main

July 12, 2021

1 GO module enrichment

```
[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

```
[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   grey   ENSG00000227232.5     WASH7P
     25   grey   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    grey   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:0:00:05.511399 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 5238 IDs … 71%  3,721 of
5,238 study items found in association
100%  5,238 of  5,238 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
   6,528 GO terms are associated with  3,721 of  5,238 study items
  METHOD fdr_bh:
      18 GO terms found significant (< 0.05=alpha) ( 15 enriched +   3
purified): statsmodels fdr_bh
     812 study items associated with significant GO IDs (enriched)
     128 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 5238 IDs … 75%  3,949 of
5,238 study items found in association
100%  5,238 of  5,238 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
   1,057 GO terms are associated with  3,949 of  5,238 study items
  METHOD fdr_bh:
      28 GO terms found significant (< 0.05=alpha) ( 23 enriched +   5
purified): statsmodels fdr_bh
   2,060 study items associated with significant GO IDs (enriched)
     737 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 5238 IDs … 72%  3,747 of
5,238 study items found in association
100%  5,238 of  5,238 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
```

```
   2,252 GO terms are associated with  3,747 of  5,238 study items
  METHOD fdr_bh:
     11 GO terms found significant (< 0.05=alpha) (  7 enriched +   4
purified): statsmodels fdr_bh
   2,899 study items associated with significant GO IDs (enriched)
     86 study items associated with significant GO IDs (purified)
Significant results[57] = 18 BP + 11 MF + 28 CC
     57 items WROTE: GO_analysis_module_grey.xlsx
     57 GOEA results for  3621 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:0:00:04.954009 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 17 IDs … 71%    12 of
17 study items found in association
100%    17 of    17 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
     44 GO terms are associated with    12 of    17 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 17 IDs … 88%    15 of
17 study items found in association
100%    17 of    17 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
     48 GO terms are associated with    15 of    17 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 17 IDs … 88%    15 of
17 study items found in association
100%    17 of     17 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
      30 GO terms are associated with     15 of     17 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_saddlebrown.xlsx
      0 GOEA results. NOT WRITING 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:0:00:04.614714 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 … 84%    298 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
   1,420 GO terms are associated with    298 of    355 study items
  METHOD fdr_bh:
      18 GO terms found significant (< 0.05=alpha) ( 18 enriched +   0
purified): statsmodels fdr_bh
      83 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 … 88%    314 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
     338 GO terms are associated with   314 of    355 study items
  METHOD fdr_bh:
      47 GO terms found significant (< 0.05=alpha) ( 47 enriched +   0
purified): statsmodels fdr_bh
     241 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 … 86%    304 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
     480 GO terms are associated with   304 of    355 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
     226 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[74] = 18 BP + 9 MF + 47 CC
      74 items WROTE: GO_analysis_module_cyan.xlsx
      74 GOEA results for   298 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:0:00:04.538422 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 786 IDs … 87%    683 of
786 study items found in association
100%    786 of    786 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
```

```
    2,664 GO terms are associated with    683 of    786 study items
  METHOD fdr_bh:
        1 GO terms found significant (< 0.05=alpha) (  1 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 786 IDs … 91%    712 of
786 study items found in association
100%    786 of    786 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
      611 GO terms are associated with    712 of    786 study items
  METHOD fdr_bh:
       29 GO terms found significant (< 0.05=alpha) ( 29 enriched +   0
purified): statsmodels fdr_bh
      620 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 786 IDs … 89%    696 of
786 study items found in association
100%    786 of    786 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
      818 GO terms are associated with    696 of    786 study items
  METHOD fdr_bh:
       10 GO terms found significant (< 0.05=alpha) (  9 enriched +   1
purified): statsmodels fdr_bh
      574 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[40] = 1 BP + 10 MF + 29 CC
      40 items WROTE: GO_analysis_module_yellow.xlsx
      40 GOEA results for   698 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:0:00:04.289541 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 1054 IDs … 85%    900 of
1,054 study items found in association
100%  1,054 of  1,054 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
   2,909 GO terms are associated with    900 of  1,054 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) ( 14 enriched +   3
purified): statsmodels fdr_bh
     202 study items associated with significant GO IDs (enriched)
       5 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1054 IDs … 91%    959 of
1,054 study items found in association
100%  1,054 of  1,054 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
     603 GO terms are associated with    959 of  1,054 study items
  METHOD fdr_bh:
      42 GO terms found significant (< 0.05=alpha) ( 42 enriched +   0
purified): statsmodels fdr_bh
     892 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 1054 IDs … 89%    938 of
1,054 study items found in association
100%  1,054 of  1,054 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
   1,009 GO terms are associated with    938 of  1,054 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  8 enriched +   1
purified): statsmodels fdr_bh
     779 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[68] = 17 BP + 9 MF + 42 CC
      68 items WROTE: GO_analysis_module_blue.xlsx
      68 GOEA results for   974 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:0:00:04.540418 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 57 IDs … 95%    54 of
57 study items found in association
100%    57 of    57 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
    356 GO terms are associated with    54 of    57 study items
  METHOD fdr_bh:
     40 GO terms found significant (< 0.05=alpha) ( 40 enriched +   0
purified): statsmodels fdr_bh
     45 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 57 IDs … 96%    55 of
57 study items found in association
100%    57 of    57 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
     89 GO terms are associated with    55 of    57 study items
  METHOD fdr_bh:
     13 GO terms found significant (< 0.05=alpha) ( 13 enriched +   0
purified): statsmodels fdr_bh
     51 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 57 IDs … 98%    56 of
57 study items found in association
100%    57 of    57 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    56 of    57 study items
  METHOD fdr_bh:
     16 GO terms found significant (< 0.05=alpha) ( 16 enriched +   0
purified): statsmodels fdr_bh
     54 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[69] = 40 BP + 16 MF + 13 CC
     69 items WROTE: GO_analysis_module_paleturquoise.xlsx
```

```
    69 GOEA results for    56 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:0:00:04.521634 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 440 IDs … 82%    363 of
440 study items found in association
100%    440 of    440 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
   1,415 GO terms are associated with    363 of    440 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 440 IDs … 87%    381 of
440 study items found in association
100%    440 of    440 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
     381 GO terms are associated with    381 of    440 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
     284 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 440 IDs … 87%    381 of
440 study items found in association
100%    440 of    440 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
      534 GO terms are associated with    381 of    440 study items
  METHOD fdr_bh:
        2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
      293 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[11] = 0 BP + 2 MF + 9 CC
       11 items WROTE: GO_analysis_module_pink.xlsx
       11 GOEA results for   354 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:0:00:04.560398 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 416 IDs … 94%    389 of
416 study items found in association
100%    416 of    416 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
   1,612 GO terms are associated with    389 of    416 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 416 IDs … 95%    397 of
416 study items found in association
100%    416 of    416 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
     389 GO terms are associated with    397 of    416 study items
  METHOD fdr_bh:
       18 GO terms found significant (< 0.05=alpha) ( 18 enriched +   0
```

```
purified): statsmodels fdr_bh
      349 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 416 IDs … 94%    390 of
416 study items found in association
100%    416 of    416 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
     525 GO terms are associated with    390 of    416 study items
  METHOD fdr_bh:
        8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
      338 study items associated with significant GO IDs (enriched)
        0 study items associated with significant GO IDs (purified)
Significant results[26] = 0 BP + 8 MF + 18 CC
      26 items WROTE: GO_analysis_module_purple.xlsx
      26 GOEA results for   387 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:0:00:04.455410 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 160 IDs … 85%    136 of
160 study items found in association
100%    160 of    160 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
     717 GO terms are associated with    136 of    160 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 160 IDs … 89%    142 of
160 study items found in association
100%    160 of    160 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
     211 GO terms are associated with    142 of    160 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
      88 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 160 IDs … 91%    145 of
160 study items found in association
100%    160 of    160 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
     322 GO terms are associated with    145 of    160 study items
  METHOD fdr_bh:
       1 GO terms found significant (< 0.05=alpha) (  1 enriched +   0
purified): statsmodels fdr_bh
     110 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[6] = 0 BP + 1 MF + 5 CC
      6 items WROTE: GO_analysis_module_darkgrey.xlsx
      6 GOEA results for    127 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:0:00:04.501407 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 1551 IDs … 81%  1,258 of
1,551 study items found in association
100%  1,551 of  1,551 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
    4,278 GO terms are associated with  1,258 of  1,551 study items
   METHOD fdr_bh:
       29 GO terms found significant (< 0.05=alpha) ( 27 enriched +   2
purified): statsmodels fdr_bh
      469 study items associated with significant GO IDs (enriched)
        5 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 1551 IDs … 85%  1,318 of
1,551 study items found in association
100%  1,551 of  1,551 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
      714 GO terms are associated with  1,318 of  1,551 study items
   METHOD fdr_bh:
       59 GO terms found significant (< 0.05=alpha) ( 59 enriched +   0
purified): statsmodels fdr_bh
    1,242 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 1551 IDs … 84%  1,305 of
1,551 study items found in association
100%  1,551 of  1,551 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
    1,304 GO terms are associated with  1,305 of  1,551 study items
   METHOD fdr_bh:
       24 GO terms found significant (< 0.05=alpha) ( 21 enriched +   3
purified): statsmodels fdr_bh
    1,117 study items associated with significant GO IDs (enriched)
       17 study items associated with significant GO IDs (purified)
Significant results[112] = 29 BP + 24 MF + 59 CC
     112 items WROTE: GO_analysis_module_turquoise.xlsx
     112 GOEA results for  1338 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:0:00:04.533948 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
```

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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 225 IDs … 90%    203 of
225 study items found in association
100%    225 of    225 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
   1,109 GO terms are associated with    203 of    225 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 225 IDs … 95%    213 of
225 study items found in association
100%    225 of    225 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
     267 GO terms are associated with    213 of    225 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     161 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 225 IDs … 93%    210 of
225 study items found in association
100%    225 of    225 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
     365 GO terms are associated with    210 of    225 study items
  METHOD fdr_bh:
       4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
     190 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[8] = 0 BP + 4 MF + 4 CC
       8 items WROTE: GO_analysis_module_royalblue.xlsx
       8 GOEA results for   203 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:0:00:04.356764 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 180 IDs … 96%    172 of
180 study items found in association
100%    180 of    180 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
   1,230 GO terms are associated with    172 of    180 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 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 CC Gene Ontology Analysis: current study set of 180 IDs … 96%    172 of
180 study items found in association
100%    180 of    180 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
     336 GO terms are associated with    172 of    180 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 30 enriched +   0
purified): statsmodels fdr_bh
     158 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 180 IDs … 94%    169 of
180 study items found in association
100%    180 of    180 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
     377 GO terms are associated with    169 of    180 study items
  METHOD fdr_bh:
       8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
```

```
    139 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[43] = 5 BP + 8 MF + 30 CC
     43 items WROTE: GO_analysis_module_darkturquoise.xlsx
     43 GOEA results for   171 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:0:00:04.562696 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 138 IDs … 82%    113 of
138 study items found in association
100%    138 of    138 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
     864 GO terms are associated with    113 of    138 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 138 IDs … 86%    118 of
138 study items found in association
100%    138 of    138 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
     183 GO terms are associated with    118 of    138 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 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 MF Gene Ontology Analysis: current study set of 138 IDs … 80%    111 of
138 study items found in association
100%    138 of    138 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
     283 GO terms are associated with    111 of    138 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    29 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:0:00:04.486028 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 327 IDs … 79%    259 of
327 study items found in association
100%    327 of    327 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
   1,395 GO terms are associated with    259 of    327 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 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 CC Gene Ontology Analysis: current study set of 327 IDs … 85%    277 of
327 study items found in association
100%    327 of    327 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    277 of    327 study items
  METHOD fdr_bh:
      10 GO terms found significant (< 0.05=alpha) ( 10 enriched +   0
purified): statsmodels fdr_bh
     163 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 327 IDs … 78%    256 of
327 study items found in association
100%    327 of    327 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
     423 GO terms are associated with    256 of    327 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[15] = 5 BP + 0 MF + 10 CC
     15 items WROTE: GO_analysis_module_midnightblue.xlsx
     15 GOEA results for   178 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:0:00:04.475668 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 567 IDs … 89%    506 of
567 study items found in association
100%    567 of    567 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
   1,901 GO terms are associated with    506 of    567 study items
  METHOD fdr_bh:
```

```
      5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
     80 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 567 IDs … 95%    537 of
567 study items found in association
100%    567 of    567 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
     478 GO terms are associated with    537 of    567 study items
  METHOD fdr_bh:
     31 GO terms found significant (< 0.05=alpha) ( 28 enriched +   3
purified): statsmodels fdr_bh
     497 study items associated with significant GO IDs (enriched)
     25 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 567 IDs … 92%    523 of
567 study items found in association
100%    567 of    567 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
     558 GO terms are associated with    523 of    567 study items
  METHOD fdr_bh:
     10 GO terms found significant (< 0.05=alpha) (  9 enriched +   1
purified): statsmodels fdr_bh
     468 study items associated with significant GO IDs (enriched)
      1 study items associated with significant GO IDs (purified)
Significant results[46] = 5 BP + 10 MF + 31 CC
     46 items WROTE: GO_analysis_module_red.xlsx
     46 GOEA results for   533 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:0:00:04.583495 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 433 IDs … 87%    376 of
433 study items found in association
100%    433 of    433 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
   1,773 GO terms are associated with    376 of    433 study items
  METHOD fdr_bh:
     51 GO terms found significant (< 0.05=alpha) ( 51 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 CC Gene Ontology Analysis: current study set of 433 IDs … 92%    398 of
433 study items found in association
100%    433 of    433 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
     395 GO terms are associated with    398 of    433 study items
  METHOD fdr_bh:
     59 GO terms found significant (< 0.05=alpha) ( 59 enriched +   0
purified): statsmodels fdr_bh
     339 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 433 IDs … 88%    379 of
433 study items found in association
100%    433 of    433 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
     528 GO terms are associated with    379 of    433 study items
  METHOD fdr_bh:
     24 GO terms found significant (< 0.05=alpha) ( 24 enriched +   0
purified): statsmodels fdr_bh
     293 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[134] = 51 BP + 24 MF + 59 CC
    134 items WROTE: GO_analysis_module_magenta.xlsx
    134 GOEA results for   384 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:0:00:04.431449 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 377 IDs … 85%    319 of
377 study items found in association
100%    377 of    377 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
   1,561 GO terms are associated with    319 of    377 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 30 enriched +   0
purified): statsmodels fdr_bh
      87 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 377 IDs … 92%    345 of
377 study items found in association
100%    377 of    377 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    345 of    377 study items
  METHOD fdr_bh:
      33 GO terms found significant (< 0.05=alpha) ( 32 enriched +   1
purified): statsmodels fdr_bh
     319 study items associated with significant GO IDs (enriched)
       4 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 377 IDs … 92%    348 of
377 study items found in association
100%    377 of    377 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
     518 GO terms are associated with    348 of    377 study items
  METHOD fdr_bh:
      24 GO terms found significant (< 0.05=alpha) ( 24 enriched +   0
purified): statsmodels fdr_bh
     305 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[87] = 30 BP + 24 MF + 33 CC
     87 items WROTE: GO_analysis_module_greenyellow.xlsx
     87 GOEA results for   344 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:0:00:04.290355 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 212 IDs … 90%    190 of
212 study items found in association
100%    212 of    212 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
   1,214 GO terms are associated with    190 of    212 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 212 IDs … 94%    200 of
212 study items found in association
100%    212 of    212 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
     338 GO terms are associated with    200 of    212 study items
  METHOD fdr_bh:
      19 GO terms found significant (< 0.05=alpha) ( 19 enriched +   0
purified): statsmodels fdr_bh
     176 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 212 IDs … 92%    196 of
212 study items found in association
100%    212 of    212 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
```

```
    401 GO terms are associated with    196 of    212 study items
  METHOD fdr_bh:
      9 GO terms found significant (< 0.05=alpha) (  9 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[29] = 1 BP + 9 MF + 19 CC
     29 items WROTE: GO_analysis_module_darkred.xlsx
     29 GOEA results for   192 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:0:00:04.558226 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 497 IDs … 88%    439 of
497 study items found in association
100%    497 of    497 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
   2,448 GO terms are associated with    439 of    497 study items
  METHOD fdr_bh:
    295 GO terms found significant (< 0.05=alpha) (295 enriched +   0
purified): statsmodels fdr_bh
    356 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 497 IDs … 94%    466 of
497 study items found in association
100%    497 of    497 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
    340 GO terms are associated with    466 of    497 study items
  METHOD fdr_bh:
     75 GO terms found significant (< 0.05=alpha) ( 75 enriched +   0
```

purified): statsmodels fdr_bh
     432 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 497 IDs … 91%   452 of
497 study items found in association
100%   497 of   497 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
     681 GO terms are associated with   452 of   497 study items
  METHOD fdr_bh:
      57 GO terms found significant (< 0.05=alpha) (57 enriched +   0
purified): statsmodels fdr_bh
     398 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[427] = 295 BP + 57 MF + 75 CC
    427 items WROTE: GO_analysis_module_black.xlsx
    427 GOEA results for   456 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:0:00:04.438400 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 518 IDs … 83%   429 of
518 study items found in association
100%   518 of   518 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
   2,501 GO terms are associated with   429 of   518 study items
  METHOD fdr_bh:
      22 GO terms found significant (< 0.05=alpha) (22 enriched +   0
purified): statsmodels fdr_bh
     171 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 518 IDs … 87%    450 of
518 study items found in association
100%    518 of    518 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
     383 GO terms are associated with    450 of    518 study items
  METHOD fdr_bh:
      26 GO terms found significant (< 0.05=alpha) ( 26 enriched +   0
purified): statsmodels fdr_bh
     393 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 518 IDs … 85%    438 of
518 study items found in association
100%    518 of    518 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
     701 GO terms are associated with    438 of    518 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
     336 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[54] = 22 BP + 6 MF + 26 CC
     54 items WROTE: GO_analysis_module_green.xlsx
     54 GOEA results for   448 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:0:00:04.612271 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 118 IDs … 93%    110 of
118 study items found in association
100%    118 of    118 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
     729 GO terms are associated with    110 of    118 study items
  METHOD fdr_bh:
      11 GO terms found significant (< 0.05=alpha) ( 11 enriched +   0
purified): statsmodels fdr_bh
      42 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 118 IDs … 96%    113 of
118 study items found in association
100%    118 of    118 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
     251 GO terms are associated with    113 of    118 study items
  METHOD fdr_bh:
      21 GO terms found significant (< 0.05=alpha) ( 21 enriched +   0
purified): statsmodels fdr_bh
     106 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 118 IDs … 92%    109 of
118 study items found in association
100%    118 of    118 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
     262 GO terms are associated with    109 of    118 study items
  METHOD fdr_bh:
      14 GO terms found significant (< 0.05=alpha) ( 14 enriched +   0
purified): statsmodels fdr_bh
      96 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[46] = 11 BP + 14 MF + 21 CC
     46 items WROTE: GO_analysis_module_white.xlsx
     46 GOEA results for   110 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:0:00:04.303362 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 250 IDs … 94%    234 of
250 study items found in association
100%    250 of    250 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
   1,123 GO terms are associated with    234 of    250 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 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 250 IDs … 97%    242 of
250 study items found in association
100%    250 of    250 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
     341 GO terms are associated with    242 of    250 study items
  METHOD fdr_bh:
      36 GO terms found significant (< 0.05=alpha) ( 36 enriched +   0
purified): statsmodels fdr_bh
     231 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 250 IDs … 94%    234 of
250 study items found in association
100%    250 of    250 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
     345 GO terms are associated with    234 of    250 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
     214 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[45] = 3 BP + 6 MF + 36 CC
      45 items WROTE: GO_analysis_module_lightgreen.xlsx
      45 GOEA results for   239 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:0:00:04.573554 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 849 IDs … 87%    738 of
849 study items found in association
100%    849 of    849 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
   2,186 GO terms are associated with    738 of    849 study items
  METHOD fdr_bh:
      12 GO terms found significant (< 0.05=alpha) ( 10 enriched +   2
purified): statsmodels fdr_bh
     236 study items associated with significant GO IDs (enriched)
       4 study items associated with significant GO IDs (purified)


Run CC Gene Ontology Analysis: current study set of 849 IDs … 92%    777 of
849 study items found in association
100%    849 of    849 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
     559 GO terms are associated with    777 of    849 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 26 enriched +   4
purified): statsmodels fdr_bh
     676 study items associated with significant GO IDs (enriched)
     126 study items associated with significant GO IDs (purified)


Run MF Gene Ontology Analysis: current study set of 849 IDs … 88%    751 of
849 study items found in association
100%    849 of    849 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
     813 GO terms are associated with    751 of    849 study items
  METHOD fdr_bh:
      22 GO terms found significant (< 0.05=alpha) ( 20 enriched +   2
purified): statsmodels fdr_bh
     651 study items associated with significant GO IDs (enriched)
       3 study items associated with significant GO IDs (purified)
```

```
Significant results[64] = 12 BP + 22 MF + 30 CC
     64 items WROTE: GO_analysis_module_brown.xlsx
     64 GOEA results for   764 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:0:00:04.497288 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 86 IDs … 79%    68 of
86 study items found in association
100%     86 of     86 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
     534 GO terms are associated with     68 of     86 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 86 IDs … 81%    70 of
86 study items found in association
100%     86 of     86 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
     118 GO terms are associated with     70 of     86 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 86 IDs … 79%    68 of
86 study items found in association
100%     86 of     86 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
     174 GO terms are associated with     68 of     86 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_skyblue.xlsx
       0 GOEA results. NOT WRITING 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:0:00:04.594846 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 112 IDs … 81%    91 of
112 study items found in association
100%    112 of    112 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
     471 GO terms are associated with     91 of    112 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 112 IDs … 86%    96 of
112 study items found in association
100%    112 of    112 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
     144 GO terms are associated with     96 of    112 study items
  METHOD fdr_bh:
```

```
      3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     60 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 112 IDs … 86%    96 of
112 study items found in association
100%    112 of    112 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
    206 GO terms are associated with    96 of    112 study items
  METHOD fdr_bh:
      3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     84 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[6] = 0 BP + 3 MF + 3 CC
      6 items WROTE: GO_analysis_module_darkorange.xlsx
      6 GOEA results for    92 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:0:00:04.529465 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 342 IDs … 95%    325 of
342 study items found in association
100%    342 of    342 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
   2,264 GO terms are associated with    325 of    342 study items
  METHOD fdr_bh:
    169 GO terms found significant (< 0.05=alpha) (169 enriched +   0
purified): statsmodels fdr_bh
    260 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 342 IDs … 97%    332 of
342 study items found in association
100%    342 of    342 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
     359 GO terms are associated with    332 of    342 study items
  METHOD fdr_bh:
      63 GO terms found significant (< 0.05=alpha) ( 63 enriched +   0
purified): statsmodels fdr_bh
     323 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 342 IDs … 96%    330 of
342 study items found in association
100%    342 of    342 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
     580 GO terms are associated with    330 of    342 study items
  METHOD fdr_bh:
      26 GO terms found significant (< 0.05=alpha) ( 26 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[258] = 169 BP + 26 MF + 63 CC
    258 items WROTE: GO_analysis_module_lightcyan.xlsx
    258 GOEA results for   331 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:0:00:04.557003 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 371 IDs … 91%    339 of
```

```
371 study items found in association
100%    371 of    371 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
   1,779 GO terms are associated with    339 of    371 study items
  METHOD fdr_bh:
      17 GO terms found significant (< 0.05=alpha) ( 17 enriched +   0
purified): statsmodels fdr_bh
     121 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 371 IDs … 94%    349 of
371 study items found in association
100%    371 of    371 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
     424 GO terms are associated with    349 of    371 study items
  METHOD fdr_bh:
      30 GO terms found significant (< 0.05=alpha) ( 30 enriched +   0
purified): statsmodels fdr_bh
     314 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 371 IDs … 93%    345 of
371 study items found in association
100%    371 of    371 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
     462 GO terms are associated with    345 of    371 study items
  METHOD fdr_bh:
      21 GO terms found significant (< 0.05=alpha) ( 21 enriched +   0
purified): statsmodels fdr_bh
     307 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[68] = 17 BP + 21 MF + 30 CC
      68 items WROTE: GO_analysis_module_salmon.xlsx
      68 GOEA results for   342 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:0:00:04.329587 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 51 IDs … 96%     49 of
51 study items found in association
100%     51 of     51 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
     319 GO terms are associated with     49 of     51 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 51 IDs …100%     51 of
51 study items found in association
100%     51 of     51 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
     137 GO terms are associated with     51 of     51 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
      36 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 51 IDs … 94%     48 of
51 study items found in association
100%     51 of     51 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
     133 GO terms are associated with     48 of     51 study items
  METHOD fdr_bh:
       8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
      43 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[11] = 0 BP + 8 MF + 3 CC
     11 items WROTE: GO_analysis_module_violet.xlsx
     11 GOEA results for    45 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:0:00:04.568103 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 195 IDs … 85%    166 of
195 study items found in association
100%    195 of    195 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
     957 GO terms are associated with    166 of    195 study items
  METHOD fdr_bh:
       7 GO terms found significant (< 0.05=alpha) (  7 enriched +   0
purified): statsmodels fdr_bh
      48 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 195 IDs … 91%    177 of
195 study items found in association
100%    195 of    195 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
     205 GO terms are associated with    177 of    195 study items
  METHOD fdr_bh:
      11 GO terms found significant (< 0.05=alpha) ( 11 enriched +   0
purified): statsmodels fdr_bh
     132 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 195 IDs … 84%    164 of
195 study items found in association
100%    195 of    195 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
     322 GO terms are associated with    164 of    195 study items
  METHOD fdr_bh:
       6 GO terms found significant (< 0.05=alpha) (  6 enriched +   0
purified): statsmodels fdr_bh
```

```
        42 study items associated with significant GO IDs (enriched)
         0 study items associated with significant GO IDs (purified)
Significant results[24] = 7 BP + 6 MF + 11 CC
      24 items WROTE: GO_analysis_module_darkgreen.xlsx
      24 GOEA results for   135 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:0:00:04.516710 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 234 IDs … 94%    221 of
234 study items found in association
100%    234 of    234 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
   1,512 GO terms are associated with    221 of    234 study items
  METHOD fdr_bh:
      80 GO terms found significant (< 0.05=alpha) ( 80 enriched +   0
purified): statsmodels fdr_bh
     149 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 234 IDs … 96%    225 of
234 study items found in association
100%    234 of    234 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
     245 GO terms are associated with    225 of    234 study items
  METHOD fdr_bh:
      38 GO terms found significant (< 0.05=alpha) ( 38 enriched +   0
purified): statsmodels fdr_bh
     205 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 234 IDs … 95%    223 of
234 study items found in association
100%    234 of    234 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
     399 GO terms are associated with    223 of    234 study items
  METHOD fdr_bh:
      20 GO terms found significant (< 0.05=alpha) ( 20 enriched +   0
purified): statsmodels fdr_bh
     190 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[138] = 80 BP + 20 MF + 38 CC
    138 items WROTE: GO_analysis_module_lightyellow.xlsx
    138 GOEA results for   229 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:0:00:04.310915 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 304 IDs … 86%    261 of
304 study items found in association
100%    304 of    304 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
   1,192 GO terms are associated with    261 of    304 study items
  METHOD fdr_bh:
       5 GO terms found significant (< 0.05=alpha) (  5 enriched +   0
purified): statsmodels fdr_bh
      76 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 304 IDs … 92%    279 of
304 study items found in association
100%    304 of    304 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
     308 GO terms are associated with    279 of    304 study items
  METHOD fdr_bh:
       9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
     226 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 304 IDs … 89%    272 of
304 study items found in association
100%    304 of    304 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
     404 GO terms are associated with    272 of    304 study items
  METHOD fdr_bh:
       3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     237 study items associated with significant GO IDs (enriched)
       0 study items associated with significant GO IDs (purified)
Significant results[17] = 5 BP + 3 MF + 9 CC
      17 items WROTE: GO_analysis_module_grey60.xlsx
      17 GOEA results for   267 study items. WROTE: 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:0:00:04.570661 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 387 IDs … 88%    339 of
387 study items found in association
100%    387 of    387 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
   1,217 GO terms are associated with    339 of    387 study items
  METHOD fdr_bh:
```

```
      3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
     27 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 387 IDs … 94%    365 of
387 study items found in association
100%    387 of    387 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
     390 GO terms are associated with    365 of    387 study items
  METHOD fdr_bh:
     21 GO terms found significant (< 0.05=alpha) ( 21 enriched +   0
purified): statsmodels fdr_bh
    318 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 387 IDs … 93%    358 of
387 study items found in association
100%    387 of    387 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
     505 GO terms are associated with    358 of    387 study items
  METHOD fdr_bh:
      3 GO terms found significant (< 0.05=alpha) (  3 enriched +   0
purified): statsmodels fdr_bh
    307 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[27] = 3 BP + 3 MF + 21 CC
     27 items WROTE: GO_analysis_module_tan.xlsx
     27 GOEA results for   360 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:0:00:04.316526 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 59 IDs … 92%     54 of
59 study items found in association
100%    59 of    59 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
    471 GO terms are associated with    54 of    59 study items
  METHOD fdr_bh:
      9 GO terms found significant (< 0.05=alpha) (  9 enriched +   0
purified): statsmodels fdr_bh
     12 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 59 IDs … 92%     54 of
59 study items found in association
100%    59 of    59 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
     79 GO terms are associated with    54 of    59 study items
  METHOD fdr_bh:
      2 GO terms found significant (< 0.05=alpha) (  2 enriched +   0
purified): statsmodels fdr_bh
     31 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 59 IDs … 90%     53 of
59 study items found in association
100%    59 of    59 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
    129 GO terms are associated with    53 of    59 study items
  METHOD fdr_bh:
      8 GO terms found significant (< 0.05=alpha) (  8 enriched +   0
purified): statsmodels fdr_bh
     44 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[19] = 9 BP + 8 MF + 2 CC
     19 items WROTE: GO_analysis_module_steelblue.xlsx
     19 GOEA results for    47 study items. WROTE:
GO_analysis_module_steelblue.txt
```

[ ]: