```
##############################
#         18S                #
#     Q2Pipe Option file     #
# Designed for Q2Pipe V0.91 #
#                            #
##############################

################################
#  Common Analysis Parameters  #
################################

ANALYSIS_NAME=BASIC_TEST
NB_THREADS=8

# Leave empty if you don't use singularity image to launch Qiime2
# To define a different temporary folder, add -B /path/to/your/folder:/tmp
SINGULARITY_COMMAND="singularity exec --cleanenv --env
MPLCONFIGDIR=/tmp,TMPDIR=/tmp -B /scratch/melnag/tmp:/tmp -B /scratch/melnag -B
/project/def-chrmarti
/project/def-chrmarti/softwares/qiime2/qiime2_2022_2_NRCAN.sif"



# Metadata must be in TSV format
# Manifest must be in CSV format
# For multiple run, seperate each run manifest by a comma (,)
METADATA_FILE_PATH=

MANIFEST_FILE_PATH=/project/def-chrmarti/melnag/Caribou2019_data/16S_workspace/
mani.csv

# Leave empty to use system's default  (/tmp)
# DO NOT SPECIFY IF YOU ARE USING SINGULARITY COMMAND
TEMPORARY_DIRECTORY=

###########################
#  Step 1 : Data Import  #
###########################

# PLACEHOLDER for single end support DO NOT CHANGE THIS, ONLY PAIRED IS SUPPORTED
DATA_TYPE=paired

# Number of sequences to use to generate quality plots (default: 10000)
p_n=10000

#########################
#  Cutadapt (Optional)  #
#########################
# This step is done during step 1.5 and step 2

RUN_CUTADAPT=false
forward_trim_param=--p-front-f
reverse_trim_param=--p-front-r

forward_primer=GTGYCAGCMGCCGCGGTAA
reverse_primer=CCGYCAATTYMTTTRAGTTT

p_discard_untrimmed=true
```

```
#########################################################
#  Step 1.5 : Dada2 Denoising Parameters Evaluation  #
#########################################################

# This step is design to work with a single manifest file
# Manifest must be in CSV format
EVAL_MANIFEST_FILE_PATH=

# if your data is single-end, only p_trim_left_f, p_trunc_len_f and p_max_ee_f will
be used in trimming

# Use 0 to bypass evaluation (will just denoise all samples)
DENOISE_EVALUATION_SAMPLE_SIZE=5
TESTFILE_PATH=
# if true, will generate a new random manifest. even if one already exists
# if false, will use the $ANALYSIS_NAME.eval_manifest.temp as subset
FORCE_RESAMPLING=false

# If true, will stop the step after generating $ANALYSIS_NAME.eval_manifest.temp
# Nothing else will be generated until DRY_RUN is switched to false again
DRY_RUN=false

#################################
#   Step 2 : Dada2 Denoising   #
#################################

# NOT FOR STEP 1.5 (YOU MUST USE TESTFILE FOR STEP 1.5)

# Number of denoising job to launch simultaneously
# Each job will use NB_THREADS / job count
# For best result, your number of job should be a multiple of your NB_THREADS
# Ex: 3 jobs should have 9, 12, 15, etc. NB_THREADS so each job have the same
number of threads
# If 1 is used, all job will run sequentially (which will be slower that having
multiple jobs)
CONCURRENT_JOBS=1

# Use 0 to deactivate parameters (should be 0 if you used CutAdapt)
p_trim_left_f=19
p_trim_left_r=20

# Use 0 to deactivate parameters
# If you have multiple run, you must input a value for each of them
# seperate them by a comma (ex 234,235,223)
# They must be in the same order then your manifest list
p_trunc_len_f=261
p_trunc_len_r=238

p_max_ee_f=2
p_max_ee_r=2
p_n_reads_learn=1000000

p_chimera_method=consensus
p_min_fold_parent_over_abundance=1.0

############################
# Step 2.5 : Run Merging  #
############################
```

```
# If true, will proceed with merging even if runs are incompatible (different
denoising parameters)
# NOT RECOMMENDED
IGNORE_INCOMPATIBILITY=false



#####################################
# Step 3 : Feature Table filtering  #
#####################################

# FUTURE DEV: REPLACE OR ADD AUTO CALCULATION ACCORDING TO VISUALIZATION DATA
# Use 0 to disable
#freq_threshold=0.0005
p_min_frequency=25


# IDEM ^^^^
# Use 0 to disable
#sample_threshold=0
p_min_samples=0

################################
# Step 4 : Denovo Clustering  #
################################

# Must be between ]0 , 1.0]
# Use NA to skip denovo clustering (you must still launch step 4)
p_perc_identity=NA

#################################
# Step 5 : Classifier Training   #
#################################

# Only Specify these if you want to train the classifier with your database
# It's recommended to use the same name (different extension) for the fasta and the
tax file
# The classifier output name must have the .qza extension

#FASTA_DATABASE_PATH=
#TAXO_DATABASE_PATH=
SEQS_QZA_PATH=
TAXO_QZA_PATH=
CLASSIFIER_OUTPUT_NAME=

#################################
# Step 6 : Taxonomy Assignment  #
#################################

# Only specify this if you skipped step 5
CLASSIFIER_DATABASE_PATH=/project/def-chrmarti/databases/qiime2/16S_18S/silva_138/
classifier_silva138_q2.qza

# Possible value [0, 1]
p_confidence=0.7

############################
```

```
# Step 7 : Taxa Filtering  #
############################

# Filter samples according to specific metadata
# ex "[subject]='subject-1' AND NOT [body-site]='gut'"
# ex "[body-site]='gut' OR [reported-antibiotic-usage]='Yes'"
# ex "[body-site] IN ('left palm', 'right palm')"
# Leave "" to ignore
p_where=""

# Never use space in the list, only comma
# p_exclude remove unwanted taxe and p_include keep only specified taxa
# You can use both option to exclude parts of the inclusion
# If both are empty, taxa filtering will be skipped
p_include=bacteria,archaea
p_exclude=eukaryota,mitochondria,chloroplast

# Must be exact or contains (default)
p_mode=contains

# Will also be used in step 8 and 10
GENERATE_PHYLOGENY=false

# RAREFACTION OVERRIDE
# true, false or both
# if you activate this option, you can ignore the next sections, skip step 8 and 9
# Use "both" without the quotes to run both with and without rarefaction in a
single run
SKIP_RAREFACTION=both
########################################
#   Step 8 : Alpha rarefaction plotting  #
########################################

p_max_depth=30000
p_steps=50
p_iterations=10
# Use this format: observed_features,shannon
# You can also leave this blank to use Qiime2 default metrics
(observed_features,shannon)
# IMPORTANT: This is NOT the metrics for step 10, this is only for the rarefaction
curve
p_metrics=observed_features,shannon

############################
# Step 9 : Data Rarefaction #
############################

p_sampling_depth=18430

########################
#   Step 10 : Metrics  #
########################

alpha_metrics=shannon,simpson,observed_features,chao1,pielou_e
beta_metrics=braycurtis,jaccard

# Relevent only if GENERATE_PHYLOGENY is activated
alpha_metrics_phylo=faith_pd
beta_metrics_phylo=weighted_unifrac,weighted_normalized_unifrac,generalized_unifrac
```

```
,unweighted_unifrac

######################
#   Step 11 : Export #
######################


## FUNGuild specific options (Fungal ITS Only)
# To use FUNGuild, Guilds_v1.1.py must be available in your path
# Recommended FUNGuild version : https://github.com/Patg13/FUNGuild
GENERATE_FUNGUILD=false
# Enter remote_fungi to use remote fungi database
(http://stbates.org/funguild_db.php)
# You can also specify a local database path
# Database must be downloaded with the provided bash script in
https://github.com/Patg13/FUNGuild
FUNGUILD_DATABASE_PATH=



## ANCOM specific options
GENERATE_ANCOM=true
# Collapse table at genus level (6)
p_level=2

# Depend on your metadata
# Specify each target column seperated by a comma
# Ex: Col1,Col2,Col3,Col4
# There will be one ANCOM by column
m_metadata_column=Sex,Population



##############################
#         ITSplante          #
#     Q2Pipe Option file     #
# Designed for Q2Pipe V0.89 #
#                            #
##############################

################################
#  Common Analysis Parameters  #
################################

ANALYSIS_NAME=Caribou_ITSPlant_Global_mai2022
NB_THREADS=4

# Leave empty if you don't use singularity image to launch Qiime2
# To define a different temporary folder, add -B /path/to/your/folder:/tmp
SINGULARITY_COMMAND="singularity exec --cleanenv --env
MPLCONFIGDIR=/mnt/pagagne/cmartineau/METB_WaterSedAbitibi_avril2022/temp,TMPDIR=/
mnt/pagagne/cmartineau/METB_WaterSedAbitibi_avril2022/temp -B /rawdata -B /mnt
/home/ubuntu/qiime2_singularity/qiime2_2022_2_NRCAN.sif"

# Metadata must be in TSV format
# Manifest must be in CSV format
METADATA_FILE_PATH=/mnt/pagagne/cmartineau/METB_Caribou_mai2022/ITS_Plant/Global/
metadata_file_ITS2Plant.txt
MANIFEST_FILE_PATH=/mnt/pagagne/cmartineau/METB_Caribou_mai2022/ITS_Plant/Global/
```

```
manifest.csv

# Leave empty to use system's default  (/tmp)
# DO NOT SPECIFY IF YOU ARE USING SINGULARITY COMMAND
TEMPORARY_DIRECTORY=

##########################
#  Step 1 : Data Import  #
##########################

# PLACEHOLDER for single end support DO NOT CHANGE THIS, ONLY PAIRED IS SUPPORTED
DATA_TYPE=paired

##########################
#  Cutadapt (Optional)  #
##########################
# This step is done during step 1.5 and step 2

SKIP_CUTADAPT=false
forward_trim_param=--p-front-f
reverse_trim_param=--p-front-r

forward_primer=ATGCGATACTTGGTGTGAAT
reverse_primer=GACGCTTCTCCAGACTACAAT

p_discard_untrimmed=true

#########################################################
#  Step 1.5 : Dada2 Denoising Parameters Evaluation  #
#########################################################

# if your data is single-end, only p_trim_left_f, p_trunc_len_f and p_max_ee_f will
be used in trimming

# Use 0 to bypass evaluation (will just denoise all samples)
DENOISE_EVALUATION_SAMPLE_SIZE=5
TESTFILE_PATH=
# if true, will generate a new random manifest. even if one already exists
# if false, will use the $ANALYSIS_NAME.eval_manifest.temp as subset
FORCE_RESAMPLING=false

# If true, will stop the step after generating $ANALYSIS_NAME.eval_manifest.temp
# Nothing else will be generated until DRY_RUN is switched to false again
DRY_RUN=false

################################
#   Step 2 : Dada2 Denoising   #
################################

# NOT FOR STEP 1.5 (YOU MUST USE TESTFILE FOR STEP 1.5)

# Use 0 to deactivate parameters (should be 0 if you used CutAdapt)
# 20 21
p_trim_left_f=0
p_trim_left_r=0

# Use 0 to deactivate parameters
p_trunc_len_f=276
p_trunc_len_r=237
```

```
#276 237
# MOD TEST 2 -> 3
p_max_ee_f=2
p_max_ee_r=2
p_n_reads_learn=1000000

p_chimera_method=consensus
p_min_fold_parent_over_abundance=1.0

####################################
# Step3  Feature Table filtering   #
####################################

# FUTURE DEV: REPLACE OR ADD AUTO CALCULATION ACCORDING TO VISUALIZATION DATA
# Use 0 to disable
#freq_threshold=0.0005
p_min_frequency=7


# IDEM ^^^^
# Use 0 to disable
#sample_threshold=0
p_min_samples=0

################################
# Step 4  Denovo Clustering   #
################################

# Must be between ]0 , 1.0]
# Use NA to skip denovo clustering (you must still launch step 4)
p_perc_identity=NA

################################
# Step 5  Classifier Training   #
################################

# Only Specify these if you want to train the classifier with your database
# It's recommended to use the same name (different extension) for the fasta and the
tax file
# The classifier output name must have the .qza extension

#FASTA_DATABASE_PATH=
#TAXO_DATABASE_PATH=
SEQS_QZA_PATH=
TAXO_QZA_PATH=
CLASSIFIER_OUTPUT_NAME=

################################
# Step 6 Taxonomy Assignment  #
################################

# Only specify this if you skipped step 5
CLASSIFIER_DATABASE_PATH=/mnt/CMartineau/Qiime2_databases/ITS2_Plant/PLANiTS/
PLANiTS_ITS2_classifier.qza

# Possible value [0, 1]
p_confidence=0.7

############################
```

```
# Step 7 Taxa Filtering    #
############################

# Never use space in the list, only comma
# p_exclude remove unwanted taxe and p_include keep only specified taxa
# You can use both option to exclude parts of the inclusion
# If both are empty, taxa filtering will be skipped
p_include=Streptophyta
p_exclude=

# Must be exact or contains (default)
p_mode=contains

# Will also be used in step 8 and 10
GENERATE_PHYLOGENY=false

# RAREFACTION OVERRIDE
# true, false or both
# if you activate this option, you can ignore the next sections, skip step 8 and 9
# Use "both" without the quotes to run both with and without rarefaction in a
single run
SKIP_RAREFACTION=both
########################################
#   Step 8 Alpha rarefaction plotting    #
########################################

p_max_depth=10000
p_steps=50
p_iterations=10
# Use this format: observed_features,shannon
# You can also leave this blank to use Qiime2 default metrics
(observed_features,shannon)
# IMPORTANT: This is NOT the metrics for step 10, this is only for the rarefaction
curve
p_metrics=observed_features,shannon

############################
# Step 9 Data Rarefaction #
############################

p_sampling_depth=3700

######################
#   Step 10 Metrics   #
######################

alpha_metrics=shannon,simpson,observed_features,chao1,pielou_e
beta_metrics=braycurtis,jaccard

# Relevent only if GENERATE_PHYLOGENY is activated
alpha_metrics_phylo=faith_pd
beta_metrics_phylo=weighted_unifrac,weighted_normalized_unifrac,generalized_unifrac
,unweighted_unifrac

######################
#   Step 11 Export   #
######################
```

```
## FUNGuild specific options (Fungal ITS Only)
# To use FUNGuild, Guilds_v1.1.py must be available in your path
# Recommended FUNGuild version : https://github.com/Patg13/FUNGuild
GENERATE_FUNGUILD=false
# Enter remote_fungi to use remote fungi database
(http://stbates.org/funguild_db.php)
# You can also specify a local database path
# Database must be downloaded with the provided bash script in
https://github.com/Patg13/FUNGuild
FUNGUILD_DATABASE_PATH=



## ANCOM specific options
GENERATE_ANCOM=false
# Collapse table at genus level (6)
p_level=6

# Depend on your metadata
# Specify each target column seperated by a comma
# Ex: Col1,Col2,Col3,Col4
# There will be one ANCOM by column
m_metadata_column=

##############################
#         ITSfungi           #
#     Q2Pipe Option file     #
# Designed for Q2Pipe V0.85 #
#                            #
##############################

################################
#  Common Analysis Parameters  #
################################

ANALYSIS_NAME=Caribou_ITS2_mai2022
NB_THREADS=2

# Leave empty if you don't use singularity image to launch Qiime2
# To define a different temporary folder, add -B /path/to/your/folder:/tmp
SINGULARITY_COMMAND="singularity exec --cleanenv --env
MPLCONFIGDIR=/mnt/pagagne/cmartineau/METB_WaterSedAbitibi_avril2022/temp,TMPDIR=/
mnt/pagagne/cmartineau/METB_WaterSedAbitibi_avril2022/temp -B /rawdata -B /mnt
/home/ubuntu/qiime2_singularity/qiime2_2022_2_NRCAN.sif"

# Metadata must be in TSV format
# Manifest must be in CSV format
METADATA_FILE_PATH=/mnt/pagagne/cmartineau/METB_Caribou_mai2022/ITS2/Global/
metadata_file_ITS2FMiSeq96.tsv
MANIFEST_FILE_PATH=/mnt/pagagne/cmartineau/METB_Caribou_mai2022/ITS2/Global/
manifest.csv

# Leave empty to use system's default  (/tmp)
# DO NOT SPECIFY IF YOU ARE USING SINGULARITY COMMAND
TEMPORARY_DIRECTORY=

#########################
#  Step 1 : Data Import  #
#########################
```

```
# PLACEHOLDER for single end support DO NOT CHANGE THIS, ONLY PAIRED IS SUPPORTED
DATA_TYPE=paired

##########################
#  Cutadapt (Optional)  #
##########################
# This step is done during step 1.5 and step 2

SKIP_CUTADAPT=false
forward_trim_param=--p-front-f
reverse_trim_param=--p-front-r

forward_primer=GAACGCAGCRAANNGYGA
reverse_primer=TCCTCCGCTTATTGATATGC

p_discard_untrimmed=true

#########################################################
