

Full GLMMs output for EMP data
Significant models (likelihood-ratio test, $p < 0.05$)

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1. DBD across different taxonomic ratios

1.1. ASV:Genus

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_ASV ~ nb_genus + (nb_genus | genus_type/emp_3) + (nb_genus |
## emp_3:PI) + (nb_genus - 1 | sample)
## Data: datsc1
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
## 290657.5 290771.1 -145316.7  290633.5    95593
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.7143 -0.3896 -0.1390  0.2107 12.0218
##
## Random effects:
## Groups          Name      Variance Std.Dev. Corr
## emp_3:genus_type (Intercept) 0.056526 0.23775
##                  nb_genus    0.020192 0.14210  0.04
## sample          nb_genus    0.004483 0.06696
## genus_type      (Intercept) 0.069547 0.26372
##                  nb_genus    0.005417 0.07360  0.56
## emp_3:PI        (Intercept) 0.016527 0.12856
##                  nb_genus    0.013038 0.11418  0.06
## Number of obs: 95605, groups:
## emp_3:genus_type, 7857; sample, 1995; genus_type, 1128; emp_3:PI, 117
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.31772    0.01822  17.441 < 2e-16 ***
## nb_genus     0.09075    0.01567   5.792 6.95e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

nb_ASV=ASV:genus, nb_genus=number of non-focal genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID.

1.2. Genus:Family

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_genus ~ nb_family + (nb_family | family_type/empo_3) + (nb_family |
##   empo_3:PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
## 277313.9 277419.8 -138646.0 277291.9   111922
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.0954 -0.2301 -0.0484  0.0452  6.2366
##
## Random effects:
## Groups             Name             Variance Std.Dev. Corr
## empo_3:family_type (Intercept) 0.022386 0.14962
##                   nb_family      0.005039 0.07099  0.08
## family_type       (Intercept) 0.049366 0.22218
##                   nb_family      0.005063 0.07115  0.74
## empo_3:PI         (Intercept) 0.001811 0.04256
##                   nb_family      0.001532 0.03914 -0.38
## Number of obs: 111933, groups:
## empo_3:family_type, 4832; family_type, 458; empo_3:PI, 117
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.167032   0.013531  12.344 < 2e-16 ***
## nb_family   0.047326   0.008007   5.911 3.41e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

nb_genus=genus:family, nb_family=number of non-focal families, family_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data.

1.3. Family:Order

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_family ~ nb_order + (nb_order | order_type/empo_3) + (nb_order -
##   1 | empo_3) + (nb_order | empo_3:PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
```

```

## 261737.7 261852.4 -130856.8 261713.7 105182
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -2.6704 -0.1386 -0.0131  0.0567  6.5306
##
## Random effects:
##   Groups          Name          Variance Std.Dev. Corr
## empo_3:order_type (Intercept) 0.0210015 0.14492
##                   nb_order     0.0084763 0.09207 -0.07
## order_type       (Intercept) 0.0837311 0.28936
##                   nb_order     0.0087631 0.09361  0.74
## empo_3:PI        (Intercept) 0.0078208 0.08844
##                   nb_order     0.0112401 0.10602  0.69
## empo_3           nb_order     0.0005462 0.02337
## Number of obs: 105194, groups:
## empo_3:order_type, 3781; order_type, 363; empo_3:PI, 117; empo_3, 17
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.19068    0.02149   8.875 < 2e-16 ***
## nb_order     0.11918    0.01702   7.001 2.54e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_family=family:order, nb_order=number of non-focal orders, order_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data.

1.4. Order:Class

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_order ~ nb_classe + (nb_classe | classe_type/empo_3) + (nb_classe -
##   1 | empo_3) + (nb_classe | empo_3:PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##           AIC          BIC    logLik deviance df.resid
## 189330.9 189441.7 -94653.5 189306.9    75369
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -2.2595 -0.1457 -0.0179  0.0429  4.1586
##
## Random effects:
##   Groups          Name          Variance Std.Dev. Corr
## empo_3:classe_type (Intercept) 0.0134159 0.11583
##                   nb_classe     0.0061698 0.07855 -0.01
## classe_type       (Intercept) 0.1122675 0.33506
##                   nb_classe     0.0199721 0.14132  0.70
## empo_3:PI        (Intercept) 0.0008366 0.02892
##                   nb_classe     0.0026542 0.05152 -0.29

```

```

## empo_3          nb_classe    0.0025565 0.05056
## Number of obs: 75381, groups:
## empo_3:classe_type, 2383; classe_type, 230; empo_3:PI, 117; empo_3, 17
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.17490    0.02499   6.998 2.61e-12 ***
## nb_classe    0.10872    0.01996   5.447 5.13e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_order=order:class, nb_classe=number of non-focal classes, classe_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data.

1.5. Class:Phylum

```

## Loading required package: lme4
## Loading required package: Matrix
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_class ~ nb_phylum + (nb_phylum | phylum_type/empo_3) + (nb_phylum |
##   empo_3:PI) + (nb_phylum - 1 | empo_3)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 99420.6 99521.7 -49698.3 99396.6   33702
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6993 -0.2934 -0.0350  0.2070  4.7465
##
## Random effects:
## Groups                Name          Variance Std.Dev. Corr
## empo_3:phylum_type (Intercept) 0.026141 0.16168
##                   nb_phylum  0.014168 0.11903 -0.36
## empo_3:PI           (Intercept) 0.009716 0.09857
##                   nb_phylum  0.013039 0.11419  0.12
## phylum_type       (Intercept) 0.234843 0.48461
##                   nb_phylum  0.030151 0.17364  0.55
## empo_3              nb_phylum  0.014234 0.11931
## Number of obs: 33714, groups:
## empo_3:phylum_type, 911; empo_3:PI, 117; phylum_type, 84; empo_3, 17
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.30488    0.05807   5.250 1.52e-07 ***
## nb_phylum   0.27186    0.04288   6.341 2.29e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_class=class:phylum, nb_phylum=number of non-focal phyla, phylum_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data.

2. ASV based analysis

2.1. ASV:Genus

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ shanon + (shanon | genus_type/empo_3) + (shanon | empo_3:PI) +
## (shanon - 1 | sample)
## Data: datsc1
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
## 290622.3 290735.9 -145299.1  290598.3    95593
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6323 -0.3883 -0.1398  0.2125 12.2095
##
## Random effects:
## Groups              Name            Variance Std.Dev. Corr
## empo_3:genus_type (Intercept) 0.056752 0.23823
##                   shanon        0.022489 0.14996 0.16
## sample            shanon        0.002968 0.05448
## genus_type       (Intercept) 0.069456 0.26355
##                   shanon        0.006445 0.08028 0.70
## empo_3:PI        (Intercept) 0.017813 0.13347
##                   shanon        0.007216 0.08495 0.20
## Number of obs: 95605, groups:
## empo_3:genus_type, 7857; sample, 1995; genus_type, 1128; empo_3:PI, 117
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.29051    0.01787   16.26 < 2e-16 ***
## shanon       0.05508    0.01272    4.33 1.49e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.2. ASV:Family

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ shanon + (shanon | famil_type/empo_3) + (shanon | empo_3:PI) +
## (shanon - 1 | sample) + (1 | obs)
## Data: datsc2
```

```

## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
## 442753.1 442878.2 -221363.5 442727.1   112008
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.6327 -0.4682 -0.1423  0.3132  3.6994
##
## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## obs              (Intercept) 0.12959  0.3600
## empo_3:famil_type (Intercept) 0.13062  0.3614
##                  shanon       0.07207  0.2685  0.01
## sample           shanon       0.01786  0.1336
## famil_type       (Intercept) 0.14374  0.3791
##                  shanon       0.03390  0.1841  0.59
## empo_3:PI        (Intercept) 0.04177  0.2044
##                  shanon       0.02556  0.1599 -0.12
## Number of obs: 112021, groups:
## obs, 112021; empo_3:famil_type, 4833; sample, 1999; famil_type, 458; empo_3:PI, 117
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.50753    0.02995  16.949 < 2e-16 ***
## shanon       0.14766    0.02275   6.491 8.51e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

2.3. ASV:Order

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ shanon + (shanon | order_type/empo_3) + (shanon | empo_3:PI) +
## (shanon - 1 | sample) + (1 | obs)
## Data: datsc2
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC    logLik deviance df.resid
## 486216.8 486341.1 -243095.4 486190.8   105181
##
## Scaled residuals:
##      Min      1Q  Median      3Q      Max
## -2.7884 -0.4696 -0.1030  0.2985  6.2226
##
## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## obs              (Intercept) 0.19691  0.4437
## empo_3:order_type (Intercept) 0.20007  0.4473
##                  shanon       0.17358  0.4166 -0.23
## sample           shanon       0.04096  0.2024

```

```

## order_type      (Intercept) 0.29459  0.5428
##                shanon      0.11600  0.3406  0.33
## empo_3:PI      (Intercept) 0.11781  0.3432
##                shanon      0.06648  0.2578  0.09
## Number of obs: 105194, groups:
## obs, 105194; empo_3:order_type, 3781; sample, 2000; order_type, 363; empo_3:PI, 117
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.60375    0.04820  12.527 <2e-16 ***
## shanon       0.37796    0.03832   9.864 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

2.4. ASV:Class

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ shanon + (shanon | clas_type/empo_3) + (shanon | empo_3:PI) +
## (shanon - 1 | sample) + (1 | obs)
## Data: datsc2
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##           AIC          BIC    logLik deviance df.resid
## 396695.5 396815.5 -198334.7 396669.5    75368
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5231 -0.4443 -0.0711  0.2558  8.3789
##
## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## obs              (Intercept) 0.25714  0.5071
## empo_3:clas_type (Intercept) 0.22980  0.4794
##                  shanon       0.21214  0.4606  -0.19
## sample           shanon       0.06879  0.2623
## clas_type        (Intercept) 0.50950  0.7138
##                  shanon       0.13654  0.3695  0.32
## empo_3:PI        (Intercept) 0.19611  0.4428
##                  shanon       0.10615  0.3258  0.05
## Number of obs: 75381, groups:
## obs, 75381; empo_3:clas_type, 2383; sample, 2000; clas_type, 230; empo_3:PI, 117
##
## Fixed effects:
##           Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.63017    0.06863   9.182 < 2e-16 ***
## shanon       0.39836    0.04996   7.973 1.54e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

2.5. ASV:Phylum

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ shanon + (shanon | phylum_type/emp3) + (shanon | emp3:PI) +
## (shanon - 1 | emp3) + (shanon - 1 | sample) + (1 | obs)
## Data: datsc2
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC    logLik deviance df.resid
## 211526.8 211644.8 -105749.4  211498.8   33700
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.3449 -0.3817 -0.0319  0.1921  3.1857
##
## Random effects:
## Groups           Name      Variance Std.Dev. Corr
## obs              (Intercept) 0.31503  0.5613
## sample           shanon      0.14296  0.3781
## emp3:phylum_type (Intercept) 0.28560  0.5344
##                  shanon      0.25029  0.5003  -0.27
## emp3:PI          (Intercept) 0.34088  0.5838
##                  shanon      0.24545  0.4954  -0.11
## phylum_type    (Intercept) 1.13499  1.0654
##                  shanon      0.10031  0.3167  0.32
## emp3             shanon      0.02871  0.1694
## Number of obs: 33714, groups:
## obs, 33714; sample, 2000; emp3:phylum_type, 911; emp3:PI, 117; phylum_type, 84; emp3, 17
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.5874    0.1360   4.320 1.56e-05 ***
## shanon       0.3187    0.0882   3.614 0.000302 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
shanon=Shannon diversity of non focal lineages
```

3. DBD is strongest in low-diversity environments

3.1. Family:Order

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_family ~ nb_order * emp3 + (nb_order | order_type) + (1 |
## PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
```



```

##          AIC          BIC    logLik deviance df.resid
## 266705.4 267068.8 -133314.7 266629.4 105156
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.7214 -0.1772 -0.0173  0.0831  6.7579
##
## Random effects:
## Groups      Name          Variance Std.Dev. Corr
## order_type (Intercept) 0.08678  0.2946
##          nb_order      0.01197  0.1094  0.45
## PI          (Intercept) 0.00624  0.0790
## Number of obs: 105194, groups: order_type, 363; PI, 61
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.28087   0.02779  10.105 < 2e-16 ***
## nb_order          0.13404   0.02016   6.648 2.97e-11 ***
## empo_3Animal corpus      0.46962   0.10479   4.481 7.42e-06 ***
## empo_3Animal distal gut   0.30468   0.10115   3.012 0.002594 **
## empo_3Animal proximal gut  0.37860   0.09115   4.154 3.27e-05 ***
## empo_3Animal secretion    0.09225   0.03392   2.720 0.006536 **
## empo_3Animal surface      0.12120   0.02693   4.500 6.79e-06 ***
## empo_3Hypersaline (saline) -0.10911  0.09228  -1.182 0.237064
## empo_3Plant corpus        0.19482   0.03569   5.459 4.79e-08 ***
## empo_3Plant rhizosphere   -0.08185  0.02477  -3.304 0.000954 ***
## empo_3Plant surface      -0.01899  0.05932  -0.320 0.748923
## empo_3Sediment (non-saline) -0.20406  0.02320  -8.797 < 2e-16 ***
## empo_3Sediment (saline)   -0.20619  0.02398  -8.597 < 2e-16 ***
## empo_3Soil (non-saline)   -0.09221  0.02214  -4.164 3.12e-05 ***
## empo_3Surface (non-saline) -0.05198  0.02204  -2.358 0.018377 *
## empo_3Surface (saline)    -0.17916  0.05188  -3.453 0.000553 ***
## empo_3Water (non-saline)  -0.15775  0.02111  -7.474 7.79e-14 ***
## empo_3Water (saline)     -0.21450  0.02908  -7.377 1.62e-13 ***
## nb_order:empo_3Animal corpus  0.50958  0.07198   7.080 1.45e-12 ***
## nb_order:empo_3Animal distal gut  0.23727  0.07222   3.285 0.001019 **
## nb_order:empo_3Animal proximal gut  0.26375  0.06295   4.190 2.80e-05 ***
## nb_order:empo_3Animal secretion  0.15239  0.03171   4.806 1.54e-06 ***
## nb_order:empo_3Animal surface  0.12136  0.02909   4.172 3.02e-05 ***
## nb_order:empo_3Hypersaline (saline)  0.10875  0.10081   1.079 0.280678
## nb_order:empo_3Plant corpus  0.35619  0.03506  10.160 < 2e-16 ***
## nb_order:empo_3Plant rhizosphere -0.15332  0.02421  -6.334 2.39e-10 ***
## nb_order:empo_3Plant surface  0.05029  0.03689   1.363 0.172749
## nb_order:empo_3Sediment (non-saline) -0.11854  0.02391  -4.958 7.14e-07 ***
## nb_order:empo_3Sediment (saline)  -0.03690  0.02397  -1.540 0.123657
## nb_order:empo_3Soil (non-saline)  -0.12247  0.02296  -5.335 9.56e-08 ***
## nb_order:empo_3Surface (non-saline) -0.03367  0.02665  -1.263 0.206472
## nb_order:empo_3Surface (saline)  -0.03563  0.02335  -1.526 0.127049
## nb_order:empo_3Water (non-saline) -0.09724  0.02315  -4.200 2.66e-05 ***
## nb_order:empo_3Water (saline)  -0.06915  0.02919  -2.369 0.017848 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##

```

```

## Correlation matrix not shown by default, as p = 34 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it

## convergence code: 0
## Model failed to converge with max|grad| = 0.00393273 (tol = 0.001, component 1)

nb_family=family:order, nb_order=number of non-focal orders, order_type=Lineage, empo_3=Environment,
PI=laboratory that submitted the data.

```

3.2. Order:Class

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_order ~ nb_classe * empo_3 + (nb_classe | classe_type) + (1 |
##   PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC   logLik deviance df.resid
## 190975.6 191326.4 -95449.8 190899.6    75343
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.4132 -0.1695 -0.0178  0.0773  3.7208
##
## Random effects:
## Groups      Name          Variance Std.Dev. Corr
## classe_type (Intercept) 0.115704 0.34015
##              nb_classe   0.024655 0.15702  0.59
## PI           (Intercept) 0.001917 0.04378
## Number of obs: 75381, groups:  classe_type, 230; PI, 61
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.1788354  0.0355370   5.032 4.84e-07
## nb_classe      0.1202961  0.0271894   4.424 9.67e-06
## empo_3Animal corpus    0.3129449  0.1011805   3.093 0.00198
## empo_3Animal distal gut 0.5368501  0.1310345   4.097 4.19e-05
## empo_3Animal proximal gut 0.1279622  0.1130821   1.132 0.25781
## empo_3Animal secretion 0.0687260  0.0435475   1.578 0.11452
## empo_3Animal surface   0.0593722  0.0360301   1.648 0.09938
## empo_3Hypersaline (saline) 0.0005382  0.0728933   0.007 0.99411
## empo_3Plant corpus     0.0833159  0.0434269   1.919 0.05504
## empo_3Plant rhizosphere 0.0515817  0.0301697   1.710 0.08732
## empo_3Plant surface    0.0891866  0.0593787   1.502 0.13310
## empo_3Sediment (non-saline) 0.0326726  0.0290694   1.124 0.26103
## empo_3Sediment (saline) -0.0258649  0.0288895  -0.895 0.37062
## empo_3Soil (non-saline) -0.0103278  0.0275593  -0.375 0.70785
## empo_3Surface (non-saline) 0.0546641  0.0282431   1.935 0.05293
## empo_3Surface (saline)  0.0178921  0.0428232   0.418 0.67608
## empo_3Water (non-saline) -0.0136723  0.0266687  -0.513 0.60818
## empo_3Water (saline)    0.0320635  0.0328420   0.976 0.32892

```

```

## nb_classe:empo_3Animal corpus          0.3679761  0.0689111  5.340 9.30e-08
## nb_classe:empo_3Animal distal gut      0.5279010  0.0948001  5.569 2.57e-08
## nb_classe:empo_3Animal proximal gut    0.2401076  0.0805145  2.982 0.00286
## nb_classe:empo_3Animal secretion       0.1582968  0.0394070  4.017 5.90e-05
## nb_classe:empo_3Animal surface         0.0860404  0.0363760  2.365 0.01801
## nb_classe:empo_3Hypersaline (saline)   0.0578305  0.0884959  0.653 0.51345
## nb_classe:empo_3Plant corpus           0.3087379  0.0391894  7.878 3.32e-15
## nb_classe:empo_3Plant rhizosphere      -0.1322135  0.0289678 -4.564 5.02e-06
## nb_classe:empo_3Plant surface          -0.0327739  0.0407867 -0.804 0.42166
## nb_classe:empo_3Sediment (non-saline) -0.1197560  0.0289740 -4.133 3.58e-05
## nb_classe:empo_3Sediment (saline)      -0.0562754  0.0283242 -1.987 0.04694
## nb_classe:empo_3Soil (non-saline)     -0.0634347  0.0282739 -2.244 0.02486
## nb_classe:empo_3Surface (non-saline)   0.0329599  0.0323289  1.020 0.30796
## nb_classe:empo_3Surface (saline)       -0.0448347  0.0277785 -1.614 0.10653
## nb_classe:empo_3Water (non-saline)    -0.0844399  0.0277276 -3.045 0.00232
## nb_classe:empo_3Water (saline)        -0.0921891  0.0313269 -2.943 0.00325
##
## (Intercept)                            ***
## nb_classe                               ***
## empo_3Animal corpus                     **
## empo_3Animal distal gut                 ***
## empo_3Animal proximal gut
## empo_3Animal secretion
## empo_3Animal surface                    .
## empo_3Hypersaline (saline)
## empo_3Plant corpus                       .
## empo_3Plant rhizosphere                  .
## empo_3Plant surface
## empo_3Sediment (non-saline)
## empo_3Sediment (saline)
## empo_3Soil (non-saline)
## empo_3Surface (non-saline)              .
## empo_3Surface (saline)
## empo_3Water (non-saline)
## empo_3Water (saline)
## nb_classe:empo_3Animal corpus           ***
## nb_classe:empo_3Animal distal gut       ***
## nb_classe:empo_3Animal proximal gut     **
## nb_classe:empo_3Animal secretion        ***
## nb_classe:empo_3Animal surface          *
## nb_classe:empo_3Hypersaline (saline)    ***
## nb_classe:empo_3Plant corpus            ***
## nb_classe:empo_3Plant rhizosphere       ***
## nb_classe:empo_3Plant surface
## nb_classe:empo_3Sediment (non-saline)   ***
## nb_classe:empo_3Sediment (saline)       *
## nb_classe:empo_3Soil (non-saline)      *
## nb_classe:empo_3Surface (non-saline)
## nb_classe:empo_3Surface (saline)
## nb_classe:empo_3Water (non-saline)     **
## nb_classe:empo_3Water (saline)         **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 34 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x)           if you need it

## convergence code: 0
## Model failed to converge with max|grad| = 0.00163613 (tol = 0.001, component 1)

nb_order=order:class, nb_classe=number of non-focal classes, classe_type=Lineage, empo_3=Environment,
PI=laboratory that submitted the data.

```

3.3. Class:Phylum

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_class ~ nb_phylum * empo_3 + (nb_phylum | phylum_type) + (1 |
##   PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 1e+05))
##
##      AIC      BIC   logLik deviance df.resid
## 101518.6 101838.8 -50721.3 101442.6   33676
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.6499 -0.3520 -0.0525  0.2605  4.3900
##
## Random effects:
## Groups      Name          Variance Std.Dev. Corr
## phylum_type (Intercept) 0.23697  0.48680
##               nb_phylum 0.03750  0.19364  0.42
## PI           (Intercept) 0.00701  0.08373
## Number of obs: 33714, groups:  phylum_type, 84; PI, 61
##
## Fixed effects:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.28661   0.06589   4.350 1.36e-05 ***
## nb_phylum       0.33731   0.04234   7.968 1.62e-15 ***
## empo_3Animal corpus      0.25901   0.10148   2.552 0.010698 *
## empo_3Animal distal gut   0.18777   0.11532   1.628 0.103483
## empo_3Animal proximal gut 0.16148   0.11773   1.372 0.170165
## empo_3Animal secretion    0.03595   0.05218   0.689 0.490780
## empo_3Animal surface      0.10572   0.04419   2.392 0.016748 *
## empo_3Hypersaline (saline) -0.12403   0.06233  -1.990 0.046581 *
## empo_3Plant corpus        0.37243   0.05786   6.437 1.22e-10 ***
## empo_3Plant rhizosphere    0.10504   0.03769   2.787 0.005319 **
## empo_3Plant surface        0.22745   0.08505   2.674 0.007487 **
## empo_3Sediment (non-saline) 0.13989   0.03634   3.849 0.000119 ***
## empo_3Sediment (saline)   -0.06715   0.03792  -1.771 0.076606 .
## empo_3Soil (non-saline)    0.09999   0.03523   2.838 0.004539 **
## empo_3Surface (non-saline) 0.11125   0.03711   2.998 0.002718 **
## empo_3Surface (saline)    -0.07392   0.06465  -1.144 0.252824
## empo_3Water (non-saline)  -0.04040   0.03464  -1.166 0.243522

```

```

## empo_3Water (saline) -0.14358 0.03964 -3.622 0.000292 ***
## nb_phylum:empo_3Animal corpus 0.36484 0.07850 4.647 3.36e-06 ***
## nb_phylum:empo_3Animal distal gut 0.18855 0.09250 2.038 0.041520 *
## nb_phylum:empo_3Animal proximal gut 0.18888 0.09837 1.920 0.054862 .
## nb_phylum:empo_3Animal secretion 0.06901 0.05120 1.348 0.177706
## nb_phylum:empo_3Animal surface 0.11961 0.05051 2.368 0.017892 *
## nb_phylum:empo_3Hypersaline (saline) -0.14872 0.08425 -1.765 0.077524 .
## nb_phylum:empo_3Plant corpus 0.50461 0.05625 8.970 < 2e-16 ***
## nb_phylum:empo_3Plant rhizosphere -0.25721 0.04138 -6.216 5.09e-10 ***
## nb_phylum:empo_3Plant surface 0.06277 0.05969 1.051 0.293046
## nb_phylum:empo_3Sediment (non-saline) -0.36355 0.03785 -9.605 < 2e-16 ***
## nb_phylum:empo_3Sediment (saline) -0.27209 0.03771 -7.215 5.38e-13 ***
## nb_phylum:empo_3Soil (non-saline) -0.25006 0.03936 -6.353 2.11e-10 ***
## nb_phylum:empo_3Surface (non-saline) -0.04118 0.04476 -0.920 0.357563
## nb_phylum:empo_3Surface (saline) -0.19153 0.03754 -5.102 3.35e-07 ***
## nb_phylum:empo_3Water (non-saline) -0.20028 0.03837 -5.220 1.79e-07 ***
## nb_phylum:empo_3Water (saline) -0.21296 0.04117 -5.173 2.30e-07 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

##
## Correlation matrix not shown by default, as p = 34 > 12.
## Use print(x, correlation=TRUE) or
##     vcov(x)         if you need it

```

nb_class=class:phylum, nb_phylum=number of non-focal phyla, phylum_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data.

4. Abiotic factors analysis

4.1. ASV:Genus

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_ASV ~ nb_genus + temperature_deg_c + nb_genus:temperature_deg_c +
##     nb_genus:latitude_deg + nb_genus:elevation_m + (1 | genus_type/empo_3) +
##     (1 | empo_3:PI) + (1 | sample)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 27838.5 27909.7 -13909.3 27818.5     9112
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3363 -0.3680 -0.1554  0.1999  8.9640
##
## Random effects:
## Groups              Name              Variance Std.Dev.
## empo_3:genus_type (Intercept) 0.087128 0.29517
## genus_type        (Intercept) 0.091049 0.30174
## sample            (Intercept) 0.004665 0.06830

```

```

## empo_3:PI (Intercept) 0.003740 0.06116
## Number of obs: 9122, groups:
## empo_3:genus_type, 1740; genus_type, 651; sample, 192; empo_3:PI, 16
##
## Fixed effects:
##
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.32688 0.02773 11.788 < 2e-16 ***
## nb_genus 0.12837 0.01330 9.652 < 2e-16 ***
## temperature_deg_c 0.03995 0.01416 2.821 0.00479 **
## nb_genus:temperature_deg_c 0.04340 0.01387 3.129 0.00175 **
## nb_genus:latitude_deg 0.03112 0.01350 2.305 0.02119 *
## nb_genus:elevation_m -0.03137 0.01430 -2.193 0.02829 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_ASV=ASV:family, nb_genus=number of non-focal genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID, temperature_deg_c=temperature, latitude_deg=latitude, elevation_m=elevation.

4.2. Genus:Family

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_genus ~ nb_family + temperature_deg_c + ph + (1 | family_type/empo_3)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
## AIC BIC logLik deviance df.resid
## 31081.0 31125.7 -15534.5 31069.0 12624
##
## Scaled residuals:
## Min 1Q Median 3Q Max
## -1.6402 -0.2080 -0.0755 0.0507 5.2865
##
## Random effects:
## Groups Name Variance Std.Dev.
## empo_3:family_type (Intercept) 0.02926 0.1711
## family_type (Intercept) 0.05404 0.2325
## Number of obs: 12630, groups: empo_3:family_type, 1582; family_type, 389
##
## Fixed effects:
##
## Estimate Std. Error z value Pr(>|z|)
## (Intercept) 0.175100 0.017917 9.773 < 2e-16 ***
## nb_family 0.094498 0.008669 10.901 < 2e-16 ***
## temperature_deg_c 0.026323 0.008768 3.002 0.00268 **
## ph -0.041609 0.009184 -4.531 5.88e-06 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_genus=genus:family, nb_family=number of non-focal families, family_type=Lineage, empo_3=Environment, temperature_deg_c=temperature, latitude_deg=latitude, elevation_m=elevation.

4.3. Family:Order

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_family ~ nb_order + (1 | order_type/emp_3) + (1 | emp_3:PI)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 32598.6 32636.0 -16294.3 32588.6   12985
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.6667 -0.1693 -0.0398  0.0872  3.9125
##
## Random effects:
## Groups           Name          Variance Std.Dev.
## emp_3:order_type (Intercept) 0.02992  0.1730
## order_type       (Intercept) 0.09716  0.3117
## emp_3:PI         (Intercept) 0.01017  0.1008
## Number of obs: 12990, groups:
## emp_3:order_type, 1360; order_type, 323; emp_3:PI, 16
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.17547    0.03567   4.919 8.69e-07 ***
## nb_order     0.13134    0.01092  12.028 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

nb_family=family:order, nb_order=number of non-focal orders, order_type=Lineage, emp_3=Environment, PI=laboratory that submitted the data, temperature_deg_c=temperature, latitude_deg=latitude, elevation_m=elevation.

4.4. Order:Class

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_order ~ nb_classe + nb_classe:temperature_deg_c + nb_classe:latitude_deg +
## (1 | classe_type/emp_3)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 24298.7 24341.6 -12143.3 24286.7   9453
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.9938 -0.1883 -0.0498  0.1533  3.3081
##
## Random effects:
```

```

## Groups           Name          Variance Std.Dev.
## empo_3:classe_type (Intercept) 0.03287  0.1813
## classe_type      (Intercept) 0.15383  0.3922
## Number of obs: 9459, groups:  empo_3:classe_type, 941; classe_type, 206
##
## Fixed effects:
##
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.151710   0.033274   4.559 5.13e-06 ***
## nb_classe        0.184448   0.009933  18.570 < 2e-16 ***
## nb_classe:temperature_deg_c 0.031932   0.009550   3.344 0.000827 ***
## nb_classe:latitude_deg     0.023453   0.008431   2.782 0.005403 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_order=order:class, nb_classe=number of non-focal classes, classe_type=Lineage, empo_3=Environment, temperature_deg_c=temperature, latitude_deg=latitude, elevation_m=elevation.

4.5. Class:Phylum

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_class ~ nb_phylum + nb_phylum:temperature_deg_c + nb_phylum:latitude_deg +
##   nb_phylum:ph + (1 | phylum_type/empo_3)
## Data: datsc
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 12482.4 12526.7 -6234.2 12468.4    4101
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.5567 -0.3108 -0.0519  0.2560  3.7076
##
## Random effects:
## Groups           Name          Variance Std.Dev.
## empo_3:phylum_type (Intercept) 0.04314  0.2077
## phylum_type      (Intercept) 0.31013  0.5569
## Number of obs: 4108, groups:  empo_3:phylum_type, 367; phylum_type, 78
##
## Fixed effects:
##
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.25091   0.07113   3.527 0.00042 ***
## nb_phylum       0.23662   0.01191  19.864 < 2e-16 ***
## nb_phylum:temperature_deg_c 0.05921   0.01394   4.249 2.15e-05 ***
## nb_phylum:latitude_deg     0.03013   0.01151   2.618 0.00884 **
## nb_phylum:ph          0.01263   0.01090   1.159 0.24661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_class=class:phylum, nb_phylum=number of non-focal phyla, phylum_type=Lineage, empo_3=Environment, temperature_deg_c=temperature, latitude_deg=latitude, elevation_m=elevation.

5. DBD in resident genera versus non-resident genera

5.1. Animal cluster

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_ASV ~ nb_genus * status + (nb_genus | genus_type/empo_3) +
## (nb_genus | empo_3:PI) + (nb_genus - 1 | sample)
## Data: datsc1
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC   logLik deviance df.resid
## 98718.5 98853.1 -49343.2 98686.5   33295
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.0576 -0.3761 -0.1504  0.2038  8.2981
##
## Random effects:
## Groups          Name      Variance Std.Dev. Corr
## empo_3:genus_type (Intercept) 0.039726 0.19931
##                  nb_genus    0.008227 0.09070  0.17
## genus_type      (Intercept) 0.063582 0.25216
##                  nb_genus    0.007117 0.08436  0.88
## sample          nb_genus    0.004299 0.06557
## empo_3:PI       (Intercept) 0.028807 0.16973
##                  nb_genus    0.007302 0.08545  0.11
## Number of obs: 33311, groups:
## empo_3:genus_type, 3196; genus_type, 850; sample, 795; empo_3:PI, 35
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      0.25300   0.03799   6.659 2.75e-11 ***
## nb_genus          0.01619   0.02505   0.646  0.518
## statusMigrant     0.04152   0.03492   1.189  0.234
## statusNative      0.15219   0.03129   4.863 1.15e-06 ***
## nb_genus:statusMigrant -0.01142  0.02018  -0.566  0.571
## nb_genus:statusNative  0.11791   0.01661   7.100 1.25e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

nb_ASV=ASV:genus, nb_genus=number of non-focal native genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID, status=Migrant/Native (Resident)/Generalist.

5.2. Saline cluster

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_ASV ~ nb_genus * status + (nb_genus | genus_type/empo_3) +
## (nb_genus | empo_3:PI) + (nb_genus - 1 | sample)
```

```

## Data: datscl
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 57099.8 57225.9 -28533.9 57067.8 19486
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.3816 -0.3677 -0.1566  0.1609  8.1450
##
## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## empo_3:genus_type (Intercept) 0.037468 0.19357
##                  nb_genus     0.005197 0.07209 -0.15
## genus_type       (Intercept) 0.080367 0.28349
##                  nb_genus     0.006384 0.07990 0.36
## sample           nb_genus     0.004304 0.06561
## empo_3:PI        (Intercept) 0.013523 0.11629
##                  nb_genus     0.004867 0.06976 -0.41
## Number of obs: 19502, groups:
## empo_3:genus_type, 1998; genus_type, 788; sample, 498; empo_3:PI, 26
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.270074  0.033510   8.060 7.65e-16 ***
## nb_genus       0.006229  0.022320   0.279 0.780173
## statusMigrant  -0.006777  0.038090  -0.178 0.858789
## statusNative   -0.005741  0.043218  -0.133 0.894323
## nb_genus:statusMigrant -0.070906  0.022200  -3.194 0.001404 **
## nb_genus:statusNative  0.071725  0.021632   3.316 0.000914 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_ASV=ASV:genus, nb_genus=number of non-focal native genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID, status=Migrant/Native (Resident)/Generalist.

5.3. Non saline cluster

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula: nb_ASV ~ nb_genus * status + (nb_genus | genus_type/empo_3) +
##          (nb_genus | empo_3:PI) + (nb_genus - 1 | sample)
## Data: datscl
## Control: glmerControl(optimizer = "bobyqa")
##
##      AIC      BIC  logLik deviance df.resid
## 131340.7 131479.0 -65654.3 131308.7 42063
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.4818 -0.3928 -0.1428  0.2505 10.2862
##

```

```

## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## empo_3:genus_type (Intercept) 0.042733 0.20672
##                  nb_genus      0.029340 0.17129 0.04
## genus_type      (Intercept) 0.097078 0.31157
##                  nb_genus      0.008959 0.09465 0.70
## sample          nb_genus      0.001827 0.04274
## empo_3:PI       (Intercept) 0.011668 0.10802
##                  nb_genus      0.013691 0.11701 0.04
## Number of obs: 42079, groups:
## empo_3:genus_type, 2611; genus_type, 870; sample, 637; empo_3:PI, 55
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.251500   0.028175   8.926 < 2e-16 ***
## nb_genus       0.008664   0.025004   0.347 0.72896
## statusMigrant  0.020687   0.044937   0.460 0.64527
## statusNative   0.233262   0.035794   6.517 7.19e-11 ***
## nb_genus:statusMigrant -0.079900 0.028135  -2.840 0.00451 **
## nb_genus:statusNative  0.141488  0.019904   7.109 1.17e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_ASV=ASV:genus, nb_genus=number of non-focal native genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID, status=Migrant/Native (Resident)/Generalist.

6. Genome size analysis

```

## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: poisson ( log )
## Formula:
## nb_ASV ~ nb_genus * size + (nb_genus | genus_type/empo_3) + (nb_genus |
##   empo_3:PI) + (nb_genus - 1 | sample)
## Data: datsc1
## Control: glmerControl(optimizer = "bobyqa")
##
##          AIC          BIC    logLik deviance df.resid
## 240595.8 240725.6 -120283.9 240567.8    78199
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -3.6998 -0.4020 -0.1466  0.2450 11.9407
##
## Random effects:
## Groups          Name          Variance Std.Dev. Corr
## empo_3:genus_type (Intercept) 0.059649 0.24423
##                  nb_genus      0.021223 0.14568 0.05
## sample          nb_genus      0.002721 0.05216
## genus_type      (Intercept) 0.074050 0.27212
##                  nb_genus      0.005595 0.07480 0.60
## empo_3:PI       (Intercept) 0.017041 0.13054

```

```

##                nb_genus    0.013100 0.11445  0.18
## Number of obs: 78213, groups:
## empo_3:genus_type, 5501; sample, 1993; genus_type, 576; empo_3:PI, 117
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.371754   0.020487  18.145 < 2e-16 ***
## nb_genus     0.113302   0.016313   6.945 3.77e-12 ***
## size         0.001268   0.014027   0.090  0.9280
## nb_genus:size 0.015908   0.006342   2.508  0.0121 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

nb_ASV=ASV:genus, nb_genus=number of non-focal genera, genus_type=Lineage, empo_3=Environment, PI=laboratory that submitted the data, sample=EMP sample ID, size=genome size.