

Pre-processing of *Strongyloides papillosus* bulk RNAseq via an alignment-free analysis pipeline

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1 Introduction

The goal of this file is to pre-process the *Strongyloides papillosus* RNAseq dataset originally analyzed by Hunt *et al* 2016.

2 Pre-processing Methods Overview

Raw reads are aligned to the *S. papillosus* reference transcriptome (PRJEB525.WBPS14.mRNA_transcripts, downloaded from WormBase Parasite on 17 August 2020), using Kallisto. Kallisto alignments are imported into the R environment and annotated with information imported via the Wormbase ParaSite BioMaRT. Annotation information includes: *C. elegans* homologs/percent homology, UniProtKB number, Interpro terms, GO terms, and general Description information. Hunt *et al* 2016 establishes two distinct subclades from the four sequenced *Strongyloides* species: *S. venezuelensis*-*S. papillosus* and *S. ratti*-*S. stercoralis*. Thus, we also include annotation information for the appropriate in-group (here, *S. venezuelensis*), and a reference member of the out-group (*S. stercoralis*). Annotation information is saved as an R object that is passed to a Shiny Web App for downstream browsing and on-demand analysis. Note: Raw count data is be saved as a digital gene expression list.

Raw reads were quantified as counts per million using the EdgeR package, then filtered to remove transcripts with low counts (less than 1 count-per-million in at least 2 samples). A list of discarded genes and their expression values across life stages is saved. Non-discarded gene values are normalized using the trimmed

mean of M-values method (TMM, Robinson and Oshlack) to permit between-samples comparisons. The mean-variance relationship was modeled using a precision weights approach Law *et al* 2014.

A variance-stabilized, condensed DGEList object is saved; this file is passed to a Shiny Web App for downstream browsing and on-demand analysis.

3 Results/Analysis

3.1 Kallisto read mapping

This shell script checks the quality of the fastq files and performs an alignment to the *Strongyloides papillosus* cDNA transcriptome reference with Kallisto; to work, it needs to be saved as an .sh file in a folder containing required raw files. This script is reproduced here to demonstrate the QC and alignment process.

3.2 Import Kallisto reads into R

Import Kallisto transcript counts into R using Tximport. Counts are generated from abundance files using the `lengthScaledTPM` option. This code chunk is not evaluated each time, instead it was run once and an object containing the transcripts per million data is saved. In subsequent chunks, that file is loaded, and analysis progresses. The point of this is so that folks attempting to rerun this analysis do not need to have abundance files loaded on their local machines (and we do not have to upload abundance files to github).

3.3 Gene Annotation

Import gene annotation information for *S. papillosus* genes, including:

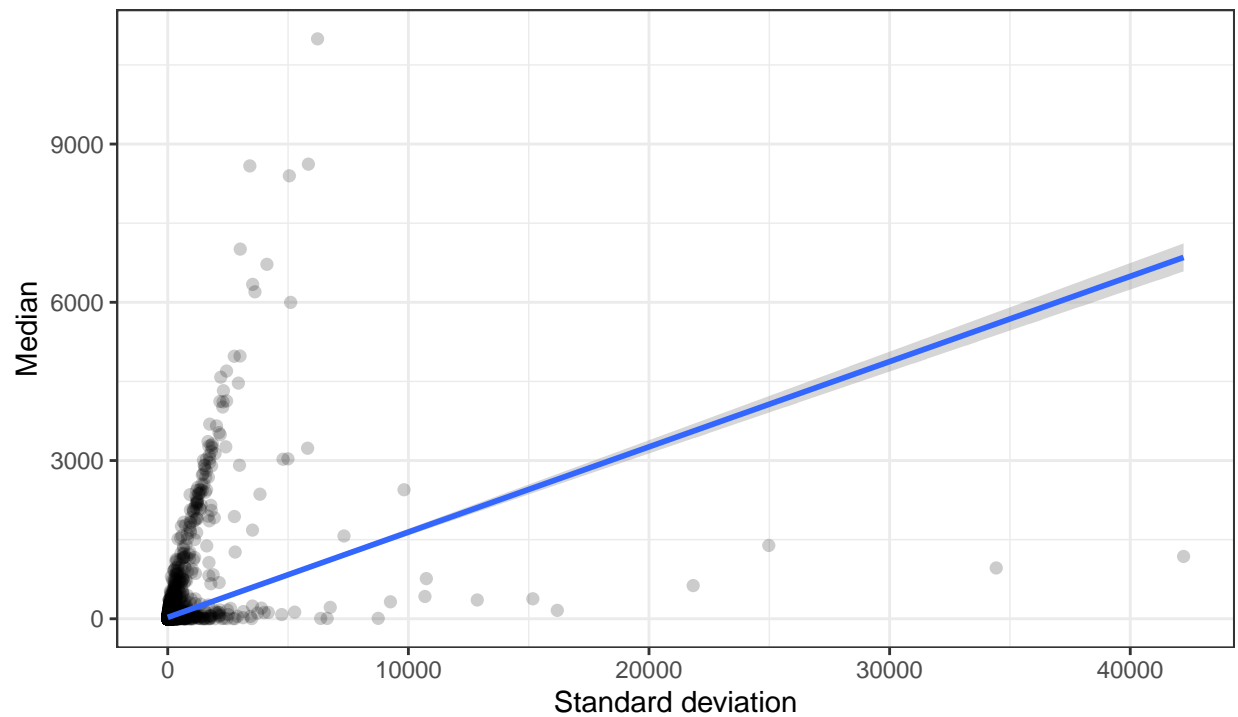
- * *C. elegans* homologs/percent homology
- * *S. venezuelensis* homologs/percent homology
- * *S. stercoralis* homologs/percent homology
- * UniProtKB number
- * Interpro terms
- * GO terms
- * general Description information using biomaRt.

3.4 Generate Digital Gene Expression List

This chunk of code generates a digital gene expression list that could be easily shared/loaded for downstream filtering/normalization. It generates a scatter plot of unfiltered and non-normalized transcripts per million data.

S. papillosus: Transcripts per million (TPM)

unfiltered, non-normalized data



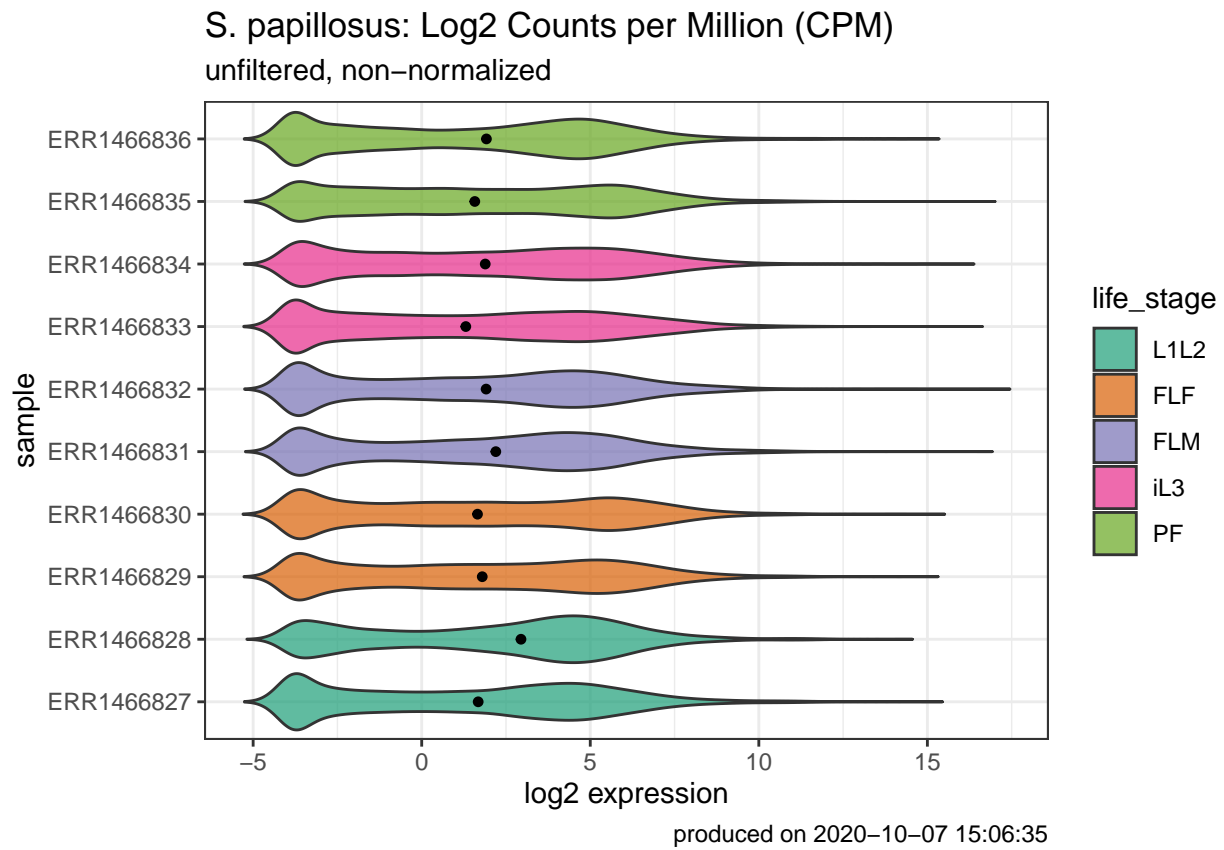
S. papillosus RNAseq Dataset

3.5 Data Filtering and Normalization

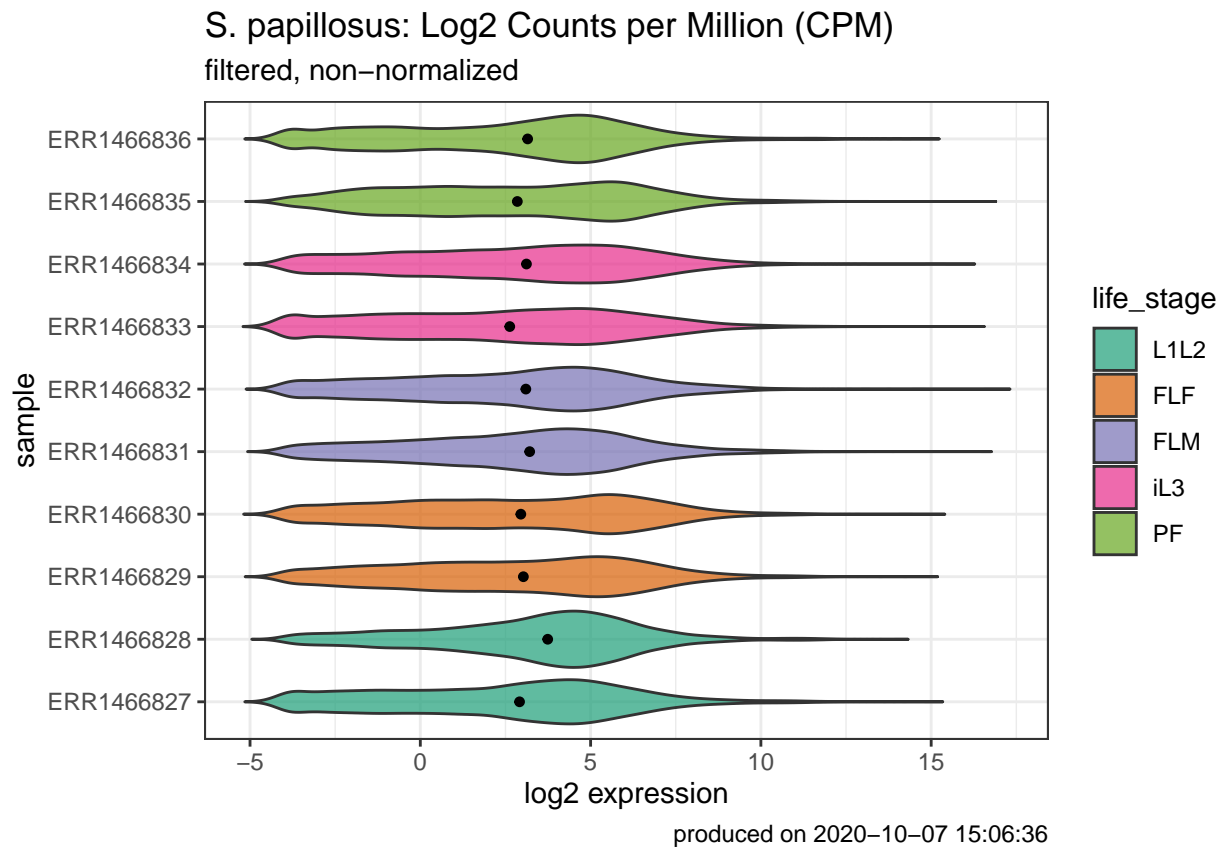
The goal of this chunk is to:

1. Filter and normalize data
2. Use `ggplot2` to visualize the impact of filtering and normalization on the data.

3.5.1 Plot of unfiltered, non-normalized log2CPM data by life stage



3.5.2 Plot of filtered, non-normalized log2CPM data by life stage

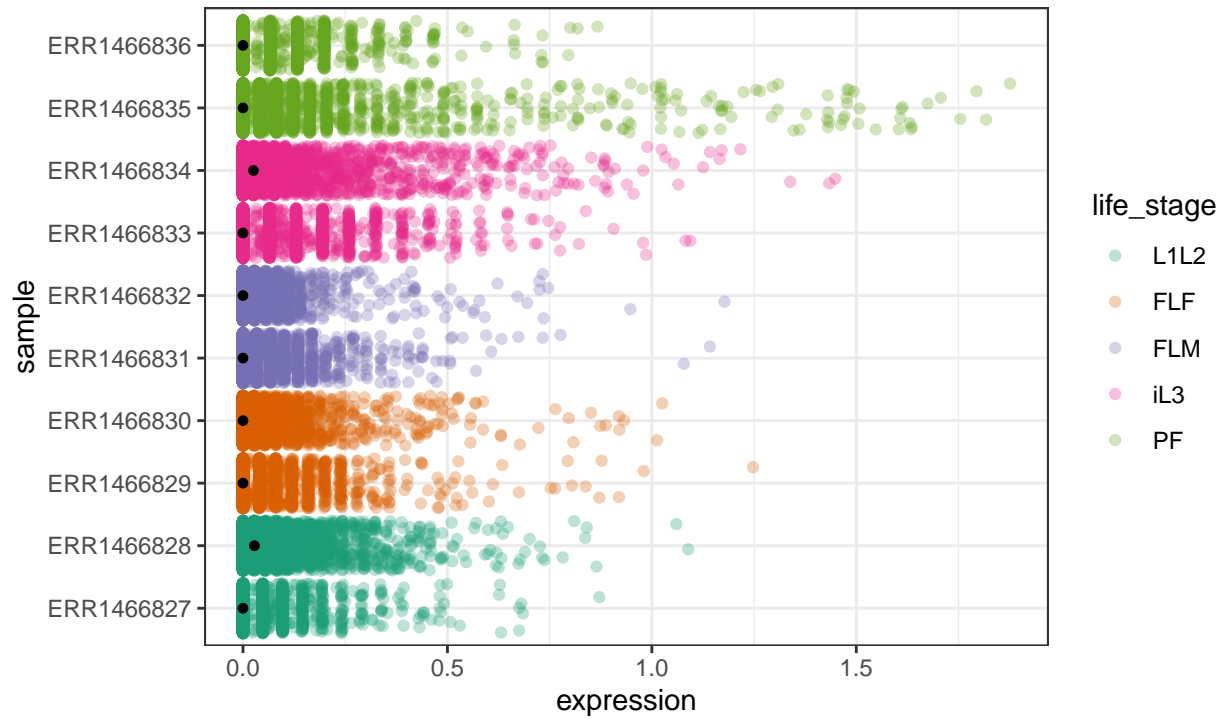


3.5.3 Plot of genes discarded by low-copy filtering step

The low copy number filtering step excluded a total of `dim(myDGEList.discarded)[[1]]` genes.

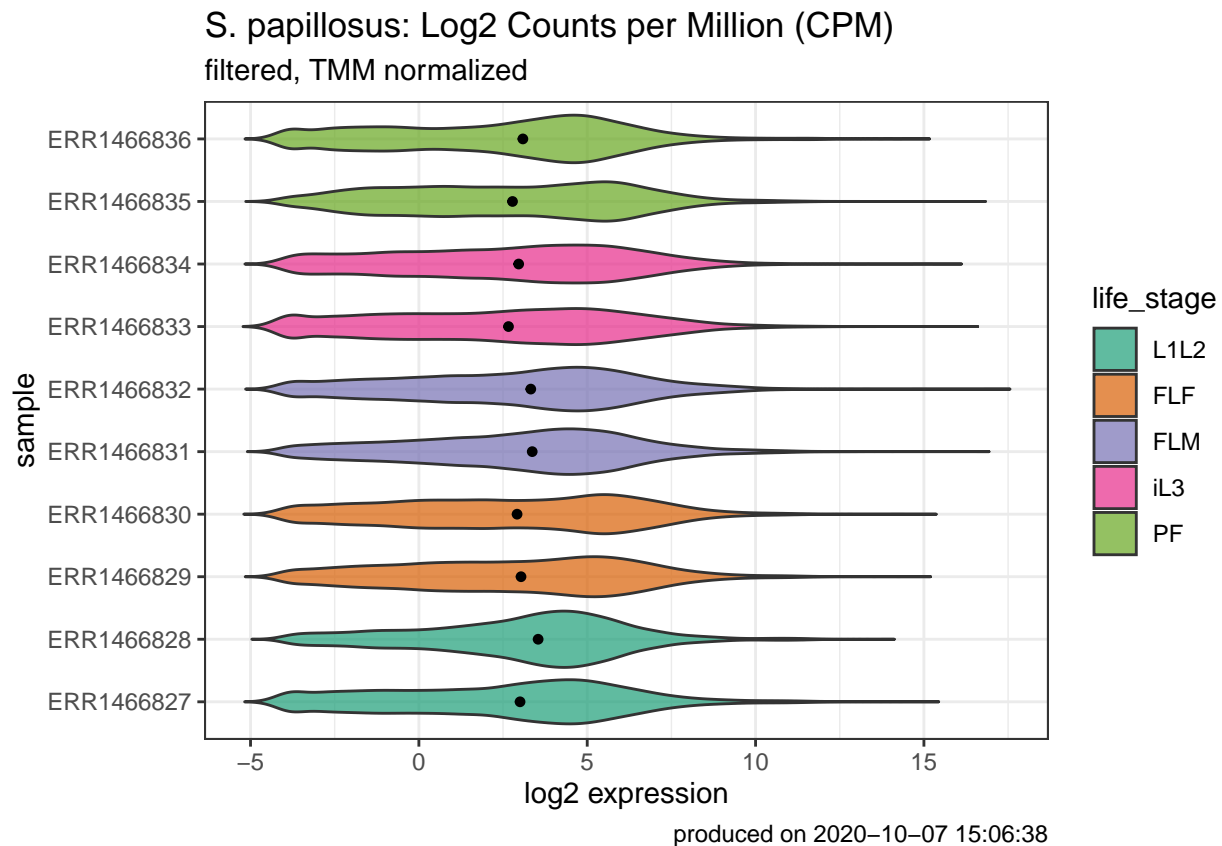
S. papillosus: Counts per Million (CPM)

genes excluded by low count filtering step, non-normalized



produced on 2020-10-07 15:06:37

3.5.4 Plot of filtered, normalized log2CPM data by life stage



3.6 Compute and Save Variance-Stabilized DGEList Object

This chunk uses a DGEList of filtered and normalized abundance data. It will fit data to a linear model for responsively detecting differentially expressed genes (DEGs).

3.7 Save Filtered Data and Annotations

This code chunk saves data and annotations, generated in code chunks above. The filtered data and annotation information is required for downstream analyses. It enables users to not have to re-import and re-align raw read files every time the code is run. The variance-stabilized vDGEList can be imported into a Shiny data browsing/analysis app.

4 Appendix I : All code for this report

```
knitr::opts_chunk$set(echo = FALSE, message = FALSE, warning = FALSE)

# This script checks the quality of the fastq files and performs an alignment
# to the Strongyloides papillosus cDNA transcriptome reference with Kallisto.

# To run this 'shell script' you will need to open your terminal and
# navigate to the directory where this script resides on your computer.
# This should be the same directory where you fastq files and reference
# fasta file are found.
```

```

# Change permissions on your computer so that you can run a
# shell script by typing: 'chmod u+x readMapping.sh' (without the quotes)
# at the terminal prompt
# Then type './readMapping.sh' (without the quotes) at the prompt.

# first use fastqc to check the quality of the fastq files:
fastqc *.gz -t 14

# build index from the reference fasta file
kallisto index -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index
strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.fa

# map reads to the indexed reference host transcriptome

# L1/L2s: Biological Replicates 1-2
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466827 -t 14 ERR1466827_1.fastq.gz ERR1466827_2.fastq.gz&> ERR1466827.log
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466828 -t 14 ERR1466828_1.fastq.gz ERR1466828_2.fastq.gz&> ERR1466828.log

# Free-living Females: Biological Replicates 1-2
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466829 -t 14 ERR1466829_1.fastq.gz ERR1466829_2.fastq.gz&> ERR1466829.log
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466830 -t 14 ERR1466830_1.fastq.gz ERR1466830_2.fastq.gz&> ERR1466830.log

# Free-living Males: Biological Replicates 1-2
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466831 -t 14 ERR1466831_1.fastq.gz ERR1466831_2.fastq.gz&> ERR1466831.log
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466832 -t 14 ERR1466832_1.fastq.gz ERR1466832_2.fastq.gz&> ERR1466832.log

# iL3s: Biological Replicates 1-2
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466833 -t 14 ERR1466833_1.fastq.gz ERR1466833_2.fastq.gz&> ERR1466833.log
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466834 -t 14 ERR1466834_1.fastq.gz ERR1466834_2.fastq.gz&> ERR1466834.log

# Parasitic Females: biological Replicates 1-2
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466835 -t 14 ERR1466835_1.fastq.gz ERR1466835_2.fastq.gz&> ERR1466835.log
kallisto quant -i strongyloides_papillosus.PRJEB525.WBPS14.mRNA_transcripts.index -o
ERR1466836 -t 14 ERR1466836_1.fastq.gz ERR1466836_2.fastq.gz&> ERR1466836.log

# summarize fastqc and kallisto mapping results using MultiQC
multiqc -d .

echo "Finished"
# load packages ----
suppressPackageStartupMessages({
  library(tidyverse)
  library(tximport)

```



```

library(ensembladb)
library(biomaRt)
library(magrittr)
})
# read in the study design ----
targets <- read_tsv("../Data/S_papillosus/Study_Design/PRJEB14543_study_design.txt",
                    na = c("", "NA", "na"))
# create file paths to the abundance files generated by
# Kallisto using the 'file.path' function
path <- file.path("../Data/S_papillosus/Reads", targets$sample, "abundance.tsv")

# get annotations using organism-specific package ----
Tx.Sp <- getBM(attributes=c('wbps_transcript_id',
                           'wbps_gene_id'),
               # grab the ensembl annotations for Wormbase Parasite genes
               mart = useMart(biomart="parasite_mart",
                              dataset = "wbps_gene",
                              host="https://parasite.wormbase.org",
                              port = 443),
               filters = c('species_id_1010'),
               value = list('stpapiprjeb525')) %>%
as_tibble() %>%
#we need to rename the columns retrieved from biomaRt
dplyr::rename(target_id = wbps_transcript_id,
              WB_geneID = wbps_gene_id) %>%
dplyr::mutate(gene_name = str_remove_all(target_id, "\\.[0-9]$")) %>%
dplyr::mutate(gene_name = str_remove_all(gene_name, "[a-c]$")) %>%
dplyr::select(!WB_geneID)

# import Kallisto transcript counts into R using Tximport ----
# copy the abundance files to the working directory and
# rename so that each sample has a unique name
Tx_gene <- tximport(path,
                    type = "kallisto",
                    tx2gene = Tx.Sp[,1:2],
                    txOut = FALSE,
                    countsFromAbundance = "lengthScaledTPM",
                    ignoreTxVersion = FALSE)

# Save the raw transcript counts ----
save(Tx_gene,
     file = file.path("../Data/S_papillosus",
                      "SpRNAseq_TPM"))

# Introduction to this chunk -----
# This chunk imports gene annotation information
# for S. papillosus genes, including:
# C. elegans homologs/percent homology,
# S. venezuelensis homologs/percent homology,
# S. stercoralis homologs/percent homology,
# UniProtKB number, Interpro terms, GO terms,

```

```

# and general Description information using biomaRt.
# It will generate a table that can be saved.

# Load packages -----
suppressPackageStartupMessages({
  library(tidyverse)
  library(tximport)
  library(ensembladb)
  library(biomaRt)
  library(magrittr)
})

# Load data & study design ----
load(file = file.path("../Data/S_papillosus",
                      "SpRNAseq_TPM"))

targets <- read_tsv("../Data/S_papillosus/Study_Design/PRJEB14543_study_design.txt",
                    na = c("", "NA", "na"))

# Get In-subclade group homologs for S. papillosus genes
# from BioMart and filter -----
Annt.temp.1 <- getBM(attributes=c('wbps_gene_id',
                                'stvenepjeb530_gene',
                                'stvenepjeb530_homolog_perc_id'),
                    # grab the ensembl annotations for Wormbase Parasite genes
                    mart = useMart(biomart="parasite_mart",
                                dataset = "wbps_gene",
                                host="https://parasite.wormbase.org",
                                port = 443),
                    filters = c('species_id_1010'),
                    value = list('stpapiprjeb525')) %>%

as_tibble() %>%
#rename columns
dplyr::rename(geneID = wbps_gene_id,
              In.subclade_geneID = stvenepjeb530_gene,
              In.subclade_percent_homology= stvenepjeb530_homolog_perc_id
) %>%
dplyr::group_by(geneID)

# Get Out-subclade group homologs for S. papillosus genes
# from BioMart and filter -----
Annt.temp.2 <- getBM(attributes=c('wbps_gene_id',
                                'ststerprjeb528_gene',
                                'ststerprjeb528_homolog_perc_id'
                                ),
                    # grab the ensembl annotations for Wormbase Parasite genes
                    mart = useMart(biomart="parasite_mart",
                                dataset = "wbps_gene",
                                host="https://parasite.wormbase.org",
                                port = 443),
                    filters = c('species_id_1010'),
                    value = list('stpapiprjeb525')) %>%

as_tibble() %>%

```

```

#rename columns
dplyr::rename(geneID = wbps_gene_id,
              Out.subclade_geneID = ststerprjeb528_gene,
              Out.subclade_percent_homology= ststerprjeb528_homolog_perc_id
) %>%
dplyr::group_by(geneID)

# Get C. elegans homologs and gene information for S. papillosus genes
# from BioMart and filter -----
Annt.temp.3 <- getBM(attributes=c('wbps_gene_id',
                                'caelegprjna13758_gene_name',
                                'caelegprjna13758_homolog_perc_id',
                                'description',
                                'interpro_short_description',
                                'go_name_1006',
                                'uniprot_sptrembl'),
                    # grab the ensembl annotations for Wormbase Parasite genes
                    mart = useMart(biomart="parasite_mart",
                                   dataset = "wbps_gene",
                                   host="https://parasite.wormbase.org",
                                   port = 443),
                    filters = c('species_id_1010'),
                    value = list('stpapiprjeb525')) %>%

as_tibble() %>%
#rename columns
dplyr::rename(geneID = wbps_gene_id,
              Ce_geneID = caelegprjna13758_gene_name,
              Ce_percent_homology = caelegprjna13758_homolog_perc_id,
              Description = description,
              GO_term = go_name_1006,
              UniProtKB = uniprot_sptrembl
) %>%
dplyr::group_by(geneID)

Annt.import <- full_join(Annt.temp.1, Annt.temp.2, by = "geneID") %>%
  full_join(Annt.temp.3, by = "geneID")

Annt.import$geneID <- str_remove_all(Annt.import$geneID, "\\.[0-9]$")
Annt.import$geneID <- str_remove_all(Annt.import$geneID, "[a-z]$")

# Replace empty string values (mostly in Ce_geneID column) with NAs
Annt.import[Annt.import == ""]<-NA

# Remove any duplications in the possible homolog matches.
# Select based on highest % homology.
# #Give fake value here to make sure genes
# without homologs aren't filtered out
Annt.import$Ce_percent_homology[
  is.na(Annt.import$Ce_percent_homology)] <- 1000
Annt.import$In.subclade_percent_homology[
  is.na(Annt.import$In.subclade_percent_homology)] <- 1000
Annt.import$Out.subclade_percent_homology[
  is.na(Annt.import$Out.subclade_percent_homology)] <- 1000

```

```

Annt.logs <-Annt.import %>%
  dplyr::select(!c(interpro_short_description:GO_term))%>%
  group_by(geneID) %>%
  slice_max(n = 1, order_by = Ce_percent_homology,
            with_ties = FALSE) %>%
  slice_max(n = 1, order_by = In.subclade_percent_homology,
            with_ties = FALSE) %>%
  slice_max(n = 1, order_by = Out.subclade_percent_homology,
            with_ties = FALSE) %>%
  group_by(geneID, Ce_geneID)

# Remove source code to shorten the description
Annt.logs$Description<- Annt.logs$Description %>%
  str_replace_all(string = .,
                  pattern = " \\[Source:.*\\]",
                  replacement = "") %>%
  cbind()

Annt.logs$Ce_percent_homology[
  Annt.logs$Ce_percent_homology == 1000] <- NA
Annt.logs$In.subclade_percent_homology[
  Annt.logs$In.subclade_percent_homology == 1000]<- NA
Annt.logs$Out.subclade_percent_homology[
  Annt.logs$Out.subclade_percent_homology == 1000]<- NA

# Clean up interprotKB terms, removing duplications and collapsing to one line
Annt.interpro<-Annt.import %>%
  dplyr::select(geneID, Ce_geneID, interpro_short_description) %>%
  group_by(geneID, Ce_geneID) %>%
  dplyr::distinct(interpro_short_description, .keep_all = TRUE) %>%
  dplyr::summarise(InterPro = paste(interpro_short_description,
                                   collapse = ', '))

# Clean up GO terms, removing duplications and collapsing to one line
Annt.goterms<-Annt.import %>%
  dplyr::select(geneID, Ce_geneID, GO_term) %>%
  group_by(geneID, Ce_geneID) %>%
  dplyr::distinct(GO_term, .keep_all = TRUE) %>%
  dplyr::summarise(GO_term = paste(GO_term, collapse = ', '))

annotations<-dplyr::left_join(Annt.logs, Annt.interpro) %>%
  dplyr::left_join(.,Annt.goterms) %>%
  ungroup() %>%
  dplyr::relocate(In.subclade_geneID,
                  In.subclade_percent_homology,
                  Out.subclade_geneID,
                  Out.subclade_percent_homology,
                  .after = geneID) %>%
  column_to_rownames(var = "geneID")

# List of S. papillosus genes is longer than the number of
# genes in the RNAseq dataset. So subset the
# annotations by the geneIDs in Txi_gene
annotations<-annotations[

```

```

rownames(annotations) %in% rownames(Txi_gene$counts),]

# Goals of this chunk:
# Generate and save a digital gene expression list that can be easily
# shared/loaded for downstream filtering/normalization

# Load packages -----
suppressPackageStartupMessages({
  library(tidyverse)
  library(edgeR)
  library(matrixStats)
  library(cowplot)
  library(ggthemes)
  library(RColorBrewer)
  library(gprofiler2)
})

# Generate and plot summary stats for the data ----
myTPM.stats <- transform(Txi_gene$abundance,
                        SD=rowSds(Txi_gene$abundance),
                        AVG=rowMeans(Txi_gene$abundance),
                        MED=rowMedians(Txi_gene$abundance))

# produce a scatter plot of the transformed data
p1<-ggplot(myTPM.stats) +
  aes(x = SD, y = MED) +
  geom_point(shape=16, size=2, alpha = 0.2) +
  geom_smooth(method=lm) +
  labs(y="Median", x = "Standard deviation",
       title="S. papillosus: Transcripts per million (TPM)",
       subtitle="unfiltered, non-normalized data",
       caption="S. papillosus RNAseq Dataset") +
  theme_bw()
p1

# make a Digital Gene Expression list using the raw counts and plot ----
myDGEList <- DGEList(Txi_gene$counts,
                    samples = targets$sample,
                    group = targets$group,
                    genes = annotations)

# Goals of this chunk:
# 1 - Filter and normalize data
# 2 - use ggplot2 to visualize the impact of filtering and normalization on the data.

# Notes:
# recall that abundance data are TPM, while the counts
# are read counts mapping to each gene or transcript

# Load packages -----
suppressPackageStartupMessages({
  library(tidyverse)
  library(edgeR)

```

```

library(matrixStats)
library(cowplot)
library(ggthemes)
library(RColorBrewer)
library(gprofiler2)
})

# If it's not available, read in the study design file ----
if (!exists("targets")){
  targets <- read_tsv(
    "../Data/S_papillosus/Study_Design/PRJEB14543_study_design.txt",
    na = c("", "NA", "na"))
}

# calculate and plot log2 counts per million ----

# Generate life stage IDs
ids <- rep(cbind(targets$group),
           times = nrow(myDGEList$counts)) %>%
  as_factor()

# use the 'cpm' function from EdgeR to get log2 counts per million
# then coerce into a tibble
# add sample names to the dataframe
# tidy up the dataframe into a tibble
log2.cpm.df.pivot <-cpm(myDGEList, log=TRUE) %>%
  as_tibble(rownames = "geneID") %>%
  setNames(nm = c("geneID", targets$sample)) %>%
  pivot_longer(cols = -geneID,
               names_to = "samples",
               values_to = "expression") %>%
  add_column(life_stage = ids)

# plot the pivoted data
p2 <- ggplot(log2.cpm.df.pivot) +
  aes(x=samples, y=expression, fill=life_stage) +
  geom_violin(trim = FALSE, show.legend = T, alpha= 0.7) +
  stat_summary(fun = "median",
               geom = "point",
               shape = 20,
               size = 2,
               color = "black",
               show.legend = FALSE) +
  labs(y="log2 expression", x = "sample",
       title="S. papillosus: Log2 Counts per Million (CPM)",
       subtitle="unfiltered, non-normalized",
       caption=paste0("produced on ", Sys.time())) +
  theme_bw() +
  scale_fill_brewer(palette = "Dark2") +
  coord_flip()
p2

```

```

# Filter the data ----
# filter genes/transcripts with low counts
# how many genes had more than 1 CPM (TRUE) in at least n samples
# Note: The cutoff "n" is adjusted for the number of
# samples in the smallest group of comparison.
keepers <- cpm(myDGEList) %>%
  rowSums(>1)>=2

myDGEList.filtered <- myDGEList[keepers,]

ids.filtered <- rep(cbind(targets$group),
  times = nrow(myDGEList.filtered)) %>%
  as_factor()

log2.cpm.filtered.df.pivot <- cpm(myDGEList.filtered, log=TRUE) %>%
  as_tibble(rownames = "geneID") %>%
  setNames(nm = c("geneID", targets$sample)) %>%
  pivot_longer(cols = -geneID,
    names_to = "samples",
    values_to = "expression") %>%
  add_column(life_stage = ids.filtered)

p3 <- ggplot(log2.cpm.filtered.df.pivot) +
  aes(x=samples, y=expression, fill=life_stage) +
  geom_violin(trim = FALSE, show.legend = T, alpha= 0.7) +
  stat_summary(fun = "median",
    geom = "point",
    shape = 20,
    size = 2,
    color = "black",
    show.legend = FALSE) +
  labs(y="log2 expression", x = "sample",
    title="S. papillosus: Log2 Counts per Million (CPM)",
    subtitle="filtered, non-normalized",
    caption=paste0("produced on ", Sys.time())) +
  theme_bw() +
  scale_fill_brewer(palette = "Dark2") +
  coord_flip()
p3

# Look at the genes excluded by the filtering step ----
# just to check that there aren't any with
# high expression that are in few samples
# Discarded genes
myDGEList.discarded <- myDGEList[!keepers,]

ids.discarded <- rep(cbind(targets$group),
  times = nrow(myDGEList.discarded)) %>%
  as_factor()

log2.cpm.discarded.df.pivot <- cpm(myDGEList.discarded, log=F) %>%
  as_tibble(rownames = "geneID") %>%

```

```

setNames(nm = c("geneID", targets$sample)) %>%
pivot_longer(cols = -geneID,
              names_to = "samples",
              values_to = "expression") %>%
add_column(life_stage = ids.discarded)

p.discarded <- ggplot(log2.cpm.discarded.df.pivot) +
  aes(x=samples, y=expression, color=life_stage) +
  #geom_violin(trim = FALSE, show.legend = T, alpha= 0.7) +
  geom_jitter(alpha = 0.3, show.legend = T)+
  stat_summary(fun = "median",
              geom = "point",
              shape = 20,
              size = 2,
              color = "black",
              show.legend = FALSE) +
  labs(y="expression", x = "sample",
       title="S. papillosus: Counts per Million (CPM)",
       subtitle="genes excluded by low count filtering step, non-normalized",
       caption=paste0("produced on ", Sys.time())) +
  theme_bw() +
  scale_color_brewer(palette = "Dark2") +
  coord_flip()
p.discarded

# # Carry out GO enrichment of discarded gene set using gProfiler2 ----
# discarded.geneID <- unique(log2.cpm.discarded.df.pivot$geneID)
# gost.res <- gost(list(Discarded_genes = discarded.geneID),
#                   organism = "stpapiprjeb525",
#                   correction_method = "fdr")
# gostplot(gost.res, interactive = T, capped = T)

# Generate a matrix of discarded genes and their raw counts ----
discarded.gene.df <-log2.cpm.discarded.df.pivot %>%
  pivot_wider(names_from = c(life_stage, samples),
              names_sep = "-",
              values_from = expression,
              id_cols = geneID)

# Normalize the data using a between samples normalization ----
# Source for TMM sample normalization here:
# https://genomebiology.biomedcentral.com/articles/10.1186/gb-2010-11-3-r25
myDGEList.filtered.norm <- calcNormFactors(myDGEList.filtered, method = "TMM")

log2.cpm.filtered.norm <- cpm(myDGEList.filtered.norm, log=TRUE)

log2.cpm.filtered.norm.df<- cpm(myDGEList.filtered.norm, log=TRUE) %>%
  as_tibble(rownames = "geneID") %>%
  setNames(nm = c("geneID", targets$sample))

log2.cpm.filtered.norm.df.pivot<-log2.cpm.filtered.norm.df %>%
  pivot_longer(cols = -geneID,

```



```

        names_to = "samples",
        values_to = "expression") %>%
add_column(life_stage = ids.filtered)

p4 <- ggplot(log2.cpm.filtered.norm.df.pivot) +
  aes(x=samples, y=expression, fill=life_stage) +
  geom_violin(trim = FALSE, show.legend = T, alpha = 0.7) +
  stat_summary(fun = "median",
    geom = "point",
    shape = 20,
    size = 2,
    color = "black",
    show.legend = FALSE) +
  labs(y="log2 expression", x = "sample",
    title="S. papillosus: Log2 Counts per Million (CPM)",
    subtitle="filtered, TMM normalized",
    caption=paste0("produced on ", Sys.time())) +
  theme_bw() +
  scale_fill_brewer(palette = "Dark2") +
  coord_flip()
p4

# Introduction to this chunk ----
# This chunk uses a DGEList of filtered and normalized abundance data
# It will fit data to a linear model for responsively detecting
# differentially expressed genes (DEGs)

# Load packages ----
suppressPackageStartupMessages({
  library(tidyverse)
  library(limma) # differential gene expression using linear modeling
  library(edgeR)
})

# Set up the design matrix ----
group <- factor(targets$group)
design <- model.matrix(~0 + group)
colnames(design) <- levels(group)

# Model mean-variance trend and fit linear model to data ----
colnames(myDGEList.filtered.norm$counts) <- targets$group

v.DGEList.filtered.norm <- voom(counts = myDGEList.filtered.norm,
  design = design, plot = F)
colnames(v.DGEList.filtered.norm)<-targets$sample
colnames(v.DGEList.filtered.norm$E) <- paste(targets$group,
  targets$sample, sep = '-')

# Check for presence of output folder, generate if it doesn't exist
output.path <- "../Outputs"
if (!dir.exists(output.path)){
  dir.create(output.path)
}

```

```

# Save full gene annotations ----
save(annotations,
     file = file.path(output.path,
                       "Sp_geneAnnotations"))

# Save DGEList of raw counts ----
save(myDGEList,
     file = file.path(output.path,
                       "SpRNAseq_DGEList"))

# Save a matrix of discarded genes and their raw counts ----
discarded.gene.df %>%
write.csv(file = file.path(output.path,
                           "SpRNAseq_discardedGene_counts.csv"))

# This data is required for downstream analyses in this file.
# It enables users to not have to re-import and
# re-align raw read files every time the code is run.
#
SpRNAseq.preprocessed.data <- list(targets = targets,
                                   annotations = annotations,
                                   log2.cpm.filtered.norm = log2.cpm.filtered.norm,
                                   myDGEList.filtered.norm = myDGEList.filtered.norm
)
save(SpRNAseq.preprocessed.data,
     file = file.path(output.path,
                       "SpRNAseq_data_preprocessed"))

# Save matrix of genes and their filtered, normalized counts ----
colnames(log2.cpm.filtered.norm)<-paste(targets$group,
                                       targets$sample,
                                       sep = "-")

write.csv(log2.cpm.filtered.norm,
          file = file.path(output.path,
                           "SpRNAseq_log2cpm_filtered_norm.csv"))

# Save v.DEGList ----
# This file will be imported into Shiny App
save(v.DEGList.filtered.norm,
     file = file.path(output.path,
                       "Sp_vDGEList"))

sessionInfo()

```

5 Appendix II: Session Info

```

## R version 3.6.3 (2020-02-29)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.5
##
## Matrix products: default

```

```

## BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats4 parallel stats graphics grDevices utils datasets
## [8] methods base
##
## other attached packages:
## [1] gprofiler2_0.1.9 RColorBrewer_1.1-2 ggthemes_4.2.0
## [4] cowplot_1.0.0 matrixStats_0.56.0 edgeR_3.28.1
## [7] limma_3.42.2 magrittr_1.5 biomaRt_2.42.1
## [10] ensemblDb_2.10.2 AnnotationFilter_1.10.0 GenomicFeatures_1.38.2
## [13] AnnotationDbi_1.48.0 Biobase_2.46.0 GenomicRanges_1.38.0
## [16] GenomeInfoDb_1.22.1 IRanges_2.20.2 S4Vectors_0.24.4
## [19] BiocGenerics_0.32.0 tximport_1.14.2 forcats_0.5.0
## [22] stringr_1.4.0 dplyr_1.0.1 purrr_0.3.4
## [25] readr_1.3.1 tidyr_1.1.1 tibble_3.0.3
## [28] ggplot2_3.3.2 tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] colorspace_1.4-1 ellipsis_0.3.1
## [3] XVector_0.26.0 fs_1.4.2
## [5] rstudioapi_0.11 farver_2.0.3
## [7] bit64_0.9-7 fansi_0.4.1
## [9] lubridate_1.7.9 xml2_1.3.2
## [11] splines_3.6.3 knitr_1.29
## [13] jsonlite_1.7.0 Rsamtools_2.2.3
## [15] broom_0.5.6 dbplyr_1.4.4
## [17] compiler_3.6.3 httr_1.4.2
## [19] backports_1.1.8 assertthat_0.2.1
## [21] Matrix_1.2-18 lazyeval_0.2.2
## [23] cli_2.0.2 htmltools_0.5.0
## [25] prettyunits_1.1.1 tools_3.6.3
## [27] gtable_0.3.0 glue_1.4.1
## [29] GenomeInfoDbData_1.2.2 rappdirs_0.3.1
## [31] Rcpp_1.0.5 cellranger_1.1.0
## [33] vctrs_0.3.2 Biostrings_2.54.0
## [35] nlme_3.1-148 rtracklayer_1.46.0
## [37] xfun_0.15 rvest_0.3.5
## [39] lifecycle_0.2.0 XML_3.99-0.3
## [41] zlibbioc_1.32.0 scales_1.1.1
## [43] hms_0.5.3 ProtGenerics_1.18.0
## [45] SummarizedExperiment_1.16.1 yaml_2.2.1
## [47] curl_4.3 memoise_1.1.0
## [49] stringi_1.4.6 RSQLite_2.2.0
## [51] BiocParallel_1.20.1 rlang_0.4.7
## [53] pkgconfig_2.0.3 bitops_1.0-6
## [55] evaluate_0.14 lattice_0.20-41
## [57] labeling_0.3 GenomicAlignments_1.22.1
## [59] htmlwidgets_1.5.1.9001 bit_1.1-15.2
## [61] tidyselect_1.1.0 R6_2.4.1

```

## [63] generics_0.0.2	DelayedArray_0.12.3
## [65] DBI_1.1.0	mgcv_1.8-31
## [67] pillar_1.4.6	haven_2.3.1
## [69] withr_2.2.0	RCurl_1.98-1.2
## [71] modelr_0.1.8	crayon_1.3.4
## [73] BiocFileCache_1.10.2	plotly_4.9.2.9000
## [75] rmarkdown_2.3	progress_1.2.2
## [77] locfit_1.5-9.4	grid_3.6.3
## [79] readxl_1.3.1	data.table_1.12.8
## [81] blob_1.2.1	reprex_0.3.0
## [83] digest_0.6.25	openssl_1.4.2
## [85] munsell_0.5.0	viridisLite_0.3.0
## [87] askpass_1.1	