

main

September 24, 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(2)
```

A data.table: 2 × 4

id	Afr	Eur	group
<chr>	<dbl>	<dbl>	<chr>
Br2374	0.007	0.993	CAUC
Br1857	0.001	0.999	CAUC

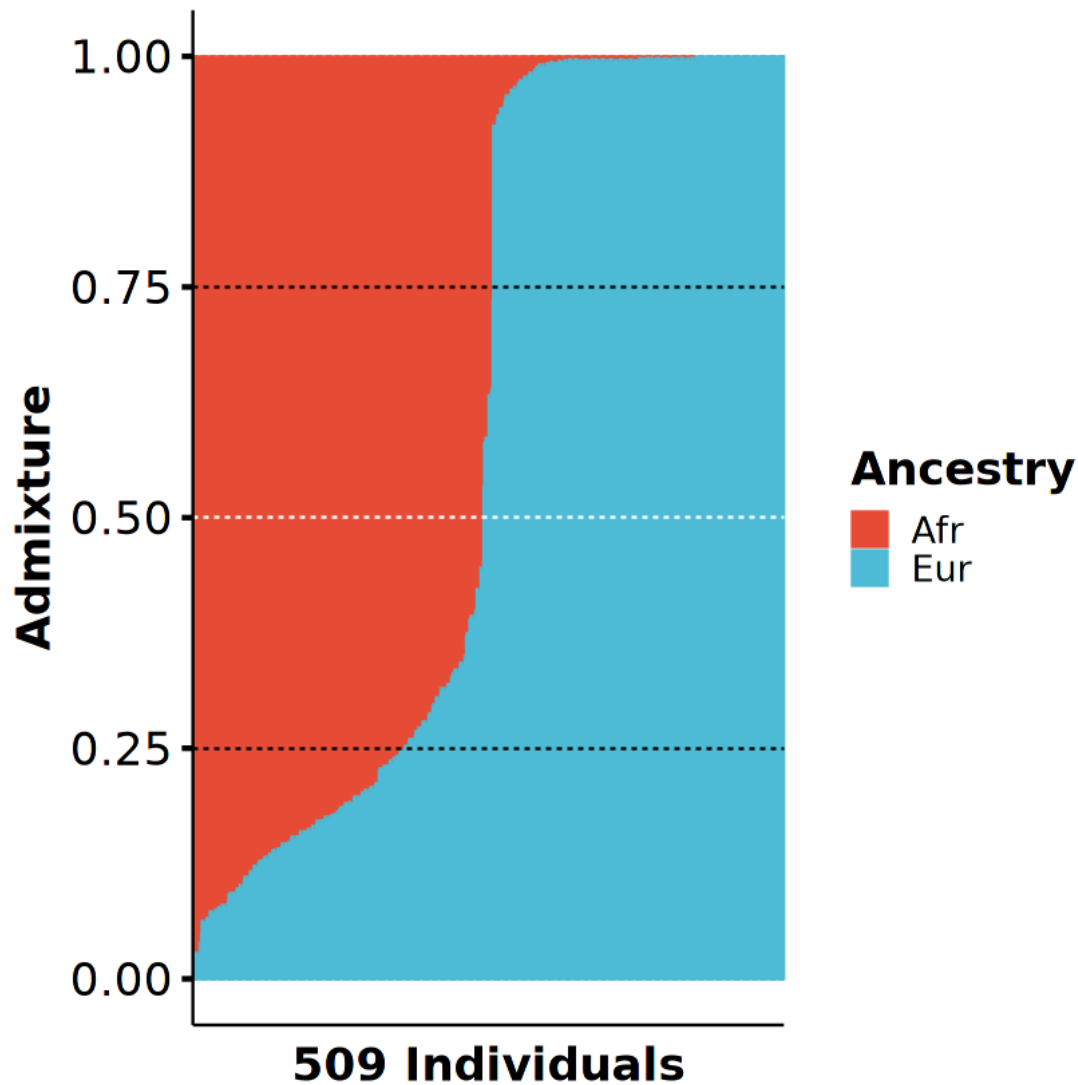
```
[9]: ancestry %>% mutate_if(is.character, as.factor) %>%
  group_by(group) %>% summarize(AA=mean(Afr), EA=mean(Eur))
```

	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))
```

