# KECHIR KHELOUDJA

# Dans cette première étape, nous chargeons les packages nécessaires (DADA2 et d’autres) et définissons le chemin d’accès au dossier contenant les fichiers de séquences.

# Charger le package DADA2  
# Le packageVersion permet de vérifier la version de dada2 installée.  
 library(dada2); packageVersion("dada2")

## Loading required package: Rcpp  
  
## [1] '1.28.0'

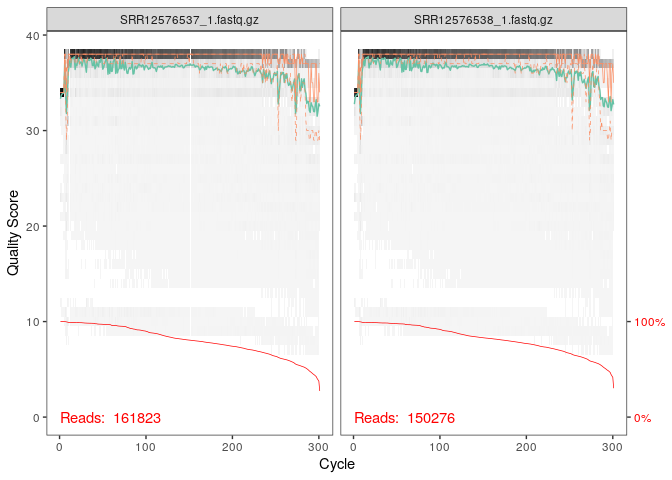
# Nous listons les fichiers .fastq.gz pour les lectures forward (fnFs) et reverse (fnRs) et extrayons les noms des échantillons à partir des noms de fichiers

# Définir le chemin vers le dossier contenant les séquences  
path <- "/home/rstudio/DADA2-et-Phyloseq" # Modifier le chemin si nécessaire  
  
# Lister les fichiers forward et reverse  
fnFs <- sort(list.files(path, pattern = "\_1.fastq.gz", full.names = TRUE)) # Lectures forward  
fnRs <- sort(list.files(path, pattern = "\_2.fastq.gz", full.names = TRUE)) # Lectures reverse

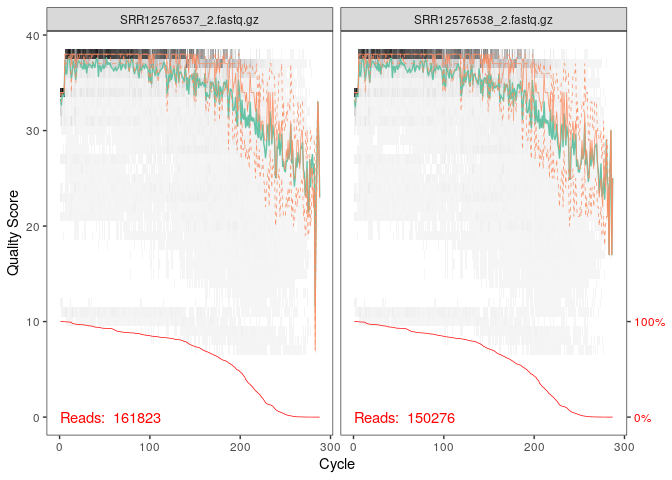
# Extraire les noms d'échantillons à partir des fichiers  
sample.names <- sapply(strsplit(basename(fnFs), "\_"), `[`, 1)

# étape permet de visualiser les profils de qualité des séquences avant de procéder au filtrage. Cela aide à déterminer les seuils de filtrage optimaux pour chaque jeu de données

# Visualiser la qualité des premiers fichiers forward  
plotQualityProfile(fnFs[1:2])



# Visualiser la qualité des premiers fichiers reverse  
plotQualityProfile(fnRs[1:2])



# Dans cette étape, nous filtrons et trimmons les séquences en fonction des seuils de qualité observés dans l’étape précédente. Cela permet de supprimer les bases de faible qualité, les séquences trop courtes et les séquences contenant trop d’erreurs.

# Définir le répertoire de sortie pour les fichiers filtrés  
filtFs <- file.path(path, "filtered", paste0(sample.names, "\_F\_filt.fastq.gz"))  
filtRs <- file.path(path, "filtered", paste0(sample.names, "\_R\_filt.fastq.gz"))

# Créer le répertoire de sortie s'il n'existe pas  
if (!dir.exists(file.path(path, "filtered"))) dir.create(file.path(path, "filtered"))

# Filtrer et trimmer les séquences  
out <- filterAndTrim(fnFs, filtFs, fnRs, filtRs, truncLen=c(240, 160),  
 maxN=0, maxEE=c(2,2), truncQ=2, rm.phix=TRUE,  
 compress=TRUE, multithread=TRUE)

# Nous utilisons les fichiers filtrés pour apprendre les modèles d’erreurs des séquences forward (errF) et reverse (errR). Ensuite, nous appliquons le débruitage (denoising) pour corriger les erreurs de séquençage et obtenir des séquences uniques.

# Apprentissage des erreurs pour les lectures forward  
errF <- learnErrors(filtFs, multithread=TRUE)

## 107393760 total bases in 447474 reads from 6 samples will be used for learning the error rates.

# Apprentissage des erreurs pour les lectures reverse  
errR <- learnErrors(filtRs, multithread=TRUE)

## 71595840 total bases in 447474 reads from 6 samples will be used for learning the error rates.

# Denoising pour les lectures forward  
dadaFs <- dada(filtFs, err=errF, multithread=TRUE)

## Sample 1 - 93851 reads in 33557 unique sequences.  
## Sample 2 - 87167 reads in 29598 unique sequences.  
## Sample 3 - 62603 reads in 22362 unique sequences.  
## Sample 4 - 66861 reads in 20537 unique sequences.  
## Sample 5 - 70356 reads in 21462 unique sequences.  
## Sample 6 - 66636 reads in 19607 unique sequences.

# Denoising pour les lectures reverse  
dadaRs <- dada(filtRs, err=errR, multithread=TRUE)

## Sample 1 - 93851 reads in 25645 unique sequences.  
## Sample 2 - 87167 reads in 24507 unique sequences.  
## Sample 3 - 62603 reads in 18475 unique sequences.  
## Sample 4 - 66861 reads in 14943 unique sequences.  
## Sample 5 - 70356 reads in 14989 unique sequences.  
## Sample 6 - 66636 reads in 15319 unique sequences.

# Dans cette étape, nous créons une table de séquences (ASV table) à partir des séquences débruitées et fusionnons les lectures forward et reverse.

# Construire la table des séquences (ASV table)  
seqtab <- makeSequenceTable(dadaFs)  
  
# Afficher la dimension de la table  
dim(seqtab)

## [1] 6 4174

# Fusionner les lectures forward et reverse  
mergers <- mergePairs(dadaFs, filtFs, dadaRs, filtRs, verbose=TRUE)

## 57 paired-reads (in 21 unique pairings) successfully merged out of 85739 (in 17529 pairings) input.  
  
## 49 paired-reads (in 22 unique pairings) successfully merged out of 78658 (in 14203 pairings) input.  
  
## 52 paired-reads (in 26 unique pairings) successfully merged out of 56398 (in 10306 pairings) input.  
  
## 7 paired-reads (in 3 unique pairings) successfully merged out of 62394 (in 10706 pairings) input.  
  
## 2 paired-reads (in 1 unique pairings) successfully merged out of 66112 (in 10248 pairings) input.  
  
## 10 paired-reads (in 4 unique pairings) successfully merged out of 62387 (in 9626 pairings) input.

# Construire la table des séquences après fusion  
seqtab.merged <- makeSequenceTable(mergers)  
  
# Afficher la dimension de la table fusionnée  
dim(seqtab.merged)

## [1] 6 75

#Les chimères sont des artefacts de PCR qui peuvent introduire des biais dans l’analyse. Nous utilisons removeBimeraDenovo() pour supprimer les chimères de la table des séquences

# Retirer les chimères de la table  
seqtab.nochim <- removeBimeraDenovo(seqtab.merged, method="consensus", multithread=TRUE, verbose=TRUE)

## Identified 19 bimeras out of 75 input sequences.

# Calculer le pourcentage de séquences non-chimériques  
sum(seqtab.nochim)/sum(seqtab.merged)

## [1] 0.8813559

if (!requireNamespace("BiocManager", quietly = TRUE))  
 install.packages("BiocManager")  
BiocManager::install("dada2")

## 'getOption("repos")' replaces Bioconductor standard repositories, see  
## 'help("repositories", package = "BiocManager")' for details.  
## Replacement repositories:  
## CRAN: https://packagemanager.posit.co/cran/\_\_linux\_\_/jammy/latest  
  
## Bioconductor version 3.17 (BiocManager 1.30.22), R 4.3.1 (2023-06-16)  
  
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## `force = TRUE` to re-install: 'dada2'  
  
## Installation paths not writeable, unable to update packages  
## path: /usr/local/lib/R/library  
## packages:  
## boot, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nlme, rpart,  
## survival  
  
## Old packages: 'abind', 'adegraphics', 'adephylo', 'adespatial', 'ANCOMBC',  
## 'aplot', 'arrow', 'askpass', 'backports', 'bayesm', 'BH', 'BiocManager',  
## 'BiodiversityR', 'bit', 'bit64', 'bitops', 'brew', 'brio', 'broom', 'Cairo',  
## 'callr', 'car', 'caTools', 'checkmate', 'circlize', 'classInt', 'cli',  
## 'clock', 'clue', 'coin', 'colorspace', 'commonmark', 'compositions',  
## 'corrplot', 'cowplot', 'crayon', 'credentials', 'crosstalk', 'curl', 'CVXR',  
## 'data.table', 'DBI', 'dbplyr', 'DelayedMatrixStats', 'deldir', 'dendextend',  
## 'DEoptimR', 'desc', 'DescTools', 'digest', 'diptest', 'downlit', 'dqrng',  
## 'DT', 'duckdb', 'dunn.test', 'ecodist', 'emmeans', 'energy', 'estimability',  
## 'evaluate', 'Exact', 'expm', 'FactoMineR', 'fansi', 'farver', 'fBasics',  
## 'filelock', 'FNN', 'fpc', 'fs', 'FSA', 'fstcore', 'future', 'future.apply',  
## 'GenomeInfoDb', 'GenomicRanges', 'geometry', 'gert', 'ggfittext', 'ggfun',  
## 'ggnewscale', 'ggpmisc', 'ggpp', 'ggsci', 'gh', 'globals', 'glue', 'gmp',  
## 'gplots', 'gss', 'gtable', 'gtools', 'GUniFrac', 'hardhat', 'haven', 'highr',  
## 'Hmisc', 'htmlTable', 'htmlwidgets', 'httpuv', 'httr2', 'insight', 'interp',  
## 'ipred', 'jsonlite', 'kernlab', 'knitr', 'labeling', 'Lahman', 'later',  
## 'lava', 'leaps', 'libcoin', 'lifecycle', 'listenv', 'littler', 'lme4',  
## 'lmom', 'locfit', 'lpSolve', 'lubridate', 'markdown', 'MatrixModels',  
## 'matrixStats', 'mclust', 'MicrobiotaProcess', 'minpack.lm', 'minqa',  
## 'modEvA', 'multcomp', 'multcompView', 'munsell', 'mvtnorm', 'nloptr',  
## 'openssl', 'osqp', 'parallelly', 'patchwork', 'pbkrtest', 'phylobase',  
## 'pixmap', 'pkgbuild', 'pkgdown', 'pkgload', 'plotly', 'plotrix', 'plotROC',  
## 'plyr', 'prabclus', 'prettyunits', 'pROC', 'processx', 'prodlim', 'profvis',  
## 'progress', 'promises', 'ps', 'quantreg', 'ragg', 'rbibutils', 'rcdd',  
## 'Rcmdr', 'RcmdrMisc', 'Rcpp', 'RcppAnnoy', 'RcppArmadillo', 'RcppEigen',  
## 'RcppHNSW', 'RcppParallel', 'RCurl', 'Rdpack', 'readr', 'recipes', 'rematch',  
## 'remotes', 'renv', 'reprex', 'reticulate', 'Rfast', 'Rhdf5lib', 'rjson',  
## 'rlang', 'RMariaDB', 'rmarkdown', 'Rmpfr', 'robustbase', 'rootSolve',  
## 'roxygen2', 'RPostgres', 'rprojroot', 'RSQLite', 'rstudioapi', 'Rtsne',  
## 'rvest', 's2', 'S4Arrays', 'S4Vectors', 'sandwich', 'scuttle', 'segmented',  
## 'seqinr', 'sf', 'shape', 'sp', 'SparseM', 'spData', 'spdep', 'splus2R',  
## 'stabledist', 'statnet.common', 'stringi', 'stringr', 'survey', 'sys',  
## 'systemfonts', 'tensorA', 'terra', 'testthat', 'textshaping', 'tidyr',  
## 'tidyselect', 'tidytree', 'timechange', 'timeDate', 'timeSeries', 'tinytex',  
## 'treemapify', 'units', 'usethis', 'utf8', 'uuid', 'uwot', 'vipor', 'viridis',  
## 'vroom', 'waldo', 'withr', 'wk', 'xfun', 'XML', 'xml2', 'xopen', 'xts',  
## 'yaml', 'yulab.utils', 'zCompositions', 'zip'

BiocManager::install("ShortRead")

## 'getOption("repos")' replaces Bioconductor standard repositories, see  
## 'help("repositories", package = "BiocManager")' for details.  
## Replacement repositories:  
## CRAN: https://packagemanager.posit.co/cran/\_\_linux\_\_/jammy/latest  
  
## Bioconductor version 3.17 (BiocManager 1.30.22), R 4.3.1 (2023-06-16)  
  
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## `force = TRUE` to re-install: 'ShortRead'  
  
## Installation paths not writeable, unable to update packages  
## path: /usr/local/lib/R/library  
## packages:  
## boot, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nlme, rpart,  
## survival  
  
## Old packages: 'abind', 'adegraphics', 'adephylo', 'adespatial', 'ANCOMBC',  
## 'aplot', 'arrow', 'askpass', 'backports', 'bayesm', 'BH', 'BiocManager',  
## 'BiodiversityR', 'bit', 'bit64', 'bitops', 'brew', 'brio', 'broom', 'Cairo',  
## 'callr', 'car', 'caTools', 'checkmate', 'circlize', 'classInt', 'cli',  
## 'clock', 'clue', 'coin', 'colorspace', 'commonmark', 'compositions',  
## 'corrplot', 'cowplot', 'crayon', 'credentials', 'crosstalk', 'curl', 'CVXR',  
## 'data.table', 'DBI', 'dbplyr', 'DelayedMatrixStats', 'deldir', 'dendextend',  
## 'DEoptimR', 'desc', 'DescTools', 'digest', 'diptest', 'downlit', 'dqrng',  
## 'DT', 'duckdb', 'dunn.test', 'ecodist', 'emmeans', 'energy', 'estimability',  
## 'evaluate', 'Exact', 'expm', 'FactoMineR', 'fansi', 'farver', 'fBasics',  
## 'filelock', 'FNN', 'fpc', 'fs', 'FSA', 'fstcore', 'future', 'future.apply',  
## 'GenomeInfoDb', 'GenomicRanges', 'geometry', 'gert', 'ggfittext', 'ggfun',  
## 'ggnewscale', 'ggpmisc', 'ggpp', 'ggsci', 'gh', 'globals', 'glue', 'gmp',  
## 'gplots', 'gss', 'gtable', 'gtools', 'GUniFrac', 'hardhat', 'haven', 'highr',  
## 'Hmisc', 'htmlTable', 'htmlwidgets', 'httpuv', 'httr2', 'insight', 'interp',  
## 'ipred', 'jsonlite', 'kernlab', 'knitr', 'labeling', 'Lahman', 'later',  
## 'lava', 'leaps', 'libcoin', 'lifecycle', 'listenv', 'littler', 'lme4',  
## 'lmom', 'locfit', 'lpSolve', 'lubridate', 'markdown', 'MatrixModels',  
## 'matrixStats', 'mclust', 'MicrobiotaProcess', 'minpack.lm', 'minqa',  
## 'modEvA', 'multcomp', 'multcompView', 'munsell', 'mvtnorm', 'nloptr',  
## 'openssl', 'osqp', 'parallelly', 'patchwork', 'pbkrtest', 'phylobase',  
## 'pixmap', 'pkgbuild', 'pkgdown', 'pkgload', 'plotly', 'plotrix', 'plotROC',  
## 'plyr', 'prabclus', 'prettyunits', 'pROC', 'processx', 'prodlim', 'profvis',  
## 'progress', 'promises', 'ps', 'quantreg', 'ragg', 'rbibutils', 'rcdd',  
## 'Rcmdr', 'RcmdrMisc', 'Rcpp', 'RcppAnnoy', 'RcppArmadillo', 'RcppEigen',  
## 'RcppHNSW', 'RcppParallel', 'RCurl', 'Rdpack', 'readr', 'recipes', 'rematch',  
## 'remotes', 'renv', 'reprex', 'reticulate', 'Rfast', 'Rhdf5lib', 'rjson',  
## 'rlang', 'RMariaDB', 'rmarkdown', 'Rmpfr', 'robustbase', 'rootSolve',  
## 'roxygen2', 'RPostgres', 'rprojroot', 'RSQLite', 'rstudioapi', 'Rtsne',  
## 'rvest', 's2', 'S4Arrays', 'S4Vectors', 'sandwich', 'scuttle', 'segmented',  
## 'seqinr', 'sf', 'shape', 'sp', 'SparseM', 'spData', 'spdep', 'splus2R',  
## 'stabledist', 'statnet.common', 'stringi', 'stringr', 'survey', 'sys',  
## 'systemfonts', 'tensorA', 'terra', 'testthat', 'textshaping', 'tidyr',  
## 'tidyselect', 'tidytree', 'timechange', 'timeDate', 'timeSeries', 'tinytex',  
## 'treemapify', 'units', 'usethis', 'utf8', 'uuid', 'uwot', 'vipor', 'viridis',  
## 'vroom', 'waldo', 'withr', 'wk', 'xfun', 'XML', 'xml2', 'xopen', 'xts',  
## 'yaml', 'yulab.utils', 'zCompositions', 'zip'

BiocManager::install("Biostrings")

## 'getOption("repos")' replaces Bioconductor standard repositories, see  
## 'help("repositories", package = "BiocManager")' for details.  
## Replacement repositories:  
## CRAN: https://packagemanager.posit.co/cran/\_\_linux\_\_/jammy/latest  
  
## Bioconductor version 3.17 (BiocManager 1.30.22), R 4.3.1 (2023-06-16)  
  
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## `force = TRUE` to re-install: 'Biostrings'  
  
## Installation paths not writeable, unable to update packages  
## path: /usr/local/lib/R/library  
## packages:  
## boot, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nlme, rpart,  
## survival  
  
## Old packages: 'abind', 'adegraphics', 'adephylo', 'adespatial', 'ANCOMBC',  
## 'aplot', 'arrow', 'askpass', 'backports', 'bayesm', 'BH', 'BiocManager',  
## 'BiodiversityR', 'bit', 'bit64', 'bitops', 'brew', 'brio', 'broom', 'Cairo',  
## 'callr', 'car', 'caTools', 'checkmate', 'circlize', 'classInt', 'cli',  
## 'clock', 'clue', 'coin', 'colorspace', 'commonmark', 'compositions',  
## 'corrplot', 'cowplot', 'crayon', 'credentials', 'crosstalk', 'curl', 'CVXR',  
## 'data.table', 'DBI', 'dbplyr', 'DelayedMatrixStats', 'deldir', 'dendextend',  
## 'DEoptimR', 'desc', 'DescTools', 'digest', 'diptest', 'downlit', 'dqrng',  
## 'DT', 'duckdb', 'dunn.test', 'ecodist', 'emmeans', 'energy', 'estimability',  
## 'evaluate', 'Exact', 'expm', 'FactoMineR', 'fansi', 'farver', 'fBasics',  
## 'filelock', 'FNN', 'fpc', 'fs', 'FSA', 'fstcore', 'future', 'future.apply',  
## 'GenomeInfoDb', 'GenomicRanges', 'geometry', 'gert', 'ggfittext', 'ggfun',  
## 'ggnewscale', 'ggpmisc', 'ggpp', 'ggsci', 'gh', 'globals', 'glue', 'gmp',  
## 'gplots', 'gss', 'gtable', 'gtools', 'GUniFrac', 'hardhat', 'haven', 'highr',  
## 'Hmisc', 'htmlTable', 'htmlwidgets', 'httpuv', 'httr2', 'insight', 'interp',  
## 'ipred', 'jsonlite', 'kernlab', 'knitr', 'labeling', 'Lahman', 'later',  
## 'lava', 'leaps', 'libcoin', 'lifecycle', 'listenv', 'littler', 'lme4',  
## 'lmom', 'locfit', 'lpSolve', 'lubridate', 'markdown', 'MatrixModels',  
## 'matrixStats', 'mclust', 'MicrobiotaProcess', 'minpack.lm', 'minqa',  
## 'modEvA', 'multcomp', 'multcompView', 'munsell', 'mvtnorm', 'nloptr',  
## 'openssl', 'osqp', 'parallelly', 'patchwork', 'pbkrtest', 'phylobase',  
## 'pixmap', 'pkgbuild', 'pkgdown', 'pkgload', 'plotly', 'plotrix', 'plotROC',  
## 'plyr', 'prabclus', 'prettyunits', 'pROC', 'processx', 'prodlim', 'profvis',  
## 'progress', 'promises', 'ps', 'quantreg', 'ragg', 'rbibutils', 'rcdd',  
## 'Rcmdr', 'RcmdrMisc', 'Rcpp', 'RcppAnnoy', 'RcppArmadillo', 'RcppEigen',  
## 'RcppHNSW', 'RcppParallel', 'RCurl', 'Rdpack', 'readr', 'recipes', 'rematch',  
## 'remotes', 'renv', 'reprex', 'reticulate', 'Rfast', 'Rhdf5lib', 'rjson',  
## 'rlang', 'RMariaDB', 'rmarkdown', 'Rmpfr', 'robustbase', 'rootSolve',  
## 'roxygen2', 'RPostgres', 'rprojroot', 'RSQLite', 'rstudioapi', 'Rtsne',  
## 'rvest', 's2', 'S4Arrays', 'S4Vectors', 'sandwich', 'scuttle', 'segmented',  
## 'seqinr', 'sf', 'shape', 'sp', 'SparseM', 'spData', 'spdep', 'splus2R',  
## 'stabledist', 'statnet.common', 'stringi', 'stringr', 'survey', 'sys',  
## 'systemfonts', 'tensorA', 'terra', 'testthat', 'textshaping', 'tidyr',  
## 'tidyselect', 'tidytree', 'timechange', 'timeDate', 'timeSeries', 'tinytex',  
## 'treemapify', 'units', 'usethis', 'utf8', 'uuid', 'uwot', 'vipor', 'viridis',  
## 'vroom', 'waldo', 'withr', 'wk', 'xfun', 'XML', 'xml2', 'xopen', 'xts',  
## 'yaml', 'yulab.utils', 'zCompositions', 'zip'

BiocManager::install("DECIPHER")

## 'getOption("repos")' replaces Bioconductor standard repositories, see  
## 'help("repositories", package = "BiocManager")' for details.  
## Replacement repositories:  
## CRAN: https://packagemanager.posit.co/cran/\_\_linux\_\_/jammy/latest  
  
## Bioconductor version 3.17 (BiocManager 1.30.22), R 4.3.1 (2023-06-16)  
  
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## `force = TRUE` to re-install: 'DECIPHER'  
  
## Installation paths not writeable, unable to update packages  
## path: /usr/local/lib/R/library  
## packages:  
## boot, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nlme, rpart,  
## survival  
  
## Old packages: 'abind', 'adegraphics', 'adephylo', 'adespatial', 'ANCOMBC',  
## 'aplot', 'arrow', 'askpass', 'backports', 'bayesm', 'BH', 'BiocManager',  
## 'BiodiversityR', 'bit', 'bit64', 'bitops', 'brew', 'brio', 'broom', 'Cairo',  
## 'callr', 'car', 'caTools', 'checkmate', 'circlize', 'classInt', 'cli',  
## 'clock', 'clue', 'coin', 'colorspace', 'commonmark', 'compositions',  
## 'corrplot', 'cowplot', 'crayon', 'credentials', 'crosstalk', 'curl', 'CVXR',  
## 'data.table', 'DBI', 'dbplyr', 'DelayedMatrixStats', 'deldir', 'dendextend',  
## 'DEoptimR', 'desc', 'DescTools', 'digest', 'diptest', 'downlit', 'dqrng',  
## 'DT', 'duckdb', 'dunn.test', 'ecodist', 'emmeans', 'energy', 'estimability',  
## 'evaluate', 'Exact', 'expm', 'FactoMineR', 'fansi', 'farver', 'fBasics',  
## 'filelock', 'FNN', 'fpc', 'fs', 'FSA', 'fstcore', 'future', 'future.apply',  
## 'GenomeInfoDb', 'GenomicRanges', 'geometry', 'gert', 'ggfittext', 'ggfun',  
## 'ggnewscale', 'ggpmisc', 'ggpp', 'ggsci', 'gh', 'globals', 'glue', 'gmp',  
## 'gplots', 'gss', 'gtable', 'gtools', 'GUniFrac', 'hardhat', 'haven', 'highr',  
## 'Hmisc', 'htmlTable', 'htmlwidgets', 'httpuv', 'httr2', 'insight', 'interp',  
## 'ipred', 'jsonlite', 'kernlab', 'knitr', 'labeling', 'Lahman', 'later',  
## 'lava', 'leaps', 'libcoin', 'lifecycle', 'listenv', 'littler', 'lme4',  
## 'lmom', 'locfit', 'lpSolve', 'lubridate', 'markdown', 'MatrixModels',  
## 'matrixStats', 'mclust', 'MicrobiotaProcess', 'minpack.lm', 'minqa',  
## 'modEvA', 'multcomp', 'multcompView', 'munsell', 'mvtnorm', 'nloptr',  
## 'openssl', 'osqp', 'parallelly', 'patchwork', 'pbkrtest', 'phylobase',  
## 'pixmap', 'pkgbuild', 'pkgdown', 'pkgload', 'plotly', 'plotrix', 'plotROC',  
## 'plyr', 'prabclus', 'prettyunits', 'pROC', 'processx', 'prodlim', 'profvis',  
## 'progress', 'promises', 'ps', 'quantreg', 'ragg', 'rbibutils', 'rcdd',  
## 'Rcmdr', 'RcmdrMisc', 'Rcpp', 'RcppAnnoy', 'RcppArmadillo', 'RcppEigen',  
## 'RcppHNSW', 'RcppParallel', 'RCurl', 'Rdpack', 'readr', 'recipes', 'rematch',  
## 'remotes', 'renv', 'reprex', 'reticulate', 'Rfast', 'Rhdf5lib', 'rjson',  
## 'rlang', 'RMariaDB', 'rmarkdown', 'Rmpfr', 'robustbase', 'rootSolve',  
## 'roxygen2', 'RPostgres', 'rprojroot', 'RSQLite', 'rstudioapi', 'Rtsne',  
## 'rvest', 's2', 'S4Arrays', 'S4Vectors', 'sandwich', 'scuttle', 'segmented',  
## 'seqinr', 'sf', 'shape', 'sp', 'SparseM', 'spData', 'spdep', 'splus2R',  
## 'stabledist', 'statnet.common', 'stringi', 'stringr', 'survey', 'sys',  
## 'systemfonts', 'tensorA', 'terra', 'testthat', 'textshaping', 'tidyr',  
## 'tidyselect', 'tidytree', 'timechange', 'timeDate', 'timeSeries', 'tinytex',  
## 'treemapify', 'units', 'usethis', 'utf8', 'uuid', 'uwot', 'vipor', 'viridis',  
## 'vroom', 'waldo', 'withr', 'wk', 'xfun', 'XML', 'xml2', 'xopen', 'xts',  
## 'yaml', 'yulab.utils', 'zCompositions', 'zip'

install.packages("ggplot2")

## Installing package into '/usr/local/lib/R/site-library'  
## (as 'lib' is unspecified)

BiocManager::install("phyloseq")

## 'getOption("repos")' replaces Bioconductor standard repositories, see  
## 'help("repositories", package = "BiocManager")' for details.  
## Replacement repositories:  
## CRAN: https://packagemanager.posit.co/cran/\_\_linux\_\_/jammy/latest  
  
## Bioconductor version 3.17 (BiocManager 1.30.22), R 4.3.1 (2023-06-16)  
  
## Warning: package(s) not installed when version(s) same as or greater than current; use  
## `force = TRUE` to re-install: 'phyloseq'  
  
## Installation paths not writeable, unable to update packages  
## path: /usr/local/lib/R/library  
## packages:  
## boot, cluster, codetools, foreign, KernSmooth, lattice, mgcv, nlme, rpart,  
## survival  
  
## Old packages: 'abind', 'adegraphics', 'adephylo', 'adespatial', 'ANCOMBC',  
## 'aplot', 'arrow', 'askpass', 'backports', 'bayesm', 'BH', 'BiocManager',  
## 'BiodiversityR', 'bit', 'bit64', 'bitops', 'brew', 'brio', 'broom', 'Cairo',  
## 'callr', 'car', 'caTools', 'checkmate', 'circlize', 'classInt', 'cli',  
## 'clock', 'clue', 'coin', 'colorspace', 'commonmark', 'compositions',  
## 'corrplot', 'cowplot', 'crayon', 'credentials', 'crosstalk', 'curl', 'CVXR',  
## 'data.table', 'DBI', 'dbplyr', 'DelayedMatrixStats', 'deldir', 'dendextend',  
## 'DEoptimR', 'desc', 'DescTools', 'digest', 'diptest', 'downlit', 'dqrng',  
## 'DT', 'duckdb', 'dunn.test', 'ecodist', 'emmeans', 'energy', 'estimability',  
## 'evaluate', 'Exact', 'expm', 'FactoMineR', 'fansi', 'farver', 'fBasics',  
## 'filelock', 'FNN', 'fpc', 'fs', 'FSA', 'fstcore', 'future', 'future.apply',  
## 'GenomeInfoDb', 'GenomicRanges', 'geometry', 'gert', 'ggfittext', 'ggfun',  
## 'ggnewscale', 'ggpmisc', 'ggpp', 'ggsci', 'gh', 'globals', 'glue', 'gmp',  
## 'gplots', 'gss', 'gtable', 'gtools', 'GUniFrac', 'hardhat', 'haven', 'highr',  
## 'Hmisc', 'htmlTable', 'htmlwidgets', 'httpuv', 'httr2', 'insight', 'interp',  
## 'ipred', 'jsonlite', 'kernlab', 'knitr', 'labeling', 'Lahman', 'later',  
## 'lava', 'leaps', 'libcoin', 'lifecycle', 'listenv', 'littler', 'lme4',  
## 'lmom', 'locfit', 'lpSolve', 'lubridate', 'markdown', 'MatrixModels',  
## 'matrixStats', 'mclust', 'MicrobiotaProcess', 'minpack.lm', 'minqa',  
## 'modEvA', 'multcomp', 'multcompView', 'munsell', 'mvtnorm', 'nloptr',  
## 'openssl', 'osqp', 'parallelly', 'patchwork', 'pbkrtest', 'phylobase',  
## 'pixmap', 'pkgbuild', 'pkgdown', 'pkgload', 'plotly', 'plotrix', 'plotROC',  
## 'plyr', 'prabclus', 'prettyunits', 'pROC', 'processx', 'prodlim', 'profvis',  
## 'progress', 'promises', 'ps', 'quantreg', 'ragg', 'rbibutils', 'rcdd',  
## 'Rcmdr', 'RcmdrMisc', 'Rcpp', 'RcppAnnoy', 'RcppArmadillo', 'RcppEigen',  
## 'RcppHNSW', 'RcppParallel', 'RCurl', 'Rdpack', 'readr', 'recipes', 'rematch',  
## 'remotes', 'renv', 'reprex', 'reticulate', 'Rfast', 'Rhdf5lib', 'rjson',  
## 'rlang', 'RMariaDB', 'rmarkdown', 'Rmpfr', 'robustbase', 'rootSolve',  
## 'roxygen2', 'RPostgres', 'rprojroot', 'RSQLite', 'rstudioapi', 'Rtsne',  
## 'rvest', 's2', 'S4Arrays', 'S4Vectors', 'sandwich', 'scuttle', 'segmented',  
## 'seqinr', 'sf', 'shape', 'sp', 'SparseM', 'spData', 'spdep', 'splus2R',  
## 'stabledist', 'statnet.common', 'stringi', 'stringr', 'survey', 'sys',  
## 'systemfonts', 'tensorA', 'terra', 'testthat', 'textshaping', 'tidyr',  
## 'tidyselect', 'tidytree', 'timechange', 'timeDate', 'timeSeries', 'tinytex',  
## 'treemapify', 'units', 'usethis', 'utf8', 'uuid', 'uwot', 'vipor', 'viridis',  
## 'vroom', 'waldo', 'withr', 'wk', 'xfun', 'XML', 'xml2', 'xopen', 'xts',  
## 'yaml', 'yulab.utils', 'zCompositions', 'zip'

list.files("/home/rstudio/DADA2-et-Phyloseq")

## [1] "1er partie dada2.RData"   
## [2] "article"   
## [3] "CC2\_MAD\_files"   
## [4] "CC2\_MAD.md"   
## [5] "CC2\_MAD.Rmd"   
## [6] "core"   
## [7] "dada2"   
## [8] "dada2\_V1.RData"   
## [9] "dada2\_V2.RData"   
## [10] "dada2\_Vfinal\_.RData"   
## [11] "DADA2-et-Phyloseq.Rproj"   
## [12] "data-url.text"   
## [13] "filtered"   
## [14] "MiSeq\_SOP"   
## [15] "rdp\_train\_set\_16.fa.gz"   
## [16] "README.md"   
## [17] "silva\_nr\_v128\_train\_set.fa.gz"   
## [18] "silva\_species\_assignment\_v138.1 (1).fa.gz"  
## [19] "silva\_species\_assignment\_v138.1.fa.gz"   
## [20] "SRR12576537\_1.fastq.gz"   
## [21] "SRR12576537\_2.fastq.gz"   
## [22] "SRR12576538\_1.fastq.gz"   
## [23] "SRR12576538\_2.fastq.gz"   
## [24] "SRR12576539\_1.fastq.gz"   
## [25] "SRR12576539\_2.fastq.gz"   
## [26] "SRR12576540\_1.fastq.gz"   
## [27] "SRR12576540\_2.fastq.gz"   
## [28] "SRR12576541\_1.fastq.gz"   
## [29] "SRR12576541\_2.fastq.gz"   
## [30] "SRR12576542\_1.fastq.gz"   
## [31] "SRR12576542\_2.fastq.gz"

download.file("https://zenodo.org/record/1172783/files/silva\_nr\_v132\_train\_set.fa.gz",   
 destfile = "~/tax/silva\_nr\_v132\_train\_set.fa.gz", method = "auto")

# Définir le chemin complet du fichier Silva  
refFasta <- "~/tax/silva\_nr\_v132\_train\_set.fa.gz"

# Dans cette étape, nous assignons les séquences non-chimiériques à des taxons en utilisant la base de données Silva.

taxonomy <- dada2::assignTaxonomy(  
 seqs = seqtab.nochim,  
 refFasta = refFasta, # Utilisation du chemin défini correctement  
 taxLevels = c("Kingdom", "Phylum", "Class",   
 "Order", "Family", "Genus",   
 "Species"),  
 multithread = TRUE,  
 minBoot = 60  
)

head(taxonomy)

## Kingdom   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Bacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC "Eukaryota"  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Bacteria"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC "Eukaryota"  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Bacteria"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC "Eukaryota"  
## Phylum   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Proteobacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Firmicutes"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellaeota"  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Class   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Gammaproteobacteria"  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichia"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellae"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Order   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "SAR86\_clade"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichales"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "WCHB1-41"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Family   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Genus   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae\_UCG-004"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA

taxonomy\_df <- as.data.frame(taxonomy)  
head(taxonomy\_df)

## Kingdom  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC Bacteria  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC Eukaryota  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Bacteria  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC Eukaryota  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC Bacteria  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC Eukaryota  
## Phylum  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC Proteobacteria  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC <NA>  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Firmicutes  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC <NA>  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC Kiritimatiellaeota  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC <NA>  
## Class  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC Gammaproteobacteria  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC <NA>  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Erysipelotrichia  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC <NA>  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC Kiritimatiellae  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC <NA>  
## Order  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC SAR86\_clade  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC <NA>  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Erysipelotrichales  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC <NA>  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC WCHB1-41  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC <NA>  
## Family  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC <NA>  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC <NA>  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Erysipelotrichaceae  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC <NA>  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC <NA>  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC <NA>  
## Genus  
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC <NA>  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC <NA>  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC Erysipelotrichaceae\_UCG-004  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC <NA>  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC <NA>  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC <NA>

write.csv(taxonomy, file = "~/taxonomic\_assignment.csv")

# Nous utilisons l’objet phyloseq pour combiner la table de séquences, la taxonomie et les métadonnées, et pour visualiser la composition taxonomique des échantillons.

library(phyloseq)  
  
# Créer un objet phyloseq avec les données de séquence et de taxonomie  
physeq <- phyloseq(otu\_table(seqtab.nochim, taxa\_are\_rows = FALSE),   
 tax\_table(taxonomy))  
  
# Visualiser l'objet phyloseq  
physeq

## phyloseq-class experiment-level object  
## otu\_table() OTU Table: [ 56 taxa and 6 samples ]  
## tax\_table() Taxonomy Table: [ 56 taxa by 6 taxonomic ranks ]

# Sauvegarde de l’Objet phyloseq

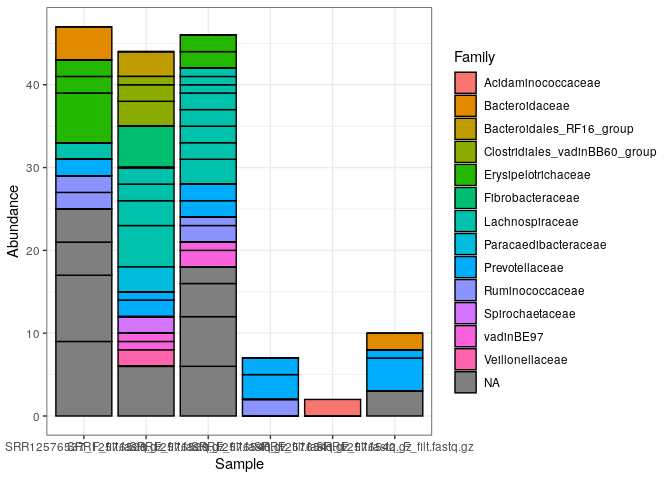
saveRDS(physeq, file = "~/phyloseq\_object.rds")

# Installation et Chargement de ggplot2 pour la Visualisation

# Installer ggplot2 s'il n'est pas encore installé  
if (!requireNamespace("ggplot2", quietly = TRUE)) {  
 install.packages("ggplot2")  
}  
  
# Charger ggplot2  
library(ggplot2)

# Visualisation de la Composition Taxonomique

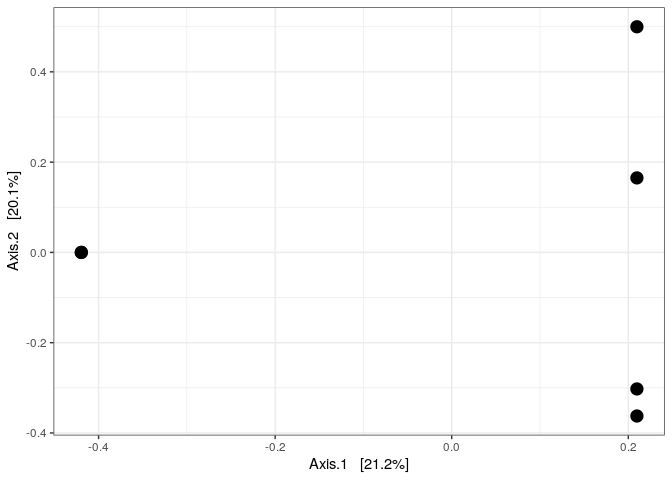
# Visualiser la composition taxonomique au niveau de la famille  
plot\_bar(physeq, fill = "Family") + theme\_bw()



# Analyse de la Diversité Beta avec PCoA

# Créer une ordination PCoA basée sur la distance de Bray-Curtis  
ordination <- ordinate(physeq, method = "PCoA", distance = "bray")  
  
# Visualiser l'ordination avec les échantillons colorés par type d'échantillon  
# Remplacez "SampleType" par le nom réel de la variable que vous voulez utiliser pour la couleur  
plot\_ordination(physeq, ordination, color = "SampleType") +   
 geom\_point(size = 4) +   
 theme\_bw()

## Warning in plot\_ordination(physeq, ordination, color = "SampleType"): Color  
## variable was not found in the available data you provided.No color mapped.  
  
## No available covariate data to map on the points for this plot `type`



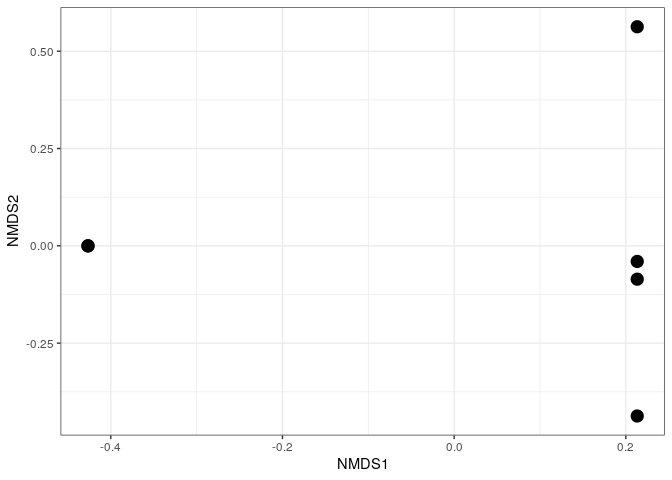
# Analyse NMDS de la Diversité Beta

# Calculer la distance Bray-Curtis  
bray\_dist <- distance(physeq, method = "bray")  
  
# Réaliser une analyse NMDS  
nmds\_ordination <- ordinate(physeq, method = "NMDS", distance = bray\_dist)

## Run 0 stress 0   
## Run 1 stress 0   
## ... Procrustes: rmse 0.3043451 max resid 0.603842   
## Run 2 stress 0   
## ... Procrustes: rmse 0.3048957 max resid 0.3889696   
## Run 3 stress 0   
## ... Procrustes: rmse 0.3599646 max resid 0.6200608   
## Run 4 stress 0   
## ... Procrustes: rmse 0.3425506 max resid 0.4058872   
## Run 5 stress 0   
## ... Procrustes: rmse 0.3138011 max resid 0.4831336   
## Run 6 stress 0   
## ... Procrustes: rmse 0.306433 max resid 0.4159327   
## Run 7 stress 0   
## ... Procrustes: rmse 0.2396962 max resid 0.4441453   
## Run 8 stress 0   
## ... Procrustes: rmse 0.2853872 max resid 0.4825211   
## Run 9 stress 0   
## ... Procrustes: rmse 0.3844613 max resid 0.4365894   
## Run 10 stress 0   
## ... Procrustes: rmse 0.3701655 max resid 0.6791305   
## Run 11 stress 0   
## ... Procrustes: rmse 0.3516983 max resid 0.6485093   
## Run 12 stress 0   
## ... Procrustes: rmse 0.2781688 max resid 0.4863696   
## Run 13 stress 0   
## ... Procrustes: rmse 0.265472 max resid 0.491285   
## Run 14 stress 0   
## ... Procrustes: rmse 0.3326913 max resid 0.4228548   
## Run 15 stress 0   
## ... Procrustes: rmse 0.3077626 max resid 0.454737   
## Run 16 stress 0   
## ... Procrustes: rmse 0.2674659 max resid 0.4002595   
## Run 17 stress 0   
## ... Procrustes: rmse 0.3723324 max resid 0.530064   
## Run 18 stress 0   
## ... Procrustes: rmse 0.348153 max resid 0.5384146   
## Run 19 stress 0   
## ... Procrustes: rmse 0.3422854 max resid 0.5739728   
## Run 20 stress 0   
## ... Procrustes: rmse 0.3237002 max resid 0.4675835   
## \*\*\* Best solution was not repeated -- monoMDS stopping criteria:  
## 20: stress < smin  
  
## Warning in metaMDS(ps.dist): stress is (nearly) zero: you may have insufficient  
## data  
  
## Warning in postMDS(out$points, dis, plot = max(0, plot - 1), ...): skipping  
## half-change scaling: too few points below threshold

# Visualiser l'ordination NMDS  
plot\_ordination(physeq, nmds\_ordination, color = "SampleType") +   
 geom\_point(size = 4) +   
 theme\_bw()

## Warning in plot\_ordination(physeq, nmds\_ordination, color = "SampleType"):  
## Color variable was not found in the available data you provided.No color  
## mapped.  
  
## No available covariate data to map on the points for this plot `type`



# Sauvegarde et Chargement de l’Objet phyloseq

# Sauvegarder l'objet phyloseq  
saveRDS(physeq, file = "~/phyloseq\_object.rds")  
  
# Charger l'objet phyloseq si besoin  
physeq <- readRDS("~/phyloseq\_object.rds")

# Afficher et Vérifier les Objets Importants

# Afficher les dimensions et quelques lignes des objets principaux  
dim(seqtab.nochim)

## [1] 6 56

head(seqtab.nochim)

## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC  
## SRR12576537\_F\_filt.fastq.gz 9  
## SRR12576538\_F\_filt.fastq.gz 0  
## SRR12576539\_F\_filt.fastq.gz 0  
## SRR12576540\_F\_filt.fastq.gz 0  
## SRR12576541\_F\_filt.fastq.gz 0  
## SRR12576542\_F\_filt.fastq.gz 0  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC  
## SRR12576537\_F\_filt.fastq.gz 8  
## SRR12576538\_F\_filt.fastq.gz 0  
## SRR12576539\_F\_filt.fastq.gz 0  
## SRR12576540\_F\_filt.fastq.gz 0  
## SRR12576541\_F\_filt.fastq.gz 0  
## SRR12576542\_F\_filt.fastq.gz 0  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC  
## SRR12576537\_F\_filt.fastq.gz 6  
## SRR12576538\_F\_filt.fastq.gz 0  
## SRR12576539\_F\_filt.fastq.gz 0  
## SRR12576540\_F\_filt.fastq.gz 0  
## SRR12576541\_F\_filt.fastq.gz 0  
## SRR12576542\_F\_filt.fastq.gz 0  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC  
## SRR12576537\_F\_filt.fastq.gz 0  
## SRR12576538\_F\_filt.fastq.gz 6  
## SRR12576539\_F\_filt.fastq.gz 0  
## SRR12576540\_F\_filt.fastq.gz 0  
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## SRR12576542\_F\_filt.fastq.gz 0  
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head(taxonomy)

## Kingdom   
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## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
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## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Gammaproteobacteria"  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichia"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellae"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Order   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "SAR86\_clade"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichales"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "WCHB1-41"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Family   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Genus   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae\_UCG-004"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA

head(tax\_table(physeq))

## Taxonomy Table: [6 taxa by 6 taxonomic ranks]:  
## Kingdom   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Bacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC "Eukaryota"  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Bacteria"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC "Eukaryota"  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Bacteria"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC "Eukaryota"  
## Phylum   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Proteobacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Firmicutes"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellaeota"  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Class   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Gammaproteobacteria"  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichia"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellae"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Order   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "SAR86\_clade"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichales"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "WCHB1-41"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Family   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Genus   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae\_UCG-004"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA

# Vérification de la Correspondance entre les Colonnes et les Lignes

# Vérifier la correspondance des noms de colonnes et lignes  
identical(colnames(seqtab.nochim), rownames(taxonomy))

## [1] TRUE

# Création d’une Table de Métadonnées

# Créer une table de métadonnées fictive avec des informations sur chaque échantillon  
sample\_names <- colnames(seqtab.nochim) # Utiliser les noms de colonnes de votre séquence  
metadata <- data.frame(  
 SampleID = sample\_names,  
 SampleType = factor(rep(c("Type1", "Type2"), length.out = length(sample\_names)))  
)  
  
# Définir les noms des lignes de la table de métadonnées pour qu'ils correspondent à ceux de seqtab.nochim  
rownames(metadata) <- sample\_names

#Création et Visualisation de Tableaux de Données

#Ces sections de code permettent de créer des tableaux fictifs pour illustrer les différentes comparaisons entre les échantillons, par exemple, les changements dans les paramètres physico-chimiques ou la diversité alpha.

# Créer un tableau pour les paramètres physico-chimiques  
physico\_chemical\_data <- data.frame(  
 Parameter = c("Salinity (ppt)", "Precipitation (mm)", "pH",   
 "Total suspended solids (mg/L)", "Turbidity (UNT)",   
 "Apparent color (UC)", "Conductivity (µS/cm)",   
 "Total phosphorous (mg/L)", "Ammonium (mg/L)",   
 "Nitrate (mg/L)", "Nitrite (mg/L)", "Total nitrogen (mg/L)"),  
 T1\_Dry\_Season = c(9.6, 2, 6.6, 27.66, 4.56, 10.73, 247.33, 1.36, 1.03, 1.76, 0.007, 3.23),  
 T2\_Rainy\_Season = c(4.43, 5.1, 6.36, 172.66, 162.66, 241, 369, 0.34, 1.9, 1.23, 0.003, 2.4),  
 Fold\_Change = c(-2.17, NA, NA, 6.24, 35.67, 22.46, 1.49, -4.0, 1.84, -1.43, NA, NA)  
)  
  
# Afficher le tableau  
print(physico\_chemical\_data)

## Parameter T1\_Dry\_Season T2\_Rainy\_Season Fold\_Change  
## 1 Salinity (ppt) 9.600 4.430 -2.17  
## 2 Precipitation (mm) 2.000 5.100 NA  
## 3 pH 6.600 6.360 NA  
## 4 Total suspended solids (mg/L) 27.660 172.660 6.24  
## 5 Turbidity (UNT) 4.560 162.660 35.67  
## 6 Apparent color (UC) 10.730 241.000 22.46  
## 7 Conductivity (µS/cm) 247.330 369.000 1.49  
## 8 Total phosphorous (mg/L) 1.360 0.340 -4.00  
## 9 Ammonium (mg/L) 1.030 1.900 1.84  
## 10 Nitrate (mg/L) 1.760 1.230 -1.43  
## 11 Nitrite (mg/L) 0.007 0.003 NA  
## 12 Total nitrogen (mg/L) 3.230 2.400 NA

# Le tableau de diversité alpha montre les indices de diversité tels que Chao1, Shannon et Simpson pour chaque saison.

# Créer un tableau pour les indices de diversité alpha  
alpha\_diversity\_data <- data.frame(  
 Index = c("Chao1", "Shannon", "Simpson"),  
 T1\_Dry\_Season = c(85.5, 3.2, 0.78),  
 T2\_Rainy\_Season = c(123.4, 4.1, 0.85)  
)  
  
# Afficher le tableau  
print(alpha\_diversity\_data)

## Index T1\_Dry\_Season T2\_Rainy\_Season  
## 1 Chao1 85.50 123.40  
## 2 Shannon 3.20 4.10  
## 3 Simpson 0.78 0.85

# Création d’un Tableau pour les Abondances des Phylums Bactériens

# Créer un tableau pour les abondances de phylums bactériens  
bacterial\_abundance\_data <- data.frame(  
 Phylum = c("Firmicutes", "Bacteroidetes", "Proteobacteria", "Actinobacteria", "Elusimicrobia", "Tenericutes", "Lentisphaerae"),  
 T1\_Dry\_Season = c(30, 25, 20, 10, 5, 5, 5), # Exemple de valeurs d'abondance pour chaque phylum  
 T2\_Rainy\_Season = c(25, 30, 15, 10, 10, 5, 5) # Modifier selon les valeurs exactes  
)  
  
# Afficher le tableau  
print(bacterial\_abundance\_data)

## Phylum T1\_Dry\_Season T2\_Rainy\_Season  
## 1 Firmicutes 30 25  
## 2 Bacteroidetes 25 30  
## 3 Proteobacteria 20 15  
## 4 Actinobacteria 10 10  
## 5 Elusimicrobia 5 10  
## 6 Tenericutes 5 5  
## 7 Lentisphaerae 5 5

# Exporter les tableaux créés pour les paramètres physico-chimiques, la diversité alpha et l’abondance des phylums bactériens en fichiers CSV.

# Ces fichiers peuvent être utilisés pour un traitement ou une visualisation ultérieure dans d’autres outils.

# Exporter les données en CSV  
write.csv(physico\_chemical\_data, file = "~/physico\_chemical\_data.csv", row.names = FALSE)  
write.csv(alpha\_diversity\_data, file = "~/alpha\_diversity\_data.csv", row.names = FALSE)  
write.csv(bacterial\_abundance\_data, file = "~/bacterial\_abundance\_data.csv", row.names = FALSE)

# Calculer la différence directe entre les saisons sèche et pluvieuse pour chaque paramètre physico-chimique.Cela permet de visualiser comment chaque paramètre change entre les saisons.

# Calculer la différence directe entre T1 et T2 pour chaque paramètre  
difference <- physico\_chemical\_data$T2\_Rainy\_Season - physico\_chemical\_data$T1\_Dry\_Season  
  
# Ajouter la différence au tableau  
physico\_chemical\_data$Difference <- difference  
  
# Afficher les résultats  
print(physico\_chemical\_data)

## Parameter T1\_Dry\_Season T2\_Rainy\_Season Fold\_Change  
## 1 Salinity (ppt) 9.600 4.430 -2.17  
## 2 Precipitation (mm) 2.000 5.100 NA  
## 3 pH 6.600 6.360 NA  
## 4 Total suspended solids (mg/L) 27.660 172.660 6.24  
## 5 Turbidity (UNT) 4.560 162.660 35.67  
## 6 Apparent color (UC) 10.730 241.000 22.46  
## 7 Conductivity (µS/cm) 247.330 369.000 1.49  
## 8 Total phosphorous (mg/L) 1.360 0.340 -4.00  
## 9 Ammonium (mg/L) 1.030 1.900 1.84  
## 10 Nitrate (mg/L) 1.760 1.230 -1.43  
## 11 Nitrite (mg/L) 0.007 0.003 NA  
## 12 Total nitrogen (mg/L) 3.230 2.400 NA  
## Difference  
## 1 -5.170  
## 2 3.100  
## 3 -0.240  
## 4 145.000  
## 5 158.100  
## 6 230.270  
## 7 121.670  
## 8 -1.020  
## 9 0.870  
## 10 -0.530  
## 11 -0.004  
## 12 -0.830

# Exemple de Tableau de Données Étendues pour Comparaison de Saisons

# Exemple de tableau avec plusieurs observations pour chaque saison et chaque paramètre  
physico\_chemical\_data\_extended <- data.frame(  
 Parameter = rep(c("Salinity", "pH", "Total suspended solids"), each = 6), # 6 répétitions pour chaque paramètre  
 Season = rep(c("Dry", "Rainy"), each = 3, times = 3), # 3 répétitions pour chaque saison, répété pour chaque paramètre  
 Value = c(9.6, 9.7, 9.8, 4.4, 4.5, 4.6, 6.5, 6.6, 6.7, 6.2, 6.3, 6.4,   
 27.5, 27.7, 27.8, 172.5, 172.6, 172.7) # 6 valeurs pour chaque paramètre  
)  
  
# Afficher le tableau de données  
print(physico\_chemical\_data\_extended)

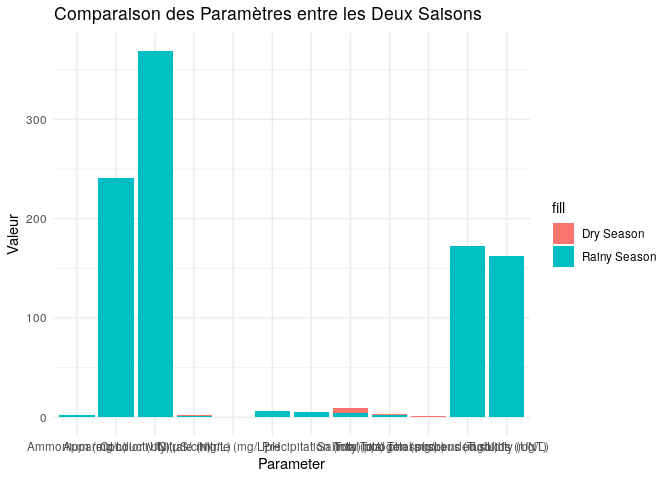
## Parameter Season Value  
## 1 Salinity Dry 9.6  
## 2 Salinity Dry 9.7  
## 3 Salinity Dry 9.8  
## 4 Salinity Rainy 4.4  
## 5 Salinity Rainy 4.5  
## 6 Salinity Rainy 4.6  
## 7 pH Dry 6.5  
## 8 pH Dry 6.6  
## 9 pH Dry 6.7  
## 10 pH Rainy 6.2  
## 11 pH Rainy 6.3  
## 12 pH Rainy 6.4  
## 13 Total suspended solids Dry 27.5  
## 14 Total suspended solids Dry 27.7  
## 15 Total suspended solids Dry 27.8  
## 16 Total suspended solids Rainy 172.5  
## 17 Total suspended solids Rainy 172.6  
## 18 Total suspended solids Rainy 172.7

# Utiliser le test t sur les nouvelles données  
t\_test\_results <- t.test(Value ~ Season, data = physico\_chemical\_data\_extended)  
  
# Afficher les résultats du test t  
print(t\_test\_results)

##   
## Welch Two Sample t-test  
##   
## data: Value by Season  
## t = -1.6563, df = 8.2221, p-value = 0.1352  
## alternative hypothesis: true difference in means between group Dry and group Rainy is not equal to 0  
## 95 percent confidence interval:  
## -110.88283 17.92728  
## sample estimates:  
## mean in group Dry mean in group Rainy   
## 14.65556 61.13333

# Visualisation des Paramètres Physico-Chimiques entre les Saisons

# Charger ggplot2  
library(ggplot2)  
  
# Créer un graphique pour comparer visuellement les deux saisons  
ggplot(physico\_chemical\_data, aes(x = Parameter)) +  
 geom\_bar(aes(y = T1\_Dry\_Season, fill = "Dry Season"), stat = "identity", position = "dodge") +  
 geom\_bar(aes(y = T2\_Rainy\_Season, fill = "Rainy Season"), stat = "identity", position = "dodge") +  
 labs(title = "Comparaison des Paramètres entre les Deux Saisons", y = "Valeur") +  
 theme\_minimal()



# Construction de la Table des Séquences DADA2 (ASV Table)

# Construire la table des séquences  
seqtab <- makeSequenceTable(dadaFs)  
  
# Afficher les dimensions de la table de séquences  
print(dim(seqtab))

## [1] 6 4174

# Assignation Taxonomique aux Séquences Non-Chimiériques

# Assigner la taxonomie aux séquences non-chimiériques  
taxa <- assignTaxonomy(  
 seqtab.nochim, # Table des séquences non-chimiériques  
 refFasta = "~/tax/silva\_nr\_v132\_train\_set.fa.gz", # Chemin vers le fichier de référence Silva  
 multithread = TRUE  
)  
  
# Afficher les premières lignes de la table de taxonomie  
head(taxa)

## Kingdom   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Bacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC "Eukaryota"  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Bacteria"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC "Eukaryota"  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Bacteria"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC "Eukaryota"  
## Phylum   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Proteobacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Firmicutes"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellaeota"  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Class   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Gammaproteobacteria"  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichia"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellae"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Order   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "SAR86\_clade"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichales"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "WCHB1-41"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Family   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Genus   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae\_UCG-004"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA

# Vérification des Dimensions et de la Taxonomie

# Vérification de la dimension et des échantillons de la table des séquences  
dim(seqtab.nochim)

## [1] 6 56

summary(rowSums(seqtab.nochim))

## Min. 1st Qu. Median Mean 3rd Qu. Max.   
## 2.00 7.75 27.00 26.00 45.50 47.00

# Vérification des premiers rangs taxonomiques assignés  
head(taxa)

## Kingdom   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Bacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC "Eukaryota"  
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Bacteria"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC "Eukaryota"  
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Bacteria"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC "Eukaryota"  
## Phylum   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Proteobacteria"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Firmicutes"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellaeota"  
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Class   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "Gammaproteobacteria"  
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichia"   
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "Kiritimatiellae"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Order   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC "SAR86\_clade"   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichales"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC "WCHB1-41"   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Family   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA   
## Genus   
## CCTACGGGAGGCTGCAGCCGCGGTAATACGGAAGGTCCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTTTATTAAGTTGGGTGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGATTCACTAGAGTACGAAAGAGGGAGGTAGAATTCACAGTGTAGCGGTGGAATGCGTAGATATTGTGAAGAATACCAATGGCGAAGGCAGCCTCCTGGTTCTGTACTGACACTGAGGTGCGAAAGCGTGGGTAGCGAACAGGATTAGATACCCTAGTAGTC NA   
## CCTACGGGCGGCTGCGTCCGCAAGGATCCTTCCGGCAATATCACCCCCGGAAAAGCCTTCCCCGCCGGGGCTGTCACCGACCGGGAAACCGTCCCCGGCATGACCTGCGGCAAGGCATTTCGCCGCAGTCTGTGGGGAAATCTCCAATTCCCCACGGGTTACTGGTACGAGGACTCCGTAATCTCTCAGATTCTGCTGCCTATGGCAAAGCGTATTTACGCCATCGATACCCTAGTAGTC NA   
## CCTACGGGGGGCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGTGAGCAGGCGGTTATTTAAGTCTGAAGTCAAAGGCTATGGCTCAACCATAGTTCGCTTTGGAAACTGGATGACTAGAGTGCGAGAGAGGTAAGCGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTTACTAGCTCGTAACTGACGCTCAGTCACGAAAGCGTGGGTAGCAAATAGGATTAGATACCCCAGTAGTC "Erysipelotrichaceae\_UCG-004"  
## CCTACGGGTGGCTGCGGCACGCAGGTATCCGACGTGAACCAGCTGCTGAGGCAGTTCGACCAGATGCAGAAAATGATGAAGCAATTCGGTCTGGGCGGAAAAAATCTGCACGGCAAGAAAGCGCGCATGAACCGCGCGGGAATGCTAAAACTCATGGGCGGTATGCCTAAGAAATAAGATTTGAACCGCTTTGCGGCTTAAATACAAAAAGTATGATGATGGAGGTGAATTTAAAATGGCAGTAAAGATCAGACTGAGAAGAATGGGCGCTAAGAAGGCTCCTTTTTACAGAATAGTTGTTGCTGATTCCAGATACCCTTGTAGTC NA   
## CCTACGGGGGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGCCCGTAGCGTTGTTCGGATTTACTGGGCGTAAAGGGCGCGTAGGCGGTCCTGCGTGTCGGATGTGAAATCTCCGGGCTCAACCCGGAAAGTGCGTCCGAAACTGCAAGGCTCGAGTGCGGGATGGGGAAGGGGAATGCAGGGTGTAGCGGTGAAATGCGTTGATATCCTGCAGAACACCGGAGGCGAAGGCGCCTTCCTGGAACGCAACTGACGCTGAGGCGCGAAAGCCGGGGGAGCAAACAGGATTAGATACCCCTGTAGTC NA   
## CCTACGGGAGGCTGCAGATGTGGAATACTACGGACTGGGAGAATAATCTGCAGACAGACGGAATAACCGATCAGGATGAATACTACCGCAAGGACAGATACAACAGGAAAATACCTGAGAAGTGGGGGAAAACGCAGATGACAGGACTGGATCAGCGTTCATTTATTCTGGGCATGATCACGGCCTTCTGCGAATGCGTGGCGGGCGGATGCAAGCGGCTGGCGCTCTCACCGCCGCTGCGGCATGCAGATTATGAACGGATTTCGGCTCAAGCGTATGAGCTGATCGGGAAACACGGGCTGGTGCATTATCATGAAGAAAACCTGGACCGGCCCGCAGATACCCCTGTAGTC NA

# Création et Visualisation de l’Objet Phyloseq

library(phyloseq)  
  
# Créer un objet phyloseq avec la table des séquences (ASV) et la table de taxonomie  
physeq <- phyloseq(otu\_table(seqtab.nochim, taxa\_are\_rows = FALSE),   
 tax\_table(taxa))  
  
# Afficher un résumé de l'objet phyloseq  
print(physeq)

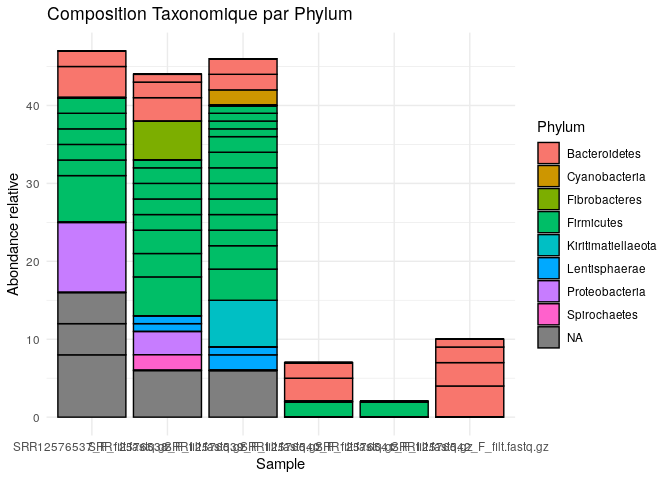
## phyloseq-class experiment-level object  
## otu\_table() OTU Table: [ 56 taxa and 6 samples ]  
## tax\_table() Taxonomy Table: [ 56 taxa by 6 taxonomic ranks ]

# Créer un graphique en barres montrant la composition taxonomique des échantillons au niveau du phylum.

# Le paramètre “fill = Phylum” indique que chaque barre sera colorée en fonction des phylums bactériens.

# Cela permet de comparer visuellement la proportion de chaque phylum dans les différents échantillons.

plot\_bar(physeq, fill = "Phylum") +   
 theme\_minimal() +  
 labs(title = "Composition Taxonomique par Phylum", y = "Abondance relative")



# Calculer la richesse alpha pour chaque échantillon à l’aide de la fonction estimate\_richness de phyloseq.

# La richesse alpha mesure la diversité au sein d’un échantillon individuel.

# Elle inclut des indices comme le Chao1, Shannon et Simpson, qui prennent en compte le nombre d’espèces et leur abondance

# Calculer la richesse alpha pour chaque échantillon  
alpha\_diversity <- estimate\_richness(physeq)

## Warning in sqrt(sum(Deriv.Ch1 %\*% t(Deriv.Ch1) \* (diag(a) - a %\*%  
## t(a)/S.ACE))): NaNs produced

# Afficher les premières lignes de la diversité alpha  
head(alpha\_diversity)

## Observed Chao1 se.chao1 ACE se.ACE  
## SRR12576537\_F\_filt.fastq.gz 12 12.00000 0.0000000 12.000000 NaN  
## SRR12576538\_F\_filt.fastq.gz 17 17.85714 1.3920402 18.909767 1.539855e+00  
## SRR12576539\_F\_filt.fastq.gz 20 20.83333 1.2592865 22.910305 1.956149e+00  
## SRR12576540\_F\_filt.fastq.gz 3 3.00000 0.0000000 3.000000 1.490116e-08  
## SRR12576541\_F\_filt.fastq.gz 1 1.00000 0.0000000 1.000000 0.000000e+00  
## SRR12576542\_F\_filt.fastq.gz 4 4.00000 0.2165064 4.444444 7.672053e-01  
## Shannon Simpson InvSimpson Fisher  
## SRR12576537\_F\_filt.fastq.gz 2.315798 0.8854685 8.731225 5.2046916  
## SRR12576538\_F\_filt.fastq.gz 2.685416 0.9225207 12.906667 10.1569815  
## SRR12576539\_F\_filt.fastq.gz 2.837525 0.9310019 14.493151 13.4657221  
## SRR12576540\_F\_filt.fastq.gz 1.078992 0.6530612 2.882353 1.9887982  
## SRR12576541\_F\_filt.fastq.gz 0.000000 0.0000000 1.000000 0.7959019  
## SRR12576542\_F\_filt.fastq.gz 1.279854 0.7000000 3.333333 2.4709922