Visualisation of mapped sequencing reads

The following packages were used for this anlysis: ggplot2, dplyr, purrr, here, ape, ggrepel, ggpubr.

Please define your in and output directories

```
output <- here("output/img")

##Genome Input
inputGenome <- here("data/Ecoli_genome.fasta")

##input from summary from mapping.py
inputMap <- here("output/2023-01-27_NC_000913.3 Escherichia coli str. K-12 substr. MG1655, complete gen

if (file.exists(output)){

} else {
    dir.create(file.path(output))

}
```

```
## NULL
```

```
genome <- read.dna(inputGenome,format="fasta")
sequence <- as.character(genome)
genome_length <- length(sequence)
```

Importing data from /output/*.csv

```
mapped <- read.csv(inputMap,sep = ";")

# mapped = mapped[50:60,]

mapped = mapped %>% mutate_at(vars(Sense, Antisense), ~map(strsplit(. ,split=","), ~map_int(.x, as.inte
# mapped %>% str()

sense = unlist(mapped$Sense)
anti = unlist(mapped$Antisense)

sense %>% length()
```

```
## [1] 820
```

```
anti %>% length()
```

```
## [1] 171
```

```
reads <- data.frame(pos = c(sense, anti), strand = as.factor(rep(c("s","a"),times = c(length(sense),len
```

Plotting mapped reads

```
p1 <- ggplot(reads, aes(x = pos, y = ..density..)) +
  geom_histogram(bins = 155, color = "green4", fill = "green2") +
  geom_density(color = "darkgreen", lwd=1.3, bw = 70000)+
                # geom_histogram(reads)
```

```
  labs(x = "Genome Position in Mb", y = "Density of reads mapped", caption = "Fig. 1: Density of the rea
  theme_classic()


p2 <- ggplot(reads) +
  geom_histogram(data = reads[reads$strand == "s",],aes(x = pos/10^6, y = ..count..), bins = 155,color=
  # geom_density(data = reads[reads$strand == "s",], color="lightblue") +
  geom_histogram(data = reads[reads$strand == "a",],aes(x = pos/10^6, y = -..count..), bins = 155,color=
  scale_y_continuous(labels = abs) +
  labs(x = "Genome Position in Mb", y = "reads mapped per 30 Kb segment", caption = "Fig 2: Orientation
  theme_classic()

ggsave("F1_Genome_pos_total.png",p1, device = "png", dpi = 300, path = output)
```

```
## Saving 6.5 x 4.5 in image
```

```
ggsave("F2_Genome_pos_orient.png",p2, device = "png", dpi = 300, path = output)
```

```
## Saving 6.5 x 4.5 in image
```

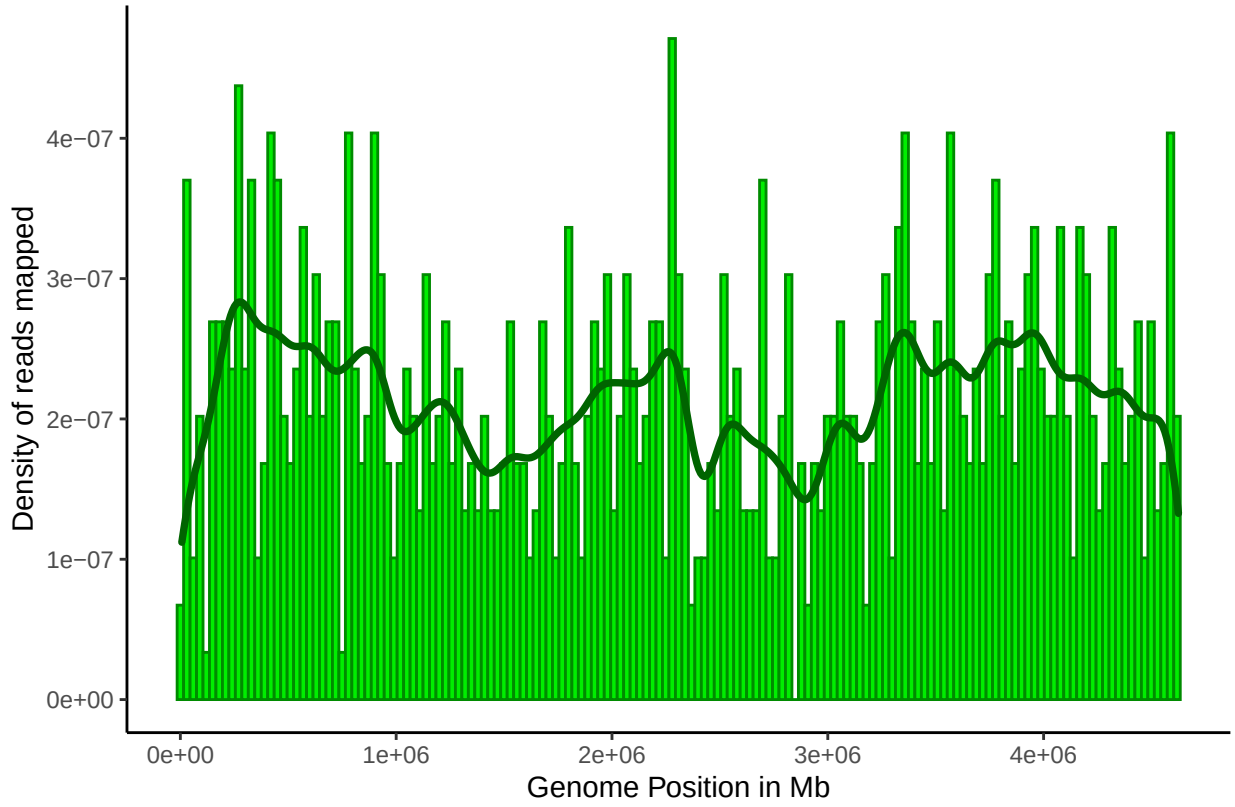


Fig. 1: Density of the reads mapped to the E.coli genome.

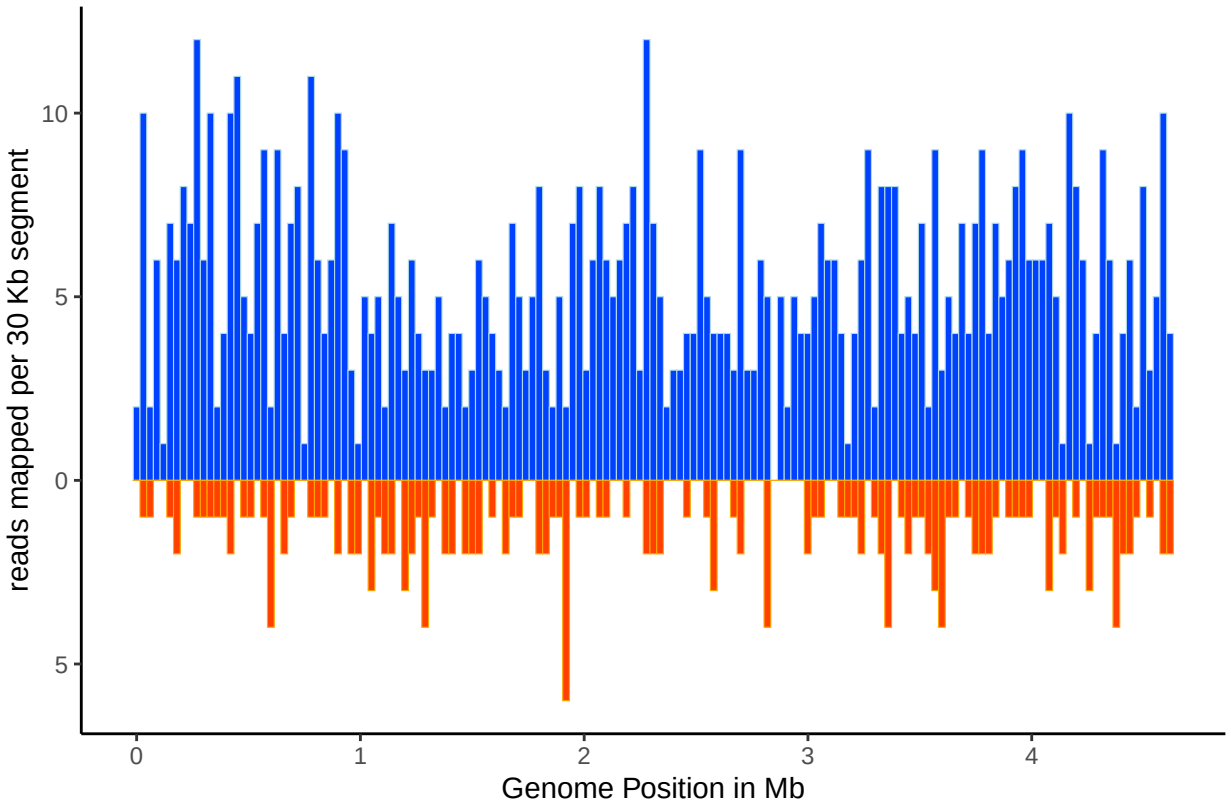


Fig 2: Orientation of mapped Reads

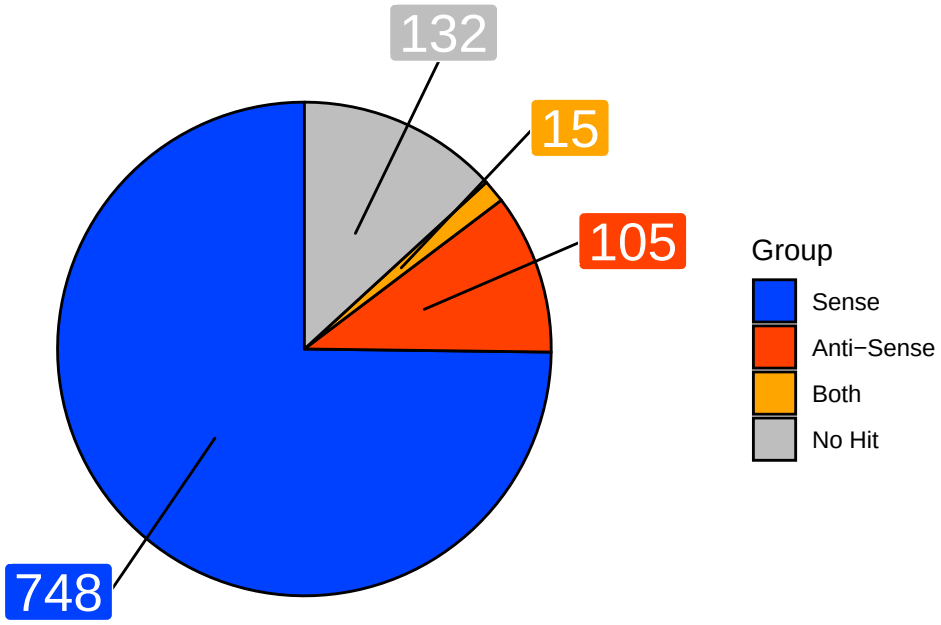
Description Fig 1: Density of reads mapped to the E.coli genome. Each bin size represents a 30 kb long segment along the genome. Description Fig 2: Sense vs. Antisense density of mapped reads. The y-axis shows a number of counts per 30 Kb segment.

```
p3 <- ggplot(pie1, aes(x="", y=amount, fill=Group)) +
  geom_bar(stat="identity", width=1, color = "black") +
  coord_polar("y", start=0)+
  theme_void()+
  ## theme(legend.position="bottom",legend.key.size = unit(1,'cm'), legend.text = element_text(size = 1
  ## theme(legend.title= element_blank()) +
  geom_text(aes(x = 1, y = ypos, label = amount), color = "white", size=5)+
  scale_fill_manual(values= c("#ff4000","#0040ff"))# +
  # labs(caption = "Fig 3")

pie2$Group <- factor(pie2$Group, levels = c("Sense", "Anti-Sense", "Both", "No Hit"))

p4 <- ggplot(pie2, aes(x="", y=value, fill=Group)) +
  geom_bar(stat="identity", width=1, color = "black") +
  coord_polar("y", start=0)+
  theme_void()+
  # theme(legend.position="bottom") +
  # theme(legend.title= element_blank()) +
  geom_label_repel(aes(y=ypos, label = value), colour = "white",
                   segment.colour = "black",size = 7, nudge_x = 0.9, show.legend = FALSE) +
  # geom_text(aes(x = 1.15, y = ypos, label = value), color = "white", size=5)+
  scale_fill_manual(values= c("#0040ff","#ff4000","orange","grey"))#+
  # labs(caption = "Fig 4")
```

```
p4
```




```
p5 <- ggplot(MapNum, aes(x = factor(Mappings),y=Hits, fill=factor(Mappings))) +
  geom_bar(stat="identity", width=1, color = "black") +
  # coord_polar("y", start=0)+
  theme_classic()+
  scale_fill_brewer(name="Frequency of read",palette="Greens")+
  geom_label_repel(data = MapNum,
                   aes(y = pos, label = paste0(Hits, " (",Fraction, "%)")),
                   size = 5, nudge_y = 3, show.legend = FALSE) +
labs(x = "Number of hits per read", caption = "Fig 5")
p5
```

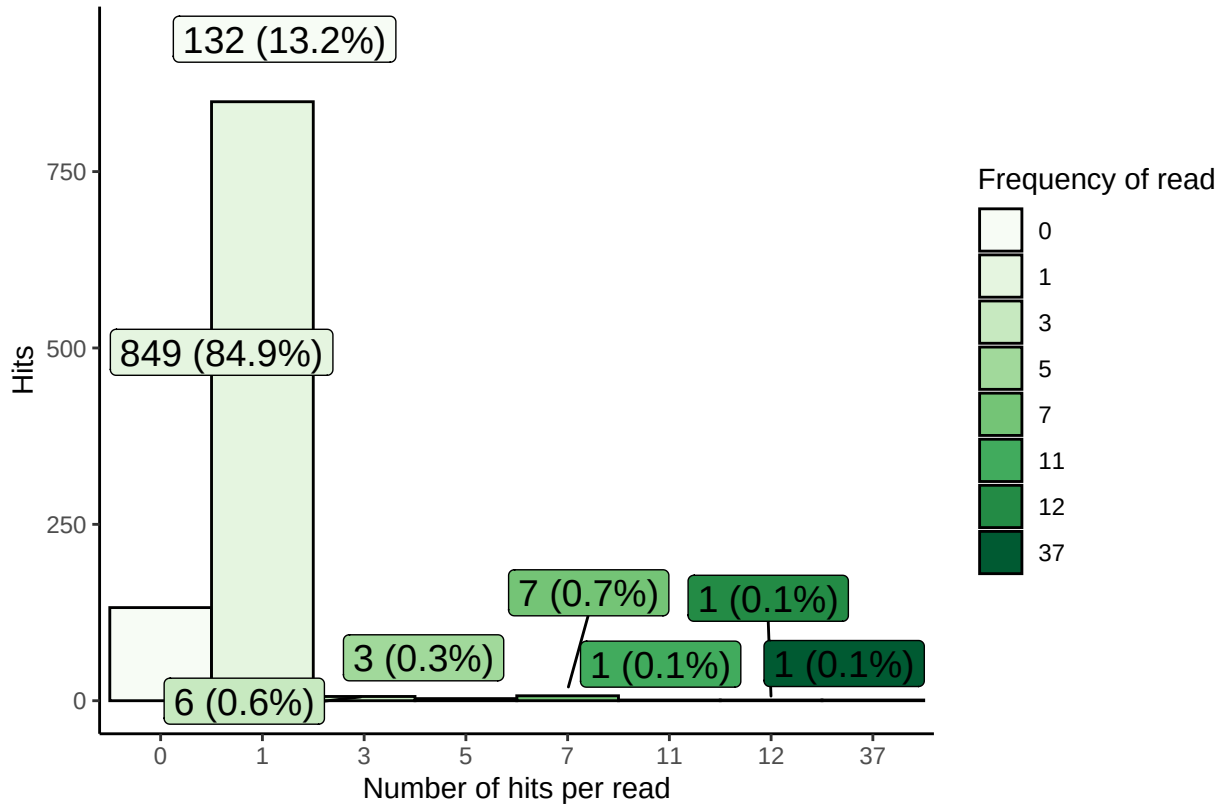


Fig 5

```
ggsave("F3_Hits_sense_vs_antisense.png",p3 ,device = "png", dpi = 300, path = output)
```

```
## Saving 6.5 x 4.5 in image
```

```
ggsave("F4_Read_distribution.png",p4, device = "png", dpi = 300, path = output)
```

```
## Saving 6.5 x 4.5 in image
```

```
ggsave("F5_Reads_by_number_of_hits.png",p5 ,device = "png", height = 10, width = 10, dpi = 300, path = o

p2p3 <- ggpubr::ggarrange(p2,p3,nrow = 1, widths = c(1,0.5), align = "h", common.legend = TRUE)
p2p3
```

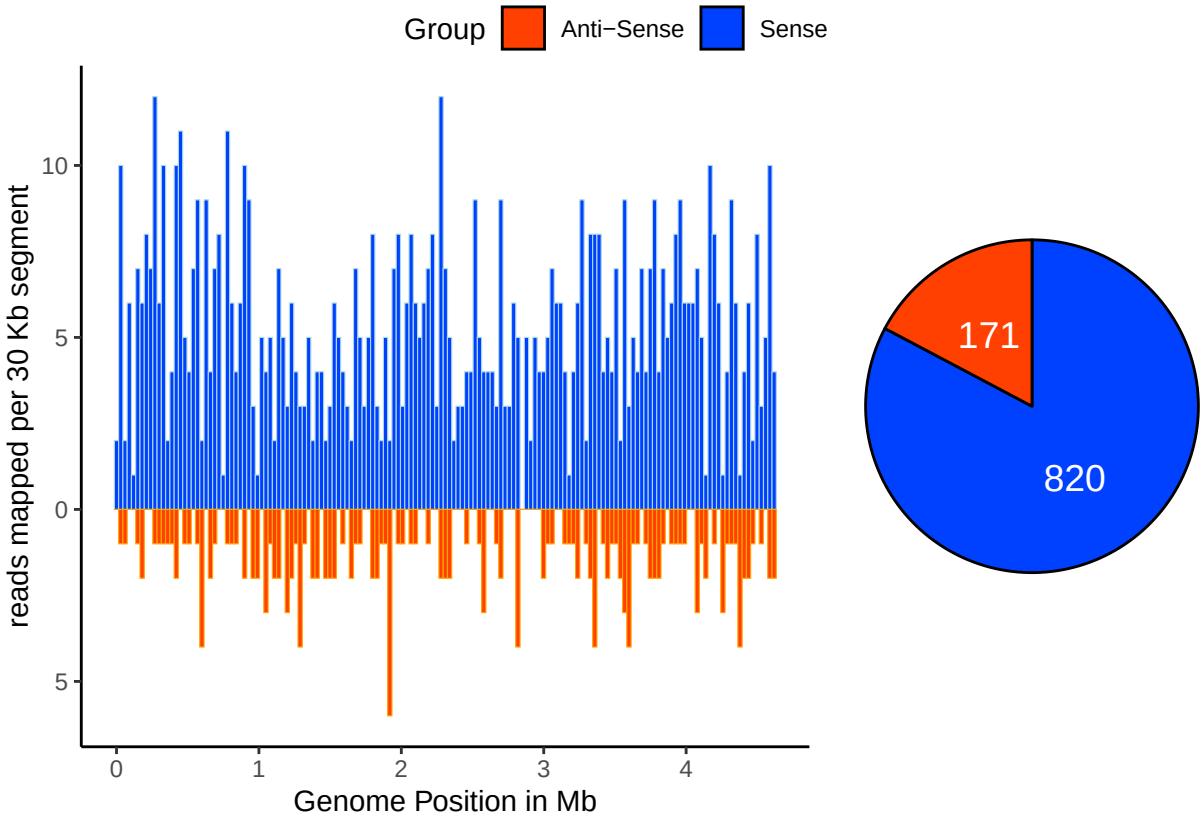


Fig 2: Orientation of mapped Reads

```
p1p4 <- ggpubr::ggarrange(p1,p4, nrow = 1, widths = c(1,1),heights = c(1,10), align = "v", common.legend
p1p4
```

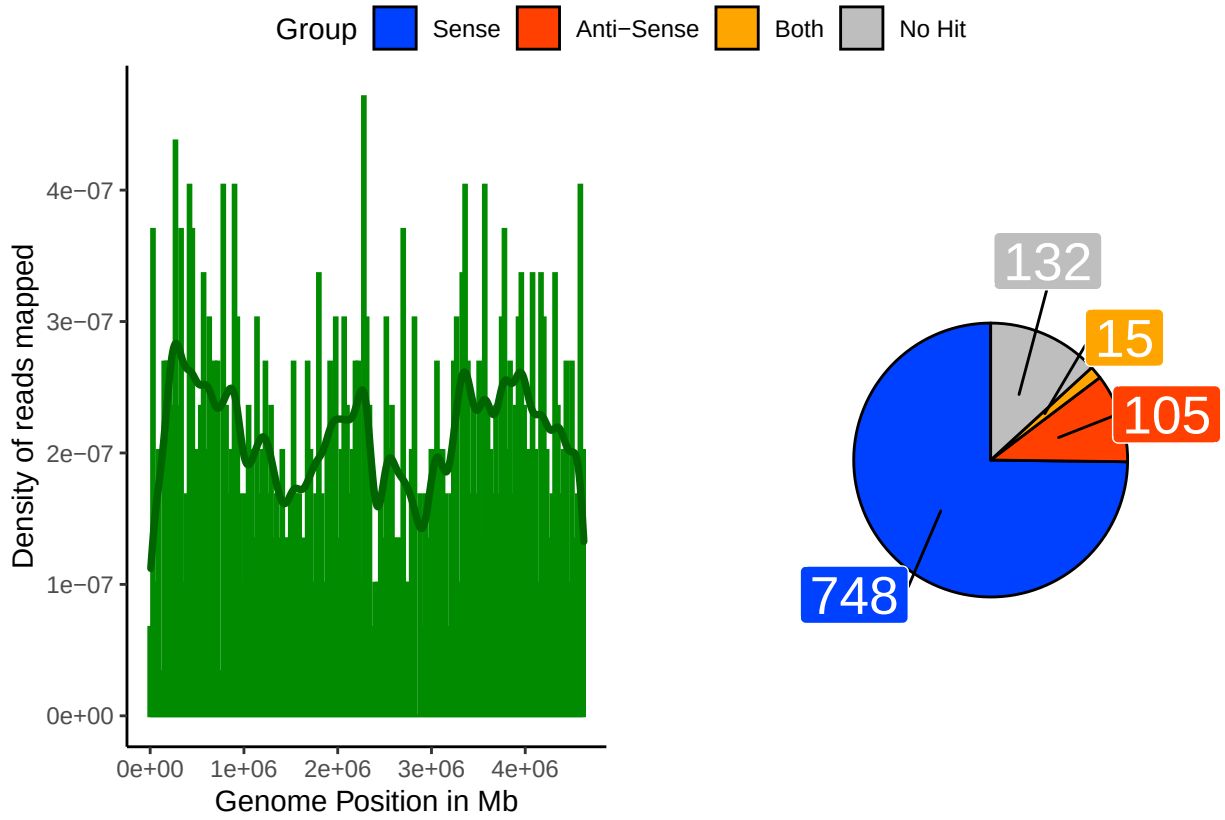


Fig. 1: Density of the reads mapped to the E.coli genome.

```
ggsave("F1_and_F4_reads.png", p1p4, device = "png", dpi = 300, path = here("doc/"))
```

```
## Saving 6.5 x 4.5 in image
```

```
ggsave("F2_and_F3_orient.png", p2p3, device = "png", dpi = 300, path = here("doc/"))
```

```
## Saving 6.5 x 4.5 in image
```

Description Fig 3: Number of successful hits to sense or anti-sense strand. Description Fig 4: Number of reads mapped to sense strand, anti-sense strand, both strands or none in Genome Description Fig 5: Frequency of hits per read.