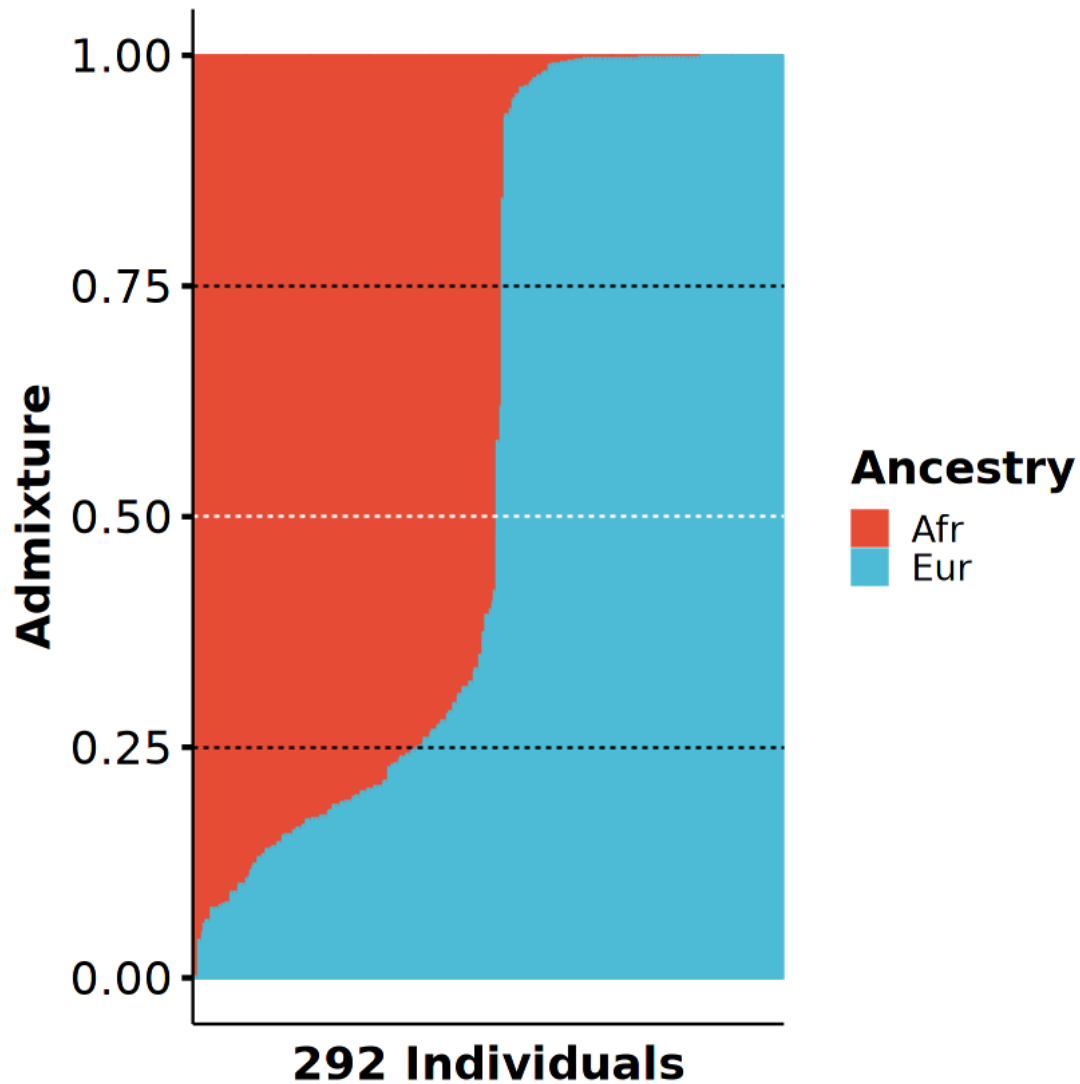
	group	AA_mean	AA_sd	AA_max	AA_min	EA_mean	EA_sd	EA_max
	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
A tibble: 2 × 9	AA	0.78962609	0.10611682	0.999	0.381	0.2103739	0.10611682	0.619
	CAUC	0.03087879	0.02997578	0.156	0.001	0.9691212	0.02997578	0.999

```
[11]: brp = ancestry %>% inner_join(pheno, by=c("id"="BrNum")) %>%
  select(id, Race, Afr, Eur) %>%
  mutate_if(is.character, as.factor) %>% distinct %>%
  pivot_longer(-c("Race", "id"), names_to="Ancestry", values_to="Proportion")
  ↪%>%
  mutate_if(is.character, as.factor) %>% group_by(Ancestry) %>%
  mutate(ID = fct_reorder(id, desc(Proportion))) %>%
  ggbarplot(x="ID", y="Proportion", fill = "Ancestry", color="Ancestry",
  palette="npg", ylab="Admixture", xlab="509 Individuals",
  ggtheme=theme_pubr(base_size=20), legend="right") +
  geom_hline(yintercept=0.5, linetype="dashed", color="white") +
  geom_hline(yintercept=0.75, linetype="dashed", color="black") +
  geom_hline(yintercept=0.25, linetype="dashed", color="black") +
  font("xy.title", face="bold") + font("legend.title", face="bold") +
  rremove("x.text") + rremove("x.ticks")
save_ggplots(brp, "ancestry_structure_barplot_eqtl", 12, 5)
brp
```



```
[12]: brp = 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")
  ↪ %>%
  mutate_if(is.character, as.factor) %>% group_by(Ancestry) %>%
  mutate(ID = fct_reorder(id, desc(Proportion))) %>%
  ggbarplot(x="ID", y="Proportion", fill = "Ancestry", color="Ancestry",
    palette="npg", ylab="Admixture", xlab="292 Individuals",
    ggtheme=theme_pubr(base_size=20), legend="right") +
  geom_hline(yintercept=0.5, linetype="dashed", color="white") +
  geom_hline(yintercept=0.75, linetype="dashed", color="black") +
  geom_hline(yintercept=0.25, linetype="dashed", color="black") +
```

```
font("xy.title", face="bold") + font("legend.title", face="bold") +
  rremove("x.text") + rremove("x.ticks")
save_ggplots(brp, "ancestry_structure_barplot", 12, 5)
brp
```

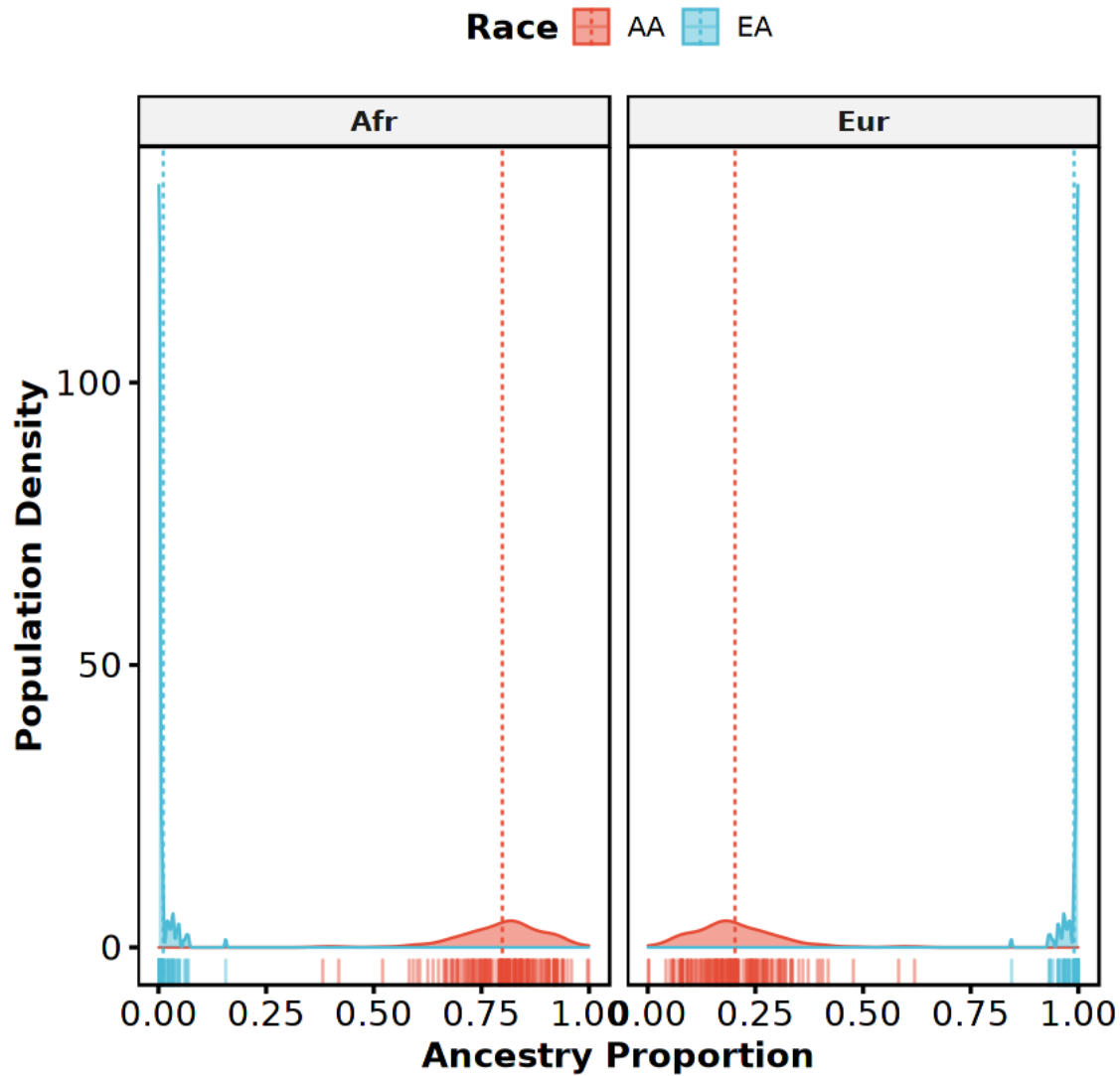


```
[13]: bxp = ancestry %>% inner_join(pheno, by=c("id"="BrNum")) %>%
  filter(Age > 17, Dx == "Control") %>% select(id, Race, Afr, Eur) %>%
  mutate_if(is.character, as.factor) %>% distinct %>%
  pivot_longer(-c("Race", "id"), names_to="Ancestry", values_to="Proportion")
  → %>%
  ggdensity(x="Proportion", 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

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

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

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

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

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

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

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

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

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

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

