

Broliden_5325

14 October, 2020

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

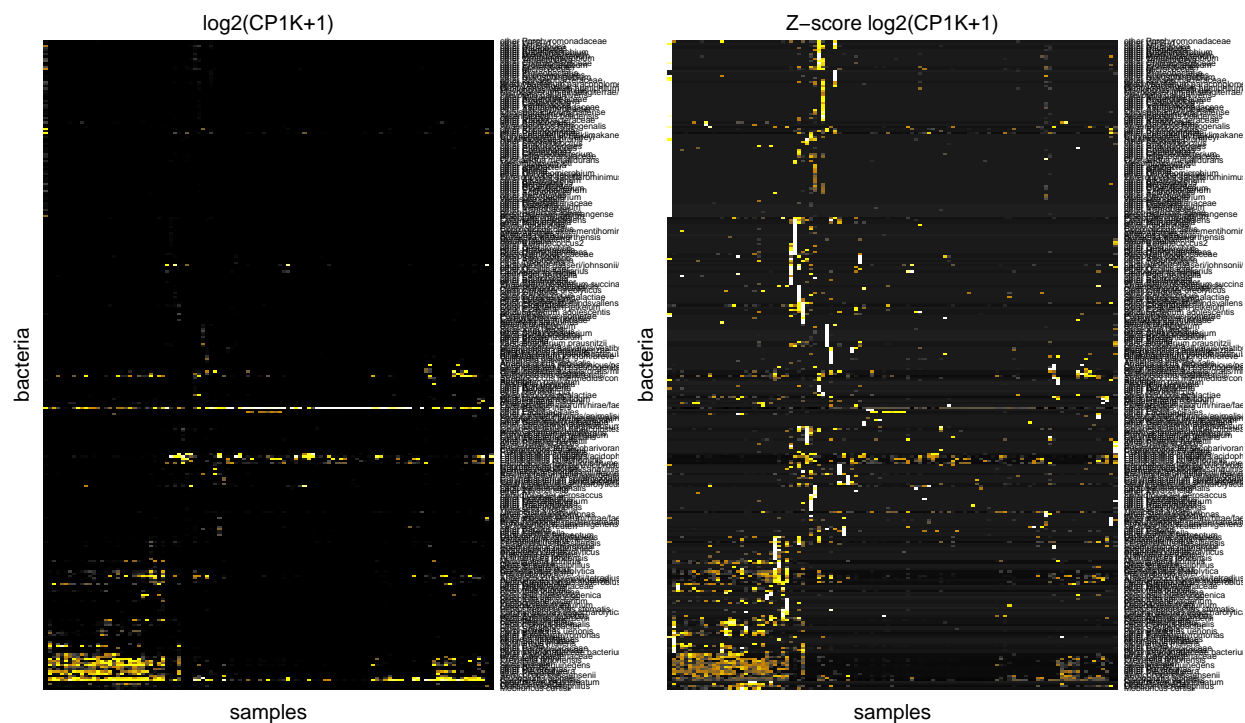
Loading data and metadata

```
## $ASV_tissue_V3_normalized_batch_corrected.csv
## [1] 767 96
##
## $ASV_CVL_V3_normalized_batch_corrected.csv
## [1] 767 111
##
## $ASV_CVL_V2_normalized_batch_corrected.csv
## [1] 767 111
##
## $ASV_CVL_V2_normalized_NOT_batch_corrected.csv
## [1] 767 111
```

