

# Maaslin 2 Analysis of GO Terms for COVIRT19

Lets install some R packages that we are gonna need to run this analysis

```
if(!requireNamespace("BiocManager", quietly = TRUE))
```

```
install.packages("BiocManager")
```

```
In [1]: #BiocManager::install("Maaslin2")
#BiocManager::install('DESeq2')
#BiocManager::install('phyloseq')
#BiocManager::install('microbiome')
```

```
In [2]: #install.packages("remotes")
#remotes::install_github("mikemc/speedyseq")
```

Now lets load our libraries and set out environment

```
In [3]: library(tidyverse)
library(phyloseq)
library(microbiome)
library(DESeq2)
library(Maaslin2)
```

— Attaching packages — tidyverse 1.3.0 —

```
✓ ggplot2 3.3.2    ✓ purrr   0.3.4
✓ tibble  3.0.4    ✓ dplyr   1.0.2
✓ tidyr   1.1.2    ✓ stringr 1.4.0
✓ readr   1.4.0    ✓ forcats 0.5.0
```

— Conflicts — tidyverse\_conflicts() —

```
✗ dplyr::filter() masks stats::filter()
✗ dplyr::lag()     masks stats::lag()
```

microbiome R package (microbiome.github.com)

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Sudarshan Shetty et al. <microbiome.github.io>

Attaching package: 'microbiome'

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

alpha

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

transform

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, colnames,  
dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,  
grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,  
order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,  
rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,  
union, unique, unsplit, which.max, which.min
```

Attaching package: 'S4Vectors'

The following objects are masked from 'package:dplyr':

first, rename

The following object is masked from 'package:tidyr':

expand

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

expand.grid

Loading required package: IRanges

Attaching package: 'IRanges'

The following object is masked from 'package:microbiome':

coverage

The following object is masked from 'package:phyloseq':

distance

The following objects are masked from 'package:dplyr':

collapse, desc, slice

The following object is masked from 'package:purrr':

reduce

Loading required package: GenomicRanges

Loading required package: GenomeInfoDb

Loading required package: SummarizedExperiment

Loading required package: MatrixGenerics

Loading required package: matrixStats

Attaching package: 'matrixStats'

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

count

Attaching package: 'MatrixGenerics'

The following objects are masked from 'package:matrixStats':

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

Loading required package: Biobase

Welcome to Bioconductor

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

Attaching package: 'Biobase'

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

rowMedians

The following objects are masked from 'package:matrixStats':

anyMissing, rowMedians

The following object is masked from 'package:phyloseq':

sampleNames

```
In [4]: setwd('/media//jochum00/Aagaard_Raid3/microbial/GO_term_analysis/')
```

```
In [5]: raw<-as_tibble(read.table("Combined_BALF_GO_Terms_parent_propagated.tsv", sep = "\t", row.names = NULL, header = T, quote
```

A tibble: 47,233 x 2,020 # good so far now do a little regex and fix some stuff

```
In [6]: colnames(raw)<-gsub("NA_tax","unclass", colnames(raw))%>%str_replace_all("NC1_SRR7796663", "NC1.SRR7796663")
```

Transform the raw table by type of count (euk, term, bac, arc)

```
In [7]: df<-raw %>%
  select(GO_term,namespace,depth,name,ends_with("_counts"))%>%
  pivot_longer(cols = -c(GO_term,namespace,depth,name),
    names_to = c("sample","type","abund"),#c("Total", "Archaea","Bacteria","Eukarya", "Viridae", "Unclassified"),
    names_pattern = "(.*)_(.*)_(.*)")%>%
  select(-abund)%>%
  filter(value>1)%>%
  pivot_wider(names_from = sample, values_from=value, values_fill=0)
#SIDE NOTE:There are multiple processes and values for a single sample so you cant convert the sample to columns
```

Make individual tibbles for biological processes and molecular fxn

```
In [8]: bio<-filter(df, namespace=="biological_process")
        mol<-filter(df, namespace=="molecular_function")
```

make individual tibbles for each type (bac, euk, term, arc, vir, etc)

```
In [9]: bio_bac<-bio%>%filter(type=="bac")%>%select(-type)
        bio_term<-bio%>%filter(type=="term")%>%select(-type)
        mol_bac<-mol%>%filter(type=="bac")%>%select(-type)
        mol_term<-mol%>%filter(type=="term")%>%select(-type)
```

subselect tibbles for only the counts and go terminology

```
In [10]: bio_bac_counts<-bio_bac%>%select(-c(namespace,depth,name))
         bio_bac_tax<-bio_bac%>%select(GO_term,namespace,depth,name)
         mol_bac_counts<-mol_bac%>%select(-c(namespace,depth,name))
         mol_bac_tax<-mol_bac%>%select(GO_term,namespace,depth,name)
```

convert them to dataframes for downstream import to phyloseq

```
In [11]: bio_bac_counts<-data.frame(bio_bac_counts, row.names=1)
         bio_bac_tax<-data.frame(bio_bac_tax, row.names=1)
         mol_bac_counts<-data.frame(mol_bac_counts, row.names=1)
         mol_bac_tax<-data.frame(mol_bac_tax, row.names=1)
```

convert the dataframes into phyloseq formats

```
In [12]: bio_bac_counts_phy <- otu_table(bio_bac_counts, taxa_are_rows=TRUE)
         bio_bac_tax_phy <- tax_table(as.matrix(bio_bac_tax), errorIfNULL=TRUE)
         mol_bac_counts_phy<-otu_table(mol_bac_counts, taxa_are_rows = T)
         mol_bac_tax_phy<-tax_table(as.matrix(mol_bac_tax), errorIfNULL = T)
```

import your metadata

```
In [13]: bio_bac_sam<-as.data.frame(read.table("Combined_BALF_GO_Terms_metadata.txt",header = T, sep = "\t",row.names = 1))
```

a little regex to fix the stupid filename

```
In [14]: rownames(bio_bac_sam)<-rownames(bio_bac_sam)%>%str_replace_all("NC1_SRR7796663", "NC1.SRR7796663")
         bio_bac_sam$accession<-rownames(bio_bac_sam)
```

making physeq object



IT FIXED THE BATCH EFFECT!

Dont worry about the limma batch effect correction step, I think I found a better way by including it in the multivariate model

```
In [21]: #vst_trans_count_tab2 <- limma::removeBatchEffect(vst_trans_count_tab, sample_info_tab$publication)
```

```
In [26]: vst_count_phy <- otu_table(vst_trans_count_tab, taxa_are_rows=T)
vst_tax_phy <- tax_table(bac_pseq_no_neg)
vst_physeq <- phyloseq(vst_count_phy, vst_tax_phy, sample_data(bac_pseq_no_neg))
vst_physeq_comp <- microbiome::transform(x = vst_physeq, transform = "compositional")
```

## MaAsLIN2

```
In [27]: dir.create("R_Maaslin2") # Create a new directory
setwd("R_Maaslin2") # Change the current working directory
getwd() #check if directory has been successfully changed
```

Warning message in dir.create("R\_Maaslin2"):

“'R\_Maaslin2' already exists”

'/media/jochum00/Aggaard\_Raid3/microbial/GO\_term\_analysis/R\_Maaslin2'

```
In [28]: df_input_data2 <- data.frame(t(otu_table(vst_physeq_comp)))
df_input_metadata2 <- data.frame(sample_data(vst_physeq_comp))
```

ok so here are the parameters you want to manipulate:

min abundance= the min rel abund hits (1%) #filters out XXXX GO\_terms \ min prevalence = Min samples required with min abundance for a feature not to be filtered (0.1=10%=14.1000 samples) \ max\_significance = the maximum p adjusted value to be significant \

This will filter our 13779 GO TERMS \

***normalization = CLR transformation \***

**CORRECTION** dont normalize here, just use the VST transformed counts

correction = the mutiple test correction method to be done (BH=Benjamini-Hochberg)

