Correlations

Daniel Flores Orozco

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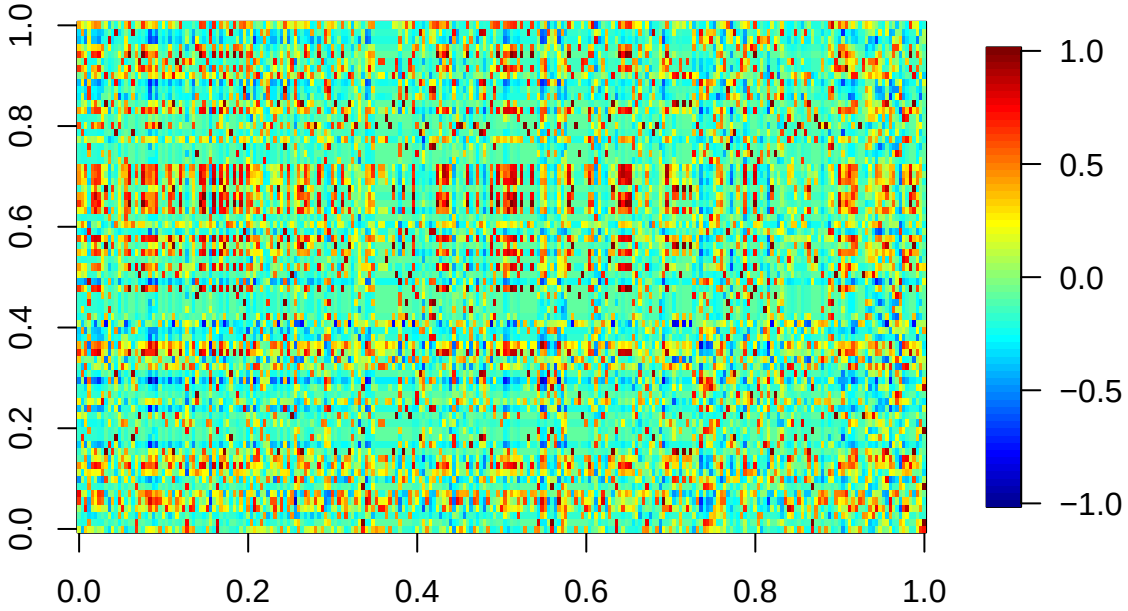
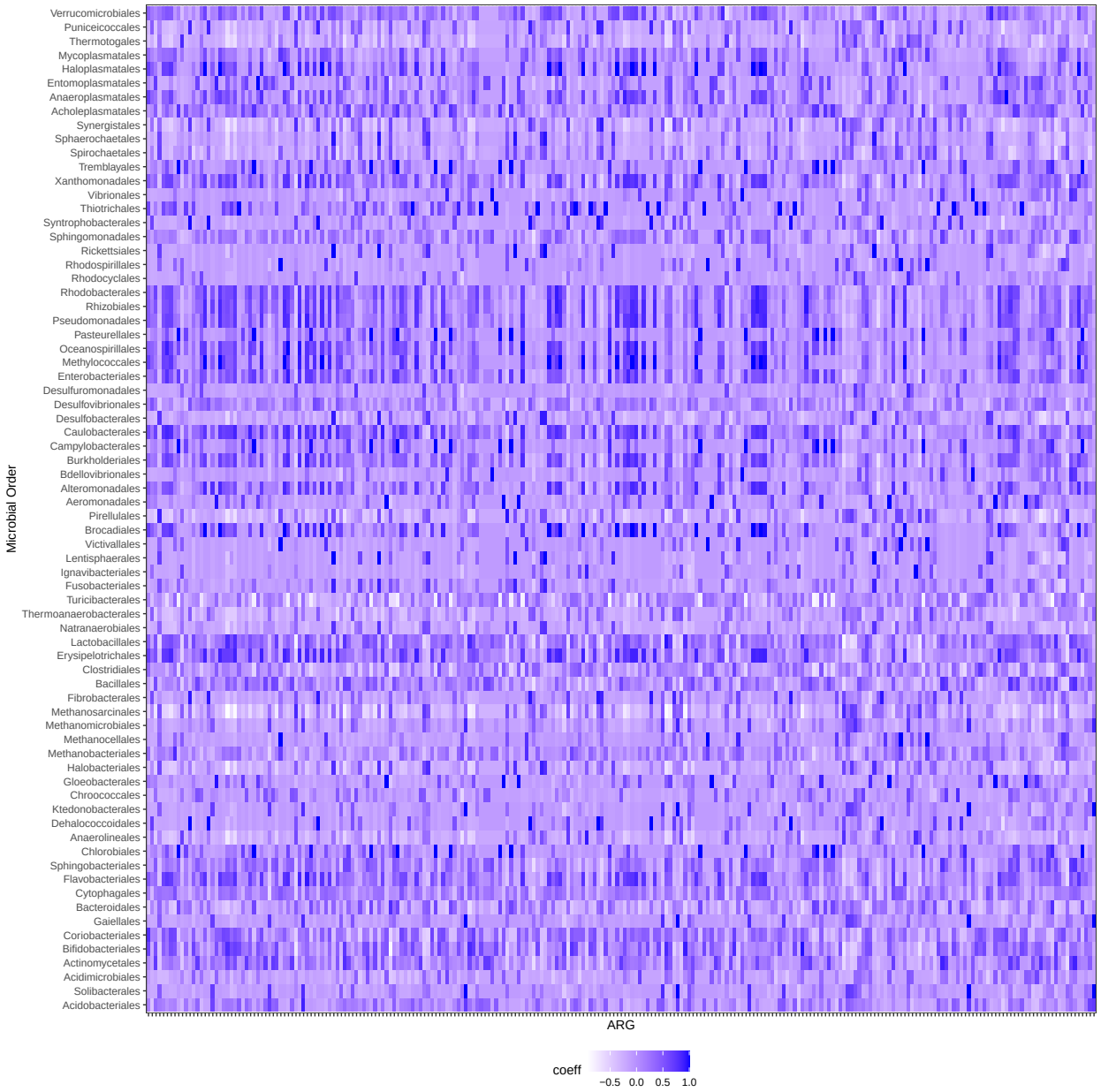



```
## Joining, by = "microbe"
```

```
## Joining, by = "gene_id"
```




```
## Warning: Setting row names on a tibble is deprecated.

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## Warning in brewer.pal(ColourCount1, "Paired"): n too large, allowed maximum for palette Paired is 12
## Returning the palette you asked for with that many colors
```
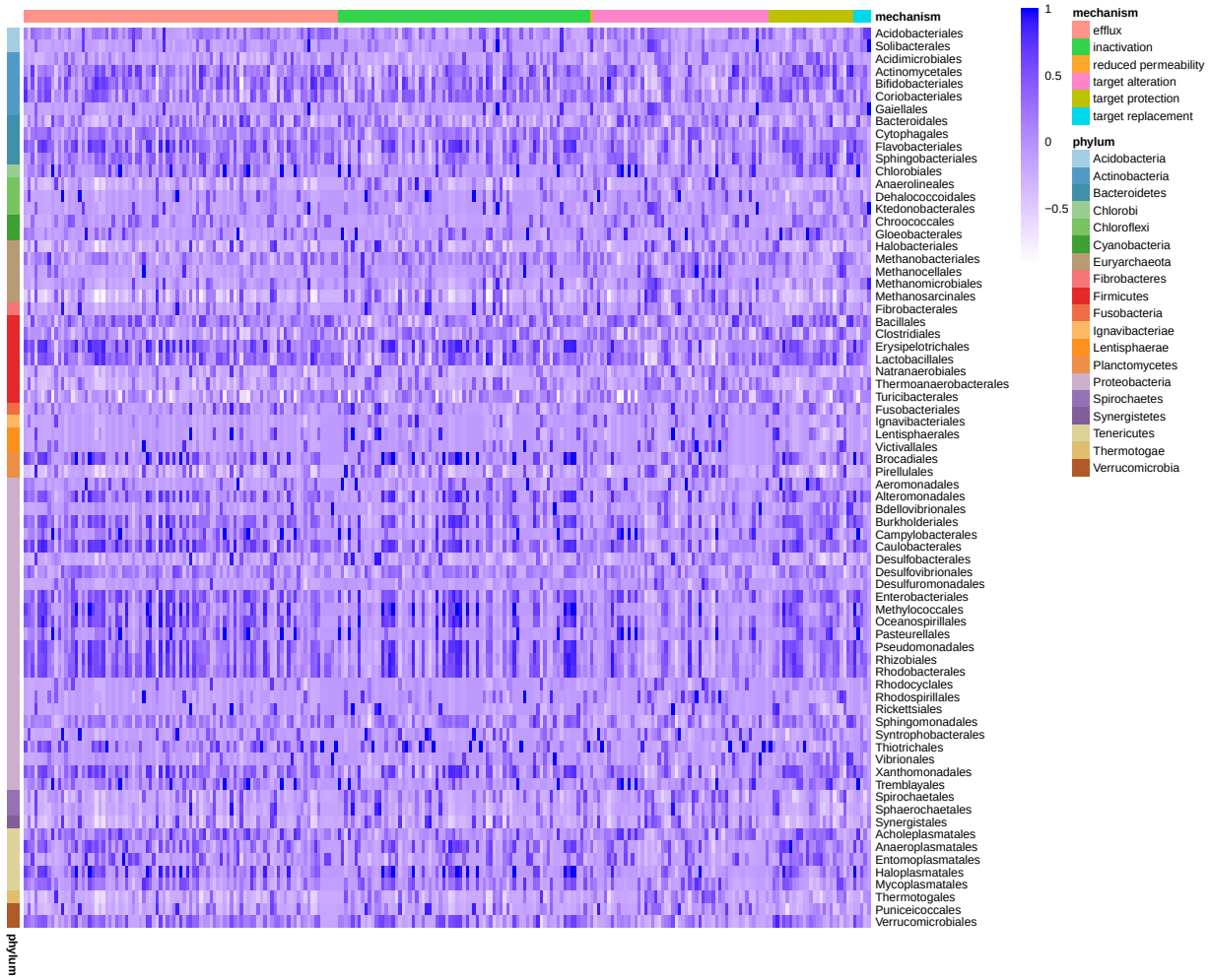
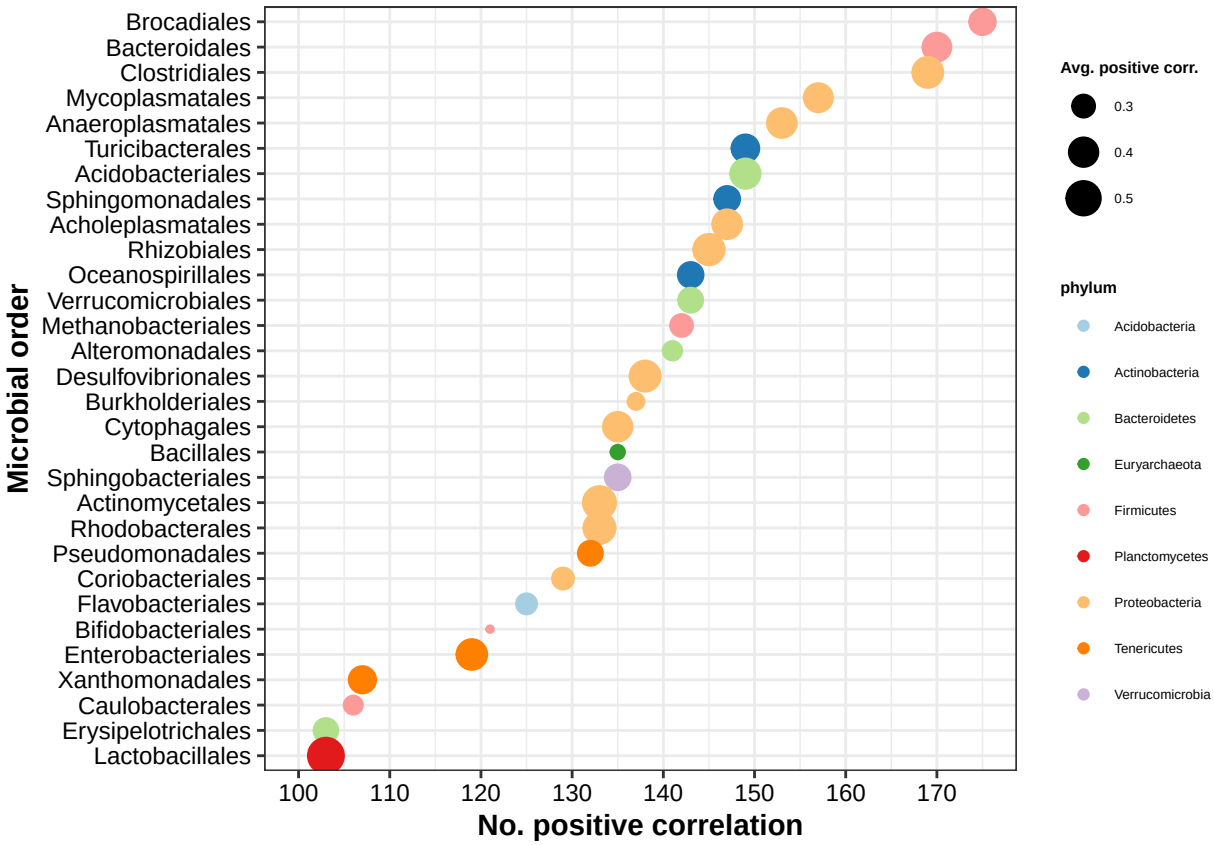



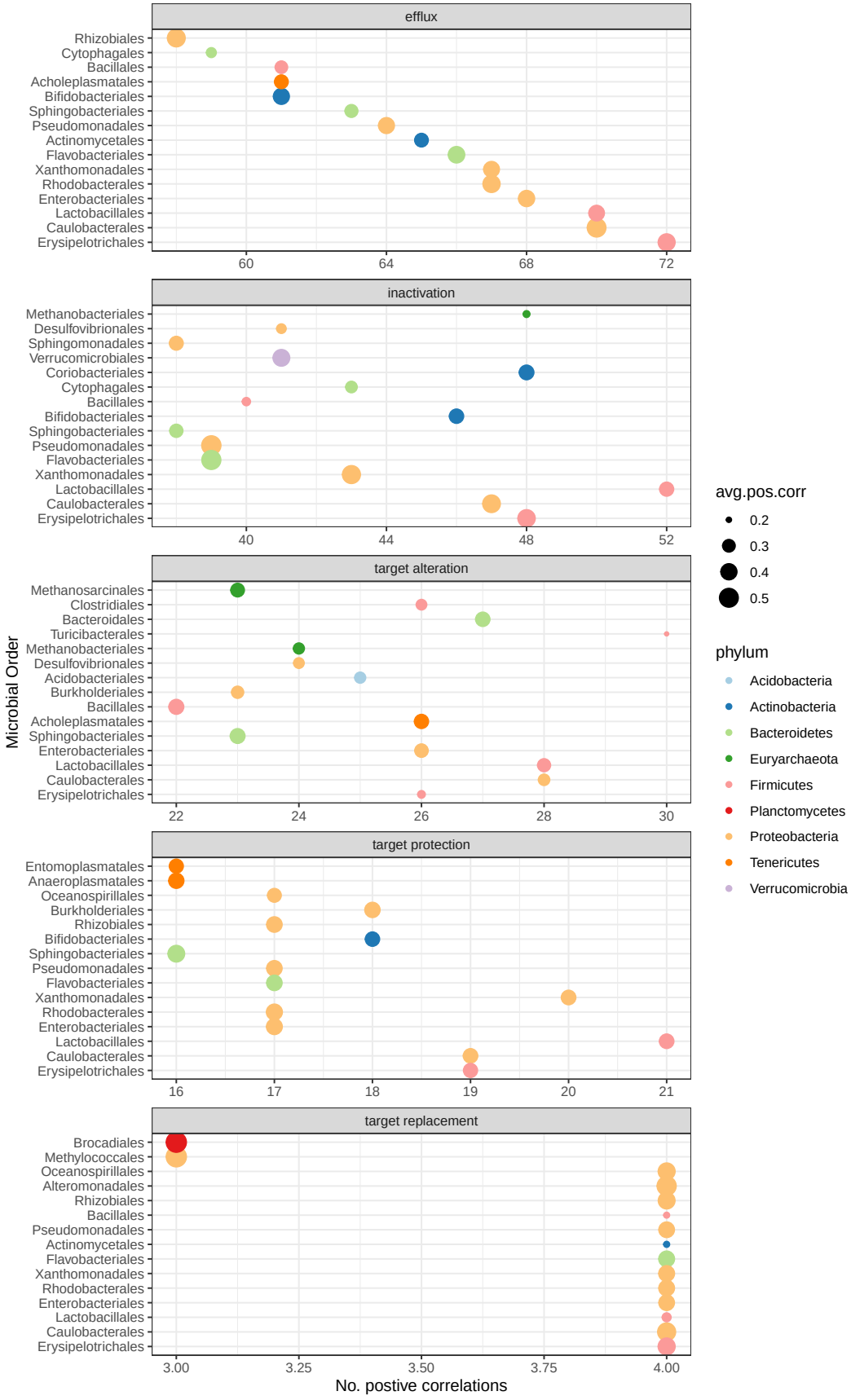
2. Summary of the correlations

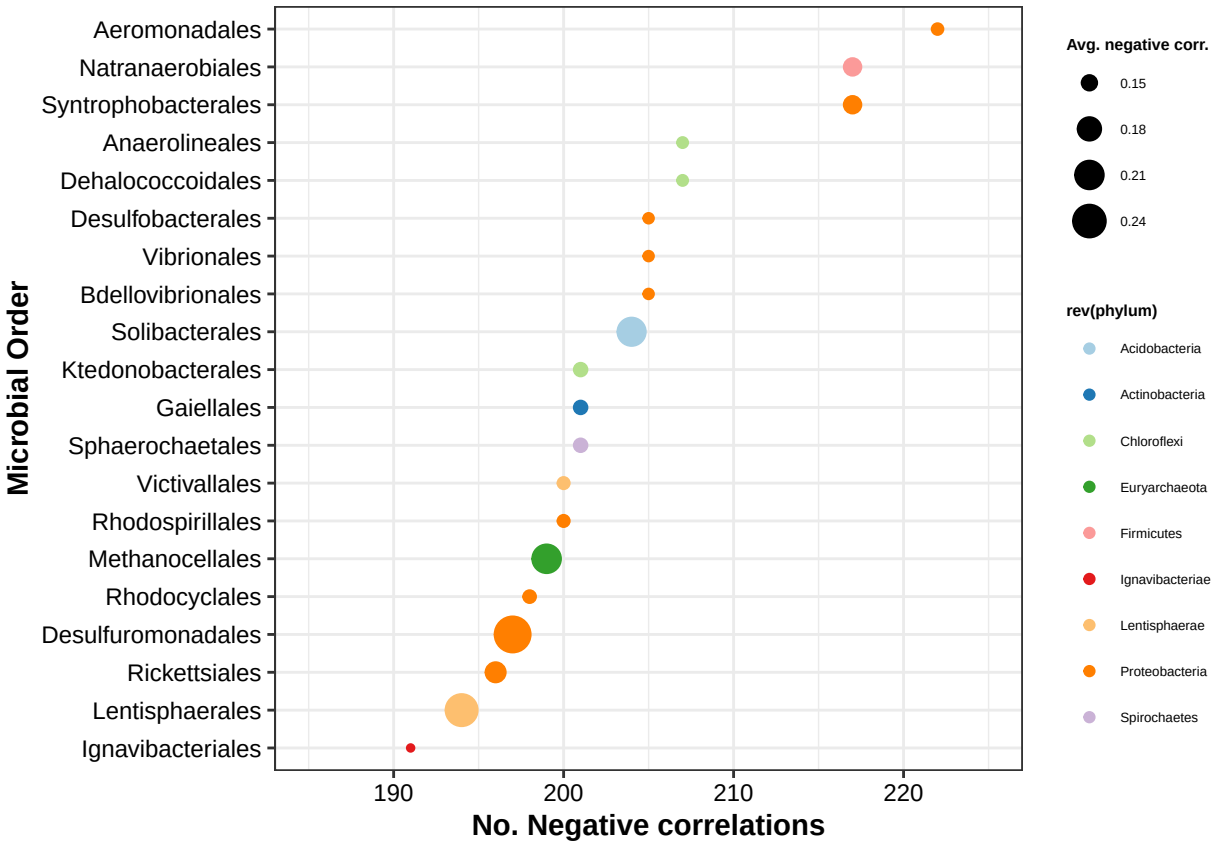
2.1 Microbes vs No. positive correlations

```
## `summarise()` has grouped output by 'microbe'. You can override using the `.groups` argument.
```




```
## `summarise()` has grouped output by 'mechanism', 'microbe'. You can override using the `.groups` argu
```


efflux
Rhizobiales
Cytophagales
Bacillales
Acholeplasmatales
Bifidobacteriales
Sphingobacteriales
Pseudomonadales
Actinomycetales
Flavobacteriales
Xanthomonadales
Rhodobacterales
Enterobacteriales
Lactobacillales
Caulobacterales
Erysipelotrichales
60
64
68
72
inactivation
Methanobacteriales
Desulfovibrionales
Sphingomonadales
Verrucomicrobiales
Coriobacteriales
Cytophagales
Bacillales
Bifidobacteriales
Sphingobacteriales
Pseudomonadales
Flavobacteriales
Xanthomonadales
Lactobacillales
Caulobacterales
Erysipelotrichales
40
44
48
52
target alteration
Methanosarcinales
Clostridiales
Bacteroidales
Turicibacterales
Methanobacteriales
Desulfovibrionales
Acidobacteriales
Burkholderiales
Bacillales
Acholeplasmatales
Sphingobacteriales
Enterobacteriales
Lactobacillales
Caulobacterales
Erysipelotrichales
22
24
26
28
30
target protection
Entomoplasmatales
Anaeroplasmatales
Oceanospirillales
Burkholderiales
Rhizobiales
Bifidobacteriales
Sphingobacteriales
Pseudomonadales
Flavobacteriales
Xanthomonadales
Rhodobacterales
Enterobacteriales
Lactobacillales
Caulobacterales
Erysipelotrichales
16
17
18
19
20
21
target replacement
Brocadiales
Methylococcales
Oceanospirillales
Alteromonadales
Rhizobiales
Bacillales
Pseudomonadales
Actinomycetales
Flavobacteriales
Xanthomonadales
Rhodobacterales
Enterobacteriales
Lactobacillales
Caulobacterales
Erysipelotrichales
3.00
3.25
3.50
3.75
4.00
Microbial Order
No. postive correlations
avg.pos.corr
0.2
0.3
0.4
0.5
phylum
Acidobacteria
Actinobacteria
Bacteroidetes
Euryarchaeota
Firmicutes
Planctomycetes
Proteobacteria
Tenericutes
Verrucomicrobia

2 Negative correlations

```
## `summarise()` has grouped output by 'microbe'. You can override using the `.groups` argument.
```