main

July 12, 2021

1 GO module enrichment

```python
[1]: import functools
     import numpy as np
     import pandas as pd
     import collections as cx
     from pybiomart import Dataset
     from gtfparse import read_gtf
     from scipy.stats import fisher_exact
     from statsmodels.stats.multitest import multipletests

     # GO analysis
     from goatools.base import download_go_basic_obo
     from goatools.base import download_ncbi_associations
     from goatools.obo_parser import GODag
     from goatools.anno.genetogo_reader import Gene2GoReader
     from goatools.goea.go_enrichment_ns import GOEnrichmentStudyNS
```

1.1 Functions

1.1.1 Cached functions

```python
[2]: @functools.lru_cache()
     def get_gtf_genes_df():
         gtf_df = read_gtf("/ceph/genome/human/gencode25/gtf.CHR/_m/gencode.v25.
      ↪annotation.gtf")
         return gtf_df[gtf_df["feature"] == "gene"][['gene_id', 'gene_name']]


     @functools.lru_cache()
     def get_wgcna_modules():
         return pd.read_csv("../../_m/modules.csv", index_col=0)


     @functools.lru_cache()
     def get_database():
         dataset = Dataset(name="hsapiens_gene_ensembl",
                           host="http://www.ensembl.org",
```

```
                                use_cache=True)
        db = dataset.query(attributes=["ensembl_gene_id",
                                       "external_gene_name",
                                       "entrezgene_id"],
                           use_attr_names=True).dropna(subset=['entrezgene_id'])
        return db
```

1.1.2 Simple functions

```
[3]: def convert2entrez(mod):
         df = get_wgcna_modules()[(get_wgcna_modules().module) == mod].copy()
         df["ensemblID"] = df.index.str.replace("\\..*", "", regex=True)
         return df.merge(get_database(), left_on='ensemblID',
                         right_on='ensembl_gene_id')


     def obo_annotation(alpha=0.05):
         # database annotation
         fn_obo = download_go_basic_obo()
         fn_gene2go = download_ncbi_associations() # must be gunzip to work
         obodag = GODag(fn_obo) # downloads most up-to-date
         anno_hs = Gene2GoReader(fn_gene2go, taxids=[9606])
         # get associations
         ns2assoc = anno_hs.get_ns2assc()
         for nspc, id2gos in ns2assoc.items():
             print("{NS} {N:,} annotated human genes".format(NS=nspc, N=len(id2gos)))
         goeaobj = GOEnrichmentStudyNS(
             get_database()['entrezgene_id'], # List of human genes with entrez IDs
             ns2assoc, # geneid/GO associations
             obodag, # Ontologies
             propagate_counts = False,
             alpha = alpha, # default significance cut-off
             methods = ['fdr_bh'])
         return goeaobj


     def run_goea(mod):
         df = convert2entrez(mod)
         geneids_study = {z[0]:z[1] for z in zip(df['entrezgene_id'],
     ↪df['external_gene_name'])}
         goeaobj = obo_annotation()
         goea_results_all = goeaobj.run_study(geneids_study)
         goea_results_sig = [r for r in goea_results_all if r.p_fdr_bh < 0.05]
         ctr = cx.Counter([r.NS for r in goea_results_sig])
         print('Significant results[{TOTAL}] = {BP} BP + {MF} MF + {CC} CC'.format(
             TOTAL=len(goea_results_sig),
             BP=ctr['BP'],  # biological_process
```

```
        MF=ctr['MF'],  # molecular_function
        CC=ctr['CC'])) # cellular_component
    goeaobj.wr_xlsx("GO_analysis_module_%s.xlsx" % mod, goea_results_sig)
    goeaobj.wr_txt("GO_analysis_module_%s.txt" % mod, goea_results_sig)
```

1.2 Gene annotation

```
[4]: gtf = get_gtf_genes_df()
     gtf.head(2)
```

```
INFO:root:Extracted GTF attributes: ['gene_id', 'gene_type', 'gene_status',
'gene_name', 'level', 'havana_gene', 'transcript_id', 'transcript_type',
'transcript_status', 'transcript_name', 'transcript_support_level', 'tag',
'havana_transcript', 'exon_number', 'exon_id', 'ont', 'protein_id', 'ccdsid']
```

```
[4]:            gene_id gene_name
     0   ENSG00000223972.5    DDX11L1
     12  ENSG00000227232.5     WASH7P
```

1.2.1 Load WGCNA module

```
[5]: wgcna_df = get_wgcna_modules().merge(gtf, left_index=True, right_on="gene_id",␣
     ↪how="left")
     wgcna_df.head(2)
```

```
[5]:         module              gene_id  gene_name
     12  greenyellow  ENSG00000227232.5      WASH7P
     25       brown  ENSG00000278267.1  MIR6859-1
```

```
[6]: wgcna_df[(wgcna_df.gene_id.str.startswith("chr"))]
```

```
[6]: Empty DataFrame
     Columns: [module, gene_id, gene_name]
     Index: []
```

```
[7]: wgcna_df[(wgcna_df.gene_name == 'DRD2')]
```

```
[7]:         module              gene_id gene_name
     1445279  brown  ENSG00000149295.13      DRD2
```

```
[8]: wgcna_df.to_csv("module_annotated.csv", index=False)
```

1.3 GO enrichment for each cluster

```
[9]: for mod in get_wgcna_modules().module.unique():
         run_goea(mod)
```

```
requests.get(http://purl.obolibrary.org/obo/go/go-basic.obo, stream=True)
  WROTE: go-basic.obo
```

```
FTP RETR ftp.ncbi.nlm.nih.gov gene/DATA gene2go.gz -> gene2go.gz
  gunzip gene2go.gz
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.345673 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 406 IDs … 90%    366 of
406 study items found in association
100%    406 of    406 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,573 GO terms are associated with    366 of    406 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      29 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 406 IDs … 93%    379 of
406 study items found in association
100%    406 of    406 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     449 GO terms are associated with    379 of    406 study items
  METHOD fdr_bh:
      32 GO terms found significant (< 0.05=alpha) ( 32 enriched +   0
purified): statsmodels fdr_bh
     357 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 406 IDs … 94%    381 of
406 study items found in association
100%    406 of    406 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
```

```
      557 GO terms are associated with    381 of    406 study items
   METHOD fdr_bh:
        4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
      330 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[38] = 2 BP + 4 MF + 32 CC
       38 items WROTE: GO_analysis_module_greenyellow.xlsx
       38 GOEA results for    385 study items. WROTE:
GO_analysis_module_greenyellow.txt
   EXISTS: go-basic.obo
   EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:06.186145 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1194 IDs … 81%    962 of
1,194 study items found in association
100%  1,194 of  1,194 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   3,203 GO terms are associated with    962 of  1,194 study items
   METHOD fdr_bh:
        9 GO terms found significant (< 0.05=alpha) (  8 enriched +   1
purified): statsmodels fdr_bh
      166 study items associated with significant GO IDs (enriched)
        1 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1194 IDs … 85%  1,015 of
1,194 study items found in association
100%  1,194 of  1,194 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     641 GO terms are associated with  1,015 of  1,194 study items
   METHOD fdr_bh:
       21 GO terms found significant (< 0.05=alpha) ( 21 enriched +   0
```

purified): statsmodels fdr_bh
        838 study items associated with significant GO IDs (enriched)
          0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1194 IDs … 84% 1,003 of
1,194 study items found in association
100% 1,194 of 1,194 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
   1,097 GO terms are associated with 1,003 of 1,194 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) (15 enriched +   2
purified): statsmodels fdr_bh
        864 study items associated with significant GO IDs (enriched)
         10 study items associated with significant GO IDs (purified)
Significant results[47] = 9 BP + 17 MF + 21 CC
      47 items WROTE: GO_analysis_module_brown.xlsx
      47 GOEA results for 1007 study items. WROTE: GO_analysis_module_brown.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.742197 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 3509 IDs … 74% 2,609 of
3,509 study items found in association
100% 3,509 of 3,509 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   5,348 GO terms are associated with 2,609 of 3,509 study items
  METHOD fdr_bh:
      12 GO terms found significant (< 0.05=alpha) (9 enriched +   3
purified): statsmodels fdr_bh
      589 study items associated with significant GO IDs (enriched)
      103 study items associated with significant GO IDs (purified)

```
Run CC Gene Ontology Analysis: current study set of 3509 IDs … 79%  2,773 of
3,509 study items found in association
100%  3,509 of  3,509 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     932 GO terms are associated with  2,773 of  3,509 study items
  METHOD fdr_bh:
      28 GO terms found significant (< 0.05=alpha) ( 26 enriched +   2
purified): statsmodels fdr_bh
   1,952 study items associated with significant GO IDs (enriched)
      20 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 3509 IDs … 74%  2,612 of
3,509 study items found in association
100%  3,509 of  3,509 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
   1,876 GO terms are associated with  2,612 of  3,509 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  5 enriched +   2
purified): statsmodels fdr_bh
   2,049 study items associated with significant GO IDs (enriched)
      24 study items associated with significant GO IDs (purified)
Significant results[47] = 12 BP + 7 MF + 28 CC
     47 items WROTE: GO_analysis_module_grey.xlsx
     47 GOEA results for  2546 study items. WROTE: GO_analysis_module_grey.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:06.288791 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1507 IDs … 82%  1,236 of
1,507 study items found in association
100%  1,507 of  1,507 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
```

```
    12,438 GO terms are associated with 17,849 of 29,107 population items
     4,323 GO terms are associated with  1,236 of  1,507 study items
   METHOD fdr_bh:
       17 GO terms found significant (< 0.05=alpha) ( 15 enriched +   2
purified): statsmodels fdr_bh
      281 study items associated with significant GO IDs (enriched)
        8 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 1507 IDs … 85%  1,277 of
1,507 study items found in association
100%  1,507 of  1,507 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
      696 GO terms are associated with  1,277 of  1,507 study items
   METHOD fdr_bh:
       53 GO terms found significant (< 0.05=alpha) ( 53 enriched +   0
purified): statsmodels fdr_bh
    1,223 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 1507 IDs … 82%  1,236 of
1,507 study items found in association
100%  1,507 of  1,507 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
    1,290 GO terms are associated with  1,236 of  1,507 study items
   METHOD fdr_bh:
       18 GO terms found significant (< 0.05=alpha) ( 16 enriched +   2
purified): statsmodels fdr_bh
      979 study items associated with significant GO IDs (enriched)
        2 study items associated with significant GO IDs (purified)
Significant results[88] = 17 BP + 18 MF + 53 CC
       88 items WROTE: GO_analysis_module_blue.xlsx
       88 GOEA results for  1297 study items. WROTE: GO_analysis_module_blue.txt
   EXISTS: go-basic.obo
   EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:07.435127 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association
```

```
Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 99 IDs … 86%     85 of
99 study items found in association
100%     99 of     99 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     402 GO terms are associated with     85 of     99 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
       9 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 99 IDs … 87%     86 of
99 study items found in association
100%     99 of     99 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     160 GO terms are associated with     86 of     99 study items
  METHOD fdr_bh:
       8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
      53 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 99 IDs … 81%     80 of
99 study items found in association
100%     99 of     99 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     164 GO terms are associated with     80 of     99 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
      67 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[16] = 3 BP + 5 MF + 8 CC
     16 items WROTE: GO_analysis_module_darkgreen.xlsx
     16 GOEA results for    80 study items. WROTE:
GO_analysis_module_darkgreen.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:06.436543 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
```

```
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 214 IDs … 89%    191 of
214 study items found in association
100%    214 of    214 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,571 GO terms are associated with    191 of    214 study items
  METHOD fdr_bh:
     177 GO terms found significant (< 0.05=alpha) (177 enriched +   0
purified): statsmodels fdr_bh
     154 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 214 IDs … 93%    199 of
214 study items found in association
100%    214 of    214 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     229 GO terms are associated with    199 of    214 study items
  METHOD fdr_bh:
      46 GO terms found significant (< 0.05=alpha) ( 46 enriched +   0
purified): statsmodels fdr_bh
     187 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 214 IDs … 90%    193 of
214 study items found in association
100%    214 of    214 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     380 GO terms are associated with    193 of    214 study items
  METHOD fdr_bh:
      33 GO terms found significant (< 0.05=alpha) ( 33 enriched +   0
purified): statsmodels fdr_bh
     175 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Significant results[256] = 177 BP + 33 MF + 46 CC
    256 items WROTE: GO_analysis_module_lightcyan.xlsx
    256 GOEA results for   198 study items. WROTE:
GO_analysis_module_lightcyan.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:08.690241 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1933 IDs … 84%  1,626 of
1,933 study items found in association
100%  1,933 of  1,933 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   4,585 GO terms are associated with  1,626 of  1,933 study items
  METHOD fdr_bh:
      36 GO terms found significant (< 0.05=alpha) ( 33 enriched +   3
purified): statsmodels fdr_bh
     733 study items associated with significant GO IDs (enriched)
      16 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1933 IDs … 89%  1,718 of
1,933 study items found in association
100%  1,933 of  1,933 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     816 GO terms are associated with  1,718 of  1,933 study items
  METHOD fdr_bh:
      57 GO terms found significant (< 0.05=alpha) ( 57 enriched +   0
purified): statsmodels fdr_bh
   1,631 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1933 IDs … 86%  1,666 of
1,933 study items found in association
```

```
100%  1,933 of  1,933 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
   1,391 GO terms are associated with  1,666 of  1,933 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 28 enriched +   2
purified): statsmodels fdr_bh
   1,446 study items associated with significant GO IDs (enriched)
       4 study items associated with significant GO IDs (purified)
Significant results[123] = 36 BP + 30 MF + 57 CC
    123 items WROTE: GO_analysis_module_turquoise.xlsx
    123 GOEA results for  1755 study items. WROTE:
GO_analysis_module_turquoise.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.387755 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 423 IDs … 85%    361 of
423 study items found in association
100%    423 of    423 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,435 GO terms are associated with    361 of    423 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      23 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 423 IDs … 88%    374 of
423 study items found in association
100%    423 of    423 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
```

```
    377 GO terms are associated with     374 of     423 study items
  METHOD fdr_bh:
      7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
    233 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 423 IDs … 89%     375 of
423 study items found in association
100%     423 of     423 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,839 of 29,107 population items
    567 GO terms are associated with     375 of     423 study items
  METHOD fdr_bh:
      2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
    277 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[11] = 2 BP + 2 MF + 7 CC
    11 items WROTE: GO_analysis_module_pink.xlsx
    11 GOEA results for   347 study items. WROTE: GO_analysis_module_pink.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.575022 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 61 IDs … 87%     53 of
61 study items found in association
100%     61 of     61 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
    292 GO terms are associated with     53 of     61 study items
  METHOD fdr_bh:
      1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
```

3 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 61 IDs … 97%   59 of
61 study items found in association
100%   61 of   61 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
      109 GO terms are associated with   59 of   61 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 61 IDs … 84%   51 of
61 study items found in association
100%   61 of   61 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
      111 GO terms are associated with   51 of   61 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[1] = 1 BP + 0 MF + 0 CC
      1 items WROTE: GO_analysis_module_violet.xlsx
      1 GOEA results for   3 study items. WROTE: GO_analysis_module_violet.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.735098 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 453 IDs … 91%   414 of

```
453 study items found in association
100%    453 of    453 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   2,731 GO terms are associated with    414 of    453 study items
  METHOD fdr_bh:
     104 GO terms found significant (< 0.05=alpha) (103 enriched +   1
purified): statsmodels fdr_bh
     251 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 453 IDs … 94%    427 of
453 study items found in association
100%    453 of    453 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     378 GO terms are associated with    427 of    453 study items
  METHOD fdr_bh:
      55 GO terms found significant (< 0.05=alpha) ( 55 enriched +   0
purified): statsmodels fdr_bh
     395 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 453 IDs … 92%    416 of
453 study items found in association
100%    453 of    453 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     726 GO terms are associated with    416 of    453 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) ( 17 enriched +   0
purified): statsmodels fdr_bh
     350 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[176] = 104 BP + 17 MF + 55 CC
    176 items WROTE: GO_analysis_module_magenta.xlsx
    176 GOEA results for   421 study items. WROTE:
GO_analysis_module_magenta.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.832440 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
```

```
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 127 IDs … 72%     92 of
127 study items found in association
100%    127 of    127 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     631 GO terms are associated with    92 of    127 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 127 IDs … 72%     92 of
127 study items found in association
100%    127 of    127 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     195 GO terms are associated with    92 of    127 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 127 IDs … 74%     94 of
127 study items found in association
100%    127 of    127 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     168 GO terms are associated with    94 of    127 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
      0 items. NOT WRITING GO_analysis_module_grey60.xlsx
      0 GOEA results. NOT WRITING GO_analysis_module_grey60.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
```

```
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.922303 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 267 IDs … 78%    209 of
267 study items found in association
100%    267 of    267 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     997 GO terms are associated with    209 of    267 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 267 IDs … 82%    220 of
267 study items found in association
100%    267 of    267 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     299 GO terms are associated with    220 of    267 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     122 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 267 IDs … 81%    216 of
267 study items found in association
100%    267 of    267 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     388 GO terms are associated with    216 of    267 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
```

purified): statsmodels fdr_bh
       164 study items associated with significant GO IDs (enriched)
         0 study items associated with significant GO IDs (purified)
Significant results[5] = 0 BP + 1 MF + 4 CC
       5 items WROTE: GO_analysis_module_salmon.xlsx
       5 GOEA results for   187 study items. WROTE: GO_analysis_module_salmon.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.328531 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 143 IDs … 95%   136 of
143 study items found in association
100%   143 of   143 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     991 GO terms are associated with   136 of   143 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (2 enriched +   0
purified): statsmodels fdr_bh
       5 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 143 IDs … 97%   138 of
143 study items found in association
100%   143 of   143 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     272 GO terms are associated with   138 of   143 study items
  METHOD fdr_bh:
      16 GO terms found significant (< 0.05=alpha) (16 enriched +   0
purified): statsmodels fdr_bh
     126 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

```
Run MF Gene Ontology Analysis: current study set of 143 IDs … 97%    139 of
143 study items found in association
100%    143 of    143 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     282 GO terms are associated with    139 of    143 study items
  METHOD fdr_bh:
      10 GO terms found significant (< 0.05=alpha) ( 10 enriched +   0
purified): statsmodels fdr_bh
     128 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[28] = 2 BP + 10 MF + 16 CC
     28 items WROTE: GO_analysis_module_royalblue.xlsx
     28 GOEA results for   139 study items. WROTE:
GO_analysis_module_royalblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.401638 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 85 IDs … 92%    78 of
85 study items found in association
100%    85 of    85 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     551 GO terms are associated with    78 of    85 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 85 IDs … 92%    78 of
85 study items found in association
100%    85 of    85 study items found in population(29107)
```

```
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     195 GO terms are associated with     78 of     85 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
      50 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 85 IDs … 89%     76 of
85 study items found in association
100%     85 of     85 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     186 GO terms are associated with     76 of     85 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      65 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[4] = 0 BP + 1 MF + 3 CC
       4 items WROTE: GO_analysis_module_darkorange.xlsx
       4 GOEA results for    72 study items. WROTE:
GO_analysis_module_darkorange.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.536354 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 73 IDs … 86%     63 of
73 study items found in association
100%     73 of     73 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     518 GO terms are associated with     63 of     73 study items
```

```
  METHOD fdr_bh:
      16 GO terms found significant (< 0.05=alpha) ( 16 enriched +   0
purified): statsmodels fdr_bh
      28 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 73 IDs … 95%     69 of
73 study items found in association
100%     73 of     73 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     112 GO terms are associated with     69 of     73 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
      19 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 73 IDs … 90%     66 of
73 study items found in association
100%     73 of     73 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     199 GO terms are associated with     66 of     73 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[19] = 16 BP + 0 MF + 3 CC
      19 items WROTE: GO_analysis_module_saddlebrown.xlsx
      19 GOEA results for    33 study items. WROTE:
GO_analysis_module_saddlebrown.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.451756 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association
```

```
Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 107 IDs … 85%     91 of
107 study items found in association
100%     107 of     107 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     455 GO terms are associated with     91 of     107 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
       3 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 107 IDs … 90%     96 of
107 study items found in association
100%     107 of     107 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     169 GO terms are associated with     96 of     107 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 107 IDs … 88%     94 of
107 study items found in association
100%     107 of     107 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     187 GO terms are associated with     94 of     107 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[1] = 1 BP + 0 MF + 0 CC
      1 items WROTE: GO_analysis_module_darkturquoise.xlsx
      1 GOEA results for     3 study items. WROTE:
GO_analysis_module_darkturquoise.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.873166 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
```

```
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 737 IDs … 68%    498 of
737 study items found in association
100%    737 of    737 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,739 GO terms are associated with   498 of    737 study items
  METHOD fdr_bh:
      0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
      0 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 737 IDs … 74%    544 of
737 study items found in association
100%    737 of    737 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     415 GO terms are associated with   544 of    737 study items
  METHOD fdr_bh:
      2 GO terms found significant (< 0.05=alpha) (  1 enriched +   1
purified): statsmodels fdr_bh
    189 study items associated with significant GO IDs (enriched)
     71 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 737 IDs … 72%    529 of
737 study items found in association
100%    737 of    737 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     608 GO terms are associated with   529 of    737 study items
  METHOD fdr_bh:
      2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
    409 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[4] = 0 BP + 2 MF + 2 CC
```

```
     4 items WROTE: GO_analysis_module_yellow.xlsx
     4 GOEA results for   450 study items. WROTE: GO_analysis_module_yellow.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.974234 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 98 IDs … 86%     84 of
98 study items found in association
100%     98 of     98 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     536 GO terms are associated with     84 of     98 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 98 IDs … 87%     85 of
98 study items found in association
100%     98 of     98 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     161 GO terms are associated with     85 of     98 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 98 IDs … 89%     87 of
98 study items found in association
100%     98 of     98 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
```

```
   4,434 GO terms are associated with 17,839 of 29,107 population items
     180 GO terms are associated with     87 of     98 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      67 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[1] = 0 BP + 1 MF + 0 CC
       1 items WROTE: GO_analysis_module_darkgrey.xlsx
       1 GOEA results for    67 study items. WROTE:
GO_analysis_module_darkgrey.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.290376 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 341 IDs … 74%    252 of
341 study items found in association
100%    341 of    341 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,227 GO terms are associated with    252 of    341 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 341 IDs … 82%    279 of
341 study items found in association
100%    341 of    341 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     337 GO terms are associated with    279 of    341 study items
  METHOD fdr_bh:
```

```
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     141 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 341 IDs … 77%    261 of
341 study items found in association
100%    341 of    341 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     436 GO terms are associated with    261 of    341 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
     192 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[4] = 0 BP + 1 MF + 3 CC
       4 items WROTE: GO_analysis_module_black.xlsx
       4 GOEA results for   229 study items. WROTE: GO_analysis_module_black.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.075495 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 911 IDs … 92%    834 of
911 study items found in association
100%    911 of    911 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   2,843 GO terms are associated with    834 of    911 study items
  METHOD fdr_bh:
      45 GO terms found significant (< 0.05=alpha) ( 42 enriched +   3
purified): statsmodels fdr_bh
     409 study items associated with significant GO IDs (enriched)
       8 study items associated with significant GO IDs (purified)
```

```
Run CC Gene Ontology Analysis: current study set of 911 IDs … 95%    861 of
911 study items found in association
100%    911 of    911 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     668 GO terms are associated with    861 of    911 study items
  METHOD fdr_bh:
      49 GO terms found significant (< 0.05=alpha) ( 48 enriched +   1
purified): statsmodels fdr_bh
     804 study items associated with significant GO IDs (enriched)
      18 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 911 IDs … 93%    843 of
911 study items found in association
100%    911 of    911 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     901 GO terms are associated with    843 of    911 study items
  METHOD fdr_bh:
      55 GO terms found significant (< 0.05=alpha) ( 53 enriched +   2
purified): statsmodels fdr_bh
     786 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[149] = 45 BP + 55 MF + 49 CC
    149 items WROTE: GO_analysis_module_green.xlsx
    149 GOEA results for   862 study items. WROTE: GO_analysis_module_green.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.103439 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 44 IDs … 89%    39 of
44 study items found in association
100%    44 of    44 study items found in population(29107)
```

```
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     331 GO terms are associated with     39 of     44 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
       3 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 44 IDs … 93%     41 of
44 study items found in association
100%     44 of     44 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     142 GO terms are associated with     41 of     44 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      26 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 44 IDs … 91%     40 of
44 study items found in association
100%     44 of     44 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     124 GO terms are associated with     40 of     44 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[3] = 1 BP + 0 MF + 2 CC
       3 items WROTE: GO_analysis_module_plum1.xlsx
       3 GOEA results for    27 study items. WROTE: GO_analysis_module_plum1.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.497804 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
```

```
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 355 IDs … 91%    324 of
355 study items found in association
100%    355 of    355 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,606 GO terms are associated with    324 of    355 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
      79 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 355 IDs … 95%    337 of
355 study items found in association
100%    355 of    355 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     469 GO terms are associated with    337 of    355 study items
  METHOD fdr_bh:
      40 GO terms found significant (< 0.05=alpha) ( 40 enriched +   0
purified): statsmodels fdr_bh
     319 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 355 IDs … 90%    321 of
355 study items found in association
100%    355 of    355 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     529 GO terms are associated with    321 of    355 study items
  METHOD fdr_bh:
      10 GO terms found significant (< 0.05=alpha) ( 10 enriched +   0
purified): statsmodels fdr_bh
     288 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[59] = 9 BP + 10 MF + 40 CC
      59 items WROTE: GO_analysis_module_tan.xlsx
      59 GOEA results for   333 study items. WROTE: GO_analysis_module_tan.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.366670 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
```

```
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 89 IDs … 96%     85 of
89 study items found in association
100%     89 of     89 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     585 GO terms are associated with     85 of     89 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
       5 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 89 IDs … 97%     86 of
89 study items found in association
100%     89 of     89 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     169 GO terms are associated with     86 of     89 study items
  METHOD fdr_bh:
       8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
      67 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 89 IDs … 98%     87 of
89 study items found in association
100%     89 of     89 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     188 GO terms are associated with     87 of     89 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      74 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Significant results[10] = 1 BP + 1 MF + 8 CC
     10 items WROTE: GO_analysis_module_white.xlsx
     10 GOEA results for    81 study items. WROTE: GO_analysis_module_white.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.643448 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 782 IDs … 88%    692 of
782 study items found in association
100%    782 of    782 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   2,882 GO terms are associated with    692 of    782 study items
  METHOD fdr_bh:
      26 GO terms found significant (< 0.05=alpha) ( 25 enriched +   1
purified): statsmodels fdr_bh
     249 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 782 IDs … 93%    727 of
782 study items found in association
100%    782 of    782 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     577 GO terms are associated with    727 of    782 study items
  METHOD fdr_bh:
      44 GO terms found significant (< 0.05=alpha) ( 44 enriched +   0
purified): statsmodels fdr_bh
     687 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 782 IDs … 91%    713 of
782 study items found in association
100%    782 of    782 study items found in population(29107)
```

```
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     897 GO terms are associated with    713 of    782 study items
  METHOD fdr_bh:
      11 GO terms found significant (< 0.05=alpha) ( 10 enriched +   1
purified): statsmodels fdr_bh
     598 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[81] = 26 BP + 11 MF + 44 CC
     81 items WROTE: GO_analysis_module_red.xlsx
     81 GOEA results for   734 study items. WROTE: GO_analysis_module_red.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.669227 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 365 IDs … 78%    286 of
365 study items found in association
100%    365 of    365 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     938 GO terms are associated with    286 of    365 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      56 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 365 IDs … 83%    304 of
365 study items found in association
100%    365 of    365 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     291 GO terms are associated with    304 of    365 study items
  METHOD fdr_bh:
```

```
     6 GO terms found significant (< 0.05=alpha) (  5 enriched +   1
purified): statsmodels fdr_bh
     187 study items associated with significant GO IDs (enriched)
      28 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 365 IDs … 86%    315 of
365 study items found in association
100%    365 of    365 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     366 GO terms are associated with    315 of    365 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
     264 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[13] = 1 BP + 6 MF + 6 CC
      13 items WROTE: GO_analysis_module_purple.xlsx
      13 GOEA results for   287 study items. WROTE: GO_analysis_module_purple.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.247703 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 79 IDs … 92%     73 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     518 GO terms are associated with     73 of     79 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      14 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Run CC Gene Ontology Analysis: current study set of 79 IDs … 96%    76 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     133 GO terms are associated with    76 of    79 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
      33 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 79 IDs … 94%    74 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     177 GO terms are associated with    74 of    79 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[2] = 1 BP + 0 MF + 1 CC
      2 items WROTE: GO_analysis_module_skyblue.xlsx
      2 GOEA results for    44 study items. WROTE:
GO_analysis_module_skyblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.228906 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 140 IDs … 86%    121 of
140 study items found in association
```

```
100%    140 of    140 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     702 GO terms are associated with    121 of    140 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 140 IDs … 91%    127 of
140 study items found in association
100%    140 of    140 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     215 GO terms are associated with    127 of    140 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      71 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 140 IDs … 89%    125 of
140 study items found in association
100%    140 of    140 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     239 GO terms are associated with    125 of    140 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
     104 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[3] = 0 BP + 1 MF + 2 CC
       3 items WROTE: GO_analysis_module_lightyellow.xlsx
       3 GOEA results for   112 study items. WROTE:
GO_analysis_module_lightyellow.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.777264 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association
```

```
Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 249 IDs … 92%     228 of
249 study items found in association
100%     249 of     249 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
   1,466 GO terms are associated with     228 of     249 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
      23 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 249 IDs … 94%     233 of
249 study items found in association
100%     249 of     249 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     298 GO terms are associated with     233 of     249 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
     181 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 249 IDs … 93%     232 of
249 study items found in association
100%     249 of     249 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     436 GO terms are associated with     232 of     249 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
     187 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[12] = 3 BP + 2 MF + 7 CC
     12 items WROTE: GO_analysis_module_midnightblue.xlsx
     12 GOEA results for   216 study items. WROTE:
GO_analysis_module_midnightblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
```

```
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.045340 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 74 IDs … 96%    71 of
74 study items found in association
100%    74 of    74 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
    423 GO terms are associated with    71 of    74 study items
  METHOD fdr_bh:
     10 GO terms found significant (< 0.05=alpha) ( 10 enriched +   0
purified): statsmodels fdr_bh
     32 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 74 IDs … 97%    72 of
74 study items found in association
100%    74 of    74 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
    165 GO terms are associated with    72 of    74 study items
  METHOD fdr_bh:
     28 GO terms found significant (< 0.05=alpha) ( 28 enriched +   0
purified): statsmodels fdr_bh
     69 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 74 IDs … 97%    72 of
74 study items found in association
100%    74 of    74 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
    131 GO terms are associated with    72 of    74 study items
  METHOD fdr_bh:
      7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
```

```
purified): statsmodels fdr_bh
      70 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[45] = 10 BP + 7 MF + 28 CC
     45 items WROTE: GO_analysis_module_paleturquoise.xlsx
     45 GOEA results for    73 study items. WROTE:
GO_analysis_module_paleturquoise.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.419518 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 43 IDs … 81%    35 of
43 study items found in association
100%    43 of    43 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     341 GO terms are associated with    35 of    43 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 43 IDs … 81%    35 of
43 study items found in association
100%    43 of    43 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
      96 GO terms are associated with    35 of    43 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Run MF Gene Ontology Analysis: current study set of 43 IDs … 84%     36 of
43 study items found in association
100%     43 of     43 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     113 GO terms are associated with     36 of     43 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
      0 items. NOT WRITING GO_analysis_module_darkolivegreen.xlsx
      0 GOEA results. NOT WRITING GO_analysis_module_darkolivegreen.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.553703 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 275 IDs … 87%     240 of
275 study items found in association
100%     275 of     275 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     875 GO terms are associated with    240 of     275 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      59 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 275 IDs … 92%     254 of
275 study items found in association
100%     275 of     275 study items found in population(29107)
```

```
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     273 GO terms are associated with    254 of    275 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
     187 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 275 IDs … 89%    244 of
275 study items found in association
100%    275 of    275 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     319 GO terms are associated with    244 of    275 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
     221 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[13] = 2 BP + 6 MF + 5 CC
     13 items WROTE: GO_analysis_module_cyan.xlsx
     13 GOEA results for   237 study items. WROTE: GO_analysis_module_cyan.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.340845 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 79 IDs … 89%    70 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     601 GO terms are associated with     70 of     79 study items
  METHOD fdr_bh:
```

```
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 79 IDs … 91%     72 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     155 GO terms are associated with     72 of     79 study items
  METHOD fdr_bh:
        3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
       47 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 79 IDs … 85%     67 of
79 study items found in association
100%     79 of     79 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     181 GO terms are associated with     67 of     79 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[3] = 0 BP + 0 MF + 3 CC
        3 items WROTE: GO_analysis_module_orange.xlsx
        3 GOEA results for    47 study items. WROTE: GO_analysis_module_orange.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.016457 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association
```

Run BP Gene Ontology Analysis: current study set of 78 IDs … 72%   56 of
78 study items found in association
100%   78 of   78 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     255 GO terms are associated with   56 of   78 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 78 IDs … 85%   66 of
78 study items found in association
100%   78 of   78 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
      92 GO terms are associated with   66 of   78 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 78 IDs … 85%   66 of
78 study items found in association
100%   78 of   78 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     117 GO terms are associated with   66 of   78 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
      0 items. NOT WRITING GO_analysis_module_steelblue.xlsx
      0 GOEA results. NOT WRITING GO_analysis_module_steelblue.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.794144 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

```
Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 165 IDs … 91%    150 of
165 study items found in association
100%     165 of     165 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     893 GO terms are associated with    150 of    165 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      16 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 165 IDs … 94%    155 of
165 study items found in association
100%     165 of     165 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     277 GO terms are associated with    155 of    165 study items
  METHOD fdr_bh:
      16 GO terms found significant (< 0.05=alpha) ( 16 enriched +   0
purified): statsmodels fdr_bh
     137 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 165 IDs … 93%    154 of
165 study items found in association
100%     165 of     165 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     304 GO terms are associated with    154 of    165 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     129 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[22] = 2 BP + 4 MF + 16 CC
      22 items WROTE: GO_analysis_module_lightgreen.xlsx
      22 GOEA results for   150 study items. WROTE:
GO_analysis_module_lightgreen.txt
```

```
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.215976 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes


Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association


Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association


Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association


Run BP Gene Ontology Analysis: current study set of 139 IDs … 90%    125 of
139 study items found in association
100%    139 of    139 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     666 GO terms are associated with    125 of    139 study items
  METHOD fdr_bh:
       0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
       0 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 139 IDs … 93%    129 of
139 study items found in association
100%    139 of    139 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     226 GO terms are associated with    129 of    139 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
      91 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 139 IDs … 89%    124 of
139 study items found in association
100%    139 of    139 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     221 GO terms are associated with    124 of    139 study items
```

```
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
     107 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[5] = 0 BP + 1 MF + 4 CC
      5 items WROTE: GO_analysis_module_darkred.xlsx
      5 GOEA results for   121 study items. WROTE:
GO_analysis_module_darkred.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.205761 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 48 IDs … 85%     41 of
48 study items found in association
100%     48 of     48 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     482 GO terms are associated with     41 of     48 study items
  METHOD fdr_bh:
      23 GO terms found significant (< 0.05=alpha) ( 23 enriched +   0
purified): statsmodels fdr_bh
      19 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 48 IDs … 90%     43 of
48 study items found in association
100%     48 of     48 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     124 GO terms are associated with     43 of     48 study items
  METHOD fdr_bh:
      15 GO terms found significant (< 0.05=alpha) ( 15 enriched +   0
purified): statsmodels fdr_bh
```

```
        38 study items associated with significant GO IDs (enriched)
         0 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 48 IDs … 94%    45 of
48 study items found in association
100%    48 of    48 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     159 GO terms are associated with    45 of    48 study items
  METHOD fdr_bh:
      22 GO terms found significant (< 0.05=alpha) ( 22 enriched +   0
purified): statsmodels fdr_bh
      41 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[60] = 23 BP + 22 MF + 15 CC
     60 items WROTE: GO_analysis_module_darkmagenta.xlsx
     60 GOEA results for    43 study items. WROTE:
GO_analysis_module_darkmagenta.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.537411 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 45 IDs … 96%    43 of
45 study items found in association
100%    45 of    45 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,849 of 29,107 population items
     380 GO terms are associated with    43 of    45 study items
  METHOD fdr_bh:
       2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
       5 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
```

```
Run CC Gene Ontology Analysis: current study set of 45 IDs … 96%      43 of
45 study items found in association
100%      45 of      45 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
   1,756 GO terms are associated with 18,713 of 29,107 population items
     115 GO terms are associated with      43 of      45 study items
  METHOD fdr_bh:
       8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
      35 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 45 IDs … 91%      41 of
45 study items found in association
100%      45 of      45 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
   4,434 GO terms are associated with 17,839 of 29,107 population items
     100 GO terms are associated with      41 of      45 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
      36 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[17] = 2 BP + 7 MF + 8 CC
      17 items WROTE: GO_analysis_module_yellowgreen.xlsx
      17 GOEA results for    40 study items. WROTE:
GO_analysis_module_yellowgreen.txt
  EXISTS: go-basic.obo
  EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.739587 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association

Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 46 IDs … 85%      39 of
46 study items found in association
100%      46 of      46 study items found in population(29107)
```

```
Calculating 12,438 uncorrected p-values using fisher
   12,438 GO terms are associated with 17,849 of 29,107 population items
      393 GO terms are associated with      39 of      46 study items
   METHOD fdr_bh:
        8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
       15 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 46 IDs … 98%     45 of
46 study items found in association
100%     46 of     46 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
       91 GO terms are associated with     45 of     46 study items
   METHOD fdr_bh:
        6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
       24 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 46 IDs … 93%     43 of
46 study items found in association
100%     46 of     46 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
      108 GO terms are associated with     43 of     46 study items
   METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[14] = 8 BP + 0 MF + 6 CC
      14 items WROTE: GO_analysis_module_sienna3.xlsx
      14 GOEA results for    28 study items. WROTE:
GO_analysis_module_sienna3.txt
   EXISTS: go-basic.obo
   EXISTS: gene2go
go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:05.058004 330,320 annotations, 20,687 genes, 18,684 GOs, 1 taxids READ:
gene2go
MF 18,191 annotated human genes
CC 19,424 annotated human genes
BP 18,506 annotated human genes

Load BP Gene Ontology Analysis …
 70% 20,237 of 29,107 population items found in association
```

```
Load CC Gene Ontology Analysis …
 74% 21,430 of 29,107 population items found in association

Load MF Gene Ontology Analysis …
 70% 20,355 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 43 IDs … 88%     38 of
43 study items found in association
100%     43 of     43 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
   12,438 GO terms are associated with 17,849 of 29,107 population items
      245 GO terms are associated with     38 of     43 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 43 IDs … 91%     39 of
43 study items found in association
100%     43 of     43 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,713 of 29,107 population items
       94 GO terms are associated with     39 of     43 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 43 IDs … 86%     37 of
43 study items found in association
100%     43 of     43 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,839 of 29,107 population items
       97 GO terms are associated with     37 of     43 study items
  METHOD fdr_bh:
        0 GO terms found significant (< 0.05=alpha) (  0 enriched +   0
purified): statsmodels fdr_bh
        0 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[0] = 0 BP + 0 MF + 0 CC
      0 items. NOT WRITING GO_analysis_module_skyblue3.xlsx
      0 GOEA results. NOT WRITING GO_analysis_module_skyblue3.txt
```

[ ]: