Clustering of modENCODE/Reinke ChIP-seq peaks

DC King - Onish lab

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Script version and versions

This repo is from 'bash `git remote -v`\`\`. Using R version 4.0.0 (2020-04-24)'.

Process data

The source data is a BED file corresponding to the basewise UNION of LE, L1, and L3 IDR peak files, run through an aggregate function (mod'd javaGenomicToolkit) that calculates summary information for each of the above ranges.

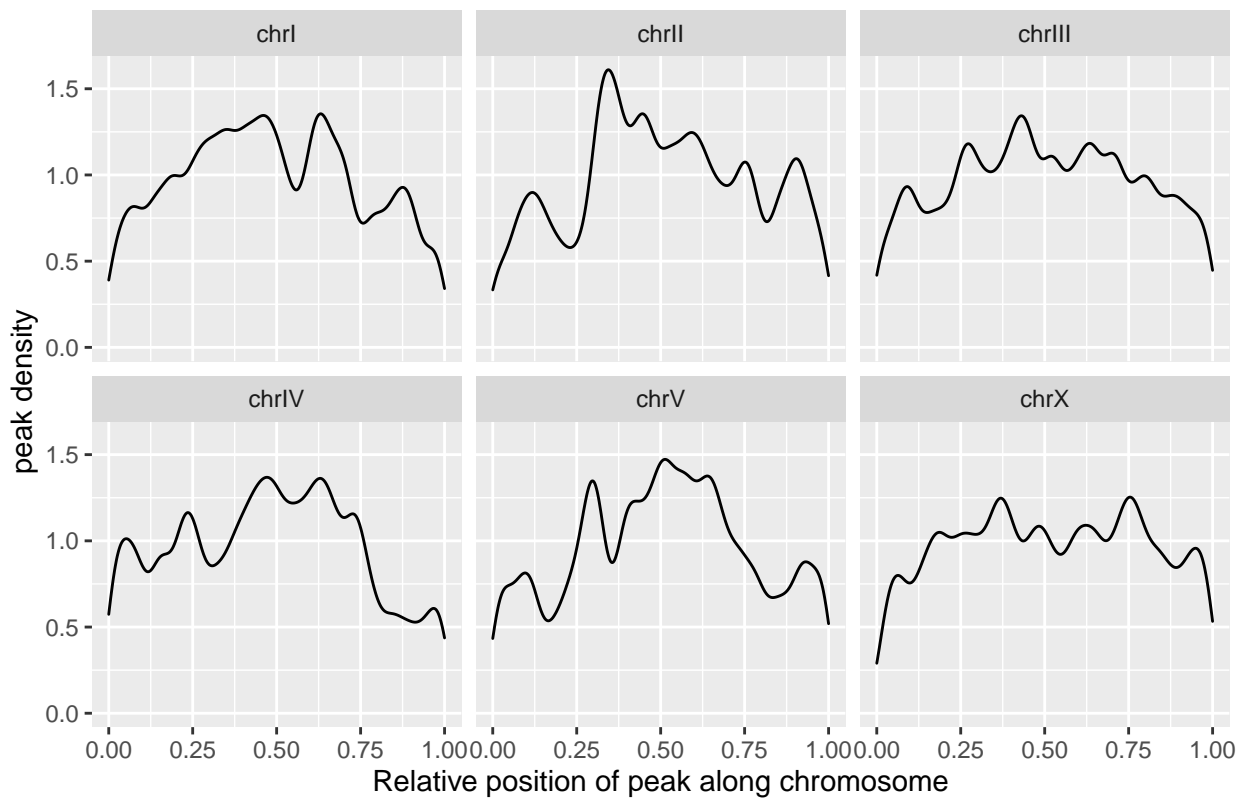The original IDR peaks are rescanned to determine the composition of each peak.

```
## [1] 11015
```
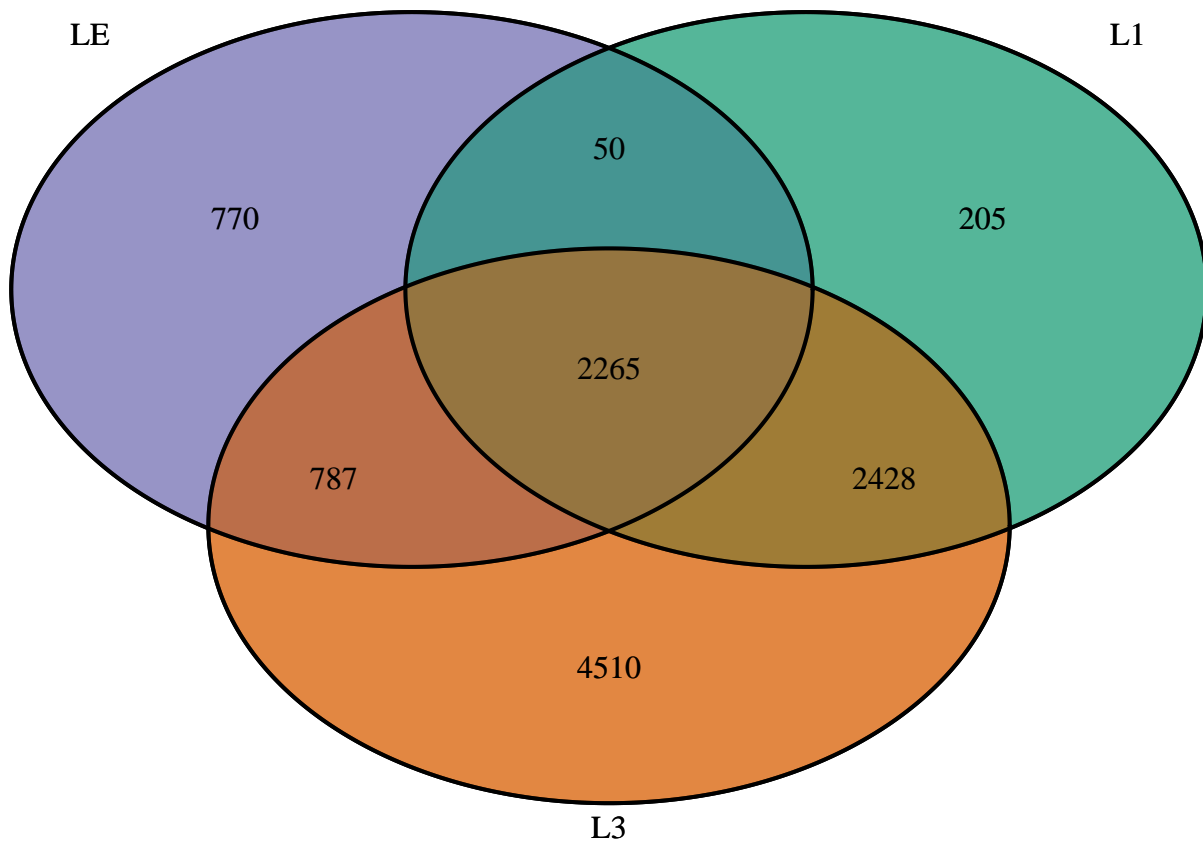
Genomic properties of peaks
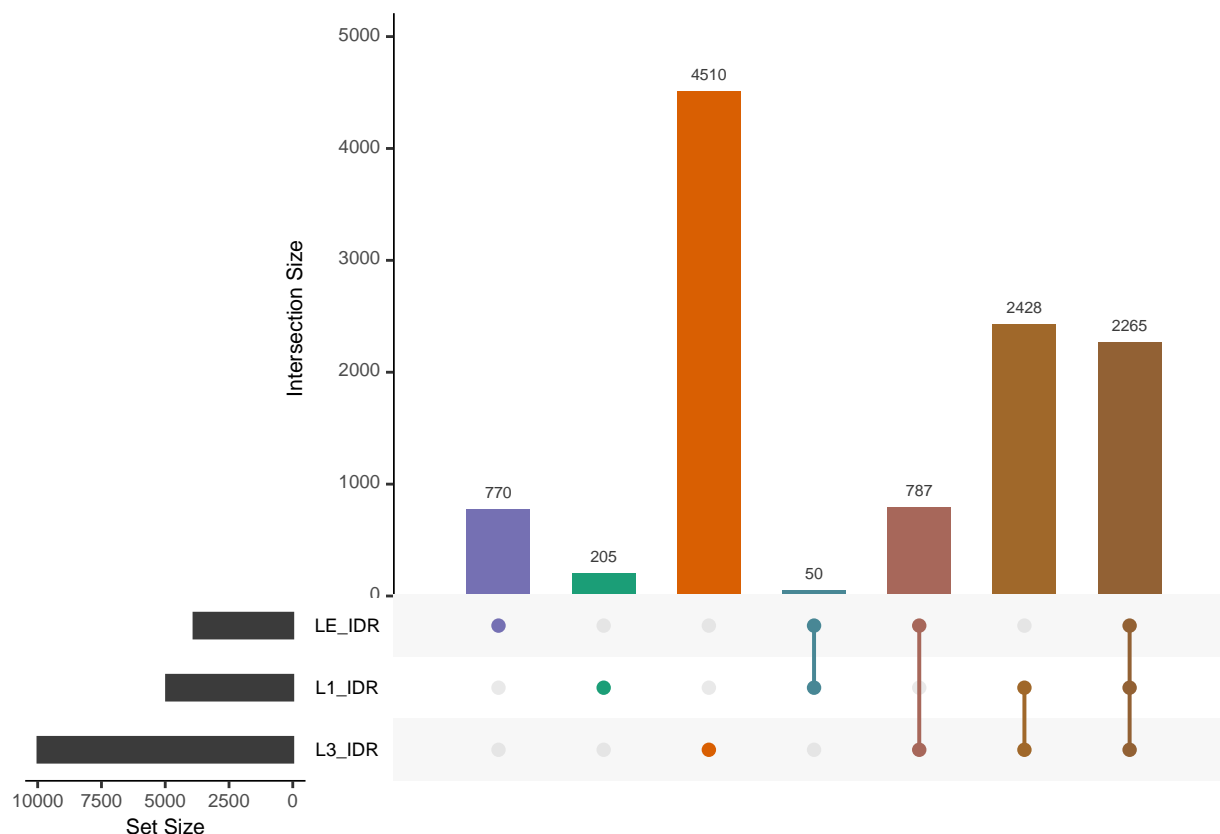
Number of peaks versus chromosome length
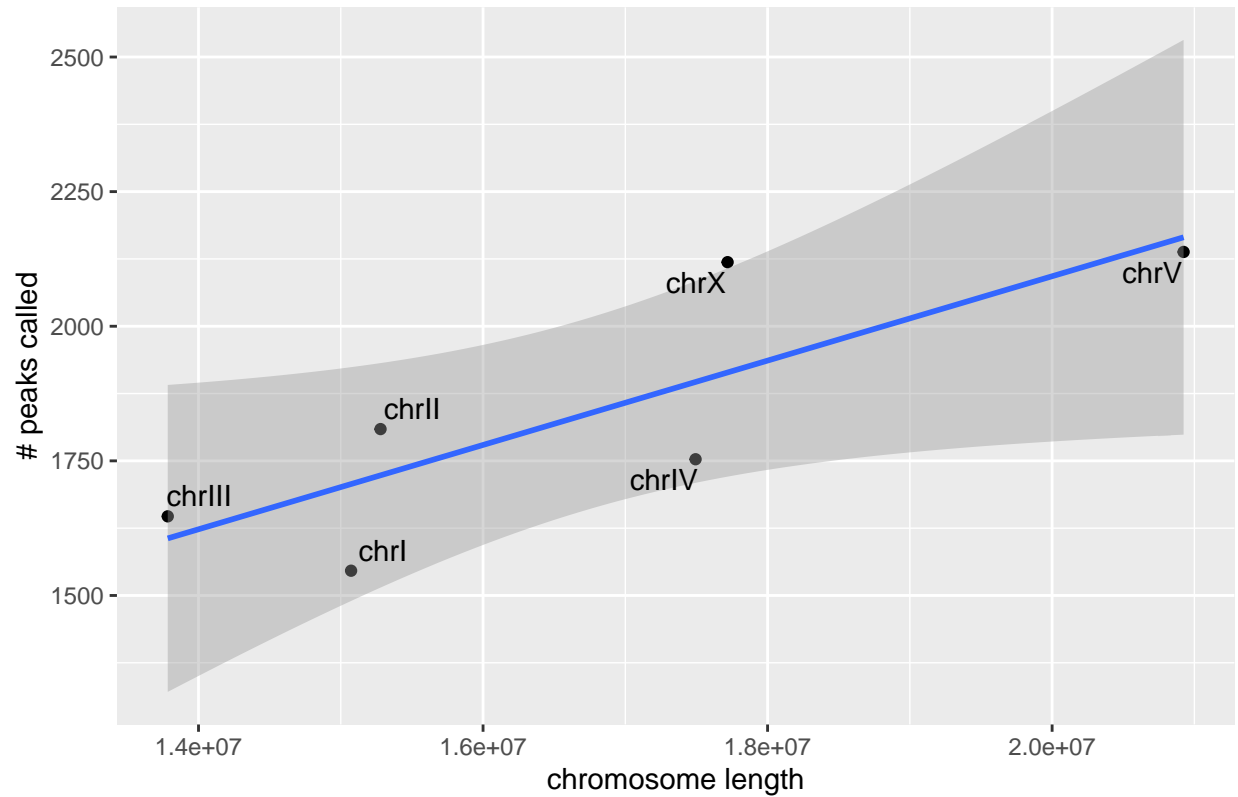
Peaks favor chromosome centers

Peaks are equally distributed across the nuclear chromosomes, accounting for the chromosome size in bases.
Peaks favor the centers of chromosomes.

LE

L1

50

770

205

2265

787

2428

4510

L3

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

The overlap between the different IDR-vetted peaks is not uniform. Individually, the number of peaks called at each stage increases through developmental time, ranging from 3,889, 5,063, and 10,342 for late embryo, L1, and L3, respectively. The total number of merged peaks is 11,015. 4,510 are stage-specific; 1,624 are called in at least two stages. A large class is present in all three stages, 2,265, representing 21% of total.

current wording in text

The overlap between the different IDR-vetted peaks at different stages is not uniform. Individually, the number of peaks called at each stage increases through developmental time, ranging from 3,889, to 5,063, to 10,342 for LE, L1, and L3, respectively. The total number of merged peaks is 11,015. The largest individual class is the set of 4,510 peaks called in L3 without LE or L1 counterparts by overlapping position. A large class is present in all three stages, 2,265, representing 21% of total.

Post-scaling of data

Now the quantitative data represents 3 timepoints, 2 replicates each. Each value is the input and read-depth normalized pileups (signal) computed per basepair. The maximum value within a peak is the value used. There are 11,015 peaks, (and therefore rows).

Next we want to filter the lesser 5% invariant rows, and then normalize the values by row.

K-means clustering

Perform K-means on the peaks that vary throughout the timecourse.

```
## Warning: Quick-TRANSfer stage steps exceeded maximum (= 523200)
```

```
## Warning: Quick-TRANSfer stage steps exceeded maximum (= 523200)
```

Skree plot for cluster number

total within groups sum−of−squares

number of clusters
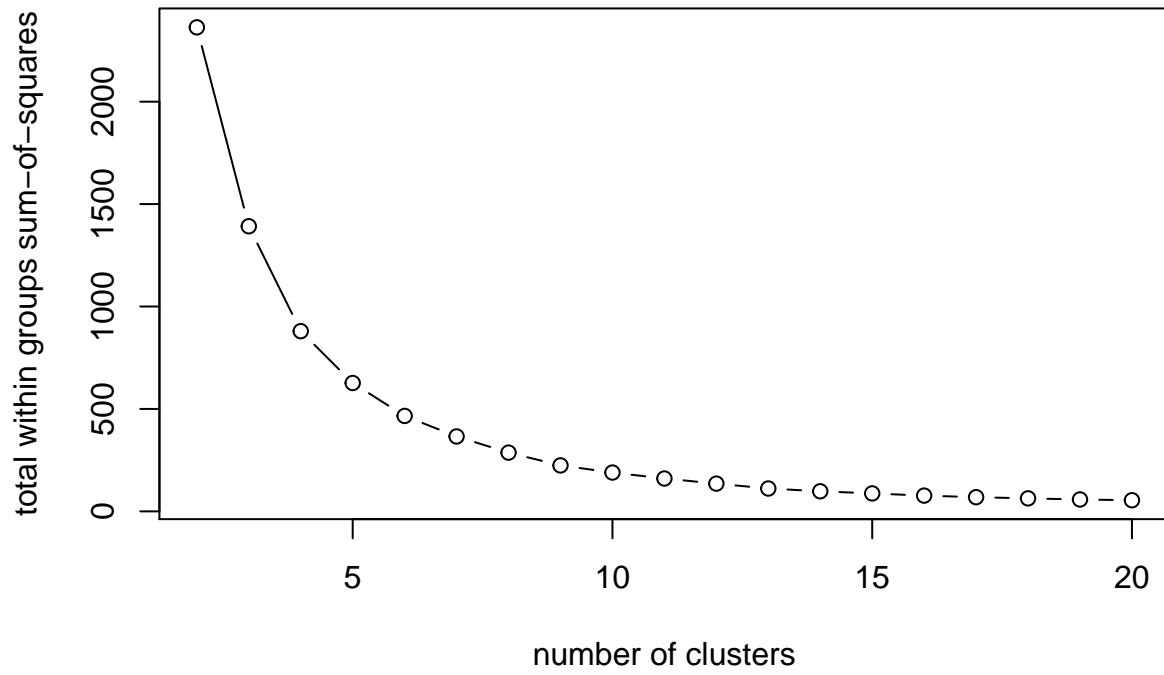
ieans clusters at std. dev. > 0.383, (excludes lower 5.0%)

Kmeans cluster centers (k=4)

78.0% variance explained

Kmeans cluster centers (k=4)
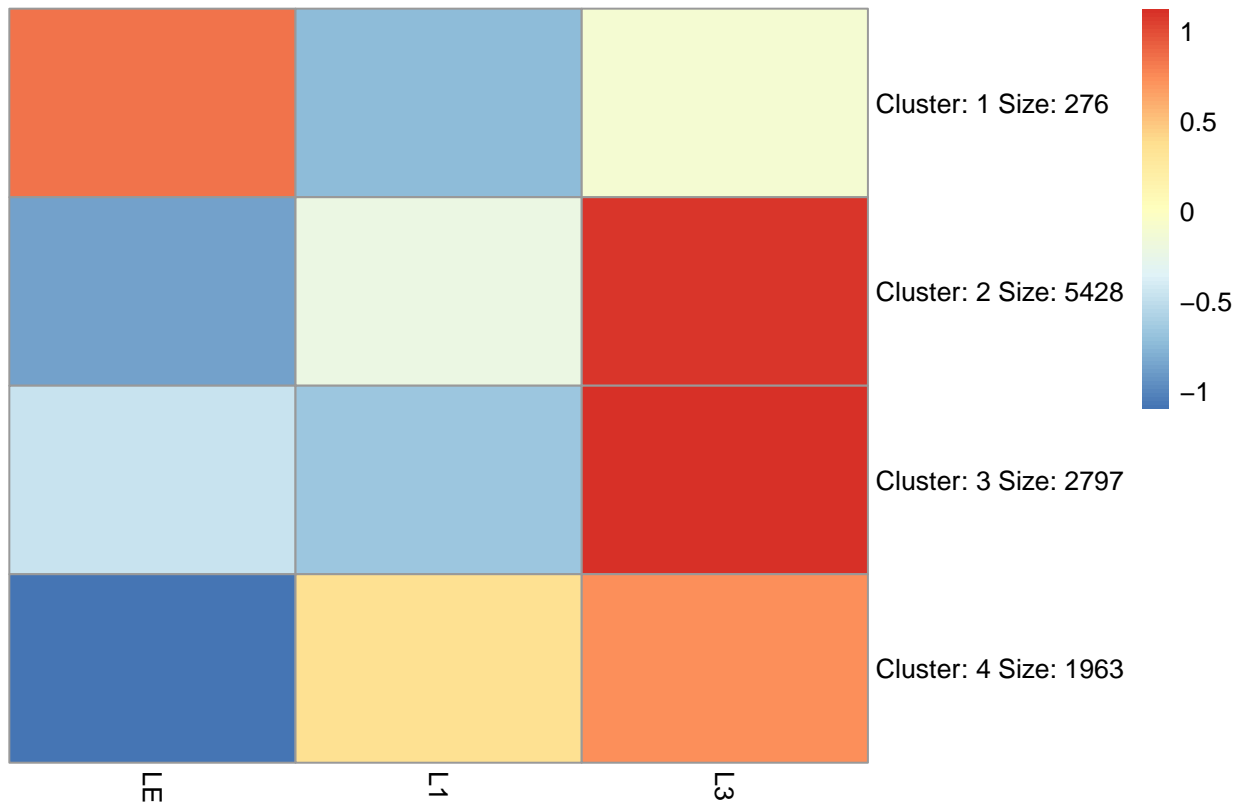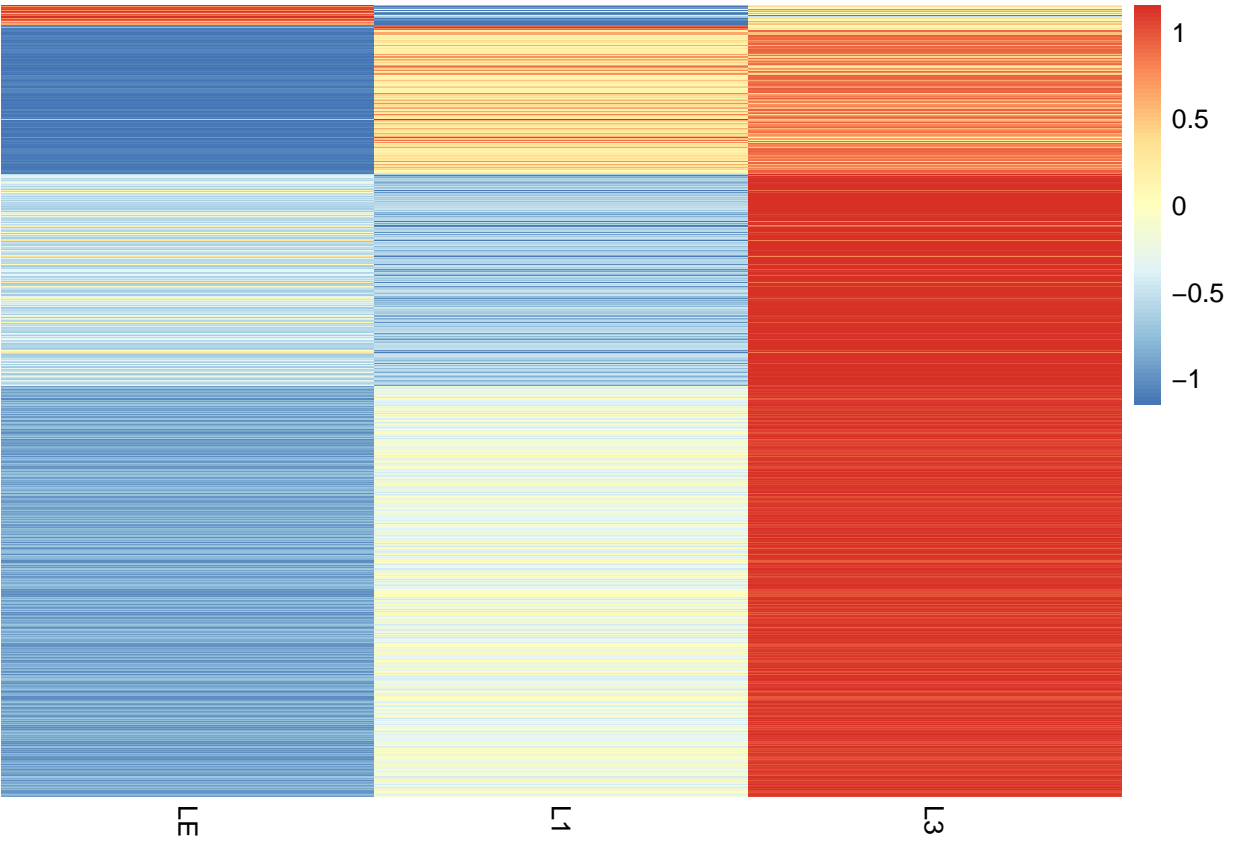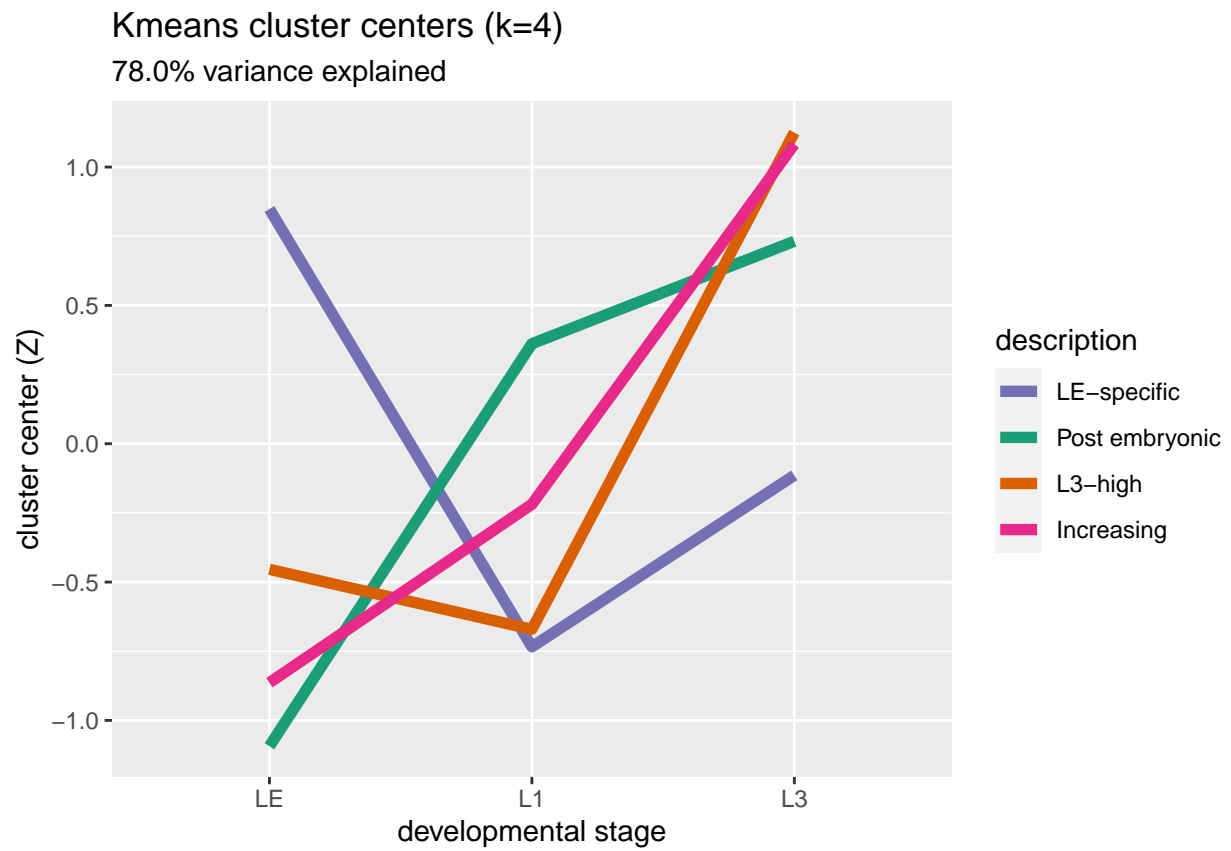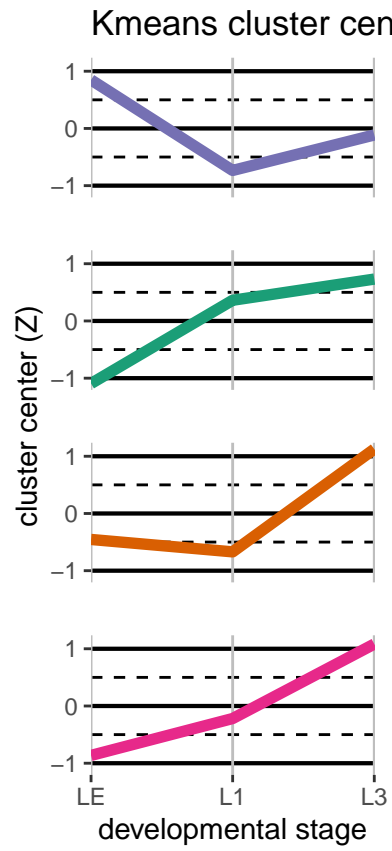

```
## Using label as id variables
```

Kmeans cluster centers (k=6)

88.3% variance explained

cluster Id (size)

1 (170)
2 (455)
3 (720)
4 (2437)
5 (2624)
6 (4058)
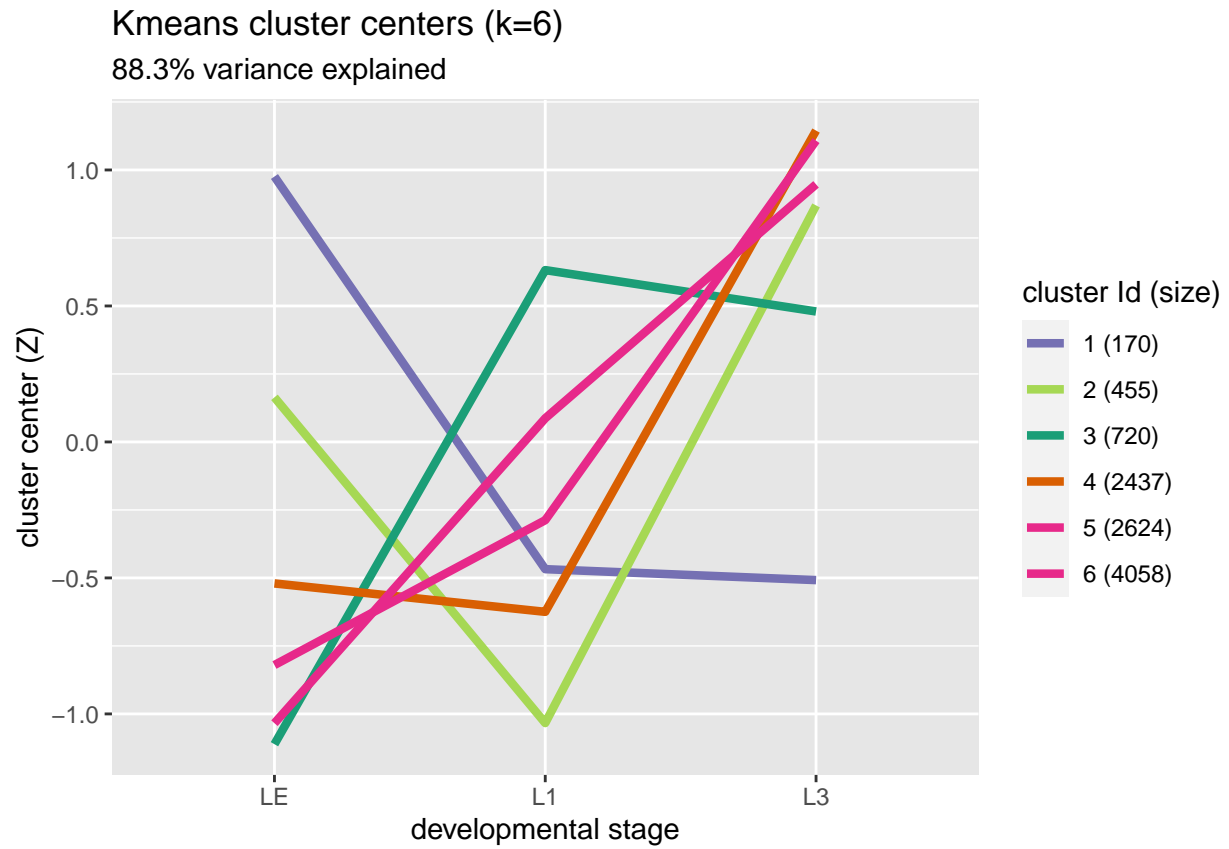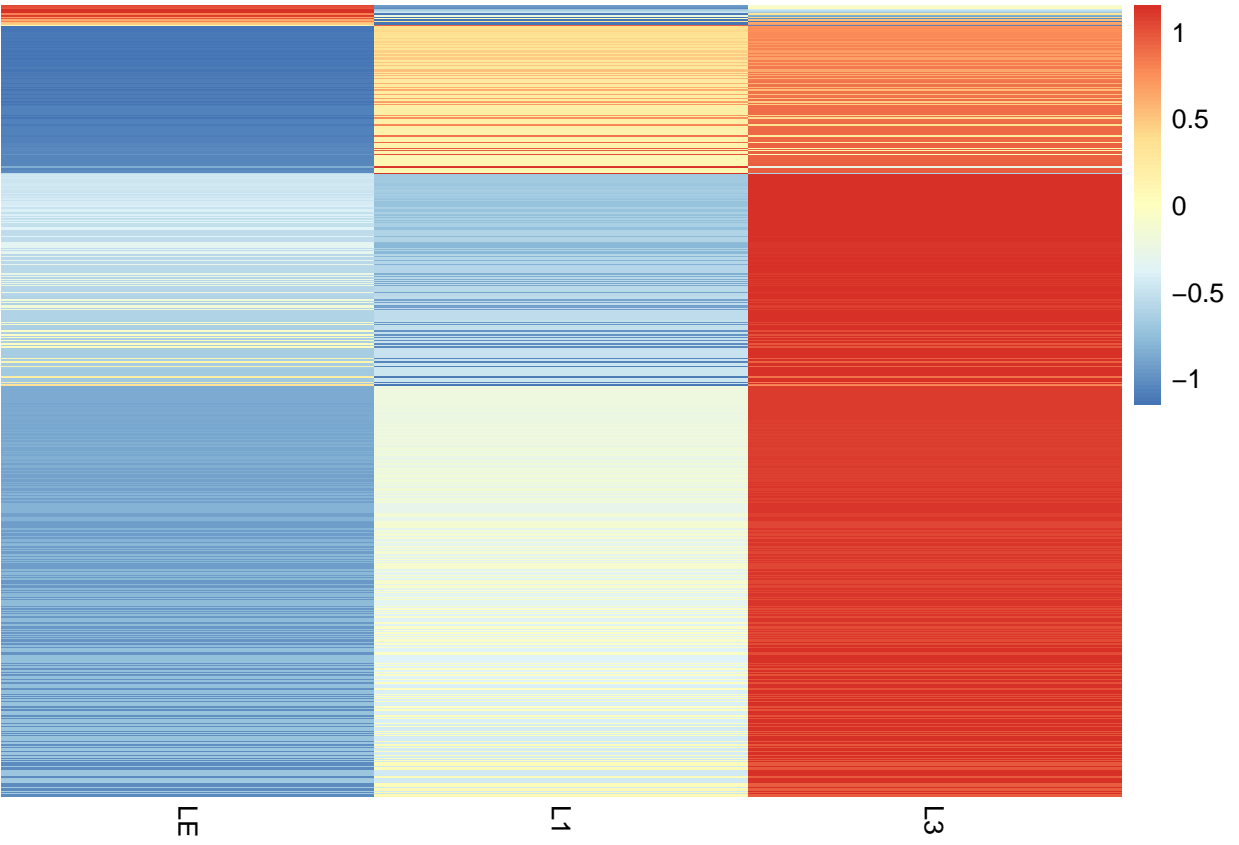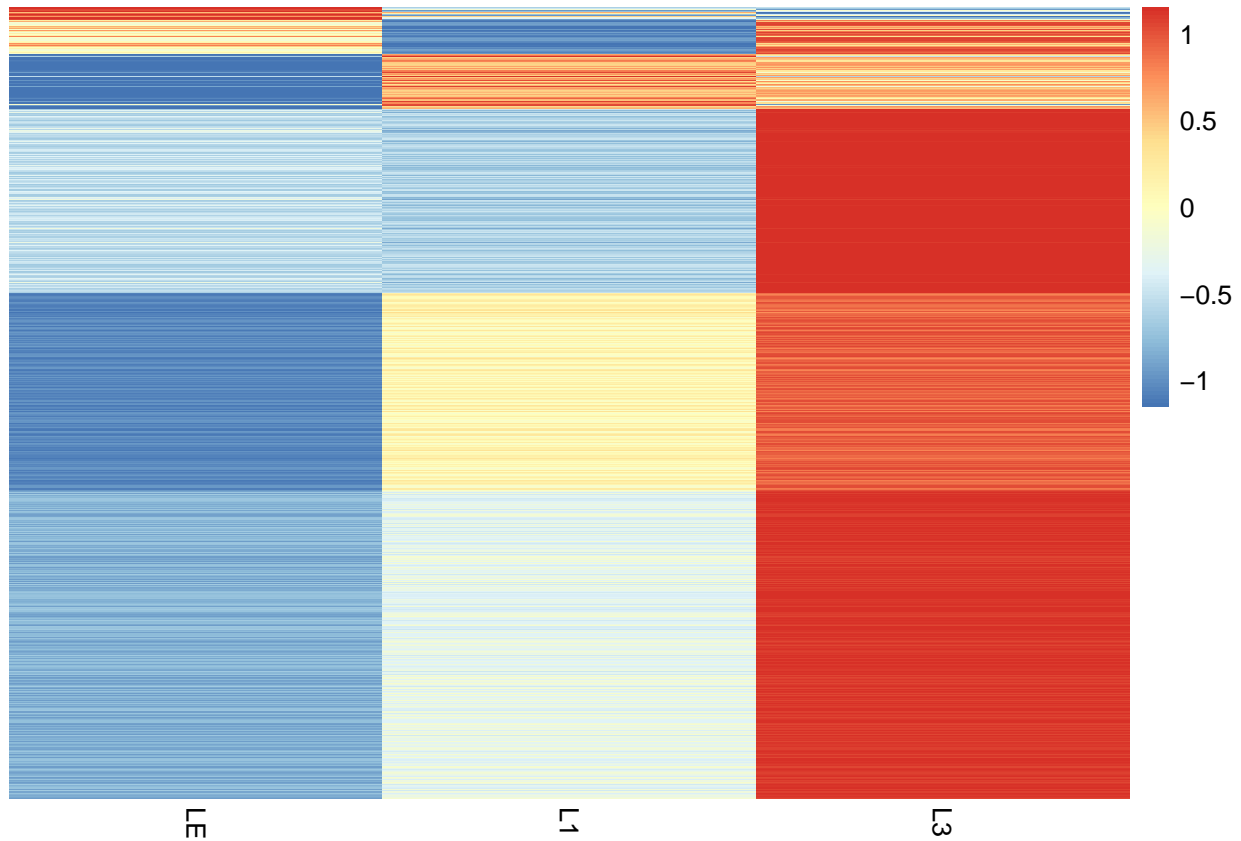
Prepare data structures to output bigBed files.

Custom tracks are served locally (but world-readable). The chunk currently also maps peaks to genes through the "scripts/getCodingGenes.R".

```
## Warning in annotatePeakInBatch(peaks, AnnotationData = all_CDS_genes, bindingRegions = c(-within_gene
##                   in the AnnotationData.

## Warning in FUN(extractROWS(unlisted_X, IRanges(X_elt_start[i], X_elt_end[i])), : not all the seqname
##                   in the AnnotationData.

## Warning in FUN(extractROWS(unlisted_X, IRanges(X_elt_start[i], X_elt_end[i])), : not all the seqname
##                   in the AnnotationData.

## Warning in FUN(extractROWS(unlisted_X, IRanges(X_elt_start[i], X_elt_end[i])), : not all the seqname
##                   in the AnnotationData.

## Warning in annotatePeakInBatch(no_overlap_peaks, AnnotationData = all_CDS_genes, : not all the seqnar
##                   in the AnnotationData.

## Warning in annotatePeakInBatch(no_overlap_peaks, AnnotationData = all_CDS_genes, : not all the seqnar
##                   in the AnnotationData.

## Warning in annotatePeakInBatch(no_overlap_peaks, AnnotationData = all_CDS_genes, : not all the seqnar
##                   in the AnnotationData.

## Warning in annotatePeakInBatch(no_overlap_peaks, AnnotationData = all_CDS_genes, : not all the seqnar
##                   in the AnnotationData.
```

```
##    user  system elapsed
##   3.910   0.095   4.018
```

Gene features at or near ELT–2 occupied peaks
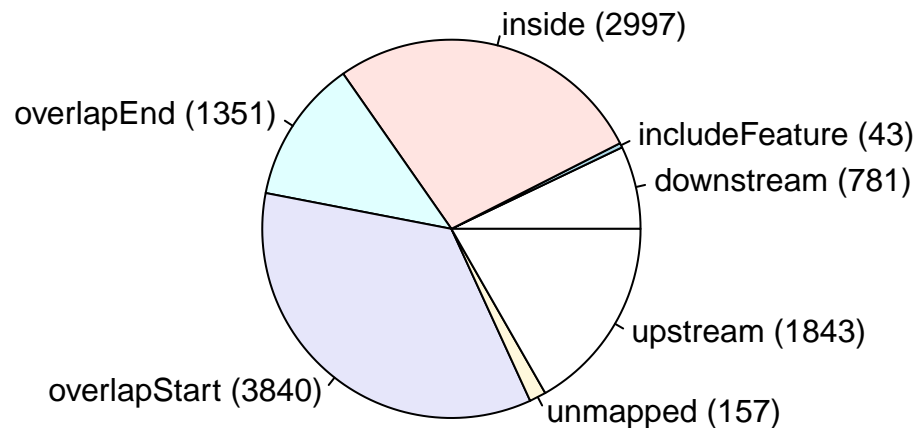
The closest feature to a peak is mapped unless farther than 5KB.
Feature" means the peak completely encompasses the gene (might be a consequence o

A BASH chunk, bedToBigBed

Run UCSC-user apps tools.

```
## pass1 - making usageList (6 chroms): 2 millis
## pass2 - checking and writing primary data (11012 records, 12 fields): 30 millis
## Sorting and writing extra index 0: 2 millis
```

Plot gene mapping stats.

Pie chart for the relative locations and counts of how the peaks mapped to genes.

```
## The following objects are masked from annotatedPeaks (pos = 3):
##
##     all_CDS_genes, ap, stacked_nr

## pdf
##   2

## [1] 525
## [1] 264
## [1] 1688
## [1] 2462
## [1] 3919
```

Peaks mapping nearest to a gene

inside (3040)

upstream (5683)

downstream (2132)

unmapped (157)
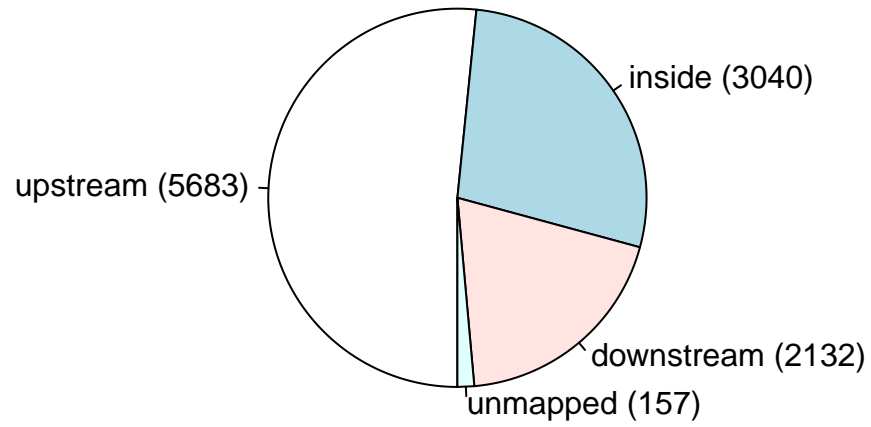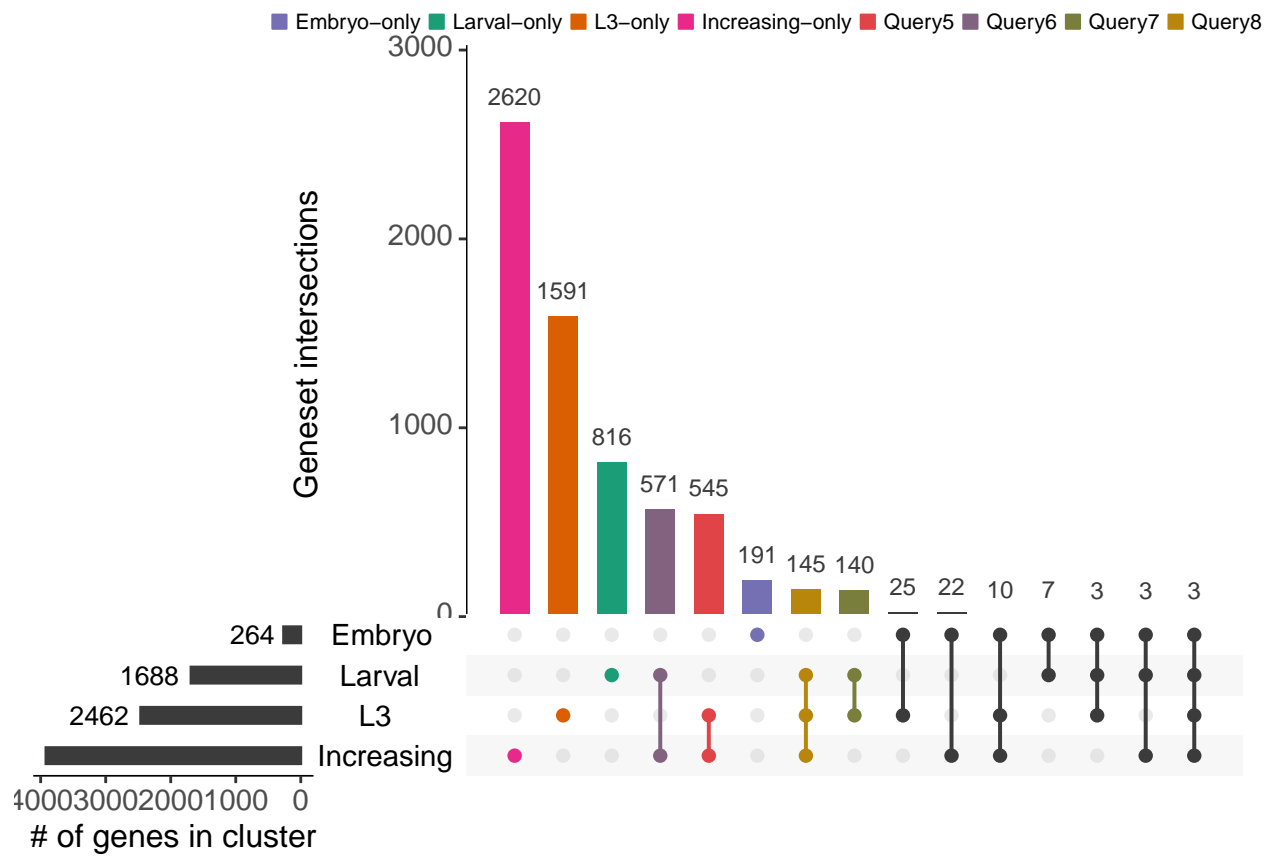
[1] 2329

Genes tend to have a single peak mapped to them
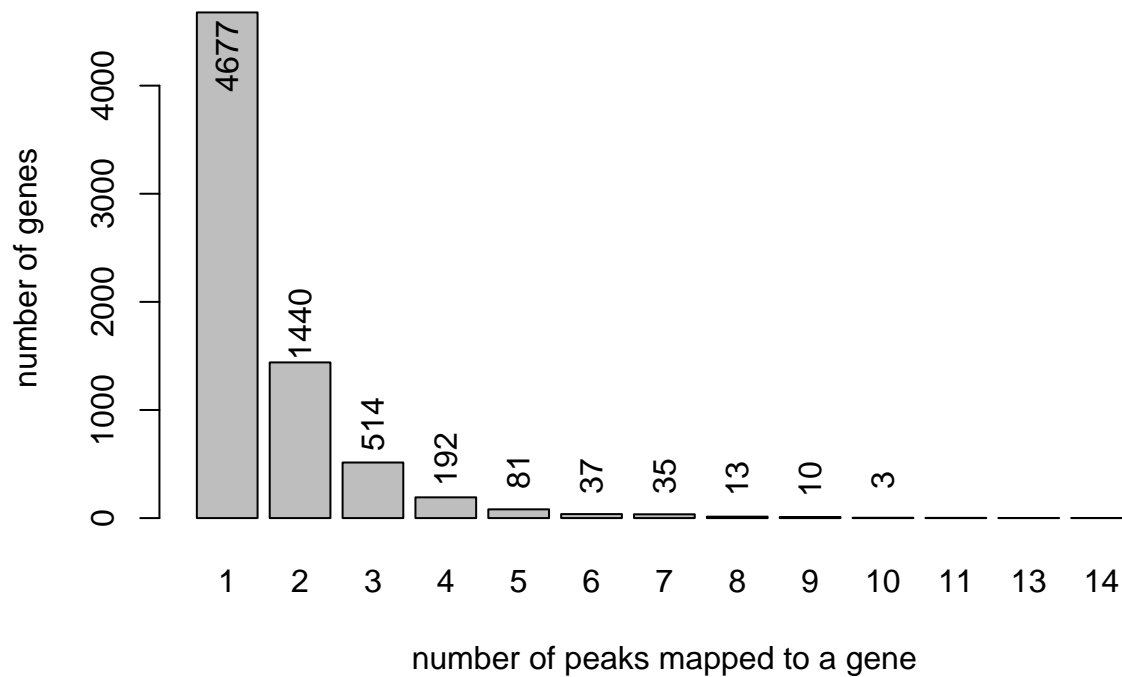

```
annotatedPeaks$ap$k4labels[annotatedPeaks$ap$k4labels == "Post-embryonic"] <- "Larval"
annotatedPeaks$ap$k4labels = factor(annotatedPeaks$ap$k4labels, levels=c("LE-specific","Larval","L3-high
lapply(split(annotatedPeaks$ap$feature, annotatedPeaks$ap$k4labels),unique) -> ap.split
lapply(ap.split, length)
```

```
## $`LE-specific`
## [1] 264
##
## $Larval
## [1] 1688
##
## $`L3-high`
## [1] 2462
##
## $Increasing
## [1] 3919
##
## $`Not-changing or not IDR-passing`
## [1] 525
```

```
sum(unlist(.Last.value))
```

```
## [1] 0
```

```
gene.df <- lapply( ap.split, function(WBGeneID){ bitr(WBGeneID,
    fromType = "WORMBASE",
    toType = "ENTREZID",
    OrgDb = org.Ce.eg.db)})
```

```
## 'select()' returned 1:many mapping between keys and columns
## 'select()' returned 1:many mapping between keys and columns
## 'select()' returned 1:many mapping between keys and columns

## Warning in bitr(WBGeneID, fromType = "WORMBASE", toType = "ENTREZID", OrgDb =
## org.Ce.eg.db): 0.16% of input gene IDs are fail to map...

## 'select()' returned 1:many mapping between keys and columns

## Warning in bitr(WBGeneID, fromType = "WORMBASE", toType = "ENTREZID", OrgDb =
## org.Ce.eg.db): 0.05% of input gene IDs are fail to map...

## 'select()' returned 1:many mapping between keys and columns
```

```r
lapply(gene.df,nrow)
```

```
## $`LE-specific`
## [1] 269
##
## $Larval
## [1] 1707
##
## $`L3-high`
## [1] 2504
##
## $Increasing
## [1] 3952
##
## $`Not-changing or not IDR-passing`
## [1] 529
```

```r
sum(unlist(.Last.value))
```

```
## [1] 0
```

```r
gene.df$`Not-changing or not IDR-passing` = NULL
system.time(
{compareCluster(lapply(gene.df, function(x) x$ENTREZID),
                fun = "enrichGO",
                pvalueCutoff = 0.05,
                keyType = "ENTREZID",
                ont="MF",
                OrgDb = org.Ce.eg.db,
                pAdjustMethod = "BH",
                minGSSize = 5,
                maxGSSize = 150,
                readable=TRUE) -> compClust.MF})
```

```
##    user  system elapsed
##   9.104   1.101  10.462
```

```r
# MF:
#   user  system elapsed
# 16.542   2.653 128.106
system.time(
{compareCluster(lapply(gene.df, function(x) x$ENTREZID),
                fun = "enrichGO",
```

```
                  pvalueCutoff = 0.05,
                  keyType = "ENTREZID",
                  ont="BP",
                  OrgDb = org.Ce.eg.db,
                  pAdjustMethod = "BH",
                  minGSSize = 5,
                  maxGSSize = 150,
                  readable=TRUE) -> compClust.BP})
```

```
##     user  system elapsed
##   20.047   2.837  23.019
```

```r
# BP:
#   user  system elapsed
# 30.142   5.171 149.272
# 33.919   6.138 236.847  (had readable=T)
# 26.847   4.398  39.339  (had readable=T)
# 27.766   4.445  40.864  (had readable=T)
# 32.690   5.623 107.306
system.time(
{compareCluster(lapply(gene.df, function(x) x$ENTREZID),
                fun = "enrichGO",
                pvalueCutoff = 0.05,
                keyType = "ENTREZID",
                ont="CC",
                OrgDb = org.Ce.eg.db,
                pAdjustMethod = "BH",
                minGSSize = 5,
                maxGSSize = 150,
                readable=TRUE) -> compClust.CC})
```

```
##     user  system elapsed
##    7.617   0.736   8.416
```

```r
compClust.simp = simplify(compClust.MF,cutoff=.25)
dotplot(compClust.simp, showCategory=10, includeAll=T,by="count") + theme(axis.text.x = element_text(an
```

Molecular Function (GO)
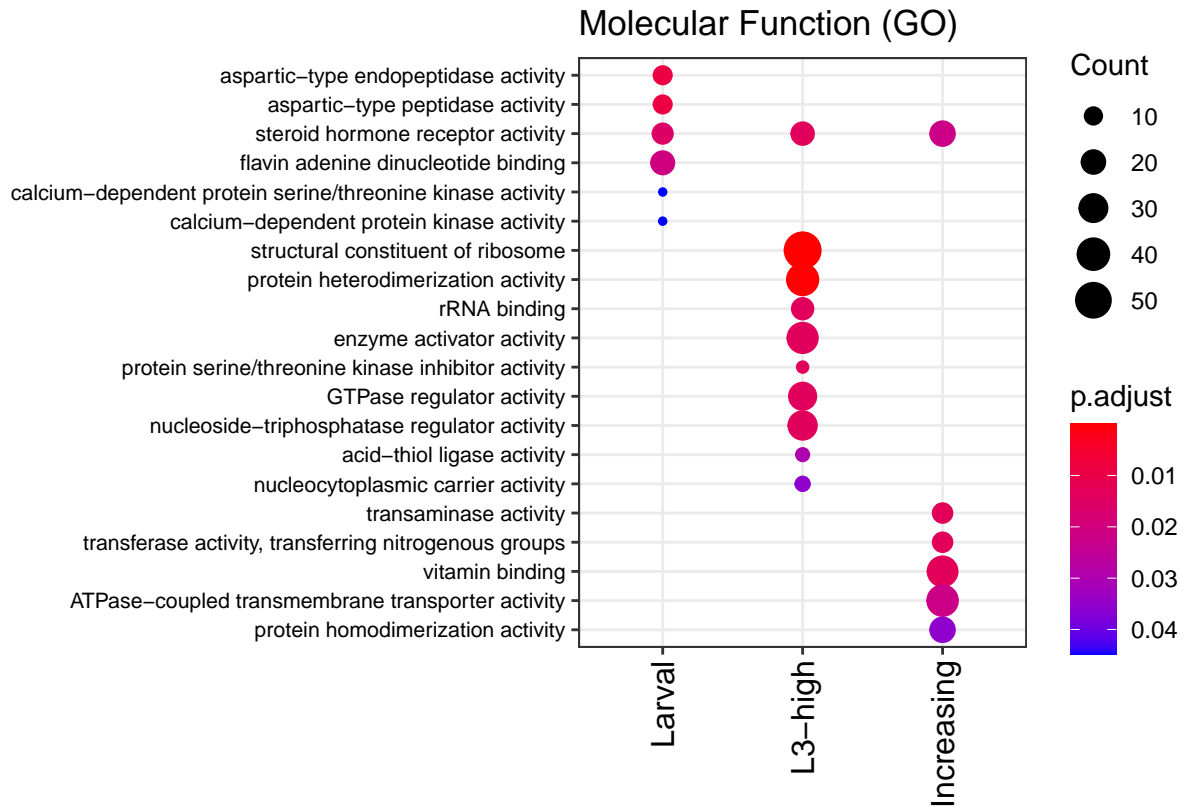

```
compClust.simp = simplify(compClust.BP,cutoff=.3)
dotplot(compClust.simp, showCategory=10, includeAll=T,by="count") + theme(axis.text.x = element_text(ang
```

Biological Process (GO)
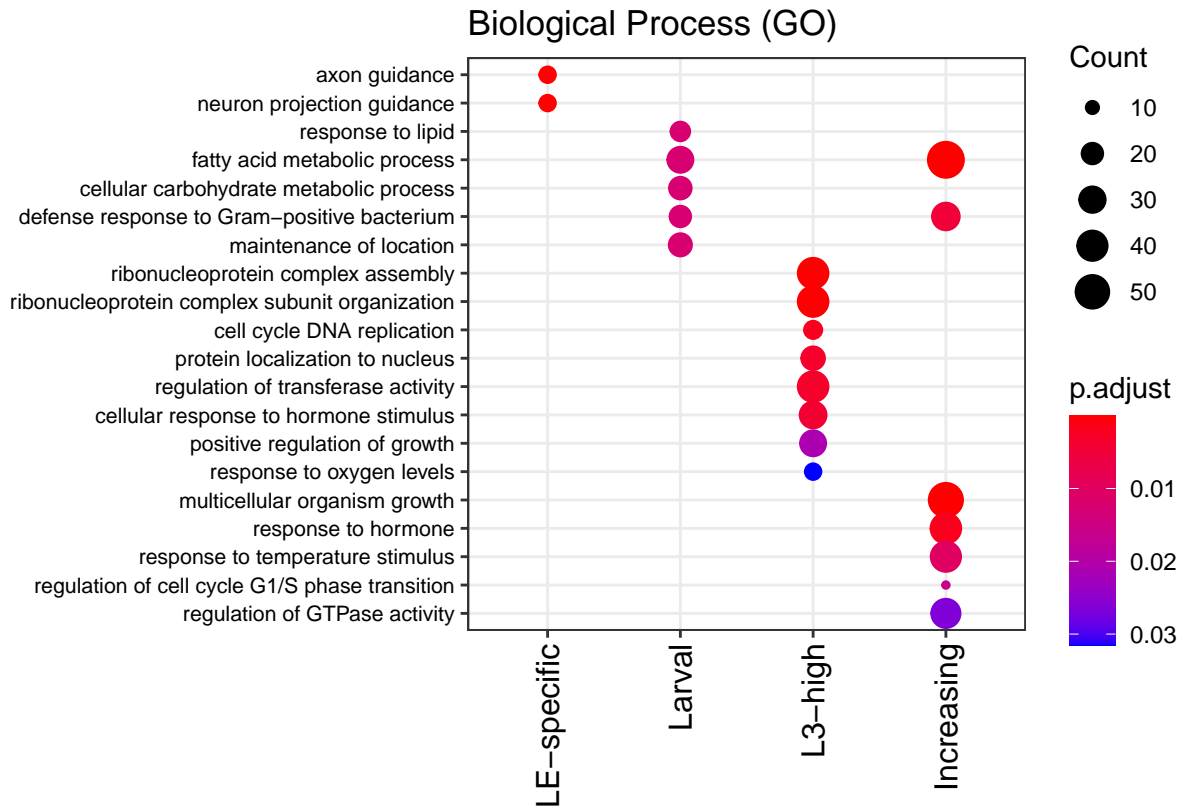
```
compClust.simp = simplify(compClust.CC,cutoff=.7)
dotplot(compClust.simp, showCategory=10, includeAll=T,by="count") + theme(axis.text.x = element_text(an
```

Cellular Component (GO)

```
dotplot(compClust.simp, showCategory=10, includeAll=T,by="count") + theme(axis.text.x = element_text(ang
```

GO (BP)
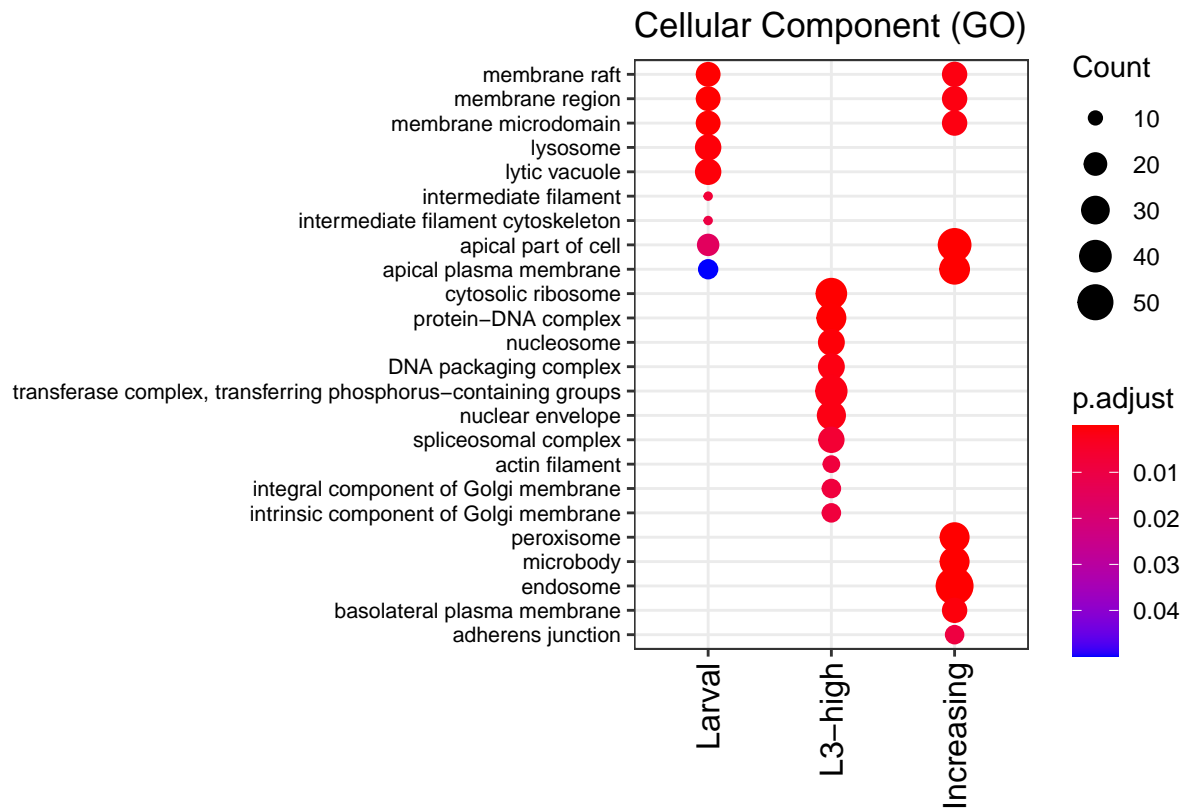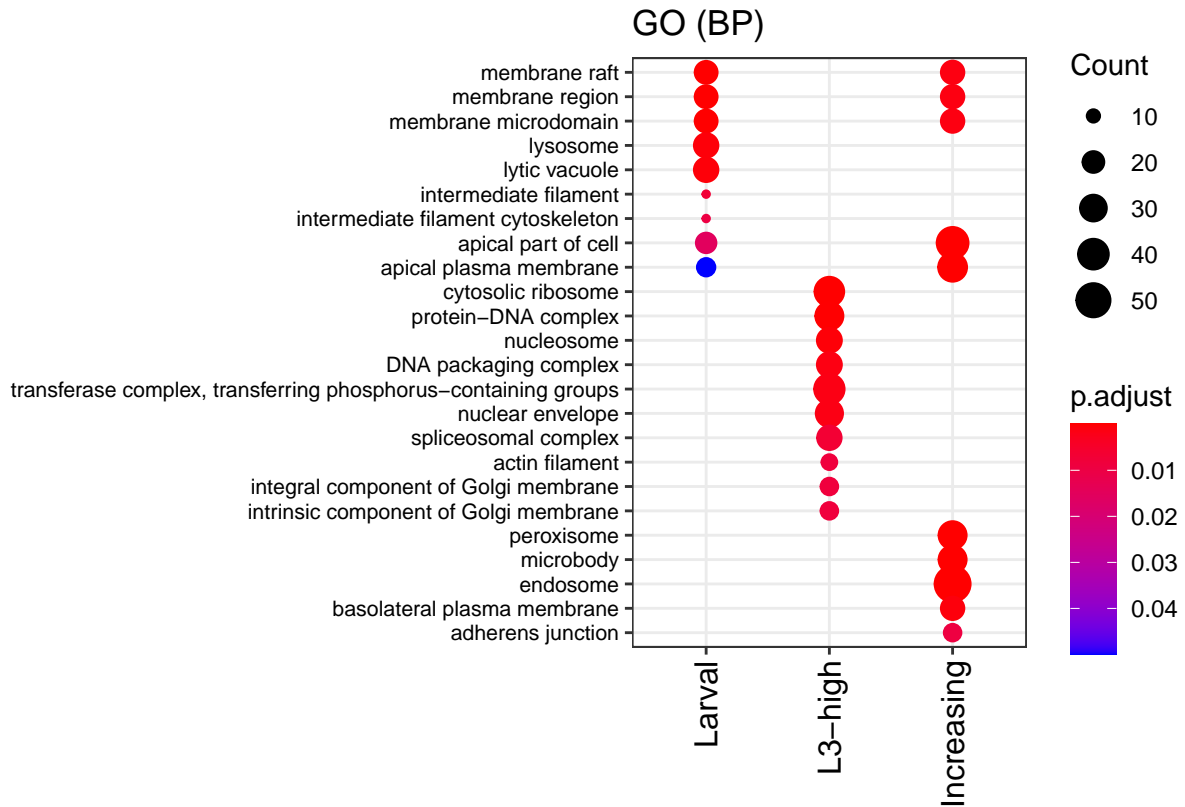
```
c_eK<- compareCluster(geneClusters = lapply(gene.df, function(x) x$ENTREZID),
                      fun="enrichKEGG",
                      organism = "cel",
                      pvalueCutoff = 0.05,
                      keyType = "ncbi-geneid",
                      pAdjustMethod = "BH",
                      minGSSize = 5,
                      maxGSSize = 150)
dotplot(c_eK) + ggtitle("KEGG pathways")
```

KEGG pathways
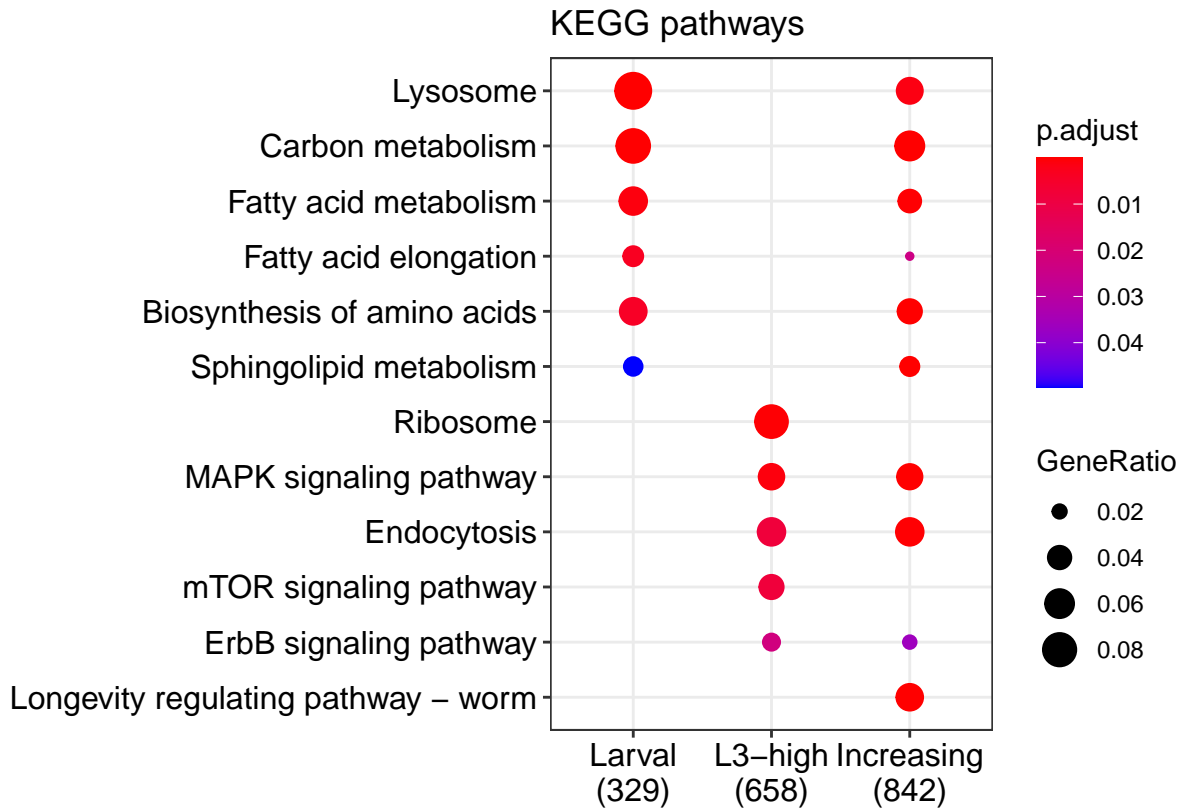
```
gene.df.ENTREZID = lapply(gene.df, function(x) x$ENTREZID)

kegg.readable = lapply(gene.df.ENTREZID, function(clust.entrez.ids) {
  as.data.frame(setReadable(
    enrichKEGG(clust.entrez.ids,
               organism = 'cel',
               keyType = 'ncbi-geneid'),
    OrgDb = org.Ce.eg.db,
    keyType = "ENTREZID"
  ))
})
# switch to kables
#View(kegg.readable$`LE-specific`) # empty
#View(kegg.readable$`Larval`)
#View(kegg.readable$`L3-high`)
#View(kegg.readable$Increasing)
```

GO data and processing functions

Data is from paramart, the functions are necessary to make the topGO analysis easier to repeat across the clusters.

```
##    user  system elapsed
##   1.206   0.025   4.274

##    user  system elapsed
##   0.417   0.010   0.439
```

Perform GO-term enrichment analyses

Run the topGO analyses using the above functions.

```
chip_v_genome_wide=mkGO(unique.ap.wbid, all.genes)
```

```
##
## Building most specific GOs .....
##  ( 3774 GO terms found. )
##
## Build GO DAG topology ..........
##  ( 6446 GO terms and 14504 relations. )
##
## Annotating nodes ...............
##  ( 9515 genes annotated to the GO terms. )
##
## Building most specific GOs .....
##  ( 2144 GO terms found. )
##
## Build GO DAG topology ..........
##  ( 2640 GO terms and 3441 relations. )
##
## Annotating nodes ...............
##  ( 10468 genes annotated to the GO terms. )
##
## Building most specific GOs .....
##  ( 955 GO terms found. )
##
## Build GO DAG topology ..........
##  ( 1195 GO terms and 2107 relations. )
##
## Annotating nodes ...............
##  ( 12007 genes annotated to the GO terms. )
```

```
gBP = GOSummary(chip_v_genome_wide$BP,1000)
```

```
##
##              -- Classic Algorithm --
##
##          the algorithm is scoring 5581 nontrivial nodes
##          parameters:
##              test statistic: fisher
##
##
##              -- Weight01 Algorithm --
##
##          the algorithm is scoring 5581 nontrivial nodes
##          parameters:
```

```
##              test statistic: fisher

##
##    Level 18:  1 nodes to be scored     (0 eliminated genes)

##
##    Level 17:  10 nodes to be scored    (0 eliminated genes)

##
##    Level 16:  27 nodes to be scored    (3 eliminated genes)

##
##    Level 15:  50 nodes to be scored    (38 eliminated genes)

##
##    Level 14:  102 nodes to be scored   (93 eliminated genes)

##
##    Level 13:  179 nodes to be scored   (254 eliminated genes)

##
##    Level 12:  352 nodes to be scored   (544 eliminated genes)

##
##    Level 11:  507 nodes to be scored   (1230 eliminated genes)

##
##    Level 10:  714 nodes to be scored   (2161 eliminated genes)

##
##    Level 9:   800 nodes to be scored   (3318 eliminated genes)

##
##    Level 8:   790 nodes to be scored   (4625 eliminated genes)

##
##    Level 7:   756 nodes to be scored   (5748 eliminated genes)

##
##    Level 6:   595 nodes to be scored   (6887 eliminated genes)

##
##    Level 5:   385 nodes to be scored   (7693 eliminated genes)

##
##    Level 4:   199 nodes to be scored   (8735 eliminated genes)

##
##    Level 3:   93 nodes to be scored    (9103 eliminated genes)

##
##    Level 2:   20 nodes to be scored    (9241 eliminated genes)

##
##    Level 1:   1 nodes to be scored     (9479 eliminated genes)
```

```r
goID="GO:0050769"
neurogo=c('GO:0007218','GO:0033563','GO:0048665','GO:0097376','GO:0050769','GO:0007416','GO:0050769','GO
gene.universe = genes(chip_v_genome_wide$BP)
go.genes <- genesInTerm(chip_v_genome_wide$BP, goID)[[1]]
sig.genes <- sigGenes(chip_v_genome_wide$BP)
my.group <- new("classicCount", testStatistic = GOFisherTest, name = "fisher",
                allMembers = gene.universe, groupMembers = go.genes,
```

```
                sigMembers = sig.genes)
contTable(my.group)
```

```
##          sig notSig
## anno      43     18
## notAnno 4206   5248
```

```
runTest(my.group)
```

```
## [1] 3.81941e-05
```

```
dataset=mkGO(unique.clust_1_wbid,unique.ap.wbid)
```

```
##
## Building most specific GOs .....
```

```
##   ( 3042 GO terms found. )
```

```
##
## Build GO DAG topology ..........
```

```
##   ( 5581 GO terms and 12485 relations. )
```

```
##
## Annotating nodes ..............
```

```
##   ( 4249 genes annotated to the GO terms. )
```

```
##
## Building most specific GOs .....
```

```
##   ( 1695 GO terms found. )
```

```
##
## Build GO DAG topology ..........
```

```
##   ( 2190 GO terms and 2875 relations. )
```

```
##
## Annotating nodes ..............
```

```
##   ( 4542 genes annotated to the GO terms. )
```

```
##
## Building most specific GOs .....
```

```
##   ( 780 GO terms found. )
```

```
##
## Build GO DAG topology ..........
```

```
##   ( 1024 GO terms and 1813 relations. )
```

```
##
## Annotating nodes ..............
```

```
##   ( 4616 genes annotated to the GO terms. )
```

```
neurogo=c('GO:0007218','GO:0033563','GO:0048665','GO:0097376','GO:0050769','GO:0007416','GO:0050769','GO
neuroterms=genesInTerm(dataset$BP, neurogo)
neurogenes=c()
# neuropeptide signaling pathway
neuroterms$`GO:0007218`[neuroterms$`GO:0007218` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# dorsal/ventral axon guidance
```

```r
neuroterms$`GO:0033563`[neuroterms$`GO:0033563` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# neuron fate specification
neuroterms$`GO:0048665`[neuroterms$`GO:0048665` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# interneuron axon guidance
neuroterms$`GO:0097376`[neuroterms$`GO:0097376` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# synapse assembly
neuroterms$`GO:0007416`[neuroterms$`GO:0007416` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# GO:0050769     positive regulation of neurogenesis
neuroterms$`GO:0050769`[neuroterms$`GO:0050769` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
# GO:0003388     neuron development involved in amphid se...   2   2
neuroterms$`GO:0003388`[neuroterms$`GO:0003388` %in% unique.clust_1_wbid] %>% c(neurogenes) -> neurogene
neurogenes=unique(neurogenes)

# in K3:
# GO:0007212     dopamine receptor signaling pathway

# in K4: reproduction-
# GO:1905516     positive regulation of fertilization
# and GO:0000003     reproduction     461 262
# in K4: neuro-
# GO:0007614     short-term memory 9 8
# GO:0042048     olfactory behavior   20   17

# These values are used in the text below.
# neuroterms "found in "significantly enriched" in Embryo cluster that are significantly enriched in th
n_neuroterms_all = omigod[['all']] %>% filter(GO.ID %in% neurogo) %>% nrow # 0
n_0050769 = length(genesInTerm(dataset$BP,"GO:0050769")[[1]]) # 43
n_0050769_genome = length(genesInTerm(all.GO$BP,"GO:0050769")[[1]]) # 61
stats_0050769_k1 = omigod[['K1']] %>% select(-classicFisher,-'Rank in elim') %>% rename(pval=elim) %>%

# The genes with this term are:
annotatedPeaks$all_CDS_genes[neuroterms$`GO:0050769`[neuroterms$`GO:0050769` %in% unique.clust_1_wbid]]
```

```
## GRanges object with 4 ranges and 4 metadata columns:
##                   seqnames            ranges strand |  wbps_gene_id
##                      <Rle>         <IRanges>  <Rle> |   <character>
##   WBGene00003006      chrI   2706883-2717549      + | WBGene00003006
##   WBGene00013082      chrV 18592754-18614101      + | WBGene00013082
##   WBGene00016633    chrIII   3155268-3158393      + | WBGene00016633
##   WBGene00017381      chrX   3315321-3324229      + | WBGene00017381
##                   wormbase_gseq wormbase_locus        name
##                      <character>    <character> <character>
##   WBGene00003006       Y71F9B.5          lin-17      lin-17
##   WBGene00013082      Y51A2D.15          grdn-1      grdn-1
##   WBGene00016633       C44B11.1                     C44B11.1
##   WBGene00017381        F11D5.3           ddr-2       ddr-2
##   -------
##   seqinfo: 6 sequences from an unspecified genome; no seqlengths
```

We find some GO terms are enriched in some of the clusters versus the ELT-2 peaks at-large (all clusters). However, those terms *ARE NOT enriched* in ELT-2 peaks (all clusters) versus the genome (there are 1 enriched).

For example, having 43 genes annotated with the term "GO:0050769: positive regulation of neurogenesis" in the ELT-2 peaks is not *enriched* versus the whole genome (61 genes).

However, having of those genes near Embryo-high peaks, relative to expected, gives a p-value of using the elimination method implemented in topGO.

Output GO term enrichment results. Also, write files to paste into Revigo analysis, which collapses terms.

Paste output two-column files (GO-term p-like-value) into the form at. http://revigo.irb.hr/index.jsp

```
innate_immune_response = 'GO:0045087'
dataset=mkGO(unique.clust_2_wbid,unique.ap.wbid)
```

```
##
## Building most specific GOs .....

##   ( 3042 GO terms found. )

##
## Build GO DAG topology ..........

##   ( 5581 GO terms and 12485 relations. )

##
## Annotating nodes ...............

##   ( 4249 genes annotated to the GO terms. )

##
## Building most specific GOs .....

##   ( 1695 GO terms found. )

##
## Build GO DAG topology ..........

##   ( 2190 GO terms and 2875 relations. )

##
## Annotating nodes ...............

##   ( 4542 genes annotated to the GO terms. )

##
## Building most specific GOs .....

##   ( 780 GO terms found. )

##
## Build GO DAG topology ..........

##   ( 1024 GO terms and 1813 relations. )

##
## Annotating nodes ...............

##   ( 4616 genes annotated to the GO terms. )
```

```
immune_genes_chip = genesInTerm(dataset$BP, innate_immune_response)[[1]] # 170
immune_genes_larval = immune_genes_chip[immune_genes_chip %in% unique.clust_2_wbid] # 65
immune_peaks_chip = ap[ap$feature %in% immune_genes_chip] # 305

length(immune_genes_chip)
```

```
## [1] 169
```

```r
length(immune_genes_larval)
```

```
## [1] 65
```

```r
immune_peaks_larval = ap[ap$feature %in% immune_genes_larval] # 144
write.table(immune_peaks_larval$name, "peaklists/immune_peaks_larval.txt",row.names=F,col.names=F,quote=


immune_genes_L3 = immune_genes_chip[immune_genes_chip %in% unique.clust_3_wbid] # 31
immune_peaks_L3 = ap[ap$feature %in% immune_genes_L3] # 92
write.table(immune_peaks_L3$name, "peaklists/immune_peaks_L3.txt",row.names=F,col.names=F,quote=F)


immune_genes_increasing = immune_genes_chip[immune_genes_chip %in% unique.clust_4_wbid] # 248
immune_peaks_increasing = ap[ap$feature %in% immune_genes_increasing] # 92
write.table(immune_peaks_increasing$name, "peaklists/immune_peaks_increasing.txt",row.names=F,col.names=


immune_genes_labelled = data.frame(embryo=immune_genes_chip %in% unique.clust_1_wbid)
immune_genes_labelled %>%
  mutate(larval=(immune_genes_chip %in% unique.clust_2_wbid)) %>%
  mutate(L3=immune_genes_chip %in% unique.clust_3_wbid) %>%
  mutate(increasing=immune_genes_chip %in% unique.clust_4_wbid) -> immune_genes_labelled
rownames(immune_genes_labelled) <- immune_genes_chip
```

```r
zeroIfError = function(expr)
{
  suppressWarnings(tryCatch(expr, error=function(e){0}))
}

### here's the function
getGenesAndWBIDs_for_GOterm = function(term_id, GO_obj,ap.obj=ap)
{

  # WORMGO is the biomart result that contains the GO term name
  if( ! ("WORMGO" %in% ls(envir = .GlobalEnv)) ){
    stop("WORMGO is not in the global environment. Execute the 'GO functions' chunk.")
  }

  description=WORMGO %>% filter(go_accession == term_id) %>% select('go_name_1006') %>% unique %>% unlis

  termGenes = c() # initialize
  if (zeroIfError(length(genesInTerm(dataset$MF, term_id)[[1]])) > 0)
  {
    termGenes = genesInTerm(dataset$MF, term_id)[[1]]
  }
  else if (zeroIfError(length(genesInTerm(dataset$BP, term_id)[[1]])) > 0)
  {
    termGenes = genesInTerm(dataset$BP, term_id)[[1]]
  }
  else if (zeroIfError(length(genesInTerm(dataset$CC, term_id)[[1]])) > 0) {
    termGenes = genesInTerm(dataset$CC, term_id)[[1]]
  }
  else {
```

```r
    stop("GO term ID:",term_id, " not found in GO_obj")
  }

  peaks_ChIP = ap.obj[ap.obj$feature %in% termGenes]

  # get WBIDs for each cluster
  unique.clust_1_wbid = unique((ap.obj %>% filter(k4cluster == 1))$feature)
  unique.clust_2_wbid = unique((ap.obj %>% filter(k4cluster == 2))$feature)
  unique.clust_3_wbid = unique((ap.obj %>% filter(k4cluster == 3))$feature)
  unique.clust_4_wbid = unique((ap.obj %>% filter(k4cluster == 4))$feature)

  termGenes_notchanging = intersect(termGenes,unique.clust_0_wbid)
  termGenes_embryo = intersect(termGenes,unique.clust_1_wbid)
  termGenes_larval = intersect(termGenes,unique.clust_2_wbid)
  termGenes_L3 = intersect(termGenes,unique.clust_3_wbid)
  termGenes_increasing = intersect(termGenes,unique.clust_4_wbid)

  # tidy %>% .select can't get into the GRanges obj, so $ accessor outside of ()
  termPeaks_notchanging    = (ap.obj %>% filter(feature %in% termGenes_notchanging))$name
  termPeaks_embryo      = (ap.obj %>% filter(feature %in% termGenes_embryo))$name
  termPeaks_larval      = (ap.obj %>% filter(feature %in% termGenes_larval))$name
  termPeaks_L3          = (ap.obj %>% filter(feature %in% termGenes_L3))$name
  termPeaks_increasing = (ap.obj %>% filter(feature %in% termGenes_increasing))$name

  dir_friendly_GOID = stringr::str_replace(term_id, ":","")
  dir_friendly_desc = stringr::str_replace_all(description, " ", "_")
  dir_friendly_desc = stringr::str_replace_all(dir_friendly_desc, "/", "_")
  outdirname = sprintf("GO_split_lists/%s_%s", dir_friendly_GOID, dir_friendly_desc)
  if(! dir.exists(outdirname))
  {
    cat("writing directory:", outdirname)
    dir.create(outdirname)
  }
  wt = function(obj, filepath) {
    write.table(obj, filepath,row.names=F,col.names=F,quote=F)
  }

  for (varstr in c("termGenes_notchanging", "termGenes_embryo", "termGenes_larval",
                   "termGenes_L3", "termGenes_increasing",
                   "termPeaks_notchanging", "termPeaks_embryo", "termPeaks_larval",
                   "termPeaks_L3", "termPeaks_increasing"))
  {
      outobj=get(varstr)
      outpath = sprintf("%s/%s_%s.txt", outdirname,
                        dir_friendly_GOID,
                        str_replace(varstr, "term", ""))
      wt(outobj, outpath)
      cat("wrote", outpath, ".", length(outobj), "IDs.\n")
  }

}

DNA_transcription_factor_activity = 'GO:0000981'
TF_genes_chip = genesInTerm(dataset$MF, DNA_transcription_factor_activity)[[1]]
```

```
TF_genes_embryo = TF_genes_chip[TF_genes_chip %in% unique.clust_1_wbid]
TF_genes_larval = TF_genes_chip[TF_genes_chip %in% unique.clust_2_wbid]
TF_genes_L3 = TF_genes_chip[TF_genes_chip %in% unique.clust_3_wbid]
TF_genes_increasing = TF_genes_chip[TF_genes_chip %in% unique.clust_4_wbid]

TF_peaks_chip = ap[ap$feature %in% TF_genes_chip]

TF_peaks_embryo = ap[ap$feature %in% TF_genes_embryo]
TF_peaks_larval = ap[ap$feature %in% TF_genes_larval]
TF_peaks_L3 = ap[ap$feature %in% TF_genes_L3]
TF_peaks_increasing = ap[ap$feature %in% TF_genes_increasing]

write.table(TF_peaks_embryo$name,
            "peaklists/TF_peaks_embryo.txt",
            row.names=F,col.names=F,quote=F)
write.table(TF_peaks_larval$name,
            "peaklists/TF_peaks_larval.txt",
            row.names=F,col.names=F,quote=F)
write.table(TF_peaks_L3$name,
            "peaklists/TF_peaks_L3.txt",
            row.names=F,col.names=F,quote=F)
write.table(TF_peaks_increasing$name,
            "peaklists/TF_peaks_increasing.txt",
            row.names=F,col.names=F,quote=F)
```

Table 1: Dataset versus genome

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0032991	protein-containing complex	2178	1057	837.32	0.9867900	0.0000000	CC
GO: 0005488	binding	6909	3251	2997.77	1.0000000	0.0000000	MF
GO: 0005829	cytosol	579	339	222.59	0.0000000	0.0000000	CC
GO: 0043167	ion binding	2867	1467	1243.97	1.0000000	0.0000000	MF
GO: 0031090	organelle membrane	906	489	348.30	1.0000000	0.0000000	CC
GO: 0006629	lipid metabolic process	527	334	235.34	0.0141200	0.0000000	BP
GO: 0045087	innate immune response	231	169	103.15	0.0000000	0.0000000	BP
GO: 0098805	whole membrane	303	190	116.49	1.0000000	0.0000000	CC
GO: 0006955	immune response	241	173	107.62	0.3878100	0.0000000	BP
GO: 0002376	immune system process	243	174	108.51	1.0000000	0.0000000	BP
GO: 0008152	metabolic process	5706	2751	2548.06	0.3062600	0.0000000	BP
GO: 0044255	cellular lipid metabolic process	409	265	182.64	0.0013500	0.0000000	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0044281	small molecule metabolic process	791	465	353.23	1.0000000	0.0000000	BP
GO: 0097159	organic cyclic compound binding	3200	1580	1388.46	1.0000000	0.0000000	MF
GO: 0003824	catalytic activity	4125	1992	1789.81	0.0024800	0.0000000	MF
GO: 1901363	heterocyclic compound binding	3189	1574	1383.69	1.0000000	0.0000000	MF
GO: 0050793	regulation of developmental process	562	344	250.97	1.0000000	0.0000000	BP
GO: 0009056	catabolic process	986	560	440.31	0.5802200	0.0000000	BP
GO: 0019752	carboxylic acid metabolic process	394	254	175.94	0.7255000	0.0000000	BP
GO: 0043169	cation binding	1729	900	750.20	0.3763900	0.0000000	MF
GO: 0044237	cellular metabolic process	4912	2385	2193.49	1.0000000	0.0000000	BP
GO: 0032787	monocarboxylic acid metabolic process	201	144	89.76	1.0000000	0.0000000	BP
GO: 0048856	anatomical structure development	1811	957	808.72	0.0018100	0.0000000	BP
GO: 0007275	multicellular organism development	1643	876	733.69	0.9690700	0.0000000	BP
GO: 0009607	response to biotic stimulus	293	195	130.84	1.0000000	0.0000000	BP
GO: 0043207	response to external biotic stimulus	293	195	130.84	1.0000000	0.0000000	BP
GO: 0051707	response to other organism	293	195	130.84	1.0000000	0.0000000	BP
GO: 0046872	metal ion binding	1708	882	741.09	0.0000001	0.0000000	MF
GO: 0044419	interspecies interaction between organis...	297	196	132.63	1.0000000	0.0000000	BP
GO: 0098542	defense response to other organism	288	191	128.61	1.0000000	0.0000000	BP
GO: 0005739	mitochondrion	671	351	257.96	0.0000000	0.0000000	CC
GO: 0043168	anion binding	1446	758	627.41	1.0000000	0.0000000	MF
GO: 0005773	vacuole	181	119	69.58	0.1447900	0.0000000	CC
GO: 0043228	non-membrane-bounded organelle	1482	701	569.74	1.0000000	0.0000000	CC
GO: 0043232	intracellular non-membrane-bounded organ...	1482	701	569.74	1.0000000	0.0000000	CC
GO: 0071704	organic substance metabolic process	5228	2513	2334.61	1.0000000	0.0000000	BP
GO: 0006952	defense response	295	194	131.73	0.5378800	0.0000000	BP
GO: 0032502	developmental process	1941	1011	866.77	0.5718300	0.0000000	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0071840	cellular component organization or bioge...	2127	1098	949.83	1.0000000	0.0000000	BP
GO: 0031974	membrane-enclosed lumen	850	427	326.78	0.3755200	0.0000000	CC
GO: 1901575	organic substance catabolic process	834	472	372.43	1.0000000	0.0000000	BP
GO: 0006950	response to stress	975	542	435.39	1.0000000	0.0000000	BP
GO: 0005783	endoplasmic reticulum	417	232	160.31	0.0000000	0.0000000	CC
GO: 0016043	cellular component organization	1988	1030	887.76	1.0000000	0.0000000	BP
GO: 0043233	organelle lumen	849	426	326.39	1.0000000	0.0000000	CC
GO: 0006631	fatty acid metabolic process	146	108	65.20	0.0003500	0.0000000	BP
GO: 0070013	intracellular organelle lumen	847	425	325.62	1.0000000	0.0000000	CC
GO: 0051239	regulation of multicellular organismal p...	617	361	275.53	1.0000000	0.0000000	BP
GO: 0098588	bounding membrane of organelle	430	237	165.31	1.0000000	0.0000000	CC
GO: 0002119	nematode larval development	457	278	204.08	0.0000000	0.0000000	BP
GO: 0002164	larval development	463	280	206.76	0.9441500	0.0000000	BP
GO: 0019899	enzyme binding	454	269	196.99	0.2871900	0.0000000	MF
GO: 0044248	cellular catabolic process	833	467	371.98	0.4356800	0.0000000	BP
GO: 2000026	regulation of multicellular organismal d...	409	250	182.64	1.0000000	0.0000000	BP
GO: 0009791	post-embryonic development	486	290	217.03	0.3518200	0.0000000	BP
GO: 0005777	peroxisome	67	53	25.76	0.0000000	0.0000000	CC
GO: 0042579	microbody	67	53	25.76	1.0000000	0.0000000	CC
GO: 0034641	cellular nitrogen compound metabolic pro...	2585	1298	1154.35	1.0000000	0.0000000	BP
GO: 0048731	system development	718	405	320.63	1.0000000	0.0000000	BP
GO: 0043436	oxoacid metabolic process	431	258	192.47	1.0000000	0.0000000	BP
GO: 0007568	aging	250	162	111.64	0.6877000	0.0000000	BP
GO: 0008340	determination of adult lifespan	247	160	110.30	0.0000000	0.0000000	BP
GO: 0010259	multicellular organism aging	247	160	110.30	1.0000000	0.0000000	BP
GO: 0036094	small molecule binding	1460	746	633.48	1.0000000	0.0000000	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0009605	response to external stimulus	627	357	279.99	1.0000000	0.0000000	BP
GO: 0006082	organic acid metabolic process	470	276	209.88	0.4504900	0.0000000	BP
GO: 0044238	primary metabolic process	4933	2354	2202.87	1.0000000	0.0000000	BP
GO: 0006996	organelle organization	1386	726	618.93	0.8181000	0.0000000	BP
GO: 0031410	cytoplasmic vesicle	382	206	146.86	0.0416900	0.0000000	CC
GO: 0097708	intracellular vesicle	382	206	146.86	1.0000000	0.0000000	CC
GO: 0009790	embryo development	505	293	225.51	1.0000000	0.0000000	BP
GO: 0031982	vesicle	390	209	149.93	0.6400800	0.0000000	CC
GO: 1990904	ribonucleoprotein complex	421	223	161.85	0.0163900	0.0000000	CC
GO: 0005515	protein binding	3520	1674	1527.31	0.1291200	0.0000000	MF
GO: 0040007	growth	218	142	97.35	1.0000000	0.0000000	BP
GO: 0051240	positive regulation of multicellular org...	323	198	144.24	1.0000000	0.0000000	BP
GO: 0005768	endosome	167	103	64.20	0.0013900	0.0000000	CC
GO: 0051094	positive regulation of developmental pro...	286	178	127.72	1.0000000	0.0000000	BP
GO: 0019637	organophosphate metabolic process	428	252	191.13	1.0000000	0.0000000	BP
GO: 0048513	animal organ development	399	237	178.18	1.0000000	0.0000000	BP
GO: 0051641	cellular localization	889	482	396.99	1.0000000	0.0000000	BP
GO: 0008289	lipid binding	182	119	78.97	0.0778600	0.0000000	MF
GO: 0042175	nuclear outer membrane-endoplasmic retic...	268	151	103.03	0.3804100	0.0000000	CC
GO: 1901576	organic substance biosynthetic process	2245	1125	1002.52	1.0000000	0.0000000	BP
GO: 0000166	nucleotide binding	1325	675	574.91	0.3977800	0.0000000	MF
GO: 1901265	nucleoside phosphate binding	1325	675	574.91	1.0000000	0.0000000	MF
GO: 0051128	regulation of cellular component organiz...	507	291	226.40	1.0000000	0.0000000	BP
GO: 0005789	endoplasmic reticulum membrane	263	148	101.11	0.0000230	0.0000000	CC
GO: 0055086	nucleobase-containing small molecule met...	270	168	120.57	1.0000000	0.0000000	BP
GO: 0045121	membrane raft	52	41	19.99	0.0000000	0.0000000	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0098589	membrane region	52	41	19.99	1.0000000	0.0000000	CC
GO: 0098857	membrane microdomain	52	41	19.99	1.0000000	0.0000000	CC
GO: 0048878	chemical homeostasis	189	124	84.40	1.0000000	0.0000000	BP
GO: 0009058	biosynthetic process	2292	1144	1023.51	0.7712600	0.0000000	BP
GO: 1901360	organic cyclic compound metabolic proces. . .	2247	1123	1003.42	1.0000000	0.0000000	BP
GO: 0040008	regulation of growth	173	115	77.25	0.4425800	0.0000000	BP
GO: 0045927	positive regulation of growth	93	69	41.53	1.0000000	0.0000000	BP
GO: 0046907	intracellular transport	523	297	233.55	0.8239300	0.0000000	BP
GO: 0005764	lysosome	132	83	50.75	0.0000059	0.0000000	CC
GO: 0006139	nucleobase-containing compound metabolic. . .	2147	1073	958.76	0.6763500	0.0000000	BP
GO: 0033036	macromolecule localization	902	483	402.80	1.0000000	0.0000000	BP
GO: 0046483	heterocycle metabolic process	2197	1096	981.09	1.0000000	0.0000000	BP
GO: 0031967	organelle envelope	348	185	133.79	1.0000000	0.0000000	CC
GO: 0031975	envelope	348	185	133.79	1.0000000	0.0000000	CC
GO: 0006725	cellular aromatic compound metabolic pro. . .	2198	1096	981.53	1.0000000	0.0000000	BP
GO: 0044271	cellular nitrogen compound biosynthetic . . .	1657	843	739.95	1.0000000	0.0000000	BP
GO: 0051649	establishment of localization in cell	685	376	305.89	1.0000000	0.0000000	BP
GO: 0009792	embryo development ending in birth or eg. . .	305	184	136.20	0.0000000	0.0000000	BP
GO: 0035264	multicellular organism growth	103	74	46.00	0.0227100	0.0000000	BP
GO: 0071702	organic substance transport	804	434	359.03	1.0000000	0.0000000	BP
GO: 0008104	protein localization	756	410	337.60	0.3084100	0.0000000	BP
GO: 0000323	lytic vacuole	134	83	51.52	1.0000000	0.0000000	CC
GO: 0050662	coenzyme binding	211	131	91.55	0.9657000	0.0000000	MF
GO: 0005635	nuclear envelope	103	67	39.60	0.0027600	0.0000000	CC
GO: 0048639	positive regulation of developmental gro. . .	72	55	32.15	0.4166500	0.0000000	BP
GO: 0044249	cellular biosynthetic process	2212	1098	987.79	1.0000000	0.0000000	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0019222	regulation of metabolic process	1872	939	835.96	1.0000000	0.0000001	BP
GO: 0042592	homeostatic process	309	184	137.99	1.0000000	0.0000001	BP
GO: 0055114	oxidation-reduction process	657	359	293.39	0.0000740	0.0000001	BP
GO: 0016236	macroautophagy	58	46	25.90	0.6913800	0.0000001	BP
GO: 0040028	regulation of vulval development	105	74	46.89	0.0116700	0.0000001	BP
GO: 1902494	catalytic complex	651	315	250.27	1.0000000	0.0000001	CC
GO: 0044283	small molecule biosynthetic process	205	129	91.54	1.0000000	0.0000001	BP
GO: 0048589	developmental growth	192	122	85.74	0.0170300	0.0000001	BP
GO: 0044282	small molecule catabolic process	161	105	71.90	1.0000000	0.0000001	BP
GO: 0016491	oxidoreductase activity	570	308	247.32	0.0933200	0.0000001	MF
GO: 0009653	anatomical structure morphogenesis	657	358	293.39	0.9679400	0.0000001	BP
GO: 0071705	nitrogen compound transport	668	363	298.30	1.0000000	0.0000001	BP
GO: 0048518	positive regulation of biological proces...	1237	637	552.39	1.0000000	0.0000001	BP
GO: 1901657	glycosyl compound metabolic process	43	36	19.20	1.0000000	0.0000001	BP
GO: 0099080	supramolecular complex	457	229	175.69	1.0000000	0.0000002	CC
GO: 0045177	apical part of cell	90	59	34.60	0.1385000	0.0000002	CC
GO: 0007033	vacuole organization	74	55	33.05	0.6911600	0.0000002	BP
GO: 0032553	ribonucleotide binding	1188	598	515.47	1.0000000	0.0000002	MF
GO: 0048037	cofactor binding	425	236	184.40	0.5738900	0.0000002	MF
GO: 0048569	post-embryonic animal organ development	174	111	77.70	1.0000000	0.0000002	BP
GO: 0051179	localization	2358	1159	1052.98	1.0000000	0.0000002	BP
GO: 0072521	purine-containing compound metabolic pro...	176	112	78.59	1.0000000	0.0000002	BP
GO: 0040014	regulation of multicellular organism gro...	88	63	39.30	0.0256300	0.0000003	BP
GO: 0019693	ribose phosphate metabolic process	169	108	75.47	0.6898800	0.0000003	BP
GO: 0070887	cellular response to chemical stimulus	446	251	199.16	1.0000000	0.0000003	BP
GO: 0032879	regulation of localization	466	261	208.10	1.0000000	0.0000003	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0040025	vulval development	171	109	76.36	0.0795100	0.0000003	BP
GO: 0045184	establishment of protein localization	495	275	221.05	0.4113900	0.0000004	BP
GO: 0017076	purine nucleotide binding	1176	590	510.26	0.4253700	0.0000004	MF
GO: 0048522	positive regulation of cellular process	991	516	442.54	1.0000000	0.0000004	BP
GO: 0030554	adenyl nucleotide binding	981	499	425.65	1.0000000	0.0000005	MF
GO: 0009117	nucleotide metabolic process	217	133	96.90	0.5970600	0.0000005	BP
GO: 0042886	amide transport	500	277	223.28	1.0000000	0.0000005	BP
GO: 0015833	peptide transport	494	274	220.60	0.0856300	0.0000005	BP
GO: 0006753	nucleoside phosphate metabolic process	221	135	98.69	0.6894000	0.0000005	BP
GO: 0003676	nucleic acid binding	1833	890	795.33	0.2332300	0.0000006	MF
GO: 0009116	nucleoside metabolic process	32	28	14.29	0.0015500	0.0000006	BP
GO: 0009259	ribonucleotide metabolic process	165	105	73.68	0.4432700	0.0000006	BP
GO: 0008610	lipid biosynthetic process	197	122	87.97	0.7330700	0.0000006	BP
GO: 0048638	regulation of developmental growth	147	95	65.64	1.0000000	0.0000007	BP
GO: 0022603	regulation of anatomical structure morph…	203	125	90.65	1.0000000	0.0000007	BP
GO: 0032559	adenyl ribonucleotide binding	978	496	424.35	1.0000000	0.0000008	MF
GO: 0032555	purine ribonucleotide binding	1172	586	508.52	1.0000000	0.0000008	MF
GO: 0009894	regulation of catabolic process	129	85	57.61	1.0000000	0.0000008	BP
GO: 0007548	sex differentiation	263	156	117.44	0.1079000	0.0000009	BP
GO: 0006637	acyl-CoA metabolic process	37	31	16.52	0.0009800	0.0000010	BP
GO: 0035383	thioester metabolic process	37	31	16.52	1.0000000	0.0000010	BP
GO: 0060255	regulation of macromolecule metabolic pr…	1761	876	786.39	1.0000000	0.0000012	BP
GO: 0045595	regulation of cell differentiation	260	154	116.11	0.8902000	0.0000012	BP
GO: 0022626	cytosolic ribosome	80	52	30.76	0.0560800	0.0000013	CC
GO: 0031981	nuclear lumen	642	304	246.81	1.0000000	0.0000014	CC
GO: 0006807	nitrogen compound metabolic process	4512	2128	2014.87	0.4240600	0.0000016	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005643	nuclear pore	36	28	13.84	0.0019200	0.0000017	CC
GO: 0009057	macromolecule catabolic process	518	283	231.32	1.0000000	0.0000018	BP
GO: 0015031	protein transport	482	265	215.24	0.2062200	0.0000020	BP
GO: 0010033	response to organic substance	360	204	160.76	1.0000000	0.0000021	BP
GO: 0016323	basolateral plasma membrane	45	33	17.30	0.0000054	0.0000021	CC
GO: 0016324	apical plasma membrane	77	50	29.60	0.0000290	0.0000021	CC
GO: 1901362	organic cyclic compound biosynthetic pro...	1339	676	597.94	1.0000000	0.0000022	BP
GO: 0030258	lipid modification	95	65	42.42	0.1255700	0.0000023	BP
GO: 1902531	regulation of intracellular signal trans...	159	100	71.00	0.6903000	0.0000024	BP
GO: 0005776	autophagosome	17	16	6.54	0.0751600	0.0000024	CC
GO: 0007044	cell-substrate junction assembly	16	16	7.14	1.0000000	0.0000025	BP
GO: 0150115	cell-substrate junction organization	16	16	7.14	1.0000000	0.0000025	BP
GO: 0019900	kinase binding	114	74	49.46	0.4315800	0.0000027	MF
GO: 0018130	heterocycle biosynthetic process	1309	661	584.54	1.0000000	0.0000029	BP
GO: 0003723	RNA binding	618	323	268.15	0.0000990	0.0000030	MF
GO: 0043603	cellular amide metabolic process	531	288	237.12	1.0000000	0.0000032	BP
GO: 0034654	nucleobase-containing compound biosynthe...	1272	643	568.02	1.0000000	0.0000034	BP
GO: 1901565	organonitrogen compound catabolic proces...	519	282	231.76	0.6875300	0.0000034	BP
GO: 0010467	gene expression	2124	1040	948.49	1.0000000	0.0000034	BP
GO: 0005774	vacuolar membrane	76	49	29.22	0.0071000	0.0000037	CC
GO: 0006163	purine nucleotide metabolic process	162	101	72.34	0.9466100	0.0000038	BP
GO: 0098771	inorganic ion homeostasis	149	94	66.54	1.0000000	0.0000039	BP
GO: 0005543	phospholipid binding	100	66	43.39	0.0146400	0.0000039	MF
GO: 0019901	protein kinase binding	113	73	49.03	0.0178000	0.0000040	MF
GO: 0000902	cell morphogenesis	233	138	104.05	0.1026300	0.0000043	BP
GO: 0009150	purine ribonucleotide metabolic process	153	96	68.32	1.0000000	0.0000044	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0071310	cellular response to organic substance	290	167	129.50	0.4425500	0.0000049	BP
GO: 0019438	aromatic compound biosynthetic process	1301	655	580.97	1.0000000	0.0000053	BP
GO: 0031581	hemidesmosome assembly	15	15	6.70	0.0000055	0.0000055	BP
GO: 0070727	cellular macromolecule localization	550	296	245.61	1.0000000	0.0000056	BP
GO: 0035639	purine ribonucleoside triphosphate bindi...	1145	567	496.81	1.0000000	0.0000057	MF
GO: 0048580	regulation of post-embryonic development	165	102	73.68	1.0000000	0.0000058	BP
GO: 0061062	regulation of nematode larval developmen...	165	102	73.68	0.3951500	0.0000058	BP
GO: 0055080	cation homeostasis	150	94	66.98	1.0000000	0.0000059	BP
GO: 0019725	cellular homeostasis	234	138	104.49	1.0000000	0.0000059	BP
GO: 0005524	ATP binding	957	480	415.24	0.0000059	0.0000059	MF
GO: 0051235	maintenance of location	95	64	42.42	1.0000000	0.0000061	BP
GO: 0010468	regulation of gene expression	1411	706	630.09	0.0221900	0.0000063	BP
GO: 0018995	host cellular component	337	169	129.56	1.0000000	0.0000063	CC
GO: 0033643	host cell part	337	169	129.56	1.0000000	0.0000063	CC
GO: 0033646	host intracellular part	337	169	129.56	1.0000000	0.0000063	CC
GO: 0033647	host intracellular organelle	337	169	129.56	1.0000000	0.0000063	CC
GO: 0033648	host intracellular membrane-bounded orga...	337	169	129.56	1.0000000	0.0000063	CC
GO: 0042025	host cell nucleus	337	169	129.56	0.0000063	0.0000063	CC
GO: 0043656	host intracellular region	337	169	129.56	1.0000000	0.0000063	CC
GO: 0043657	host cell	337	169	129.56	1.0000000	0.0000063	CC
GO: 0016192	vesicle-mediated transport	449	246	200.50	0.6637200	0.0000065	BP
GO: 0035556	intracellular signal transduction	506	274	225.96	0.6381600	0.0000067	BP
GO: 0034613	cellular protein localization	545	293	243.37	0.9268300	0.0000070	BP
GO: 0009161	ribonucleoside monophosphate metabolic p...	28	24	12.50	1.0000000	0.0000084	BP
GO: 0042802	identical protein binding	124	78	53.80	0.0006100	0.0000085	MF
GO: 0050801	ion homeostasis	153	95	68.32	0.4437700	0.0000093	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005794	Golgi apparatus	339	169	130.33	0.0776400	0.0000098	CC
GO: 0022625	cytosolic large ribosomal subunit	47	33	18.07	0.0000098	0.0000098	CC
GO: 0046914	transition metal ion binding	718	367	311.54	0.4282600	0.0000098	MF
GO: 0005694	chromosome	459	221	176.46	0.2850900	0.0000100	CC
GO: 0040018	positive regulation of multicellular org. . .	49	37	21.88	0.0000110	0.0000110	BP
GO: 0030148	sphingolipid biosynthetic process	36	29	16.08	0.1055800	0.0000110	BP
GO: 0009896	positive regulation of catabolic process	73	51	32.60	1.0000000	0.0000110	BP
GO: 0006457	protein folding	98	65	43.76	0.0040500	0.0000110	BP
GO: 0097367	carbohydrate derivative binding	1274	624	552.78	0.8110400	0.0000110	MF
GO: 0046394	carboxylic acid biosynthetic process	120	77	53.59	1.0000000	0.0000120	BP
GO: 0051962	positive regulation of nervous system de. . .	75	52	33.49	1.0000000	0.0000130	BP
GO: 0000045	autophagosome assembly	41	32	18.31	0.0003900	0.0000130	BP
GO: 1905037	autophagosome organization	41	32	18.31	1.0000000	0.0000130	BP
GO: 0006665	sphingolipid metabolic process	56	41	25.01	0.1582000	0.0000130	BP
GO: 0051020	GTPase binding	148	90	64.22	0.6767300	0.0000130	MF
GO: 0071396	cellular response to lipid	46	35	20.54	1.0000000	0.0000140	BP
GO: 0055082	cellular chemical homeostasis	141	88	62.96	1.0000000	0.0000150	BP
GO: 0031329	regulation of cellular catabolic process	115	74	51.35	1.0000000	0.0000150	BP
GO: 0046513	ceramide biosynthetic process	21	19	9.38	0.0002500	0.0000150	BP
GO: 0035091	phosphatidylinositol binding	61	43	26.47	0.0080100	0.0000160	MF
GO: 0016070	RNA metabolic process	1666	821	743.97	0.6827900	0.0000170	BP
GO: 0016053	organic acid biosynthetic process	121	77	54.03	1.0000000	0.0000180	BP
GO: 0044265	cellular macromolecule catabolic process	458	248	204.52	1.0000000	0.0000180	BP
GO: 0048608	reproductive structure development	136	85	60.73	1.0000000	0.0000190	BP
GO: 0061458	reproductive system development	136	85	60.73	1.0000000	0.0000190	BP
GO: 0031323	regulation of cellular metabolic process	1620	799	723.42	1.0000000	0.0000200	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0000003	reproduction	903	462	403.24	0.1019200	0.0000220	BP
GO: 0060284	regulation of cell development	182	109	81.27	0.4436500	0.0000220	BP
GO: 0009617	response to bacterium	55	40	24.56	1.0000000	0.0000220	BP
GO: 0006914	autophagy	103	67	46.00	0.8351700	0.0000220	BP
GO: 0061919	process utilizing autophagic mechanism	103	67	46.00	1.0000000	0.0000220	BP
GO: 1990234	transferase complex	359	176	138.01	0.9438300	0.0000220	CC
GO: 0030163	protein catabolic process	384	211	171.48	0.0111900	0.0000230	BP
GO: 0009123	nucleoside monophosphate metabolic proce...	40	31	17.86	1.0000000	0.0000230	BP
GO: 0000407	phagophore assembly site	20	17	7.69	0.0055300	0.0000250	CC
GO: 0006873	cellular ion homeostasis	133	83	59.39	1.0000000	0.0000260	BP
GO: 0030003	cellular cation homeostasis	133	83	59.39	1.0000000	0.0000260	BP
GO: 0048666	neuron development	249	143	111.19	0.3992700	0.0000280	BP
GO: 0072329	monocarboxylic acid catabolic process	64	45	28.58	1.0000000	0.0000280	BP
GO: 0051186	cofactor metabolic process	206	121	91.99	1.0000000	0.0000280	BP
GO: 0008144	drug binding	1114	547	483.36	0.8119700	0.0000290	MF
GO: 0006886	intracellular protein transport	361	199	161.21	0.0180100	0.0000300	BP
GO: 0051960	regulation of nervous system development	160	97	71.45	1.0000000	0.0000310	BP
GO: 0006900	vesicle budding from membrane	20	18	8.93	0.1269800	0.0000310	BP
GO: 1901659	glycosyl compound biosynthetic process	20	18	8.93	1.0000000	0.0000310	BP
GO: 0006643	membrane lipid metabolic process	91	60	40.64	1.0000000	0.0000320	BP
GO: 0031175	neuron projection development	226	131	100.92	0.2444900	0.0000330	BP
GO: 0032990	cell part morphogenesis	195	115	87.08	1.0000000	0.0000350	BP
GO: 0045597	positive regulation of cell differentiat...	104	67	46.44	0.1975500	0.0000350	BP
GO: 0060627	regulation of vesicle-mediated transport	104	67	46.44	1.0000000	0.0000350	BP
GO: 0003707	steroid hormone receptor activity	43	32	18.66	0.0000350	0.0000350	MF
GO: 1901566	organonitrogen compound biosynthetic pro...	856	438	382.25	1.0000000	0.0000360	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0048583	regulation of response to stimulus	490	262	218.81	1.0000000	0.0000360	BP
GO: 0050769	positive regulation of neurogenesis	61	43	27.24	0.4449500	0.0000380	BP
GO: 0006732	coenzyme metabolic process	108	69	48.23	1.0000000	0.0000410	BP
GO: 0033865	nucleoside bisphosphate metabolic proces...	44	33	19.65	1.0000000	0.0000410	BP
GO: 0033875	ribonucleoside bisphosphate metabolic pr...	44	33	19.65	1.0000000	0.0000410	BP
GO: 0034032	purine nucleoside bisphosphate metabolic...	44	33	19.65	1.0000000	0.0000410	BP
GO: 0009893	positive regulation of metabolic process	654	341	292.05	1.0000000	0.0000410	BP
GO: 0043087	regulation of GTPase activity	97	63	43.32	0.2463500	0.0000420	BP
GO: 0019842	vitamin binding	77	51	33.41	1.0000000	0.0000420	MF
GO: 0061564	axon development	188	111	83.95	0.4437200	0.0000440	BP
GO: 0048585	negative regulation of response to stimu...	163	98	72.79	1.0000000	0.0000450	BP
GO: 0099512	supramolecular fiber	310	153	119.18	1.0000000	0.0000490	CC
GO: 0080090	regulation of primary metabolic process	1547	761	690.83	1.0000000	0.0000510	BP
GO: 0031331	positive regulation of cellular cataboli...	65	45	29.03	1.0000000	0.0000520	BP
GO: 0051130	positive regulation of cellular componen...	210	122	93.78	1.0000000	0.0000530	BP
GO: 0009112	nucleobase metabolic process	28	23	12.50	1.0000000	0.0000530	BP
GO: 0065008	regulation of biological quality	857	437	382.70	1.0000000	0.0000560	BP
GO: 0016787	hydrolase activity	1637	782	710.28	0.4298900	0.0000570	MF
GO: 0016054	organic acid catabolic process	120	75	53.59	1.0000000	0.0000580	BP
GO: 0046395	carboxylic acid catabolic process	120	75	53.59	1.0000000	0.0000580	BP
GO: 0099081	supramolecular polymer	311	153	119.56	1.0000000	0.0000600	CC
GO: 0051082	unfolded protein binding	56	39	24.30	0.0000620	0.0000620	MF
GO: 0005759	mitochondrial matrix	141	77	54.21	0.0000022	0.0000660	CC
GO: 0015934	large ribosomal subunit	82	49	31.52	1.0000000	0.0000720	CC
GO: 0008483	transaminase activity	18	16	7.81	0.0813100	0.0000840	MF
GO: 0016769	transferase activity, transferring nitro...	18	16	7.81	1.0000000	0.0000840	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0060589	nucleoside-triphosphatase regulator acti...	99	62	42.96	1.0000000	0.0000840	MF
GO: 0000139	Golgi membrane	178	93	68.43	0.0047400	0.0001100	CC
GO: 0005654	nucleoplasm	310	151	119.18	0.1127800	0.0001200	CC
GO: 0005096	GTPase activator activity	78	50	33.84	0.0001700	0.0001700	MF
GO: 0008270	zinc ion binding	557	283	241.68	0.0001800	0.0001800	MF
GO: 0000287	magnesium ion binding	49	34	21.26	0.0002100	0.0002100	MF
GO: 0030695	GTPase regulator activity	86	54	37.31	0.8961200	0.0002200	MF
GO: 0015399	primary active transmembrane transporter...	88	55	38.18	1.0000000	0.0002300	MF
GO: 0030170	pyridoxal phosphate binding	51	35	22.13	0.0002300	0.0002300	MF
GO: 0070279	vitamin B6 binding	51	35	22.13	1.0000000	0.0002300	MF
GO: 0003682	chromatin binding	90	56	39.05	0.0003700	0.0002300	MF
GO: 0044391	ribosomal subunit	141	75	54.21	1.0000000	0.0002500	CC
GO: 0019829	ATPase-coupled cation transmembrane tran...	32	24	13.88	1.0000000	0.0002800	MF
GO: 0042625	ATPase-coupled ion transmembrane transpo...	32	24	13.88	1.0000000	0.0002800	MF
GO: 0055037	recycling endosome	35	24	13.46	0.0252500	0.0002900	CC
GO: 0015078	proton transmembrane transporter activit...	68	44	29.50	0.4502500	0.0003100	MF
GO: 0042626	ATPase-coupled transmembrane transporter...	85	53	36.88	0.1077900	0.0003200	MF
GO: 0048471	perinuclear region of cytoplasm	90	51	34.60	0.0002600	0.0003300	CC
GO: 0070161	anchoring junction	105	58	40.37	1.0000000	0.0003400	CC
GO: 0031406	carboxylic acid binding	34	25	14.75	1.0000000	0.0003500	MF
GO: 0043177	organic acid binding	34	25	14.75	1.0000000	0.0003500	MF
GO: 0005788	endoplasmic reticulum lumen	26	19	10.00	0.0003600	0.0003600	CC
GO: 0005840	ribosome	178	91	68.43	0.3462800	0.0003600	CC
GO: 0005778	peroxisomal membrane	19	15	7.30	0.0055400	0.0003800	CC
GO: 0031903	microbody membrane	19	15	7.30	1.0000000	0.0003800	CC
GO: 0005938	cell cortex	134	71	51.52	0.0085900	0.0004100	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0016887	ATPase activity	281	150	121.92	0.0000990	0.0004100	MF
GO: 0017016	Ras GTPase binding	107	64	46.43	0.7164000	0.0004300	MF
GO: 0031267	small GTPase binding	109	65	47.29	0.6776200	0.0004400	MF
GO: 0016614	oxidoreductase activity, acting on CH-OH. . .	71	45	30.81	0.4325800	0.0005300	MF
GO: 0004679	AMP-activated protein kinase activity	9	9	3.91	0.0005400	0.0005400	MF
GO: 0035097	histone methyltransferase complex	23	17	8.84	0.3288700	0.0005900	CC
GO: 0010008	endosome membrane	81	46	31.14	0.8400300	0.0006000	CC
GO: 0030424	axon	212	105	81.50	0.0017700	0.0006000	CC
GO: 0098796	membrane protein complex	432	199	166.08	1.0000000	0.0006000	CC
GO: 0005770	late endosome	52	32	19.99	0.3399300	0.0006100	CC
GO: 1901981	phosphatidylinositol phosphate binding	42	29	18.22	0.3999900	0.0006800	MF
GO: 0098590	plasma membrane region	259	125	99.57	1.0000000	0.0007200	CC
GO: 0046527	glucosyltransferase activity	15	13	6.51	1.0000000	0.0007200	MF
GO: 0035251	UDP-glucosyltransferase activity	12	11	5.21	1.0000000	0.0007400	MF
GO: 0034708	methyltransferase complex	29	20	11.15	1.0000000	0.0008400	CC
GO: 0016776	phosphotransferase activity, phosphate g. . .	30	22	13.02	1.0000000	0.0008600	MF
GO: 0000785	chromatin	214	105	82.27	0.0618400	0.0009100	CC
GO: 0016829	lyase activity	131	75	56.84	0.1141900	0.0009100	MF
GO: 0009678	pyrophosphate hydrolysis-driven proton t. . .	20	16	8.68	1.0000000	0.0009400	MF
GO: 0005811	lipid droplet	20	15	7.69	0.0009900	0.0009900	CC
GO: 0005912	adherens junction	39	25	14.99	0.0010200	0.0010200	CC
GO: 0030684	preribosome	72	41	27.68	1.0000000	0.0010800	CC
GO: 0022804	active transmembrane transporter activit. . .	211	114	91.55	1.0000000	0.0010900	MF
GO: 0005740	mitochondrial envelope	245	118	94.19	0.3824700	0.0011000	CC
GO: 0016616	oxidoreductase activity, acting on the C. . .	67	42	29.07	0.9930900	0.0011100	MF
GO: 0005911	cell-cell junction	85	47	32.68	0.0248300	0.0011500	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0044769	ATPase activity, coupled to transmembran...	17	14	7.38	1.0000000	0.0012000	MF
GO: 0046961	proton-transporting ATPase activity, rot...	17	14	7.38	0.0012000	0.0012000	MF
GO: 0047617	acyl-CoA hydrolase activity	17	14	7.38	0.0023000	0.0012000	MF
GO: 0031588	nucleotide-activated protein kinase comp...	7	7	2.69	0.0012400	0.0012400	CC
GO: 0034045	phagophore assembly site membrane	7	7	2.69	0.0032200	0.0012400	CC
GO: 0071617	lysophospholipid acyltransferase activit...	8	8	3.47	0.1879600	0.0012500	MF
GO: 0016798	hydrolase activity, acting on glycosyl b...	77	47	33.41	0.0350600	0.0013200	MF
GO: 0033293	monocarboxylic acid binding	14	12	6.07	1.0000000	0.0014500	MF
GO: 0070603	SWI/SNF superfamily-type complex	28	19	10.76	1.0000000	0.0015300	CC
GO: 1904949	ATPase complex	28	19	10.76	1.0000000	0.0015300	CC
GO: 0031227	intrinsic component of endoplasmic retic...	73	41	28.06	0.3834100	0.0015600	CC
GO: 0000932	P-body	34	22	13.07	0.0017000	0.0017000	CC
GO: 0030173	integral component of Golgi membrane	38	24	14.61	0.0017400	0.0017400	CC
GO: 0031228	intrinsic component of Golgi membrane	38	24	14.61	1.0000000	0.0017400	CC
GO: 0031300	intrinsic component of organelle membran...	153	77	58.82	1.0000000	0.0017400	CC
GO: 0031593	polyubiquitin modification-dependent pro...	19	15	8.24	0.1413100	0.0017500	MF
GO: 0050660	flavin adenine dinucleotide binding	76	46	32.98	0.0181100	0.0018900	MF
GO: 0036452	ESCRT complex	19	14	7.30	1.0000000	0.0019600	CC
GO: 0044666	MLL3/4 complex	12	10	4.61	0.0019700	0.0019700	CC
GO: 0035770	ribonucleoprotein granule	102	54	39.21	1.0000000	0.0019800	CC
GO: 0003735	structural constituent of ribosome	146	81	63.35	0.0020500	0.0020500	MF
GO: 0015629	actin cytoskeleton	120	62	46.13	0.0239200	0.0021100	CC
GO: 0000118	histone deacetylase complex	21	15	8.07	0.0438100	0.0022300	CC
GO: 0061695	transferase complex, transferring phosph...	145	73	55.74	1.0000000	0.0022300	CC
GO: 0031966	mitochondrial membrane	228	109	87.65	0.0110400	0.0022800	CC
GO: 0008022	protein C-terminus binding	16	13	6.94	0.0023000	0.0023000	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0017056	structural constituent of nuclear pore	16	13	6.94	0.0023000	0.0023000	MF
GO: 0030176	integral component of endoplasmic reticu...	72	40	27.68	0.0022900	0.0023200	CC
GO: 0016289	CoA hydrolase activity	21	16	9.11	1.0000000	0.0023500	MF
GO: 0051536	iron-sulfur cluster binding	48	31	20.83	0.6784600	0.0024500	MF
GO: 0051540	metal cluster binding	48	31	20.83	1.0000000	0.0024500	MF
GO: 0031301	integral component of organelle membrane	150	75	57.67	1.0000000	0.0024700	CC
GO: 0005681	spliceosomal complex	94	50	36.14	0.0082500	0.0025100	CC
GO: 0004553	hydrolase activity, hydrolyzing O-glycos...	69	42	29.94	0.9965400	0.0025200	MF
GO: 0008081	phosphoric diester hydrolase activity	37	25	16.05	0.2291300	0.0025600	MF
GO: 0036464	cytoplasmic ribonucleoprotein granule	101	53	38.83	1.0000000	0.0027900	CC
GO: 0043292	contractile fiber	162	80	62.28	0.4204700	0.0028100	CC
GO: 0016705	oxidoreductase activity, acting on paire...	135	75	58.58	0.1969300	0.0028100	MF
GO: 0015020	glucuronosyltransferase activity	39	26	16.92	0.0004900	0.0028100	MF
GO: 0000803	sex chromosome	9	8	3.46	1.0000000	0.0028200	CC
GO: 0022853	active ion transmembrane transporter act...	131	73	56.84	1.0000000	0.0028500	MF
GO: 0003997	acyl-CoA oxidase activity	7	7	3.04	0.0066600	0.0028900	MF
GO: 0051019	mitogen-activated protein kinase binding	7	7	3.04	0.0028900	0.0028900	MF
GO: 0070530	K63-linked polyubiquitin modification-de...	7	7	3.04	0.0028900	0.0028900	MF
GO: 0005080	protein kinase C binding	13	11	5.64	0.0029000	0.0029000	MF
GO: 0048365	Rac GTPase binding	13	11	5.64	0.0069100	0.0029000	MF
GO: 0030117	membrane coat	37	23	14.22	0.3837600	0.0029200	CC
GO: 0048475	coated membrane	37	23	14.22	1.0000000	0.0029200	CC
GO: 0032040	small-subunit processome	35	22	13.46	0.0029300	0.0029300	CC
GO: 0046915	transition metal ion transmembrane trans...	41	27	17.79	1.0000000	0.0030600	MF
GO: 0000421	autophagosome membrane	6	6	2.31	0.0032200	0.0032200	CC
GO: 0000805	X chromosome	6	6	2.31	0.0032200	0.0032200	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005775	vacuolar lumen	6	6	2.31	1.0000000	0.0032200	CC
GO: 0016234	inclusion body	6	6	2.31	1.0000000	0.0032200	CC
GO: 0016235	aggresome	6	6	2.31	0.0032200	0.0032200	CC
GO: 0043202	lysosomal lumen	6	6	2.31	0.0032200	0.0032200	CC
GO: 0044753	amphisome	6	6	2.31	0.0032200	0.0032200	CC
GO: 0031625	ubiquitin protein ligase binding	43	28	18.66	0.0032900	0.0032900	MF
GO: 0042803	protein homodimerization activity	43	28	18.66	0.0032900	0.0032900	MF
GO: 0010494	cytoplasmic stress granule	16	12	6.15	0.0033000	0.0033000	CC
GO: 0031312	extrinsic component of organelle membran...	16	12	6.15	1.0000000	0.0033000	CC
GO: 0009931	calcium-dependent protein serine/threoni...	10	9	4.34	0.0353400	0.0033100	MF
GO: 0010857	calcium-dependent protein kinase activit...	10	9	4.34	1.0000000	0.0033100	MF
GO: 0061659	ubiquitin-like protein ligase activity	62	38	26.90	1.0000000	0.0033500	MF
GO: 0099513	polymeric cytoskeletal fiber	154	76	59.20	1.0000000	0.0036000	CC
GO: 0030135	coated vesicle	69	38	26.53	1.0000000	0.0036200	CC
GO: 1901681	sulfur compound binding	34	23	14.75	1.0000000	0.0036900	MF
GO: 0005769	early endosome	52	30	19.99	0.0407800	0.0037200	CC
GO: 1903293	phosphatase complex	18	13	6.92	0.3839900	0.0038100	CC
GO: 0003677	DNA binding	1007	477	436.93	0.0072000	0.0041400	MF
GO: 0016878	acid-thiol ligase activity	20	15	8.68	1.0000000	0.0041900	MF
GO: 0008374	O-acyltransferase activity	27	19	11.72	0.6787700	0.0042000	MF
GO: 0033176	proton-transporting V-type ATPase comple...	20	14	7.69	0.3839700	0.0042200	CC
GO: 0045335	phagocytic vesicle	20	14	7.69	0.5447300	0.0042200	CC
GO: 0008092	cytoskeletal protein binding	247	128	107.17	0.8487900	0.0042700	MF
GO: 0005682	U5 snRNP	11	9	4.23	0.0043100	0.0043100	CC
GO: 0045239	tricarboxylic acid cycle enzyme complex	11	9	4.23	0.3841000	0.0043100	CC
GO: 1904115	axon cytoplasm	11	9	4.23	0.0043100	0.0043100	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0031965	nuclear membrane	44	26	16.92	0.0084300	0.0043300	CC
GO: 0000228	nuclear chromosome	220	104	84.58	0.2573900	0.0043700	CC
GO: 0042887	amide transmembrane transporter activity	15	12	6.51	1.0000000	0.0043800	MF
GO: 0055120	striated muscle dense body	96	50	36.91	0.0044000	0.0044000	CC
GO: 0016469	proton-transporting two-sector ATPase co. . .	40	24	15.38	1.0000000	0.0046100	CC
GO: 0016409	palmitoyltransferase activity	29	20	12.58	1.0000000	0.0047900	MF
GO: 0008134	transcription factor binding	164	88	71.16	0.0051400	0.0049000	MF
GO: 0044389	ubiquitin-like protein ligase binding	44	28	19.09	1.0000000	0.0053400	MF
GO: 0005516	calmodulin binding	46	29	19.96	0.0056100	0.0056100	MF
GO: 0005504	fatty acid binding	12	10	5.21	0.0069200	0.0057200	MF
GO: 0019200	carbohydrate kinase activity	12	10	5.21	1.0000000	0.0057200	MF
GO: 0051287	NAD binding	33	22	14.32	0.1013800	0.0058800	MF
GO: 0005667	transcription regulator complex	152	74	58.44	0.0010000	0.0061700	CC
GO: 0016740	transferase activity	1680	776	728.94	0.2106300	0.0062500	MF
GO: 0030056	hemidesmosome	15	11	5.77	0.0065600	0.0065600	CC
GO: 0000159	protein phosphatase type 2A complex	8	7	3.08	0.0065700	0.0065700	CC
GO: 0004348	glucosylceramidase activity	6	6	2.60	0.0066600	0.0066600	MF
GO: 0004448	isocitrate dehydrogenase activity	6	6	2.60	1.0000000	0.0066600	MF
GO: 0004709	MAP kinase kinase kinase activity	6	6	2.60	0.0066600	0.0066600	MF
GO: 0016842	amidine-lyase activity	6	6	2.60	1.0000000	0.0066600	MF
GO: 0016846	carbon-sulfur lyase activity	6	6	2.60	0.1880500	0.0066600	MF
GO: 0042171	lysophosphatidic acid acyltransferase ac. . .	6	6	2.60	0.0815600	0.0066600	MF
GO: 0016877	ligase activity, forming carbon-sulfur b. . .	37	24	16.05	1.0000000	0.0068400	MF
GO: 0061630	ubiquitin protein ligase activity	60	36	26.03	0.0190000	0.0069200	MF
GO: 0016408	C-acyltransferase activity	9	8	3.91	1.0000000	0.0069300	MF
GO: 0070403	NAD+ binding	9	8	3.91	0.0069300	0.0069300	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0019866	organelle inner membrane	204	96	78.43	1.0000000	0.0070200	CC
GO: 0016604	nuclear body	41	24	15.76	0.0814800	0.0071000	CC
GO: 0000790	nuclear chromatin	116	58	44.60	0.2152600	0.0071900	CC
GO: 0140110	transcription regulator activity	673	323	292.01	1.0000000	0.0072400	MF
GO: 0008287	protein serine/threonine phosphatase com. . .	17	12	6.54	0.7662600	0.0073100	CC
GO: 0017053	transcription repressor complex	17	12	6.54	0.1579300	0.0073100	CC
GO: 0019904	protein domain specific binding	68	40	29.50	0.2250800	0.0073100	MF
GO: 0030139	endocytic vesicle	39	23	14.99	0.5153600	0.0073700	CC
GO: 0015662	ion transmembrane transporter activity, . . .	19	14	8.24	1.0000000	0.0073900	MF
GO: 0008194	UDP-glycosyltransferase activity	135	73	58.58	0.1462900	0.0077000	MF
GO: 0098793	presynapse	105	53	40.37	0.0195900	0.0078200	CC
GO: 0005730	nucleolus	172	82	66.12	0.0622100	0.0080900	CC
GO: 0044841	gut granule membrane	5	5	1.92	0.0083900	0.0083900	CC
GO: 0031902	late endosome membrane	25	16	9.61	0.0045200	0.0084900	CC
GO: 0016746	transferase activity, transferring acyl . . .	232	119	100.66	0.0147500	0.0086500	MF
GO: 0019205	nucleobase-containing compound kinase ac. . .	21	15	9.11	1.0000000	0.0088100	MF
GO: 0005813	centrosome	83	43	31.91	0.0217900	0.0089000	CC
GO: 0017111	nucleoside-triphosphatase activity	454	222	196.99	1.0000000	0.0089900	MF
GO: 0015630	microtubule cytoskeleton	265	121	101.88	0.4202000	0.0091400	CC
GO: 0005869	dynactin complex	10	8	3.84	0.0093100	0.0093100	CC
GO: 0016462	pyrophosphatase activity	485	236	210.44	0.8954200	0.0095300	MF
GO: 0016853	isomerase activity	99	55	42.96	0.7172400	0.0096100	MF
GO: 0005765	lysosomal membrane	44	25	16.92	0.0101100	0.0101100	CC
GO: 0098852	lytic vacuole membrane	44	25	16.92	1.0000000	0.0101100	CC
GO: 0005085	guanyl-nucleotide exchange factor activi. . .	67	39	29.07	0.0976500	0.0101500	MF
GO: 0019843	rRNA binding	36	23	15.62	0.0023500	0.0104800	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0010181	FMN binding	16	12	6.94	0.0105900	0.0105900	MF
GO: 0016817	hydrolase activity, acting on acid anhyd...	486	236	210.87	1.0000000	0.0106700	MF
GO: 0016818	hydrolase activity, acting on acid anhyd...	486	236	210.87	1.0000000	0.0106700	MF
GO: 0003756	protein disulfide isomerase activity	11	9	4.77	0.0111500	0.0111500	MF
GO: 0008013	beta-catenin binding	11	9	4.77	0.0111500	0.0111500	MF
GO: 0016864	intramolecular oxidoreductase activity, ...	11	9	4.77	1.0000000	0.0111500	MF
GO: 0005743	mitochondrial inner membrane	188	88	72.28	0.0130200	0.0112700	CC
GO: 0120111	neuron projection cytoplasm	12	9	4.61	1.0000000	0.0113500	CC
GO: 0030662	coated vesicle membrane	38	22	14.61	1.0000000	0.0116200	CC
GO: 0030054	cell junction	454	198	174.54	0.0244400	0.0123500	CC
GO: 0030666	endocytic vesicle membrane	14	10	5.38	1.0000000	0.0127900	CC
GO: 0055038	recycling endosome membrane	14	10	5.38	0.0127900	0.0127900	CC
GO: 1902936	phosphatidylinositol bisphosphate bindin...	18	13	7.81	1.0000000	0.0128200	MF
GO: 0016208	AMP binding	8	7	3.47	0.0143400	0.0143400	MF
GO: 0016634	oxidoreductase activity, acting on the C...	8	7	3.47	1.0000000	0.0143400	MF
GO: 0016801	hydrolase activity, acting on ether bond...	8	7	3.47	1.0000000	0.0143400	MF
GO: 0030544	Hsp70 protein binding	8	7	3.47	0.0143400	0.0143400	MF
GO: 0016879	ligase activity, forming carbon-nitrogen...	31	20	13.45	1.0000000	0.0143500	MF
GO: 0012506	vesicle membrane	110	54	42.29	1.0000000	0.0144200	CC
GO: 0030659	cytoplasmic vesicle membrane	110	54	42.29	0.3720400	0.0144200	CC
GO: 0097526	spliceosomal tri-snRNP complex	24	15	9.23	0.2902300	0.0145100	CC
GO: 0005856	cytoskeleton	527	227	202.60	0.9069200	0.0147100	CC
GO: 0045179	apical cortex	7	6	2.69	0.0151300	0.0151300	CC
GO: 0015562	efflux transmembrane transporter activit...	13	10	5.64	0.0292500	0.0151300	MF
GO: 0050145	nucleoside monophosphate kinase activity	13	10	5.64	0.4335300	0.0151300	MF
GO: 1904680	peptide transmembrane transporter activi...	13	10	5.64	0.2200000	0.0151300	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0016836	hydro-lyase activity	33	21	14.32	1.0000000	0.0151500	MF
GO: 0005324	long-chain fatty acid transporter activi...	5	5	2.17	0.0153600	0.0153600	MF
GO: 0030291	protein serine/threonine kinase inhibito...	5	5	2.17	1.0000000	0.0153600	MF
GO: 0030976	thiamine pyrophosphate binding	5	5	2.17	0.0153600	0.0153600	MF
GO: 0042813	Wnt-activated receptor activity	5	5	2.17	0.0153600	0.0153600	MF
GO: 0016835	carbon-oxygen lyase activity	37	23	16.05	1.0000000	0.0164600	MF
GO: 0051087	chaperone binding	22	15	9.55	0.0166500	0.0166500	MF
GO: 0017048	Rho GTPase binding	39	24	16.92	0.5991500	0.0169900	MF
GO: 0140030	modification-dependent protein binding	39	24	16.92	1.0000000	0.0169900	MF
GO: 0000502	proteasome complex	39	22	14.99	0.3839100	0.0171100	CC
GO: 0004842	ubiquitin-protein transferase activity	122	65	52.94	0.0686500	0.0171600	MF
GO: 0008047	enzyme activator activity	120	64	52.07	0.8964500	0.0174600	MF
GO: 0000987	cis-regulatory region sequence-specific ...	81	45	35.15	0.2193200	0.0180400	MF
GO: 0005496	steroid binding	15	11	6.51	1.0000000	0.0187200	MF
GO: 1902911	protein kinase complex	48	26	18.45	1.0000000	0.0192400	CC
GO: 0030014	CCR4-NOT complex	9	7	3.46	0.0567300	0.0197200	CC
GO: 0030670	phagocytic vesicle membrane	9	7	3.46	0.0197200	0.0197200	CC
GO: 0098687	chromosomal region	100	49	38.44	1.0000000	0.0198800	CC
GO: 0030133	transport vesicle	84	42	32.29	0.4964100	0.0201100	CC
GO: 0005802	trans-Golgi network	31	18	11.92	0.0529400	0.0208400	CC
GO: 0004652	polynucleotide adenylyltransferase activ...	10	8	4.34	0.0402500	0.0213900	MF
GO: 0005375	copper ion transmembrane transporter act...	10	8	4.34	0.0402500	0.0213900	MF
GO: 0015926	glucosidase activity	10	8	4.34	1.0000000	0.0213900	MF
GO: 0016406	carnitine O-acyltransferase activity	10	8	4.34	1.0000000	0.0213900	MF
GO: 0016638	oxidoreductase activity, acting on the C...	10	8	4.34	1.0000000	0.0213900	MF
GO: 0036002	pre-mRNA binding	10	8	4.34	0.4336000	0.0213900	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0030120	vesicle coat	29	17	11.15	1.0000000	0.0217800	CC
GO: 0030134	COPII-coated ER to Golgi transport vesic...	29	17	11.15	0.2648500	0.0217800	CC
GO: 0005967	mitochondrial pyruvate dehydrogenase com...	4	4	1.54	0.0218300	0.0218300	CC
GO: 0034663	endoplasmic reticulum chaperone complex	4	4	1.54	0.0218300	0.0218300	CC
GO: 0045252	oxoglutarate dehydrogenase complex	4	4	1.54	0.0218300	0.0218300	CC
GO: 0045254	pyruvate dehydrogenase complex	4	4	1.54	1.0000000	0.0218300	CC
GO: 0051184	cofactor transmembrane transporter activ...	17	12	7.38	0.3571300	0.0218600	MF
GO: 0051539	4 iron, 4 sulfur cluster binding	30	19	13.02	0.0219500	0.0219500	MF
GO: 0003700	DNA-binding transcription factor activit...	568	270	246.45	0.0003300	0.0226300	MF
GO: 0005771	multivesicular body	11	8	4.23	0.0226400	0.0226400	CC
GO: 0005798	Golgi-associated vesicle	53	28	20.38	0.3838600	0.0231000	CC
GO: 0000978	RNA polymerase II cis-regulatory region ...	76	42	32.98	0.0318500	0.0243200	MF
GO: 0031624	ubiquitin conjugating enzyme binding	19	13	8.24	0.0245800	0.0245800	MF
GO: 0030674	protein-macromolecule adaptor activity	74	41	32.11	0.4689100	0.0245900	MF
GO: 0045178	basal part of cell	21	13	8.07	0.0754200	0.0249500	CC
GO: 0005849	mRNA cleavage factor complex	15	10	5.77	0.1614500	0.0252400	CC
GO: 0012507	ER to Golgi transport vesicle membrane	15	10	5.77	0.2344000	0.0252400	CC
GO: 0016407	acetyltransferase activity	68	38	29.50	0.0812900	0.0253300	MF
GO: 0046540	U4/U6 x U5 tri-snRNP complex	19	12	7.30	0.0253800	0.0253800	CC
GO: 0005844	polysome	17	11	6.54	0.0113500	0.0255200	CC
GO: 0003743	translation initiation factor activity	46	27	19.96	0.0260800	0.0260800	MF
GO: 0043204	perikaryon	76	38	29.22	0.0261700	0.0261700	CC
GO: 0017137	Rab GTPase binding	50	29	21.69	0.0119200	0.0263000	MF
GO: 0016417	S-acyltransferase activity	21	14	9.11	1.0000000	0.0269100	MF
GO: 0005381	iron ion transmembrane transporter activ...	12	9	5.21	0.0587800	0.0274300	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005546	phosphatidylinositol-4,5-bisphosphate bi...	12	9	5.21	0.0274300	0.0274300	MF
GO: 0140142	nucleocytoplasmic carrier activity	12	9	5.21	1.0000000	0.0274300	MF
GO: 0004095	carnitine O-palmitoyltransferase activit...	7	6	3.04	0.0293000	0.0293000	MF
GO: 0008553	proton-exporting ATPase activity, phosph...	7	6	3.04	0.0293000	0.0293000	MF
GO: 0015232	heme transporter activity	7	6	3.04	0.0588200	0.0293000	MF
GO: 0016416	O-palmitoyltransferase activity	7	6	3.04	1.0000000	0.0293000	MF
GO: 0016597	amino acid binding	7	6	3.04	0.4010900	0.0293000	MF
GO: 0016722	oxidoreductase activity, oxidizing metal...	7	6	3.04	1.0000000	0.0293000	MF
GO: 0016803	ether hydrolase activity	7	6	3.04	1.0000000	0.0293000	MF
GO: 0016868	intramolecular transferase activity, pho...	7	6	3.04	0.4010900	0.0293000	MF
GO: 0035257	nuclear hormone receptor binding	7	6	3.04	0.2201700	0.0293000	MF
GO: 0090482	vitamin transmembrane transporter activi...	7	6	3.04	0.2201700	0.0293000	MF
GO: 0016405	CoA-ligase activity	25	16	10.85	0.5996000	0.0305300	MF
GO: 0031984	organelle subcompartment	79	39	30.37	1.0000000	0.0307800	CC
GO: 0004190	aspartic-type endopeptidase activity	27	17	11.72	0.0305200	0.0319100	MF
GO: 0019903	protein phosphatase binding	27	17	11.72	0.0841100	0.0319100	MF
GO: 0070001	aspartic-type peptidase activity	27	17	11.72	1.0000000	0.0319100	MF
GO: 0000062	fatty-acyl-CoA binding	14	10	6.07	0.0324600	0.0324600	MF
GO: 0003993	acid phosphatase activity	14	10	6.07	0.0324600	0.0324600	MF
GO: 0015645	fatty acid ligase activity	14	10	6.07	1.0000000	0.0324600	MF
GO: 0032452	histone demethylase activity	14	10	6.07	1.0000000	0.0324600	MF
GO: 0140457	protein demethylase activity	14	10	6.07	1.0000000	0.0324600	MF
GO: 1905369	endopeptidase complex	41	22	15.76	1.0000000	0.0339700	CC
GO: 0000243	commitment complex	6	5	2.31	0.0342100	0.0342100	CC
GO: 0000813	ESCRT I complex	6	5	2.31	0.0342100	0.0342100	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0016342	catenin complex	6	5	2.31	0.0342100	0.0342100	CC
GO: 0030127	COPII vesicle coat	6	5	2.31	0.0342100	0.0342100	CC
GO: 0031080	nuclear pore outer ring	6	5	2.31	0.0342100	0.0342100	CC
GO: 0044214	spanning component of plasma membrane	6	5	2.31	0.0342100	0.0342100	CC
GO: 0044840	gut granule	6	5	2.31	1.0000000	0.0342100	CC
GO: 0045240	dihydrolipoyl dehydrogenase complex	6	5	2.31	1.0000000	0.0342100	CC
GO: 0089717	spanning component of membrane	6	5	2.31	1.0000000	0.0342100	CC
GO: 0098592	cytoplasmic side of apical plasma membra...	6	5	2.31	0.0342100	0.0342100	CC
GO: 1990204	oxidoreductase complex	73	36	28.06	1.0000000	0.0376100	CC
GO: 0000235	astral microtubule	8	6	3.08	0.0407900	0.0407900	CC

Table 2: Not changing versus whole dataset

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0008045	motor neuron axon guidance	20	8	1.56	0.000068	0.000068	BP
GO: 0008083	growth factor activity	3	3	0.23	0.000450	0.000450	MF
GO: 0030628	pre-mRNA 3'-splice site binding	3	3	0.23	0.000450	0.000450	MF
GO: 0007399	nervous system development	207	32	16.13	0.002600	0.000100	BP
GO: 0008584	male gonad development	5	3	0.39	0.004200	0.004160	BP
GO: 0030150	protein import into mitochondrial matrix	5	3	0.39	0.004200	0.004160	BP
GO: 0030121	AP-1 adaptor complex	2	2	0.15	0.005900	0.005930	CC
GO: 0089701	U2AF	2	2	0.15	0.005900	0.005930	CC
GO: 0004831	tyrosine-tRNA ligase activity	2	2	0.15	0.005920	0.005920	MF
GO: 0006437	tyrosyl-tRNA aminoacylation	2	2	0.16	0.006100	0.006050	BP
GO: 0010696	positive regulation of mitotic spindle p...	2	2	0.16	0.006100	0.006050	BP
GO: 0010862	positive regulation of pathway-restricte...	2	2	0.16	0.006100	0.006050	BP
GO: 0060395	SMAD protein signal transduction	2	2	0.16	0.006100	0.006050	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0072321	chaperone-mediated protein transport	2	2	0.16	0.006100	0.006050	BP
GO: 0043025	neuronal cell body	92	13	7.10	0.006400	0.023060	CC
GO: 0005515	protein binding	1674	160	129.00	0.006800	0.000250	MF
GO: 0035335	peptidyl-tyrosine dephosphorylation	30	7	2.34	0.006900	0.006940	BP
GO: 0043022	ribosome binding	11	4	0.85	0.007400	0.007400	MF
GO: 0030950	establishment or maintenance of actin cy...	6	3	0.47	0.007800	0.007840	BP
GO: 0031115	negative regulation of microtubule polym...	6	3	0.47	0.007800	0.007840	BP
GO: 0061643	chemorepulsion of axon	6	3	0.47	0.007800	0.007840	BP
GO: 1905815	regulation of dorsal/ventral axon guidan...	6	3	0.47	0.007800	0.007840	BP
GO: 0030687	preribosome, large subunit precursor	12	4	0.93	0.010500	0.010460	CC
GO: 0005736	RNA polymerase I complex	7	3	0.54	0.012600	0.012590	CC
GO: 0007419	ventral cord development	7	3	0.55	0.012900	0.012940	BP
GO: 0005125	cytokine activity	3	2	0.23	0.016860	0.016860	MF
GO: 0019784	NEDD8-specific protease activity	3	2	0.23	0.016860	0.016860	MF
GO: 0030993	axonemal heterotrimeric kinesin-II compl...	3	2	0.23	0.016900	0.016890	CC
GO: 0071565	nBAF complex	3	2	0.23	0.016900	0.016890	CC
GO: 1990423	RZZ complex	3	2	0.23	0.016900	0.016890	CC
GO: 0007274	neuromuscular synaptic transmission	6	3	0.47	0.017100	0.007840	BP
GO: 0030970	retrograde protein transport, ER to cyto...	3	2	0.23	0.017200	0.017220	BP
GO: 0032968	positive regulation of transcription elo...	3	2	0.23	0.017200	0.017220	BP
GO: 0048730	epidermis morphogenesis	3	2	0.23	0.017200	0.017220	BP
GO: 0071108	protein K48-linked deubiquitination	3	2	0.23	0.017200	0.017220	BP
GO: 1903394	protein localization to kinetochore invo...	3	2	0.23	0.017200	0.017220	BP
GO: 1905342	positive regulation of protein localizat...	3	2	0.23	0.017200	0.017220	BP
GO: 0005770	late endosome	32	6	2.47	0.018800	0.032930	CC
GO: 0008355	olfactory learning	8	3	0.62	0.019500	0.019530	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005524	ATP binding	480	49	36.99	0.021420	0.021420	MF
GO: 1904115	axon cytoplasm	9	3	0.69	0.026900	0.026920	CC
GO: 0038007	netrin-activated signaling pathway	9	3	0.70	0.027600	0.027630	BP
GO: 0005744	TIM23 mitochondrial import inner membran. . .	5	3	0.39	0.031900	0.004050	CC
GO: 0016477	cell migration	109	18	8.49	0.032000	0.001640	BP
GO: 0008353	RNA polymerase II CTD heptapeptide repea. . .	4	2	0.31	0.032010	0.032010	MF
GO: 0030553	cGMP binding	4	2	0.31	0.032010	0.032010	MF
GO: 0046785	microtubule polymerization	10	5	0.78	0.032200	0.000510	BP
GO: 0008543	fibroblast growth factor receptor signal. . .	4	2	0.31	0.032700	0.032670	BP
GO: 0010754	negative regulation of cGMP-mediated sig. . .	4	2	0.31	0.032700	0.032670	BP
GO: 0042074	cell migration involved in gastrulation	4	2	0.31	0.032700	0.032670	BP

Table 3: Embryo cluster versus whole dataset

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005001	transmembrane receptor protein tyrosine . . .	2	2	0.07	0.0012	0.00117	MF
GO: 0010172	embryonic body morphogenesis	27	5	1.02	0.0029	0.00293	BP
GO: 0038007	netrin-activated signaling pathway	9	3	0.34	0.0037	0.00372	BP
GO: 0007218	neuropeptide signaling pathway	18	4	0.68	0.0039	0.00392	BP
GO: 0005604	basement membrane	9	3	0.35	0.0042	0.00420	CC
GO: 0033563	dorsal/ventral axon guidance	16	4	0.60	0.0051	0.00247	BP
GO: 0004115	3',5'-cyclic-AMP phosphodiesterase activ. . .	4	2	0.14	0.0067	0.00672	MF
GO: 0040022	feminization of hermaphroditic germ-line	4	2	0.15	0.0080	0.00804	BP
GO: 0048665	neuron fate specification	4	2	0.15	0.0080	0.00804	BP
GO: 0097376	interneuron axon guidance	4	2	0.15	0.0080	0.00804	BP
GO: 0006730	one-carbon metabolic process	12	3	0.45	0.0090	0.00897	BP
GO: 0005576	extracellular region	197	13	7.72	0.0126	0.04420	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0004930	G protein-coupled receptor activity	73	7	2.51	0.0133	0.01200	MF
GO: 0009952	anterior/posterior pattern specification	36	4	1.36	0.0189	0.04473	BP
GO: 0070006	metalloaminopeptidase activity	8	2	0.27	0.0286	0.02864	MF
GO: 0001228	DNA-binding transcription activator acti. . .	21	3	0.72	0.0336	0.03357	MF
GO: 0000035	acyl binding	1	1	0.03	0.0343	0.03435	MF
GO: 0000036	acyl carrier activity	1	1	0.03	0.0343	0.03435	MF
GO: 0003827	alpha-1,3-mannosylglycoprotein 2-beta-N-. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0004504	peptidylglycine monooxygenase activity	1	1	0.03	0.0343	0.03435	MF
GO: 0004566	beta-glucuronidase activity	1	1	0.03	0.0343	0.03435	MF
GO: 0004616	phosphogluconate dehydrogenase (decarbox. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0004719	protein-L-isoaspartate (D-aspartate) O-m. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0004818	glutamate-tRNA ligase activity	1	1	0.03	0.0343	0.03435	MF
GO: 0004935	adrenergic receptor activity	1	1	0.03	0.0343	0.03435	MF
GO: 0004989	octopamine receptor activity	1	1	0.03	0.0343	0.03435	MF
GO: 0005005	transmembrane-ephrin receptor activity	1	1	0.03	0.0343	0.03435	MF
GO: 0008226	tyramine receptor activity	1	1	0.03	0.0343	0.03435	MF
GO: 0008467	[heparan sulfate]-glucosamine 3-sulfotra. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0016155	formyltetrahydrofolate dehydrogenase act. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0018738	S-formylglutathione hydrolase activity	1	1	0.03	0.0343	0.03435	MF
GO: 0019799	tubulin N-acetyltransferase activity	1	1	0.03	0.0343	0.03435	MF
GO: 0032216	glucosaminyl-phosphatidylinositol O-acyl. . .	1	1	0.03	0.0343	0.03435	MF
GO: 0042923	neuropeptide binding	1	1	0.03	0.0343	0.03435	MF
GO: 0048101	calcium- and calmodulin-regulated 3',5'-. . .	1	1	0.03	0.0343	0.03435	MF
GO: 1990890	netrin receptor binding	1	1	0.03	0.0343	0.03435	MF
GO: 0033613	activating transcription factor binding	9	2	0.31	0.0360	0.03601	MF
GO: 0003388	neuron development involved in amphid se. . .	2	2	0.08	0.0374	0.00141	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0032878	regulation of establishment or maintenan...	8	2	0.30	0.0375	0.03398	BP
GO: 0000390	spliceosomal complex disassembly	1	1	0.04	0.0377	0.03766	BP
GO: 0000493	box H/ACA snoRNP assembly	1	1	0.04	0.0377	0.03766	BP
GO: 0001966	thigmotaxis	1	1	0.04	0.0377	0.03766	BP
GO: 0003391	amphid sensory organ dendrite retrograde...	1	1	0.04	0.0377	0.03766	BP
GO: 0006198	cAMP catabolic process	1	1	0.04	0.0377	0.03766	BP
GO: 0006424	glutamyl-tRNA aminoacylation	1	1	0.04	0.0377	0.03766	BP
GO: 0009051	pentose-phosphate shunt, oxidative branc...	1	1	0.04	0.0377	0.03766	BP
GO: 0009258	10-formyltetrahydrofolate catabolic proc...	1	1	0.04	0.0377	0.03766	BP
GO: 0019391	glucuronoside catabolic process	1	1	0.04	0.0377	0.03766	BP
GO: 0031640	killing of cells of other organism	1	1	0.04	0.0377	0.03766	BP
GO: 0035332	positive regulation of hippo signaling	1	1	0.04	0.0377	0.03766	BP

Table 4: Larval cluster versus whole dataset

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0030246	carbohydrate binding	118	60	28.76	0.000000	0.0000000	MF
GO: 0045087	innate immune response	169	65	40.13	0.000005	0.0000094	BP
GO: 0045121	membrane raft	41	22	9.53	0.000011	0.0000220	CC
GO: 0000977	RNA polymerase II transcription regulato...	111	46	27.05	0.000320	0.0000450	MF
GO: 0000122	negative regulation of transcription by ...	74	31	17.57	0.000680	0.0003800	BP
GO: 0005882	intermediate filament	10	8	2.32	0.000820	0.0002400	CC
GO: 0004190	aspartic-type endopeptidase activity	17	11	4.14	0.001300	0.0004800	MF
GO: 0000981	DNA-binding transcription factor activit...	78	29	19.01	0.001740	0.0075000	MF
GO: 0004185	serine-type carboxypeptidase activity	8	6	1.95	0.003650	0.0036500	MF
GO: 0005576	extracellular region	197	67	45.79	0.005950	0.0002900	CC
GO: 0030163	protein catabolic process	211	61	50.11	0.006220	0.0443700	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0042761	very long-chain fatty acid biosynthetic . . .	9	6	2.14	0.007580	0.0075800	BP
GO: 0043401	steroid hormone mediated signaling pathw. . .	32	14	7.60	0.009790	0.0097900	BP
GO: 0003707	steroid hormone receptor activity	32	14	7.80	0.012400	0.0124000	MF
GO: 0050830	defense response to Gram-positive bacter. . .	15	8	3.56	0.012490	0.0124900	BP
GO: 0030590	first cell cycle pseudocleavage	5	4	1.19	0.012830	0.0128300	BP
GO: 1901216	positive regulation of neuron death	5	4	1.19	0.012830	0.0128300	BP
GO: 0035461	vitamin transmembrane transport	3	3	0.71	0.013360	0.0133600	BP
GO: 0043327	chemotaxis to cAMP	3	3	0.71	0.013360	0.0133600	BP
GO: 0070781	response to biotin	3	3	0.71	0.013360	0.0133600	BP
GO: 1905803	negative regulation of cellular response. . .	3	3	0.71	0.013360	0.0133600	BP
GO: 0008107	galactoside 2-alpha-L-fucosyltransferase. . .	5	4	1.22	0.014150	0.0141500	MF
GO: 0005381	iron ion transmembrane transporter activ. . .	9	5	2.19	0.014150	0.0440400	MF
GO: 0004022	alcohol dehydrogenase (NAD+) activity	3	3	0.73	0.014450	0.0144500	MF
GO: 0005542	folic acid binding	3	3	0.73	0.014450	0.0144500	MF
GO: 0008270	zinc ion binding	283	85	68.97	0.014530	0.0145300	MF
GO: 0071949	FAD binding	18	9	4.39	0.016210	0.0162100	MF
GO: 0005615	extracellular space	115	37	26.73	0.016810	0.0168100	CC
GO: 0005764	lysosome	83	27	19.29	0.020500	0.0327200	CC
GO: 0008340	determination of adult lifespan	160	49	37.99	0.025560	0.0255600	BP
GO: 0040034	regulation of development, heterochronic	15	8	3.56	0.029000	0.0124900	BP
GO: 0045944	positive regulation of transcription by . . .	136	43	32.30	0.030660	0.0205700	BP
GO: 0007160	cell-matrix adhesion	7	5	1.66	0.031190	0.0101600	BP
GO: 0007168	receptor guanylyl cyclase signaling path. . .	6	4	1.42	0.031270	0.0312700	BP
GO: 0005516	calmodulin binding	29	12	7.07	0.032040	0.0320400	MF
GO: 0005524	ATP binding	480	134	116.99	0.032940	0.0329400	MF
GO: 0016324	apical plasma membrane	50	18	11.62	0.033550	0.0279100	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0004523	RNA-DNA hybrid ribonuclease activity	6	4	1.46	0.034290	0.0342900	MF
GO: 0017147	Wnt-protein binding	6	4	1.46	0.034290	0.0342900	MF
GO: 0009062	fatty acid catabolic process	38	14	9.02	0.039300	0.0479100	BP
GO: 0046856	phosphatidylinositol dephosphorylation	9	5	2.14	0.039640	0.0396400	BP
GO: 0000307	cyclin-dependent protein kinase holoenzy. . .	8	5	1.86	0.041300	0.0199300	CC
GO: 0009931	calcium-dependent protein serine/threoni. . .	9	6	2.19	0.047040	0.0086900	MF
GO: 0038023	signaling receptor activity	193	62	47.04	0.047070	0.0077800	MF
GO: 0033613	activating transcription factor binding	9	5	2.19	0.047160	0.0440400	MF
GO: 0004439	phosphatidylinositol-4,5-bisphosphate 5-. . .	4	3	0.97	0.047250	0.0472500	MF
GO: 0015271	outward rectifier potassium channel acti. . .	4	3	0.97	0.047250	0.0472500	MF
GO: 0097730	non-motile cilium	22	9	5.11	0.049250	0.0492500	CC
GO: 0005201	extracellular matrix structural constitu. . .	15	7	3.66	0.049710	0.0497100	MF
GO: 0000978	RNA polymerase II cis-regulatory region . . .	42	16	10.24	0.053800	0.0328600	MF

Table 5: L3 cluster versus whole dataset

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0003735	structural constituent of ribosome	81	54	30.41	0.0000001	0.0000001	MF
GO: 0006412	translation	174	100	66.34	0.0000001	0.0000001	BP
GO: 0003677	DNA binding	477	210	179.06	0.0000160	0.0012700	MF
GO: 0003697	single-stranded DNA binding	20	15	7.51	0.0000550	0.0007200	MF
GO: 0005634	nucleus	1307	581	489.84	0.0001200	0.0000000	CC
GO: 0022625	cytosolic large ribosomal subunit	33	23	12.37	0.0001700	0.0001700	CC
GO: 0000786	nucleosome	37	25	13.87	0.0001900	0.0001900	CC
GO: 0006334	nucleosome assembly	29	20	11.06	0.0003100	0.0007200	BP
GO: 0046982	protein heterodimerization activity	48	30	18.02	0.0003700	0.0003700	MF
GO: 0003688	DNA replication origin binding	8	8	3.00	0.0003900	0.0003900	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0008340	determination of adult lifespan	160	82	61.00	0.0004000	0.0004000	BP
GO: 0005840	ribosome	91	61	34.11	0.0006000	0.0000000	CC
GO: 0009792	embryo development ending in birth or eg...	184	91	70.15	0.0009000	0.0009000	BP
GO: 0005737	cytoplasm	2126	902	796.79	0.0009300	0.0000000	CC
GO: 0033290	eukaryotic 48S preinitiation complex	7	7	2.62	0.0010300	0.0010300	CC
GO: 0000398	mRNA splicing, via spliceosome	75	43	28.59	0.0024000	0.0005200	BP
GO: 0022627	cytosolic small ribosomal subunit	16	12	6.00	0.0025400	0.0025400	CC
GO: 0005669	transcription factor TFIID complex	6	6	2.25	0.0027600	0.0027600	CC
GO: 0016282	eukaryotic 43S preinitiation complex	6	6	2.25	0.0027600	0.0027600	CC
GO: 0051123	RNA polymerase II preinitiation complex ...	9	8	3.43	0.0030400	0.0026300	BP
GO: 0000794	condensed nuclear chromosome	24	14	8.99	0.0044600	0.0302300	CC
GO: 0046716	muscle cell cellular homeostasis	8	7	3.05	0.0062000	0.0062000	BP
GO: 0080008	Cul4-RING E3 ubiquitin ligase complex	6	6	2.25	0.0073500	0.0027600	CC
GO: 0005687	U4 snRNP	5	5	1.87	0.0073700	0.0073700	CC
GO: 0008157	protein phosphatase 1 binding	5	5	1.88	0.0074300	0.0074300	MF
GO: 0061608	nuclear import signal receptor activity	5	5	1.88	0.0074300	0.0074300	MF
GO: 0071011	precatalytic spliceosome	11	9	4.12	0.0077400	0.0035000	CC
GO: 0000727	double-strand break repair via break-ind...	5	5	1.91	0.0080300	0.0080300	BP
GO: 0000462	maturation of SSU-rRNA from tricistronic...	12	10	4.58	0.0087000	0.0018100	BP
GO: 0000028	ribosomal small subunit assembly	10	8	3.81	0.0087400	0.0087400	BP
GO: 0019843	rRNA binding	23	15	8.63	0.0110900	0.0064300	MF
GO: 0071013	catalytic step 2 spliceosome	20	13	7.50	0.0113200	0.0114100	CC
GO: 0005686	U2 snRNP	7	6	2.62	0.0131100	0.0131100	CC
GO: 0008139	nuclear localization sequence binding	7	6	2.63	0.0132300	0.0132300	MF
GO: 0017025	TBP-class protein binding	7	6	2.63	0.0132300	0.0132300	MF
GO: 0072686	mitotic spindle	13	9	4.87	0.0168300	0.0203100	CC

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0005682	U5 snRNP	9	7	3.37	0.0168600	0.0168600	CC
GO: 0005814	centriole	9	7	3.37	0.0168600	0.0168600	CC
GO: 1904115	axon cytoplasm	9	7	3.37	0.0168600	0.0168600	CC
GO: 0003725	double-stranded RNA binding	9	7	3.38	0.0170300	0.0170300	MF
GO: 0003743	translation initiation factor activity	27	16	10.14	0.0176500	0.0176500	MF
GO: 0003682	chromatin binding	56	30	21.02	0.0177600	0.0101600	MF
GO: 0002119	nematode larval development	278	126	105.99	0.0189700	0.0067000	BP
GO: 0005884	actin filament	15	11	5.62	0.0190000	0.0051900	CC
GO: 0034719	SMN-Sm protein complex	4	4	1.50	0.0196900	0.0196900	CC
GO: 0042555	MCM complex	4	4	1.50	0.0196900	0.0196900	CC
GO: 0004861	cyclin-dependent protein serine/threonin...	4	4	1.50	0.0198100	0.0198100	MF
GO: 0017124	SH3 domain binding	4	4	1.50	0.0198100	0.0198100	MF
GO: 0003723	RNA binding	323	163	121.25	0.0198900	0.0000006	MF
GO: 0051539	4 iron, 4 sulfur cluster binding	19	12	7.13	0.0206600	0.0206600	MF

Table 6: Increasing cluster versus whole dataset

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0003700	DNA-binding transcription factor activit...	270	191	152.42	0.0000002	0.0000005	MF
GO: 0006355	regulation of transcription, DNA-templat...	486	315	270.17	0.0000016	0.0000072	BP
GO: 0042025	host cell nucleus	169	119	93.21	0.0000250	0.0000250	CC
GO: 0043565	sequence-specific DNA binding	279	187	157.50	0.0000620	0.0001300	MF
GO: 0045087	innate immune response	169	115	93.95	0.0010000	0.0005000	BP
GO: 0046777	protein autophosphorylation	25	19	13.90	0.0019000	0.0290900	BP
GO: 0016324	apical plasma membrane	50	39	27.58	0.0051000	0.0006400	CC
GO: 0000977	RNA polymerase II transcription regulato...	111	77	62.66	0.0054000	0.0032600	MF
GO: 0042048	olfactory behavior	20	17	11.12	0.0091000	0.0056200	BP

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0018105	peptidyl-serine phosphorylation	53	38	29.46	0.0094000	0.0115400	BP
GO: 0042803	protein homodimerization activity	28	22	15.81	0.0126000	0.0126200	MF
GO: 0008270	zinc ion binding	283	178	159.76	0.0136000	0.0136200	MF
GO: 0035556	intracellular signal transduction	274	171	152.32	0.0139000	0.0108000	BP
GO: 0016311	dephosphorylation	115	75	63.93	0.0140000	0.0213600	BP
GO: 0045167	asymmetric protein localization involved...	13	11	7.23	0.0152000	0.0294200	BP
GO: 0006636	unsaturated fatty acid biosynthetic proc...	7	7	3.89	0.0163000	0.0163400	BP
GO: 0006629	lipid metabolic process	334	219	185.67	0.0164000	0.0000720	BP
GO: 0040024	dauer larval development	57	44	31.69	0.0190000	0.0005500	BP
GO: 0030968	endoplasmic reticulum unfolded protein r...	35	26	19.46	0.0196000	0.0177000	BP
GO: 0032436	positive regulation of proteasomal ubiqu...	22	17	12.23	0.0212000	0.0303500	BP
GO: 0005912	adherens junction	25	19	13.79	0.0264000	0.0263800	CC
GO: 0035869	ciliary transition zone	6	6	3.31	0.0281000	0.0280800	CC
GO: 0045179	apical cortex	6	6	3.31	0.0281000	0.0280800	CC
GO: 0055114	oxidation-reduction process	359	217	199.57	0.0293000	0.0297000	BP
GO: 0006559	L-phenylalanine catabolic process	6	6	3.34	0.0294000	0.0294300	BP
GO: 0019367	fatty acid elongation, saturated fatty a...	6	6	3.34	0.0294000	0.0294300	BP
GO: 0034625	fatty acid elongation, monounsaturated f...	6	6	3.34	0.0294000	0.0294300	BP
GO: 0034626	fatty acid elongation, polyunsaturated f...	6	6	3.34	0.0294000	0.0294300	BP
GO: 1905516	positive regulation of fertilization	6	6	3.34	0.0294000	0.0294300	BP
GO: 0006357	regulation of transcription by RNA polym...	292	184	162.32	0.0318000	0.0046600	BP
GO: 0009922	fatty acid elongase activity	6	6	3.39	0.0323000	0.0322800	MF
GO: 0102336	3-oxo-arachidoyl-CoA synthase activity	6	6	3.39	0.0323000	0.0322800	MF
GO: 0102337	3-oxo-cerotoyl-CoA synthase activity	6	6	3.39	0.0323000	0.0322800	MF
GO: 0102338	3-oxo-lignoceronyl-CoA synthase activity	6	6	3.39	0.0323000	0.0322800	MF
GO: 0102756	very-long-chain 3-ketoacyl-CoA synthase ...	6	6	3.39	0.0323000	0.0322800	MF

GO.ID	Term	Annotated	Significant	Expected	pval	fisher	DB
GO: 0010468	regulation of gene expression	706	431	392.46	0.0351000	0.0007700	BP
GO: 0000132	establishment of mitotic spindle orienta...	27	20	15.01	0.0382000	0.0381700	BP
GO: 1990573	potassium ion import across plasma membr...	10	9	5.56	0.0413000	0.0252000	BP
GO: 0010494	cytoplasmic stress granule	12	10	6.62	0.0429000	0.0429100	CC
GO: 0046513	ceramide biosynthetic process	19	16	10.56	0.0461000	0.0087300	BP
GO: 2000294	positive regulation of defecation	6	6	3.34	0.0529000	0.0294300	BP
GO: 0002119	nematode larval development	278	182	154.54	0.0542000	0.0003400	BP
GO: 0035264	multicellular organism growth	74	53	41.14	0.0682000	0.0031700	BP
GO: 0048566	embryonic digestive tract development	20	16	11.12	0.0949000	0.0211500	BP
GO: 0042626	ATPase-coupled transmembrane transporter...	53	37	29.92	0.0996000	0.0317600	MF
GO: 0006631	fatty acid metabolic process	108	73	60.04	0.1128000	0.0067100	BP
GO: 0048856	anatomical structure development	957	567	531.99	0.1255000	0.0053000	BP
GO: 0040014	regulation of multicellular organism gro...	63	44	35.02	0.1551000	0.0140900	BP
GO: 0071944	cell periphery	632	369	348.59	0.1595000	0.0430000	CC
GO: 0045177	apical part of cell	59	47	32.54	0.1619000	0.0000690	CC

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