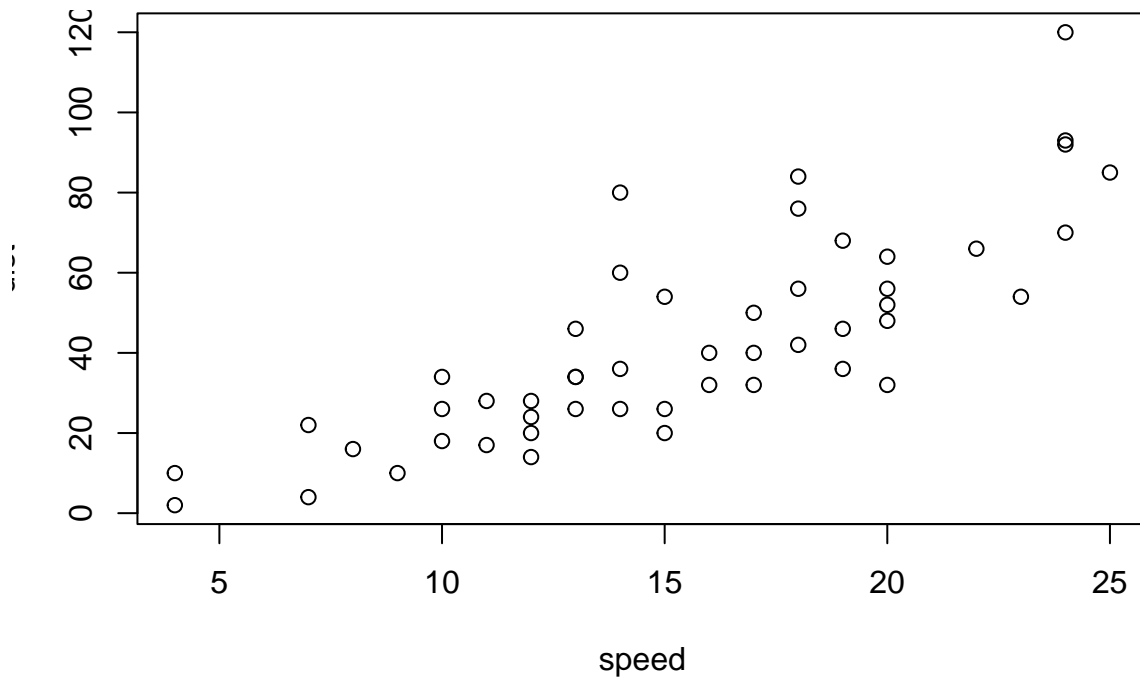# R Notebook

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

```
plot(cars)
```



Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- Conflicts ------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(cowplot)
```

```
##
## Attaching package: 'cowplot'
##
## The following object is masked from 'package:lubridate':
##
##      stamp
```

```r
emai<-read_tsv("~/bigdata/Genomecontent/GCcontent/Occultercut - Emai.tsv",col_names = c("GC","Proportion
```

```
## Rows: 100 Columns: 2
## -- Column specification ----------------------------------------------------
## Delimiter: "\t"
## dbl (2): GC, Proportion
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
emaigc<-emai%>%ggplot(aes(x=GC,y=Proportion)) +
  geom_histogram(stat = "identity",fill="purple") +
  geom_line(color="green")+
  theme_cowplot(16)+
  xlab("GC (%)") +
  ylab("Proportion of genome")
```

```
## Warning in geom_histogram(stat = "identity", fill = "purple"): Ignoring unknown
## parameters: `binwidth`, `bins`, and `pad`
```
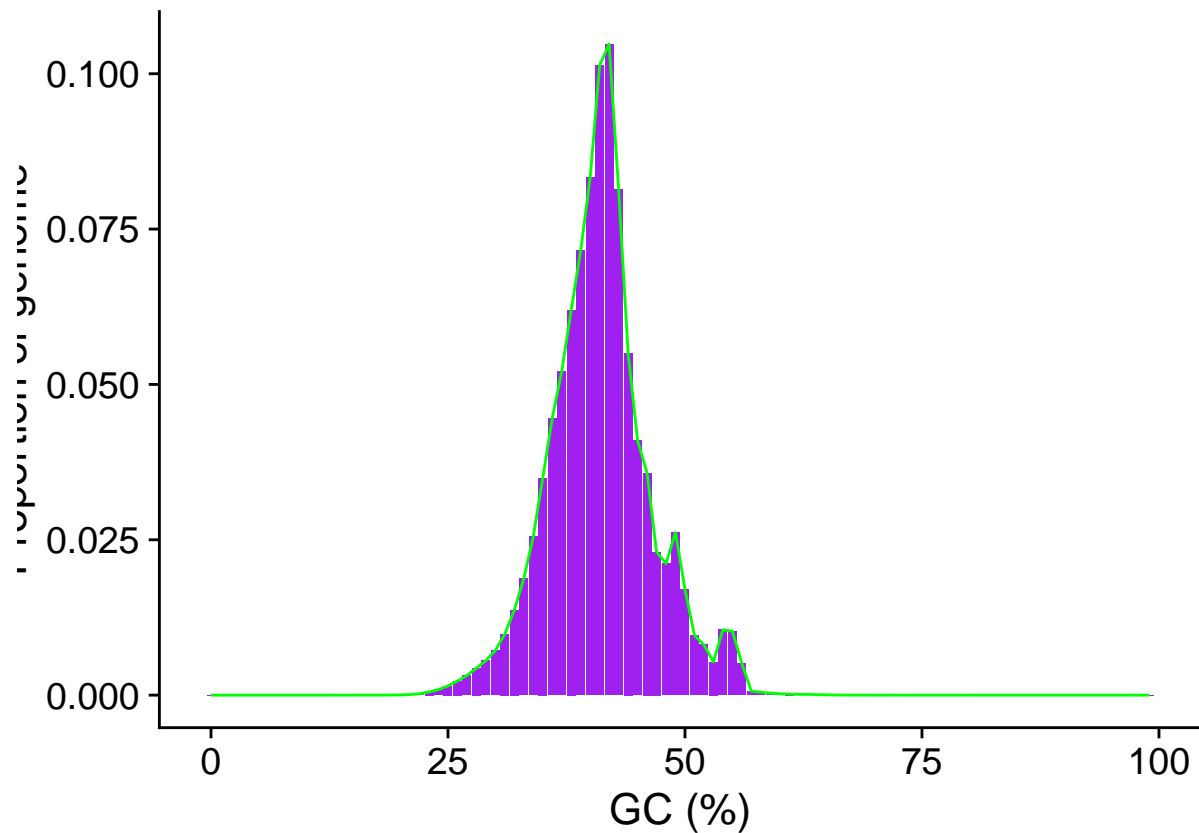
```r
print(emaigc)
```
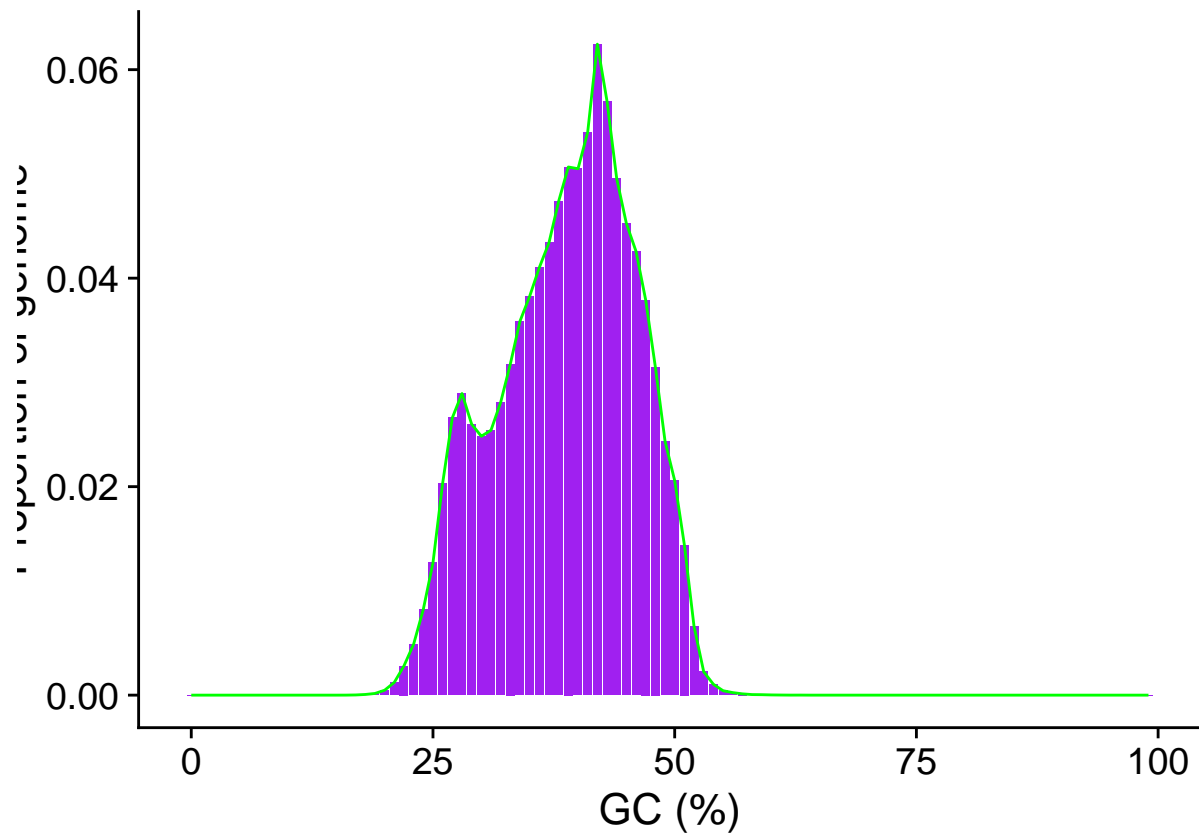
```
mcic<-read_tsv("~/bigdata/Genomecontent/GCcontent/Occultercut - Mcic.tsv",col_names = c("GC","Proportion
```