#  Step 1.5 : Dada2 Denoising Parameters Evaluation  #
#########################################################

# if your data is single-end, only p_trim_left_f, p_trunc_len_f and p_max_ee_f will
be used in trimming

# Use 0 to bypass evaluation (will just denoise all samples)
DENOISE_EVALUATION_SAMPLE_SIZE=20
TESTFILE_PATH=/mnt/pagagne/cmartineau/METB_LivingLab/16S/testlist.txt
# if true, will generate a new random manifest. even if one already exists
# if false, will use the $ANALYSIS_NAME.eval_manifest.temp as subset
FORCE_RESAMPLING=false

DRY_RUN=false

#################################
#   Step 2 : Dada2 Denoising   #
#################################

# NOT FOR STEP 1.5 (YOU MUST USE TESTFILE FOR STEP 1.5)

p_trim_left_f=0
p_trim_left_r=0

p_trunc_len_f=270
p_trunc_len_r=217

p_max_ee_f=2
p_max_ee_r=2
p_n_reads_learn=1000000

p_chimera_method=consensus
p_min_fold_parent_over_abundance=1.0

#####################################
# Step3  Feature Table filtering   #
#####################################

# FUTURE DEV: REPLACE OR ADD AUTO CALCULATION ACCORDING TO VISUALIZATION DATA
# Use 0 to disable
```

```
#freq_threshold=0.0005
# Mean frequency: 29,732.395833333332 * 0.0005 = 14.86619
p_min_frequency=20


# IDEM ^^^^
# Use 0 to disable
#sample_threshold=0
p_min_samples=0

################################
# Step 4  Denovo Clustering   #
################################

# Must be between ]0 , 1.0]
# Use NA to skip denovo clustering (you must still launch step 4)
p_perc_identity=NA

################################
# Step 5  Classifier Training   #
################################

# Only Specify these if you want to train the classifier with your database
# It's recommended to use the same name (different extension) for the fasta and the
tax file
# The classifier output name must have the .qza extension

#FASTA_DATABASE_PATH=
#TAXO_DATABASE_PATH=
SEQS_QZA_PATH=
TAXO_QZA_PATH=
CLASSIFIER_OUTPUT_NAME=

################################
# Step 6 Taxonomy Assignment  #
################################

# Only specify this if you skipped step 5
CLASSIFIER_DATABASE_PATH=/mnt/CMartineau/Qiime2_databases/ITS_Fungi/
unite_v8_ajout/classifier_ajouts_unite_ver8_dynamic_10.05.2021.qza

#############################
# Step 7 Taxa Filtering    #
#############################

p_where=""

p_confidence=0.7
# Never use space in the list, only comma
# p_exclude remove unwanted taxe and p_include keep only specified taxa
# You can use both option to exclude parts of the inclusion
# If both are empty, taxa filtering will be skipped
p_include=fungi
p_exclude=

# Must be exact or contains (default)
p_mode=contains

# Will also be used in step 8 and 10
```

```
GENERATE_PHYLOGENY=false

# RAREFACTION OVERRIDE
# if you activate this option, you can ignore the next sections, skip step 8 and 9
SKIP_RAREFACTION=both
# Les deux ont ete fait (avec et sans)

########################################
#   Step 8 Alpha rarefaction plotting    #
########################################

p_max_depth=25000
p_steps=50
p_iterations=10
# Use this format: observed_features,shannon
# You can also leave this blank to use Qiime2 default metrics
(observed_features,shannon)
# IMPORTANT: This is NOT the metrics for step 10, this is only for the rarefaction
curve
p_metrics=observed_features,shannon

############################
# Step 9 Data Rarefaction #
############################

p_sampling_depth=7100

#######################
#   Step 10 Metrics   #
#######################

# Maniuplation necessaire en raison de bug avec qzv pielou_e non rarefie
alpha_metrics=shannon,simpson,observed_features,chao1,pielou_e

beta_metrics=braycurtis,jaccard

# Relevent only if GENERATE_PHYLOGENY is activated
alpha_metrics_phylo=faith_pd
beta_metrics_phylo=weighted_unifrac,weighted_normalized_unifrac,generalized_unifrac
,unweighted_unifrac

#######################
#   Step 11 Export   #
#######################


# ANCOM specific options
GENERATE_ANCOM=false
# Collapse table at genus level (6)
p_level=6

# Depend on your metadata
# Specify each target column seperated by a comma
GENERATE_FUNGUILD=true
# Ex: Col1,Col2,Col3,Col4
# There will be one ANCOM by column
m_metadata_column=
FUNGUILD_DATABASE_PATH=/mnt/CMartineau/Qiime2_databases/Funguild/
FUNguild_db_stbates.Jan-2022.json
```

```
##############################
#          16S               #
#     Q2Pipe Option file     #
# Designed for Q2Pipe V0.91 #
#                            #
##############################

################################
#  Common Analysis Parameters  #
################################

ANALYSIS_NAME=BASIC_TEST
NB_THREADS=8

# Leave empty if you don't use singularity image to launch Qiime2
# To define a different temporary folder, add -B /path/to/your/folder:/tmp
SINGULARITY_COMMAND="singularity exec --cleanenv --env
MPLCONFIGDIR=/tmp,TMPDIR=/tmp -B /scratch/melnag/tmp:/tmp -B /scratch/melnag -B
/project/def-chrmarti
/project/def-chrmarti/softwares/qiime2/qiime2_2022_2_NRCAN.sif"



# Metadata must be in TSV format
# Manifest must be in CSV format
# For multiple run, seperate each run manifest by a comma (,)
METADATA_FILE_PATH=

MANIFEST_FILE_PATH=/project/def-chrmarti/melnag/Caribou2019_data/16S_workspace/
mani.csv

# Leave empty to use system's default  (/tmp)
# DO NOT SPECIFY IF YOU ARE USING SINGULARITY COMMAND
TEMPORARY_DIRECTORY=

############################
#  Step 1 : Data Import  #
############################

# PLACEHOLDER for single end support DO NOT CHANGE THIS, ONLY PAIRED IS SUPPORTED
DATA_TYPE=paired

# Number of sequences to use to generate quality plots (default: 10000)
p_n=10000

############################
#  Cutadapt (Optional)  #
############################
# This step is done during step 1.5 and step 2

RUN_CUTADAPT=false
forward_trim_param=--p-front-f
reverse_trim_param=--p-front-r

forward_primer=GTGYCAGCMGCCGCGGTAA
```

```
reverse_primer=CCGYCAATTYMTTTRAGTTT

p_discard_untrimmed=true

#########################################################
#  Step 1.5 : Dada2 Denoising Parameters Evaluation  #
#########################################################

# This step is design to work with a single manifest file
# Manifest must be in CSV format
EVAL_MANIFEST_FILE_PATH=

# if your data is single-end, only p_trim_left_f, p_trunc_len_f and p_max_ee_f will
be used in trimming

# Use 0 to bypass evaluation (will just denoise all samples)
DENOISE_EVALUATION_SAMPLE_SIZE=5
TESTFILE_PATH=
# if true, will generate a new random manifest. even if one already exists
# if false, will use the $ANALYSIS_NAME.eval_manifest.temp as subset
FORCE_RESAMPLING=false

# If true, will stop the step after generating $ANALYSIS_NAME.eval_manifest.temp
# Nothing else will be generated until DRY_RUN is switched to false again
DRY_RUN=false

#################################
#   Step 2 : Dada2 Denoising   #
#################################

# NOT FOR STEP 1.5 (YOU MUST USE TESTFILE FOR STEP 1.5)

# Number of denoising job to launch simultaneously
# Each job will use NB_THREADS / job count
# For best result, your number of job should be a multiple of your NB_THREADS
# Ex: 3 jobs should have 9, 12, 15, etc. NB_THREADS so each job have the same
number of threads
# If 1 is used, all job will run sequentially (which will be slower that having
multiple jobs)
CONCURRENT_JOBS=1

# Use 0 to deactivate parameters (should be 0 if you used CutAdapt)
p_trim_left_f=19
p_trim_left_r=20

# Use 0 to deactivate parameters
# If you have multiple run, you must input a value for each of them
# seperate them by a comma (ex 234,235,223)
# They must be in the same order then your manifest list
p_trunc_len_f=261
p_trunc_len_r=238

p_max_ee_f=2
p_max_ee_r=2
p_n_reads_learn=1000000

p_chimera_method=consensus
p_min_fold_parent_over_abundance=1.0
```

```
############################
# Step 2.5 : Run Merging  #
############################


# If true, will proceed with merging even if runs are incompatible (different
denoising parameters)
# NOT RECOMMENDED
IGNORE_INCOMPATIBILITY=false



####################################
# Step 3 : Feature Table filtering  #
####################################

# FUTURE DEV: REPLACE OR ADD AUTO CALCULATION ACCORDING TO VISUALIZATION DATA
# Use 0 to disable
#freq_threshold=0.0005
p_min_frequency=25


# IDEM ^^^^
# Use 0 to disable
#sample_threshold=0
p_min_samples=0

################################
# Step 4 : Denovo Clustering  #
################################

# Must be between ]0 , 1.0]
# Use NA to skip denovo clustering (you must still launch step 4)
p_perc_identity=NA

##################################
# Step 5 : Classifier Training   #
##################################

# Only Specify these if you want to train the classifier with your database
# It's recommended to use the same name (different extension) for the fasta and the
tax file
# The classifier output name must have the .qza extension

#FASTA_DATABASE_PATH=
#TAXO_DATABASE_PATH=
SEQS_QZA_PATH=
TAXO_QZA_PATH=
CLASSIFIER_OUTPUT_NAME=

################################
# Step 6 : Taxonomy Assignment  #
################################

# Only specify this if you skipped step 5
CLASSIFIER_DATABASE_PATH=/project/def-chrmarti/databases/qiime2/16S_18S/silva_138/
classifier_silva138_q2.qza

# Possible value [0, 1]
```

```
p_confidence=0.7

############################
# Step 7 : Taxa Filtering  #
############################

# Filter samples according to specific metadata
# ex "[subject]='subject-1' AND NOT [body-site]='gut'"
# ex "[body-site]='gut' OR [reported-antibiotic-usage]='Yes'"
# ex "[body-site] IN ('left palm', 'right palm')"
# Leave "" to ignore
p_where=""

# Never use space in the list, only comma
# p_exclude remove unwanted taxe and p_include keep only specified taxa
# You can use both option to exclude parts of the inclusion
# If both are empty, taxa filtering will be skipped
p_include=bacteria,archaea
p_exclude=eukaryota,mitochondria,chloroplast

# Must be exact or contains (default)
p_mode=contains

# Will also be used in step 8 and 10
GENERATE_PHYLOGENY=false

# RAREFACTION OVERRIDE
# true, false or both
# if you activate this option, you can ignore the next sections, skip step 8 and 9
# Use "both" without the quotes to run both with and without rarefaction in a
single run
SKIP_RAREFACTION=both
########################################
#   Step 8 : Alpha rarefaction plotting  #
########################################

p_max_depth=30000
p_steps=50
p_iterations=10
# Use this format: observed_features,shannon
# You can also leave this blank to use Qiime2 default metrics
(observed_features,shannon)
# IMPORTANT: This is NOT the metrics for step 10, this is only for the rarefaction
curve
p_metrics=observed_features,shannon

############################
# Step 9 : Data Rarefaction #
############################

p_sampling_depth=18430

########################
#   Step 10 : Metrics  #
########################

alpha_metrics=shannon,simpson,observed_features,chao1,pielou_e
beta_metrics=braycurtis,jaccard
```

```
# Relevent only if GENERATE_PHYLOGENY is activated
alpha_metrics_phylo=faith_pd
beta_metrics_phylo=weighted_unifrac,weighted_normalized_unifrac,generalized_unifrac
,unweighted_unifrac

######################
#   Step 11 : Export #
######################


## FUNGuild specific options (Fungal ITS Only)
# To use FUNGuild, Guilds_v1.1.py must be available in your path
# Recommended FUNGuild version : https://github.com/Patg13/FUNGuild
GENERATE_FUNGUILD=false
# Enter remote_fungi to use remote fungi database
(http://stbates.org/funguild_db.php)
# You can also specify a local database path
# Database must be downloaded with the provided bash script in
https://github.com/Patg13/FUNGuild
FUNGUILD_DATABASE_PATH=



## ANCOM specific options
GENERATE_ANCOM=true
# Collapse table at genus level (6)
p_level=2

# Depend on your metadata
# Specify each target column seperated by a comma
# Ex: Col1,Col2,Col3,Col4
# There will be one ANCOM by column
m_metadata_column=Sex,Population
```