Код для R:

```r
dds <- DESeqDataSetFromMatrix(counts, design, design = ~ group)

# calculating deseq ----------------------------------------------------

dds <- DESeq(dds)
resultsNames(dds)

# retrieving results ----------------------------------------------------

res <- results(dds) %>% as.data.frame() %>%
  add_genesym() %>% rownames_to_column("gene.id") %>%
  arrange(log2FoldChange, padj) %>% as_tibble()

# filtering significant ----------------------------------------------------

dge <- list()

dge$upreg <- dplyr::filter(res, log2FoldChange > 1.3 & pvalue < 0.05)
dge$downreg <- dplyr::filter(res, log2FoldChange < -1.3 & pvalue < 0.05)

dge$upreg <- dplyr::filter(res, log2FoldChange > 1.3 & padj  < 0.05)
dge$downreg <- dplyr::filter(res, log2FoldChange < -1.3 & padj < 0.05)


nrow(dge$upreg)

nrow(dge$downreg)



# Volcano plot ----------------------------------------------------

#write.csv(x = signGenes, file = "./signGenes.csv", row.names = TRUE)


pval = 0.05
lfc = 1.3
res$signGenes = (abs(res$log2FoldChange) > lfc & -log10(res$padj) > -log10(pval))
pdf("Volcano_plot_after_DES_p=0,05.pdf")
res <- res[is.na((res$signGenes))==FALSE,]
ggplot(res, aes(x=log2FoldChange,y=-log10(padj))) +
  geom_jitter(aes(colour = signGenes), size =3) +
  geom_hline(yintercept = -log10(pval), color = "green4", size = 1) +
  geom_vline(xintercept = c(-lfc, lfc), linetype='dotted', color = "blue", size = 1) +
  ggtitle(sprintf("%s", "Volcano Plot")) +
  theme(axis.text.x = element_text(size = rel(1.5), angle = 0, vjust = 0.5)) +
  theme(axis.text.y = element_text(angle = 0, vjust = 0.5, size = 8)) +
```

```
  xlim(-5,5) +

  theme_bw() + scale_fill_grey()
dev.off()
```

Кол-во ап и даунрегулированных при параметрах:
- lof2FC = 1.3
- padj = 0.05

```
> nrow(dge$upreg)
[1] 143
> nrow(dge$downreg)
[1] 90
```

При параметрах
- lof2FC = 1.3
- pval = 0.05

```
> nrow(dge$upreg)
[1] 683
> nrow(dge$downreg)
[1] 901
>
```

Построенный volcano plot при pvalue 0.05 показывает отсечку, на каком значении гены можно считать значимыми: