main_junctions

September 8, 2021

1 eQTL boxplot: Enrichment and Overlap of PGC2+CLOZUK

This is script ported from python to fix unknown plotting error.

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

1.1 Functions

```
[2]: feature = "junctions"
```

1.1.1 Cached functions

```
[3]: get_de_df <- function(){
         de_file = paste0("../../differential_expression/_m/", feature,
                          "/diffExpr_szVctl_full.txt")
         return(data.table::fread(de_file))
     }
     memDE <- memoise::memoise(get_de_df)

     get_eqtl_df <- function(){
         eGenes_file = paste0('../../eqtl/caudate/summary_table/_m/',
                              'Brainseq_LIBD_caudate_4features.signifpairs.txt.gz')
         eGenes = data.table::fread(eGenes_file) %>%
             filter(Type == feature_map(feature)) %>%
             arrange(pval_nominal)
         return(eGenes)
     }
     memEQTL <- memoise::memoise(get_eqtl_df)

     get_pheno_df <- function(){
         phenotype_file = paste0('/ceph/projects/v4_phase3_paper/inputs/',
                                 'phenotypes/_m/merged_phenotypes.csv')
         return(data.table::fread(phenotype_file))
     }
     memPHENO <- memoise::memoise(get_pheno_df)
```

```r
get_residualized_df <- function(){
    expr_file = paste0("../../differential_expression/_m/", feature,
                       "/residualized_expression.tsv")
    return(data.table::fread(expr_file) %>% column_to_rownames("V1"))
}
memRES <- memoise::memoise(get_residualized_df)

get_genotypes <- function(){
    traw_file = paste0("/ceph/projects/brainseq/genotype/download/topmed/
 ↪convert2plink/",
                       "filter_maf_01/a_transpose/_m/LIBD_Brain_TopMed.traw")
    traw = data.table::fread(traw_file) %>% rename_with(~ gsub('\\_.*', '', .x))
    return(traw)
}
memSNPs <- memoise::memoise(get_genotypes)

get_gwas_snps <- function(){
    gwas_snp_file = paste0('/ceph/projects/v4_phase3_paper/inputs/sz_gwas/',
                           'pgc2_clozuk/map_phase3/_m/libd_hg38_pgc2sz_snps.tsv')
    gwas_df = data.table::fread(gwas_snp_file) %>% arrange(P)
    return(gwas_df)
}
memGWAS <- memoise::memoise(get_gwas_snps)

get_integration_df <- function(){
    return(inner_join(memGWAS(), memEQTL(),
                      by=c("our_snp_id"="variant_id"),
                      suffix=c("_PGC2", "_eQTL")) %>%
           inner_join(memDE(), by=c("gene_id"="V1")) %>%
           mutate(agree_direction=sign(OR -1) * sign(slope) * sign(t) *␣
 ↪ifelse(pgc2_a1_same_as_our_counted, 1, -1)))
}
memMERGE <- memoise::memoise(get_integration_df)

get_snp_df <- function(variant_id, gene_id){
    zz = get_geno_annot() %>% filter(SNP == variant_id)
    xx = get_snps_df() %>% filter(SNP == variant_id) %>%
        column_to_rownames("SNP") %>% t %>% as.data.frame %>%
        rownames_to_column("BrNum") %>% mutate(COUNTED=zz$COUNTED, ALT=zz$ALT)␣
 ↪%>%
        rename("SNP"=all_of(variant_id))
    yy = memRES()[gene_id, ] %>% t %>% as.data.frame %>%
        rownames_to_column("RNum") %>% inner_join(memPHENO(), by="RNum")
    ## Annotated SNPs
    letters = c()
    for(ii in seq_along(xx$COUNTED)){
```

```
        a0 = xx$COUNTED[ii]; a1 = xx$ALT[ii]; number = xx$SNP[ii]
        letters <- append(letters, letter_snp(number, a0, a1))
    }
    xx = xx %>% mutate(LETTER=letters, ID=paste(SNP, LETTER, sep="\n"))
    df = inner_join(xx, yy, by="BrNum") %>% mutate_if(is.character, as.factor)
    return(df)
}
memDF <- memoise::memoise(get_snp_df)
```

1.1.2 Simple functions

```
[4]: feature_map <- function(feature){
    return(list("genes"="Gene", "transcripts"= "Transcript",
                "exons"= "Exon", "junctions"= "Junction")[[feature]])
}

get_geno_annot <- function(){
    return(memSNPs() %>% select(CHR, SNP, POS, COUNTED, ALT))
}

get_snps_df <- function(){
    return(memSNPs() %>% select("SNP", starts_with("Br")))
}

letter_snp <- function(number, a0, a1){
    if(is.na(number)){ return(NA) }
    if( length(a0) == 1 & length(a1) == 1){
        seps = ""; collapse=""
    } else {
        seps = " "; collapse=NULL
    }
    return(paste(paste0(rep(a0, number), collapse = collapse),
                 paste0(rep(a1, (2-number)), collapse = collapse), sep=seps))
}

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

get_biomart_df <- function(){
    biomart = data.table::fread("../_h/biomart.csv")
}
memMART <- memoise::memoise(get_biomart_df)

get_gene_symbol <- function(gene_id){
```

```r
        ensemblID = gsub("\\..*", "", gene_id)
        geneid = memMART() %>% filter(ensembl_gene_id == gsub("\\..*", "", gene_id))
        if(dim(geneid)[1] == 0){
            return("")
        } else {
            return(geneid$external_gene_name)
        }
}

plot_simple_eqtl <- function(fn, gene_id, variant_id, eqtl_annot){
    bxp = memDF(variant_id, gene_id) %>%
        ggboxplot(x="ID", y=gene_id, fill="red", add="jitter", xlab="",
                  ylab="Residualized Expression", outlier.shape=NA,
                  add.params=list(alpha=0.5), alpha=0.4,
                  ggtheme=theme_pubr(base_size=20, border=TRUE)) +
        font("xy.title", face="bold") +
        ggtitle(paste(get_gene_symbol(gene_id), gene_id, eqtl_annot, sep='\n'))␣
 ↪+
        theme(plot.title = element_text(hjust = 0.5, face="bold"))
    print(bxp)
    save_ggplots(fn, bxp, 7, 7)
}
```

1.1.3 GWAS plots

```r
[5]: get_risk_allele <- function(OR, A1, A2){
    ra = ifelse(OR > 1, A1, A2)
    return(ra)
}

get_df <- function(){
    return(memEQTL() %>% inner_join(memGWAS(), by="variant_id"))
}

get_gwas_ordered_snp_df <- function(variant_id, gene_id,␣
 ↪pgc2_a1_same_as_our_counted, OR){
    df = memDF(variant_id, gene_id)
    if(!pgc2_a1_same_as_our_counted){ # Fix bug with matching alleles!
        if(OR < 1){ df = df %>% mutate(SNP = 2-SNP, ID=paste(SNP, LETTER,␣
 ↪sep="\n")) }
    } else {
        if(OR > 1){ df = df %>% mutate(SNP = 2-SNP, ID=paste(SNP, LETTER,␣
 ↪sep="\n")) }
    }
    return(df)
}
```

4

```
plot_gwas_eqtl_pheno <- function(fn, gene_id, variant_id,␣
 ↪pgc2_a1_same_as_our_counted, OR, title){
     bxp = get_gwas_ordered_snp_df(variant_id, gene_id,␣
 ↪pgc2_a1_same_as_our_counted, OR) %>%
         mutate_if(is.character, as.factor) %>% filter(Dx %in% c("CTL", "SZ"),␣
 ↪Age > 17) %>%
         ggboxplot(x="ID", y=gene_id, fill="Dx", color="Dx", add="jitter",␣
 ↪xlab=variant_id,
                   ylab="Residualized Expression", outlier.shape=NA,
                   add.params=list(alpha=0.5), alpha=0.4, legend="bottom",
                   ggtheme=theme_pubr(base_size=20, border=TRUE)) +
         font("xy.title", face="bold") + ggtitle(title) +
         theme(plot.title = element_text(hjust = 0.5, face="bold"))
     print(bxp)
     save_ggplots(fn, bxp, 7, 9)
}
```

1.2 Integration analysis

```
[6]: dir.create(feature)
```

1.2.1 Enrichment

Integrate DEG with PGC2+CLOZUK SNPs

```
[7]: dft = memMERGE() %>% mutate(agree_direction=ifelse(agree_direction == 1, "Yes",␣
 ↪ifelse(agree_direction == -1, "No", 0)))
dim(dft)
```

1. 3190613 2. 58

```
[8]: table(dft$agree_direction)
```

```
      0       No      Yes
   3267 1557478 1629868
```

```
[9]: table = matrix(c(sum((dft$P<5e-8)  & (dft$adj.P.Val < 0.05)),
                  sum((dft$P>=5e-8) & (dft$adj.P.Val < 0.05)),
                  sum((dft$P<5e-8)  & (dft$adj.P.Val >= 0.05)),
                  sum((dft$P>=5e-8) & (dft$adj.P.Val >= 0.05))),
              nrow=2)
print(table)
fisher.test(table)
```

```
        [,1]    [,2]
[1,]    5196   74475
[2,] 122145 2988797
```

```
        Fisher's Exact Test for Count Data

data:  table
p-value < 2.2e-16
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 1.658580 1.756912
sample estimates:
odds ratio
  1.707175
```

```
[10]: dft2 = dft %>% filter(P <= 5e-8, `adj.P.Val` < 0.05) %>%
          mutate(eqtl_gwas_dir=sign(OR -1) * sign(slope) *␣
      ↪ifelse(pgc2_a1_same_as_our_counted, 1, -1),
                 de_dir=sign(t), eqtl_slope=sign(OR␣
      ↪-1)*sign(slope)*ifelse(pgc2_a1_same_as_our_counted, 1, -1)) %>%
          #rowwise() %>% mutate(risk_allele=get_risk_allele(our_snp_id)) %>%
          select(gene_id, newGeneSymbol, our_snp_id, rsid, A1, A2, OR, P,␣
      ↪pval_nominal, adj.P.Val, logFC,
                 t, eqtl_slope, de_dir, eqtl_gwas_dir, agree_direction,␣
      ↪pgc2_a1_same_as_our_counted) %>%
          rename("variant_id"="our_snp_id", "Symbol"="newGeneSymbol") %>%␣
      ↪mutate_all(list(~na_if(.,""))) %>%
          mutate(Symbol = coalesce(Symbol,gene_id))
      dft2 %>% data.table::fwrite(paste0(feature, "/integration_by_symbol.txt"),␣
      ↪sep='\t')
      dim(dft2)
```

1. 5196 2. 17

```
[11]: df = dft2 %>% group_by(Symbol) %>% slice(1) %>% arrange(P)
      table(df$agree_direction)
```

```
 No Yes
  9  12
```

```
[12]: df
```

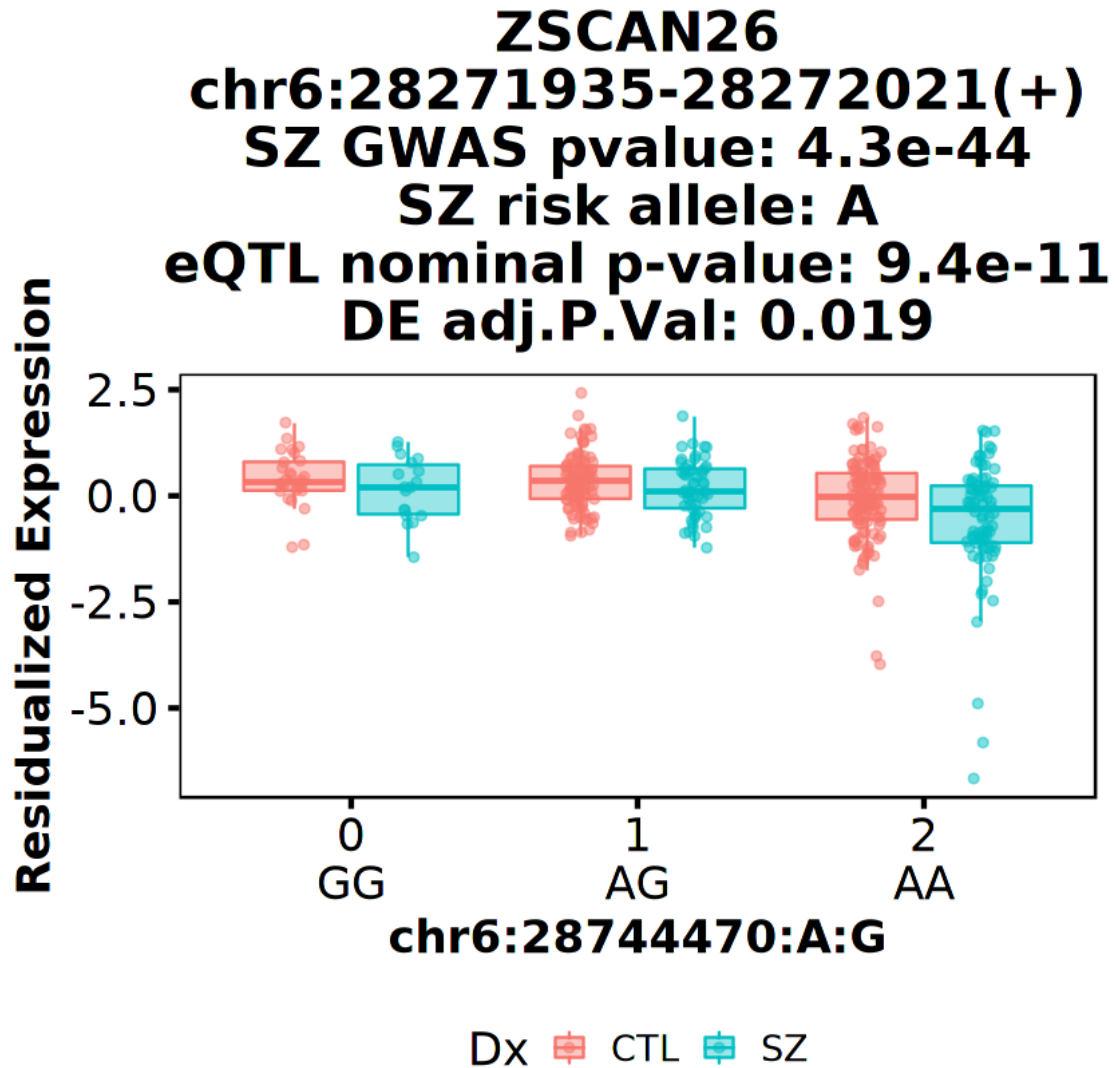|	gene_id	Symbol	variant_id	rsid
	<chr>	<chr>	<chr>	<chr>
	chr6:28271935-28272021(+)	ZSCAN26	chr6:28744470:A:G	rs1233578
	chr6:31270086-31270209(-)	HLA-C	chr6:31348749:T:C	rs9265994
	chr6:31651777-31652399(-)	BAG6	chr6:31793436:G:A	rs2607014
	chr6:31996112-31996206(+)	C4A	chr6:31793436:G:A	rs2607014
	chr6:32024325-32024469(+)	C4B	chr6:31793436:G:A	rs2607014
	chr14:103729183-103729792(+)	ZFYVE21	chr14:103762504:C:T	rs7142769
	chr14:103520312-103520468(-)	CKB	chr14:103710761:G:T	rs4900592
	chr2:232888108-232891357(-)	NGEF	chr2:232926898:C:G	rs1878289
	chr11:113412884-113415420(-)	DRD2	chr11:113522272:C:T	rs2514218
A grouped_df: 21 × 17	chr3:136262066-136283836(+)	PCCB	chr3:136569563:G:A	rs7432375
	chr6:83346335-83352063(-)	ME1	chr6:83668266:G:A	rs217300
	chr1:2497011-2497501(+)	PLCH2	chr1:2441515:A:G	rs6673661
	chr6:33080535-33080671(+)	HLA-DPB1	chr6:33020111:A:G	rs17214290
	chr16:58510684-58511421(+)	NDRG4	chr16:58511522:A:G	rs42945
	chr6:33728301-33735277(-)	IP6K3	chr6:33773939:A:G	rs4711350
	chr2:58048968-58084088(+)	VRK2	chr2:57939634:T:C	rs28718871
	chr1:8359987-8360111(-)	RERE	chr1:8443182:G:A	rs301818
	chr11:47180691-47182402(-)	PACSIN3	chr11:46729945:T:TAGG	rs3136476
	chr5:138445599-138445682(+)	REEP2	chr5:138439892:C:G	rs982085
	chr13:79551123-79552515(+)	NDFIP2	chr13:79285321:A:C	rs9545047
	chr7:24641869-24649611(+)	MPP6	chr7:24737470:CA:C	rs146678232

1.2.2 Plot with PGC2 risk allele

```
[13]: for(num in seq_along(df$gene_id)){
          variant_id = df$variant_id[num]
          gene_id = df$gene_id[num]
          gene_name = df$Symbol[num]
          pgc2_a1_same_as_our_counted = df$pgc2_a1_same_as_our_counted[num]
          OR = df$OR[num]; A1 = df$A1[num]; A2 = df$A2[num]
          fn = paste0(feature, "/eqtl_gwas_", gsub("\\.", "_", gene_name))
          de_annot = paste('DE adj.P.Val:', signif(df$adj.P.Val[num], 2))
          eqtl_annot = paste("eQTL nominal p-value:", signif(df$pval_nominal[num], 2))
          gwas_annot = paste("SZ GWAS pvalue:", signif(df$P[num], 2))
          risk_annot = paste("SZ risk allele:", get_risk_allele(OR, A1, A2))
          title = paste(gene_name, gene_id, gwas_annot,
                        risk_annot, eqtl_annot, de_annot, sep='\n')
          plot_gwas_eqtl_pheno(fn, gene_id, variant_id, pgc2_a1_same_as_our_counted,␣
       ↪OR, title)
          #print(title)
      }
```

Warning message in data.table::fread(expr_file):
"Detected 393 column names but the data has 394 columns (i.e. invalid file).
Added 1 extra default column name for the first column which is guessed to be
row names or an index. Use setnames() afterwards if this guess is not correct,

ZSCAN26
chr6:28271935-28272021(+)
SZ GWAS pvalue: 4.3e-44
SZ risk allele: A
eQTL nominal p-value: 9.4e-11
DE adj.P.Val: 0.019

HLA-C
chr6:31270086-31270209(-)
SZ GWAS pvalue: 1e-32
SZ risk allele: T
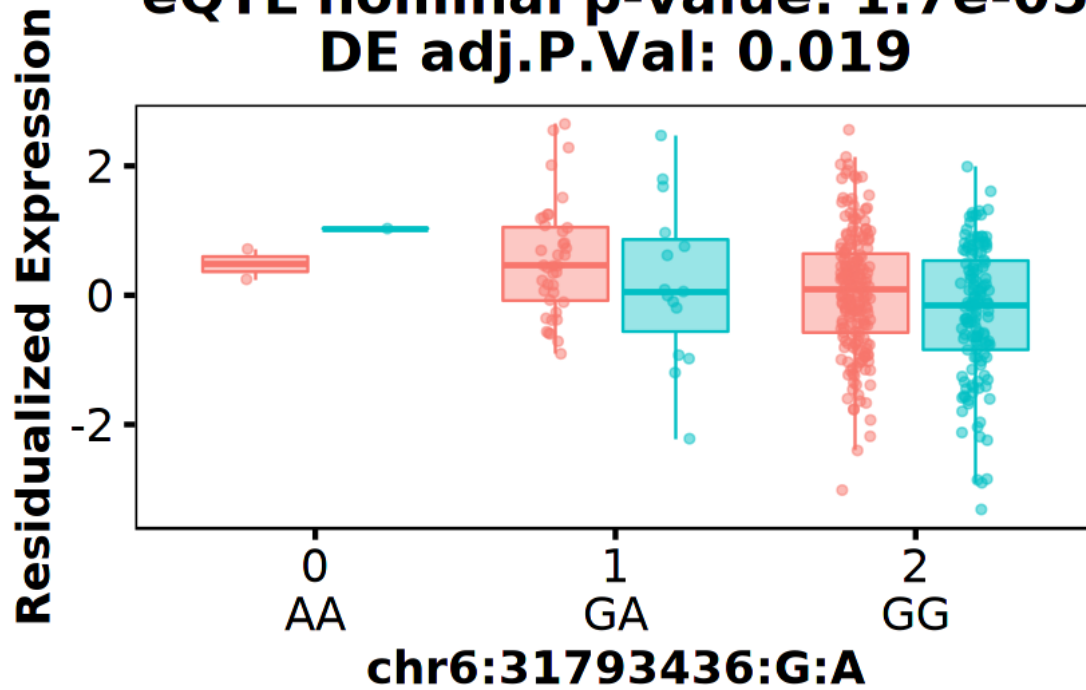**eQTL nominal p-value: 9.4e-14**
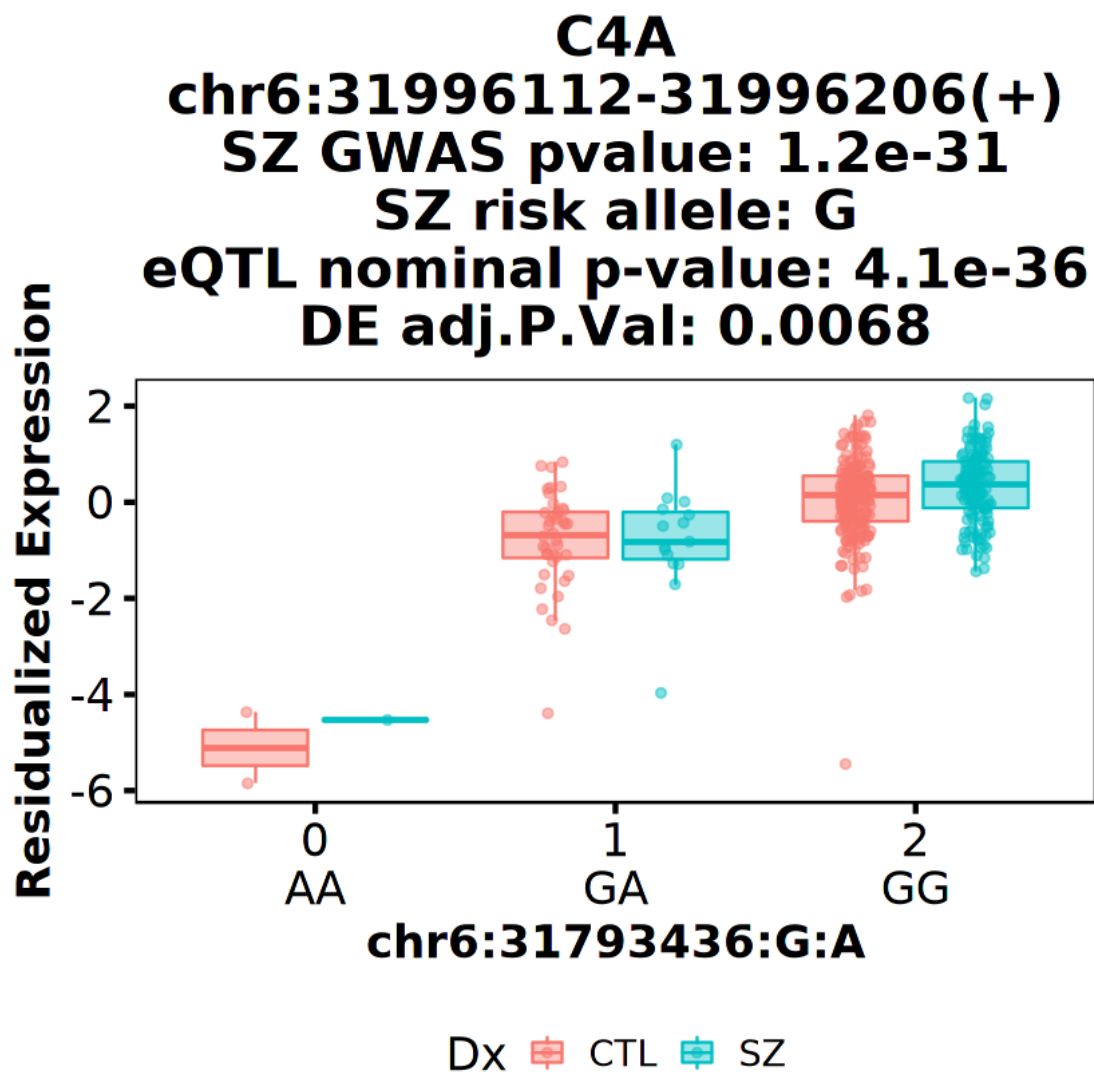**DE adj.P.Val: 0.037**
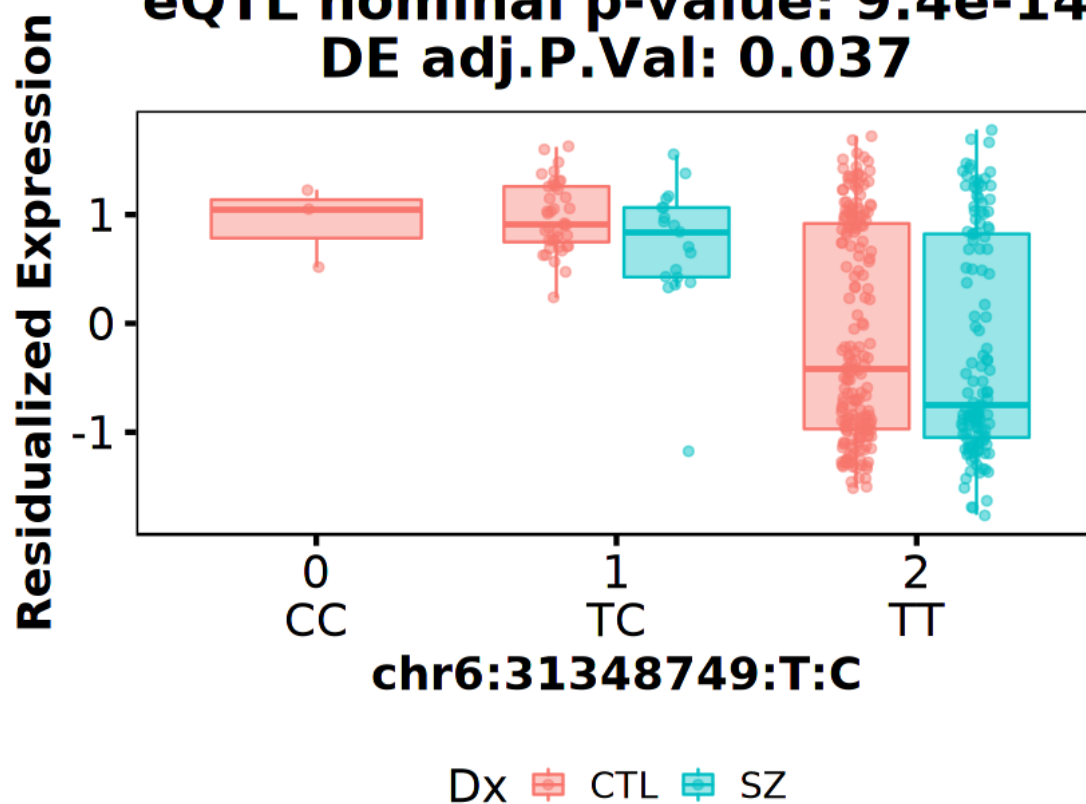
BAG6
chr6:31651777-31652399(-)
SZ GWAS pvalue: 1.2e-31
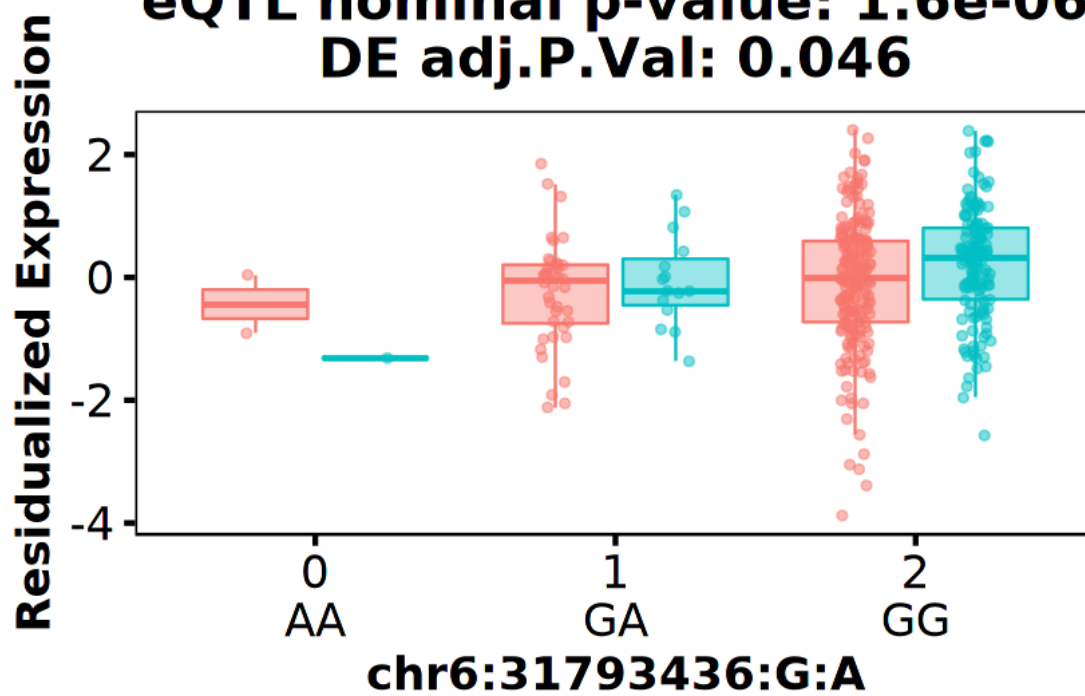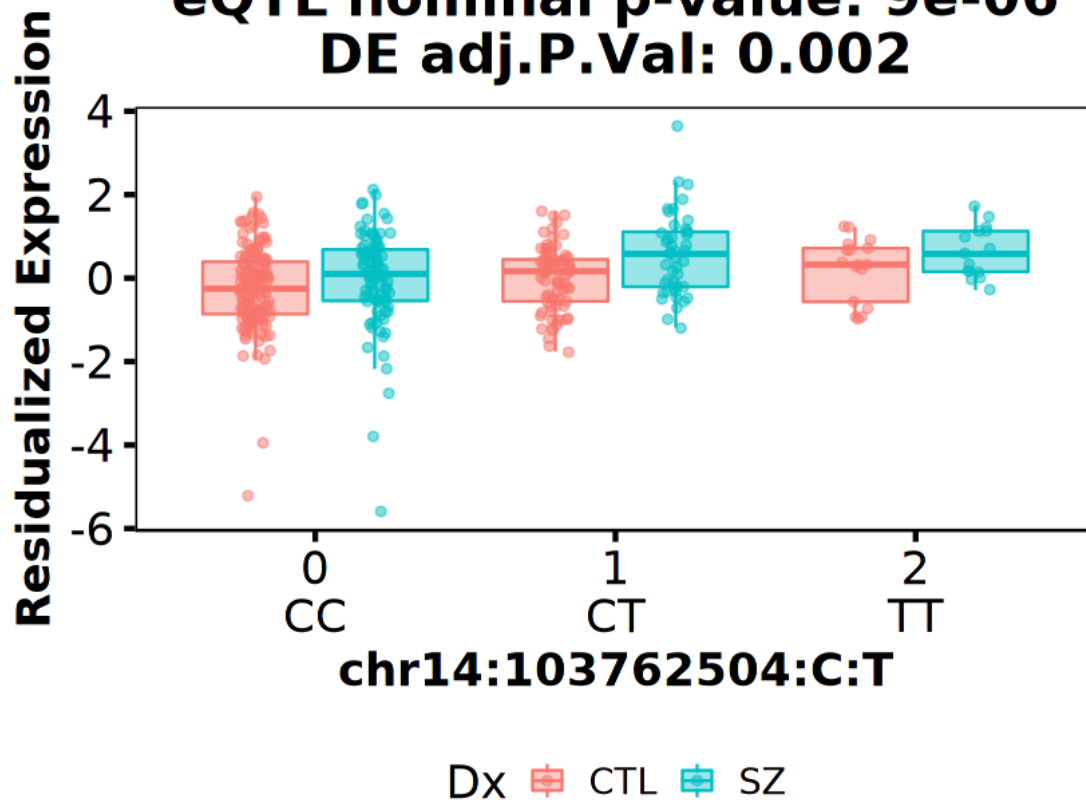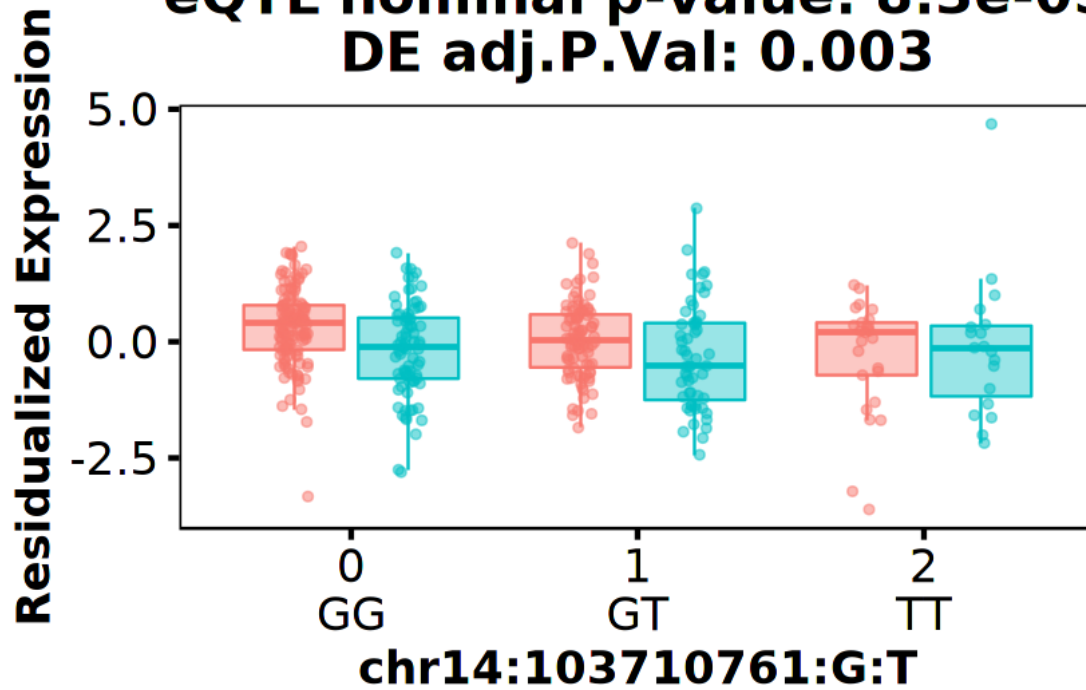SZ risk allele: G
eQTL nominal p-value: 1.7e-05
DE adj.P.Val: 0.019

C4A
chr6:31996112-31996206(+)
SZ GWAS pvalue: 1.2e-31
SZ risk allele: G
eQTL nominal p-value: 4.1e-36
DE adj.P.Val: 0.0068

C4B
chr6:32024325-32024469(+)
SZ GWAS pvalue: 1.2e-31
SZ risk allele: G
eQTL nominal p-value: 1.6e-06
DE adj.P.Val: 0.046

ZFYVE21
chr14:103729183-103729792(+)
SZ GWAS pvalue: 4.5e-14
SZ risk allele: T
eQTL nominal p-value: 9e-06
DE adj.P.Val: 0.002

CKB
chr14:103520312-103520468(-)
SZ GWAS pvalue: 3.3e-13
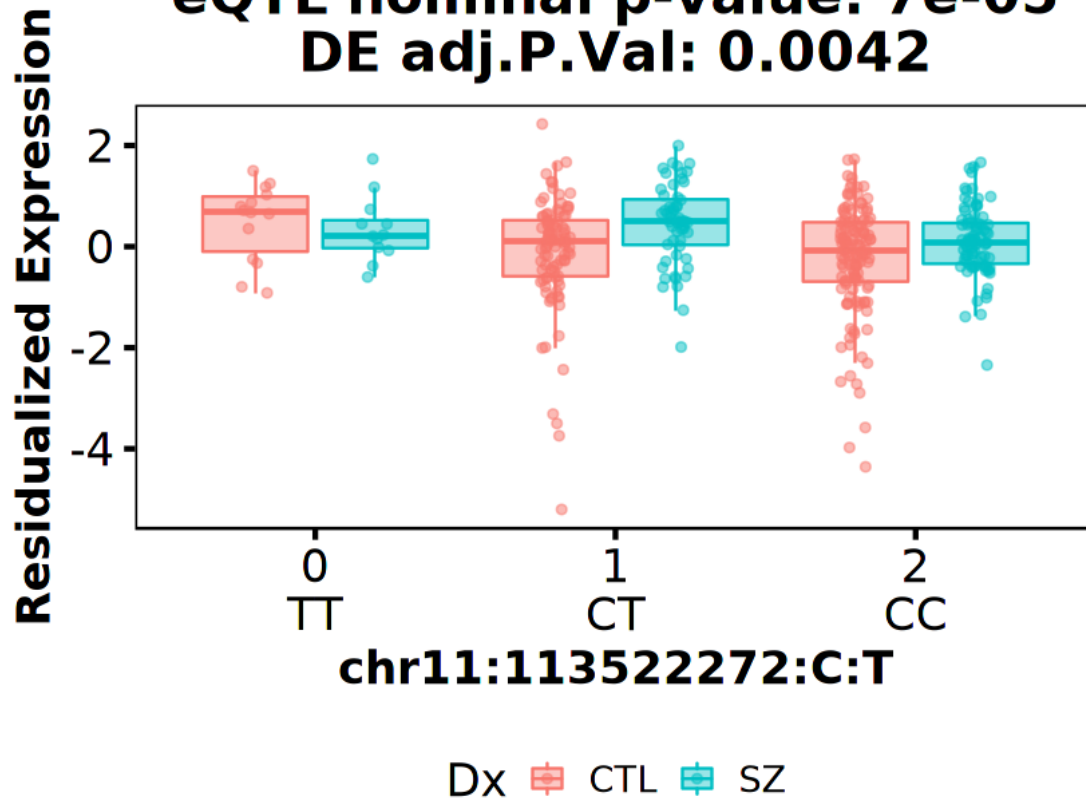SZ risk allele: T
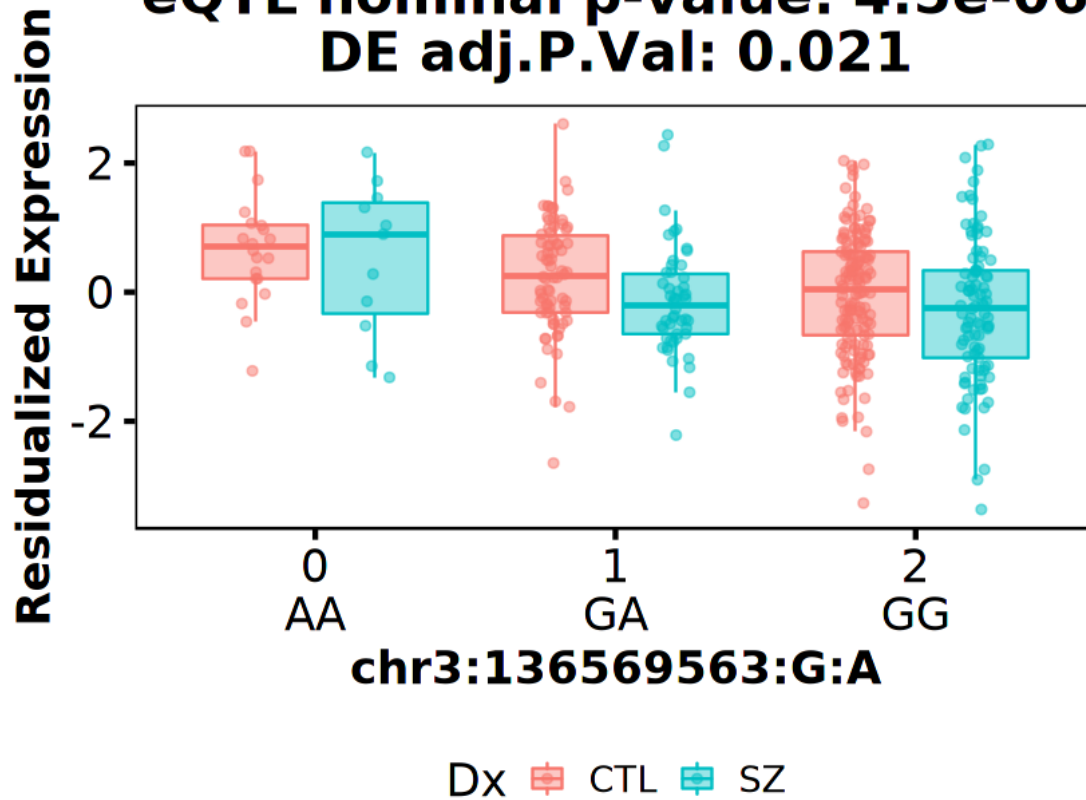eQTL nominal p-value: 8.3e-05
DE adj.P.Val: 0.003

chr14:103710761:G:T

Dx ▣ CTL ▣ SZ

NGEF
chr2:232888108-232891357(-)
SZ GWAS pvalue: 1.3e-12
SZ risk allele: G
eQTL nominal p-value: 1.6e-05
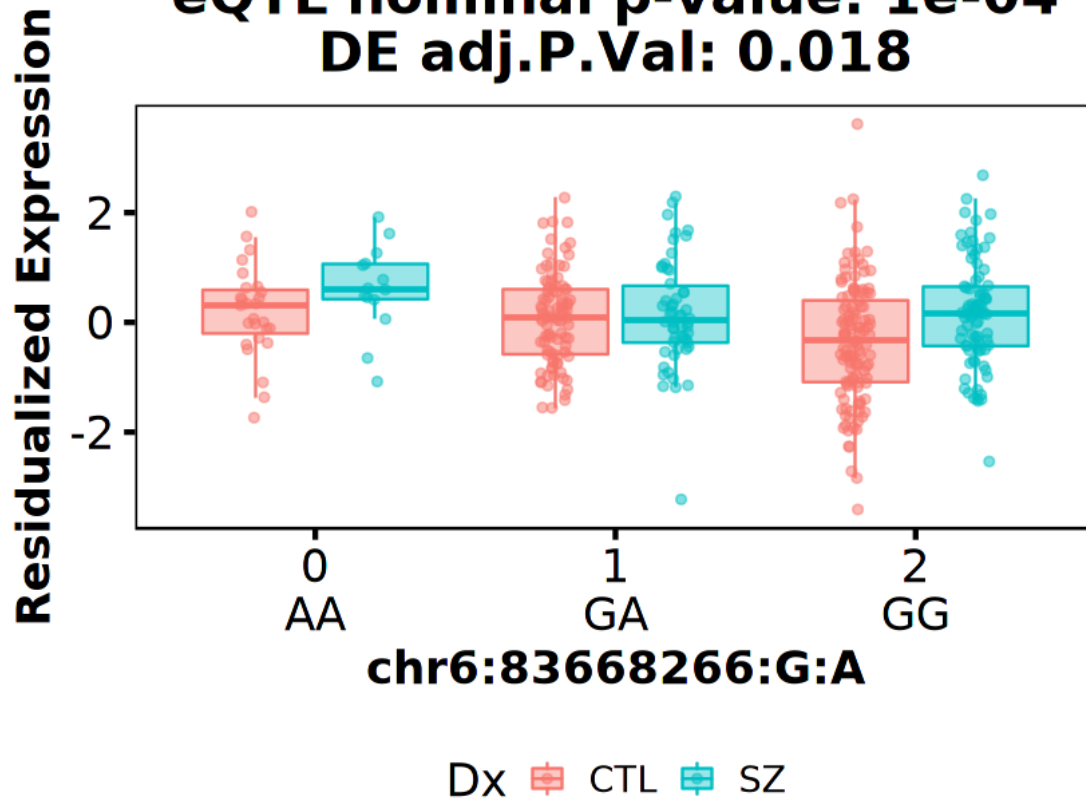DE adj.P.Val: 0.0095

chr2:232926898:C:G

Dx ⬜ CTL ⬜ SZ
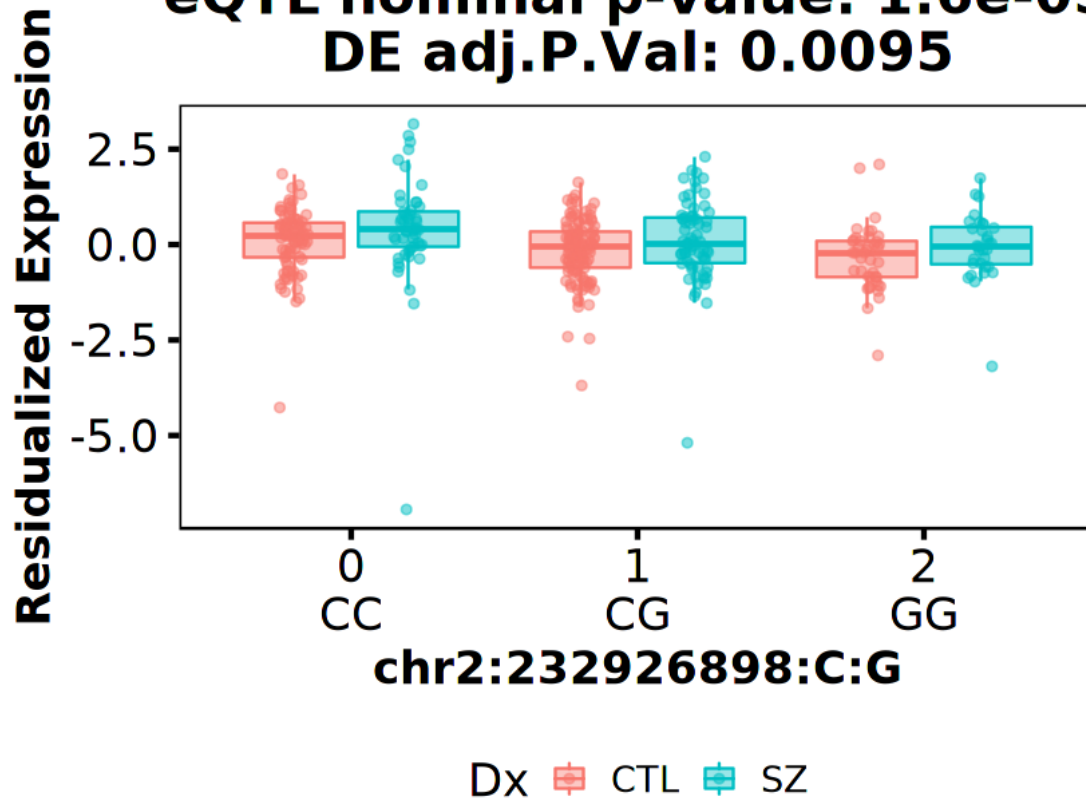
DRD2
chr11:113412884-113415420(-)
SZ GWAS pvalue: 2.4e-12
SZ risk allele: C
eQTL nominal p-value: 7e-05
DE adj.P.Val: 0.0042

