Hierarchical clustering of samples when limited to InnateDB genes

Load required libraries

```r
library(plyr)
library(dplyr)
```

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

## The following objects are masked from 'package:plyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

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

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

```r
library(tibble)
library(stringr)
library(biomaRt)
library(genefilter)
library(DESeq2)
```

```
## Loading required package: S4Vectors

## Loading required package: stats4

## Loading required package: BiocGenerics

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB

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

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

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

##
## Attaching package: 'S4Vectors'

## The following objects are masked from 'package:dplyr':
##
##     first, rename

## The following object is masked from 'package:plyr':
##
##     rename

## The following object is masked from 'package:base':
##
##     expand.grid

## Loading required package: IRanges

##
## Attaching package: 'IRanges'

## The following objects are masked from 'package:dplyr':
##
##     collapse, desc, slice

## The following object is masked from 'package:plyr':
##
##     desc

## Loading required package: GenomicRanges

## Loading required package: GenomeInfoDb

## Loading required package: SummarizedExperiment

## Loading required package: Biobase

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

## Loading required package: DelayedArray

## Loading required package: matrixStats

##
## Attaching package: 'matrixStats'

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

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

```
##     rowSds, rowVars

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

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

## Loading required package: BiocParallel

##
## Attaching package: 'DelayedArray'

## The following objects are masked from 'package:matrixStats':
##
##     colMaxs, colMins, colRanges, rowMaxs, rowMins, rowRanges

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

```r
library(gplots)
```

```
##
## Attaching package: 'gplots'

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

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

## The following object is masked from 'package:stats':
##
##     lowess
```

```r
library(ggplot2)
library(RColorBrewer)
library(stringr)
library(devtools)
library(reshape2)
library(data.table)
```

```
##
## Attaching package: 'data.table'

## The following objects are masked from 'package:reshape2':
##
##     dcast, melt

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

## The following object is masked from 'package:GenomicRanges':
##
##     shift
## The following object is masked from 'package:IRanges':
##
##     shift
## The following objects are masked from 'package:S4Vectors':
##
##     first, second
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```
library(purrr)
```

```
##
## Attaching package: 'purrr'
## The following object is masked from 'package:data.table':
##
##     transpose
## The following object is masked from 'package:DelayedArray':
##
##     simplify
## The following object is masked from 'package:GenomicRanges':
##
##     reduce
## The following object is masked from 'package:IRanges':
##
##     reduce
## The following object is masked from 'package:plyr':
##
##     compact
```

```
library(ape)
```

Purpose

To compare more closely using dendrograms the hierarchical clustering of the different samples after aligning to the human genome or the species-specific genome and then limiting the subsequent RNA-Seq read counts to genes that have a one-to-one human ortholog in ALL NHP species AND fall into the InnateDB list.

```
##Read in the previously generated rlog(dds, blind = TRUE) outputs

##From mapping to human genome
##dds1 <- DESeqDataSetFromMatrix(countData = dd,
                              ##colData = sampleTable_setup_again,
                              ##design = ~species + species:donor.n + species:treatment)
##rld_dds1 <- rlog(dds1, blind = TRUE)
rld_dds1_human <-
  get(load("dds_outputs_humanalignments/2019-05-27_rld_dds1_mappedTohuman.Rdata"))

##From mapping to species-specific genomes
##dds1 <- DESeqDataSetFromMatrix(countData = dd,
                              ##colData = sampleTable_setup_again,
                              ##design = ~species + species:donor.n + species:treatment)
##rld_dds1 <- rlog(dds1, blind = TRUE)
rld_dds1_species <-
  get(load("dds_outputs_speciesspecificalignments/2019-05-26_rld_dds1_mappedTospecies.Rdata"))

##Folder for putting generated plots into
output_dir <- "PCA_output"

##Function to make rld outputs into format acceptable for further analysis
matrix_df <- function(input) {
matrix_made <- assay(input)
matrix_df <- as.data.frame(matrix_made)
matrix_df
}

species_df <- matrix_df(rld_dds1_species)
human_df <- matrix_df(rld_dds1_human)

##Getting column order to be in alphabetical order (so the same) in both data frames
human_df <- human_df[,order(colnames(human_df))]
species_df <- species_df[,order(colnames(species_df))]
```

Setting up our color scheme to use in the dendrogram, with each species having a different color.

```
##Setting the color scheme for the donors
colcoloring = function(donor) {
  ifelse(grepl("AG07923|AG08490|PR0058", donor), "darkolivegreen3",
      ifelse(grepl("PR00033|PR00036|PR00039", donor), "darkgreen",
        ifelse(grepl("AG05311|SQMA|SQMB", donor), "purple",
          ifelse(grepl("AG06105|PR00054|PR01109", donor), "#bee1f4",
             ifelse(grepl("PR230|PR0230|PR573|PR00573|PR107|PR00107", donor), "#7dc3e8",
               ifelse(grepl("PR111|PR235|PR248|PR00248", donor), "#0088ce",
                 ifelse(grepl("S4933|S004933|S3611|S003611|S3649|S003649", donor), "#00659c",
                   ifelse(grepl("AG08308|AG08312|AG08305", donor), "forestgreen",
                     ifelse(grepl("NHDF|AF|SR", donor), "#004368", "grey")))))))))
}
```

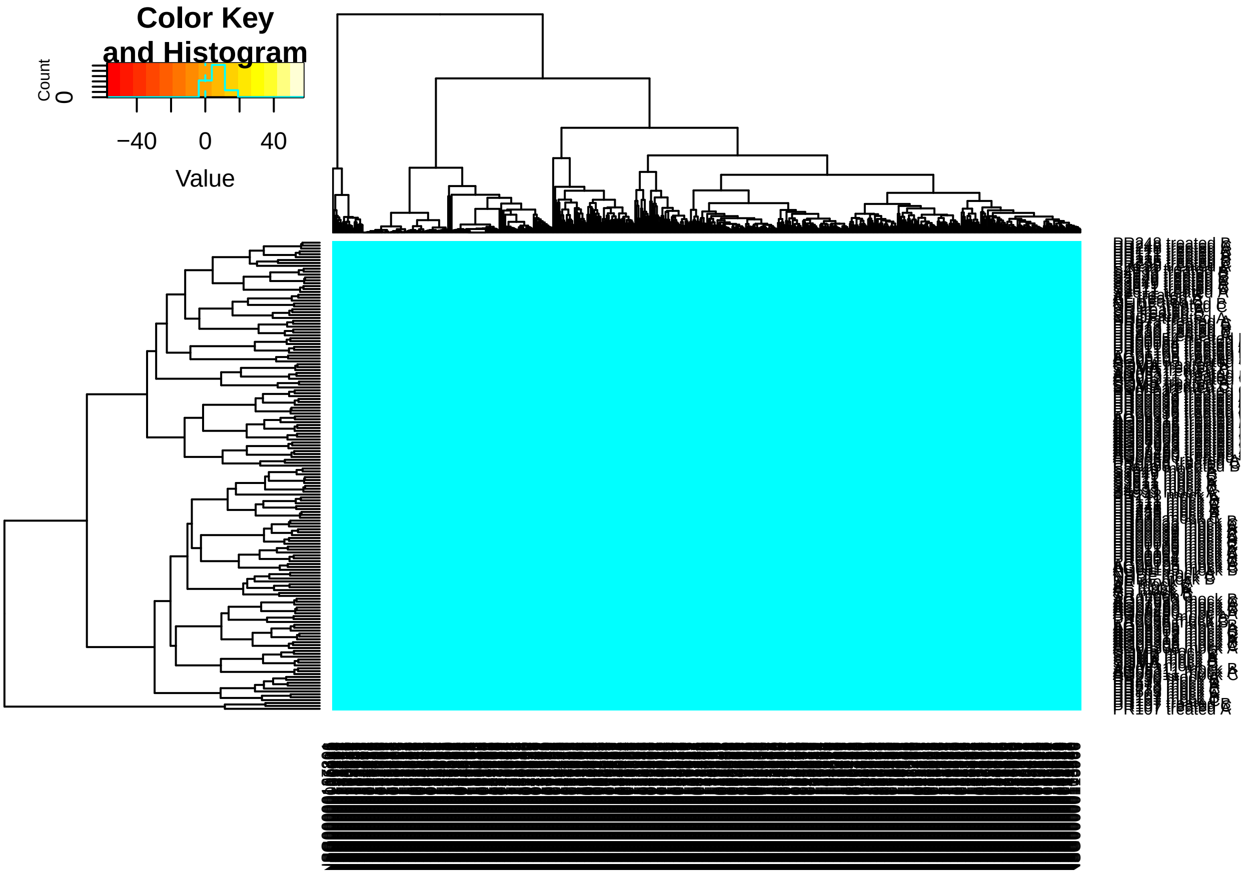
Selecting from our rlog output of genes that have a one-to-one human ortholog across ALL species the innate genes that we want to look at more closely.

```
##Download the InnateDB file of human innate gene symbols
innate <- read.csv(file = "innatedb_curated_genes.csv") %>%
  filter(Species == "9606") %>%
  distinct(Gene.Symbol, .keep_all = TRUE)

##Specifying that we want to work with the ENSEMBL database -- want to use ENSEMBL 96
##since this was the  version we used for processing our RNASeq reads.
#ensembl <- useMart("ENSEMBL_MART_ENSEMBL",
 #         host = "http://apr2019.archive.ensembl.org",
  #        ensemblRedirect = FALSE)
#human_ensembl <- useDataset("hsapiens_gene_ensembl", mart = ensembl)

##The innate gene list that was downloaded from innateDB only listed the gene symbol
##and gave no other identifier. Here, we wrote a function to pull in the ENSEMBL ID, biotype, gene name
##and description for each of the innate gene symbols in our document we read in as "innate"
```

