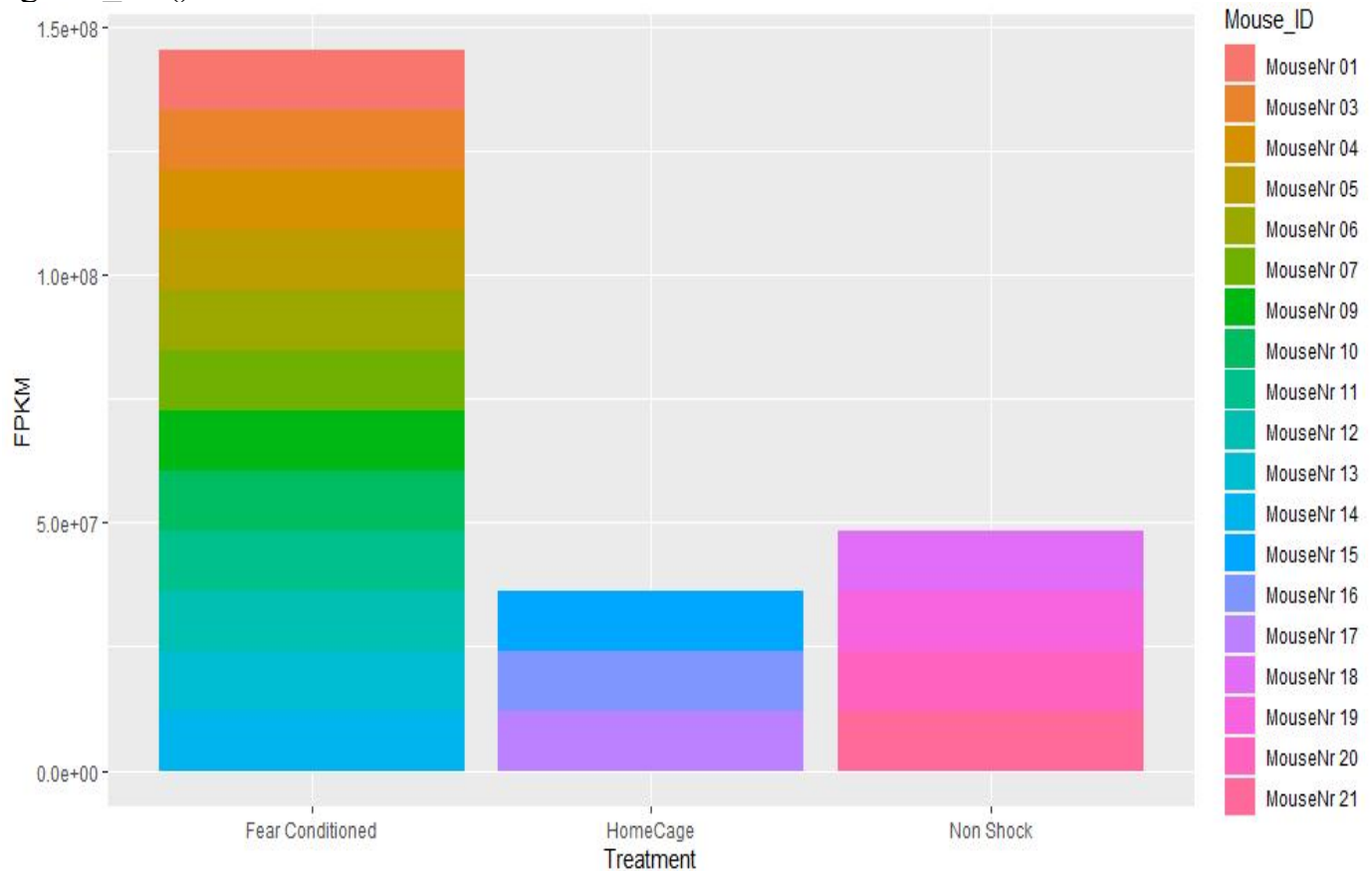


# HackBio Transcriptomics Task 3 Visualization

## # 1. Bar plot

```
dat.long %>%  
  filter(FPKM >= 50) %>%  
  filter(!is.na(Treatment)) %>%  
  ggplot(., aes(x = Treatment, y = FPKM, fill = Mouse_ID)) +  
  geom_col()
```

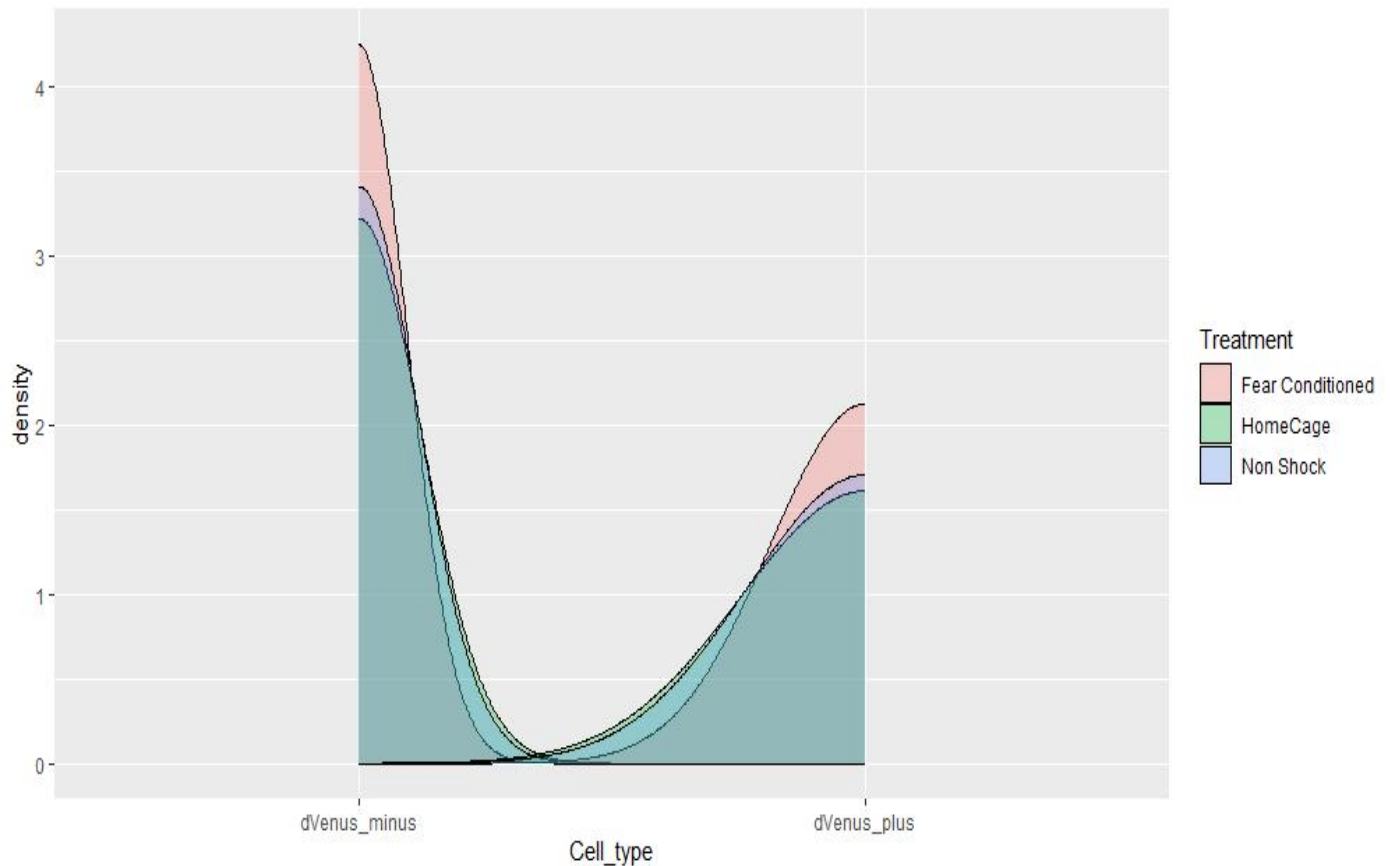


This plot shows the gene counts for the fear conditioned, home caged, and non-shocked treatment. It also fills in the Mouse\_ID to show us how the types of mice that were used for the experiment compare to each other based on the treatments they underwent.

As we can see from this plot, the mice that were treated under fear condition had the highest gene counts followed by the non-shocked mice, while the home caged mice showed the least gene counts.

## # 2. Density plot

```
dat.long %>%  
  filter(FPKM >= 50) %>%  
  filter(!is.na(Treatment)) %>%  
  ggplot(., aes(x = Cell_type, fill = Treatment)) +  
  geom_density(alpha = 0.3)
```

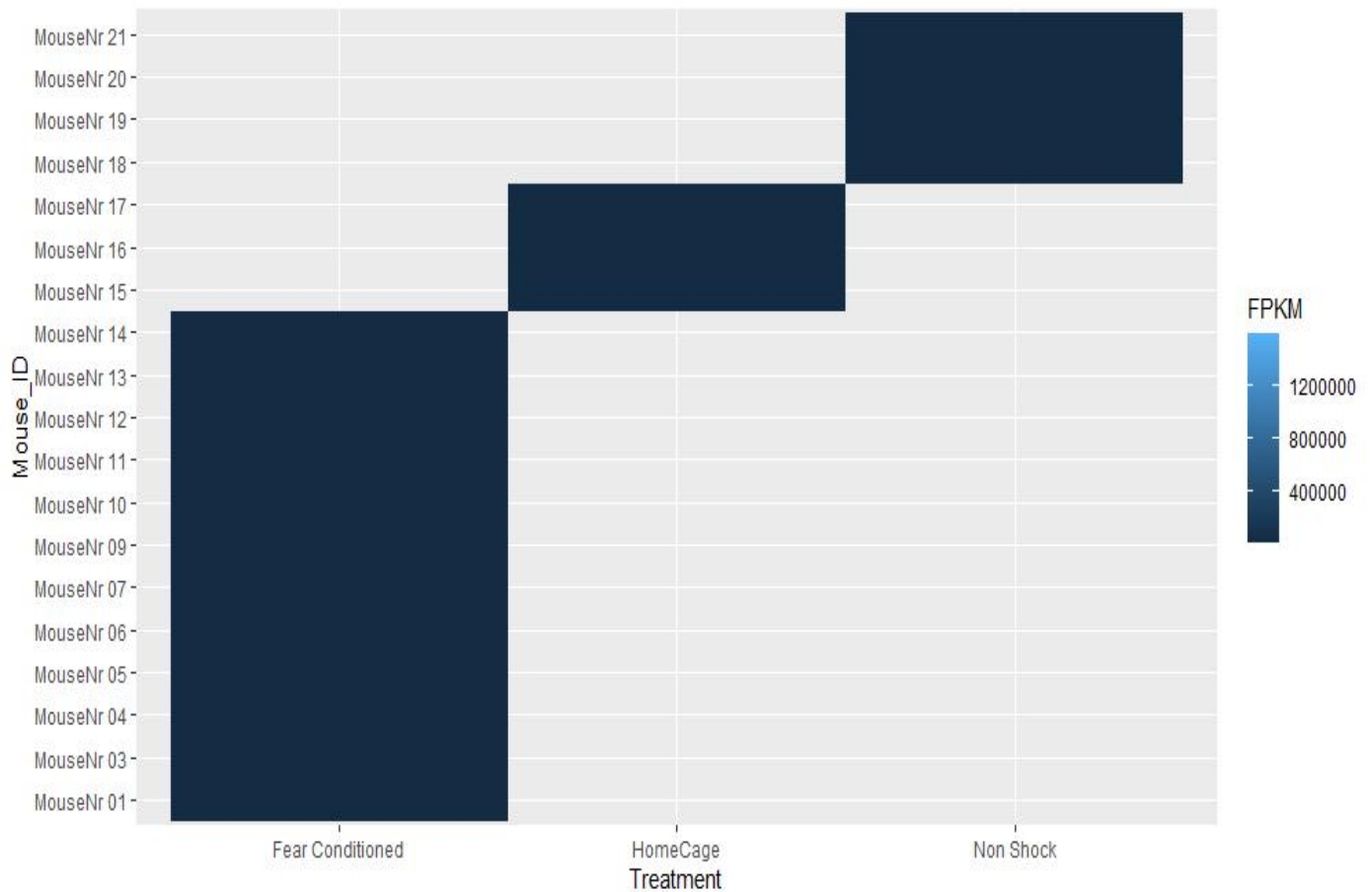


The density plot represents a comparison between our cell types. The two cell types used for this analysis are dVenus\_minus and dVenus\_plus. dVenus\_minus from the plot can be seen to be denser than dVenus\_plus. Also, this plot is filled with the “Treatment” to show the distribution of the treatments. We can see that the fear conditioned mice showed the highest distribution of cell types followed by the home caged and finally the Non-shock treated mice.

### # 3. Heat map

```
mouse.of.interest <- c("MouseNr 01","MouseNr 02","MouseNr 03","MouseNr 04",
  "MouseNr 05","MouseNr 06","MouseNr 07","MouseNr 08",
  "MouseNr 09","MouseNr 10","MouseNr 11","MouseNr 12",
  "MouseNr 13","MouseNr 14","MouseNr 15","MouseNr 16",
  "MouseNr 17","MouseNr 18","MouseNr 19","MouseNr 20",
  "MouseNr 21")

dat.long %>%
  filter(Mouse_ID%in%mouse.of.interest) %>%
  filter(FPKM >= 50) %>%
  filter(!is.na(Mouse_ID)) %>%
  ggplot(., aes(x = Treatment, y = Mouse_ID, fill = FPKM)) +
  geom_tile()
```



The heat map generated shows that the gene count for all the samples are below 400,000. Fear condition showed the highest and was used on Mice with ID numbers “MouseNr01 to MouseNr14”. The non-shocked had the moderate gene count that were expressed in “MouseNr18 to MouseNr21”. Finally, the home cage mice posses the lowest gene count for “MouseNr15 to MouseNr17”.