

Enriched GO

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This code for GO enriched genes in samples compared to control; the excel sheet for this is uploaded on github called “genego”, make sure you have the required packages installed.

```
“{r setup, include=FALSE} knitr::opts_chunk$set(echo = TRUE) library(clusterProfiler) library(org.Mm.eg.db) library(ggplot2) library(gprofiler2) library(gProfileR) library(tidyverse) geneontology <- read.csv(“genego.csv”)
```

```
## R Markdown
```

```
```{r GO}
```

```
up_genes <- filter(geneontology, logFC > 0)
down_genes <- filter(geneontology, logFC < 0)
up_enrich <- enrichGO(up_genes$gene_symbol , OrgDb = org.Mm.eg.db, keyType = "SYMBOL", ont = "BP")
down_enrich <- enrichGO(down_genes$gene_symbol , OrgDb = org.Mm.eg.db, keyType = "SYMBOL", ont = "BP")
up_terms <- rev(up_enrich@result$Description)
down_terms <- rev(down_enrich@result$Description)
up_pvals <- rev(up_enrich@result$pvalue)
down_pvals <- rev(down_enrich@result$pvalue)
```

```
par(mar = c(4, 10, 2, 2) + 0.1)
barplot(-log10(up_pvals), horiz = TRUE, names.arg = up_terms, col = "blue", xlim = c(0, max(-log10(up_pvals))))
barplot(-log10(down_pvals), horiz = TRUE, names.arg = down_terms, col = "red",
ylab = "GO Terms (Down-regulated)", las = 1, cex.names = 0.7)
```