

```
In [ ]: #install.packages("data.table")
#install.packages("qqman")
#install.packages("dplyr")
```

```
In [ ]: library(data.table)
vcf <- fread(file='sample.vcf', sep='\\t', header = TRUE, skip = '#CHROM', fill=TRUE)
vcf
```

```
In [ ]: library(qqman)
GwasResults <- read.delim("gwasResults")
```

```
In [ ]: head(GwasResults)
```

```
In [ ]: manhattan(GwasResults,
  chr="X.CHROM",
  bp="POS",
  snp="ID",
  p="P")
```

```
In [ ]: manhattan(GwasResults,
  chr="X.CHROM",
  bp="POS",
  snp="ID",
  p="P",
  annotatePval = 5e-08,
  main = "Manhattan Plot", ylim = c(0, 9), #cex = 0.6, cex.axis = 0.9,
  col = c("blue4", "orange3"))
#suggestiveline = -log10(1e-05),
#genomewideline = -log10(5e-08),
```