Supplemental File of

Use ggbreak to effectively utilize plotting space to deal with large datasets and outliers

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1 Example1: automatically wrap plot with long x axis scale

```
library(ggplot2)
library(ggbreak)
library(aplot)

# import output data from Protscale
data <- read.table(file = "../data/7MWE_A.csv", sep = ",", header = F, fill = T)
colnames(data) <- c("Position","Score")
head(data)
```

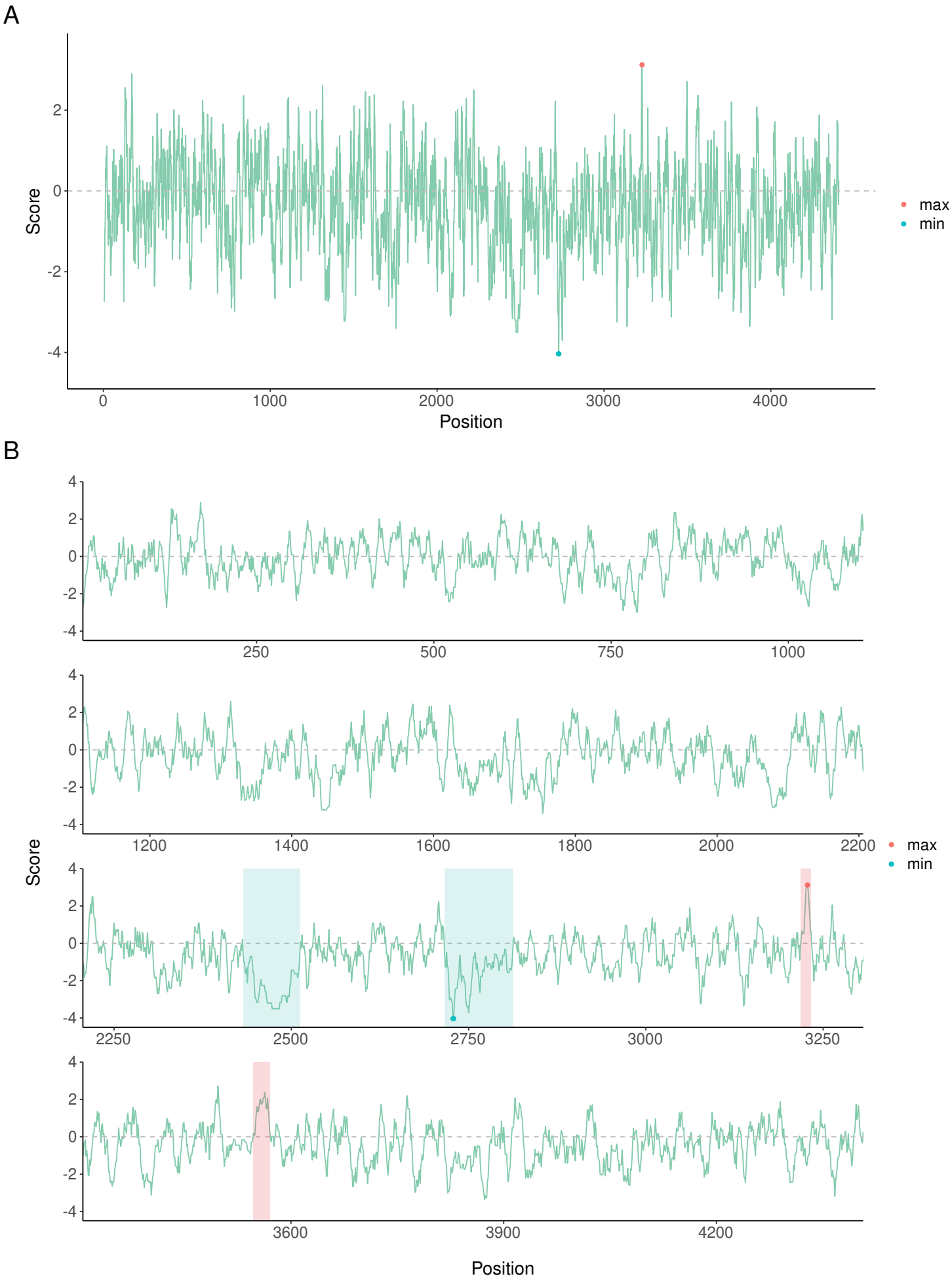
```
##   Position  Score
## 1        5 -2.744
## 2        6 -2.533
## 3        7 -1.944
## 4        8 -1.600
## 5        9 -0.967
## 6       10 -0.967
```

```
data2 <- data.frame(c(2728,2729,3228),c(-4.033,-4.033,3.122),c("min","min","max"))
colnames(data2) <- c("Position","Score","Type")

p <- ggplot(data=data) +
    geom_line(mapping=aes(x=Position,y=Score),color="#83cbac",stat="identity") +
    geom_point(data=data2,mapping = aes(x=Position,y=Score,color=Type)) +
    theme_classic() +
    geom_hline(yintercept=0,color="grey",linetype="dashed") +
    expand_limits(y=c(-4.5,3.5)) +
    theme(axis.text.x = element_text(size = 14),
          axis.text.y = element_text(size=14),
          axis.title.x = element_text(size = 16),
          axis.title.y = element_text(size = 16),
          legend.title=element_blank(),
          legend.text=element_text(size=14))

p1 <- p + scale_wrap(n=4) +
    annotate("rect", xmin=2432, xmax=2512, ymin=-4.5, ymax=4,fill='#57c3c2',alpha = 0.2) +
    annotate("rect", xmin=2716, xmax=2813, ymin=-4.5, ymax=4,fill='#57c3c2',alpha = 0.2) +
    annotate("rect", xmin=3219, xmax=3233, ymin=-4.5, ymax=4,fill='#ef475d',alpha = 0.2) +
    annotate("rect", xmin=3547, xmax=3571, ymin=-4.5, ymax=4,fill='#ef475d',alpha = 0.2)

plot_list(p, p1, ncol=1, tag_levels = 'A', tag_size = rel(2), heights=c(1,2))
```

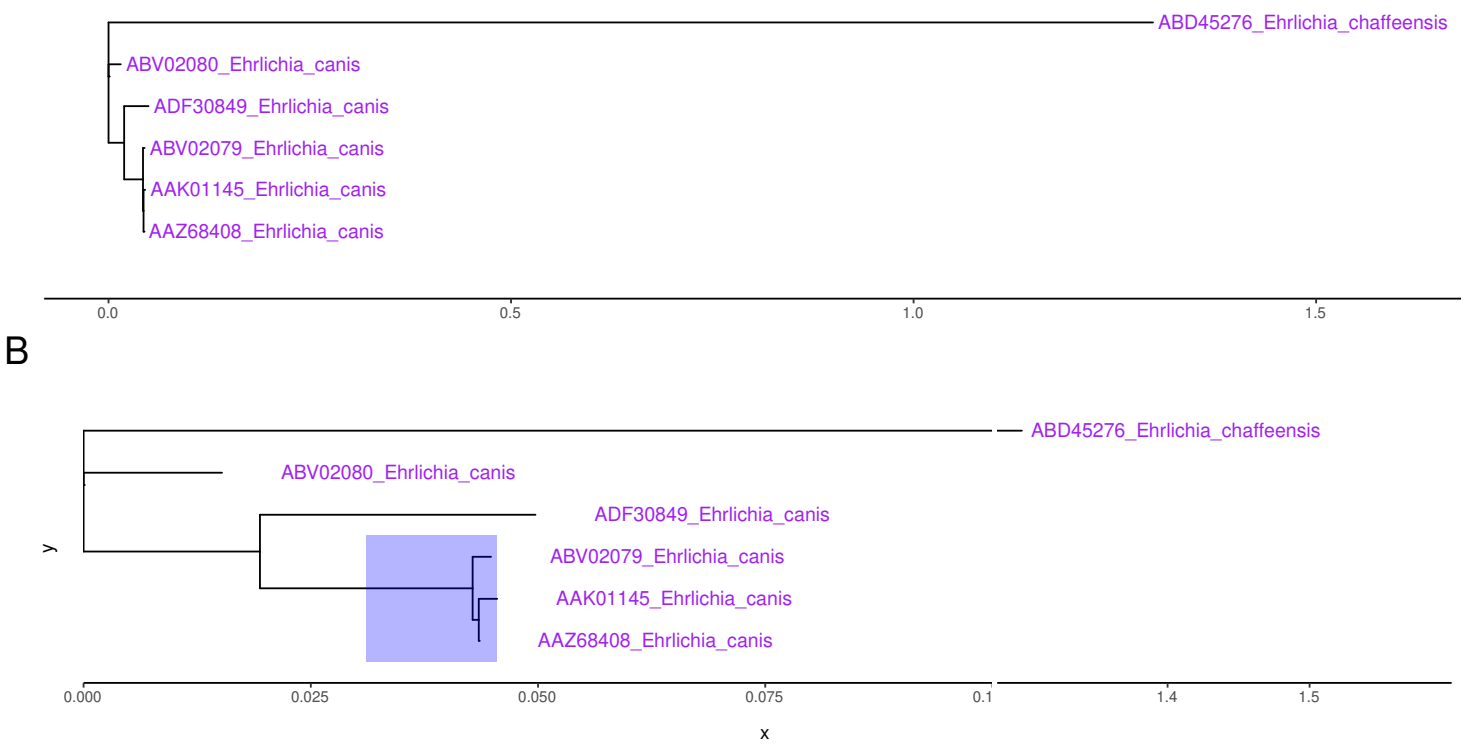

A
Score
Position
max
min
B
Score
Position
max
min

2 Example 2: Shrank outlier branch of phylogenetic tree

```
library("ggtree")
library("treeio")
library("ggbreak")
library("aplot")
library("ggplot2")

treedata <- read.newick(file = "../data/gp200.nwk")
p <- ggtree(treedata,ladderize=FALSE) +
    expand_limits(x=c(0,1.6), y=c(0,7)) +
    geom_tiplab(size=4,color="purple")  +
    theme_tree2()

p1 <- p + scale_x_break(breaks = c(0.1,1.28),
                        ticklabels = c(1.4,1.5),scales = 0.5) +
    geom_highlight(node=9,fill="blue",alpha = 0.3) +
    theme(
        plot.margin = margin(t = 2,
                             r = 2,
                             b = 2,
                             l = 2,
                             unit = "cm"))
plot_list(p, p1, ncol=1, tag_levels = 'A', tag_size = rel(2))
```



3 Example3: Cut Manhattan plot to create more space for annotation

```
library("ggbreak")
library("aplot")
library("ggplot2")
library("dplyr")
```

```
snp <- read.table(file = "../data/GCST90007012_buildGRCh37.tsv",
                  header = T, fill = T)
head(snp)
```

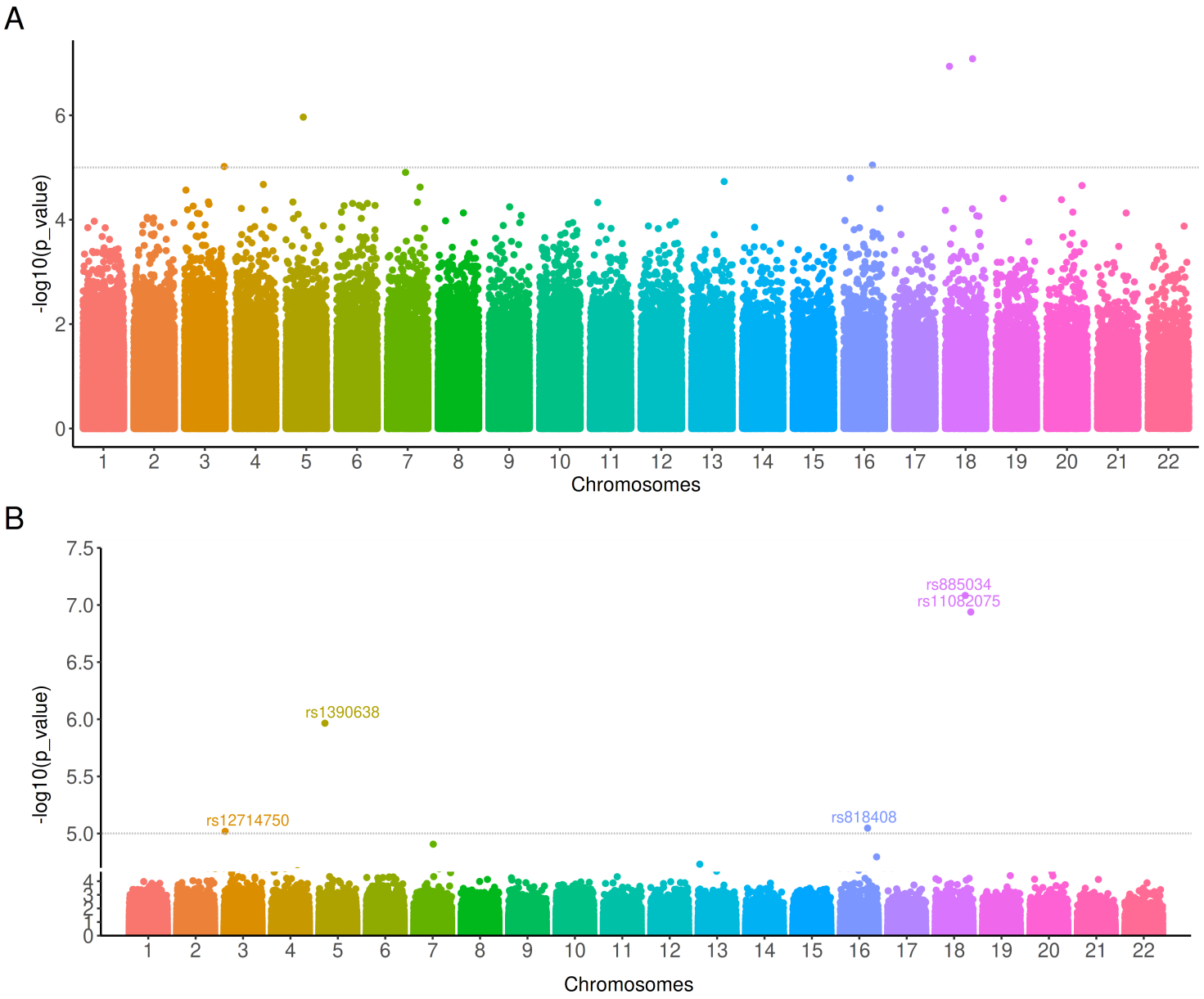
```
##   variant_id p_value chromosome base_pair_location effect_allele    beta
## 1  rs3131972  0.3586          1             752721             A  10.880
## 2 rs11240777  0.4565          1             798959             A   8.063
## 3  rs4970383  0.3810          1             838555             A -10.080
## 4  rs4475691  0.8293          1             846808             T   3.277
## 5  rs7537756  0.2872          1             854250             G  14.660
## 6 rs13302982  0.8938          1             861808             A   1.374
##   standard_error
## 1          11.85
## 2          10.82
## 3          11.49
## 4          15.19
## 5          13.76
## 6          10.28
```

```
snp$chromosome <- factor(snp$chromosome,
                         levels = sort(unique(snp$chromosome)))

p1 <- ggplot(snp, aes(x=chromosome, y = -log10(p_value))) +
    geom_jitter(data=snp,
                aes(x=chromosome, y = -log10(p_value),color=chromosome)) +
    theme_classic() + xlab("Chromosomes") +
    geom_abline(intercept=5,slope = 0,color="grey",linetype="dashed") +
    theme(legend.position="none",
          axis.title.y = element_text(size = 14),
          axis.title.x = element_text(size = 14),
          axis.text = element_text(size = 14))

p2 <- p1 + scale_y_cut(breaks=c(4.7),which=c(2),scales=c(0.2)) +
    geom_text(data=snp%>%filter(-log10(p_value) >= 5),
              aes(x=chromosome, y = -log10(p_value),
                  color=chromosome, label=variant_id),
              nudge_x =0.1,nudge_y = 0.1) +
    expand_limits(x=c(0, 23),y=c(0,7.5))

plot_list(p1, p2, ncol=1, tag_levels = 'A', tag_size = rel(2))
```



4 Example 4: Inserting broken axes in barplot with ggbreak

```
library("ggprism")
library("ggbreak")
library("ggplot2")

data1 <- read.table(file = "../data/data1.txt",
                    header = TRUE, sep = "\t", dec = ".")
data1$Species.name <- factor(data1$Species.name,
                             levels = rev(unique(data1$Species.name)))
load("../data/sigdata.rda")

p1 <- ggplot(data=data1,aes(x=Species.name,weight = Mean, fill = group)) +
    geom_bar(position = 'dodge') +
    labs( y = 'Relative abundance(%)', x = NULL) +
    coord_flip() +
    theme_prism()

p2 <- ggplot(data=data1,aes(x=Species.name,weight = log10(Mean+1), fill = group)) +
    geom_bar(position = 'dodge') +
```

```
    labs( y = 'log10(Relative abundance+1)', x = NULL) +
    coord_flip() +
    theme_prism()

p3 <- p1 + scale_y_break(c(32, 84),scales=0.5,ticklabels=c(84,85,86)) +
    scale_y_break(c(3.5, 10),scales=0.5,ticklabels = c(15,25))

p4 <- p3 + geom_text(data=sigdata,mapping=aes(x=Species,y=Mean,label=sig),vjust=-0.1)

plot_list(p1, p2, p3, p4, byrow=T, tag_levels = 'A', tag_size = rel(2))
```