

Contents

Loading data and metadata	1
Merging microbiome datasets	2
Organise the datasets	2
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Computing a SNN graph from sample correlations	3
Visualise the data	4
Computing differential expression across clusters	5
Plotting the most significant bacteria across clusters	9
Saving clusters and differentially expressed bacteria	13
#Load libraries and other scripts	
#Defining some variables for the analysis	

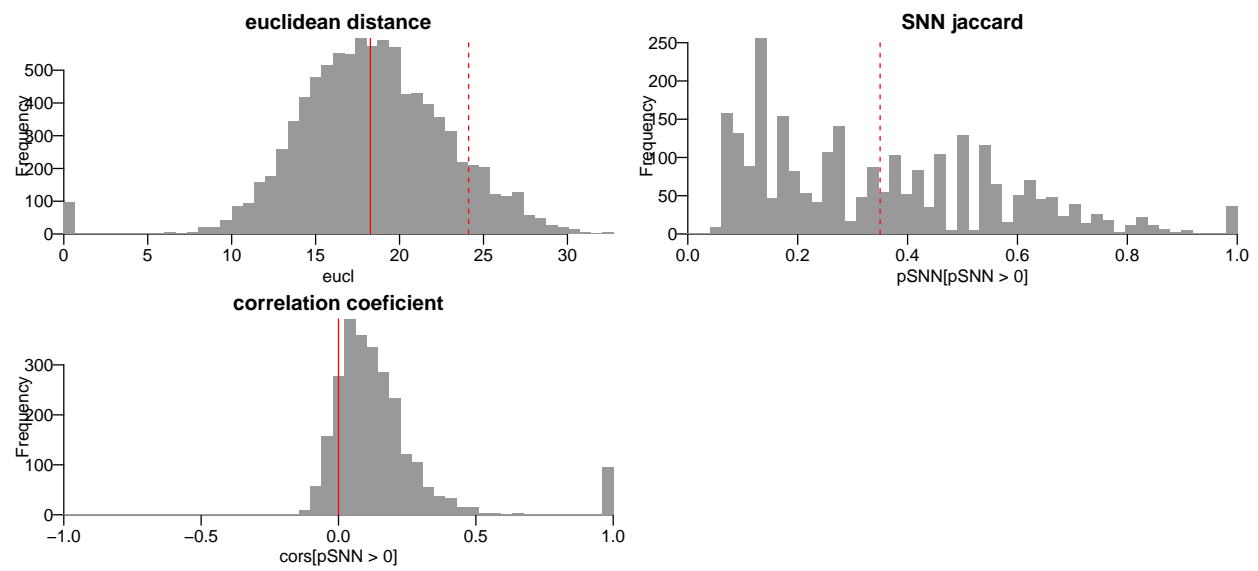
Loading data and metadata

```
## $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
```

Organise the datasets

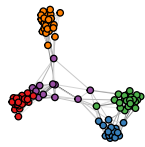


Computing a SNN graph from sample correlations



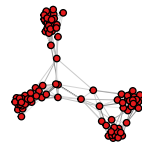
Visualise the data

Louvain clusters



- 1
- 2
- 3
- 4
- 5

dataset

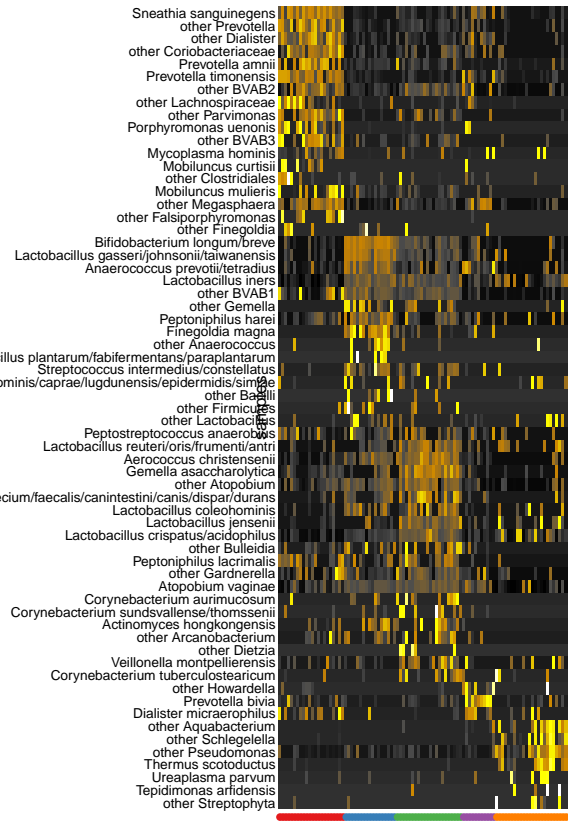
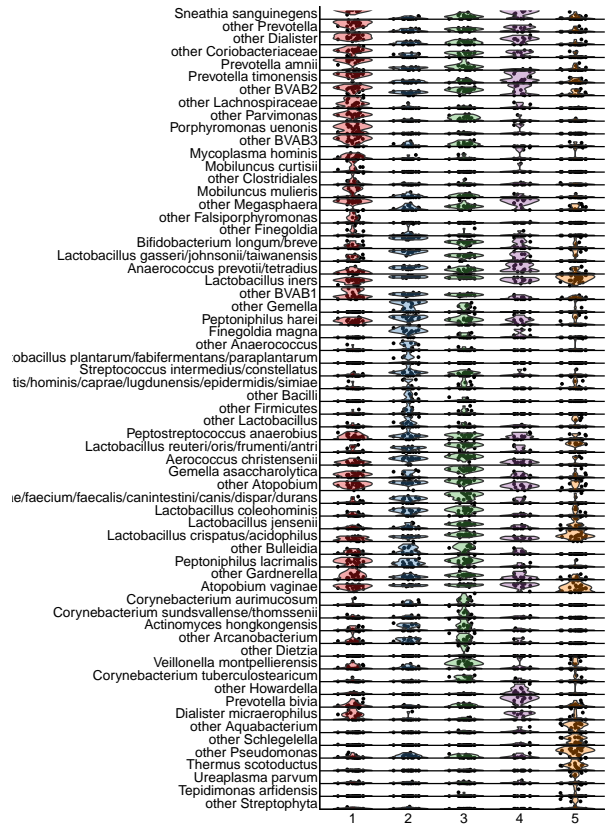
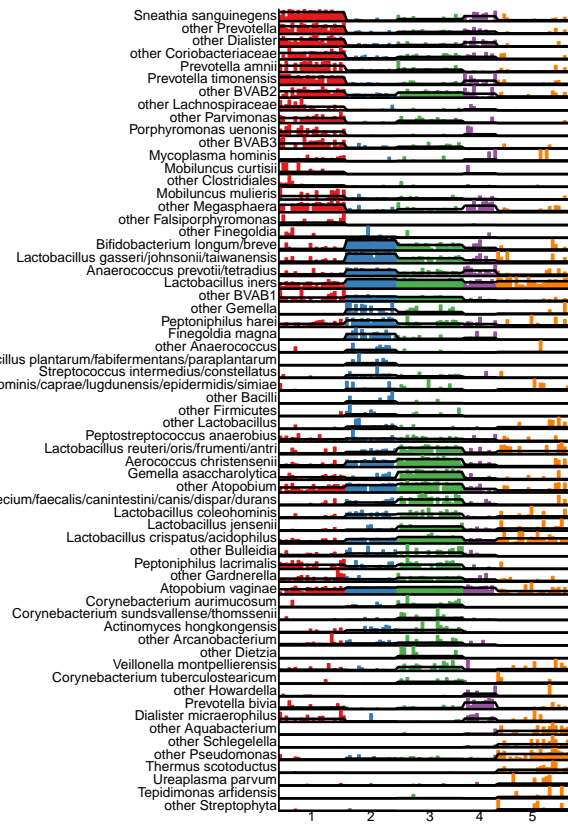
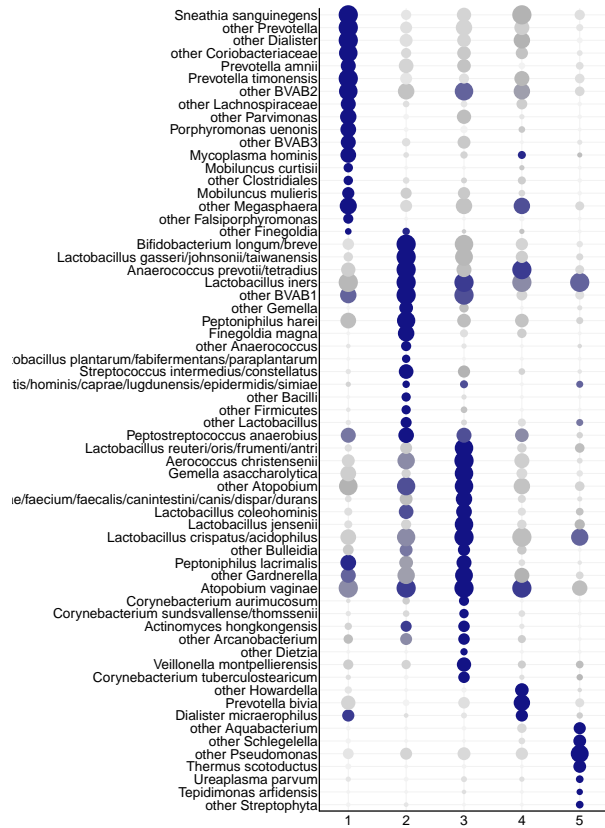


- ASV_CVL_\

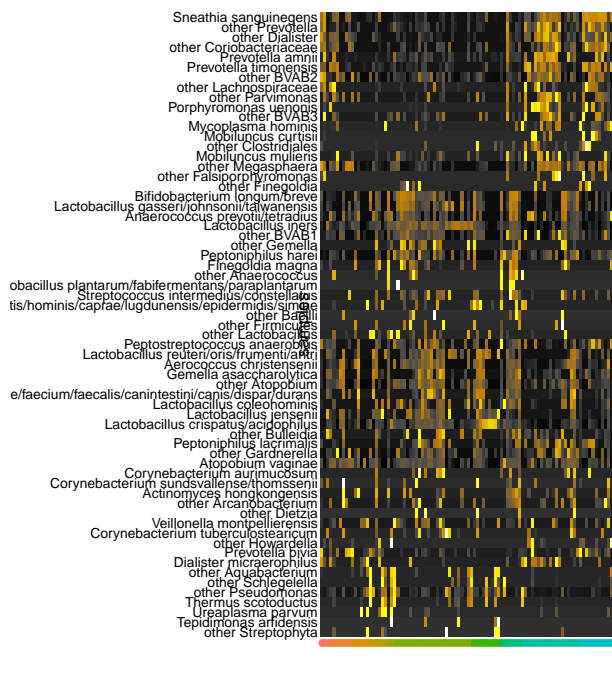
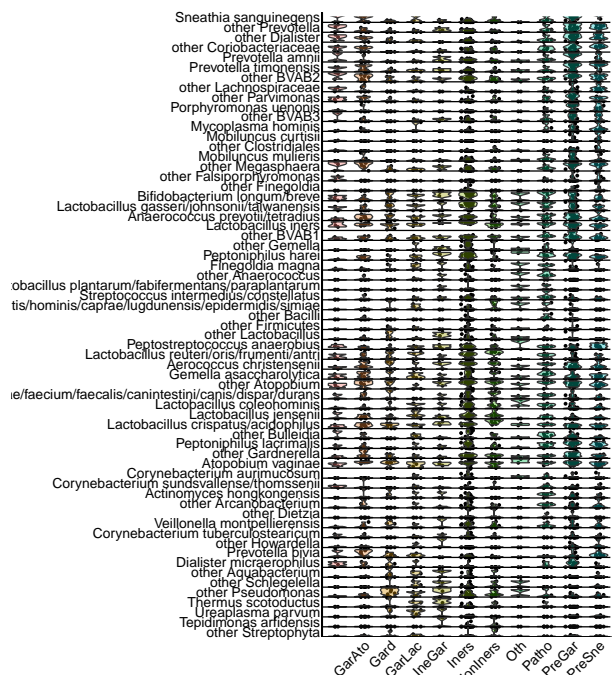
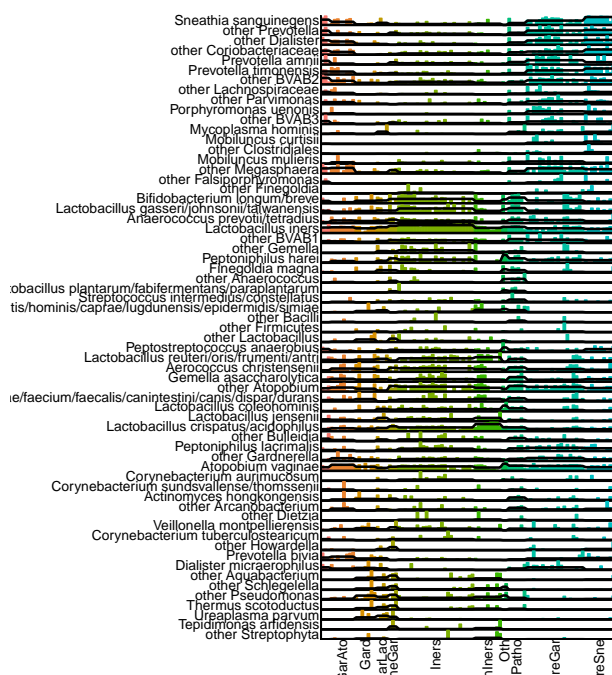
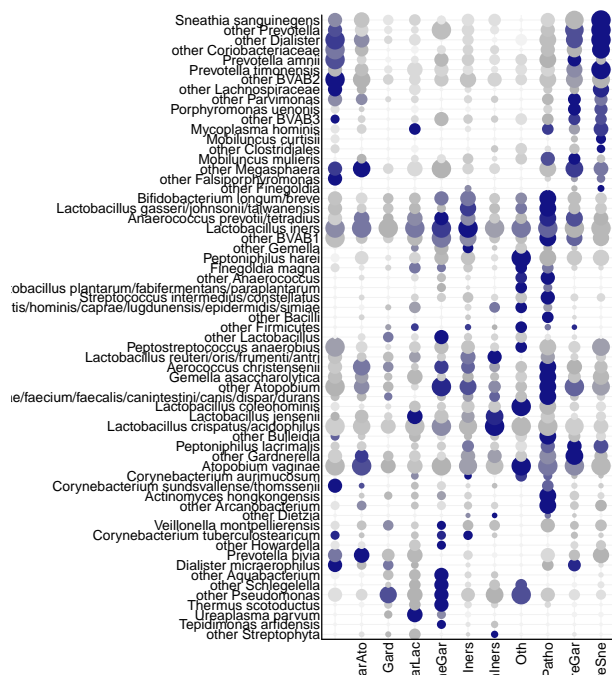
Computing differential expression across clusters

```
## [1] 100 8
```

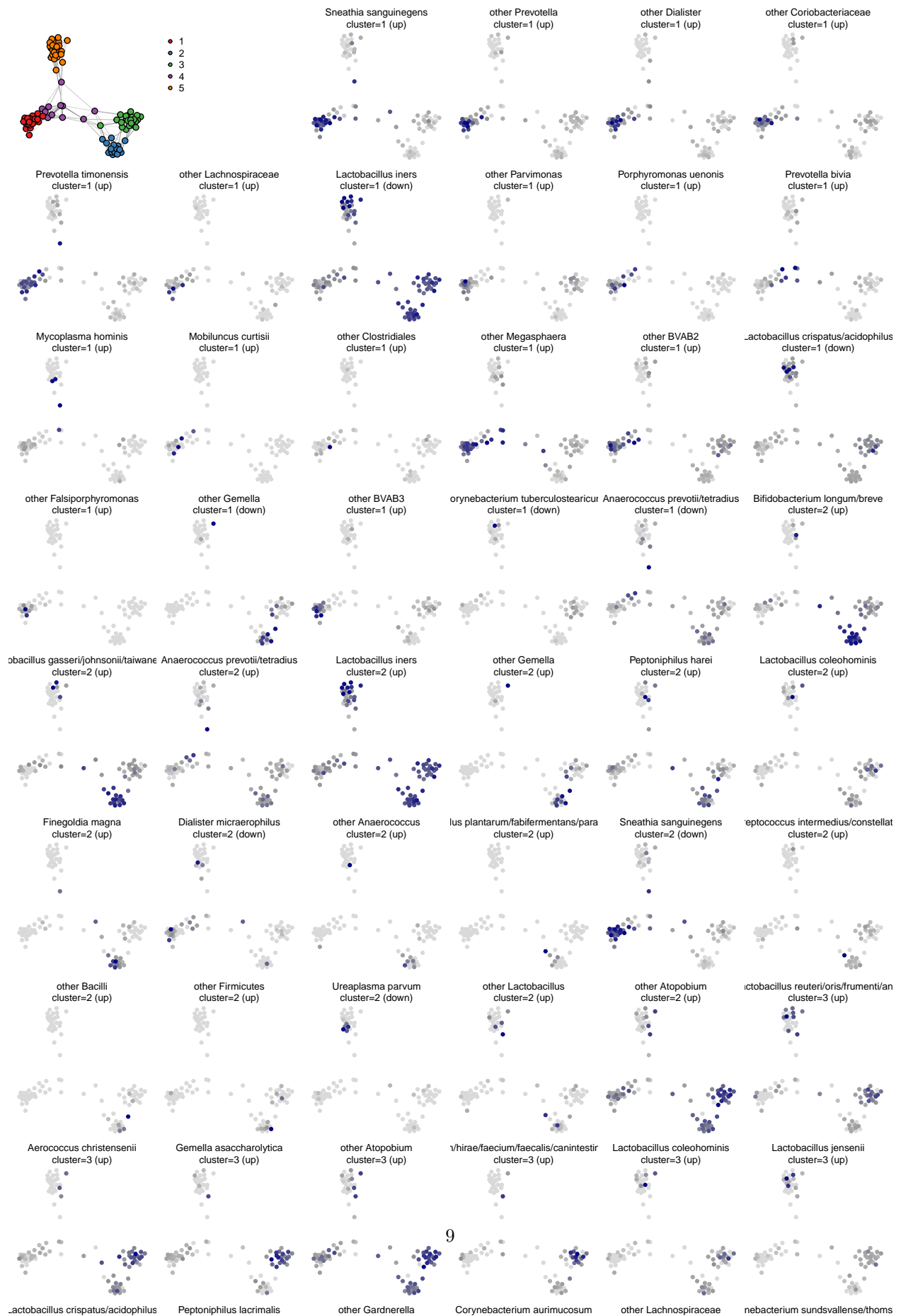
```
#Plotting the most significant bacteria across clusters
```

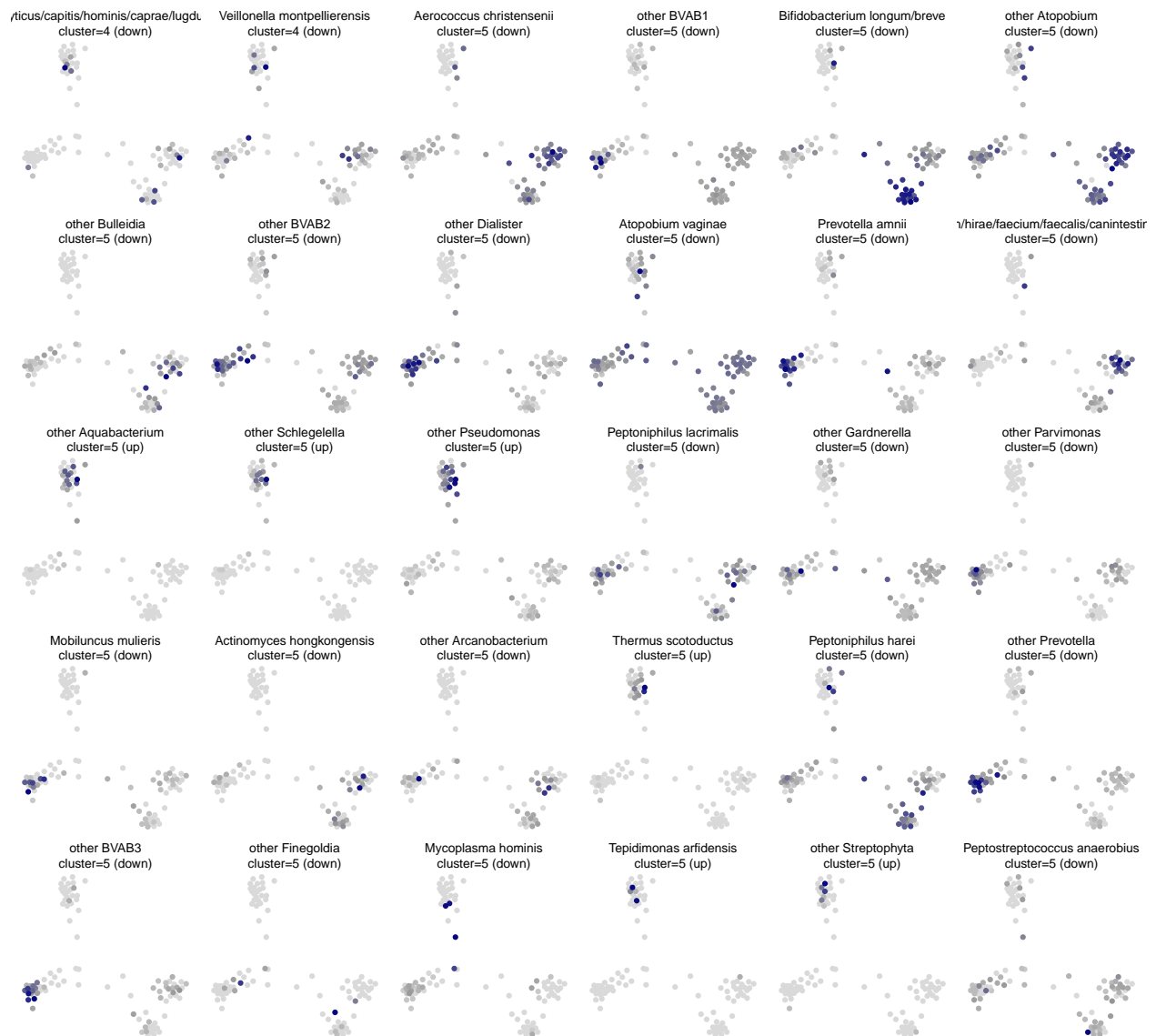


#Plotting the most significant bacteria across PREVIOUS ANNOTATION

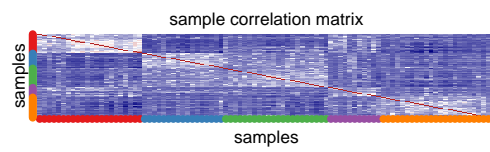
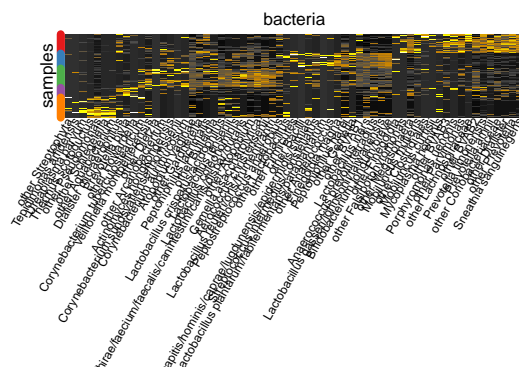


Plotting the most significant bacteria across clusters



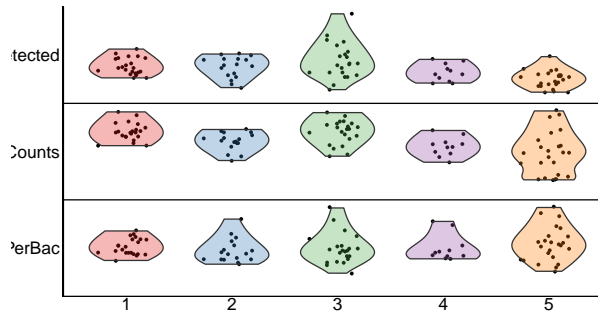
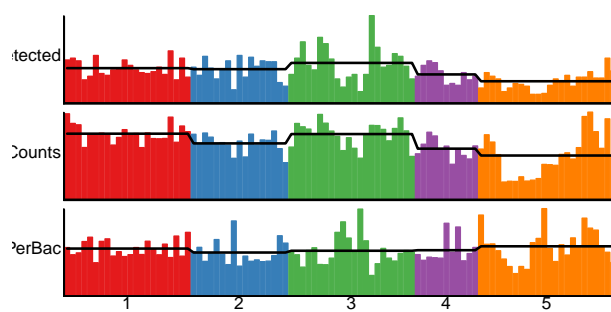
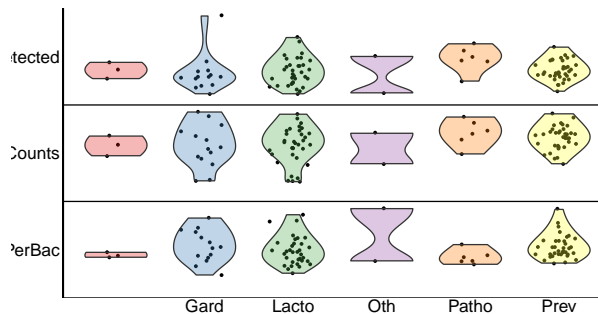
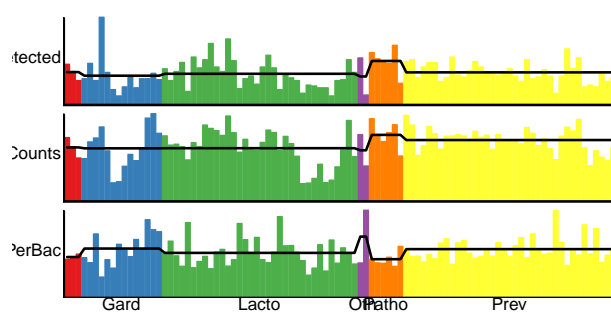


#Plotting bacteria across clusters



[1] -0.01536842

#Plotting bacteria across clusters



##	.2						
##	.1	Gard	Lacto	Oth	Patho	Prev	
##	1	1	0	0	0	1	20
##	2	0	2	9	1	3	2
##	3	1	2	12	0	1	6
##	4	1	1	0	0	0	9
##	5	0	9	13	1	1	0

Saving clusters and differentially expressed bacteria