PCCB
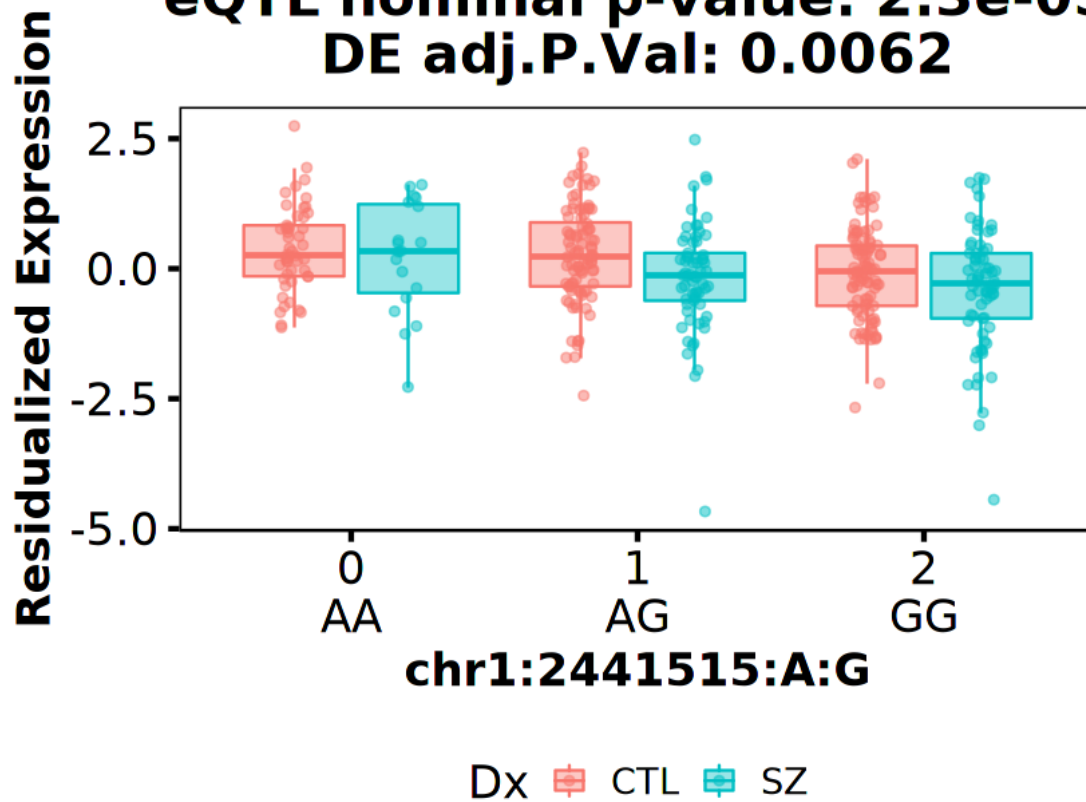**chr3:136262066-136283836(+)**
SZ GWAS pvalue: 4.1e-12
SZ risk allele: G
eQTL nominal p-value: 4.5e-06
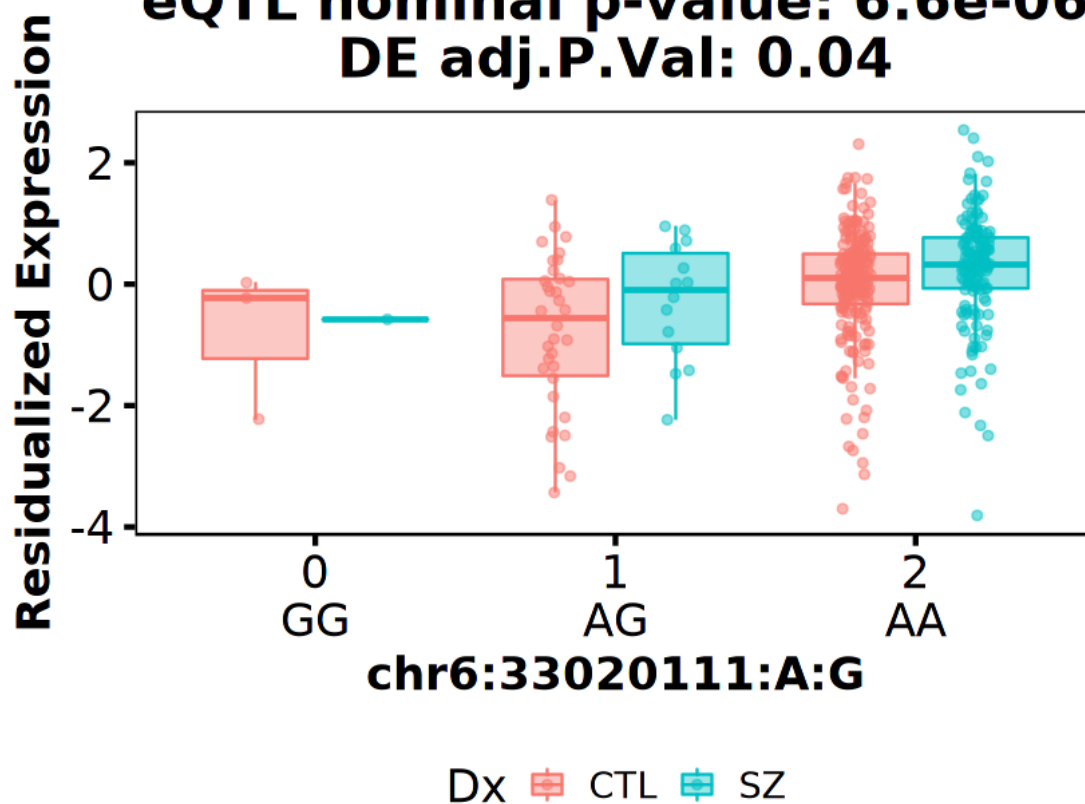**DE adj.P.Val: 0.021**

ME1
chr6:83346335-83352063(-)
SZ GWAS pvalue: 4.2e-12
SZ risk allele: G
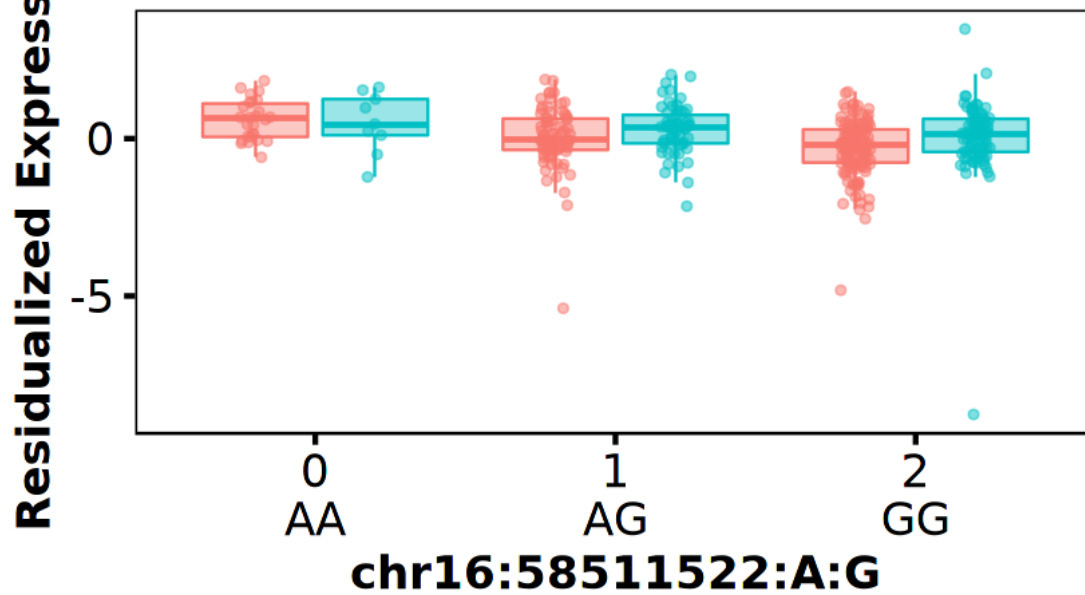eQTL nominal p-value: 1e-04
DE adj.P.Val: 0.018

PLCH2
chr1:2497011-2497501(+)
SZ GWAS pvalue: 3.7e-11
SZ risk allele: G
eQTL nominal p-value: 2.3e-05
DE adj.P.Val: 0.0062

HLA-DPB1
chr6:33080535-33080671(+)
SZ GWAS pvalue: 2.2e-10
SZ risk allele: A
eQTL nominal p-value: 6.6e-06
DE adj.P.Val: 0.04

NDRG4
chr16:58510684-58511421(+)
SZ GWAS pvalue: 2.2e-10
SZ risk allele: G
eQTL nominal p-value: 2.3e-16
DE adj.P.Val: 0.028

IP6K3
chr6:33728301-33735277(-)
SZ GWAS pvalue: 2.3e-10
SZ risk allele: G
eQTL nominal p-value: 1.2e-05
DE adj.P.Val: 0.0047
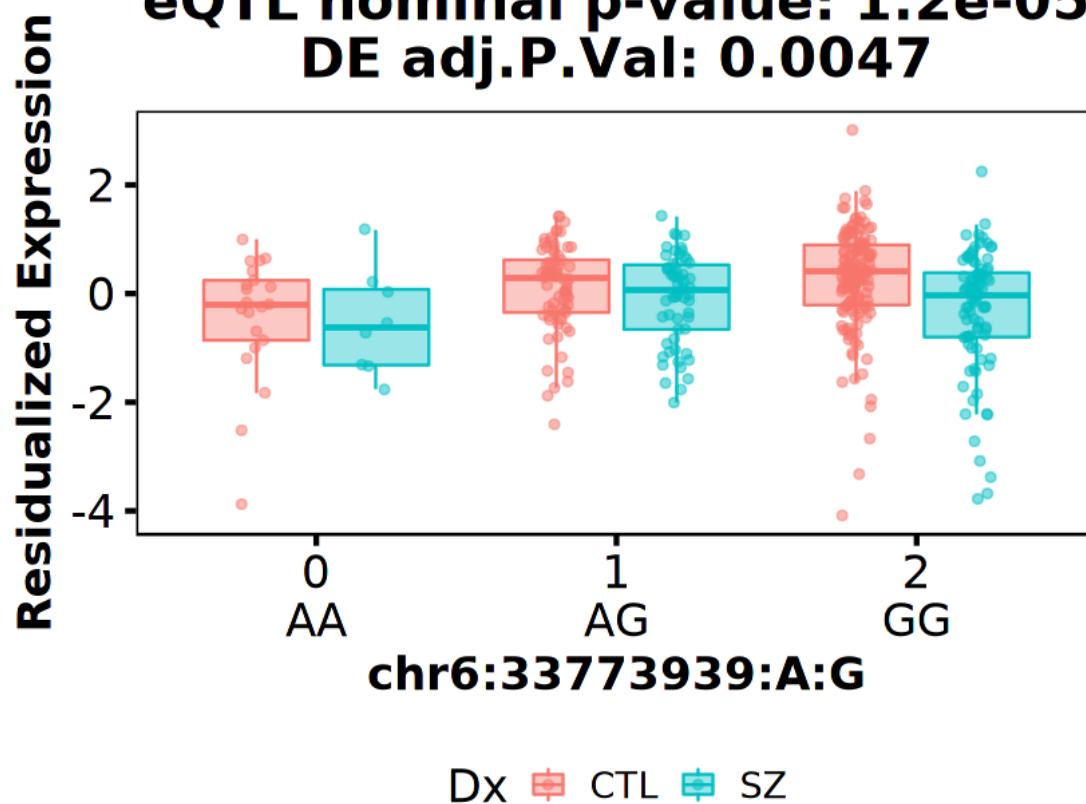
VRK2
chr2:58048968-58084088(+)
SZ GWAS pvalue: 7.5e-10
SZ risk allele: C
eQTL nominal p-value: 6.4e-05
DE adj.P.Val: 0.042

RERE
chr1:8359987-8360111(-)
SZ GWAS pvalue: 3.8e-09
SZ risk allele: A
eQTL nominal p-value: 3.7e-06
DE adj.P.Val: 0.02
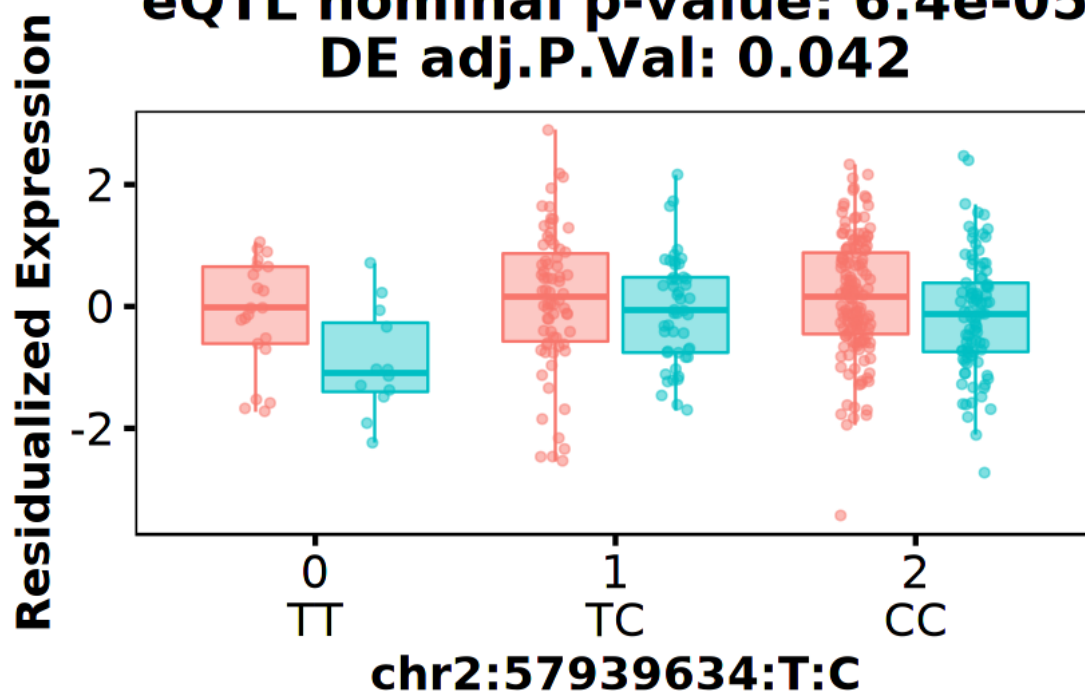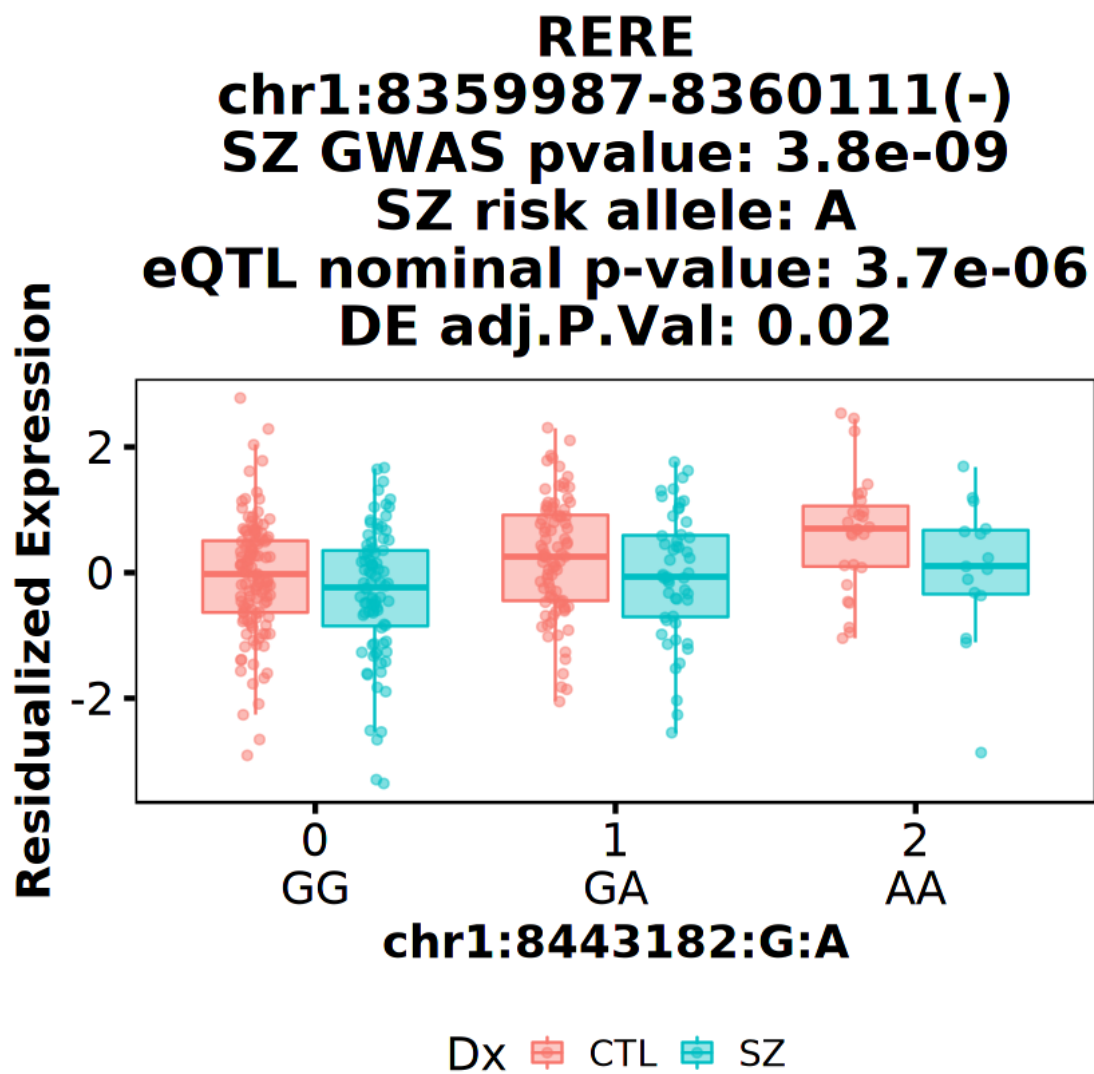
PACSIN3
chr11:47180691-47182402(-)
SZ GWAS pvalue: 3.9e-09
SZ risk allele: TAGG
eQTL nominal p-value: 0.00022
DE adj.P.Val: 0.023
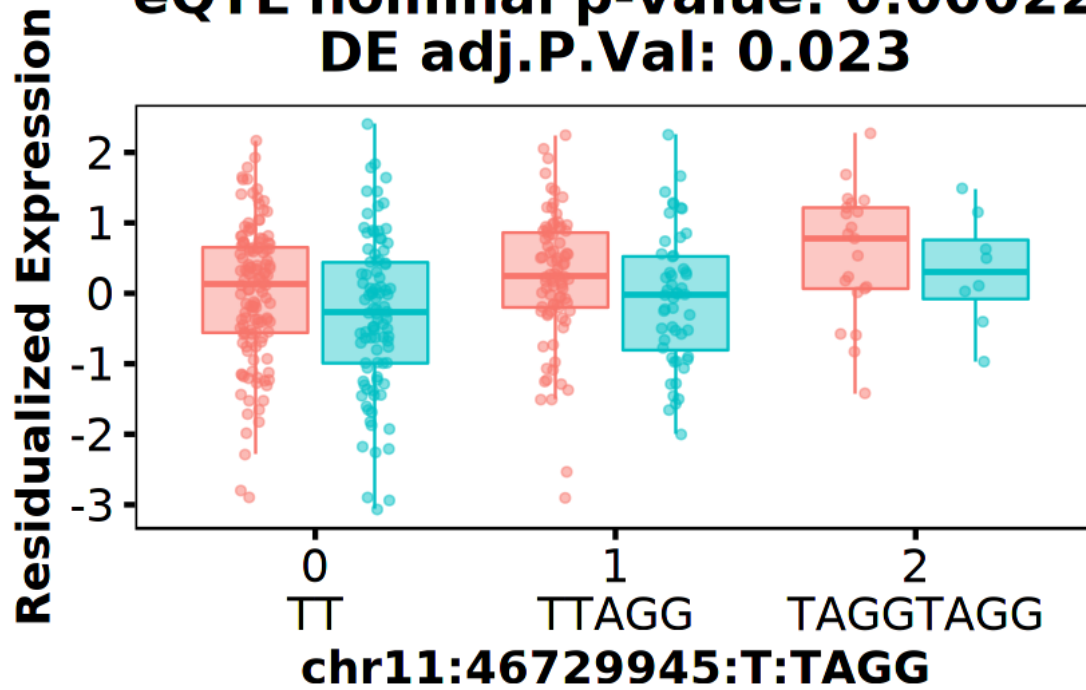
REEP2
chr5:138445599-138445682(+)
SZ GWAS pvalue: 1e-08
SZ risk allele: C
eQTL nominal p-value: 3.6e-05
DE adj.P.Val: 1.1e-05
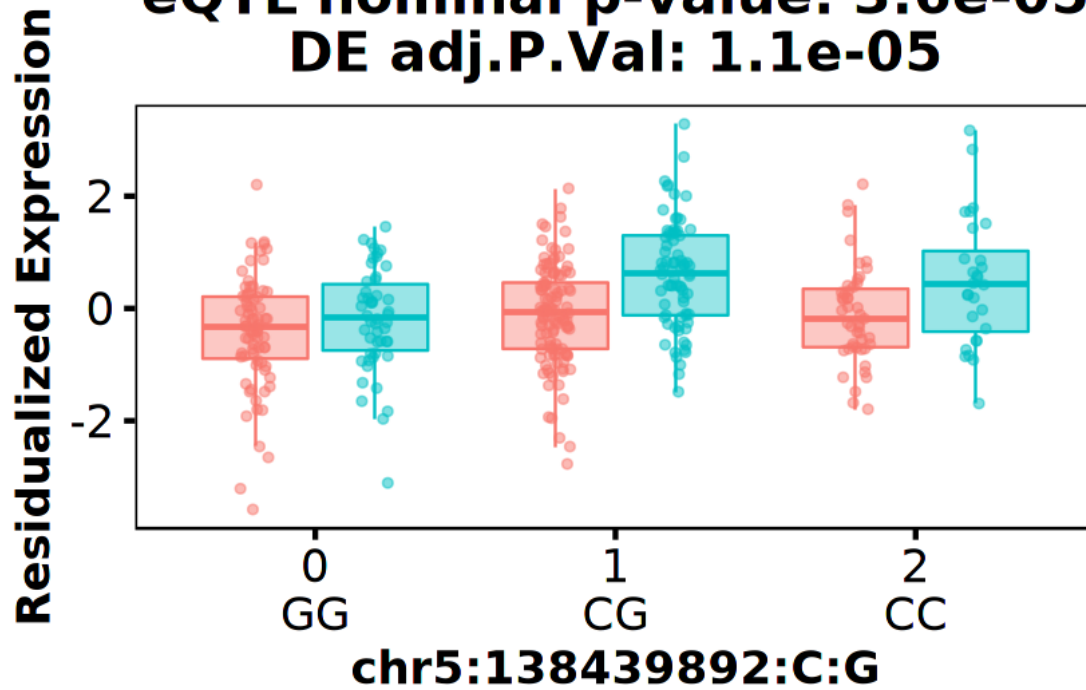
NDFIP2
chr13:79551123-79552515(+)
SZ GWAS pvalue: 1.2e-08
SZ risk allele: A
eQTL nominal p-value: 5.3e-05
DE adj.P.Val: 0.029

MPP6
chr7:24641869-24649611(+)
SZ GWAS pvalue: 1.6e-08
SZ risk allele: C
eQTL nominal p-value: 4.8e-06
DE adj.P.Val: 0.044
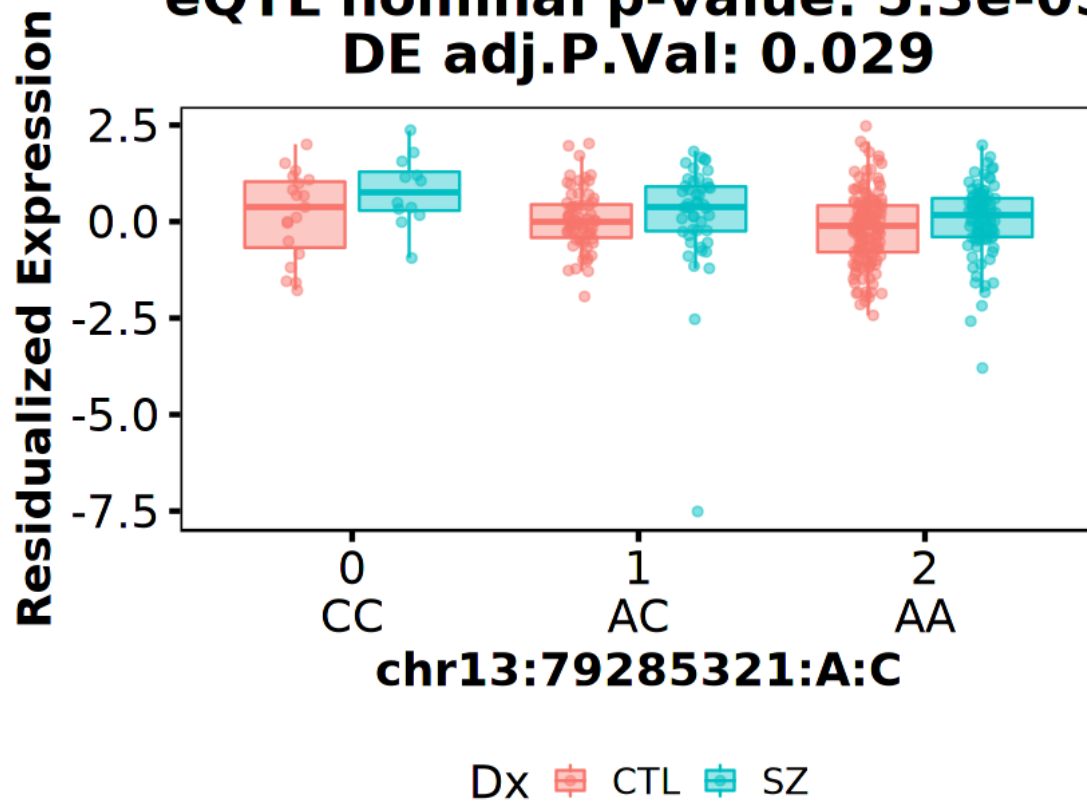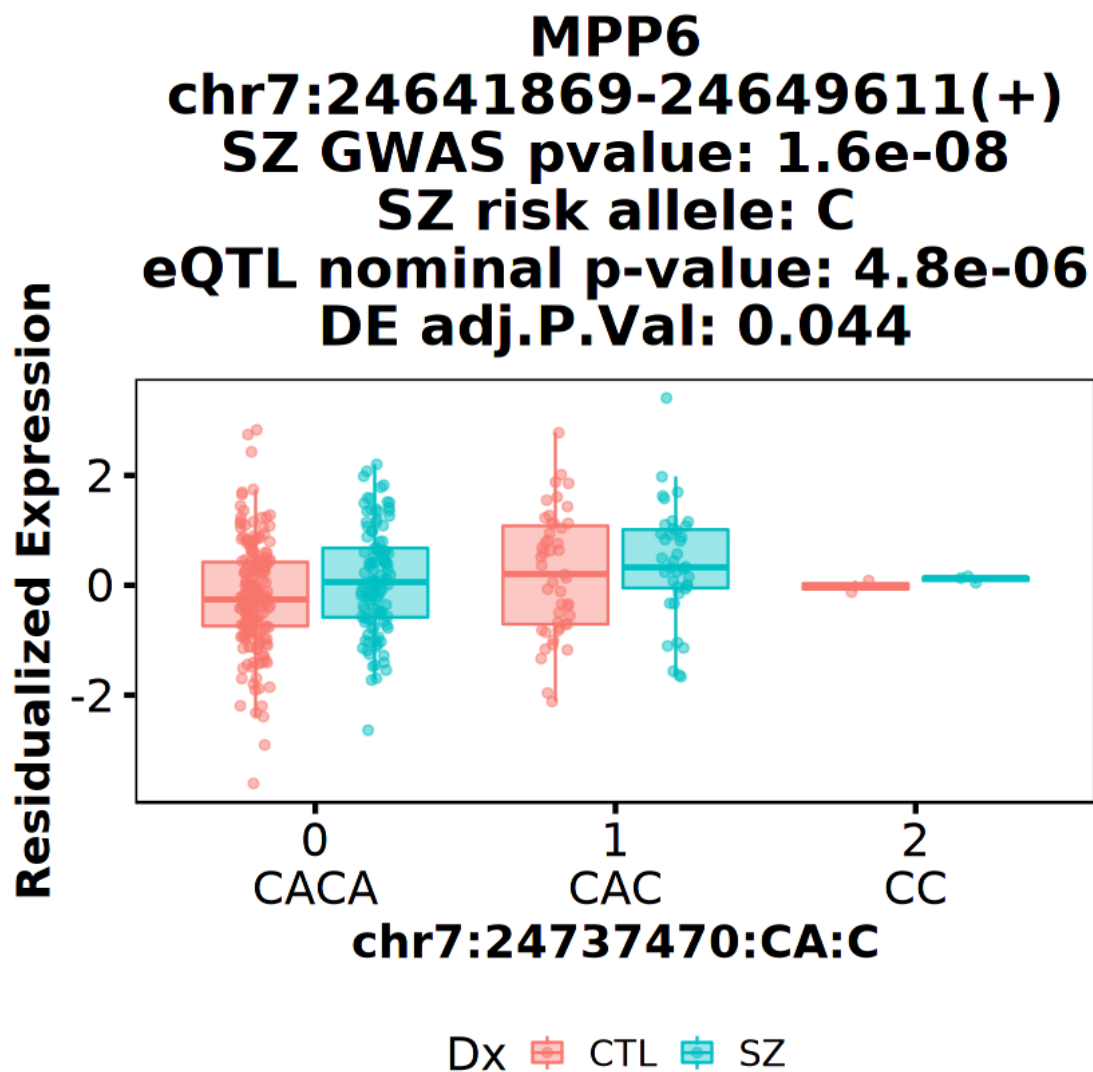
1.3 Session Info

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

[1] "2021-09-08 11:24:25 EDT"

```
    user   system  elapsed
8671.188 4339.813 1869.688
```

 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     2021-09-08

 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)
broom          0.7.9   2021-07-27 [1] CRAN (R 4.0.3)
cachem         1.0.6   2021-08-19 [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)
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)
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)
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)
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)
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)
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)
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)
memoise         2.0.0     2021-01-26 [1] CRAN (R 4.0.2)
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)
R.methodsS3     1.8.1     2020-08-26 [1] CRAN (R 4.0.3)
R.oo            1.24.0    2020-08-26 [1] CRAN (R 4.0.3)
R.utils         2.10.1    2020-08-26 [1] CRAN (R 4.0.3)
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)
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)
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)
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)
zip             2.2.0     2021-05-31 [1] CRAN (R 4.0.3)
```

```
[1] /home/jbenja13/R/x86_64-pc-linux-gnu-library/4.0
[2] /usr/lib/R/library
```