

# Figure 1 for Deleterious Alleles paper

```
#setwd("~/Documents/Github/pvpDiallel/")
knitr::opts_knit$set(root.dir=normalizePath('../'))
```

To reproduce the figures, we should set `pvpDiallel` as the root path, i.e. `setwd("~/Documents/Github/pvpDiallel/")`. And then use `knitr` package to knit a pdf file. Or simply click Knit PDF icon in RStudio. Note, to generate each panel into separate pdf files, we should turn `getpdf` into `TRUE` (i.e. `getpdf=TRUE`) when calling the plotting functions.

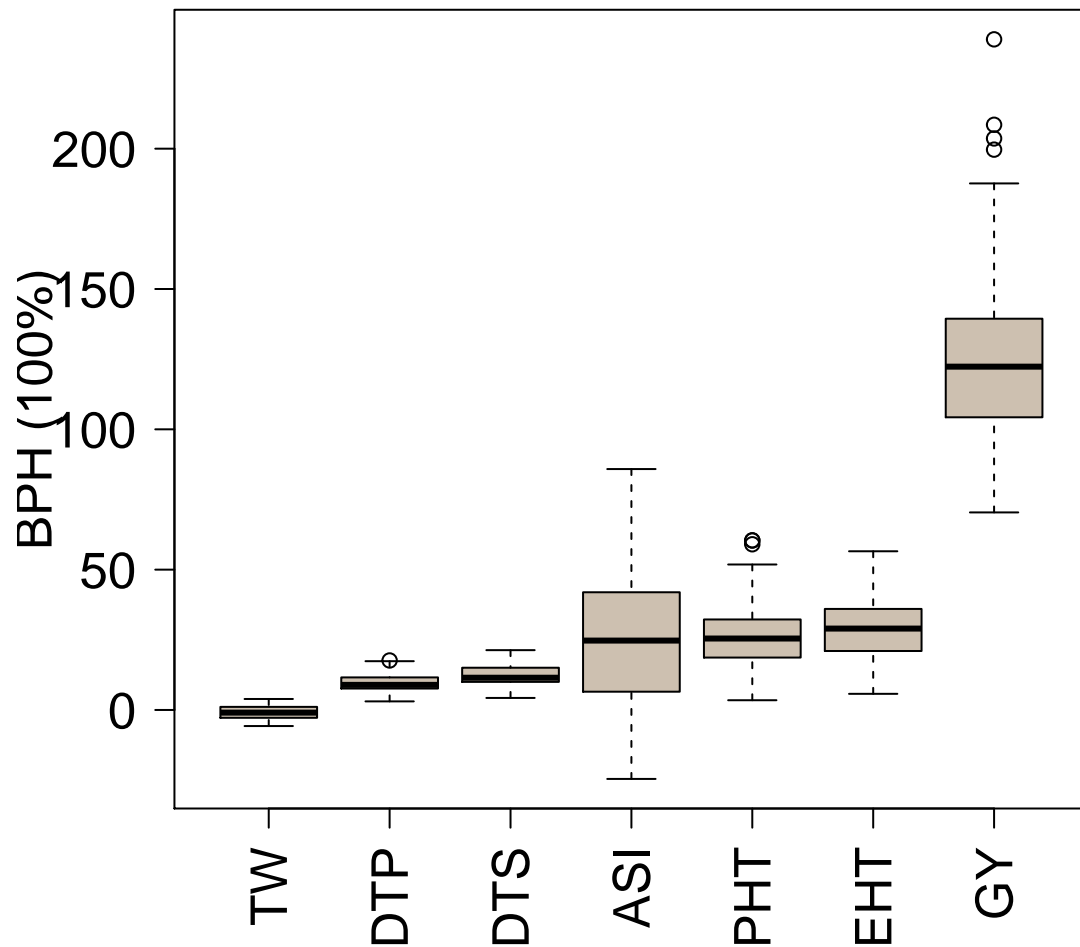
First of all, determine font size and set the `getpdf` option:

```
#par(mar=c(5,4,4,2))
par(font= 2, font.lab= 2, font.axis= 2)
fs <- 1.6 # times bigger than default
ht= 6; wt= 6 #figure height and weight
getpdf <- TRUE # get figures in separated pdf [TRUE] or not [FALSE]
```

## Figure 1a

```
plotloh <- function(getpdf, outfile, ...){
  trait <- read.csv("cache/STable_heterosis.csv")
  bymed2 <- with(trait, reorder(trait, pBPH, median))
  boxplot(pBPH ~ bymed2, data=trait,
          xlab = "", ylab= "BPH (100%)", col="antiquewhite3",
          ...)
  if(getpdf == TRUE){
    pdf(outfile, width=ht, height=wt)
    par(mar=c(5,5,4,2))
    boxplot(pBPH ~ bymed2, data=trait,
            xlab = "", ylab= "BPH (100%)", col="antiquewhite3",
            ...)
    dev.off()
  }
}

plotloh(getpdf, outfile="graphs/Fig1a_v3.pdf",
        main="", cex.axis=fs, cex.lab=fs, las=2)
```



```
## pdf
## 2
```

Figure 1b

```
plotReg <- function(getpdf, outfile, ...){
  snptab <- read.csv("cache/daf_gerp2.csv")
  snptab <- snptab[order(snptab$GERP2),]
  plx <- predict(loess(snptab$meandaf ~ snptab$GERP2), se=T)
  x <- snptab$GERP2
  y <- snptab$meandaf

  plot(x, y, ...)
  lines(snptab$GERP2, plx$fit, col="cornflowerblue", lwd=2)
  lines(snptab$GERP2, plx$fit - qt(0.975,plx$df)*plx$se, lty=2, lwd=2, col="black")
  lines(snptab$GERP2, plx$fit + qt(0.975,plx$df)*plx$se, lty=2, lwd=2, col="black")

  if(getpdf == TRUE){
    pdf(outfile, width=wt, height=ht)
    par(mar=c(5,5,4,2))
  }
}
```

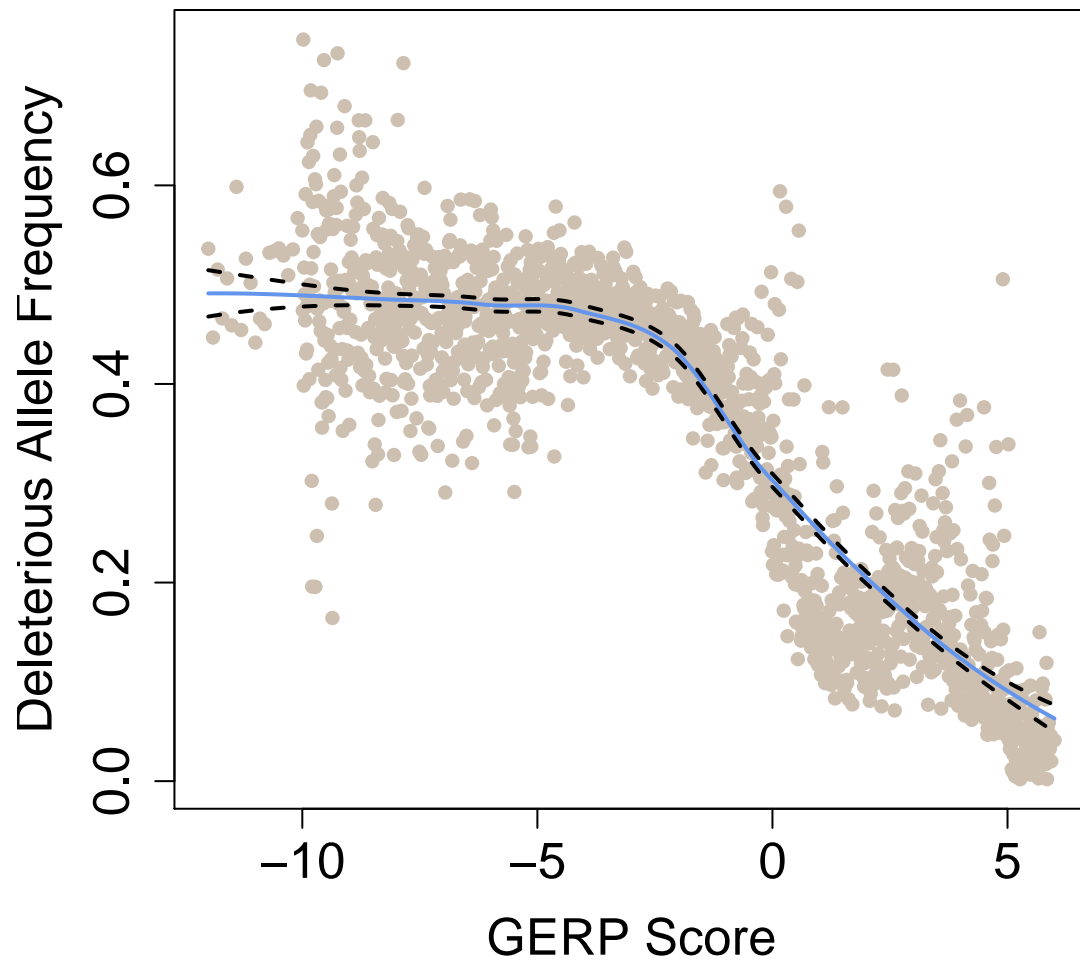
```

plot(x, y, ...)
lines(snptab$GERP2, plx$fit, col="cornflowerblue", lwd=2)
lines(snptab$GERP2, plx$fit - qt(0.975,plx$df)*plx$se, lty=2, lwd=2, col="black")
lines(snptab$GERP2, plx$fit + qt(0.975,plx$df)*plx$se, lty=2, lwd=2, col="black")

dev.off()
}
}

plotReg(getpdf, outfile="graphs/Fig1b_v3.pdf",
        pch=16, col="antiquewhite3", xlab="GERP Score", ylab="Deleterious Allele Frequency",
        main="", cex.axis=fs, cex.lab=fs)

```



```

## pdf
## 2

```

**Figure 1c**

To run this chunk, we need to install `beanplot` package.

```

library("beanplot")
plotbeans <- function(getpdf, outfile, ...){

  res <- read.csv("cache/mgerp_cm.csv")
  cutoff <- quantile(res$gen, c(0.25, 0.5, 0.75))
  res$sq <- 0
  res[res$gen < cutoff[1], ]$sq <- 1
  res[res$gen >= cutoff[1] & res$gen < cutoff[2], ]$sq <- 2
  res[res$gen >= cutoff[2] & res$gen < cutoff[3], ]$sq <- 3
  res[res$gen >= cutoff[3], ]$sq <- 4

  beanplot(mgerp ~ sq, data = res, kernel="cosine", ll = 0.04, cex=fs, side = "no", cut=10, ylim=c(0.5,
    border = NA, col=list("#cd5b45", "antiquewhite3", "antiquewhite3", "antiquewhite3"),
    xaxt="n", ...)
  axis(side=1, at =1:4, labels =c("25", "50", "75", "100"), cex.axis=fs)

  if(getpdf == TRUE){
    pdf(outfile, width=wt, height=ht)
    par(mar=c(5,5,4,2))
    beanplot(mgerp ~ sq, data = res, kernel="cosine", ll = 0.04, cex=1.5, side = "no", cut=10, ylim=c(0.5,
      border = NA, col=list("#cd5b45", "antiquewhite3", "antiquewhite3", "antiquewhite3"),
      xaxt="n", ...)
    axis(side=1, at =1:4, labels =c("25", "50", "75", "100"), cex.axis=fs)
    dev.off()
  }
}

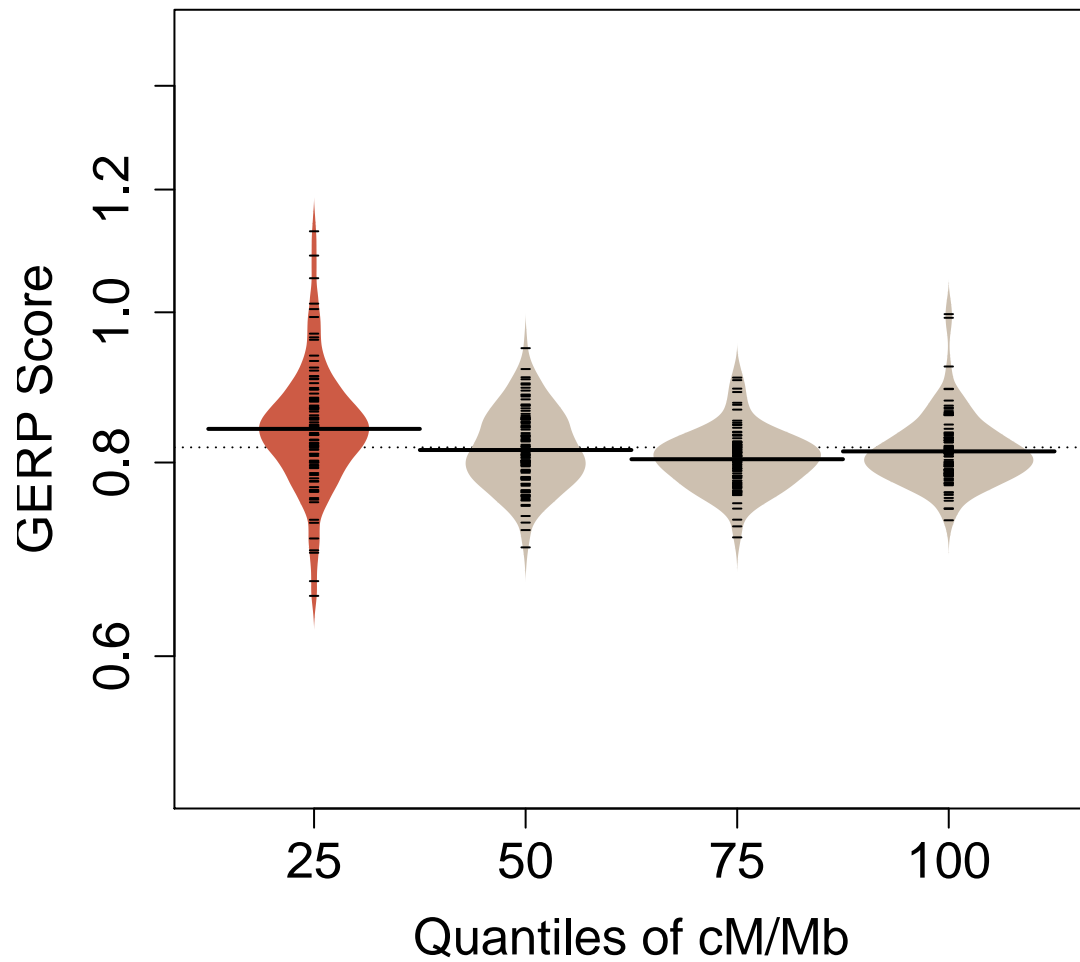
plotbeans(getpdf, outfile="graphs/Fig1c_v3.pdf",
  ylab="GERP Score", xlab="Quantiles of cM/Mb",
  cex.axis=fs, cex.lab=fs)

```

```

## log="y" selected
## log="y" selected

```



```
## pdf
## 2
```

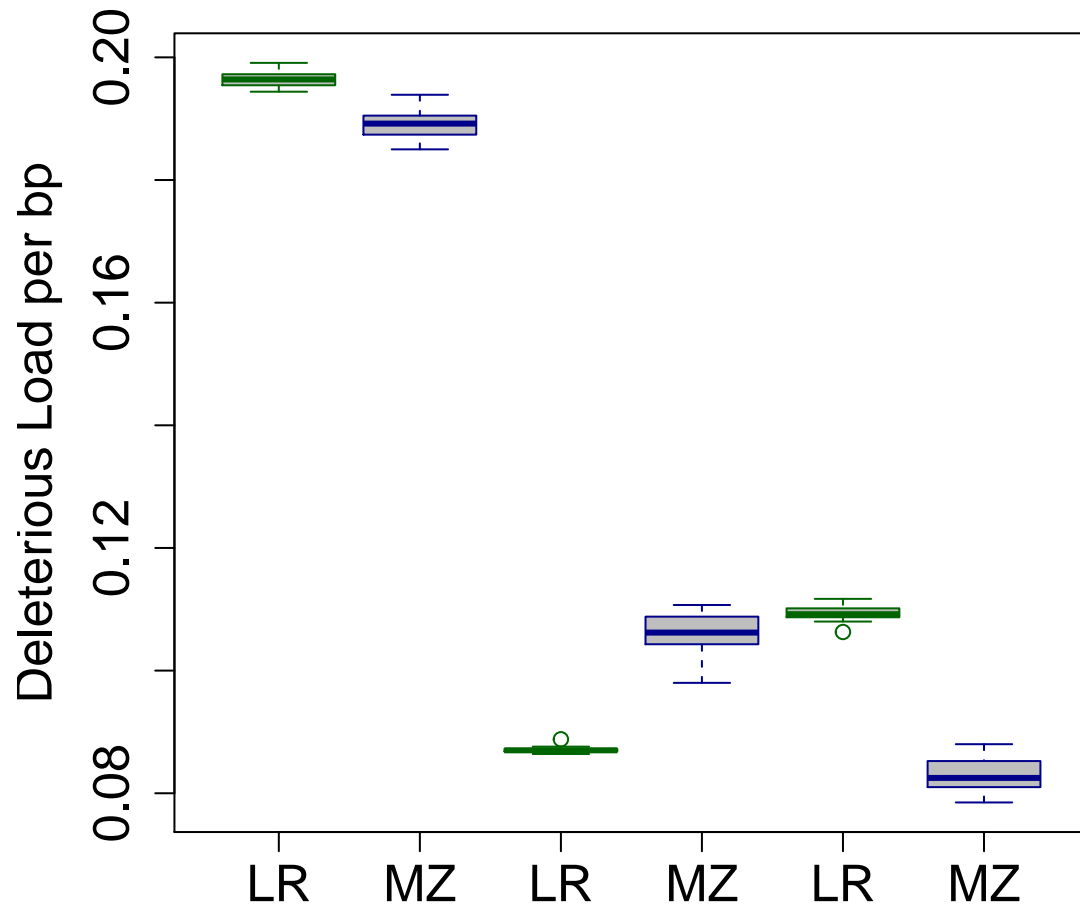
Figure 1d

```
plot_load <- function(getpdf, outfile, ...){
  dres <- read.table("data/sup_deleterious_hmp3.txt", header=T)

  boxplot(DR ~ geno*ordered, data=dres, border=c("darkgreen","darkblue"), col="grey", ...)
  #text(cew=fs, x=x-.25, y=-1.25, H2$Traits, xpd=TRUE, srt=45, pos=2)
  if(getpdf == TRUE){
    pdf(outfile, width=ht, height=wt)
    par(mar=c(5,5,4,2))
    boxplot(DR ~ geno*ordered, data=dres, border=c("darkgreen","darkblue"), col="grey", ...)

    box()
    dev.off()
  }
}
```

```
plot_load(getpdf, outfile="graphs/Fig1d_v3.pdf",
names=c("LR", "MZ", "LR", "MZ", "LR", "MZ"),
xlab="", ylab="Deleterious Load per bp",
main="", cex.axis=fs, cex.lab=fs)
```



```
## pdf
## 2
```