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

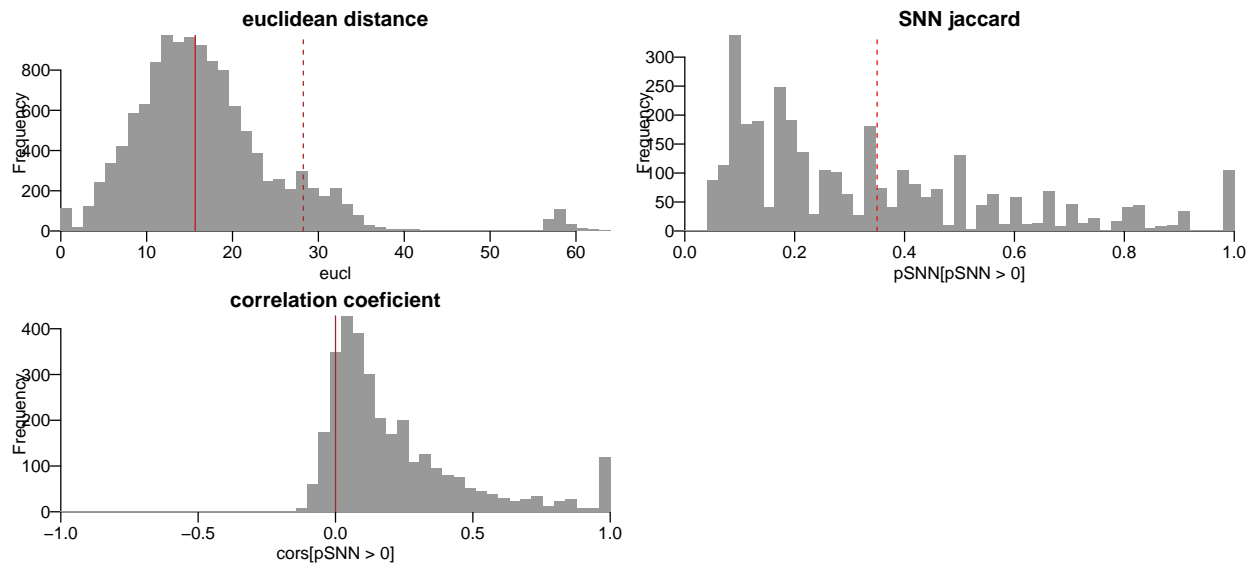
Loading data and metadata

```
## $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
```

Organise the datasets

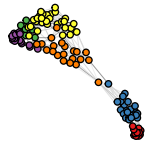


Computing a SNN graph from sample correlations



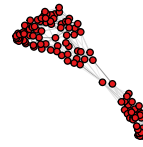
Visualise the data

Louvain clusters



- 1
- 2
- 3
- 4
- 5
- 6

dataset



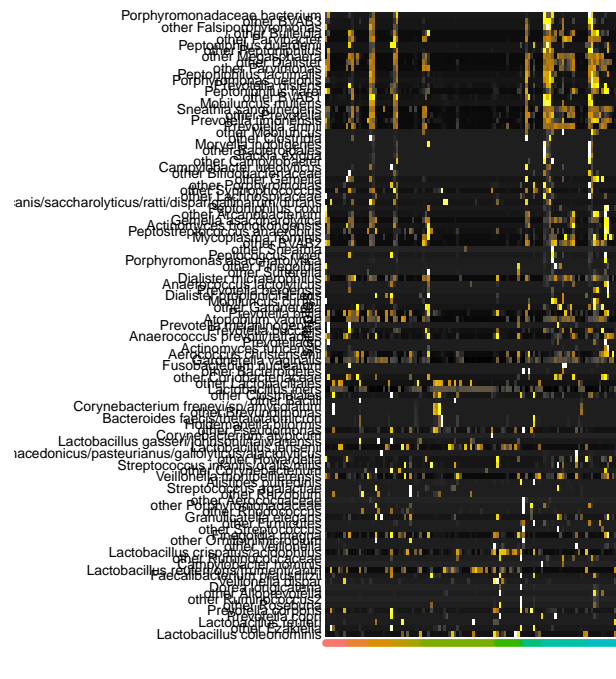
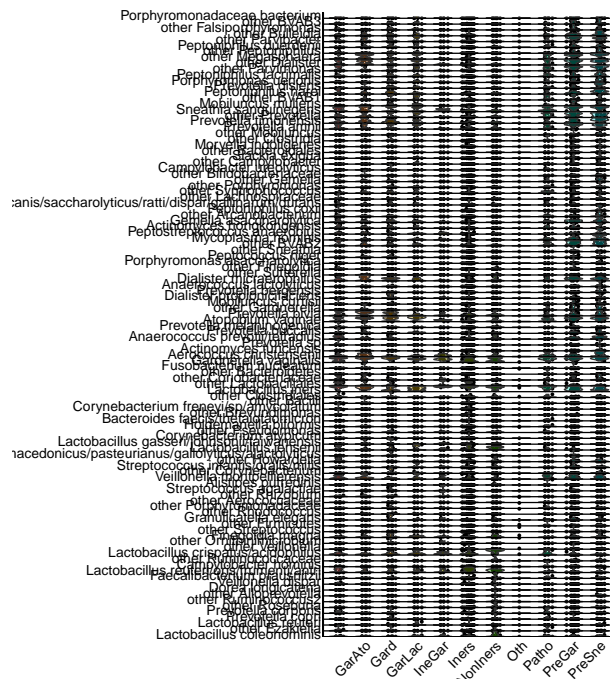
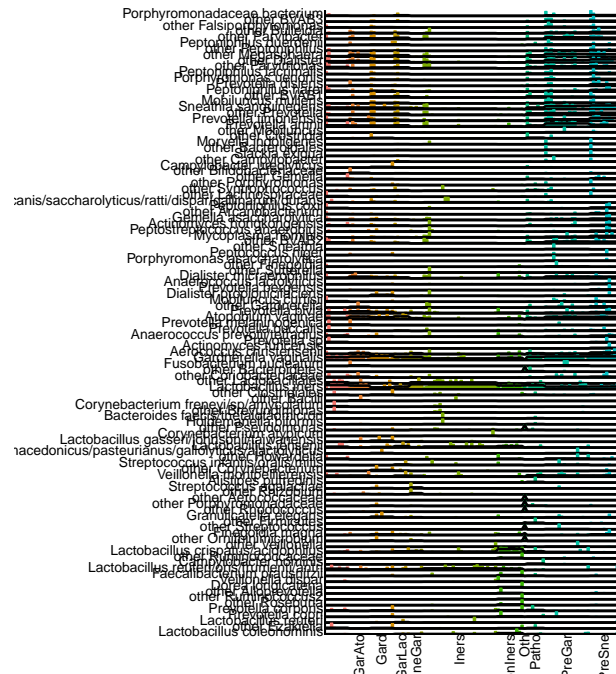
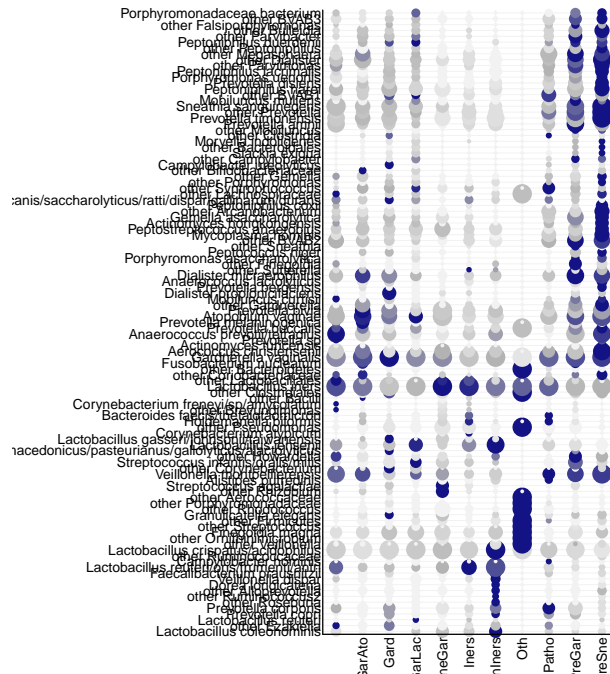
- ASV_CVL_\\

Computing differential expression across clusters

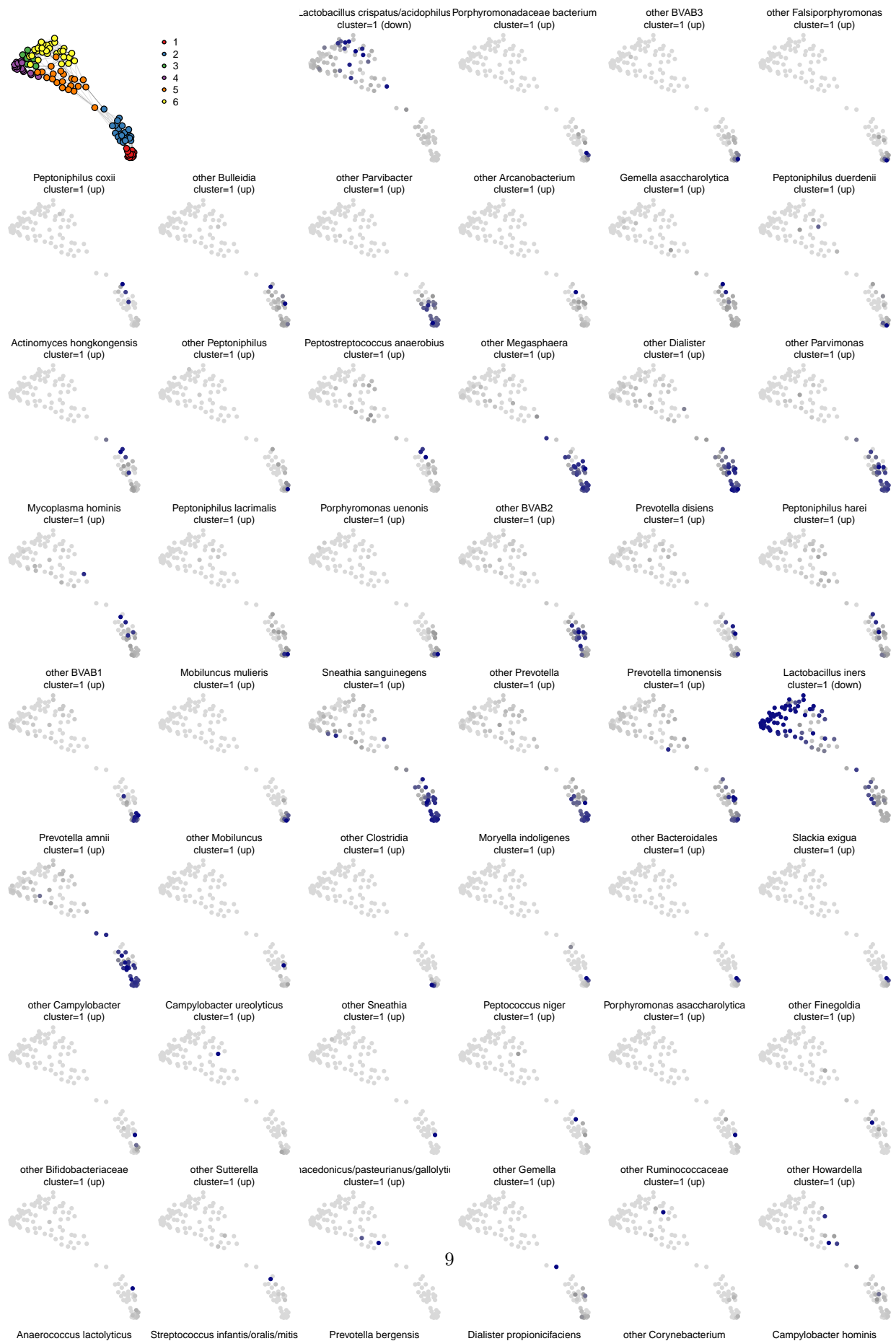
```
## [1] 162 8
```

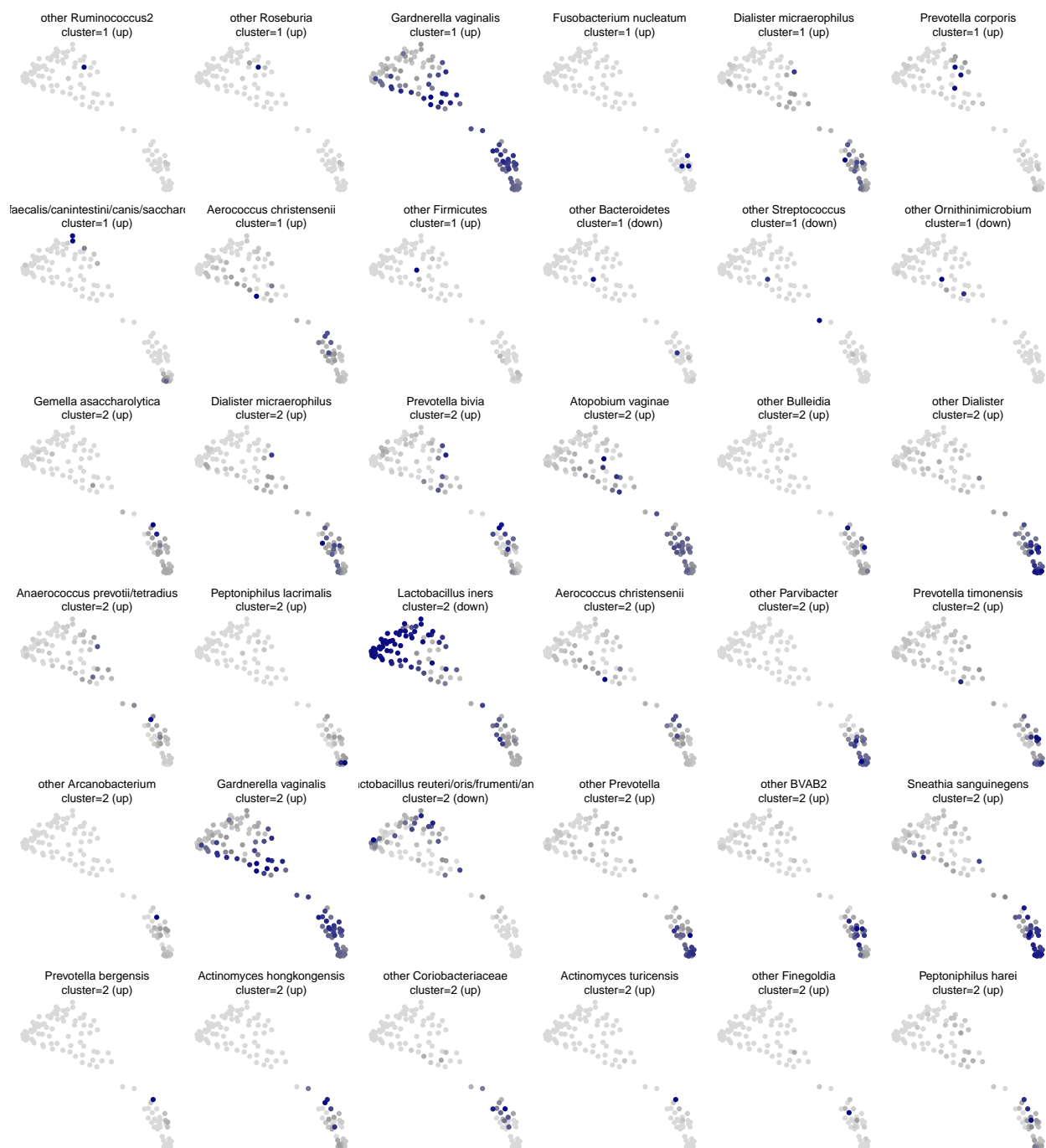
```
#Plotting the most significant bacteria across clusters
```

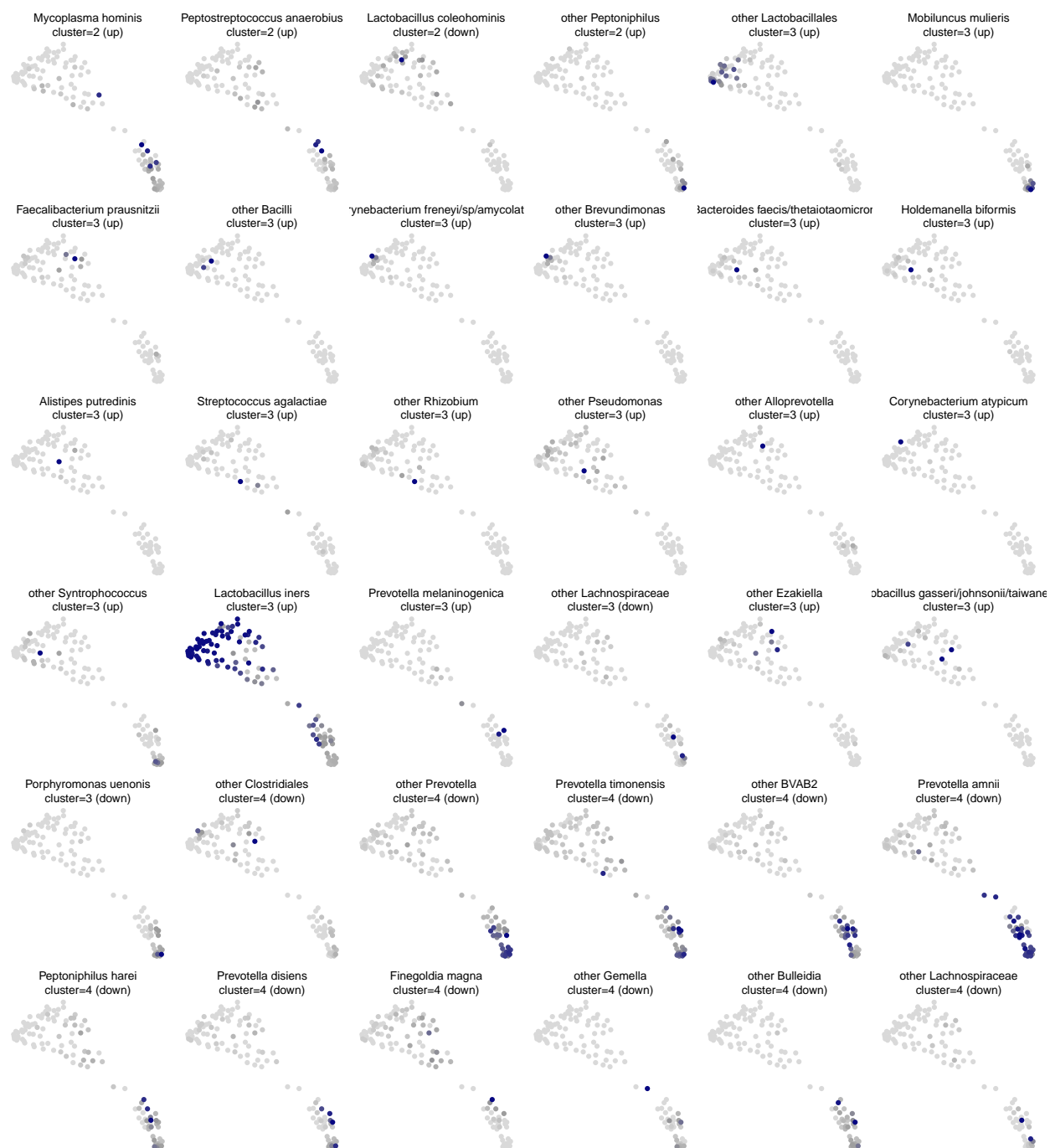

#Plotting the most significant bacteria across PREVIOUS ANNOTATION

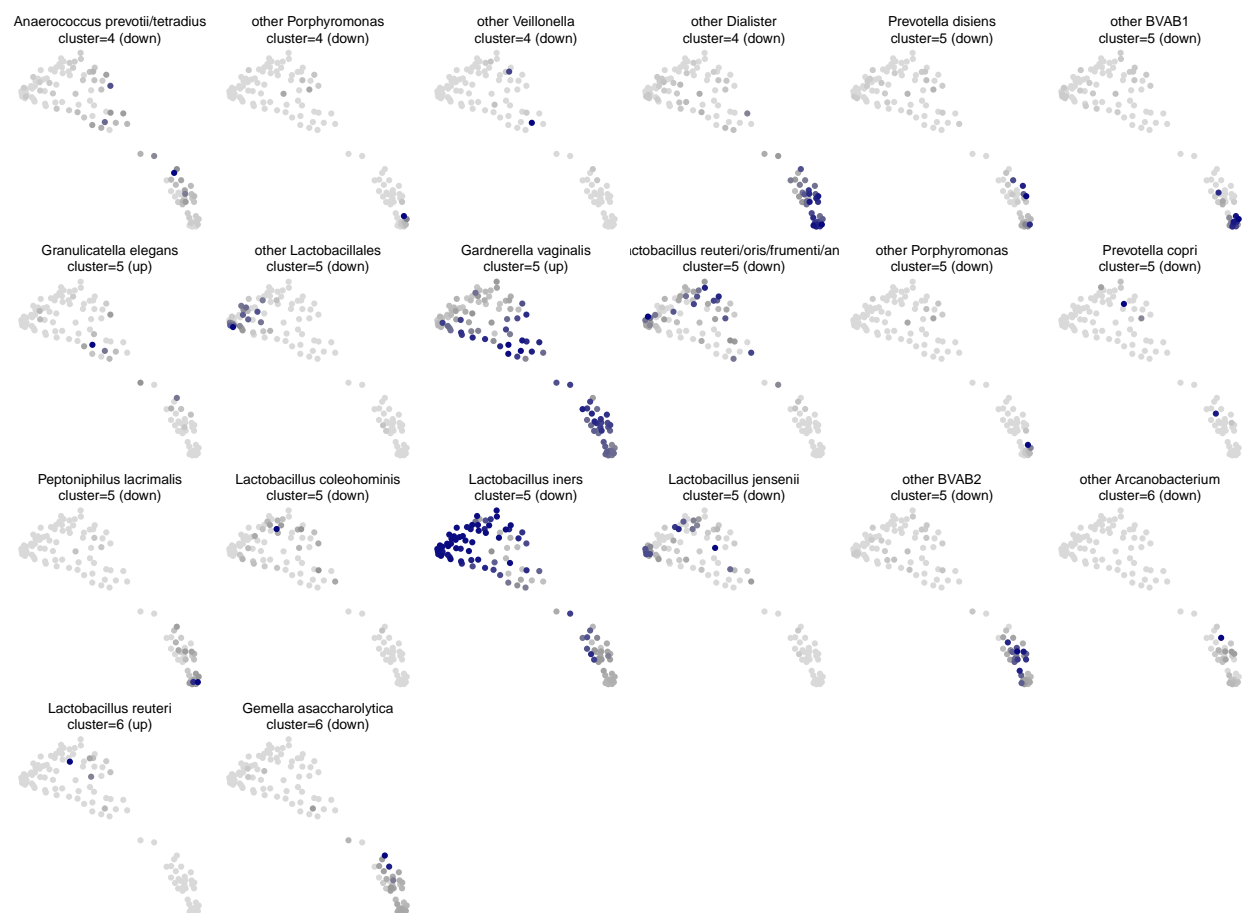


Plotting the most significant bacteria across clusters

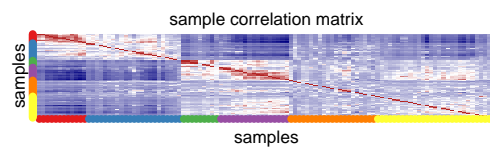
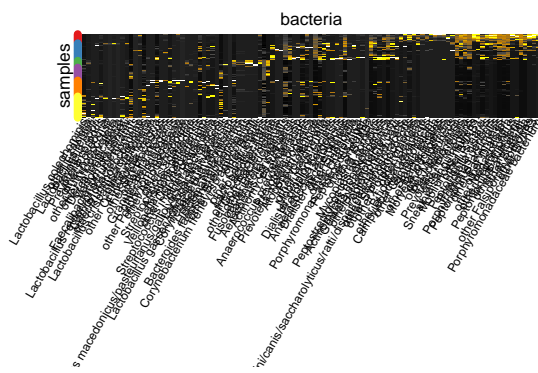






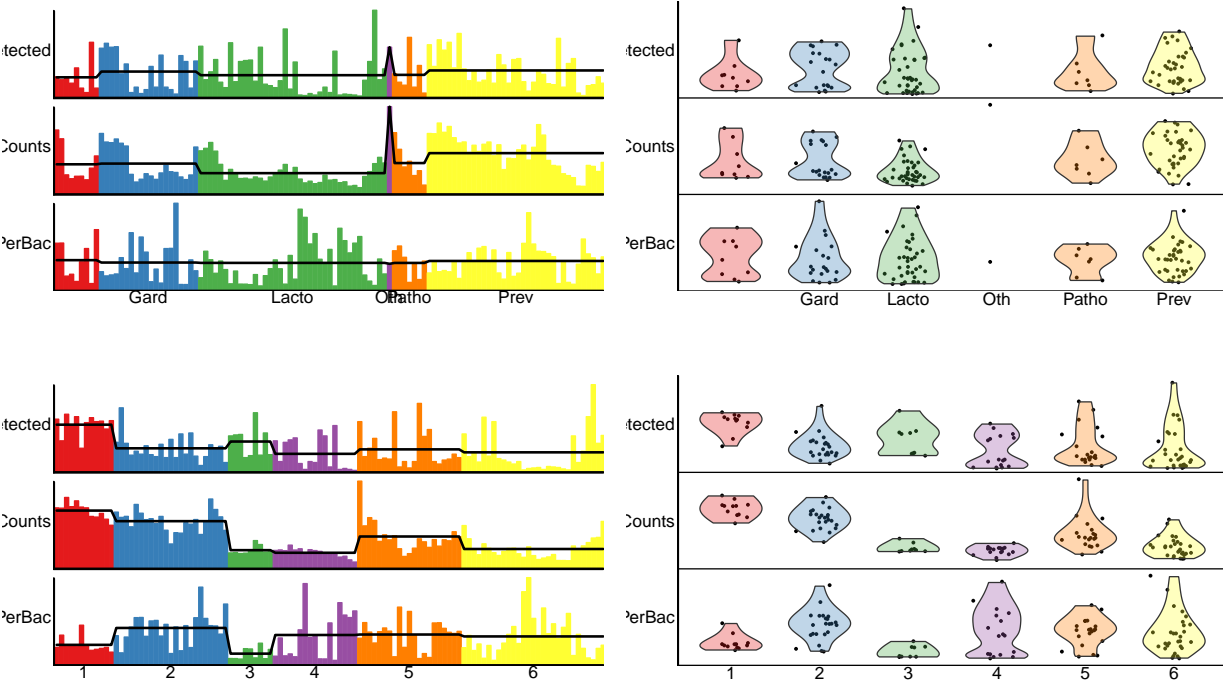


#Plotting bacteria across clusters



[1] -0.01463636

#Plotting bacteria across clusters



##	.2						
##	.1		Gard	Lacto	Oth	Patho	Prev
##	1	0	4	1	0	1	6
##	2	3	0	2	0	1	17
##	3	1	0	6	0	0	2
##	4	3	3	8	0	2	1
##	5	0	8	3	1	2	7
##	6	2	5	18	0	1	3

Saving clusters and differentially expressed bacteria