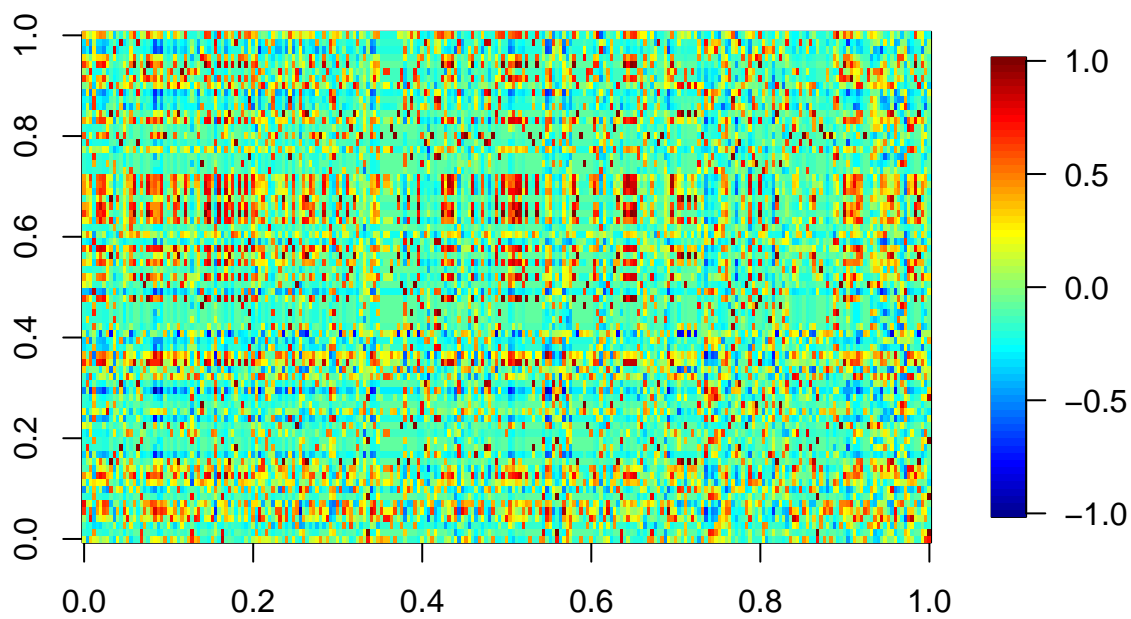


Correlations

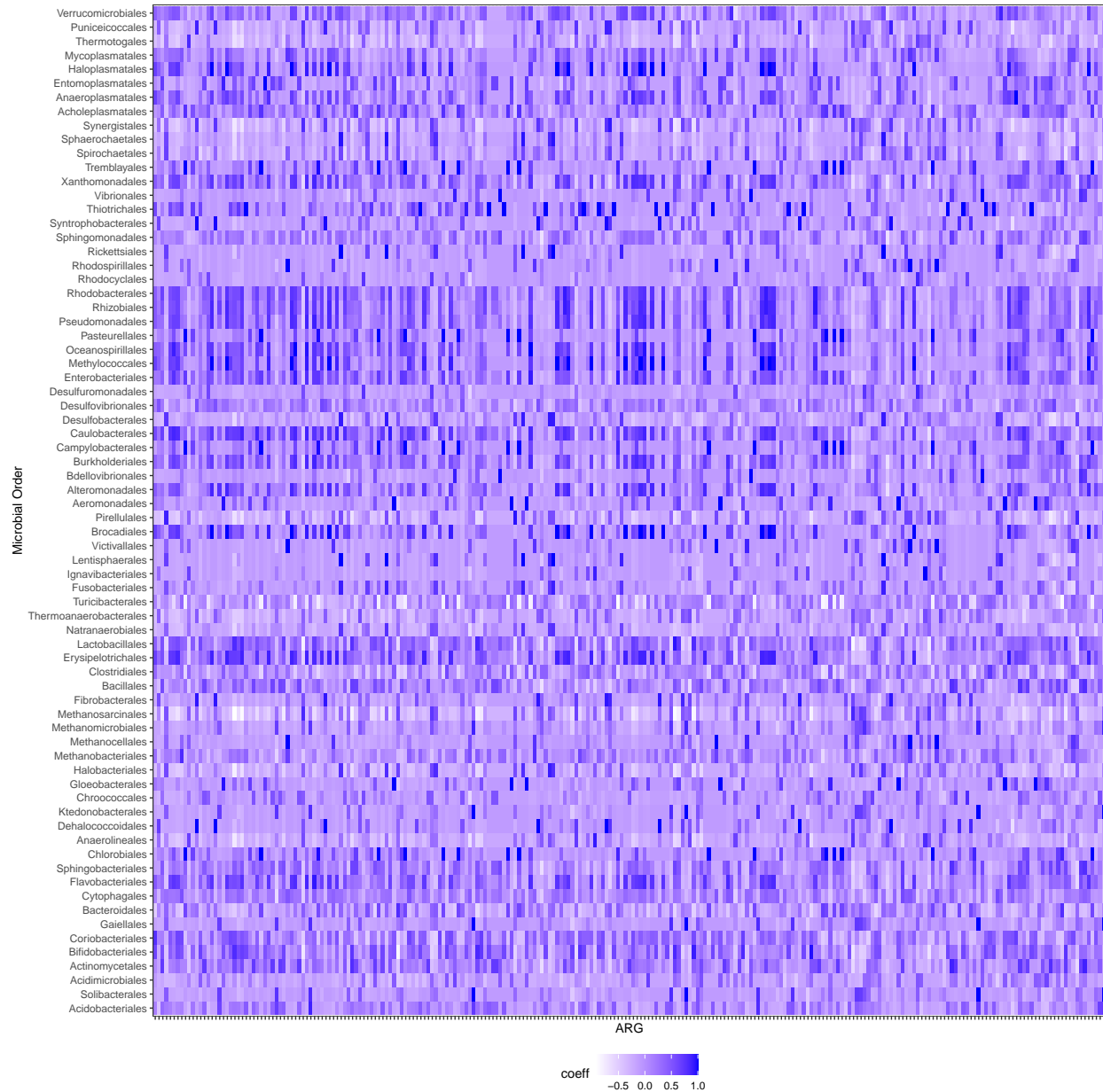
Daniel Flores Orozco

08/02/2022



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

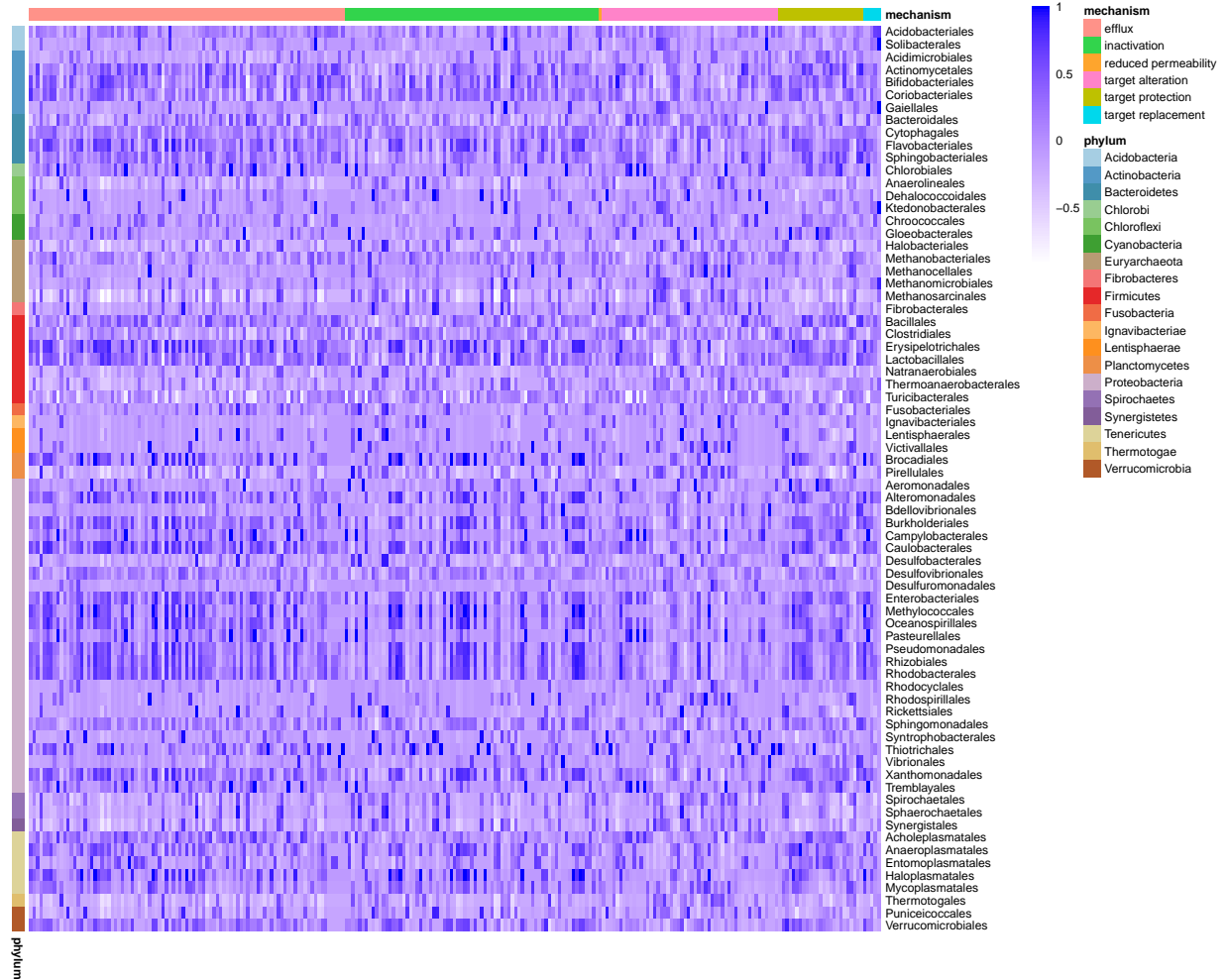
```
## Joining, by = "gene_id"
```



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

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

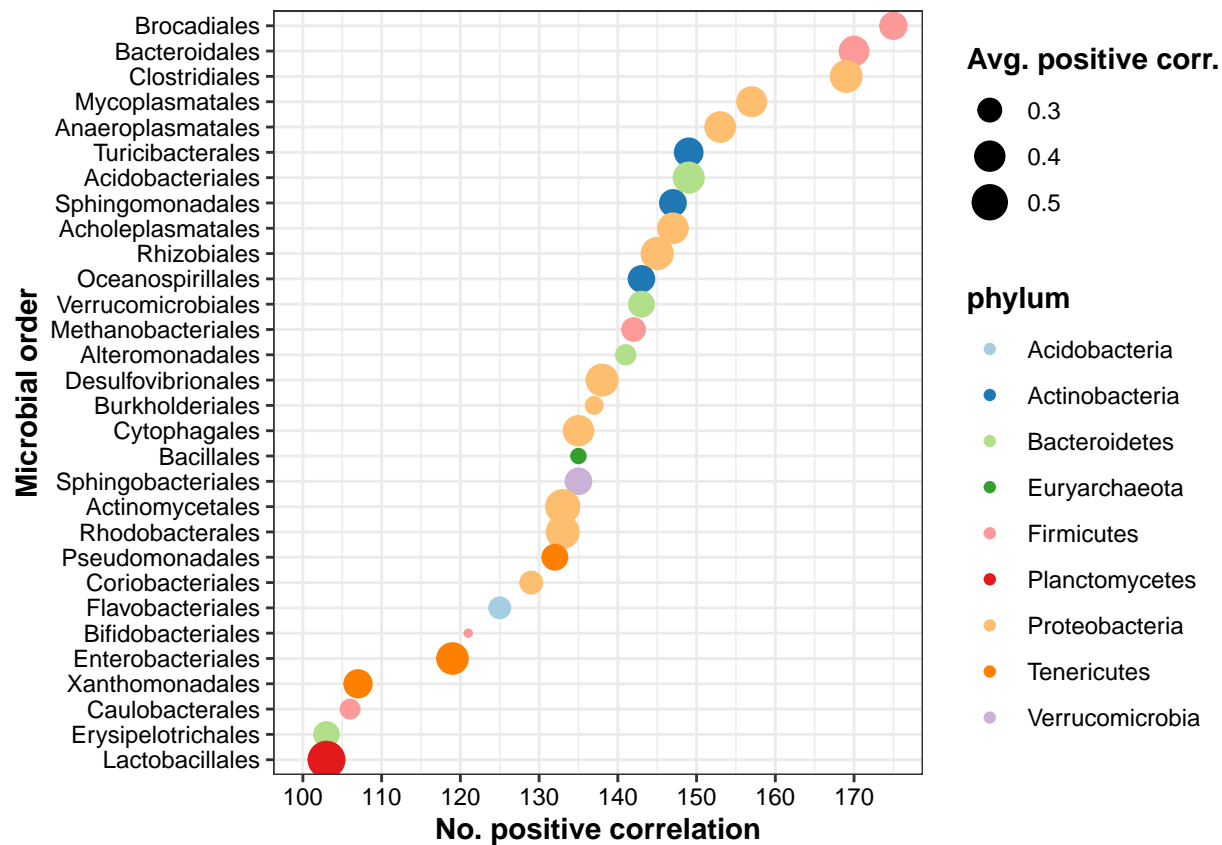
```
## Warning in brewer.pal(ColourCount1, "Paired"): n too large, allowed maximum for palette Paired is 12
## Returning the palette you asked for with that many colors
```



2. Summary of the correlations

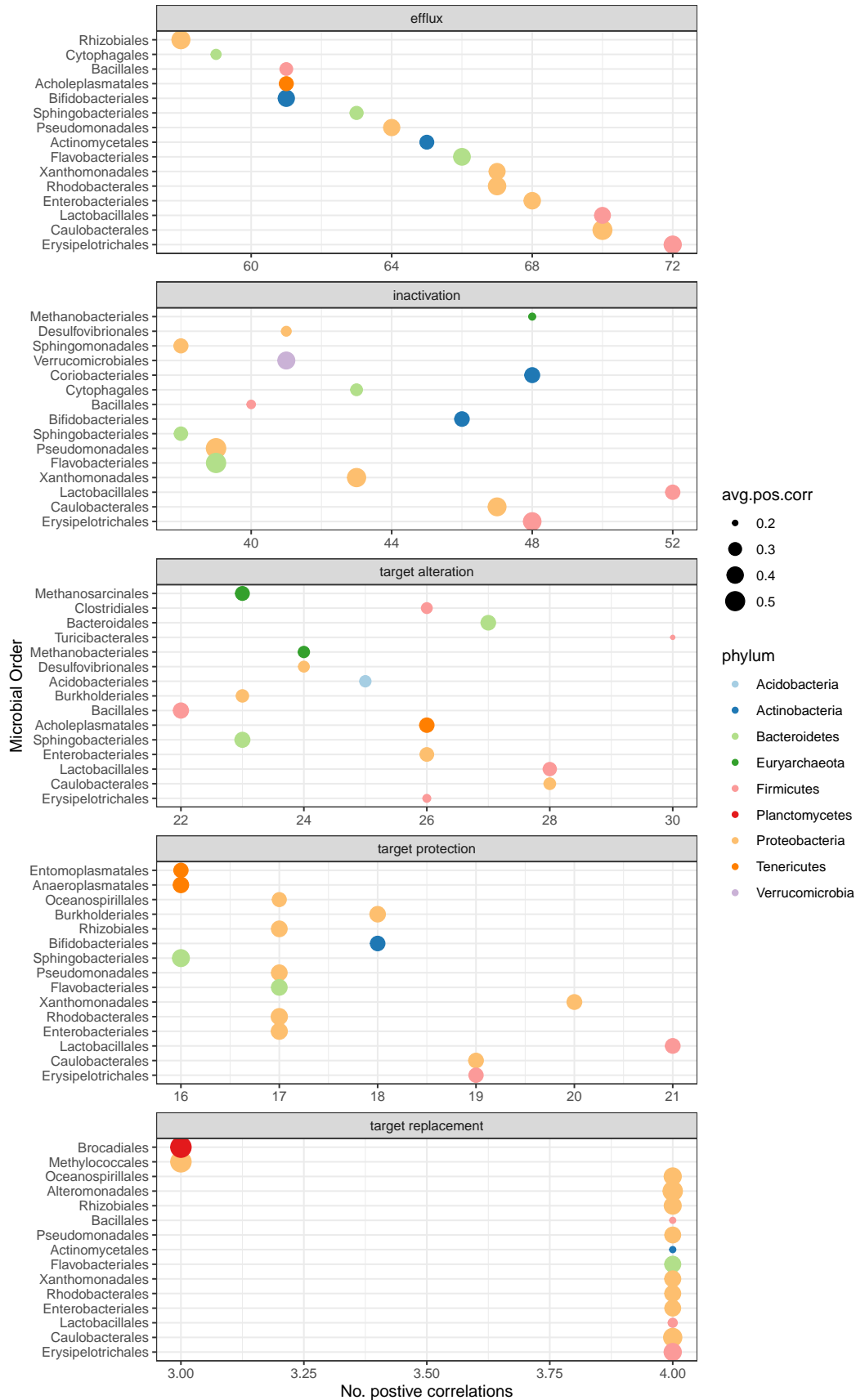
2.1 Microbes vs No. positive correlations

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



```
## pdf
## 2
```

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



2 Negative correlations

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

