

Comparison of the frequency vectors between Bellairs and Cement.

Hallett group

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We perform some cursory exploration of the frequency tables obtained from Bracken (REF) and Kraken for the Barbados and Cement reef marine samples. The code to perform this analysis is primarily in `src/exp-4/percolate.R`, as some of the routines are too time consuming to be performed within the R markdown setting here. Column names from Bracken have been modified for readability below. Some of the code is reproduced here to explain the series of steps. We begin by reading in the two Bracken files from the `data` directory.

```
options(warn = -1)
setwd("~/repo/reefmicrobiome/experiments/exp4-species_abundance")
library(xtable)
source("../src/functions.R")

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

##
## Attaching package: 'reshape'

## The following object is masked from 'package:dplyr':
##
##   rename
```

The final tree will always be kept in `repo/reefmicrobiome/data/tree.latest`. This data.frame contains all the information we have about our samples. It was generated using the code in `ad_hoc_scripts.R` and the functions in `functions.R`

```
# load the finalized tree computed in percolate.R with functions from abundance_comparison.R
load("~/repo/reefmicrobiome/data/tree.latest")
tree[1:10, 1:7 ]

##           name tax_id parent      rank embl_code
## 1          root      1    NA      no rank
## 2         Bacteria      2 131567 superkingdom
## 3   Azorhizobium      6 335928      genus
## 4 Azorhizobium caulinodans      7      6      species      AC
## 5         Buchnera aphidicola      9 32199      species      BA
## 6         Cellvibrio     10 1706371      genus
## 7   Cellulomonas gilvus      11    1707      species      CG
## 8         Dictyoglomus     13 203488      genus
## 9 Dictyoglomus thermophilum     14     13      species      DT
## 10        Methylophilus     16 32011      genus
##  division_id br_bel
```

```
## 1      8 4708322
## 2      0 3246493
## 3      0    641
## 4      0    641
## 5      0   3666
## 6      0   1376
## 7      0    412
## 8      0    526
## 9      0    259
## 10     0    334
```

The `make_table()` function takes as input a `tax_id` and pretty prints the information regarding the children of that node.

```
root <- make_table( 1 ); # 1 is the root
make_table( 131567 ) # superkingdoms 131567

##      Name Tax. Id. Parent      Rank Local.Freq.Bel Local.Freq.May
## 1  Bacteria      2 131567 superkingdom      0.700      0.772
## 2  Eukaryota    2759 131567 superkingdom      0.292      0.224
## 3  Archaea     2157 131567 superkingdom      0.008      0.004
##  log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1    -0.097      0.690      0.754    -0.064
## 2     0.266      0.288      0.219     0.069
## 3     0.560      0.007      0.004     0.003

make_table( 2, precision = 4) # 2 is tax_id for bacteria

##      Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1  Proteobacteria    1224      2 phylum      0.4711
## 2  Terrabacteria group 1783272      2 no rank      0.4097
## 3      FCB group    1783270      2 no rank      0.1018
## 4      PVC group    1783257      2 no rank      0.0065
## 5  Fusobacteria     32066      2 phylum      0.0030
## 6  Spirochaetes    203691      2 phylum      0.0028
## 7  Acidobacteria    57723      2 phylum      0.0011
## 8  Thermotogae     200918      2 phylum      0.0011
## 9  Aquificae       200783      2 phylum      0.0006
## 10 Nitrospirae      40117      2 phylum      0.0005
## 11 Deferribacteres   200930      2 phylum      0.0004
## 12 unclassified Bacteria 2323      2 no rank      0.0004
## 13 Thermodesulfobacteria 200940      2 phylum      0.0003
## 14 Synergistetes    508458      2 phylum      0.0002
## 15 Dictyoglomi      68297      2 phylum      0.0002
## 16 Elusimicrobia    74152      2 phylum      0.0001
## 17 Calditrichaeota  1930617      2 phylum      0.0001
## 18 Chrysiogenetes    200938      2 phylum      0.0001
## 19      <NA>       2498710      2 no rank      0.0000
## 20      <NA>       2138240      2 phylum      0.0000
##  Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.2274    0.7283      0.3248      0.1714    0.1534
## 2      0.7208   -0.5650      0.2825      0.5432   -0.2608
## 3      0.0421    0.8830      0.0702      0.0317    0.0385
## 4      0.0026    0.9281      0.0045      0.0019    0.0025
## 5      0.0022    0.3204      0.0021      0.0016    0.0004
## 6      0.0019    0.4096      0.0020      0.0014    0.0005
## 7      0.0004    0.9659      0.0008      0.0003    0.0005
## 8      0.0008    0.3351      0.0007      0.0006    0.0002
```

```
## 9      0.0005    0.2574      0.0004      0.0004    0.0001
## 10     0.0003    0.6869      0.0004      0.0002    0.0002
## 11     0.0003    0.3271      0.0003      0.0002    0.0001
## 12     0.0002    0.5097      0.0003      0.0002    0.0001
## 13     0.0002    0.2875      0.0002      0.0002    0.0000
## 14     0.0001    0.5971      0.0002      0.0001    0.0001
## 15     0.0001    0.3099      0.0001      0.0001    0.0000
## 16     0.0001    0.2919      0.0001      0.0001    0.0000
## 17     0.0001    0.6934      0.0001      0.0000    0.0000
## 18     0.0000    0.9773      0.0000      0.0000    0.0000
## 19     0.0000    0.1993      0.0000      0.0000    0.0000
## 20     0.0000    0.0431      0.0000      0.0000   -0.0000
```

```
make_table( 1224, precision = 4) # proteobacteris is 1224
```

```
##          Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Alphaproteobacteria   28211  1224    class      0.5338
## 2      Gammaproteobacteria    1236  1224    class      0.3094
## 3      Betaproteobacteria   28216  1224    class      0.1063
## 4 delta/epsilon subdivisions  68525  1224 subphylum  0.0476
## 5          Oligoflexia  1553900  1224    class      0.0022
## 6      Acidithiobacillia  1807140  1224    class      0.0004
## 7      Zetaproteobacteria   580370  1224    class      0.0002
## 8          <NA>  2008785  1224    class      0.0001
## Local.Freq.May log(BvSM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.5267    0.0133      0.1734      0.0903    0.0831
## 2      0.2993    0.0334      0.1005      0.0513    0.0492
## 3      0.1137   -0.0673      0.0345      0.0195    0.0150
## 4      0.0571   -0.1824      0.0155      0.0098    0.0057
## 5      0.0025   -0.1496      0.0007      0.0004    0.0003
## 6      0.0004    0.0057      0.0001      0.0001    0.0001
## 7      0.0002    0.0303      0.0001      0.0000    0.0000
## 8      0.0001    0.3257      0.0000      0.0000    0.0000
```

```
make_table( 1218 ) # 1218 is the tax_id of Prochlorococcus
```

```
##          Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Prochlorococcus marinus    1219  1218 species    0.774
## 2 Prochlorococcus sp. MIT 0604  1501268  1218 species    0.127
## 3      Prochlorococcus sp. RS50  1924285  1218 species    0.099
## 4 Prochlorococcus sp. MIT 0801  1501269  1218 species    0.001
## Local.Freq.May log(BvSM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.778   -0.004      0.088      0.300   -0.212
## 2      0.125    0.010      0.014      0.048   -0.034
## 3      0.097    0.018      0.011      0.037   -0.026
## 4      0.000    0.619      0.000      0.000   -0.000
```

```
make_table( 10239 ) # Viruses is tax_id 10239
```

```
##          Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Caudovirales    28883  10239 order      0.946
## 2      Phycodnaviridae  10501  10239 family     0.017
## 3      Mimiviridae    549779  10239 family     0.009
## 4          <NA>  2204151  10239 no rank     0.008
## 5      Poxviridae    10240  10239 family     0.007
## 6      Baculoviridae  10442  10239 family     0.003
## 7      Herpesvirales   548681  10239 order     0.002
## 8 unclassified viruses   12429  10239 no rank     0.001
## 9      Nudiviridae   1511852  10239 family     0.001
```

```

## 10      <NA> 2559587 10239 no rank 0.001
## 11      Iridoviridae 10486 10239 family 0.001
## 12      Polydnviridae 10482 10239 family 0.001
## 13      Marseilleviridae 944644 10239 family 0.000
## 14      Nimaviridae 196937 10239 family 0.000
## 15      Hytrosaviridae 1285590 10239 family 0.000
## 16      Parvoviridae 10780 10239 family 0.000
## 17      Adenoviridae 10508 10239 family 0.000
## 18      Bicaudaviridae 423358 10239 family 0.000
## 19      Alphasatellitidae 1458186 10239 family 0.000
## 20      Ascoviridae 43682 10239 family 0.000
## 21      Ligamenvirales 1511857 10239 order 0.000
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.962 -0.017 0.014 0.022 -0.008
## 2      0.013 0.264 0.000 0.000 -0.000
## 3      0.005 0.545 0.000 0.000 0.000
## 4      0.005 0.463 0.000 0.000 0.000
## 5      0.005 0.463 0.000 0.000 0.000
## 6      0.003 0.235 0.000 0.000 -0.000
## 7      0.003 -0.010 0.000 0.000 -0.000
## 8      0.001 0.625 0.000 0.000 0.000
## 9      0.000 1.034 0.000 0.000 0.000
## 10     0.001 0.111 0.000 0.000 -0.000
## 11     0.001 -0.141 0.000 0.000 -0.000
## 12     0.000 0.635 0.000 0.000 0.000
## 13     0.000 0.179 0.000 0.000 -0.000
## 14     0.000 0.678 0.000 0.000 0.000
## 15     0.000 0.956 0.000 0.000 0.000
## 16     0.000 0.364 0.000 0.000 -0.000
## 17     0.000 -0.470 0.000 0.000 -0.000
## 18     0.000 -Inf 0.000 0.000 -0.000
## 19     0.000 -Inf 0.000 0.000 -0.000
## 20     0.000 -Inf 0.000 0.000 -0.000
## 21     0.000 -Inf 0.000 0.000 -0.000

```

```
make_table( 2157 ) # Archaea
```

```

##      Name Tax. Id. Parent Rank Local.Freq.Bel
## 1      Euryarchaeota 28890 2157 phylum 0.731
## 2      TACK group 1783275 2157 no rank 0.263
## 3      unclassified Archaea 29294 2157 no rank 0.005
## 4      DPANN group 1783276 2157 no rank 0.001
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.848 -0.149 0.005 0.004 0.002
## 2      0.146 0.591 0.002 0.001 0.001
## 3      0.004 0.045 0.000 0.000 0.000
## 4      0.002 -0.416 0.000 0.000 0.000

```

```
make_table( 2759 ) # Eukaryota
```

```

##      Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May
## 1      Viridiplantae 33090 2759 kingdom 0.853 0.859
## 2      Opisthokonta 33154 2759 no rank 0.112 0.110
## 3      Alveolata 33630 2759 no rank 0.019 0.019
## 4      Euglenozoa 33682 2759 no rank 0.005 0.007
## 5      Stramenopiles 33634 2759 no rank 0.005 0.002
## 6      Amoebozoa 554915 2759 no rank 0.003 0.002
## 7      Cryptophyta 3027 2759 phylum 0.002 0.001

```

```
## 8 Rhizaria 543769 2759 no rank 0.000 0.000
## 9 Rhodophyta 2763 2759 phylum 0.000 0.000
## log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1 -0.006 0.246 0.188 0.058
## 2 0.016 0.032 0.024 0.008
## 3 0.017 0.006 0.004 0.001
## 4 -0.276 0.001 0.001 -0.000
## 5 0.992 0.001 0.000 0.001
## 6 0.344 0.001 0.001 0.000
## 7 0.706 0.001 0.000 0.000
## 8 0.798 0.000 0.000 0.000
## 9 -0.128 0.000 0.000 0.000

make_table( 33154 ) # parent of fungi

## Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May log(BvsM)
## 1 Metazoa 33208 33154 kingdom 0.694 0.668 0.038
## 2 Fungi 4751 33154 kingdom 0.306 0.332 -0.082
## Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1 0.022 0.016 0.006
## 2 0.010 0.008 0.002

make_table( 4751 ) # fungi

## Name Tax. Id. Parent Rank Local.Freq.Bel
## 1 Dikarya 451864 4751 subkingdom 0.996
## 2 Fungi incertae sedis 112252 4751 no rank 0.004
## Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1 0.996 -0.000 0.010 0.008 0.002
## 2 0.004 0.097 0.000 0.000 0.000
```

You can easily then send these tables to file using the `write.csv()` function.

1 Background: how the tree was constructed

We now describe how we built the data.frame `tree` and describe the purpose of each of its columns.

1.1 NCBI Taxonomy

```
tree[1,]

## name tax_id parent rank embl_code division_id br_bel br_may
## 1 root 1 NA no rank 8 4708322 10181105
## br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1 0 0 NA NA 1
## Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1 1 0 0 NA NA root

tree[1, 1:6]
```

All of these fields originate from the NCBI Taxonomy download. File `ad_hoc_scripts.R` contains code that added the names of each taxa after trying to find the scientific name amongst synonyms. The column `tax_id` is used throughout the code to find taxa of interest. The `parent` column defines the structure of the tree (each node points to its unique parent).

1.2 Importing the Bracken counts for our two sites

I have never observed a big difference in the results if I look at Kraken versus Bracken. The script `script_bracken.bash` contains the shell commands used to generate these files. Therefore, I suggest we use only the Bracken mappings of reads to nodes in the tree from here on in.

```
tree[1,]
##   name tax_id parent    rank embl_code division_id br_bel  br_may
## 1 root      1      NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0              NA              NA              1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0          NA          NA root

tree[1, 7:8]
##   br_bel  br_may
## 1 4708322 10181105
```

These two fields represent the Bracken counts from Bellairs and Maycocks respectively. The first step was to assign the `est_reads` from the `bellairs.bracken` and `cement.bracken` files (cement was the earlier name for Maycocks). This information was renamed `br_bel` and `br_may`. At the same time the `fraction` fields of the Bracken files were assigned to variables `br_bel_frac` and `br_may_frac`. These reads were assigned to the leaves of `tree`. The code is located in `ad_hoc_scripts.R`.

The next step was to percolate these reads “up” the tree of life to the root. More precisely, consider a node t with children c_1, \dots, c_k . At the Bellairs site child c_i has with read count `br_beli`. Then, `br_bel` for node t is $\sum_{1 \leq i \leq k} \text{br_bel}_i$. This is defined analogously for Maycocks.

Before doing this, the root of the tree of life was manually set to NA (see `ad_hoc_scripts.R`), as there was a mistake in the NCBI download (the root pointed to itself which causes a problem for recursion).

```
tree[1,]
##   name tax_id parent    rank embl_code division_id br_bel  br_may
## 1 root      1      NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0              NA              NA              1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0          NA          NA root

#percolate(1) # note that this function takes about 1 day to run.
tree[1,]
##   name tax_id parent    rank embl_code division_id br_bel  br_may
## 1 root      1      NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0              NA              NA              1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0          NA          NA root
```

Next nodes with 0 counts for both Bellairs and Maycocks were removed (see `ad_hoc_scripts.R`). Columns were rearranged and the scientific name from NCBI Taxonomy was assigned, if it existed (see comment above and `ad_hoc_scripts.R`).

1.3 Global versus Local Frequencies

There are two distinct concepts of frequencies that each have advantages and disadvantages. Consider a node t with total reads r and children c_1, \dots, c_k with total reads r_1, \dots, r_k respectively. The local frequency f_i for child c_i is

equal to $\frac{f_i}{R}$. The global frequency f_i for child c_i is equal to $\frac{f_i}{R}$ where R is the total number of reads at the root of the tree of life.

The local frequencies were assigned to the **tree** as follows.

```
#void <- local_frequencies(1)
tree[1, ]

##   name tax_id parent    rank embl_code division_id br_bel  br_may
## 1 root      1     NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0             NA             NA             1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0             NA             NA root

# Local.Freq.Bel and Local.Freq.May
```

The global frequencies were assigned as follows.

```
#void <- global_frequencies(1)
tree[1, ]

##   name tax_id parent    rank embl_code division_id br_bel  br_may
## 1 root      1     NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0             NA             NA             1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0             NA             NA root

# Glob.Freq.Bel and Glob.Freq.May, Delta.Freq
```

For convenience, I added a column to the **tree** data.frame to record the difference in global frequencies between the two sites.

```
# tree$DeltaFreq <- tree$Glob.Freq.Bel - tree$Glob.Freq.May
top <- tree[ order( -abs(tree$DeltaFreq) ), ]
top[1:max(which(top$DeltaFreq > 0.01)), c(1,2,3, 13:15) ]

##           name tax_id parent Glob.Freq.Bel
## 1540538 Synechococcales 1890424 1117 0.14656687
## 867 Cyanobacteria 1117 1798711 0.15879989
## 1458333 Cyanobacteria/Melainabacteria group 1798711 1783272 0.15879989
## 933 Prochloraceae 1213 1890424 0.11365748
## 937 Prochlorococcus 1218 1213 0.11365748
## 1446826 Terrabacteria group 1783272 2 0.28247325
## 938 Prochlorococcus marinus 1219 1218 0.08797742
## 942 Proteobacteria 1224 2 0.32480340
## 12016 Alphaproteobacteria 28211 1224 0.17337408
## 2189 Eukaryota 2759 131567 0.28780721
## 2 Bacteria 2 131567 0.68952230
## 2531 Embryophyta 3193 131221 0.23357175
## 17254 Streptophyta 35493 33090 0.23357175
## 100789 Streptophytina 131221 35493 0.23357175
## 2706 Magnoliopsida 3398 58024 0.22972261
## 36888 Tracheophyta 58023 3193 0.22972261
## 36889 Spermatophyta 58024 78536 0.22972261
## 54511 Euphyllophyta 78536 58023 0.22972261
## 1142173 Mesangiospermae 1437183 3398 0.22972261
## 15400 Viridiplantae 33090 2759 0.24550360
## 47939 eudicotyledons 71240 1437183 0.18665567
## 66320 Gunneridae 91827 71240 0.18665567
```

## 1142189	Pentapetalae	1437201	91827	0.18665567
## 949	Gammaproteobacteria	1236	1224	0.10050821
## 1540539	Synechococcaceae	1890426	1890424	0.03123172
## 878	Synechococcus	1129	1890426	0.03060581
## 166576	Rhodobacterales	204455	28211	0.04930207
## 14804	Rhodobacteraceae	31989	204455	0.04829576
## 1446824	FCB group	1783270	2	0.07017829
## 45553	Bacteroidetes/Chlorobi group	68336	1783270	0.06970296
## 752	Bacteroidetes	976	68336	0.06895365
## 1199462	Prochlorococcus sp. MIT 0604	1501268	1218	0.01437922
## 47969	rosids	71275	1437201	0.12093289
## 88883	Flavobacteriia	117743	976	0.05279652
## 163073	Flavobacteriales	200644	117743	0.05279652
## 29439	Flavobacteriaceae	49546	200644	0.05163963
## 1570271	Prochlorococcus sp. RS50	1924285	1218	0.01119698
## 163583	Actinobacteria	201174	1783272	0.06144971
## 1380	Actinobacteria	1760	201174	0.05967221
## 66328	fabids	91835	71275	0.07810235
## 274	Rhizobiales	356	28211	0.03040298
## 47968	asterids	71274	1437201	0.06215293
## 952	Firmicutes	1239	1783272	0.05579674
## 48874	Pseudomonadales	72274	1236	0.03367420
## 12020	Betaproteobacteria	28216	1224	0.03452164
## 3064	Fabaceae	3803	72025	0.05438604
## 3075	Papilionoideae	3814	3803	0.05438604
## 48652	Fabales	72025	91835	0.05438604
## 1823180	<NA>	2231393	3814	0.05438604
## 104687	Pseudomonadaceae	135621	72274	0.02585252
## 226	Pseudomonas	286	135621	0.02558300
## 65606	Bacilli	91061	1239	0.03928045
## 131932	Synechococcus sp. WH 8109	166314	1129	0.01126091
## 66370	lamiids	91888	71274	0.04599962
## 56568	Burkholderiales	80840	28216	0.02855540
## 1073	Bacillales	1385	91061	0.03134068
## 66329	malvids	91836	71275	0.03985284
## 105784	Pseudomonas aeruginosa group	136841	286	0.01764238
##	Glob.Freq.May	DeltaFreq		
## 1540538	0.458586961	-0.31202009		
## 867	0.462612162	-0.30381228		
## 1458333	0.462612162	-0.30381228		
## 933	0.386067721	-0.27241024		
## 937	0.386067721	-0.27241024		
## 1446826	0.543244569	-0.26077132		
## 938	0.300176749	-0.21219933		
## 942	0.171382871	0.15342053		
## 12016	0.090270948	0.08310313		
## 2189	0.218706025	0.06910118		
## 2	0.753719365	-0.06419707		
## 2531	0.173892028	0.05967972		
## 17254	0.173892028	0.05967972		
## 100789	0.173892028	0.05967972		
## 2706	0.170825858	0.05889675		
## 36888	0.170825858	0.05889675		
## 36889	0.170825858	0.05889675		
## 54511	0.170825858	0.05889675		
## 1142173	0.170825858	0.05889675		


```
## 15400      0.187763018  0.05774058
## 47939      0.135790565  0.05086511
## 66320      0.135790565  0.05086511
## 1142189    0.135790565  0.05086511
## 949        0.051290503  0.04921770
## 1540539    0.072151598 -0.04091988
## 878        0.071415529 -0.04080972
## 166576     0.008688644  0.04061342
## 14804      0.008428358  0.03986740
## 1446824    0.031722785  0.03845551
## 45553      0.031467901  0.03823506
## 752        0.031018048  0.03793561
## 1199462    0.048339056 -0.03395984
## 47969      0.088740171  0.03219272
## 88883      0.023318687  0.02947783
## 163073     0.023318687  0.02947783
## 29439      0.022535078  0.02910455
## 1570271    0.037361858 -0.02616488
## 163583     0.037575686  0.02387402
## 1380       0.036654666  0.02301755
## 66328      0.057000100  0.02110225
## 274        0.011290228  0.01911275
## 47968      0.044611661  0.01754127
## 952        0.038596891  0.01719985
## 48874      0.016558026  0.01711618
## 12020      0.019484133  0.01503751
## 3064       0.039867775  0.01451827
## 3075       0.039867775  0.01451827
## 48652      0.039867775  0.01451827
## 1823180    0.039867775  0.01451827
## 104687     0.011436971  0.01441555
## 226        0.011304765  0.01427823
## 65606      0.025871357  0.01340909
## 131932     0.024298639 -0.01303773
## 66370      0.033032858  0.01296676
## 56568      0.016331528  0.01222387
## 1073       0.020381776  0.01095890
## 66329      0.029517621  0.01033522
## 105784     0.007581986  0.01006039
```

1.4 The Multinomial Statistic

I implemented the multinomial test and applied it to each node in the `tree` datastructure. The relevant function is in `functions.R`.

```
#multinomial_tree_test(1)
# Fraction significant
length(which(tree$Multinom < 0.01)) / nrow(tree)
## [1] 0.07789474
```

1.5 The Adjusted Polarity Statistic

Next I implemented the polarity statistic. It adds two columns. `Polarity` is the estimated p-value calculated on the local frequencies of the children at each taxa. `Adj.Polarity` is the p-value estimated after removing the “outlier”

children and recomputing the binomial test.

That is, those children that represent that are in the minority. For example, if 3 of 7 children are lower at Bellairs than Maycocks, those 3 are removed. The binomial is recomputed after re-normalizing the frequencies. (Note: we should also re-compute the multinomial here.)

```
# void <- polarity_test( 1 )
tree[1,]

##   name tax_id parent      rank embl_code division_id br_bel  br_may
## 1 root      1      NA no rank                8 4708322 10181105
##   br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 1           0           0           NA           NA           1
##   Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj path
## 1           1           0           0           NA           NA root
```

The intuition of the adjusted polarity statistic is as follows. When a node is deemed significant by the polarity statistic, we can test the hypothesis that the “peak” taxa in the “losing” site drain reads from the other taxa at the losing site, making it seem that the other site is the winner.

Let’s focus on the Bacteria, the second row of **tree**. We know that Bacteria is in fact significant for the polarity statistic, making it a good example here.

```
parent <- 2
c <- p2c( parent ); c_i <- t2i(c); ind <- t2i( parent )

M <- as.table(rbind(tree[c_i, "br_bel"], tree[c_i, "br_may"]))
if (sum(M[1,]) == 0) M[1,] <- 0 else M[1,] <- M[1,] / sum(M[1,])
if (sum(M[2,]) == 0) M[2,] <- 0 else M[2,] <- M[2,] / sum(M[2,])
X <- sum(M[1,] < M[2,])
(X)

## [1] 1

(polarity.orig <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value)
## [1] 4.005432e-05

(M)

##           A           B           C           D           E
## A 4.710557e-01 3.837988e-04 2.983219e-03 5.144012e-04 1.148316e-03
## B 2.273829e-01 2.305278e-04 2.165449e-03 2.588062e-04 4.370775e-04
##           F           G           H           I           J
## A 1.620210e-04 1.259821e-04 6.345309e-04 1.074390e-03 4.155253e-04
## B 1.188476e-04 9.408765e-05 4.905068e-04 7.684693e-04 2.995949e-04
##           K           L           M           N           O
## A 5.852469e-05 2.769142e-04 2.842144e-03 2.251660e-04 6.486692e-03
## B 2.202329e-05 2.077226e-04 1.886966e-03 1.239299e-04 2.564214e-03
##           P           Q           R           S           T
## A 1.017781e-01 4.096651e-01 1.034963e-04 2.217778e-05 4.373951e-05
## B 4.208832e-02 7.207518e-01 5.173517e-05 2.124139e-05 3.583671e-05
```

Bellairs is almost always bigger than Maycocks, and is significant for the polarity test. In fact, only 1 of 20 taxa is more prevalent at Maycocks than Bellairs (17th). Now we remove entires where Bellairs is smaller than Maycocks, renormalize and recompute the polarity statistic.

```
M <- M[ , -which(M[1,]<M[2,])]
# renormalize
M[1,] <- M[1,] / sum(M[1,]); M[2,] <- M[2,] / sum(M[2,])

# and re-test
X <- sum(M[1,] < M[2,])
```

```

(X)
## [1] 15

polarity.new <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value
(polarity.orig); (polarity.new)

## [1] 4.005432e-05
## [1] 0.01921082

```

After adjustment, in fact 15 of 19 species have a lower frequency at Bellairs than Maycocks! The Bacteria node is no longer significant under the polarity test after adjustment. The function `polarity_test()` computes this at every node in `tree`.

So now let's look at all the taxa that are significant under the Polarity statistic and how they behave when adjusted.

```

leave <- setdiff( which(tree$Polarity < 0.01), which(tree$Polarity.Adj < 0.01) )
remain <- intersect( which(tree$Polarity < 0.01), which(tree$Polarity.Adj < 0.01))

```

(Some nodes that weren't significant became significant but these are not interesting.) Nodes 519 (Synechococcus) and 1622 (Burkholderia) both remain significant. Let's look Synechococcus first.

```

parent <- tree[519, "tax_id"]
make_table( parent)

```

##	Name	Tax. Id.	Parent	Rank	
## 1	Synechococcus sp. WH 8109	166314	1129	species	
## 2	Synechococcus sp. CC9605	110662	1129	species	
## 3	Synechococcus sp. WH 8103	29410	1129	species	
## 4	Synechococcus sp. KORDI-52	585425	1129	species	
## 5	Synechococcus sp. WH 8102	84588	1129	species	
## 6	Synechococcus sp. KORDI-100	1280380	1129	species	
## 7	Synechococcus sp. KORDI-49	585423	1129	species	
## 8	Synechococcus sp. WH 8101	59932	1129	species	
## 9	Synechococcus sp. CB0101	232348	1129	species	
## 10	Synechococcus sp. WH 7803	32051	1129	species	
## 11	Synechococcus sp. RCC307	316278	1129	species	
## 12	Synechococcus sp. CC9902	316279	1129	species	
## 13	Synechococcus sp. SynAce01	1916956	1129	species	
## 14	Synechococcus sp. PCC 7336	195250	1129	species	
## 15	Synechococcus sp. WH 8020	32052	1129	species	
## 16	Synechococcus sp. CC9311	64471	1129	species	
## 17	Synechococcus sp. PCC 7502	1173263	1129	species	
## 18	Synechococcus sp. NIES-970	1827144	1129	species	
## 19	Synechococcus sp. JA-2-3B'a(2-13)	321332	1129	species	
## 20	Synechococcus lividus	33070	1129	species	
## 21	Synechococcus sp. PCC 6312	195253	1129	species	
## 22	Synechococcus sp. PCC 7003	374981	1129	species	
## 23	Synechococcus sp. JA-3-3Ab	321327	1129	species	
## 24	Synechococcus elongatus	32046	1129	species	
## 25	Synechococcus sp. PCC 73109	374982	1129	species	
## 26	Synechococcus sp. PCC 7002	32049	1129	species	
## 27	<NA>	2579791	1129	species	
## 28	Synechococcus sp. PCC 7117	195498	1129	species	
## 29	Synechococcus sp. PCC 8807	195248	1129	species	
##	Local.Freq.Bel	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May
## 1	0.368	0.340	0.078	0.011	0.024
## 2	0.175	0.169	0.036	0.005	0.012
## 3	0.082	0.101	-0.215	0.002	0.007

## 4	0.078	0.074	0.057	0.002	0.005
## 5	0.075	0.097	-0.264	0.002	0.007
## 6	0.054	0.077	-0.357	0.002	0.006
## 7	0.052	0.060	-0.144	0.002	0.004
## 8	0.021	0.017	0.171	0.001	0.001
## 9	0.016	0.012	0.299	0.000	0.001
## 10	0.016	0.014	0.144	0.000	0.001
## 11	0.014	0.014	-0.038	0.000	0.001
## 12	0.009	0.008	0.128	0.000	0.001
## 13	0.008	0.006	0.253	0.000	0.000
## 14	0.005	0.000	2.337	0.000	0.000
## 15	0.004	0.003	0.133	0.000	0.000
## 16	0.003	0.003	0.252	0.000	0.000
## 17	0.003	0.001	1.548	0.000	0.000
## 18	0.002	0.000	2.106	0.000	0.000
## 19	0.002	0.000	1.729	0.000	0.000
## 20	0.002	0.000	2.205	0.000	0.000
## 21	0.002	0.000	1.828	0.000	0.000
## 22	0.002	0.000	2.288	0.000	0.000
## 23	0.002	0.001	1.222	0.000	0.000
## 24	0.001	0.000	1.335	0.000	0.000
## 25	0.001	0.000	2.306	0.000	0.000
## 26	0.001	0.000	2.164	0.000	0.000
## 27	0.001	0.000	2.113	0.000	0.000
## 28	0.001	0.000	1.757	0.000	0.000
## 29	0.001	0.000	1.921	0.000	0.000
##	DeltaFreq				
## 1	-0.013				
## 2	-0.007				
## 3	-0.005				
## 4	-0.003				
## 5	-0.005				
## 6	-0.004				
## 7	-0.003				
## 8	-0.001				
## 9	-0.000				
## 10	-0.001				
## 11	-0.001				
## 12	-0.000				
## 13	-0.000				
## 14	0.000				
## 15	-0.000				
## 16	-0.000				
## 17	0.000				
## 18	0.000				
## 19	0.000				
## 20	0.000				
## 21	0.000				
## 22	0.000				
## 23	0.000				
## 24	0.000				
## 25	0.000				
## 26	0.000				
## 27	0.000				
## 28	0.000				
## 29	0.000				

```

c <- p2c( parent ); c_i <- t2i(c); ind <- t2i( parent )

M <- as.table(rbind(tree[c_i, "br_bel"], tree[c_i, "br_may"]))
if (sum(M[1,]) == 0) M[1,] <- 0 else M[1,] <- M[1,] / sum(M[1,])
if (sum(M[2,]) == 0) M[2,] <- 0 else M[2,] <- M[2,] / sum(M[2,])
X <- sum(M[1,] < M[2,])
(X); length(M[1,])

## [1] 5
## [1] 29

```

Only 5 times (of 29) is Bellairs smaller than Maycocks. So Bellairs has the more polarized distribution.

```

(polarity.orig <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value)

## [1] 0.0005461127

```

It is significant. Now adjusting by removing the 5 taxa less frequent at Bellairs.

```

M <- M[ ,~which(M[1,]<M[2,])]
# renormalize
M[1,] <- M[1,] / sum(M[1,]); M[2,] <- M[2,] / sum(M[2,])

# and re-test
X <- sum(M[1,] < M[2,])
(X); length(M[1,])

## [1] 3
## [1] 24

```

Now Bellairs is smaller 3 times (out of are remainig 24). It remains significant.

```

polarity.new <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value
(polarity.orig); (polarity.new)

## [1] 0.0005461127
## [1] 0.0002771616

```

Now let's look at 1622, the Burkholderia genus.

```

parent <- tree[1622, "tax_id"]
make_table( parent)

```

##	Name	Tax. Id.	Parent	Rank
## 1	Burkholderia cepacia complex	87882	32008	species group
## 2	pseudomallei group	111527	32008	species group
## 3	Burkholderia gladioli	28095	32008	species
## 4	Burkholderia plantarii	41899	32008	species
## 5	<NA>	2571746	32008	species
## 6	Burkholderia glumae	337	32008	species
## 7	Burkholderia insecticola	758793	32008	species
## 8	Burkholderia sp. AD24	1528693	32008	species
## 9	Burkholderia sp. ID03	1705310	32008	species
## 10	Burkholderia sp. CCGE1003	640512	32008	species
## 11	Burkholderia sp. OLGA172	1804984	32008	species
## 12	Burkholderia sp. CCGE1001	640510	32008	species
## 13	Burkholderia sp. Bp7605	1740163	32008	species
## 14	Burkholderia sp. HB1	1678678	32008	species
## 15	<NA>	2217913	32008	species
## 16	Burkholderia sp. KK1	1855726	32008	species
## 17	Burkholderia sp. RPE67	758796	32008	species
## 18	Burkholderia sp. YI23	1097668	32008	species

```

## 19 Burkholderia sp. PAMC 26561 1795043 32008 species
## 20 Burkholderia sp. PAMC 28687 1795874 32008 species
## 21 Burkholderia sp. KJ006 416344 32008 species
## Local.Freq.Bel Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May
## 1 0.715 0.769 -0.072 0.006 0.005
## 2 0.143 0.133 0.078 0.001 0.001
## 3 0.027 0.018 0.364 0.000 0.000
## 4 0.015 0.010 0.419 0.000 0.000
## 5 0.010 0.006 0.504 0.000 0.000
## 6 0.008 0.007 0.208 0.000 0.000
## 7 0.008 0.006 0.341 0.000 0.000
## 8 0.008 0.006 0.372 0.000 0.000
## 9 0.008 0.006 0.264 0.000 0.000
## 10 0.007 0.005 0.278 0.000 0.000
## 11 0.007 0.004 0.572 0.000 0.000
## 12 0.006 0.004 0.395 0.000 0.000
## 13 0.006 0.005 0.167 0.000 0.000
## 14 0.006 0.004 0.315 0.000 0.000
## 15 0.006 0.004 0.427 0.000 0.000
## 16 0.005 0.004 0.316 0.000 0.000
## 17 0.004 0.003 0.415 0.000 0.000
## 18 0.003 0.002 0.271 0.000 0.000
## 19 0.003 0.002 0.478 0.000 0.000
## 20 0.003 0.002 0.549 0.000 0.000
## 21 0.002 0.002 0.092 0.000 0.000
## DeltaFreq
## 1 0.001
## 2 0.000
## 3 0.000
## 4 0.000
## 5 0.000
## 6 0.000
## 7 0.000
## 8 0.000
## 9 0.000
## 10 0.000
## 11 0.000
## 12 0.000
## 13 0.000
## 14 0.000
## 15 0.000
## 16 0.000
## 17 0.000
## 18 0.000
## 19 0.000
## 20 0.000
## 21 0.000

c <- p2c( parent ); c_i <- t2i(c); ind <- t2i( parent )

M <- as.table(rbind(tree[c_i, "br_bel"], tree[c_i, "br_may"]))
if (sum(M[1,]) == 0) M[1,] <- 0 else M[1,] <- M[1,] / sum(M[1,])
if (sum(M[2,]) == 0) M[2,] <- 0 else M[2,] <- M[2,] / sum(M[2,])
X <- sum(M[1,] < M[2,])
(X); length(M[1,])

## [1] 1

```

```
## [1] 21
```

Only 1 time (of 21) is Bellairs smaller than Maycocks. So Bellairs has the more polarized distribution.

```
(polarity.orig <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value)
## [1] 2.098083e-05
```

It is significant. Now adjusting by removing the 5 taxa less frequent at Bellairs.

```
M <- M[ , -which(M[1,]<M[2,])]
# renormalize
M[1,] <- M[1,] / sum(M[1,]); M[2,] <- M[2,] / sum(M[2,])

# and re-test
X <- sum(M[1,] < M[2,])
(X); length(M[1,])

## [1] 3
## [1] 20
```

Now Bellairs is smaller 3 times (out of are remainig 20). It remains significant.

```
polarity.new <- binom.test(x=X, n=ncol(M), p=0.5, alternative="two.sided" )$p.value
(polarity.orig); (polarity.new)

## [1] 2.098083e-05
## [1] 0.002576828
```

However, of the 10 significant taxa under the polarity statistic ($p < 0.01$), 8 do not retain significance when adjusted.

```
tree[leave, c("Polarity", "Polarity.Adj")]

##          Polarity Polarity.Adj
## 2      4.005432e-05 0.01921082
## 422     4.077315e-03 0.26317596
## 519     2.102402e-03 0.45312500
## 1074    6.855642e-04 0.53270926
## 1303    2.746582e-04      NA
## 1380    7.197380e-03 1.00000000
## 62785   1.211166e-04 0.82380295
## 105786  7.537842e-03 1.00000000
```

1.6 Taxa Path to Root

Finally, I added a character to the `tree` data.frame that describes the phylogenetic path to the root.

```
# tree$path <- unlist(lapply( tree$tax_id, FUN = function(x) { return(paste(path2root(x)$name, collapse="
```

2 Taxa with Differential Behavior

2.1 Taxa more frequent at Maycocks

Across the entire Tree of Life, we first identify the taxa that have the biggest shift in frequencies towards Maycocks.

```
may.big <- tree[ which(tree$DeltaFreq < -0.001), ] ; nrow(may.big)
## [1] 32
```

```
may.big <- may.big[ order( may.big$path, may.big$DeltaFreq ), ]
may.big[ , c(1:4,15 )]
```

##		name	tax_id	parent	rank
## 2		Bacteria	2	131567	superkingdom
## 1446826		Terrabacteria group	1783272	2	no rank
## 1458333		Cyanobacteria/Melainabacteria group	1798711	1783272	no rank
## 867		Cyanobacteria	1117	1798711	phylum
## 1540538		Synechococcales	1890424	1117	order
## 933		Prochloraceae	1213	1890424	family
## 937		Prochlorococcus	1218	1213	genus
## 938		Prochlorococcus marinus	1219	1218	species
## 1199462		Prochlorococcus sp. MIT 0604	1501268	1218	species
## 1570271		Prochlorococcus sp. RS50	1924285	1218	species
## 1540539		Synechococcaceae	1890426	1890424	family
## 878		Synechococcus	1129	1890426	genus
## 82778		Synechococcus sp. CC9605	110662	1129	species
## 1007225		Synechococcus sp. KORDI-100	1280380	1129	species
## 496092		Synechococcus sp. KORDI-49	585423	1129	species
## 496094		Synechococcus sp. KORDI-52	585425	1129	species
## 59859		Synechococcus sp. WH 8102	84588	1129	species
## 12954		Synechococcus sp. WH 8103	29410	1129	species
## 131932		Synechococcus sp. WH 8109	166314	1129	species
## 2402		Chlorophyta	3041	33090	phylum
## 797843		Mamiellophyceae	1035538	3041	class
## 10591		Mamiellales	13792	1035538	order
## 22758		Mamiellaceae	41873	13792	family
## 20093		Micromonas	38832	41873	genus
## 245354		Micromonas commoda	296587	38832	species
## 8295		Viruses	10239	1	superkingdom
## 12521		Caudovirales	28883	10239	order
## 8614		Myoviridae	10662	28883	family
## 159561		unclassified Myoviridae	196896	10662	no rank
## 687482		Prochlorococcus phage MED4-213	889956	196896	species
## 379172		Prochlorococcus phage P-HM1	445700	196896	species
## 379167		Synechococcus phage S-SSM7	445686	196896	species
##	DeltaFreq				
## 2	-0.064197069				
## 1446826	-0.260771323				
## 1458333	-0.303812276				
## 867	-0.303812276				
## 1540538	-0.312020095				
## 933	-0.272410243				
## 937	-0.272410243				
## 938	-0.212199334				
## 1199462	-0.033959835				
## 1570271	-0.026164875				
## 1540539	-0.040919877				
## 878	-0.040809721				
## 82778	-0.006717490				
## 1007225	-0.003866433				
## 496092	-0.002700047				
## 496094	-0.002868768				
## 59859	-0.004662019				
## 12954	-0.004728312				
## 131932	-0.013037727				


```
## 2402      -0.001939138
## 797843    -0.001939138
## 10591     -0.001939138
## 22758     -0.001994242
## 20093     -0.001994242
## 245354    -0.001994242
## 8295      -0.008112324
## 12521     -0.008049537
## 8614      -0.008996657
## 159561    -0.009238802
## 687482    -0.001042721
## 379172    -0.001080761
## 379167    -0.001718189
```

There is a large increase in the fraction of bacteria at Maycocks (6%) but the distribution within Bacteria is remarkably different between the two sites especially with respect to the Synechococcales and Prochloraceae (Terrabacteria group/Cyanobacteria). Within Eukaryota, the Chlorophyta are slightly increased at Maycocks (0.2%), specifically *Micromonas commoda* (genome size of 19Mb). Wrt viruses, both Prochlorococcus and Synechococcus phage viruses are slightly elevated at Maycocks.

2.2 Taxa more frequent at Bellairs

We repeat the above analysis for Bellairs.

```
bel.big <- tree[ which(tree$DeltaFreq > 0.001), ]; nrow(bel.big)
## [1] 350

bel.big <- bel.big[ order( -bel.big$DeltaFreq ), ]
bel.big[, c(1:4,15 )]
```

##	name	tax_id	parent	rank
## 942	Proteobacteria	1224	2	phylum
## 12016	Alphaproteobacteria	28211	1224	class
## 2189	Eukaryota	2759	131567	superkingdom
## 2531	Embryophyta	3193	131221	no rank
## 17254	Streptophyta	35493	33090	phylum
## 100789	Streptophytina	131221	35493	subphylum
## 2706	Magnoliopsida	3398	58024	no rank
## 36888	Tracheophyta	58023	3193	no rank
## 36889	Spermatophyta	58024	78536	no rank
## 54511	Euphyllophyta	78536	58023	no rank
## 1142173	Mesangiospermae	1437183	3398	no rank
## 15400	Viridiplantae	33090	2759	kingdom
## 47939	eudicotyledons	71240	1437183	no rank
## 66320	Gunneridae	91827	71240	no rank
## 1142189	Pentapetalae	1437201	91827	no rank
## 949	Gammaproteobacteria	1236	1224	class
## 166576	Rhodobacterales	204455	28211	order
## 14804	Rhodobacteraceae	31989	204455	family
## 1446824	FCB group	1783270	2	no rank
## 45553	Bacteroidetes/Chlorobi group	68336	1783270	no rank
## 752	Bacteroidetes	976	68336	phylum
## 47969	rosids	71275	1437201	no rank
## 88883	Flavobacteriia	117743	976	class
## 163073	Flavobacteriales	200644	117743	order
## 29439	Flavobacteriaceae	49546	200644	family

## 163583	Actinobacteria	201174	1783272	phylum
## 1380	Actinobacteria	1760	201174	class
## 66328	fabids	91835	71275	no rank
## 274	Rhizobiales	356	28211	order
## 47968	asterids	71274	1437201	no rank
## 952	Firmicutes	1239	1783272	phylum
## 48874	Pseudomonadales	72274	1236	order
## 12020	Betaproteobacteria	28216	1224	class
## 3064	Fabaceae	3803	72025	family
## 3075	Papilionoideae	3814	3803	subfamily
## 48652	Fabales	72025	91835	order
## 1823180	<NA>	2231393	3814	no rank
## 104687	Pseudomonadaceae	135621	72274	family
## 226	Pseudomonas	286	135621	genus
## 65606	Bacilli	91061	1239	class
## 66370	lamiids	91888	71274	no rank
## 56568	Burkholderiales	80840	28216	order
## 1073	Bacillales	1385	91061	order
## 66329	malvids	91836	71275	no rank
## 105784	Pseudomonas aeruginosa group	136841	286	species group
## 3311	Solanales	4069	91888	order
## 3312	Solanaceae	4070	4069	family
## 32798	Pseudomonas resinovorans	53412	136841	species
## 1823169	<NA>	2231382	2231393	no rank
## 33769	Pelagibacterales	54526	28211	order
## 1335441	Pelagibacteraceae	1655514	54526	family
## 101088	cellular organisms	131567	1	no rank
## 15464	Opisthokonta	33154	2759	no rank
## 360071	Solanoideae	424551	4070	subfamily
## 160842	Candidatus Pelagibacter	198251	1655514	genus
## 129670	Phaseoleae	163735	2233855	tribe
## 1824645	<NA>	2233855	2231382	no rank
## 166578	Sphingomonadales	204457	28211	order
## 4896	Eumetazoa	6072	33208	no rank
## 6209	Chordata	7711	33511	phylum
## 6238	Vertebrata	7742	89593	no rank
## 6258	Gnathostomata	7776	7742	no rank
## 6664	Sarcopterygii	8287	117571	superclass
## 7552	Eutheria	9347	32525	no rank
## 7639	Primates	9443	314146	order
## 7705	Catarrhini	9526	314293	parvorder
## 7768	Hominidae	9604	314295	family
## 7769	Homo	9605	207598	genus
## 7770	Homo sapiens	9606	9605	species
## 15231	Tetrapoda	32523	1338369	no rank
## 15232	Amniota	32524	32523	no rank
## 15233	Theria	32525	40674	no rank
## 15503	Metazoa	33208	33154	kingdom
## 15505	Bilateria	33213	6072	no rank
## 15683	Deuterostomia	33511	33213	no rank
## 21676	Mammalia	40674	32524	class
## 64277	Craniata	89593	7711	subphylum
## 88716	Teleostomi	117570	7776	no rank
## 88717	Euteleostomi	117571	117570	no rank
## 169391	Homininae	207598	9604	subfamily
## 261158	Euarchontoglires	314146	1437010	superorder

## 261292	Simiiformes	314293	376913	infraorder
## 261294	Hominoidea	314295	9526	superfamily
## 317280	Haplorrhini	376913	9443	suborder
## 1059069	Dipnotetrapodomorpha	1338369	8287	no rank
## 1142005	Boreoeutheria	1437010	9347	no rank
## 1621	Streptomycetaceae	2062	85011	family
## 60252	Streptomycetales	85011	1760	order
## 150594	Paenibacillaceae	186822	1385	family
## 501	Vibrionaceae	641	135623	family
## 104689	Vibrionales	135623	1236	order
## 1482	Streptomyces	1883	2062	genus
## 24794	Paenibacillus	44249	186822	genus
## 65880	Enterobacteriales	91347	1236	order
## 45715	delta/epsilon subdivisions	68525	1224	subphylum
## 3639	Liliopsida	4447	1437183	class
## 1142187	Petrosaviidae	1437197	4447	subclass
## 2913	Malvaceae	3629	41938	family
## 22820	Malvales	41938	91836	order
## 104685	Oceanospirillales	135619	1236	order
## 1137	Paenibacillus larvae	1464	44249	species
## 3313	Capsicum	4071	424564	genus
## 3314	Capsicum annuum	4072	4071	species
## 360083	Capsiceae	424564	424551	tribe
## 519	Vibrio	662	641	genus
## 2916	Gossypium	3633	214907	genus
## 176137	Malvoideae	214907	3629	subfamily
## 60247	Micrococcales	85006	1760	order
## 66366	campanulids	91882	71274	no rank
## 166566	Rhodospirillales	204441	28211	order
## 104688	Alteromonadales	135622	1236	order
## 57581	Rhizobiaceae	82115	356	family
## 60248	Corynebacteriales	85007	1760	order
## 3885	commelinids	4734	1437197	no rank
## 2975	Brassicales	3699	91836	order
## 2976	Brassicaceae	3700	3699	family
## 38748	Sulfitobacter	60136	31989	genus
## 895	Nostocales	1161	1117	order
## 12023	Deltaproteobacteria	28221	68525	class
## 22258	Sphingomonadaceae	41297	204457	family
## 12048	Halomonadaceae	28256	135619	family
## 1616664	<NA>	1977864	198251	species
## 3436	Asterales	4209	91882	order
## 3437	Asteraceae	4210	4209	family
## 90081	Burkholderiaceae	119060	80840	family
## 3078	Arachis	3817	2231390	genus
## 129662	Dalbergieae	163725	2231387	tribe
## 1823174	<NA>	2231387	2231393	no rank
## 1823177	<NA>	2231390	163725	no rank
## 615008	Cytophagia	768503	976	class
## 615011	Cytophagales	768507	768503	order
## 3015	Rosales	3744	91835	order
## 250565	Phaeobacter	302485	31989	genus
## 22255	Bradyrhizobiaceae	41294	356	family
## 1702	Archaea	2157	131567	superkingdom
## 187	Flavobacterium	237	49546	genus
## 211	Paracoccus	265	31989	genus

## 187051	Rhizobium/Agrobacterium group	227290	82115	no rank
## 56588	Comamonadaceae	80864	80840	family
## 150576	Clostridia	186801	1239	class
## 2981	Brassica	3705	981071	genus
## 755366	Brassicaceae	981071	3700	tribe
## 46253	Phyllobacteriaceae	69277	356	family
## 3172	Vigna	3913	163735	genus
## 422	Enterobacteriaceae	543	91347	family
## 85788	Zymobacter group	114403	28256	no rank
## 66335	Candidatus Portiera aleyrodidarum	91844	235572	species
## 85784	whitefly endosymbionts	114399	114403	no rank
## 194293	Candidatus Portiera	235572	114399	genus
## 3457	Helianthus	4231	102814	genus
## 3458	Helianthus annuus	4232	4231	species
## 76005	Asteroideae	102804	4210	subfamily
## 76014	Heliantheae	102814	911341	tribe
## 702345	Heliantheae alliance	911341	102804	no rank
## 1025557	Oscillatoriophyceae	1301283	1117	subclass
## 1514	Streptomyces lividans	1916	1883	species
## 22256	Rhodospirillaceae	41295	204441	family
## 150577	Clostridiales	186802	186801	order
## 51905	Oxalobacteraceae	75682	80840	family
## 104680	Xanthomonadales	135614	1236	order
## 3016	Rosaceae	3745	3744	family
## 358	Moraxellaceae	468	72274	family
## 90066	Methylobacteriaceae	119045	356	family
## 3343	Solanum	4107	424574	genus
## 29229	Lycopersicon	49274	4107	subgenus
## 360093	Solaneae	424574	424551	tribe
## 150590	Bacillaceae	186817	1385	family
## 1446811	PVC group	1783257	2	no rank
## 2767	Papaveraceae	3465	41768	family
## 2770	Papaver	3468	1462614	genus
## 2771	Papaver somniferum	3469	3468	species
## 22665	Ranunculales	41768	1437183	order
## 1165039	Papaveroideae	1462614	3465	subfamily
## 150598	Lactobacillales	186826	91061	order
## 280865	Erythrobacteraceae	335929	204457	family
## 20086	Poales	38820	4734	order
## 2918	Gossypium hirsutum	3635	3633	species
## 359	Acinetobacter	469	468	genus
## 32390	Polaribacter	52959	49546	genus
## 14836	Xanthomonadaceae	32033	135614	family
## 38415	Chryseobacterium	59732	49546	genus
## 22	Myxococcales	29	28221	order
## 674403	Celeribacter	875170	31989	genus
## 588253	Vibrio harveyi group	717610	662	species group
## 914	Rivulariaceae	1185	1161	family
## 1824628	<NA>	2233838	2231382	no rank
## 1824629	<NA>	2233839	2233838	no rank
## 3372	Lamiales	4143	91888	order
## 60250	Propionibacteriales	85009	1760	order
## 3325	Nicotiana	4085	424562	genus
## 29353	Nicotiana attenuata	49451	4085	species
## 360074	Nicotianoideae	424554	4070	subfamily
## 360082	Nicotianeae	424562	424554	tribe

## 283	Bradyrhizobium	374	41294	genus
## 45508	Mesorhizobium	68287	69277	genus
## 104679	Chromatiales	135613	1236	order
## 3106	Glycine	3846	163735	genus
## 1165036	Soja	1462606	3846	subgenus
## 77200	Tenacibaculum	104267	49546	genus
## 60264	Microbacteriaceae	85023	85006	family
## 117021	Massilia	149698	75682	genus
## 3663	Poaceae	4479	38820	family
## 2927	Malpighiales	3646	91835	order
## 3898	Fungi	4751	33154	kingdom
## 4014	Ascomycota	4890	451864	phylum
## 12526	Euryarchaeota	28890	2157	phylum
## 384478	Dikarya	451864	4751	subkingdom
## 288	Rhizobium	379	227290	genus
## 587287	saccharomyceta	716545	4890	no rank
## 59838	Sphingobacteriaceae	84566	200666	family
## 88886	Sphingobacteriia	117747	976	class
## 163094	Sphingobacteriales	200666	117747	order
## 1381	Mycobacteriaceae	1762	85007	family
## 327	Acetobacteraceae	433	204441	family
## 100097	Arachis ipaensis	130454	3817	species
## 1074	Bacillus	1386	186817	genus
## 71047	Ruegeria	97050	31989	genus
## 163072	Bacteroidia	200643	976	class
## 393	Alcaligenaceae	506	80840	family
## 165851	Planctomycetes	203682	1783257	phylum
## 1626	Pseudonocardiaceae	2070	85010	family
## 60251	Pseudonocardiales	85010	1760	order
## 2986	Brassica rapa	3711	3705	species
## 136645	Amygdaloideae	171637	3745	subfamily
## 819	Rhodobacter	1060	31989	genus
## 53004	Caulobacteraceae	76892	204458	family
## 166579	Caulobacterales	204458	28211	order
## 3373	Oleaceae	4144	4143	family
## 3374	Olea	4145	426106	genus
## 3375	Olea europaea	4146	4145	species
## 361490	Oleeae	426106	4144	tribe
## 60256	Nocardoidaceae	85015	85009	family
## 154451	Leisingera	191028	31989	genus
## 48875	Alteromonadaceae	72275	135622	family
## 85	Planctomycetales	112	203683	order
## 165852	Planctomycetia	203683	203682	class
## 868	Chroococcales	1118	1301283	order
## 11897	Micromonosporaceae	28056	85008	family
## 60249	Micromonosporales	85008	1760	order
## 896	Nostocaceae	1162	1161	family
## 3865	Arecaceae	4710	40551	family
## 21578	Arecales	40551	4734	order
## 31486	Elaeis	51952	169729	genus
## 31487	Elaeis guineensis	51953	51952	species
## 134884	Arecoideae	169697	4710	subfamily
## 134891	Cocoseae	169705	169697	tribe
## 134908	Elaeidinae	169729	169705	subtribe
## 136571	Bacteroidales	171549	200643	order
## 3129	Lupinus	3869	163729	genus

## 3131	Lupinus angustifolius	3871	3869	species
## 129665	Genisteae	163729	2231385	tribe
## 1823171	<NA>	2231384	2231393	no rank
## 1823172	<NA>	2231385	2231384	no rank
## 12212	Solanum pennellii	28526	49274	species
## 15788	Alveolata	33630	2759	no rank
## 13062	Epsilonproteobacteria	29547	68525	class
## 33288	Octadecabacter	53945	31989	genus
## 4680	Apicomplexa	5794	33630	phylum
## 548	Pasteurellaceae	712	135625	family
## 104691	Pasteurellales	135625	1236	order
## 13226	Gossypium arboreum	29729	3633	species
## 3079	Arachis hypogaea	3818	3817	species
## 37628	unclassified Rhodobacteraceae	58840	31989	no rank
## 1379335	Cellvibrionales	1706369	1236	order
## 1446829	TACK group	1783275	2157	no rank
## 14817	Burkholderia	32008	119060	genus
## 754509	Camelineae	980083	3700	tribe
## 39437	Phaeobacter gallaeciensis	60890	302485	species
## 915	Calothrix	1186	1185	genus
## 886	Oscillatoriales	1150	1301283	order
## 175148	Campylobacterales	213849	29547	order
## 1335443	unclassified Pelagibacteraceae	1655516	1655514	no rank
## 115177	Panicoideae	147369	147370	subfamily
## 115178	PACMAD clade	147370	4479	no rank
## 358308	Aconoidasida	422676	5794	class
## 14795	Clostridiaceae	31979	186802	family
## 60266	Nocardiaceae	85025	85007	family
## 975	Micrococcaceae	1268	85006	family
## 2931	Cucurbitaceae	3650	71239	family
## 47938	Cucurbitales	71239	91835	order
## 1616665	<NA>	1977865	198251	species
## 3300	Gentianales	4055	91888	order
## 10278	Coffea	13442	169640	genus
## 11175	Rubiaceae	24966	4055	family
## 134815	Ixoroideae	169618	24966	subfamily
## 134834	Coffeeae	169640	1968428	tribe
## 1608226	<NA>	1968428	1968429	no rank
## 1608227	<NA>	1968429	169618	no rank
## 3321	Solanum lycopersicum	4081	49274	species
## 10498	Sphingomonas	13687	41297	genus
## 1869404	<NA>	2290931	28890	no rank
## 531588	Thaumarchaeota	651137	1783275	phylum
## 223017	Shewanellaceae	267890	135622	family
## 25774	Hyphomicrobiaceae	45401	356	family
## 150451	Microvirga	186650	119045	genus
## 4015	Saccharomycetes	4891	147537	class
## 4016	Saccharomycetales	4892	4891	order
## 115327	Saccharomycotina	147537	716545	subphylum
## 307	Methylobacterium	407	119045	genus
## 209106	Maribacter	252356	49546	genus
## 3143	Phaseolus	3883	163735	genus
## 3145	Phaseolus vulgaris	3885	3883	species
## 3086	Cicer	3826	163722	genus
## 3087	Cicer arietinum	3827	3826	species
## 129660	Cicereae	163722	2233839	tribe

## 2821	Caryophyllales	3524	1437201	order
## 2849	Beta	3554	1804621	genus
## 128004	Beta vulgaris	161934	3554	species
## 1463833	Betoideae	1804621	1804623	subfamily
## 1463835	Chenopodiaceae	1804623	3524	family
## 305242	Nonlabens	363408	49546	genus
## 1507401	Hymenobacteraceae	1853232	768507	family
## 3176	Vigna unguiculata	3917	3913	species
## 4701	Haemosporida	5819	422676	order
## 4702	Plasmodium	5820	1639119	genus
## 1321768	Plasmodiidae	1639119	5819	family
## 56540	Cystobacterineae	80811	29	suborder
## 236174	Winogradskyella	286104	49546	genus
## 1153	Clostridium	1485	31979	genus
## 3843	Asparagus	4685	703533	genus
## 3844	Asparagus officinalis	4686	4685	species
## 21579	Asparagaceae	40552	73496	family
## 49992	Asparagales	73496	1437197	order
## 576395	Asparagoideae	703533	40552	subfamily
## 786	Capnocytophaga	1016	49546	genus
## 804	Erythrobacter	1041	335929	genus
## 187053	Sinorhizobium/Ensifer group	227292	82115	no rank
## 150	Azospirillum	191	41295	genus
## 3080	Cajanus	3820	163735	genus
## 3081	Cajanus cajan	3821	3820	species
## 16	Shewanella	22	267890	genus
## 275	Agrobacterium	357	227290	genus
## 224	Comamonas	283	80864	genus
## 32661	Pseudoalteromonas	53246	267888	genus
## 223015	Pseudoalteromonadaceae	267888	135622	family
## 1533643	Microvirga ossetica	1882682	186650	species
## 57583	unclassified Alphaproteobacteria	82117	28211	no rank
## 136646	Rosoideae	171638	3745	subfamily
## 3107	Glycine max	3847	1462606	species
## 48011	Camelina	71323	980083	genus
## 65253	Camelina sativa	90675	71323	species
## 660968	alpha proteobacterium HIMB5	859653	1655516	species
## 1099318	Candidatus Pelagibacter sp. HIMB1321	1388755	198251	species
## 131414	Sphingobium	165695	41297	genus
## 48892	Campylobacteraceae	72294	213849	family
## 124275	Vigna radiata	157791	3913	species
## 13227	Gossypium raimondii	29730	3633	species
## 1929	Roseobacter	2433	31989	genus
## 14770	Nitrosopumilales	31932	651137	order
## 282896	Nitrosopumilaceae	338190	31932	family
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## 942	0.153420531			
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## 36888	0.058896748			
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## 1142005	0.006253884
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## 3639	0.005534685
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## 38748	0.004420362
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## 12048	0.004058154
## 1616664	0.003898152

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## 129662	0.003773391
## 1823174	0.003773391
## 1823177	0.003773391
## 615008	0.003682363
## 615011	0.003682363
## 3015	0.003464338
## 250565	0.003424529
## 22255	0.003378390
## 1702	0.003208212
## 187	0.003200099
## 211	0.003170896
## 187051	0.003167235
## 56588	0.003158796
## 150576	0.003136441
## 2981	0.003103686
## 755366	0.003103686
## 46253	0.003055389
## 3172	0.002985382
## 422	0.002968178
## 85788	0.002957673
## 66335	0.002936547
## 85784	0.002936547
## 194293	0.002936547
## 3457	0.002860277
## 3458	0.002860277
## 76005	0.002860277
## 76014	0.002860277
## 702345	0.002860277
## 1025557	0.002838350
## 1514	0.002820092
## 22256	0.002732465
## 150577	0.002730762
## 51905	0.002727829
## 104680	0.002727466
## 3016	0.002726521
## 358	0.002700627
## 90066	0.002691670
## 3343	0.002650088
## 29229	0.002650088
## 360093	0.002650088
## 150590	0.002573046
## 1446811	0.002540021
## 2767	0.002496957
## 2770	0.002496957
## 2771	0.002496957
## 22665	0.002496957
## 1165039	0.002496957
## 150598	0.002450190
## 280865	0.002412569
## 20086	0.002337784
## 2918	0.002331198
## 359	0.002321968

## 32390	0.002270205
## 14836	0.002249584
## 38415	0.002226066
## 22	0.002199627
## 674403	0.002193732
## 588253	0.002148913
## 914	0.002147986
## 1824628	0.002137061
## 1824629	0.002137061
## 3372	0.002103994
## 60250	0.002090733
## 3325	0.001996887
## 29353	0.001996887
## 360074	0.001996887
## 360082	0.001996887
## 283	0.001982107
## 45508	0.001978904
## 104679	0.001973515
## 3106	0.001962825
## 1165036	0.001962825
## 77200	0.001926942
## 60264	0.001920323
## 117021	0.001903160
## 3663	0.001901600
## 2927	0.001879242
## 3898	0.001853988
## 4014	0.001853716
## 12526	0.001852961
## 384478	0.001842582
## 288	0.001839986
## 587287	0.001818065
## 59838	0.001814395
## 88886	0.001814395
## 163094	0.001814395
## 1381	0.001799948
## 327	0.001797159
## 100097	0.001789172
## 1074	0.001730223
## 71047	0.001724716
## 163072	0.001717996
## 393	0.001716190
## 165851	0.001712554
## 1626	0.001699455
## 60251	0.001699455
## 2986	0.001690903
## 136645	0.001679943
## 819	0.001665289
## 53004	0.001614090
## 166579	0.001614090
## 3373	0.001575690
## 3374	0.001575690
## 3375	0.001575690
## 361490	0.001575690
## 60256	0.001542569
## 154451	0.001525678
## 48875	0.001515642

## 85	0.001515365
## 165852	0.001515365
## 868	0.001512814
## 11897	0.001507654
## 60249	0.001507654
## 896	0.001495913
## 3865	0.001494775
## 21578	0.001494775
## 31486	0.001494775
## 31487	0.001494775
## 134884	0.001494775
## 134891	0.001494775
## 134908	0.001494775
## 136571	0.001474898
## 3129	0.001436244
## 3131	0.001436244
## 129665	0.001436244
## 1823171	0.001436244
## 1823172	0.001436244
## 12212	0.001432255
## 15788	0.001415183
## 13062	0.001414379
## 33288	0.001411668
## 4680	0.001410198
## 548	0.001390229
## 104691	0.001390229
## 13226	0.001383619
## 3079	0.001374020
## 37628	0.001357546
## 1379335	0.001341095
## 1446829	0.001338132
## 14817	0.001337408
## 754509	0.001331653
## 39437	0.001331396
## 915	0.001330072
## 886	0.001325536
## 175148	0.001324073
## 1335443	0.001316368
## 115177	0.001314962
## 115178	0.001314962
## 358308	0.001298758
## 14795	0.001282597
## 60266	0.001275871
## 975	0.001250900
## 2931	0.001240400
## 47938	0.001240400
## 1616665	0.001226266
## 3300	0.001225214
## 10278	0.001225214
## 11175	0.001225214
## 134815	0.001225214
## 134834	0.001225214
## 1608226	0.001225214
## 1608227	0.001225214
## 3321	0.001217834
## 10498	0.001216907

1869404 0.001212329
531588 0.001206082
223017 0.001189713
25774 0.001187282
150451 0.001173278
4015 0.001168460
4016 0.001168460
115327 0.001168460
307 0.001165213
209106 0.001154702
3143 0.001146930
3145 0.001146930
3086 0.001146491
3087 0.001146491
129660 0.001146491
2821 0.001131116
2849 0.001131116
128004 0.001131116
1463833 0.001131116
1463835 0.001131116
305242 0.001129519
1507401 0.001127524
3176 0.001124486
4701 0.001123461
4702 0.001123461
1321768 0.001123461
56540 0.001117197
236174 0.001114821
1153 0.001111238
3843 0.001097747
3844 0.001097747
21579 0.001097747
49992 0.001097747
576395 0.001097747
786 0.001088732
804 0.001079616
187053 0.001078580
150 0.001078148
3080 0.001076433
3081 0.001076433
16 0.001071787
275 0.001069879
224 0.001069807
32661 0.001057498
223015 0.001057498
1533643 0.001054460
57583 0.001050297
136646 0.001046579
3107 0.001032758
48011 0.001032436
65253 0.001032436
660968 0.001026429
1099318 0.001022868
131414 0.001022280
48892 0.001021303
124275 0.001016212

```
## 13227 0.001015412
## 1929 0.001008921
## 14770 0.001002616
## 282896 0.001002616
```

First we note that Bellairs has many more taxa that have higher frequency at this site and which pass the threshold of 0.1% change (n= 350 vs 32). The major changes include large increases the the frequency of Proteobacteria (15%), more specifically Alphaproteobacteria (8%), Betaproteobacteria (2%), and Gammaproteobacteria (5%). To better identify the key taxa here, we repeated the analysis with a higher threshold.

```
bel.big <- tree[ which(trees$DeltaFreq > 0.01), ]; nrow(bel.big)
## [1] 45

bel.big <- bel.big[ order( bel.big$path, bel.big$DeltaFreq ), ]
bel.big[ , c(1:4,15 )]
```

##		name	tax_id	parent	rank
## 1446824		FCB group	1783270	2	no rank
## 45553	Bacteroidetes/Chlorobi group		68336	1783270	no rank
## 752	Bacteroidetes		976	68336	phylum
## 88883	Flavobacteriia		117743	976	class
## 163073	Flavobacteriales		200644	117743	order
## 29439	Flavobacteriaceae		49546	200644	family
## 942	Proteobacteria		1224	2	phylum
## 12016	Alphaproteobacteria		28211	1224	class
## 274	Rhizobiales		356	28211	order
## 166576	Rhodobacterales		204455	28211	order
## 14804	Rhodobacteraceae		31989	204455	family
## 12020	Betaproteobacteria		28216	1224	class
## 56568	Burkholderiales		80840	28216	order
## 949	Gammaproteobacteria		1236	1224	class
## 48874	Pseudomonadales		72274	1236	order
## 104687	Pseudomonadaceae		135621	72274	family
## 226	Pseudomonas		286	135621	genus
## 105784	Pseudomonas aeruginosa group		136841	286	species group
## 163583	Actinobacteria		201174	1783272	phylum
## 1380	Actinobacteria		1760	201174	class
## 952	Firmicutes		1239	1783272	phylum
## 65606	Bacilli		91061	1239	class
## 1073	Bacillales		1385	91061	order
## 2189	Eukaryota		2759	131567	superkingdom
## 15400	Viridiplantae		33090	2759	kingdom
## 17254	Streptophyta		35493	33090	phylum
## 100789	Streptophytina		131221	35493	subphylum
## 2531	Embryophyta		3193	131221	no rank
## 36888	Tracheophyta		58023	3193	no rank
## 54511	Euphyllophyta		78536	58023	no rank
## 36889	Spermatophyta		58024	78536	no rank
## 2706	Magnoliopsida		3398	58024	no rank
## 1142173	Mesangiospermae		1437183	3398	no rank
## 47939	eudicotyledons		71240	1437183	no rank
## 66320	Gunneridae		91827	71240	no rank
## 1142189	Pentapetalae		1437201	91827	no rank
## 47968	asterids		71274	1437201	no rank
## 66370	lamiids		91888	71274	no rank
## 47969	rosids		71275	1437201	no rank
## 66328	fabids		91835	71275	no rank

## 48652	Fabales	72025	91835	order
## 3064	Fabaceae	3803	72025	family
## 3075	Papilionoideae	3814	3803	subfamily
## 1823180	<NA>	2231393	3814	no rank
## 66329	malvids	91836	71275	no rank

##	DeltaFreq
## 1446824	0.03845551
## 45553	0.03823506
## 752	0.03793561
## 88883	0.02947783
## 163073	0.02947783
## 29439	0.02910455
## 942	0.15342053
## 12016	0.08310313
## 274	0.01911275
## 166576	0.04061342
## 14804	0.03986740
## 12020	0.01503751
## 56568	0.01222387
## 949	0.04921770
## 48874	0.01711618
## 104687	0.01441555
## 226	0.01427823
## 105784	0.01006039
## 163583	0.02387402
## 1380	0.02301755
## 952	0.01719985
## 65606	0.01340909
## 1073	0.01095890
## 2189	0.06910118
## 15400	0.05774058
## 17254	0.05967972
## 100789	0.05967972
## 2531	0.05967972
## 36888	0.05889675
## 54511	0.05889675
## 36889	0.05889675
## 2706	0.05889675
## 1142173	0.05889675
## 47939	0.05086511
## 66320	0.05086511
## 1142189	0.05086511
## 47968	0.01754127
## 66370	0.01296676
## 47969	0.03219272
## 66328	0.02110225
## 48652	0.01451827
## 3064	0.01451827
## 3075	0.01451827
## 1823180	0.01451827
## 66329	0.01033522

Wrt Bacteria, this highlights the Flavobacteriaceae (FCB group), Rhodobacteraceae (Betaproteo-), Pseudomonas aeruginosa (Gammaproteo-), and Bacillales (Terrabacteria). Wrt Eukaryota, this highlights Fabaceae and malvids; several trees of the Fabaceae family are growing on the shore where the sample at Bellairs was collected. It seems that many of the plants are higher at Bellairs. Is this due to closer proximity to shore plants? Check for the malvids

too.

2.2.1 Largest Archae Changes in Global Frequencies

Archae represent only 0.7% of the reads at Bellairs and 0.4% at Maycocks. Not surprisingly, we did not observe Archae in the global rankings due to their low frequency. Here we restrict our attention to this superkingdom to identify subtle changes in frequency between the sites. We ask which Archae taxa are most prevalent at either site.

```
arch <- induce_tree(2157) # tax_id of Archae
big.bel <- arch[ order(-arch$Glob.Freq.Bel), ]
big.may <- arch[ order(-arch$Glob.Freq.May), ]
big.diff <- arch[ order(-abs(arch$DeltaFreq)), ]
```

There is more Archae at Maycocks than Bellairs (0.003%) absolute change but only 18 Archae taxa are more frequent at Maycocks

```
may.big <- arch[ which(arch$DeltaFreq < -0.00), ] ; nrow(may.big) # 0.001 was too stringent
## [1] 22
```

```
may.big <- may.big[ order( may.big$path, may.big$DeltaFreq ), ]
may.big[ , c(1:4,15 )] #CHANGE
```

##		name	tax_id	parent	rank
##	1039701	Archaeoglobus sulfaticallidus	1316941	2233	species
##	92485	Haloterrigena thermotolerans	121872	121871	species
##	1675461	<NA>	2044521	253106	species
##	1559450	Methanobacterium sp. MZ-A1	1911685	2160	species
##	667073	Methanothermobacter sp. CaT2	866790	145260	species
##	113317	Methanothermobacter thermautotrophicus	145262	145260	species
##	1728	Methanocaldococcus jannaschii	2190	196118	species
##	23658	Methanococcus aeolicus	42879	2184	species
##	71352	Ferroplasma acidarmanus	97393	74968	species
##	26863	Picrophilaceae	46630	2301	family
##	26864	Picrophilus	46631	46630	genus
##	57546	Picrophilus torridus	82076	46631	species
##	258578	Thermococcus kodakarensis	311400	2263	species
##	33294	Thermococcus peptonophilus	53952	2263	species
##	33519	Ignicoccus	54258	2272	genus
##	126439	Ignicoccus hospitalis	160233	54258	species
##	33508	Hyperthermus	54247	2307	genus
##	33509	Hyperthermus butylicus	54248	54247	species
##	22588	Acidianus brierleyi	41673	12914	species
##	55451	Metallosphaera hakonensis	79601	41980	species
##	10576	Pyrobaculum aerophilum	13773	2276	species
##	148140	Thermoproteus uzoniensis	184117	2270	species
##		DeltaFreq			
##	1039701	-5.969006e-06			
##	92485	-1.669760e-06			
##	1675461	-1.225031e-06			
##	1559450	-6.580818e-06			
##	667073	-1.767981e-06			
##	113317	-5.205722e-06			
##	1728	-7.373800e-06			
##	23658	-2.866609e-07			
##	71352	-1.055412e-06			
##	26863	-2.268720e-07			


```

## 1446830      no rank 1.259125e-06
## 1461129      phylum 1.259125e-06
## 2044869      genus 1.259125e-06
## 1566992      species 1.259125e-06
## 1824         species 1.208746e-06
## 20834        -2.268720e-07 1.165975e-06
## 1743386      -2.268720e-07 1.118132e-06
## 215378       -5.012290e-07 9.930876e-07
## 1521469      -5.994702e-07 9.735339e-07
## 31498        -1.164806e-06 9.242258e-07
## 126439       -1.762187e-06 9.242258e-07
## 436437       -5.465899e-07 9.242258e-07
## 93939        -5.465899e-07 8.075212e-07
## 12888        -1.039729e-06 7.647502e-07
## 88580        -1.207281e-06 5.976671e-07
## 10976        -6.029900e-07 5.755777e-07
## 145140       -3.602588e-07 5.179293e-07
## 33515        species 5.179293e-07
This highlights Thermococcus, Methanothermobacter, Methanocaldococcus, and others with very small differences.
## 1788        species 3.725982e-07
The Archae with highest change in frequency towards Bellairs are as follows.
## 1792        species 3.374346e-07

```

Here 405 taxa are more frequent at Bellairs. The major changes in frequency are within the TACK group and the Euryarchaeota.

2.2.2 Largest Viral Changes in Global Frequencies

Here we restrict our attention to Viruses to identify subtle changes in frequency between the sites. We ask which Viruses taxa are most prevalent at either site.

```

virus <- induce_tree(10239) # tax_id of Virus
(big.bel <- virus[ order(-virus$Glob.Freq.Bel), c(1:4,15 ) ] )

##              name tax_id
## 8295          Viruses 10239
## 12521      Caudovirales 28883
## 8614        Myoviridae 10662
## 159561 unclassified Myoviridae 196896
## 1236470 Prochlorococcus phage P-TIM68 1542477
## 8671        Podoviridae 10744
## 462518 Autographivirinae 542835
## 879134 unclassified Autographivirinae 1132574
## 379167 Synechococcus phage S-SSM7 445686
## 223779 Prochlorococcus phage P-SSM4 268747
## 379172 Prochlorococcus phage P-HM1 445700
## 687482 Prochlorococcus phage MED4-213 889956
## 223778 Prochlorococcus phage P-SSM2 268746
## 379171 Prochlorococcus phage P-HM2 445696
## 322098 Prochlorococcus phage P-GSP1 382262
## 1009728 Pelagibacter phage HTVC008M 1283076
## 457445 Prochlorococcus phage P-SSM3 536453
## 378414 Prochlorococcus phage P-RSM4 444862
## 378412 Synechococcus phage S-SM2 444860
## 159560 unclassified Podoviridae 196895
## 603221 Synechococcus phage S-SKS1 754042
## 8639      Siphoviridae 10699
## 8501      Phycodnaviridae 10501
## 719290 Cyanophage P-RSM6 929832
## 1559892 Lubbockvirus 1912144
## 1559894 unclassified Lubbockvirus 1912146
## 1118976 Clostridium phage CDMH1 1411095
## 1009729 Pelagibacter phage HTVC010P 1283077

```

## 159559	unclassified Siphoviridae	196894
## 379168	Prochlorococcus phage P-SSM7	445688
## 1276788	Cyanophage P-TIM40	1589733
## 223780	Prochlorococcus virus PSSP7	268748
## 1192468	Synechococcus phage ACG-2014j	1493514
## 1534232	Synechococcus phage S-CAM9	1883369
## 836422	Synechococcus phage metaG-MbCM1	1079999
## 378416	Cyanophage P-SSP2	444876
## 387538	unclassified Phycodnaviridae	455363
## 322108	Prochlorococcus phage P-SSP3	382273
## 468533	Mimiviridae	549779
## 457458	Synechococcus phage S-SSM4	536466
## 1798558	<NA>	2204151
## 31012	unclassified dsDNA viruses	51368
## 735496	Puniceispirillum phage HMO-2011	948071
## 1687017	<NA>	2060084
## 8296	Poxviridae	10240
## 687480	Cyanophage MED4-117	889954
## 262244	Mimivirus	315393
## 387539	Chrysochromulina ericina virus	455364
## 457436	Cyanophage P-RSM1	536444
## 687481	Prochlorococcus phage MED4-184	889955
## 2053675	<NA>	2501774
## 1534230	Synechococcus phage S-CAM4	1883367
## 197065	Synechococcus phage S-PM2	238854
## 473450	Synechococcus phage S-RSM4	555387
## 836421	Synechococcus phage ACG-2014c	1079998
## 379166	Synechococcus phage S-SSM5	445685
## 1060842	Synechococcus phage ACG-2014h	1340810
## 1534231	Synechococcus phage S-CAM7	1883368
## 1192467	Synechococcus phage ACG-2014i	1493513
## 1534229	Synechococcus phage S-CAM3	1883366
## 145322	Prasinovirus	181084
## 379165	Synechococcus phage Syn19	445684
## 378417	Prochlorococcus phage Syn33	444878
## 8463	Baculoviridae	10442
## 8338	Entomopoxvirinae	10284
## 1192465	Synechococcus phage ACG-2014f	1493511
## 475679	Alphabaculovirus	558016
## 678635	unclassified Prasinovirus	880158
## 378413	Prochlorococcus phage Syn1	444861
## 457466	Cyanophage Syn30	536474
## 1005392	Cyanophage S-RIM32	1278479
## 603216	Synechococcus phage S-CAM1	754037
## 8297	Chordopoxvirinae	10241
## 379164	Synechococcus phage S-ShM2	445683
## 1534228	Synechococcus phage S-CAM22	1883365
## 1473409	Synechococcus phage S-WAM1	1815521
## 934114	Tevenvirinae	1198136
## 322189	Synechococcus phage syn9	382359
## 1473410	Synechococcus phage S-WAM2	1815522
## 467626	Herpesvirales	548681
## 1192464	Synechococcus phage ACG-2014e	1493510
## 1192463	Synechococcus phage ACG-2014d	1493509
## 145324	Prymnesiovirus	181086
## 300575	unclassified Prymnesiovirus	358403

## 208529	Phaeocystis globosa virus	251749
## 603217	Synechococcus phage S-CAM8	754038
## 1192466	Synechococcus phage ACG-2014g	1493512
## 848500	Megavirus chiliensis	1094892
## 997642	Acanthamoeba polyphaga moumouvirus	1269028
## 379170	Cyanophage NATL1A-7	445693
## 678638	Micromonas sp. RCC1109 virus MpV1	880161
## 8343	Herpesviridae	10292
## 790044	Synechococcus phage S-CRM01	1026955
## 1068364	Pandoravirus salinus	1349410
## 8339	Betaentomopoxvirus	10286
## 669494	Synechococcus phage S-RIM2 R1_1999	869662
## 603218	Synechococcus phage S-IOM18	754039
## 379169	Cyanophage NATL2A-133	445692
## 683915	Prochlorococcus phage P-SSP10	885867
## 378411	Synechococcus phage S-SM1	444859
## 1192462	Synechococcus phage ACG-2014b	1493508
## 2104542	<NA>	2560128
## 1657371	<NA>	2023057
## 603220	Synechococcus phage S-RIP1	754041
## 563395	Cyanophage S-RIM50	687803
## 1210391	Cafeteriavirus	1513234
## 1210392	Cafeteria roenbergensis virus	1513235
## 1060844	Synechococcus phage S-MbCM100	1340812
## 1009730	Pelagibacter phage HTVC011P	1283078
## 1068363	Pandoravirus dulcis	1349409
## 9825	unclassified viruses	12429
## 1209012	Nudiviridae	1511852
## 378415	Cyanophage 9515-10a	444875
## 173522	Acanthamoeba polyphaga mimivirus	212035
## 2104539	<NA>	2560124
## 2104744	<NA>	2560427
## 603237	Synechococcus phage S-CBP4	754059
## 1176678	Aureococcus anophagefferens virus	1474867
## 669544	Synechococcus phage S-RIM8 A.HR1	869724
## 1726857	<NA>	2107709
## 145321	Chlorovirus	181083
## 8393	Betaherpesvirinae	10357
## 1542319	unclassified Teenvirinae	1892568
## 21152	unclassified Poxviridae	40069
## 2104158	<NA>	2559587
## 940040	Clostridium phage phiMMP04	1204535
## 1291601	Pandoravirus inopinatum	1605721
## 875414	Mimivirus terra2	1128151
## 8489	Iridoviridae	10486
## 861174	unclassified Nudiviridae	1110703
## 8485	Polydnviridae	10482
## 2105025	<NA>	2560849
## 1561548	Dhakavirus	1914165
## 1561571	Escherichia virus VR5	1914195
## 8316	Avipoxvirus	10260
## 8344	Alphaherpesvirinae	10293
## 1726856	<NA>	2107708
## 2120242	<NA>	2585030
## 1568411	unclassified RNA viruses ShiM-2016	1922348
## 839518	Bacillus virus G	1084719

## 153940	Clostridium phage phi3626	190478
## 1726855	<NA>	2107707
## 21153	unclassified Chordopoxvirinae	40070
## 44717	BeAn 58058 virus	67082
## 58589	Melanoplus sanguinipes entomopoxvirus	83191
## 1505477	Catopsilia pomona nucleopolyhedrovirus	1850906
## 1653197	<NA>	2017757
## 8488	Bracovirus	10485
## 605035	Synechococcus phage S-CBP3	756276
## 604342	Micromonas pusilla virus 12T	755272
## 1578174	Pacmanvirus A23	1932881
## 2106561	<NA>	2562654
## 8368	Varicellovirus	10319
## 1631196	<NA>	1993630
## 1642509	<NA>	2005509
## 918102	Mythimna separata entomopoxvirus	1179664
## 1307641	Timquatrovirus	1623306
## 2106591	<NA>	2562717
## 1186356	Mycobacterium phage OkiRoe	1486473
## 30959	Helicoverpa armigera nucleopolyhedrovirus	51313
## 883569	Cyanophage S-TIM5	1137745
## 1051112	Eptesipox virus	1329402
## 1354297	Mollivirus sibericum	1678078
## 1559687	Vequintavirinae	1911928
## 2104607	<NA>	2560207
## 2104663	<NA>	2560286
## 1565537	Cbastvirus	1918718
## 1565538	Cellulophaga virus ST	1918720
## 8493	Chloriridovirus	10491
## 2104968	<NA>	2560751
## 1009731	Pelagibacter phage HTVC019P	1283079
## 40455	Alphaentomopoxvirus	62098
## 40456	Anomala cuprea entomopoxvirus	62099
## 26327	Paramecium bursaria Chlorella virus NY2A	46021
## 169792	Agrotis ipsilon multiple nucleopolyhedrovirus	208013
## 1075906	Caulobacter phage Cr30	1357714
## 510604	Cyanophage SS120-1	616674
## 1620894	<NA>	1982587
## 1853472	<NA>	2269062
## 1525883	Pseudoalteromonas phage PH1	1874540
## 8430	Tupaiid betaherpesvirus 1	10397
## 281375	unclassified Avipoxvirus	336487
## 529863	Penguinpox virus	648998
## 20606	Cotia virus	39444
## 934115	Schizotequatrovirus	1198137
## 1561419	Vibrio virus ValKK3	1914021
## 1452629	Pectobacterium phage CBB	1792242
## 1616799	<NA>	1978007
## 1049926	Cellulophaga phage phi14:2	1327990
## 314601	Micromonas pusilla virus SP1	373996
## 12080	Amsacta moorei entomopoxvirus	28321
## 1631197	<NA>	1993631
## 732438	Marseilleviridae	944644
## 852827	Apis mellifera filamentous virus	1100043
## 1659386	<NA>	2025358
## 1659387	<NA>	2025359

## 18001	Chelonus inanitus bracovirus	36344
## 487253	Raphidovirus	573012
## 71182	Heterosigma akashiwo virus 01	97195
## 1562148	Certrevirus	1914850
## 1619492	<NA>	1980961
## 2111825	<NA>	2570372
## 289623	Invertebrate iridescent virus 30	345585
## 135457	Canid alphaherpesvirus 1	170325
## 1239831	Tipula oleracea nudivirus	1546257
## 1209014	Betanudivirus	1511854
## 12831	Heliothis zea nudivirus	29250
## 159600	Nimaviridae	196937
## 206416	Whispovirus	249585
## 286729	White spot syndrome virus	342409
## 1657483	<NA>	2023203
## 8340	Choristoneura biennis entomopoxvirus	10288
## 722846	Bathycoccus sp. RCC1105 virus BpV	933845
## 1032431	Bacillus phage vB_BanS-Tsamsa	1308863
## 1049877	Cronobacter phage S13	1327935
## 8387	Suid alphaherpesvirus 1	10345
## 8410	Gammaherpesvirinae	10374
## 467632	Percavirus	548688
## 8407	Equid gammaherpesvirus 5	10371
## 55087	unclassified dsDNA phages	79205
## 1101730	Phormidium phage MIS-PhV1A	1391455
## 2050489	<NA>	2497569
## 1569421	Sanxia atyid shrimp virus 4	1923358
## 8467	Spodoptera exigua multiple nucleopolyhedrovirus	10454
## 1268625	Agrotis segetum nucleopolyhedrovirus B	1580580
## 470846	Leptopilina boulardi filamentous virus	552509
## 1620398	<NA>	1982076
## 1620399	<NA>	1982077
## 2104491	<NA>	2560065
## 2104503	<NA>	2560081
## 1511766	Twortvirus	1857846
## 34655	Staphylococcus virus Twort	55510
## 759776	unclassified Mimiviridae	985780
## 1274170	Yellowstone lake mimivirus	1586712
## 198509	Squirrelpox virus	240426
## 1319463	Proteus phage vB_PmiM_Pm5461	1636250
## 1366668	Brevibacillus phage Sundance	1691958
## 372872	Synechococcus virus Syn5	438482
## 1777711	<NA>	2169643
## 1778050	<NA>	2170215
## 467627	Alloherpesviridae	548682
## 567489	Cyprinivirus	692606
## 117557	Anguillid herpesvirus 1	150286
## 8336	Yatapoxvirus	10282
## 72700	Tanapox virus	99000
## 833061	Yokapox virus	1076255
## 1653196	<NA>	2017756
## 8496	Lymphocystivirus	10494
## 289723	unclassified Lymphocystivirus	345690
## 212992	Lymphocystis disease virus - isolate China	256729
## 290573	Coccolithovirus	346673
## 145320	Emiliana huxleyi virus 86	181082

## 1135710	Pectobacterium bacteriophage PM2	1429794
## 1621160	<NA>	1982876
## 1891377	<NA>	2315863
## 1166129	Mycobacterium phage Jolie1	1463812
## 8345	Simplexvirus	10294
## 8367	Cercopithecine alphaherpesvirus 2	10317
## 8394	Cytomegalovirus	10358
## 30050	Aotinae betaherpesvirus 1	50290
## 1210612	Marseillevirus	1513458
## 1471788	unclassified Marseillevirus	1813598
## 1483257	Tokyo virus A1	1826170
## 1568567	Beihai partiti-like virus 2	1922504
## 8317	Fowlpox virus	10261
## 678186	Aeromonas phage phiAS5	879630
## 1684541	<NA>	2057187
## 1569287	Hubei sobemo-like virus 37	1923224
## 487295	Cervidpoxvirus	573055
## 252296	Mule deerpox virus	304399
## 38098	Ectropis obliqua nucleopolyhedrovirus	59376
## 254981	Euproctis pseudoconsersa nucleopolyhedrovirus	307467
## 475680	Betabaculovirus	558017
## 304688	Artogeia rapae granulovirus	362830
## 8486	Ichnovirus	10483
## 8487	Campoletis sonorensis ichnovirus	10484
## 289264	Invertebrate iridescent virus 9	345195
## 2059065	<NA>	2508196
## 1390286	Klebsiella phage vB_KpnM_KB57	1719140
## 9782	Clostridium phage c-st	12336
## 1464651	Mycobacterium phage Bipper	1805457
## 1697067	<NA>	2072209
## 8329	Suipoxvirus	10275
## 8330	Swinepox virus	10276
## 268250	Acanthocystis turfacea chlorella virus 1	322019
## 321766	Paramecium bursaria Chlorella virus A1	381899
## 808604	Acinetobacter phage ZZ1	1049283
## 886589	Cronobacter phage vB_CsaM_GAP32	1141136
## 24661	Canarypox virus	44088
## 1703764	<NA>	2083300
## 290574	unclassified Chlorovirus	346674
## 1564246	Only Syngen Nebraska virus 5	1917232
## 145323	Phaeovirus	181085
## 191389	Feldmannia irregularis virus a	231992
## 216062	Aeromonas virus 65	260149
## 1307624	Liefievirus	1623288
## 1796197	<NA>	2201169
## 1328941	Mycobacterium phage Cambiare	1647305
## 1001296	Synechococcus phage S-CBP1	1273711
## 8401	Muromegalovirus	10365
## 990782	Murid betaherpesvirus 8	1261657
## 21332	Roseolovirus	40272
## 366040	unclassified Roseolovirus	431037
## 1584736	Murine roseolovirus	1940555
## 1356888	Salmon gill poxvirus	1680908
## 8468	Spodoptera frugiperda multiple nucleopolyhedrovirus	10455
## 75165	Thysanoplusia orichalcea nucleopolyhedrovirus	101850
## 1325021	Lambdina fiscellaria nucleopolyhedrovirus	1642929

## 20791	Cotesia congregata bracovirus	39640
## 8490	Iridovirus	10487
## 141287	Invertebrate iridescent virus 6	176652
## 8502	Paramecium bursaria Chlorella virus 1	10506
## 276618	Yersinia phage phiR1-37	331278
## 487396	Vibrio phage henriette 12B8	573174
## 1307615	Bronvirus	1623278
## 1796195	<NA>	2201166
## 1060858	Mycobacterium phage Whirlwind	1340826
## 1564965	Helsingorvirus	1918017
## 1565138	Cellulophaga virus Cba121	1918193
## 1012076	Hytrosaviridae	1285590
## 1012077	Glossinavirus	1285591
## 1012079	Glossina hytivirus	1285594
## 1334588	Kallithea virus	1654582
## 1464816	Pithovirus	1805626
## 1153837	Pithovirus sibericum	1450746
## 1552147	Cedratvirus A11	1903266
## 595989	unclassified Alphabaculovirus	745176
## 254975	Apocheima cinerarium nucleopolyhedrovirus	307461
## 8504	Adenoviridae	10508
## 8529	Aviadenovirus	10552
## 891963	Turkey aviadenovirus B	1146875
## 8691	Parvoviridae	10780
## 21198	Densovirinae	40120
## 149765	unclassified Densovirinae	185880
## 1556008	Parus major densovirus	1907771
## 466034	Mycobacterium phage Myrna	546805
## 940032	Streptomyces phage SV1	1204525
## 1261902	Geobacillus virus E3	1572712
## 105097	Roseobacter virus SI01	136084
## 467633	Proboscivirus	548689
## 467778	unclassified Proboscivirus	548912
## 467780	Elephant endotheliotropic herpesvirus 4	548914
## 986221	Tunisvirus	1255301
## 1209013	Alphanudivirus	1511853
## 367413	Gryllus bimaculatus nudivirus	432587
## 395652	Picornavirales	464095
## 9528	Picornaviridae	12058
## 1051673	Megrivirus	1330069
## 1051674	Melegrivirus A	1330070
## 2050490	<NA>	2497570
## 2050494	<NA>	2497574
## 8995	Mononegavirales	11157
## 526001	unassigned Mononegavirales	644608
## 1535263	Chengtivirus	1884457
## 1672183	<NA>	2040575
## 2050491	<NA>	2497571
## 2050496	<NA>	2497576
## 1618997	<NA>	1980410
## 1619001	<NA>	1980416
## 20860	unclassified Peribunyaviridae	39718
## 1293694	Huangpi Tick Virus 1	1608047
## 8298	Orthopoxvirus	10242
## 126933	Skunkpox virus	160796
## 8313	Parapoxvirus	10257

## 99426	Bovine papular stomatitis virus	129727
## 99427	Parapoxvirus of red deer in New Zealand	129728
## 279547	unclassified Parapoxvirus	334521
## 151622	Seal parapoxvirus	187984
## 8319	Pigeonpox virus	10264
## 281374	Turkeypox virus	336486
## 1686392	<NA>	2059380
## 8320	Capripoxvirus	10265
## 8321	Sheeppox virus	10266
## 8332	Molluscipoxvirus	10278
## 8333	Molluscum contagiosum virus	10279
## 20073	Yaba monkey tumor virus	38804
## 1123954	Sea otter poxvirus	1416741
## 1659388	<NA>	2025360
## 17108	unclassified Baculoviridae	35255
## 1352395	Urbanus proteus nucleopolyhedrovirus	1675866
## 8464	Lymantria dispar multiple nucleopolyhedrovirus	10449
## 8469	Spodoptera littoralis nucleopolyhedrovirus	10456
## 26528	Spodoptera litura nucleopolyhedrovirus	46242
## 36955	Choristoneura rosaceana nucleopolyhedrovirus	58094
## 50678	Buzura suppressaria nucleopolyhedrovirus	74320
## 127585	Antheraea pernyi nucleopolyhedrovirus	161494
## 381133	Mythimna unipuncta nucleopolyhedrovirus	447897
## 482324	Spodoptera litura nucleopolyhedrovirus II	566270
## 1066190	Peridroma alphabaculovirus	1346829
## 806265	Operophtera brumata nucleopolyhedrovirus	1046267
## 1031545	Leucania separata nucleopolyhedrovirus	1307956
## 1031546	Clanis bilineata nucleopolyhedrovirus	1307957
## 2104823	<NA>	2560521
## 17107	Cryptophlebia leucotreta granulovirus	35254
## 35970	Choristoneura fumiferana granulovirus	56947
## 1418509	Cnaphalocrocis medinalis granulovirus	1750712
## 1624313	<NA>	1986290
## 475682	Deltabaculovirus	558019
## 100193	Culex nigripalpus nucleopolyhedrovirus	130556
## 87958	Glyptapanteles indiensis bracovirus	116759
## 18013	Lymphocystis disease virus 1	36363
## 289268	Invertebrate iridescent virus 31	345199
## 289269	Invertebrate iridescent virus 3	345201
## 1025553	Invertebrate iridovirus 22	1301279
## 1025554	Invertebrate iridovirus 25	1301280
## 1167956	Anopheles minimus irodoovirus	1465751
## 1274171	Yellowstone lake phycodnavirus 1	1586713
## 1274173	Yellowstone lake phycodnavirus 3	1586715
## 1341546	Ostreococcus lucimarinus virus 2	1663208
## 1700527	<NA>	2079134
## 153554	Fowl aviadenovirus B	190062
## 74367	Atadenovirus	100953
## 99974	Duck atadenovirus A	130328
## 21197	Parvovirinae	40119
## 1204975	Bocaparvovirus	1507401
## 1204976	unclassified Bocaparvovirus	1507402
## 1653158	<NA>	2017714
## 573007	Thermus phage TMA	699370
## 1056379	Pseudomonas phage PaBG	1335230
## 1257002	Clostridium phage phiCT9441A	1567014

## 1473399	Bacillus phage AR9	1815509
## 187209	Aeromonas virus Aeh1	227470
## 1561418	Vibrio virus nt1	1914020
## 608459	Acinetobacter phage Acj61	760732
## 610186	Acinetobacter phage Ac42	762660
## 1181619	Serratia phage PS2	1481112
## 1506818	Morganella phage vB_MmoM_MP1	1852628
## 1623441	<NA>	1985325
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## 1852515	<NA>	2267885
## 1506815	Klebsiella phage vB_KpnM_KpV477	1852625
## 1319822	Eucampyvirinae	1636616
## 1319823	Firehammervirus	1636617
## 589962	Campylobacter virus CP220	722417
## 776286	Campylobacter virus IBB35	1006972
## 927148	Campylobacter virus CP21	1190451
## 1567806	Tegunavirus	1921704
## 1567808	Yersinia virus TG1	1921706
## 2104505	<NA>	2560086
## 2104837	<NA>	2560541
## 2106563	<NA>	2562656
## 892153	Enterobacteria phage vB_KleM-RaK2	1147094
## 2104511	<NA>	2560094
## 2104753	<NA>	2560436
## 2106453	<NA>	2562455
## 1001320	Escherichia phage PBECO 4	1273738
## 2104582	<NA>	2560175
## 2104654	<NA>	2560269
## 150549	Fromanvirus	186764
## 1631426	<NA>	1993867
## 164152	Lactococcus phage 4268	201847
## 602301	Synechococcus phage S-CBS2	753084
## 687479	Cyanophage KBS-S-2A	889953
## 755586	Tsukamurella phage TPA2	981330
## 1049906	Cellulophaga phage phi19:1	1327970
## 1049929	Cellulophaga phage phi39:1	1327993
## 1329103	Gordonia phage GTE8	1647475
## 1478927	Gordonia phage Lucky10	1821557
## 1024120	Yuavirus	1299429
## 394297	Pseudomonas virus Yua	462590
## 1161538	Mycobacterium phage Jolie2	1458831
## 1307631	Phicbkvirus	1623296
## 946343	Caulobacter virus Rogue	1211643
## 1307640	Skunavirus	1623305
## 175086	Lactococcus virus 712	213769
## 1558941	Tunavirinae	1910999
## 2104557	<NA>	2560145
## 2104978	<NA>	2560762
## 1567316	Nonanavirus	1921122
## 1567317	Salmonella virus 9NA	1921123
## 1568322	Sextaecvirus	1922243
## 1568324	Staphylococcus virus SEP9	1922247
## 1620406	<NA>	1982084
## 1620474	<NA>	1982152
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## 1620673	<NA>	1982359

## 1620674	<NA>	1982360
## 1621181	<NA>	1982898
## 1621396	<NA>	1983119
## 603231	Pseudoalteromonas phage pYD6-A	754052
## 1049919	Cellulophaga phage phi18:3	1327983
## 1891373	<NA>	2315857
## 946129	uncultured crAssphage	1211417
## 327719	Lactococcus virus KSY1	388452
## 118711	Synechococcus virus P60	151528
## 2104606	<NA>	2560206
## 2104923	<NA>	2560679
## 462519	Picovirinae	542836
## 150613	Salasvirus	186846
## 2106555	<NA>	2562647
## 1525397	Bacillus phage Stitch	1874002
## 1391394	Hollowayvirus	1720324
## 231656	Pseudomonas virus F116	280701
## 517730	Lactobacillus virus Lb338-1	632112
## 2104497	<NA>	2560073
## 1511764	Pecentumvirus	1857844
## 2104844	<NA>	2560553
## 24302	Ascoviridae	43682
## 24300	Ascovirus	43680
## 274188	unclassified Ascovirus	328613
## 274190	Trichoplusia ni ascovirus 2c	328615
## 358969	Bicaudaviridae	423358
## 871974	unclassified Bicaudaviridae	1123963
## 1456800	Acidianus tailed spindle virus	1797140
## 8391	Saimiriine alphaherpesvirus 1	10353
## 17098	Ateline alphaherpesvirus 1	35243
## 286730	unclassified Simplexvirus	342410
## 1063491	Fruit bat alphaherpesvirus 1	1343901
## 8369	Bovine alphaherpesvirus 1	10320
## 144554	Mardivirus	180252
## 67736	Columbid alphaherpesvirus 1	93386
## 8395	Human betaherpesvirus 5	10359
## 30052	Cercopithecine betaherpesvirus 5	50292
## 8402	Murid betaherpesvirus 1	10366
## 12073	Murid betaherpesvirus 2	28304
## 15846	Caviid betaherpesvirus 2	33706
## 113996	Elephantid betaherpesvirus 1	146015
## 137588	Ictalurivirus	172653
## 8432	Ictalurid herpesvirus 1	10401
## 144533	Cyprinid herpesvirus 3	180230
## 264505	Cyprinid herpesvirus 2	317878
## 467629	Malacoherpesviridae	548685
## 467630	Ostreavirus	548686
## 217565	Ostreid herpesvirus 1	261939
## 770280	Lausannevirus	999883
## 1391586	Golden Marseillevirus	1720526
## 1599198	<NA>	1955558
## 1160937	Alphasatellitidae	1458186
## 233846	Geminialphasatellitinae	283494
## 1777687	<NA>	2169619
## 1777828	<NA>	2169841
## 1209017	Ligamenvirales	1511857

## 124367		Rudiviridae	157897
## 150951		Rudivirus	187213
## 294413		unclassified Rudivirus	351054
## 1621720		<NA>	1983551
## 1751669		<NA>	2136008
## 98528		Haloviruses	128706
## 1001327		Halovirus HCTV-1	1273746
## 1001335		Halovirus HRTV-7	1273754
## 8774		Reoviridae	10880
## 18075		unclassified Reoviridae	36446
## 1322731	Grapevine Cabernet Sauvignon reovirus		1640277
## 565043		Spinareovirinae	689831
## 8841		Aquareovirus	10979
## 149679		Aquareovirus C	185782
## 8870		Partitiviridae	11012
## 1208970		Alphapartitivirus	1511808
## 234891	Cherry chlorotic rusty spot associated	partitivirus	284688
## 8898		Flaviviridae	11050
## 8938		Pestivirus	11095
## 1777967		<NA>	2170084
## 551883		Secoviridae	675072
## 551886		Comovirinae	675075
## 9721		Nepovirus	12270
## 9729		Tomato ringspot virus	12280
## 572890		Iflaviridae	699189
## 862140		unclassified Iflaviridae	1111709
## 1313349	Graminella nigrifrons virus 1		1629132
## 9215		Arenaviridae	11617
## 1333656		Mammarenavirus	1653394
## 170630		Cupixi mammarenavirus	208899
## 1618999		<NA>	1980413
## 2104498		<NA>	2560074
## 2053375		<NA>	2501368
## 2053377		<NA>	2501370
## 1619003		<NA>	1980418
## 2059713		<NA>	2509283
## 2059714		<NA>	2509284
## 2104568		<NA>	2560157
## 2104833		<NA>	2560537
## 1569223		Hubei picorna-like virus 76	1923160
##	parent	rank	DeltaFreq
## 8295	1	superkingdom	-8.112324e-03
## 12521	10239	order	-8.049537e-03
## 8614	28883	family	-8.996657e-03
## 159561	10662	no rank	-9.238802e-03
## 1236470	196896	species	-2.747998e-04
## 8671	28883	family	8.009692e-04
## 462518	10744	subfamily	5.754744e-04
## 879134	542835	no rank	5.197064e-04
## 379167	196896	species	-1.718189e-03
## 223779	196896	species	-8.455055e-04
## 379172	196896	species	-1.080761e-03
## 687482	196896	species	-1.042721e-03
## 223778	196896	species	-5.346773e-04
## 379171	196896	species	-8.511970e-04
## 322098	1132574	species	3.038549e-04

##	1009728	196896	species	1.406301e-04
##	457445	196896	species	-3.460316e-04
##	378414	196896	species	-2.786889e-04
##	378412	196896	species	-1.144479e-04
##	159560	10744	no rank	2.775774e-04
##	603221	196896	species	-2.625666e-04
##	8639	28883	family	1.487937e-04
##	8501	10239	family	-4.564866e-05
##	719290	196896	species	-1.854736e-04
##	1559892	10662	genus	2.510449e-04
##	1559894	1912144	no rank	2.510449e-04
##	1118976	1912146	species	2.510449e-04
##	1009729	196895	species	1.895863e-04
##	159559	10699	no rank	1.544434e-04
##	379168	196896	species	-1.816767e-04
##	1276788	196896	species	-1.935763e-04
##	223780	542835	species	5.697025e-05
##	1192468	196896	species	2.441881e-05
##	1534232	196896	species	-8.293692e-05
##	836422	196896	species	-1.033282e-04
##	378416	1132574	species	7.612445e-05
##	387538	10501	no rank	-3.827458e-05
##	322108	1132574	species	4.547871e-05
##	468533	10239	family	1.510409e-05
##	457458	196896	species	-1.174920e-04
##	1798558	10239	no rank	4.607100e-06
##	31012	2204151	no rank	3.993485e-06
##	735496	196895	species	9.242370e-05
##	1687017	51368	genus	-3.079600e-07
##	8296	10239	family	4.032255e-06
##	687480	196894	species	9.314241e-05
##	262244	549779	genus	1.756756e-05
##	387539	455363	species	-4.831348e-05
##	457436	196896	species	-7.320621e-05
##	687481	196894	species	7.298131e-05
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##	197065	196896	species	-3.065870e-05
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##	379166	196896	species	-4.782024e-05
##	1060842	196896	species	-9.886081e-05
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##	475679	10442	genus	-5.286135e-06
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##	457466	196896	species	-1.296333e-05
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##	603216	196896	species	-2.826735e-05
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##	379164	196896	species	-1.692988e-05
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##	1473409	196896	species	-1.885734e-05
##	934114	10662	subfamily	4.947696e-07
##	322189	196896	species	-8.066419e-06
##	1473410	196896	species	-7.189169e-05
##	467626	10239	order	-2.081669e-05
##	1192464	196896	species	-7.411635e-05
##	1192463	196896	species	-1.835862e-05
##	145324	10501	genus	-1.596688e-05
##	300575	181086	no rank	-1.596688e-05
##	208529	358403	species	-1.596688e-05
##	603217	196896	species	-1.744020e-05
##	1192466	196896	species	-1.793131e-05
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##	997642	2501774	species	7.279637e-06
##	379170	1132574	species	1.381261e-05
##	678638	880158	species	1.251979e-05
##	8343	548681	family	-1.617674e-05
##	790044	196896	species	-5.895411e-06
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##	379169	1132574	species	3.899882e-06
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##	1192462	196896	species	-1.120769e-05
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##	1657371	455363	species	7.079927e-06
##	603220	1132574	species	1.304459e-05
##	563395	196896	species	-5.272385e-06
##	1210391	549779	genus	-5.073909e-07
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##	1060844	196896	species	-1.849528e-05
##	1009730	1132574	species	1.381949e-05
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##	378415	1132574	species	9.800027e-06
##	173522	315393	species	5.772959e-06
##	2104539	10699	genus	9.489416e-06
##	2104744	2560124	species	9.489416e-06
##	603237	1132574	species	8.900089e-06
##	1176678	455363	species	2.958976e-06
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##	1726857	2060084	species	2.173207e-06
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##	1542319	1198136	no rank	-4.192685e-06
##	21152	10240	no rank	2.077522e-06
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##	940040	196896	species	1.614163e-05
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## 1561548	1198136	genus	4.689258e-06
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## 8316	10241	genus	-2.377479e-07
## 8344	10292	subfamily	-1.222073e-05
## 1726856	2060084	species	-9.252961e-07
## 2120242	2559587	no rank	5.527942e-06
## 1568411	2585030	no rank	5.527942e-06
## 839518	10662	species	4.529782e-06
## 153940	196894	species	9.342619e-06
## 1726855	2060084	species	9.778728e-07
## 21153	10241	no rank	4.301445e-06
## 44717	40070	species	5.578320e-06
## 58589	10284	species	3.908560e-06
## 1505477	558016	species	7.654829e-07
## 1653197	10486	subfamily	-9.253076e-06
## 8488	10482	genus	6.513142e-07
## 605035	1132574	species	5.660594e-06
## 604342	880158	species	1.192798e-06
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## 2106561	2560128	no rank	2.551947e-06
## 8368	10293	genus	2.928604e-07
## 1631196	10286	species	5.089750e-06
## 1642509	10241	genus	4.574077e-07
## 918102	10286	species	-1.212352e-06
## 1307641	10699	genus	5.745403e-06
## 2106591	1623306	no rank	5.745403e-06
## 1186356	2562717	species	5.745403e-06
## 30959	558016	species	6.220561e-06
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## 1051112	40069	species	-6.708678e-07
## 1354297	12429	species	5.077861e-07
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## 2104607	10662	genus	-8.154086e-08
## 2104663	2560207	species	-8.154086e-08
## 1565537	10699	genus	4.043748e-06
## 1565538	1918718	species	4.043748e-06
## 8493	2017757	genus	-6.776528e-06
## 2104968	2560128	species	2.554483e-06
## 1009731	1132574	species	5.697560e-06
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## 40456	62098	species	1.819092e-06
## 26327	181083	species	3.194189e-06
## 169792	558016	species	3.080020e-06
## 1075906	196896	species	1.901366e-06
## 510604	1132574	species	3.964010e-06
## 1620894	10744	genus	4.455116e-06
## 1853472	1982587	no rank	4.455116e-06
## 1525883	2269062	species	4.455116e-06
## 8430	10357	species	-2.594998e-07
## 281375	10260	no rank	1.492534e-06
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##	1561419	1198137	species	6.584087e-06
##	1452629	2562654	species	2.737514e-06
##	1616799	196895	no rank	2.049965e-06
##	1049926	1978007	species	3.719725e-06
##	314601	181084	species	7.411952e-07
##	12080	10286	species	3.377219e-06
##	1631197	10286	species	1.359206e-07
##	732438	10239	family	-1.549787e-06
##	852827	51368	species	1.298627e-06
##	1659386	2005509	no rank	-5.835226e-07
##	1659387	2025358	species	2.363112e-06
##	18001	10485	species	3.132934e-06
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##	71182	573012	species	-1.090576e-06
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##	135457	10319	species	1.152563e-06
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##	1209014	1511852	genus	3.706314e-06
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##	1657483	51368	family	3.002818e-06
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##	55087	2204151	no rank	2.970923e-06
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##	34655	1857846	species	1.383436e-06
##	759776	549779	no rank	-1.956083e-06
##	1274170	985780	species	-1.956083e-06
##	198509	10241	species	-7.607406e-09
##	1319463	1892568	species	6.799408e-07
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##	117557	692606	species	2.530195e-06
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##	833061	2005509	species	1.040930e-06
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##	8496	2017756	genus	-1.119935e-06
##	289723	10494	no rank	5.871864e-08
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##	1135710	1892568	species	1.139151e-06
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##	8345	10293	genus	-8.781186e-06
##	8367	10294	species	-2.359449e-07
##	8394	10357	genus	-1.611041e-06
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##	1568567	1922348	species	3.398238e-06
##	8317	10260	species	1.516089e-06
##	678186	1892568	species	1.908973e-06
##	1684541	1110703	species	1.221425e-06
##	1569287	1922348	species	1.024983e-06
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##	304688	558017	species	1.009035e-06
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##	268250	181083	species	1.582415e-06
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##	24661	10260	species	-1.032928e-07
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##	1307624	10699	genus	-1.183726e-06
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##	990782	10365	species	2.548679e-06
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##	366040	40272	no rank	1.271804e-06
##	1584736	431037	species	1.271804e-06
##	1356888	40069	species	7.647502e-07
##	8468	558016	species	1.754232e-07
##	75165	558016	species	9.611925e-07
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##	8490	2017757	genus	-2.476548e-06
##	141287	10487	species	-5.121250e-07
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##	1564965	10699	genus	3.718655e-07
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##	1012076	10239	family	9.611925e-07
##	1012077	1285590	genus	9.611925e-07
##	1012079	1285591	species	9.611925e-07
##	1334588	1110703	species	7.647502e-07
##	1464816	2023203	genus	6.665290e-07
##	1153837	1805626	species	6.665290e-07
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##	254975	745176	species	7.488026e-07
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##	891963	10552	species	8.470238e-07
##	8691	10239	family	-1.351879e-07
##	21198	10780	subfamily	1.043466e-06
##	149765	40120	no rank	1.043466e-06
##	1556008	185880	species	1.043466e-06
##	466034	196896	species	-1.351879e-07
##	940032	196894	species	-6.262937e-07
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##	105097	10744	species	2.123899e-06
##	467633	10357	genus	-1.215621e-06
##	467778	548689	no rank	-3.696673e-08
##	467780	548912	species	-3.696673e-08
##	986221	944644	species	2.123899e-06
##	1209013	1511852	genus	3.559179e-07
##	367413	1511853	species	3.559179e-07
##	395652	2559587	order	-1.804948e-06
##	9528	464095	family	2.123899e-06
##	1051673	12058	genus	2.123899e-06
##	1051674	1330069	species	2.123899e-06
##	2050490	2497569	subphylum	8.470238e-07
##	2050494	2497570	class	8.470238e-07

##	8995	2497574	order	8.470238e-07
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##	2050496	2497571	class	-3.671150e-06
##	1618997	2497576	order	-3.671150e-06
##	1619001	1980410	family	2.123899e-06
##	20860	1980416	no rank	2.123899e-06
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##	126933	10242	species	-4.223510e-06
##	8313	10241	genus	-6.384376e-06
##	99426	10257	species	-3.437741e-06
##	99427	10257	species	-1.571539e-06
##	279547	10257	no rank	-1.375096e-06
##	151622	334521	species	-1.375096e-06
##	8319	10260	species	-1.473317e-06
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##	8332	10241	genus	-1.767981e-06
##	8333	10278	species	-1.767981e-06
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##	8469	558016	species	-1.767981e-06
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##	2104823	558016	species	-3.437741e-06
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##	21197	10780	subfamily	-1.178654e-06
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##	1204976	1507401	no rank	-1.178654e-06
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##	573007	196896	species	-2.946635e-06
##	1056379	196896	species	-9.822117e-07
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##	608459	1892568	species	-1.080433e-06
##	610186	1892568	species	-1.571539e-06
##	1181619	1892568	species	-1.669760e-06
##	1506818	1892568	species	-3.241298e-06
##	1623441	1198136	genus	-4.419952e-06
##	1623442	1985325	species	-2.160866e-06
##	1852515	1985325	no rank	-2.259087e-06
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## 1236470	Prochlorococcus phage P-TIM68	1542477
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## 379172	Prochlorococcus phage P-HM1	445700
## 687482	Prochlorococcus phage MED4-213	889956
## 379171	Prochlorococcus phage P-HM2	445696
## 223778	Prochlorococcus phage P-SSM2	268746
## 8671	Podoviridae	10744
## 457445	Prochlorococcus phage P-SSM3	536453
## 462518	Autographivirinae	542835
## 378414	Prochlorococcus phage P-RSM4	444862
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## 603221	Synechococcus phage S-SKS1	754042
## 378412	Synechococcus phage S-SM2	444860
## 719290	Cyanophage P-RSM6	929832
## 1009728	Pelagibacter phage HTVC008M	1283076
## 379168	Prochlorococcus phage P-SSM7	445688
## 1276788	Cyanophage P-TIM40	1589733
## 322098	Prochlorococcus phage P-GSP1	382262
## 8501	Phycodnaviridae	10501
## 836422	Synechococcus phage metaG-MbCM1	1079999
## 457458	Synechococcus phage S-SSM4	536466
## 1534232	Synechococcus phage S-CAM9	1883369
## 473450	Synechococcus phage S-RSM4	555387
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## 1060842	Synechococcus phage ACG-2014h	1340810
## 387539	Chrysochromulina ericina virus	455364
## 1192468	Synechococcus phage ACG-2014j	1493514
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## 1473410	Synechococcus phage S-WAM2	1815522
## 8296	Poxviridae	10240
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## 223780	Prochlorococcus virus PSSP7	268748
## 379165	Synechococcus phage Syn19	445684
## 378413	Prochlorococcus phage Syn1	444861
## 322108	Prochlorococcus phage P-SSP3	382273
## 262244	Mimivirus	315393
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## 1005392	Cyanophage S-RIM32	1278479
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## 1192465	Synechococcus phage ACG-2014f	1493511
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## 836421	Synechococcus phage ACG-2014c	1079998
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## 669494	Synechococcus phage S-RIM2 R1_1999	869662
## 1060844	Synechococcus phage S-MbCM100	1340812
## 1192462	Synechococcus phage ACG-2014b	1493508
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## 934114	Tevenvirinae	1198136
## 603218	Synechococcus phage S-IOM18	754039
## 8338	Entomopoxvirinae	10284
## 1068364	Pandoravirus salinus	1349410
## 563395	Cyanophage S-RIM50	687803
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## 848500	Megavirus chiliensis	1094892
## 379169	Cyanophage NATL2A-133	445692
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## 8493	Chloriridovirus	10491
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## 1257002	Clostridium phage phiCT9441A	1567014
## 603220	Synechococcus phage S-RIP1	754041
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## 164152	Lactococcus phage 4268	201847
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## 1051112	Eptesipox virus	1329402
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## 1319823	Firehammervirus	1636617
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## 1166129	Mycobacterium phage Joliel	1463812
## 58589	Melanoplus sanguinipes entomopoxvirus	83191
## 487253	Raphidovirus	573012
## 71182	Heterosigma akashiwo virus 01	97195
## 839518	Bacillus virus G	1084719
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## 1274170	Yellowstone lake mimivirus	1586712
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## 126933	Skunkpox virus	160796
## 595989	unclassified Alphabaculovirus	745176
## 852827	Apis mellifera filamentous virus	1100043
## 1025553	Invertebrate iridovirus 22	1301279
## 722846	Bathycoccus sp. RCC1105 virus BpV	933845

## 26327	Paramecium bursaria Chlorella virus NY2A	46021
## 1565537	Cbastvirus	1918718
## 1565538	Cellulophaga virus ST	1918720
## 169792	Agrotis ipsilon multiple nucleopolyhedrovirus	208013
## 589962	Campylobacter virus CP220	722417
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## 395652	Picornavirales	464095
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## 8336	Yatapoxvirus	10282
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## 159600	Nimaviridae	196937
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## 286729	White spot syndrome virus	342409
## 8367	Cercopithecine alphaherpesvirus 2	10317
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## 467632	Percavirus	548688
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## 99426	Bovine papular stomatitis virus	129727
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## 145320	Emiliana huxleyi virus 86	181082
## 529863	Penguinpox virus	648998
## 20791	Cotesia congregata bracovirus	39640
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## 212992	Lymphocystis disease virus - isolate China	256729
## 467633	Proboscivirus	548689
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## 1506818	Morganella phage vB_MmoM_MP1	1852628
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## 175086	Lactococcus virus 712	213769
## 487295	Cervidpoxvirus	573055
## 252296	Mule deerpox virus	304399
## 1319463	Proteus phage vB_PmiM_Pm5461	1636250
## 470846	Leptopilina boulardi filamentous virus	552509
## 510604	Cyanophage SS120-1	616674
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## 1568324	Staphylococcus virus SEP9	1922247

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## 1322731	Grapevine Cabernet Sauvignon reovirus	1640277
## 8464	Lymantria dispar multiple nucleopolyhedrovirus	10449
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## 940032	Streptomyces phage SV1	1204525
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## 833061	Yokapox virus	1076255
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## 1561418	Vibrio virus nt1	1914020
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## 1009731	Pelagibacter phage HTVC019P	1283079
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## 1569287	Hubei sobemo-like virus 37	1923224
## 72700	Tanapox virus	99000
## 30959	Helicoverpa armigera nucleopolyhedrovirus	51313
## 50678	Buzura suppressaria nucleopolyhedrovirus	74320
## 254981	Euproctis pseudoconsersa nucleopolyhedrovirus	307467
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## 1564246	Only Syngen Nebraska virus 5	1917232
## 602301	Synechococcus phage S-CBS2	753084
## 1328941	Mycobacterium phage Cambiare	1647305
## 1564965	Helsingorvirus	1918017
## 1565138	Cellulophaga virus Cba121	1918193
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## 1063491	Fruit bat alphaherpesvirus 1	1343901
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## 1049929	Cellulophaga phage phi39:1	1327993
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## 281374	Turkeypox virus	336486
## 381133	Mythimna unipuncta nucleopolyhedrovirus	447897
## 1268625	Agrotis segetum nucleopolyhedrovirus B	1580580

## 321766	Paramecium bursaria Chlorella virus A1	381899
## 1181619	Serratia phage PS2	1481112
## 1024120	Yuavirus	1299429
## 394297	Pseudomonas virus Yua	462590
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## 1208970	Alphapartitivirus	1511808
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## 99427	Parapoxvirus of red deer in New Zealand	129728
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## 216062	Aeromonas virus 65	260149
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## 36955	Choristoneura rosaceana nucleopolyhedrovirus	58094
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## 1329103	Gordonia phage GTE8	1647475
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## 1584736	Murine roseolovirus	1940555
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## 467630	Ostreavirus	548686
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## 268250	Acanthocystis turfacea chlorella virus 1	322019
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## 159561 unclassified Myoviridae 196896
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## 379171 Prochlorococcus phage P-HM2 445696
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## 1009728	Pelagibacter phage HTVC008M	1283076
## 473450	Synechococcus phage S-RSM4	555387
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## 378412	Synechococcus phage S-SM2	444860
## 836422	Synechococcus phage metaG-MbCM1	1079999
## 1060842	Synechococcus phage ACG-2014h	1340810
## 687480	Cyanophage MED4-117	889954
## 735496	Puniceispirillum phage HMO-2011	948071
## 1534232	Synechococcus phage S-CAM9	1883369
## 378416	Cyanophage P-SSP2	444876
## 1534230	Synechococcus phage S-CAM4	1883367
## 1192464	Synechococcus phage ACG-2014e	1493510
## 457436	Cyanophage P-RSM1	536444
## 687481	Prochlorococcus phage MED4-184	889955
## 1473410	Synechococcus phage S-WAM2	1815522
## 1192467	Synechococcus phage ACG-2014i	1493513
## 1534229	Synechococcus phage S-CAM3	1883366
## 223780	Prochlorococcus virus PSSP7	268748
## 379165	Synechococcus phage Syn19	445684
## 1391394	Hollowayvirus	1720324
## 231656	Pseudomonas virus F116	280701
## 387539	Chrysochromulina ericina virus	455364
## 379166	Synechococcus phage S-SSM5	445685
## 378413	Prochlorococcus phage Syn1	444861
## 8501	Phycodnaviridae	10501
## 322108	Prochlorococcus phage P-SSP3	382273
## 387538	unclassified Phycodnaviridae	455363
## 1005392	Cyanophage S-RIM32	1278479
## 1534231	Synechococcus phage S-CAM7	1883368
## 1192465	Synechococcus phage ACG-2014f	1493511
## 197065	Synechococcus phage S-PM2	238854
## 603216	Synechococcus phage S-CAM1	754037
## 378417	Prochlorococcus phage Syn33	444878
## 1192468	Synechococcus phage ACG-2014j	1493514
## 378411	Synechococcus phage S-SM1	444859
## 467626	Herpesvirales	548681
## 1473409	Synechococcus phage S-WAM1	1815521
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## 1192463	Synechococcus phage ACG-2014d	1493509
## 1192466	Synechococcus phage ACG-2014g	1493512
## 262244	Mimivirus	315393
## 603217	Synechococcus phage S-CAM8	754038
## 379164	Synechococcus phage S-ShM2	445683
## 8343	Herpesviridae	10292
## 940040	Clostridium phage phiMMP04	1204535
## 145324	Prymnesiovirus	181086
## 300575	unclassified Prymnesiovirus	358403
## 208529	Phaeocystis globosa virus	251749
## 683915	Prochlorococcus phage P-SSP10	885867
## 468533	Mimiviridae	549779
## 836421	Synechococcus phage ACG-2014c	1079998
## 1534228	Synechococcus phage S-CAM22	1883365
## 1009730	Pelagibacter phage HTVC011P	1283078
## 379170	Cyanophage NATL1A-7	445693
## 8338	Entomopoxvirinae	10284
## 603220	Synechococcus phage S-RIP1	754041

## 1257002	Clostridium phage phiCT9441A	1567014
## 457466	Cyanophage Syn30	536474
## 669494	Synechococcus phage S-RIM2 R1_1999	869662
## 678638	Micromonas sp. RCC1109 virus MpV1	880161
## 8344	Alphaherpesvirinae	10293
## 164152	Lactococcus phage 4268	201847
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## 322189	Synechococcus phage syn9	382359
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## 1049906	Cellulophaga phage phi19:1	1327970
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## 1319823	Firehammervirus	1636617
## 848500	Megavirus chiliensis	1094892
## 997642	Acanthamoeba polyphaga moumouvirus	1269028
## 1657371	<NA>	2023057
## 145321	Chlorovirus	181083
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## 603218	Synechococcus phage S-IOM18	754039
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## 30959	Helicoverpa armigera nucleopolyhedrovirus	51313
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## 2111825	<NA>	2570372
## 790044	Synechococcus phage S-CRM01	1026955
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## 1307641	Timquatrovirus	1623306
## 2106591	<NA>	2562717
## 1186356	Mycobacterium phage OkiRoe	1486473
## 1009731	Pelagibacter phage HTVC019P	1283079
## 605035	Synechococcus phage S-CBP3	756276
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## 2120242	<NA>	2585030
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## 1390286	Klebsiella phage vB_KpnM_KB57	1719140
## 1049919	Cellulophaga phage phi18:3	1327983
## 669544	Synechococcus phage S-RIM8 A.HR1	869724
## 1561548	Dhakavirus	1914165
## 1561571	Escherichia virus VR5	1914195
## 8393	Betaherpesvirinae	10357
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## 1307631	Phicbkvirus	1623296
## 946343	Caulobacter virus Rogue	1211643
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## 126933	Skunkpox virus	160796
## 1542319	unclassified Tevenvirinae	1892568
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## 1565538	Cellulophaga virus ST	1918720
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## 8296	Poxviridae	10240
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## 589962	Campylobacter virus CP220	722417
## 8774	Reoviridae	10880
## 58589	Melanoplus sanguinipes entomopoxvirus	83191
## 379169	Cyanophage NATL2A-133	445692
## 9825	unclassified viruses	12429
## 144554	Mardivirus	180252
## 67736	Columbid alphaherpesvirus 1	93386
## 1049926	Cellulophaga phage phi14:2	1327990
## 1209014	Betanudivirus	1511854
## 12831	Heliothis zea nudivirus	29250
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## 529863	Penguinpox virus	648998
## 99426	Bovine papular stomatitis virus	129727
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## 1506818	Morganella phage vB_MmoM_MP1	1852628
## 1307640	Skunavirus	1623305
## 175086	Lactococcus virus 712	213769
## 26327	Paramecium bursaria Chlorella virus NY2A	46021
## 18001	Chelonus inanitus bracovirus	36344
## 8504	Adenoviridae	10508
## 169792	Agrotis ipsilon multiple nucleopolyhedrovirus	208013
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## 1101730	Phormidium phage MIS-PhV1A	1391455
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## 26528	Spodoptera litura nucleopolyhedrovirus	46242
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## 927148	Campylobacter virus CP21	1190451
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## 8469	Spodoptera littoralis nucleopolyhedrovirus	10456
## 1274173	Yellowstone lake phycodnavirus 3	1586715
## 1161538	Mycobacterium phage Jolie2	1458831
## 1464651	Mycobacterium phage Bipper	1805457
## 281374	Turkeypox virus	336486
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## 1181619	Serratia phage PS2	1481112
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## 394297	Pseudomonas virus Yua	462590
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## 268250	Acanthocystis turfacea chlorella virus 1	322019
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## 20073	Yaba monkey tumor virus	38804
## 127585	Antheraea pernyi nucleopolyhedrovirus	161494
## 610186	Acinetobacter phage Ac42	762660
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## 1123954	Sea otter poxvirus	1416741
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## 153554	Fowl aviadenovirus B	190062
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## 21332	Roseolovirus	40272
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## 1584736	Murine roseolovirus	1940555
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## 487253	Raphidovirus	573012
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## 87958	Glyptapanteles indiensis bracovirus	116759
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## 304688	Artogeia rapae granulovirus	362830
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## 470846	Leptopilina boulardi filamentous virus	552509
## 482324	Spodoptera litura nucleopolyhedrovirus II	566270
## 806265	Operophtera brumata nucleopolyhedrovirus	1046267
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## 1777828	<NA>	2169841
## 9215	Arenaviridae	11617
## 1333656	Mammarenavirus	1653394
## 170630	Cupixi mammarenavirus	208899
## 2059713	<NA>	2509283
## 2059714	<NA>	2509284
## 1726855	<NA>	2107707
## 216062	Aeromonas virus 65	260149
## 75165	Thysanoplusia orichalcea nucleopolyhedrovirus	101850
## 276618	Yersinia phage phiR1-37	331278
## 1012076	Hytrosaviridae	1285590
## 1012077	Glossinavirus	1285591
## 1012079	Glossina hytivirus	1285594
## 1726856	<NA>	2107708
## 254981	Euproctis pseudoconsersa nucleopolyhedrovirus	307467
## 372872	Synechococcus virus Syn5	438482
## 883569	Cyanophage S-TIM5	1137745
## 891963	Turkey aviadenovirus B	1146875
## 2050490	<NA>	2497570
## 2050494	<NA>	2497574
## 8995	Mononegavirales	11157
## 526001	unassigned Mononegavirales	644608
## 1535263	Chengtivirus	1884457
## 1672183	<NA>	2040575
## 1505477	Catopsilia pomona nucleopolyhedrovirus	1850906
## 1356888	Salmon gill poxvirus	1680908
## 1334588	Kallithea virus	1654582
## 254975	Apocheima cinerarium nucleopolyhedrovirus	307461
## 314601	Micromonas pusilla virus SP1	373996
## 9782	Clostridium phage c-st	12336
## 8410	Gammaherpesvirinae	10374
## 467632	Percavirus	548688
## 8407	Equid gammaherpesvirus 5	10371
## 678635	unclassified Prasinovirus	880158
## 1068364	Pandoravirus salinus	1349410
## 1319463	Proteus phage vB_PmiM_Pm5461	1636250
## 1051112	Eptesipox virus	1329402
## 1464816	Pithovirus	1805626
## 1153837	Pithovirus sibericum	1450746
## 8488	Bracovirus	10485
## 30050	Aotine betaherpesvirus 1	50290
## 8340	Choristoneura biennis entomopoxvirus	10288
## 940032	Streptomyces phage SV1	1204525
## 290574	unclassified Chlorovirus	346674
## 1564246	Only Syngen Nebraska virus 5	1917232
## 1328941	Mycobacterium phage Cambiare	1647305
## 1659386	<NA>	2025358
## 141287	Invertebrate iridescent virus 6	176652
## 1354297	Mollivirus sibericum	1678078
## 1210391	Cafeteriavirus	1513234
## 1210392	Cafeteria roenbergensis virus	1513235
## 934114	Tevenvirinae	1198136

## 8502	Paramecium bursaria Chlorella virus 1	10506
## 487396	Vibrio phage henriette 12B8	573174
## 1049877	Cronobacter phage S13	1327935
## 1642509	<NA>	2005509
## 8529	Aviadenovirus	10552
## 1697067	<NA>	2072209
## 1703764	<NA>	2083300
## 1564965	Helsingorvirus	1918017
## 1565138	Cellulophaga virus Cba121	1918193
## 1209013	Alphanudivirus	1511853
## 367413	Gryllus bimaculatus nudivirus	432587
## 722846	Bathycoccus sp. RCC1105 virus BpV	933845
## 1261902	Geobacillus virus E3	1572712
## 1687017	<NA>	2060084
## 8368	Varicellovirus	10319
## 8430	Tupaiid betaherpesvirus 1	10397
## 8316	Avipoxvirus	10260
## 8336	Yatapoxvirus	10282
## 8367	Cercopithecine alphaherpesvirus 2	10317
## 289264	Invertebrate iridescent virus 9	345195
## 1001296	Synechococcus phage S-CBP1	1273711
## 886589	Cronobacter phage vB_CsaM_GAP32	1141136
## 1068363	Pandoravirus dulcis	1349409
## 8468	Spodoptera frugiperda multiple nucleopolyhedrovirus	10455
## 487295	Cervidpoxvirus	573055
## 252296	Mule deerpox virus	304399
## 1631197	<NA>	1993631
## 8691	Parvoviridae	10780
## 466034	Mycobacterium phage Myrna	546805
## 808604	Acinetobacter phage ZZ1	1049283
## 24661	Canarypox virus	44088
## 2104607	<NA>	2560207
## 2104663	<NA>	2560286
## 289723	unclassified Lymphocystivirus	345690
## 212992	Lymphocystis disease virus - isolate China	256729
## 290573	Coccolithovirus	346673
## 145320	Emiliana huxleyi virus 86	181082
## 467778	unclassified Proboscivirus	548912
## 467780	Elephant endotheliotropic herpesvirus 4	548914
## 198509	Squirrelpox virus	240426
##	parent rank DeltaFreq	
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## 8295	1 superkingdom	-8.112324e-03
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## 223778	196896 species	-5.346773e-04
## 879134	542835 no rank	5.197064e-04
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## 1564965    10699      genus  3.718655e-07
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## 289723     10494     no rank  5.871864e-08
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## 145320    346673     species -3.950253e-08
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## 198509     10241     species -7.607406e-09

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may.big <- virus[ which(virus$DeltaFreq < -0.00), ] ; nrow(may.big) # 0.001 was too stringent
## [1] 355

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may.big <- may.big[ order( may.big$path, may.big$DeltaFreq ), ]
may.big[ , c(1:4,15 )]

##                                name  tax_id
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## 8504                        Adenoviridae  10508
## 74367                      Atadenovirus  100953
## 99974                    Duck atadenovirus A  130328
## 8529                      Aviadenovirus  10552
## 153554                  Fowl aviadenovirus B  190062
## 1160937                Alphasatellitidae  1458186
## 233846          Geminialphasatellitinae  283494
## 1777687                <NA> 2169619
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## 24300                  Ascovirus  43680
## 274188                unclassified Ascovirus  328613
## 274190          Trichoplusia ni ascovirus 2c  328615
## 8463                    Baculoviridae  10442
## 475679                Alhabaculovirus  558016
## 127585          Antheraea pernyi nucleopolyhedrovirus  161494
## 50678          Buzura suppressaria nucleopolyhedrovirus  74320
## 36955          Choristoneura rosaceana nucleopolyhedrovirus  58094
## 1031546        Clanis bilineata nucleopolyhedrovirus  1307957
## 1031545        Leucania separata nucleopolyhedrovirus  1307956
## 8464          Lymantria dispar multiple nucleopolyhedrovirus  10449
## 381133        Mythimna unipuncta nucleopolyhedrovirus  447897
## 2104823                <NA> 2560521
## 806265          Operophtera brumata nucleopolyhedrovirus  1046267
## 8469          Spodoptera littoralis nucleopolyhedrovirus  10456
## 26528          Spodoptera litura nucleopolyhedrovirus  46242
## 595989                unclassified Alhabaculovirus  745176
## 1066190          Peridroma alhabaculovirus  1346829
## 482324          Spodoptera litura nucleopolyhedrovirus II  566270
## 475680          Betabaculovirus  558017
## 35970          Choristoneura fumiferana granulovirus  56947
## 1418509        Cnaphalocrocis medinalis granulovirus  1750712
## 17107          Cryptophlebia leucotreta granulovirus  35254
## 1624313                <NA> 1986290
## 475682          Deltabaculovirus  558019
## 100193          Culex nigripalpus nucleopolyhedrovirus  130556
## 17108                unclassified Baculoviridae  35255
## 1352395          Urbanus proteus nucleopolyhedrovirus  1675866
## 358969          Bicaudaviridae  423358
## 871974                unclassified Bicaudaviridae  1123963
## 1456800        Acidianus tailed spindle virus  1797140
## 12521                Caudovirales  28883
## 8614                Myoviridae  10662
## 1319822          Eucampyvirinae  1636616
## 1319823          Firehammervirus  1636617
## 927148          Campylobacter virus CP21  1190451
## 589962          Campylobacter virus CP220  722417
## 776286          Campylobacter virus IBB35  1006972
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## 892153	Enterobacteria phage vB_KleM-RaK2	1147094
## 1001320	Escherichia phage PBECO 4	1273738
## 1567806	Tegunavirus	1921704
## 1567808	Yersinia virus TG1	1921706
## 187209	Aeromonas virus Aeh1	227470
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## 1506815	Klebsiella phage vB_KpnM_KpV477	1852625
## 1561418	Vibrio virus nt1	1914020
## 1542319	unclassified Tevenvirinae	1892568
## 610186	Acinetobacter phage Ac42	762660
## 608459	Acinetobacter phage Acj61	760732
## 1049877	Cronobacter phage S13	1327935
## 1506818	Morganella phage vB_MmoM_MP1	1852628
## 1181619	Serratia phage PS2	1481112
## 159561	unclassified Myoviridae	196896
## 1473399	Bacillus phage AR9	1815509
## 1257002	Clostridium phage phiCT9441A	1567014
## 457436	Cyanophage P-RSM1	536444
## 719290	Cyanophage P-RSM6	929832
## 1276788	Cyanophage P-TIM40	1589733
## 1005392	Cyanophage S-RIM32	1278479
## 563395	Cyanophage S-RIM50	687803
## 883569	Cyanophage S-TIM5	1137745
## 457466	Cyanophage Syn30	536474
## 466034	Mycobacterium phage Myrna	546805
## 687482	Prochlorococcus phage MED4-213	889956
## 379172	Prochlorococcus phage P-HM1	445700
## 379171	Prochlorococcus phage P-HM2	445696
## 378414	Prochlorococcus phage P-RSM4	444862
## 223778	Prochlorococcus phage P-SSM2	268746
## 457445	Prochlorococcus phage P-SSM3	536453
## 223779	Prochlorococcus phage P-SSM4	268747
## 379168	Prochlorococcus phage P-SSM7	445688
## 1236470	Prochlorococcus phage P-TIM68	1542477
## 378413	Prochlorococcus phage Syn1	444861
## 378417	Prochlorococcus phage Syn33	444878
## 1056379	Pseudomonas phage PaBG	1335230
## 1192462	Synechococcus phage ACG-2014b	1493508
## 836421	Synechococcus phage ACG-2014c	1079998
## 1192463	Synechococcus phage ACG-2014d	1493509
## 1192464	Synechococcus phage ACG-2014e	1493510
## 1192465	Synechococcus phage ACG-2014f	1493511
## 1192466	Synechococcus phage ACG-2014g	1493512
## 1060842	Synechococcus phage ACG-2014h	1340810
## 1192467	Synechococcus phage ACG-2014i	1493513
## 836422	Synechococcus phage metaG-MbCM1	1079999

## 603216	Synechococcus phage S-CAM1	754037
## 1534228	Synechococcus phage S-CAM22	1883365
## 1534229	Synechococcus phage S-CAM3	1883366
## 1534230	Synechococcus phage S-CAM4	1883367
## 1534231	Synechococcus phage S-CAM7	1883368
## 603217	Synechococcus phage S-CAM8	754038
## 1534232	Synechococcus phage S-CAM9	1883369
## 790044	Synechococcus phage S-CRM01	1026955
## 603218	Synechococcus phage S-IOM18	754039
## 1060844	Synechococcus phage S-MbCM100	1340812
## 197065	Synechococcus phage S-PM2	238854
## 669494	Synechococcus phage S-RIM2 R1_1999	869662
## 669544	Synechococcus phage S-RIM8 A.HR1	869724
## 473450	Synechococcus phage S-RSM4	555387
## 379164	Synechococcus phage S-ShM2	445683
## 603221	Synechococcus phage S-SKS1	754042
## 378411	Synechococcus phage S-SM1	444859
## 378412	Synechococcus phage S-SM2	444860
## 457458	Synechococcus phage S-SSM4	536466
## 379166	Synechococcus phage S-SSM5	445685
## 379167	Synechococcus phage S-SSM7	445686
## 1473409	Synechococcus phage S-WAM1	1815521
## 1473410	Synechococcus phage S-WAM2	1815522
## 379165	Synechococcus phage Syn19	445684
## 322189	Synechococcus phage syn9	382359
## 573007	Thermus phage TMA	699370
## 1559687	Vequintavirinae	1911928
## 2059065	<NA>	2508196
## 1390286	Klebsiella phage vB_KpnM_KB57	1719140
## 2104491	<NA>	2560065
## 517730	Lactobacillus virus Lb338-1	632112
## 2104497	<NA>	2560073
## 1511764	Pecentumvirus	1857844
## 2104844	<NA>	2560553
## 2104606	<NA>	2560206
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## 118711	Synechococcus virus P60	151528
## 1391394	Hollowayvirus	1720324
## 231656	Pseudomonas virus F116	280701
## 327719	Lactococcus virus KSY1	388452
## 1777711	<NA>	2169643
## 1778050	<NA>	2170215
## 462519	Picovirinae	542836
## 150613	Salasvirus	186846
## 2106555	<NA>	2562647
## 1525397	Bacillus phage Stitch	1874002
## 1049919	Cellulophaga phage phi18:3	1327983
## 1891373	<NA>	2315857
## 946129	uncultured crAssphage	1211417
## 603231	Pseudoalteromonas phage pYD6-A	754052
## 150549	Fromanvirus	186764
## 1631426	<NA>	1993867
## 1307624	Liefievirus	1623288
## 1796197	<NA>	2201169
## 1161538	Mycobacterium phage Jolie2	1458831
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## 1166129	Mycobacterium phage Joliel	1463812
## 1621396	<NA>	1983119
## 1567316	Nonanavirus	1921122
## 1567317	Salmonella virus 9NA	1921123
## 1307631	Phicbkvirus	1623296
## 946343	Caulobacter virus Rogue	1211643
## 1568322	Sextaecvirus	1922243
## 1568324	Staphylococcus virus SEP9	1922247
## 1307640	Skunavirus	1623305
## 175086	Lactococcus virus 712	213769
## 1558941	Tunavirinae	1910999
## 2104557	<NA>	2560145
## 2104978	<NA>	2560762
## 1049906	Cellulophaga phage phi19:1	1327970
## 1049929	Cellulophaga phage phi39:1	1327993
## 687479	Cyanophage KBS-S-2A	889953
## 1261902	Geobacillus virus E3	1572712
## 1329103	Gordonia phage GTE8	1647475
## 1478927	Gordonia phage Lucky10	1821557
## 164152	Lactococcus phage 4268	201847
## 940032	Streptomyces phage SV1	1204525
## 602301	Synechococcus phage S-CBS2	753084
## 755586	Tsukamurella phage TPA2	981330
## 1024120	Yuavirus	1299429
## 394297	Pseudomonas virus Yua	462590
## 467626	Herpesvirales	548681
## 467627	Alloherpesviridae	548682
## 567489	Cyprinivirus	692606
## 264505	Cyprinid herpesvirus 2	317878
## 144533	Cyprinid herpesvirus 3	180230
## 137588	Ictalurivirus	172653
## 8432	Ictalurid herpesvirus 1	10401
## 8343	Herpesviridae	10292
## 8344	Alphaherpesvirinae	10293
## 144554	Mardivirus	180252
## 67736	Columbid alphaherpesvirus 1	93386
## 8345	Simplexvirus	10294
## 17098	Ateline alphaherpesvirus 1	35243
## 8367	Cercopithecine alphaherpesvirus 2	10317
## 8391	Saimiriine alphaherpesvirus 1	10353
## 286730	unclassified Simplexvirus	342410
## 1063491	Fruit bat alphaherpesvirus 1	1343901
## 8369	Bovine alphaherpesvirus 1	10320
## 8393	Betaherpesvirinae	10357
## 15846	Caviid betaherpesvirus 2	33706
## 8394	Cytomegalovirus	10358
## 30052	Cercopithecine betaherpesvirus 5	50292
## 8395	Human betaherpesvirus 5	10359
## 8401	Muromegalovirus	10365

## 8402	Murid betaherpesvirus 1	10366
## 12073	Murid betaherpesvirus 2	28304
## 467633	Proboscivirus	548689
## 113996	Elephantid betaherpesvirus 1	146015
## 467778	unclassified Proboscivirus	548912
## 467780	Elephant endotheliotropic herpesvirus 4	548914
## 8430	Tupaiaid betaherpesvirus 1	10397
## 467629	Malacoherpesviridae	548685
## 467630	Ostreavirus	548686
## 217565	Ostreid herpesvirus 1	261939
## 8489	Iridoviridae	10486
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## 8493	Chloriridovirus	10491
## 289269	Invertebrate iridescent virus 3	345201
## 2111825	<NA>	2570372
## 1167956	Anopheles minimus irodovirus	1465751
## 1025553	Invertebrate iridovirus 22	1301279
## 1025554	Invertebrate iridovirus 25	1301280
## 8490	Iridovirus	10487
## 289268	Invertebrate iridescent virus 31	345199
## 141287	Invertebrate iridescent virus 6	176652
## 8496	Lymphocystivirus	10494
## 18013	Lymphocystis disease virus 1	36363
## 1209017	Ligamenvirales	1511857
## 124367	Rudiviridae	157897
## 150951	Rudivirus	187213
## 294413	unclassified Rudivirus	351054
## 1621720	<NA>	1983551
## 732438	Marseilleviridae	944644
## 770280	Lausannevirus	999883
## 1210612	Marseillevirus	1513458
## 1471788	unclassified Marseillevirus	1813598
## 1391586	Golden Marseillevirus	1720526
## 1599198	<NA>	1955558
## 1210391	Cafeteriavirus	1513234
## 1210392	Cafeteria roenbergensis virus	1513235
## 875414	Mimivirus terra2	1128151
## 759776	unclassified Mimiviridae	985780
## 1274170	Yellowstone lake mimivirus	1586712
## 2104158	<NA>	2559587
## 8898	Flaviviridae	11050
## 8938	Pestivirus	11095
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## 98528	Haloviruses	128706
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## 1001335	Halovirus HRTV-7	1273754
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## 9215	Arenaviridae	11617
## 1333656	Mammarenavirus	1653394
## 170630	Cupixi mammarenavirus	208899
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## 1569223	Hubei picorna-like virus 76		1923160
## 8870	Partitiviridae		11012
## 1208970	Alphapartitivirus		1511808
## 234891	Cherry chlorotic rusty spot associated partitivirus		284688
## 395652	Picornavirales		464095
## 572890	Iflaviridae		699189
## 862140	unclassified Iflaviridae		1111709
## 1313349	Graminella nigrifrons virus 1		1629132
## 551883	Secoviridae		675072
## 551886	Comovirinae		675075
## 9721	Nepovirus		12270
## 9729	Tomato ringspot virus		12280
## 8774	Reoviridae		10880
## 565043	Spinareovirinae		689831
## 8841	Aquareovirus		10979
## 149679	Aquareovirus C		185782
## 18075	unclassified Reoviridae		36446
## 1322731	Grapevine Cabernet Sauvignon reovirus		1640277
## 1687017		<NA>	2060084
## 1726856		<NA>	2107708
## 1068363	Pandoravirus dulcis		1349409
## 1291601	Pandoravirus inopinatum		1605721
## 8691	Parvoviridae		10780
## 21197	Parvovirinae		40119
## 1204975	Bocaparvovirus		1507401
## 1204976	unclassified Bocaparvovirus		1507402
## 1653158		<NA>	2017714
## 8501	Phycodnaviridae		10501
## 290573	Coccolithovirus		346673
## 145320	Emiliana huxleyi virus 86		181082
## 1700527		<NA>	2079134
## 1341546	Ostreococcus lucimarinus virus 2		1663208
## 1274171	Yellowstone lake phycodnavirus 1		1586713
## 1274173	Yellowstone lake phycodnavirus 3		1586715
## 145324	Prymnesiovirus		181086
## 300575	unclassified Prymnesiovirus		358403
## 208529	Phaeocystis globosa virus		251749
## 487253	Raphidovirus		573012
## 71182	Heterosigma akashiwo virus 01		97195
## 387538	unclassified Phycodnaviridae		455363
## 387539	Chrysochromulina ericina virus		455364
## 20791	Cotesia congregata bracovirus		39640
## 87958	Glyptapanteles indiensis bracovirus		116759
## 1703764		<NA>	2083300
## 8297	Chordopoxvirinae		10241
## 8316	Avipoxvirus		10260
## 24661	Canarypox virus		44088
## 8319	Pigeonpox virus		10264

## 281374		Turkeypox virus	336486
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## 8320		Capripoxvirus	10265
## 8321		Sheeppox virus	10266
## 487295		Cervidpoxvirus	573055
## 252296		Mule deerpox virus	304399
## 8332		Molluscipoxvirus	10278
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## 126933		Skunkpox virus	160796
## 8313		Parapoxvirus	10257
## 99426		Bovine papular stomatitis virus	129727
## 99427		Parapoxvirus of red deer in New Zealand	129728
## 279547		unclassified Parapoxvirus	334521
## 151622		Seal parapoxvirus	187984
## 198509		Squirrelepox virus	240426
## 1123954		Sea otter poxvirus	1416741
## 8336		Yatapoxvirus	10282
## 20073		Yaba monkey tumor virus	38804
## 918102		Mythimna separata entomopoxvirus	1179664
## 1051112		Eptesipox virus	1329402
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## 806265	558016	species	-9.822117e-07
## 8469	558016	species	-1.767981e-06
## 26528	558016	species	-2.455529e-06
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##	286730	10294	no rank	-1.964423e-06
##	1063491	342410	species	-1.964423e-06
##	8369	10319	species	-2.455529e-06
##	8393	10292	subfamily	-4.667844e-06
##	15846	10357	species	-1.669760e-06
##	8394	10357	genus	-1.611041e-06
##	30052	10358	species	-9.822117e-07
##	8395	10358	species	-1.276875e-06
##	8401	10357	genus	-1.183726e-06
##	8402	10365	species	-1.669760e-06
##	12073	10365	species	-2.062644e-06
##	467633	10357	genus	-1.215621e-06
##	113996	548689	species	-1.178654e-06
##	467778	548689	no rank	-3.696673e-08
##	467780	548912	species	-3.696673e-08
##	8430	10357	species	-2.594998e-07
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##	467630	548685	genus	-1.276875e-06
##	217565	548686	species	-1.276875e-06
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##	1653196	10486	subfamily	-1.119935e-06
##	8493	2017757	genus	-6.776528e-06
##	289269	10491	species	-9.822117e-07
##	2111825	10491	no rank	-6.017582e-06
##	1167956	2570372	species	-9.822117e-07
##	1025553	2570372	species	-4.125289e-06
##	1025554	2570372	species	-2.062644e-06
##	8490	2017757	genus	-2.476548e-06
##	289268	10487	species	-1.964423e-06
##	141287	10487	species	-5.121250e-07
##	8496	2017756	genus	-1.119935e-06
##	18013	10494	species	-1.178654e-06
##	1209017	10239	order	-1.964423e-06
##	124367	1511857	family	-1.964423e-06
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##	294413	187213	no rank	-1.964423e-06
##	1621720	351054	species	-1.964423e-06
##	732438	10239	family	-1.549787e-06
##	770280	944644	species	-2.455529e-06
##	1210612	944644	genus	-1.218157e-06
##	1471788	1513458	no rank	-1.218157e-06
##	1391586	1813598	species	-1.178654e-06
##	1599198	1813598	species	-1.375096e-06
##	1210391	549779	genus	-5.073909e-07

##	1210392	1513234	species	-5.073909e-07
##	875414	2501774	species	-2.862896e-06
##	759776	549779	no rank	-1.956083e-06
##	1274170	985780	species	-1.956083e-06
##	2104158	10239	no rank	-6.369499e-06
##	8898	2559587	family	-1.669760e-06
##	8938	11050	genus	-1.669760e-06
##	1777967	11095	species	-1.669760e-06
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##	1751669	2204151	no rank	-2.357308e-06
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##	1001327	128706	species	-1.178654e-06
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##	2050491	2497569	subphylum	-3.671150e-06
##	2050496	2497571	class	-3.671150e-06
##	1618997	2497576	order	-3.671150e-06
##	9215	1980410	family	-9.822117e-07
##	1333656	11617	genus	-9.822117e-07
##	170630	1653394	species	-9.822117e-07
##	1619003	1980410	family	-3.339520e-06
##	1618999	1980410	family	-1.473317e-06
##	2104568	1980418	genus	-2.357308e-06
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##	2104833	2560157	species	-2.357308e-06
##	2053375	2560074	genus	-1.473317e-06
##	2059714	2509283	species	-9.822117e-07
##	2053377	2501368	species	-1.473317e-06
##	1569223	1922348	species	-1.571539e-06
##	8870	2559587	family	-1.669760e-06
##	1208970	11012	genus	-1.669760e-06
##	234891	1511808	species	-1.669760e-06
##	395652	2559587	order	-1.804948e-06
##	572890	464095	family	-2.750193e-06
##	862140	699189	no rank	-2.750193e-06
##	1313349	1111709	species	-2.750193e-06
##	551883	464095	family	-1.178654e-06
##	551886	675072	subfamily	-1.178654e-06
##	9721	675075	genus	-1.178654e-06
##	9729	12270	species	-1.178654e-06
##	8774	2559587	family	-3.928847e-06
##	565043	10880	subfamily	-1.080433e-06
##	8841	689831	genus	-1.080433e-06
##	149679	10979	species	-1.080433e-06
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##	1322731	36446	species	-2.848414e-06
##	1687017	51368	genus	-3.079600e-07
##	1726856	2060084	species	-9.252961e-07
##	1068363	2060084	species	-1.757607e-07
##	1291601	2060084	species	-3.043391e-06
##	8691	10239	family	-1.351879e-07
##	21197	10780	subfamily	-1.178654e-06
##	1204975	40119	genus	-1.178654e-06
##	1204976	1507401	no rank	-1.178654e-06
##	1653158	1507402	species	-1.178654e-06
##	8501	10239	family	-4.564866e-05

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## 290573      10501      genus -3.950253e-08
## 145320      346673     species -3.950253e-08
## 1700527     880158     species -1.080433e-06
## 1341546     880158     species -9.527453e-06
## 1274171     880158     species -9.822117e-07
## 1274173     880158     species -1.767981e-06
## 145324      10501      genus -1.596688e-05
## 300575      181086     no rank -1.596688e-05
## 208529      358403     species -1.596688e-05
## 487253      10501      genus -1.090576e-06
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## 387538      10501      no rank -3.827458e-05
## 387539      455363     species -4.831348e-05
## 20791       10485      species -1.003231e-06
## 87958       10485      species -1.080433e-06
## 1703764     10485      species -3.979563e-07
## 8297        10240      subfamily -1.179302e-05
## 8316        10241      genus -2.377479e-07
## 24661       10260      species -1.032928e-07
## 8319        10260      species -1.473317e-06
## 281374      10260      species -1.669760e-06
## 1686392     336487     species -1.964423e-06
## 8320        10241      genus -5.009279e-06
## 8321        10265      species -5.009279e-06
## 487295      10241      genus -1.696188e-07
## 252296     573055      species -1.696188e-07
## 8332        10241      genus -1.767981e-06
## 8333        10278      species -1.767981e-06
## 1659386     2005509     no rank -5.835226e-07
## 1659388     2025358     species -2.946635e-06
## 8298        10241      genus -4.223510e-06
## 126933      10242      species -4.223510e-06
## 8313        10241      genus -6.384376e-06
## 99426       10257      species -3.437741e-06
## 99427       10257      species -1.571539e-06
## 279547      10257      no rank -1.375096e-06
## 151622      334521      species -1.375096e-06
## 198509      10241      species -7.607406e-09
## 1123954     40070      species -1.276875e-06
## 8336        10241      genus -2.359449e-07
## 20073       10282      species -1.571539e-06
## 918102      10286      species -1.212352e-06
## 1051112     40069      species -6.708678e-07
```

```
bel.big <- virus[ which(virus$DeltaFreq > -0.00), ] ; nrow(bel.big) # 0.001 was too stringent
```

```
## [1] 217
```

```
bel.big <- bel.big[ order( -bel.big$DeltaFreq ), ]
```

```
bel.big[ , c(1:4,15 )]
```

```
##
##                                name  tax_id
## 8671                          Podoviridae  10744
## 462518                        Autographivirinae  542835
## 879134      unclassified Autographivirinae  1132574
## 322098      Prochlorococcus phage P-GSP1  382262
## 159560      unclassified Podoviridae  196895
## 1559892      Lubbockvirus  1912144
```

## 1559894	unclassified Lubbockvirus	1912146
## 1118976	Clostridium phage CDMH1	1411095
## 1009729	Pelagibacter phage HTVC010P	1283077
## 159559	unclassified Siphoviridae	196894
## 8639	Siphoviridae	10699
## 1009728	Pelagibacter phage HTVC008M	1283076
## 687480	Cyanophage MED4-117	889954
## 735496	Puniceispirillum phage HMO-2011	948071
## 378416	Cyanophage P-SSP2	444876
## 687481	Prochlorococcus phage MED4-184	889955
## 223780	Prochlorococcus virus PSSP7	268748
## 322108	Prochlorococcus phage P-SSP3	382273
## 1192468	Synechococcus phage ACG-2014j	1493514
## 262244	Mimivirus	315393
## 940040	Clostridium phage phiMMP04	1204535
## 683915	Prochlorococcus phage P-SSP10	885867
## 468533	Mimiviridae	549779
## 1009730	Pelagibacter phage HTVC011P	1283078
## 379170	Cyanophage NATL1A-7	445693
## 8338	Entomopoxvirinae	10284
## 603220	Synechococcus phage S-RIP1	754041
## 678638	Micromonas sp. RCC1109 virus MpV1	880161
## 2053675	<NA>	2501774
## 378415	Cyanophage 9515-10a	444875
## 2104539	<NA>	2560124
## 2104744	<NA>	2560427
## 153940	Clostridium phage phi3626	190478
## 1209012	Nudiviridae	1511852
## 603237	Synechococcus phage S-CBP4	754059
## 2104542	<NA>	2560128
## 8339	Betaentomopoxvirus	10286
## 848500	Megavirus chiliensis	1094892
## 997642	Acanthamoeba polyphaga mounouvirus	1269028
## 1657371	<NA>	2023057
## 145321	Chlorovirus	181083
## 1561419	Vibrio virus ValKK3	1914021
## 30959	Helicoverpa armigera nucleopolyhedrovirus	51313
## 173522	Acanthamoeba polyphaga mimivirus	212035
## 1307641	Timquatrovirus	1623306
## 2106591	<NA>	2562717
## 1186356	Mycobacterium phage OkiRoe	1486473
## 1009731	Pelagibacter phage HTVC019P	1283079
## 605035	Synechococcus phage S-CBP3	756276
## 44717	BeAn 58058 virus	67082
## 2120242	<NA>	2585030
## 1568411	unclassified RNA viruses ShiM-2016	1922348
## 861174	unclassified Nudiviridae	1110703
## 1631196	<NA>	1993630
## 1561548	Dhakavirus	1914165
## 1561571	Escherichia virus VR5	1914195
## 1798558	<NA>	2204151
## 839518	Bacillus virus G	1084719
## 1620894	<NA>	1982587
## 1853472	<NA>	2269062
## 1525883	Pseudoalteromonas phage PH1	1874540
## 934115	Schizotequatrovirus	1198137

## 21153	unclassified Chordopoxvirinae	40070
## 1565537	Cbastvirus	1918718
## 1565538	Cellulophaga virus ST	1918720
## 1620399	<NA>	1982077
## 8296	Poxviridae	10240
## 31012	unclassified dsDNA viruses	51368
## 510604	Cyanophage SS120-1	616674
## 58589	Melanoplus sanguinipes entomopoxvirus	83191
## 379169	Cyanophage NATL2A-133	445692
## 9825	unclassified viruses	12429
## 1049926	Cellulophaga phage phi14:2	1327990
## 1209014	Betanudivirus	1511854
## 12831	Heliothis zea nudivirus	29250
## 1366668	Brevibacillus phage Sundance	1691958
## 2105025	<NA>	2560849
## 529863	Penguinpox virus	648998
## 1568567	Beihai partiti-like virus 2	1922504
## 12080	Amsacta moorei entomopoxvirus	28321
## 1562148	Certrevirus	1914850
## 1619492	<NA>	1980961
## 1032431	Bacillus phage vB_BanS-Tsamsa	1308863
## 26327	Paramecium bursaria Chlorella virus NY2A	46021
## 18001	Chelonus inanitus bracovirus	36344
## 169792	Agrotis ipsilon multiple nucleopolyhedrovirus	208013
## 1657483	<NA>	2023203
## 55087	unclassified dsDNA phages	79205
## 1101730	Phormidium phage MIS-PhV1A	1391455
## 1176678	Aureococcus anophagefferens virus	1474867
## 1239831	Tipula oleracea nudivirus	1546257
## 1620398	<NA>	1982076
## 1452629	Pectobacterium phage CBB	1792242
## 1569421	Sanxia atyid shrimp virus 4	1923358
## 2104968	<NA>	2560751
## 2106561	<NA>	2562654
## 990782	Murid betaherpesvirus 8	1261657
## 117557	Anguillid herpesvirus 1	150286
## 8485	Polydnviridae	10482
## 1578174	Pacmanvirus A23	1932881
## 1268625	Agrotis segetum nucleopolyhedrovirus B	1580580
## 1659387	<NA>	2025359
## 1307615	Bronvirus	1623278
## 1796195	<NA>	2201166
## 1060858	Mycobacterium phage Whirlwind	1340826
## 1552147	Cedratvirus A11	1903266
## 1726857	<NA>	2107709
## 105097	Roseobacter virus SI01	136084
## 986221	Tunisvirus	1255301
## 9528	Picornaviridae	12058
## 1051673	Megrivirus	1330069
## 1051674	Melegrivirus A	1330070
## 1619001	<NA>	1980416
## 20860	unclassified Peribunyaviridae	39718
## 1293694	Huangpi Tick Virus 1	1608047
## 21152	unclassified Poxviridae	40069
## 1616799	<NA>	1978007
## 20606	Cotia virus	39444

## 678186	Aeromonas phage phiAS5	879630
## 1075906	Caulobacter phage Cr30	1357714
## 40455	Alphaentomopoxvirus	62098
## 40456	Anomala cuprea entomopoxvirus	62099
## 8486	Ichnovirus	10483
## 8487	Campoletis sonorensis ichnovirus	10484
## 1464651	Mycobacterium phage Bipper	1805457
## 8387	Suid alphaherpesvirus 1	10345
## 268250	Acanthocystis turfacea chlorella virus 1	322019
## 8317	Fowlpox virus	10261
## 281375	unclassified Avipoxvirus	336487
## 8329	Suipoxvirus	10275
## 8330	Swinepox virus	10276
## 145322	Prasinovirus	181084
## 8467	Spodoptera exigua multiple nucleopolyhedrovirus	10454
## 2104503	<NA>	2560081
## 1511766	Twortvirus	1857846
## 34655	Staphylococcus virus Twort	55510
## 145323	Phaeovirus	181085
## 191389	Feldmannia irregularis virus a	231992
## 72700	Tanapox virus	99000
## 1483257	Tokyo virus A1	1826170
## 852827	Apis mellifera filamentous virus	1100043
## 21332	Roseolovirus	40272
## 366040	unclassified Roseolovirus	431037
## 1584736	Murine roseolovirus	1940555
## 1325021	Lambdina fiscellaria nucleopolyhedrovirus	1642929
## 1684541	<NA>	2057187
## 604342	Micromonas pusilla virus 12T	755272
## 289623	Invertebrate iridescent virus 30	345585
## 135457	Canid alphaherpesvirus 1	170325
## 1135710	Pectobacterium bacteriophage PM2	1429794
## 38098	Ectropis obliqua nucleopolyhedrovirus	59376
## 321766	Paramecium bursaria Chlorella virus A1	381899
## 21198	Densovirinae	40120
## 149765	unclassified Densovirinae	185880
## 1556008	Parus major densovirus	1907771
## 833061	Yokapox virus	1076255
## 159600	Nimaviridae	196937
## 206416	Whispovirus	249585
## 286729	White spot syndrome virus	342409
## 1569287	Hubei sobemo-like virus 37	1923224
## 304688	Artogeia rapae granulovirus	362830
## 470846	Leptopilina boulardi filamentous virus	552509
## 1726855	<NA>	2107707
## 216062	Aeromonas virus 65	260149
## 75165	Thysanoplusia orichalcea nucleopolyhedrovirus	101850
## 276618	Yersinia phage phiR1-37	331278
## 1012076	Hytrosaviridae	1285590
## 1012077	Glossinavirus	1285591
## 1012079	Glossina hytrovirus	1285594
## 254981	Euproctis pseudoconsersa nucleopolyhedrovirus	307467
## 372872	Synechococcus virus Syn5	438482
## 891963	Turkey aviadenovirus B	1146875
## 2050490	<NA>	2497570
## 2050494	<NA>	2497574

## 8995		Mononegavirales	11157
## 526001		unassigned Mononegavirales	644608
## 1535263		Chengtivirus	1884457
## 1672183		<NA>	2040575
## 1505477	Catopsilia pomona	nucleopolyhedrovirus	1850906
## 1356888		Salmon gill poxvirus	1680908
## 1334588		Kallithea virus	1654582
## 254975	Apocheima cinerarium	nucleopolyhedrovirus	307461
## 314601	Micromonas pusilla	virus SP1	373996
## 9782		Clostridium phage c-st	12336
## 8410		Gammaherpesvirinae	10374
## 467632		Percavirus	548688
## 8407		Equid gammaherpesvirus 5	10371
## 678635		unclassified Prasinovirus	880158
## 1068364		Pandoravirus salinus	1349410
## 1319463	Proteus phage vB_PmiM_Pm5461		1636250
## 1464816		Pithovirus	1805626
## 1153837		Pithovirus sibericum	1450746
## 8488		Bracovirus	10485
## 30050		Aotine betaherpesvirus 1	50290
## 8340	Choristoneura biennis	entomopoxvirus	10288
## 290574		unclassified Chlorovirus	346674
## 1564246	Only Syngen Nebraska	virus 5	1917232
## 1328941	Mycobacterium phage Cambiare		1647305
## 1354297		Mollivirus sibericum	1678078
## 934114		Tevenvirinae	1198136
## 8502	Paramecium bursaria	Chlorella virus 1	10506
## 487396		Vibrio phage henriette 12B8	573174
## 1642509		<NA>	2005509
## 1697067		<NA>	2072209
## 1564965		Helsingorvirus	1918017
## 1565138		Cellulophaga virus Cba121	1918193
## 1209013		Alphanudivirus	1511853
## 367413	Gryllus bimaculatus	nudivirus	432587
## 722846	Bathycoccus sp. RCC1105	virus BpV	933845
## 8368		Varicellovirus	10319
## 289264	Invertebrate iridescent	virus 9	345195
## 1001296	Synechococcus phage S-CBP1		1273711
## 8468	Spodoptera frugiperda	multiple nucleopolyhedrovirus	10455
## 1631197		<NA>	1993631
## 808604		Acinetobacter phage ZZ1	1049283
## 289723		unclassified Lymphocystivirus	345690
## 212992	Lymphocystis disease virus - isolate China		256729
##	parent	rank	DeltaFreq
## 8671	28883	family	8.009692e-04
## 462518	10744	subfamily	5.754744e-04
## 879134	542835	no rank	5.197064e-04
## 322098	1132574	species	3.038549e-04
## 159560	10744	no rank	2.775774e-04
## 1559892	10662	genus	2.510449e-04
## 1559894	1912144	no rank	2.510449e-04
## 1118976	1912146	species	2.510449e-04
## 1009729	196895	species	1.895863e-04
## 159559	10699	no rank	1.544434e-04
## 8639	28883	family	1.487937e-04
## 1009728	196896	species	1.406301e-04

##	687480	196894	species	9.314241e-05
##	735496	196895	species	9.242370e-05
##	378416	1132574	species	7.612445e-05
##	687481	196894	species	7.298131e-05
##	223780	542835	species	5.697025e-05
##	322108	1132574	species	4.547871e-05
##	1192468	196896	species	2.441881e-05
##	262244	549779	genus	1.756756e-05
##	940040	196896	species	1.614163e-05
##	683915	1132574	species	1.545808e-05
##	468533	10239	family	1.510409e-05
##	1009730	1132574	species	1.381949e-05
##	379170	1132574	species	1.381261e-05
##	8338	10240	subfamily	1.374775e-05
##	603220	1132574	species	1.304459e-05
##	678638	880158	species	1.251979e-05
##	2053675	315393	no rank	1.179460e-05
##	378415	1132574	species	9.800027e-06
##	2104539	10699	genus	9.489416e-06
##	2104744	2560124	species	9.489416e-06
##	153940	196894	species	9.342619e-06
##	1209012	10239	family	9.290438e-06
##	603237	1132574	species	8.900089e-06
##	2104542	10662	genus	8.632982e-06
##	8339	10284	genus	8.020100e-06
##	848500	2501774	species	7.377859e-06
##	997642	2501774	species	7.279637e-06
##	1657371	455363	species	7.079927e-06
##	145321	10501	genus	6.922254e-06
##	1561419	1198137	species	6.584087e-06
##	30959	558016	species	6.220561e-06
##	173522	315393	species	5.772959e-06
##	1307641	10699	genus	5.745403e-06
##	2106591	1623306	no rank	5.745403e-06
##	1186356	2562717	species	5.745403e-06
##	1009731	1132574	species	5.697560e-06
##	605035	1132574	species	5.660594e-06
##	44717	40070	species	5.578320e-06
##	2120242	2559587	no rank	5.527942e-06
##	1568411	2585030	no rank	5.527942e-06
##	861174	1511852	no rank	5.228206e-06
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##	1561548	1198136	genus	4.689258e-06
##	1561571	1914165	species	4.689258e-06
##	1798558	10239	no rank	4.607100e-06
##	839518	10662	species	4.529782e-06
##	1620894	10744	genus	4.455116e-06
##	1853472	1982587	no rank	4.455116e-06
##	1525883	2269062	species	4.455116e-06
##	934115	1198136	genus	4.423221e-06
##	21153	10241	no rank	4.301445e-06
##	1565537	10699	genus	4.043748e-06
##	1565538	1918718	species	4.043748e-06
##	1620399	1982076	species	4.035408e-06
##	8296	10239	family	4.032255e-06
##	31012	2204151	no rank	3.993485e-06

##	510604	1132574	species	3.964010e-06
##	58589	10284	species	3.908560e-06
##	379169	1132574	species	3.899882e-06
##	9825	10239	no rank	3.869790e-06
##	1049926	1978007	species	3.719725e-06
##	1209014	1511852	genus	3.706314e-06
##	12831	1511854	species	3.706314e-06
##	1366668	196894	species	3.610628e-06
##	2105025	2560128	species	3.526552e-06
##	529863	336487	species	3.456957e-06
##	1568567	1922348	species	3.398238e-06
##	12080	10286	species	3.377219e-06
##	1562148	1911928	genus	3.329376e-06
##	1619492	1914850	species	3.329376e-06
##	1032431	196894	species	3.281534e-06
##	26327	181083	species	3.194189e-06
##	18001	10485	species	3.132934e-06
##	169792	558016	species	3.080020e-06
##	1657483	51368	family	3.002818e-06
##	55087	2204151	no rank	2.970923e-06
##	1101730	79205	species	2.970923e-06
##	1176678	455363	species	2.958976e-06
##	1239831	1110703	species	2.822323e-06
##	1620398	10699	genus	2.758533e-06
##	1452629	2562654	species	2.737514e-06
##	1569421	1922348	species	2.676259e-06
##	2104968	2560128	species	2.554483e-06
##	2106561	2560128	no rank	2.551947e-06
##	990782	10365	species	2.548679e-06
##	117557	692606	species	2.530195e-06
##	8485	10239	family	2.446119e-06
##	1578174	12429	species	2.371452e-06
##	1268625	558016	species	2.365648e-06
##	1659387	2025358	species	2.363112e-06
##	1307615	10699	genus	2.336289e-06
##	1796195	1623278	no rank	2.336289e-06
##	1060858	2201166	species	2.336289e-06
##	1552147	2023203	species	2.336289e-06
##	1726857	2060084	species	2.173207e-06
##	105097	10744	species	2.123899e-06
##	986221	944644	species	2.123899e-06
##	9528	464095	family	2.123899e-06
##	1051673	12058	genus	2.123899e-06
##	1051674	1330069	species	2.123899e-06
##	1619001	1980410	family	2.123899e-06
##	20860	1980416	no rank	2.123899e-06
##	1293694	39718	species	2.123899e-06
##	21152	10240	no rank	2.077522e-06
##	1616799	196895	no rank	2.049965e-06
##	20606	40069	species	1.983639e-06
##	678186	1892568	species	1.908973e-06
##	1075906	196896	species	1.901366e-06
##	40455	10284	genus	1.819092e-06
##	40456	62098	species	1.819092e-06
##	8486	10482	genus	1.794804e-06
##	8487	10483	species	1.794804e-06

##	1464651	196894	species	1.696583e-06
##	8387	10319	species	1.595826e-06
##	268250	181083	species	1.582415e-06
##	8317	10260	species	1.516089e-06
##	281375	10260	no rank	1.492534e-06
##	8329	10241	genus	1.484193e-06
##	8330	10275	species	1.484193e-06
##	145322	10501	genus	1.430604e-06
##	8467	558016	species	1.383436e-06
##	2104503	2560065	subfamily	1.383436e-06
##	1511766	2560081	genus	1.383436e-06
##	34655	1857846	species	1.383436e-06
##	145323	10501	genus	1.370025e-06
##	191389	181085	species	1.370025e-06
##	72700	10282	species	1.335594e-06
##	1483257	1813598	species	1.335594e-06
##	852827	51368	species	1.298627e-06
##	21332	10357	genus	1.271804e-06
##	366040	40272	no rank	1.271804e-06
##	1584736	431037	species	1.271804e-06
##	1325021	558016	species	1.255856e-06
##	1684541	1110703	species	1.221425e-06
##	604342	880158	species	1.192798e-06
##	289623	2570372	species	1.152563e-06
##	135457	10319	species	1.152563e-06
##	1135710	1892568	species	1.139151e-06
##	38098	558016	species	1.107256e-06
##	321766	181083	species	1.091309e-06
##	21198	10780	subfamily	1.043466e-06
##	149765	40120	no rank	1.043466e-06
##	1556008	185880	species	1.043466e-06
##	833061	2005509	species	1.040930e-06
##	159600	10239	family	1.038394e-06
##	206416	196937	genus	1.038394e-06
##	286729	249585	species	1.038394e-06
##	1569287	1922348	species	1.024983e-06
##	304688	558017	species	1.009035e-06
##	470846	12429	species	9.905518e-07
##	1726855	2060084	species	9.778728e-07
##	216062	1198136	species	9.771401e-07
##	75165	558016	species	9.611925e-07
##	276618	196896	species	9.611925e-07
##	1012076	10239	family	9.611925e-07
##	1012077	1285590	genus	9.611925e-07
##	1012079	1285591	species	9.611925e-07
##	254981	558016	species	9.108140e-07
##	372872	542835	species	8.604355e-07
##	891963	10552	species	8.470238e-07
##	2050490	2497569	subphylum	8.470238e-07
##	2050494	2497570	class	8.470238e-07
##	8995	2497574	order	8.470238e-07
##	526001	11157	no rank	8.470238e-07
##	1535263	644608	genus	8.470238e-07
##	1672183	1884457	species	8.470238e-07
##	1505477	558016	species	7.654829e-07
##	1356888	40069	species	7.647502e-07

```

## [532] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota"
## [533] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Ascomycota saccharomyceta Saccharomycota"
## [534] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Ascomycota saccharomyceta Saccharomycota"
## [535] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [536] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [537] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [538] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [539] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [540] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [541] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [542] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [543] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [544] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [545] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [546] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [547] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [548] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [549] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [550] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [551] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [552] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [553] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [554] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [555] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [556] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [557] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [558] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [559] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [560] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [561] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [562] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [563] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [564] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [565] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [566] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [567] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [568] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [569] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [570] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [571] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [572] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [573] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [574] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [575] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [576] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [577] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [578] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [579] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [580] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [581] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [582] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [583] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"
## [584] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Agaricomycotina Tremetaceae"

```

There are generally a higher frequency of viruses at Maycocks than at Bellairs. (Recall that almost all taxa are higher at Bellairs than Maycocks.) Adenoviridae, Alphaviridae, Baculoviridae are higher at Maycocks. CHECK THEIR HOSTS. Caudovirales are consistently higher at Bellairs. We should investigate this Shawn - it seems that they are known to infect reefs. <https://www.sciencedirect.com/topics/biochemistry-genetics-and-molecular-biology/>

```

## [574] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria"
## [575] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria Myxogastromycetidae"
## [576] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria Myxogastromycetidae"
## [577] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria Myxogastromycetidae"
## [578] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria Myxogastromycetidae"
## [579] "root cellular organisms Eukaryota Amoebozoa Mycetozoa Myxogastria Myxogastromycetidae"
## [580] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Ustilaginomycotina"
## [581] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Ustilaginomycotina"
## [582] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Ustilaginomycotina"
## [583] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Ustilaginomycotina"
## [584] "root cellular organisms Eukaryota Opisthokonta Fungi Dikarya Basidiomycota Ustilaginomycotina"

```

Bellairs has a higher fraction of Eukaryota than Maycocks (7%) and most of this change is in the Viridiplantae as discussed above. Phylum Chlorophyta is one of the few cases where the frequency is higher at Maycocks. The analysis here also highlights *Nicotiana attenuata*, *Olea europaea*, *Elaeis guineensis*, *Arachis ipaensis*, *Cajanus cajan*, *Gossypium raimondii*, *Malus domestica*, *Cynara cardunculus*.

```

may.big <- euk[ which(euk$DeltaFreq < -0.00), ] ; nrow(may.big) # 0.001 was too stringent
## [1] 59

```

```
may.big <- may.big[ order( may.big$path, may.big$DeltaFreq ), ]
may.big[ , c(1:4,15 )]
```

##		name	tax_id	parent
## 15829		Myxogastria	33680	142796
## 106512		Myxogastromycetidae	137627	33680
## 4675		Physariida	5789	137627
## 865673		Physaraceae	1115744	5789
## 4676		Physarum	5790	1115744
## 4677		Physarum polycephalum	5791	5790
## 15830		Euglenozoa	33682	2759
## 4571		Kinetoplastida	5653	33682
## 4572		Trypanosomatidae	5654	5653
## 1012741		Leishmaniinae	1286322	5654
## 4576		Leishmania	5658	1286322
## 19857		Leishmania	38568	5658
## 19860	Leishmania donovani species complex		38574	38568
## 4586		Leishmania infantum	5671	38574
## 19865	Leishmania major species complex		38581	38568
## 4581		Leishmania major	5664	38581
## 19866	Leishmania mexicana species complex		38582	38568
## 4582		Leishmania mexicana	5665	38582
## 19058		Viannia	37616	5658
## 19059	Leishmania braziliensis species complex		37617	37616
## 4578		Leishmania braziliensis	5660	37617
## 806957		Zymoseptoria	1047167	93133
## 806961		Zymoseptoria tritici	1047171	1047167
## 17430		Chaetomiaceae	35718	5139
## 1566519		Thermothelomyces	1920207	35718
## 54552	Thermothelomyces thermophilus		78579	1920207
## 17431		Thielavia	35719	35718
## 17432		Thielavia terrestris	35720	35719
## 15475		Eremothecium gossypii	33169	33170
## 347659		Trichomonascaceae	410830	4892
## 347658		Sugiyamaella	410829	410830
## 616748	Sugiyamaella lignohabitans		796027	410829
## 4242		Basidiomycota	5204	451864
## 384832		Ustilaginomycotina	452284	5204
## 1232386		Malasseziomycetes	1538075	452284
## 128470		Malasseziales	162474	1538075
## 593868		Malasseziaceae	742845	162474
## 34359		Malassezia	55193	742845
## 52906	Malassezia restricta		76775	55193
## 4283		Ustilaginomycetes	5257	452284
## 4293		Ustilaginales	5267	5257
## 4294		Ustilaginaceae	5268	5267
## 41505		Sporisorium	63265	5268
## 231048	Sporisorium graminicola		280036	63265
## 4295		Ustilago	5269	5268
## 4296	Ustilago maydis		5270	5269
## 2402		Chlorophyta	3041	33090
## 797843		Mamiellophyceae	1035538	3041
## 10591		Mamiellales	13792	1035538
## 47250		Ostreococcus	70447	1525212
## 1853330		<NA>	2268852	70447
## 199954	Ostreococcus sp. 'lucimarinus'		242159	2268852

## 47251		Ostreococcus tauri	70448	70447
## 22758		Mamiellaceae	41873	13792
## 20093		Micromonas	38832	41873
## 245354		Micromonas commoda	296587	38832
## 1329630		Sorghinae	1648028	147429
## 3726		Sorghum	4557	1648028
## 3727		Sorghum bicolor	4558	4557
##	rank	DeltaFreq		
## 15829	no rank	-1.080433e-06		
## 106512	subclass	-1.080433e-06		
## 4675	order	-1.080433e-06		
## 865673	family	-1.080433e-06		
## 4676	genus	-1.080433e-06		
## 4677	species	-1.080433e-06		
## 15830	no rank	-2.256913e-06		
## 4571	order	-2.256913e-06		
## 4572	family	-2.256913e-06		
## 1012741	subfamily	-6.810950e-05		
## 4576	genus	-6.810950e-05		
## 19857	subgenus	-4.183369e-05		
## 19860	species group	-2.443317e-05		
## 4586	species	-3.156145e-05		
## 19865	species group	-1.717314e-06		
## 4581	species	-1.717314e-06		
## 19866	species group	-1.568320e-05		
## 4582	species	-1.568320e-05		
## 19058	subgenus	-2.627582e-05		
## 19059	species group	-2.988408e-05		
## 4578	species	-2.988408e-05		
## 806957	genus	-6.695209e-06		
## 806961	species	-6.695209e-06		
## 17430	family	-5.301423e-05		
## 1566519	genus	-3.172301e-05		
## 54552	species	-3.172301e-05		
## 17431	genus	-2.129122e-05		
## 17432	species	-2.129122e-05		
## 15475	species	-2.084419e-05		
## 347659	family	-2.792396e-06		
## 347658	genus	-2.792396e-06		
## 616748	species	-2.792396e-06		
## 4242	phylum	-1.113386e-05		
## 384832	subphylum	-4.586995e-05		
## 1232386	class	-2.072606e-07		
## 128470	order	-2.072606e-07		
## 593868	family	-2.072606e-07		
## 34359	genus	-2.072606e-07		
## 52906	species	-2.072606e-07		
## 4283	class	-4.566269e-05		
## 4293	order	-4.566269e-05		
## 4294	family	-4.566269e-05		
## 41505	genus	-6.575178e-06		
## 231048	species	-6.575178e-06		
## 4295	genus	-3.908751e-05		
## 4296	species	-3.908751e-05		
## 2402	phylum	-1.939138e-03		
## 797843	class	-1.939138e-03		

```
## 10591      order -1.939138e-03
## 47250      genus -1.445043e-04
## 1853330    no rank -1.279097e-04
## 199954     species -1.279097e-04
## 47251     species -1.659463e-05
## 22758      family -1.994242e-03
## 20093      genus -1.994242e-03
## 245354     species -1.994242e-03
## 1329630    subtribe -9.637653e-06
## 3726       genus -9.637653e-06
## 3727       species -9.637653e-06
```

```
bel.big <- euk[ which(euk$DeltaFreq > -0.00), ] ; nrow(bel.big) # 0.001 was too stringent
```

```
## [1] 525
```

```
bel.big <- bel.big[ order( -bel.big$DeltaFreq ), ]
```

```
bel.big[ , c(1:4,15 )]
```

```
##           name  tax_id  parent
## 2189      Eukaryota    2759  131567
## 17254     Streptophyta  35493   33090
## 100789    Streptophytina 131221   35493
## 2531      Embryophyta   3193  131221
## 36888     Tracheophyta  58023   3193
## 54511     Euphyllophyta 78536   58023
## 36889     Spermatophyta 58024   78536
## 2706      Magnoliopsida  3398   58024
## 1142173   Mesangiospermae 1437183   3398
## 15400     Viridiplantae  33090   2759
## 47939     eudicotyledons 71240  1437183
## 66320     Gunneridae    91827   71240
## 1142189   Pentapetalae 1437201   91827
## 47969     rosids        71275  1437201
## 66328     fabids        91835   71275
## 47968     asterids      71274  1437201
## 48652     Fabales       72025   91835
## 3064      Fabaceae      3803    72025
## 3075      Papilionoideae 3814    3803
## 1823180   <NA> 2231393    3814
## 66370     lamiids       91888   71274
## 66329     malvids       91836   71275
## 3311      Solanales     4069   91888
## 3312      Solanaceae    4070    4069
## 1823169   <NA> 2231382  2231393
## 15464     Opisthokonta  33154   2759
## 360071     Solanoideae  424551   4070
## 1824645   <NA> 2233855  2231382
## 129670     Phaseoleae   163735  2233855
## 15503      Metazoa      33208   33154
## 4896      Eumetazoa     6072   33208
## 15505      Bilateria    33213   6072
## 15683      Deuterostomia 33511   33213
## 6209      Chordata      7711   33511
## 64277      Craniata     89593   7711
## 6238      Vertebrata    7742   89593
## 6258      Gnathostomata 7776    7742
## 88716     Teleostomi   117570   7776
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## 88717	Euteleostomi	117571	117570
## 6664	Sarcopterygii	8287	117571
## 1059069	Dipnotetrapodomorpha	1338369	8287
## 15231	Tetrapoda	32523	1338369
## 15232	Amniota	32524	32523
## 21676	Mammalia	40674	32524
## 15233	Theria	32525	40674
## 7552	Eutheria	9347	32525
## 1142005	Boreoeutheria	1437010	9347
## 261158	Euarchontoglires	314146	1437010
## 7639	Primates	9443	314146
## 317280	Haplorrhini	376913	9443
## 261292	Simiiformes	314293	376913
## 7705	Catarrhini	9526	314293
## 261294	Hominoidea	314295	9526
## 7768	Hominidae	9604	314295
## 169391	Homininae	207598	9604
## 7769	Homo	9605	207598
## 7770	Homo sapiens	9606	9605
## 3639	Liliopsida	4447	1437183
## 1142187	Petrosaviidae	1437197	4447
## 22820	Malvales	41938	91836
## 2913	Malvaceae	3629	41938
## 360083	Capsiceae	424564	424551
## 3313	Capsicum	4071	424564
## 3314	Capsicum annuum	4072	4071
## 176137	Malvoideae	214907	3629
## 2916	Gossypium	3633	214907
## 66366	campanulids	91882	71274
## 3885	commelinids	4734	1437197
## 2975	Brassicales	3699	91836
## 2976	Brassicaceae	3700	3699
## 3436	Asterales	4209	91882
## 3437	Asteraceae	4210	4209
## 1823174	<NA>	2231387	2231393
## 129662	Dalbergieae	163725	2231387
## 1823177	<NA>	2231390	163725
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## 3015	Rosales	3744	91835
## 755366	Brassicaceae	981071	3700
## 2981	Brassica	3705	981071
## 3172	Vigna	3913	163735
## 76005	Asteroideae	102804	4210
## 702345	Heliantheae alliance	911341	102804
## 76014	Heliantheae	102814	911341
## 3457	Helianthus	4231	102814
## 3458	Helianthus annuus	4232	4231
## 3016	Rosaceae	3745	3744
## 360093	Solaneae	424574	424551
## 3343	Solanum	4107	424574
## 29229	Lycopersicon	49274	4107
## 22665	Ranunculales	41768	1437183
## 2767	Papaveraceae	3465	41768
## 1165039	Papaveroideae	1462614	3465
## 2770	Papaver	3468	1462614
## 2771	Papaver somniferum	3469	3468

## 20086	Poales	38820	4734
## 2918	Gossypium hirsutum	3635	3633
## 1824628	<NA>	2233838	2231382
## 1824629	<NA>	2233839	2233838
## 3372	Lamiales	4143	91888
## 360074	Nicotianoideae	424554	4070
## 360082	Nicotianeae	424562	424554
## 3325	Nicotiana	4085	424562
## 29353	Nicotiana attenuata	49451	4085
## 3106	Glycine	3846	163735
## 1165036	Soja	1462606	3846
## 3663	Poaceae	4479	38820
## 2927	Malpighiales	3646	91835
## 3898	Fungi	4751	33154
## 4014	Ascomycota	4890	451864
## 384478	Dikarya	451864	4751
## 587287	saccharomyceta	716545	4890
## 100097	Arachis ipaensis	130454	3817
## 2986	Brassica rapa	3711	3705
## 136645	Amygdaloideae	171637	3745
## 3373	Oleaceae	4144	4143
## 361490	Oleeae	426106	4144
## 3374	Olea	4145	426106
## 3375	Olea europaea	4146	4145
## 21578	Arecales	40551	4734
## 3865	Arecaceae	4710	40551
## 134884	Arecoideae	169697	4710
## 134891	Cocoseae	169705	169697
## 134908	Elaeidinae	169729	169705
## 31486	Elaeis	51952	169729
## 31487	Elaeis guineensis	51953	51952
## 1823171	<NA>	2231384	2231393
## 1823172	<NA>	2231385	2231384
## 129665	Genisteae	163729	2231385
## 3129	Lupinus	3869	163729
## 3131	Lupinus angustifolius	3871	3869
## 12212	Solanum pennellii	28526	49274
## 15788	Alveolata	33630	2759
## 4680	Apicomplexa	5794	33630
## 13226	Gossypium arboreum	29729	3633
## 3079	Arachis hypogaea	3818	3817
## 754509	Camelineae	980083	3700
## 115178	PACMAD clade	147370	4479
## 115177	Panicoideae	147369	147370
## 358308	Aconoidasida	422676	5794
## 47938	Cucurbitales	71239	91835
## 2931	Cucurbitaceae	3650	71239
## 3300	Gentianales	4055	91888
## 11175	Rubiaceae	24966	4055
## 134815	Ixoroideae	169618	24966
## 1608227	<NA>	1968429	169618
## 1608226	<NA>	1968428	1968429
## 134834	Coffeeae	169640	1968428
## 10278	Coffea	13442	169640
## 3321	Solanum lycopersicum	4081	49274
## 115327	Saccharomycotina	147537	716545

## 4015	Saccharomycetes	4891	147537
## 4016	Saccharomycetales	4892	4891
## 3143	Phaseolus	3883	163735
## 3145	Phaseolus vulgaris	3885	3883
## 129660	Cicereae	163722	2233839
## 3086	Cicer	3826	163722
## 3087	Cicer arietinum	3827	3826
## 2821	Caryophyllales	3524	1437201
## 1463835	Chenopodiaceae	1804623	3524
## 1463833	Betoideae	1804621	1804623
## 2849	Beta	3554	1804621
## 128004	Beta vulgaris	161934	3554
## 3176	Vigna unguiculata	3917	3913
## 4701	Haemosporida	5819	422676
## 1321768	Plasmodiidae	1639119	5819
## 4702	Plasmodium	5820	1639119
## 49992	Asparagales	73496	1437197
## 21579	Asparagaceae	40552	73496
## 576395	Asparagoideae	703533	40552
## 3843	Asparagus	4685	703533
## 3844	Asparagus officinalis	4686	4685
## 3080	Cajanus	3820	163735
## 3081	Cajanus cajan	3821	3820
## 136646	Rosoideae	171638	3745
## 3107	Glycine max	3847	1462606
## 48011	Camelina	71323	980083
## 65253	Camelina sativa	90675	71323
## 124275	Vigna radiata	157791	3913
## 13227	Gossypium raimondii	29730	3633
## 129676	Trifolieae	163742	2233839
## 3137	Medicago	3877	163742
## 3140	Medicago truncatula	3880	3877
## 180011	Carduoideae	219103	4210
## 76017	Cardueae	102818	219103
## 593122	Carduinae	742010	102818
## 3488	Cynara	4264	742010
## 3489	Cynara cardunculus	4265	4264
## 589651	Maleae	721813	171637
## 3019	Malus	3749	721813
## 3020	Malus domestica	3750	3749
## 15792	Stramenopiles	33634	2759
## 2252	Bacillariophyta	2836	33634
## 2966	Salicaceae	3688	3646
## 196545	Saliceae	238069	3688
## 2967	Populus	3689	238069
## 2971	Populus trichocarpa	3694	3689
## 3108	Glycine soja	3848	1462606
## 3227	Euphorbiaceae	3977	3646
## 194343	Crotonoideae	235631	3977
## 194585	Manihoteae	235883	235631
## 3232	Manihot	3982	235883
## 3233	Manihot esculenta	3983	3982
## 2983	Brassica napus	3708	3705
## 3173	Vigna angularis	3914	3913
## 15944	Coscinodiscophyceae	33836	2836
## 15954	Thalassiosirophycidae	33846	33836

## 15955	Thalassiosirales	33847	33846
## 12790	Thalassiosiraceae	29202	33847
## 16991	Thalassiosira	35127	29202
## 16992	Thalassiosira pseudonana	35128	35127
## 2542	Bryophyta	3208	3193
## 341946	Bryophytina	404260	3208
## 2547	Bryopsida	3214	404260
## 86017	Funariidae	114656	3214
## 2548	Funariales	3215	114656
## 2549	Funariaceae	3216	3215
## 2550	Physcomitrella	3217	3216
## 2551	Physcomitrella patens	3218	3217
## 10279	Coffea arabica	13443	13442
## 66327	rosids incertae sedis	91834	71275
## 341373	Vitales	403667	91834
## 2891	Vitaceae	3602	403667
## 1880857	<NA>	2304100	3602
## 2892	Vitis	3603	2304100
## 13250	Vitis vinifera	29760	3603
## 1329631	Tripsacinae	1648029	147429
## 3741	Zea	4575	1648029
## 3743	Zea mays	4577	4575
## 1329634	Andropogonodae	1648033	147369
## 115227	Andropogoneae	147429	1648033
## 2897	Rhamnaceae	3608	3744
## 271226	Paliureae	325284	3608
## 48781	Ziziphus	72171	325284
## 272773	Ziziphus jujuba	326968	72171
## 3281	Apiales	4036	91882
## 306060	Apiineae	364270	4036
## 3282	Apiaceae	4037	364270
## 199700	Apiioideae	241778	4037
## 199711	Scandiceae	241789	241778
## 199718	Daucinae	241799	241789
## 3283	Daucus	4038	241799
## 1524889	Daucus sect. Daucus	1873447	4038
## 3284	Daucus carota	4039	1873447
## 589645	Amygdaleae	721805	171637
## 3023	Prunus	3754	721805
## 915507	Rosoideae incertae sedis	1176516	171638
## 3032	Rosa	3764	1176516
## 50962	Rosa chinensis	74649	3764
## 4017	Saccharomycetaceae	4893	4892
## 115328	Pezizomycotina	147538	716545
## 587288	leotiomyceta	716546	147538
## 773580	Cucurbiteae	1003878	3650
## 2941	Cucurbita	3660	1003878
## 2944	Cucurbita pepo	3663	3660
## 22819	Sapindales	41937	91836
## 11123	Rutaceae	23513	41937
## 1399065	Aurantioideae	1728959	23513
## 2151	Citrus	2706	1728959
## 2155	Citrus sinensis	2711	2706
## 100096	Arachis duranensis	130453	3817
## 3778	Zingiberales	4618	4734
## 3797	Musaceae	4637	4618

## 3800	Musa	4640	4637
## 3801	Musa acuminata	4641	4640
## 773579	Benincaseae	1003877	3650
## 2936	Cucumis	3655	1003877
## 2940	Cucumis sativus	3659	3655
## 301288	BOP clade	359160	4479
## 586732	sordariomyceta	715989	716546
## 1329637	Panicodae	1648036	147369
## 115226	Paniceae	147428	1648036
## 176139	Byttnerioideae	214909	3629
## 2922	Theobroma	3640	214909
## 2923	Theobroma cacao	3641	3640
## 2987	Brassica oleracea	3712	3705
## 3407	Pedaliaceae	4180	4143
## 3408	Sesamum	4181	4180
## 3409	Sesamum indicum	4182	4181
## 115337	Sordariomycetes	147550	715989
## 29287	Coffea eugenoides	49369	13442
## 15397	Dictyostelids	33083	142796
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## 473000	Amoebozoa	554915	2759
## 111164	Mycetozoa	142796	554915
## 613480	Debaryomycetaceae	766764	4892
## 3773	Bromeliaceae	4613	38820
## 1557430	Bromelioideae	1909378	4613
## 3774	Ananas	4614	1909378
## 3775	Ananas comosus	4615	4614
## 1229909	Candida/Lodderomyces clade	1535325	766764
## 1229910	Candida	1535326	1535325
## 1019009	Cenchrinae	1293361	147428
## 3723	Setaria	4554	1293361
## 3724	Setaria italica	4555	4554
## 182805	Hypocreomycetidae	222543	147550
## 589630	Potentilleae	721789	171638
## 921645	Fragariinae	1184124	721789
## 3017	Fragaria	3746	1184124
## 36788	Fragaria vesca	57918	3746
## 354355	Plasmodium (Plasmodium)	418103	5820
## 75387	Prunus mume	102107	3754
## 3028	Prunus persica	3760	3754
## 4178	Hypocreales	5125	222543
## 82735	Nectriaceae	110618	5125
## 4478	Fusarium	5506	110618
## 2388	Cryptophyta	3027	2759
## 115176	Pooideae	147368	359160
## 115193	Brachypodieae	147385	147368
## 10678	Brachypodium	15367	147385
## 10679	Brachypodium distachyon	15368	15367
## 2977	Arabidopsis	3701	980083
## 2978	Arabidopsis thaliana	3702	3701
## 354353	Plasmodium (Vinckeia)	418101	5820
## 115175	Oryzoideae	147367	359160
## 115188	Oryzeae	147380	147367

## 1329623	Oryzinae	1648021	147380
## 3699	Oryza	4527	1648021
## 499512	Pyrenomonadales	589342	3027
## 499513	Geminigeraceae	589343	589342
## 34671	Guillardia	55528	589343
## 34672	Guillardia theta	55529	55528
## 484048	Fusarium sambucinum species complex	569360	5506
## 4737	Plasmodium malariae	5858	418103
## 22759	Bathycoccus	41874	1525212
## 22760	Bathycoccus prasinos	41875	41874
## 354359	Plasmodium (Laverania)	418107	5820
## 1019013	Panicinae	1293365	147428
## 3710	Panicum	4539	1293365
## 1720017	<NA>	2100772	4539
## 168043	Panicum hallii	206008	2100772
## 15957	Bacillariophyceae	33849	2836
## 15958	Bacillariophycidae	33850	33849
## 20026	Naviculales	38748	33850
## 20027	Phaeodactylaceae	38749	38748
## 2256	Phaeodactylum	2849	38749
## 2257	Phaeodactylum tricornutum	2850	2849
## 4742	Piroplasmida	5863	422676
## 170214	Plasmodium coatneyi	208452	5820
## 85396	Tetrapisispora	113604	4893
## 23209	Candida dubliniensis	42374	1535326
## 74433	Fusarium pseudograminearum	101028	569360
## 3704	Oryza brachyantha	4533	4527
## 4456	Candida albicans	5476	1535326
## 229507	Naumovozyma	278028	4893
## 3702	Oryza sativa	4530	4527
## 11846	Theileriidae	27994	5863
## 4752	Theileria	5873	27994
## 4740	Plasmodium yoelii	5861	418101
## 354356	Plasmodium (Haemamoeba)	418104	5820
## 60678	Plasmodium relictum	85471	418104
## 115335	Leotiomycetes	147548	715989
## 4221	Helotiales	5178	147548
## 12607	Sclerotiniaceae	28983	5178
## 15497	Botrytis	33196	28983
## 21584	Botrytis cinerea	40559	33196
## 1007254	Conoidasida	1280412	5794
## 4681	Coccidia	5796	1280412
## 51953	Eucoccidiorida	75739	5796
## 358684	Eimeriorina	423054	75739
## 828763	Tetrapisispora blattae	1071379	113604
## 4703	Plasmodium berghei	5821	418101
## 182806	Sordariomycetidae	222544	147550
## 11289	Naumovozyma dairenensis	27289	278028
## 521307	Magnaporthales	639021	222544
## 2076680	<NA>	2528436	639021
## 28582	Pyricularia	48558	2528436
## 463345	Rhizaria	543769	2759
## 105404	Cercozoa	136419	543769
## 12785	Chlorarachniophyceae	29197	136419
## 186868	Bigelowiella	227085	29197
## 186869	Bigelowiella natans	227086	227085

## 4706	Plasmodium chabaudi	5825	418101
## 499516	Cryptomonadales	589350	3027
## 47942	Kazachstania	71245	4893
## 136639	Fusarium fujikuroi species complex	171627	5506
## 4599	Trypanosoma	5690	5654
## 20843	Trypanozoon	39700	5690
## 4600	Trypanosoma brucei	5691	39700
## 4041	Saccharomyces	4930	4893
## 11288	Naumovozya castellii	27288	278028
## 227908	Candida orthopsilosis	273371	1535326
## 85400	Tetrapisispora phaffii	113608	113604
## 16948	Cryptosporidiidae	35082	423054
## 4688	Cryptosporidium	5806	35082
## 4689	Cryptosporidium parvum	5807	5806
## 115332	Eurotiomycetes	147545	716546
## 384485	Eurotiomycetidae	451871	147545
## 4116	Eurotiales	5042	451871
## 878136	Aspergillaceae	1131492	5042
## 4124	Aspergillus	5052	1131492
## 4197	Sordariaceae	5148	5139
## 4189	Neurospora	5140	5148
## 4190	Neurospora crassa	5141	5140
## 2293	Cryptomonadaceae	2896	589350
## 2391	Cryptomonas	3030	2896
## 2295	Cryptomonas paramecium	2898	3030
## 315016	Nakaseomyces	374468	4893
## 506759	Nakaseomyces/Candida clade	600669	374468
## 4458	[Candida] glabrata	5478	600669
## 4735	Plasmodium vivax	5855	418103
## 4730	Plasmodium knowlesi	5850	418103
## 528223	Plasmodium gaboni	647221	418107
## 1221289	Bathycoccaceae	1525212	13792
## 265362	Pyricularia oryzae	318829	48558
## 15279	Babesiidae	32594	5863
## 4743	Babesia	5864	32594
## 15476	Eremothecium	33170	4893
## 4691	Sarcocystidae	5809	423054
## 4714	Plasmodium falciparum	5833	418107
## 678953	Plasmodium sp. gorilla clade G2	880535	418107
## 4026	Kluyveromyces	4910	4893
## 4734	Plasmodium reichenowi	5854	418107
## 88353	Fusarium verticillioides	117187	171627
## 4754	Theileria parva	5875	5873
## 136641	Fusarium oxysporum species complex	171631	5506
## 4479	Fusarium oxysporum	5507	171631
## 25680	Eremothecium sinicaudum	45286	33170
## 613451	Scheffersomyces	766733	766764
## 4036	Scheffersomyces stipitis	4924	766733
## 1267340	Pyricularia pennisetigena	1578925	48558
## 4753	Theileria annulata	5874	5873
## 4708	Plasmodium cynomolgi	5827	418103
## 366985	Kazachstania africana	432096	71245
## 384480	Taphrinomycotina	451866	4890
## 115340	Schizosaccharomycetes	147554	451866
## 16395	Schizosaccharomycetales	34346	147554
## 4018	Schizosaccharomycetaceae	4894	34346

## 4019	Schizosaccharomyces	4895	4894
## 4020	Schizosaccharomyces pombe	4896	4895
## 4314	Agaricomycotina	5302	5204
## 122408	Tremellomycetes	155616	5302
## 4265	Tremellales	5234	155616
## 1535429	Cryptococcaceae	1884633	5234
## 4243	Cryptococcus	5206	1884633
## 898164	Pichiaceae	1156497	4892
## 4043	Saccharomyces cerevisiae	4932	4930
## 498932	Kazachstania naganishii	588726	71245
## 25679	Eremothecium cymbalariae	45285	33170
## 4031	Pichia	4919	1156497
## 4025	Pichia kudriavzevii	4909	4919
## 4132	Aspergillus oryzae	5062	5052
## 836747	Saccharomyces eubayanus	1080349	4930
## 4484	Fusarium graminearum	5518	569360
## 596780	Aspergillus fumigatus	746128	5052
## 45940	Theileria orientalis	68886	5873
## 4027	Kluyveromyces marxianus	4911	4910
## 791259	Glomerellales	1028384	222543
## 558234	Glomerellaceae	681950	1028384
## 4441	Colletotrichum	5455	681950
## 56608	Colletotrichum higginsianum	80884	5455
## 4049	Torulaspora	4948	4893
## 4050	Torulaspora delbrueckii	4950	4948
## 1546369	Cryptococcus neoformans species complex	1897064	5206
## 4244	Cryptococcus neoformans	5207	1897064
## 16399	Dipodascaceae	34353	4892
## 4051	Yarrowia	4951	34353
## 4052	Yarrowia lipolytica	4952	4951
## 4053	Zygosaccharomyces	4953	4893
## 4056	Zygosaccharomyces rouxii	4956	4953
## 16424	Clavicipitaceae	34397	5125
## 200634	Pochonia	243023	34397
## 231704	Pochonia chlamydosporia	280754	243023
## 4692	Toxoplasma	5810	5809
## 4693	Toxoplasma gondii	5811	5810
## 35705	Fusarium venenatum	56646	569360
## 4179	Fusarium fujikuroi	5127	171627
## 12622	Cercospora	29002	93133
## 92895	Cercospora beticola	122368	29002
## 499517	Hemiselmidae	589351	589350
## 53942	Hemiselmis	77924	589351
## 396410	Hemiselmis andersenii	464988	77924
## 4745	Babesia bigemina	5866	5864
## 12765	Neospora	29175	5809
## 12766	Neospora caninum	29176	29175
## 12609	Kluyveromyces lactis	28985	4910
## 4747	Babesia microti	5868	5864
## 4751	Theileria equi	5872	5873
## 4058	Debaryomyces	4958	766764
## 4059	Debaryomyces hansenii	4959	4958
## 4744	Babesia bovis	5865	5864
## 2192	Rhodophyta	2763	2759
## 2218	Bangiophyceae	2797	2763
## 220605	Cyanidiales	265318	2797

## 220603	Cyanidiaceae	265316	265318
## 25565	Cyanidioschyzon	45156	265316
## 25566	Cyanidioschyzon merolae	45157	45156
## 586705	dothideomyceta	715962	716546
## 115330	Dothideomycetes	147541	715962
## 384481	Dothideomycetidae	451867	147541
## 103498	Capnodiales	134362	451867
## 67504	Mycosphaerellaceae	93133	134362
## 84230	Fungi incertae sedis	112252	4751
## 4865	Microsporidia	6029	112252
## 4866	Apansporoblastina	6032	6029
## 18281	Unikaryonidae	36734	6032
## 4867	Encephalitozoon	6033	36734
## 248502	Lachancea	300275	4893
## 321041	Lachancea thermotolerans	381046	300275
## 1535432	Cryptococcus gattii species complex	1884637	5206
## 19183	Cryptococcus gattii VGI	37769	1884637
## 68881	Besnoitia	94642	5809
## 68882	Besnoitia besnoiti	94643	94642
## 4579	Leishmania donovani	5661	38574
## 87076	Phaffomycetaceae	115784	4892
## 392352	Komagataella	460517	115784
## 392353	Komagataella phaffii	460519	460517
## 4188	Sordariales	5139	222544
## 4757	Ciliophora	5878	33630
## 366796	Intramacronucleata	431838	5878
## 4859	Oligohymenophorea	6020	431838
## 15934	Peniculida	33825	6020
## 284599	Parameciidae	340080	33825
## 4760	Paramecium	5884	340080
## 4764	Paramecium tetraurelia	5888	5884
## 4868	Encephalitozoon cuniculi	6035	6033
## 19863	Leishmania guyanensis species complex	38579	37616
## 4590	Leishmania panamensis	5679	38579
## 37627	Encephalitozoon intestinalis	58839	6033
## 486263	Encephalitozoon romaleae	571949	6033
## 393054	Ogataea	461281	1156497
## 775499	Ogataea parapolyomorpha	1005962	461281
## 11830	Encephalitozoon hellem	27973	6033
##	rank DeltaFreq		
## 2189	superkingdom	6.910118e-02	
## 17254	phylum	5.967972e-02	
## 100789	subphylum	5.967972e-02	
## 2531	no rank	5.967972e-02	
## 36888	no rank	5.889675e-02	
## 54511	no rank	5.889675e-02	
## 36889	no rank	5.889675e-02	
## 2706	no rank	5.889675e-02	
## 1142173	no rank	5.889675e-02	
## 15400	kingdom	5.774058e-02	
## 47939	no rank	5.086511e-02	
## 66320	no rank	5.086511e-02	
## 1142189	no rank	5.086511e-02	
## 47969	no rank	3.219272e-02	
## 66328	no rank	2.110225e-02	
## 47968	no rank	1.754127e-02	

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## 48652      order 1.451827e-02
## 3064       family 1.451827e-02
## 3075      subfamily 1.451827e-02
## 1823180    no rank 1.451827e-02
## 66370     no rank 1.296676e-02
## 66329     no rank 1.033522e-02
## 3311      order 9.637549e-03
## 3312      family 9.637549e-03
## 1823169    no rank 9.308632e-03
## 15464     no rank 8.107872e-03
## 360071     subfamily 7.640661e-03
## 1824645    no rank 7.171571e-03
## 129670     tribe 7.171571e-03
## 15503     kingdom 6.253884e-03
## 4896      no rank 6.253884e-03
## 15505     no rank 6.253884e-03
## 15683     no rank 6.253884e-03
## 6209      phylum 6.253884e-03
## 64277     subphylum 6.253884e-03
## 6238      no rank 6.253884e-03
## 6258      no rank 6.253884e-03
## 88716     no rank 6.253884e-03
## 88717     no rank 6.253884e-03
## 6664      superclass 6.253884e-03
## 1059069    no rank 6.253884e-03
## 15231     no rank 6.253884e-03
## 15232     no rank 6.253884e-03
## 21676     class 6.253884e-03
## 15233     no rank 6.253884e-03
## 7552      no rank 6.253884e-03
## 1142005    no rank 6.253884e-03
## 261158    superorder 6.253884e-03
## 7639      order 6.253884e-03
## 317280    suborder 6.253884e-03
## 261292    infraorder 6.253884e-03
## 7705      parvorder 6.253884e-03
## 261294    superfamily 6.253884e-03
## 7768      family 6.253884e-03
## 169391    subfamily 6.253884e-03
## 7769      genus 6.253884e-03
## 7770      species 6.253884e-03
## 3639      class 5.534685e-03
## 1142187    subclass 5.534685e-03
## 22820     order 5.288041e-03
## 2913      family 5.288041e-03
## 360083     tribe 4.990573e-03
## 3313      genus 4.990573e-03
## 3314      species 4.990573e-03
## 176137    subfamily 4.730230e-03
## 2916      genus 4.730230e-03
## 66366     no rank 4.574511e-03
## 3885      no rank 4.436938e-03
## 2975      order 4.435340e-03
## 2976      family 4.435340e-03
## 3436      order 3.845460e-03
## 3437      family 3.845460e-03

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## 1823174	no rank	3.773391e-03
## 129662	tribe	3.773391e-03
## 1823177	no rank	3.773391e-03
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## 3015	order	3.464338e-03
## 755366	tribe	3.103686e-03
## 2981	genus	3.103686e-03
## 3172	genus	2.985382e-03
## 76005	subfamily	2.860277e-03
## 702345	no rank	2.860277e-03
## 76014	tribe	2.860277e-03
## 3457	genus	2.860277e-03
## 3458	species	2.860277e-03
## 3016	family	2.726521e-03
## 360093	tribe	2.650088e-03
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## 29229	subgenus	2.650088e-03
## 22665	order	2.496957e-03
## 2767	family	2.496957e-03
## 1165039	subfamily	2.496957e-03
## 2770	genus	2.496957e-03
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## 360082	tribe	1.996887e-03
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## 29353	species	1.996887e-03
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## 1165036	subgenus	1.962825e-03
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## 2927	order	1.879242e-03
## 3898	kingdom	1.853988e-03
## 4014	phylum	1.853716e-03
## 384478	subkingdom	1.842582e-03
## 587287	no rank	1.818065e-03
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## 3373	family	1.575690e-03
## 361490	tribe	1.575690e-03
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## 31487	species	1.494775e-03
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## 1823172	no rank	1.436244e-03
## 129665	tribe	1.436244e-03

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## 3131	species	1.436244e-03
## 12212	species	1.432255e-03
## 15788	no rank	1.415183e-03
## 4680	phylum	1.410198e-03
## 13226	species	1.383619e-03
## 3079	species	1.374020e-03
## 754509	tribe	1.331653e-03
## 115178	no rank	1.314962e-03
## 115177	subfamily	1.314962e-03
## 358308	class	1.298758e-03
## 47938	order	1.240400e-03
## 2931	family	1.240400e-03
## 3300	order	1.225214e-03
## 11175	family	1.225214e-03
## 134815	subfamily	1.225214e-03
## 1608227	no rank	1.225214e-03
## 1608226	no rank	1.225214e-03
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## 3143	genus	1.146930e-03
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## 1463835	family	1.131116e-03
## 1463833	subfamily	1.131116e-03
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## 128004	species	1.131116e-03
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## 4701	order	1.123461e-03
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## 21579	family	1.097747e-03
## 576395	subfamily	1.097747e-03
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## 76017	tribe	9.851834e-04

## 593122	subtribe	9.851834e-04
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## 15954	subclass	7.878171e-04
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## 16991	genus	7.878171e-04
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## 2892	genus	7.552560e-04
## 13250	species	7.552560e-04
## 1329631	subtribe	7.542927e-04
## 3741	genus	7.542927e-04
## 3743	species	7.542927e-04
## 1329634	no rank	7.446551e-04
## 115227	tribe	7.446551e-04
## 2897	family	7.378168e-04
## 271226	tribe	7.378168e-04
## 48781	genus	7.378168e-04
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## 306060	suborder	7.290509e-04
## 3282	family	7.290509e-04
## 199700	subfamily	7.290509e-04
## 199711	tribe	7.290509e-04
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## 1524889	section	7.290509e-04
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## 11123	family	6.118372e-04
## 1399065	subfamily	6.118372e-04
## 2151	genus	6.118372e-04
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## 3797	family	6.043787e-04
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## 1329637	no rank	5.703071e-04
## 115226	tribe	5.703071e-04
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## 2923	species	5.578117e-04
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## 3407	family	5.283037e-04
## 3408	genus	5.283037e-04
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## 921645	subtribe	3.611975e-04
## 3017	genus	3.611975e-04
## 36788	species	3.611975e-04
## 354355	subgenus	3.527411e-04
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## 4178	order	3.417820e-04
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## 1329623	subtribe	2.822263e-04
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## 354359	subgenus	1.949851e-04
## 1019013	subtribe	1.926268e-04
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## 11846	family	1.229787e-04
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## 354356	subgenus	1.124125e-04

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## 4599        genus 6.585259e-05
## 20843       subgenus 6.585259e-05
## 4600        species 6.585259e-05
## 4041        genus 6.502952e-05
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## 227908      species 6.261636e-05
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## 4688        genus 6.114124e-05
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## 878136      family 6.061430e-05
## 4124        genus 6.061430e-05
## 4197        family 5.895373e-05
## 4189        genus 5.895373e-05
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## 2391        genus 5.881898e-05
## 2295        species 5.881898e-05
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## 506759      no rank 5.813910e-05
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## 4735        species 5.671301e-05
## 4730        species 5.610367e-05
## 528223      species 5.597215e-05
## 1221289     family 5.510426e-05
## 265362      species 5.235471e-05
## 15279       family 5.231909e-05

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## 678953        species 4.630117e-05
## 4026          genus 4.556217e-05
## 4734          species 4.529501e-05
## 88353         species 4.491153e-05
## 4754          species 4.088768e-05
## 136641 species group 4.064272e-05
## 4479          species 4.064272e-05
## 25680         species 3.888409e-05
## 613451        genus 3.731689e-05
## 4036          species 3.731689e-05
## 1267340       species 3.718001e-05
## 4753          species 3.689031e-05
## 4708          species 3.639357e-05
## 366985        species 3.573848e-05
## 384480        subphylum 3.565113e-05
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## 596780        species 2.883944e-05
## 45940         species 2.806488e-05
## 4027          species 2.725962e-05
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## 558234        family 2.644168e-05
## 4441          genus 2.644168e-05
## 56608         species 2.644168e-05
## 4049          genus 2.539223e-05
## 4050          species 2.539223e-05
## 1546369 species group 2.492874e-05
## 4244          species 2.492874e-05
## 16399         family 2.466670e-05
## 4051          genus 2.466670e-05
## 4052          species 2.466670e-05
## 4053          genus 2.328394e-05
## 4056          species 2.328394e-05
## 16424         family 2.279909e-05
## 200634        genus 2.279909e-05

```

## 231704	species	2.279909e-05
## 4692	genus	2.229069e-05
## 4693	species	2.229069e-05
## 35705	species	2.210073e-05
## 4179	species	2.113114e-05
## 12622	genus	2.048450e-05
## 92895	species	2.048450e-05
## 499517	family	1.999621e-05
## 53942	genus	1.999621e-05
## 396410	species	1.999621e-05
## 4745	species	1.910574e-05
## 12765	genus	1.850385e-05
## 12766	species	1.850385e-05
## 12609	species	1.830256e-05
## 4747	species	1.824310e-05
## 4751	species	1.713585e-05
## 4058	genus	1.558212e-05
## 4059	species	1.558212e-05
## 4744	species	1.497025e-05
## 2192	phylum	1.418273e-05
## 2218	class	1.418273e-05
## 220605	order	1.418273e-05
## 220603	family	1.418273e-05
## 25565	genus	1.418273e-05
## 25566	species	1.418273e-05
## 586705	no rank	1.378929e-05
## 115330	class	1.378929e-05
## 384481	subclass	1.378929e-05
## 103498	order	1.378929e-05
## 67504	family	1.378929e-05
## 84230	no rank	1.140566e-05
## 4865	phylum	1.140566e-05
## 4866	suborder	1.140566e-05
## 18281	family	1.140566e-05
## 4867	genus	1.140566e-05
## 248502	genus	1.089173e-05
## 321041	species	1.089173e-05
## 1535432	species group	9.807355e-06
## 19183	species	9.807355e-06
## 68881	genus	9.503849e-06
## 68882	species	9.503849e-06
## 4579	species	7.128280e-06
## 87076	family	6.171311e-06
## 392352	genus	6.171311e-06
## 392353	species	6.171311e-06
## 4188	order	5.939499e-06
## 4757	phylum	4.984654e-06
## 366796	subphylum	4.984654e-06
## 4859	class	4.984654e-06
## 15934	order	4.984654e-06
## 284599	family	4.984654e-06
## 4760	genus	4.984654e-06
## 4764	species	4.984654e-06
## 4868	species	4.447509e-06
## 19863	species group	3.608265e-06
## 4590	species	3.608265e-06


```
## 37627      species 3.526552e-06
## 486263     species 2.023875e-06
## 393054      genus 1.825292e-06
## 775499     species 1.825292e-06
## 11830      species 1.407724e-06
```

3 Comaprison with the Spermonde Archipelago

The following investigates some of the findings from Kegler et al. (Spermonde Archipelago) in our data. First, they mention two OTUs that dominated the bacterial community composition: *Escheria/Shigella* (gamma proteo bacteria) and *Ralstonia* (beta proteobacteria)

```
idx <- grep("Ralstonia", tree$name); tree[idx,]

##              name tax_id parent  rank embl_code
## 240      Ralstonia solanacearum    305  48736 species      RS
## 257      Ralstonia pickettii     329  48736 species      RP
## 28748      Ralstonia      48736 119060  genus
## 78032  Ralstonia mannitolilytica 105219 48736 species      RM
## 154166      Ralstonia insidiosa 190721 48736 species      RI
## 171442  unclassified Ralstonia 209769 48736 no rank
## 1033409 Ralstonia pseudosolanacearum 1310165 48736 species      RP
##      division_id br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 240              0   1770   2635    0.00038    0.00026    0.50155852
## 257              0    780    717    0.00017    0.00007    0.22102579
## 28748             0   3529   4331    0.00000    0.00000    0.05490471
## 78032             0    353    365    0.00008    0.00004    0.10002834
## 154166            0    423    486    0.00009    0.00005    0.11986398
## 171442            0     61     61    0.00000    0.00000    0.01728535
## 1033409           0    142     67    0.00003    0.00001    0.04023803
##      Local.Freq.May Glob.Freq.Bel Glob.Freq.May  DeltaFreq
## 240      0.60840453  3.759301e-04  2.588128e-04  1.171173e-04
## 257      0.16555068  1.656641e-04  7.042458e-05  9.523954e-05
## 28748      0.04322571  7.495239e-04  4.253959e-04  3.241281e-04
## 78032      0.08427615  7.497363e-05  3.585073e-05  3.912291e-05
## 154166      0.11221427  8.984092e-05  4.773549e-05  4.210544e-05
## 171442      0.01408451  1.295578e-05  5.991491e-06  6.964292e-06
## 1033409      0.01546987  3.015936e-05  6.580818e-06  2.357855e-05
##      Multinom Polarity Polarity.Adj
## 240              NA      NA      NA
## 257              NA      NA      NA
## 28748  5.851432e-25  0.21875      1
## 78032              NA      NA      NA
## 154166             NA      NA      NA
## 171442  1.000000e+00      NA      NA
## 1033409            NA      NA      NA
##
## 240      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 257      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 28748      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 78032      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 154166      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 171442      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 1033409      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia

ral_tax_id <- 48736 # I think this is it.
```

```

make_table(ral_tax_id)

##           Name Tax. Id. Parent   Rank Local.Freq.Bel
## 1      Ralstonia solanacearum      305 48736 species      0.502
## 2      Ralstonia pickettii       329 48736 species      0.221
## 3      Ralstonia insidiosa    190721 48736 species      0.120
## 4      Ralstonia mannitolilytica 105219 48736 species      0.100
## 5      Ralstonia pseudosolanacearum 1310165 48736 species      0.040
## 6      unclassified Ralstonia   209769 48736 no rank      0.017
##   Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1           0.608    -0.193         0.000         0.000     0.000
## 2           0.166     0.289         0.000         0.000     0.000
## 3           0.112     0.066         0.000         0.000     0.000
## 4           0.084     0.171         0.000         0.000     0.000
## 5           0.015     0.956         0.000         0.000     0.000
## 6           0.014     0.205         0.000         0.000     0.000

make_table( tree[idx[3], "parent" ] )

##           Name Tax. Id. Parent   Rank Local.Freq.Bel Local.Freq.May
## 1      Burkholderia      32008 119060 genus      0.606      0.705
## 2      Cupriavidus     106589 119060 genus      0.136      0.096
## 3      Paraburkholderia 1822464 119060 genus      0.095      0.070
## 4      Ralstonia       48736 119060 genus      0.055      0.043
## 5      Pandoraea       93217 119060 genus      0.047      0.034
## 6      Polynucleobacter 44013 119060 genus      0.047      0.042
## 7      Hydromonas     1910924 119060 genus      0.004      0.003
## 8      Lautropia      47670 119060 genus      0.004      0.002
## 9      Mycoavidus     1810868 119060 genus      0.003      0.003
## 10     <NA>          2571159 119060 genus      0.003      0.002
##   log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1     -0.151         0.008         0.007     0.001
## 2      0.343         0.002         0.001     0.001
## 3      0.302         0.001         0.001     0.001
## 4      0.239         0.001         0.000     0.000
## 5      0.347         0.001         0.000     0.000
## 6      0.119         0.001         0.000     0.000
## 7      0.241         0.000         0.000     0.000
## 8      0.462         0.000         0.000     0.000
## 9      0.155         0.000         0.000     0.000
## 10     0.577         0.000         0.000     0.000

parent <- indexOfParent( 32008 )
tree[parent,]

##           name tax_id parent   rank embl_code division_id br_bel
## 90081 Burkholderiaceae 119060 80840 family           0 64275
##           br_may br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May
## 90081 100195           0           0      0.4780659      0.6025933
##           Glob.Freq.Bel Glob.Freq.May DeltaFreq Multinom Polarity
## 90081 0.01365136      0.00984127 0.003810091           0 0.02148438
##           Polarity.Adj
## 90081           1
##
## 90081 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiaceae

```

So we can see that *Ralstonia* genus is present in our data at 5% of the Burkholderiaceae family but the *Burkholderia* genus is much more prevalent in our data at 60.6%. The absolute fraction of reads is approx. 0.01%. Burkholderiaceae is also highlighted by the polarity statistic.

So now we focus on the Escheria/Shigella (gamma proteo bacteria). The absolute fraction is very small at 0.2%.

```
idx <- grep("Escherichia", tree$name); tree[idx,]

##          name tax_id parent  rank embl_code
## 437      Escherichia    561    543   genus
## 438      Escherichia coli    562    561 species      EC
## 440      Escherichia fergusonii    564    561 species      EF
## 170690      Escherichia albertii    208962    561 species      EA
## 1001320 Escherichia phage PBECO 4    1273738    2562455 species      EP
## 1198247      Escherichia marmotae    1499973    561 species      EM
## 1561571      Escherichia virus VR5    1914195    1914165 species      EV
##      division_id br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 437              0   8337   10660      0.00000      0.00000      0.20115331
## 438              0   7739    9800      0.00164      0.00096      0.92827156
## 440              0    194     326      0.00004      0.00003      0.02326976
## 170690           0    276     372      0.00006      0.00004      0.03310543
## 1001320          3      0      21      0.00000      0.00000             NaN
## 1198247          0     36      44      0.00001      0.00000      0.00431810
## 1561571          3     60      82      0.00001      0.00001      1.00000000
##      Local.Freq.May Glob.Freq.Bel Glob.Freq.May      DeltaFreq
## 437      0.17945524  1.770695e-03  1.047038e-03  7.236569e-04
## 438      0.91932458  1.643685e-03  9.625674e-04  6.811179e-04
## 440      0.03058161  4.120364e-05  3.202010e-05  9.183539e-06
## 170690      0.03489681  5.861961e-05  3.653827e-05  2.208134e-05
## 1001320      1.00000000  0.000000e+00  2.062644e-06 -2.062644e-06
## 1198247      0.00412758  7.646036e-06  4.321731e-06  3.324305e-06
## 1561571      1.00000000  1.274339e-05  8.054136e-06  4.689258e-06
##      Multinom Polarity Polarity.Adj
## 437      0.04002761      1      1
## 438      NA      NA      NA
## 440      NA      NA      NA
## 170690      NA      NA      NA
## 1001320      NA      NA      NA
## 1198247      NA      NA      NA
## 1561571      NA      NA      NA
##
## 437      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae
## 438      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae
## 440      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae
## 170690      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae
## 1001320      root Viruses Caudovirales
## 1198247      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae
## 1561571      root Viruses Caudovirales Myoviridae Te...
```

```
esch_tax_id <- 561 # I think this is it.
make_table(esch_tax_id)

##          Name Tax. Id. Parent  Rank Local.Freq.Bel
## 1      Escherichia coli    562    561 species      0.928
## 2      Escherichia albertii    208962    561 species      0.033
## 3      Escherichia fergusonii    564    561 species      0.023
## 4      <NA>    2044467    561 species      0.011
## 5      Escherichia marmotae    1499973    561 species      0.004
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.919      0.010      0.002      0.001      0.001
## 2      0.035     -0.053      0.000      0.000      0.000
## 3      0.031     -0.273      0.000      0.000      0.000
```

```
## 4      0.011   -0.003      0.000      0.000      0.000
## 5      0.004      0.045      0.000      0.000      0.000
```

```
make_table( tree[idx[1], "parent"] )
```

##	Name	Tax.	Id.	Parent	Rank	Local.Freq.Bel
## 1	Salmonella		590	543	genus	0.214
## 2	Escherichia		561	543	genus	0.201
## 3	Klebsiella		570	543	genus	0.140
## 4	Enterobacter		547	543	genus	0.106
## 5	unclassified Enterobacteriaceae		191675	543	no rank	0.085
## 6	Citrobacter		544	543	genus	0.058
## 7	Leclercia		83654	543	genus	0.040
## 8	Cronobacter		413496	543	genus	0.023
## 9	Shigella		620	543	genus	0.019
## 10	Kosakonia		1330547	543	genus	0.016
## 11	Cedecea		158483	543	genus	0.014
## 12	Raoultella		160674	543	genus	0.013
## 13	Lelliottia		1330545	543	genus	0.012
## 14	Pluralibacter		1330546	543	genus	0.011
## 15	Candidatus Riesia		401618	543	genus	0.009
## 16	Candidatus Ishikawaella		409304	543	genus	0.006
## 17	Izhakiella		1780190	543	genus	0.005
## 18	Gibbsiella		929812	543	genus	0.004
## 19	Buttiauxella		82976	543	genus	0.004
## 20	Shimwellia		1335483	543	genus	0.004
## 21	Atlantibacter		1903434	543	genus	0.003
## 22	<NA>		2055876	543	genus	0.003
## 23	Kluyvera		579	543	genus	0.003
## 24	<NA>		2172100	543	genus	0.003
## 25	Candidatus Moranella		1048757	543	genus	0.002
##	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq	
## 1	0.291	-0.310	0.002	0.002	0.000	
## 2	0.179	0.114	0.002	0.001	0.001	
## 3	0.121	0.149	0.001	0.001	0.001	
## 4	0.081	0.277	0.001	0.000	0.000	
## 5	0.103	-0.195	0.001	0.001	0.000	
## 6	0.048	0.205	0.001	0.000	0.000	
## 7	0.015	1.011	0.000	0.000	0.000	
## 8	0.019	0.205	0.000	0.000	0.000	
## 9	0.054	-1.029	0.000	0.000	-0.000	
## 10	0.012	0.266	0.000	0.000	0.000	
## 11	0.010	0.353	0.000	0.000	0.000	
## 12	0.011	0.192	0.000	0.000	0.000	
## 13	0.008	0.354	0.000	0.000	0.000	
## 14	0.008	0.351	0.000	0.000	0.000	
## 15	0.011	-0.271	0.000	0.000	0.000	
## 16	0.007	-0.198	0.000	0.000	0.000	
## 17	0.003	0.548	0.000	0.000	0.000	
## 18	0.003	0.323	0.000	0.000	0.000	
## 19	0.003	0.249	0.000	0.000	0.000	
## 20	0.002	0.544	0.000	0.000	0.000	
## 21	0.003	0.300	0.000	0.000	0.000	
## 22	0.001	1.074	0.000	0.000	0.000	
## 23	0.003	0.116	0.000	0.000	0.000	
## 24	0.002	0.274	0.000	0.000	0.000	
## 25	0.002	0.051	0.000	0.000	0.000	

In our data, Salmonella is highest at both sites. Escherichia is second with approximately 20% and 17.8% at Bellairs and Maycock. This is not surprising as these two species are the most common in the environment.

So in conclusion, we do not observe that these two species are overwhelmingly present. It is interesting to note that both Shigella and Escheria are descendants of Enterobacteriaceae.

3.1 Water Column, Fungia Mucus, Reef Sediments

In Kegler et al, Gammaproteobacteria ranged from 29% at 6km to 69% at the 27km station. (So gamma- would be predicted to be lower at Bellairs.) Alphaproteobacteria ranged from 22% at 6km to 5% at 19km. (So alpha- on the other hand would be predicted to be higher at Bellairs.) Betaproteobacteria did not have a trend.

Let's adjust to make all frequencies relative to Bacteria.

```
make_table(2, relative_taxa = 2) # 2 is tax id for bacteria
```

##	Name	Tax. Id.	Parent	Rank	Local.Freq.Bel
## 1	Proteobacteria	1224	2	phylum	0.471
## 2	Terrabacteria group	1783272	2	no rank	0.410
## 3	FCB group	1783270	2	no rank	0.102
## 4	PVC group	1783257	2	no rank	0.006
## 5	Fusobacteria	32066	2	phylum	0.003
## 6	Spirochaetes	203691	2	phylum	0.003
## 7	Acidobacteria	57723	2	phylum	0.001
## 8	Thermotogae	200918	2	phylum	0.001
## 9	Aquificae	200783	2	phylum	0.001
## 10	Nitrospirae	40117	2	phylum	0.001
## 11	Deferribacteres	200930	2	phylum	0.000
## 12	unclassified Bacteria	2323	2	no rank	0.000
## 13	Thermodesulfobacteria	200940	2	phylum	0.000
## 14	Synergistetes	508458	2	phylum	0.000
## 15	Dictyoglomi	68297	2	phylum	0.000
## 16	Elusimicrobia	74152	2	phylum	0.000
## 17	Calditrichaeota	1930617	2	phylum	0.000
## 18	Chrysiogenetes	200938	2	phylum	0.000
## 19	<NA>	2498710	2	no rank	0.000
## 20	<NA>	2138240	2	phylum	0.000
##	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq
## 1	0.227	0.728	0.325	0.171	0.153
## 2	0.721	-0.565	0.282	0.543	-0.261
## 3	0.042	0.883	0.070	0.032	0.038
## 4	0.003	0.928	0.004	0.002	0.003
## 5	0.002	0.320	0.002	0.002	0.000
## 6	0.002	0.410	0.002	0.001	0.001
## 7	0.000	0.966	0.001	0.000	0.000
## 8	0.001	0.335	0.001	0.001	0.000
## 9	0.000	0.257	0.000	0.000	0.000
## 10	0.000	0.687	0.000	0.000	0.000
## 11	0.000	0.327	0.000	0.000	0.000
## 12	0.000	0.510	0.000	0.000	0.000
## 13	0.000	0.288	0.000	0.000	0.000
## 14	0.000	0.597	0.000	0.000	0.000
## 15	0.000	0.310	0.000	0.000	0.000
## 16	0.000	0.292	0.000	0.000	0.000
## 17	0.000	0.693	0.000	0.000	0.000
## 18	0.000	0.977	0.000	0.000	0.000
## 19	0.000	0.199	0.000	0.000	0.000
## 20	0.000	0.043	0.000	0.000	-0.000
##	Rel.Freq.Bel	Rel.Freq.May	Rel.DeltaFreq		

```
## 1      0.471      0.227      0.244
## 2      0.410      0.721     -0.311
## 3      0.102      0.042      0.060
## 4      0.006      0.003      0.003
## 5      0.003      0.002      0.001
## 6      0.003      0.002      0.001
## 7      0.001      0.000      0.001
## 8      0.001      0.001      0.000
## 9      0.001      0.000      0.001
## 10     0.001      0.000      0.001
## 11     0.000      0.000      0.000
## 12     0.000      0.000      0.000
## 13     0.000      0.000      0.000
## 14     0.000      0.000      0.000
## 15     0.000      0.000      0.000
## 16     0.000      0.000      0.000
## 17     0.000      0.000      0.000
## 18     0.000      0.000      0.000
## 19     0.000      0.000      0.000
## 20     0.000      0.000      0.000
```

In our dataset, we can see that both locations primarily break into three Bacterial groups: Proteo- (47,23%), Terra- (41,72%) and FCB group (10,4%). FCB and Terra- are not commented upon in the Kegler et al. effort. We now restrict our attention just to Proteo-,

```
make_table(2, relative_taxa = 2) # 2 is tax id for bacteria

##           Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Proteobacteria      1224      2 phylum      0.471
## 2      Terrabacteria group 1783272      2 no rank      0.410
## 3           FCB group 1783270      2 no rank      0.102
## 4          PVC group 1783257      2 no rank      0.006
## 5      Fusobacteria      32066      2 phylum      0.003
## 6      Spirochaetes      203691      2 phylum      0.003
## 7      Acidobacteria      57723      2 phylum      0.001
## 8      Thermotogae      200918      2 phylum      0.001
## 9      Aquificae      200783      2 phylum      0.001
## 10     Nitrospirae      40117      2 phylum      0.001
## 11     Deferribacteres      200930      2 phylum      0.000
## 12 unclassified Bacteria      2323      2 no rank      0.000
## 13 Thermodesulfobacteria      200940      2 phylum      0.000
## 14      Synergistetes      508458      2 phylum      0.000
## 15      Dictyoglomi      68297      2 phylum      0.000
## 16      Elusimicrobia      74152      2 phylum      0.000
## 17      Calditrichaeota      1930617      2 phylum      0.000
## 18      Chrysiogenetes      200938      2 phylum      0.000
## 19      <NA>      2498710      2 no rank      0.000
## 20      <NA>      2138240      2 phylum      0.000

##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.227      0.728      0.325      0.171      0.153
## 2      0.721     -0.565      0.282      0.543     -0.261
## 3      0.042      0.883      0.070      0.032      0.038
## 4      0.003      0.928      0.004      0.002      0.003
## 5      0.002      0.320      0.002      0.002      0.000
## 6      0.002      0.410      0.002      0.001      0.001
## 7      0.000      0.966      0.001      0.000      0.000
## 8      0.001      0.335      0.001      0.001      0.000
```

```
## 9      0.000      0.257      0.000      0.000      0.000
## 10     0.000      0.687      0.000      0.000      0.000
## 11     0.000      0.327      0.000      0.000      0.000
## 12     0.000      0.510      0.000      0.000      0.000
## 13     0.000      0.288      0.000      0.000      0.000
## 14     0.000      0.597      0.000      0.000      0.000
## 15     0.000      0.310      0.000      0.000      0.000
## 16     0.000      0.292      0.000      0.000      0.000
## 17     0.000      0.693      0.000      0.000      0.000
## 18     0.000      0.977      0.000      0.000      0.000
## 19     0.000      0.199      0.000      0.000      0.000
## 20     0.000      0.043      0.000      0.000     -0.000
```

```
##      Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.471      0.227      0.244
## 2      0.410      0.721     -0.311
## 3      0.102      0.042      0.060
## 4      0.006      0.003      0.003
## 5      0.003      0.002      0.001
## 6      0.003      0.002      0.001
## 7      0.001      0.000      0.001
## 8      0.001      0.001      0.000
## 9      0.001      0.000      0.001
## 10     0.001      0.000      0.001
## 11     0.000      0.000      0.000
## 12     0.000      0.000      0.000
## 13     0.000      0.000      0.000
## 14     0.000      0.000      0.000
## 15     0.000      0.000      0.000
## 16     0.000      0.000      0.000
## 17     0.000      0.000      0.000
## 18     0.000      0.000      0.000
## 19     0.000      0.000      0.000
## 20     0.000      0.000      0.000
```

```
make_table(1224, relative_taxa = 2) # 1224 is proteobacteria
```

```
##      Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Alphaproteobacteria 28211 1224      class      0.534
## 2      Gammaproteobacteria 1236 1224      class      0.309
## 3      Betaproteobacteria 28216 1224      class      0.106
## 4 delta/epsilon subdivisions 68525 1224 subphylum 0.048
## 5      Oligoflexia 1553900 1224      class      0.002
## 6      Acidithiobacillia 1807140 1224      class      0.000
## 7      Zetaproteobacteria 580370 1224      class      0.000
## 8      <NA> 2008785 1224      class      0.000
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.527      0.013      0.173      0.090      0.083
## 2      0.299      0.033      0.101      0.051      0.049
## 3      0.114     -0.067      0.035      0.019      0.015
## 4      0.057     -0.182      0.015      0.010      0.006
## 5      0.003     -0.150      0.001      0.000      0.000
## 6      0.000      0.006      0.000      0.000      0.000
## 7      0.000      0.030      0.000      0.000      0.000
## 8      0.000      0.326      0.000      0.000      0.000
##      Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.251      0.120      0.131
## 2      0.146      0.068      0.078
```

## 3	0.050	0.026	0.024
## 4	0.022	0.013	0.009
## 5	0.001	0.001	0.000
## 6	0.000	0.000	0.000
## 7	0.000	0.000	0.000
## 8	0.000	0.000	0.000

Alpha- is higher at Bellairs but so are Gamma- and Beta-.

Several human pathogenic bacteria were observed at high frequencies in the Indonesian study. This includes Escherichia, Shigella, Ralstonia, Stenotrophomonas, and Phenyllobacterium. They did not have absolute counts in our data. As stated above, for Escherichia the absolute read counts are 0.2% at both locations. For Shigella, Stenotrophomonas and Phenyllobacterium, this is very close to 0%.

```
make_table(28211, relative_taxa = 2) # alpha
```

##	Name	Tax. Id.	Parent	Rank	Local.Freq.Bel
## 1	Pelagibacterales	54526	28211	order	0.392
## 2	Rhodobacterales	204455	28211	order	0.284
## 3	Rhizobiales	356	28211	order	0.175
## 4	Sphingomonadales	204457	28211	order	0.060
## 5	Rhodospirillales	204441	28211	order	0.045
## 6	Caulobacterales	204458	28211	order	0.015
## 7	Rickettsiales	766	28211	order	0.014
## 8	unclassified Alphaproteobacteria	82117	28211	no rank	0.010
## 9	Holospirales	1921002	28211	order	0.002
## 10	<NA>	2066490	28211	order	0.001
## 11	Parvularculales	255473	28211	order	0.000
## 12	Magnetococcales	1191478	28211	order	0.000

##	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq
## 1	0.654	-0.512	0.068	0.059	0.009
## 2	0.096	1.083	0.049	0.009	0.041
## 3	0.125	0.338	0.030	0.011	0.019
## 4	0.043	0.326	0.010	0.004	0.007
## 5	0.037	0.205	0.008	0.003	0.005
## 6	0.011	0.340	0.003	0.001	0.002
## 7	0.022	-0.457	0.002	0.002	0.000
## 8	0.008	0.256	0.002	0.001	0.001
## 9	0.002	-0.283	0.000	0.000	0.000
## 10	0.001	0.366	0.000	0.000	0.000
## 11	0.000	0.566	0.000	0.000	0.000
## 12	0.000	0.104	0.000	0.000	0.000

##	Rel.Freq.Bel	Rel.Freq.May	Rel.DeltaFreq
## 1	0.099	0.078	0.021
## 2	0.072	0.012	0.060
## 3	0.044	0.015	0.029
## 4	0.015	0.005	0.010
## 5	0.011	0.004	0.007
## 6	0.004	0.001	0.003
## 7	0.004	0.003	0.001
## 8	0.003	0.001	0.002
## 9	0.000	0.000	0.000
## 10	0.000	0.000	0.000
## 11	0.000	0.000	0.000
## 12	0.000	0.000	0.000

```
make_table(1236, relative_taxa = 2) # gamma
```

##	Name	Tax. Id.	Parent	Rank	Local.Freq.Bel
----	------	----------	--------	------	----------------

## 1	Pseudomonadales	72274	1236	order	0.335
## 2	Enterobacterales	91347	1236	order	0.155
## 3	Oceanospirillales	135619	1236	order	0.106
## 4	Alteromonadales	135622	1236	order	0.091
## 5	Vibrionales	135623	1236	order	0.083
## 6	Xanthomonadales	135614	1236	order	0.051
## 7	Pasteurellales	135625	1236	order	0.036
## 8	Chromatiales	135613	1236	order	0.031
## 9	Cellvibrionales	1706369	1236	order	0.023
## 10	Thiotrichales	72273	1236	order	0.023
## 11	Legionellales	118969	1236	order	0.019
## 12	unclassified Gammaproteobacteria	118884	1236	no rank	0.017
## 13	Aeromonadales	135624	1236	order	0.013
## 14	Methylococcales	135618	1236	order	0.007
## 15	Acidiferrobacterales	1692040	1236	order	0.003
## 16	Orbales	1240482	1236	order	0.002
## 17	Nevskiales	1775403	1236	order	0.002
## 18	Immundisolibacterales	1934945	1236	order	0.001
## 19	Cardiobacteriales	135615	1236	order	0.001
## 20	Salinisphaerales	742030	1236	order	0.001
##	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq
## 1	0.323	0.037	0.034	0.017	0.017
## 2	0.192	-0.212	0.016	0.010	0.006
## 3	0.106	0.004	0.011	0.005	0.005
## 4	0.091	0.002	0.009	0.005	0.005
## 5	0.046	0.581	0.008	0.002	0.006
## 6	0.047	0.081	0.005	0.002	0.003
## 7	0.043	-0.185	0.004	0.002	0.001
## 8	0.022	0.327	0.003	0.001	0.002
## 9	0.019	0.190	0.002	0.001	0.001
## 10	0.033	-0.375	0.002	0.002	0.001
## 11	0.028	-0.400	0.002	0.001	0.000
## 12	0.022	-0.295	0.002	0.001	0.001
## 13	0.011	0.102	0.001	0.001	0.001
## 14	0.006	0.247	0.001	0.000	0.000
## 15	0.002	0.308	0.000	0.000	0.000
## 16	0.003	-0.353	0.000	0.000	0.000
## 17	0.002	0.300	0.000	0.000	0.000
## 18	0.001	0.179	0.000	0.000	0.000
## 19	0.001	-0.045	0.000	0.000	0.000
## 20	0.001	0.056	0.000	0.000	0.000
##	Rel.Freq.Bel	Rel.Freq.May	Rel.DeltaFreq		
## 1	0.049	0.022	0.027		
## 2	0.023	0.013	0.010		
## 3	0.015	0.007	0.008		
## 4	0.013	0.006	0.007		
## 5	0.012	0.003	0.009		
## 6	0.007	0.003	0.004		
## 7	0.005	0.003	0.002		
## 8	0.005	0.002	0.003		
## 9	0.003	0.001	0.002		
## 10	0.003	0.002	0.001		
## 11	0.003	0.002	0.001		
## 12	0.002	0.002	0.000		
## 13	0.002	0.001	0.001		
## 14	0.001	0.000	0.001		

```
## 15      0.000      0.000      0.000
## 16      0.000      0.000      0.000
## 17      0.000      0.000      0.000
## 18      0.000      0.000      0.000
## 19      0.000      0.000      0.000
## 20      0.000      0.000      0.000

make_table(28216, relative_taxa = 2) # beta

##              Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Burkholderiales      80840 28216  order      0.827
## 2      Neisseriales      206351 28216  order      0.056
## 3      Nitrosomonadales      32003 28216  order      0.051
## 4      Rhodocyclales      206389 28216  order      0.044
## 5 unclassified Betaproteobacteria 119066 28216 no rank      0.022
##  Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.838      -0.013      0.029      0.016      0.012
## 2      0.050      0.111      0.002      0.001      0.001
## 3      0.049      0.037      0.002      0.001      0.001
## 4      0.032      0.318      0.002      0.001      0.001
## 5      0.031      -0.329      0.001      0.001      0.000
##  Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.041      0.022      0.019
## 2      0.003      0.001      0.002
## 3      0.003      0.001      0.002
## 4      0.002      0.001      0.001
## 5      0.001      0.001      0.000

idx <- grep("Ralstonia", tree$name); tree[idx,] # within beta proteo

##              name tax_id parent      rank embl_code
## 240      Ralstonia solanacearum      305 48736 species      RS
## 257      Ralstonia pickettii      329 48736 species      RP
## 28748      Ralstonia      48736 119060 genus
## 78032      Ralstonia mannitolilytica 105219 48736 species      RM
## 154166      Ralstonia insidiosa 190721 48736 species      RI
## 171442      unclassified Ralstonia 209769 48736 no rank
## 1033409 Ralstonia pseudosolanacearum 1310165 48736 species      RP
##  division_id br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 240      0      1770      2635      0.00038      0.00026      0.50155852
## 257      0      780      717      0.00017      0.00007      0.22102579
## 28748      0      3529      4331      0.00000      0.00000      0.05490471
## 78032      0      353      365      0.00008      0.00004      0.10002834
## 154166      0      423      486      0.00009      0.00005      0.11986398
## 171442      0      61      61      0.00000      0.00000      0.01728535
## 1033409      0      142      67      0.00003      0.00001      0.04023803
##  Local.Freq.May Glob.Freq.Bel Glob.Freq.May      DeltaFreq
## 240      0.60840453 3.759301e-04 2.588128e-04 1.171173e-04
## 257      0.16555068 1.656641e-04 7.042458e-05 9.523954e-05
## 28748      0.04322571 7.495239e-04 4.253959e-04 3.241281e-04
## 78032      0.08427615 7.497363e-05 3.585073e-05 3.912291e-05
## 154166      0.11221427 8.984092e-05 4.773549e-05 4.210544e-05
## 171442      0.01408451 1.295578e-05 5.991491e-06 6.964292e-06
## 1033409      0.01546987 3.015936e-05 6.580818e-06 2.357855e-05
##  Multinom Polarity Polarity.Adj
## 240      NA      NA      NA
## 257      NA      NA      NA
## 28748 5.851432e-25 0.21875      1
```

```

## 78032      NA      NA      NA
## 154166     NA      NA      NA
## 171442  1.000000e+00      NA      NA
## 1033409    NA      NA      NA
##
## 240      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 257      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 28748      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 78032      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 154166      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 171442      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 1033409 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales

tid <- 48736 # I think this is it.
path2root(48736)

##      name tax_id parent      rank embl_code division_id
## 1      root      1      NA      no rank      8
## 101088 cellular organisms 131567      1      no rank      8
## 2      Bacteria      2 131567 superkingdom      0
## 942      Proteobacteria      1224      2      phylum      0
## 12020 Betaproteobacteria      28216      1224      class      0
## 56568 Burkholderiales      80840      28216      order      0
## 90081 Burkholderiaceae 119060      80840      family      0
## 28748 Ralstonia      48736 119060      genus      0
##      br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 1      4708322 10181105      0      0      NA
## 101088 4636449 9943097      0      0      0.98473490
## 2      3246493 7673696      0      0      0.70021109
## 942      1529279 1744867      0      0      0.47105569
## 12020      162539 198370      0      0      0.10628473
## 56568      134448 166273      0      0      0.82717379
## 90081      64275 100195      0      0      0.47806587
## 28748      3529 4331      0      0      0.05490471
##      Local.Freq.May Glob.Freq.Bel Glob.Freq.May      DeltaFreq
## 1      NA 1.0000000000 1.0000000000 0.0000000000
## 101088 0.97662258 0.9847349013 0.9766225768 0.0081123245
## 2      0.77176115 0.6895222969 0.7537193654 -0.0641970685
## 942      0.22738287 0.3248034013 0.1713828705 0.1534205308
## 12020 0.11368775 0.0345216406 0.0194841326 0.0150375080
## 56568 0.83819630 0.0285553962 0.0163315279 0.0122238683
## 90081 0.60259333 0.0136513603 0.0098412697 0.0038100906
## 28748 0.04322571 0.0007495239 0.0004253959 0.0003241281
##      Multinom      Polarity Polarity.Adj
## 1      0.000000e+00      NA      NA
## 101088 0.000000e+00 1.000000e+00 1.00000000
## 2      0.000000e+00 4.005432e-05 0.01921082
## 942      0.000000e+00 7.265625e-01 1.00000000
## 12020 1.165388e-142 1.000000e+00 1.00000000
## 56568 0.000000e+00 2.187500e-01 0.37500000
## 90081 0.000000e+00 2.148438e-02 1.00000000
## 28748 5.851432e-25 2.187500e-01 1.00000000
##
## 1
## 101088      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 2      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales
## 942      root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiales

```

```
## 12020 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 56568 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 90081 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
## 28748 root cellular organisms Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderia
```

```
make_table(119060 , relative_taxa=2) # parent of
```

```
##      Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May
## 1 Burkholderia 32008 119060 genus 0.606 0.705
## 2 Cupriavidus 106589 119060 genus 0.136 0.096
## 3 Paraburkholderia 1822464 119060 genus 0.095 0.070
## 4 Ralstonia 48736 119060 genus 0.055 0.043
## 5 Pandoraea 93217 119060 genus 0.047 0.034
## 6 Polynucleobacter 44013 119060 genus 0.047 0.042
## 7 Hydromonas 1910924 119060 genus 0.004 0.003
## 8 Lautropia 47670 119060 genus 0.004 0.002
## 9 Mycoavidus 1810868 119060 genus 0.003 0.003
## 10 <NA> 2571159 119060 genus 0.003 0.002
```

```
##      log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq Rel.Freq.Bel
## 1 -0.151 0.008 0.007 0.001 0.012
## 2 0.343 0.002 0.001 0.001 0.003
## 3 0.302 0.001 0.001 0.001 0.002
## 4 0.239 0.001 0.000 0.000 0.001
## 5 0.347 0.001 0.000 0.000 0.001
## 6 0.119 0.001 0.000 0.000 0.001
## 7 0.241 0.000 0.000 0.000 0.000
## 8 0.462 0.000 0.000 0.000 0.000
## 9 0.155 0.000 0.000 0.000 0.000
## 10 0.577 0.000 0.000 0.000 0.000
```

```
##      Rel.Freq.May Rel.DeltaFreq
## 1 0.009 0.003
## 2 0.001 0.002
## 3 0.001 0.001
## 4 0.001 0.000
## 5 0.000 0.001
## 6 0.001 0.000
## 7 0.000 0.000
## 8 0.000 0.000
## 9 0.000 0.000
## 10 0.000 0.000
```

```
idx <- grep("Stenotrophomonas", tree$name); tree[idx,] # within gamma proteo
```

```
##      name tax_id parent rank
## 21375 Stenotrophomonas 40323 32033 genus
## 21376 Stenotrophomonas maltophilia 40324 995085 species
## 98595 Stenotrophomonas acidaminiphila 128780 40323 species
## 177834 Stenotrophomonas rhizophila 216778 40323 species
## 766770 Stenotrophomonas maltophilia group 995085 40323 species group
## 1484328 Stenotrophomonas sp. MYb57 1827305 40323 species
## 1553536 Stenotrophomonas sp. LM091 1904944 40323 species
```

```
##      embl_code division_id br_bel br_may br_bel_frac br_may_frac
## 21375 0 6320 6530 0.00000 0.00000
## 21376 SM 0 2537 2569 0.00054 0.00025
## 98595 SA 0 879 762 0.00019 0.00007
## 177834 SR 0 513 541 0.00011 0.00005
## 766770 0 3713 3815 0.00000 0.00000
## 1484328 SS 0 135 157 0.00003 0.00002
```

```

## 1553536      SS      0      250      303      0.00005      0.00003
##      Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 21375      0.30989507      0.30807700      1.342304e-03      6.413842e-04
## 21376      0.68327498      0.67339450      5.388332e-04      2.523302e-04
## 98595      0.13908228      0.11669219      1.866907e-04      7.484453e-05
## 177834      0.08117089      0.08284839      1.089560e-04      5.313765e-05
## 766770      0.58750000      0.58422665      7.886037e-04      3.747137e-04
## 1484328      0.02136076      0.02404288      2.867264e-05      1.542072e-05
## 1553536      0.03955696      0.04640123      5.309747e-05      2.976101e-05
##      DeltaFreq      Multinom      Polarity Polarity.Adj
## 21375      7.009199e-04      2.959003e-35      0.7744141      0.375
## 21376      2.865030e-04      NA      NA      NA
## 98595      1.118462e-04      NA      NA      NA
## 177834      5.581836e-05      NA      NA      NA
## 766770      4.138899e-04      1.828599e-02      1.0000000      0.375
## 1484328      1.325191e-05      NA      NA      NA
## 1553536      2.333646e-05      NA      NA      NA
##
## 21375      root cellular organisms Bacteria
## 21376      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria Xanthomonadales Xanthomonadales
## 98595      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria
## 177834      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria
## 766770      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria
## 1484328      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria
## 1553536      root cellular organisms Bacteria Proteobacteria Gammaproteobacteria

tid <- 40323 # I think this is it.
make_table(32033, relative_taxa=2) # parent of

##      Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1      Stenotrophomonas      40323      32033      genus      0.310
## 2      Xanthomonas      338      32033      genus      0.290
## 3      Lysobacter      68      32033      genus      0.200
## 4      Luteimonas      83614      32033      genus      0.084
## 5      Pseudoxanthomonas      83618      32033      genus      0.055
## 6      Xylella      2370      32033      genus      0.023
## 7      Thermomonas      141948      32033      genus      0.019
## 8 unclassified Xanthomonadaceae      191676      32033 no rank      0.018
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.308      0.006      0.001      0.001      0.001
## 2      0.324      -0.113      0.001      0.001      0.001
## 3      0.184      0.087      0.001      0.000      0.000
## 4      0.071      0.177      0.000      0.000      0.000
## 5      0.054      0.030      0.000      0.000      0.000
## 6      0.031      -0.304      0.000      0.000      0.000
## 7      0.016      0.194      0.000      0.000      0.000
## 8      0.012      0.376      0.000      0.000      0.000
##      Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.002      0.001      0.001
## 2      0.002      0.001      0.001
## 3      0.001      0.001      0.000
## 4      0.001      0.000      0.001
## 5      0.000      0.000      0.000
## 6      0.000      0.000      0.000
## 7      0.000      0.000      0.000
## 8      0.000      0.000      0.000

```

```

idx <- grep("Phenylobacterium", tree$name); tree[idx,] # within alpha proteo

##
##          name tax_id parent      rank embl_code
## 14          Phenylobacterium      20 76892      genus
## 234275 Phenylobacterium zucineum 284016      20 species      PZ
##          division_id br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 14              0      1305      992      0.00000      0e+00      0.1080924
## 234275              0      855      680      0.00018      7e-05      0.6551724
##          Local.Freq.May Glob.Freq.Bel Glob.Freq.May      DeltaFreq Multinom
## 14          0.1025535      0.0002771688      9.743540e-05      0.0001797334      0.137916
## 234275          0.6854839      0.0001815934      6.679039e-05      0.0001148030      NA
##          Polarity Polarity.Adj
## 14              NA              NA
## 234275          NA              NA
##
## 14          root cellular organisms Bacteria Proteobacteria Alphaproteobacteria Ca
## 234275 root cellular organisms Bacteria Proteobacteria Alphaproteobacteria Caulobacterales Caulobactera

tid <- 20 # I think this is it.
make_table( 76892, relative_taxa=2)

##
##          Name Tax. Id. Parent      Rank Local.Freq.Bel
## 1          Brevundimonas      41275      76892      genus      0.453
## 2          Caulobacter      75      76892      genus      0.361
## 3          Phenylobacterium      20      76892      genus      0.108
## 4          Asticcacaulis      76890      76892      genus      0.049
## 5 unclassified Caulobacteraceae      81440      76892 no rank      0.030
##          Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1          0.407      0.107      0.001      0.000      0.001
## 2          0.400      -0.103      0.001      0.000      0.001
## 3          0.103      0.053      0.000      0.000      0.000
## 4          0.048      0.018      0.000      0.000      0.000
## 5          0.043      -0.367      0.000      0.000      0.000
##          Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1          0.002      0.001      0.001
## 2          0.001      0.001      0.000
## 3          0.000      0.000      0.000
## 4          0.000      0.000      0.000
## 5          0.000      0.000      0.000

idx <- grep("Mycobacterium", tree$name); tree[idx,] # Terra Actino

##
##          name      tax_id      parent      rank
## 1382          Mycobacterium      1763      1762      genus
## 1383          Mycobacterium avium      1764      120793      species
## 1386          Mycobacterium intracellulare      1767      120793      species
## 1387          Mycobacterium kansasii      1768      1763      species
## 1388          Mycobacterium leprae      1769      1763      species
## 1392          Mycobacterium tuberculosis      1773      77643      species
## 1400          Mycobacterium marinum      1781      1763      species
## 1425          Mycobacterium ulcerans      1809      1763      species
## 12869          Mycobacterium haemophilum      29311      1763      species
## 42667          Mycobacterium lepraemurium      64667      120793      species
## 53688          Mycobacterium tuberculosis complex      77643      1763 species group
## 54333          Mycobacterium canettii      78331      77643      species
## 91516          Mycobacterium avium complex (MAC)      120793      1763 species group
## 130563          Mycobacterium sp. JLS      164757      1763      species
## 174180          Mycobacterium sp. JS623      212767      1763      species

```

## 183028	Mycobacterium chimaera	222805	120793	species		
## 217216	Mycobacterium liflandii	261524	1763	species		
## 221185	Mycobacterium pseudoshottsii	265949	1763	species		
## 283911	Mycobacterium colombiense	339268	120793	species		
## 411643	Mycobacterium dioxanotrophicus	482462	1763	species		
## 466034	Mycobacterium phage Myrna	546805	196896	species		
## 574428	Mycobacterium marseillense	701042	120793	species		
## 590236	Mycobacterium shigaense	722731	2249310	species		
## 884138	Mycobacterium paraintracellulare	1138383	120793	species		
## 908773	Mycobacterium sp. MOTT36Y	1168287	1763	species		
## 1001273	Mycobacterium sp. VKM Ac-1817D	1273687	1763	species		
## 1060858	Mycobacterium phage Whirlwind	1340826	2201166	species		
## 1100201	Mycobacterium paragordona	1389713	1763	species		
## 1161538	Mycobacterium phage Jolie2	1458831	2201169	species		
## 1166129	Mycobacterium phage Jolie1	1463812	2315863	species		
## 1186356	Mycobacterium phage OkiRoe	1486473	2562717	species		
## 1217231	[Mycobacterium] stephanolepidis	1520670	670516	species		
## 1239376	Mycobacterium sp. EPa45	1545728	1763	species		
## 1251868	Mycobacterium sp. QIA-37	1561223	1763	species		
## 1328941	Mycobacterium phage Cambiare	1647305	2201169	species		
## 1358042	Mycobacterium sp. YC-RL4	1682113	1763	species		
## 1464651	Mycobacterium phage Bipper	1805457	196894	species		
## 1530219	Mycobacterium sp. djl-10	1879023	1763	species		
## 1566916	Mycobacterium sp. WY10	1920667	1763	species		
## 1580953	Mycobacterium sp. MS1601	1936029	1763	species		
##	embl_code	division_id	br_bel	br_may	br_bel_frac	br_may_frac
## 1382		0	8057	9290	0.00000	0.00000
## 1383	MA	0	496	675	0.00011	0.00007
## 1386	MI	0	339	341	0.00007	0.00003
## 1387	MK	0	333	400	0.00007	0.00004
## 1388	ML	0	59	79	0.00001	0.00001
## 1392	MT	0	1991	2243	0.00042	0.00022
## 1400	MM	0	126	223	0.00003	0.00002
## 1425	MU	0	50	87	0.00001	0.00001
## 12869	MH	0	163	164	0.00003	0.00002
## 42667	ML	0	71	96	0.00002	0.00001
## 53688		0	2103	2381	0.00000	0.00000
## 54333	MC	0	112	138	0.00002	0.00001
## 91516		0	1686	2133	0.00000	0.00000
## 130563	MS	0	95	109	0.00002	0.00001
## 174180	MS	0	340	379	0.00007	0.00004
## 183028	MC	0	226	343	0.00005	0.00003
## 217216	ML	0	0	14	0.00000	0.00000
## 221185	MP	0	13	17	0.00000	0.00000
## 283911	MC	0	320	364	0.00007	0.00004
## 411643	MD	0	393	418	0.00008	0.00004
## 466034	MP	3	10	23	0.00000	0.00000
## 574428	MM	0	182	276	0.00004	0.00003
## 590236	MS	0	297	310	0.00006	0.00003
## 884138	MP	0	52	38	0.00001	0.00000
## 908773	MS	0	16	22	0.00000	0.00000
## 1001273	MS	0	82	87	0.00002	0.00001
## 1060858	MP	3	11	0	0.00000	0.00000
## 1100201	MP	0	366	420	0.00008	0.00004
## 1161538	MP	3	0	18	0.00000	0.00000
## 1166129	MP	3	16	65	0.00000	0.00001

##	1186356	MP	3	40	28	0.00001	0.00000
##	1217231	MS	0	89	144	0.00002	0.00001
##	1239376	MS	0	355	383	0.00008	0.00004
##	1251868	MS	0	35	33	0.00001	0.00000
##	1328941	MP	3	12	20	0.00000	0.00000
##	1358042	MS	0	361	333	0.00008	0.00003
##	1464651	MP	3	14	13	0.00000	0.00000
##	1530219	MS	0	397	414	0.00008	0.00004
##	1566916	MS	0	67	62	0.00001	0.00001
##	1580953	MS	0	321	370	0.00007	0.00004
##		Local.Freq.Bel	Local.Freq.May	Glob.Freq.Bel	Glob.Freq.May		
##	1382	0.4490080250	0.4537018949	1.711225e-03	9.124746e-04		
##	1383	0.2941874259	0.3164556962	1.053454e-04	6.629929e-05		
##	1386	0.2010676157	0.1598687295	7.200017e-05	3.349342e-05		
##	1387	0.0413305200	0.0430570506	7.072583e-05	3.928847e-05		
##	1388	0.0073228249	0.0085037675	1.253100e-05	7.759472e-06		
##	1392	0.9467427485	0.9420411592	4.228683e-04	2.203101e-04		
##	1400	0.0156385752	0.0240043057	2.676113e-05	2.190332e-05		
##	1425	0.0062057838	0.0093649085	1.061949e-05	8.545241e-06		
##	12869	0.0202308552	0.0176533907	3.461955e-05	1.610827e-05		
##	42667	0.0421115065	0.0450070323	1.507968e-05	9.429232e-06		
##	53688	0.2610152662	0.2562970936	4.466559e-04	2.338646e-04		
##	54333	0.0532572515	0.0579588408	2.378767e-05	1.355452e-05		
##	91516	0.2092590294	0.2296017223	3.580894e-04	2.095057e-04		
##	130563	0.0117909892	0.0117330463	2.017704e-05	1.070611e-05		
##	174180	0.0421993298	0.0407965554	7.221256e-05	3.722582e-05		
##	183028	0.1340450771	0.1608063760	4.800012e-05	3.368986e-05		
##	217216	0.0000000000	0.0015069968	0.000000e+00	1.375096e-06		
##	221185	0.0016135038	0.0018299247	2.761069e-06	1.669760e-06		
##	283911	0.1897983393	0.1706516643	6.796477e-05	3.575250e-05		
##	411643	0.0487774606	0.0449946179	8.346923e-05	4.105645e-05		
##	466034	0.0001750026	0.0001056874	2.123899e-06	2.259087e-06		
##	574428	0.1079478055	0.1293952180	3.865496e-05	2.710904e-05		
##	590236	1.0000000000	1.0000000000	6.307980e-05	3.044856e-05		
##	884138	0.0308422301	0.0178152836	1.104427e-05	3.732404e-06		
##	908773	0.0019858508	0.0023681378	3.398238e-06	2.160866e-06		
##	1001273	0.0101774854	0.0093649085	1.741597e-05	8.545241e-06		
##	1060858	1.0000000000	NaN	2.336289e-06	0.000000e+00		
##	1100201	0.0454263373	0.0452099031	7.773470e-05	4.125289e-05		
##	1161538	0.0000000000	0.4736842105	0.000000e+00	1.767981e-06		
##	1166129	1.0000000000	1.0000000000	3.398238e-06	6.384376e-06		
##	1186356	1.0000000000	1.0000000000	8.495596e-06	2.750193e-06		
##	1217231	0.0264016612	0.0390243902	1.890270e-05	1.414385e-05		
##	1239376	0.0440610649	0.0412271259	7.539841e-05	3.761871e-05		
##	1251868	0.0043440487	0.0035522067	7.433646e-06	3.241298e-06		
##	1328941	1.0000000000	0.5263157895	2.548679e-06	1.964423e-06		
##	1358042	0.0448057590	0.0358449946	7.667275e-05	3.270765e-05		
##	1464651	0.0131086142	0.0176390773	2.973458e-06	1.276875e-06		
##	1530219	0.0492739233	0.0445640474	8.431879e-05	4.066356e-05		
##	1566916	0.0083157503	0.0066738428	1.423012e-05	6.089712e-06		
##	1580953	0.0398411319	0.0398277718	6.817716e-05	3.634183e-05		
##		DeltaFreq	Multinom	Polarity	Polarity.Adj		
##	1382	7.987507e-04	9.624260e-06	0.3074563	0.3017578		
##	1383	3.904610e-05	NA	NA	NA		
##	1386	3.850676e-05	NA	NA	NA		
##	1387	3.143737e-05	NA	NA	NA		

## 1388	4.771532e-06	NA	NA	NA
## 1392	2.025582e-04	NA	NA	NA
## 1400	4.857806e-06	NA	NA	NA
## 1425	2.074253e-06	NA	NA	NA
## 12869	1.851128e-05	NA	NA	NA
## 42667	5.650450e-06	NA	NA	NA
## 53688	2.127913e-04	5.355623e-01	NA	NA
## 54333	1.023315e-05	NA	NA	NA
## 91516	1.485836e-04	1.153435e-04	1.0000000	1.0000000
## 130563	9.470933e-06	NA	NA	NA
## 174180	3.498674e-05	NA	NA	NA
## 183028	1.431026e-05	NA	NA	NA
## 217216	-1.375096e-06	NA	NA	NA
## 221185	1.091309e-06	NA	NA	NA
## 283911	3.221226e-05	NA	NA	NA
## 411643	4.241278e-05	NA	NA	NA
## 466034	-1.351879e-07	NA	NA	NA
## 574428	1.154592e-05	NA	NA	NA
## 590236	3.263124e-05	NA	NA	NA
## 884138	7.311870e-06	NA	NA	NA
## 908773	1.237373e-06	NA	NA	NA
## 1001273	8.870730e-06	NA	NA	NA
## 1060858	2.336289e-06	NA	NA	NA
## 1100201	3.648181e-05	NA	NA	NA
## 1161538	-1.767981e-06	NA	NA	NA
## 1166129	-2.986137e-06	NA	NA	NA
## 1186356	5.745403e-06	NA	NA	NA
## 1217231	4.758853e-06	NA	NA	NA
## 1239376	3.777971e-05	NA	NA	NA
## 1251868	4.192348e-06	NA	NA	NA
## 1328941	5.842554e-07	NA	NA	NA
## 1358042	4.396510e-05	NA	NA	NA
## 1464651	1.696583e-06	NA	NA	NA
## 1530219	4.365522e-05	NA	NA	NA
## 1566916	8.140410e-06	NA	NA	NA
## 1580953	3.183532e-05	NA	NA	NA
##				
## 1382				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1383				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1386				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1387				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1388				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1392				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1400				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 1425				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 12869				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 42667				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 53688				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 54333				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 91516				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 130563				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 174180				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 183028				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 217216				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 221185				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium
## 283911				root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacterium

```

## 411643 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 466034
## 574428 root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacteriales
## 590236 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 884138 root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacteriales
## 908773 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1001273 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1060858
## 1100201 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1161538
## 1166129
## 1186356
## 1217231 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1239376 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1251868 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1328941
## 1358042 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1464651
## 1530219 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1566916 root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1580953 root cellular organisms Bacteria Terrabacteria group Actinobacteria

```

```

tid <- 1763 # I think this is it.
path2root(1763)

```

##		name	tax_id	parent	rank	embl_code
## 1		root	1	NA	no rank	
## 101088	cellular organisms		131567	1	no rank	
## 2	Bacteria		2	131567	superkingdom	
## 1446826	Terrabacteria group		1783272	2	no rank	
## 163583	Actinobacteria		201174	1783272	phylum	
## 1380	Actinobacteria		1760	201174	class	
## 60248	Corynebacteriales		85007	1760	order	
## 1381	Mycobacteriaceae		1762	85007	family	
## 1382	Mycobacterium		1763	1762	genus	
##	division_id	br_bel	br_may	br_bel_frac	br_may_frac	
## 1	8	4708322	10181105	0	0	
## 101088	8	4636449	9943097	0	0	
## 2	0	3246493	7673696	0	0	
## 1446826	0	1329975	5530830	0	0	
## 163583	0	289325	382562	0	0	
## 1380	0	280956	373185	0	0	
## 60248	0	47993	58237	0	0	
## 1381	0	17944	20476	0	0	
## 1382	0	8057	9290	0	0	
##	Local.Freq.Bel	Local.Freq.May	Glob.Freq.Bel	Glob.Freq.May		
## 1	NA	NA	1.000000000	1.000000000		
## 101088	0.9847349	0.9766226	0.984734901	0.9766225768		
## 2	0.7002111	0.7717612	0.689522297	0.7537193654		
## 1446826	0.4096651	0.7207518	0.282473246	0.5432445692		
## 163583	0.2175417	0.0691690	0.061449705	0.0375756855		
## 1380	0.9710741	0.9754889	0.059672214	0.0366546657		
## 60248	0.1708203	0.1560540	0.010193228	0.0057201060		
## 1381	0.3738879	0.3515978	0.003811124	0.0020111766		
## 1382	0.4490080	0.4537019	0.001711225	0.0009124746		
##	DeltaFreq	Multinom	Polarity	Polarity.Adj		
## 1	0.0000000000	0.000000e+00	NA	NA		

```

## 101088 0.0081123245 0.000000e+00 1.000000e+00 1.00000000
## 2 -0.0641970685 0.000000e+00 4.005432e-05 0.01921082
## 1446826 -0.2607713229 0.000000e+00 7.031250e-02 1.00000000
## 163583 0.0238740199 4.282119e-47 4.531250e-01 1.00000000
## 1380 0.0230175488 0.000000e+00 7.197380e-03 1.00000000
## 60248 0.0044731221 5.413778e-20 7.265625e-01 1.00000000
## 1381 0.0017999476 1.434105e-01 1.000000e+00 1.00000000
## 1382 0.0007987507 9.624260e-06 3.074563e-01 0.30175781
##
## 1
## 101088
## 2
## 1446826 root cellular org
## 163583 root cellular organisms Bacteri
## 1380 root cellular organisms Bacteria Terrabacteria
## 60248 root cellular organisms Bacteria Terrabacteria group Actinobacte
## 1381 root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteri
## 1382 root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Corynebacter

make_table(1762, relative_taxa=2) # parent of

##      Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May
## 1 Mycobacterium 1763 1762 genus 0.449 0.454
## 2 Mycolicibacterium 1866885 1762 genus 0.322 0.322
## 3 Mycobacteroides 670516 1762 genus 0.188 0.180
## 4 Mycolicibacter 1073531 1762 genus 0.031 0.033
## 5 Hoyosella 697025 1762 genus 0.010 0.011
## log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq Rel.Freq.Bel
## 1 -0.010 0.002 0.001 0.001 0.002
## 2 0.001 0.001 0.001 0.001 0.002
## 3 0.042 0.001 0.000 0.000 0.001
## 4 -0.045 0.000 0.000 0.000 0.000
## 5 -0.166 0.000 0.000 0.000 0.000
## Rel.Freq.May Rel.DeltaFreq
## 1 0.001 0.001
## 2 0.001 0.001
## 3 0.000 0.001
## 4 0.000 0.000
## 5 0.000 0.000

make_table(85007, relative_taxa=2) # parent of

##      Name Tax. Id. Parent Rank Local.Freq.Bel
## 1 Mycobacteriaceae 1762 85007 family 0.374
## 2 Nocardiaceae 85025 85007 family 0.295
## 3 Corynebacteriaceae 1653 85007 family 0.195
## 4 Gordoniaceae 85026 85007 family 0.080
## 5 Dietziaceae 85029 85007 family 0.026
## 6 Tsukamurellaceae 85028 85007 family 0.024
## 7 Segniliparaceae 316606 85007 family 0.004
## 8 unclassified Corynebacteriales 697024 85007 no rank 0.002
## Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1 0.352 0.061 0.004 0.002 0.002
## 2 0.302 -0.025 0.003 0.002 0.001
## 3 0.211 -0.083 0.002 0.001 0.001
## 4 0.074 0.088 0.001 0.000 0.000
## 5 0.027 -0.050 0.000 0.000 0.000
## 6 0.026 -0.097 0.000 0.000 0.000

```

```
## 7      0.005    -0.205      0.000      0.000      0.000
## 8      0.002      0.001      0.000      0.000      0.000
## Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.006      0.003      0.003
## 2      0.004      0.002      0.002
## 3      0.003      0.002      0.001
## 4      0.001      0.001      0.000
## 5      0.000      0.000      0.000
## 6      0.000      0.000      0.000
## 7      0.000      0.000      0.000
## 8      0.000      0.000      0.000
```

```
idx <- grep("Staphylococcus", tree$name); tree[idx,] #Terra Firmicutes
```

```
##          name tax_id parent rank embl_code
## 984      Staphylococcus 1279 90964 genus
## 985      Staphylococcus aureus 1280 1279 species SA
## 986      Staphylococcus carnosus 1281 1279 species SC
## 987      Staphylococcus epidermidis 1282 1279 species SE
## 988      Staphylococcus haemolyticus 1283 1279 species SH
## 989      Staphylococcus hyicus 1284 1279 species SH
## 991      Staphylococcus simulans 1286 1279 species SS
## 993      Staphylococcus xylosus 1288 1279 species SX
## 994      Staphylococcus hominis 1290 1279 species SH
## 995      Staphylococcus warneri 1292 1279 species SW
## 997      Staphylococcus muscae 1294 1279 species SM
## 998      Staphylococcus schleiferi 1295 1279 species SS
## 999      Staphylococcus sciuri 1296 1279 species SS
## 11882      Staphylococcus lugdunensis 28035 1279 species SL
## 12927      Staphylococcus arlettae 29378 1279 species SA
## 12928      Staphylococcus auricularis 29379 1279 species SA
## 12929      Staphylococcus caprae 29380 1279 species SC
## 12930      Staphylococcus cohnii 29382 1279 species SC
## 12932      Staphylococcus kloosii 29384 1279 species SK
## 12933      Staphylococcus saprophyticus 29385 1279 species SS
## 12935      Staphylococcus capitis 29388 1279 species SC
## 26288      Staphylococcus pasteurii 45972 1279 species SP
## 26425      Staphylococcus felis 46127 1279 species SF
## 32738      Staphylococcus delphini 53344 1279 species SD
## 34655      Staphylococcus virus Twort 55510 1857846 species SV
## 39537      Staphylococcus succinus 61015 1279 species SS
## 47074      Staphylococcus condimenti 70255 1279 species SC
## 47077      Staphylococcus piscifermentans 70258 1279 species SP
## 121954      Staphylococcus lutrae 155085 1279 species SL
## 135685      Staphylococcus pettenkoferi 170573 1279 species SP
## 175740      Staphylococcus nepalensis 214473 1279 species SN
## 203616      Staphylococcus equorum 246432 1279 species SE
## 234062      Staphylococcus pseudintermedius 283734 1279 species SP
## 255789      Staphylococcus simiae 308354 1279 species SS
## 524780      Staphylococcus stepanovicii 643214 1279 species SS
## 759016      Staphylococcus argenteus 985002 1279 species SA
## 759758      Staphylococcus agnetis 985762 1279 species SA
## 1334421      Staphylococcus schweitzeri 1654388 1279 species SS
## 1387655      Staphylococcus sp. AntiMn-1 1715860 1279 species SS
## 1568324      Staphylococcus virus SEP9 1922247 1922243 species SV
## division_id br_bel br_may br_bel_frac br_may_frac Local.Freq.Bel
## 984          0 20913 36854 0.00000 0.00000 0.950029528
```

## 985	0	8257	16497	0.00175	0.00162	0.394826185
## 986	0	237	329	0.00005	0.00003	0.011332664
## 987	0	922	1752	0.00020	0.00017	0.044087410
## 988	0	412	670	0.00009	0.00007	0.019700665
## 989	0	263	481	0.00006	0.00005	0.012575910
## 991	0	130	204	0.00003	0.00002	0.006216229
## 993	0	518	887	0.00011	0.00009	0.024769282
## 994	0	431	741	0.00009	0.00007	0.020609190
## 995	0	630	753	0.00013	0.00007	0.030124803
## 997	0	214	324	0.00005	0.00003	0.010232870
## 998	0	307	465	0.00007	0.00005	0.014679864
## 999	0	494	708	0.00010	0.00007	0.023621671
## 11882	0	405	619	0.00009	0.00006	0.019365945
## 12927	0	245	461	0.00005	0.00005	0.011715201
## 12928	0	149	228	0.00003	0.00002	0.007124755
## 12929	0	227	414	0.00005	0.00004	0.010854492
## 12930	0	557	876	0.00012	0.00009	0.026634151
## 12932	0	267	520	0.00006	0.00005	0.012767178
## 12933	0	411	701	0.00009	0.00007	0.019652848
## 12935	0	389	741	0.00008	0.00007	0.018600870
## 26288	0	1705	2311	0.00036	0.00023	0.081528236
## 26425	0	192	317	0.00004	0.00003	0.009180892
## 32738	0	108	157	0.00002	0.00002	0.005164252
## 34655	3	19	27	0.00000	0.00000	1.000000000
## 39537	0	194	334	0.00004	0.00003	0.009276527
## 47074	0	197	350	0.00004	0.00003	0.009419978
## 47077	0	111	166	0.00002	0.00002	0.005307703
## 121954	0	161	201	0.00003	0.00002	0.007698561
## 135685	0	116	176	0.00002	0.00002	0.005546789
## 175740	0	228	438	0.00005	0.00004	0.010902310
## 203616	0	249	561	0.00005	0.00006	0.011906470
## 234062	0	380	557	0.00008	0.00005	0.018170516
## 255789	0	318	503	0.00007	0.00005	0.015205853
## 524780	0	321	534	0.00007	0.00005	0.015349304
## 759016	0	275	496	0.00006	0.00005	0.013149715
## 759758	0	184	291	0.00004	0.00003	0.008798355
## 1334421	0	170	305	0.00004	0.00003	0.008128915
## 1387655	0	124	171	0.00003	0.00002	0.005929326
## 1568324	3	0	30	0.00000	0.00000	NaN
##	Local.Freq.May	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq		
## 984	0.956327685	4.441710e-03	3.619843e-03	8.218670e-04		
## 985	0.447631193	1.753703e-03	1.620355e-03	1.333488e-04		
## 986	0.008927118	5.033640e-05	3.231476e-05	1.802164e-05		
## 987	0.047538937	1.958235e-04	1.720835e-04	2.374000e-05		
## 988	0.018179845	8.750464e-05	6.580818e-05	2.169645e-05		
## 989	0.013051501	5.585854e-05	4.724438e-05	8.614161e-06		
## 991	0.005535356	2.761069e-05	2.003712e-05	7.573568e-06		
## 993	0.024067944	1.100180e-04	8.712217e-05	2.289579e-05		
## 994	0.020106366	9.154004e-05	7.278188e-05	1.875816e-05		
## 995	0.020431975	1.338056e-04	7.396054e-05	5.984509e-05		
## 997	0.008791447	4.545144e-05	3.182366e-05	1.362778e-05		
## 998	0.012617355	6.520370e-05	4.567284e-05	1.953085e-05		
## 999	0.019210940	1.049206e-04	6.954059e-05	3.538002e-05		
## 11882	0.016796006	8.601791e-05	6.079890e-05	2.521900e-05		
## 12927	0.012508819	5.203552e-05	4.527996e-05	6.755566e-06		
## 12928	0.006186574	3.164609e-05	2.239443e-05	9.251668e-06		

## 12929	0.011233516	4.821251e-05	4.066356e-05	7.548943e-06
## 12930	0.023769469	1.183012e-04	8.604174e-05	3.225943e-05
## 12932	0.014109730	5.670810e-05	5.107501e-05	5.633095e-06
## 12933	0.019021002	8.729225e-05	6.885304e-05	1.843921e-05
## 12935	0.020106366	8.261967e-05	7.278188e-05	9.837784e-06
## 26288	0.062706897	3.621248e-04	2.269891e-04	1.351357e-04
## 26425	0.008601509	4.077886e-05	3.113611e-05	9.642750e-06
## 32738	0.004260053	2.293811e-05	1.542072e-05	7.517385e-06
## 34655	1.000000000	4.035408e-06	2.651971e-06	1.383436e-06
## 39537	0.009062788	4.120364e-05	3.280587e-05	8.397770e-06
## 47074	0.009496934	4.184081e-05	3.437741e-05	7.463401e-06
## 47077	0.004504260	2.357528e-05	1.630471e-05	7.270565e-06
## 121954	0.005453953	3.419477e-05	1.974245e-05	1.445232e-05
## 135685	0.004775601	2.463723e-05	1.728693e-05	7.350302e-06
## 175740	0.011884734	4.842490e-05	4.302087e-05	5.404025e-06
## 203616	0.015222228	5.288508e-05	5.510207e-05	-2.216991e-06
## 234062	0.015113692	8.070816e-05	5.470919e-05	2.599897e-05
## 255789	0.013648451	6.753999e-05	4.940525e-05	1.813474e-05
## 524780	0.014489608	6.817716e-05	5.245010e-05	1.572705e-05
## 759016	0.013458512	5.840722e-05	4.871770e-05	9.689522e-06
## 759758	0.007896022	3.907974e-05	2.858236e-05	1.049738e-05
## 1334421	0.008275899	3.610628e-05	2.995746e-05	6.148826e-06
## 1387655	0.004639931	2.633635e-05	1.679582e-05	9.540527e-06
## 1568324	1.000000000	0.000000e+00	2.946635e-06	-2.946635e-06
##	Multinom Polarity Polarity.Adj			
## 984	9.034546e-45	0.0237027	0.2477886	
## 985	NA	NA	NA	
## 986	NA	NA	NA	
## 987	NA	NA	NA	
## 988	NA	NA	NA	
## 989	NA	NA	NA	
## 991	NA	NA	NA	
## 993	NA	NA	NA	
## 994	NA	NA	NA	
## 995	NA	NA	NA	
## 997	NA	NA	NA	
## 998	NA	NA	NA	
## 999	NA	NA	NA	
## 11882	NA	NA	NA	
## 12927	NA	NA	NA	
## 12928	NA	NA	NA	
## 12929	NA	NA	NA	
## 12930	NA	NA	NA	
## 12932	NA	NA	NA	
## 12933	NA	NA	NA	
## 12935	NA	NA	NA	
## 26288	NA	NA	NA	
## 26425	NA	NA	NA	
## 32738	NA	NA	NA	
## 34655	NA	NA	NA	
## 39537	NA	NA	NA	
## 47074	NA	NA	NA	
## 47077	NA	NA	NA	
## 121954	NA	NA	NA	
## 135685	NA	NA	NA	
## 175740	NA	NA	NA	

```

## 203616      NA      NA      NA
## 234062      NA      NA      NA
## 255789      NA      NA      NA
## 524780      NA      NA      NA
## 759016      NA      NA      NA
## 759758      NA      NA      NA
## 1334421     NA      NA      NA
## 1387655     NA      NA      NA
## 1568324     NA      NA      NA
##
## 984          root cellular organisms Bacteria Terrabacteria group Firmicutes
## 985          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 986          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 987          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 988          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 989          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 991          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 993          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 994          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 995          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 997          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 998          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 999          root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 11882        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12927        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12928        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12929        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12930        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12932        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12933        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 12935        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 26288        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 26425        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 32738        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 34655        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 39537        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 47074        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 47077        root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 121954       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 135685       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 175740       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 203616       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 234062       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 255789       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 524780       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 759016       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 759758       root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 1334421     root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 1387655     root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 1568324     root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococci
## 1568324     root Viruses Caudovirales

tid <- 1279 # I think this is it.
path2root(1279)

##          name tax_id parent      rank embl_code
## 1          root      1     NA    no rank
## 101088 cellular organisms 131567      1    no rank

```

```

## 2          Bacteria          2 131567 superkingdom
## 1446826 Terrabacteria group 1783272      2      no rank
## 952          Firmicutes      1239 1783272      phylum
## 65606          Bacilli      91061      1239      class
## 1073          Bacillales      1385      91061      order
## 65515          Staphylococcaceae 90964      1385      family
## 984          Staphylococcus      1279      90964      genus
##          division_id br_bel br_may br_bel_frac br_may_frac
## 1          8 4708322 10181105      0      0
## 101088      8 4636449 9943097      0      0
## 2          0 3246493 7673696      0      0
## 1446826      0 1329975 5530830      0      0
## 952          0 262709 392959      0      0
## 65606      0 184945 263399      0      0
## 1073      0 147562 207509      0      0
## 65515      0 22013 38537      0      0
## 984          0 20913 36854      0      0
##          Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1          NA          NA      1.000000000      1.000000000
## 101088      0.9847349      0.97662258      0.984734901      0.976622577
## 2          0.7002111      0.77176115      0.689522297      0.753719365
## 1446826      0.4096651      0.72075177      0.282473246      0.543244569
## 952          0.1975293      0.07104883      0.055796736      0.038596891
## 65606      0.7039919      0.67029639      0.039280449      0.025871357
## 1073      0.7978696      0.78781241      0.031340677      0.020381776
## 65515      0.1491780      0.18571243      0.004675339      0.003785149
## 984          0.9500295      0.95632769      0.004441710      0.003619843
##          DeltaFreq      Multinom      Polarity Polarity.Adj
## 1          0.000000000      0.000000e+00      NA      NA
## 101088      0.0081123245      0.000000e+00      1.000000e+00      1.000000000
## 2          -0.0641970685      0.000000e+00      4.005432e-05      0.01921082
## 1446826      -0.2607713229      0.000000e+00      7.031250e-02      1.000000000
## 952          0.0171998451      8.646919e-191      4.531250e-01      1.000000000
## 65606      0.0134090917      3.253669e-16      NA      NA
## 1073      0.0109589014      0.000000e+00      5.078125e-01      1.000000000
## 65515      0.0008901896      9.951119e-03      3.750000e-01      0.625000000
## 984          0.0008218670      9.034546e-45      2.370270e-02      0.24778856
##
## 1
## 101088
## 2
## 1446826
## 952
## 65606
## 1073
## 65515
## 984
root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Bacillales Staphylococcus
make_table(90964 , relative_taxa=2) # parent of
##          Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May
## 1 Staphylococcus      1279 90964 genus      0.950      0.956
## 2 Macrococcus      69965 90964 genus      0.031      0.027
## 3 <NA>      2005363 90964 genus      0.011      0.009
## 4 Salinicoccus      45669 90964 genus      0.005      0.005
## 5 Jeotgalicoccus      227979 90964 genus      0.003      0.003
## log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq Rel.Freq.Bel

```



```
## 1      -0.007      0.004      0.004      0.001      0.006
## 2      0.132      0.000      0.000      0.000      0.000
## 3      0.180      0.000      0.000      0.000      0.000
## 4      0.109      0.000      0.000      0.000      0.000
## 5      0.058      0.000      0.000      0.000      0.000
## Rel.Freq.May Rel.DeltaFreq
## 1      0.005      0.001
## 2      0.000      0.000
## 3      0.000      0.000
## 4      0.000      0.000
## 5      0.000      0.000

idx <- grep("Propionibacterium", tree$name); tree[idx,] #Terra Actinobacteria

##              name tax_id parent    rank
## 1368          Propionibacterium 1743 31957  genus
## 1369    Propionibacterium freudenreichii 1744 1743 species
## 90821    Propionibacterium australiense 119981 1743 species
## 474424    Propionibacterium acidifaciens 556499 1743 species
## 548526 Propionibacterium sp. oral taxon 193 671223 1743 species
##      embl_code division_id br_bel br_may br_bel_frac br_may_frac
## 1368              0      881    940      0e+00      0e+00
## 1369      PF              0      284    300      6e-05      3e-05
## 90821      PA              0      241    235      5e-05      2e-05
## 474424      PA              0      295    348      6e-05      3e-05
## 548526      PS              0       61     57      1e-05      1e-05
##      Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1368      0.1690979      0.1653474 1.871155e-04 9.232790e-05
## 1369      0.3223610      0.3191489 6.031873e-05 2.946635e-05
## 90821      0.2735528      0.2500000 5.118596e-05 2.308197e-05
## 474424      0.3348468      0.3702128 6.265502e-05 3.418097e-05
## 548526      0.0692395      0.0606383 1.295578e-05 5.598606e-06
##      DeltaFreq Multinom Polarity Polarity.Adj
## 1368 9.478760e-05 0.3749978      0.625      1
## 1369 3.085238e-05      NA      NA      NA
## 90821 2.810399e-05      NA      NA      NA
## 474424 2.847405e-05      NA      NA      NA
## 548526 7.357177e-06      NA      NA      NA
##
## 1368          root cellular organisms Bacteria Terrabacteria group Actinobacteria
## 1369    root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Propionibacterium
## 90821    root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Propionibacterium
## 474424    root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Propionibacterium
## 548526 root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Propionibacterium

tid <- 1743 # I think this is it.
path2root(1743)

##      name tax_id parent    rank embl_code
## 1      root      1      NA    no rank
## 101088 cellular organisms 131567      1    no rank
## 2      Bacteria      2 131567 superkingdom
## 1446826 Terrabacteria group 1783272      2    no rank
## 163583  Actinobacteria 201174 1783272  phylum
## 1380  Actinobacteria 1760 201174    class
## 60250  Propionibacteriales 85009 1760    order
## 14779  Propionibacteriaceae 31957 85009  family
## 1368  Propionibacterium 1743 31957    genus
```

```

##      division_id br_bel   br_may br_bel_frac br_may_frac
## 1              8 4708322 10181105          0          0
## 101088         8 4636449  9943097          0          0
## 2              0 3246493  7673696          0          0
## 1446826        0 1329975  5530830          0          0
## 163583         0  289325   382562          0          0
## 1380           0  280956   373185          0          0
## 60250          0  18754    19267          0          0
## 14779          0   5210     5685          0          0
## 1368           0    881     940          0          0
##      Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1              NA              NA  1.0000000000  1.0000000000
## 101088         0.98473490      0.97662258  0.9847349013  0.9766225768
## 2              0.70021109      0.77176115  0.6895222969  0.7537193654
## 1446826        0.40966514      0.72075177  0.2824732463  0.5432445692
## 163583         0.21754168      0.06916900  0.0614497054  0.0375756855
## 1380           0.97107405      0.97548894  0.0596722144  0.0366546657
## 60250          0.06675067      0.05162855  0.0039831600  0.0018924272
## 14779          0.27780740      0.29506410  0.0011065513  0.0005583873
## 1368           0.16909789      0.16534741  0.0001871155  0.0000923279
##      DeltaFreq      Multinom      Polarity Polarity.Adj
## 1      0.0000000000  0.000000e+00          NA          NA
## 101088  0.0081123245  0.000000e+00  1.000000e+00  1.000000000
## 2      -0.0641970685  0.000000e+00  4.005432e-05  0.01921082
## 1446826 -0.2607713229  0.000000e+00  7.031250e-02  1.000000000
## 163583  0.0238740199  4.282119e-47  4.531250e-01  1.000000000
## 1380     0.0230175488  0.000000e+00  7.197380e-03  1.000000000
## 60250     0.0020907328  2.078406e-04          NA          NA
## 14779     0.0005481640  3.801651e-17  1.000000e+00  0.625000000
## 1368     0.0000947876  3.749978e-01  6.250000e-01  1.000000000
##
## 1
## 101088
## 2
## 1446826
## 163583
## 1380
## 60250
## 14779
## 1368
root cellular organisms Bacteria Terrabacteria group Actinobacteria
root cellular organisms Bacteria Terrabacteria group Actinobacteria Actinobacteria Propionibacterium

make_table(31957 , relative_taxa=2) # parent of

##      Name Tax. Id. Parent Rank Local.Freq.Bel
## 1      Tessaracoccus  72763  31957 genus      0.249
## 2      Propionibacterium  1743  31957 genus      0.169
## 3      Microlunatus  29404  31957 genus      0.166
## 4      Acidipropionibacterium 1912215 31957 genus      0.155
## 5      Cutibacterium  1912216 31957 genus      0.115
## 6      Auraticoccus  1278221 31957 genus      0.085
## 7      Pseudopropionibacterium 1912217 31957 genus      0.048
## 8      Propionimicrobium  203133 31957 genus      0.014
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.291      -0.158          0.000          0.000      0.000
## 2      0.165       0.022          0.000          0.000      0.000
## 3      0.114       0.376          0.000          0.000      0.000
## 4      0.174      -0.121          0.000          0.000      0.000

```

```

## 5      0.100      0.139      0.000      0.000      0.000
## 6      0.098     -0.141      0.000      0.000      0.000
## 7      0.041      0.158      0.000      0.000      0.000
## 8      0.016     -0.150      0.000      0.000      0.000
## Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.000      0.000      0.000
## 2      0.000      0.000      0.000
## 3      0.000      0.000      0.000
## 4      0.000      0.000      0.000
## 5      0.000      0.000      0.000
## 6      0.000      0.000      0.000
## 7      0.000      0.000      0.000
## 8      0.000      0.000      0.000

idx <- grep("Planctomycetes", tree$name); tree[idx,] # PVC group

##          name tax_id parent rank embl_code division_id br_bel
## 165851 Planctomycetes 203682 1783257 phylum 0 12002
##          br_may br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May
## 165851 8517 0 0 0.5699226 0.4328404
##          Glob.Freq.Bel Glob.Freq.May DeltaFreq Multinom Polarity
## 165851 0.002549103 0.0008365497 0.001712554 1.002846e-20 1
##          Polarity.Adj
## 165851 NA
##
## path
## 165851 root cellular organisms Bacteria PVC group Planctomycetes

tid <- 203682 # I think this is it.
path2root(203682)

##          name tax_id parent rank embl_code
## 1          root 1 NA no rank
## 101088 cellular organisms 131567 1 no rank
## 2          Bacteria 2 131567 superkingdom
## 1446811 PVC group 1783257 2 no rank
## 165851 Planctomycetes 203682 1783257 phylum
##          division_id br_bel br_may br_bel_frac br_may_frac
## 1 8 4708322 10181105 0 0
## 101088 8 4636449 9943097 0 0
## 2 0 3246493 7673696 0 0
## 1446811 0 21059 19677 0 0
## 165851 0 12002 8517 0 0
##          Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1 NA NA 1.000000000 1.000000000
## 101088 0.984734901 0.976622577 0.984734901 0.9766225768
## 2 0.700211088 0.771761152 0.689522297 0.7537193654
## 1446811 0.006486692 0.002564214 0.004472719 0.0019326979
## 165851 0.569922598 0.432840372 0.002549103 0.0008365497
##          DeltaFreq Multinom Polarity Polarity.Adj
## 1 0.000000000 0.000000e+00 NA NA
## 101088 0.008112324 0.000000e+00 1.000000e+00 1.000000000
## 2 -0.064197069 0.000000e+00 4.005432e-05 0.01921082
## 1446811 0.002540021 1.910166e-180 1.000000e+00 1.000000000
## 165851 0.001712554 1.002846e-20 1.000000e+00 NA
##
## path
## 1 root
## 101088 root cellular organisms
## 2 root cellular organisms Bacteria

```

```

## 1446811      root cellular organisms Bacteria PVC group
## 165851  root cellular organisms Bacteria PVC group Planctomycetes

make_table(1783257 , relative_taxa=2) #

##           Name Tax. Id.  Parent  Rank Local.Freq.Bel Local.Freq.May
## 1      Planctomycetes  203682 1783257 phylum      0.570      0.433
## 2      Verrucomicrobia   74201 1783257 phylum      0.290      0.364
## 3          Chlamydiae  204428 1783257 phylum      0.108      0.171
## 4 Kiritimatiellaeota  134625 1783257 phylum      0.018      0.017
## 5      Lentisphaerae  256845 1783257 phylum      0.014      0.016
## log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq Rel.Freq.Bel
## 1      0.275      0.003      0.001      0.002      0.004
## 2     -0.227      0.001      0.001      0.001      0.002
## 3     -0.456      0.000      0.000      0.000      0.001
## 4      0.057      0.000      0.000      0.000      0.000
## 5     -0.107      0.000      0.000      0.000      0.000
## Rel.Freq.May Rel.DeltaFreq
## 1      0.001      0.003
## 2      0.001      0.001
## 3      0.000      0.001
## 4      0.000      0.000
## 5      0.000      0.000

idx <- grep("Bacteroidetes", tree$name); tree[idx,] # Bacteria FCB group

##           name tax_id parent  rank
## 752      Bacteroidetes   976  68336 phylum
## 45553      Bacteroidetes/Chlorobi group  68336 1783270 no rank
## 852851 Bacteroidetes Order II. Incertae sedis 1100069   976  order
##           embl_code division_id br_bel br_may br_bel_frac br_may_frac
## 752           0 324656 315798      0      0
## 45553          0 328184 320378      0      0
## 852851          0  3021  2448      0      0
##           Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 752      0.989249933      0.985704387  0.0689536527  0.0310180476
## 45553      0.993226843      0.991965273  0.0697029642  0.0314679006
## 852851      0.009305234      0.007751791  0.0006416299  0.0002404454
##           DeltaFreq Multinom Polarity Polarity.Adj
## 752      0.0379356051 5.693315e-102      1.000      1
## 45553      0.0382350637 1.910047e-46      0.625      NA
## 852851      0.0004011844 1.000000e+00      NA      NA
##
## 752      root cellular organisms Bacteria FCB group Bacteroidetes/
## 45553      root cellular organisms Bacteria FCB group l
## 852851 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes Bacteroidetes

tid <- 976 # I think this is it.
path2root(976)

##           name tax_id parent  rank
## 1      root      1      NA  no rank
## 101088 cellular organisms 131567      1  no rank
## 2      Bacteria      2 131567 superkingdom
## 1446824 FCB group 1783270      2  no rank
## 45553 Bacteroidetes/Chlorobi group  68336 1783270  no rank
## 752      Bacteroidetes   976  68336  phylum
##           embl_code division_id br_bel br_may br_bel_frac br_may_frac
## 1           8 4708322 10181105      0      0

```

```

## 101088      8 4636449 9943097      0      0
## 2           0 3246493 7673696      0      0
## 1446824     0 330422 322973      0      0
## 45553       0 328184 320378      0      0
## 752         0 324656 315798      0      0
##           Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1           NA           NA      1.00000000 1.00000000
## 101088      0.9847349    0.97662258    0.98473490 0.97662258
## 2           0.7002111    0.77176115    0.68952230 0.75371937
## 1446824     0.1017781    0.04208832    0.07017829 0.03172278
## 45553       0.9932268    0.99196527    0.06970296 0.03146790
## 752         0.9892499    0.98570439    0.06895365 0.03101805
##           DeltaFreq      Multinom      Polarity Polarity.Adj
## 1           0.00000000 0.000000e+00      NA      NA
## 101088      0.008112324 0.000000e+00 1.000000e+00 1.00000000
## 2          -0.064197069 0.000000e+00 4.005432e-05 0.01921082
## 1446824     0.038455508 1.585467e-11 6.250000e-01      NA
## 45553       0.038235064 1.910047e-46 6.250000e-01      NA
## 752         0.037935605 5.693315e-102 1.000000e+00 1.00000000
##
## path
## 1 root
## 101088 root cellular organisms
## 2 root cellular organisms Bacteria
## 1446824 root cellular organisms Bacteria FCB group
## 45553 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group
## 752 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes

make_table(68336 , relative_taxa=2) #

##           Name Tax. Id. Parent Rank Local.Freq.Bel Local.Freq.May
## 1 Bacteroidetes 976 68336 phylum 0.989 0.986
## 2 Chlorobi 1090 68336 phylum 0.007 0.008
## 3 Ignavibacteriae 1134404 68336 phylum 0.003 0.005
## 4 Balneolaeota 1936987 68336 phylum 0.001 0.001
## log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq Rel.Freq.Bel
## 1 0.004 0.069 0.031 0.038 0.100
## 2 -0.195 0.000 0.000 0.000 0.001
## 3 -0.533 0.000 0.000 0.000 0.000
## 4 -0.095 0.000 0.000 0.000 0.000
## Rel.Freq.May Rel.DeltaFreq
## 1 0.041 0.059
## 2 0.000 0.001
## 3 0.000 0.000
## 4 0.000 0.000

idx <- grep("Deltaproteobacteria", tree$name); tree[idx,] # Proteo

##           name tax_id parent rank embl_code division_id br_bel
## 12023 Deltaproteobacteria 28221 68525 class 0 41552
## br_may br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May
## 12023 46557 0 0 0.5711851 0.4673834
## Glob.Freq.Bel Glob.Freq.May DeltaFreq Multinom Polarity
## 12023 0.008825225 0.004572883 0.004252342 1.270886e-69 0.5078125
## Polarity.Adj
## 12023 1
##
## path
## 12023 root cellular organisms Bacteria Proteobacteria delta/epsilon subdivisions Deltaproteobacteria

```

```

tid <- 28221 # I think this is it.
path2root(28221 )

##          name tax_id parent      rank embl_code
## 1          root      1    NA      no rank
## 101088 cellular organisms 131567    1      no rank
## 2          Bacteria      2 131567 superkingdom
## 942       Proteobacteria 1224    2      phylum
## 45715 delta/epsilon subdivisions 68525 1224 subphylum
## 12023 Deltaproteobacteria 28221 68525    class
##      division_id br_bel  br_may br_bel_frac br_may_frac Local.Freq.Bel
## 1              8 4708322 10181105          0          0          NA
## 101088          8 4636449 9943097          0          0      0.98473490
## 2              0 3246493 7673696          0          0      0.70021109
## 942              0 1529279 1744867          0          0      0.47105569
## 45715           0  72747   99612          0          0      0.04756948
## 12023           0  41552   46557          0          0      0.57118507
##      Local.Freq.May Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1              NA      1.000000000      1.000000000 0.000000000
## 101088          0.97662258      0.984734901      0.976622577 0.008112324
## 2              0.77176115      0.689522297      0.753719365 -0.064197069
## 942              0.22738287      0.324803401      0.171382871 0.153420531
## 45715           0.05708859      0.015450727      0.009784007 0.005666721
## 12023           0.46738345      0.008825225      0.004572883 0.004252342
##      Multinom      Polarity Polarity.Adj
## 1      0.000000e+00      NA      NA
## 101088 0.000000e+00 1.000000e+00      1.00000000
## 2      0.000000e+00 4.005432e-05      0.01921082
## 942      0.000000e+00 7.265625e-01      1.00000000
## 45715      0.000000e+00      NA      NA
## 12023      1.270886e-69 5.078125e-01      1.00000000
##
## path
## 1          root
## 101088      root cellular organisms
## 2          root cellular organisms Bacteria
## 942          root cellular organisms Bacteria Proteobacteria
## 45715      root cellular organisms Bacteria Proteobacteria delta/epsilon subdivisions
## 12023      root cellular organisms Bacteria Proteobacteria delta/epsilon subdivisions Deltaproteobacteria

make_table(68525 , relative_taxa=2) #

##      Name Tax. Id. Parent Rank Local.Freq.Bel
## 1 Deltaproteobacteria 28221 68525 class      0.571
## 2 Epsilonproteobacteria 29547 68525 class      0.429
##      Local.Freq.May log(BvsM) Glob.Freq.Bel Glob.Freq.May DeltaFreq
## 1      0.467      0.201      0.009      0.005      0.004
## 2      0.533     -0.217      0.007      0.005      0.001
##      Rel.Freq.Bel Rel.Freq.May Rel.DeltaFreq
## 1      0.013      0.006      0.007
## 2      0.010      0.007      0.003

idx <- grep("Muriicola", tree$name); tree[idx,] # Proteo

##      name tax_id parent rank embl_code division_id br_bel br_may
## 610168 Muriicola 762641 49546 genus          0 971 610
##      br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May Glob.Freq.Bel
## 610168          0          0      0.00399365      0.00265874 0.0002062306
##      Glob.Freq.May DeltaFreq Multinom Polarity Polarity.Adj

```

```
## 610168 5.991491e-05 0.0001463157 1 NA NA
##
## 610168 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes Flavobacteri
tid <- 762641 # I think this is it.
path2root(762641 )

##          name tax_id parent      rank
## 1          root      1     NA    no rank
## 101088 cellular organisms 131567      1    no rank
## 2          Bacteria      2  131567 superkingdom
## 1446824 FCB group 1783270      2    no rank
## 45553 Bacteroidetes/Chlorobi group 68336 1783270    no rank
## 752 Bacteroidetes      976  68336    phylum
## 88883 Flavobacteriia 117743      976    class
## 163073 Flavobacteriales 200644 117743    order
## 29439 Flavobacteriaceae 49546 200644    family
## 610168 Muriicola 762641 49546    genus
##      embl_code division_id br_bel br_may br_bel_frac br_may_frac
## 1          8 4708322 10181105      0      0
## 101088      8 4636449 9943097      0      0
## 2          0 3246493 7673696      0      0
## 1446824      0 330422 322973      0      0
## 45553      0 328184 320378      0      0
## 752      0 324656 315798      0      0
## 88883      0 248583 237410      0      0
## 163073      0 248583 237410      0      0
## 29439      0 243136 229432      0      0
## 610168      0 971 610      0      0
##      Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1          NA      NA 1.0000000000 1.000000e+00
## 101088 0.98473490 0.97662258 0.9847349013 9.766226e-01
## 2 0.70021109 0.77176115 0.6895222969 7.537194e-01
## 1446824 0.10177813 0.04208832 0.0701782928 3.172278e-02
## 45553 0.99322684 0.99196527 0.0697029642 3.146790e-02
## 752 0.98924993 0.98570439 0.0689536527 3.101805e-02
## 88883 0.76568121 0.75177804 0.0527965165 2.331869e-02
## 163073 1.00000000 1.00000000 0.0527965165 2.331869e-02
## 29439 0.97808780 0.96639569 0.0516396287 2.253508e-02
## 610168 0.00399365 0.00265874 0.0002062306 5.991491e-05
##      DeltaFreq Multinom Polarity Polarity.Adj
## 1 0.0000000000 0.000000e+00      NA      NA
## 101088 0.0081123245 0.000000e+00 1.000000e+00 1.00000000
## 2 -0.0641970685 0.000000e+00 4.005432e-05 0.01921082
## 1446824 0.0384555083 1.585467e-11 6.250000e-01      NA
## 45553 0.0382350637 1.910047e-46 6.250000e-01      NA
## 752 0.0379356051 5.693315e-102 1.000000e+00 1.00000000
## 88883 0.0294778295 1.000000e+00      NA      NA
## 163073 0.0294778295 2.338465e-171 6.875000e-01 1.00000000
## 29439 0.0291045503 0.000000e+00 9.191455e-02 0.86005007
## 610168 0.0001463157 1.000000e+00      NA      NA
##
## 1
## 101088
## 2
## 1446824
## 45553
```

root cellular organism

```
## 752 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes
## 88883 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes
## 163073 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes
## 29439 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes
## 610168 root cellular organisms Bacteria FCB group Bacteroidetes/Chlorobi group Bacteroidetes Flavobacteriia
```

```
make_table(49546 , relative_taxa=2) #
```

##	Name	Tax. Id.	Parent	Rank	Local.Freq.	Bel
## 1	Flavobacterium	237	49546	genus	0.115	
## 2	Chryseobacterium	59732	49546	genus	0.098	
## 3	Polaribacter	52959	49546	genus	0.083	
## 4	Tenacibaculum	104267	49546	genus	0.062	
## 5	Maribacter	252356	49546	genus	0.037	
## 6	Winogradskyella	286104	49546	genus	0.037	
## 7	Capnocytophaga	1016	49546	genus	0.036	
## 8	Nonlabens	363408	49546	genus	0.035	
## 9	unclassified Flavobacteriaceae	61432	49546	no rank	0.035	
## 10	Gramella	292691	49546	genus	0.029	
## 11	Formosa	225842	49546	genus	0.029	
## 12	Cellulophaga	104264	49546	genus	0.028	
## 13	Aquimarina	290174	49546	genus	0.028	
## 14	Lacinutrix	291183	49546	genus	0.026	
## 15	Olleya	336276	49546	genus	0.021	
## 16	Lutibacter	358023	49546	genus	0.019	
## 17	Elizabethkingia	308865	49546	genus	0.018	
## 18	Dokdonia	326319	49546	genus	0.016	
## 19	Salagentibacter	143222	49546	genus	0.015	
## 20	Muricauda	111500	49546	genus	0.012	
## 21	Kordia	221065	49546	genus	0.012	
## 22	Myroides	76831	49546	genus	0.011	
## 23	Psychroserpens	49277	49546	genus	0.011	
## 24	Zunongwangia	417127	49546	genus	0.011	
## 25	Algibacter	261827	49546	genus	0.010	
## 26	Aequorivita	153265	49546	genus	0.010	
## 27	Seonamhaeicola	1649495	49546	genus	0.009	
## 28	Euzebyella	1287916	49546	genus	0.009	
## 29	Flavivirga	1209327	49546	genus	0.008	
## 30	Ornithobacterium	28250	49546	genus	0.008	
## 31	Gilvibacter	379070	49546	genus	0.008	
## 32	Siansivirga	1204360	49546	genus	0.008	
## 33	Wenyingzhuangia	1518147	49546	genus	0.008	
## 34	Riemerella	34084	49546	genus	0.008	
## 35	<NA>	2049301	49546	genus	0.007	
## 36	Mariniflexile	527198	49546	genus	0.007	
## 37	Croceibacter	216431	49546	genus	0.007	
## 38	Gillisia	244698	49546	genus	0.007	
## 39	Tamlana	393005	49546	genus	0.007	
## 40	Arenibacter	178469	49546	genus	0.006	
## 41	Flagellimonas	444459	49546	genus	0.006	
## 42	Sediminicola	389486	49546	genus	0.006	
## 43	Psychroflexus	83612	49546	genus	0.006	
## 44	Aureitalea	1176327	49546	genus	0.005	
## 45	Zobellia	112040	49546	genus	0.005	
## 46	<NA>	2058174	49546	genus	0.004	
## 47	Cloacibacterium	501783	49546	genus	0.004	
## 48	Muriicola	762641	49546	genus	0.004	

## 49		Apibacter	1778601	49546	genus	0.004
## 50		Robiginitalea	252306	49546	genus	0.003
## 51		Weeksella	1013	49546	genus	0.003
##	Local.Freq.May	log(BvsM)	Glob.Freq.Bel	Glob.Freq.May	DeltaFreq	
## 1	0.122	-0.058	0.006	0.003	0.003	
## 2	0.125	-0.246	0.005	0.003	0.002	
## 3	0.090	-0.081	0.004	0.002	0.002	
## 4	0.057	0.090	0.003	0.001	0.002	
## 5	0.034	0.092	0.002	0.001	0.001	
## 6	0.035	0.046	0.002	0.001	0.001	
## 7	0.033	0.071	0.002	0.001	0.001	
## 8	0.030	0.145	0.002	0.001	0.001	
## 9	0.036	-0.038	0.002	0.001	0.001	
## 10	0.026	0.133	0.002	0.001	0.001	
## 11	0.028	0.036	0.001	0.001	0.001	
## 12	0.026	0.080	0.001	0.001	0.001	
## 13	0.028	0.024	0.001	0.001	0.001	
## 14	0.028	-0.054	0.001	0.001	0.001	
## 15	0.022	-0.061	0.001	0.000	0.001	
## 16	0.024	-0.233	0.001	0.001	0.000	
## 17	0.023	-0.249	0.001	0.001	0.000	
## 18	0.015	0.053	0.001	0.000	0.000	
## 19	0.013	0.180	0.001	0.000	0.000	
## 20	0.007	0.566	0.001	0.000	0.000	
## 21	0.006	0.608	0.001	0.000	0.000	
## 22	0.013	-0.160	0.001	0.000	0.000	
## 23	0.010	0.093	0.001	0.000	0.000	
## 24	0.011	0.010	0.001	0.000	0.000	
## 25	0.011	-0.117	0.001	0.000	0.000	
## 26	0.008	0.183	0.001	0.000	0.000	
## 27	0.009	-0.004	0.000	0.000	0.000	
## 28	0.006	0.377	0.000	0.000	0.000	
## 29	0.008	0.049	0.000	0.000	0.000	
## 30	0.006	0.326	0.000	0.000	0.000	
## 31	0.004	0.631	0.000	0.000	0.000	
## 32	0.007	0.052	0.000	0.000	0.000	
## 33	0.008	-0.006	0.000	0.000	0.000	
## 34	0.008	-0.013	0.000	0.000	0.000	
## 35	0.006	0.130	0.000	0.000	0.000	
## 36	0.006	0.131	0.000	0.000	0.000	
## 37	0.007	-0.001	0.000	0.000	0.000	
## 38	0.007	-0.117	0.000	0.000	0.000	
## 39	0.005	0.202	0.000	0.000	0.000	
## 40	0.005	0.264	0.000	0.000	0.000	
## 41	0.005	0.175	0.000	0.000	0.000	
## 42	0.004	0.331	0.000	0.000	0.000	
## 43	0.006	-0.123	0.000	0.000	0.000	
## 44	0.003	0.483	0.000	0.000	0.000	
## 45	0.003	0.492	0.000	0.000	0.000	
## 46	0.004	0.086	0.000	0.000	0.000	
## 47	0.006	-0.309	0.000	0.000	0.000	
## 48	0.003	0.407	0.000	0.000	0.000	
## 49	0.005	-0.332	0.000	0.000	0.000	
## 50	0.003	0.125	0.000	0.000	0.000	
## 51	0.003	-0.225	0.000	0.000	0.000	
##	Rel.Freq.Bel	Rel.Freq.May	Rel.DeltaFreq			

```
## 1      0.009      0.004      0.005
## 2      0.007      0.004      0.003
## 3      0.006      0.003      0.003
## 4      0.005      0.002      0.003
## 5      0.003      0.001      0.002
## 6      0.003      0.001      0.002
## 7      0.003      0.001      0.002
## 8      0.003      0.001      0.002
## 9      0.003      0.001      0.002
## 10     0.002      0.001      0.001
## 11     0.002      0.001      0.001
## 12     0.002      0.001      0.001
## 13     0.002      0.001      0.001
## 14     0.002      0.001      0.001
## 15     0.002      0.001      0.001
## 16     0.001      0.001      0.000
## 17     0.001      0.001      0.000
## 18     0.001      0.000      0.001
## 19     0.001      0.000      0.001
## 20     0.001      0.000      0.001
## 21     0.001      0.000      0.001
## 22     0.001      0.000      0.001
## 23     0.001      0.000      0.001
## 24     0.001      0.000      0.001
## 25     0.001      0.000      0.001
## 26     0.001      0.000      0.001
## 27     0.001      0.000      0.001
## 28     0.001      0.000      0.001
## 29     0.001      0.000      0.001
## 30     0.001      0.000      0.001
## 31     0.001      0.000      0.001
## 32     0.001      0.000      0.001
## 33     0.001      0.000      0.001
## 34     0.001      0.000      0.001
## 35     0.001      0.000      0.001
## 36     0.001      0.000      0.001
## 37     0.001      0.000      0.001
## 38     0.000      0.000      0.000
## 39     0.000      0.000      0.000
## 40     0.000      0.000      0.000
## 41     0.000      0.000      0.000
## 42     0.000      0.000      0.000
## 43     0.000      0.000      0.000
## 44     0.000      0.000      0.000
## 45     0.000      0.000      0.000
## 46     0.000      0.000      0.000
## 47     0.000      0.000      0.000
## 48     0.000      0.000      0.000
## 49     0.000      0.000      0.000
## 50     0.000      0.000      0.000
## 51     0.000      0.000      0.000
```

```
idx <- grep("Carnobacteriaceae", tree$name); tree[idx,] # Proteo
```

```
##           name tax_id parent   rank embl_code division_id br_bel
## 150600 Carnobacteriaceae 186828 186826 family           0   2014
##           br_may br_bel_frac br_may_frac Local.Freq.Bel Local.Freq.May
```

```

## 150600      3216          0          0      0.05387476      0.0575416
##           Glob.Freq.Bel Glob.Freq.May   DeltaFreq      Multinom Polarity
## 150600      0.0004277532  0.0003158793  0.000111874  0.0003866219      1
##           Polarity.Adj
## 150600          1
##
## 150600 root cellular organisms Bacteria Terrabacteria group Firmicutes Bacilli Lactobacillales Carnobac

tid <- 186828 # I think this is it.
path2root(762641 )

##           name tax_id parent      rank
## 1           root      1      NA      no rank
## 101088      cellular organisms 131567      1      no rank
## 2           Bacteria      2 131567 superkingdom
## 1446824      FCB group 1783270      2      no rank
## 45553      Bacteroidetes/Chlorobi group 68336 1783270      no rank
## 752         Bacteroidetes      976 68336      phylum
## 88883         Flavobacteriia 117743      976      class
## 163073         Flavobacteriales 200644 117743      order
## 29439         Flavobacteriaceae 49546 200644      family
## 610168         Muriicola 762641 49546      genus
##           embl_code division_id br_bel      br_may br_bel_frac br_may_frac
## 1           8 4708322 10181105      0      0
## 101088      8 4636449 9943097      0      0
## 2           0 3246493 7673696      0      0
## 1446824      0 330422 322973      0      0
## 45553      0 328184 320378      0      0
## 752         0 324656 315798      0      0
## 88883      0 248583 237410      0      0
## 163073      0 248583 237410      0      0
## 29439      0 243136 229432      0      0
## 610168      0 971 610      0      0
##           Local.Freq.Bel Local.Freq.May Glob.Freq.Bel Glob.Freq.May
## 1           NA      NA      1.0000000000 1.000000e+00
## 101088      0.98473490 0.97662258 0.9847349013 9.766226e-01
## 2           0.70021109 0.77176115 0.6895222969 7.537194e-01
## 1446824      0.10177813 0.04208832 0.0701782928 3.172278e-02
## 45553      0.99322684 0.99196527 0.0697029642 3.146790e-02
## 752         0.98924993 0.98570439 0.0689536527 3.101805e-02
## 88883      0.76568121 0.75177804 0.0527965165 2.331869e-02
## 163073      1.00000000 1.00000000 0.0527965165 2.331869e-02
## 29439      0.97808780 0.96639569 0.0516396287 2.253508e-02
## 610168      0.00399365 0.00265874 0.0002062306 5.991491e-05
##           DeltaFreq      Multinom      Polarity Polarity.Adj
## 1           0.0000000000 0.000000e+00      NA      NA
## 101088      0.0081123245 0.000000e+00 1.000000e+00 1.00000000
## 2           -0.0641970685 0.000000e+00 4.005432e-05 0.01921082
## 1446824      0.0384555083 1.585467e-11 6.250000e-01      NA
## 45553      0.0382350637 1.910047e-46 6.250000e-01      NA
## 752         0.0379356051 5.693315e-102 1.000000e+00 1.00000000
## 88883      0.0294778295 1.000000e+00      NA      NA
## 163073      0.0294778295 2.338465e-171 6.875000e-01 1.00000000
## 29439      0.0291045503 0.000000e+00 9.191455e-02 0.86005007
## 610168      0.0001463157 1.000000e+00      NA      NA
##
## 1

```