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

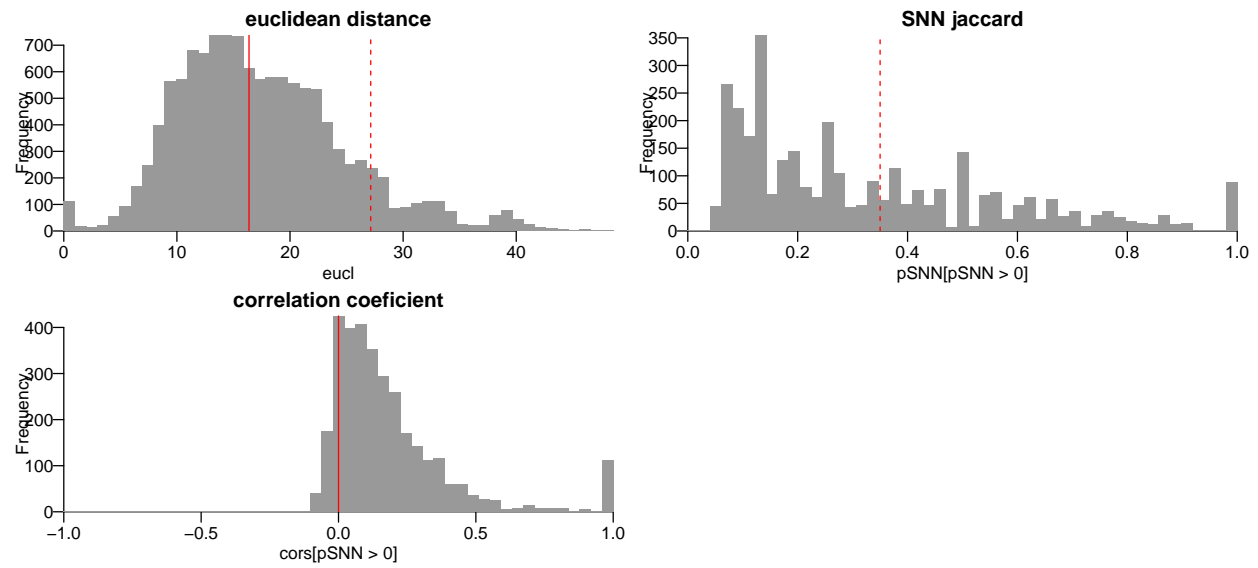
Loading data and metadata

```
## $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

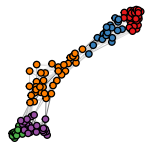


Computing a SNN graph from sample correlations



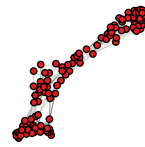
Visualise the data

Louvain clusters



- 1
- 2
- 3
- 4
- 5

dataset

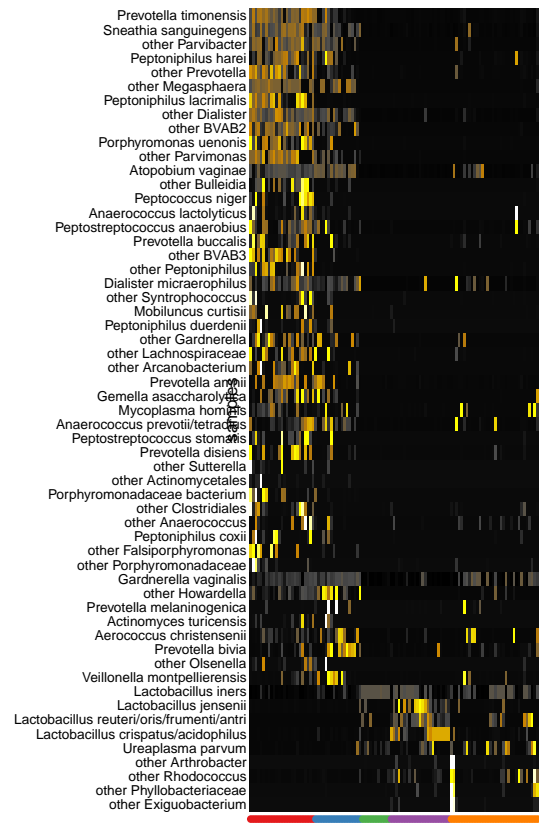
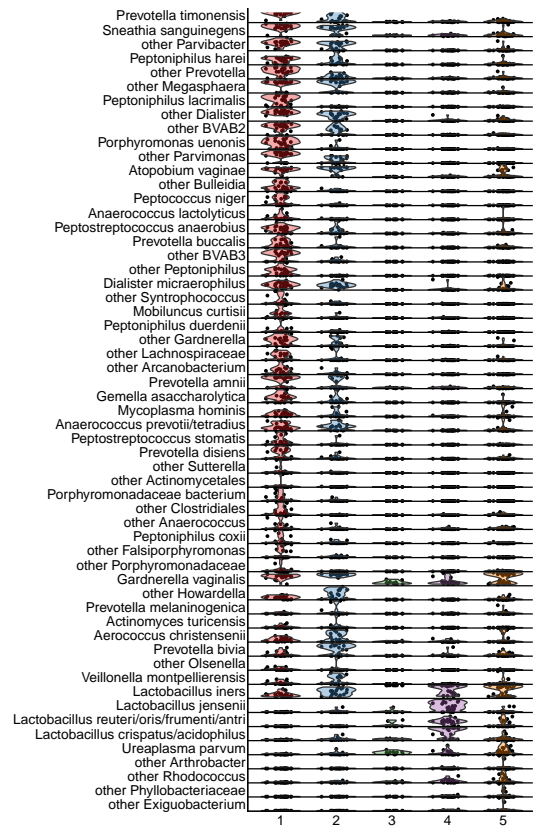
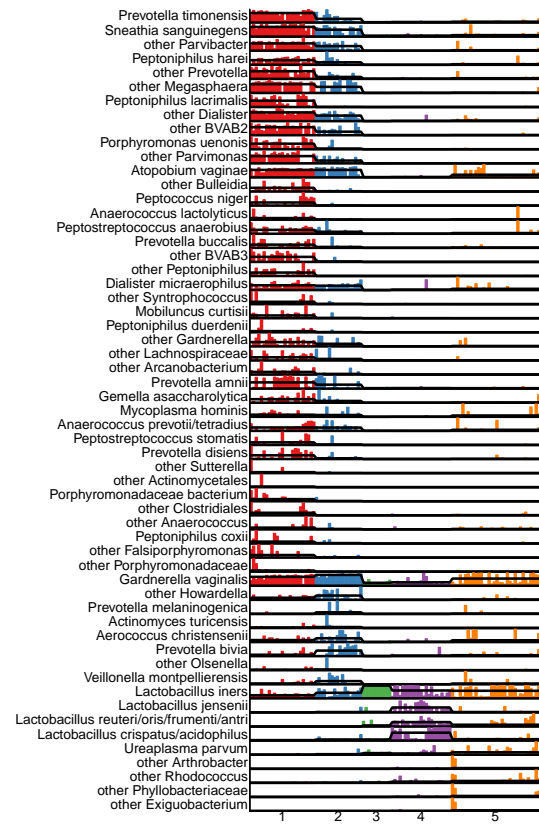


- ASV_CVL_\

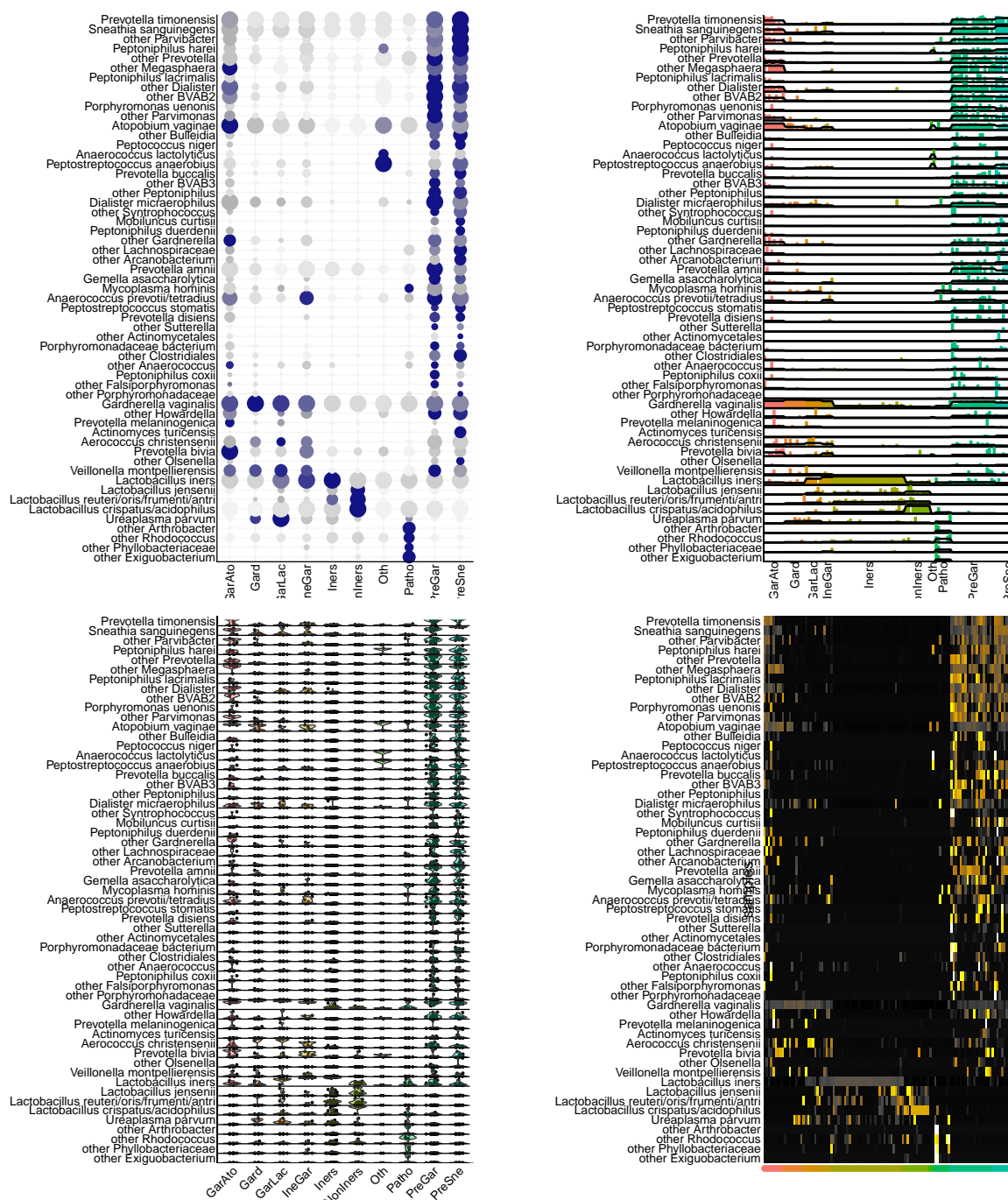
Computing differential expression across clusters

```
## [1] 92 8
```

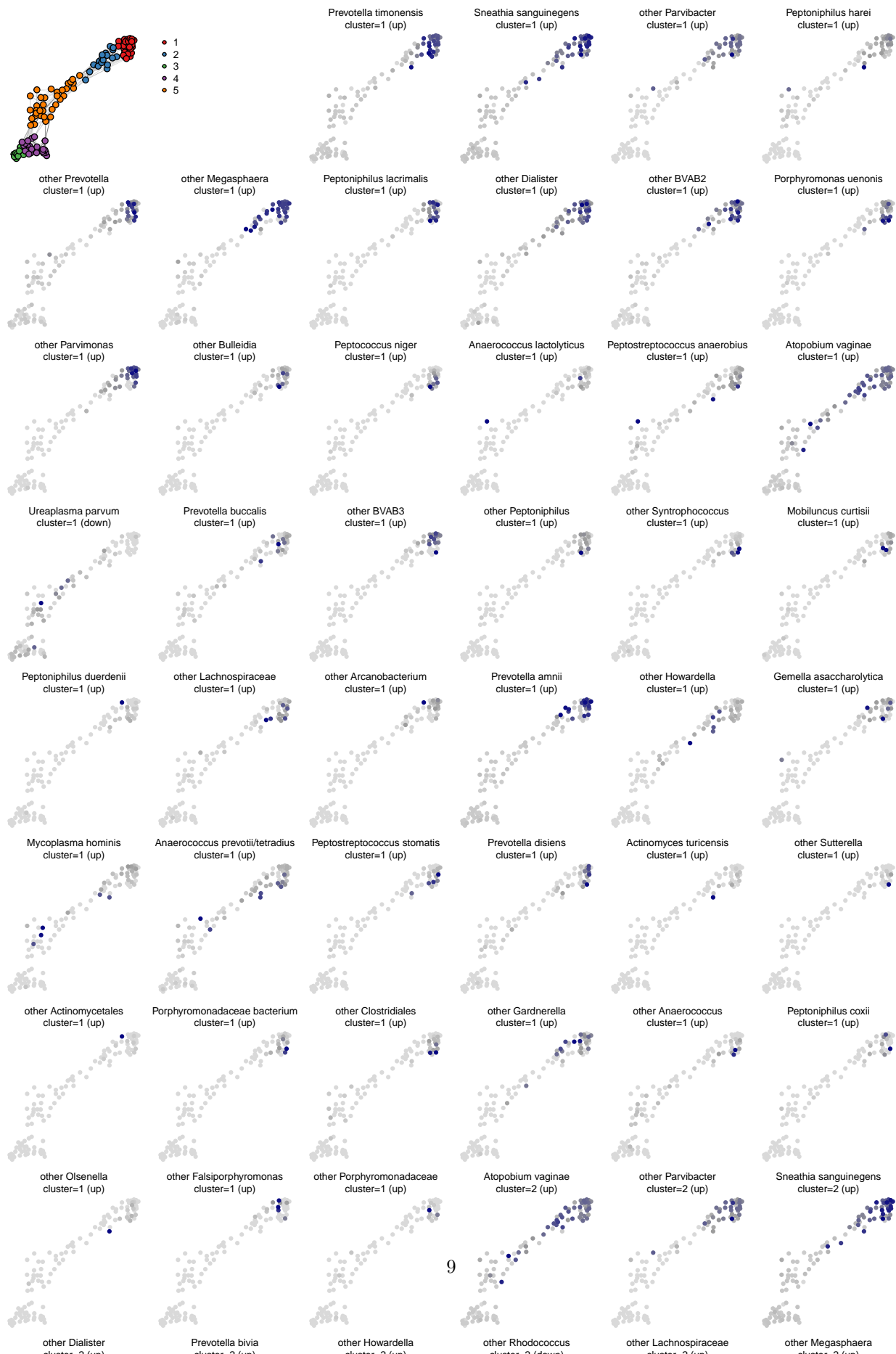
```
#Plotting the most significant bacteria across clusters
```

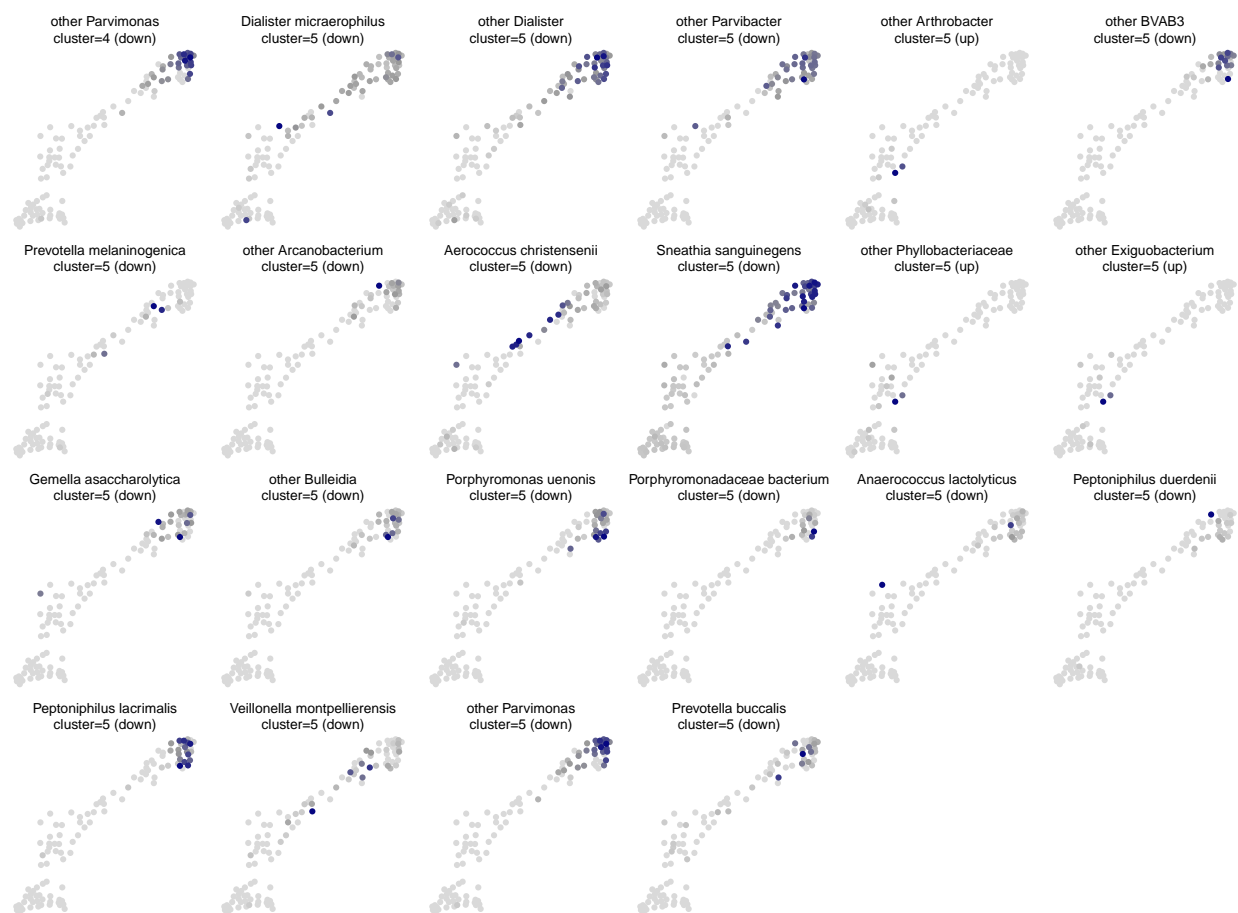


#Plotting the most significant bacteria across PREVIOUS ANNOTATION

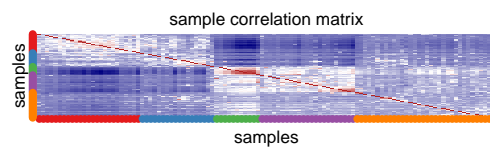
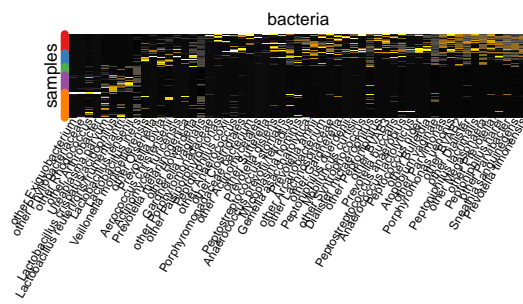


Plotting the most significant bacteria across clusters



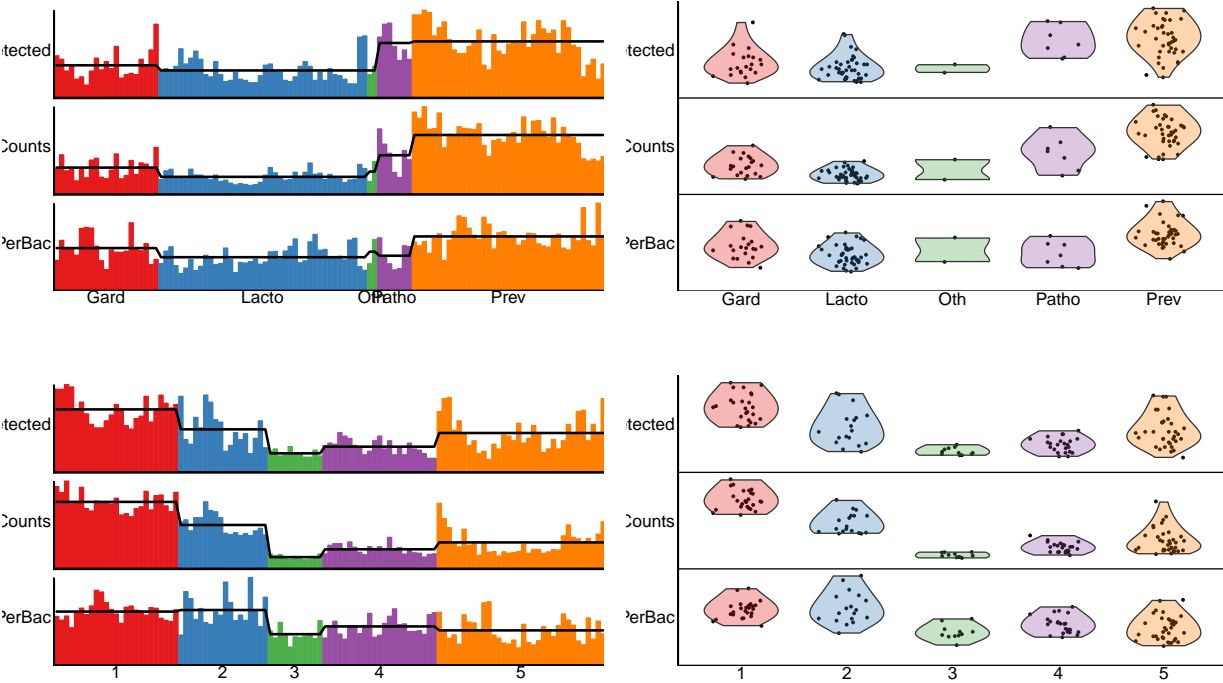


#Plotting bacteria across clusters



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

#Plotting bacteria across clusters



##	.2						
##	.1	Gard	Lacto	Oth	Patho	Prev	
##	1	0	0	0	0	25	
##	2	0	4	0	0	14	
##	3	0	0	11	0	0	
##	4	0	1	22	0	0	
##	5	0	16	9	2	7	0

Saving clusters and differentially expressed bacteria