

main

August 11, 2021

## 1 Enrichment in GWAS, TWAS, and DE

```
[1]: import functools
import numpy as np
import pandas as pd
import collections as cx
from pybiomart import Dataset
from gtftparse 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

```
[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

```

```

[3]: def fet(a, b, u):
    # a, b, u are sets
    # u is the universe
    yes_a = u.intersection(a)
    yes_b = u.intersection(b)
    no_a = u - a
    no_b = u - b
    m = [[len(yes_a.intersection(yes_b)), len(no_a.intersection(yes_b)) ],
          [len(yes_a.intersection(no_b)), len(no_a.intersection(no_b))]]
    return fisher_exact(m)

def enrichment_rows():
    mod = get_wgcna_modules().module.unique()
    u = set(get_wgcna_modules().index)
    for ii in range(len(mod)): # for each module
        a = set(get_wgcna_modules()[get_wgcna_modules().module == mod[ii]].
→index)
        yield (mod[ii],
               len(a),
               *fet(a, gwas_genes, u),
               *fet(a, twas_genes, u),
               *fet(a, de_genes, u),
               )

def enrichment_rows_nomhc():
    mod = get_wgcna_modules().module.unique()
    u = set(get_wgcna_modules().index) - mhc_genes
    for ii in range(len(mod)): # for each module
        a = set(get_wgcna_modules()[get_wgcna_modules().module == mod[ii]].
→index) - mhc_genes
        yield (mod[ii],
               len(a),
               *fet(a, gwas_genes - mhc_genes, u),
               *fet(a, twas_genes - mhc_genes, u),
               *fet(a, de_genes - mhc_genes, u),
               )

def convert2entrez(mod):

```

```

df = get_wgcna_modules()[get_wgcna_modules().module == mod].copy()
df["ensemblID"] = df.index.str.replace("\\.*", "")
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_ns2assoc()
    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
```

## 1.3 GWAS, TWAS and DE enrichment

### 1.3.1 Load DE, TWAS, and GWAS genes

```
[5]: de_genes = set(pd.read_csv('../../differential_expression/_m/genes/
    ↪diffExpr_szVct1_FDR05.txt',
                        sep='\t', usecols=[0], index_col=0).index)
len(de_genes)
```

```
[5]: 2701
```

```
[6]: gwas_genes = set(pd.read_csv('/ceph/projects/v3_phase3_paper/inputs/gwas/
    ↪PGC2_CLOZUK/table_s3/hg38/genes/_m/gwas_genes.csv')['gene_id'])
len(gwas_genes)
```

```
[6]: 2000
```

```
[7]: mhc_genes = set(pd.read_csv('/ceph/projects/v4_phase3_paper/inputs/counts/
    ↪mhc_region_genes/_m/mhc_genes.csv')['gene_id'])
len(mhc_genes)
```

```
[7]: 383
```

```
[8]: annot = pd.read_csv("/ceph/projects/v4_phase3_paper/inputs/counts/
    ↪text_files_counts/_m/caudate/gene.bed",
                        sep='\t', index_col=0)
annot["Feature"] = annot.gene_id.str.replace("\\\\.*", "", regex=True)
twas = pd.read_csv("../../twas/feature_comparison/manuscript_supp_data/_m/"+
    ↪"BrainSeq_Phase3_Caudate_TWAS_associations_allFeatures.txt.
    ↪gz", sep='\t')
twas = twas[(twas["FDR"] < 0.05) & (twas["Type"] == "Gene")].merge(annot,
    ↪on="Feature")
twas_genes = set(twas['gene_id'])
len(twas_genes)
```

INFO:numexpr.utils>Note: NumExpr detected 64 cores but "NUMEXPR\_MAX\_THREADS" not set, so enforcing safe limit of 8.

INFO:numexpr.utils:NumExpr defaulting to 8 threads.

[8]: 684

### 1.3.2 Load WGCNA module

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

```
[9]:      module      gene_id  gene_name
12.0    grey  ENSG00000227232.5    WASH7P
25.0    yellow  ENSG00000278267.1  MIR6859-1
```

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

```
[10]:      module      gene_id  gene_name
NaN  lightgreen  chr11:113412884-113414374(-)    NaN
NaN  lightgreen  chr11:113412884-113415420(-)    NaN
NaN  lightgreen  chr11:113414462-113415420(-)    NaN
```

```
[11]: wgcna_df[(wgcna_df.gene_name == 'SETD1A')]
```

```
[11]:      module      gene_id  gene_name
1914770.0  yellow  ENSG00000099381.16    SETD1A
```

### 1.3.3 Enrichment

```
[12]: edf1 = pd.DataFrame.from_records(enrichment_rows(),
    columns=['module_id', 'n_genes', 'gwas_or', 'gwas_p',
    ↳'gwas_fdr_bh', 'twas_or', 'twas_p', 'de_or', 'de_p'],
    index='module_id')
edf1['twas_fdr_bh'] = multipletests(edf1['twas_p'], method='fdr_bh')[1]
edf1['gwas_fdr_bh'] = multipletests(edf1['gwas_p'], method='fdr_bh')[1]
edf1['de_fdr_bh'] = multipletests(edf1['de_p'], method='fdr_bh')[1]
edf1[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
    ↳'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']].
    ↳to_csv('wgcna_module_enrichment.csv')
edf1[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
    ↳'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']]
```

```
[12]:      n_genes  gwas_or  gwas_p  gwas_fdr_bh  twas_or  twas_p  \
module_id
grey      3940  0.892699  0.214026    0.523174  1.082137  0.439890
yellow    1587  1.127312  0.308776    0.617552  1.111805  0.444625
```

turquoise	3334	0.864652	0.142167	0.390959	0.877289	0.270678
cyan	375	1.172909	0.522217	0.691577	0.983961	1.000000
green	1568	1.245199	0.063396	0.232452	0.889608	0.537755
brown	2253	0.767852	0.025971	0.142843	0.864100	0.327368
black	1022	1.108971	0.480575	0.691577	1.127104	0.509117
midnightblue	370	1.463223	0.093245	0.293057	1.189579	0.535008
lightyellow	226	0.908099	1.000000	1.000000	0.584393	0.426782
tan	411	1.003817	0.903400	0.973690	1.415578	0.184201
royalblue	217	0.728610	0.505137	0.691577	0.609334	0.422714
magenta	679	0.623757	0.044510	0.195843	0.528732	0.037884
darkred	204	1.879159	0.023150	0.142843	1.688871	0.140537
pink	793	1.012345	0.929431	0.973690	1.293422	0.167399
blue	2532	1.351950	0.001631	0.035874	1.165965	0.192978
lightgreen	227	0.193191	0.004850	0.053345	0.731567	0.692431
lightcyan	339	1.014813	0.893464	0.973690	0.784640	0.628696
purple	484	1.146919	0.499134	0.691577	0.611986	0.174787
red	1260	0.841721	0.287101	0.617552	1.072040	0.669600
grey60	302	1.229691	0.394382	0.691577	1.234897	0.492128
salmon	398	1.162782	0.534400	0.691577	0.837017	0.764880
greenyellow	440	0.878693	0.723219	0.883934	1.071803	0.776149

	twas_fdr_bh	de_or	de_p	de_fdr_bh
module_id				
grey	0.739413	0.676330	2.572857e-11	8.086121e-11
yellow	0.739413	0.567600	1.189145e-09	2.906798e-09
turquoise	0.739413	0.303677	3.095585e-57	3.405144e-56
cyan	1.000000	1.867858	7.274883e-06	1.150205e-05
green	0.739413	0.379828	4.231908e-21	1.862039e-20
brown	0.739413	2.935529	7.804697e-79	1.717033e-77
black	0.739413	2.301877	1.466545e-23	8.065996e-23
midnightblue	0.739413	1.491874	7.027371e-03	8.136956e-03
lightyellow	0.739413	1.826881	8.007519e-04	9.786968e-04
tan	0.707588	1.956593	3.824870e-07	7.649741e-07
royalblue	0.739413	0.844996	5.253517e-01	5.253517e-01
magenta	0.707588	0.449134	1.162519e-07	2.557542e-07
darkred	0.707588	2.019585	1.683286e-04	2.178370e-04
pink	0.707588	3.497723	1.153651e-46	8.460107e-46
blue	0.707588	0.729929	7.319488e-06	1.150205e-05
lightgreen	0.801762	2.029721	4.559218e-05	6.686852e-05
lightcyan	0.801762	2.727243	1.836597e-13	6.734189e-13
purple	0.707588	0.437539	4.324439e-06	7.928138e-06
red	0.801762	0.683561	1.292860e-04	1.777682e-04
grey60	0.739413	0.150158	3.957232e-10	1.088239e-09
salmon	0.813108	1.393123	2.245696e-02	2.470266e-02
greenyellow	0.813108	0.767239	1.164459e-01	1.219909e-01

### 1.3.4 No MHC region

```
[13]: edf2 = pd.DataFrame.from_records(enrichment_rows_nomhc(),
                                     columns=['module_id', 'n_genes', 'gwas_or', 'gwas_p',
                                     'twas_or', 'twas_p', 'de_or', 'de_p'],
                                     index='module_id')
edf2['twas_fdr_bh'] = multipletests(edf2['twas_p'], method='fdr_bh')[1]
edf2['gwas_fdr_bh'] = multipletests(edf2['gwas_p'], method='fdr_bh')[1]
edf2['de_fdr_bh'] = multipletests(edf2['de_p'], method='fdr_bh')[1]
edf2[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
      'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']].
    to_csv('wgcn_module_enrichment_excluding_mhc_region.csv')
edf2[['n_genes', 'gwas_or', 'gwas_p', 'gwas_fdr_bh', 'twas_or', 'twas_p',
      'twas_fdr_bh', 'de_or', 'de_p', 'de_fdr_bh']]
```

```
[13]:
```

	n_genes	gwas_or	gwas_p	gwas_fdr_bh	twas_or	twas_p	\
module_id							
grey	3909	0.850262	0.102202	0.281057	1.032990	0.746956	
yellow	1569	1.025675	0.834775	0.931585	1.103254	0.521159	
turquoise	3313	0.865699	0.177595	0.390709	0.834726	0.150140	
cyan	373	1.256521	0.331638	0.561233	0.976909	1.000000	
green	1563	1.415003	0.006436	0.070794	0.901696	0.629698	
brown	2245	0.829071	0.155947	0.381205	0.916562	0.586088	
black	1014	1.109538	0.494980	0.725971	1.124947	0.491598	
midnightblue	367	1.522798	0.090576	0.281057	1.309193	0.331022	
lightyellow	226	1.087747	0.722394	0.882926	0.636869	0.535715	
tan	408	1.000158	1.000000	1.000000	1.557566	0.089448	
royalblue	214	0.496723	0.199549	0.399097	0.501996	0.293814	
magenta	676	0.628150	0.076511	0.281057	0.471059	0.022054	
darkred	202	1.967530	0.021940	0.120667	1.663843	0.128938	
pink	788	1.038477	0.846895	0.931585	1.372737	0.118340	
blue	2511	1.381774	0.001941	0.042706	1.227438	0.091969	
lightgreen	227	0.231090	0.019341	0.120667	0.797370	0.837113	
lightcyan	338	1.134521	0.660435	0.854680	0.747402	0.612372	
purple	475	0.851828	0.622896	0.854680	0.525295	0.088751	
red	1253	0.857296	0.395329	0.621231	1.148942	0.422294	
grey60	291	0.454860	0.082625	0.281057	0.744392	0.589158	
salmon	397	1.324492	0.225311	0.413070	0.915317	1.000000	
greenyellow	438	0.927932	0.897975	0.940735	1.086932	0.766356	

  

	twas_fdr_bh	de_or	de_p	de_fdr_bh
module_id				
grey	0.887359	0.673036	1.788290e-11	5.620340e-11
yellow	0.814904	0.558072	4.513232e-10	1.241139e-09
turquoise	0.471869	0.305742	2.263035e-56	2.489338e-55
cyan	1.000000	1.880481	6.734897e-06	1.229777e-05

green	0.814904	0.381027	7.589137e-21	3.339220e-20
brown	0.814904	2.945581	6.003082e-79	1.320678e-77
black	0.814904	2.312840	1.036007e-23	5.698037e-23
midnightblue	0.809166	1.506621	5.327744e-03	6.168966e-03
lightyellow	0.814904	1.826750	8.010333e-04	9.790407e-04
tan	0.471869	1.944618	5.322901e-07	1.064580e-06
royalblue	0.807988	0.814611	4.548135e-01	4.548135e-01
magenta	0.471869	0.438756	5.544032e-08	1.219687e-07
darkred	0.471869	1.924064	4.104262e-04	5.311398e-04
pink	0.471869	3.509209	1.168000e-46	8.565331e-46
blue	0.471869	0.729536	7.825853e-06	1.229777e-05
lightgreen	0.920824	2.029600	4.564248e-05	6.694230e-05
lightcyan	0.814904	2.738411	1.682037e-13	6.167469e-13
purple	0.471869	0.446436	7.295151e-06	1.229777e-05
red	0.814904	0.673181	8.420111e-05	1.157765e-04
grey60	0.814904	0.156007	1.187735e-09	2.903353e-09
salmon	1.000000	1.397243	2.227414e-02	2.450156e-02
greenyellow	0.887359	0.771059	1.336408e-01	1.400046e-01

#### 1.4 GO enrichment for each cluster

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

```
<ipython-input-1-d33bb4f5e304>:41: FutureWarning: The default value of regex
will change from True to False in a future version.
```

```
df["ensemblID"] = df.index.str.replace("\\.*", "")
```

```
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:0:00:04.274250 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
```

```
BP 18,505 annotated human genes
```

```
MF 18,190 annotated human genes
```

```
CC 19,423 annotated human genes
```

```
Load BP Gene Ontology Analysis ...
```

```
70% 20,236 of 29,107 population items found in association
```

```
Load CC Gene Ontology Analysis ...
```

```
74% 21,429 of 29,107 population items found in association
```

```
Load MF Gene Ontology Analysis ...
```

```
70% 20,354 of 29,107 population items found in association
```



```

Run BP Gene Ontology Analysis: current study set of 2789 IDs ... 76% 2,114 of
2,789 study items found in association
100% 2,789 of 2,789 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,848 of 29,107 population items
5,619 GO terms are associated with 2,114 of 2,789 study items
METHOD fdr_bh:
26 GO terms found significant (< 0.05=alpha) ( 24 enriched + 2
purified): statsmodels fdr_bh
740 study items associated with significant GO IDs (enriched)
9 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 2789 IDs ... 80% 2,239 of
2,789 study items found in association
100% 2,789 of 2,789 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,712 of 29,107 population items
816 GO terms are associated with 2,239 of 2,789 study items
METHOD fdr_bh:
20 GO terms found significant (< 0.05=alpha) ( 20 enriched + 0
purified): statsmodels fdr_bh
2,036 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 2789 IDs ... 78% 2,163 of
2,789 study items found in association
100% 2,789 of 2,789 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,838 of 29,107 population items
1,757 GO terms are associated with 2,163 of 2,789 study items
METHOD fdr_bh:
18 GO terms found significant (< 0.05=alpha) ( 16 enriched + 2
purified): statsmodels fdr_bh
1,726 study items associated with significant GO IDs (enriched)
6 study items associated with significant GO IDs (purified)
Significant results[64] = 26 BP + 18 MF + 20 CC
64 items WROTE: GO_analysis_module_grey.xlsx
64 GOEA results for 2201 study items. WROTE: GO_analysis_module_grey.txt
EXISTS: go-basic.obo
EXISTS: gene2go

<ipython-input-1-d33bb4f5e304>:41: FutureWarning: The default value of regex
will change from True to False in a future version.
df["ensemblID"] = df.index.str.replace("\\.*", "")

go-basic.obo: fmt(1.2) rel(2021-07-02) 47,229 GO Terms
HMS:0:00:04.586515 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go

```

BP 18,505 annotated human genes  
MF 18,190 annotated human genes  
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1109 IDs ... 81% 900 of  
1,109 study items found in association  
100% 1,109 of 1,109 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,848 of 29,107 population items  
3,002 GO terms are associated with 900 of 1,109 study items  
METHOD fdr\_bh:  
20 GO terms found significant ( $< 0.05=\alpha$ ) ( 18 enriched + 2  
purified): statsmodels fdr\_bh  
280 study items associated with significant GO IDs (enriched)  
13 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 1109 IDs ... 84% 934 of  
1,109 study items found in association  
100% 1,109 of 1,109 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,712 of 29,107 population items  
566 GO terms are associated with 934 of 1,109 study items  
METHOD fdr\_bh:  
18 GO terms found significant ( $< 0.05=\alpha$ ) ( 18 enriched + 0  
purified): statsmodels fdr\_bh  
732 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 1109 IDs ... 81% 903 of  
1,109 study items found in association  
100% 1,109 of 1,109 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher  
4,434 GO terms are associated with 17,838 of 29,107 population items  
913 GO terms are associated with 903 of 1,109 study items  
METHOD fdr\_bh:  
16 GO terms found significant ( $< 0.05=\alpha$ ) ( 14 enriched + 2  
purified): statsmodels fdr\_bh  
759 study items associated with significant GO IDs (enriched)  
4 study items associated with significant GO IDs (purified)

Significant results[54] = 20 BP + 16 MF + 18 CC  
 54 items WROTE: GO\_analysis\_module\_yellow.xlsx  
 54 GOEA results for 884 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:0:00:04.527039 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,505 annotated human genes  
 MF 18,190 annotated human genes  
 CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1232 IDs ... 60% 743 of  
 1,232 study items found in association  
 100% 1,232 of 1,232 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,848 of 29,107 population items  
 2,061 GO terms are associated with 743 of 1,232 study items  
 METHOD fdr\_bh:  
 2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0  
 purified): statsmodels fdr\_bh  
 135 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 1232 IDs ... 64% 792 of  
 1,232 study items found in association  
 100% 1,232 of 1,232 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,712 of 29,107 population items  
 472 GO terms are associated with 792 of 1,232 study items  
 METHOD fdr\_bh:  
 3 GO terms found significant (< 0.05=alpha) ( 1 enriched + 2  
 purified): statsmodels fdr\_bh  
 27 study items associated with significant GO IDs (enriched)  
 196 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1232 IDs ... 59% 723 of  
 1,232 study items found in association  
 100% 1,232 of 1,232 study items found in population(29107)

```

Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  720 GO terms are associated with    723 of  1,232 study items
METHOD fdr_bh:
  6 GO terms found significant (< 0.05=alpha) (  5 enriched +  1
purified): statsmodels fdr_bh
  182 study items associated with significant GO IDs (enriched)
  440 study items associated with significant GO IDs (purified)
Significant results[11] = 2 BP + 6 MF + 3 CC
  11 items WROTE: GO_analysis_module_turquoise.xlsx
  11 GOEA results for  596 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:0:00:04.234009 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 349 IDs ... 85%    298 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  1,388 GO terms are associated with    298 of    349 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 349 IDs ... 91%    317 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
  324 GO terms are associated with    317 of    349 study items

```

```

METHOD fdr_bh:
    9 GO terms found significant (< 0.05=alpha) ( 9 enriched + 0
purified): statsmodels fdr_bh
    221 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 349 IDs ... 88%    308 of
349 study items found in association
100%    349 of    349 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    448 GO terms are associated with    308 of    349 study items
METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
    233 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_cyan.xlsx
    11 GOEA results for    293 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:0:00:04.560265 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 909 IDs ... 72%    655 of
909 study items found in association
100%    909 of    909 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,848 of 29,107 population items
    2,233 GO terms are associated with    655 of    909 study items
METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 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 909 IDs ... 75%    684 of
909 study items found in association
100%    909 of    909 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    489 GO terms are associated with    684 of    909 study items
METHOD fdr_bh:
    6 GO terms found significant (< 0.05=alpha) ( 5 enriched + 1
purified): statsmodels fdr_bh
    336 study items associated with significant GO IDs (enriched)
    23 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 909 IDs ... 74%    671 of
909 study items found in association
100%    909 of    909 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    731 GO terms are associated with    671 of    909 study items
METHOD fdr_bh:
    9 GO terms found significant (< 0.05=alpha) ( 8 enriched + 1
purified): statsmodels fdr_bh
    560 study items associated with significant GO IDs (enriched)
    1 study items associated with significant GO IDs (purified)
Significant results[18] = 3 BP + 9 MF + 6 CC
    18 items Wrote: GO_analysis_module_green.xlsx
    18 GOEA results for 605 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:0:00:04.275529 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 2007 IDs ... 86% 1,723 of
2,007 study items found in association

```

```

100% 2,007 of 2,007 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  4,754 GO terms are associated with 1,723 of 2,007 study items
  METHOD fdr_bh:
    135 GO terms found significant (< 0.05=alpha) (131 enriched + 4
purified): statsmodels fdr_bh
    986 study items associated with significant GO IDs (enriched)
    20 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 2007 IDs ... 91% 1,817 of
2,007 study items found in association
100% 2,007 of 2,007 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
  853 GO terms are associated with 1,817 of 2,007 study items
  METHOD fdr_bh:
    104 GO terms found significant (< 0.05=alpha) (103 enriched + 1
purified): statsmodels fdr_bh
    1,748 study items associated with significant GO IDs (enriched)
    84 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 2007 IDs ... 88% 1,759 of
2,007 study items found in association
100% 2,007 of 2,007 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  1,571 GO terms are associated with 1,759 of 2,007 study items
  METHOD fdr_bh:
    64 GO terms found significant (< 0.05=alpha) ( 62 enriched + 2
purified): statsmodels fdr_bh
    1,512 study items associated with significant GO IDs (enriched)
    3 study items associated with significant GO IDs (purified)
Significant results[303] = 135 BP + 64 MF + 104 CC
  303 items Wrote: GO_analysis_module_brown.xlsx
  303 GOEA results for 1857 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:0:00:04.625760 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

```

```

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 859 IDs ... 81%    695 of
859 study items found in association
100%    859 of    859 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  2,856 GO terms are associated with    695 of    859 study items
  METHOD fdr_bh:
    17 GO terms found significant (< 0.05=alpha) ( 15 enriched +  2
purified): statsmodels fdr_bh
    216 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 859 IDs ... 84%    725 of
859 study items found in association
100%    859 of    859 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
  516 GO terms are associated with    725 of    859 study items
  METHOD fdr_bh:
    20 GO terms found significant (< 0.05=alpha) ( 20 enriched +  0
purified): statsmodels fdr_bh
    608 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 859 IDs ... 84%    722 of
859 study items found in association
100%    859 of    859 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  865 GO terms are associated with    722 of    859 study items
  METHOD fdr_bh:
    22 GO terms found significant (< 0.05=alpha) ( 20 enriched +  2
purified): statsmodels fdr_bh
    617 study items associated with significant GO IDs (enriched)
    4 study items associated with significant GO IDs (purified)
Significant results[59] = 17 BP + 22 MF + 20 CC
  59 items WROTE: GO_analysis_module_black.xlsx
  59 GOEA results for  705 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:0:00:04.303239 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:

```



```

gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 348 IDs ... 87%    304 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  1,620 GO terms are associated with    304 of    348 study items
  METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) ( 1 enriched + 0
purified): statsmodels fdr_bh
    18 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 348 IDs ... 90%    314 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
  389 GO terms are associated with    314 of    348 study items
  METHOD fdr_bh:
    20 GO terms found significant (< 0.05=alpha) ( 20 enriched + 0
purified): statsmodels fdr_bh
    251 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 348 IDs ... 89%    309 of
348 study items found in association
100%    348 of    348 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  499 GO terms are associated with    309 of    348 study items
  METHOD fdr_bh:
    5 GO terms found significant (< 0.05=alpha) ( 5 enriched + 0
purified): statsmodels fdr_bh
    250 study items associated with significant GO IDs (enriched)

```

```

    0 study items associated with significant GO IDs (purified)
Significant results[26] = 1 BP + 5 MF + 20 CC
    26 items WROTE: GO_analysis_module_midnightblue.xlsx
    26 GOEA results for 306 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:0:00:04.536082 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 220 IDs ... 90%    198 of
220 study items found in association
100%    220 of    220 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,848 of 29,107 population items
    965 GO terms are associated with    198 of    220 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 220 IDs ... 94%    206 of
220 study items found in association
100%    220 of    220 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    255 GO terms are associated with    206 of    220 study items
METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
    81 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 220 IDs ... 93%    204 of

```

```

220 study items found in association
100% 220 of 220 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  350 GO terms are associated with 204 of 220 study items
  METHOD fdr_bh:
    3 GO terms found significant (< 0.05=alpha) ( 3 enriched + 0
purified): statsmodels fdr_bh
  174 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[5] = 0 BP + 3 MF + 2 CC
  5 items WROTE: GO_analysis_module_lightyellow.xlsx
  5 GOEA results for 189 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:0:00:04.306342 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 346 IDs ... 84% 292 of
346 study items found in association
100% 346 of 346 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  1,447 GO terms are associated with 292 of 346 study items
  METHOD fdr_bh:
    7 GO terms found significant (< 0.05=alpha) ( 7 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 346 IDs ... 88% 305 of
346 study items found in association
100% 346 of 346 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher

```

```

1,756 GO terms are associated with 18,712 of 29,107 population items
332 GO terms are associated with 305 of 346 study items
METHOD fdr_bh:
17 GO terms found significant (< 0.05=alpha) ( 17 enriched + 0
purified): statsmodels fdr_bh
249 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 346 IDs ... 86% 296 of
346 study items found in association
100% 346 of 346 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,838 of 29,107 population items
489 GO terms are associated with 296 of 346 study items
METHOD fdr_bh:
10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0
purified): statsmodels fdr_bh
240 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[34] = 7 BP + 10 MF + 17 CC
34 items WROTE: GO_analysis_module_tan.xlsx
34 GOEA results for 295 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:0:00:04.553416 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 197 IDs ... 85% 168 of
197 study items found in association
100% 197 of 197 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,848 of 29,107 population items
998 GO terms are associated with 168 of 197 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 197 IDs ... 91%    179 of
197 study items found in association
100%    197 of    197 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    251 GO terms are associated with    179 of    197 study items
METHOD fdr_bh:
    4 GO terms found significant (< 0.05=alpha) (  4 enriched +    0
purified): statsmodels fdr_bh
    130 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 197 IDs ... 94%    185 of
197 study items found in association
100%    197 of    197 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    351 GO terms are associated with    185 of    197 study items
METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) (  2 enriched +    0
purified): statsmodels fdr_bh
    157 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[6] = 0 BP + 2 MF + 4 CC
    6 items WROTE: GO_analysis_module_royalblue.xlsx
    6 GOEA results for    176 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:0:00:04.458184 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,354 of 29,107 population items found in association

```

```

Run BP Gene Ontology Analysis: current study set of 625 IDs ... 75%    470 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,848 of 29,107 population items
    2,054 GO terms are associated with    470 of    625 study items
METHOD fdr_bh:
    30 GO terms found significant (< 0.05=alpha) ( 30 enriched +    0
purified): statsmodels fdr_bh
    169 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 625 IDs ... 81%    506 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    370 GO terms are associated with    506 of    625 study items
METHOD fdr_bh:
    31 GO terms found significant (< 0.05=alpha) ( 30 enriched +    1
purified): statsmodels fdr_bh
    351 study items associated with significant GO IDs (enriched)
    8 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 625 IDs ... 77%    480 of
625 study items found in association
100%    625 of    625 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    566 GO terms are associated with    480 of    625 study items
METHOD fdr_bh:
    15 GO terms found significant (< 0.05=alpha) ( 14 enriched +    1
purified): statsmodels fdr_bh
    367 study items associated with significant GO IDs (enriched)
    8 study items associated with significant GO IDs (purified)
Significant results[76] = 30 BP + 15 MF + 31 CC
    76 items Wrote: GO_analysis_module_magenta.xlsx
    76 GOEA results for 465 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:0:00:04.471084 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

```

```

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 193 IDs ... 82%    158 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
    926 GO terms are associated with    158 of    193 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 193 IDs ... 91%    175 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
    235 GO terms are associated with    175 of    193 study items
  METHOD fdr_bh:
    6 GO terms found significant (< 0.05=alpha) (  6 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 MF Gene Ontology Analysis: current study set of 193 IDs ... 87%    168 of
193 study items found in association
100%    193 of    193 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
    304 GO terms are associated with    168 of    193 study items
  METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) (  1 enriched +  0
purified): statsmodels fdr_bh
    140 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[7] = 0 BP + 1 MF + 6 CC
  7 items WROTE: GO_analysis_module_darkred.xlsx
  7 GOEA results for    146 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:0:00:04.557408 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 700 IDs ... 85%    598 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  2,497 GO terms are associated with    598 of    700 study items
  METHOD fdr_bh:
    2 GO terms found significant (< 0.05=alpha) ( 2 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 700 IDs ... 90%    628 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
  539 GO terms are associated with    628 of    700 study items
  METHOD fdr_bh:
    28 GO terms found significant (< 0.05=alpha) ( 28 enriched + 0
purified): statsmodels fdr_bh
    589 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 700 IDs ... 89%    622 of
700 study items found in association
100%    700 of    700 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items

```



```

      824 GO terms are associated with      622 of      700 study items
METHOD fdr_bh:
      4 GO terms found significant (< 0.05=alpha) (  4 enriched +   0
purified): statsmodels fdr_bh
      488 study items associated with significant GO IDs (enriched)
      0 study items associated with significant GO IDs (purified)
Significant results[34] = 2 BP + 4 MF + 28 CC
      34 items WROTE: GO_analysis_module_pink.xlsx
      34 GOEA results for      629 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:0:00:04.496930 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 2211 IDs ... 87%  1,917 of
2,211 study items found in association
100%  2,211 of  2,211 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  4,074 GO terms are associated with  1,917 of  2,211 study items
METHOD fdr_bh:
  140 GO terms found significant (< 0.05=alpha) (131 enriched +   9
purified): statsmodels fdr_bh
  1,136 study items associated with significant GO IDs (enriched)
    58 study items associated with significant GO IDs (purified)

Run CC Gene Ontology Analysis: current study set of 2211 IDs ... 92%  2,034 of
2,211 study items found in association
100%  2,211 of  2,211 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
  1,756 GO terms are associated with 18,712 of 29,107 population items
    866 GO terms are associated with  2,034 of  2,211 study items
METHOD fdr_bh:
  183 GO terms found significant (< 0.05=alpha) (175 enriched +   8
purified): statsmodels fdr_bh

```

```

1,934 study items associated with significant GO IDs (enriched)
  305 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 2211 IDs ... 91% 2,008 of
2,211 study items found in association
100% 2,211 of 2,211 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  1,393 GO terms are associated with 2,008 of 2,211 study items
METHOD fdr_bh:
  95 GO terms found significant (< 0.05=alpha) ( 85 enriched + 10
purified): statsmodels fdr_bh
  1,865 study items associated with significant GO IDs (enriched)
  108 study items associated with significant GO IDs (purified)
Significant results[418] = 140 BP + 95 MF + 183 CC
  418 items WROTE: GO_analysis_module_blue.xlsx
  418 GOEA results for 2073 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:0:00:04.523578 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 184 IDs ... 78% 144 of
184 study items found in association
100% 184 of 184 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
  12,438 GO terms are associated with 17,848 of 29,107 population items
  871 GO terms are associated with 144 of 184 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 184 IDs ... 82% 150 of

```

```

184 study items found in association
100% 184 of 184 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,712 of 29,107 population items
215 GO terms are associated with 150 of 184 study items
METHOD fdr_bh:
2 GO terms found significant (< 0.05=alpha) ( 2 enriched + 0
purified): statsmodels fdr_bh
20 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 184 IDs ... 74% 136 of
184 study items found in association
100% 184 of 184 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,838 of 29,107 population items
255 GO terms are associated with 136 of 184 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] = 0 BP + 0 MF + 2 CC
2 items WROTE: GO_analysis_module_lightgreen.xlsx
2 GOEA results for 20 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:0:00:04.569436 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 307 IDs ... 89% 272 of
307 study items found in association
100% 307 of 307 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher

```

```

12,438 GO terms are associated with 17,848 of 29,107 population items
1,480 GO terms are associated with 272 of 307 study items
METHOD fdr_bh:
    20 GO terms found significant (< 0.05=alpha) ( 20 enriched + 0
purified): statsmodels fdr_bh
    77 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 307 IDs ... 92% 281 of
307 study items found in association
100% 307 of 307 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    353 GO terms are associated with 281 of 307 study items
METHOD fdr_bh:
    45 GO terms found significant (< 0.05=alpha) ( 45 enriched + 0
purified): statsmodels fdr_bh
    232 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 307 IDs ... 88% 270 of
307 study items found in association
100% 307 of 307 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    432 GO terms are associated with 270 of 307 study items
METHOD fdr_bh:
    6 GO terms found significant (< 0.05=alpha) ( 6 enriched + 0
purified): statsmodels fdr_bh
    195 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[71] = 20 BP + 6 MF + 45 CC
71 items WROTE: GO_analysis_module_lightcyan.xlsx
71 GOEA results for 271 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:0:00:04.452064 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...

```

```

74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 471 IDs ... 91%    430 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
12,438 GO terms are associated with 17,848 of 29,107 population items
2,891 GO terms are associated with    430 of    471 study items
METHOD fdr_bh:
231 GO terms found significant (< 0.05=alpha) (230 enriched + 1
purified): statsmodels fdr_bh
347 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 471 IDs ... 95%    449 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
1,756 GO terms are associated with 18,712 of 29,107 population items
423 GO terms are associated with    449 of    471 study items
METHOD fdr_bh:
69 GO terms found significant (< 0.05=alpha) ( 69 enriched + 0
purified): statsmodels fdr_bh
440 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 471 IDs ... 93%    440 of
471 study items found in association
100%    471 of    471 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
4,434 GO terms are associated with 17,838 of 29,107 population items
707 GO terms are associated with    440 of    471 study items
METHOD fdr_bh:
32 GO terms found significant (< 0.05=alpha) ( 32 enriched + 0
purified): statsmodels fdr_bh
392 study items associated with significant GO IDs (enriched)
0 study items associated with significant GO IDs (purified)
Significant results[332] = 231 BP + 32 MF + 69 CC
332 items WROTE: GO_analysis_module_purple.xlsx
332 GOEA results for 448 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:0:00:04.489237 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go

```

BP 18,505 annotated human genes  
MF 18,190 annotated human genes  
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...  
70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 1233 IDs ... 91% 1,121 of  
1,233 study items found in association  
100% 1,233 of 1,233 study items found in population(29107)

Calculating 12,438 uncorrected p-values using fisher  
12,438 GO terms are associated with 17,848 of 29,107 population items  
3,585 GO terms are associated with 1,121 of 1,233 study items  
METHOD fdr\_bh:  
61 GO terms found significant (< 0.05=alpha) ( 58 enriched + 3  
purified): statsmodels fdr\_bh  
607 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 1233 IDs ... 95% 1,176 of  
1,233 study items found in association  
100% 1,233 of 1,233 study items found in population(29107)

Calculating 1,756 uncorrected p-values using fisher  
1,756 GO terms are associated with 18,712 of 29,107 population items  
739 GO terms are associated with 1,176 of 1,233 study items  
METHOD fdr\_bh:  
110 GO terms found significant (< 0.05=alpha) (108 enriched + 2  
purified): statsmodels fdr\_bh  
1,146 study items associated with significant GO IDs (enriched)  
77 study items associated with significant GO IDs (purified)

Run MF Gene Ontology Analysis: current study set of 1233 IDs ... 94% 1,159 of  
1,233 study items found in association  
100% 1,233 of 1,233 study items found in population(29107)

Calculating 4,434 uncorrected p-values using fisher  
4,434 GO terms are associated with 17,838 of 29,107 population items  
1,118 GO terms are associated with 1,159 of 1,233 study items  
METHOD fdr\_bh:  
47 GO terms found significant (< 0.05=alpha) ( 44 enriched + 3  
purified): statsmodels fdr\_bh  
1,068 study items associated with significant GO IDs (enriched)  
3 study items associated with significant GO IDs (purified)

Significant results[218] = 61 BP + 47 MF + 110 CC  
 218 items WROTE: GO\_analysis\_module\_red.xlsx  
 218 GOEA results for 1196 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:0:00:04.691996 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:  
 gene2go  
 BP 18,505 annotated human genes  
 MF 18,190 annotated human genes  
 CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...  
 70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...  
 74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...  
 70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 290 IDs ... 90% 261 of  
 290 study items found in association  
 100% 290 of 290 study items found in population(29107)  
 Calculating 12,438 uncorrected p-values using fisher  
 12,438 GO terms are associated with 17,848 of 29,107 population items  
 1,770 GO terms are associated with 261 of 290 study items  
 METHOD fdr\_bh:  
 252 GO terms found significant (< 0.05=alpha) (252 enriched + 0  
 purified): statsmodels fdr\_bh  
 222 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 290 IDs ... 96% 277 of  
 290 study items found in association  
 100% 290 of 290 study items found in population(29107)  
 Calculating 1,756 uncorrected p-values using fisher  
 1,756 GO terms are associated with 18,712 of 29,107 population items  
 269 GO terms are associated with 277 of 290 study items  
 METHOD fdr\_bh:  
 65 GO terms found significant (< 0.05=alpha) ( 65 enriched + 0  
 purified): statsmodels fdr\_bh  
 265 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 290 IDs ... 92% 267 of  
 290 study items found in association  
 100% 290 of 290 study items found in population(29107)

```

Calculating 4,434 uncorrected p-values using fisher
  4,434 GO terms are associated with 17,838 of 29,107 population items
  468 GO terms are associated with 267 of 290 study items
METHOD fdr_bh:
  35 GO terms found significant (< 0.05=alpha) ( 35 enriched + 0
purified): statsmodels fdr_bh
  231 study items associated with significant GO IDs (enriched)
  0 study items associated with significant GO IDs (purified)
Significant results[352] = 252 BP + 35 MF + 65 CC
  352 items WROTE: GO_analysis_module_grey60.xlsx
  352 GOEA results for 275 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:0:00:04.437832 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
  70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
  74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
  70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 234 IDs ... 68% 159 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 17,848 of 29,107 population items
  635 GO terms are associated with 159 of 234 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 234 IDs ... 71% 167 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 18,712 of 29,107 population items
  168 GO terms are associated with 167 of 234 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 234 IDs ... 65%    152 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 17,838 of 29,107 population items
    283 GO terms are associated with    152 of    234 study items
METHOD fdr_bh:
    1 GO terms found significant (< 0.05=alpha) ( 1 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[1] = 0 BP + 1 MF + 0 CC
    1 items WROTE: GO_analysis_module_salmon.xlsx
    1 GOEA results for    41 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:0:00:04.556426 330,313 annotations, 20,686 genes, 18,684 GOs, 1 taxids READ:
gene2go
BP 18,505 annotated human genes
MF 18,190 annotated human genes
CC 19,423 annotated human genes

Load BP Gene Ontology Analysis ...
    70% 20,236 of 29,107 population items found in association

Load CC Gene Ontology Analysis ...
    74% 21,429 of 29,107 population items found in association

Load MF Gene Ontology Analysis ...
    70% 20,354 of 29,107 population items found in association

Run BP Gene Ontology Analysis: current study set of 417 IDs ... 88%    369 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 12,438 uncorrected p-values using fisher
    12,438 GO terms are associated with 17,848 of 29,107 population items
    1,924 GO terms are associated with    369 of    417 study items
METHOD fdr_bh:
    10 GO terms found significant (< 0.05=alpha) ( 10 enriched + 0
purified): statsmodels fdr_bh
    117 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 417 IDs ... 93%    387 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 1,756 uncorrected p-values using fisher
    1,756 GO terms are associated with 18,712 of 29,107 population items
    350 GO terms are associated with    387 of    417 study items
METHOD fdr_bh:
    18 GO terms found significant (< 0.05=alpha) ( 18 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 417 IDs ... 92%    382 of
417 study items found in association
100%    417 of    417 study items found in population(29107)
Calculating 4,434 uncorrected p-values using fisher
    4,434 GO terms are associated with 17,838 of 29,107 population items
    614 GO terms are associated with    382 of    417 study items
METHOD fdr_bh:
    12 GO terms found significant (< 0.05=alpha) ( 12 enriched + 0
purified): statsmodels fdr_bh
    314 study items associated with significant GO IDs (enriched)
    0 study items associated with significant GO IDs (purified)
Significant results[40] = 10 BP + 12 MF + 18 CC
    40 items WROTE: GO_analysis_module_greenyellow.xlsx
    40 GOEA results for 367 study items. WROTE:
GO_analysis_module_greenyellow.txt

```

[ ]: