

qc

2025-11-10

```
library(vcfR)

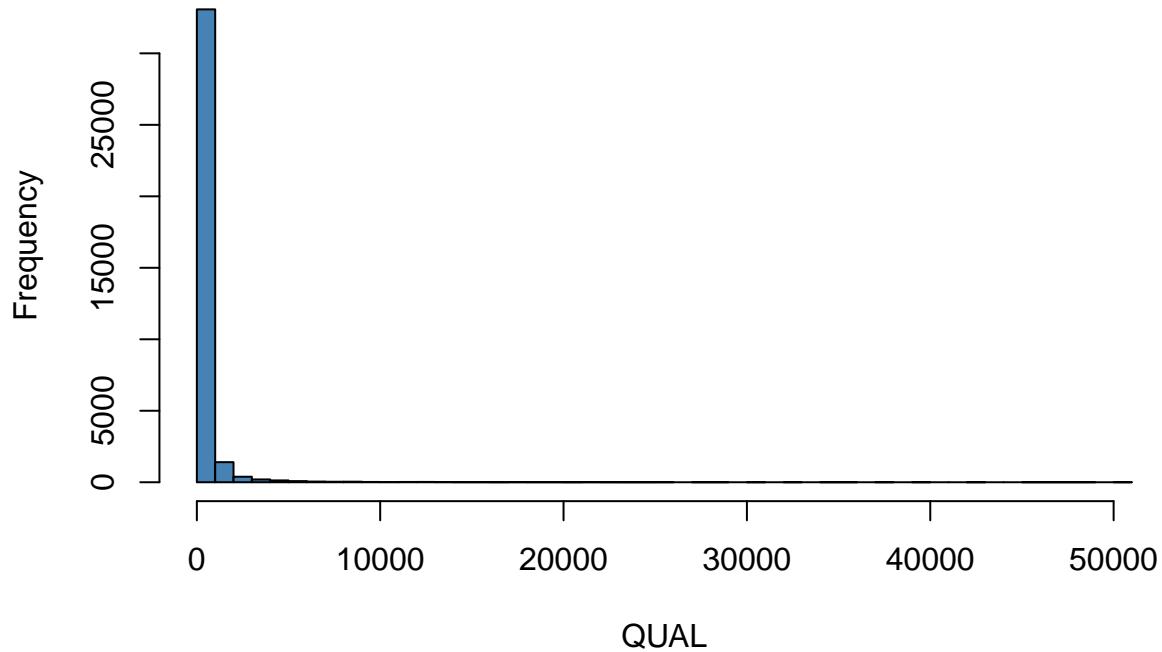
##      ****   *** vcfR   ***      ****
## This is vcfR 1.15.0
##   browseVignettes('vcfR') # Documentation
##   citation('vcfR') # Citation
##      ****   ****   ****      ****

vcf <- read.vcfR("/Users/f0052zm/Downloads/1001.hc.raw.vcf")

## Scanning file to determine attributes.
## File attributes:
##   meta lines: 219
##   header_line: 220
##   variant count: 35557
##   column count: 10
## Meta line 219 read in.
## All meta lines processed.
## gt matrix initialized.
## Character matrix gt created.
##   Character matrix gt rows: 35557
##   Character matrix gt cols: 10
##   skip: 0
##   nrows: 35557
##   row_num: 0
## Processed variant 1000Processed variant 2000Processed variant 3000Processed variant 4000Processed variant
## All variants processed

hist(getQUAL(vcf),
  breaks=50,
  col="steelblue",
  main="Distribution of variant QUAL scores",
  xlab="QUAL")
```

Distribution of variant QUAL scores



```
gt <- extract.gt(vcf)
het <- sum(gt == "0/1", na.rm=TRUE)
hom <- sum(gt == "1/1", na.rm=TRUE)
barplot(c(Heterozygous=het, Homozygous=hom),
        col=c("orange", "skyblue"),
        main="Heterozygous vs Homozygous variants",
        ylab="Count")
```

Heterozygous vs Homozygous variants