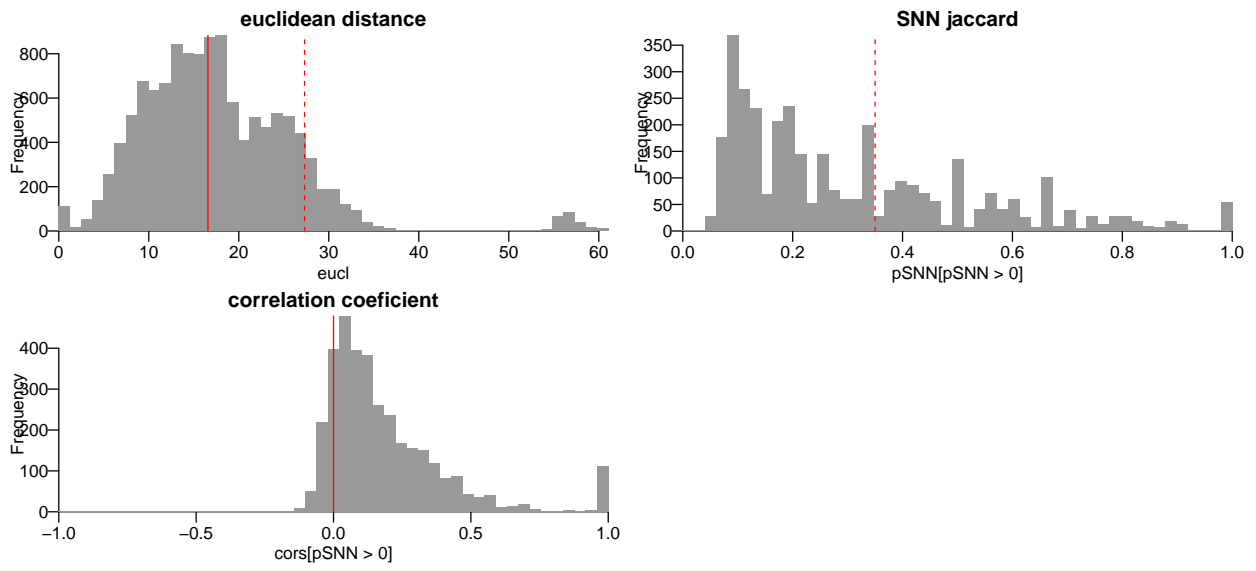
Merging microbiome datasets

Organise the datasets

Organise the datasets

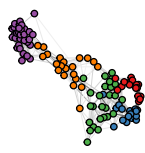


Computing a SNN graph from sample correlations



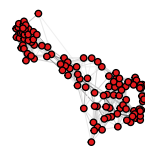
Visualise the data

Louvain clusters



- 1
- 2
- 3
- 4
- 5

dataset

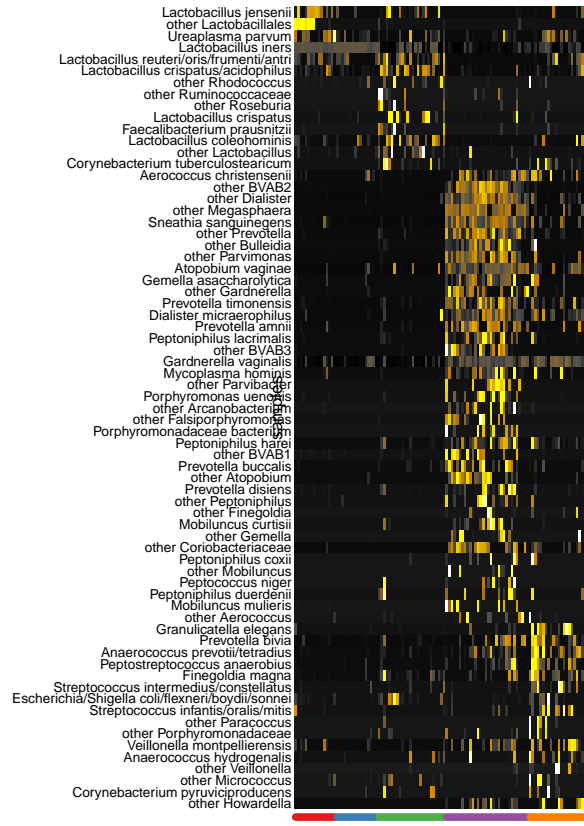
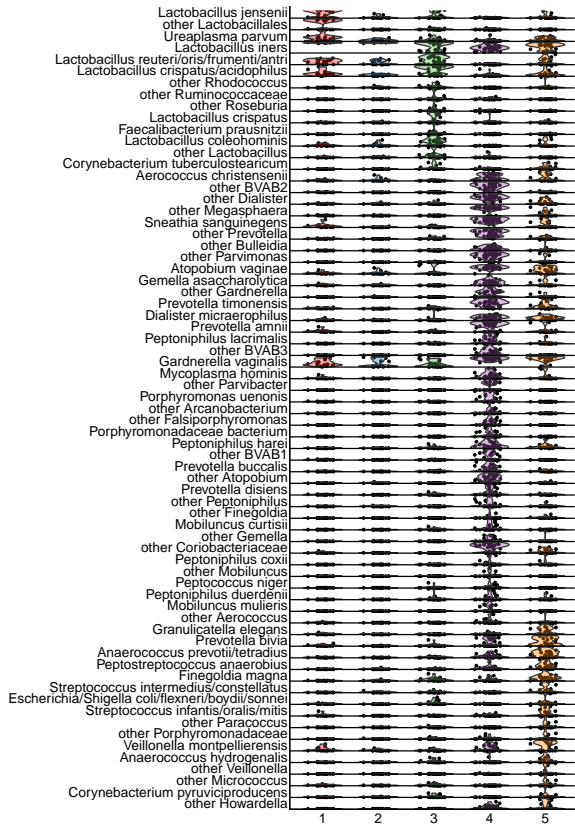
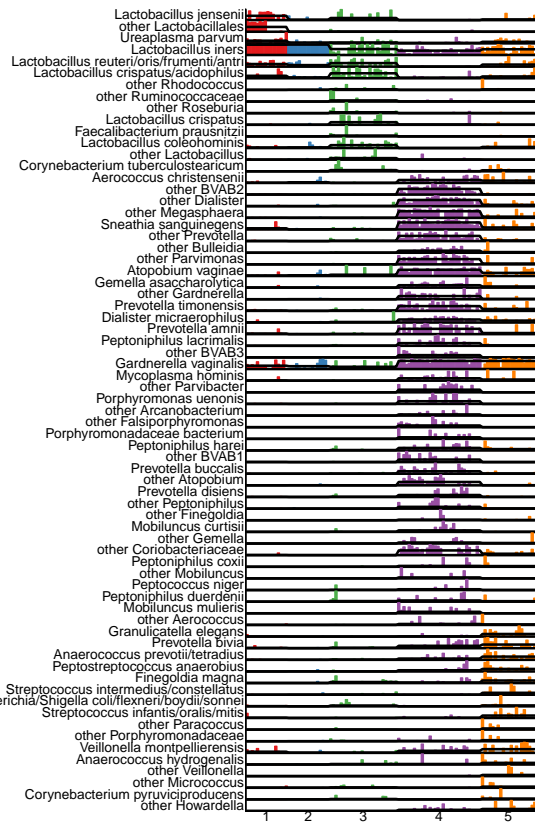
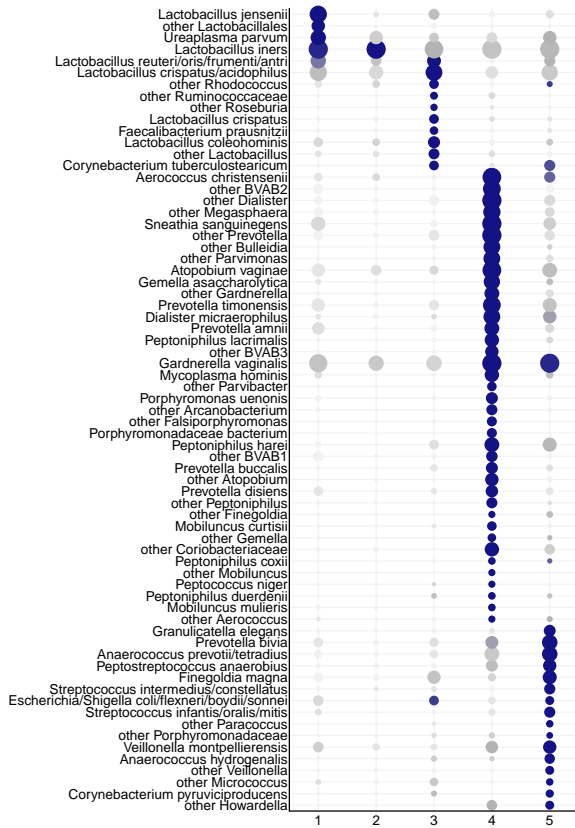


- ASV_CVL_\

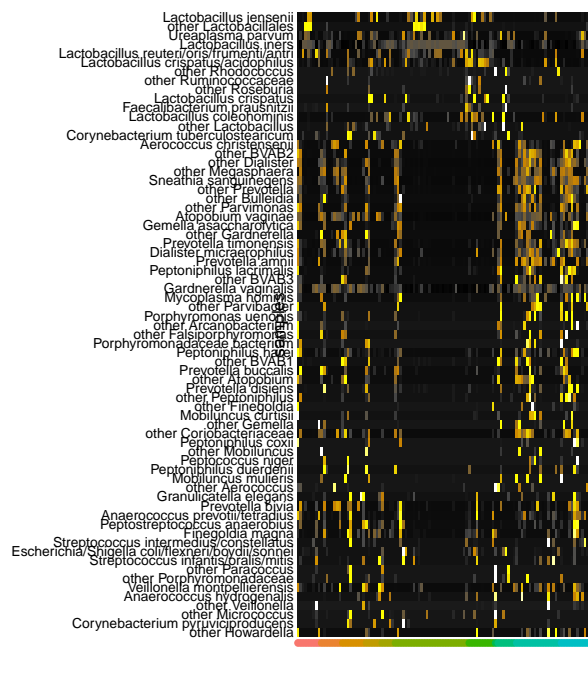
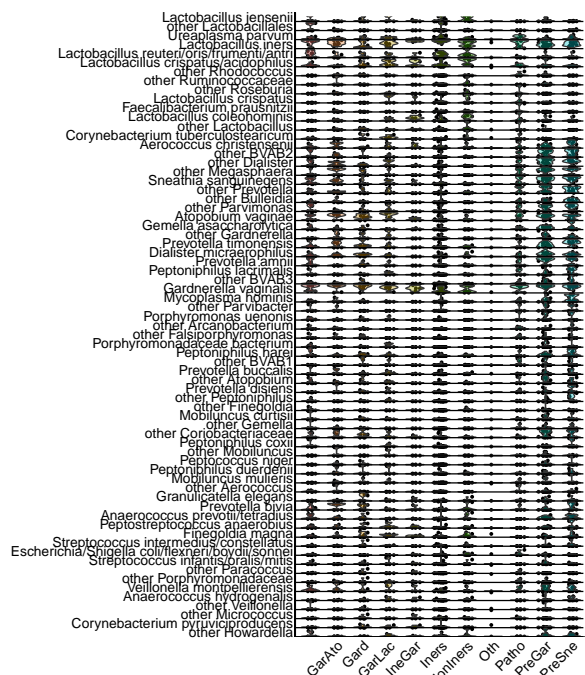
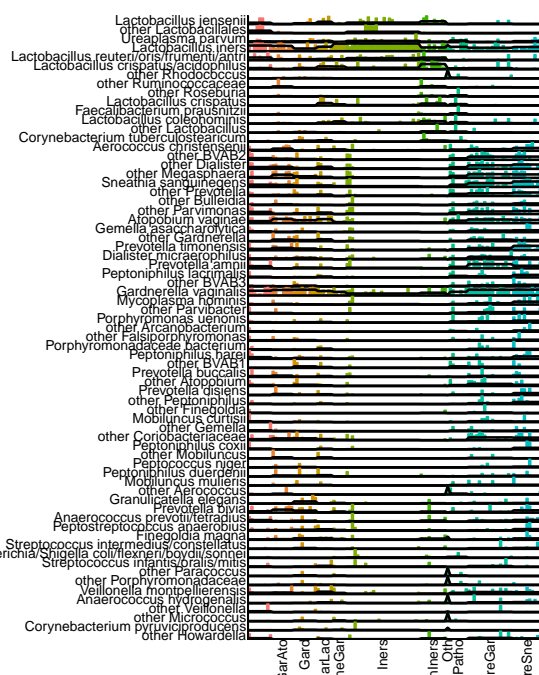
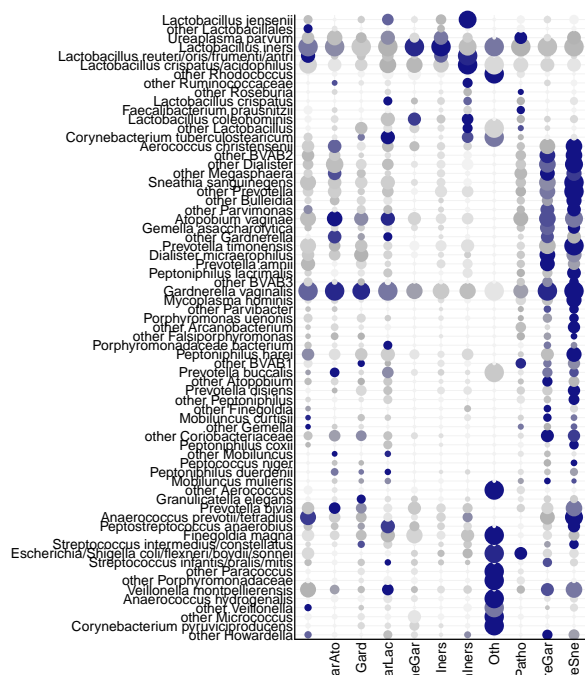
Computing differential expression across clusters

```
## [1] 120 8
```

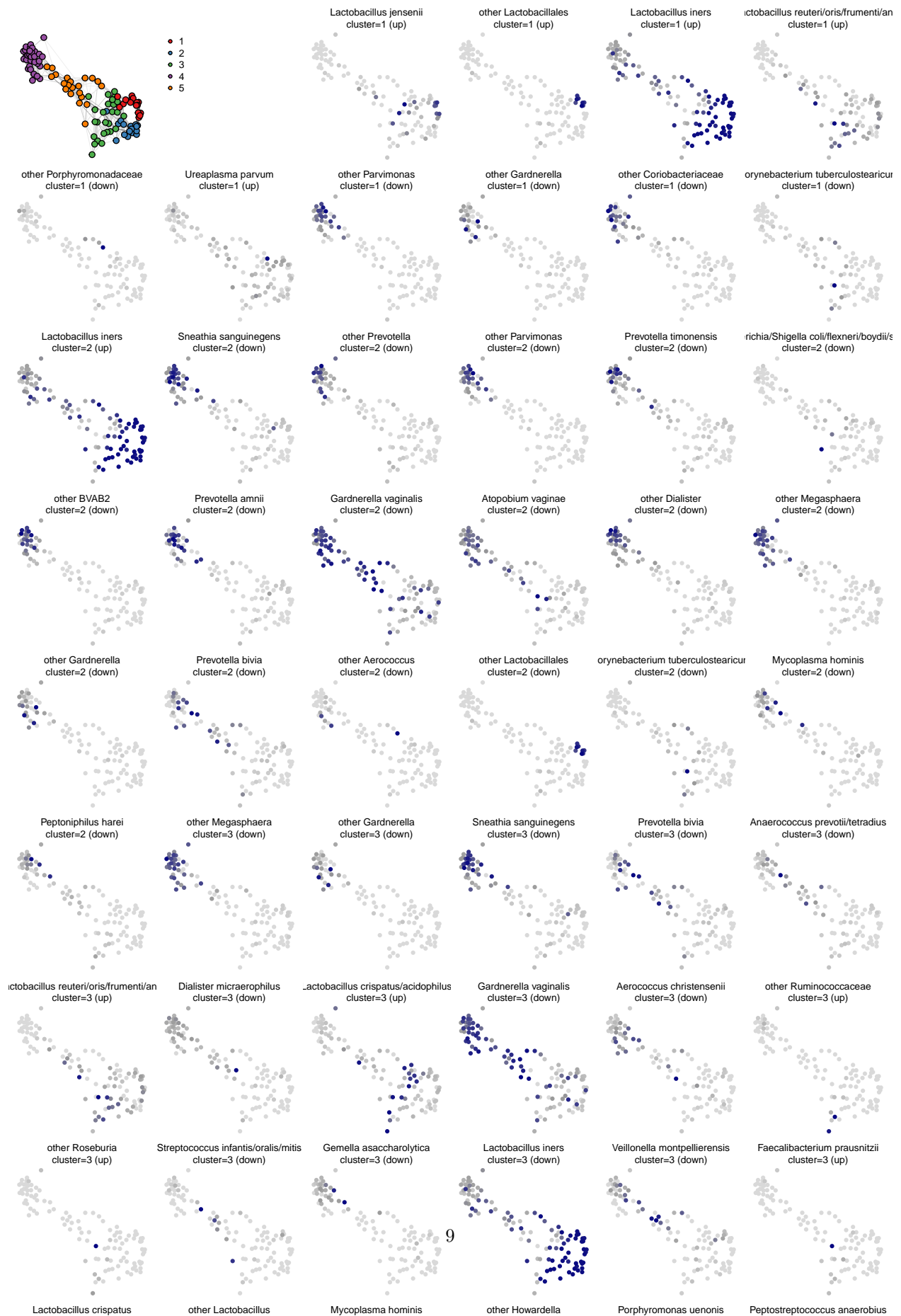
```
#Plotting the most significant bacteria across clusters
```

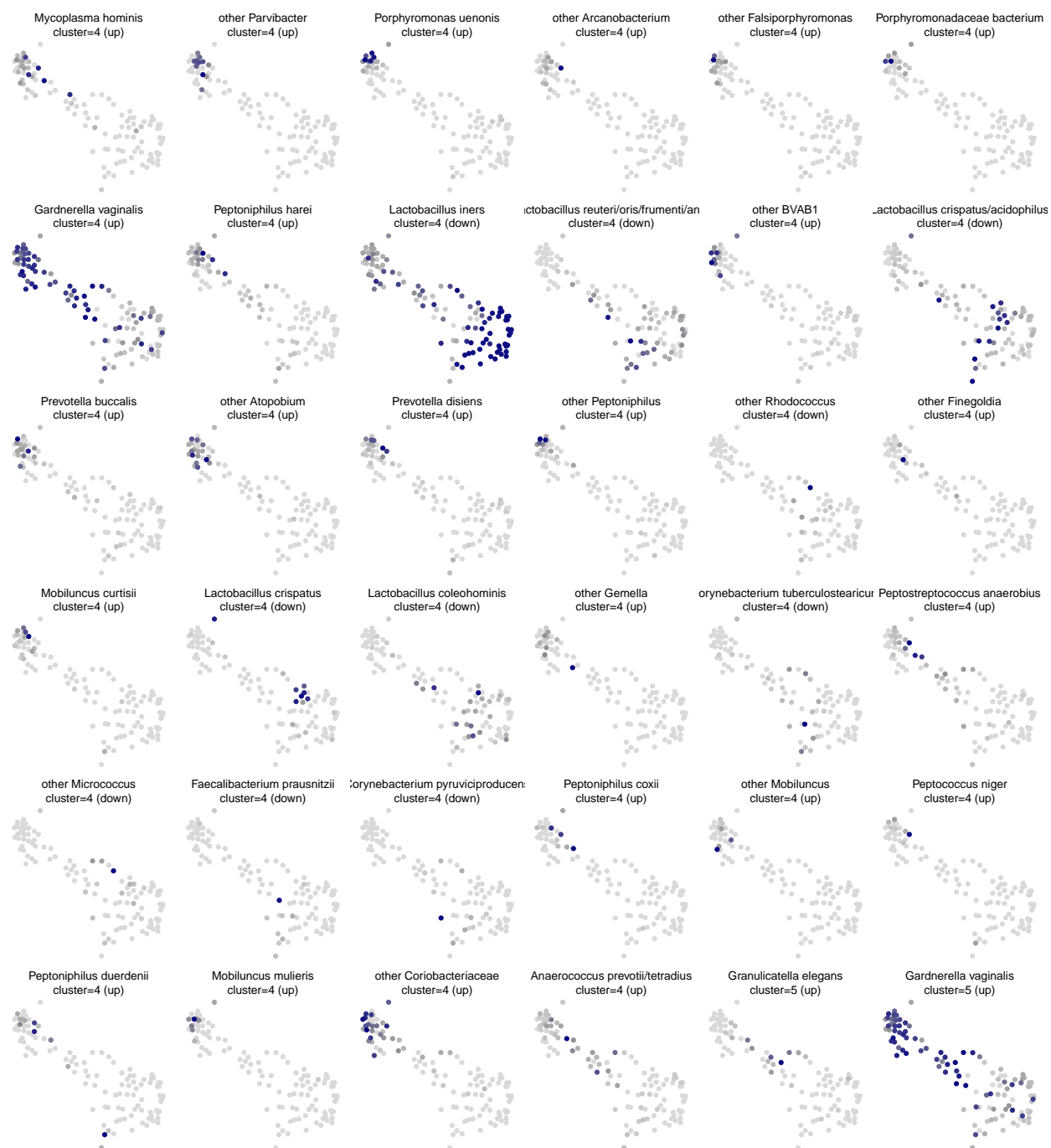


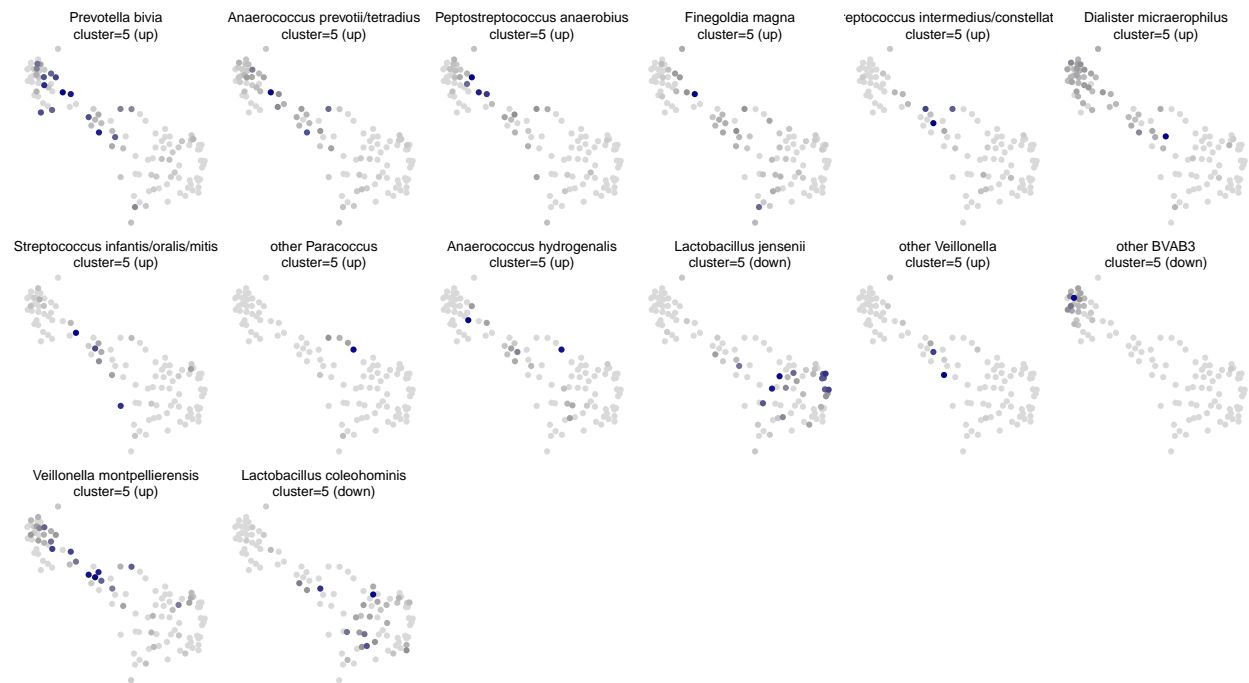
#Plotting the most significant bacteria across PREVIOUS ANNOTATION



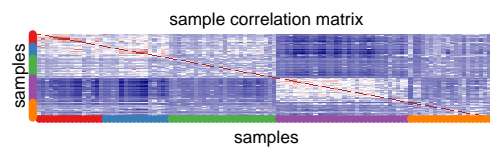
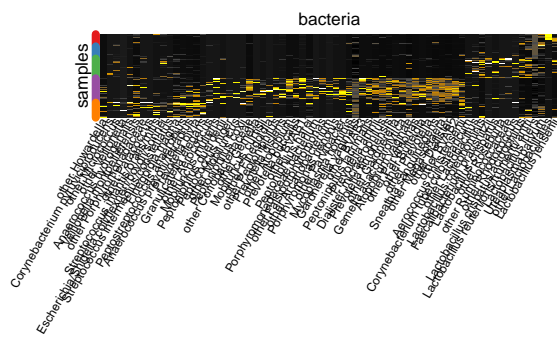
Plotting the most significant bacteria across clusters





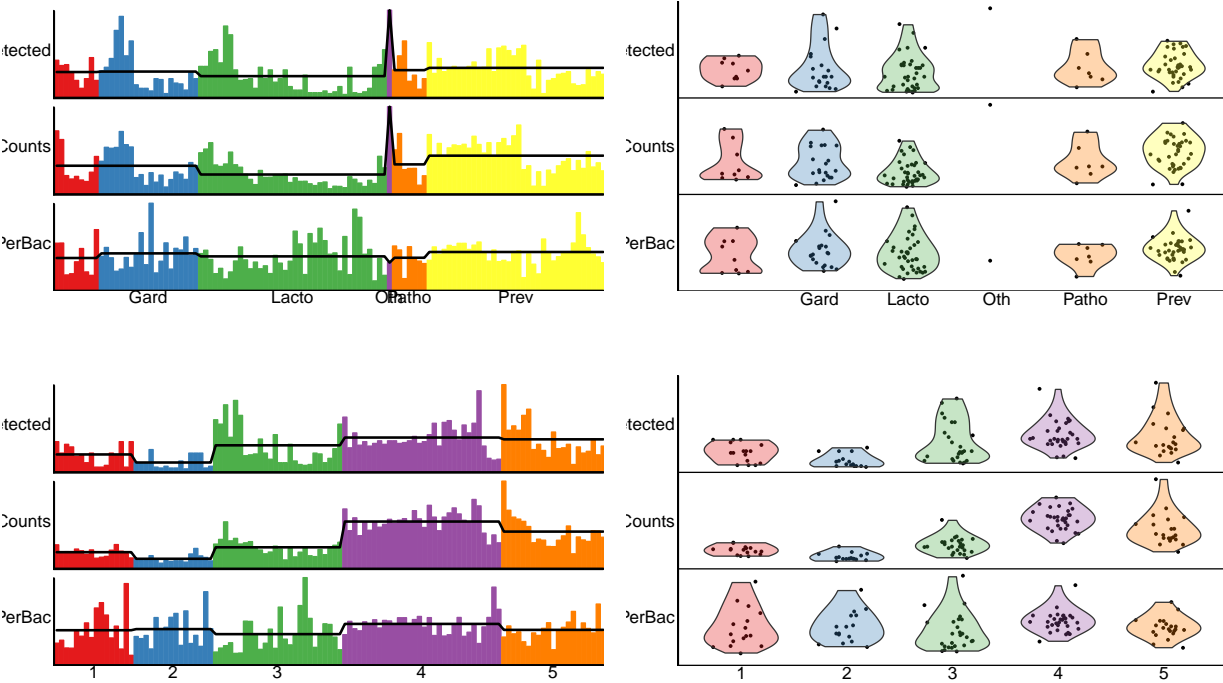


#Plotting bacteria across clusters



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

#Plotting bacteria across clusters



##	.2						
##	.1		Gard	Lacto	Oth	Patho	Prev
##	1	3	0	11	0	1	1
##	2	1	2	9	0	1	3
##	3	1	8	12	0	2	3
##	4	2	4	2	0	2	22
##	5	2	6	4	1	1	7

```
#Plotting bacteria across clusters  
#Dataset integration
```