```
In [29]: Maaslin2(
```



```

input_data = df_input_data2,
input_metadata = df_input_metadata2,
output="covirt_bac_pseq_no_neg_maaslin3",
min_abundance = 0.01,
min_prevalence = 0.01,
normalization = "NONE",
transform = "NONE",
analysis_method = "LM",
max_significance = 0.25,
random_effects = c("sample_name", "publication"),
fixed_effects = c("case"),
correction="BH",
standardize = TRUE,
cores = 48,
plot_heatmap = TRUE,
plot_scatter = TRUE,
heatmap_first_n = 50,
reference=c("case, COVID19"))

```

```

[1] "Warning: Deleting existing log file: covirt_bac_pseq_no_neg_maaslin3/maaslin2.log"
2020-11-19 01:16:52 INFO::Writing function arguments to log file
2020-11-19 01:16:52 INFO::Verifying options selected are valid
2020-11-19 01:16:53 INFO::Determining format of input files
2020-11-19 01:16:53 INFO::Input format is data samples as rows and metadata samples as rows
2020-11-19 01:16:53 INFO::Formula for random effects: expr ~ (1 | sample_name) + (1 | publication)
2020-11-19 01:16:53 INFO::Formula for fixed effects: expr ~ case
2020-11-19 01:16:53 INFO::Filter data based on min abundance and min prevalence
2020-11-19 01:16:53 INFO::Total samples in data: 141
2020-11-19 01:16:53 INFO::Min samples required with min abundance for a feature not to be filtered: 1.410000
2020-11-19 01:16:53 INFO::Total filtered features: 13730
2020-11-19 01:16:53 INFO::Filtered feature names from abundance and prevalence filtering: GO.0045212.obsolete.neurotransmitter.receptor.biosynthetic.process, GO.0001319.obsolete.inheritance.of.oxidatively.modified.proteins.involved.in.replicative.cell.aging, GO.1900008.obsolete.negative.regulation.of.extrachromosomal.rDNA.circle.accumulation.involved.in.replicative.cell.aging, GO.0001302.obsolete.replicative.cell.aging, GO.0051704.multi.organism.process, GO.0051703.intraspecies.interaction.between.organisms, GO.0110148.biomineralization, GO.0043473.pigmentation, GO.0002376.immune.system.process, GO.0044419.interspecies.interaction.between.organisms, GO.0048511.rhythmic.process, GO.0023052.signaling, GO.0007610.behavior, GO.0015976.carbon.utilization, GO.0040011.locomotion, GO.0032502.developmental.process, GO.0032501.multicellular.organismal.process, GO.0040007.growth, GO.0009758.carbohydrate.utilization, GO.0022610.biological.adhesion, GO.0022414.reproductive.process, GO.0050896.response.to.stimulus, GO.0006791.sulfur.utilization, GO.0098754.detoxification, GO.0000003.reproduction, GO.0019740.nitrogen.utilization, GO.0008340.determination.of.adult.lifespan, GO.0019748.secondary.metabolic.process, GO.0060384.innervation, GO.0022413.reproductive.process.in.single.celled.organism, GO.0009628.response.to.abiotic.stimulus, GO.0055114.oxidation.reduction.process, GO.0009791.post.embryonic.development, GO.0007585.respiratory.gaseous.exchange.by.respiratory.system, GO.0008037.cell.recognition, GO.0009605.response.to.external.stimulus, GO.0009846.pollen.germination, GO.0043335.protein.unfolding, GO.0060033.anatomical.structure.regression, GO.0071722.detoxification.of.arsenic.containing.substance, GO.0032504.multicellular.organism.reproduction, GO.0000920.septum.digestion.after.cytokinesis, GO.0003006.developmental.process.involved.in.reproduction, GO.0045494.photoreceptor.cell.maintenance, GO.0001503.ossification, GO.0007568.aging, GO.0030537.larval.behavior, GO.0097194.execution.phase.of.apoptosis, GO.0001906.cell.killing, GO.0071840.cellular.component.organization.or.biogenesis, GO.0007017.microtubule.based.process, GO.0051702.interaction.with.

```

symbiont, GO.0098727.maintenance.of.cell.number, GO.0002532.production.of.molecular.mediator.involved.in.inflammatory.res  
 ponse, GO.0010312.detoxification.of.zinc.ion, GO.0014854.response.to.inactivity, GO.0022611.dormancy.process, GO.0009653.  
 anatomical.structure.morphogenesis, GO.0009607.response.to.biotic.stimulus, GO.0007566.embryo.implantation, GO.0009566.fe  
 rtilization, GO.0051775.response.to.redox.state, GO.0036268.swimming, GO.0009847.spore.germination, GO.0016049.cell.growt  
 h, GO.0001775.cell.activation, GO.0033036.macromolecule.localization, GO.0045103.intermediate.filament.based.process, GO.  
 0019674.NAD.metabolic.process, GO.0002252.immune.effector.process, GO.0071684.organism.emergence.from.protective.structur  
 e, GO.0045730.respiratory.burst, GO.0021700.developmental.maturation, GO.0098743.cell.aggregation, GO.0010073.meristem.ma  
 intenance, GO.0051301.cell.division, GO.0048532.anatomical.structure.arrangement, GO.0008283.cell.population.proliferatio  
 n, GO.0042221.response.to.chemical, GO.0061919.process.utilizing.autophagic.mechanism, GO.0022412.cellular.process.involv  
 ed.in.reproduction.in.multicellular.organism, GO.0007155.cell.adhesion, GO.0043934.sporulation, GO.0035640.exploration.be  
 havior, GO.0051606.detection.of.stimulus, GO.0048646.anatomical.structure.formation.involved.in.morphogenesis, GO.000763  
 1.feeding.behavior, GO.0048589.developmental.growth, GO.0007154.cell.communication, GO.0007049.cell.cycle, GO.0006955.imm  
 une.response, GO.0007624.ultradian.rhythm, GO.0007163.establishment.or.maintenance.of.cell.polarity, GO.0022404.molting.c  
 ycle.process, GO.0045058.T.cell.selection, GO.0006739.NADP.metabolic.process, GO.0044110.growth.involved.in.symbiotic.int  
 eraction, GO.0042303.molting.cycle, GO.0032259.methylation, GO.0070085.glycosylation, GO.0007635.chemosensory.behavior, G  
 O.0061842.microtubule.organizing.center.localization, GO.0080190.lateral.growth, GO.0030534.adult.behavior, GO.0140253.ce  
 ll.cell.fusion, GO.0030447.filamentous.growth, GO.0035176.social.behavior, GO.0048869.cellular.developmental.process, GO.  
 0007638.mechanosensory.behavior, GO.0032505.reproduction.of.a.single.celled.organism, GO.0050817.coagulation, GO.0051716.  
 cellular.response.to.stimulus, GO.0030029.actin.filament.based.process, GO.0051641.cellular.localization, GO.0006276.plas  
 mid.maintenance, GO.0006734.NADH.metabolic.process, GO.0014823.response.to.activity, GO.0032963.collagen.metabolic.proces  
 s, GO.0009719.response.to.endogenous.stimulus, GO.0048856.anatomical.structure.development, GO.0019954.asexual.reproducti  
 on, GO.0002440.production.of.molecular.mediator.of.immune.response, GO.0009405.pathogenesis, GO.0007059.chromosome.segreg  
 ation, GO.0007389.pattern.specification.process, GO.0065009.regulation.of.molecular.function, GO.0030431.sleep, GO.009724  
 2.amyloid.beta.clearance, GO.0051189.prosthetic.group.metabolic.process, GO.0016203.muscle.attachment, GO.0065008.regulat  
 ion.of.biological.quality, GO.0140029.exocytic.process, GO.0044703.multi.organism.reproductive.process, GO.0007272.enshea  
 thment.of.neurons, GO.0090713.immunological.memory.process, GO.0035821.modulation.of.process.of.other.organism, GO.007098  
 8.demethylation, GO.0048771.tissue.remolding, GO.0046034.ATP.metabolic.process, GO.0007340.acrosome.reaction, GO.199074  
 8.cellular.detoxification, GO.0022602.ovulation.cycle.process, GO.0071554.cell.wall.organization.or.biogenesis, GO.003219  
 6.transposition, GO.0016037.light.absorption, GO.0019882.antigen.processing.and.presentation, GO.0006928.movement.of.cel  
 l.or.subcellular.component, GO.0002200.somatic.diversification.of.immune.receptors, GO.0022402.cell.cycle.process, GO.006  
