | DLPFC | F | 121 |
| | DLPFC | M | 257 |
| | HIPPO | F | 126 |
| | HIPPO | M | 269 |

```
[18]: pheno %>% group_by(Region) %>%
      summarise_at(vars(c("Age")), list(mean = mean, sd = sd))
```

| | Region <chr> | mean <dbl> | sd <dbl> |
|-----------------|-----------------|---------------|-------------|
| A tibble: 4 × 3 | Caudate | 49.12390 | 16.05379 |
| | DentateGyrus | 50.06770 | 15.43849 |
| | DLPFC | 45.83574 | 16.49445 |
| | HIPPO | 45.49527 | 16.41527 |

```
[19]: pheno %>% group_by(Region, Race) %>%
  summarise_at(vars(c("Age")), list(mean = mean, sd = sd))
```

| | Region <chr> | Race <chr> | mean <dbl> | sd <dbl> |
|---------------------|-----------------|---------------|---------------|-------------|
| A grouped_df: 8 × 4 | Caudate | AA | 48.81325 | 14.49676 |
| | Caudate | EA | 49.45376 | 17.58900 |
| | DentateGyrus | AA | 50.18423 | 15.53374 |
| | DentateGyrus | EA | 49.95819 | 15.44210 |
| | DLPFC | AA | 46.97896 | 15.34261 |
| | DLPFC | EA | 44.49542 | 17.70090 |
| | HIPPO | AA | 46.34080 | 15.61922 |
| | HIPPO | EA | 44.50571 | 17.29140 |

```
[20]: pheno %>% filter(RIN != "NA") %>% mutate("RIN"=as.numeric(unlist(RIN))) %>%
  group_by(Region) %>% summarise_at(vars(c("RIN")), list(mean = mean, sd =
  ↪sd))
```

| | Region <chr> | mean <dbl> | sd <dbl> |
|-----------------|-----------------|---------------|-------------|
| A tibble: 4 × 3 | Caudate | 7.861000 | 0.8648983 |
| | DentateGyrus | 5.208403 | 1.1871187 |
| | DLPFC | 7.699471 | 0.9340876 |
| | HIPPO | 7.616962 | 1.0311104 |

```
[21]: pheno %>% filter(RIN != "NA") %>% mutate("RIN"=as.numeric(unlist(RIN))) %>%
  group_by(Region, Race) %>% summarise_at(vars(c("RIN")), list(mean = mean,
  ↪sd = sd))
```

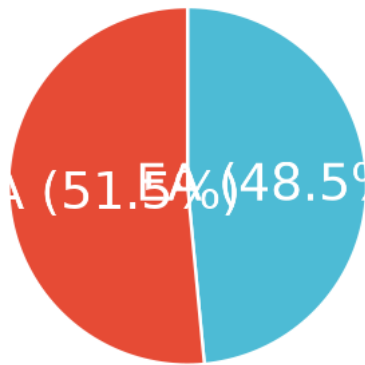
| | Region <chr> | Race <chr> | mean <dbl> | sd <dbl> |
|---------------------|-----------------|---------------|---------------|-------------|
| A grouped_df: 8 × 4 | Caudate | AA | 7.859709 | 0.8416464 |
| | Caudate | EA | 7.862371 | 0.8911055 |
| | DentateGyrus | AA | 5.206349 | 1.2062837 |
| | DentateGyrus | EA | 5.210714 | 1.1760765 |
| | DLPFC | AA | 7.678922 | 0.9445184 |
| | DLPFC | EA | 7.723563 | 0.9238440 |
| | HIPPO | AA | 7.604225 | 1.0509344 |
| | HIPPO | EA | 7.631868 | 1.0101014 |

1.3.1 Pie chart

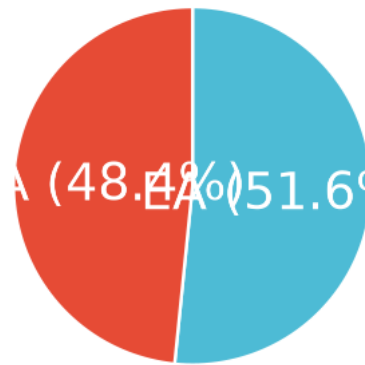
```
[22]: plot_pie <- function(tissue){
  pie = pheno %>% mutate_if(is.character, as.factor) %>% group_by(Region,
↪Race) %>%
  count %>% as.data.frame %>% group_by(Region) %>%
  transmute(Race, Percent = round(n/sum(n)*100, 1)) %>%
  mutate(Labels=paste0(Race, " (", Percent, "%)") %>% filter(Region ==
↪tissue) %>%
  ggpie("Percent", label="Labels", fill="Race", color="white",
↪palette="npg",
      lab.pos="in", lab.font=c(8, "bold", "white"),
      ggtheme=theme_pubr(base_size=20, legend="none"))
  return(pie)
}

[23]: ## Get and annotate plot
cc_pie = annotate_figure(plot_pie("Caudate"),
                        top = text_grob("Caudate", face = "bold", size = 26))
gg_pie = annotate_figure(plot_pie("DentateGyrus"),
                        top = text_grob("Dentate Gyrus", face = "bold", size =
↪26))
dd_pie = annotate_figure(plot_pie("DLPFC"),
                        top = text_grob("DLPFC", face = "bold", size = 26))
hh_pie = annotate_figure(plot_pie("HIPPO"),
                        top = text_grob("Hippocampus", face = "bold", size =
↪26))
## Arrange figure
figure <- ggarrange(cc_pie, gg_pie, dd_pie, hh_pie, ncol = 2, nrow = 2)
save_ggplots(figure, "ancestry_piecharts", 10, 10)
figure
```

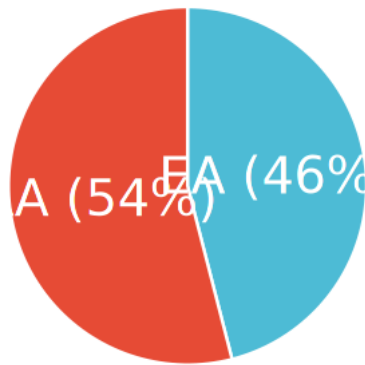
Caudate



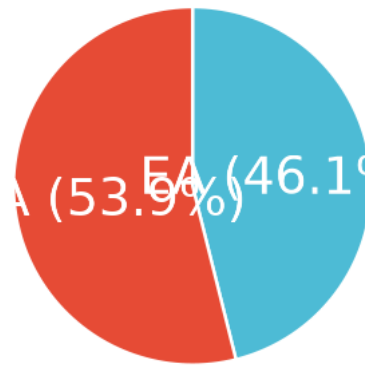
Dentate Gyrus



DLPFC



Hippocampus



1.4 Adult individuals for expression related analysis

```
[24]: pheno = pheno %>% filter(Age > 17, Dx == "Control")
      pheno %>% dim
```

```
1. 785 2. 21
```

```
[25]: print(paste("There are", unique(pheno$BrNum) %>% length, "unique BrNum."))
```

```
[1] "There are 292 unique BrNum."
```

```
[26]: pheno %>% select(BrNum, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region) %>% count()
```


| | Region | n |
|---------------------|--------------|-------|
| | <fct> | <int> |
| A grouped_df: 4 × 2 | Caudate | 240 |
| | DentateGyrus | 90 |
| | DLPFC | 212 |
| | HIPPO | 243 |

```
[27]: pheno %>% select(BrNum, Race) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Race) %>% count()
```

| | Race | n |
|---------------------|-------|-------|
| | <fct> | <int> |
| A grouped_df: 2 × 2 | AA | 151 |
| | EA | 141 |

```
[28]: pheno %>% select(BrNum, Race, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region, Race) %>% count()
```

| | Region | Race | n |
|---------------------|--------------|-------|-------|
| | <fct> | <fct> | <int> |
| A grouped_df: 8 × 3 | Caudate | AA | 122 |
| | Caudate | EA | 118 |
| | DentateGyrus | AA | 47 |
| | DentateGyrus | EA | 43 |
| | DLPFC | AA | 123 |
| | DLPFC | EA | 89 |
| | HIPPO | AA | 133 |
| | HIPPO | EA | 110 |

```
[29]: pheno %>% select(BrNum, Sex, Region) %>% distinct %>%
      mutate_if(is.character, as.factor) %>%
      group_by(Region, Sex) %>% count()
```

| | Region | Sex | n |
|---------------------|--------------|-------|-------|
| | <fct> | <fct> | <int> |
| A grouped_df: 8 × 3 | Caudate | F | 71 |
| | Caudate | M | 169 |
| | DentateGyrus | F | 26 |
| | DentateGyrus | M | 64 |
| | DLPFC | F | 66 |
| | DLPFC | M | 146 |
| | HIPPO | F | 74 |
| | HIPPO | M | 169 |

```
[30]: pheno %>% group_by(Region) %>%
      summarise_at(vars(c("Age")), list(mean = mean, sd = sd))
```

| | Region <chr> | mean <dbl> | sd <dbl> |
|-----------------|-----------------|---------------|-------------|
| A tibble: 4 × 3 | Caudate | 48.31150 | 15.84692 |
| | DentateGyrus | 47.88311 | 15.02380 |
| | DLPFC | 45.16991 | 14.76717 |
| | HIPPO | 44.56724 | 14.73045 |

```
[31]: pheno %>% group_by(Region, Race) %>%
      summarise_at(vars(c("Age")), list(mean = mean, sd = sd))
```

| | Region <chr> | Race <chr> | mean <dbl> | sd <dbl> |
|---------------------|-----------------|---------------|---------------|-------------|
| A grouped_df: 8 × 4 | Caudate | AA | 45.63770 | 14.72979 |
| | Caudate | EA | 51.07593 | 16.53588 |
| | DentateGyrus | AA | 45.85043 | 16.32827 |
| | DentateGyrus | EA | 50.10488 | 13.28980 |
| | DLPFC | AA | 44.12511 | 14.97092 |
| | DLPFC | EA | 46.61386 | 14.43996 |
| | HIPPO | AA | 43.30015 | 14.73609 |
| | HIPPO | EA | 46.09927 | 14.64404 |

```
[32]: pheno %>% filter(RIN != "NA") %>% mutate("RIN"=as.numeric(unlist(RIN))) %>%
      group_by(Region) %>% summarise_at(vars(c("RIN")), list(mean = mean, sd =
      ↪sd))
```

| | Region <chr> | mean <dbl> | sd <dbl> |
|-----------------|-----------------|---------------|-------------|
| A tibble: 4 × 3 | Caudate | 7.850000 | 0.7956997 |
| | DentateGyrus | 5.315152 | 1.2186048 |
| | DLPFC | 7.699057 | 0.8803807 |
| | HIPPO | 7.735391 | 0.9668378 |

```
[33]: pheno %>% filter(RIN != "NA") %>% mutate("RIN"=as.numeric(unlist(RIN))) %>%
      group_by(Region, Race) %>% summarise_at(vars(c("RIN")), list(mean = mean,
      ↪sd = sd))
```

| | Region <chr> | Race <chr> | mean <dbl> | sd <dbl> |
|---------------------|-----------------|---------------|---------------|-------------|
| A grouped_df: 8 × 4 | Caudate | AA | 7.829508 | 0.7993477 |
| | Caudate | EA | 7.871186 | 0.7947587 |
| | DentateGyrus | AA | 5.447368 | 1.2173824 |
| | DentateGyrus | EA | 5.135714 | 1.2190507 |
| | DLPFC | AA | 7.696748 | 0.8851169 |
| | DLPFC | EA | 7.702247 | 0.8787876 |
| | HIPPO | AA | 7.715038 | 0.9754173 |
| | HIPPO | EA | 7.760000 | 0.9602370 |

```
[34]: ## Get and annotate plot
cc_pie = annotate_figure(plot_pie("Caudate"),
```

```

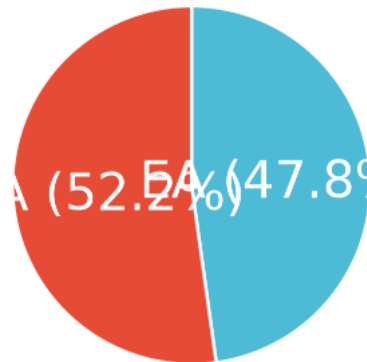
top = text_grob("Caudate", face = "bold", size = 26))
gg_pie = annotate_figure(plot_pie("DentateGyrus"),
top = text_grob("Dentate Gyrus", face = "bold", size = 26))
dd_pie = annotate_figure(plot_pie("DLPFC"),
top = text_grob("DLPFC", face = "bold", size = 26))
hh_pie = annotate_figure(plot_pie("HIPPO"),
top = text_grob("Hippocampus", face = "bold", size = 26))
## Arrange figure
figure <- ggarrange(cc_pie, gg_pie, dd_pie, hh_pie, ncol = 2, nrow = 2)
save_ggplots(figure, "ancestry_piecharts_CTL_adults", 10, 10)
figure

```

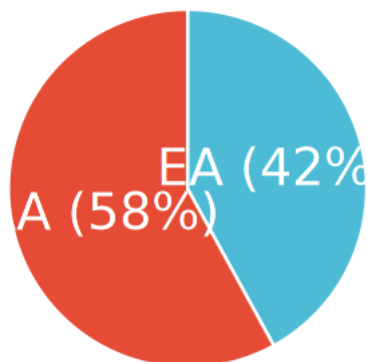
Caudate



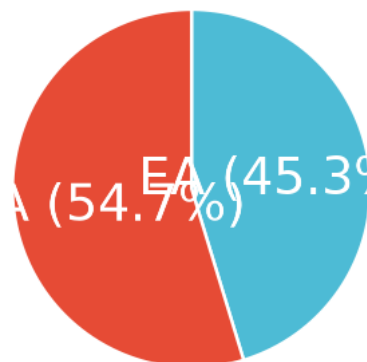
Dentate Gyrus



DLPFC



Hippocampus



1.5 Reproducibility Information

```
[35]: Sys.time()
proc.time()
options(width = 120)
sessioninfo::session_info()
```

```
[1] "2021-09-15 11:54:23 EDT"
```

```
   user  system elapsed
22.678   1.593   25.373
```

Session info

setting value

version R version 4.0.3 (2020-10-10)

os Arch Linux

system x86_64, linux-gnu

ui X11

language (EN)

collate en_US.UTF-8

ctype en_US.UTF-8

tz America/New_York

date 2021-09-15

Packages

| package | * version | date | lib | source |
|--------------|-----------|------------|-----|----------------|
| abind | 1.4-5 | 2016-07-21 | [1] | CRAN (R 4.0.2) |
| assertthat | 0.2.1 | 2019-03-21 | [1] | CRAN (R 4.0.2) |
| backports | 1.2.1 | 2020-12-09 | [1] | CRAN (R 4.0.2) |
| base64enc | 0.1-3 | 2015-07-28 | [1] | CRAN (R 4.0.2) |
| Biobase | * 2.50.0 | 2020-10-27 | [1] | Bioconductor |
| BiocGenerics | * 0.36.1 | 2021-04-16 | [1] | Bioconductor |
| bitops | 1.0-7 | 2021-04-24 | [1] | CRAN (R 4.0.3) |
| broom | 0.7.9 | 2021-07-27 | [1] | CRAN (R 4.0.3) |
| Cairo | 1.5-12.2 | 2020-07-07 | [1] | CRAN (R 4.0.2) |
| car | 3.0-11 | 2021-06-27 | [1] | CRAN (R 4.0.3) |
| carData | 3.0-4 | 2020-05-22 | [1] | CRAN (R 4.0.2) |
| cellranger | 1.1.0 | 2016-07-27 | [1] | CRAN (R 4.0.2) |
| cli | 3.0.1 | 2021-07-17 | [1] | CRAN (R 4.0.3) |
| colorspace | 2.0-2 | 2021-06-24 | [1] | CRAN (R 4.0.3) |
| cowplot | 1.1.1 | 2020-12-30 | [1] | CRAN (R 4.0.2) |
| crayon | 1.4.1 | 2021-02-08 | [1] | CRAN (R 4.0.3) |
| curl | 4.3.2 | 2021-06-23 | [1] | CRAN (R 4.0.3) |
| data.table | 1.14.0 | 2021-02-21 | [1] | CRAN (R 4.0.3) |
| DBI | 1.1.1 | 2021-01-15 | [1] | CRAN (R 4.0.2) |
| dbplyr | 2.1.1 | 2021-04-06 | [1] | CRAN (R 4.0.3) |
| DelayedArray | 0.16.3 | 2021-03-24 | [1] | Bioconductor |
| digest | 0.6.27 | 2020-10-24 | [1] | CRAN (R 4.0.2) |
| dplyr | * 1.0.7 | 2021-06-18 | [1] | CRAN (R 4.0.3) |

| | | | | | |
|------------------|----------|------------|-----|--------------|-----------|
| ellipsis | 0.3.2 | 2021-04-29 | [1] | CRAN | (R 4.0.3) |
| evaluate | 0.14 | 2019-05-28 | [1] | CRAN | (R 4.0.2) |
| fansi | 0.5.0 | 2021-05-25 | [1] | CRAN | (R 4.0.3) |
| farver | 2.1.0 | 2021-02-28 | [1] | CRAN | (R 4.0.3) |
| fastmap | 1.1.0 | 2021-01-25 | [1] | CRAN | (R 4.0.2) |
| forcats | * 0.5.1 | 2021-01-27 | [1] | CRAN | (R 4.0.2) |
| foreign | 0.8-80 | 2020-05-24 | [2] | CRAN | (R 4.0.3) |
| fs | 1.5.0 | 2020-07-31 | [1] | CRAN | (R 4.0.2) |
| generics | 0.1.0 | 2020-10-31 | [1] | CRAN | (R 4.0.2) |
| GenomeInfoDb | * 1.26.7 | 2021-04-08 | [1] | Bioconductor | |
| GenomeInfoDbData | 1.2.4 | 2021-02-02 | [1] | Bioconductor | |
| GenomicRanges | * 1.42.0 | 2020-10-27 | [1] | Bioconductor | |
| ggplot2 | * 3.3.5 | 2021-06-25 | [1] | CRAN | (R 4.0.3) |
| ggpubr | * 0.4.0 | 2020-06-27 | [1] | CRAN | (R 4.0.2) |
| ggsci | 2.9 | 2018-05-14 | [1] | CRAN | (R 4.0.2) |
| ggsignif | 0.6.2 | 2021-06-14 | [1] | CRAN | (R 4.0.3) |
| glue | 1.4.2 | 2020-08-27 | [1] | CRAN | (R 4.0.2) |
| gridExtra | 2.3 | 2017-09-09 | [1] | CRAN | (R 4.0.2) |
| gtable | 0.3.0 | 2019-03-25 | [1] | CRAN | (R 4.0.2) |
| haven | 2.4.3 | 2021-08-04 | [1] | CRAN | (R 4.0.3) |
| hms | 1.1.0 | 2021-05-17 | [1] | CRAN | (R 4.0.3) |
| htmltools | 0.5.2 | 2021-08-25 | [1] | CRAN | (R 4.0.3) |
| httr | 1.4.2 | 2020-07-20 | [1] | CRAN | (R 4.0.2) |
| IRanges | * 2.24.1 | 2020-12-12 | [1] | Bioconductor | |
| IRdisplay | 1.0 | 2021-01-20 | [1] | CRAN | (R 4.0.2) |
| IRkernel | 1.2 | 2021-05-11 | [1] | CRAN | (R 4.0.3) |
| jsonlite | 1.7.2 | 2020-12-09 | [1] | CRAN | (R 4.0.2) |
| labeling | 0.4.2 | 2020-10-20 | [1] | CRAN | (R 4.0.2) |
| lattice | 0.20-41 | 2020-04-02 | [2] | CRAN | (R 4.0.3) |
| lifecycle | 1.0.0 | 2021-02-15 | [1] | CRAN | (R 4.0.3) |
| lubridate | 1.7.10 | 2021-02-26 | [1] | CRAN | (R 4.0.3) |
| magrittr | 2.0.1 | 2020-11-17 | [1] | CRAN | (R 4.0.2) |
| Matrix | 1.3-4 | 2021-06-01 | [1] | CRAN | (R 4.0.3) |
| MatrixGenerics | * 1.2.1 | 2021-01-30 | [1] | Bioconductor | |
| matrixStats | * 0.60.1 | 2021-08-23 | [1] | CRAN | (R 4.0.3) |
| modelr | 0.1.8 | 2020-05-19 | [1] | CRAN | (R 4.0.2) |
| munsell | 0.5.0 | 2018-06-12 | [1] | CRAN | (R 4.0.2) |
| openxlsx | 4.2.4 | 2021-06-16 | [1] | CRAN | (R 4.0.3) |
| pbdZMQ | 0.3-5 | 2021-02-10 | [1] | CRAN | (R 4.0.3) |
| pillar | 1.6.2 | 2021-07-29 | [1] | CRAN | (R 4.0.3) |
| pkgconfig | 2.0.3 | 2019-09-22 | [1] | CRAN | (R 4.0.2) |
| purrr | * 0.3.4 | 2020-04-17 | [1] | CRAN | (R 4.0.2) |
| R6 | 2.5.1 | 2021-08-19 | [1] | CRAN | (R 4.0.3) |
| Rcpp | 1.0.7 | 2021-07-07 | [1] | CRAN | (R 4.0.3) |
| RCurl | 1.98-1.4 | 2021-08-17 | [1] | CRAN | (R 4.0.3) |
| readr | * 2.0.1 | 2021-08-10 | [1] | CRAN | (R 4.0.3) |
| readxl | 1.3.1 | 2019-03-13 | [1] | CRAN | (R 4.0.2) |
| repr | 1.1.3 | 2021-01-21 | [1] | CRAN | (R 4.0.2) |

| | | | | | |
|----------------------|----------|------------|-----|--------------|-----------|
| reprex | 2.0.1 | 2021-08-05 | [1] | CRAN | (R 4.0.3) |
| rio | 0.5.27 | 2021-06-21 | [1] | CRAN | (R 4.0.3) |
| rlang | 0.4.11 | 2021-04-30 | [1] | CRAN | (R 4.0.3) |
| rstatix | 0.7.0 | 2021-02-13 | [1] | CRAN | (R 4.0.3) |
| rstudioapi | 0.13 | 2020-11-12 | [1] | CRAN | (R 4.0.2) |
| rvest | 1.0.1 | 2021-07-26 | [1] | CRAN | (R 4.0.3) |
| S4Vectors | * 0.28.1 | 2020-12-09 | [1] | Bioconductor | |
| scales | 1.1.1 | 2020-05-11 | [1] | CRAN | (R 4.0.2) |
| sessioninfo | 1.1.1 | 2018-11-05 | [1] | CRAN | (R 4.0.2) |
| stringi | 1.7.4 | 2021-08-25 | [1] | CRAN | (R 4.0.3) |
| stringr | * 1.4.0 | 2019-02-10 | [1] | CRAN | (R 4.0.2) |
| SummarizedExperiment | * 1.20.0 | 2020-10-27 | [1] | Bioconductor | |
| svglite | 2.0.0 | 2021-02-20 | [1] | CRAN | (R 4.0.3) |
| systemfonts | 1.0.2 | 2021-05-11 | [1] | CRAN | (R 4.0.3) |
| tibble | * 3.1.4 | 2021-08-25 | [1] | CRAN | (R 4.0.3) |
| tidyr | * 1.1.3 | 2021-03-03 | [1] | CRAN | (R 4.0.3) |
| tidyselect | 1.1.1 | 2021-04-30 | [1] | CRAN | (R 4.0.3) |
| tidyverse | * 1.3.1 | 2021-04-15 | [1] | CRAN | (R 4.0.3) |
| tzdb | 0.1.2 | 2021-07-20 | [1] | CRAN | (R 4.0.3) |
| utf8 | 1.2.2 | 2021-07-24 | [1] | CRAN | (R 4.0.3) |
| uuid | 0.1-4 | 2020-02-26 | [1] | CRAN | (R 4.0.2) |
| vctrs | 0.3.8 | 2021-04-29 | [1] | CRAN | (R 4.0.3) |
| withr | 2.4.2 | 2021-04-18 | [1] | CRAN | (R 4.0.3) |
| xml2 | 1.3.2 | 2020-04-23 | [1] | CRAN | (R 4.0.2) |
| XVector | 0.30.0 | 2020-10-27 | [1] | Bioconductor | |
| zip | 2.2.0 | 2021-05-31 | [1] | CRAN | (R 4.0.3) |
| zlibbioc | 1.36.0 | 2020-10-27 | [1] | Bioconductor | |

[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0

[2] /usr/lib/R/library