Beta diversity variability - dehydrated food weight

Abby

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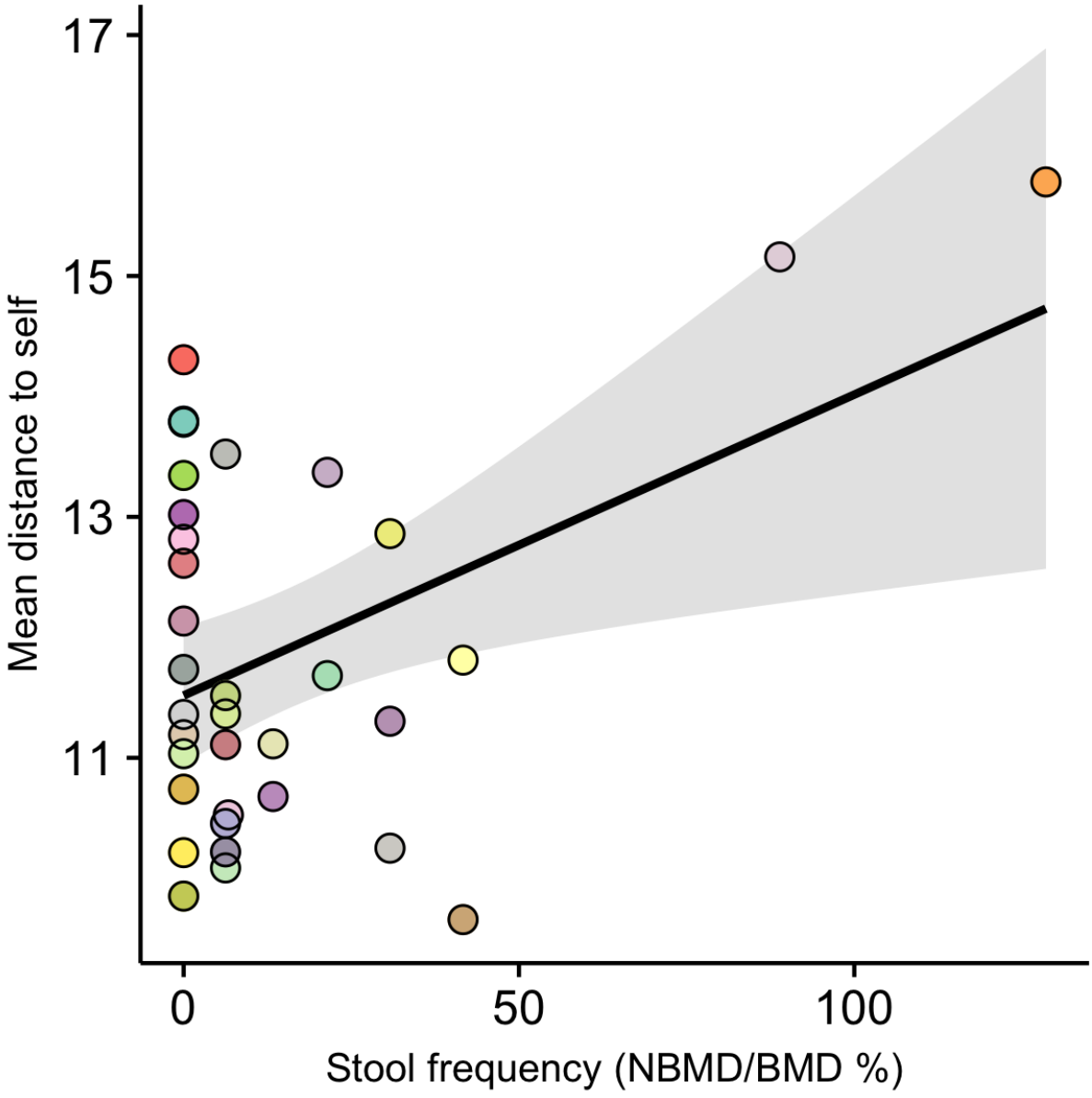
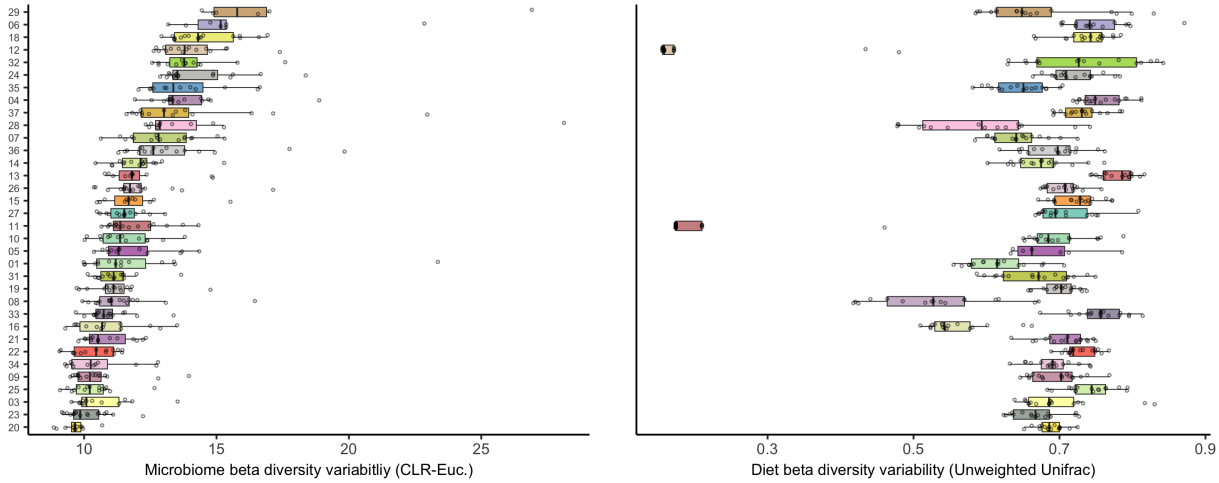
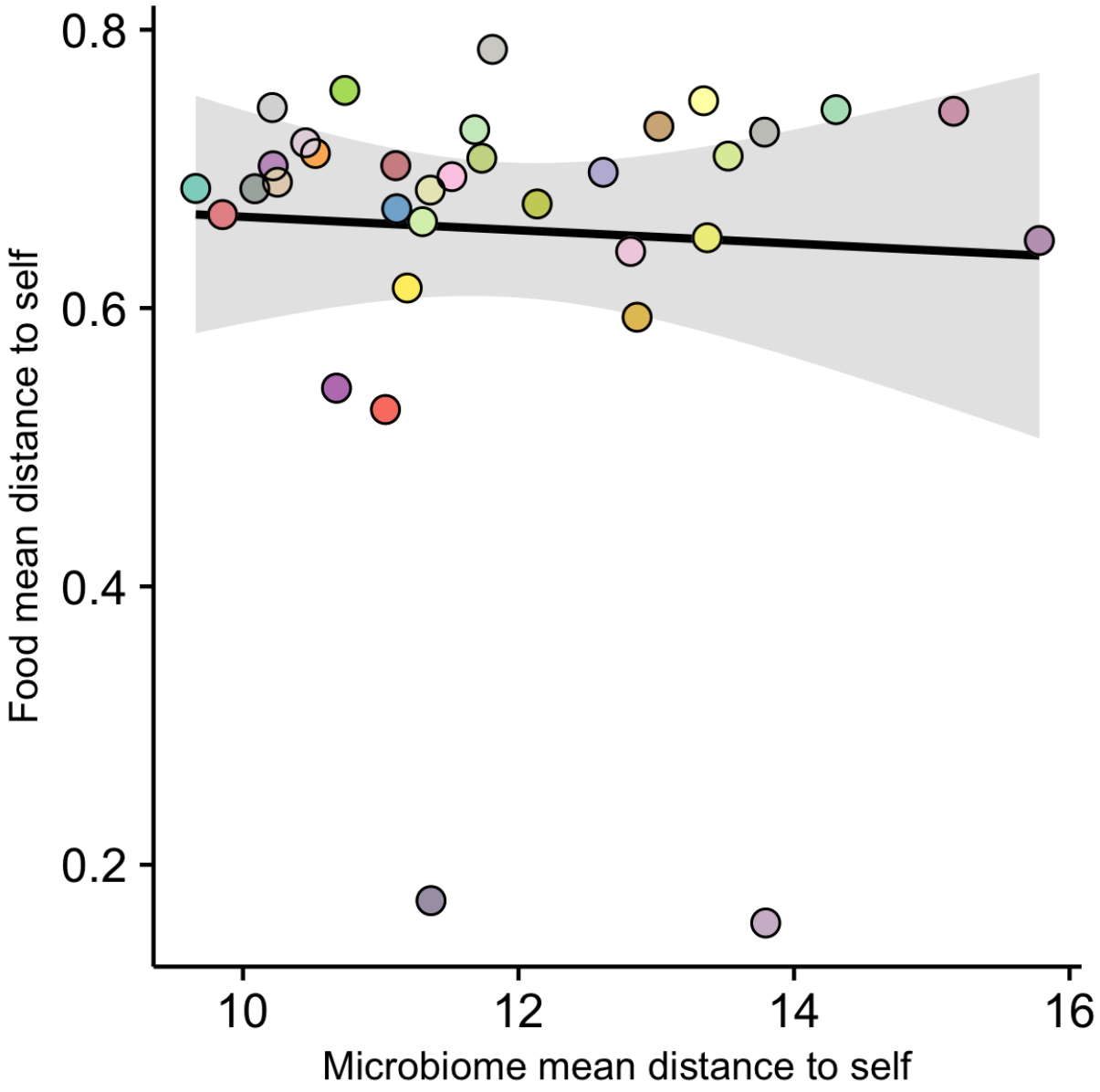



```
##
##  Spearman's rank correlation rho
##
## data:  sqrt(stool_n$percentmissed) and stool_n$ave_cloud
## S = 6770, p-value = 0.847
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
```

```
##         rho
## -0.03437358
```






```
##
##  Spearman's rank correlation rho
##
## data:  plot$food_cloud and plot$ave_cloud
## S = 6184, p-value = 0.756
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.05515661
```

```
##
##  Spearman's rank correlation rho
##
## data:  soy_plot$food_cloud and soy_plot$ave_cloud
## S = 4730, p-value = 0.4663
```

```
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.1330645
```

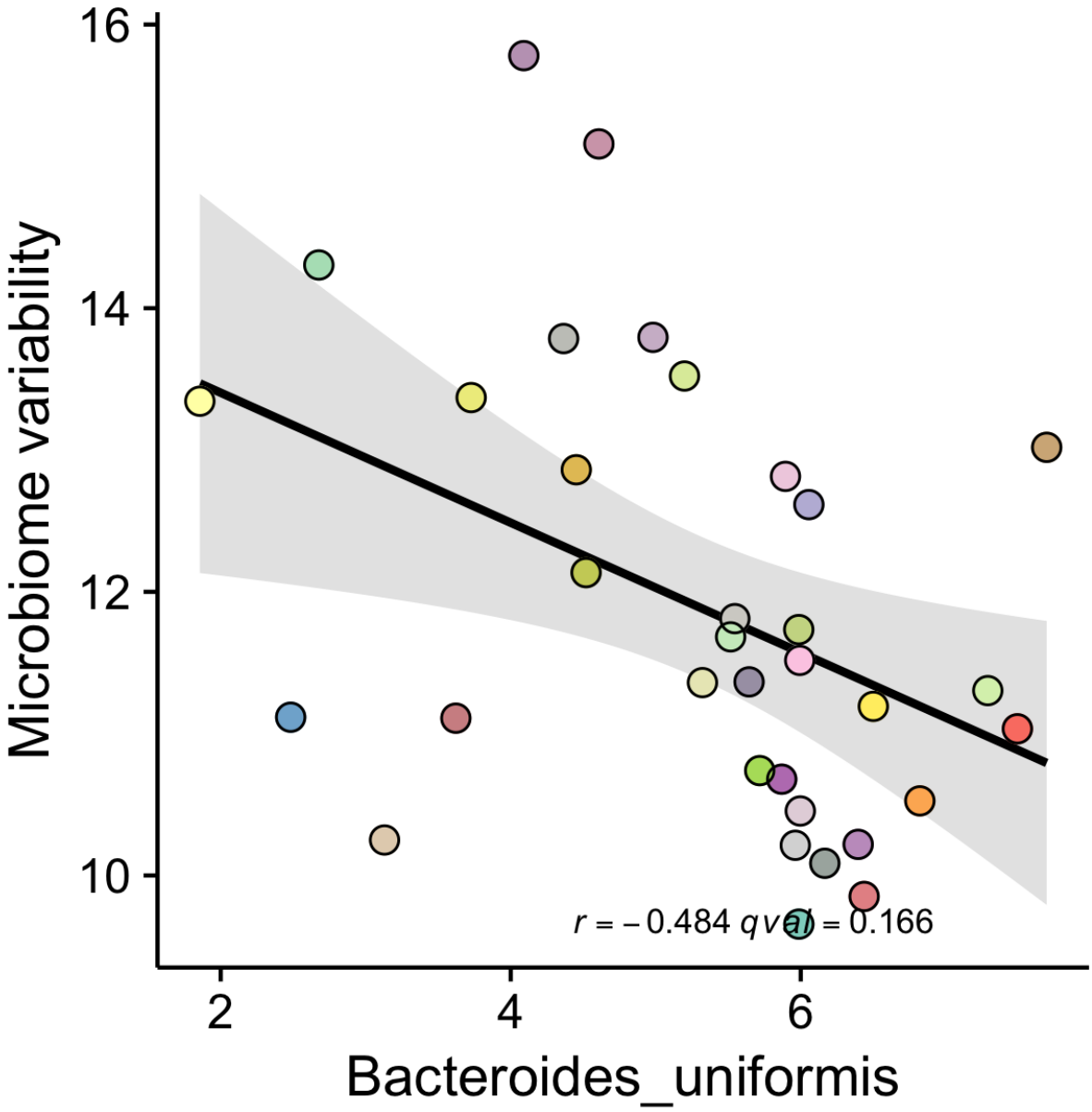
Fold difference for the variation in non-outlier microbiome cloud size:

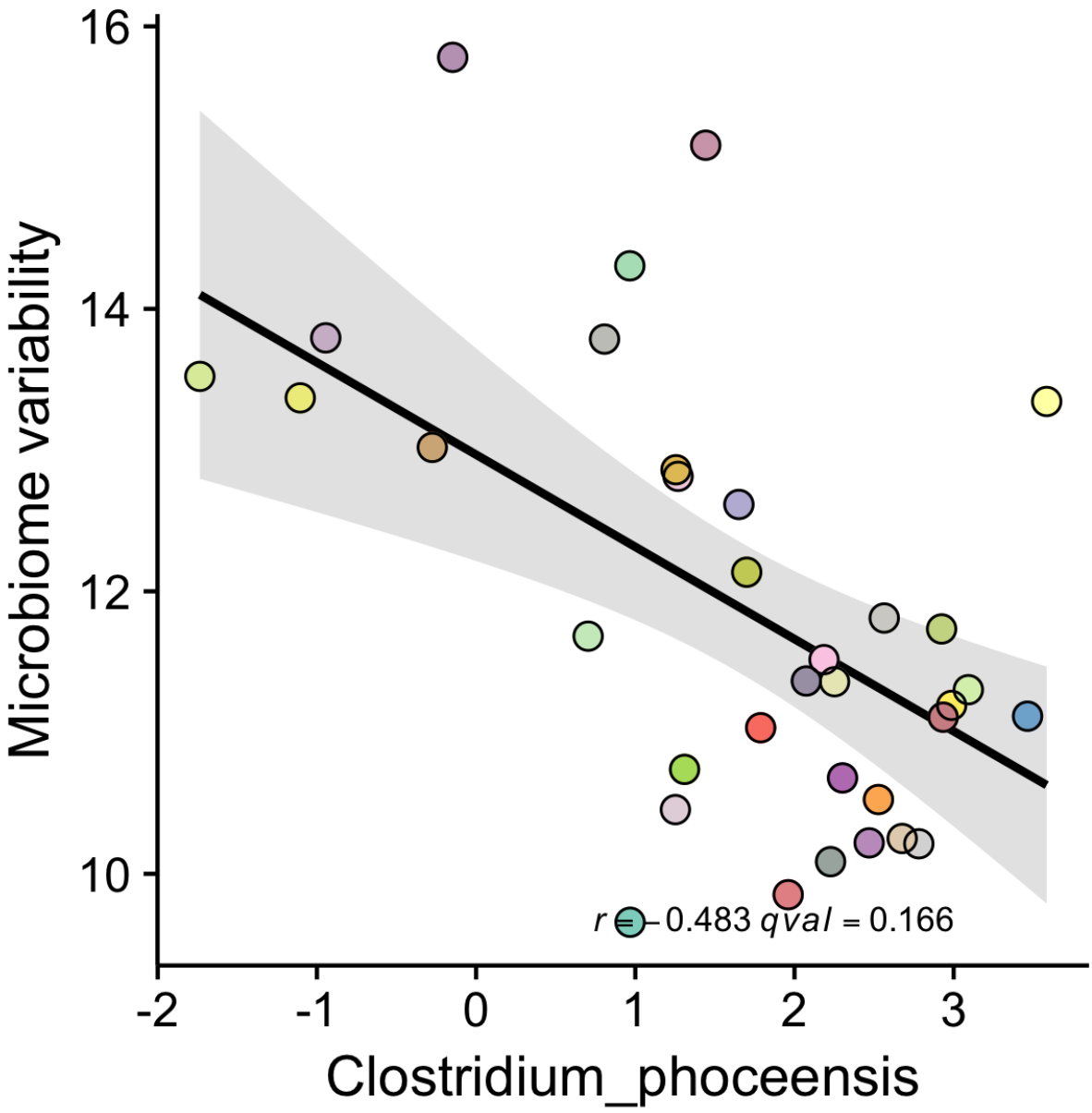
```
## [1] 1.634111
```

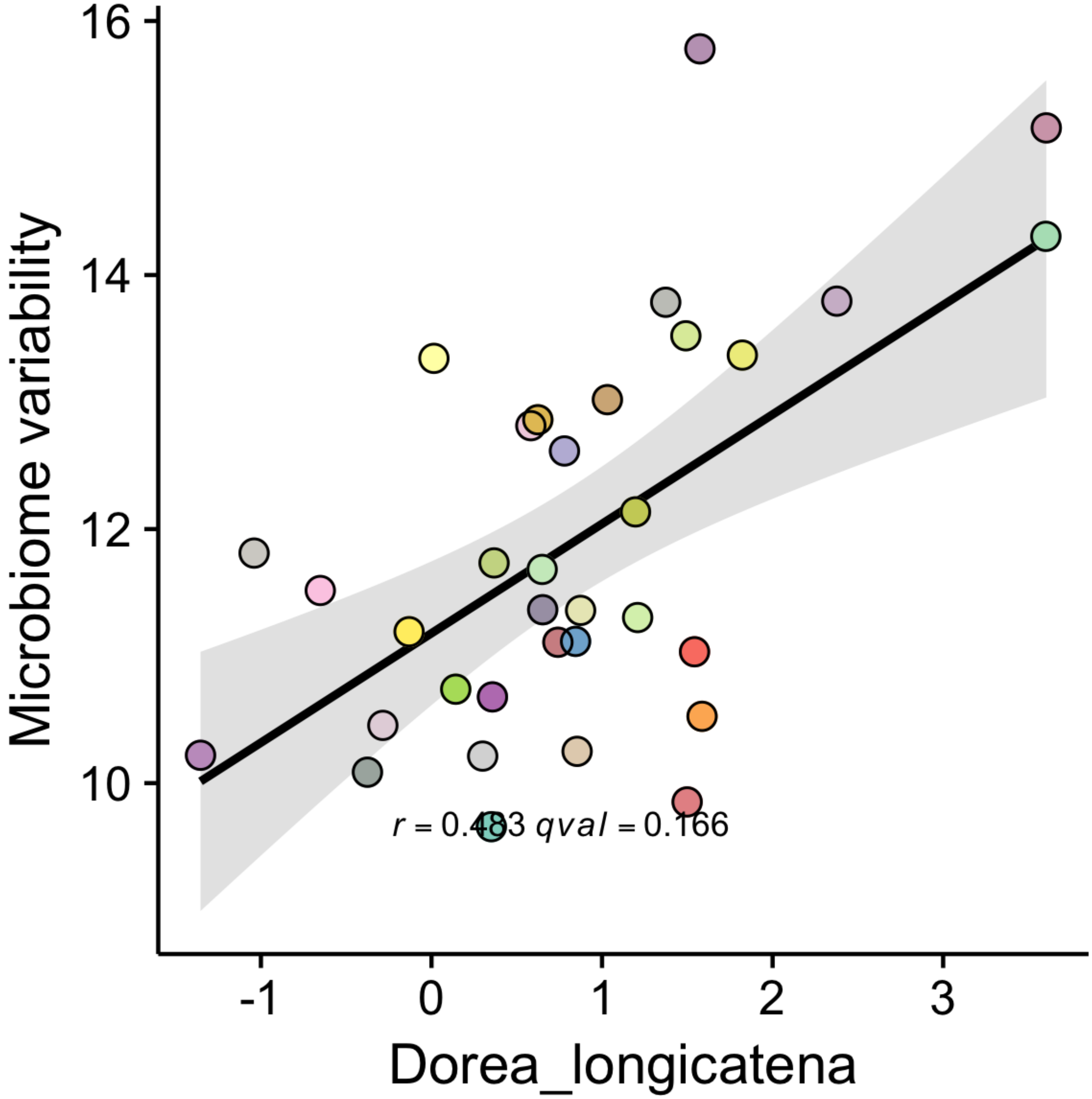
```
## [1] 4.968896
```

```
##
## 1 k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides;s__Ba
## 2    k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__Clostridium;s__Cl
## 3              k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea;s
##       qvals       cors
## 1 0.1655748 -0.4844920
## 2 0.1655748 -0.4829641
## 3 0.1655748  0.4832697
```

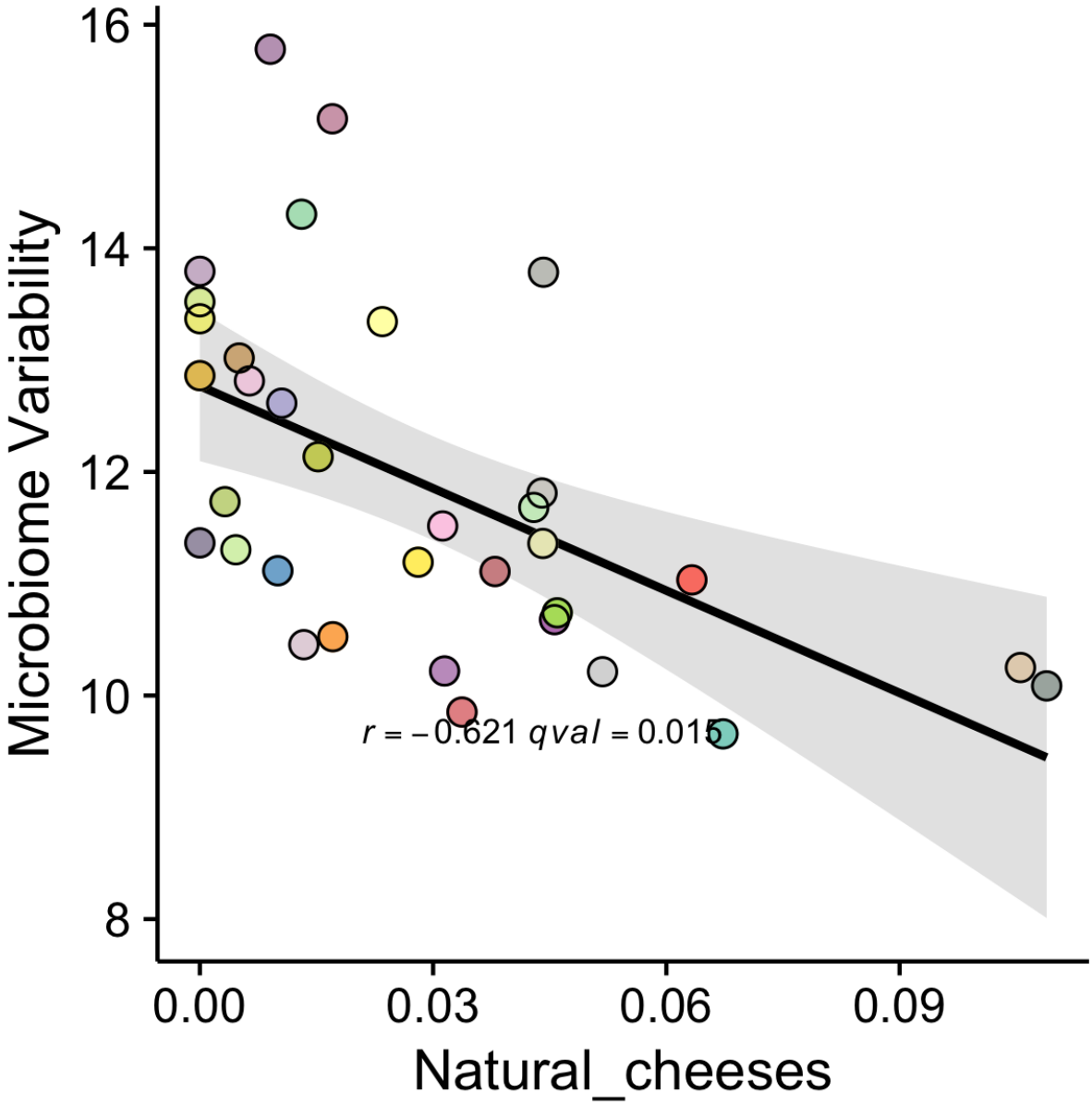
plot significant tax versus median beta diversity

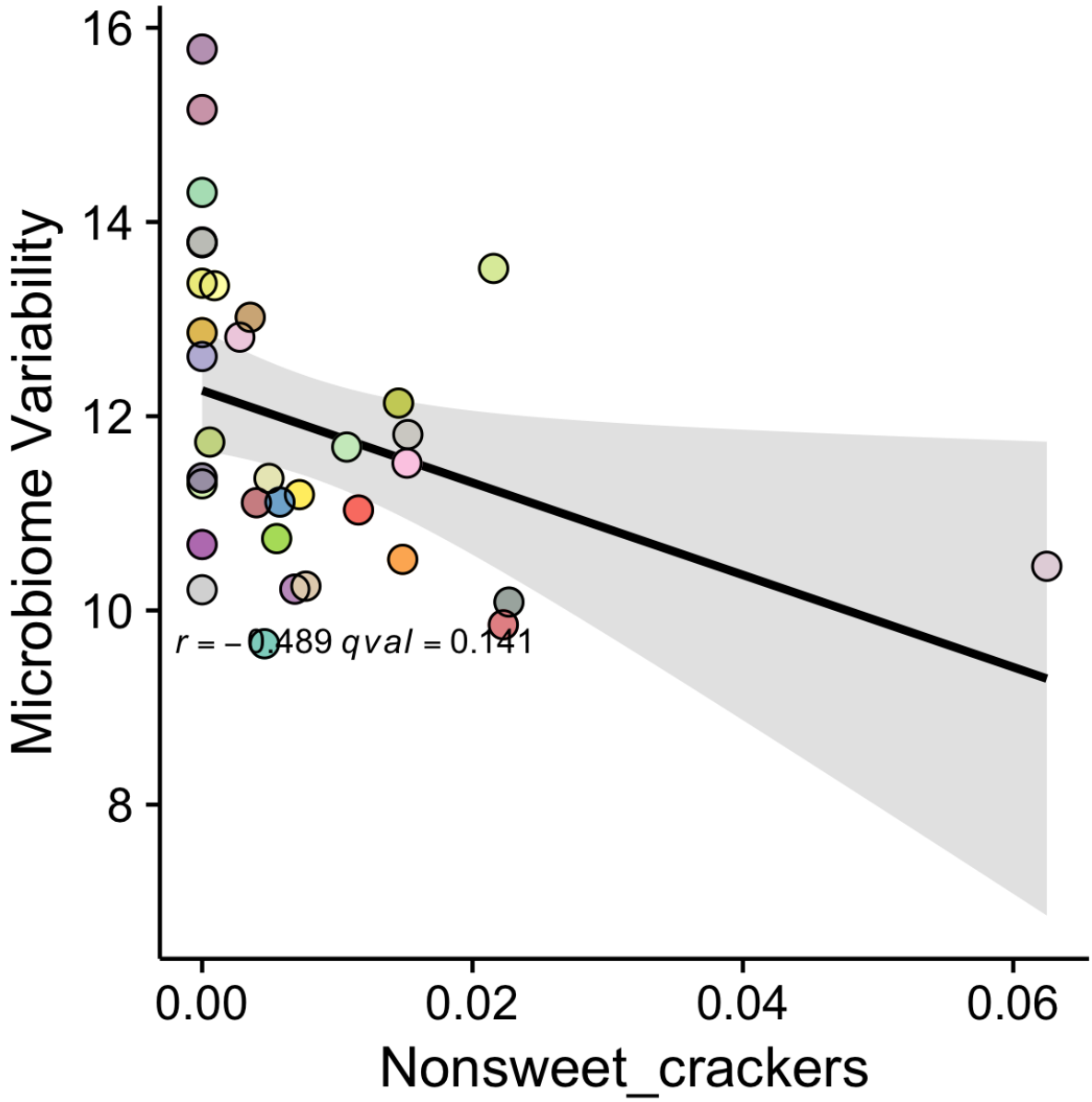


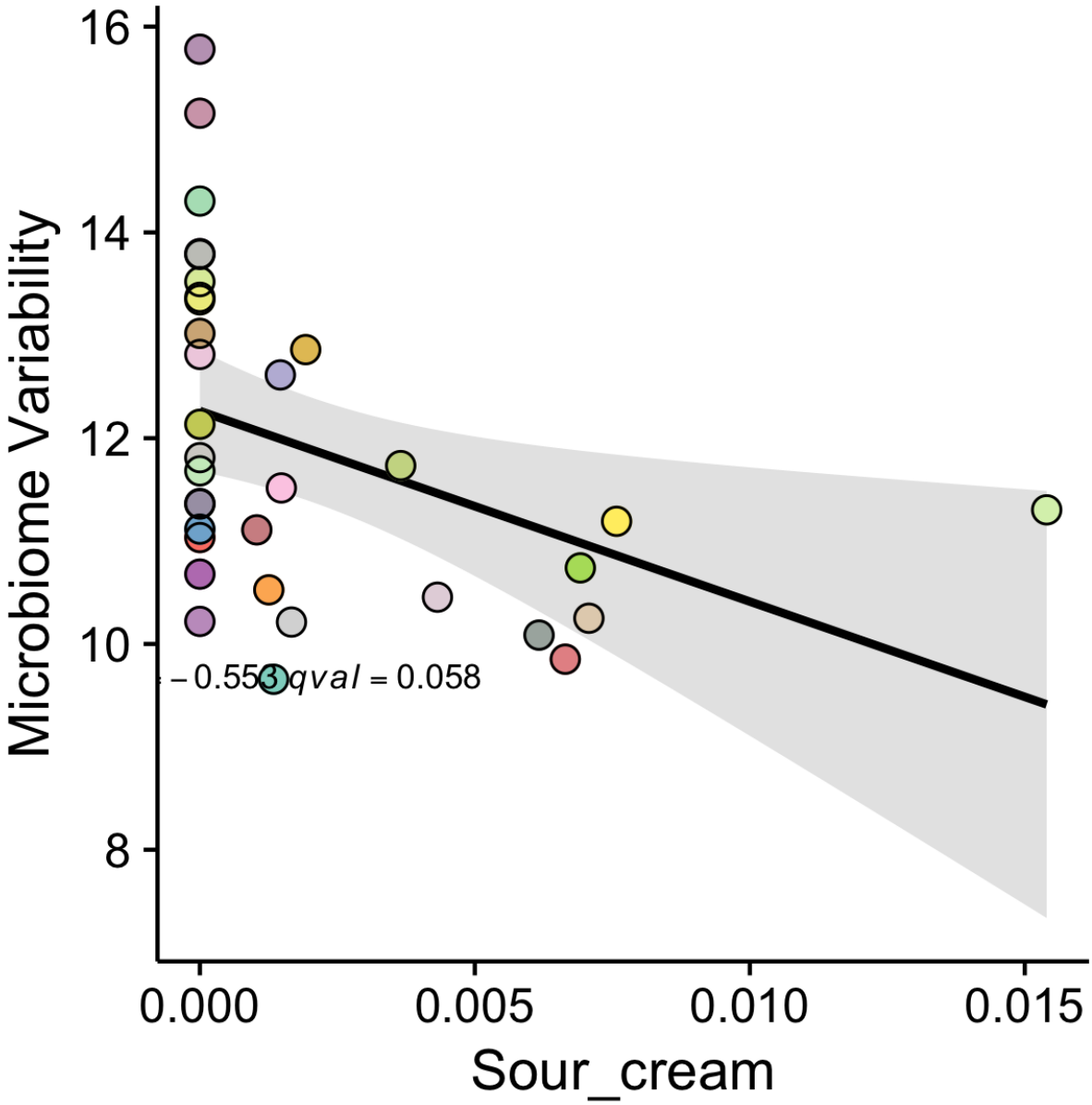

Microbiome variability
16
14
12
10
-2
-1
0
1
2
3
Clostridium_phoceensis
r = −0.483 qval = 0.166

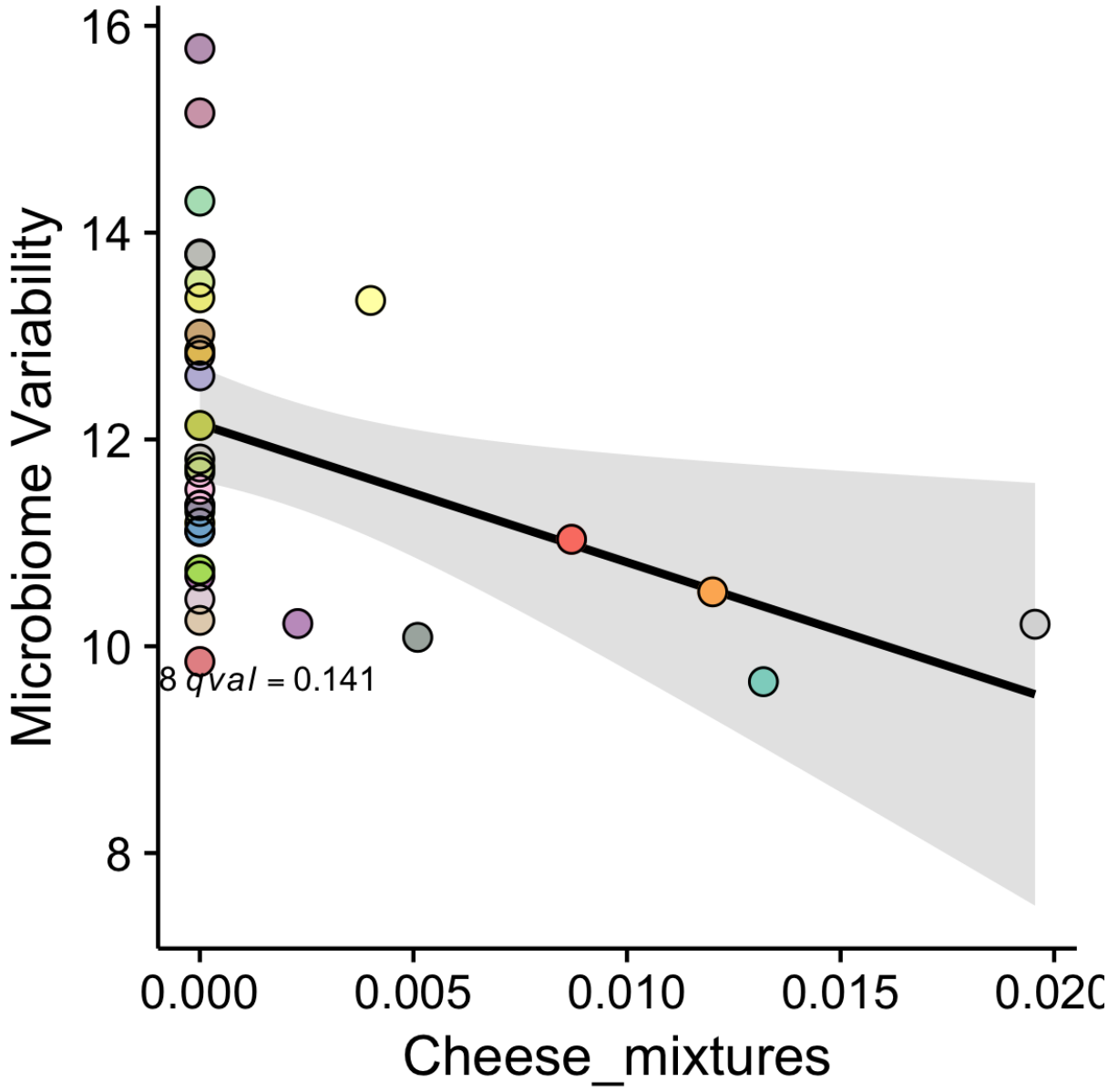



```
##                                                                       Species
## 1                          L1_Milk_and_Milk_Products;L2_Cheeses;L3_Natural_cheeses
## 2       L1_Milk_and_Milk_Products;L2_Creams_and_cream_substitutes;L3_Sour_cream
## 3 L1_Grain_Product;L2_Crackers_and_salty_snacks_from_grain;L3_Nonsweet_crackers
## 4                          L1_Milk_and_Milk_Products;L2_Cheeses;L3_Cheese_mixtures
##        qvals       cors
## 1 0.01510463 -0.6205057
## 2 0.05799252 -0.5529823
## 3 0.14133309 -0.4893442
## 4 0.14133309 -0.4883756
```

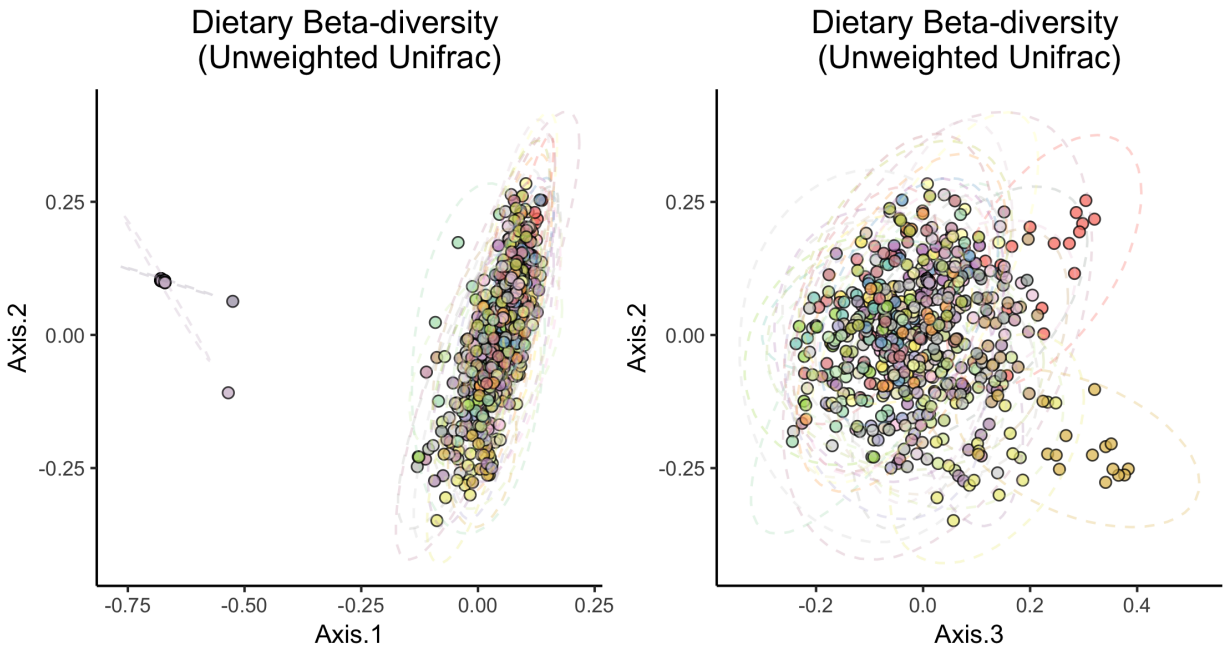

Microbiome Variability
16
14
12
10
8
0.00
0.03
0.06
0.09
Natural_cheeses
r = −0.621 qval = 0.015

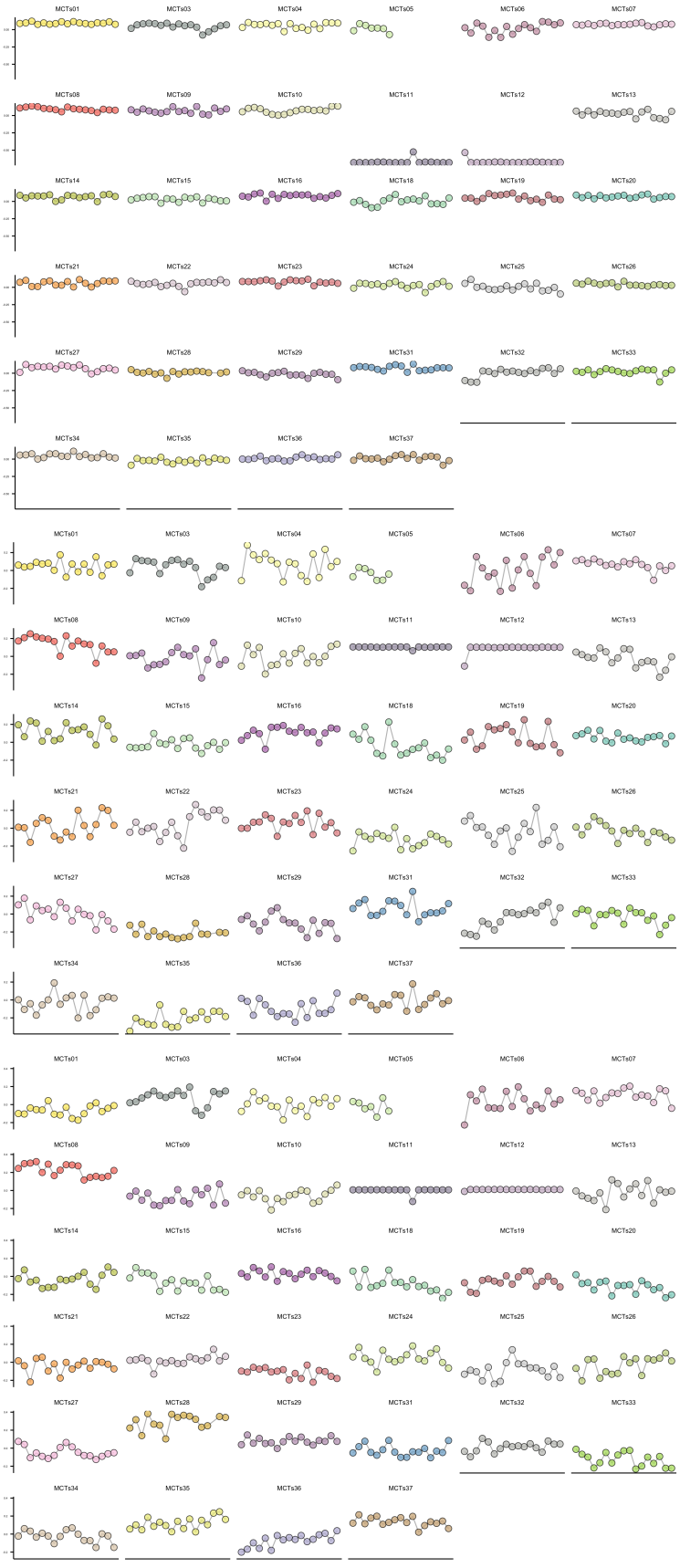

Microbiome Variability
16
14
12
10
8
r = −0.489 qval = 0.141
0.00
0.02
0.04
0.06
Nonsweet_crackers


16
14
12
10
8
Microbiome Variability
– 0.553 qval = 0.058
0.000
0.005
0.010
0.015
Sour_cream



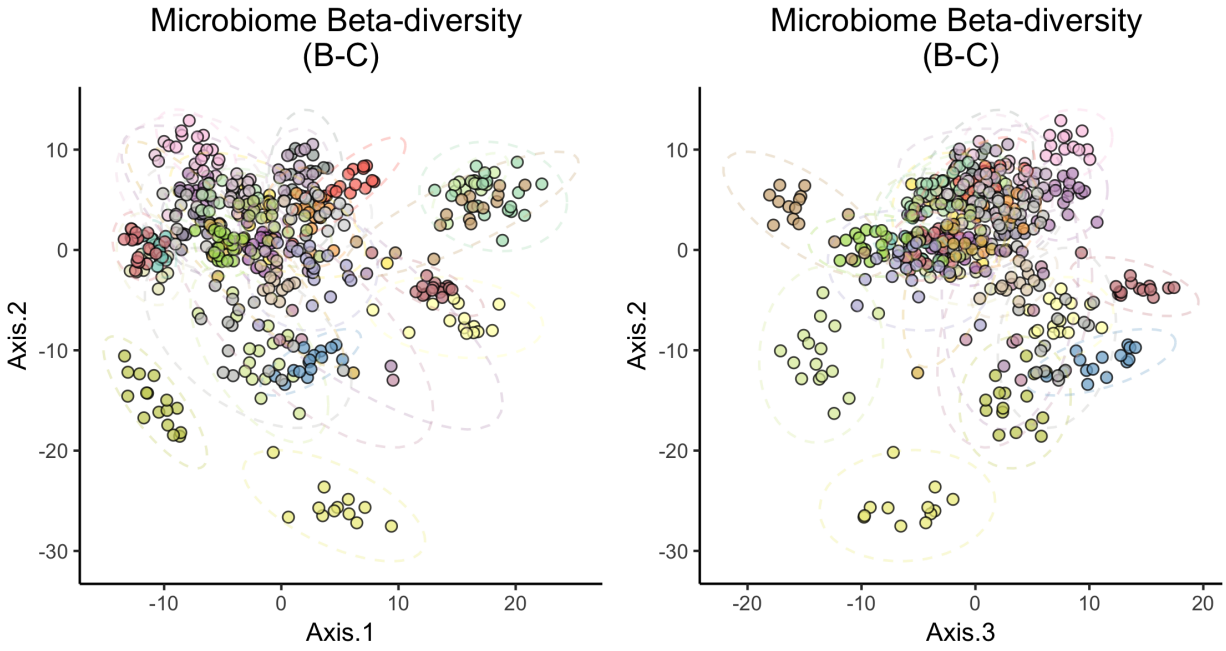

```
## Warning: Column `X.SampleID` joining character vector and factor, coercing
## into character vector
```

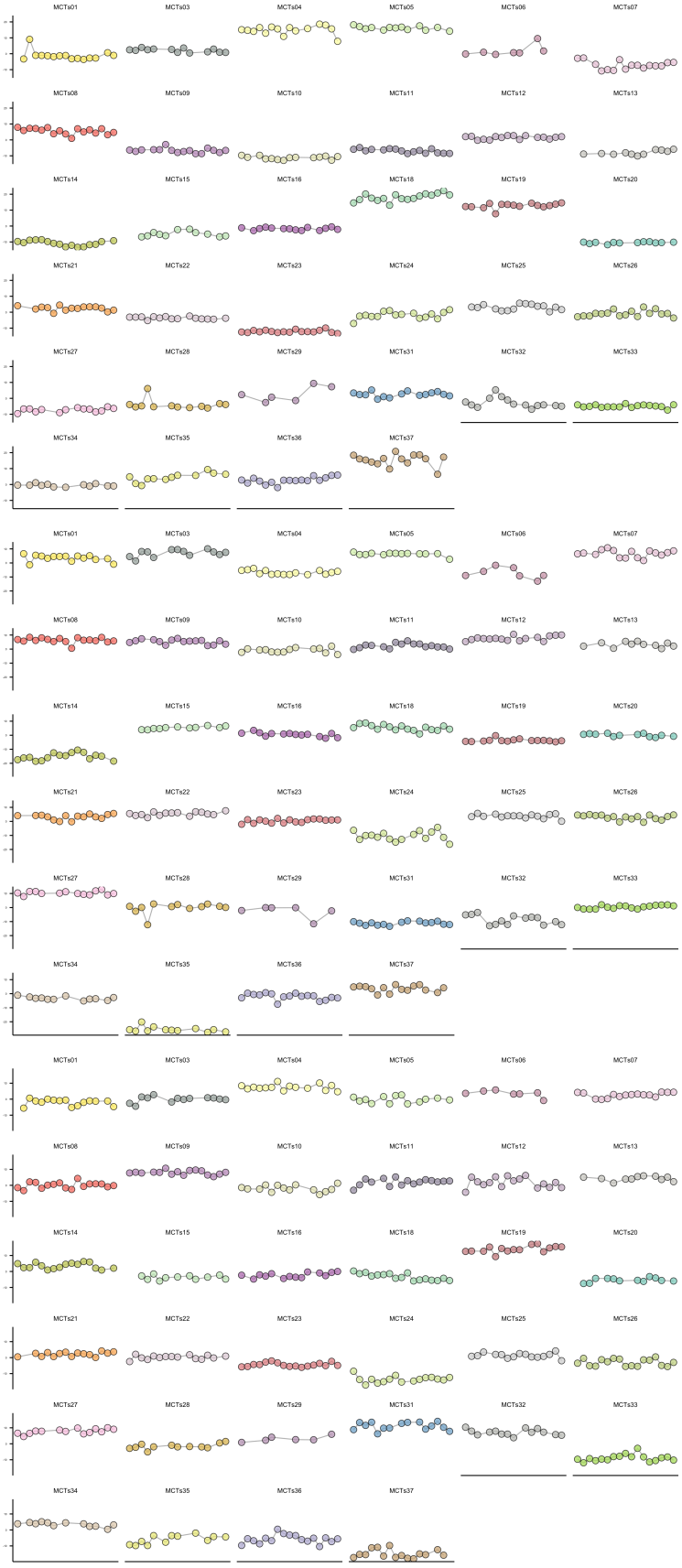

Dietary Beta-diversity
(Unweighted Unifrac)
Axis.2
0.25
0.00
-0.25
-0.75
-0.50
-0.25
0.00
0.25
Axis.1
Dietary Beta-diversity
(Unweighted Unifrac)
Axis.2
0.25
0.00
-0.25
-0.2
0.0
0.2
0.4
Axis.3


MCTs01
MCTs03
MCTs04
MCTs05
MCTs06
MCTs07
MCTs08
MCTs09
MCTs10
MCTs11
MCTs12
MCTs13
MCTs14
MCTs15
MCTs16
MCTs18
MCTs19
MCTs20
MCTs21
MCTs22
MCTs23
MCTs24
MCTs25
MCTs26
MCTs27
MCTs28
MCTs29
MCTs31
MCTs32
MCTs33
MCTs34
MCTs35
MCTs36
MCTs37

Next up, try coloring this by prevatella/bacteroides etc.

```
## Warning: Column `X.SampleID` joining character vector and factor, coercing
## into character vector
```




MCTs01
MCTs03
MCTs04
MCTs05
MCTs06
MCTs07
MCTs08
MCTs09
MCTs10
MCTs11
MCTs12
MCTs13
MCTs14
MCTs15
MCTs16
MCTs18
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MCTs34
MCTs35
MCTs36
MCTs37
MCTs01
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MCTs37
MCTs01
MCTs03
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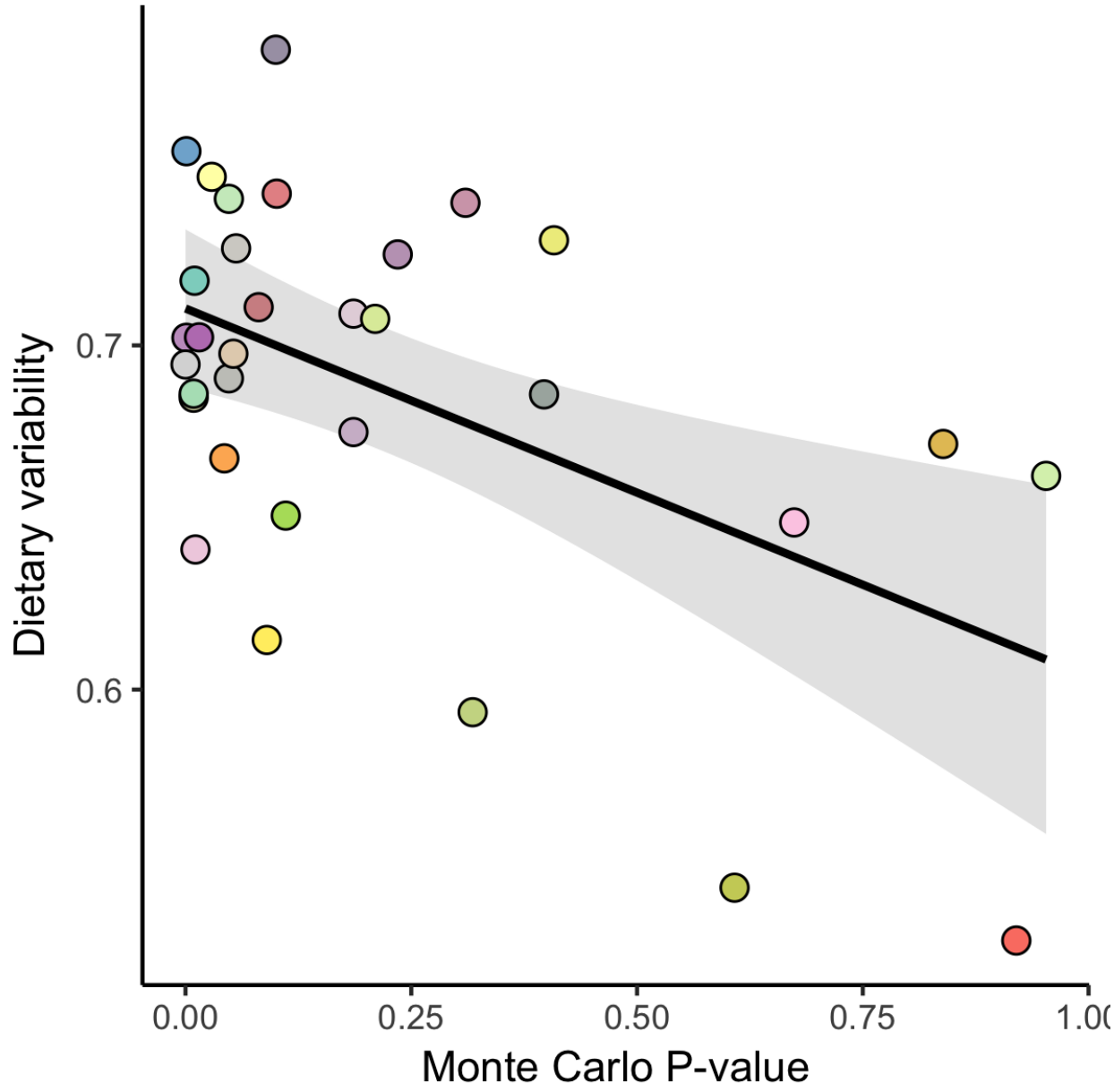
MCTs31
MCTs32
MCTs33
MCTs34
MCTs35
MCTs36
MCTs37

Is dietary beta diversity associated with the ability to sucessfully match microbiome and diet with procrutes?

```
##
##  Welch Two Sample t-test
##
## data:  procrustes$food_cloud by as.factor(procrustes$Procrustes)
## t = -1.6549, df = 25.154, p-value = 0.1104
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.068688354  0.007471224
## sample estimates:
##  mean in group ns mean in group sig
##         0.6737170         0.7043256
```

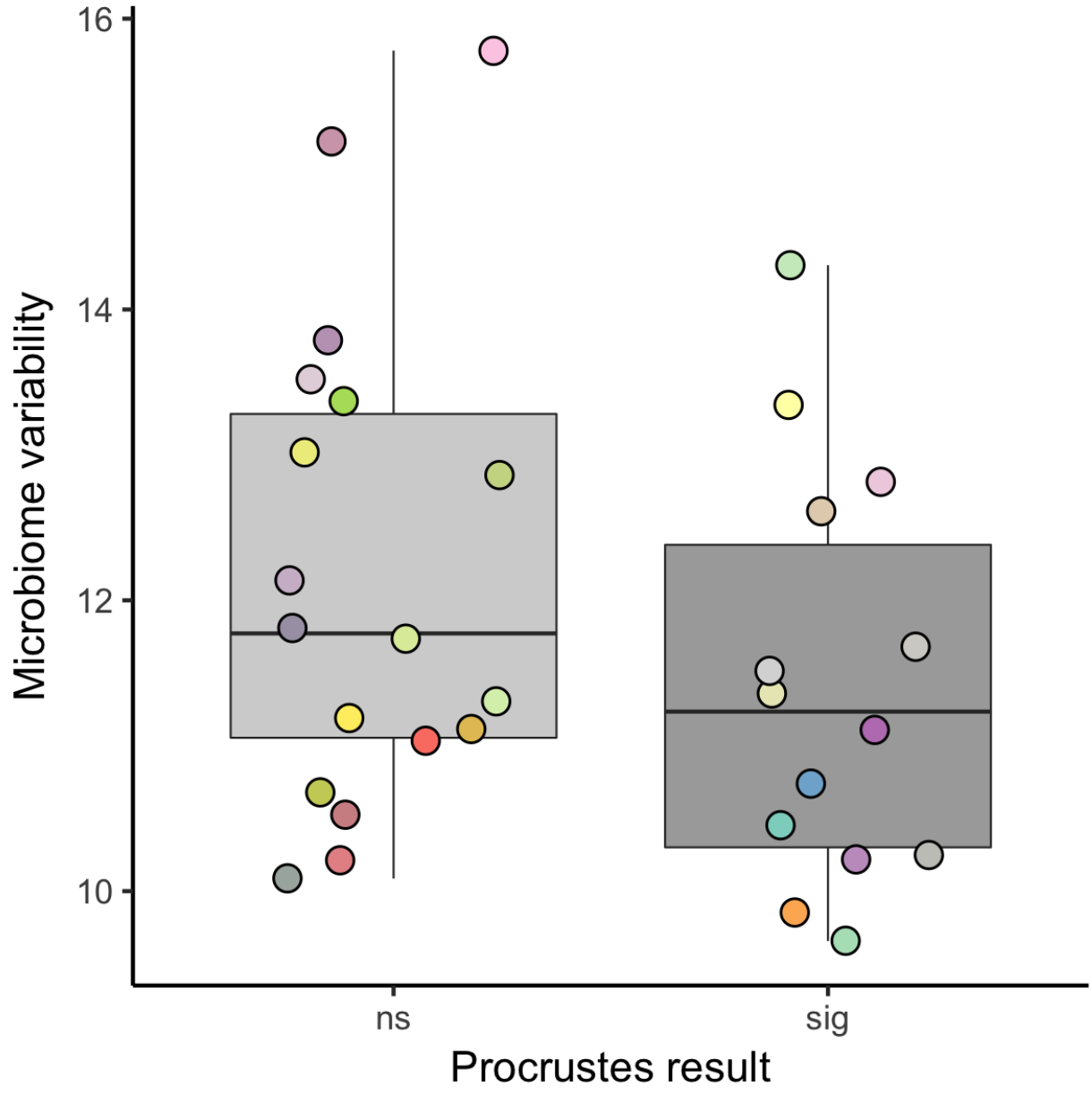
```
##
##  Pearson's product-moment correlation
##
## data:  procrustes$food_cloud and procrustes$Monte.Carlo.p.value
## t = -3.377, df = 30, p-value = 0.002043
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.7383875 -0.2155763
## sample estimates:
##        cor
## -0.5248195
```




```
##
##  Welch Two Sample t-test
##
## data:  procrustes$ave_cloud by as.factor(procrustes$Procrustes)
## t = 1.4116, df = 29.76, p-value = 0.1684
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.3408475  1.8649091
## sample estimates:
##  mean in group ns mean in group sig
##          12.18475          11.42272
```

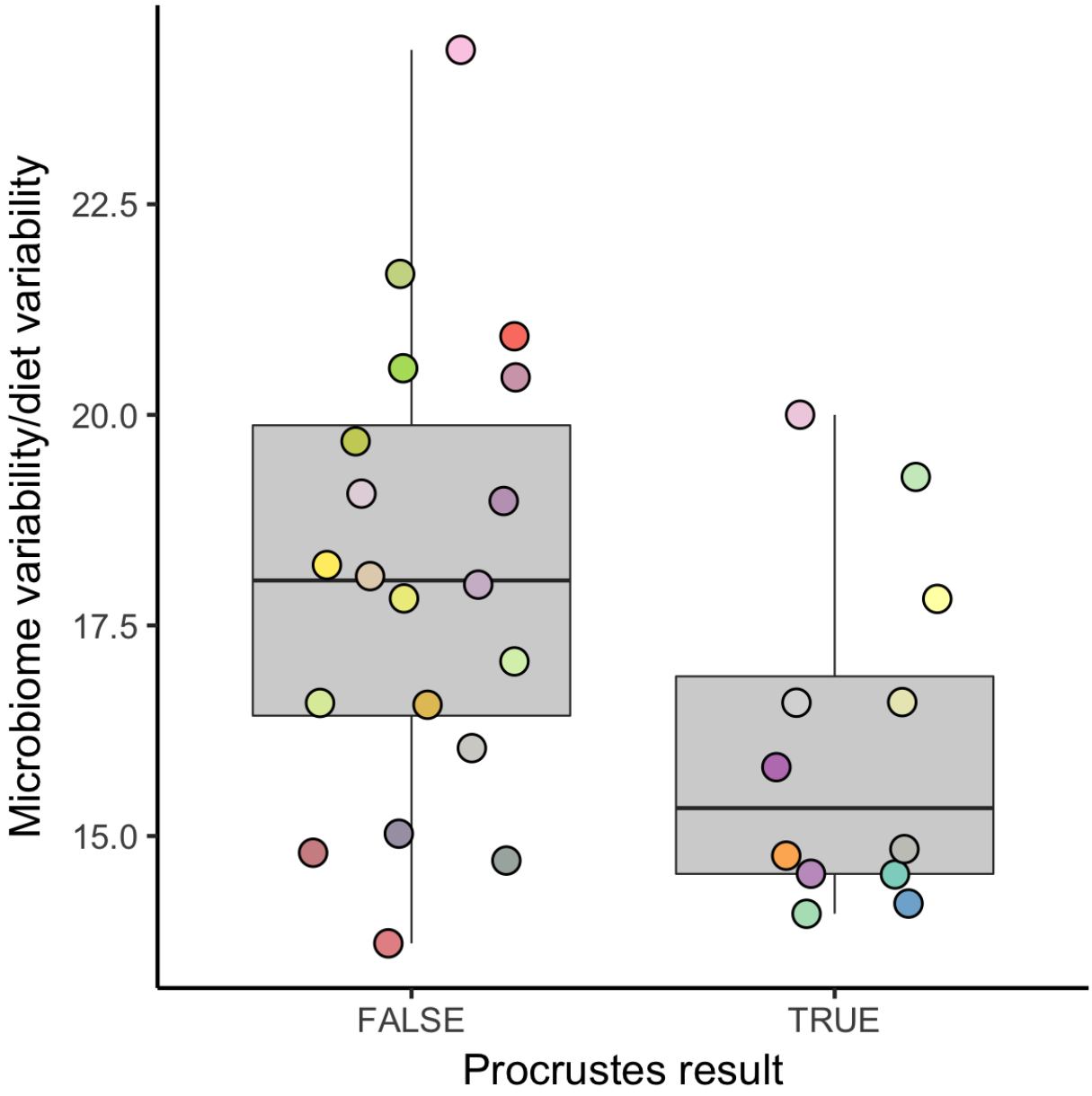
```
##
##  Spearman's rank correlation rho
##
```

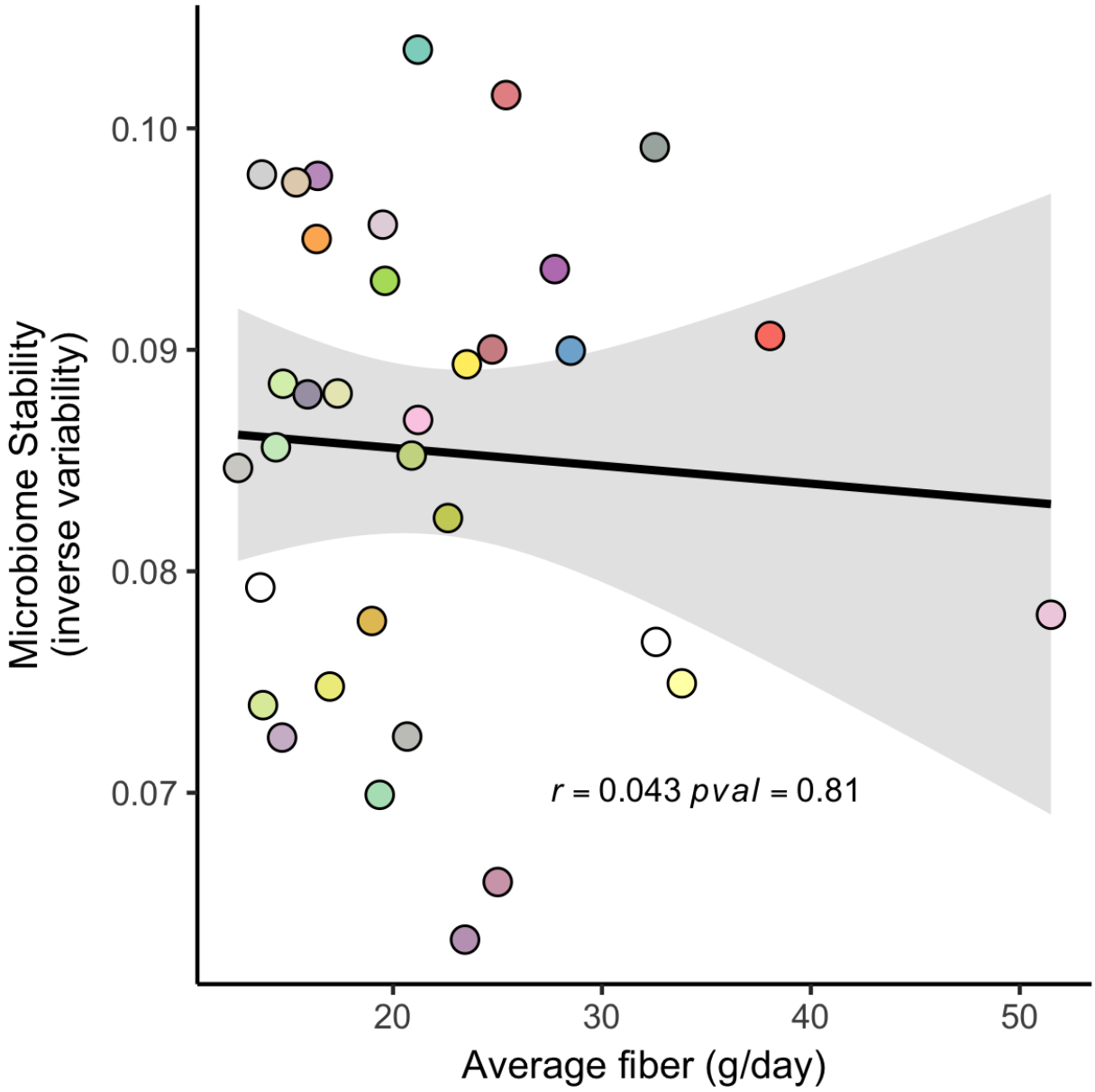
```
## data:  procrustes$ave_cloud and procrustes$Monte.Carlo.p.value
## S = 3914.4, p-value = 0.1172
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.2825449
```




```
##
##  Welch Two Sample t-test
##
## data:  procrustes$m.f by as.factor(procrustes$Monte.Carlo.p.value < 0.05)
## t = 2.4276, df = 28.299, p-value = 0.02181
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.3173275 3.7351025
```

```
## sample estimates:
## mean in group FALSE  mean in group TRUE
##            18.11426             16.08805
```




Microbiome Stability
(inverse variability)
0.10
0.09
0.08
0.07
r = 0.043 pval = 0.81
20
30
40
50
Average fiber (g/day)