

main

March 8, 2022

1 SMR manhattan plot

```
[1]: suppressMessages({  
      library(dplyr)  
      library(ggtext)  
      library(ggplot2)  
    })
```

1.1 Functions

```
[2]: save_plots <- function(p, fn){  
      for(ext in c('.png', '.pdf', '.svg')){  
        ggsave(paste0(fn,ext), p, width=30, height=15, units="cm")  
      }  
    }
```

1.2 Prepare data

1.2.1 Preparing SMR data

```
[3]: qsmr_file = "../../../../_m/eqt1_gene.Caudate.CAUC_NC_SCZ_BIP.age13.index_p1e-04.  
      ↪SCZ_PGC3_p1e-04.smr_q0.05.heidi_p0.01.csv.gz"  
qsmr_data_load <- qsmr_data_load <- data.table::fread(qsmr_file) %>% janitor::  
      ↪clean_names() %>%  
      select(probe_id, probe_bp, q_smr) %>% distinct  
  
smr_file = '../../../../_m/eqt1_gene.Caudate.CAUC_NC_SCZ_BIP.age13.index_p1e-04.  
      ↪SCZ_PGC3_p1e-04.smr.csv.gz'  
smr_data_load <- data.table::fread(smr_file) %>% janitor::clean_names() %>%  
      select(probe_id, probe_bp, probe_chr, p_smr, p_heidi, top_snp, symbol) %>%  
      ↪distinct %>%  
      rename(chr=probe_chr)  
  
data_cum <- smr_data_load %>% group_by(chr) %>% summarise(max_bp =  
      ↪max(probe_bp)) %>%  
      mutate(bp_add = lag(cumsum(as.numeric(max_bp)), default=0)) %>% select(chr,  
      ↪bp_add)
```

```
smr_data <- smr_data_load %>% inner_join(data_cum, by="chr") %>%
  mutate(bp_cum = probe_bp + bp_add) %>% left_join(qsmr_data_load,
  ↪by=c("probe_id", "probe_bp")) %>%
  mutate(q_smr = tidyr::replace_na(q_smr, 1))
smr_data %>% head(2)
```

| | probe_id | probe_bp | chr | p_smr | p_heidi | top_snp | sym |
|----------------------|--------------------|-----------|-------|-------------|------------|------------|-----|
| | <chr> | <int> | <int> | <dbl> | <dbl> | <chr> | <ch |
| A data.table: 2 × 10 | ENSG00000000971.15 | 196699691 | 1 | 0.046296670 | 0.50866940 | rs10801534 | CFH |
| | ENSG00000002822.15 | 2024518 | 7 | 0.001055838 | 0.02542476 | rs1637728 | MA |

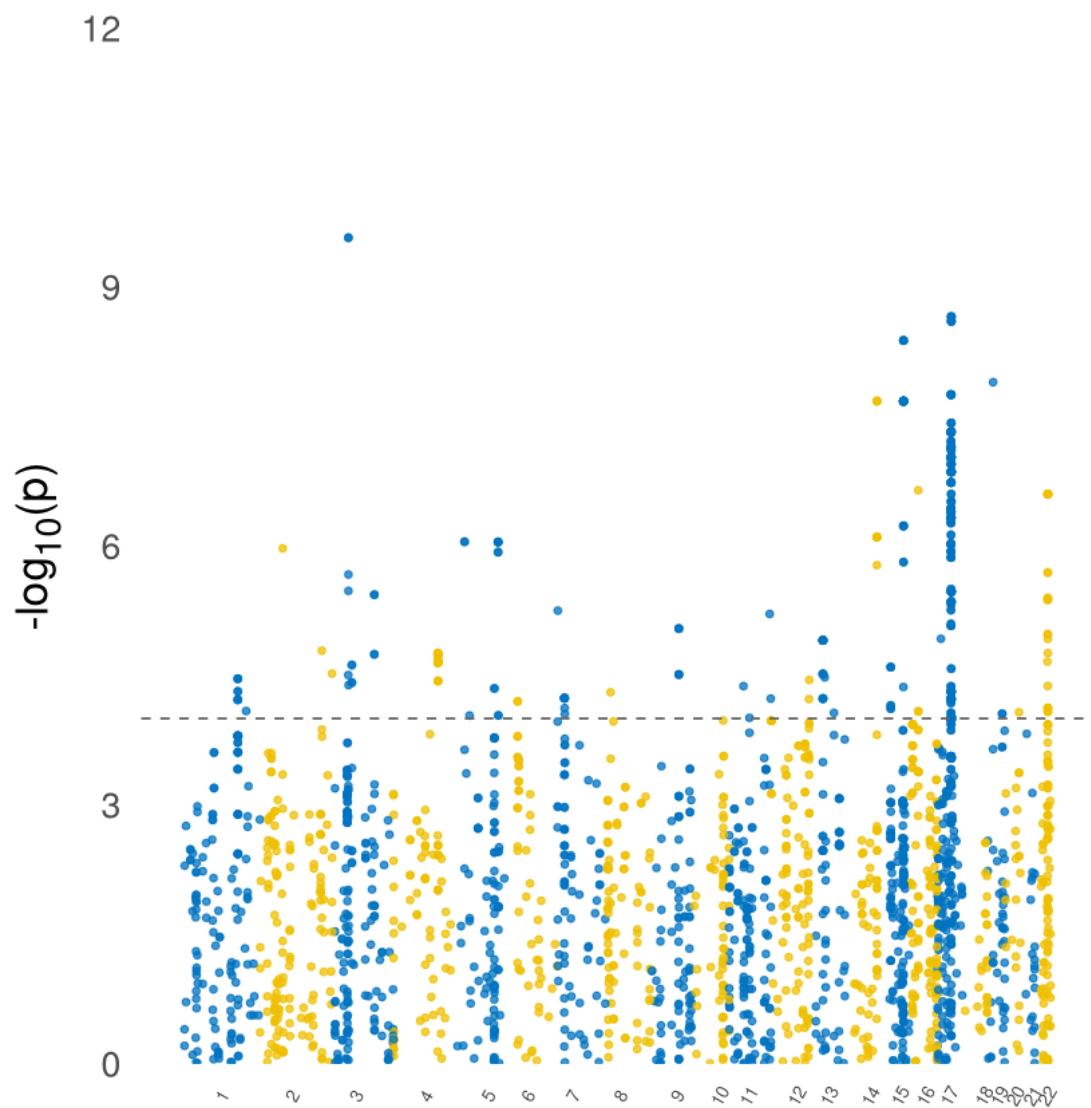
1.2.2 SMR caudate, SZ PGC3

1.2.3 Plotting settings

```
[4]: axis_set <- smr_data %>% group_by(chr) %>% summarize(center = mean(bp_cum))
ylim <- smr_data %>% filter(p_smr == min(p_smr)) %>%
  mutate(ylim = abs(floor(log10(p_smr))) + 2) %>% pull(ylim)
ylim = ylim[1]
sig <- 1e-4
```

1.2.4 Plot

```
[5]: manhplot1 <- ggplot(smr_data, aes(x=bp_cum, y=-log10(p_smr),
  ↪size=-log10(p_smr))) +
  geom_point(alpha=0.75, size=1.25, aes(color=forcats::as_factor(chr))) +
  geom_hline(yintercept = -log10(sig), color = "grey40", linetype = "dashed")
  ↪+
  scale_x_continuous(label = axis_set$chr, breaks = axis_set$center) +
  scale_y_continuous(expand = c(0,0), limits = c(0, ylim)) +
  scale_color_manual(values = rep(ggpubr::get_palette("jco", 2),
  ↪unique(length(axis_set$chr)))) +
  labs(x = NULL, y = "-log<sub>10</sub>(p)") +
  theme_minimal(base_size=20) +
  theme(
    legend.position="none", panel.border=element_blank(),
    panel.grid.major=element_blank(), panel.grid.minor=element_blank(),
    axis.title.y=element_markdown(), axis.text.x=element_text(angle=60,
  ↪size=8, vjust=0.5)
  )
manhplot1
```



```
[6]: save_plots(manhplot1, 'caudate_smr_manhattanplot')
```

```
[ ]:
```