Visualisation of mapped sequencing reads

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

Define in- and output directories in case of running script separately:

```
## [1] "C:/Users/nikla/Desktop/readmap_fin/read-mapping/data/Ecoli_genome.fasta"
```

```
## [1] "2023-01-27_NC_000913.3 Escherichia coli str. K-12 substr. MG1655, complete genome.csv"
```

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

Importing data from /output/*.csv

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

# mapped = mapped[50:60,]

mapped = mapped %>%
  mutate_at(vars(Sense, Antisense), ~map(strsplit(. ,split=","), ~map_int(.x, as.integer)))
# 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),length(anti)))))
```

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 reads mapped to the E.coli genome.") +
  theme_classic()
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
```

```
p2 <- ggplot(reads) +
  geom_histogram(data = reads[reads$strand == "s",],aes(x = pos/10^6, y = ..count..),
                 bins = 155,color="lightblue",lwd = 0.2,fill="#0040ff") +
  geom_histogram(data = reads[reads$strand == "a",],aes(x = pos/10^6, y = -..count..),
                 bins = 155,color="orange",lwd = 0.2,fill="#ff4000") +
```

```
  scale_y_continuous(labels = abs) +
  labs(x = "Genome Position in Mb", y = "reads mapped per 30 Kb segment",
       caption = "Fig 2: Orientation of mapped Reads") +
  theme_classic()


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 = 10)) +
  ## 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")

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

```
## Warning: The dot-dot notation (`..count..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(count)` instead.
```

```
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")

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", guide = "none")+
  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")
```

Saving figures to file

```
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
```

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

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

Figures 1 - 5

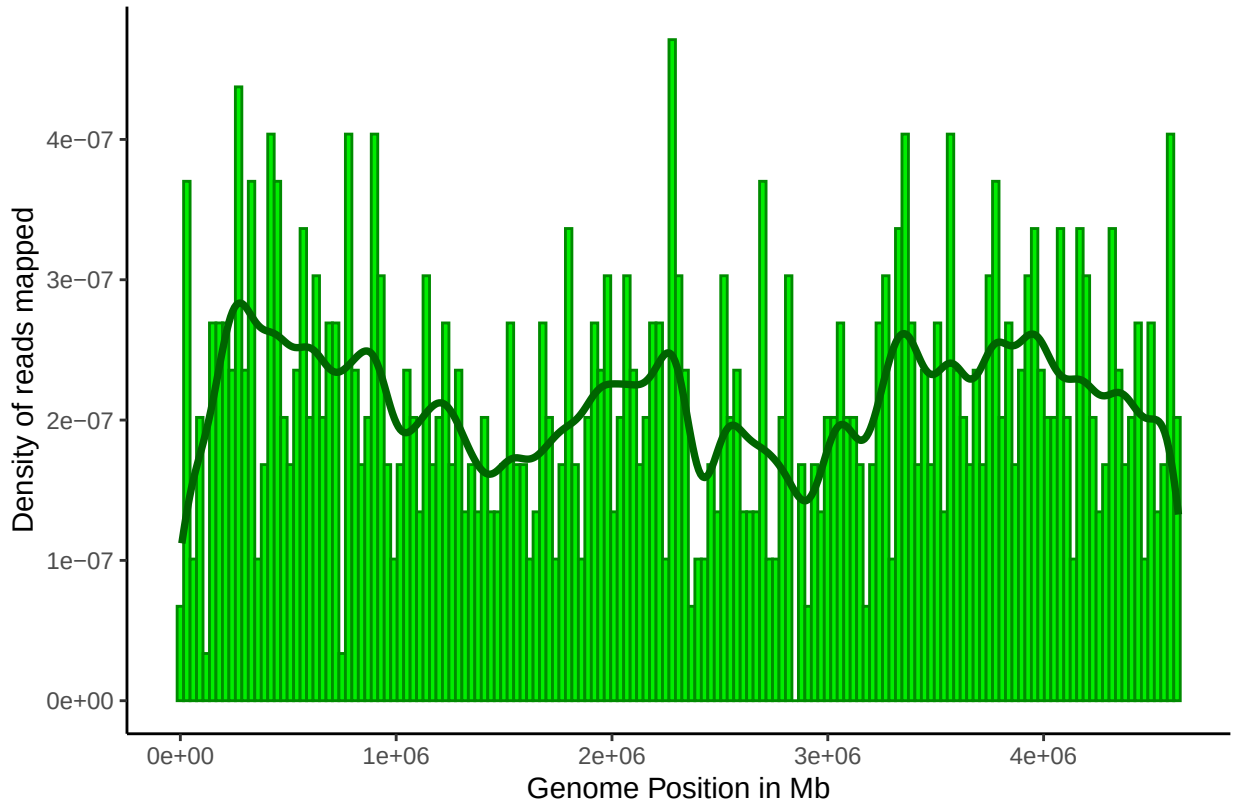


Fig. 1: Density of the reads mapped to the E.coli genome.

Description Fig 1: Density of reads mapped to the E.coli genome. Each bin size represents a 30 kb long segment along the genome.

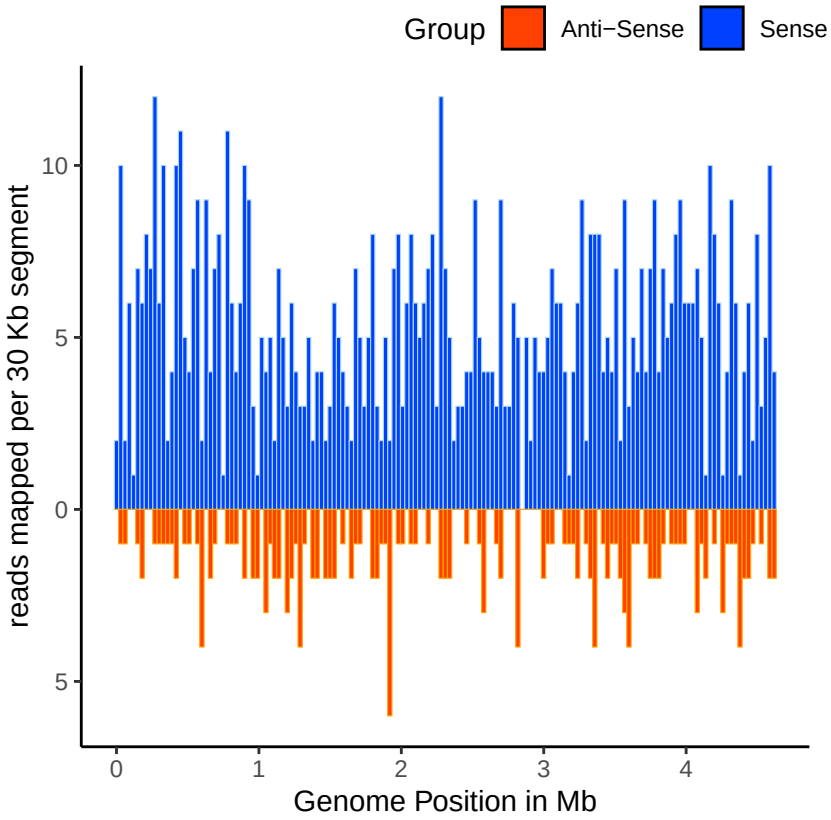


Fig 2: Orientation of mapped Reads

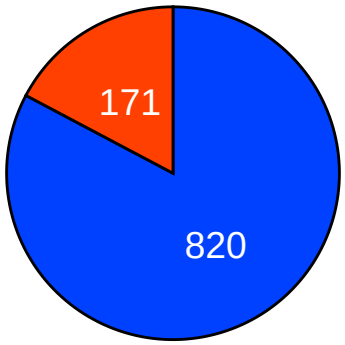
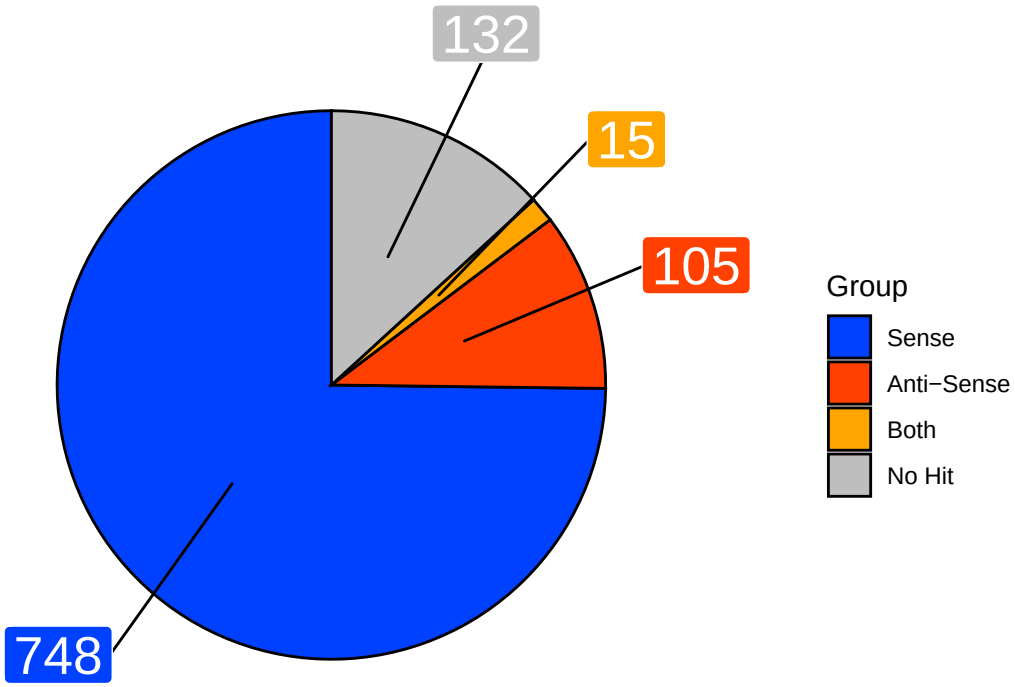
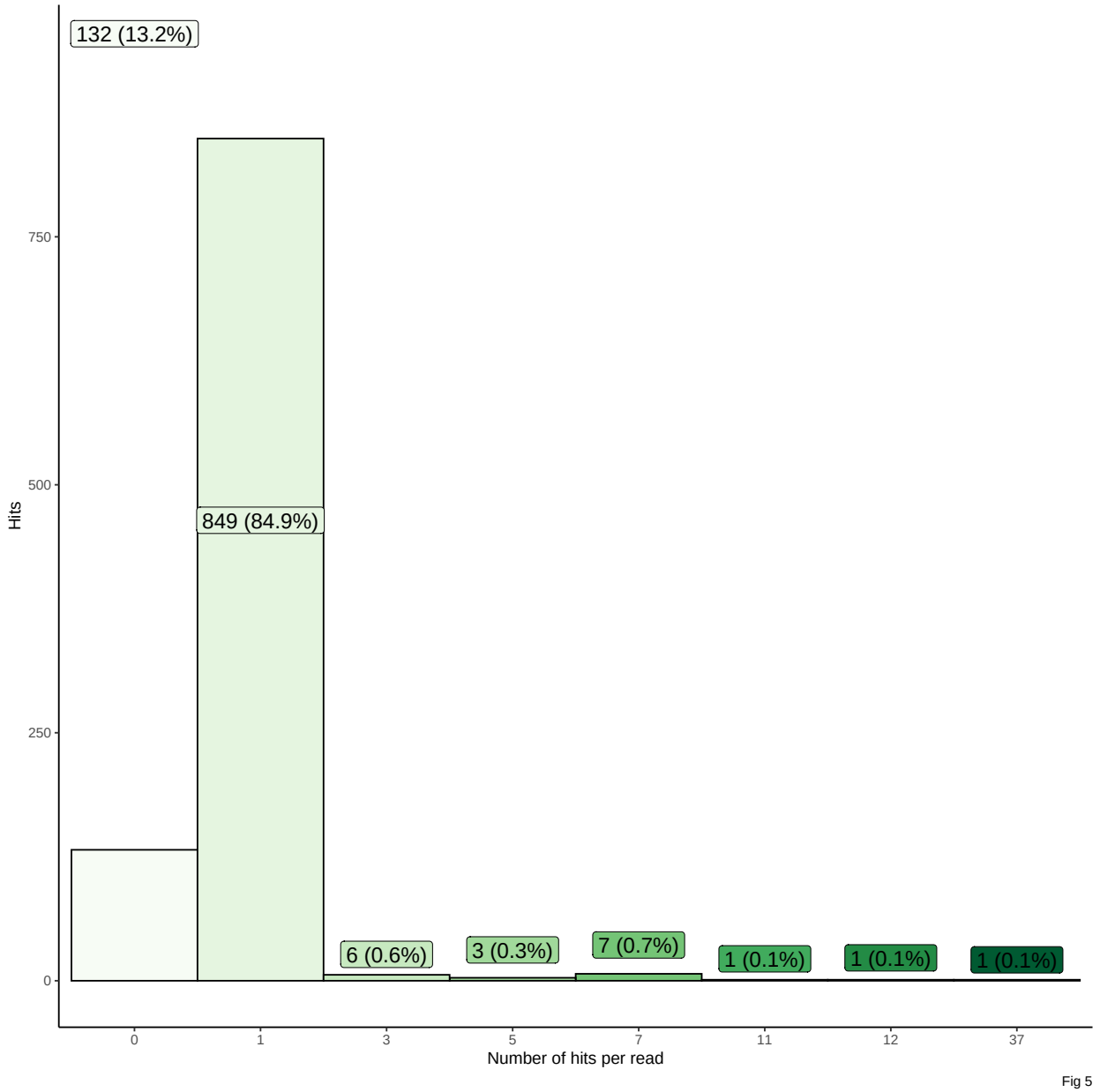


Fig 3

Description Fig 2: Sense vs. Antisense density of mapped reads. The y-axis shows a number of counts per 30 Kb segment.
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. Most reads occur once, few at higher frequencies in the genome.