Prepare data

```
## Loading required package: SummarizedExperiment

## Loading required package: MatrixGenerics

## Loading required package: matrixStats

##
## Attaching package: 'MatrixGenerics'

## The following objects are masked from 'package:matrixStats':
##
##     colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,
##     colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
##     colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
##     colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
##     colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
##     colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
##     colWeightedMeans, colWeightedMedians, colWeightedSds,
##     colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,
##     rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
##     rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
##     rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
##     rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
##     rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
##     rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
##     rowWeightedSds, rowWeightedVars

## Loading required package: GenomicRanges

## Loading required package: stats4

## Loading required package: BiocGenerics

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:stats':
##
##     IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##     anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##     dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##     grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##     order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##     rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##     union, unique, unsplit, which.max, which.min

## Loading required package: S4Vectors

##
## Attaching package: 'S4Vectors'

## The following objects are masked from 'package:base':
##
##     expand.grid, I, unname

## Loading required package: IRanges
```

```
## Loading required package: GenomeInfoDb

## Loading required package: Biobase

## Welcome to Bioconductor
##
##     Vignettes contain introductory material; view with
##     'browseVignettes()'. To cite Bioconductor, see
##     'citation("Biobase")', and for packages 'citation("pkgname")'.

##
## Attaching package: 'Biobase'

## The following object is masked from 'package:MatrixGenerics':
##
##     rowMedians

## The following objects are masked from 'package:matrixStats':
##
##     anyMissing, rowMedians

## Loading required package: SingleCellExperiment

## Loading required package: TreeSummarizedExperiment

## Loading required package: Biostrings

## Loading required package: XVector

##
## Attaching package: 'Biostrings'

## The following object is masked from 'package:base':
##
##     strsplit

## Loading required package: ggplot2

## Loading required package: ggraph

## Loading required package: MultiAssayExperiment

## snapshotDate(): 2021-07-27

## see ?microbiomeDataSets and browseVignettes('microbiomeDataSets') for documentation

## loading from cache

## see ?microbiomeDataSets and browseVignettes('microbiomeDataSets') for documentation

## loading from cache

## see ?microbiomeDataSets and browseVignettes('microbiomeDataSets') for documentation

## loading from cache
```
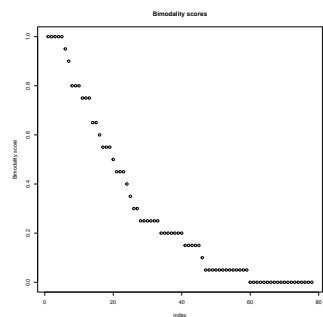
Check bimodality

```
## Loading required package: phyloseq

##
## Attaching package: 'phyloseq'
```

```
## The following object is masked from 'package:SummarizedExperiment':
##
##     distance

## The following object is masked from 'package:Biobase':
##
##     sampleNames

## The following object is masked from 'package:GenomicRanges':
##
##     distance

## The following object is masked from 'package:IRanges':
##
##     distance

##
## microbiome R package (microbiome.github.com)
##
##
##
##  Copyright (C) 2011-2021 Leo Lahti,
##     Sudarshan Shetty et al. <microbiome.github.io>

##
## Attaching package: 'microbiome'

## The following object is masked from 'package:ggplot2':
##
##     alpha

## The following object is masked from 'package:Biostrings':
##
##     coverage

## The following object is masked from 'package:SummarizedExperiment':
##
##     coverage

## The following object is masked from 'package:GenomicRanges':
##
##     coverage

## The following objects are masked from 'package:IRanges':
##
##     coverage, transform

## The following object is masked from 'package:S4Vectors':
##
##     transform

## The following object is masked from 'package:base':
##
##     transform
```
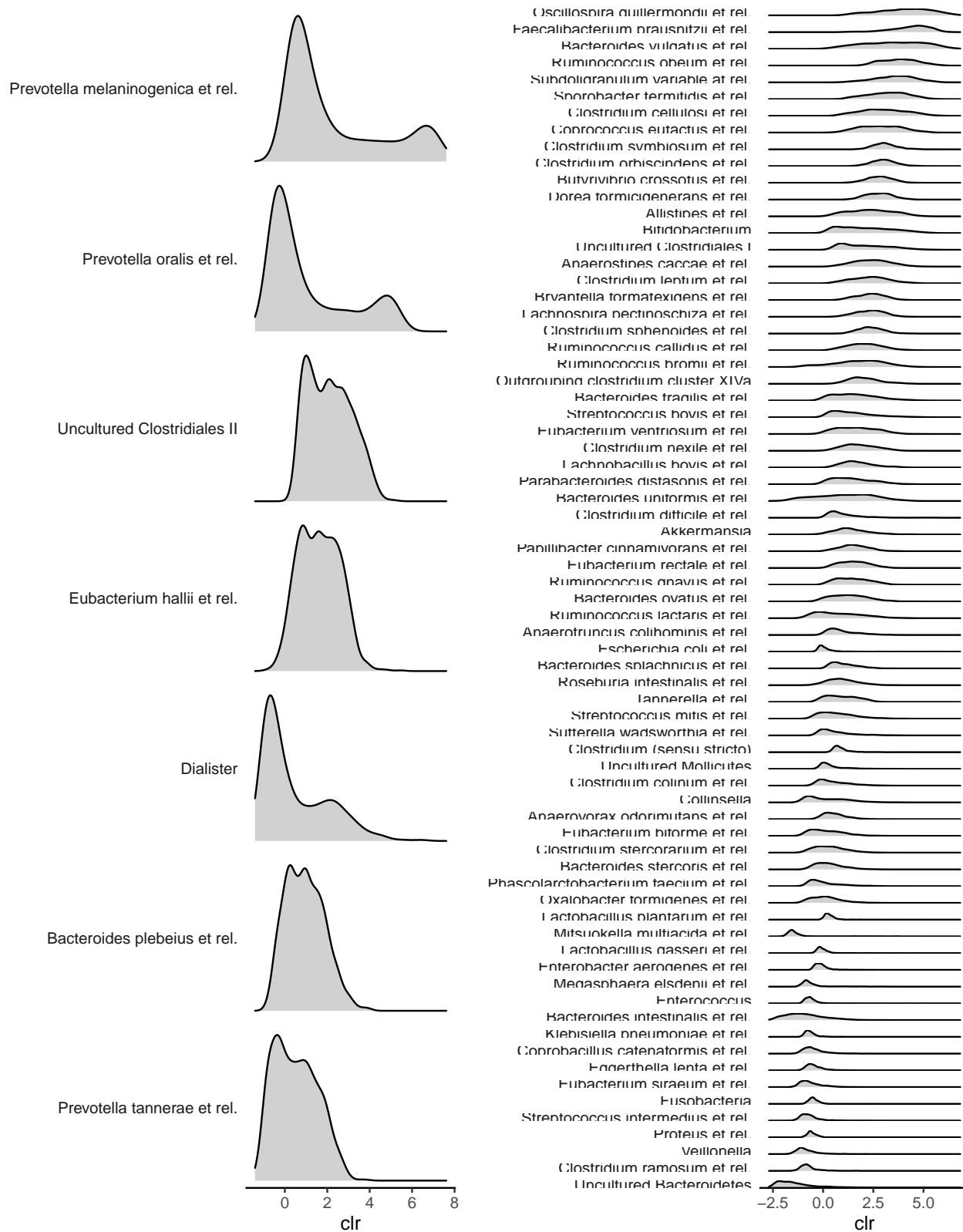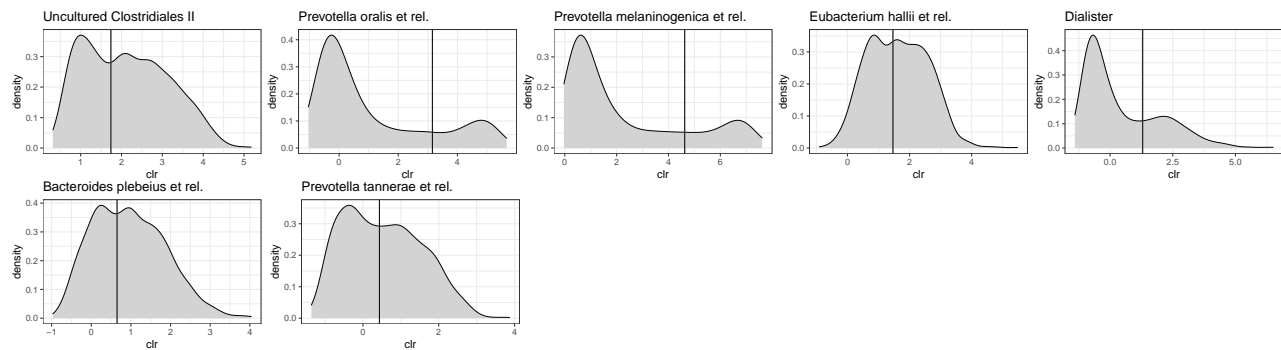
Bimodality scores

Bimodal and unimodal prevalent genera

Left panel (top to bottom):
- Prevotella melaninogenica et rel.
- Prevotella oralis et rel.
- Uncultured Clostridiales II
- Eubacterium hallii et rel.
- Dialister
- Bacteroides plebeius et rel.
- Prevotella tannerae et rel.

Right panel (top to bottom):
- Oscillospira guillermondii et rel.
- Faecalibacterium prausnitzii et rel.
- Bacteroides vulgatus et rel.
- Ruminococcus obeum et rel.
- Subdoligranulum variabile at rel.
- Sporobacter termitidis et rel.
- Clostridium cellulosi et rel.
- Coprococcus eutactus et rel.
- Clostridium symbiosum et rel.
- Clostridium orbiscindens et rel.
- Butyrivibrio crossotus et rel.
- Dorea formicigenerans et rel.
- Allistipes et rel.
- Bifidobacterium
- Uncultured Clostridiales I
- Anaerostipes caccae et rel.
- Clostridium leptum et rel.
- Bryantella formatexigens et rel.
- Lachnospira pectinoschiza et rel.
- Clostridium sphenoides et rel.
- Ruminococcus callidus et rel.
- Ruminococcus bromii et rel.
- Outgrouping clostridium cluster XIVa
- Bacteroides fragilis et rel.
- Streptococcus bovis et rel.
- Eubacterium ventriosum et rel.
- Clostridium nexile et rel.
- Lachnobacillus bovis et rel.
- Parabacteroides distasonis et rel.
- Bacteroides uniformis et rel.
- Clostridium difficile et rel.
- Akkermansia
- Papillibacter cinnamivorans et rel.
- Eubacterium rectale et rel.
- Ruminococcus gnavus et rel.
- Bacteroides ovatus et rel.
- Ruminococcus lactaris et rel.
- Anaerotruncus colihominis et rel.
- Escherichia coli et rel.
- Bacteroides splachnicus et rel.
- Roseburia intestinalis et rel.
- Tannerella et rel.
- Streptococcus mitis et rel.
- Sutterella wadsworthia et rel.
- Clostridium (sensu stricto)
- Uncultured Mollicutes
- Clostridium colinum et rel.
- Collinsella
- Anaerovorax odorimutans et rel.
- Eubacterium biforme et rel.
- Clostridium stercorarium et rel.
- Bacteroides stercoris et rel.
- Phascolarctobacterium faecium et rel.
- Oxalobacter formigenes et rel.
- Lactobacillus plantarum et rel.
- Mitsuokella multiacida et rel.
- Lactobacillus gasseri et rel.
- Enterobacter aerogenes et rel.
- Megasphaera elsdenii et rel.
- Enterococcus
- Bacteroides intestinalis et rel.
- Klebsiella pneumoniae et rel.
- Coprobacillus catenatormis et rel.
- Eggerthella lenta et rel.
- Eubacterium siraeum et rel.
- Fusobacteria
- Streptococcus intermedius et rel.
- Proteus et rel.
- Veillonella
- Clostridium ramosum et rel.
- Uncultured Bacteroidetes

Density minima

Location of the first density minimum; relative abundances are in unit interval.

```
##
## Attaching package: 'dplyr'

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

## The following object is masked from 'package:XVector':
##
##     slice

## The following object is masked from 'package:Biobase':
##
##     combine

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

## The following object is masked from 'package:GenomeInfoDb':
##
##     intersect

## The following objects are masked from 'package:IRanges':
##
##     collapse, desc, intersect, setdiff, slice, union

## The following objects are masked from 'package:S4Vectors':
##
##     first, intersect, rename, setdiff, setequal, union

## The following objects are masked from 'package:BiocGenerics':
##
##     combine, intersect, setdiff, union

## The following object is masked from 'package:matrixStats':
##
##     count

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

## The following objects are masked from 'package:base':
##
```

```
##      intersect, setdiff, setequal, union
```

tax	relab	clr
Prevotella melaninogenica et rel.	0.0695615	4.6258118
Prevotella oralis et rel.	0.0138339	3.1530291
Uncultured Clostridiales II	0.0024554	1.7397114
Eubacterium hallii et rel.	0.0018999	1.4654360
Dialister	0.0018944	1.3004911
Bacteroides plebeius et rel.	0.0008377	0.6508238
Prevotella tannerae et rel.	0.0006319	0.4354439

Abundance heatmap

With random sample subset (to speed up)

```
## Warning in metaMDS(d, wascores = FALSE, autotransform = FALSE, noshare = FALSE):
## stress is (nearly) zero: you may have insufficient data
```
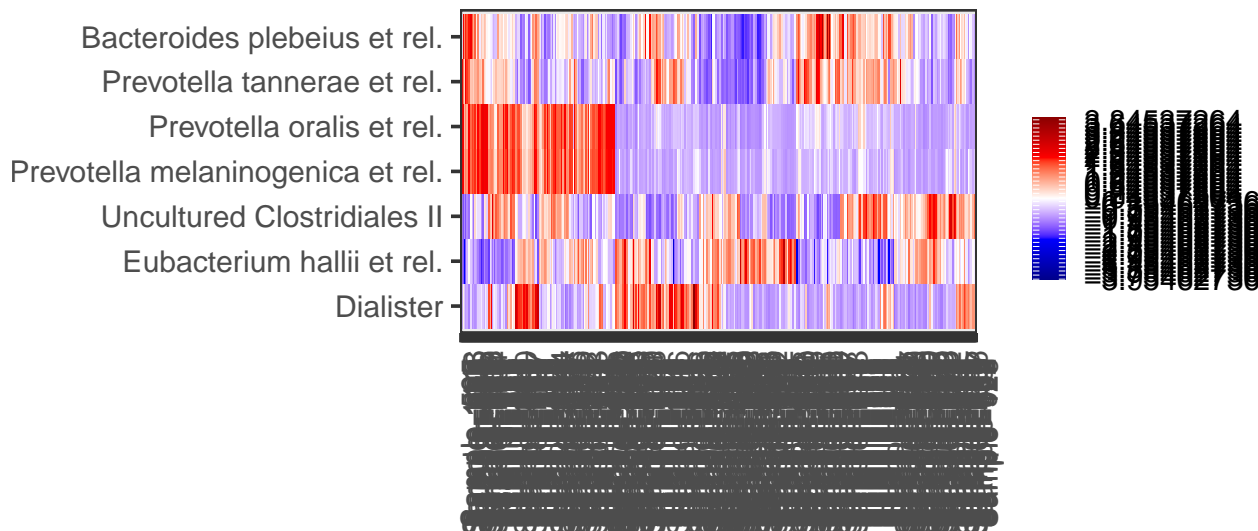

Correlations between bimodal taxa