```
## Rows: 100 Columns: 2
## -- Column specification ---------------------------------------------------
## Delimiter: "\t"
## dbl (2): GC, Proportion
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
mcicgc<-mcic%>%ggplot(aes(x=GC,y=Proportion)) +
  geom_histogram(stat = "identity",fill="purple") +
  geom_line(color="green")+
  theme_cowplot(16)+
  xlab("GC (%)") +
  ylab("Proportion of genome")
```

```
## Warning in geom_histogram(stat = "identity", fill = "purple"): Ignoring unknown
## parameters: `binwidth`, `bins`, and `pad`
```
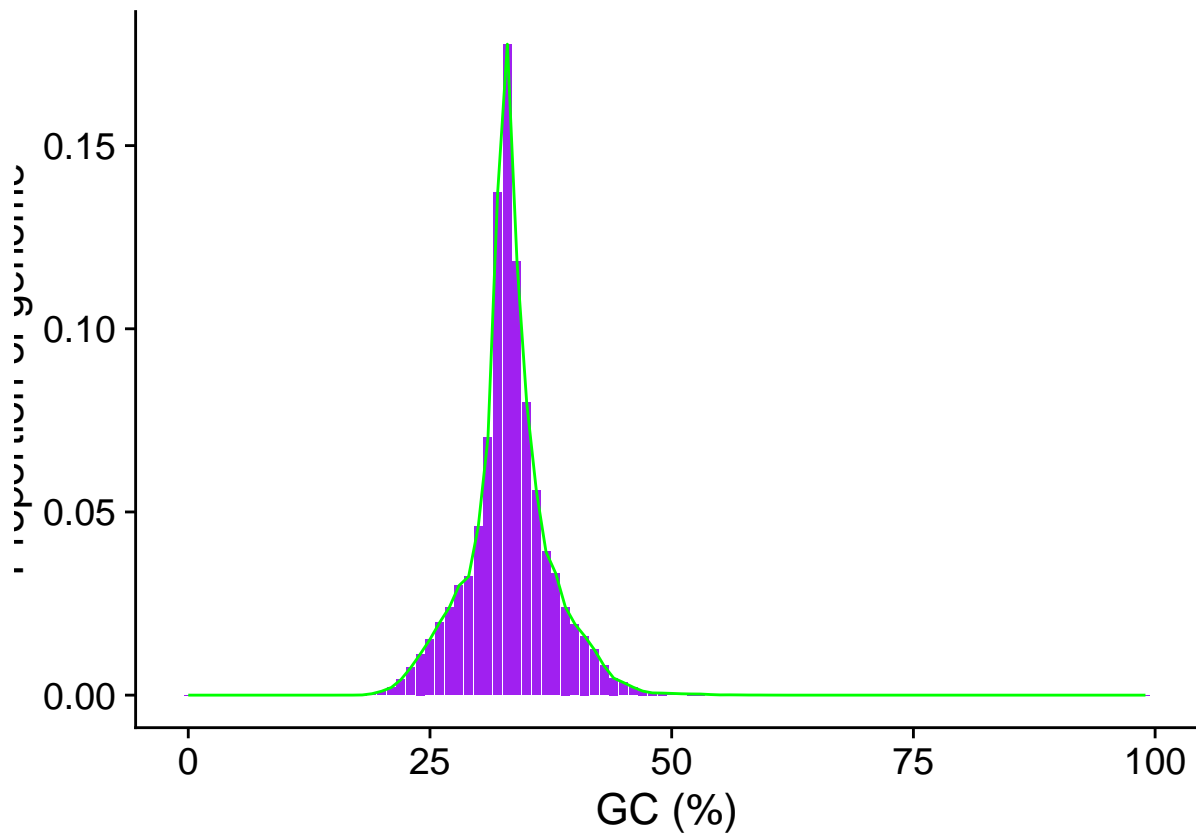
```
print(mcicgc)
```

```
zrad<-read_tsv("~/bigdata/Genomecontent/GCcontent/Occultercut - Zrad.tsv",col_names = c("GC","Proportion
```

```
## Rows: 100 Columns: 2
## -- Column specification -------------------------------------------------------
## Delimiter: "\t"
## dbl (2): GC, Proportion
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
zradgc<-zrad%>%ggplot(aes(x=GC,y=Proportion)) +
  geom_histogram(stat = "identity",fill="purple") +
  geom_line(color="green")+
  theme_cowplot(16)+
  xlab("GC (%)") +
  ylab("Proportion of genome")
```

```
## Warning in geom_histogram(stat = "identity", fill = "purple"): Ignoring unknown
## parameters: `binwidth`, `bins`, and `pad`
```
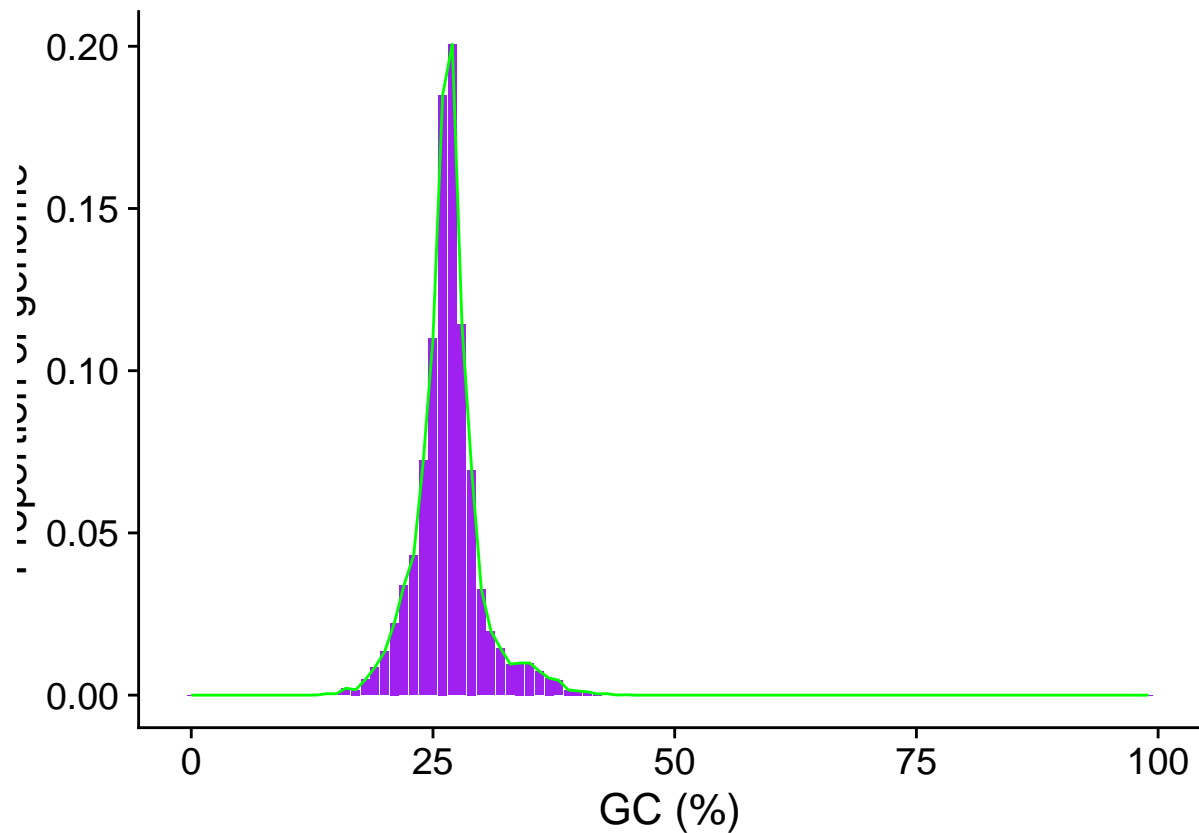
```
print(zradgc)
```

```
conth<-read_tsv("~/bigdata/Genomecontent/GCcontent/Occultercut - conth.tsv",col_names = c("GC","Proport
```

```
## Rows: 100 Columns: 2
## -- Column specification ----------------------------------------------------
## Delimiter: "\t"
## dbl (2): GC, Proportion
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
conthgc<-conth%>%ggplot(aes(x=GC,y=Proportion)) +
  geom_histogram(stat = "identity",fill="purple") +
  geom_line(color="green")+
  theme_cowplot(16)+
  xlab("GC (%)") +
  ylab("Proportion of genome")
```

```
## Warning in geom_histogram(stat = "identity", fill = "purple"): Ignoring unknown
## parameters: `binwidth`, `bins`, and `pad`
```

```r
print(conthgc)
```

```
conco<-read_tsv("~/bigdata/Genomecontent/GCcontent/Occultercut - Conco.tsv",col_names = c("GC","Proporti
```

```
## Rows: 100 Columns: 2
## -- Column specification ---------------------------------------------------------
## Delimiter: "\t"
## dbl (2): GC, Proportion
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
concogc<-conco%>%ggplot(aes(x=GC,y=Proportion)) +
  geom_histogram(stat = "identity",fill="purple") +
  geom_line(color="green")+
  theme_cowplot(16)+
  xlab("GC (%)") +
  ylab("Proportion of genome")
```

```
## Warning in geom_histogram(stat = "identity", fill = "purple"): Ignoring unknown
## parameters: `binwidth`, `bins`, and `pad`
```

```
print(concogc)
```
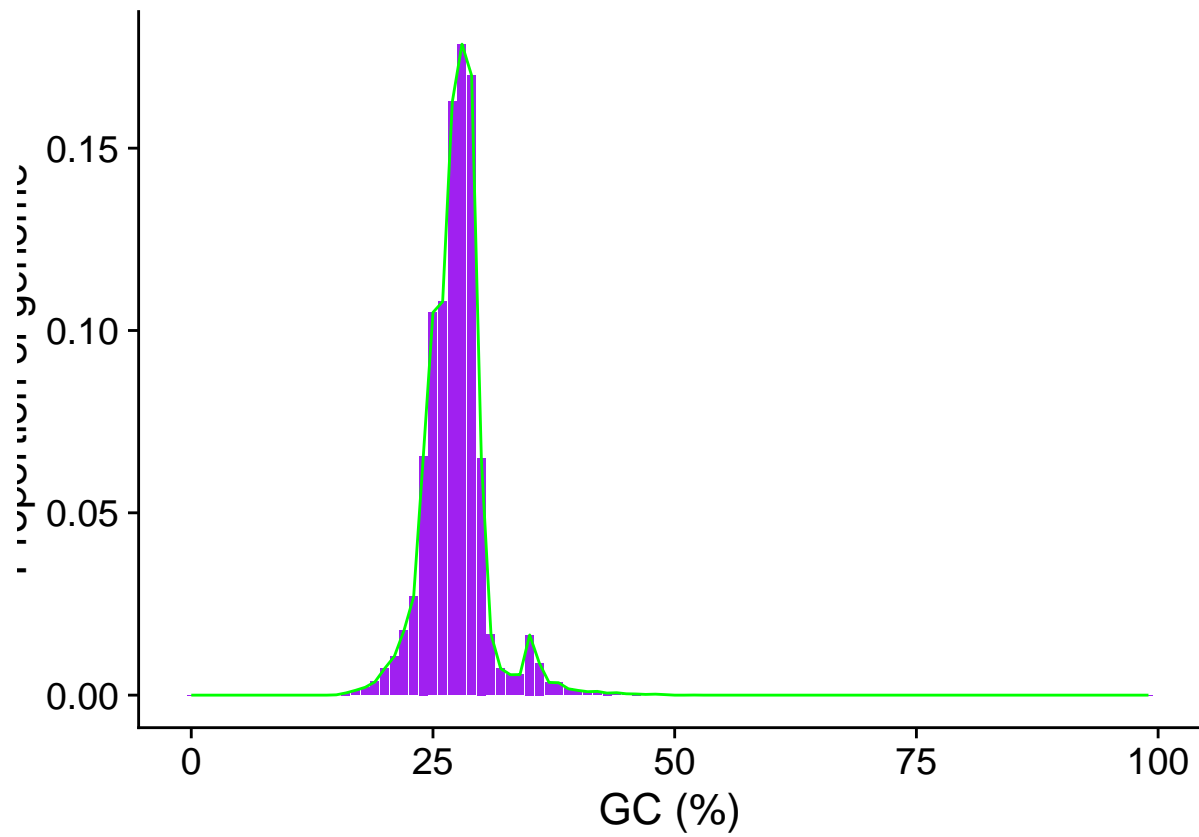
```r
gccontent<-plot_grid(emaigc,mcicgc,zradgc,conthgc,concogc,
                     labels = c("E.maimaiga","M.cicadina","Z.radicans","N.thromboides","C.coronatus"),
                     align = "hv", label_x = 0.4,
                      label_fontface = "italic",ncol = 2)
print(gccontent)
```

*E.maimaiga*

*M.cicadina*

*Z.radicans*

*N.thromboides*

*C.coronatus*

GC (%)

Proportion of ge...

Proportion of ge...
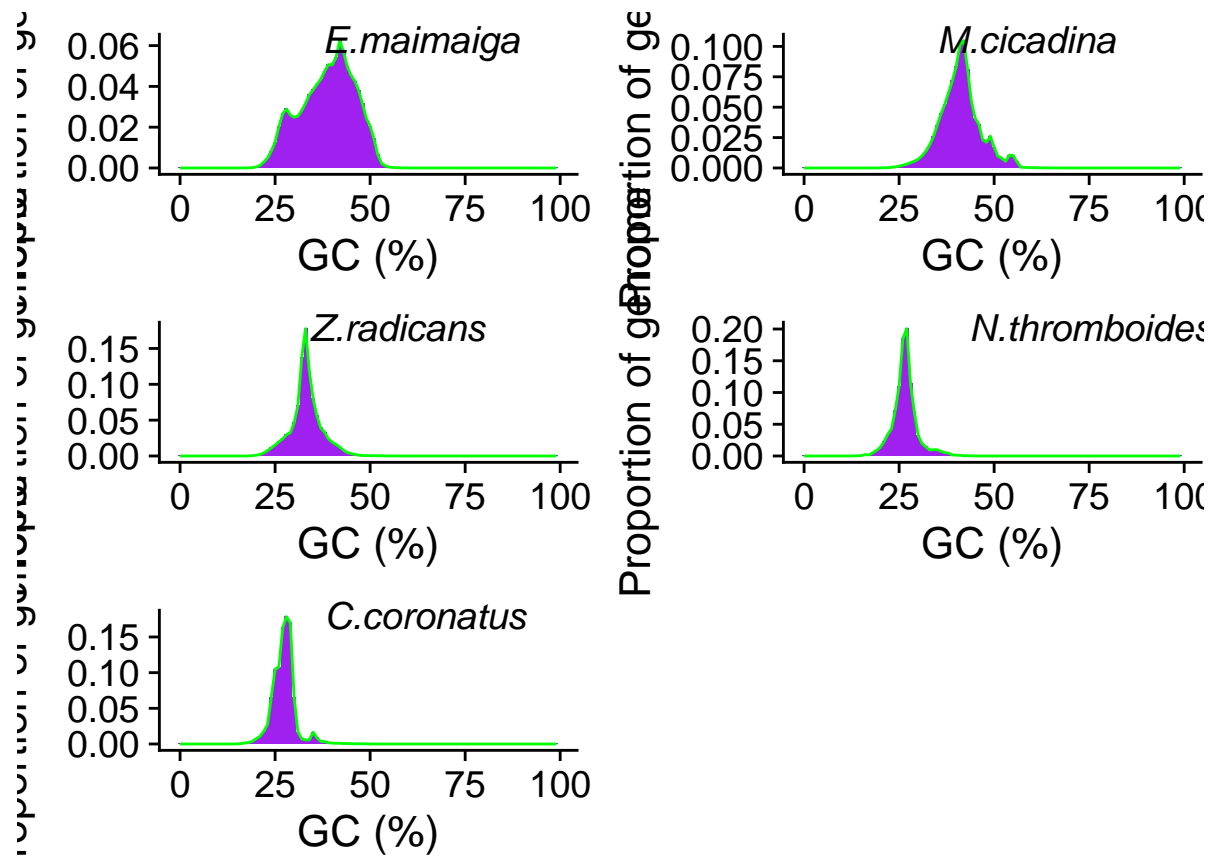
```
ggsave("GCcontent.pdf",gccontent,
        width=9,
        height = 12,
        dpi=600)
```