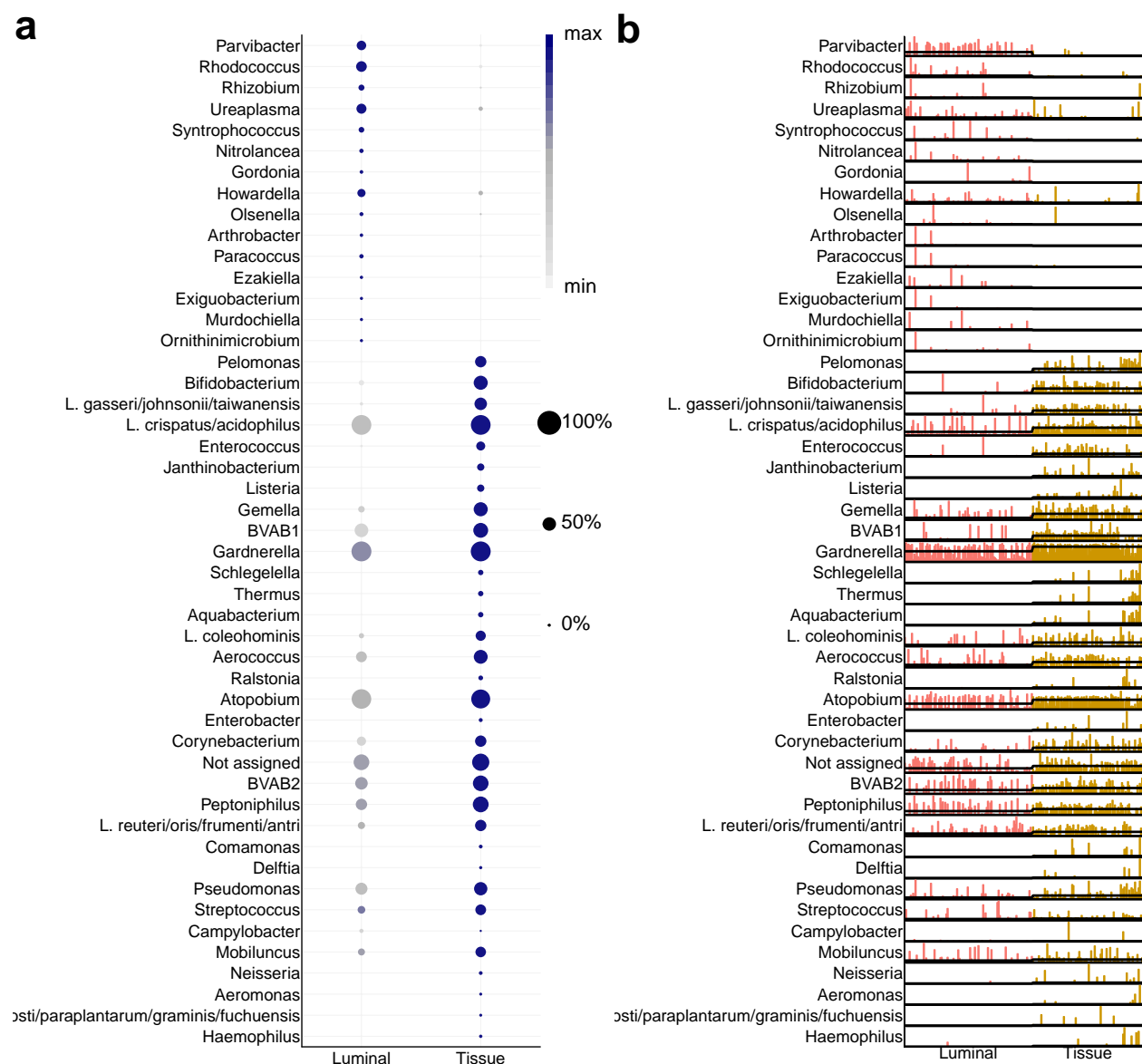# Suppl. Figure 2. Differential bacterial abundance across Tissue and Luminal microbiome

```r
knitr::opts_chunk$set(
  fig.path="./Figures/",
  fig.process = function(filename){
    new_filename <- stringr::str_remove(string = filename,
                                        pattern = "-1")
    fs::file_move(path = filename, new_path = new_filename)
    ifelse(fs::file_exists(new_filename), new_filename, filename)
})
#setwd("/Users/vilkal/work/Brolidens_work/Projects/Gabriella_repo/reports/rmarkdown/manuscript")

# setwd("/Users/vilkal/work/Brolidens_work/Projects/broliden_5325/reports/manuscript")
```

```
## null device
##           1
```

Suppl. Figure 2. Differential bacterial abundance across tissue and CVL microbiome week3 datasets. The results are shown both as **a)** Dot plots and **b)** barplots Bacteria with log2FC above 0.25 and p-value below 0.01 (from the wilcoxon test) were considered significant and were sorted by the highest expression. The colour scale indicates the difference in total abundance between the datsets as a proportion, where Max is the higest abundace of the two datasets and the other becomes a proportion of this value.The size of the dots indicates the average abundance of the given bacteria in the given dataset.