Broliden_5325

09 October, 2020

Contents

#Load libraries and other scripts

#Defining some variables for the analysis

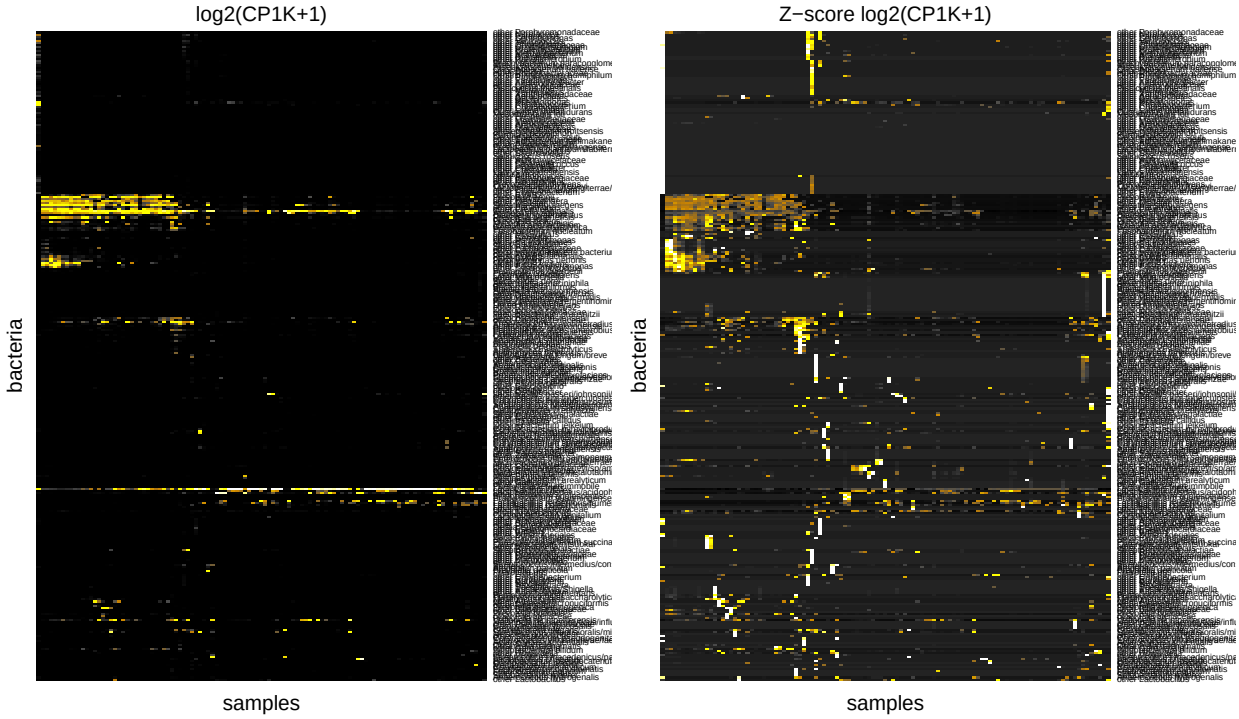
Loading data and metadata

```
## $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
```

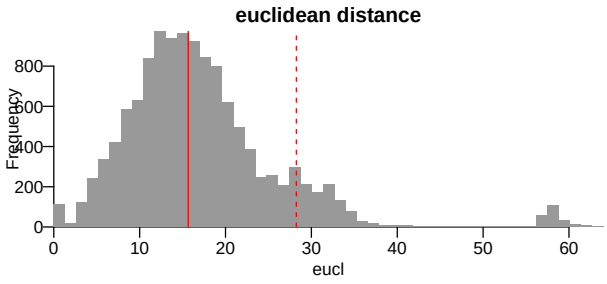
Merging microbiome datasets

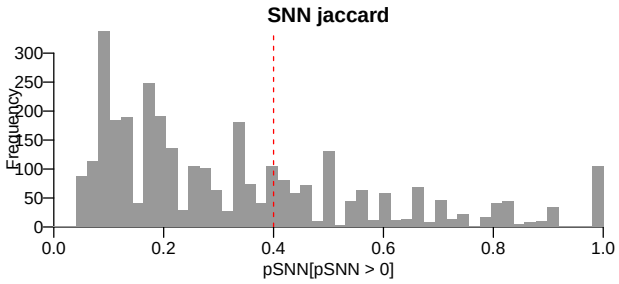
Organise the datasets

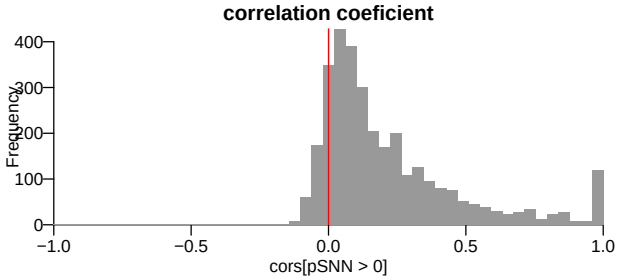
Organise the datasets



Computing a SNN graph from sample correlations





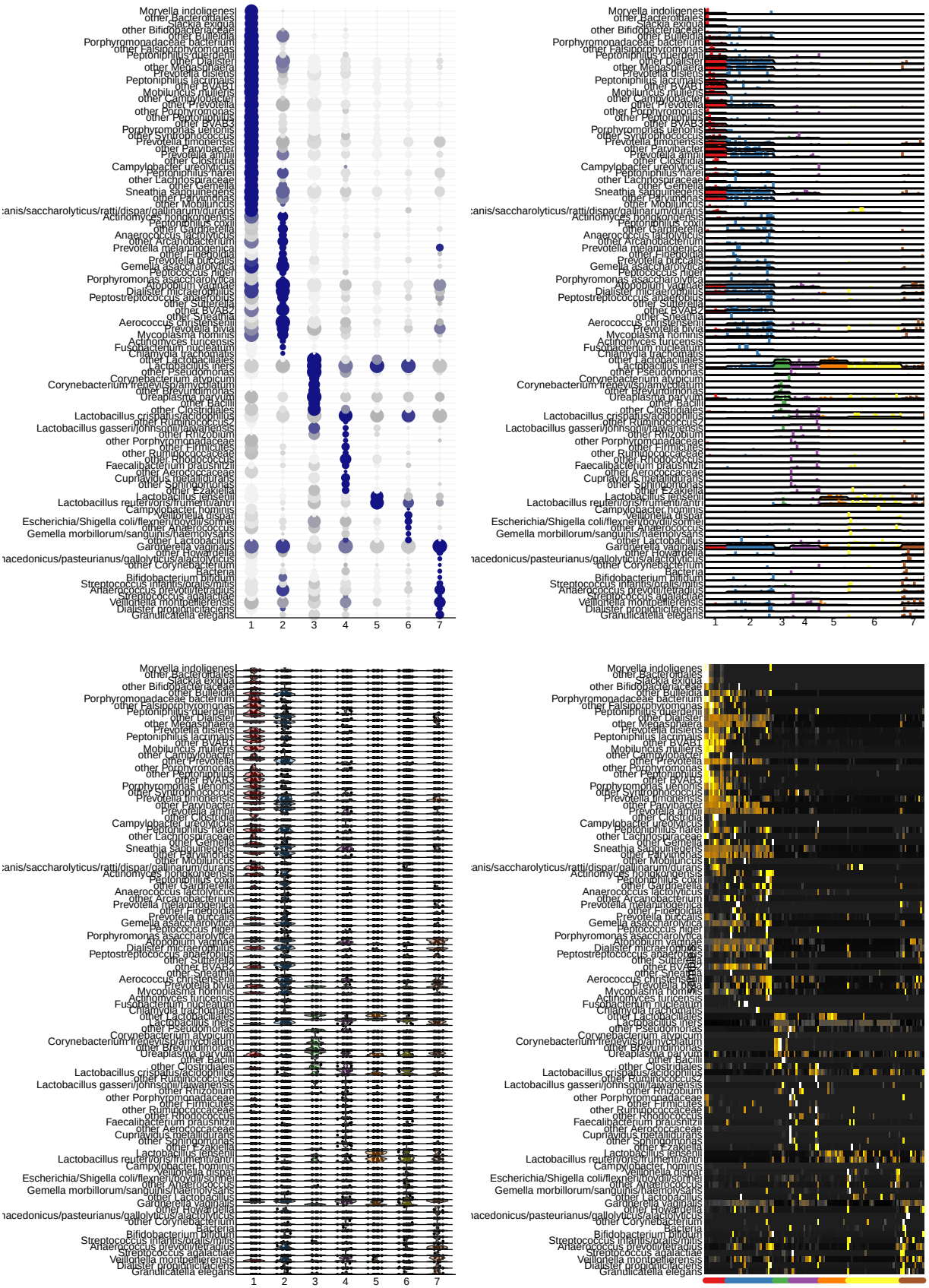


Visualise the data

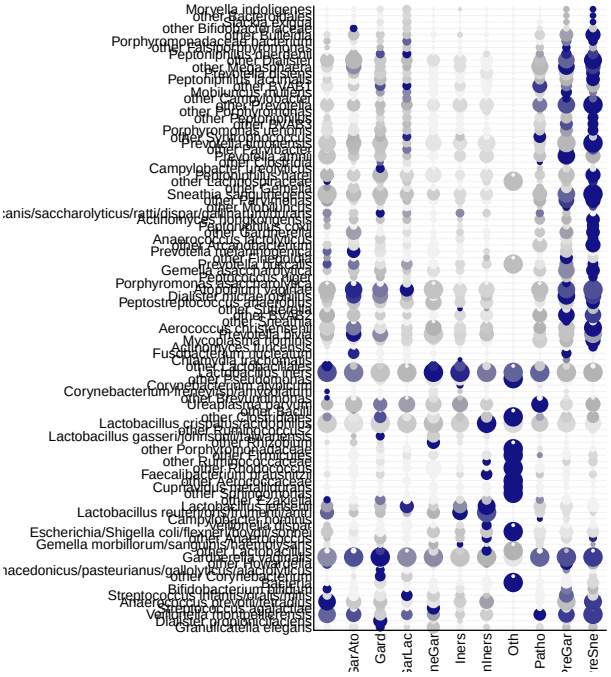
Computing differential expression across clusters

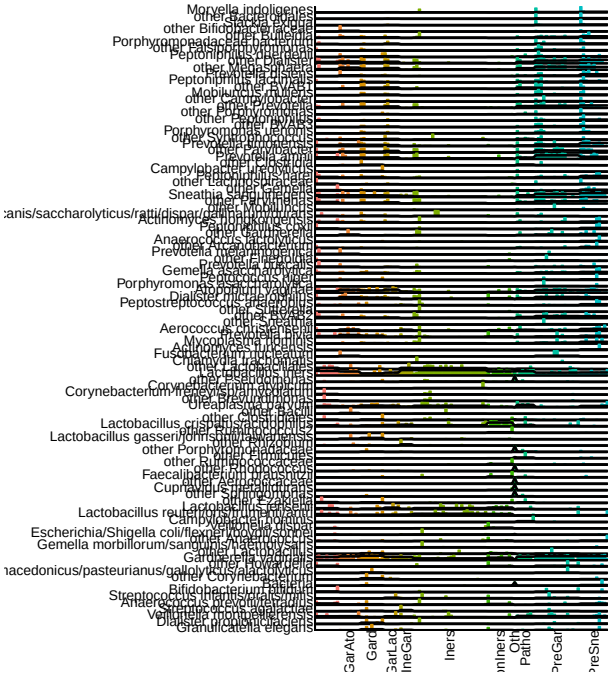
```
## [1] 130   8
```

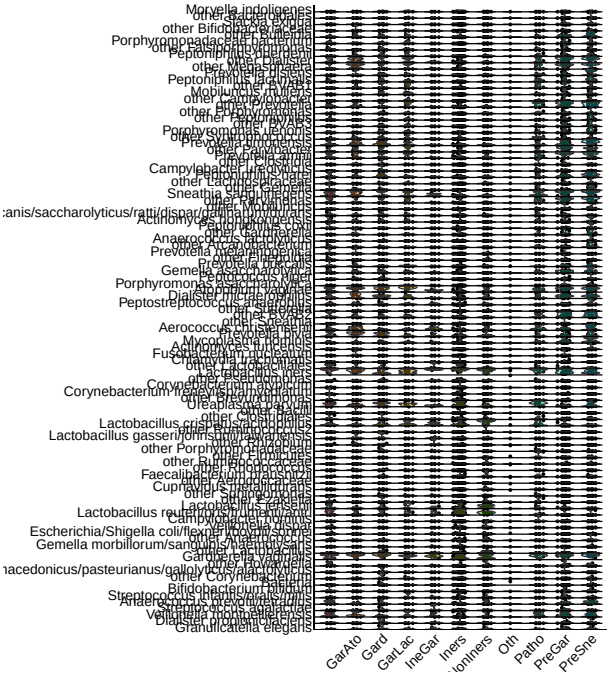
#Plotting the most significant bacteria across clusters

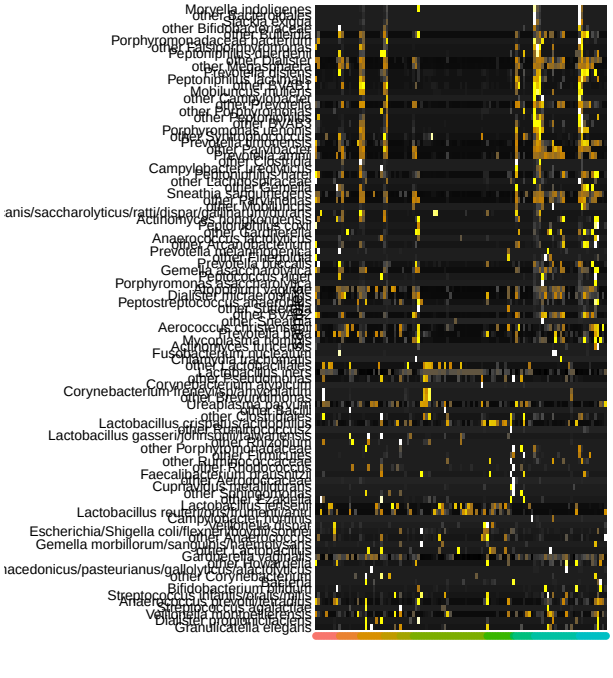

Morvella indoligenes
other Bacteroidales
Slackia exigua
other Bifidobacteriaceae
other Bulleidia
Porphyromonadaceae bacterium
other Falsiporphyromonas
Peptoniphilus duerdenii
other Dialister
other Megasphaera
Prevotella disiens
Peptoniphilus lacrimalis
other BVAB1
Mobiluncus mulieris
other Campylobacter
other Prevotella
other Porphyromonas
other Peptoniphilus
other BVAB3
Porphyromonas uenonis
other Syntrophococcus
Prevotella timonensis
other Parvibacter
Prevotella amnii
other Clostridia
Campylobacter ureolyticus
Peptoniphilus harei
other Lachnospiraceae
other Gemella
Sneathia sanguinegens
other Parvimonas
other Mobiluncus
anis/saccharolyticus/ratti/dispar/gallinarum/durans
Actinomyces hongkongensis
Peptoniphilus coxii
other Gardnerella
Anaerococcus lactolyticus
other Arcanobacterium
Prevotella melaninogenica
other Finegoldia
Prevotella buccalis
Gemella asaccharolytica
Peptococcus niger
Porphyromonas asaccharolytica
Atopobium vaginae
Dialister micraerophilus
Peptostreptococcus anaerobius
other Sutterella
other BVAB2
other Sneathia
Aerococcus christensenii
Prevotella bivia
Mycoplasma hominis
Actinomyces furcosis
Fusobacterium nucleatum
Chlamydia trachomatis
other Lactobacillales
Lactobacillus iners
other Pseudomonas
Corynebacterium atypicum
Corynebacterium freneyi/pilbarense
other Brevundimonas
Ureaplasma parvum
other Bacilli
other Clostridiales
Lactobacillus crispatus/acidophilus
other Ruminococcus2
Lactobacillus gasseri/johnsonii/taiwanensis
other Rhizobium
other Porphyromonadaceae
other Firmicutes
other Ruminococcaceae
other Rhodococcus
Faecalibacterium prausnitzii
other Aerococcaceae
Cupriavidus metallidurans
other Sphingomonas
other Ezakella
Lactobacillus jensenii
Lactobacillus reuteri/ors/frumenti/antri
Campylobacter hominis
Veillonella dispar
Escherichia/Shigella coli/flexneri/boydii/sonnei
other Anaerococcus
Gemella morbillorum/sanguinis/haemolysans
other Lactobacillus
Gardnerella vaginalis
other Howardella
acedonicus/pasteurianus/gallolyticus/alactolyticus
other Corynebacterium
Bacteria
Bifidobacterium bifidum
Streptococcus infantis/oralis/mitis
Anaerococcus prevotii/tetradius
Streptococcus agalactiae
Veillonella montpellierensis
Dialister propionicifaciens
Granulicatella elegans
1
2
3
4
5
6
7

#Plotting the most significant bacteria across PREVIOUS ANNOTATION

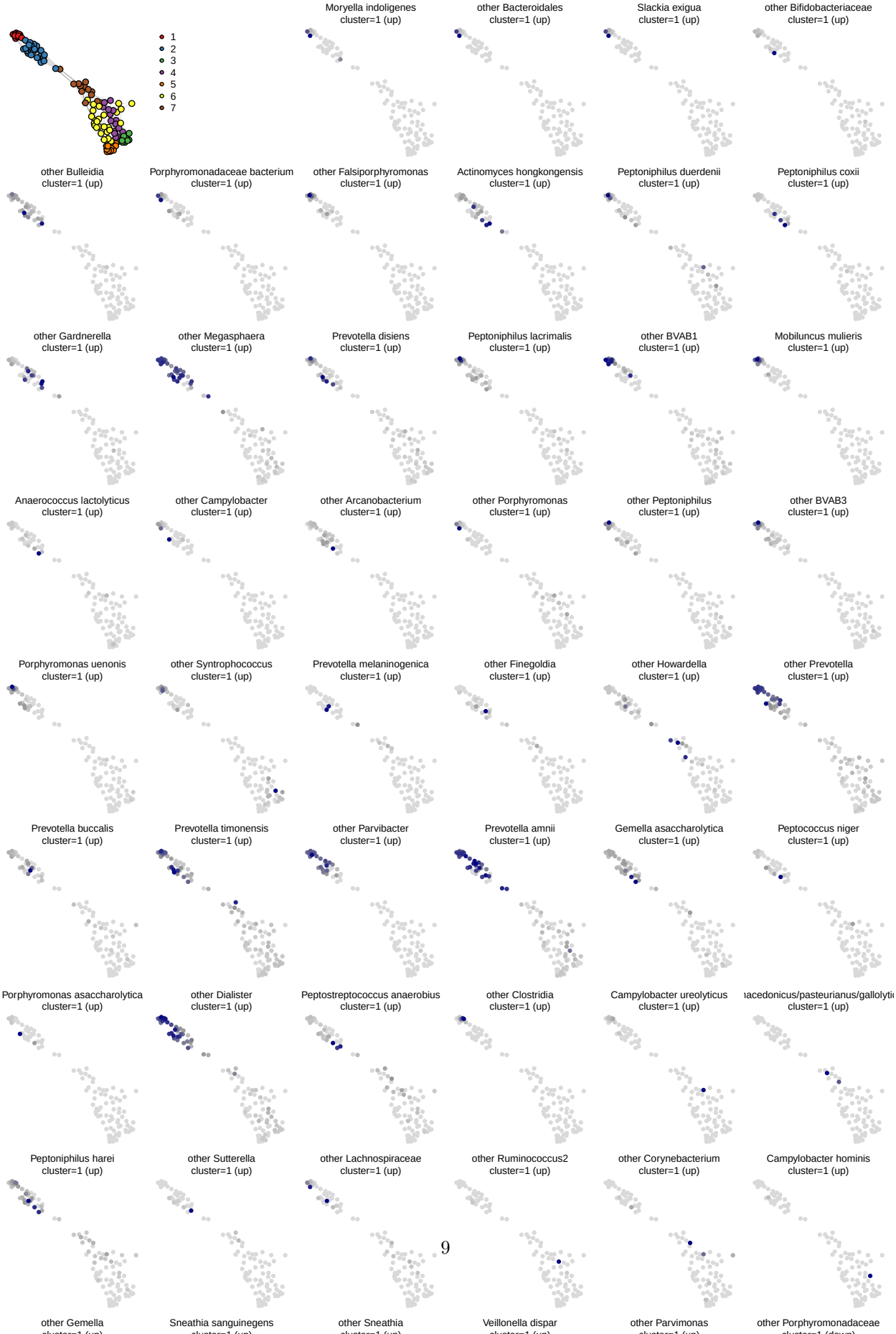


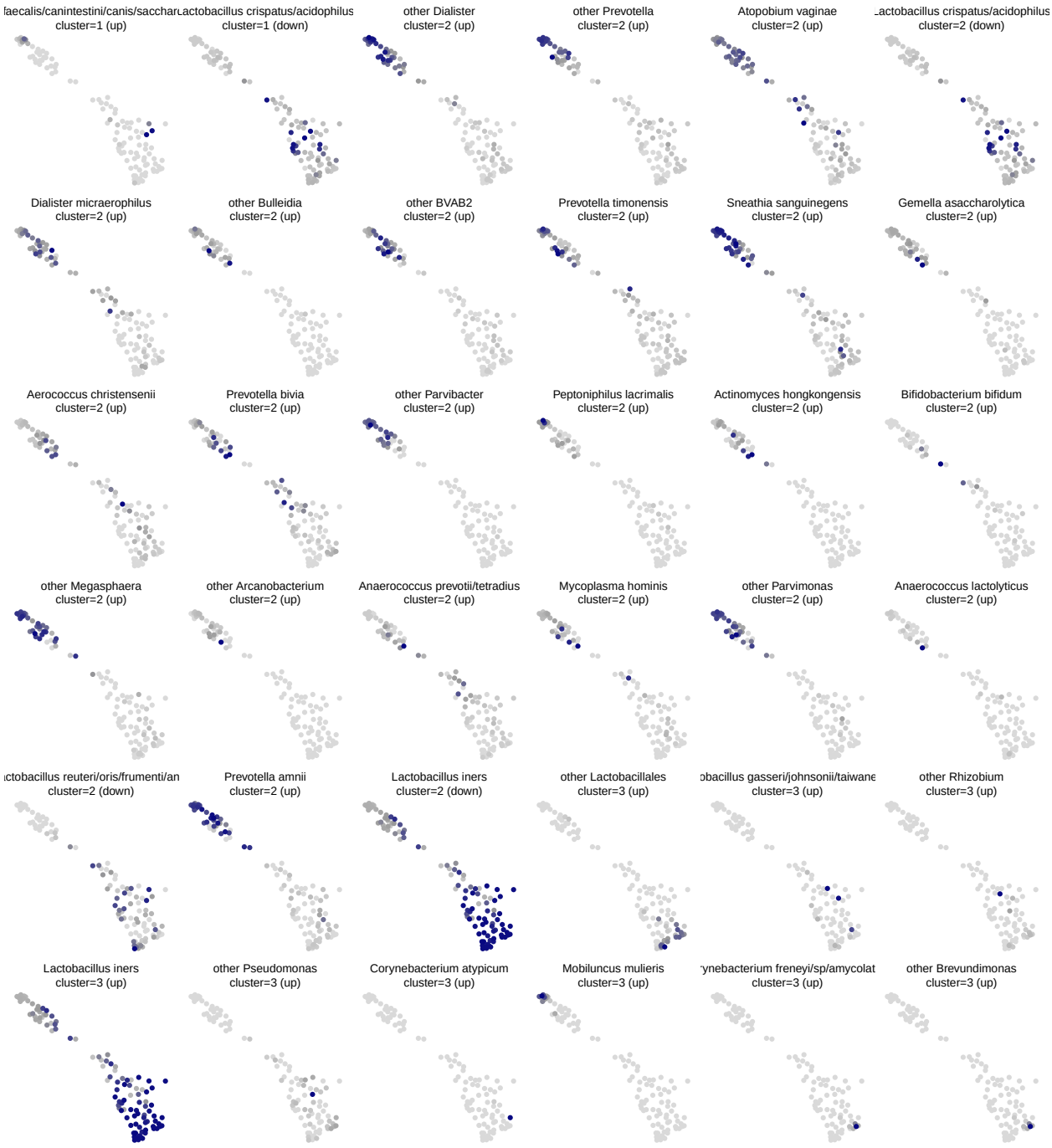


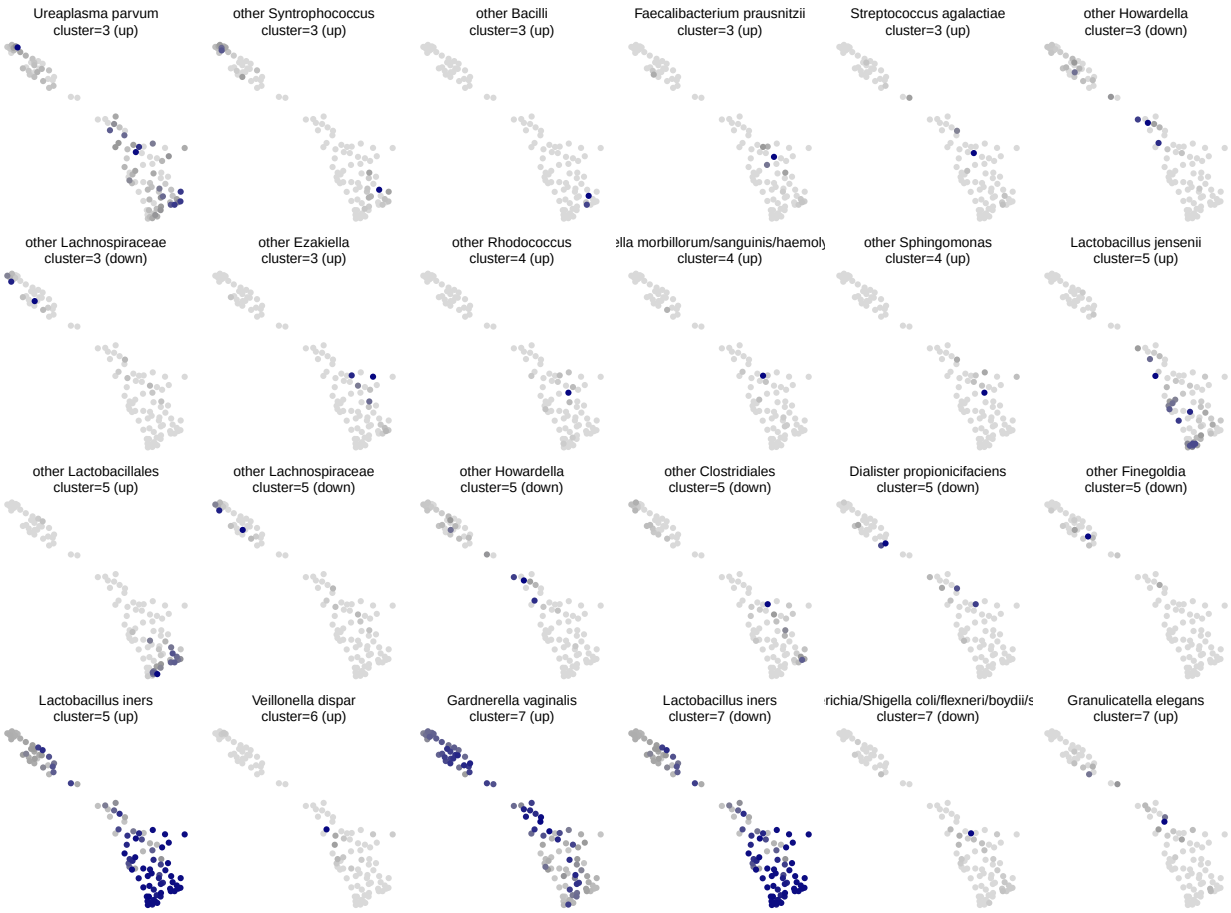




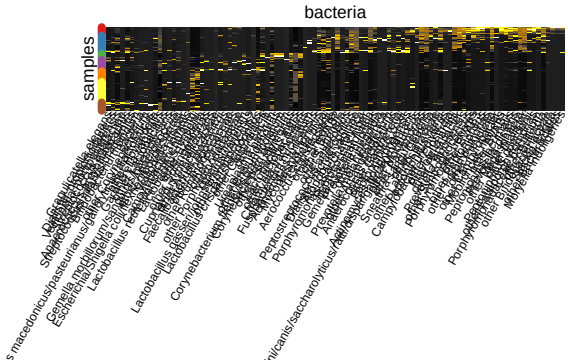
Plotting the most significant bacteria across clusters

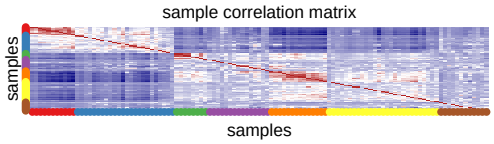



laecalis/canintestini/canis/sacchar
cluster=1 (up)
Lactobacillus crispatus/acidophilus
cluster=1 (down)
other Dialister
cluster=2 (up)
other Prevotella
cluster=2 (up)
Atopobium vaginae
cluster=2 (up)
actobacillus crispatus/acidophilus
cluster=2 (down)
Dialister micraerophilus
cluster=2 (up)
other Bulleidia
cluster=2 (up)
other BVAB2
cluster=2 (up)
Prevotella timonensis
cluster=2 (up)
Sneathia sanguinegens
cluster=2 (up)
Gemella asaccharolytica
cluster=2 (up)
Aerococcus christensenii
cluster=2 (up)
Prevotella bivia
cluster=2 (up)
other Parvibacter
cluster=2 (up)
Peptoniphilus lacrimalis
cluster=2 (up)
Actinomyces hongkongensis
cluster=2 (up)
Bifidobacterium bifidum
cluster=2 (up)
other Megasphaera
cluster=2 (up)
other Arcanobacterium
cluster=2 (up)
Anaerococcus prevotii/tetradius
cluster=2 (up)
Mycoplasma hominis
cluster=2 (up)
other Parvimonas
cluster=2 (up)
Anaerococcus lactolyticus
cluster=2 (up)
ctobacillus reuteri/oris/frumenti/an
cluster=2 (down)
Prevotella amnii
cluster=2 (up)
Lactobacillus iners
cluster=2 (down)
other Lactobacillales
cluster=3 (up)
obacillus gasseri/johnsonii/taiwane
cluster=3 (up)
other Rhizobium
cluster=3 (up)
Lactobacillus iners
cluster=3 (up)
other Pseudomonas
cluster=3 (up)
Corynebacterium atypicum
cluster=3 (up)
Mobiluncus mulieris
cluster=3 (up)
ynebacterium freneyi/sp/amycolat
cluster=3 (up)
other Brevundimonas
cluster=3 (up)


Ureaplasma parvum
cluster=3 (up)
other Syntrophococcus
cluster=3 (up)
other Bacilli
cluster=3 (up)
Faecalibacterium prausnitzii
cluster=3 (up)
Streptococcus agalactiae
cluster=3 (up)
other Howardella
cluster=3 (down)
other Lachnospiraceae
cluster=3 (down)
other Ezakiella
cluster=3 (up)
other Rhodococcus
cluster=4 (up)
ella morbillorum/sanguinis/haemoly
cluster=4 (up)
other Sphingomonas
cluster=4 (up)
Lactobacillus jensenii
cluster=5 (up)
other Lactobacillales
cluster=5 (up)
other Lachnospiraceae
cluster=5 (down)
other Howardella
cluster=5 (down)
other Clostridiales
cluster=5 (down)
Dialister propionicifaciens
cluster=5 (down)
other Finegoldia
cluster=5 (down)
Lactobacillus iners
cluster=5 (up)
Veillonella dispar
cluster=6 (up)
Gardnerella vaginalis
cluster=7 (up)
Lactobacillus iners
cluster=7 (down)
richia/Shigella coli/flexneri/boydii/s
cluster=7 (down)
Granulicatella elegans
cluster=7 (up)

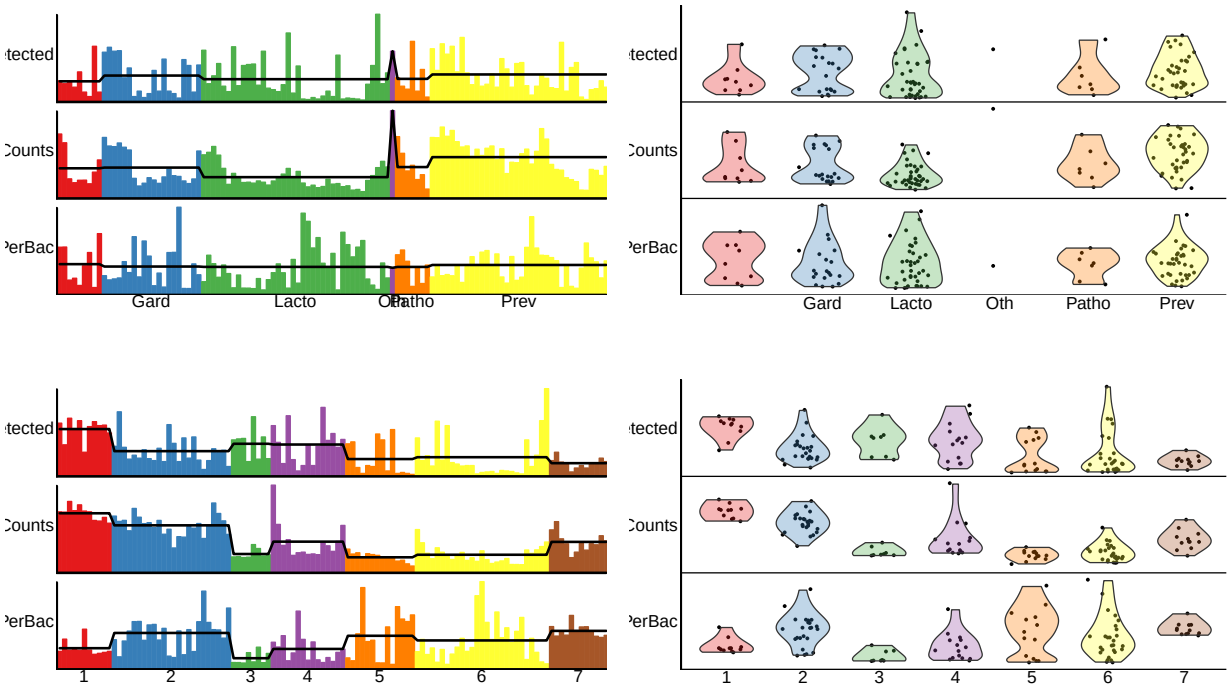
#Plotting bacteria across clusters






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

#Plotting bacteria across clusters




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

#Plotting bacteria across clusters

#Dataset integration