```
[19]: 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

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

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

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

A grouped_df: 8 × 4	Region	Race	mean	sd
	<chr>	<chr>	<dbl>	<dbl>
	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

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

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

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

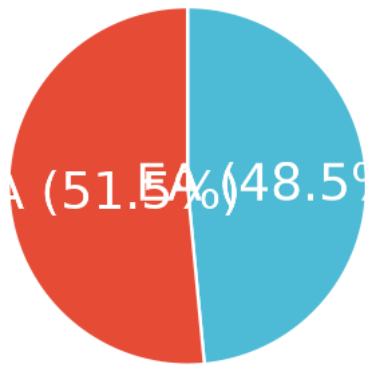

	Region <chr>	Race <chr>	mean <dbl>	sd <dbl>
A grouped_df: 8 × 4	Caudate	AA	7.859709	0.8416464
	Caudate	EA	7.862371	0.8911055
	DentateGyrus	AA	5.206349	1.2062837
	DentateGyrus	EA	5.210714	1.1760765
	DLPFC	AA	7.678922	0.9445184
	DLPFC	EA	7.723563	0.9238440
	HIPPO	AA	7.604225	1.0509344
	HIPPO	EA	7.631868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

1.3.1 Pie chart

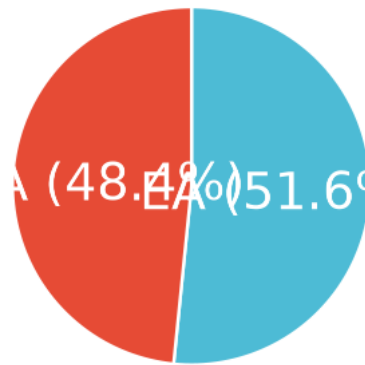
```
[24]: plot_pie <- function(tissue){
  pie = pheno %>% mutate_if(is.character, as.factor) %>% group_by(Region,
  ↪Race) %>%
    count %>% as.data.frame %>% group_by(Region) %>%
    transmute(Race, Percent = round(n/sum(n)*100, 1)) %>%
    mutate(Labels=paste0(Race, " (", Percent, "%")) %>% filter(Region ==
  ↪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)
}
```

```
[25]: ## 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
```

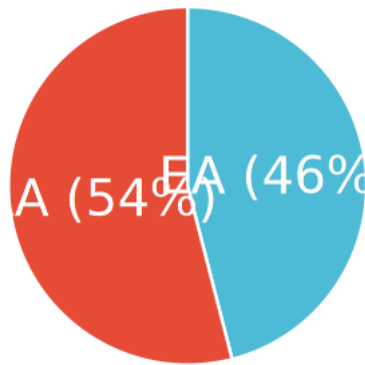
Caudate



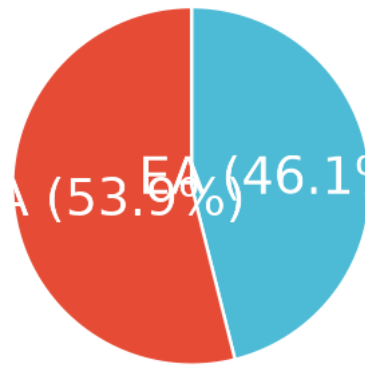
Dentate Gyrus



DLPFC



Hippocampus



1.4 Adult individuals for expression related analysis

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

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

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

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

```
[28]: 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

```
[29]: 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

```
[30]: 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

```
[31]: 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

```
[32]: 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

```
[33]: 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

```
[34]: 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

```
[35]: 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

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

```

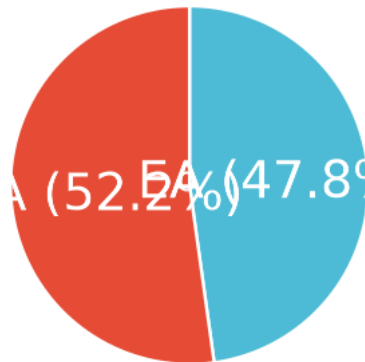
top = text_grob("Caudate", face = "bold", size = 26))
gg_pie = annotate_figure(plot_pie("DentateGyrus"),
top = text_grob("Dentate Gyrus", face = "bold", size = 26))
dd_pie = annotate_figure(plot_pie("DLPFC"),
top = text_grob("DLPFC", face = "bold", size = 26))
hh_pie = annotate_figure(plot_pie("HIPPO"),
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

```

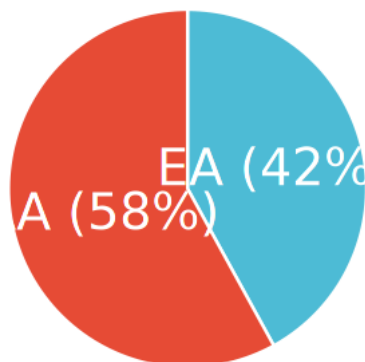
Caudate



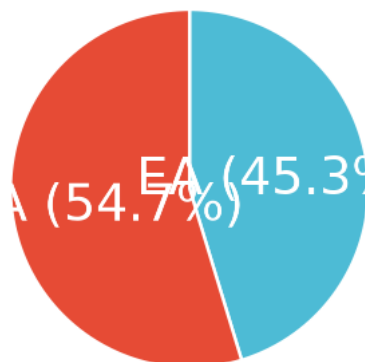
Dentate Gyrus



DLPFC



Hippocampus



1.5 Reproducibility Information

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

```
[1] "2021-09-24 13:23:00 EDT"
```

```
   user  system elapsed  
26.731   1.054   28.316
```

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 2021-09-24

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