

Suppl. Figure 1. Bacterial abundance across datasets

```
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")
```

