

```

library(ggplot2)

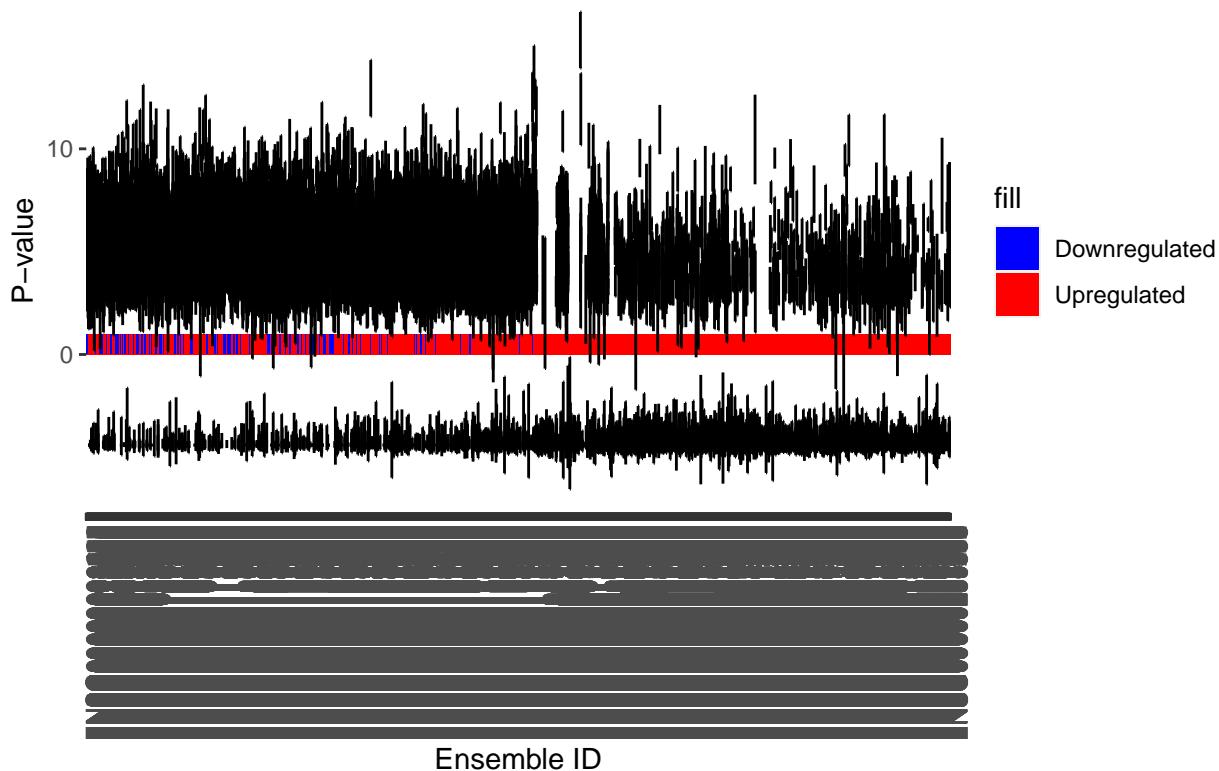
## Warning: package 'ggplot2' was built under R version 4.2.3

# Read the CSV file into a data frame
gene_data <- read.csv("results.csv")

# Create a bar plot with error bars
ggplot(gene_data, aes(x = Ensemble_id)) +
  geom_bar(aes(y = pvaldown, fill = "Downregulated"), stat = "identity", width = 0.5) +
  geom_bar(aes(y = pvalup, fill = "Upregulated"), stat = "identity", width = 0.5) +
  geom_errorbar(aes(ymin = mean - std.dev, ymax = mean + std.dev), width = 0.2) +
  labs(x = "Ensemble ID", y = "P-value") +
  scale_fill_manual(values = c("Downregulated" = "blue", "Upregulated" = "red")) +
  theme(axis.text.x = element_text(angle = 90, hjust = 1)) +
  ggtitle("Gene Expression Analysis")

```

## Gene Expression Analysis



```

# Create a scatter plot for downregulated and upregulated genes
ggplot(gene_data, aes(x = log2(mean), y = -log10(pvaldown), color = "Downregulated")) +
  geom_point() +
  geom_point(data = gene_data, aes(x = log2(mean), y = -log10(pvalup), color = "Upregulated")) +
  labs(x = "Log2 Fold Change", y = "-log10(p-value)") +
  scale_color_manual(values = c("Downregulated" = "blue", "Upregulated" = "red")) +
  ggtitle("Gene Expression Scatter Plot")

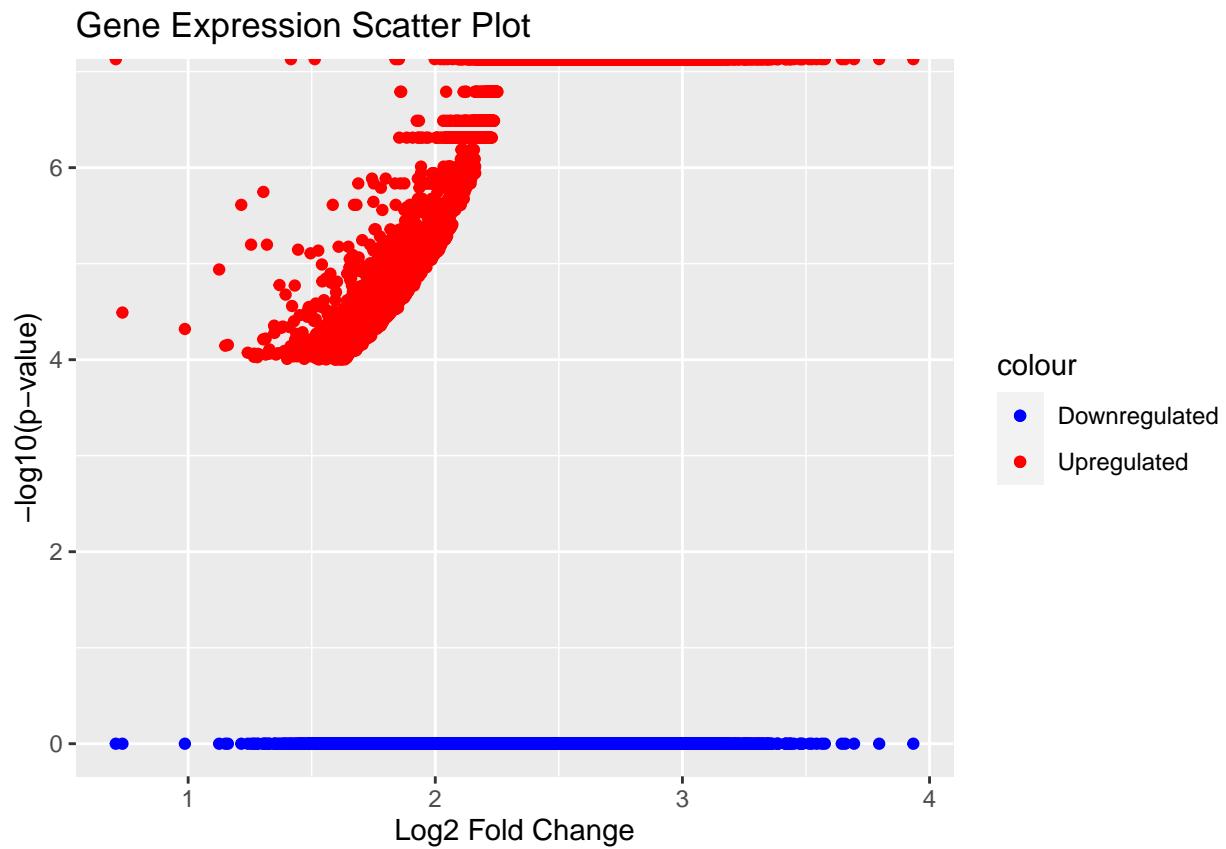
```

```

## Warning in FUN(X[[i]], ...): NaNs produced
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning in FUN(X[[i]], ...): NaNs produced

## Warning: Removed 8247 rows containing missing values ('geom_point()').
## Removed 8247 rows containing missing values ('geom_point()').

```

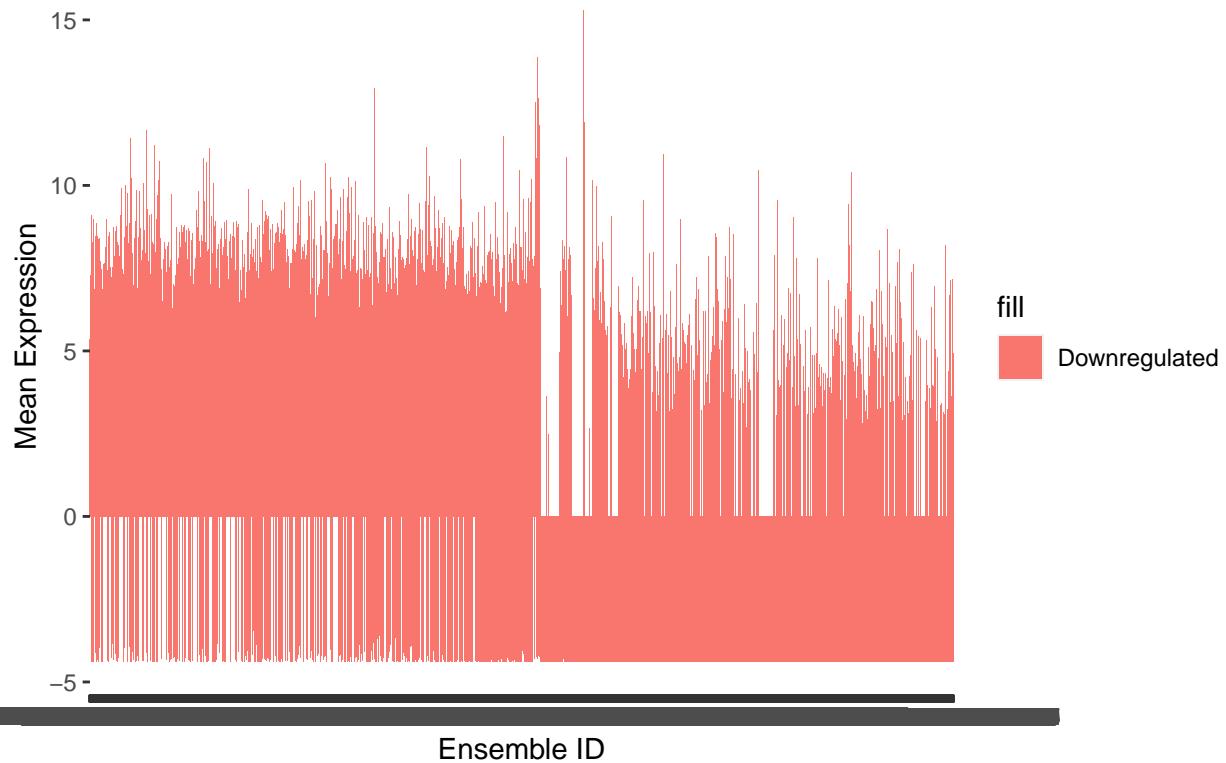


```

library(ggplot2)
ggplot(gene_data, aes(x = Ensemble_id, y = mean, fill = "Downregulated")) +
  geom_bar(stat = "identity") +
  labs(x = "Ensemble ID", y = "Mean Expression") +
  ggtitle("Mean Expression of Downregulated Genes")

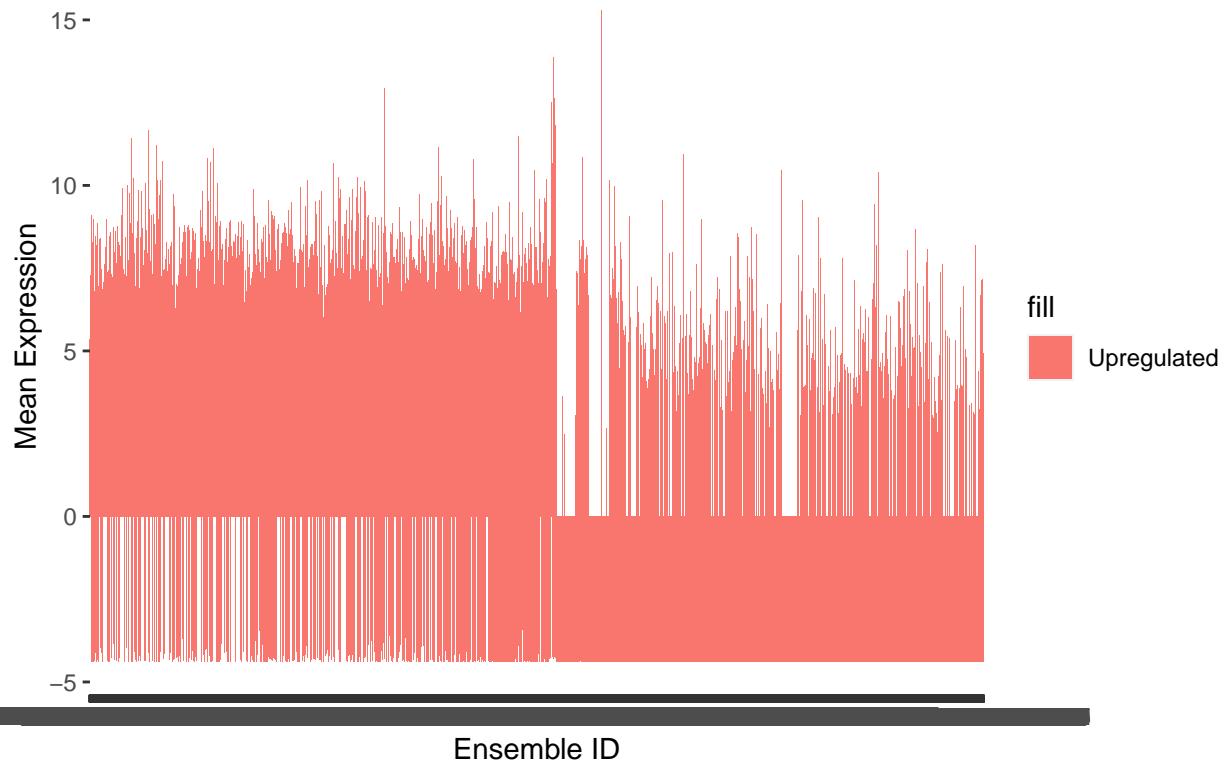
```

## Mean Expression of Downregulated Genes



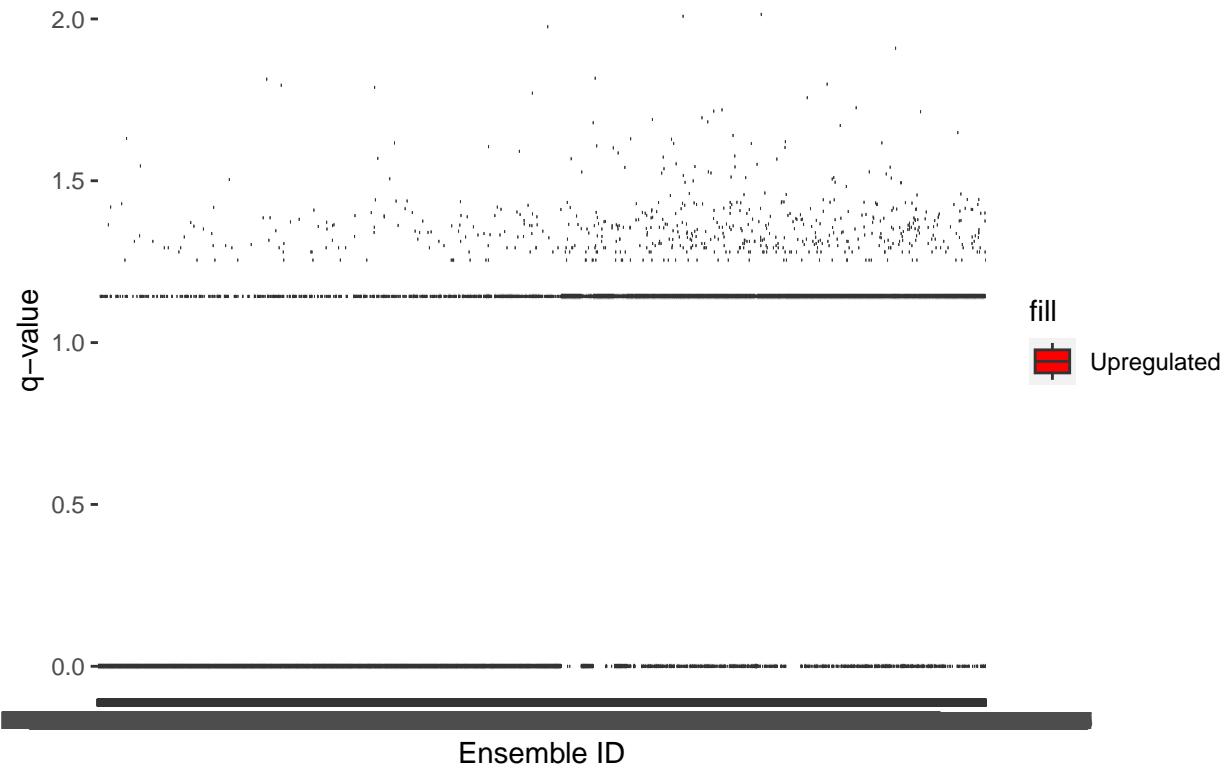
```
ggplot(gene_data, aes(x = Ensemble_id, y = mean, fill = "Upregulated")) +  
  geom_bar(stat = "identity") +  
  labs(x = "Ensemble ID", y = "Mean Expression") +  
  ggtitle("Mean Expression of Upregulated Genes")
```

## Mean Expression of Upregulated Genes

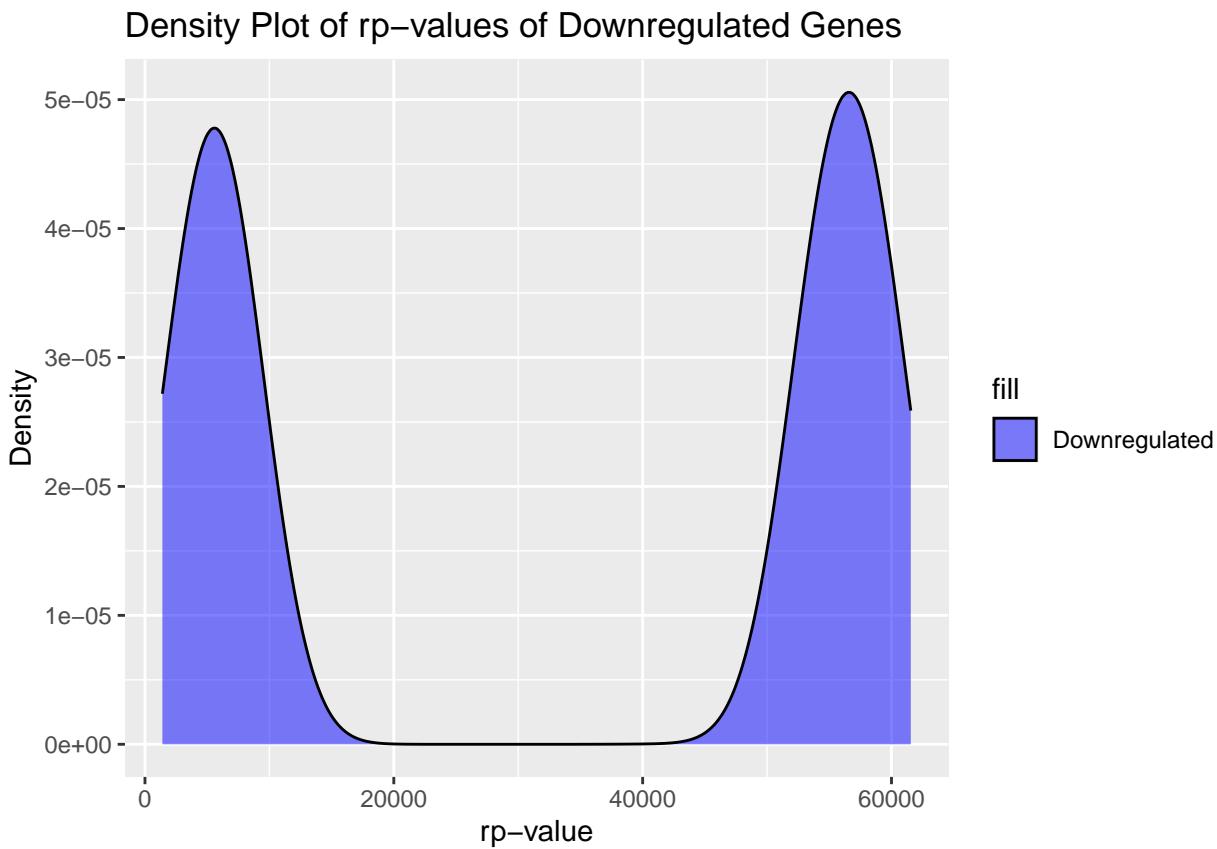


```
ggplot(gene_data, aes(x = factor(Ensemble_id), y = qvalup, fill = "Upregulated")) +  
  geom_boxplot() +  
  labs(x = "Ensemble ID", y = "q-value") +  
  scale_fill_manual(values = "red") +  
  ggtitle("q-values of Upregulated Genes")
```

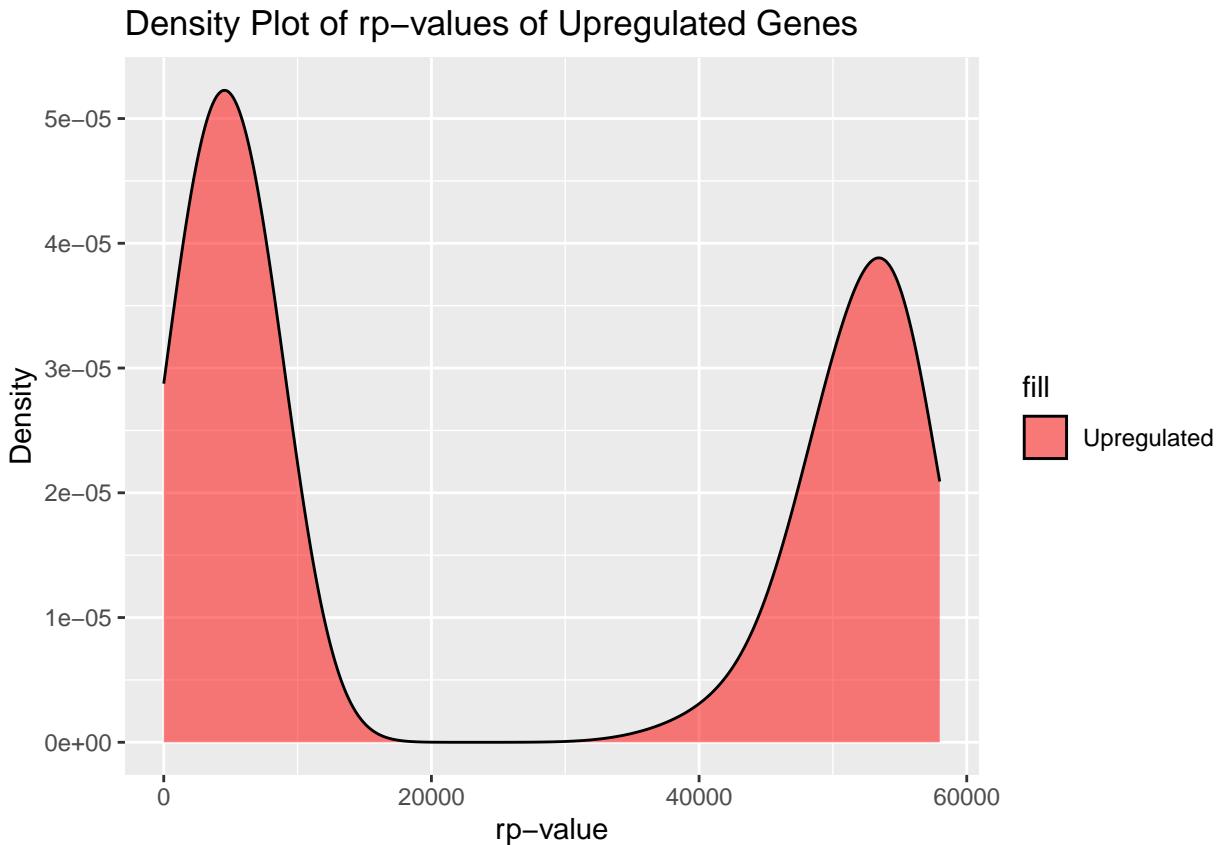
## q-values of Upregulated Genes



```
ggplot(gene_data, aes(x = rpvaldown, fill = "Downregulated")) +  
  geom_density(alpha = 0.5) +  
  labs(x = "rp-value", y = "Density") +  
  scale_fill_manual(values = "blue") +  
  ggtitle("Density Plot of rp-values of Downregulated Genes")
```

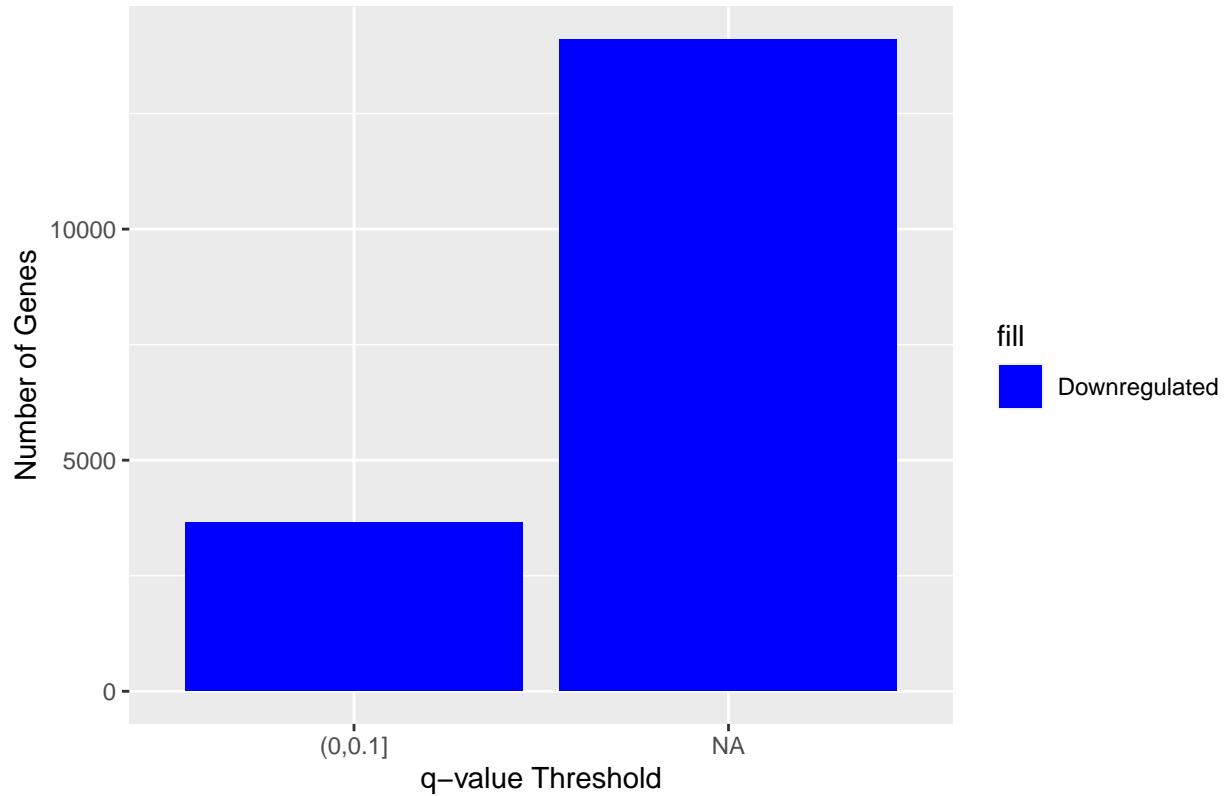


```
ggplot(gene_data, aes(x = rpvalup, fill = "Upregulated")) +  
  geom_density(alpha = 0.5) +  
  labs(x = "rp-value", y = "Density") +  
  scale_fill_manual(values = "red") +  
  ggtitle("Density Plot of rp-values of Upregulated Genes")
```

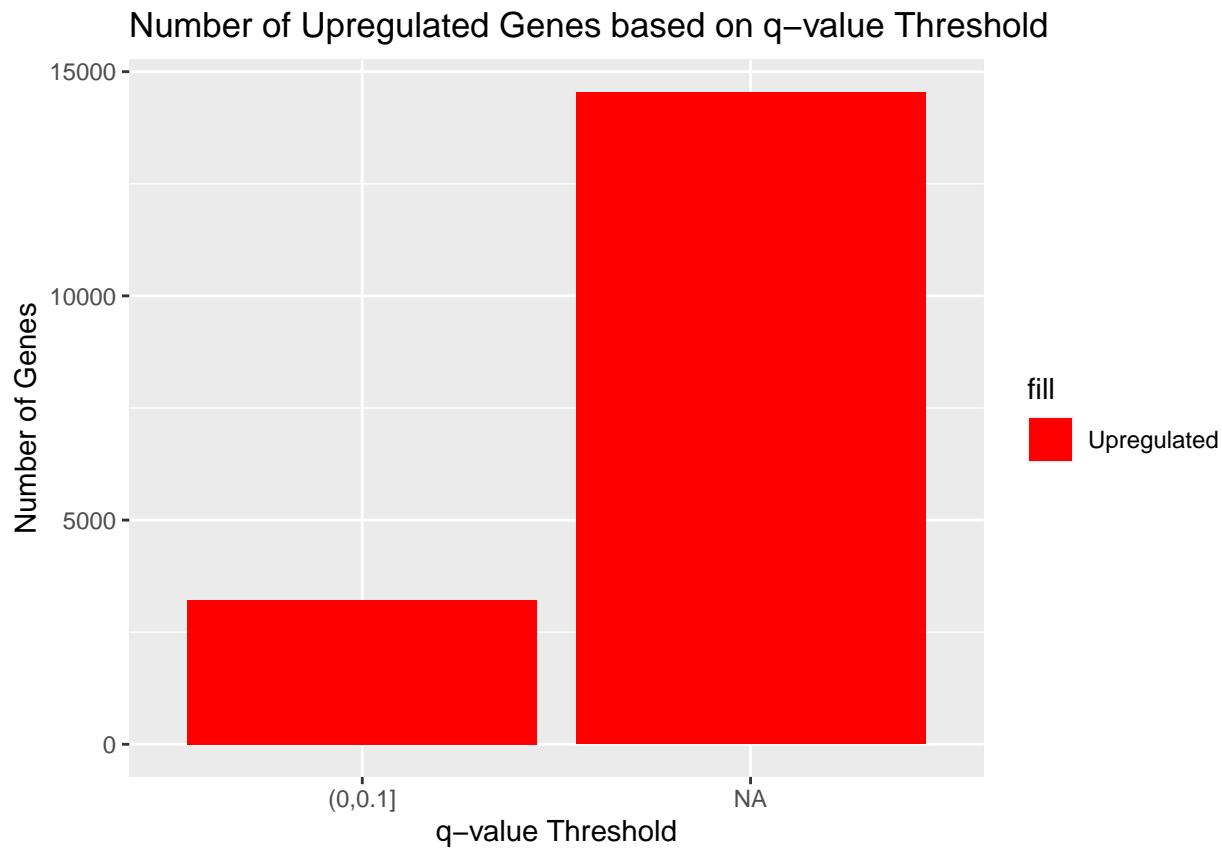


```
gene_data$qvaldown_bin <- cut(gene_data$qvaldown, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = qvaldown_bin, fill = "Downregulated")) +
  geom_bar() +
  labs(x = "q-value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = "blue") +
  ggtitle("Number of Downregulated Genes based on q-value Threshold")
```

## Number of Downregulated Genes based on q–value Threshold

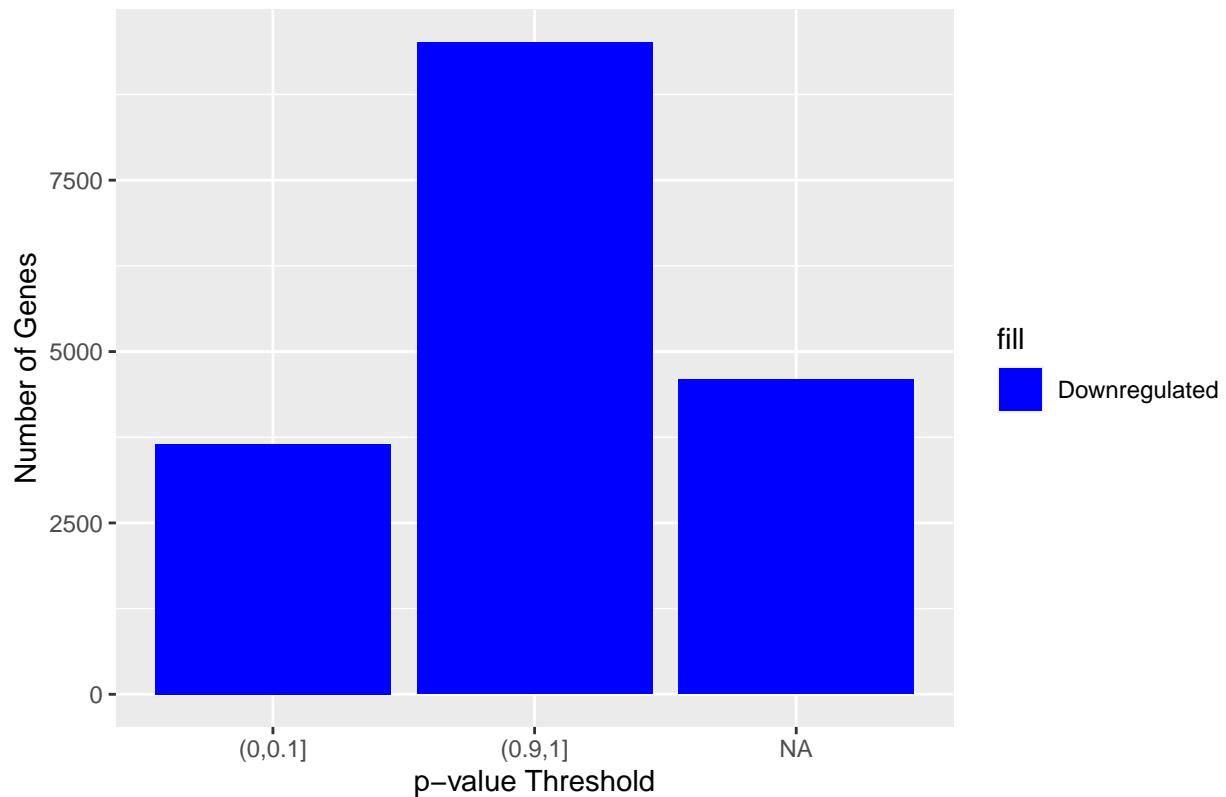


```
gene_data$qvalup_bin <- cut(gene_data$qvalup, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = qvalup_bin, fill = "Upregulated")) +
  geom_bar() +
  labs(x = "q–value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = "red") +
  ggtitle("Number of Upregulated Genes based on q–value Threshold")
```



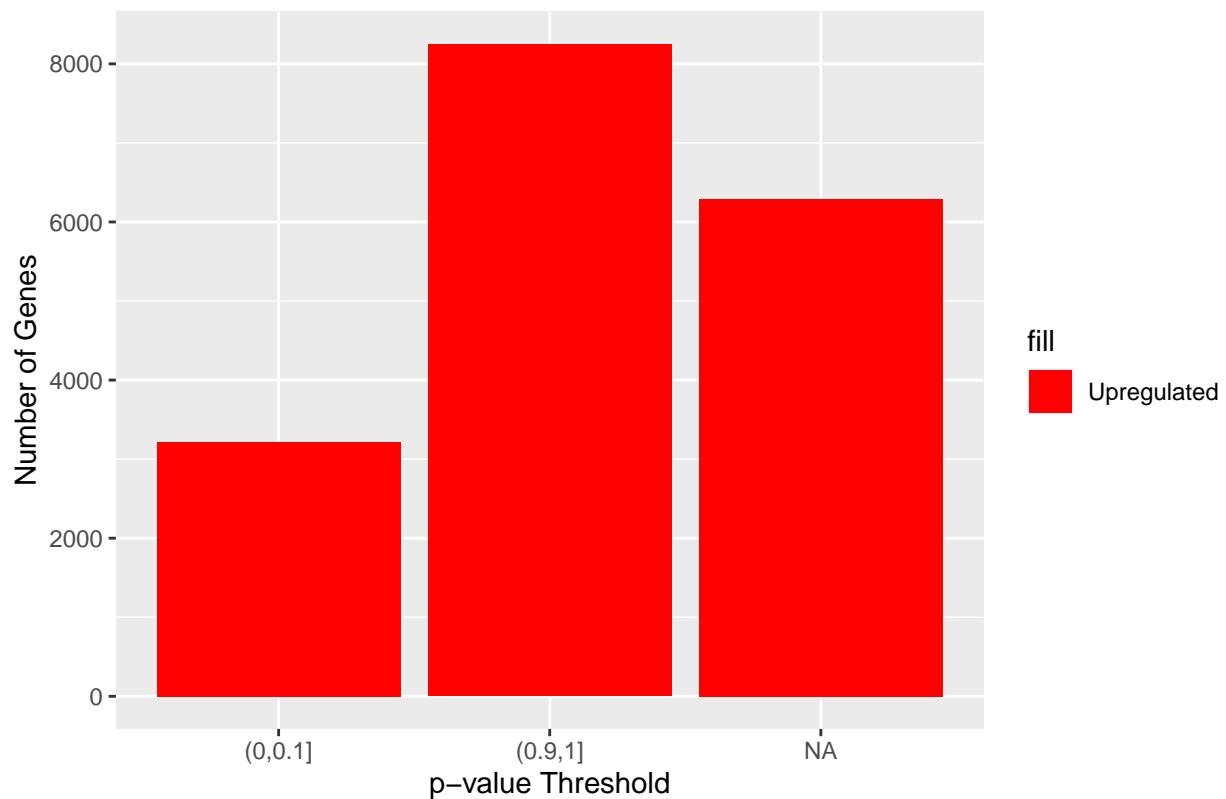
```
gene_data$pvaldown_bin <- cut(gene_data$pvaldown, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = pvaldown_bin, fill = "Downregulated")) +
  geom_bar() +
  labs(x = "p-value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = "blue") +
  ggtitle("Number of Downregulated Genes based on p-value Threshold")
```

### Number of Downregulated Genes based on p-value Threshold



```
gene_data$pvalup_bin <- cut(gene_data$pvalup, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = pvalup_bin, fill = "Upregulated")) +
  geom_bar() +
  labs(x = "p-value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = "red") +
  ggtitle("Number of Upregulated Genes based on p-value Threshold")
```

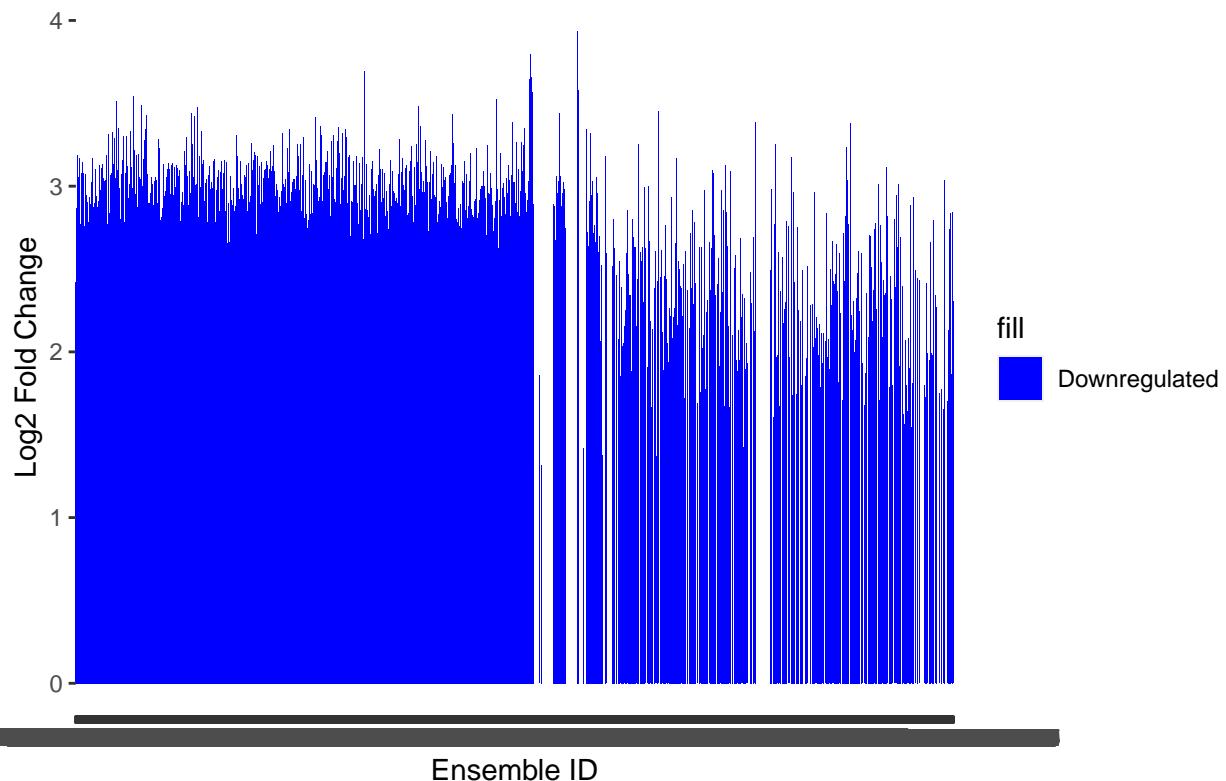
### Number of Upregulated Genes based on p-value Threshold



```
ggplot(gene_data, aes(x = Ensemble_id, y = log2(mean), fill = "Downregulated")) +  
  geom_bar(stat = "identity") +  
  labs(x = "Ensemble ID", y = "Log2 Fold Change") +  
  scale_fill_manual(values = "blue") +  
  ggtitle("Log2 Fold Change of Downregulated Genes (Bar Plot)")
```

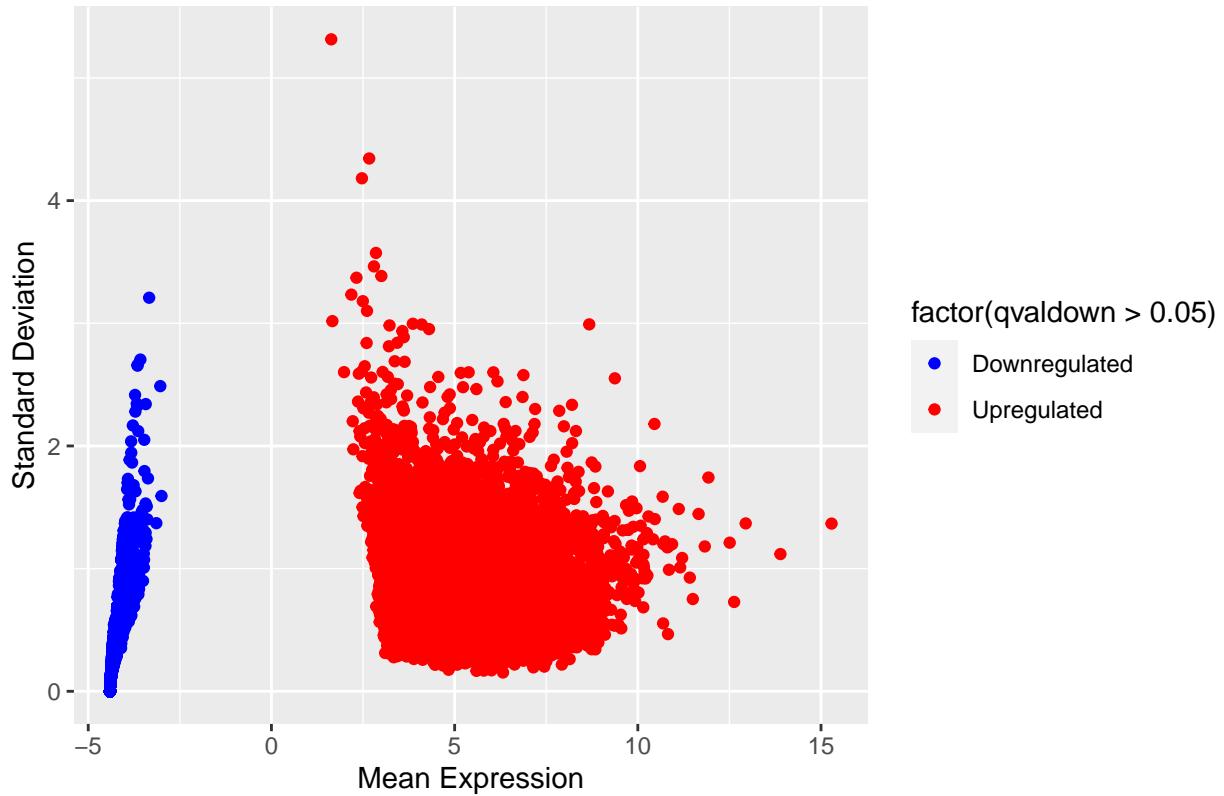
```
## Warning in FUN(X[[i]], ...): NaNs produced  
## Warning in FUN(X[[i]], ...): NaNs produced  
## Warning: Removed 8247 rows containing missing values ('position_stack()').
```

## Log2 Fold Change of Downregulated Genes (Bar Plot)



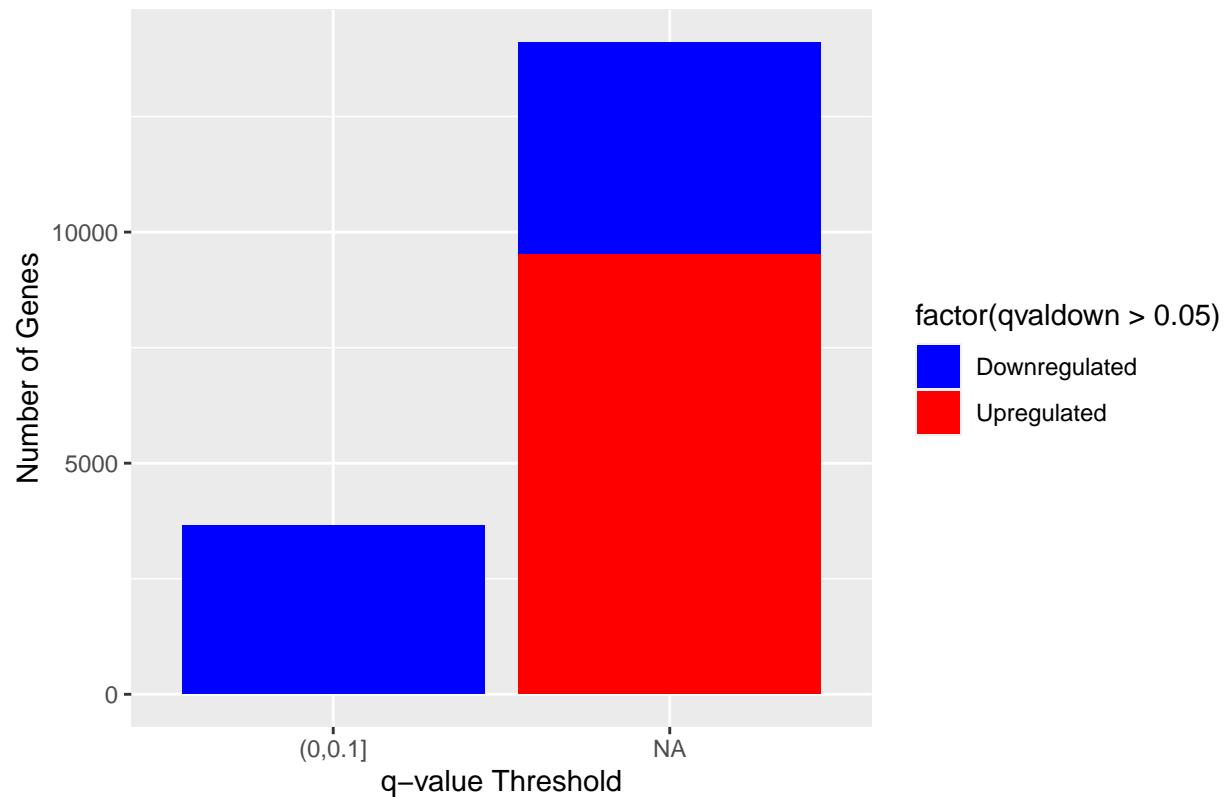
```
ggplot(gene_data, aes(x = mean, y = std.dev, color = factor(qvaldown > 0.05))) +  
  geom_point() +  
  labs(x = "Mean Expression", y = "Standard Deviation") +  
  scale_color_manual(values = c("blue", "red"), labels = c("Downregulated", "Upregulated")) +  
  ggtitle("Mean Expression vs. Standard Deviation of Genes (Color by Regulation)")
```

## Mean Expression vs. Standard Deviation of Genes (Color by Regulation)



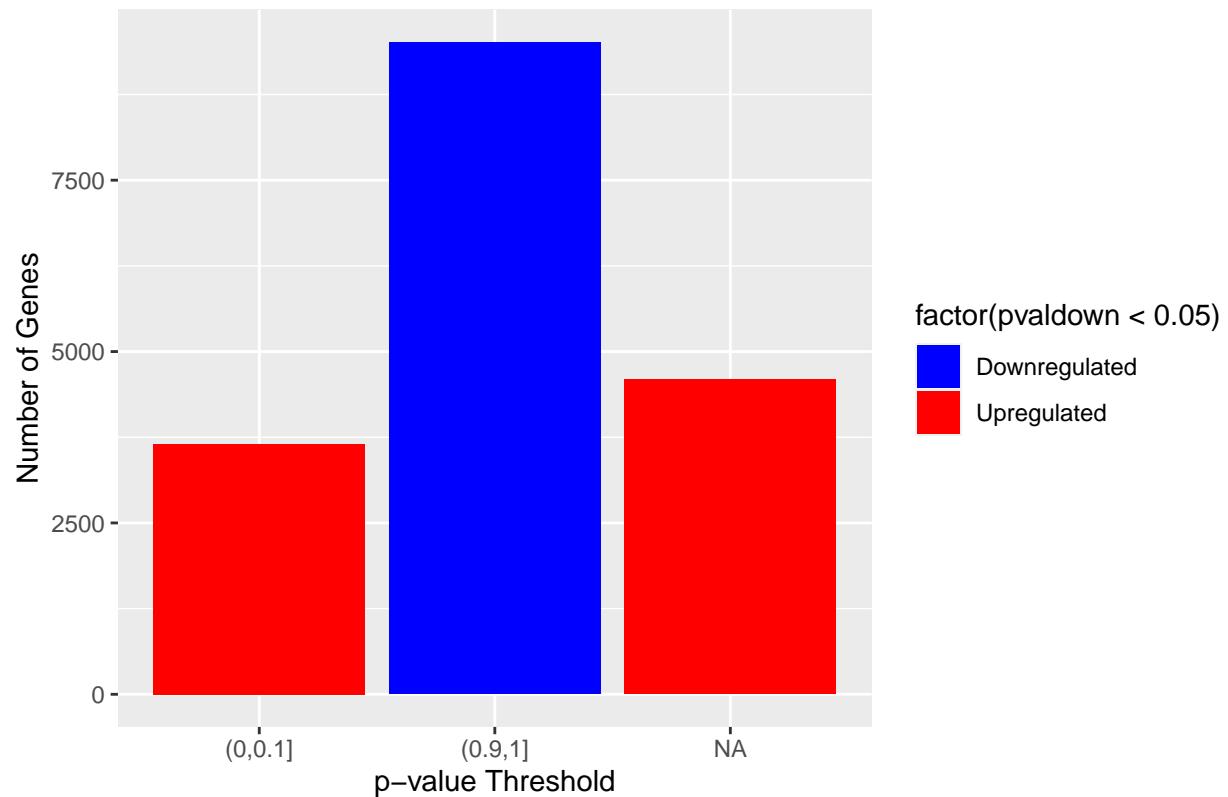
```
gene_data$qvaldown_bin <- cut(gene_data$qvaldown, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = qvaldown_bin, fill = factor(qvaldown > 0.05))) +
  geom_bar() +
  labs(x = "q-value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = c("blue", "red"), labels = c("Downregulated", "Upregulated")) +
  ggtitle("Number of Downregulated and Upregulated Genes based on q-value Threshold")
```

## Number of Downregulated and Upregulated Genes based on q-value Threshold

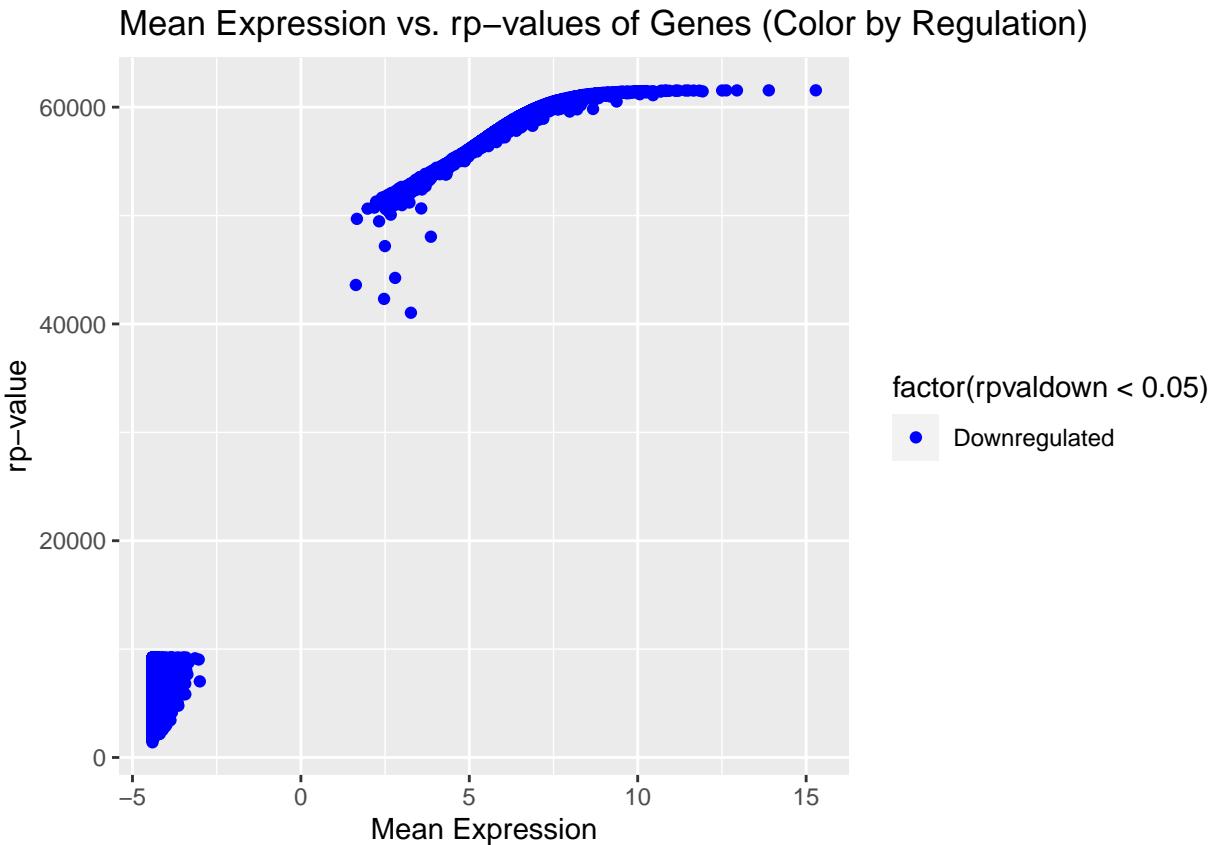


```
gene_data$pvaldown_bin <- cut(gene_data$pvaldown, breaks = seq(0, 1, by = 0.1))
ggplot(gene_data, aes(x = pvaldown_bin, fill = factor(pvaldown < 0.05))) +
  geom_bar() +
  labs(x = "p-value Threshold", y = "Number of Genes") +
  scale_fill_manual(values = c("blue", "red"), labels = c("Downregulated", "Upregulated")) +
  ggtitle("Number of Downregulated and Upregulated Genes based on p-value Threshold")
```

## Number of Downregulated and Upregulated Genes based on p-value Threshold



```
ggplot(gene_data, aes(x = mean, y = rpvaldown, color = factor(rpvaldown < 0.05))) +  
  geom_point() +  
  labs(x = "Mean Expression", y = "rp-value") +  
  scale_color_manual(values = c("blue", "red"), labels = c("Downregulated", "Upregulated")) +  
  ggtitle("Mean Expression vs. rp-values of Genes (Color by Regulation)")
```



```
ggplot(gene_data, aes(x = factor(Ensemble_id), y = log2(mean), fill = factor(qvaldown > 0.05))) +
  geom_boxplot() +
  labs(x = "Ensemble ID", y = "Log2 Fold Change") +
  scale_fill_manual(values = c("blue", "red"), labels = c("Downregulated", "Upregulated")) +
  ggtitle("Log2 Fold Change of Downregulated and Upregulated Genes (Box Plot)")
```

```
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning in FUN(X[[i]], ...): NaNs produced
## Warning: Removed 8247 rows containing non-finite values ('stat_boxplot()').
```

### Log2 Fold Change of Downregulated and Upregulated Genes (Box Plot)