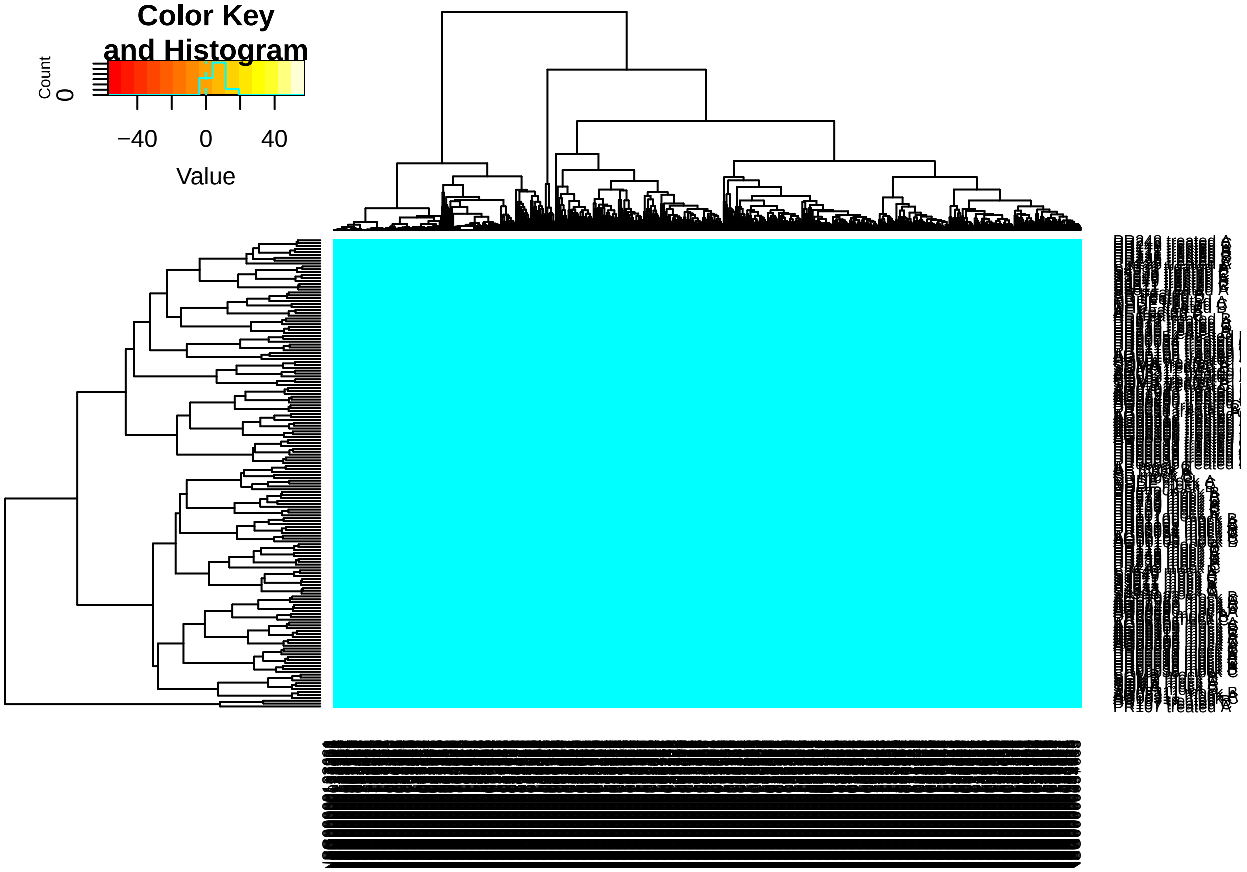
```r
#featurepage_symbol <- function(species_ensembl) {
 # getBM(attributes = c('ensembl_gene_id', 'description',
  #                            'external_gene_name', 'gene_biotype'),
   #               filters = 'external_gene_name',
    #                values = innate[,2],
     #             mart = species_ensembl)
#}

#featurepage_symbol_mouse <- function(species_ensembl) {
 # getBM(attributes = c('ensembl_gene_id', 'description',
  #                            'external_gene_name', 'gene_biotype'),
               #   filters = 'external_gene_name',
                #    values = innate_mouse[,2],
                 # mart = species_ensembl)
#}
#feature_mouse_innate <- featurepage_symbol_mouse(mouse_ensembl)

##Using the "featurepage_symbol" function to find specifically the human gene information
##for each of the InnateDB symbols in "innate."
#feature_human_innate <- featurepage_symbol(human_ensembl) %>%
 #  dplyr::rename(., hsapiens_homolog_ensembl_gene = ensembl_gene_id) %>%
  ###So when you pull the symbols from the human ENSEMBL mart that was set up, you get
  ## a class of genes known as LRG_gene which is from the Locus Reference Genomic
  ##record which is a way to distinguish between a gene that has mutliple
  ##sequence variants. Thus, all the entries where the biotype = LRG_gene can be
  ##removed for our purposes.
  #dplyr::filter_at(., vars(contains("biotype")), any_vars((. != "LRG_gene"))) %>%
  #unique() ##there were four rows that were identical
##Note that there are in some cases multiple ENSEMBL IDs for a given gene symbol. Hence,
##there are more rows in this than in the original list of innate immunity genes.
##The number of distinct gene symbols is found by this:
#distinct(feature_human_innate, external_gene_name, .keep_all = TRUE) %>%
  #nrow()
#write.csv(feature_human_innate, paste(Sys.Date(), "InnateDBGeneFeatures.csv"))

feature_human_innate <- read.csv("2019-10-20 InnateDBGeneFeatures.csv")

##With all this information fleshed out for the innateDB genes, we now want to limit
##the data frames we made from the rlog(dds) to these genes.
 innate_human_df <- human_df[rownames(human_df) %in% feature_human_innate[,2],]
 innate_species_df <- species_df[rownames(species_df) %in% feature_human_innate[,2],]
 #innate_mouse_df <- mouse_df[rownames(mouse_df) %in% feature_mouse_innate[,1],]

##Turn the species_df and human_df so that the column names are the ENSEMBL IDs and the rows
##are the samples
turned_innate_human_df <- t(innate_human_df)
turned_innate_species_df <- t(innate_species_df)
#turned_innate_mouse_df <- t(innate_mouse_df)
```

For a different visualization that takes into account all sources of variance and not just the first two principal components, I will look at a dendrogram of the rlog RNASeq read counts for each of the innate genes when aligning to either the human or the species-specific reference genome to see how the samples cluster.

```
##Heatmap data of the sample clustering can be pulled after using the heatmap.2 function
##Human genome alignment
hm_human_innate <- heatmap.2(turned_innate_human_df)
```



```
hc_human_innate <- as.hclust(hm_human_innate$rowDendrogram )

##Species-specific alignment
hm_species_innate <- heatmap.2(turned_innate_species_df)
```



```
hc_species_innate <- as.hclust(hm_species_innate$rowDendrogram )

##Setting up color schemes
cluster_labels <- function(input) {
  str_extract(input$labels, "PR\\d*|AG\\d*|S\\d{4,}|SQM\\w{1}|AF|NHDF|SR")
}

cluster_labels_species <- cluster_labels(hc_species_innate)
cluster_labels_human <- cluster_labels(hc_human_innate)

treatment_labels <- function(input) {
  ifelse(grepl("*mock|*M\\d|*M\\d\\d", input$labels), "mock", "treated")
}

treatment_labels_species <- treatment_labels(hc_species_innate)
treatment_labels_human <- treatment_labels(hc_human_innate)

treatmentcoloring = function(treatment) {
  ifelse(treatment == "mock", "orange", "red")
}

treatmentcolors_species <- unlist(lapply(treatment_labels_species, treatmentcoloring))
treatmentcolors_human <- unlist(lapply(treatment_labels_human, treatmentcoloring))

clustcolors_human <- unlist(lapply(cluster_labels_human, colcoloring))
clustcolors_human
```

```
##   [1] "#004368"         "#004368"         "#004368"        
##   [4] "#004368"         "#004368"         "#004368"        
##   [7] "purple"          "purple"          "purple"         
##  [10] "purple"          "purple"          "purple"         
##  [13] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [16] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [19] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [22] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [25] "forestgreen"     "forestgreen"     "forestgreen"    
##  [28] "forestgreen"     "forestgreen"     "forestgreen"    
##  [31] "forestgreen"     "forestgreen"     "forestgreen"    
##  [34] "forestgreen"     "forestgreen"     "forestgreen"    
##  [37] "forestgreen"     "forestgreen"     "forestgreen"    
##  [40] "forestgreen"     "forestgreen"     "forestgreen"    
##  [43] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [46] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [49] "#004368"         "#004368"         "#004368"        
##  [52] "#004368"         "#004368"         "#004368"        
##  [55] "darkgreen"       "darkgreen"       "darkgreen"      
##  [58] "darkgreen"       "darkgreen"       "darkgreen"      
##  [61] "darkgreen"       "darkgreen"       "darkgreen"      
##  [64] "darkgreen"       "darkgreen"       "darkgreen"      
##  [67] "darkgreen"       "darkgreen"       "darkgreen"      
##  [70] "darkgreen"       "darkgreen"       "darkgreen"      
##  [73] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [76] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [79] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [82] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [85] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [88] "#bee1f4"         "#bee1f4"         "#bee1f4"        
##  [91] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
##  [94] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
##  [97] "#0088ce"         "#0088ce"         "#0088ce"        
## [100] "#0088ce"         "#0088ce"         "#0088ce"        
## [103] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
## [106] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
## [109] "#0088ce"         "#0088ce"         "#0088ce"        
## [112] "#0088ce"         "#0088ce"         "#0088ce"        
## [115] "#0088ce"         "#0088ce"         "#0088ce"        
## [118] "#0088ce"         "#0088ce"         "#0088ce"        
## [121] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
## [124] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"        
## [127] "#00659c"         "#00659c"         "#00659c"        
## [130] "#00659c"         "#00659c"         "#00659c"        
## [133] "#00659c"         "#00659c"         "#00659c"        
## [136] "#00659c"         "#00659c"         "#00659c"        
## [139] "#00659c"         "#00659c"         "#00659c"        
## [142] "#00659c"         "#00659c"         "#00659c"        
## [145] "purple"          "purple"          "purple"         
## [148] "purple"          "purple"          "purple"         
## [151] "purple"          "purple"          "purple"         
## [154] "purple"          "purple"          "purple"         
## [157] "#004368"         "#004368"         "#004368"        
## [160] "#004368"         "#004368"         "#004368"        
```

```
clustcolors_species <- unlist(lapply(cluster_labels_species, colcoloring))
clustcolors_species
```

```
##   [1] "#004368"         "#004368"         "#004368"
##   [4] "#004368"         "#004368"         "#004368"
##   [7] "purple"          "purple"          "purple"
##  [10] "purple"          "purple"          "purple"
##  [13] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [16] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [19] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [22] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [25] "forestgreen"     "forestgreen"     "forestgreen"
##  [28] "forestgreen"     "forestgreen"     "forestgreen"
##  [31] "forestgreen"     "forestgreen"     "forestgreen"
##  [34] "forestgreen"     "forestgreen"     "forestgreen"
##  [37] "forestgreen"     "forestgreen"     "forestgreen"
##  [40] "forestgreen"     "forestgreen"     "forestgreen"
##  [43] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [46] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [49] "#004368"         "#004368"         "#004368"
##  [52] "#004368"         "#004368"         "#004368"
##  [55] "darkgreen"       "darkgreen"       "darkgreen"
##  [58] "darkgreen"       "darkgreen"       "darkgreen"
##  [61] "darkgreen"       "darkgreen"       "darkgreen"
##  [64] "darkgreen"       "darkgreen"       "darkgreen"
##  [67] "darkgreen"       "darkgreen"       "darkgreen"
##  [70] "darkgreen"       "darkgreen"       "darkgreen"
##  [73] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [76] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [79] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [82] "darkolivegreen3" "darkolivegreen3" "darkolivegreen3"
##  [85] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [88] "#bee1f4"         "#bee1f4"         "#bee1f4"
##  [91] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
##  [94] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
##  [97] "#0088ce"         "#0088ce"         "#0088ce"
## [100] "#0088ce"         "#0088ce"         "#0088ce"
## [103] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
## [106] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
## [109] "#0088ce"         "#0088ce"         "#0088ce"
## [112] "#0088ce"         "#0088ce"         "#0088ce"
## [115] "#0088ce"         "#0088ce"         "#0088ce"
## [118] "#0088ce"         "#0088ce"         "#0088ce"
## [121] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
## [124] "#7dc3e8"         "#7dc3e8"         "#7dc3e8"
## [127] "#00659c"         "#00659c"         "#00659c"
## [130] "#00659c"         "#00659c"         "#00659c"
## [133] "#00659c"         "#00659c"         "#00659c"
## [136] "#00659c"         "#00659c"         "#00659c"
## [139] "#00659c"         "#00659c"         "#00659c"
## [142] "#00659c"         "#00659c"         "#00659c"
## [145] "purple"          "purple"          "purple"
## [148] "purple"          "purple"          "purple"
## [151] "purple"          "purple"          "purple"
## [154] "purple"          "purple"          "purple"
## [157] "#004368"         "#004368"         "#004368"
## [160] "#004368"         "#004368"         "#004368"
```

```
##Alignment of all species with the human genome
png(file = file.path(output_dir, paste(Sys.Date(), "humanalignment_innateDBgenes_phylo.png")), units =
plot(as.phylo(hc_human_innate), tip.color = clustcolors_human, cex = 0.75, label.offset = 1, edge.lty =
     font = 1, no.margin = TRUE, direction = "downwards")
tiplabels(pch = 19, col = treatmentcolors_human)
nodelabels(pch = 15, col = "grey")
add.scale.bar()
dev.off()
```

```
## pdf
##   2
```

```
png(file = file.path(output_dir, paste(Sys.Date(), "speciesalignment_innateDBgenes_phylo.png")),
    units = 'in', height = 7,
    width = 20, res = 300)
plot(as.phylo(hc_species_innate), tip.color = clustcolors_species, cex = 0.75, label.offset = 1, edge.lt
     font = 1, no.margin = TRUE, direction = "downwards")
tiplabels(pch = 19, col = treatmentcolors_species)
nodelabels(pch = 15, col = "grey")
add.scale.bar()
dev.off()
```

```
## pdf
##   2
```

Session Info

```
sessionInfo()
```

```
## R version 3.5.2 (2018-12-20)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Sierra 10.12.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/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] parallel  stats4    stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] bindrcpp_0.2.2              ape_5.3
##  [3] purrr_0.2.5                 data.table_1.12.0
##  [5] reshape2_1.4.3              usethis_1.4.0
##  [7] devtools_2.0.1              RColorBrewer_1.1-2
##  [9] ggplot2_3.1.0               gplots_3.0.1
## [11] DESeq2_1.22.2               SummarizedExperiment_1.12.0
## [13] DelayedArray_0.8.0          BiocParallel_1.16.5
## [15] matrixStats_0.54.0          Biobase_2.42.0
## [17] GenomicRanges_1.34.0        GenomeInfoDb_1.18.1
## [19] IRanges_2.16.0              S4Vectors_0.20.1
## [21] BiocGenerics_0.28.0         genefilter_1.64.0
## [23] biomaRt_2.38.0              stringr_1.3.1
## [25] tibble_2.0.1                dplyr_0.7.8
## [27] plyr_1.8.4
##
## loaded via a namespace (and not attached):
##  [1] nlme_3.1-137           fs_1.2.6               bitops_1.0-6
##  [4] bit64_0.9-7            progress_1.2.0         httr_1.4.0
##  [7] rprojroot_1.3-2        tools_3.5.2            backports_1.1.3
## [10] R6_2.3.0               rpart_4.1-13           KernSmooth_2.23-15
## [13] Hmisc_4.1-1            DBI_1.0.0              lazyeval_0.2.1
## [16] colorspace_1.4-0       nnet_7.3-12            withr_2.1.2
## [19] processx_3.2.1         tidyselect_0.2.5       gridExtra_2.3
## [22] prettyunits_1.0.2      bit_1.1-14             compiler_3.5.2
## [25] cli_1.0.1              htmlTable_1.13.1       desc_1.2.0
## [28] caTools_1.17.1.1       scales_1.0.0           checkmate_1.9.1
## [31] callr_3.1.1            digest_0.6.18          foreign_0.8-71
## [34] rmarkdown_1.11         XVector_0.22.0         base64enc_0.1-3
## [37] pkgconfig_2.0.2        htmltools_0.3.6        sessioninfo_1.1.1
## [40] htmlwidgets_1.3        rlang_0.3.1            rstudioapi_0.9.0
## [43] RSQLite_2.1.1          bindr_0.1.1            gtools_3.8.1
## [46] acepack_1.4.1          RCurl_1.95-4.11        magrittr_1.5
## [49] GenomeInfoDbData_1.2.0 Formula_1.2-3          Matrix_1.2-15
## [52] Rcpp_1.0.0             munsell_0.5.0          stringi_1.2.4
## [55] yaml_2.2.0             zlibbioc_1.28.0        pkgbuild_1.0.2
## [58] grid_3.5.2             blob_1.1.1             gdata_2.18.0
## [61] crayon_1.3.4           lattice_0.20-38        splines_3.5.2
## [64] annotate_1.60.0        hms_0.4.2              locfit_1.5-9.1
## [67] ps_1.3.0               knitr_1.21             pillar_1.3.1
## [70] pkgload_1.0.2          geneplotter_1.60.0     XML_3.98-1.16
## [73] glue_1.3.0             evaluate_0.12          latticeExtra_0.6-28
## [76] remotes_2.0.2          gtable_0.2.0           assertthat_0.2.0
## [79] xfun_0.4               xtable_1.8-3           survival_2.43-3
## [82] AnnotationDbi_1.44.0   memoise_1.1.0          cluster_2.0.7-1
```