 1687.detoxification.of.inorganic.compound, GO.0010022.meristem.determinacy, GO.0035637.multicellular.organismal.signalin  
 g, GO.0022406.membrane.docking, GO.1902579.multi.organism.localization, GO.0048609.multicellular.organismal.reproductive.  
 process, GO.0044706.multi.multicellular.organism.process, GO.0007622.rhythmic.behavior, GO.0008219.cell.death, GO.004806  
 6.developmental.pigmentation, GO.0002118.aggressive.behavior, GO.0007626.locomotory.behavior, GO.0044403.symbiotic.proces  
 s, GO.0010127.mycothiol.dependent.detoxification, GO.0044764.multi.organism.cellular.process, GO.0014874.response.to.stim  
 ulus.involved.in.regulation.of.muscle.adaptation, GO.0003008.system.process, GO.0042440.pigment.metabolic.process, GO.001  
 0118.stomatal.movement, GO.0019835.cytolysis, GO.0042330.taxis, GO.0006950.response.to.stress, GO.0009838.abscission, GO.  
 0007623.circadian.rhythm, GO.0009056.catabolic.process, GO.0009845.seed.germination, GO.0018933.nicotine.metabolic.proces  
 s, GO.0006457.protein.folding, GO.0048870.cell.motility, GO.0010817.regulation.of.hormone.levels, GO.0048148.behavioral.r  
 esponse.to.cocaine, GO.0045196.establishment.or.maintenance.of.neuroblast.polarity, GO.0046677.response.to.antibiotic, G  
 O.0001709.cell.fate.determination, GO.0006403.RNA.localization, GO.0072593.reactive.oxygen.species.metabolic.process, GO.  
 0003002.regionalization, GO.0035878.nail.development, GO.0120252.hydrocarbon.metabolic.process, GO.0003360.brainstem.deve  
 lopment, GO.0048002.antigen.processing.and.presentation.of.peptide.antigen, GO.0044092.negative.regulation.of.molecular.f  
 unction, GO.0009292.genetic.transfer, GO.0008356.asymmetric.cell.division, GO.0021670.lateral.ventricle.development, GO.0  
 030901.midbrain.development, GO.0048286.lung.alveolus.development, GO.0035107.appendage.morphogenesis, GO.0009877.nodulat  
 ion, GO.0021508.floor.plate.formation, GO.0035902.response.to.immobilization.stress, GO.0018996.molting.cycle..collagen.a  
 nd.cuticulin.based.cuticle, GO.0070314.G1.to.G0.transition, GO.0006081.cellular.aldehyde.metabolic.process, GO.0098869.ce  
 llular.oxidant.detoxification, GO.0036342.post.anal.tail.morphogenesis, GO.0030010.establishment.of.cell.polarity, GO.009  
 8609.cell.cell.adhesion, GO.0061077.chaperone.mediated.protein.folding, GO.0001505.regulation.of.neurotransmitter.levels,

GO.0050877.nervous.system.process, GO.0099402.plant.organ.development, GO.0071216.cellular.response.to.biotic.stimulus, GO.0044282.small.molecule.catabolic.process, GO.0090659.walking.behavior, GO.0021794.thalamus.development, GO.0019883.antigen.processing.and.presentation.of.endogenous.antigen, GO.0007569.cell.aging, GO.0001708.cell.fate.specification, GO.0090693.plant.organ.senescence, GO.0009581.detection.of.external.stimulus, GO.0097502.mannosylation, GO.0044406.adhesion.of.symbiont.to.host, GO.0097485.neuron.projection.guidance, GO.0071852.fungal.type.cell.wall.organization.or.biogenesis, GO.0051649.establishment.of.localization.in.cell, GO.0048583.regulation.of.response.to.stimulus, GO.0022600.digestive.system.process, GO.0043900.regulation.of.multi.organism.process, GO.0021984.adenohypophysis.development, GO.0001966.thigmotaxis, GO.0010228.vegetative.to.reproductive.phase.transition.of.meristem, GO.0061299.retina.vasculature.morphogenesis.in.camera.type.eye, GO.0051304.chromosome.separation, GO.0061339.establishment.or.maintenance.of.monopolar.cell.polarity, GO.0032964.collagen.biosynthetic.process, GO.0006766.vitamin.metabolic.process, GO.0000320.re.entry.into.mitotic.cell.cycle, GO.0035239.tube.morphogenesis, GO.0032409.regulation.of.transporter.activity, GO.0009988.cell.cell.recognition, GO.0031640.killing.of.cells.of.other.organism, GO.0085030.symbiotic.process.benefiting.host, GO.0071495.cellular.response.to.endogenous.stimulus, GO.0048149.behavioral.response.to.ethanol, GO.0060135.maternal.process.involved.in.female.pregnancy, GO.0048070.regulation.of.developmental.pigmentation, GO.0009900.dehiscence, GO.0042755.eating.behavior, GO.0051236.establishment.of.RNA.localization, GO.0007023.post.chaperonin.tubulin.folding.pathway, GO.0120254.olefinic.compound.metabolic.process, GO.0003157.endocardium.development, GO.0042620.poly.3.hydroxyalkanoate..metabolic.process, GO.0046148.pigment.biosynthetic.process, GO.0072089.stem.cell.proliferation, GO.0006949.syncytium.formatio, GO.0009453.energy.taxis, GO.0048653.antenna.development, GO.0007379.segment.specification, GO.0021604.cranial.nerve.structural.organization, GO.0046844.chorion.micropyle.formatio, GO.0046149.pigment.catabolic.process, GO.0006450.regulation.of.translational.fidelity, GO.0003151.outflow.tract.morphogenesis, GO.0035152.regulation.of.tube.architecture..open.tracheal.system, GO.0006458.de.novo.protein.folding, GO.0019608.nicotine.catabolic.process, GO.0097164.ammonium.ion.metabolic.process, GO.0098813.nuclear.chromosome.segregation, GO.0042698.ovulation.cycle, GO.0048513.animal.organ.development, GO.0009611.response.to.wounding, GO.0008344.adult.locomotory.behavior, GO.0070265.necrotic.cell.death, GO.0007343.egg.activation, GO.0032879.regulation.of.localization, GO.0046843.dorsal.appendage.formatio, GO.0000910.cytokinesis, GO.0007618.mating, GO.0019953.sexual.reproduction, GO.0007530.sex.determination, 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GO.0016712.hydrolase.activity..acting.on.carbon.nitrogen..but.not.peptide..bonds..in.linear.amidines, GO.0017124.aldehyde.decarbonylase.activity, GO.0001108.phosphatase.activator.activity, GO.0016833.L.cystine.L.cysteine.lyase..deaminating., GO.0016724.2.octaprenyl.6.methoxyphenol.hydroxylase.activity, GO.0016298.bicarbonate.binding, GO.0047472.thiamine.transmembrane.transporter.activity, GO.0003921.homocysteine.desulphydrase.activity, GO.0033757.methylmalonyl.CoA.epimerase.activity, GO.0016034.oxidoreductase.activity..acting.on.the.CH.CH.group.of.donors..cytochrome.as.acceptor, GO.0019905.oligopeptide.binding, GO.0046566.sugar.transmembrane.transporter.activity, GO.0010329.hydrolase.activity..acting.on.acid.halide.bonds..in.C.halide.compounds, GO.0004055.signal.recognition.particle.binding, GO.0042578.PDZ.domain.binding, GO.0015267.arsenate.reductase..thioredoxin..activity, GO.0140033.oxidoreductase.activity..acting.on.other.nitrogenous.compounds.as.donors..cytochrome.as.acceptor, 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GO.0015157.phospholipid.transferase.activity, GO.0015572.D.cysteine.desulfhydrase.activity, GO.0016781.MHC.protein.binding, GO.0019135.NADPHX.epimerase.activity, GO.0015221.electron.transporter..transferring.electrons.within.cytochrome.c.oxidase.complex.activity, GO.001664

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GO.0016669.phosphotransferase.activity..alcohol.group.as.acceptor, GO.0047113.methylseleninic.acid.reductase.activity, GO.0047296.tRNA..2.methylthio.N.6..cis.hydroxy.isopentenyl.adenosine..hydroxylase.activity, GO.0015067.CTP.synthase.activity, GO.0008641.RNA.3.phosphate.cyclase.activity, GO.0047727.cation.transmembrane.transporter.activity, GO.0005186.phosphonoacetate.hydrolase.activity, GO.0016838.metal.ion.binding, GO.0090614.inositol.oxygenase.activity, GO.0033265.aspartic.type.peptidase.activity, GO.0016652.selenomethionine.adenosyltransferase.activity, GO.0008760.hydrolase.activity..acting.on.carbon.nitrogen..but.not.peptide..bonds..in.linear.amides, GO.0016878.N.acetylneuraminate.synthase.activity, GO.0019976.electron.transporter..transferring.electrons.within.the.cyclic.electron.transport.pathway.of.photosynthesis.activity, GO.0048407.C2H2.zinc.finger.domain.binding, GO.0004344.steroid.hydroxylase.activity, GO.0033765.peroxidase.activity, GO.0035014.RNA.binding, 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GO.0015647.thiolester.hydrolase.activity, GO.0016682.3.deoxy.8.phosphooctulonate.synthase.activity, GO.0047458.Notch.binding, GO.0032190.cysteine.type.peptidase.activity, GO.0044389.histone.deacetylase.binding, GO.0016641.tRNA.dihydrouridine.synthase.activity, GO.0046979.signaling.receptor.complex.adaptor.activity, GO.0032934.thiosulfate.binding, GO.0016802.oxidoreductase.activity..acting.on.paired.donors..with.incorporation.or.reduction.of.molecular.oxygen..NAD.P.H.as.one.donor..and.incorporation.of.one.atom.of.oxygen, GO.0016747.ubiquitin.binding, GO.0002060.ATPase.coupled.intramembrane.lipid.transporter.activity, GO.0034028.GABA.receptor.activity, GO.0015215.pyruvate.dehydrogenase.activity, GO.0022853.oxidoreductase.activity..acting.on.iron.sulfur.proteins.as.donors..NAD.or.NADP.as.acceptor, GO.0030248.glutathione.transferase.activity, GO.0061135.kinase.activator.activity, GO.0004930.iron.nicotianamine.transmembrane.transporter.activity, GO.0060590.acyl.carrier.activity, 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GO.0031419.vitamin.B6.binding, GO.0008933.oxidoreductase.activity..acting.on.other.nitrogenous.compounds.as.donors..oxygen.as.acceptor, GO.0019900.metalloproteinase.activity, GO.0097027.purine.nucleobase.transmembrane.transporter.activity, GO.0016708.methionine.adenosyltransferase.activity, GO.0098809.L.pipicolate.dehydrogenase.activity, GO.0016168.glycogen.synthase.activity..transferring.glucose.1.phosphate, GO.0036455.disaccharide.binding, GO.0016670.alpha.methylacyl.CoA.racemase.activity, GO.0004736.methyltransferase.activity, GO.0016715.coenzyme.F420.dependent.N5.N10.methenyltetrahydromethanopterin.reductase.activity, GO.0070012.malate.dehydrogenase.activity, GO.0016727.TAP1.binding, GO.0010328..1.4..alpha.D.glucan.1.alpha.D.glucosylmutase.activity, GO.0031406.UDPSulfoquinovose.synthase.activity, GO.0045309.clathrin.heavy.chain.binding, GO.0004087.sirohydrochlorin.ferrochelatase.activity, GO.0004462.oxidoreductase.activity..acting.on.a.sulfur.group.of.donors..disulfide.as.acceptor, 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GO.0016663.protein.deacetylase.activity, GO.0008237.syndecan.binding, GO.0005345.ubiquitin.like.protein.conjugating.enzyme.activity, GO.0004478.oxidoreductase.activity..acting.on.the.CH.NH.group.of.donors..flavin.as.acceptor, GO.0050030.telomerase.inhibitor.activity, GO.0061547.carboxylic.ester.hydrolase.activity, GO.0048030.heparin.binding, GO.0008111.oxidoreductase.activity..acting.on.the.CH.NH2.group.of.donors..iron.sulfur.protein.as.acceptor, GO.0008168.hydrolase.activity..acting.on.acid.carbon.carbon.bonds..in.ketonic.substances, GO.0018537.C3HC4.type.RING.finger.domain.binding, GO.0004012.mannan.binding, GO.0016615.2.succinyl.6.hydroxy.2.4.cyclohexadiene.1.carboxylate.synthase.activity, GO.0046978.tRNA.dimethylallyltransferase.activity, GO.0047470.cyclic.pyranopterin.monophosphate.synthase.activity, GO.0046507.muconate.cycloisomerase.activity, GO.0032050.hydrolase.activity..acting.on.carbon.nitrogen..but.not.peptide..bonds..in.cyclic.amides, GO.0051266.thiamine.binding, GO.0016671.neurotensin.receptor.activity..non.G.protein.coupled, GO.0008236.biotin.carboxylase.activity, GO.0033847.DEAD.H.box.RNA.helicase.binding, GO.0008428.blue.light.photoreceptor.activity, GO.0008812.methylation.dependent.protein.binding, GO.0019210.clathrin.adaptor.activity, GO.0016778.tRNA.2.selenouridine.synthase.activity, GO.2001062.3.phosphoshikimate.1.carboxyvinyltransferase.activity, GO.0005350.pseudouridine.synthase.activity, GO.0033850.phytoene.dehydrogenase.activity, GO.0070061.taste.receptor.activity, GO.0018551.riboflavin.binding, GO.0045158.neurotrophin.binding, GO.0016868.primary.active.transmembrane.transporter.activity, GO.0016881.oxidoreductase.activity..acting.on.single.donors.with.incorporation.of.molecular.oxygen..incorporation.of.one.atom.of.oxygen..internal.monooxygenases.or.internal.mixed.function.oxidases., GO.0003713.4.iron..4.sulfur.cluster.binding, GO.0050555.CoA.carboxylase.activity, GO.0004175.phosphotransferase.activity..phosphate.group.as.acceptor, 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GO.0033737.tRNA.Ile..lysine.synthase.activity, GO.0008066.carboxylate.reductase.activity, GO.0005528.aspartate.dehydrogenase.activity, GO.0008686.2.aminomuconate.deaminase.activity, GO.0008661.D.amino.acid.dehydrogenase.activity, GO.0017089.cystathionine.gamma.lyase.activity, GO.0018826.spectrin.binding, GO.0033734.linoleate.isomerase.activity, GO.0050418.oxidoreductase.activity..acting.on.a.heme.group.of.donors..oxygen.as.acceptor, GO.0038132.phosphotransferase.activity..nitrogenous.group.as.acceptor, GO.0019212.glycolate.dehydrogenase.activity, GO.0050334.6.7.dimethyl.8.ribityl lumazine.synthase.activity, GO.0046993.cyclosporin.A.binding, GO.0016636.phosphoribosylamine.glycine.ligase.activity, GO.0071723.L.cysteine.desulfhydrase.activity, GO.0004125.mannose.binding, GO.0042469.DNA.photolyase.activity, GO.0005158.nucleoside.transmembrane.transporter.activity, GO.0005523.oxidoreductase.activity..acting.on.the.CH.OH.group.of.donors..cytochrome.as.acceptor, 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GO.0060703.trans.octaprenyltransferase.activity, GO.0032267.peptide.hormone.binding, GO.0047770.RNA.polymerase.II.transcription.factor.binding, GO.0033735.netrin.receptor.activity, GO.0050540.GTPase.binding, GO.0008718.chloromuconate.cycloisomerase.activity, GO.0004123.transferase.activity..transferring.alkylthio.groups, GO.0003705.7.8.didemethyl.8.hydroxy.5.deazariboflavin.synthase.activity, GO.0030507.inositol.3.phosphate.synthase.activity, GO.0050058.I.SMAD.binding, GO.0016676.snRNP.binding, GO.0016775.hormone.receptor.binding, GO.0019154.spermidine.binding, GO.0000906.lipopolysaccharide.heptosyltransferase.activity, GO.0016018.thioglycosidase.binding, GO.0004637.oxidoreductase.activity..acting.on.diphenols.and.related.substances.as.donors..with.copper.protein.as.acceptor, GO.0080146.oxidoreductase.activity..acting.on.NAD.P.H..heme.protein.as.acceptor, GO.0005537.rhamnose.binding, GO.0003913.IgG.binding, GO.0005337.oxidoreductase.activity..acting.on.other.nitrogenous.compounds.as.donors..with.NAD.or.NADP.as.acceptor, GO.0016898.transferase.activity..transferring.hexosyl.groups, GO.0008504.peroxiredoxin.activity, GO.0070003.allene.oxide.cyclase.activity, GO.0070025.amidine.lyase.activity, GO.0034023.pyridoxine.5.phosphate.synthase.activity, GO.0004812.phospholipid.binding, GO.0034020.nicotinate.phosphoribosyltransferase.activity, GO.0015620.phosphate.ion.binding, GO.0043395.protoporphyrinogen.oxidase.activity, GO.0016728.peptidyl.cysteine.S.nitrosylase.activity, GO.0004408.SAM.domain.binding, GO.0009973.oxidoreductase.activity..acting.on.a.heme.group.of.donors..nitrogenous.group.as.acceptor, GO.0052890.chondroitin.sulfate.binding, GO.0102573.oxidoreductase.activity..acting.on.the.CH.CH.group.of.donors..NAD.or.NADP.as.acceptor, GO.0008849.amine.dehydrogenase.activity, GO.0002061.siderophore.uptake.transmembrane.transporter.activity, GO.0051879.capsanthin.synthase.activity, 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7.oxidoreductase.activity..acting.on.the.CH.NH2.group.of.donors..NAD.or.NADP.as.acceptor, GO.0017046.hexitol.dehydrogenase.activity, GO.0001085.taurine.dehydrogenase.activity, GO.0005042.racemase.and.epimerase.activity..acting.on.amino.acids.and.derivatives, GO.0051020.riboflavin.synthase.activity, GO.0018850.2.hydroxy.3.oxoadipate.synthase.activity, GO.0050497.1.aminocyclopropane.1.carboxylate.synthase.activity, GO.0044689.nucleotide.binding, GO.0004512.intramolecular.transferase.activity..transferring.hydroxy.groups, GO.0070411.sulfathiazole.transmembrane.transporter.activity, GO.0070990.isomaltulose.synthase.activity, GO.0051427.lycopene.beta.cyclase.activity, GO.0019809.oxidoreductase.activity..acting.on.hydrogen.as.donor..with.other.known.acceptors, GO.0008920.DNA.polymerase.binding, GO.0010180.2.succinyl.5.enolpyruvyl.6.hydroxy.3.cyclohexene.1.carboxylic.acid.synthase.activity, GO.0052880.allantoin.racemase.activity, 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GO.0004489.GDP.4.dehydro.6.deoxy.D.mannose.reductase.activity, GO.0047879.UDP.N.acetylmuramate.L.alanine.ligase.activity, GO.0019113.i.soguanine.deaminase.activity, GO.0008785.inositol.trisphosphate.kinase.activity, GO.0018669.nucleobase.containing.compound.kinase.activity, GO.0018498.adenylyl.sulfate.reductase..thioredoxin..activity, GO.0033923.NADH.peroxidase.activity, GO.0052589.methylated.histone.binding, GO.0042242.lathosterol.oxidase.activity, GO.0018481.L.L.diaminopimelate.aminotransferase.activity, GO.0004829.interleukin.17.receptor.activity, GO.0047570.RNA.polymerase.activity, GO.0001691.endoribonuclease.inhibitor.activity, GO.0052875.chemokine.receptor.binding, GO.0004815.2.chlorobenzoate.1.2.dioxygenase.activity, GO.0003729.adenosylcobinamide.GDP.ribazoletransferase.activity, GO.0047733.carbon.monoxide.oxygenase.activity, GO.0004312.D....tartrate.dehydratase.activity, GO.0050542.3.methyl.2.oxobutanoate.dehydrogenase..2.methylpropanoyl.transferring..activity, 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2020-11-19 01:16:53 INFO::Running selected normalization method: NONE

2020-11-19 01:16:53 INFO::Total filtered features with variance filtering: 0

2020-11-19 01:16:53 INFO::Filtered feature names from variance filtering:

2020-11-19 01:16:53 INFO::Applying z-score to standardize continuous metadata

2020-11-19 01:16:53 INFO::Running selected transform method: NONE

2020-11-19 01:16:53 INFO::Running selected analysis method: LM

2020-11-19 01:16:53 INFO::Creating cluster of 48 R processes

2020-11-19 01:17:57 INFO::Counting total values for each feature

2020-11-19 01:17:57 INFO::Writing residuals to file covirt\_bac\_pseq\_no\_neg\_maaslin3/residuals.rds

2020-11-19 01:17:57 INFO::Writing all results to file (ordered by increasing q-values): covirt\_bac\_pseq\_no\_neg\_maaslin3/all\_results.tsv

2020-11-19 01:17:57 INFO::Writing the significant results (those which are less than or equal to the threshold of 0.250000) to file (ordered by increasing q-values): covirt\_bac\_pseq\_no\_neg\_maaslin3/significant\_results.tsv

2020-11-19 01:17:57 INFO::Writing heatmap of significant results to file: covirt\_bac\_pseq\_no\_neg\_maaslin3/heatmap.pdf

2020-11-19 01:17:57 INFO::Writing association plots (one for each significant association) to output folder: covirt\_bac\_pseq\_no\_neg\_maaslin3

2020-11-19 01:17:57 INFO::Plotting associations from most to least significant, grouped by metadata

2020-11-19 01:17:57 INFO::Plotting data for metadata number 1, case

2020-11-19 01:17:57 INFO::Creating boxplot for categorical data, case vs GO.0034660.amino.acid.activation

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0016740.scavenger.receptor.activity

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0140098.galactoside.binding

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0043170.macromolecule.metabolic.process

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0016070.cellular.response.to.dsRNA

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0019538.non.reproductive.fruiting.body.development

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0016740.scavenger.receptor.activity

2020-11-19 01:17:58 INFO::Creating boxplot for categorical data, case vs GO.0043168.deaminase.activity

2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.1901362.organic.cyclic.compound.biosynthetic.



process

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2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0044260.cellular.macromolecule.metabolic.proc
ess
2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0003676.dynein.light.intermediate.chain.bindi
ng
2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0065007.biological.regulation
2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0003677.alcohol.dehydrogenase..acceptor..acti
vity
2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0016772.virus.receptor.activity
2020-11-19 01:17:59 INFO::Creating boxplot for categorical data, case vs GO.0009987.cellular.process
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0050794.regulation.of.cellular.process
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0090304.regulation.of.myoblast.differentiatio
n
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0050789.regulation.of.biological.process
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0044260.cellular.macromolecule.metabolic.proc
ess
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0016829.apolipoprotein.binding
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0016779.isobutyryl.CoA.mutase.activity
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0034645.negative.regulation.of.cell.activatio
n
2020-11-19 01:18:00 INFO::Creating boxplot for categorical data, case vs GO.0044281.small.molecule.metabolic.process
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0044283.small.molecule.biosynthetic.process
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0009987.cellular.process
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0009059.phenol.containing.compound.metabolic.
process
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0019438.aromatic.compound.biosynthetic.proces
s
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0044262.cellular.carbohydrate.metabolic.proce
ss
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.0019438.aromatic.compound.biosynthetic.proces
s
2020-11-19 01:18:01 INFO::Creating boxplot for categorical data, case vs GO.1901566.organonitrogen.compound.biosynthetic.
process
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0006139.response.to.ionizing.radiation
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0043168.deaminase.activity
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0034641.cellular.nitrogen.compound.metabolic.
process
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0006793.phosphorus.metabolic.process
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0006796.superoxide.metabolic.process
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.1901265.serine.hydrolase.activity
2020-11-19 01:18:02 INFO::Creating boxplot for categorical data, case vs GO.0000166.oxidoreductase.activity..acting.on.th
e.aldehyde.or.oxo.group.of.donors..disulfide.as.acceptor
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0036094.polyamine.binding
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0006082.organic.acid.metabolic.process
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0044249.cellular.biosynthetic.process
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0044281.small.molecule.metabolic.process
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0043170.macromolecule.metabolic.process
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.1901576.organic.substance.biosynthetic.proces
s

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2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0043436.oxoacid.metabolic.process
2020-11-19 01:18:03 INFO::Creating boxplot for categorical data, case vs GO.0019752.chromatin.maintenance
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.1901265.serine.hydrolase.activity
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0000166.oxidoreductase.activity..acting.on.th
e.aldehyde.or.oxo.group.of.donors..disulfide.as.acceptor
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0034660.amino.acid.activation
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0044238.primary.metabolic.process
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0005975.carbohydrate.metabolic.process
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0019538.non.reproductive.fruiting.body.develo
pment
2020-11-19 01:18:04 INFO::Creating boxplot for categorical data, case vs GO.0036094.polyamine.binding
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0008652.cholesterol.transport
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0044877.extracellular.matrix.structural.const
ituent
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0016835.catalytic.activity..acting.on.a.tRNA
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0008652.cholesterol.transport
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0046483.heterocycle.metabolic.process
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0016836.cyanate.hydratase.activity
2020-11-19 01:18:05 INFO::Creating boxplot for categorical data, case vs GO.0044283.small.molecule.biosynthetic.process
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0016053.endodermal.cell.differentiation
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0046394.1.butanol.metabolic.process
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0006520.positive.regulation.of.superoxide.dis
mutase.activity
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0016835.catalytic.activity..acting.on.a.tRNA
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0009072.myo.inositol.hexakisphosphate.metabol
ic.process
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0016836.cyanate.hydratase.activity
2020-11-19 01:18:06 INFO::Creating boxplot for categorical data, case vs GO.0046417.signal.transduction.involved.in.mitot
ic.cell.cycle.checkpoint
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0044877.extracellular.matrix.structural.const
ituent
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0009423.regulation.of.fucose.catabolic.proces
s
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0009073.methanogenesis..from.acetate
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0009423.regulation.of.fucose.catabolic.proces
s
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0003677.alcohol.dehydrogenase..acceptor..acti
vity
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0006082.organic.acid.metabolic.process
2020-11-19 01:18:07 INFO::Creating boxplot for categorical data, case vs GO.0043436.oxoacid.metabolic.process
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0043650.Malpighian.tubule.morphogenesis
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0043650.Malpighian.tubule.morphogenesis
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0003855.6.7.dihydropteridine.reductase.activi
ty
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0019752.chromatin.maintenance
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0003855.6.7.dihydropteridine.reductase.activi
ty
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0097367.lipoamide.binding
2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0097367.lipoamide.binding

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2020-11-19 01:18:08 INFO::Creating boxplot for categorical data, case vs GO.0046417.signal.transduction.involved.in.mitotic.cell.cycle.checkpoint
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0032553.imidazoleglycerol.phosphate.dehydratase.activity
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0016053.endodermal.cell.differentiation
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0046394.1.butanol.metabolic.process
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0043648.mitigation.of.host.defenses.by.symbiont
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0032553.imidazoleglycerol.phosphate.dehydratase.activity
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.0016070.cellular.response.to.dsRNA
2020-11-19 01:18:09 INFO::Creating boxplot for categorical data, case vs GO.1901566.organonitrogen.compound.biosynthetic.process
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0006807.nitrogen.compound.metabolic.process
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0003674.energy.transducer.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0032555.GDP.D.glucose.phosphorylase.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0017076.enoyl.CoA.hydratase.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0051540.protein.transporter.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0032555.GDP.D.glucose.phosphorylase.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0017076.enoyl.CoA.hydratase.activity
2020-11-19 01:18:10 INFO::Creating boxplot for categorical data, case vs GO.0004518.oxo.acid.lyase.activity
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0051536.oxidoreductase.activity..acting.on.NAD.P.H
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0035639.growth.factor.receptor.binding
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0140098.galactoside.binding
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0035639.growth.factor.receptor.binding
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0009058.biosynthetic.process
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0051539.tropomyosin.binding
2020-11-19 01:18:11 INFO::Creating boxplot for categorical data, case vs GO.0043648.mitigation.of.host.defenses.by.symbiont
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0034641.cellular.nitrogen.compound.metabolic.process
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0009072.myo.inositol.hexakisphosphate.metabolic.process
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0071941.nitrogen.cycle.metabolic.process
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0009399.nitrogen.fixation
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0009073.methanogenesis..from.acetate
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0003824.drug.binding
2020-11-19 01:18:12 INFO::Creating boxplot for categorical data, case vs GO.0065007.biological.regulation
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0050794.regulation.of.cellular.process
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0003676.dynein.light.intermediate.chain.binding
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0003824.drug.binding
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0006520.positive.regulation.of.superoxide.dismutase.activity
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0046483.heterocycle.metabolic.process
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0050789.regulation.of.biological.process
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0016874.catalytic.activity..acting.on.DNA
2020-11-19 01:18:13 INFO::Creating boxplot for categorical data, case vs GO.0051540.protein.transporter.activity

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2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0016772.virus.receptor.activity
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0051536.oxidoreductase.activity..acting.on.NA
D.P.H
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0051539.tropomyosin.binding
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0008150.biological_process
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0071941.nitrogen.cycle.metabolic.process
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0009399.nitrogen.fixation
2020-11-19 01:18:14 INFO::Creating boxplot for categorical data, case vs GO.0044271.cellular.nitrogen.compound.biosynthet
ic.process
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.1901362.organic.cyclic.compound.biosynthetic.
process
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.0044249.cellular.biosynthetic.process
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.1901576.organic.substance.biosynthetic.proces
s
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.0034645.negative.regulation.of.cell.activatio
n
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.0009059.phenol.containing.compound.metabolic.
process
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.0055086.salivary.gland.morphogenesis
2020-11-19 01:18:15 INFO::Creating boxplot for categorical data, case vs GO.0006725.cellular.aromatic.compound.metabolic.
process
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.1901564.organonitrogen.compound.metabolic.pro
cess
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0019637.organophosphate.metabolic.process
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0016788.oxygen.binding
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0016817.signaling.receptor.activator.activity
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0016818.nitrite.reductase.activity
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0006725.cellular.aromatic.compound.metabolic.
process
2020-11-19 01:18:16 INFO::Creating boxplot for categorical data, case vs GO.0006793.phosphorus.metabolic.process
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0006796.superoxide.metabolic.process
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0016462.RNA.polymerase.III.general.transcript
ion.initiation.factor.binding
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0016787.amide.binding
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0008150.biological_process
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0008233.tocopherol.cyclase.activity
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0006810.transport
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0006753.regulation.of.heterotypic.cell.cell.a
dhesion
2020-11-19 01:18:17 INFO::Creating boxplot for categorical data, case vs GO.0009117.ubiquinone.6.biosynthetic.process
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0003674.energy.transducer.activity
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0006810.transport
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0016787.amide.binding
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0051234.establishment.of.localization
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0017111.undecaprenyl.diphosphatase.activity
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0051179.localization
2020-11-19 01:18:18 INFO::Creating boxplot for categorical data, case vs GO.0043167.virion.binding
2020-11-19 01:18:19 INFO::Creating boxplot for categorical data, case vs GO.0140096.laminin.binding
2020-11-19 01:18:19 INFO::Creating boxplot for categorical data, case vs GO.0016779.isobutyryl.CoA.mutase.activity

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2020-11-19 01:18:19 INFO::Creating boxplot for categorical data, case vs GO.0072521.somatic.muscle.development

2020-11-19 01:18:19 INFO::Creating boxplot for categorical data, case vs GO.0016829.apolipoprotein.binding

## \$results

A data.frame: 232 × 10

	feature	metadata	value	coe
	<chr>	<chr>	<chr>	<dbl>
	GO.0034660.amino.acid.activation	case	Control_Healthy	0.00398172
	GO.0016740.scavenger.receptor.activity	case	Control_Sick	0.00907534
	GO.0140098.galactoside.binding	case	Control_Healthy	0.00288501
	GO.0043170.macromolecule.metabolic.process	case	Control_Healthy	0.00558945
	GO.0016070.cellular.response.to.dsRNA	case	Control_Healthy	0.00412331
	GO.0019538.non.reproductive.fruiting.body.development	case	Control_Healthy	0.00139988
	GO.0016740.scavenger.receptor.activity	case	Control_Healthy	0.00735957
	GO.0043168.deaminase.activity	case	Control_Healthy	0.00185891
	GO.1901362.organic.cyclic.compound.biosynthetic.process	case	Control_Healthy	-0.00291085
	GO.0044260.cellular.macromolecule.metabolic.process	case	Control_Healthy	0.00285043
	GO.0003676.dynein.light.intermediate.chain.binding	case	Control_Sick	-0.00297445
	GO.0065007.biological.regulation	case	Control_Healthy	0.00274794
	GO.0003677.alcohol.dehydrogenase..acceptor..activity	case	Control_Sick	-0.00222502
	GO.0016772.virus.receptor.activity	case	Control_Sick	0.00547552

	feature	metadata	value	coe
	<chr>	<chr>	<chr>	<dbl>
GO.0009987.cellular.process	case	Control_Healthy	0.00606211	
GO.0050794.regulation.of.cellular.process	case	Control_Healthy	0.00233509	
GO.0090304.regulation.of.myoblast.differentiation	case	Control_Healthy	0.00367783	
GO.0050789.regulation.of.biological.process	case	Control_Healthy	0.00232282	
GO.0044260.cellular.macromolecule.metabolic.process	case	Control_Sick	0.00237171	
GO.0016829.apolipoprotein.binding	case	Control_Healthy	-0.00464347	
GO.0016779.isobutyryl.CoA.mutase.activity	case	Control_Sick	0.00382821	
GO.0034645.negative.regulation.of.cell.activation	case	Control_Sick	0.00179341	
GO.0044281.small.molecule.metabolic.process	case	Control_Healthy	-0.00432479	
GO.0044283.small.molecule.biosynthetic.process	case	Control_Healthy	-0.00454054	
GO.0009987.cellular.process	case	Control_Sick	0.00490517	
GO.0009059.phenol.containing.compound.metabolic.process	case	Control_Sick	0.00174506	
GO.0019438.aromatic.compound.biosynthetic.process	case	Control_Healthy	-0.00205129	
GO.0044262.cellular.carbohydrate.metabolic.process	case	Control_Sick	0.00242111	
GO.0019438.aromatic.compound.biosynthetic.process	case	Control_Sick	-0.00193817	

	feature	metadata	value	coe
	<chr>	<chr>	<chr>	<dbl>
GO.1901566.organonitrogen.compound.biosynthetic.process		case	Control_Healthy	-0.00298167
:	:	:	:	:
GO.0001882.toxin.antitoxin.pair.type.II.binding		case	Control_Healthy	5.863199e-0
GO.0032549.homogentisate.1.2.dioxygenase.activity		case	Control_Healthy	5.872475e-0
GO.0019001.macrocin.O.methyltransferase.activity		case	Control_Sick	5.523391e-0
GO.0032561.abscisic.aldehyde.oxidase.activity		case	Control_Sick	5.493212e-0
GO.0043169.DNA.topoisomerase.type.I.single.strand.cut..ATP.independent..activity		case	Control_Sick	4.762072e-0
GO.0071704.organic.substance.metabolic.process		case	Control_Healthy	5.885809e-0
GO.0005215.phosphopantetheine.dependent.carrier.activity		case	Control_Sick	-2.138713e 0
GO.0001883.lipoprotein.particle.binding		case	Control_Sick	4.841929e-0
GO.0046872.endopeptidase.regulator.activity		case	Control_Sick	4.318028e-0
GO.0032550.polyphosphate.AMP.phosphotransferase.activity		case	Control_Sick	4.848646e-0
GO.0019001.macrocin.O.methyltransferase.activity		case	Control_Healthy	5.140863e-0
GO.0032561.abscisic.aldehyde.oxidase.activity		case	Control_Healthy	5.147866e-0
GO.0005525.ephrin.receptor.activity		case	Control_Sick	4.844792e-0
GO.0003924.adenyl.nucleotide.exchange.factor.activity		case	Control_Sick	4.632208e-0
GO.0001883.lipoprotein.particle.binding		case	Control_Healthy	4.579257e-0
GO.0032550.polyphosphate.AMP.phosphotransferase.activity		case	Control_Healthy	4.596168e-0
GO.0005525.ephrin.receptor.activity		case	Control_Healthy	4.587574e-0
GO.0003924.adenyl.nucleotide.exchange.factor.activity		case	Control_Healthy	4.409975e-0
GO.0006163.negative.regulation.of.muscle.cell.apoptotic.process		case	Control_Sick	-8.193882e 0
GO.0072521.somatic.muscle.development		case	Control_Sick	-7.894296e 0

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	GO.0016788.oxygen.binding	case	Control_Healthy	-1.431759e0
	GO.0006508.pentose.metabolic.process	case	Control_Sick	3.226418e-0
	GO.0009058.biosynthetic.process	case	Control_Sick	-2.985806e0
	GO.0043022.adenylate.cyclase.activity	case	Control_Sick	1.573443e-0
	GO.0043021.carbohydrate.transmembrane.transporter.activity	case	Control_Sick	1.426256e-0
	GO.1901360.organic.cyclic.compound.metabolic.process	case	Control_Sick	-9.724336e0
	GO.0043021.carbohydrate.transmembrane.transporter.activity	case	Control_Healthy	-9.348902e0
	GO.0016491.glycogen.debranching.enzyme.activity	case	Control_Healthy	-6.169740e0
	GO.0043022.adenylate.cyclase.activity	case	Control_Healthy	-6.899274e0
	GO.0044238.primary.metabolic.process	case	Control_Sick	-1.558900e0
\$residuals				1

GO.0008150.biological_process	1.050308e-03
GO.0008152.metabolic.process	1.967926e-03
GO.0051179.localization	-1.096149e-03
GO.0065007.biological.regulation	-1.735470e-04
GO.0009987.cellular.process	4.027215e-03



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<b>GO.0044237.cellular.metabolic.process</b>	3.258478e-03
<b>GO.0050789.regulation.of.biological.process</b>	-4.025308e-04
<b>GO.0044238.primary.metabolic.process</b>	-8.640054e-05
<b>GO.0071704.organic.substance.metabolic.process</b>	2.111104e-03
<b>GO.0006807.nitrogen.compound.metabolic.process</b>	5.247134e-04
<b>GO.0051234.establishment.of.localization</b>	-1.095399e-03
<b>GO.0009058.biosynthetic.process</b>	2.696740e-03
<b>GO.0044281.small.molecule.metabolic.process</b>	-4.001232e-04
<b>GO.0044283.small.molecule.biosynthetic.process</b>	3.578024e-04
<b>GO.1901360.organic.cyclic.compound.metabolic.process</b>	3.092047e-03
<b>GO.0034641.cellular.nitrogen.compound.metabolic.process</b>	3.431093e-03
<b>GO.0046483.heterocycle.metabolic.process</b>	3.578329e-03
<b>GO.0006082.organic.acid.metabolic.process</b>	-3.351721e-03
<b>GO.0043170.macromolecule.metabolic.process</b>	2.782860e-03
<b>GO.0006725.cellular.aromatic.compound.metabolic.process</b>	-7.259887e-04
<b>GO.0006810.transport</b>	-1.130341e-03

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<b>GO.0071941.nitrogen.cycle.metabolic.process</b>	-1.256314e-03
<b>GO.0044249.cellular.biosynthetic.process</b>	9.054021e-04
<b>GO.0050794.regulation.of.cellular.process</b>	-3.717222e-04
<b>GO.0005975.carbohydrate.metabolic.process</b>	1.194613e-03
<b>GO.1901564.organonitrogen.compound.metabolic.process</b>	9.787501e-04
<b>GO.0006793.phosphorus.metabolic.process</b>	1.465548e-04
<b>GO.1901576.organic.substance.biosynthetic.process</b>	9.139901e-04
<b>GO.1901362.organic.cyclic.compound.biosynthetic.process</b>	1.503030e-03
<b>GO.1901566.organonitrogen.compound.biosynthetic.process</b>	1.100834e-03
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<b>GO.0001882.toxin.antitoxin.pair.type.II.binding</b>	-3.003590e-07
<b>GO.0016788.oxygen.binding</b>	5.390783e-04
<b>GO.0043021.carbohydrate.transmembrane.transporter.activity</b>	5.093344e-08
<b>GO.1901265.serine.hydrolase.activity</b>	-2.767435e-04
<b>GO.0003676.dynein.light.intermediate.chain.binding</b>	-1.417264e-03
<b>GO.0051536.oxidoreductase.activity..acting.on.NAD.P.H</b>	-2.660612e-03

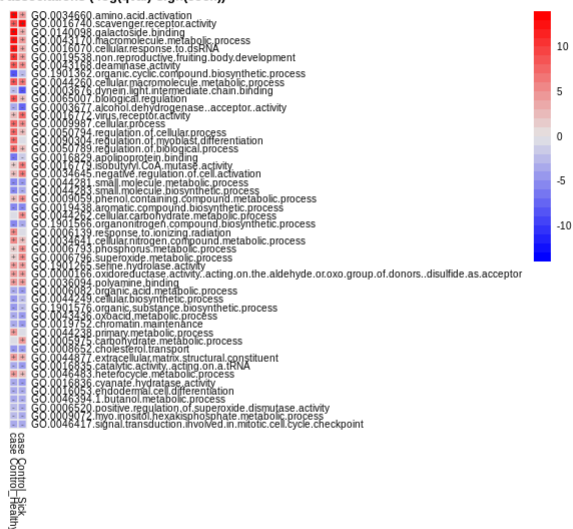
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<b>GO.0043169.DNA.topoisomerase.type.I..single.strand.cut..ATP.independent..activity</b>	2.233725e-03
<b>GO.0004518.oxo.acid.lyase.activity</b>	4.558782e-04
<b>GO.0016779.isobutyryl.CoA.mutase.activity</b>	2.006040e-04
<b>GO.0001883.lipoprotein.particle.binding</b>	-3.579259e-07
<b>GO.0046872.endopeptidase.regulator.activity</b>	2.219931e-03
<b>GO.0003677.alcohol.dehydrogenase..acceptor..activity</b>	-5.606521e-04
<b>GO.0016836.cyanate.hydration.activity</b>	-4.785183e-04
<b>GO.0043022.adenylate.cyclase.activity</b>	2.553842e-09
<b>GO.0016818.nitrite.reductase.activity</b>	-1.012493e-04
<b>GO.0035639.growth.factor.receptor.binding</b>	-8.854684e-05
<b>GO.0051539.tropomyosin.binding</b>	-1.307937e-03
<b>GO.0000166.oxidoreductase.activity..acting.on.the.aldehyde.or.oxo.group.of.donors..disulfide.as.acceptor</b>	-2.767435e-04
<b>GO.0032549.homogentisate.1.2.dioxygenase.activity</b>	-2.981624e-07
<b>GO.0016462.RNA.polymerase.III.general.transcription.initiation.factor.binding</b>	-1.055595e-04
<b>GO.0032550.polyphosphate.AMP.phosphotransferase.activity</b>	-3.557352e-07
<b>GO.0003855.6.7.dihydropteridine.reductase.activity</b>	-5.109609e-04

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<b>GO.0032553.imidazoleglycerol.phosphate.dehydratase.activity</b>	-7.401135e-05
<b>GO.0017076.enoyl.CoA.hydratase.activity</b>	-8.525448e-05
<b>GO.0032555.GDP.D.glucose.phosphorylase.activity</b>	-8.417166e-05
<b>GO.0019001.macrocin.O.methyltransferase.activity</b>	-3.225791e-07
<b>GO.0017111.undecaprenyl.diphosphatase.activity</b>	-1.094893e-04
<b>GO.0032561.abscisic.aldehyde.oxidase.activity</b>	-3.297811e-07
<b>GO.0003924.adenyl.nucleotide.exchange.factor.activity</b>	-3.044794e-07
<b>GO.0005525.ephrin.receptor.activity</b>	-3.547081e-07

atures with significant associations (-log(qval)\*sign(coeff))



OK OK OK OK NEXT I HAVE TO DO THIS ON THE COVID19 CASES ONLY (OR MAYBE ALL THE CASES AND JUST DELINEATE COVID19 BY OUTCOME) AND DO IT BY OUTCOME

In [ ]:

In [ ]: