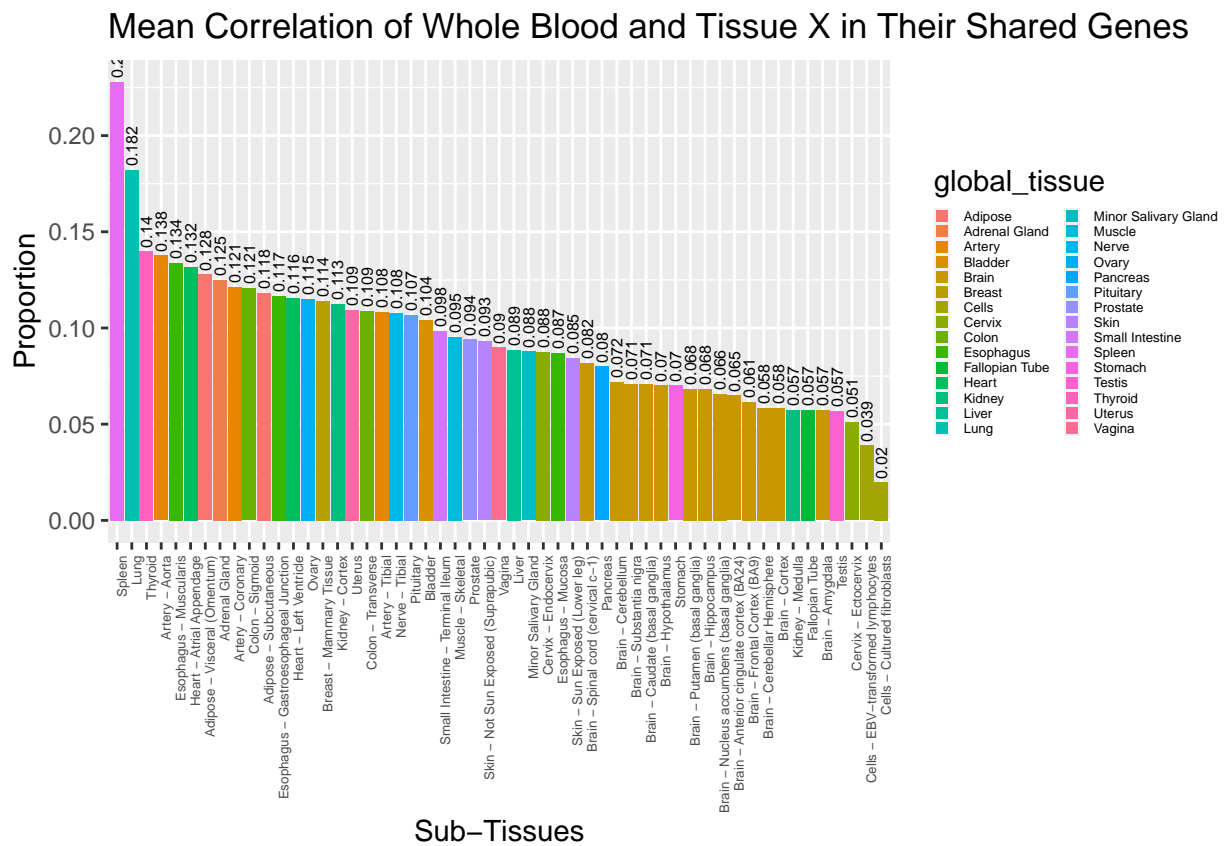# Untitled

R Markdown

```
## Loading required package: edgeR
```
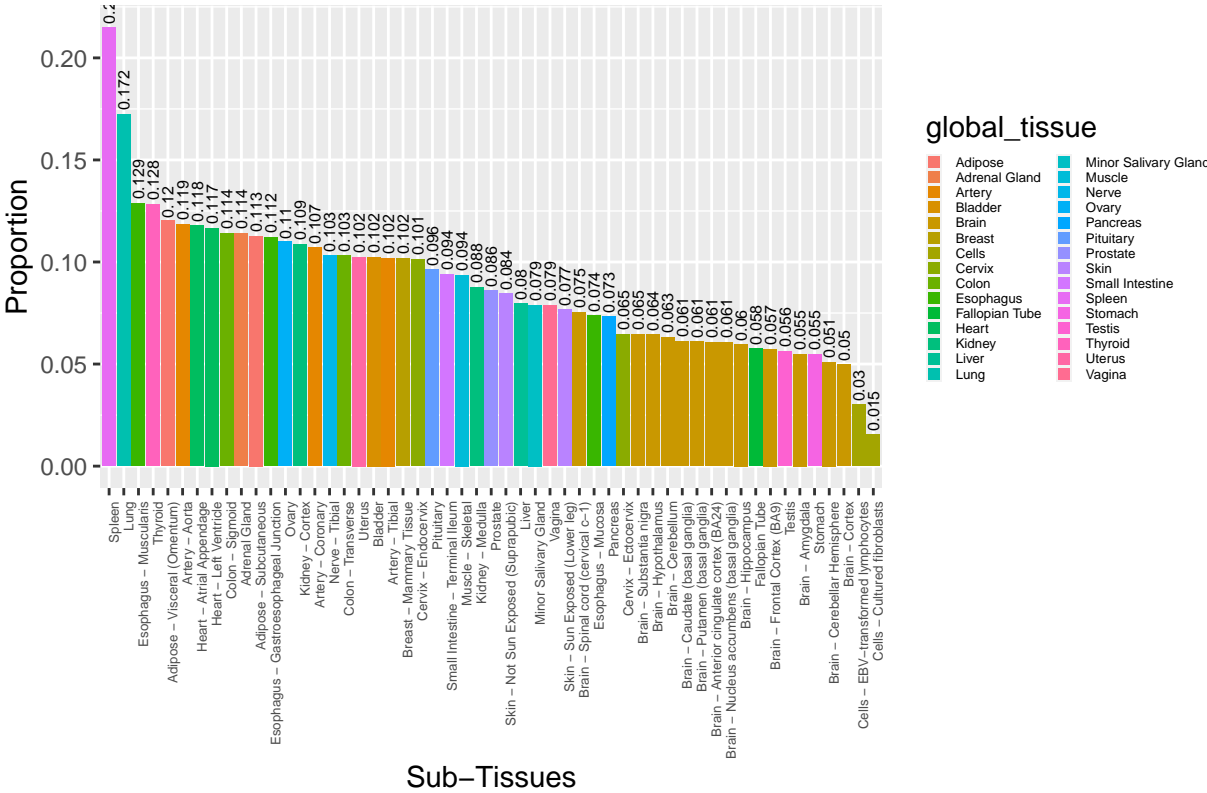
```
## Loading required package: limma
```

```r
blood_shared_genes_unique = unique(blood_shared_genes)
```
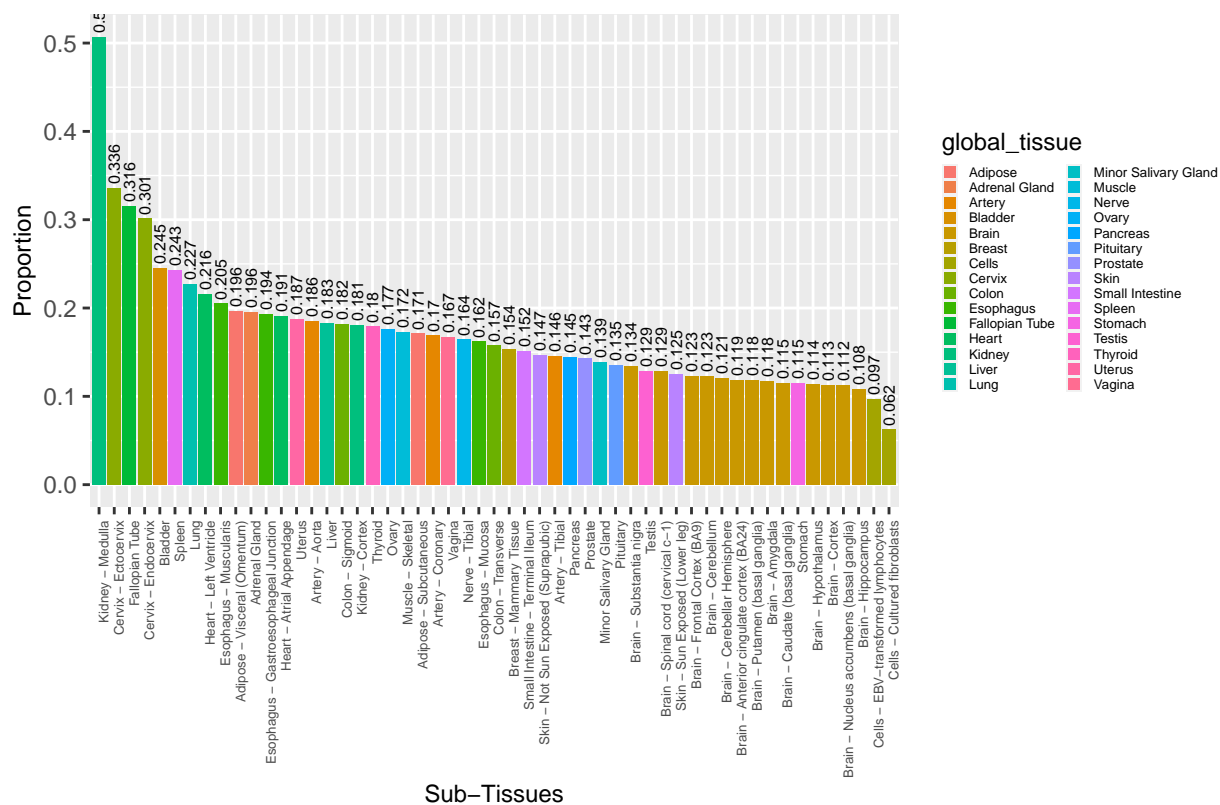
```r
corr_stats_list = corr_stats_list[!(corr_stats_list$tissueX=="Whole Blood"),]
```


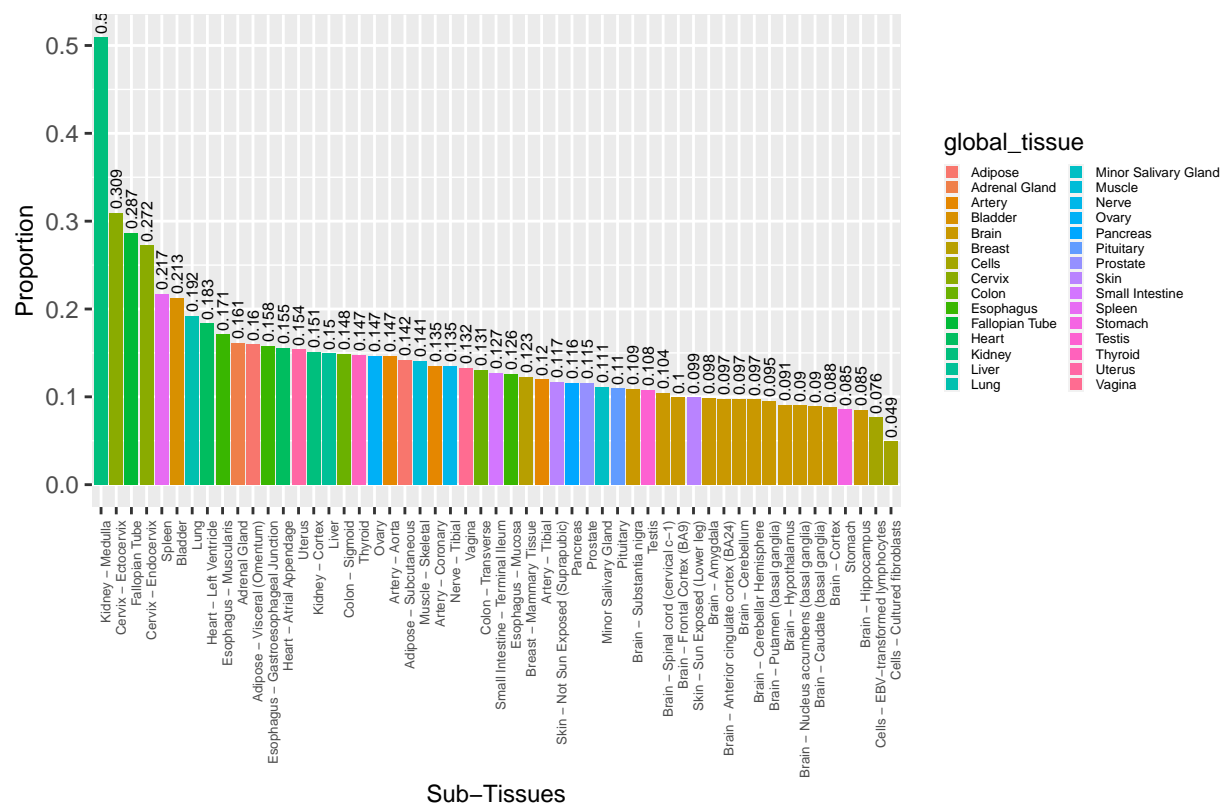Mean Correlation of Whole Blood and Tissue X in Their Shared Genes

Median Correlation of Whole Blood and Tissue X in Their Shared Genes

Mean of Absolute Correlation of Whole Blood and Tissue X in Their Shared Genes

Median of Absolute Correlation of Whole Blood and Tissue X in Their Shared Genes
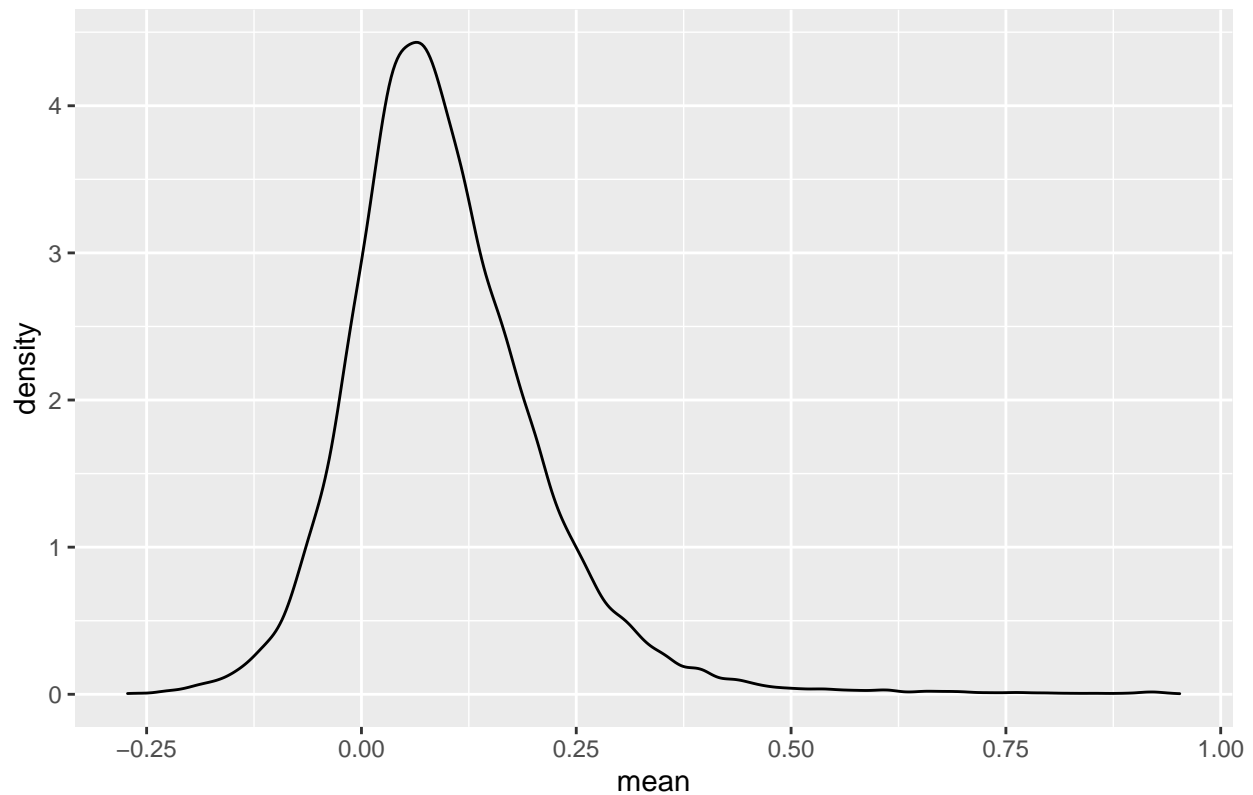


```r
mean_correlation_gene = data.frame(gene=blood_shared_genes_unique, mean=NA)
```

```r
all_mean = c()
for (gene in blood_shared_genes_unique) {
  gene_cor_list = c()
  for (i in 1:length(correlation_list)) {
  curr_df = correlation_list[[i]]
  cor = curr_df[curr_df$gene_id==gene, 2]
  gene_cor_list = c(gene_cor_list, cor)
  }
  mean_cor = mean(gene_cor_list)
  all_mean = c(all_mean, mean_cor)
}

mean_correlation_gene$mean = all_mean
```

```r
ggplot(data = mean_correlation_gene, aes(x = mean)) +
  ggtitle("Mean Correlation of Each Blood Gene with All Tissues") +
  geom_density()
```

## Mean Correlation of Each Blood Gene with All Tissues


```r
mean_abs_correlation_gene = data.frame(gene=blood_shared_genes_unique, mean=NA)
```

```r
all_mean = c()
for (gene in blood_shared_genes_unique) {
  gene_cor_list = c()
  for (i in 1:length(correlation_list)) {
  curr_df = correlation_list[[i]]
  cor = curr_df[curr_df$gene_id==gene, 2]
  cor = abs(cor)
  gene_cor_list = c(gene_cor_list, cor)
  }
  mean_cor = mean(gene_cor_list)
  all_mean = c(all_mean, mean_cor)
}

mean_abs_correlation_gene$mean = all_mean
```

```r
ggplot(data = mean_abs_correlation_gene, aes(x = mean)) +
  ggtitle("Mean Absolute Correlation of Each Blood Gene with All Tissues") +
  geom_density()
```

Mean Absolute Correlation of Each Blood Gene with All Tissues
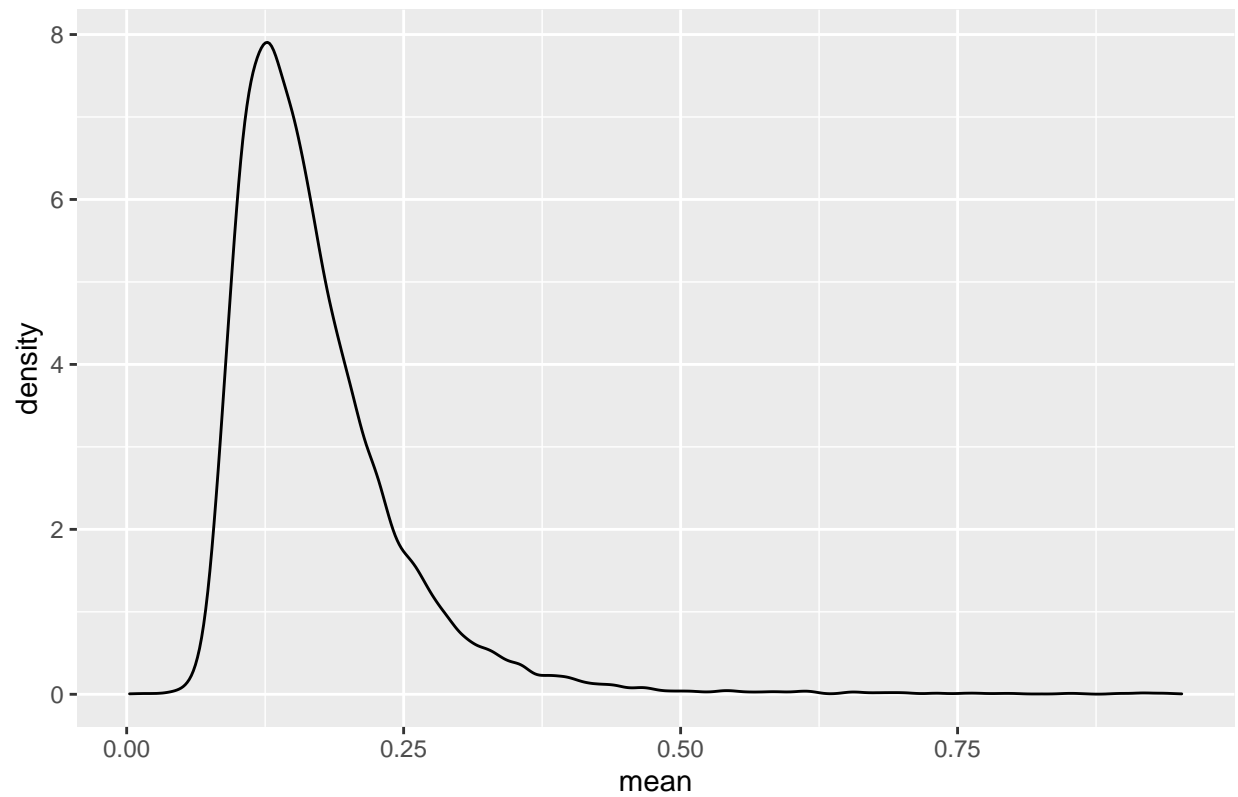

```r
save(mean_correlation_gene, file="mean_correlation_gene.Rdata")
save(mean_abs_correlation_gene, file="mean_abs_correlation_gene.Rdata")
```