

# VCFstat

Michael Hall

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```
devtools::install_github("PBGLMichaelHall/VCFstat",force = TRUE)
```

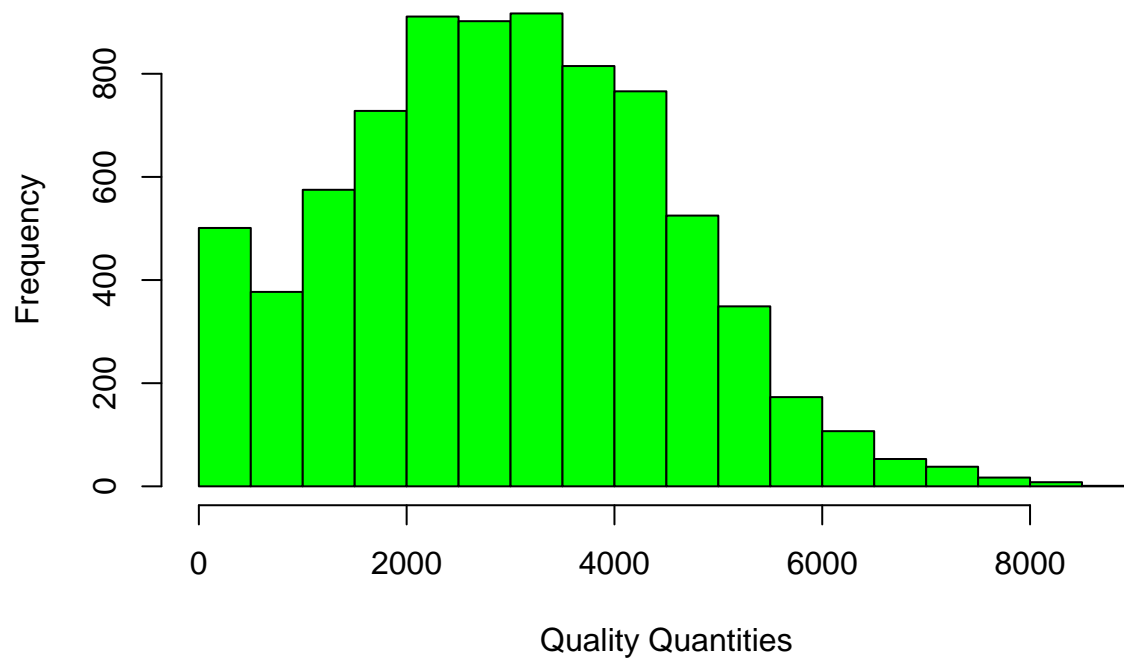
```
library(VCFstat)
library(vcfR)
library(data.table)
library(QTLseqr)
library(ggplot2)
```

```
setwd("/home/michael/Desktop/QTLseqr/extdata/")
```

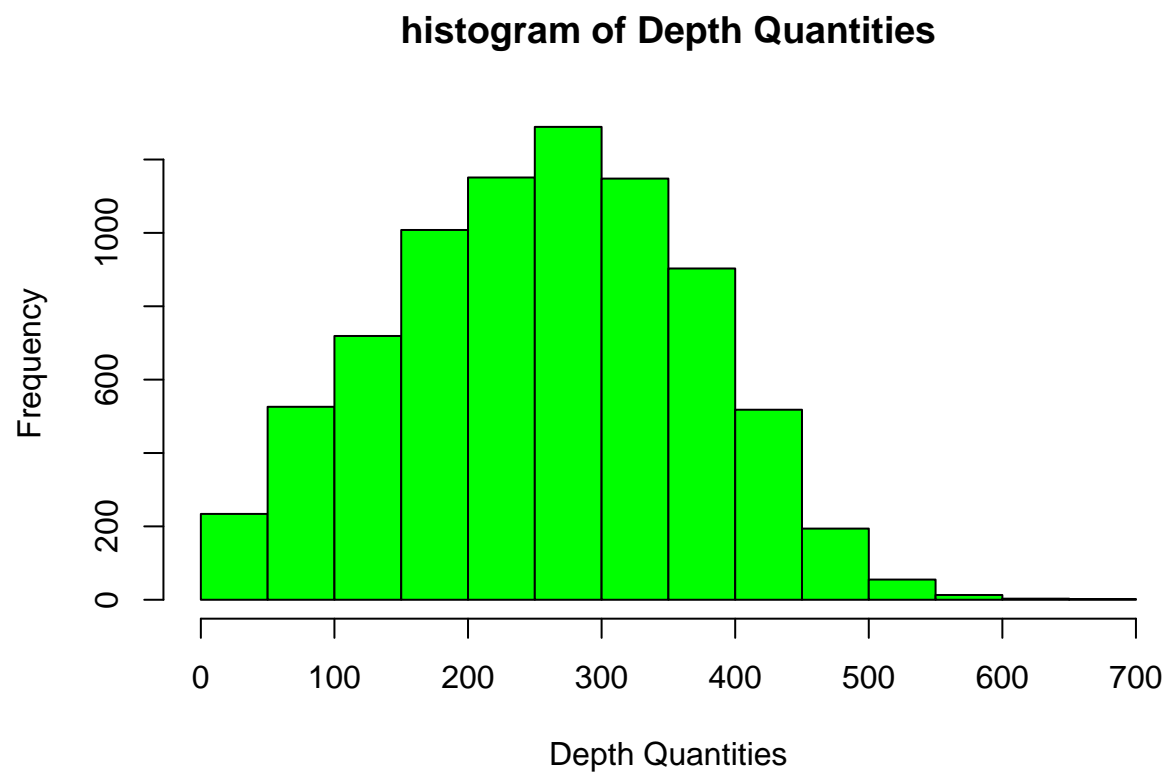
```
chromlist <- c("Chr01","Chr02","Chr03","Chr04","Chr05","Chr06","Chr07","Chr08","Chr09","Chr10")
```

```
VCFstat::ChromQual(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist,windowSize = 1e+05, binw
```

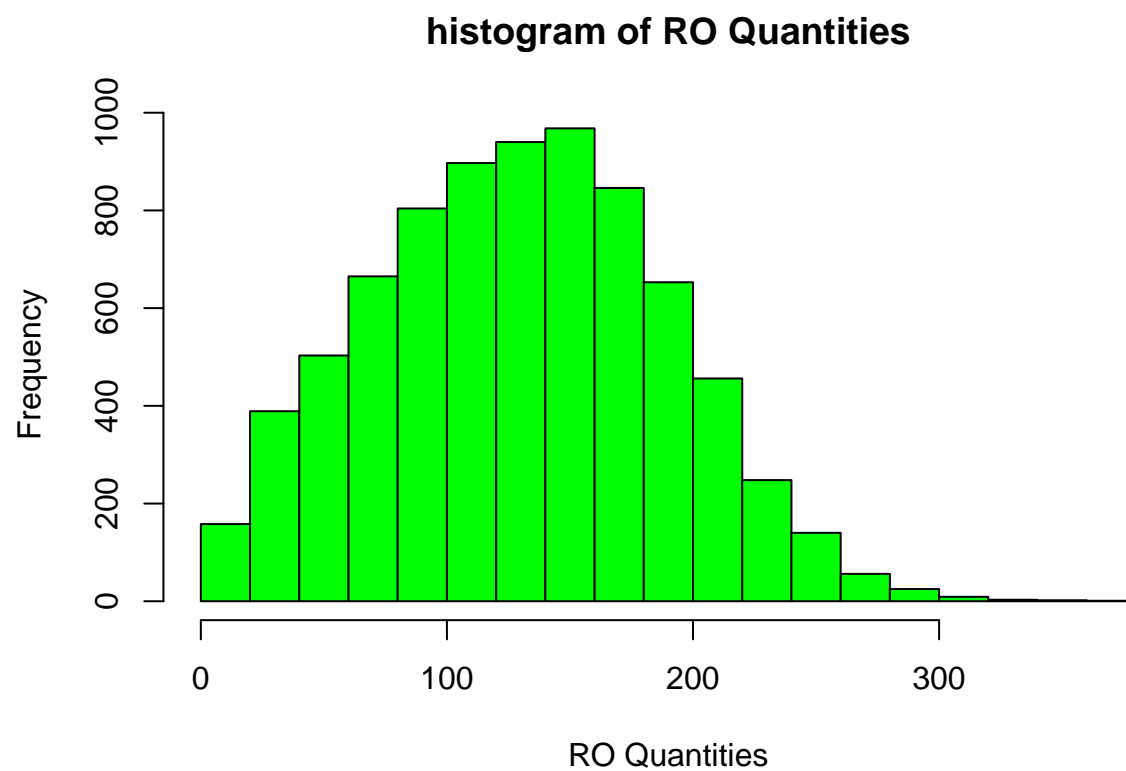
## histogram of Quality Quantities



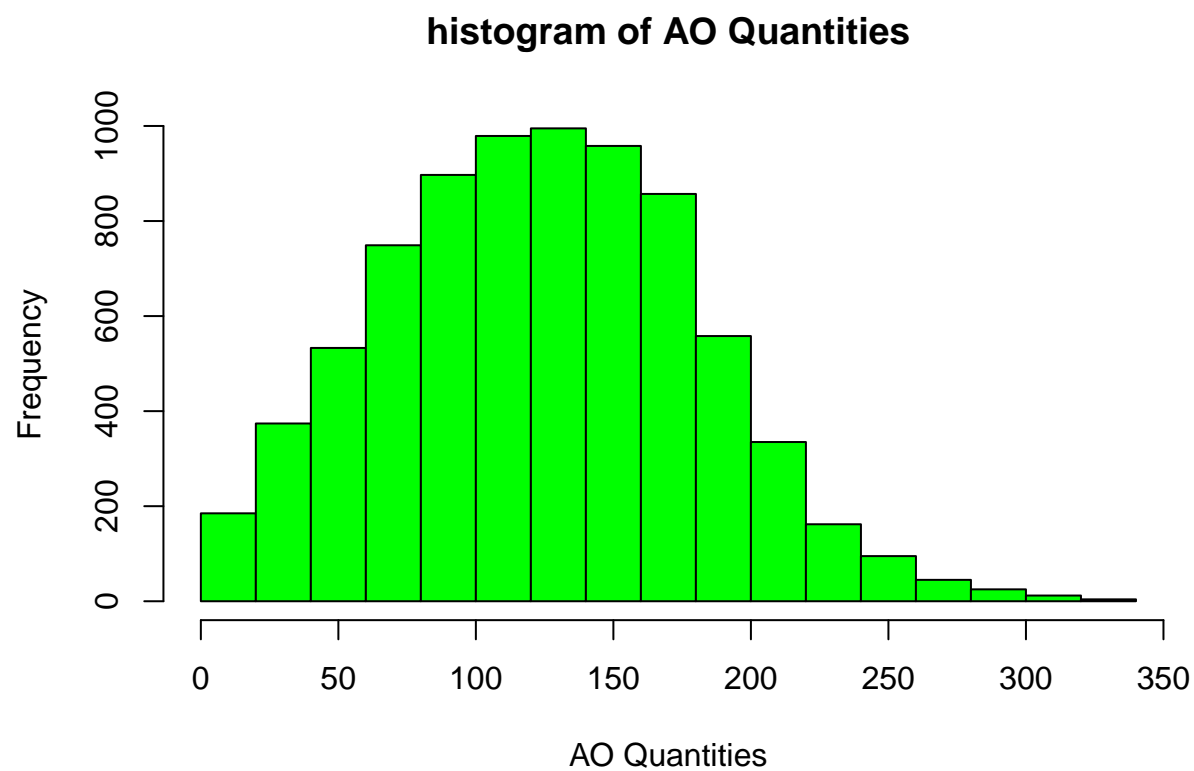
```
VCFstat::ChromDP(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwid
```



```
VCFstat::ChromRO(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwid
```

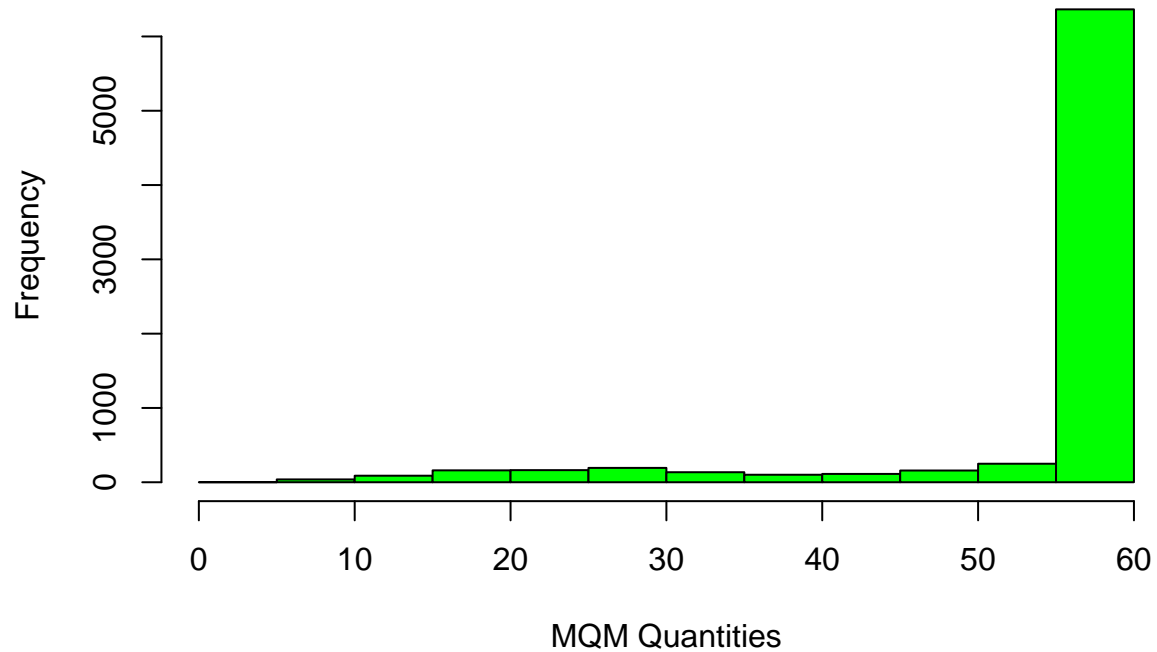


```
VCFstat::ChromAO(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwid
```

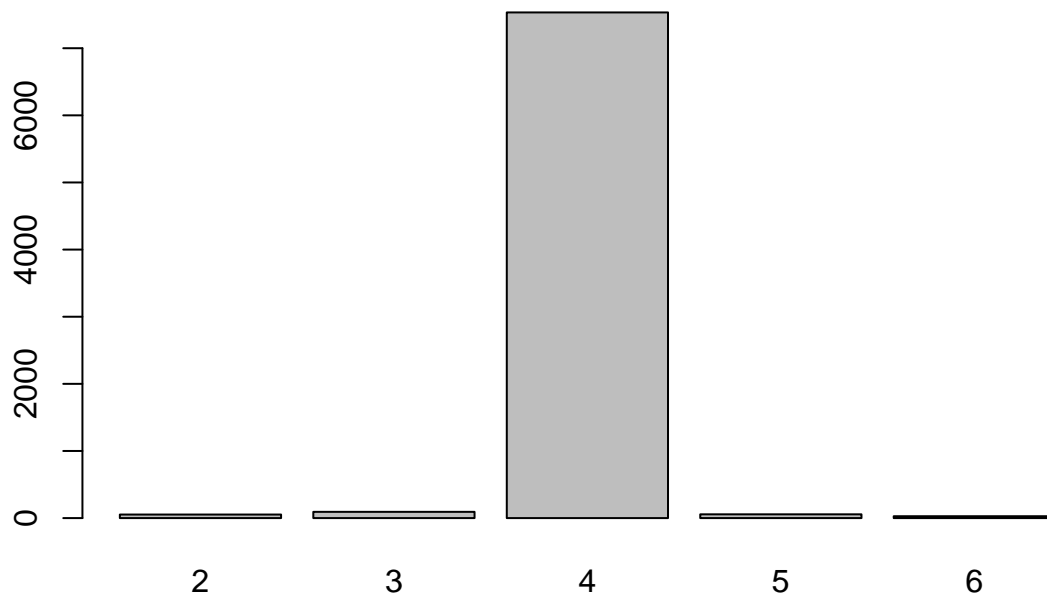


```
VCFstat::ChromMQM(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwi
```

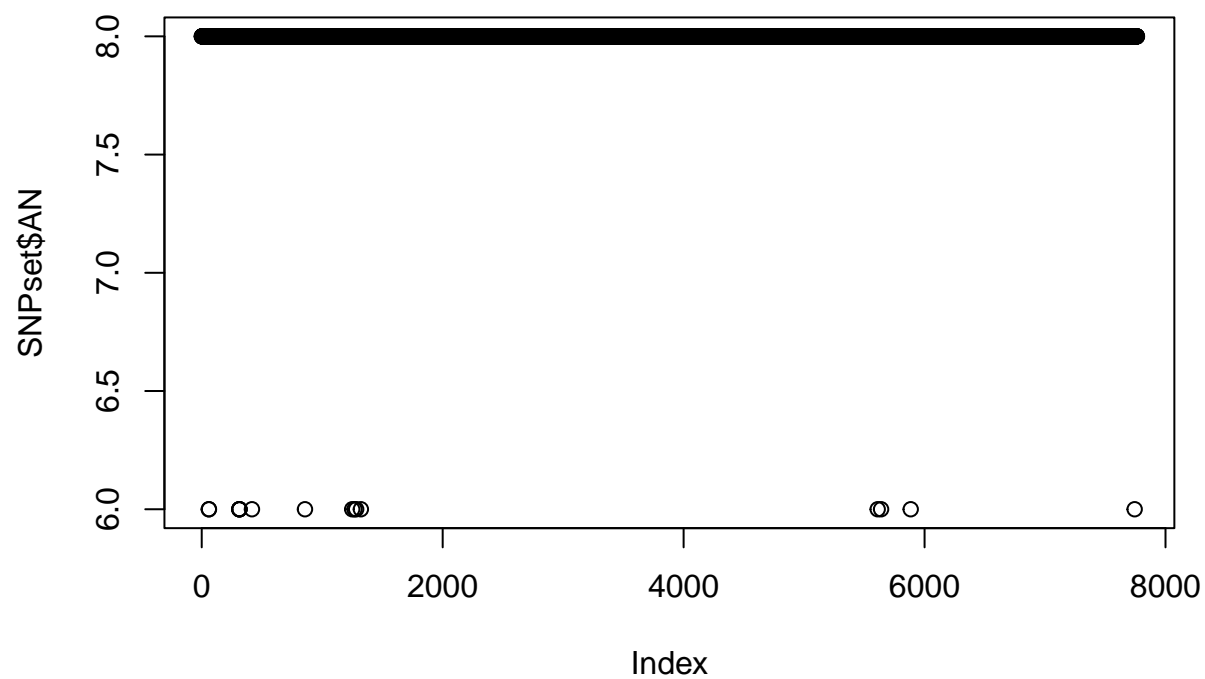
histogram of MQM Quantities



```
VCFstat::ChromAC(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwidth = 500000)
```

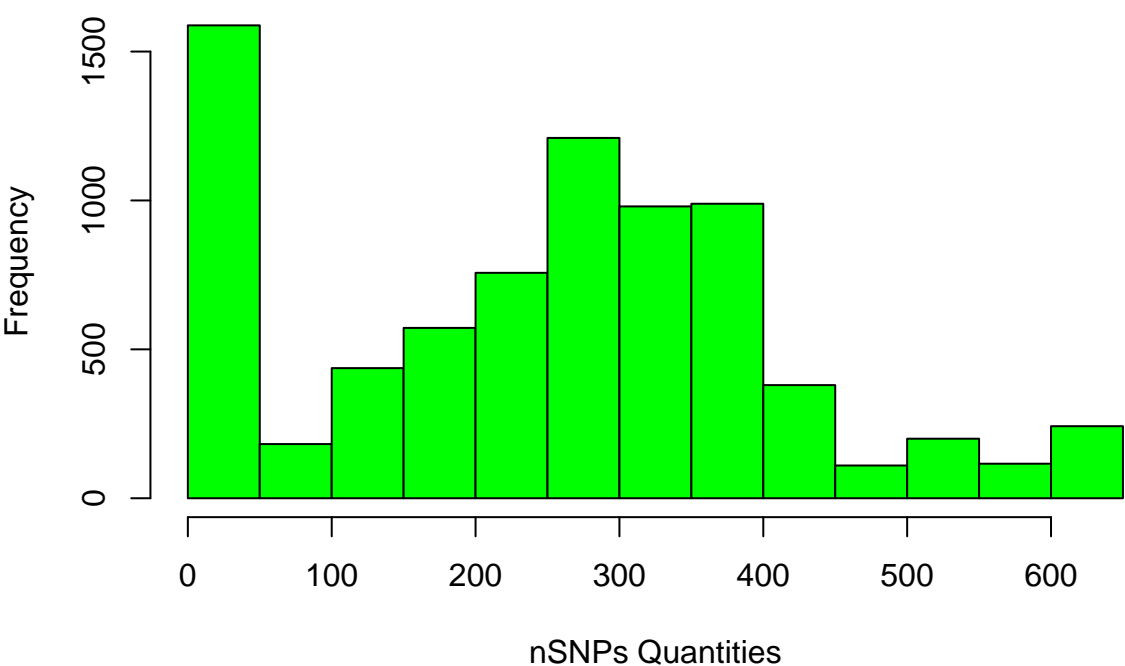


```
VCFstat::ChromAN(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, binwid
```



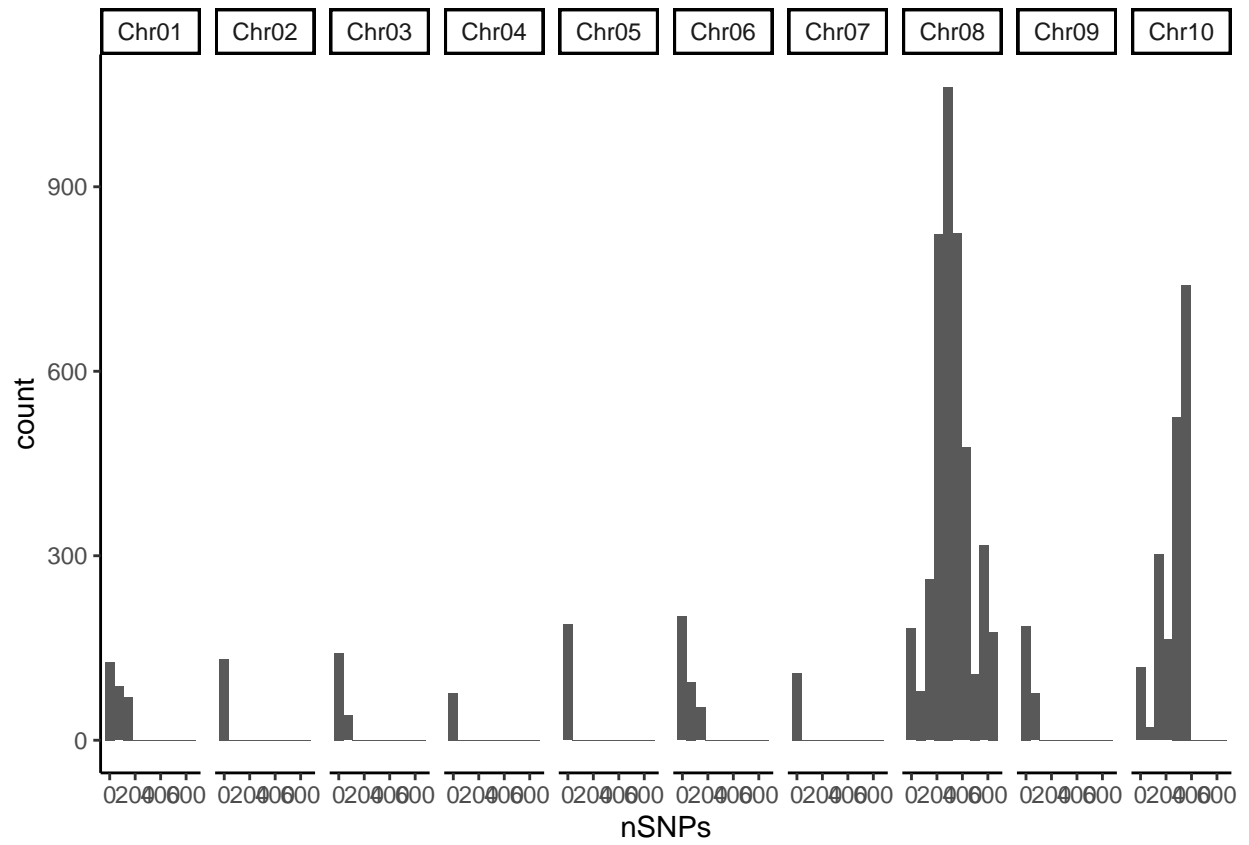
```
VCfstat::ChromnSNPs(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, bin
```

histogram of nSNPs Quantities

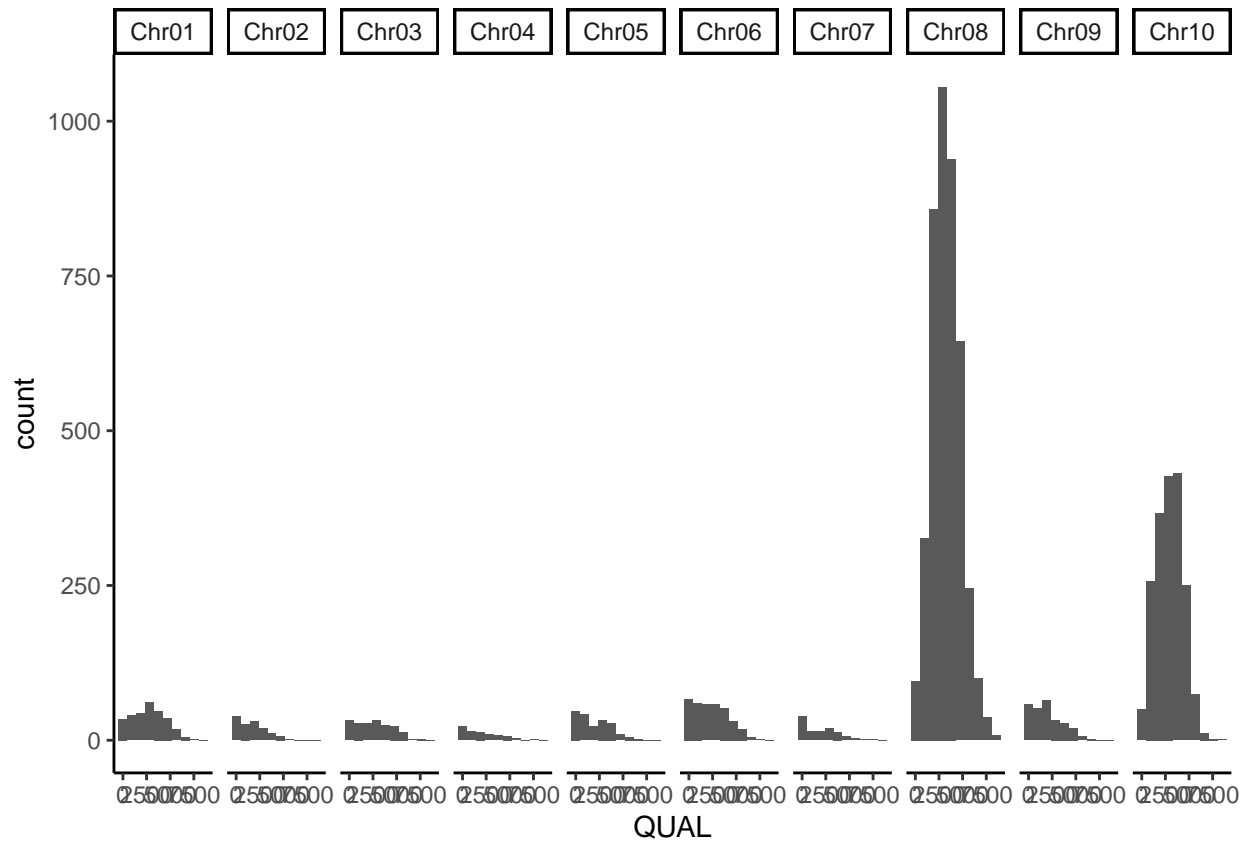


```
VCFstat::FacetChromnSNPs(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist,windowSize = 1e+05
```

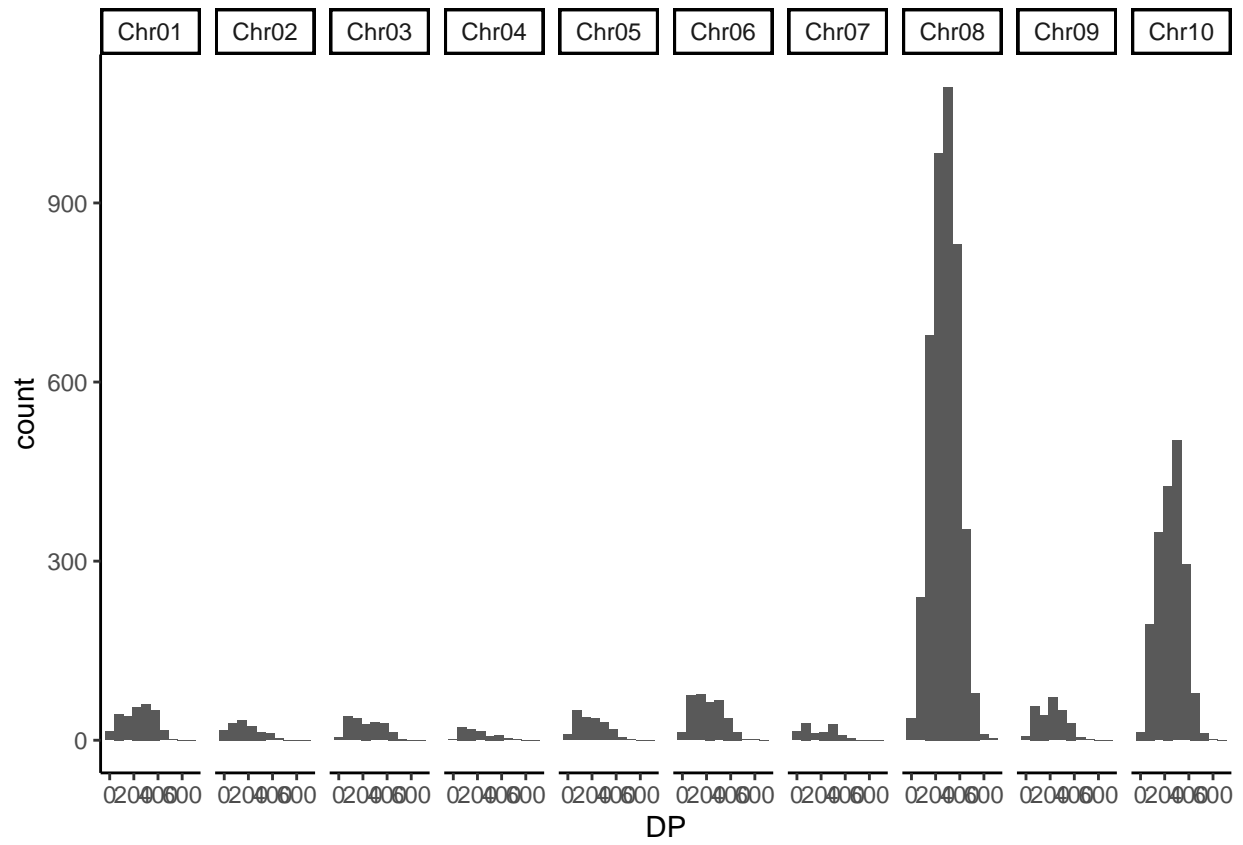




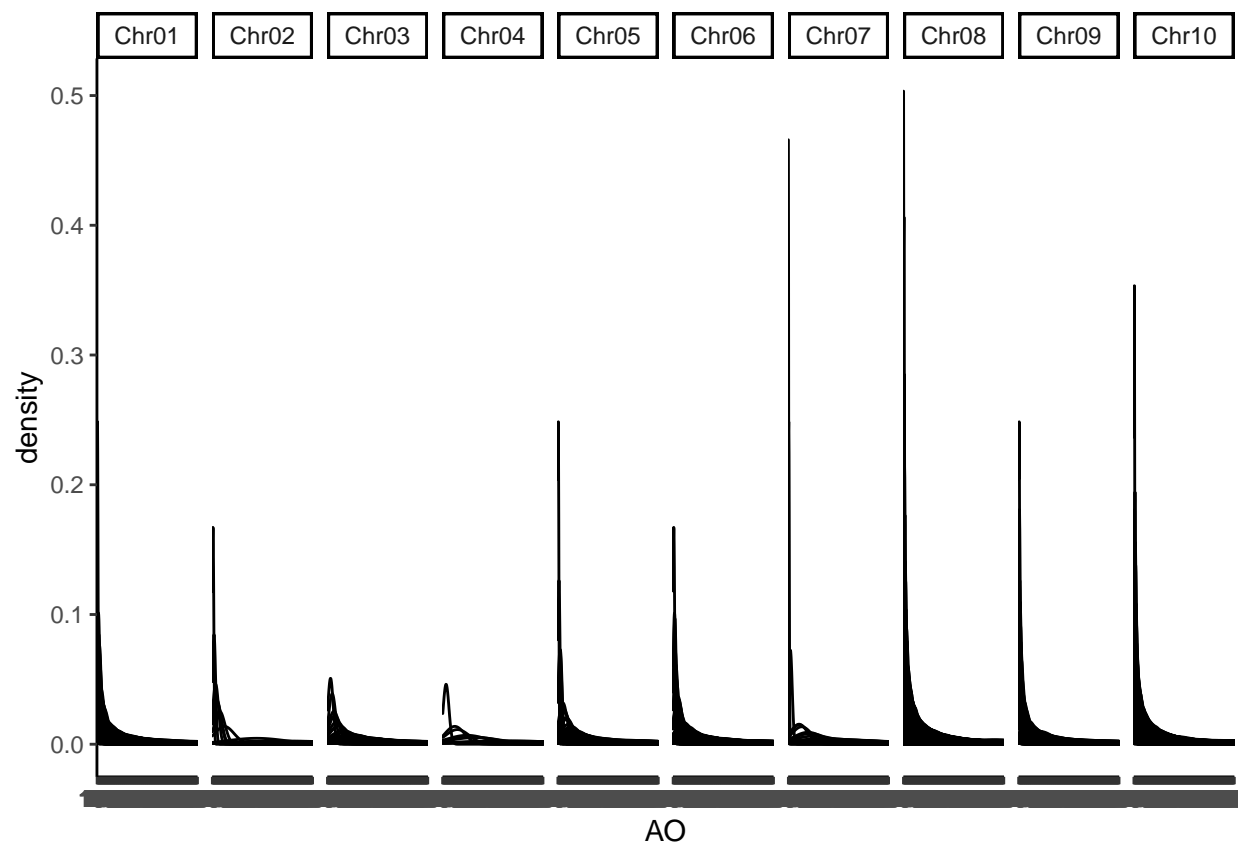
```
VCfstat::FacetChromQual(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05,
```

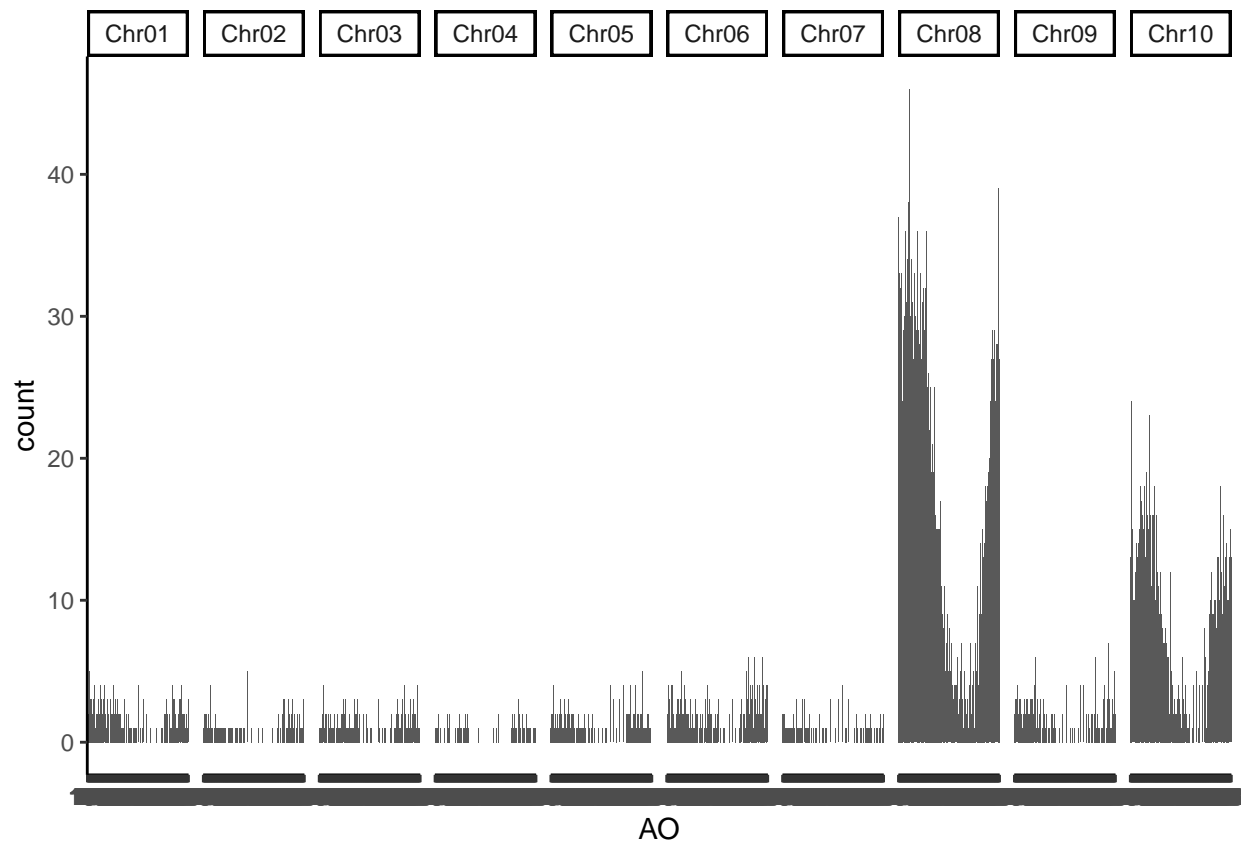


```
VCfstat::FacetChromDP(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, n
```



```
VCfstat::FacetChromA0(vcf = "freebayes_D2.filtered.vcf.gz", chromlist = chromlist, windowSize = 1e+05, n
```



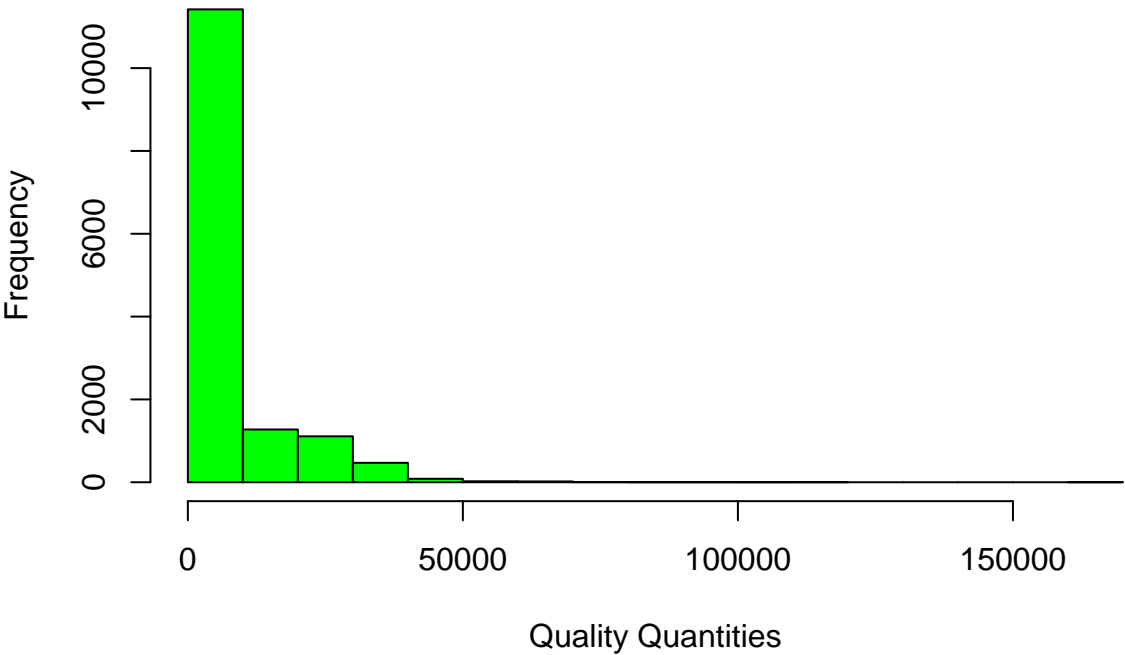


```
setwd("/home/michael/Desktop/Variants/Decompressed/")

chromlist <- c("NC_016131.3", "NC_016132.3", "NC_016133.3", "NC_016134.3", "NC_016135.3")

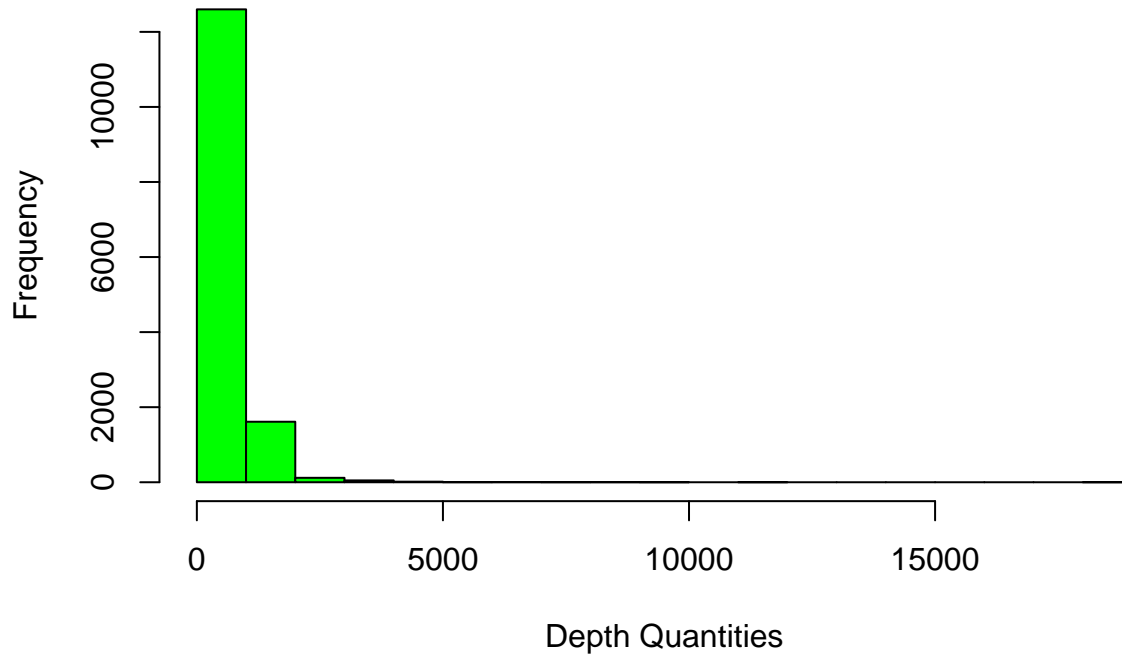
VCFstat::ChromQual(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filter
```

histogram of Quality Quantities



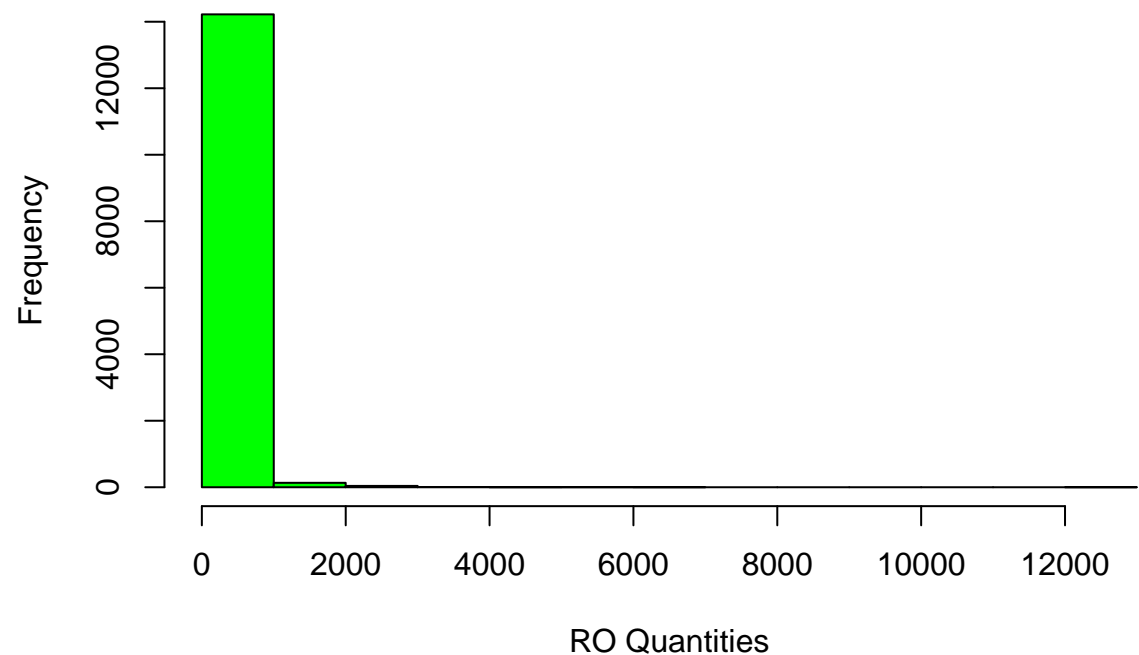
```
VCFstat::ChromDP(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered
```

histogram of Depth Quantities



```
VCFstat::ChromRO(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered
```

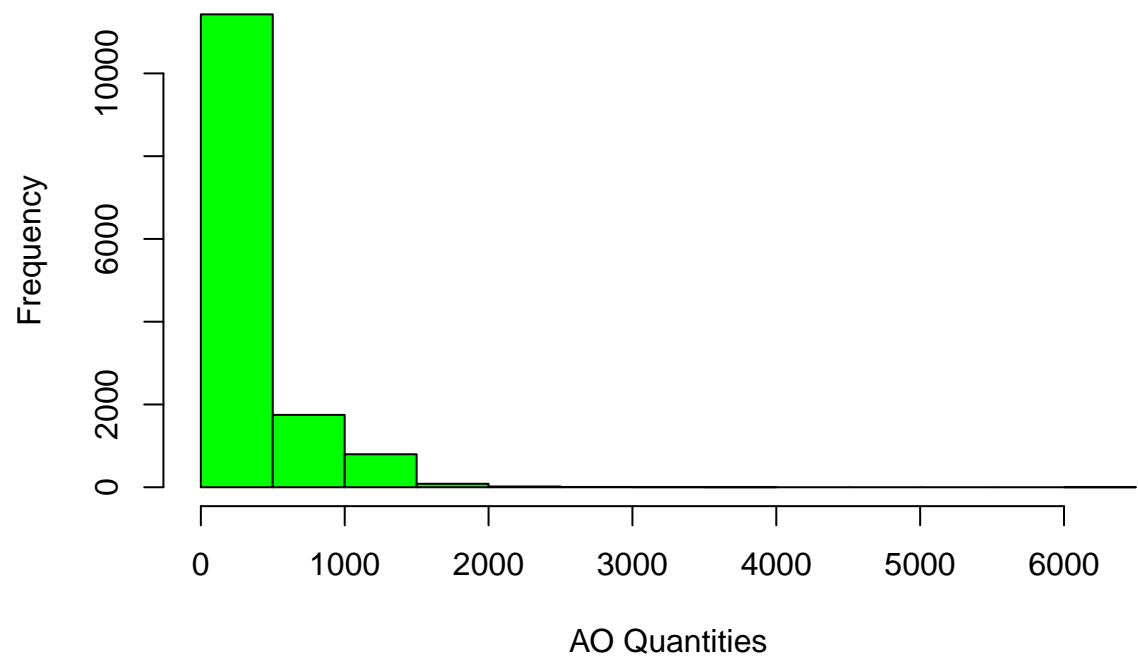
histogram of RO Quantities



```
VCFstat::ChromAO(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered
```

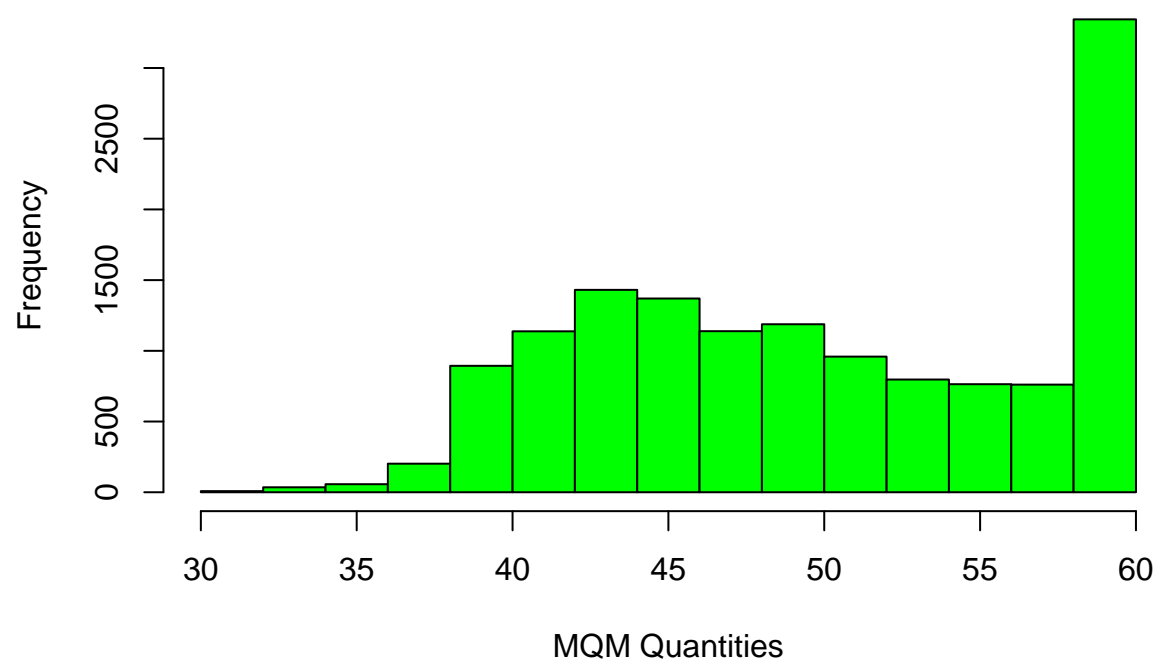


histogram of AO Quantities

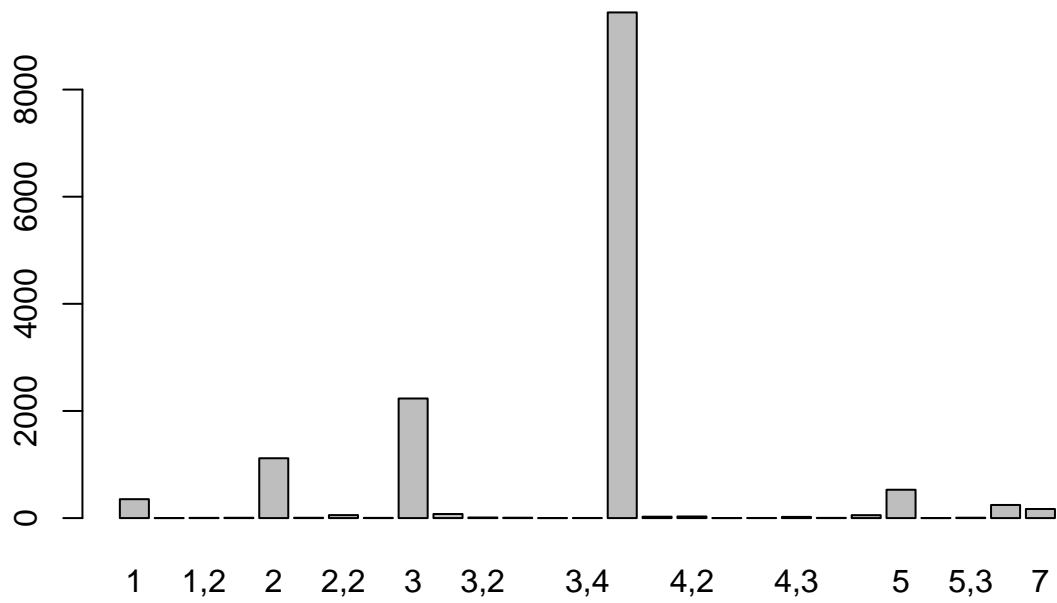


```
VCFstat::ChromMQM(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered")
```

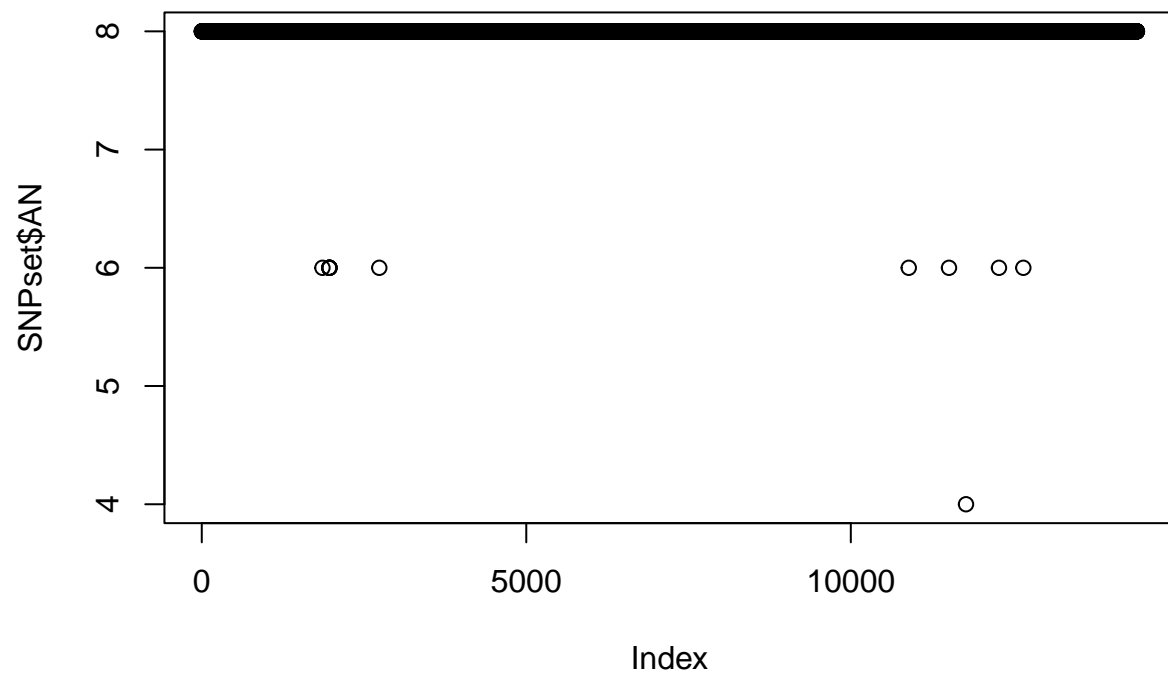
histogram of MQM Quantities



```
VCFstat::ChromAC(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered
```

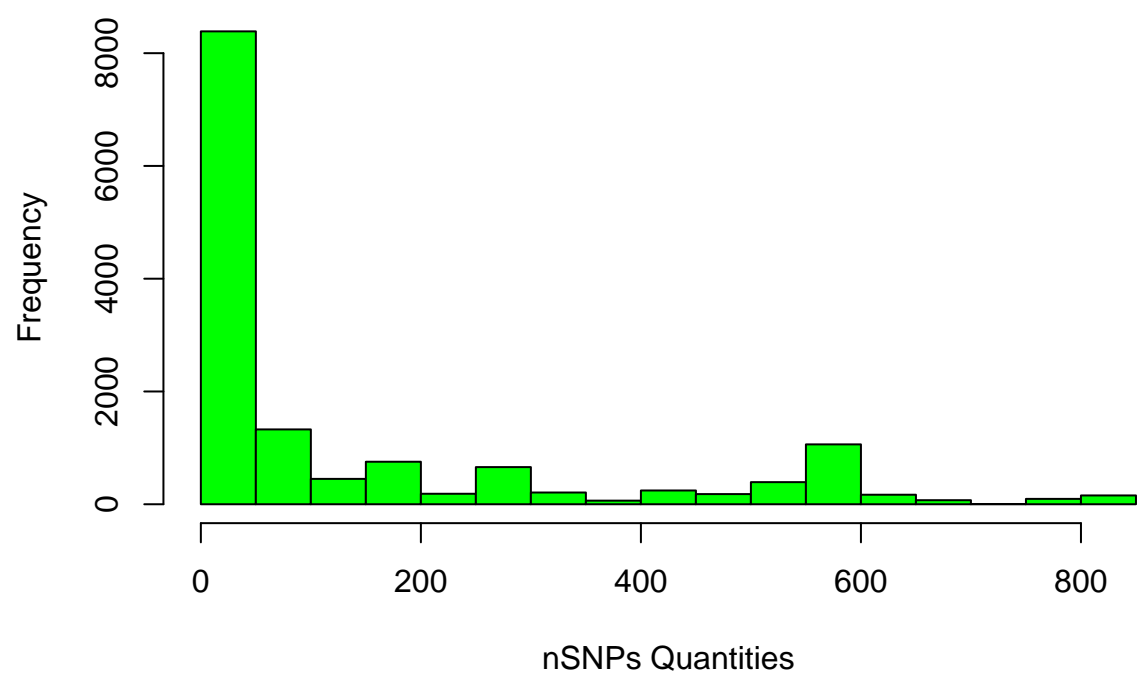


```
VCFstat::ChromAN(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered
```

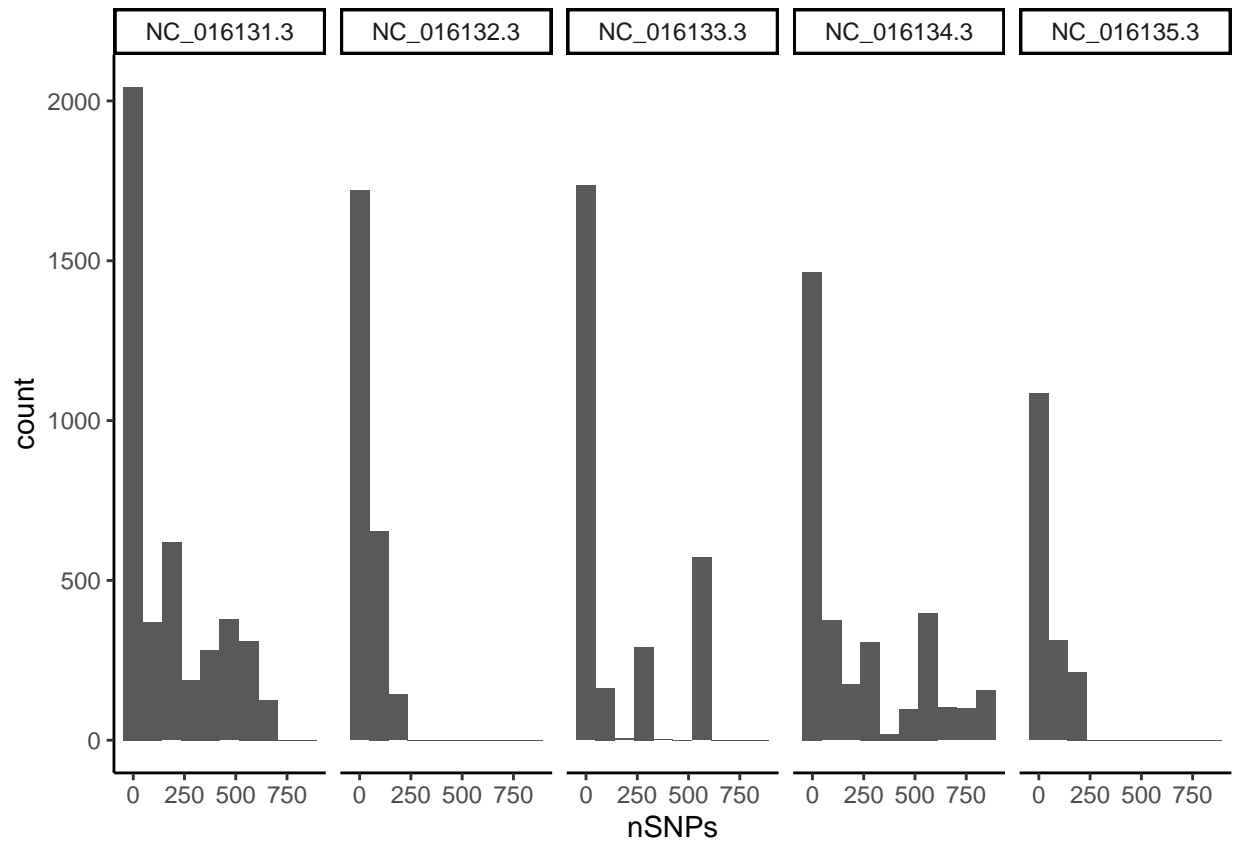


```
VCfstat::ChromnSNPs(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~filtered")
```

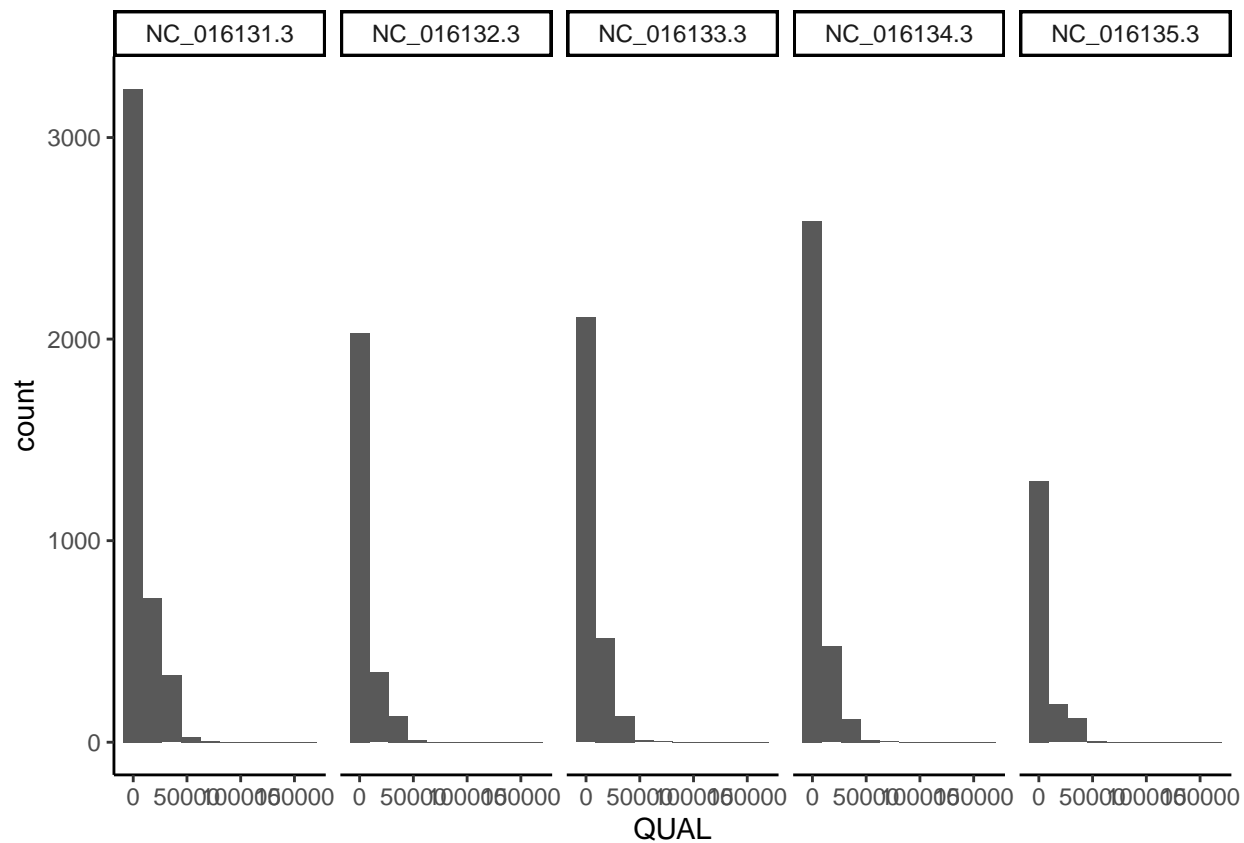
histogram of nSNPs Quantities



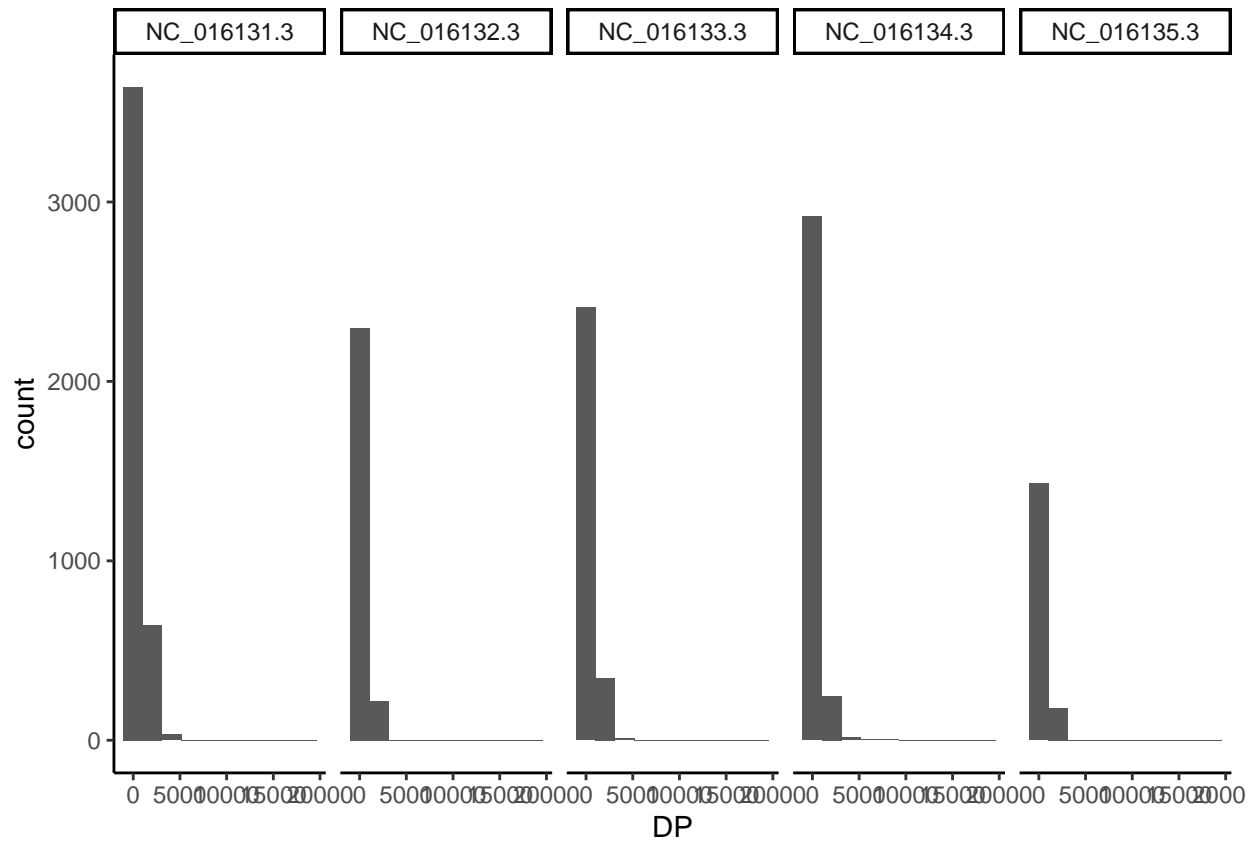
```
VCFstat::FacetChromnSNPs(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~")
```



```
VCFstat::FacetChromQual(vcf = "freebayes~bwa~GCF_000005505.3_Brachypodium_distachyon_v3.0~all_samples~f
```



VCfstat::FacetChromDP(vcf = "freebayes~bwa~GCF\_000005505.3\_Brachypodium\_distachyon\_v3.0~all\_samples~fil



VCfstat::FacetChromA0(vcf = "freebayes~bwa~GCF\_000005505.3\_Brachypodium\_distachyon\_v3.0~all\_samples~fil



