

Broliden__5325

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#Load libraries and other scripts	
#Defining some variables for the analysis	

Loading data and metadata

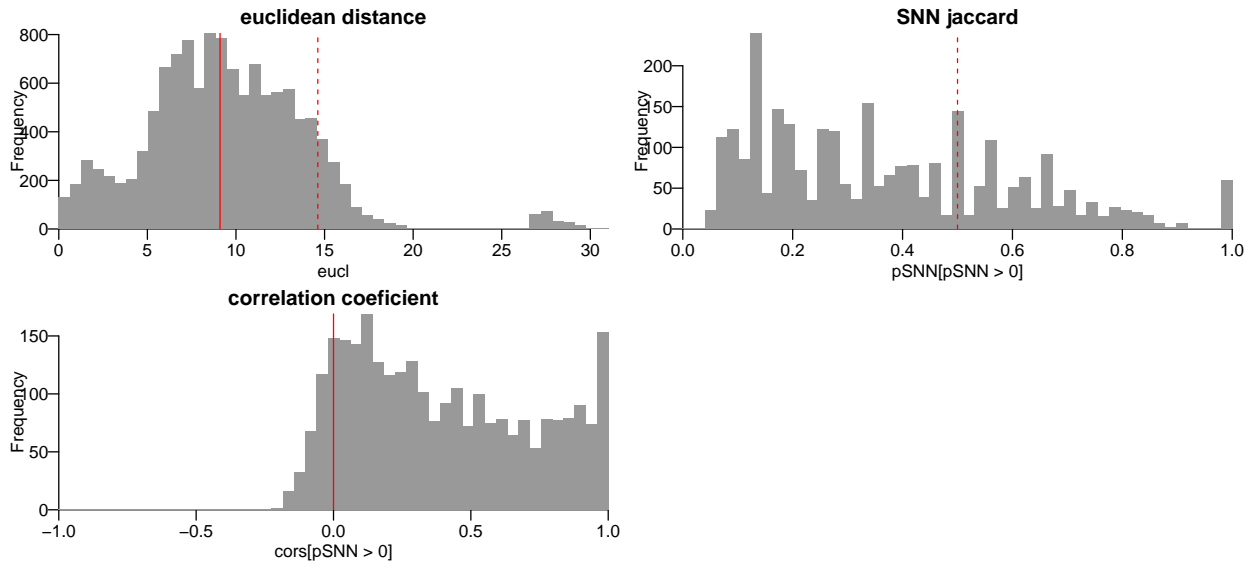
Merging microbiome datasets

Organise the datasets

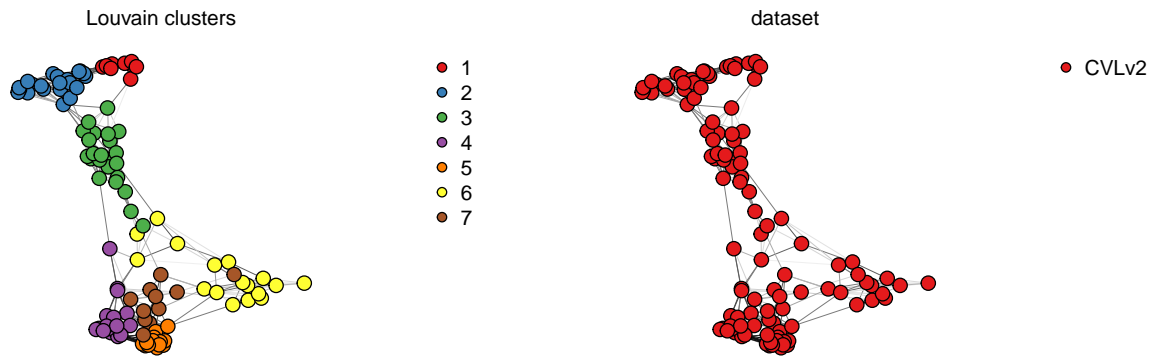
Organise the datasets



Computing a SNN graph from sample correlations



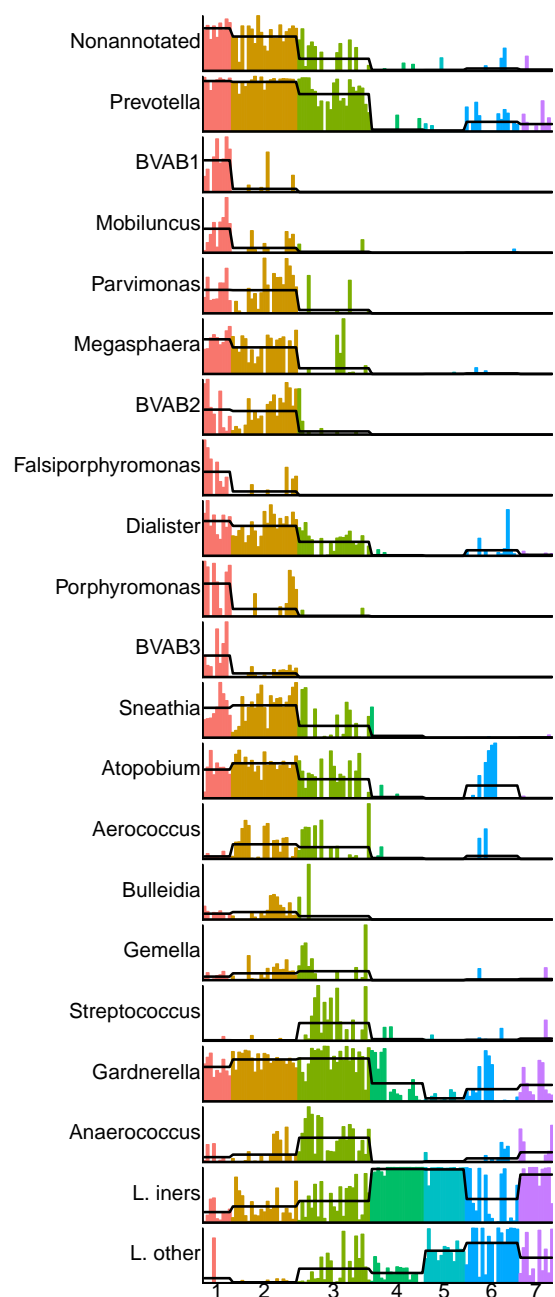
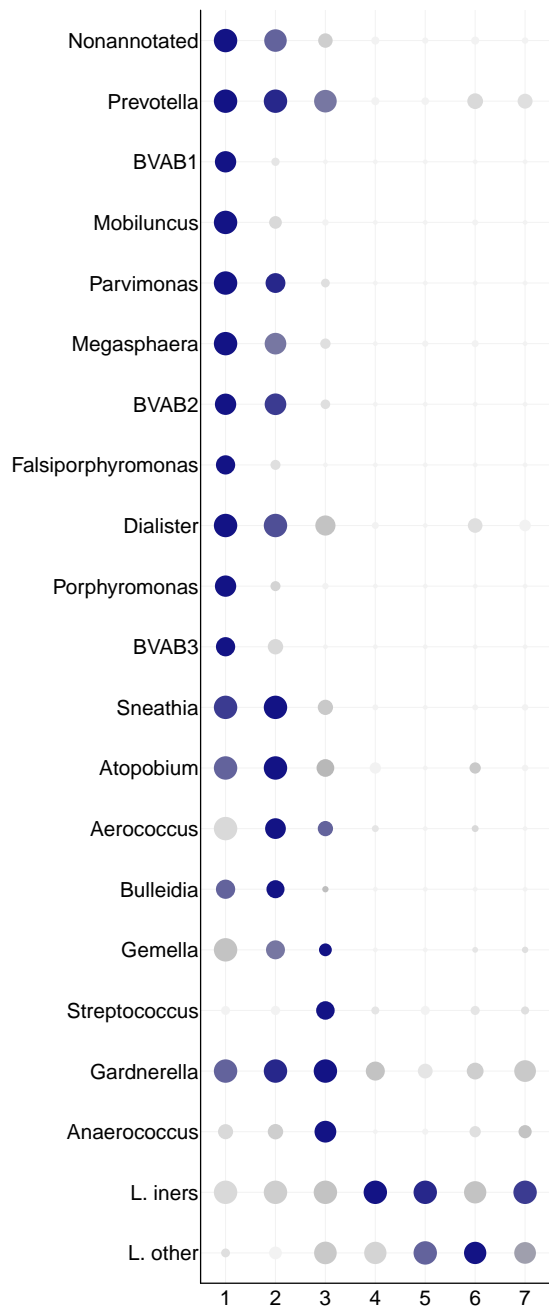
Visualise the data



Computing differential expression across clusters

```
## [1] 30 8
```

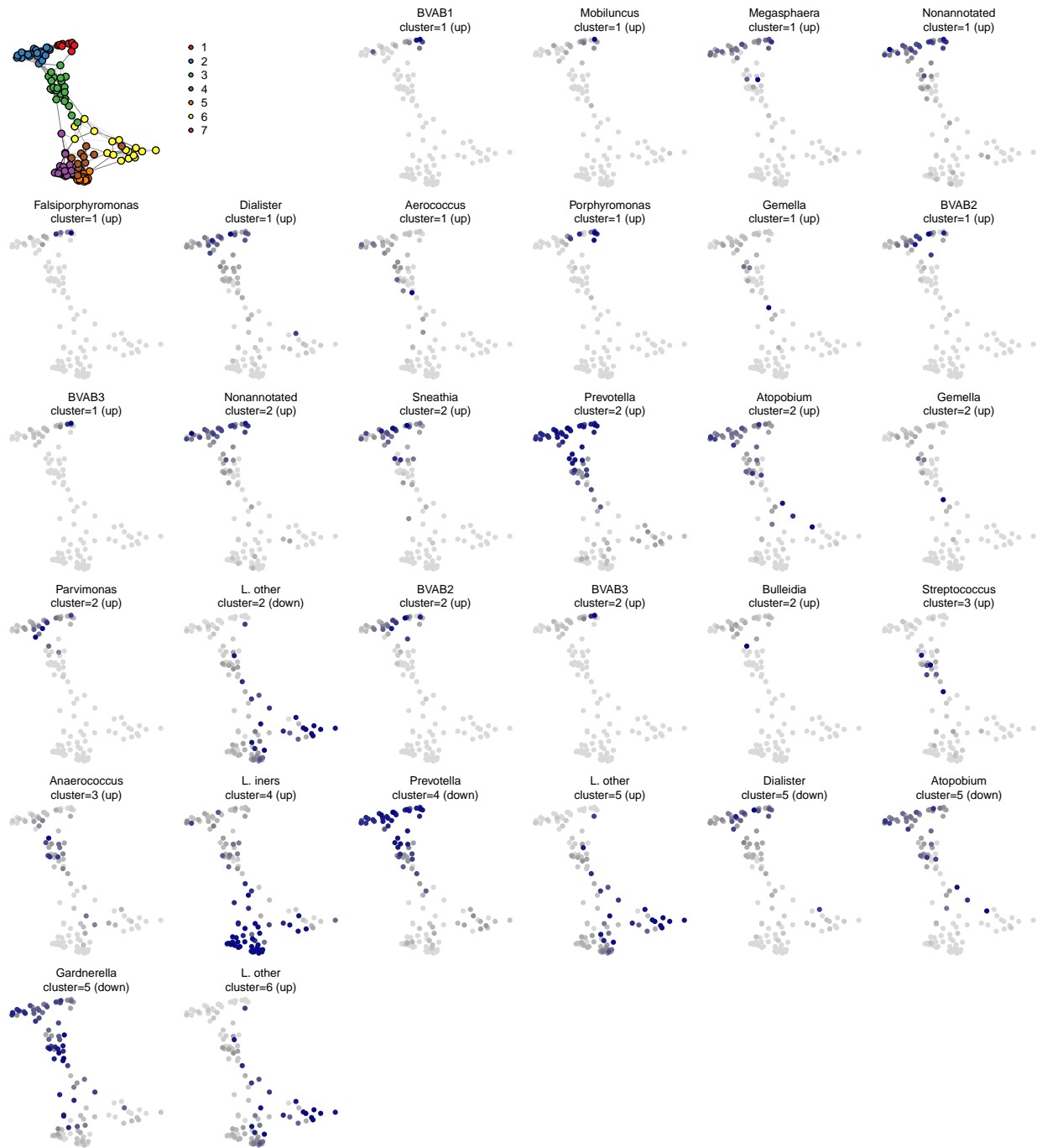
```
#Plotting the most significant bacteria across clusters
```



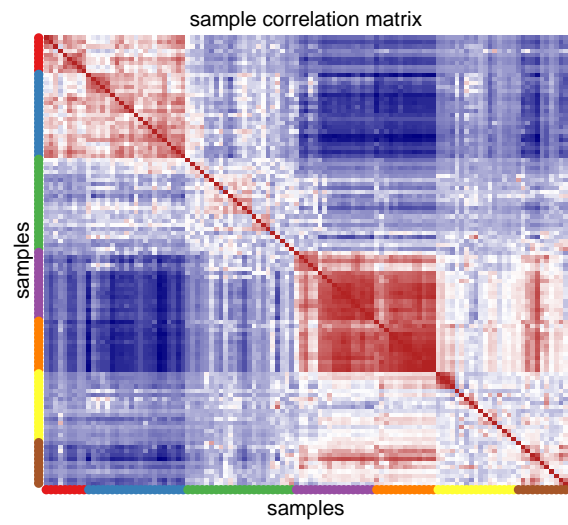
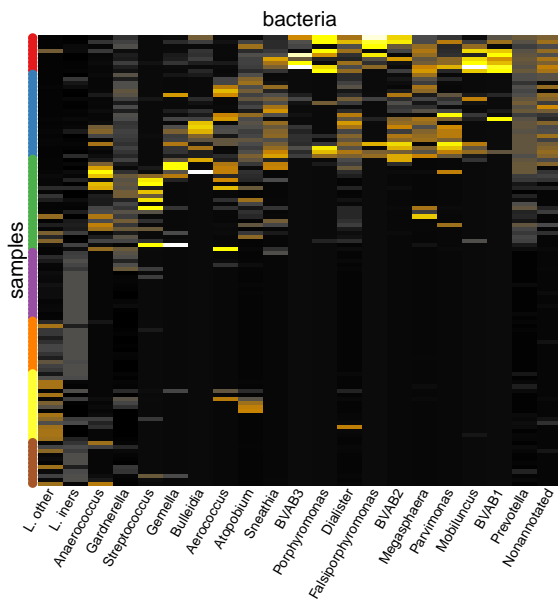
```
## [1] "1"
```

```
## [1] "2"
```

Plotting the most significant bacteria across clusters



#Plotting bacteria across clusters



```
## [1] -0.01463636
```

```
#Dataset integration
```