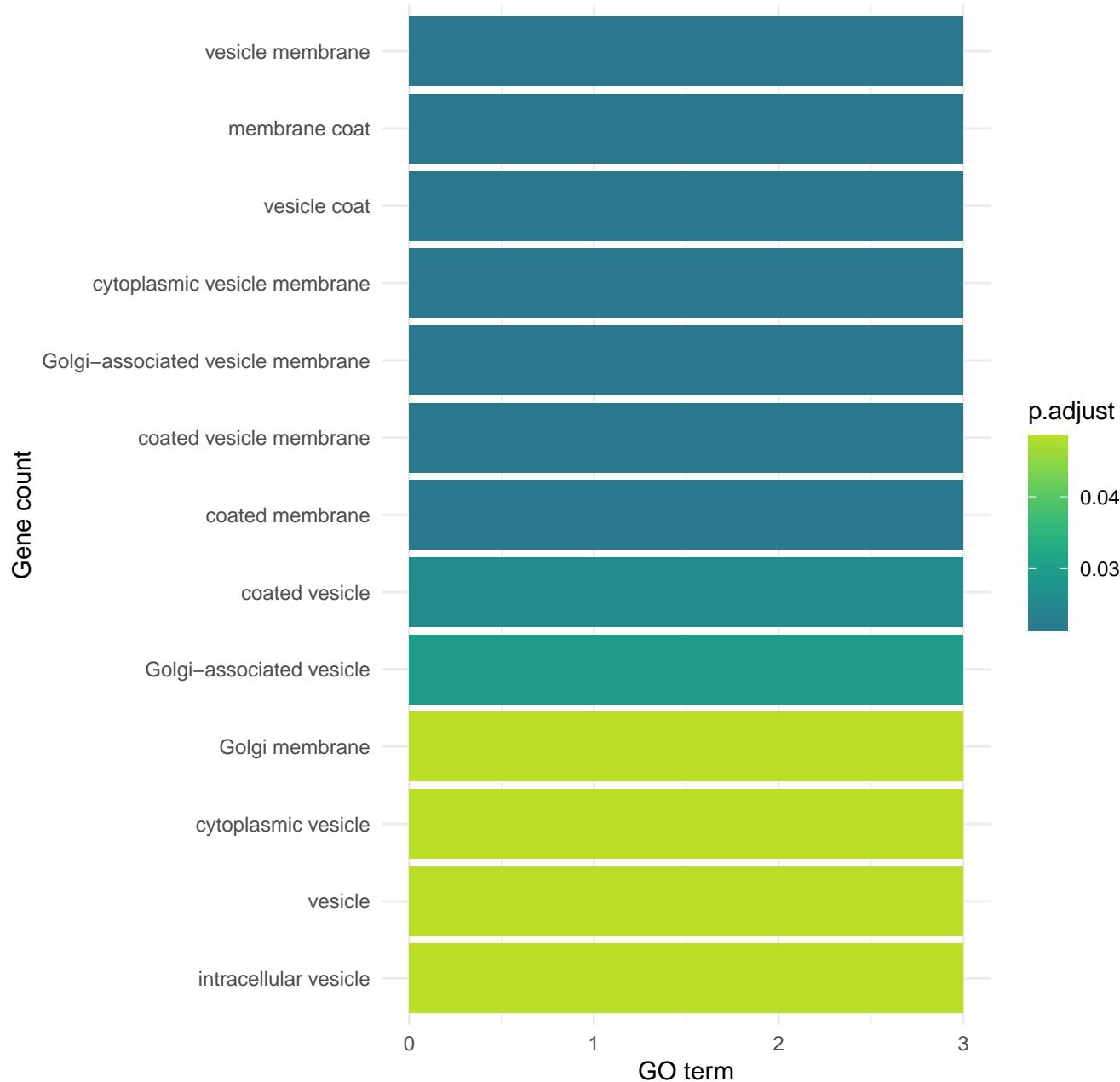
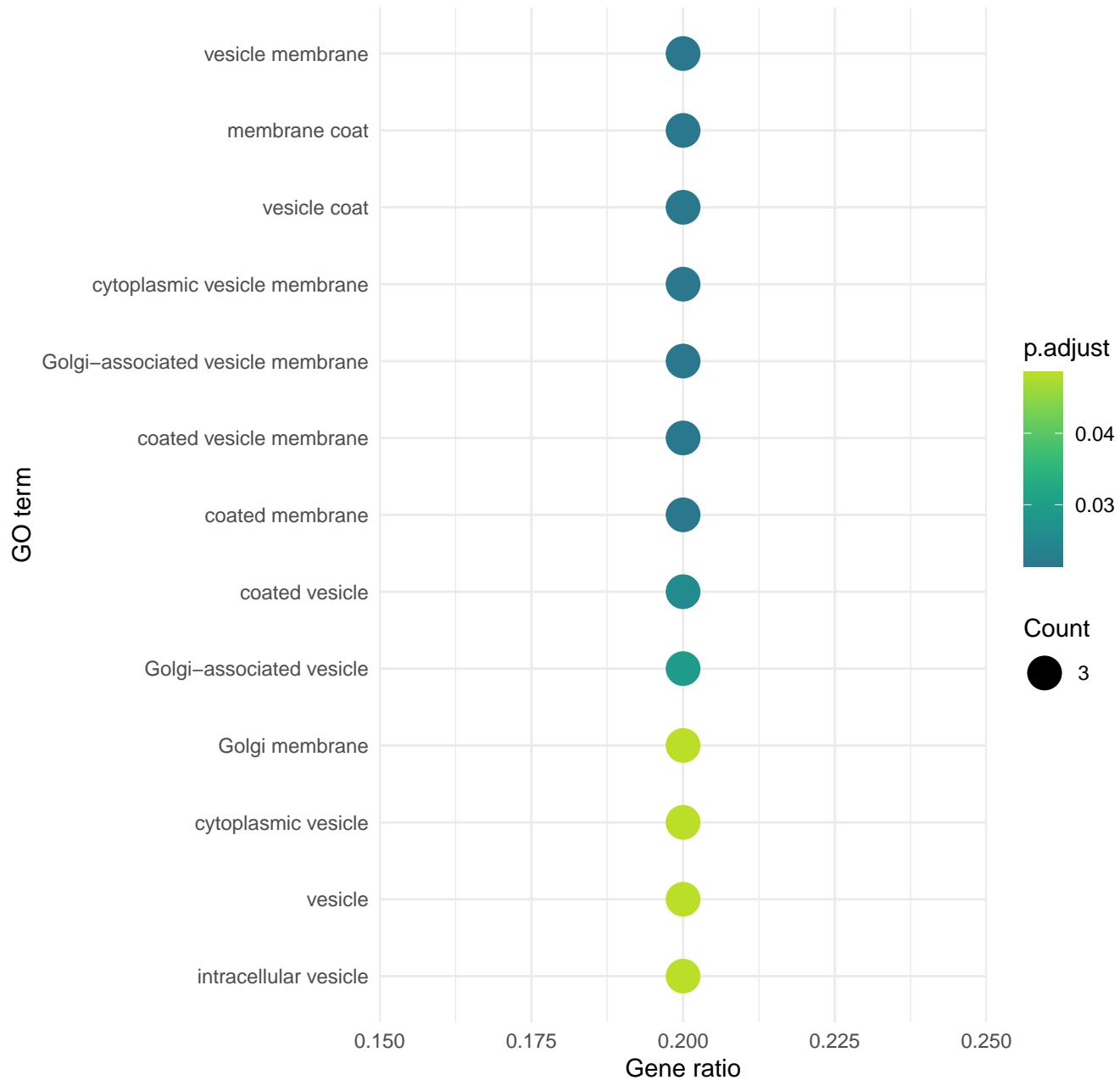


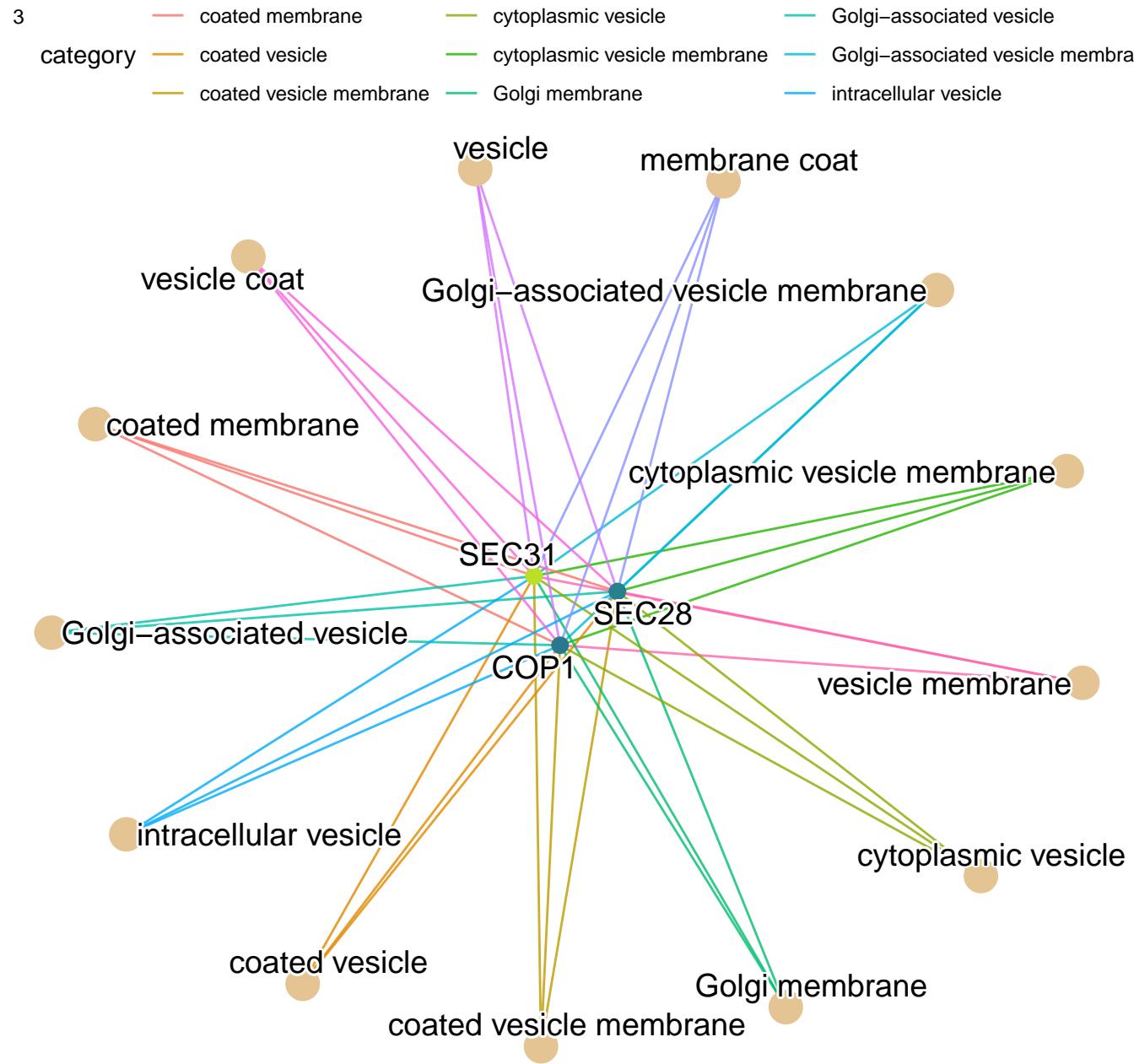
PUF3-TAP Up-regulated GO CC barplot



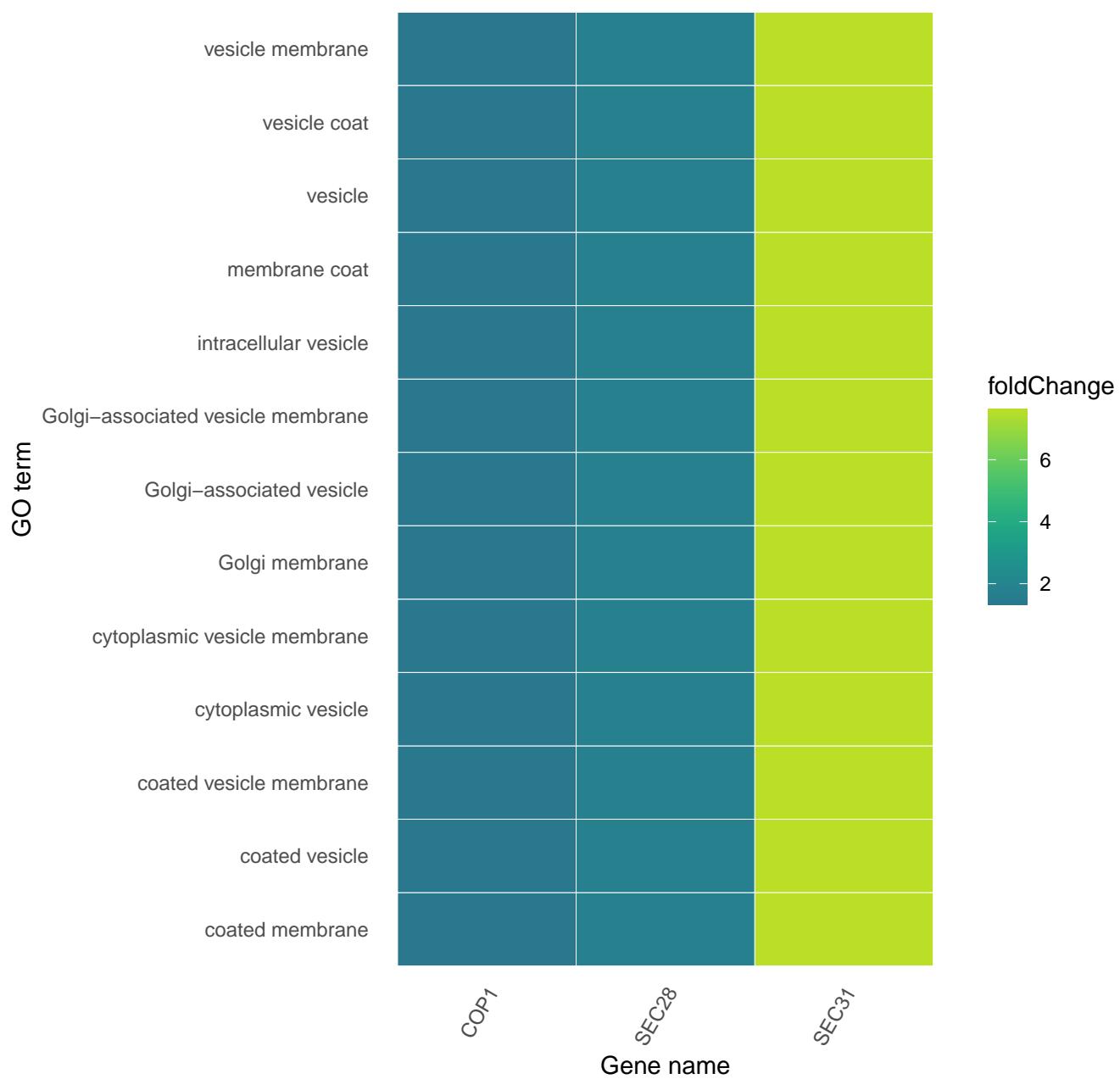
PUF3-TAP Up-regulated GO CC dotplot



PUF3-TAP Up-regulated GO CC cnetplot

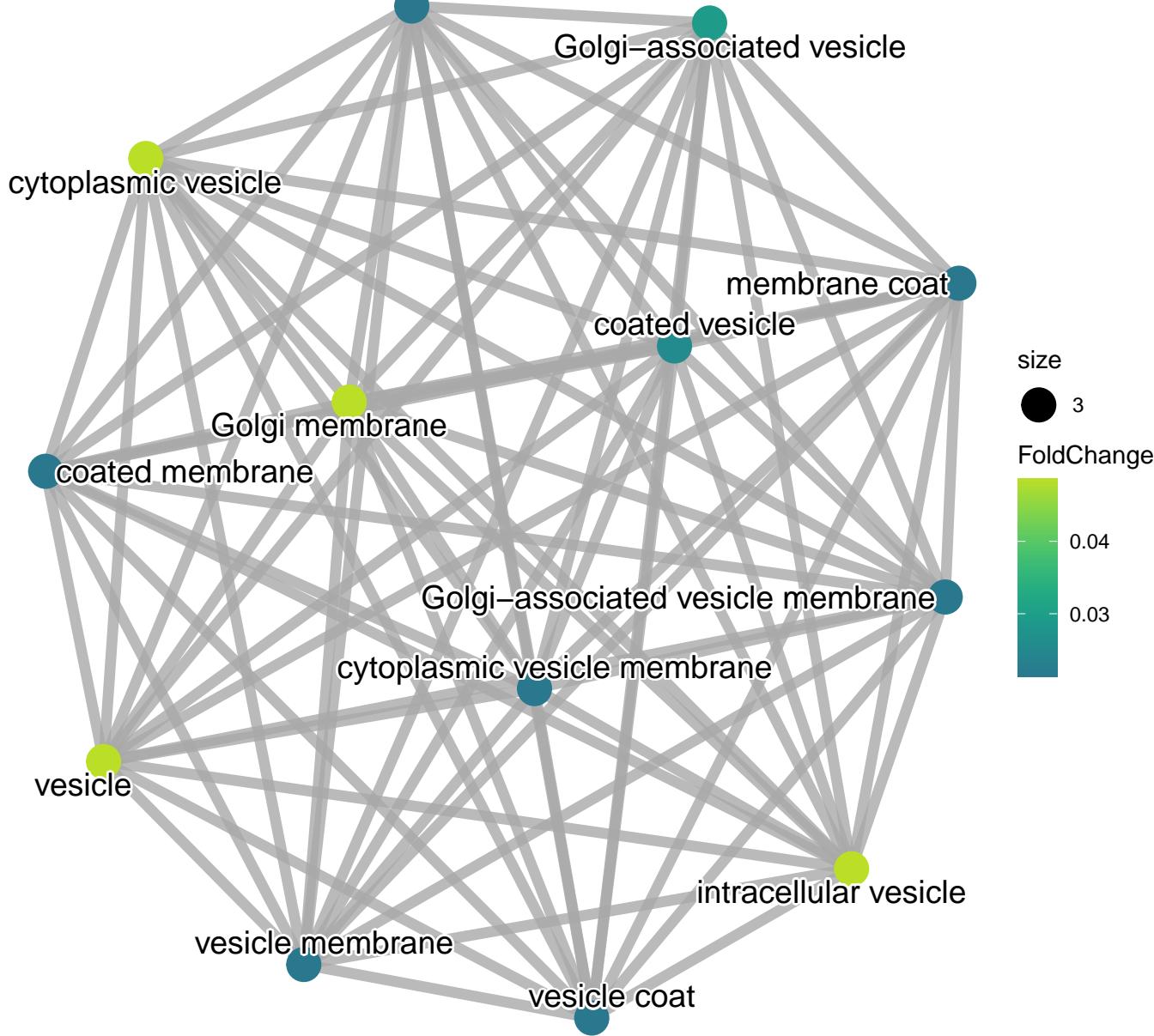


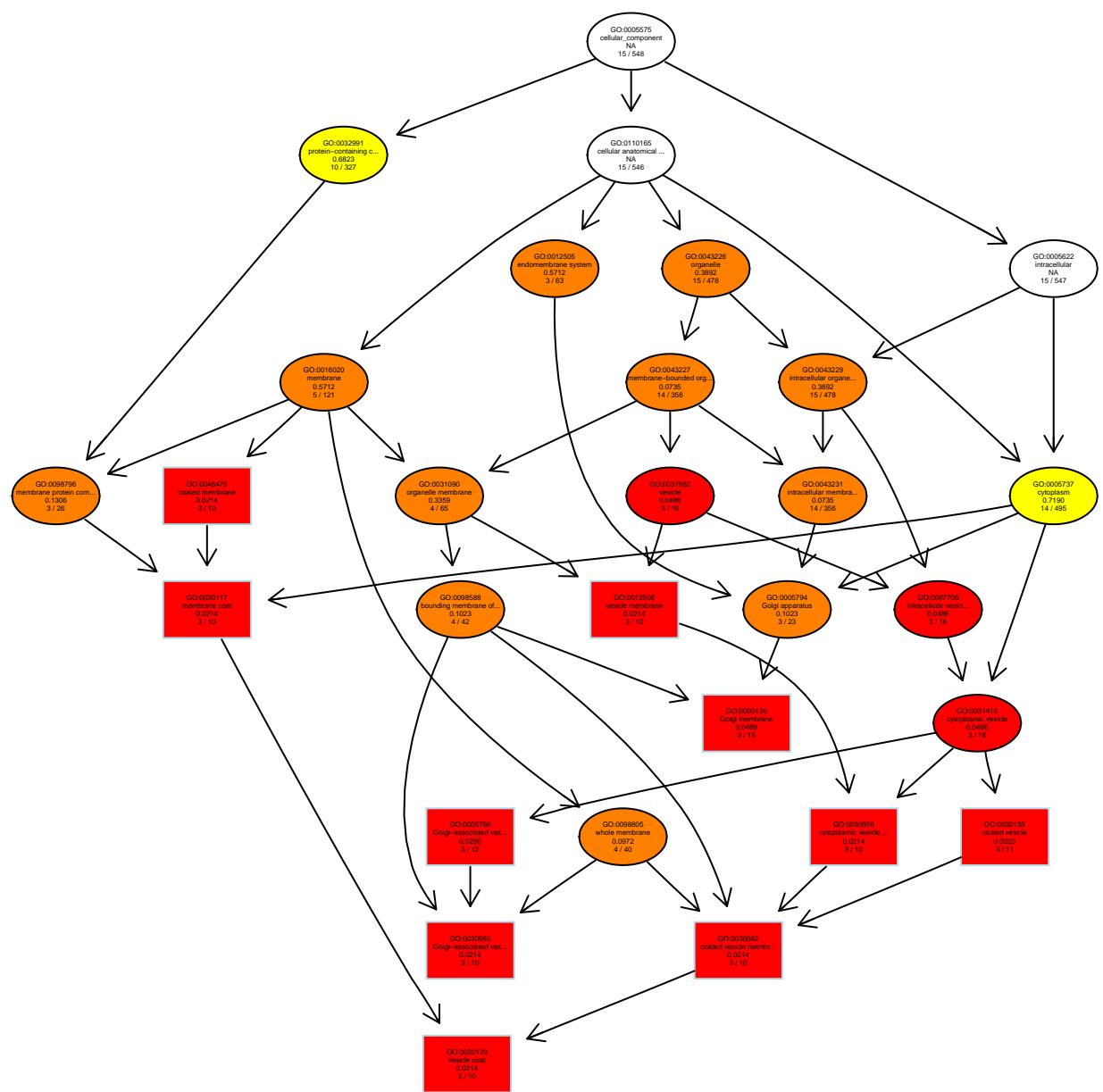
PUF3-TAP Up-regulated GO CC heatplot



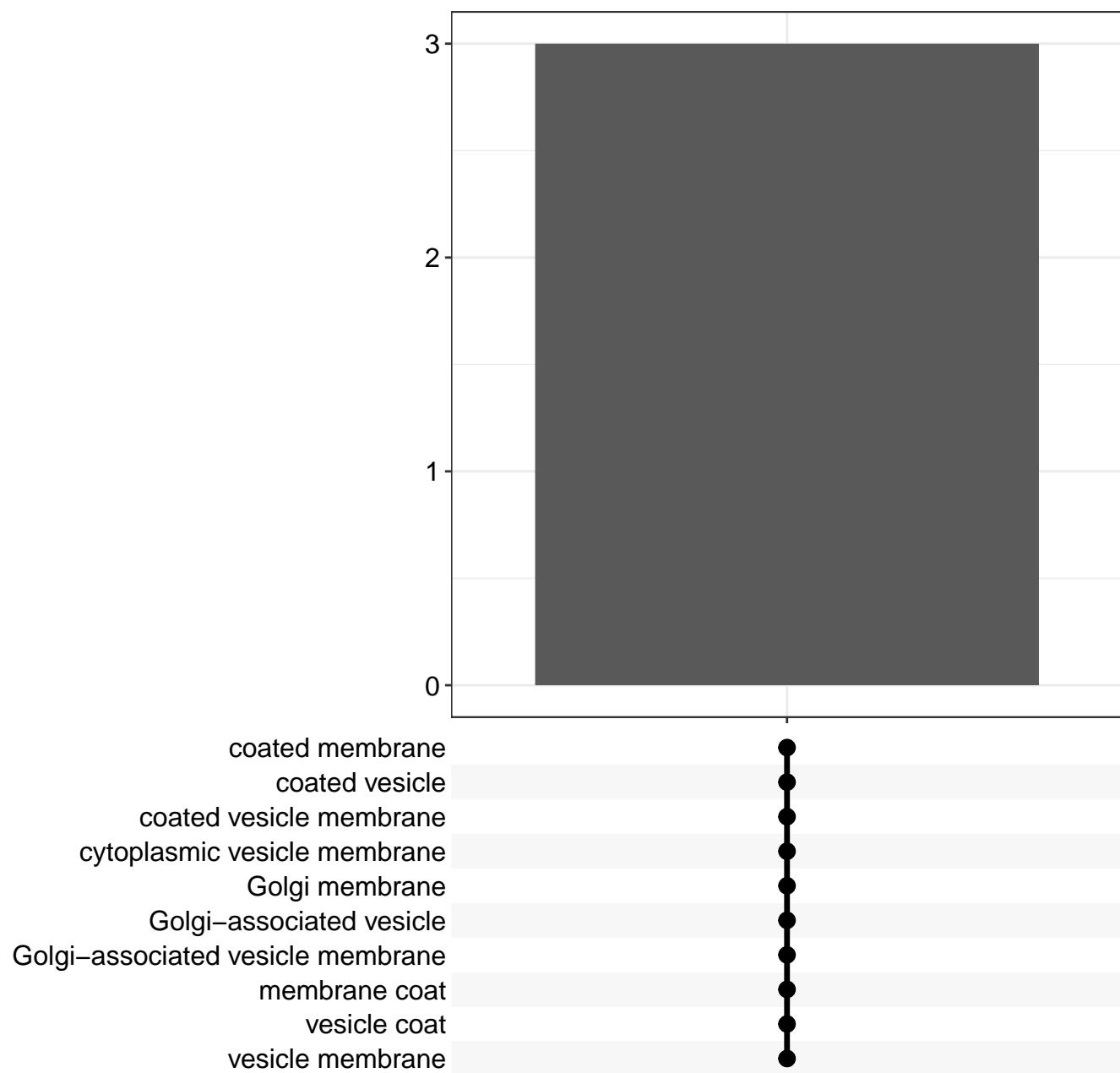
PUF3-TAP Up-regulated GO CC emapplot

coated vesicle membrane

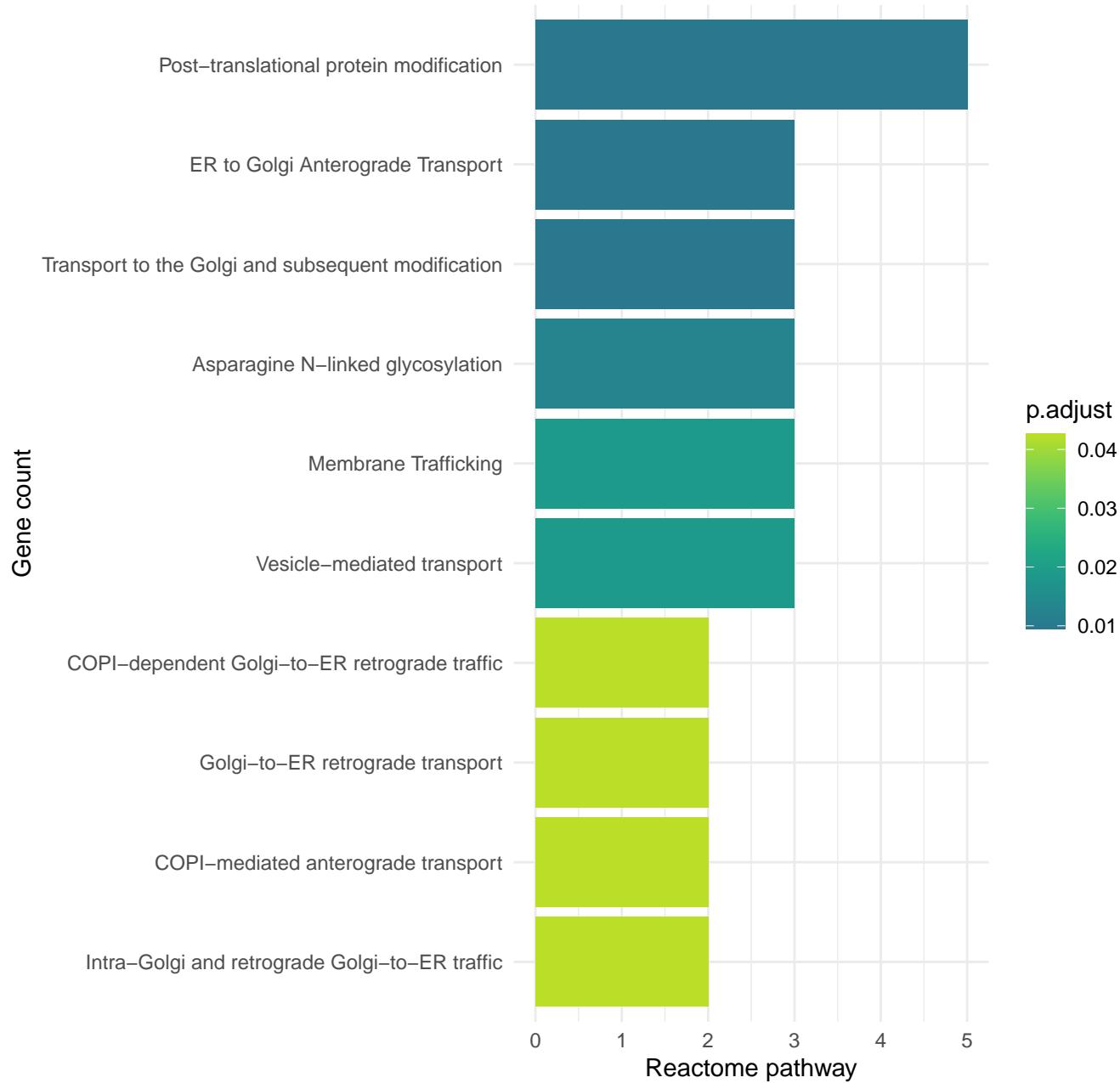




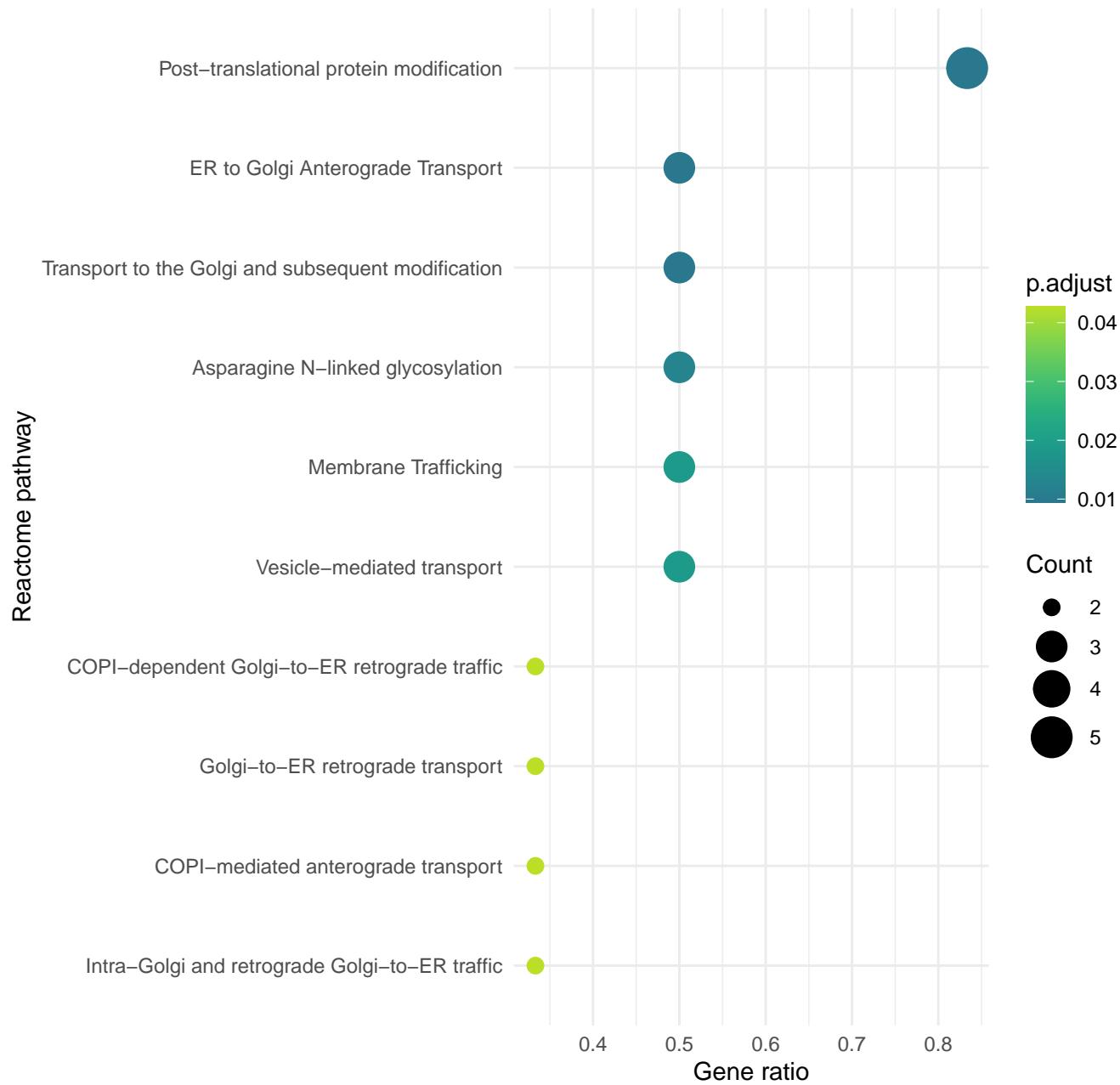
PUF3-TAP Up-regulated GO CC upsetplot



PUF3-TAP Up-regulated Reactome barplot

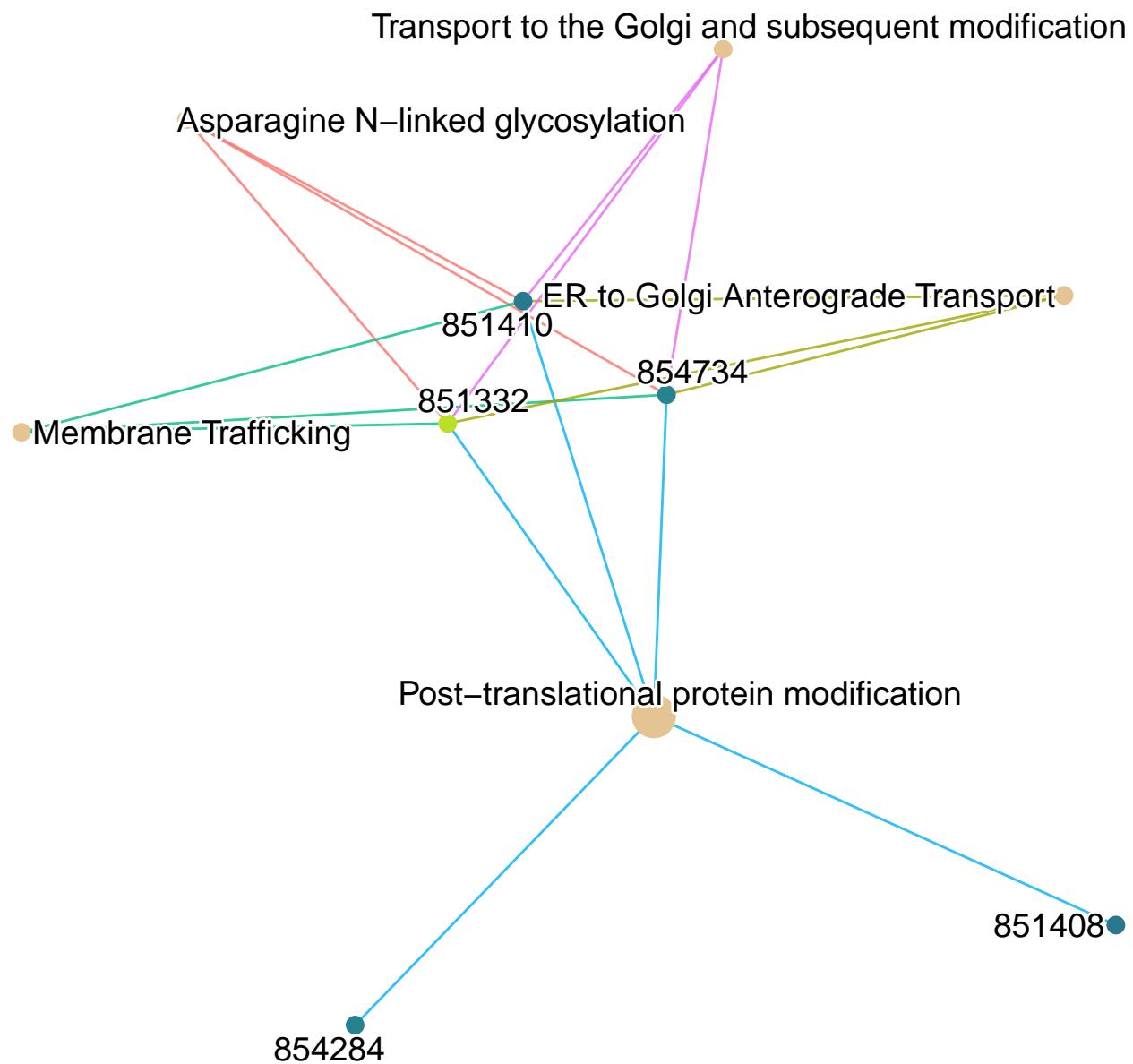


PUF3-TAP Up-regulated Reactome dotplot



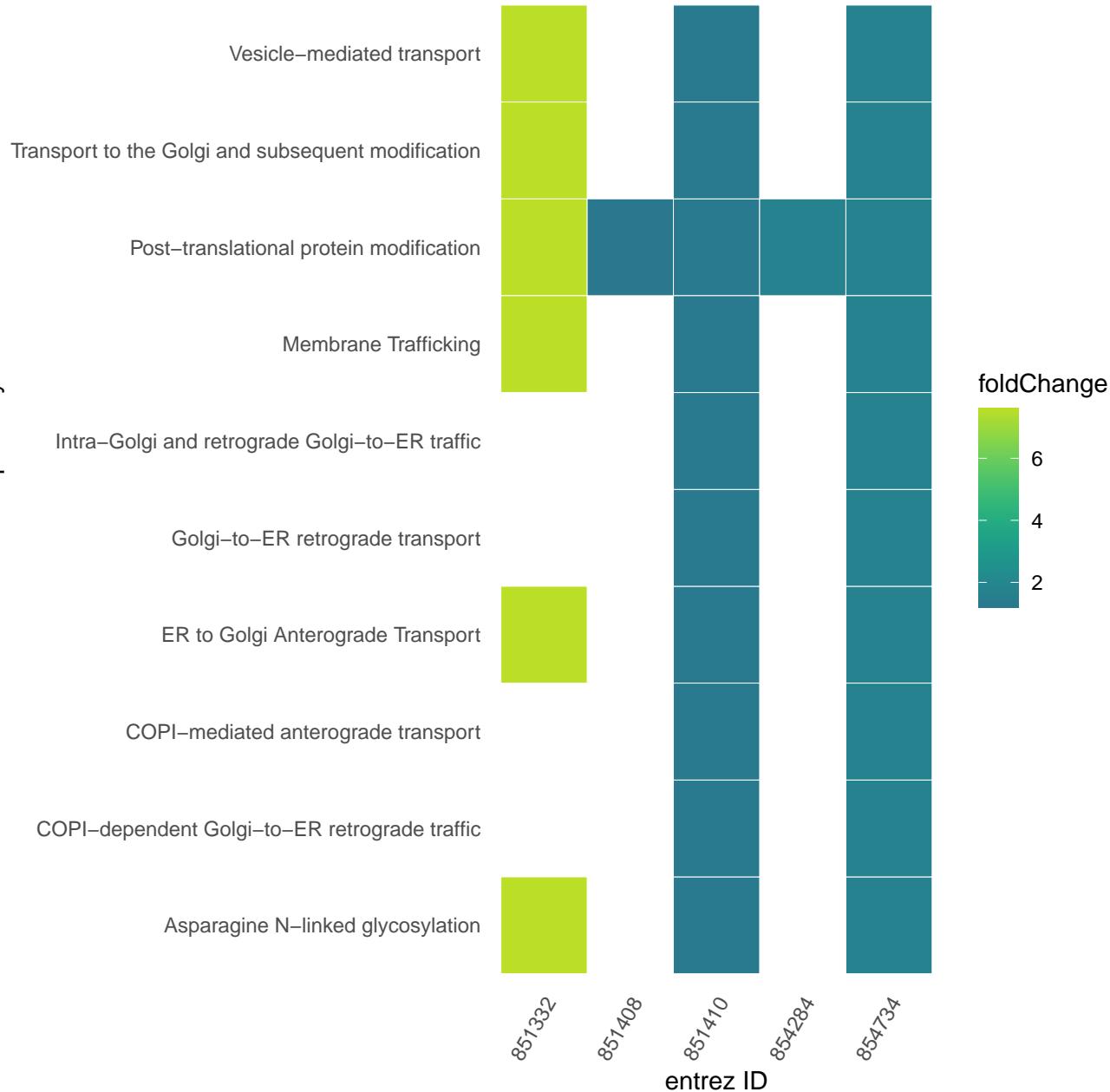
PUF3-TAP Up-regulated Reactome cnetplot

Membrane Trafficking — Post-translational protein modification — Transport to the Golgi and subsequent modification

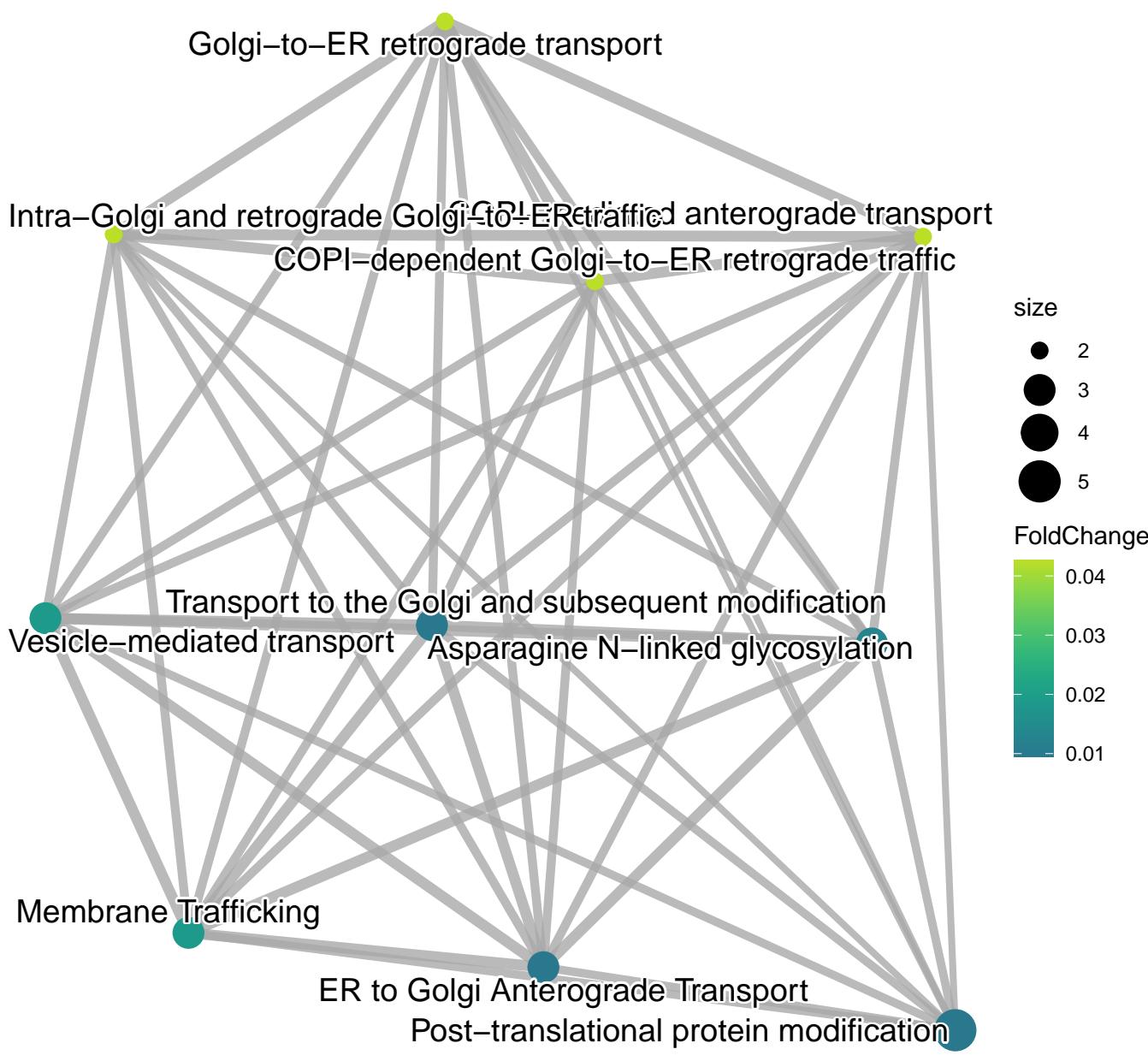


PUF3-TAP Up-regulated Reactome heatplot

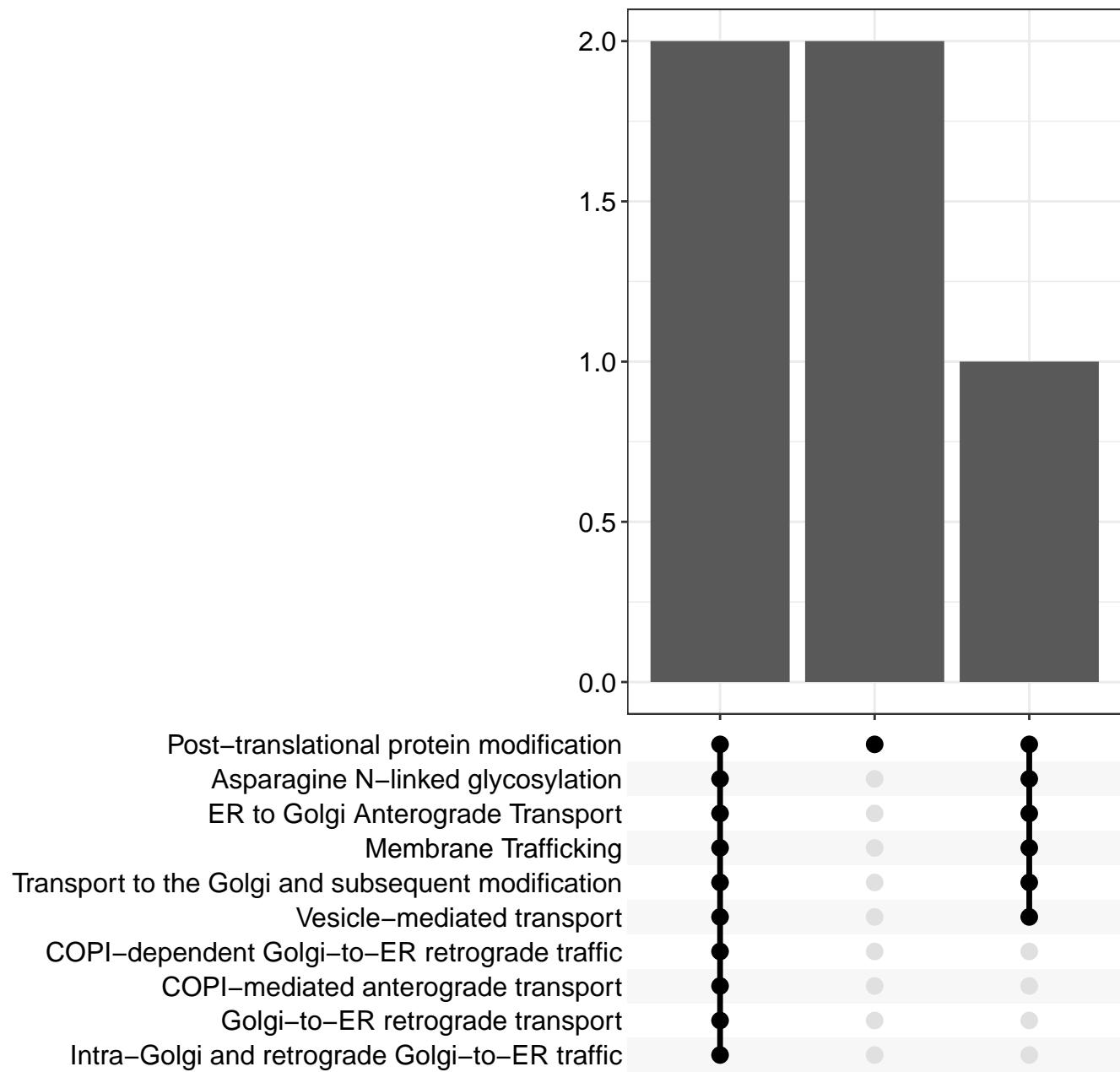
Reactome pathway



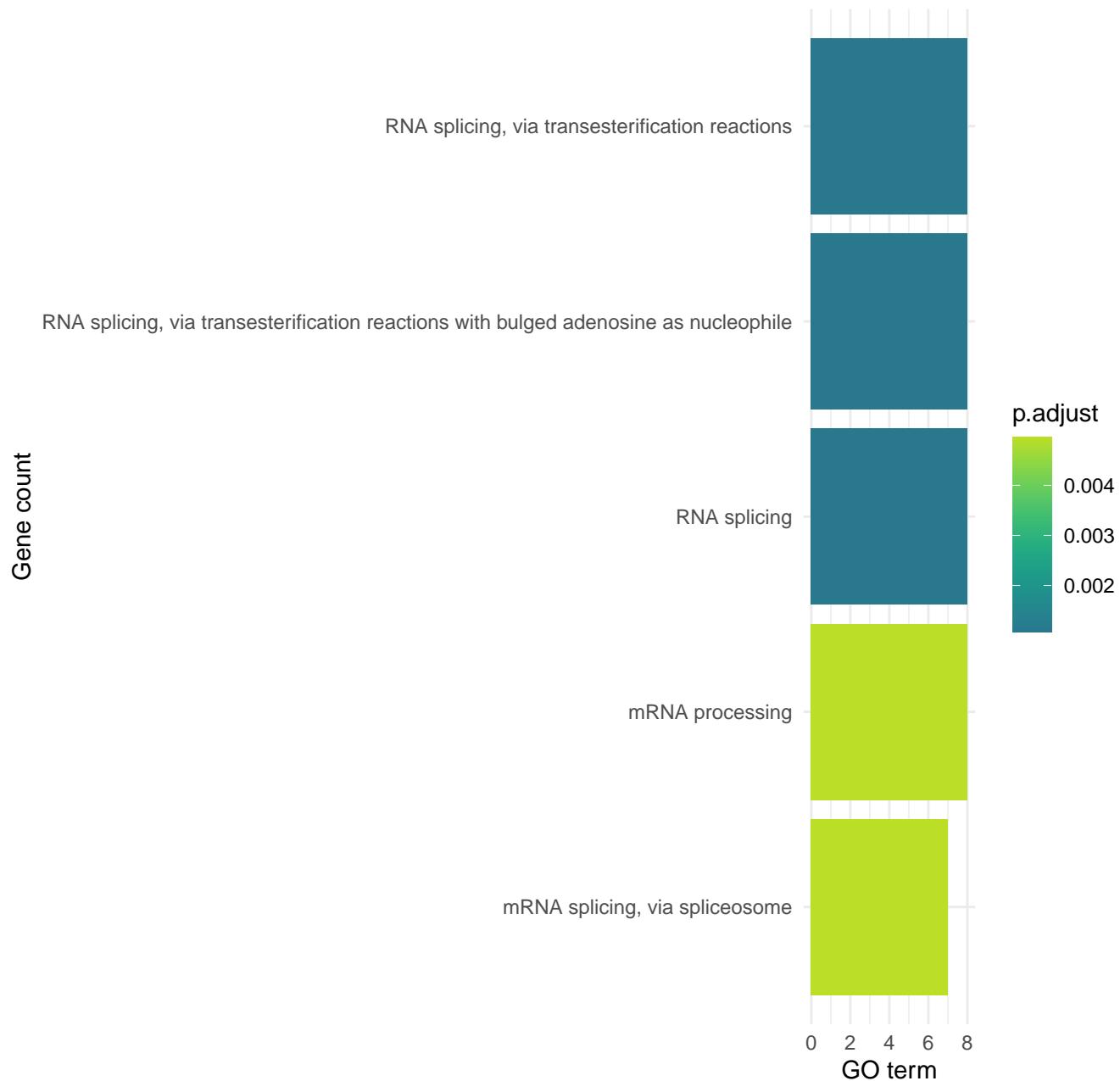
PUF3-TAP Up-regulated Reactome emapplot



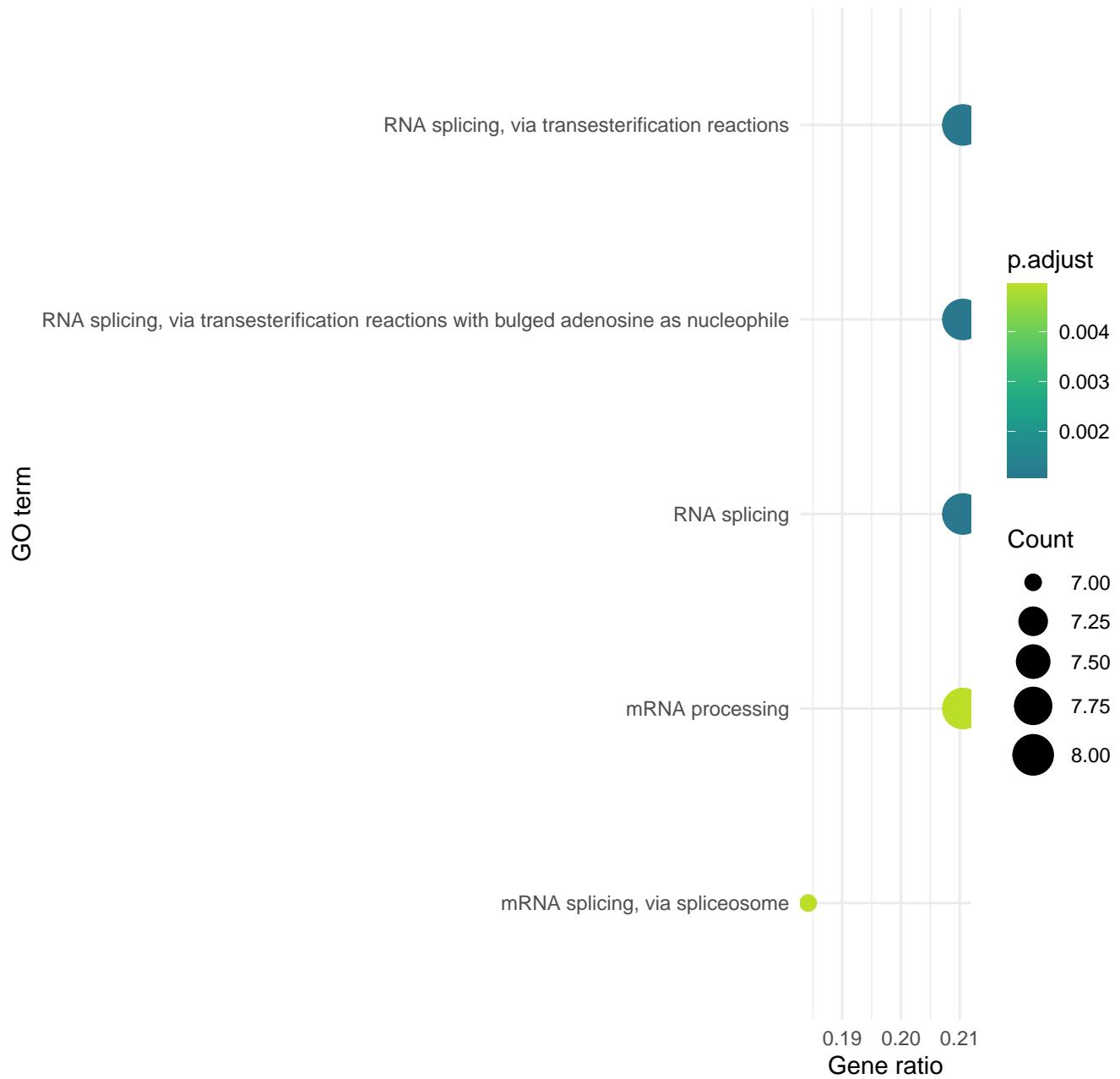
PUF3-TAP Up-regulated Reactome up



IST3-TAP Up-regulated

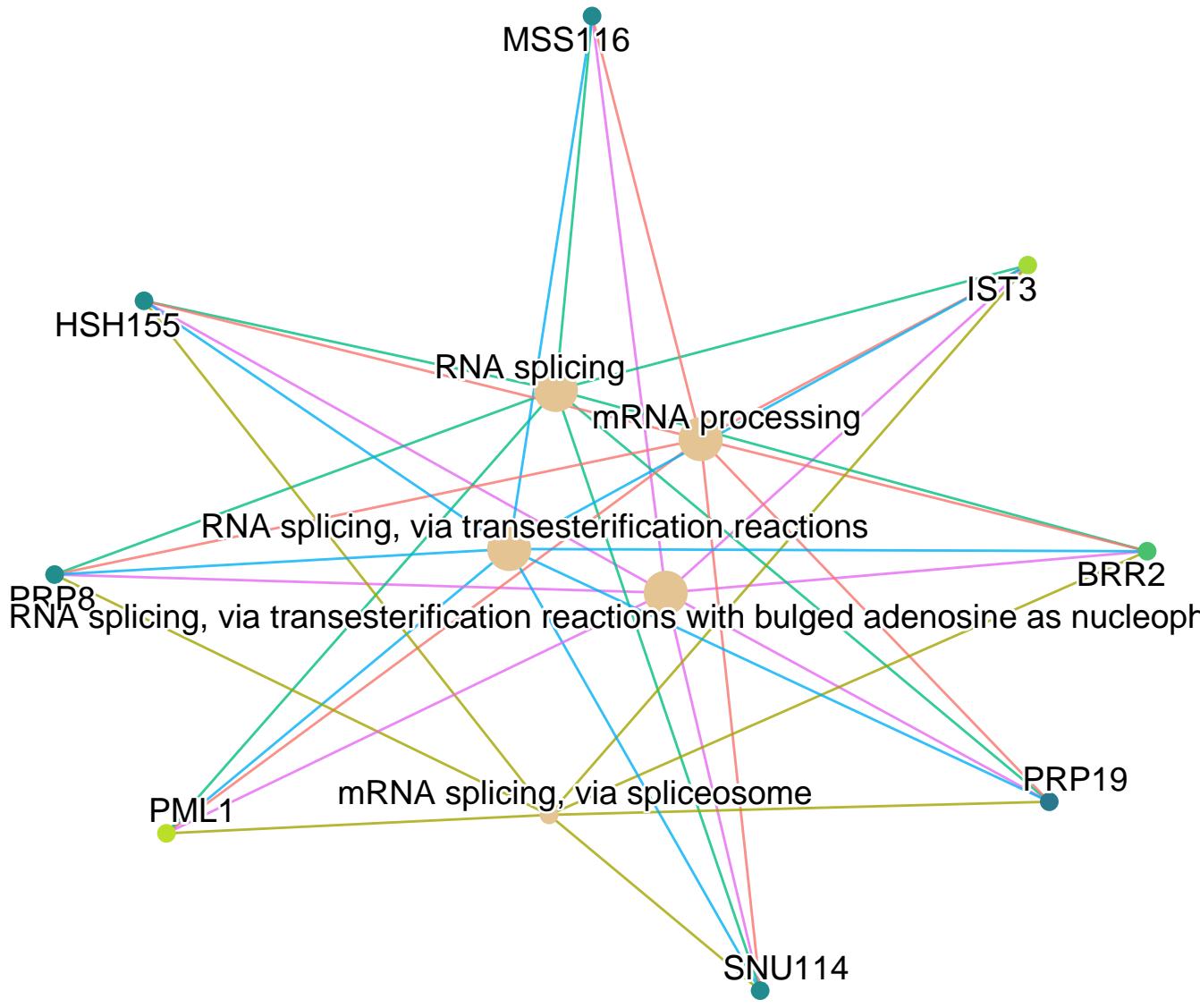


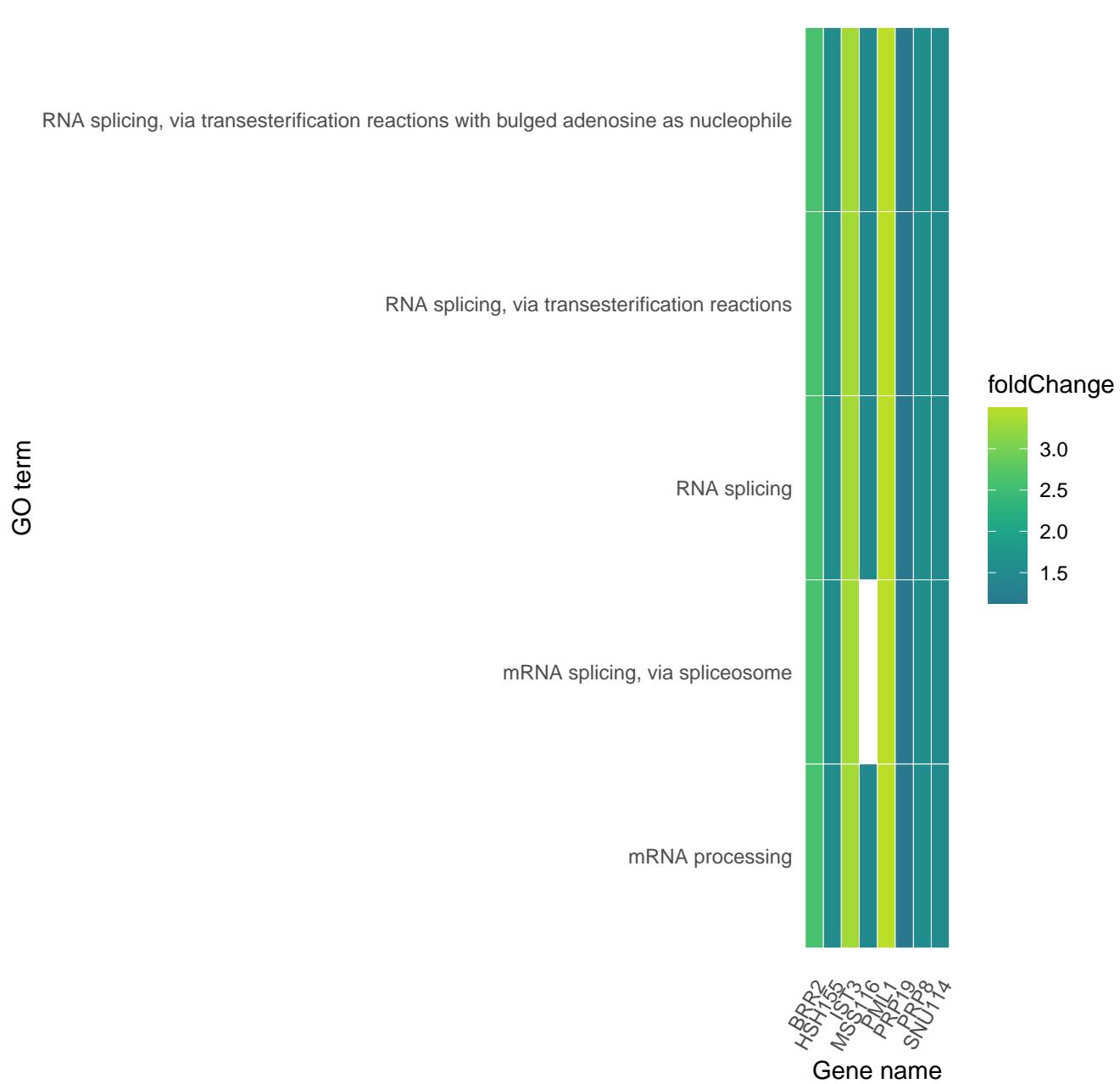
IST3-TAP Up-regulated



IST3-TAP Up-regulated GO BP cnetplot

splicing, via transesterification reactions — RNA splicing, via transesterification reactions with bulged adenosine as nucleoph





IST3-TAP Up-regulated GO BP emapplot

mRNA processing

, via transesterification reactions with bulged adenosine as nucleophile

RNA splicing

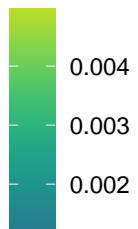
RNA splicing, via transesterification reactions

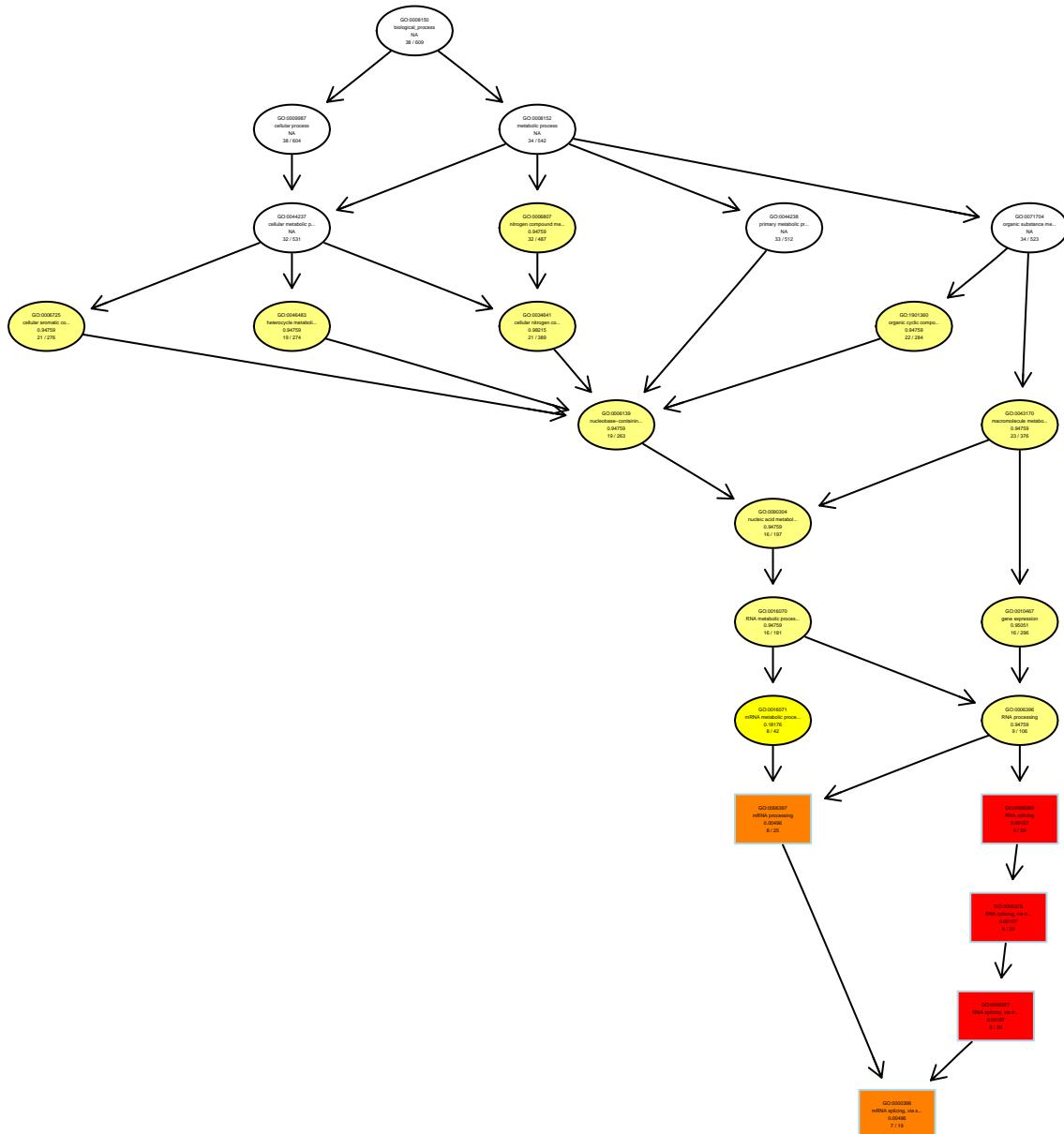
mRNA splicing, via spliceosome

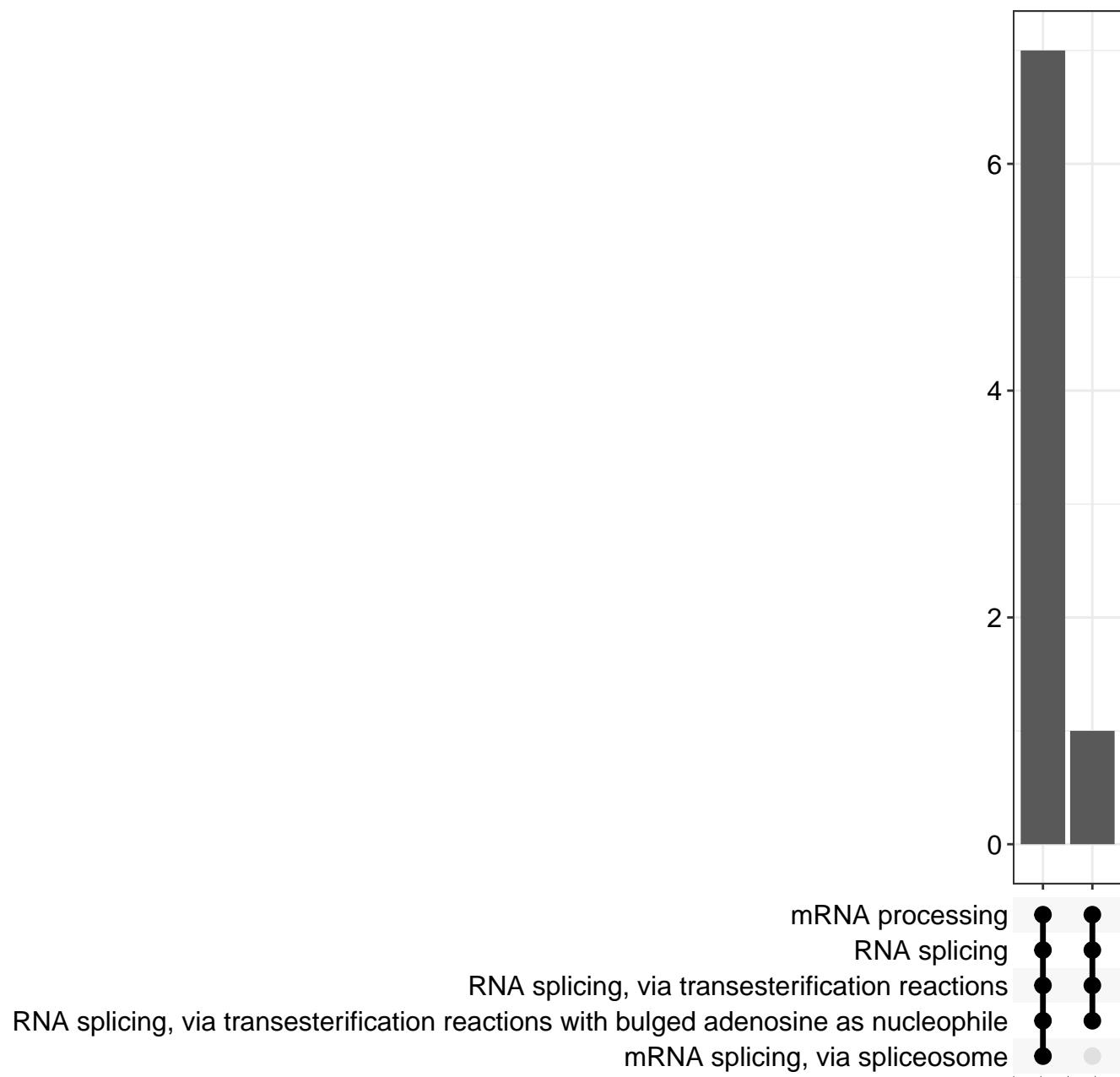
size

- 7.00
- 7.25
- 7.50
- 7.75
- 8.00

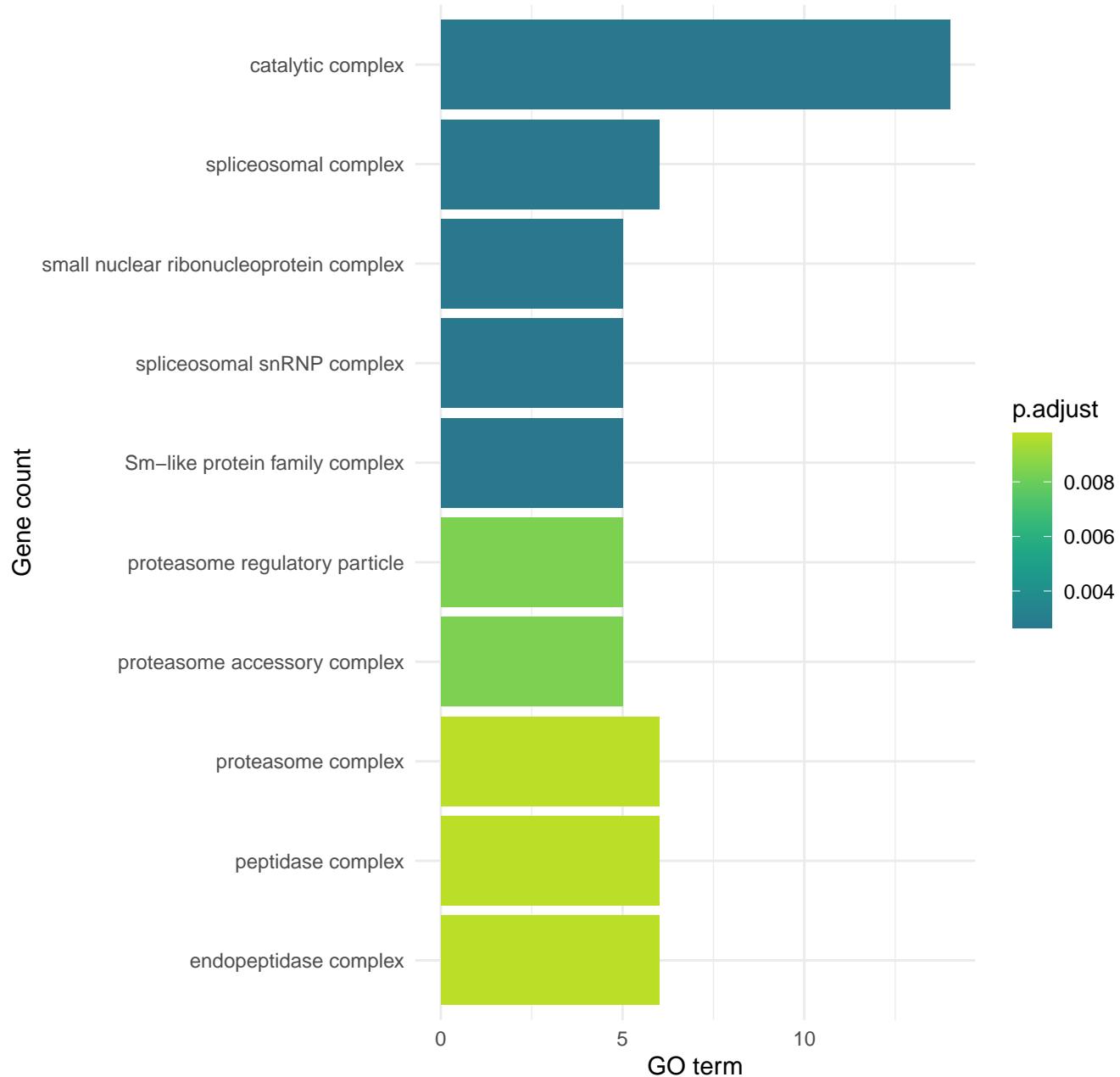
FoldChange



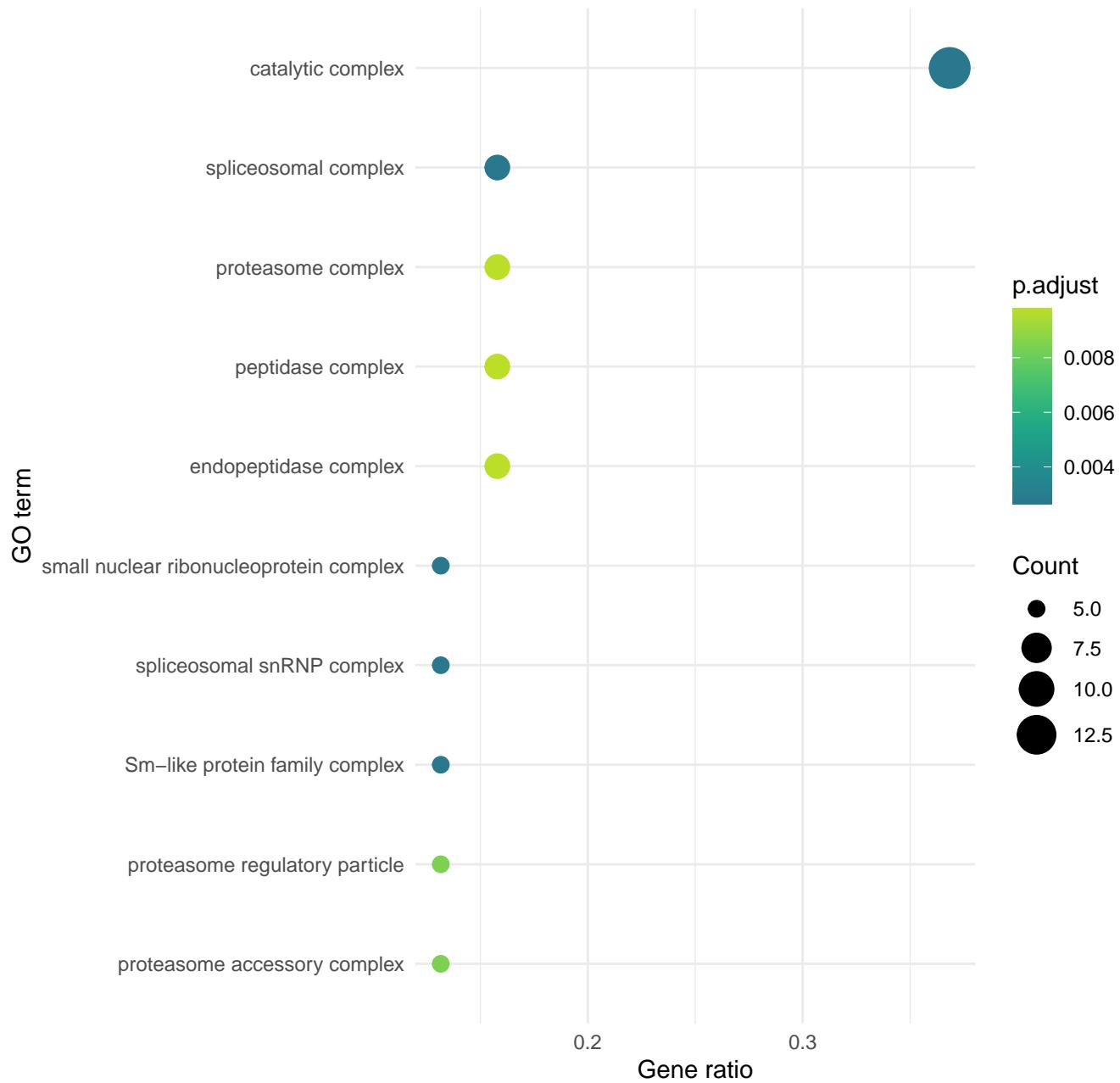




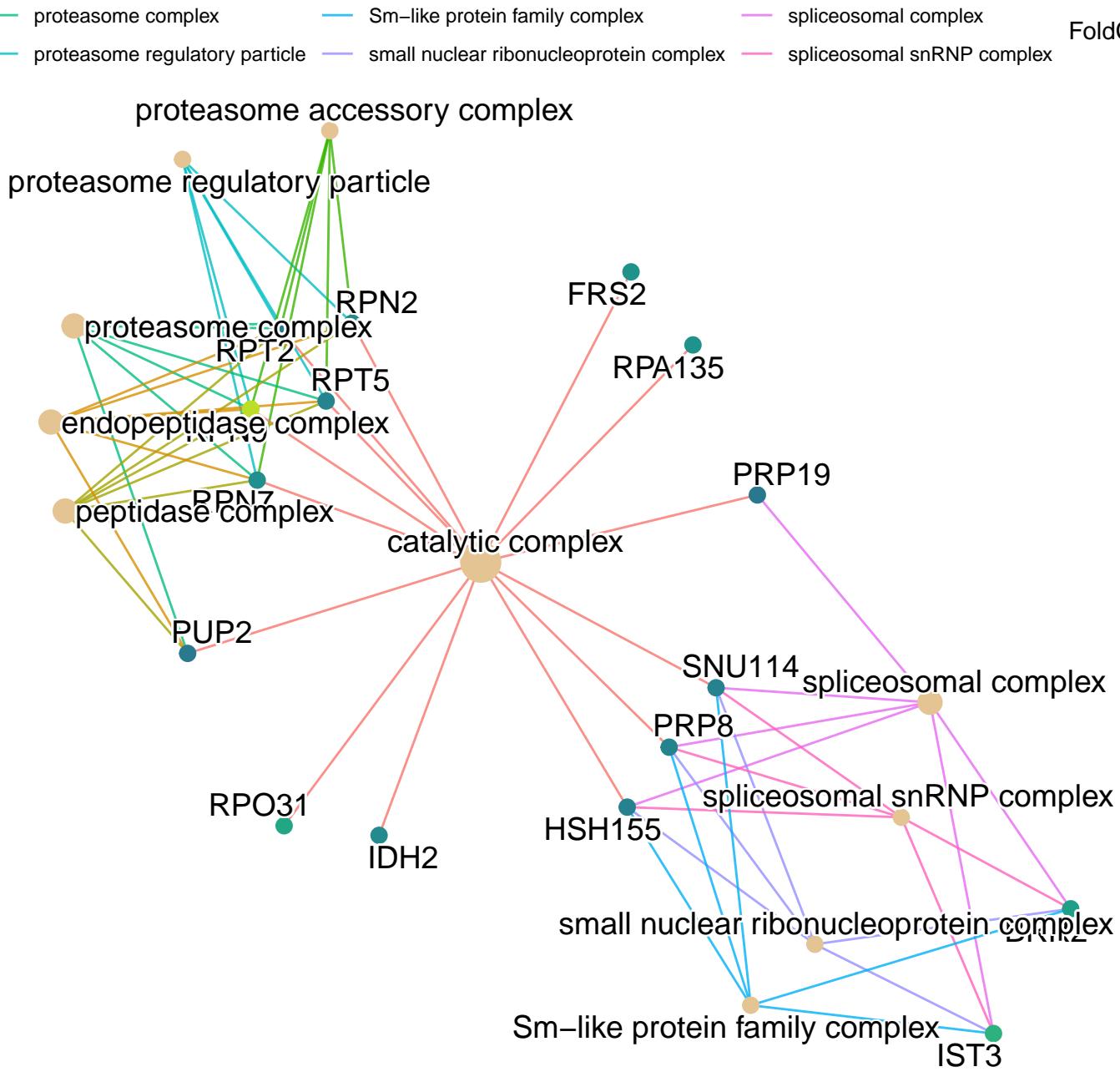
IST3-TAP Up-regulated GO CC barplot



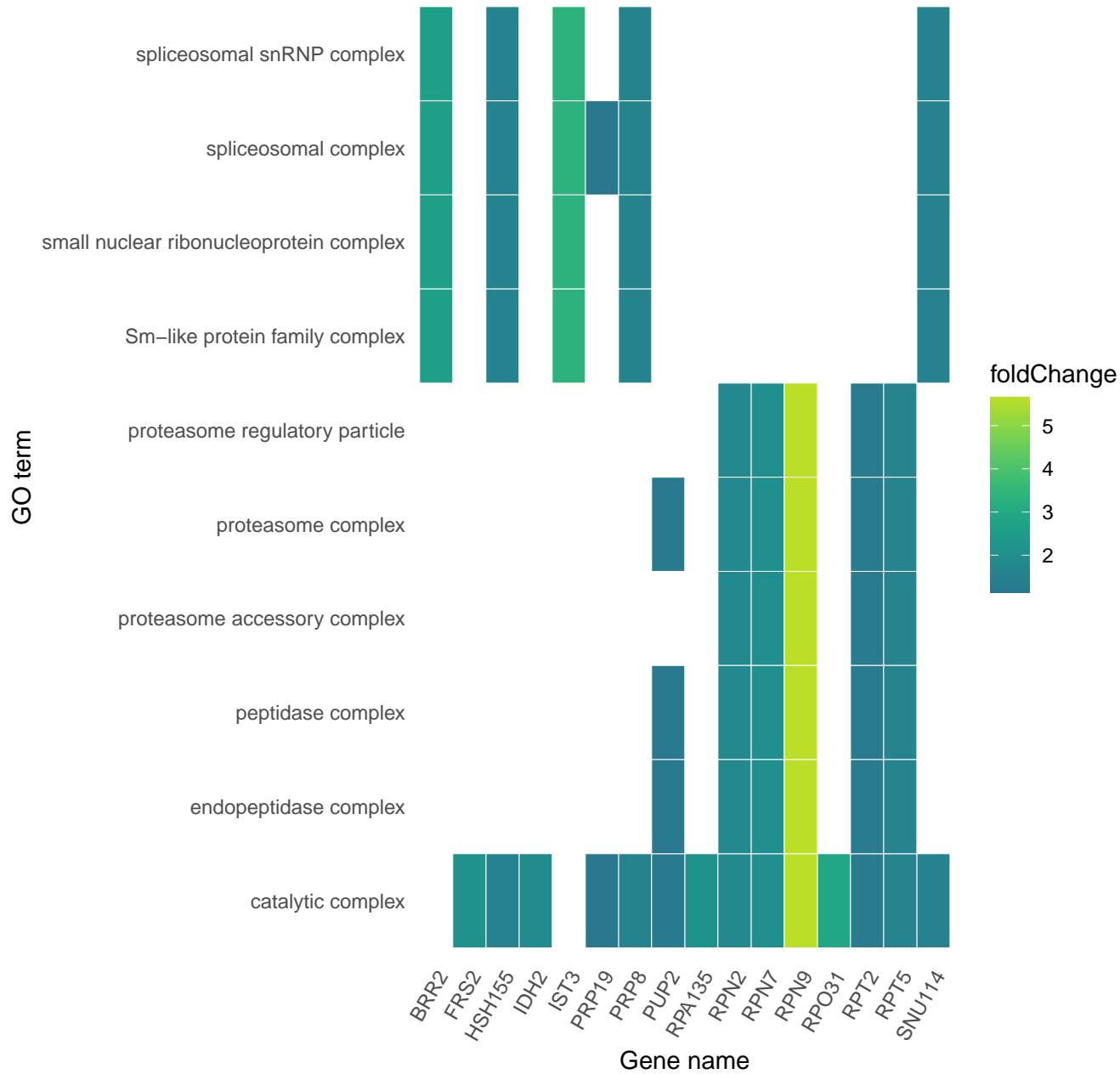
IST3-TAP Up-regulated GO CC dotplot



IST3-TAP Up-regulated GO CC cnetplot



IST3-TAP Up-regulated GO CC heatplot



IST3-TAP Up-regulated GO CC emaplot

proteasome accessory complex

proteasome regulatory particle

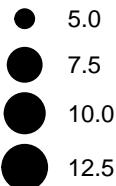
endopeptidase complex

proteasome complex

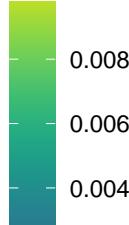
peptidase complex

catalytic complex

size



FoldChange

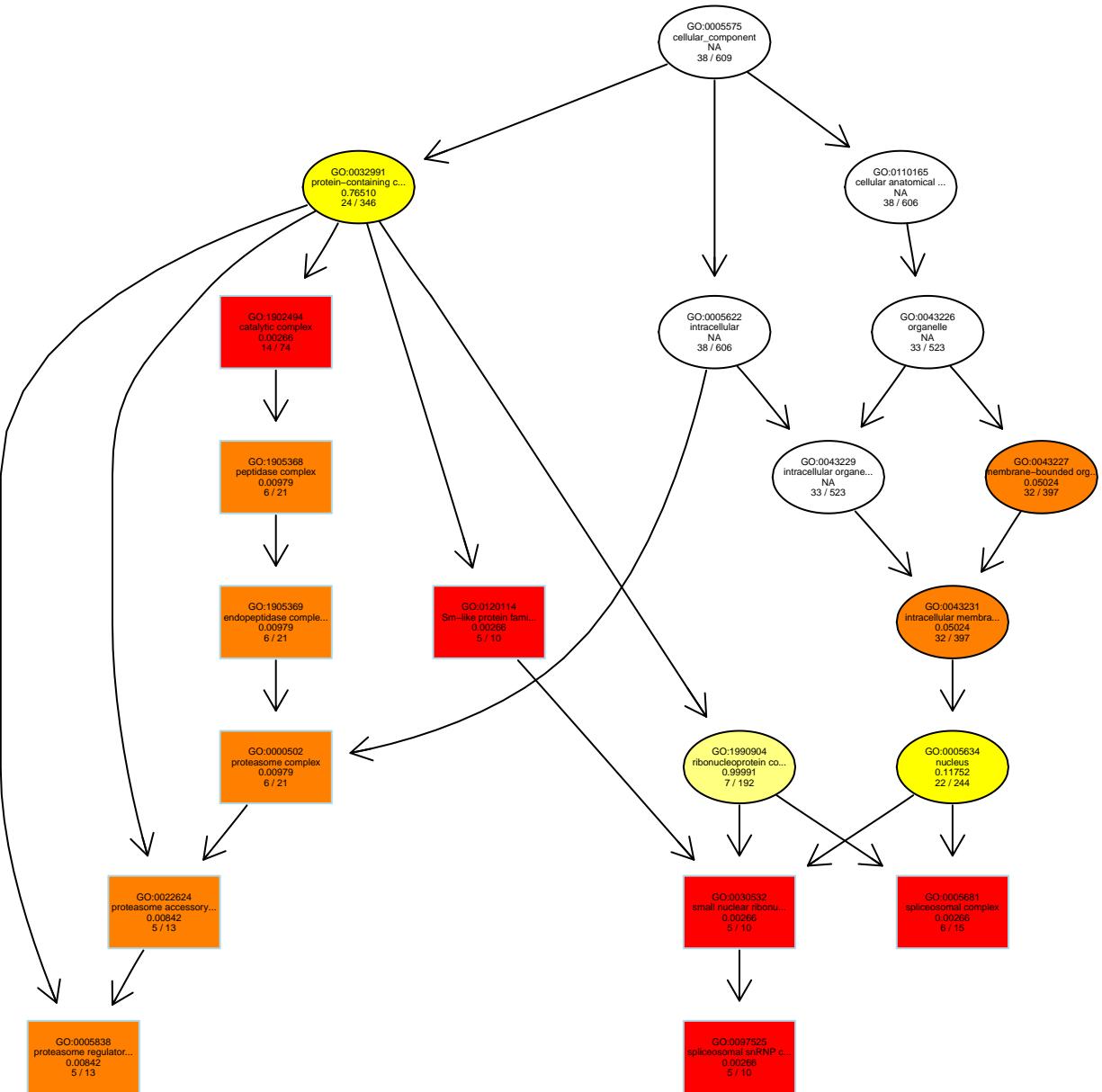


spliceosomal complex

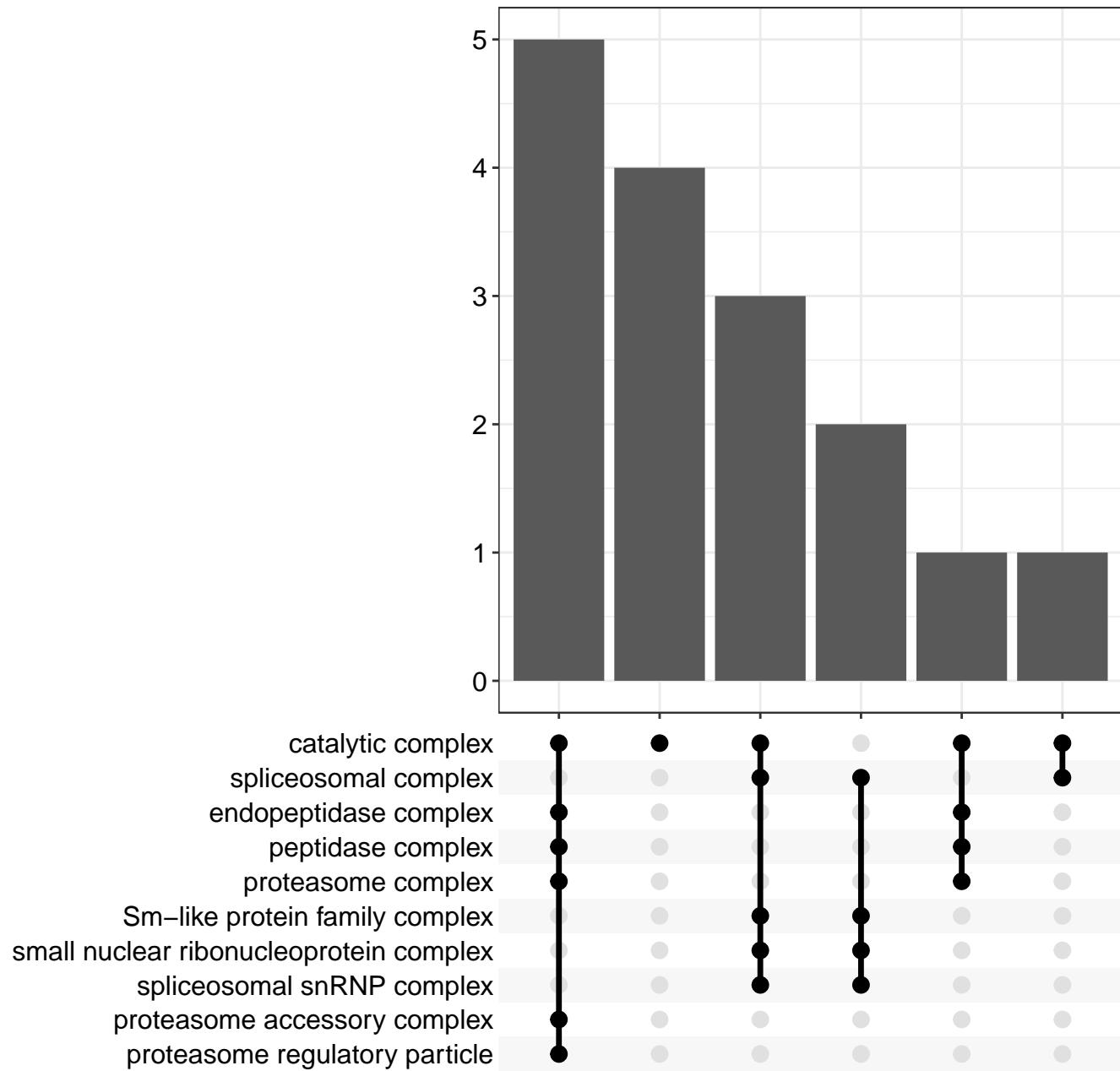
Sm-like protein family complex

small nuclear ribonucleoprotein complex

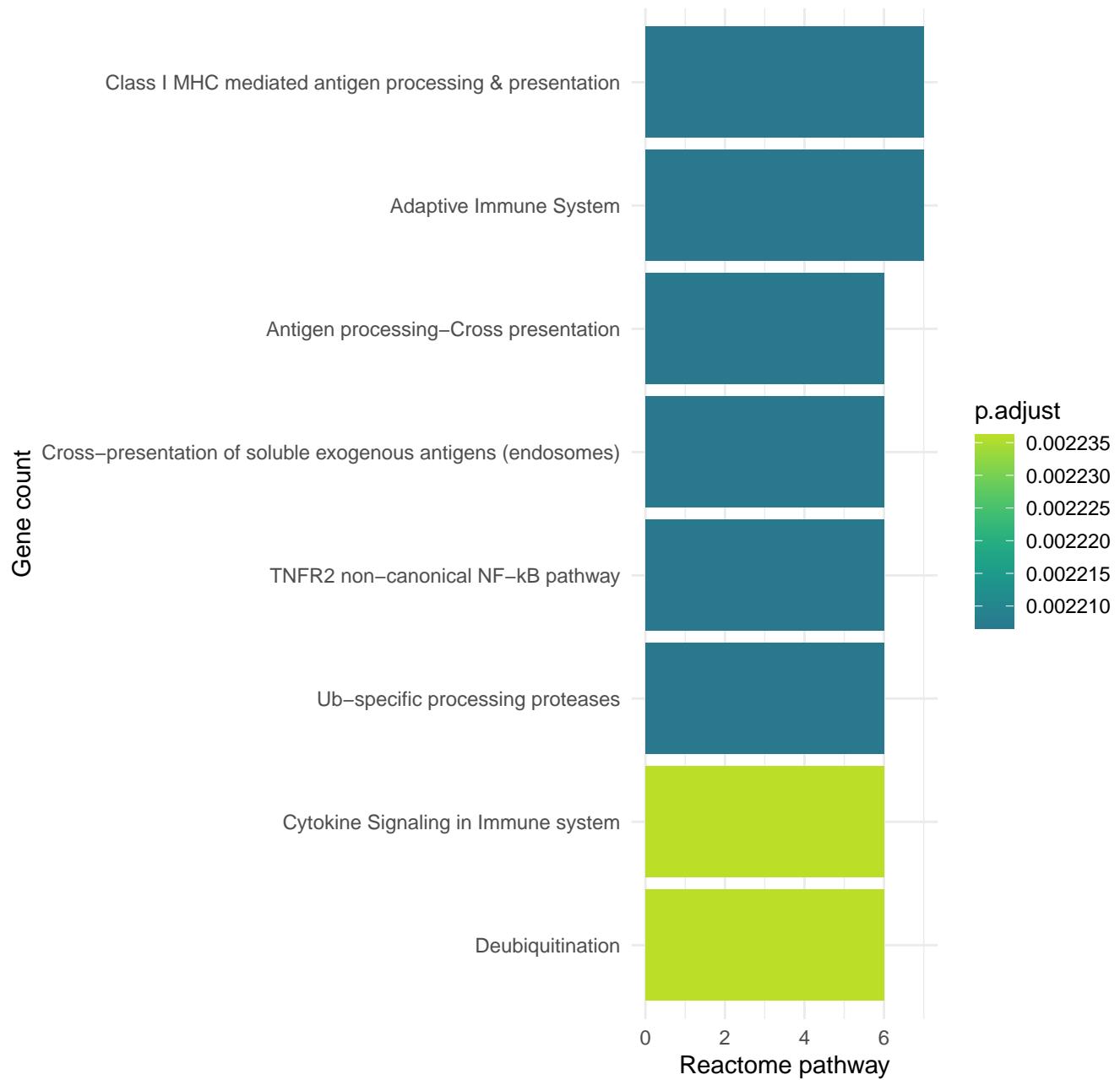
spliceosomal snRNP complex



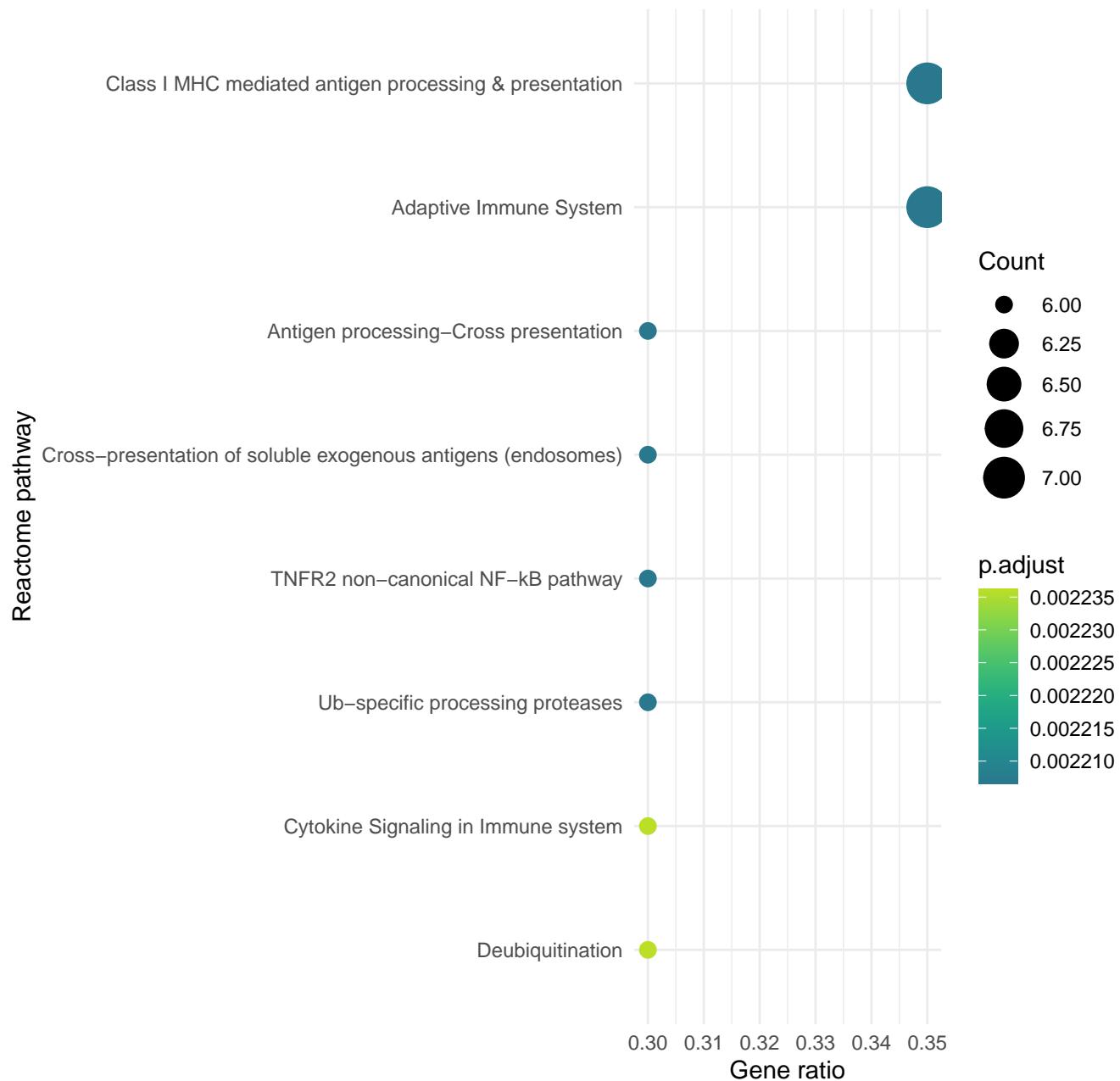
IST3-TAP Up-regulated GO CC upsetplot



IST3-TAP Up-regulated Reactome bar

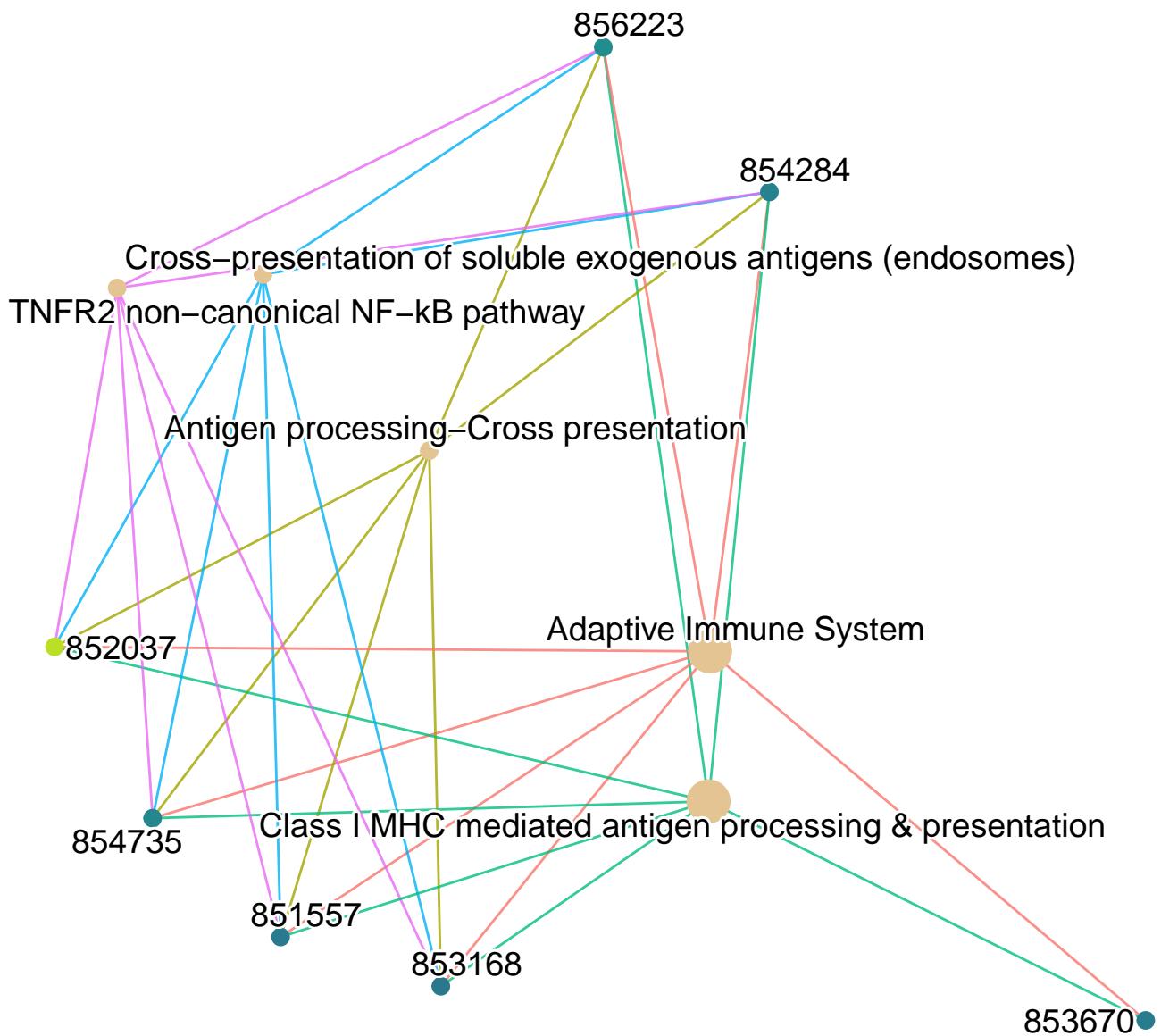


IST3-TAP Up-regulated Reactome dot

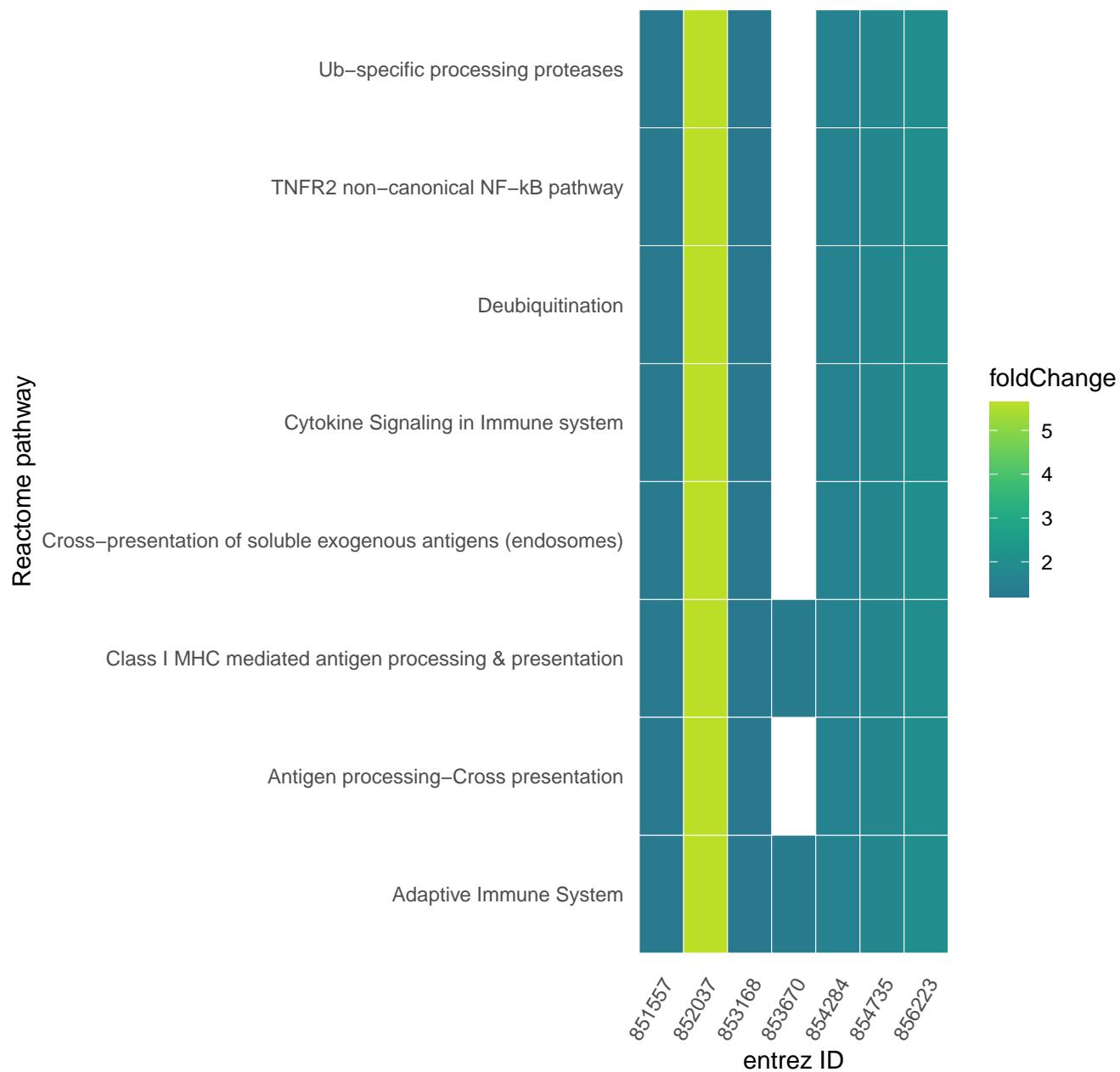


IST3-TAP Up-regulated Reactome cnetplot

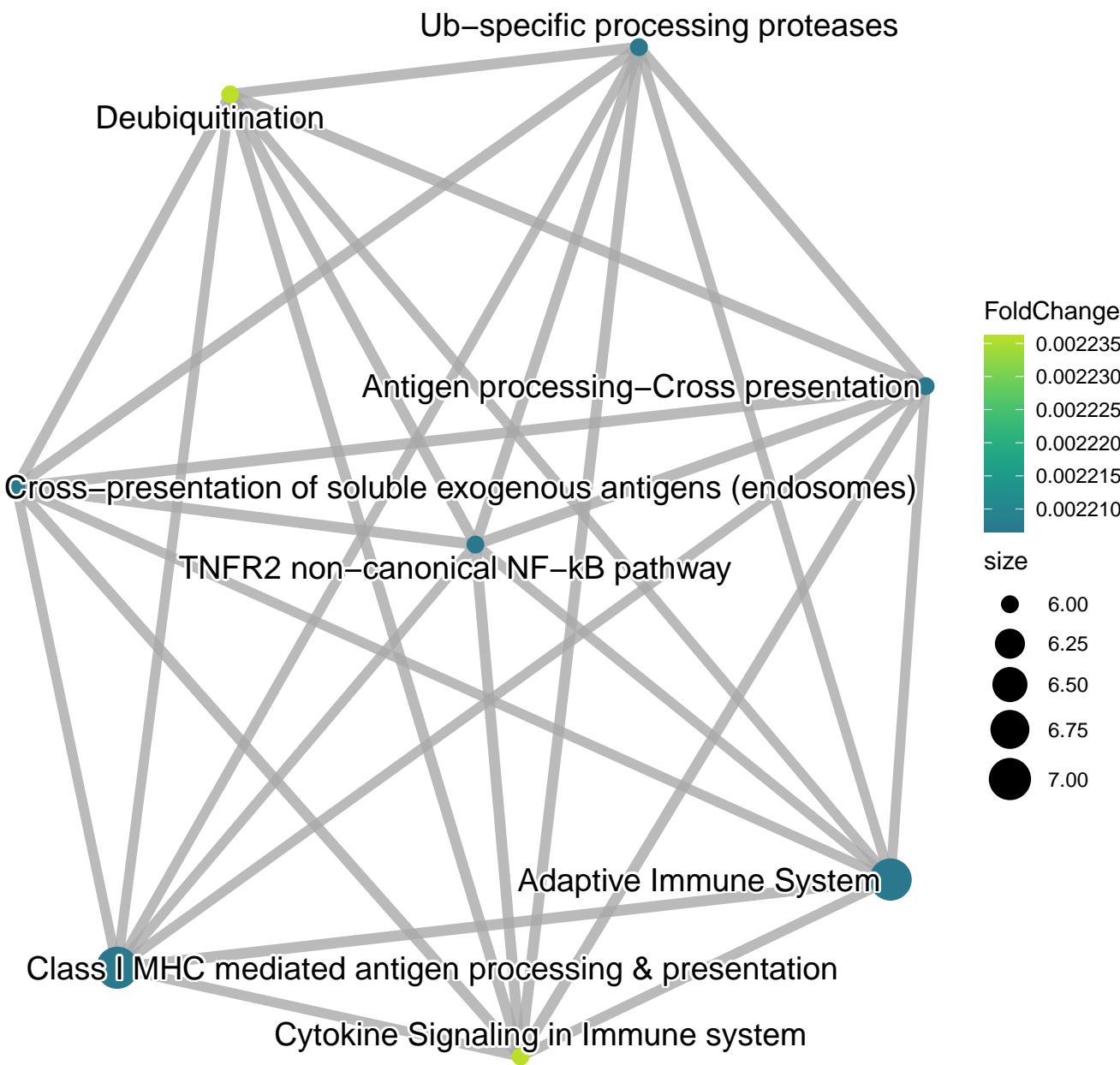
adaptive Immune System — Antigen processing—Cross presentation — Class I MHC mediated antigen processing & pres

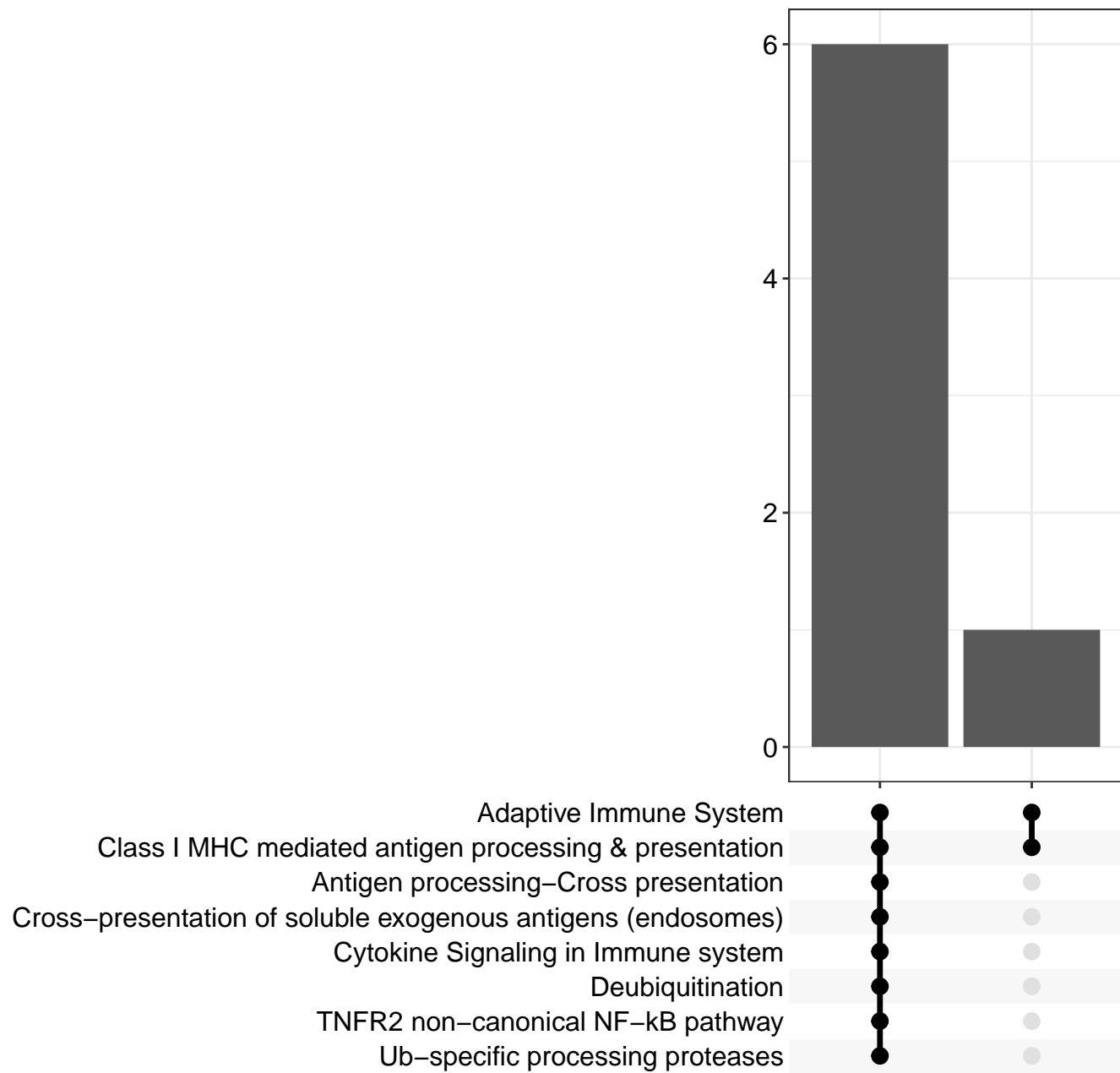


IST3-TAP Up-regulated Reactome heatmap

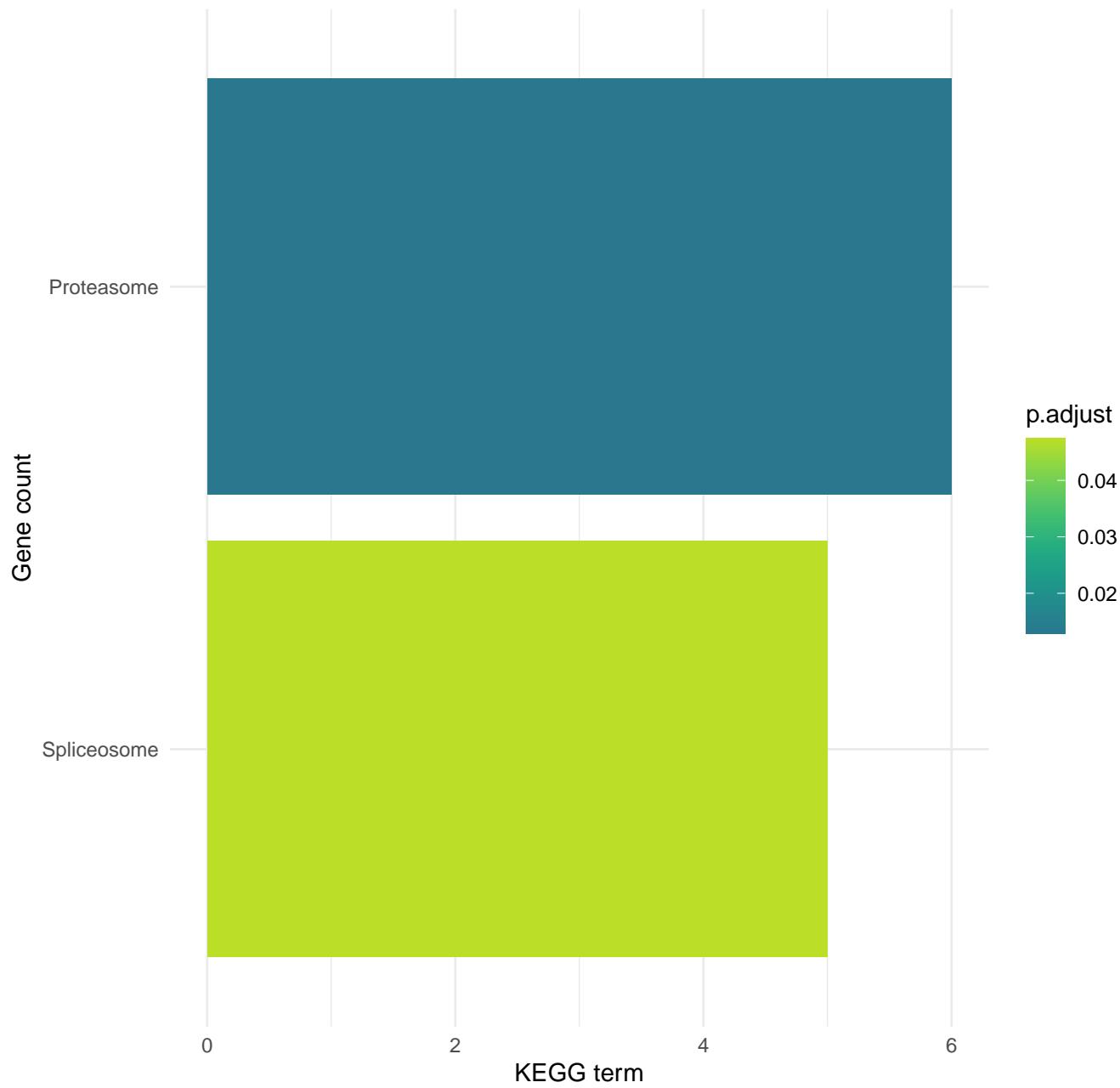


IST3-TAP Up-regulated Reactome emapplot

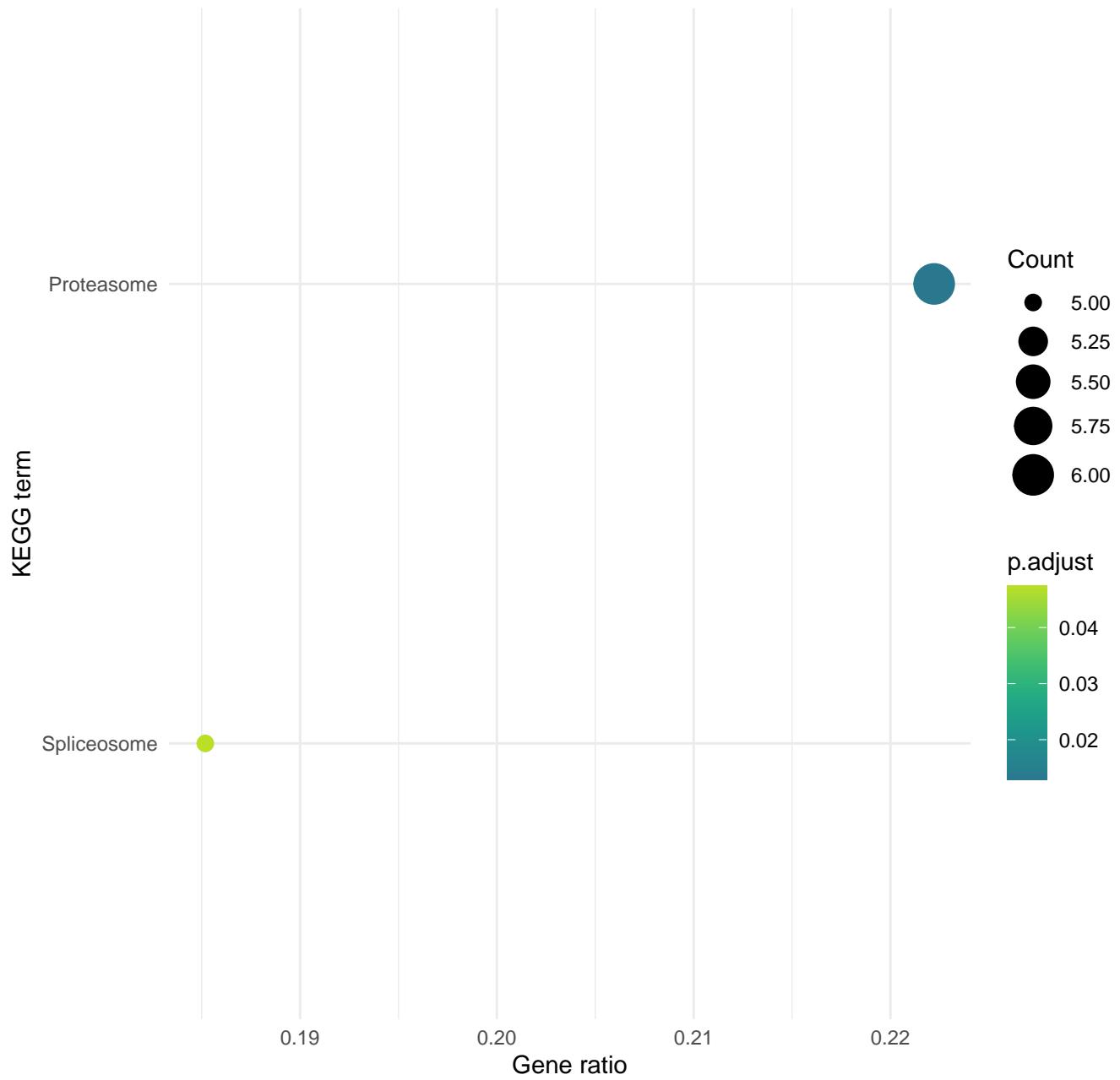


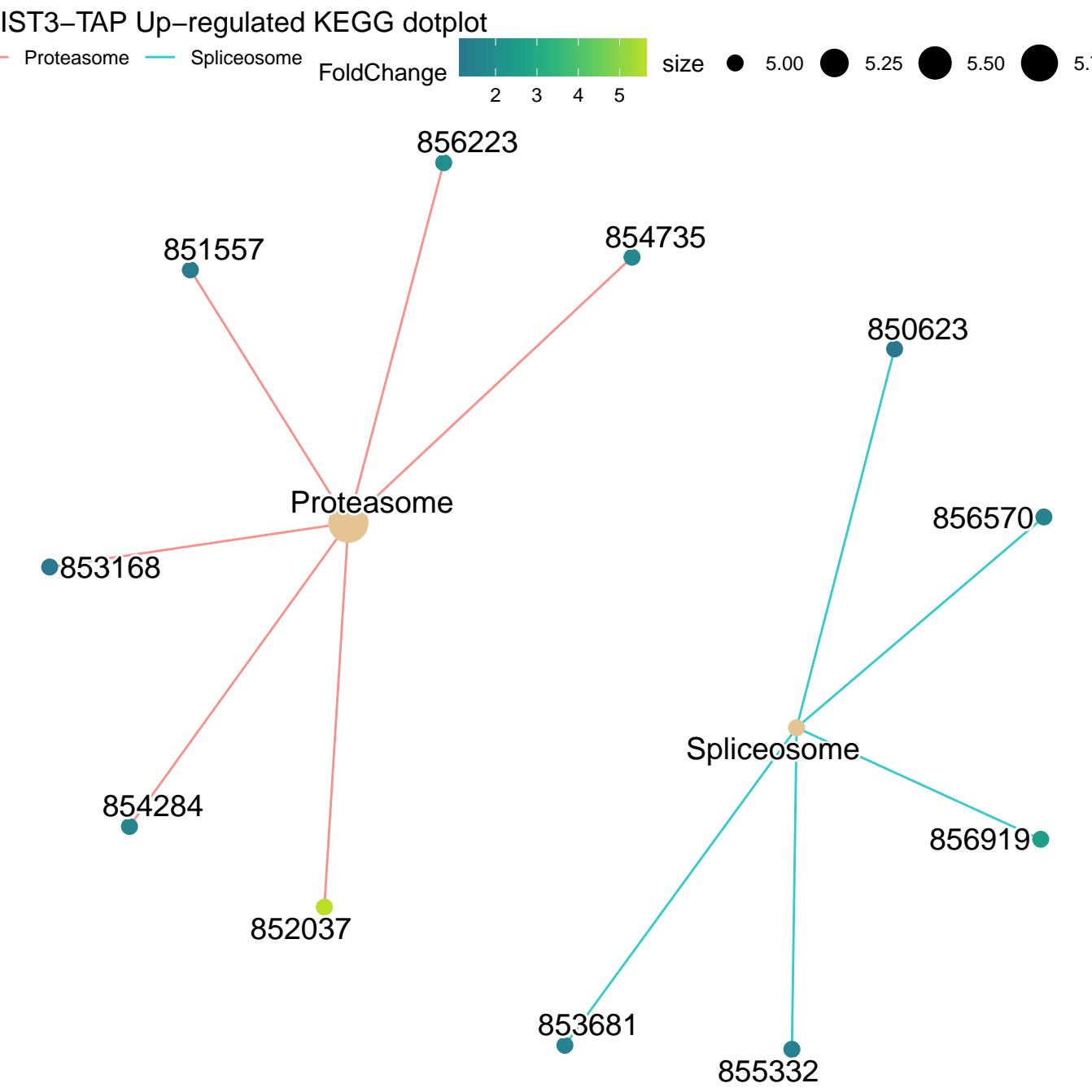


IST3-TAP Up-regulated KEGG barplot

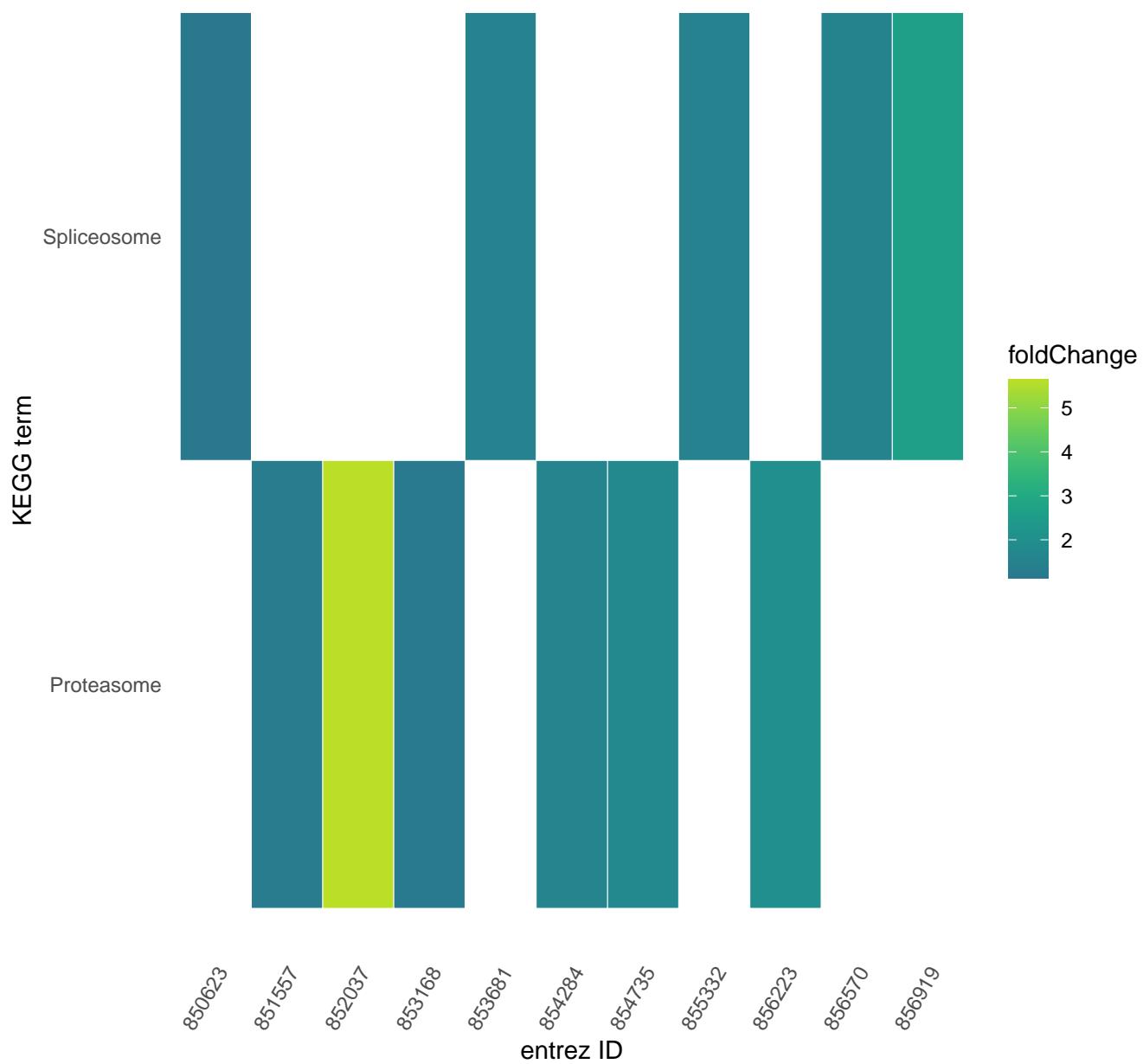


IST3-TAP Up-regulated KEGG dotplot

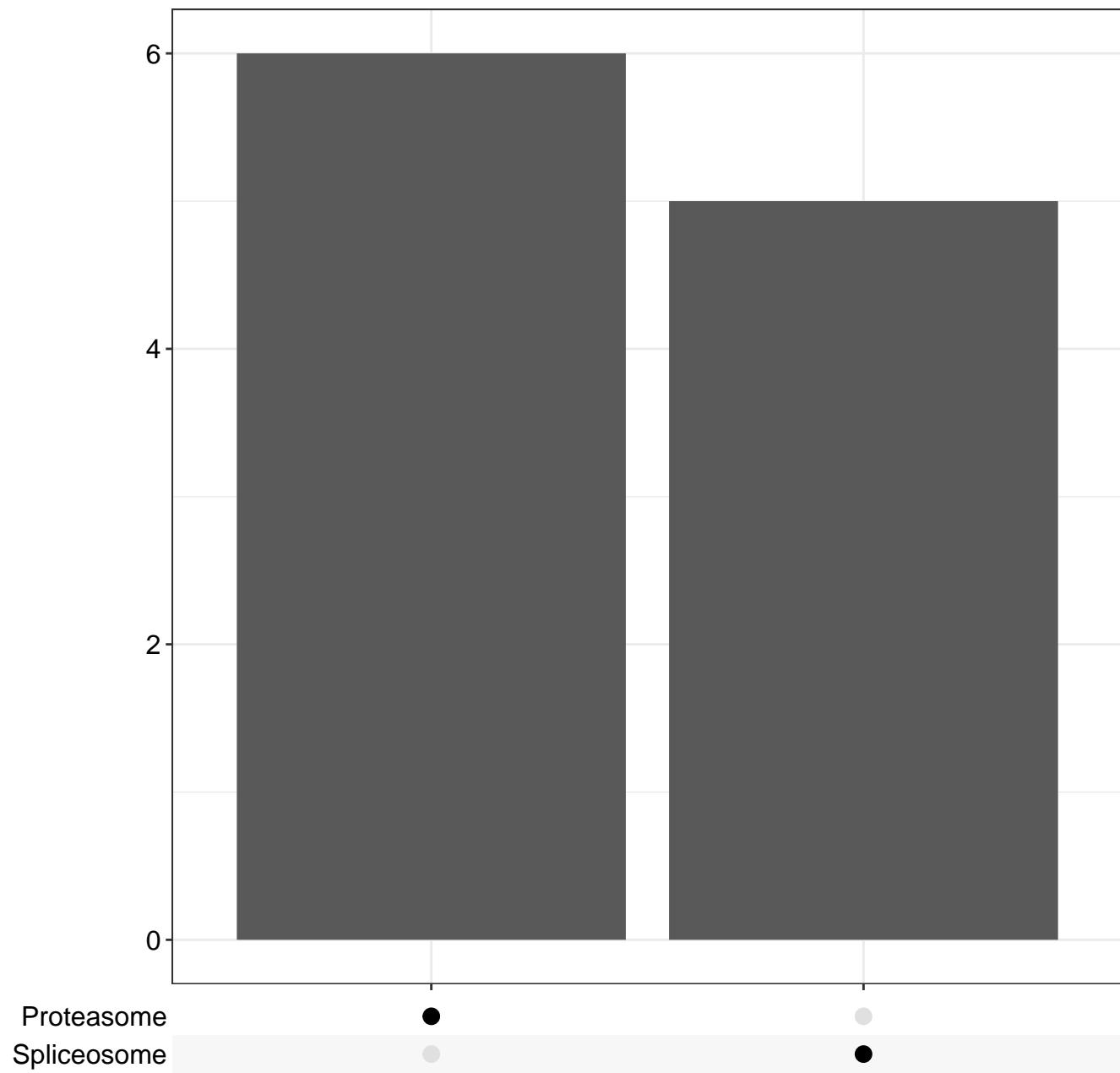




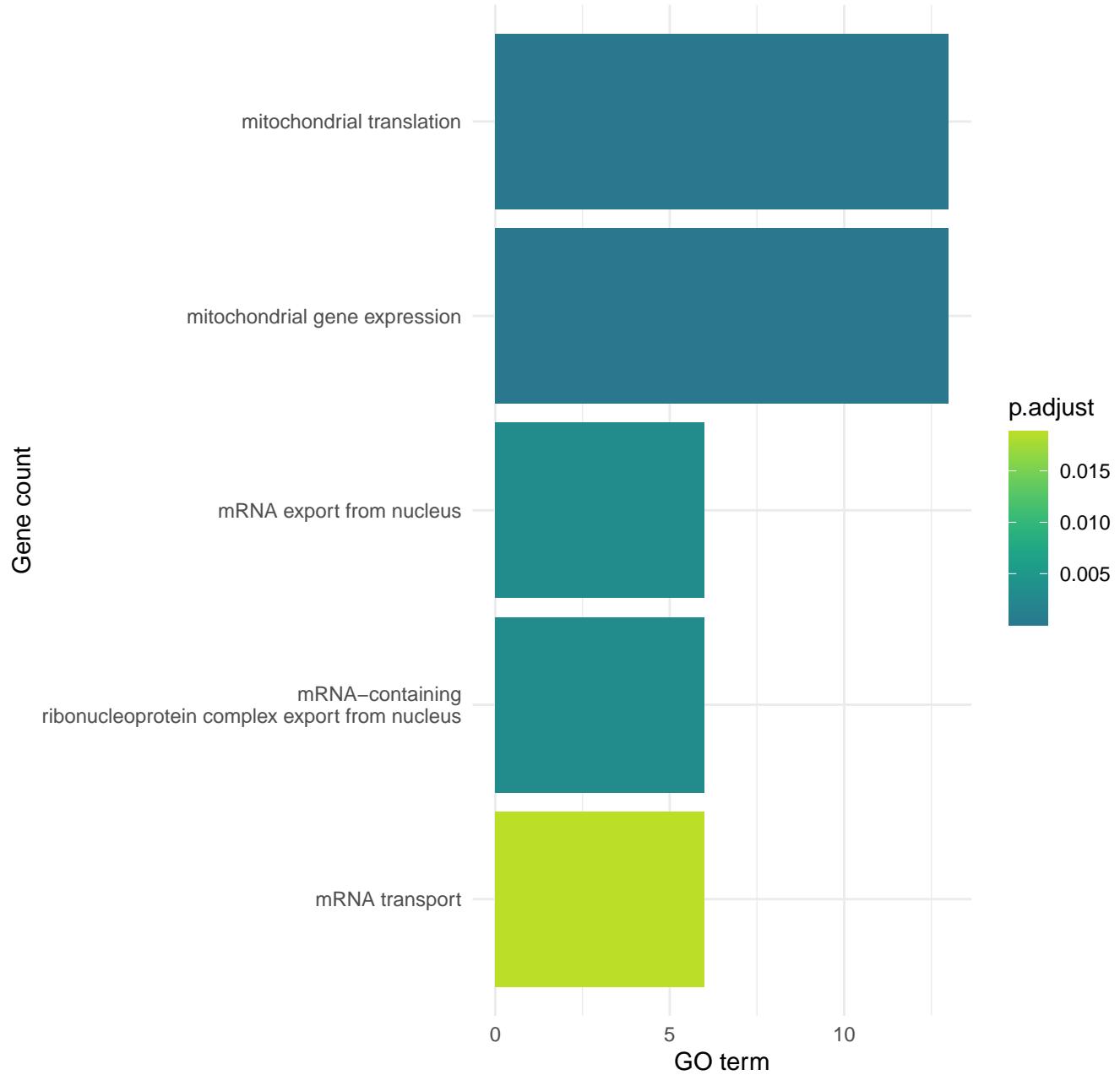
IST3-TAP Up-regulated KEGG heatplot



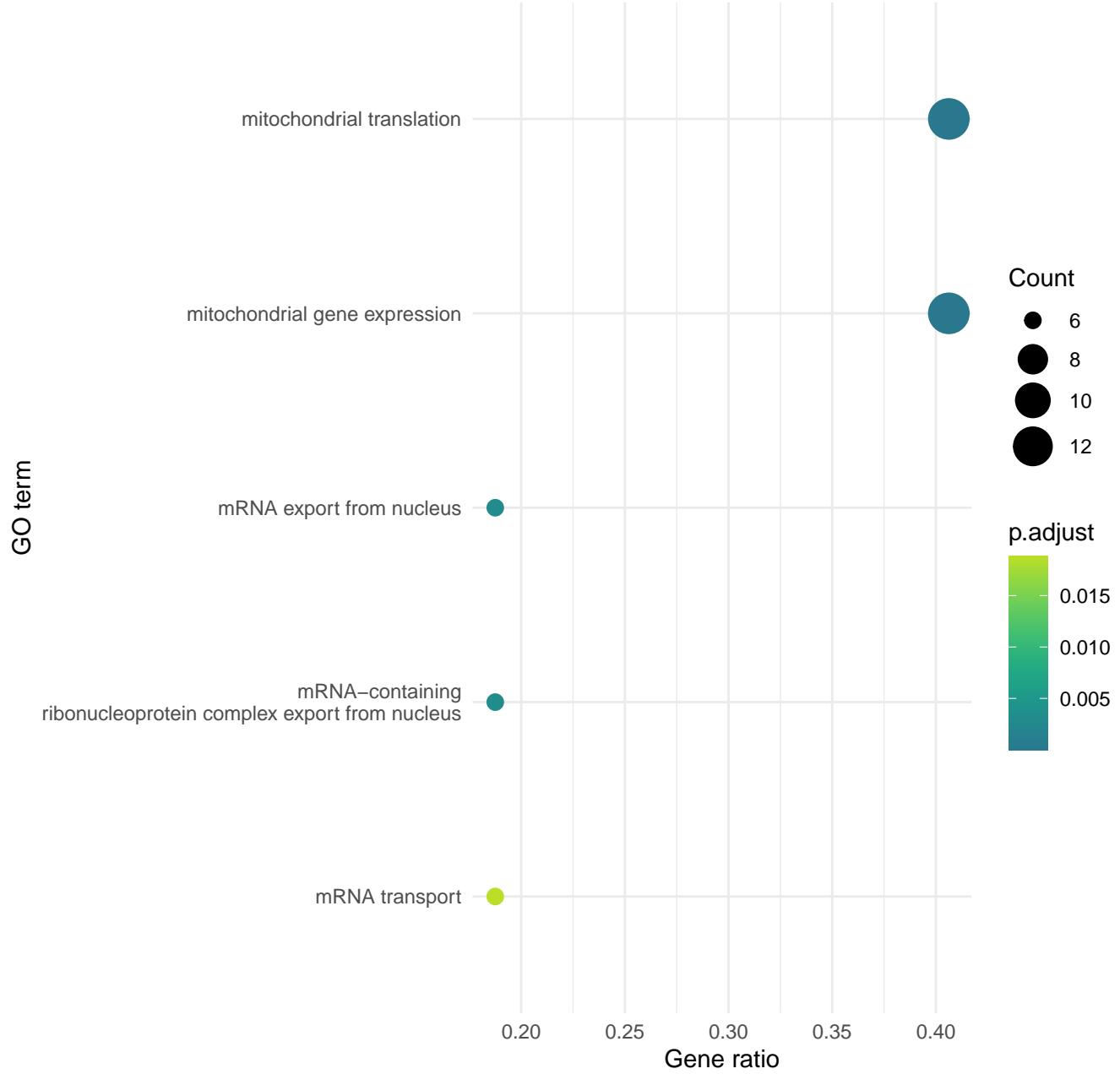
IST3-TAP Up-regulated KEGG upsetplot



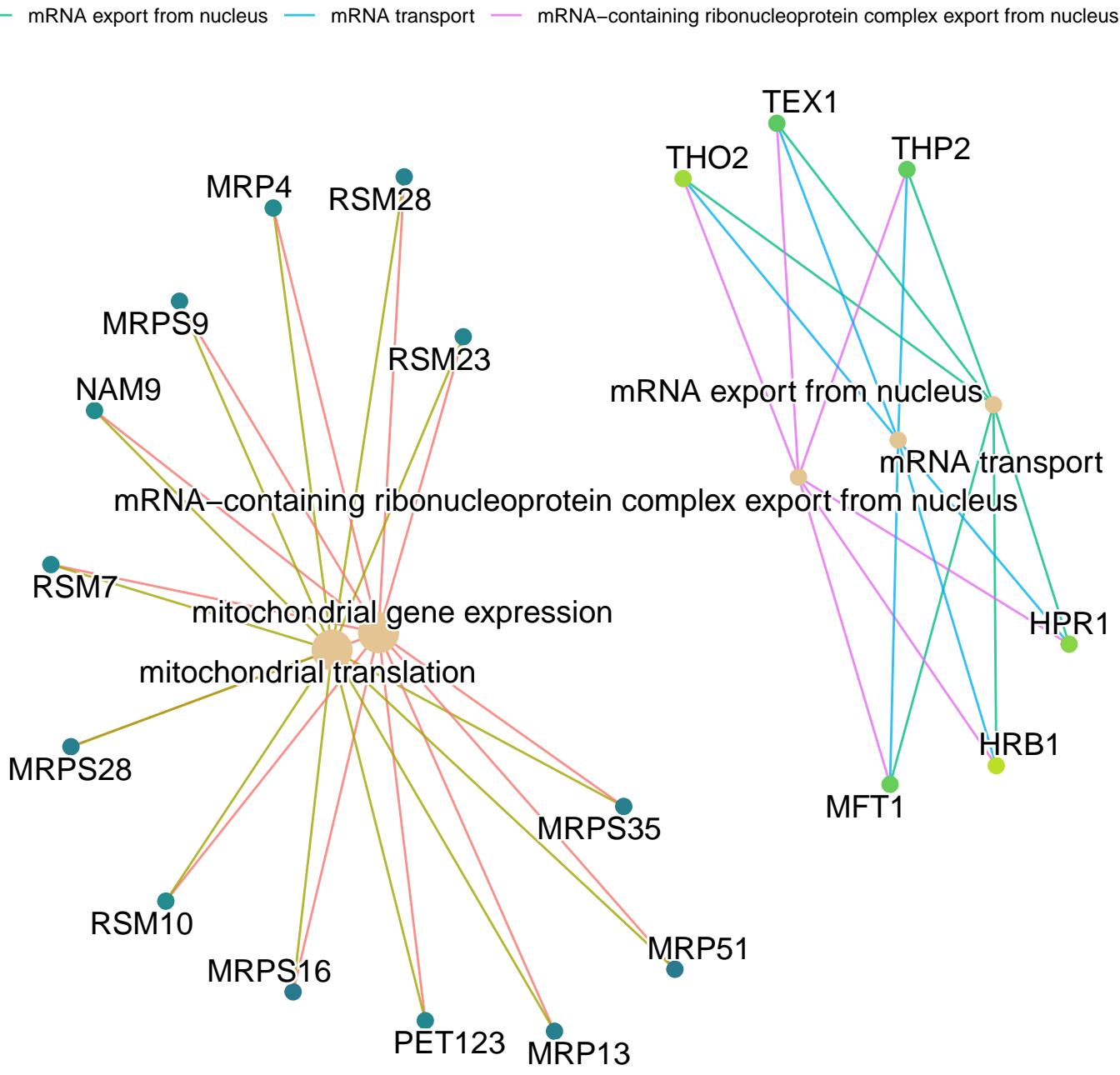
HRB1–TAP Up-regulated GO BP barplot



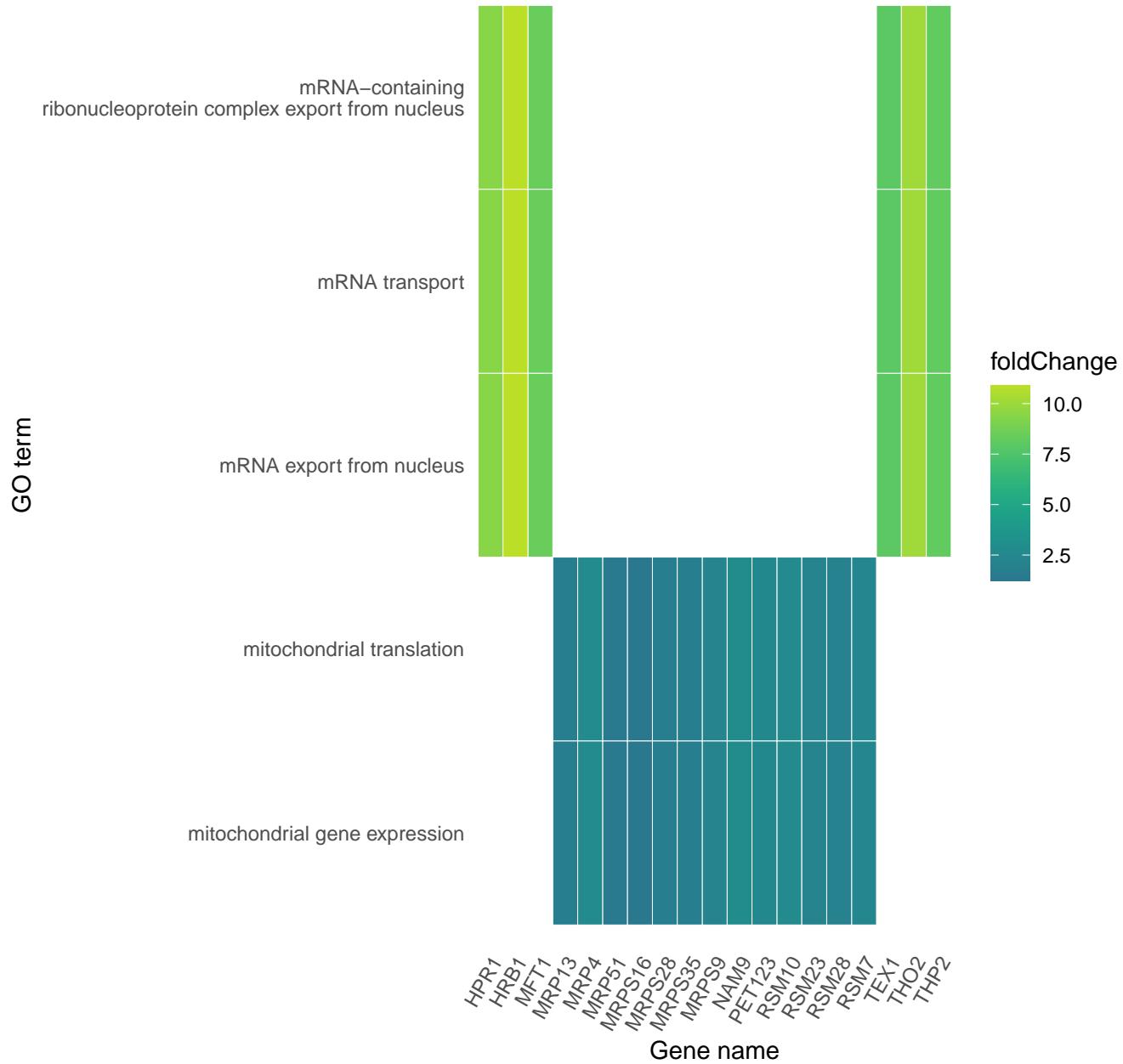
HRB1-TAP Up-regulated GO BP dotplot



HRB1-TAP Up-regulated GO BP cnetplot



HRB1-TAP Up-regulated GO BP heatplot



HRB1-TAP Up-regulated GO BP emapplot

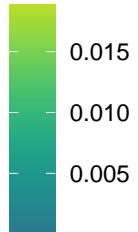
mRNA transport

mitochondrial translation

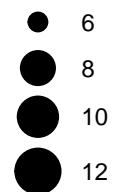
mRNA-containing ribonucleoprotein complex export from nucleus

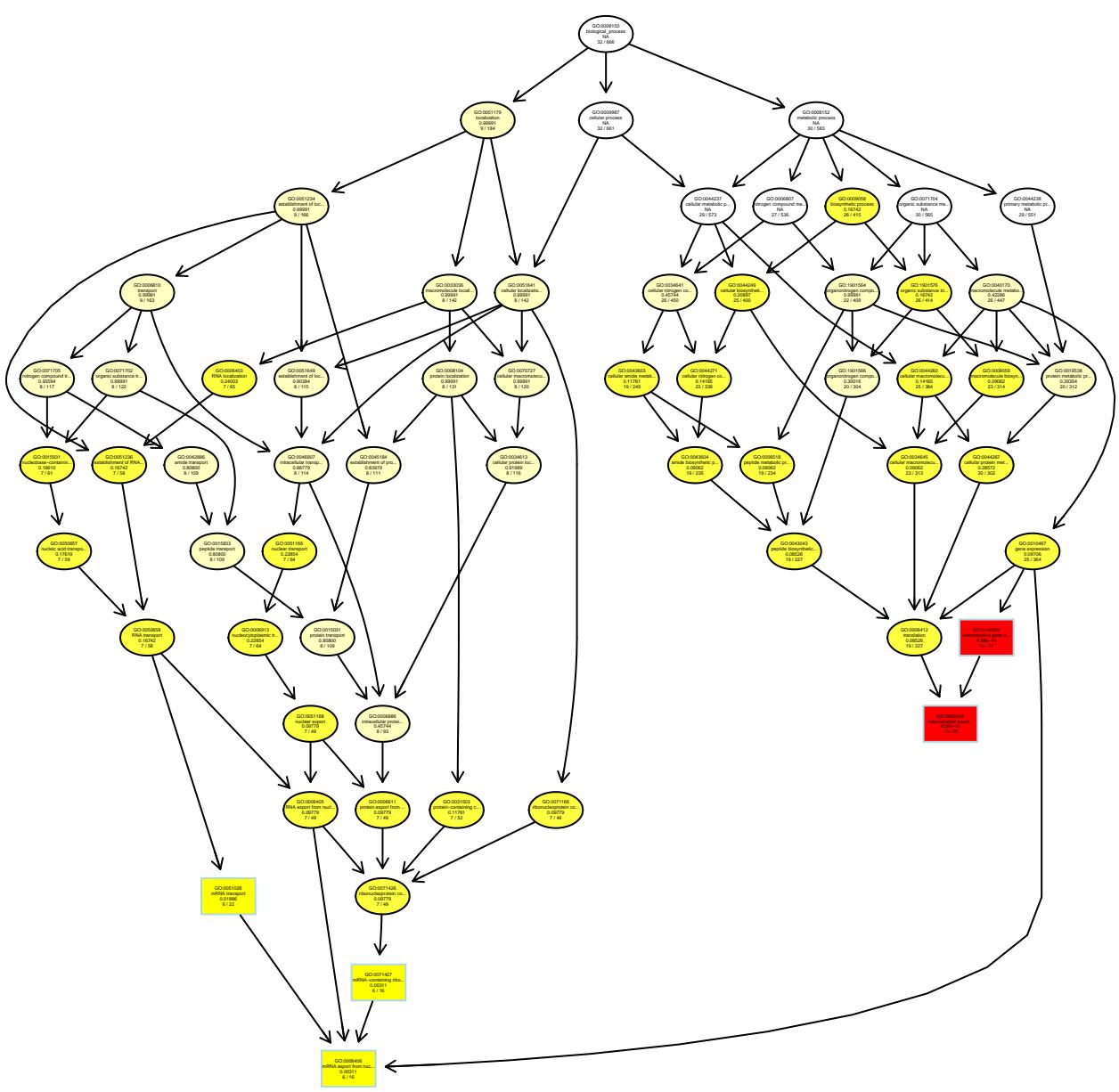
mRNA export from nucleus

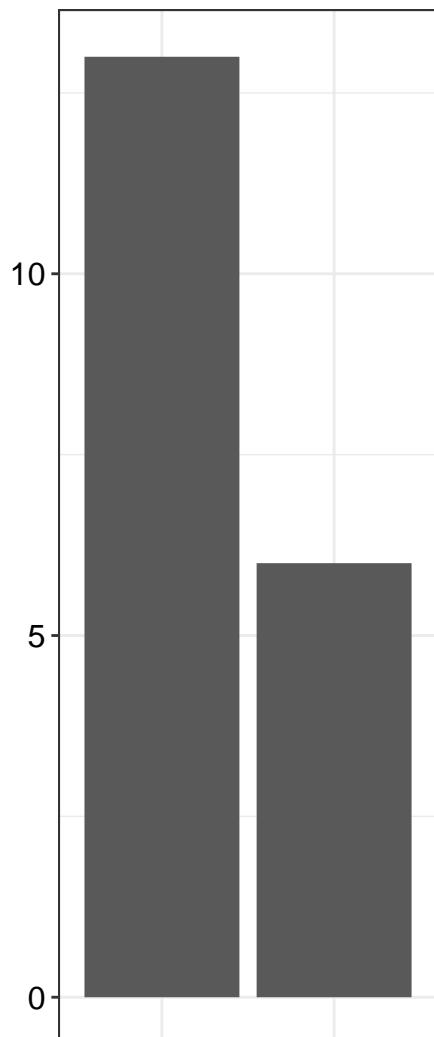
FoldChange



size







mitochondrial gene expression

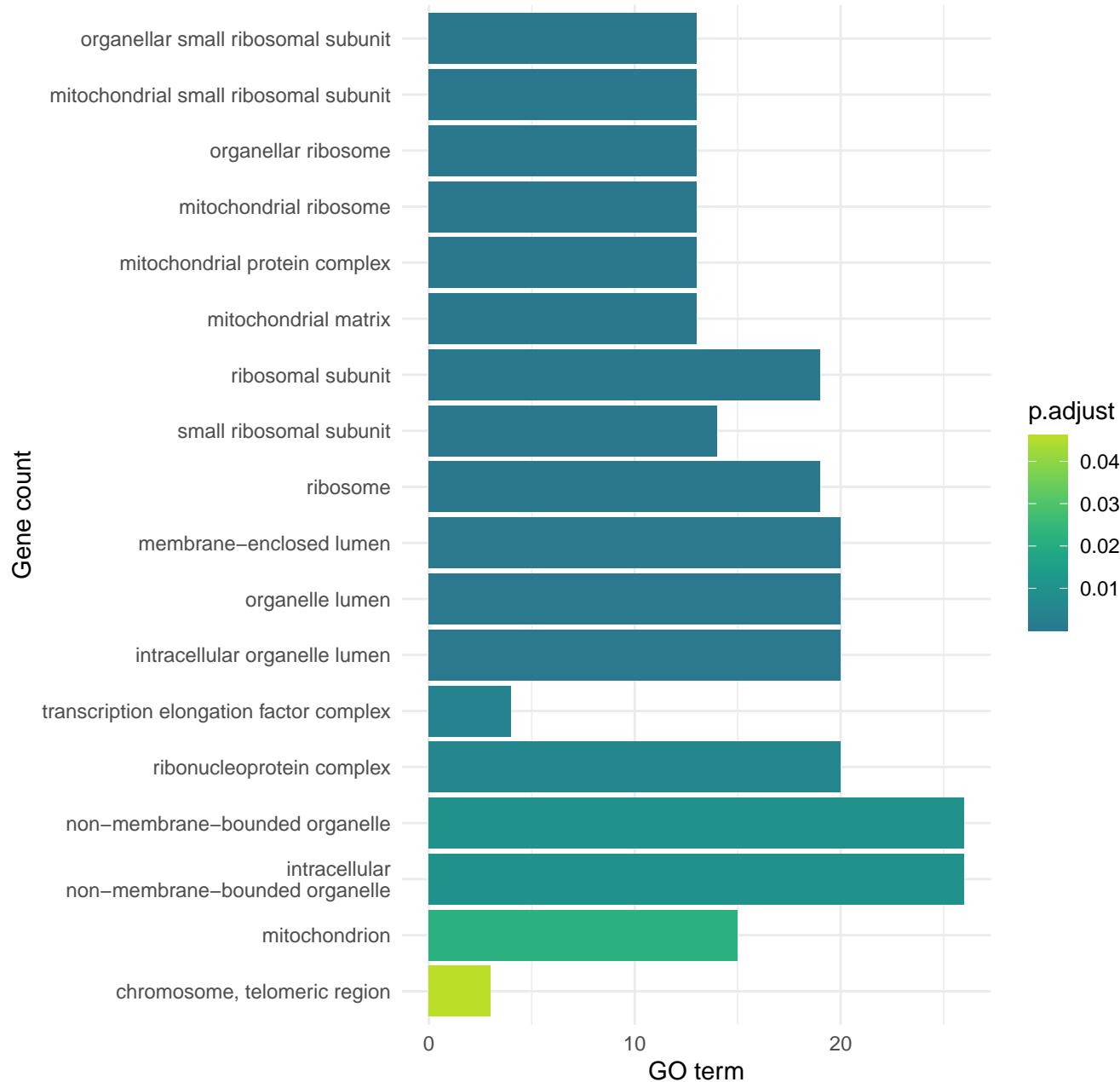
mitochondrial translation

mRNA export from nucleus

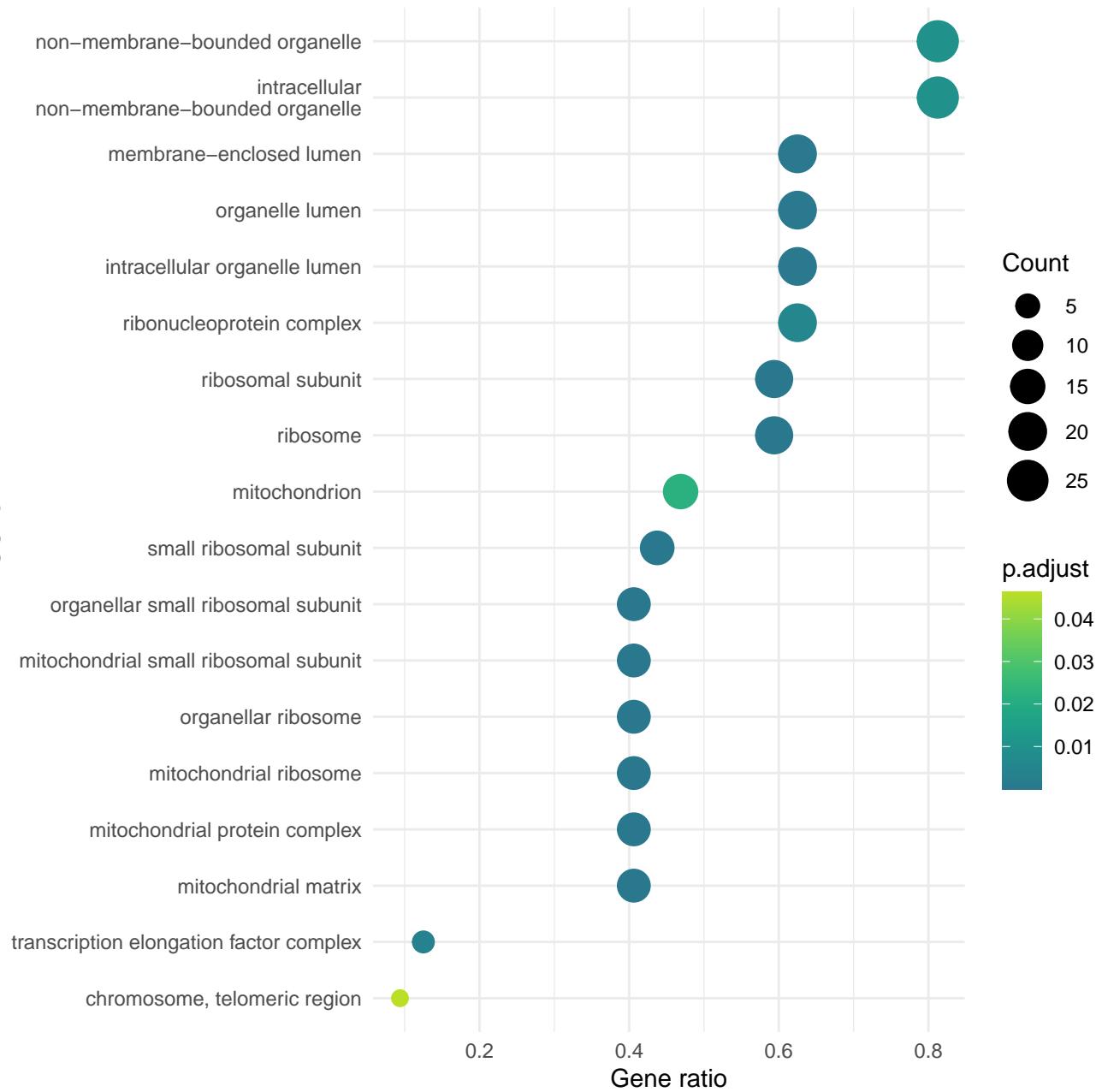
mRNA transport

mRNA-containing ribonucleoprotein complex export from nucleus

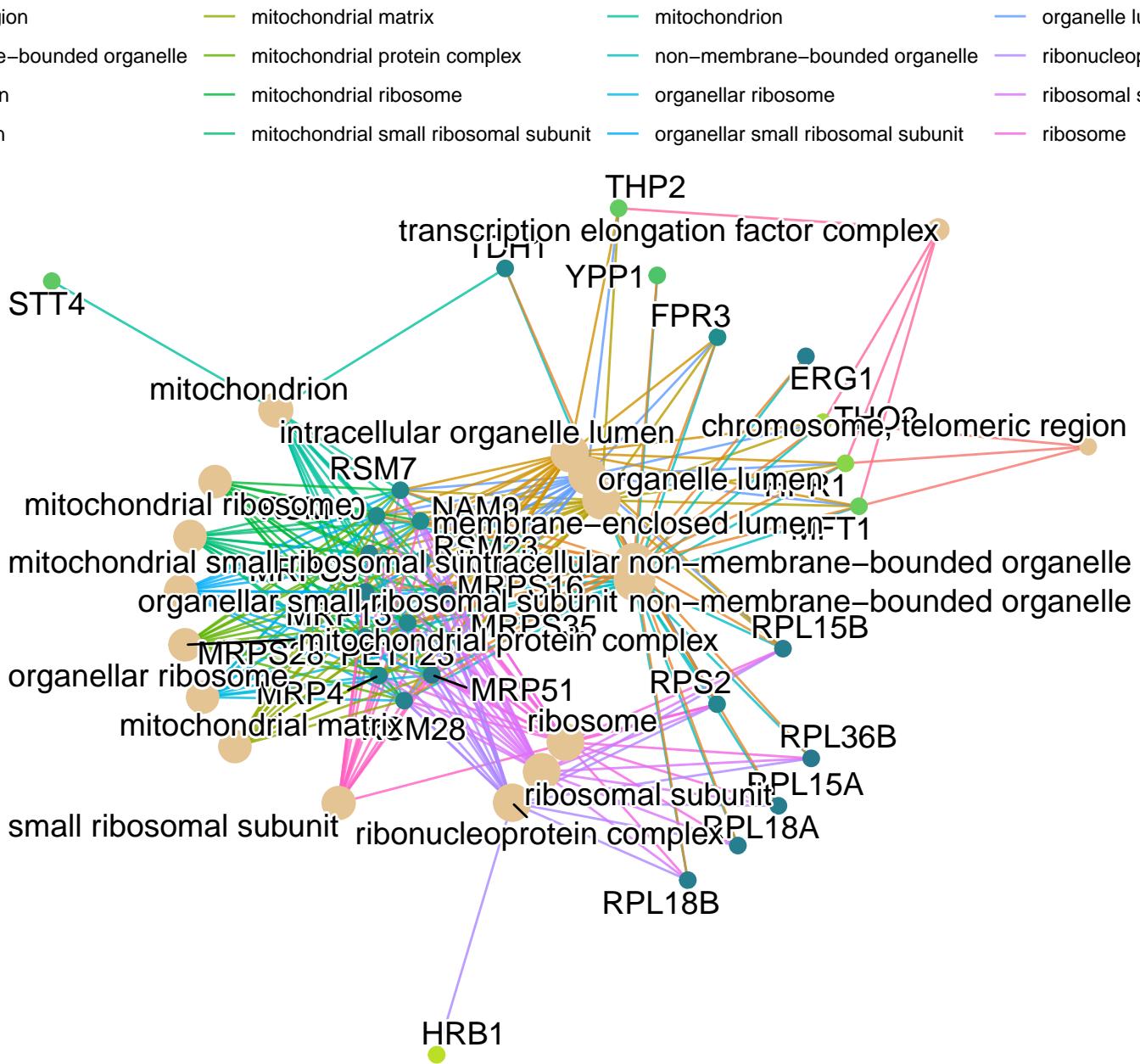
HRB1-TAP Up-regulated GO CC barplot



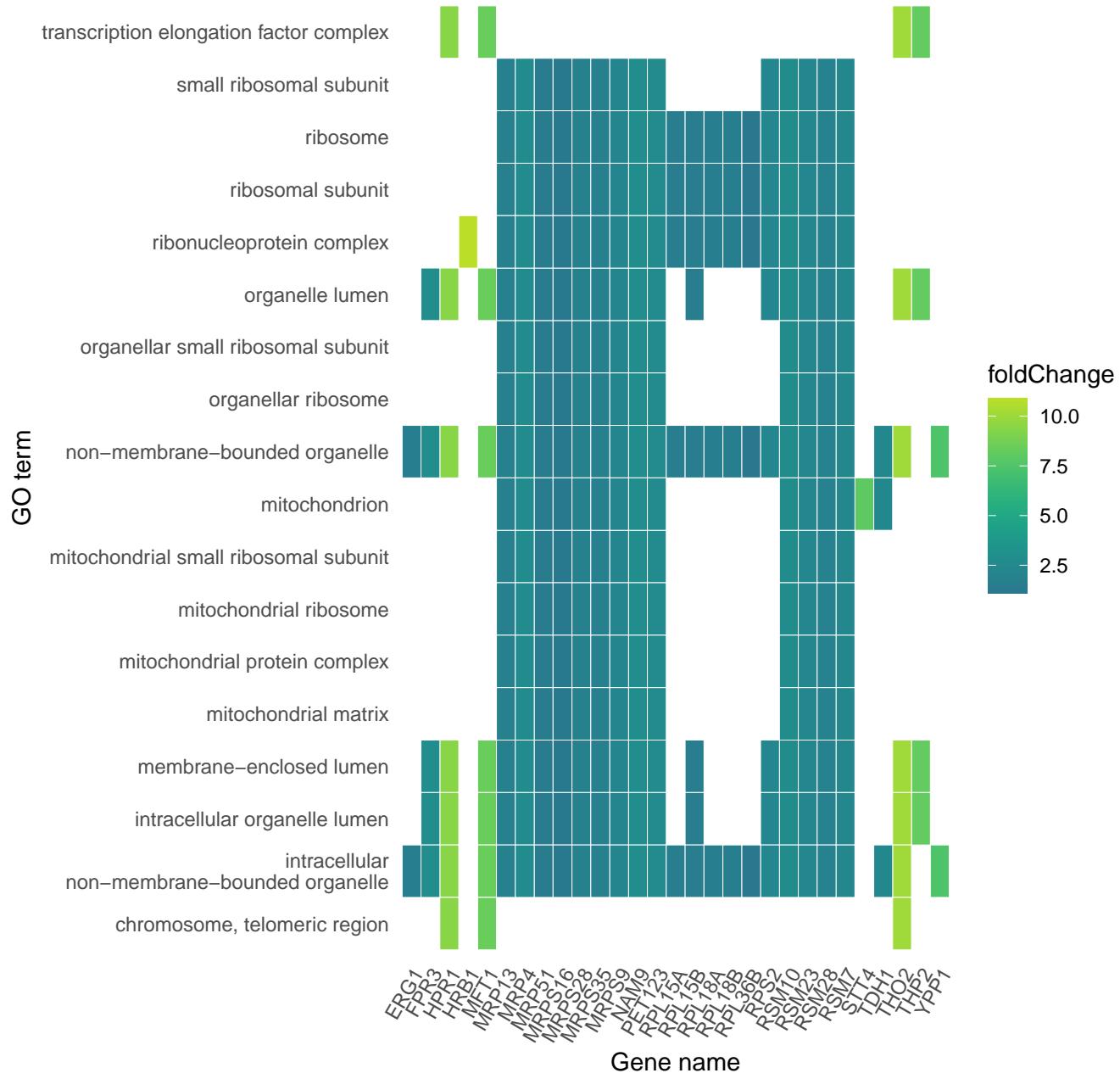
HRB1-TAP Up-regulated GO CC dotplot



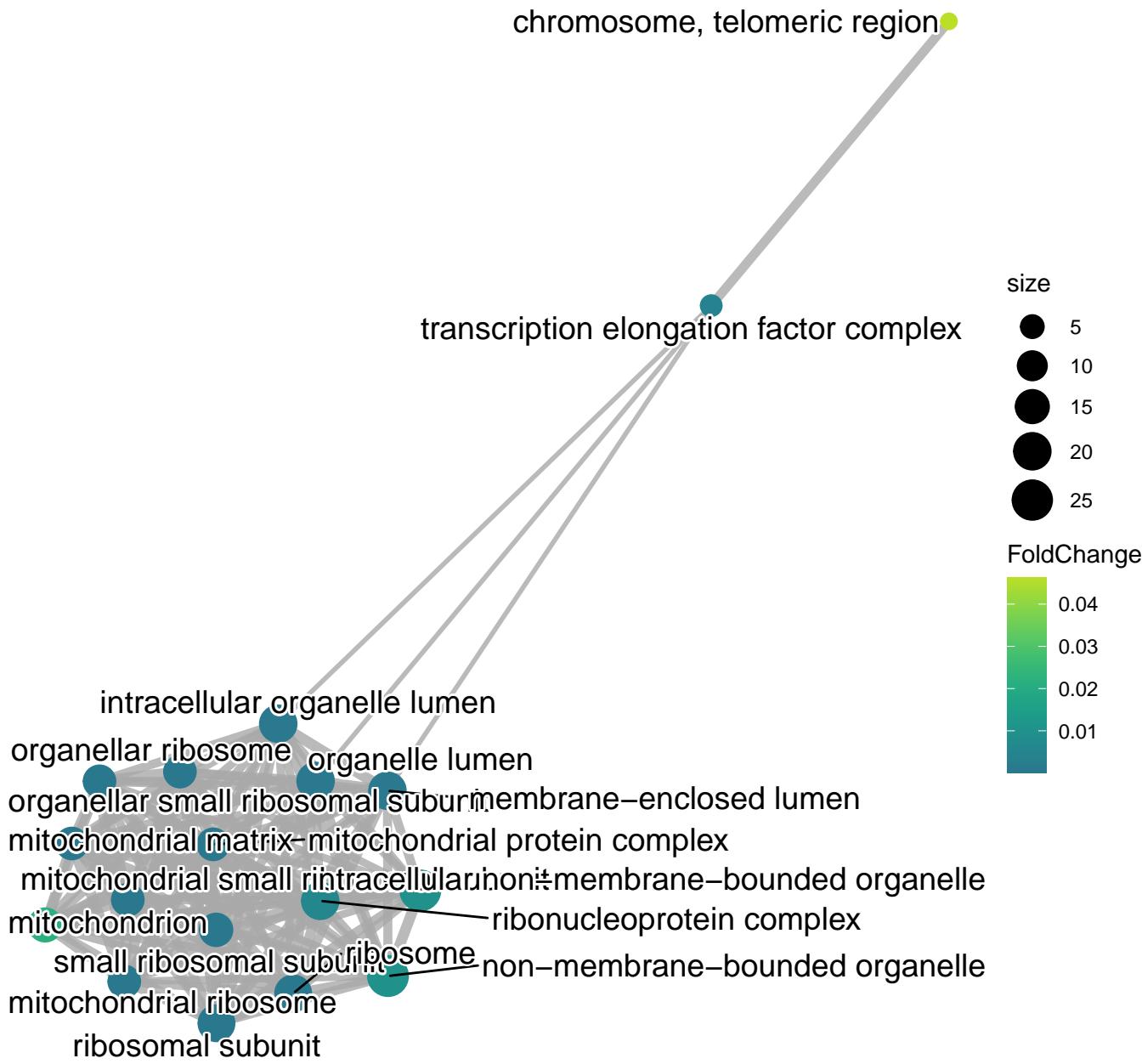
HRB1-TAP Up-regulated GO CC cnetplot

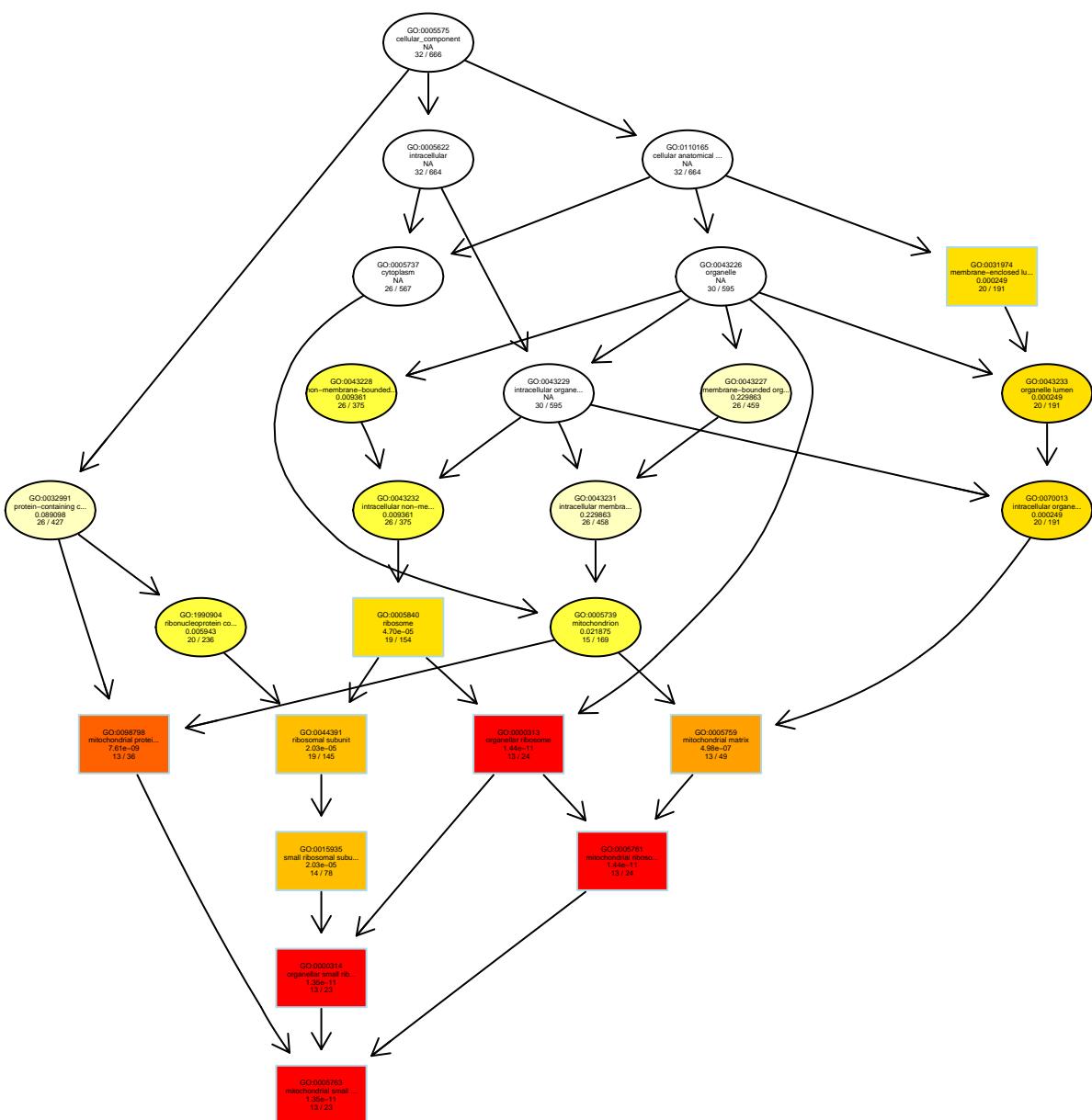


HRB1-TAP Up-regulated GO CC heatplot

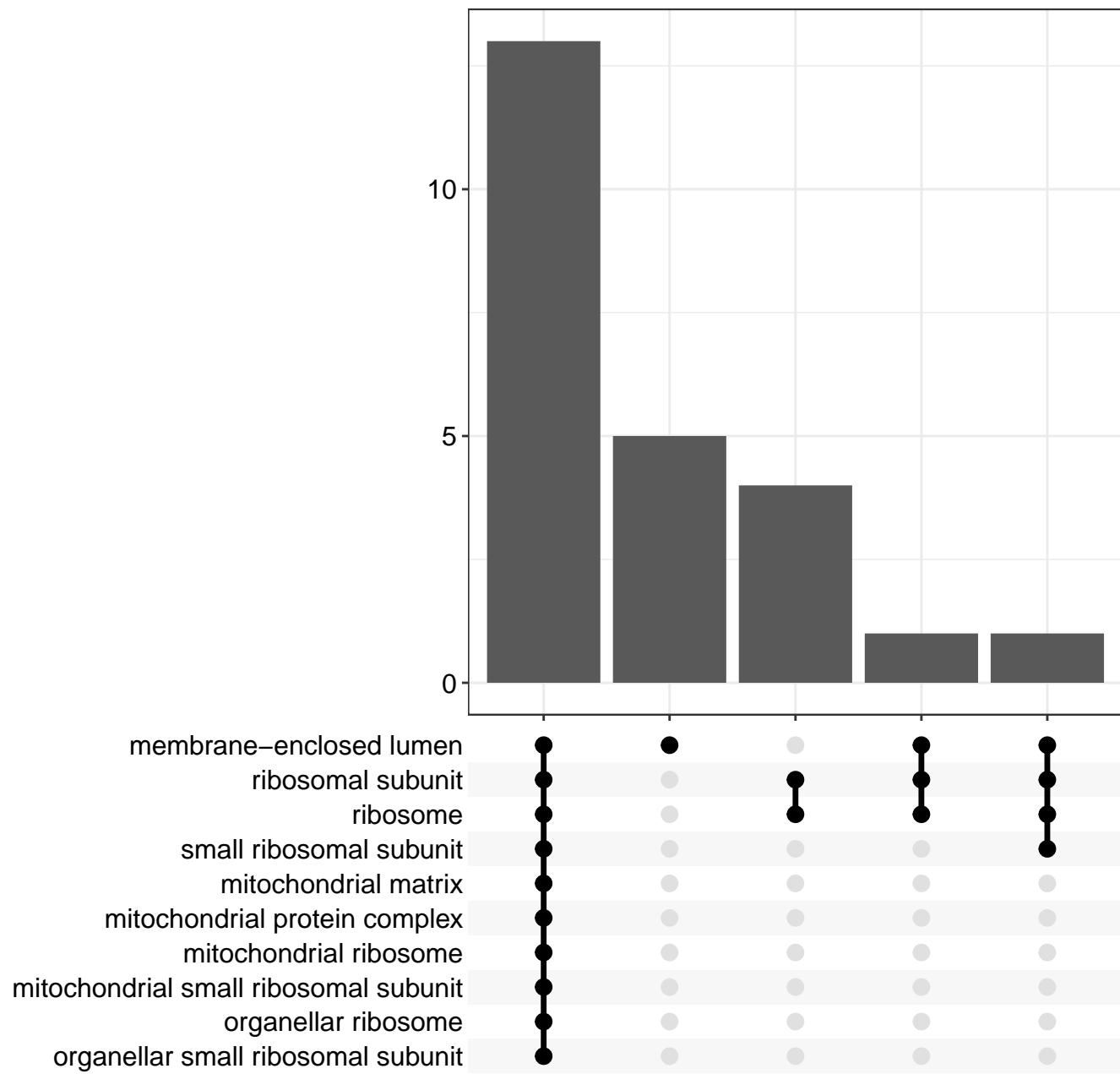


HRB1-TAP Up-regulated GO CC emapplot

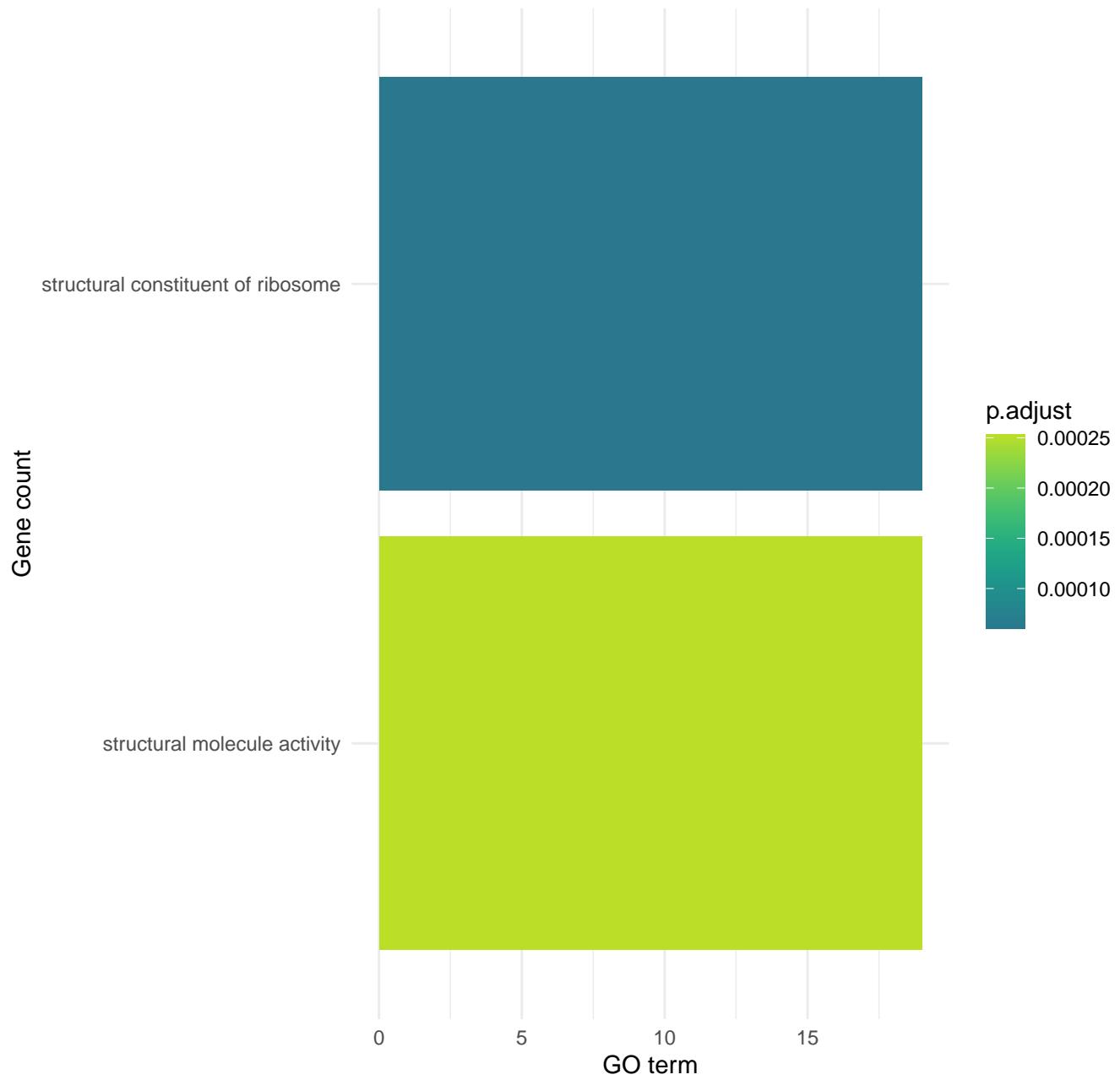




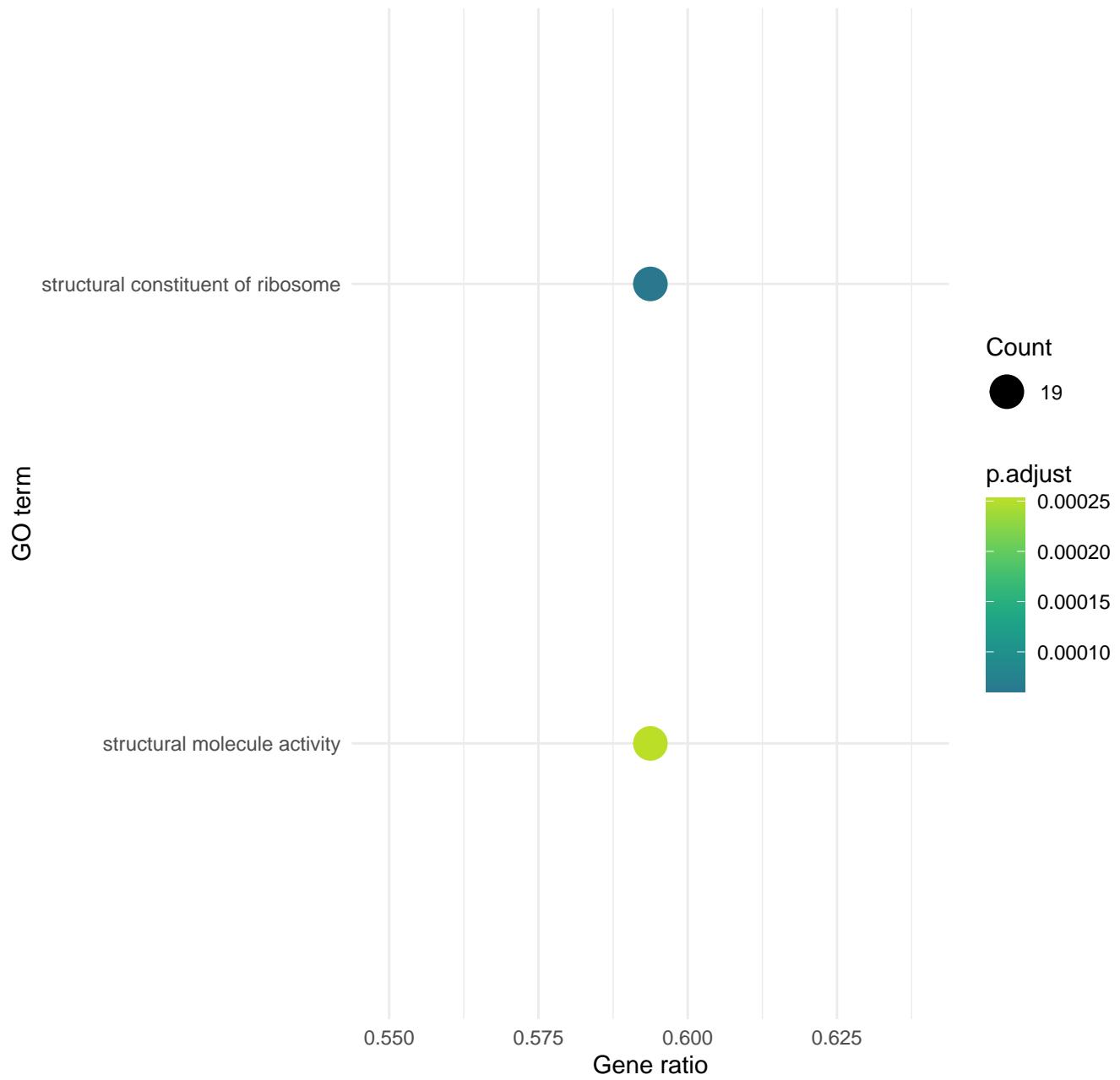
HRB1-TAP Up-regulated GO CC upsetplot



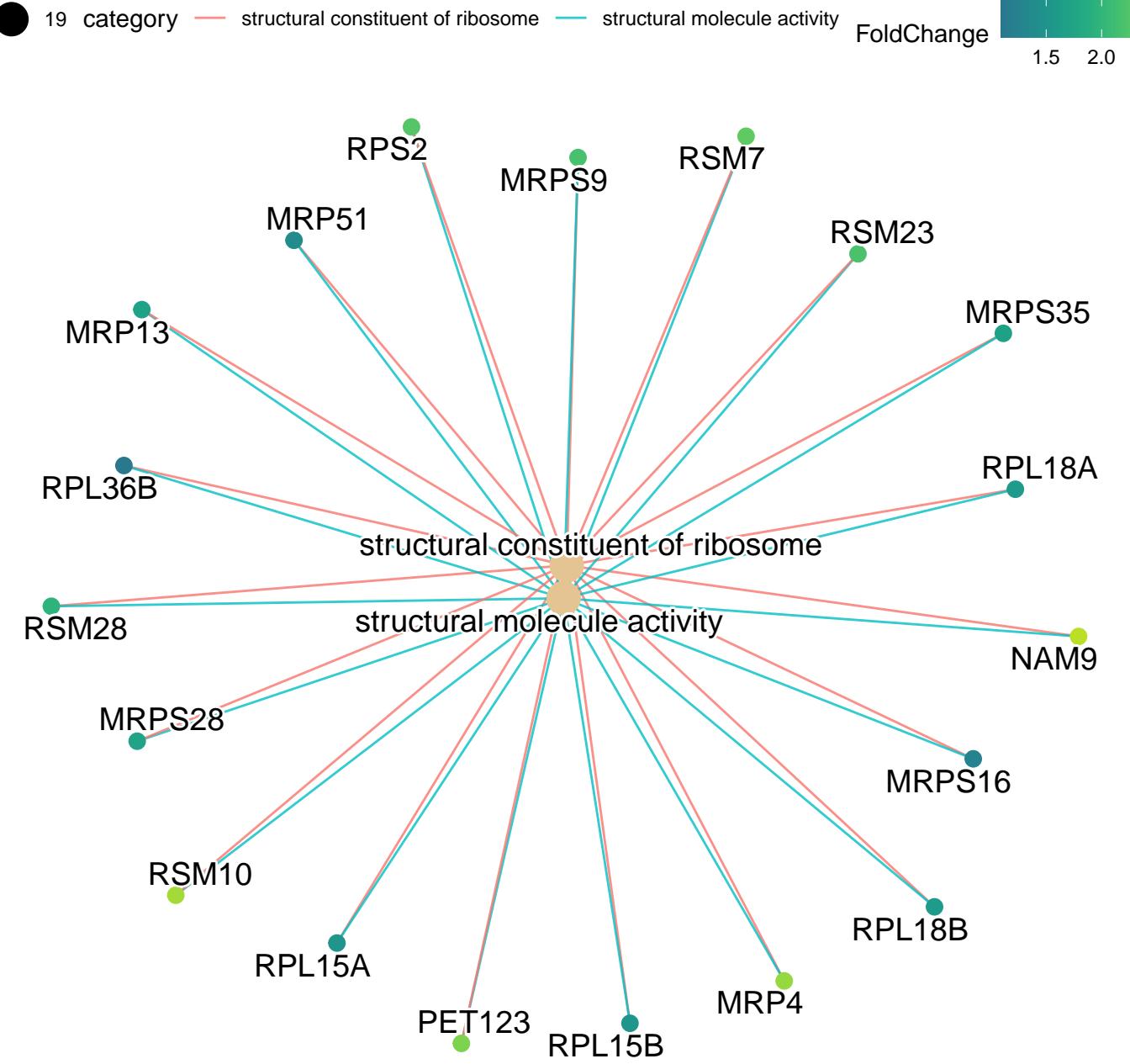
HRB1-TAP Up-regulated GO MF barplot



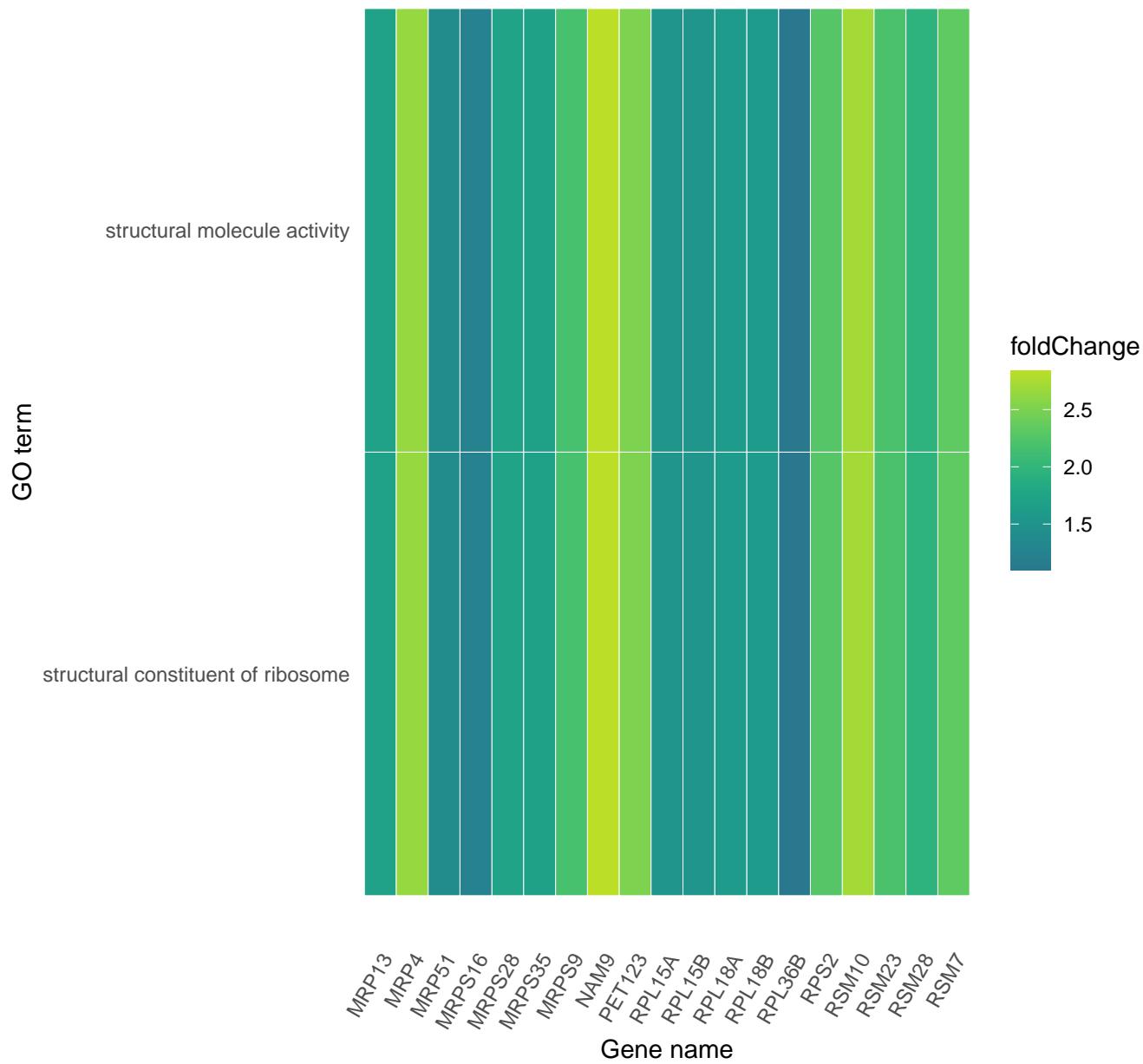
HRB1-TAP Up-regulated GO MF dotplot



HRB1-TAP Up-regulated GO MF cnetplot

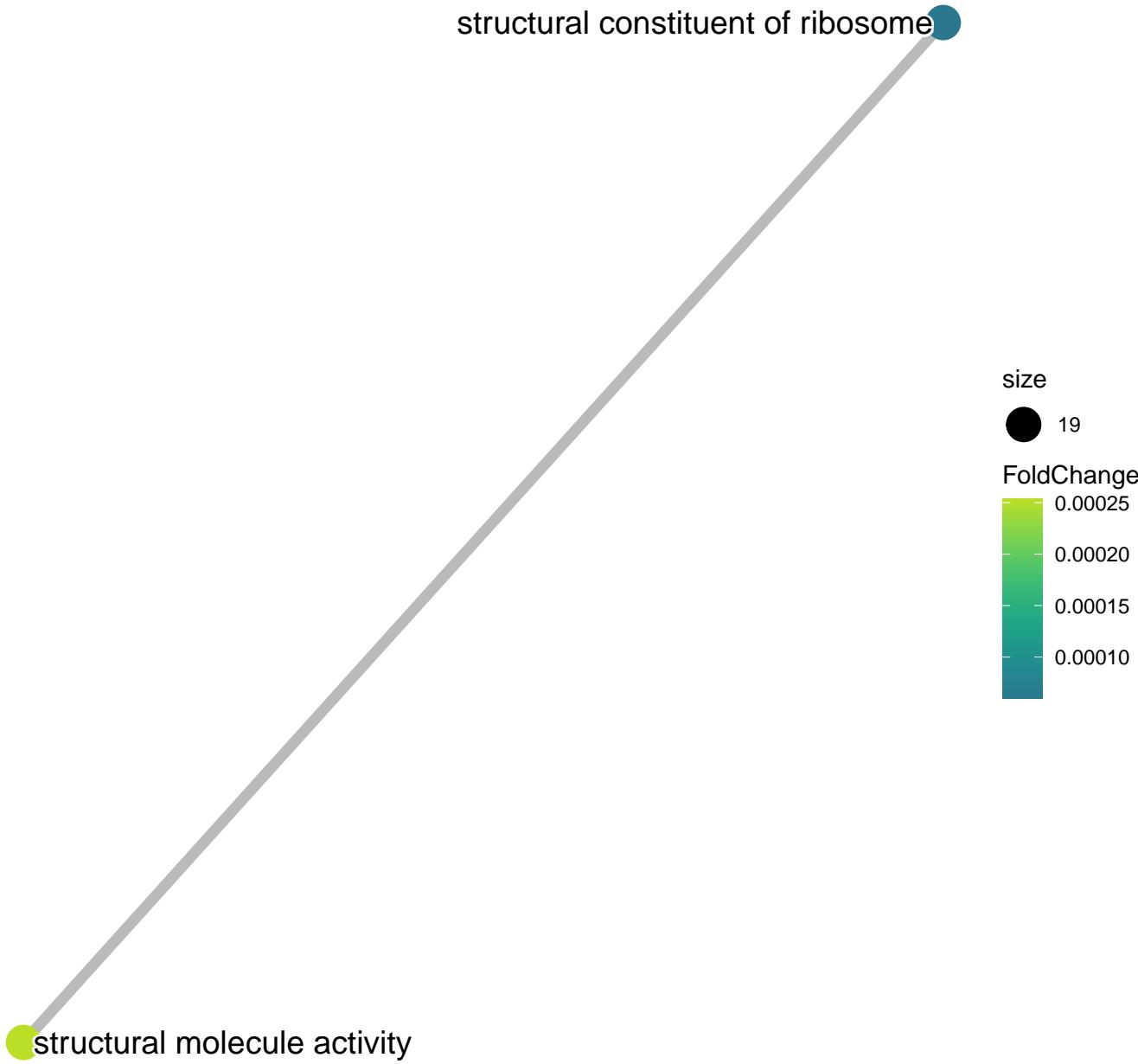


HRB1-TAP Up-regulated GO MF heatplot



HRB1-TAP Up-regulated GO MF emapplot

structural constituent of ribosome



GO:0003674
molecular_function
NA
32 / 666

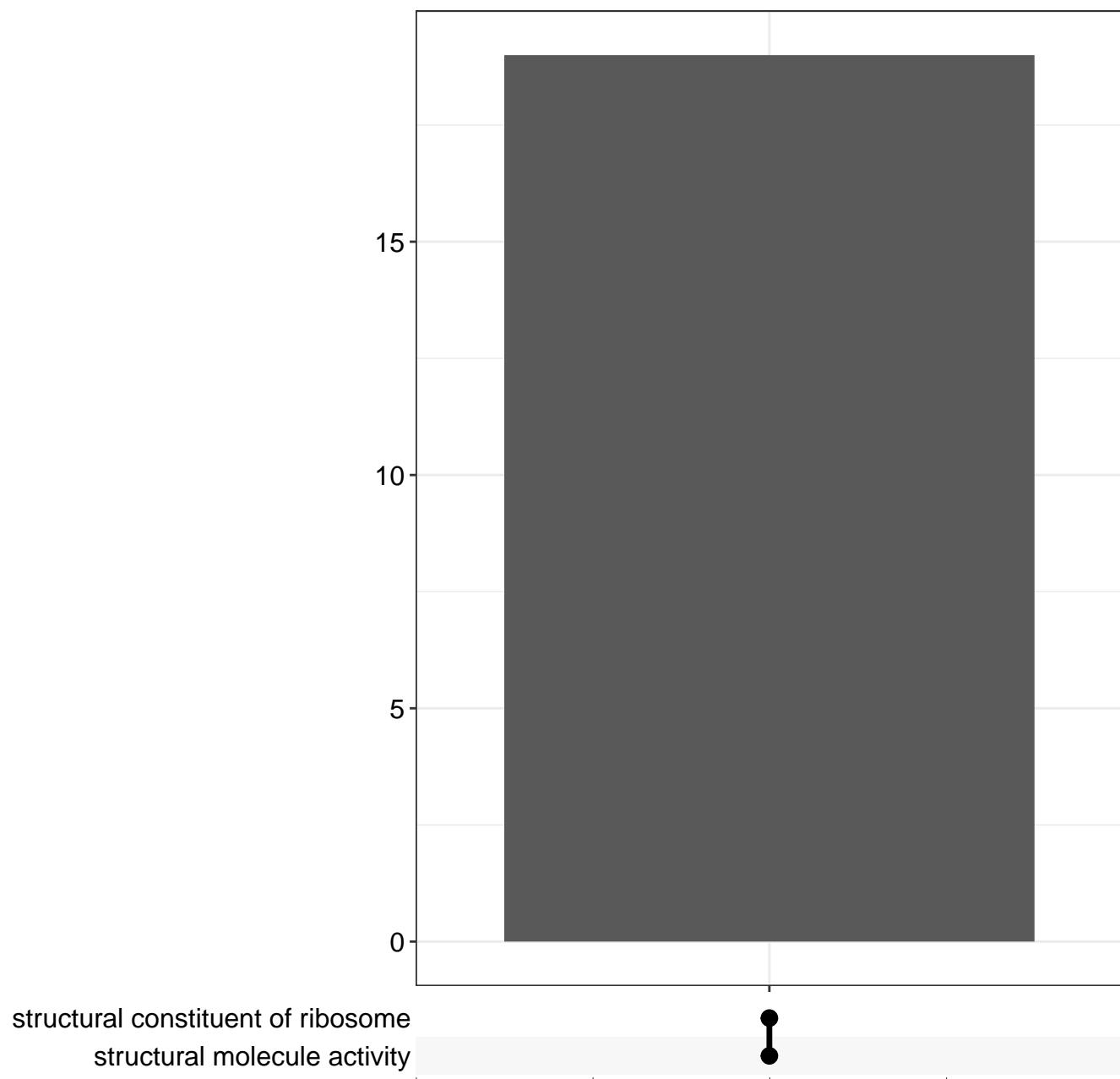


GO:0005198
structural molecule ...
0.000253
19 / 159

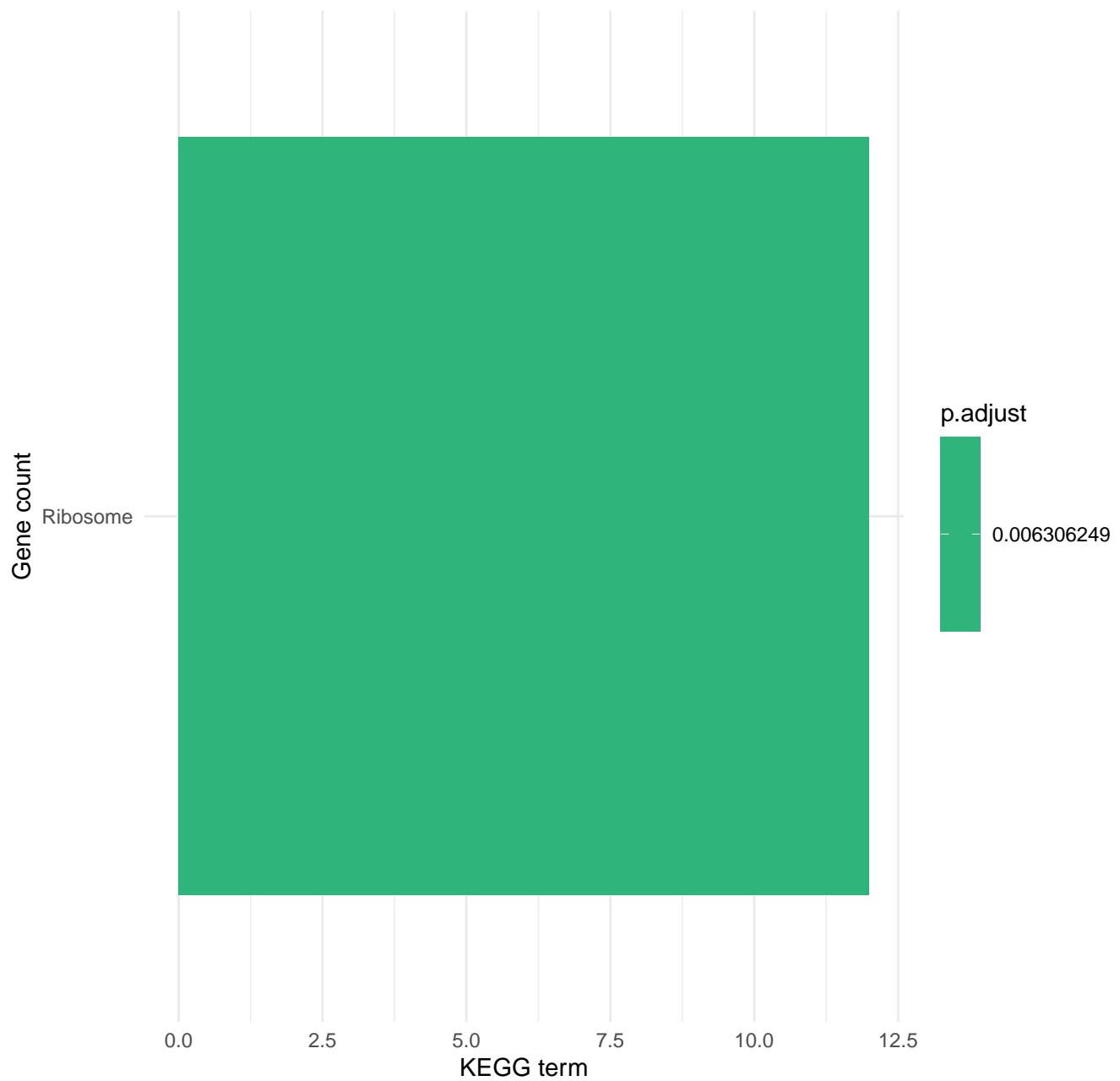


GO:0003735
structural constitue...
6.03e-05
19 / 140

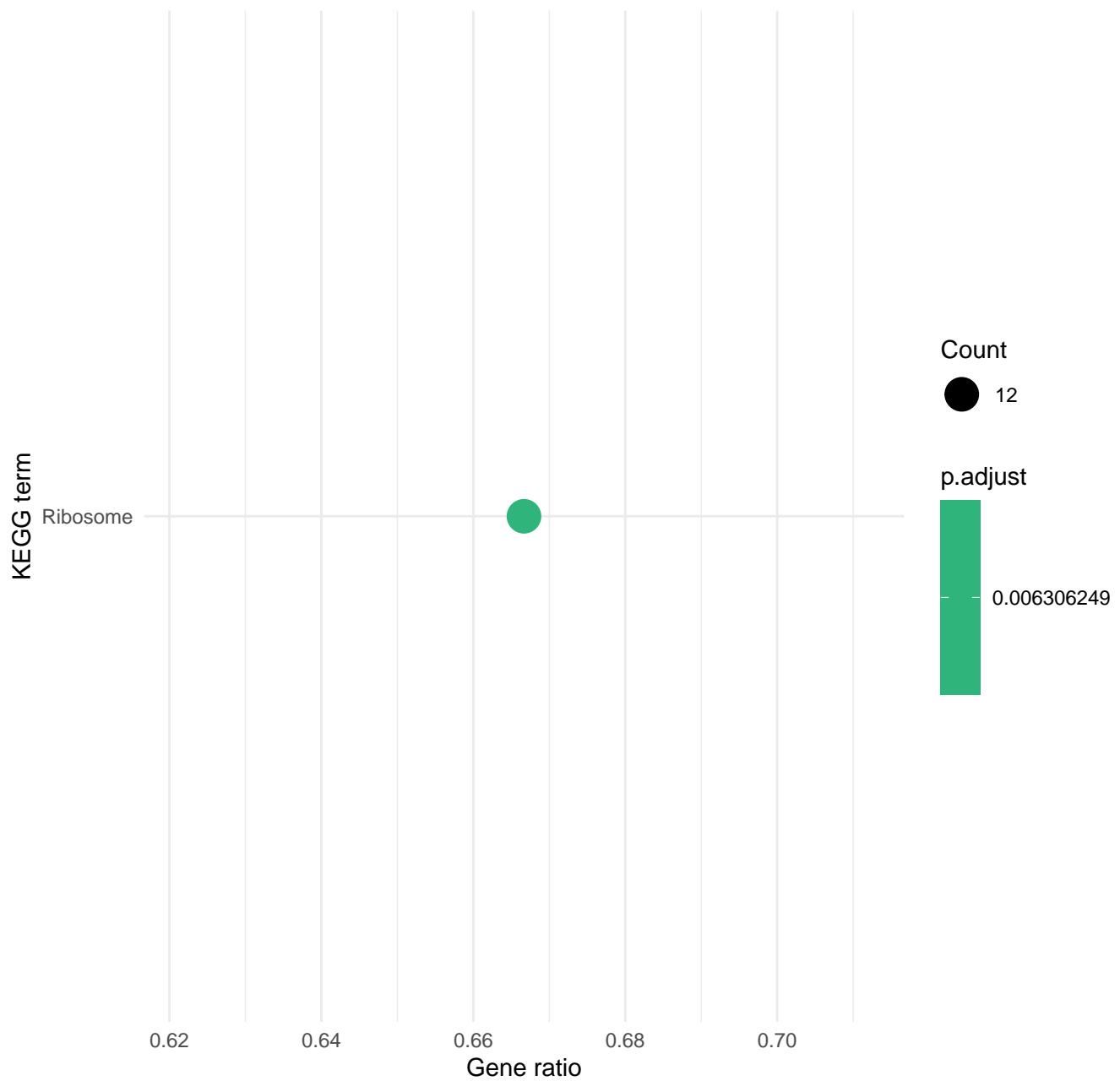
HRB1-TAP Up-regulated GO MF upsetplot



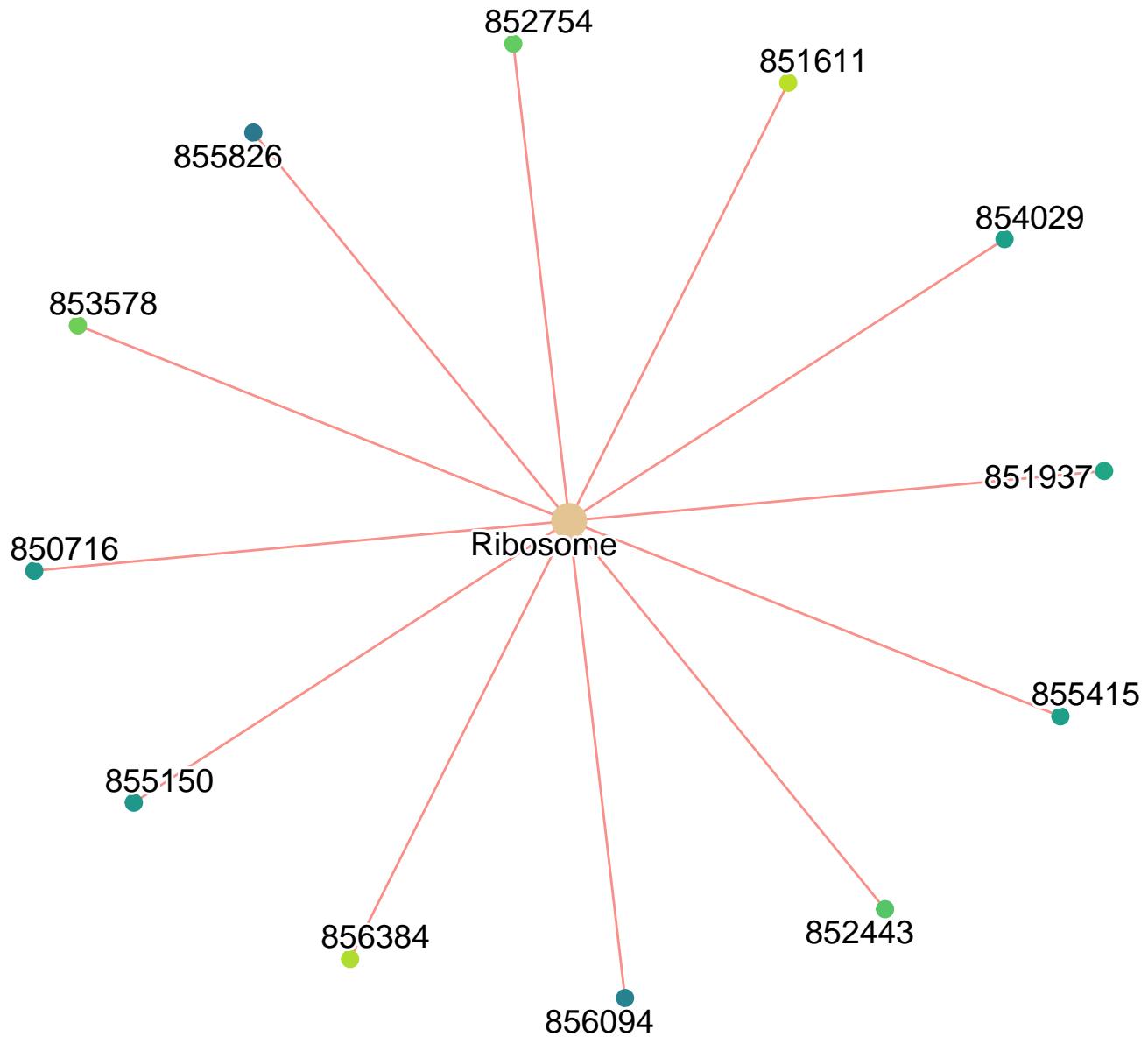
HRB1–TAP Up-regulated KEGG barplot



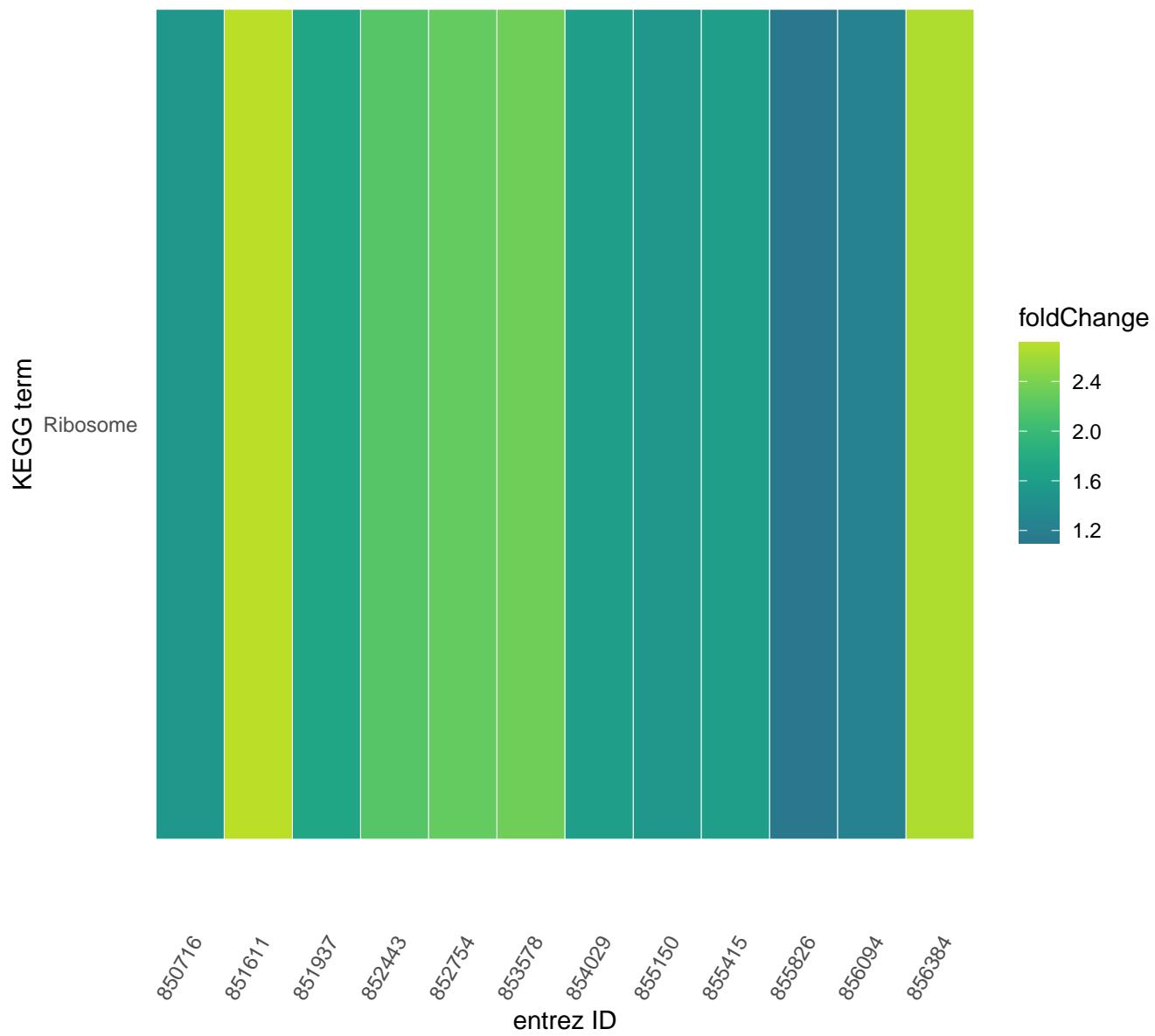
HRB1–TAP Up-regulated KEGG dotplot



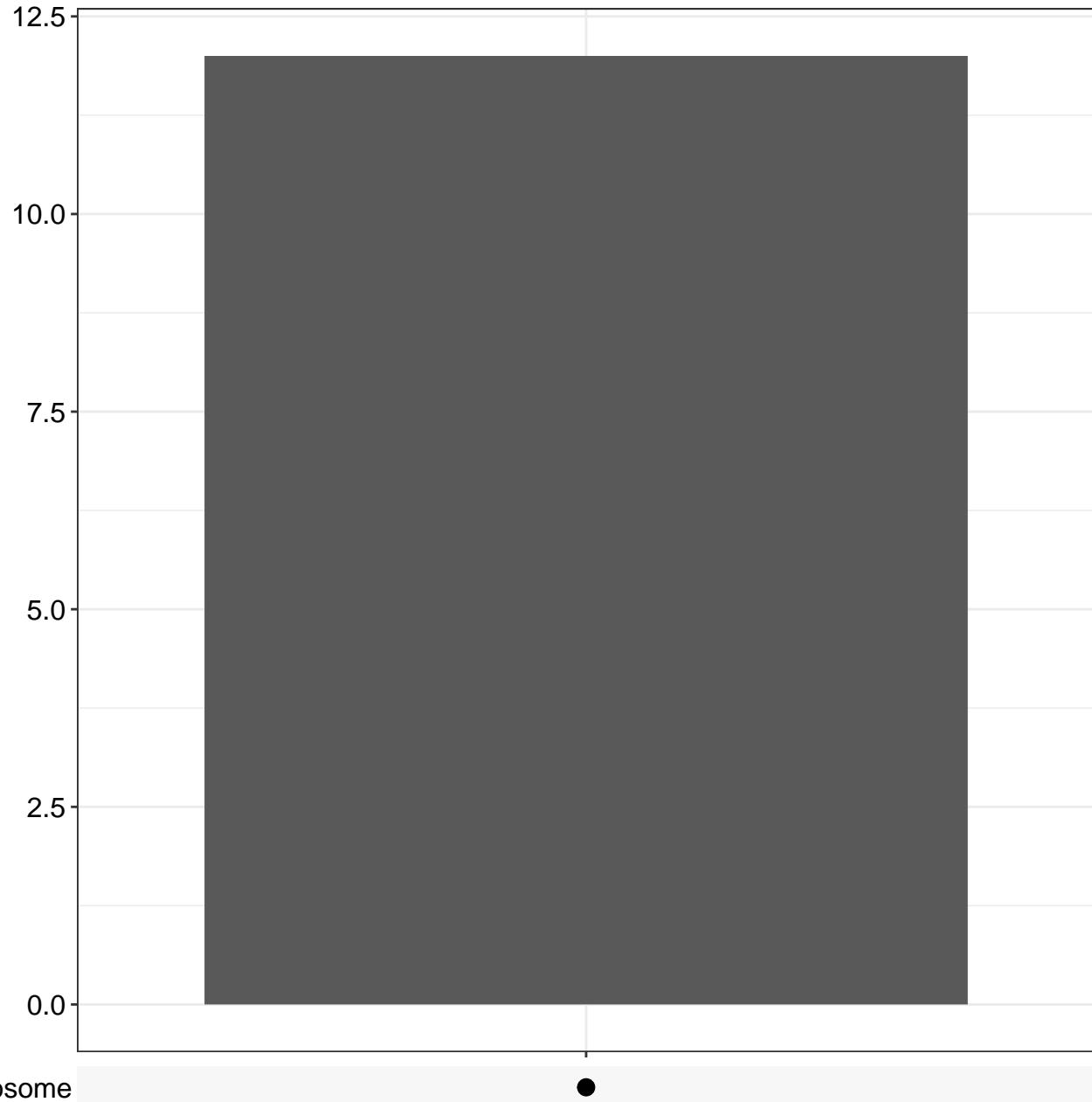
HRB1-TAP Up-regulated KEGG dotplot



HRB1-TAP Up-regulated KEGG heatplot

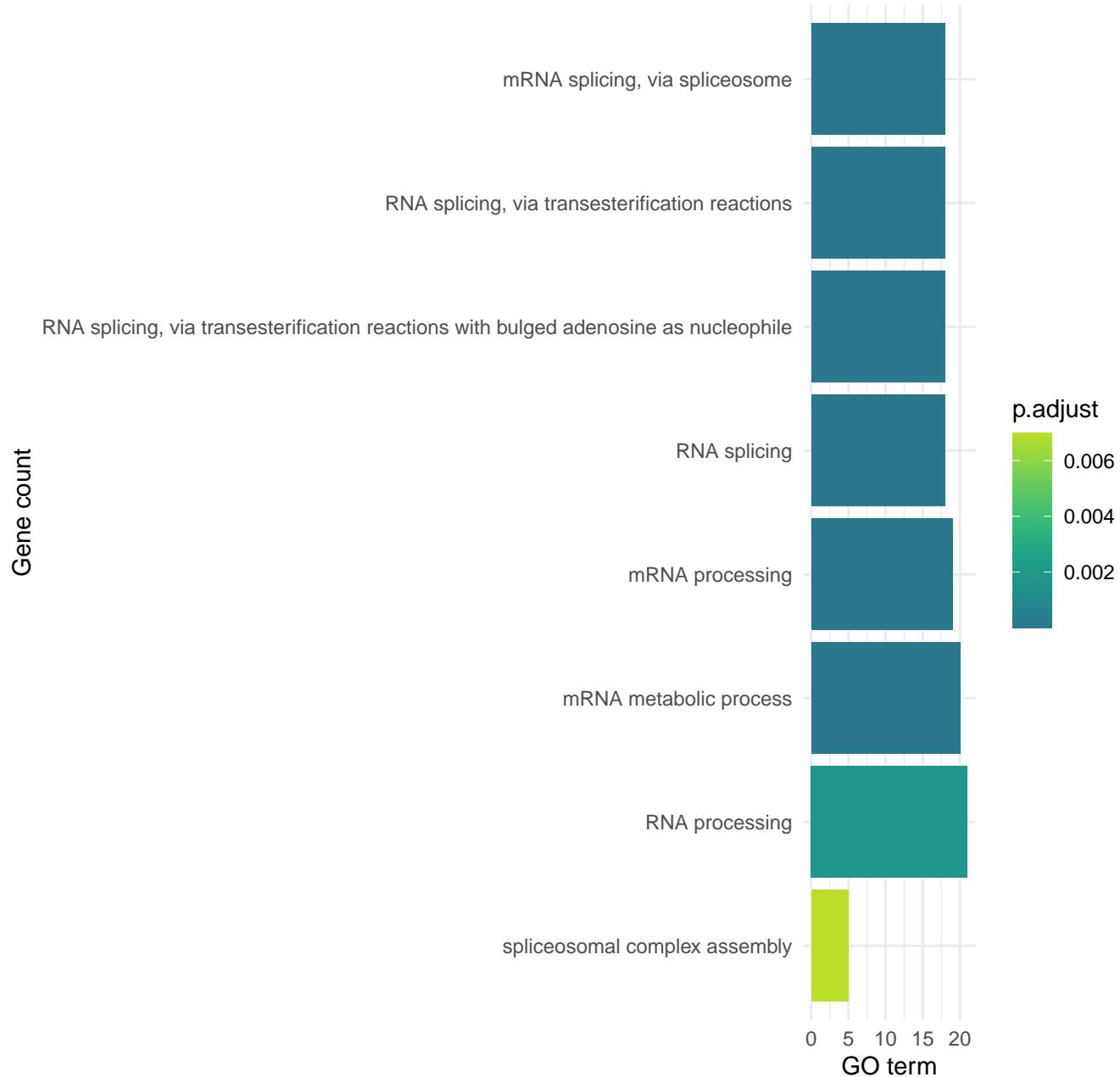


HRB1-TAP Up-regulated KEGG upsetplot

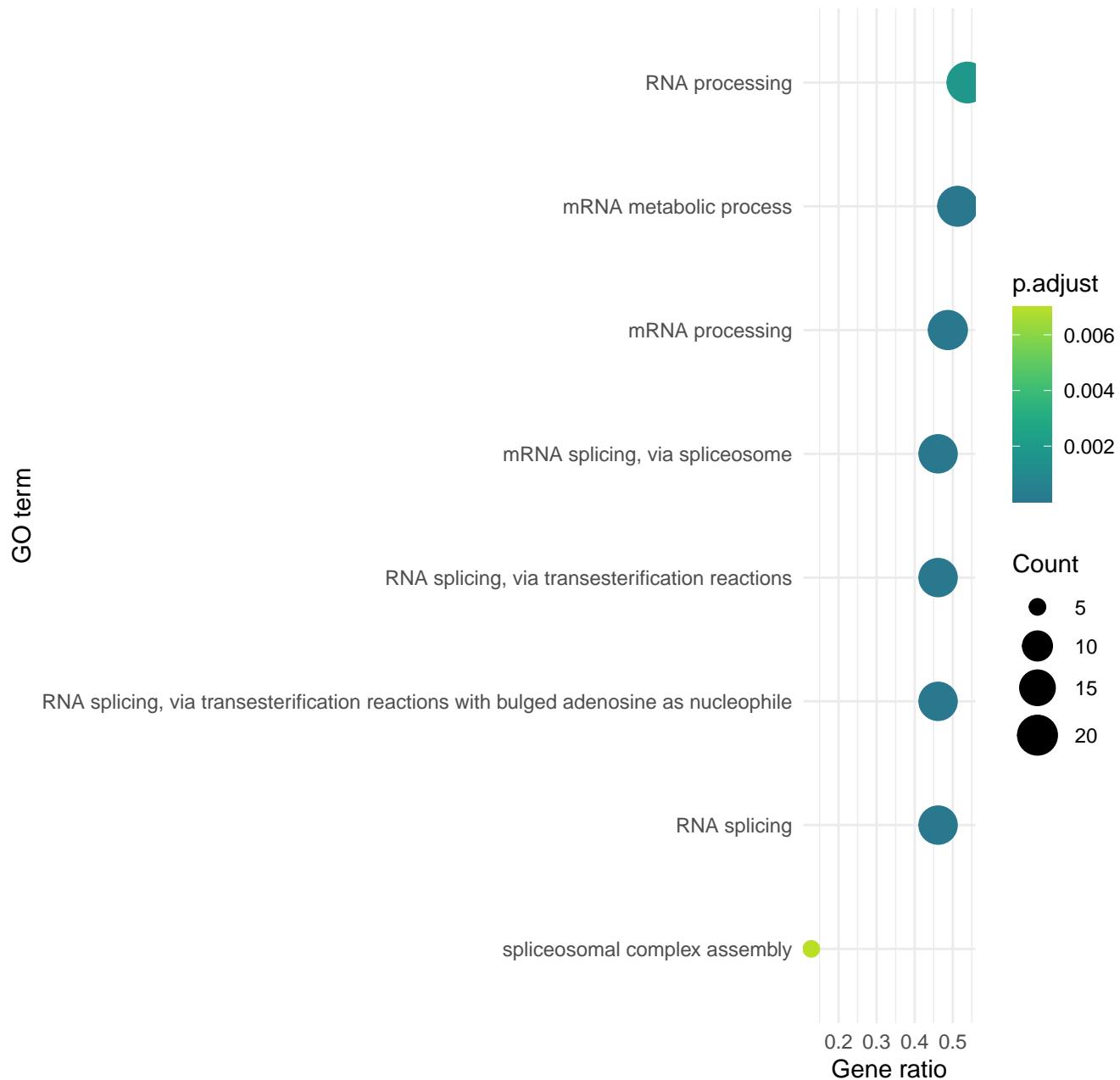


Ribosome

CBC2-TAP Up-regulated



CBC2-TAP Up-regulated



CBC2–TAP Up-regulated GO BP cnetplot

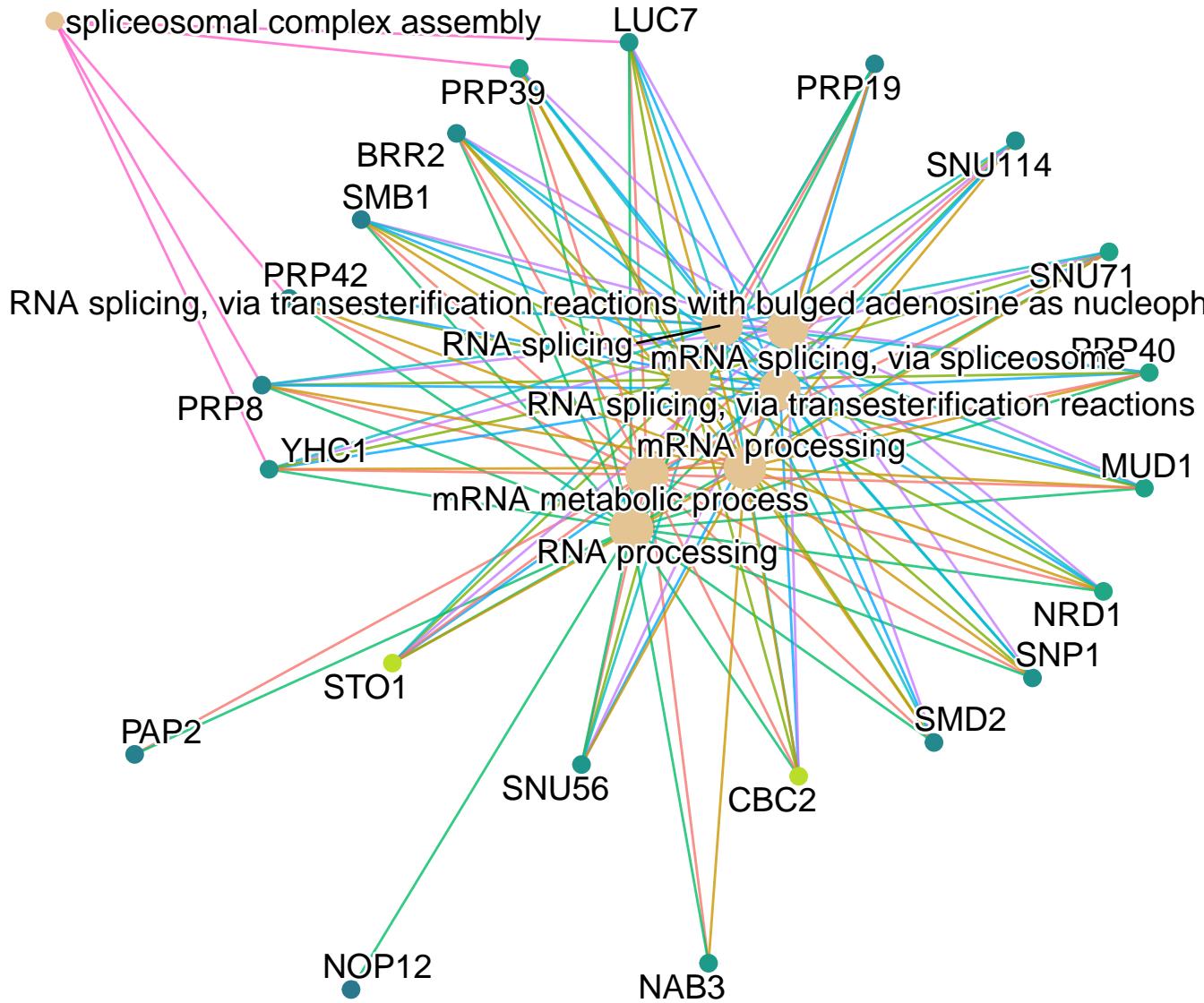
RNA splicing, via spliceosome — RNA splicing

NA processing

— RNA splicing, via transesterification reactions

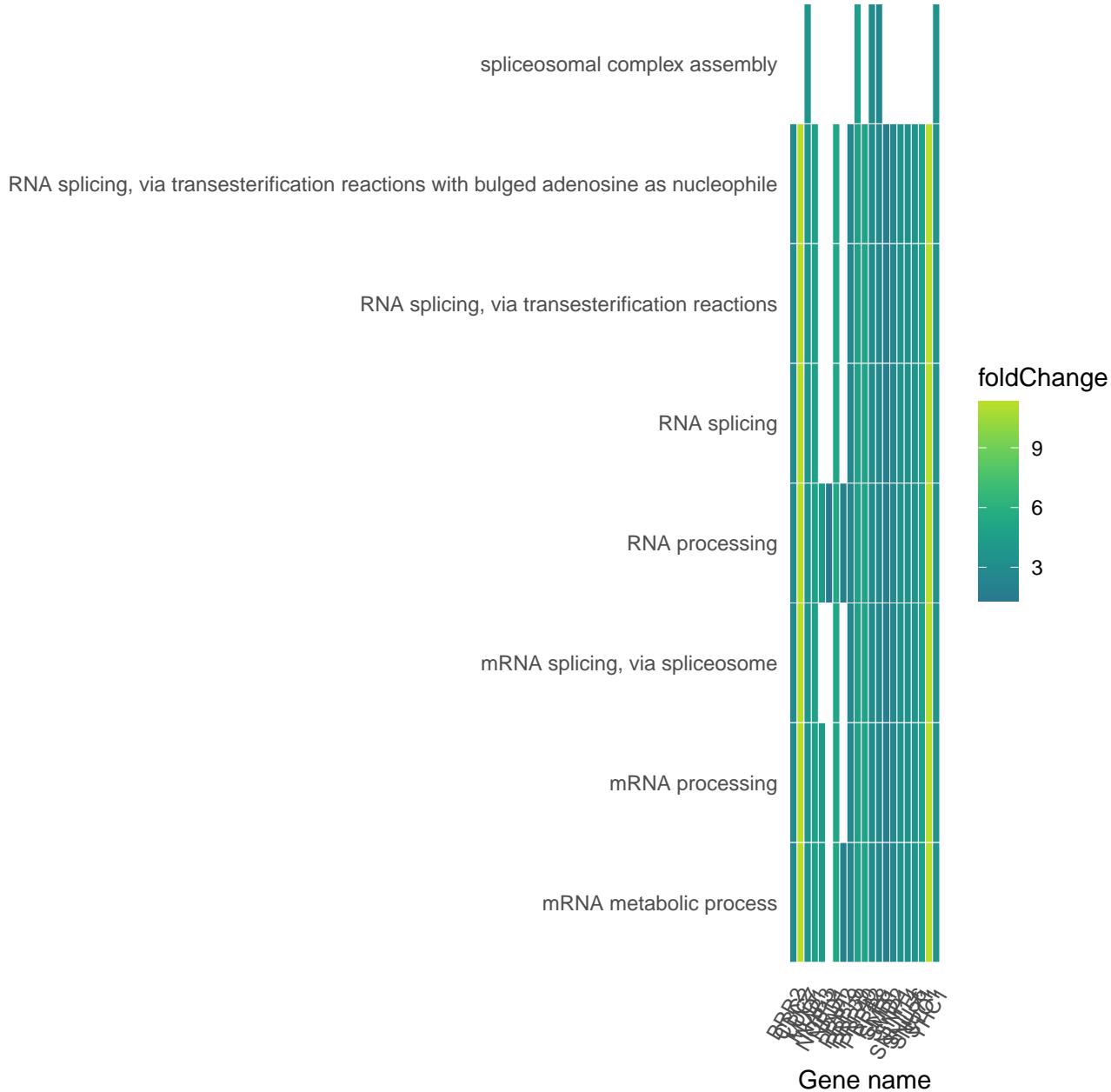
— RNA splicing, via transesterification reaction

— spliceosomal complex assembly



CBC2-TAP Up-regulated

GO term



CBC2-TAP Up-regulated GO BP emapplot

RNA processing

, via transesterification reactions with bulged adenosine as nucleophile

mRNA processing

spliceosomal complex assembly

mRNA splicing, via spliceosome

mRNA metabolic process

RNA splicing

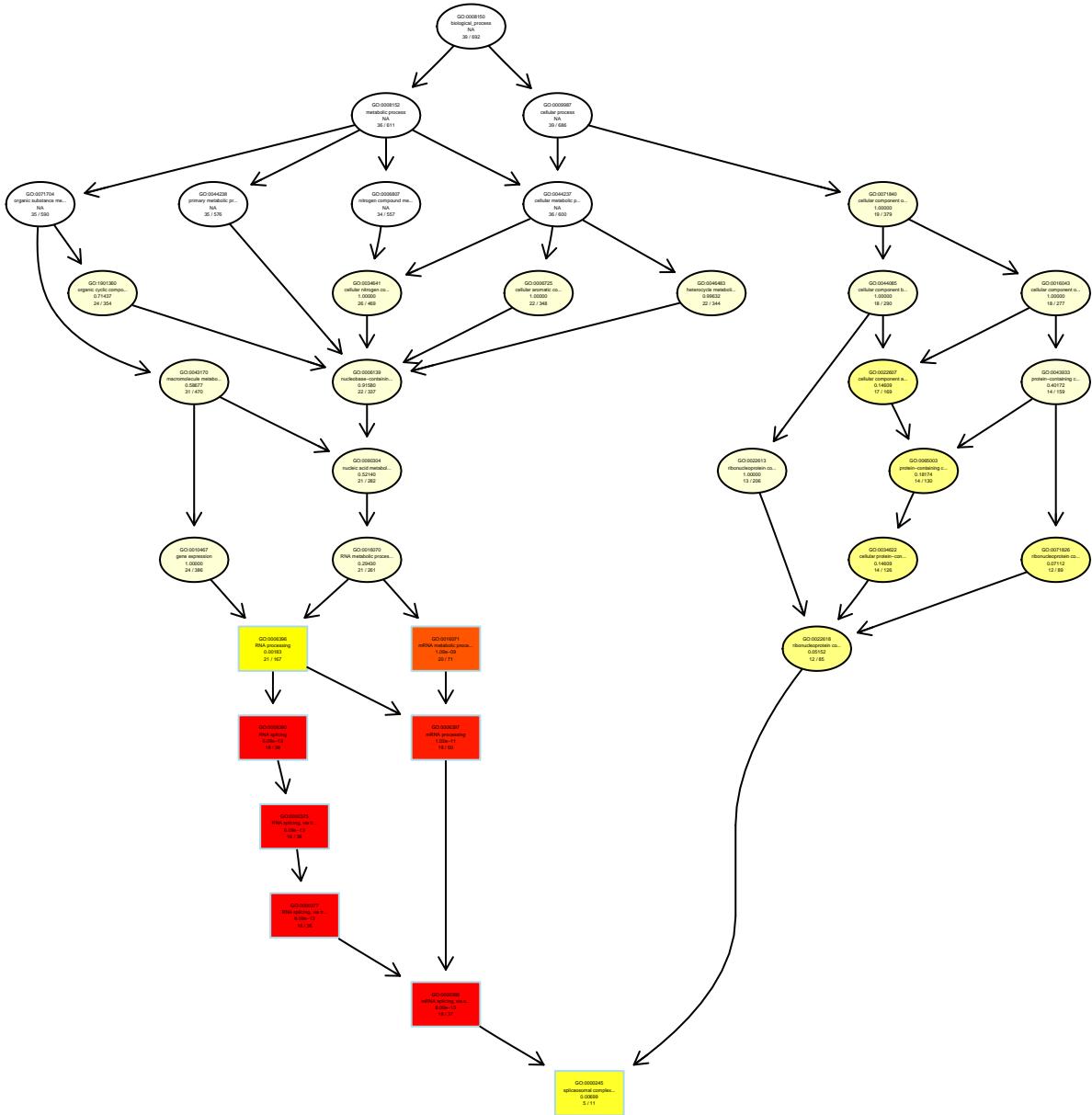
RNA splicing, via transesterification reactions

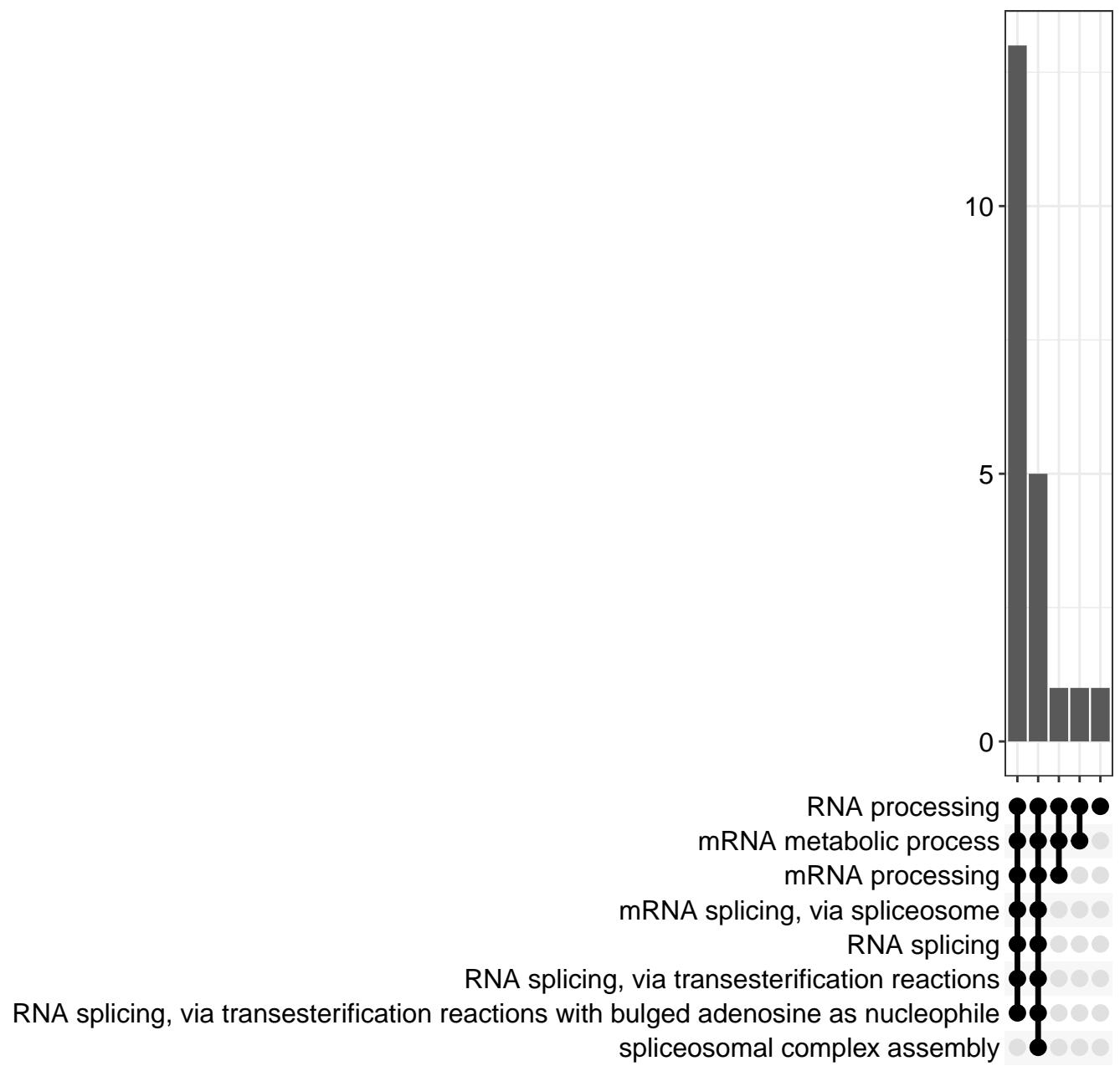
size

- 5
- 10
- 15
- 20

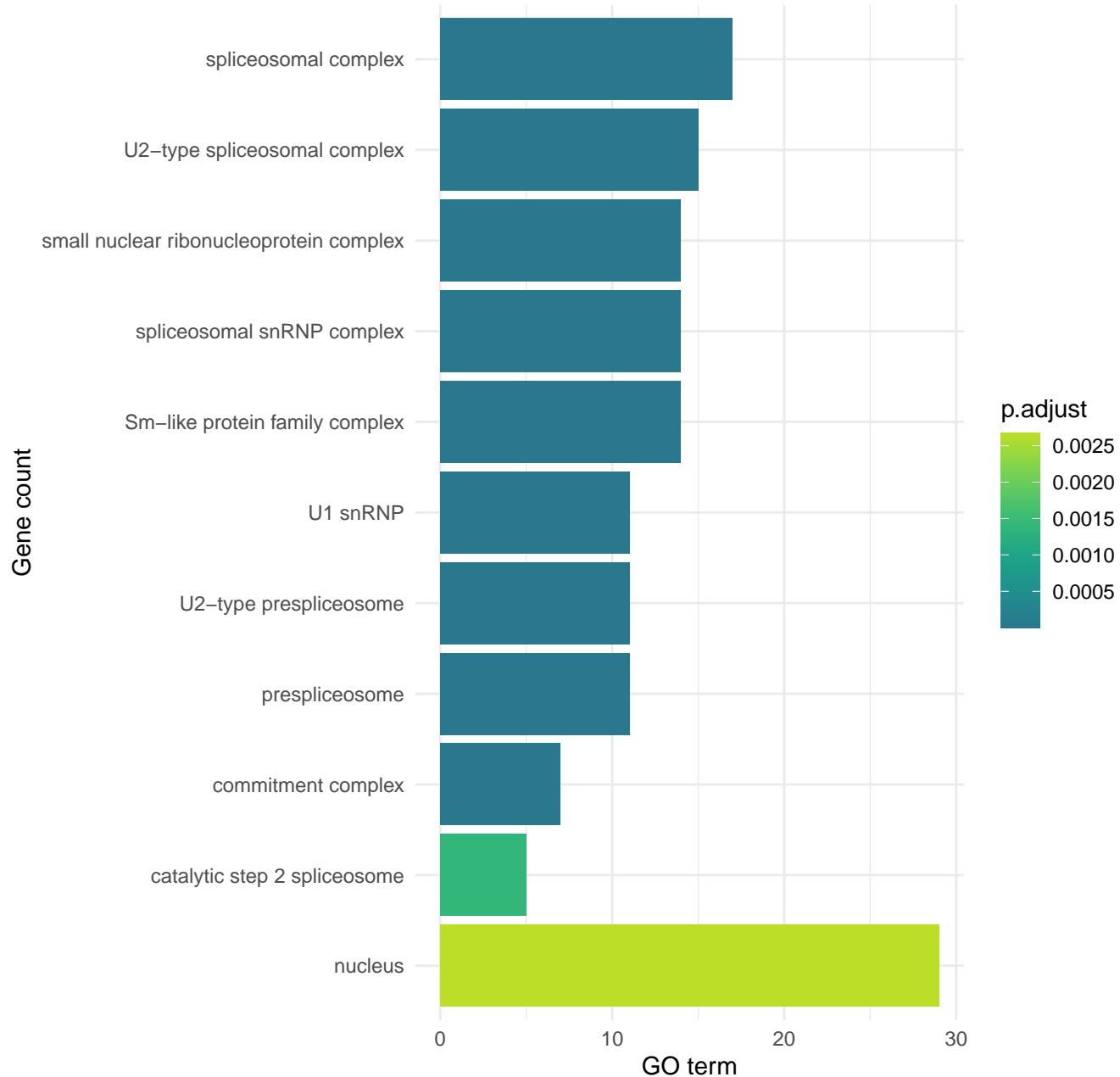
FoldChange



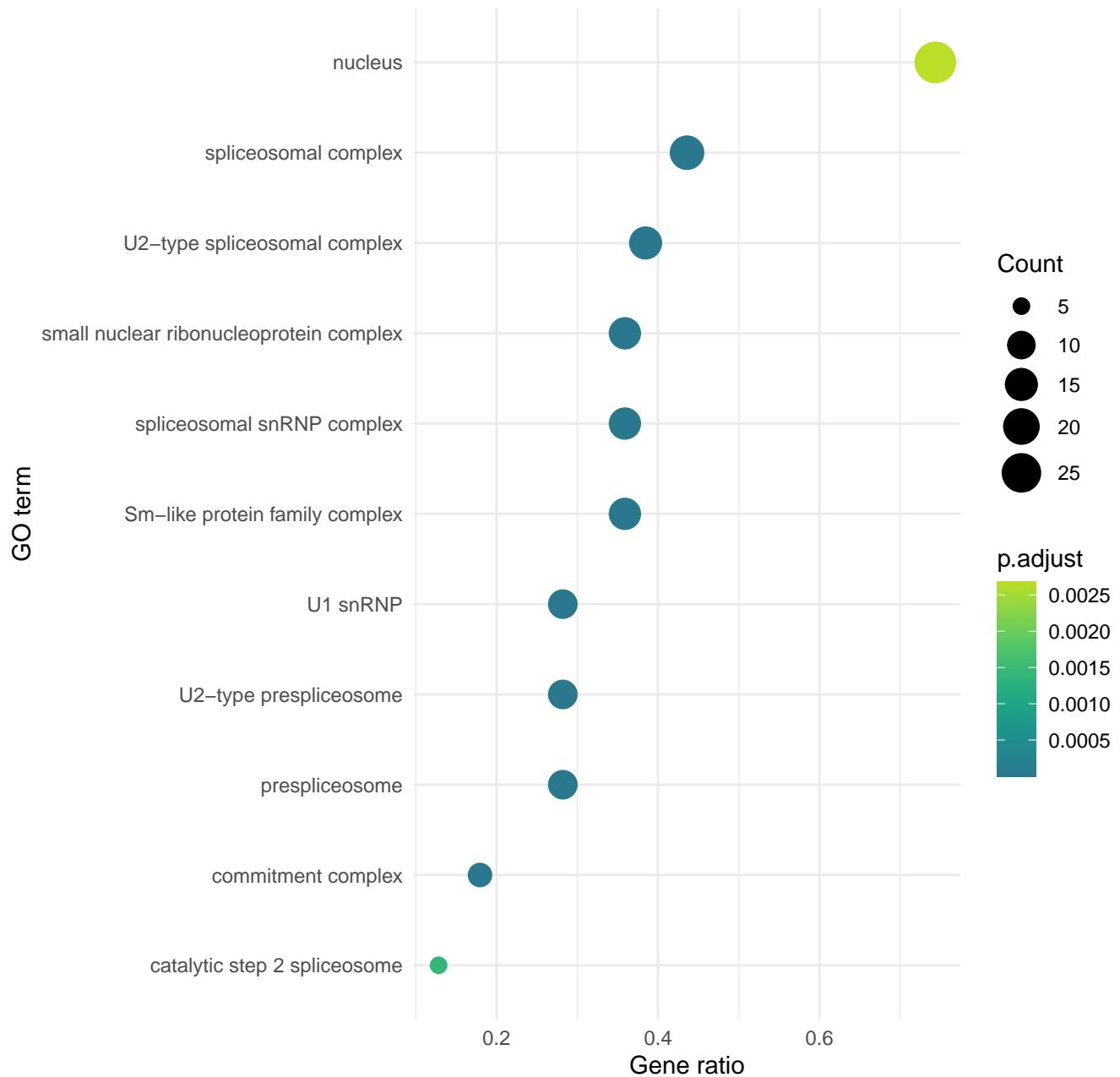




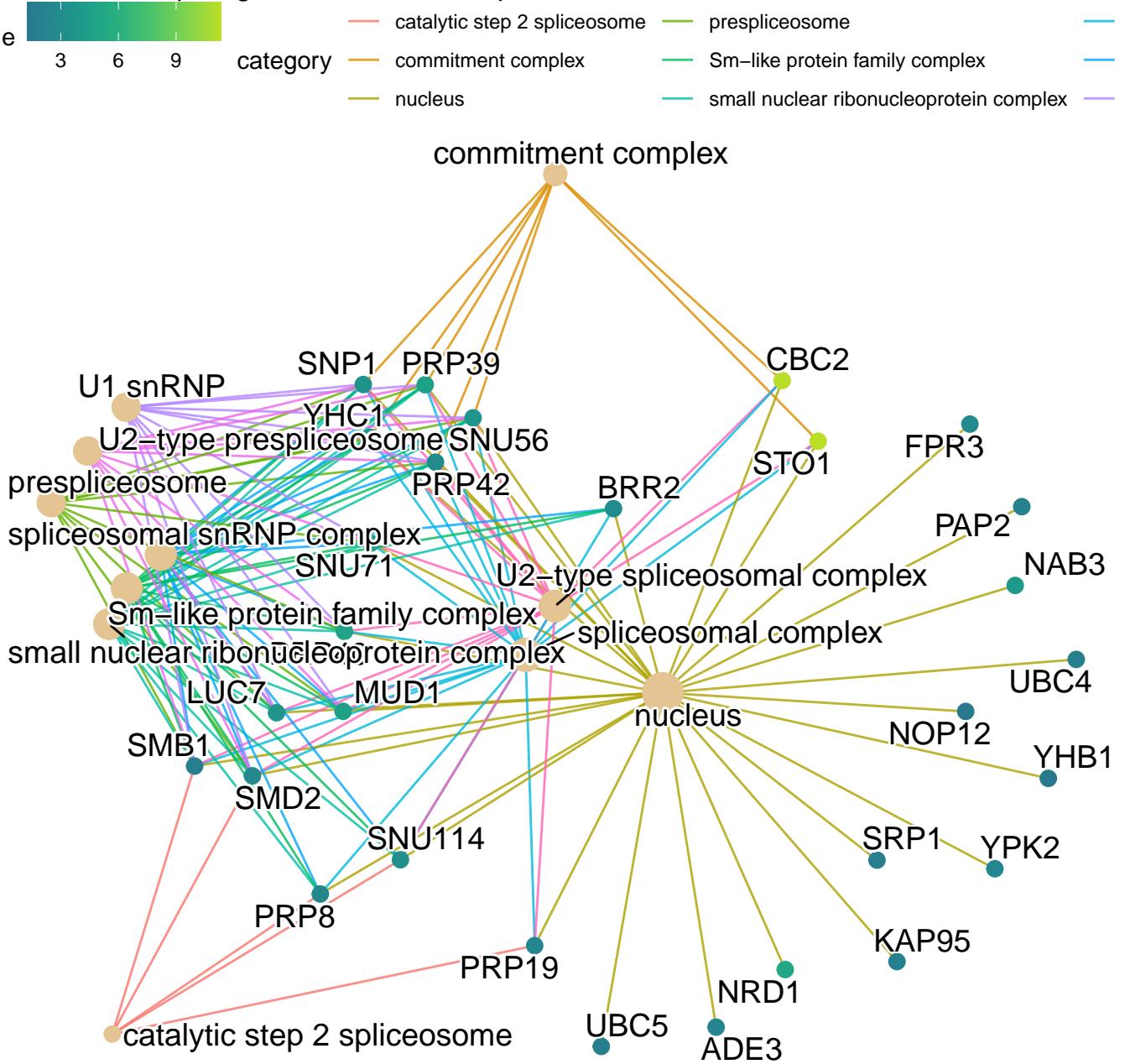
CBC2-TAP Up-regulated GO CC barplot



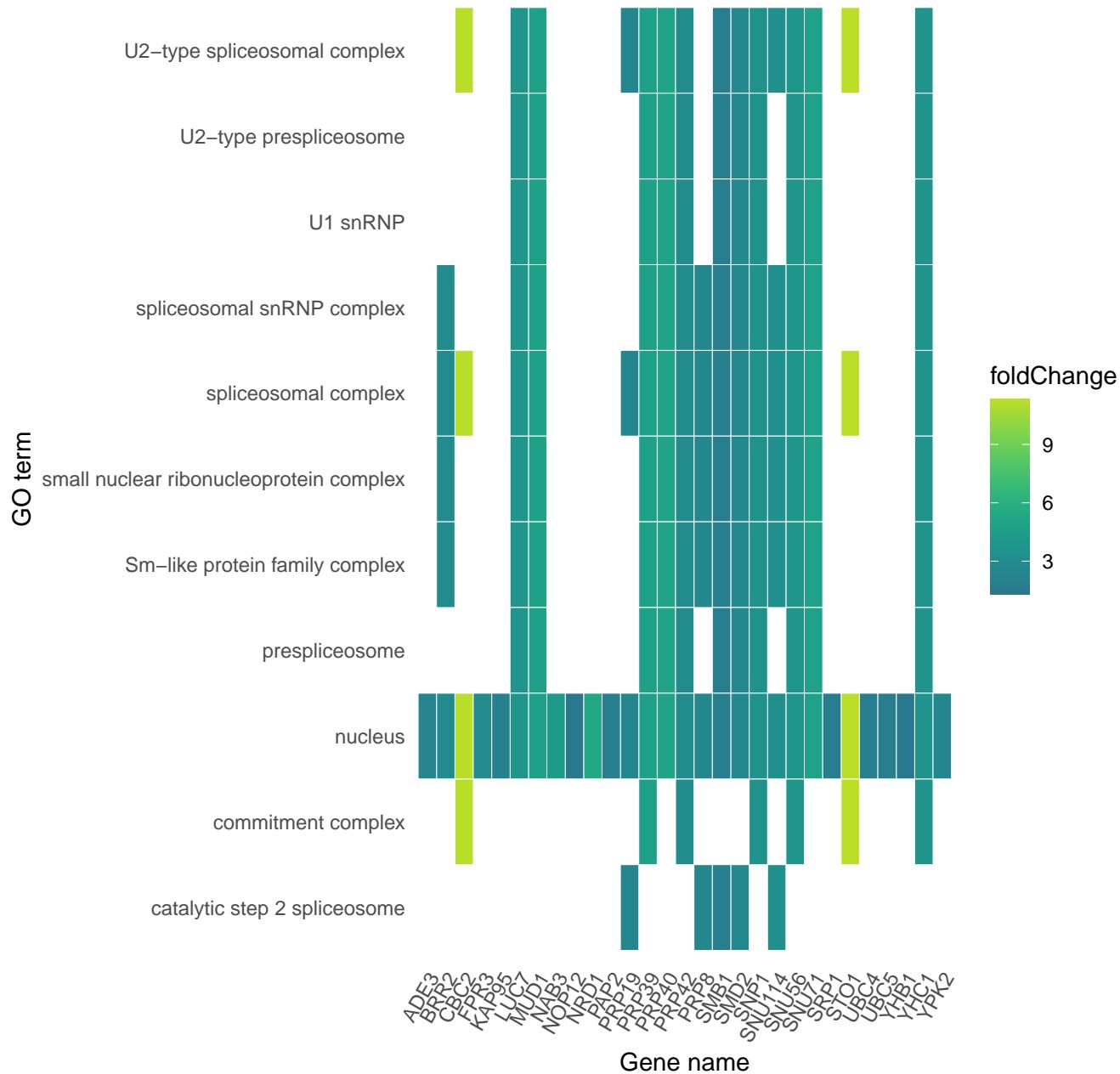
CBC2-TAP Up-regulated GO CC dotplot



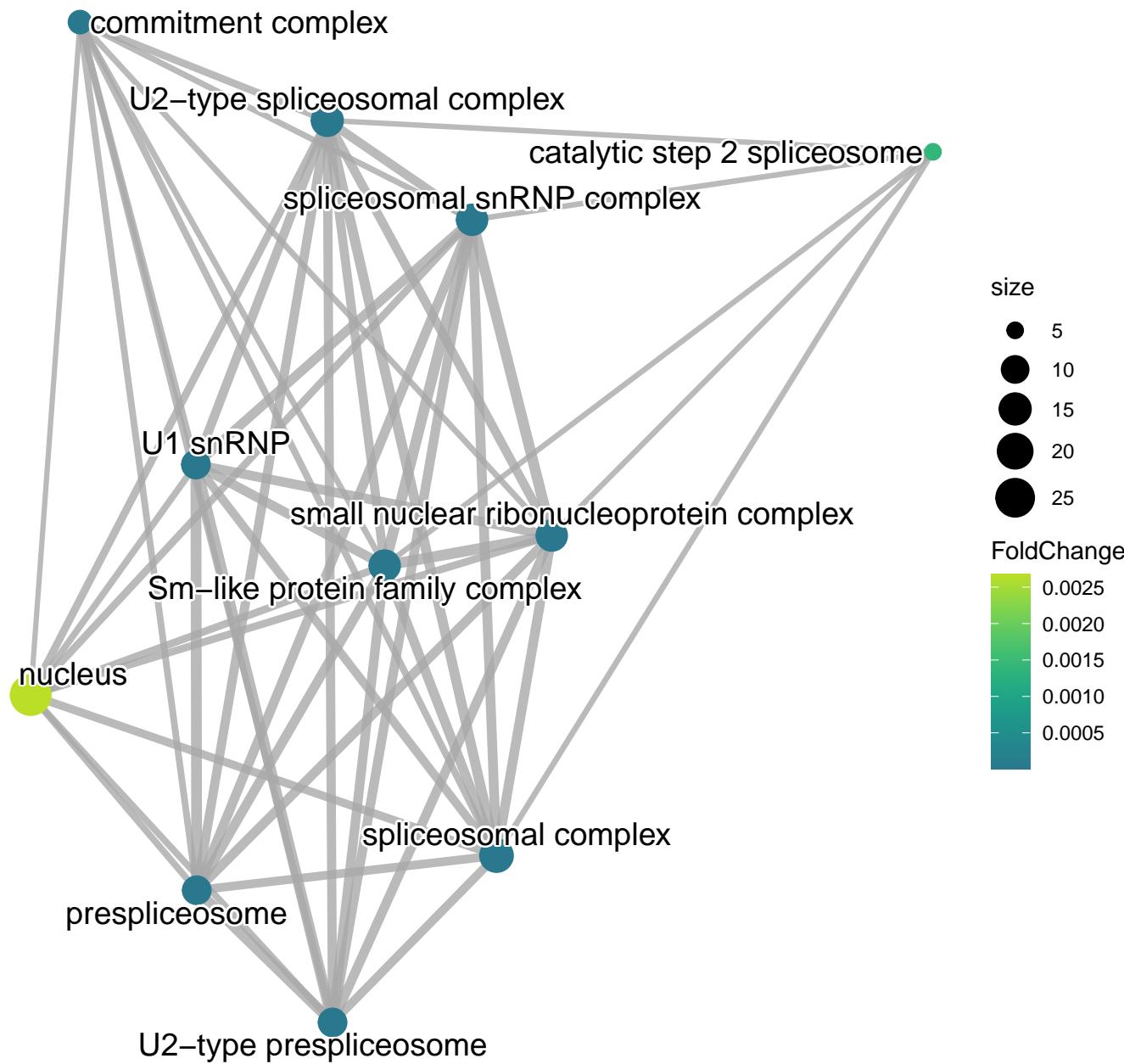
CBC2-TAP Up-regulated GO CC cnetplot

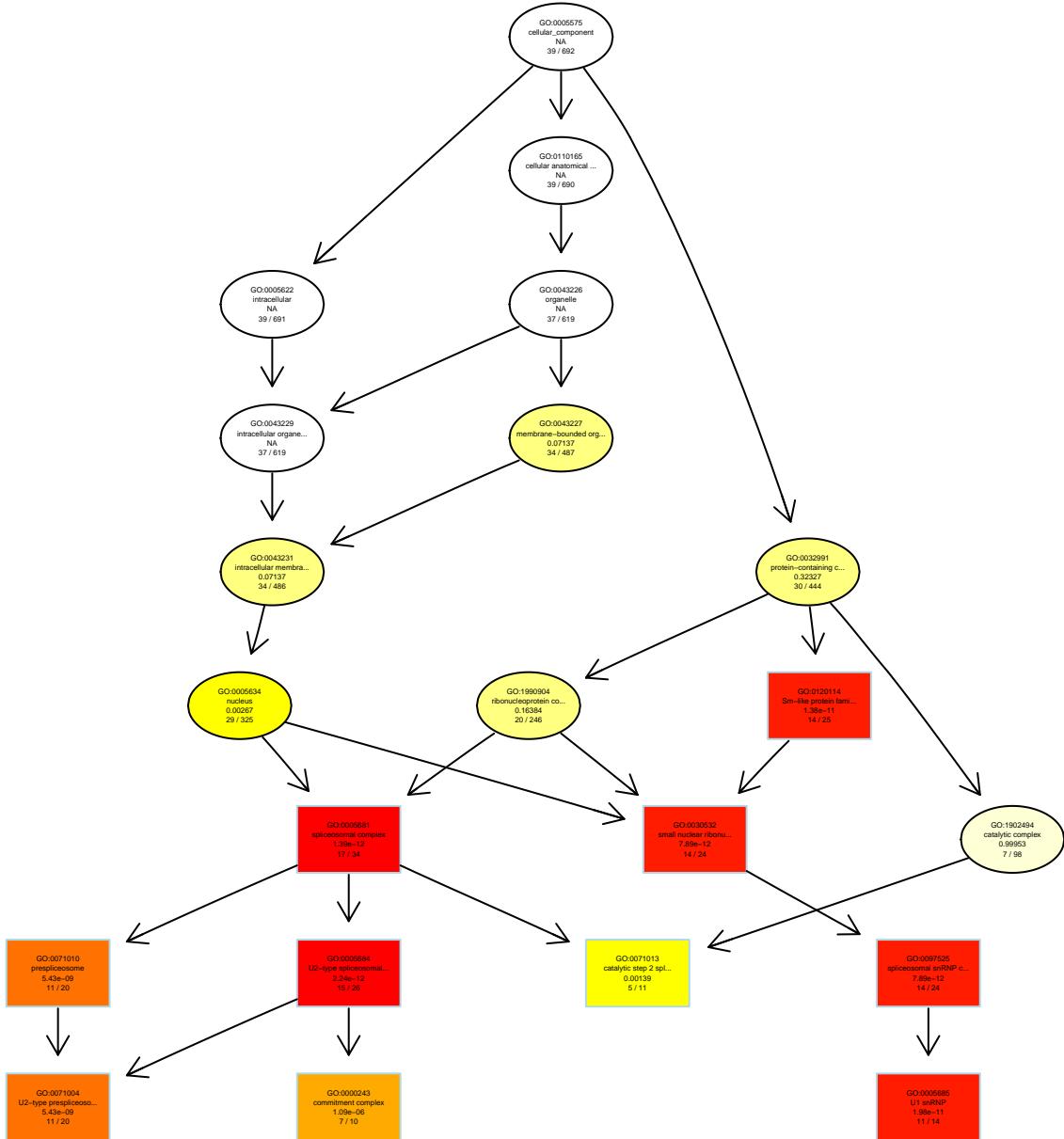


CBC2-TAP Up-regulated GO CC heatplot

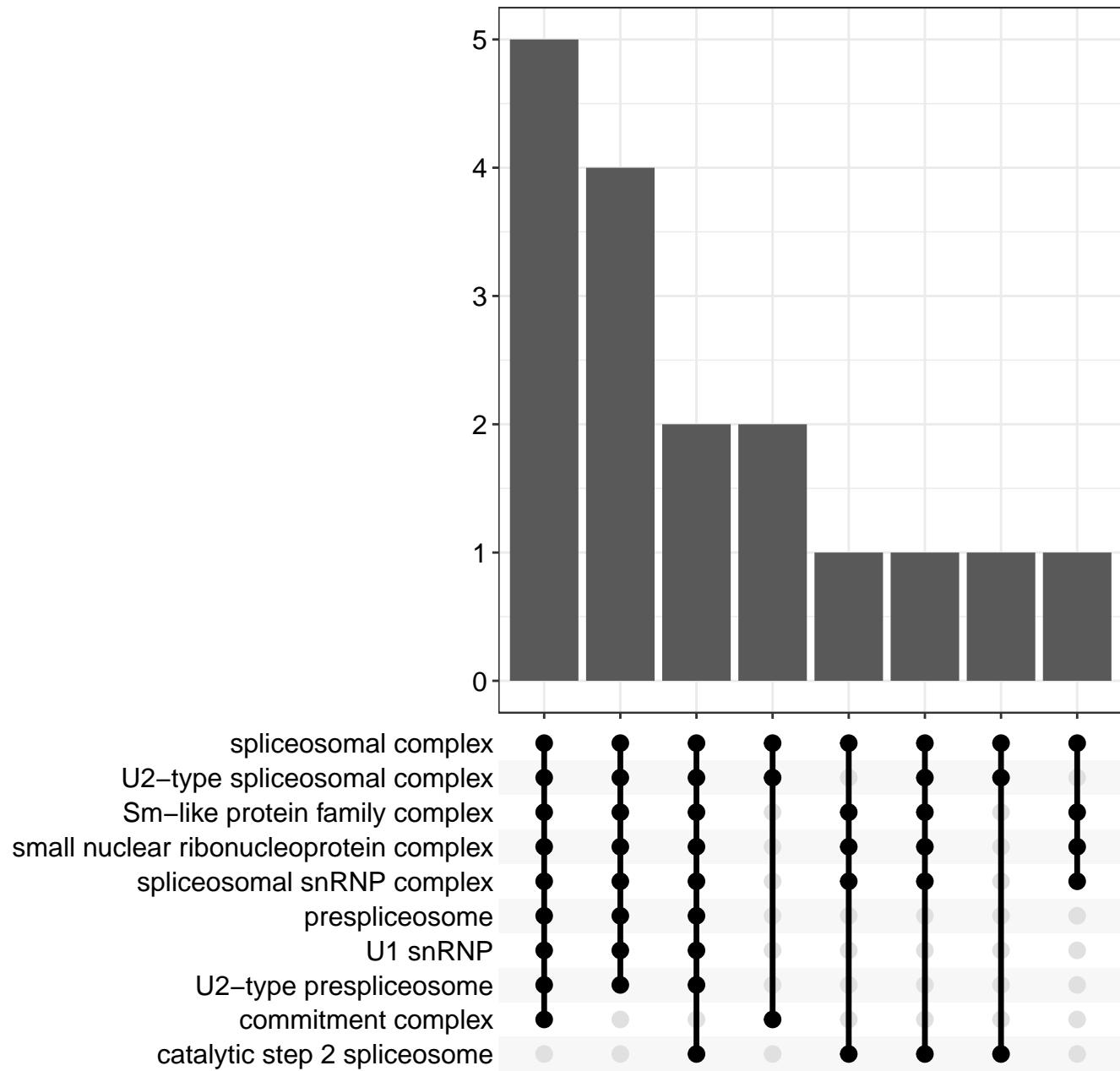


CBC2-TAP Up-regulated GO CC emapplot

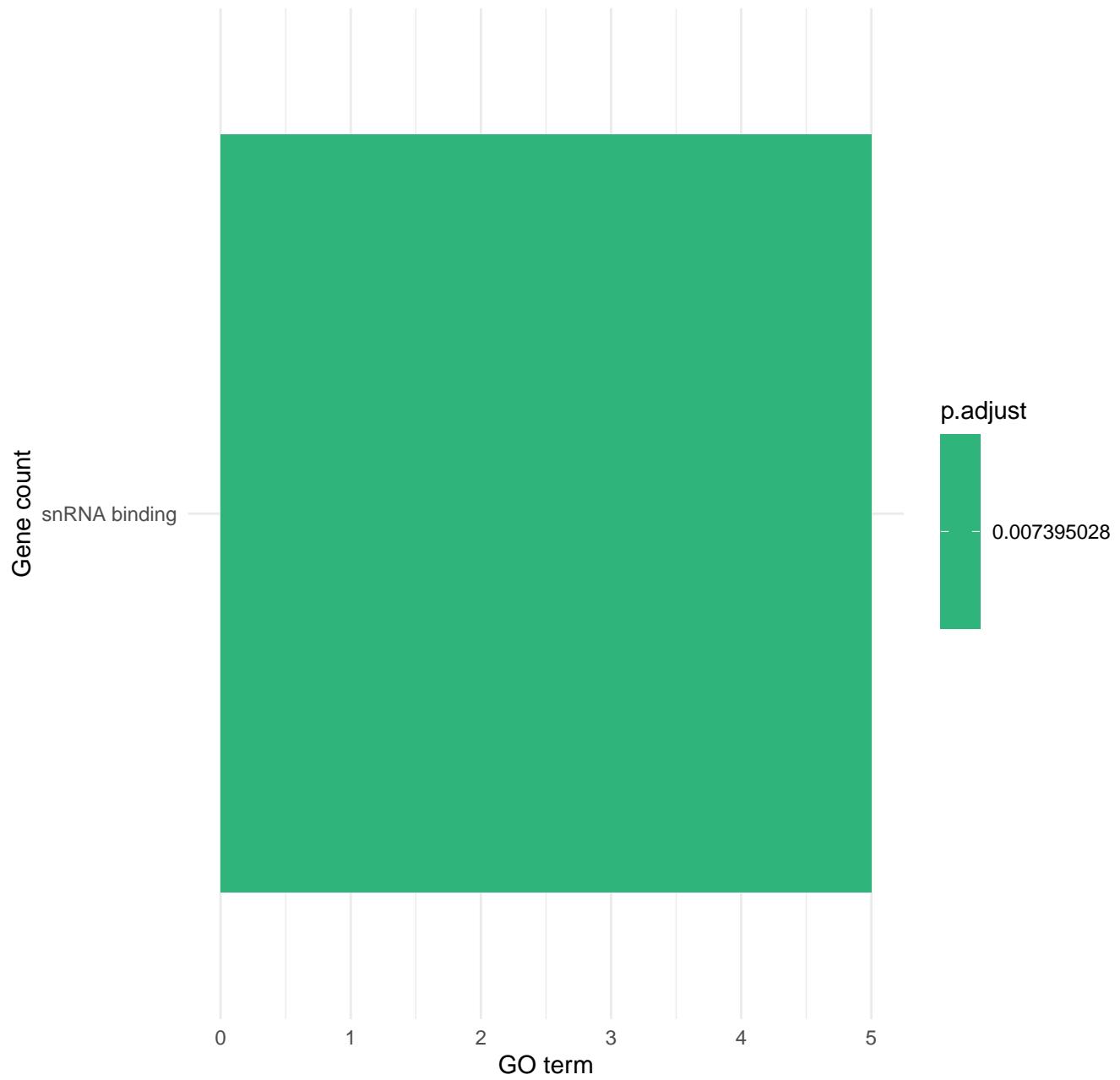




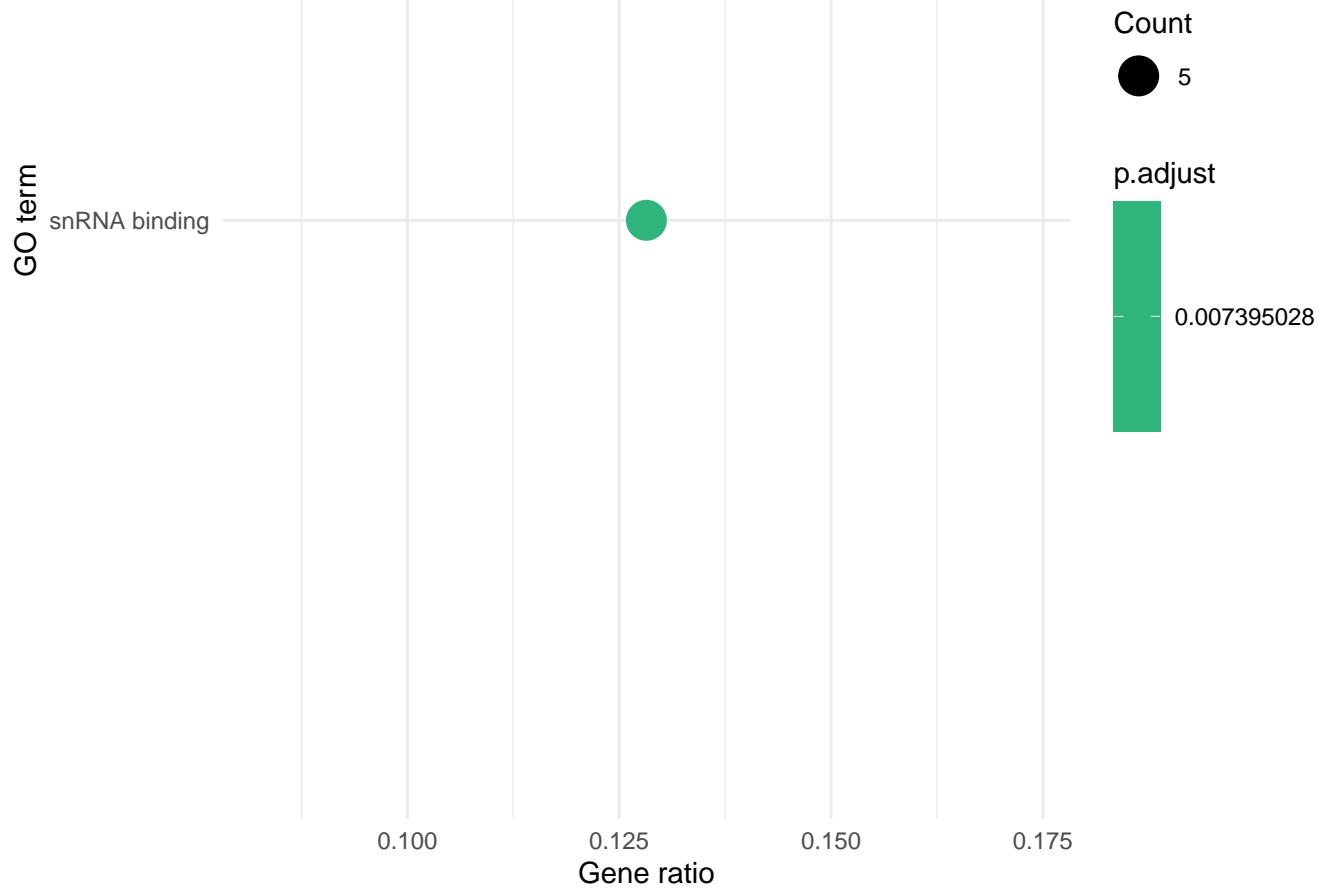
CBC2-TAP Up-regulated GO CC upsetplot



CBC2-TAP Up-regulated GO MF barplot



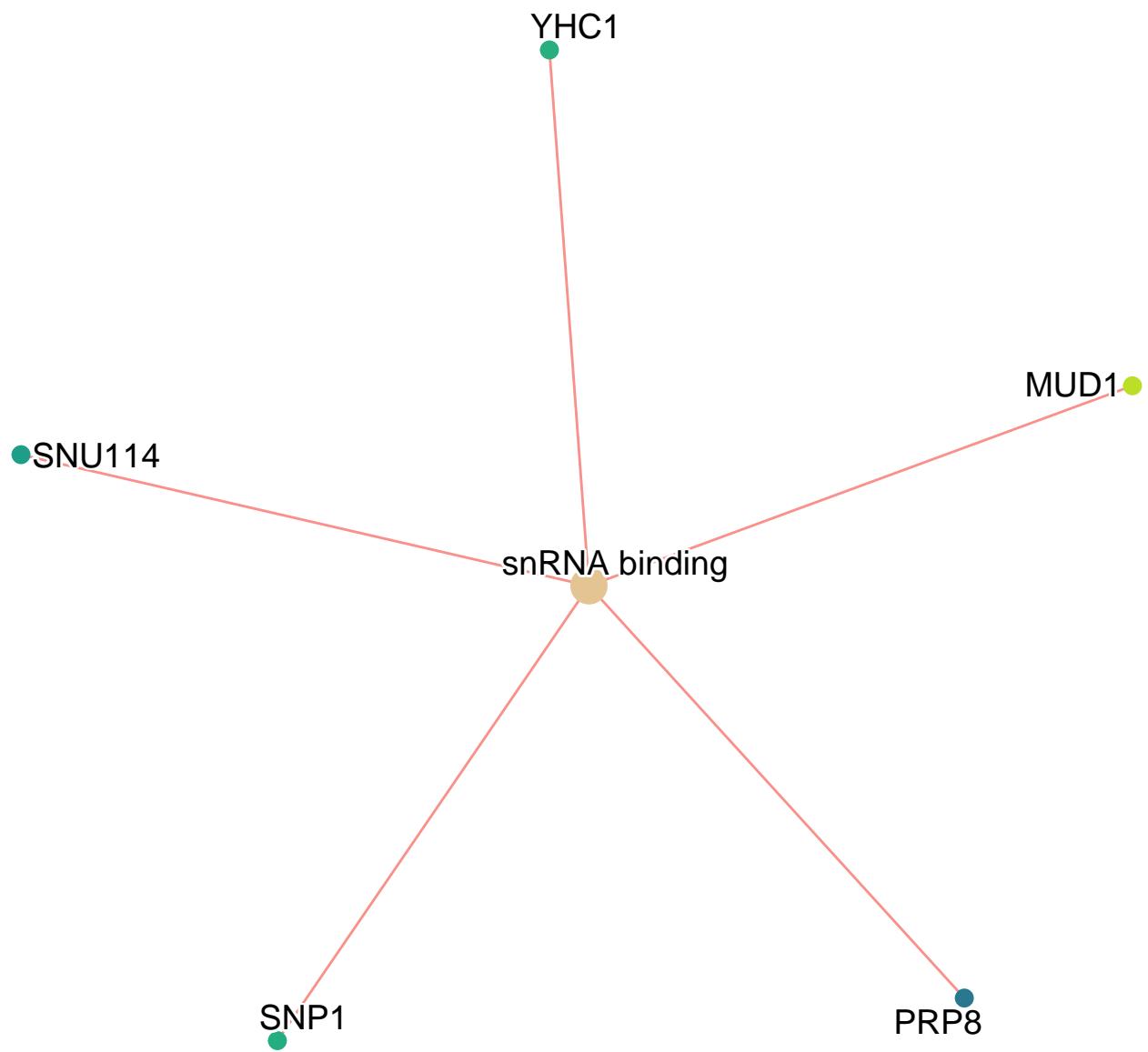
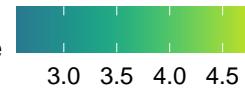
CBC2-TAP Up-regulated GO MF dotplot



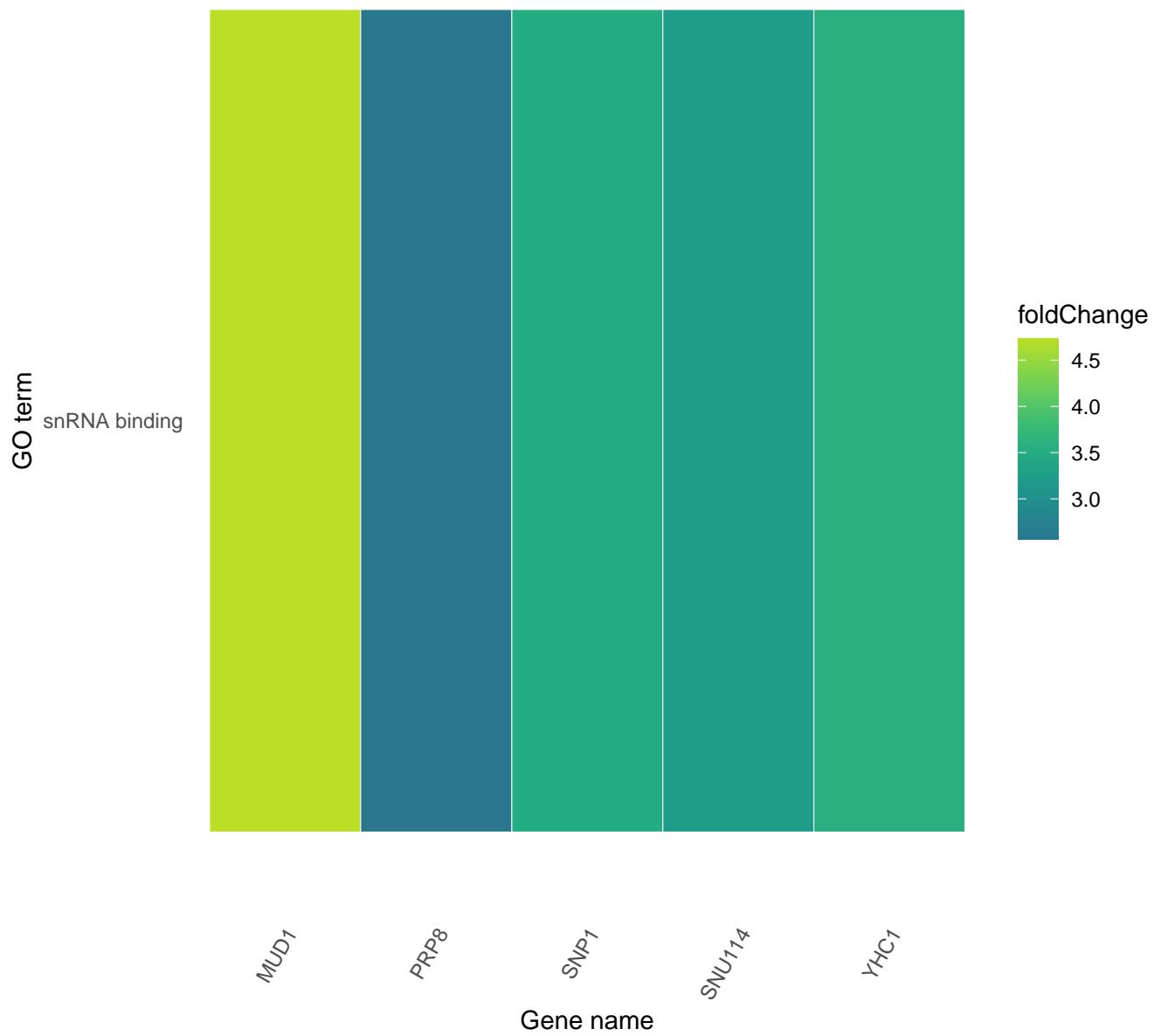
CBC2-TAP Up-regulated GO MF cnetplot

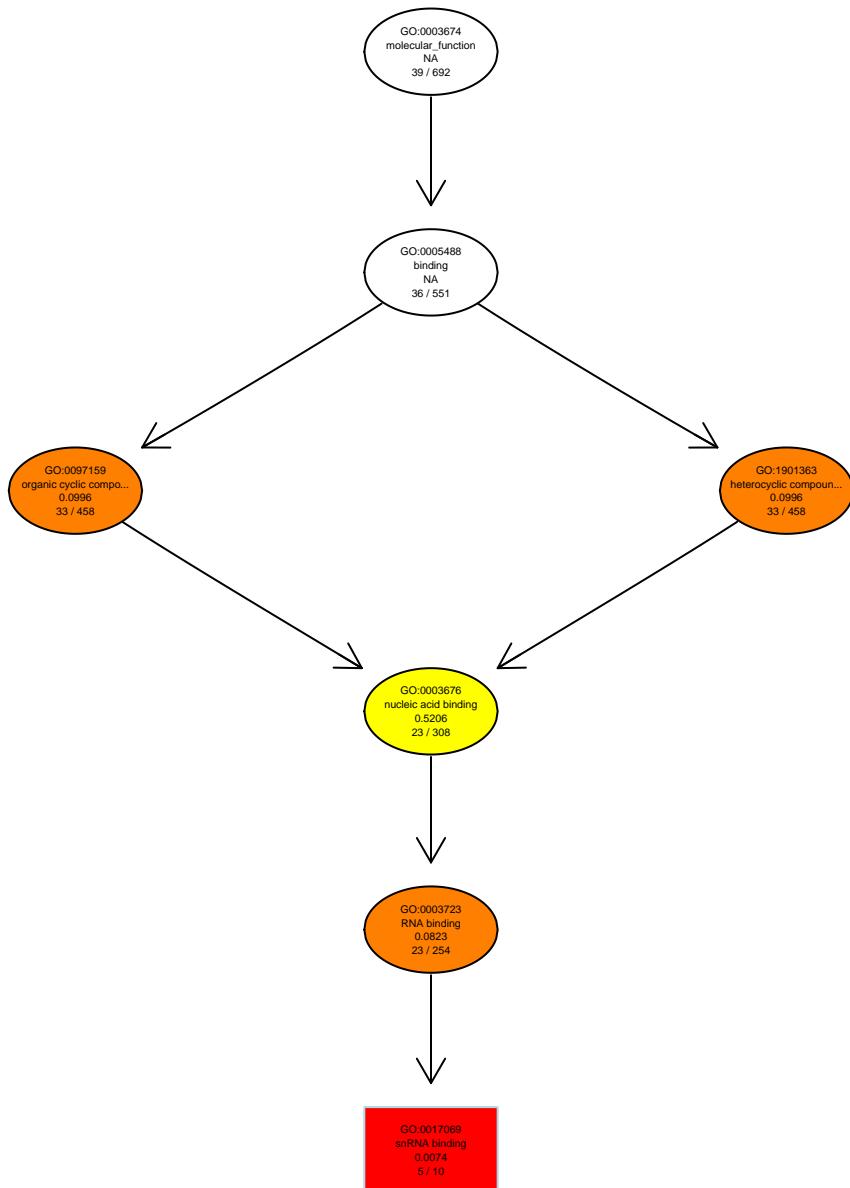
size ● 5 category — snRNA binding

FoldChange

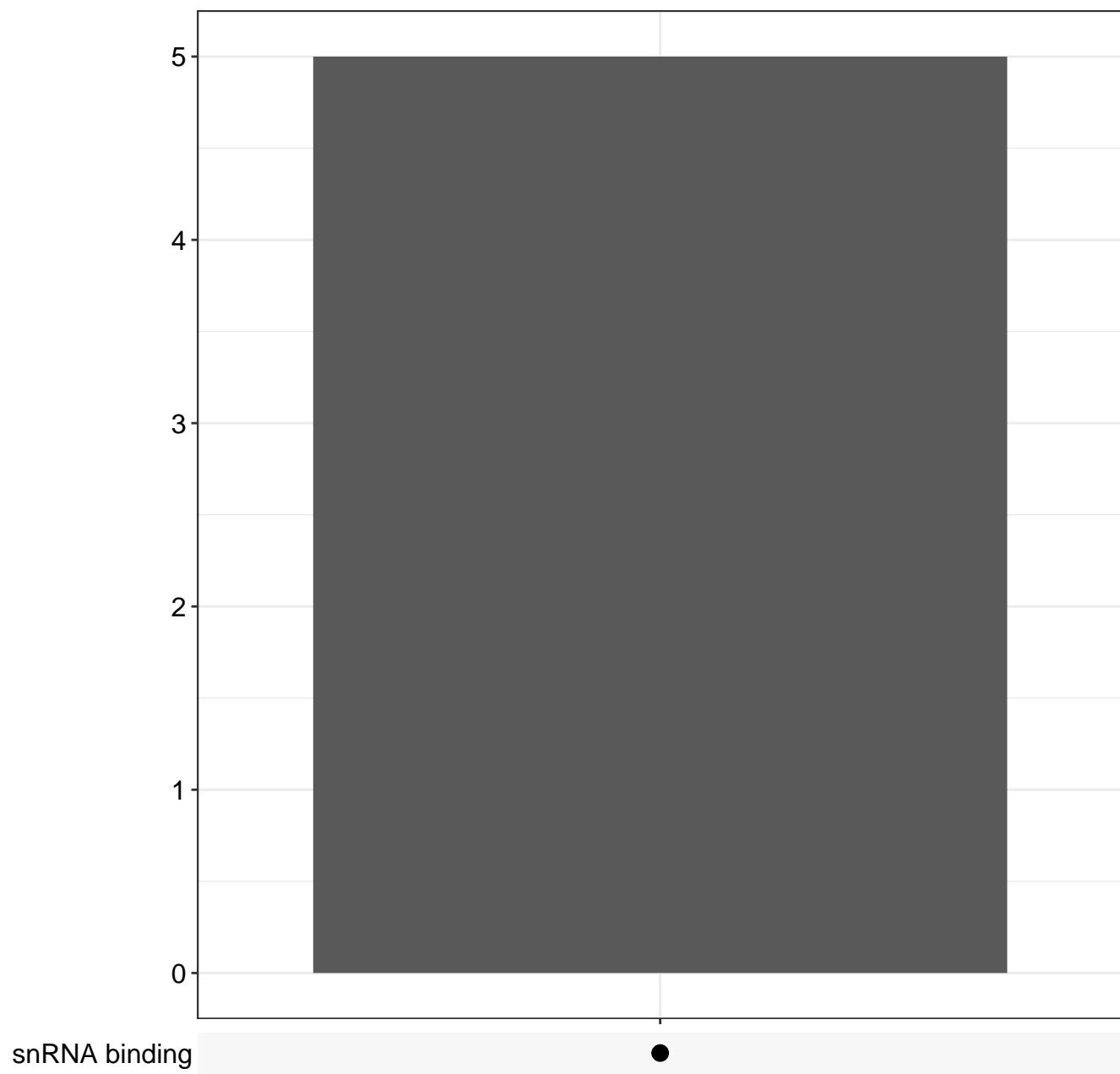


CBC2-TAP Up-regulated GO MF heatplot

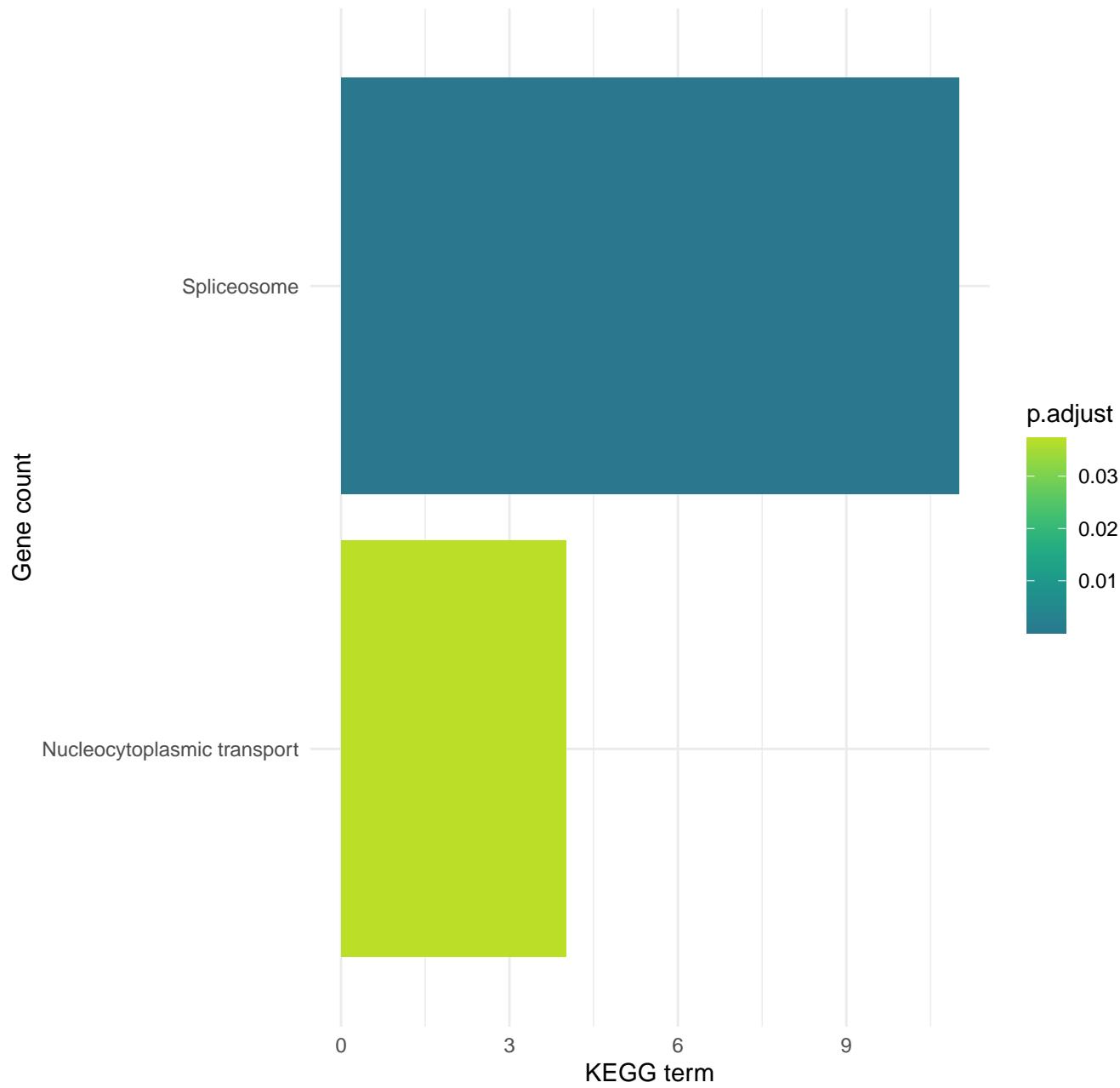




CBC2-TAP Up-regulated GO MF upsetplot



CBC2-TAP Up-regulated KEGG barplot



CBC2-TAP Up-regulated KEGG dotplot

KEGG term

Spliceosome

Nucleocytoplasmic transport

0.2

0.3

0.4

0.5

Gene ratio

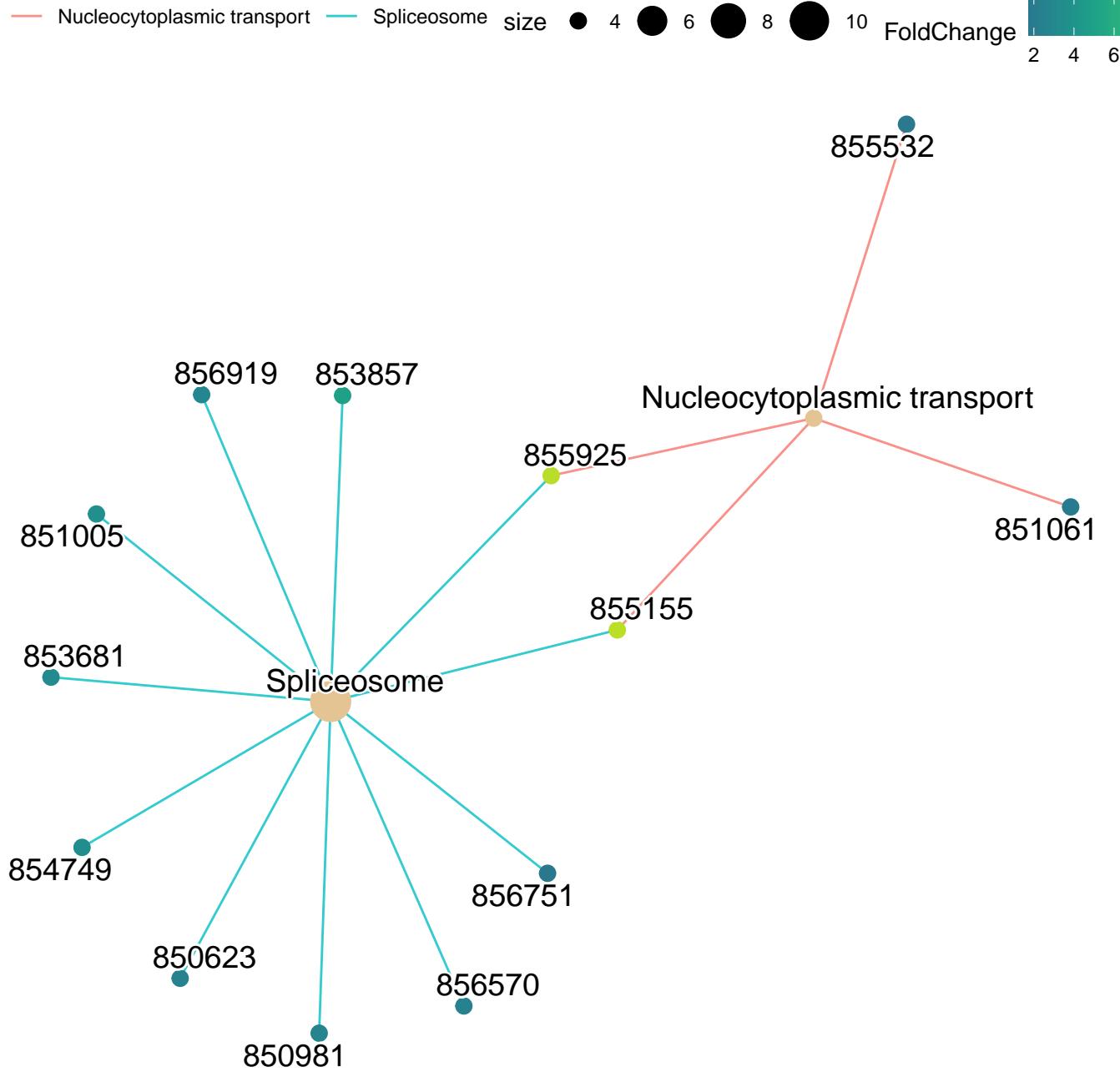
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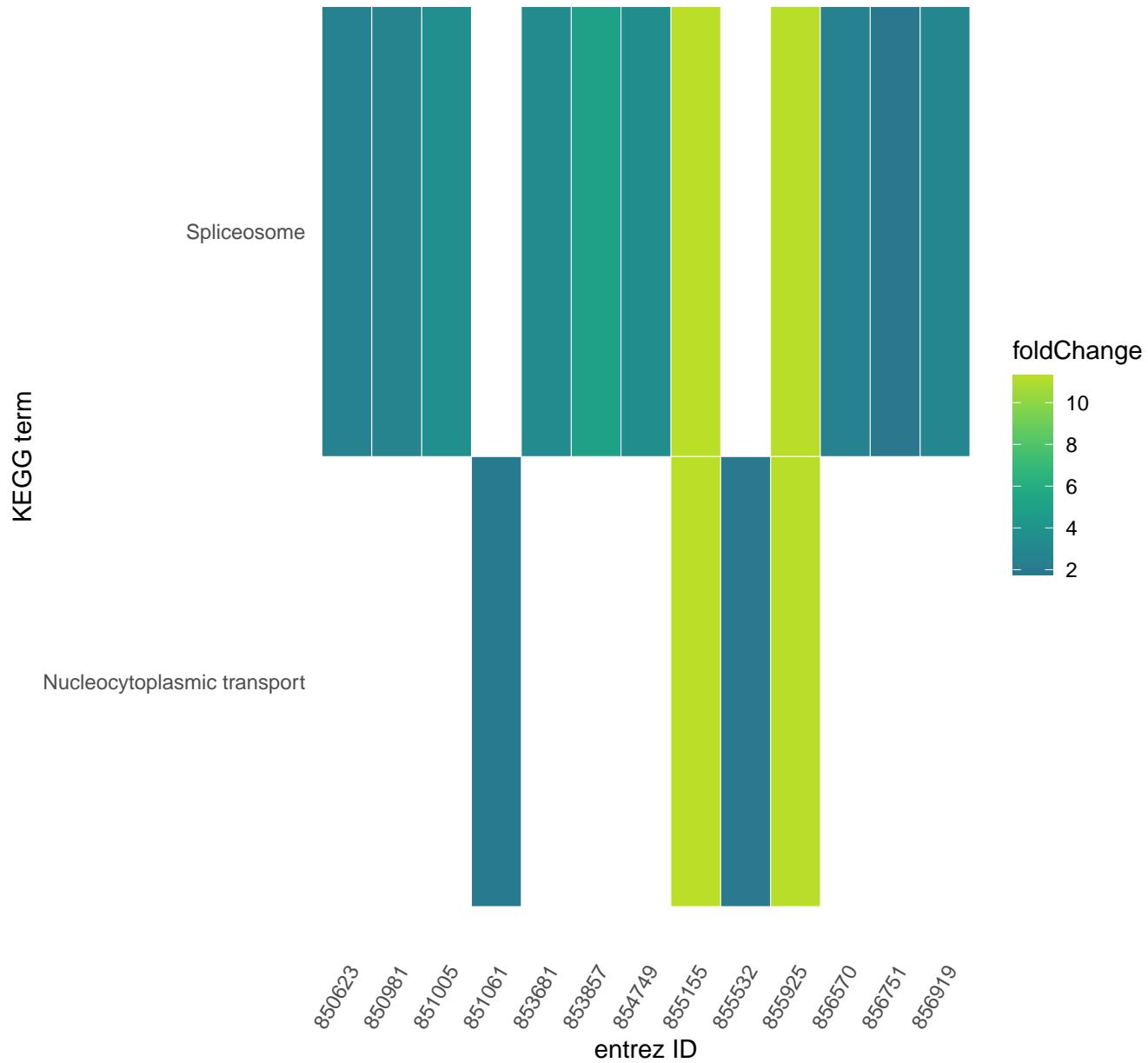
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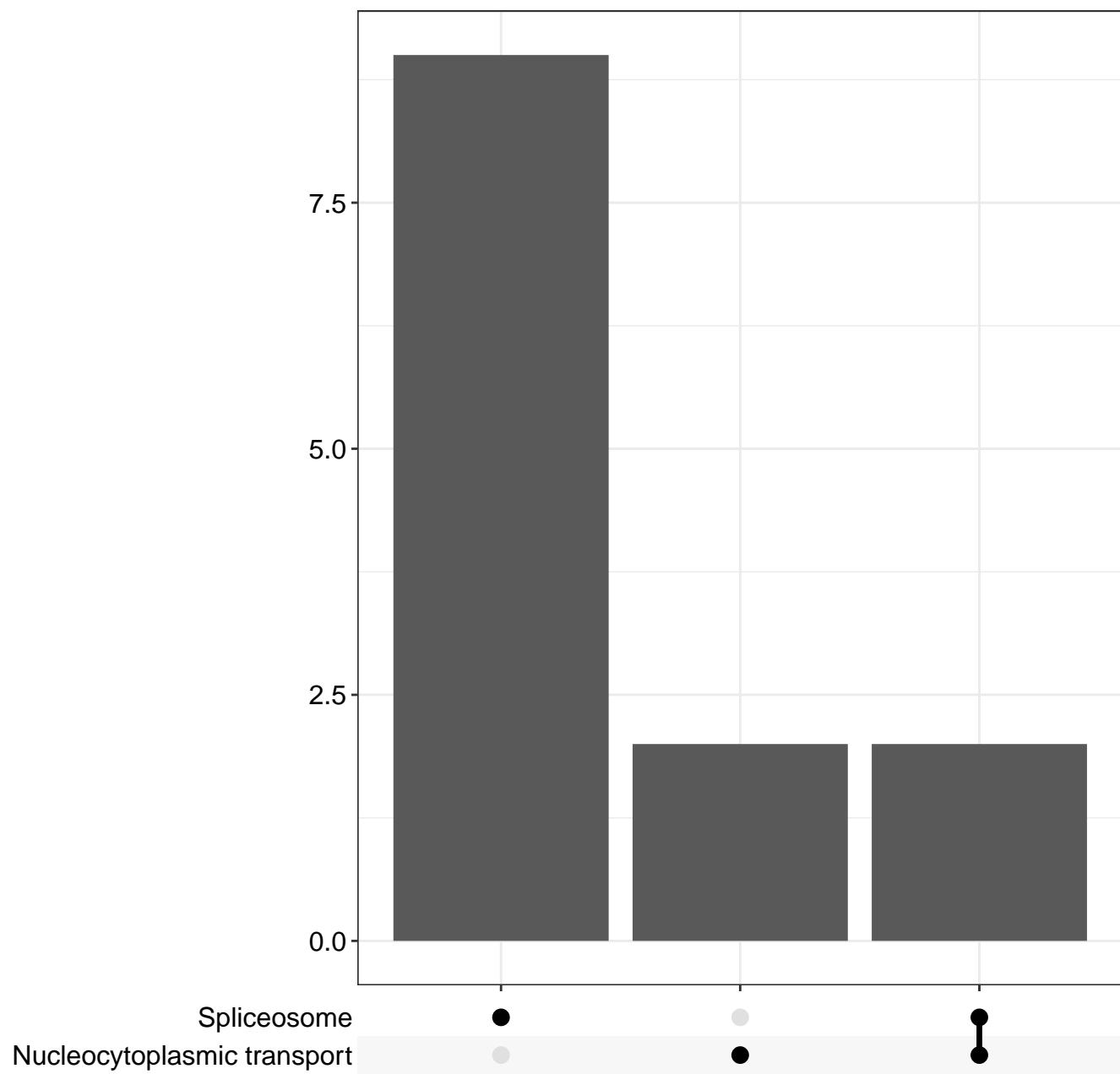
CBC2-TAP Up-regulated KEGG dotplot



CBC2-TAP Up-regulated KEGG heatplot



CBC2–TAP Up-regulated KEGG upsetplot



snRNA metabolism
nucleic acid phosphodiester bond
snoRNA metabolism
rRNA metabolism
RNA phosphodiester bond
ncRNA processing
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
RNA processing
ncRNA catabolism
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
ncRNA metabolism
rRNA 5'-end processing
rRNA catabolism
RNA 5'-end processing
ncRNA 5'-end processing
RNA surveillance
nuclear RNA surveillance
cleavage involved in rRNA processing
rRNA processing
macromolecule metabolism
nuclear mRNA surveillance
maturation of S-ribosomes
nuclear-transcribed mRNA catabolism
cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

macromolecule metabolism

RNA processing

ncRNA metabolism

rRNA metabolism

ncRNA processing

rRNA processing

nucleic acid phosphodiester bond

maturation of RNA

RNA phosphodiester bond

cleavage involved in rRNA processing

endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

rRNA 5'-end processing

RNA 5'-end processing

ncRNA 5'-end processing

cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

snRNA metabolism

nuclear-transcribed mRNA catabolism

snoRNA metabolism

ncRNA catabolism

rRNA catabolism

RNA surveillance

nuclear RNA surveillance

nuclear mRNA surveillance

MTR4-TAP Up-regulated GO BP cnetplot

RNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

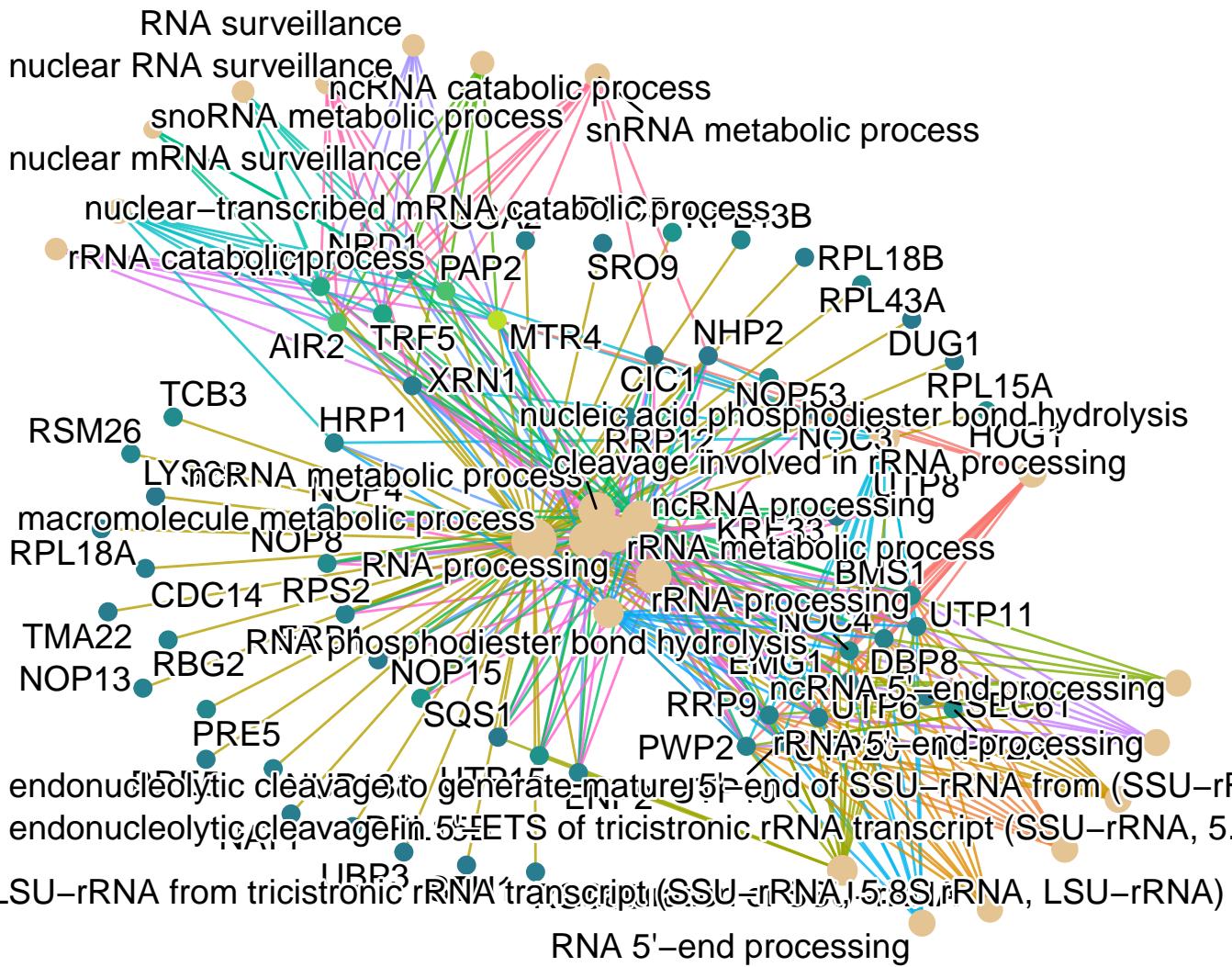
maturation

ncRNA 5'

ncRNA cat

ncRNA me

ncRNA pro



snRNA metabolic
snoRNA metabolic
rRNA processing
rRNA metabolic
rRNA catabolic
rRNA 5'-end processing
RNA surveillance
RNA processing
RNA phosphodiester bond hydrolysis
RNA 5'-end processing
nucleic acid phosphodiester bond hydrolysis
nuclear-transcribed mRNA catabolic
nuclear RNA surveillance
nuclear mRNA surveillance
ncRNA processing
ncRNA metabolic
ncRNA catabolic
ncRNA 5'-end processing
maturation of SSU-rRNA
macromolecule metabolic
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA) in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
cleavage involved in rRNA processing

MTR4-TAP Up-regulated GO BP emapplot

endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rR

endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA fro

endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSL
nucleic acid phosphodiester bond hydrolysis)

RNA phosphodiester bond hydrolysis

RNA 5'-end processing

ncRNA 5'-end processing

ncRNA processing

cleavage involved in rRNA processing

rRNA 5'-end processing

RNA processing

maturity of SSU-rRNA

rRNA metabolic process

rRNA processing

macromolecule metabolic process

rRNA catabolic process

snoRNA metabolic process

nuclear-transcribed mRNA catabolic process

ncRNA metabolic process

nuclear RNA surveillance

snRNA metabolic process

nuclear mRNA surveillance

ncRNA catabolic process

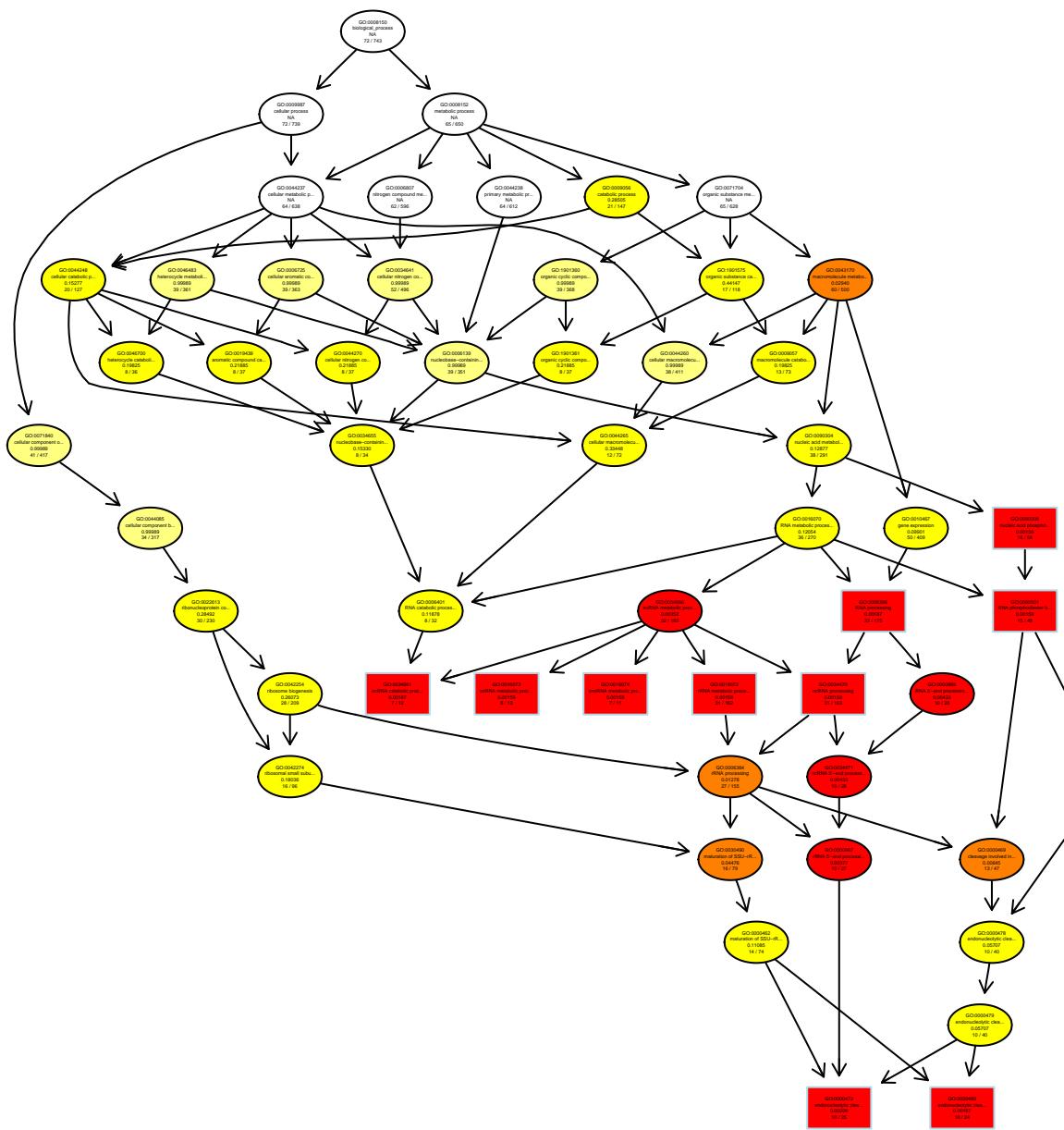
RNA surveillance

size

● 10
● 20
● 30
● 40
● 50
● 60

FoldChange

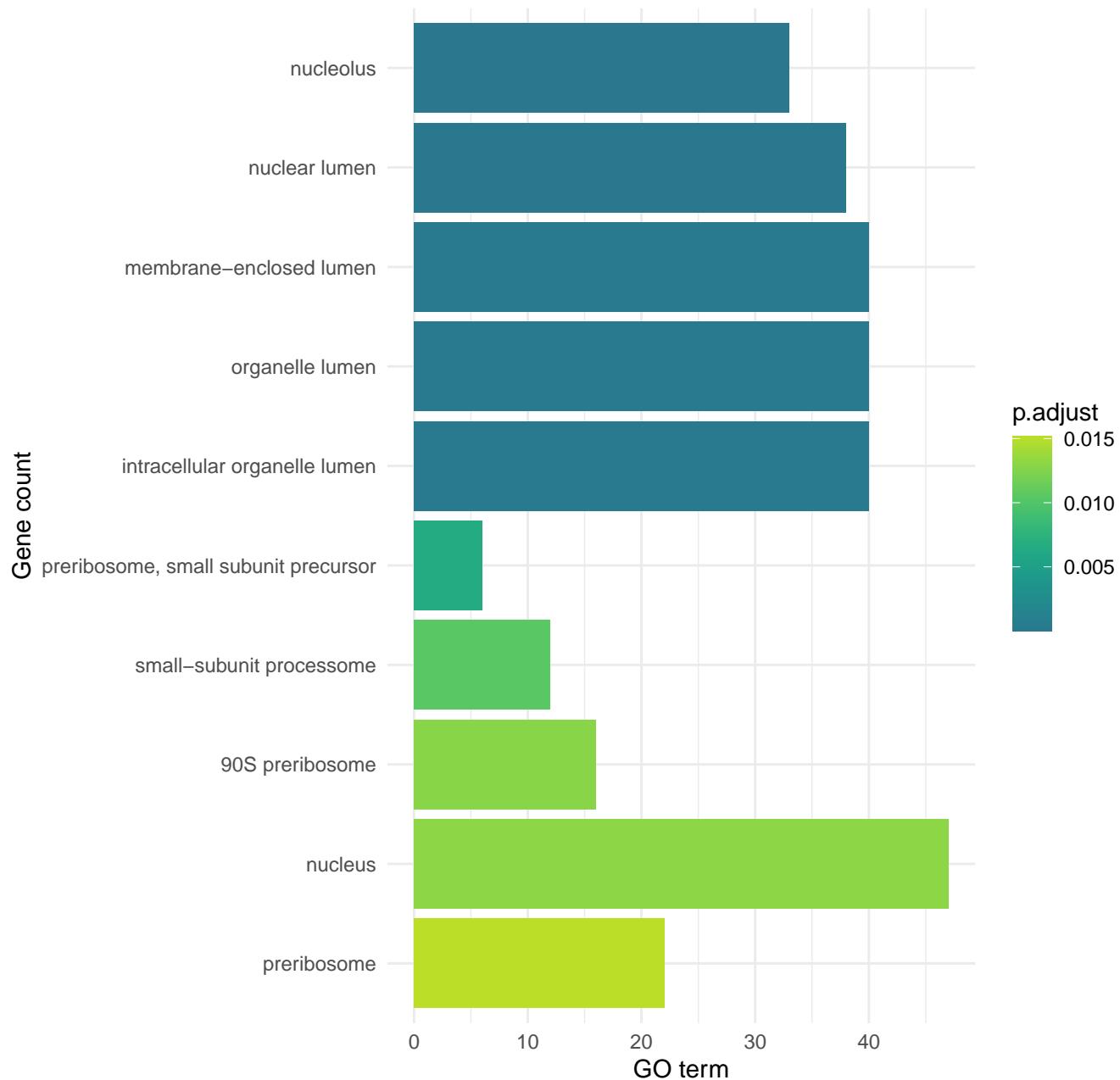
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0.03
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0.01



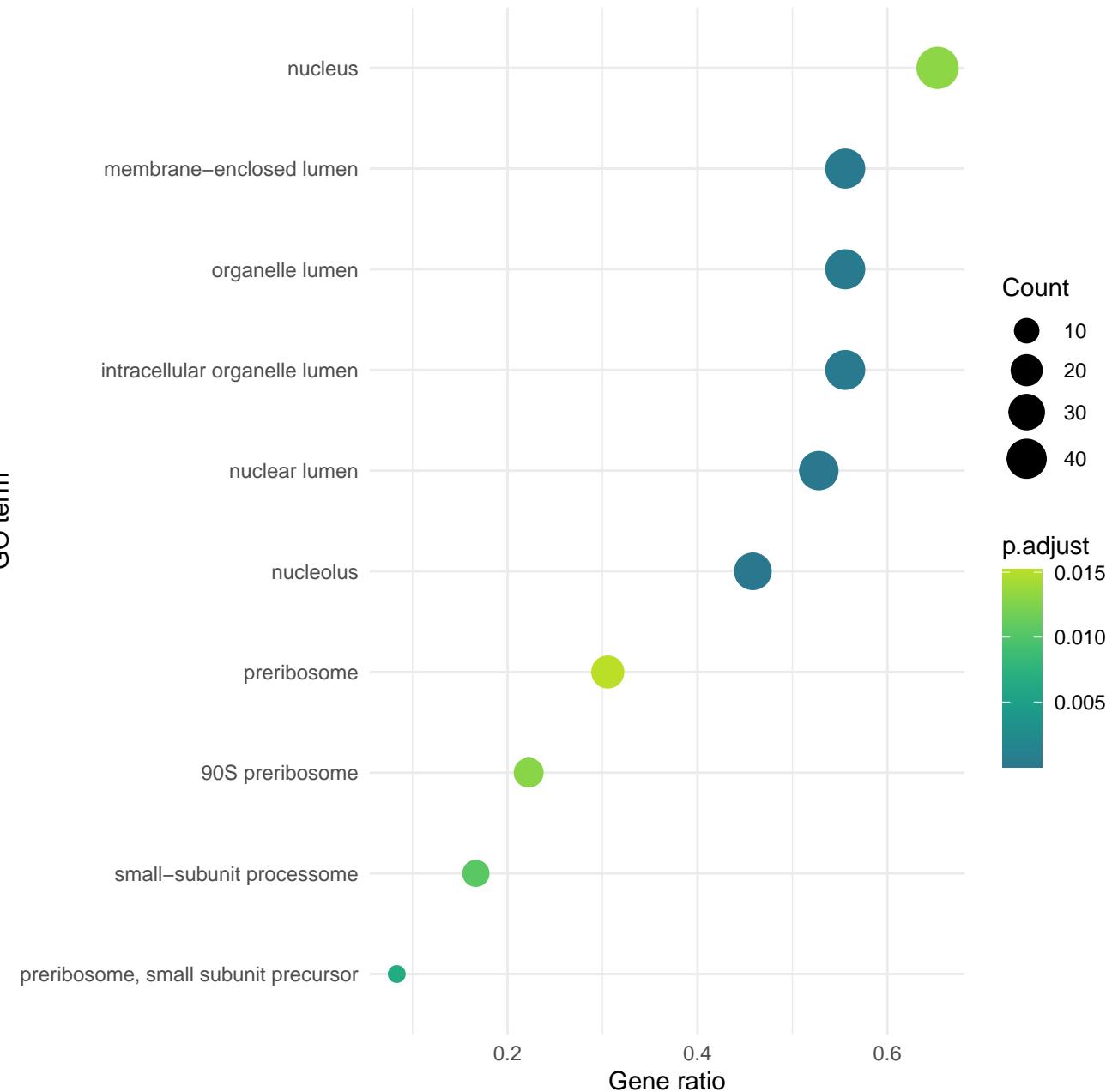
RNA processing
rRNA metabolic pathway
ncRNA processing
nucleic acid phosphodiester bond hydrolysis
RNA phosphodiester bond hydrolysis
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
cleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
snRNA metabolic pathway
ncRNA catabolic pathway
snoRNA metabolic pathway

endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
cleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

MTR4-TAP Up-regulated GO CC barplot

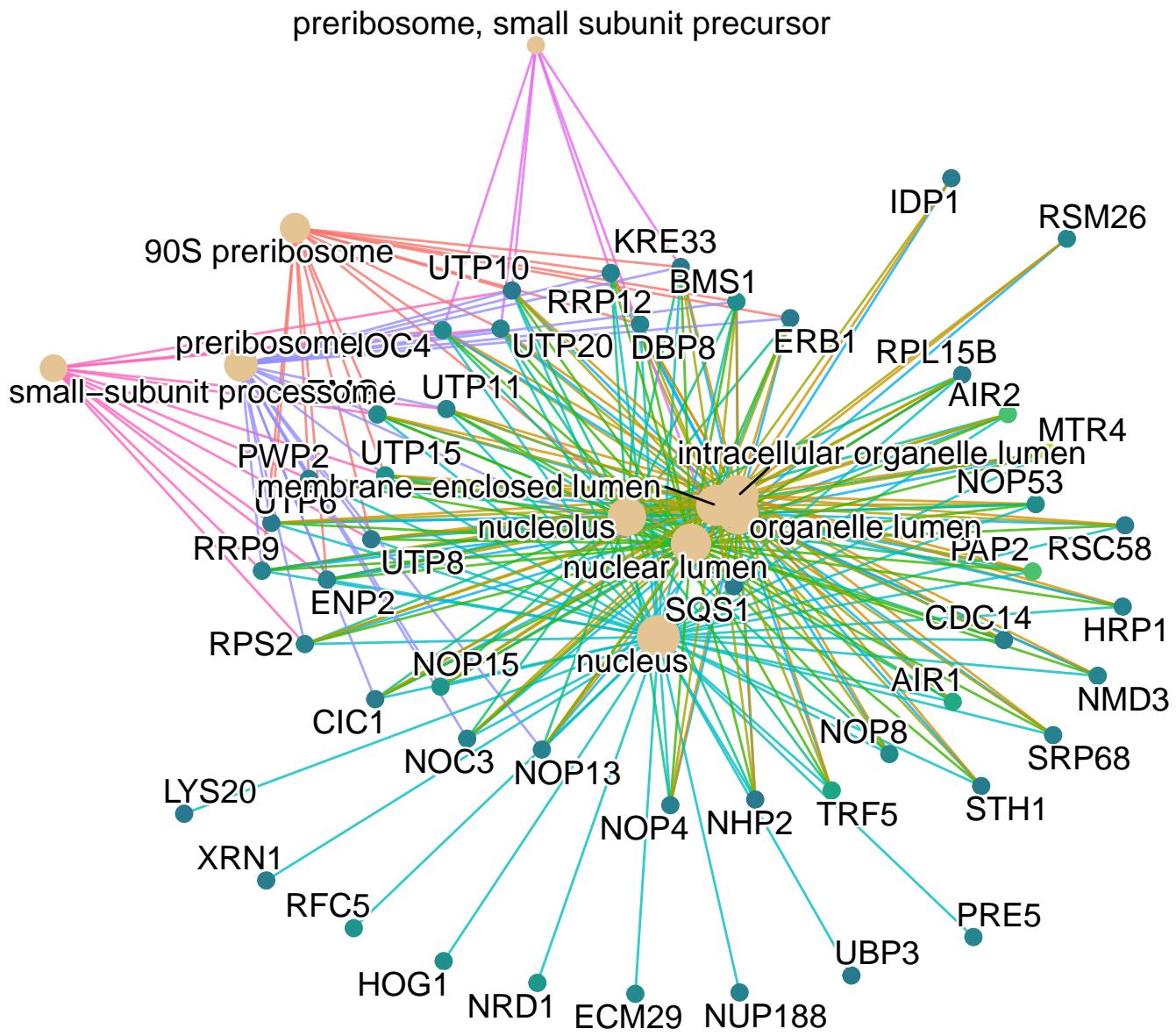


MTR4-TAP Up-regulated GO CC dotplot

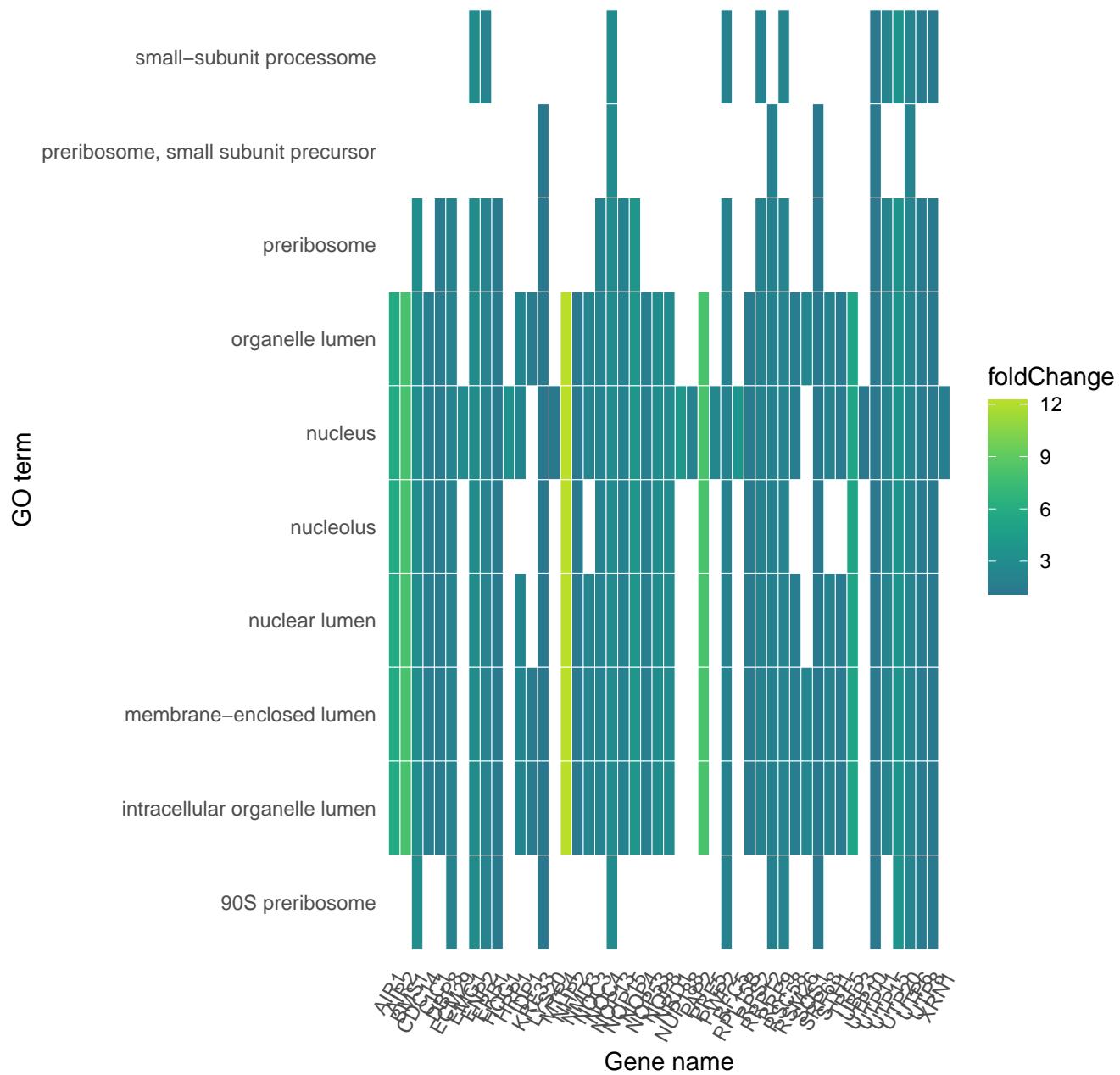


MTR4-TAP Up-regulated GO CC cnetplot

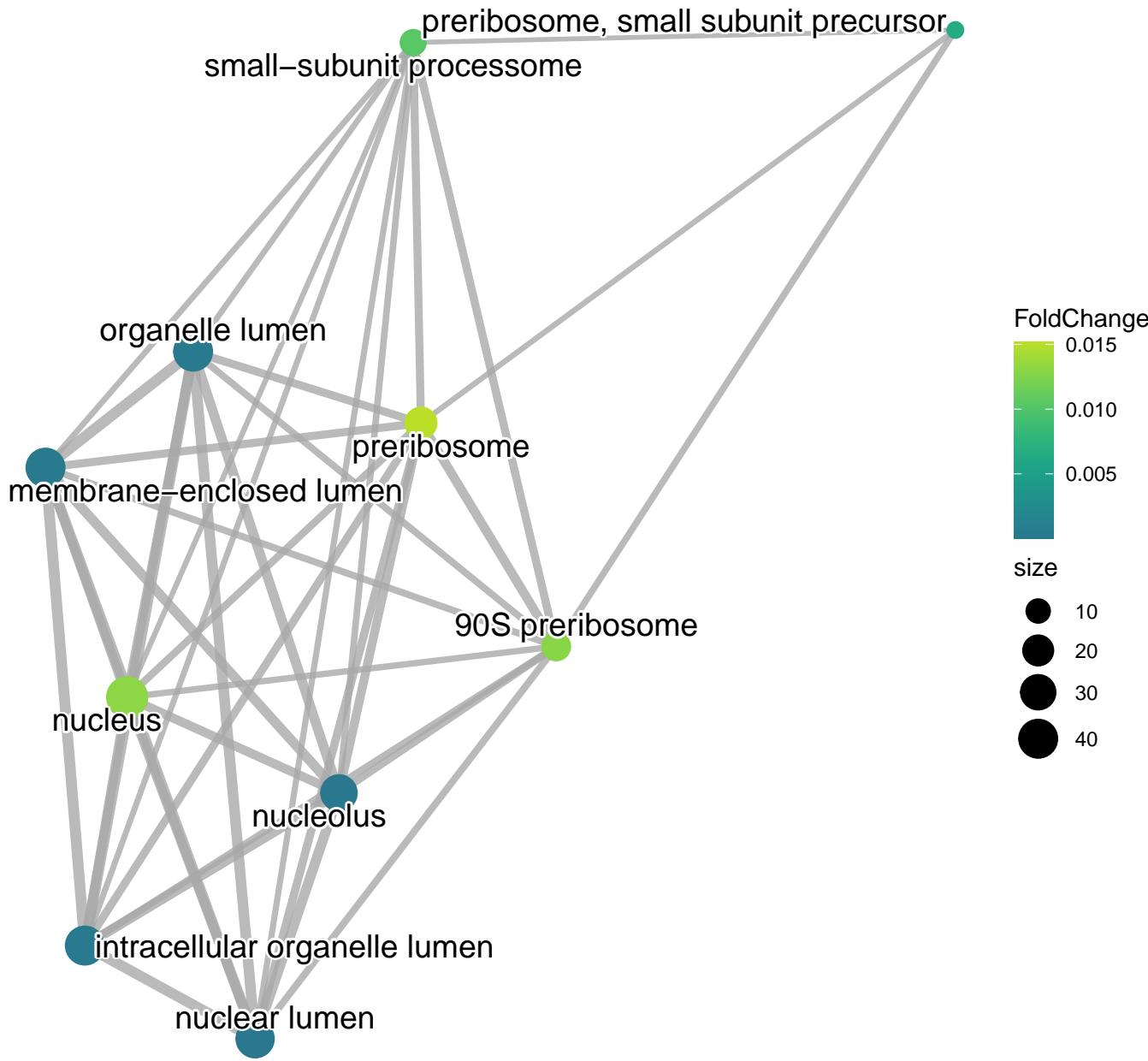
preribosome membrane-enclosed lumen nucleolus organelle lumen preribosome, small subunit
 cellular organelle lumen nuclear lumen nucleus preribosome small-subunit process

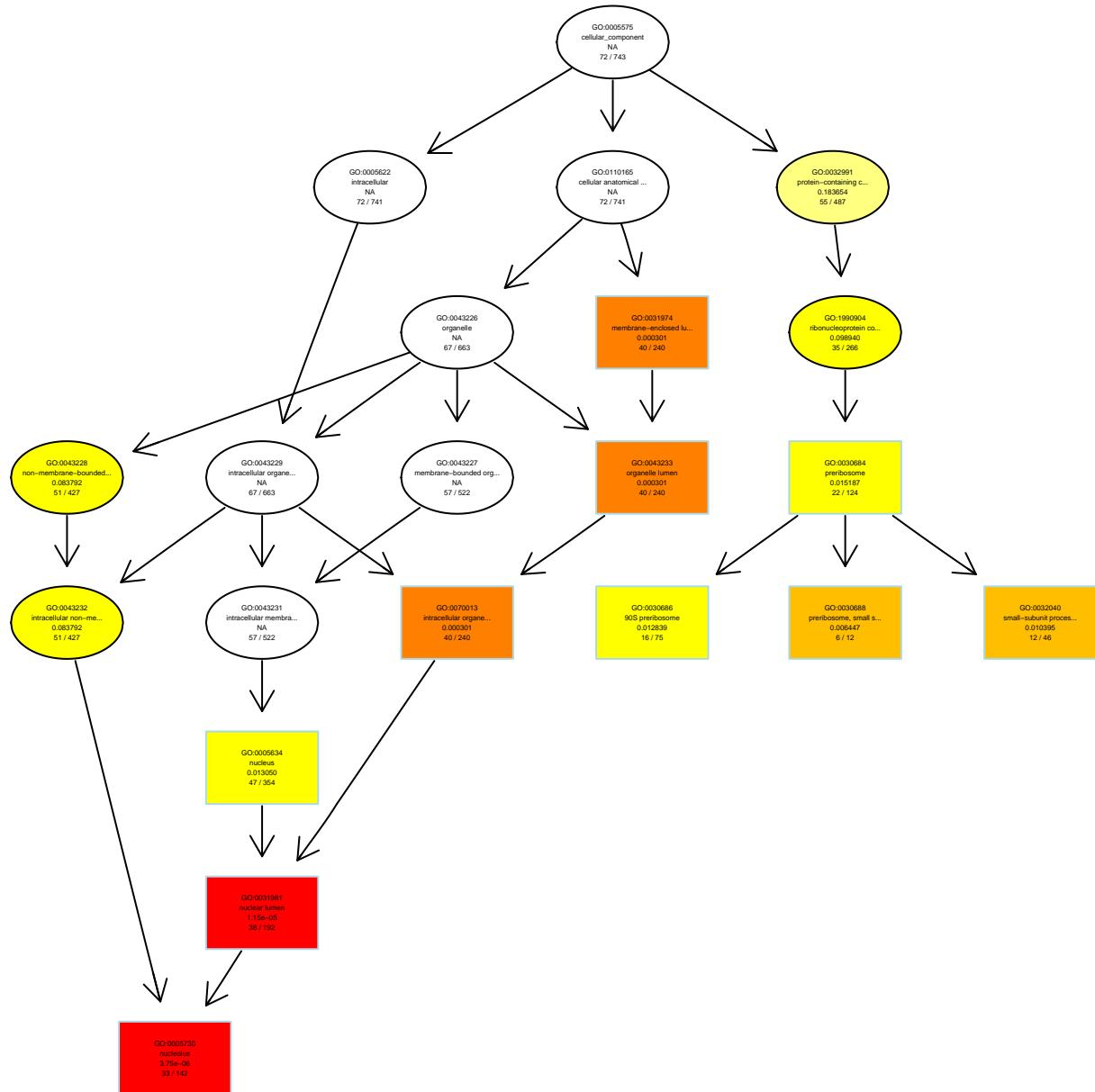


MTR4–TAP Up-regulated GO CC heatplot

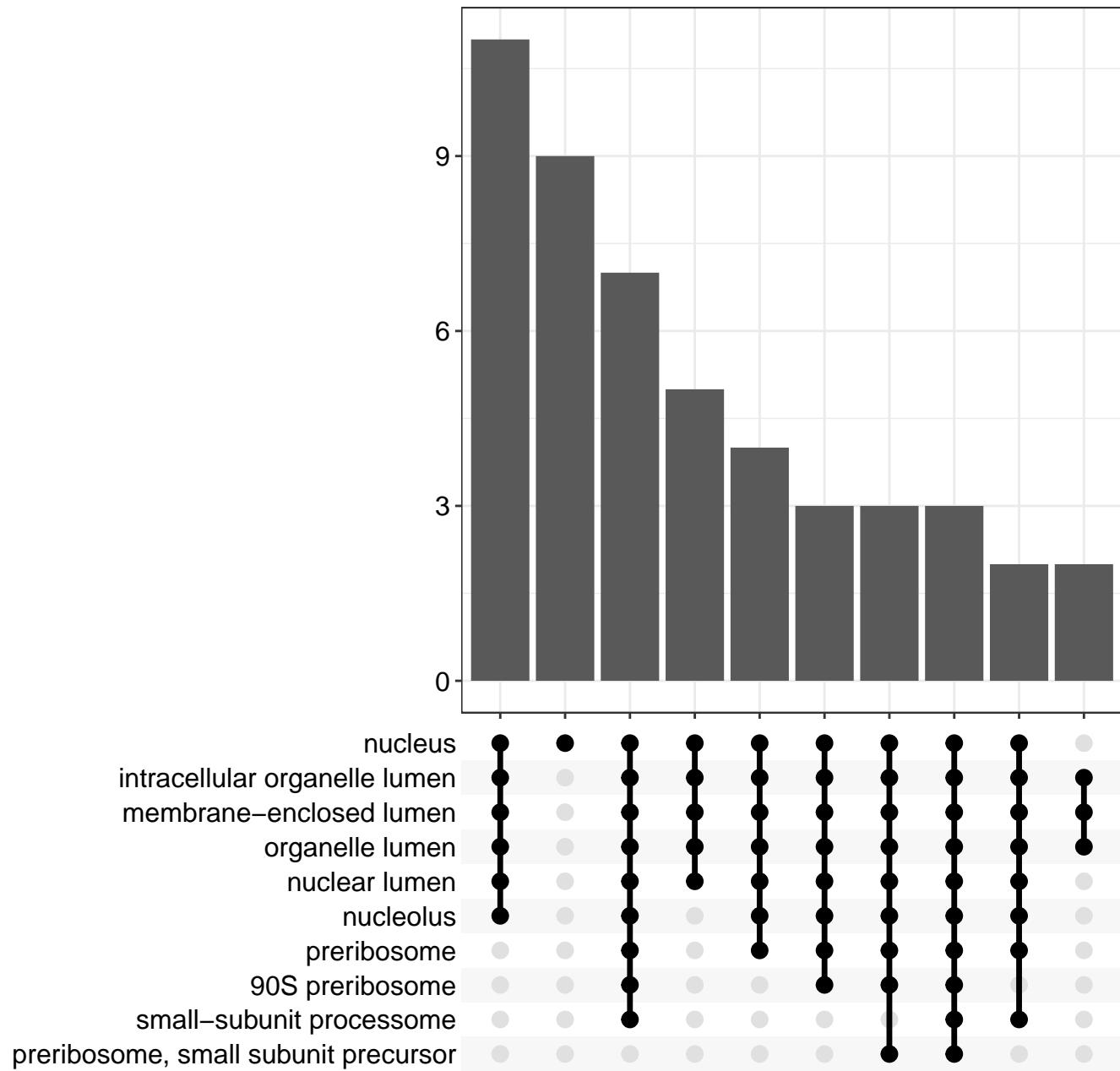


MTR4-TAP Up-regulated GO CC emapplot

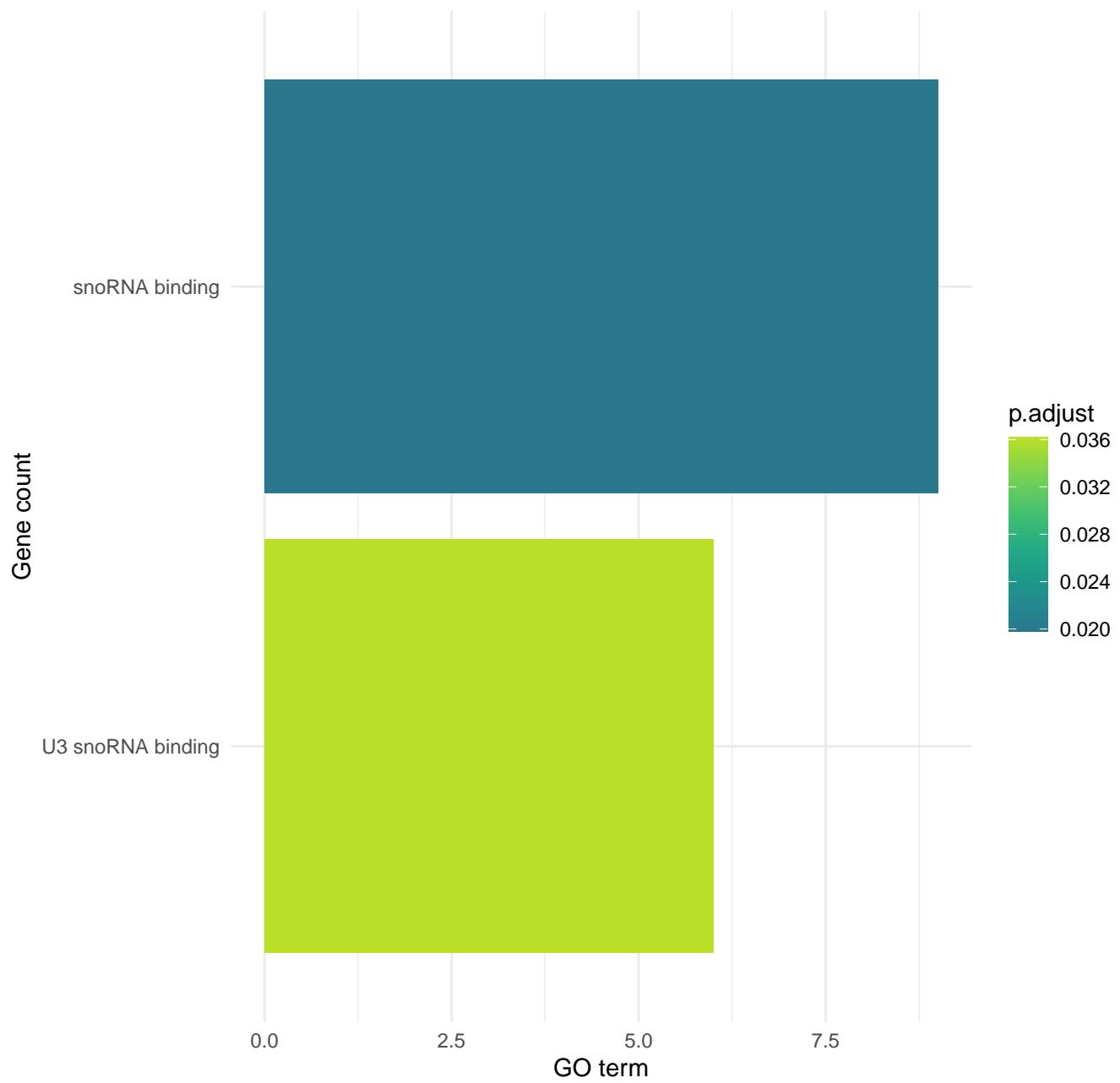




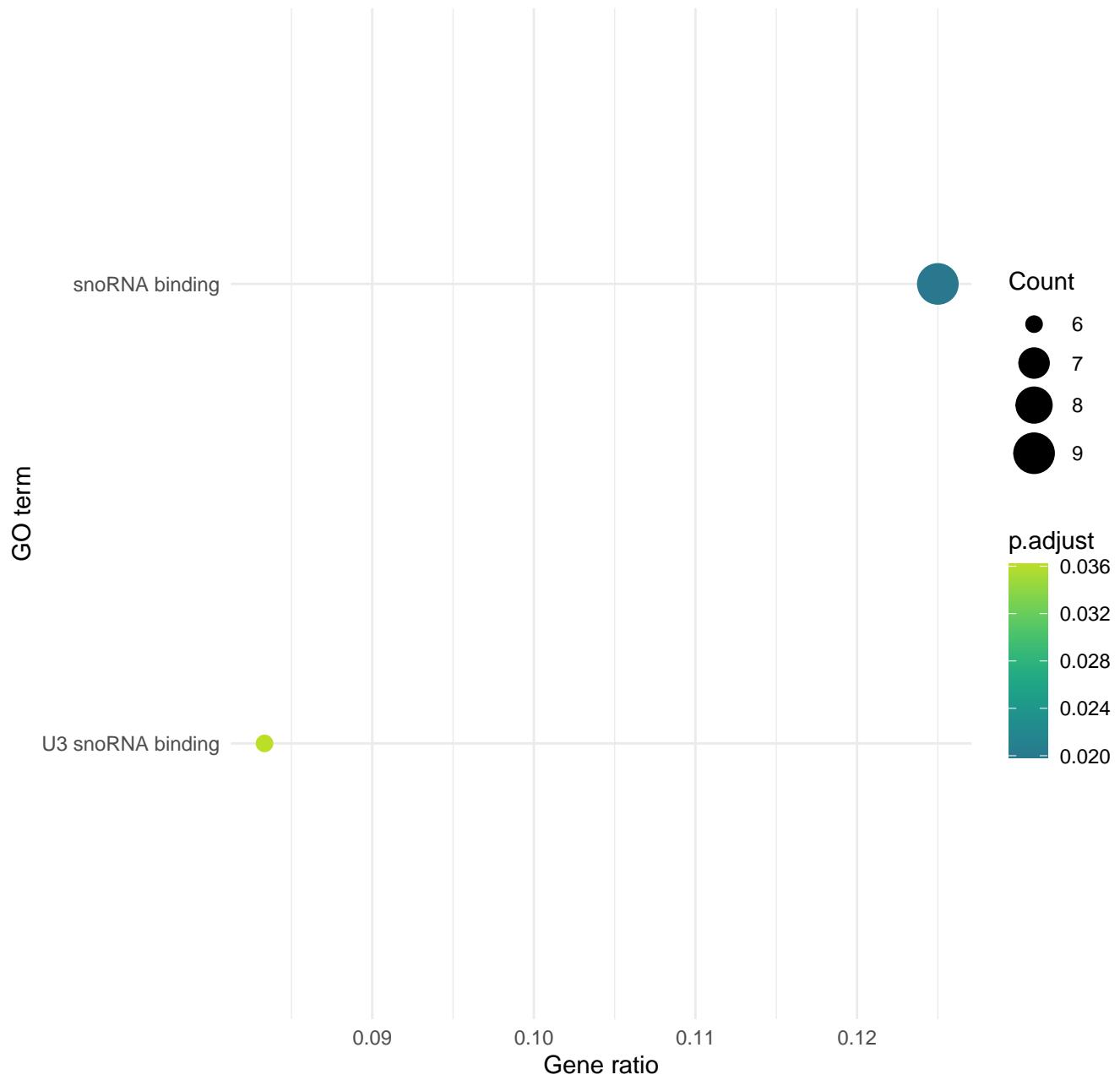
MTR4-TAP Up-regulated GO CC upsetplot



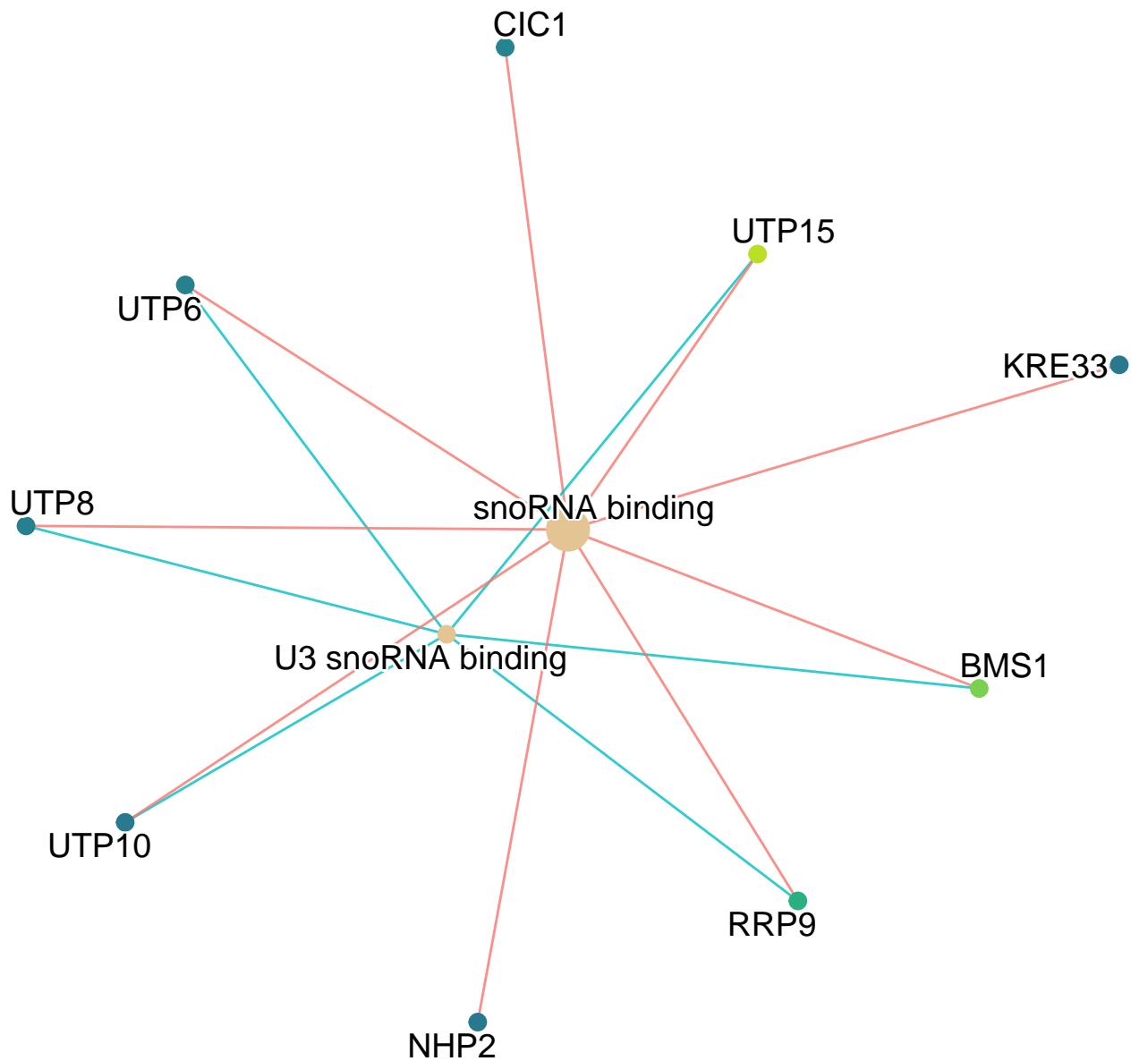
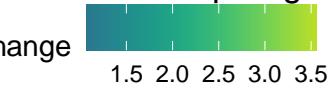
MTR4-TAP Up-regulated GO MF barplot



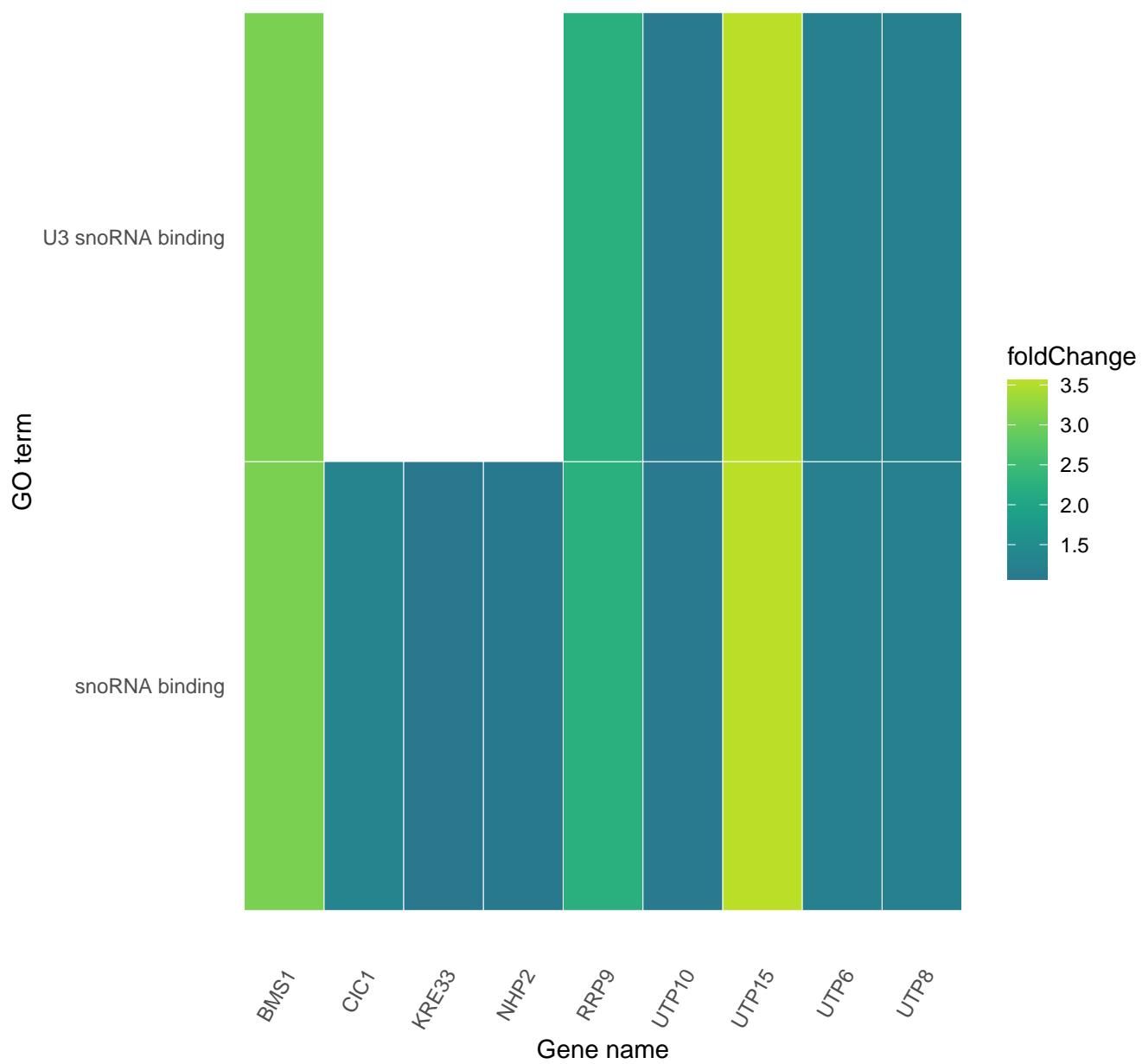
MTR4-TAP Up-regulated GO MF dotplot



MTR4-TAP Up-regulated GO MF cnetplot



MTR4-TAP Up-regulated GO MF heatplot

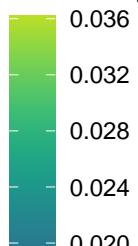


MTR4-TAP Up-regulated GO MF emapplot

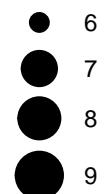
U3 snoRNA binding

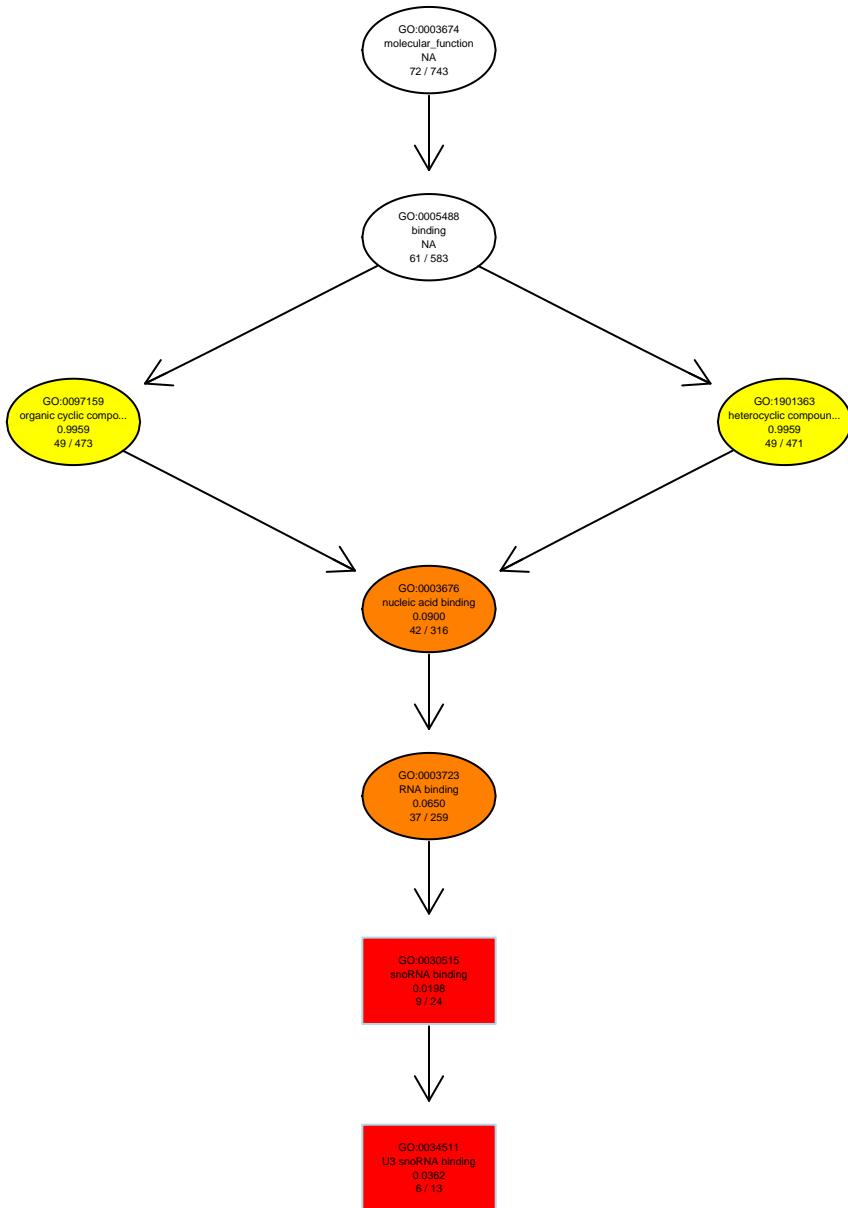
snoRNA binding

FoldChange

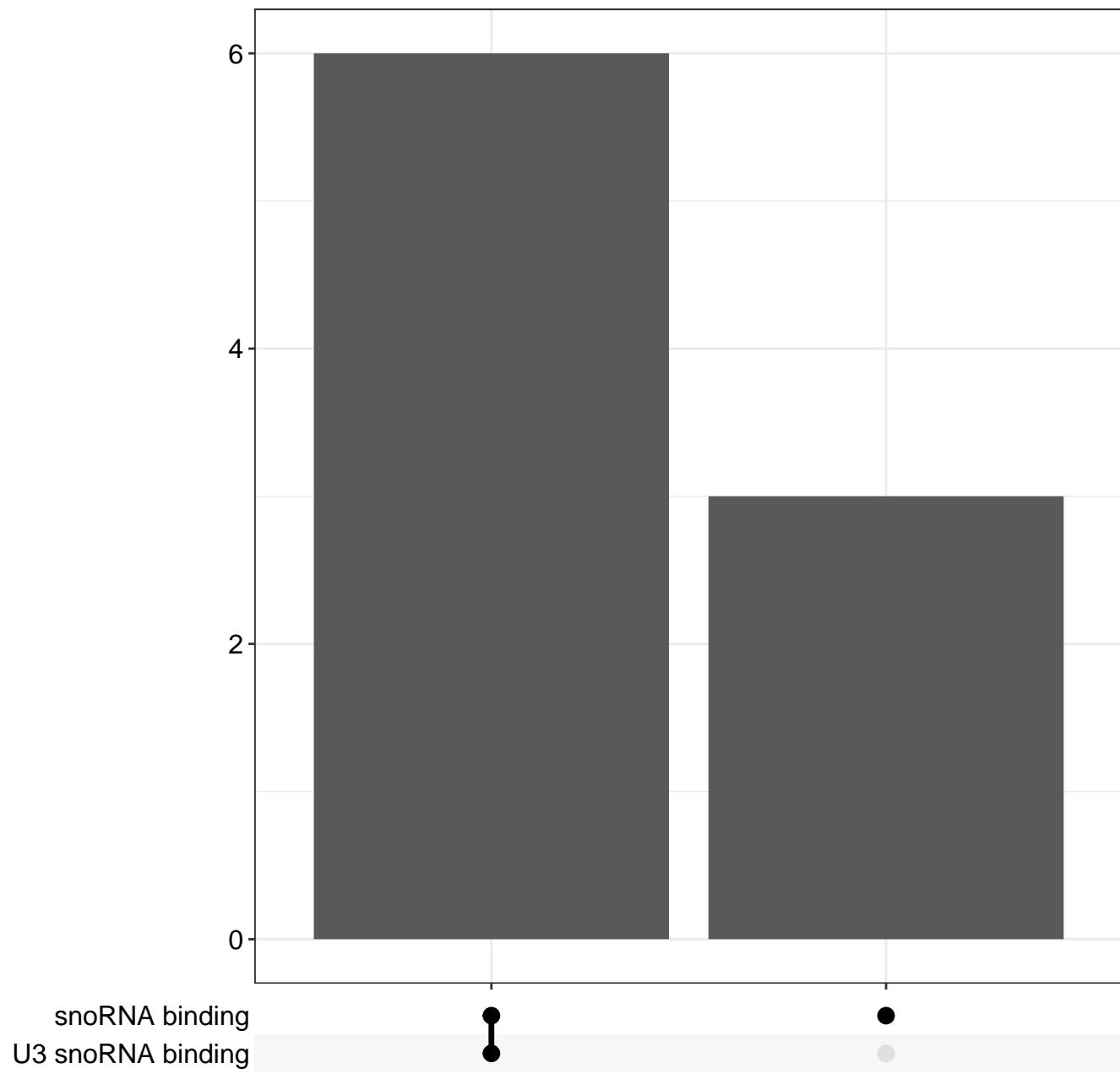


size

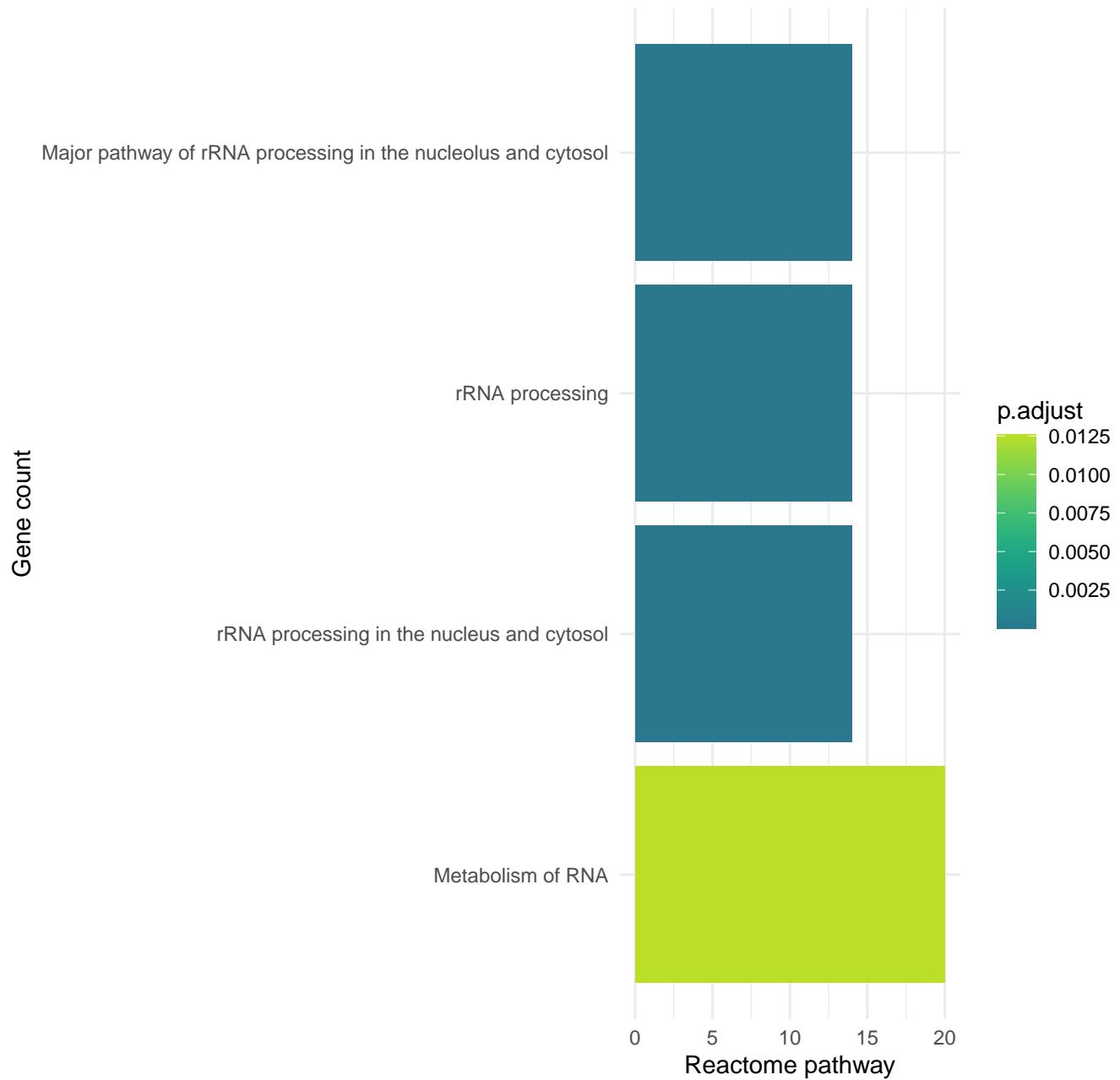




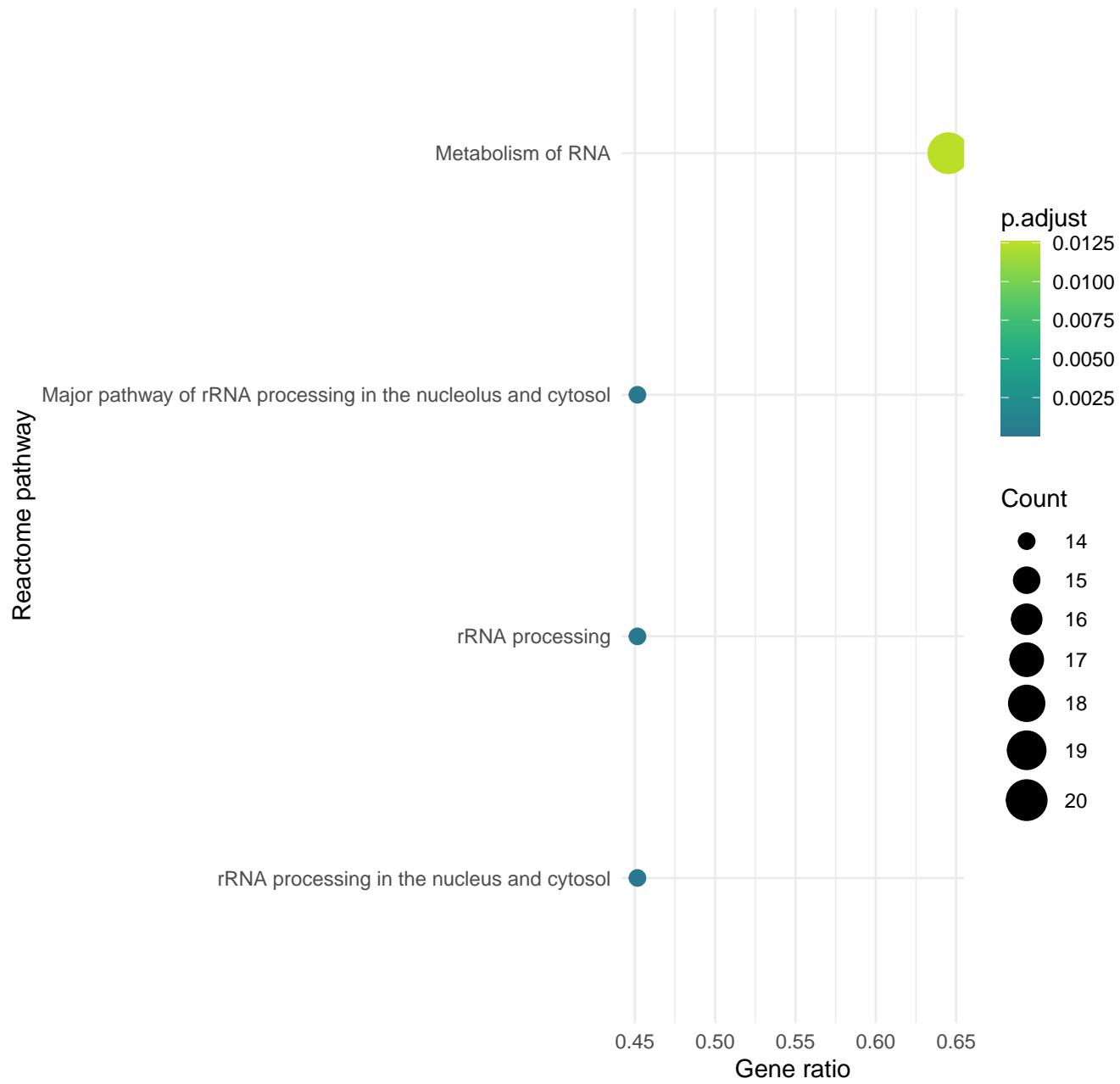
MTR4-TAP Up-regulated GO MF upsetplot



MTR4-TAP Up-regulated Reactome pathways

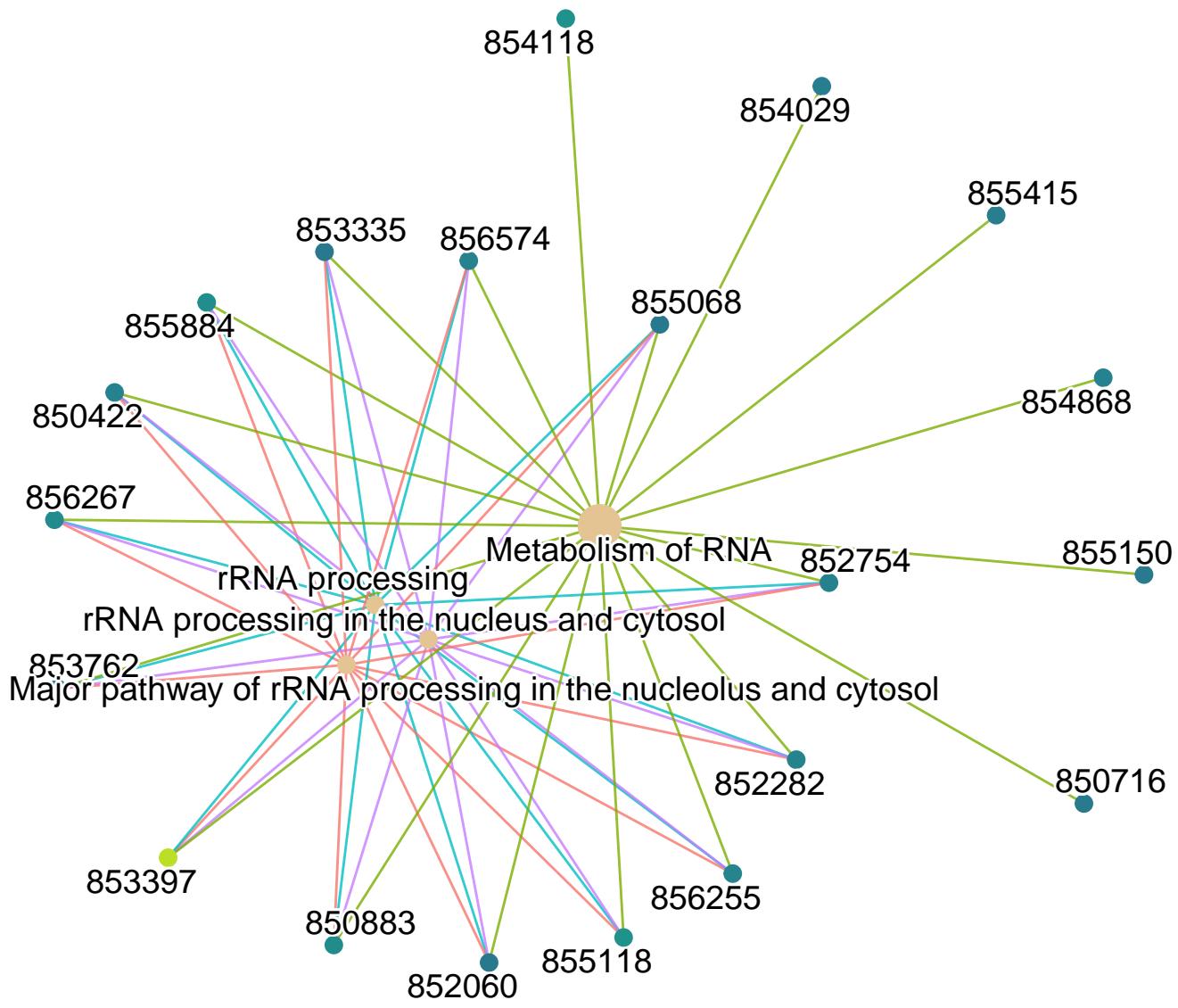


MTR4-TAP Up-regulated Reactome do



MTR4-TAP Up-regulated Reactome cnetplot

pathway of rRNA processing in the nucleolus and cytosol Metabolism of RNA rRNA processing rRNA proce



MTR4-TAP Up-regulated Reactome pathway

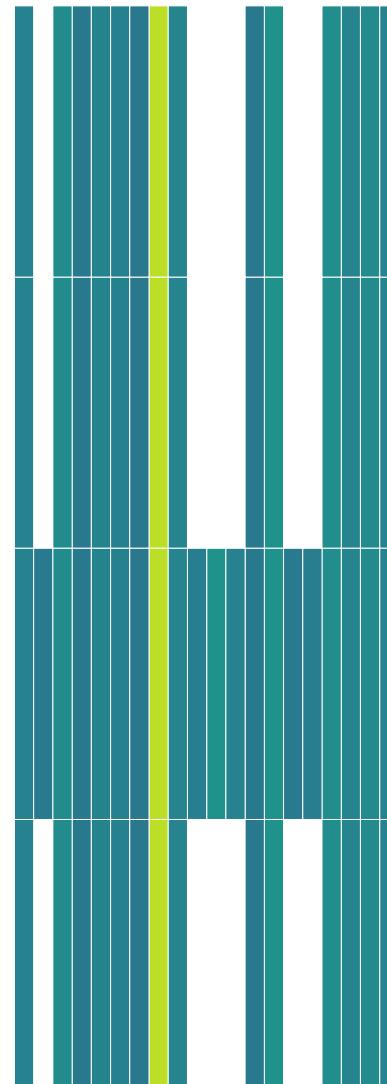
Reactome pathway

rRNA processing in the nucleus and cytosol

rRNA processing

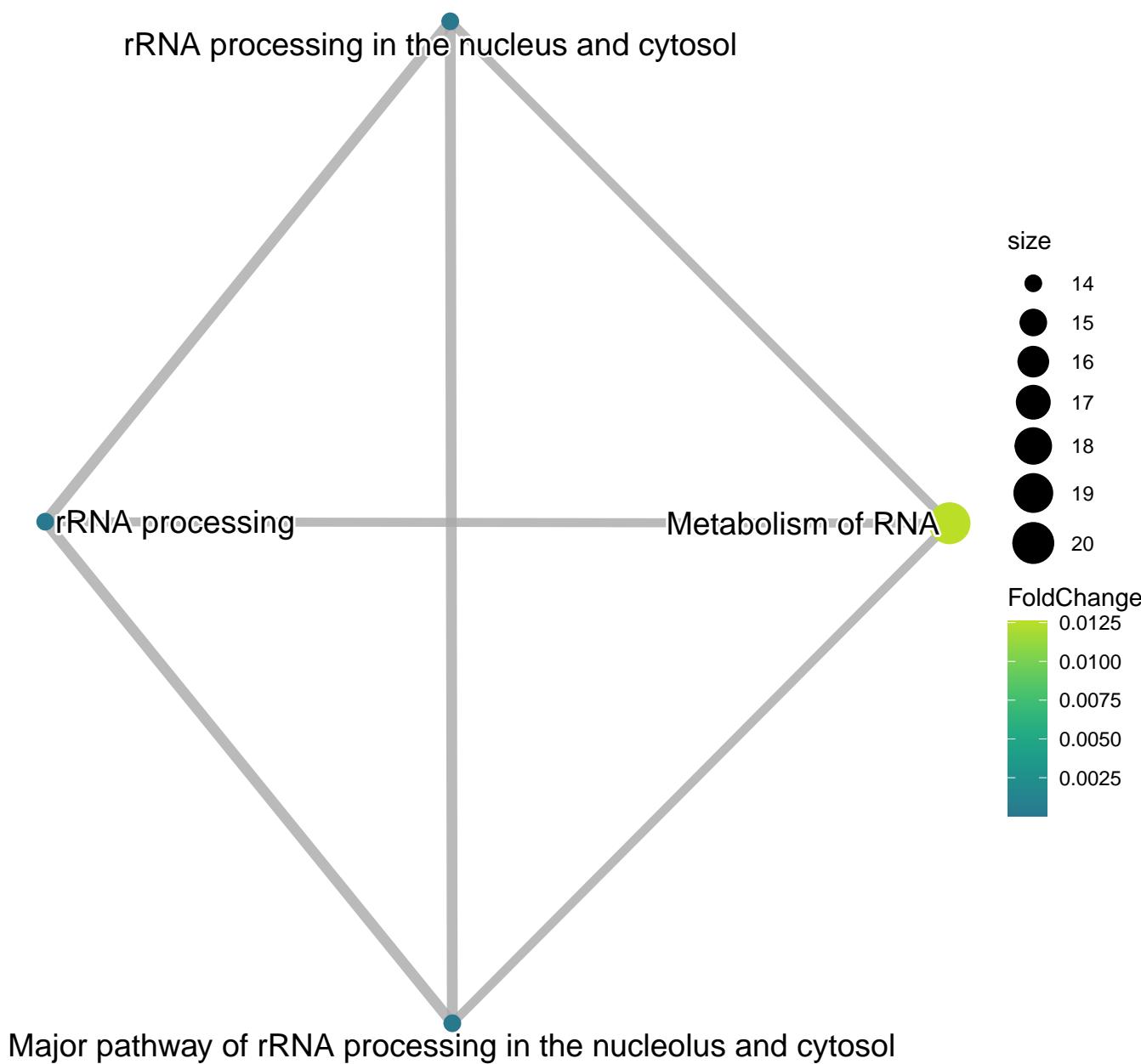
Metabolism of RNA

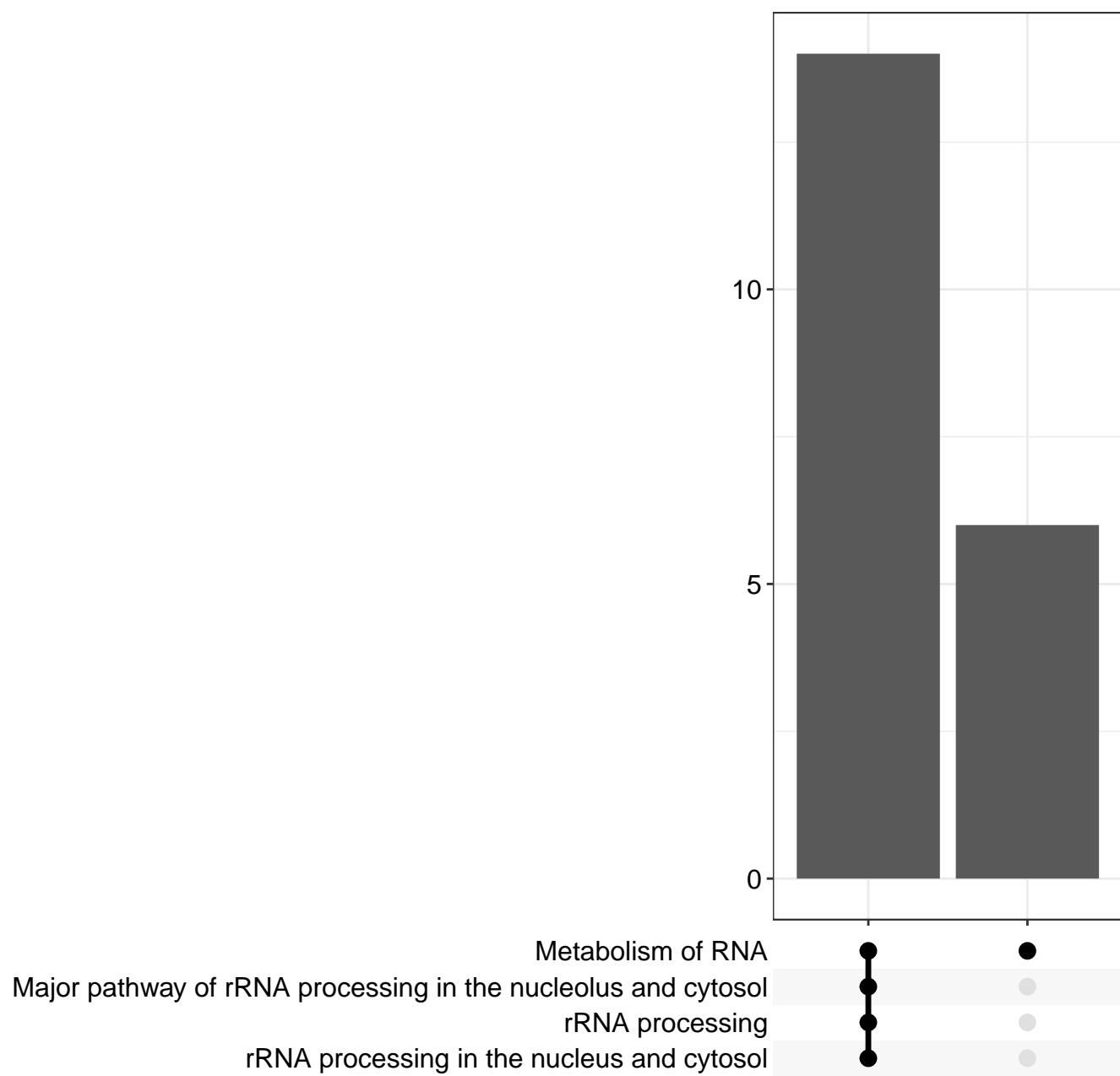
Major pathway of rRNA processing in the nucleolus and cytosol



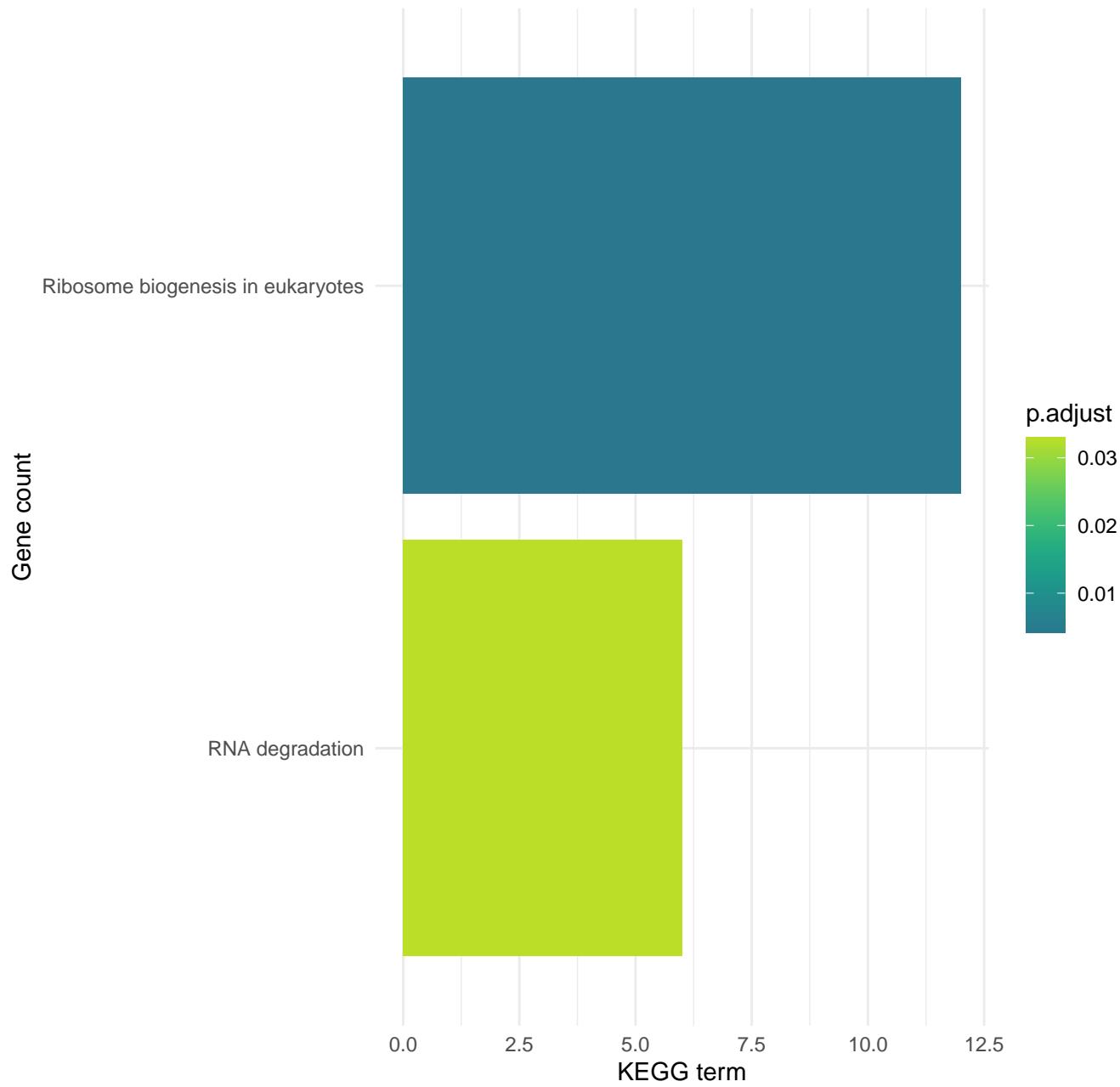
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MTR4-TAP Up-regulated Reactome emapplot





MTR4–TAP Up-regulated KEGG barplot



MTR4–TAP Up-regulated KEGG dotplot

KEGG term

Ribosome biogenesis in eukaryotes

RNA degradation

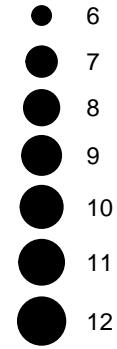
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0.20

0.25

Gene ratio

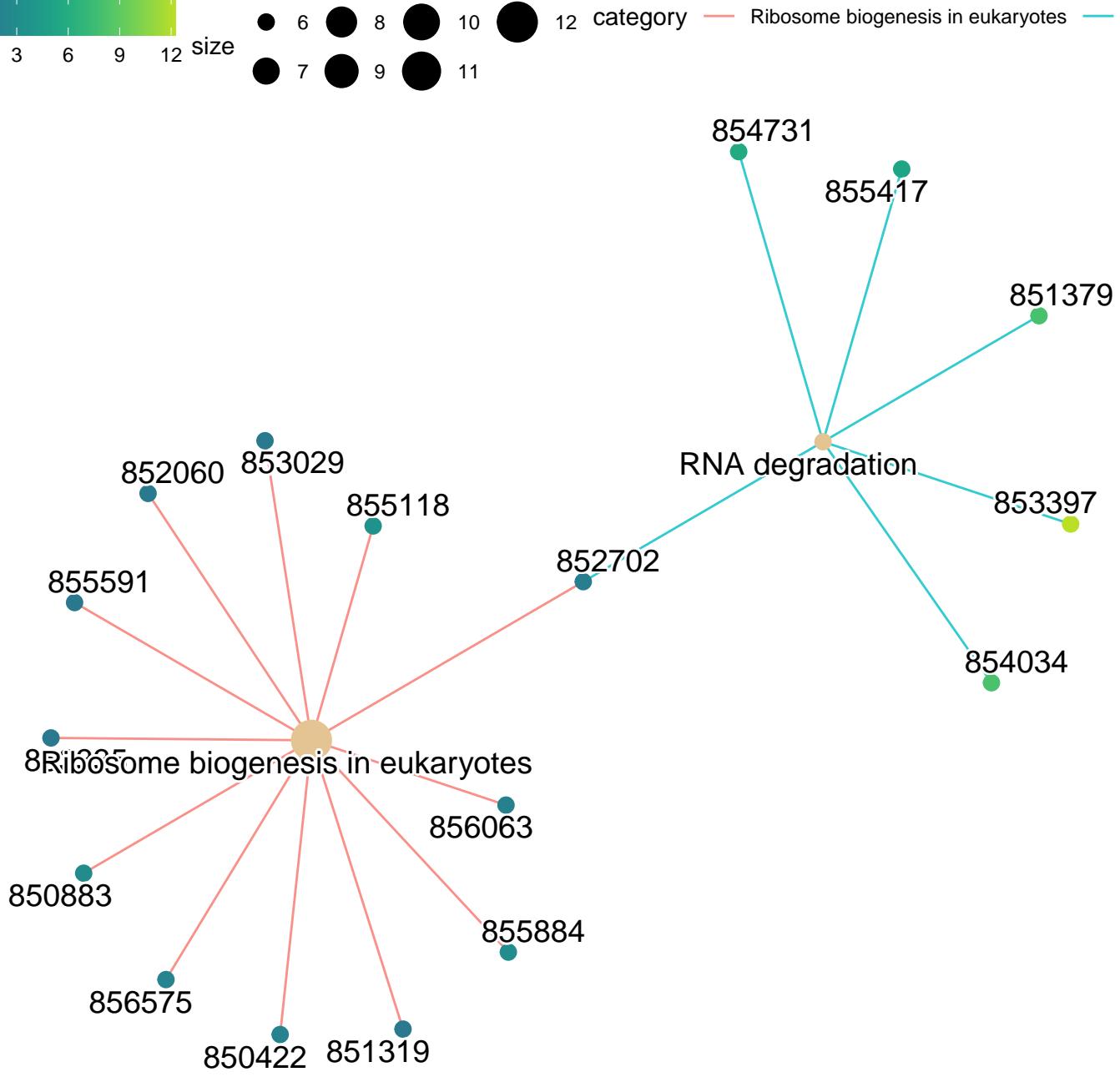
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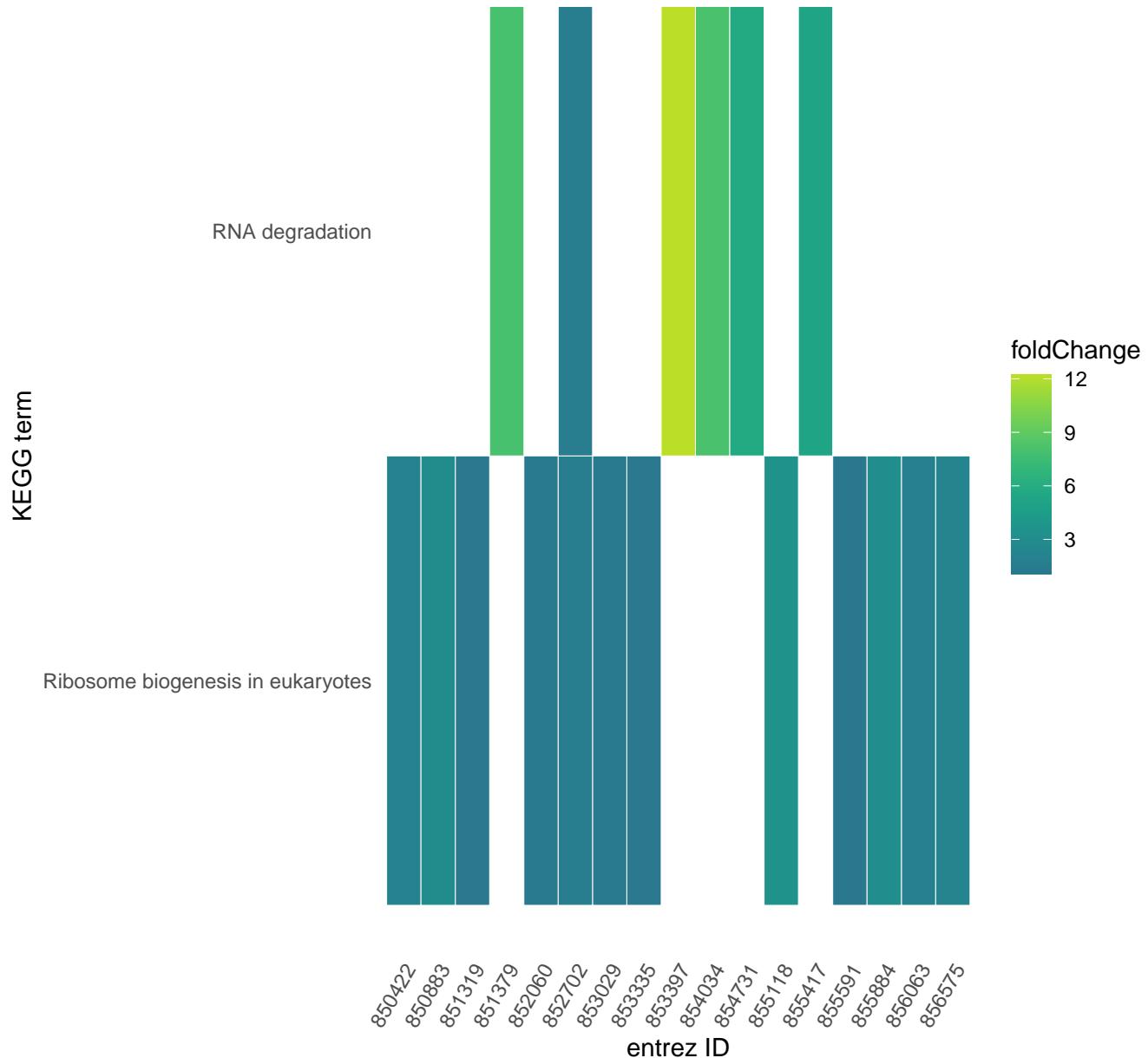
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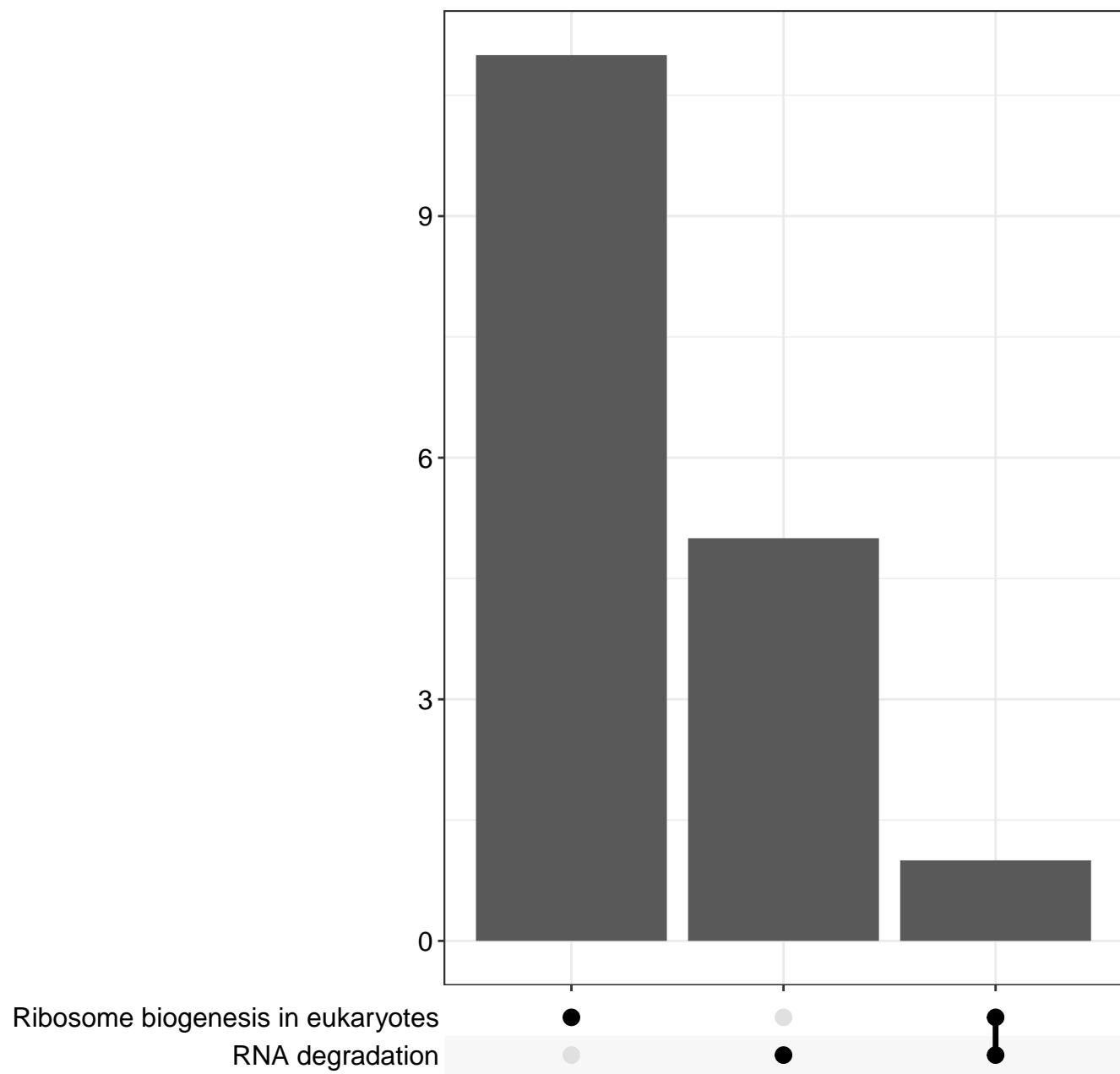
MTR4–TAP Up-regulated KEGG dotplot



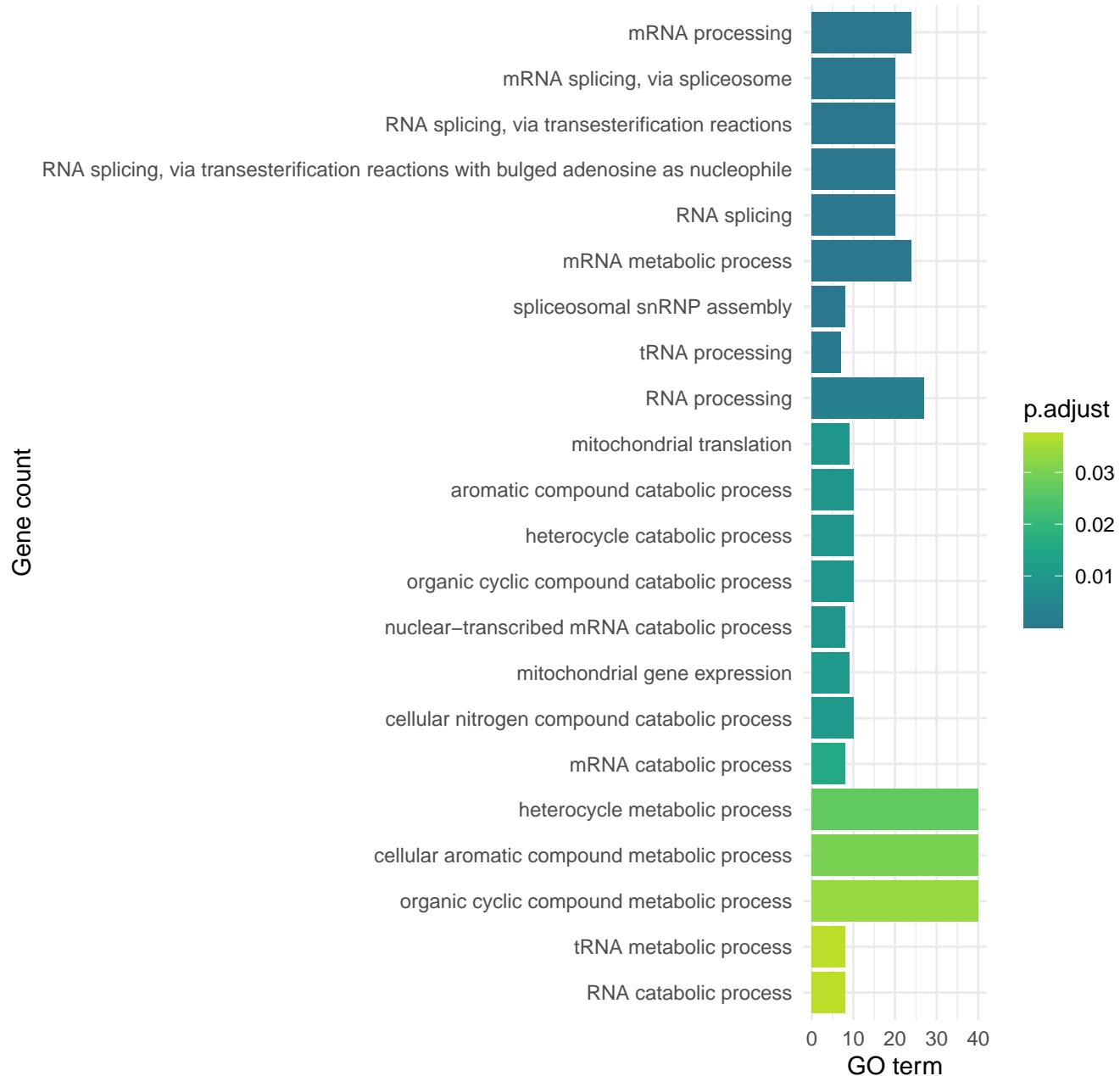
MTR4-TAP Up-regulated KEGG heatplot



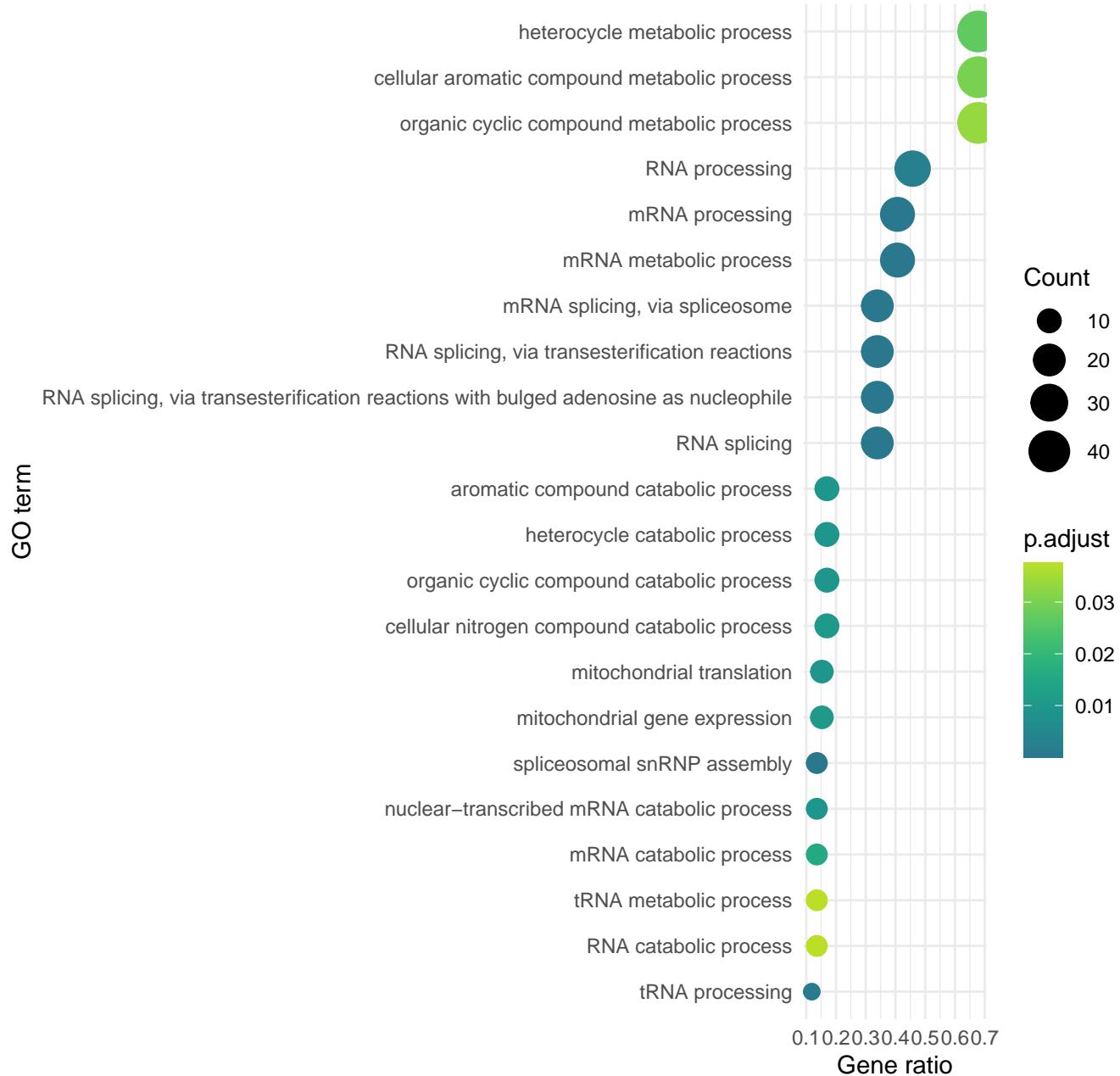
MTR4–TAP Up-regulated KEGG upsetplot



LSM2-TAP Up-regulated

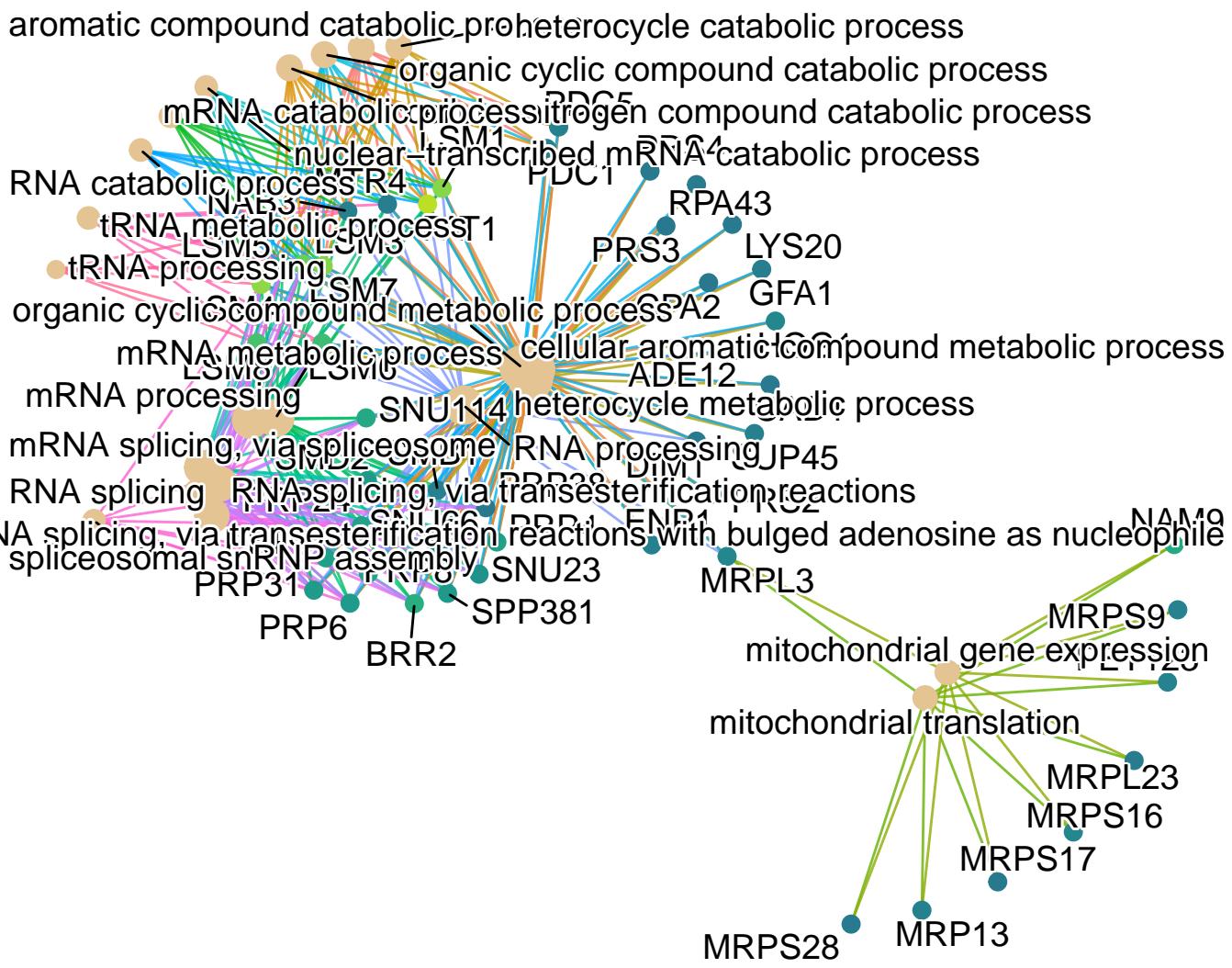


LSM2-TAP Up-regulated

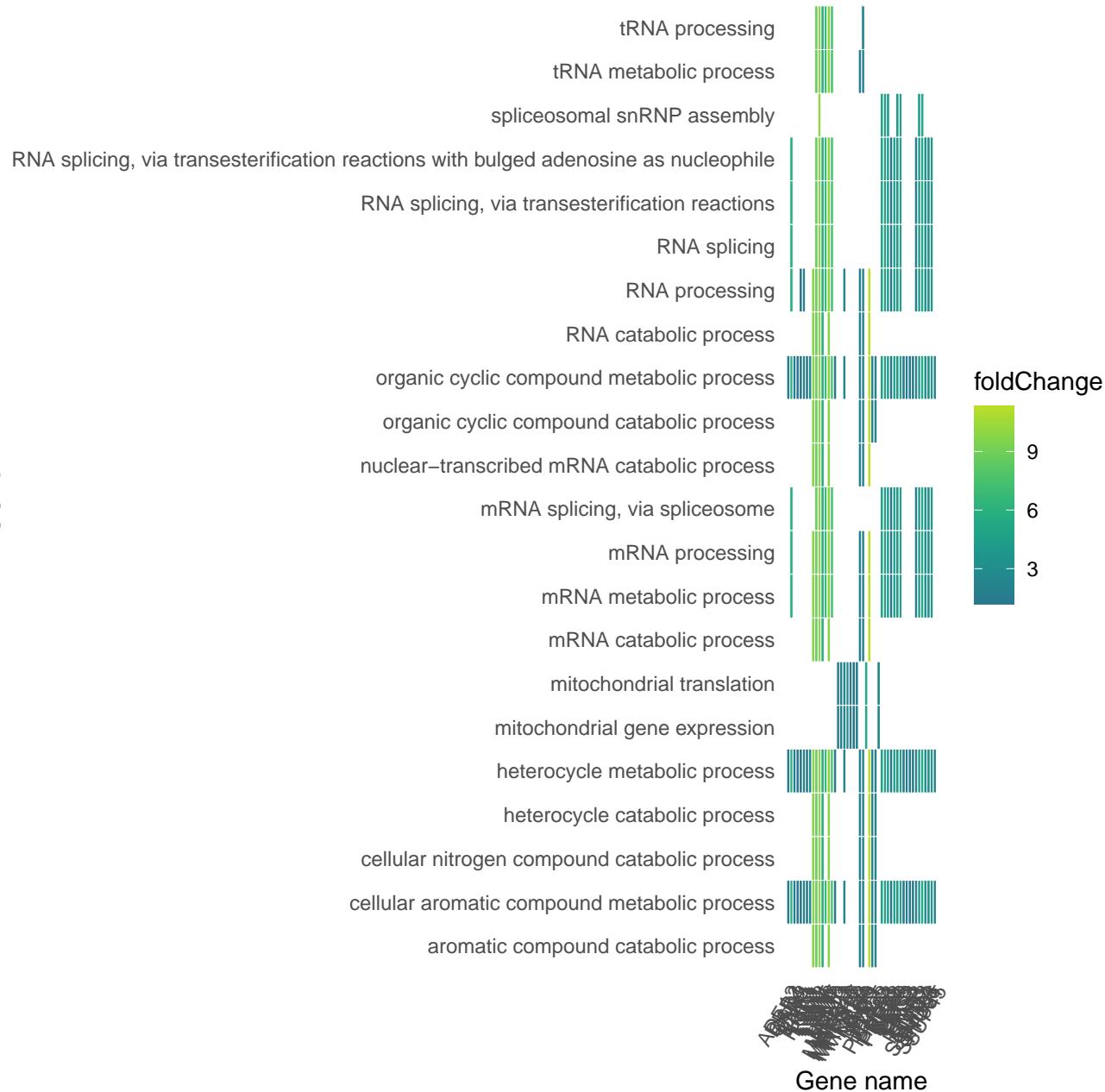


LSM2-TAP Up-regulated GO BP cnetplot

ondrial gene expression	mRNA splicing, via spliceosome	RNA processing
ondrial translation	nuclear-transcribed mRNA catabolic process	RNA splicing
catabolic process	organic cyclic compound catabolic process	RNA splicing, via transesterification reaction
metabolic process	organic cyclic compound metabolic process	RNA splicing, via transesterification reaction
processing	RNA catabolic process	spliceosomal snRNP assembly



LSM2-TAP Up-regulated

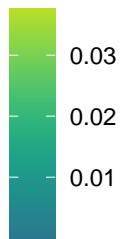


LSM2-TAP Up-regulated GO BP emapplot

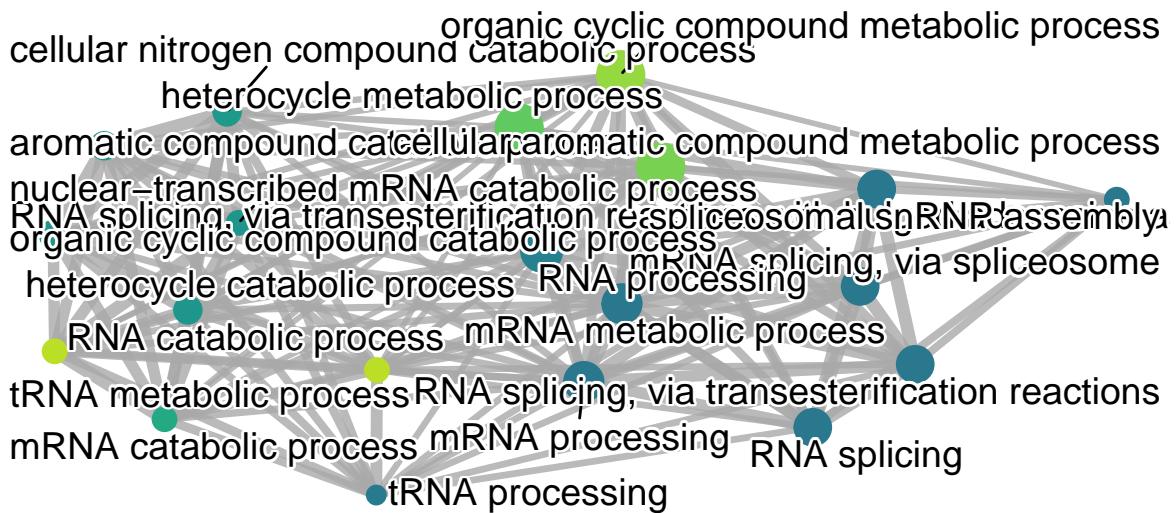
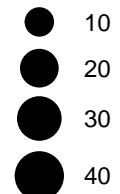
mitochondrial gene expression

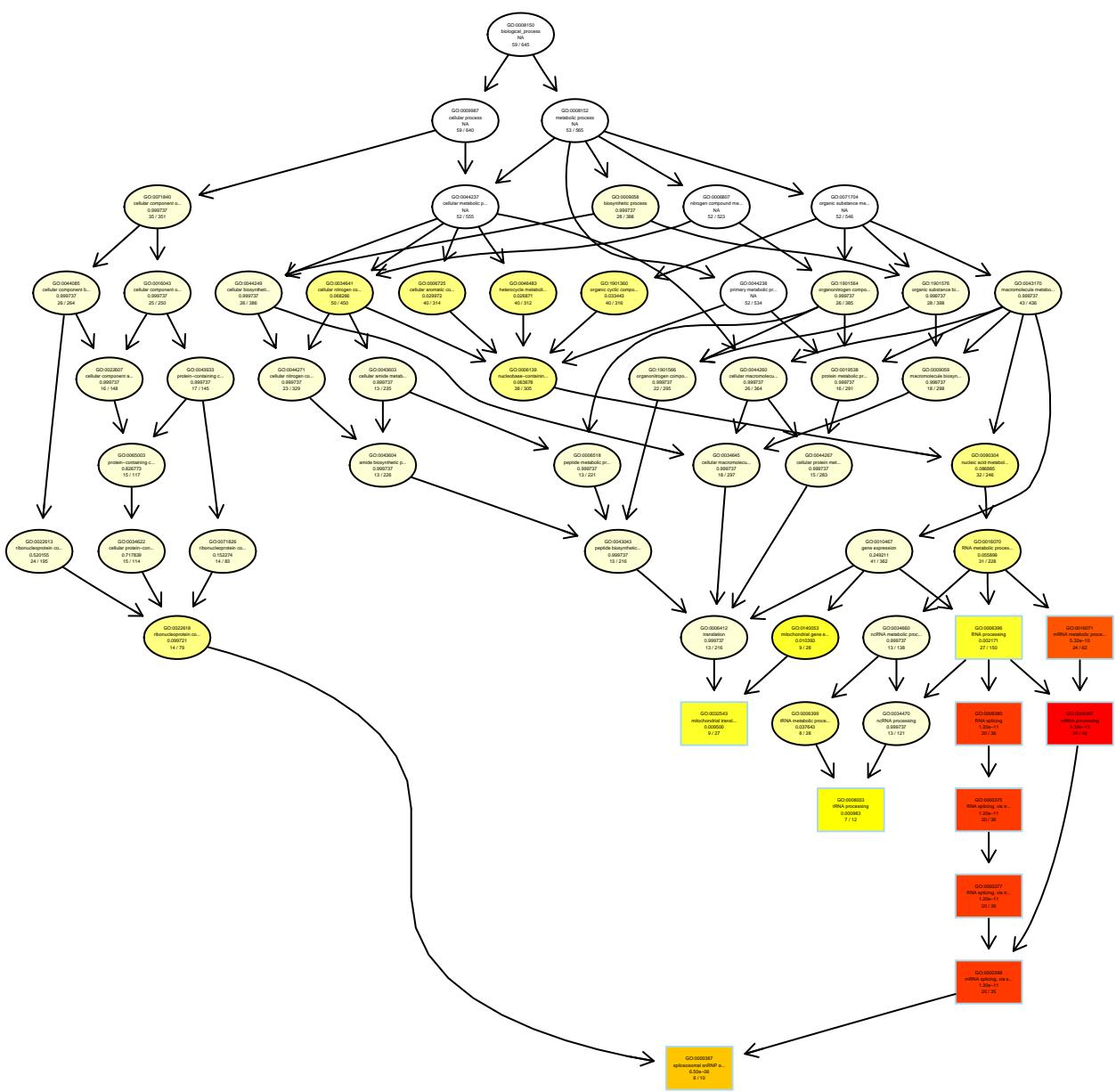
mitochondrial translation

FoldChange

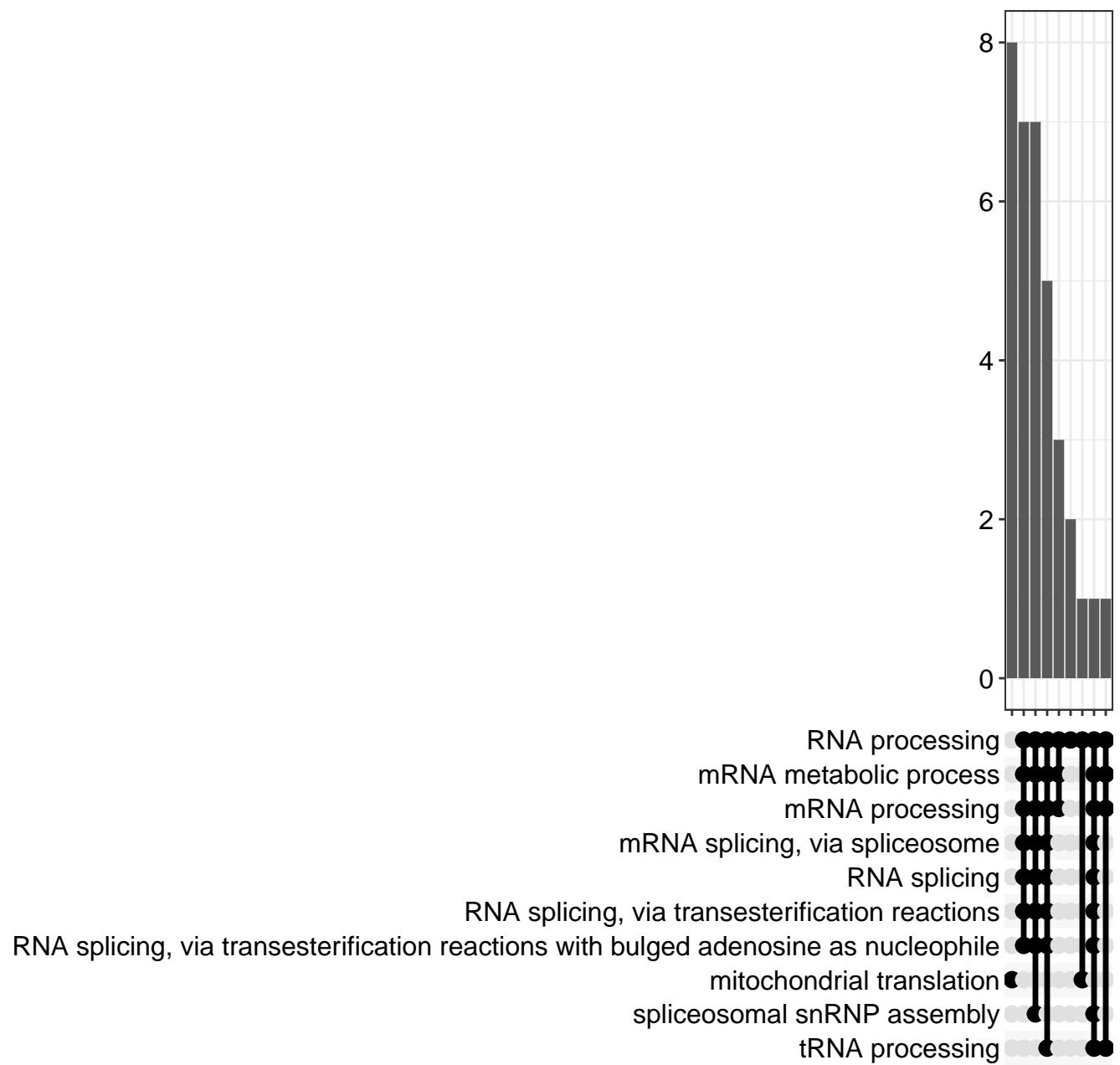


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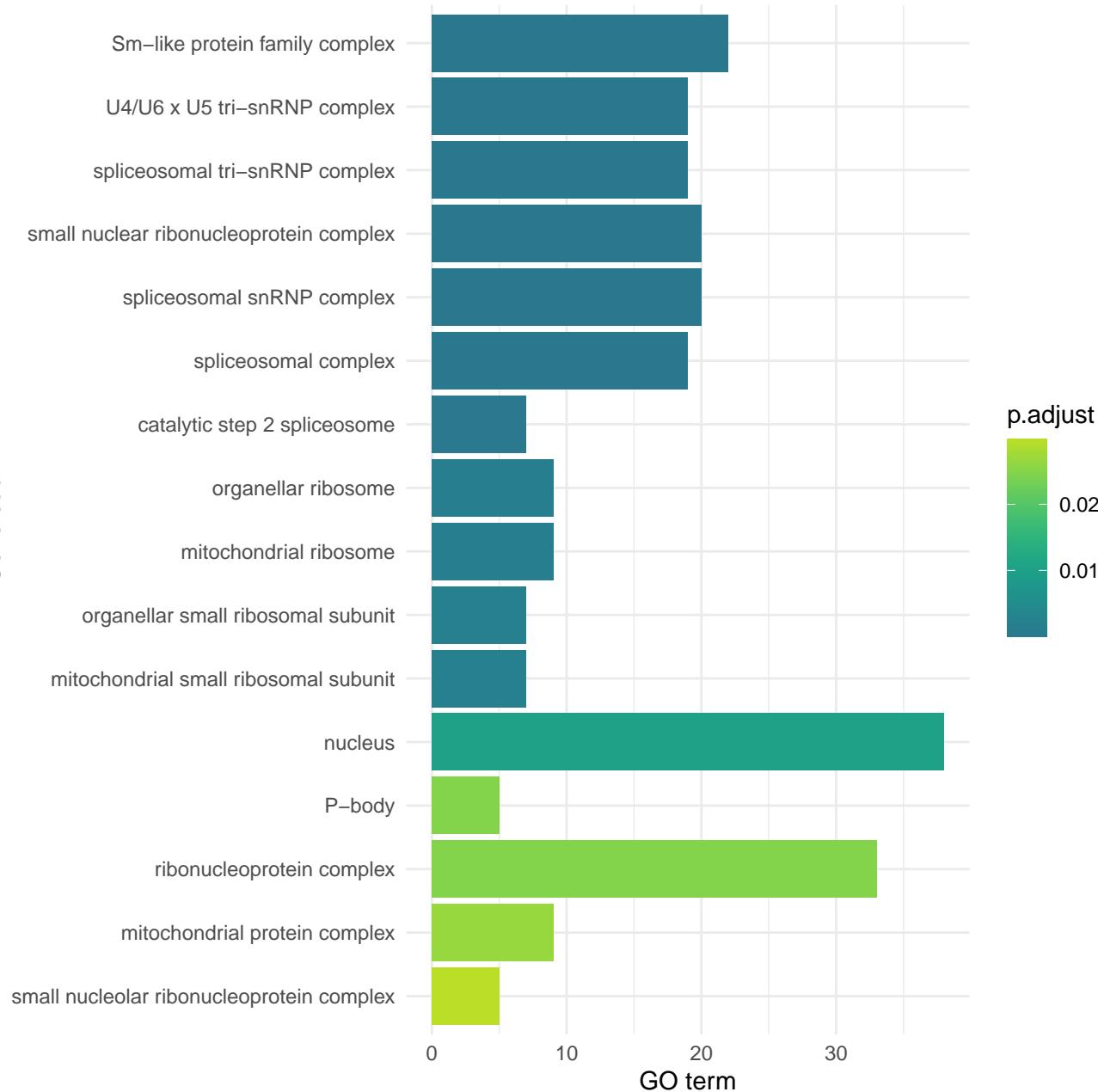




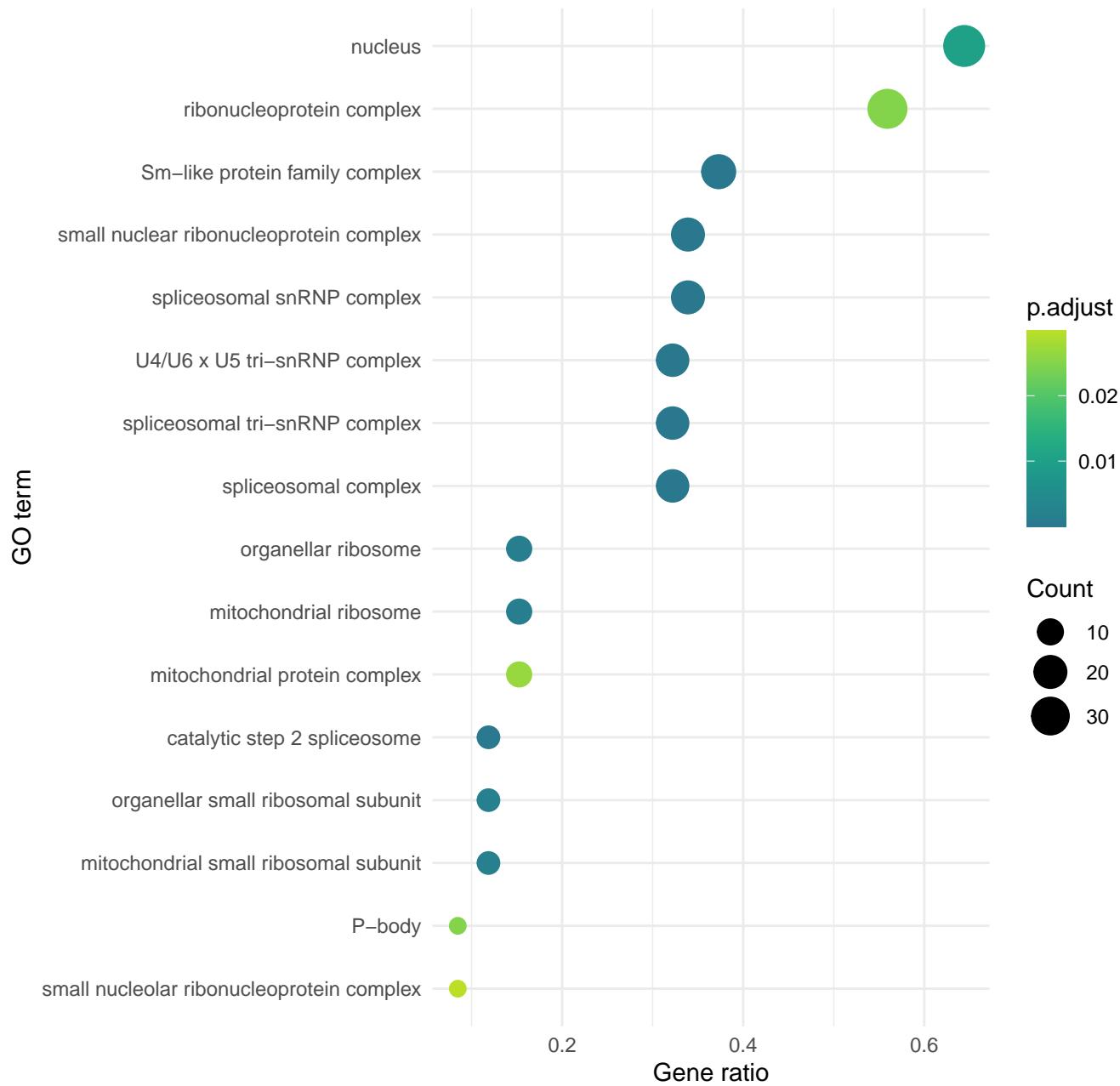
LSM2-TA



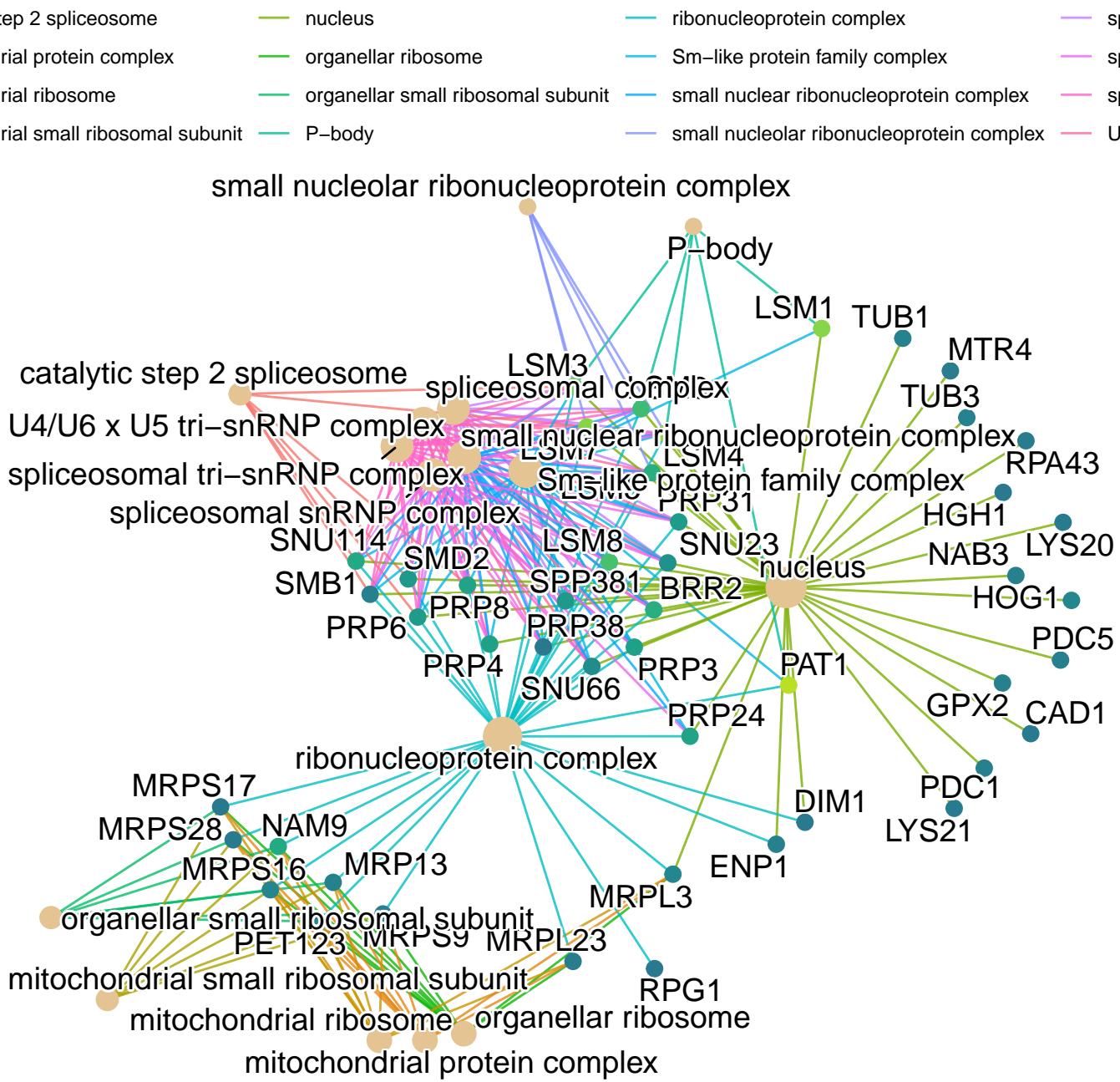
LSM2-TAP Up-regulated GO CC barplot



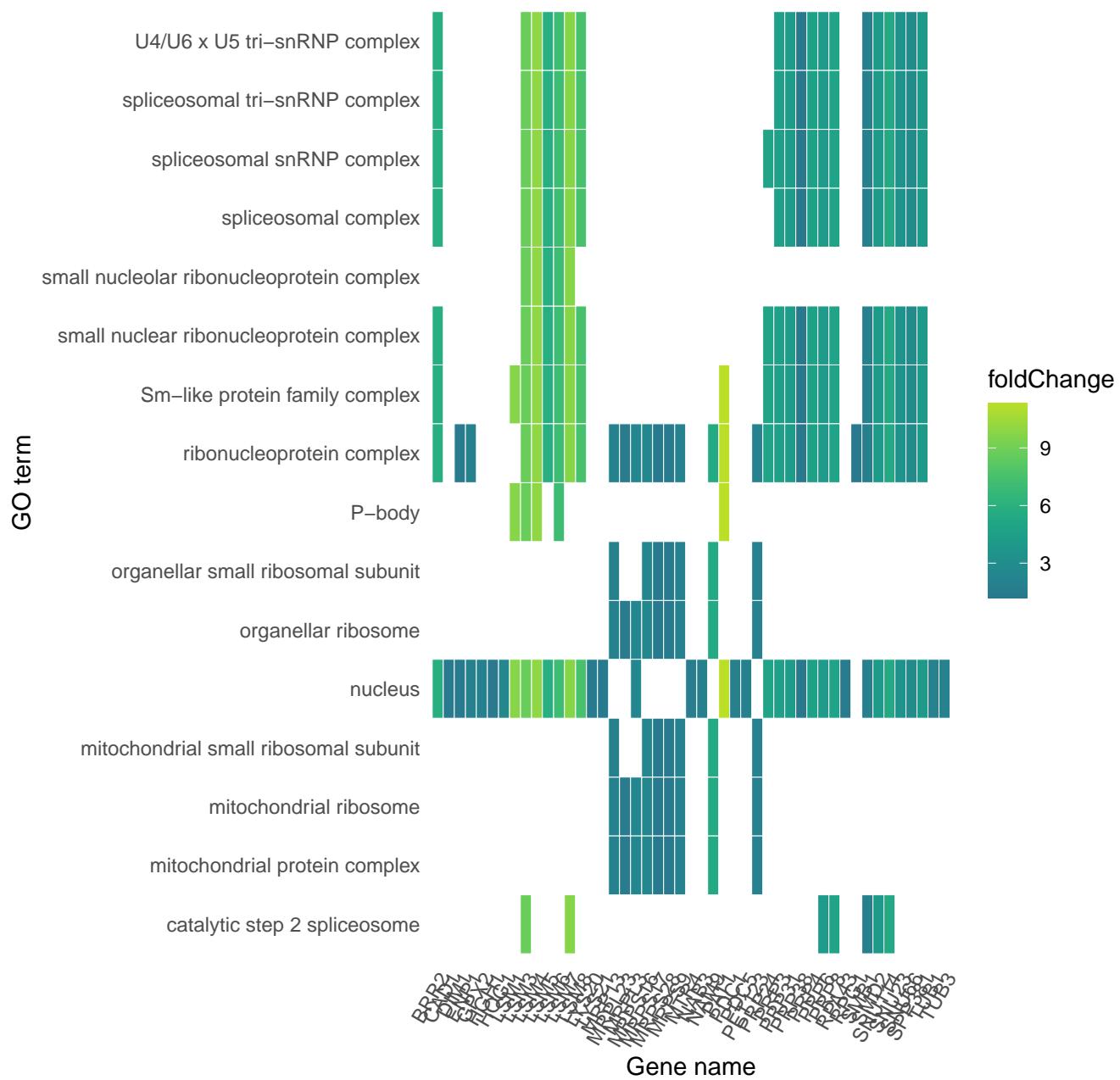
LSM2-TAP Up-regulated GO CC dotplot



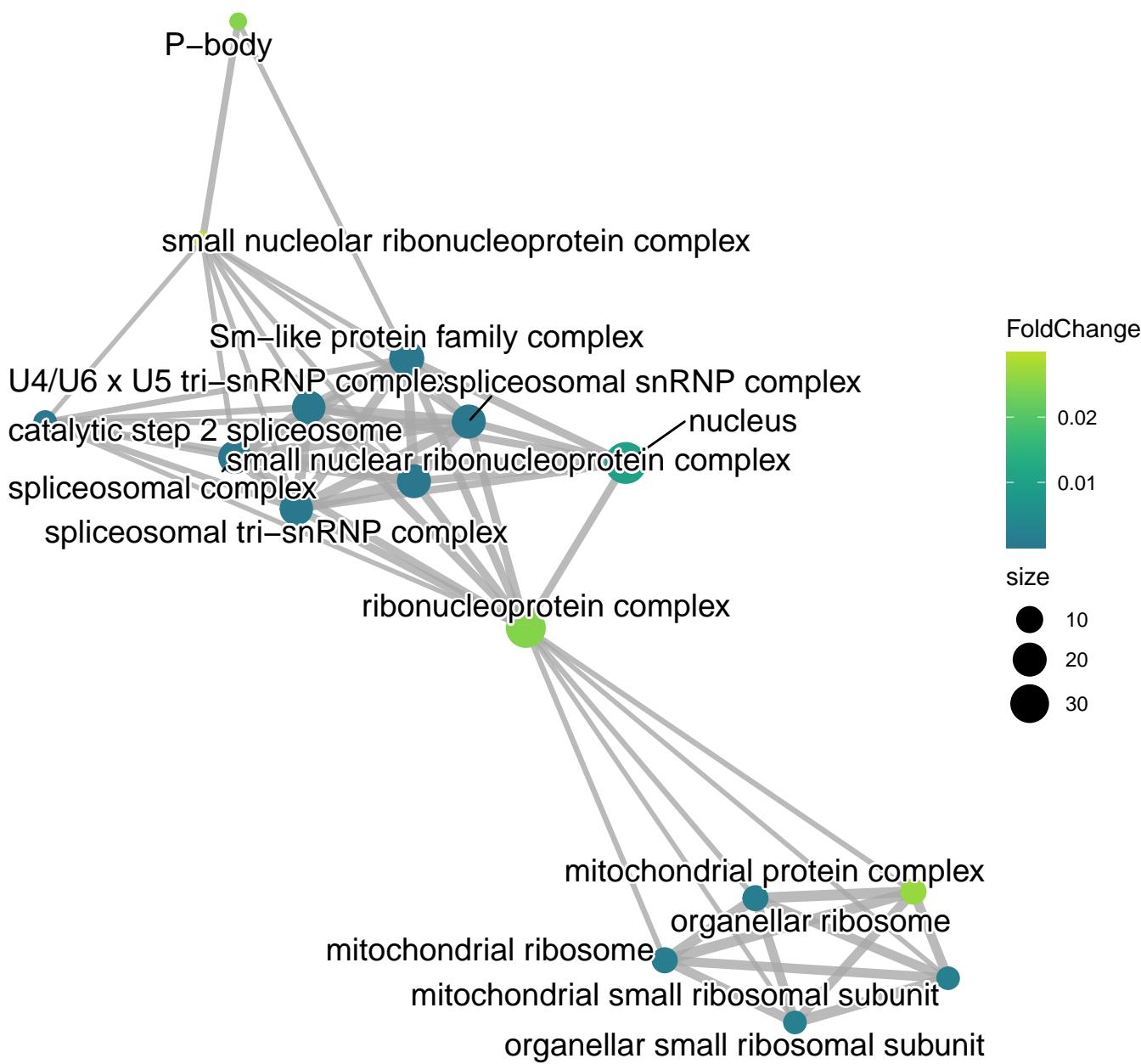
LSM2-TAP Up-regulated GO CC cnetplot

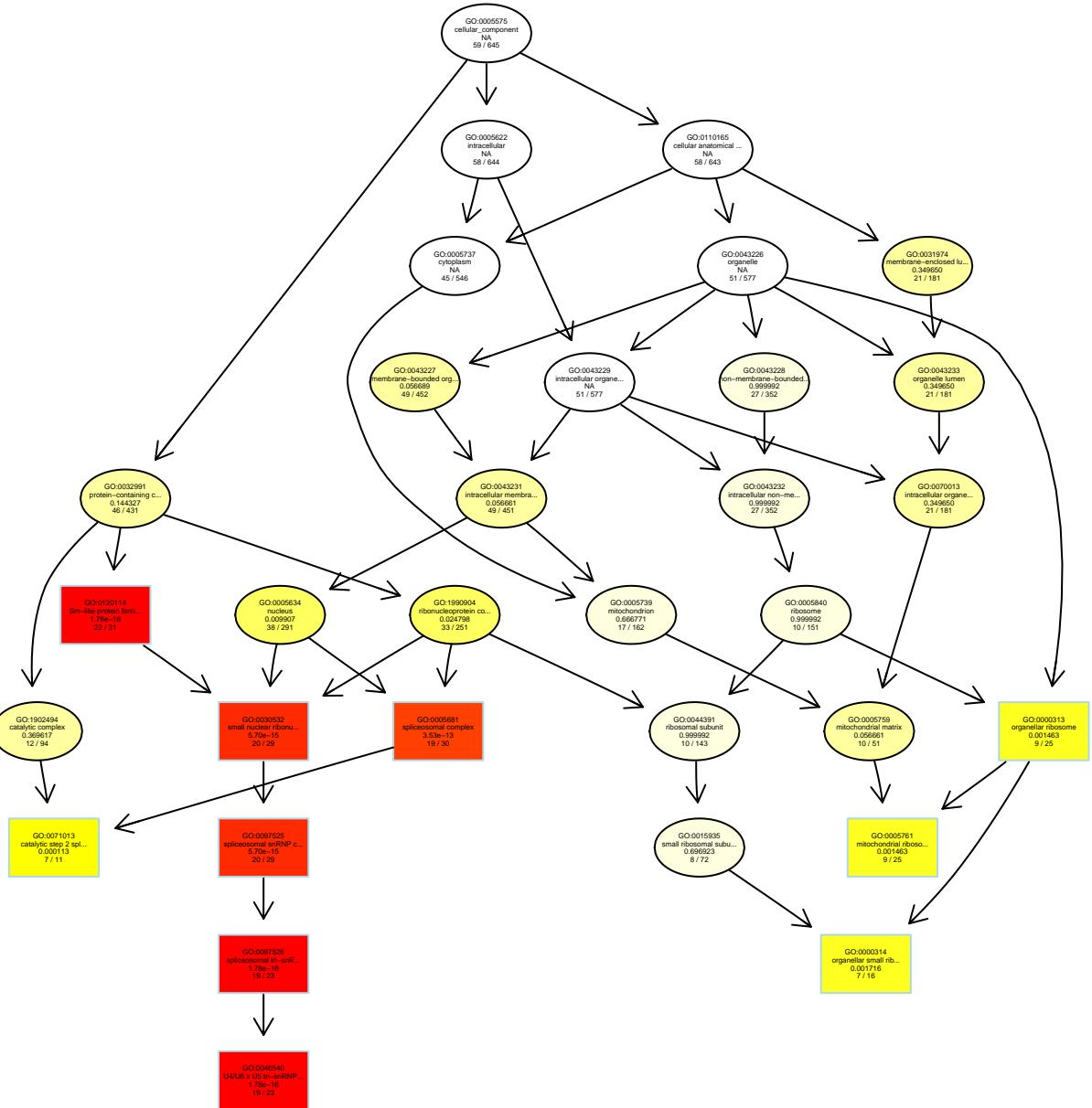


LSM2-TAP Up-regulated GO CC heatplot

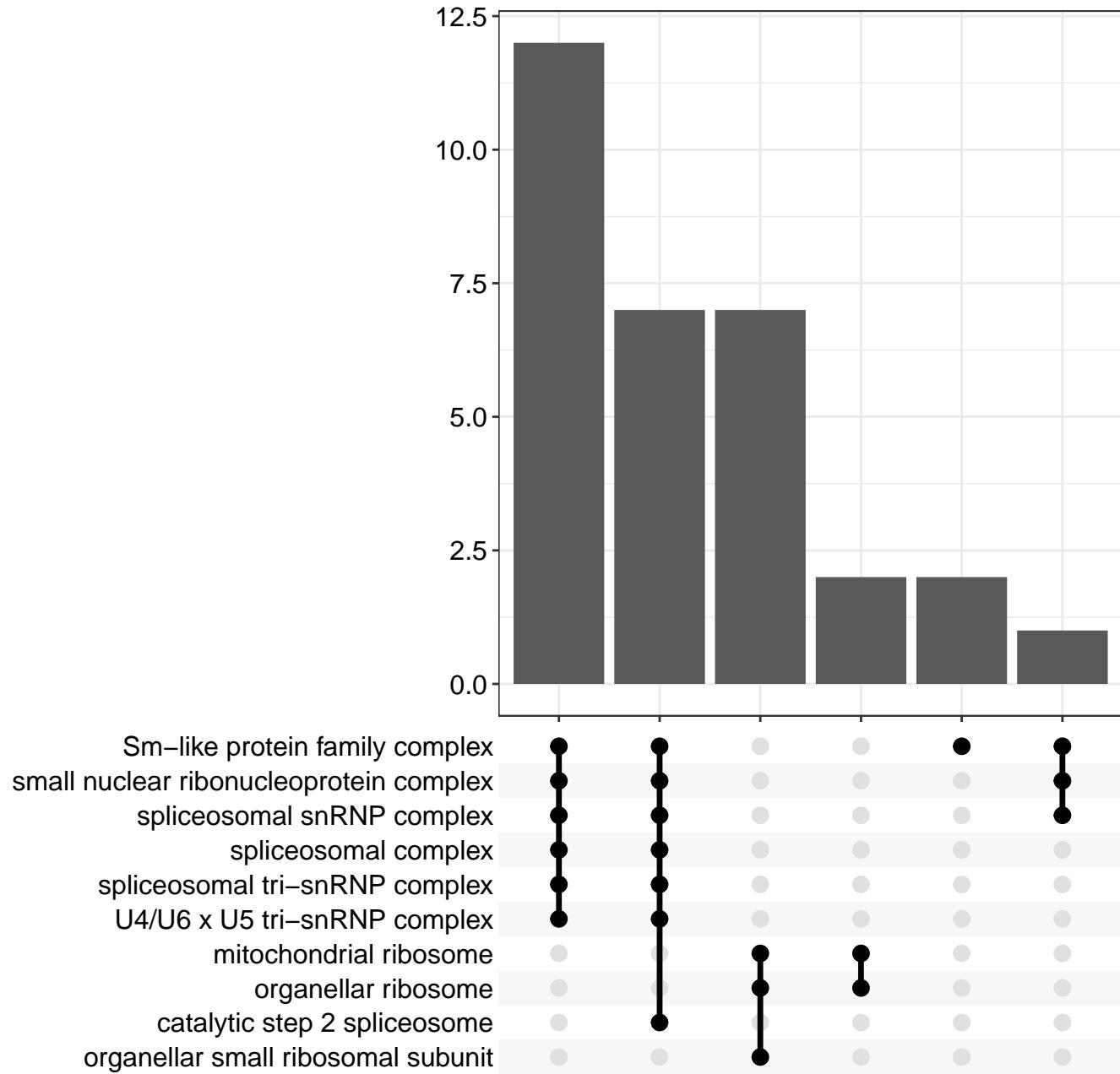


LSM2-TAP Up-regulated GO CC emapplot

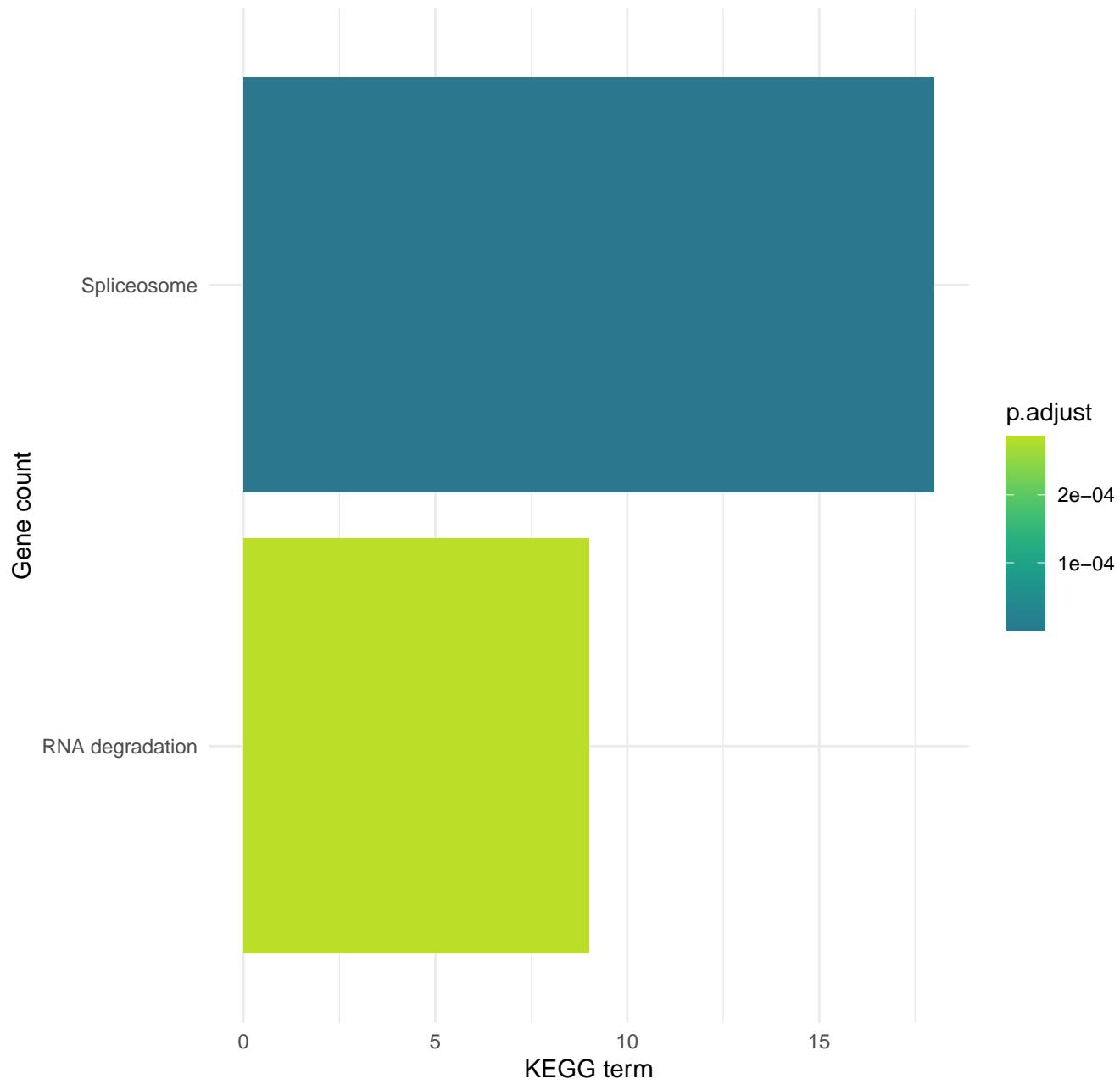




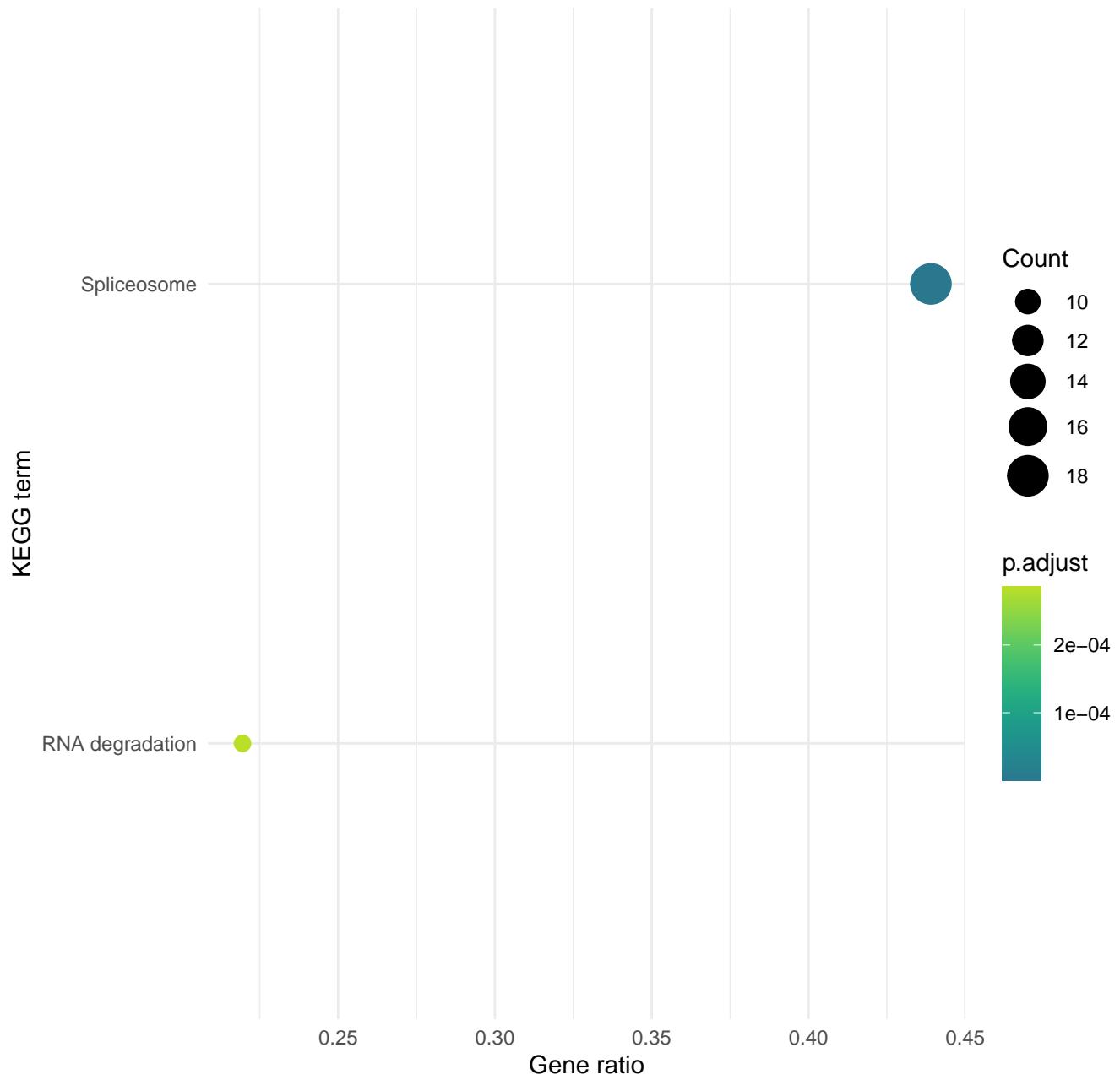
LSM2-TAP Up-regulated GO CC upsetplot



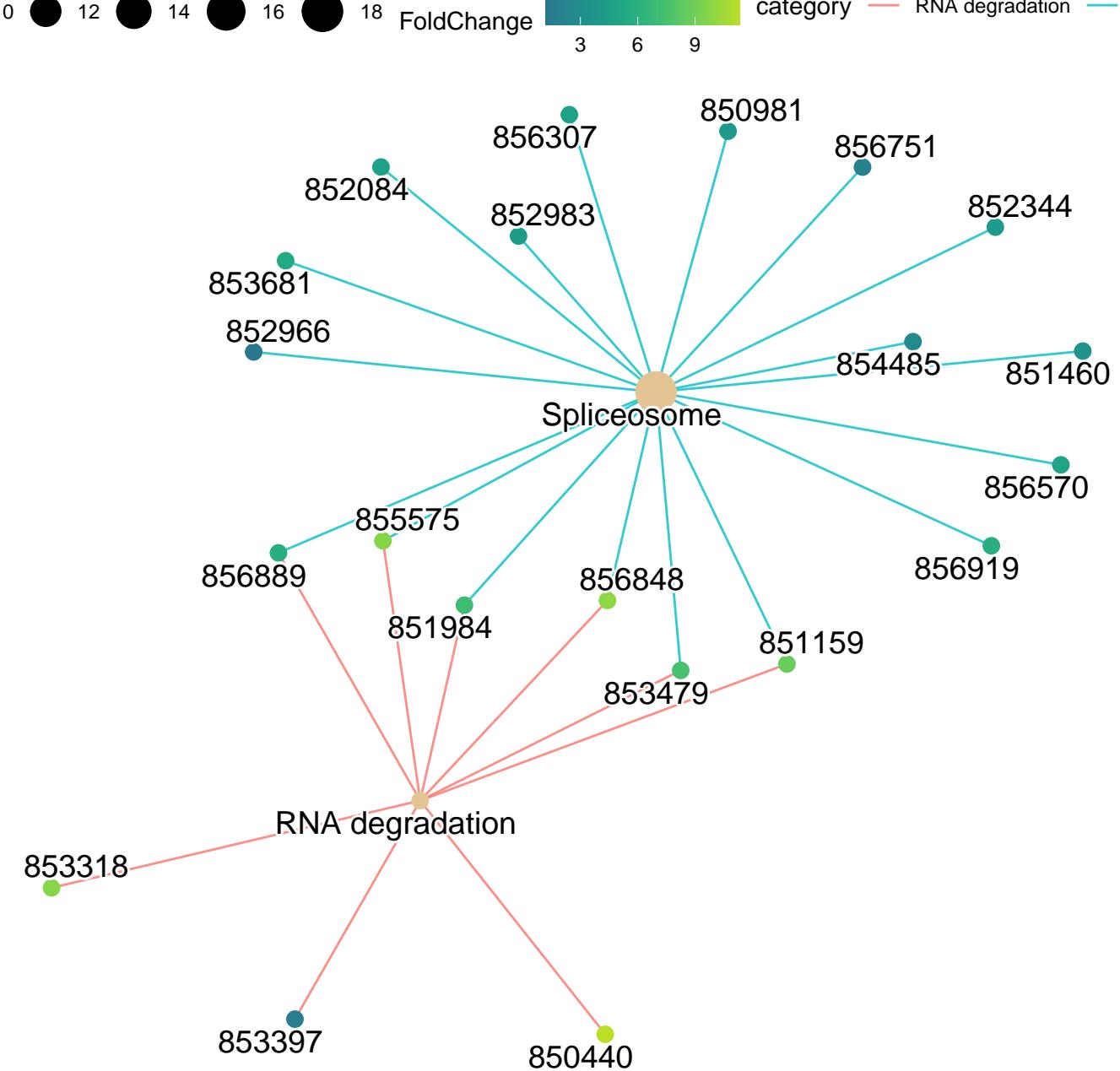
LSM2-TAP Up-regulated KEGG barplot



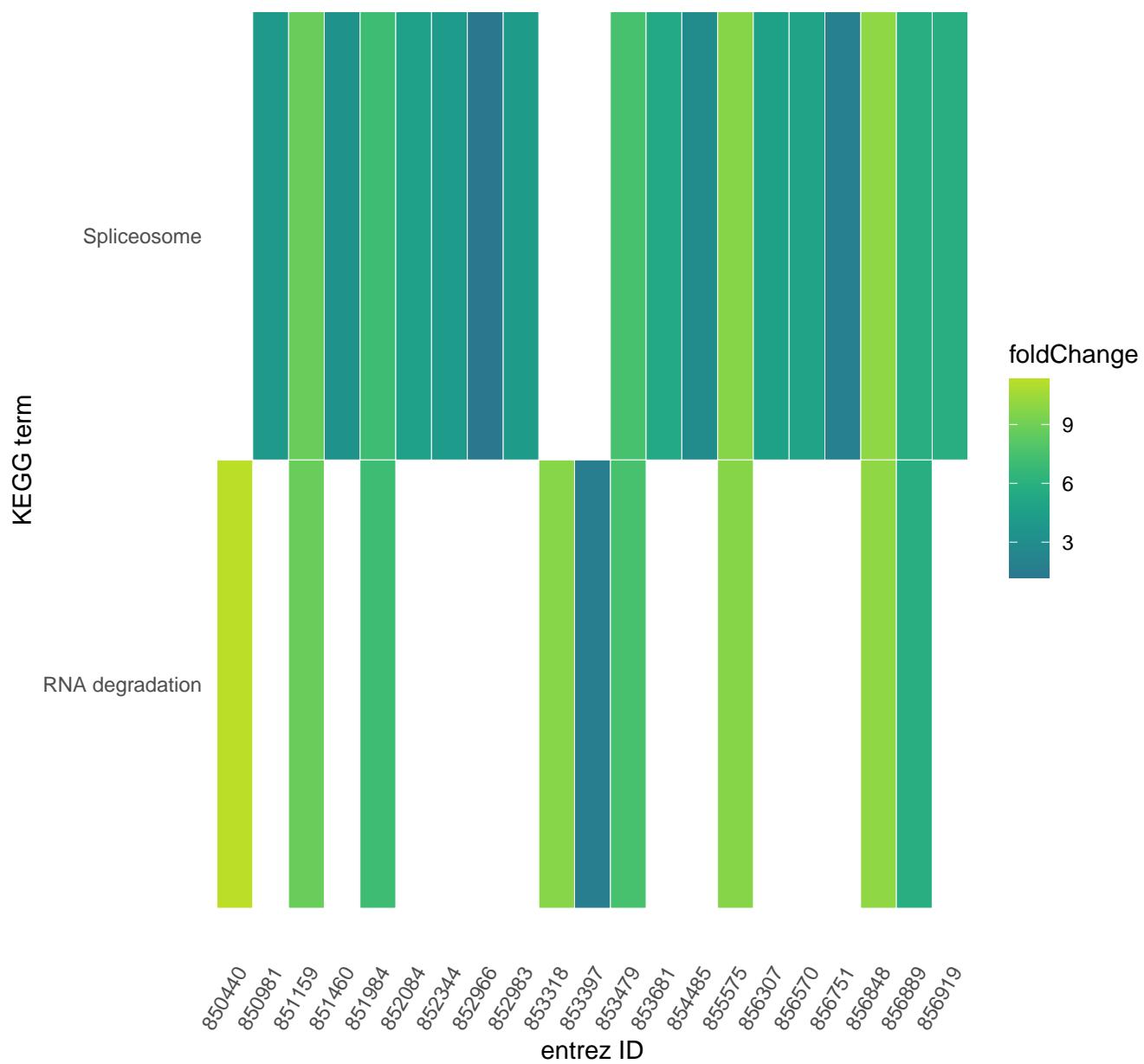
LSM2-TAP Up-regulated KEGG dotplot



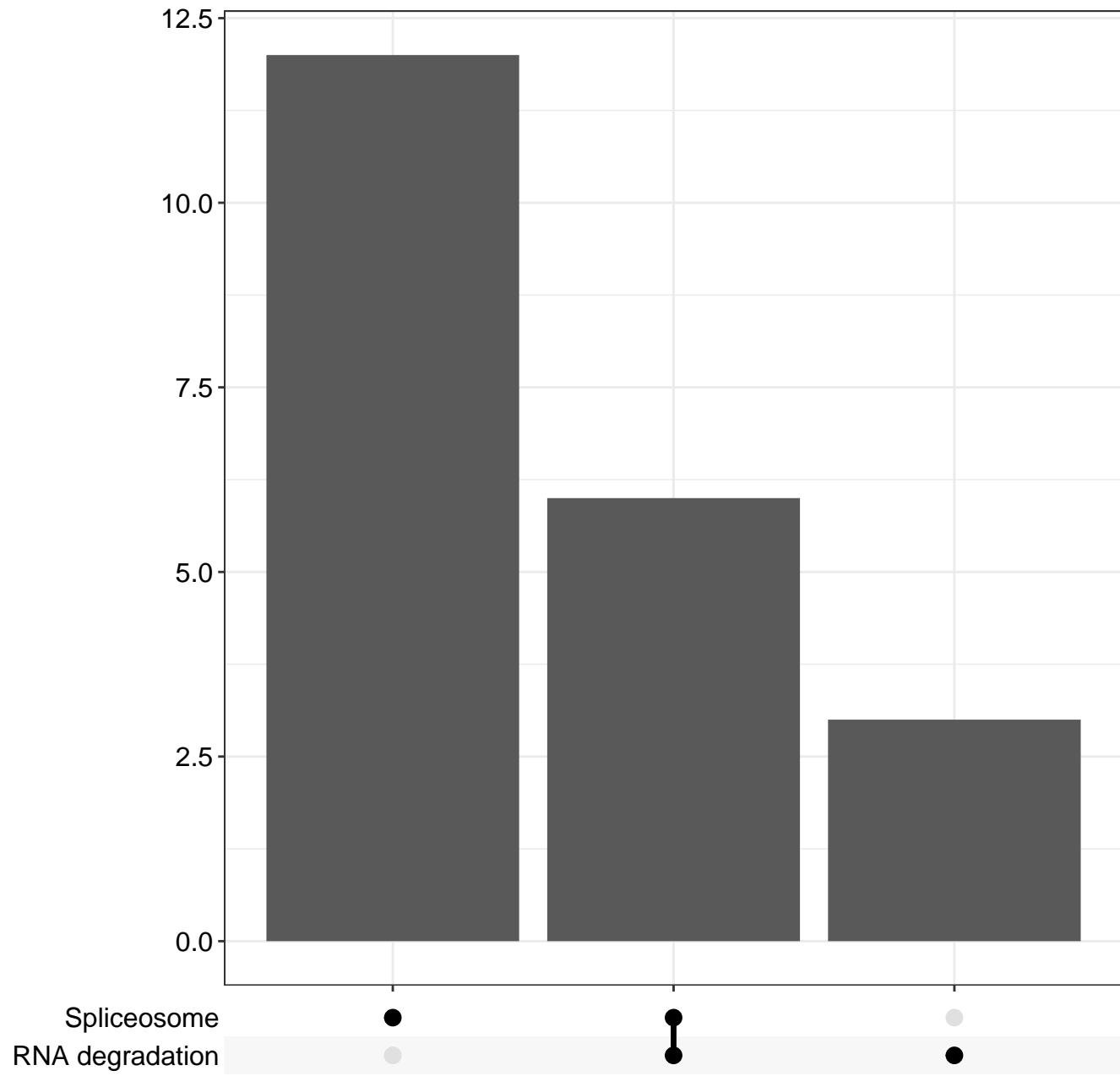
LSM2-TAP Up-regulated KEGG dotplot

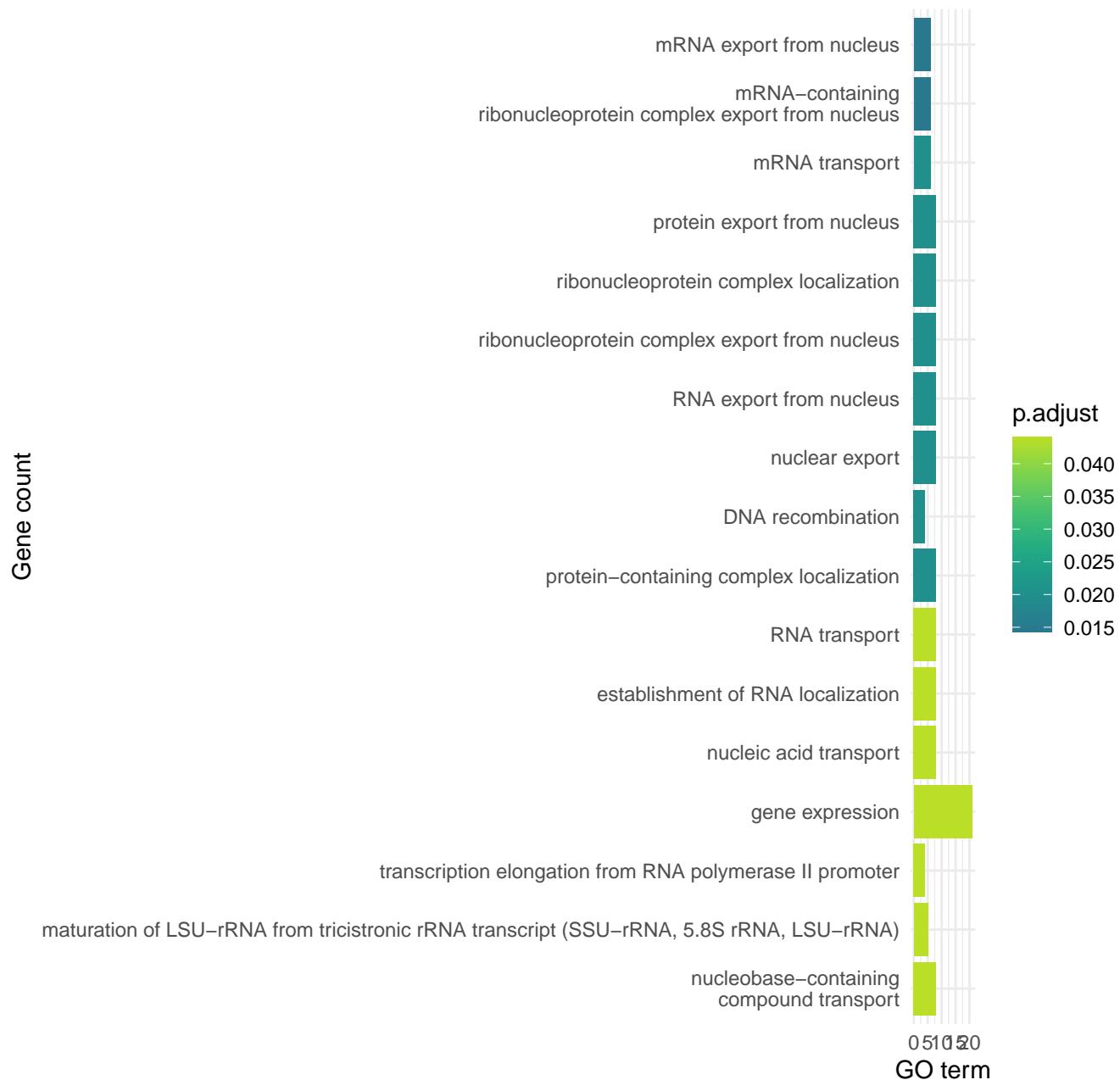


LSM2-TAP Up-regulated KEGG heatplot

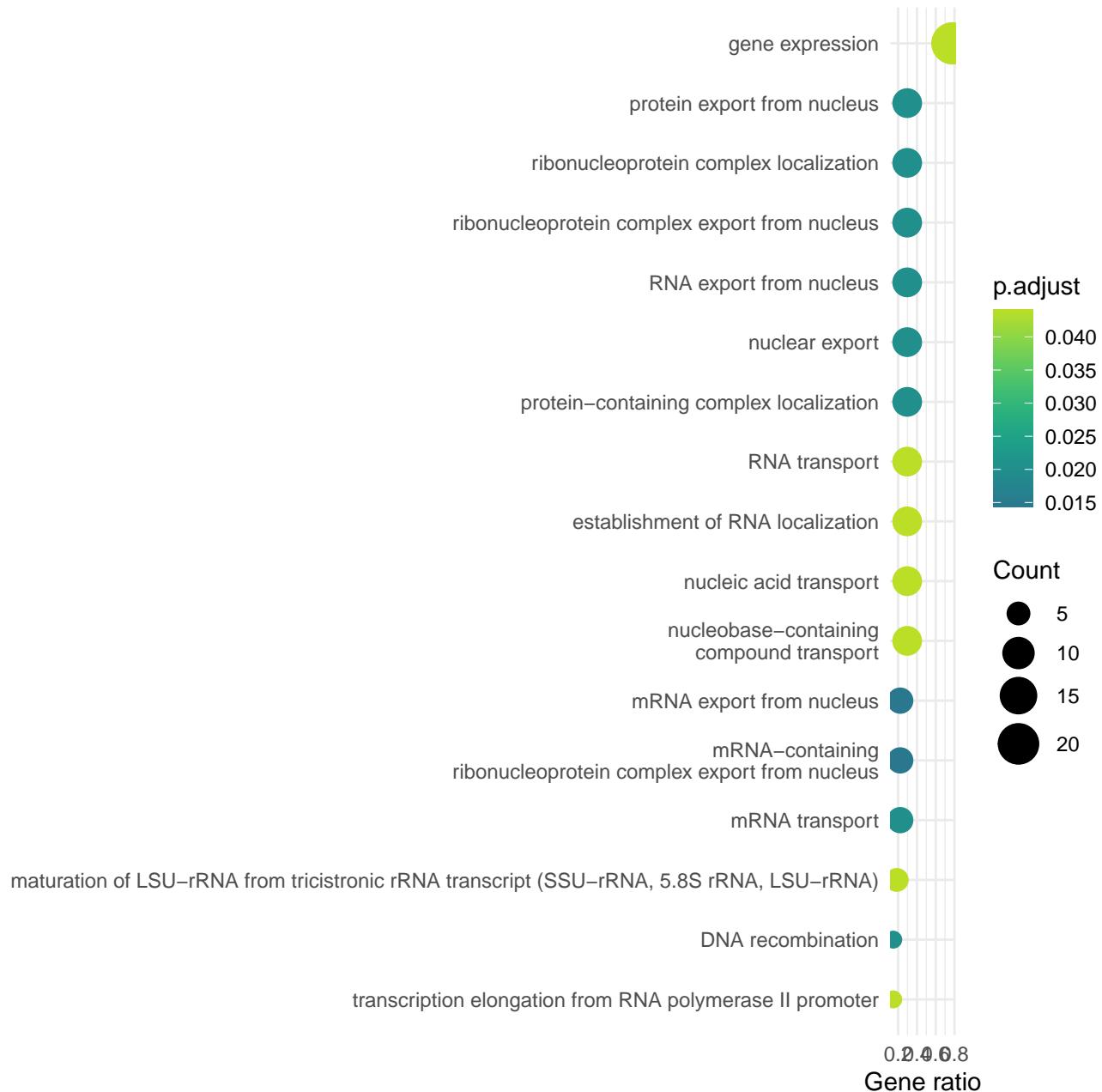


LSM2-TAP Up-regulated KEGG upsetplot



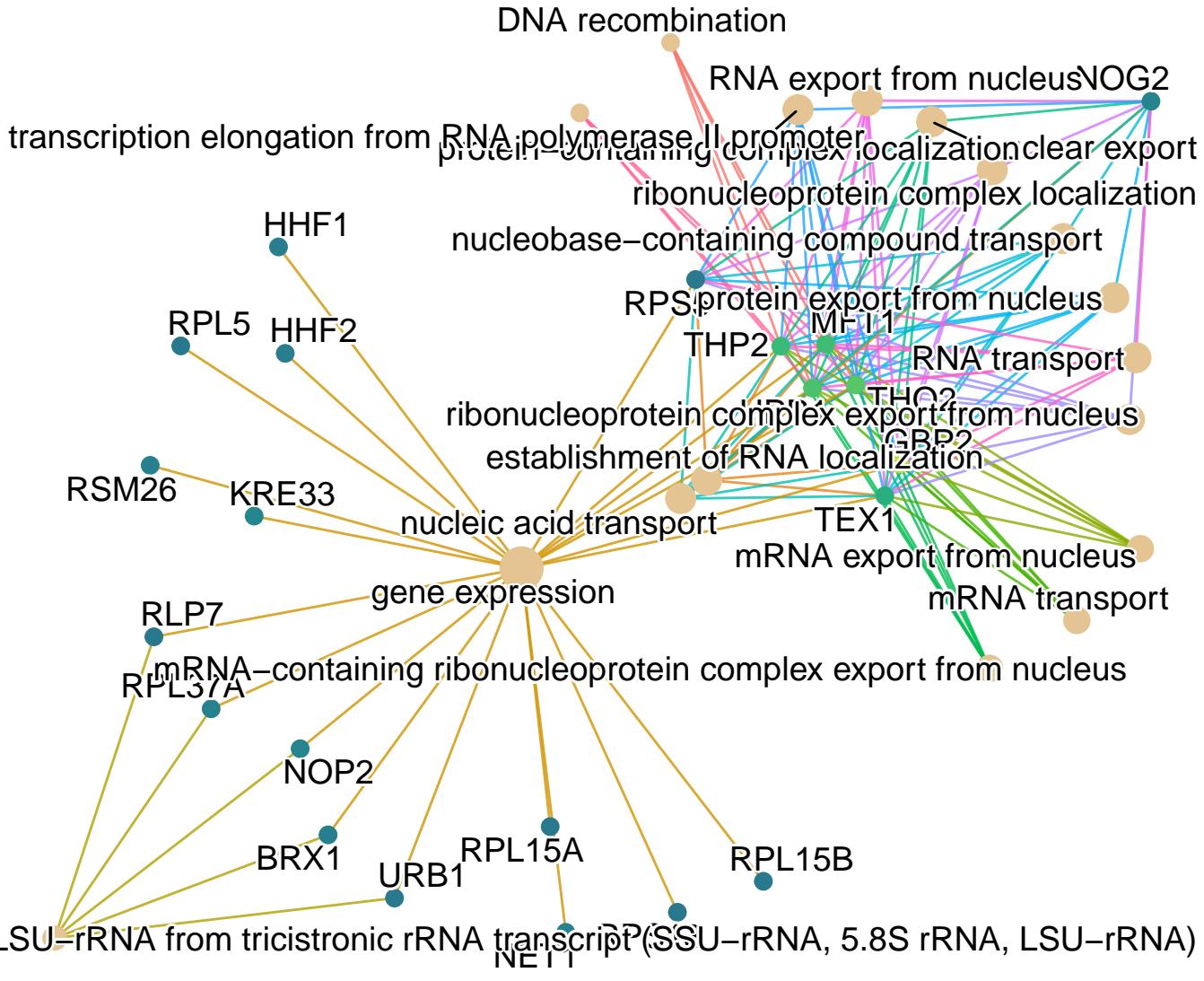
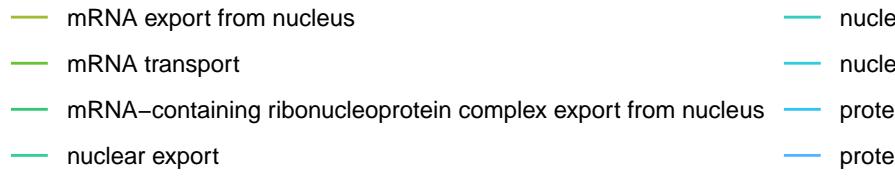


GBP2-TAP Up-



GBP2-TAP Up-regulated GO BP cnetplot

ript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)



GBP2-TAP Up-regulated

GO term

transcription elongation from RNA polymerase II promoter

RNA transport

RNA export from nucleus

ribonucleoprotein complex localization

ribonucleoprotein complex export from nucleus

protein-containing complex localization

protein export from nucleus

nucleobase-containing compound transport

nucleic acid transport

nuclear export

mRNA-containing ribonucleoprotein complex export from nucleus

mRNA transport

mRNA export from nucleus

maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

gene expression

establishment of RNA localization

DNA recombination

foldChange

9

6

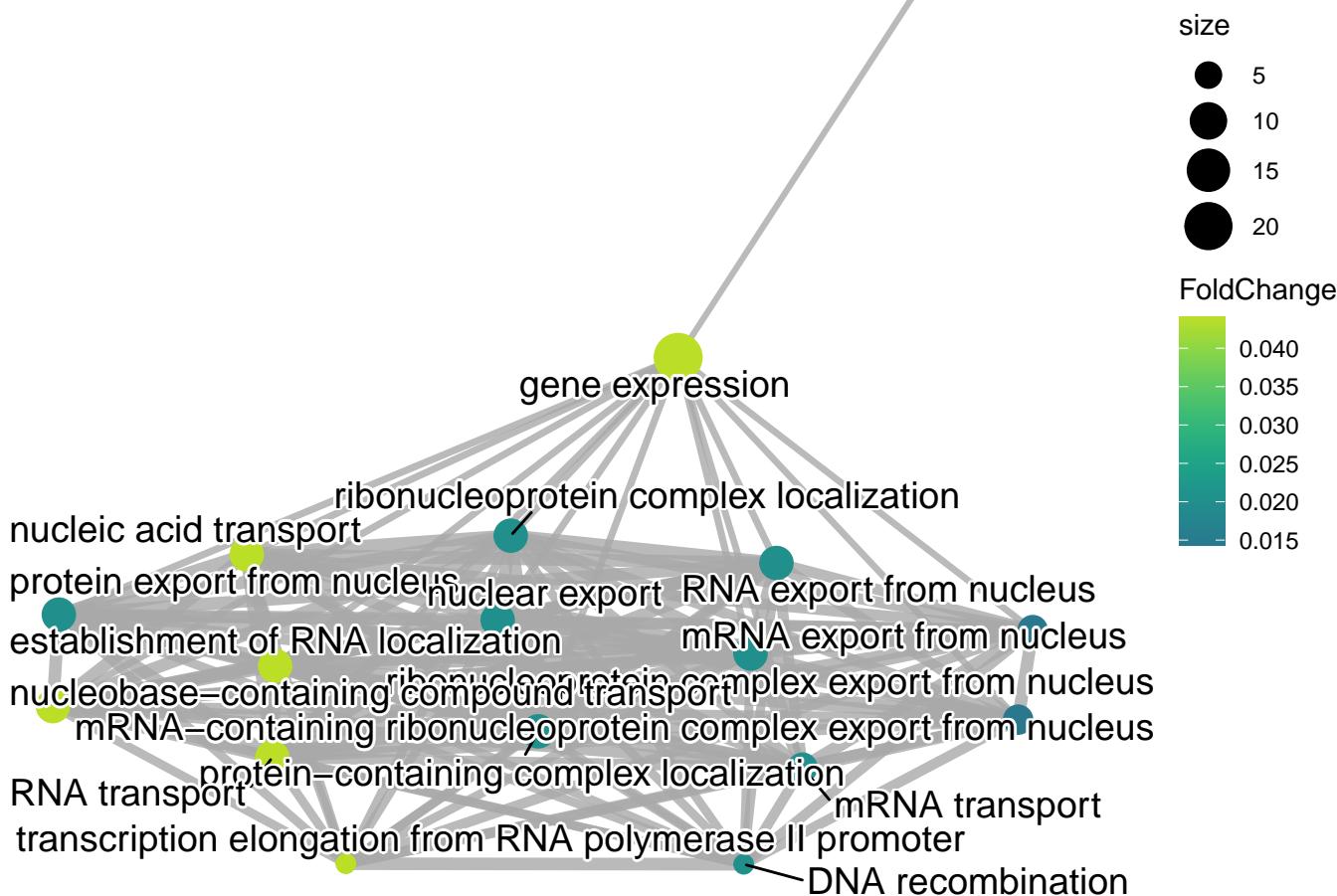
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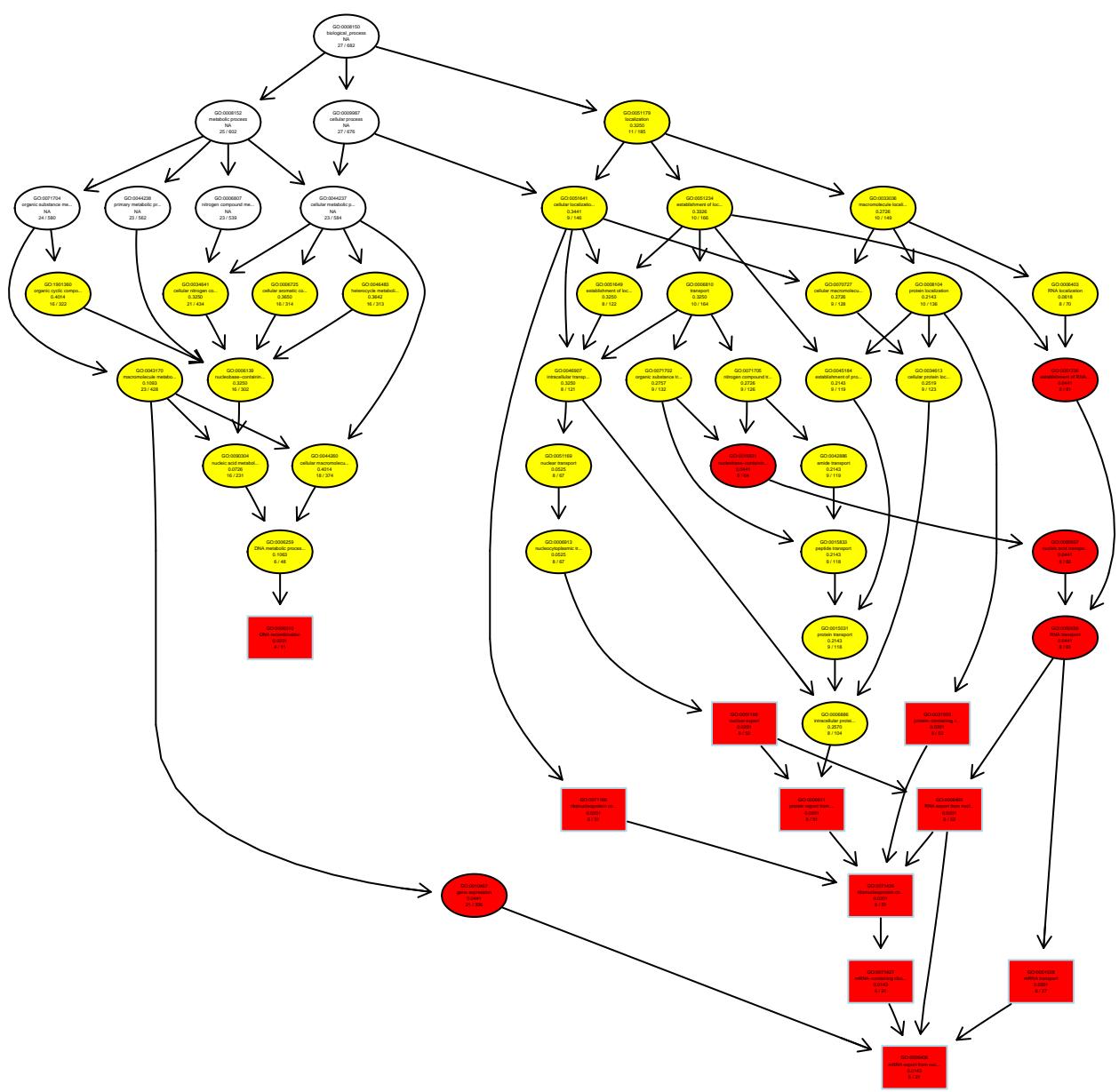


Gene name

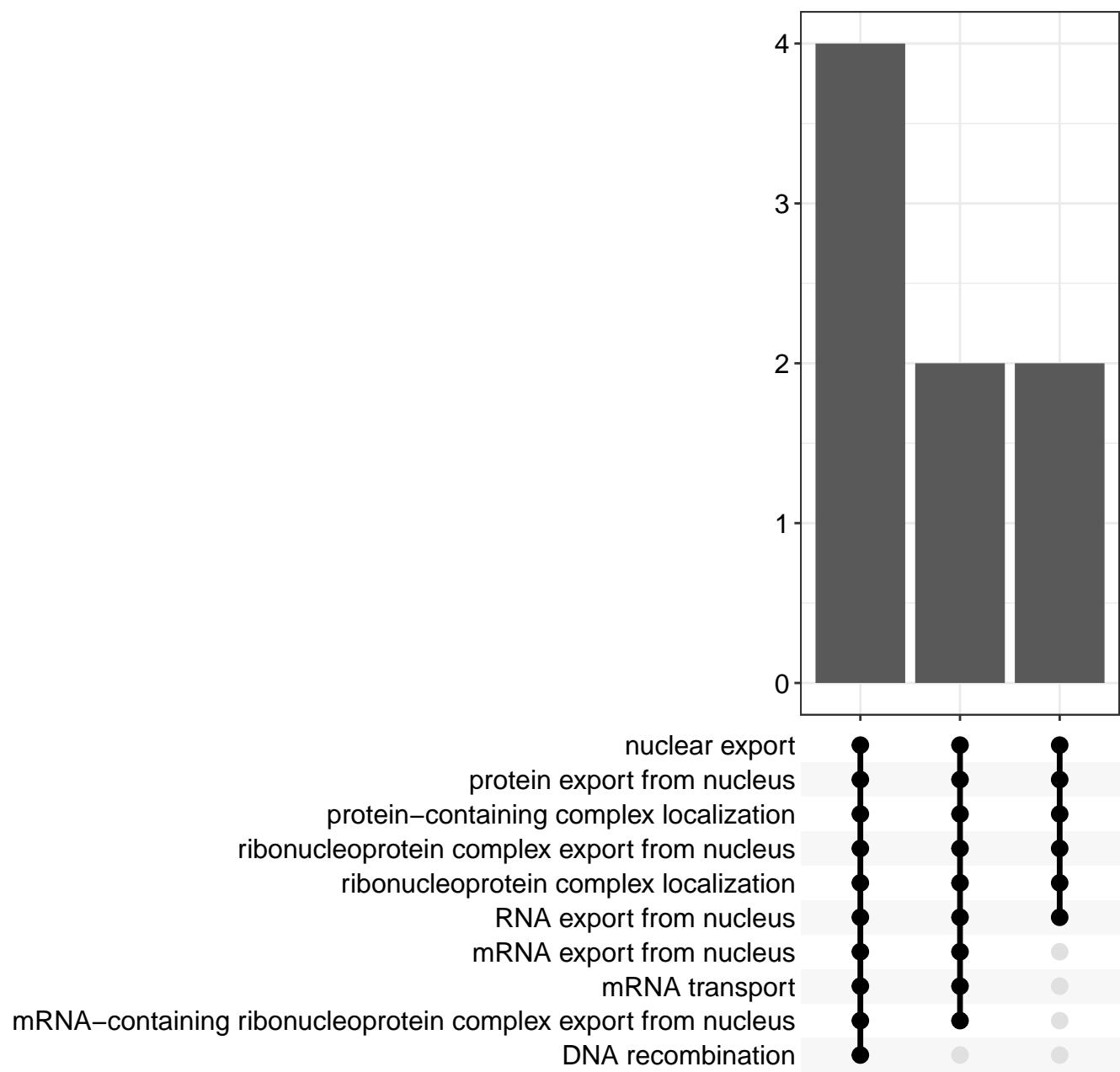
GBP2-TAP Up-regulated GO BP emapplot

maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA)

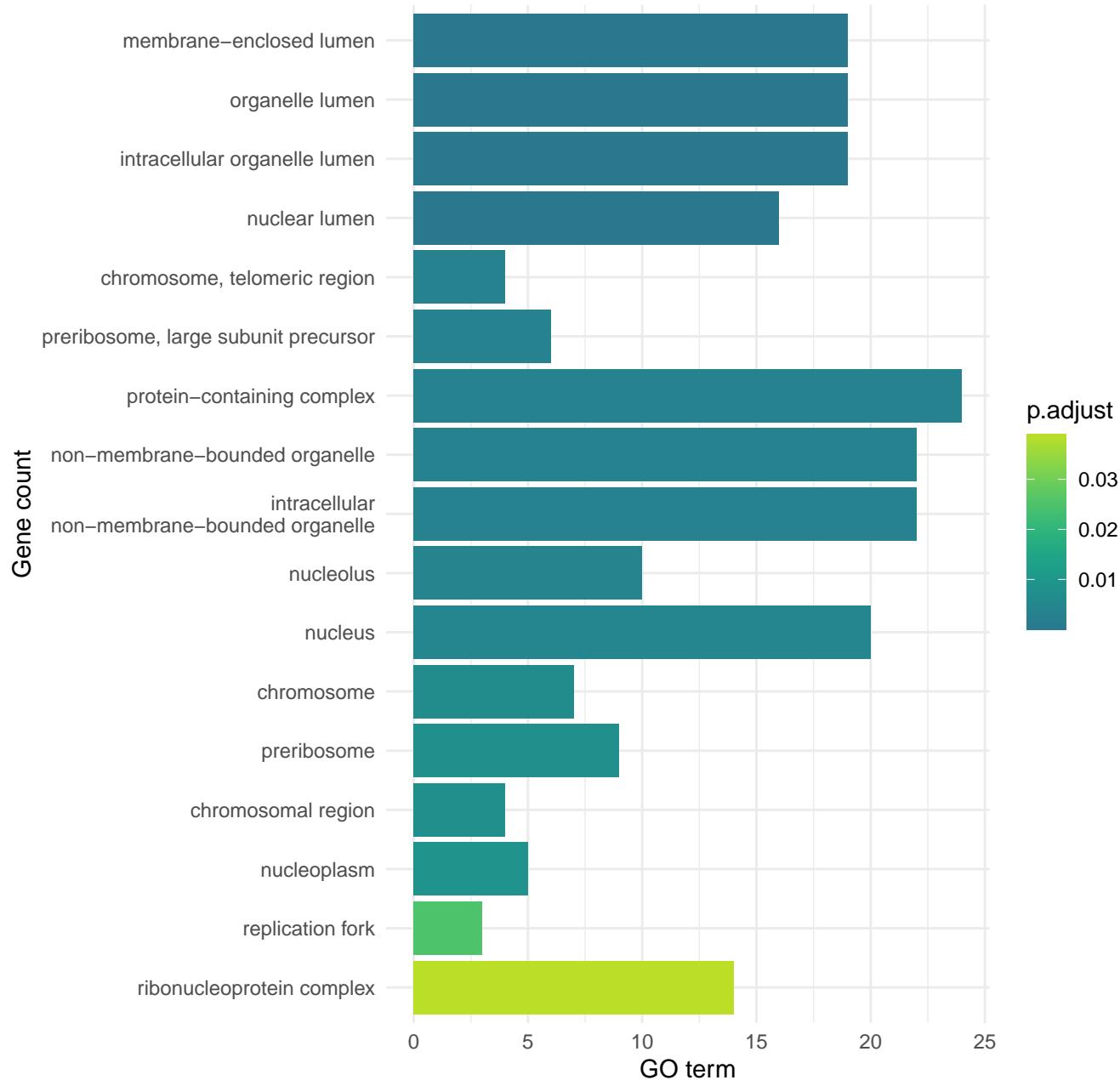




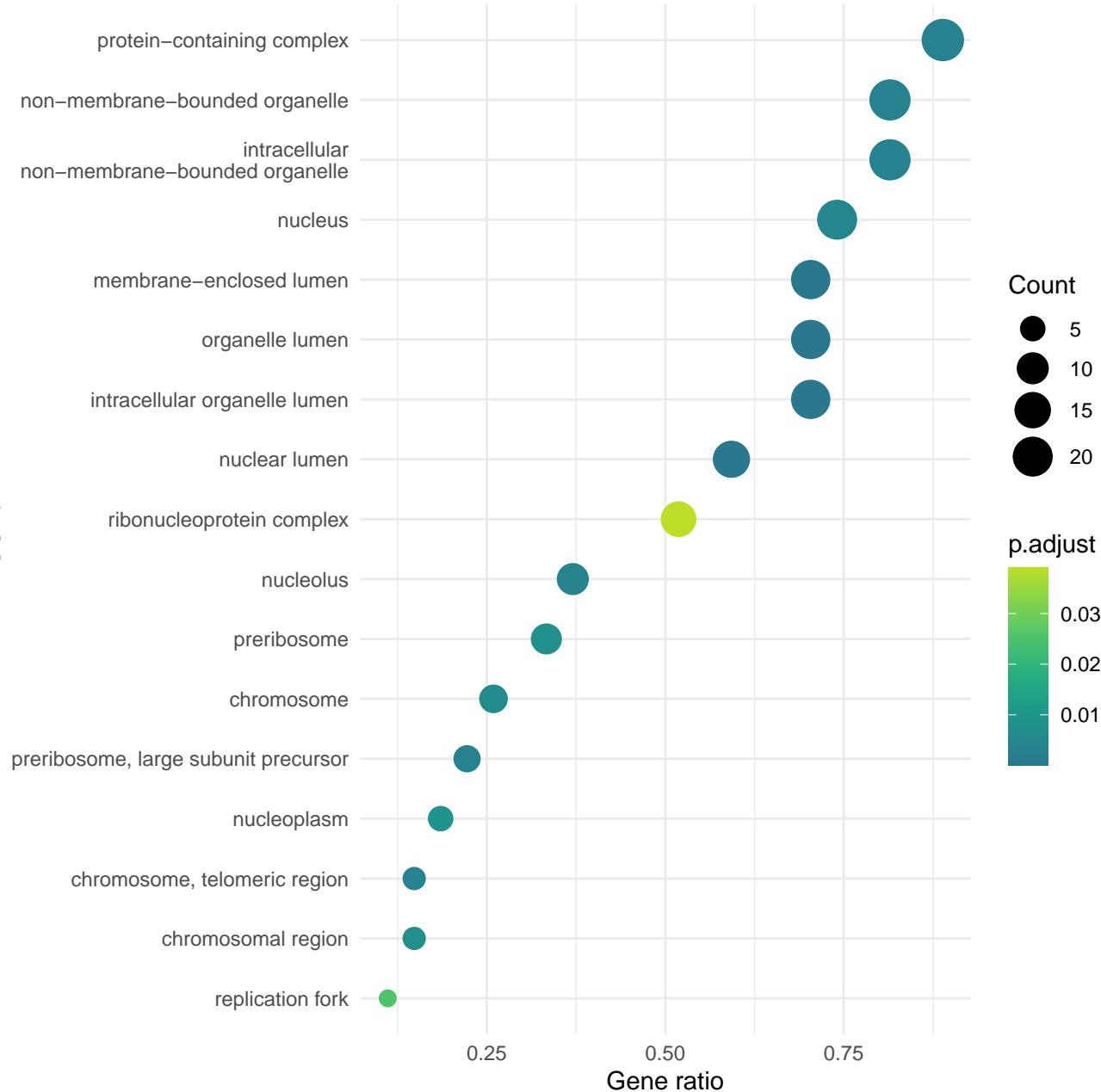
GBP2-TAP Up-regulated



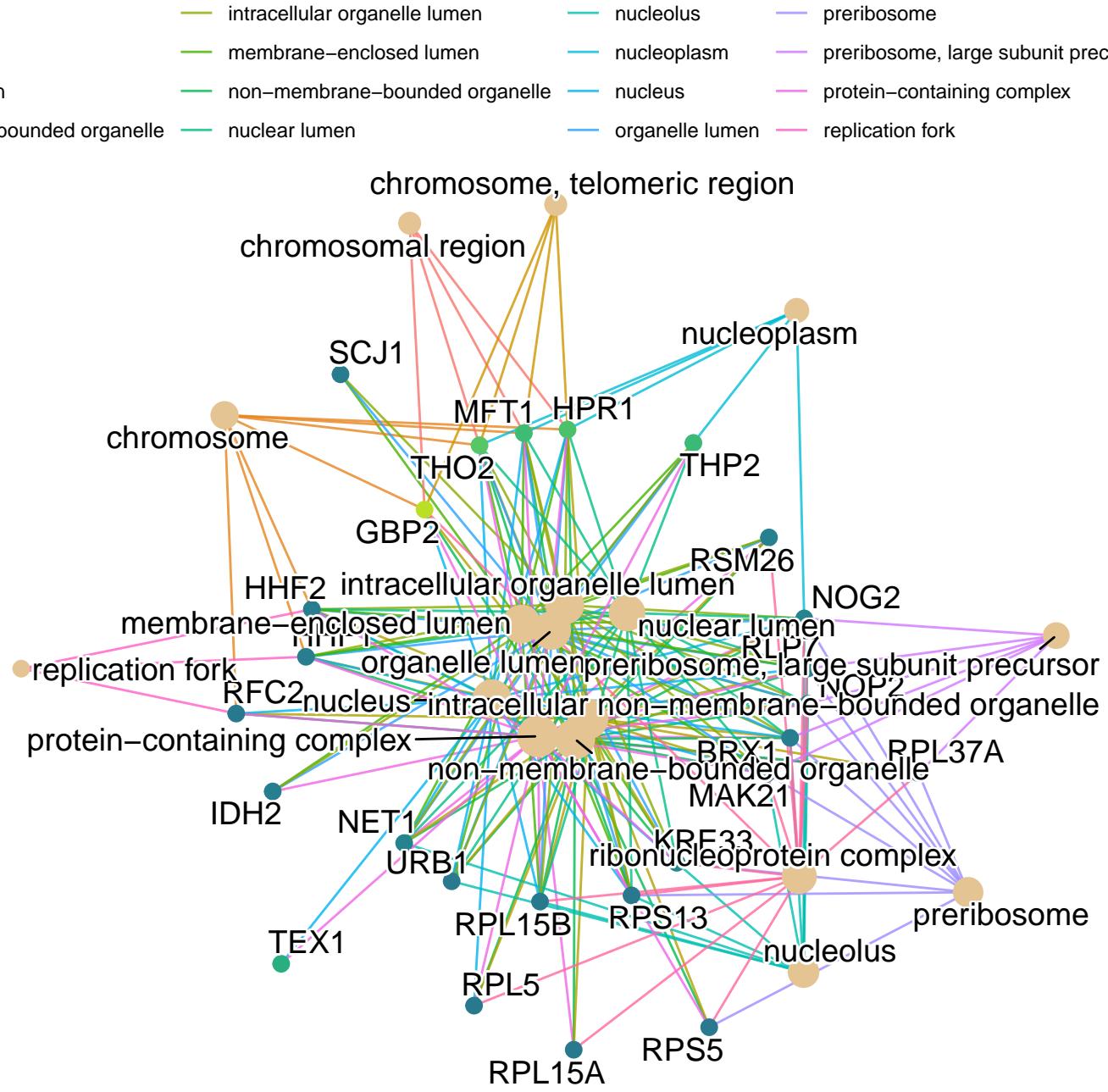
GBP2-TAP Up-regulated GO CC barplot



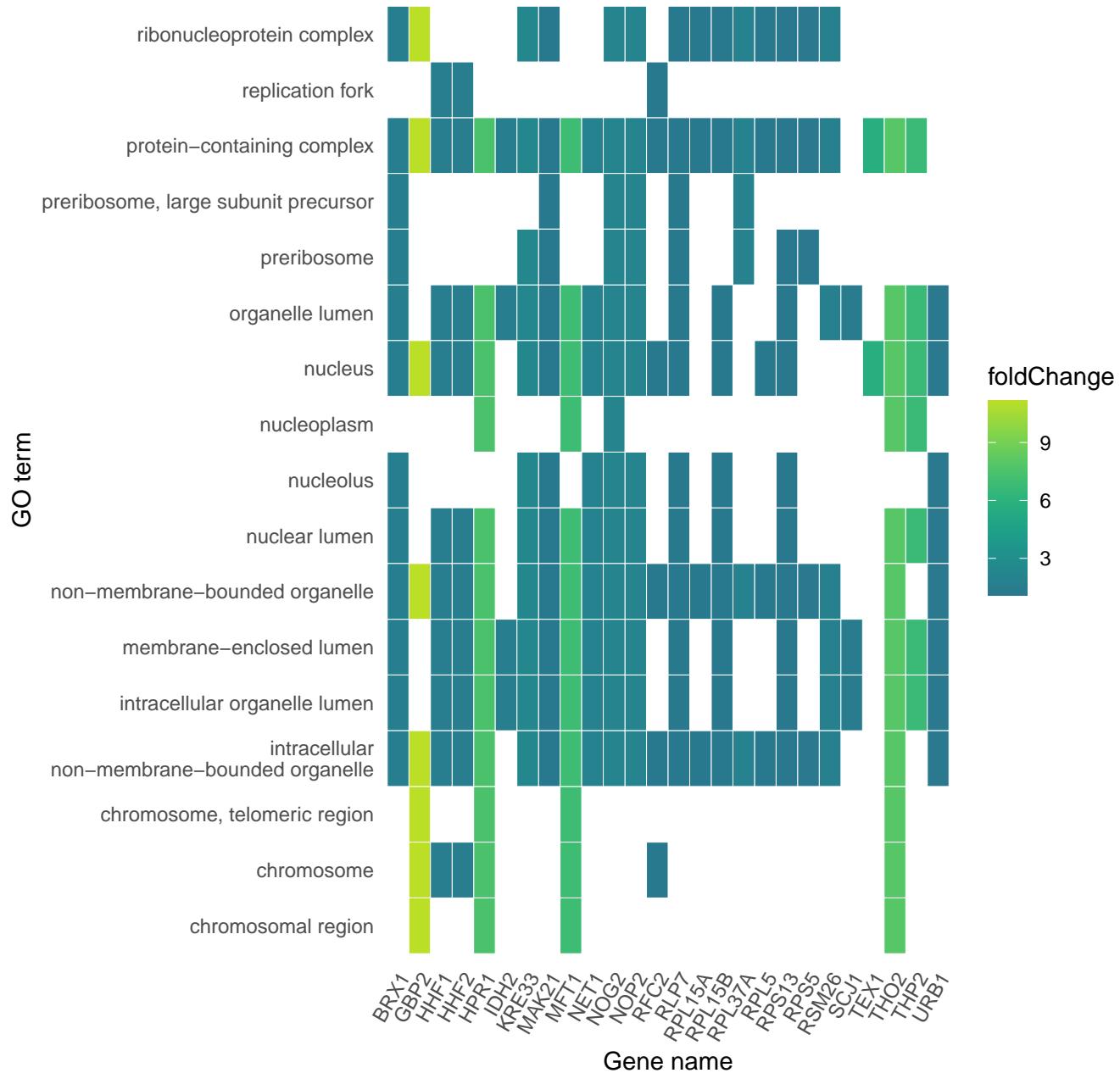
GBP2-TAP Up-regulated GO CC dotplot



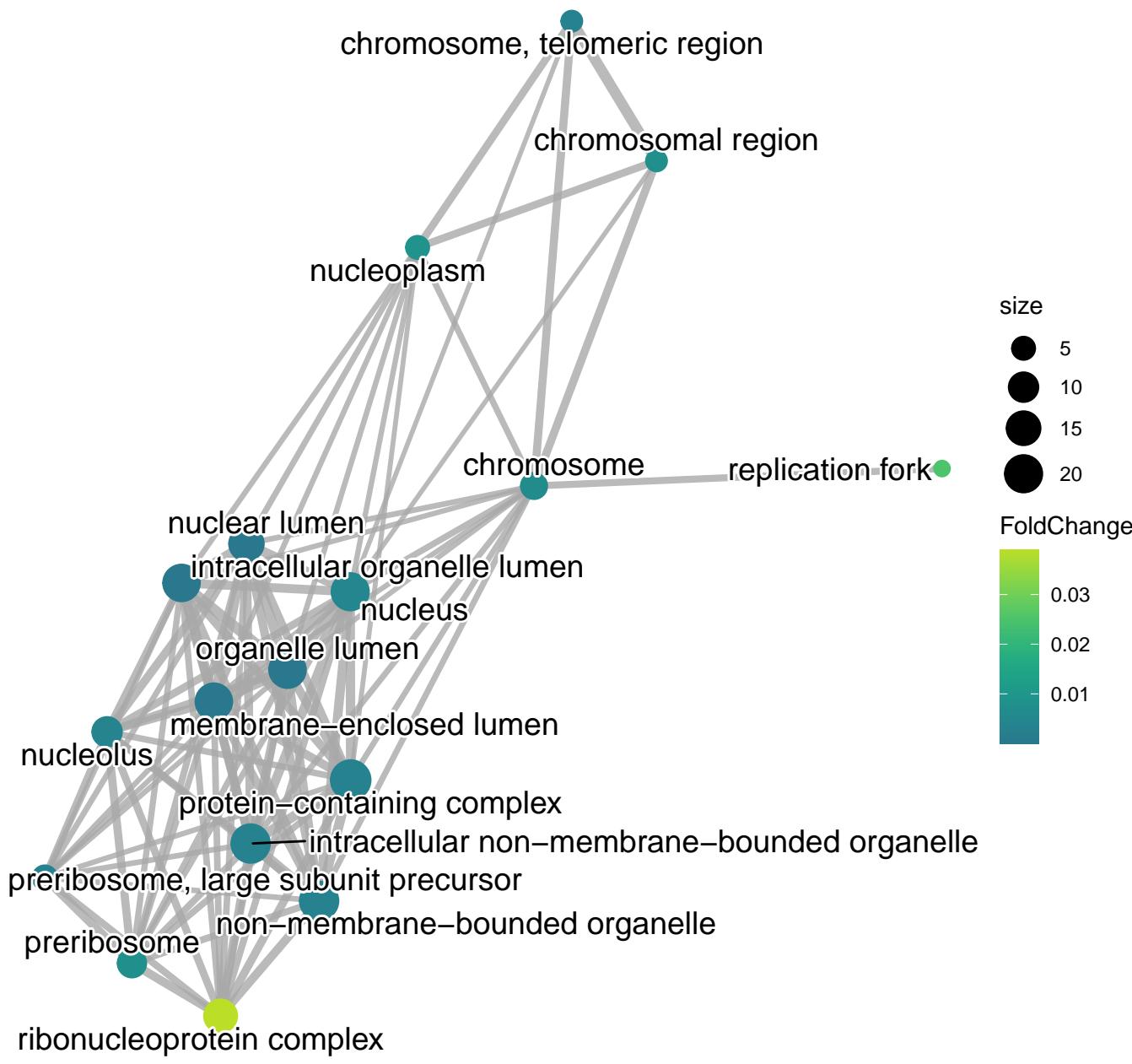
GBP2-TAP Up-regulated GO CC cnetplot

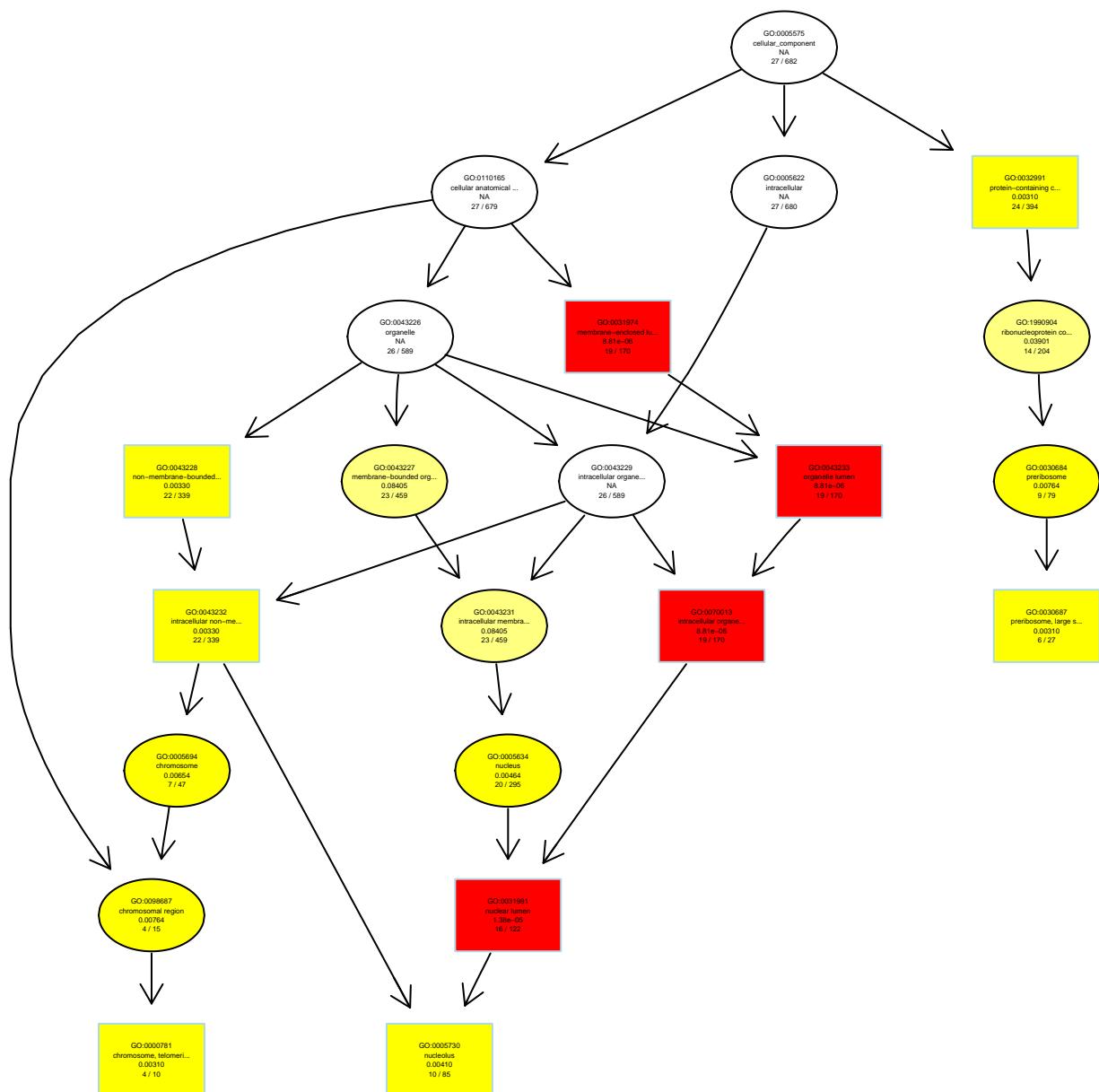


GBP2-TAP Up-regulated GO CC heatplot

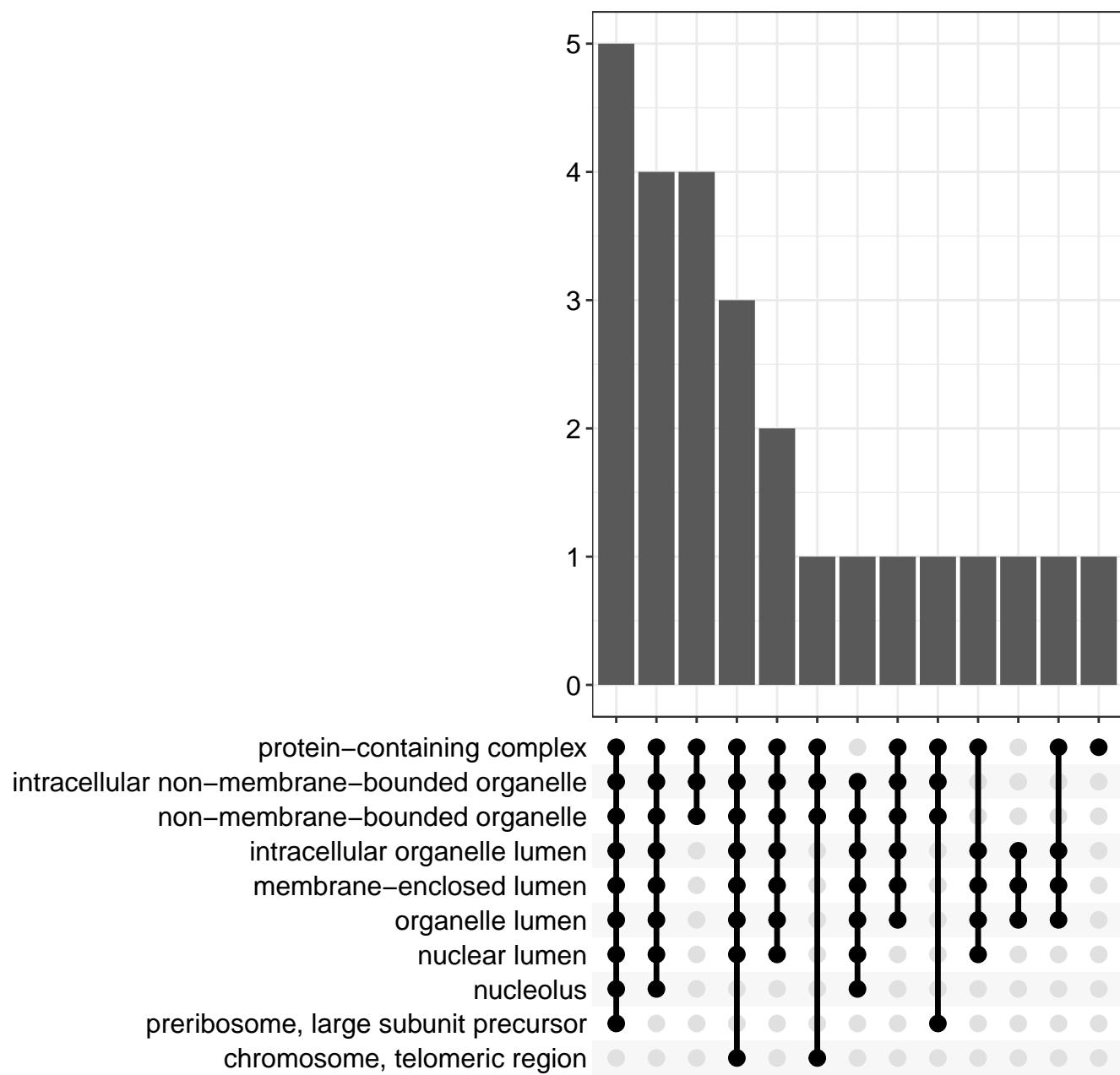


GBP2-TAP Up-regulated GO CC emapplot

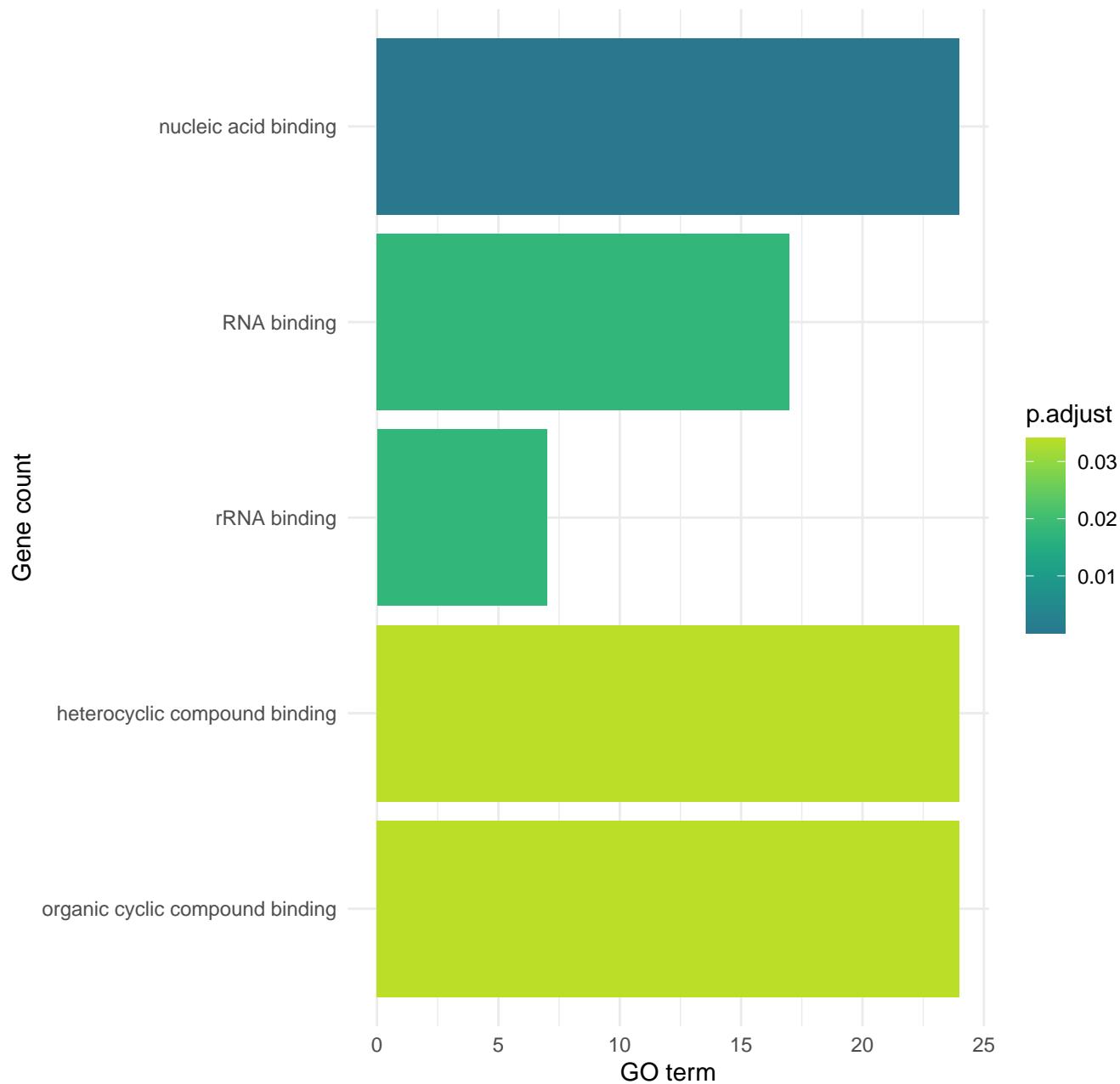




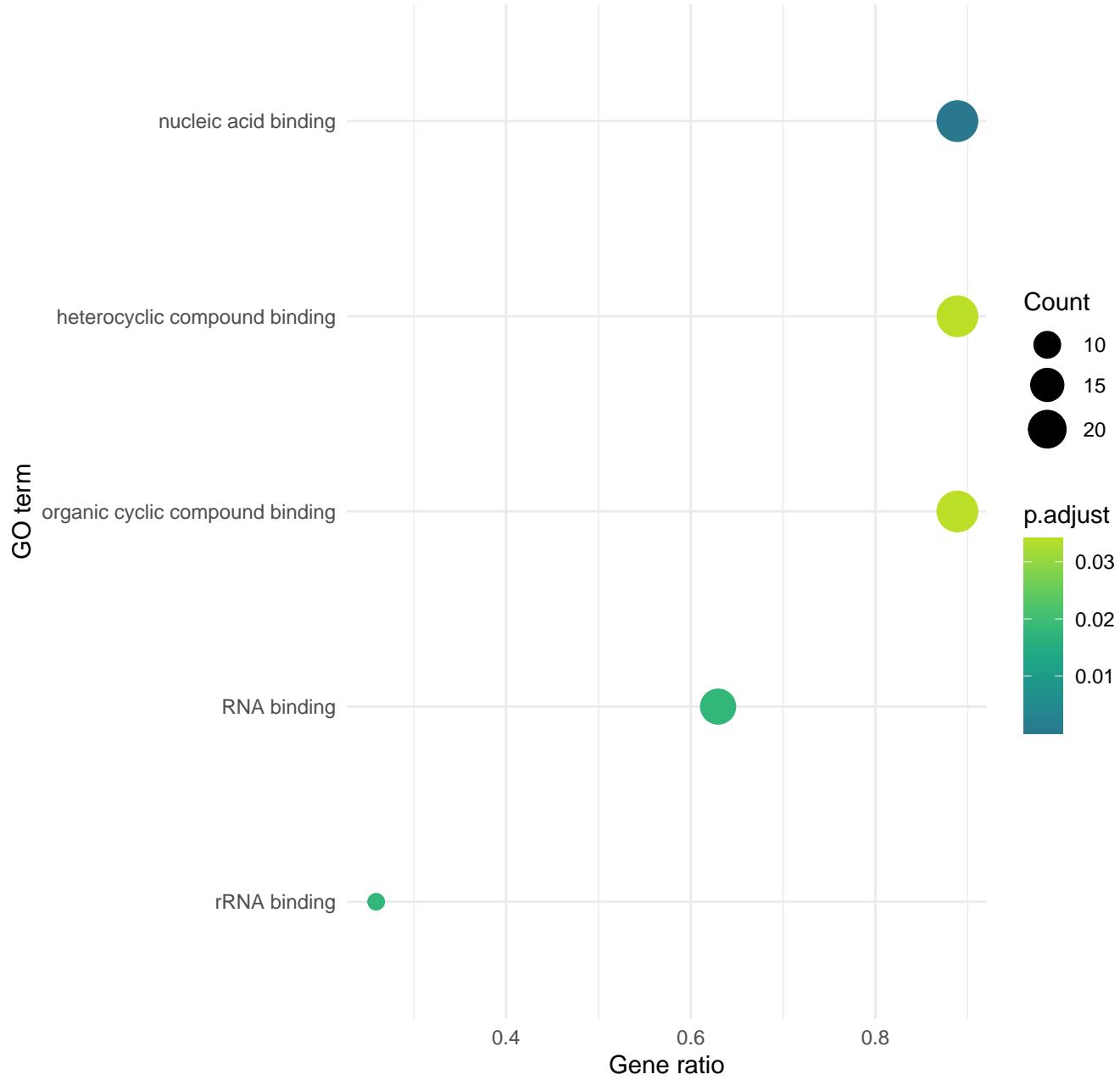
GBP2-TAP Up-regulated GO CC upsetplot



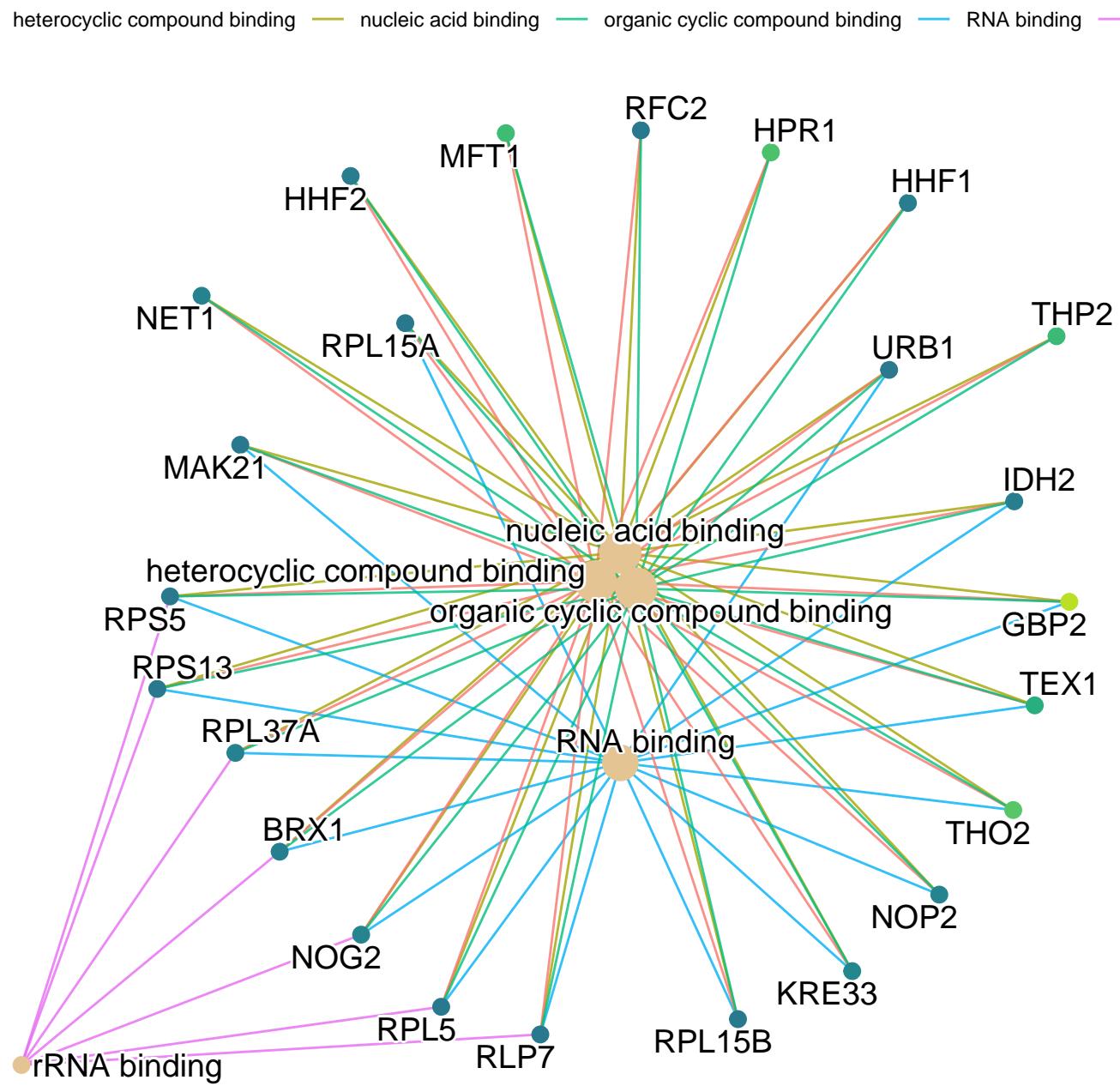
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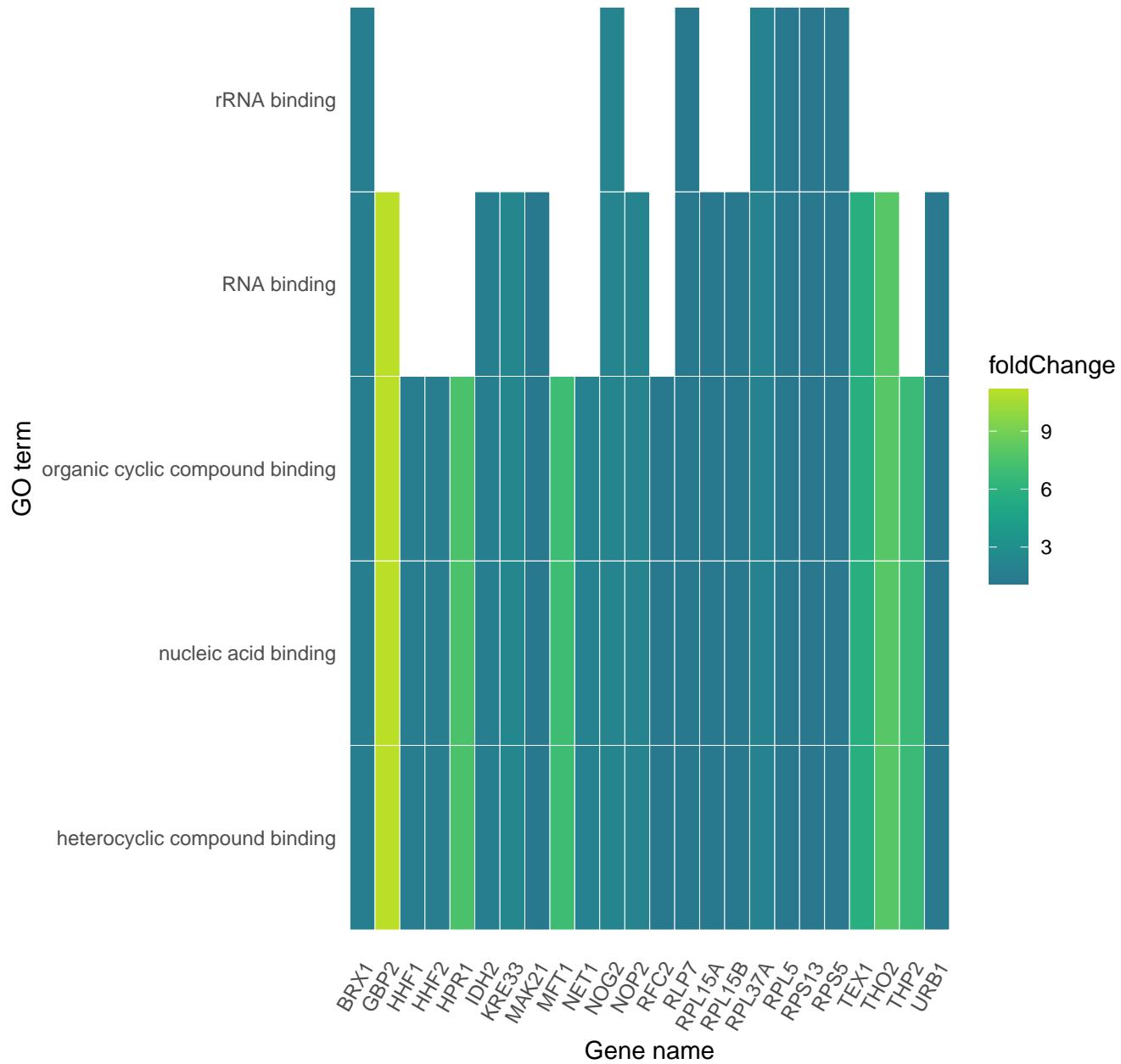
GBP2-TAP Up-regulated GO MF dotplot



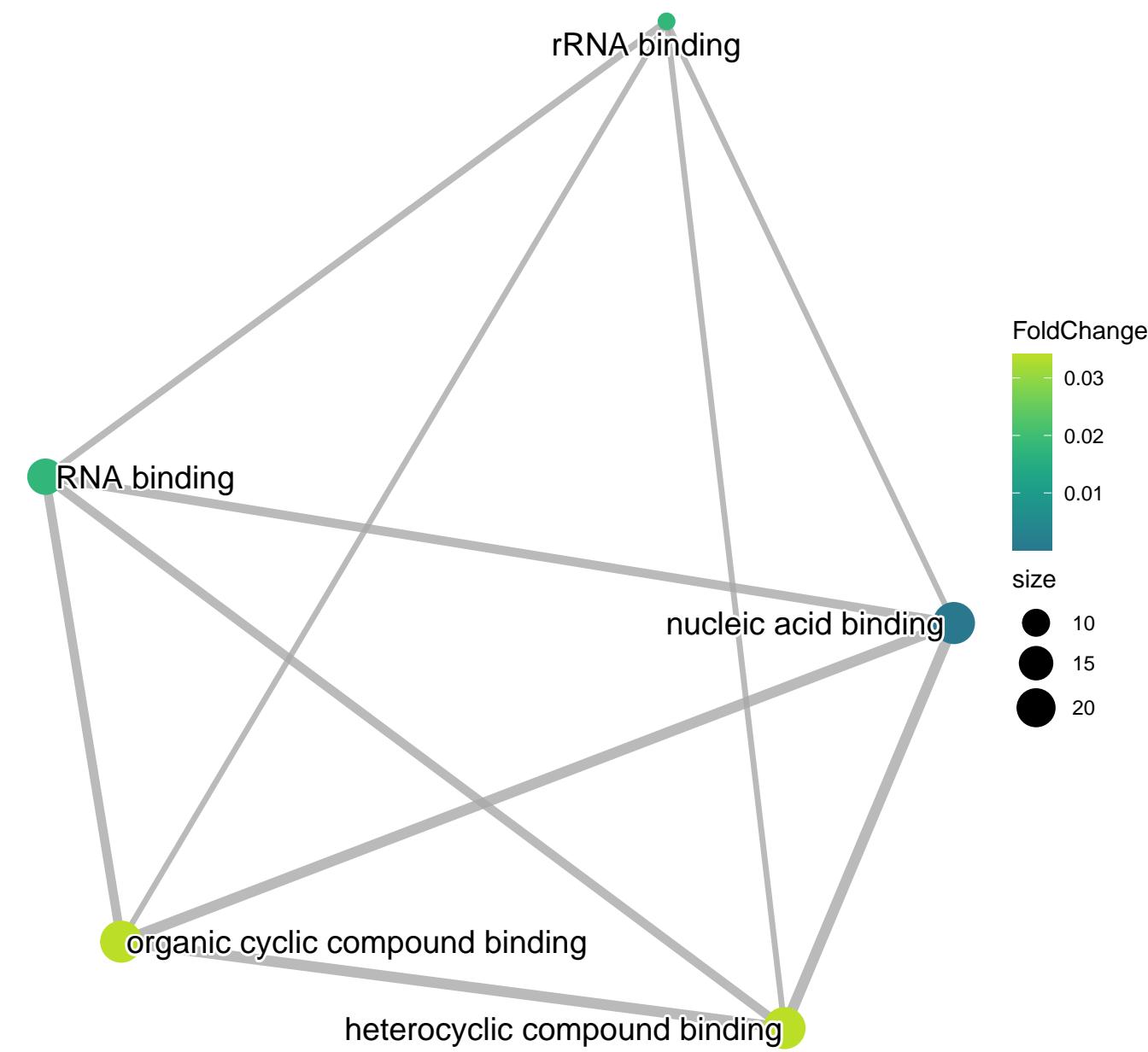
GBP2-TAP Up-regulated GO MF cnetplot

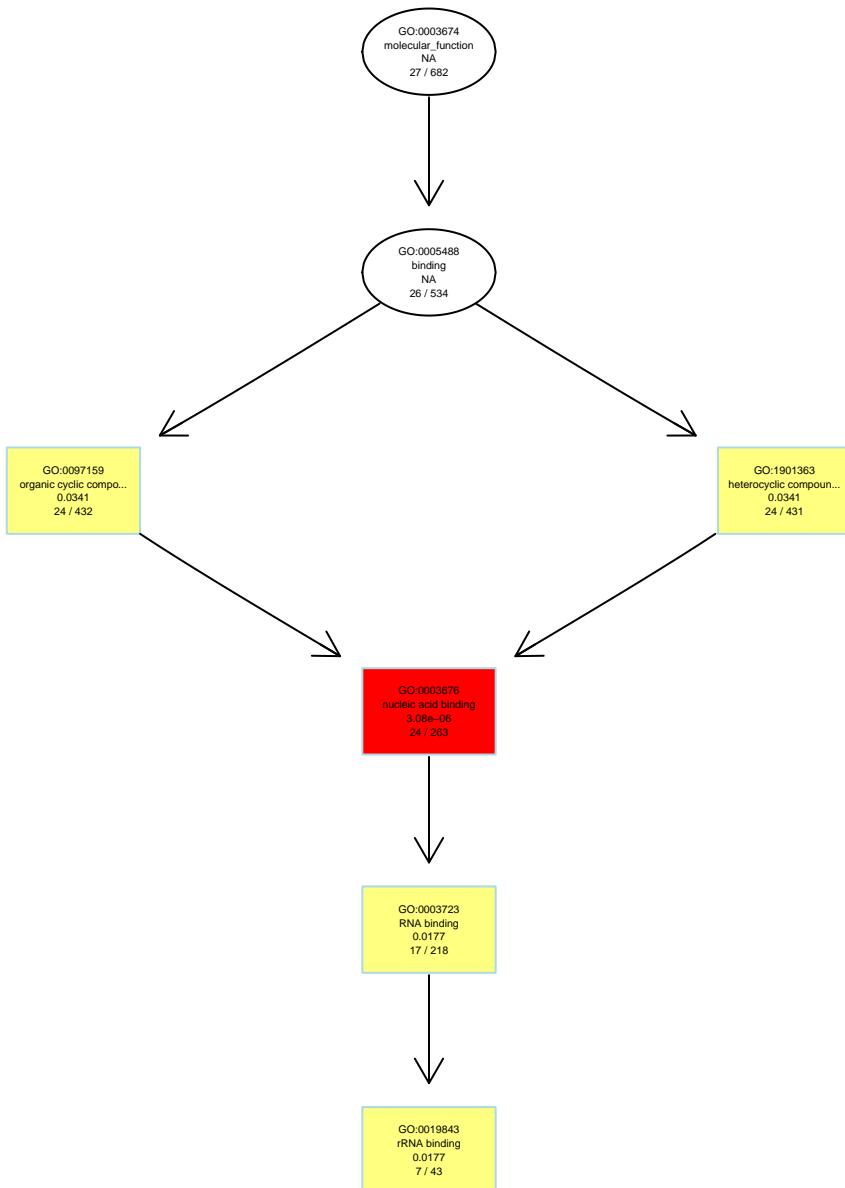


GBP2-TAP Up-regulated GO MF heatplot

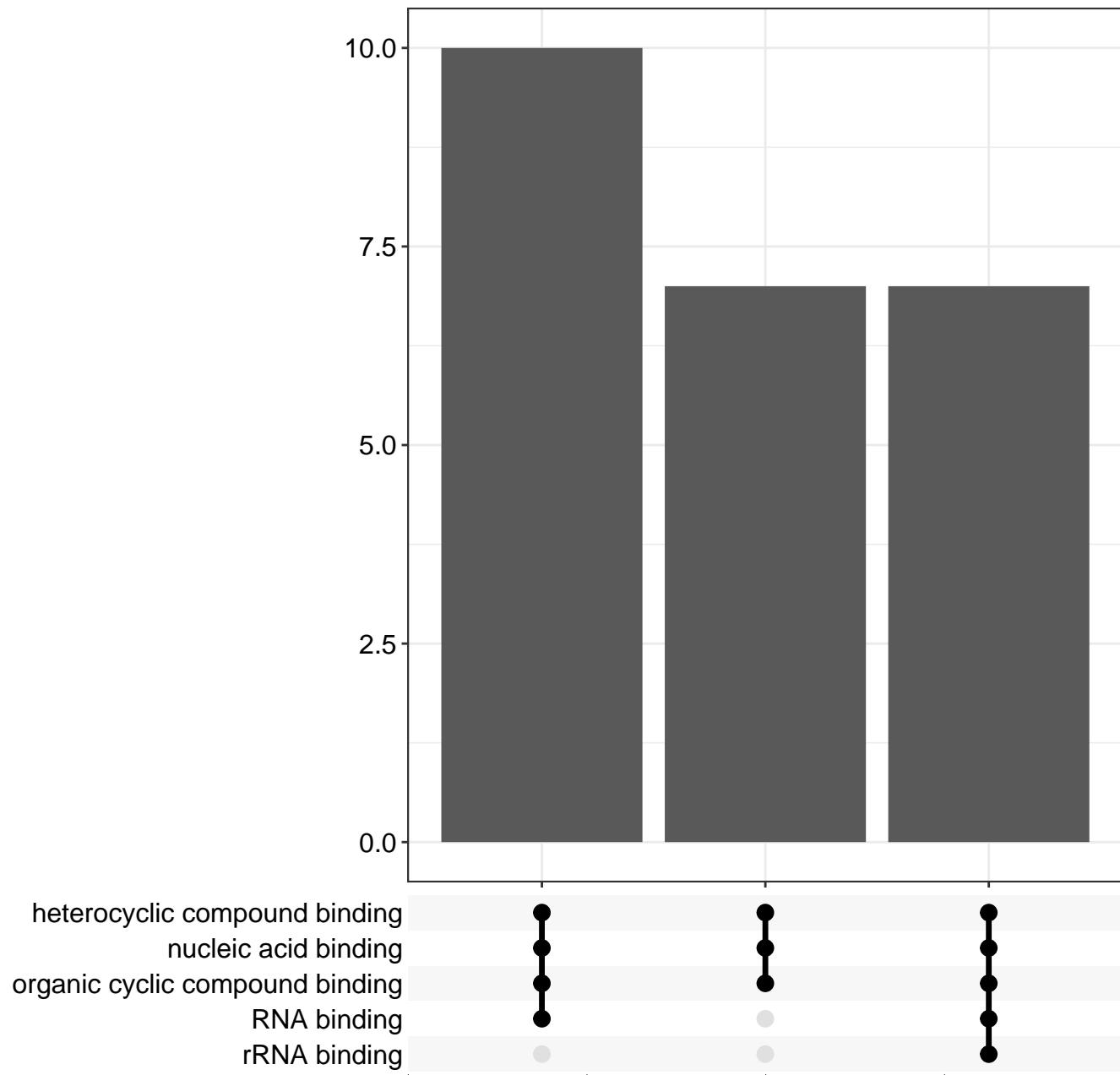


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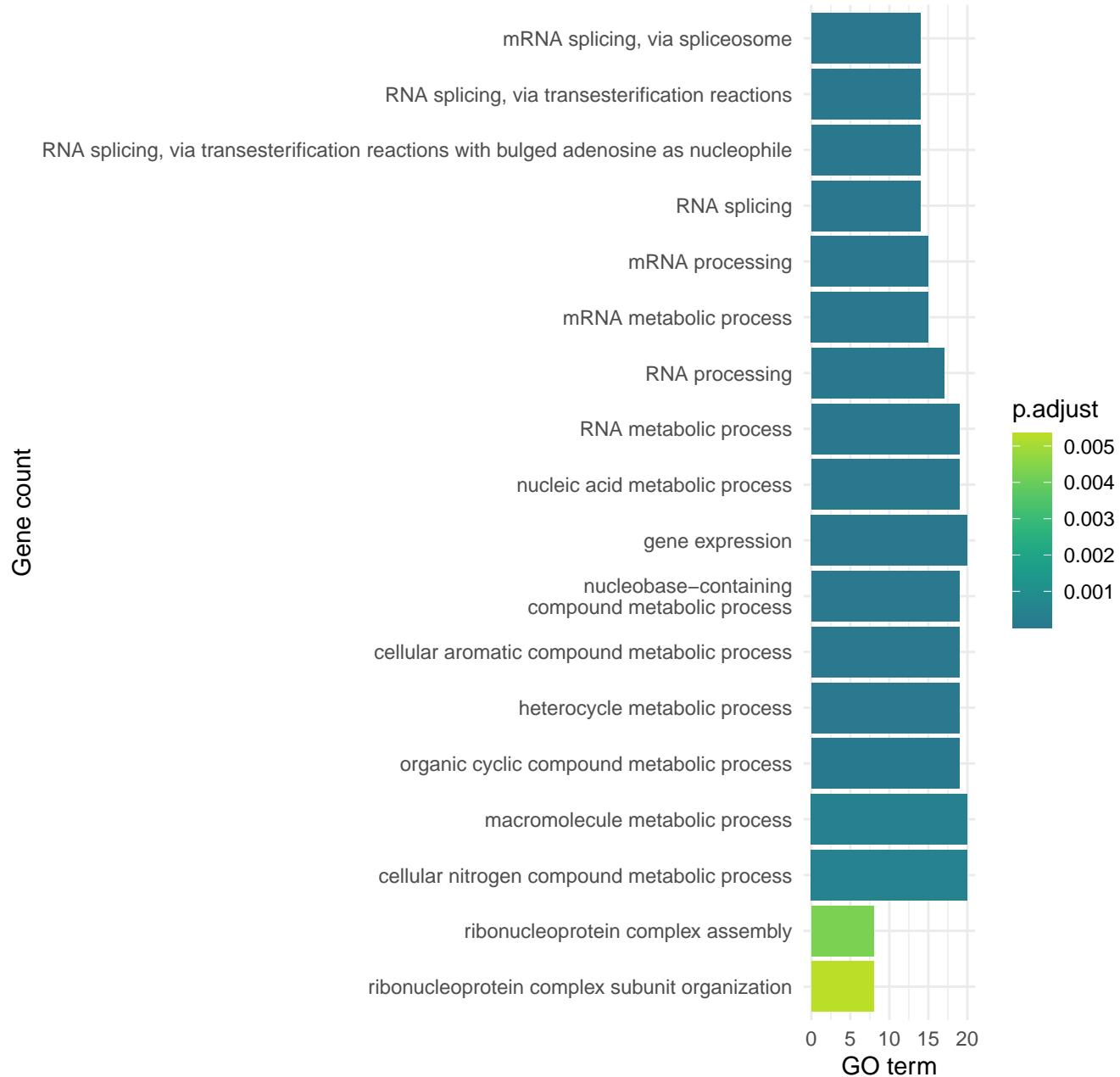




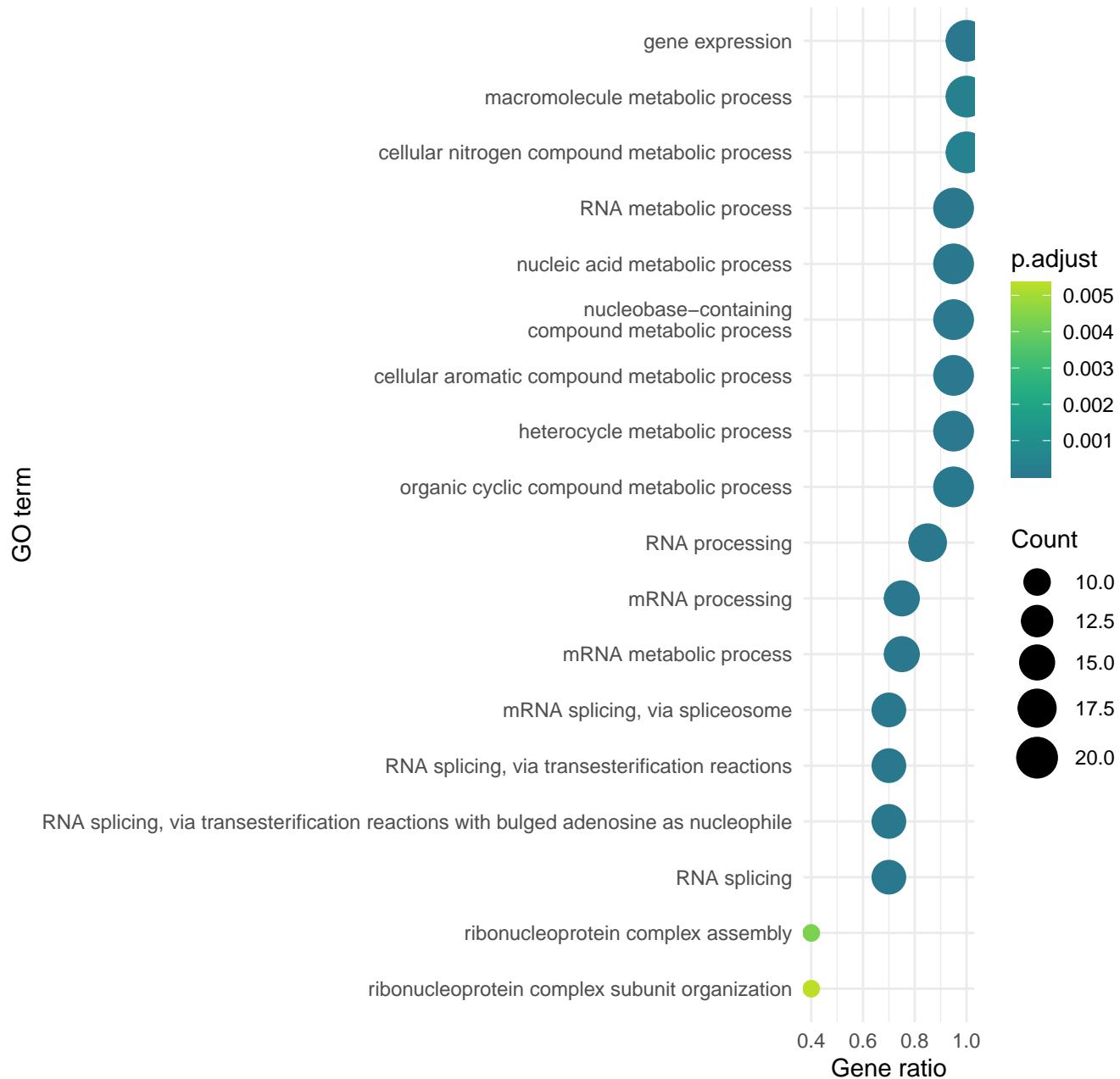
GBP2-TAP Up-regulated GO MF upsetplot



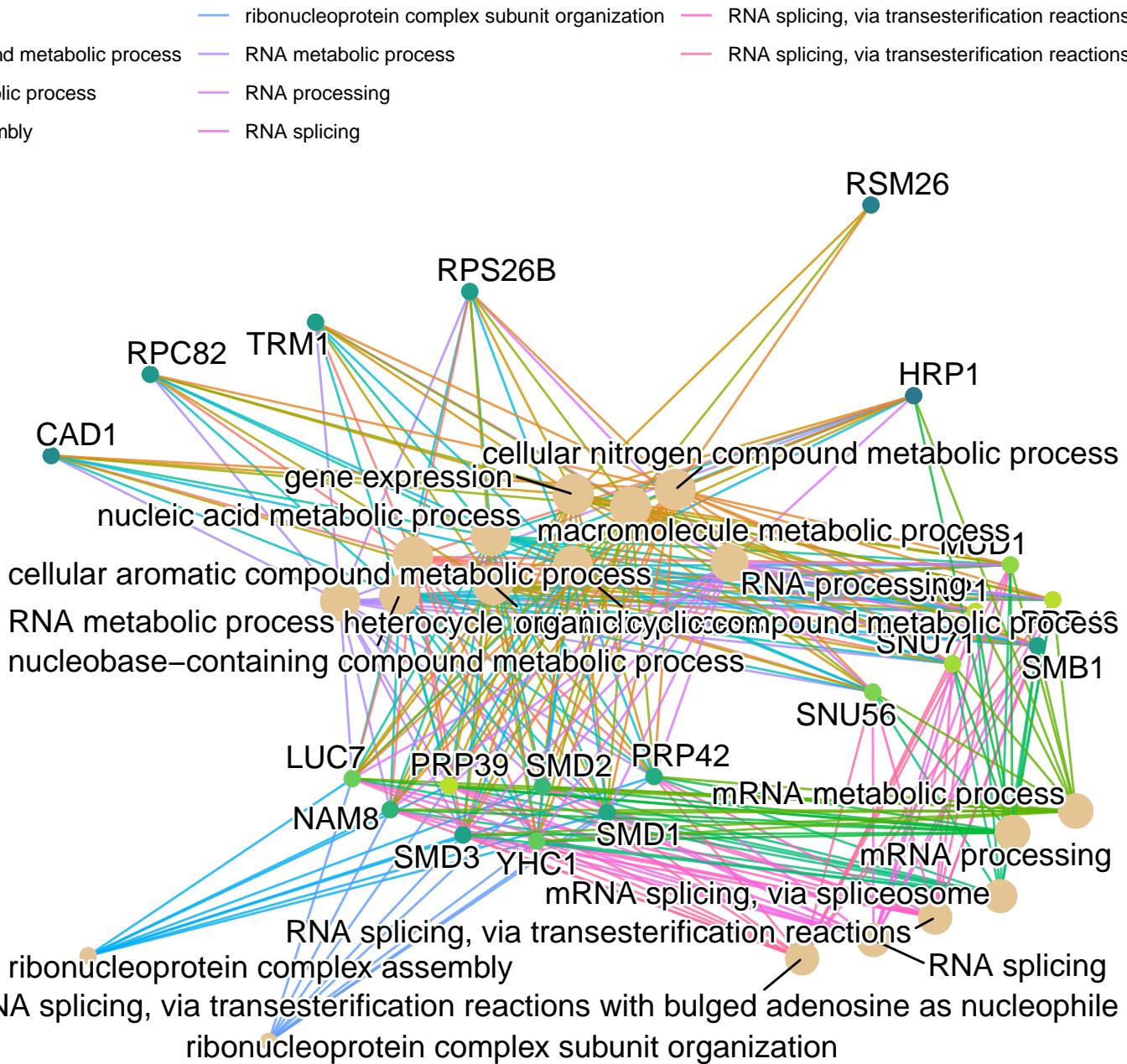
SNP1-TAP Up-regulated



SNP1-TAP Up-regulated



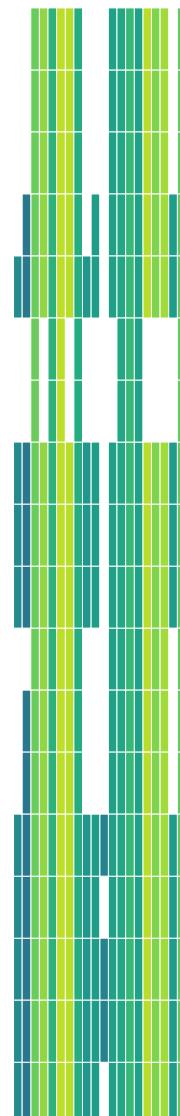
SNP1-TAP Up-regulated GO BP cnetplot



SNP1-TAP Up-regulated

GO term

RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
RNA splicing, via transesterification reactions
RNA splicing
RNA processing
RNA metabolic process
ribonucleoprotein complex subunit organization
ribonucleoprotein complex assembly
organic cyclic compound metabolic process
nucleobase-containing compound metabolic process
nucleic acid metabolic process
mRNA splicing, via spliceosome
mRNA processing
mRNA metabolic process
macromolecule metabolic process
heterocycle metabolic process
gene expression
cellular nitrogen compound metabolic process
cellular aromatic compound metabolic process



Gene name

SNP1-TAP Up-regulated GO BP emapplot

gene expression

heterocycle metabolic process

nucleic acid metabolic process

cellular nitrogen compound metabolic process

nucleobase-containing compound metabolic process

RNA processing

RNA metabolic process

mRNA metabolic process

macromolecule metabolic process

cellular aromatic compound metabolic process

organic cyclic compound metabolic process

RNA splicing, via transesterification reactions

ribonucleoprotein complex assembly

mRNA processing

RNA splicing

, via transesterification reactions with bulged adenosine as nucleophile

mRNA splicing, via spliceosome

ribonucleoprotein complex subunit organization

size

10.0

12.5

15.0

17.5

20.0

FoldChange

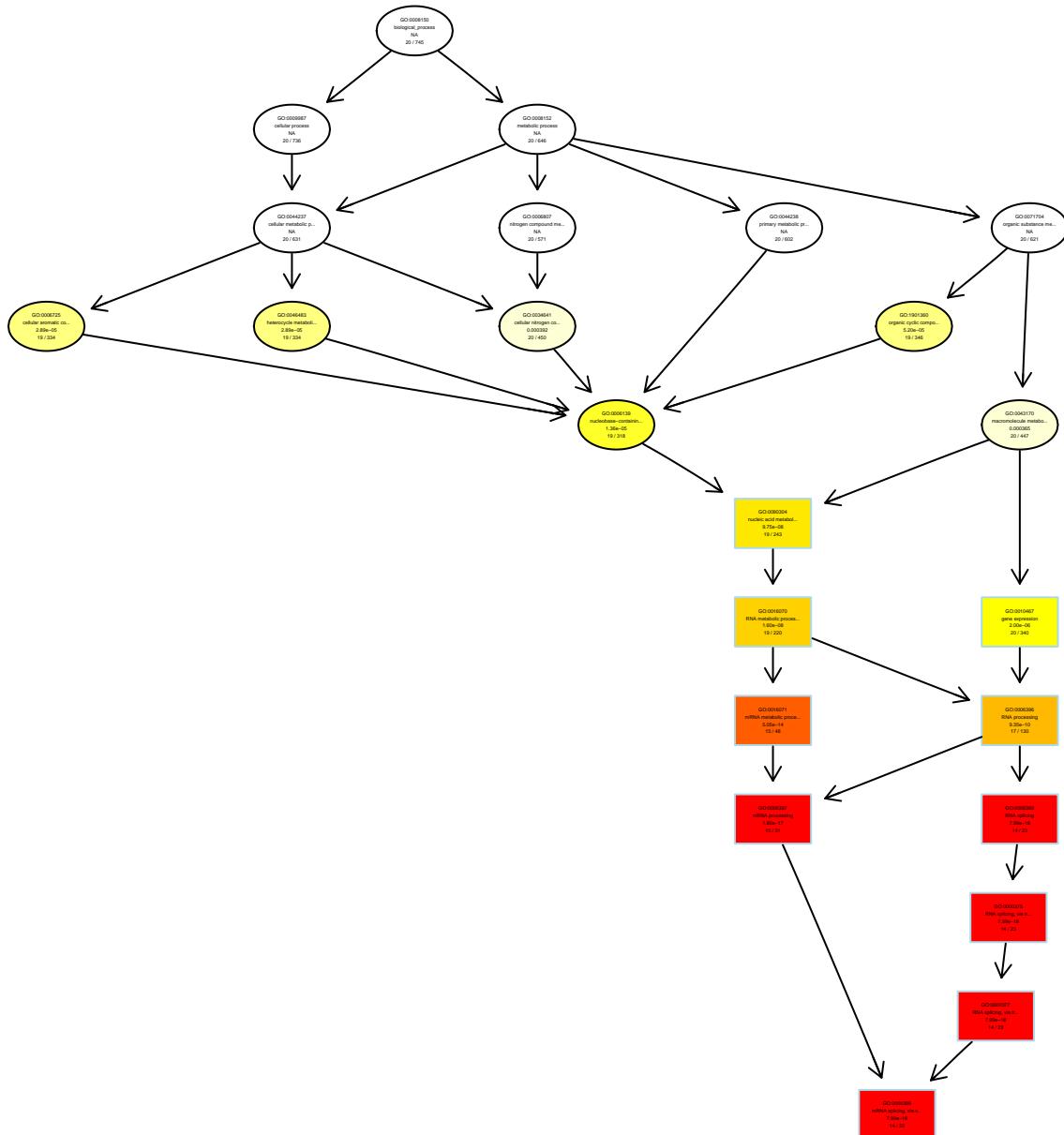
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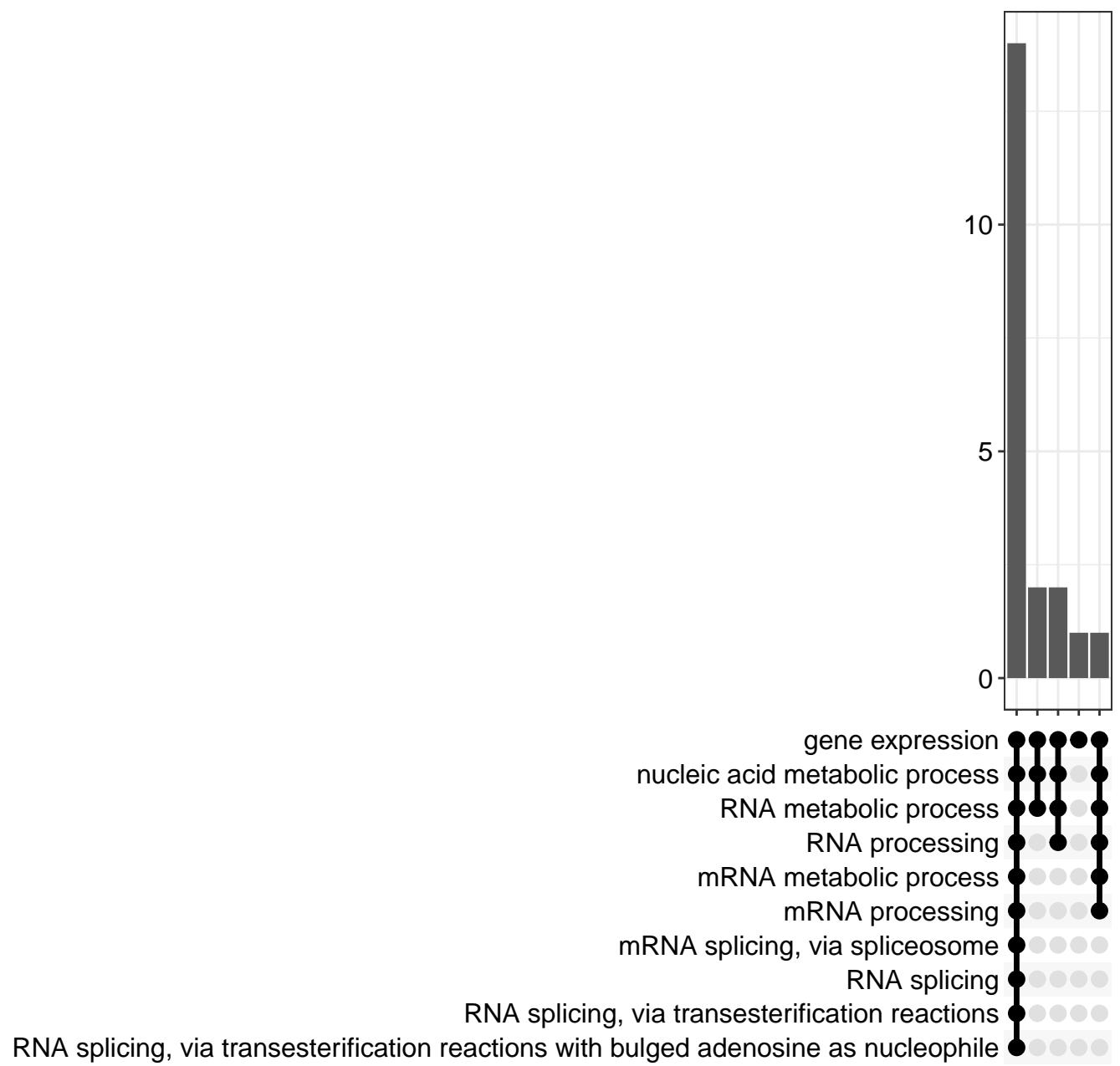
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-0.002

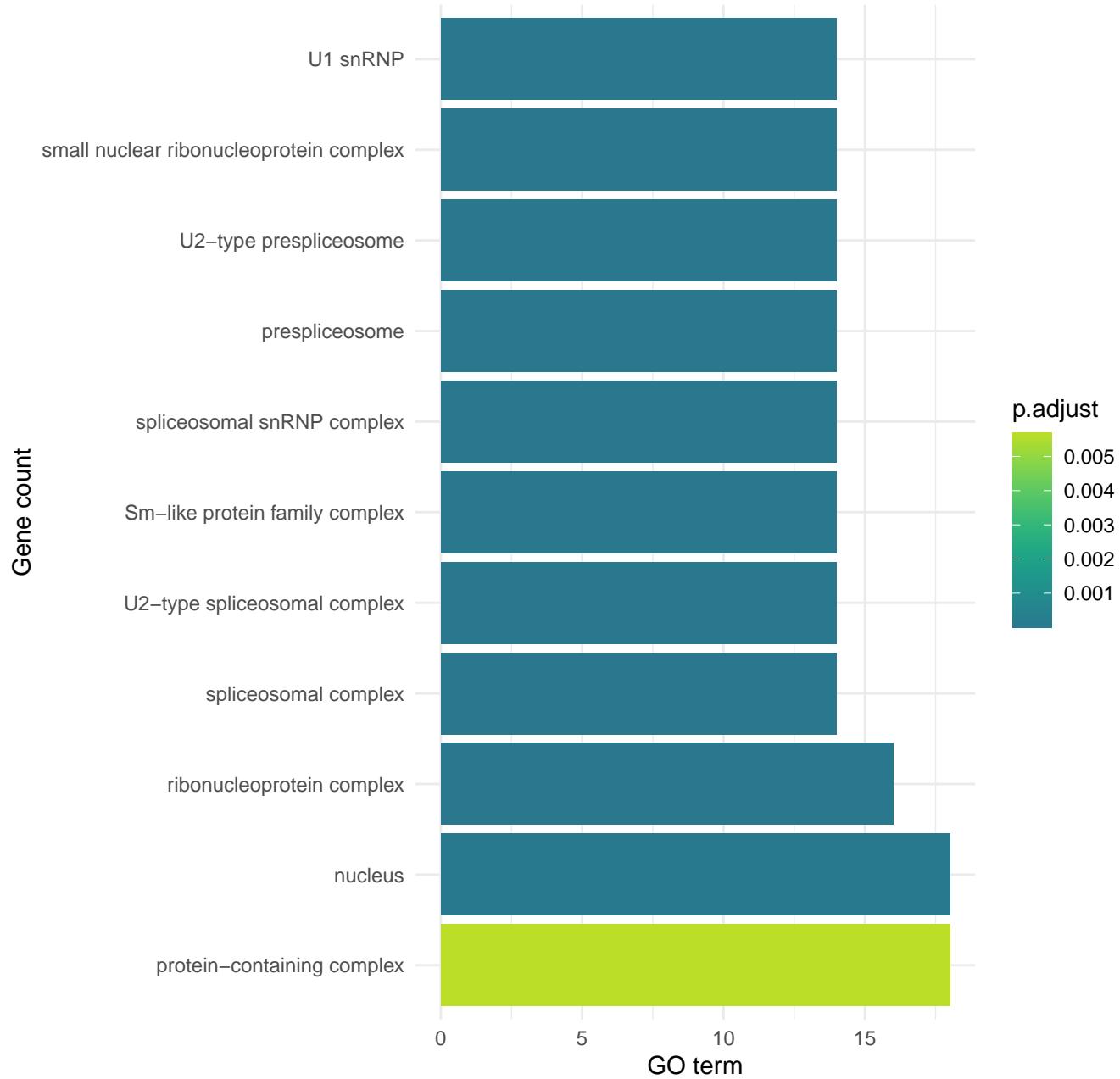
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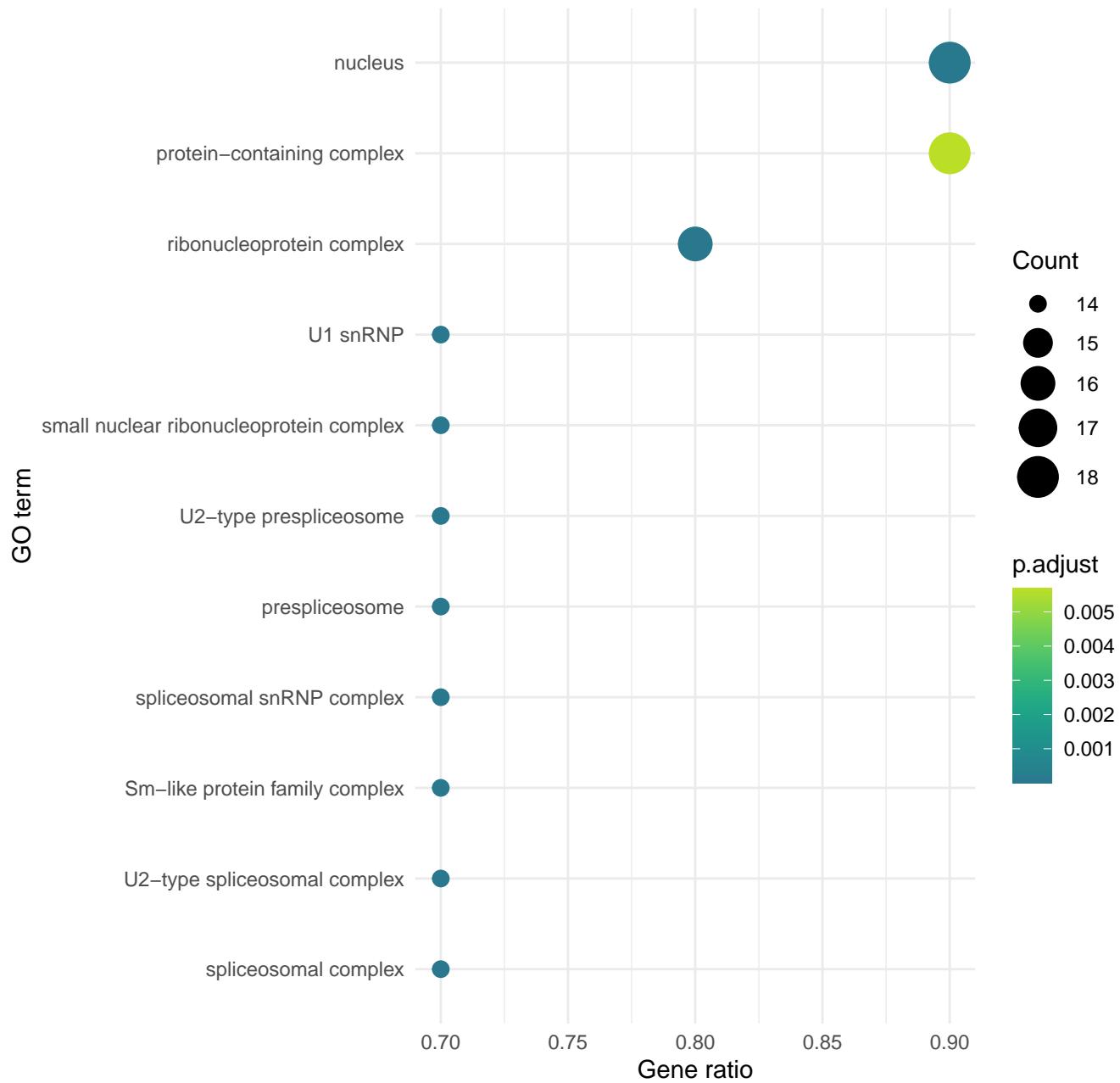
SNP1-TA



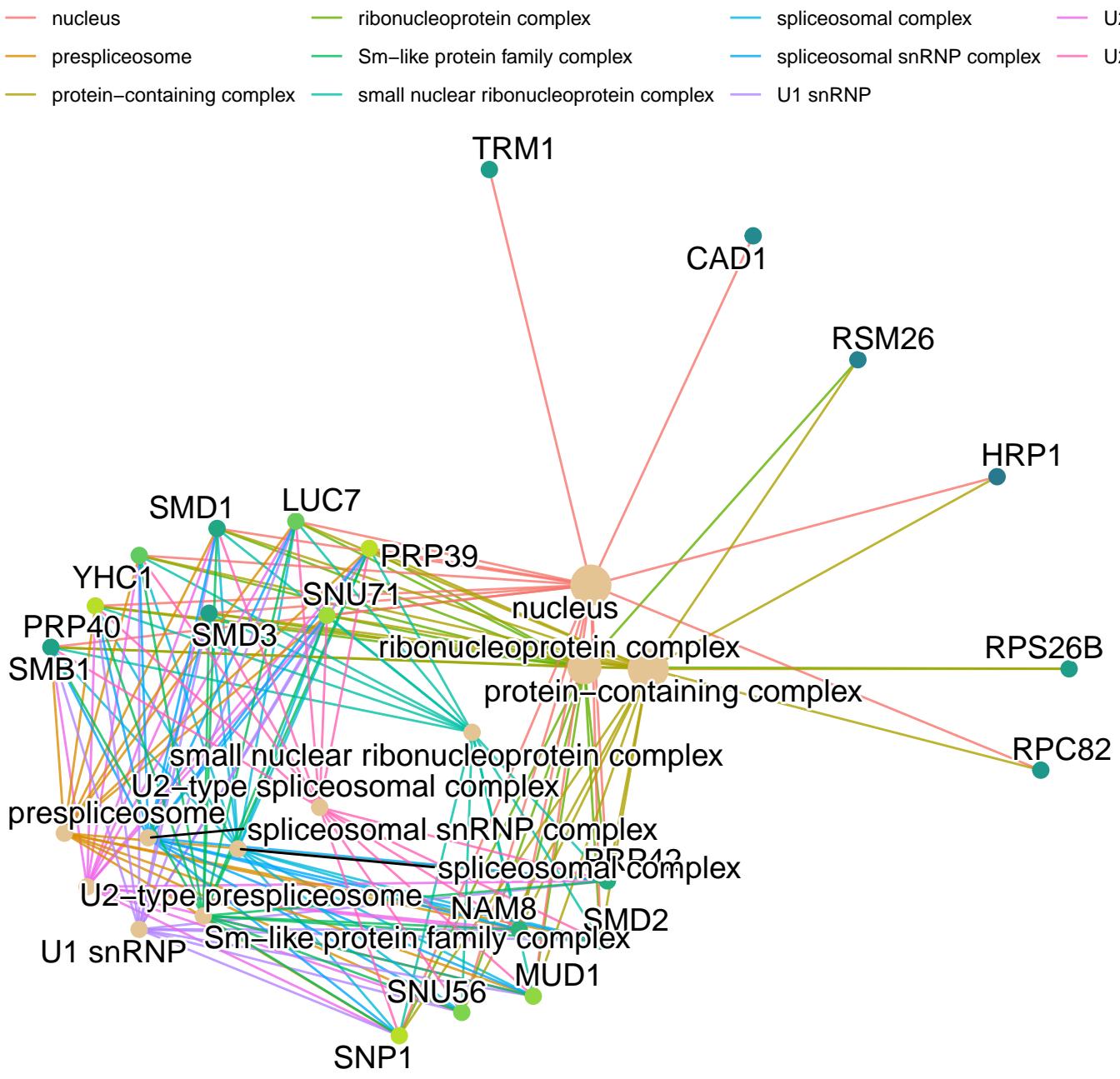
SNP1-TAP Up-regulated GO CC barplot



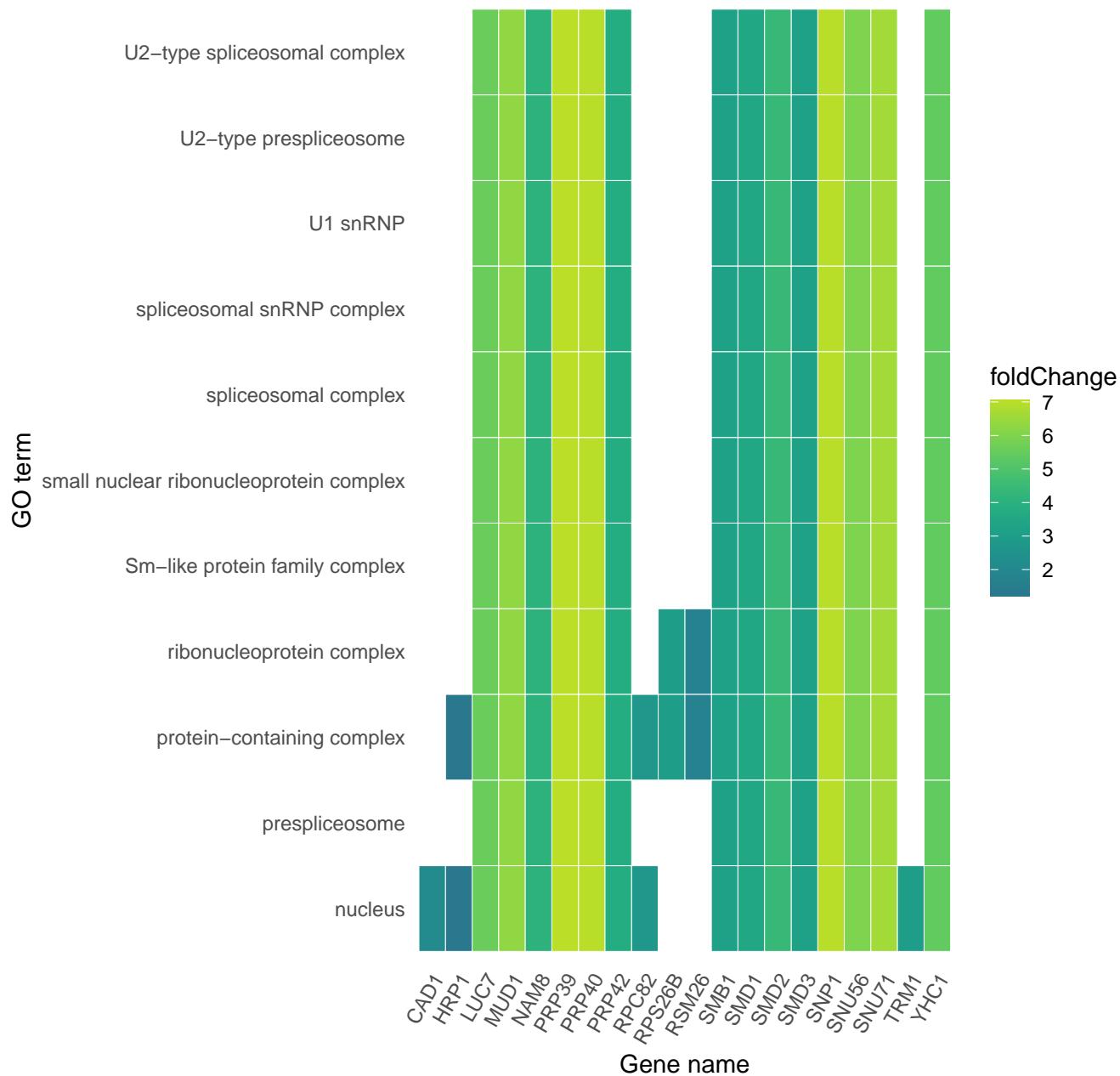
SNP1-TAP Up-regulated GO CC dotplot



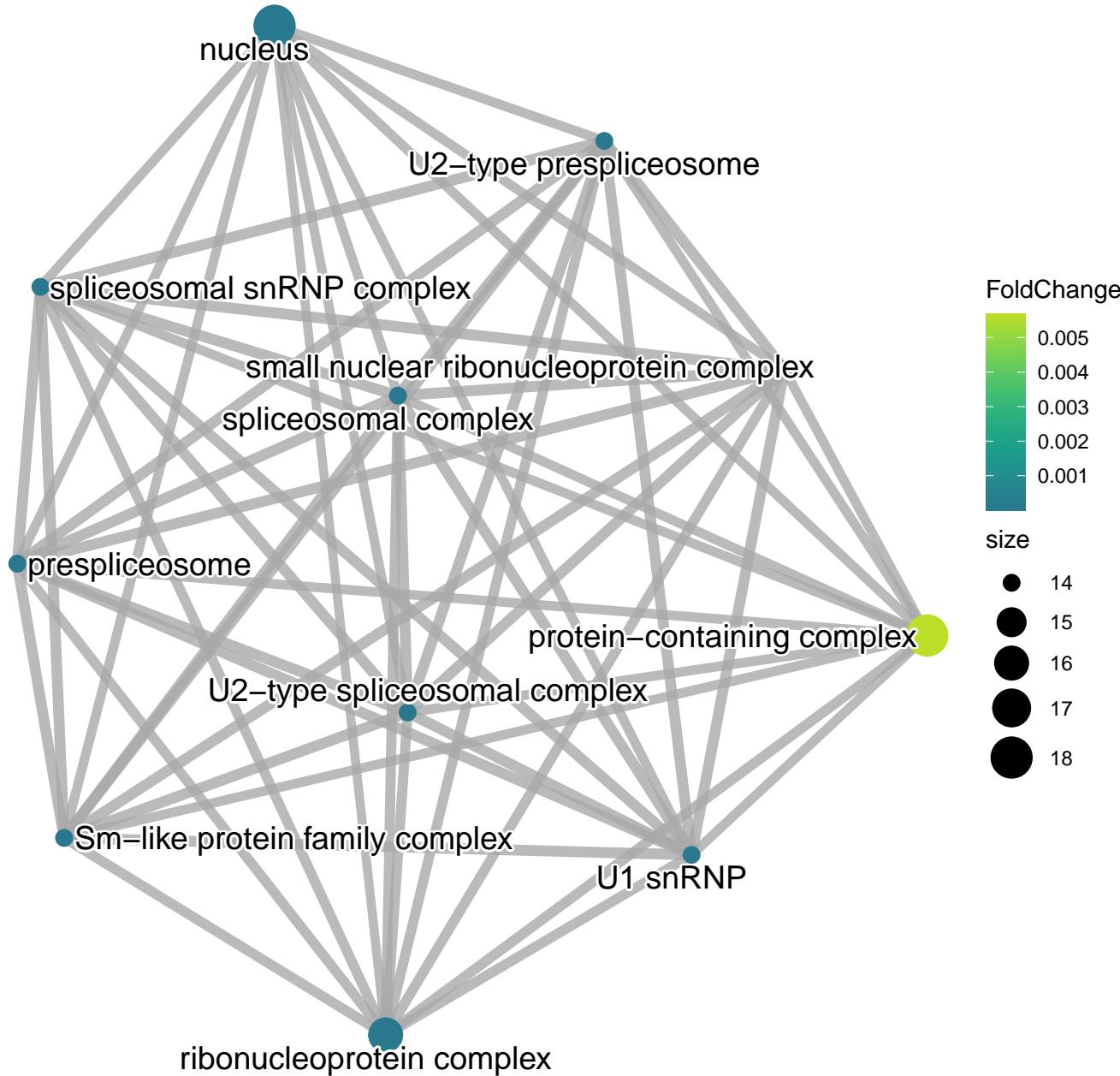
SNP1-TAP Up-regulated GO CC cnetplot

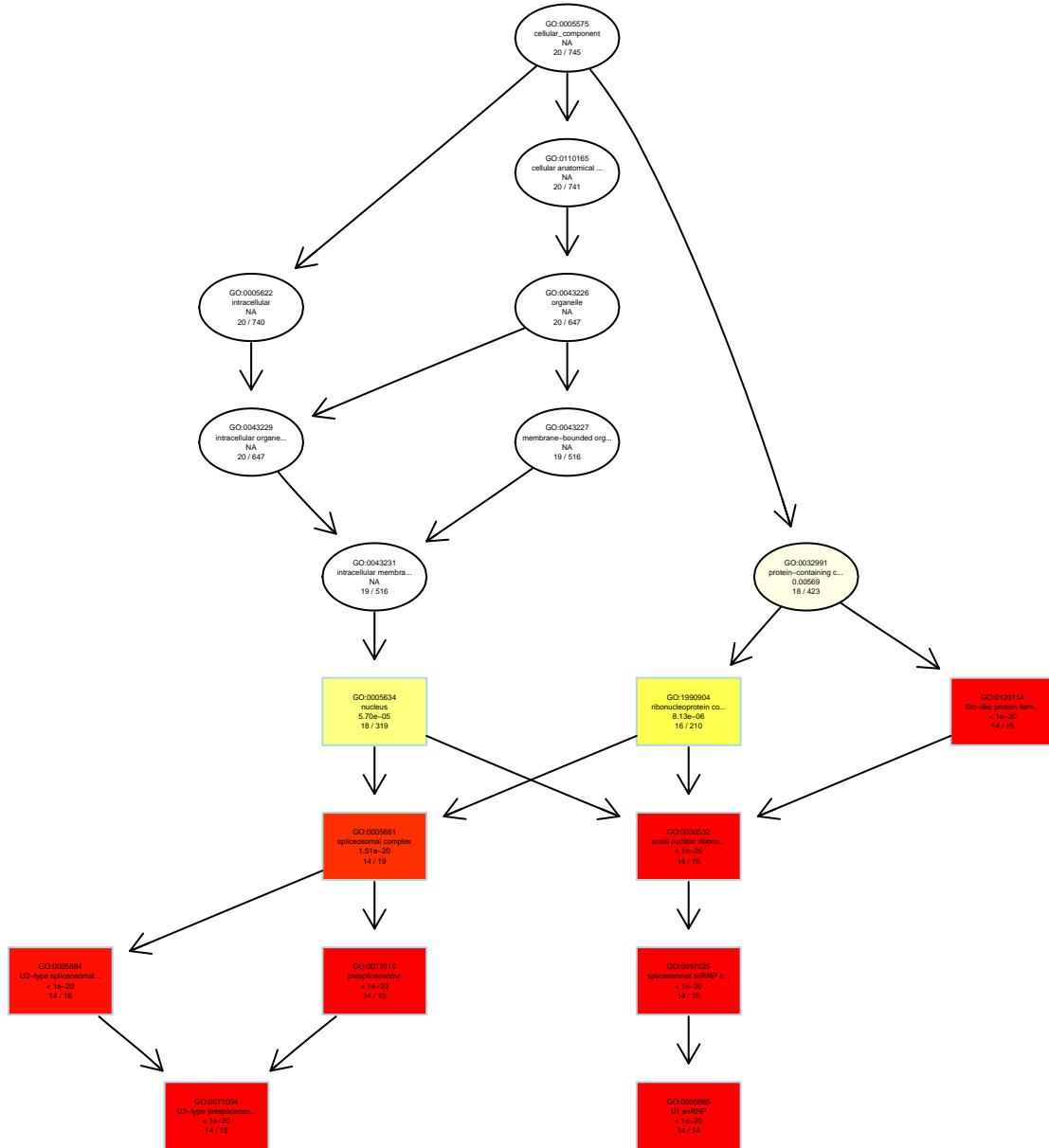


SNP1-TAP Up-regulated GO CC heatplot

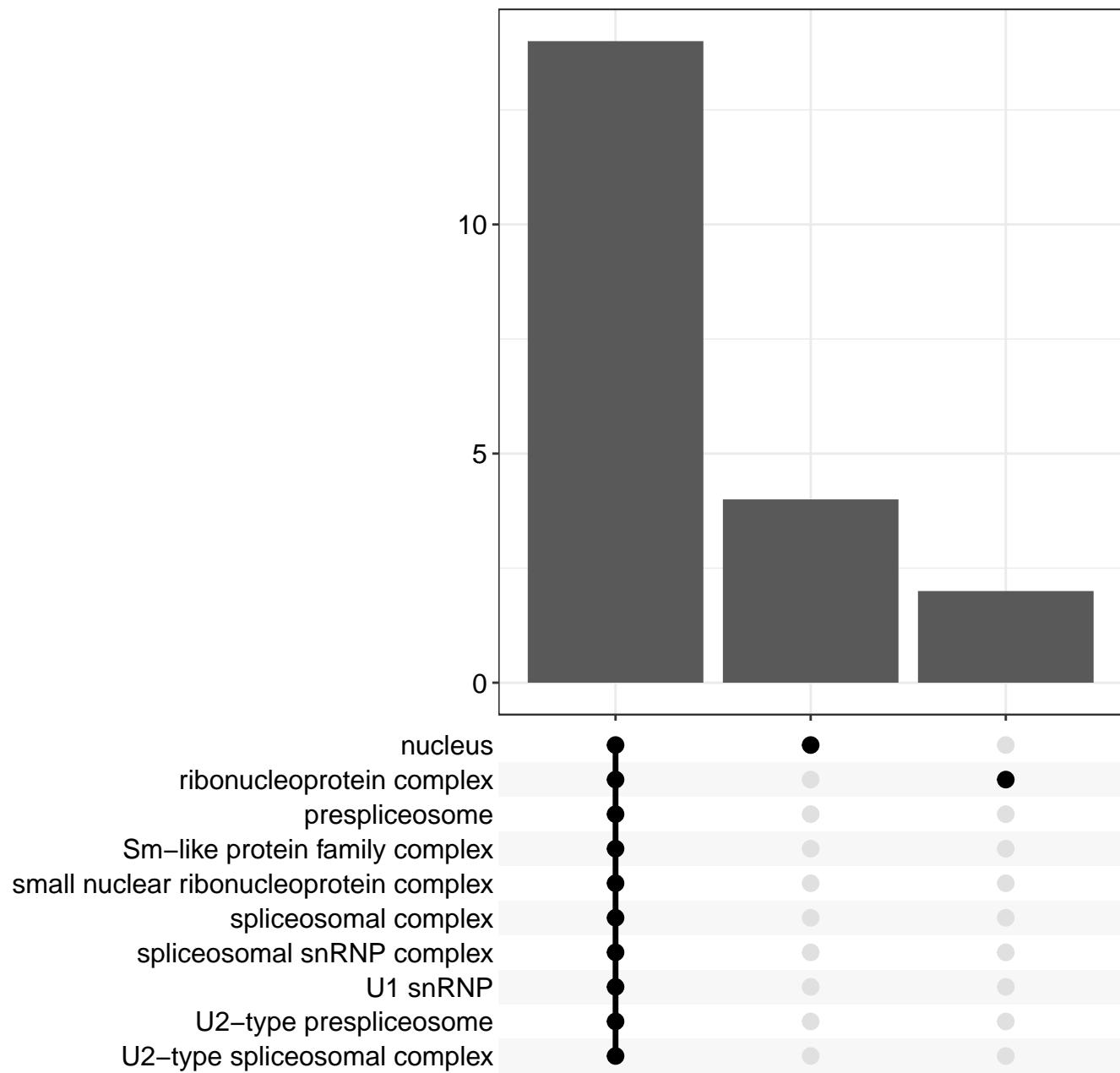


SNP1-TAP Up-regulated GO CC emapplot

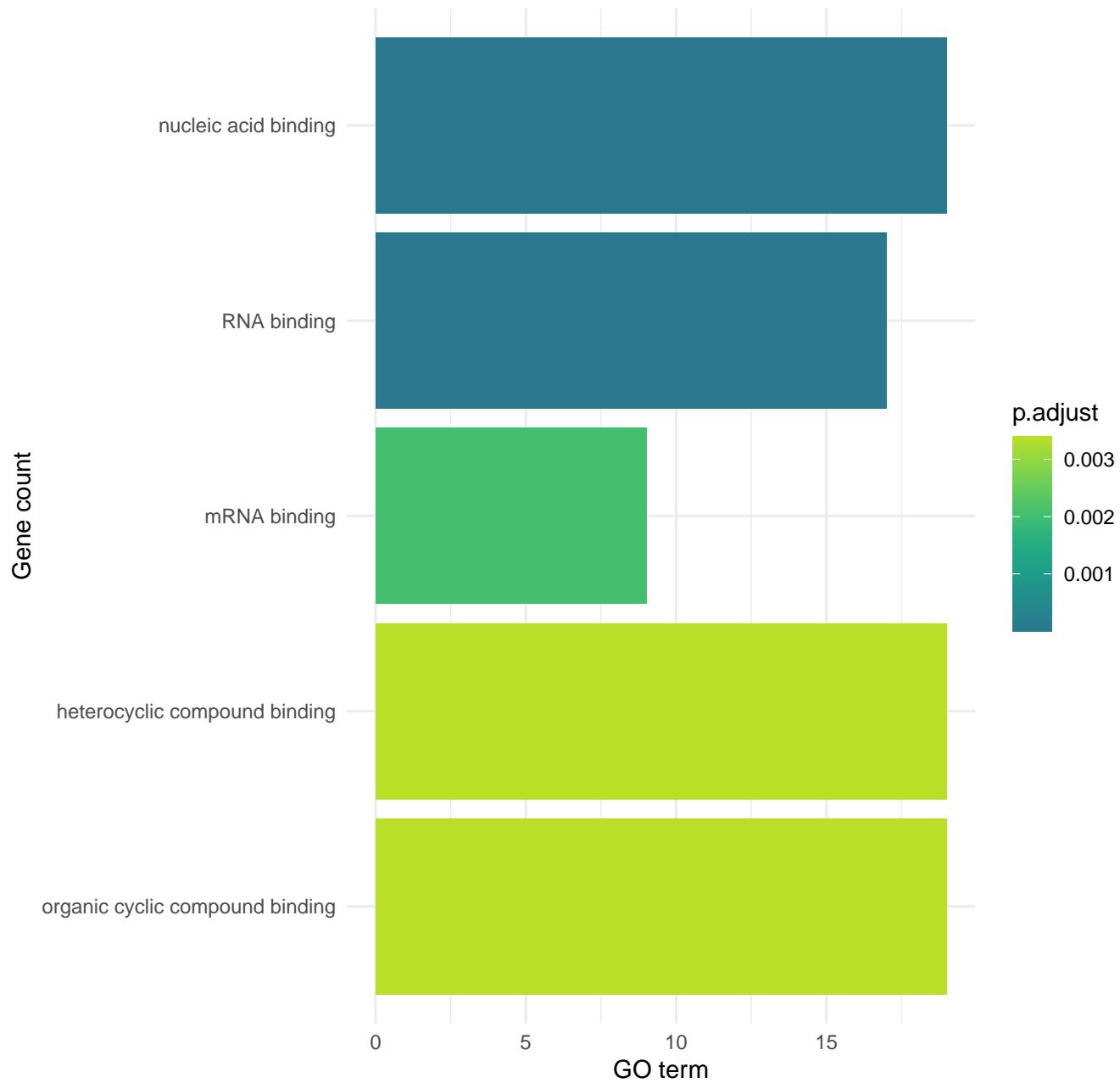




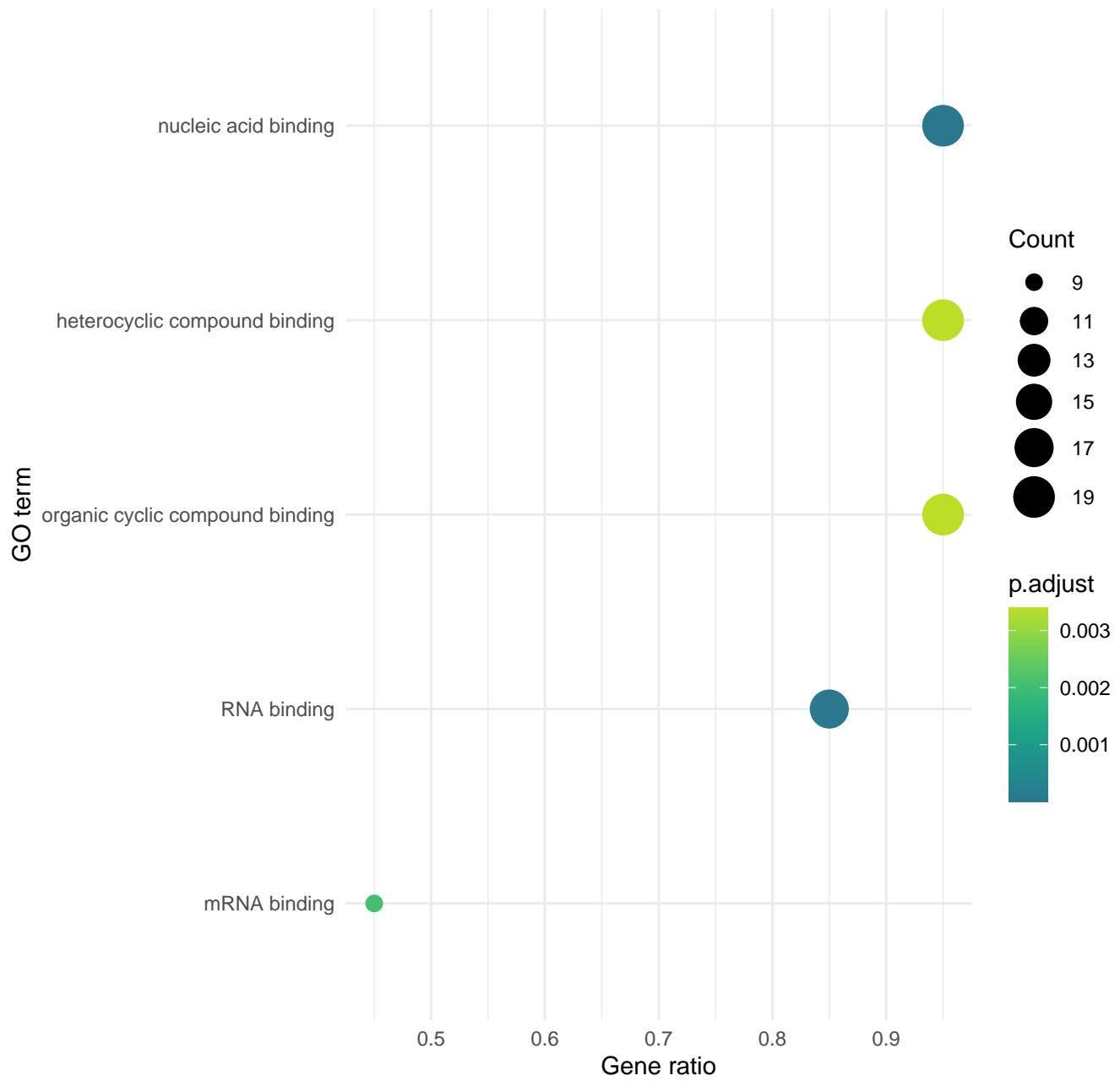
SNP1-TAP Up-regulated GO CC upsetplot



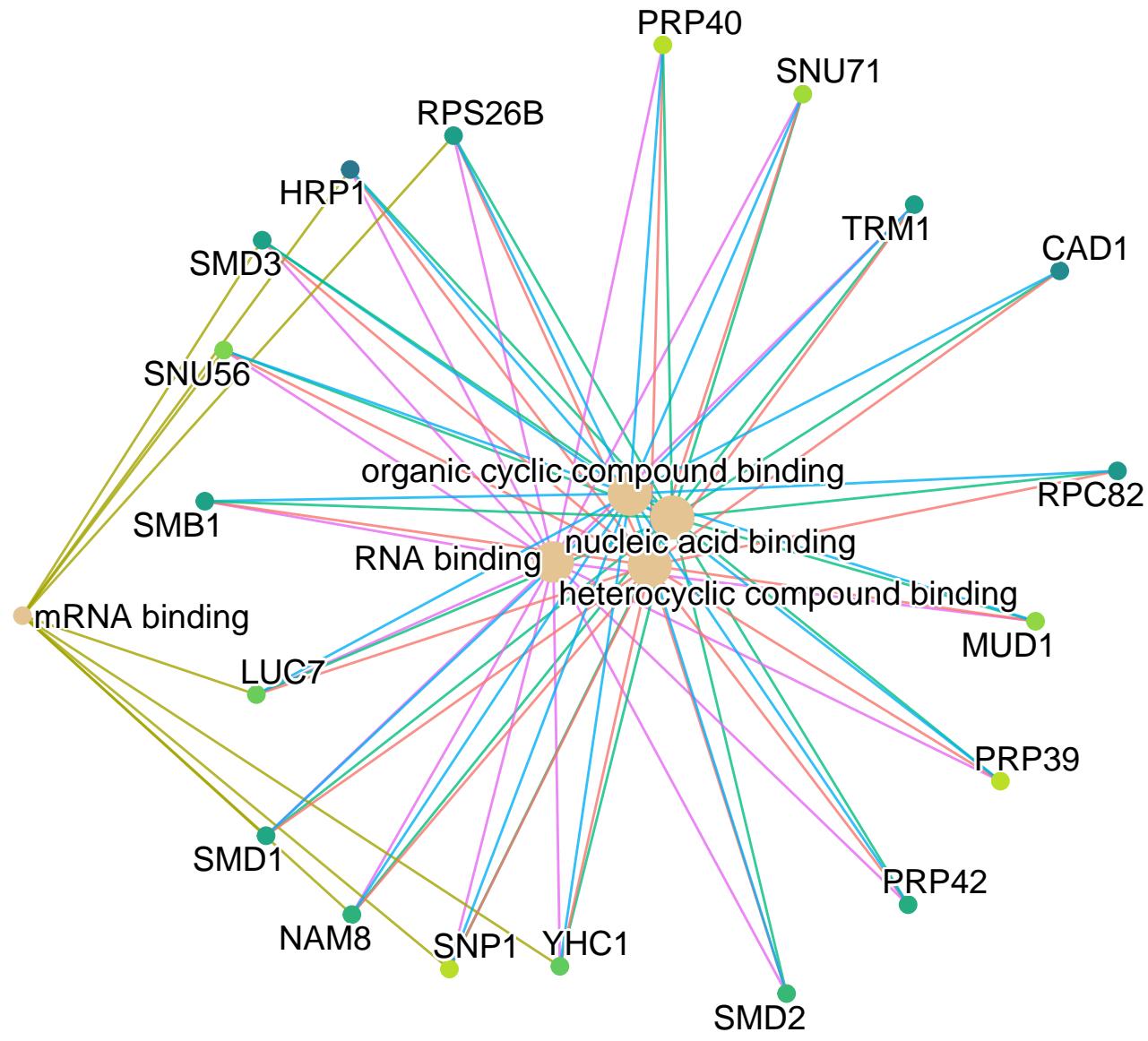
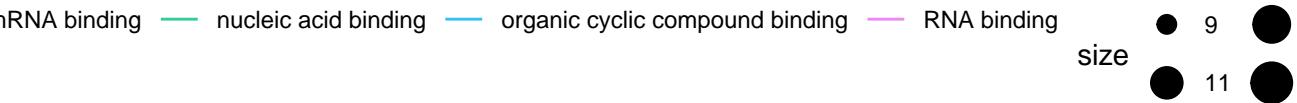
SNP1-TAP Up-regulated GO MF barplot



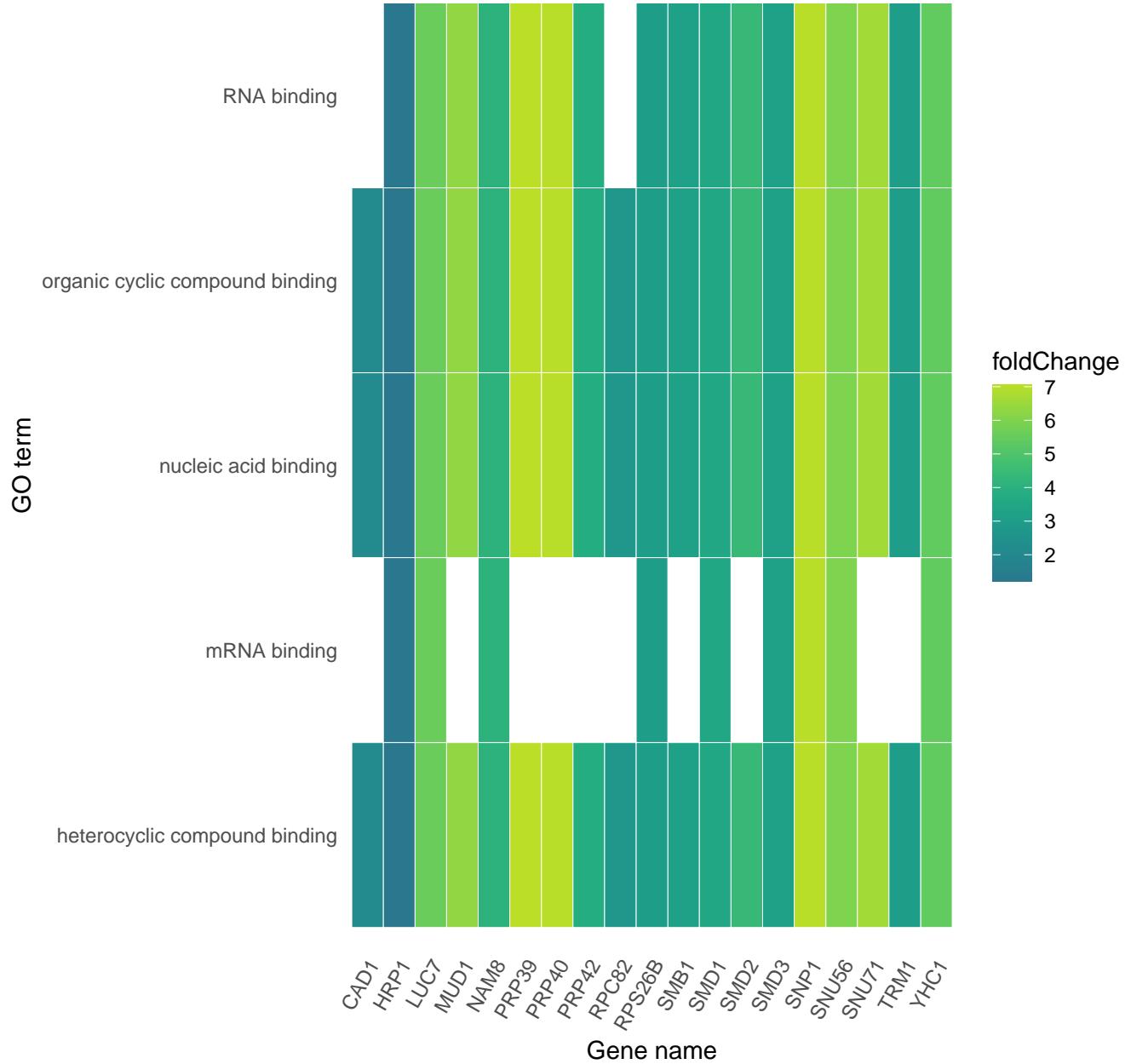
SNP1-TAP Up-regulated GO MF dotplot



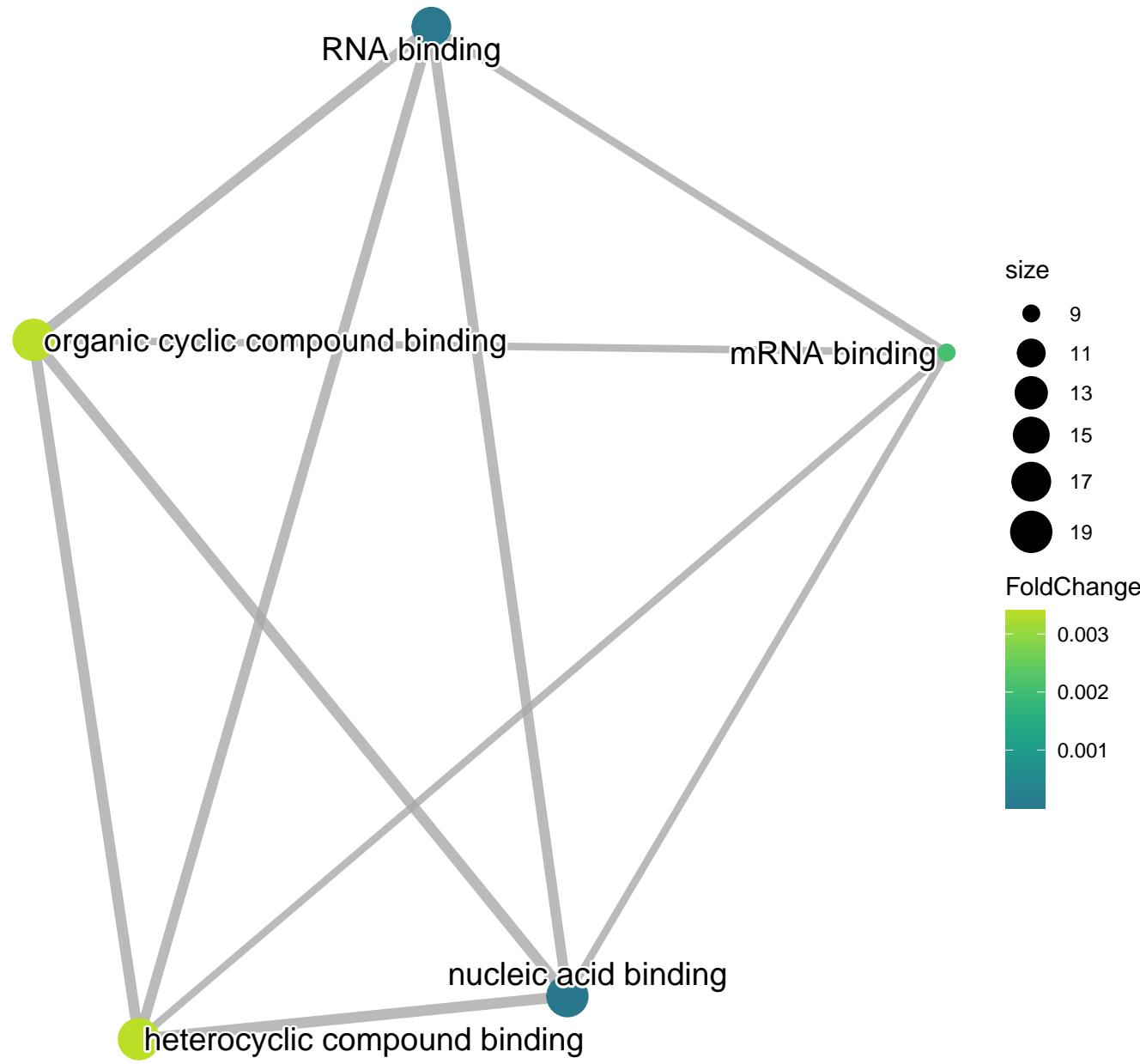
SNP1-TAP Up-regulated GO MF cnetplot

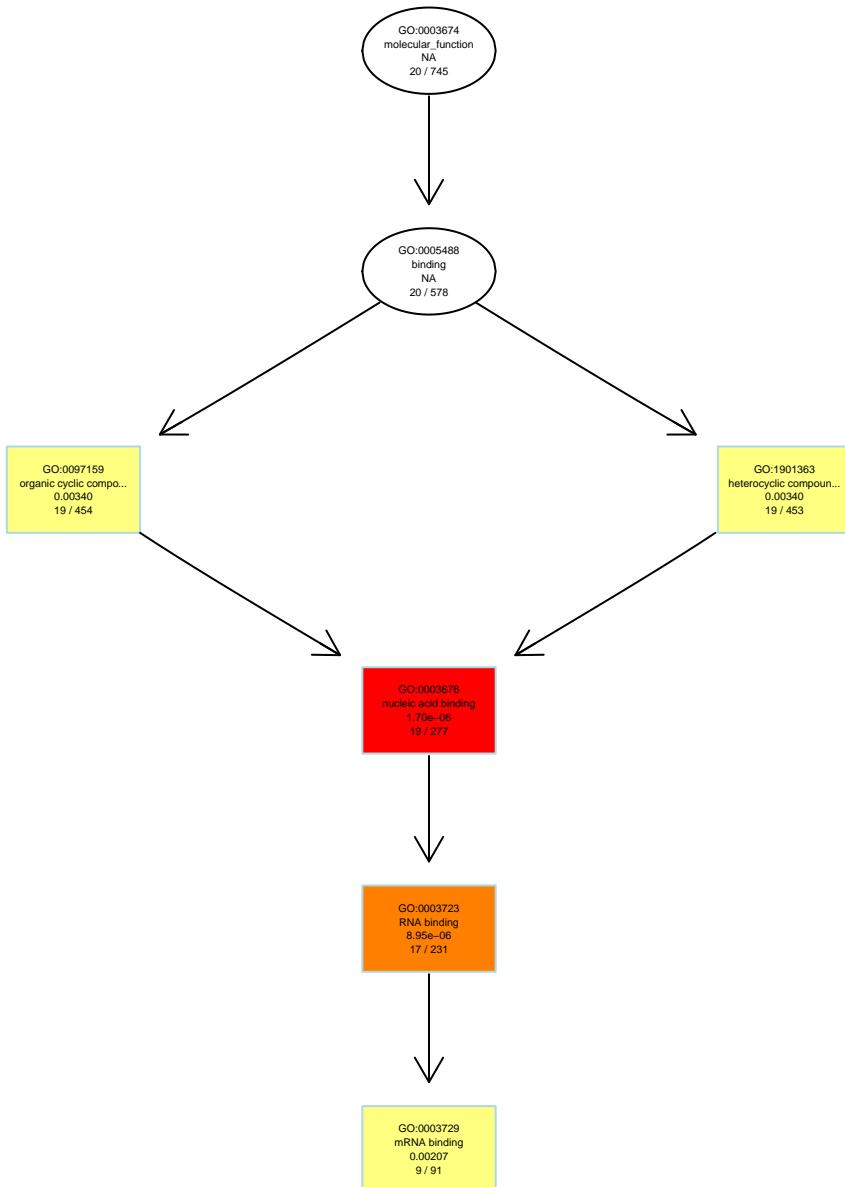


SNP1-TAP Up-regulated GO MF heatplot

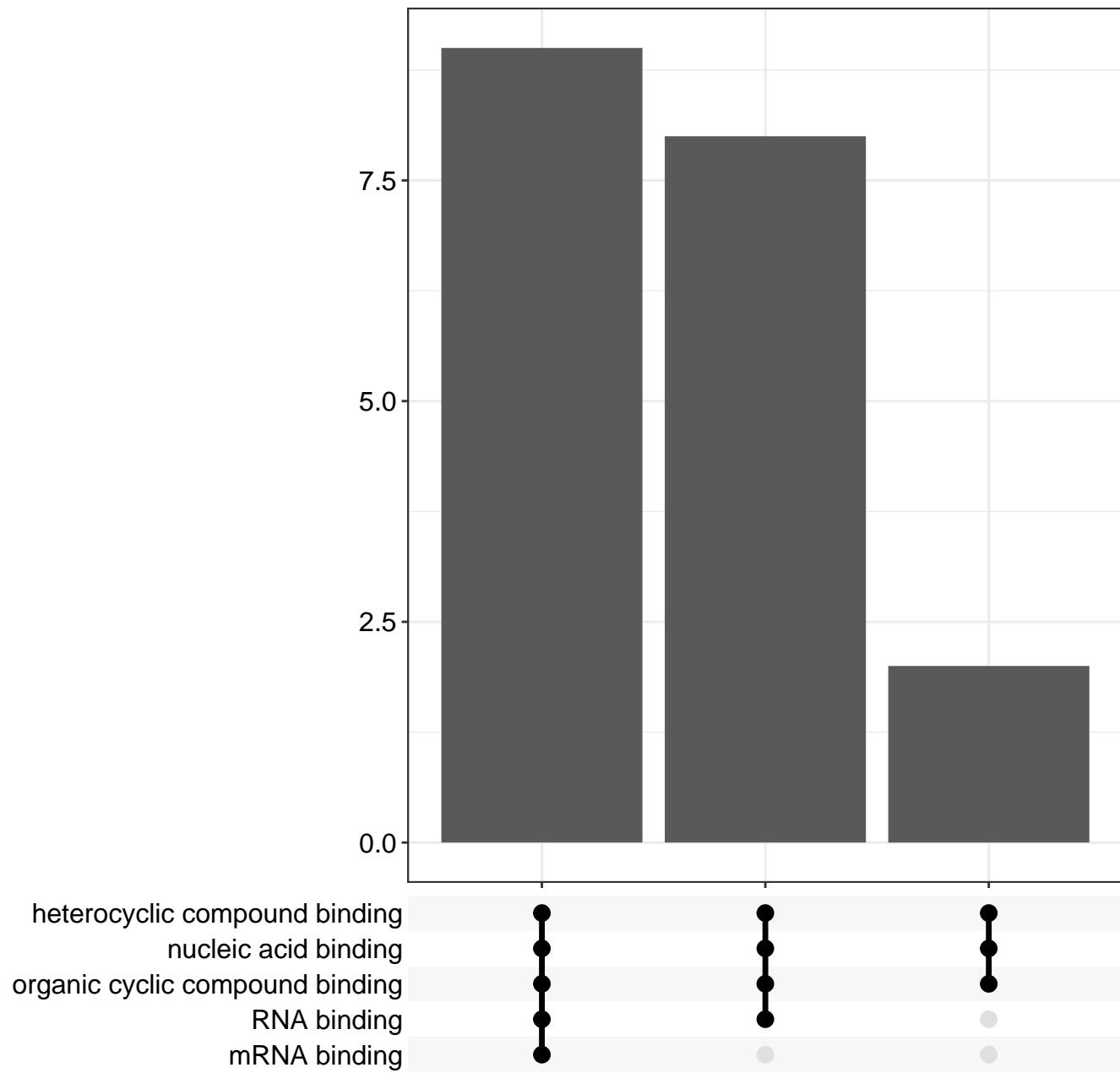


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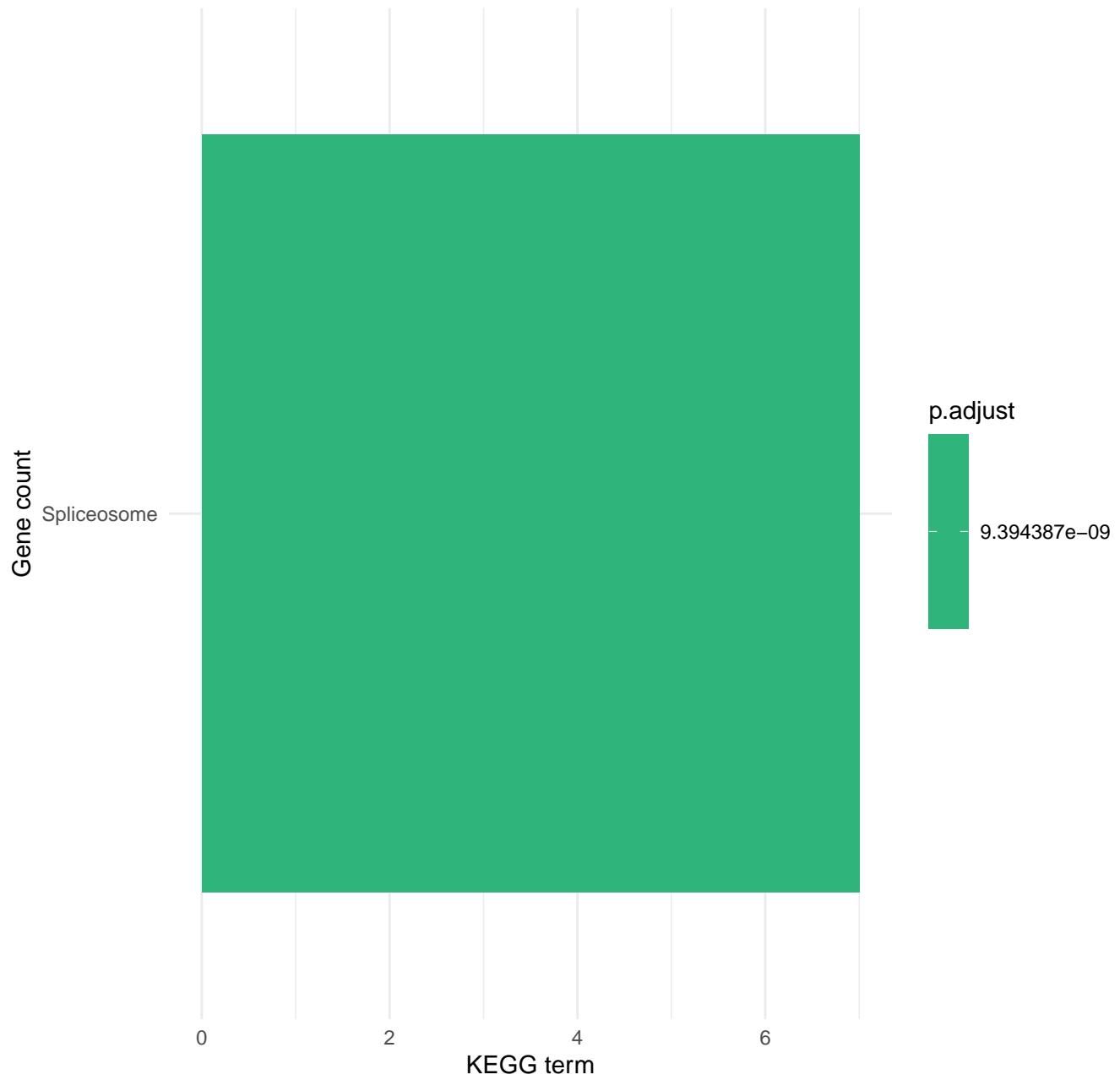




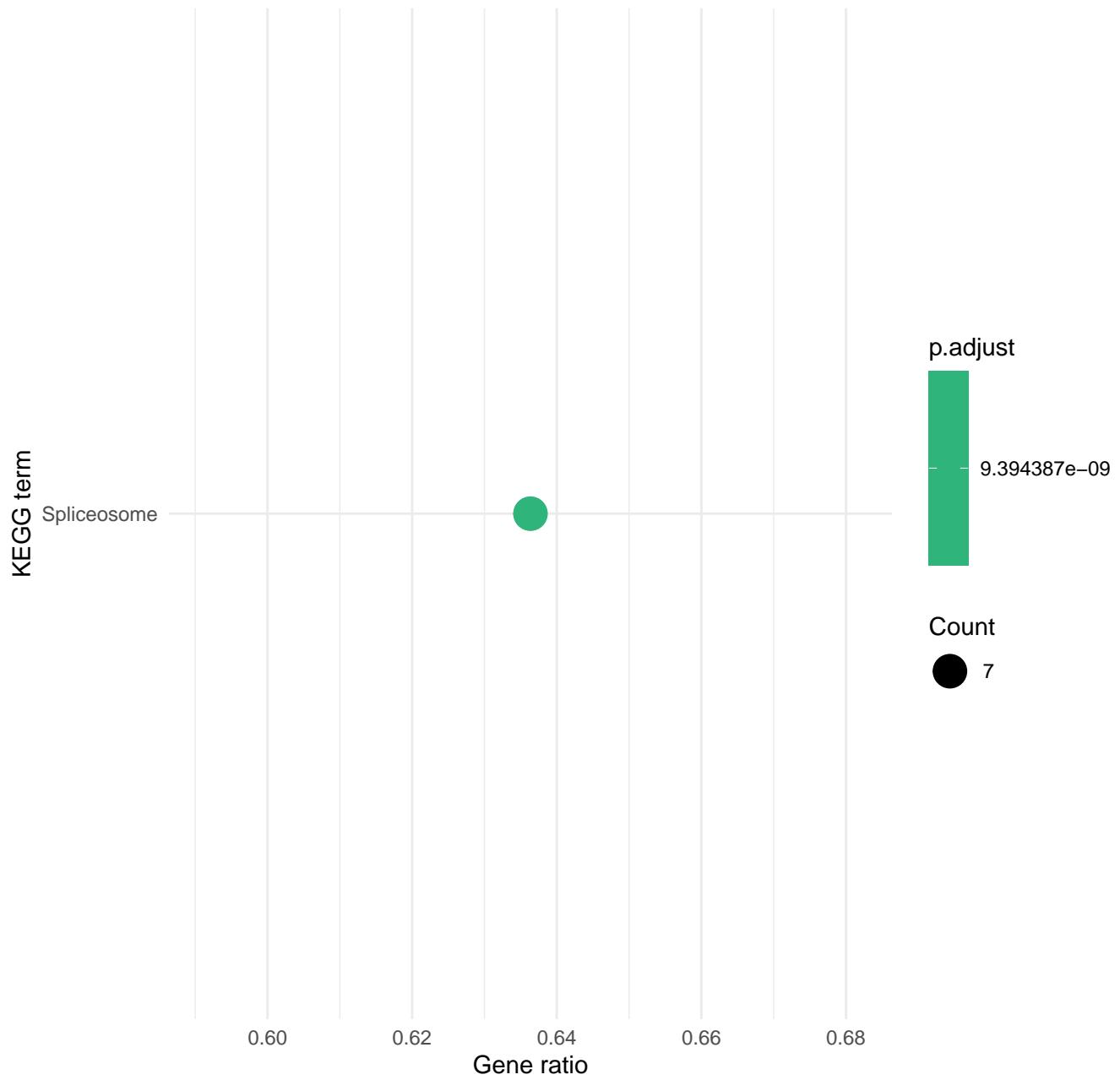
SNP1-TAP Up-regulated GO MF upsetplot



SNP1-TAP Up-regulated KEGG barplot



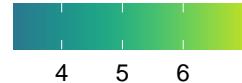
SNP1-TAP Up-regulated KEGG dotplot



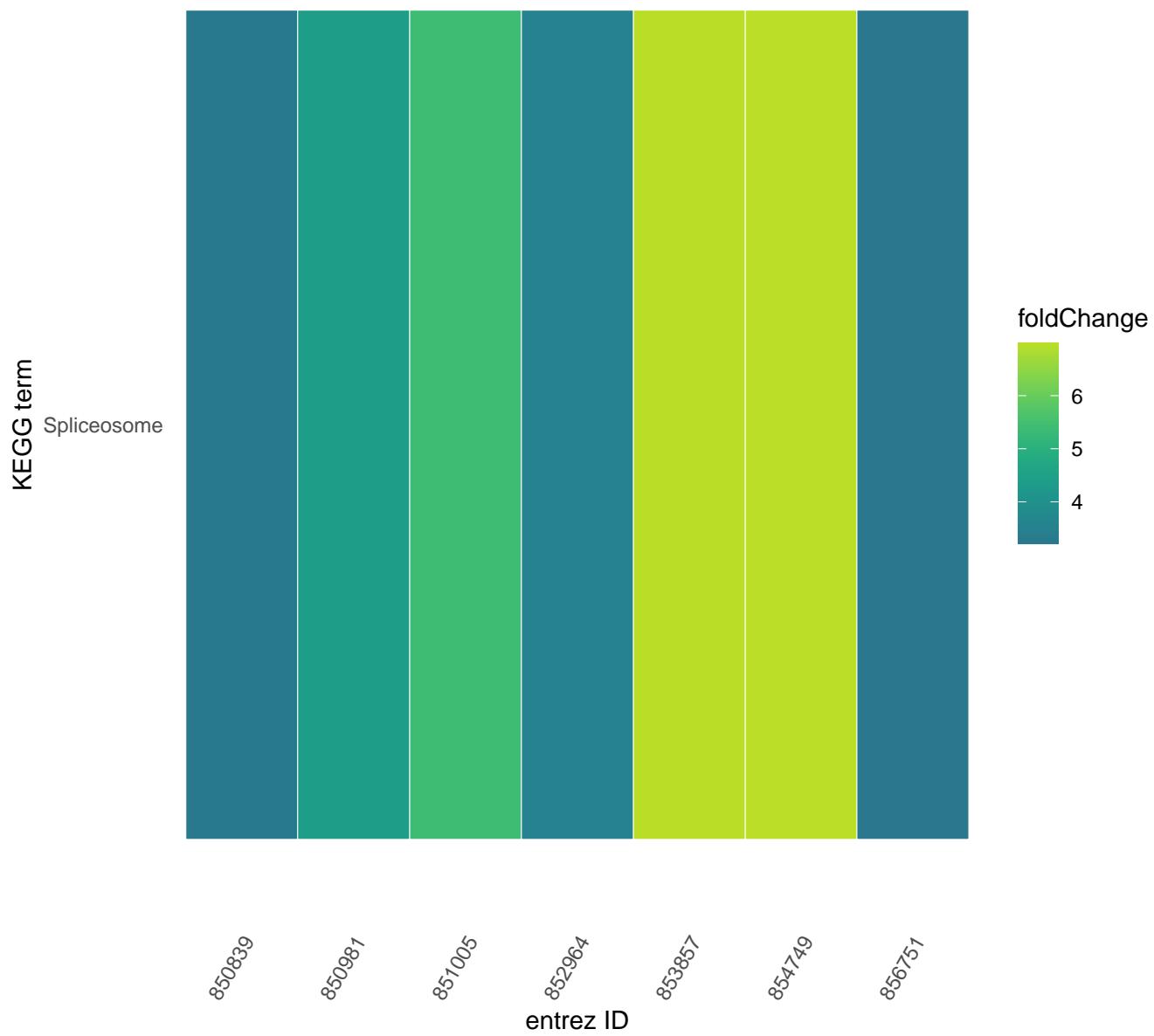
SNP1-TAP Up-regulated KEGG dotplot

size ● 7 category — Spliceosome

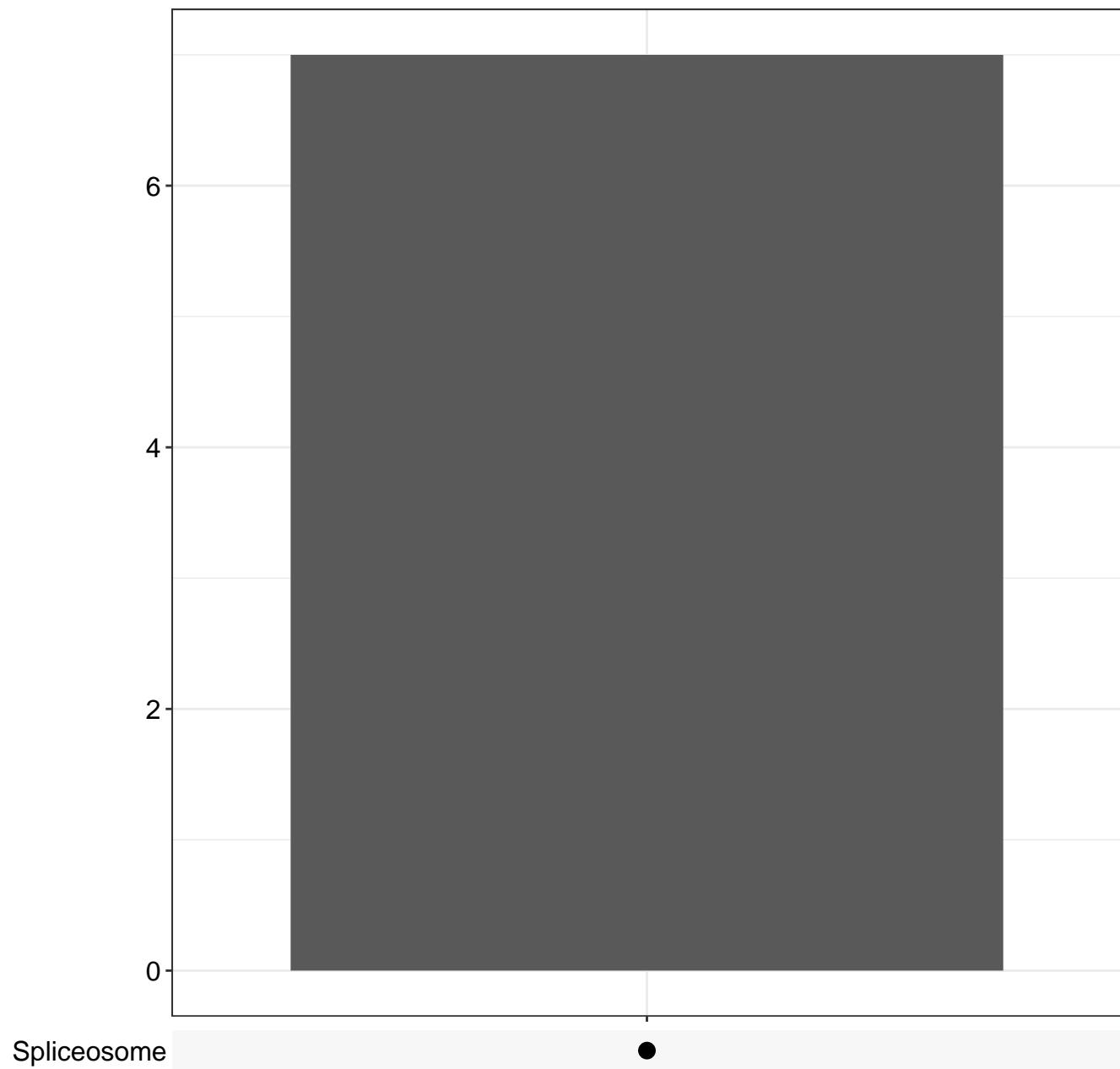
FoldChange



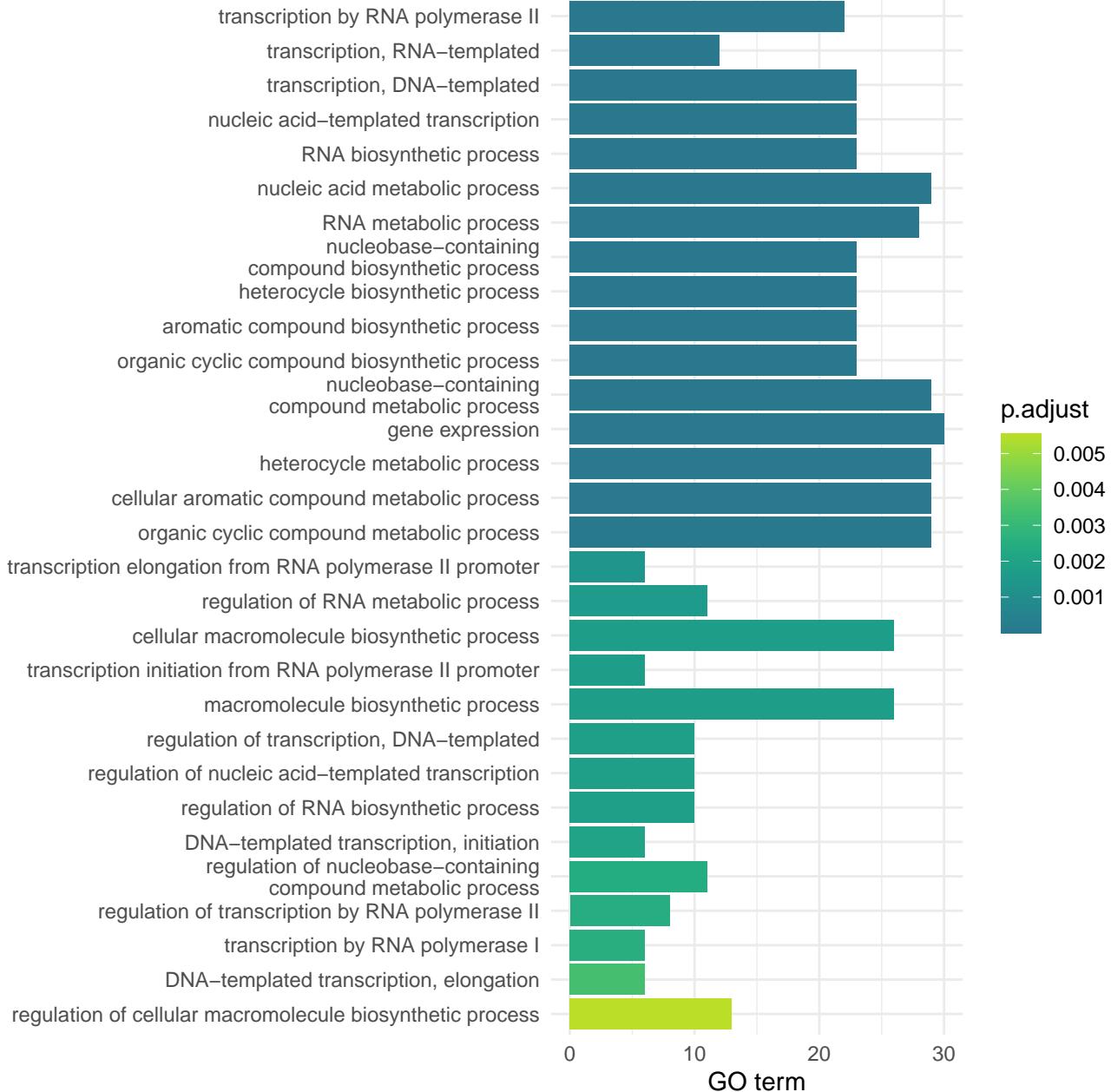
SNP1-TAP Up-regulated KEGG heatplot



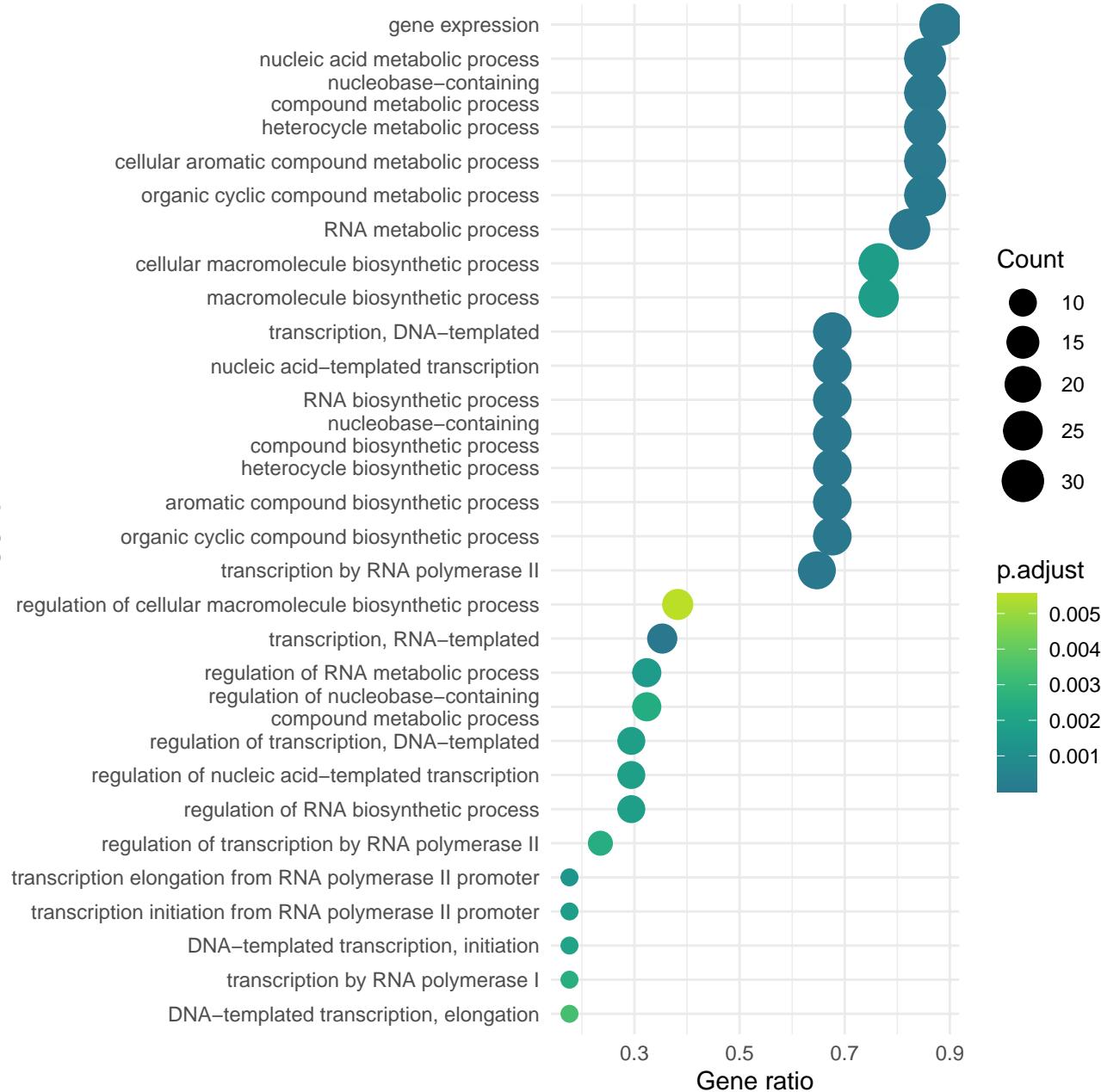
SNP1-TAP Up-regulated KEGG upsetplot



RPO21-TAP Up-regulated GO BP barplot

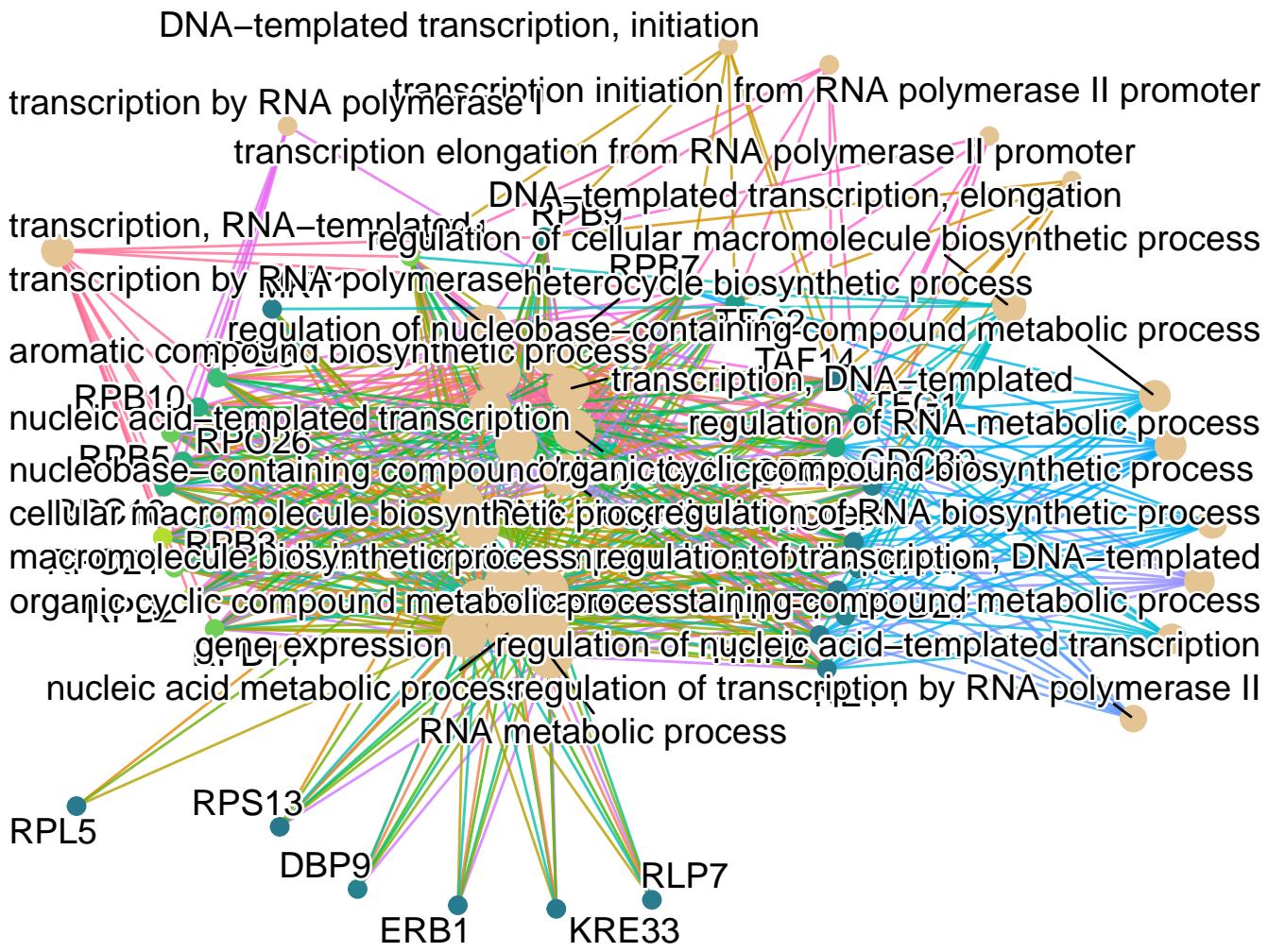


RPO21-TAP Up-regulated GO BP dotplot

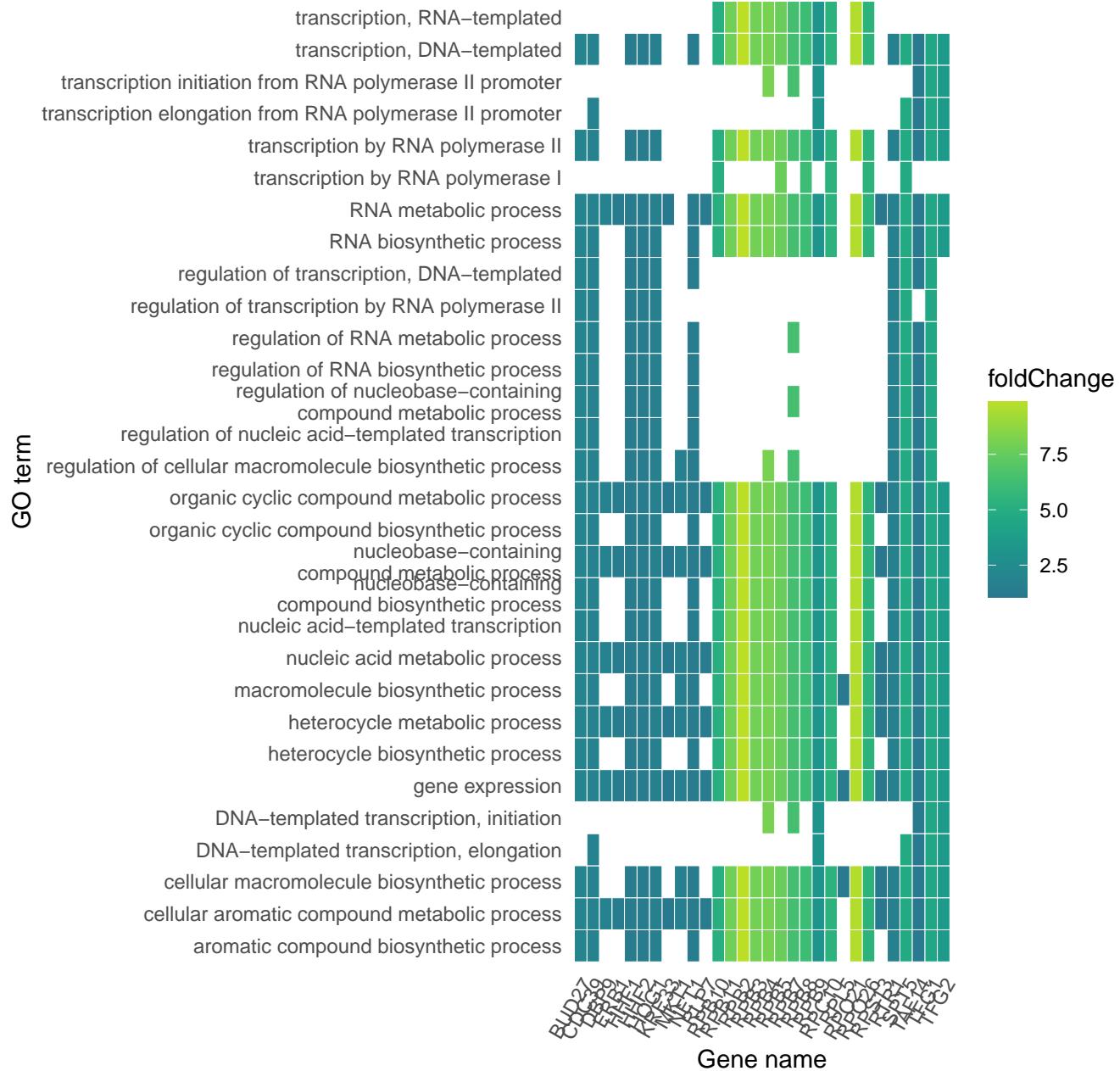


RPO21-TAP Up-regulated GO BP cnetplot

tic process	heterocycle biosynthetic process	nucleobase-containing compound metabolic process
etabolic process	heterocycle metabolic process	organic cyclic compound biosynthetic process
synthetic process	macromolecule biosynthetic process	organic cyclic compound metabolic process
elongation	nucleic acid metabolic process	regulation of cellular macromolecule biosynthesis
initiation	nucleic acid-templated transcription	regulation of nucleic acid-templated transcription
	nucleobase-containing compound biosynthetic process	regulation of nucleobase-containing compound metabolic process



RPO21-TAP Up-regulated GO BP heatplot



RPO21-TAP Up-regulated GO BP emapplot

regulation of transcription by RNA polymerase II

regulation of nucleic acid-templated transcription

regulation of RNA biosynthetic process

regulation of transcription, DNA-templated

regulation of cellular macromolecule biosynthetic process

regulation of RNA metabolic process

aromatic compound biosynthetic process

organic cyclic compound metabolic process

nucleobase-containing compound metabolic process

transcription elongation from RNA polymerase II promoter

DNA-templated transcription, elongation

heterocycle metabolic process

macromolecule biosynthetic process

gene expression

heterocycle biosynthetic process

cellular aromatic compound metabolic process

transcription elongation from RNA polymerase II promoter

RNA metabolic process

organic cyclic compound biosynthetic process

RNA biosynthetic process

transcription by RNA polymerase II

nucleobase-containing compound biosynthetic process

cellular aromatic compound metabolic process

transcription by RNA polymerase II

cellular macromolecule biosynthetic process

transcription by RNA polymerase I

transcription initiation from RNA polymerase II promoter

transcription, RNA-templated

DNA-templated transcription, initiation

FoldChange

0.005

0.004

0.003

0.002

0.001

size

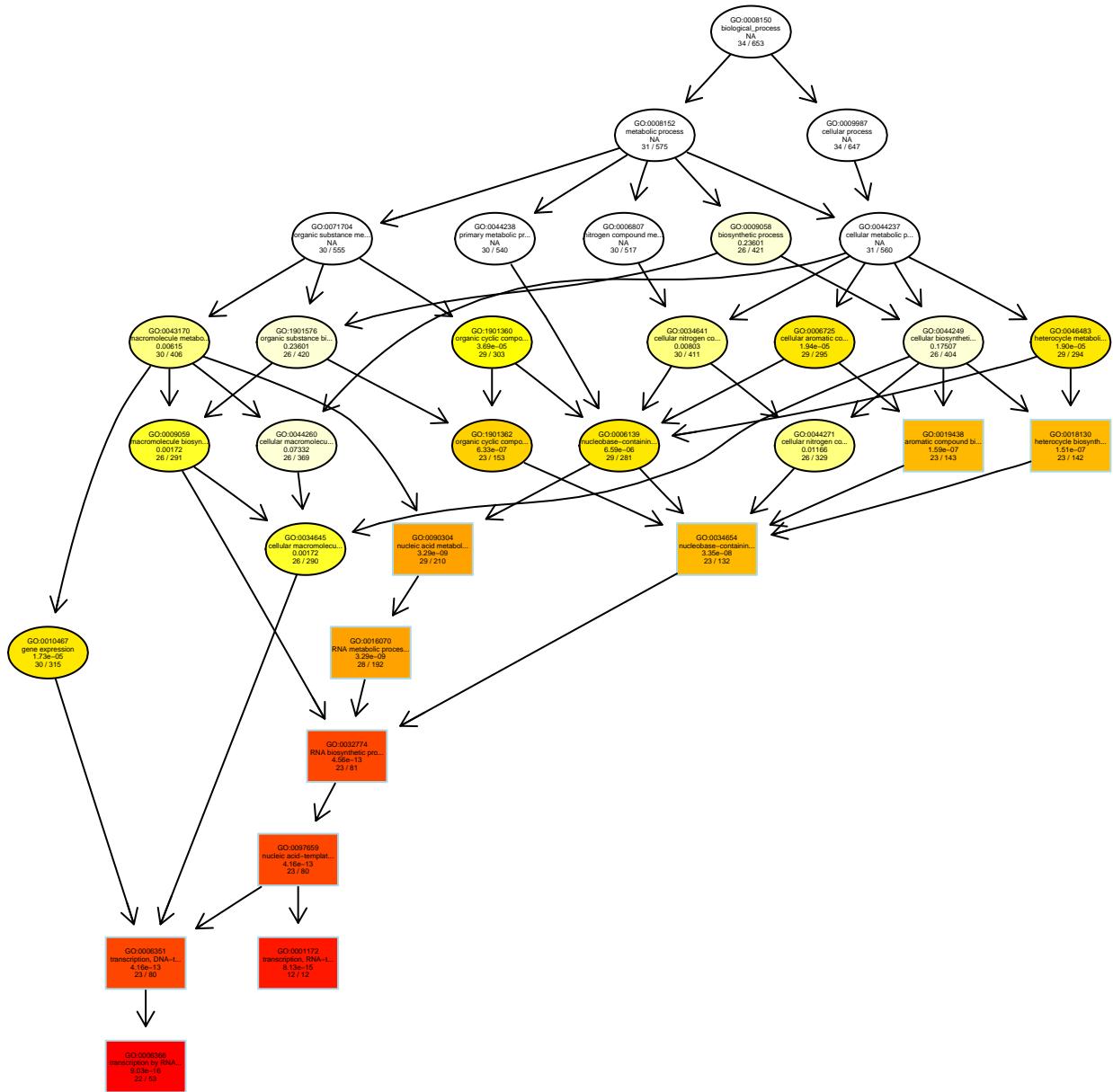
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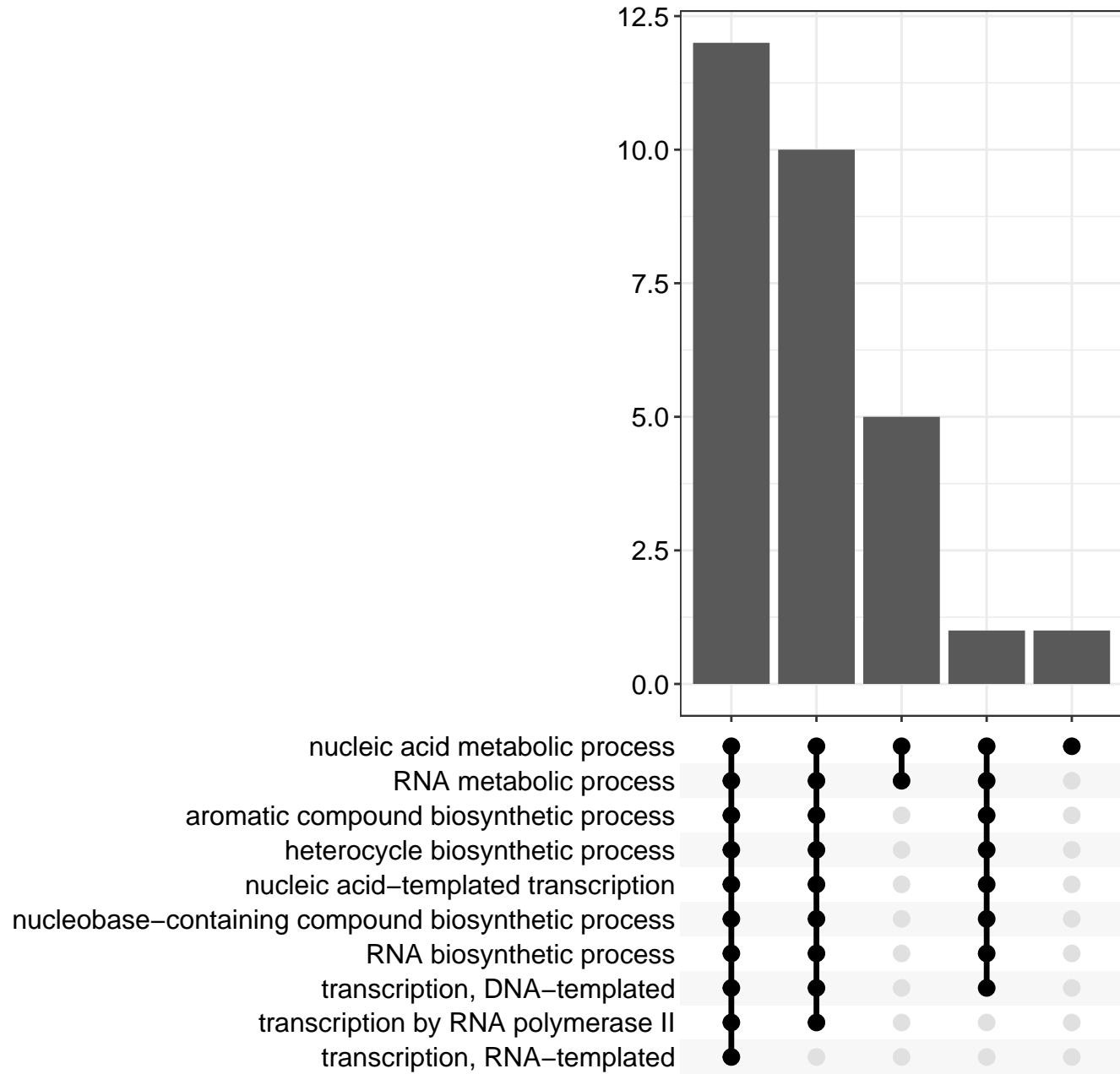
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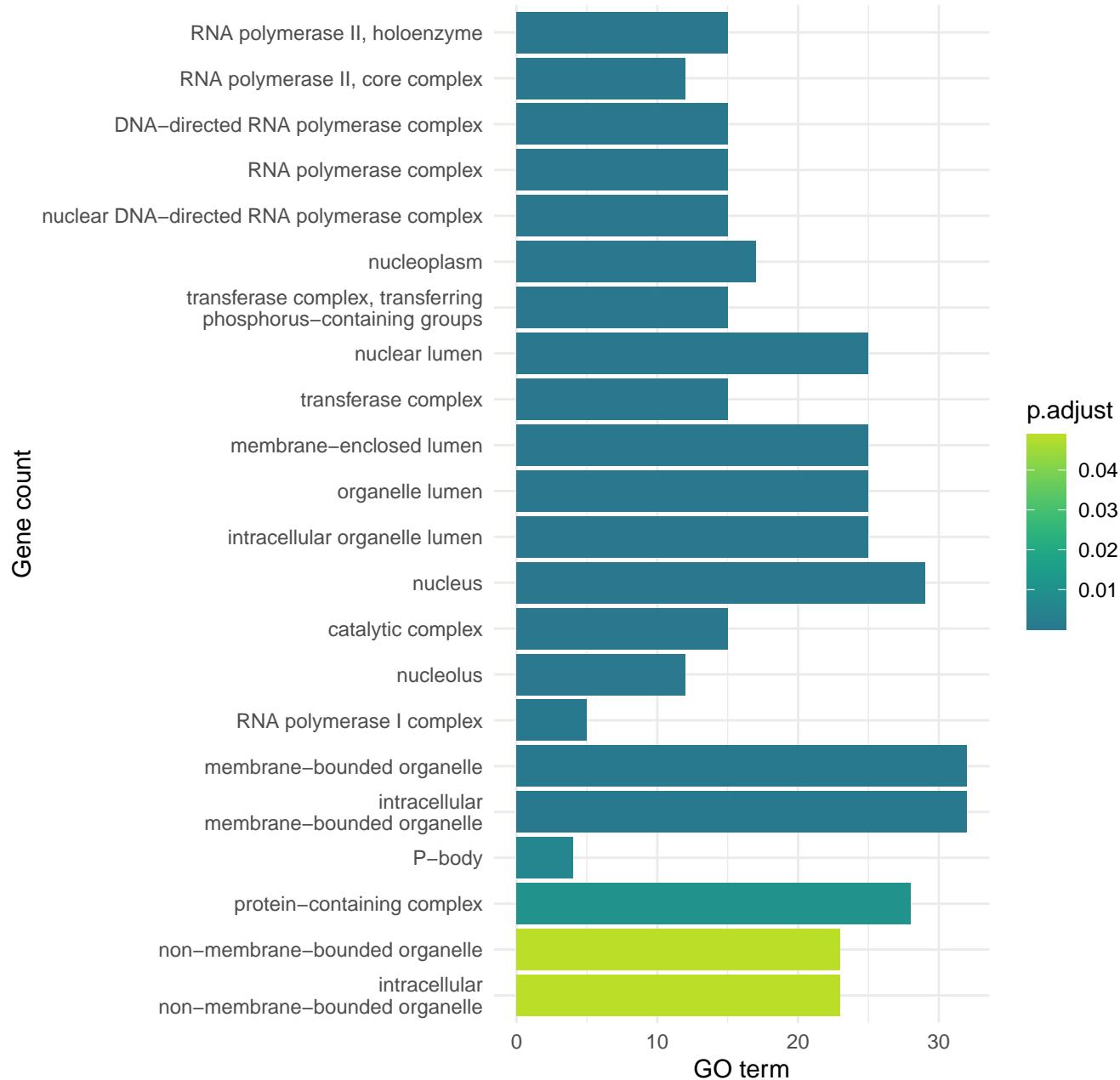
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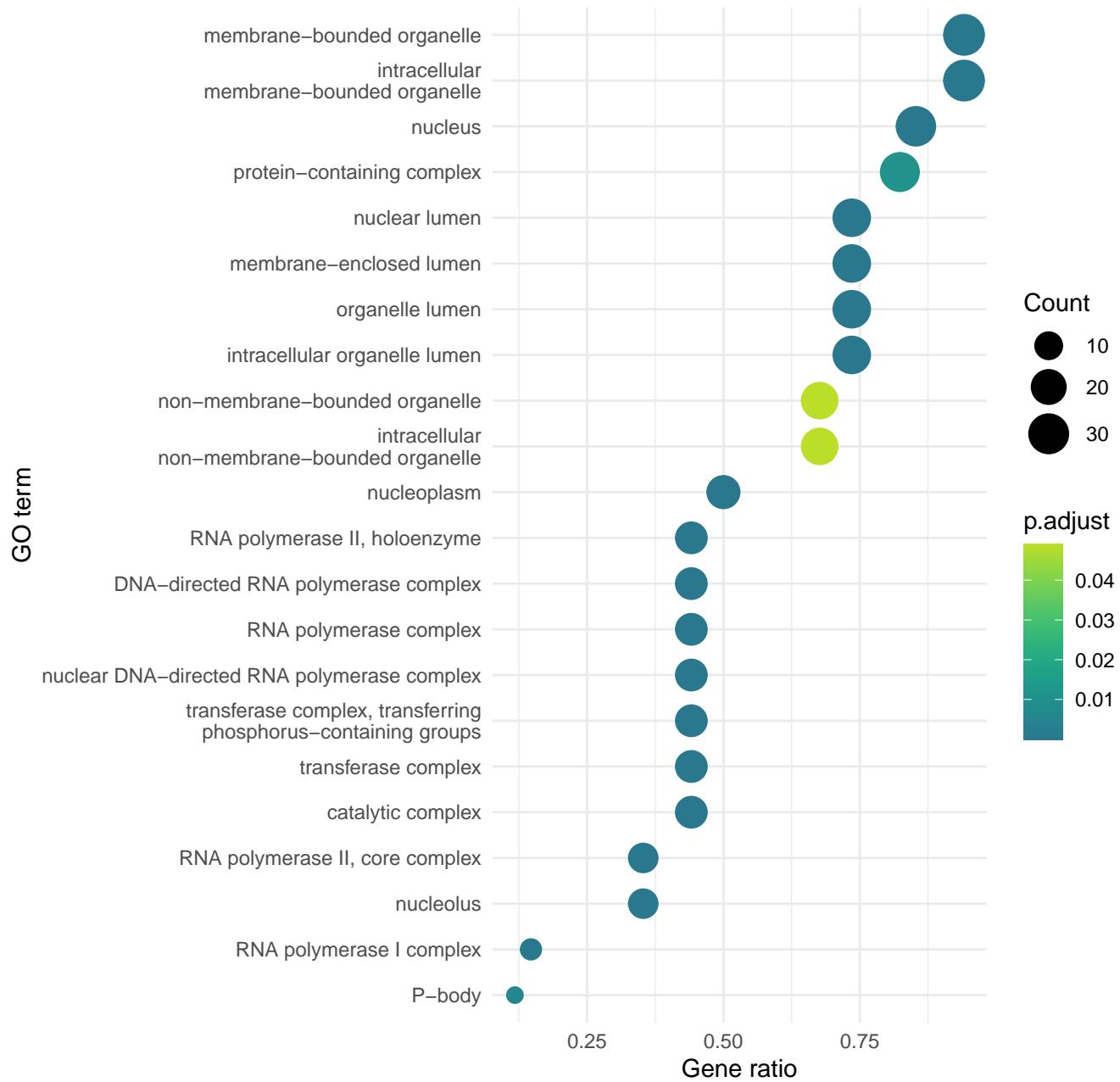
RPO21-TAP Up-regulated GO BP



RPO21-TAP Up-regulated GO CC barplot

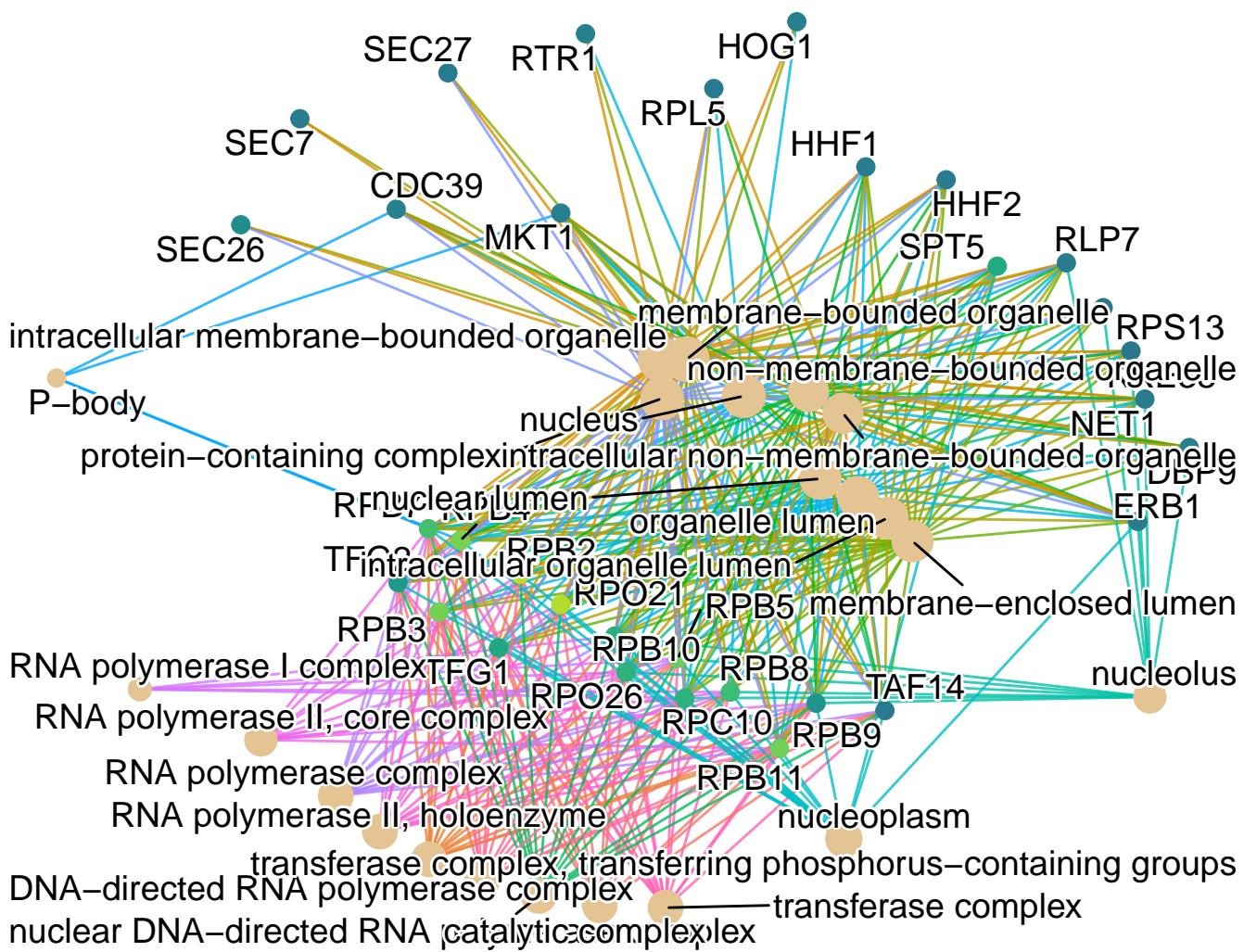


RPO21-TAP Up-regulated GO CC dotplot

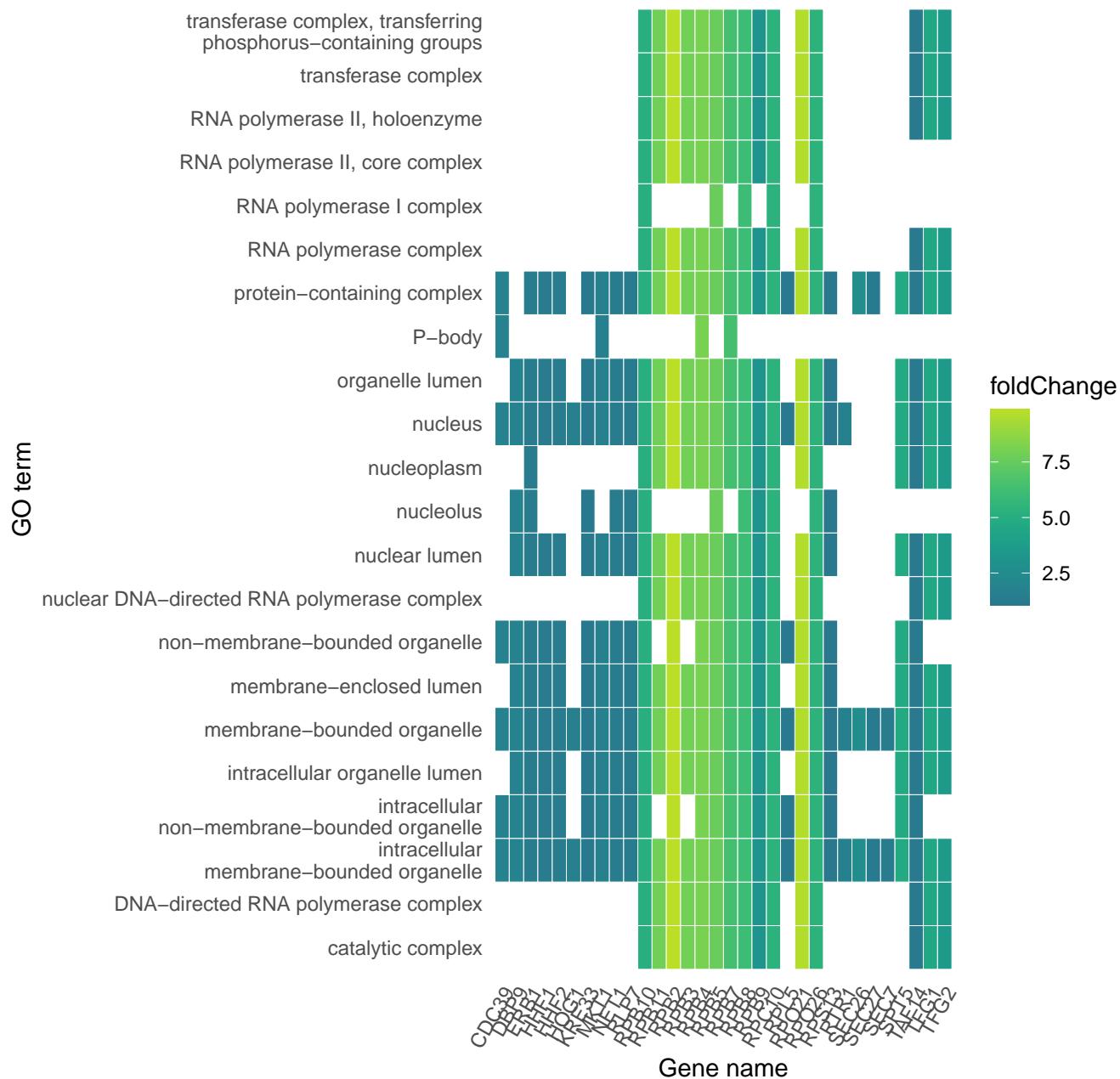


RPO21-TAP Up-regulated GO CC cnetplot

- nucleolus
- nucleoplasm
- nucleus
- organelle lumen
- P-body
- protein-containing complex
- RNA polymerase complex
- RNA polymerase I complex
- RNA polymerase II, core complex
- RNA polymerase II, holoenzyme
- transferase complex
- transferase complex, transferring phos

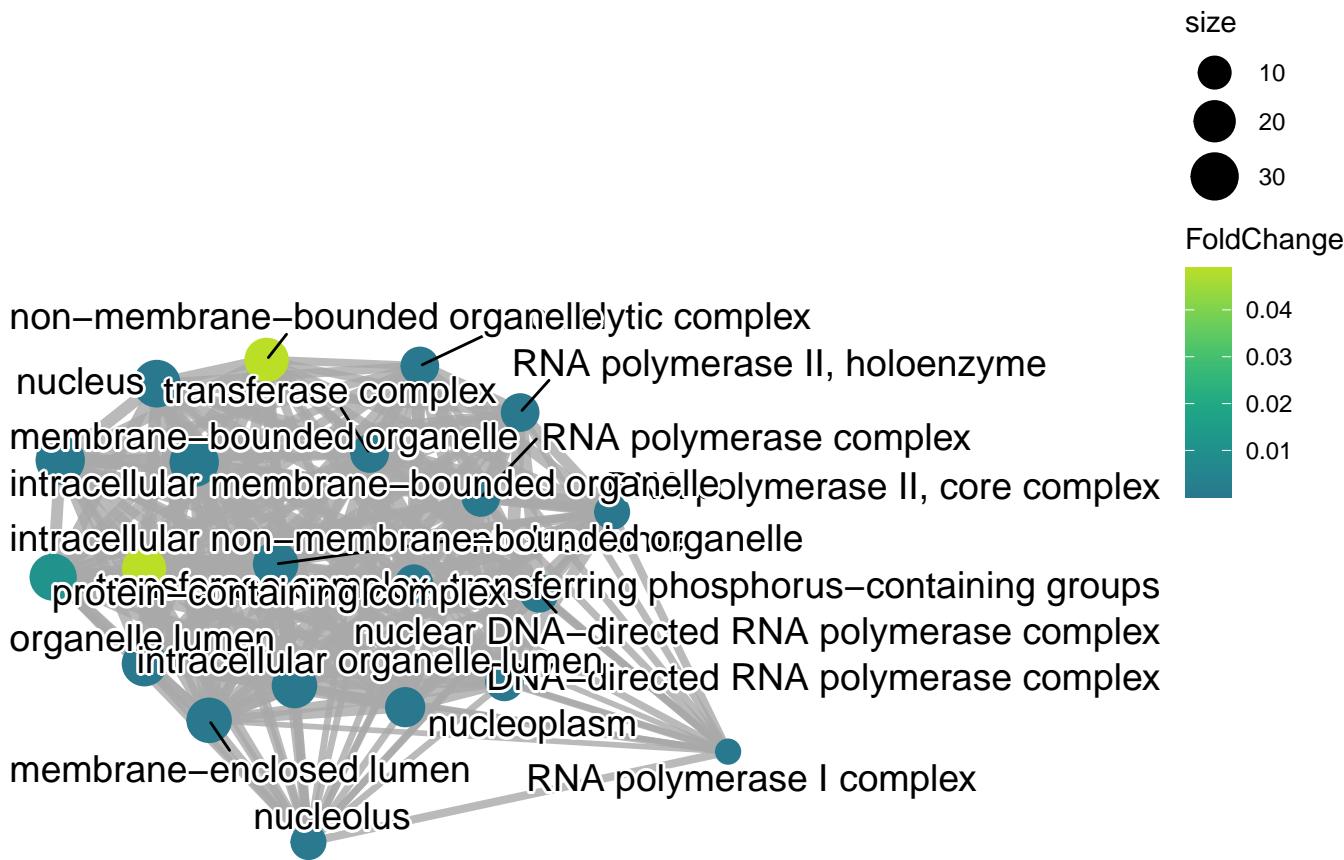


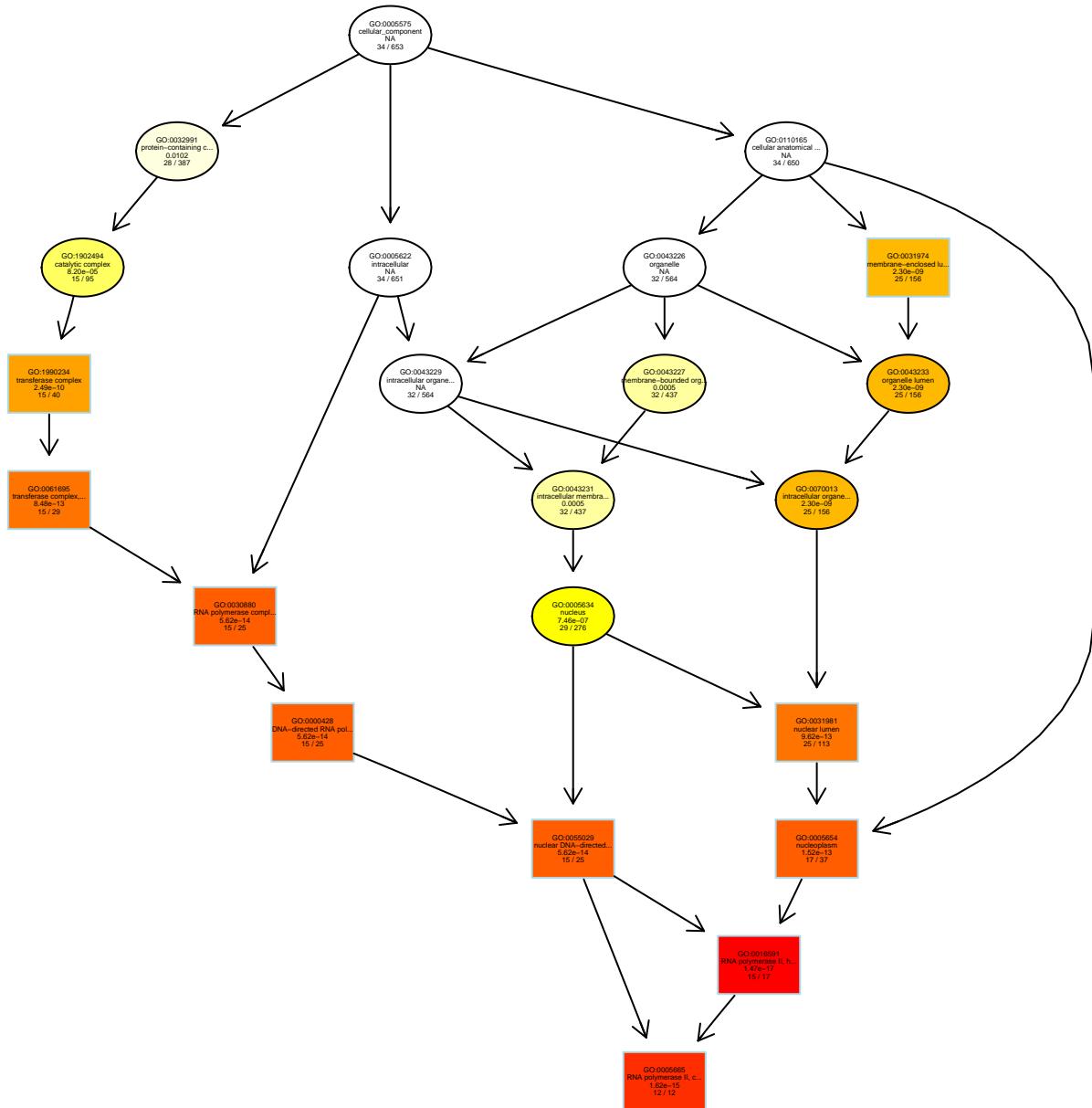
RPO21-TAP Up-regulated GO CC heatplot



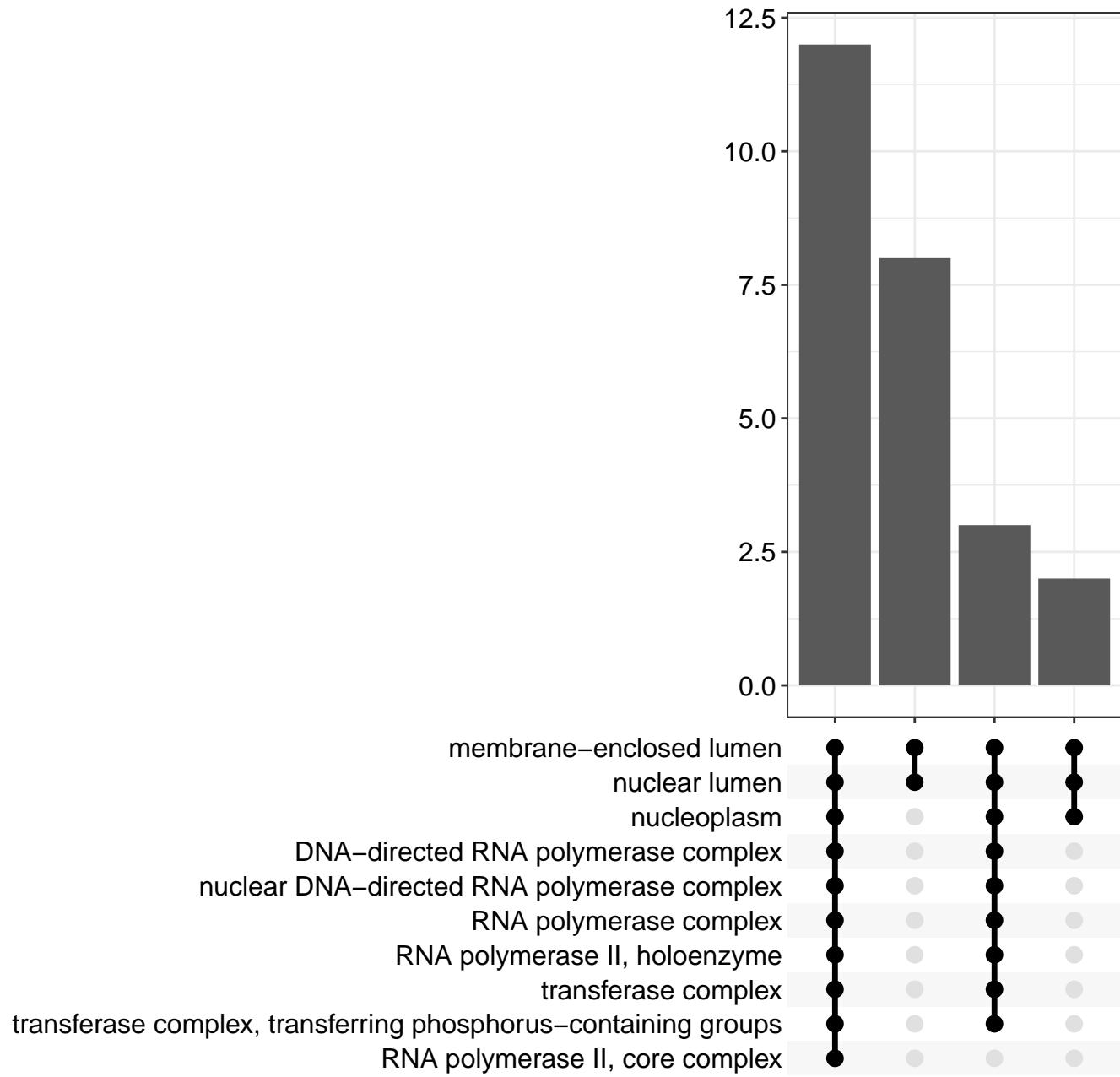
RPO21-TAP Up-regulated GO CC emapplot

P-body

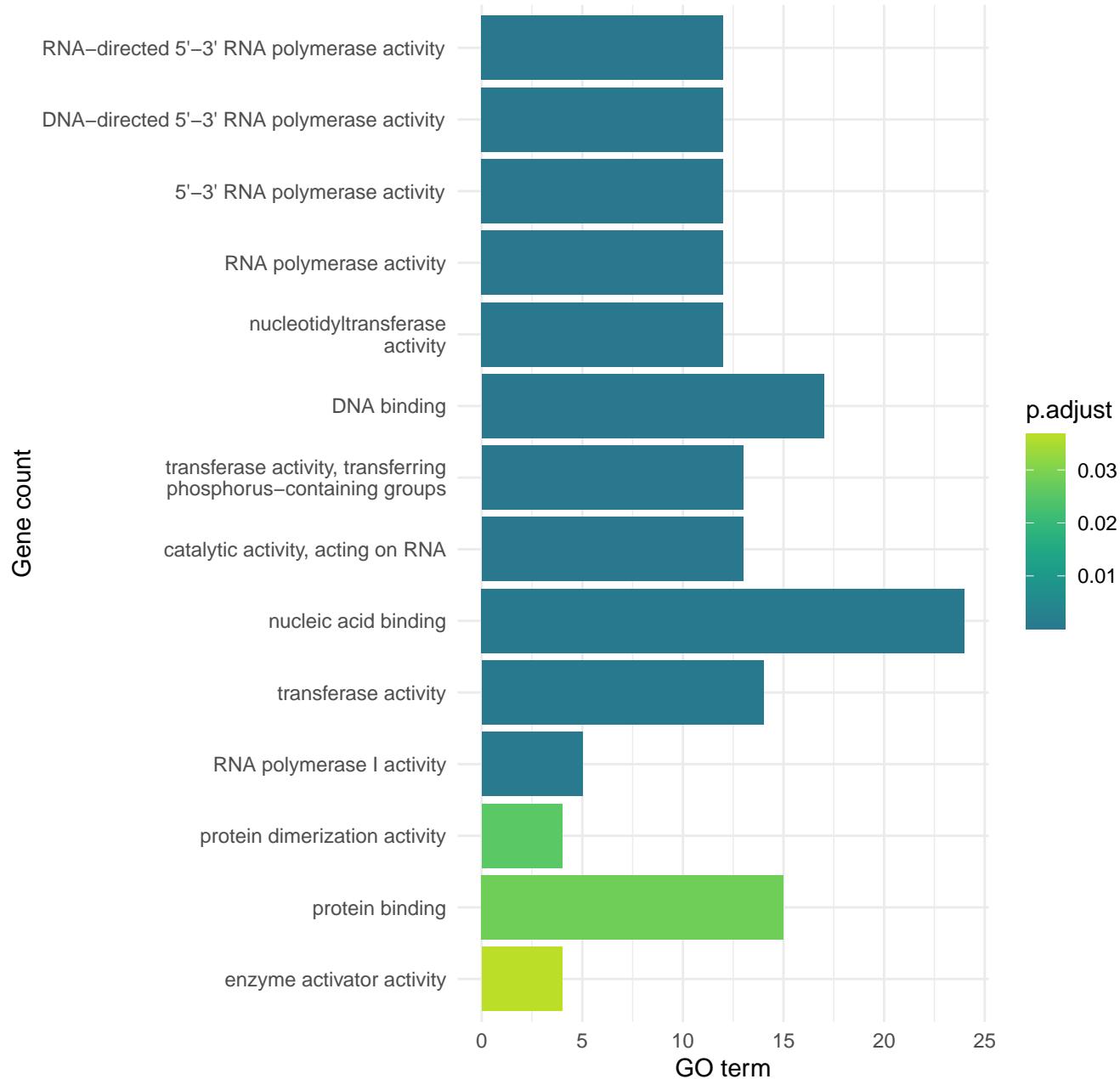




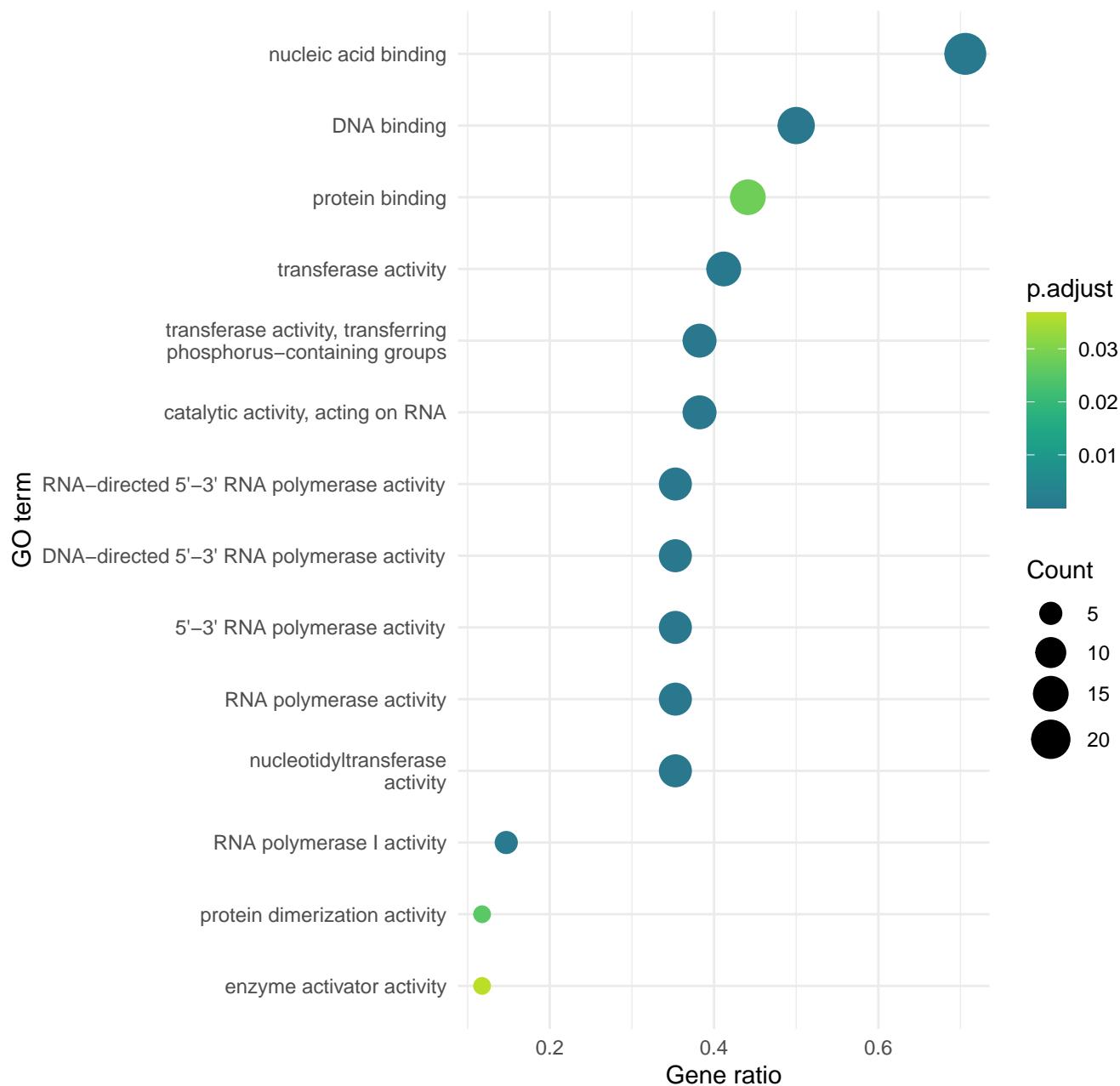
RPO21-TAP Up-regulated



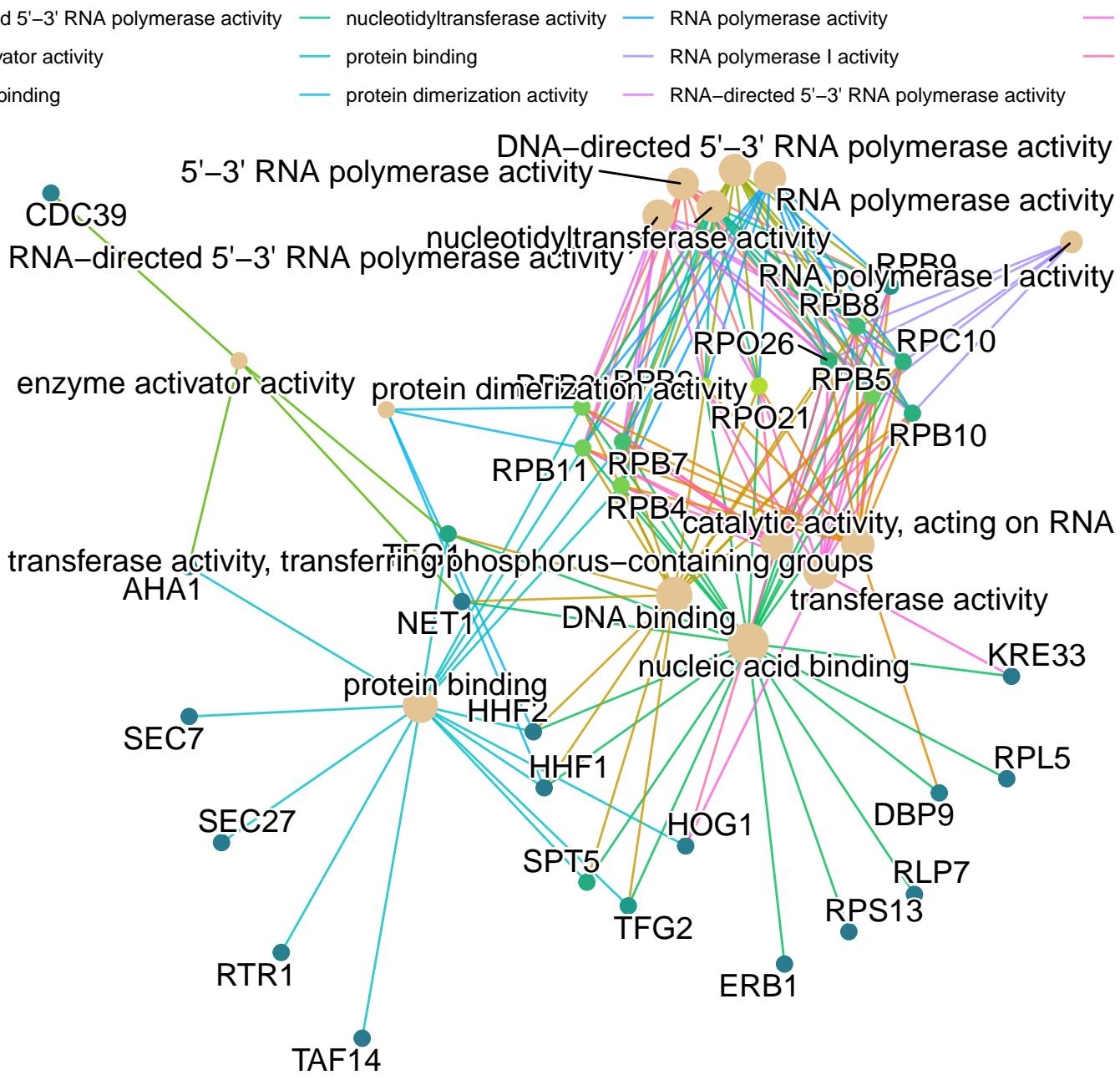
RPO21-TAP Up-regulated GO MF barplot



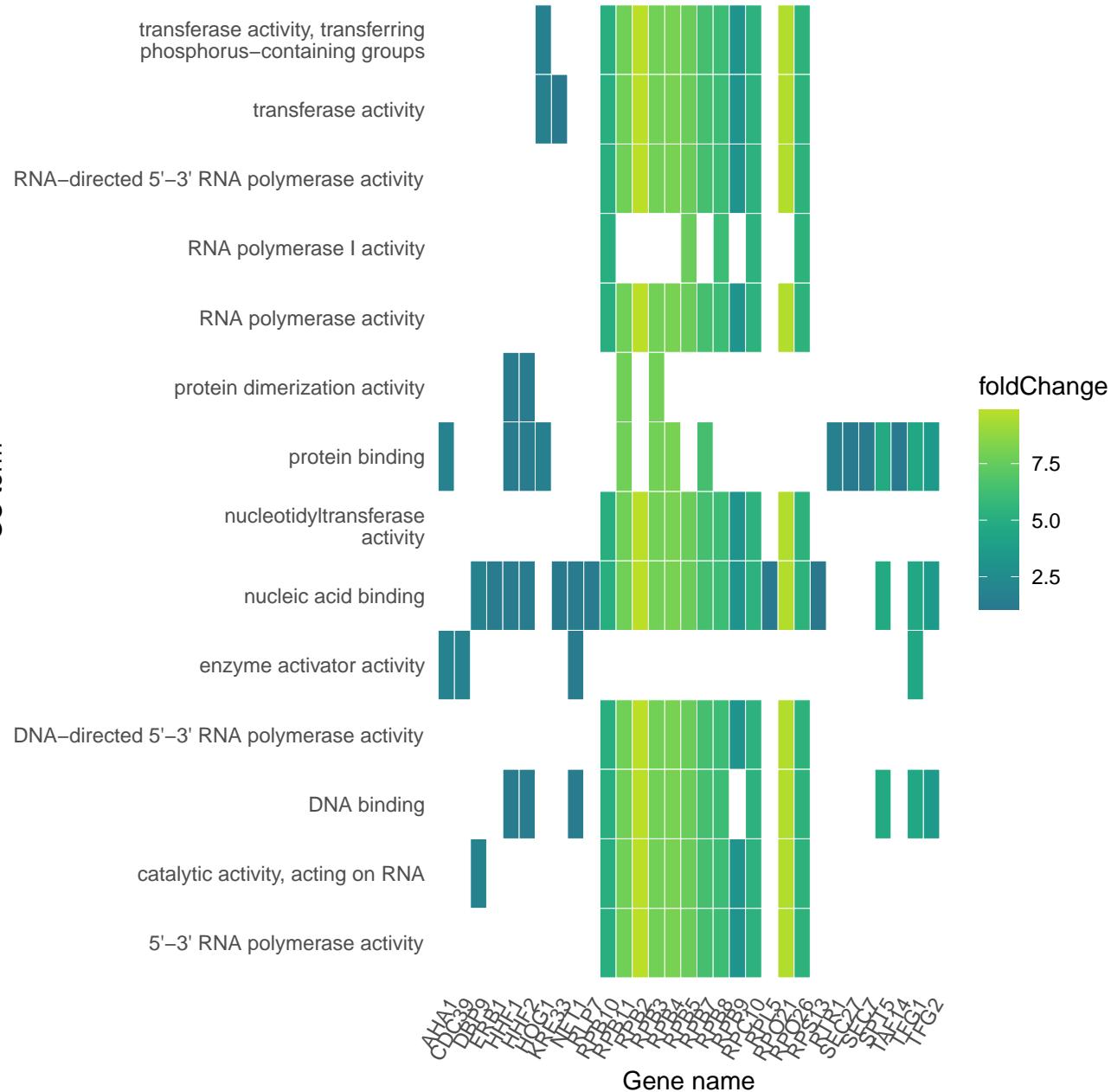
RPO21-TAP Up-regulated GO MF dotplot



RPO21-TAP Up-regulated GO MF cnetplot



RPO21-TAP Up-regulated GO MF heatplot



RPO21-TAP Up-regulated GO MF emapplot

protein dimerization activity

protein binding

DNA binding

nucleic acid binding

transferase activity

transferase activity, transferring phosphorus-containing groups

nucleotidyltransferase activity

catalytic activity, acting on RNA

RNA-directed 5'-3' RNA polymerase activity

5'-3' RNA polymerase activity

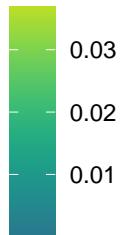
RNA polymerase activity

DNA-directed 5'-3' RNA polymerase activity

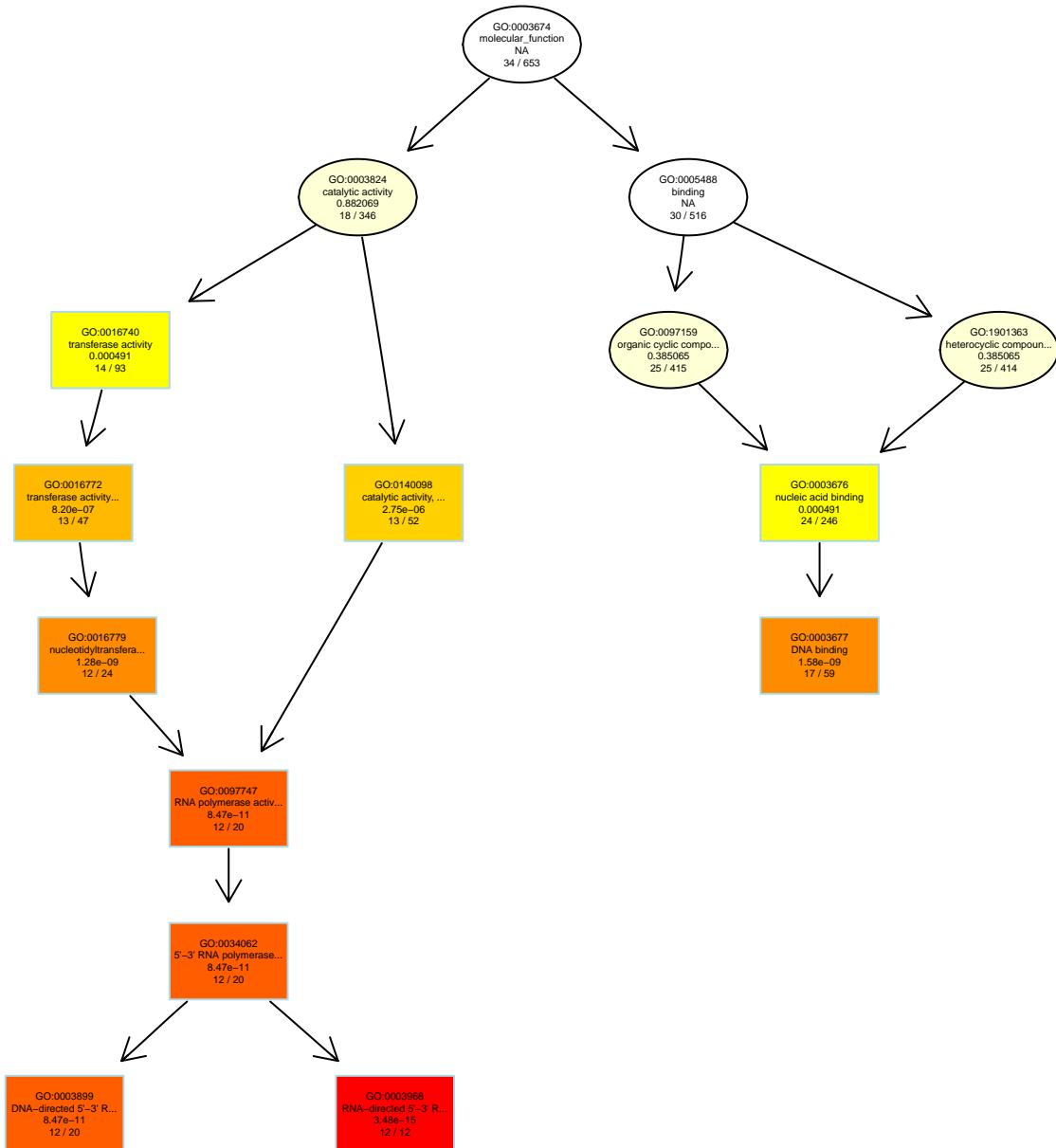
size

- 5
- 10
- 15
- 20

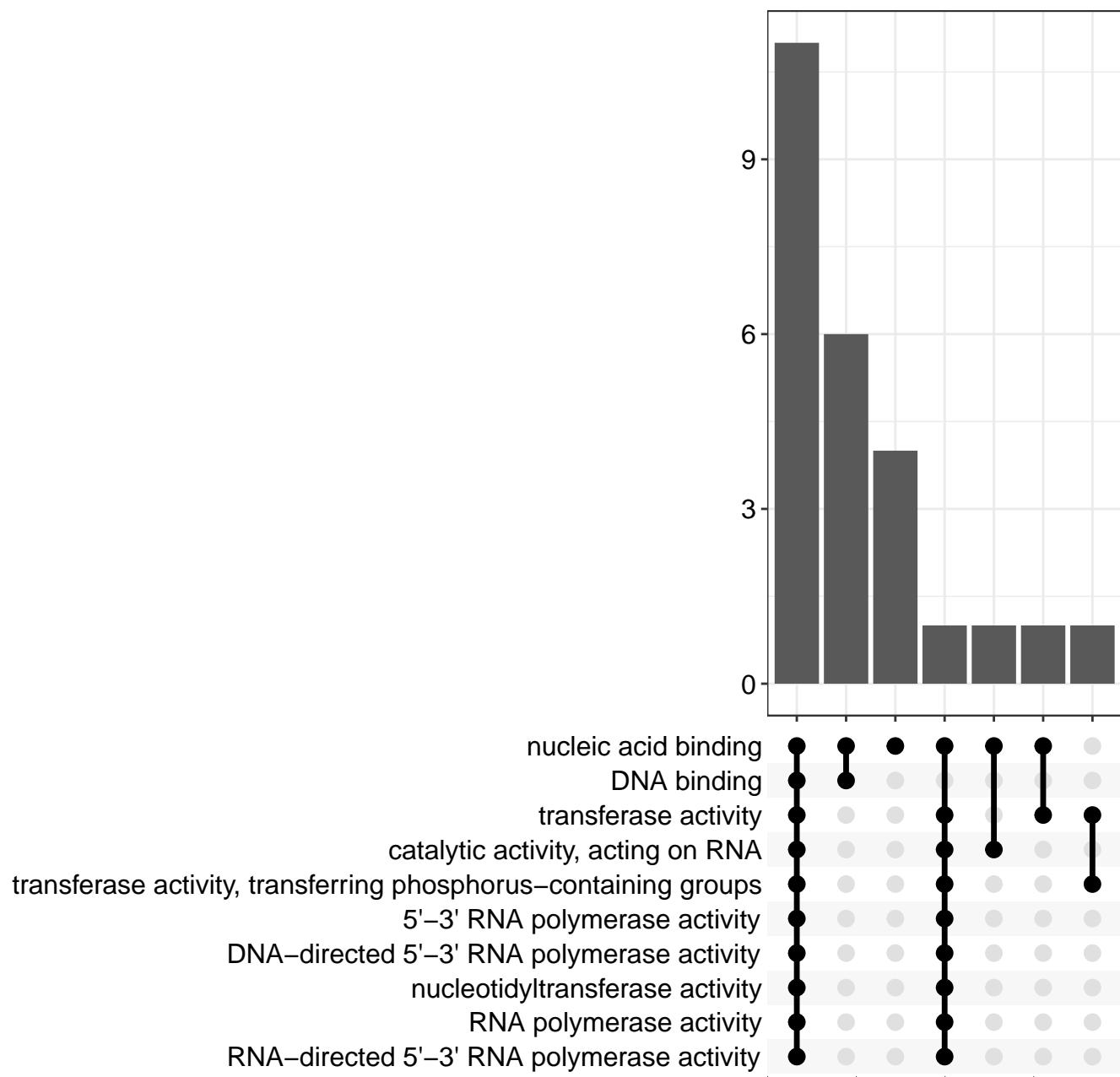
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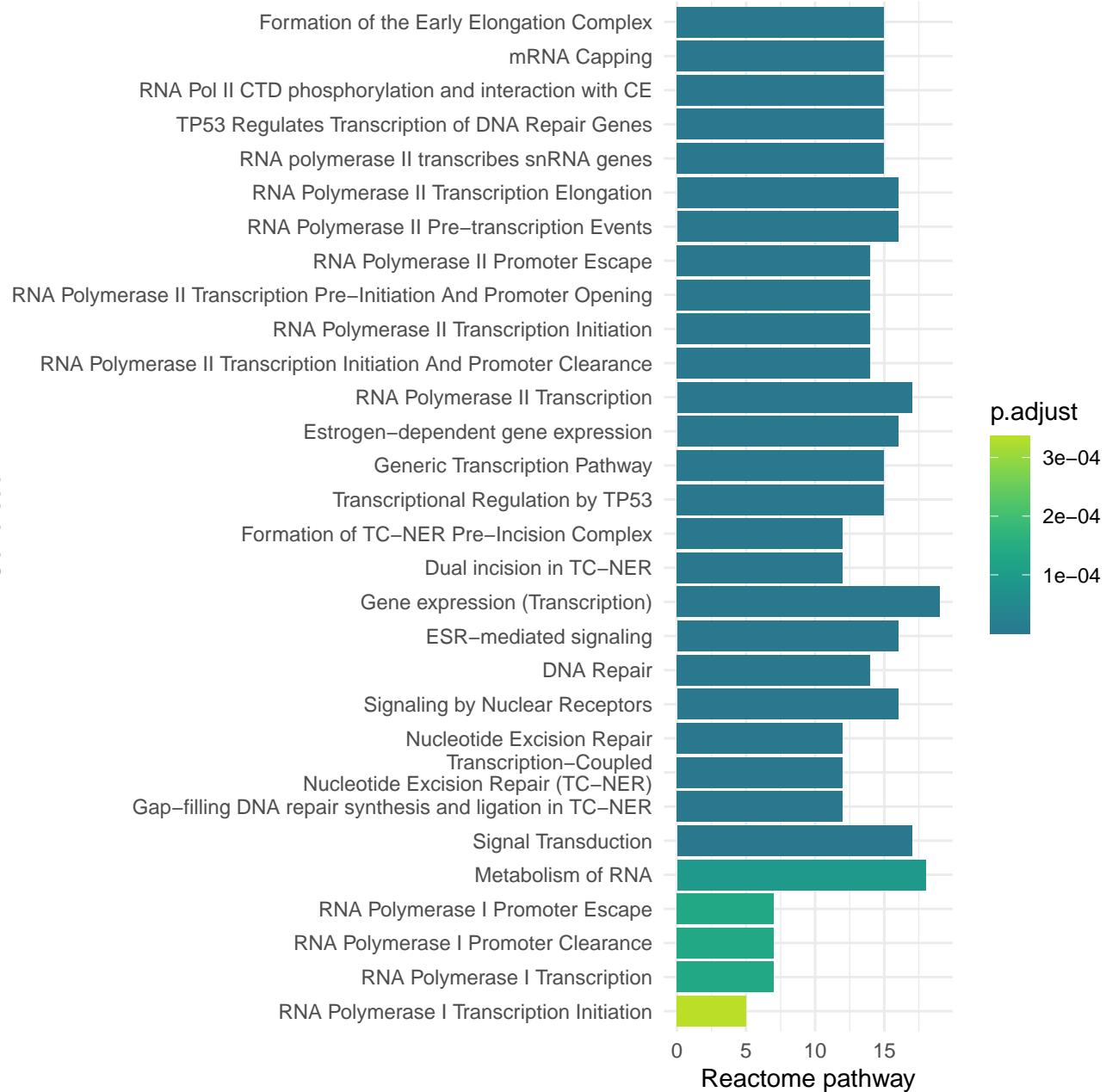
enzyme activator activity



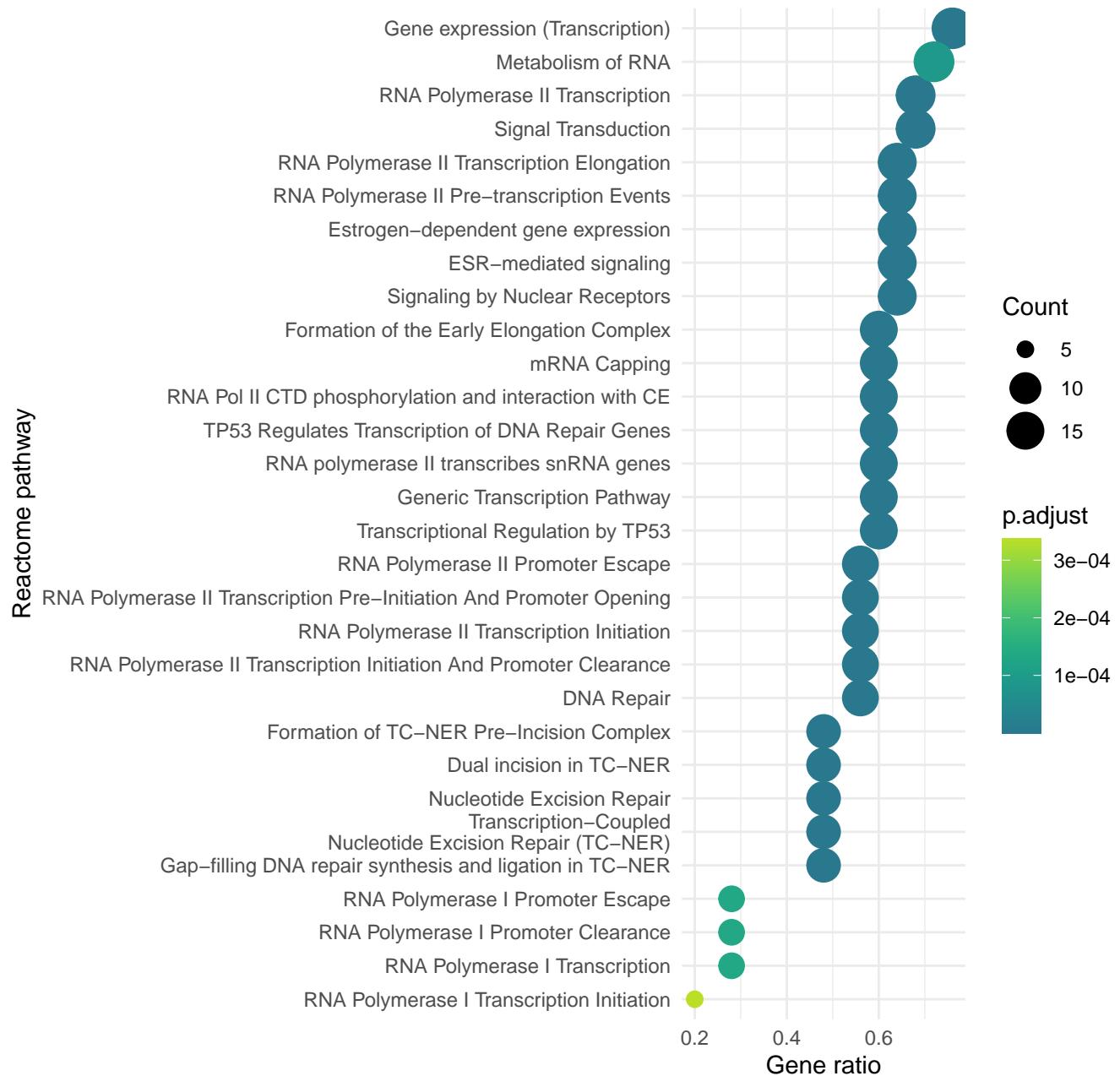
RPO21-TAP Up-regulated



RPO21-TAP Up-regulated Reactome Pathways



RPO21-TAP Up-regulated Reactome pathways

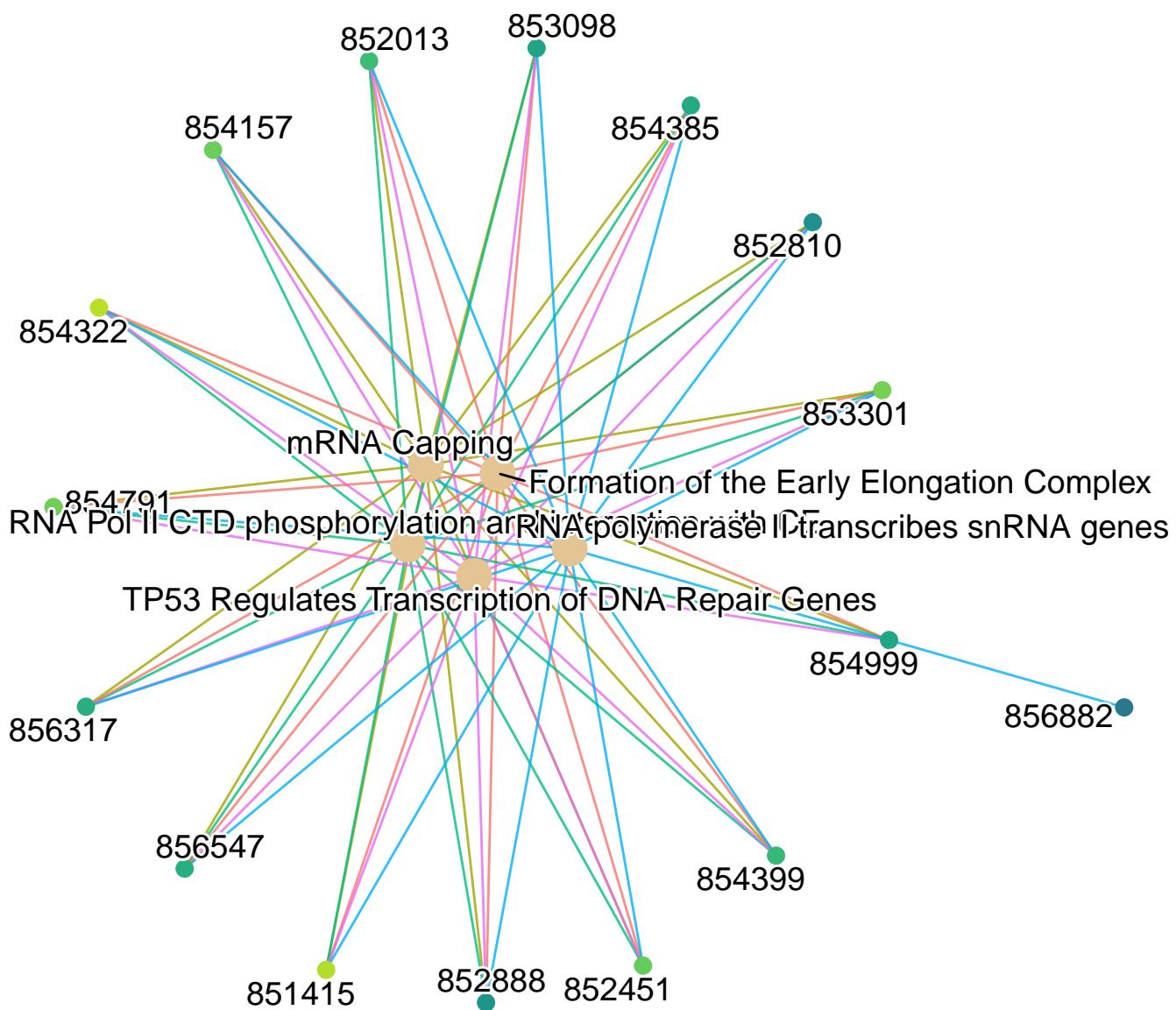


RPO21-TAP Up-regulated Reactome cnetplot

A Pol II CTD phosphorylation and interaction with CE

RNA polymerase II transcribes snRNA genes

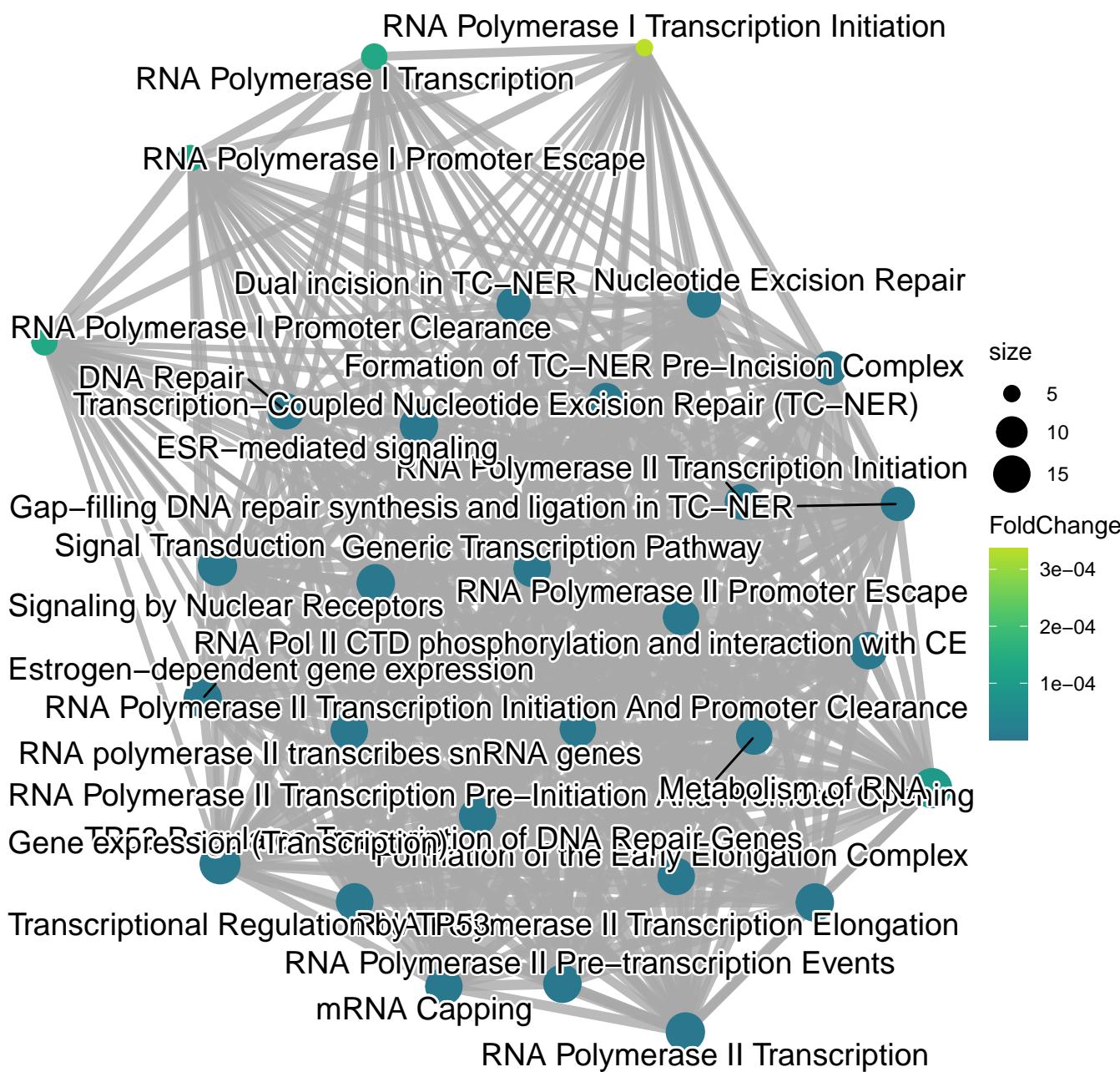
TP53 Regulates

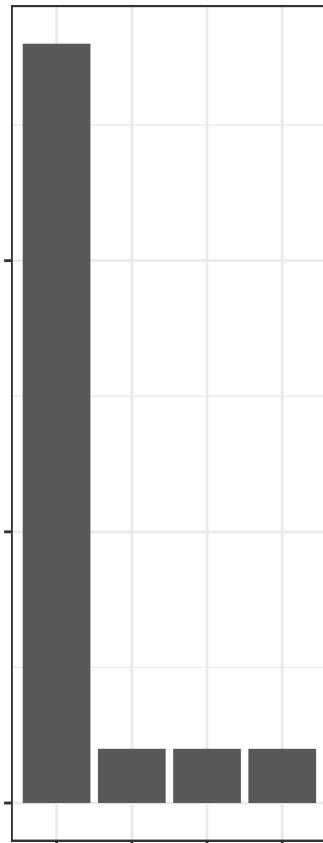


RPO21-TAP Up-regulated Reactome pathway



RPO21-TAP Up-regulated Reactome emapplot





RNA Polymerase II Pre-transcription Events

RNA Polymerase II Transcription Elongation

Formation of the Early Elongation Complex

mRNA Capping

RNA Pol II CTD phosphorylation and interaction with CE

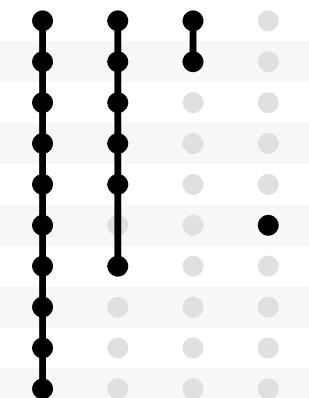
RNA polymerase II transcribes snRNA genes

TP53 Regulates Transcription of DNA Repair Genes

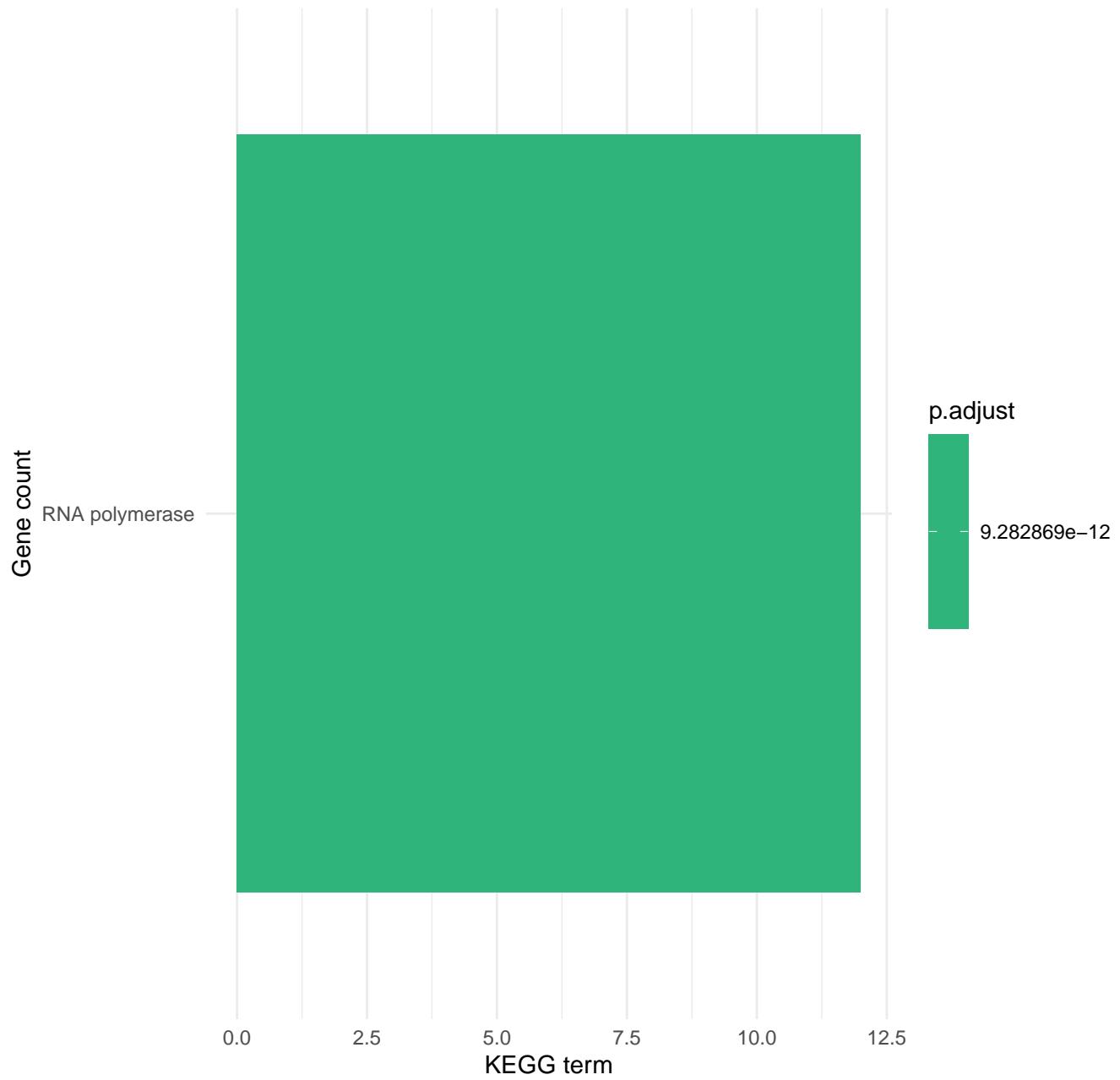
RNA Polymerase II Promoter Escape

RNA Polymerase II Transcription Initiation

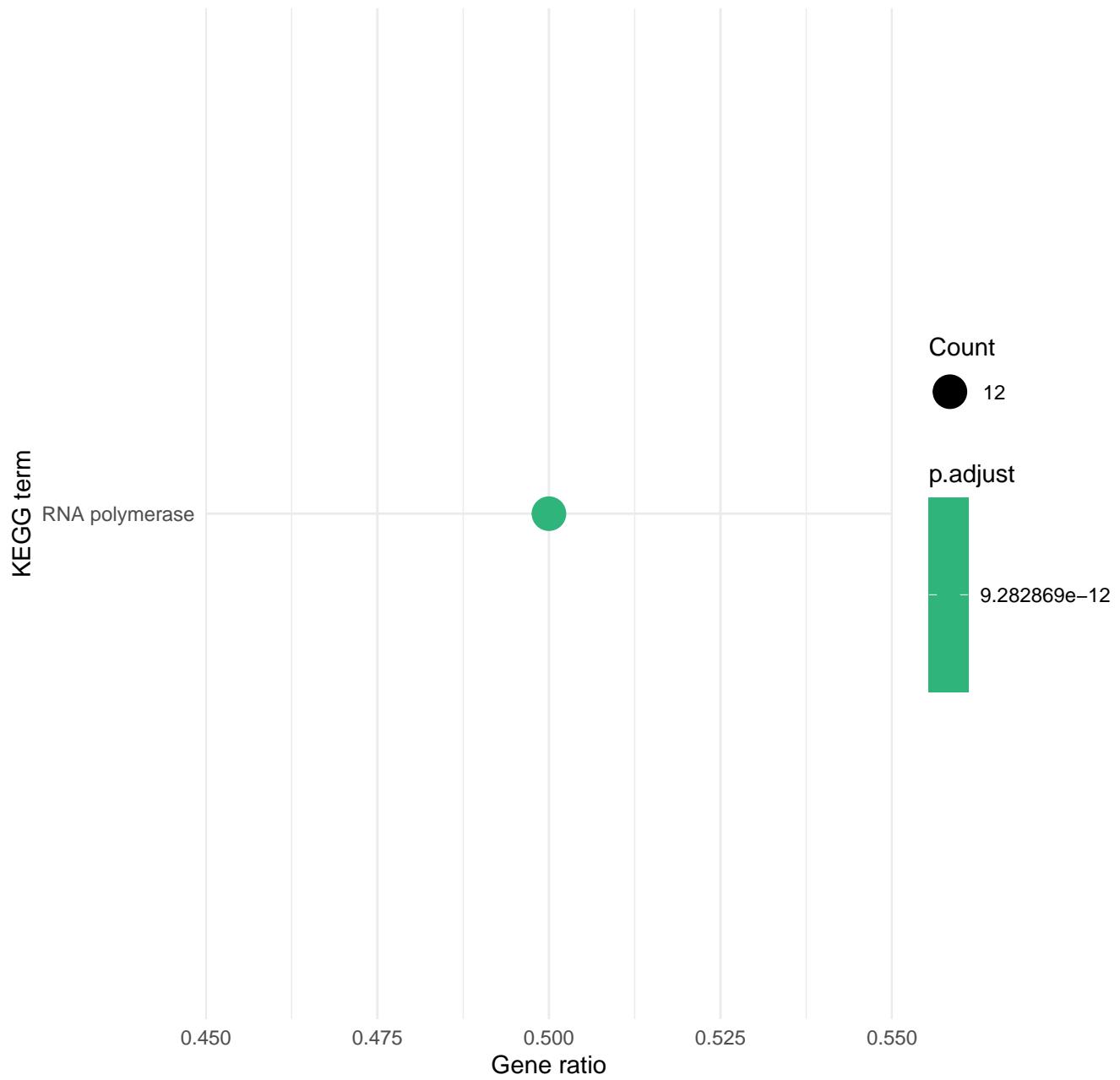
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening



RPO21-TAP Up-regulated KEGG barplot



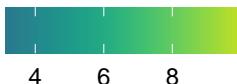
RPO21-TAP Up-regulated KEGG dotplot



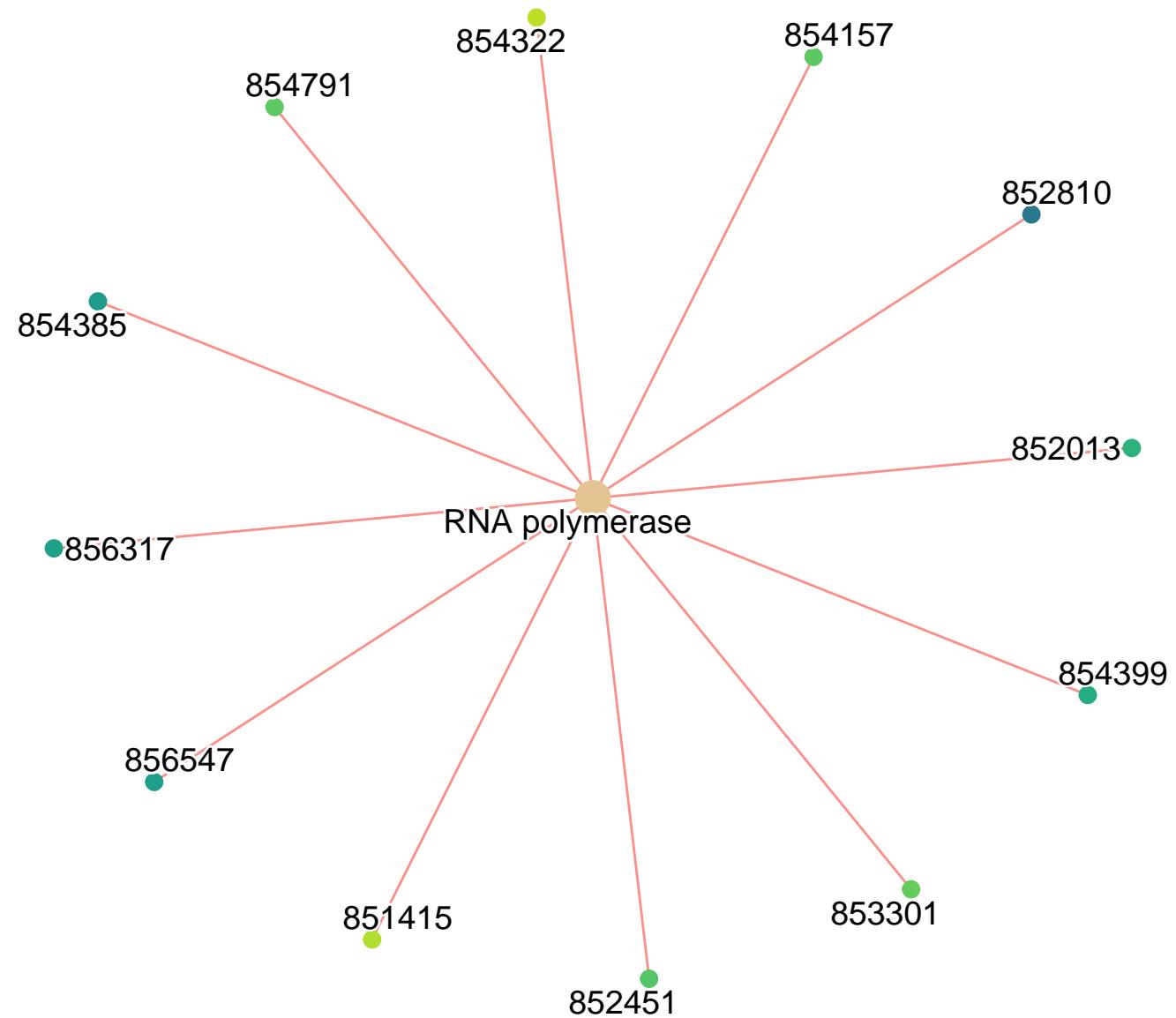
RPO21-TAP Up-regulated KEGG dotplot

category RNA polymerase

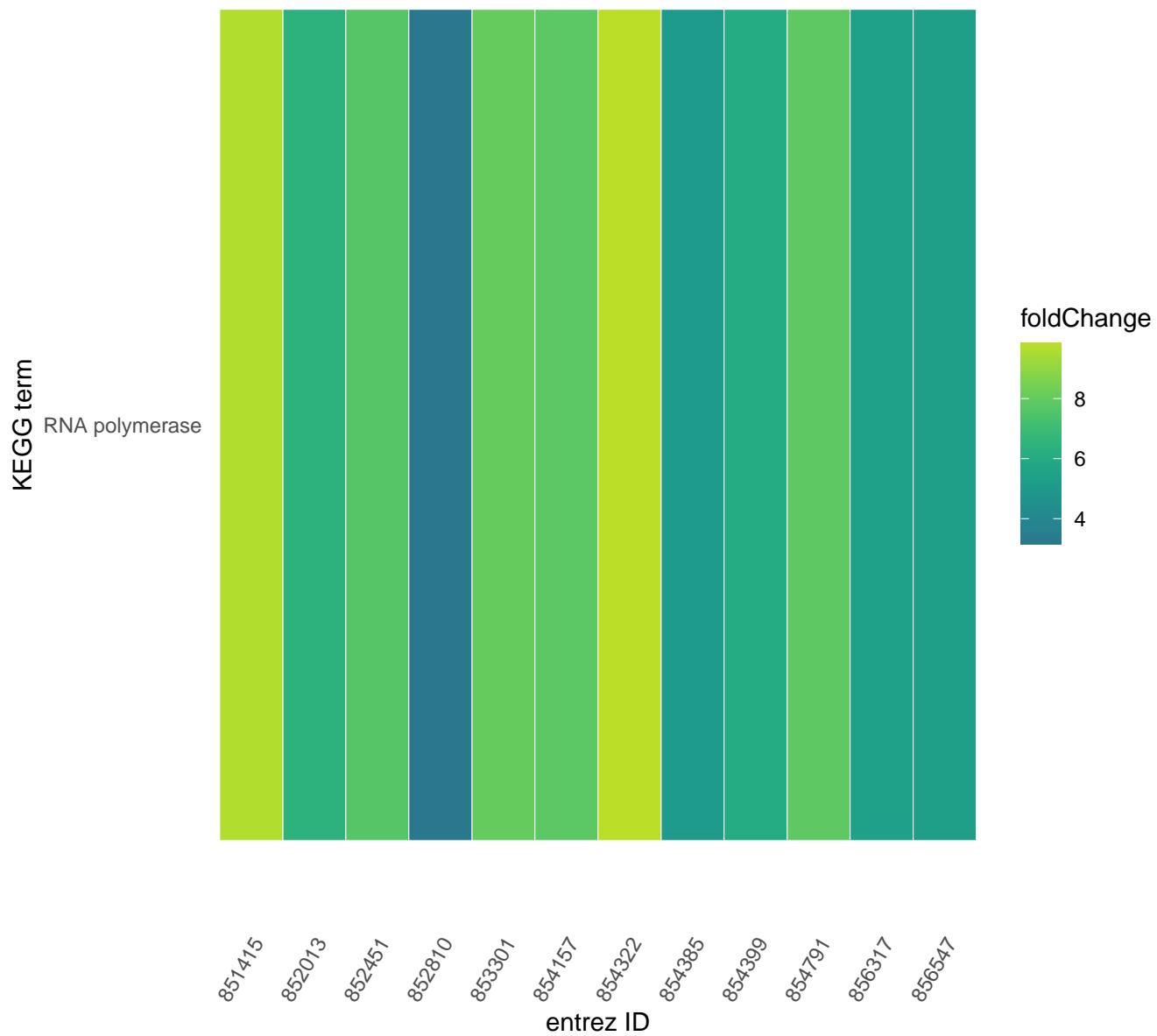
FoldChange



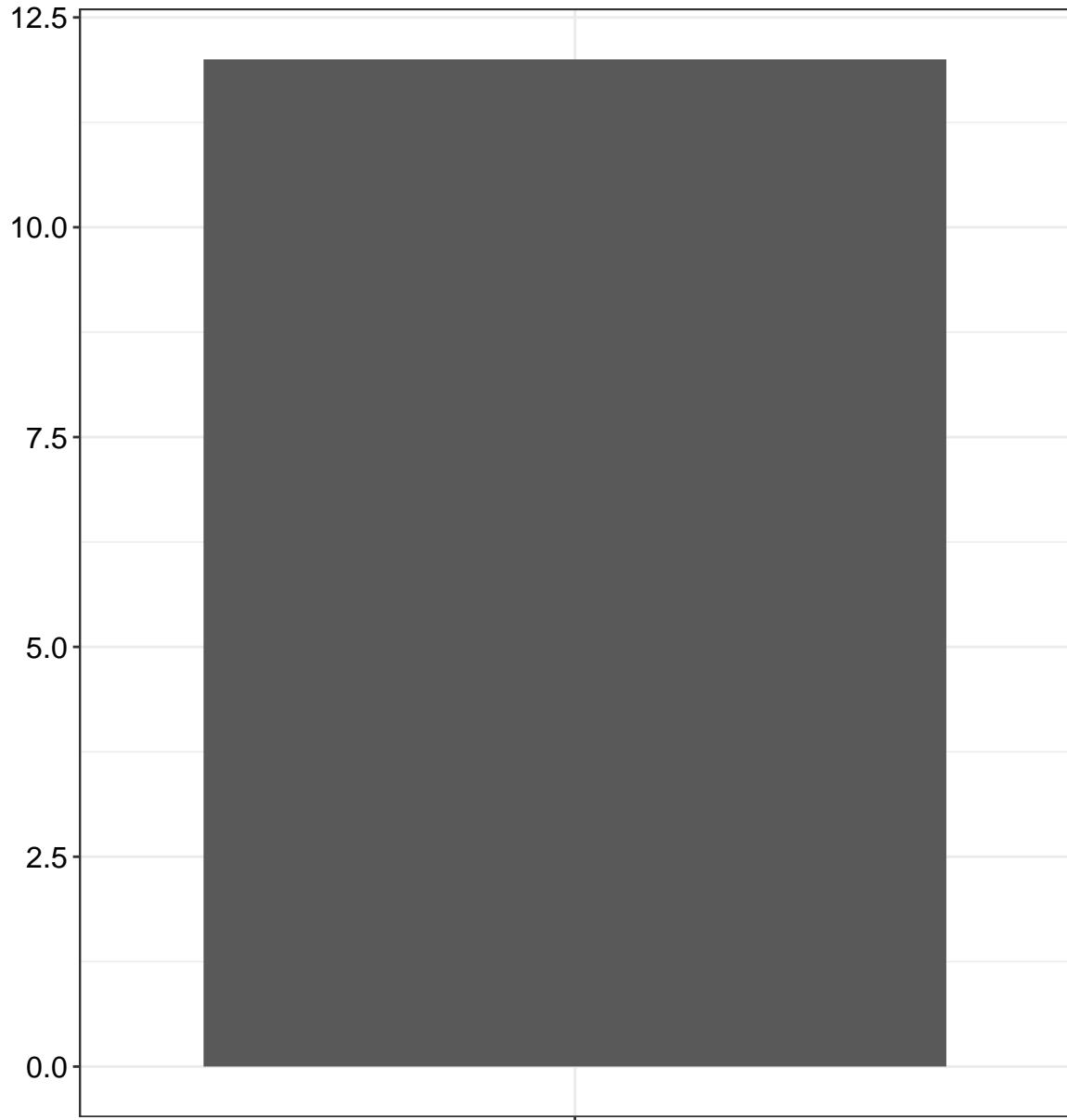
size 12



RPO21-TAP Up-regulated KEGG heatplot



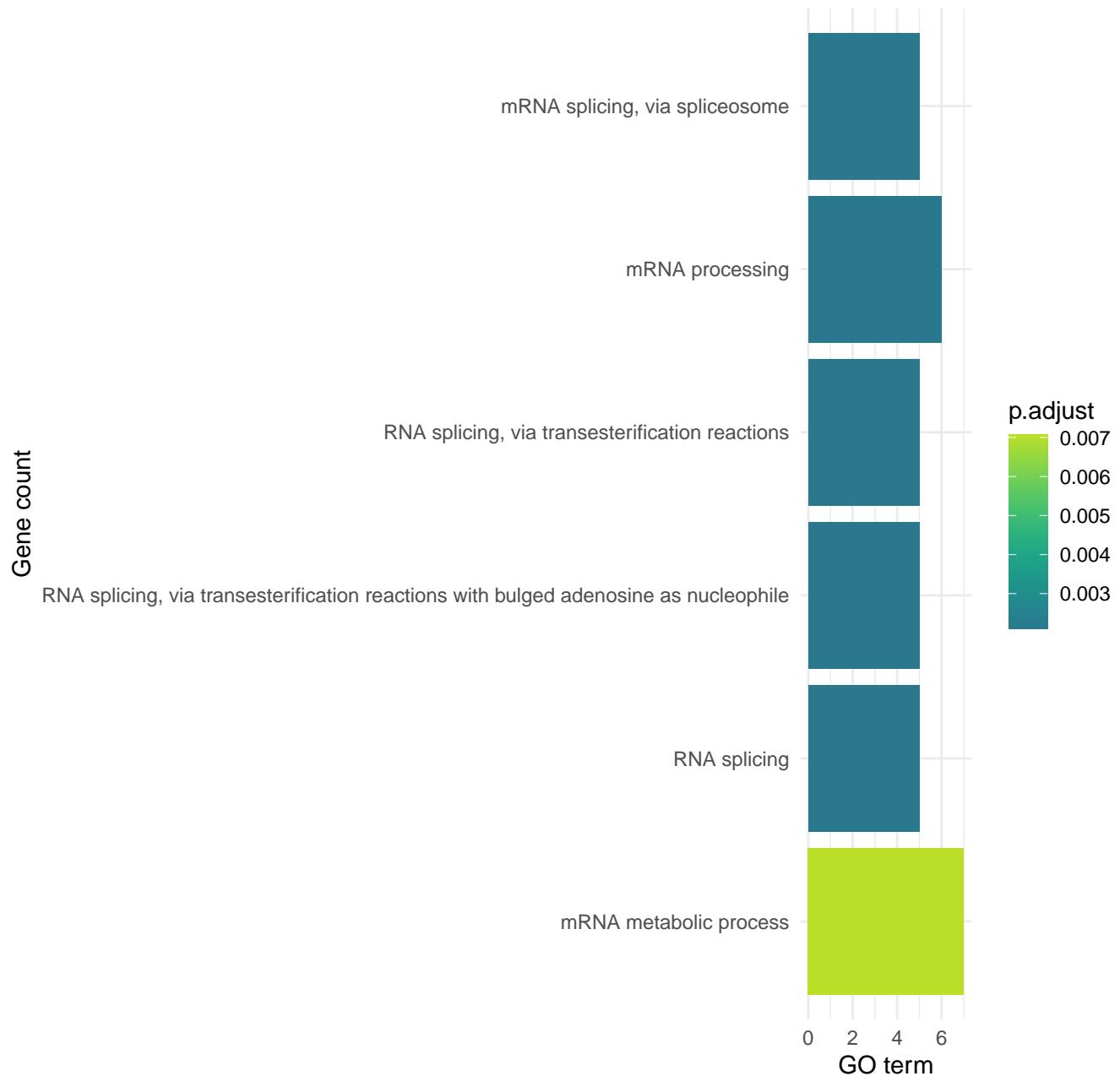
RPO21-TAP Up-regulated KEGG upsetplot



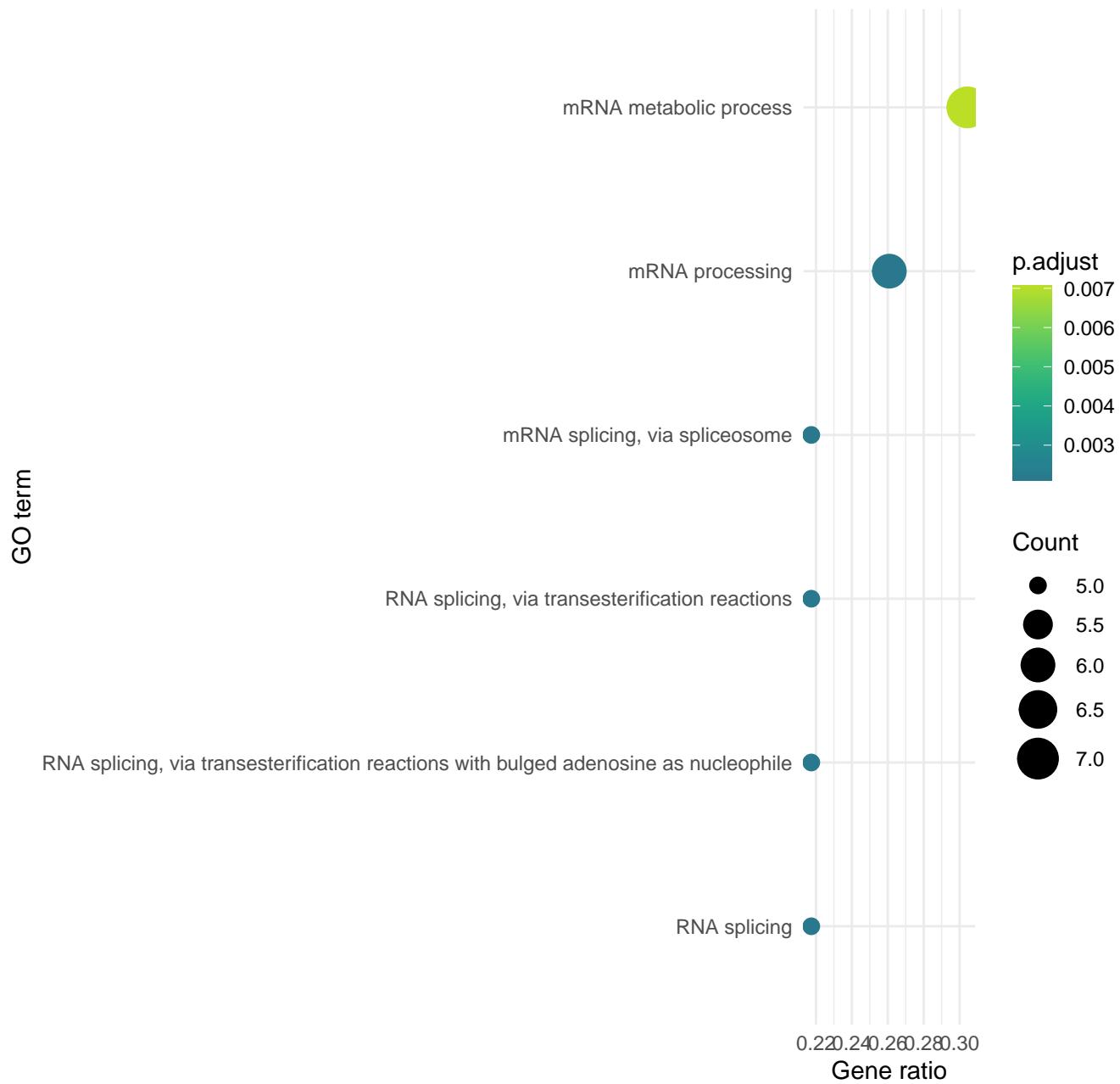
RNA polymerase



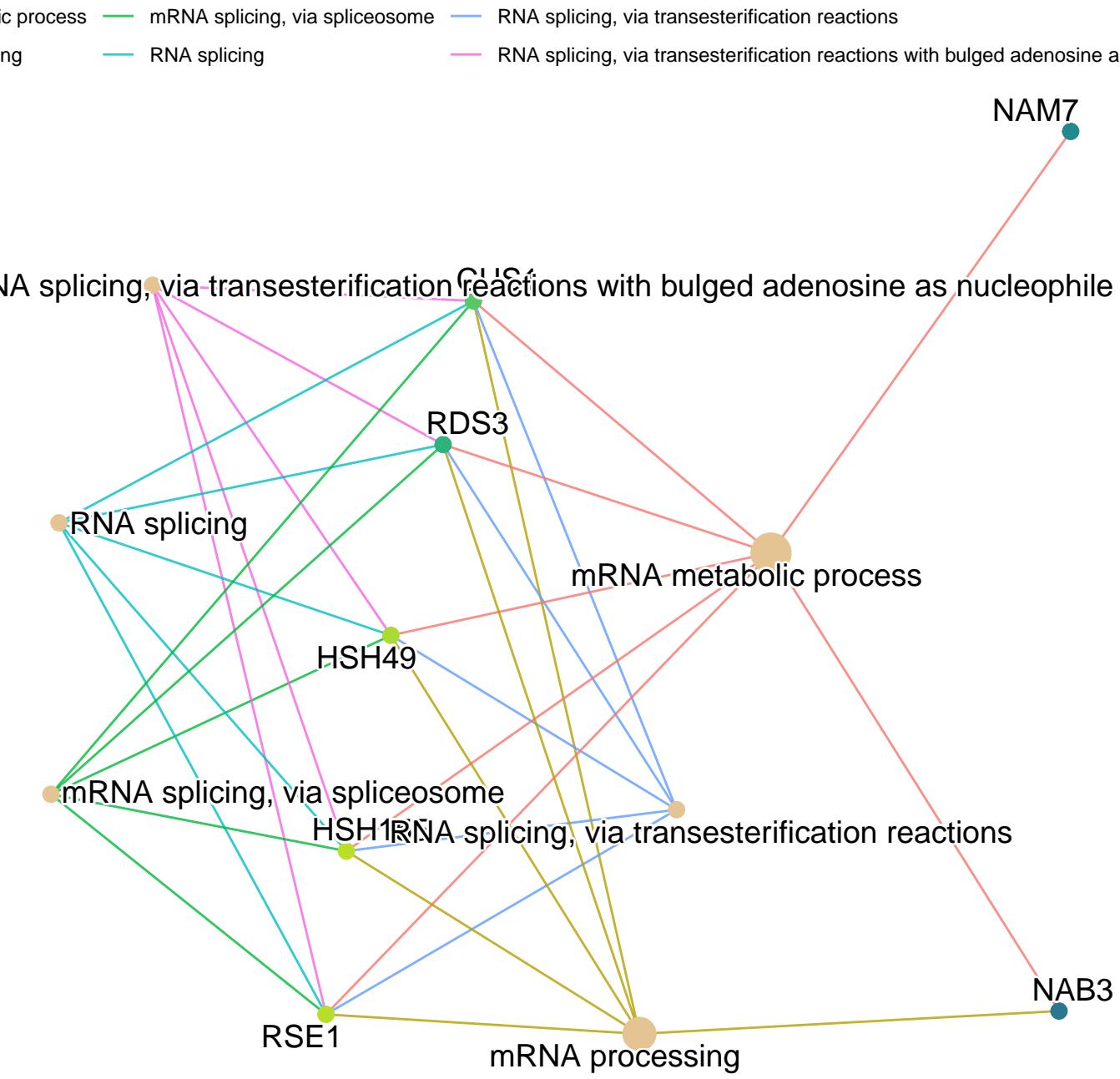
HSH49-TAP Up-regulate



HSH49-TAP Up-regulate



HSH49-TAP Up-regulated GO BP cnetplot



HSH49-TAP Up-regulate

GO term

RNA splicing, via transesterification reactions with bulged adenosine as nucleophile

RNA splicing, via transesterification reactions

RNA splicing

mRNA splicing, via spliceosome

mRNA processing

mRNA metabolic process

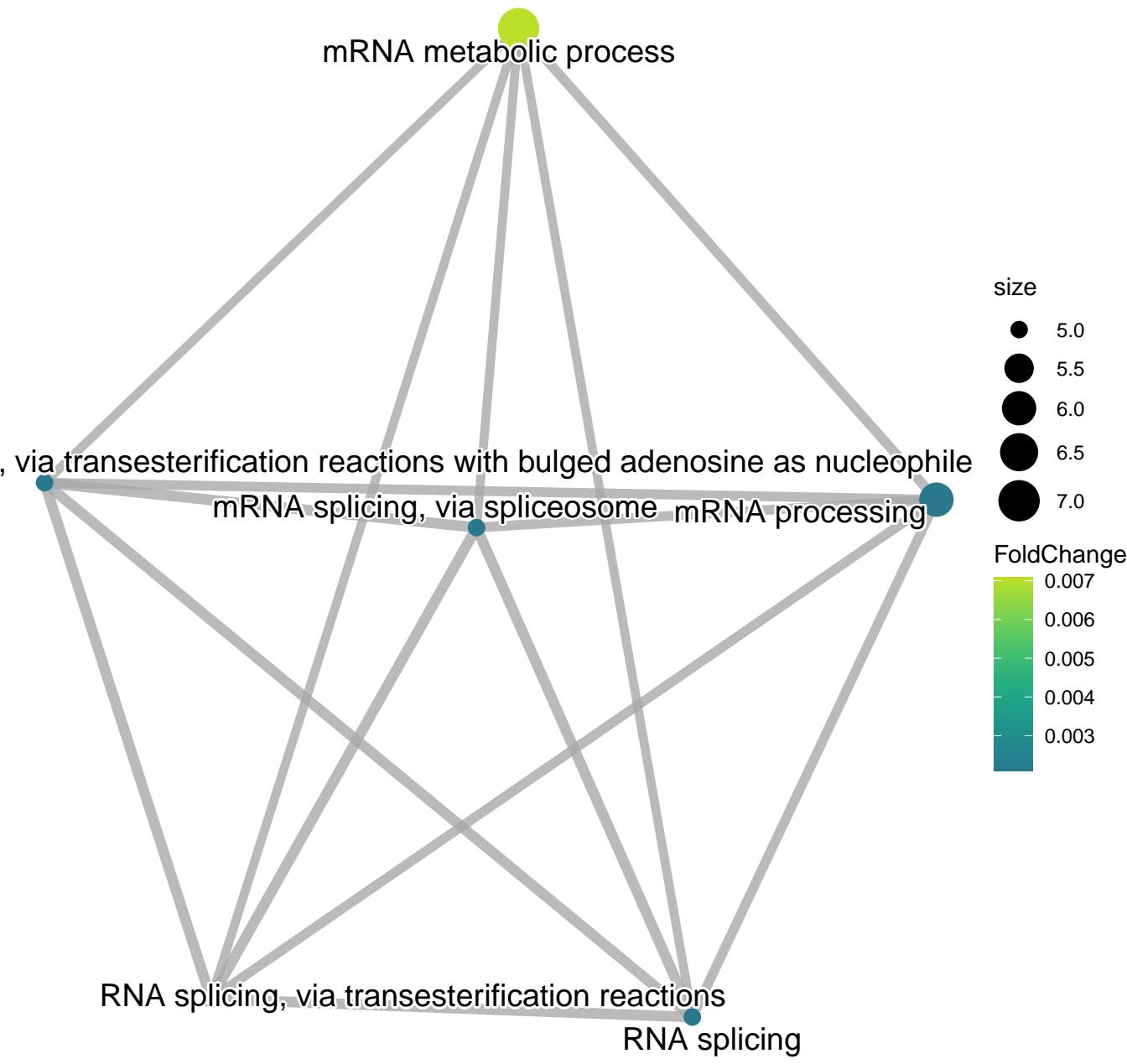
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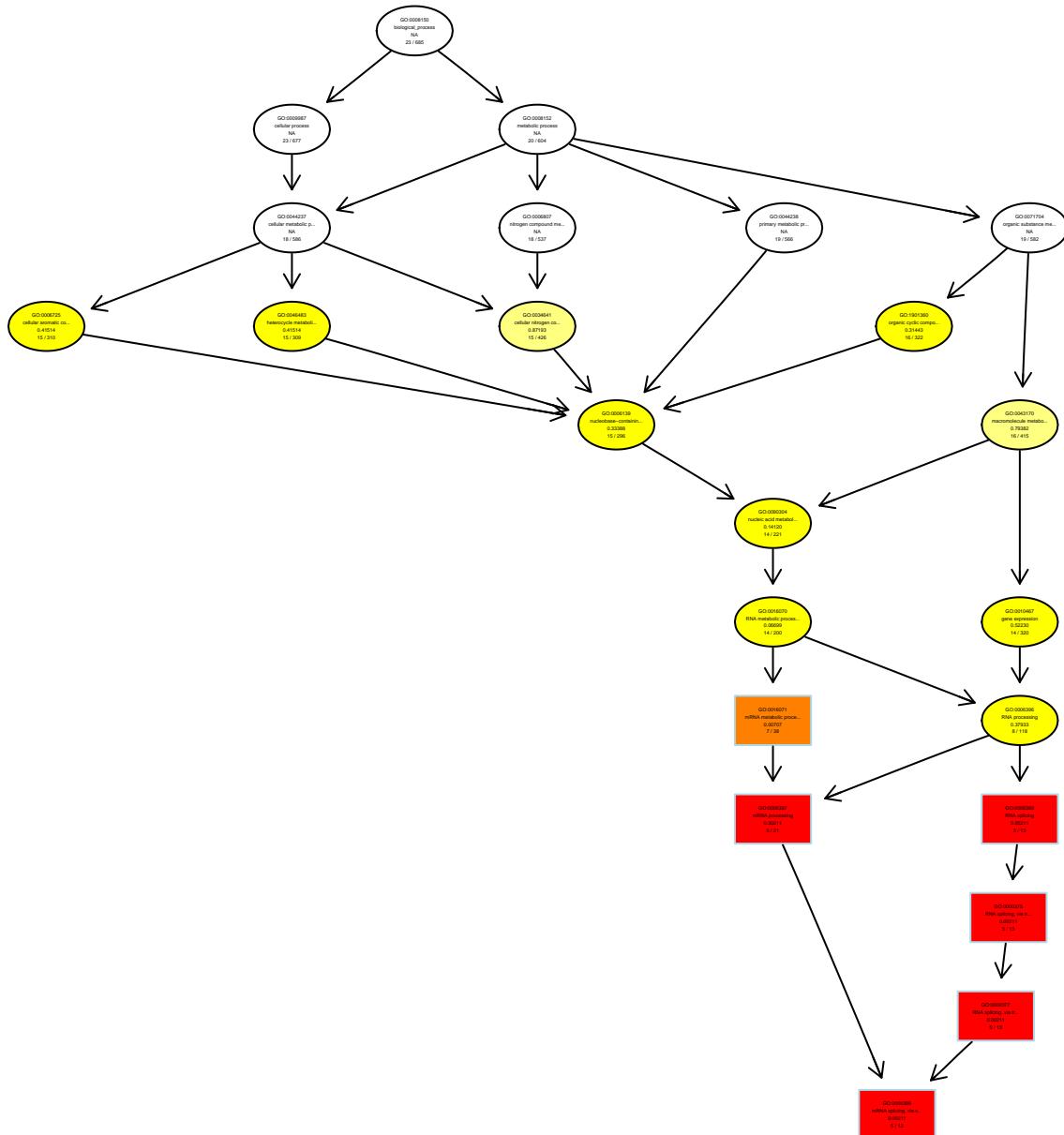


CUS1
HSH155
HSH49
NAB3
NAM7
RDS3
RSE1

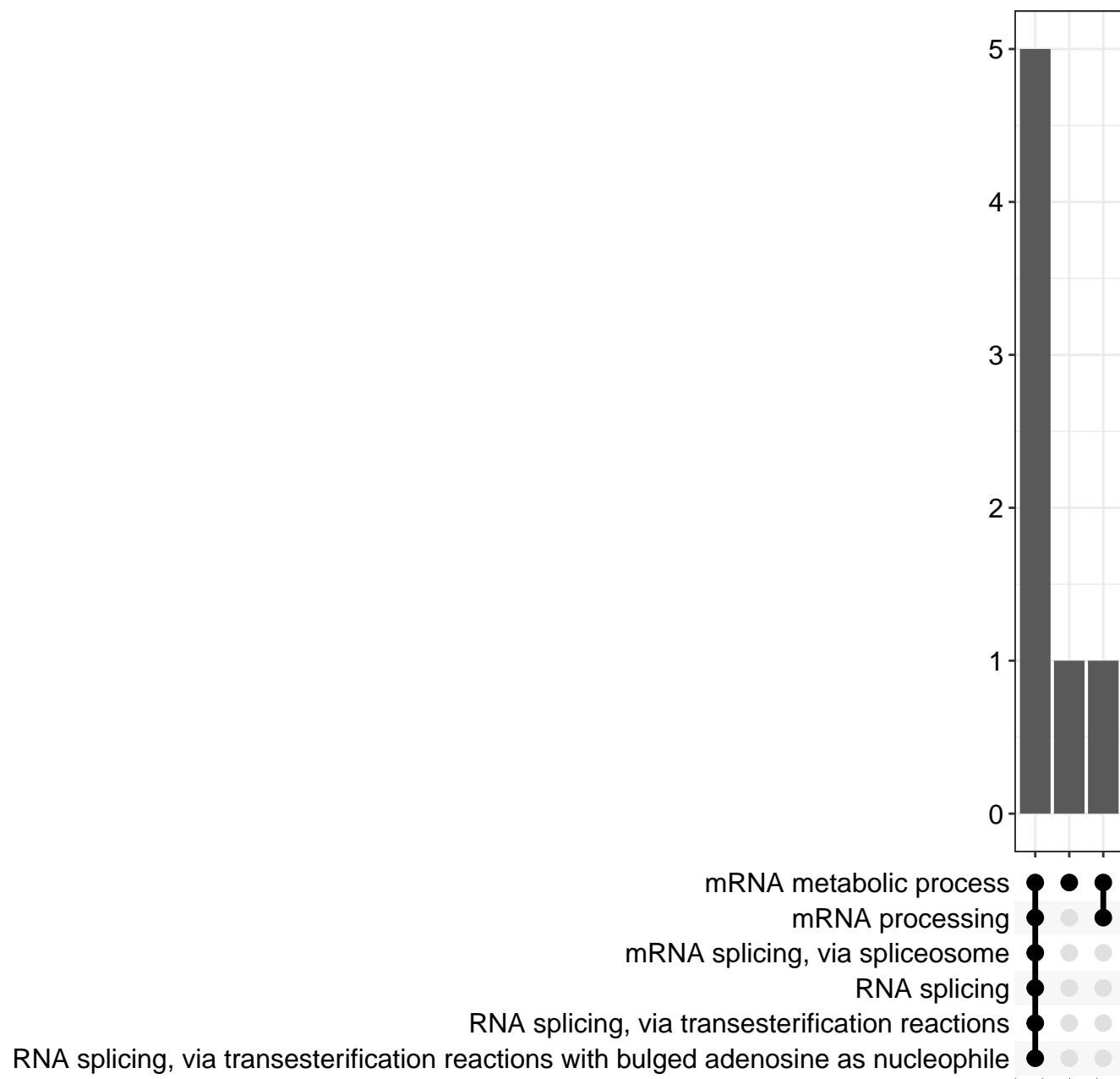
Gene name

HSH49-TAP Up-regulated GO BP emapplot

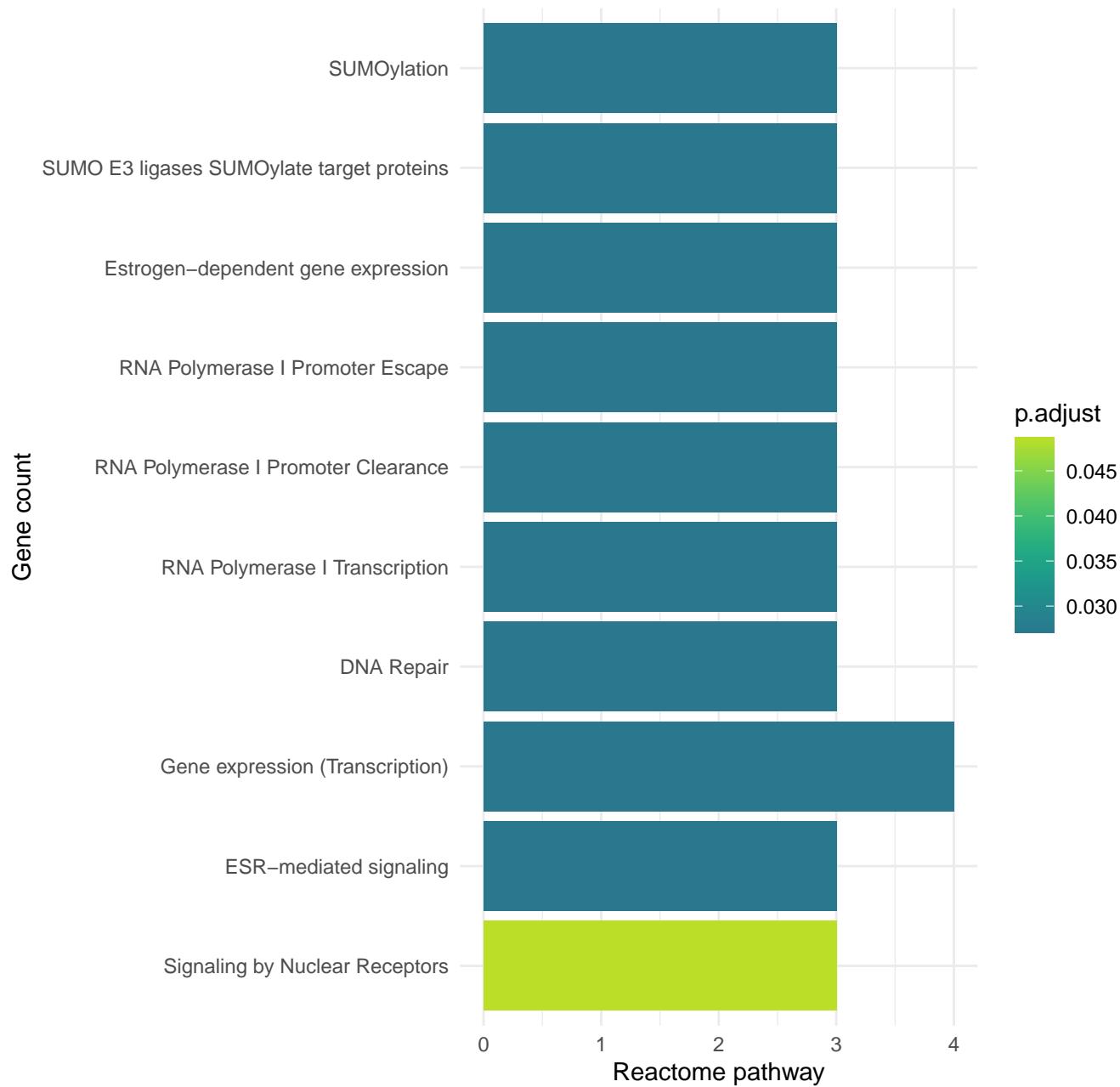




HSH49-T

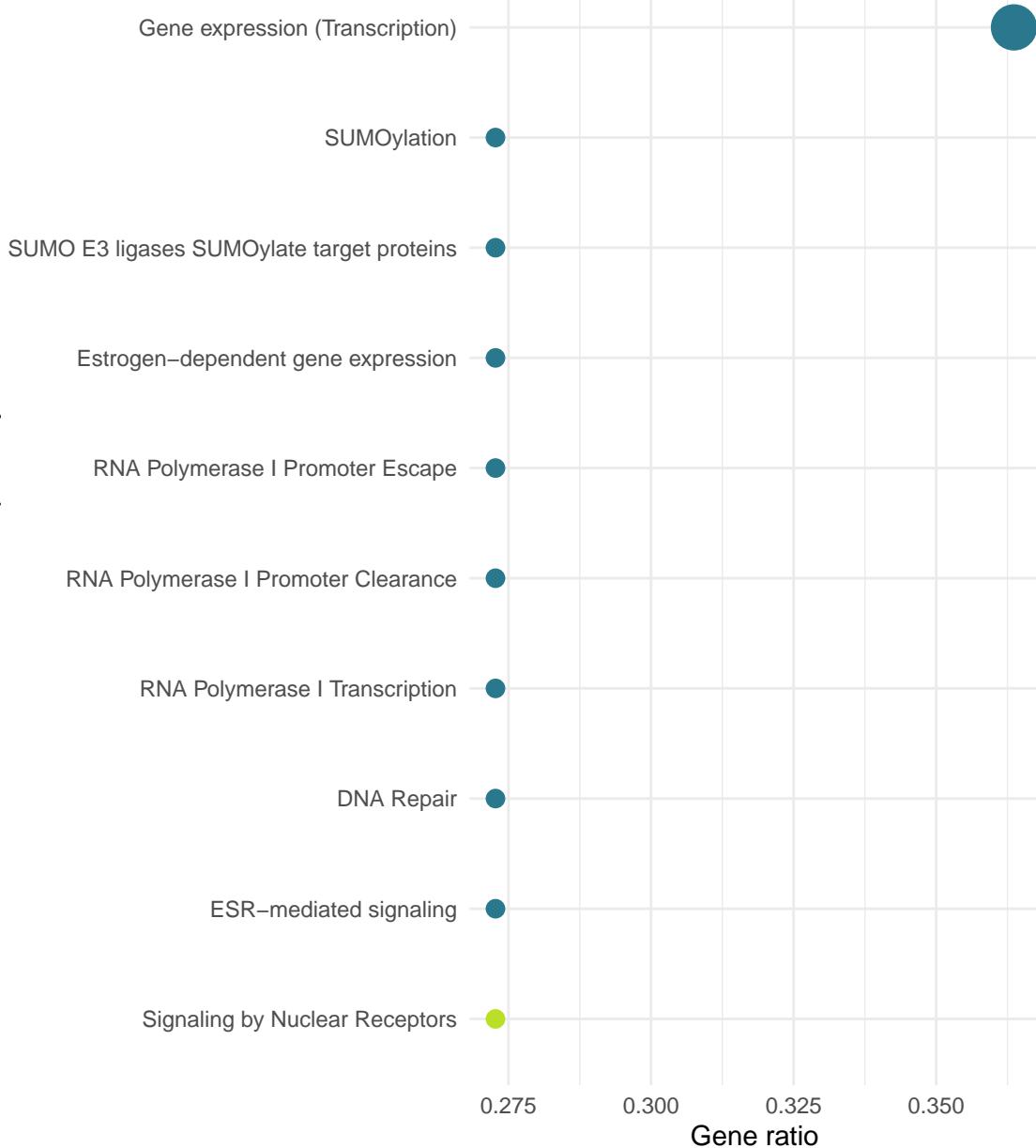


HSH49-TAP Up-regulated Reactome barplot

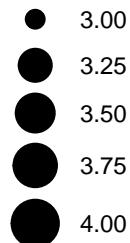


HSH49–TAP Up-regulated Reactome dotplot

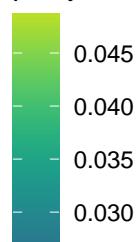
Reactome pathway



Count

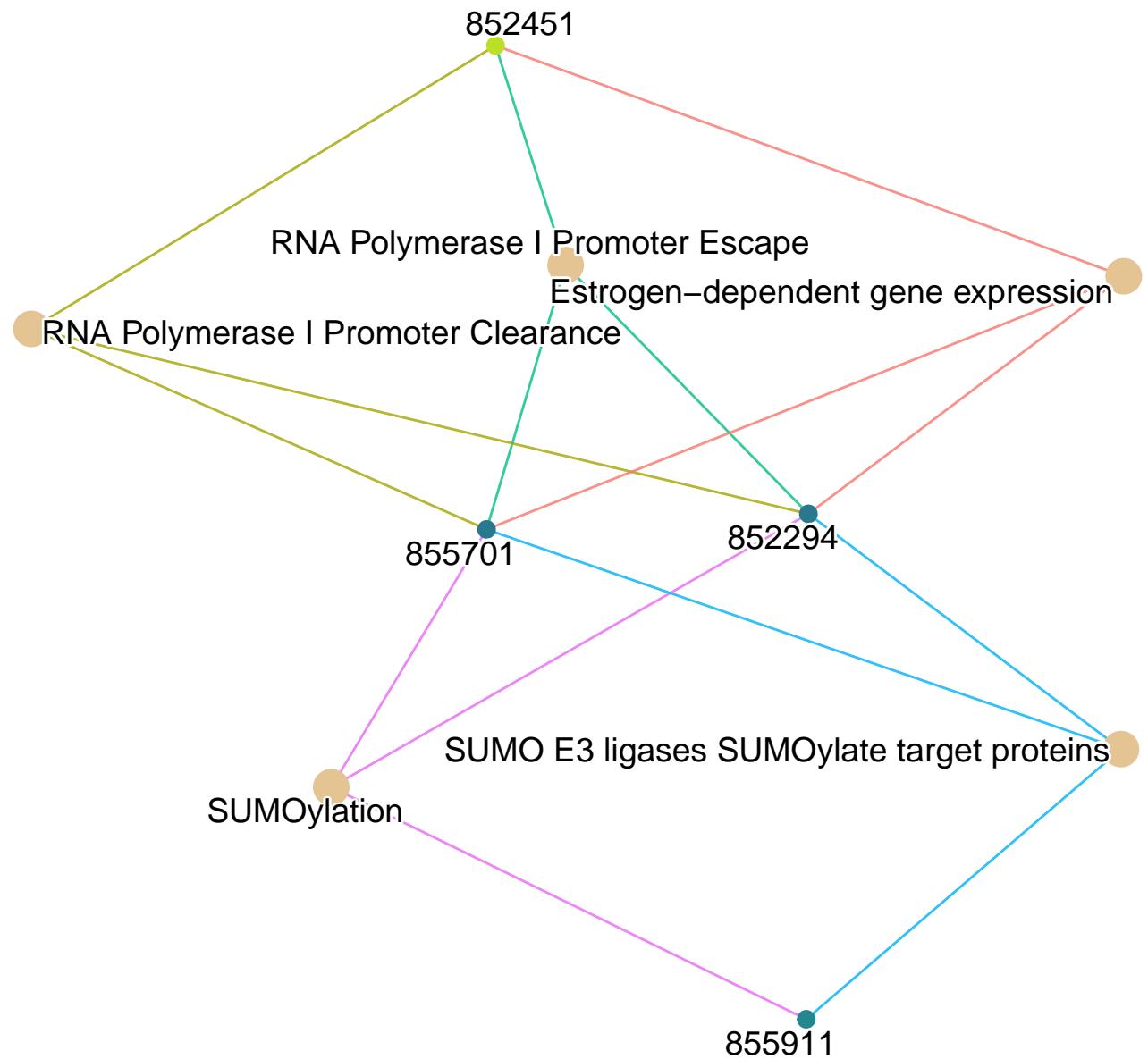


p.adjust

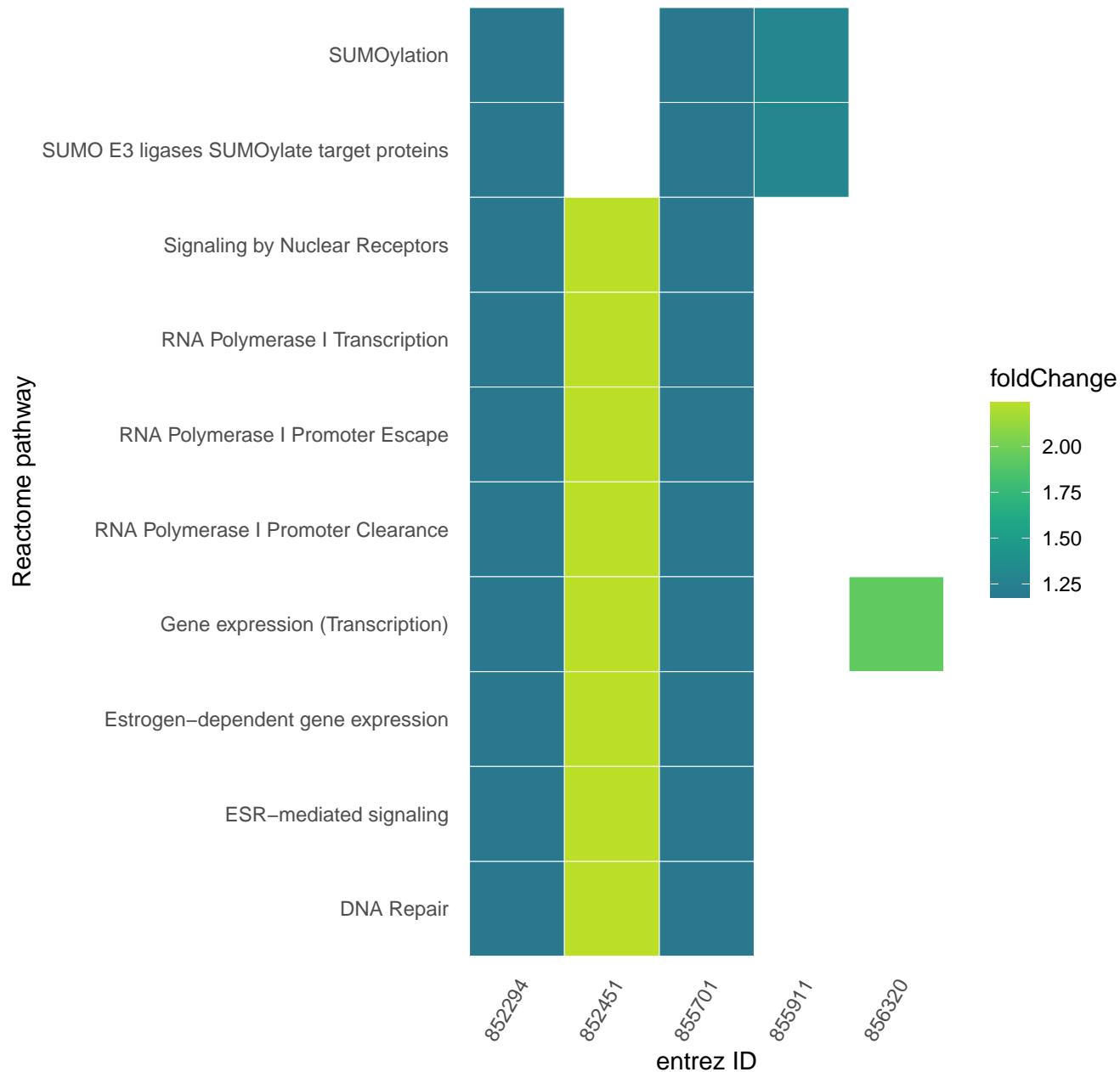


HSH49-TAP Up-regulated Reactome cnetplot

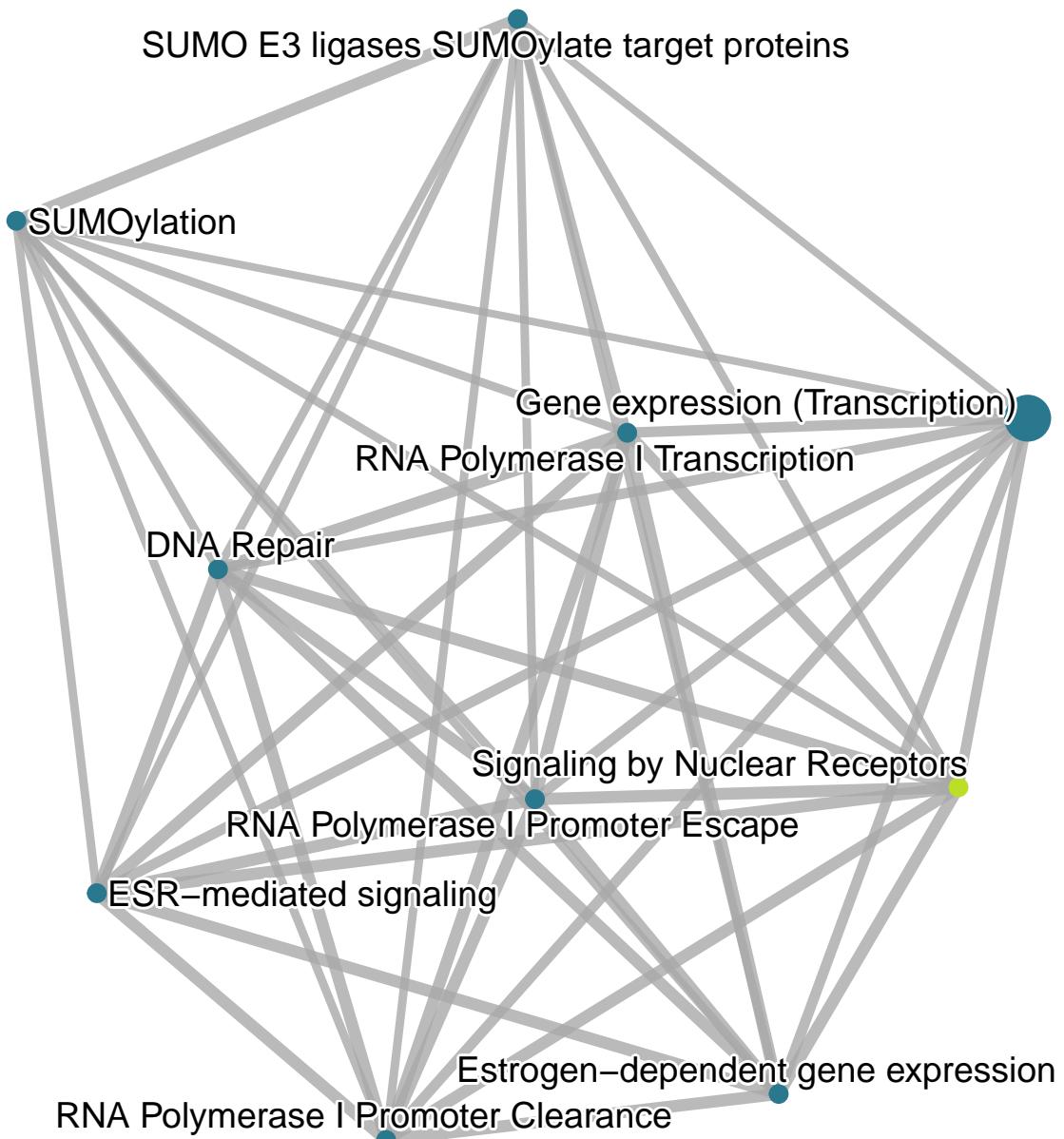
RNA Polymerase I Promoter Clearance RNA Polymerase I Promoter Escape SUMO E3 ligases SUMOylate target proteins



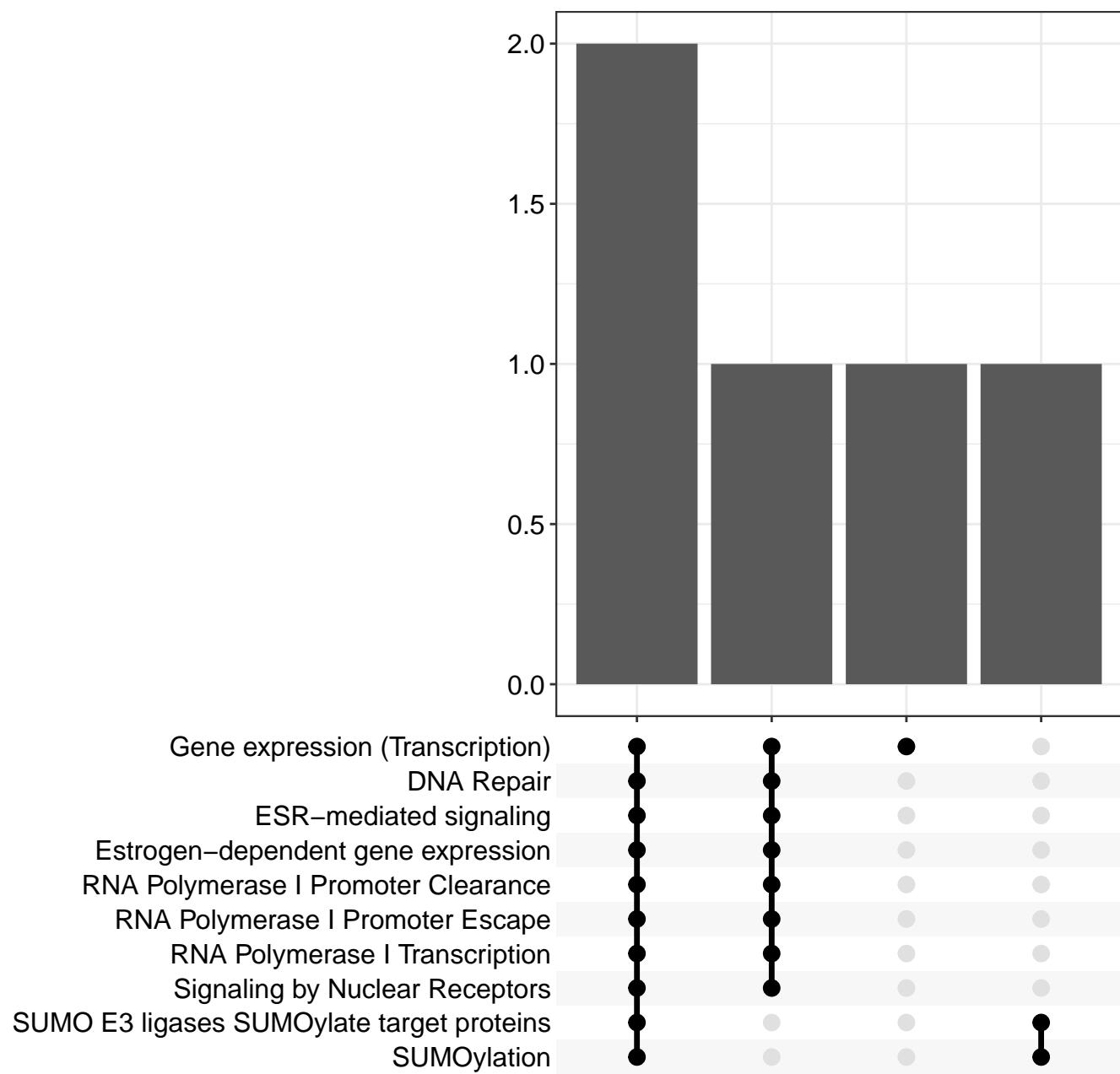
HSH49-TAP Up-regulated Reactome heatplot



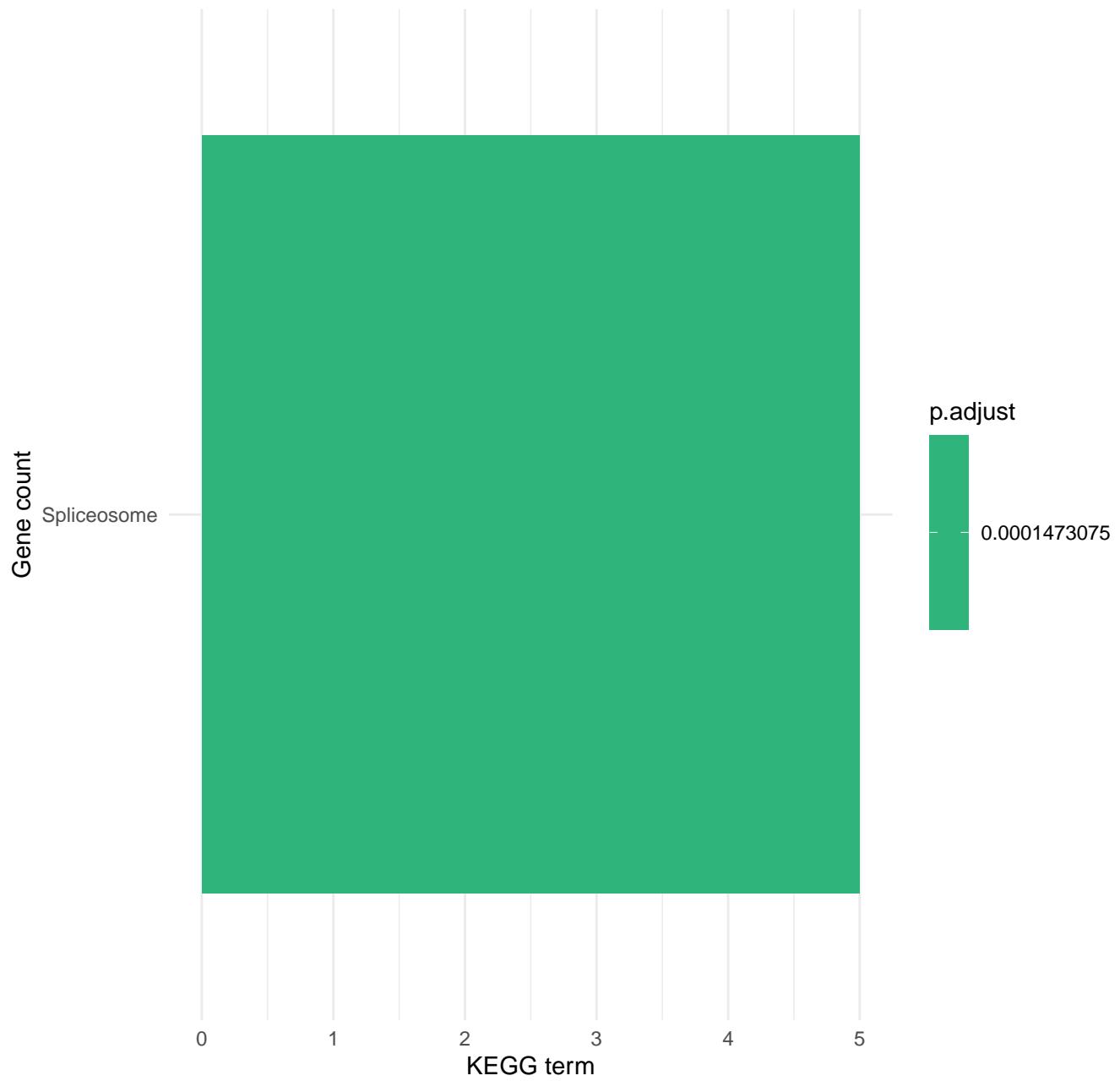
HSH49-TAP Up-regulated Reactome emapplot



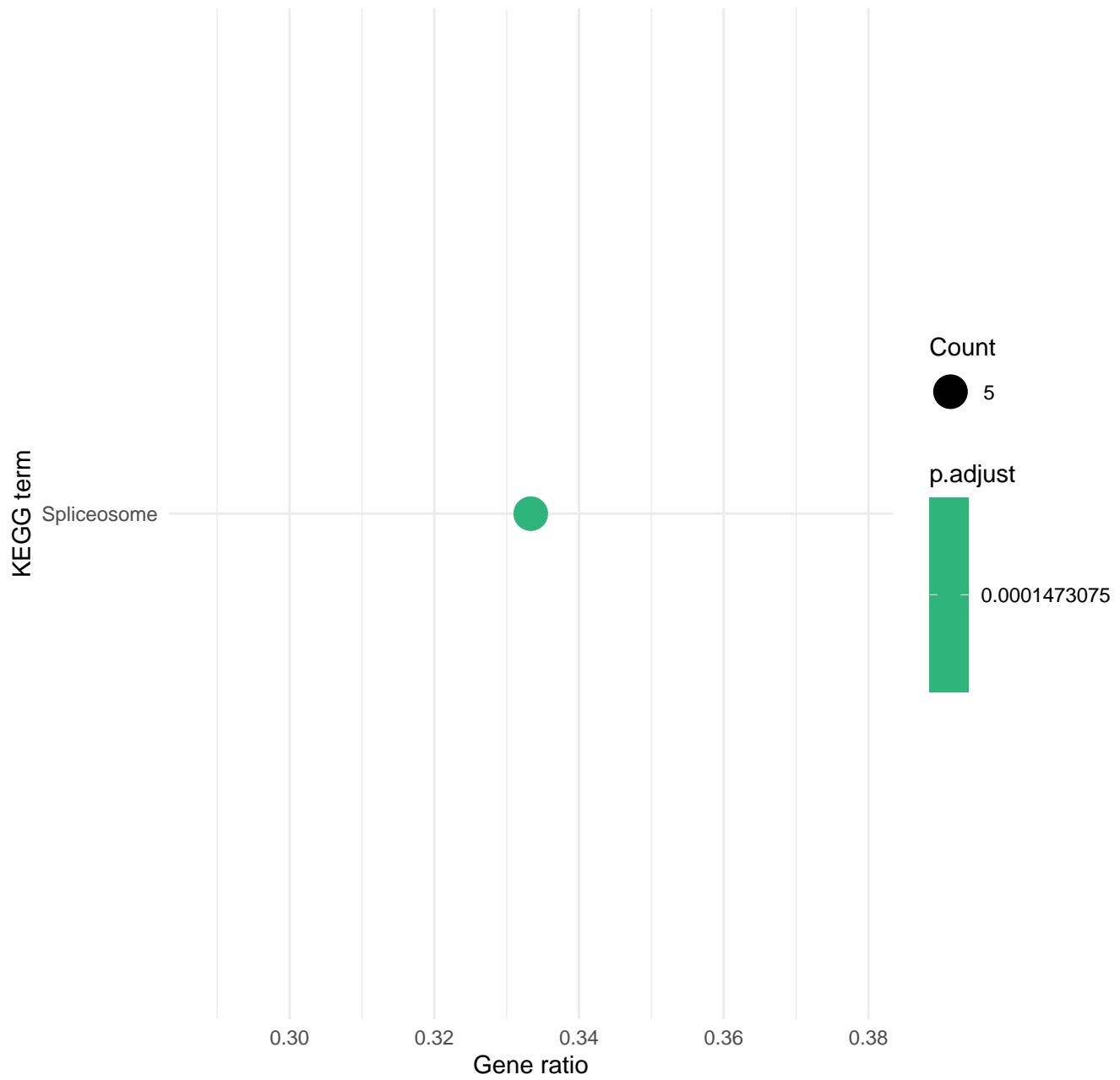
HSH49–TAP Up-regulated Reactome upsets



HSH49-TAP Up-regulated KEGG barplot



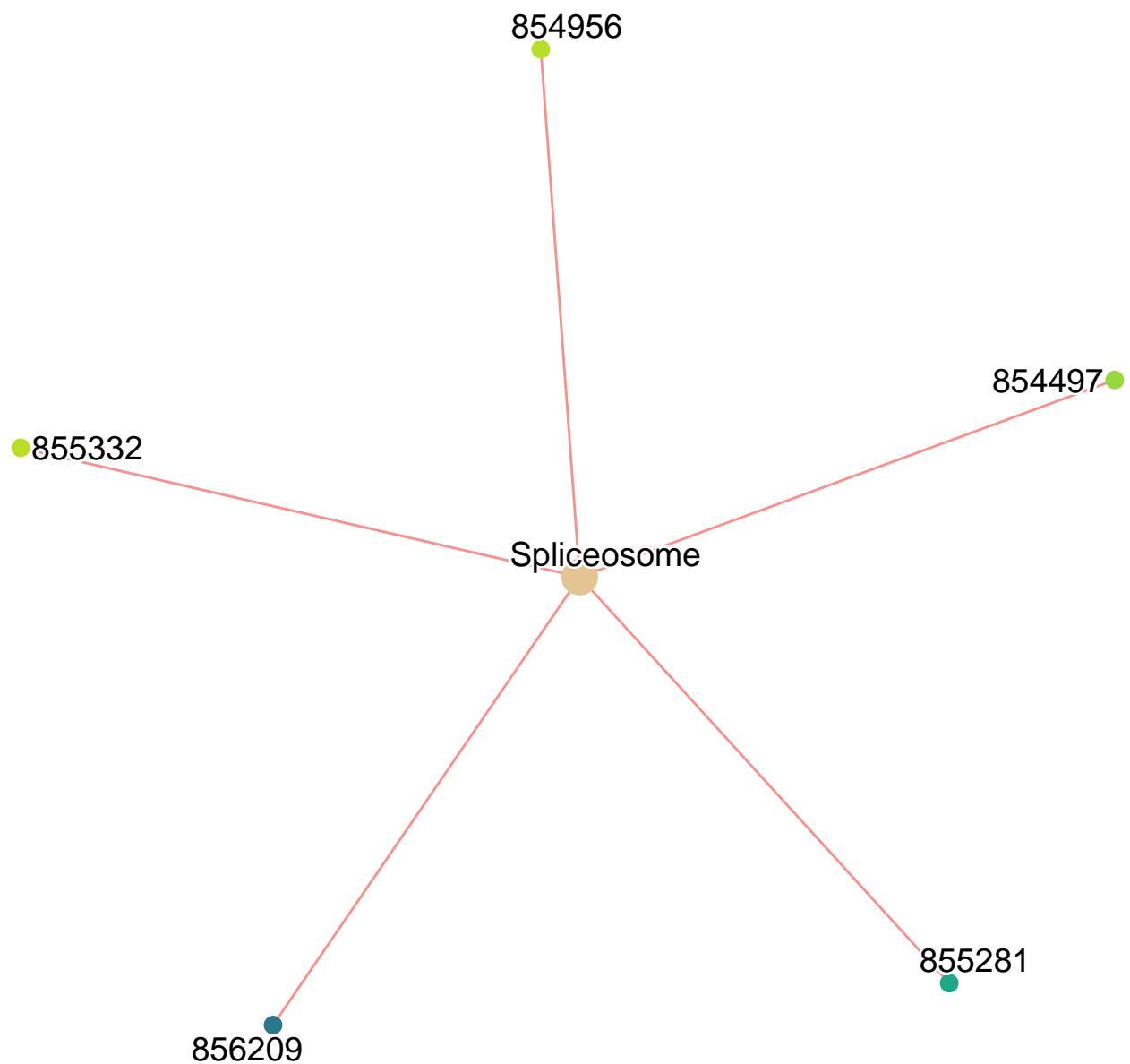
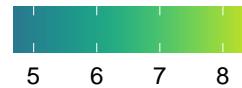
HSH49-TAP Up-regulated KEGG dotplot



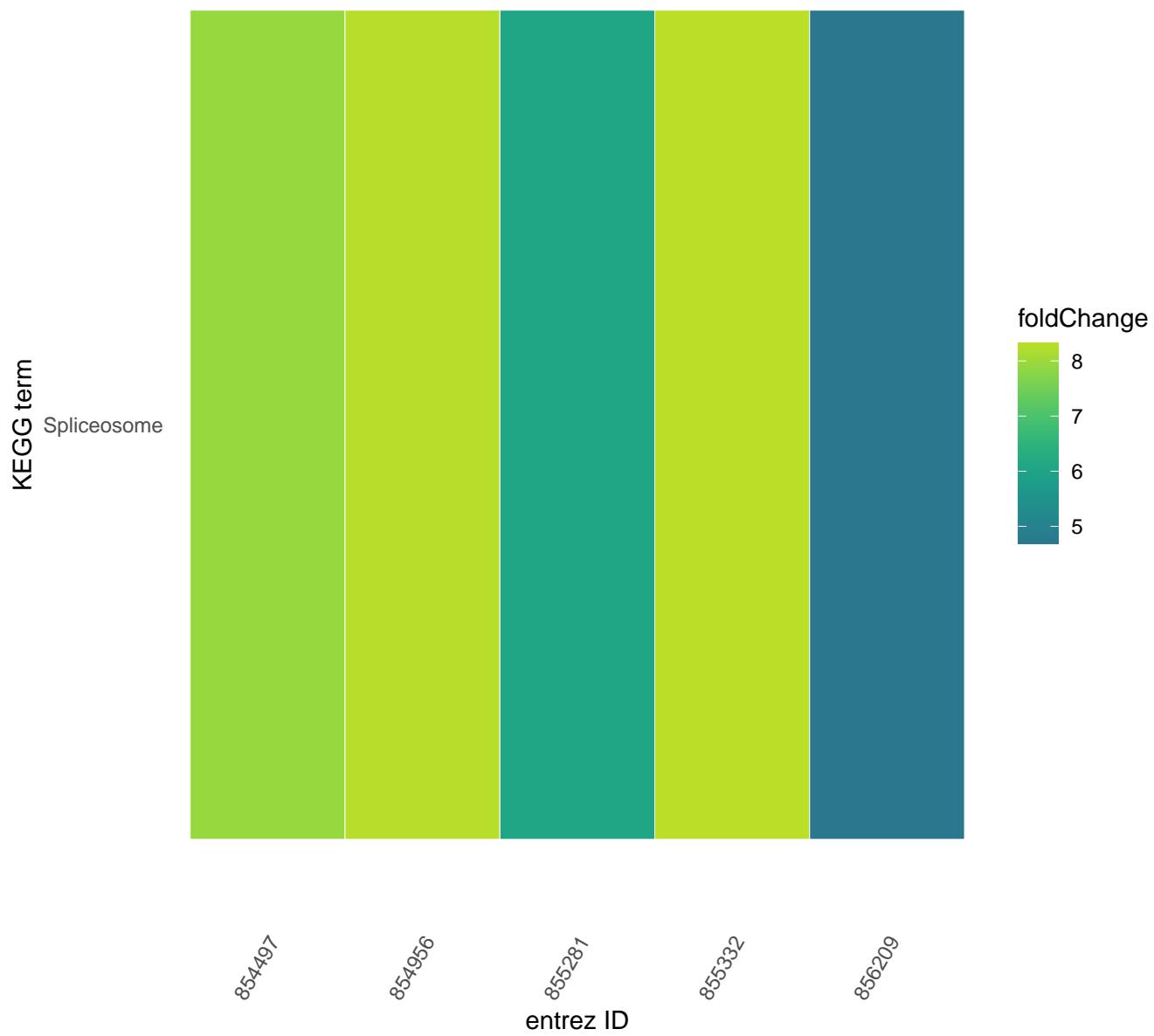
HSH49-TAP Up-regulated KEGG dotplot

size ● 5 category — Spliceosome

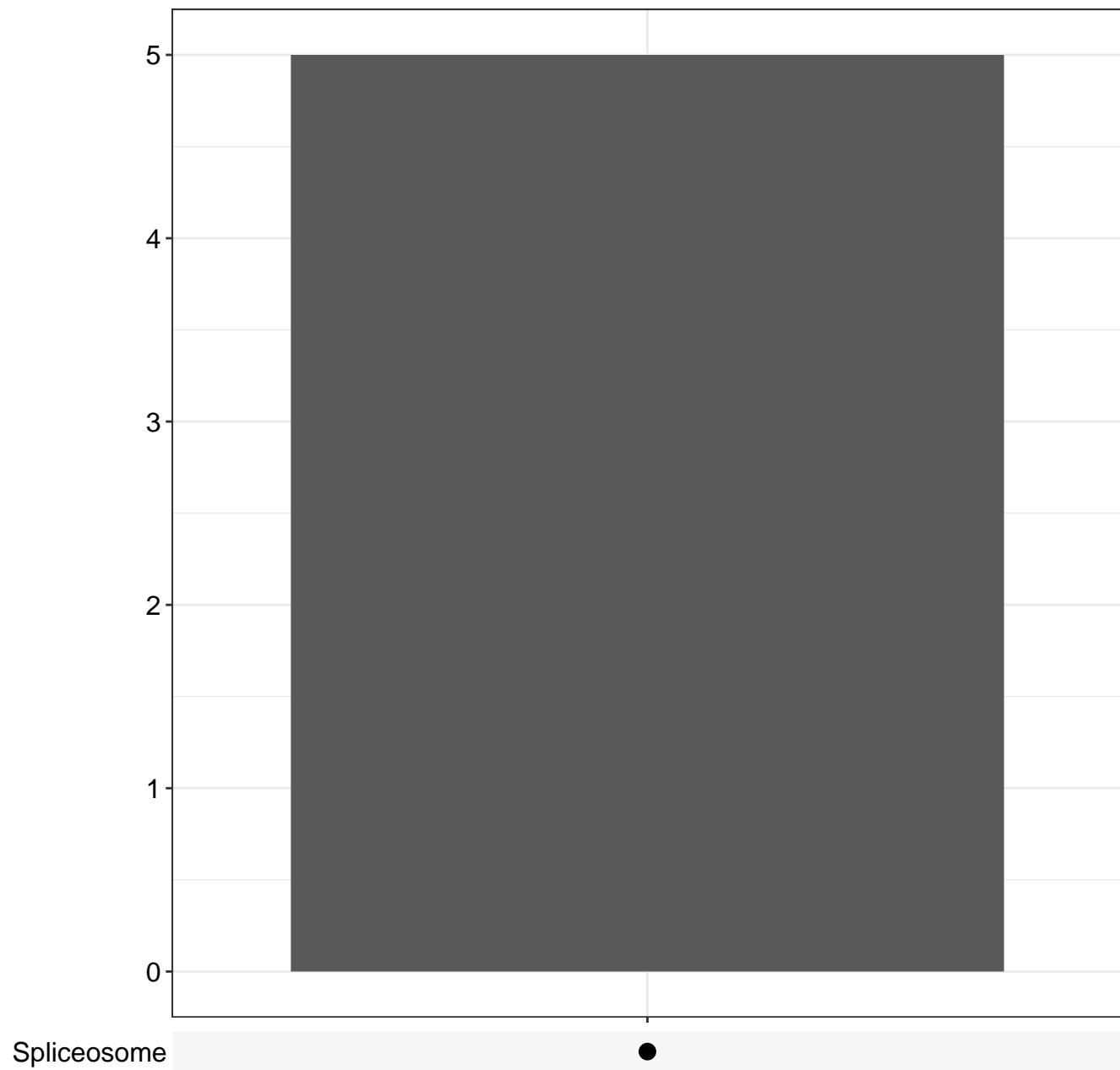
FoldChange



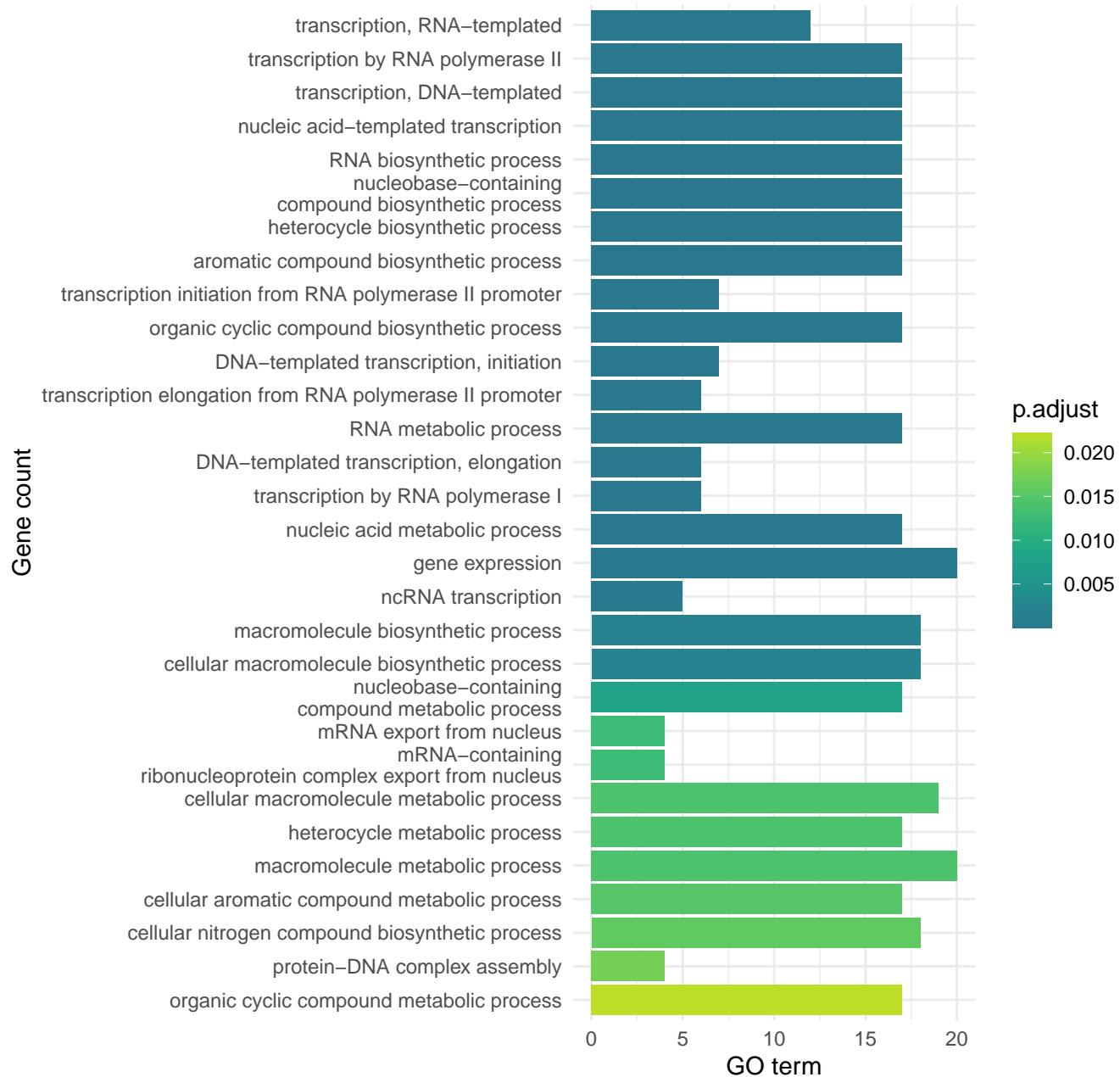
HSH49-TAP Up-regulated KEGG heatplot



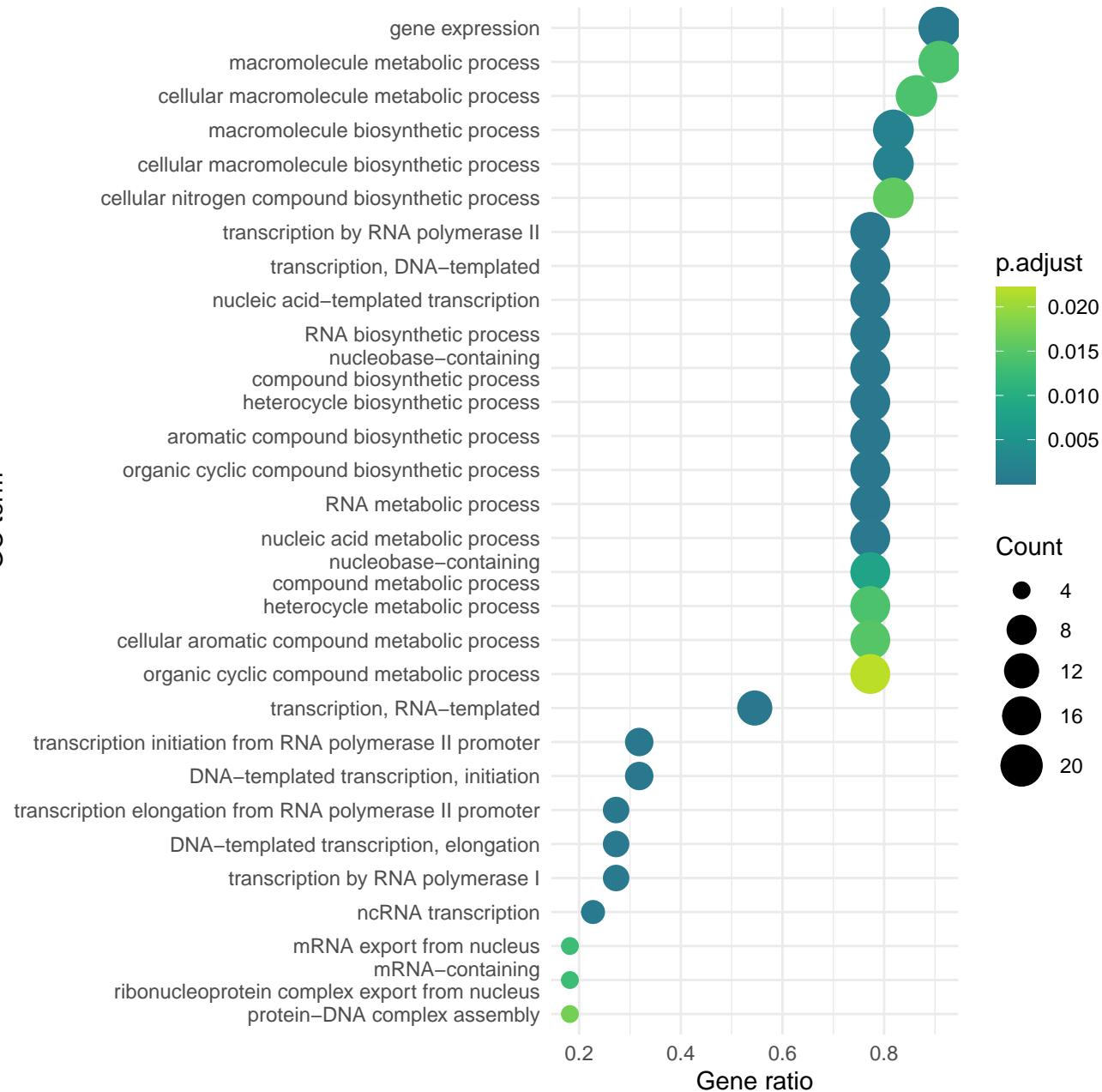
HSH49-TAP Up-regulated KEGG upsetplot



RPB7-TAP Up-regulated GO BP barplot

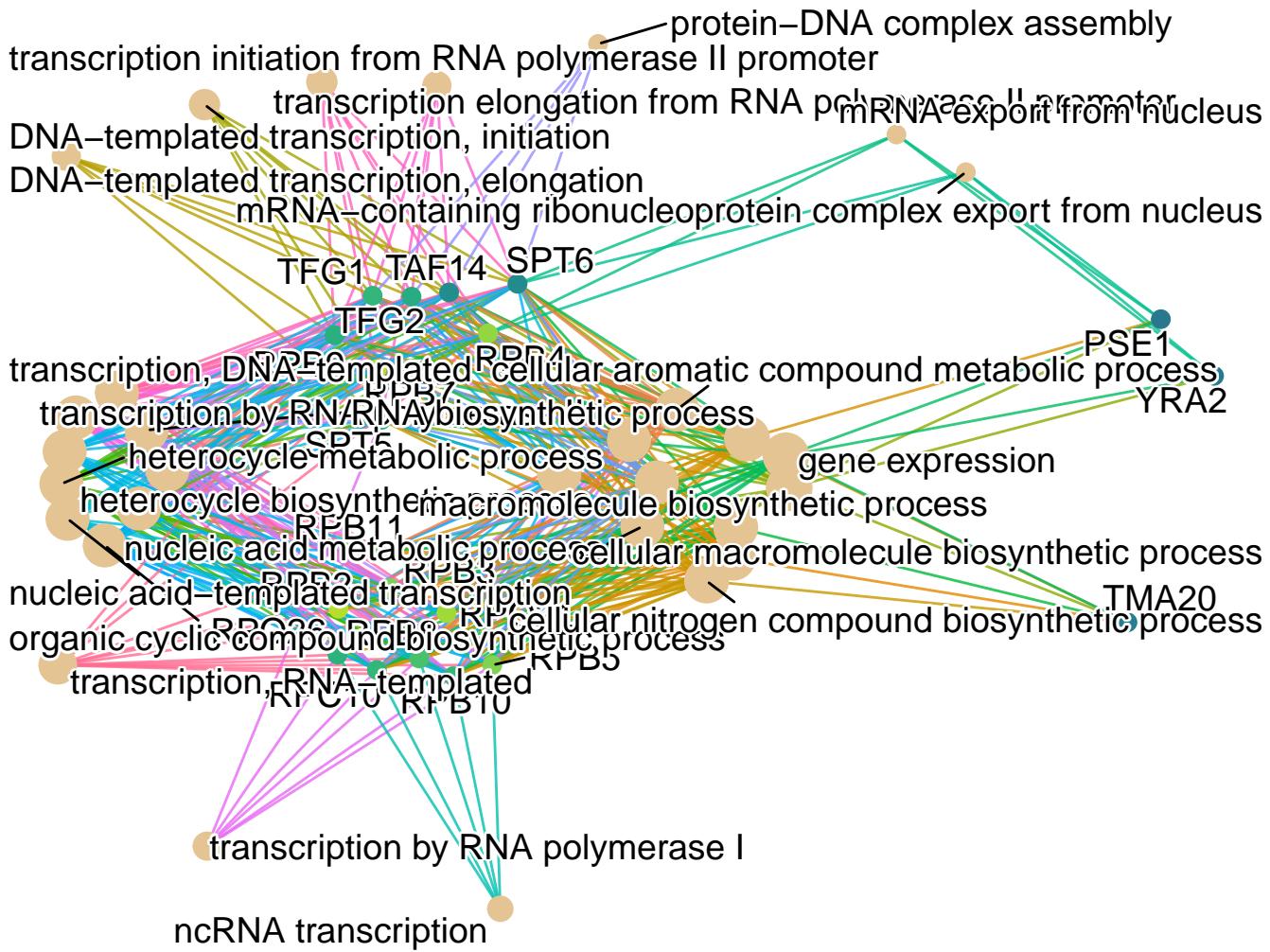


RPB7-TAP Up-regulated GO BP dotplot

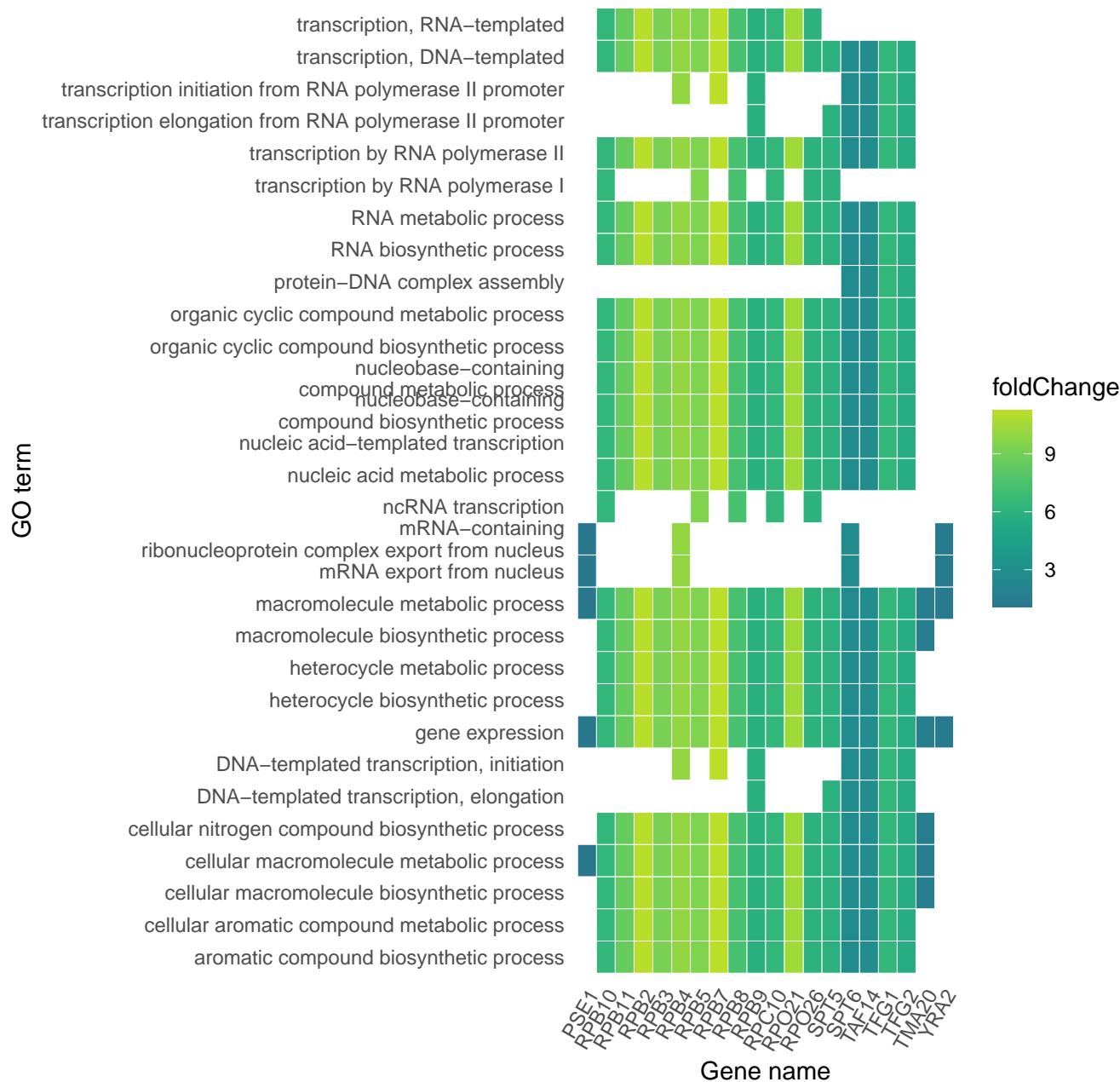


RPB7-TAP Up-regulated GO BP cnetplot

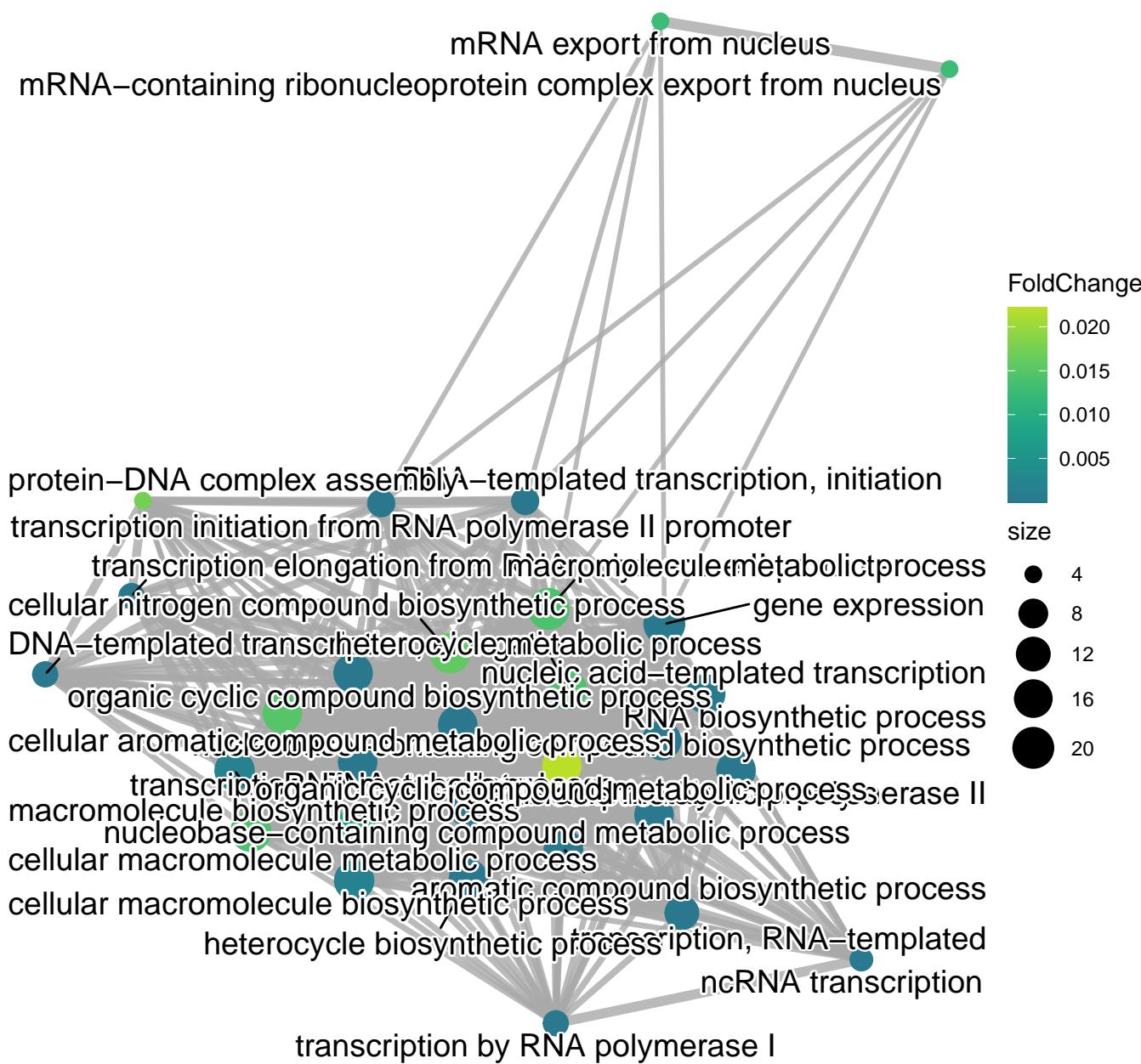
transcribed transcription, initiation	mRNA export from nucleus	nucleobase-containing compound biosynthetic process
transcription	mRNA-containing ribonucleoprotein complex export from nucleus	organic cyclic compound biosynthetic process
metabolic process	ncRNA transcription	organic cyclic compound metabolic process
metabolic process	nucleic acid metabolic process	protein-DNA complex assembly
metabolic process	nucleic acid-templated transcription	RNA biosynthetic process
metabolic process	nucleobase-containing compound biosynthetic process	RNA metabolic process

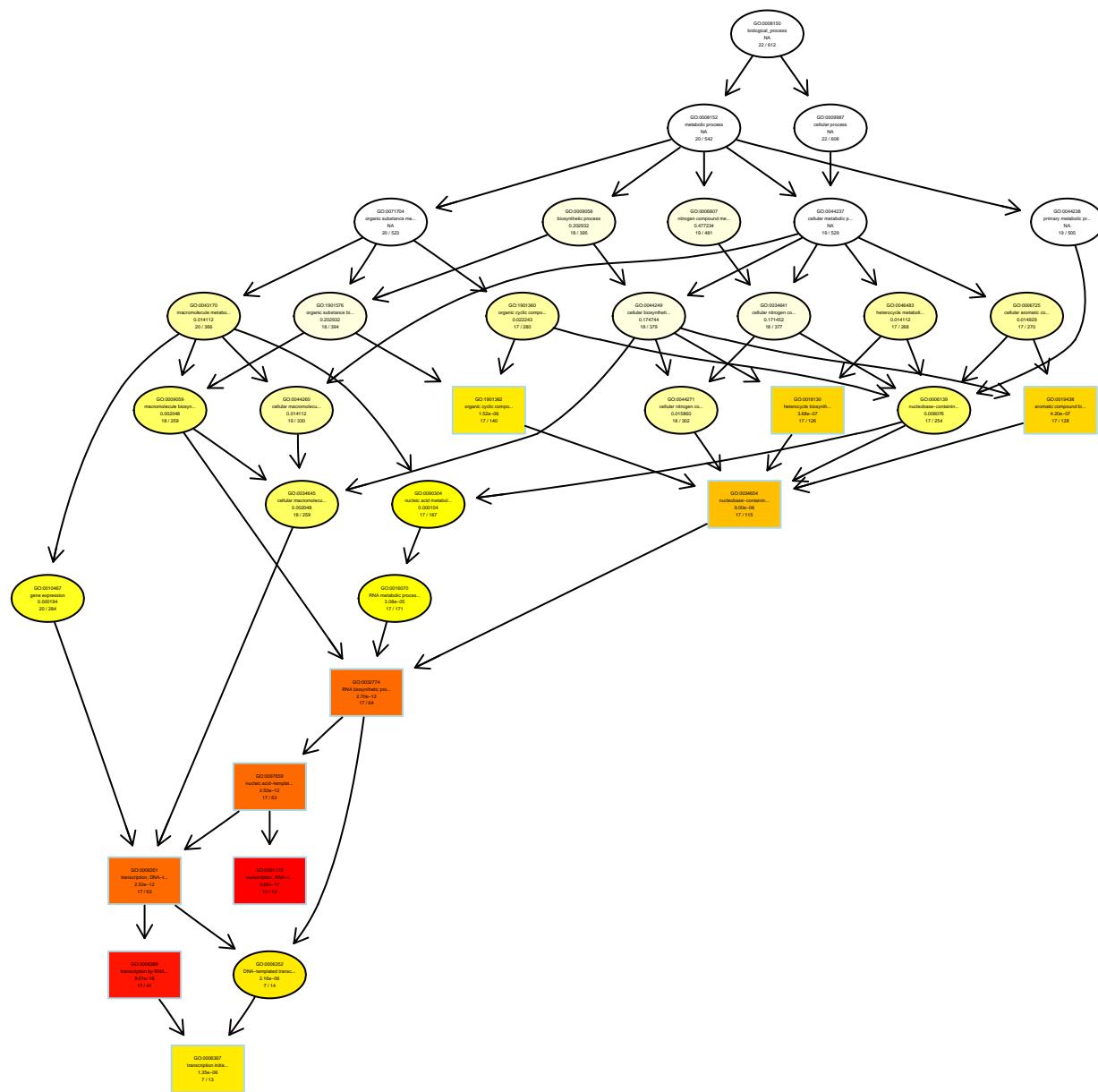


RPB7-TAP Up-regulated GO BP heatplot

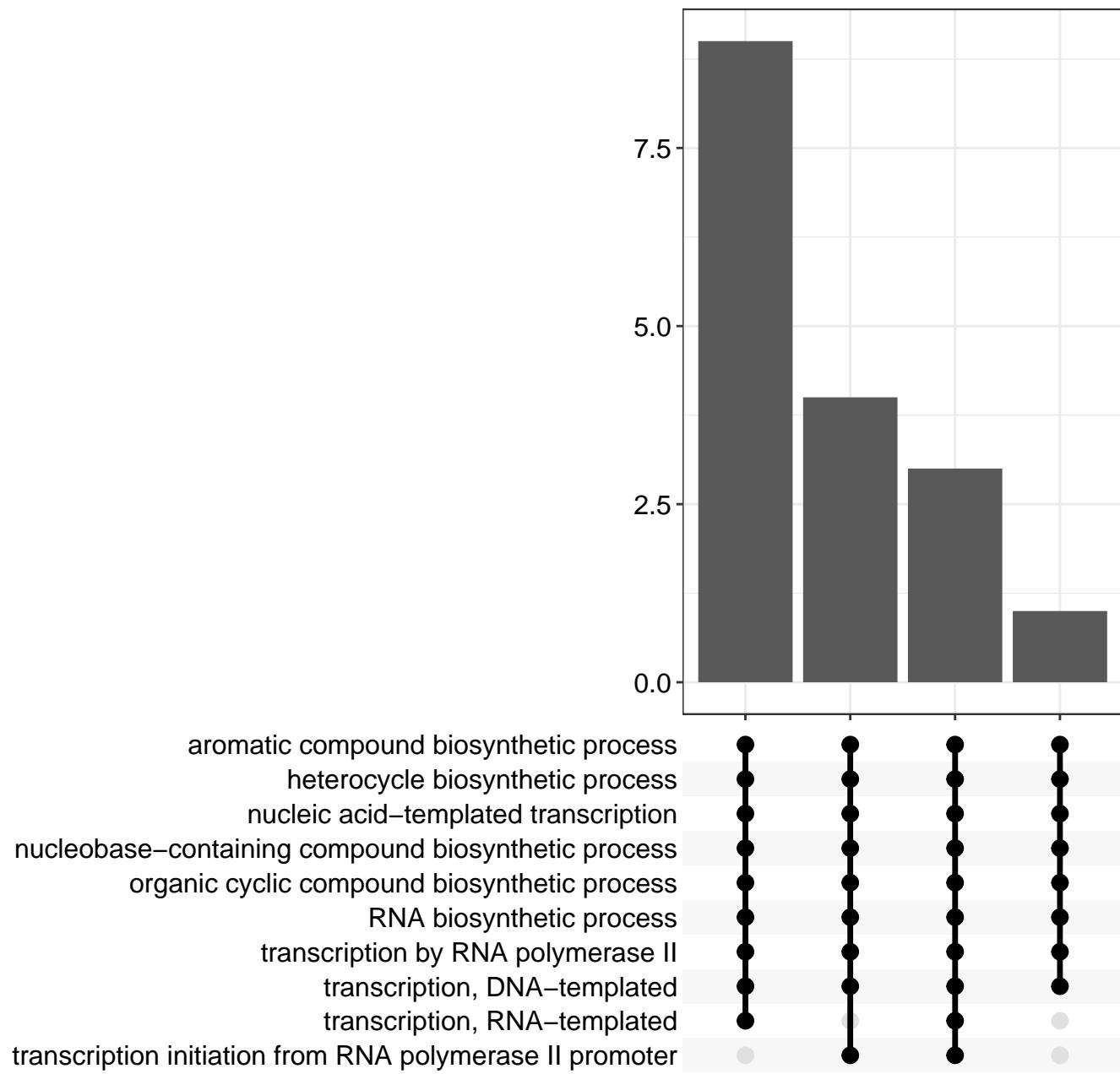


RPB7-TAP Up-regulated GO BP emapplot

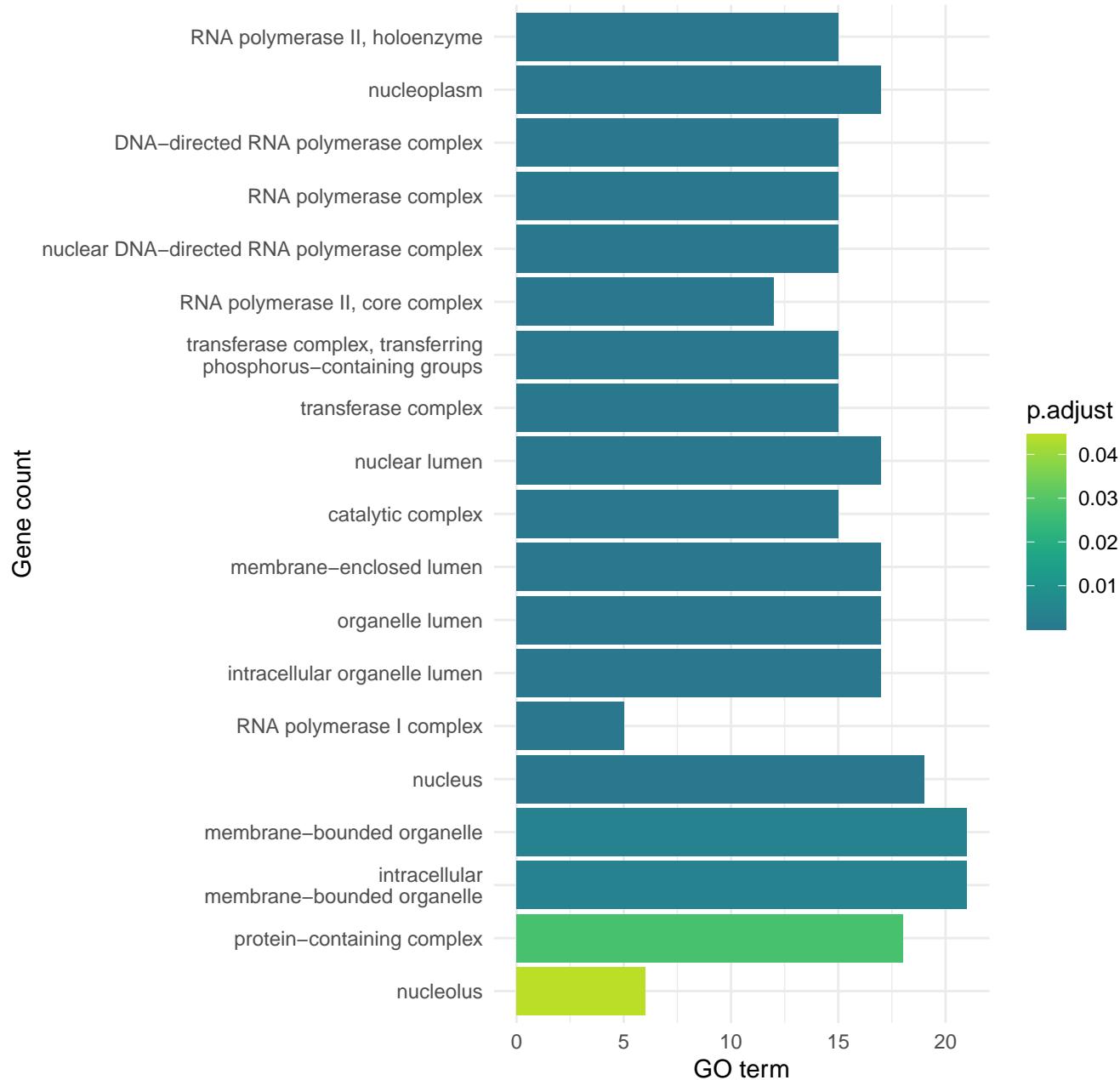




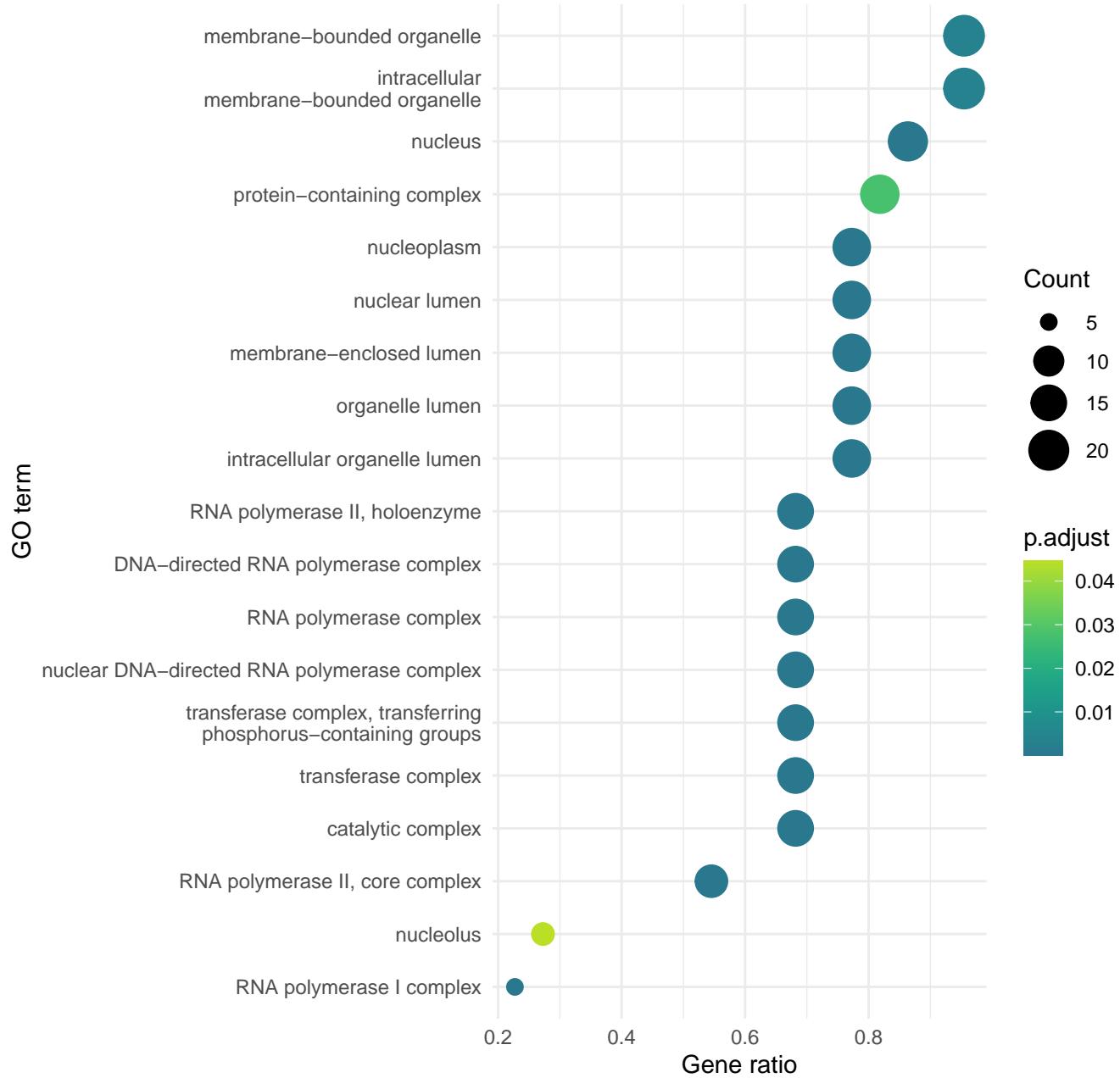
RPB7-TAP Up-regulated GO BP u



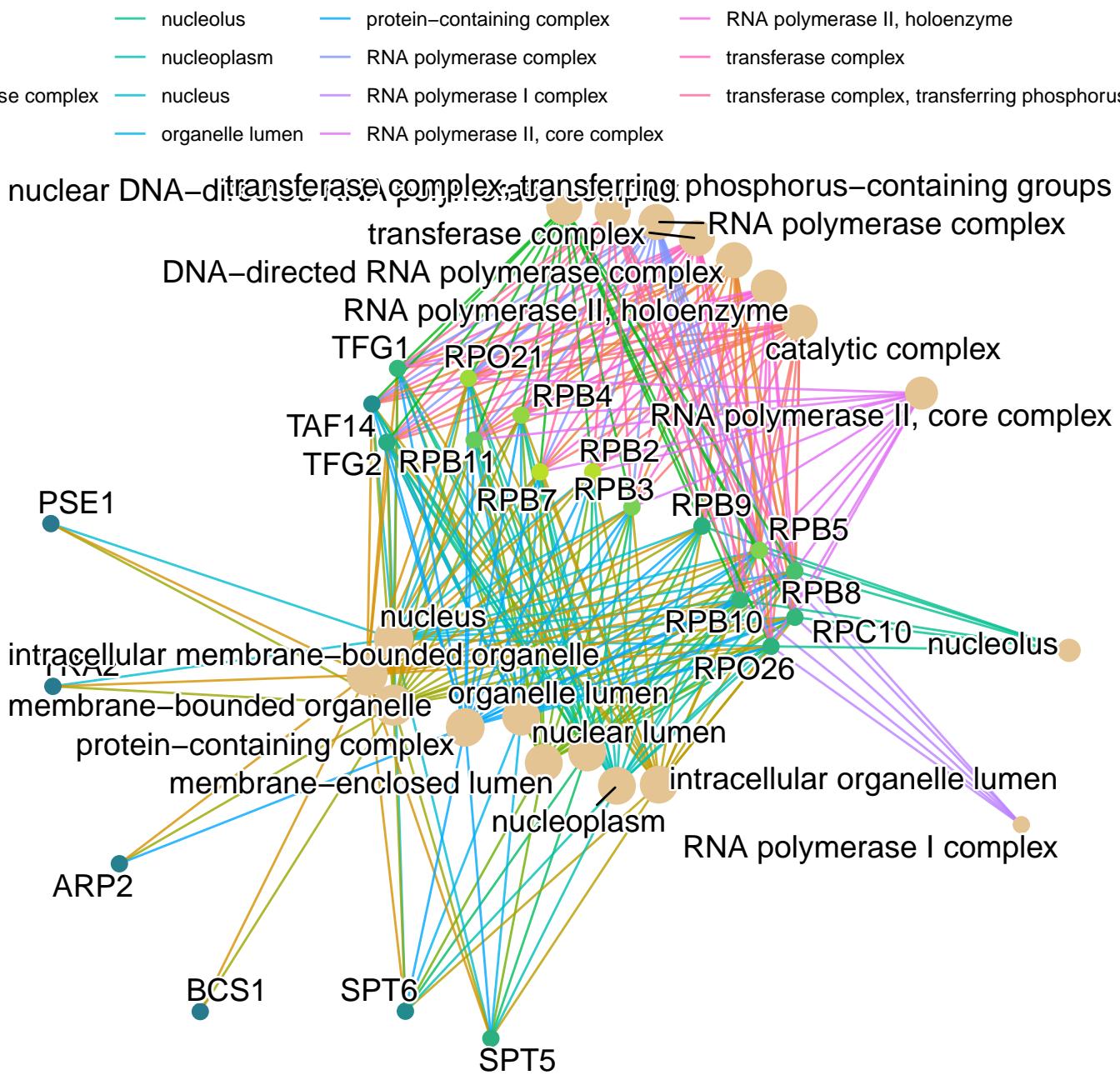
RPB7-TAP Up-regulated GO CC barplot



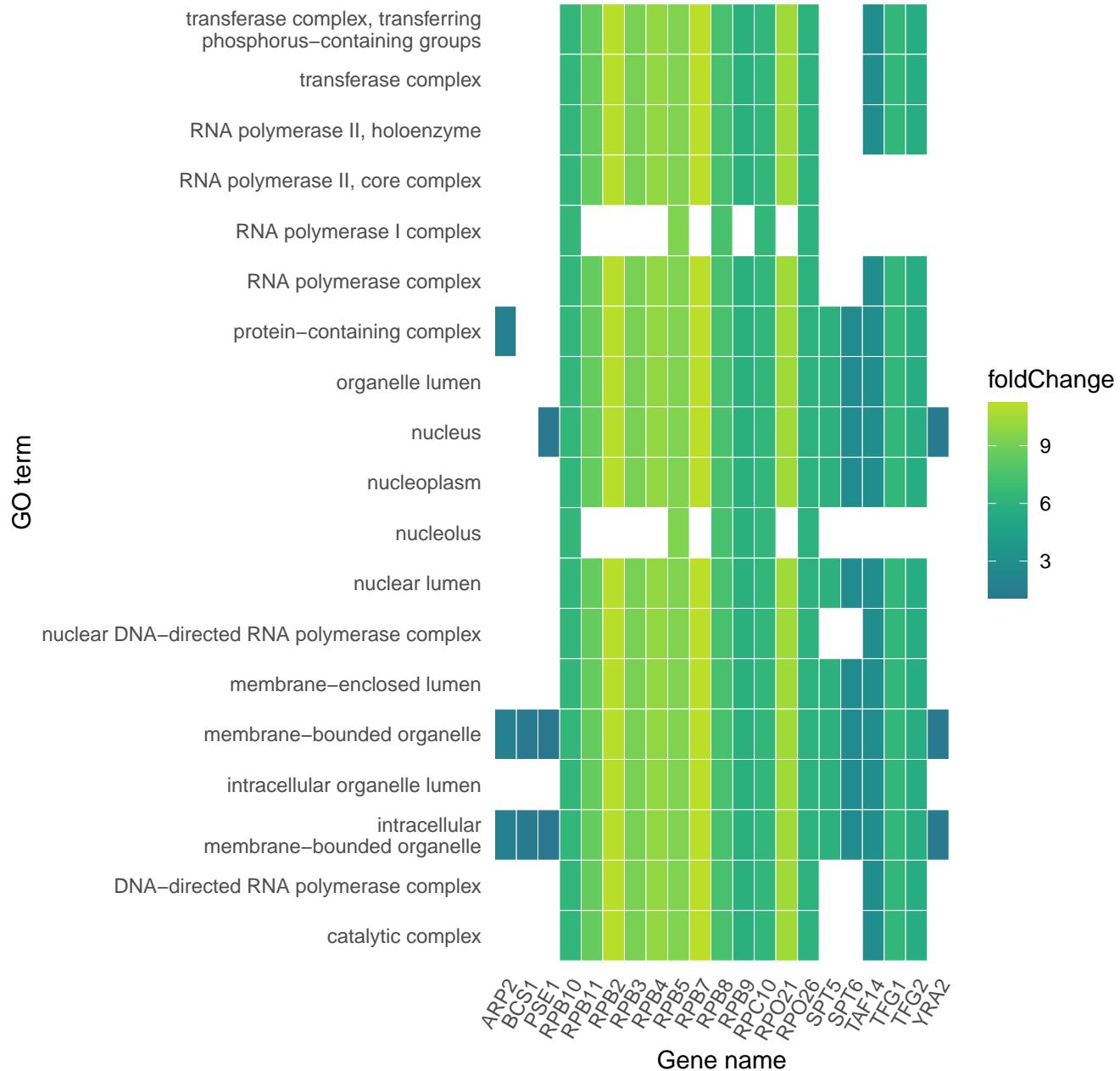
RPB7-TAP Up-regulated GO CC dotplot



RPB7-TAP Up-regulated GO CC cnetplot



RPB7–TAP Up-regulated GO CC heatplot



RPB7-TAP Up-regulated GO CC emapplot

RNA polymerase I complex

nucleolus

DNA-directed RNA polymerase complex

RNA polymerase II, holoenzyme

transferase complex

nucleus

nuclear lumen

catalytic complex

RNA polymerase II, core complex

membrane-enclosed lumen

intracellular organelle lumen

nuclear DNA-directed RNA polymerase

membrane-bounded organelle

transferase complex, transferring phosphorus-containing groups

organelle lumen

intracellular membrane-bounded organelle

RNA polymerase complex

nucleoplasm

protein-containing complex

FoldChange

0.04

0.03

0.02

0.01

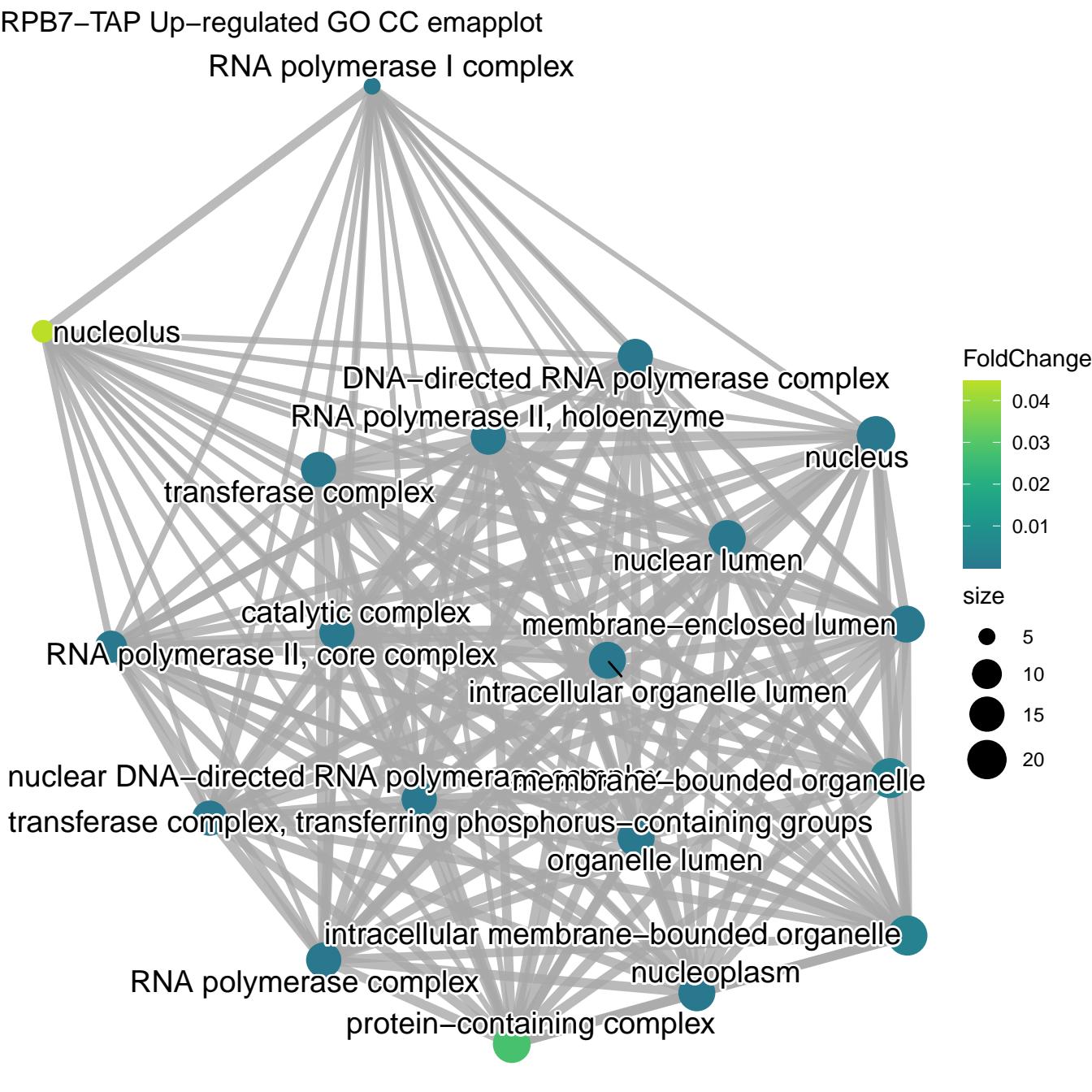
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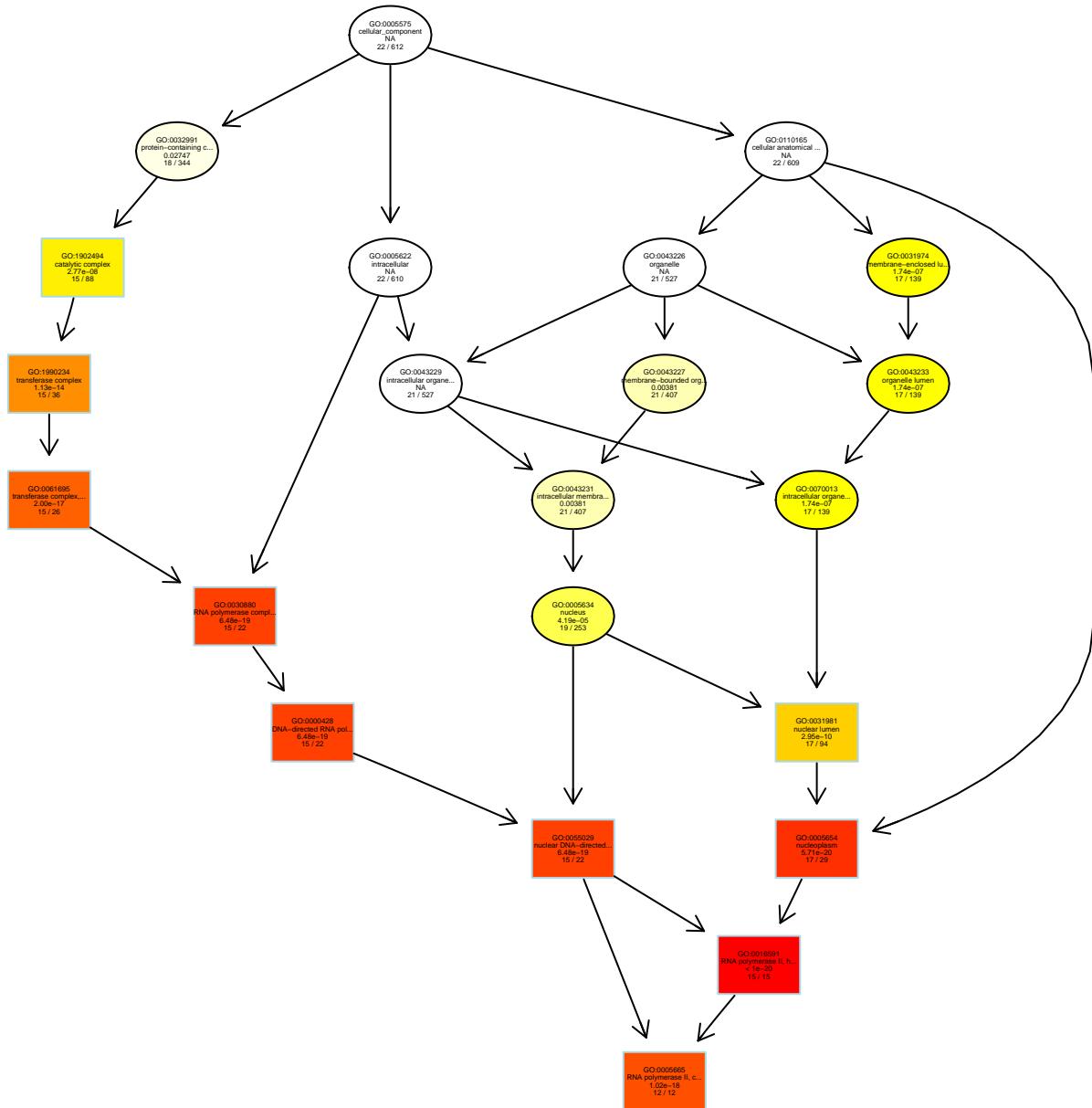
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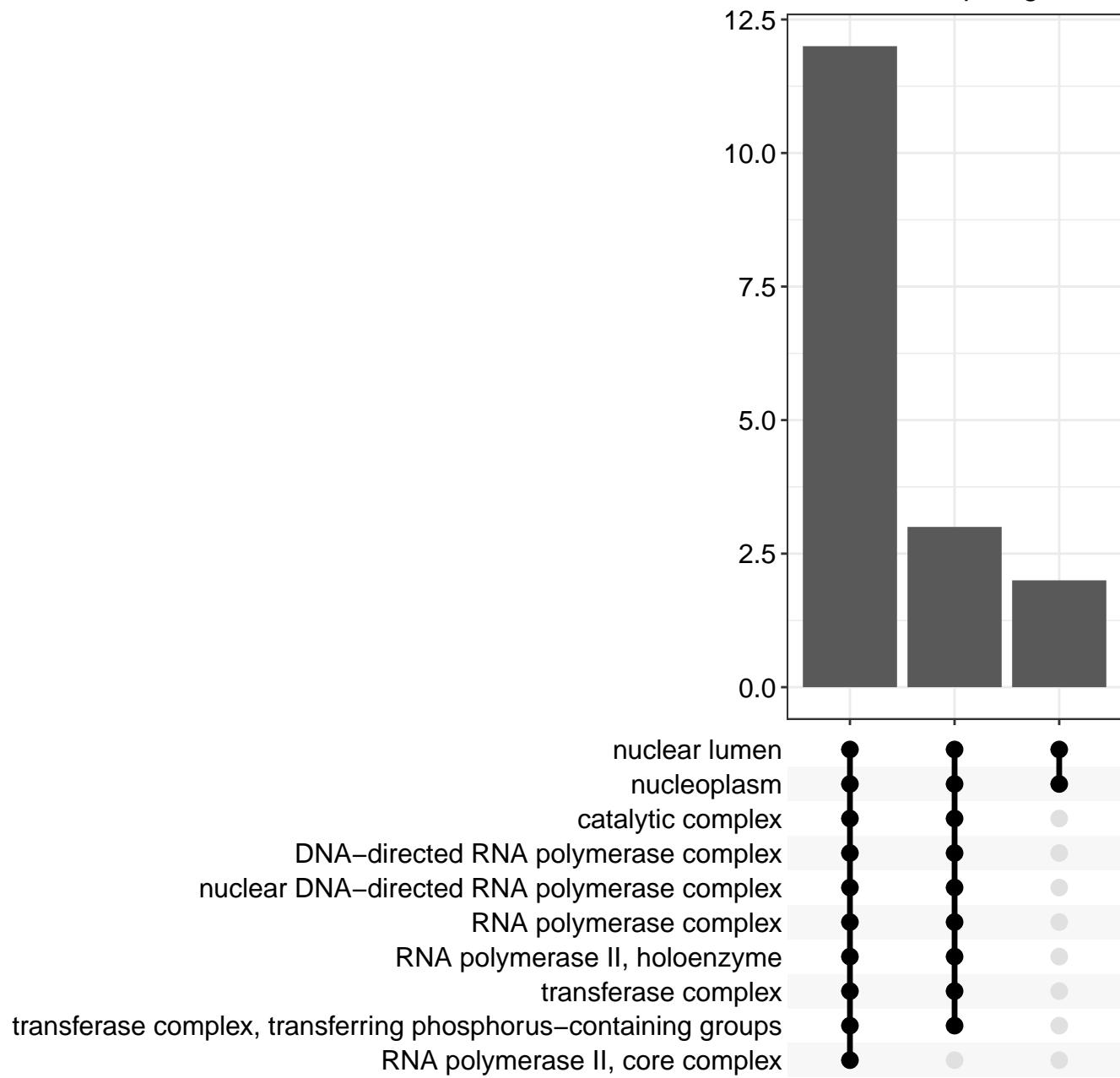
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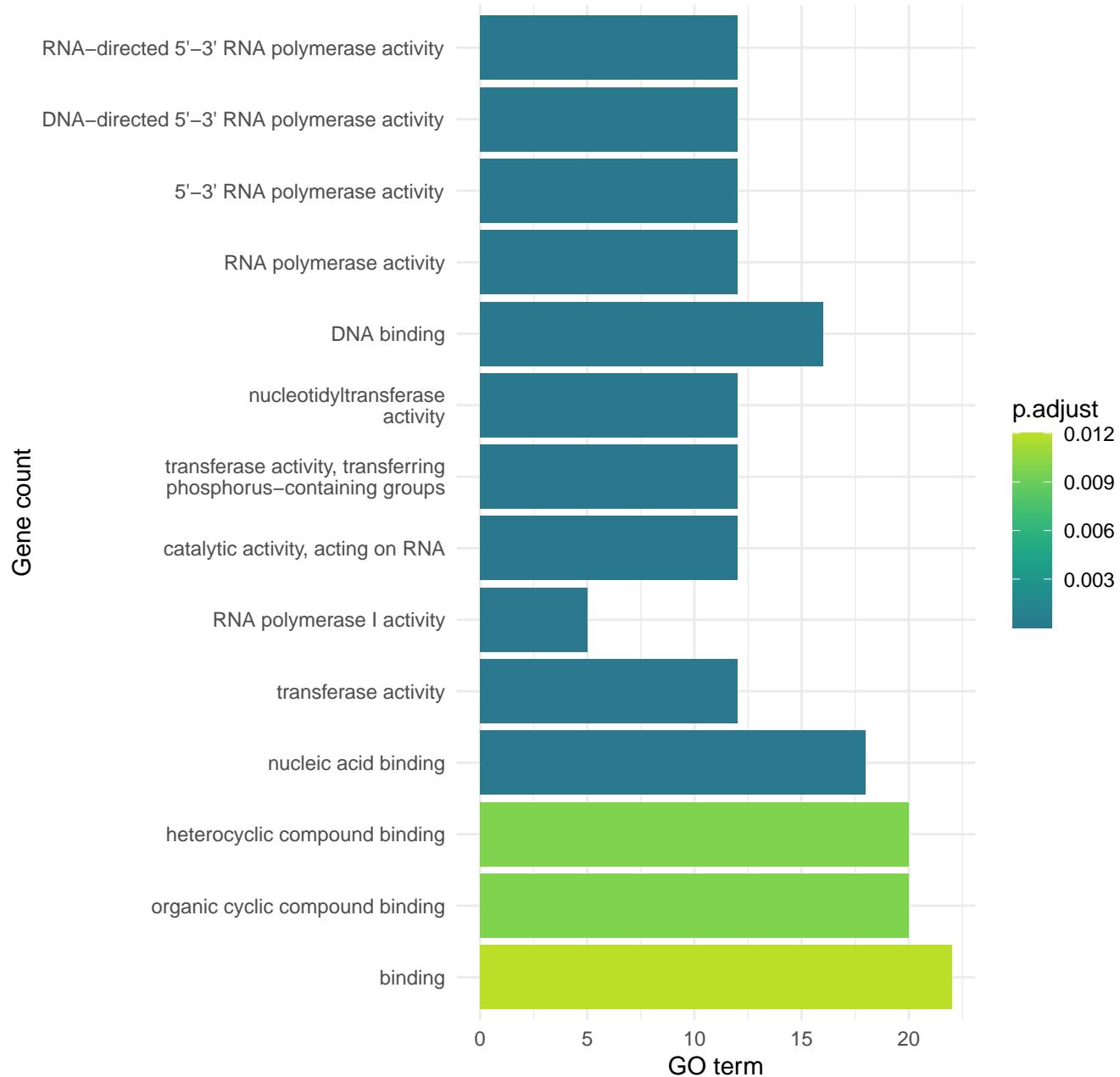




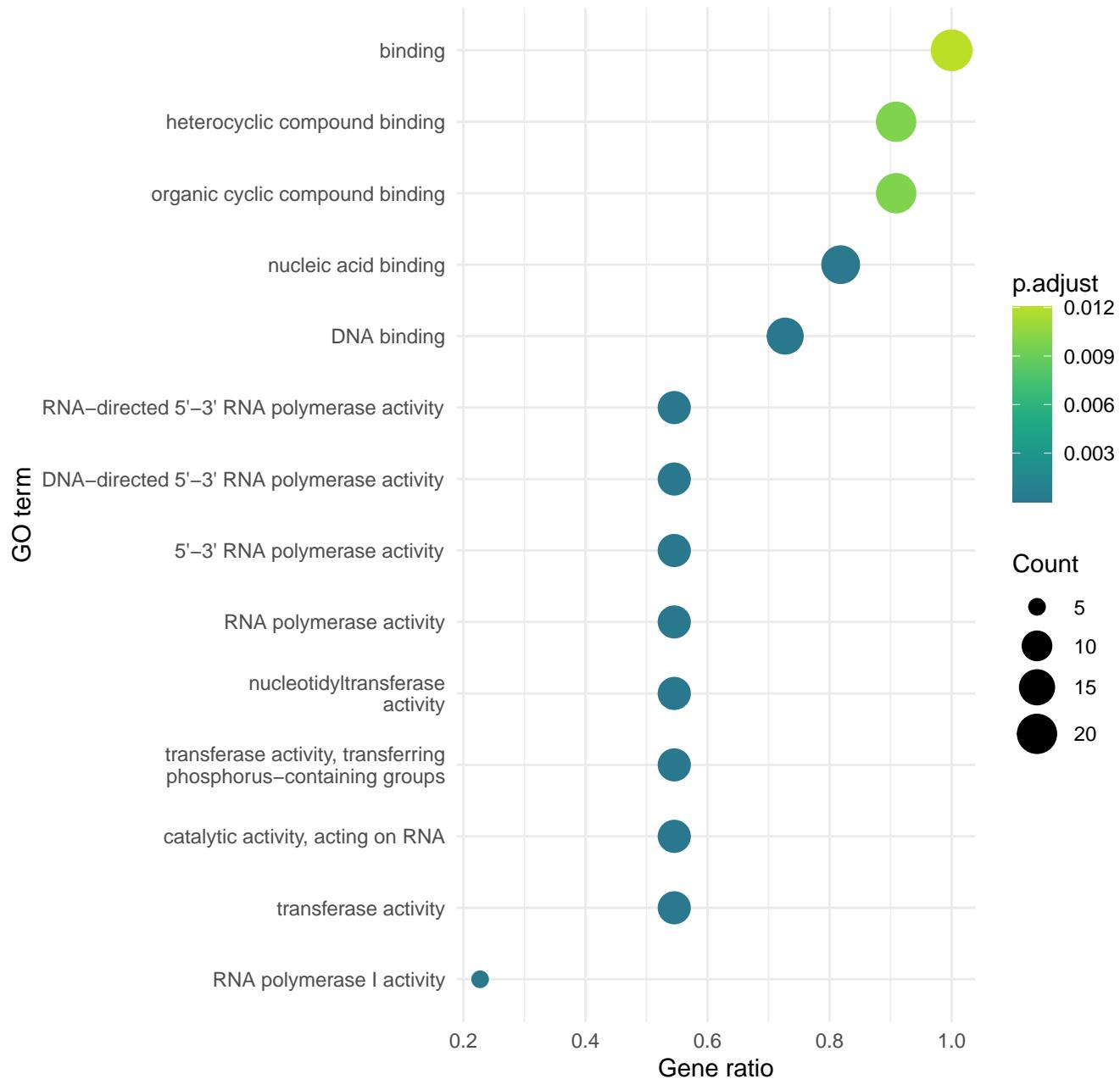
RPB7-TAP Up-regulated



RPB7-TAP Up-regulated GO MF barplot



RPB7-TAP Up-regulated GO MF dotplot



RPB7-TAP Up-regulated GO MF cnetplot

cleic acid binding

— RNA polymerase activity

— transferase activity

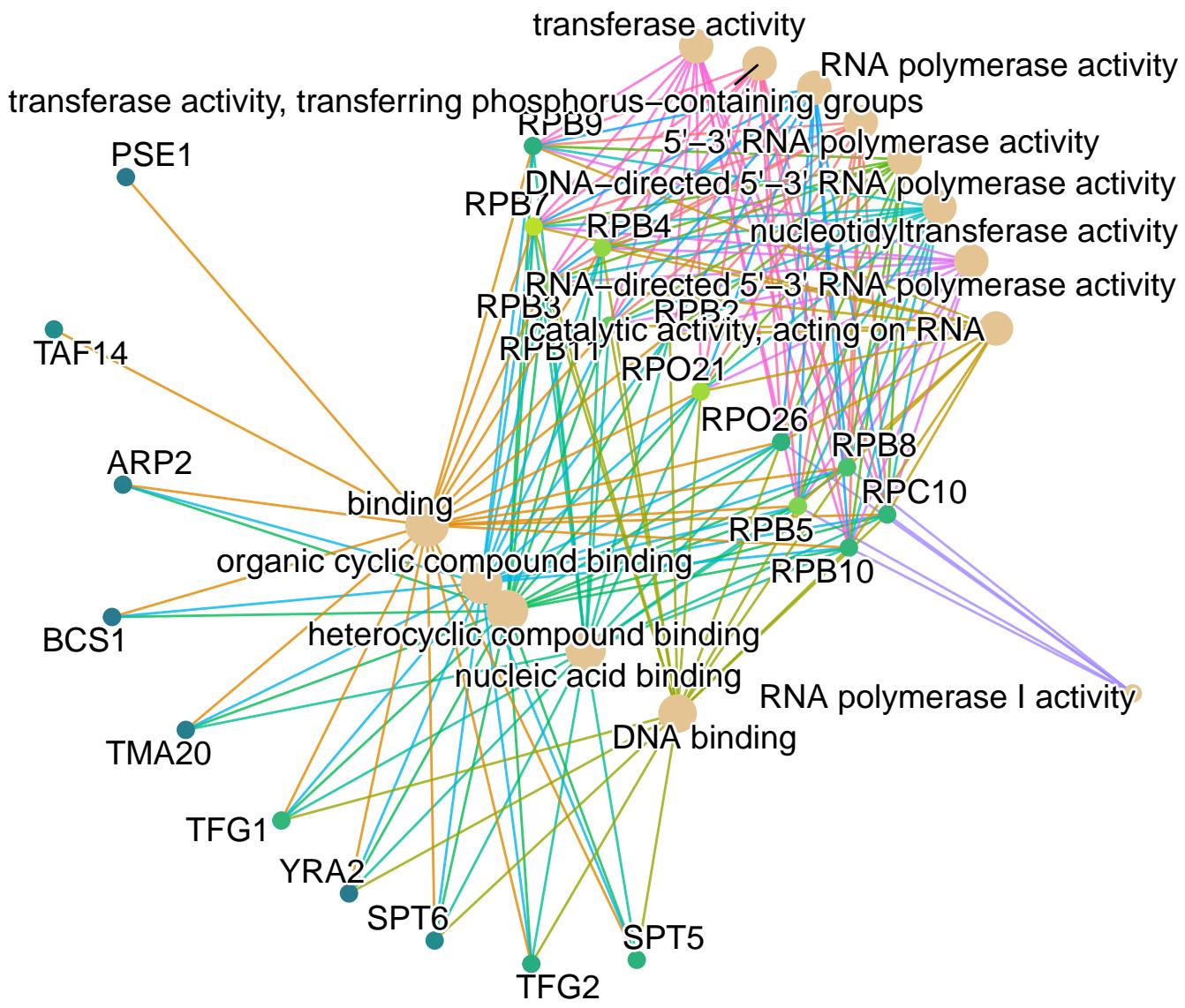
cleotidyltransferase activity

— RNA polymerase I activity

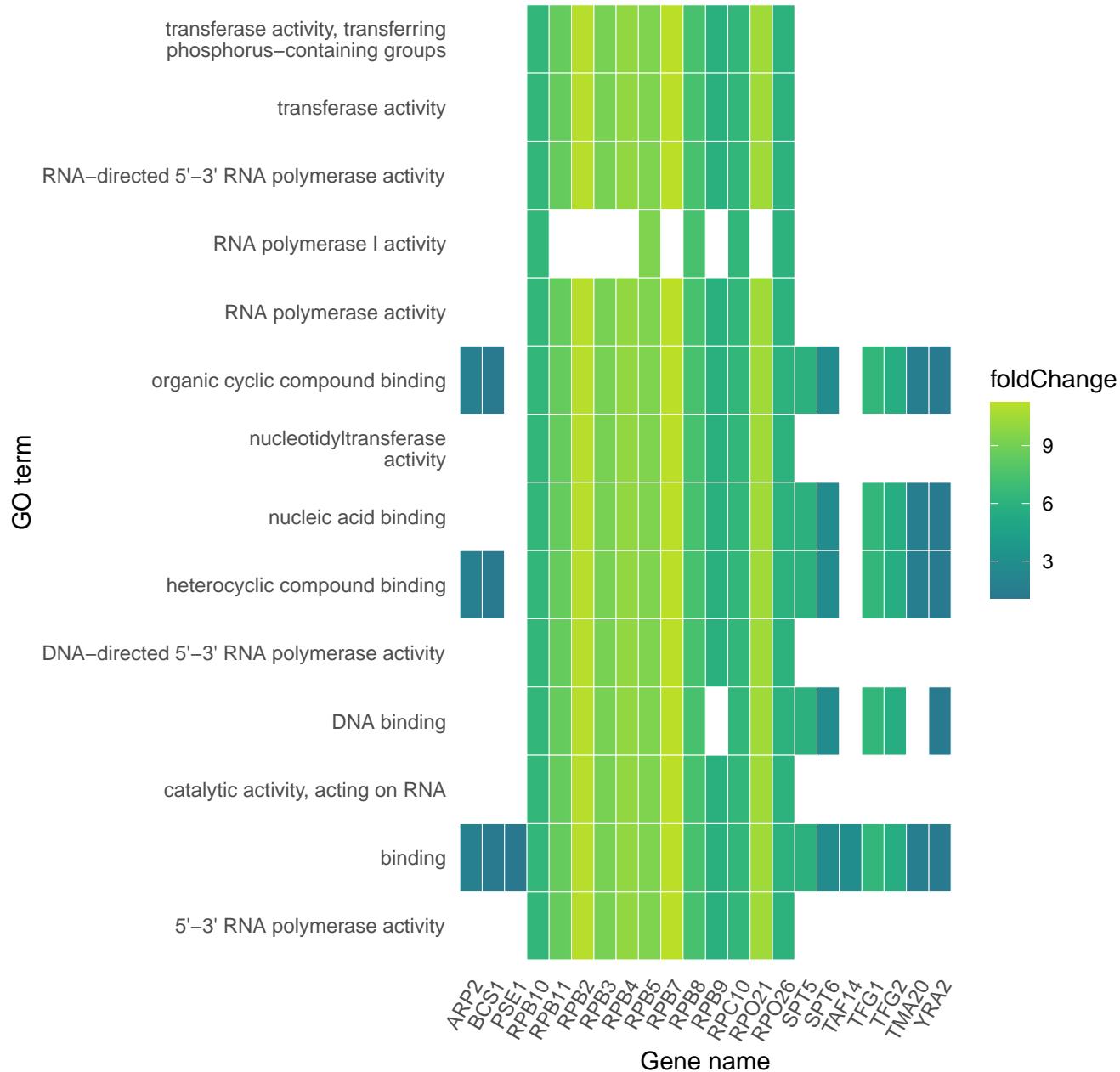
— transferase activity, transferring phosph

Organic cyclic compound binding — RNA-directed 5'-3' RNA polymerase activity

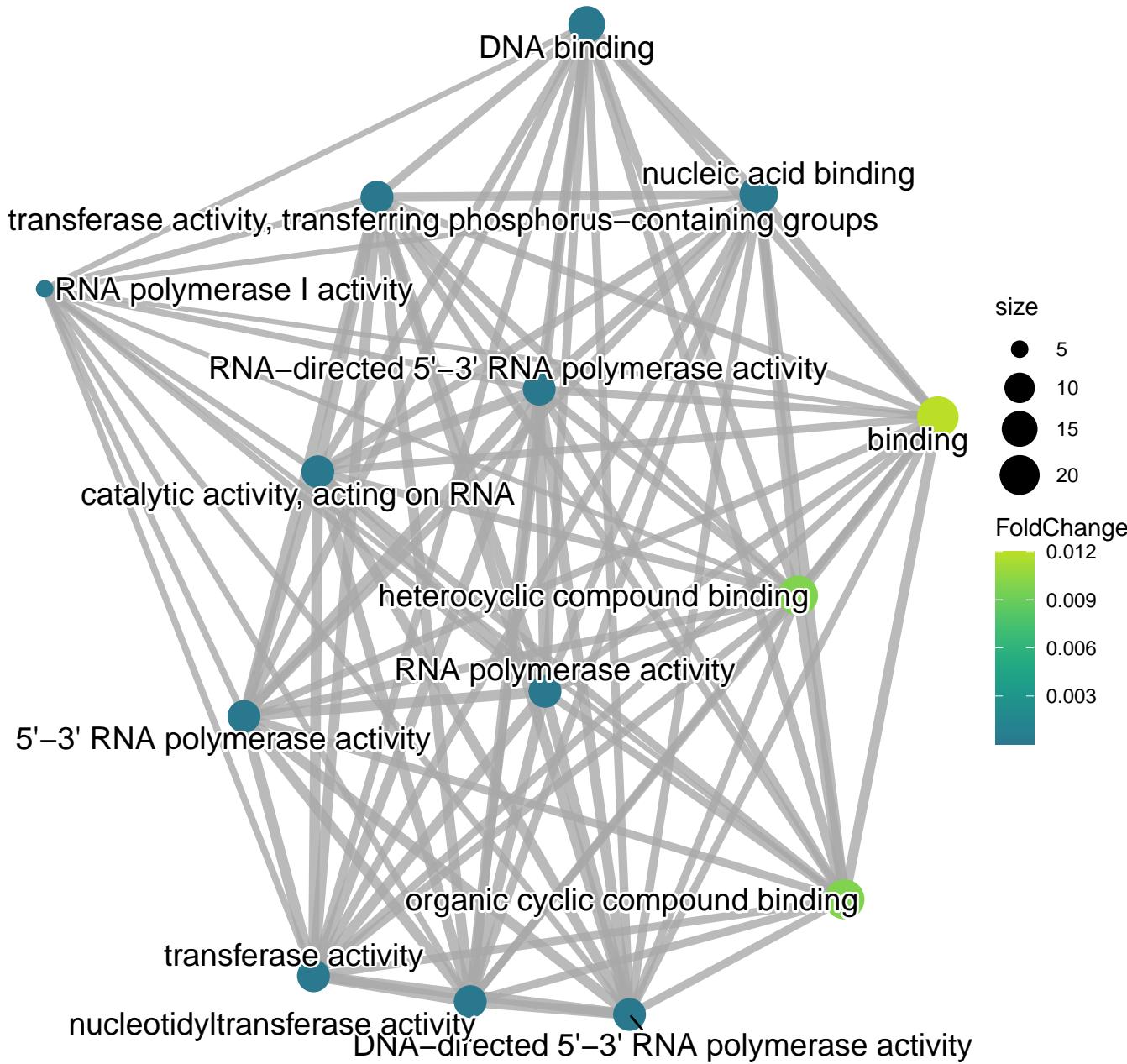
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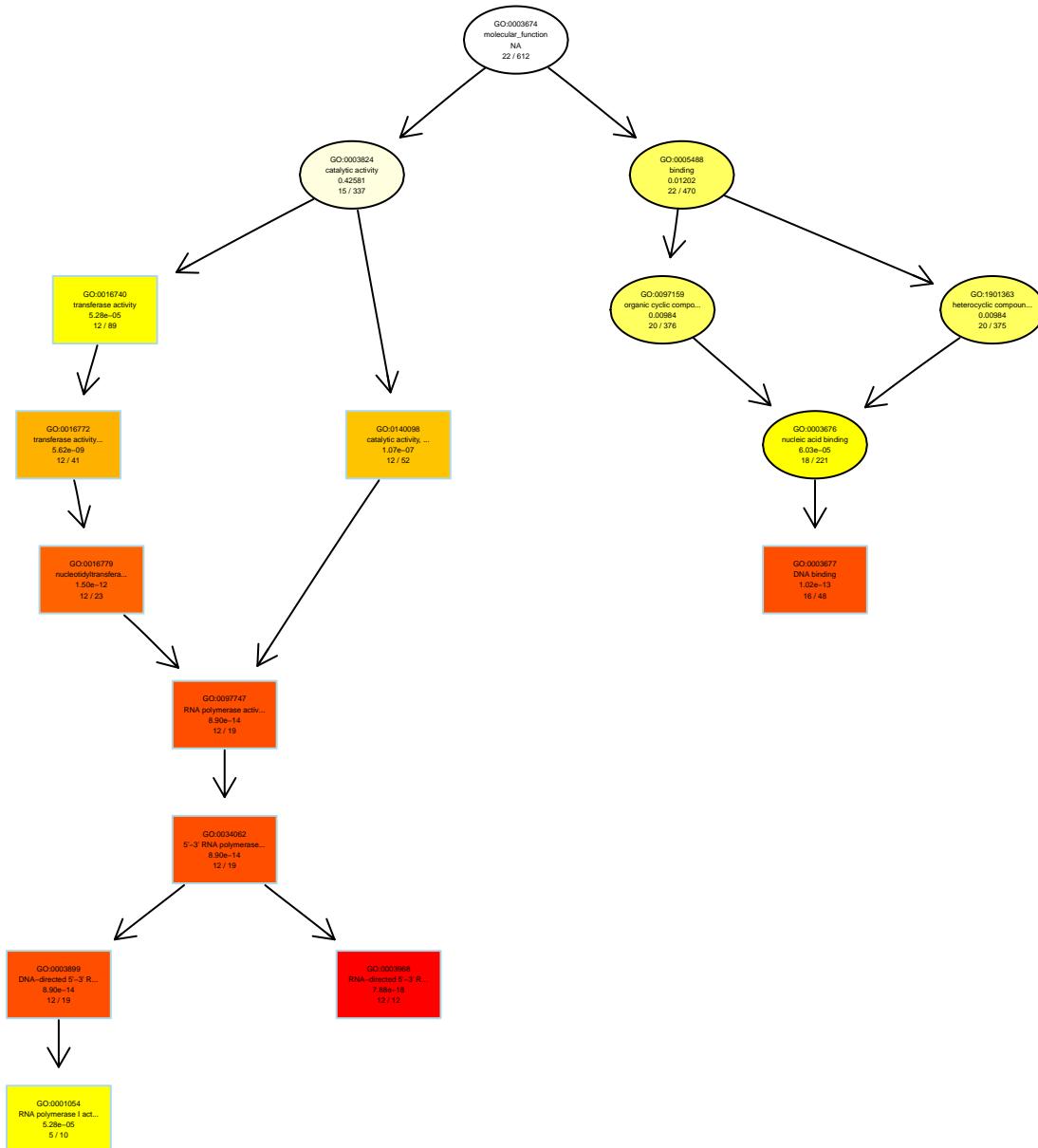


RPB7-TAP Up-regulated GO MF heatplot

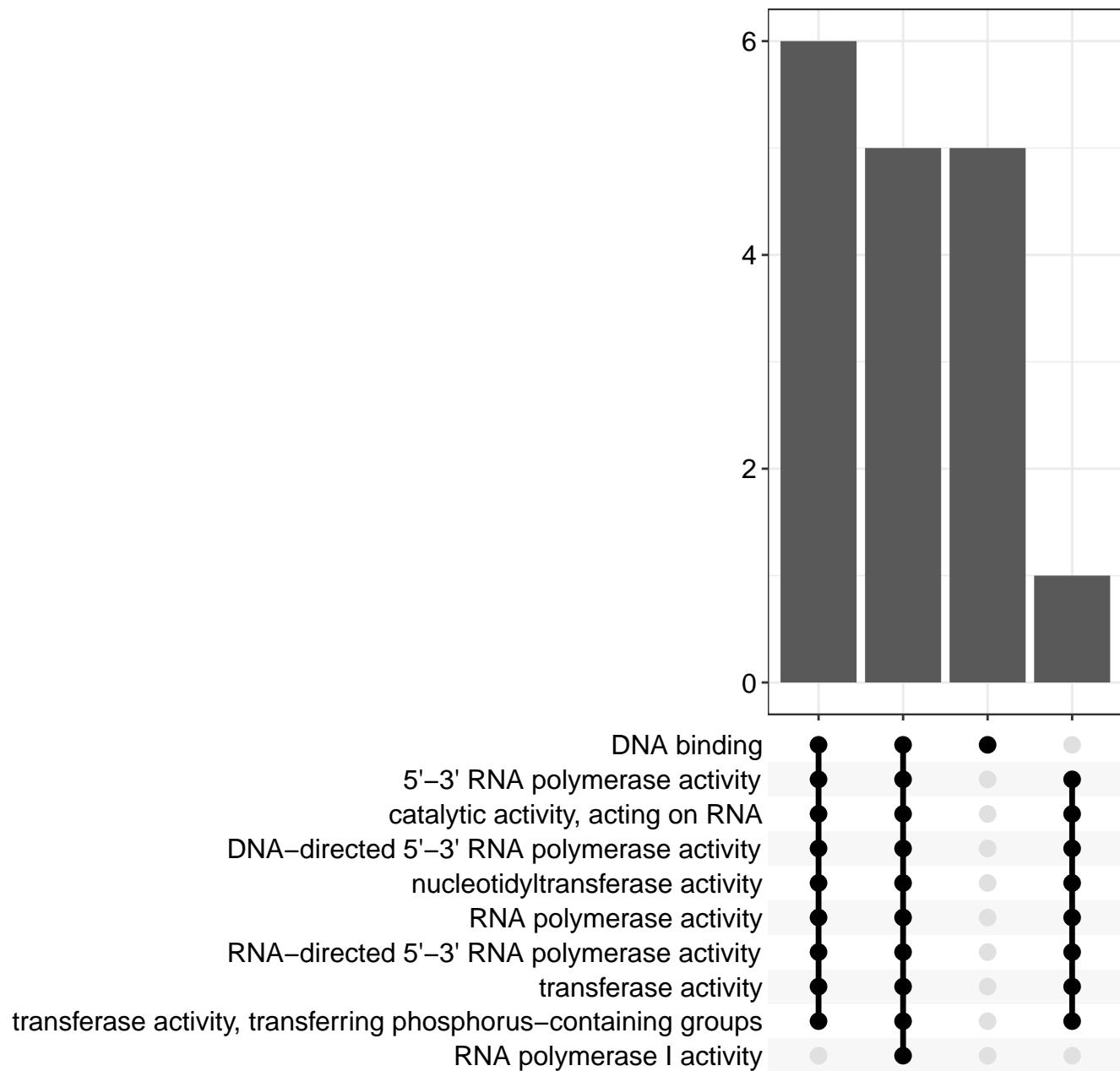


RPB7-TAP Up-regulated GO MF emapplot

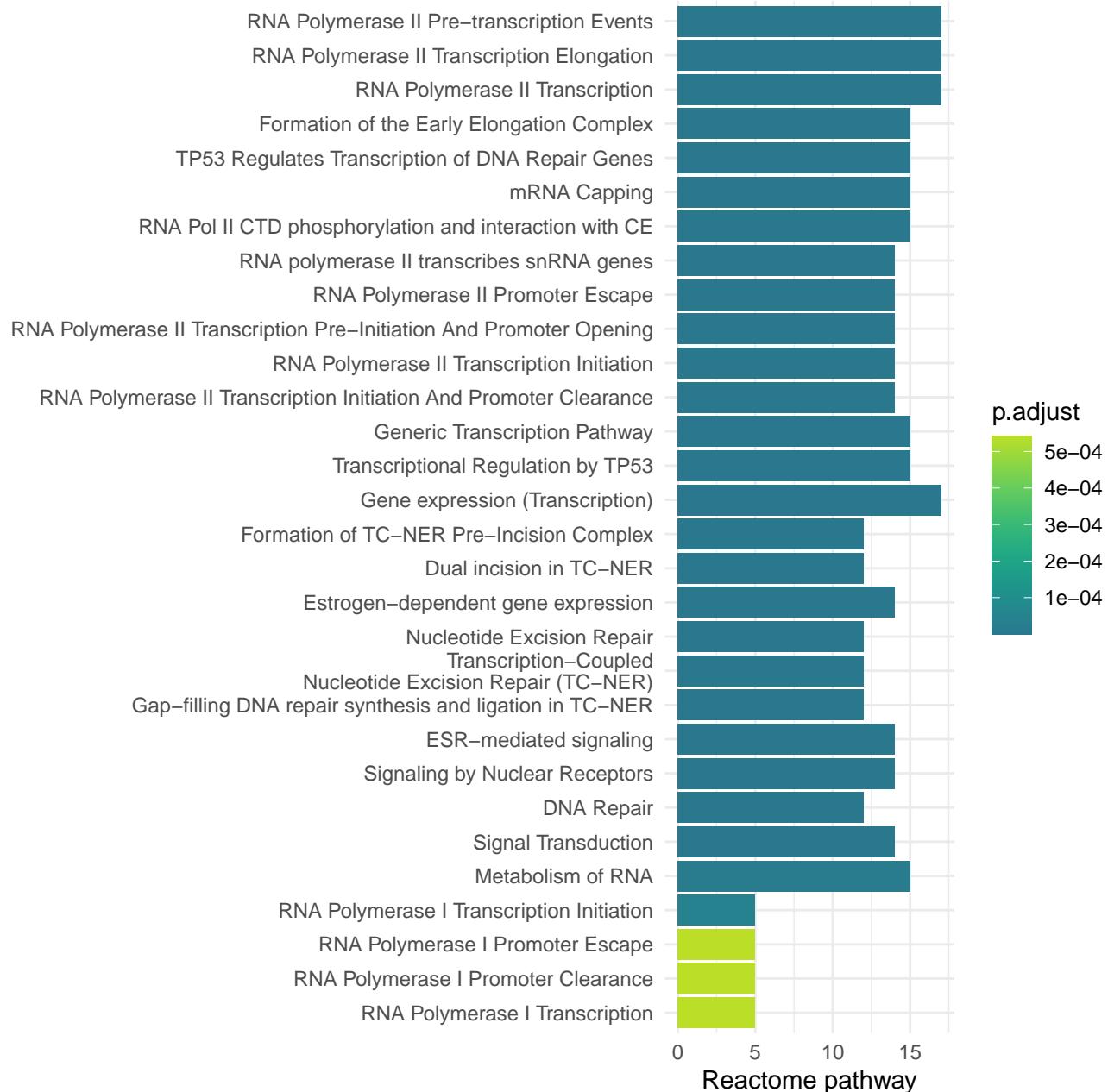




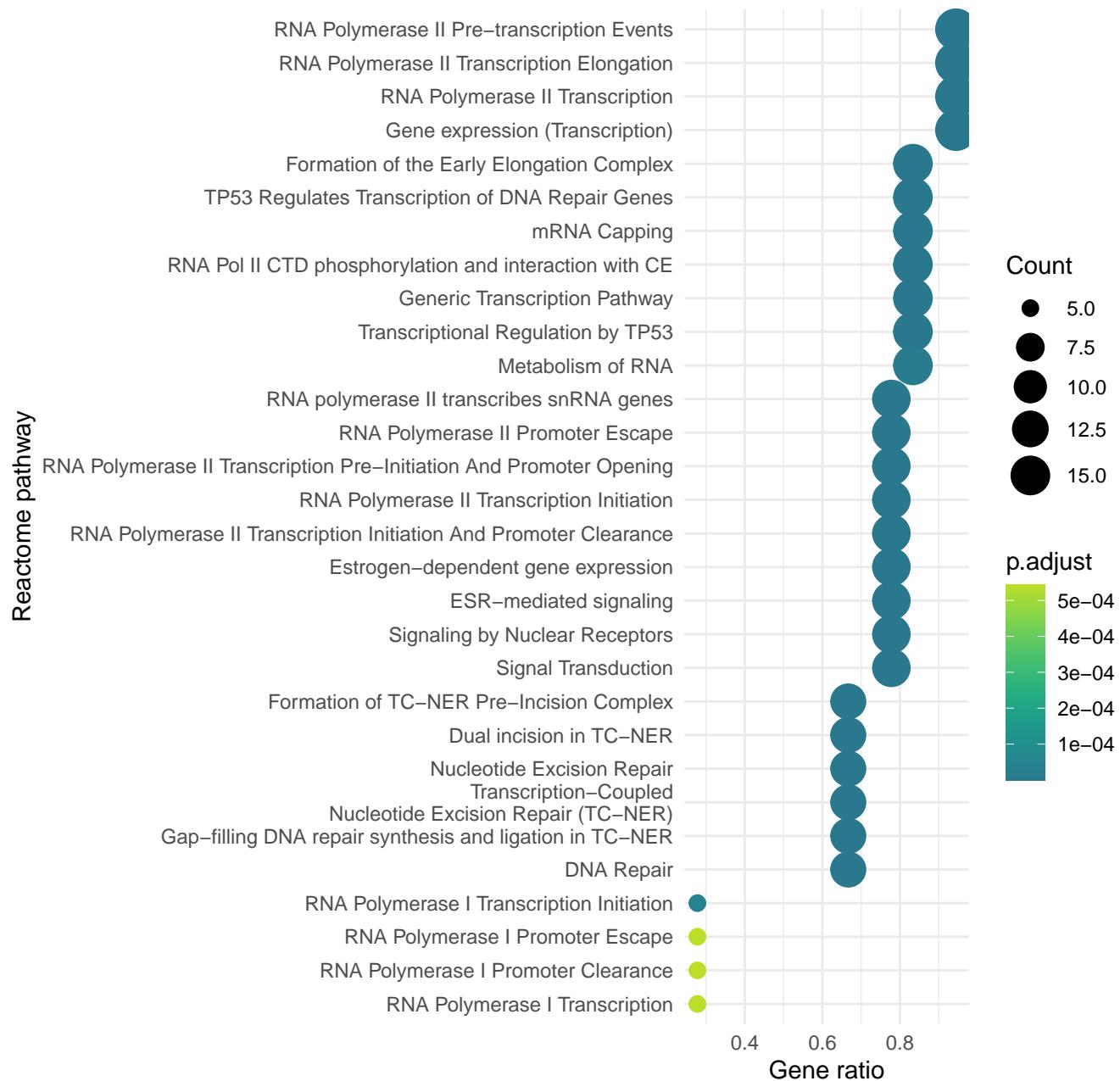
RPB7-TAP Up-regulated Genes



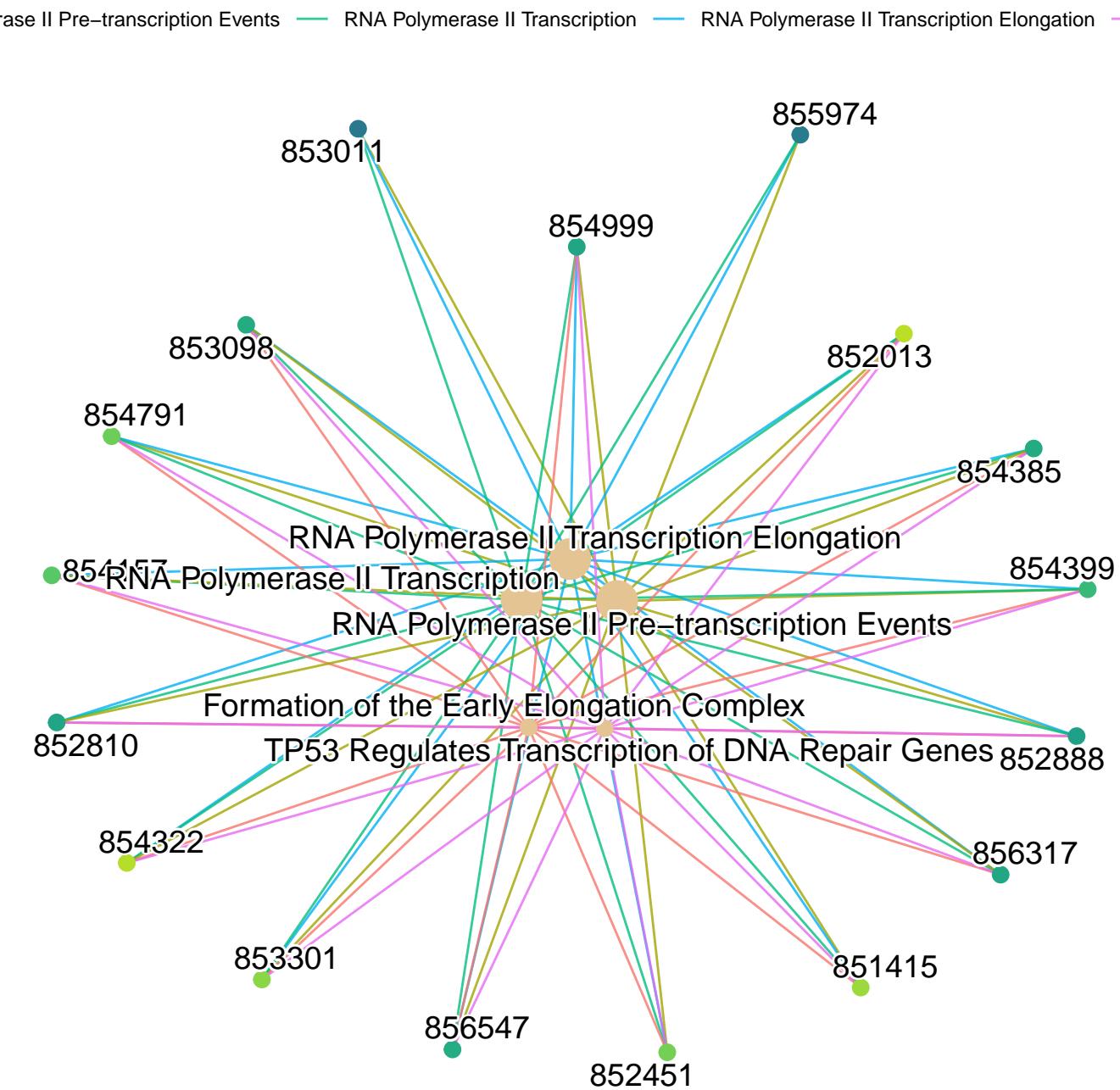
RPB7-TAP Up-regulated Reactome



RPB7-TAP Up-regulated Reactome



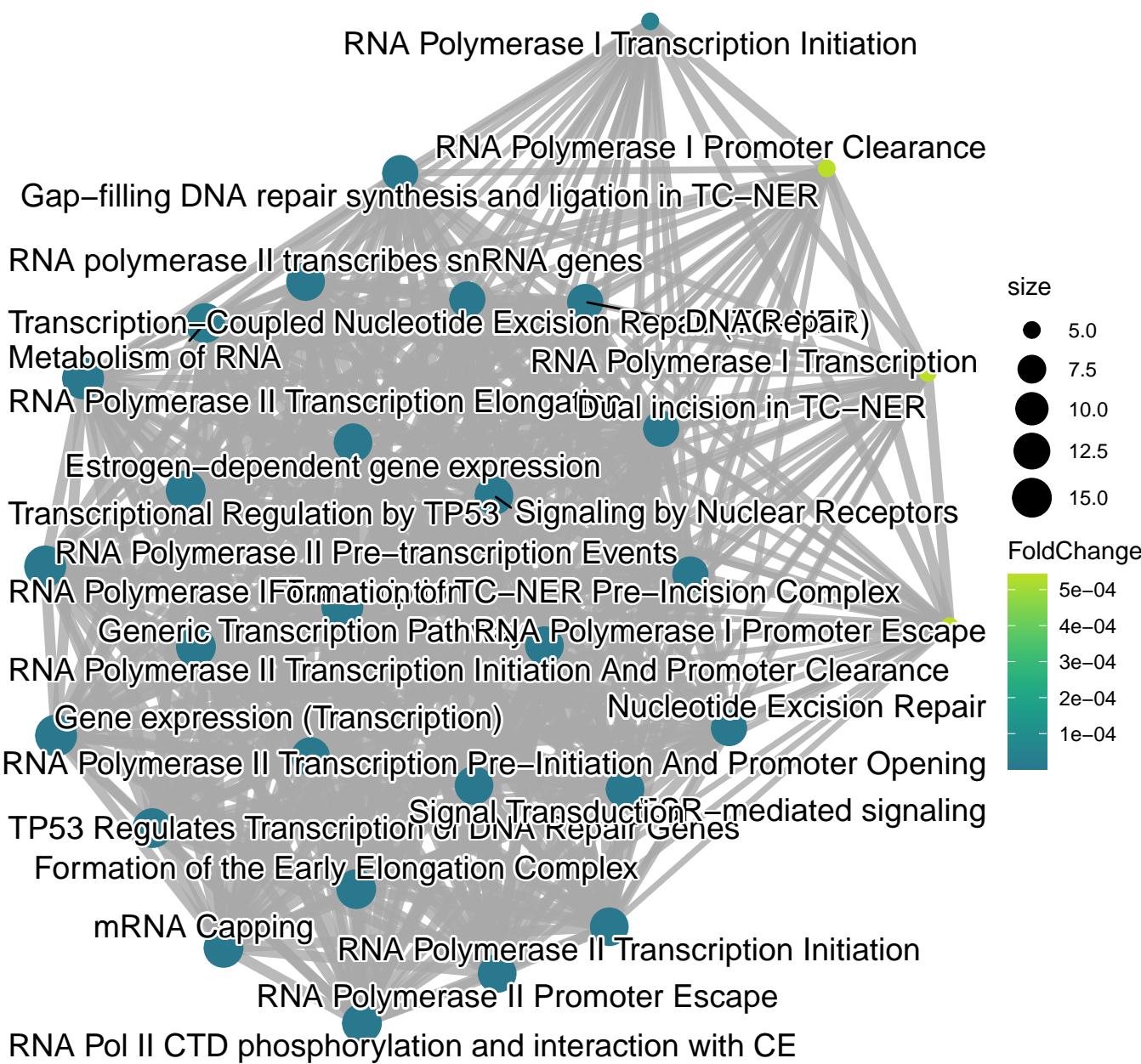
RPB7-TAP Up-regulated Reactome cnetplot

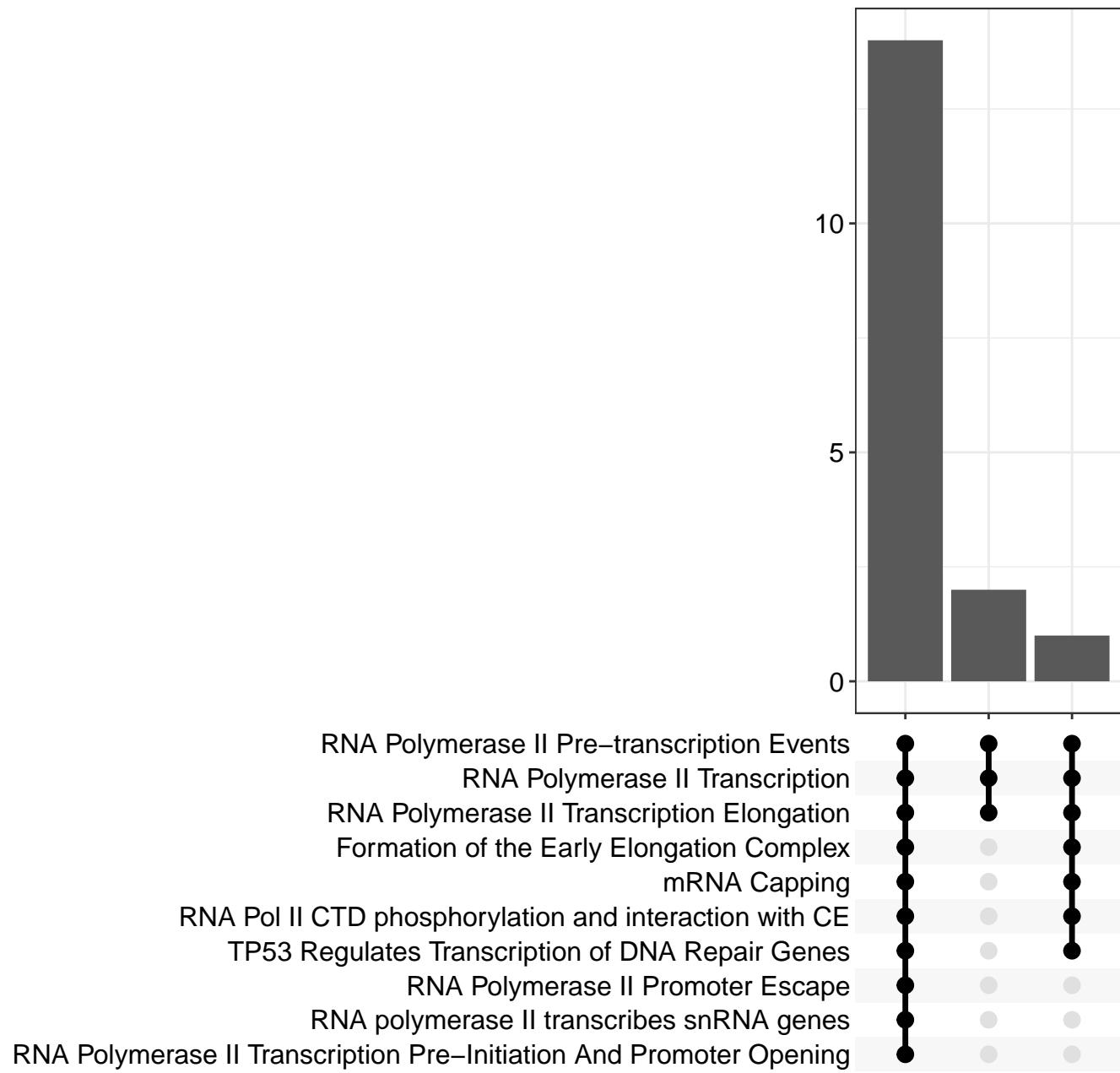


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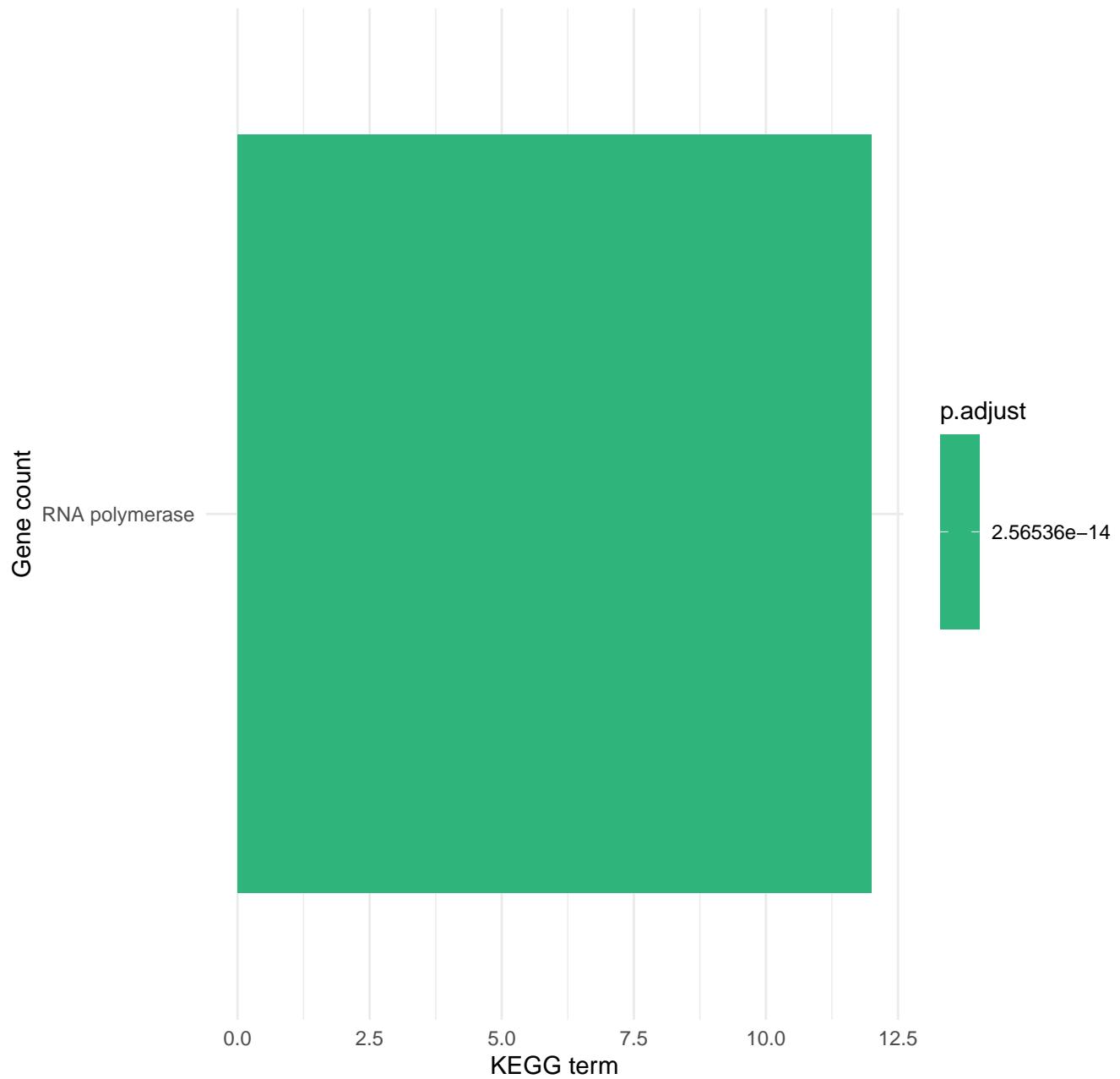


RPB7-TAP Up-regulated Reactome emapplot

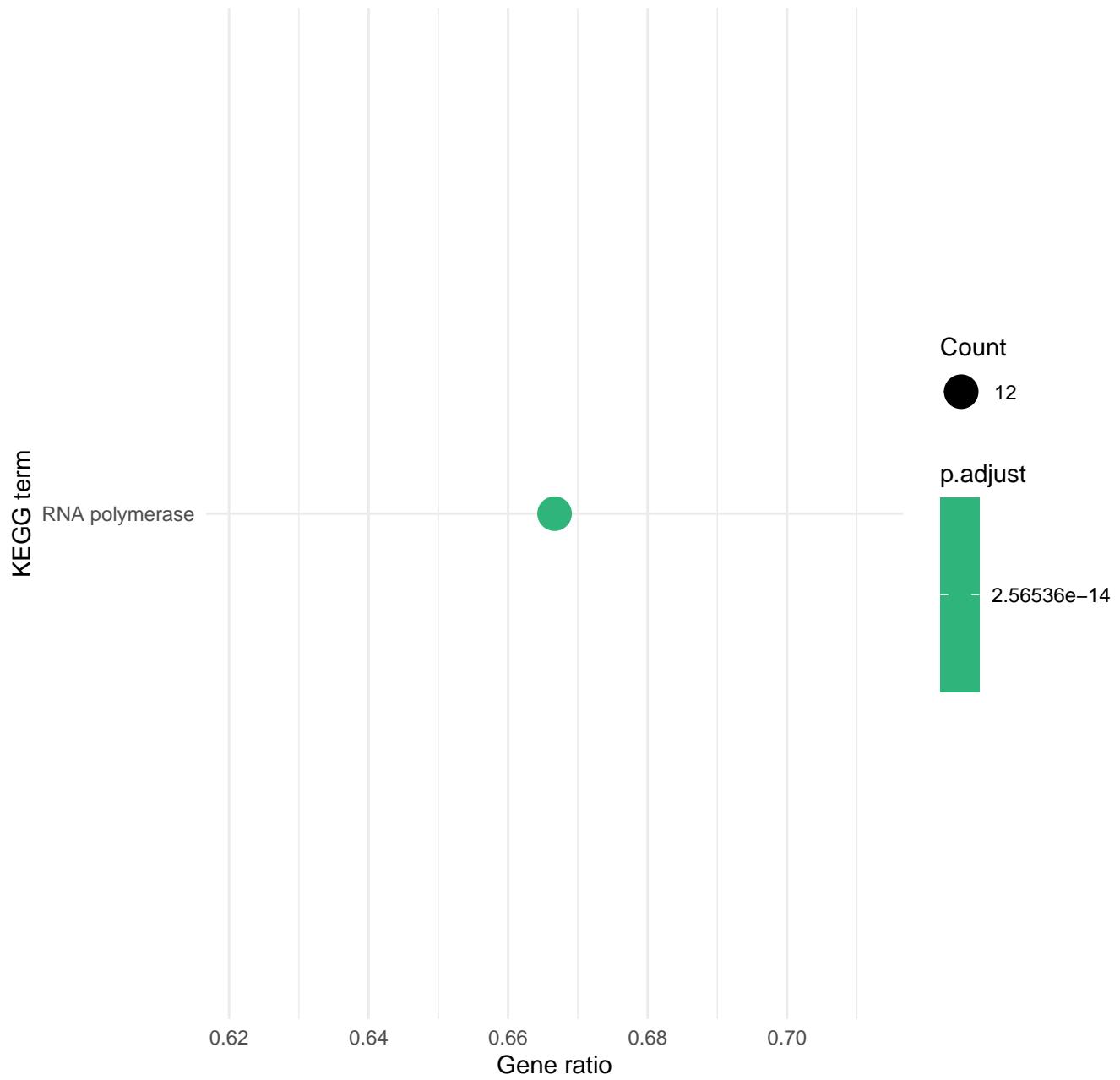




RPB7-TAP Up-regulated KEGG barplot



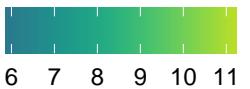
RPB7-TAP Up-regulated KEGG dotplot



RPB7-TAP Up-regulated KEGG dotplot

category RNA polymerase

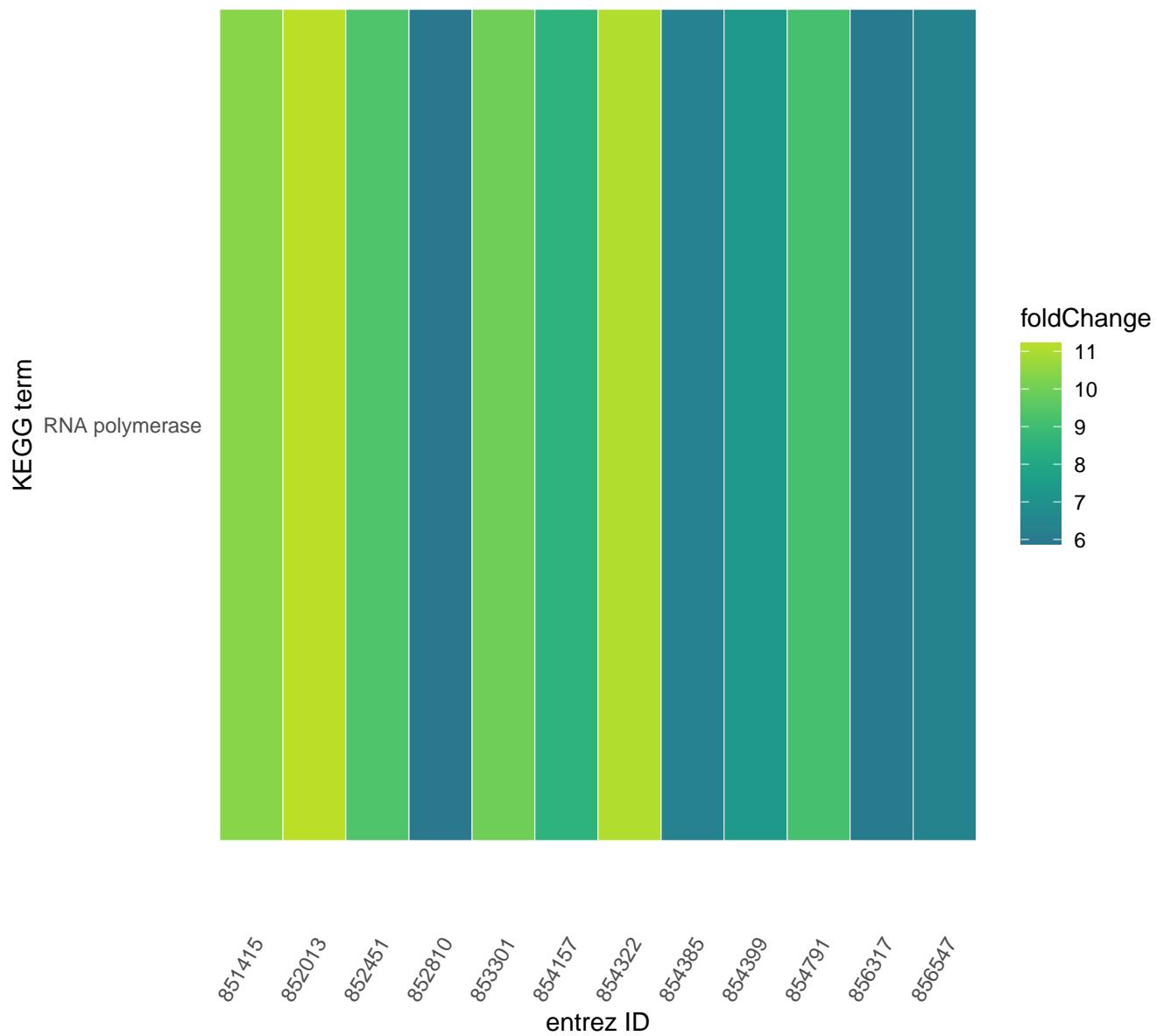
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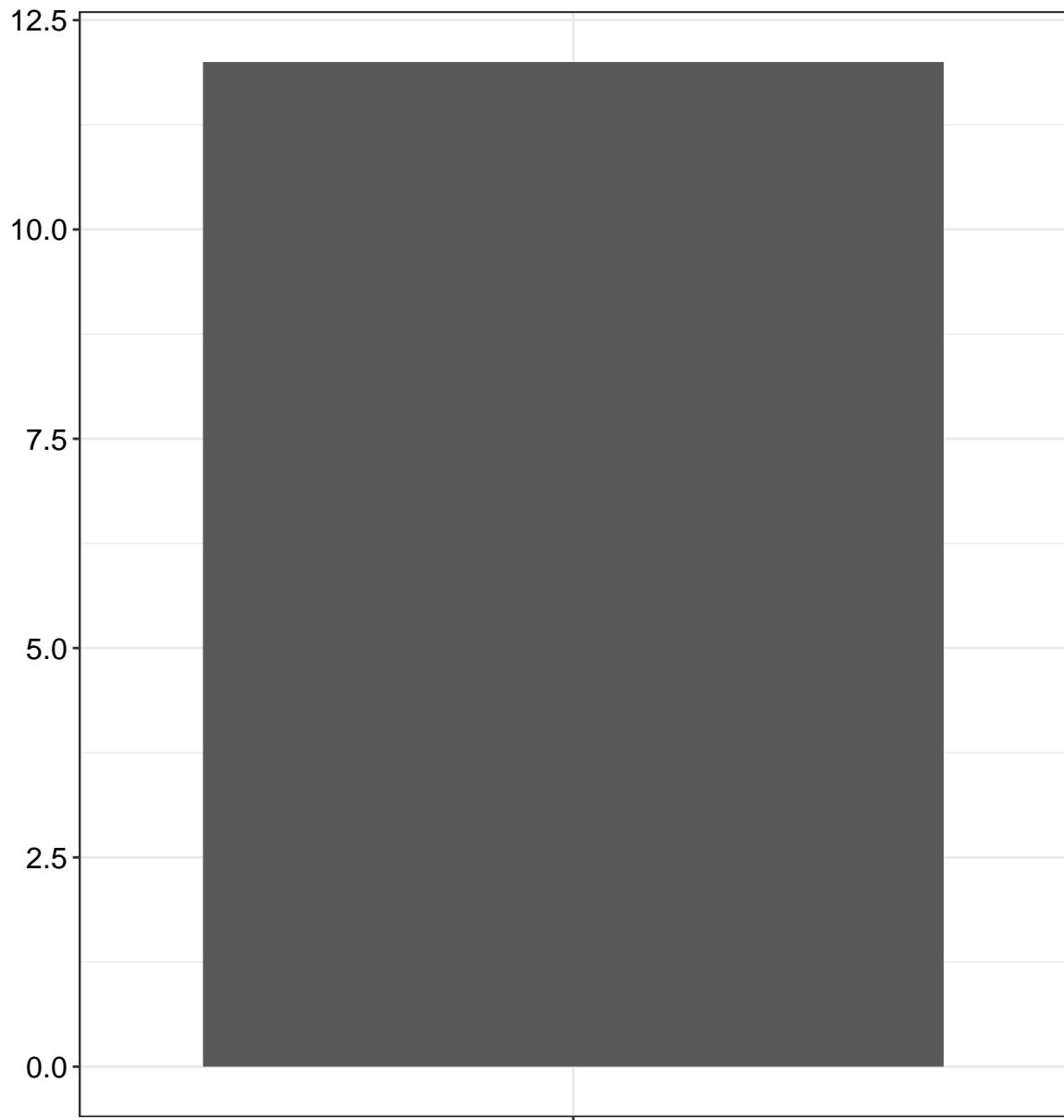
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RPB7-TAP Up-regulated KEGG heatplot



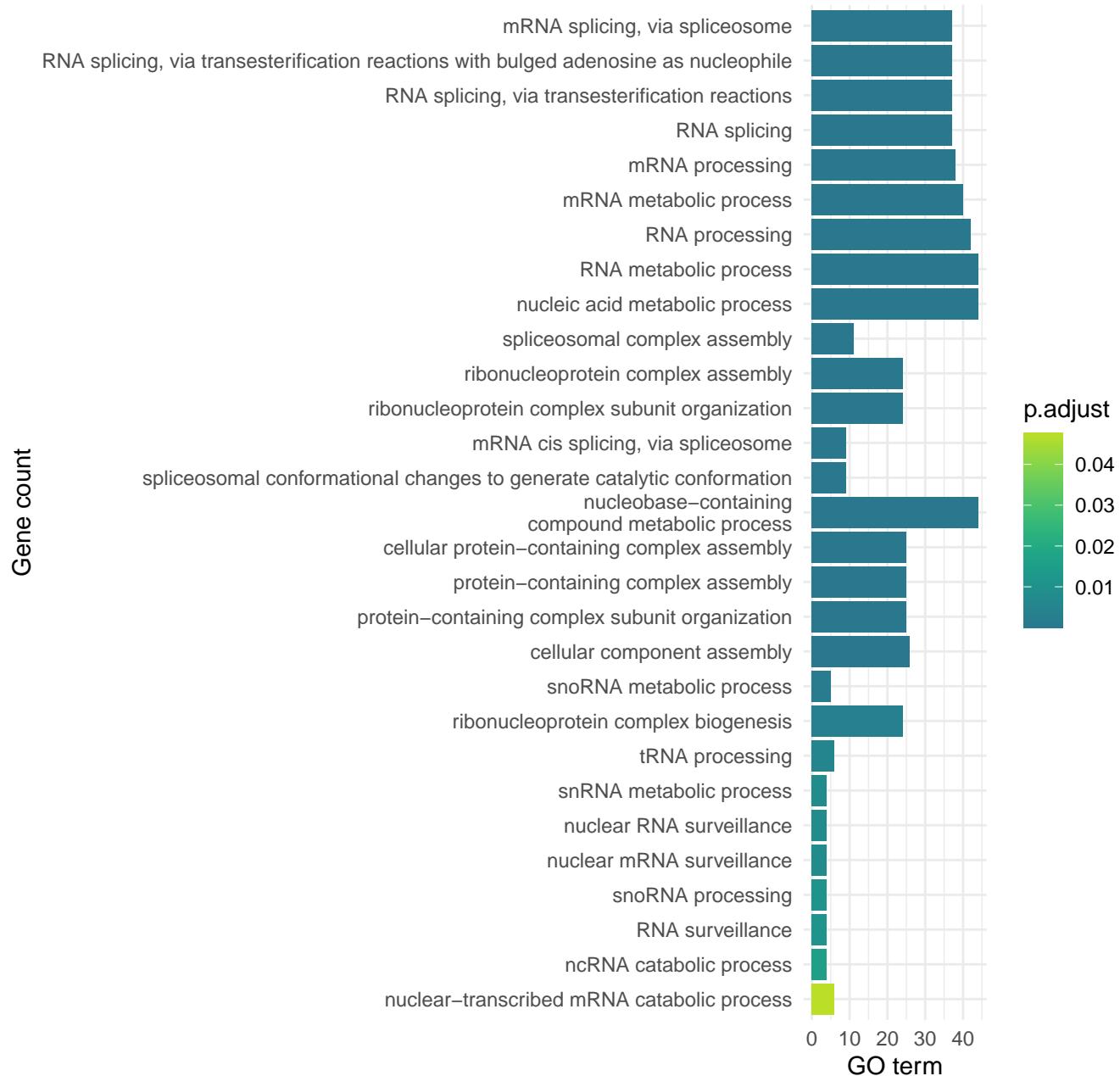
RPB7-TAP Up-regulated KEGG upsetplot



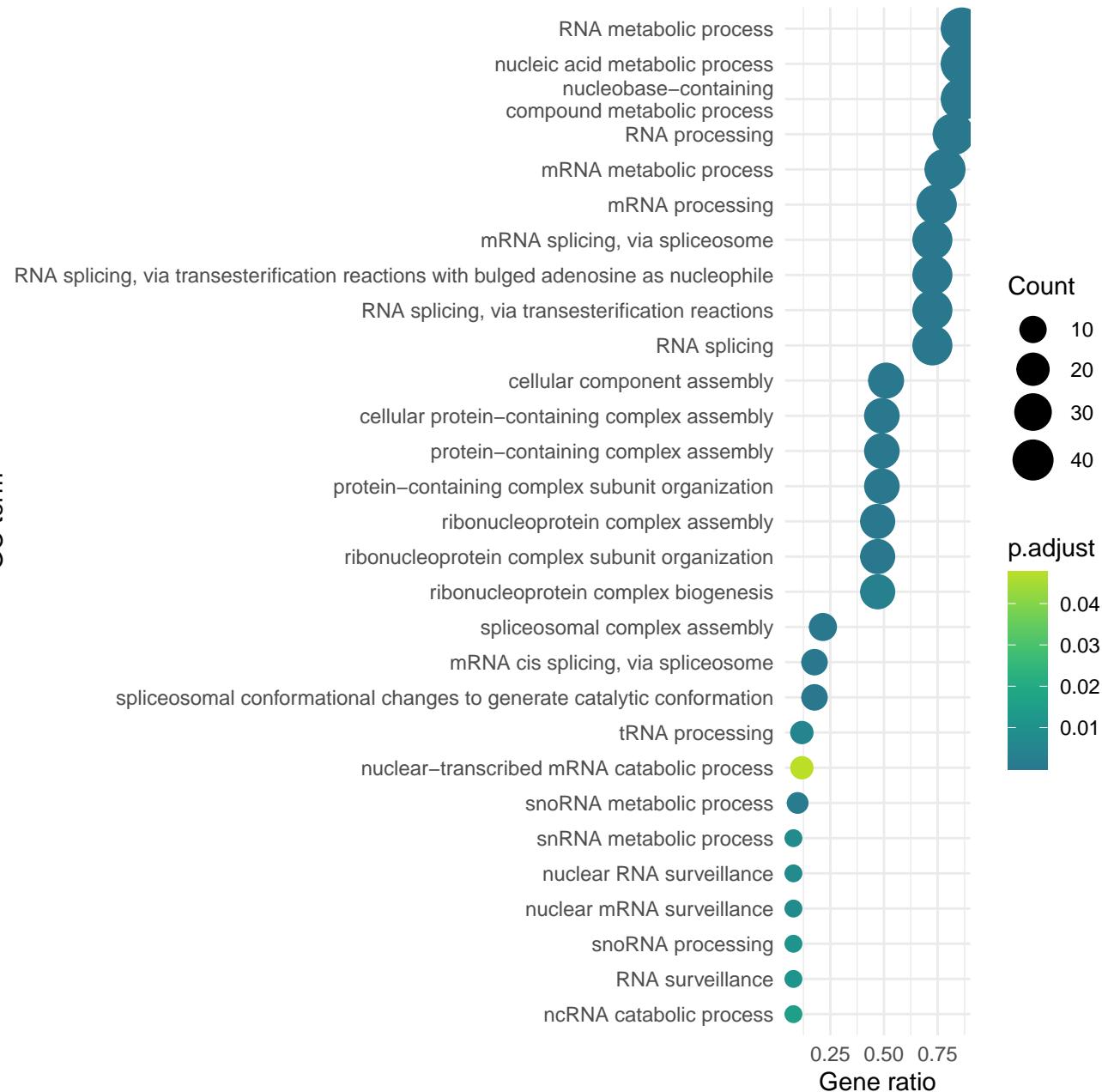
RNA polymerase

●

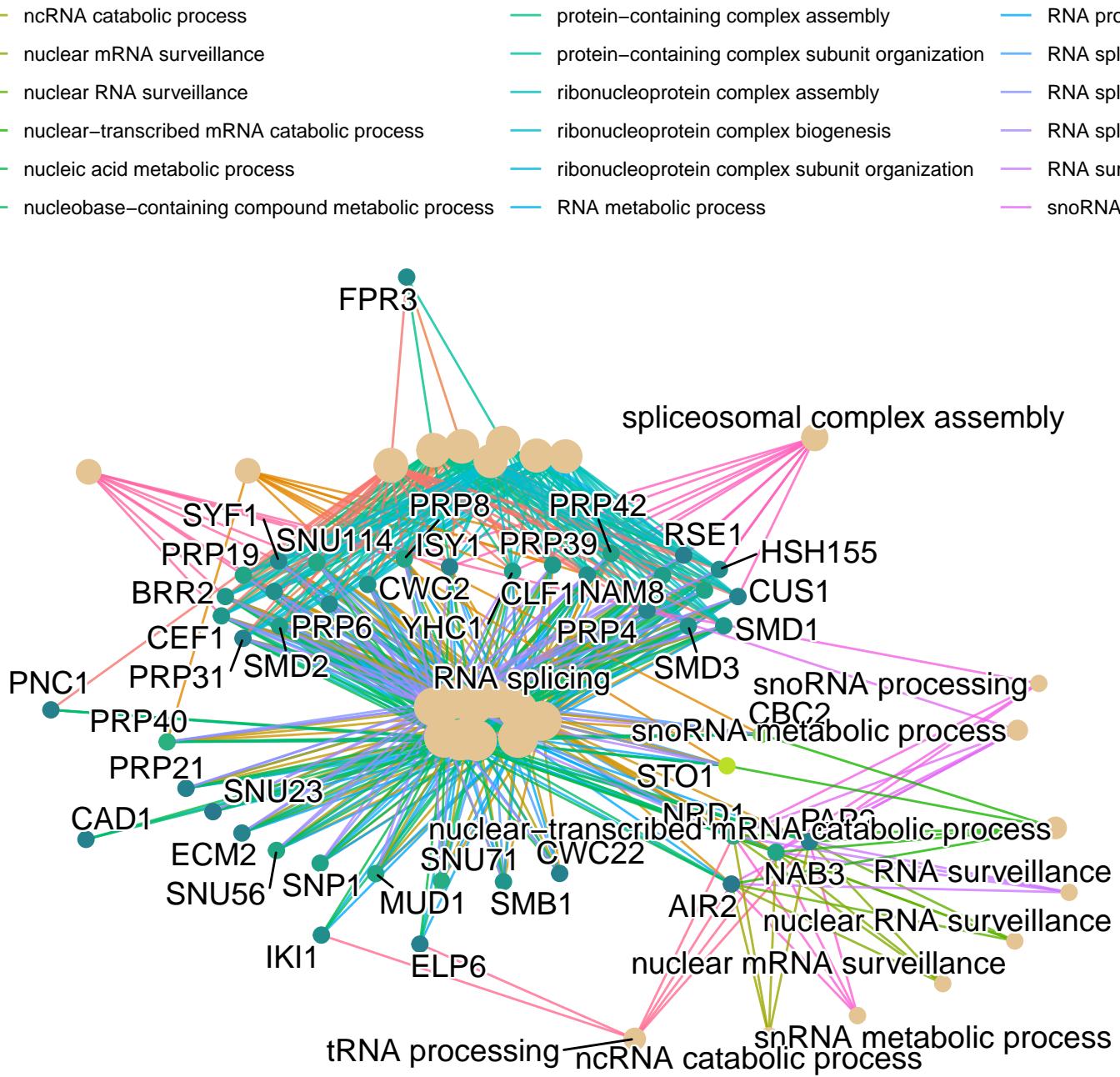
STO1-TAP Up-regulated



STO1-TAP Up-regulated



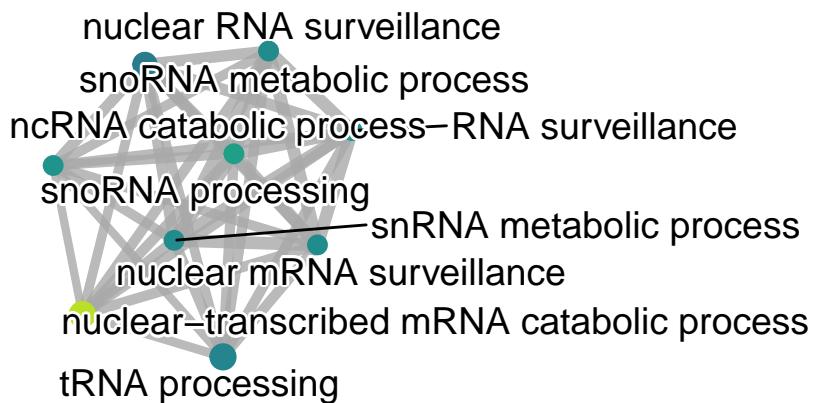
STO1-TAP Up-regulated GO BP cnetplot



STO1-TAP Up-regulated



STO1-TAP Up-regulated GO BP emapplot

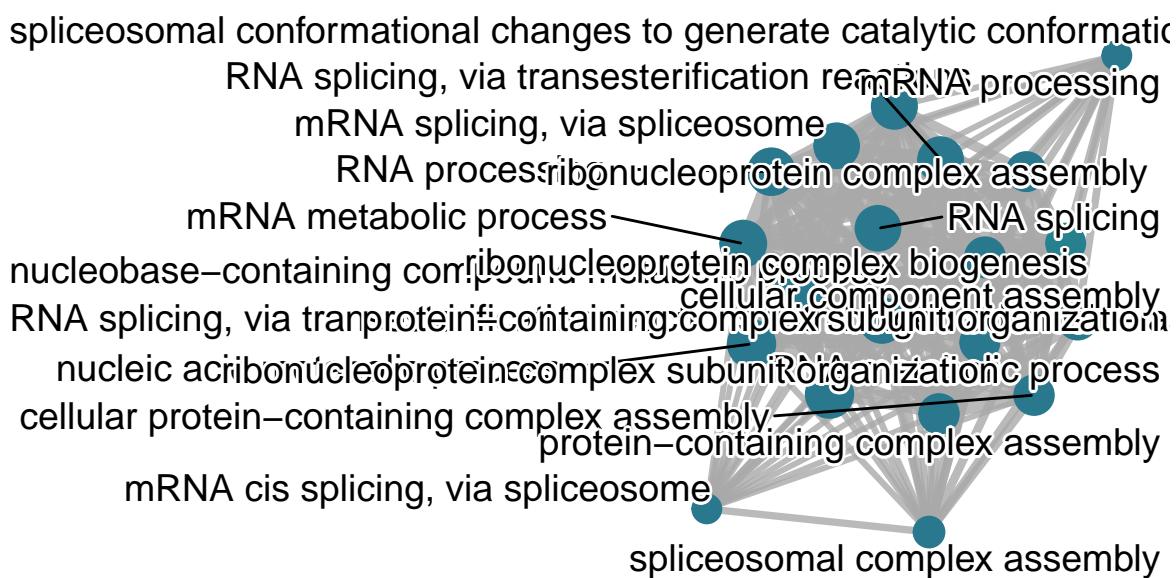


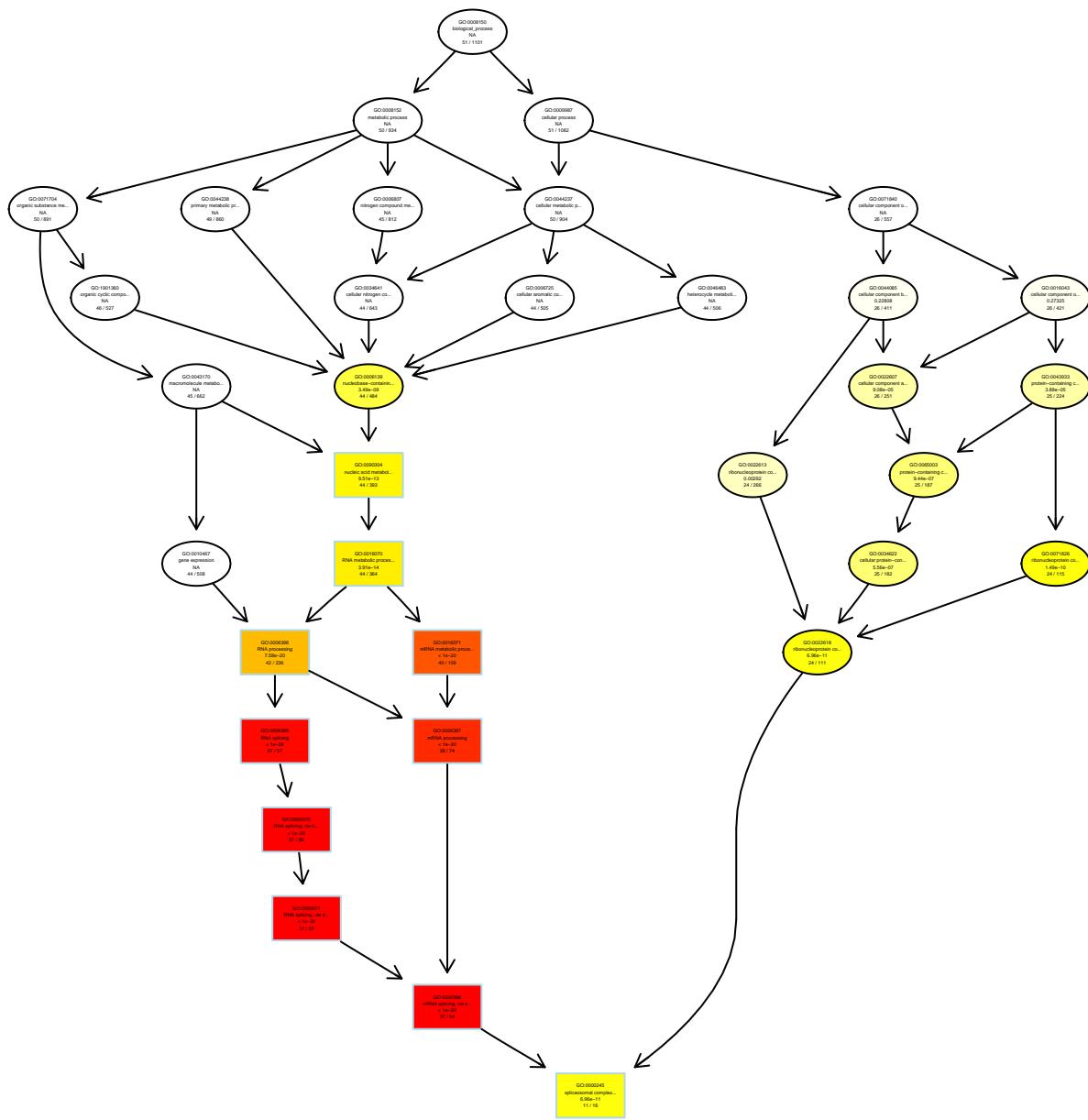
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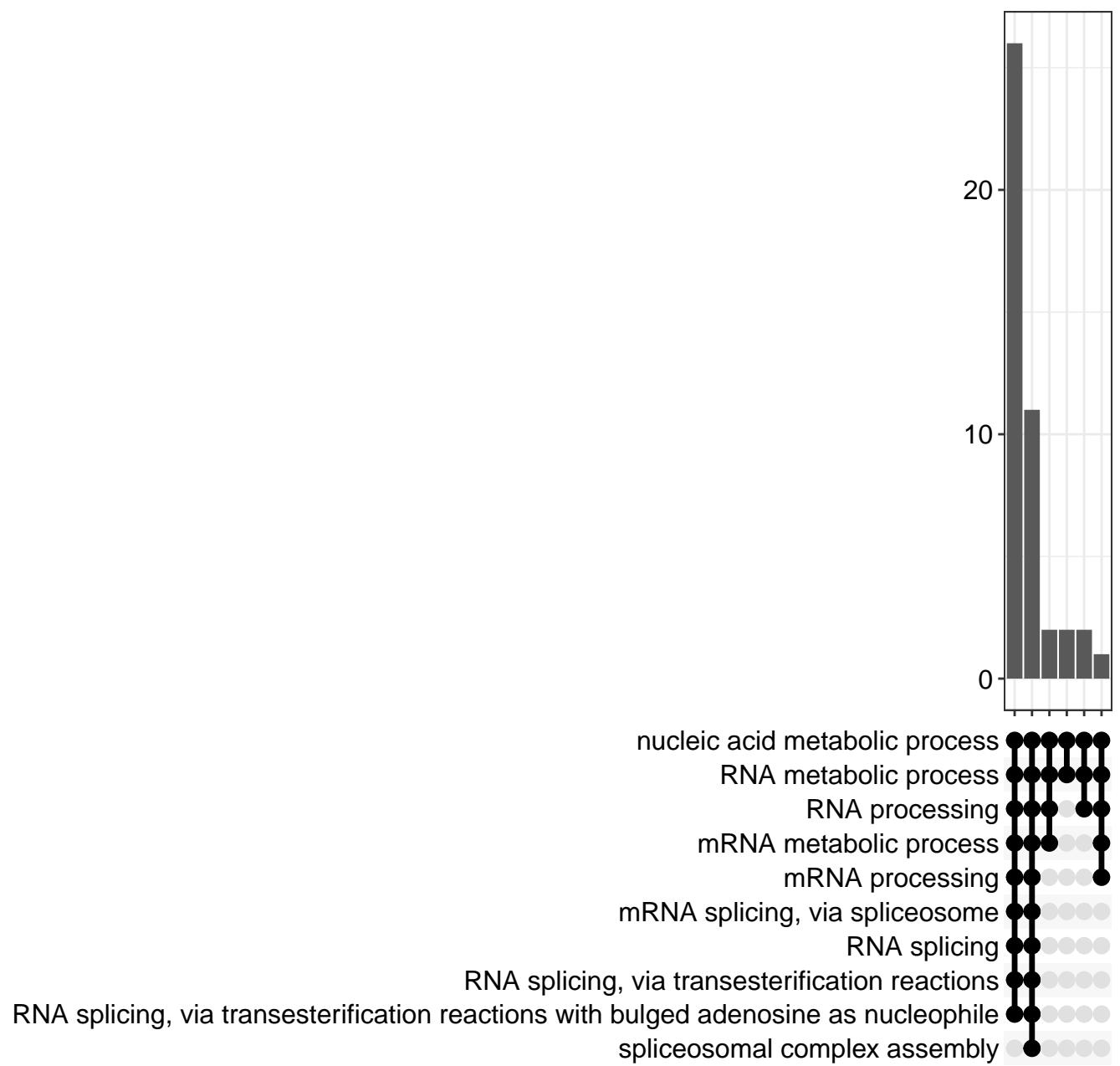
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0.01

size

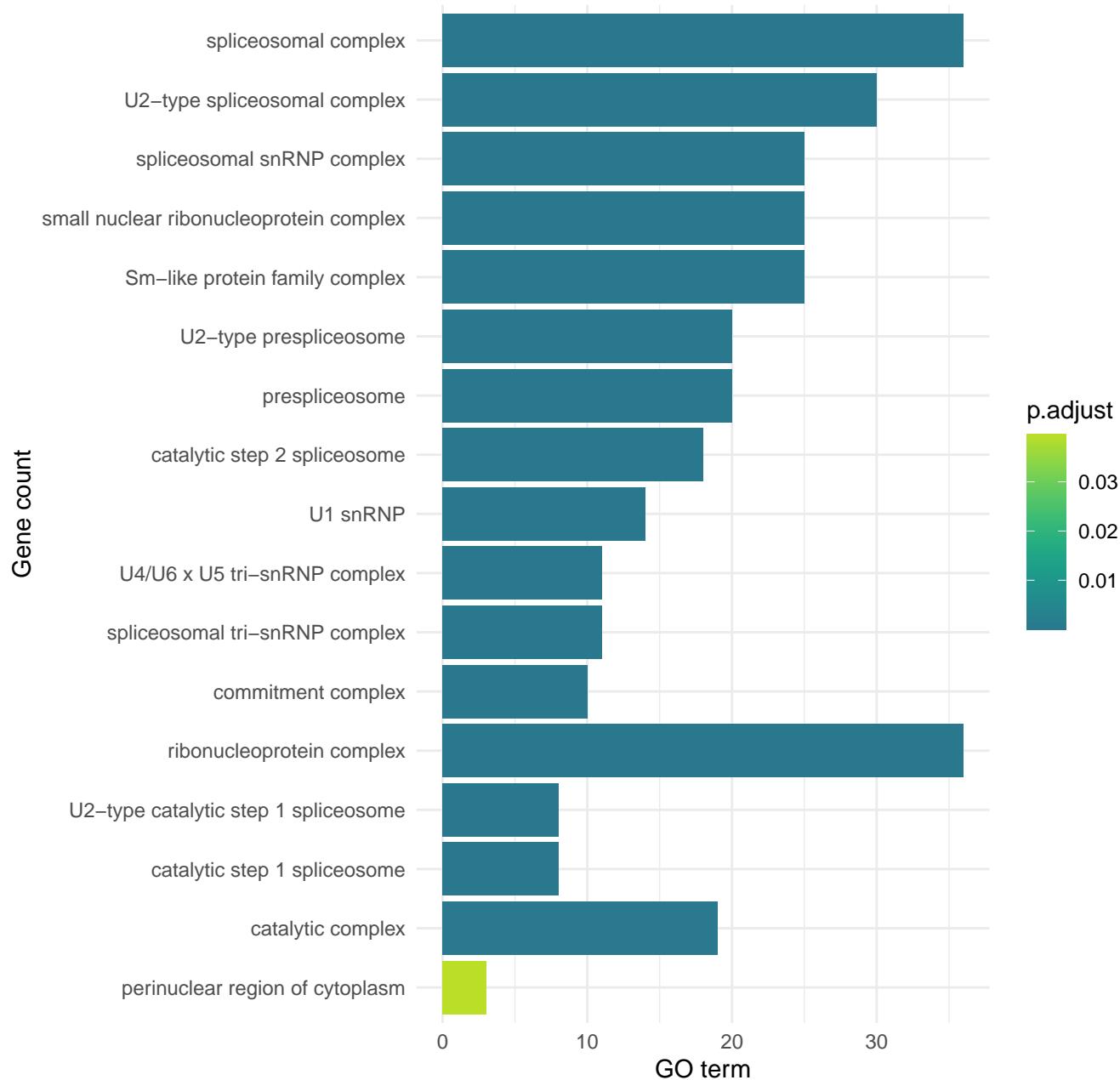
● 10
● 20
● 30
● 40



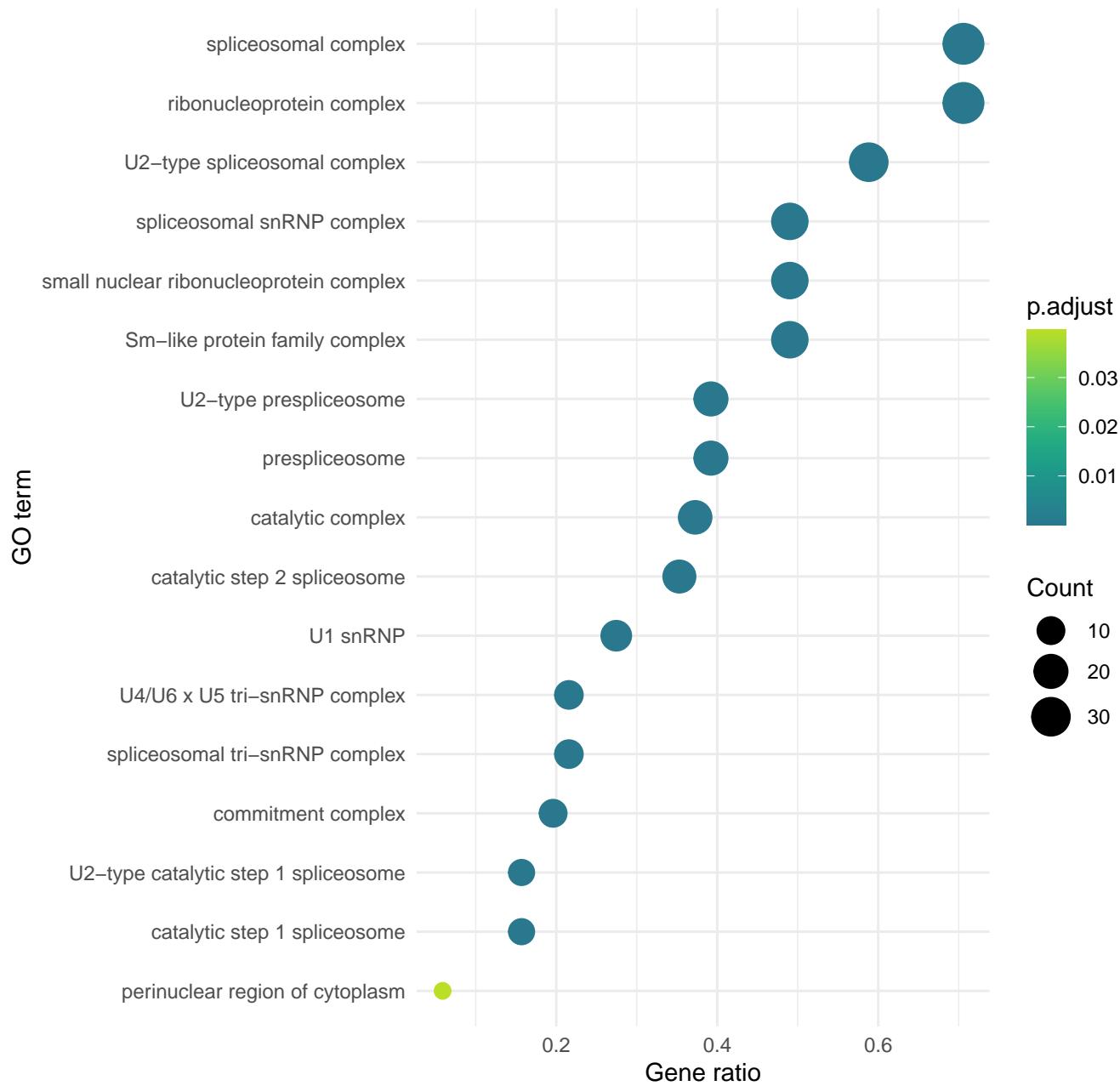




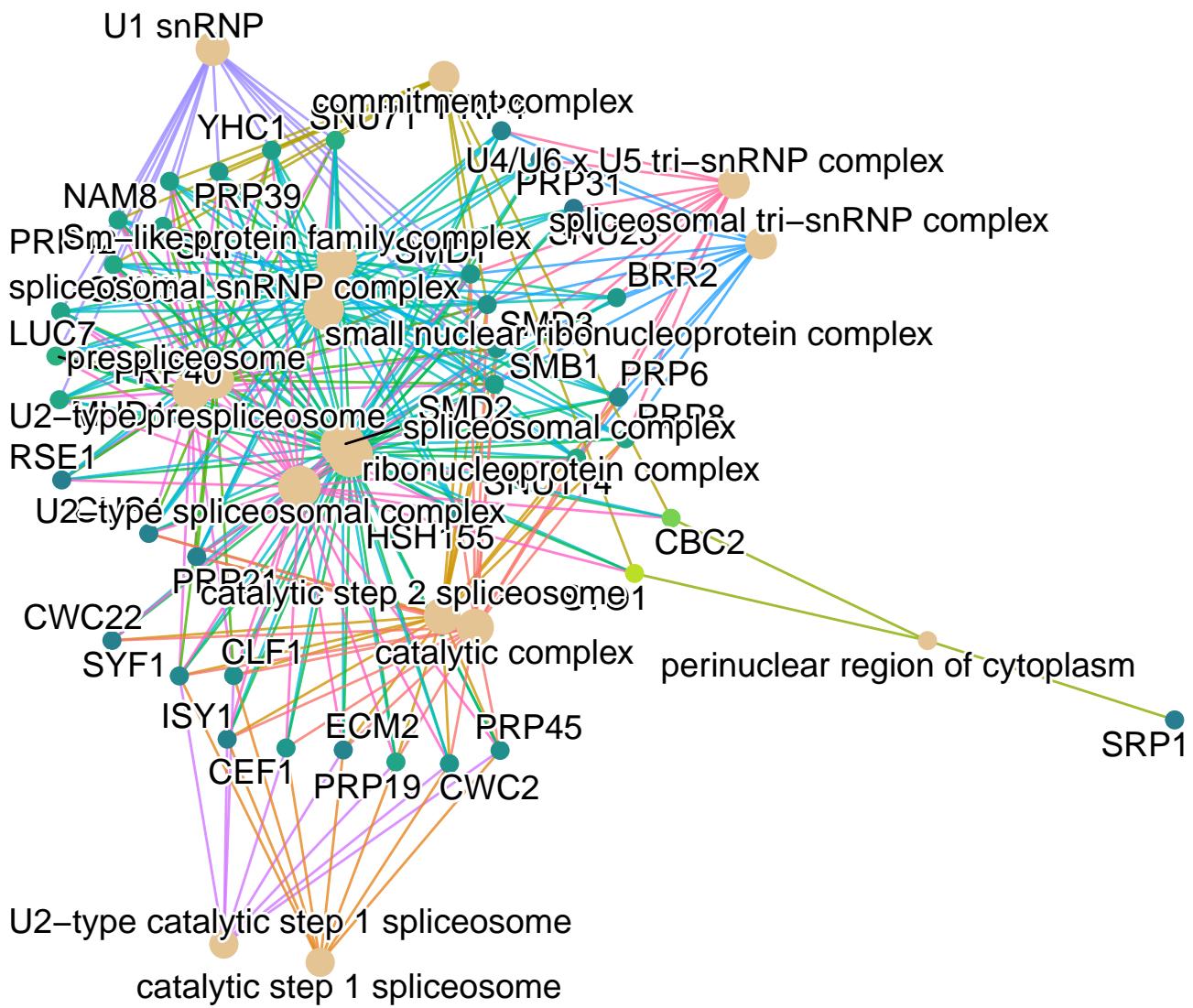
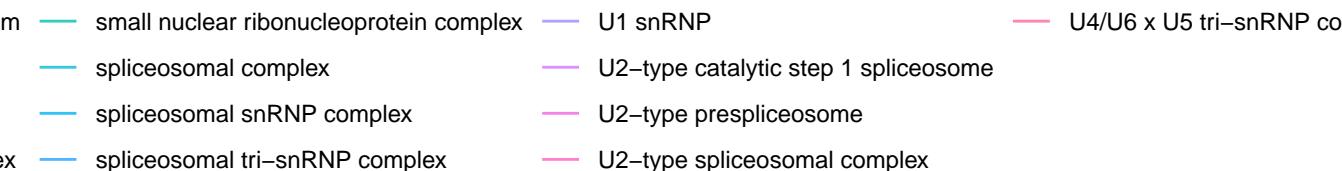
STO1-TAP Up-regulated GO CC barplot



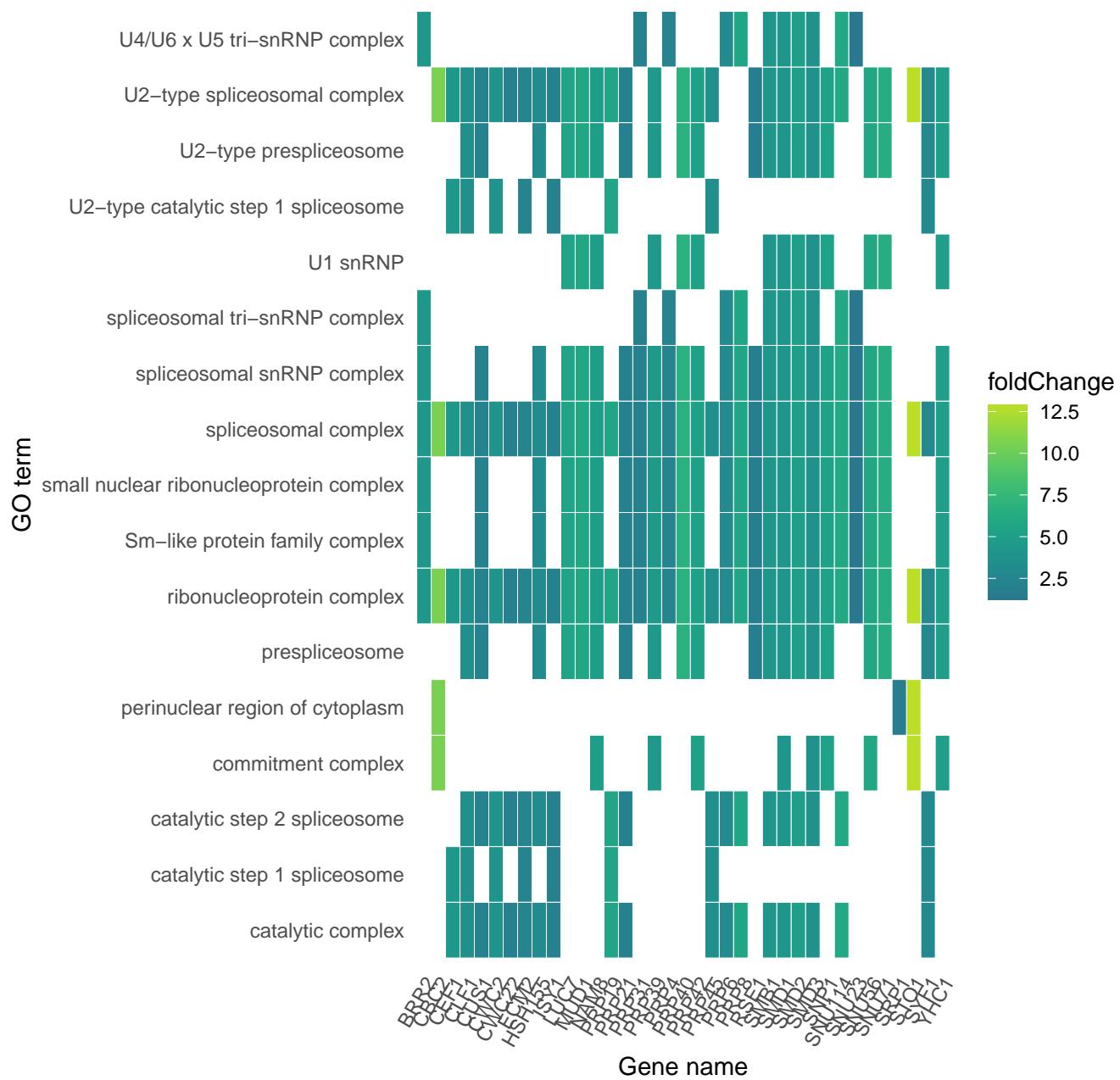
STO1-TAP Up-regulated GO CC dotplot



STO1-TAP Up-regulated GO CC cnetplot



STO1-TAP Up-regulated GO CC heatplot



STO1-TAP Up-regulated GO CC emapplot

catalytic step 1 spliceosome

U2-type catalytic step 1 spliceosome

catalytic step 2 spliceosome

U2-type spliceosomal complex

perinuclear region of cytoplasm

U2-type presspliceosome

catalytic complex

spliceosomal complex

ribonucleoprotein complex

presspliceosome

spliceosomal snRNP complex

Sm-like protein family complex

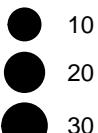
spliceosomal tri-snRNP complex

small nuclear ribonucleoprotein complex

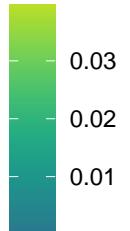
commitment complex

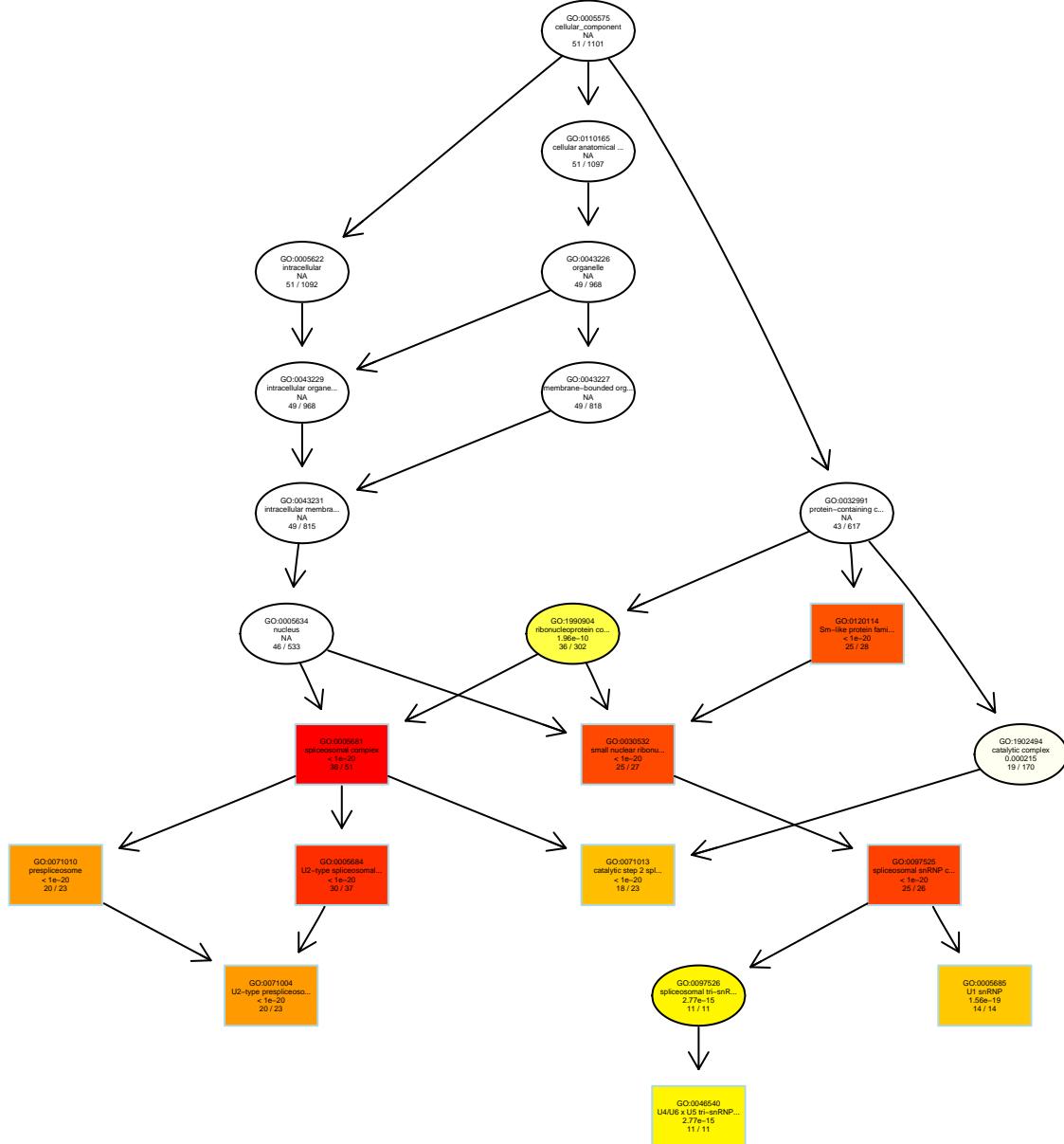
U4/U6 x U5 tri-snRNP complex

size

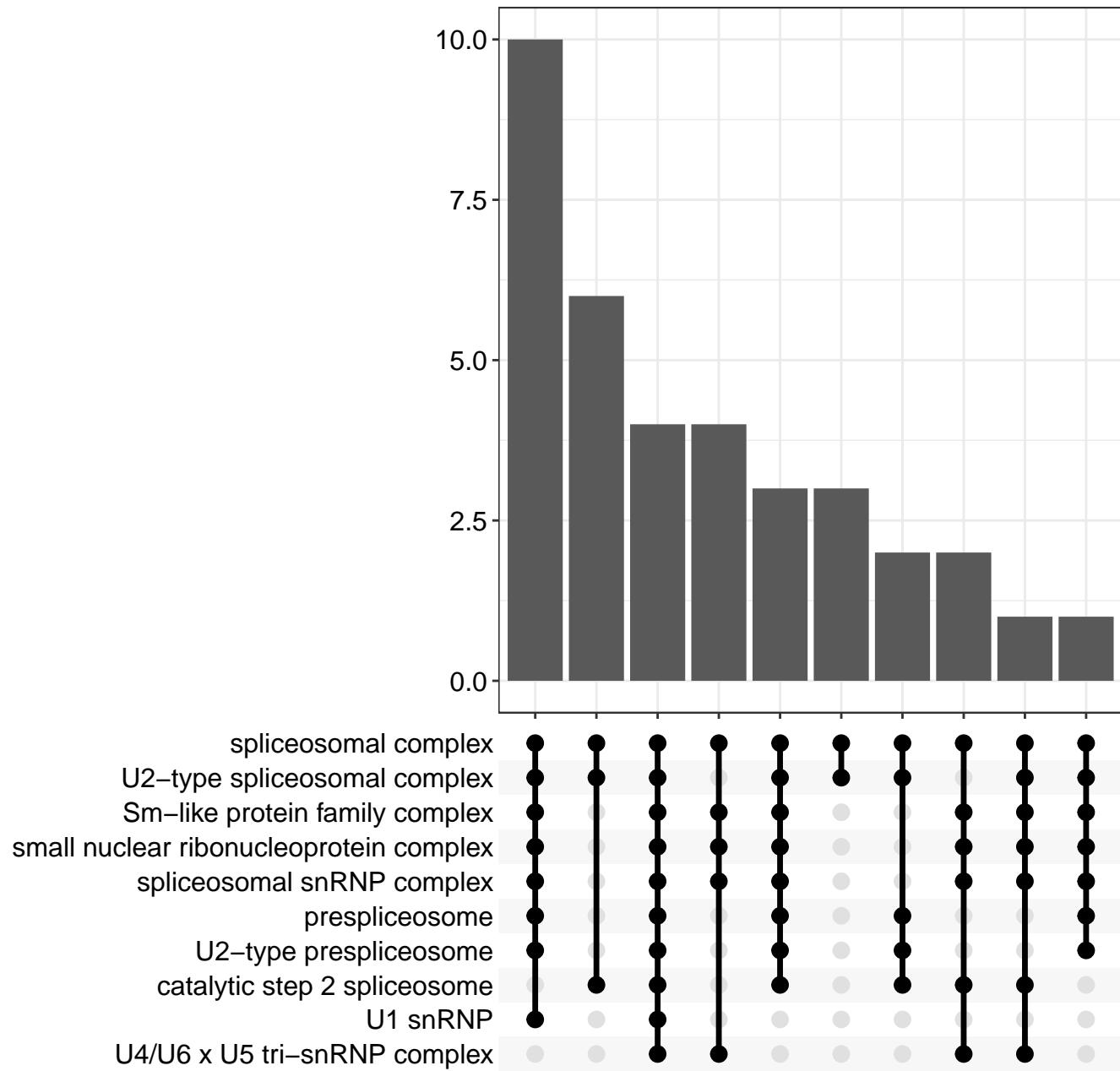


FoldChange

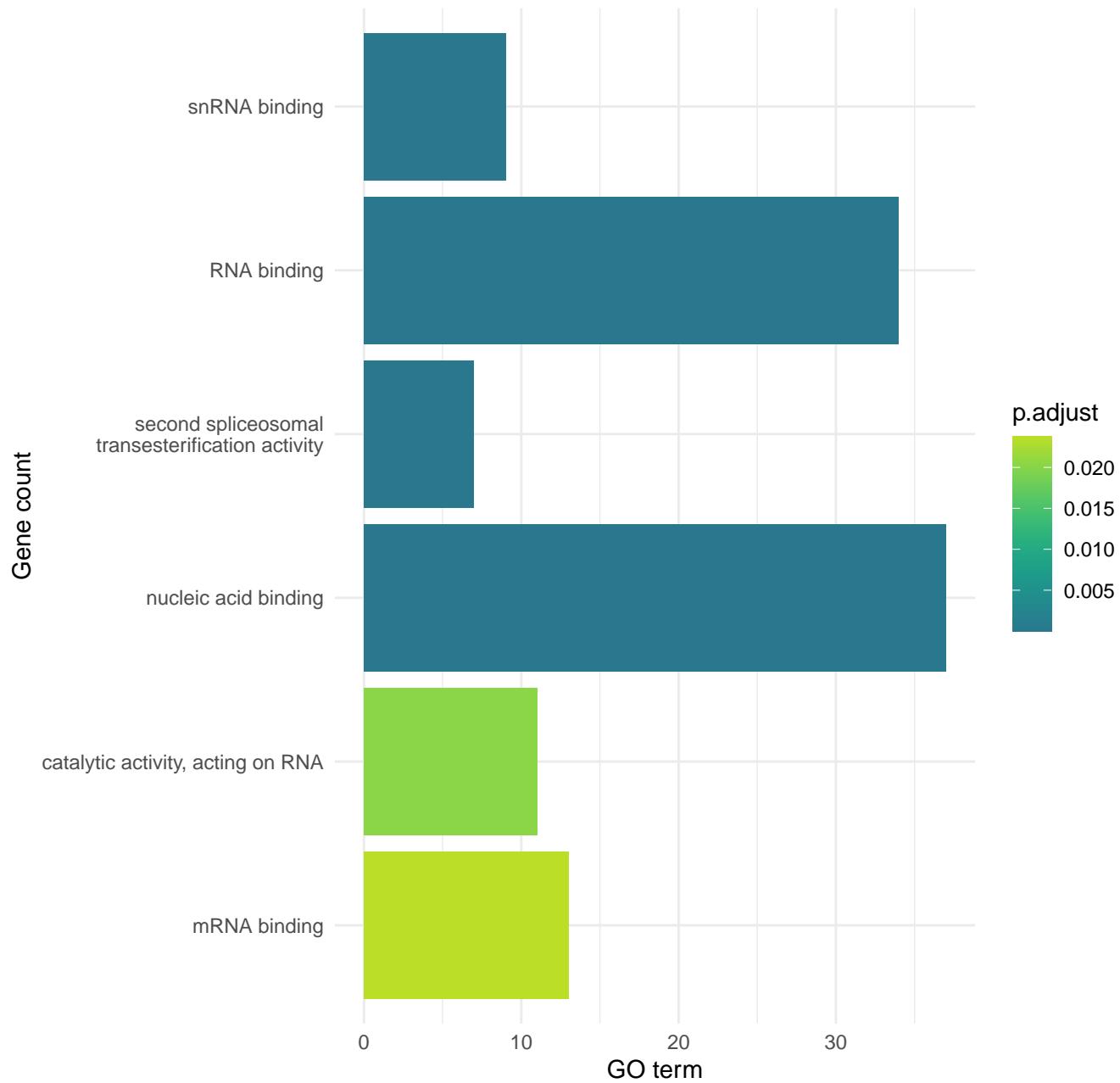




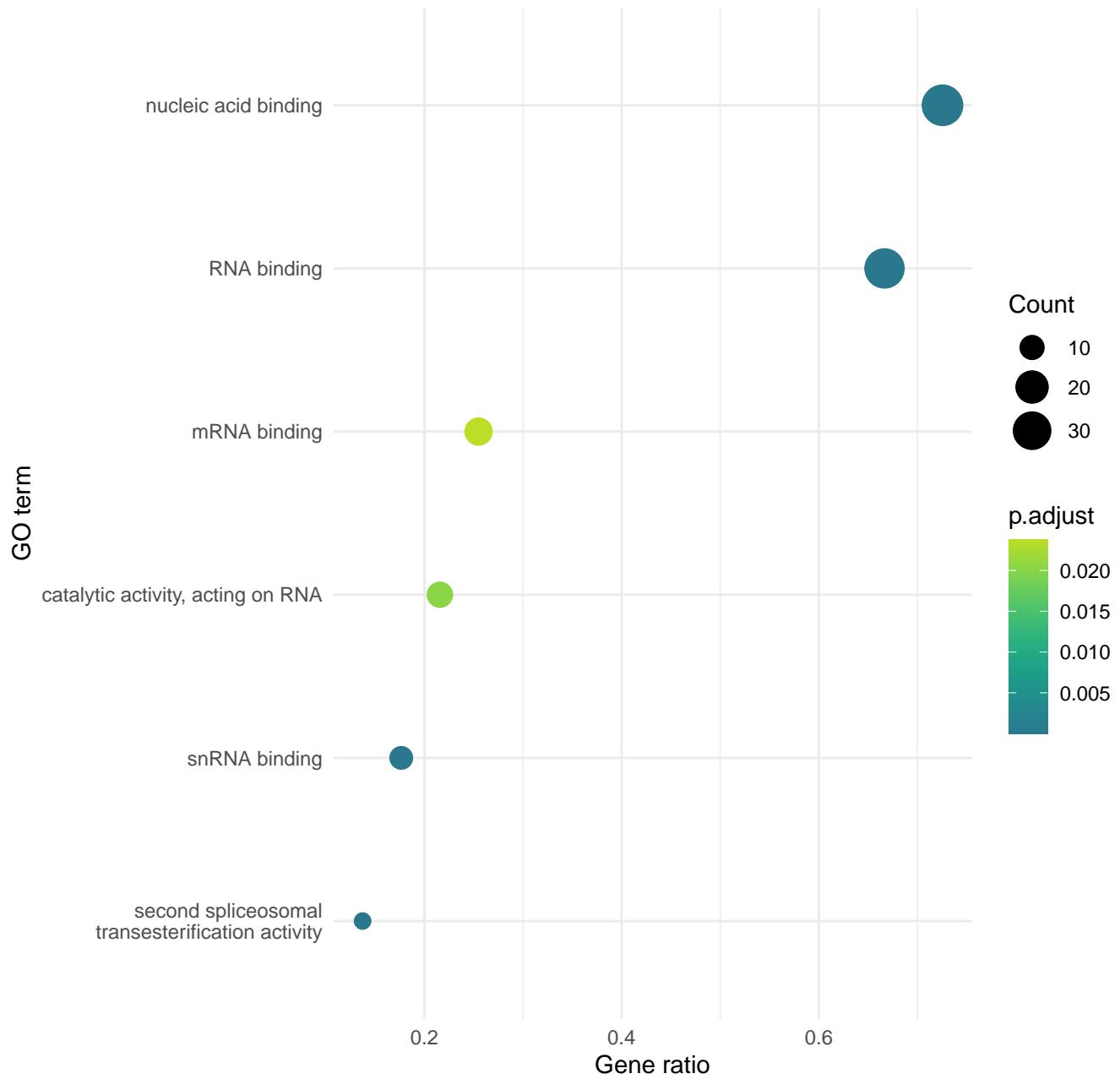
STO1-TAP Up-regulated GO CC upsetplot



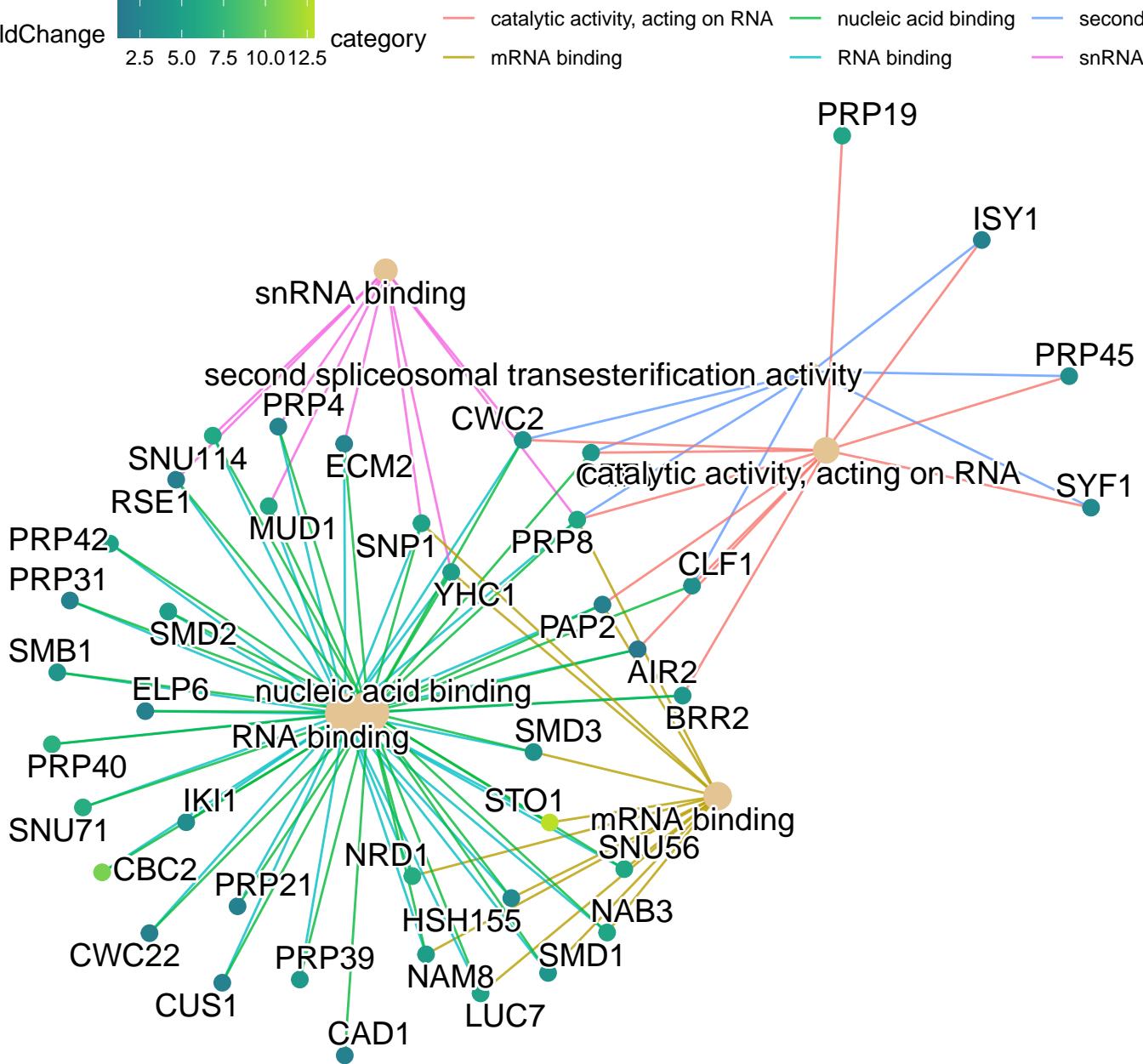
STO1-TAP Up-regulated GO MF barplot



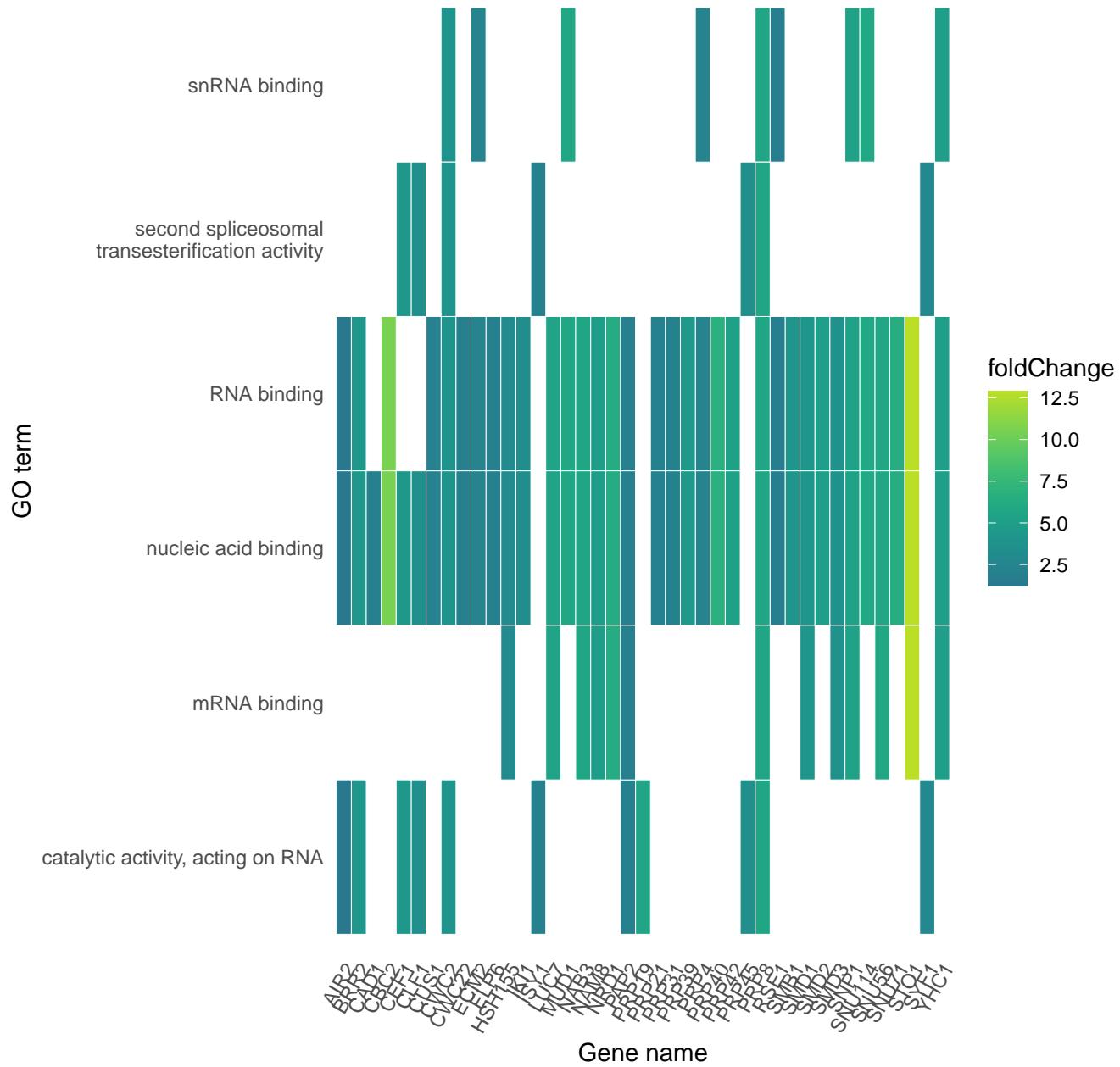
STO1-TAP Up-regulated GO MF dotplot



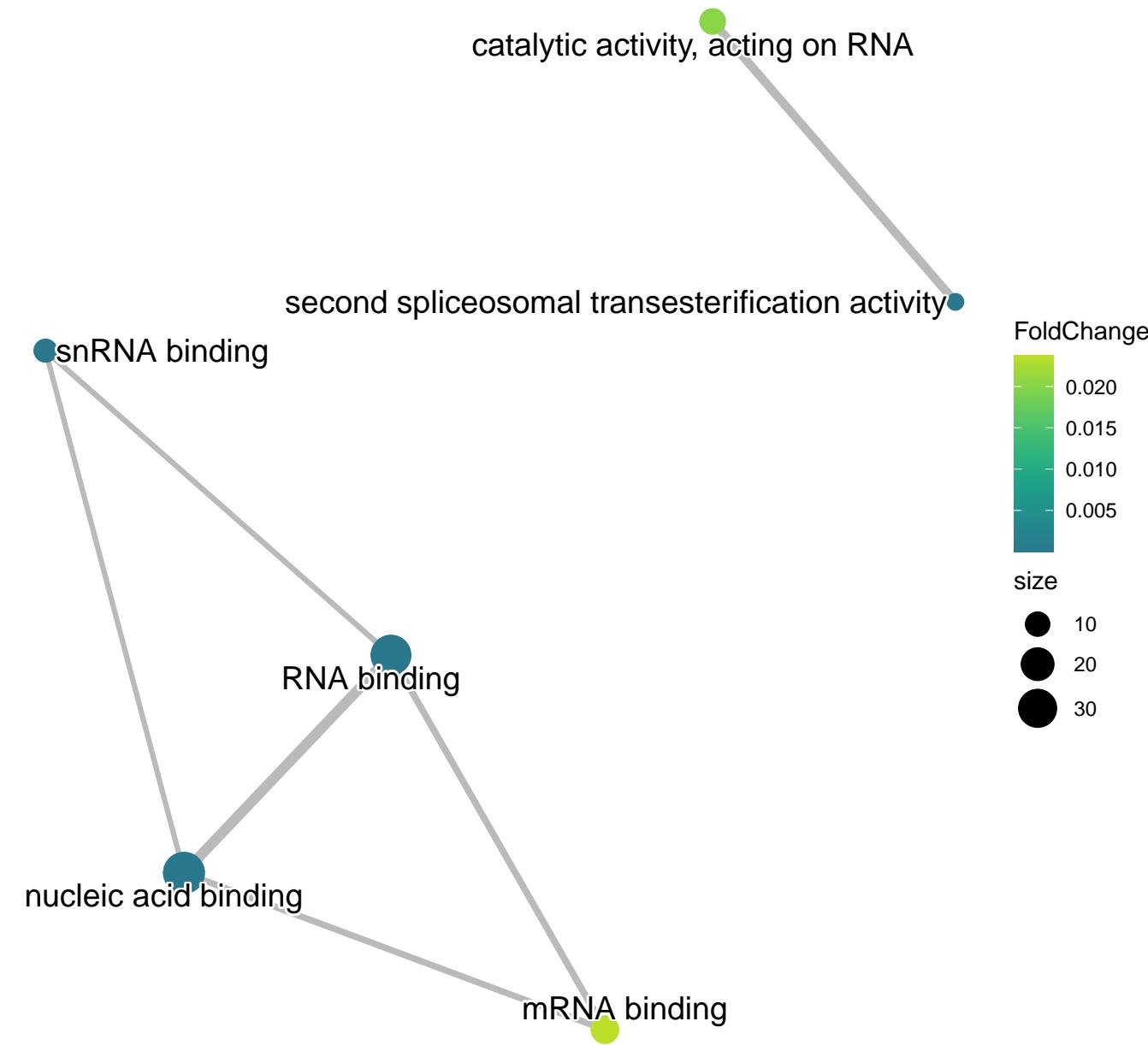
STO1-TAP Up-regulated GO MF cnetplot

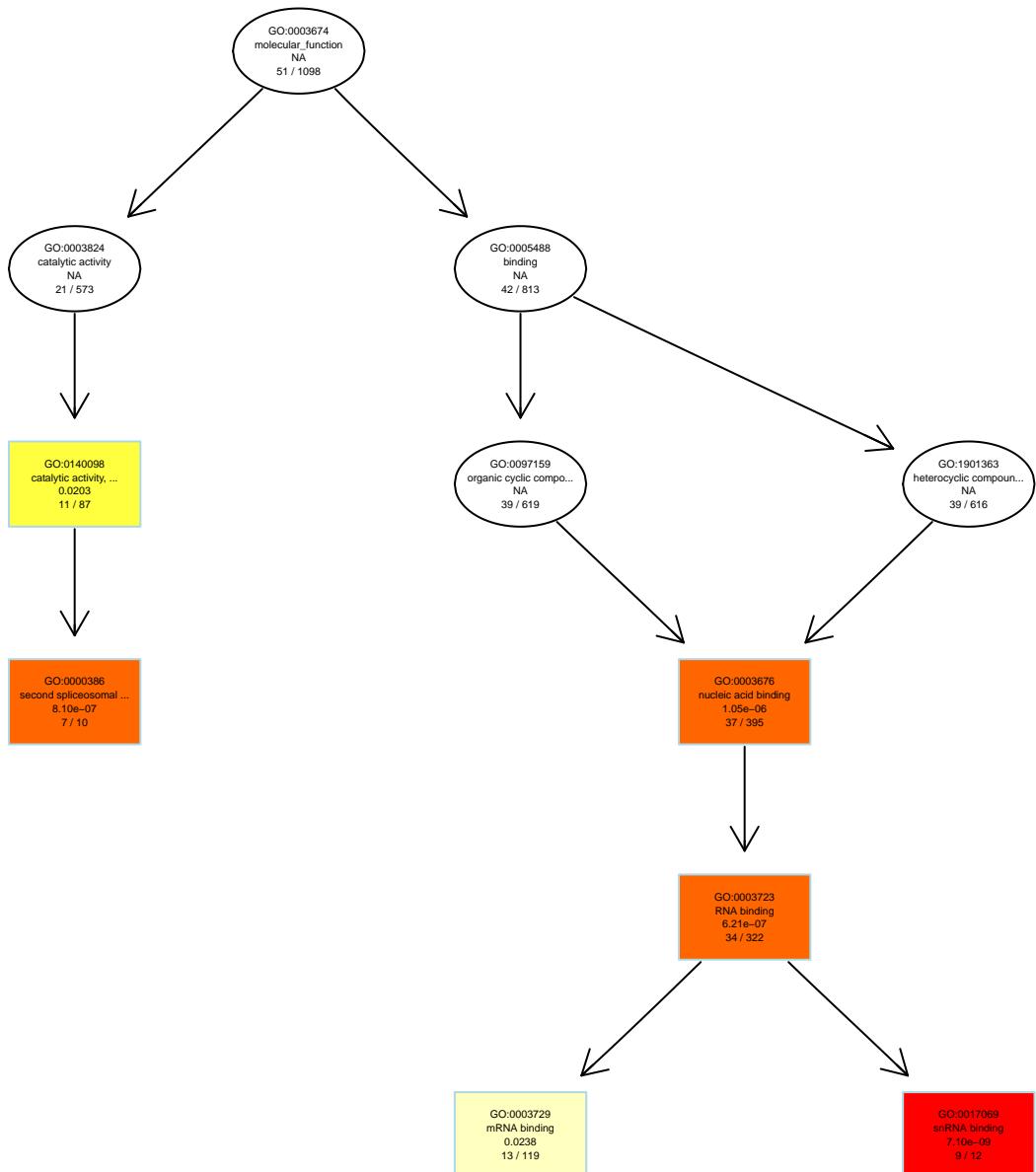


STO1-TAP Up-regulated GO MF heatplot

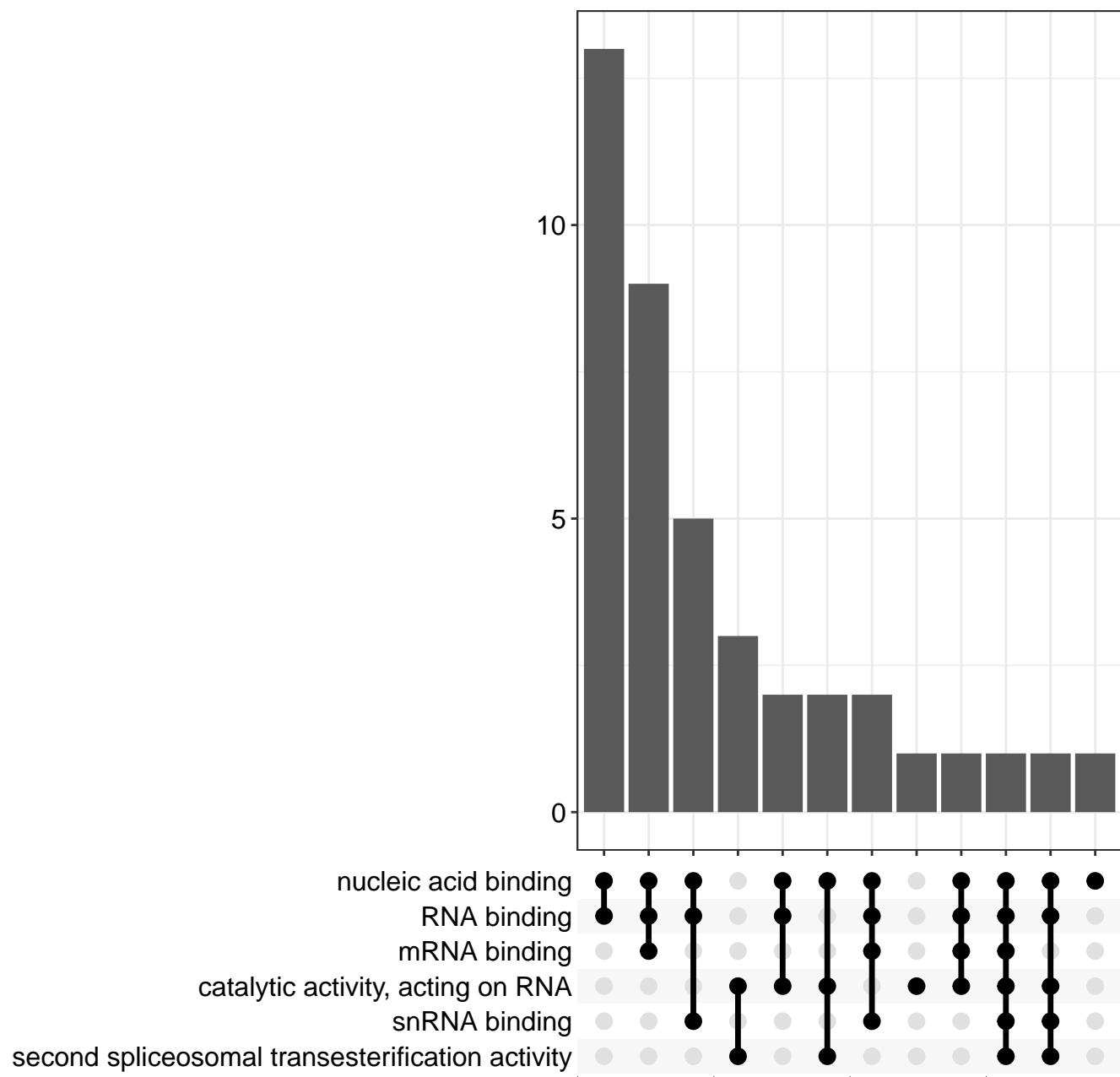


STO1-TAP Up-regulated GO MF emapplot

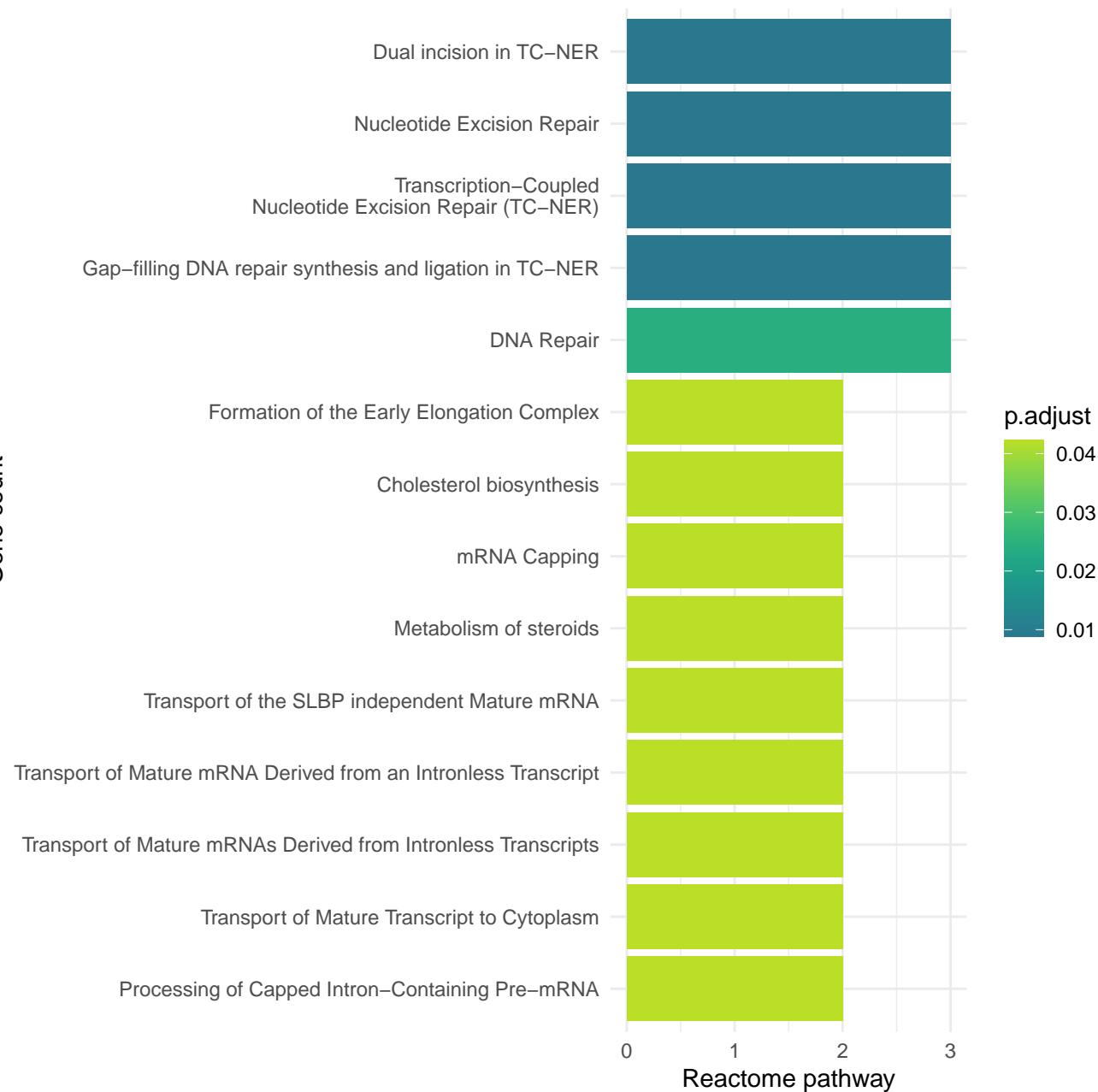




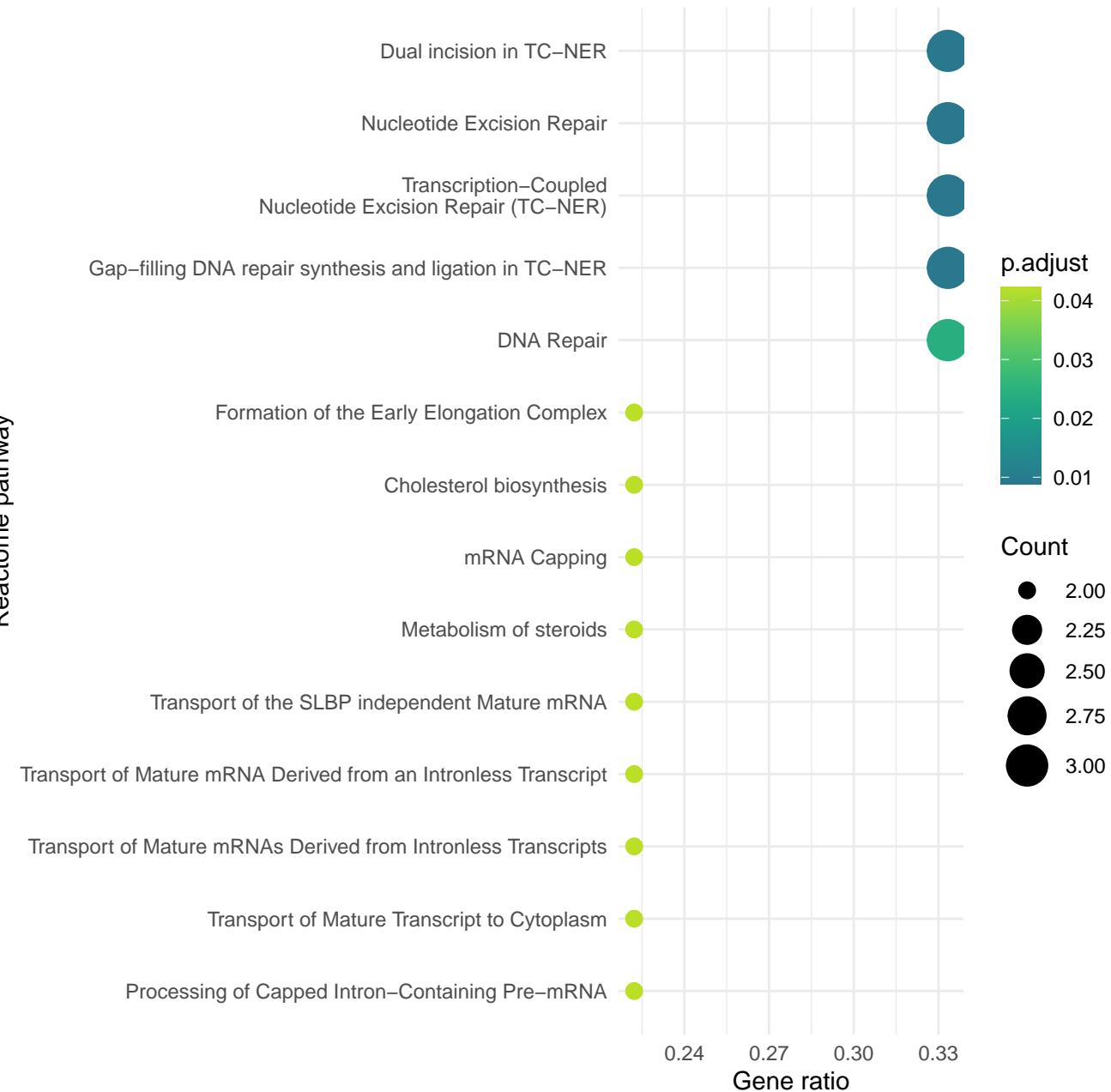
STO1-TAP Up-regulated GO MF upsetplot



STO1-TAP Up-regulated Reactome ba



STO1-TAP Up-regulated Reactome pathways



STO1-TAP Up-regulated Reactome cnetplot

Gap-filling DNA repair synthesis and ligation in TC-NER Nucleotide Excision Repair Transcription-Coupled Nucleotide Exc

Transcription–Coupled Nucleotide Excision Repair (TC–NER)

Gap-filling DNA repair synthesis and ligation in TC–NER

DNA Repair

850623

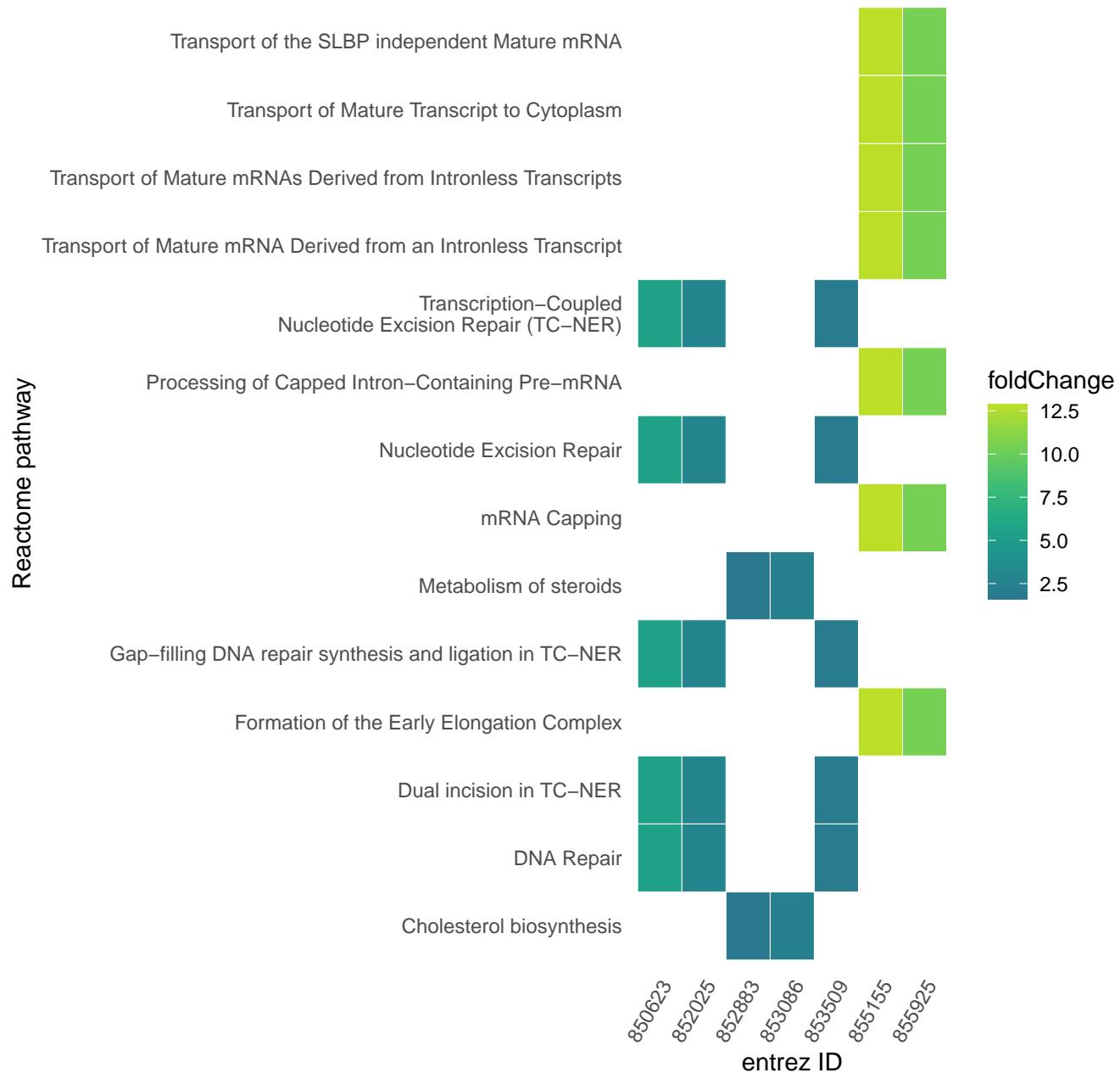
852025

853509

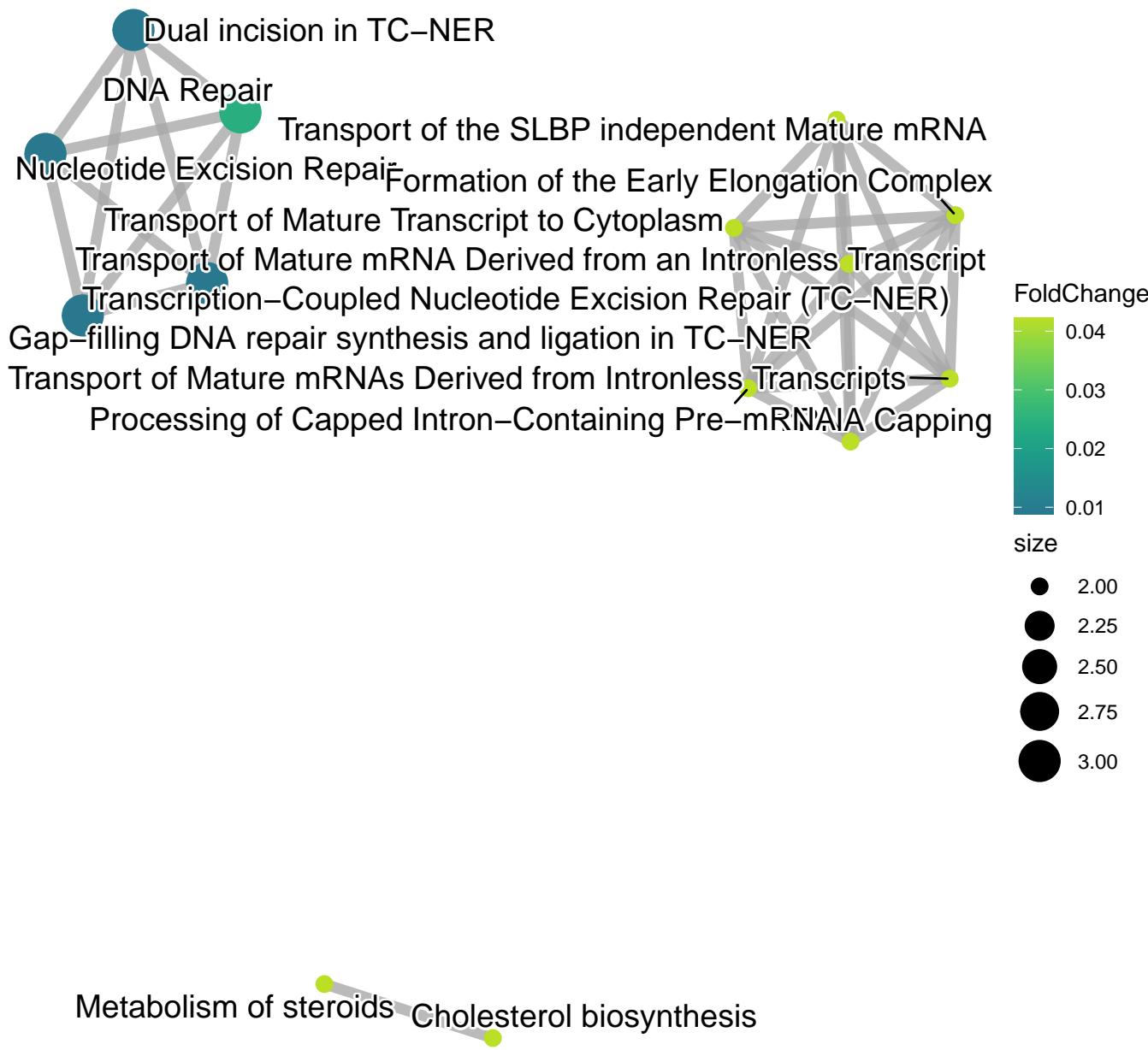
Nucleotide Excision Repair

Dual incision in TC–NER

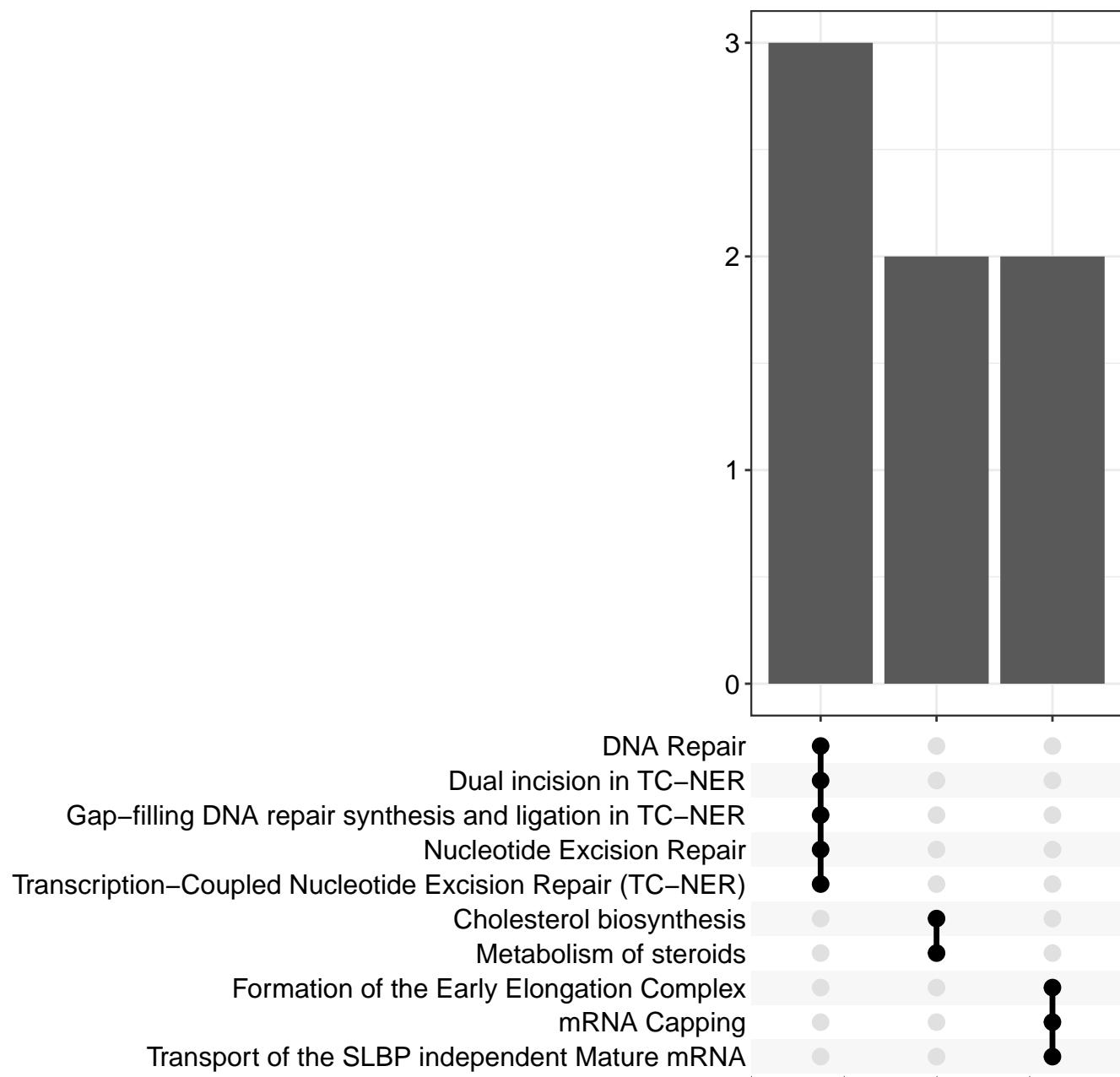
STO1-TAP Up-regulated Reactome he



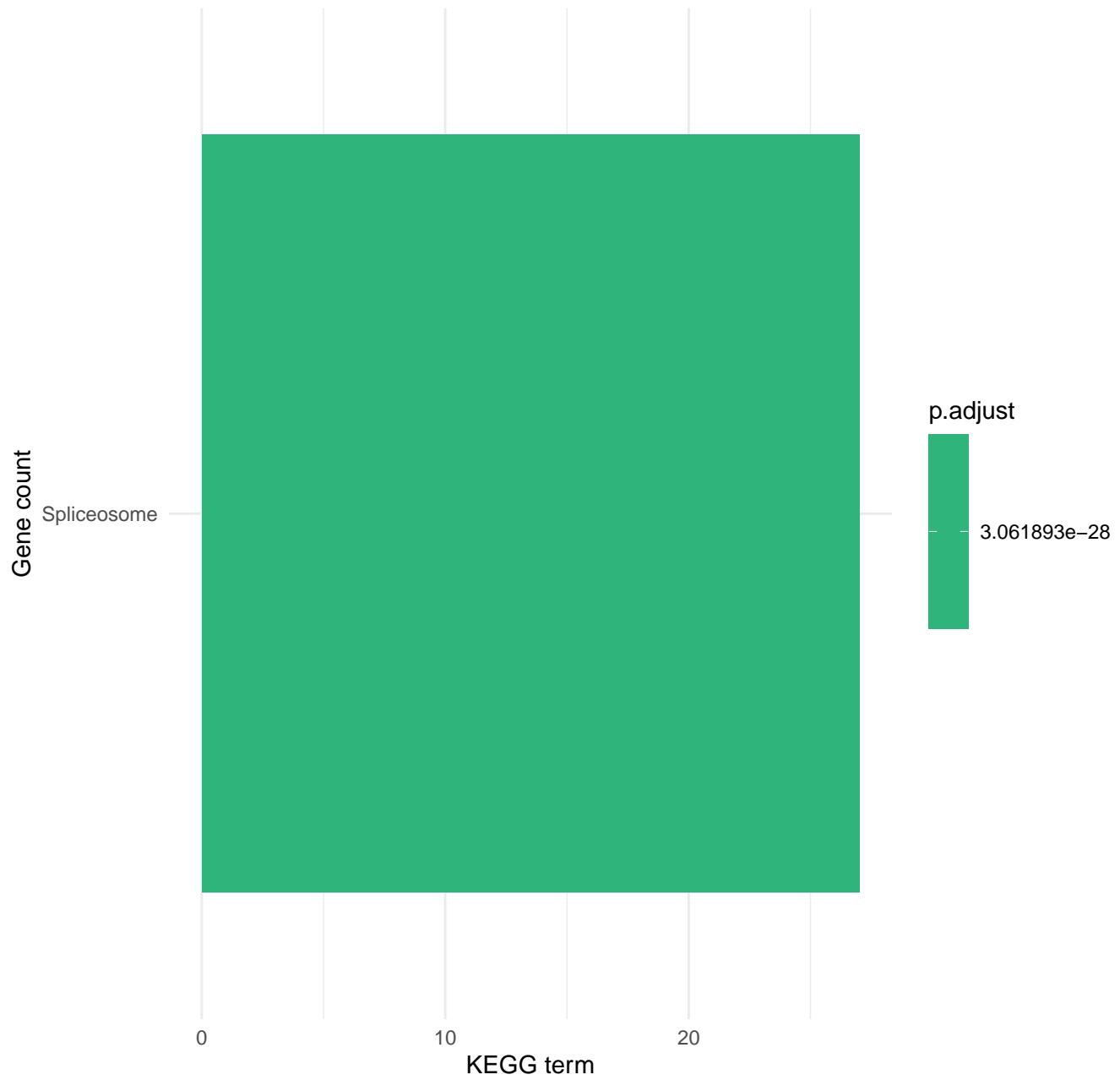
STO1-TAP Up-regulated Reactome emapplot



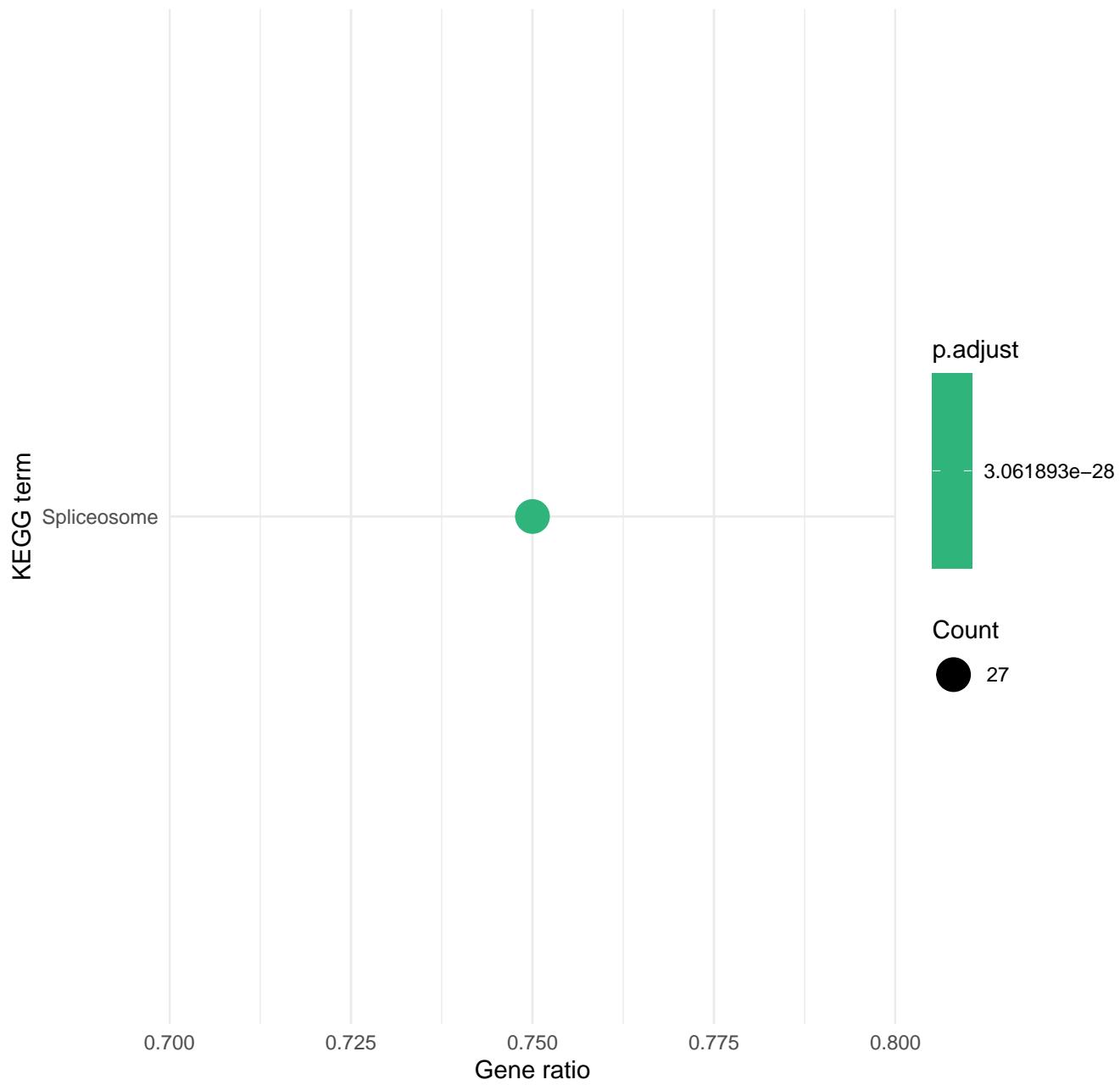
STO1-TAP Up-regulated Re



STO1-TAP Up-regulated KEGG barplot



STO1-TAP Up-regulated KEGG dotplot

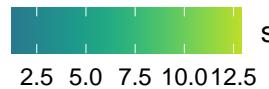


STO1-TAP Up-regulated KEGG dotplot

category

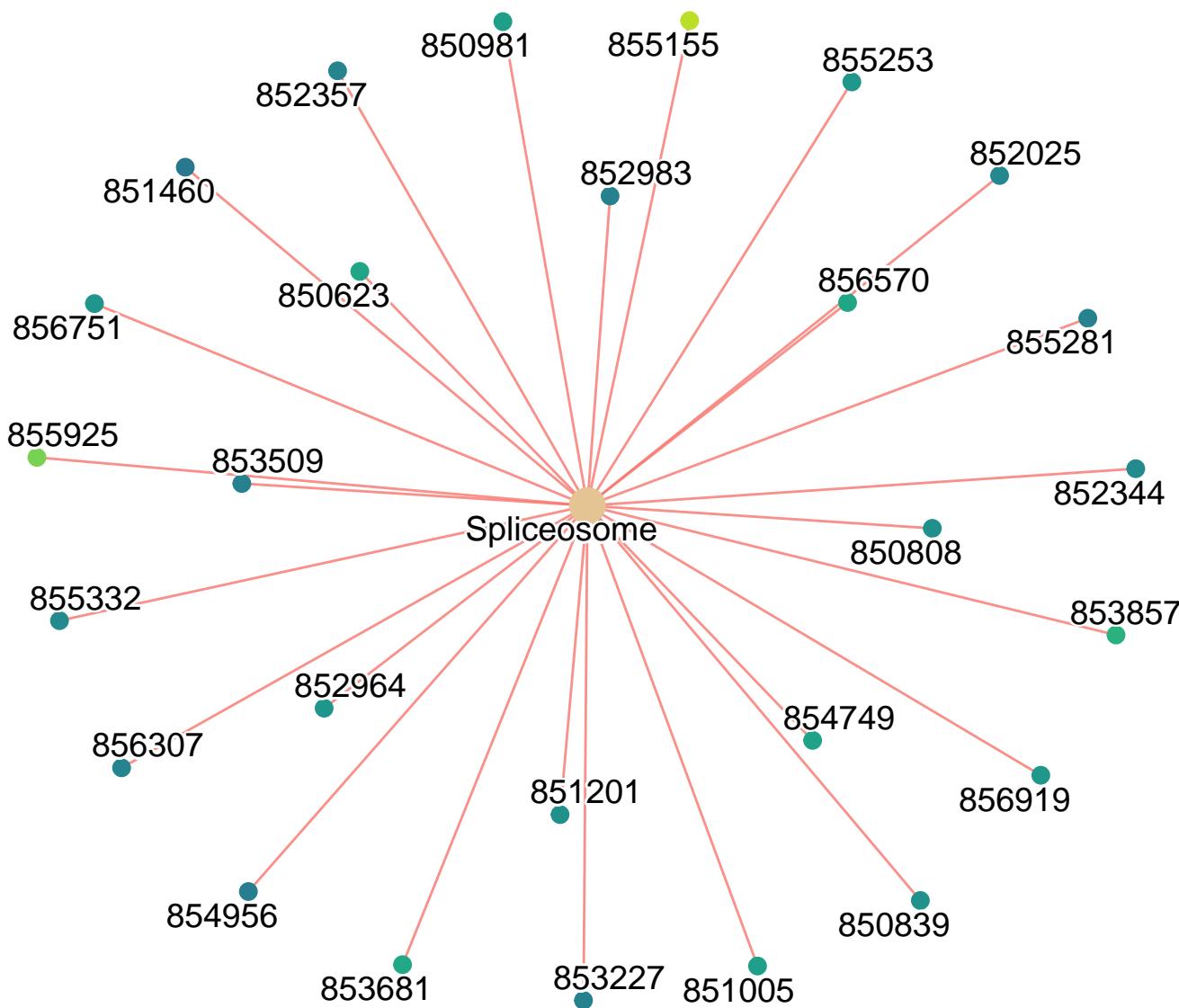
Spliceosome

FoldChange

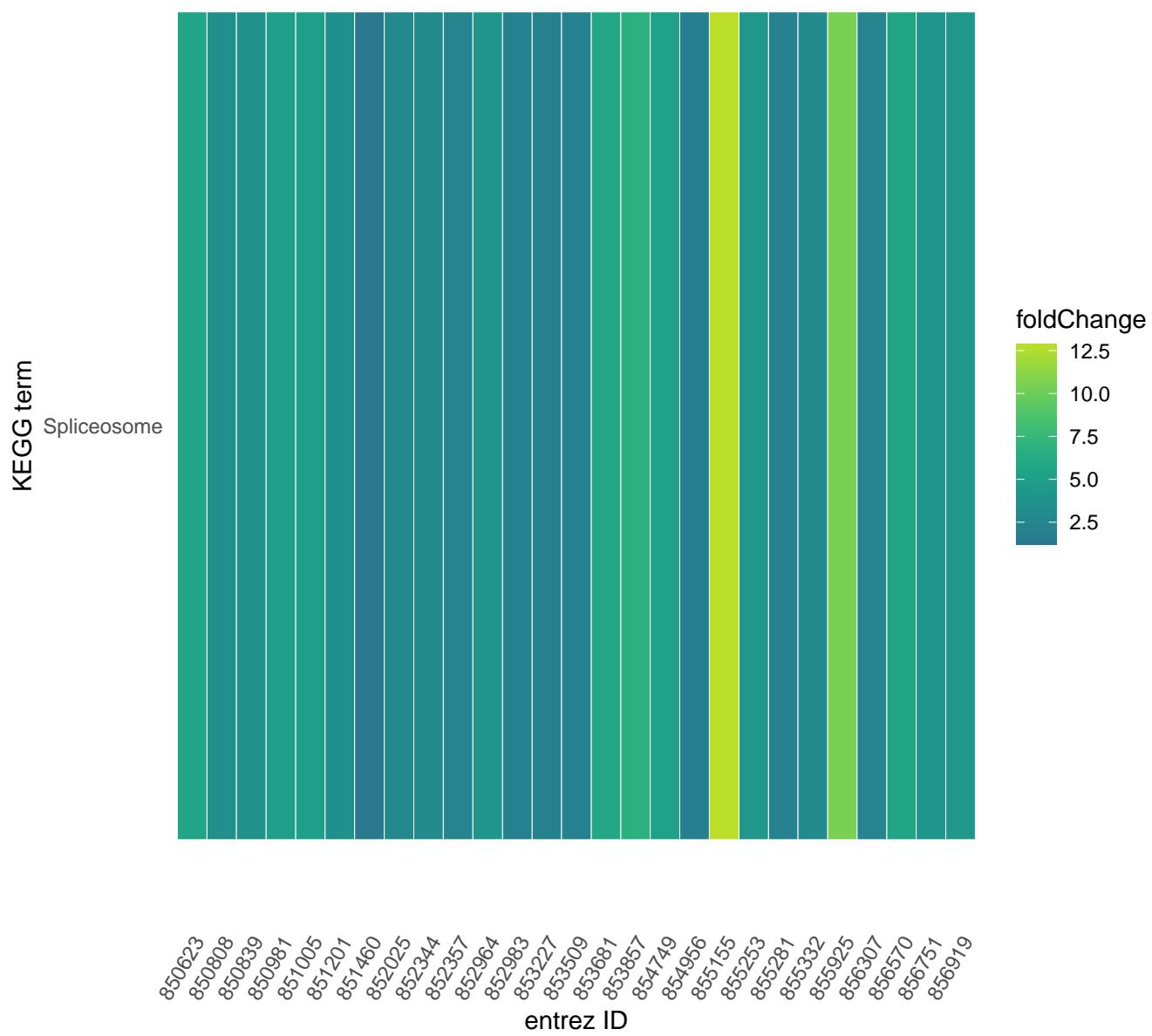


size

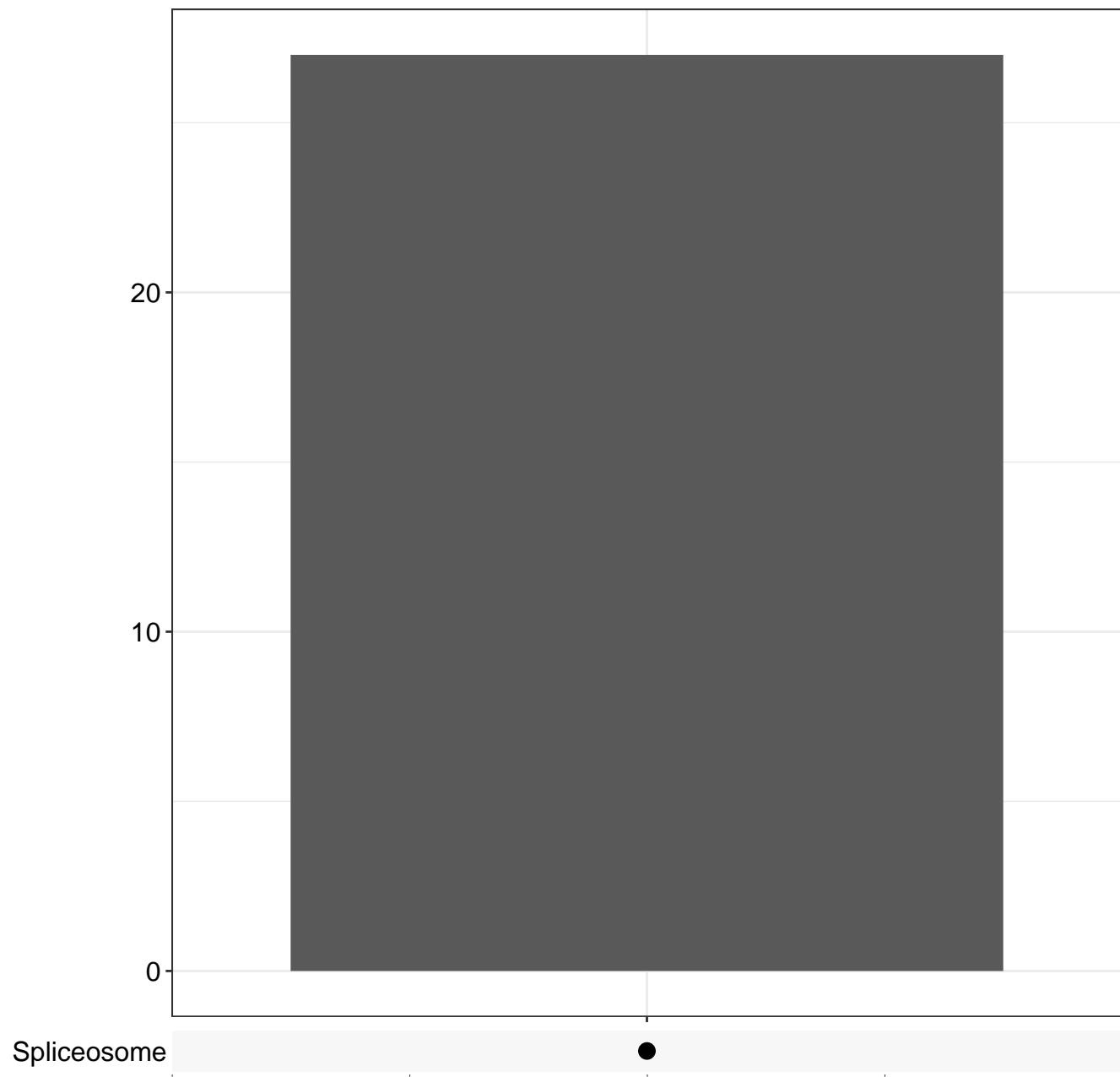
27



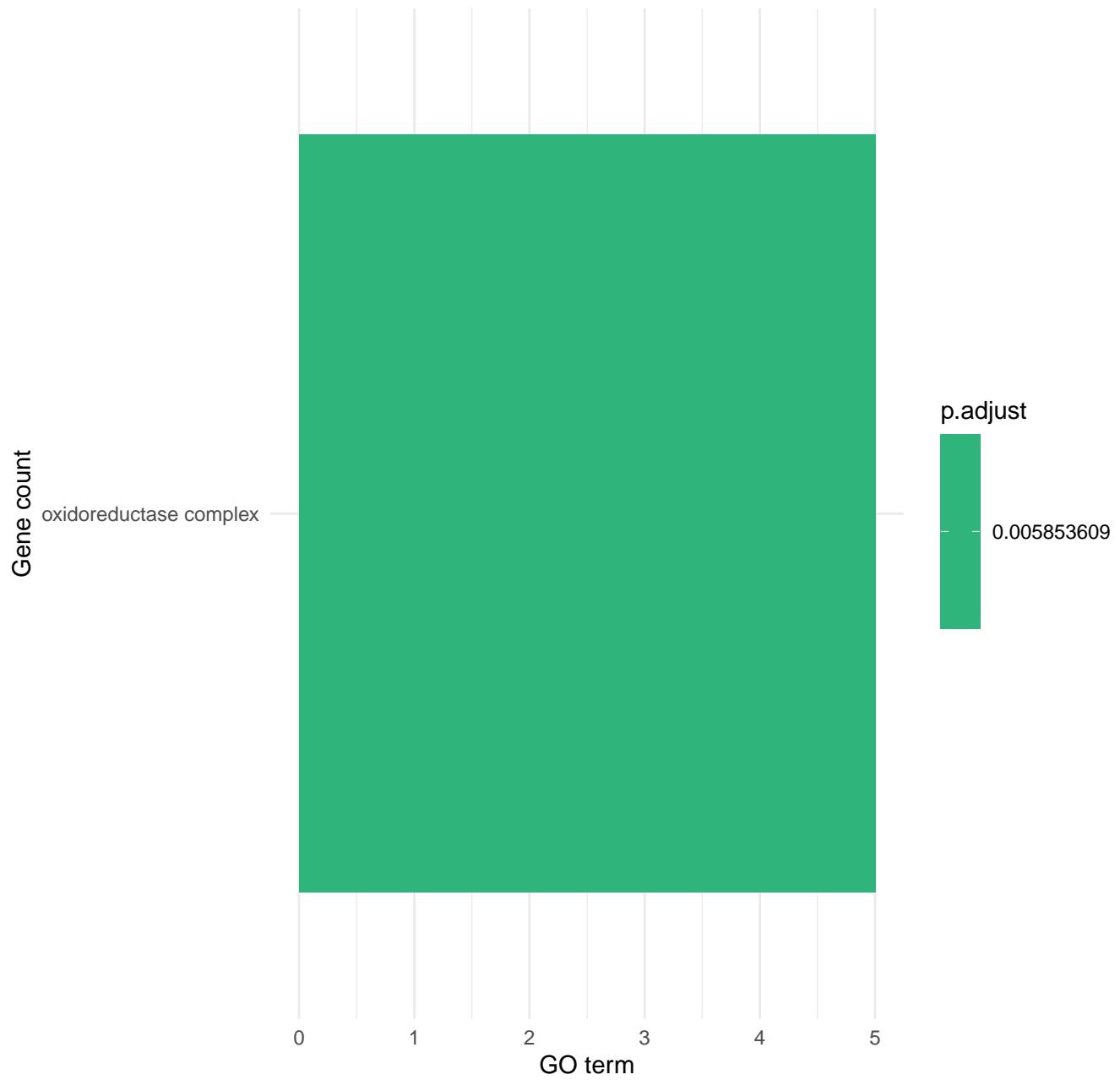
STO1-TAP Up-regulated KEGG heatplot



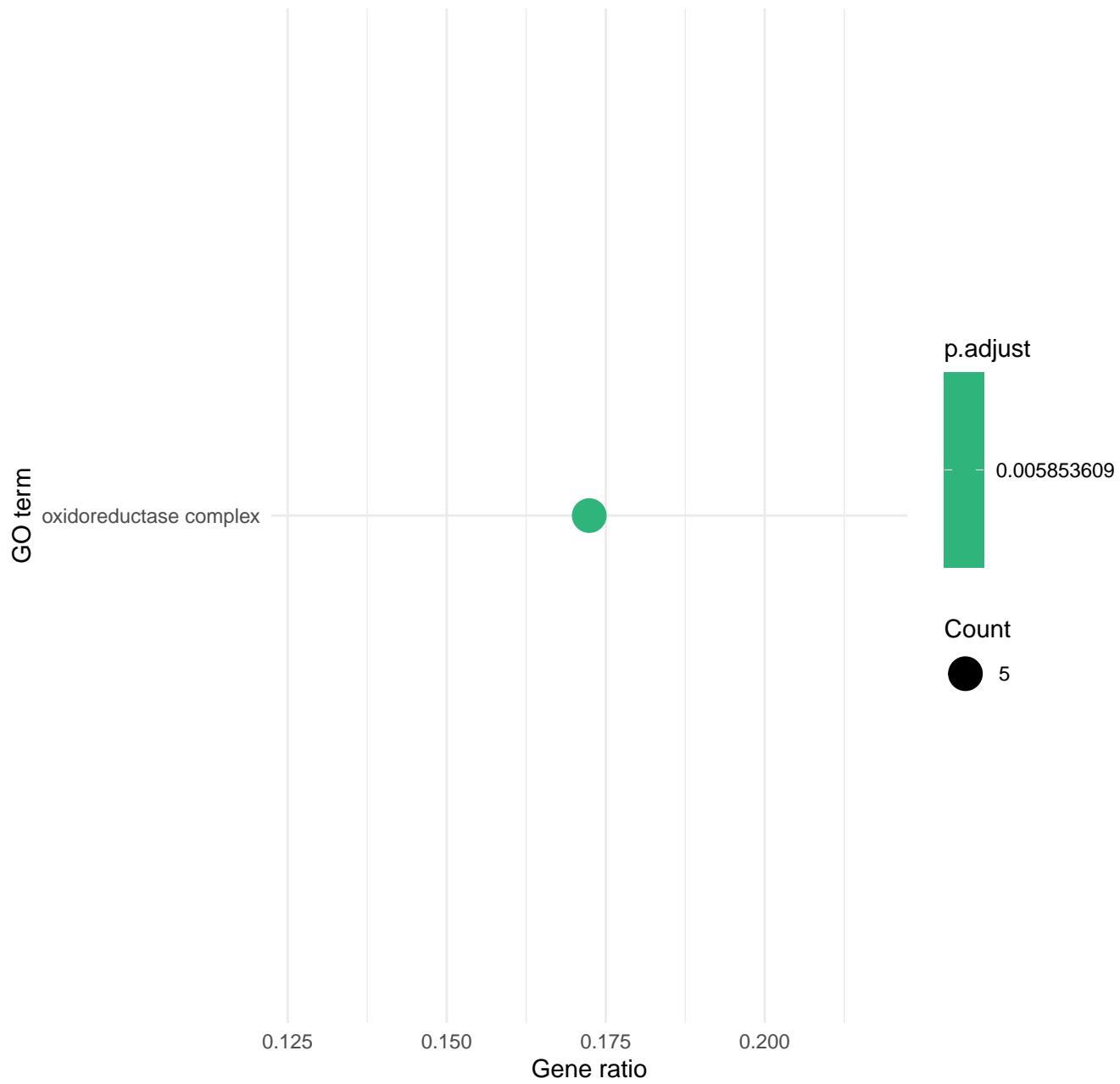
STO1–TAP Up-regulated KEGG upsetplot



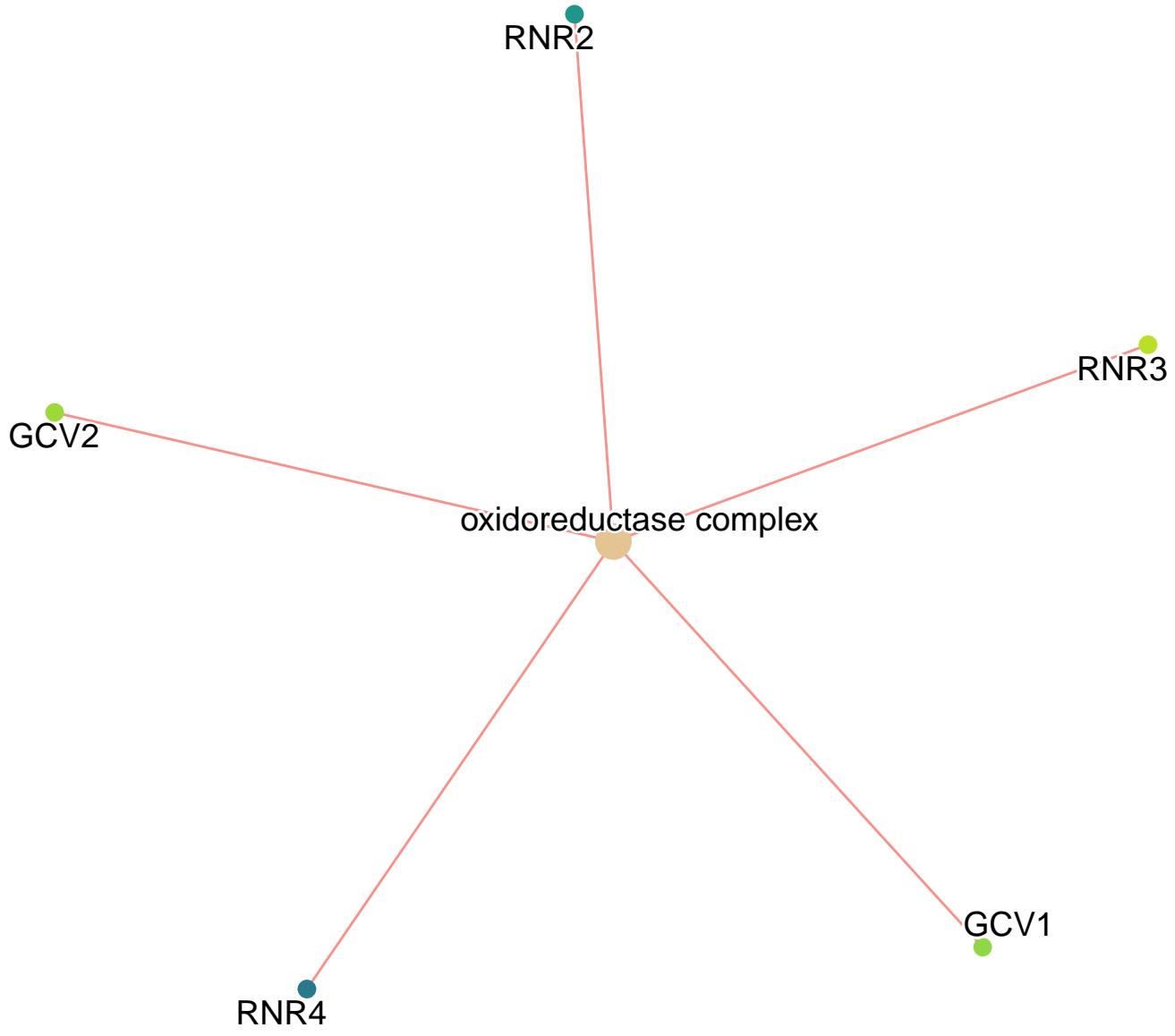
SGN1-TAP Up-regulated GO CC barplot



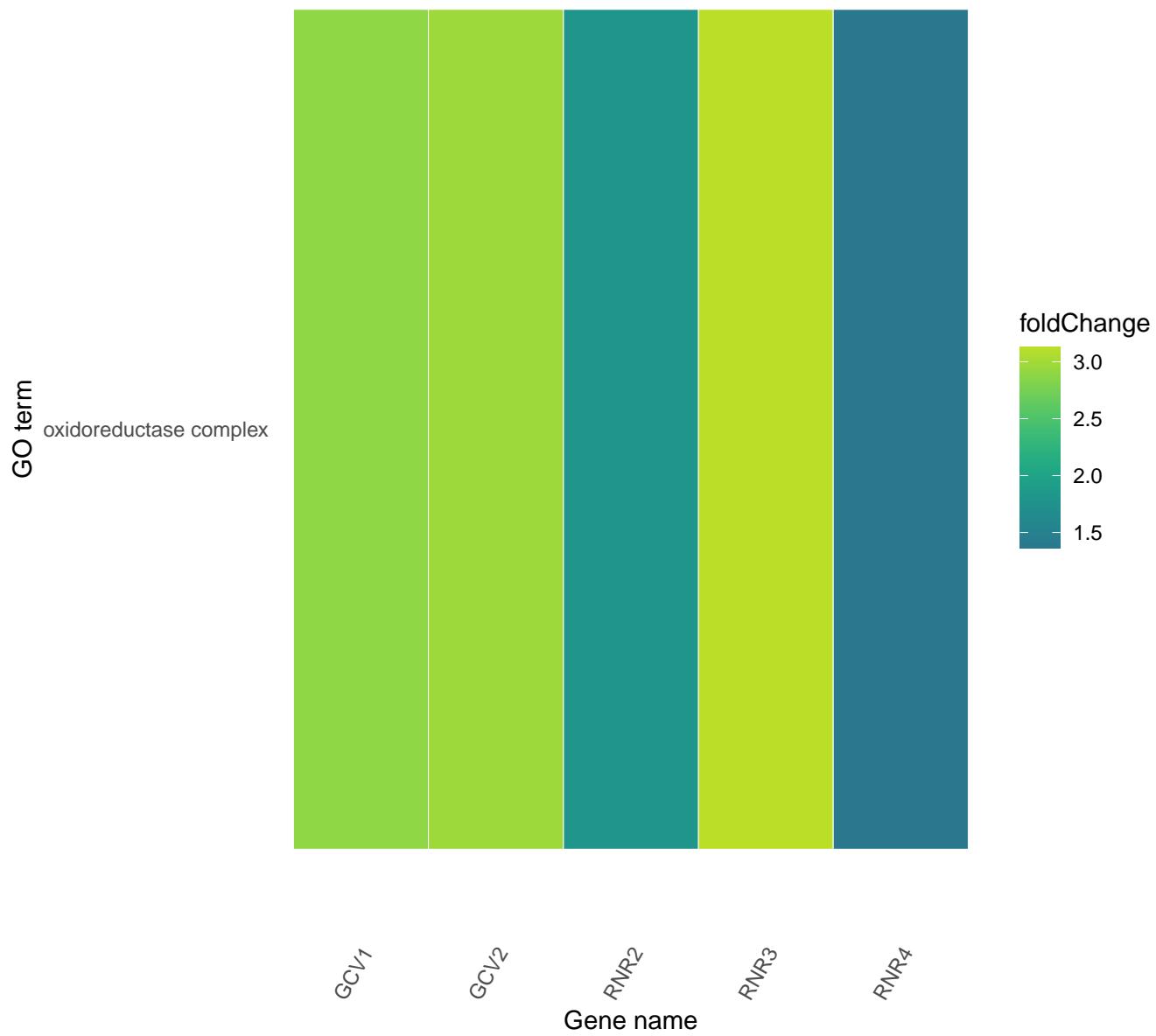
SGN1-TAP Up-regulated GO CC dotplot



SGN1-TAP Up-regulated GO CC cnetplot



SGN1-TAP Up-regulated GO CC heatplot



GO:0005575
cellular_component
NA
29 / 1087



GO:0032991
protein-containing c...
NA
10 / 583

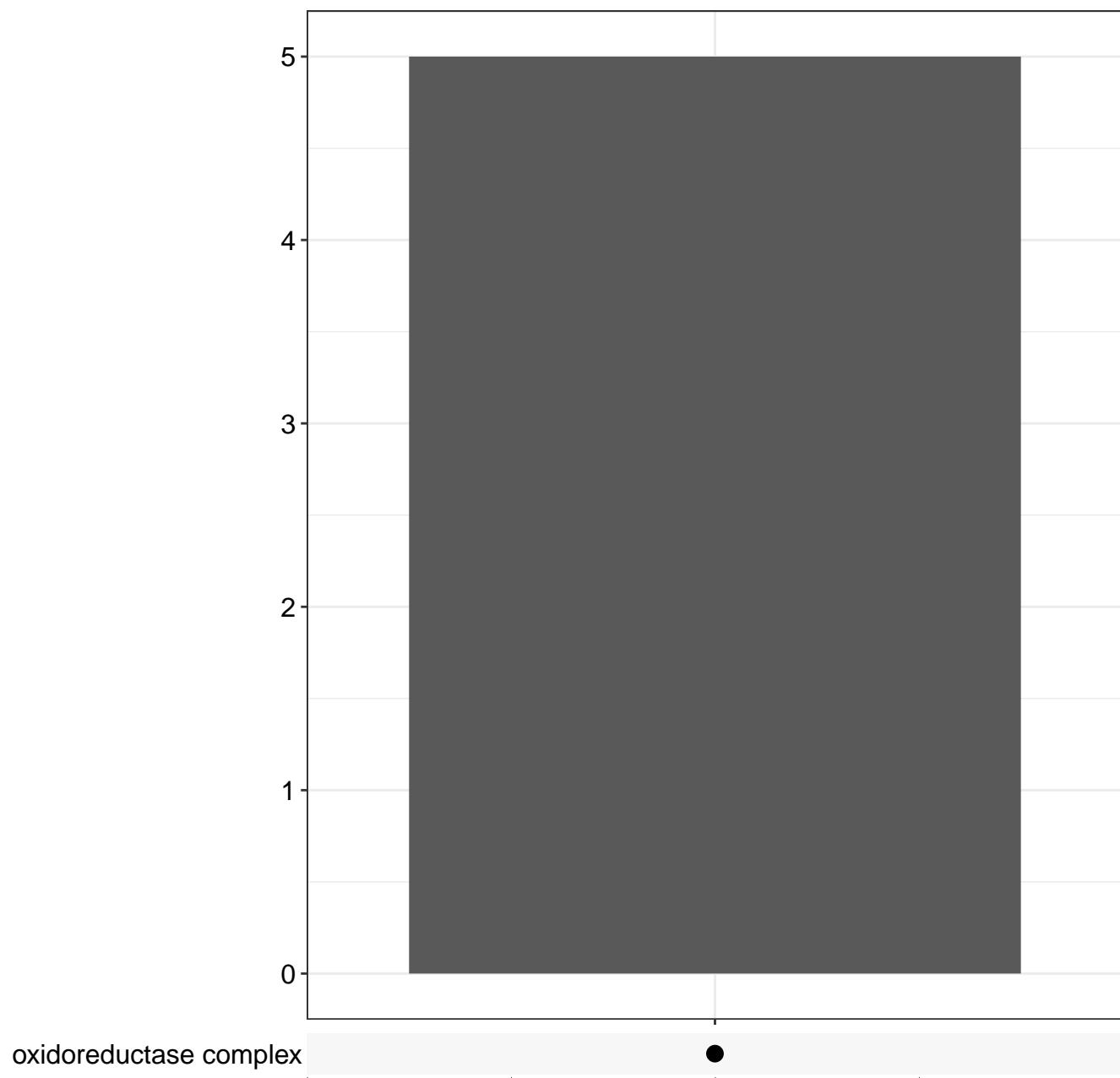


GO:1902494
catalytic complex
0.99984
6 / 148

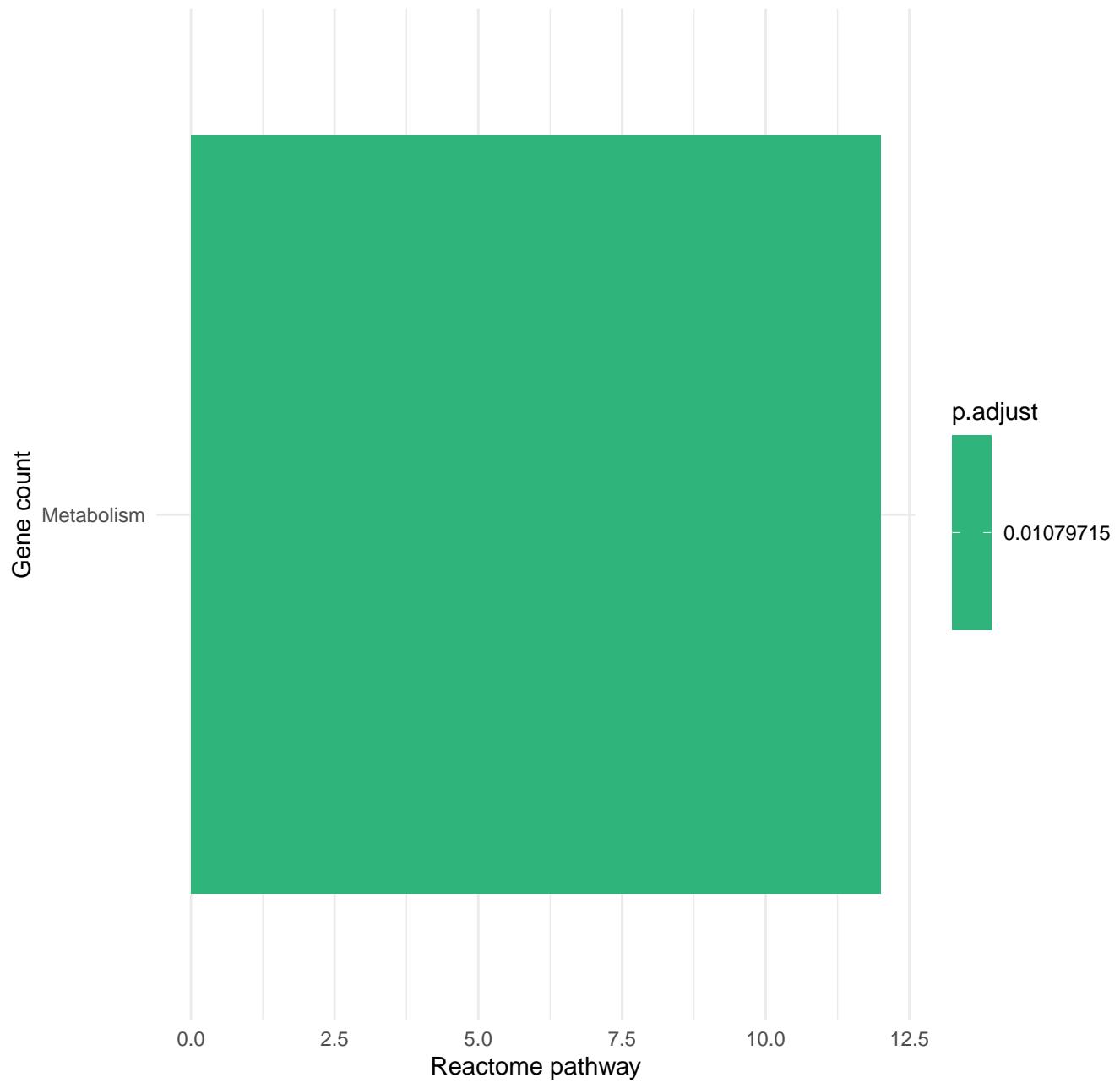


GO:1990204
oxidoreductase compl...
0.00585
5 / 19

SGN1-TAP Up-regulated GO CC upsetplot



SGN1-TAP Up-regulated Reactome barplot



SGN1-TAP Up-regulated Reactome dotplot

Reactome pathway

Metabolism

0.675

0.700

0.725

0.750

Gene ratio

Count

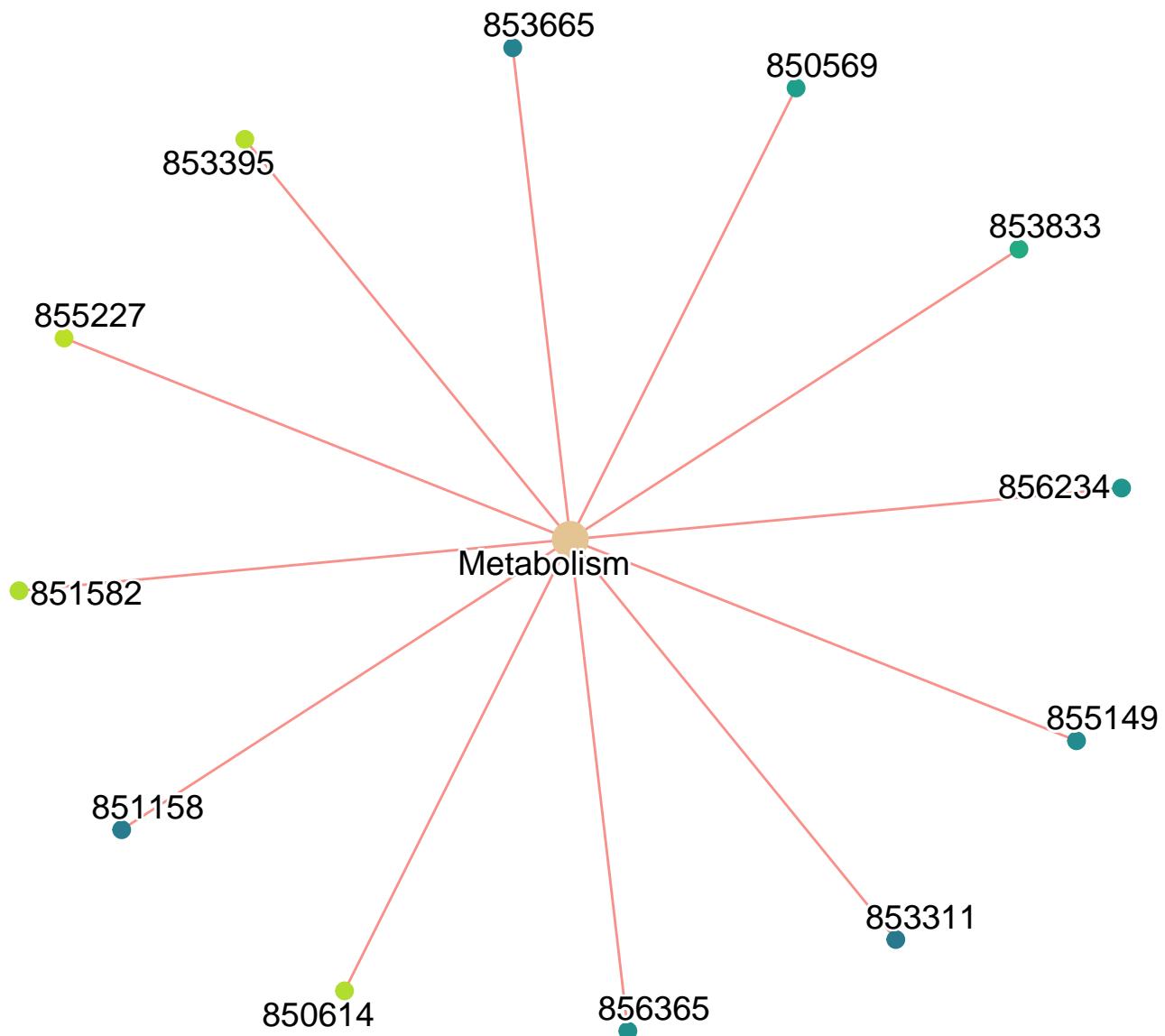
12

p.adjust

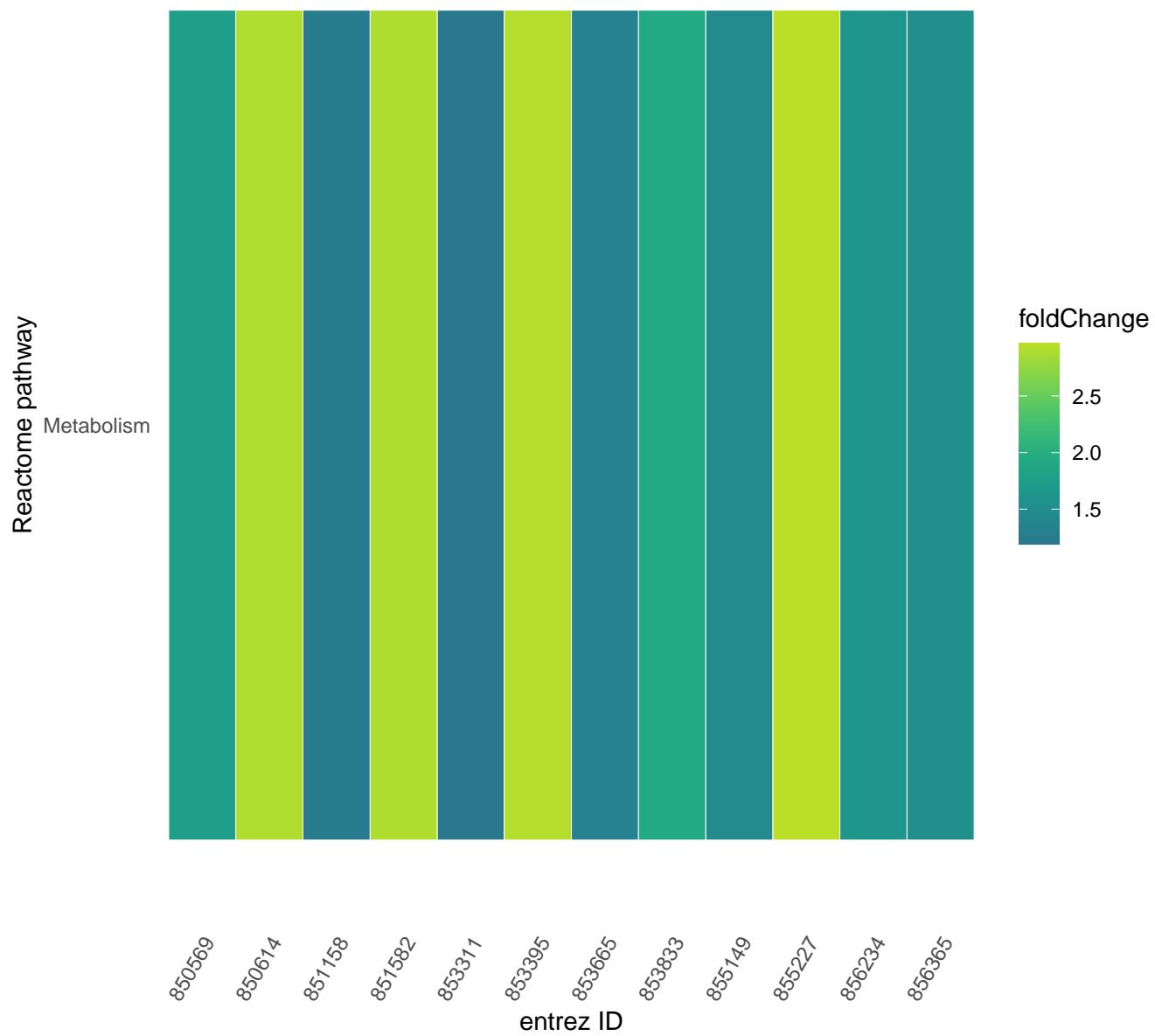
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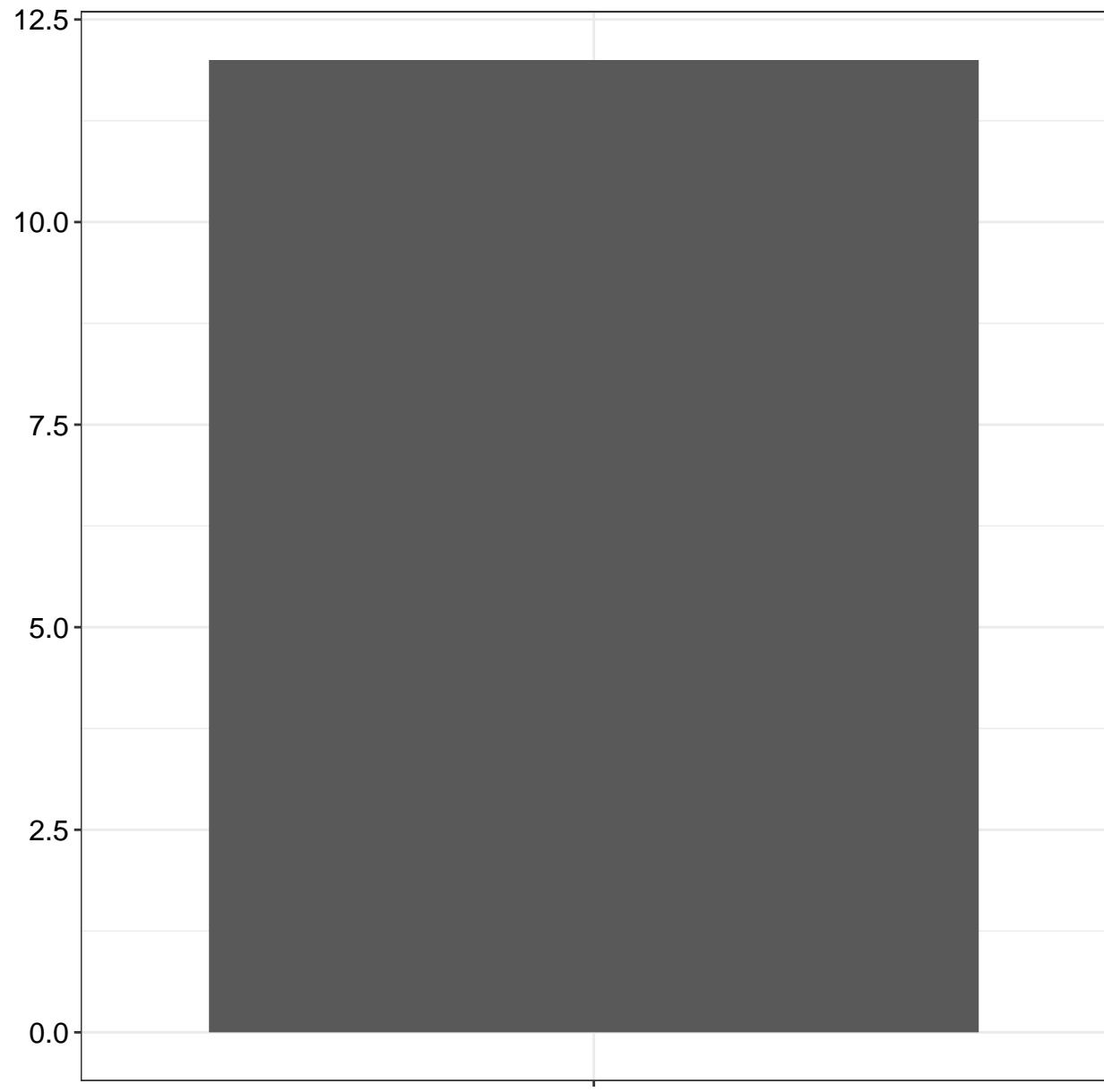
SGN1-TAP Up-regulated Reactome cnetplot



SGN1-TAP Up-regulated Reactome heatplot

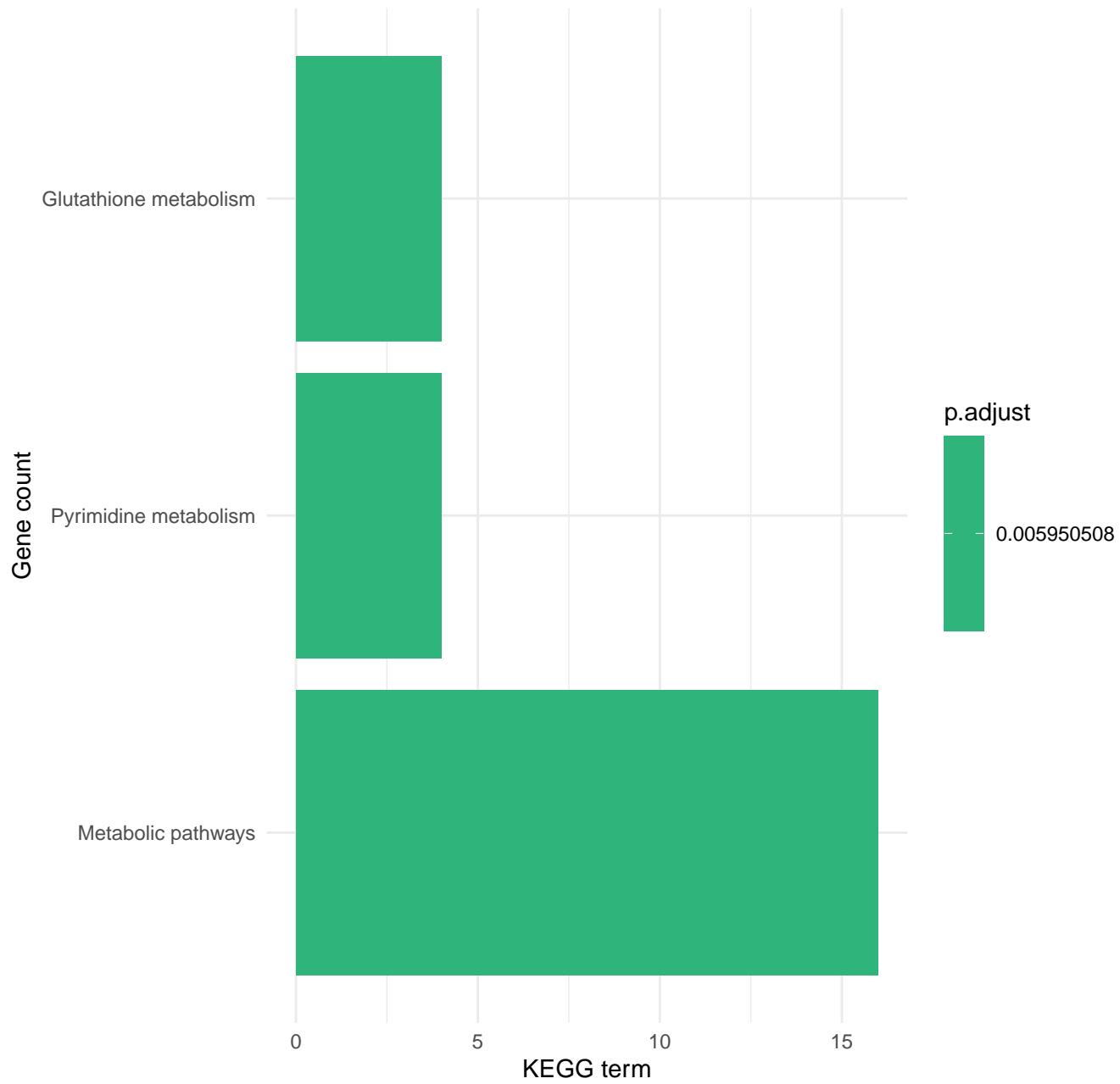


SGN1-TAP Up-regulated Reactome upsetplot

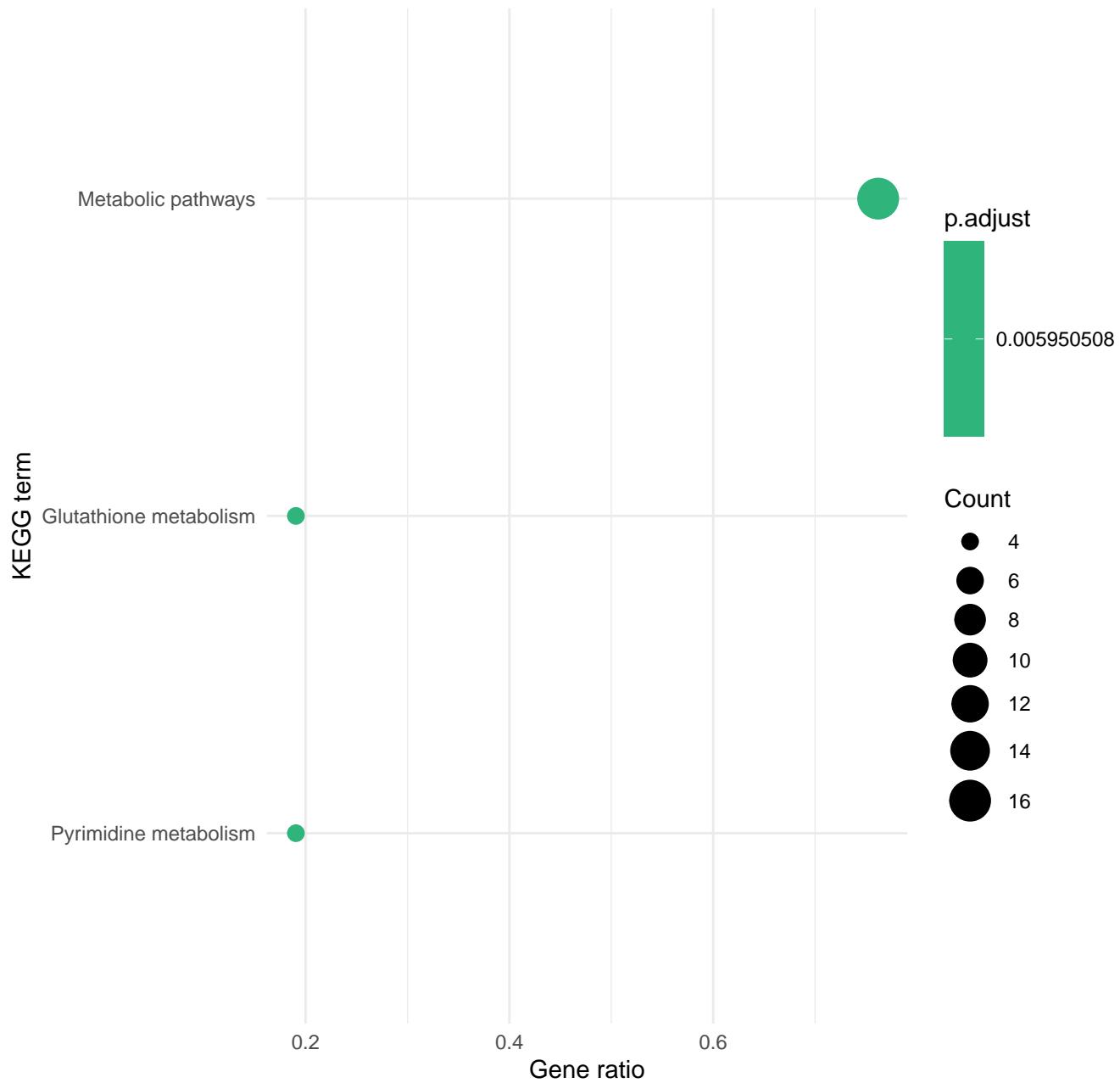


Metabolism

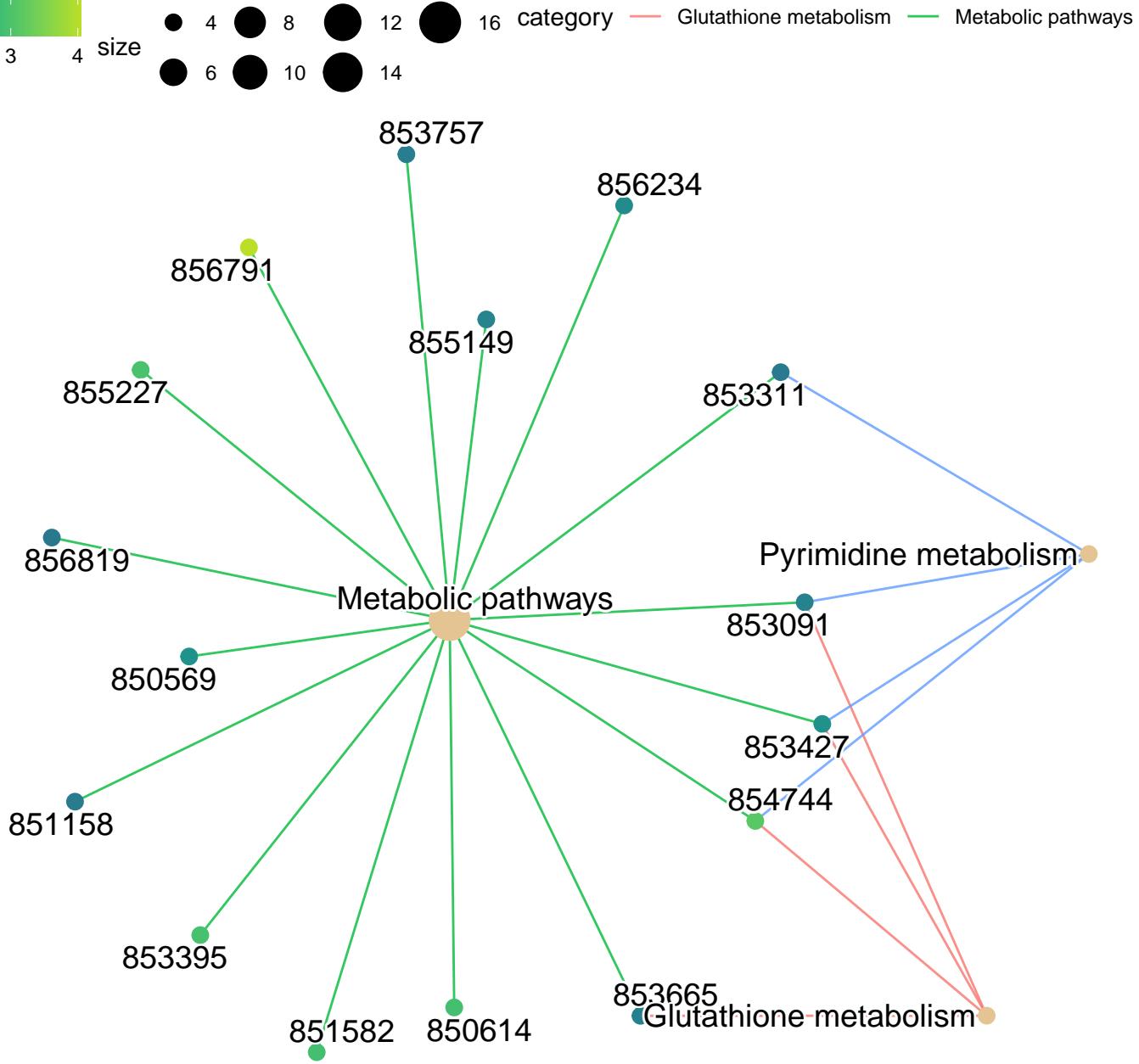
SGN1-TAP Up-regulated KEGG barplot



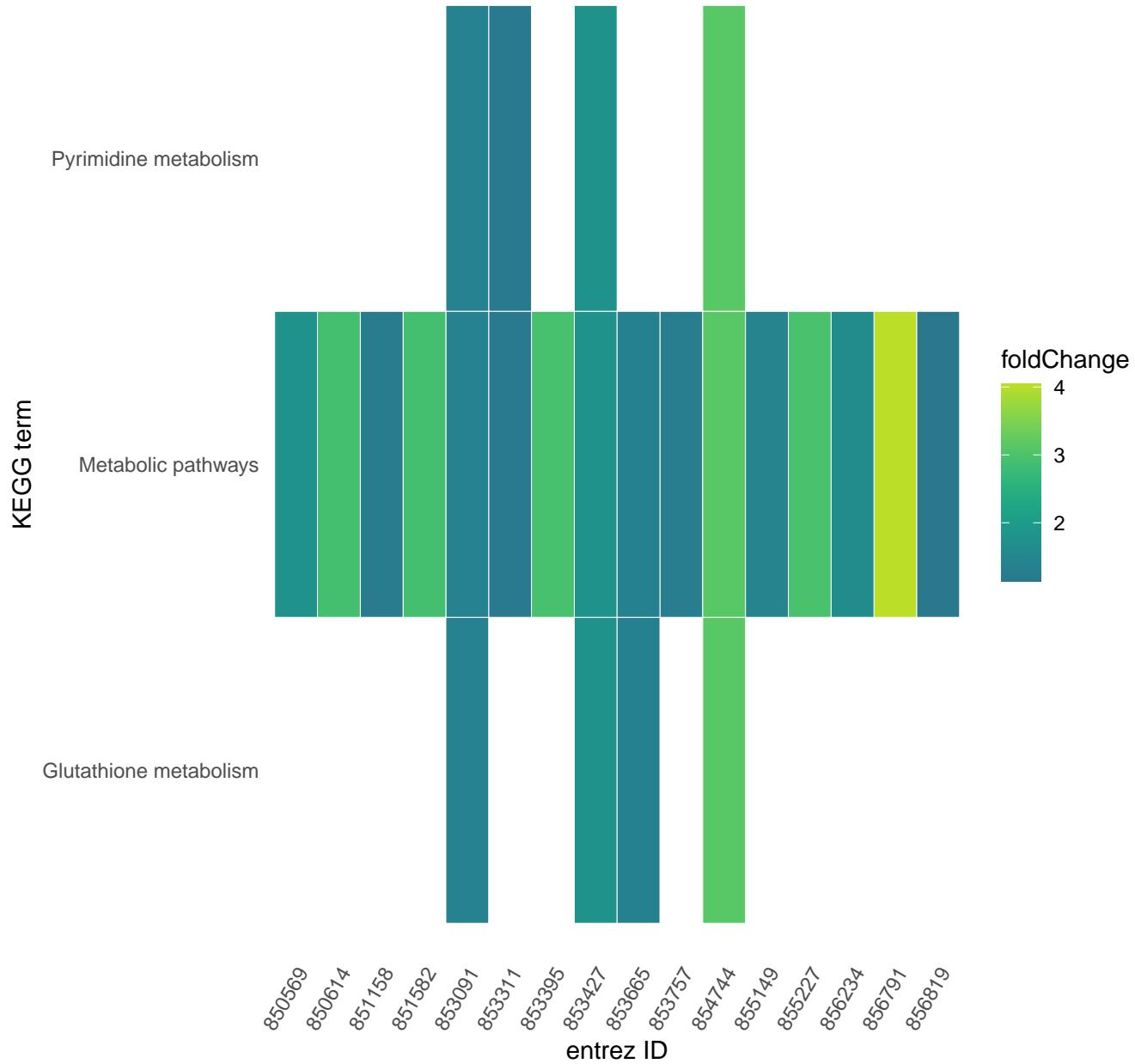
SGN1-TAP Up-regulated KEGG dotplot



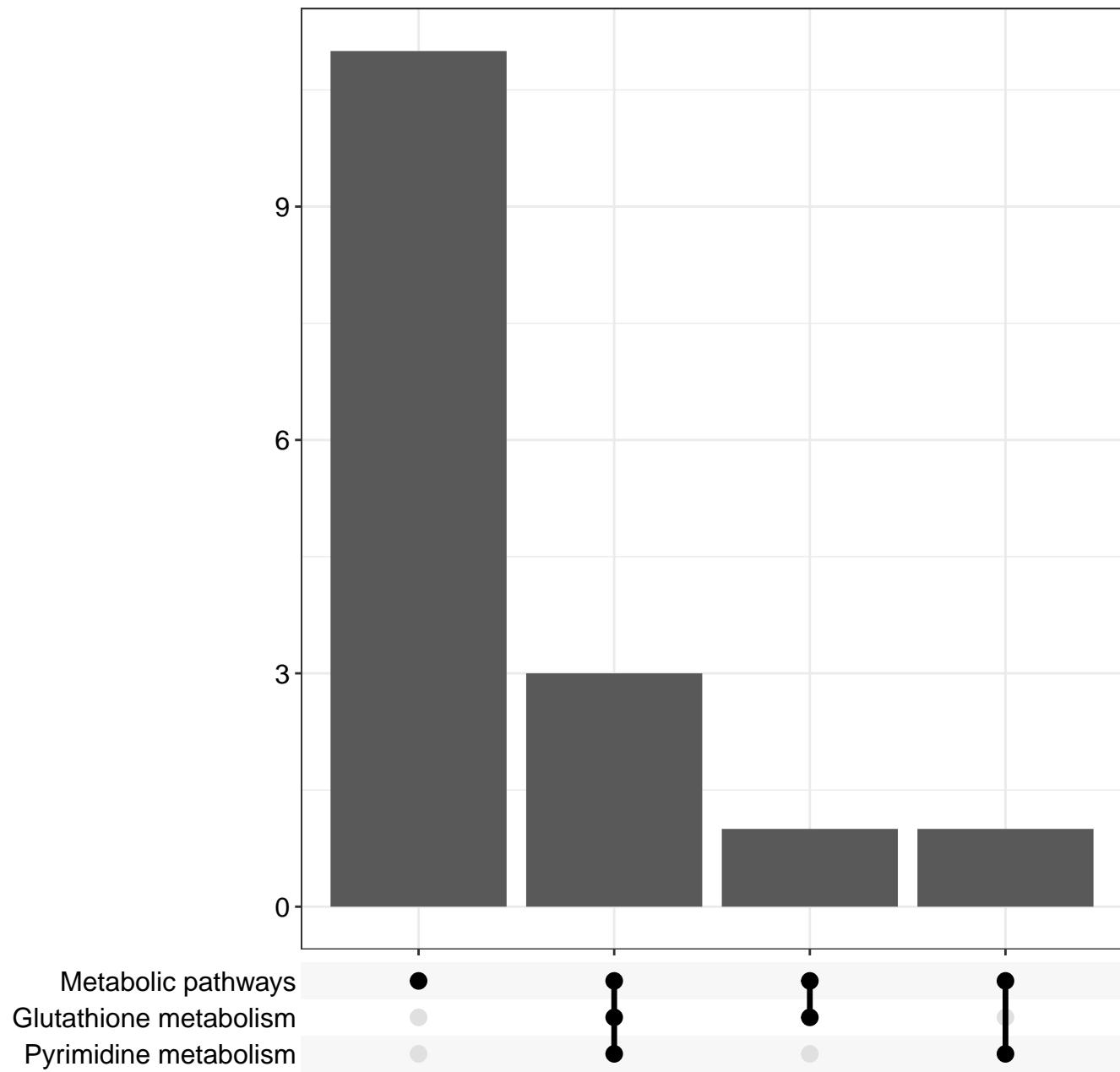
SGN1-TAP Up-regulated KEGG dotplot



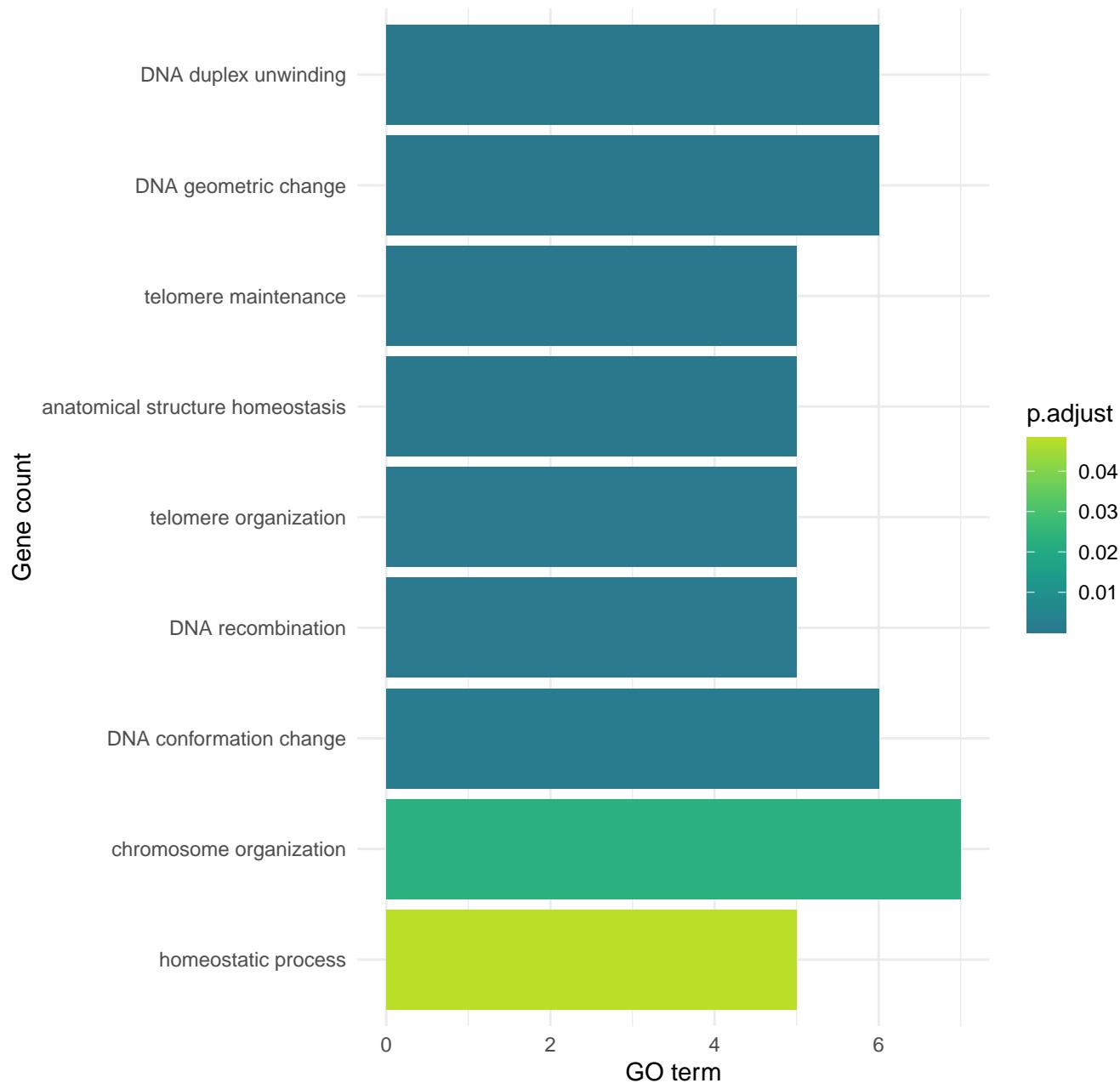
SGN1-TAP Up-regulated KEGG heatplot



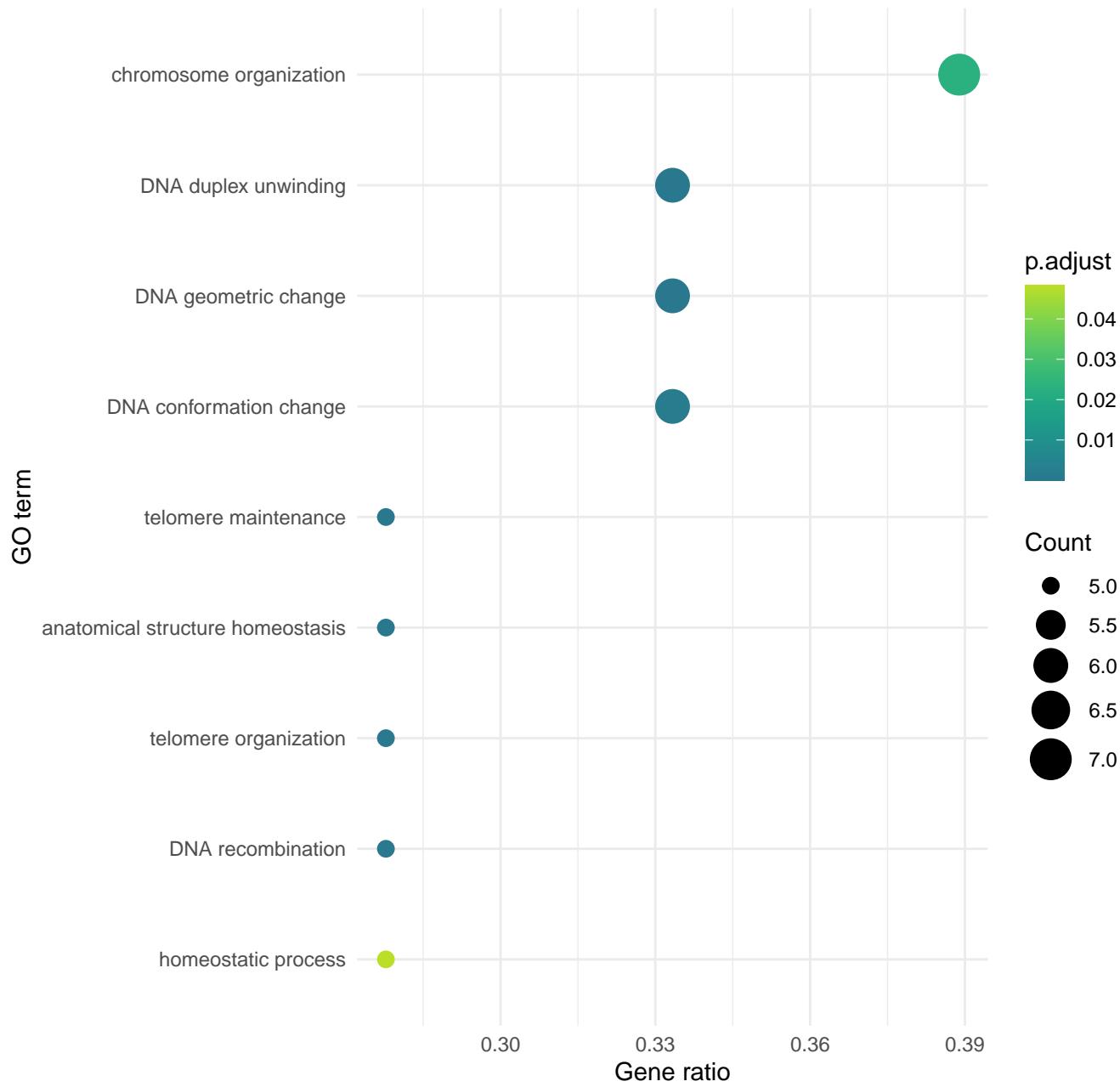
SGN1-TAP Up-regulated KEGG upsetplot



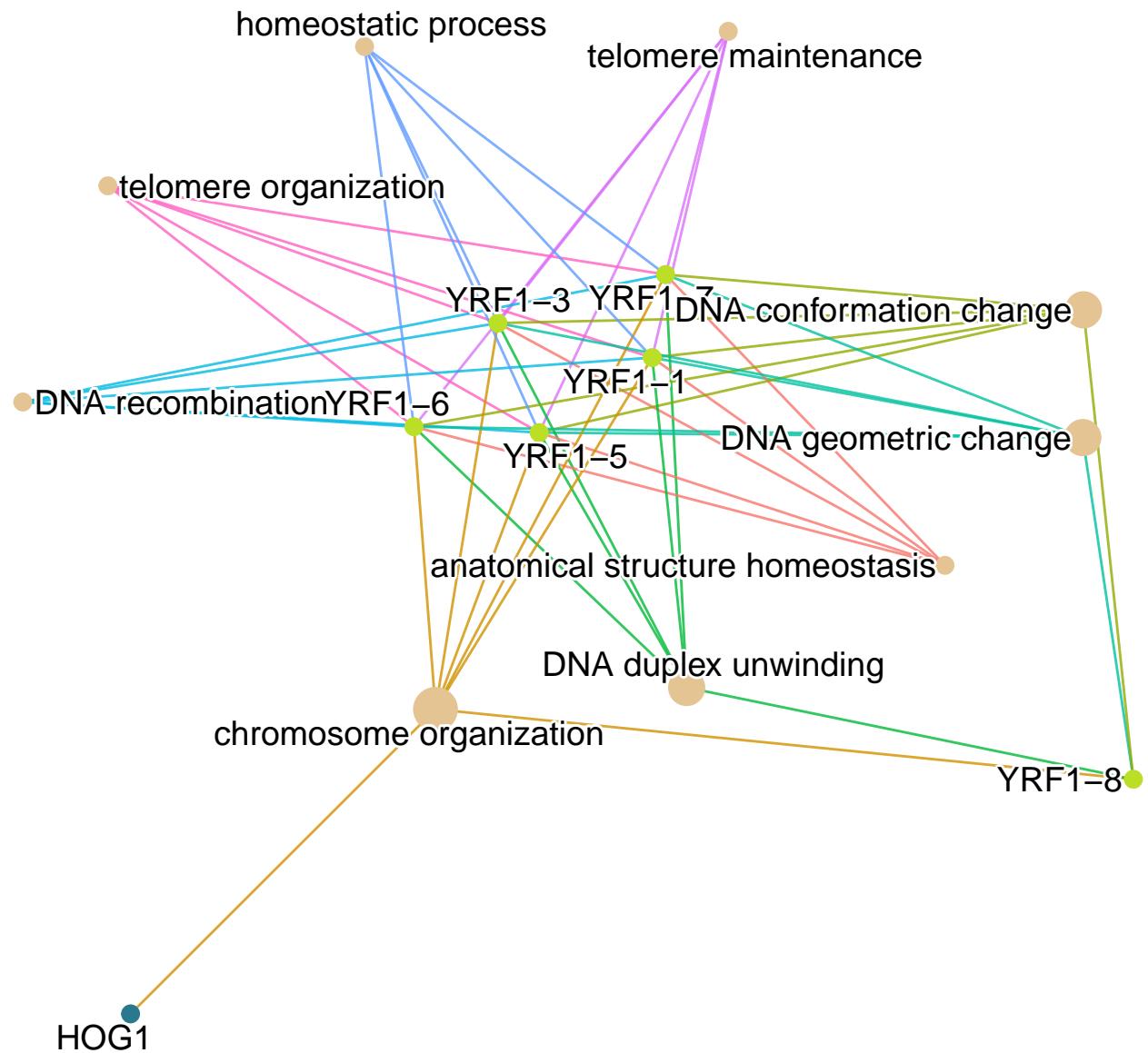
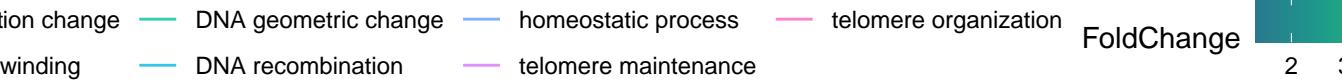
MIP6-TAP Up-regulated GO BP barplot



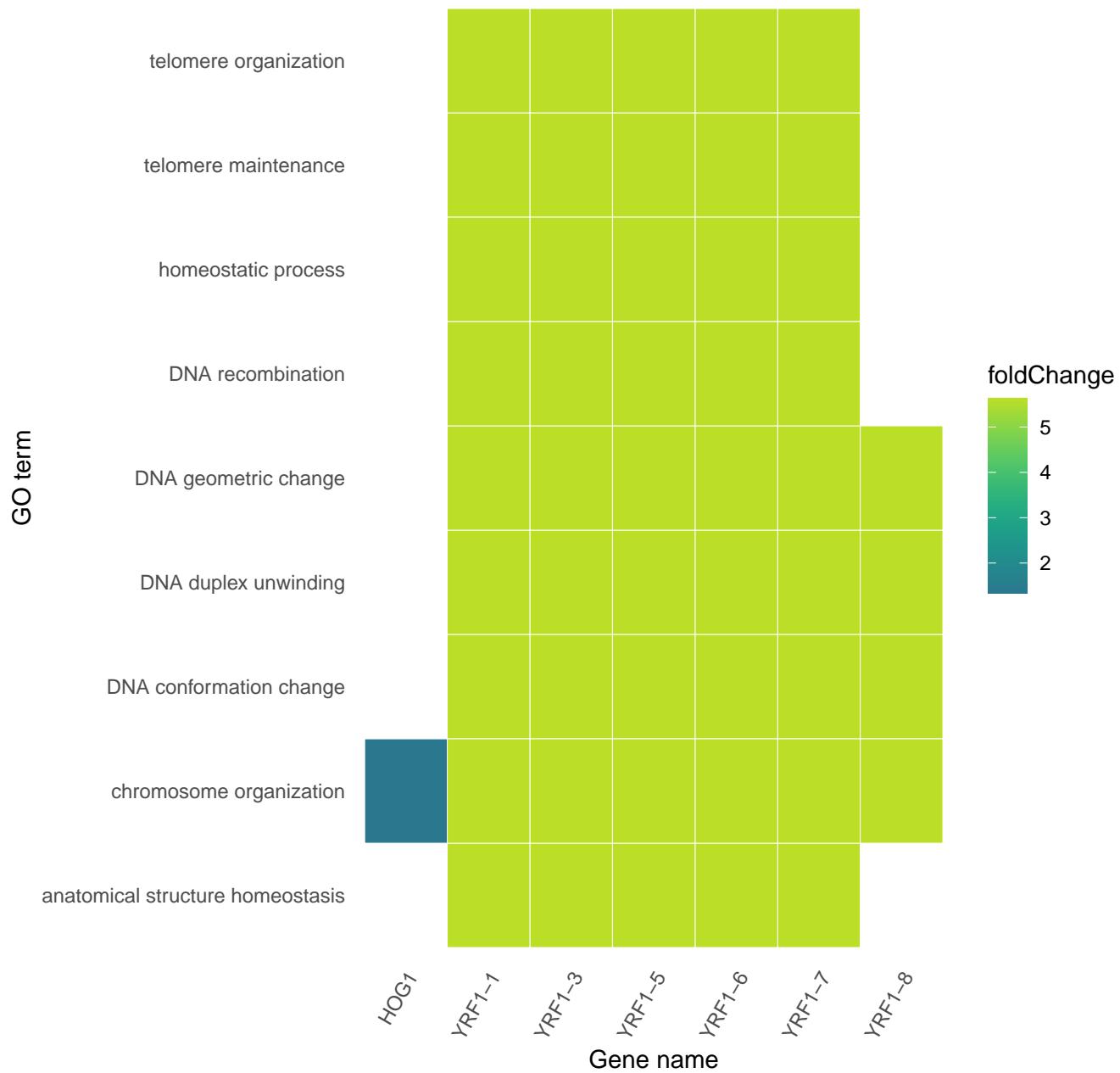
MIP6-TAP Up-regulated GO BP dotplot



MIP6-TAP Up-regulated GO BP cnetplot



MIP6-TAP Up-regulated GO BP heatplot



MIP6-TAP Up-regulated GO BP emapplot

chromosome organization

DNA conformation change

telomere organization

DNA geometric change

homeostatic process

anatomical structure homeostasis

DNA duplex unwinding

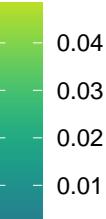
telomere maintenance

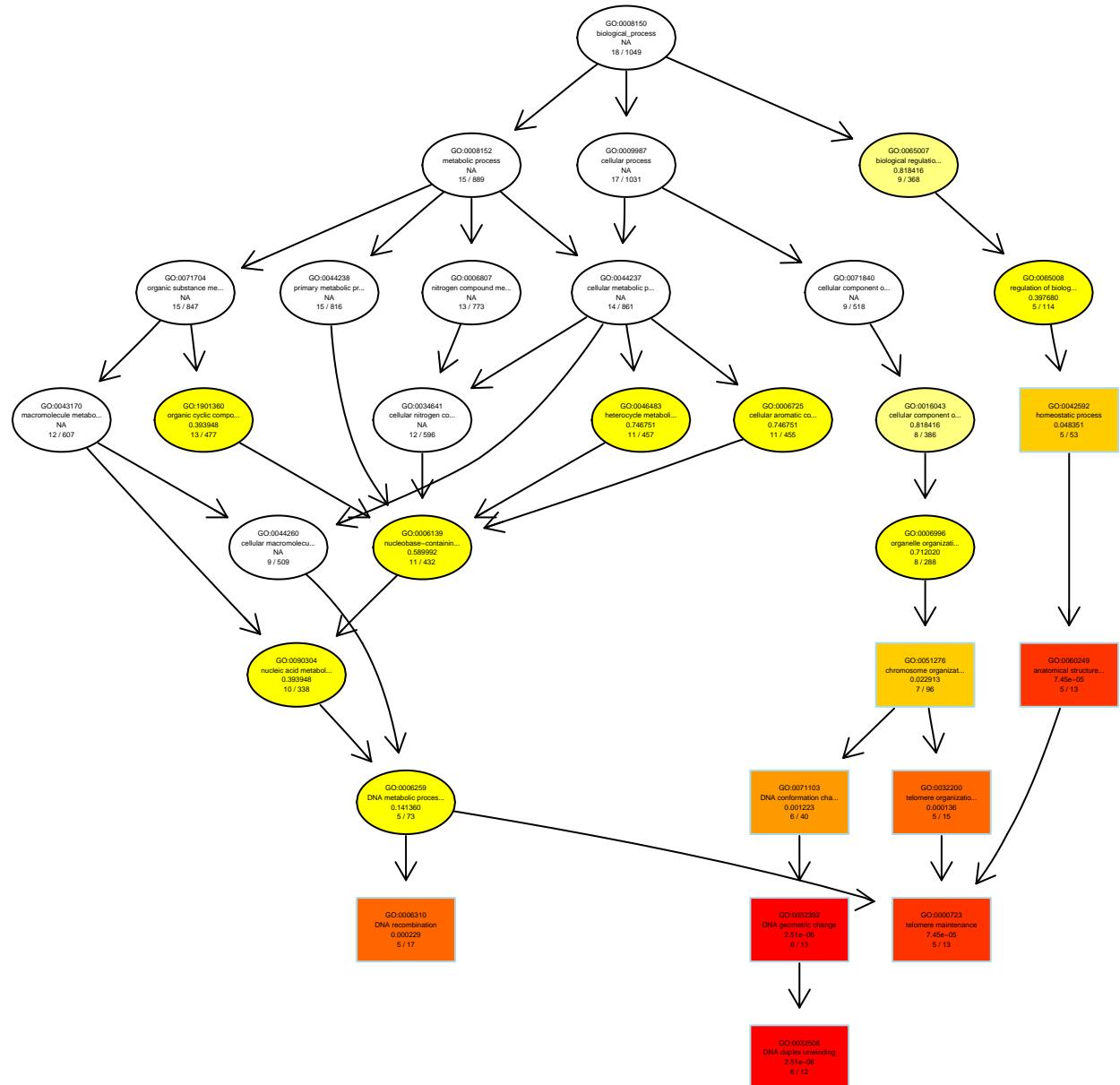
DNA recombination

size

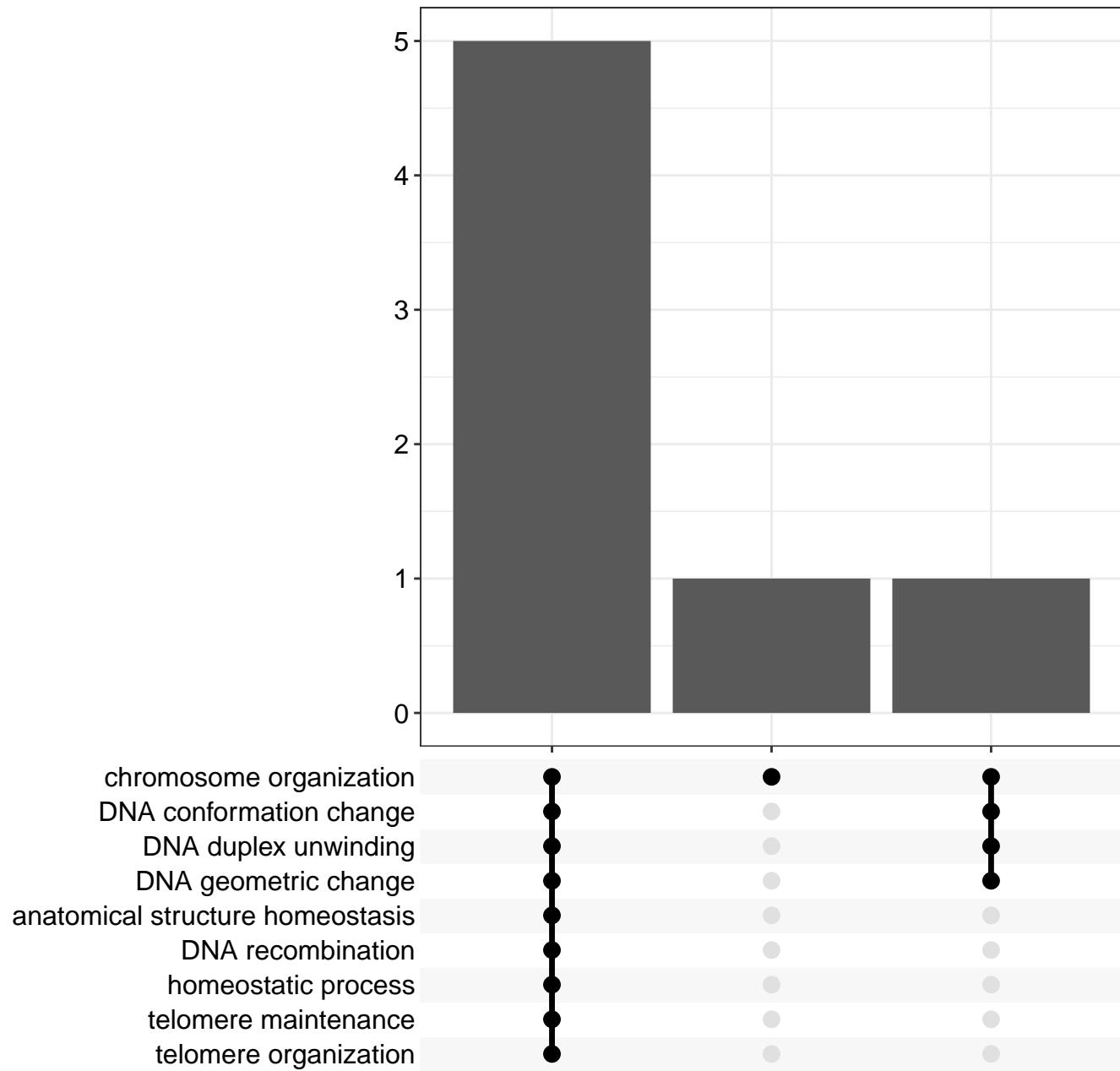
- 5.0
- 5.5
- 6.0
- 6.5
- 7.0

FoldChange

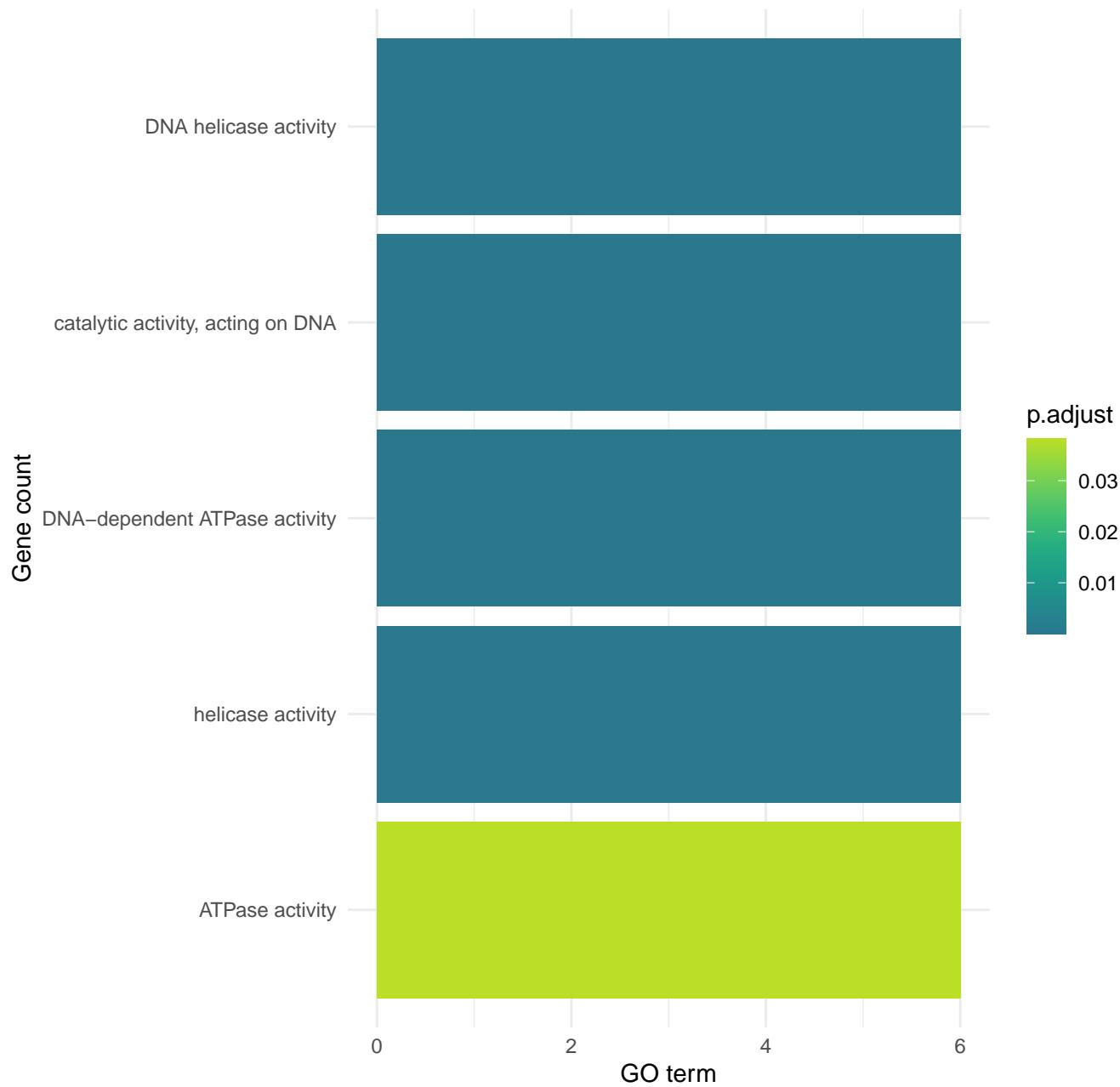




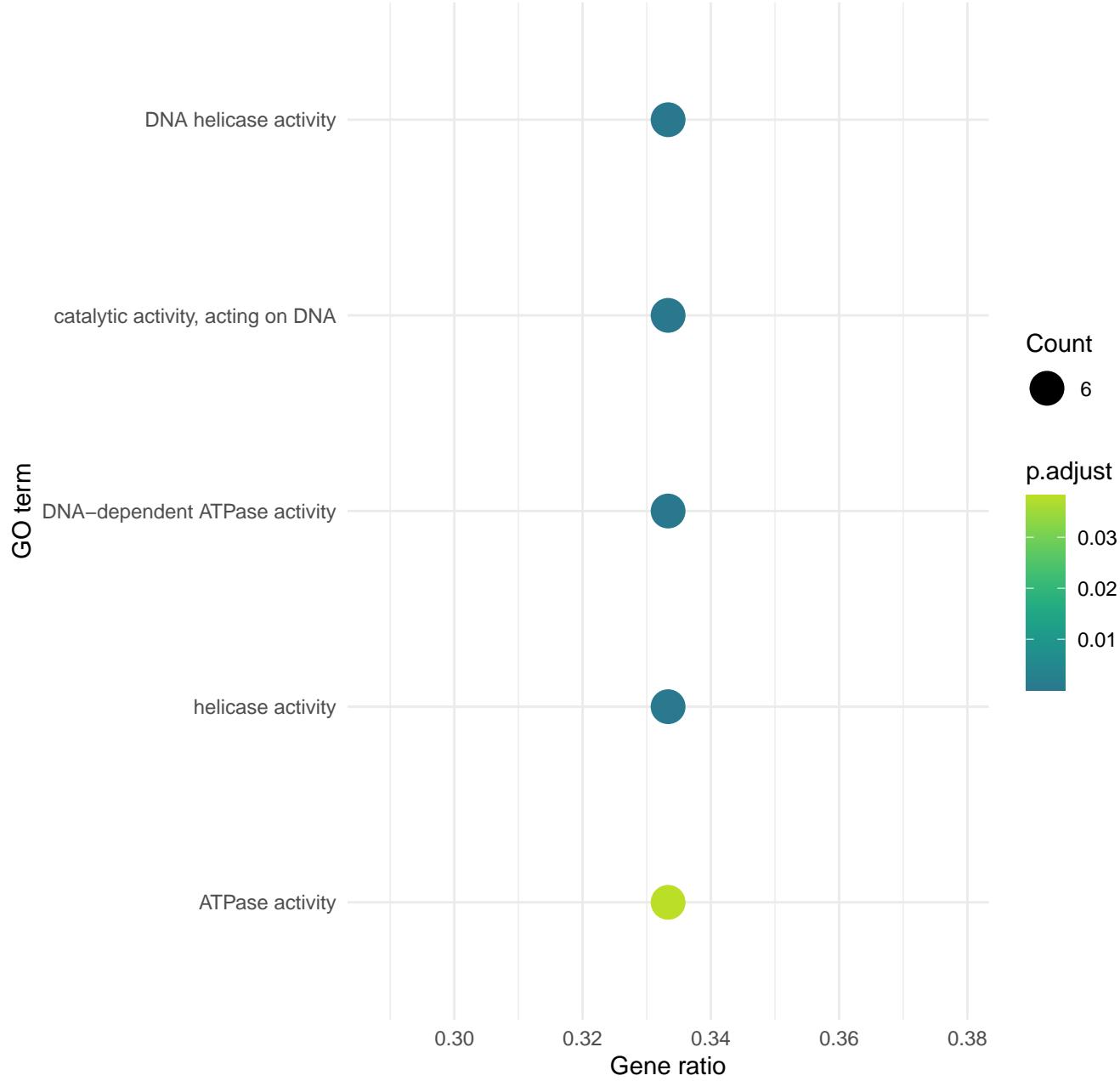
MIP6-TAP Up-regulated GO BP upsetplot



MIP6-TAP Up-regulated GO MF barplot

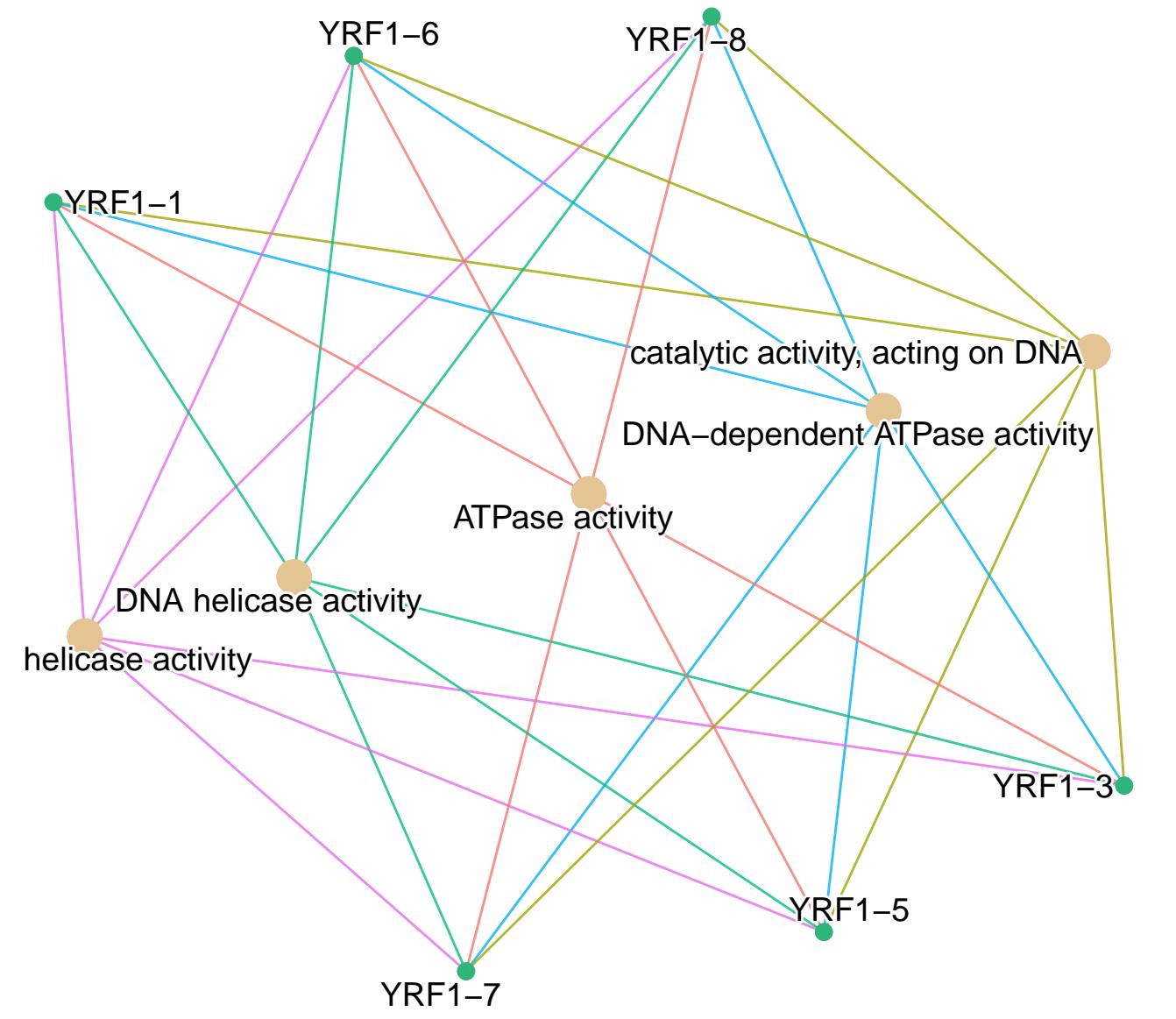


MIP6-TAP Up-regulated GO MF dotplot

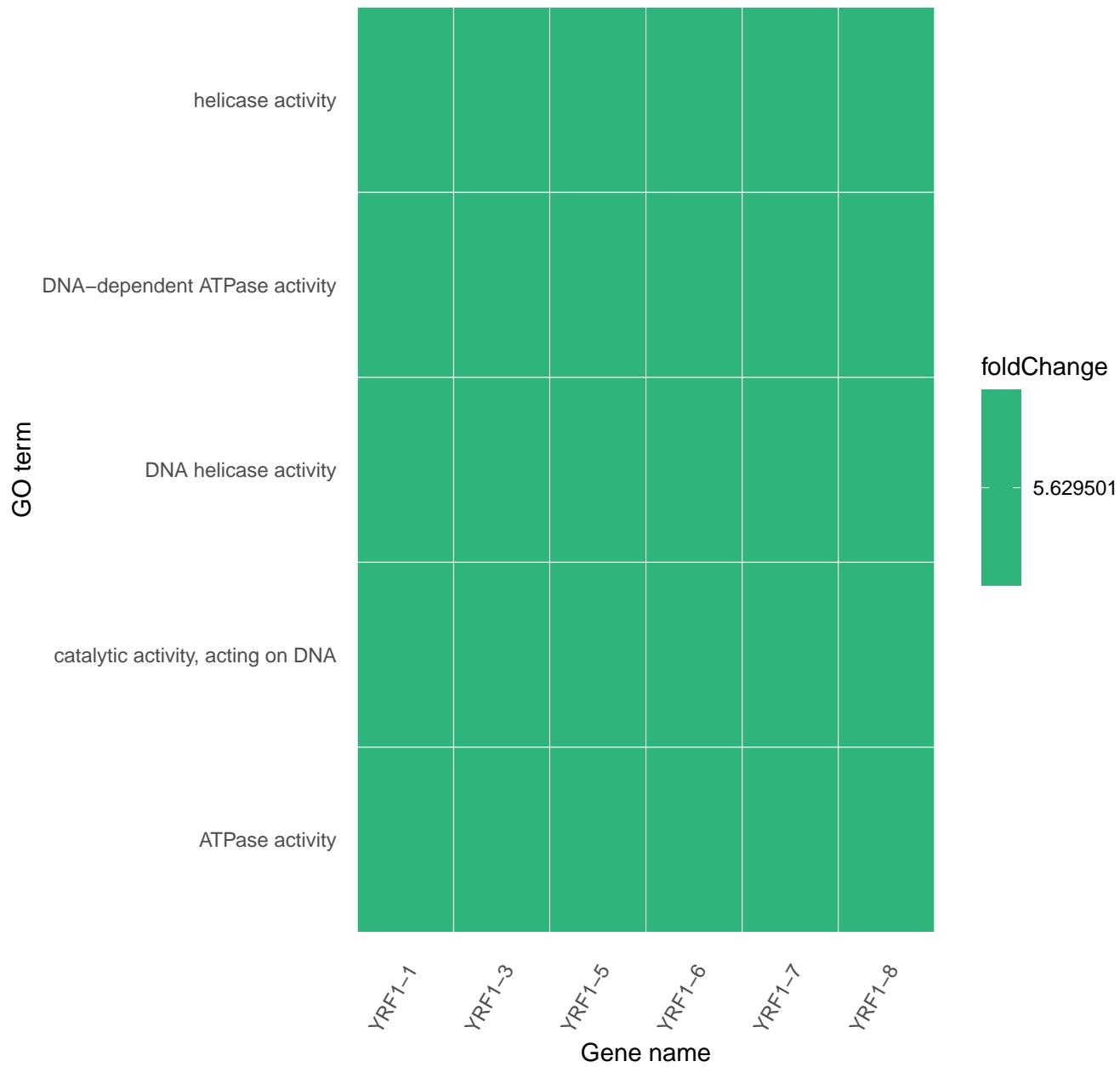


MIP6-TAP Up-regulated GO MF cnetplot

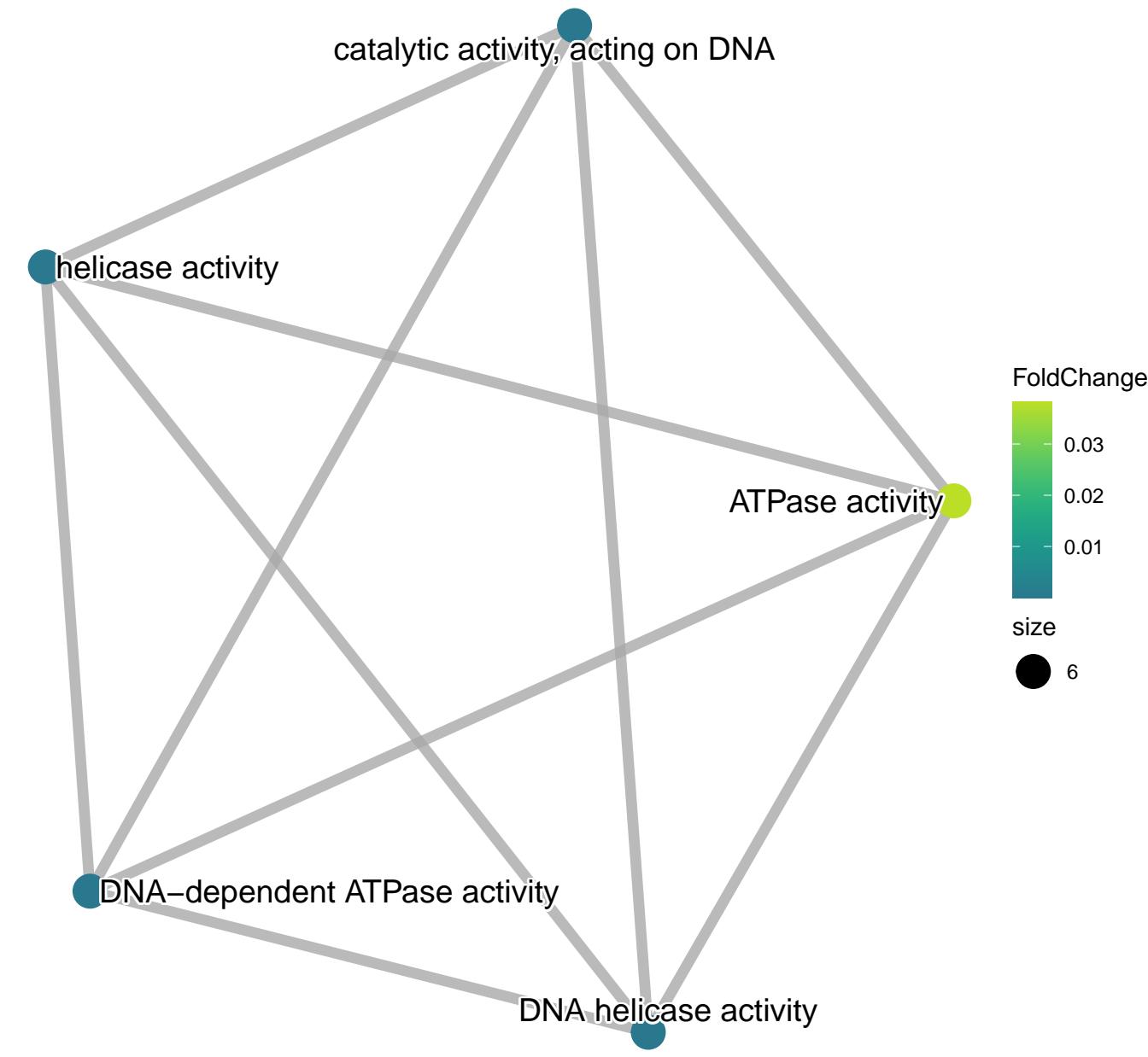
Category — ATPase activity (red), catalytic activity, acting on DNA (olive green), DNA helicase activity (teal), DNA-dependent ATPase activity (blue)

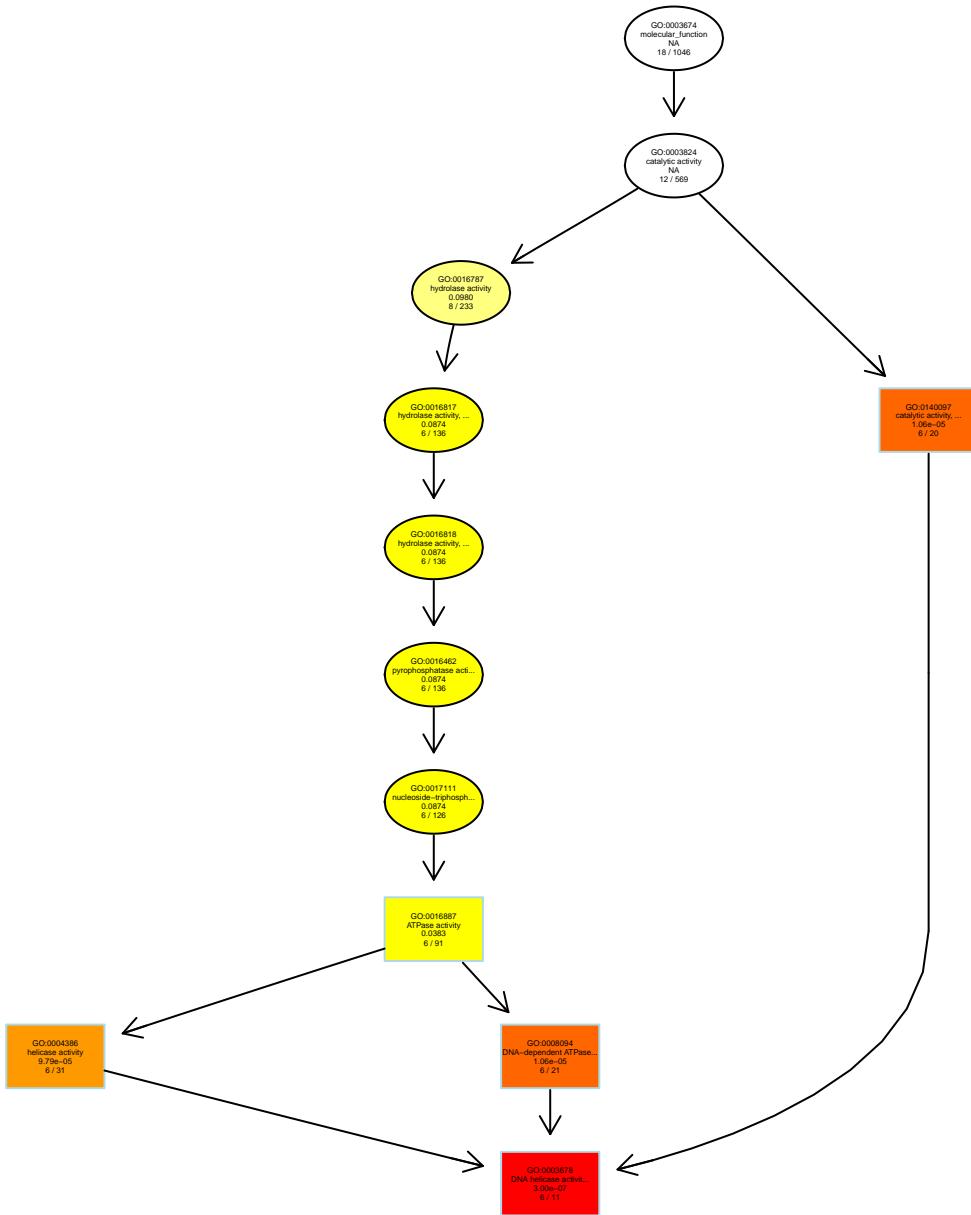


MIP6-TAP Up-regulated GO MF heatplot

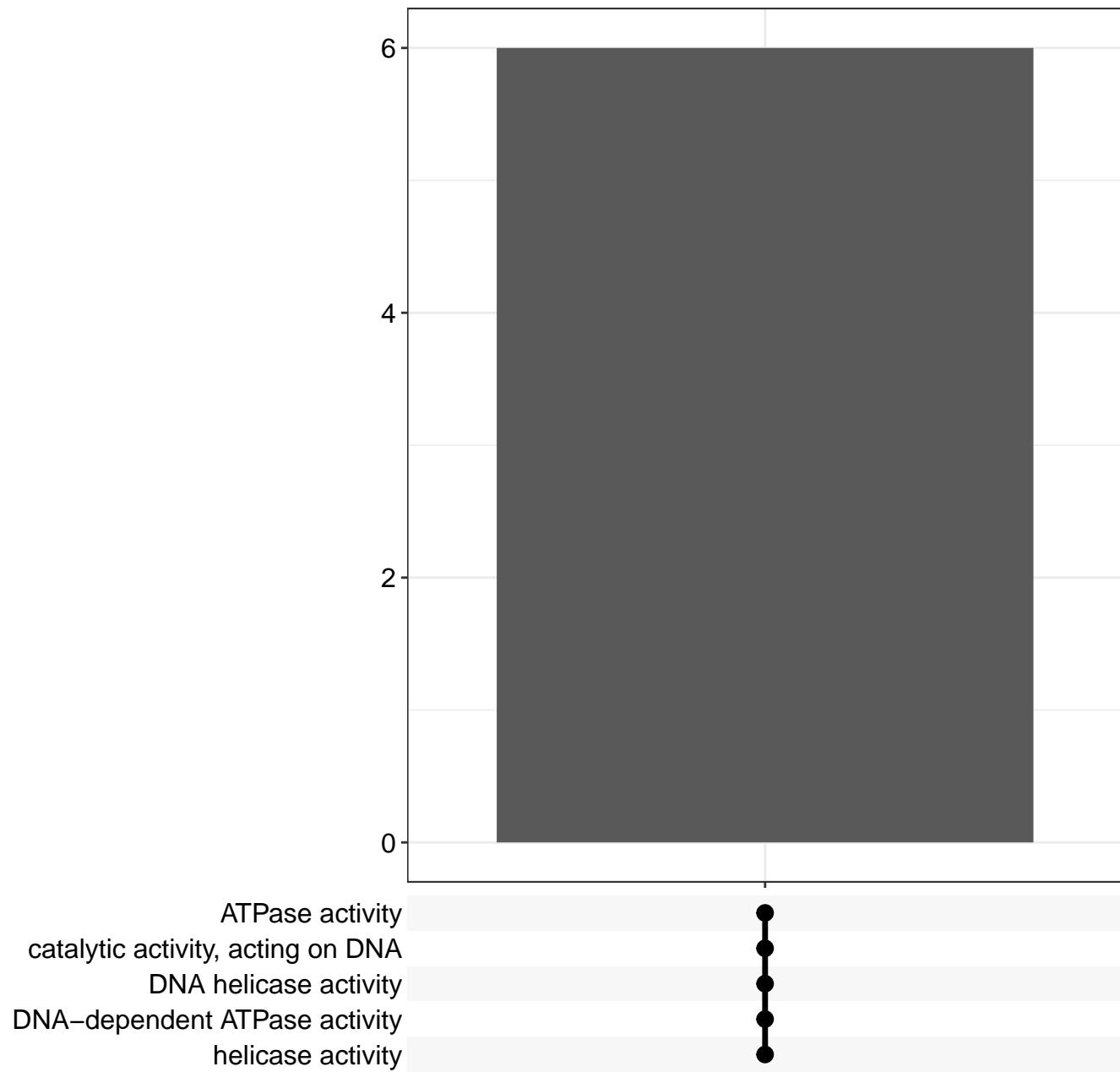


MIP6-TAP Up-regulated GO MF emapplot

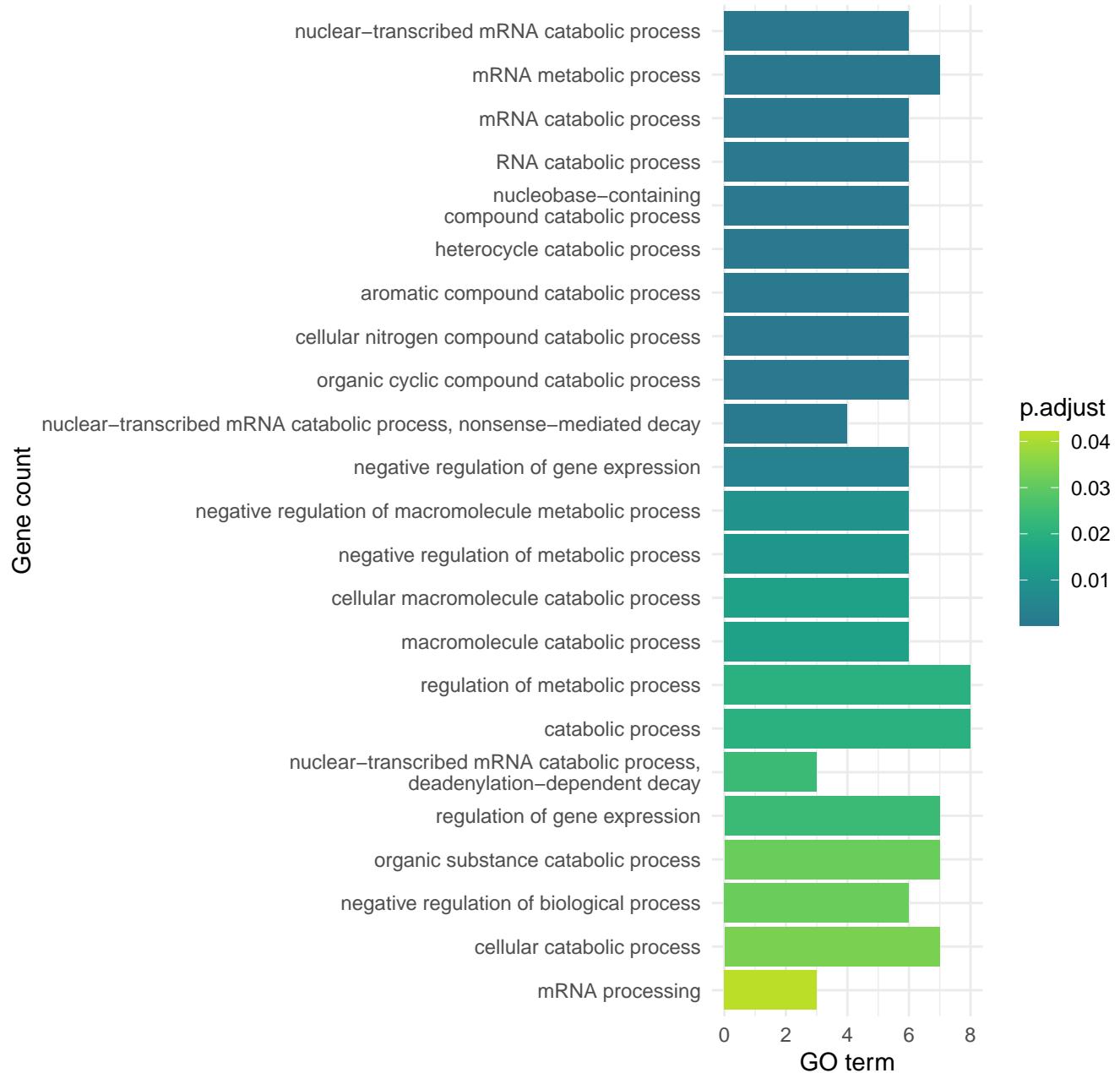




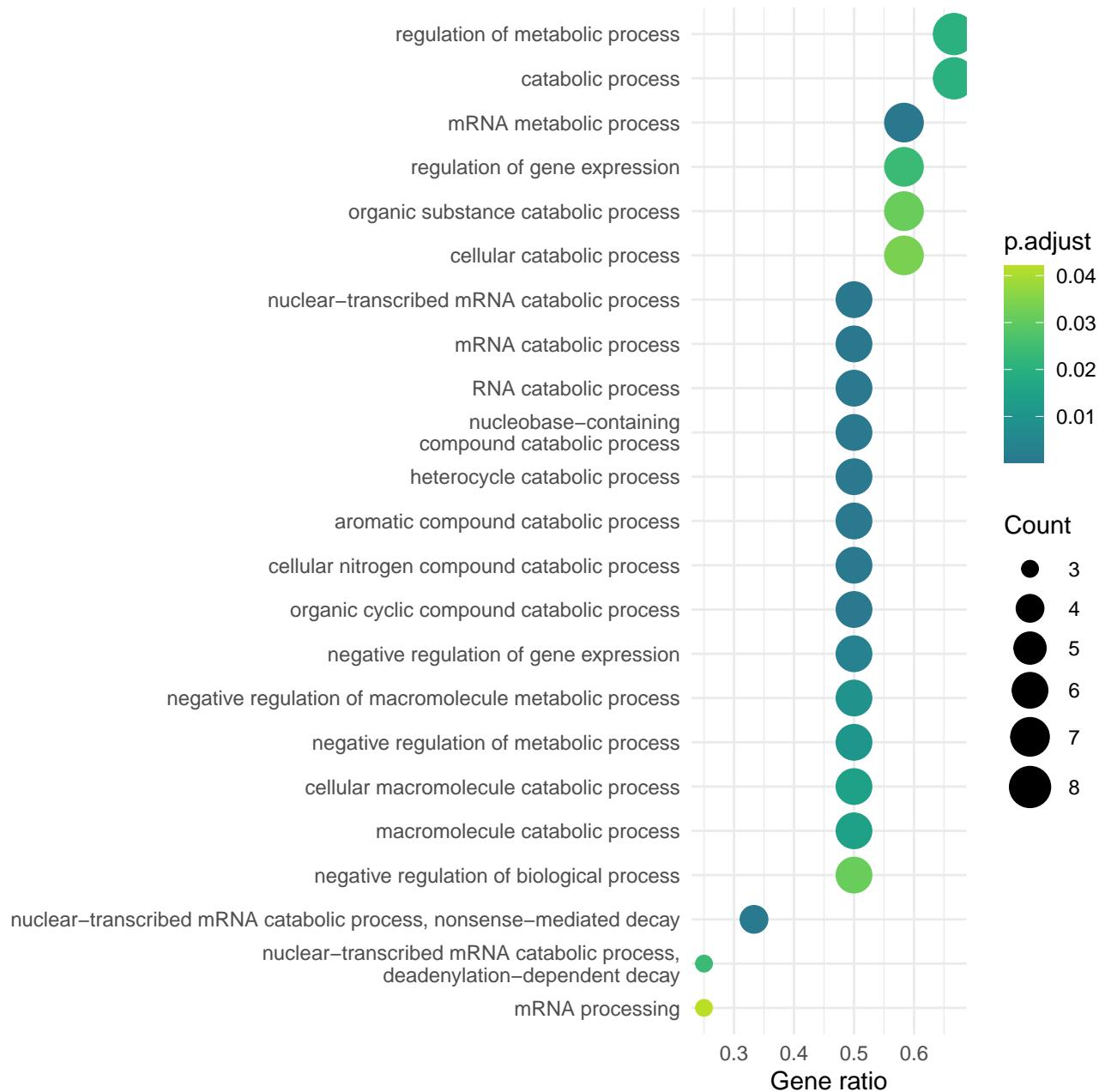
MIP6-TAP Up-regulated GO MF upsetplot



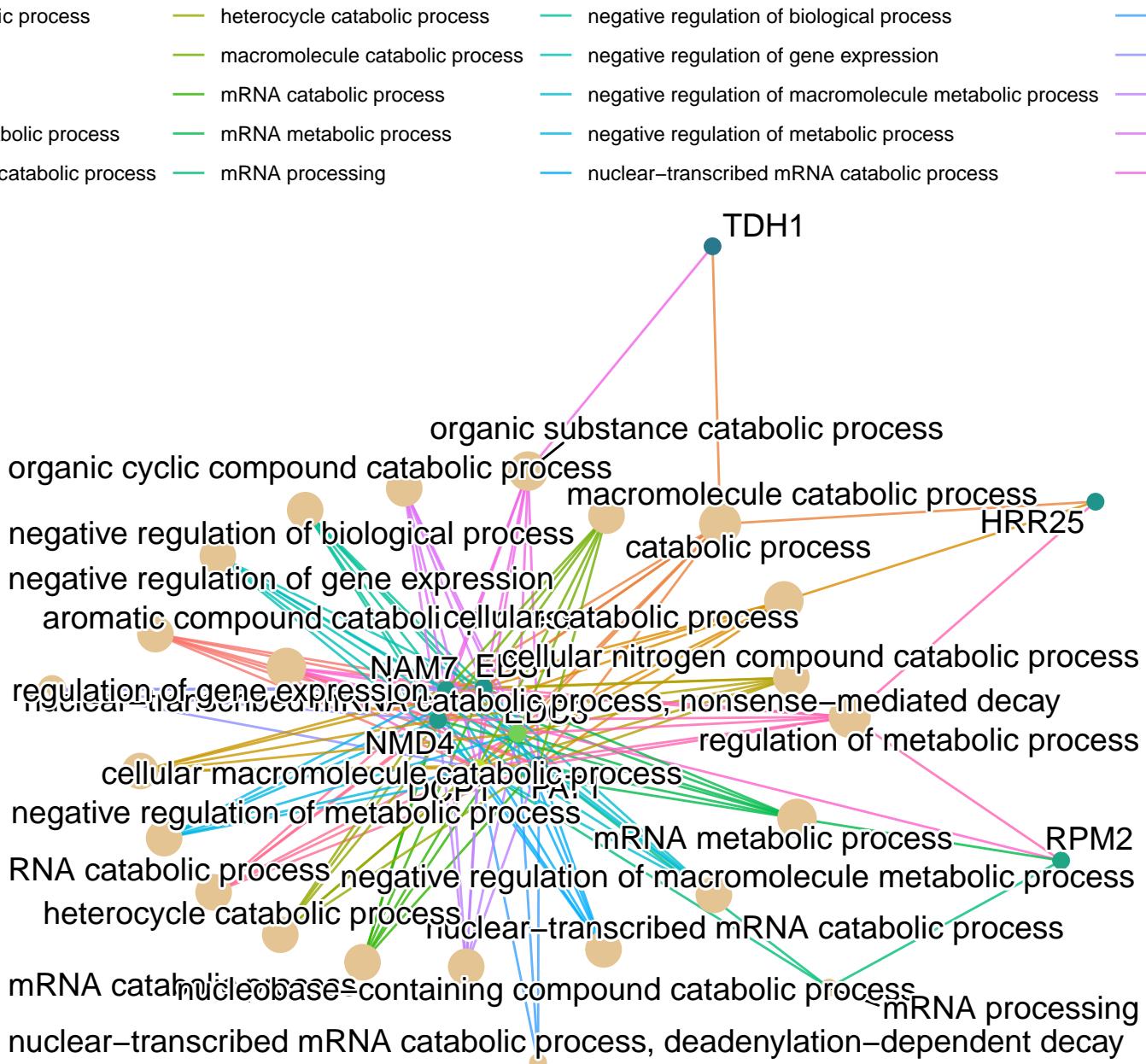
DCP2-TAP Up-regulated GO BP



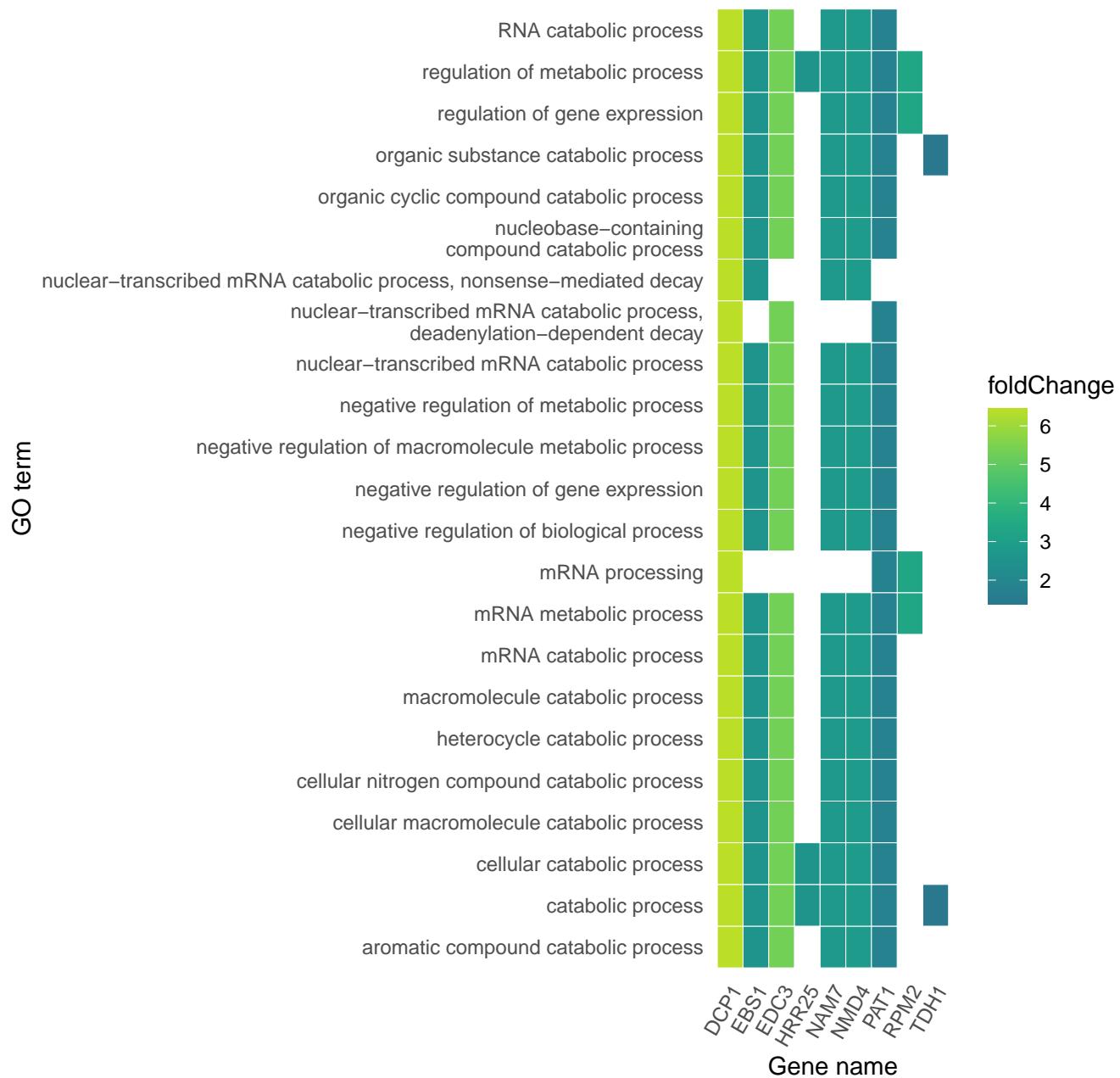
DCP2-TAP Up-regulated GO BP



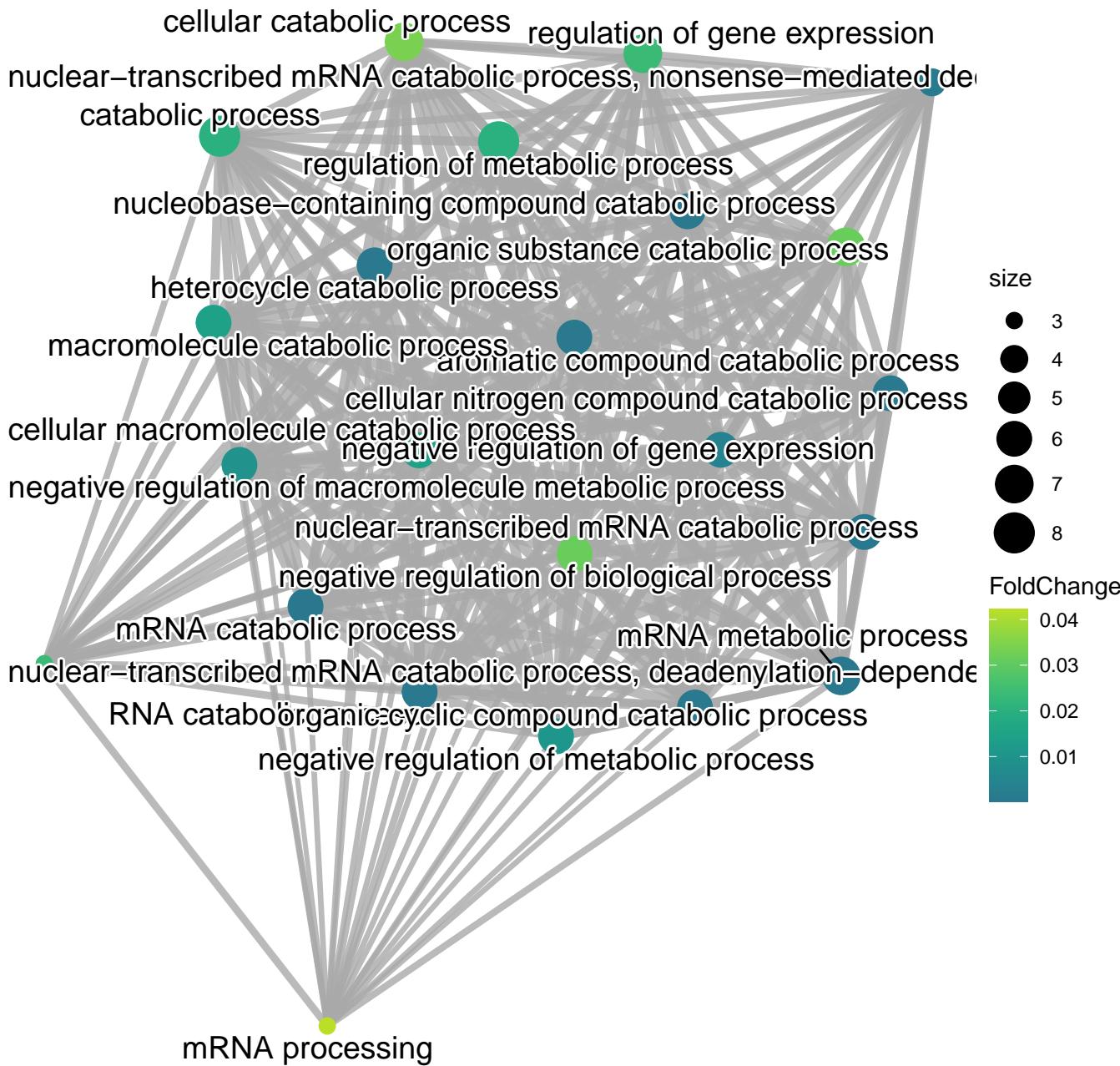
DCP2-TAP Up-regulated GO BP cnetplot

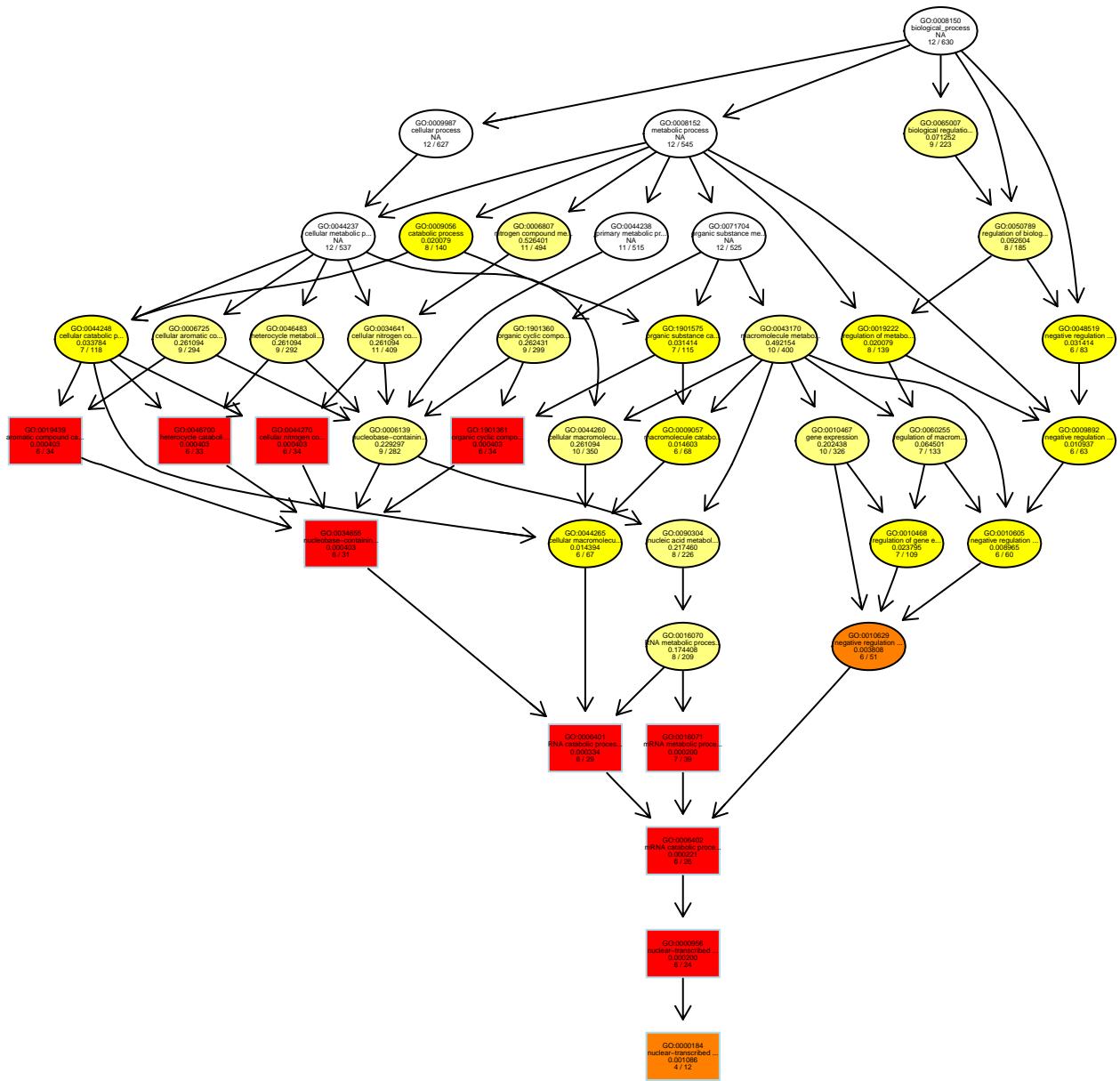


DCP2-TAP Up-regulated GO BP

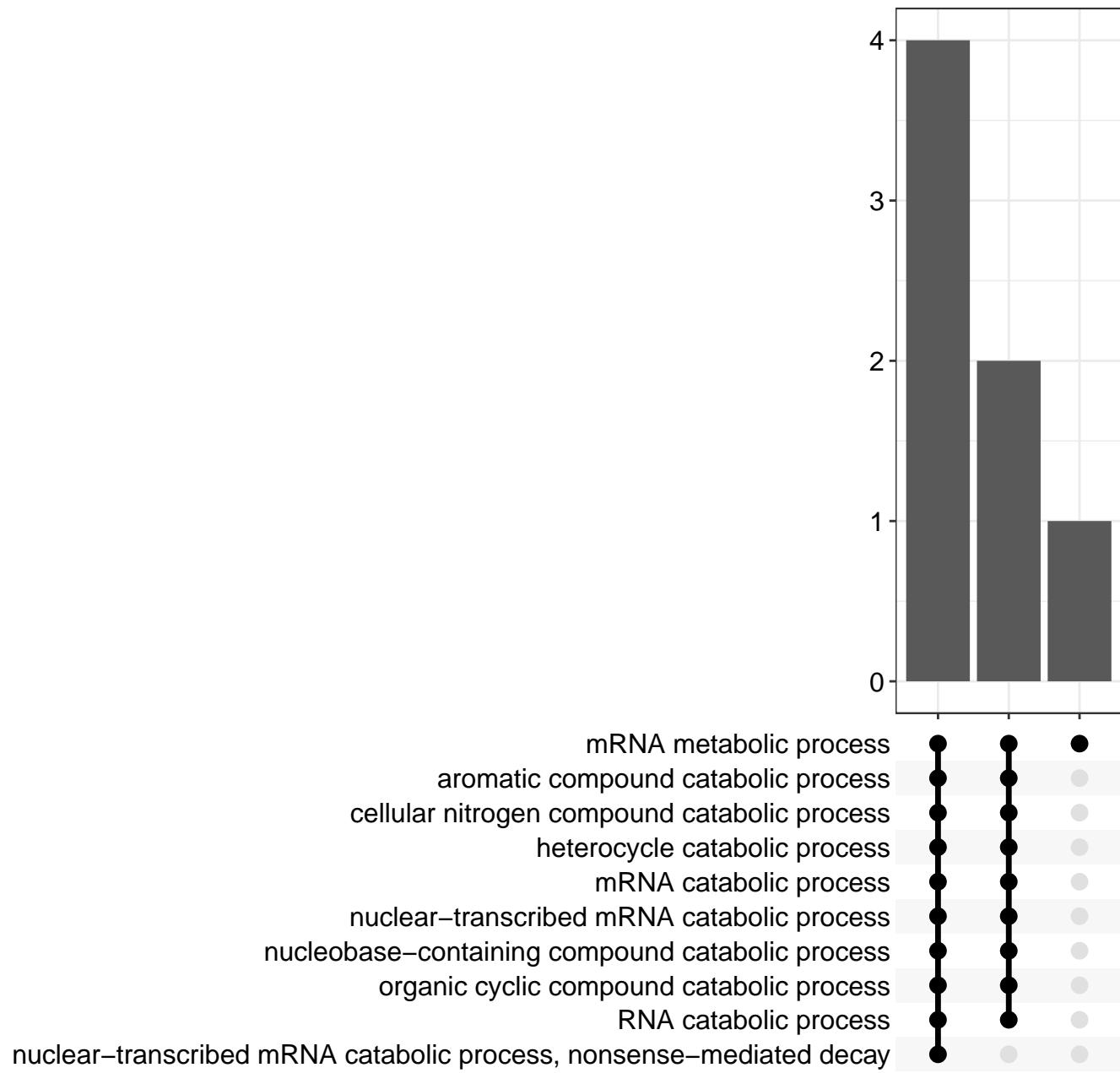


DCP2-TAP Up-regulated GO BP emapplot

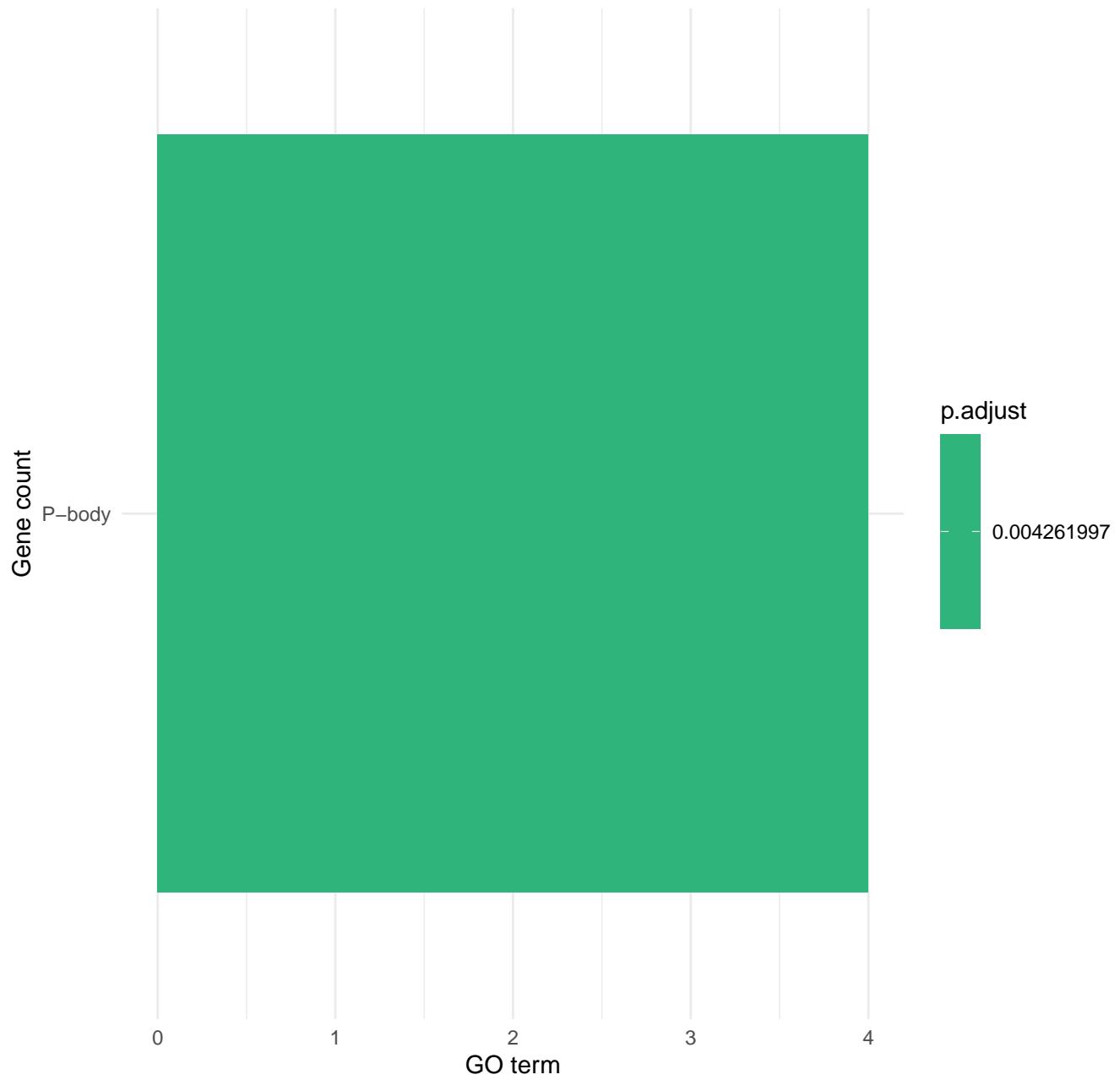




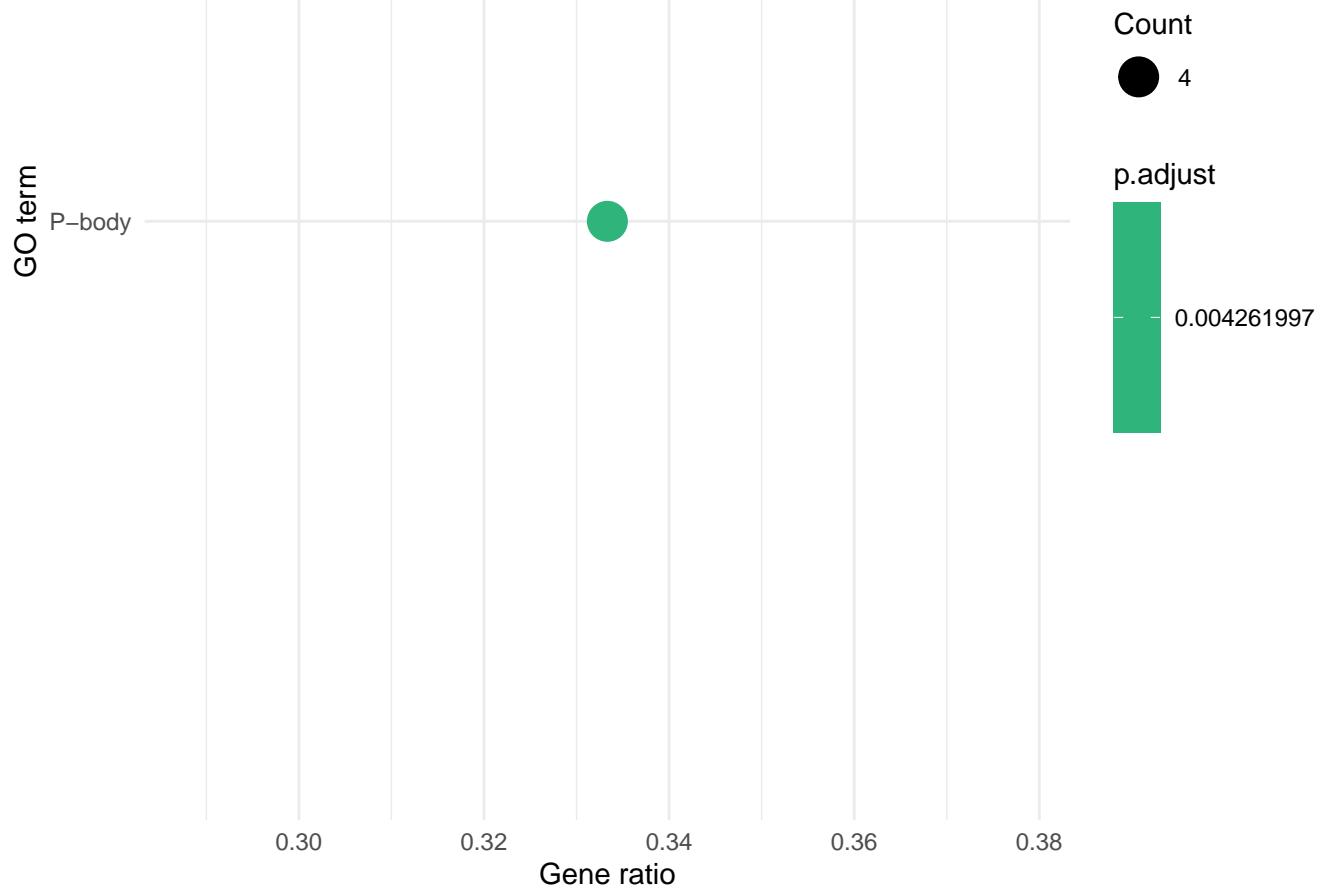
DCP2-TAP Up-re



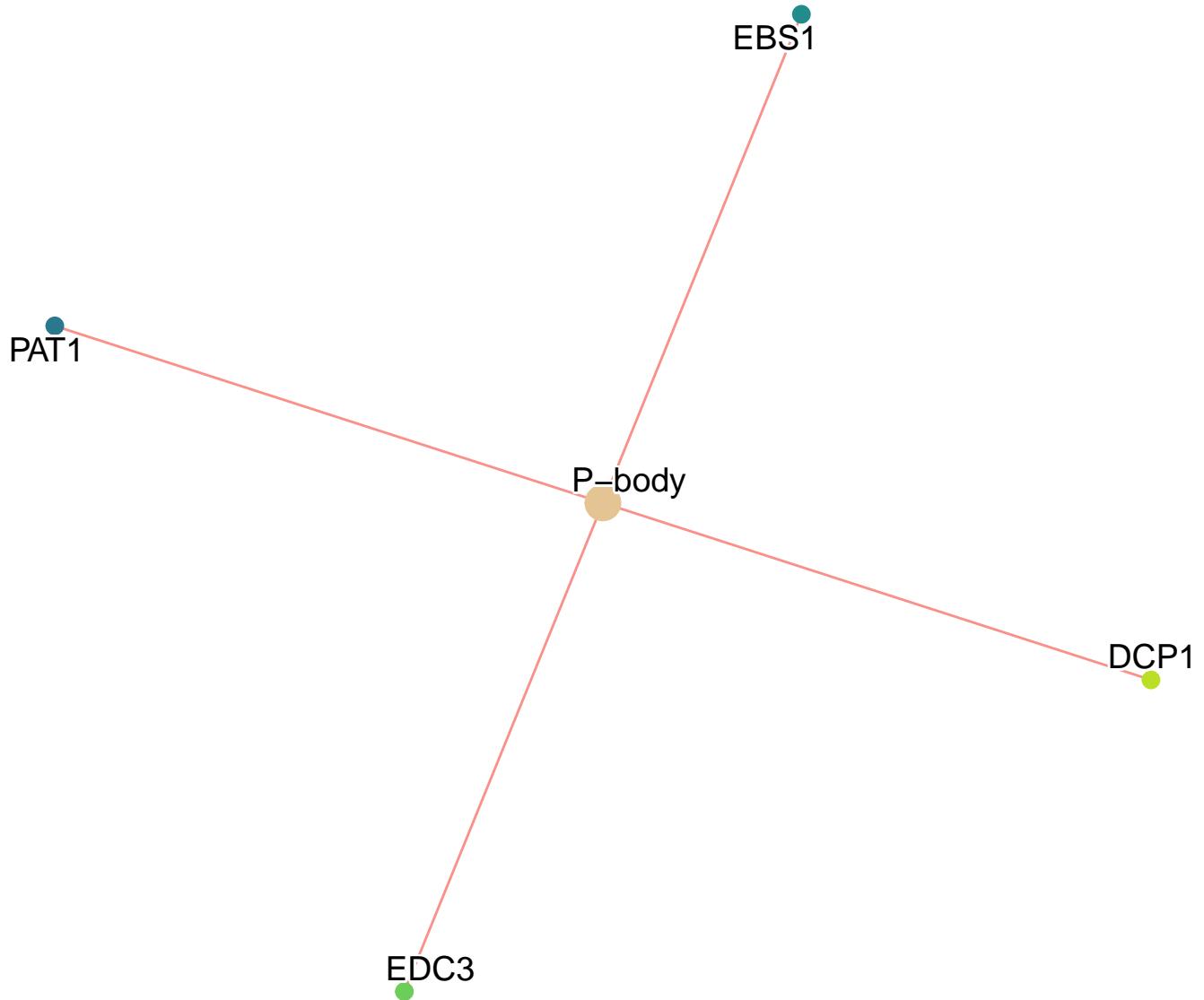
DCP2-TAP Up-regulated GO CC barplot



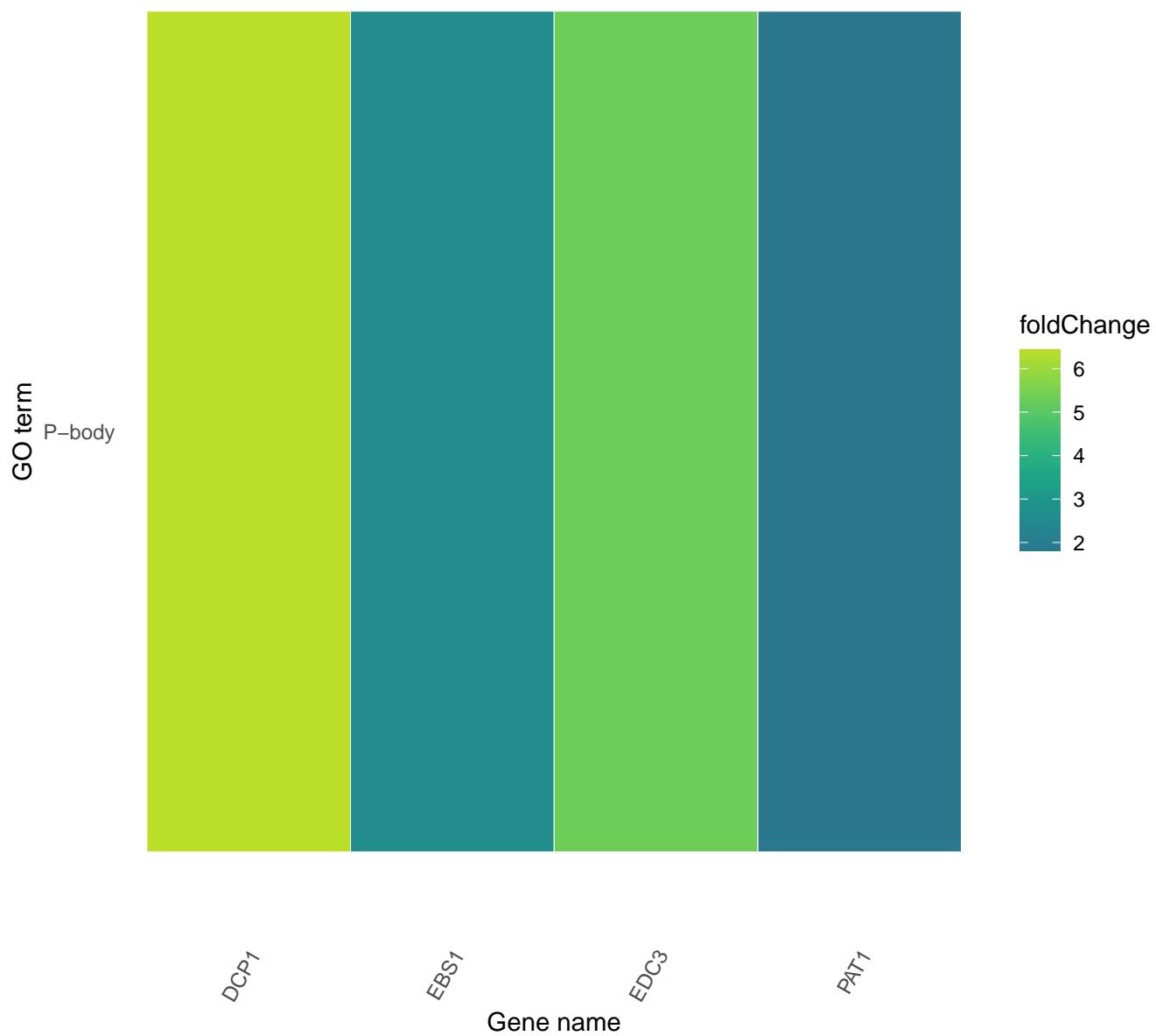
DCP2-TAP Up-regulated GO CC dotplot

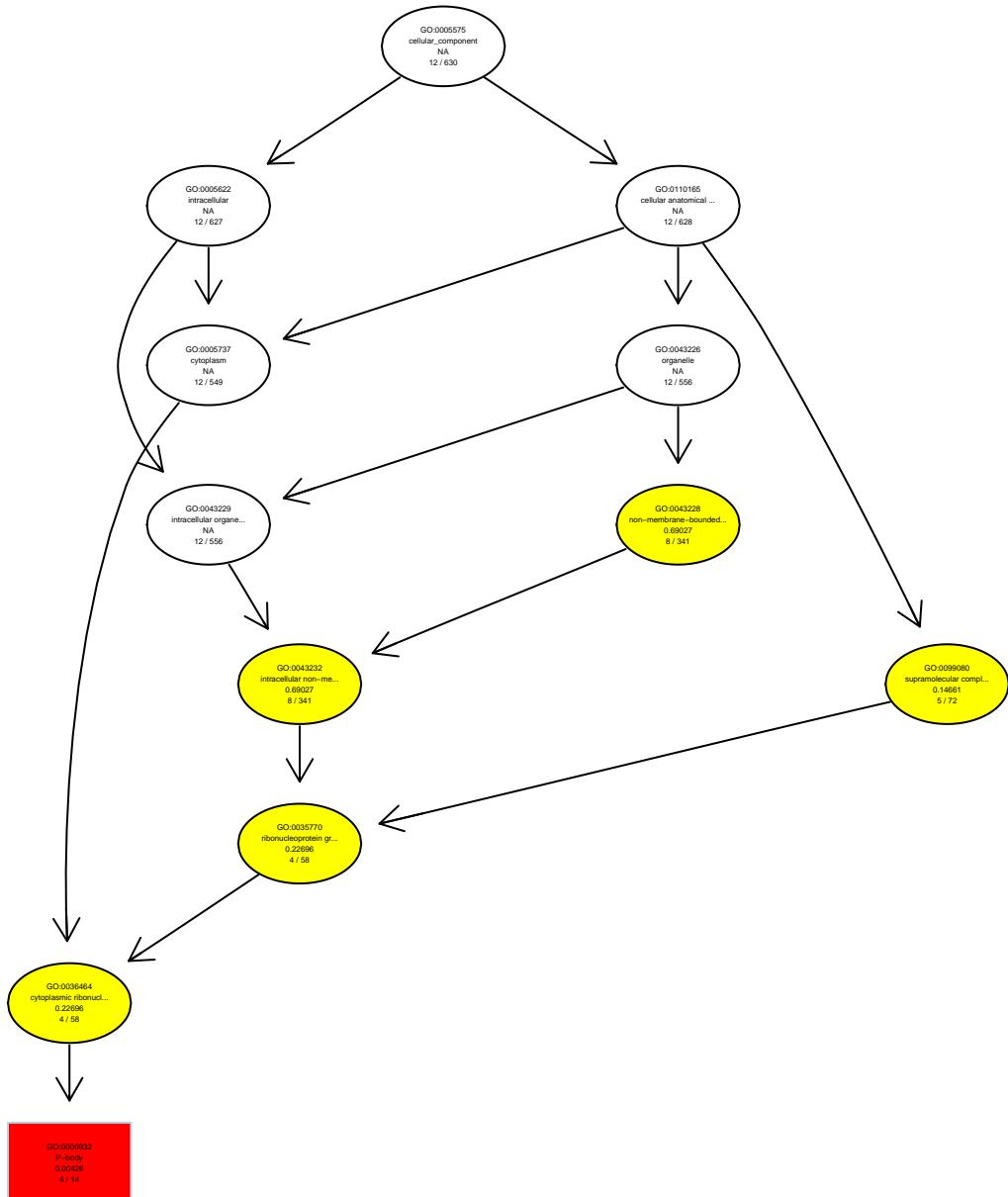


DCP2-TAP Up-regulated GO CC cnetplot

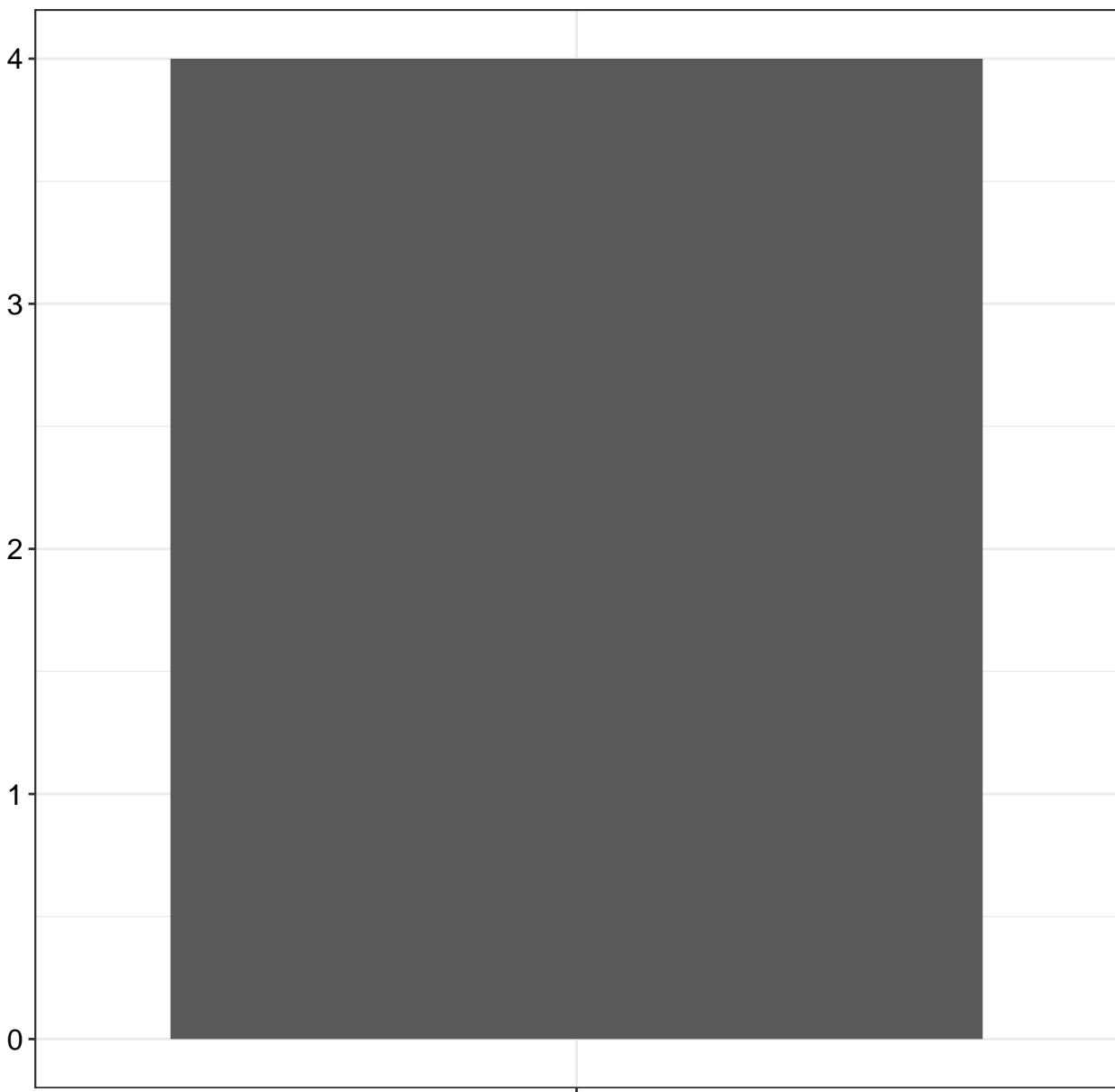


DCP2-TAP Up-regulated GO CC heatplot



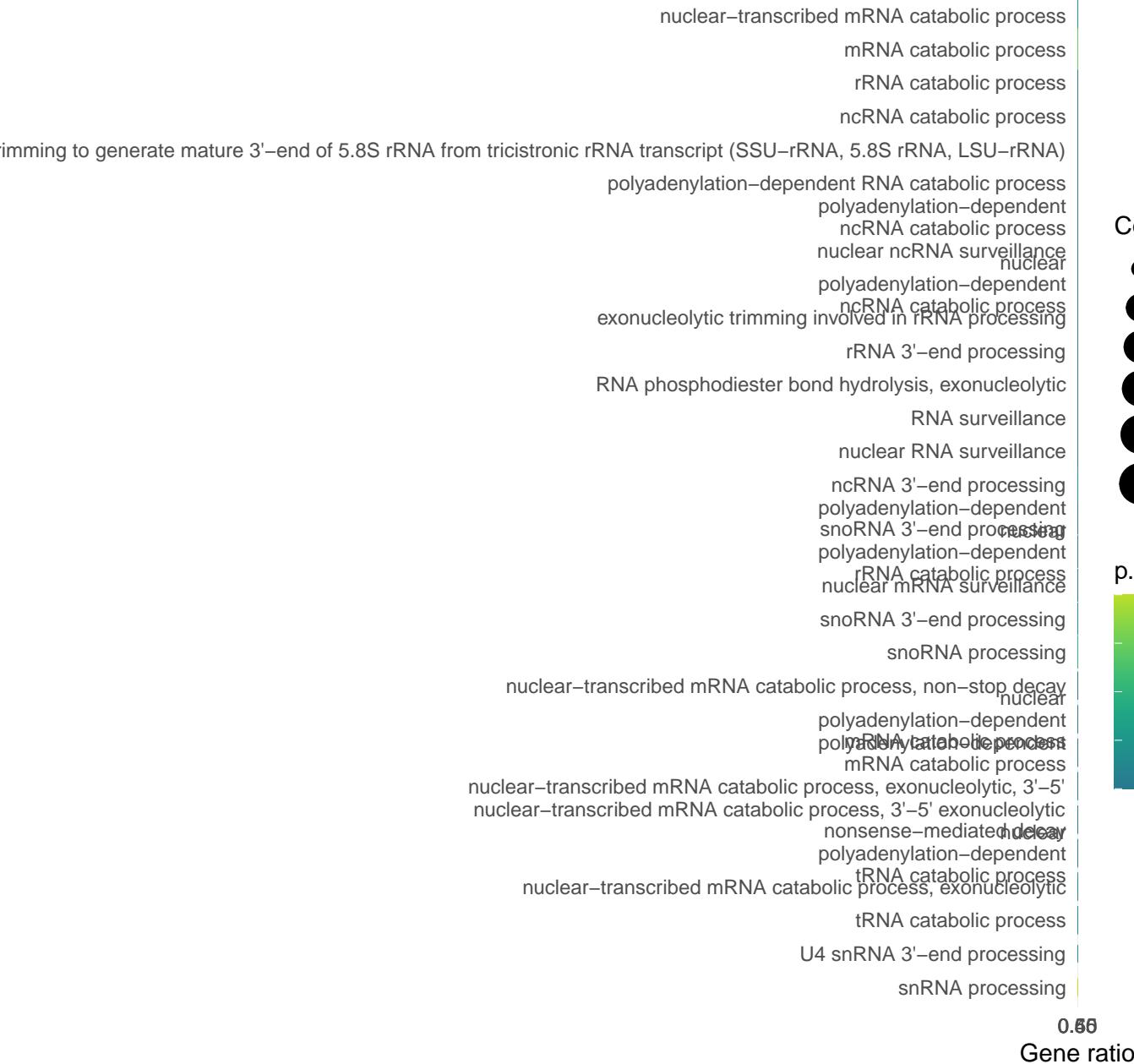


DCP2-TAP Up-regulated GO CC upsetplot

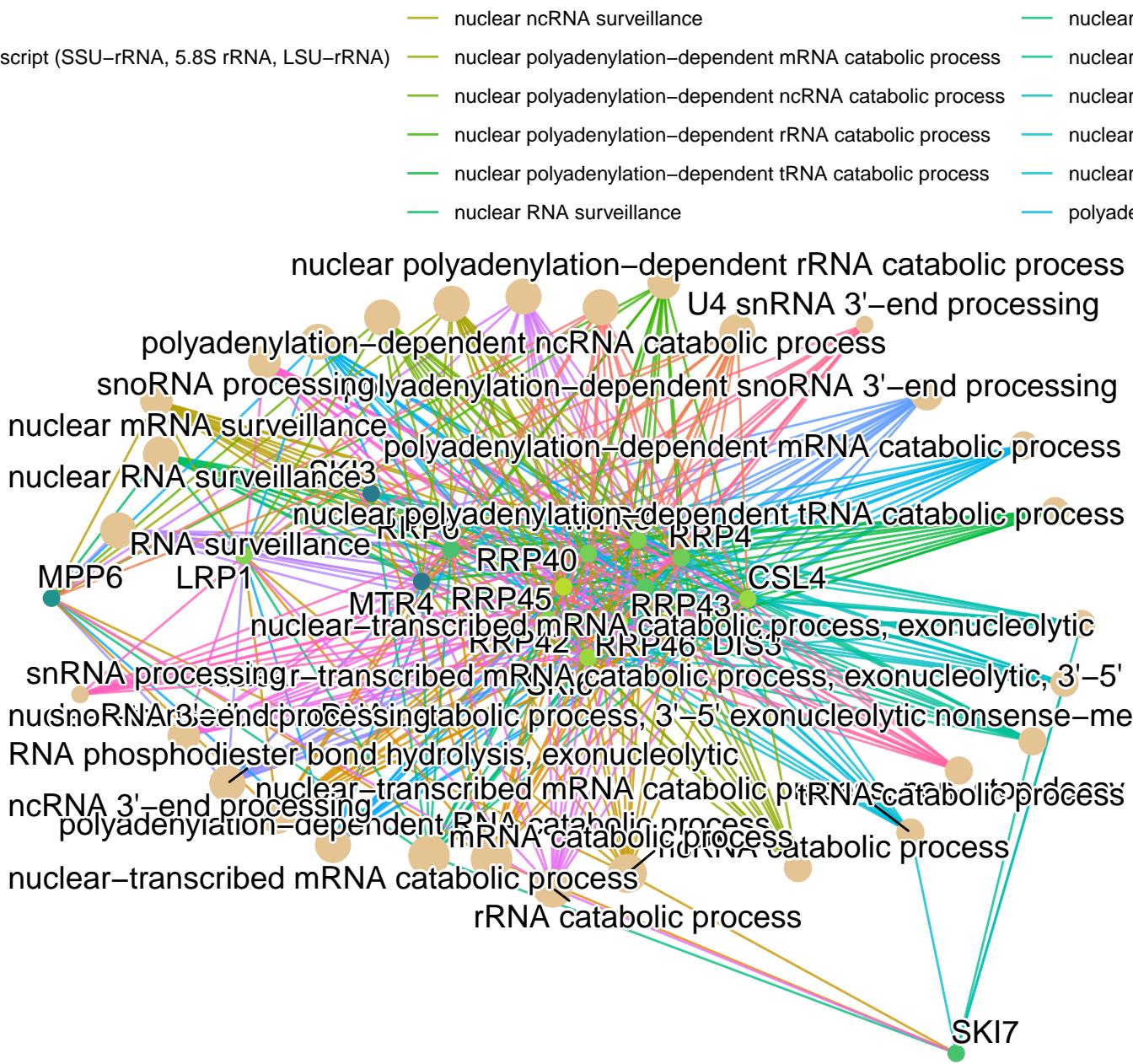


P-body

●



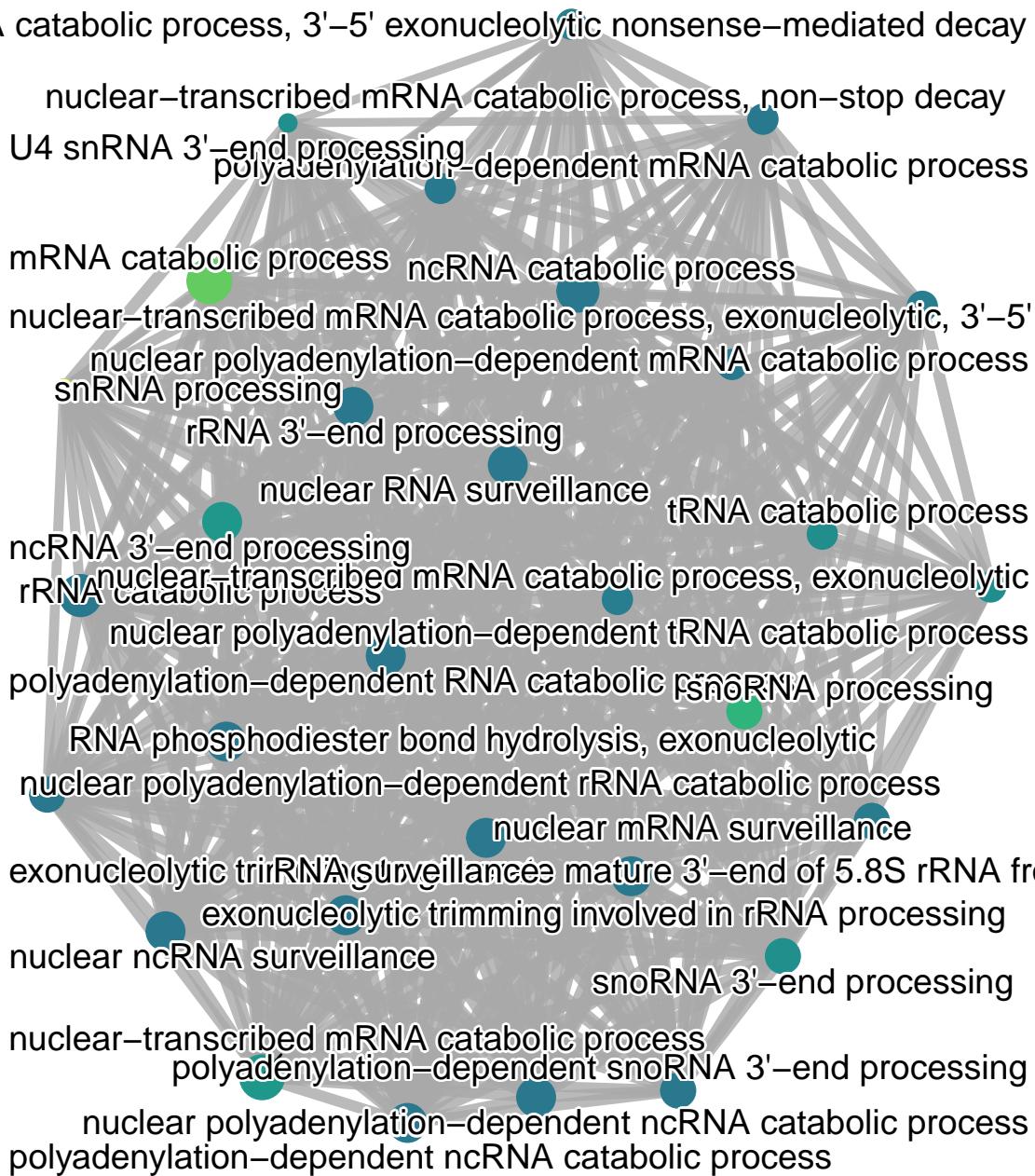
RRP40-TAP Up-regulated GO BP cnetplot

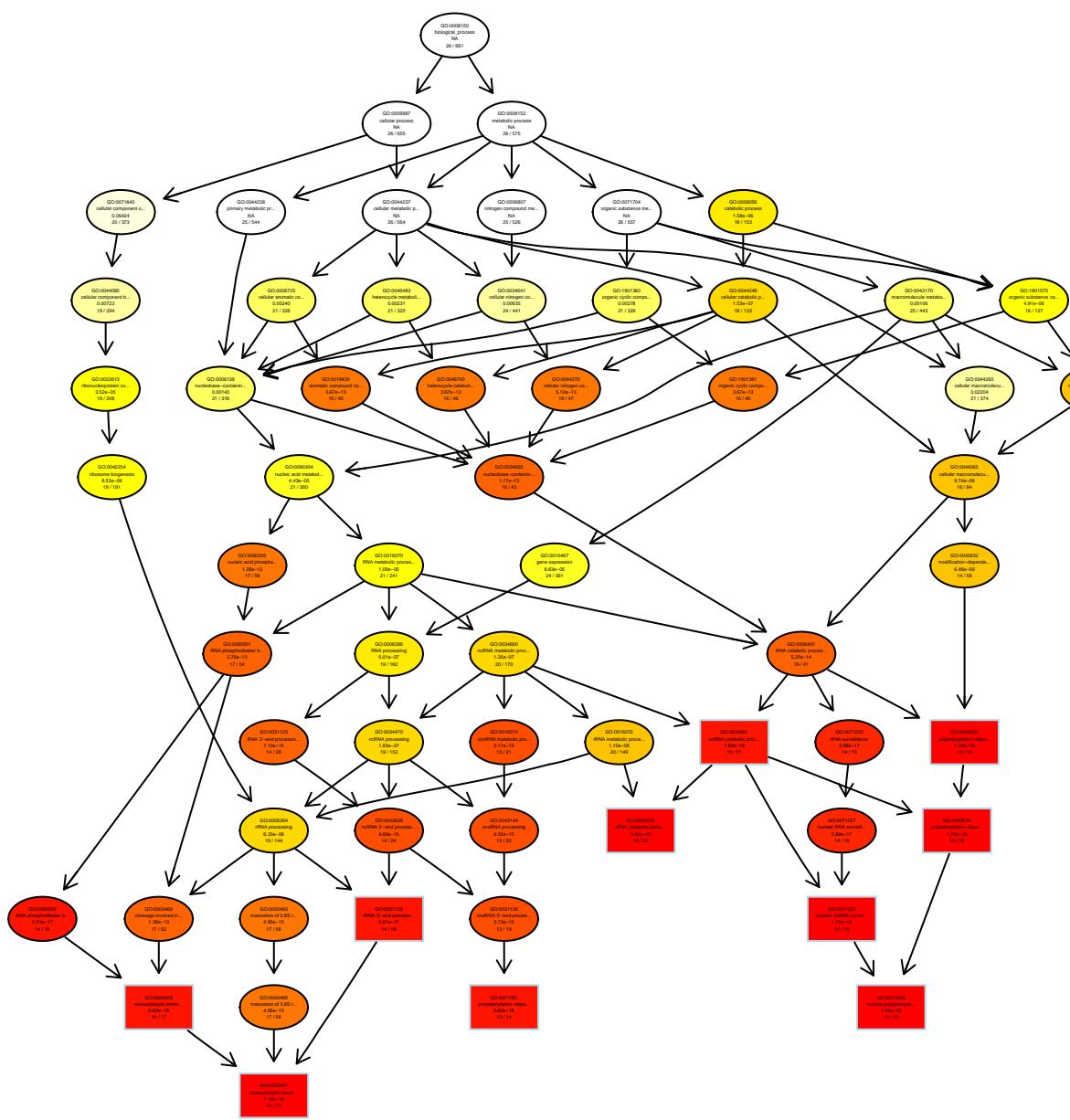


U4 snRNA 3'-end processing
tRNA catabolic process
snRNA processing
snoRNA processing
snoRNA 3'-end processing
rRNA catabolic process
rRNA 3'-end processing
RNA surveillance
RNA phosphodiester bond hydrolysis, exonucleolytic
polyadenylation-dependent snoRNA 3'-end processing
polyadenylation-dependent RNA catabolic process
polyadenylation-dependent ncRNA catabolic process
polyadenylation-dependent mRNA catabolic process
nuclear-transcribed mRNA catabolic process, non-stop decay
nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'
nuclear-transcribed mRNA catabolic process, exonucleolytic
nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic
nonsense-mediated decay
nuclear-transcribed mRNA catabolic process
nuclear RNA surveillance
nuclear polyadenylation-dependent tRNA catabolic process
nuclear polyadenylation-dependent rRNA catabolic process
nuclear polyadenylation-dependent ncRNA catabolic process
nuclear polyadenylation-dependent mRNA catabolic process
nuclear ncRNA surveillance
nuclear mRNA surveillance
ncRNA catabolic process
ncRNA 3'-end processing
mRNA catabolic process
c trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
exonucleolytic trimming involved in rRNA processing



RRP40-TAP Up-regulated GO BP emapplot





ncRN
rRN

exonucleolytic trimming involved

ing to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S
nuclear

nuclear polyadenylation-dependent ncRN

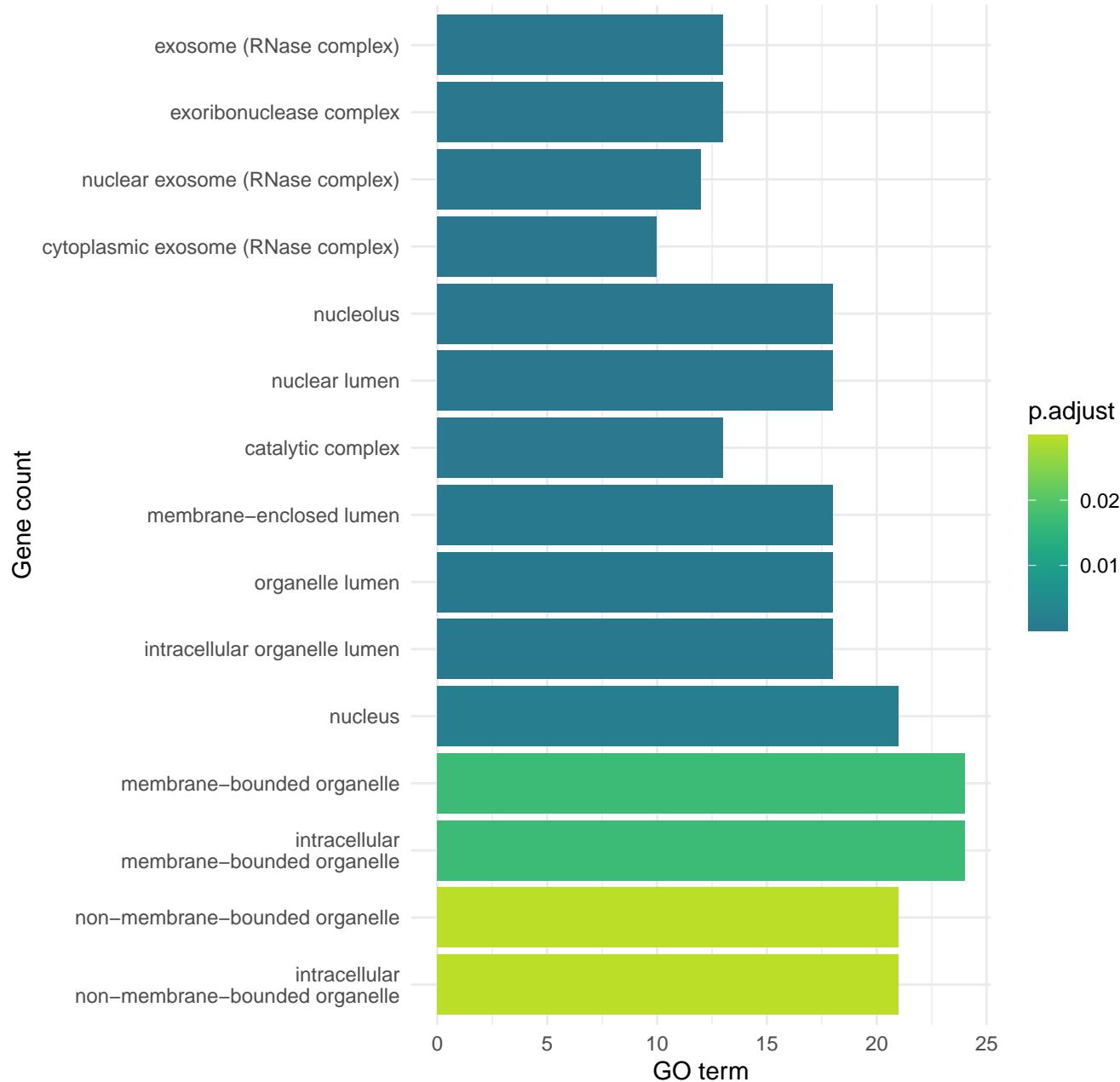
polyadenylation-dependent ncRN

polyadenylation-dependent RN

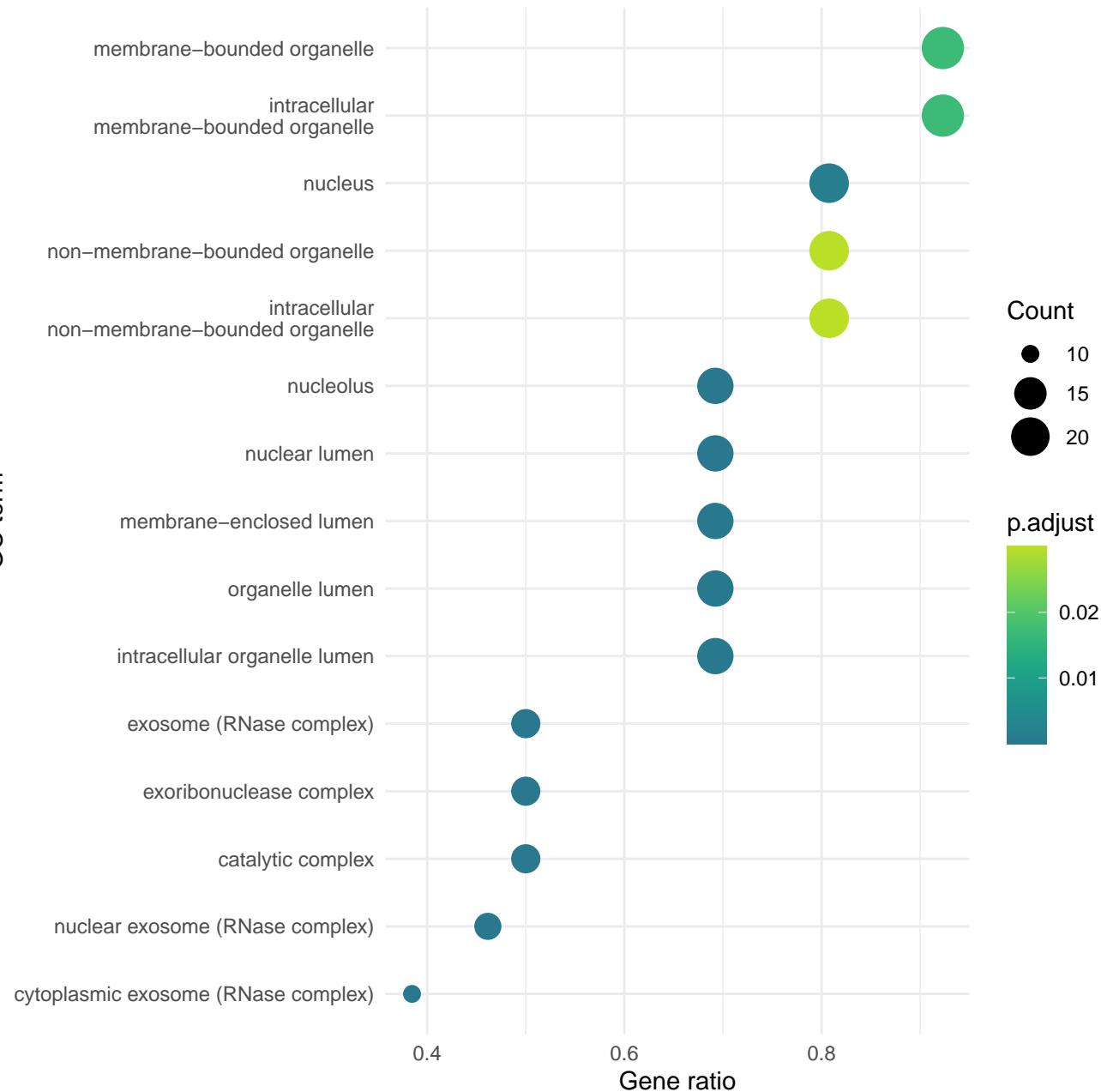
rRNA

polyadenylation-dependent snoRNA

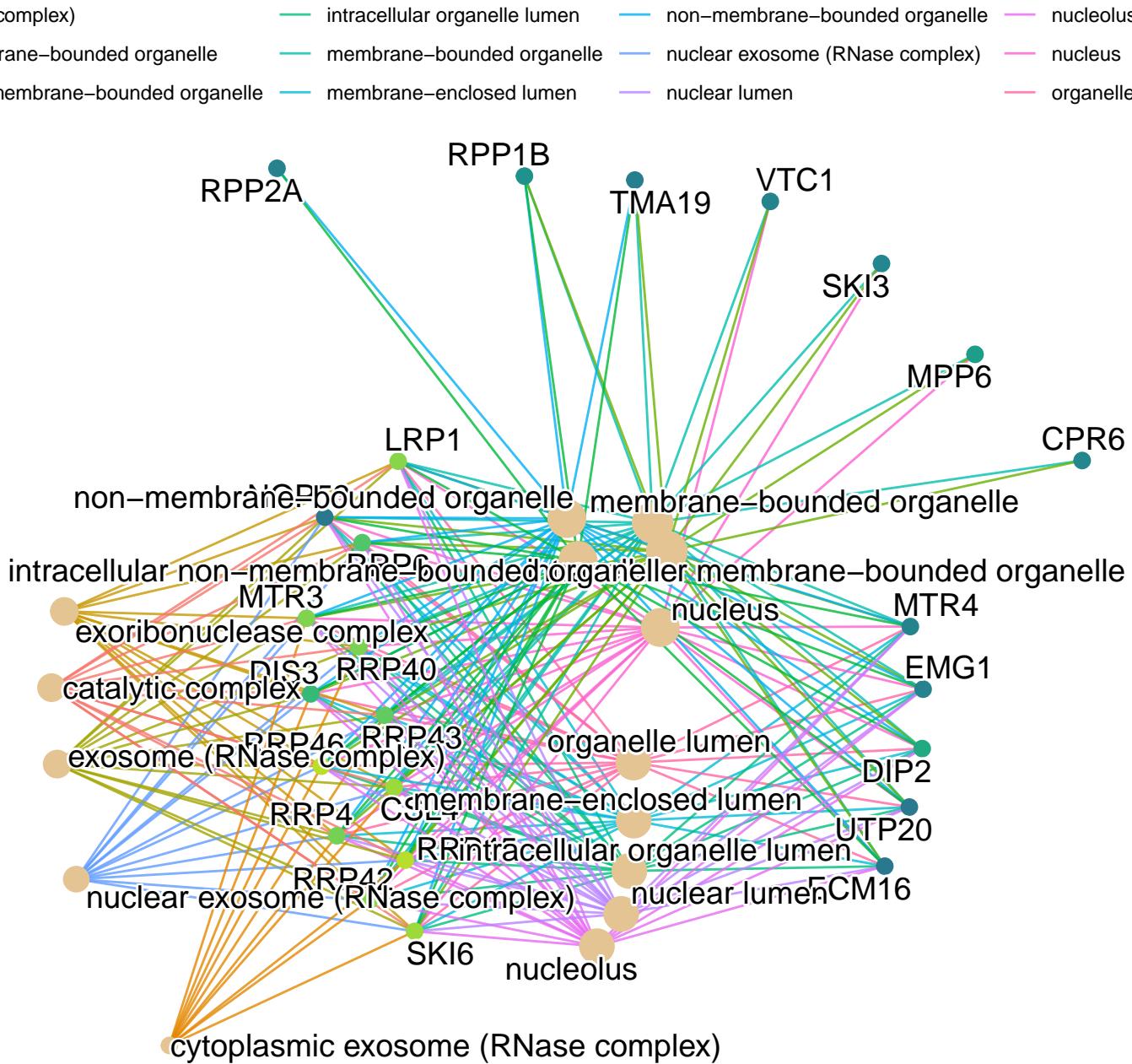
RRP40-TAP Up-regulated GO CC barplot



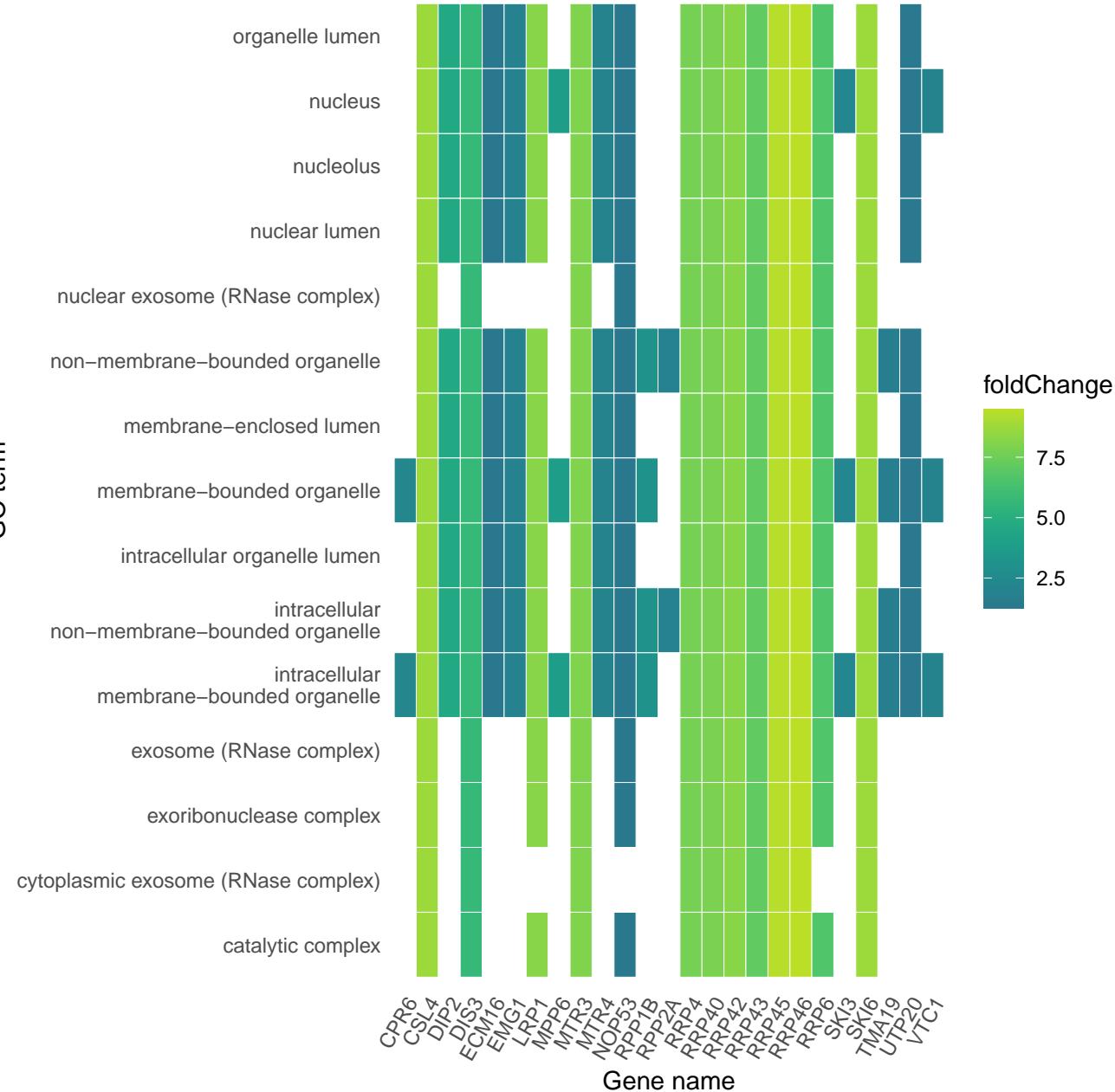
RRP40-TAP Up-regulated GO CC dotplot



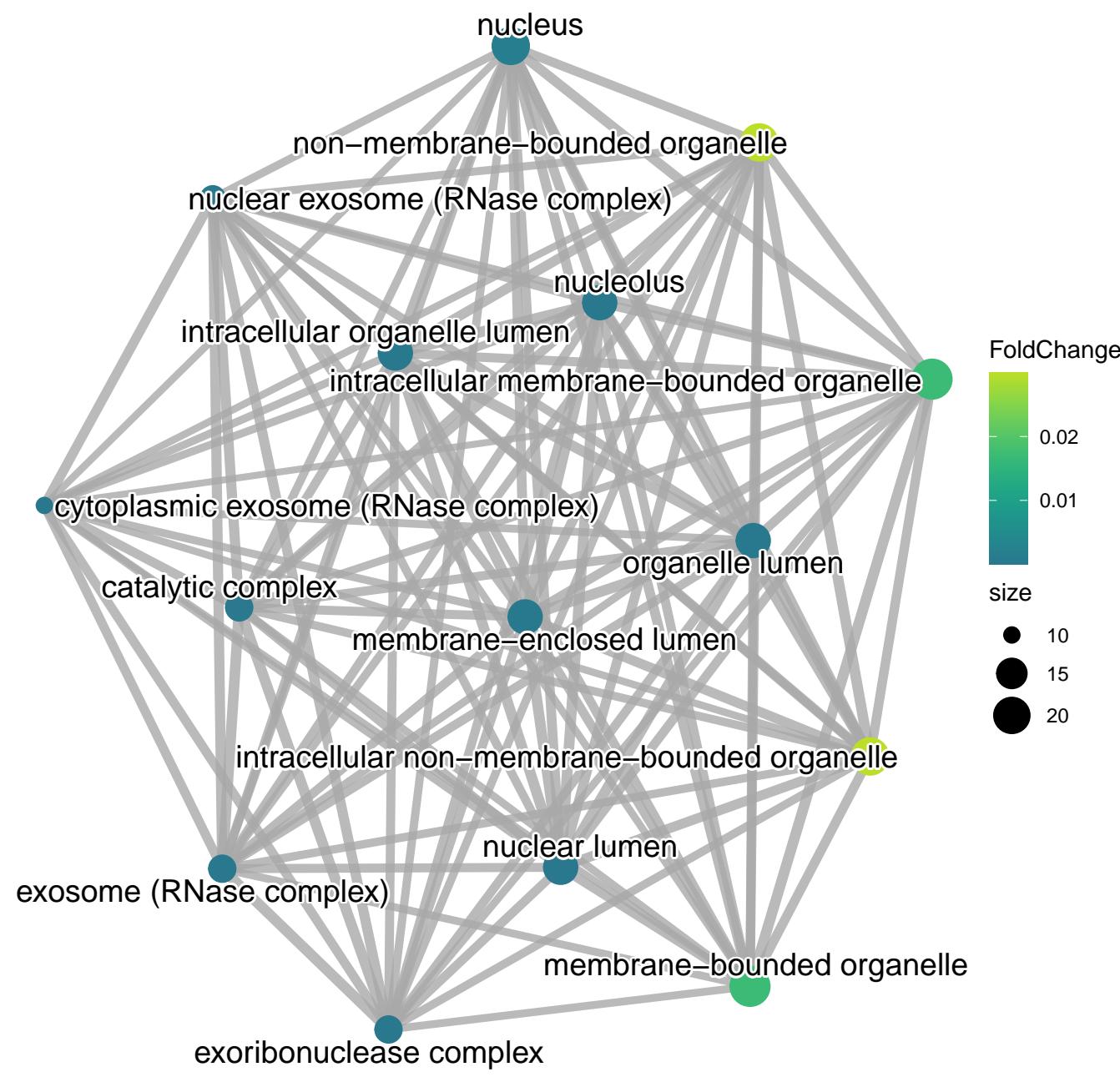
RRP40-TAP Up-regulated GO CC cnetplot

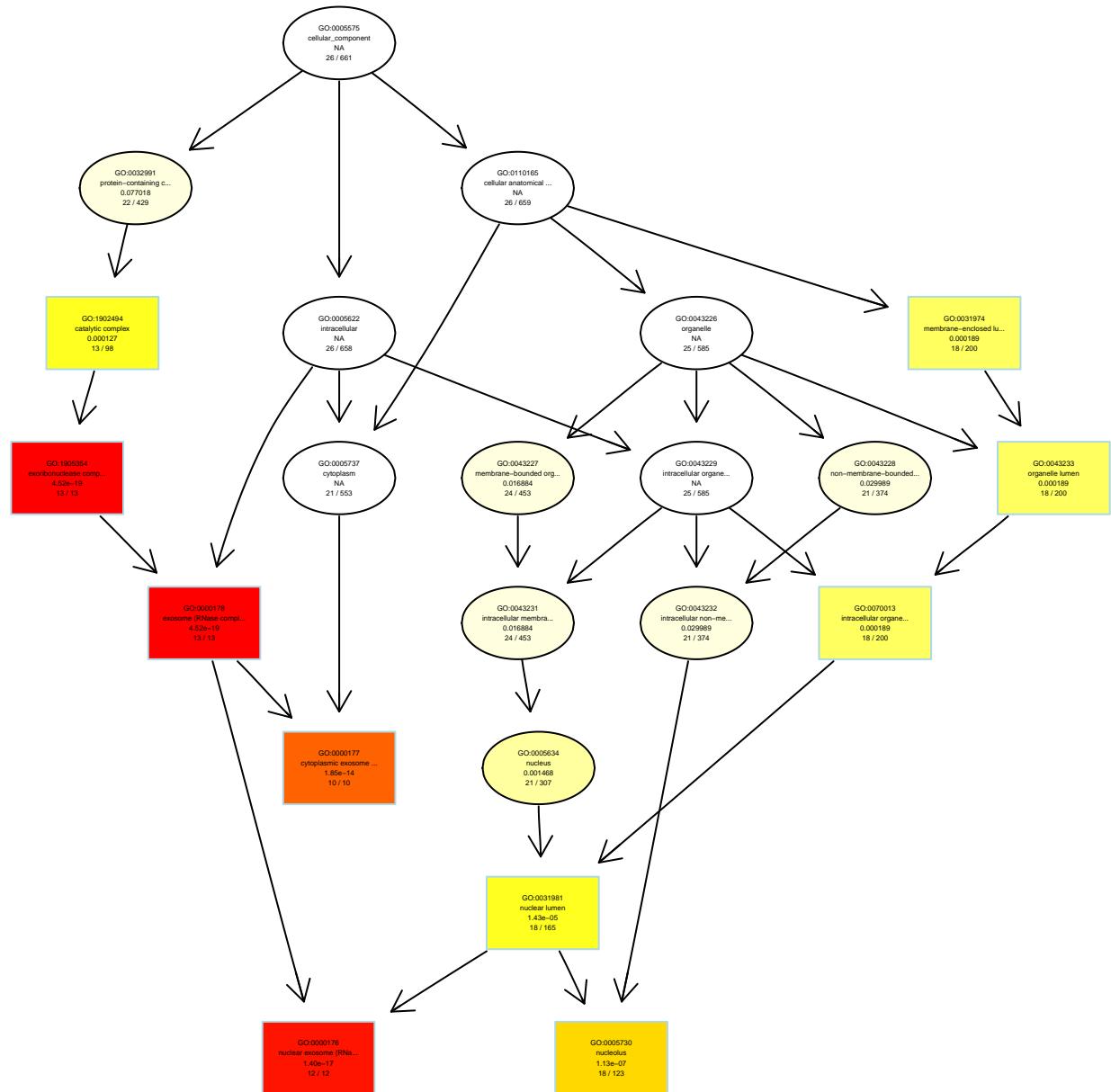


RRP40-TAP Up-regulated GO CC heatplot

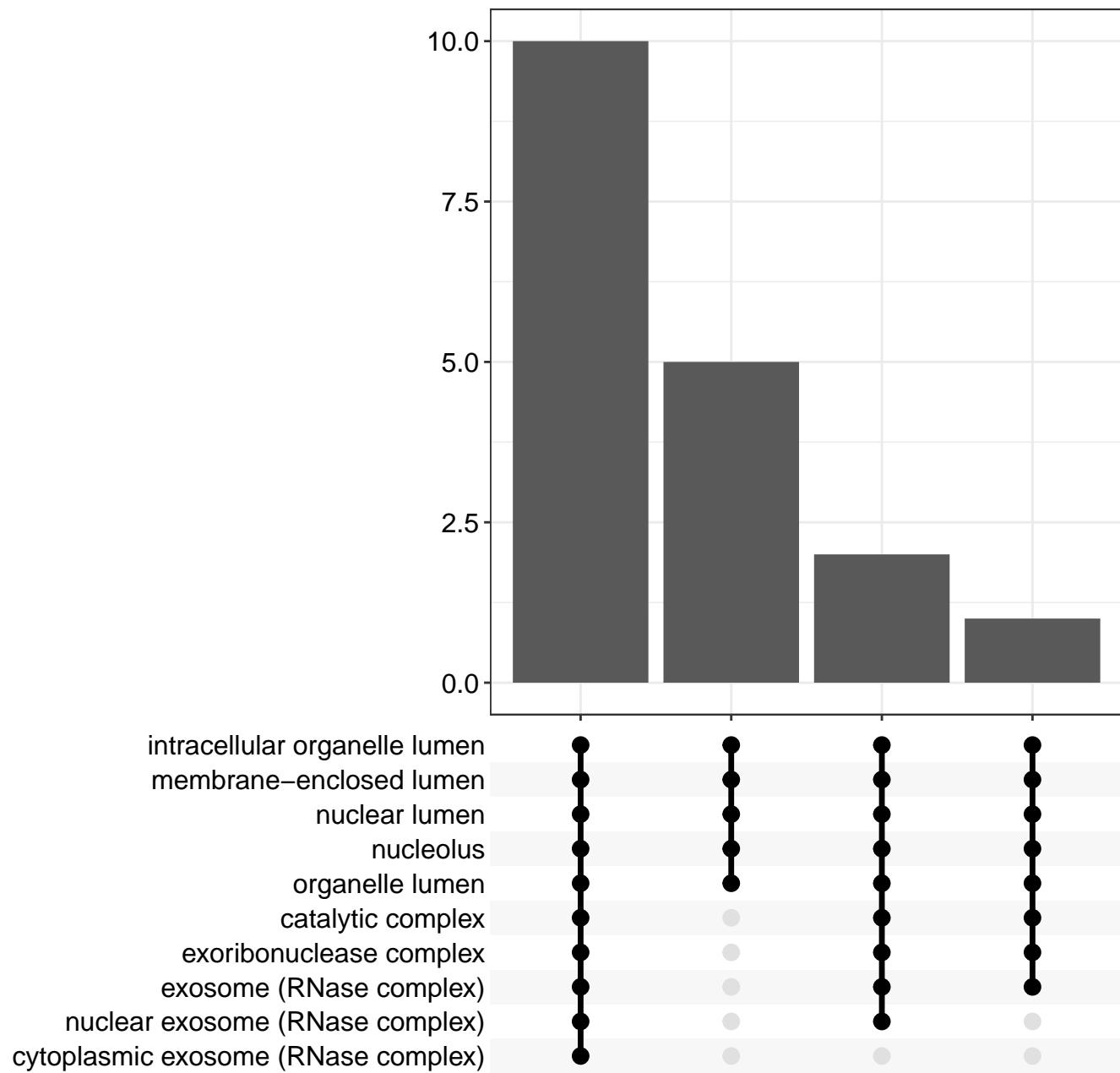


RRP40-TAP Up-regulated GO CC emapplot

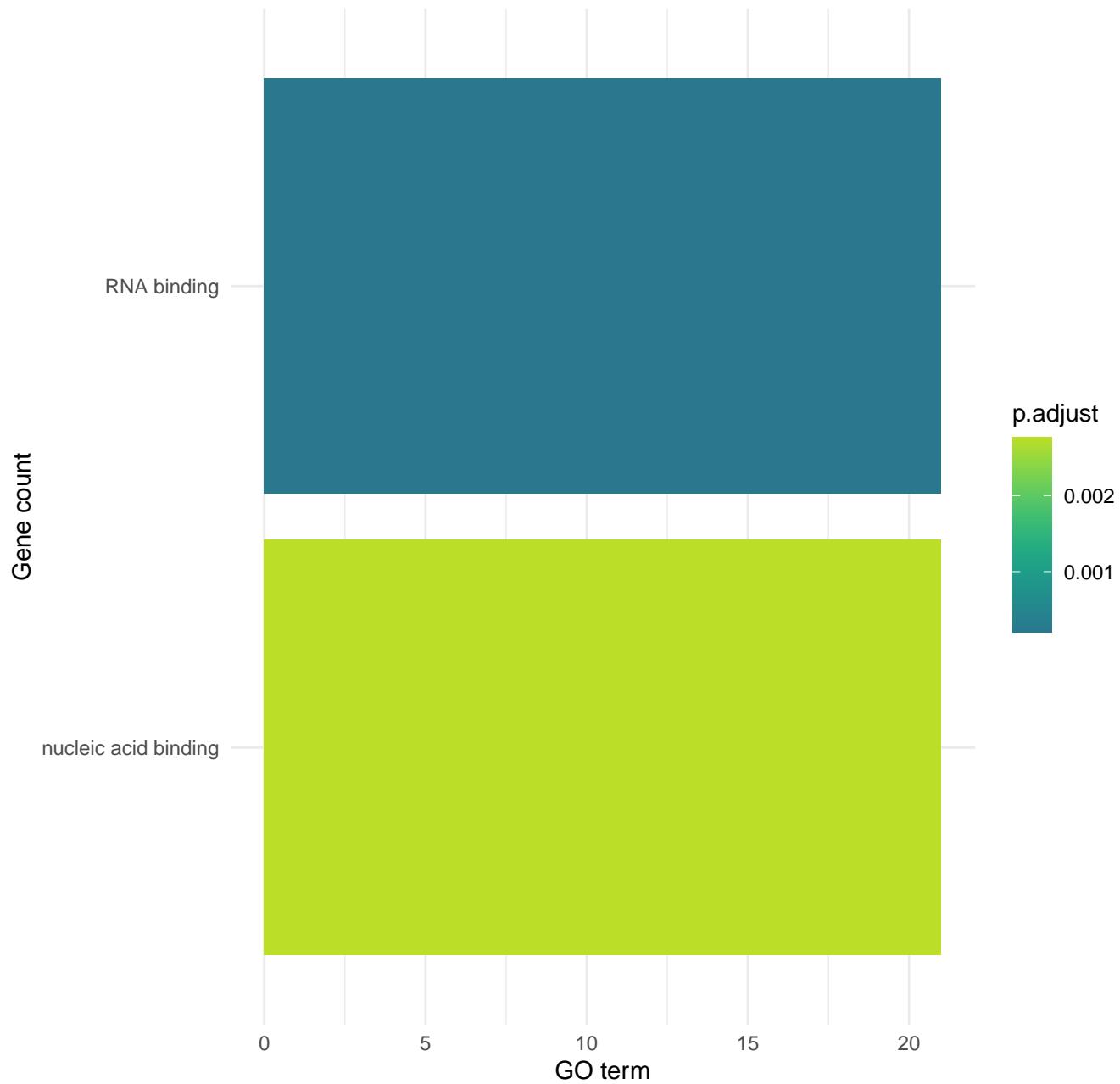




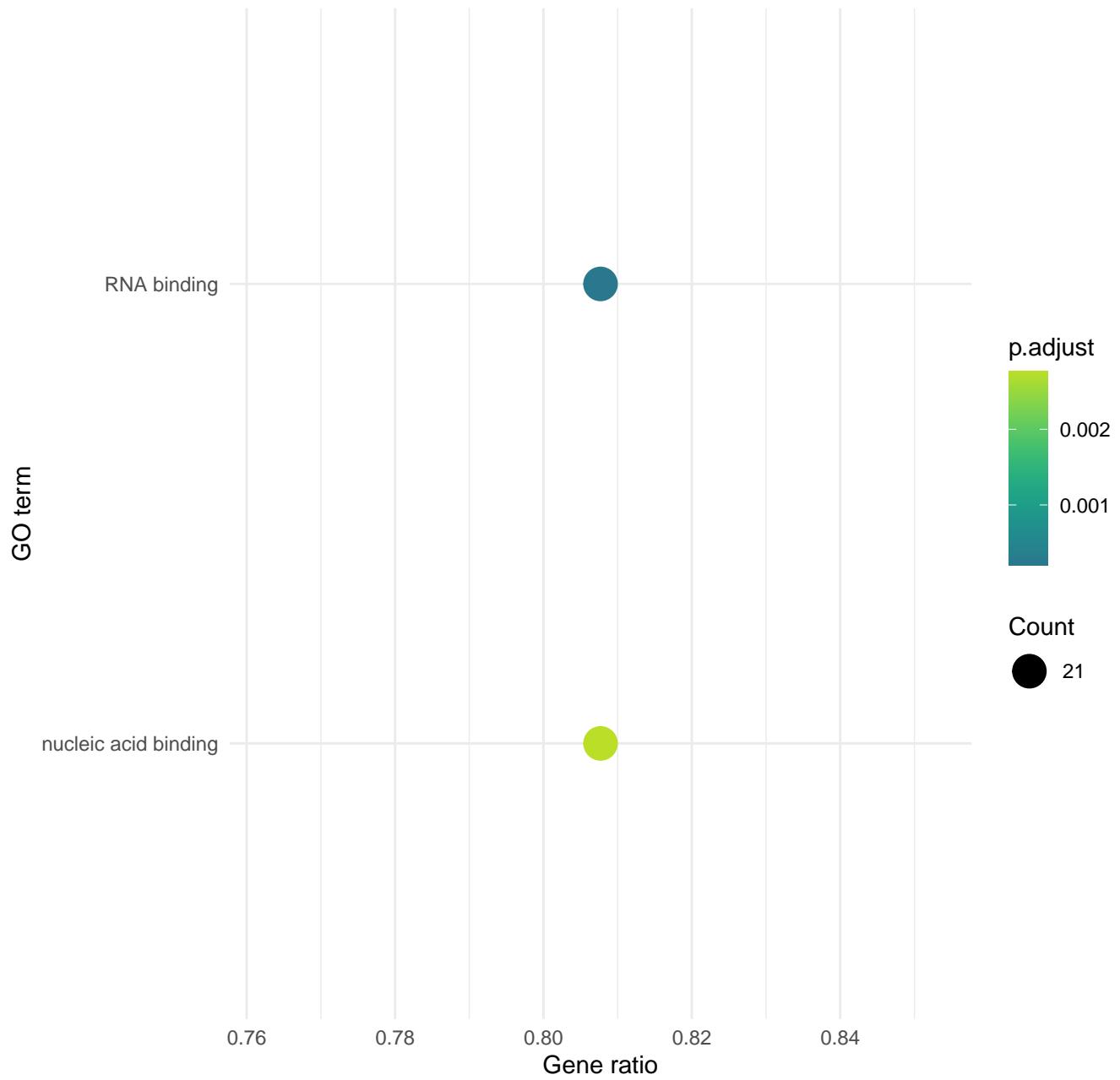
RRP40-TAP Up-regulated GO CC upsetplot



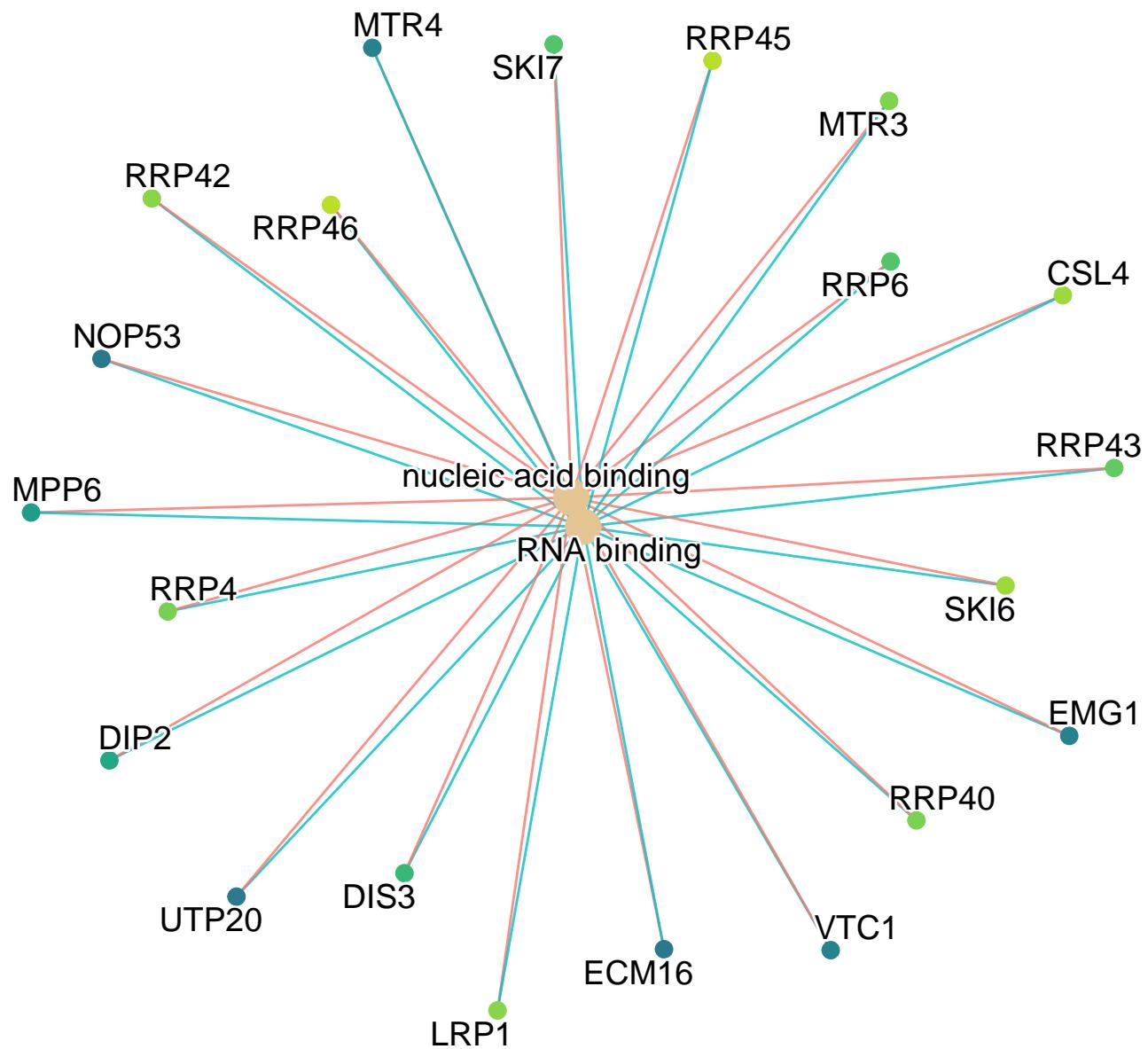
RRP40–TAP Up-regulated GO MF barplot



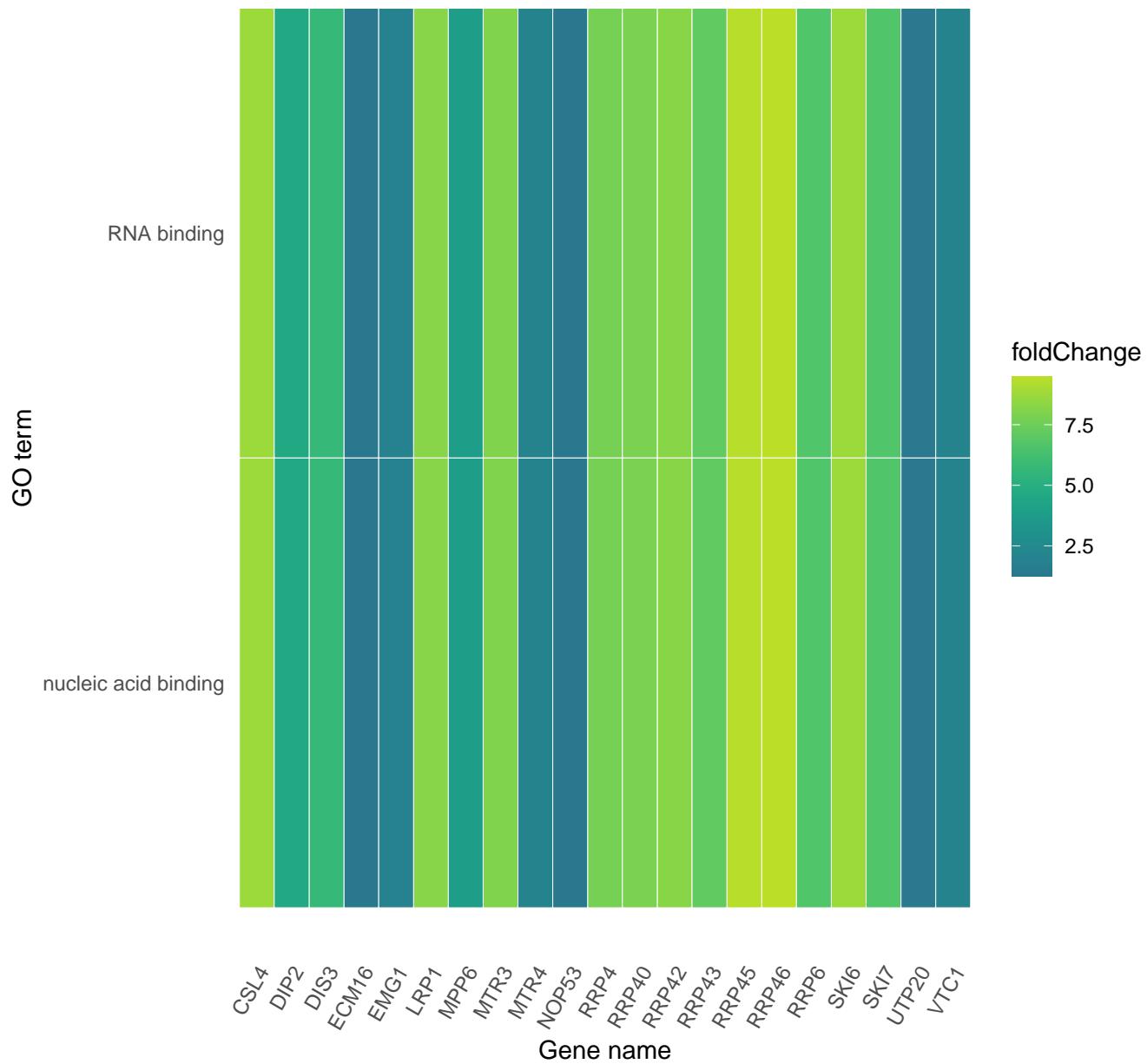
RRP40–TAP Up-regulated GO MF dotplot



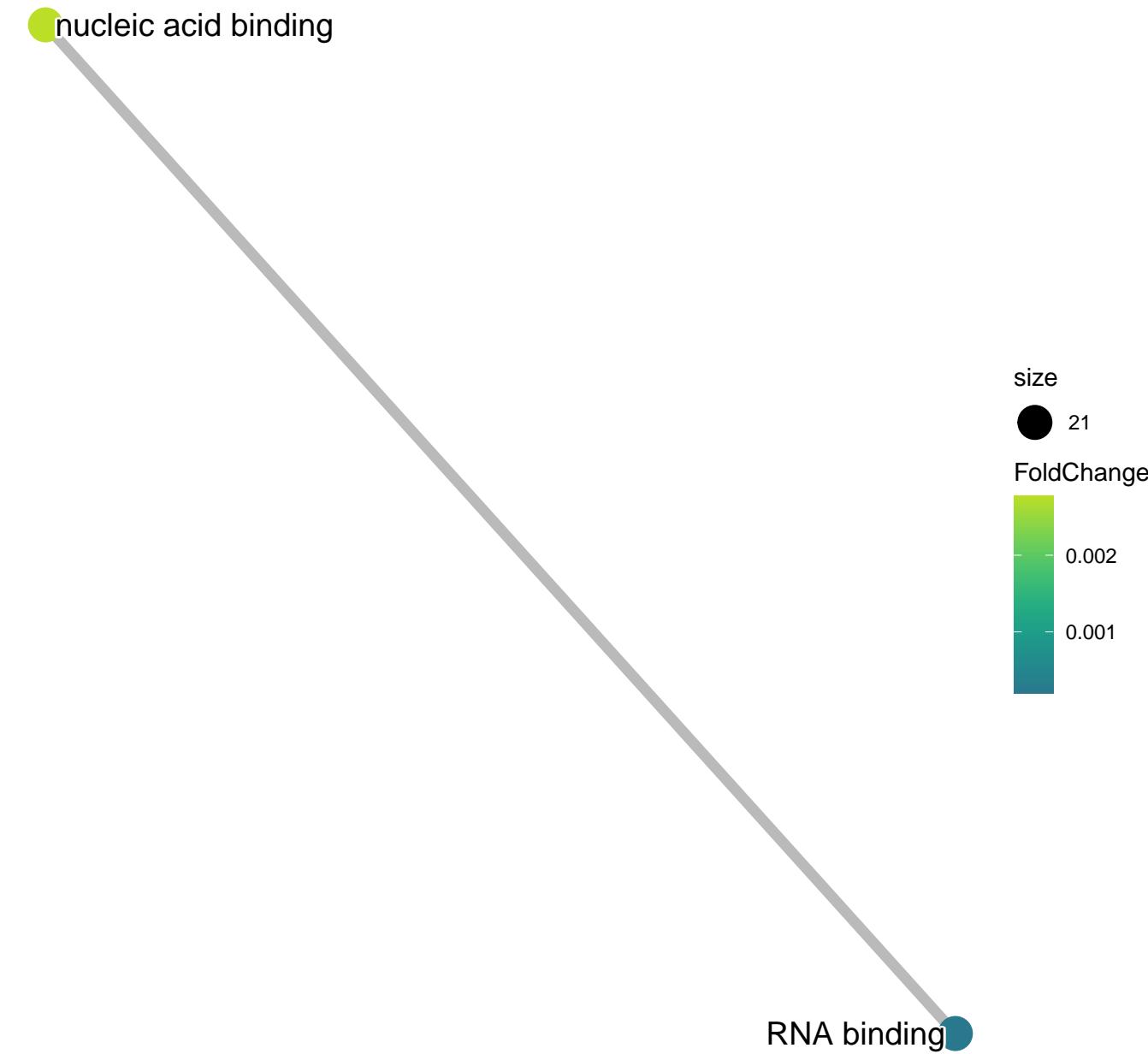
RRP40-TAP Up-regulated GO MF cnetplot

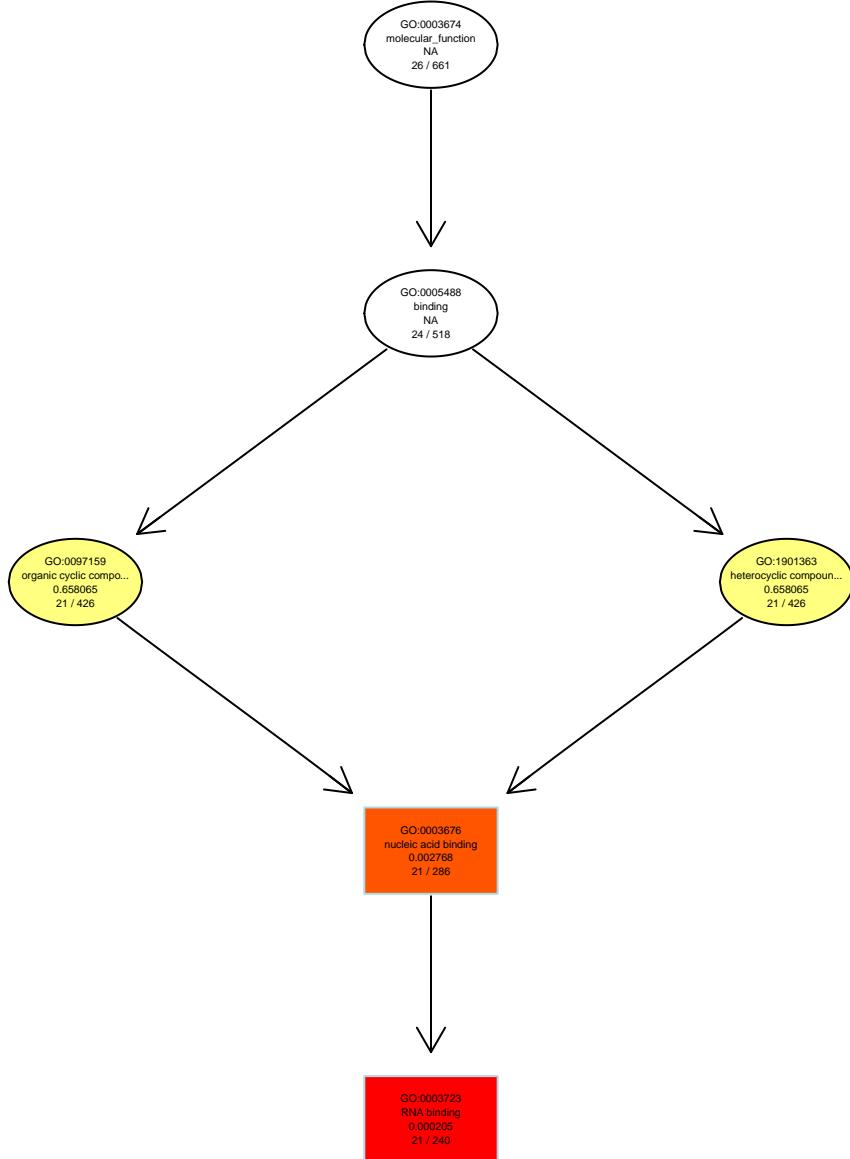


RRP40–TAP Up-regulated GO MF heatplot

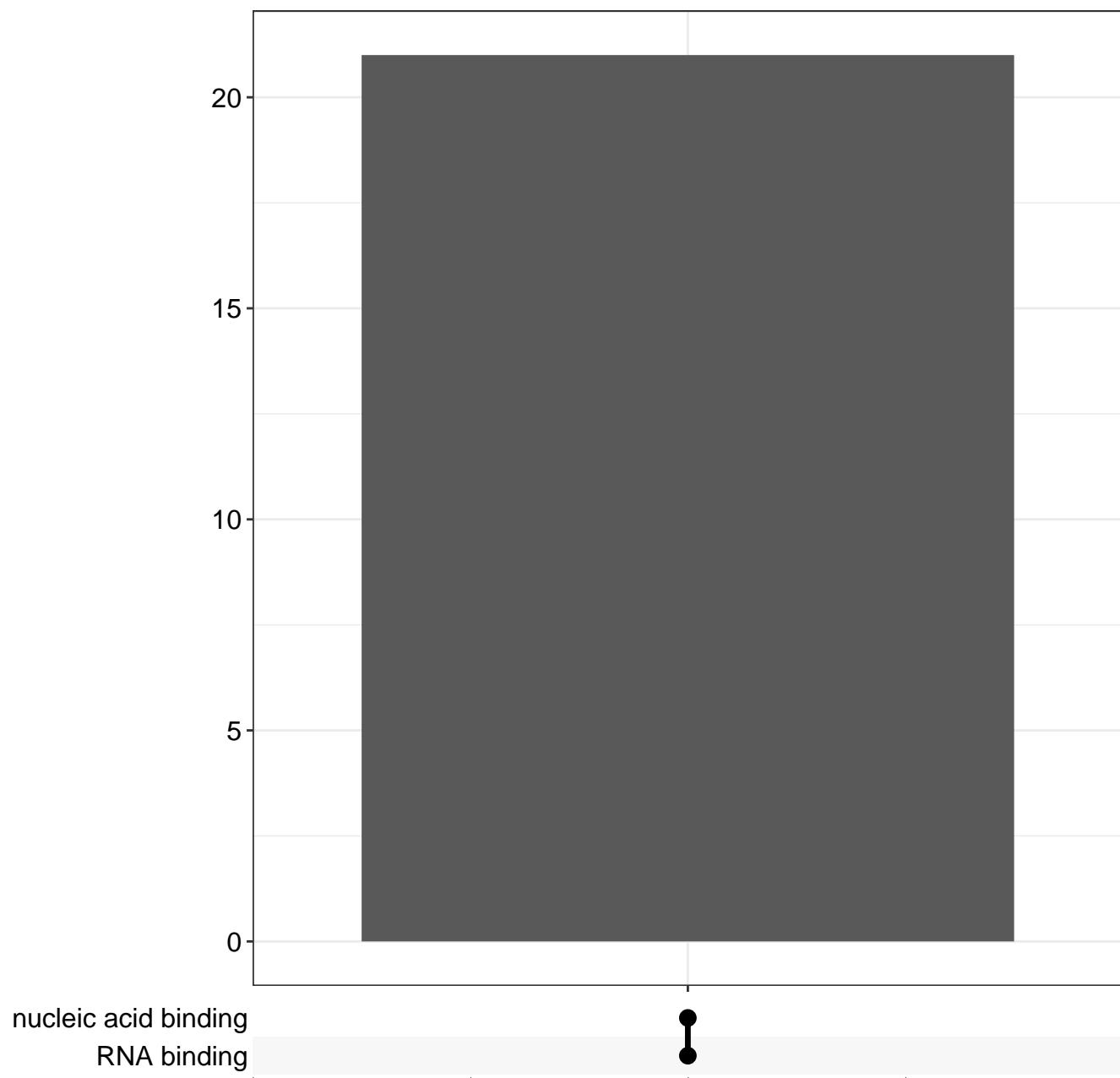


RRP40-TAP Up-regulated GO MF emapplot

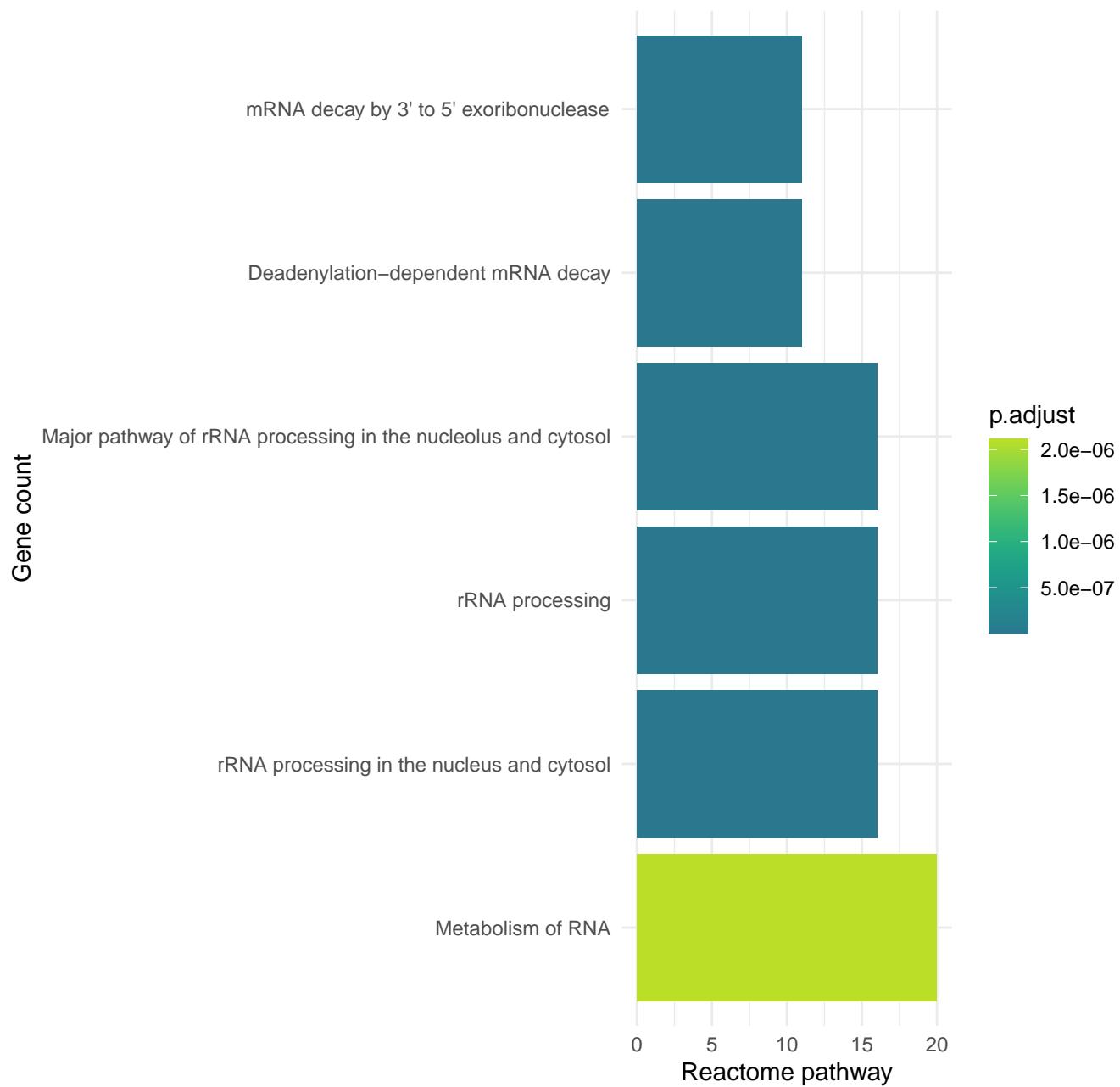




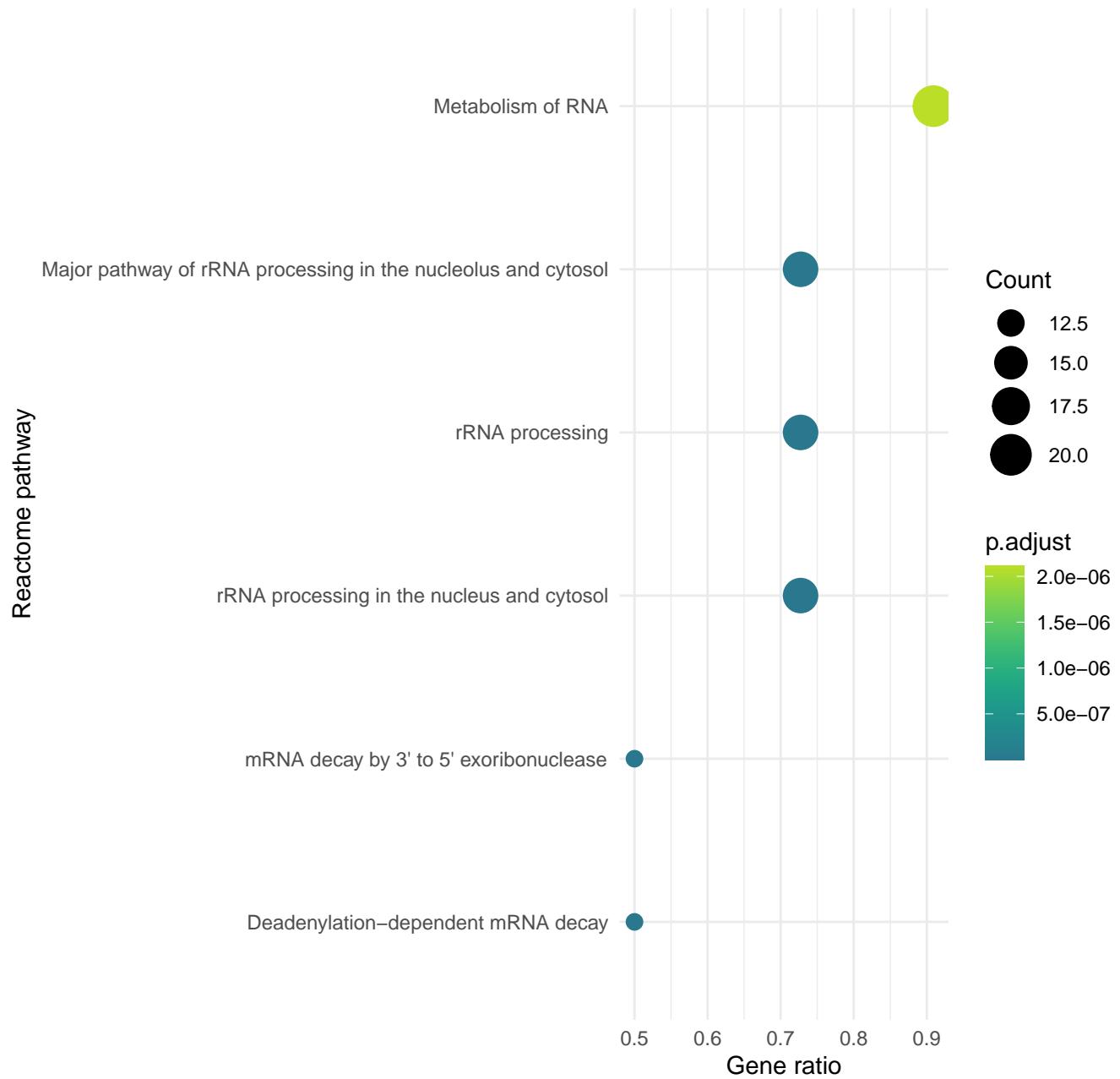
RRP40–TAP Up-regulated GO MF upsetplot



RRP40-TAP Up-regulated Reactome b

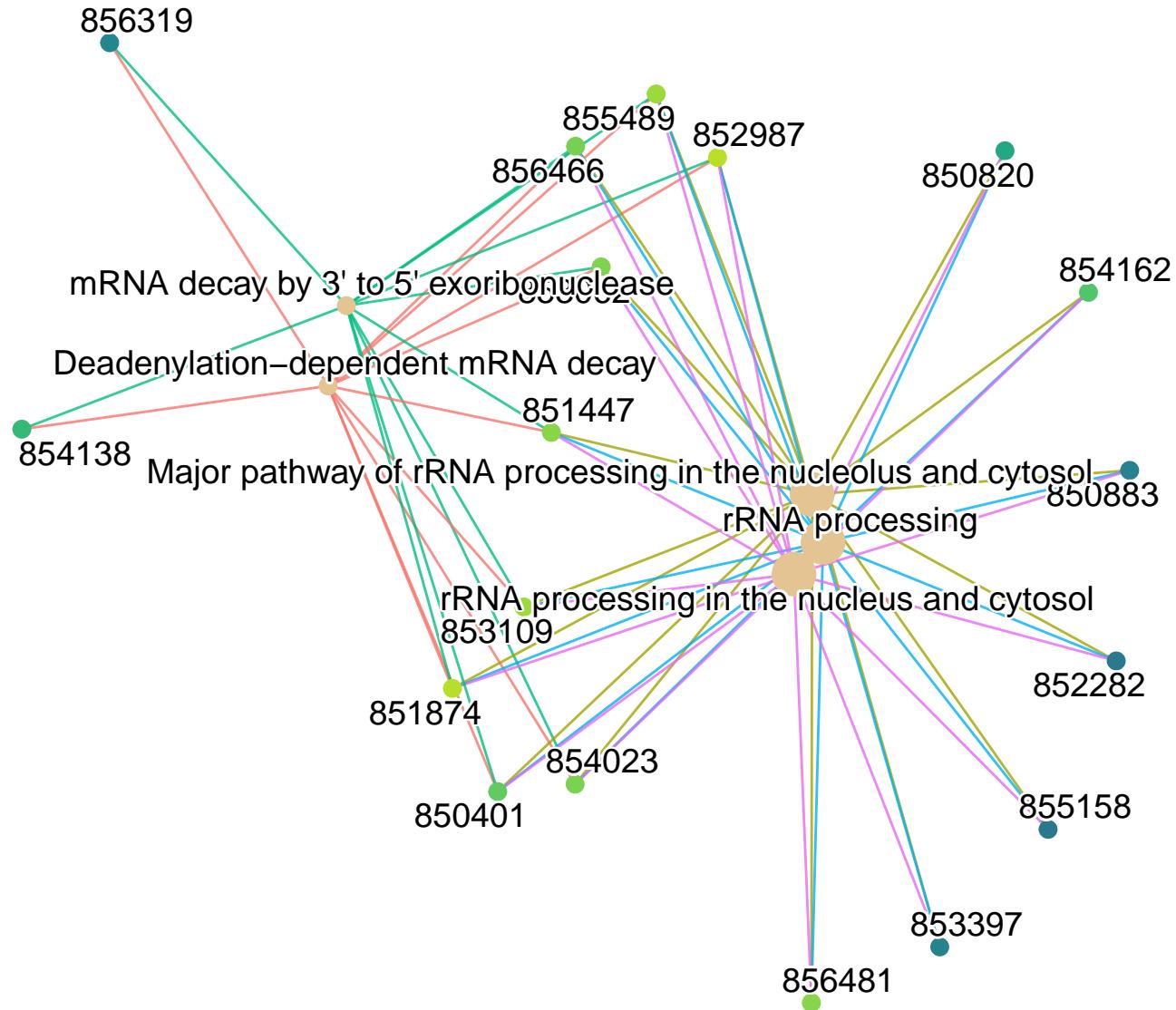


RRP40–TAP Up-regulated Reactome d



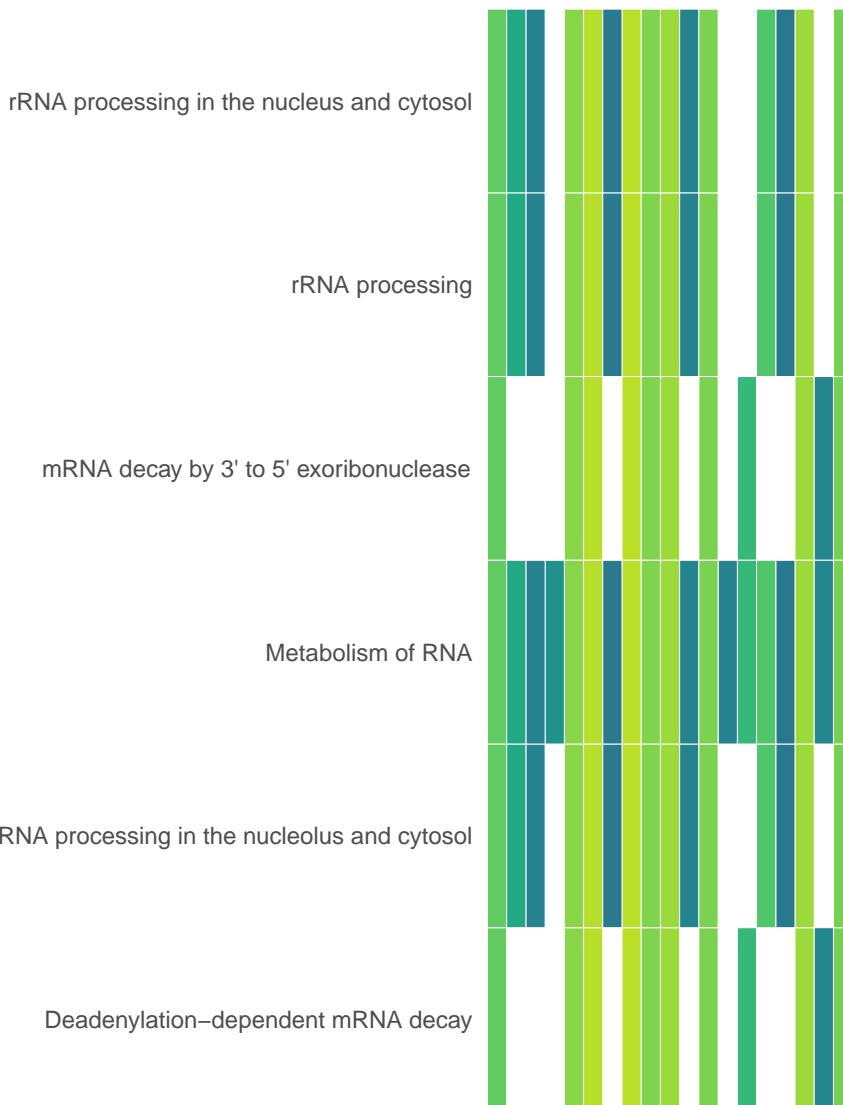
RRP40-TAP Up-regulated Reactome cnetplot

in the nucleolus and cytosol mRNA decay by 3' to 5' exoribonuclease rRNA processing rRNA processing in

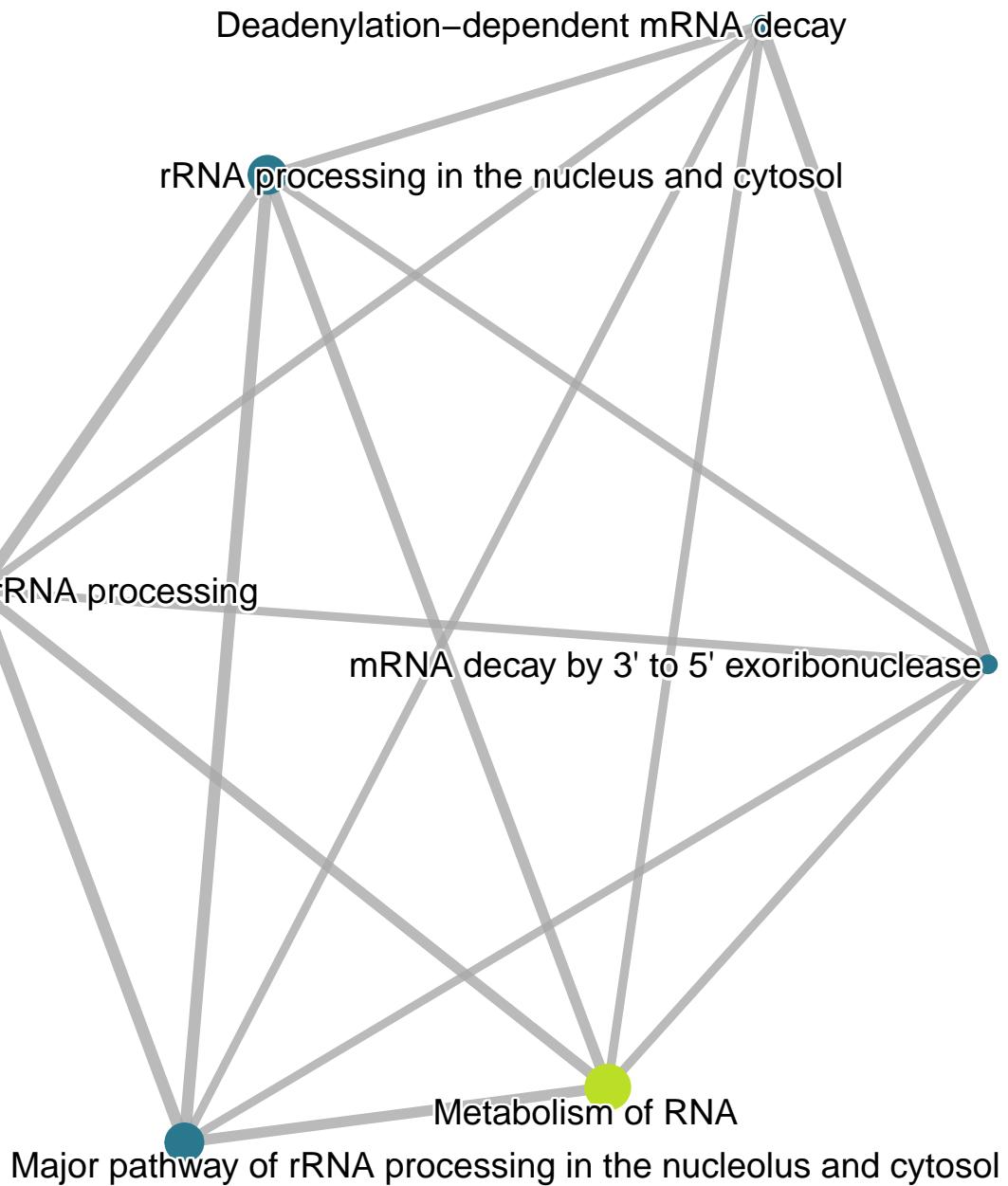


RRP40–TAP Up-regulated Reactome h

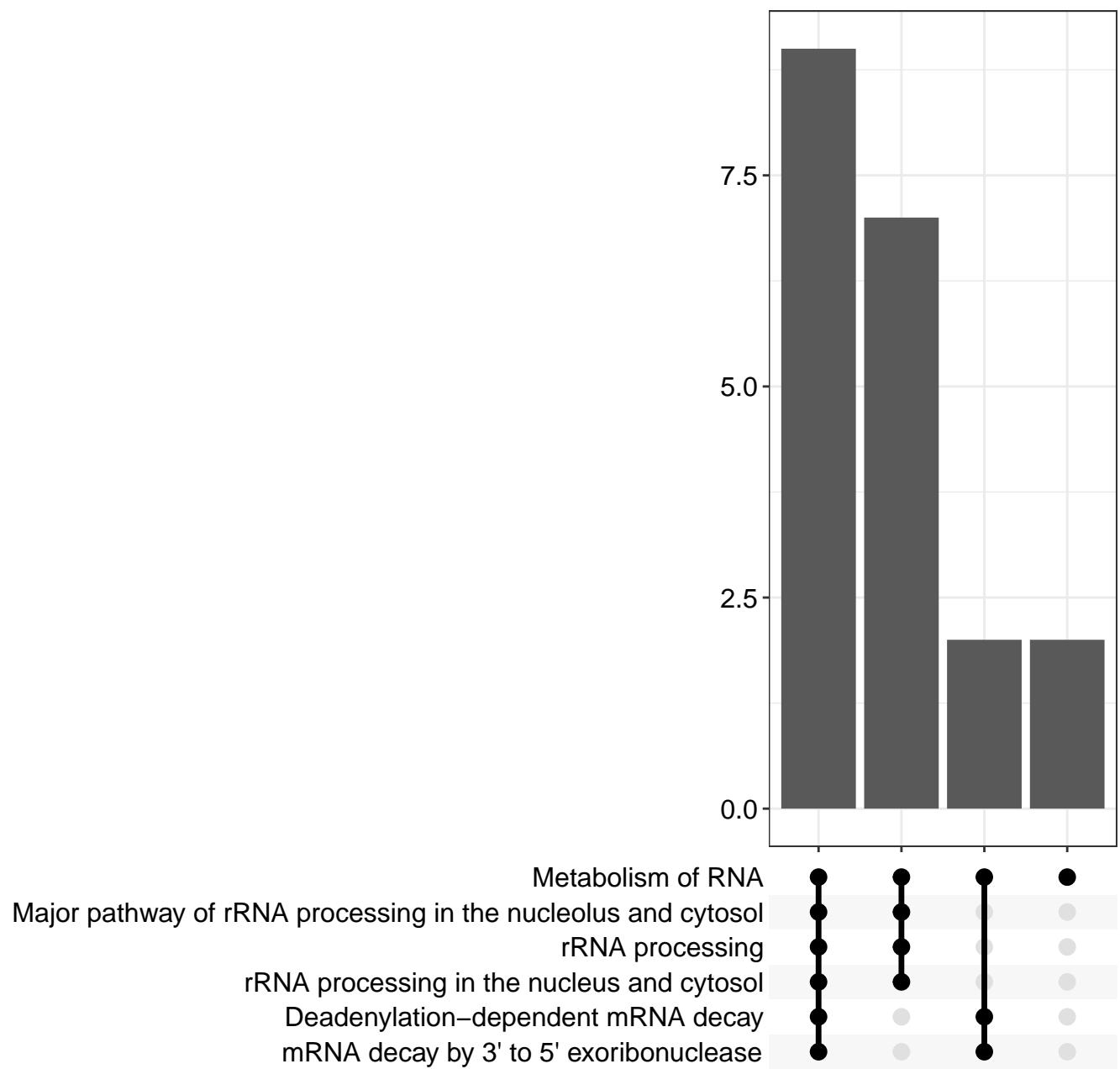
Reactome pathway



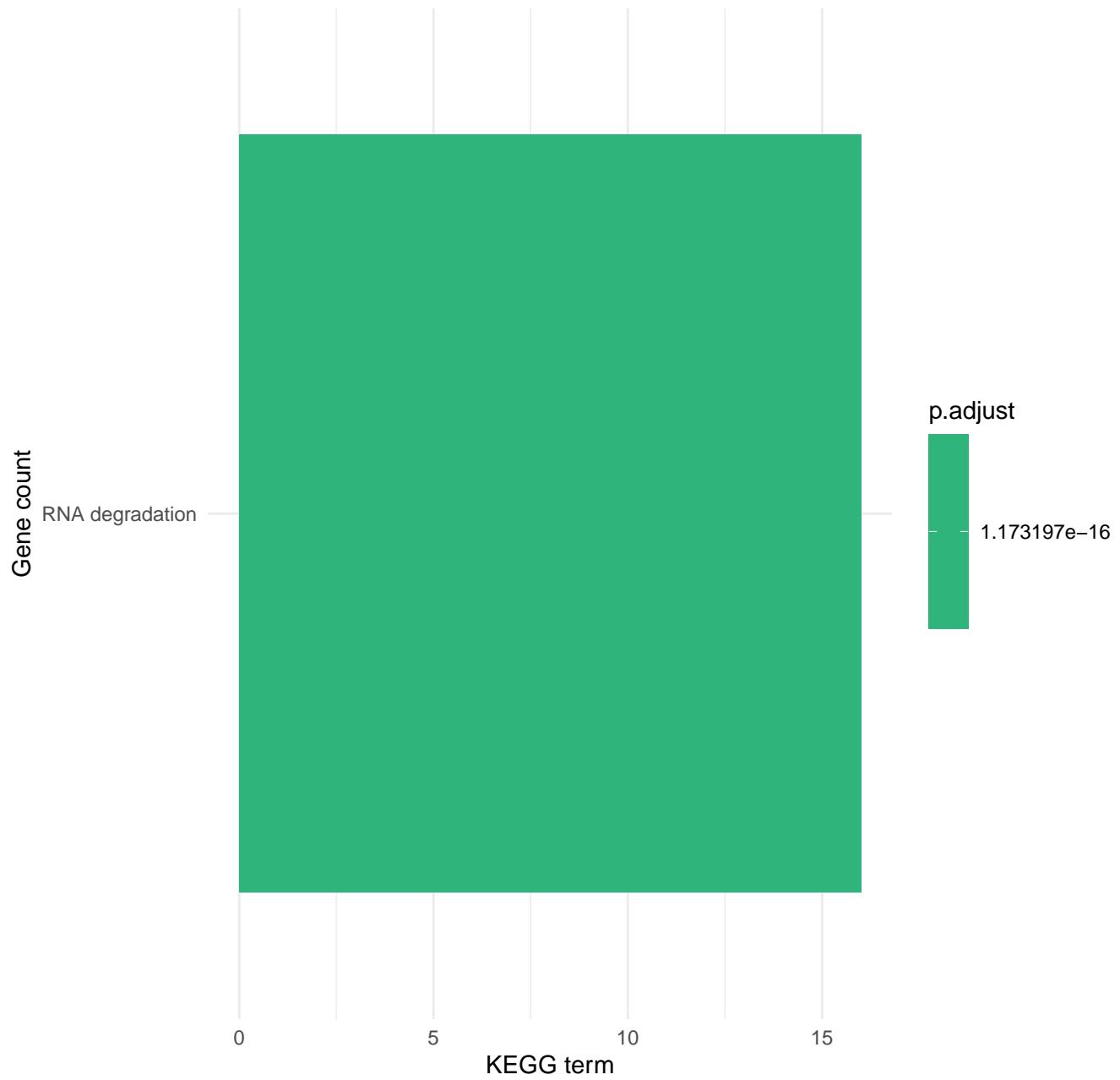
RRP40-TAP Up-regulated Reactome emapplot



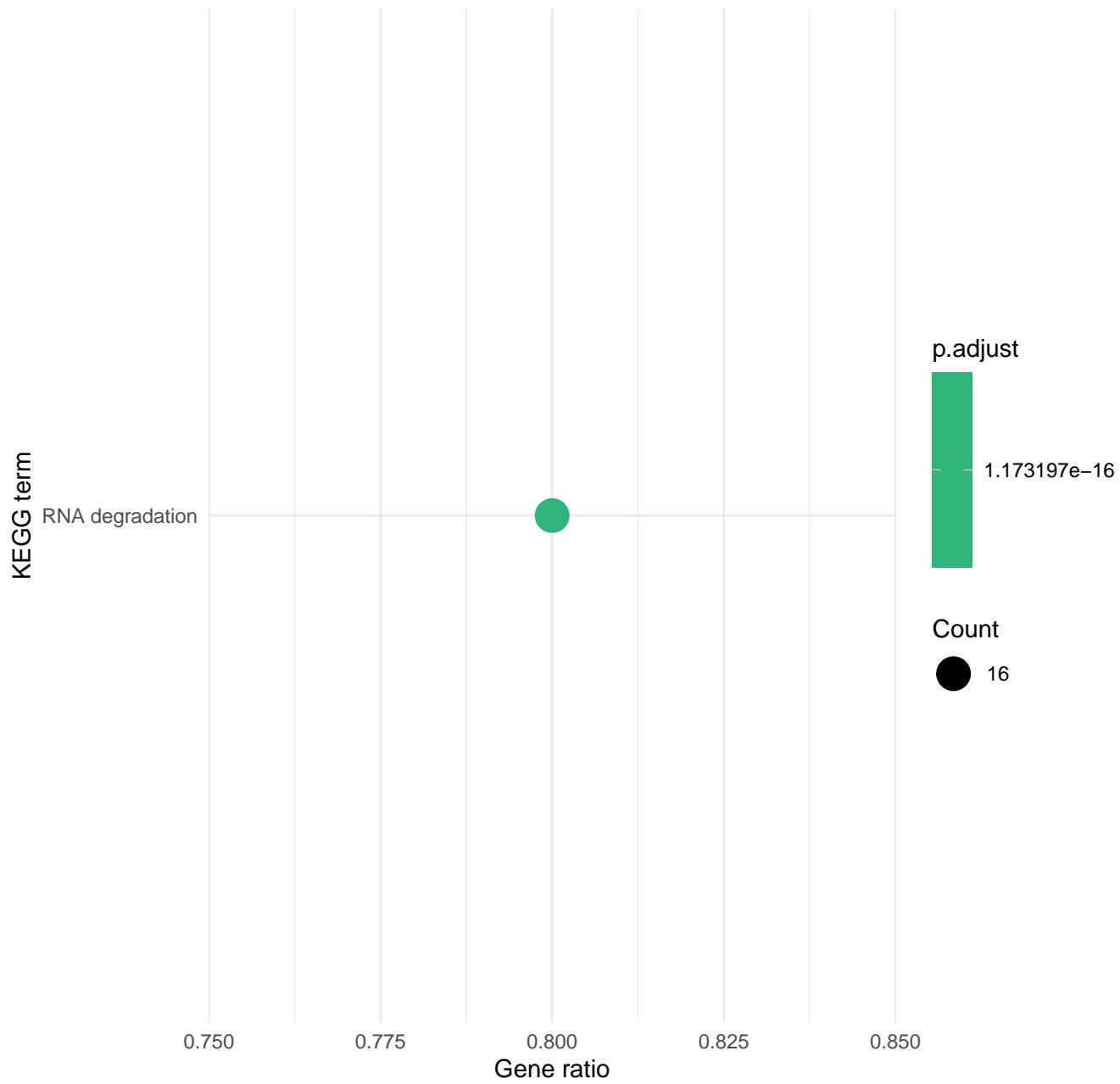
RRP40-TAP Up-regulated



RRP40–TAP Up-regulated KEGG barplot



RRP40-TAP Up-regulated KEGG dotplot



RRP40-TAP Up-regulated KEGG dotplot

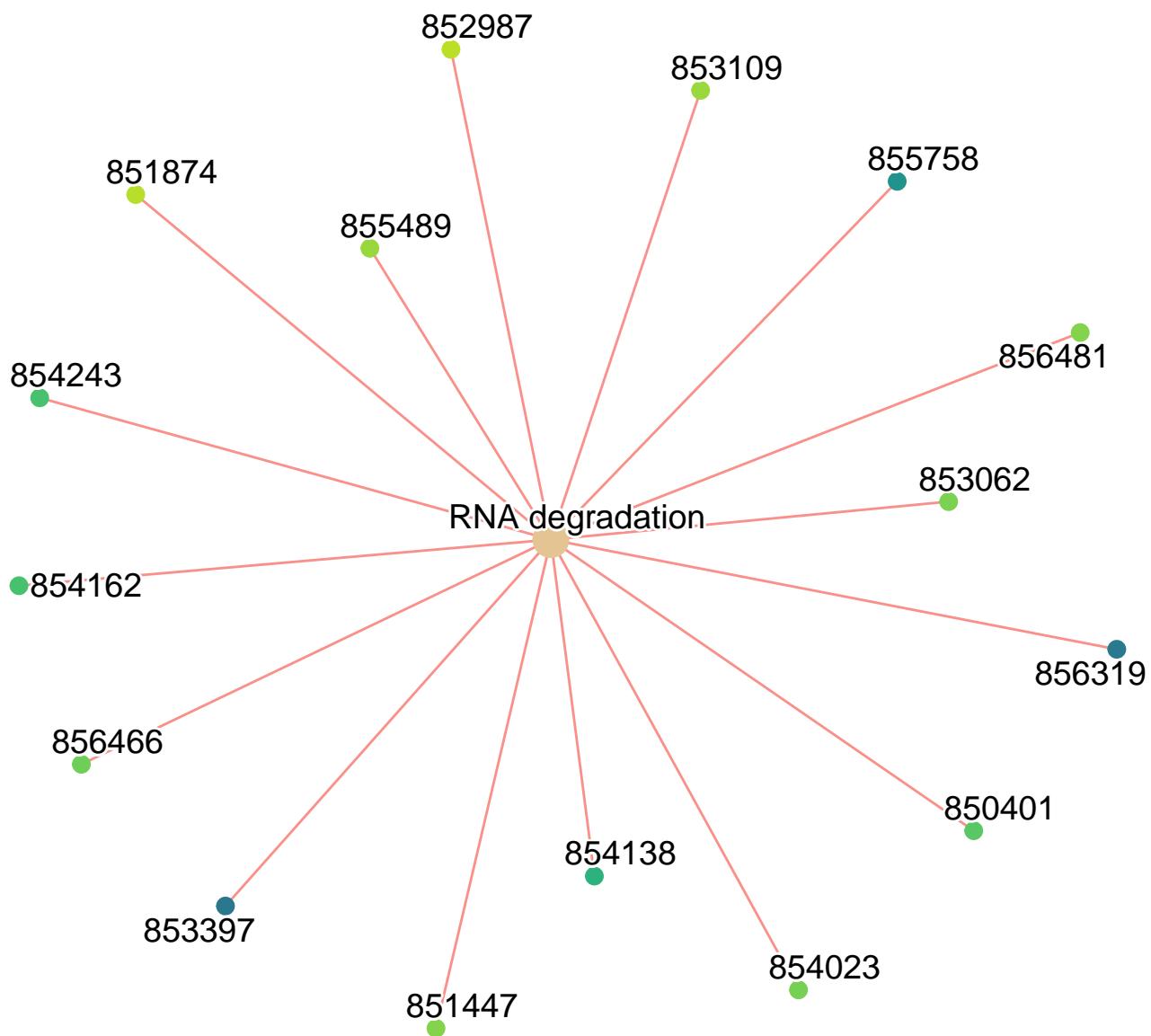
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RNA degradation

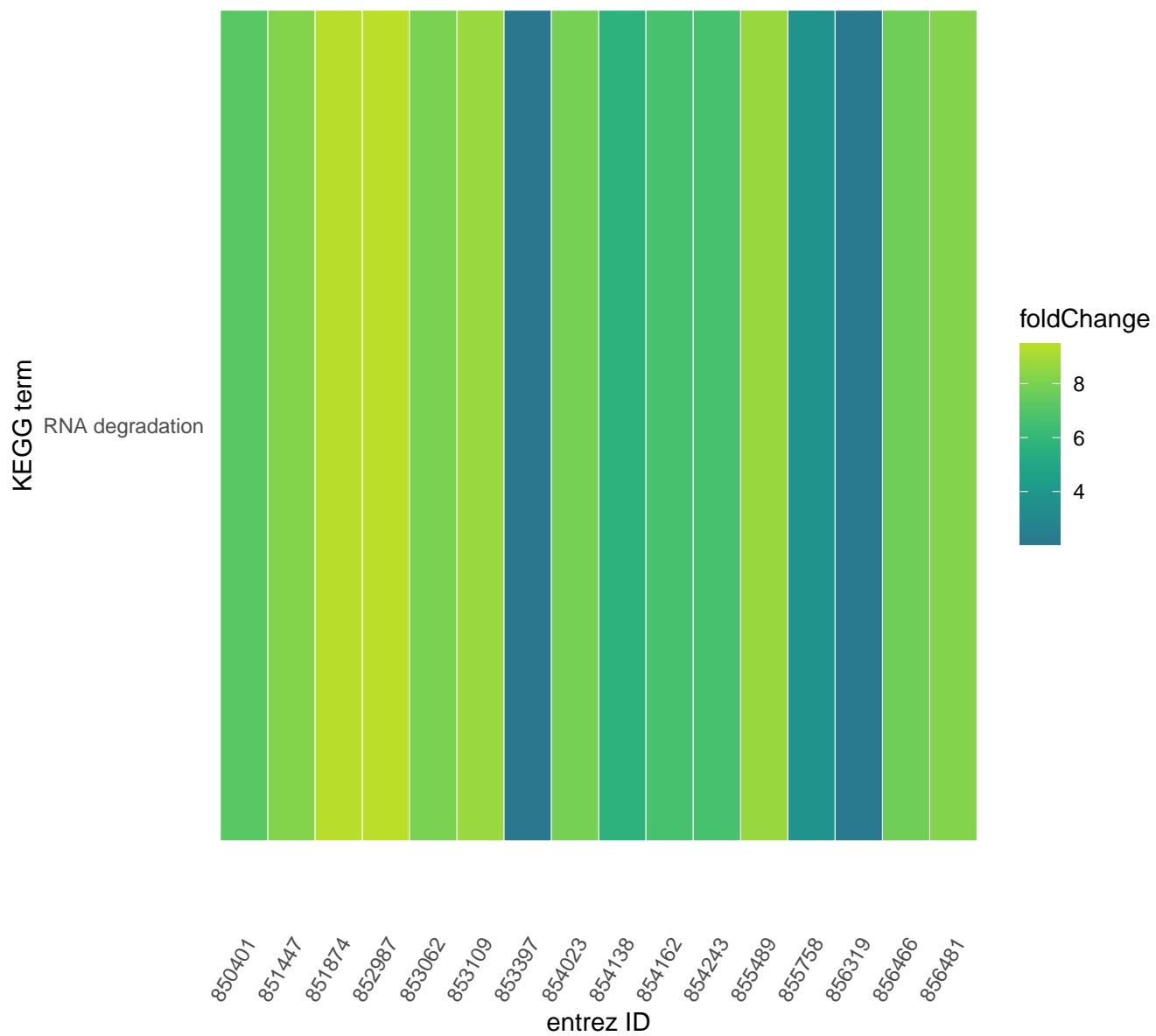
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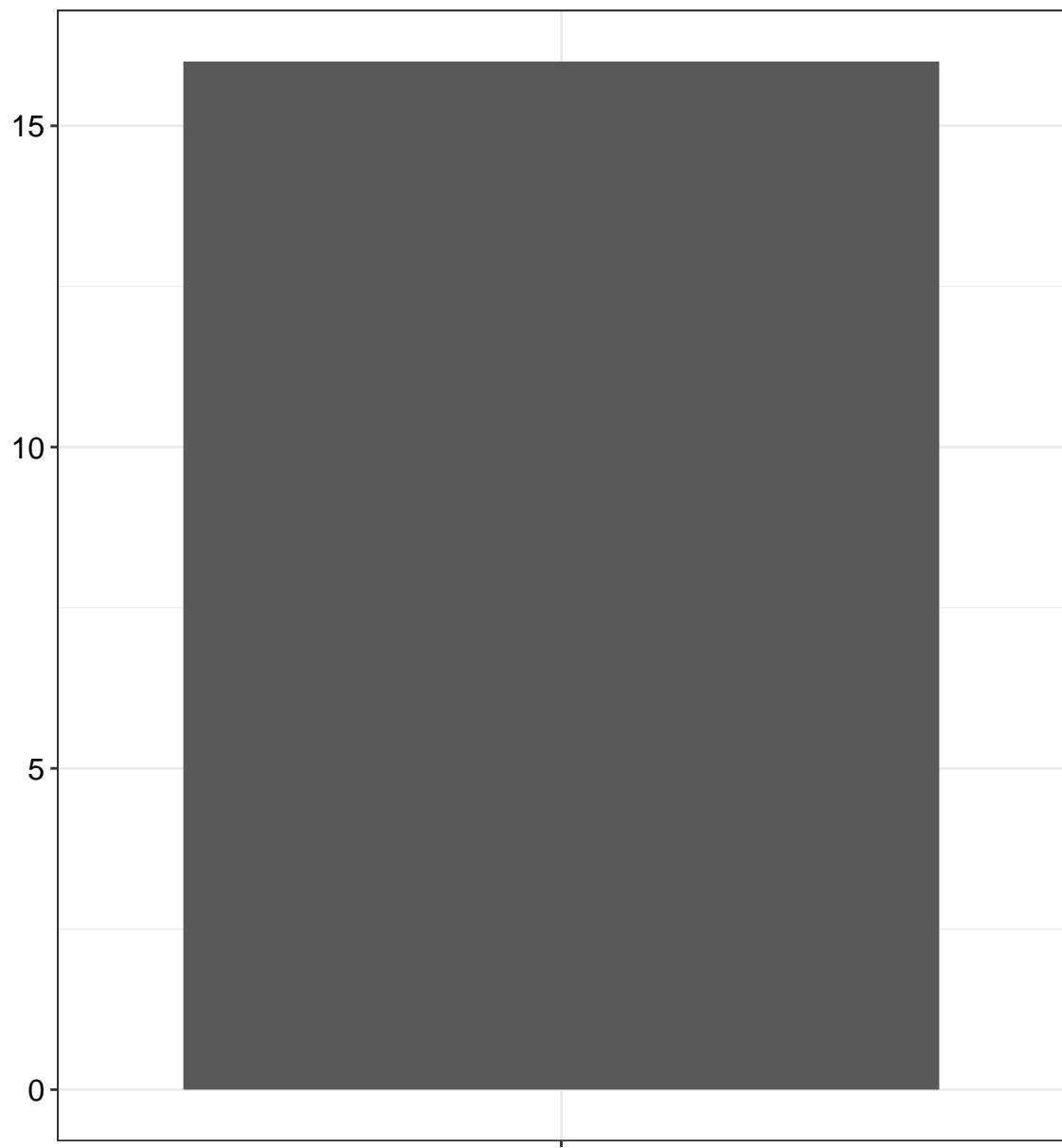
FoldChange



RRP40-TAP Up-regulated KEGG heatplot



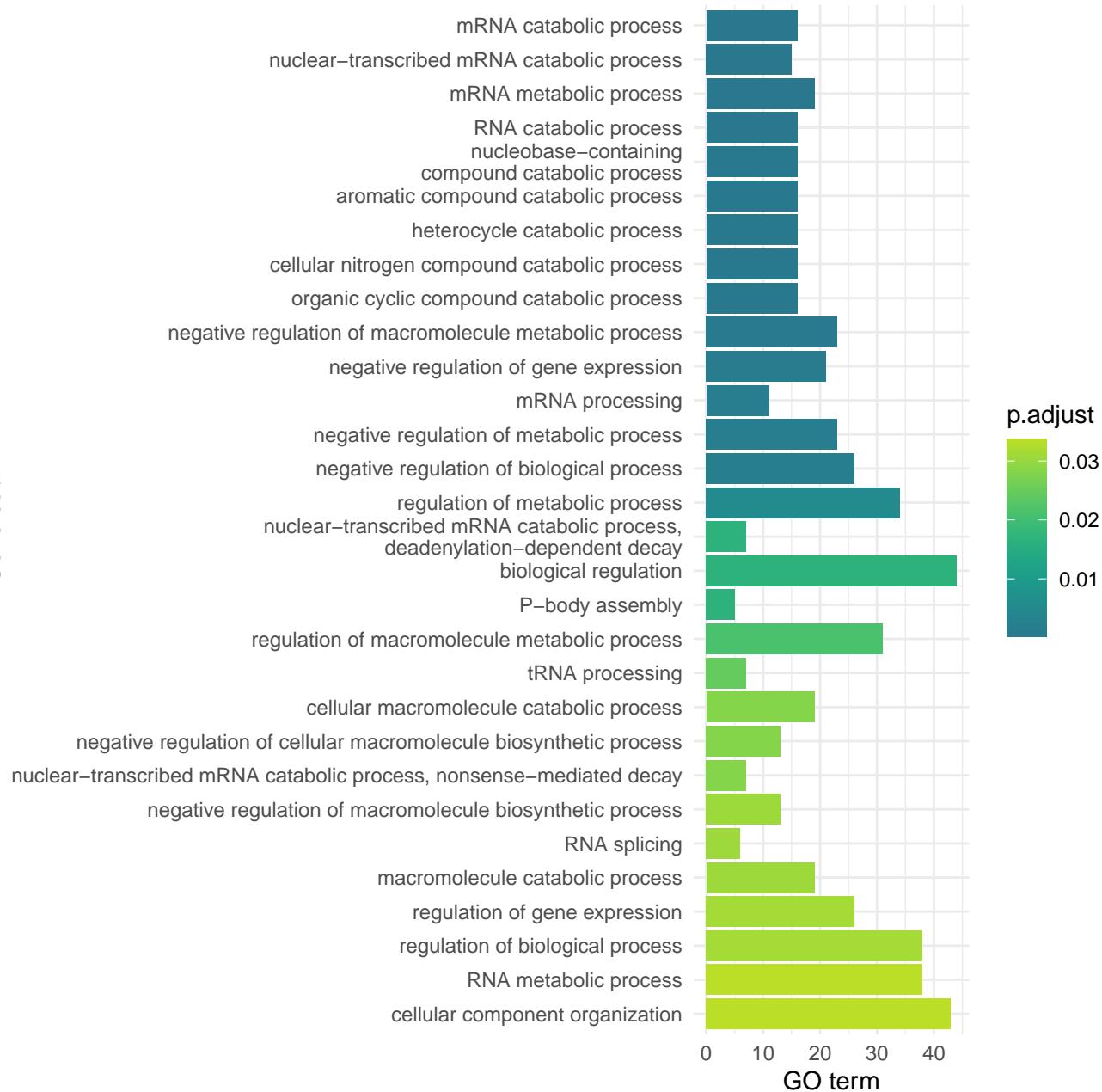
RRP40–TAP Up-regulated KEGG upsetplot



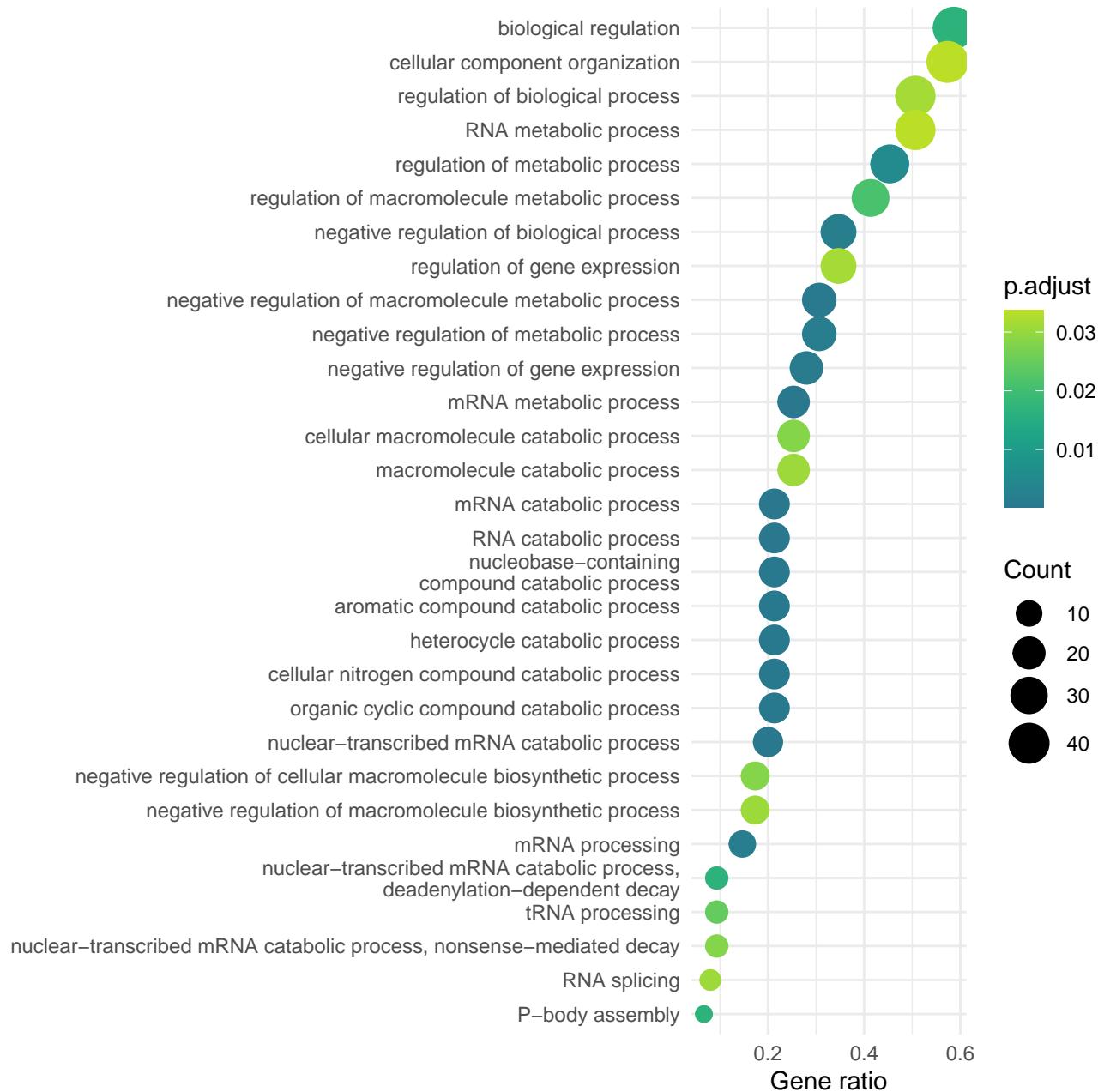
RNA degradation



DHH1-TAP Up-regulated GO BP



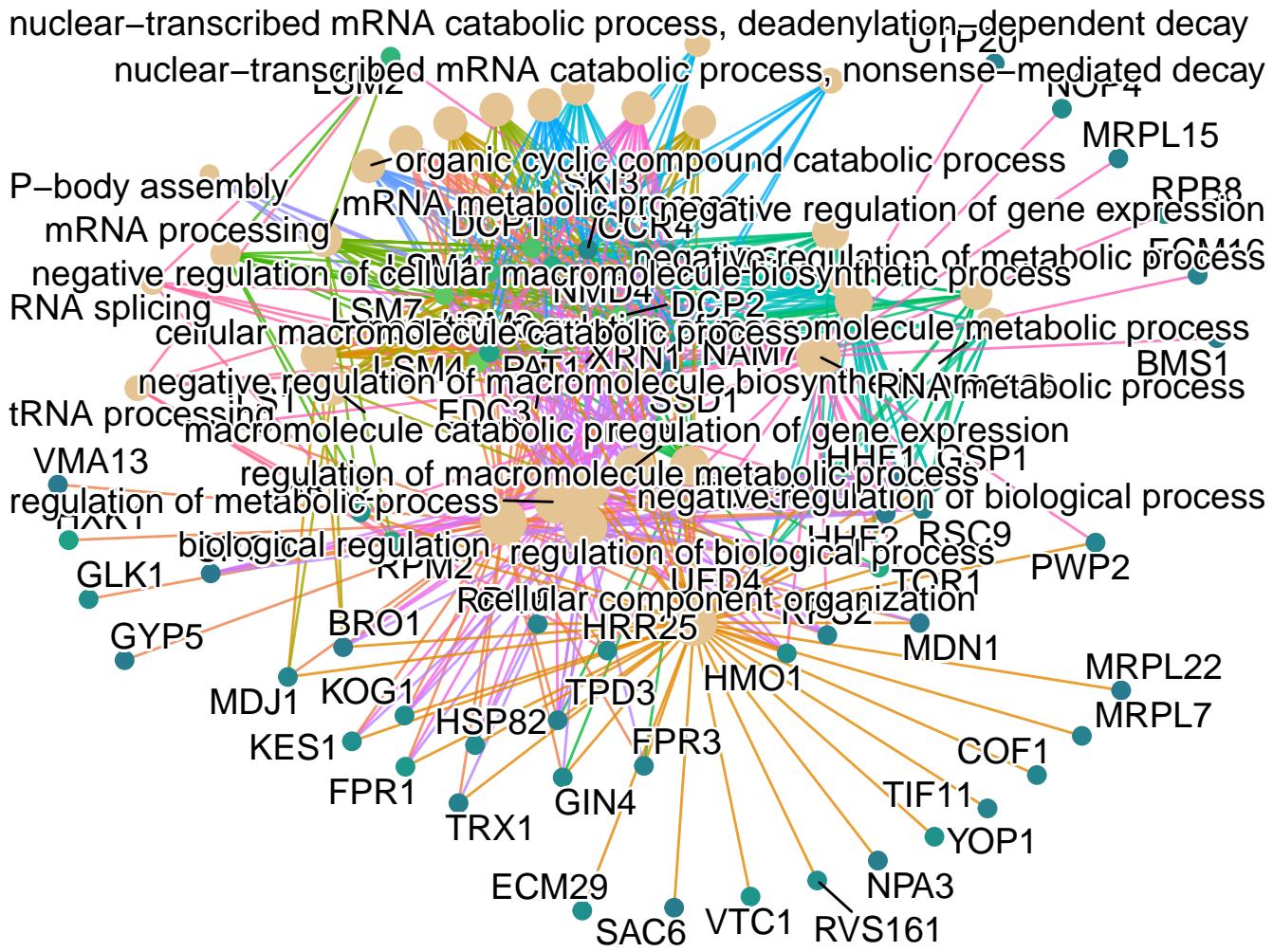
DHH1-TAP Up-regulated GO BP



DHH1-TAP Up-regulated GO BP cnetplot

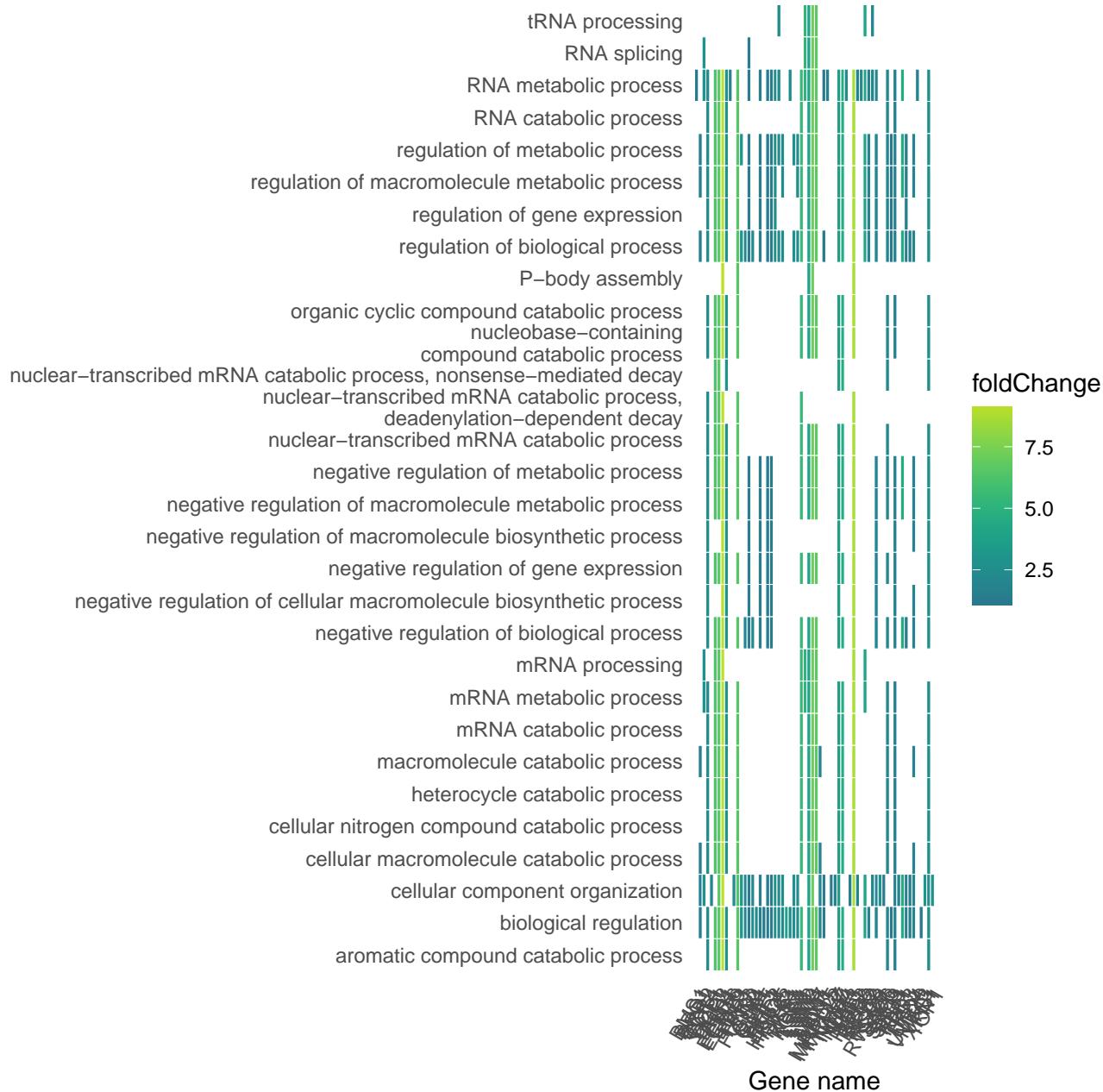
tion of gene expression
tion of macromolecule biosynthetic process
tion of macromolecule metabolic process
tion of metabolic process
cribed mRNA catabolic process
cribed mRNA catabolic process, deadenylation-dependent decay

- nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
- nucleobase-containing compound catabolic process
- organic cyclic compound catabolic process
- P-body assembly
- regulation of biological process
- regulation of gene expression

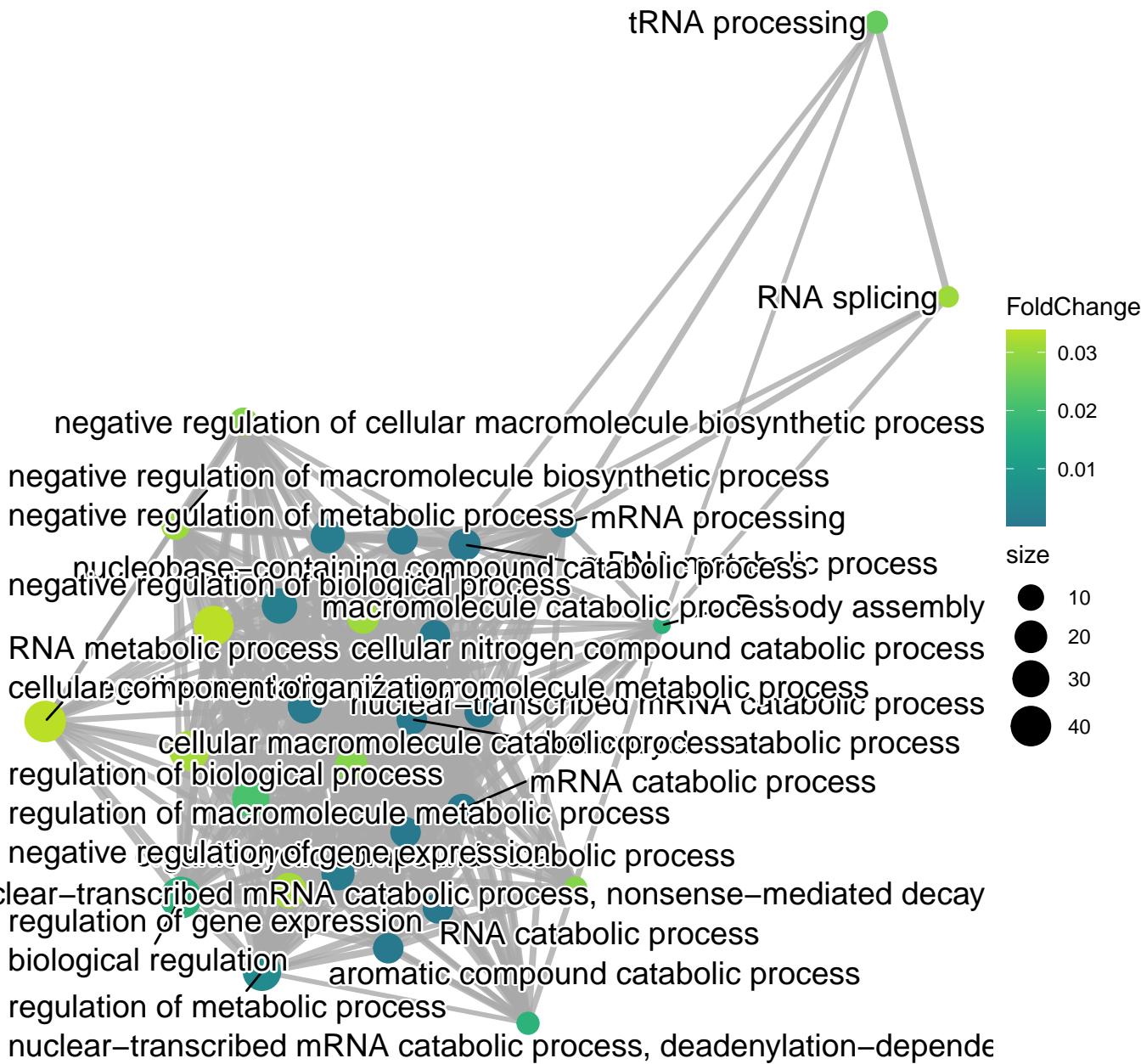


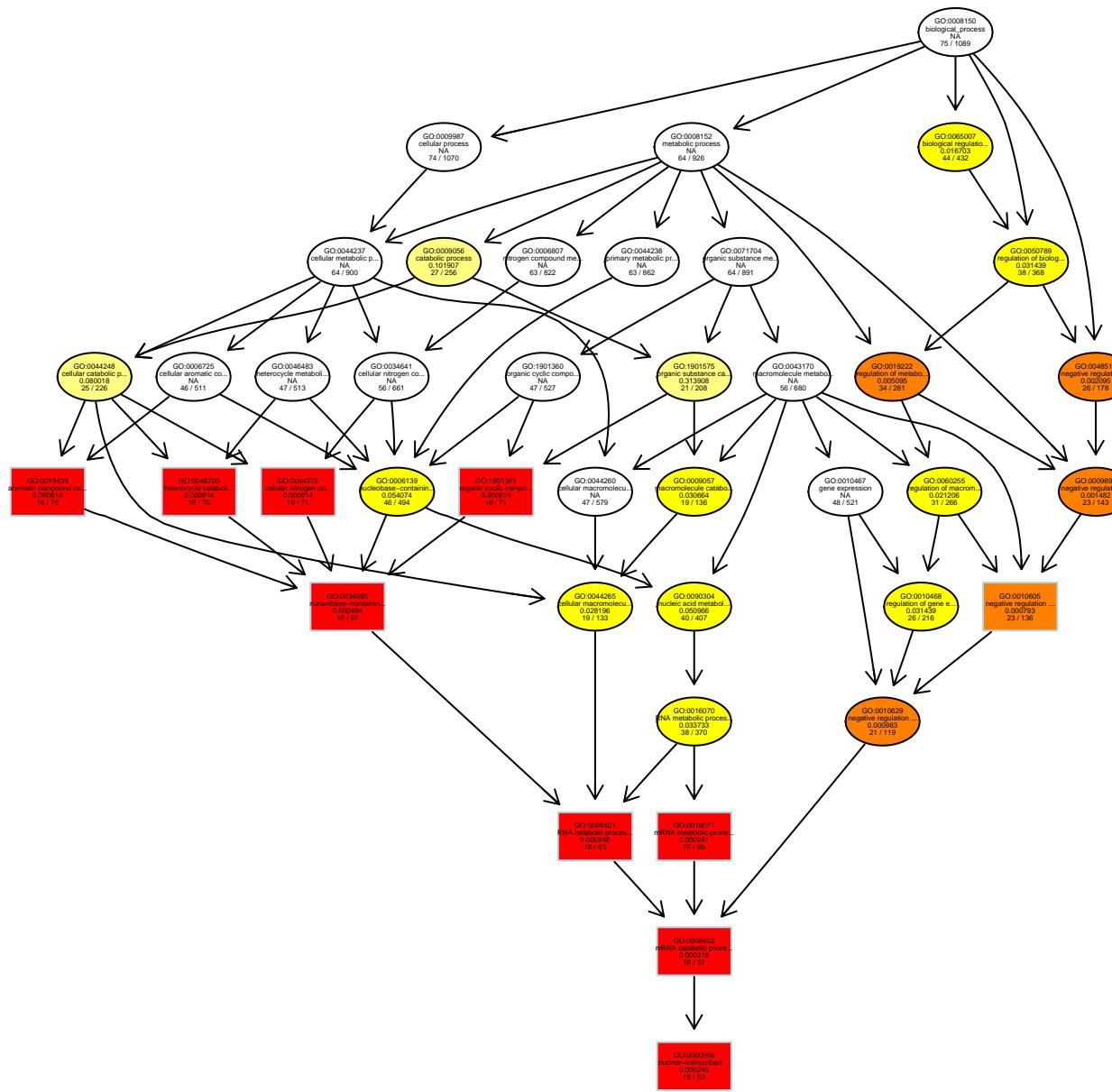
DHH1-TAP Up-regulated GO BP

GO term

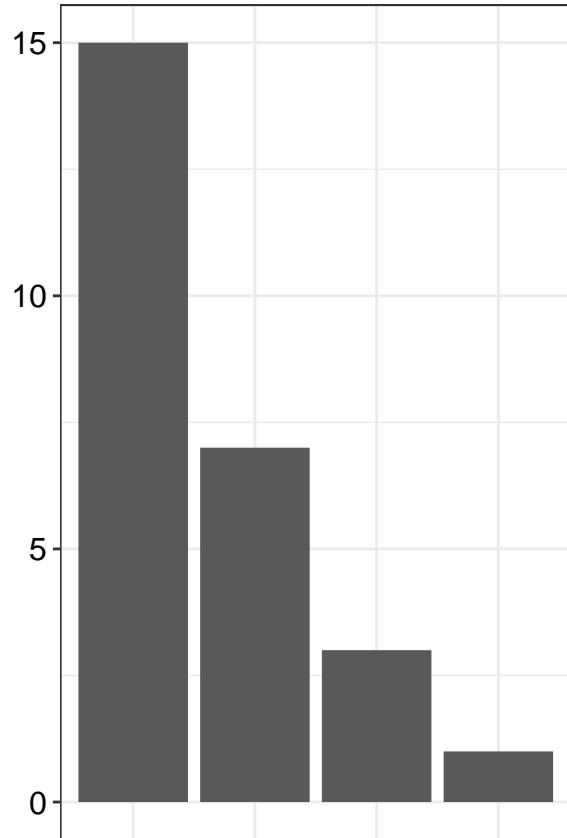


DHH1-TAP Up-regulated GO BP emapplot



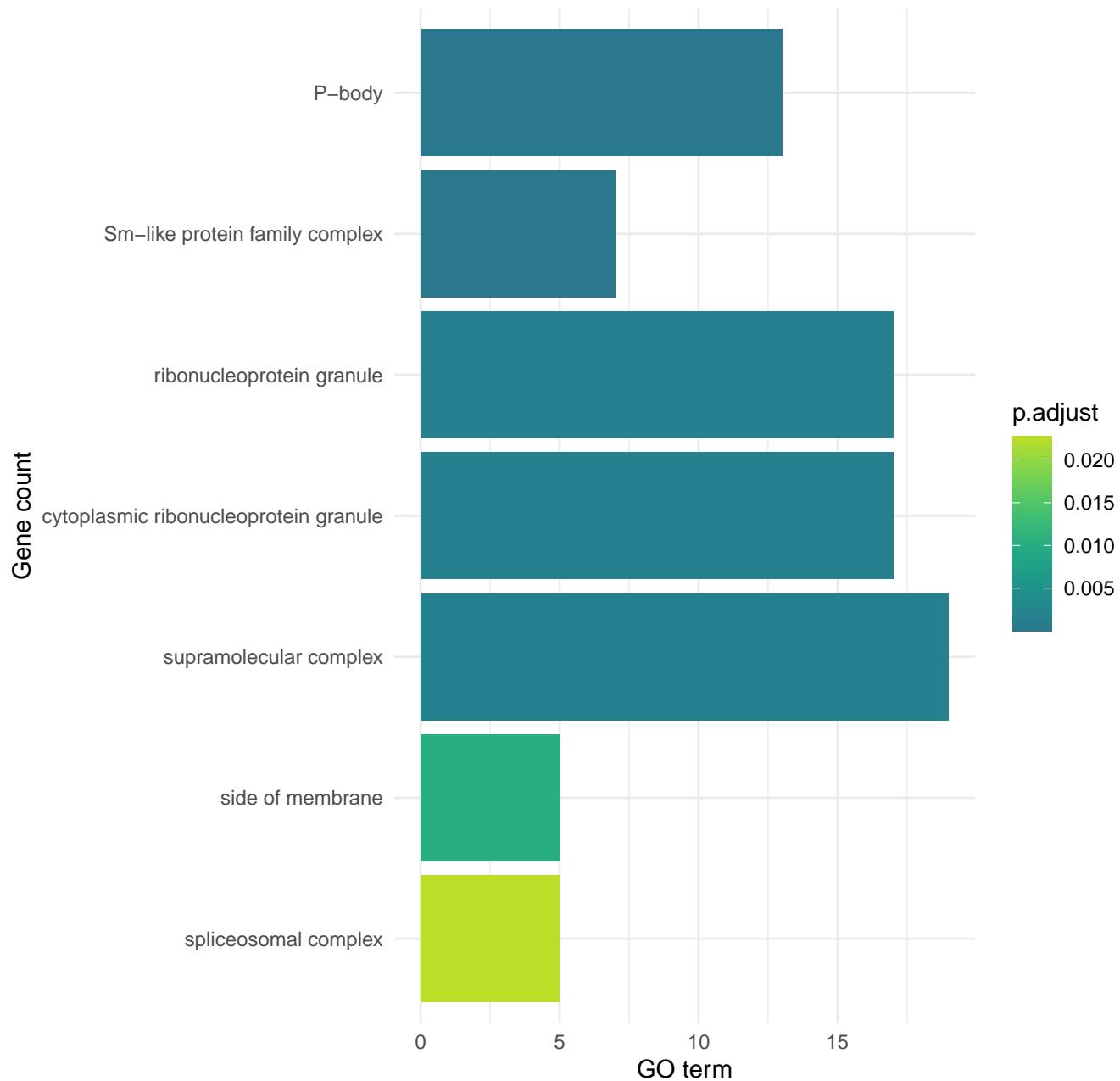


DHH1-TAP Up-regulated GO BP

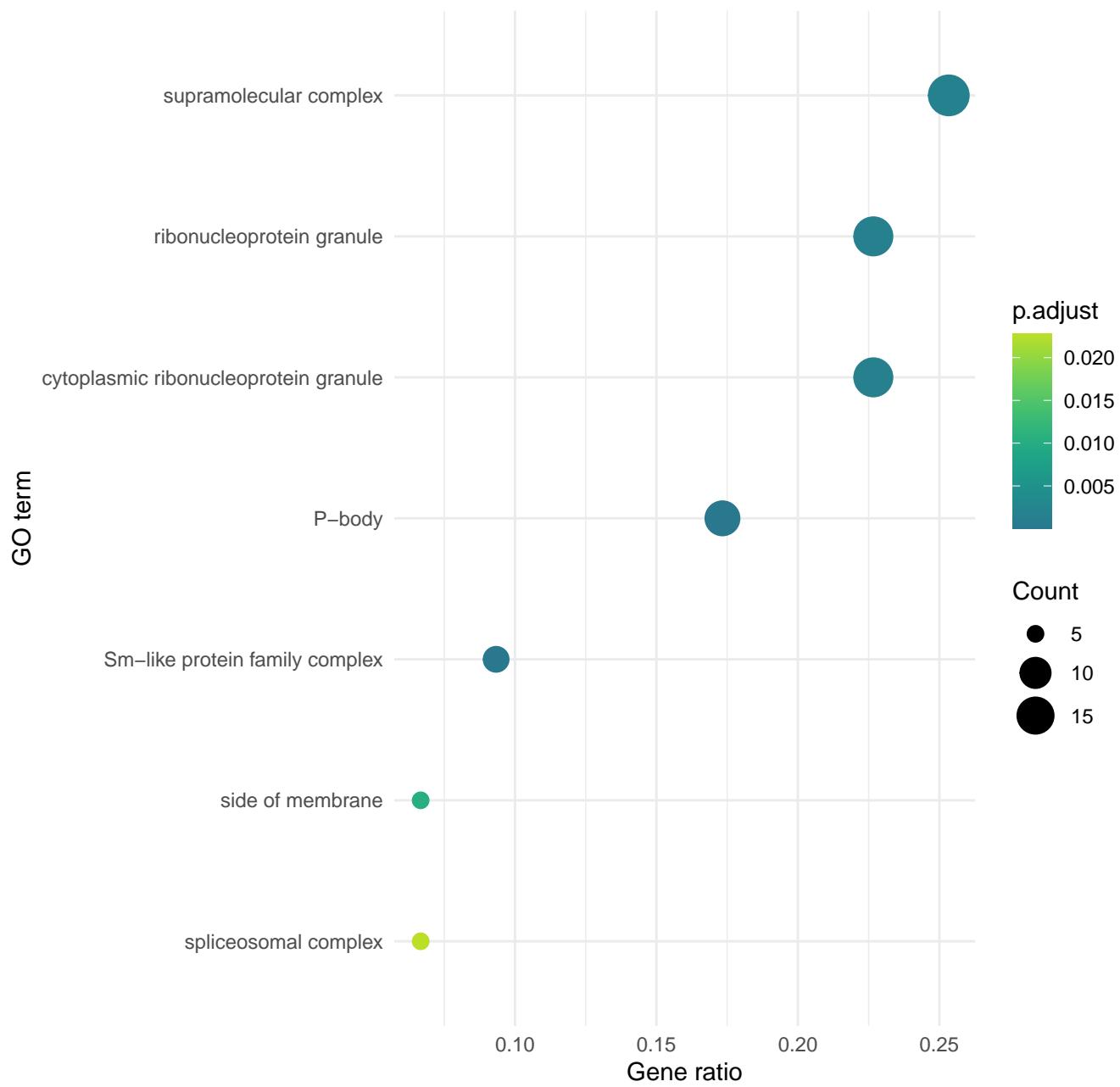


negative regulation of macromolecule metabolic process
mRNA metabolic process
aromatic compound catabolic process
cellular nitrogen compound catabolic process
heterocycle catabolic process
mRNA catabolic process
nucleobase-containing compound catabolic process
organic cyclic compound catabolic process
RNA catabolic process
nuclear-transcribed mRNA catabolic process

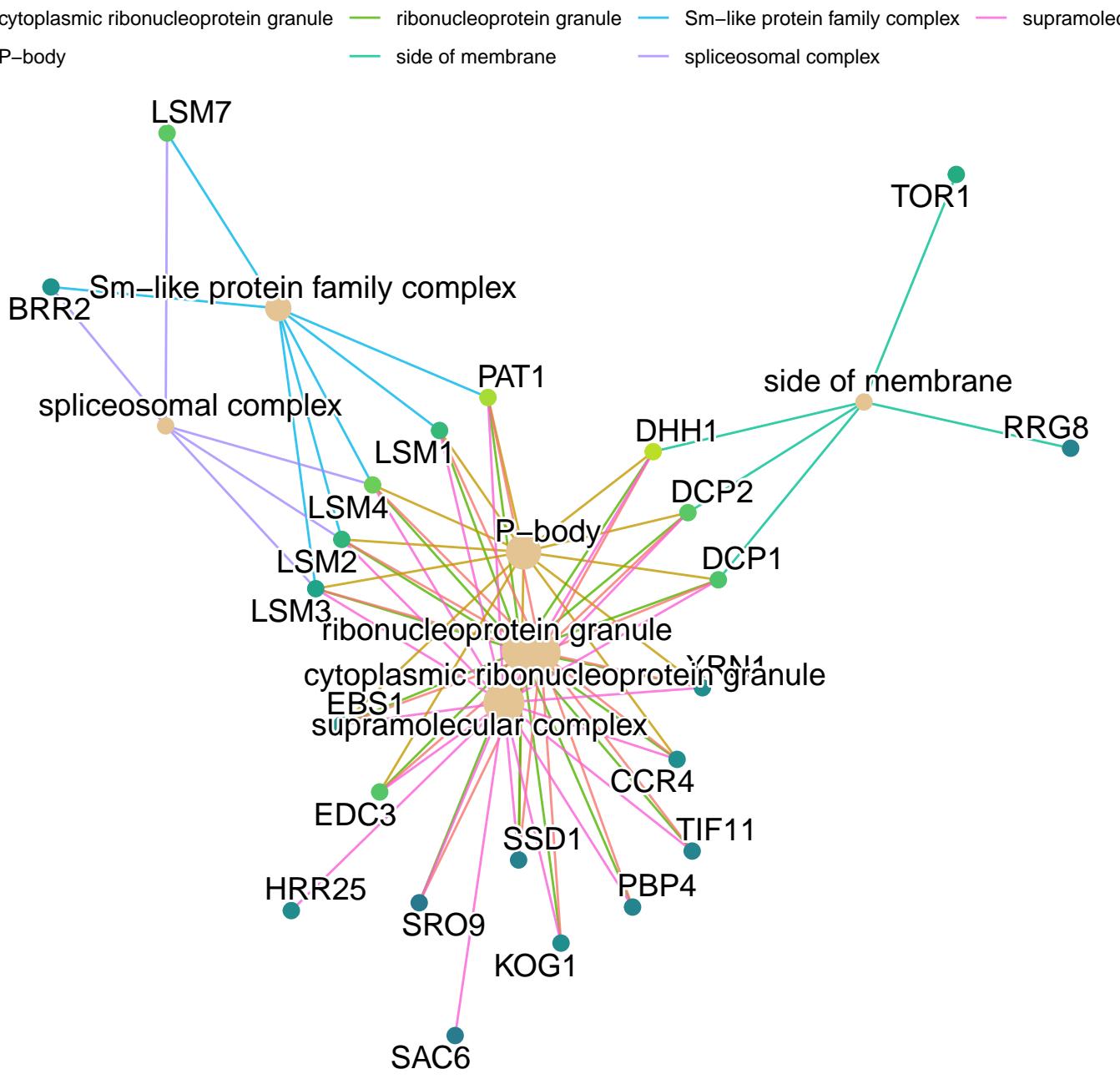
DHH1-TAP Up-regulated GO CC barplot



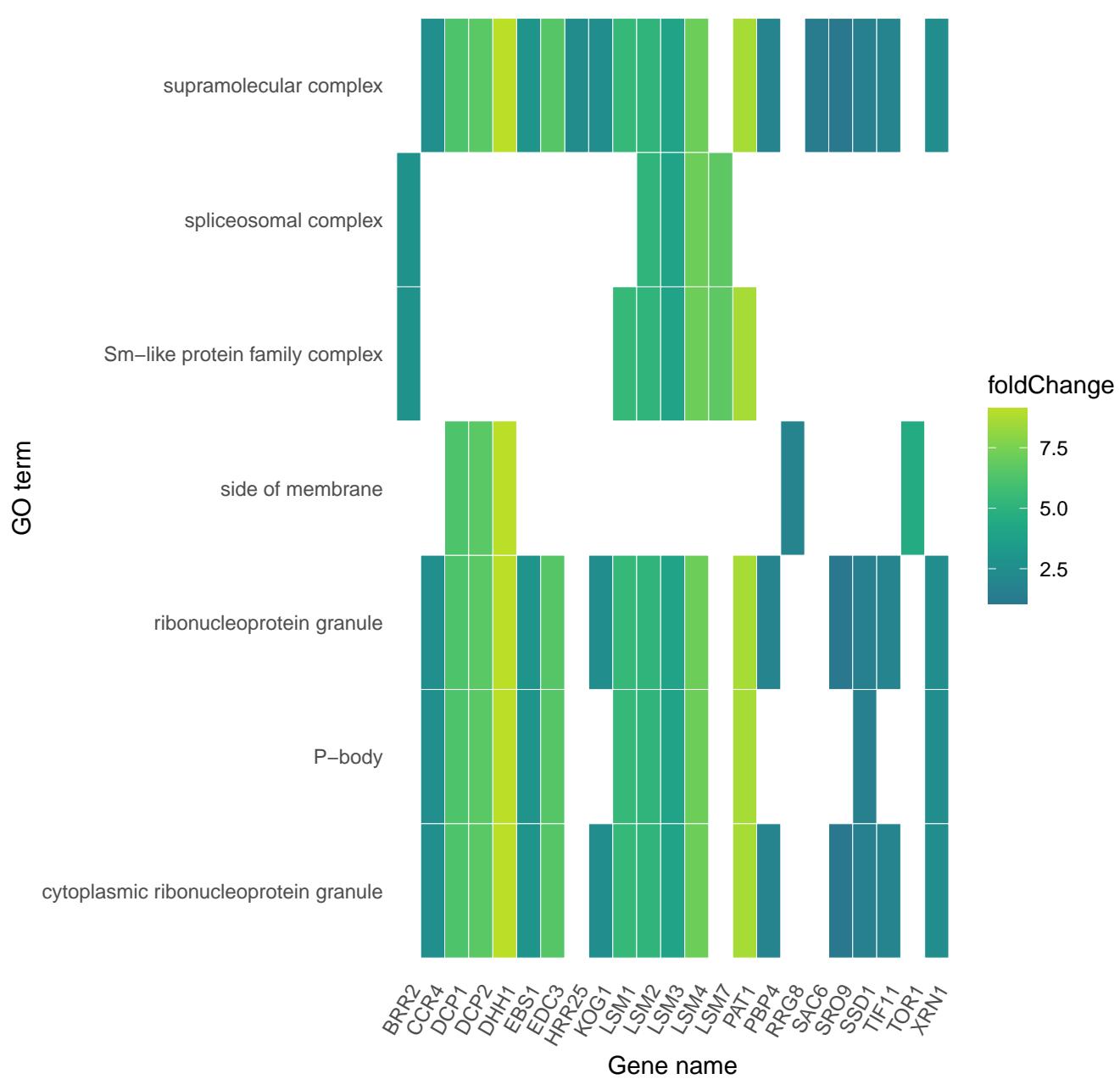
DHH1-TAP Up-regulated GO CC dotplot



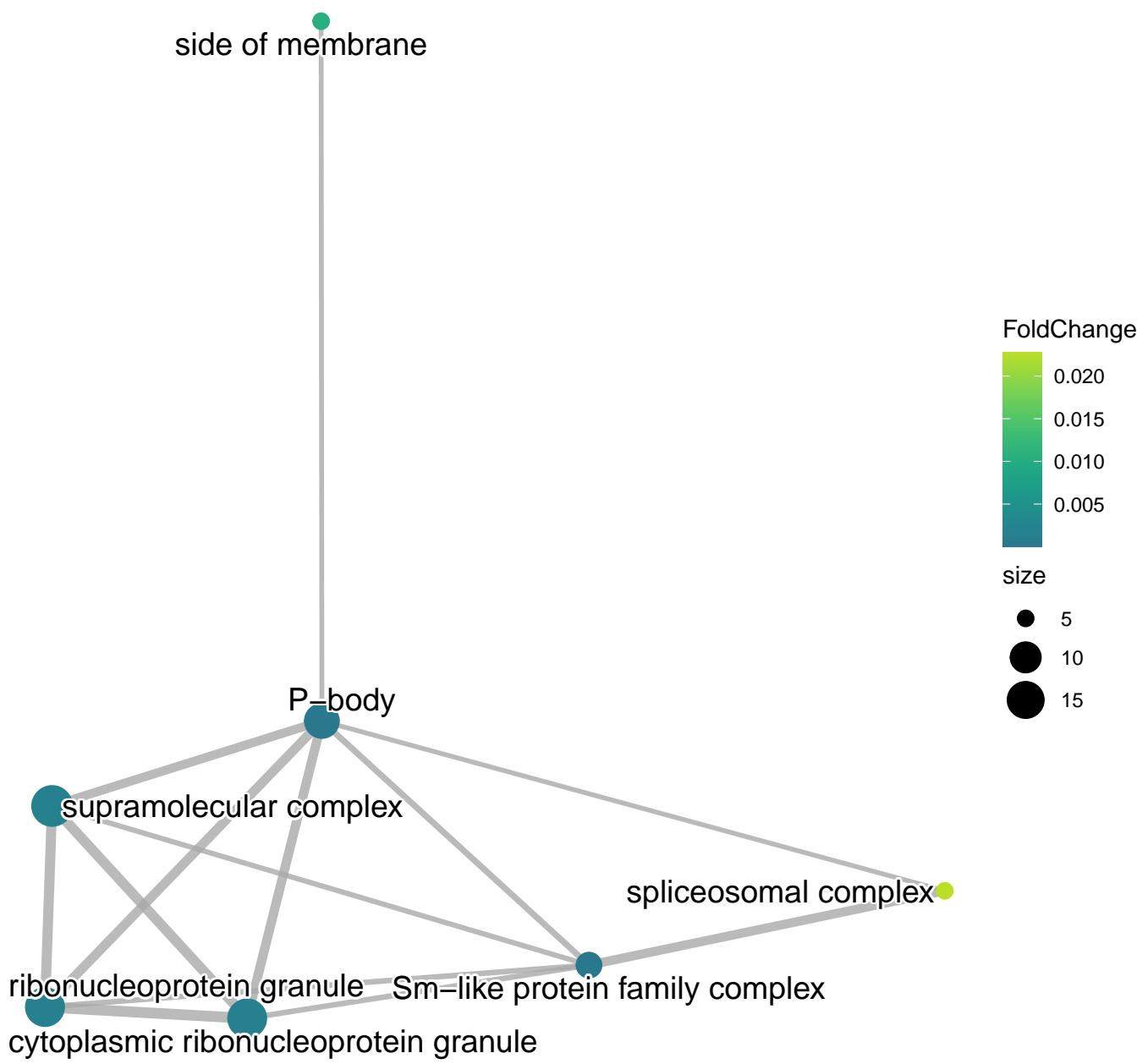
DHH1-TAP Up-regulated GO CC cnetplot

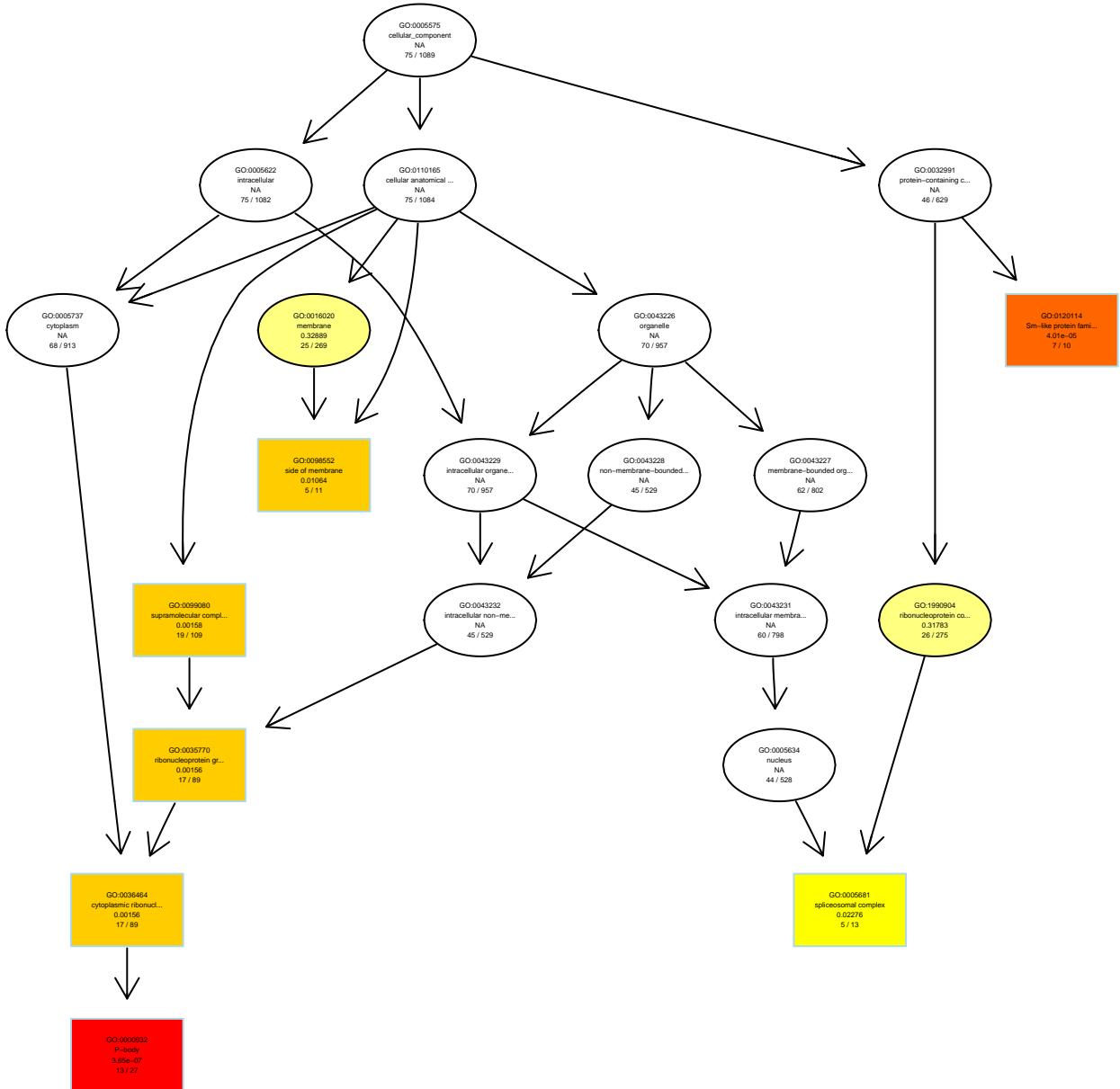


DHH1-TAP Up-regulated GO CC heatplot

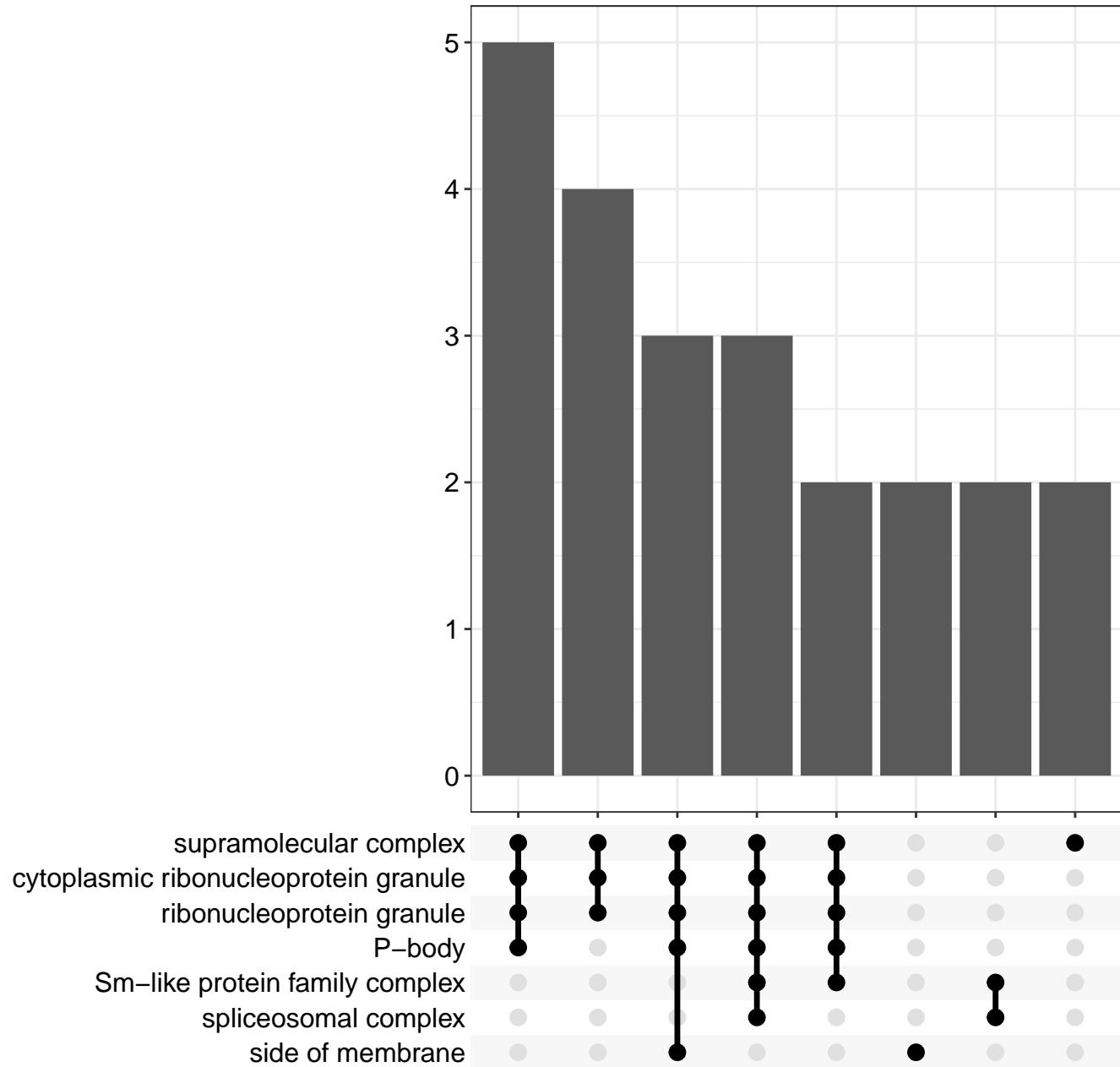


DHH1-TAP Up-regulated GO CC emapplot

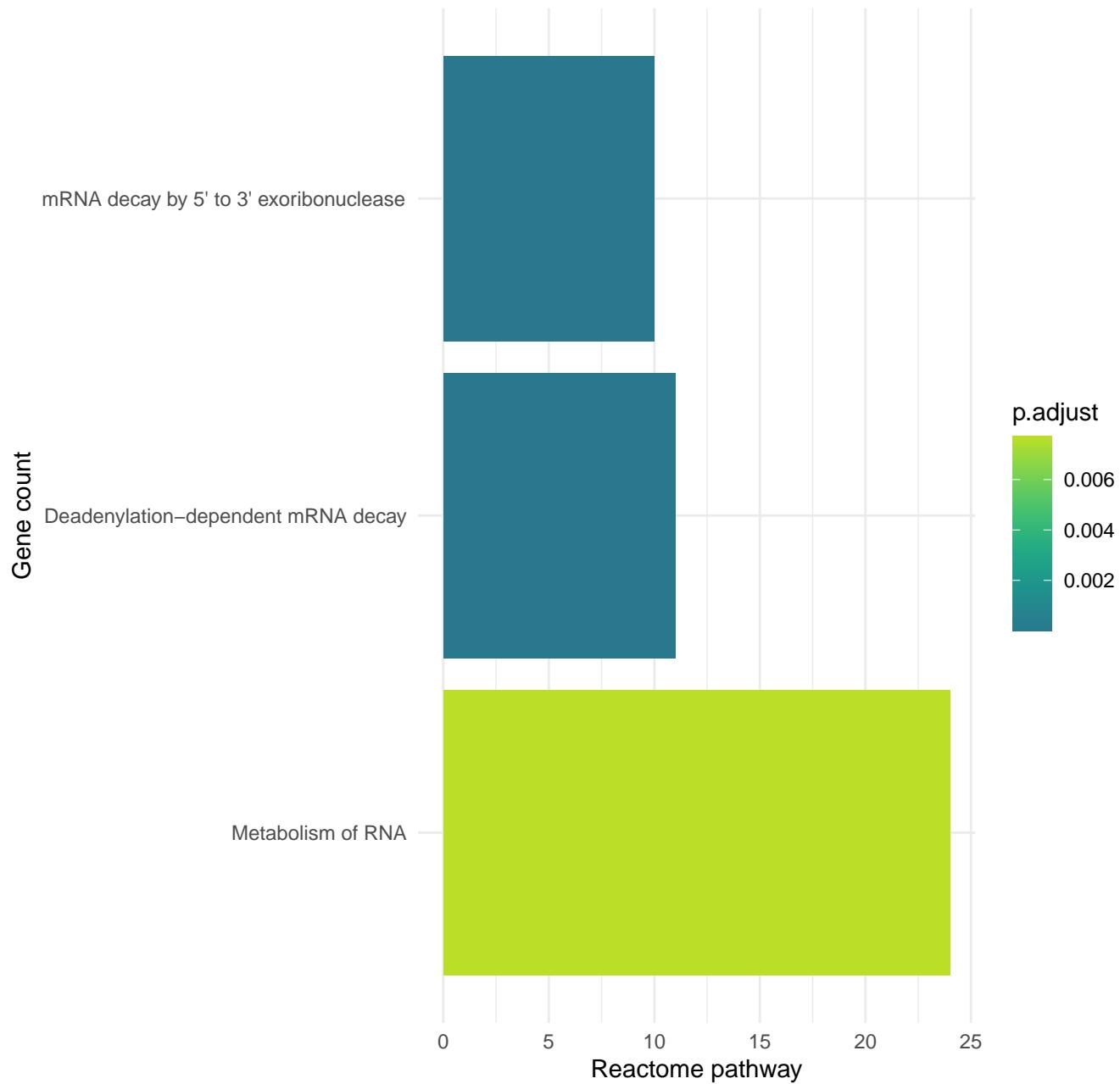




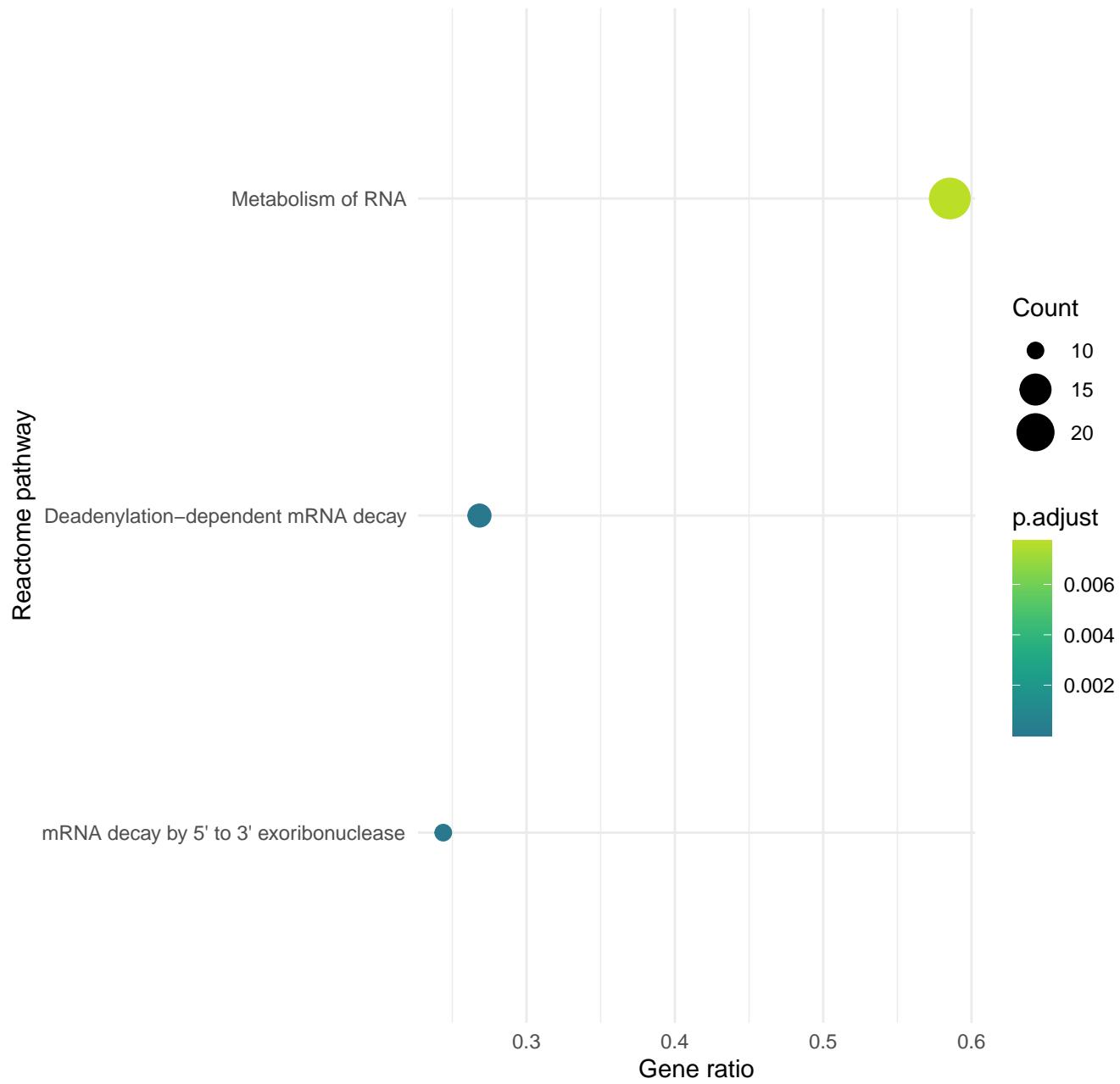
DHH1-TAP Up-regulated GO CC upsetplot



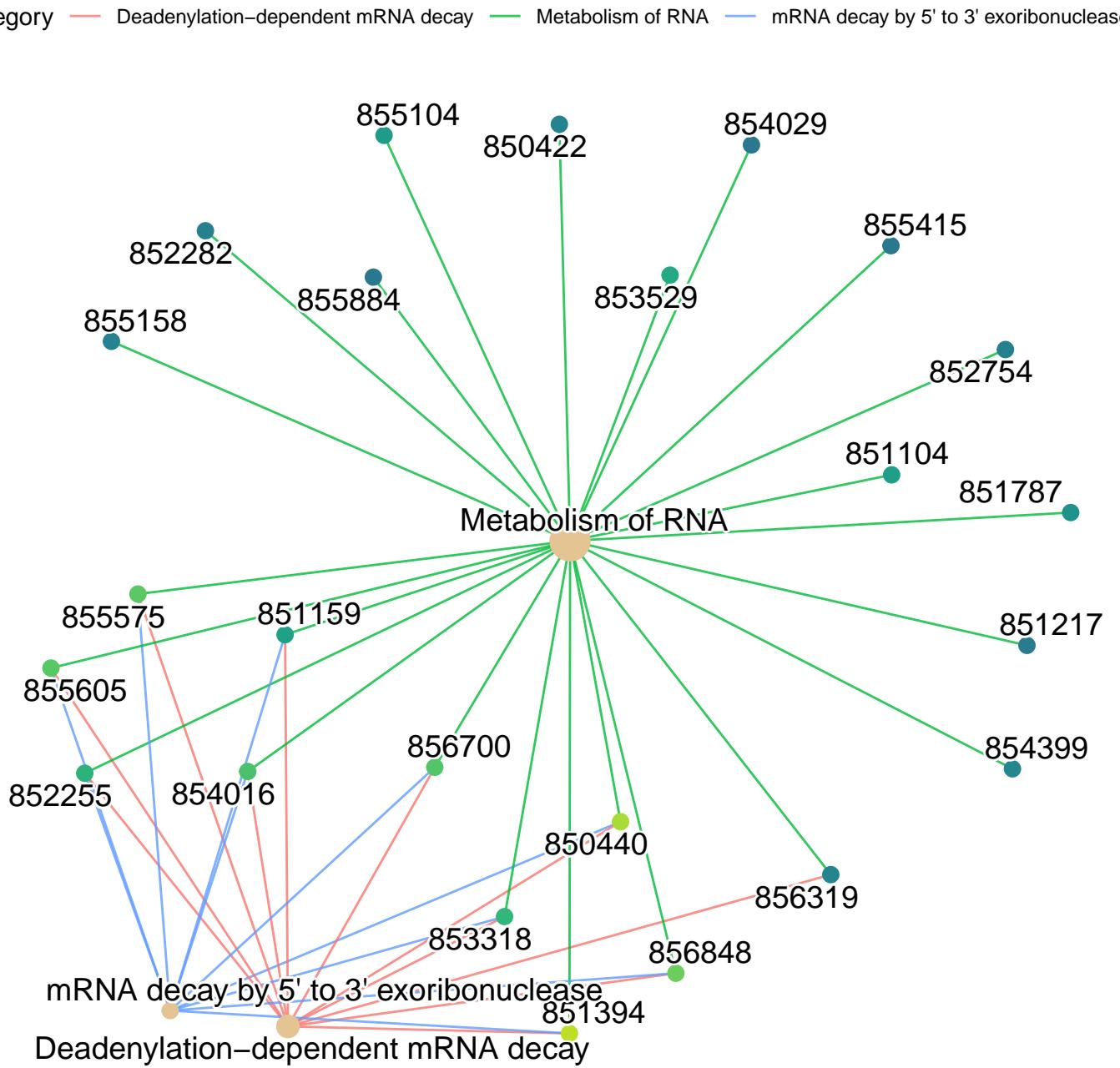
DHH1-TAP Up-regulated Reactome barplot



DHH1–TAP Up-regulated Reactome dotplot



DHH1-TAP Up-regulated Reactome cnetplot



DHH1-TAP Up-regulated Reactome heatplot

Reactome pathway

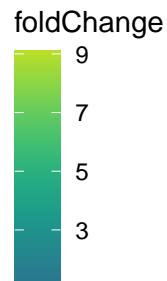
mRNA decay by 5' to 3' exoribonuclease

Metabolism of RNA

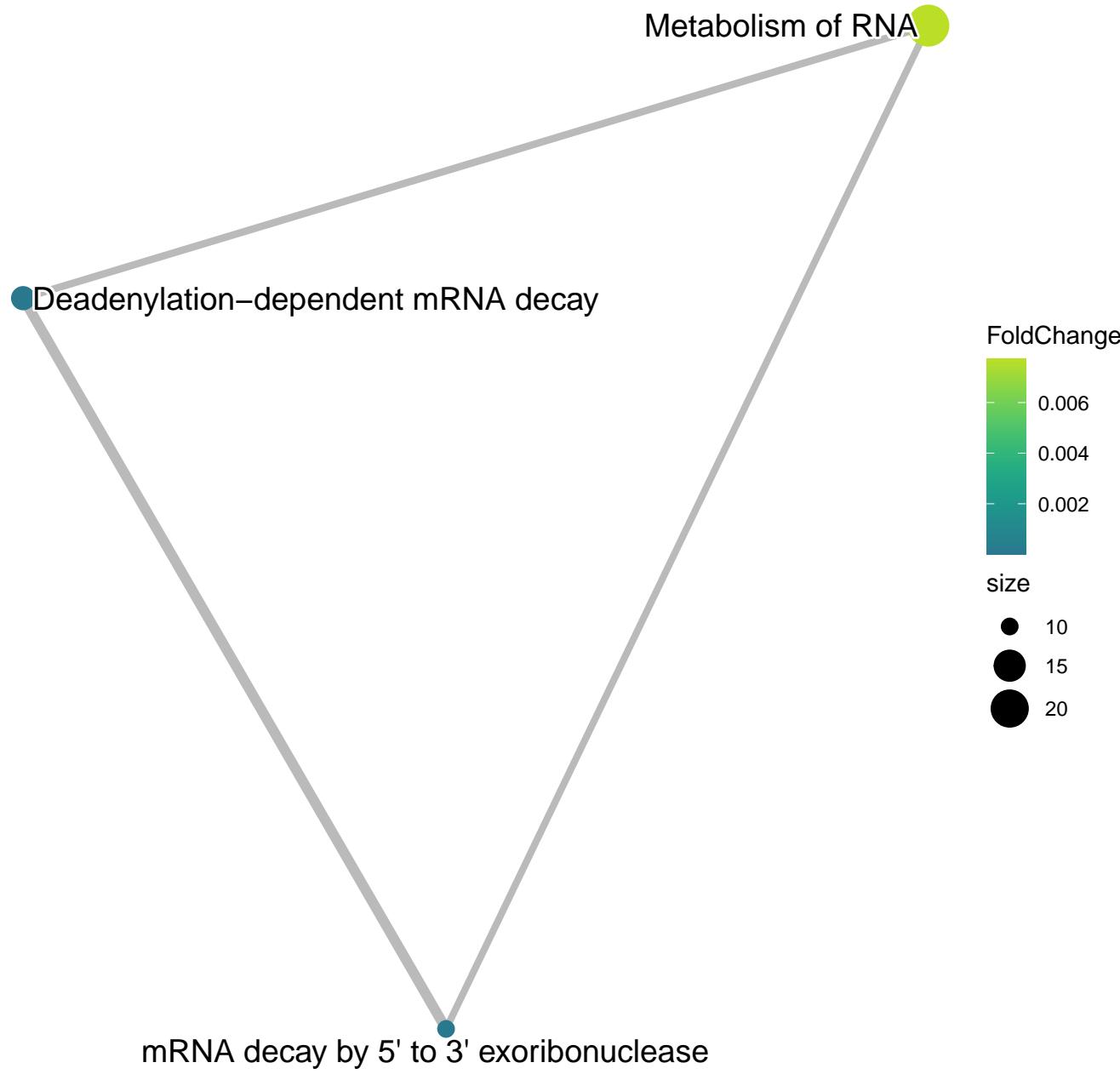
Deadenylation-dependent mRNA decay

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850440
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851159
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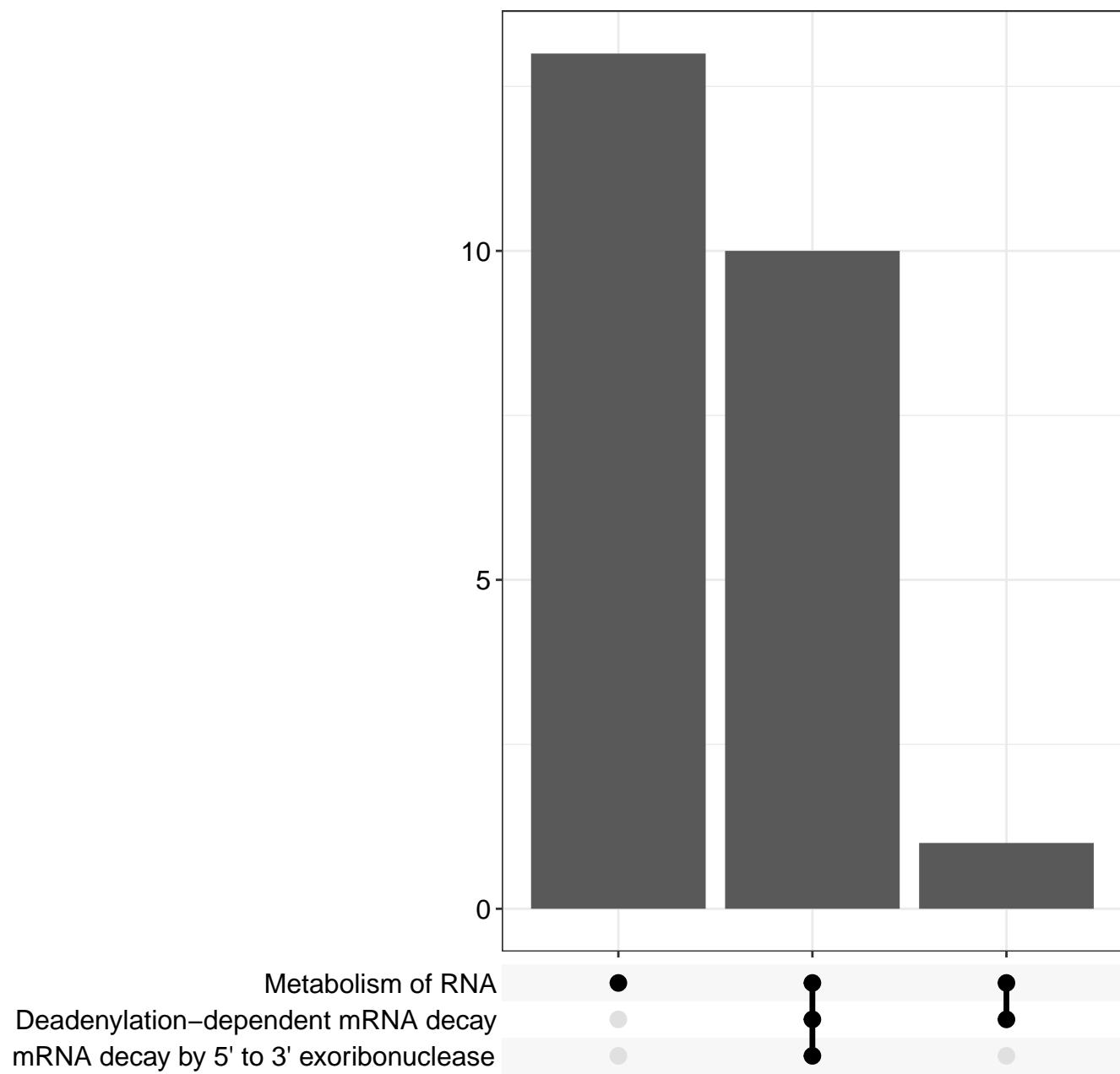
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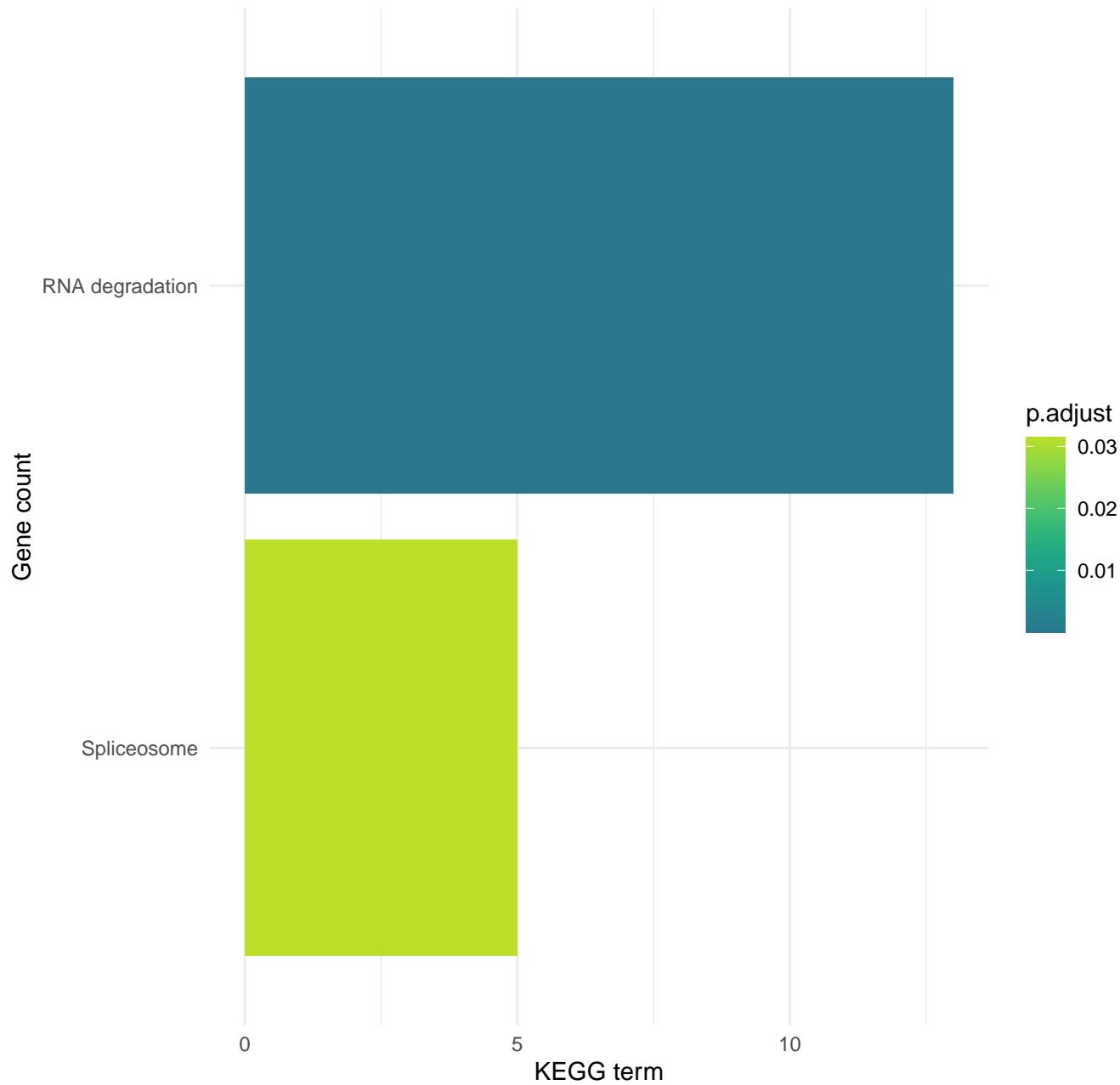
DHH1-TAP Up-regulated Reactome emapplot



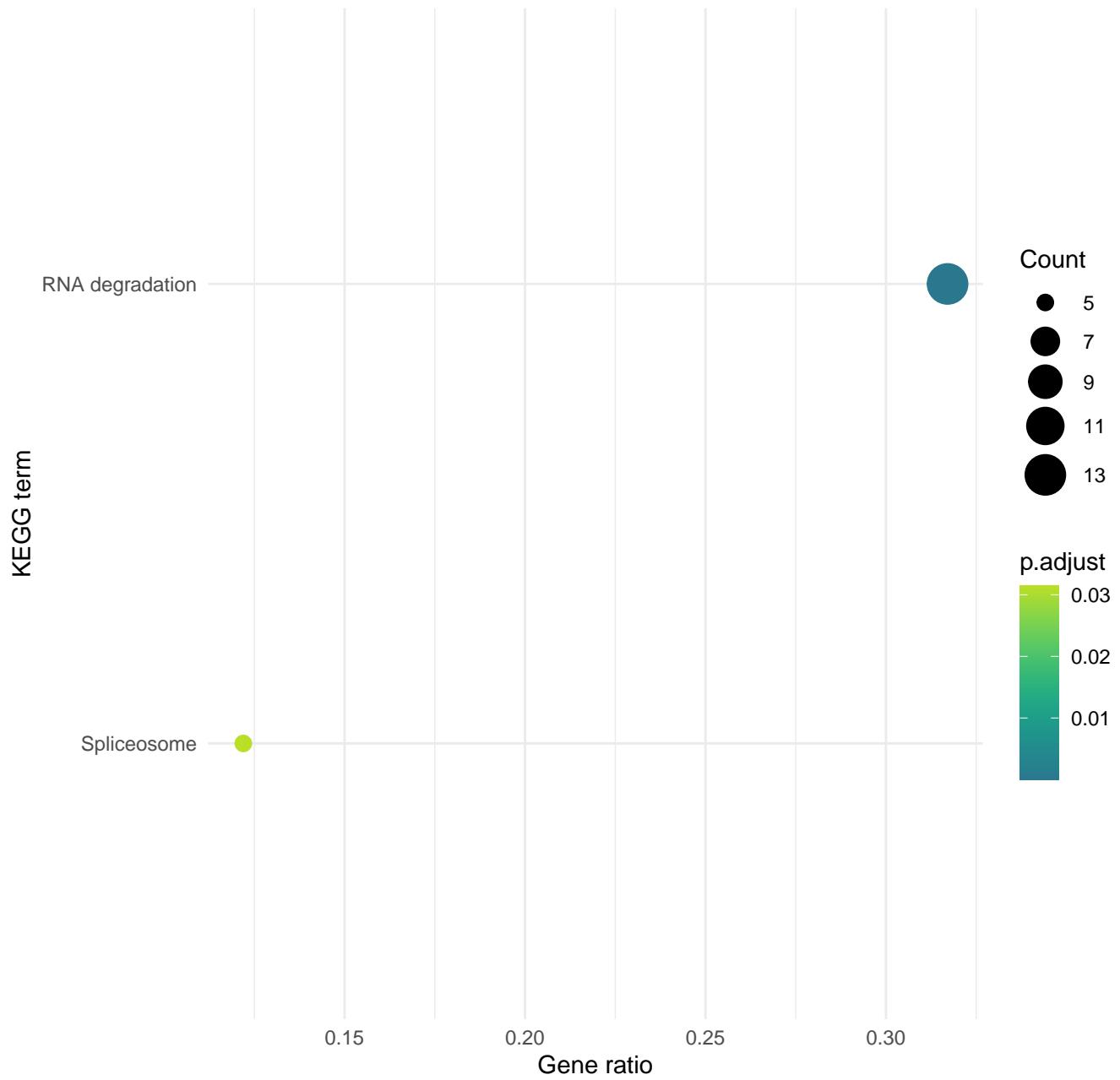
DHH1-TAP Up-regulated Reactome upsetplot



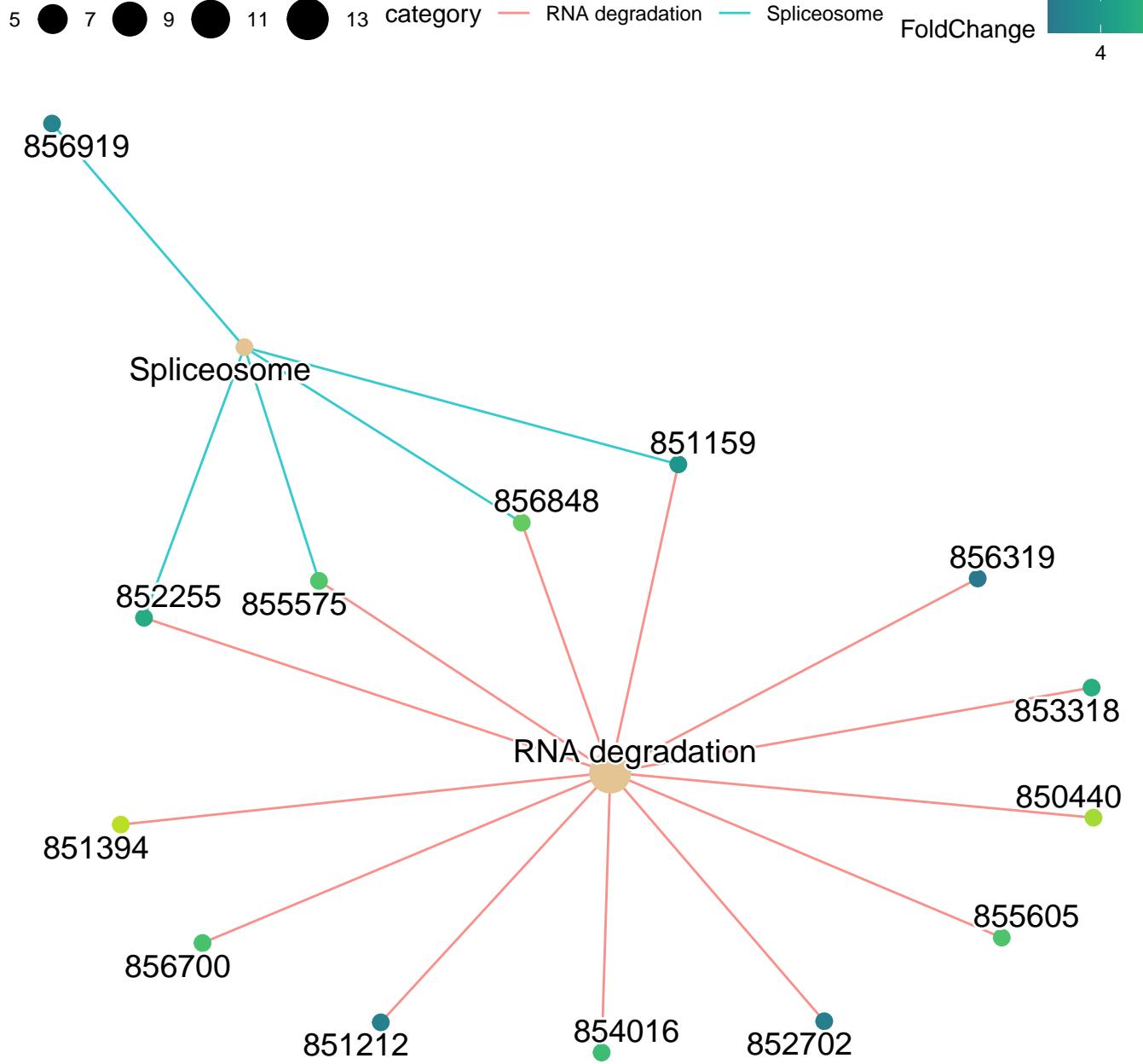
DHH1-TAP Up-regulated KEGG barplot



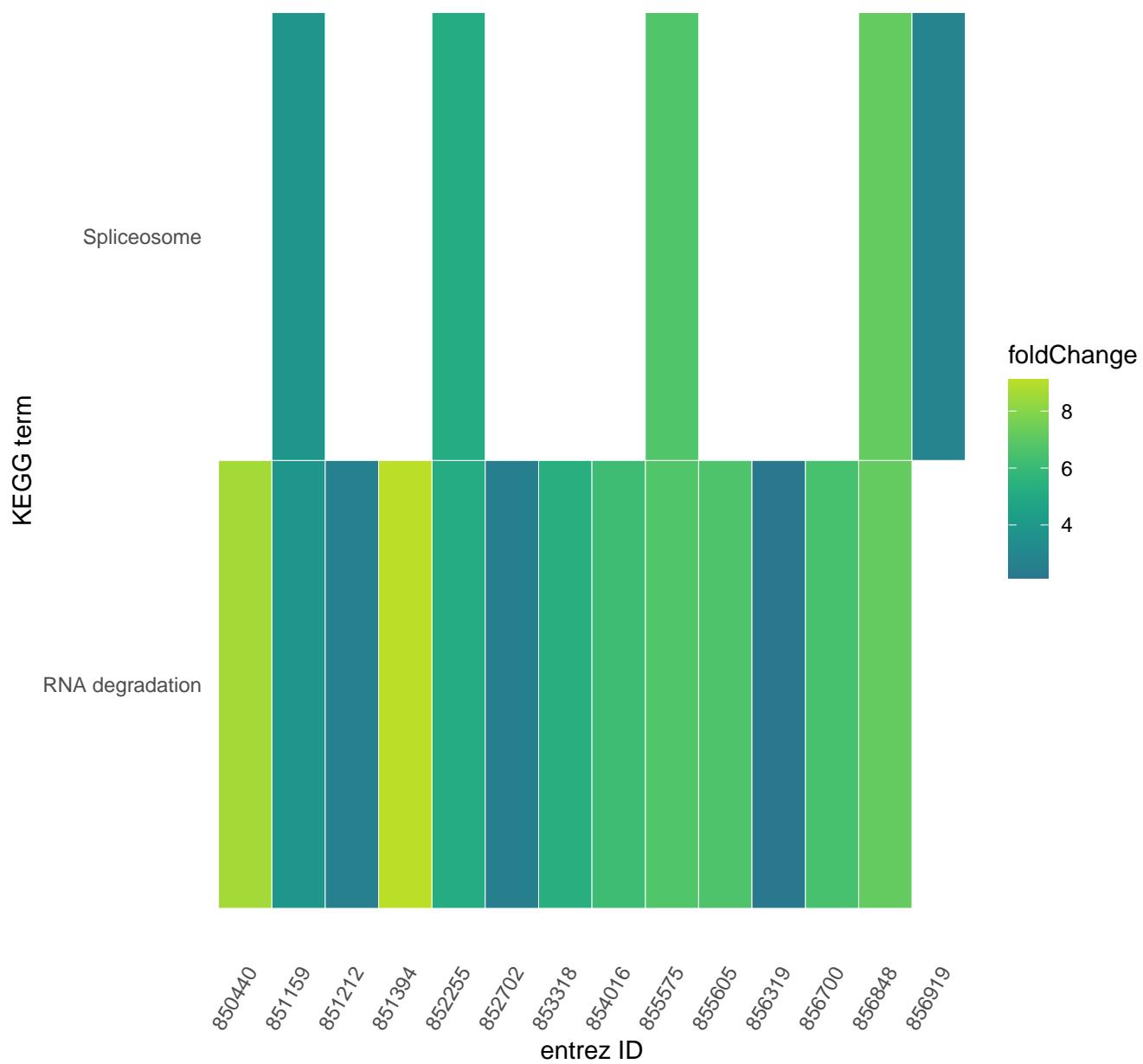
DHH1-TAP Up-regulated KEGG dotplot



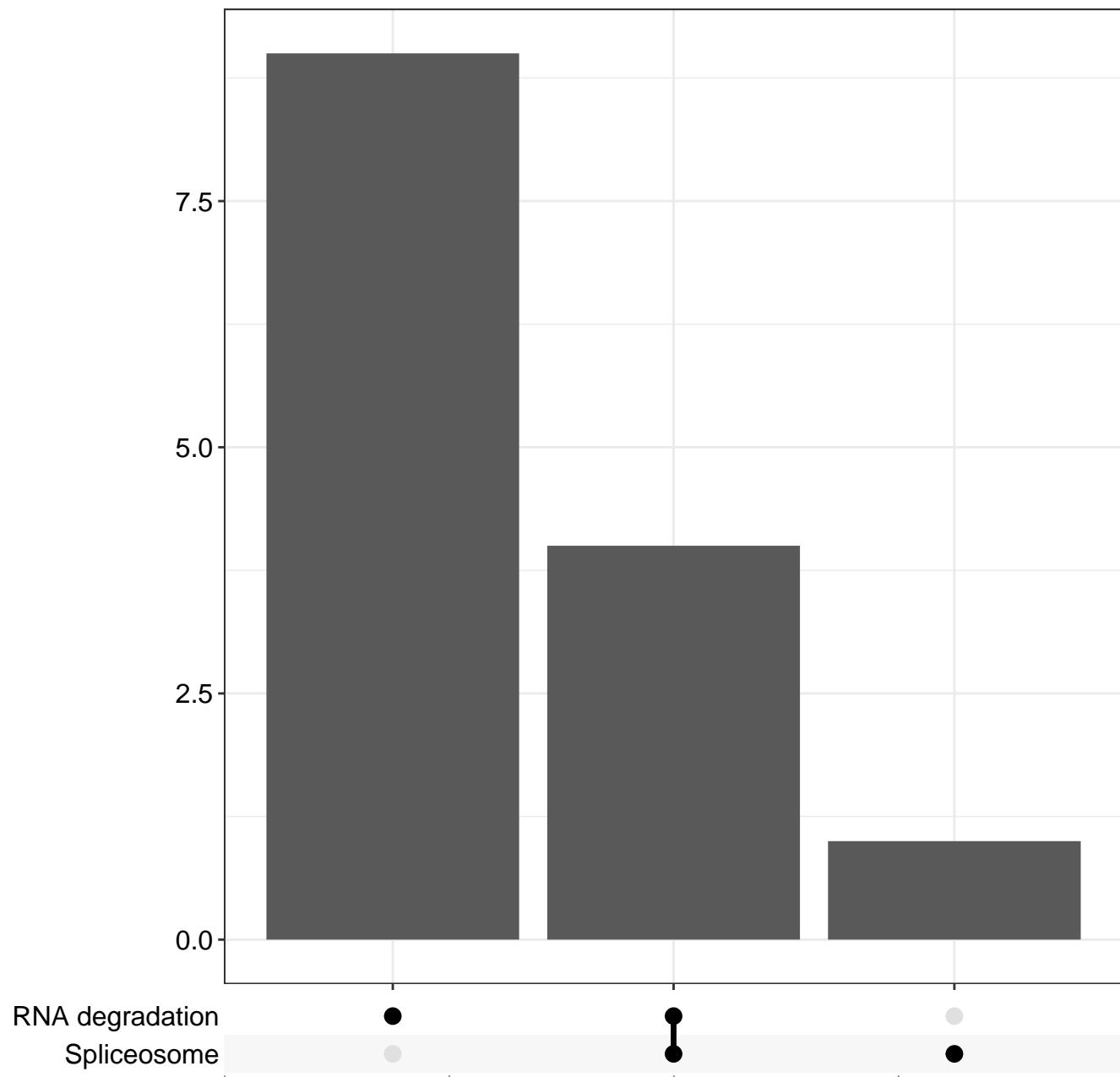
DHH1-TAP Up-regulated KEGG dotplot



DHH1-TAP Up-regulated KEGG heatplot



DHH1-TAP Up-regulated KEGG upsetplot

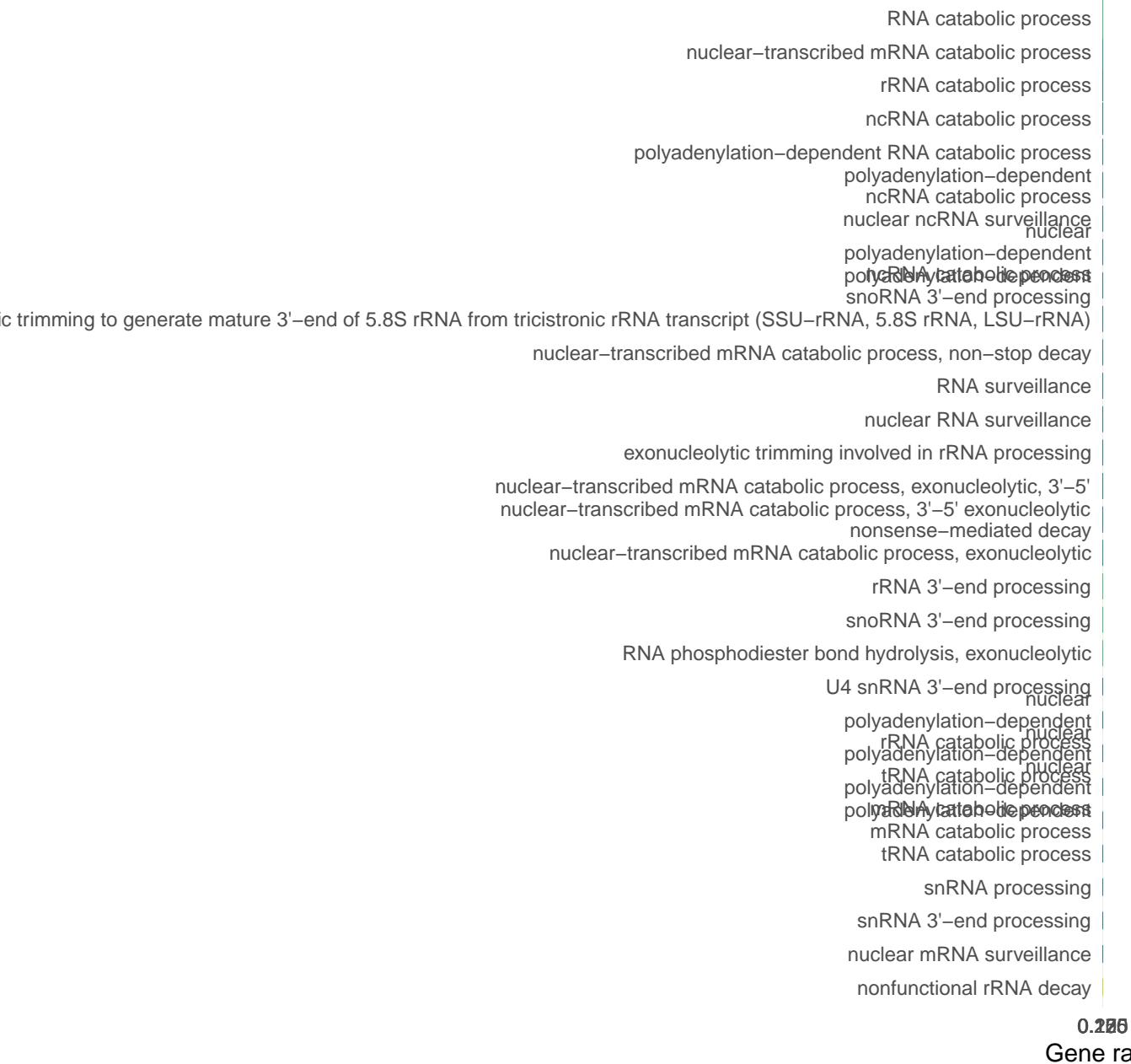


ic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

- nuclear-transcribed mRNA catabolic process, non-stop decay
- exonucleolytic trimming involved in rRNA processing
- nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'
- nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic
- nonsense-mediated decay
- tRNA catabolic process
- snRNA processing
- snRNA 3'-end processing
- nuclear mRNA surveillance
- nuclear-transcribed mRNA catabolic process, exonucleolytic
- nuclear-transcribed mRNA catabolic process
- RNA catabolic process
- rRNA 3'-end processing
- snoRNA 3'-end processing
- RNA phosphodiester bond hydrolysis, exonucleolytic
- nonfunctional rRNA decay

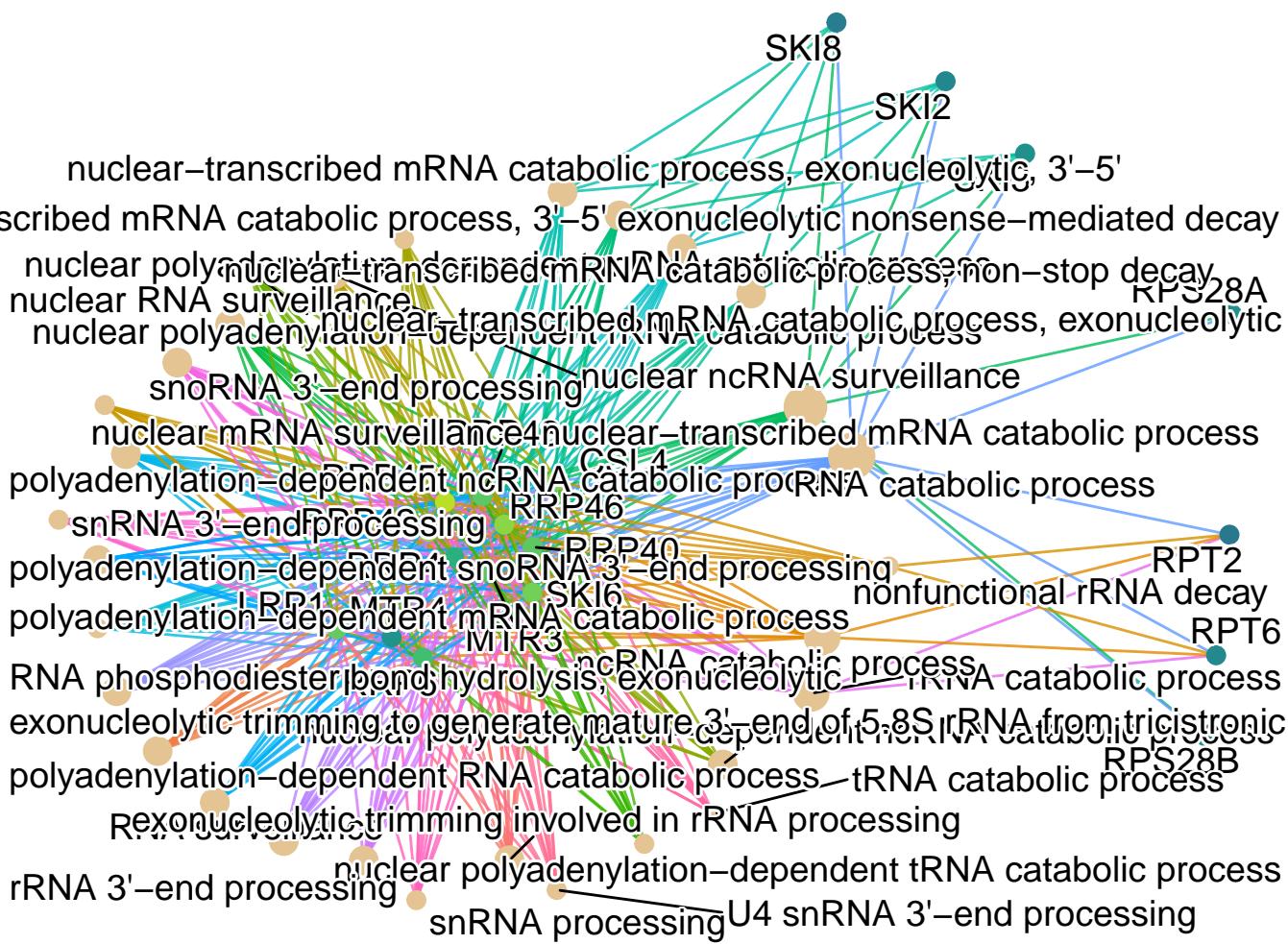
polyadenylation-dependent RNA catabolic process

- polyadenylation-dependent ncRNA catabolic process
- nuclear ncRNA surveillance
- nuclear
- polyadenylation-dependent polyA_n catabolic process
- snoRNA 3'-end processing
- U4 snRNA 3'-end processing
- nuclear
- polyadenylation-dependent nuclear rRNA catabolic process
- polyadenylation-dependent nuclear tRNA catabolic process
- polyadenylation-dependent nuclear rRNA catabolic process
- mRNA catabolic process
- rRNA catabolic process



DIS3-TAP Up-regulated GO BP cnetplot

mRNA catabolic process	nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic nonsense-mediated decay
ncRNA catabolic process	nuclear-transcribed mRNA catabolic process, exonucleolytic
rRNA catabolic process	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'
tRNA catabolic process	nuclear-transcribed mRNA catabolic process, non-stop decay
	polyadenylation-dependent mRNA catabolic process
	polyadenylation-dependent ncRNA catabolic process



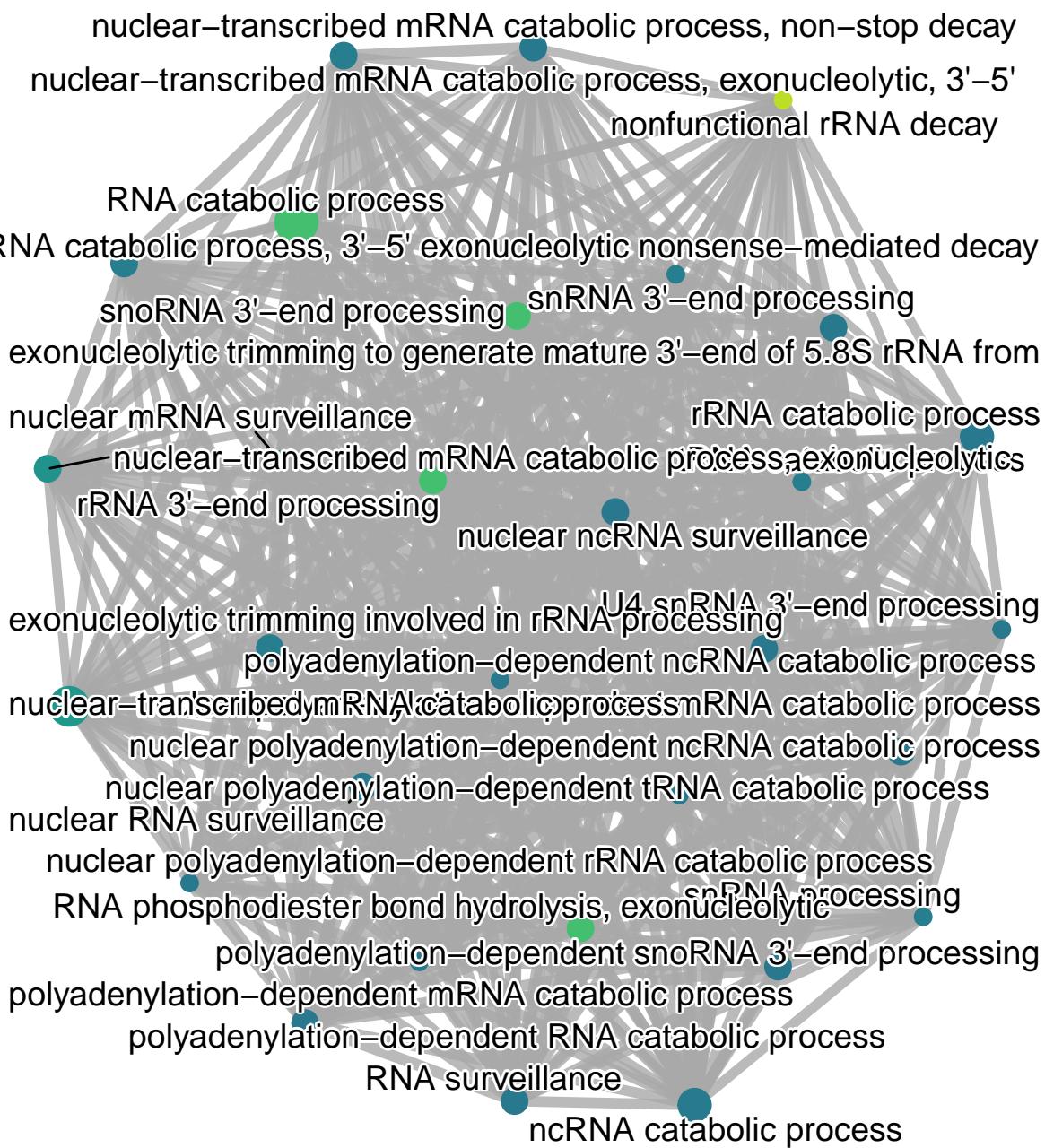
U4 snRNA 3'-end processing
tRNA catabolic process
snRNA processing
snRNA 3'-end processing
snoRNA 3'-end processing
rRNA catabolic process
rRNA 3'-end processing
RNA surveillance
RNA phosphodiester bond hydrolysis, exonucleolytic
RNA catabolic process
polyadenylation-dependent snoRNA 3'-end processing
polyadenylation-dependent RNA catabolic process
polyadenylation-dependent ncRNA catabolic process
polyadenylation-dependent mRNA catabolic process
nuclear-transcribed mRNA catabolic process, non-stop decay
nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5'
nuclear-transcribed mRNA catabolic process, exonucleolytic
nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic
nonsense-mediated decay
nuclear-transcribed mRNA catabolic process
nuclear RNA surveillance
nuclear polyadenylation-dependent tRNA catabolic process
nuclear polyadenylation-dependent rRNA catabolic process
nuclear polyadenylation-dependent ncRNA catabolic process
nuclear polyadenylation-dependent mRNA catabolic process
nuclear ncRNA surveillance
nuclear mRNA surveillance
nonfunctional rRNA decay
ncRNA catabolic process

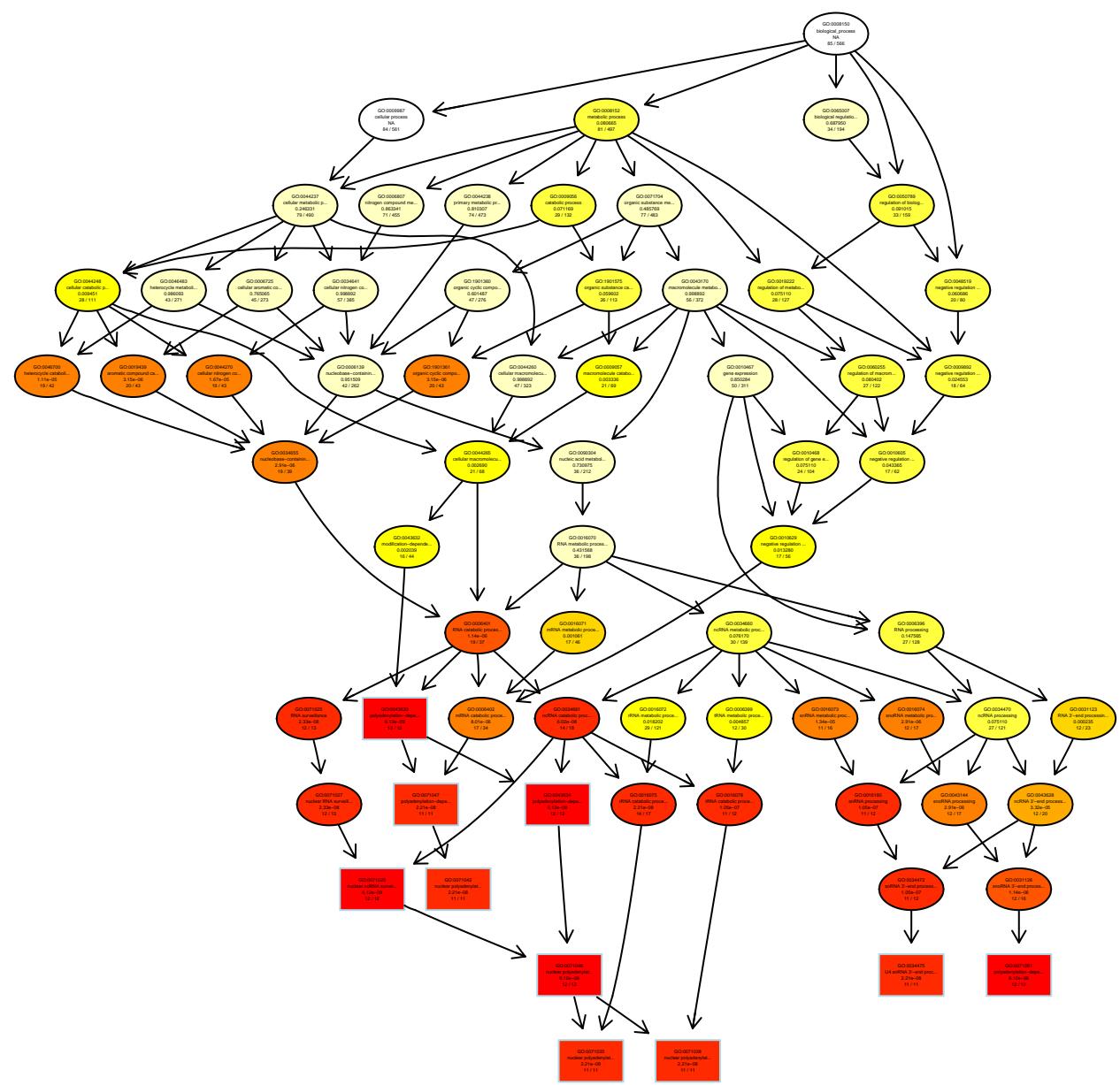
c trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
exonucleolytic trimming involved in rRNA processing

RN

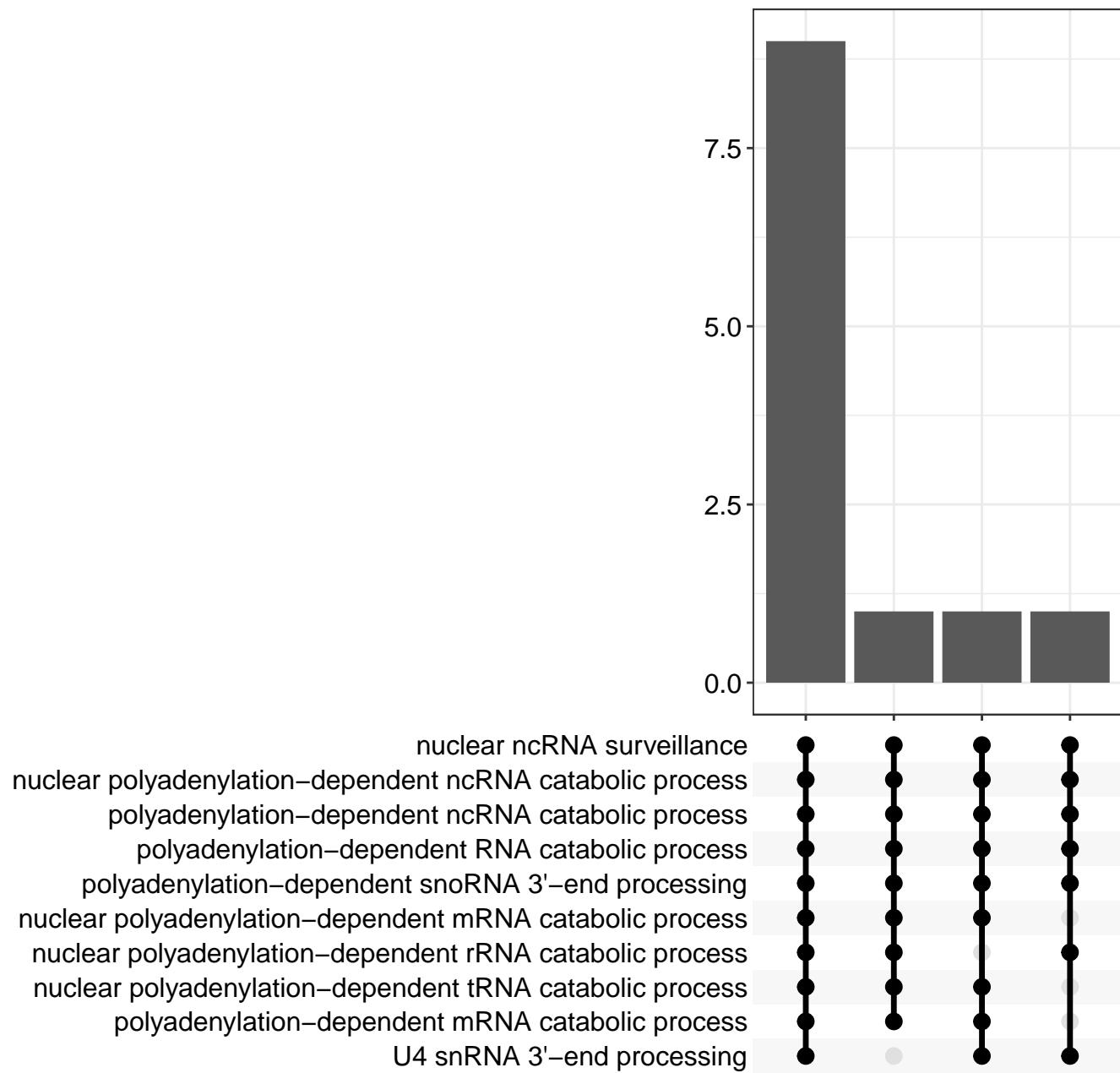
Gene na

DIS3-TAP Up-regulated GO BP emapplot

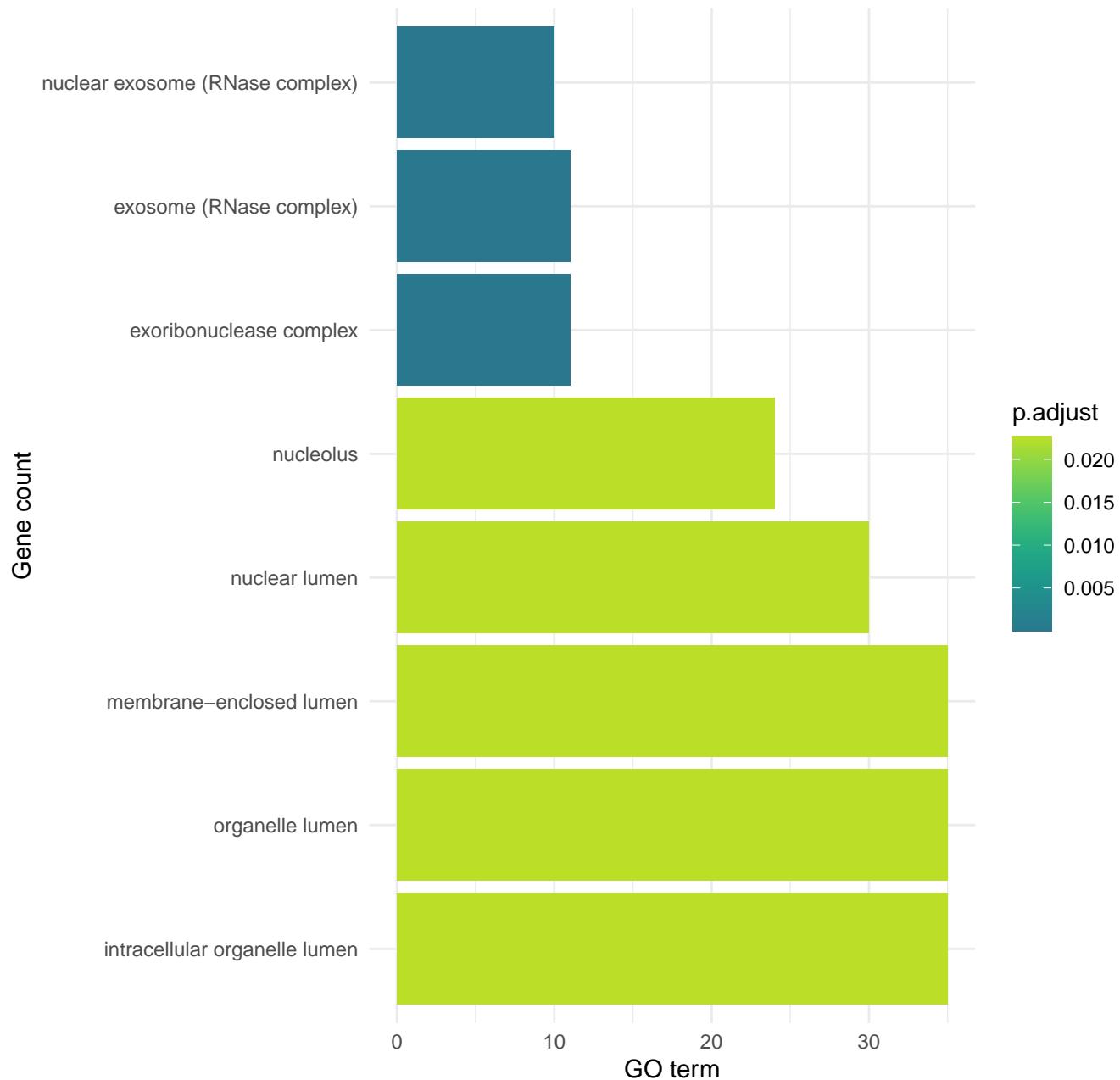




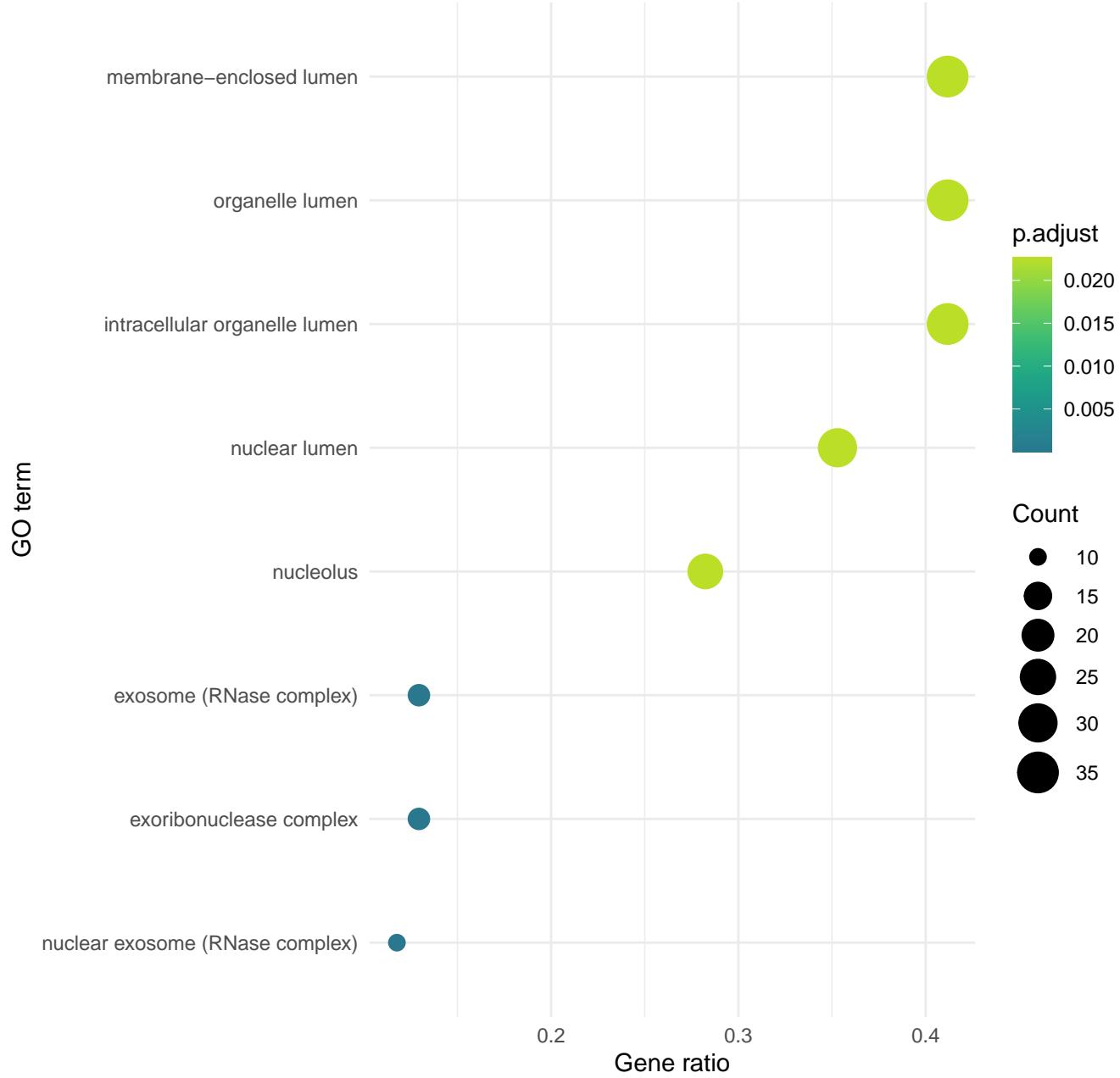
DIS3-TAP Up-regulated GO



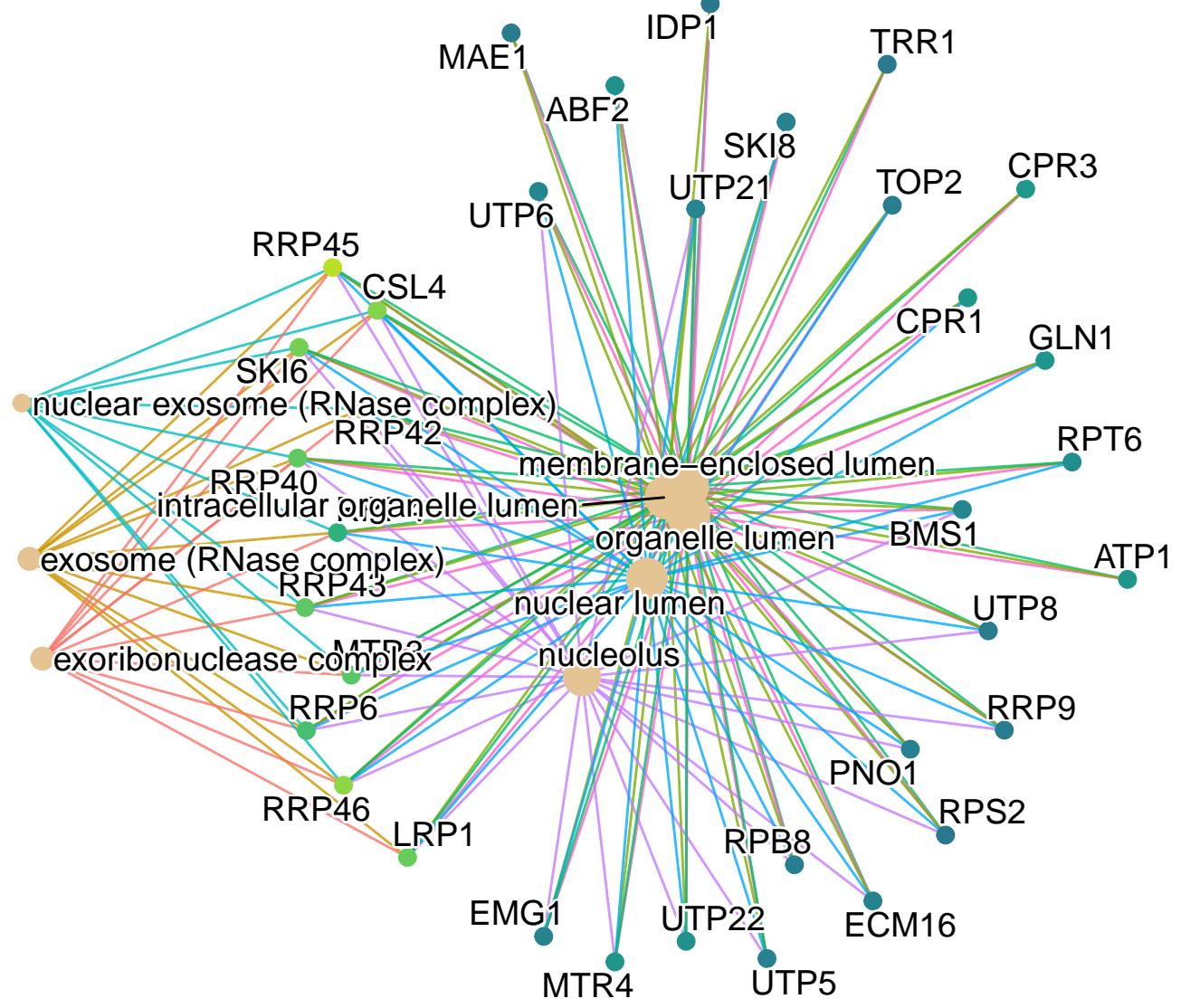
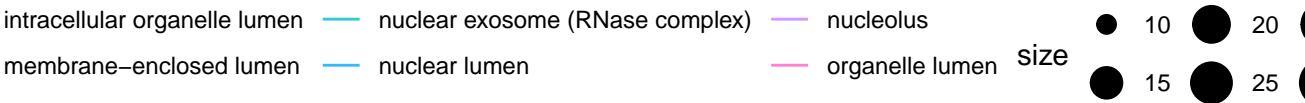
DIS3-TAP Up-regulated GO CC barplot



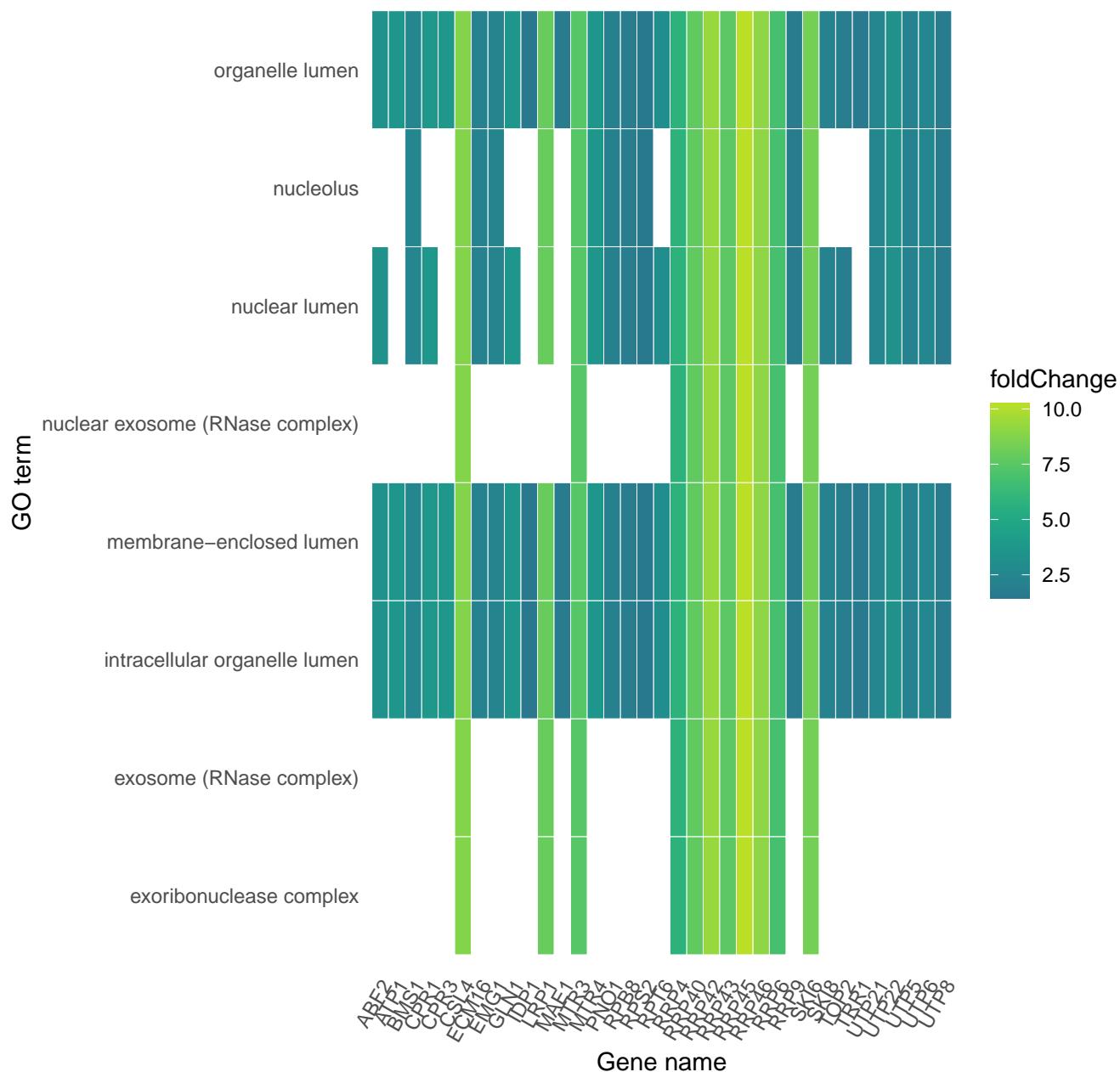
DIS3-TAP Up-regulated GO CC dotplot



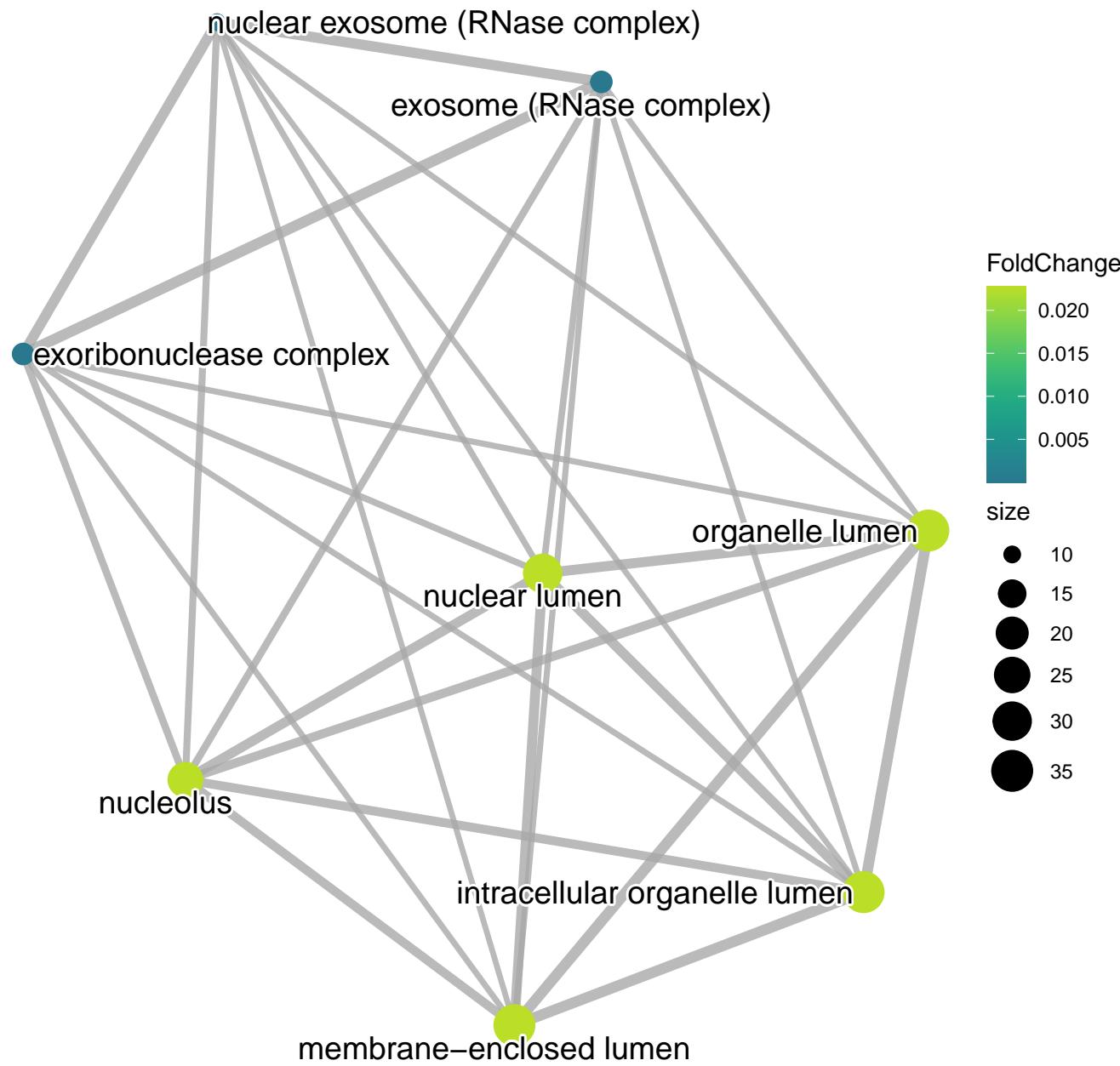
DIS3-TAP Up-regulated GO CC cnetplot

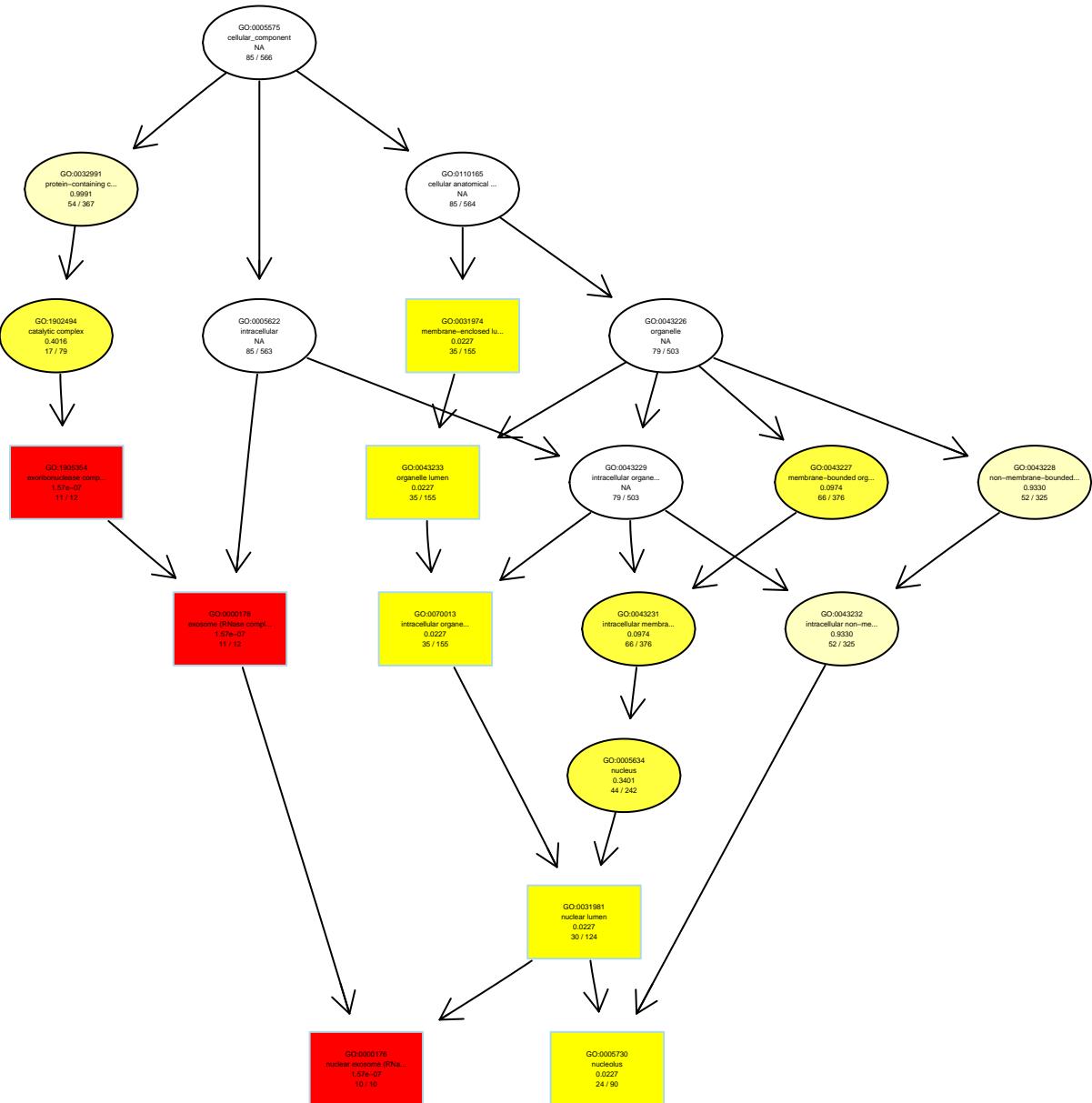


DIS3-TAP Up-regulated GO CC heatplot

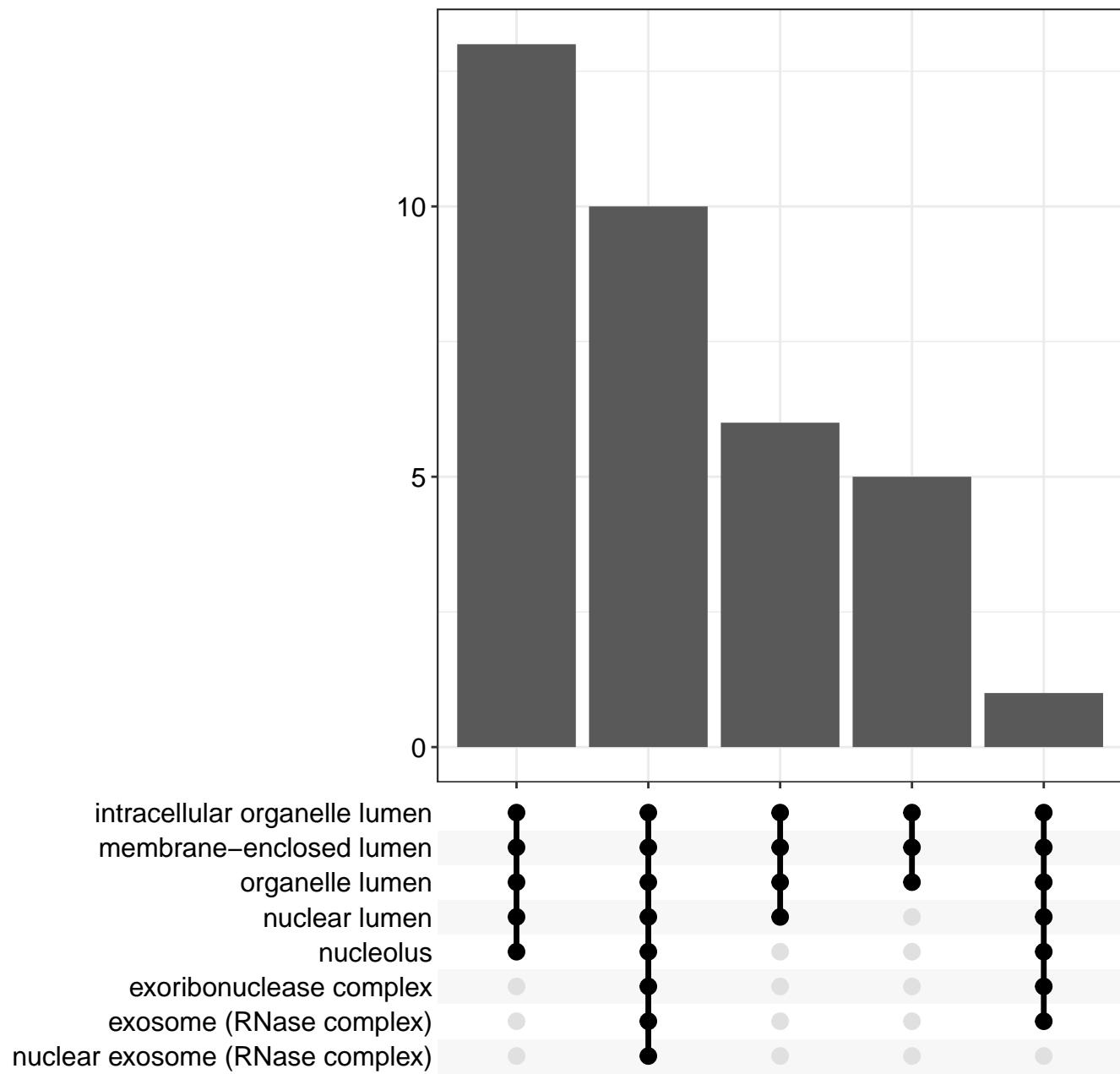


DIS3-TAP Up-regulated GO CC emapplot

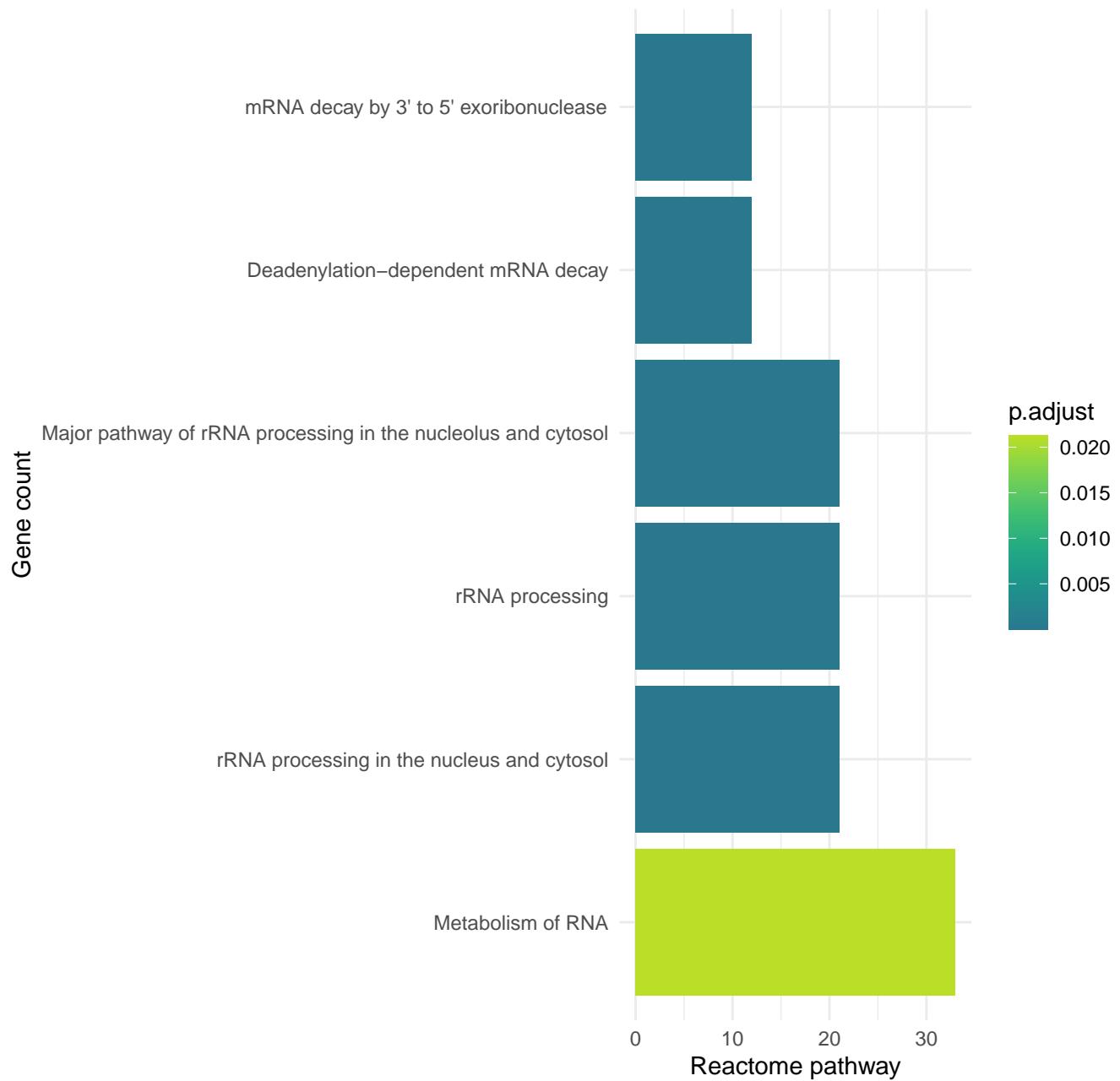




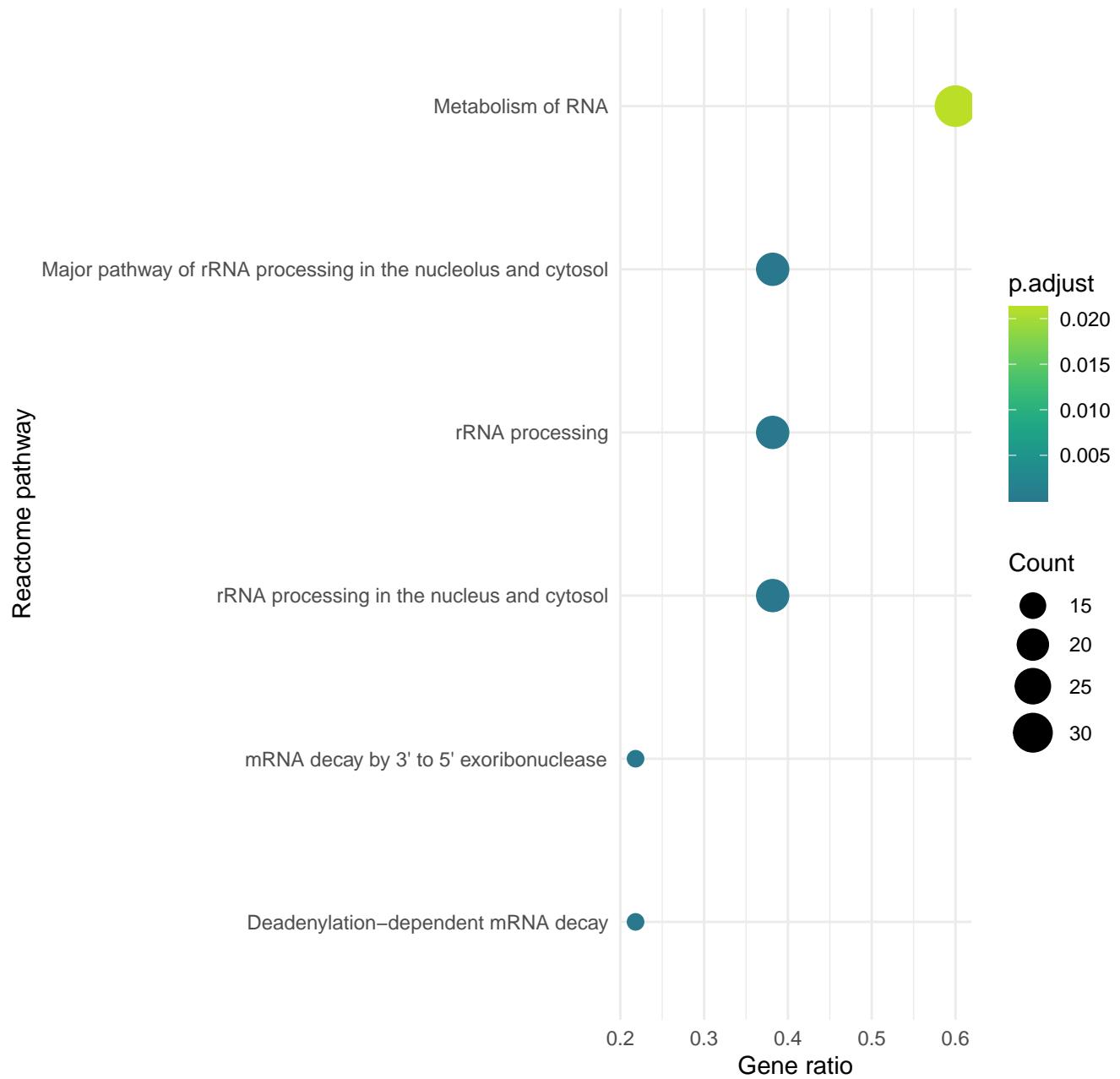
DIS3-TAP Up-regulated GO CC upsetplot



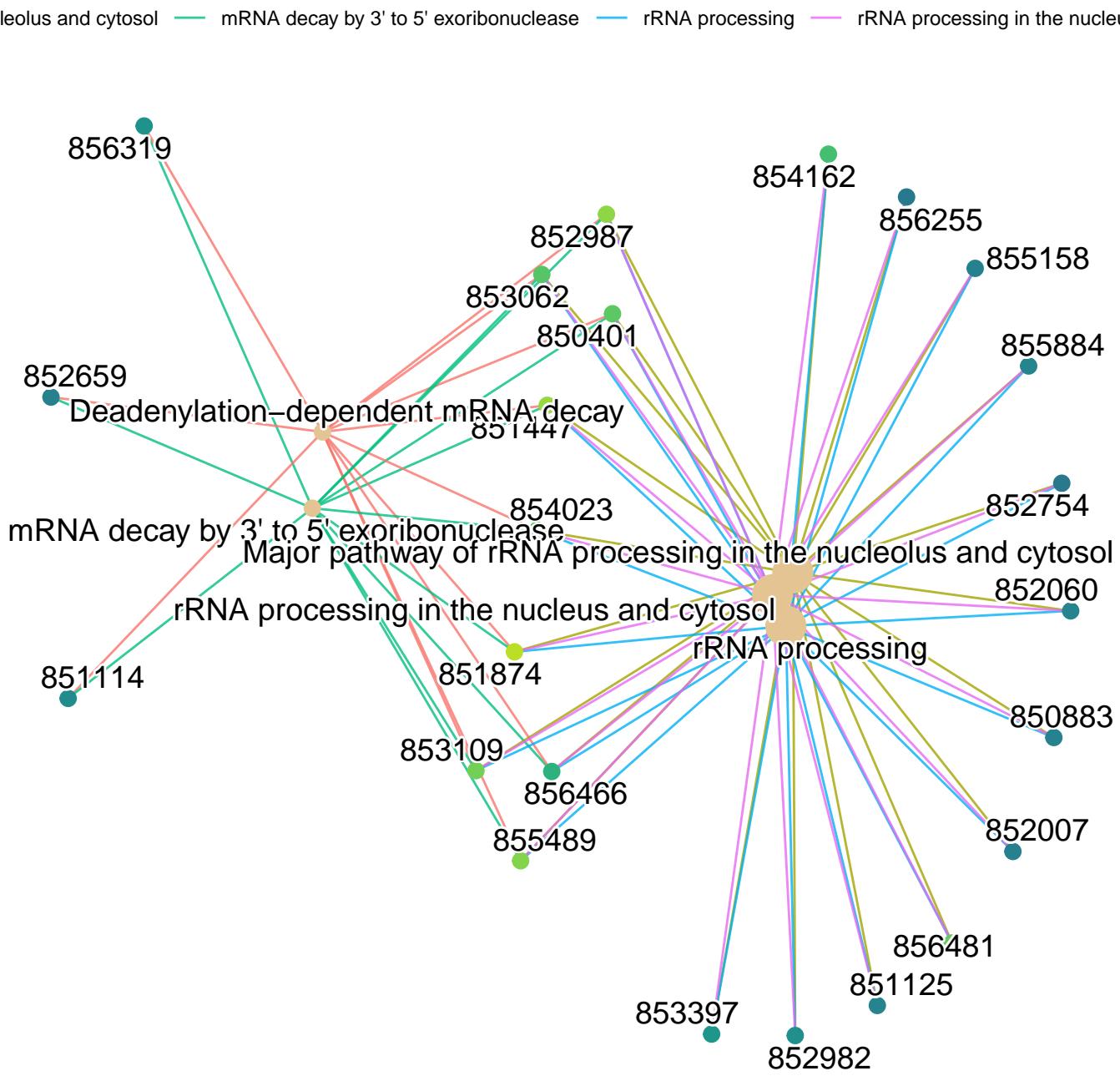
DIS3-TAP Up-regulated Reactome bar



DIS3-TAP Up-regulated Reactome dotp

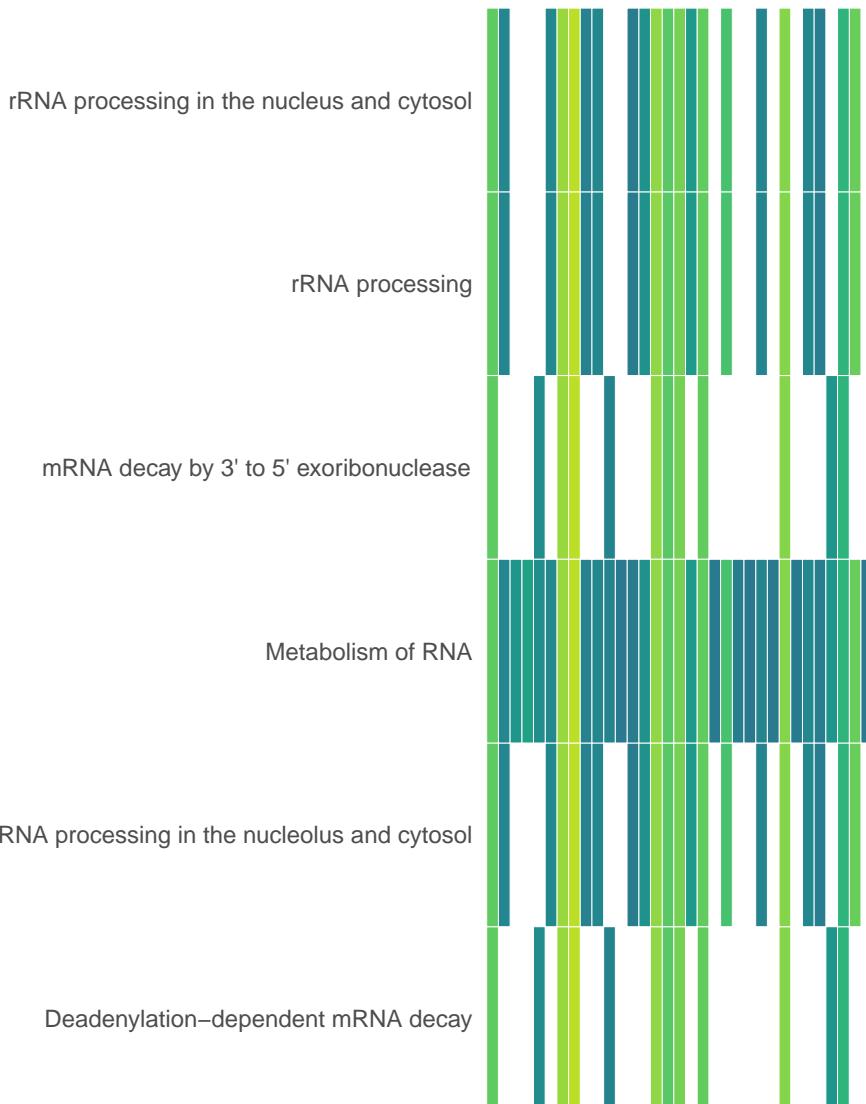


DIS3-TAP Up-regulated Reactome cnetplot



DIS3-TAP Up-regulated Reactome head

Reactome pathway



entrez ID

DIS3-TAP Up-regulated Reactome emapplot

Deadenylation-dependent mRNA decay

rRNA processing

Major pathway of rRNA processing in the nucleolus and cytosol

mRNA decay by 3' to 5' exoribonuclease

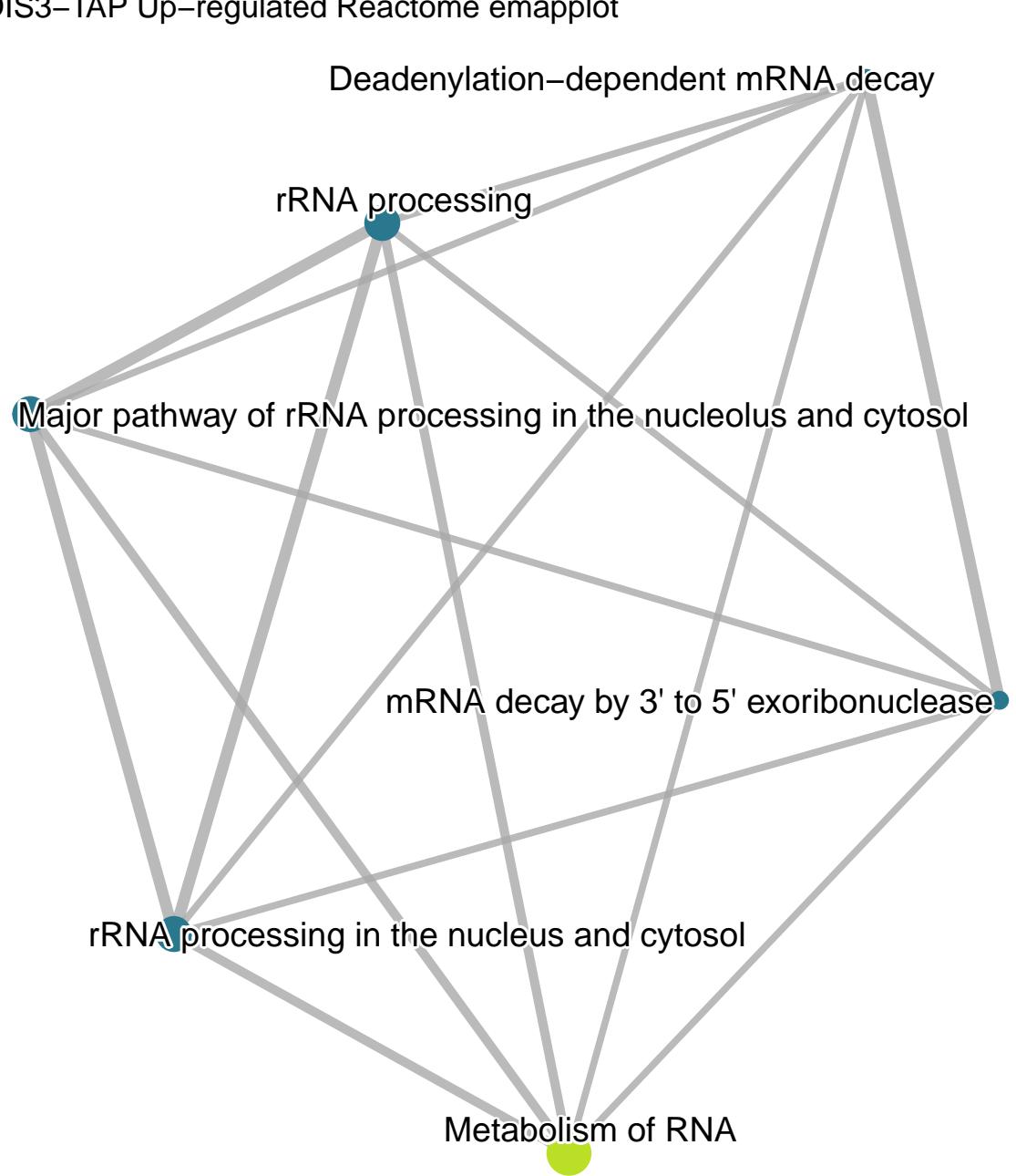
rRNA processing in the nucleus and cytosol

Metabolism of RNA

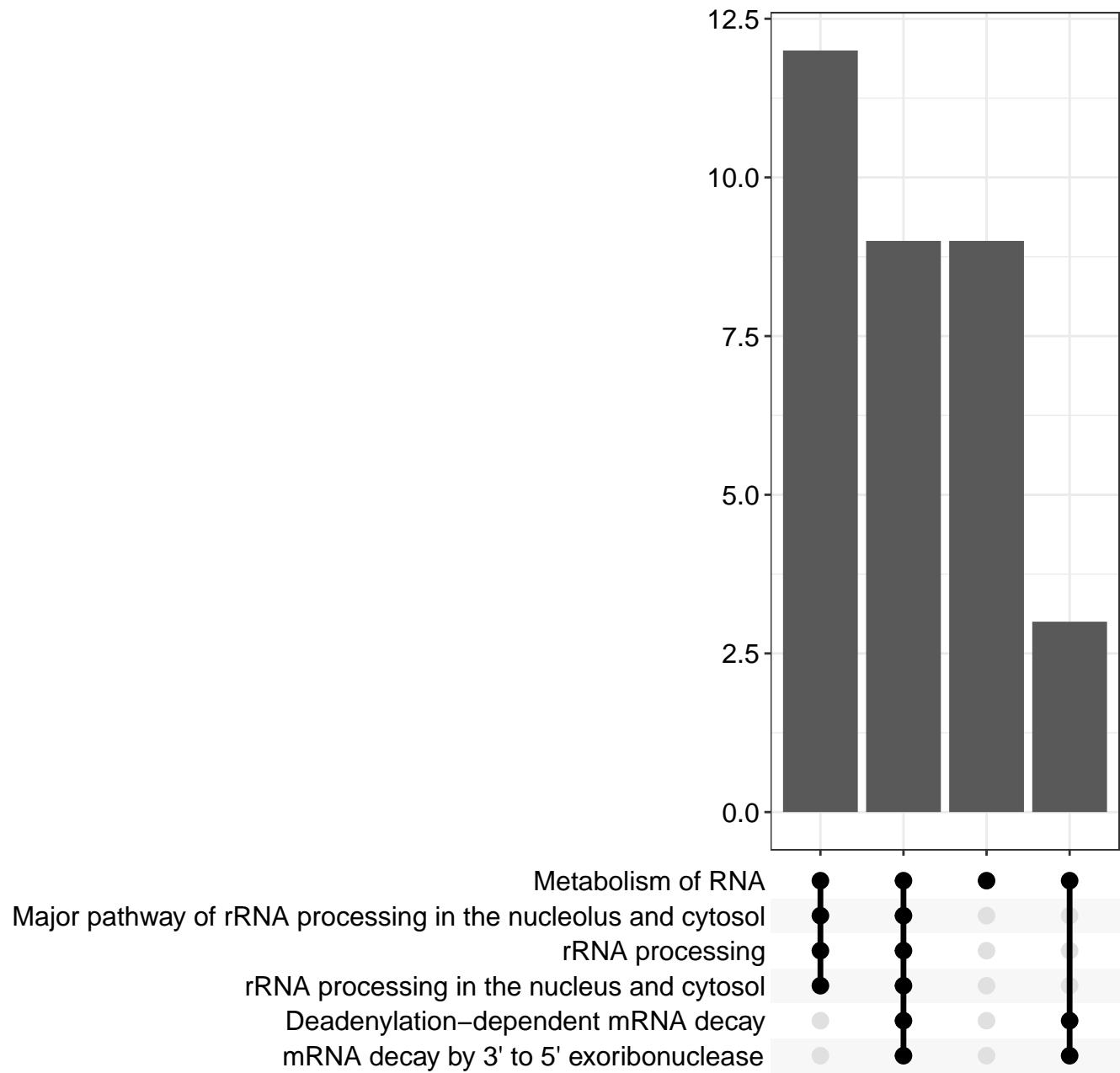
size

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- 20
- 25
- 30

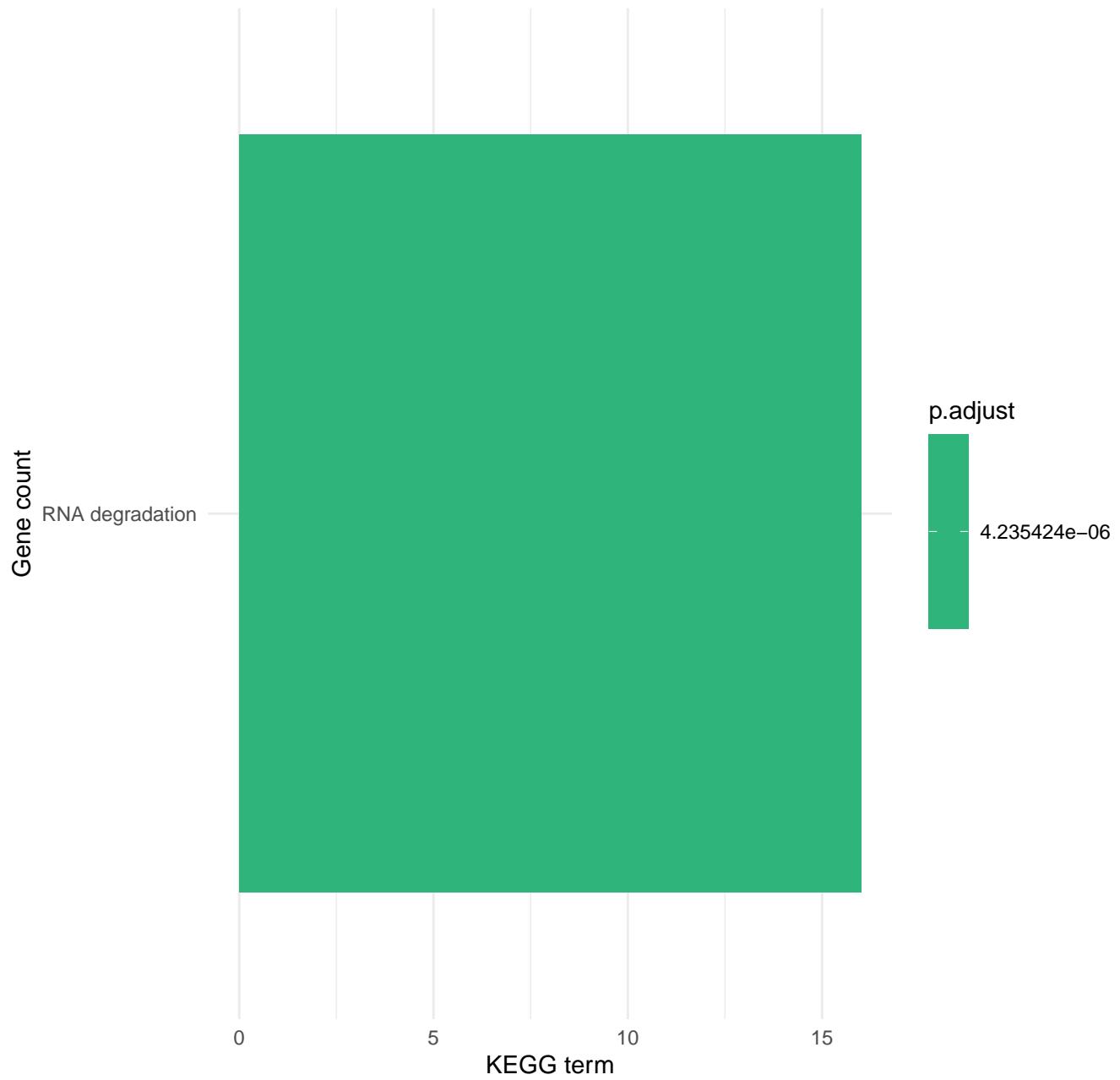
FoldChange



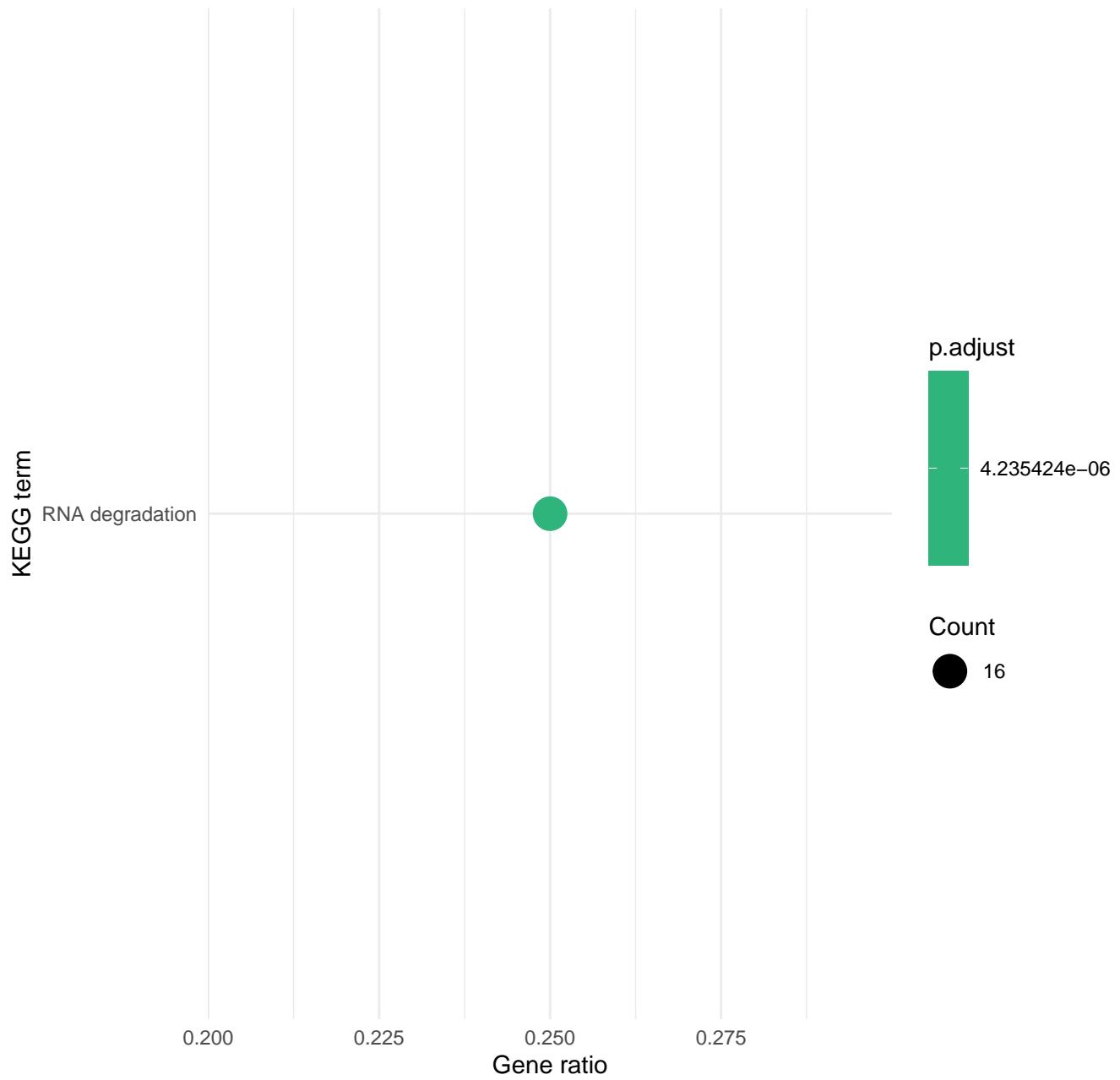
DIS3-TAP Up-regulated Re



DIS3-TAP Up-regulated KEGG barplot

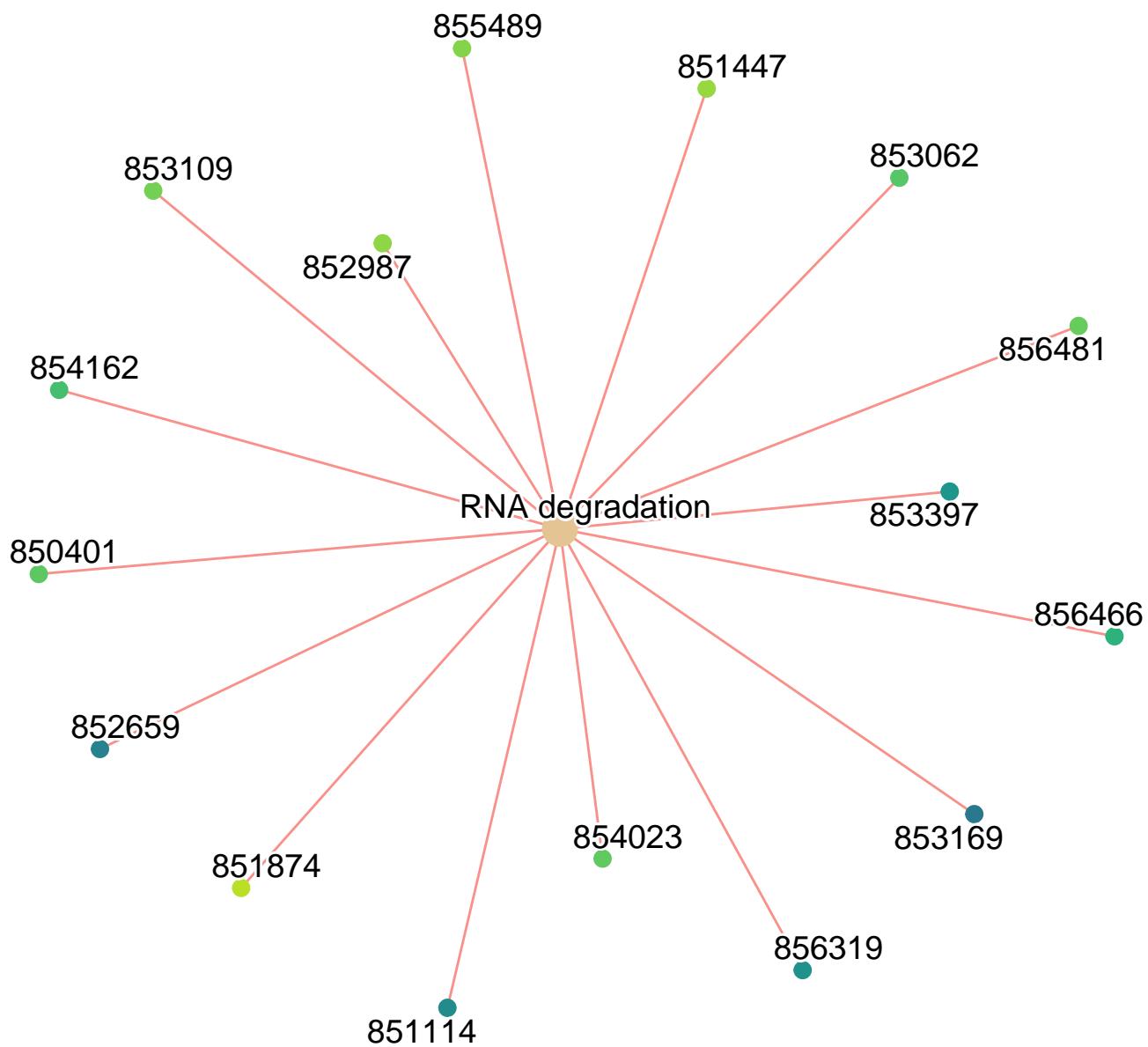


DIS3-TAP Up-regulated KEGG dotplot

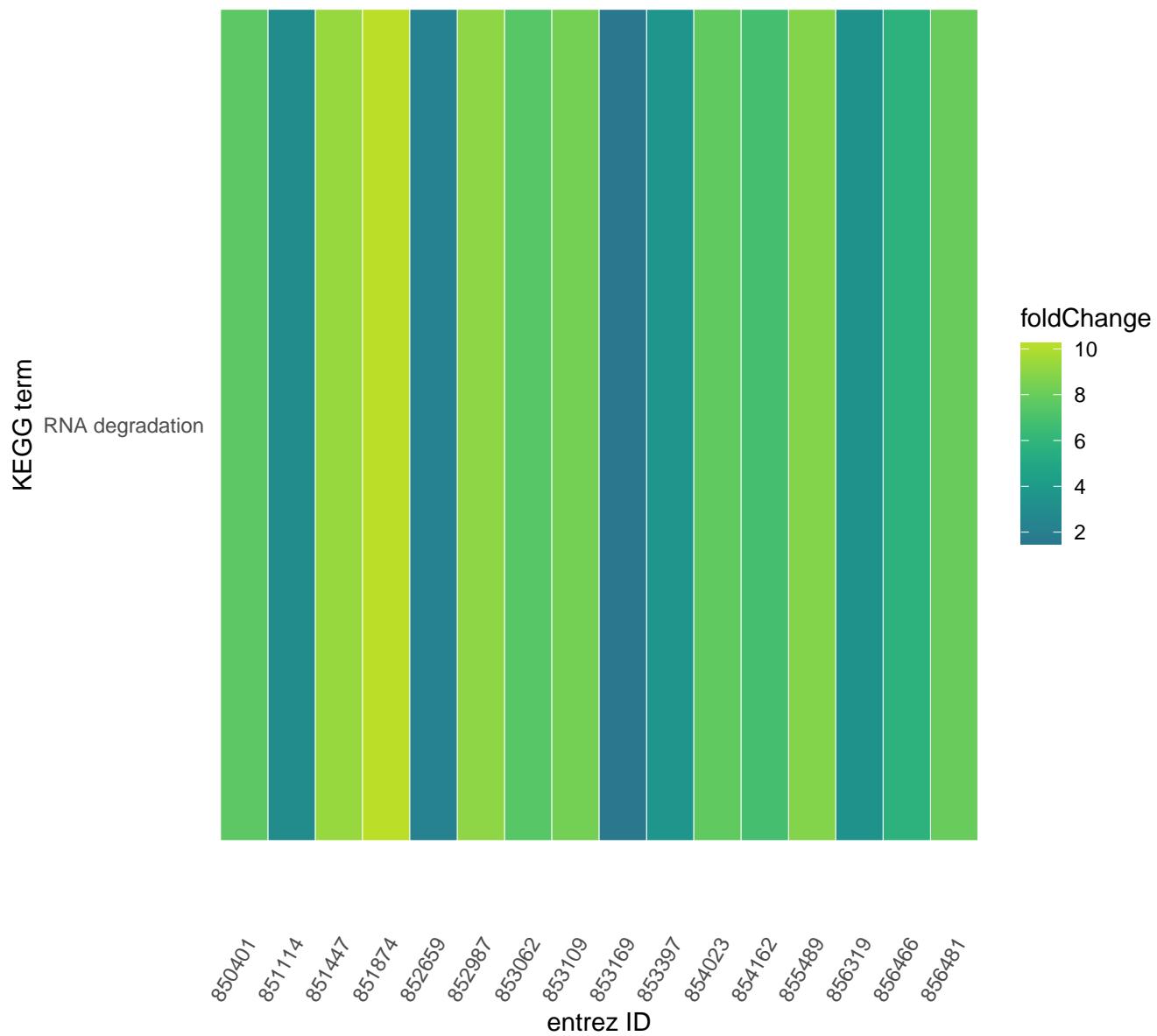


DIS3-TAP Up-regulated KEGG dotplot

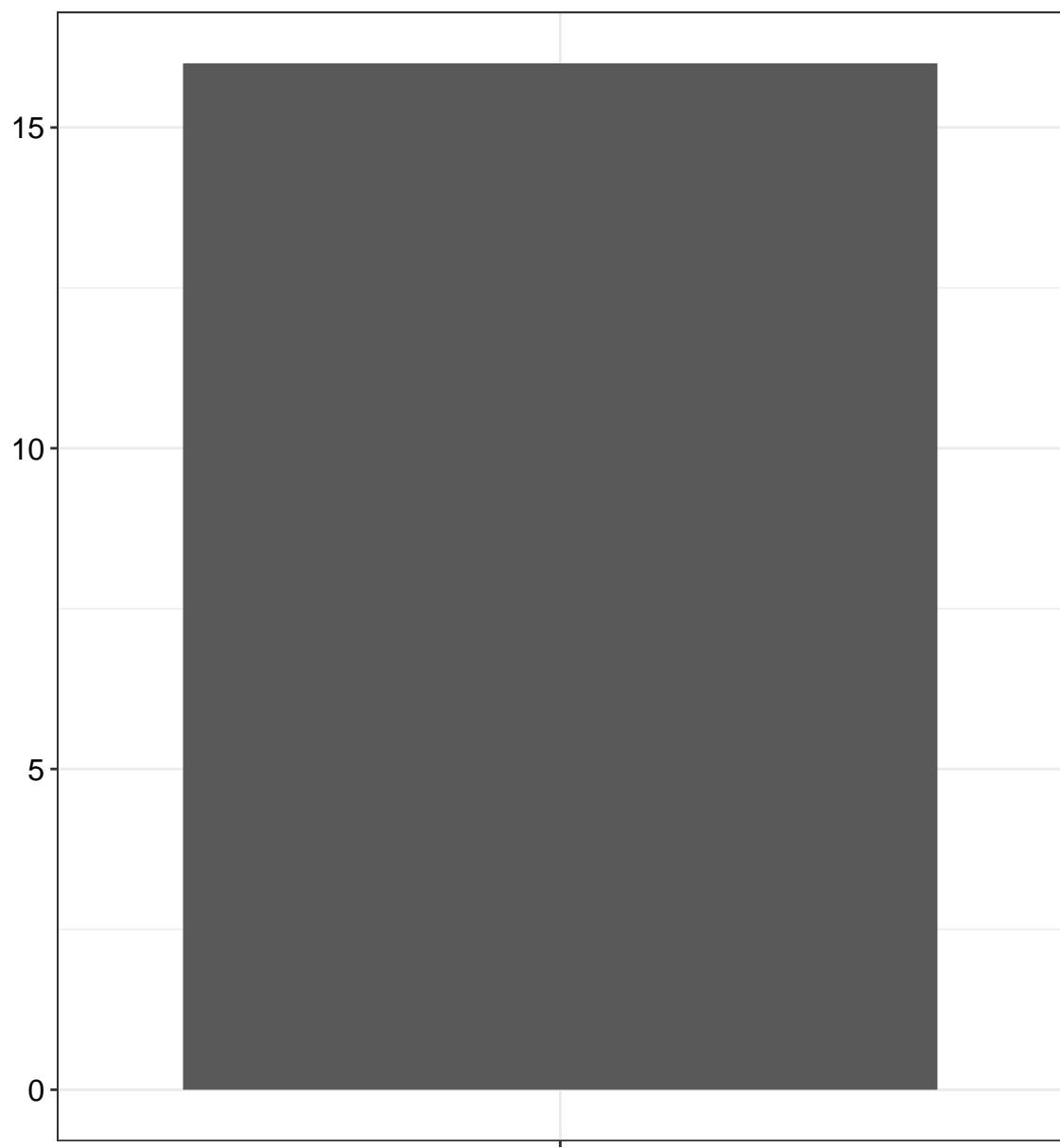
category RNA degradation size ● 16 FoldChange 2 4 6 8 10



DIS3-TAP Up-regulated KEGG heatplot

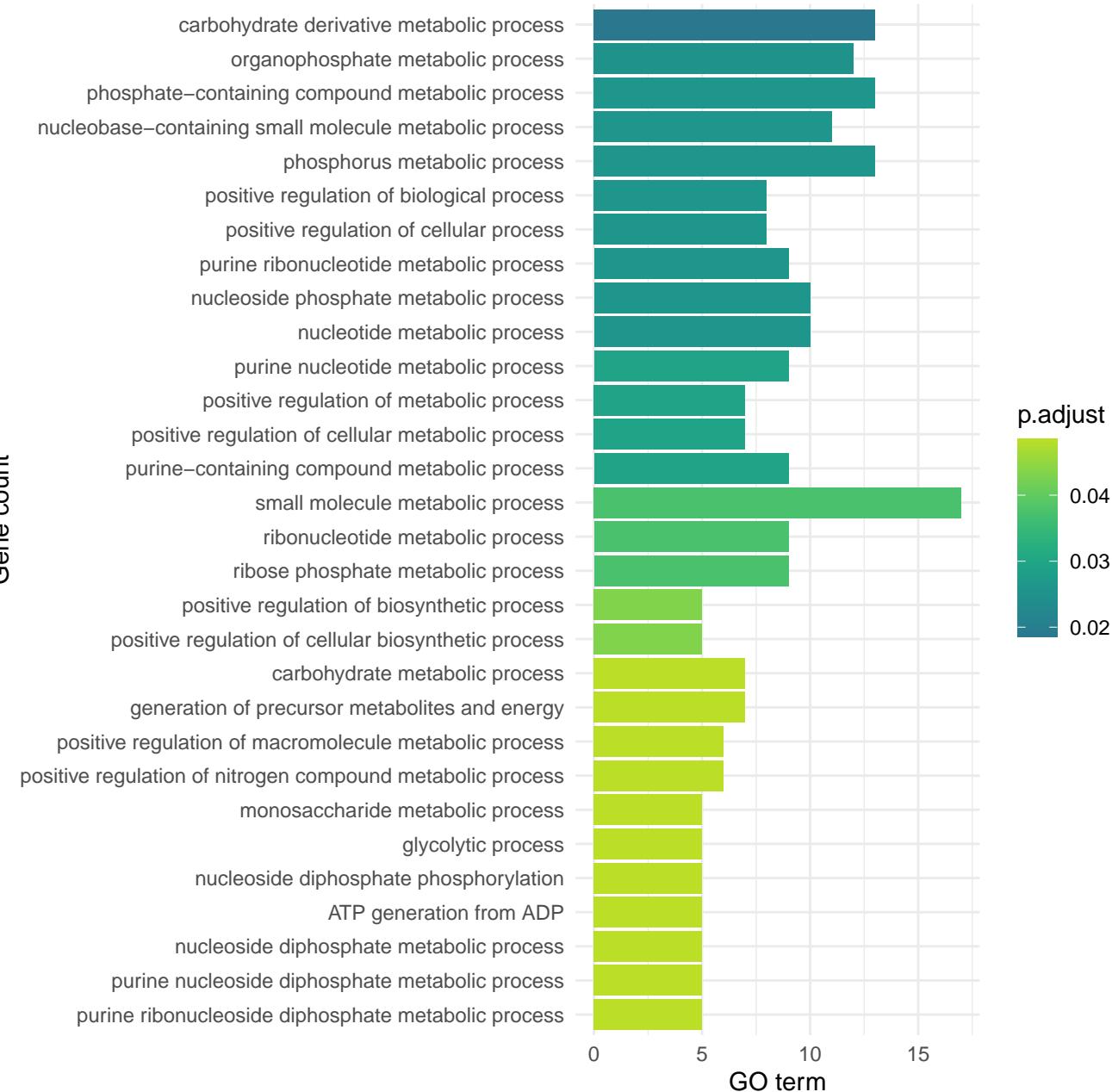


DIS3-TAP Up-regulated KEGG upsetplot

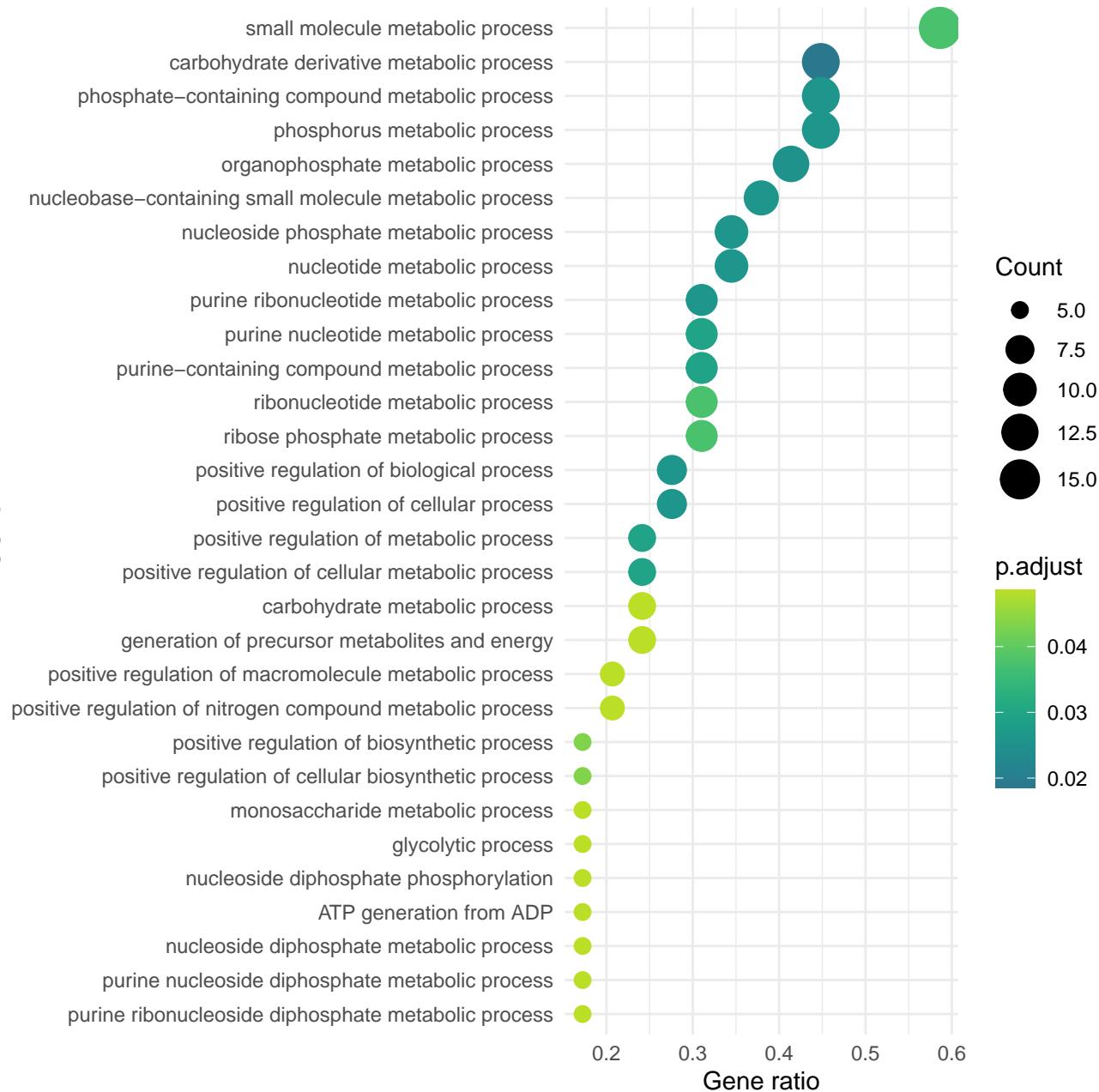


RNA degradation

FAL1-TAP Up-regulated GO BP barplot

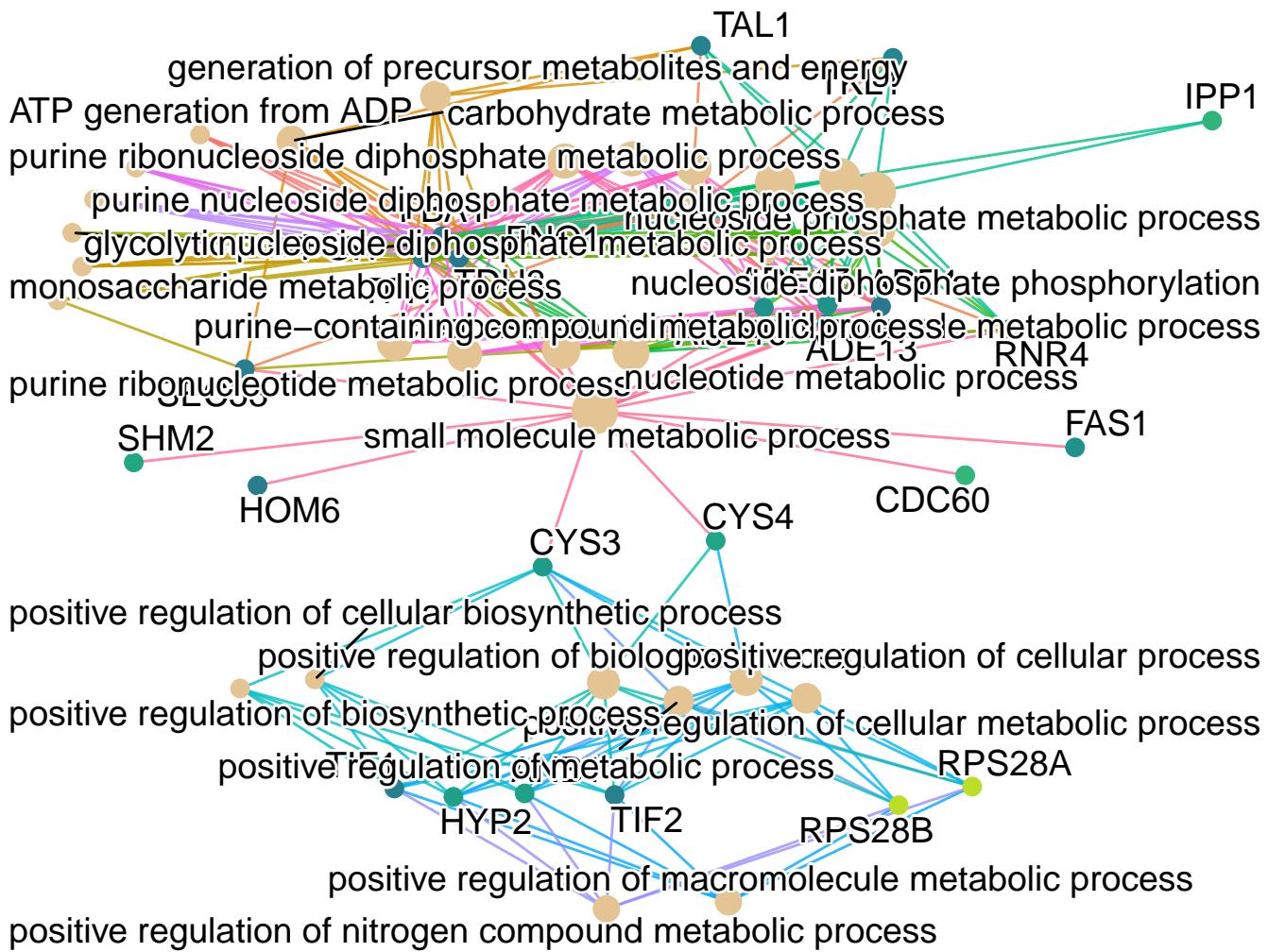


FAL1-TAP Up-regulated GO BP dotplot



FAL1-TAP Up-regulated GO BP cnetplot

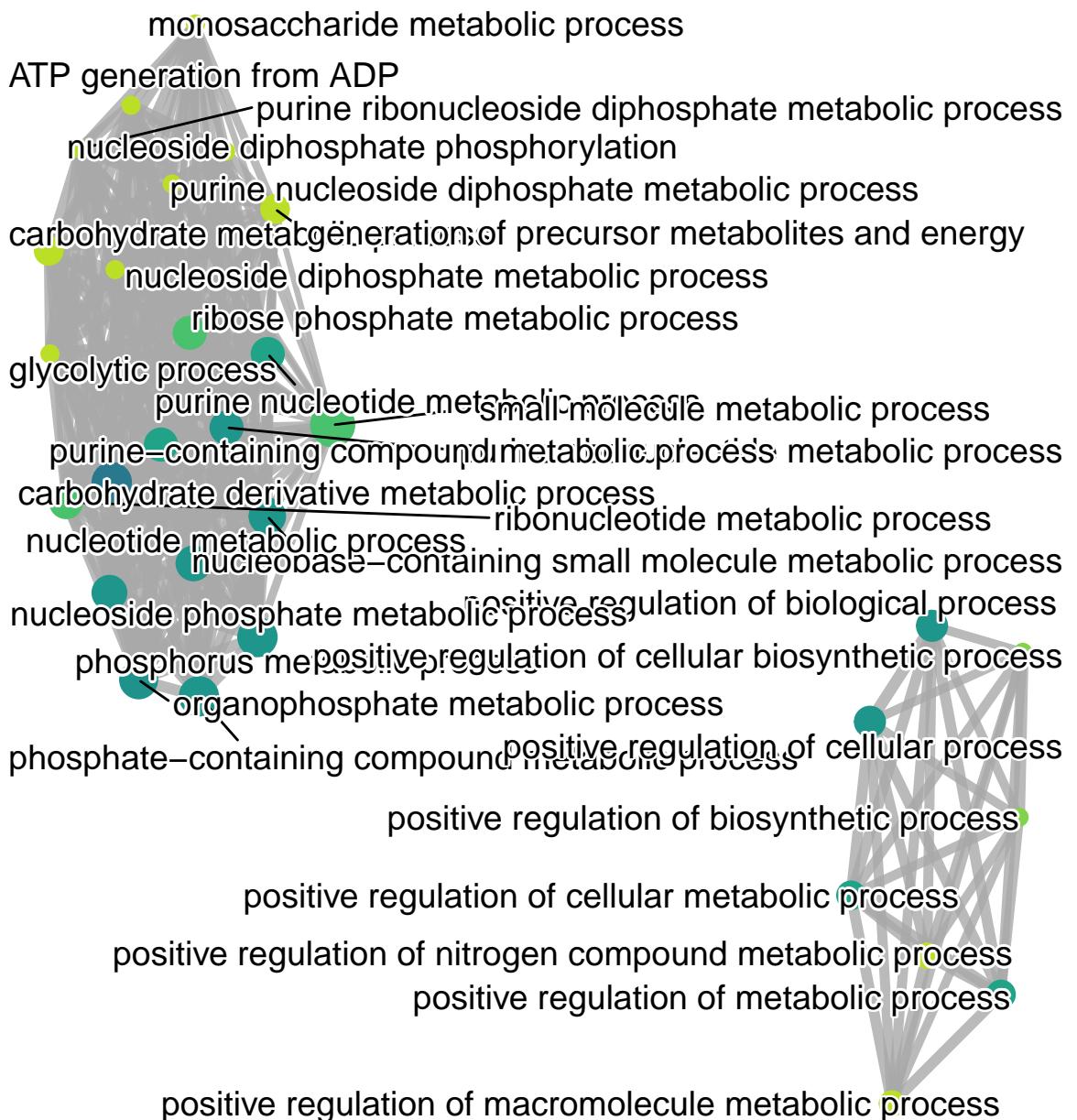
e-containing compound metabolic process	positive regulation of cellular process	purine ribo
us metabolic process	positive regulation of macromolecule metabolic process	purine ribo
regulation of biological process	positive regulation of metabolic process	purine-co
regulation of biosynthetic process	positive regulation of nitrogen compound metabolic process	ribonucle
regulation of cellular biosynthetic process	purine nucleoside diphosphate metabolic process	ribose pho
regulation of cellular metabolic process	purine nucleotide metabolic process	small mole

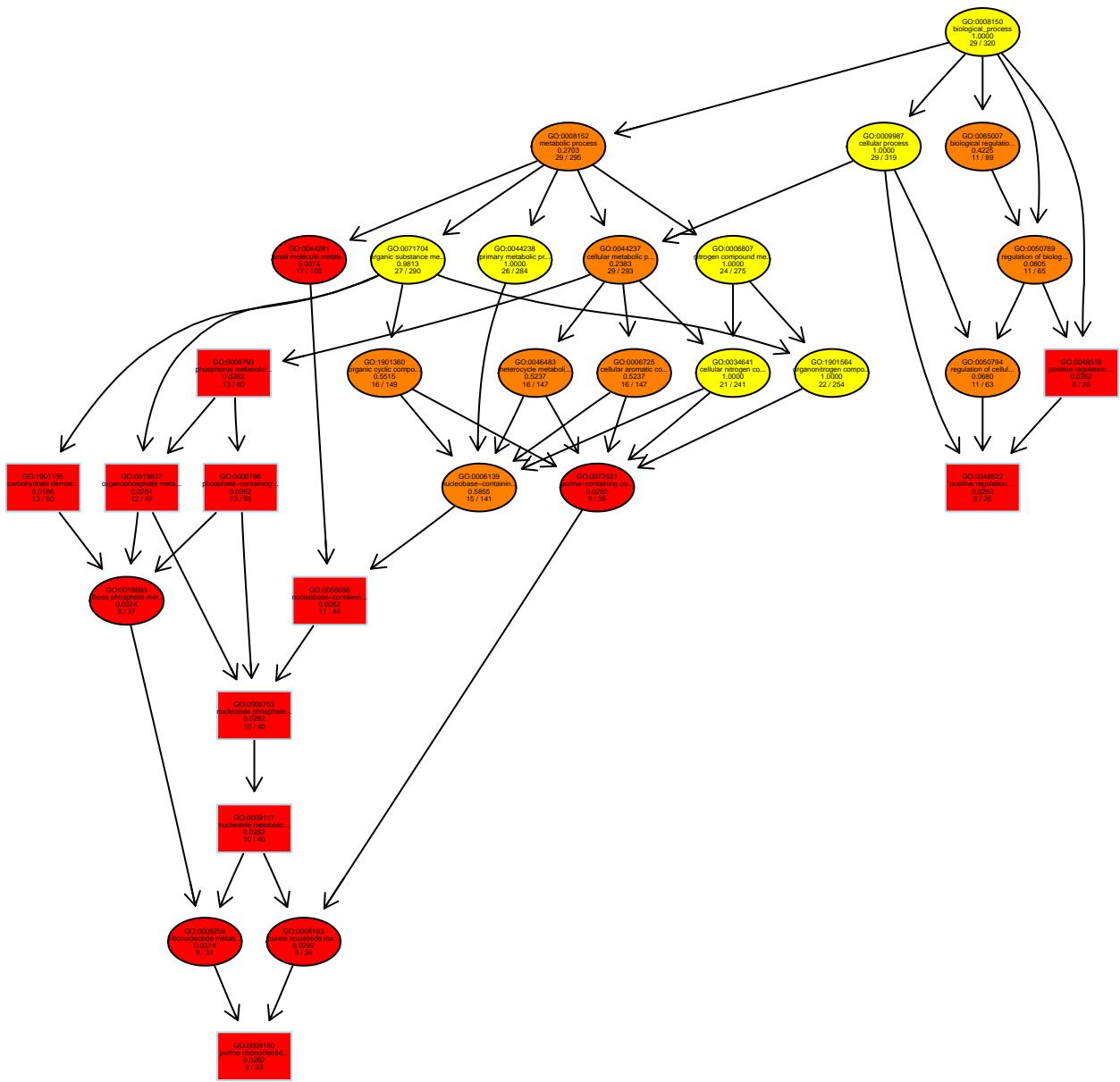


FAL1-TAP Up-regulated GO BP heatplot

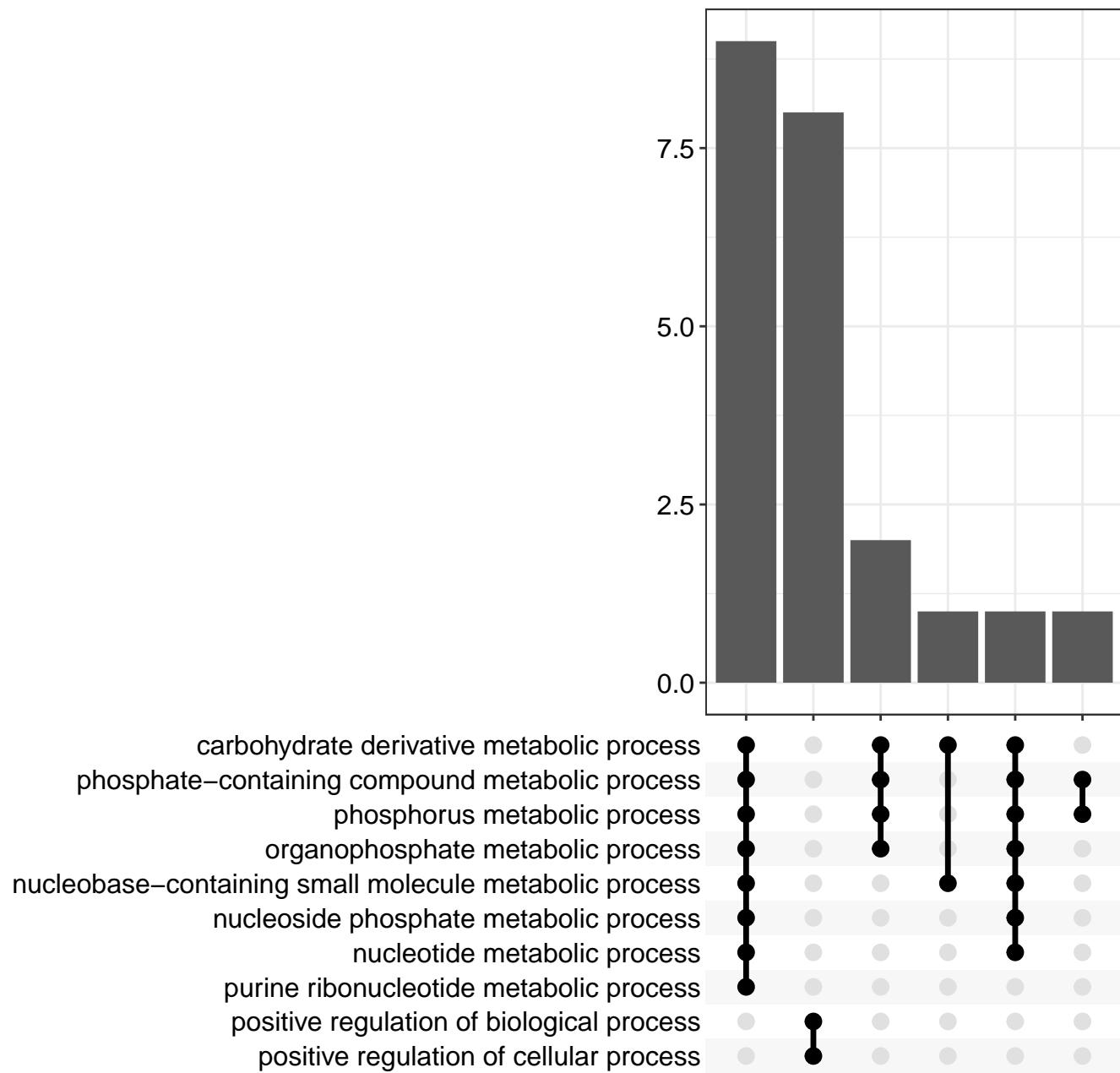


FAL1-TAP Up-regulated GO BP emapplot

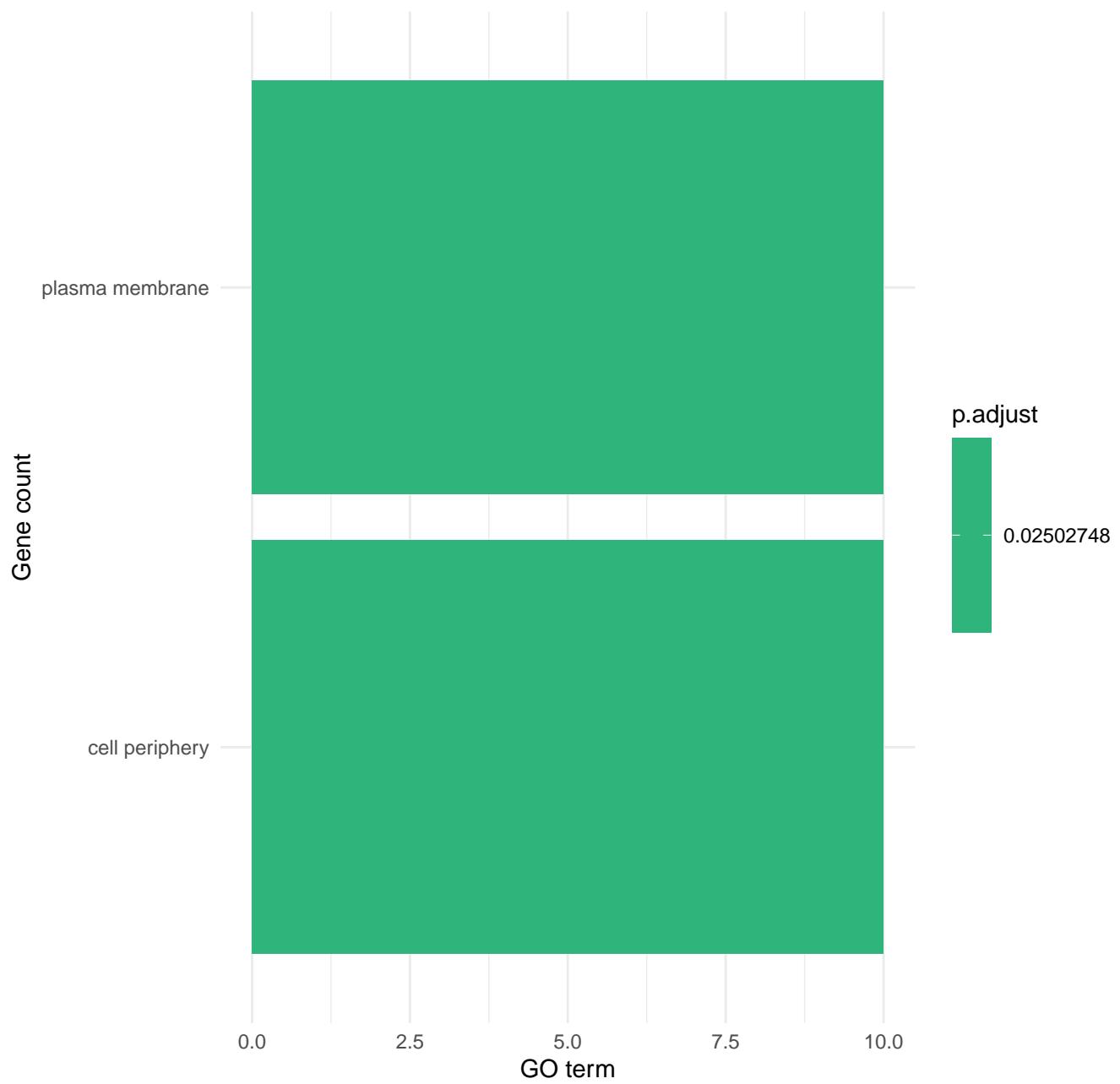




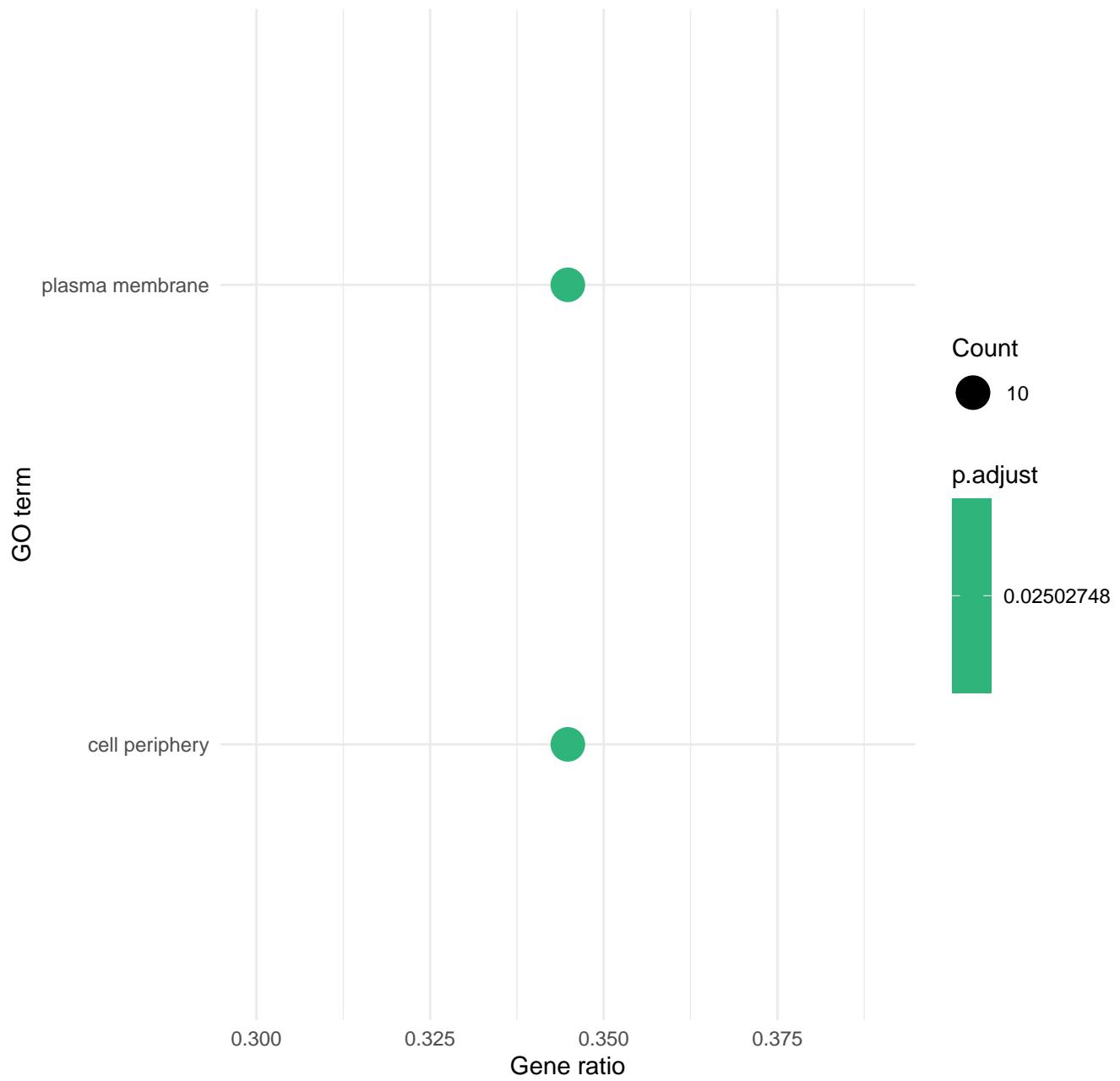
FAL1-TAP Up-regulated GO BP



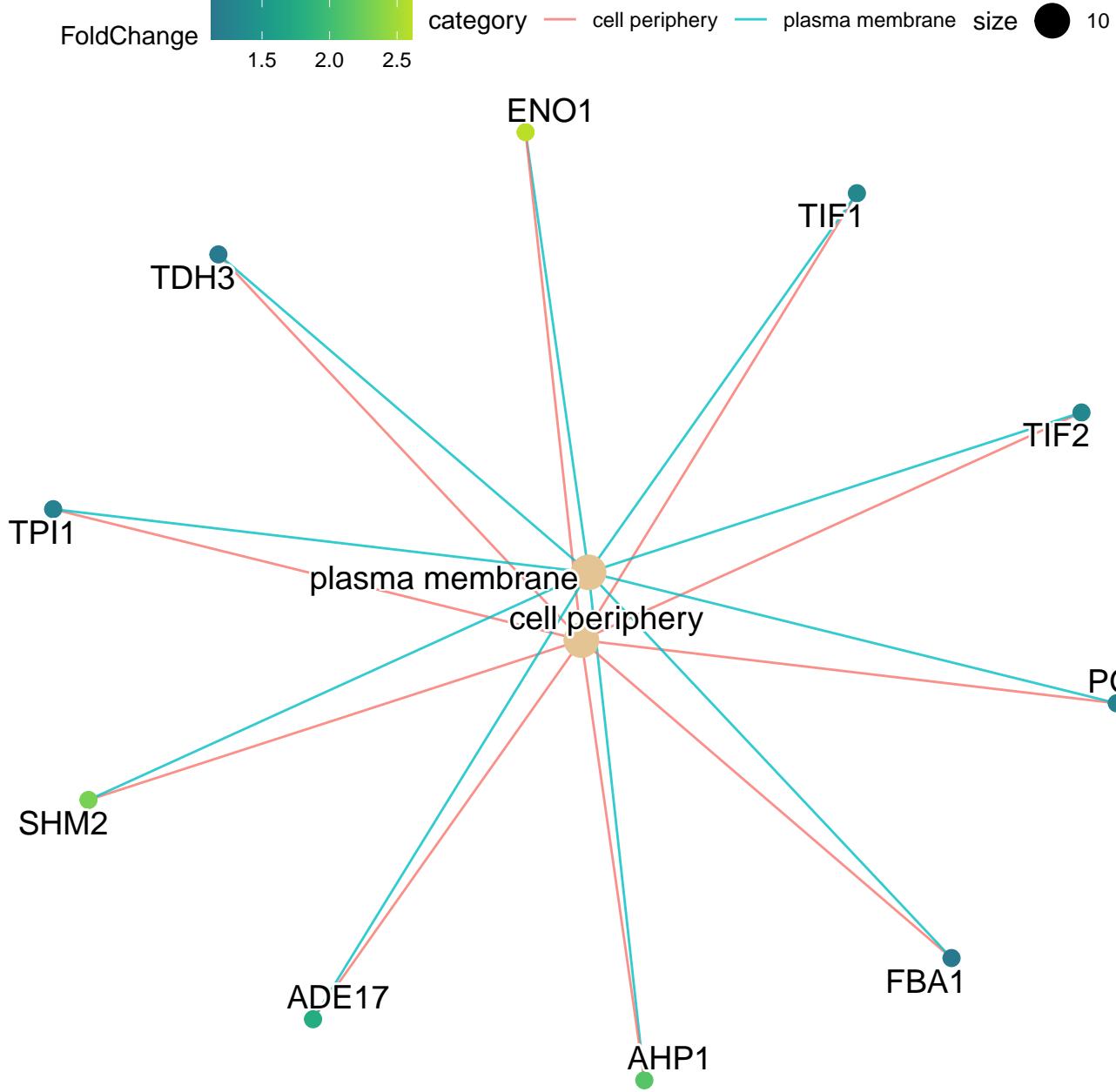
FAL1-TAP Up-regulated GO CC barplot



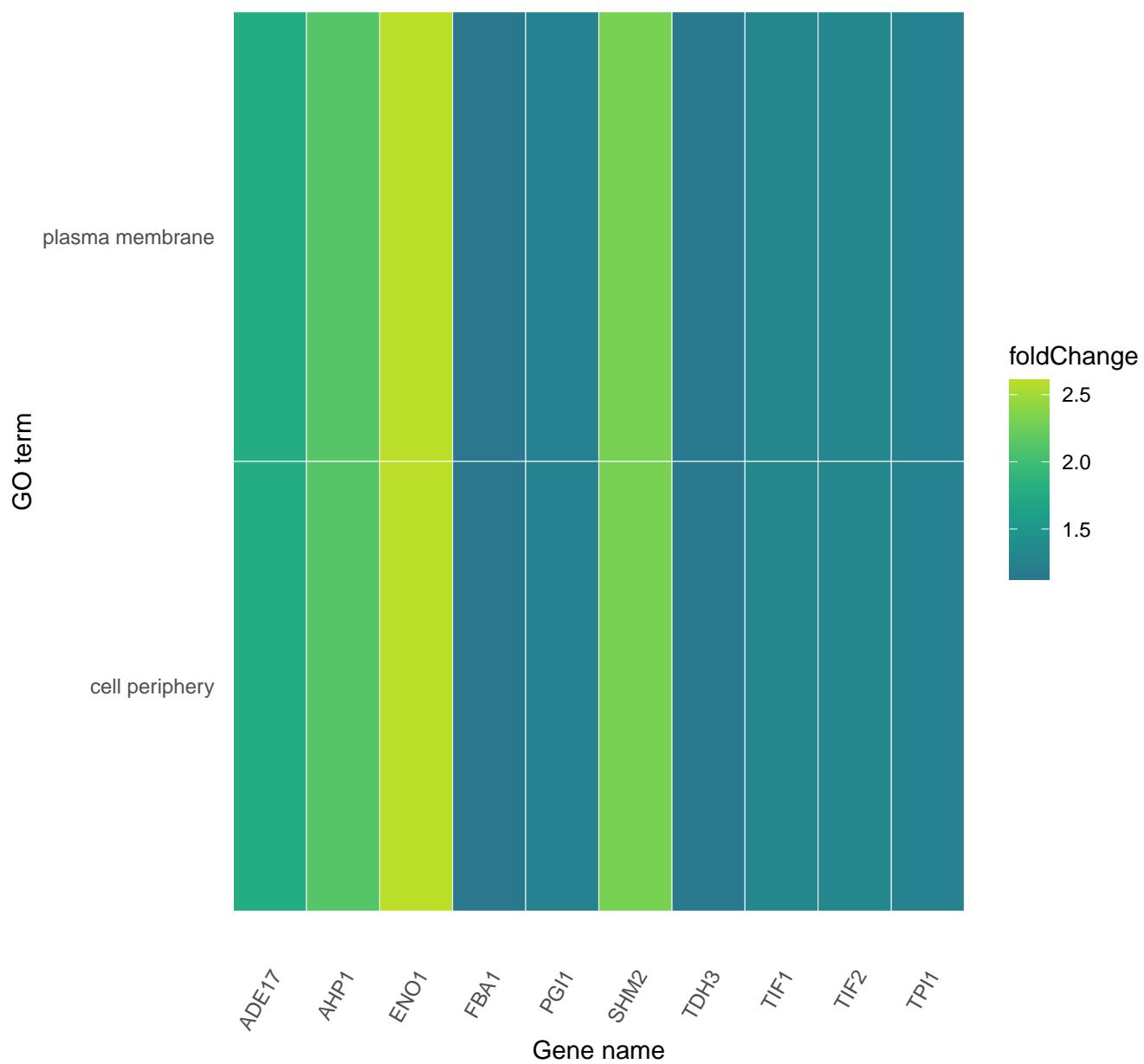
FAL1-TAP Up-regulated GO CC dotplot



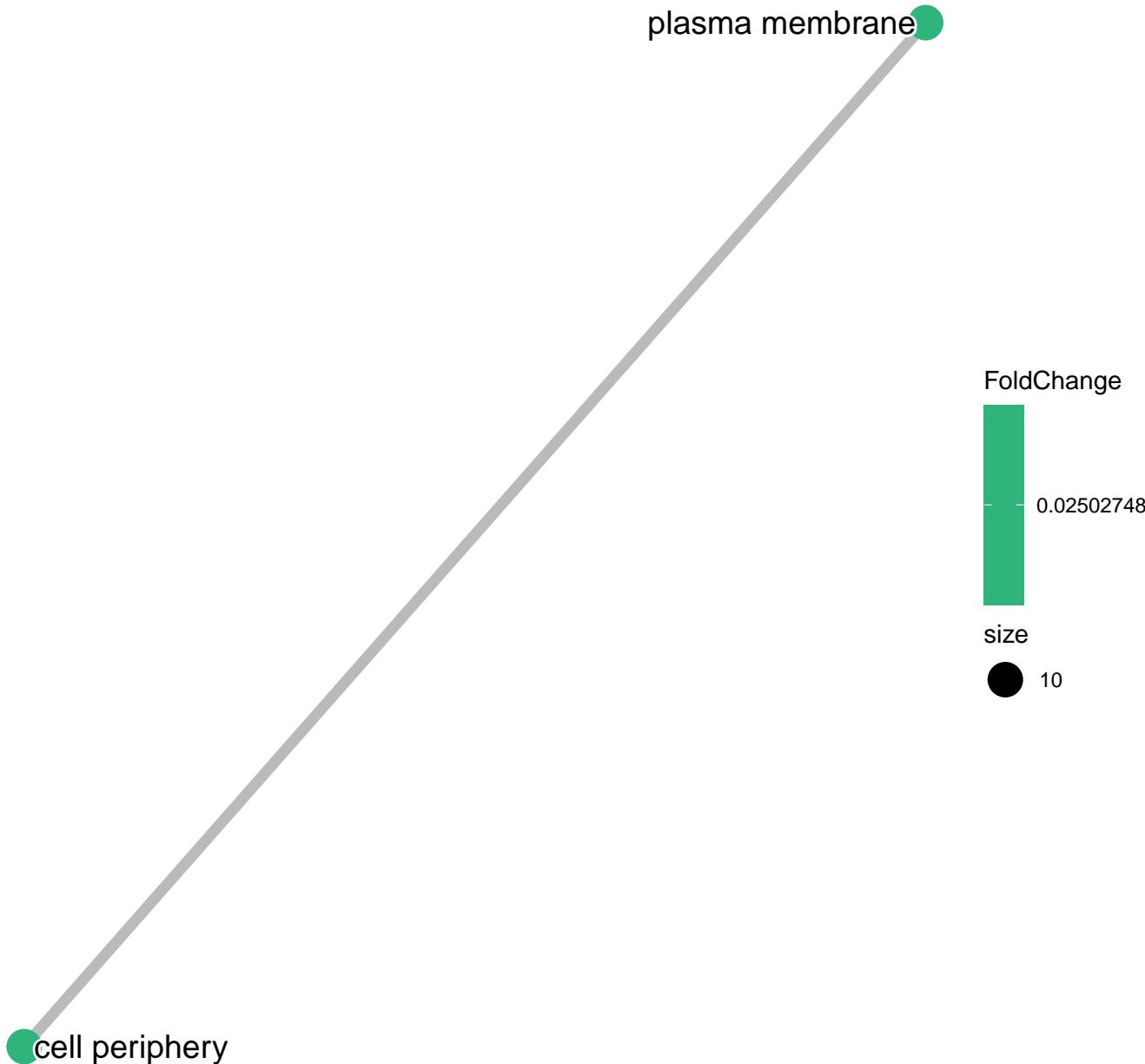
FAL1-TAP Up-regulated GO CC cnetplot

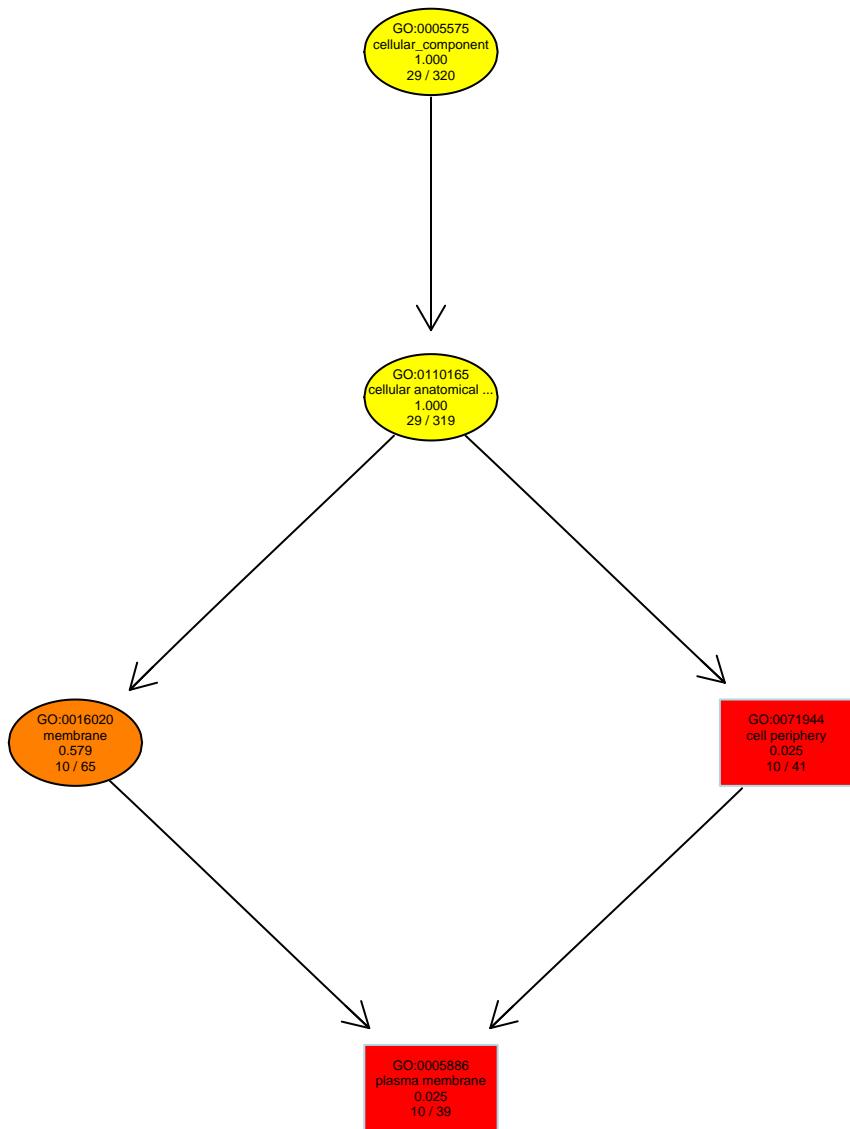


FAL1-TAP Up-regulated GO CC heatplot

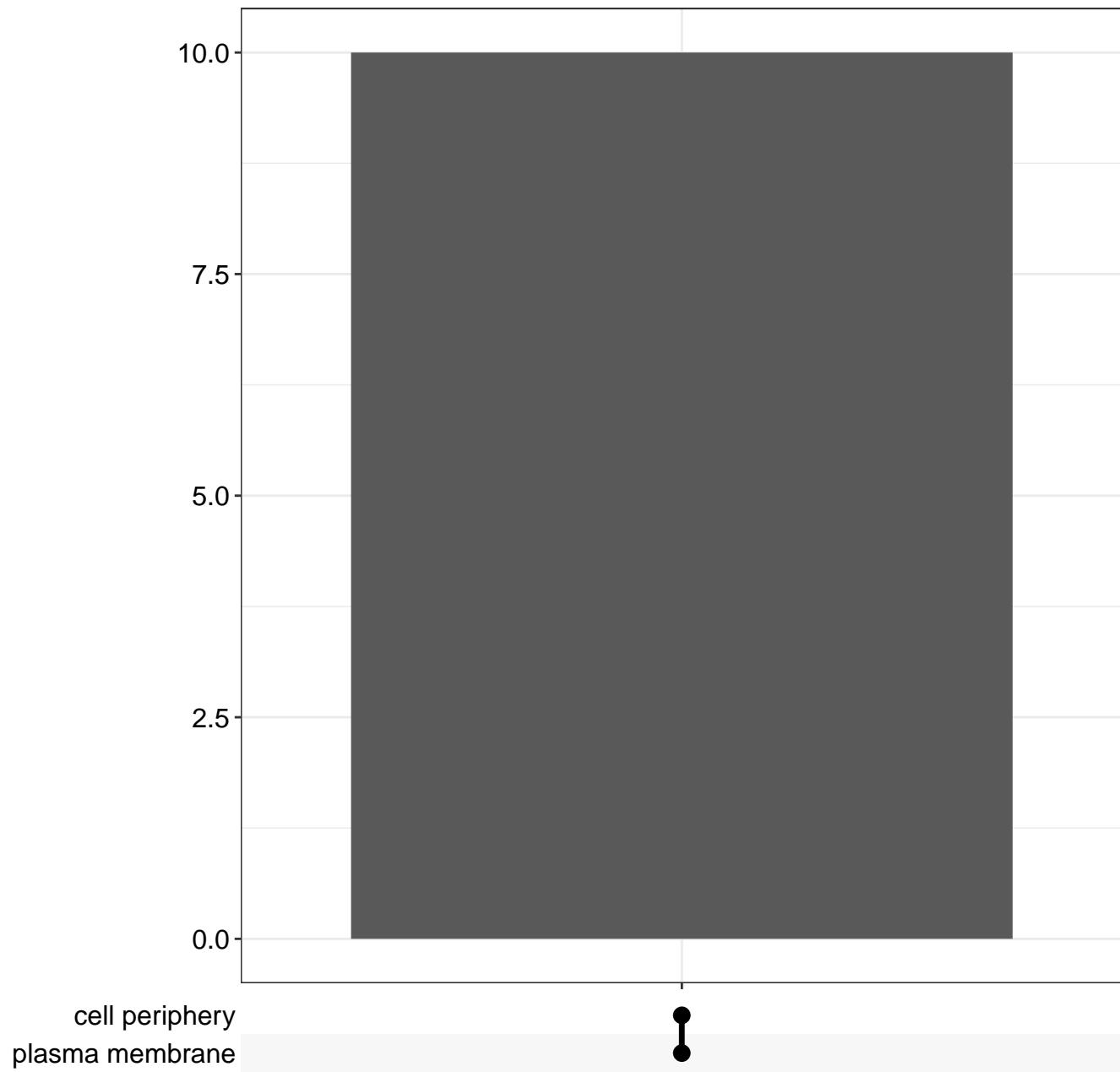


FAL1-TAP Up-regulated GO CC emapplot

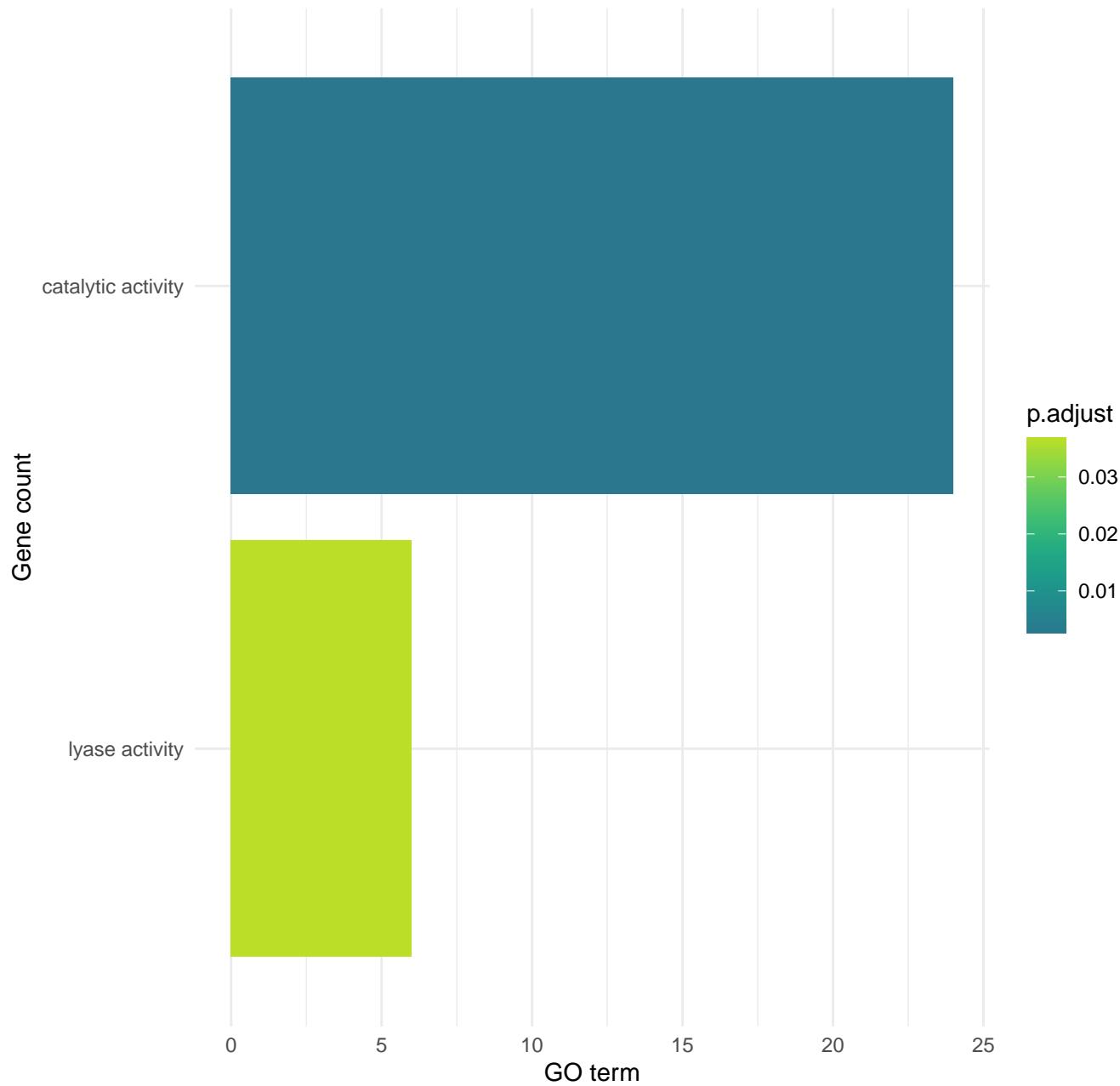




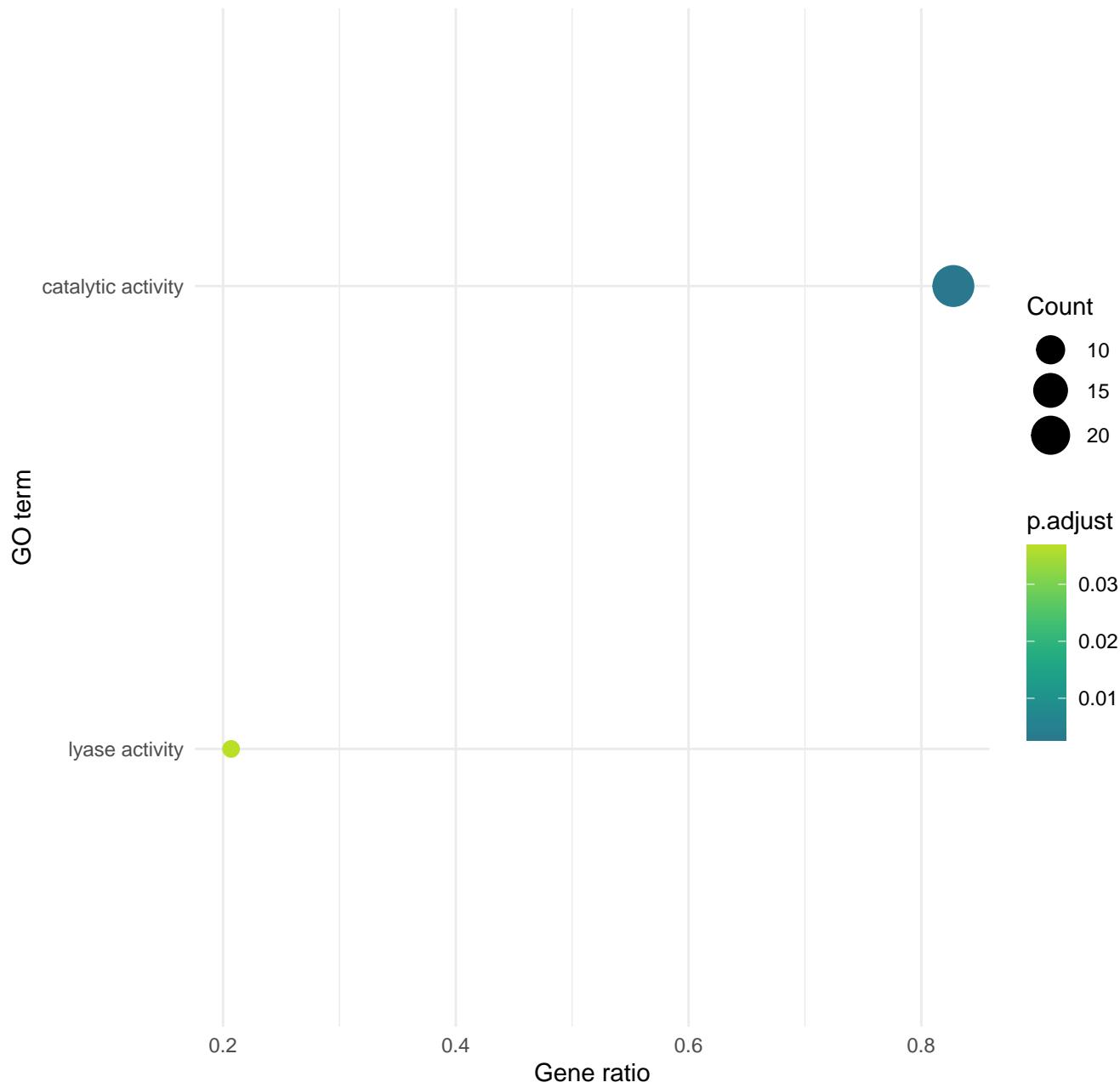
FAL1-TAP Up-regulated GO CC upsetplot



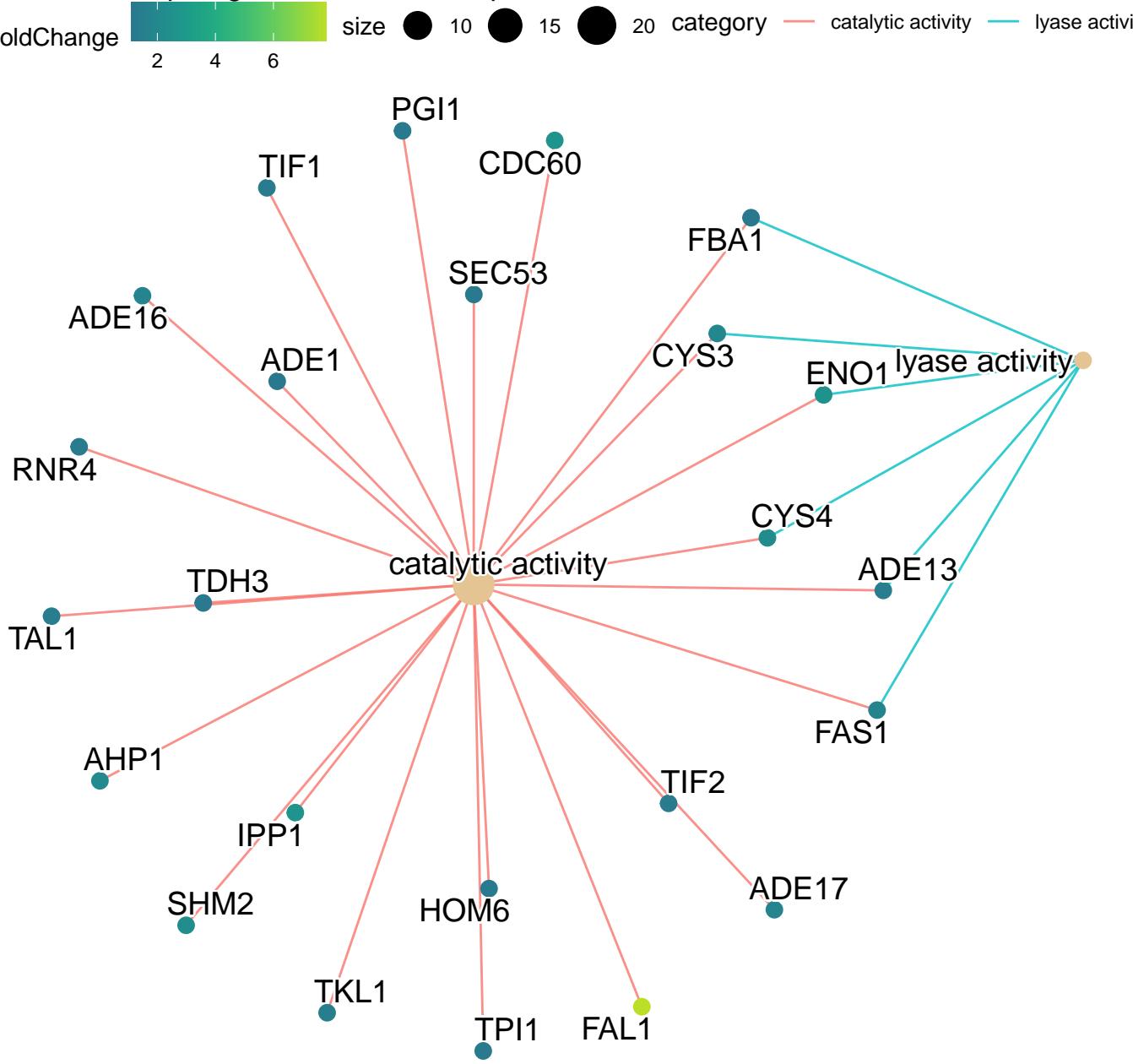
FAL1-TAP Up-regulated GO MF barplot



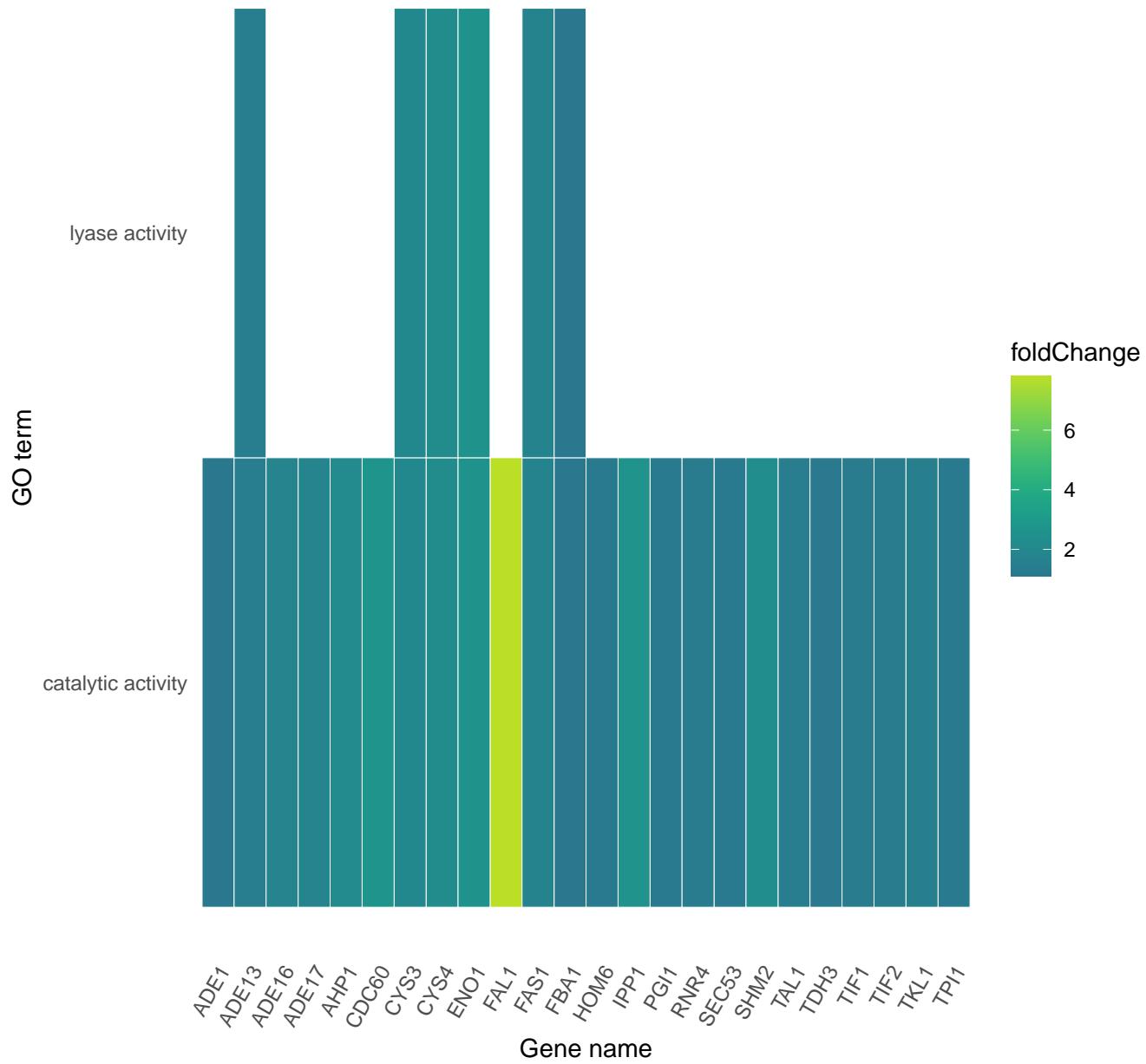
FAL1-TAP Up-regulated GO MF dotplot



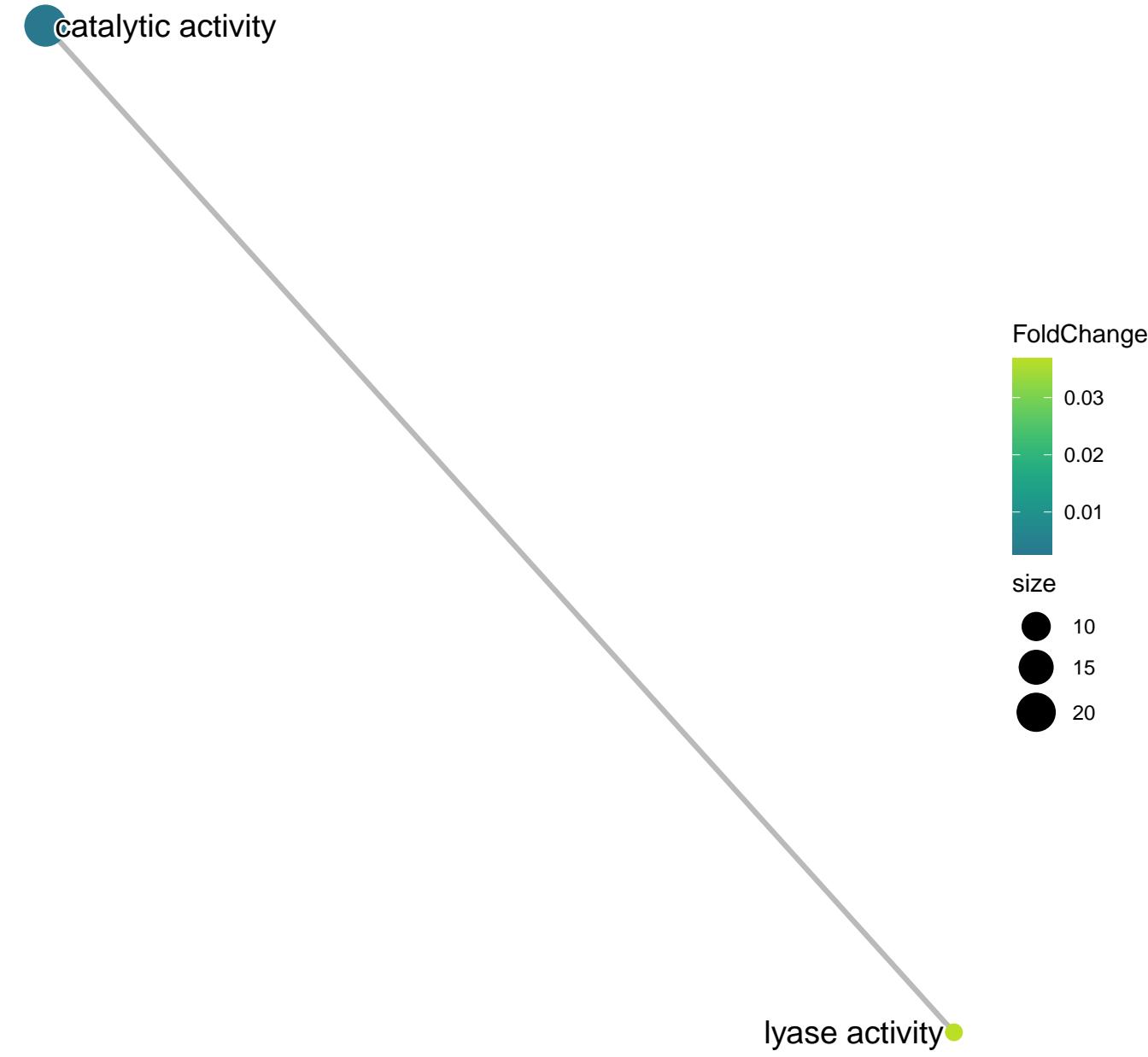
FAL1-TAP Up-regulated GO MF cnetplot



FAL1-TAP Up-regulated GO MF heatplot



FAL1-TAP Up-regulated GO MF emapplot



GO:0003674
molecular_function
1.00000
29 / 320

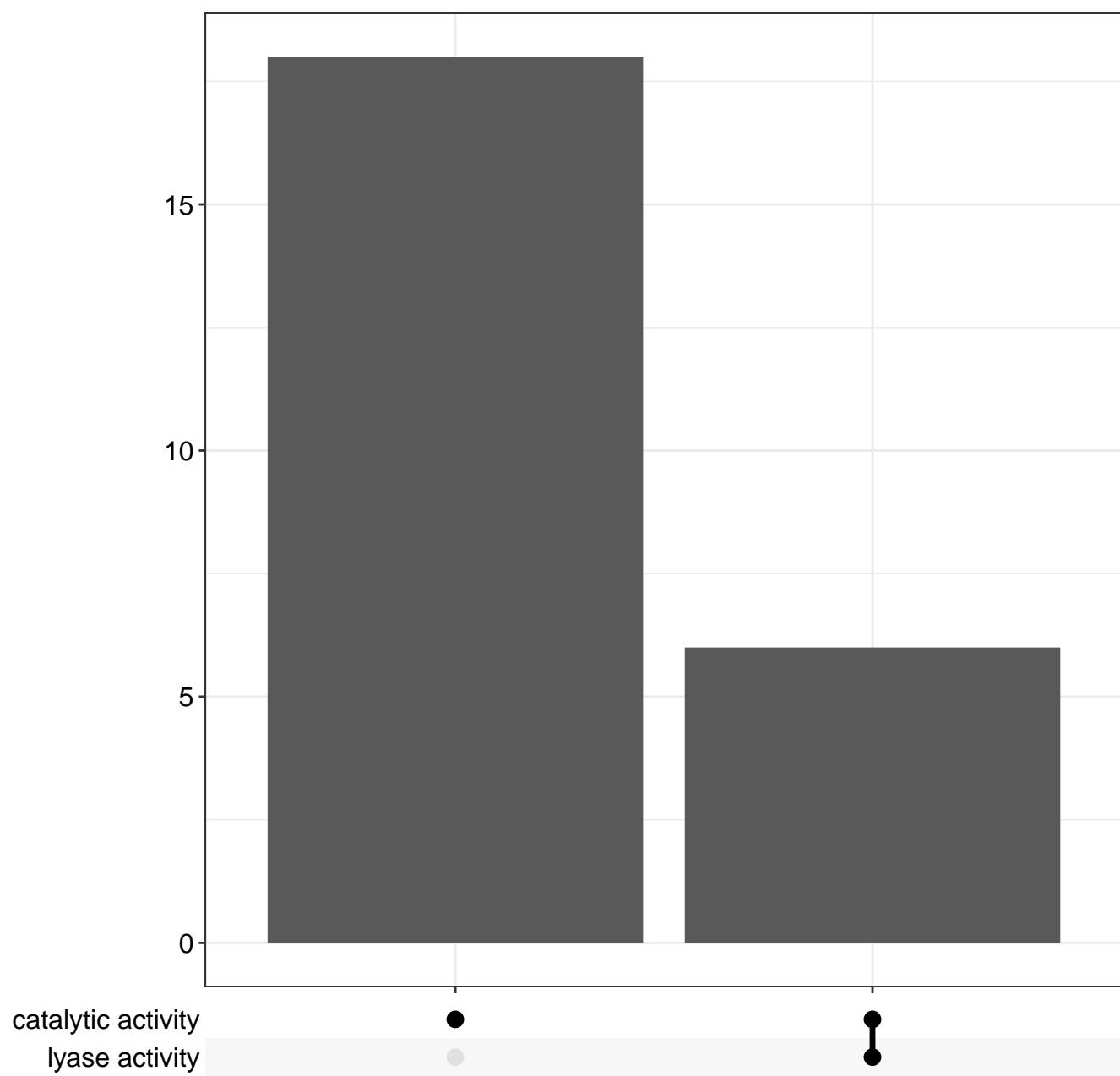


GO:0003824
catalytic activity
0.00263
24 / 152

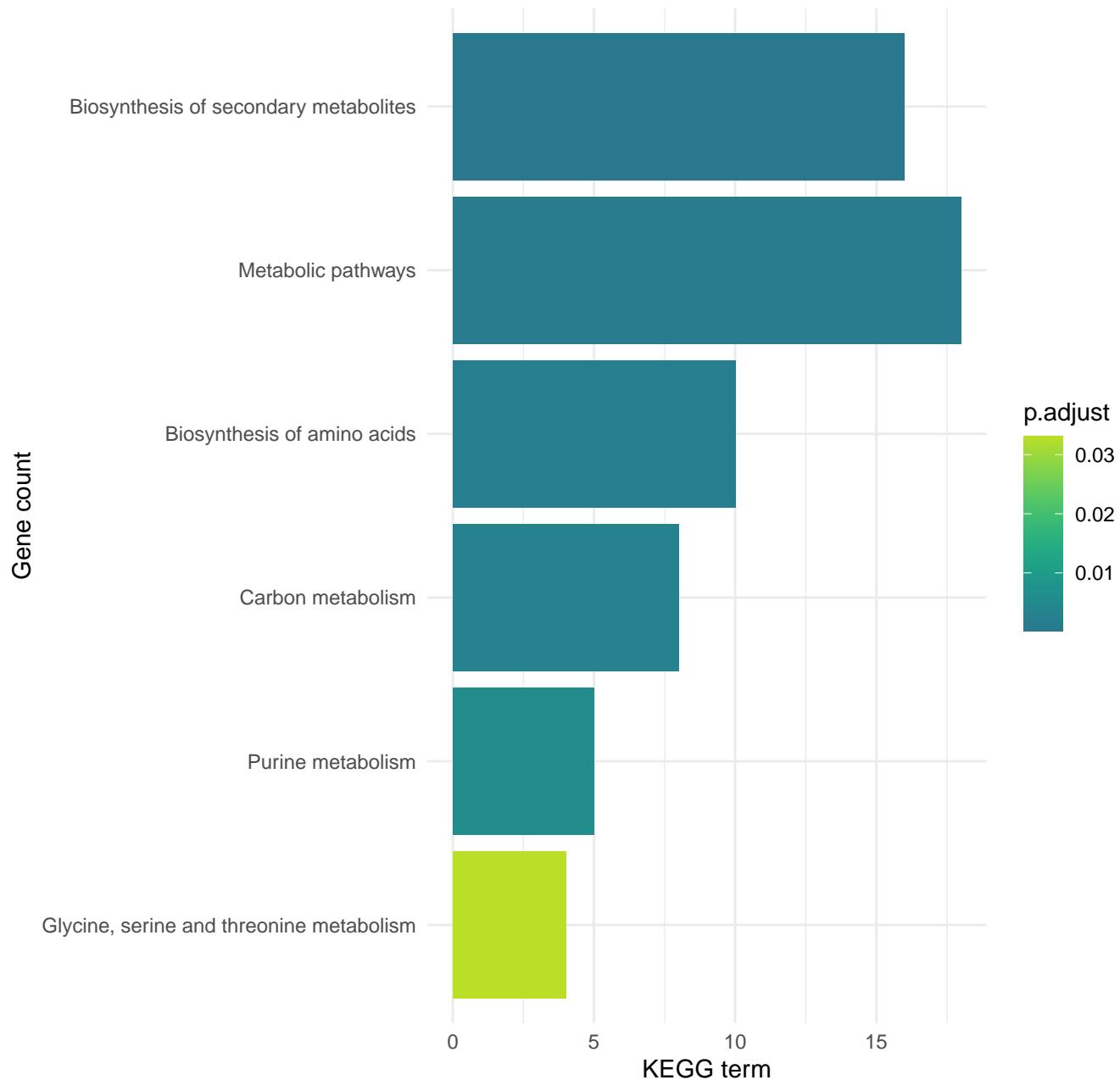


GO:0016829
lyase activity
0.03690
6 / 16

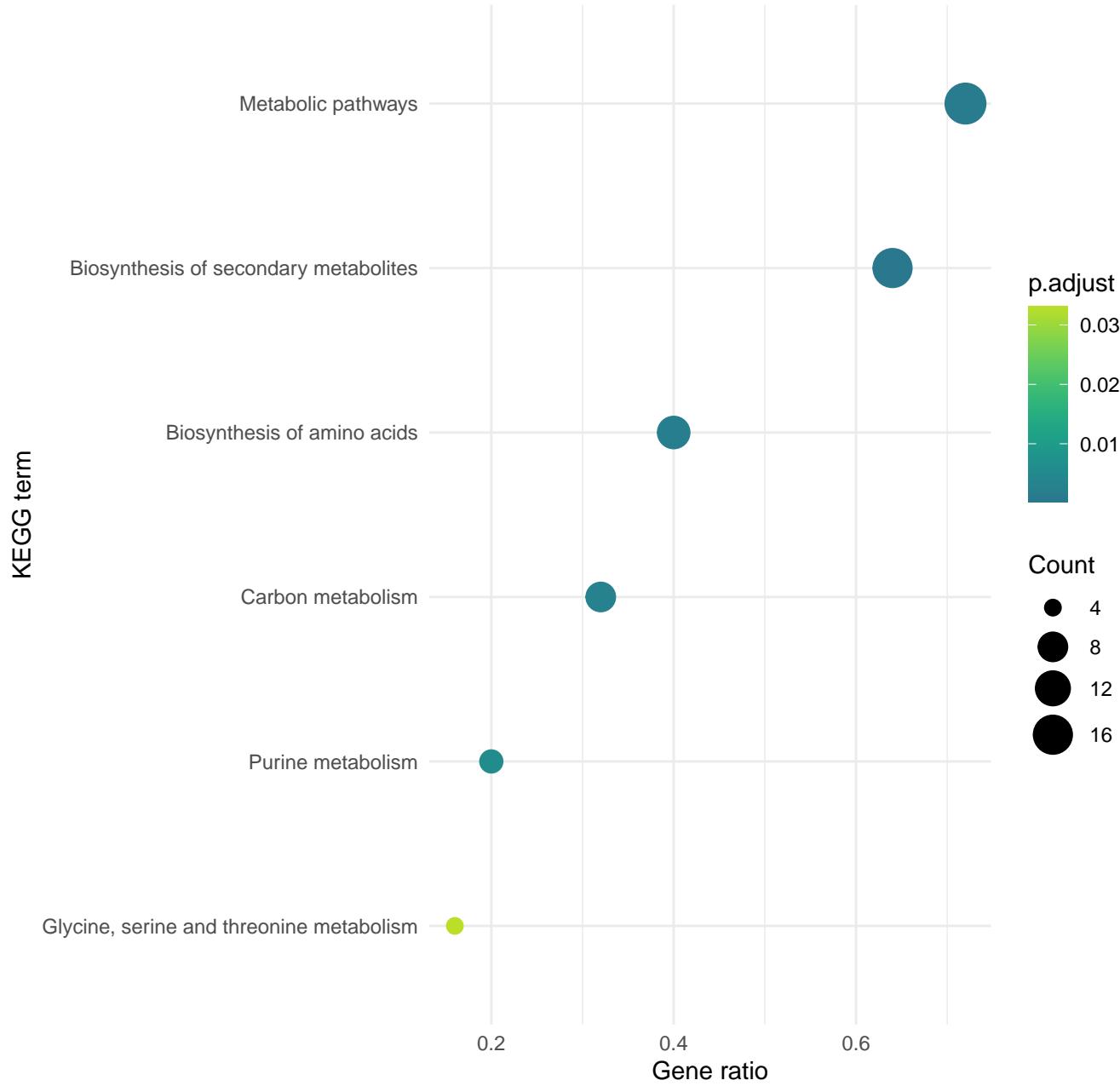
FAL1-TAP Up-regulated GO MF upsetplot



FAL1-TAP Up-regulated KEGG barplot



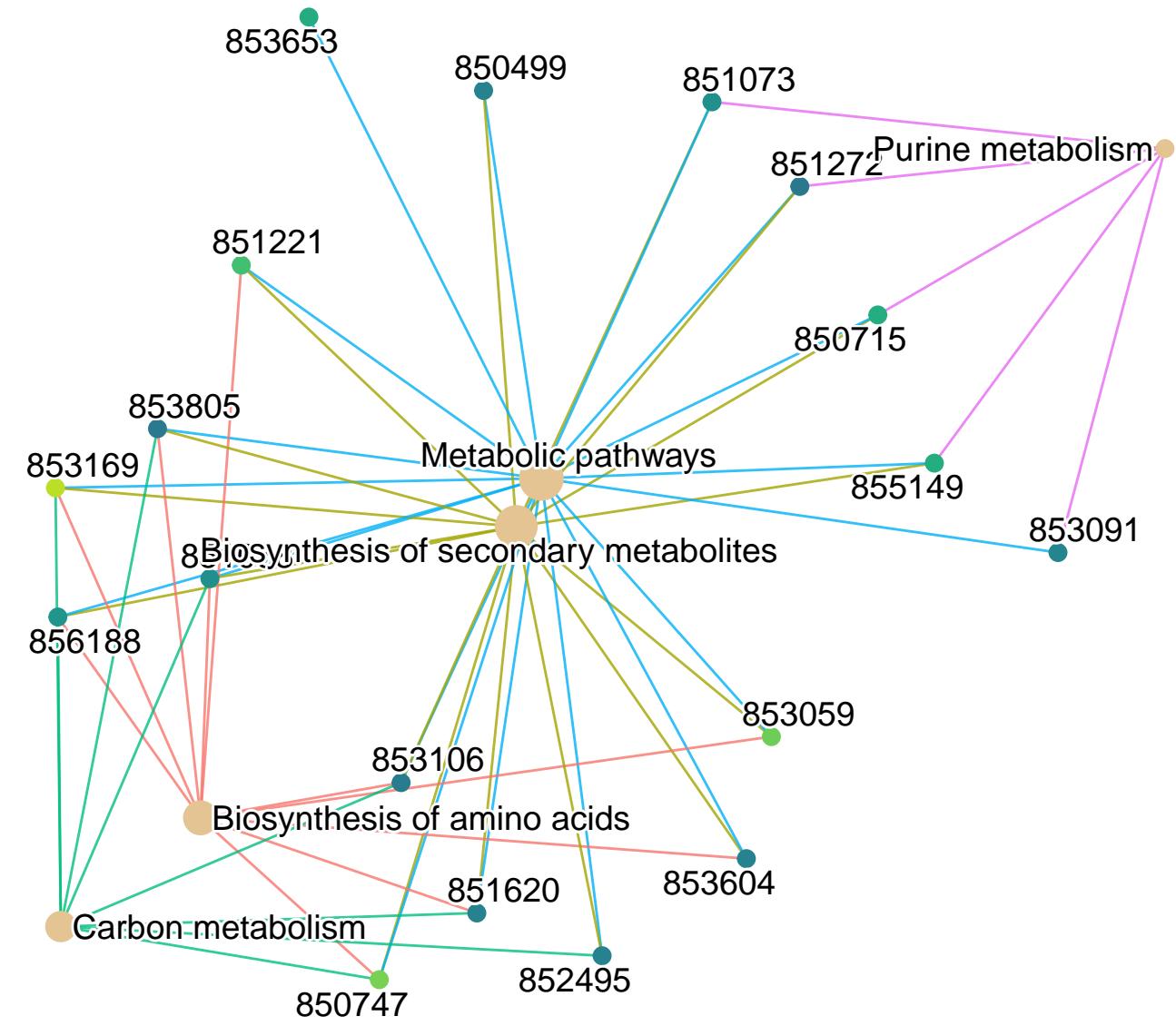
FAL1-TAP Up-regulated KEGG dotplot



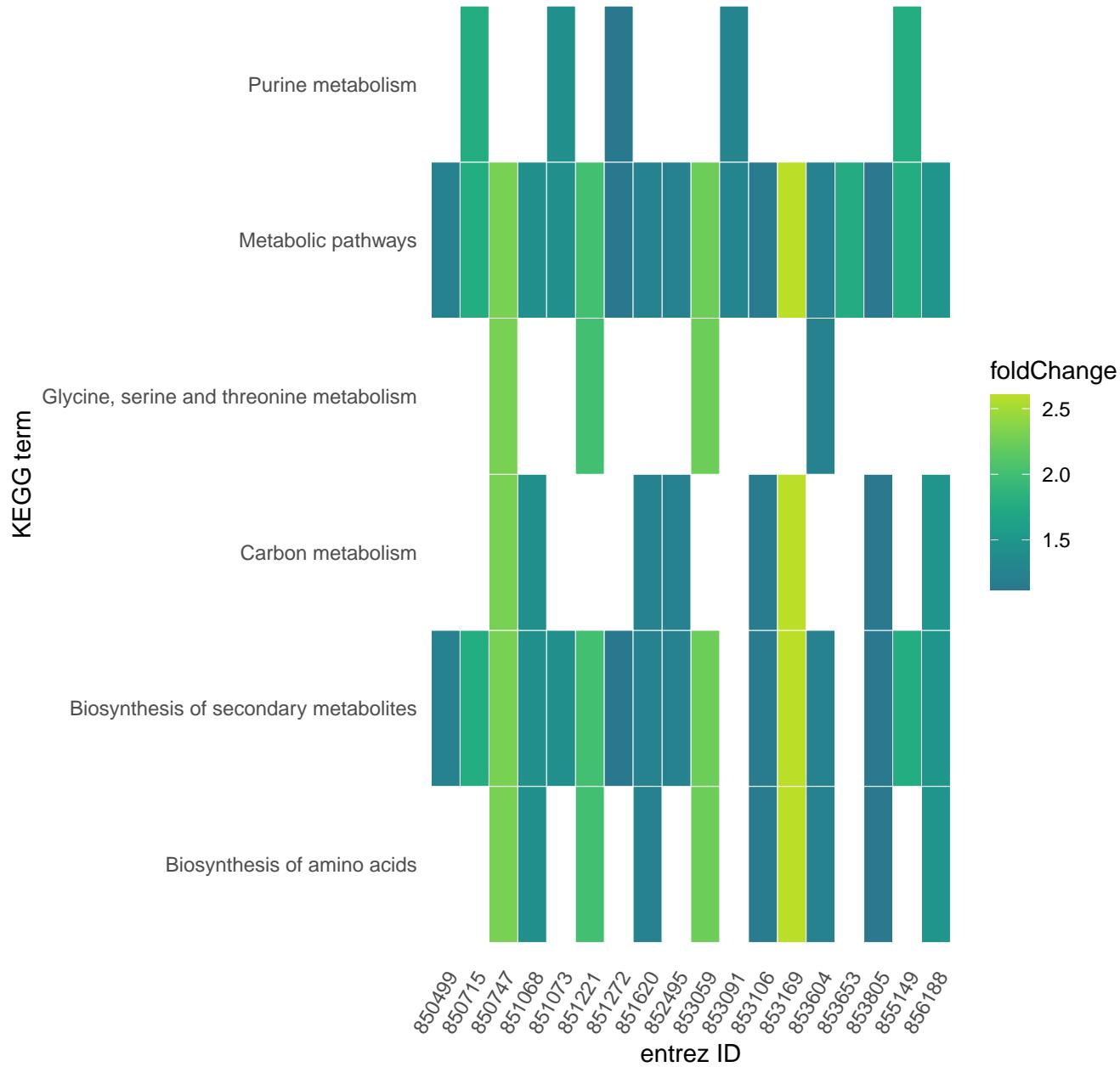
FAL1-TAP Up-regulated KEGG dotplot

Biosynthesis of secondary metabolites Carbon metabolism Metabolic pathways Purine metabolism

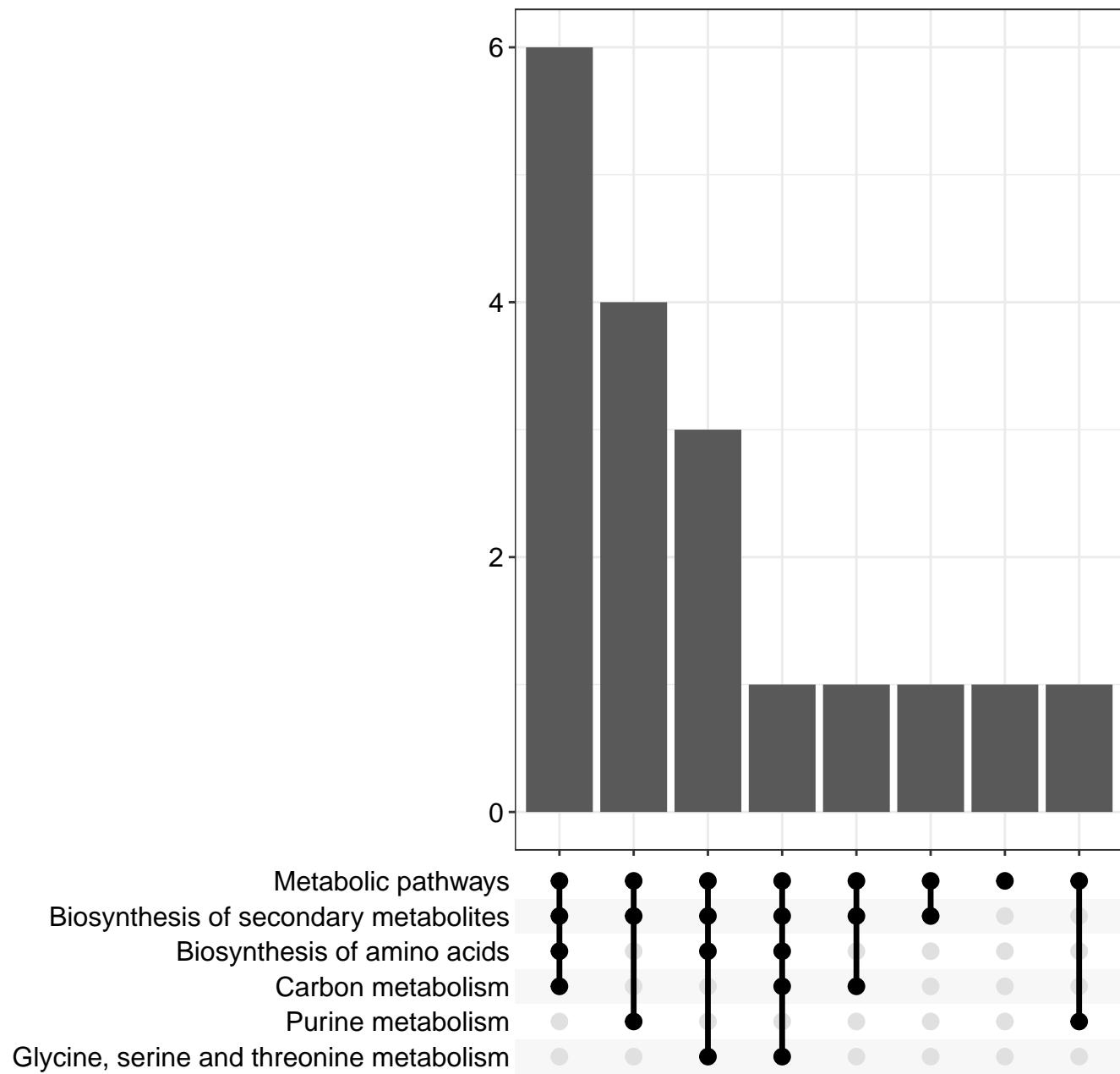
size
● 5.0
● 7.5



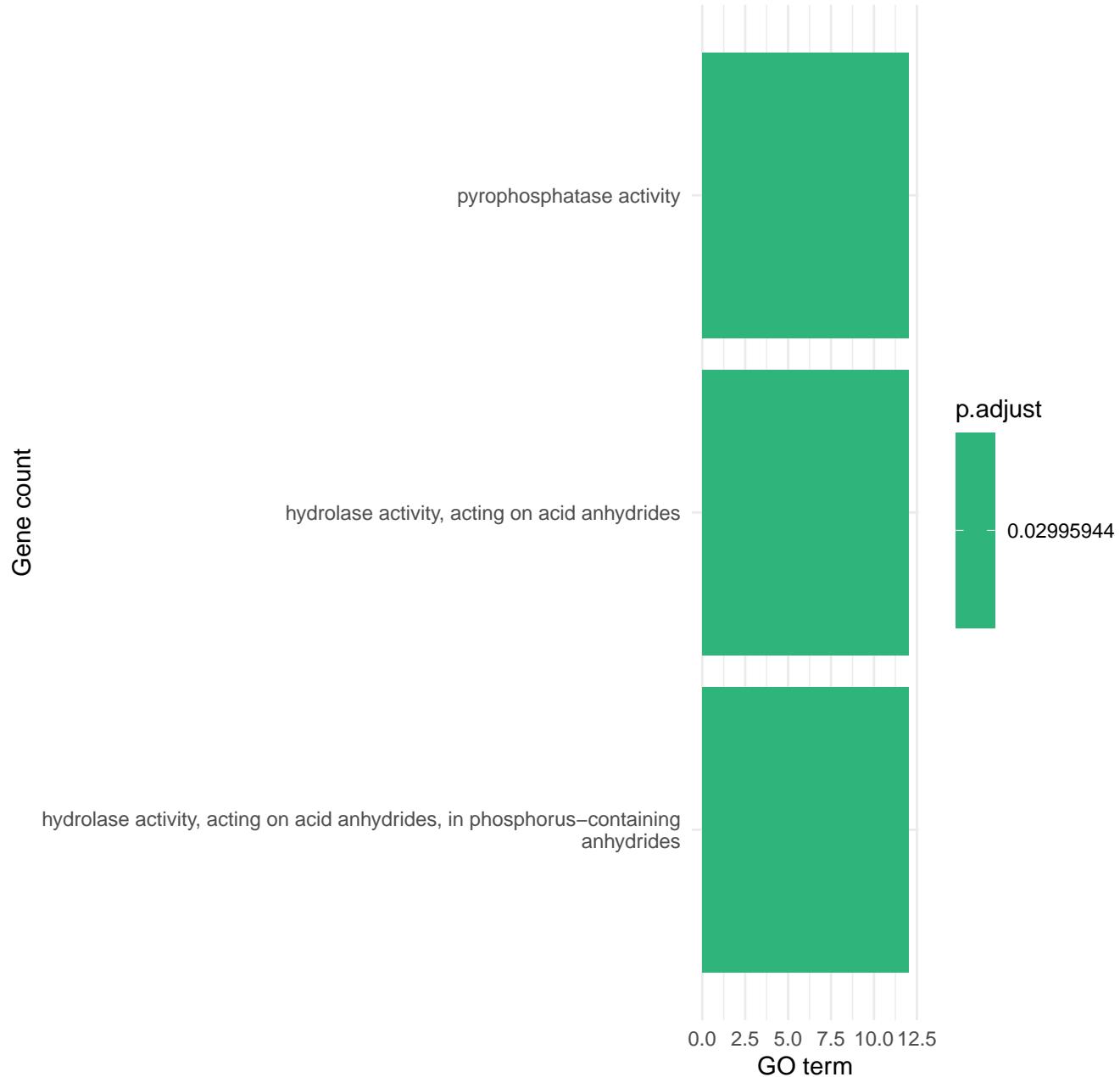
FAL1-TAP Up-regulated KEGG heatplot



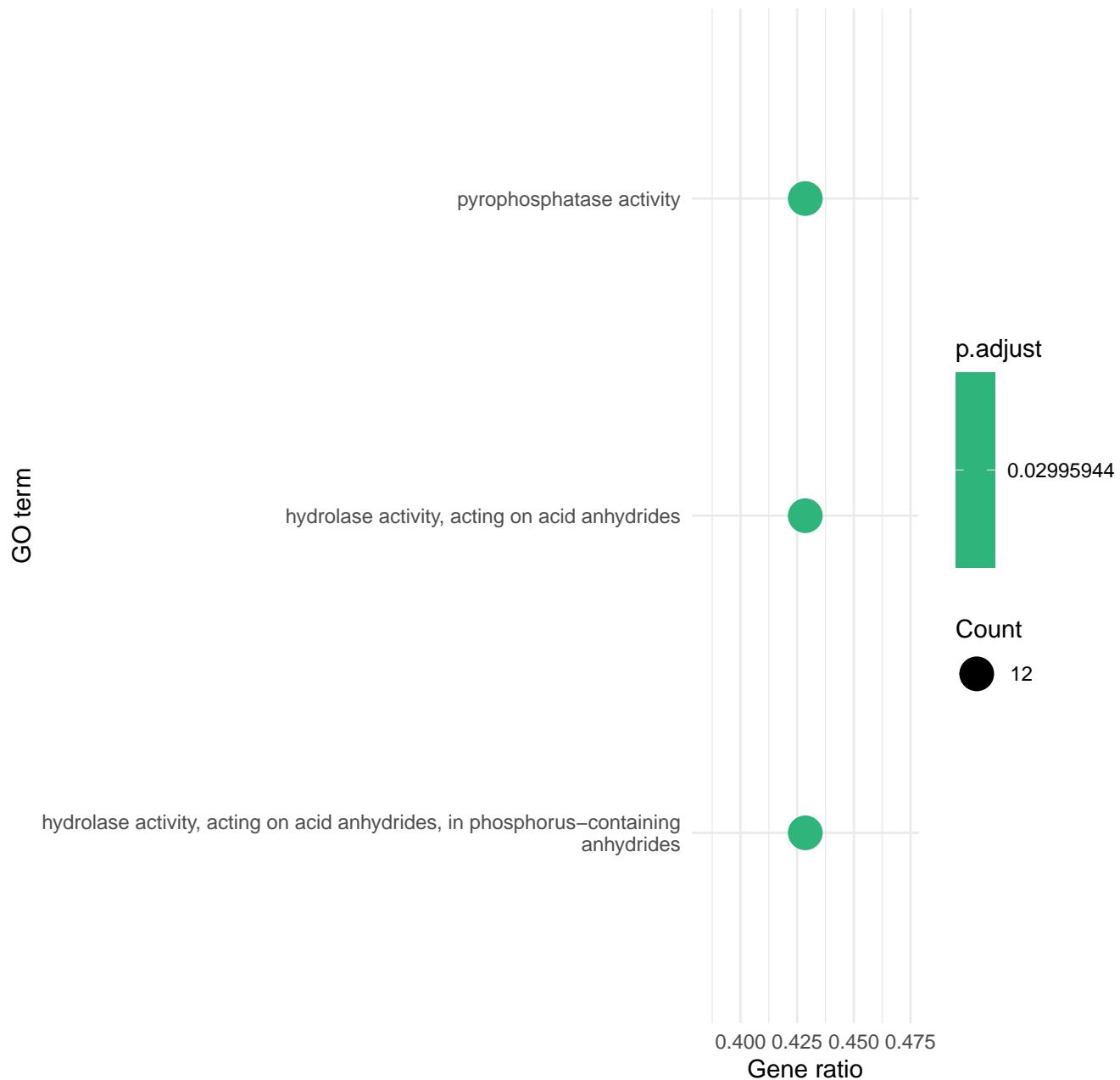
FAL1-TAP Up-regulated KEGG upsetplot



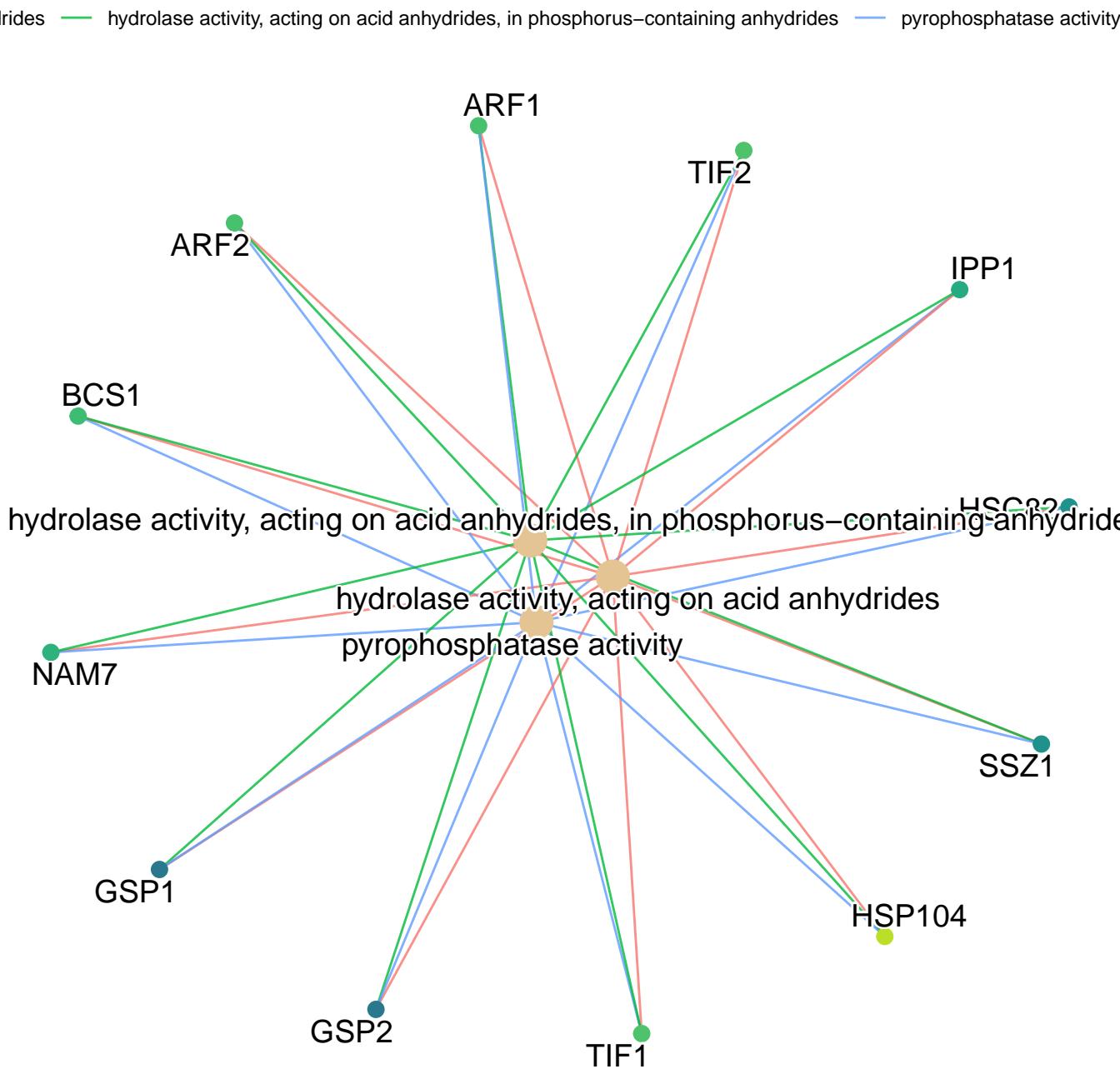
NMD2-TAP Up-regulated GO MF



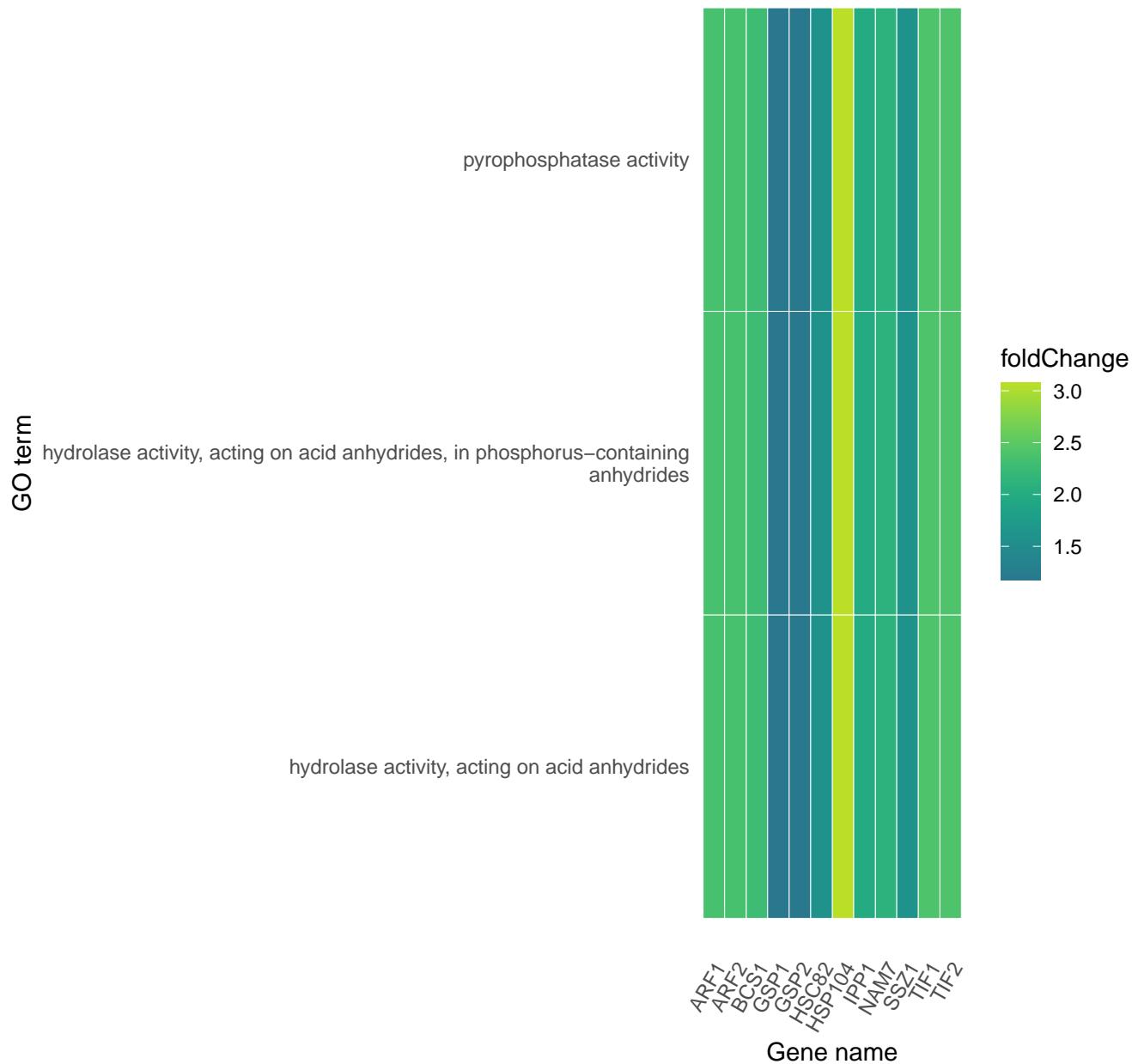
NMD2-TAP Up-regulated GO MF



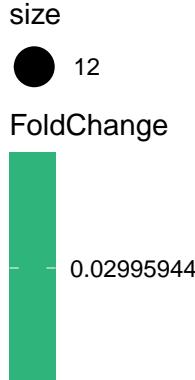
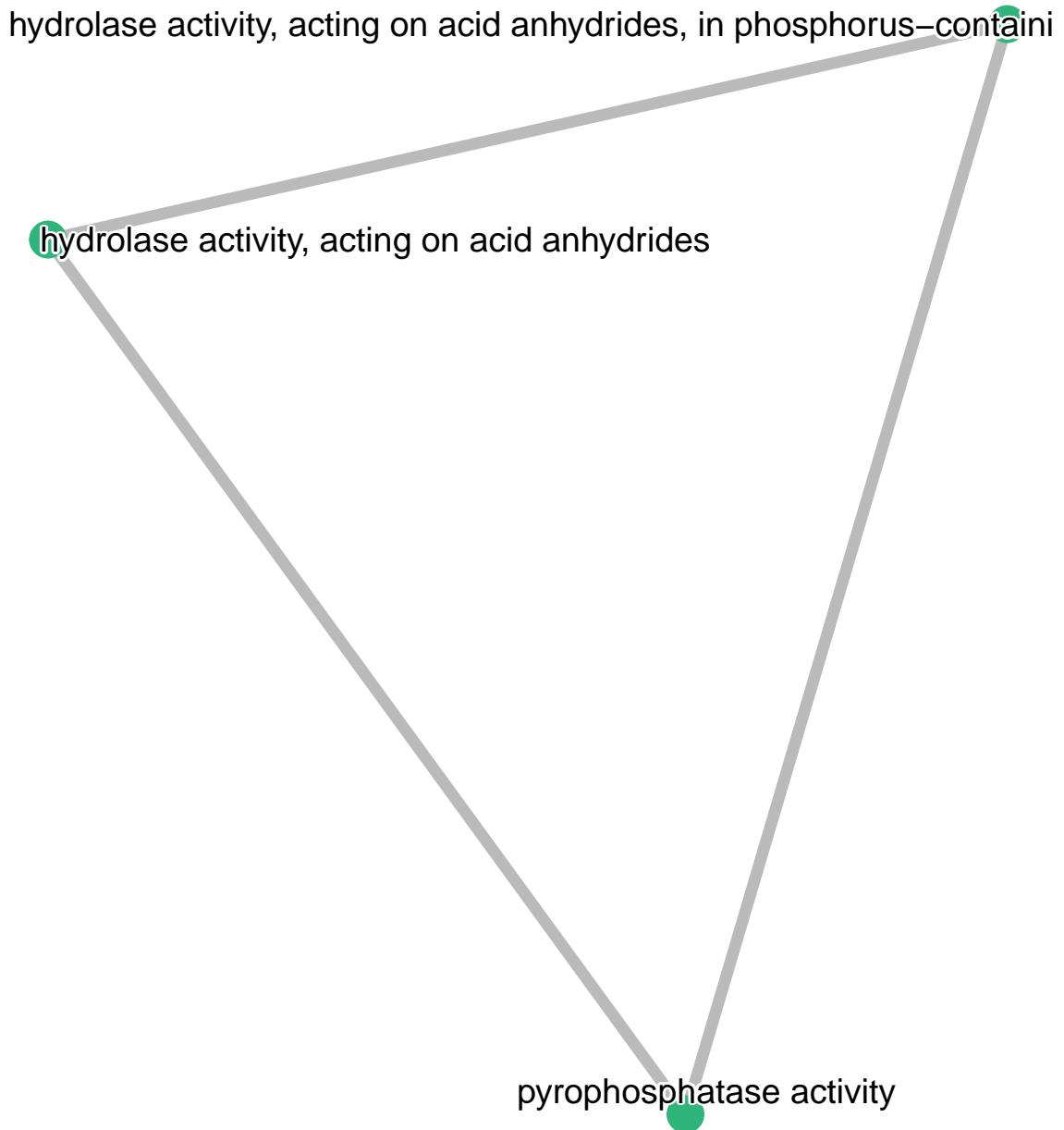
NMD2-TAP Up-regulated GO MF cnetplot



NMD2-TAP Up-regulated GO MF



NMD2-TAP Up-regulated GO MF emapplot



GO:0003674
molecular_function
1.0000
28 / 378

GO:0003824
catalytic_activity
0.0780
20 / 183

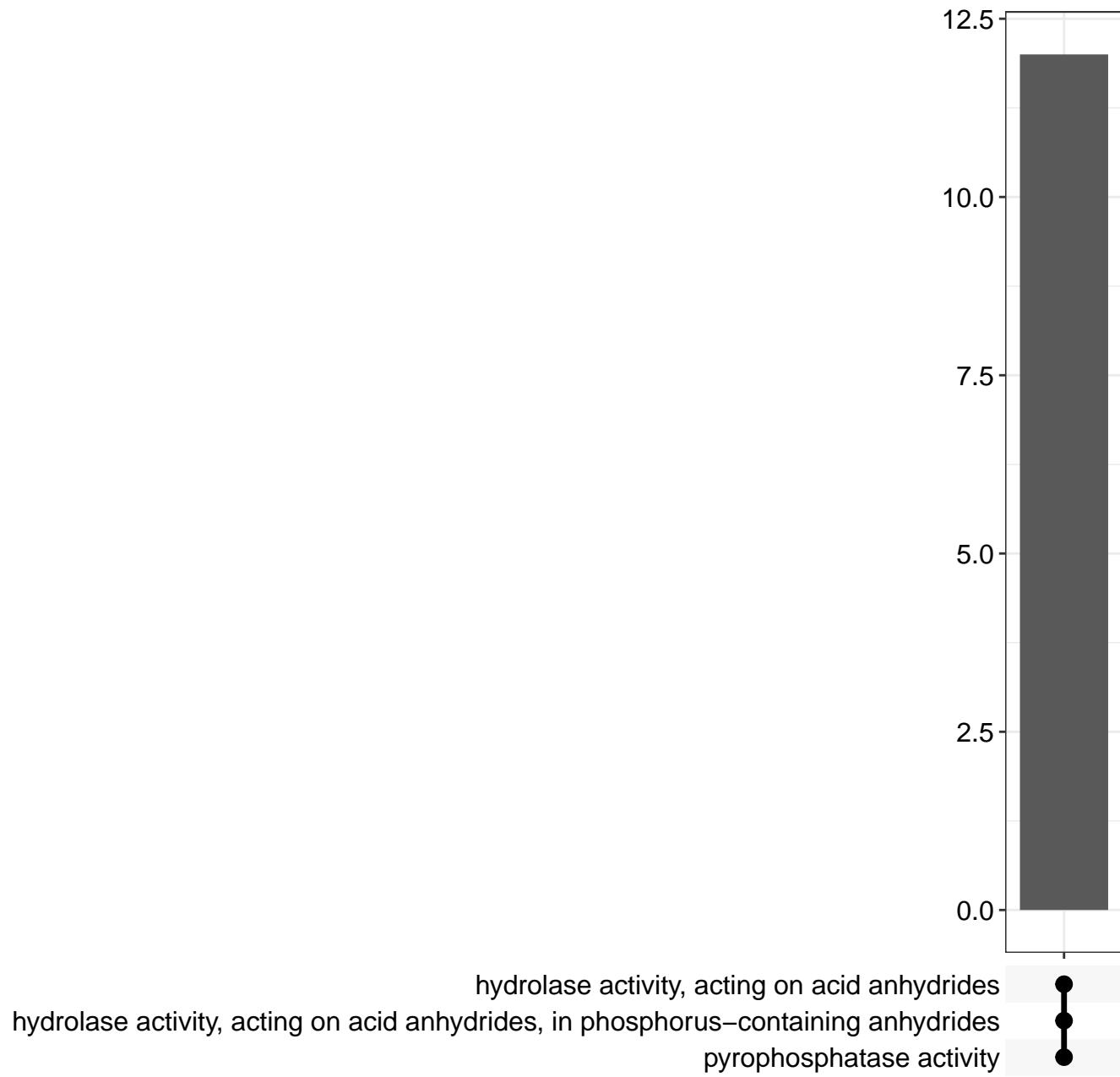
GO:0016787
hydrolase_activity
0.0394
12 / 90

GO:0016817
hydrolase_activity, ...
0.0300
12 / 68

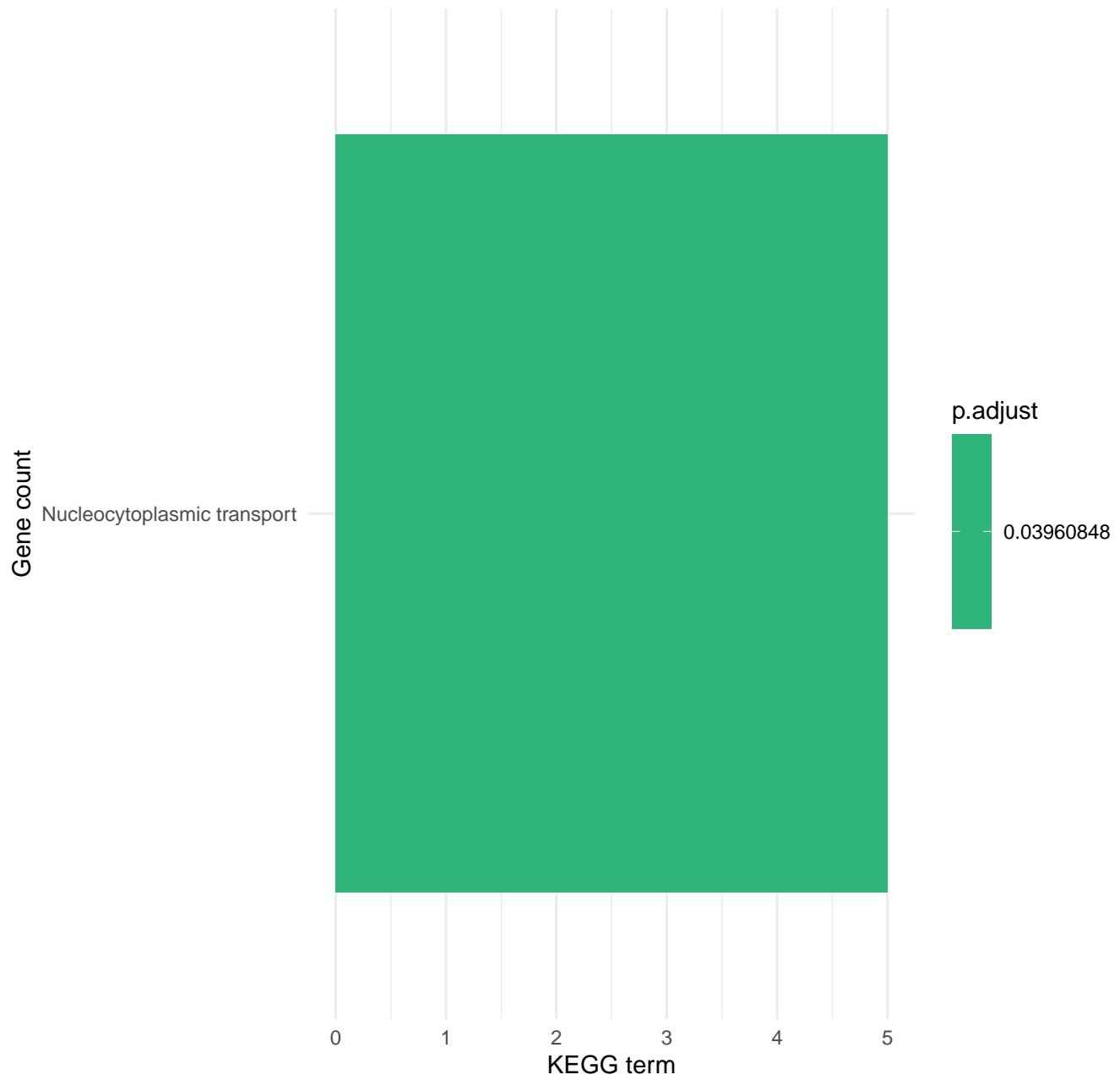
GO:0016818
hydrolase_activity, ...
0.0300
12 / 68

GO:0016462
pyrophosphatase_acid...
0.0300
12 / 68

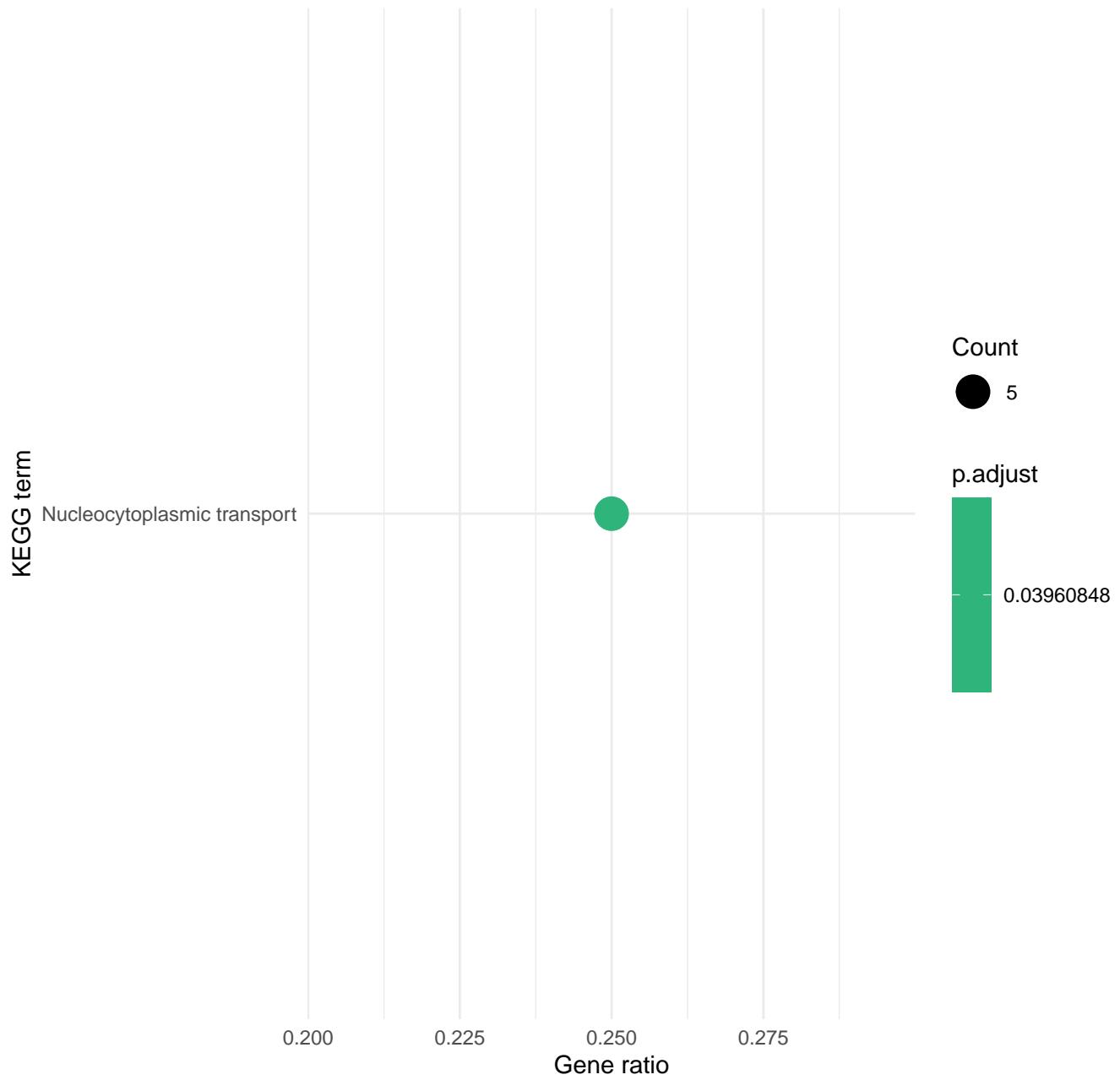
NMD2-TA



NMD2-TAP Up-regulated KEGG barplot

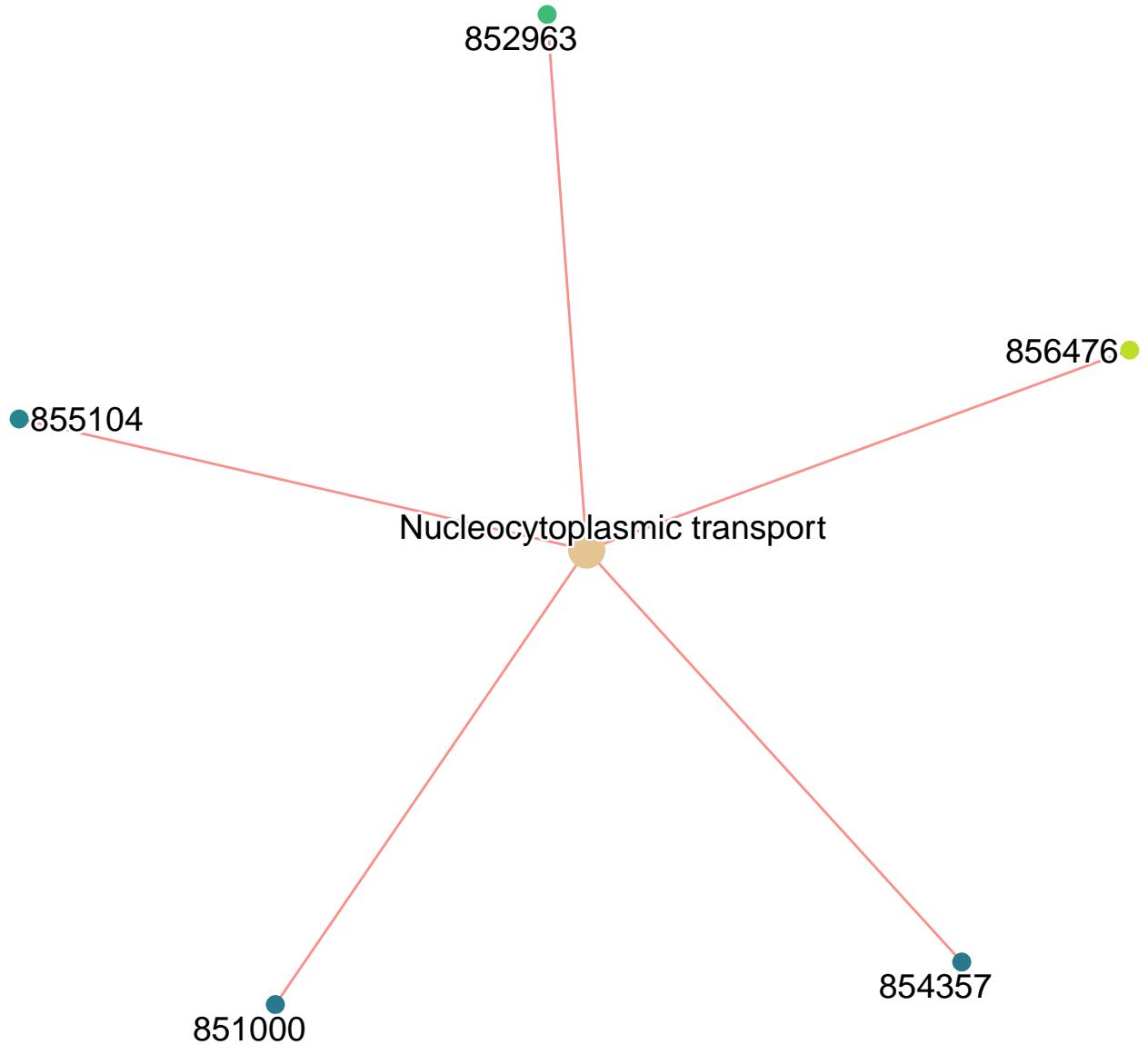


NMD2-TAP Up-regulated KEGG dotplot

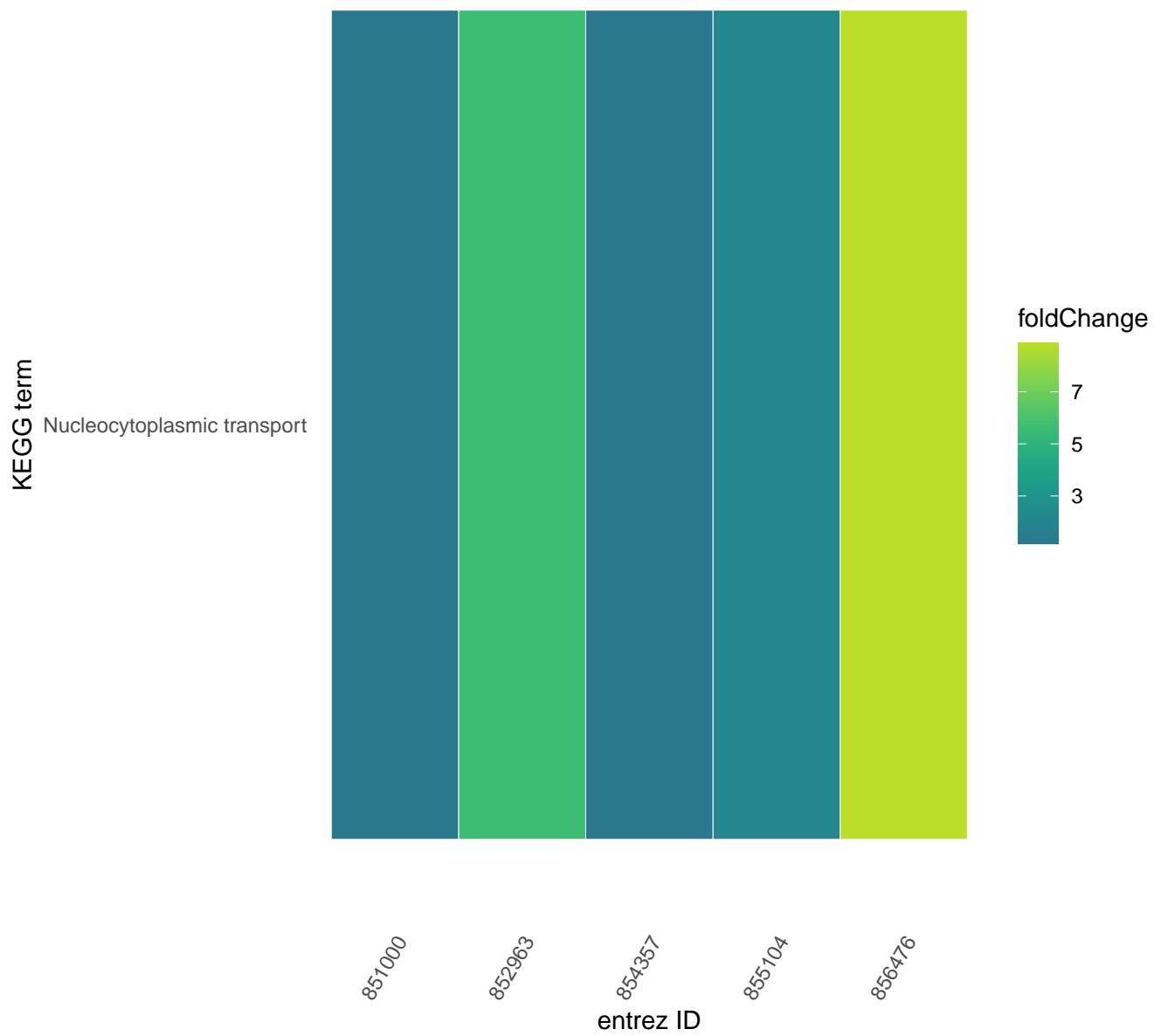


NMD2-TAP Up-regulated KEGG dotplot

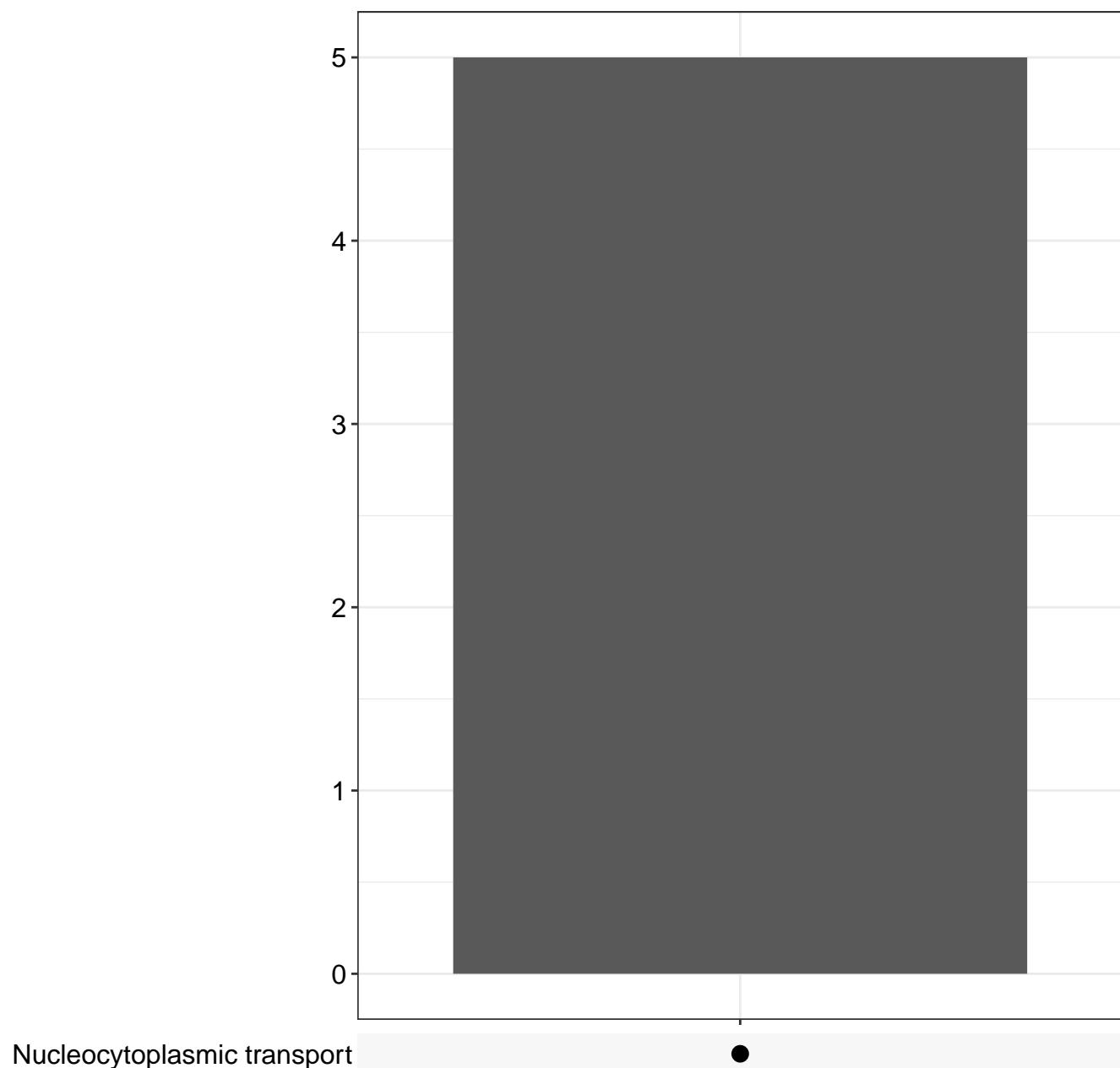
FoldChange [3 5 7] size ● 5 category — Nucleocytoplasmic transport



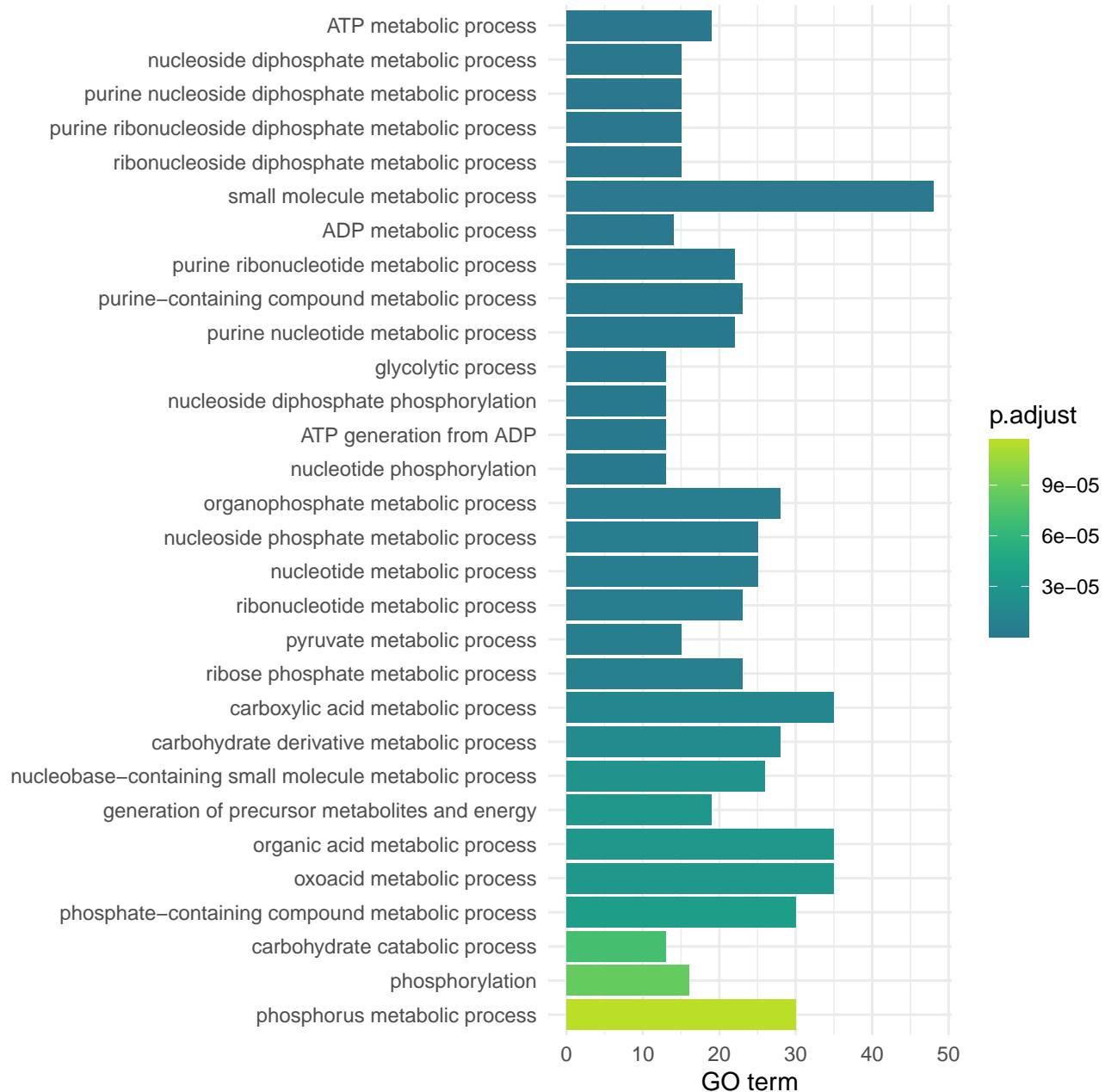
NMD2-TAP Up-regulated KEGG heatplot



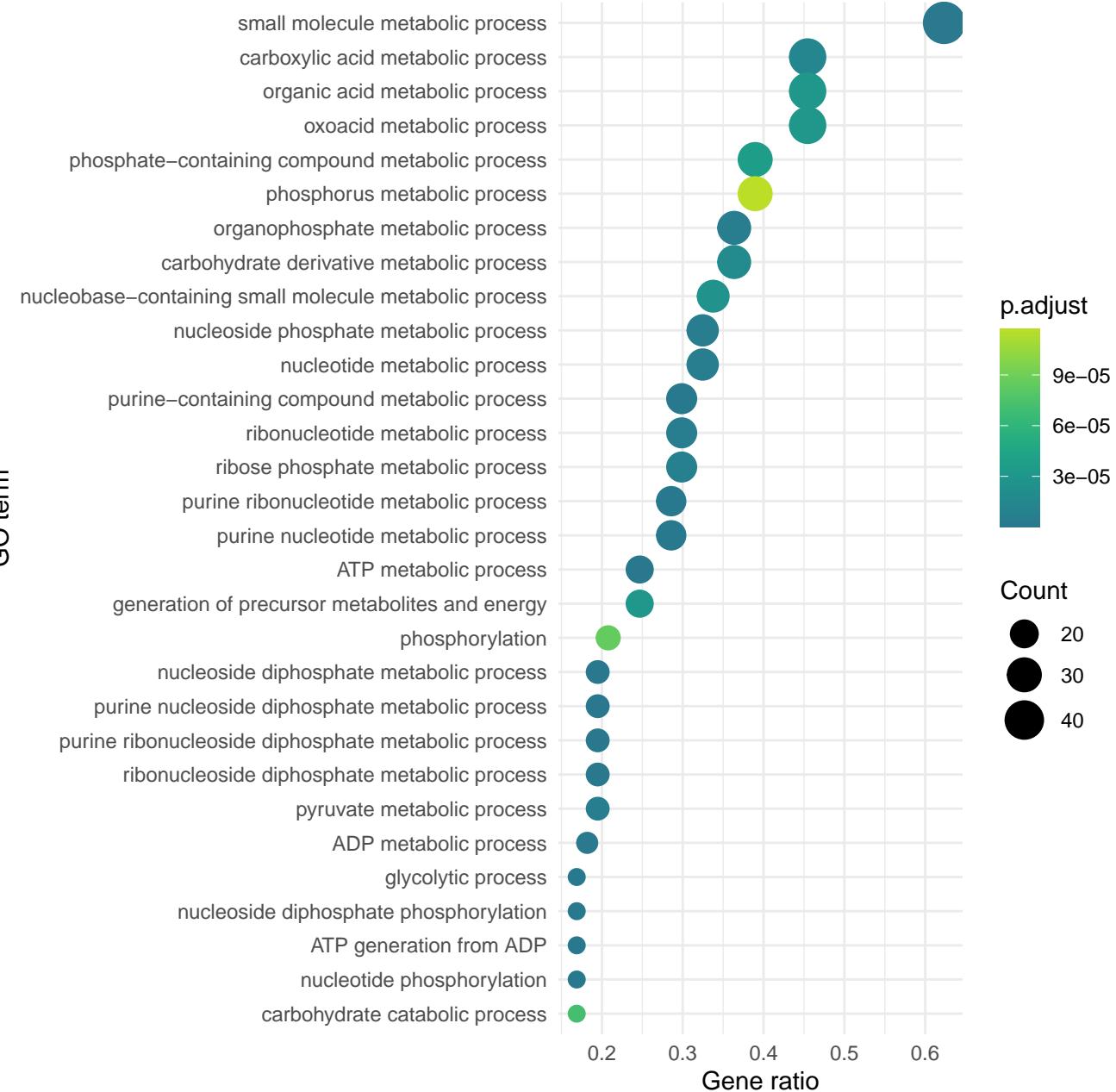
NMD2-TAP Up-regulated KEGG upsetplot



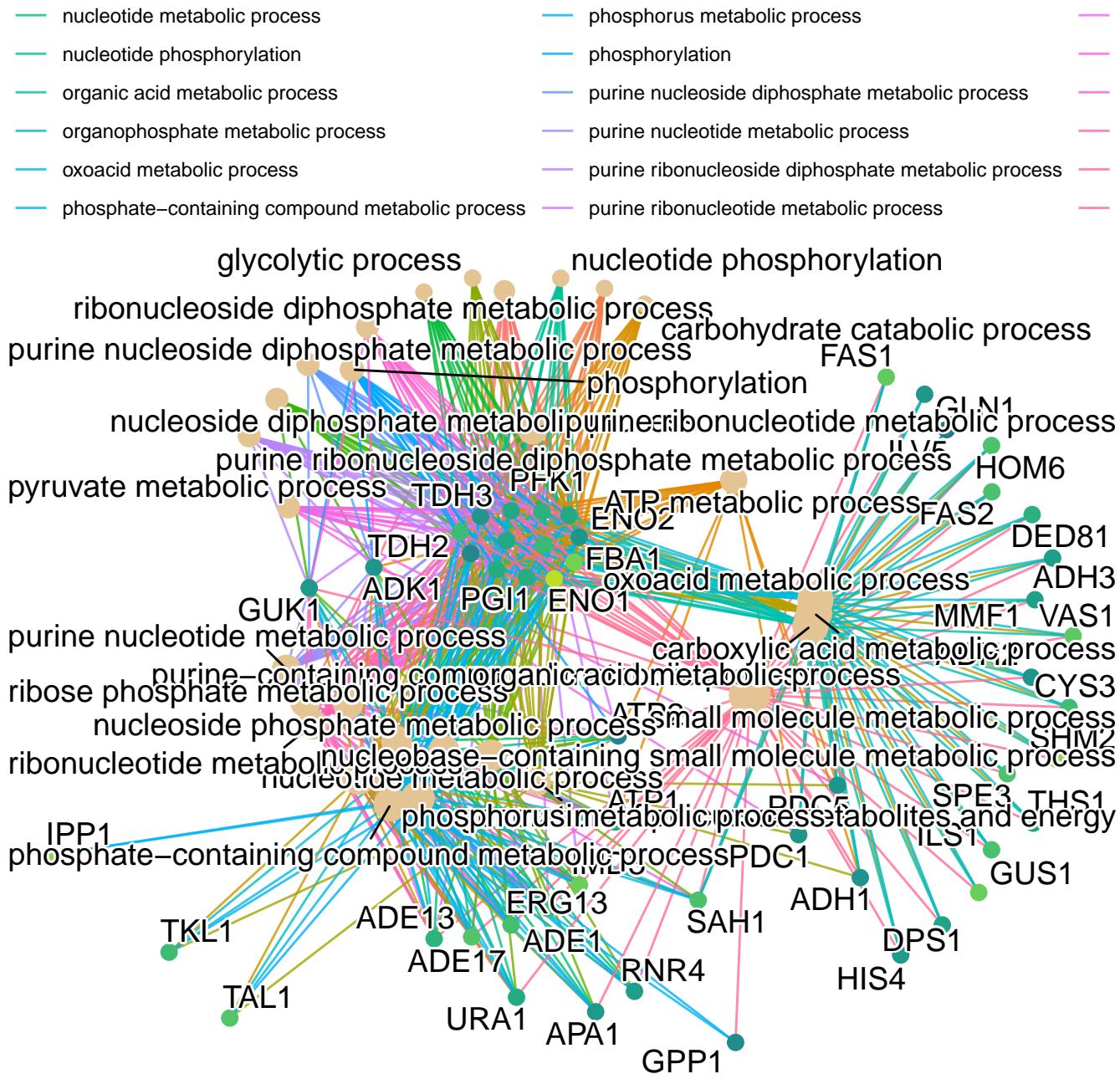
UPF3-TAP Up-regulated GO BP barplot



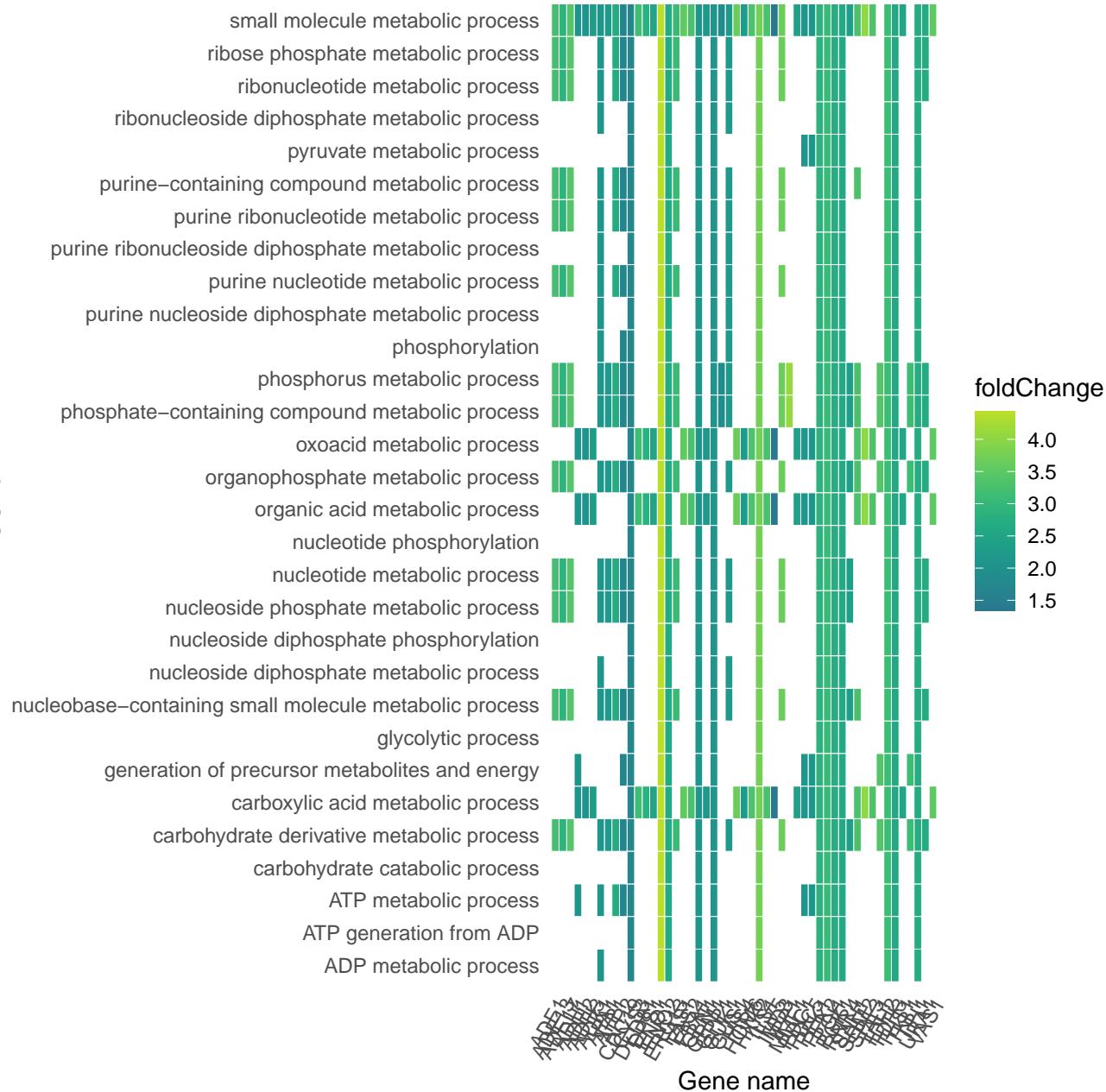
UPF3-TAP Up-regulated GO BP dotplot



UPF3-TAP Up-regulated GO BP cnetplot



UPF3-TAP Up-regulated GO BP heatplot



UPF3-TAP Up-regulated GO BP emapplot

phosphate-containing compound metabolic process

organophosphate metabolic process

carbohydrate derivative metabolic process

nucleoside phosphate metabolic process

nucleotide metabolic process

containing compound metabolic process

nucleobase-containing small molecule metabolic process

purine nucleotide metabolic process

purine nucleoside diphosphate metabolic process

small molecule metabolic process

side diphosphate metabolic process

ribose phosphate metabolic process

nucleoside diphosphate metabolic process

ATP generation from ADP phosphorylation

ATP metabolic process

purine ribonucleoside diphosphate metabolic process

oxoacid metabolic process

ADP metabolic process

nucleoside diphosphate phosphorylation

generation of precursor metabolites and energy

carbohydrate catabolic process

carboxylic acid metabolic process

nucleotide phosphorylation

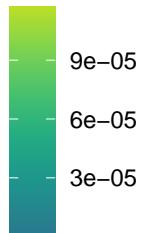
pyruvate metabolic process

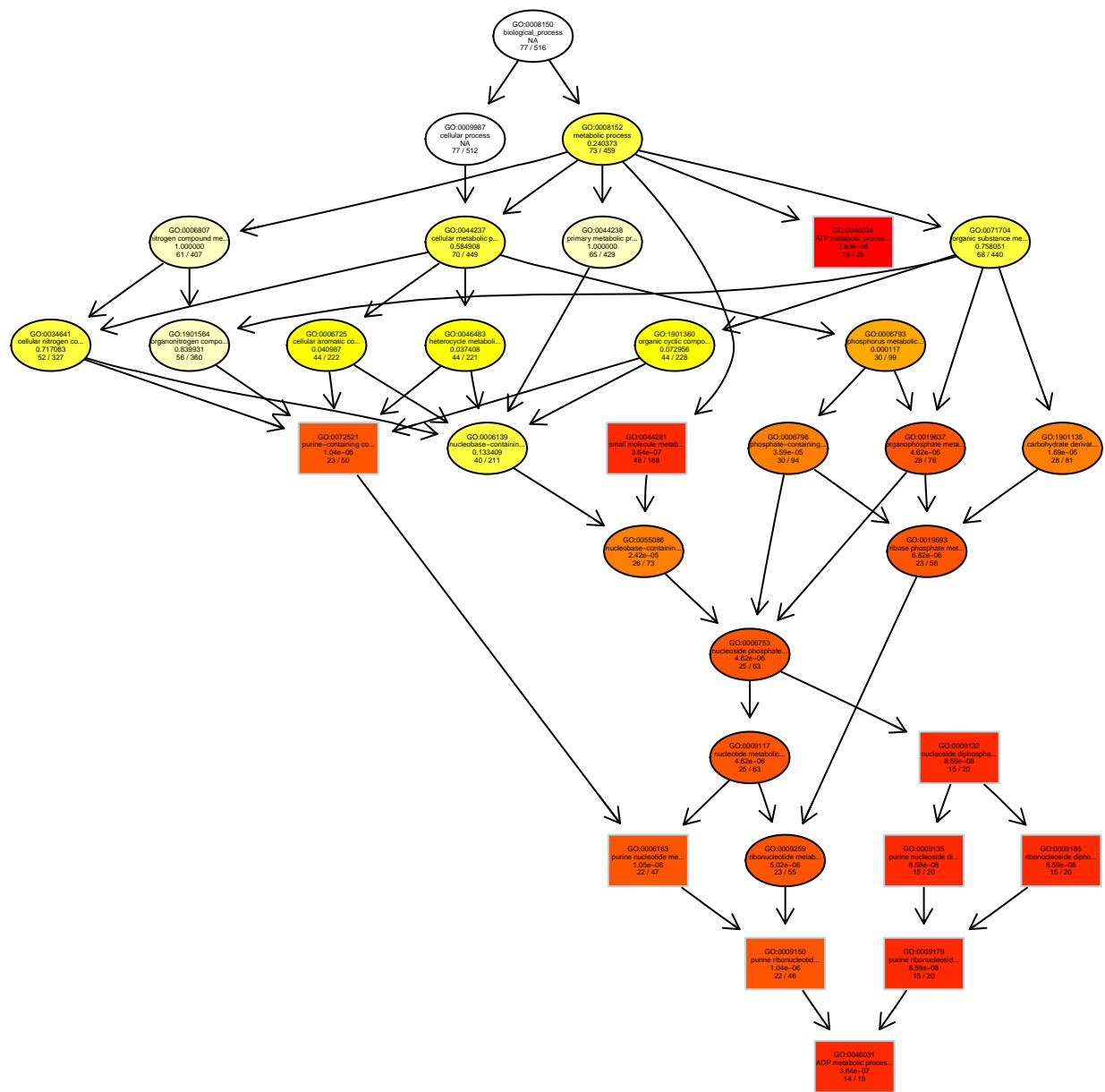
organic acid metabolic process

size

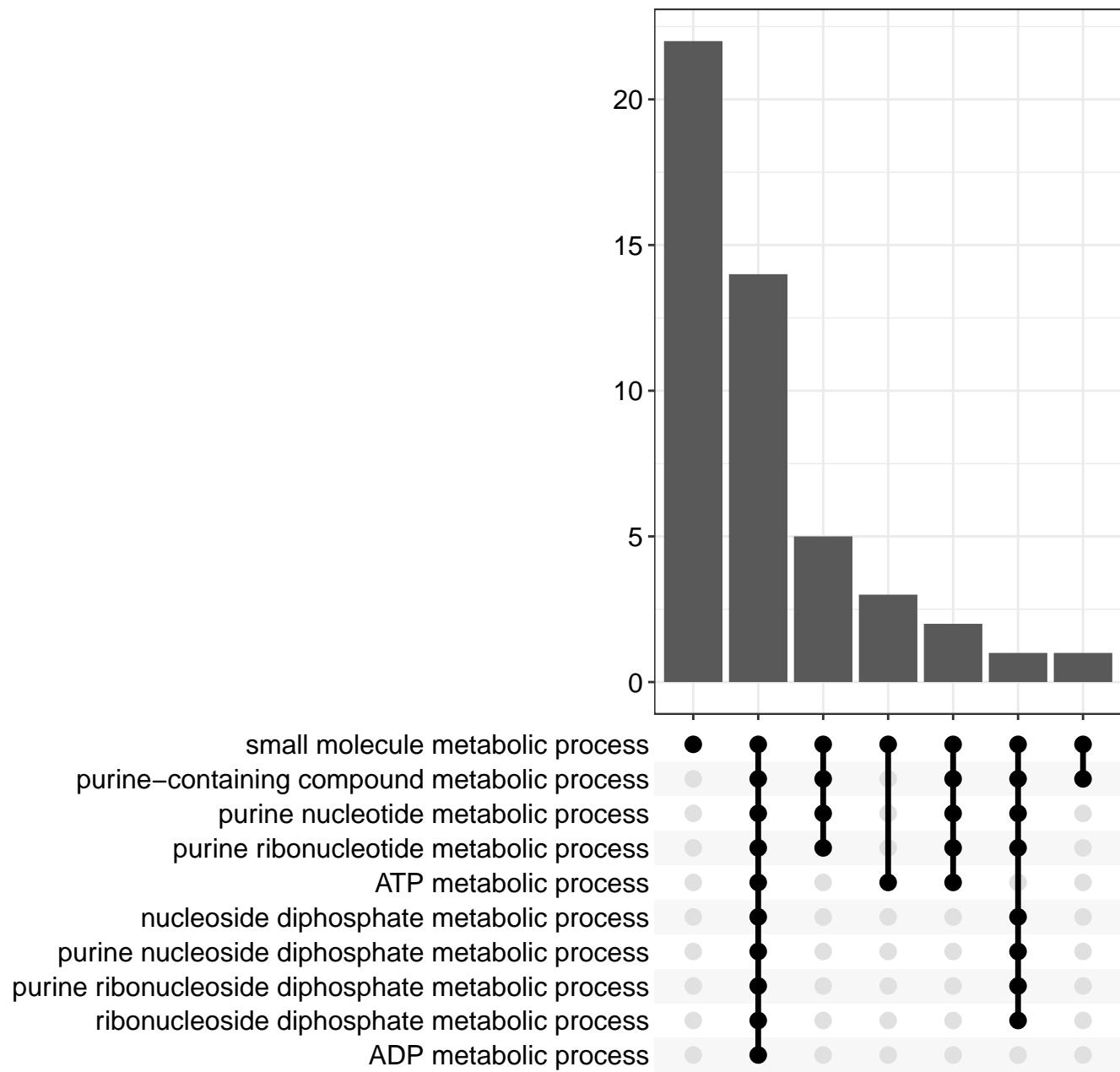


FoldChange

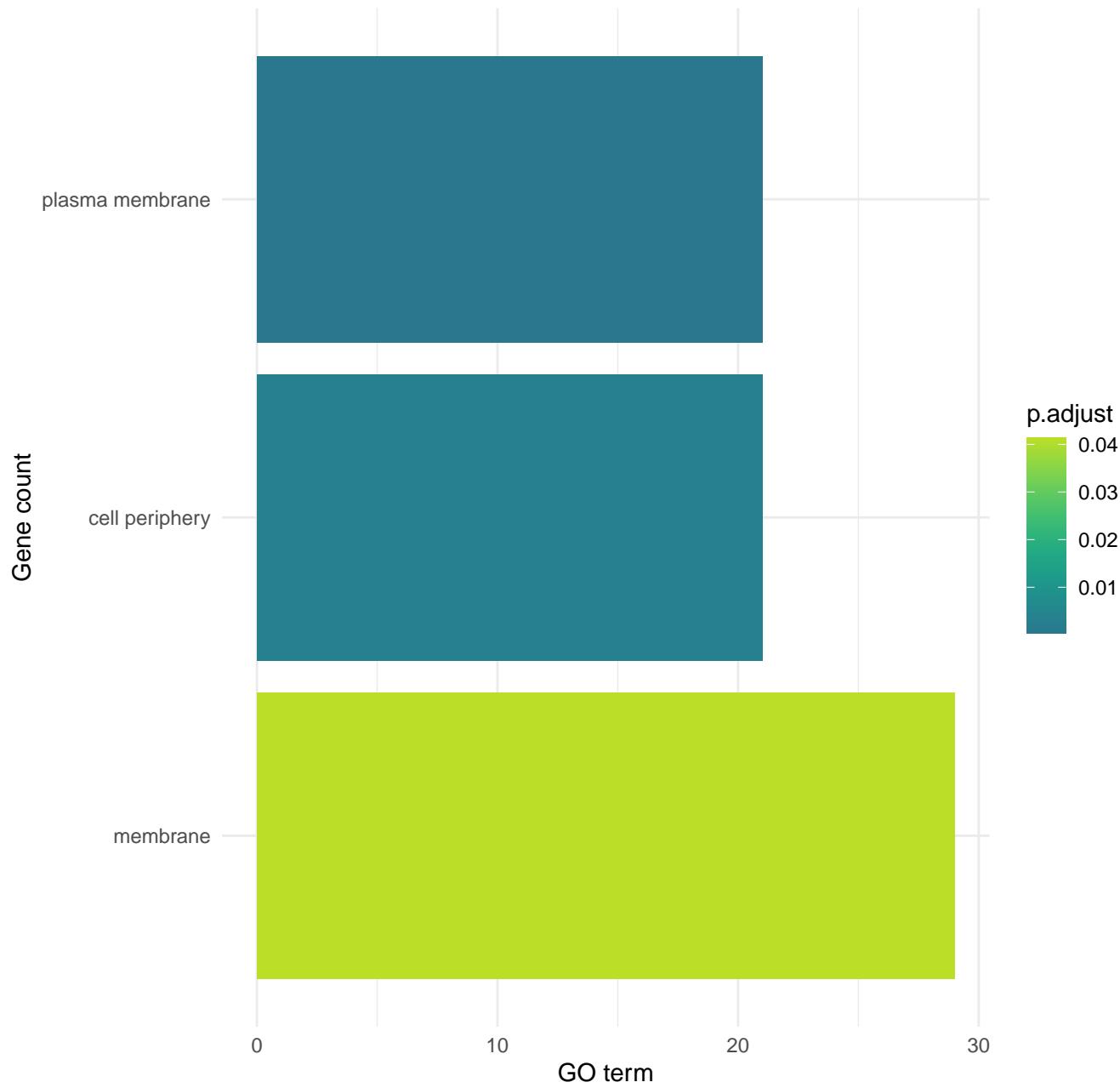




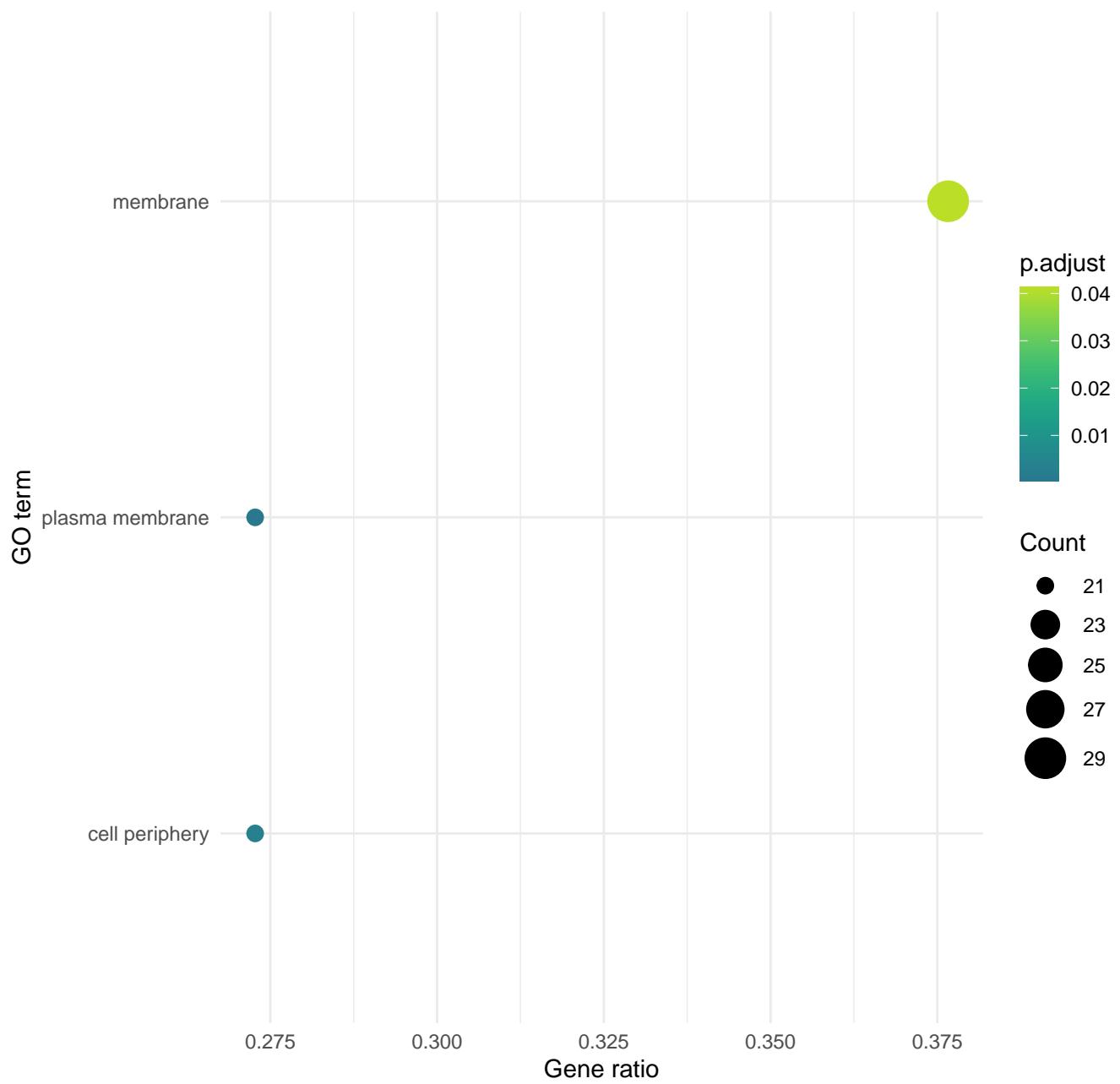
UPF3-TAP Up-regulated GO BP ups



UPF3-TAP Up-regulated GO CC barplot



UPF3-TAP Up-regulated GO CC dotplot



UPF3-TAP Up-regulated GO CC cnetplot



size

● 21

● 23

● 25

● 27

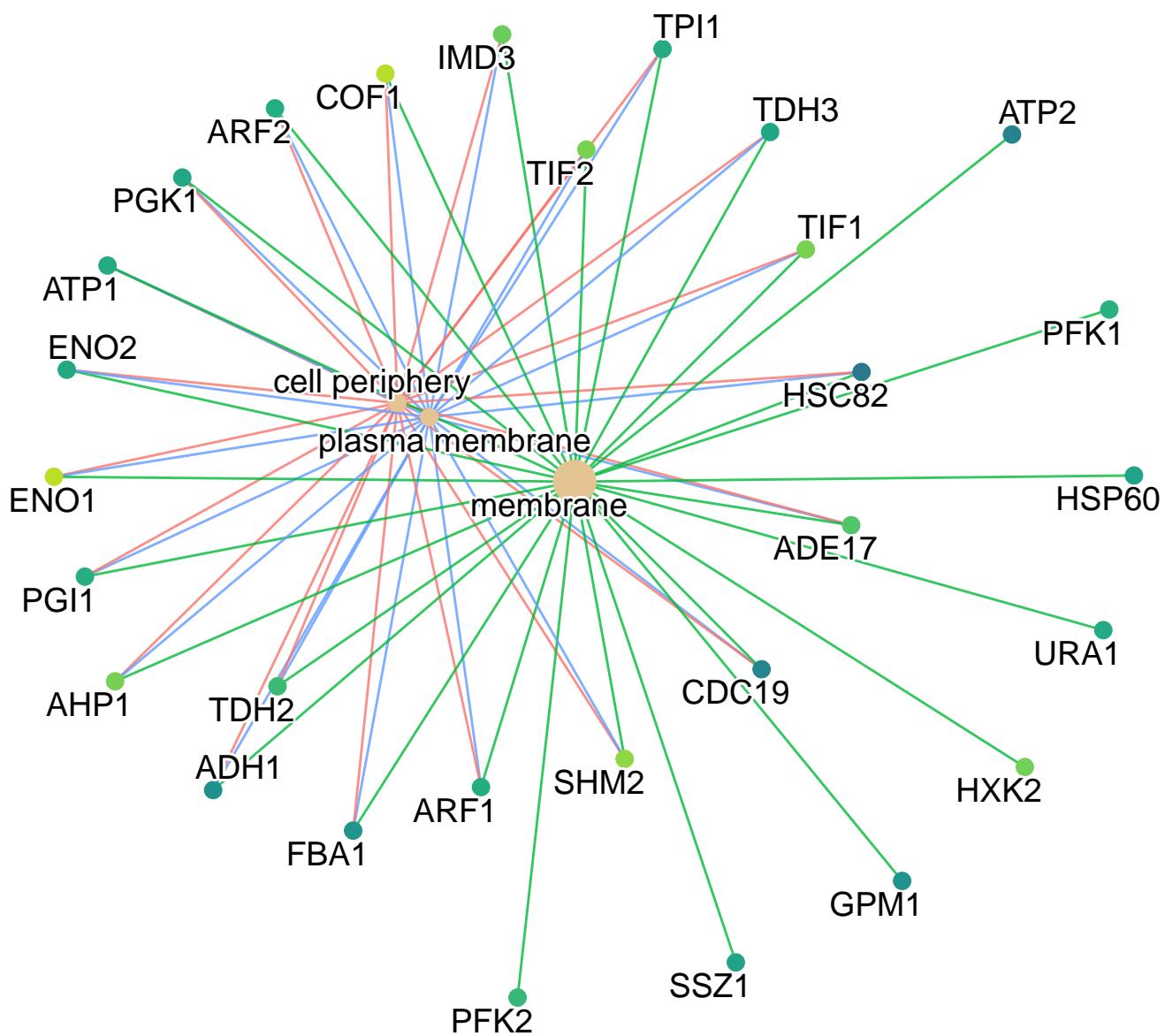
● 29

category

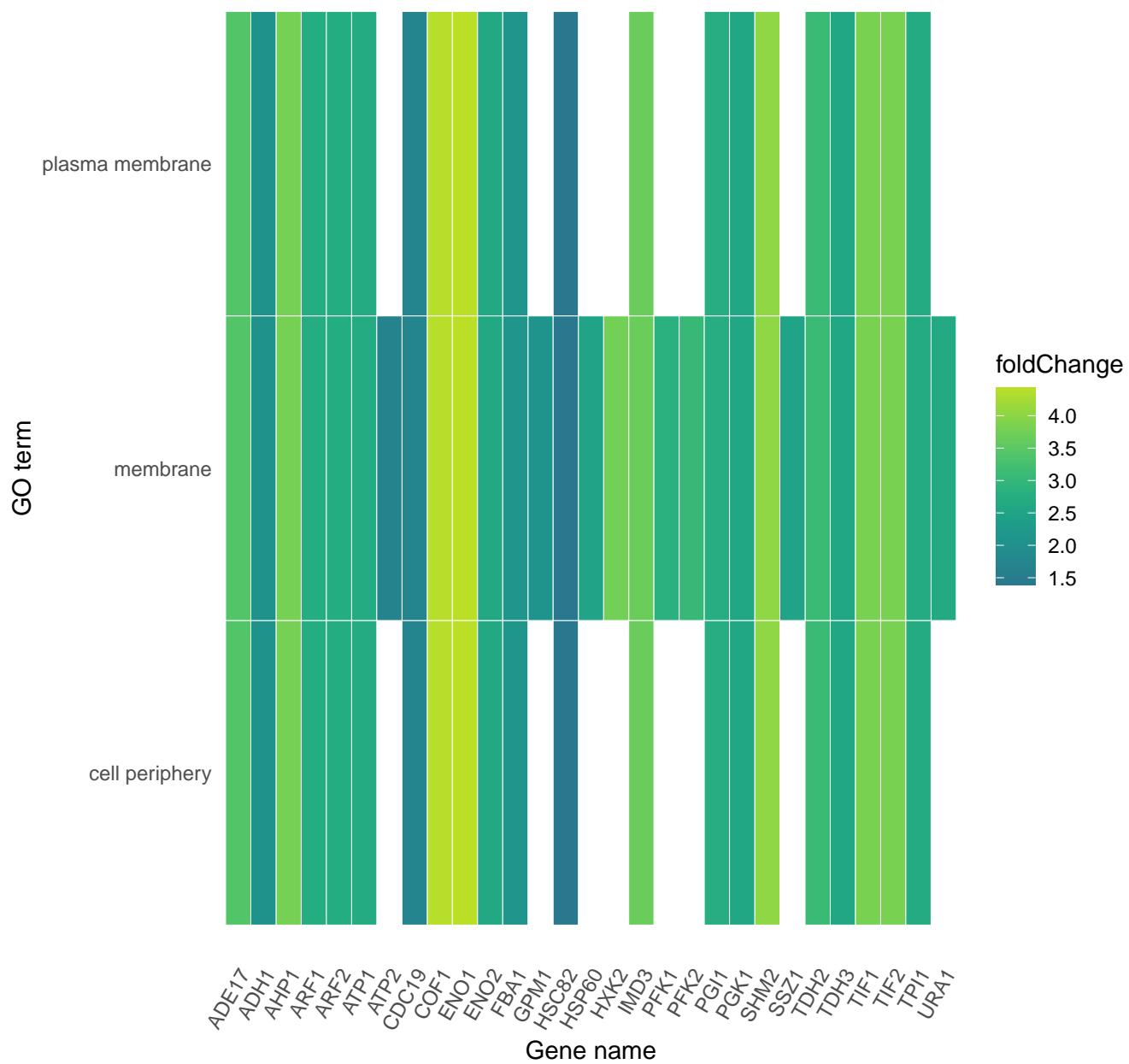
cell periphery

membrane

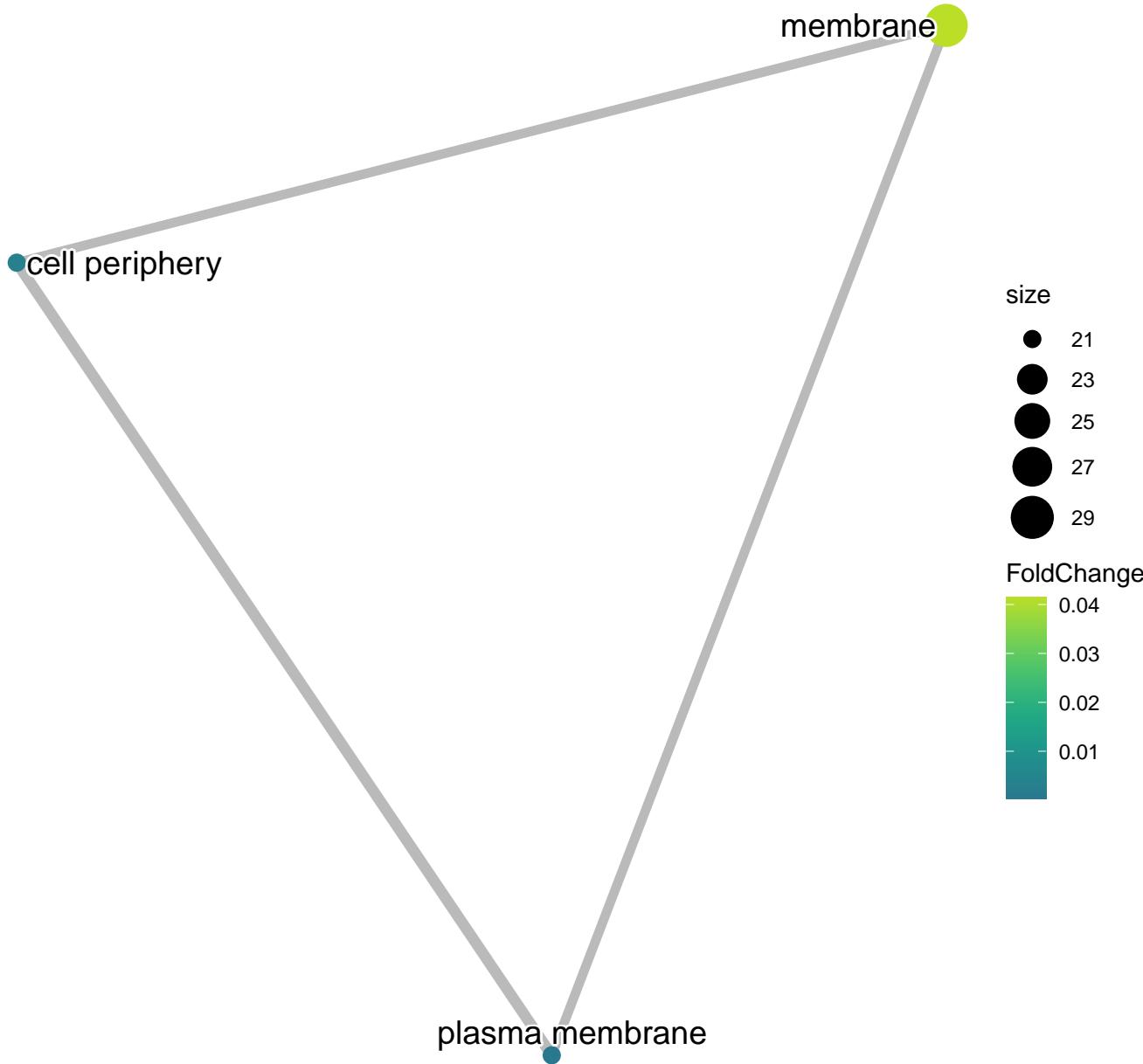
2.5 3.0 3.5 4.0

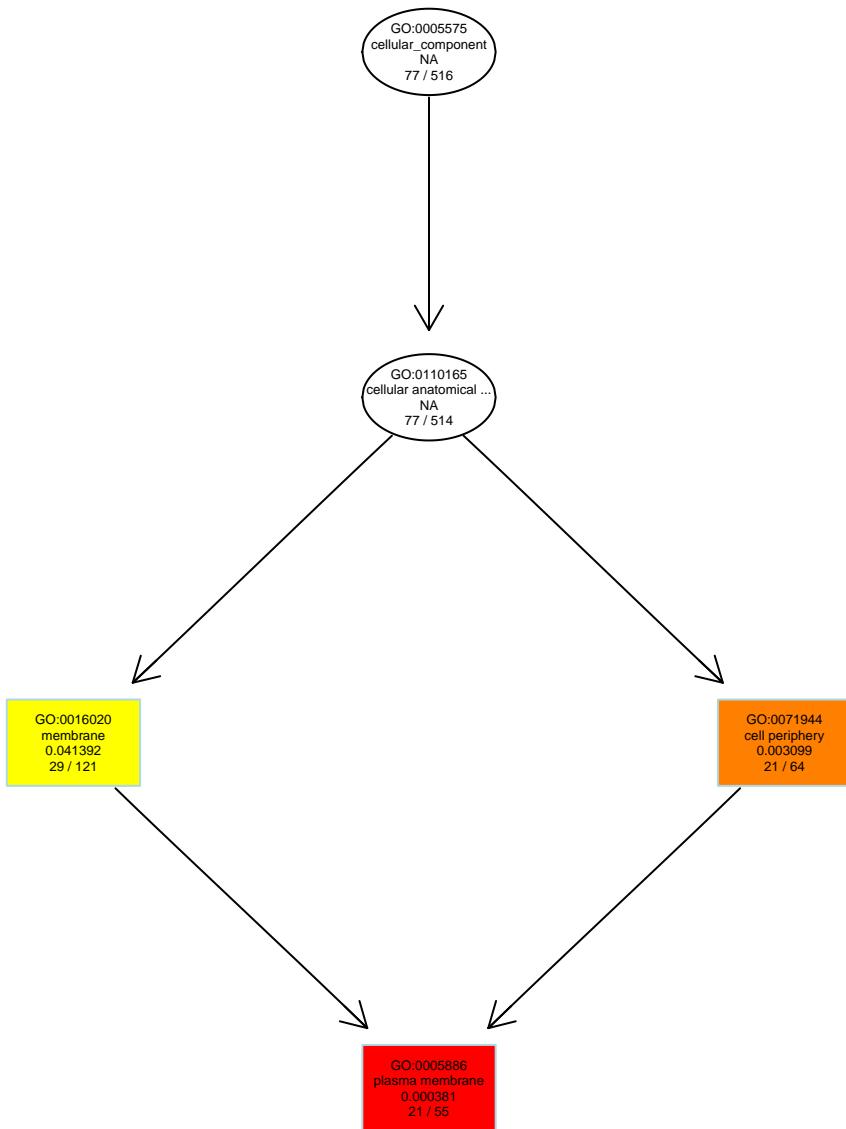


UPF3-TAP Up-regulated GO CC heatplot

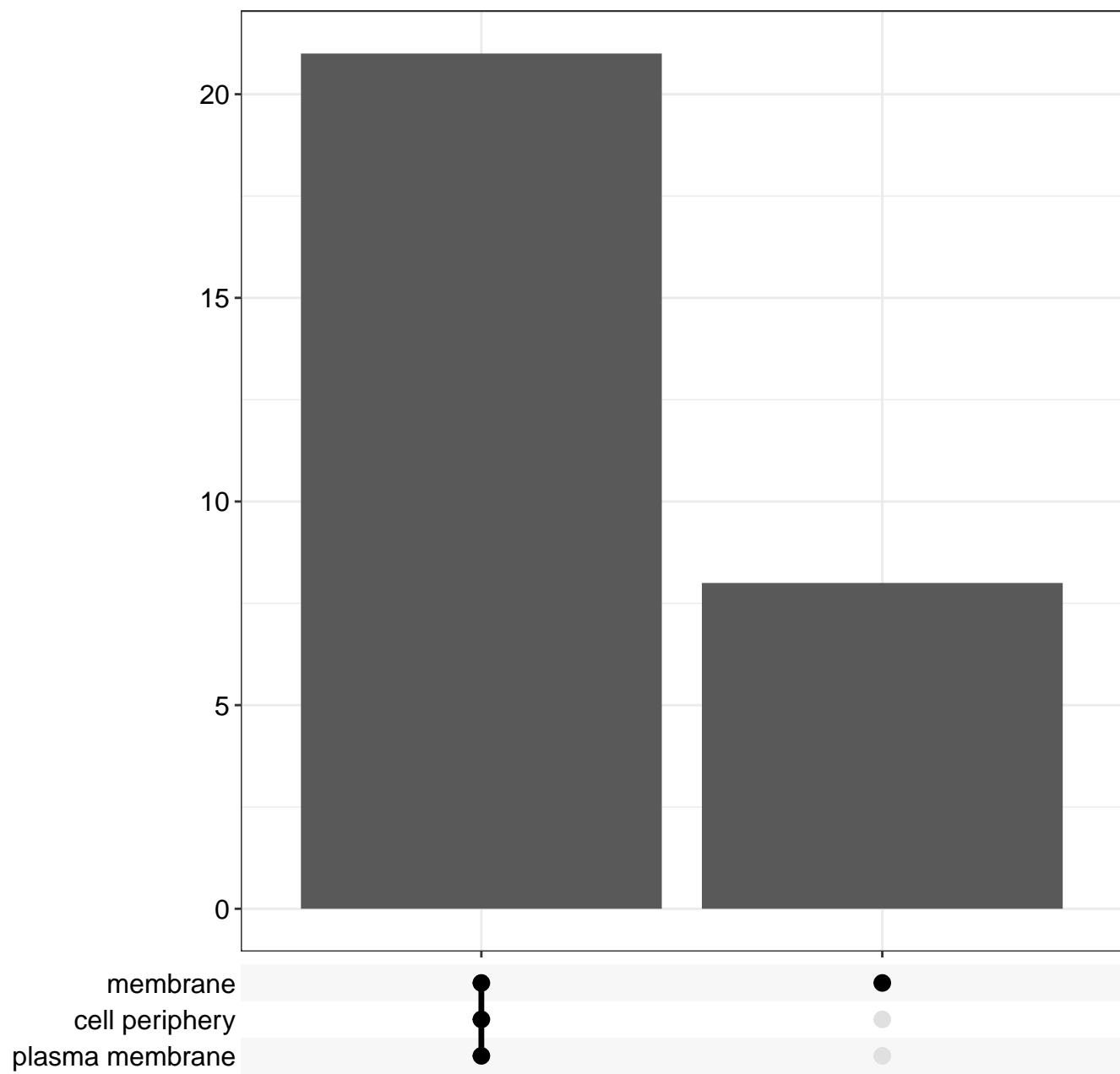


UPF3-TAP Up-regulated GO CC emapplot

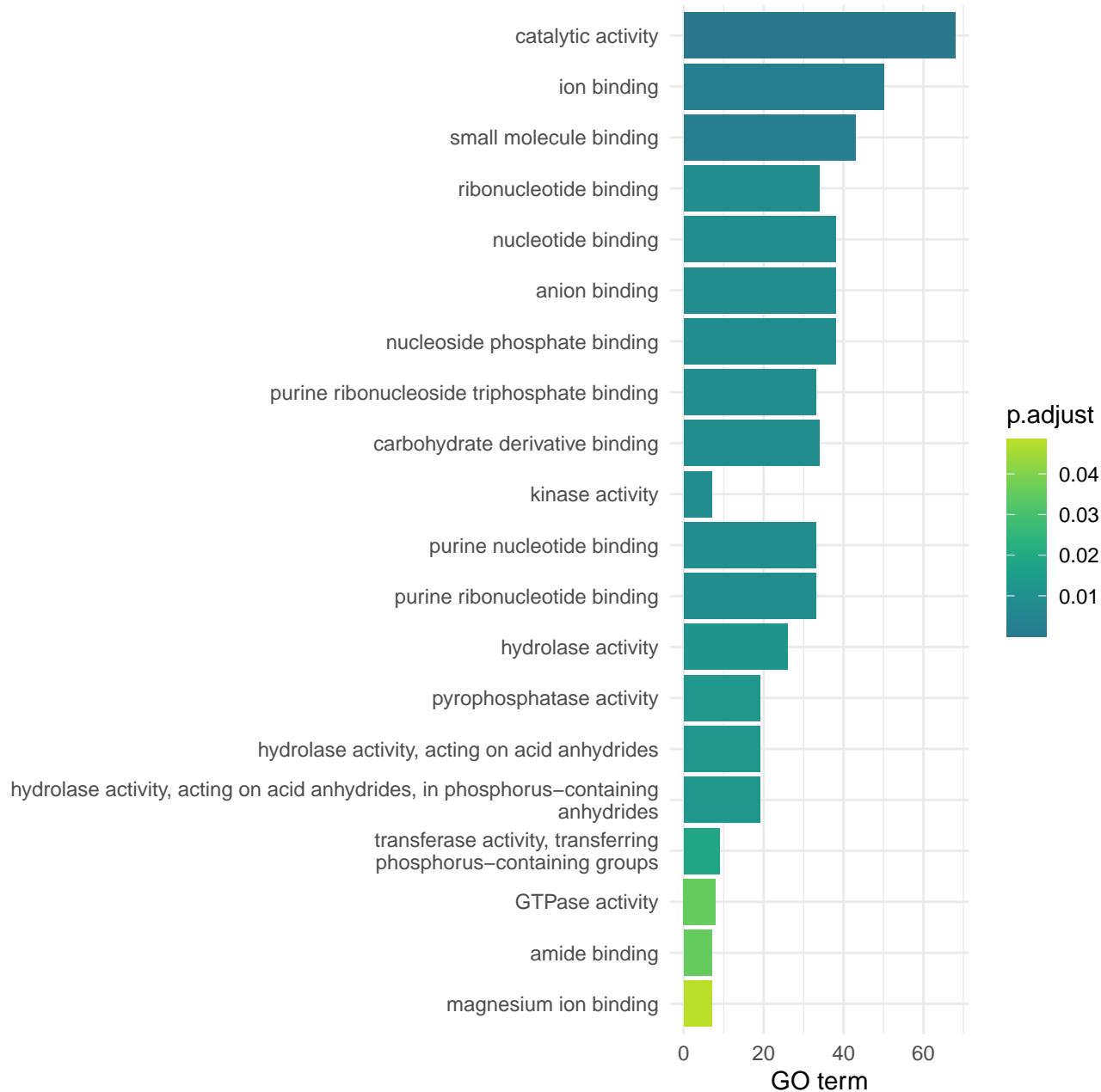




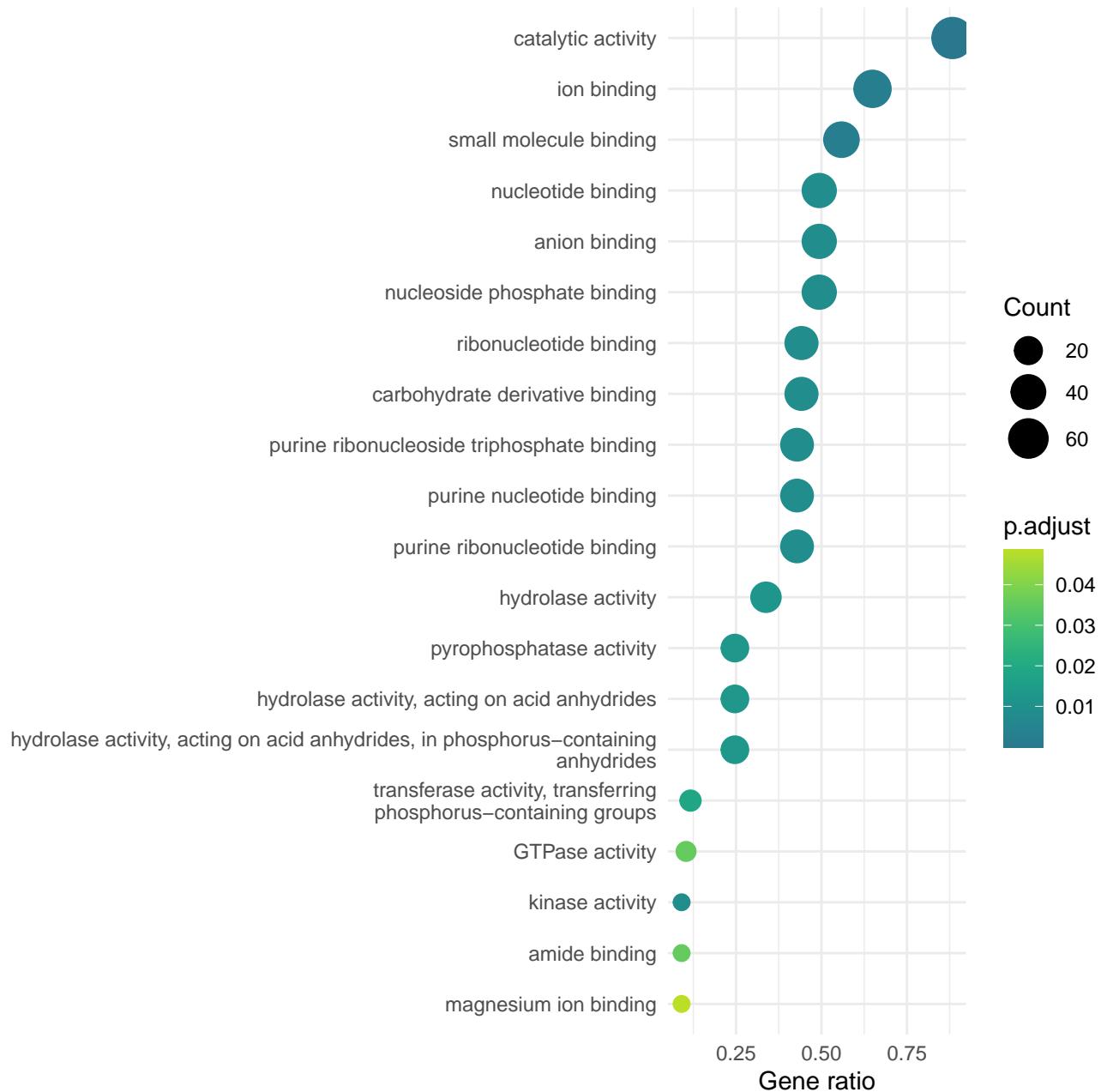
UPF3-TAP Up-regulated GO CC upsetplot



UPF3-TAP Up-regulated GO MF



UPF3-TAP Up-regulated GO MF



UPF3-TAP Up-regulated GO MF cnetplot

acid anhydrides

acid anhydrides, in phosphorus-containing anhydrides

ion binding

kinase activity

magnesium ion binding

nucleoside phosphate binding

nucleotide binding

purine nucleotide binding

purine ribonucleoside triphosphate binding

purine ribonucleotide binding

hydrolase activity, acting on acid anhydrides

hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides
pyrophosphatase activity

GTPase activity, transferring phosphorus-containing groups

kinase activity

purine nucleotide binding, purine ribonucleotide binding

GSP1 TIF2 IPP1

EFT1 SSZ1 APA1 kinase activity

TU31 purine ribonucleoside triphosphate binding

ribonucleotide binding, carbohydrate derivative binding

ARF2 HIS4 anion binding

HCP60 HCP104 nucleotide binding

HSC82 nucleotide binding

ADE1 GLN1 nucleoside phosphate binding

DED81 DPS1 catalytic activity

GUS1 VAS1 THS1 small molecule binding

FAS1 SAH1 ion binding

MMF1 ADE17 OYE2

SAH1 GPP1 SHM2

FAS1 ADE17 TKL1

MMF1 ADE17 HOM6

SAH1 ADE17 IMD3

FAS1 ADE17 TDH3

MMF1 ADE17 ENO1

SAH1 ADE17 FBA1

FAS1 ADE17 ADH1

MMF1 ADE17 CPR1

SAH1 ADE17 amide binding

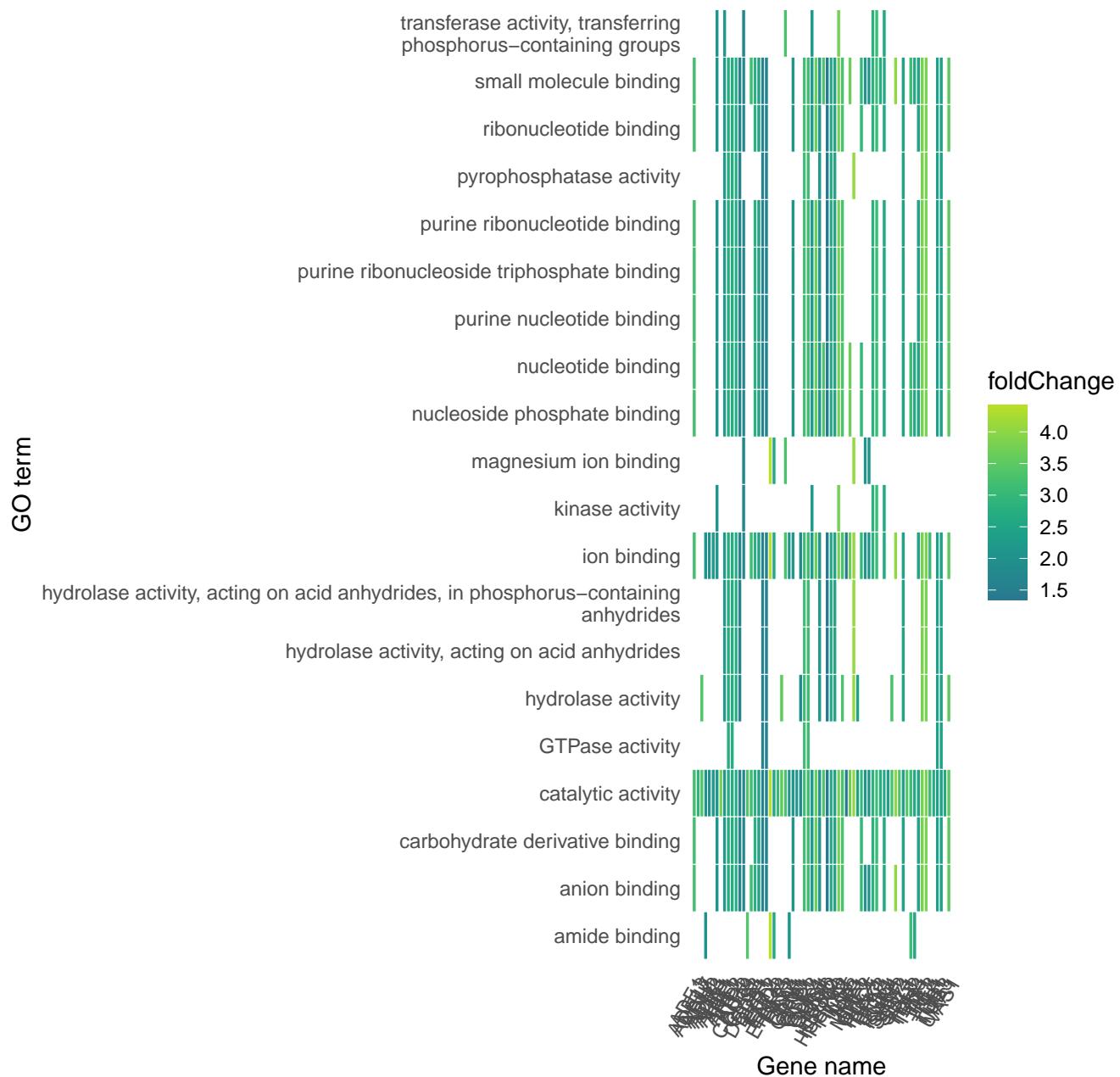
FAS1 ADE17

MMF1 ADE17

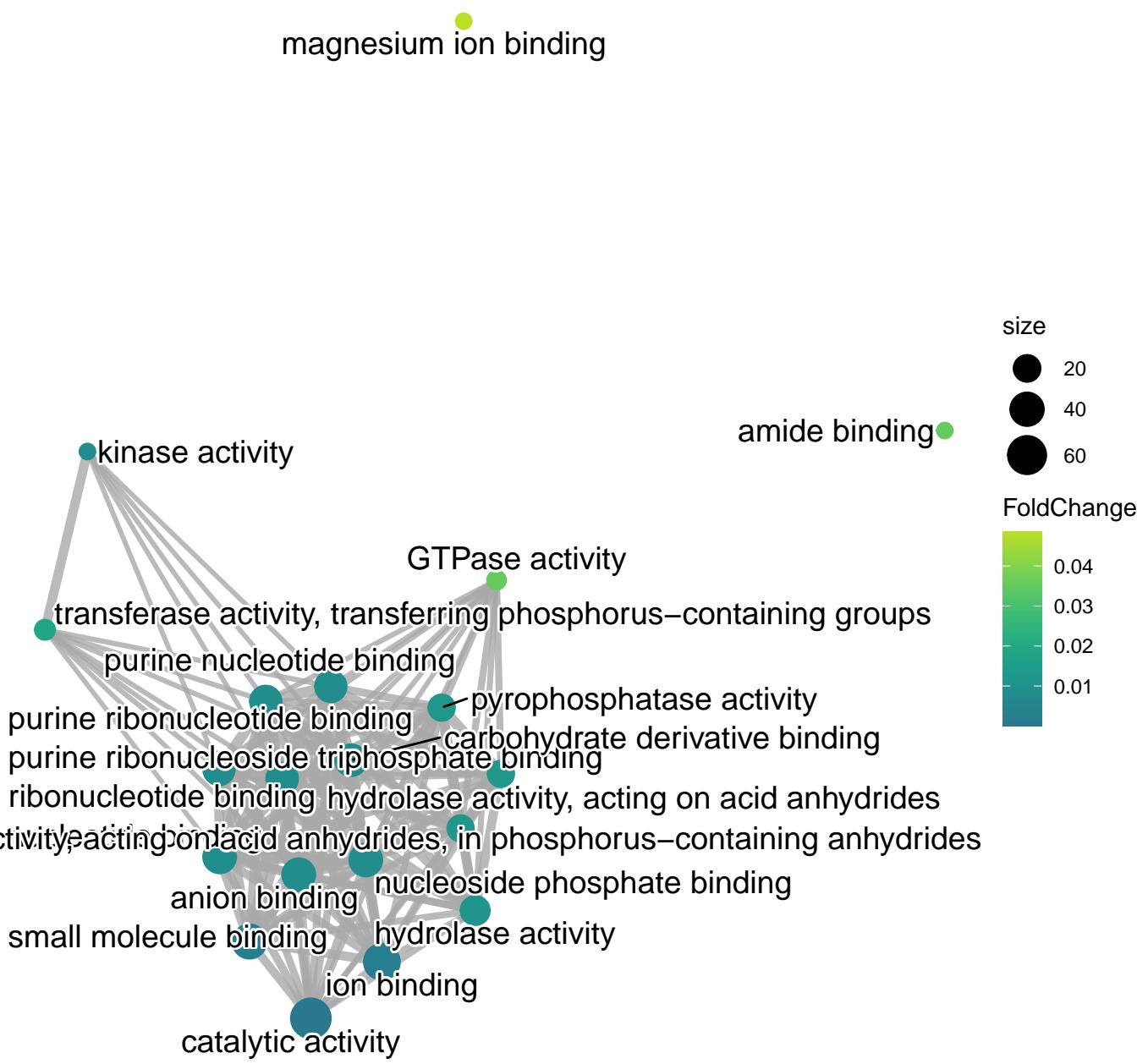
SAH1 ADE17

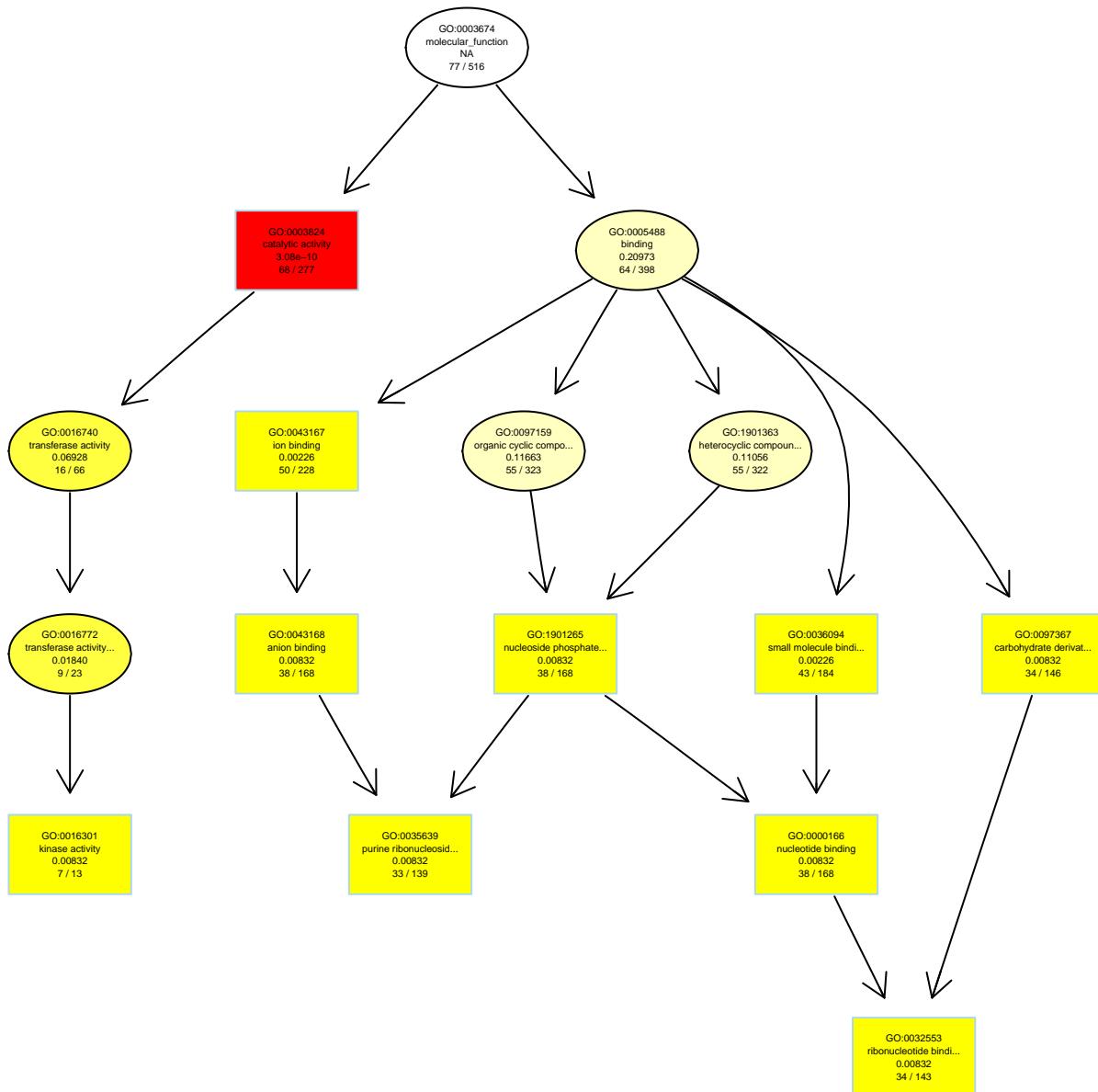
FAS1 ADE17</p

UPF3-TAP Up-regulated GO MF

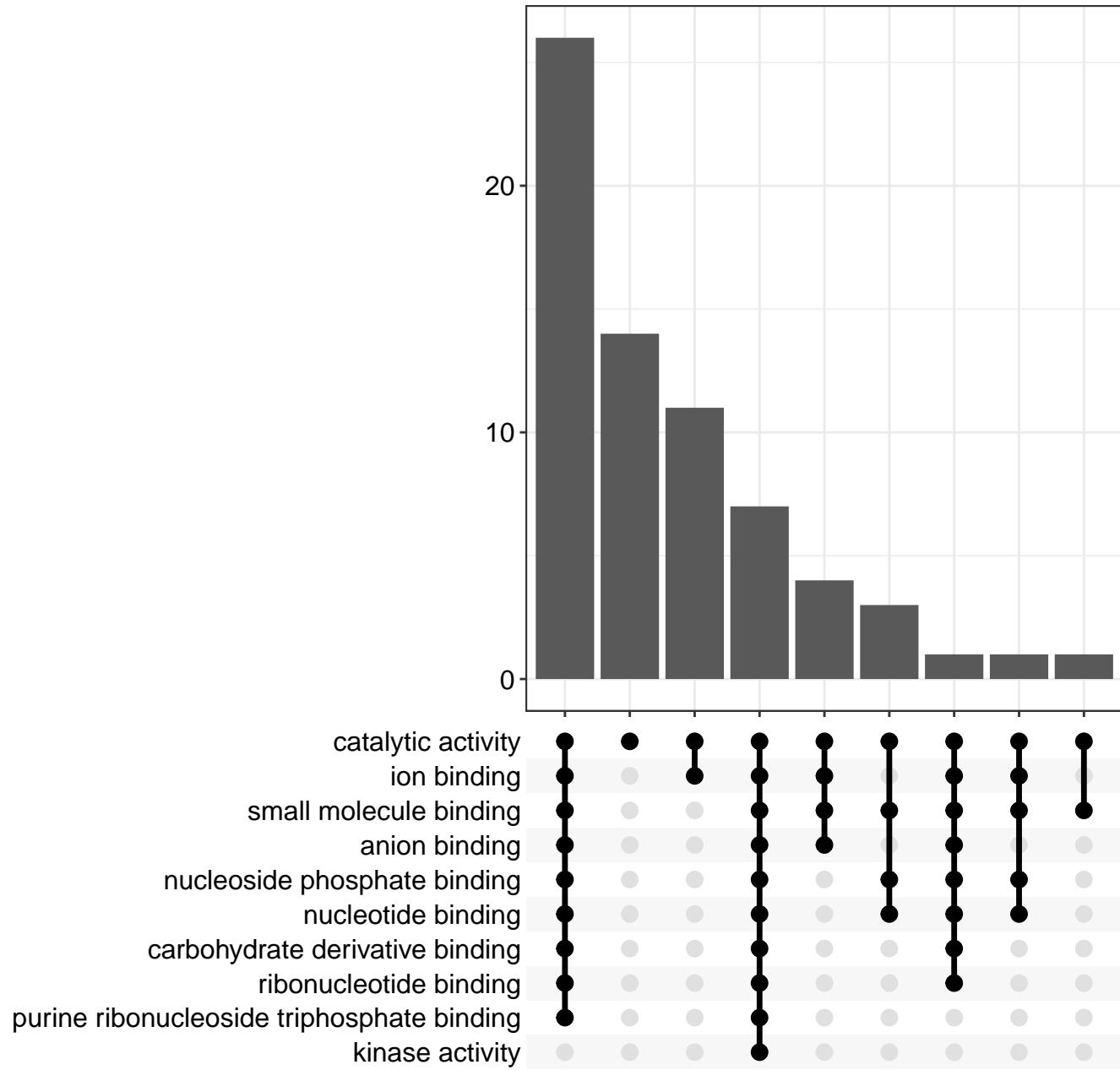


UPF3-TAP Up-regulated GO MF emapplot

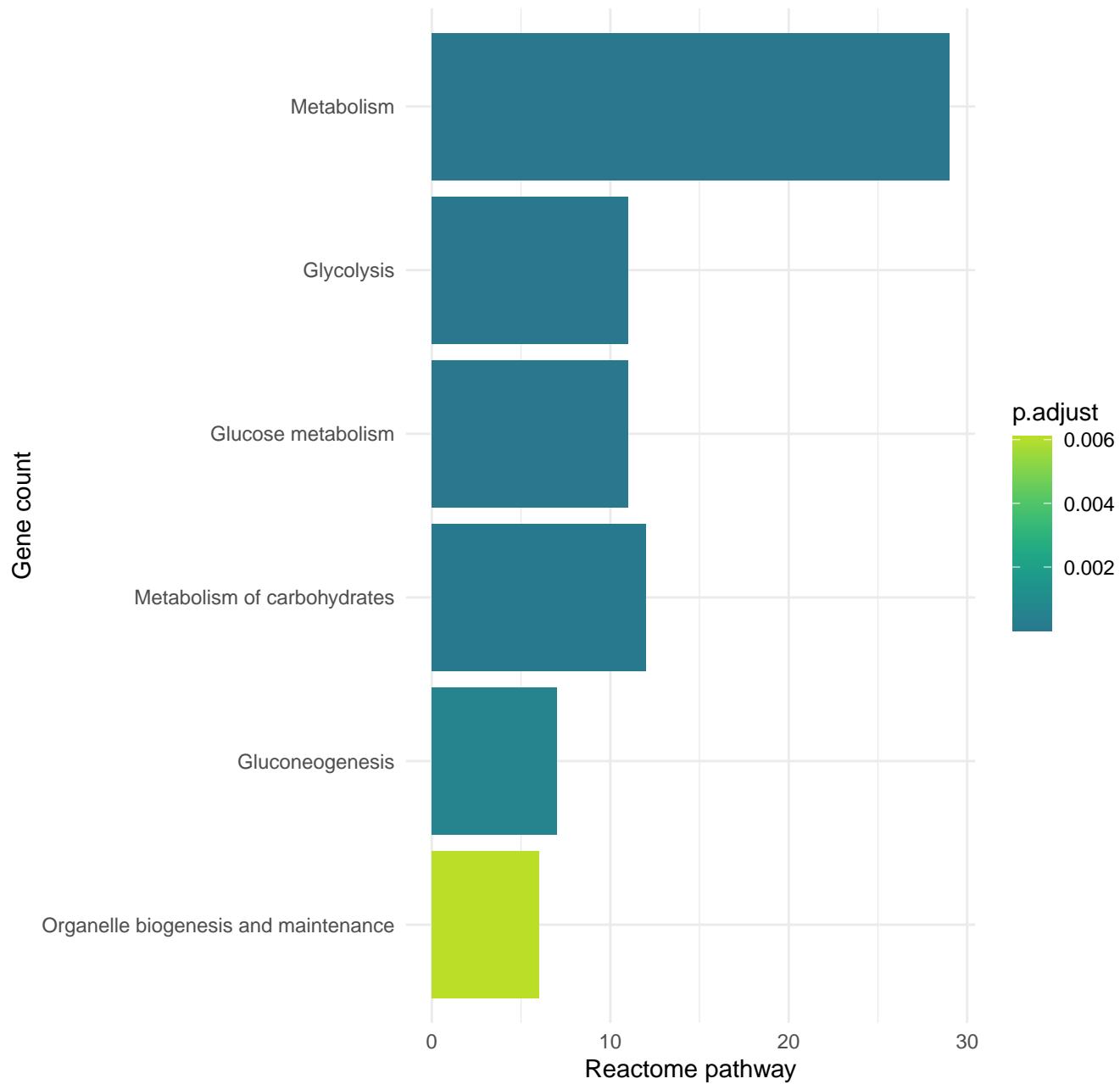




UPF3-TAP Up-regulated GO MF upsetplot

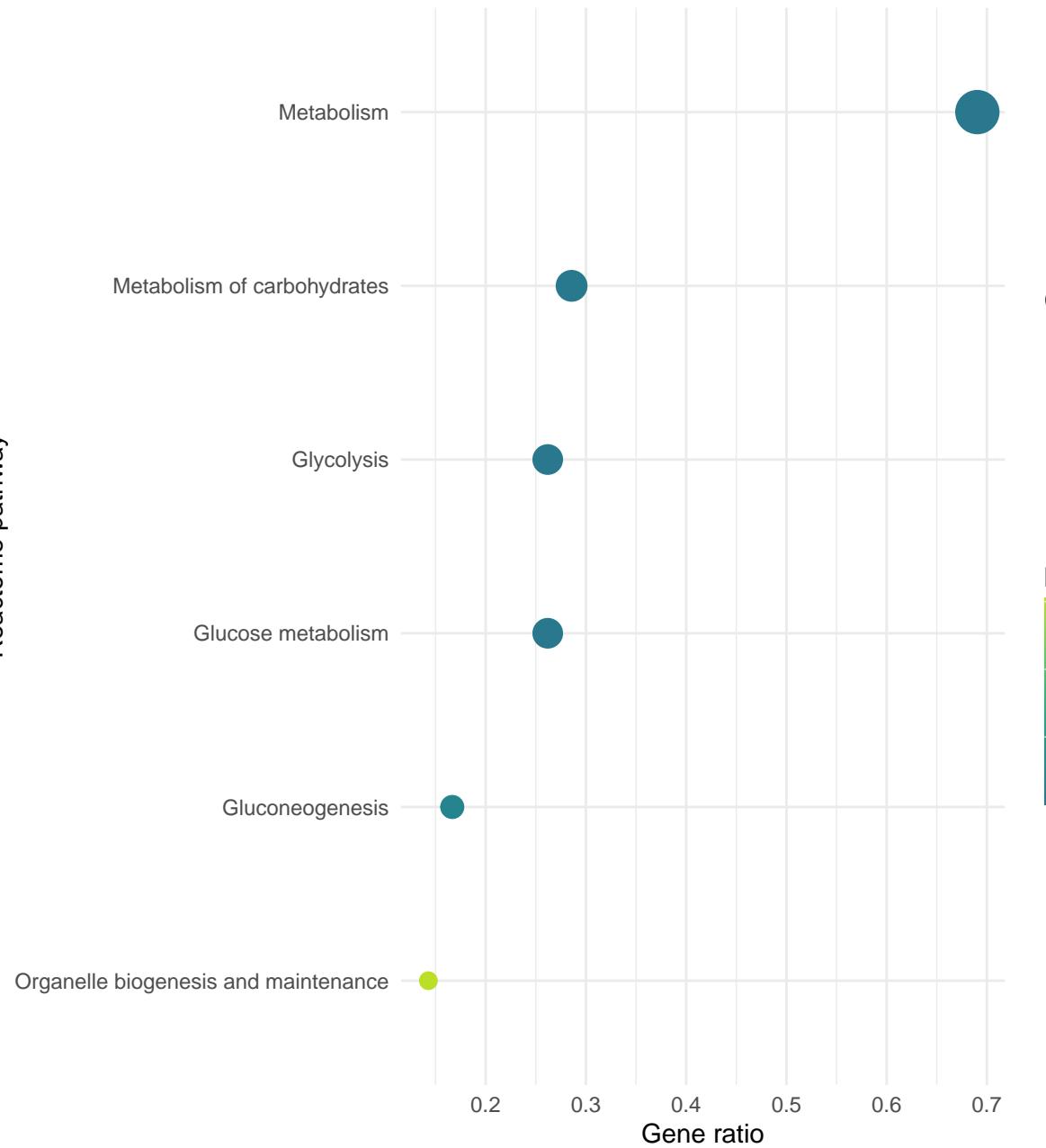


UPF3-TAP Up-regulated Reactome barplot

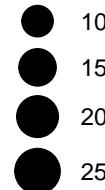


UPF3-TAP Up-regulated Reactome dotplot

Reactome pathway



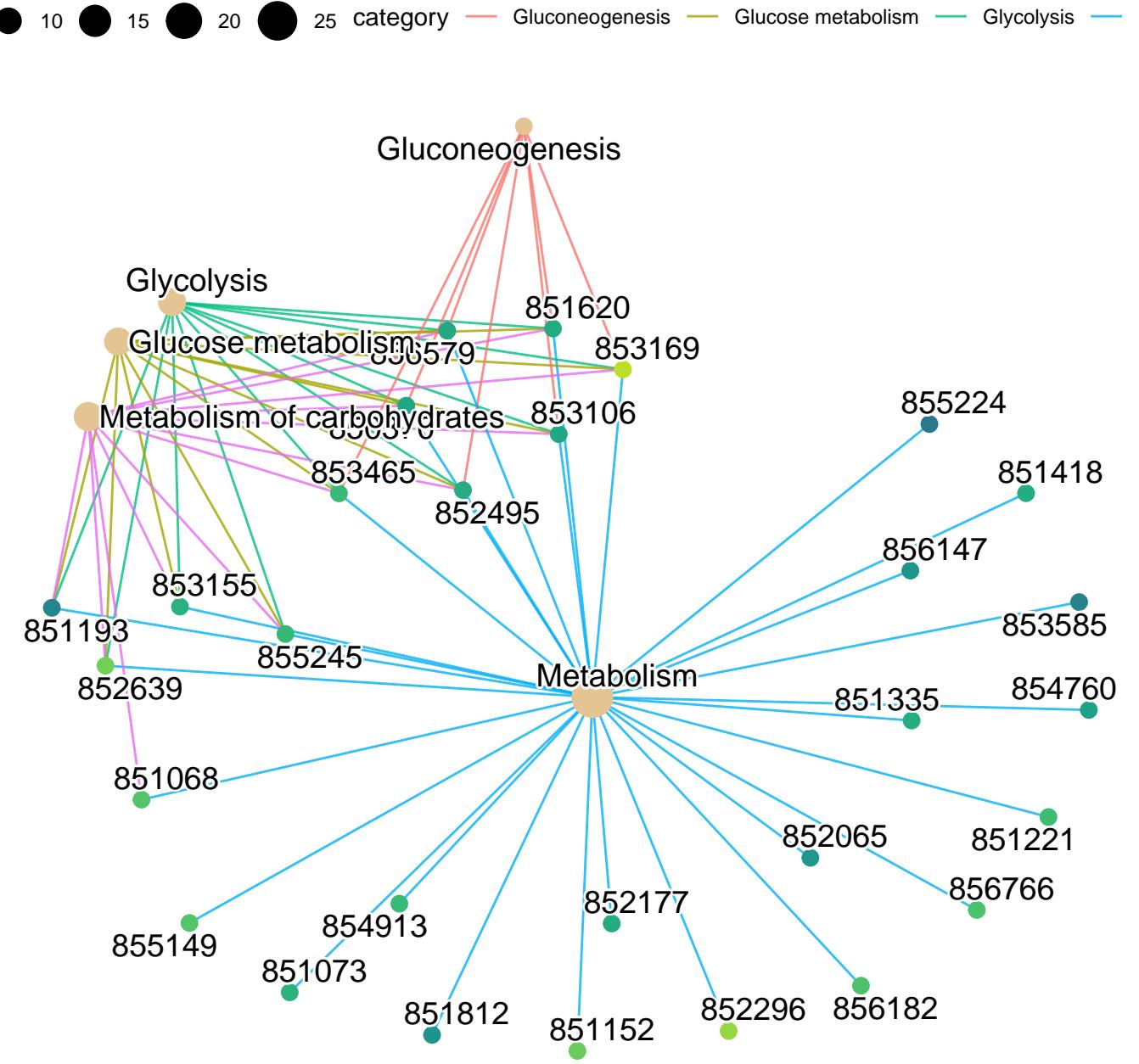
Count



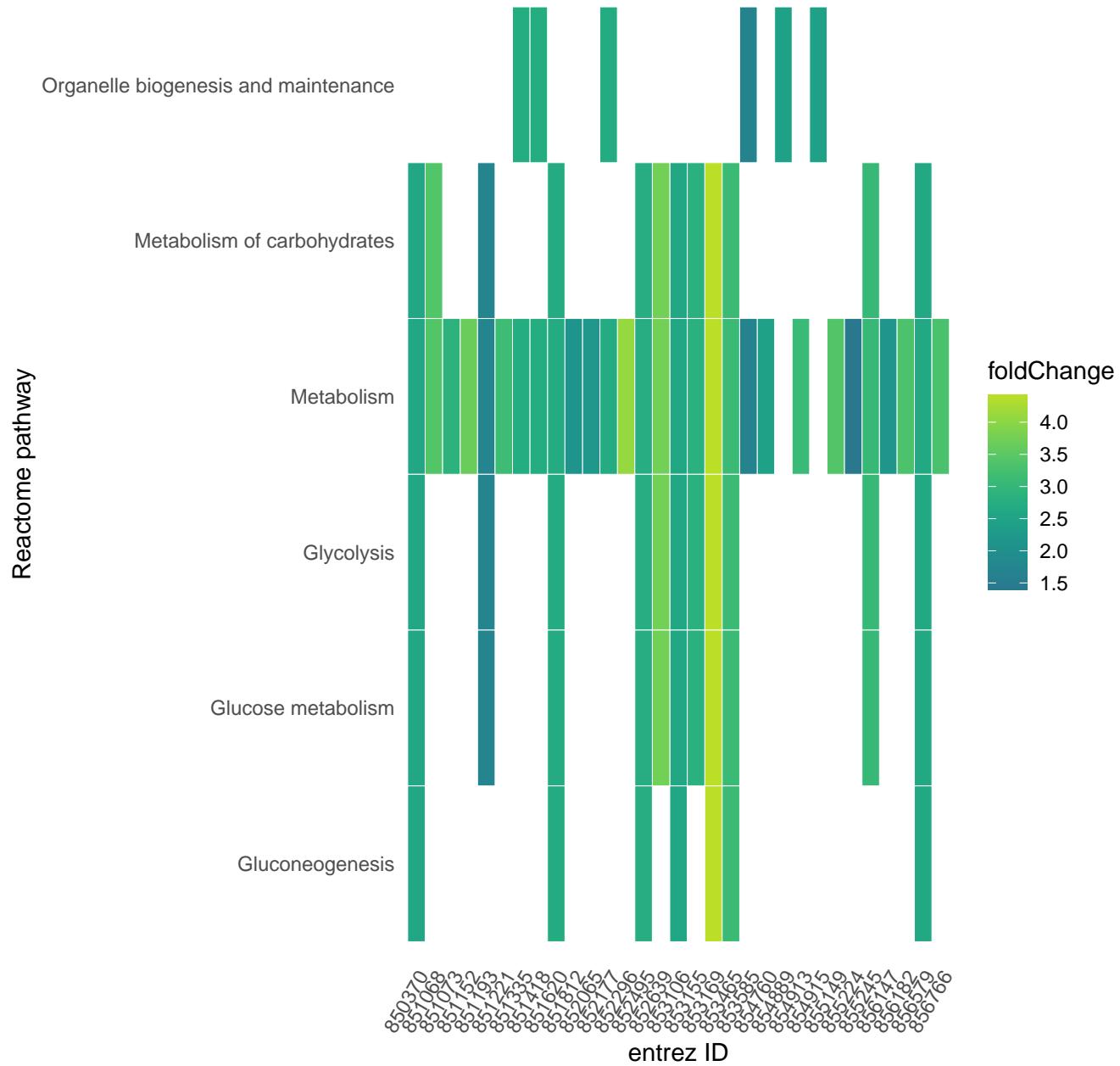
p.adjust



UPF3-TAP Up-regulated Reactome cnetplot

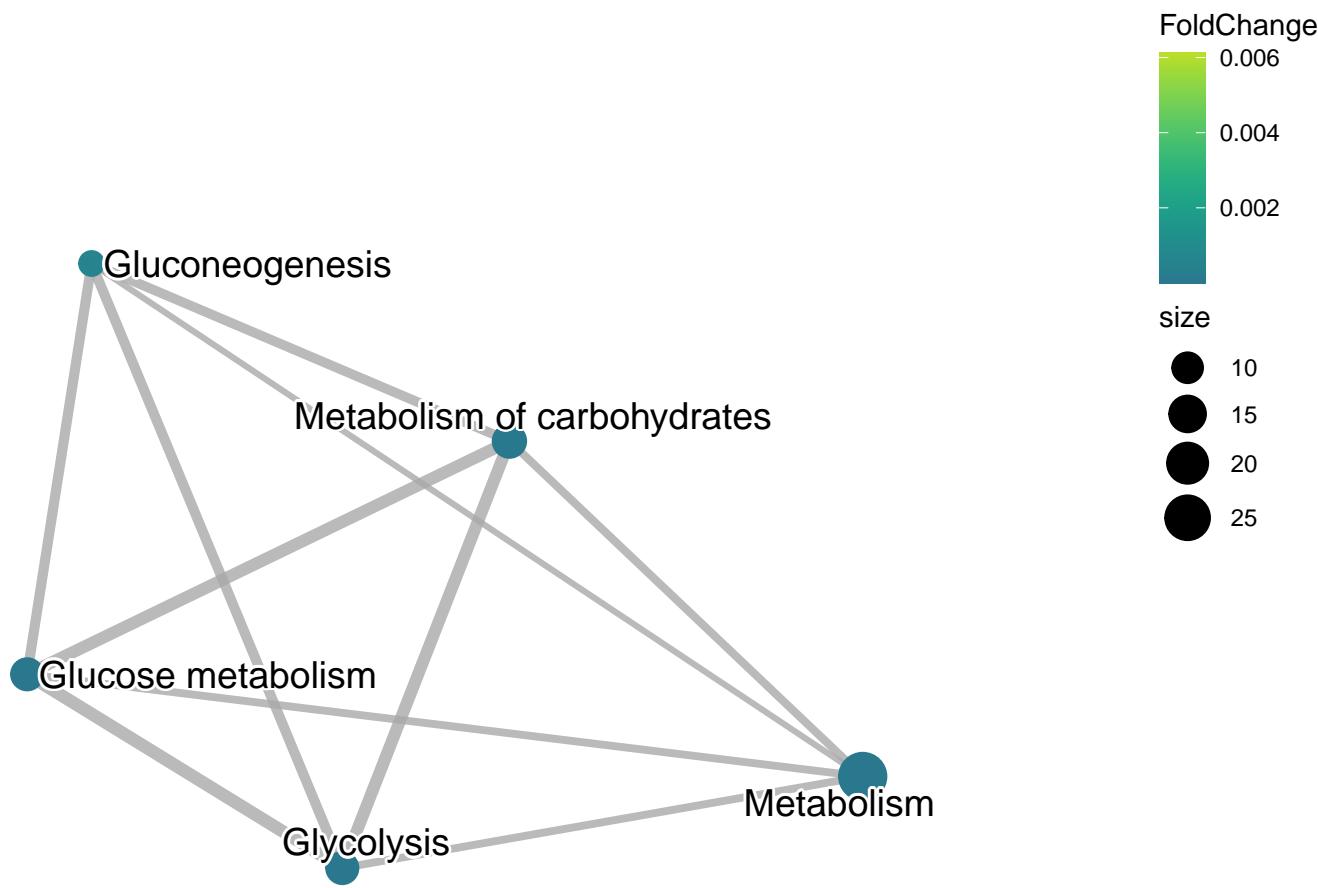


UPF3-TAP Up-regulated Reactome heatplot

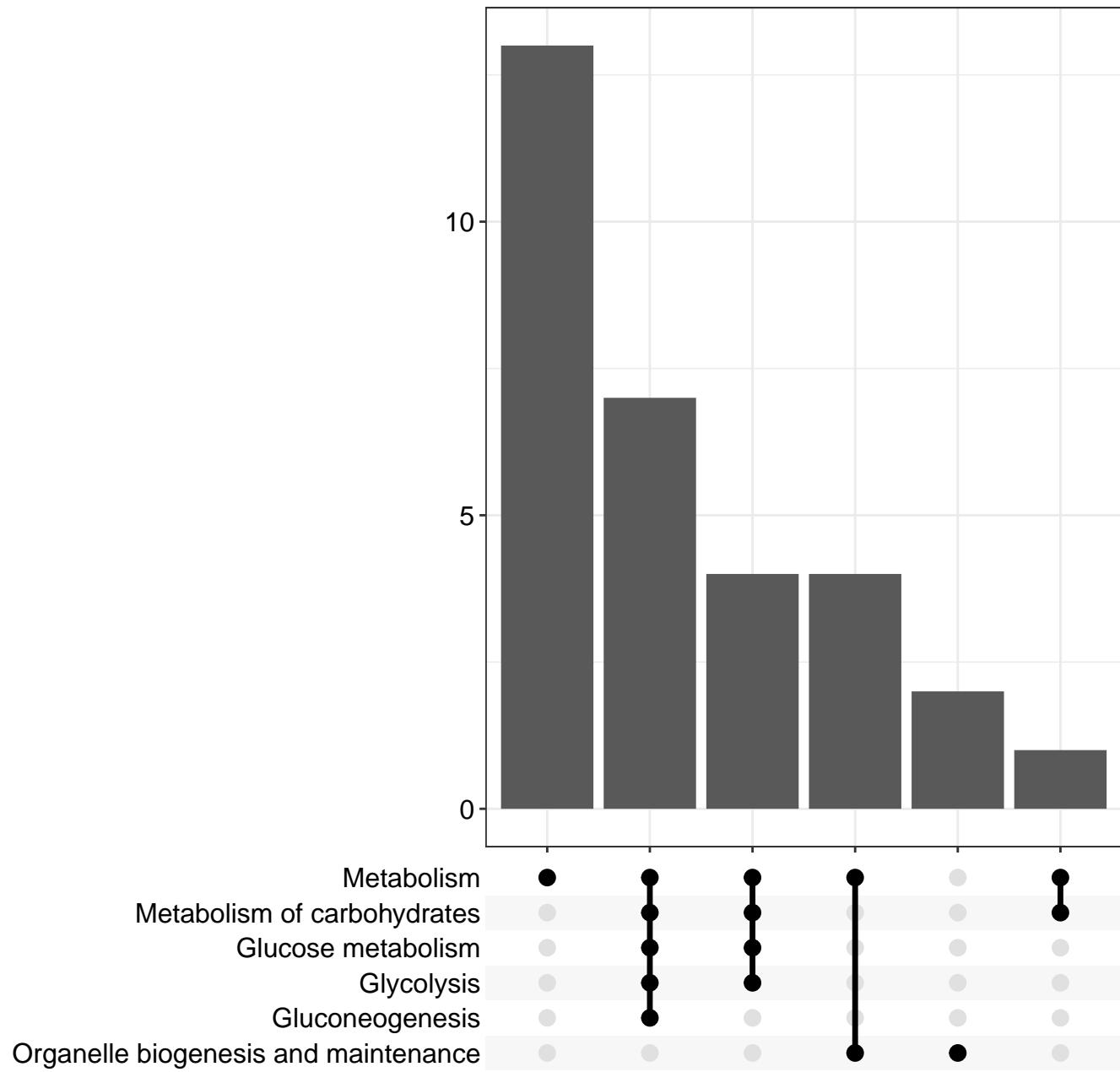


UPF3-TAP Up-regulated Reactome emapplot

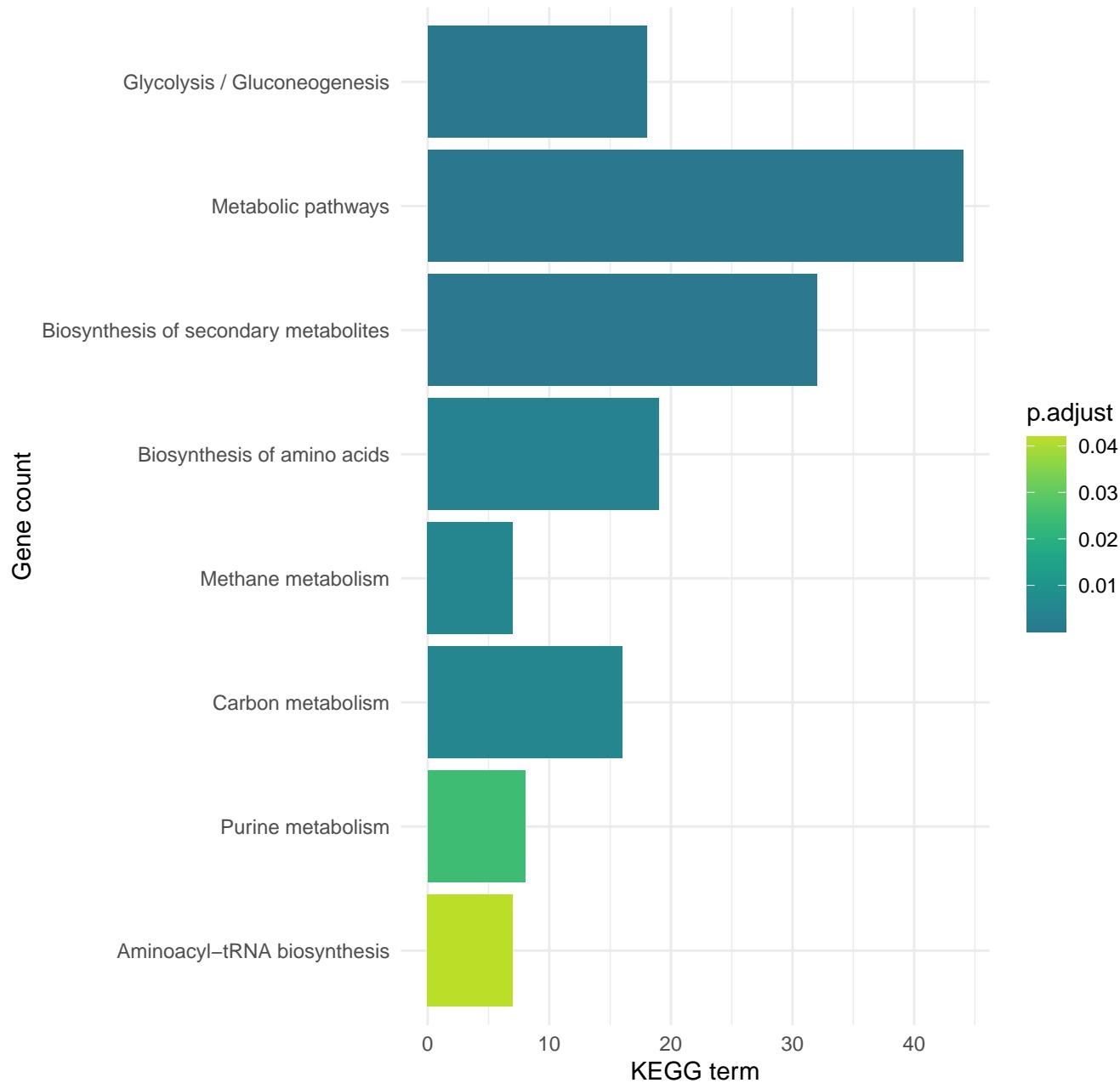
Organelle biogenesis and maintenance ●



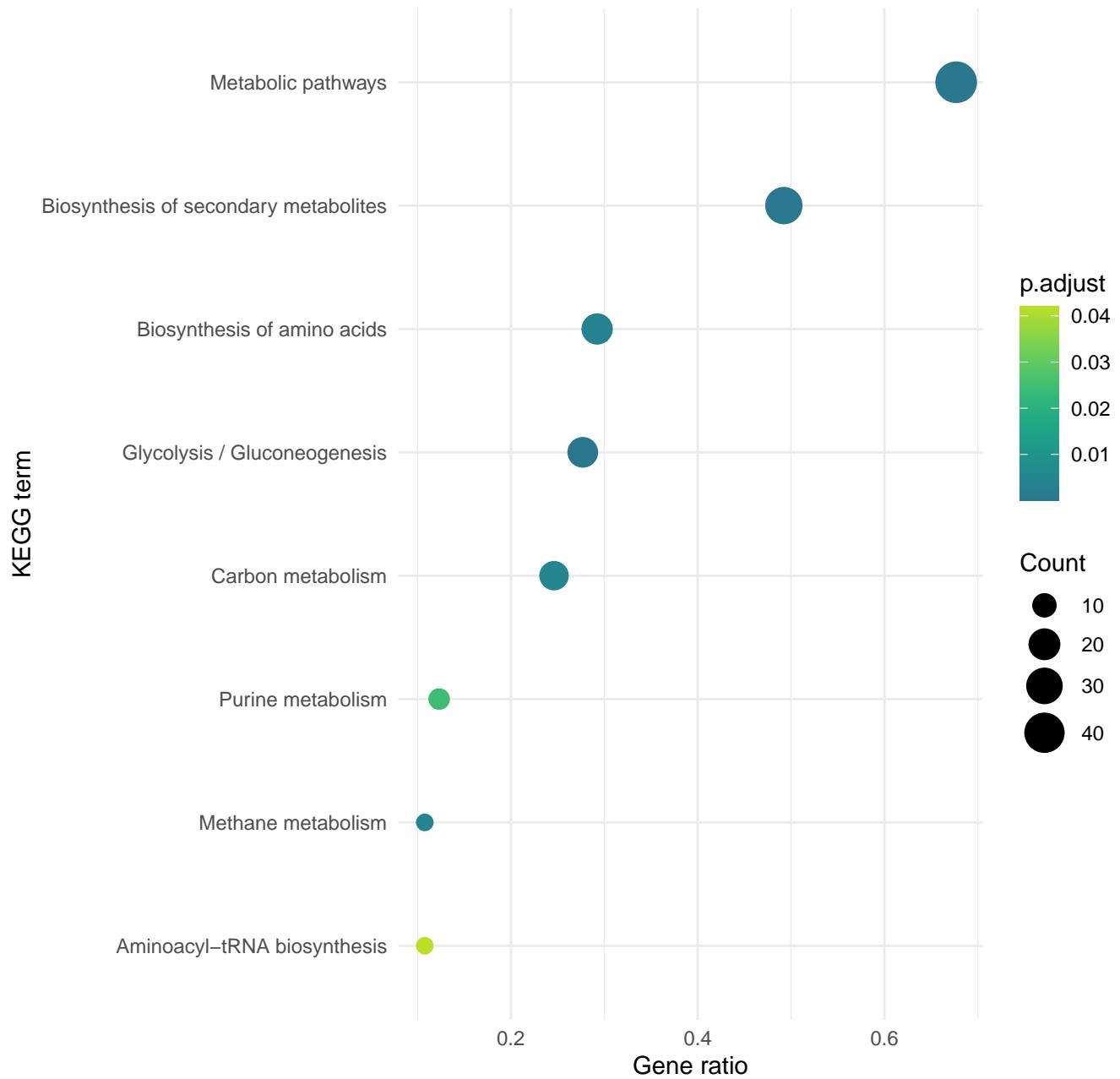
UPF3-TAP Up-regulated Reactome upsetplot



UPF3-TAP Up-regulated KEGG barplot

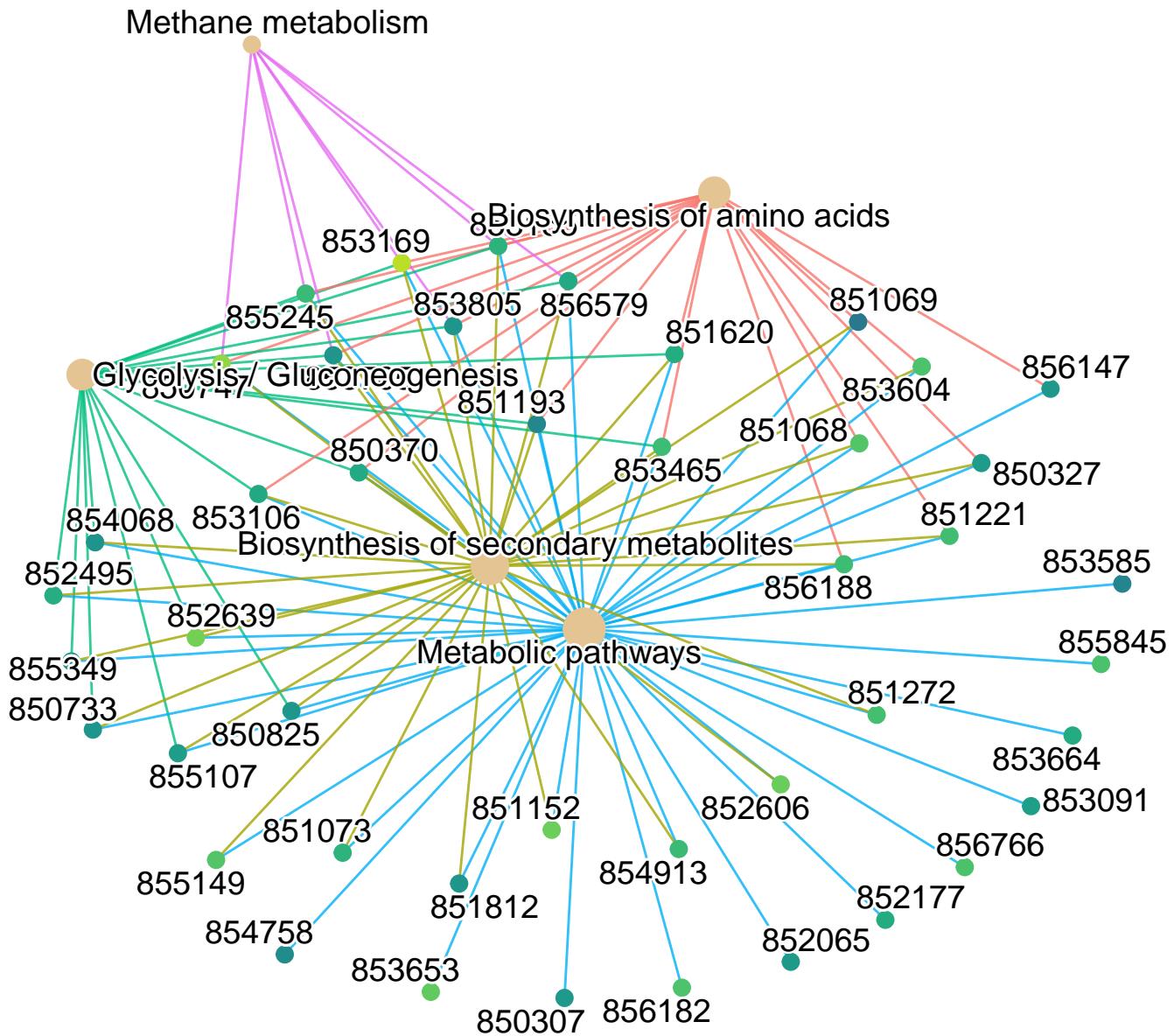


UPF3-TAP Up-regulated KEGG dotplot



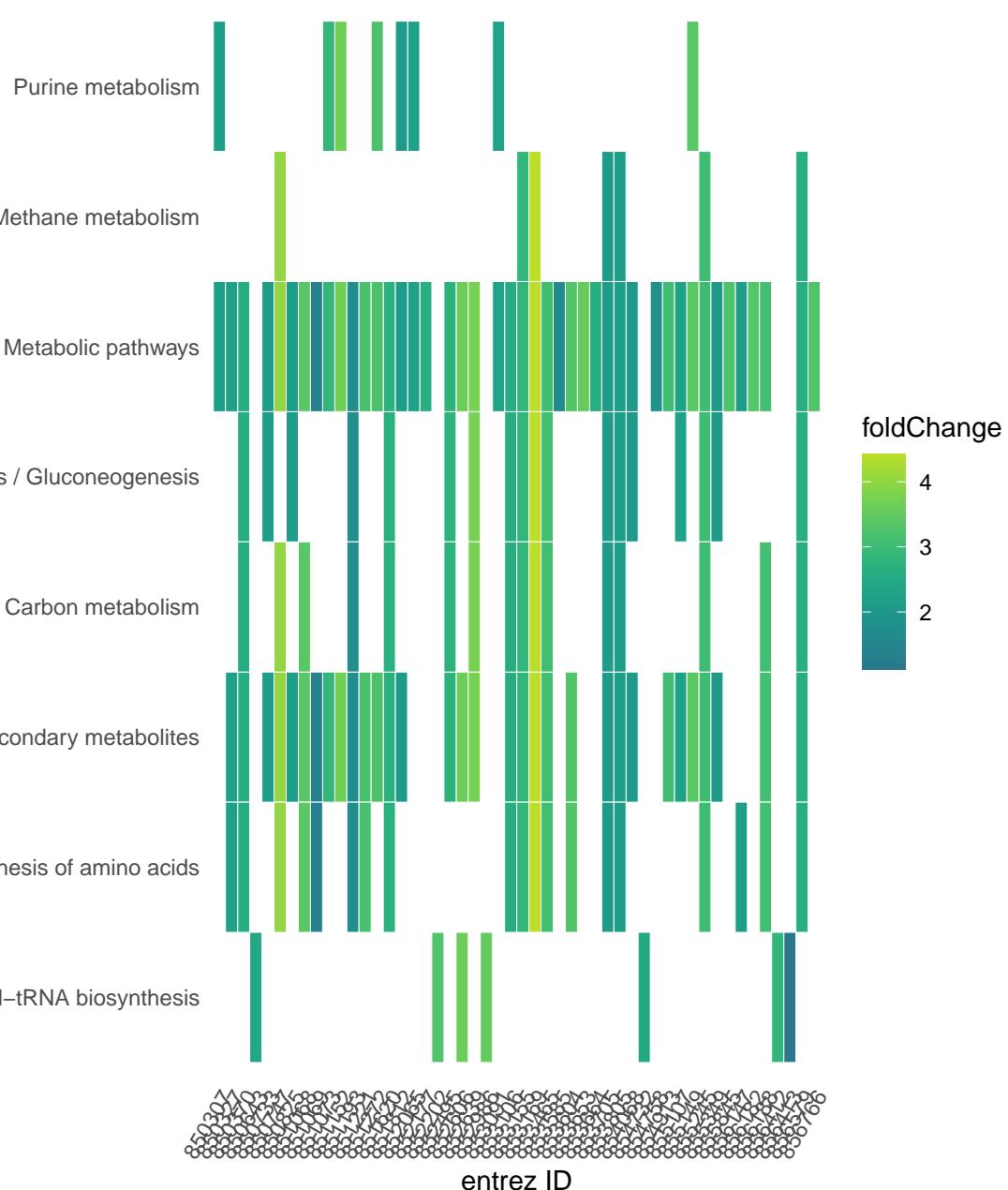
UPF3-TAP Up-regulated KEGG dotplot

secondary metabolites — Glycolysis / Gluconeogenesis — Metabolic pathways — Methane metabolism FoldChange

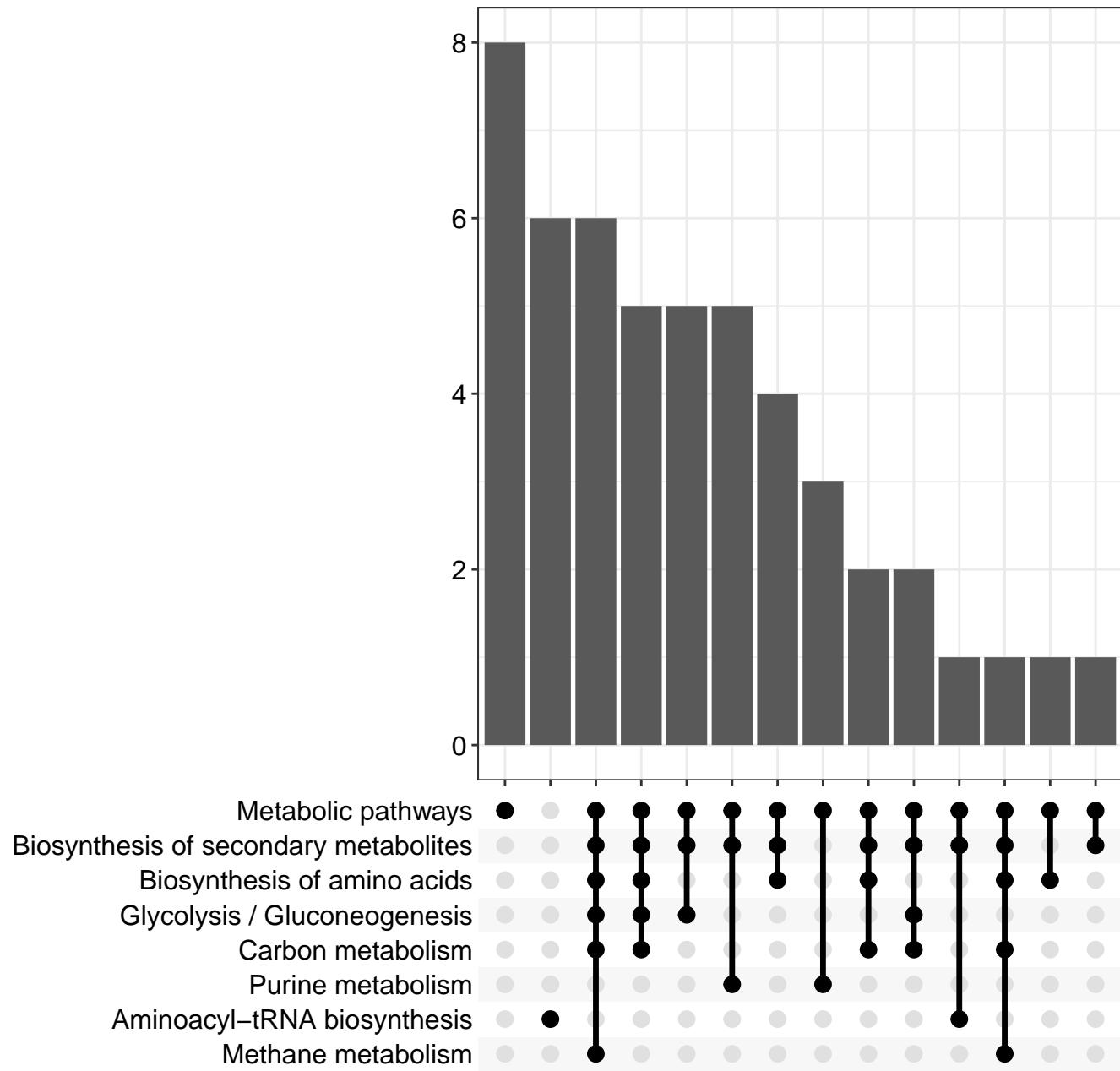


UPF3-TAP Up-regulated KEGG heatplot

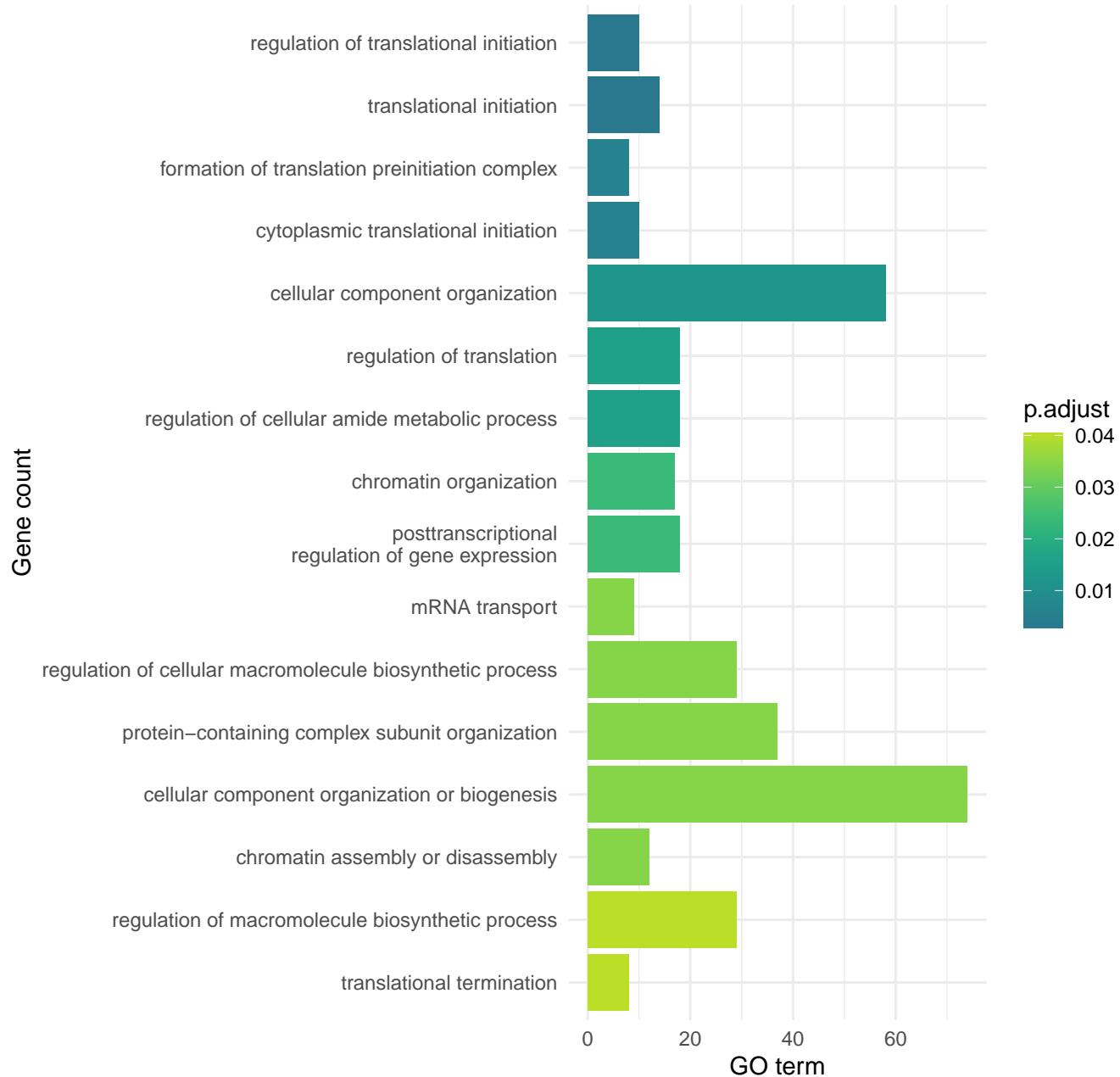
KEGG term



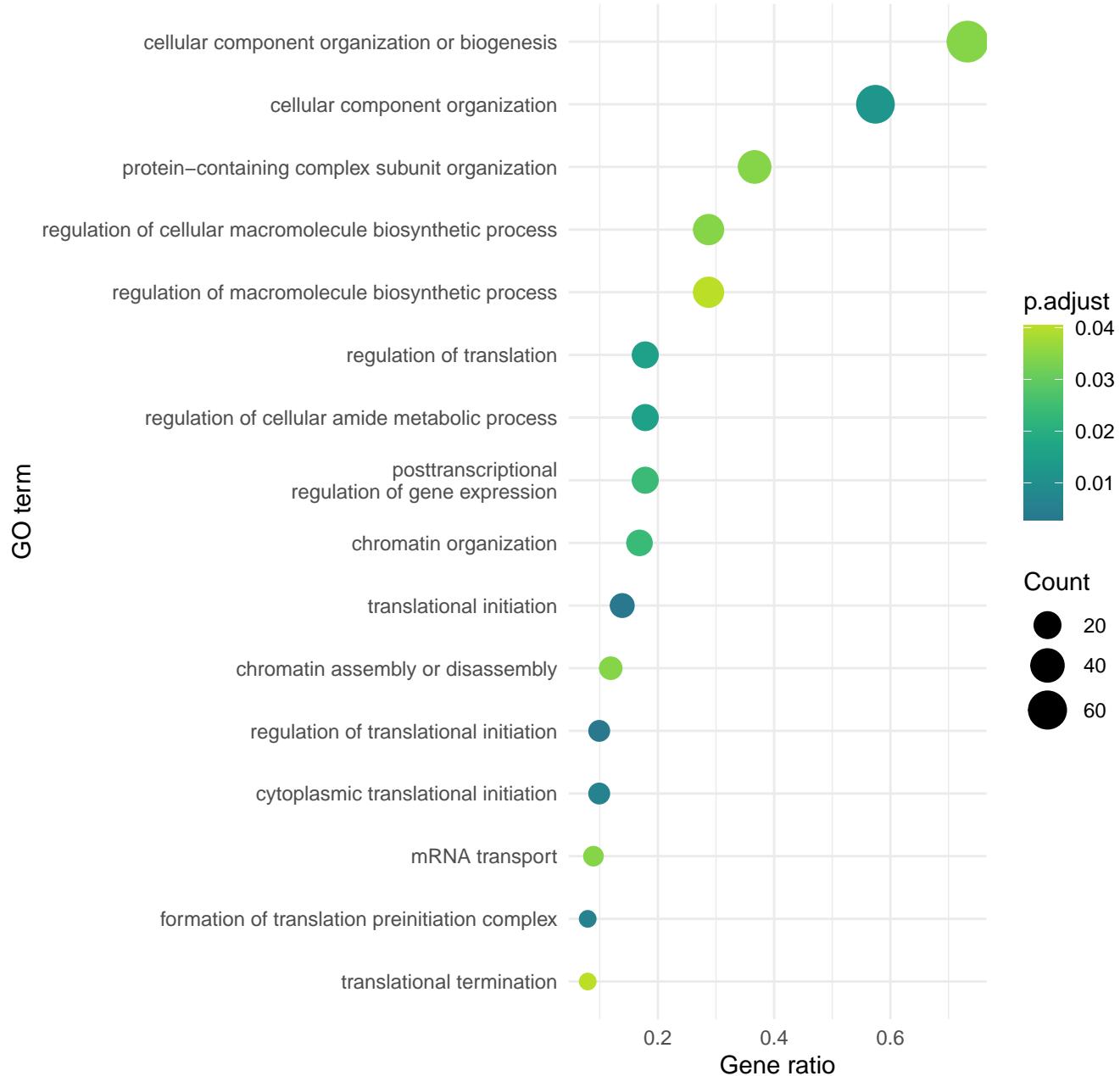
UPF3-TAP Up-regulated KEGG upsetplot



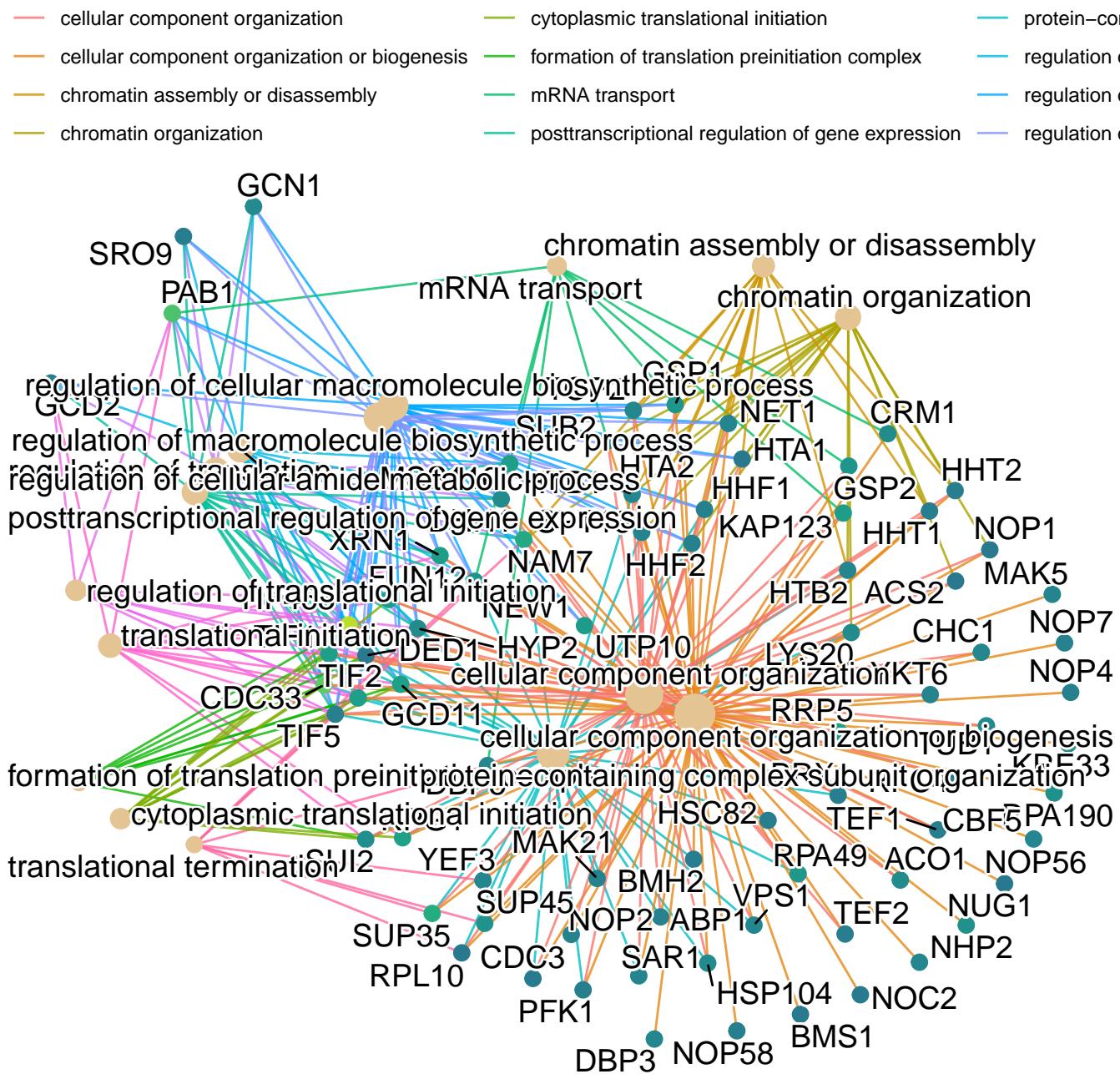
TIF4631-TAP Up-regulated GO BP barplot



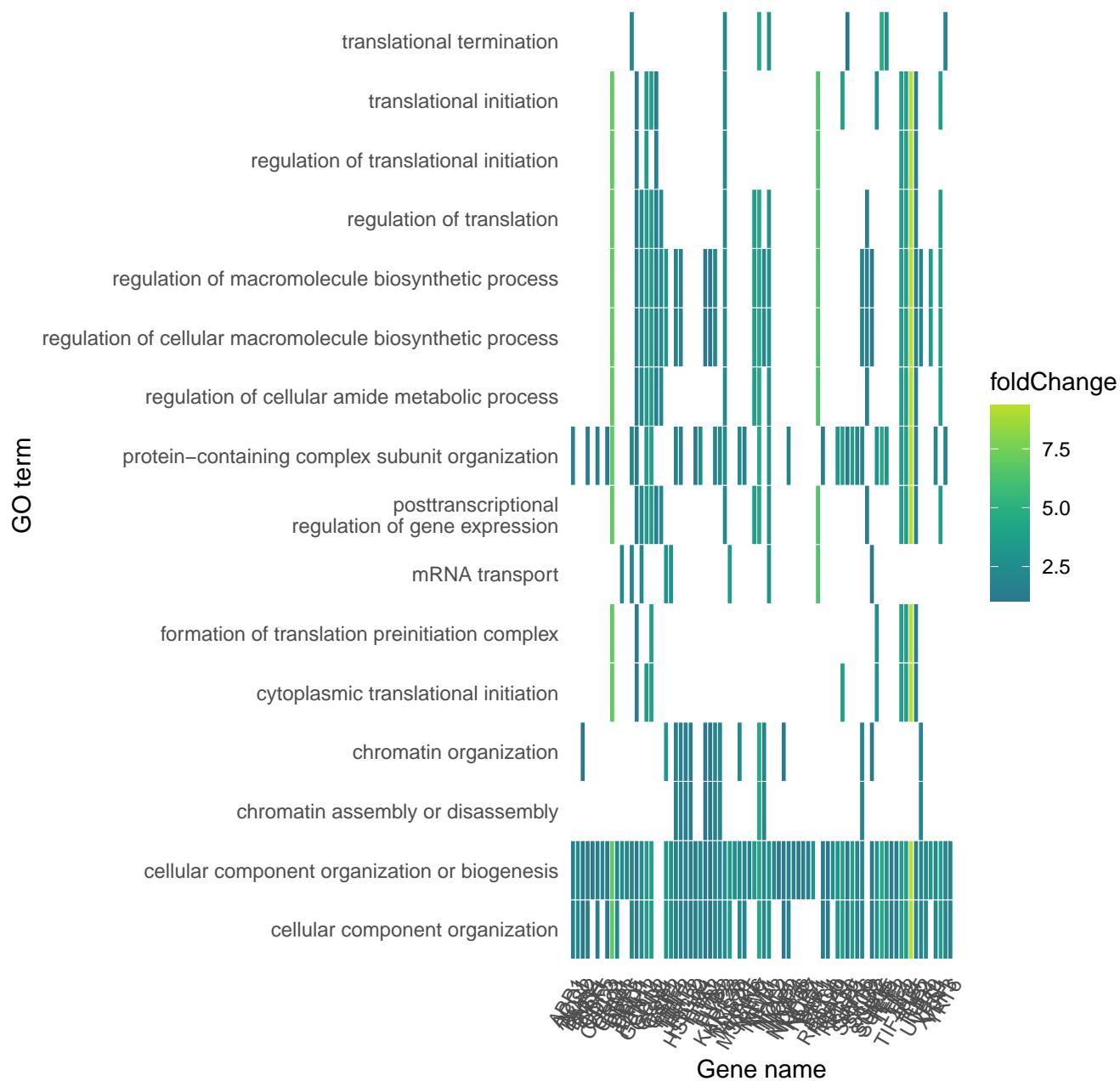
TIF4631-TAP Up-regulated GO BP dotplot



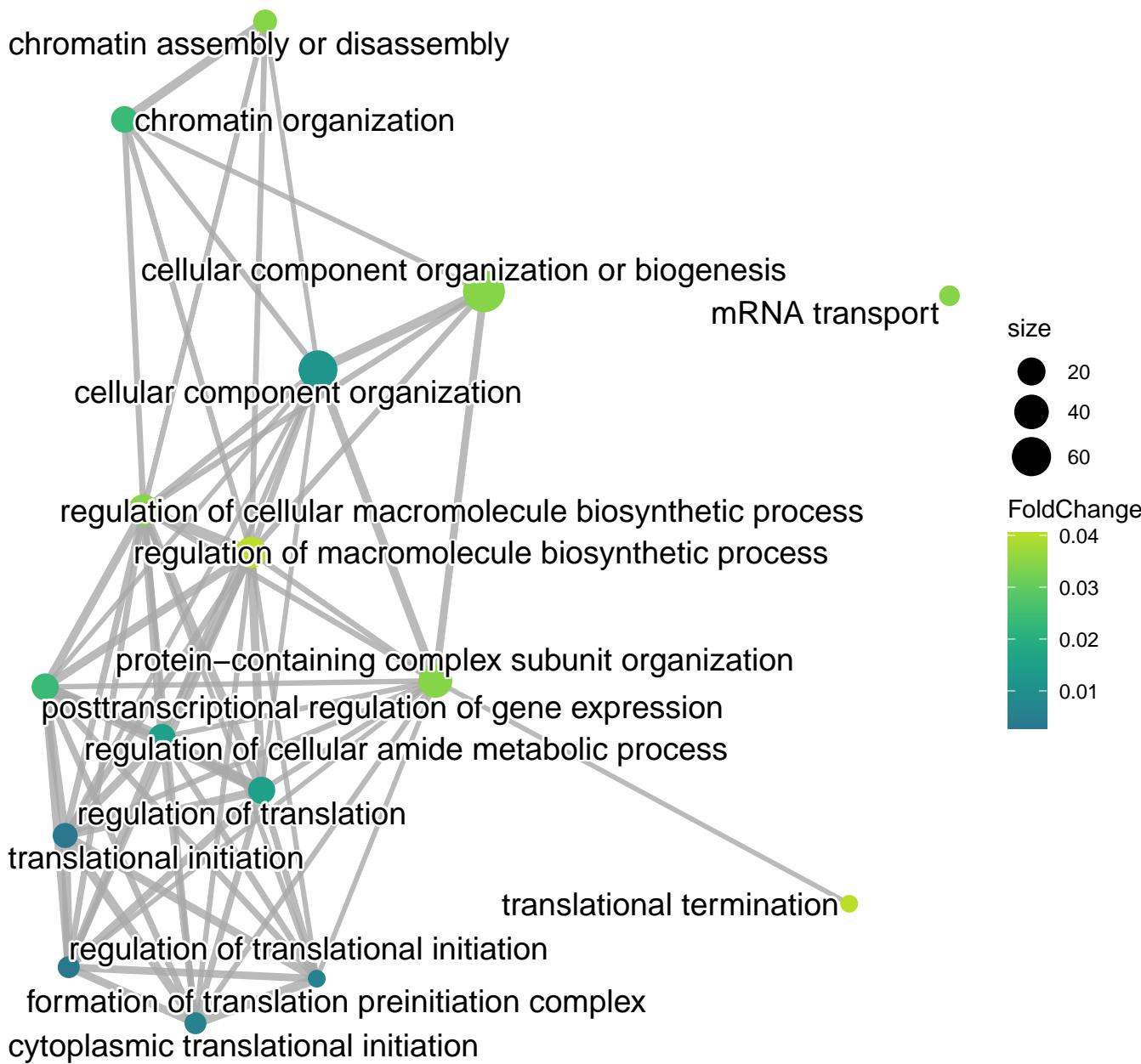
TIF4631-TAP Up-regulated GO BP cnetplot

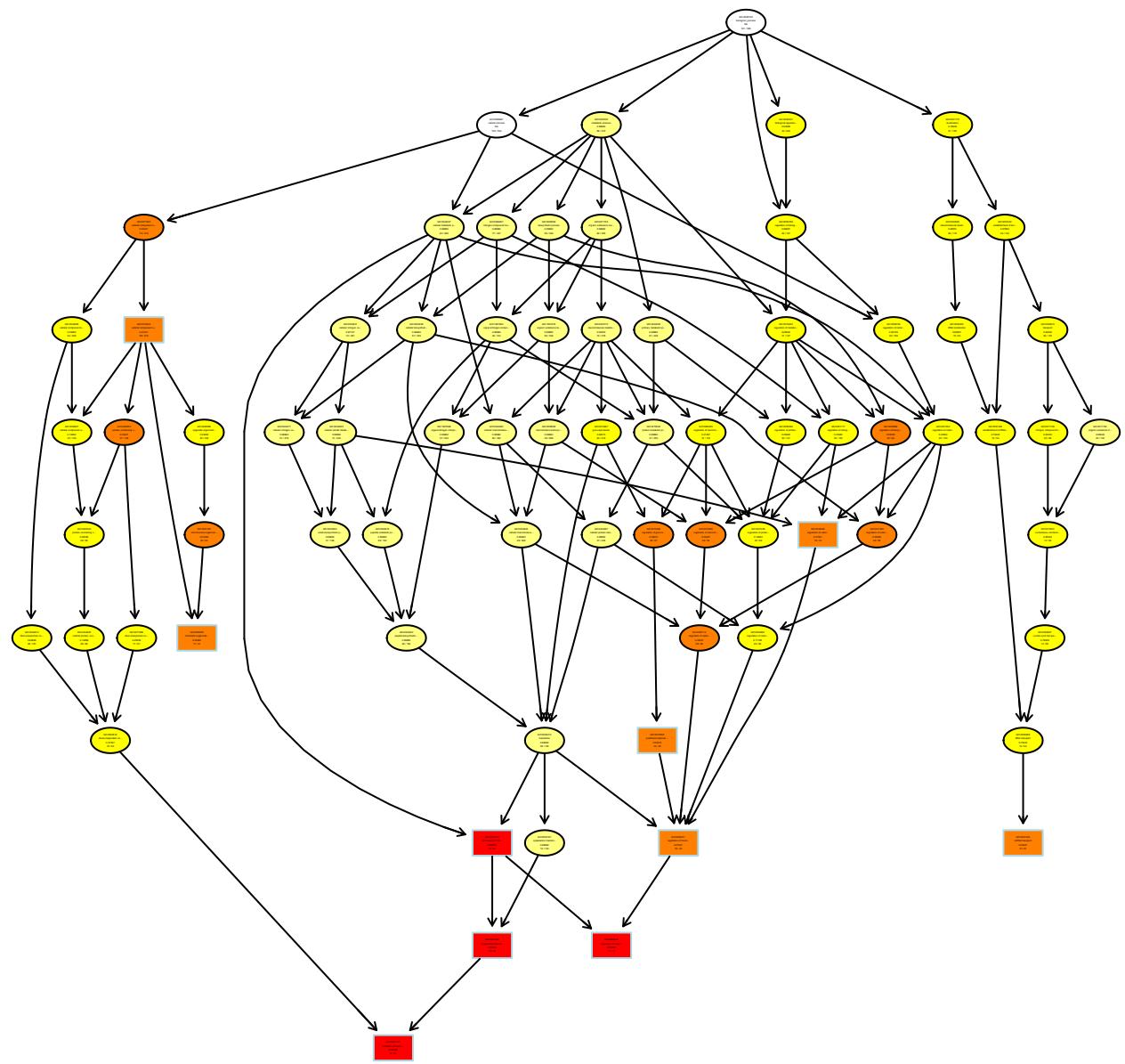


TIF4631-TAP Up-regulated GO BP heatmap

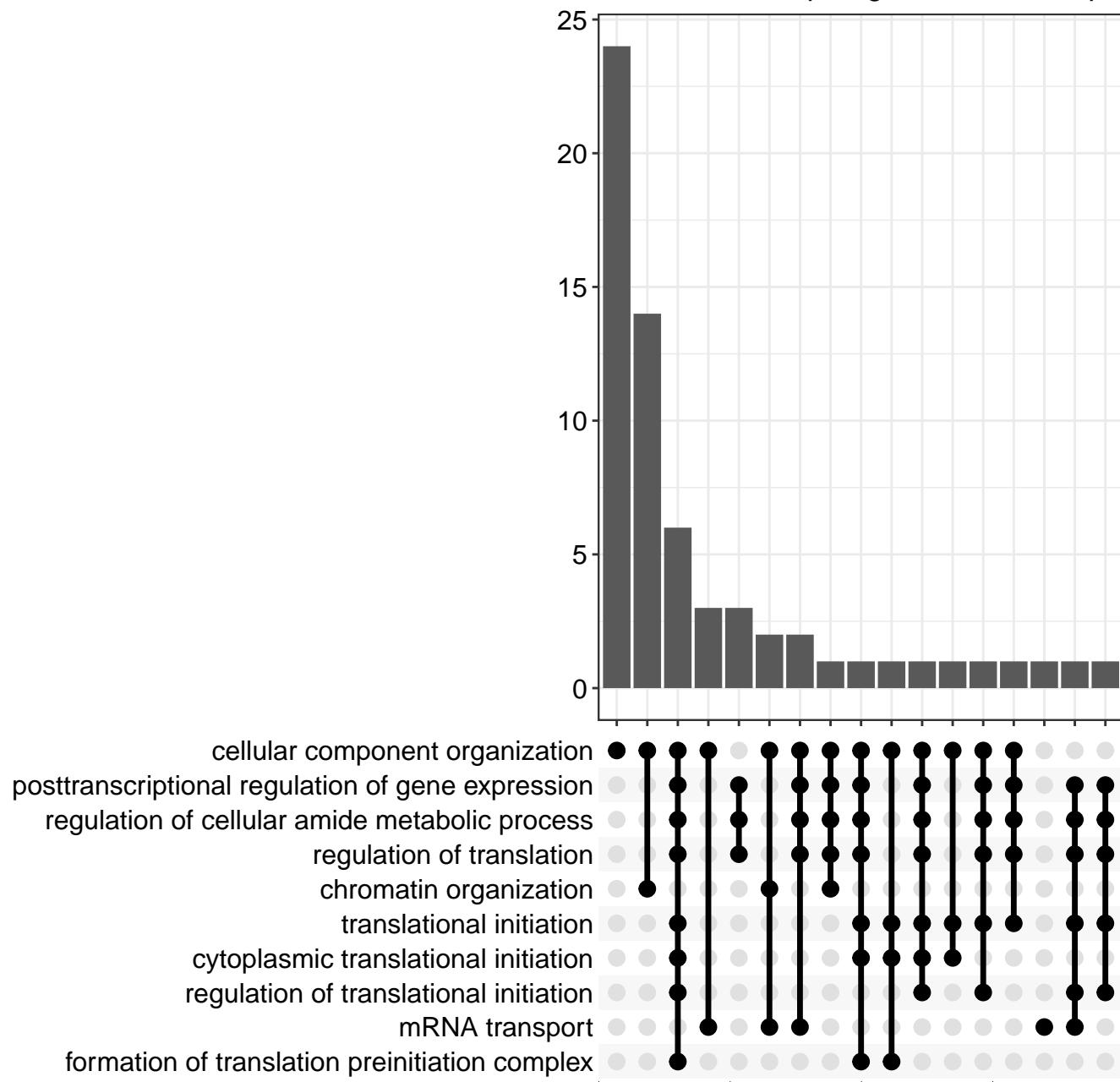


TIF4631-TAP Up-regulated GO BP emapplot

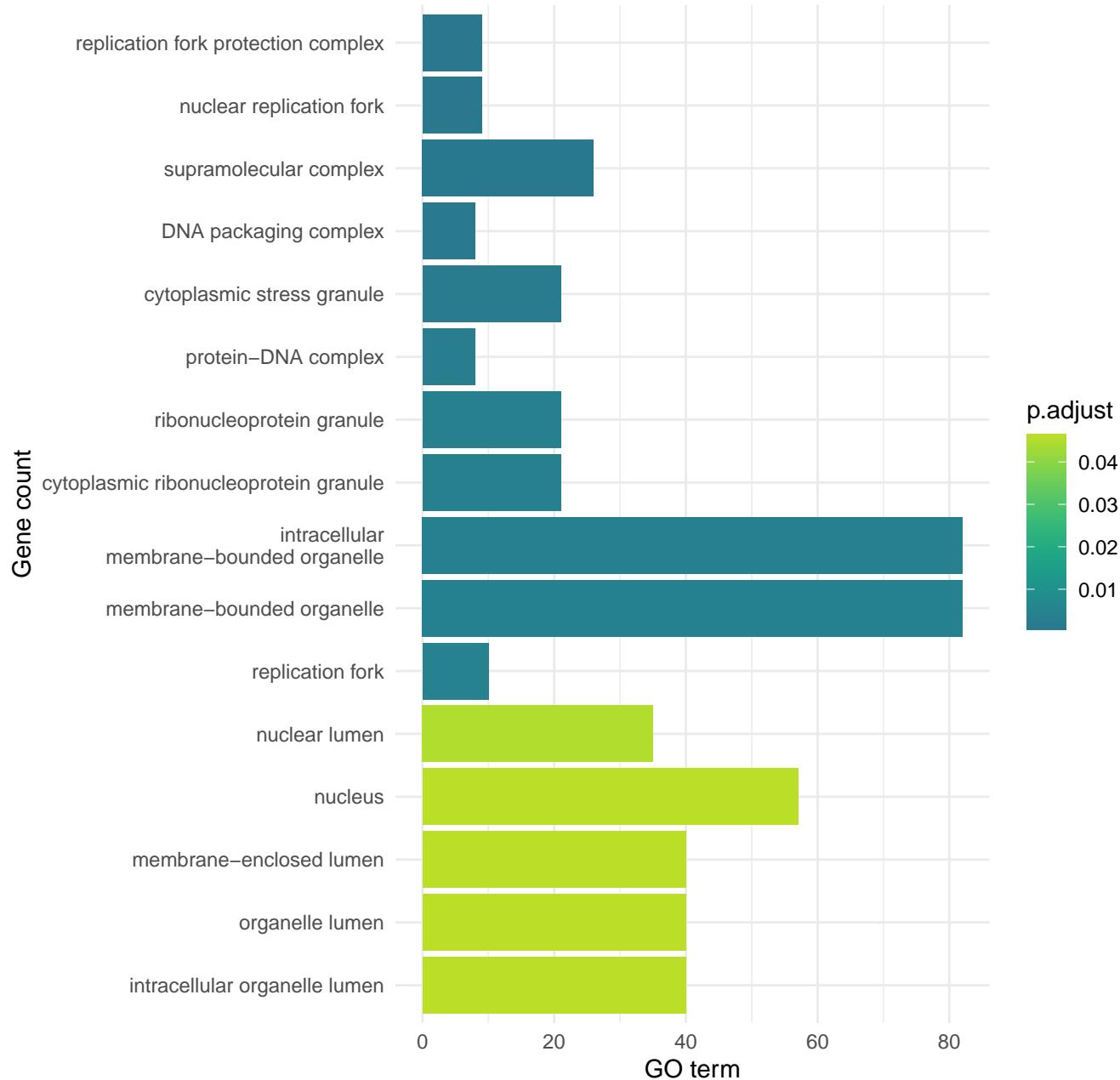




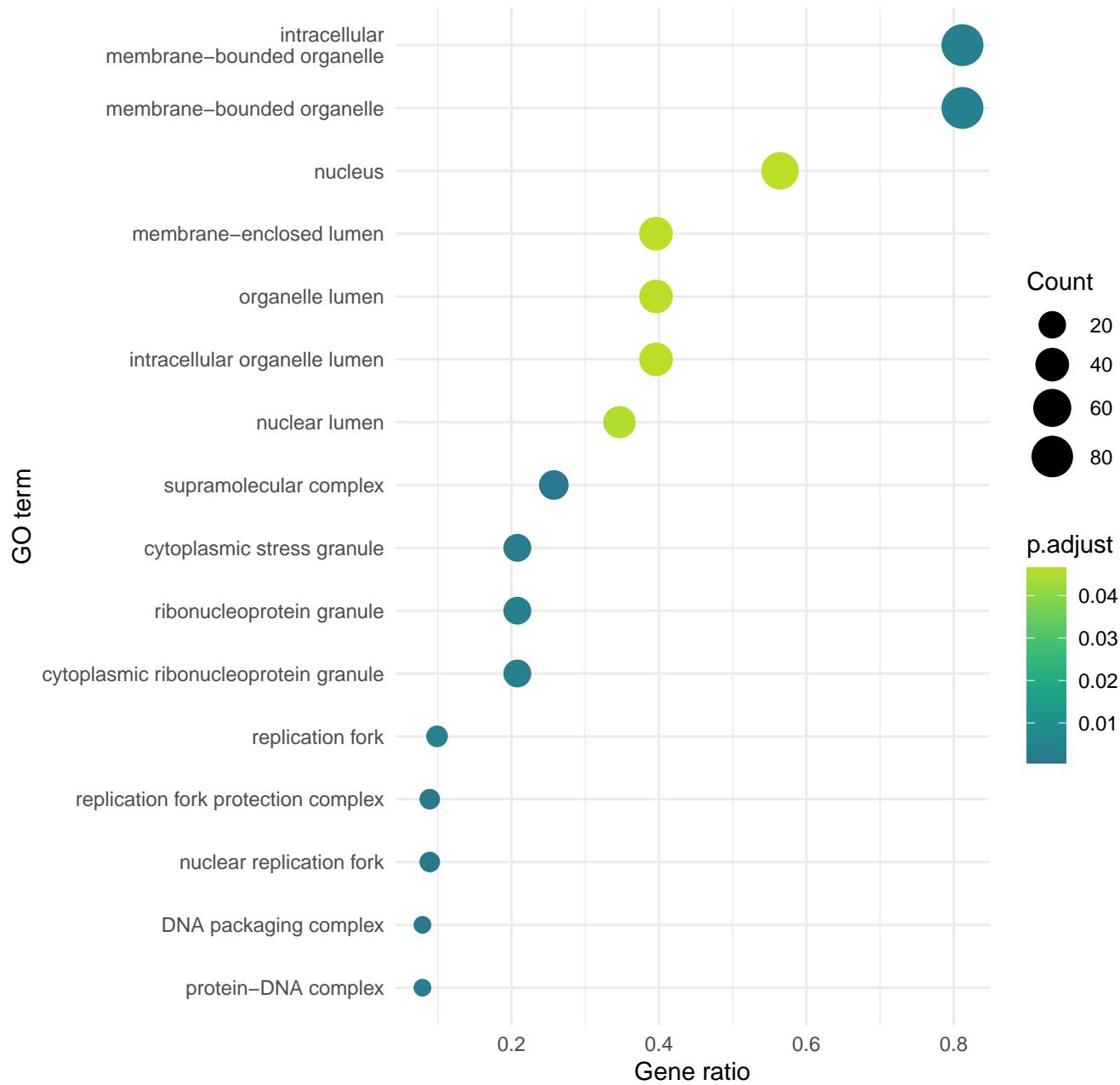
TIF4631–TAP Up-regulated GO BP upse



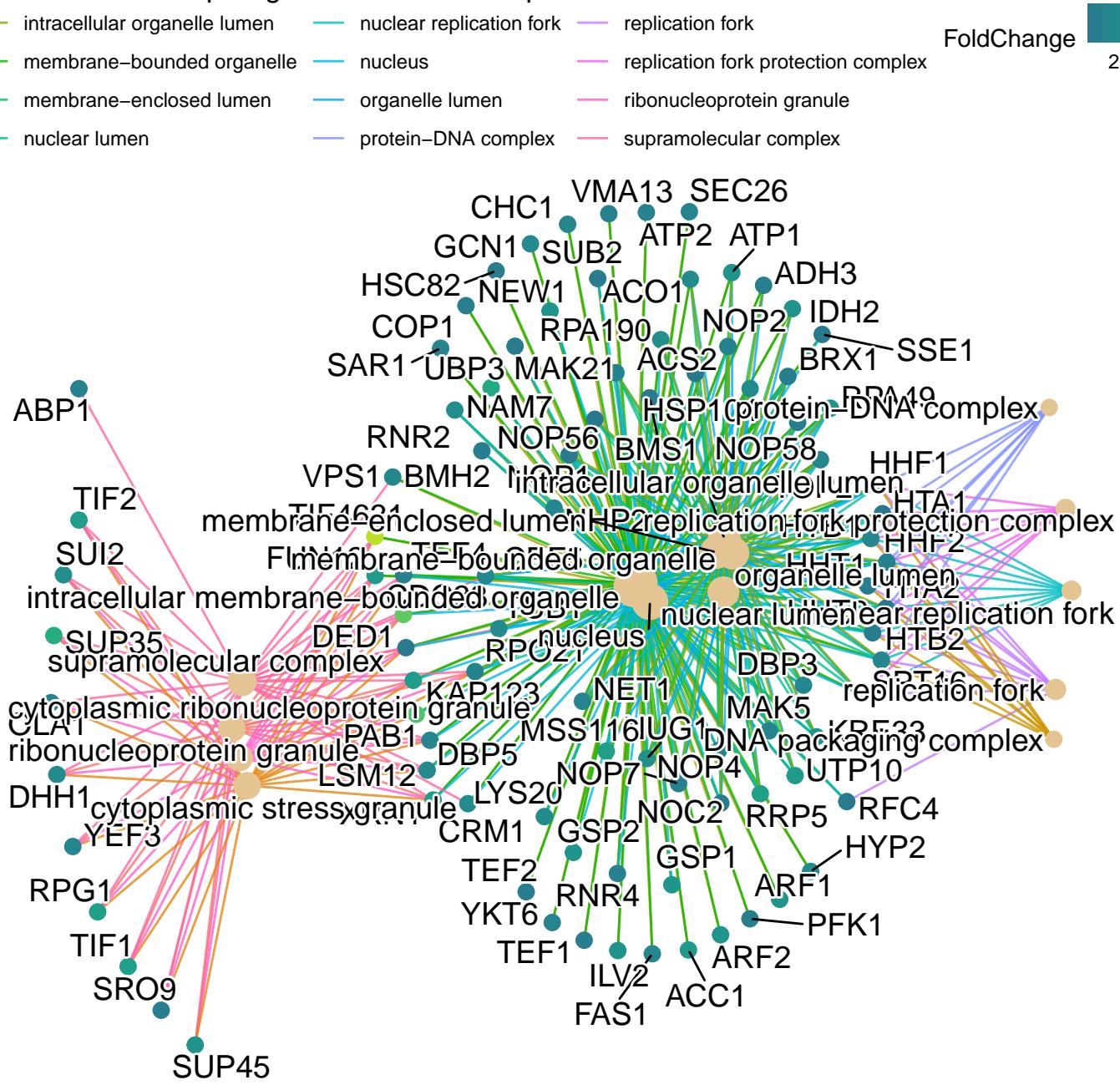
TIF4631-TAP Up-regulated GO CC barplot



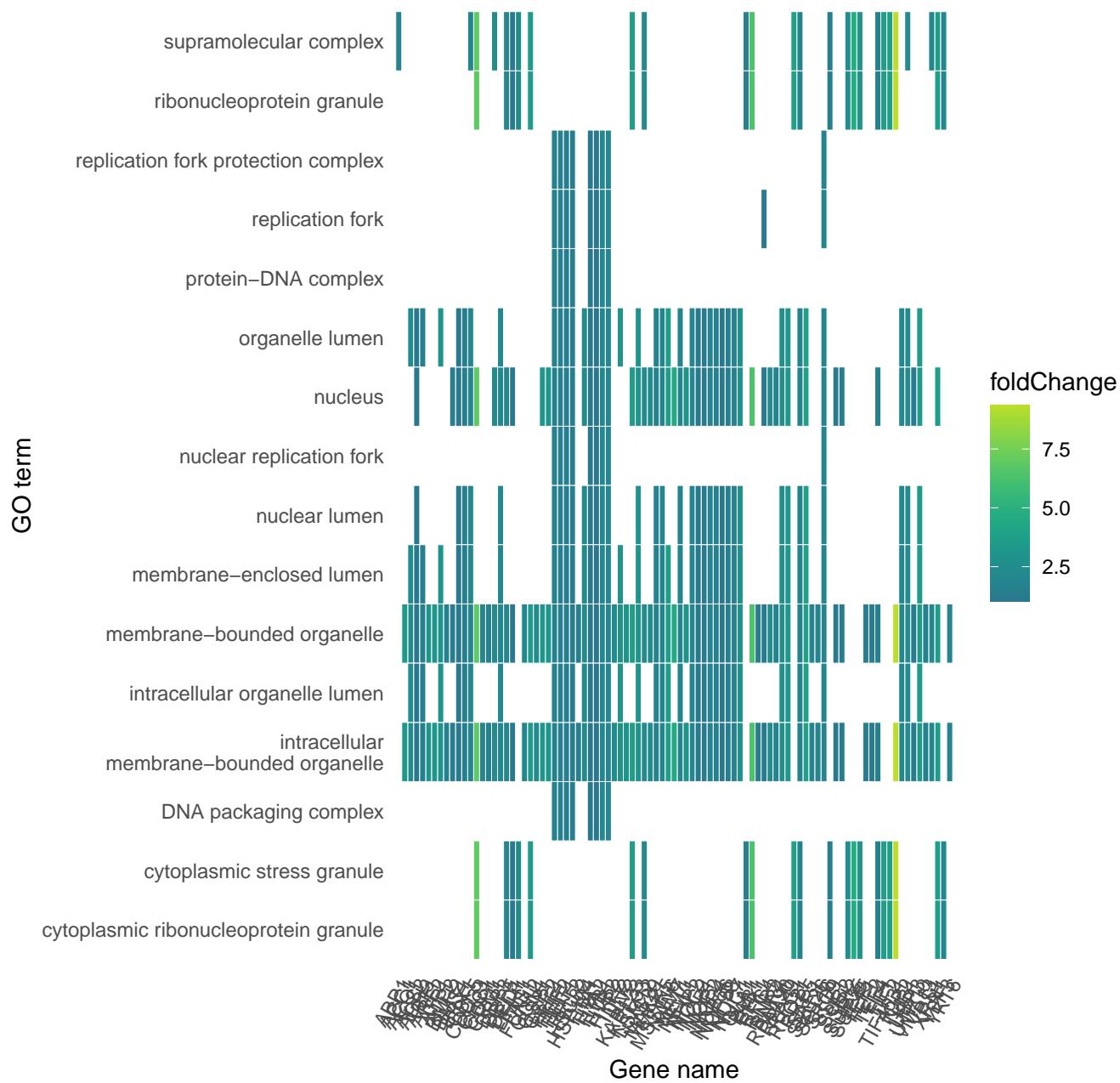
TIF4631-TAP Up-regulated GO CC dotplot



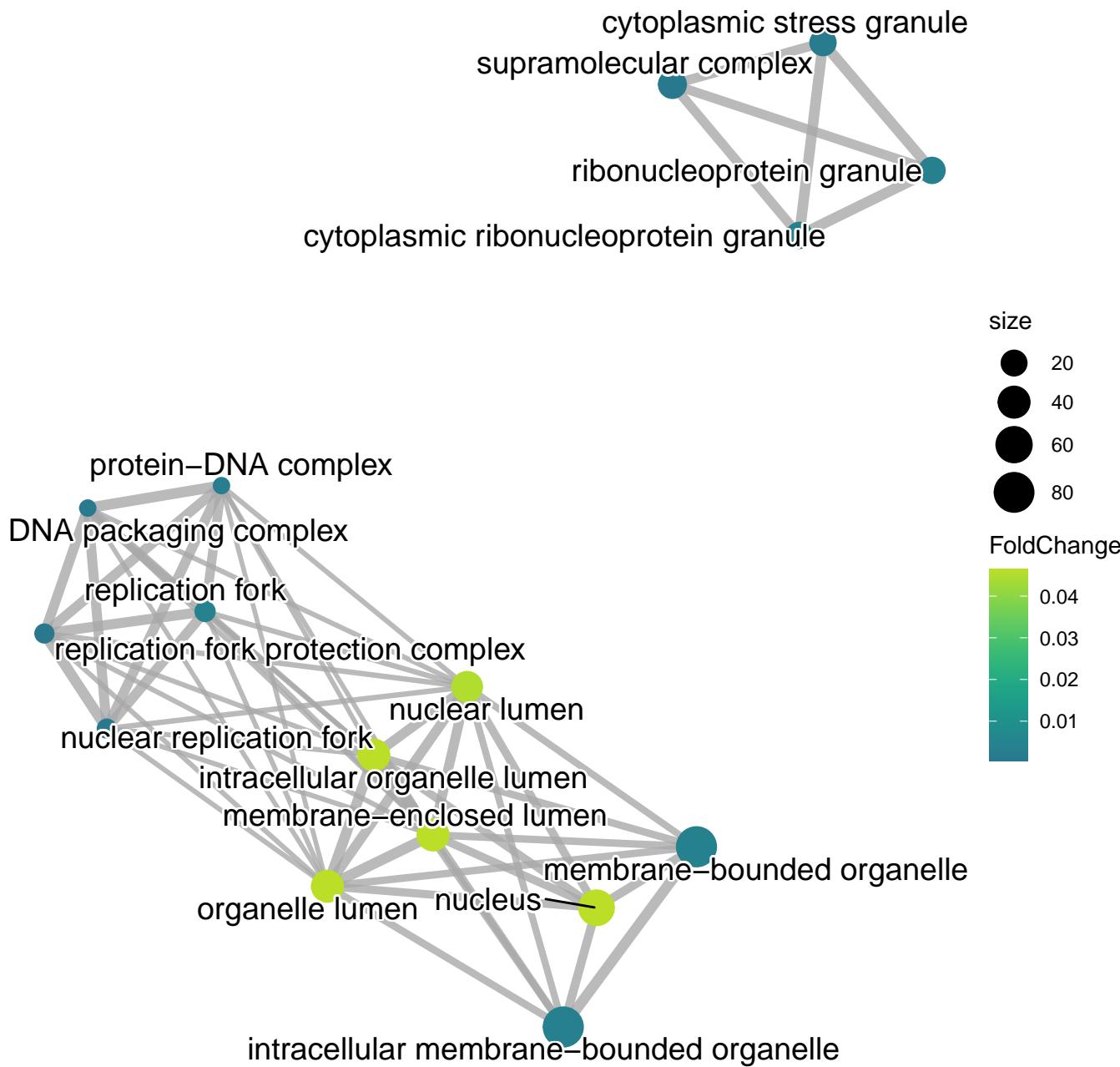
TIF4631-TAP Up-regulated GO CC cnetplot

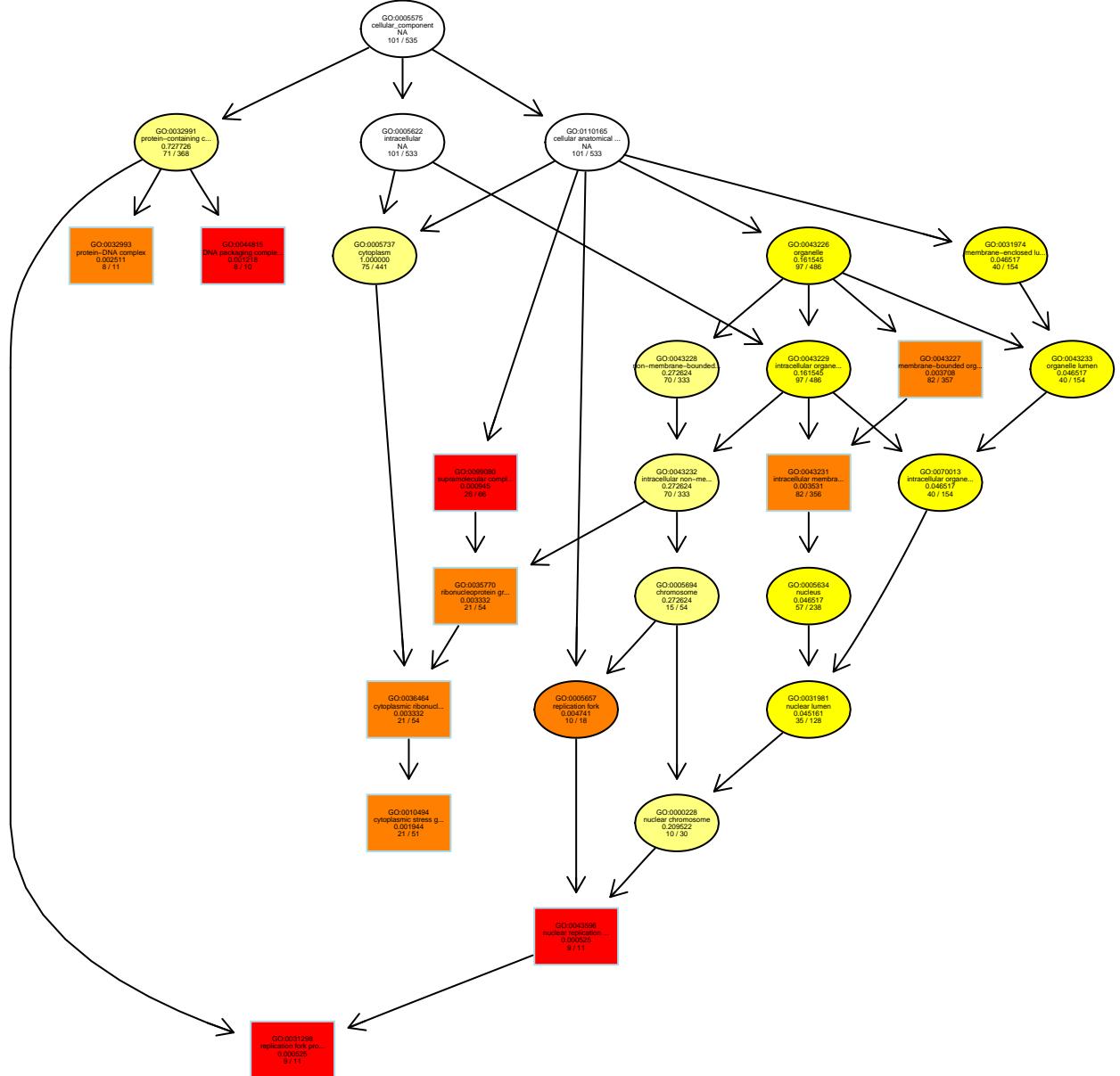


TIF4631-TAP Up-regulated GO CC heatplot

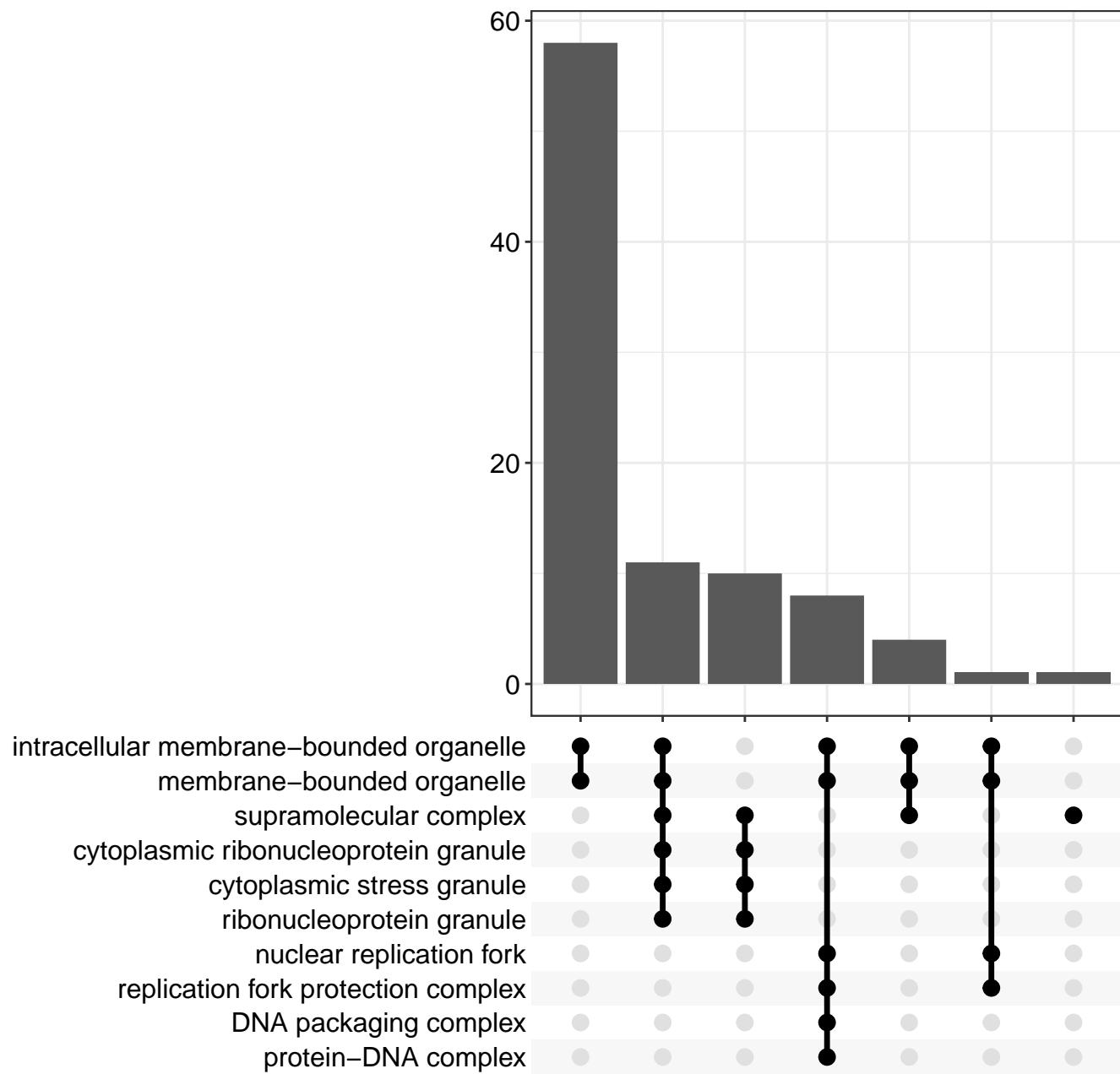


TIF4631-TAP Up-regulated GO CC emapplot

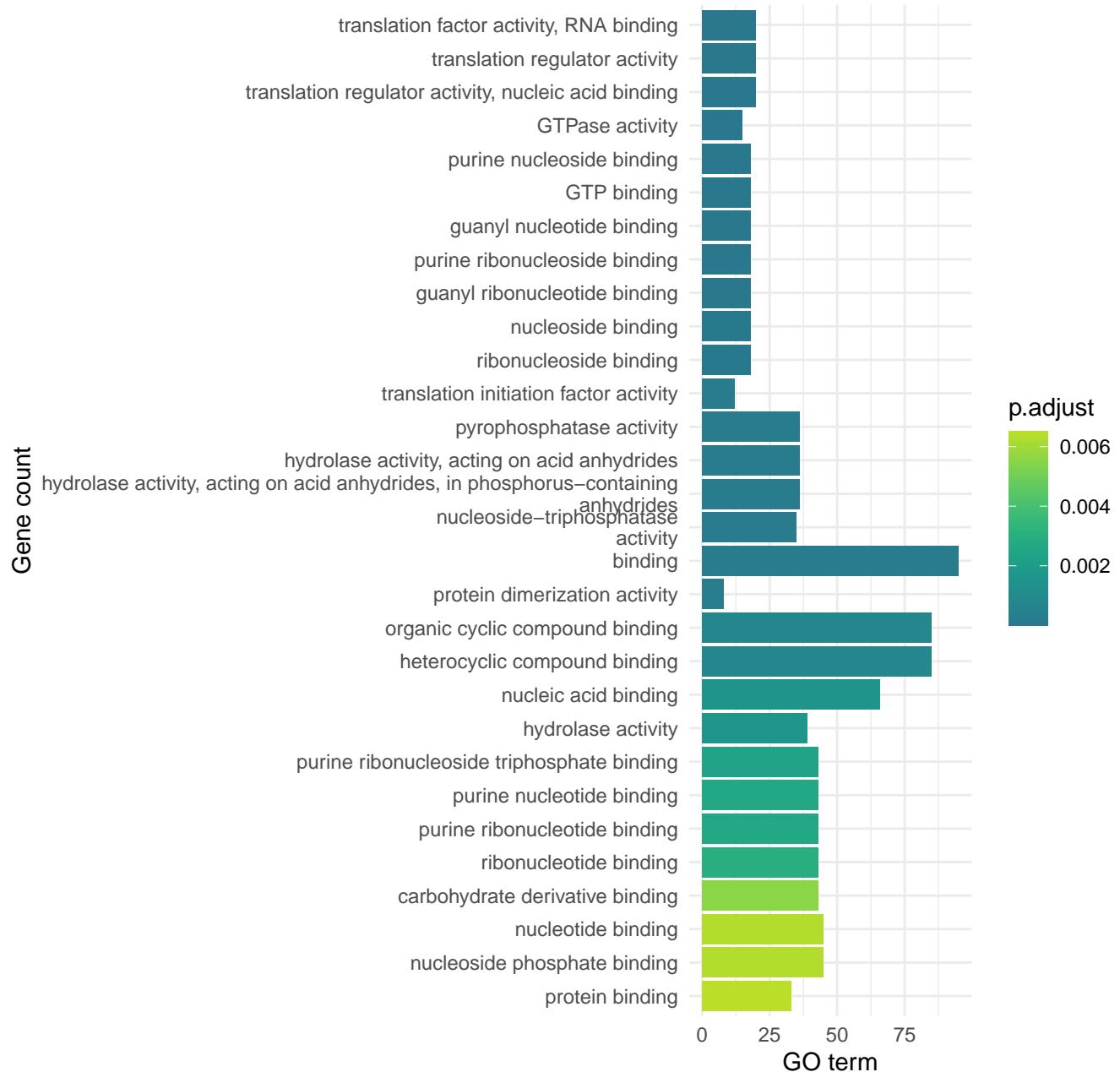




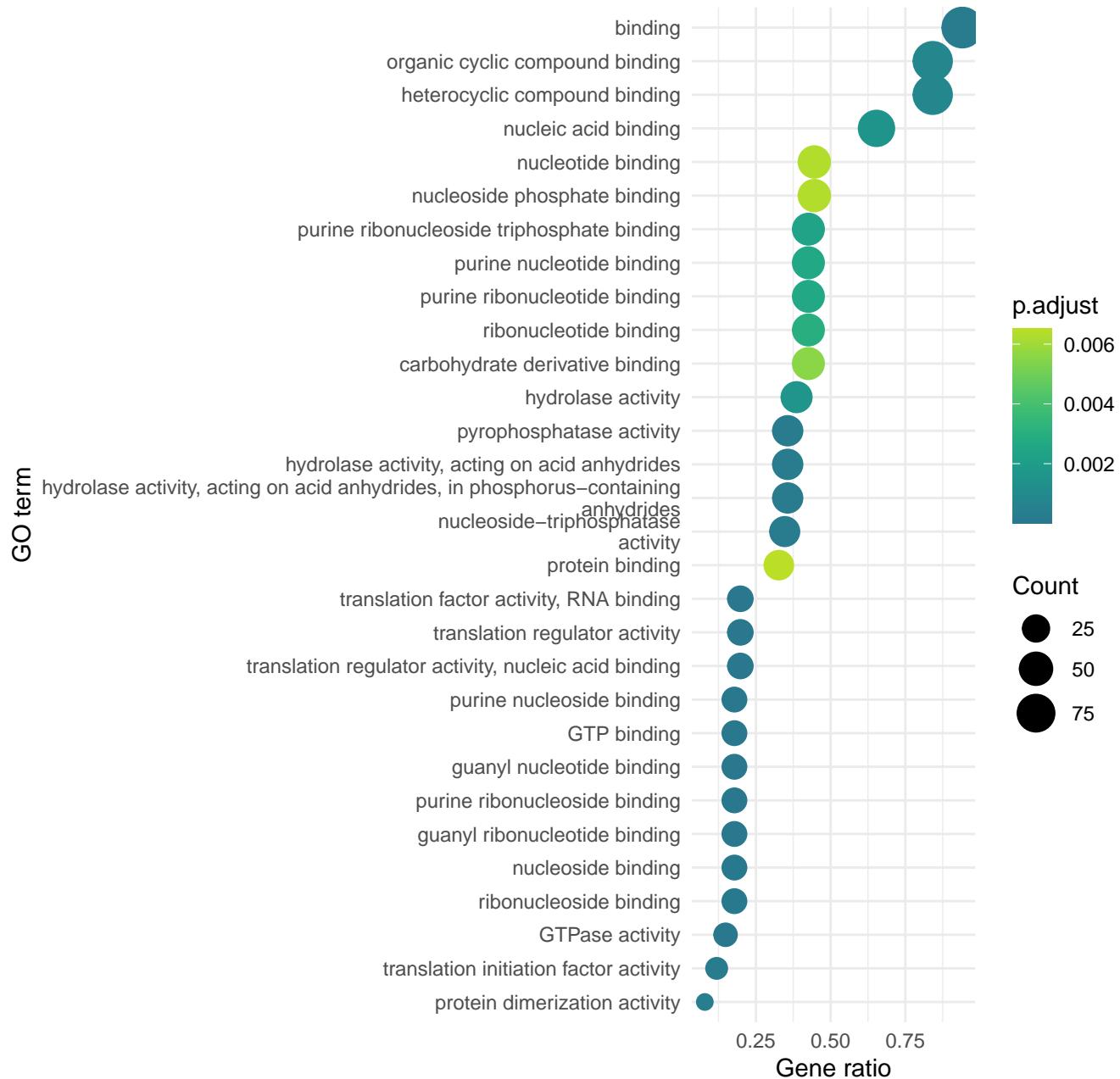
TIF4631-TAP Up-regulated GO CC upsetplot



TIF4631-TAP Up-regulated GO M

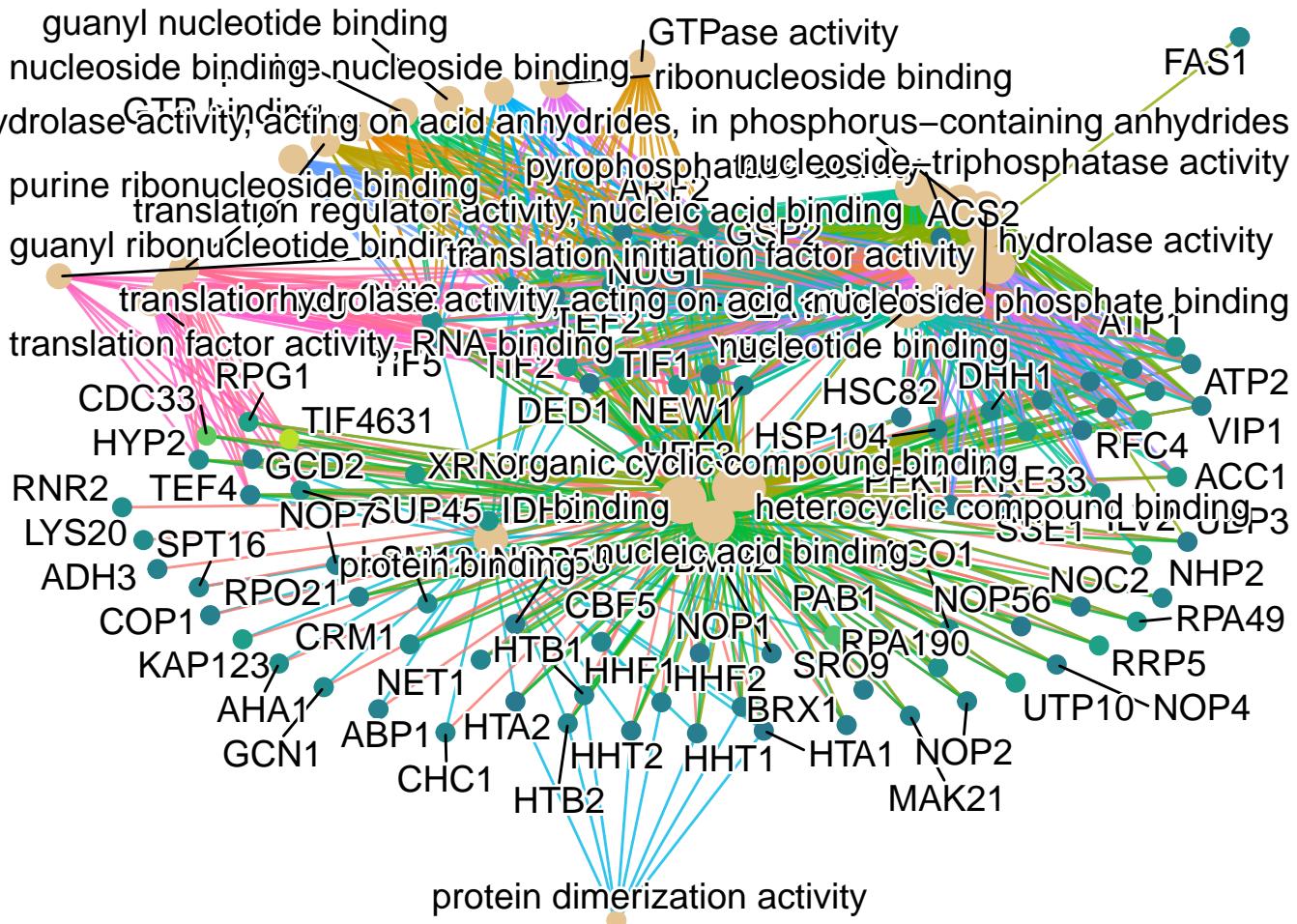


TIF4631-TAP Up-regulated GO M

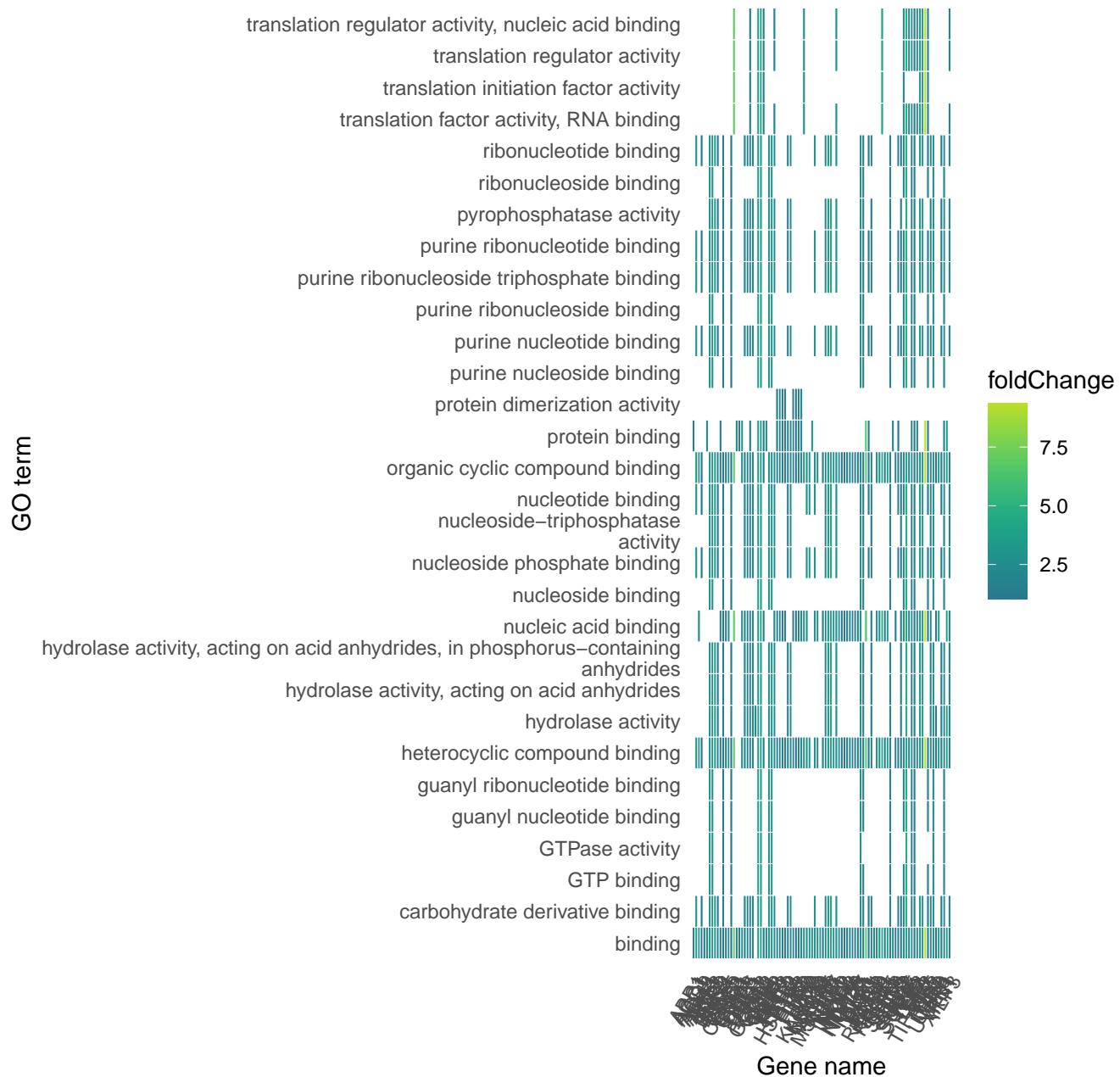


TIF4631-TAP Up-regulated GO MF cnetplot

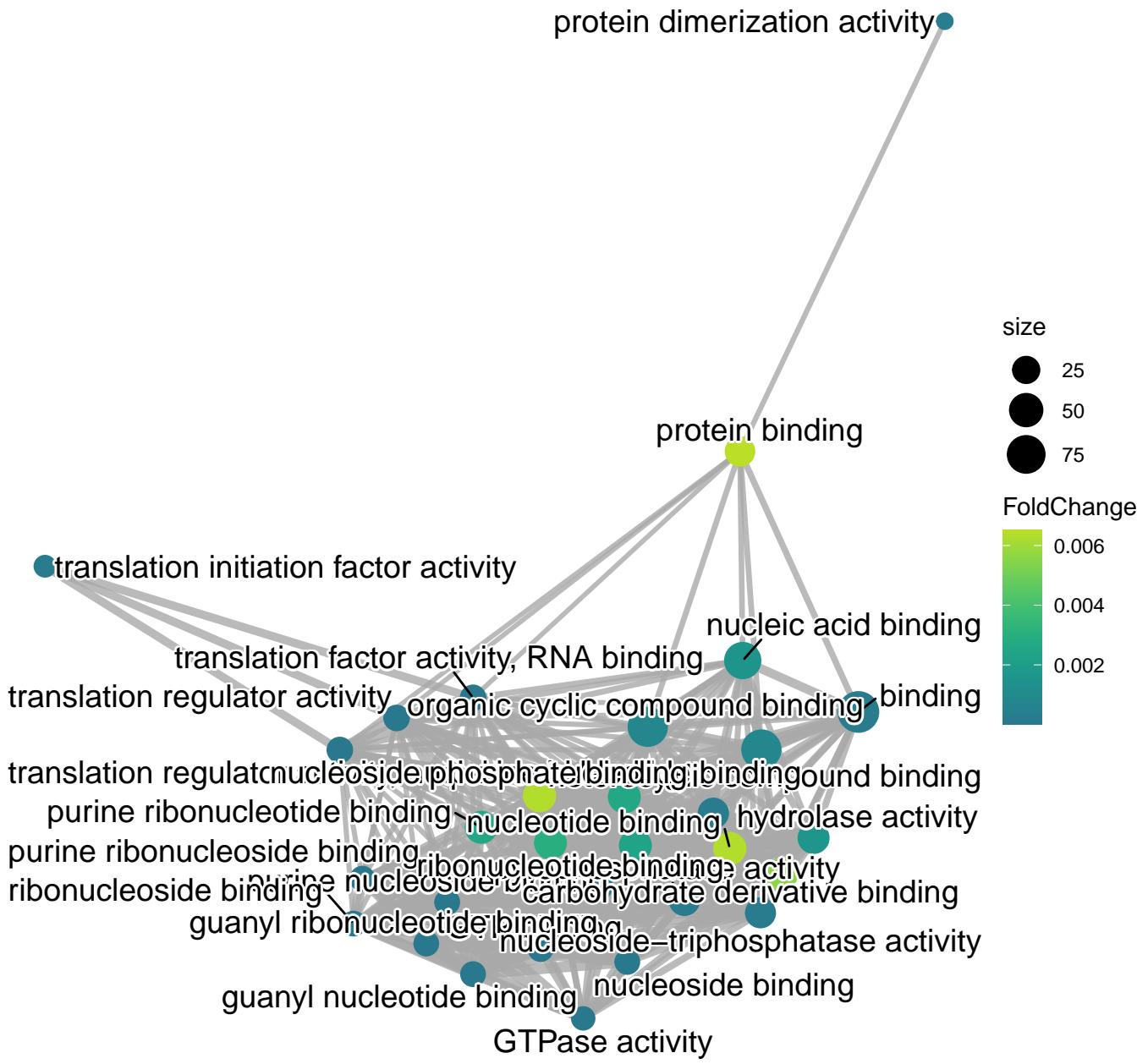
- | | | |
|---------|--|-------------------------------|
| binding | heterocyclic compound binding | nucleoside phosphate |
| | hydrolase activity | nucleoside-triphosphate |
| | hydrolase activity, acting on acid anhydrides | nucleotide binding |
| | hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | organic cyclic compound |
| ing | nucleic acid binding | protein binding |
| inding | nucleoside binding | protein dimerization activity |

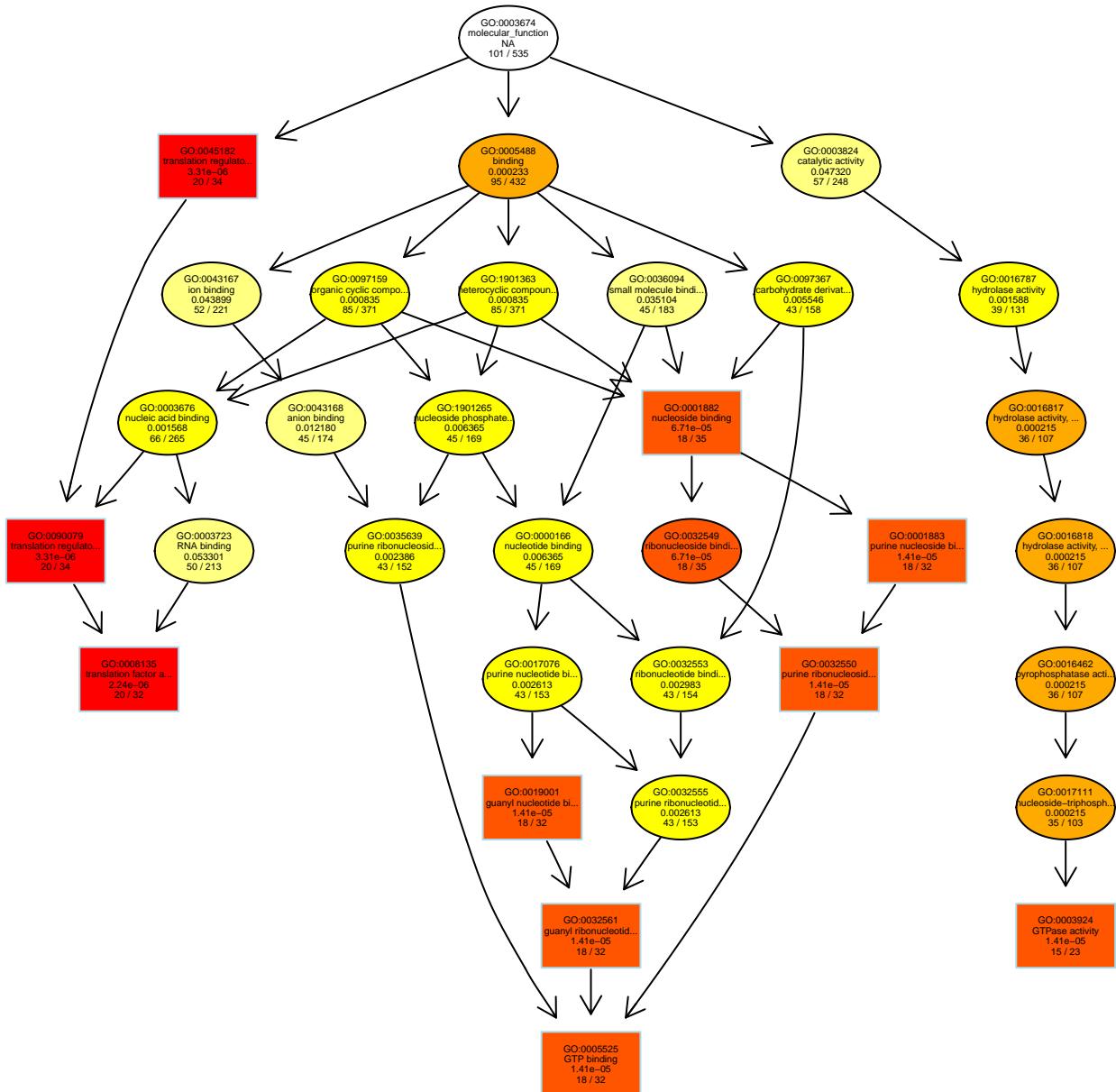


TIF4631-TAP Up-regulated GO M

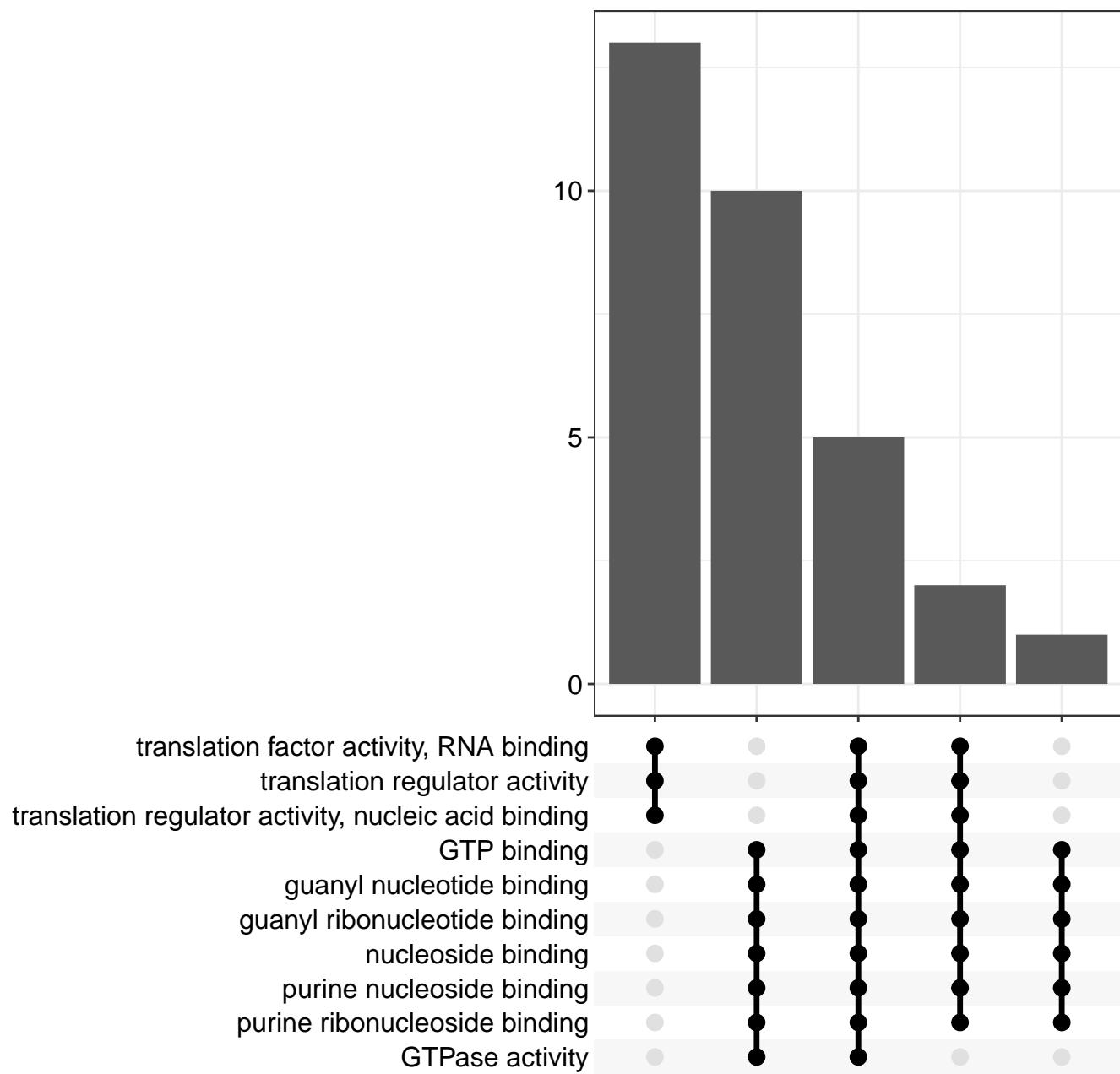


TIF4631-TAP Up-regulated GO MF emapplot

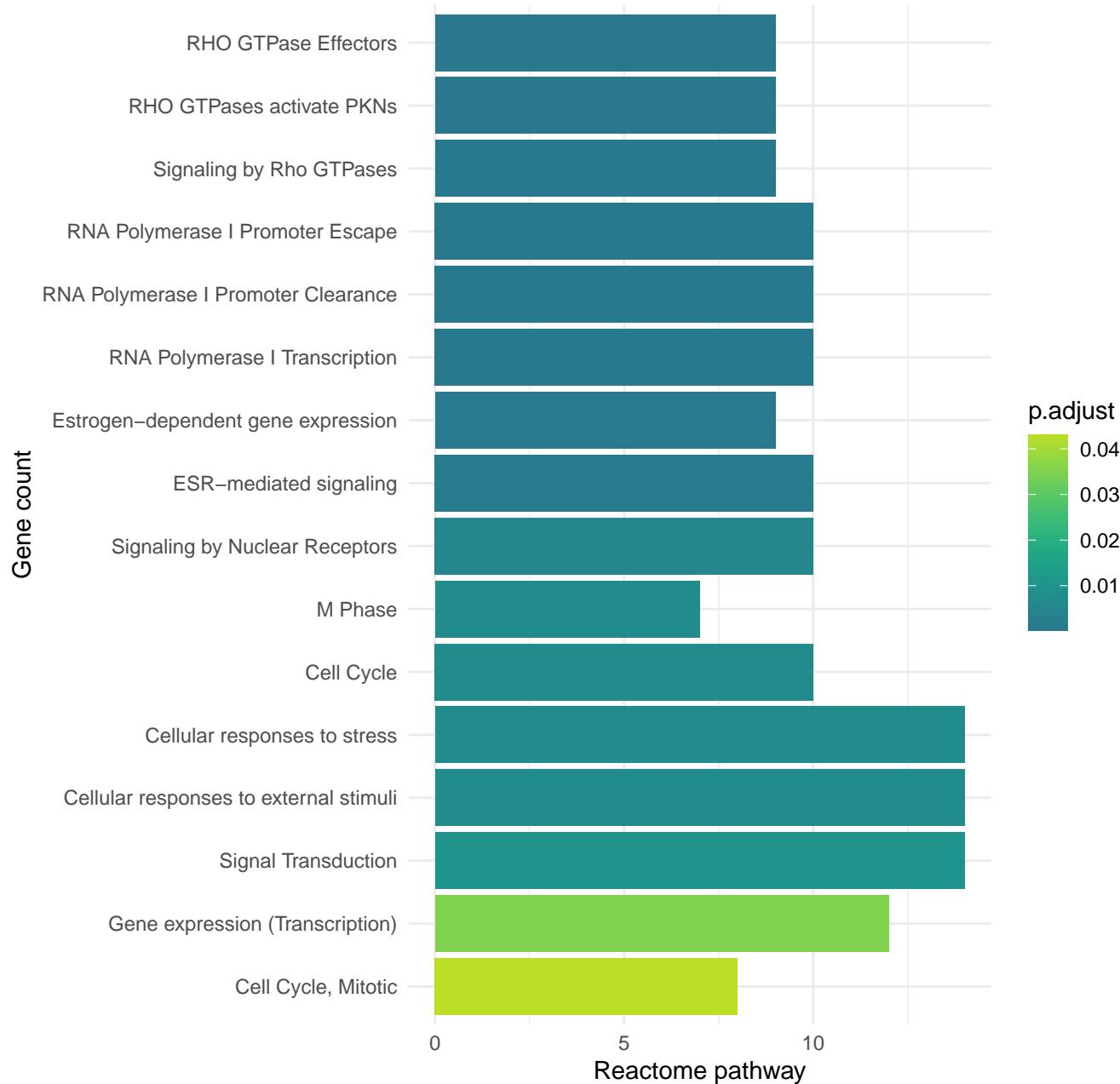




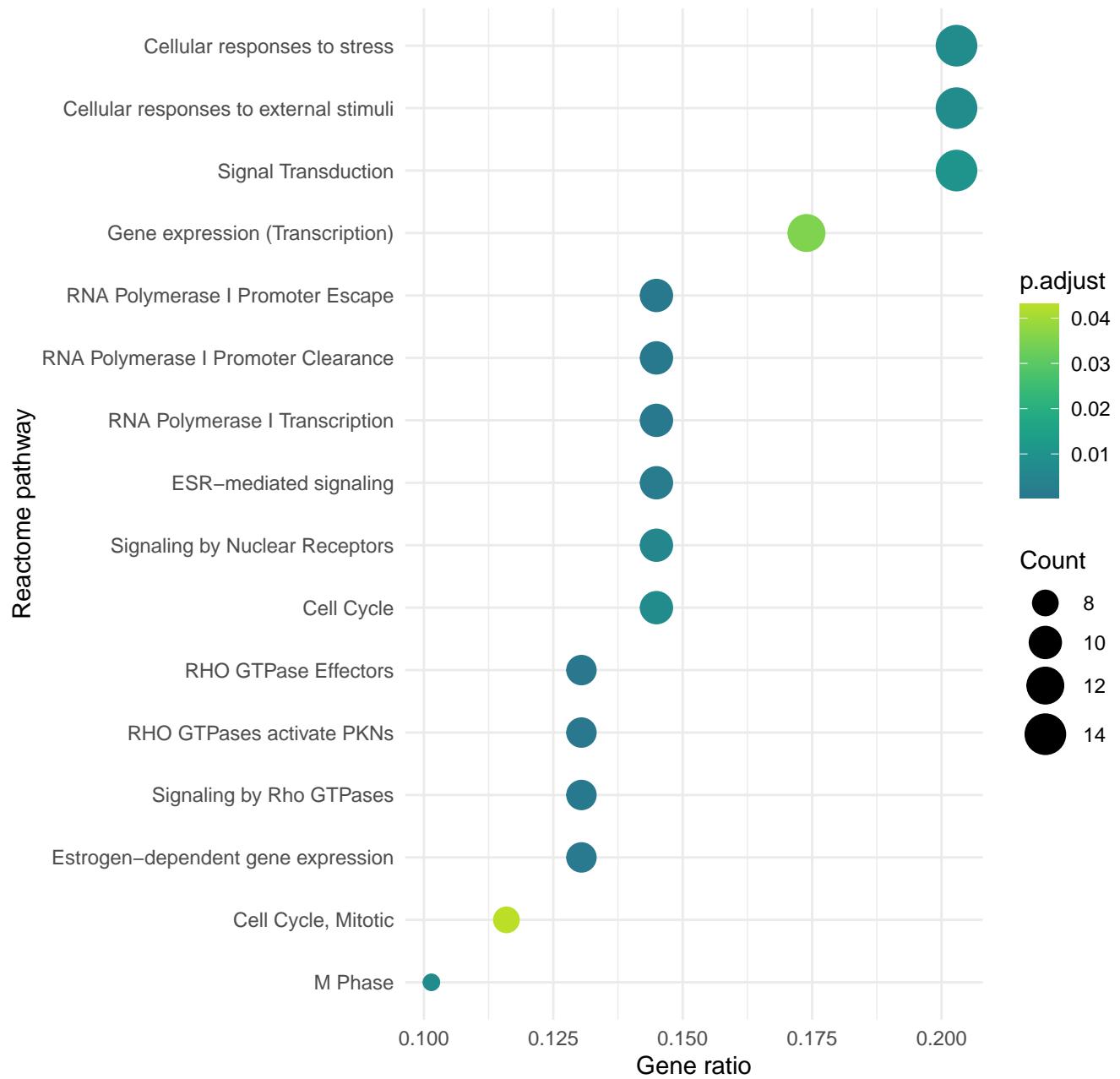
TIF4631-TAP Up-regulated GO MF upse



TIF4631-TAP Up-regulated Reactome barplot

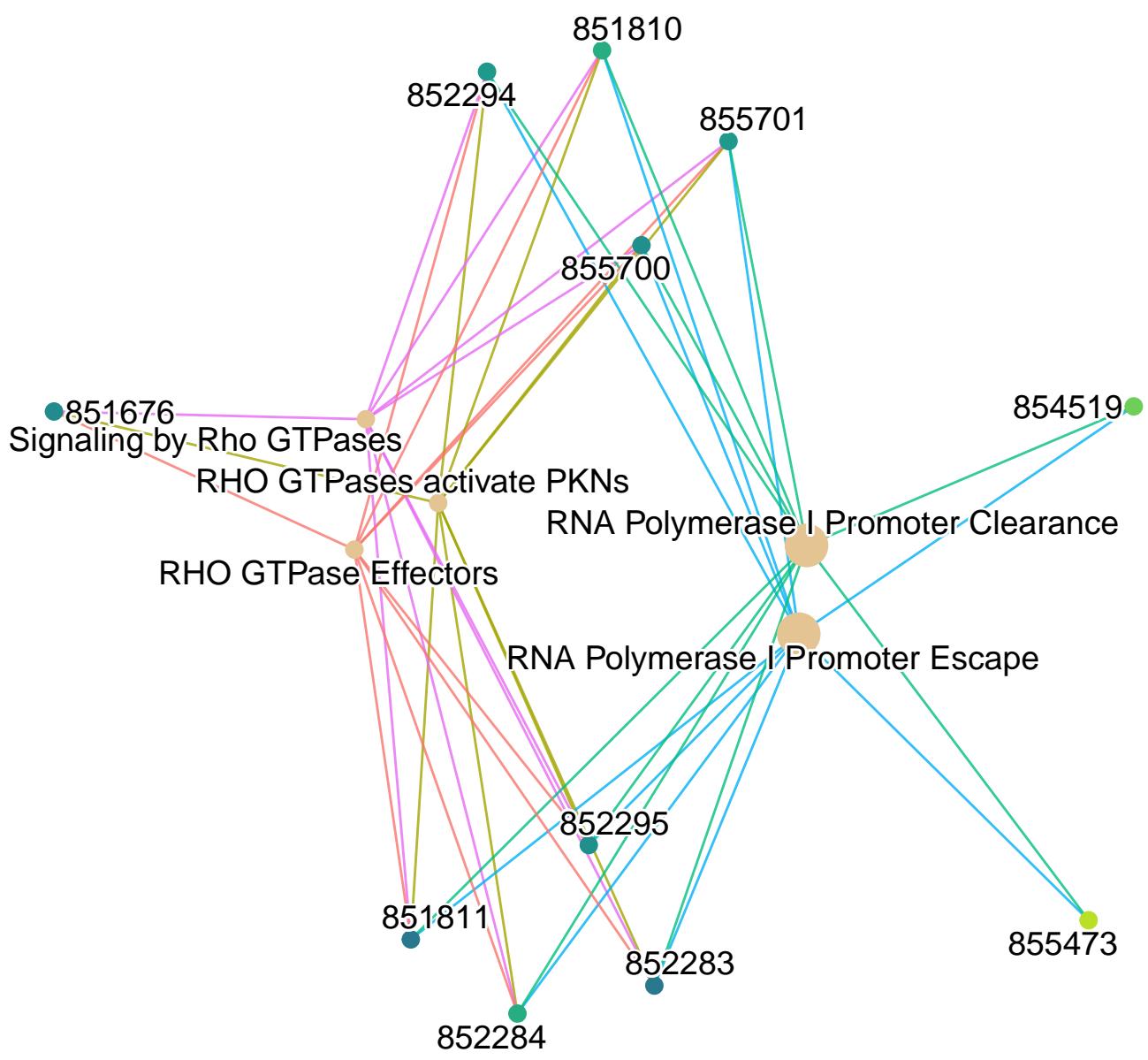


TIF4631-TAP Up-regulated Reactome dotplot

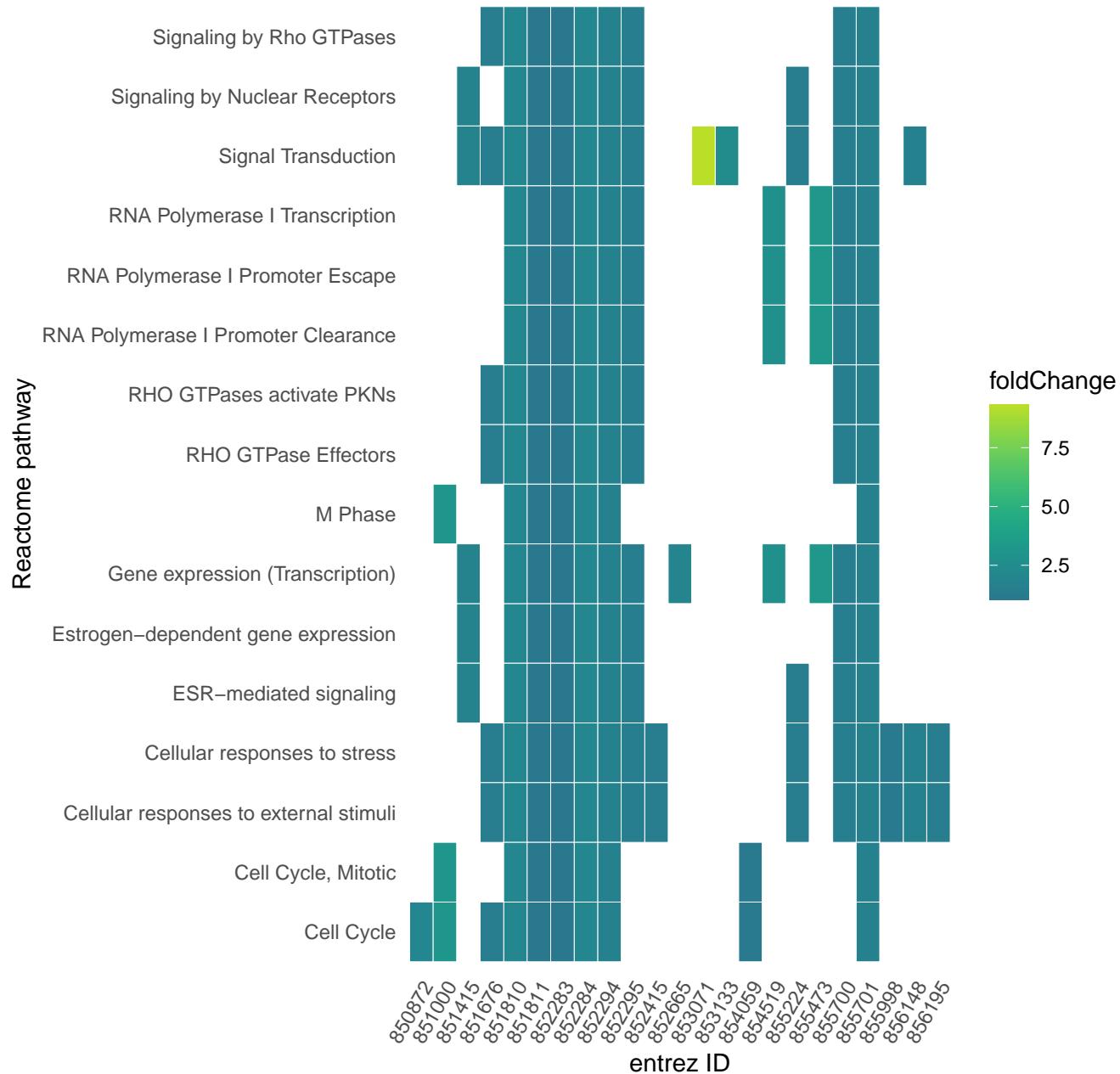


TIF4631-TAP Up-regulated Reactome cnetplot

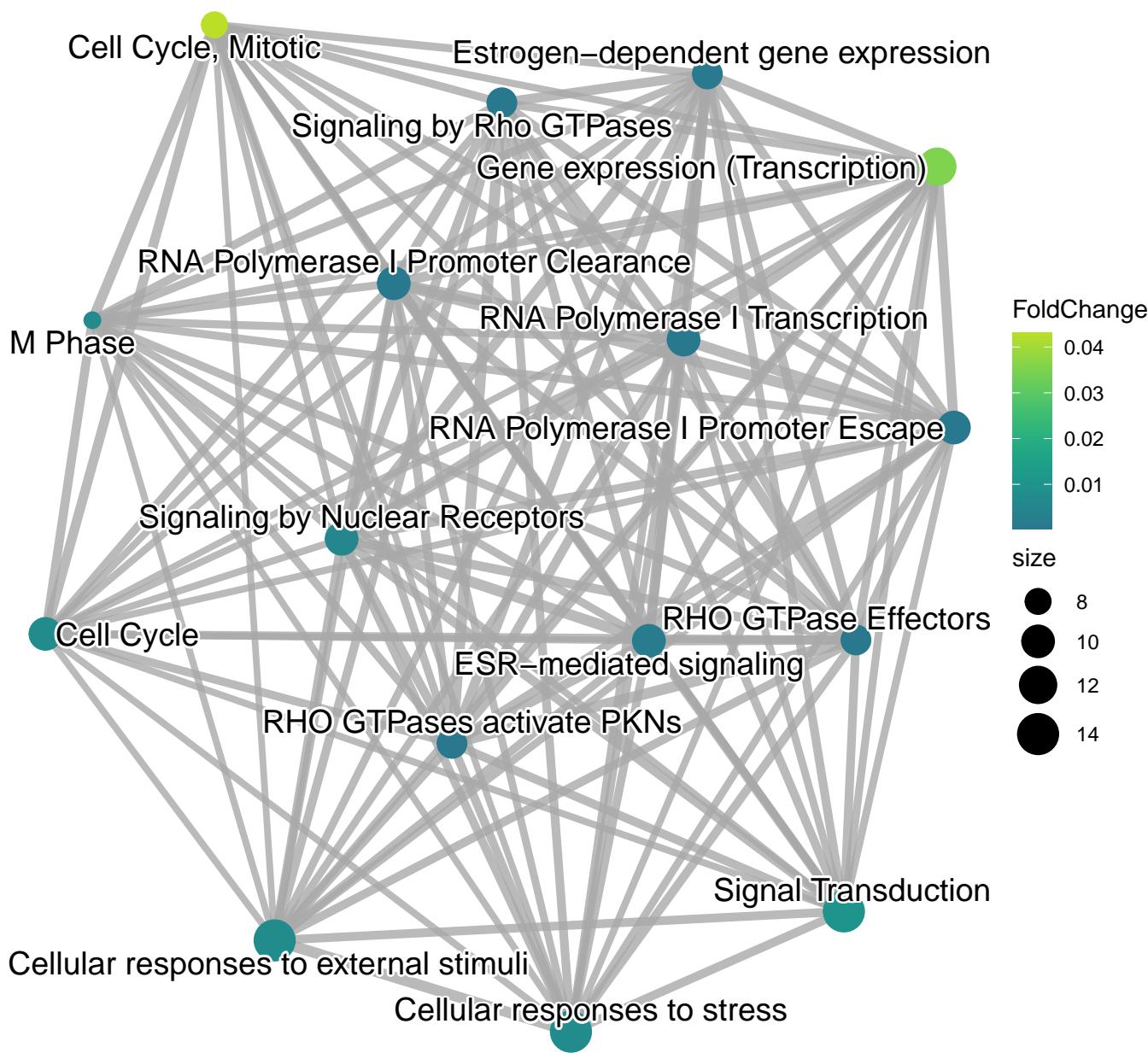
GTPase Effectors — RHO GTPases activate PKNs — RNA Polymerase I Promoter Clearance — RNA Polymerase I



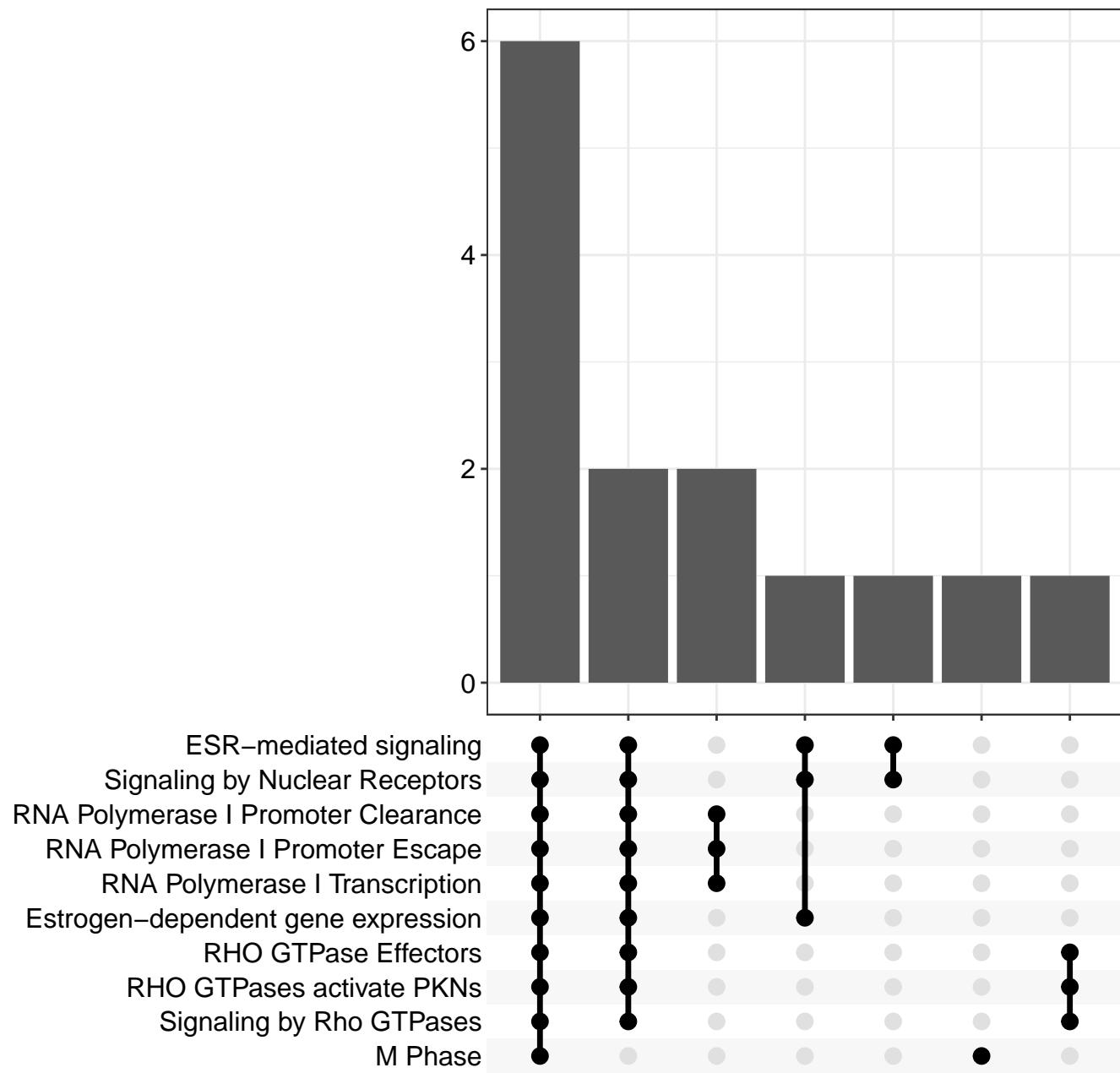
TIF4631-TAP Up-regulated Reactome heatplot



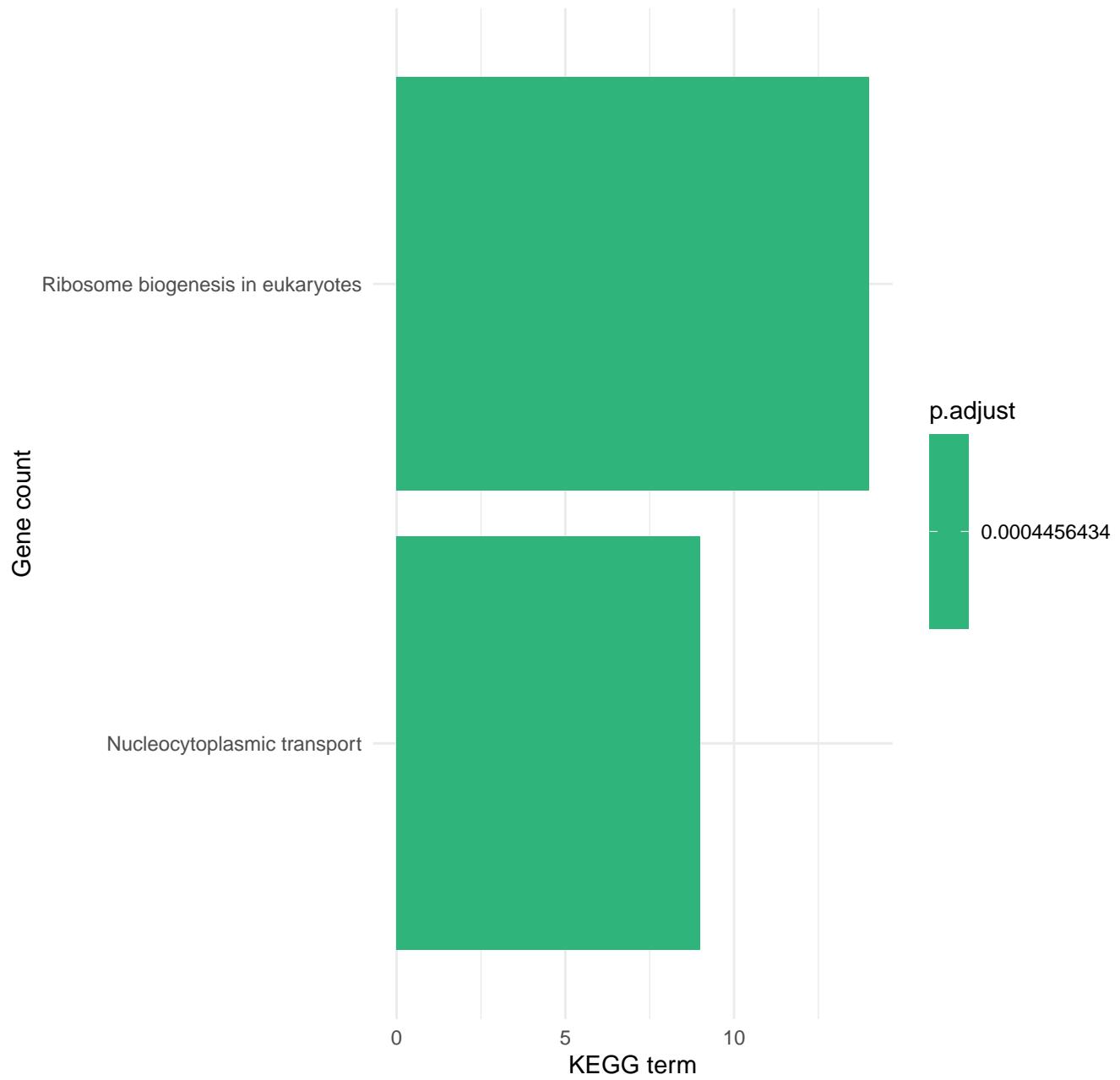
TIF4631-TAP Up-regulated Reactome emapplot



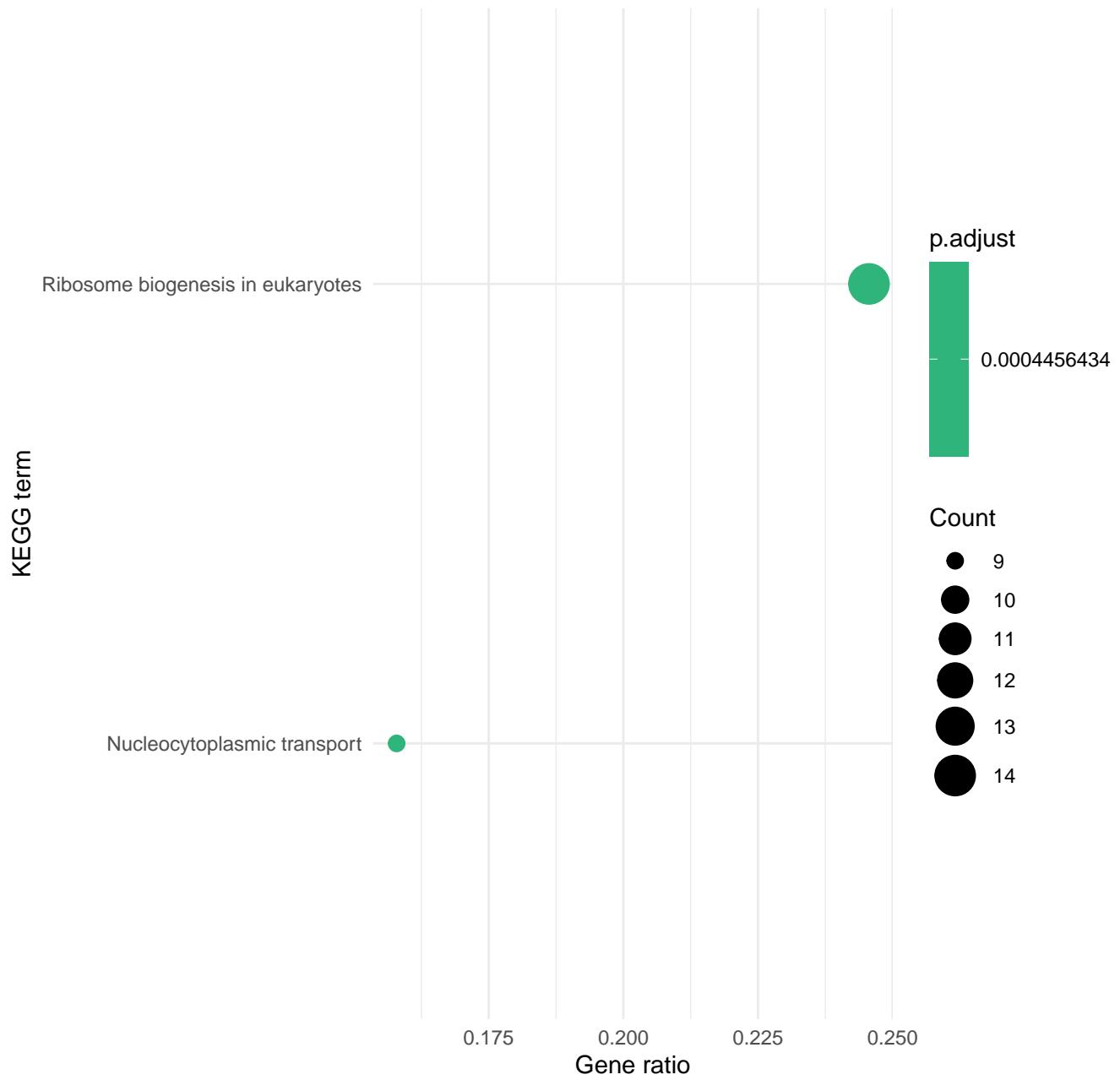
TIF4631-TAP Up-regulated Reactome upsetplot



TIF4631-TAP Up-regulated KEGG barplot

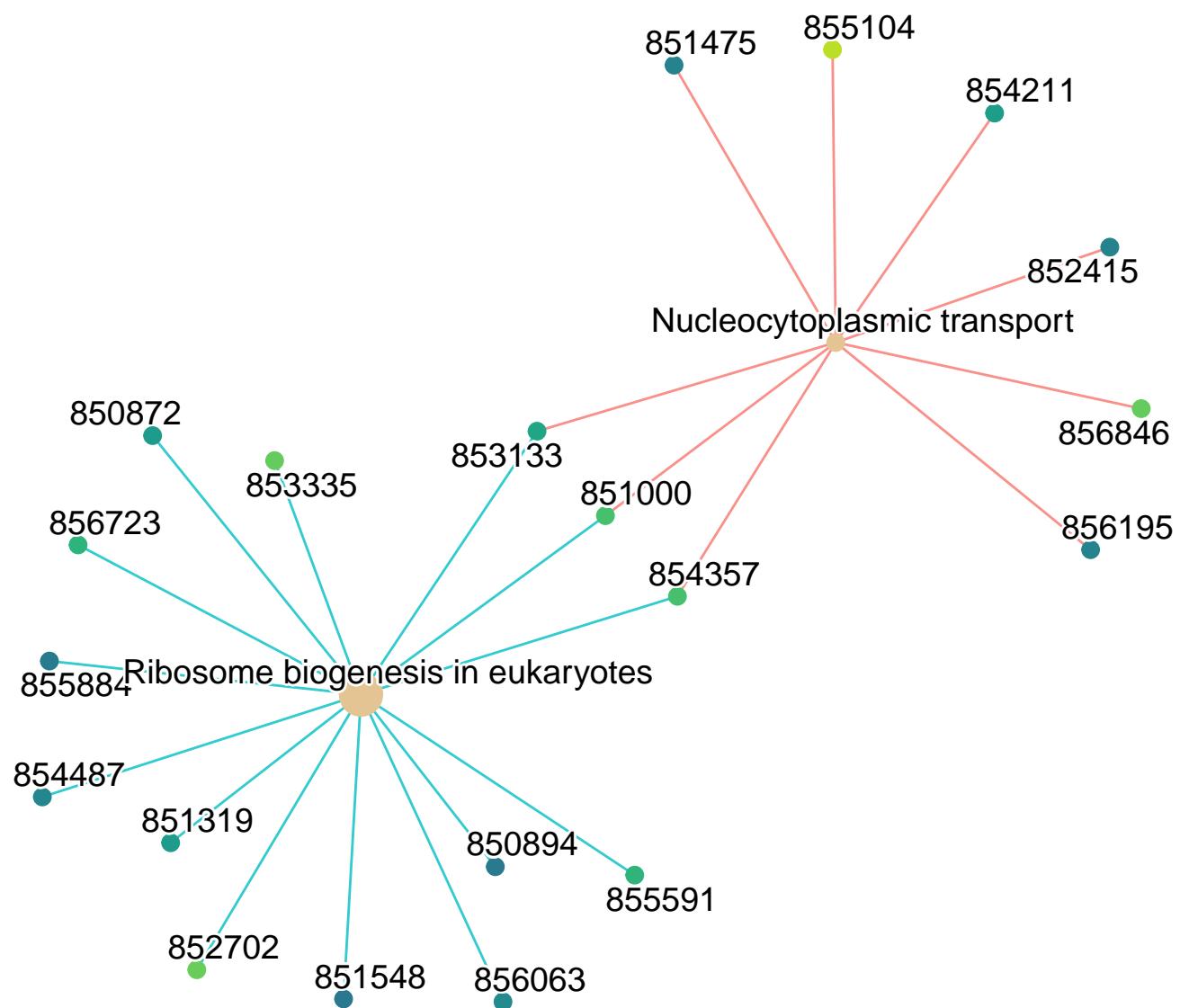


TIF4631–TAP Up-regulated KEGG dotplot

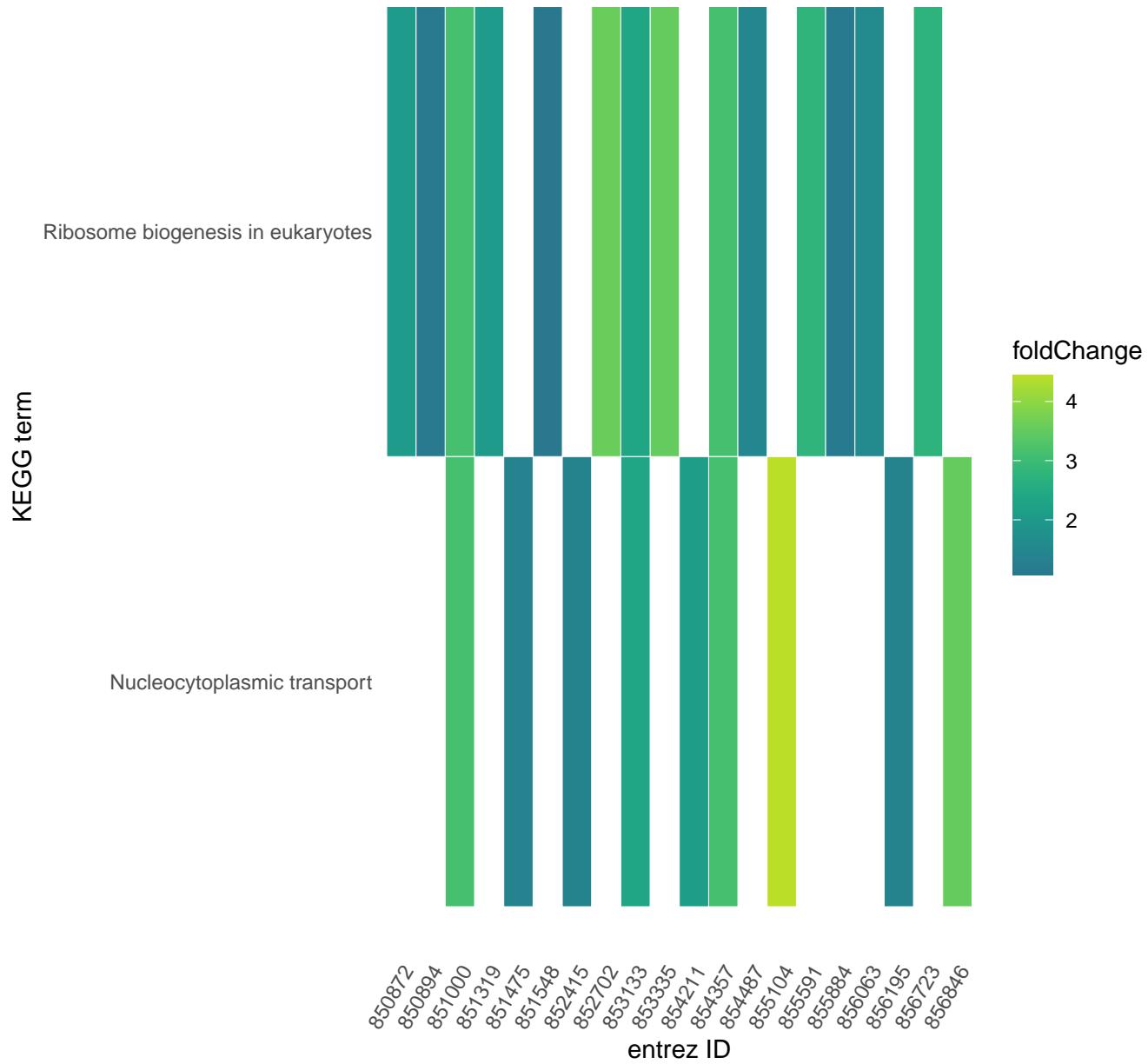


TIF4631-TAP Up-regulated KEGG dotplot

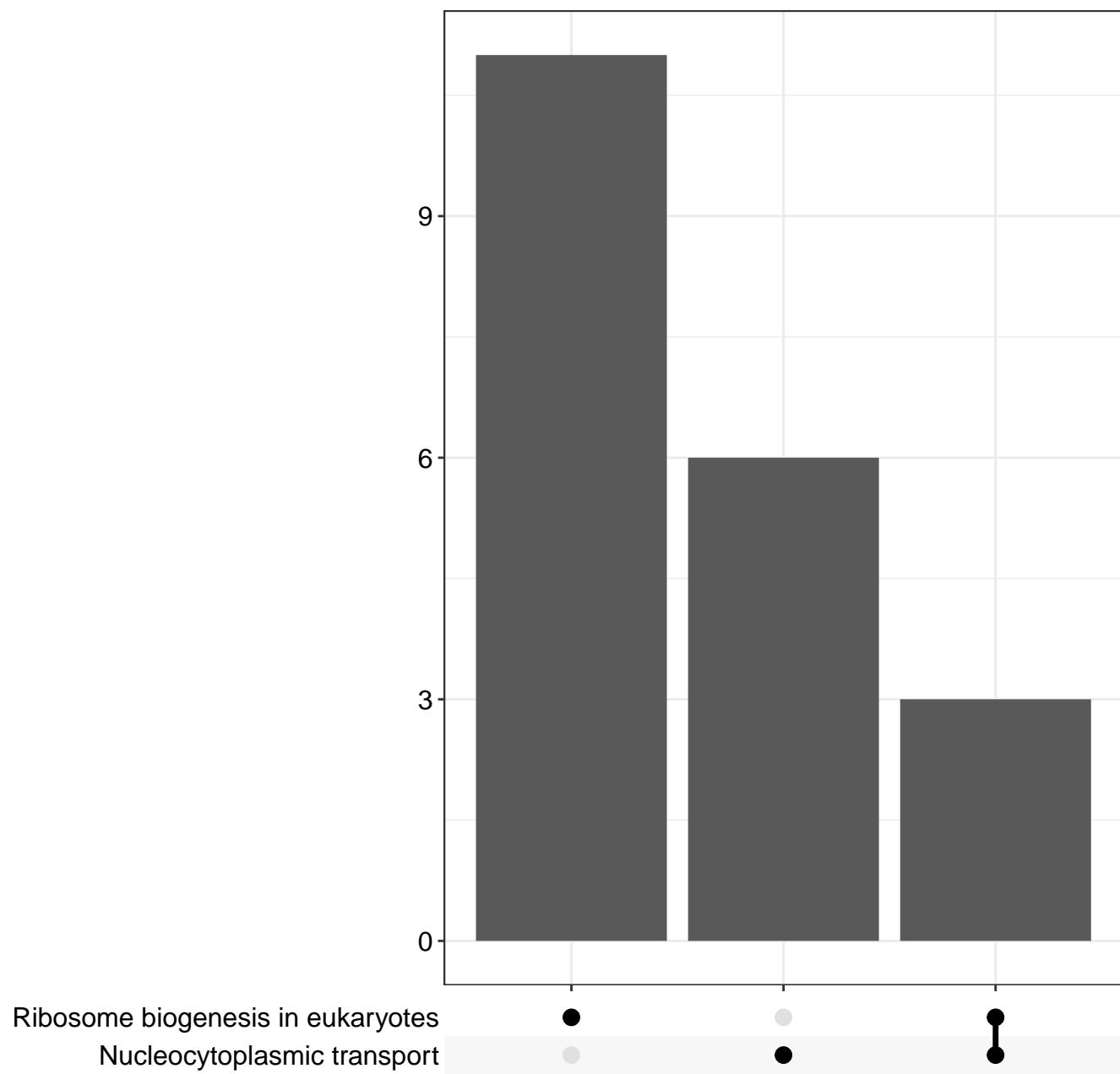
Nucleocytoplasmic transport — Ribosome biogenesis in eukaryotes



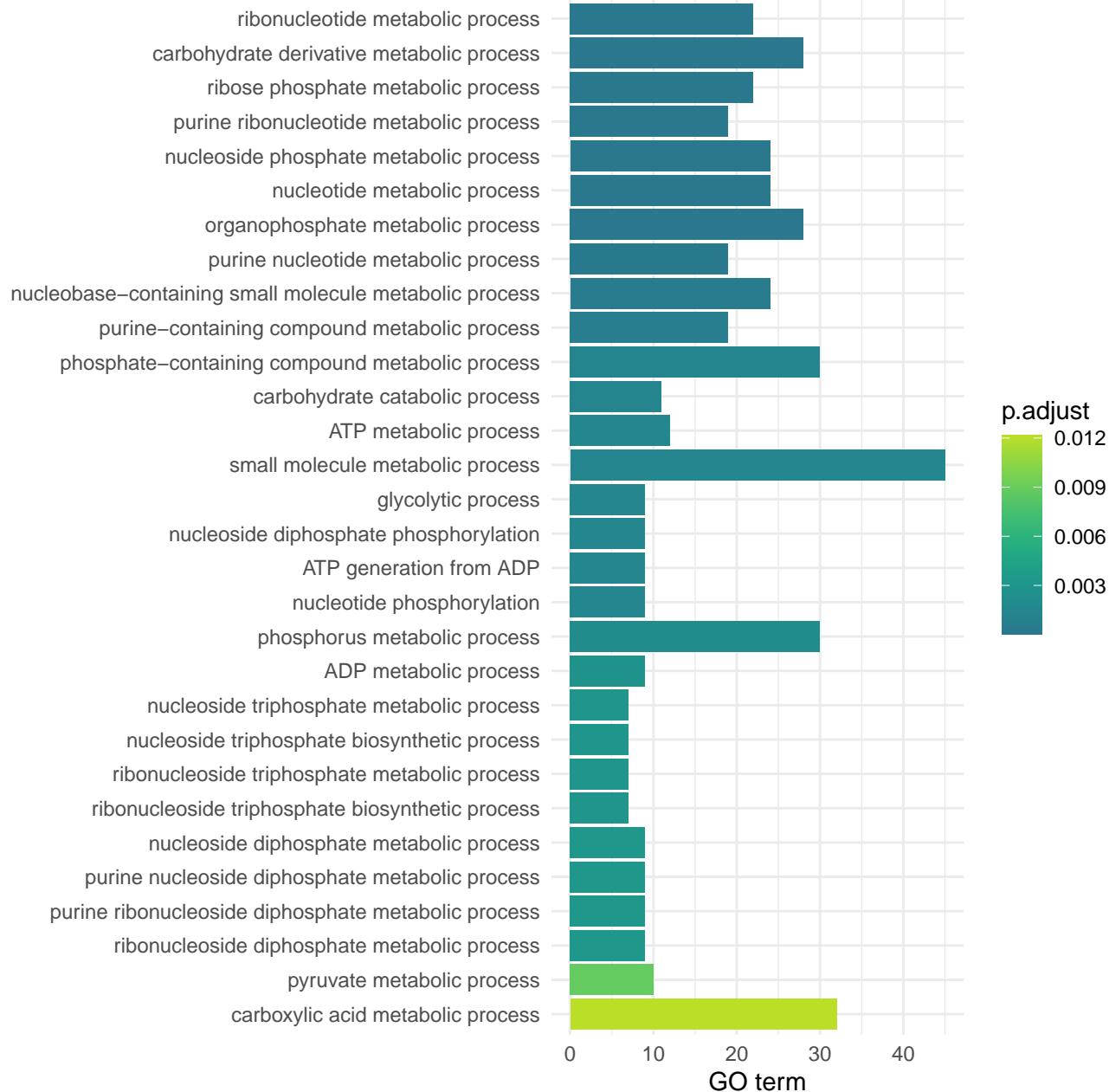
TIF4631-TAP Up-regulated KEGG heatplot



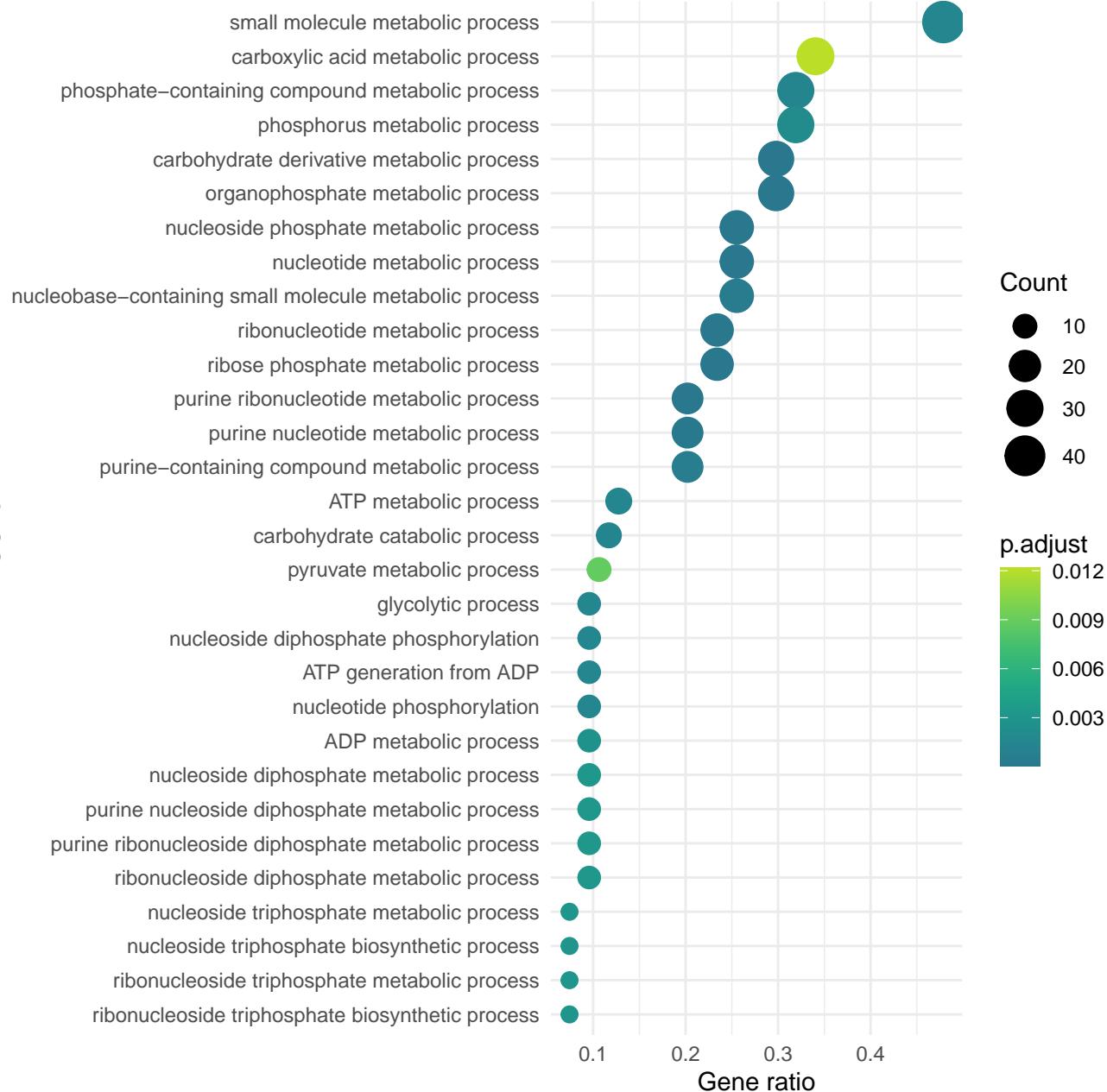
TIF4631-TAP Up-regulated KEGG upsetplot



NAM7-TAP Up-regulated GO BP barplot



NAM7-TAP Up-regulated GO BP dotplot



NAM7-TAP Up-regulated GO BP cnetplot

nucleoside triphosphate metabolic process

— purine nucleoside diphosphate metabolic process

- ribonu

nucleotide metabolic process

— purine nucleotide metabolic process

- ribonu

nucleotide phosphorylation

— purine ribonucleoside diphosphate metabolic process

- ribonu

organophosphate metabolic process

Purine ribonucleotide metabolic process

- ribonu

phosphate-containing compound metabolic process

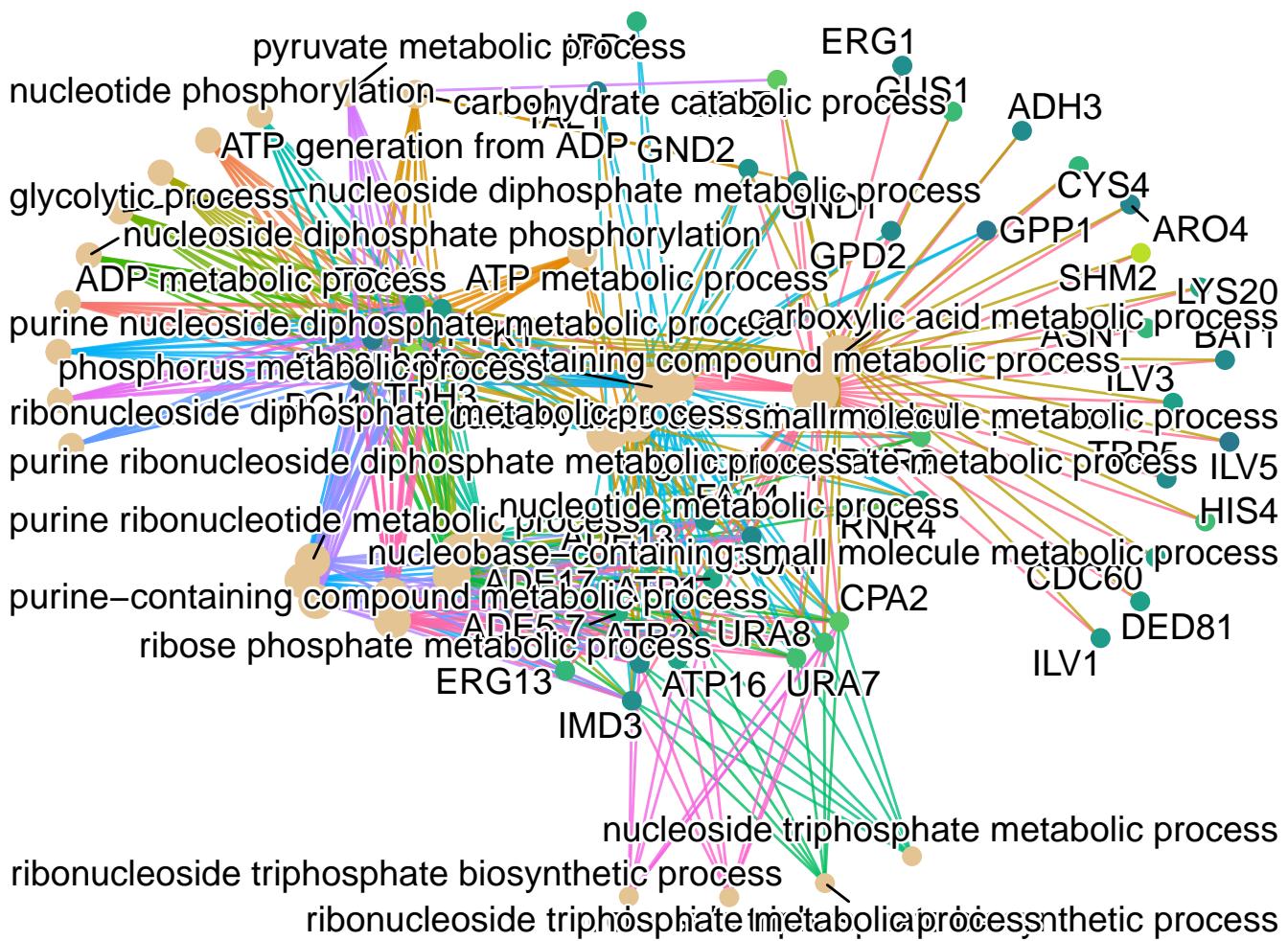
— purine-containing compound metabolic process

- ribose

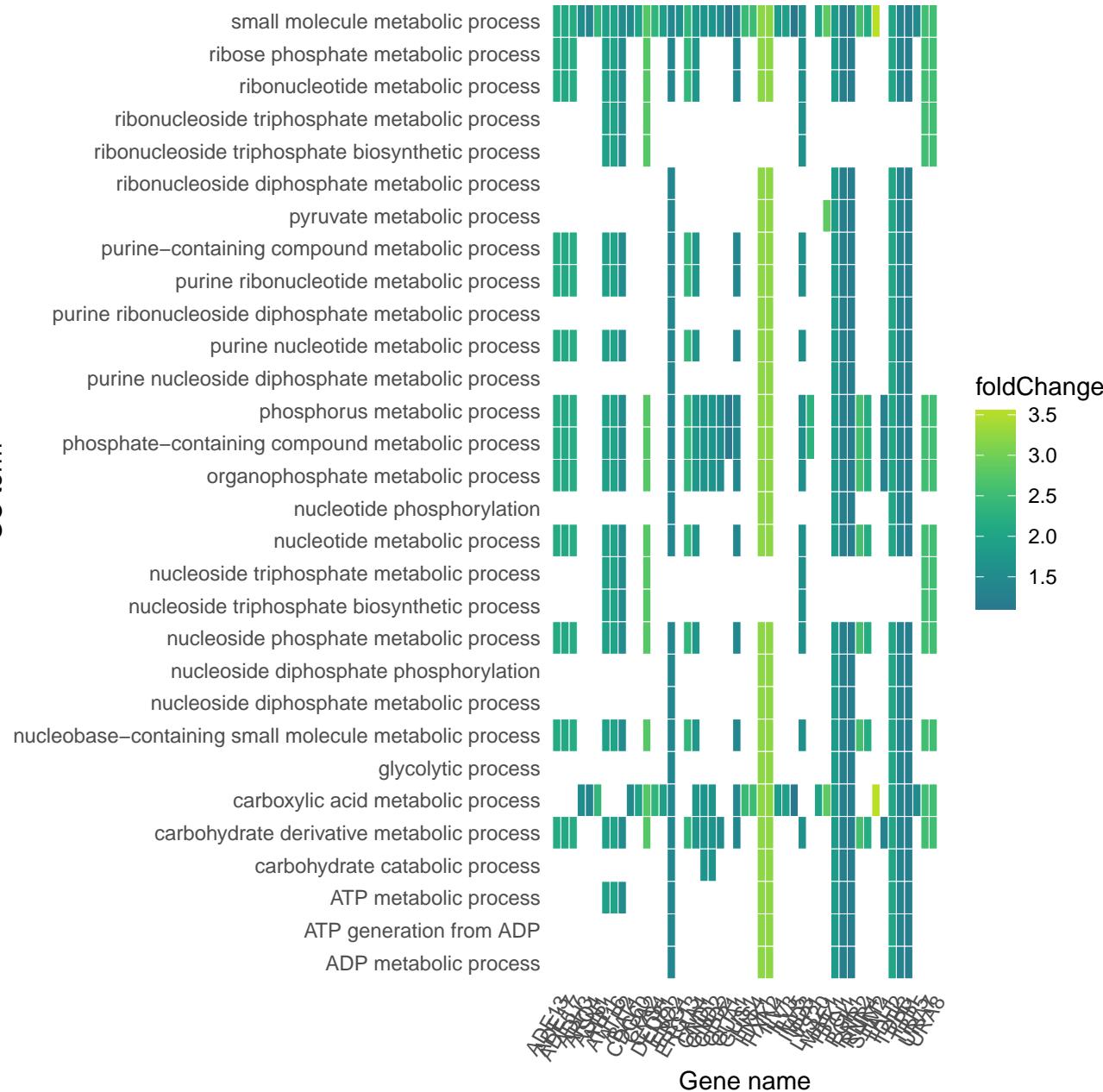
phosphorus metabolic process

— pyruvate metabolic process

- small



NAM7-TAP Up-regulated GO BP heatplot



NAM7-TAP Up-regulated GO BP emapplot

nucleoside diphosphate phosphorylation

ATP generation from ADP, carboxylic acid metabolic process
purine ribonucleoside diphosphate metabolic process

nucleoside diphosphate metabolic process, ADP metabolic process
nucleotide phosphorylation, carbohydrate catabolic process

purine nucleoside diphosphate metabolic process, small molecule metabolic process
glycolytic process

pyruvate metabolic process, peptide metabolic process

ATP metabolic process, compound metabolic process

ribonucleoside diphosphate metabolic process, carbohydrate metabolic process

ribose phosphate metabolic process

phosphorus metabolic process, purine ribonucleotide metabolic process
organophosphate metabolic process, carbohydrate derivative metabolic process

nucleotide metabolic process

nucleobase-containing compound metabolic process

nucleoside phosphate metabolic process

size

10

20

30

40

FoldChange

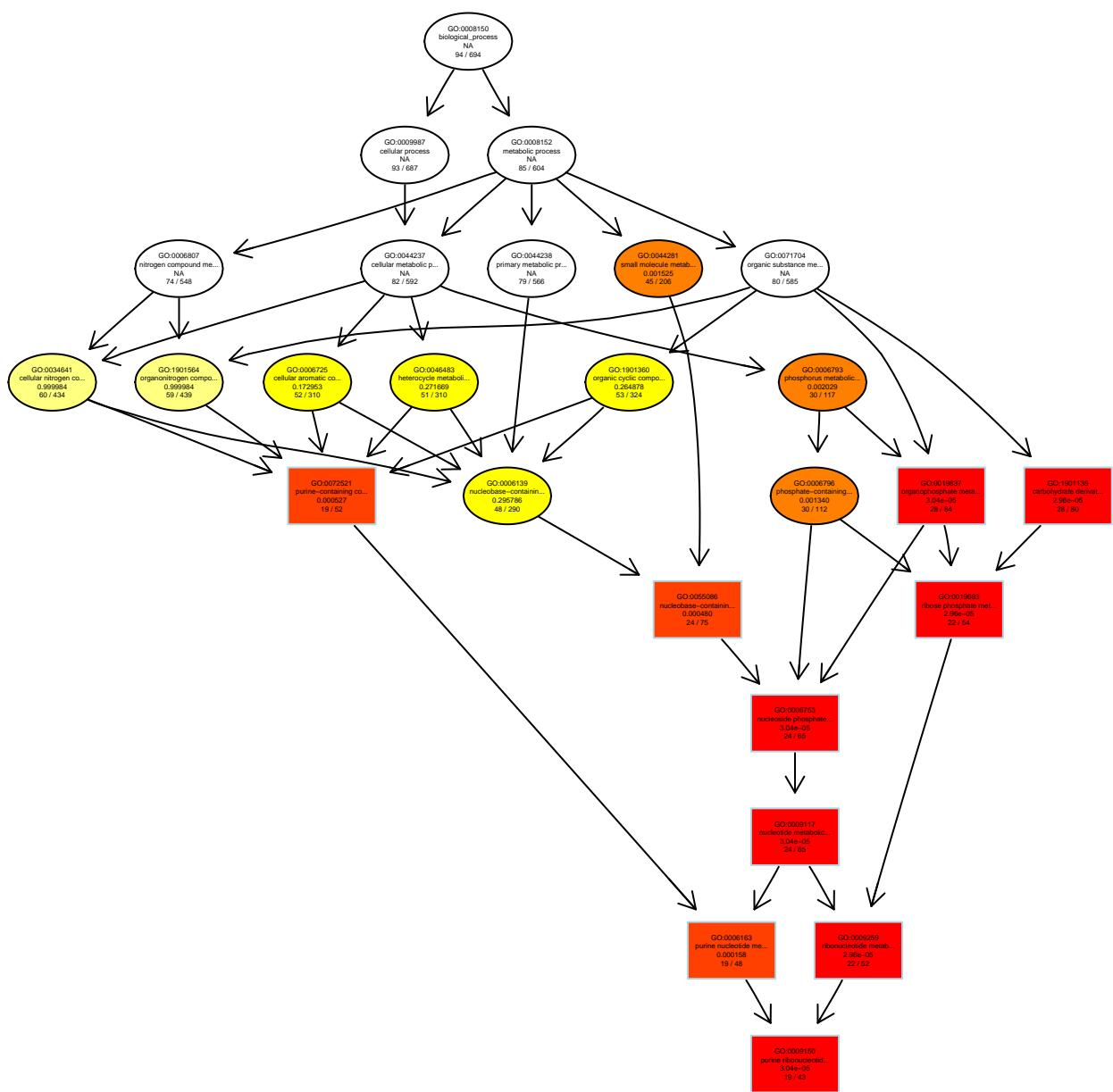


ribonucleoside triphosphate biosynthetic process

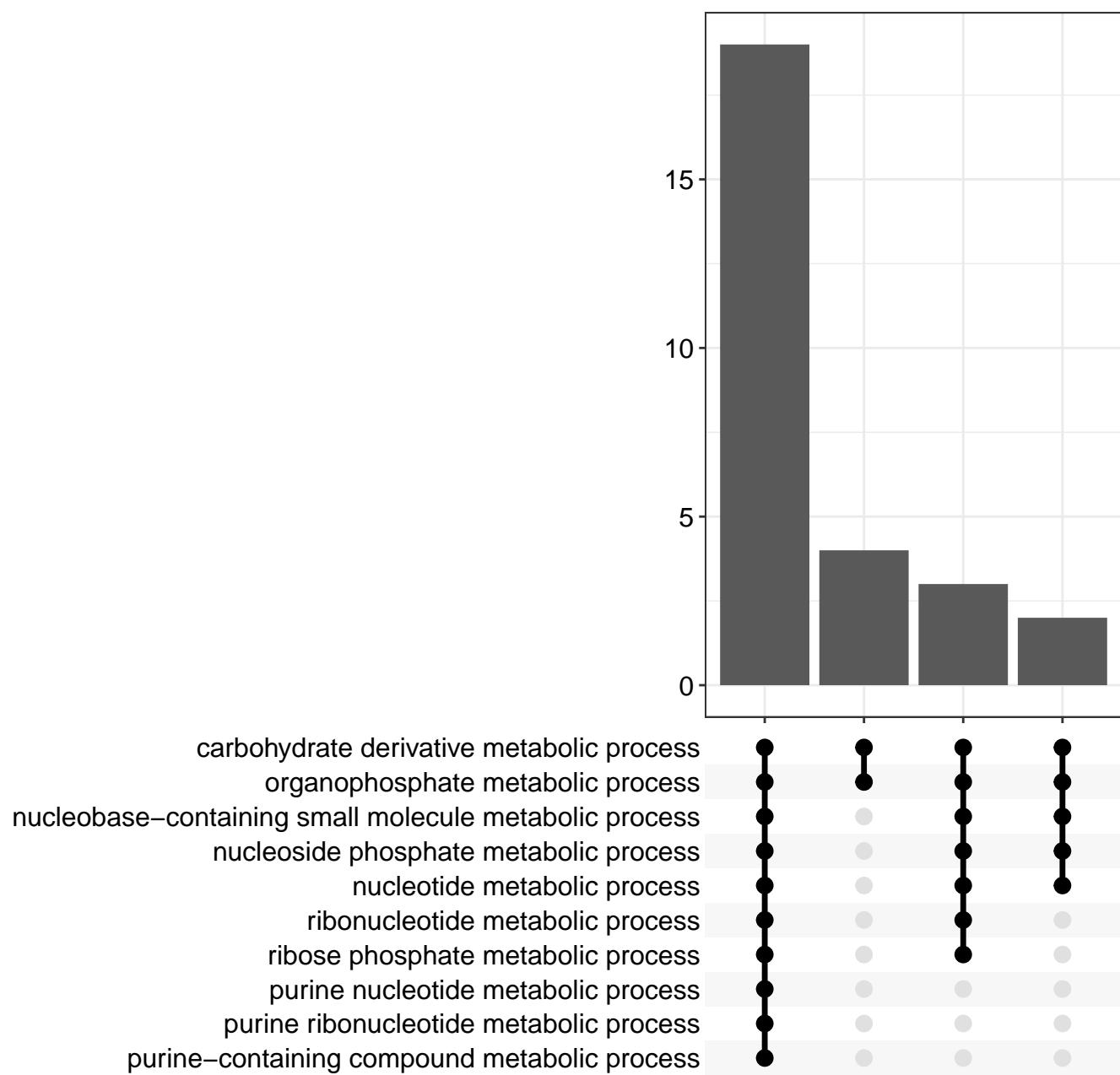
nucleoside triphosphate biosynthetic process

nucleoside triphosphate metabolic process

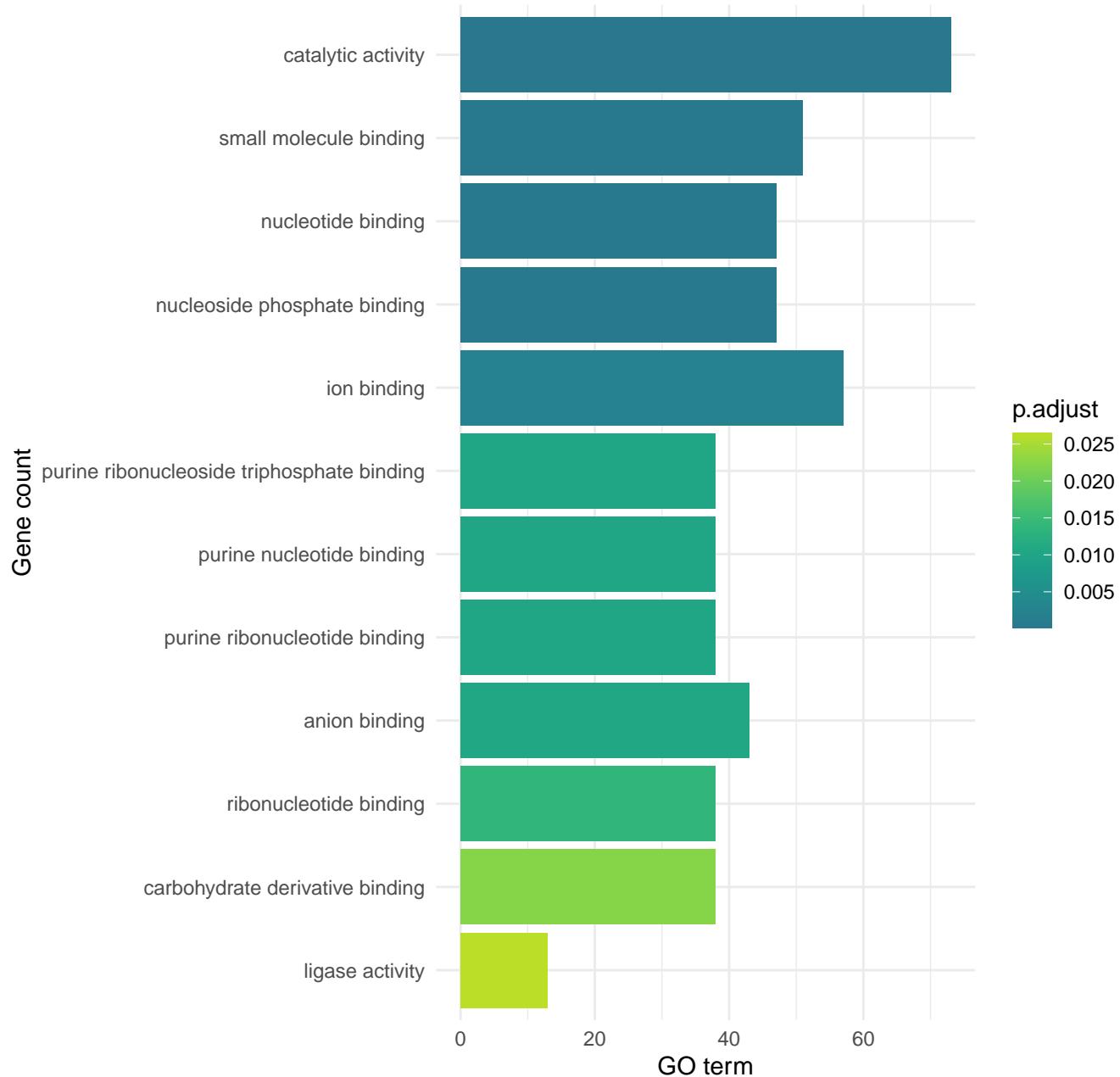
ribonucleoside triphosphate metabolic process



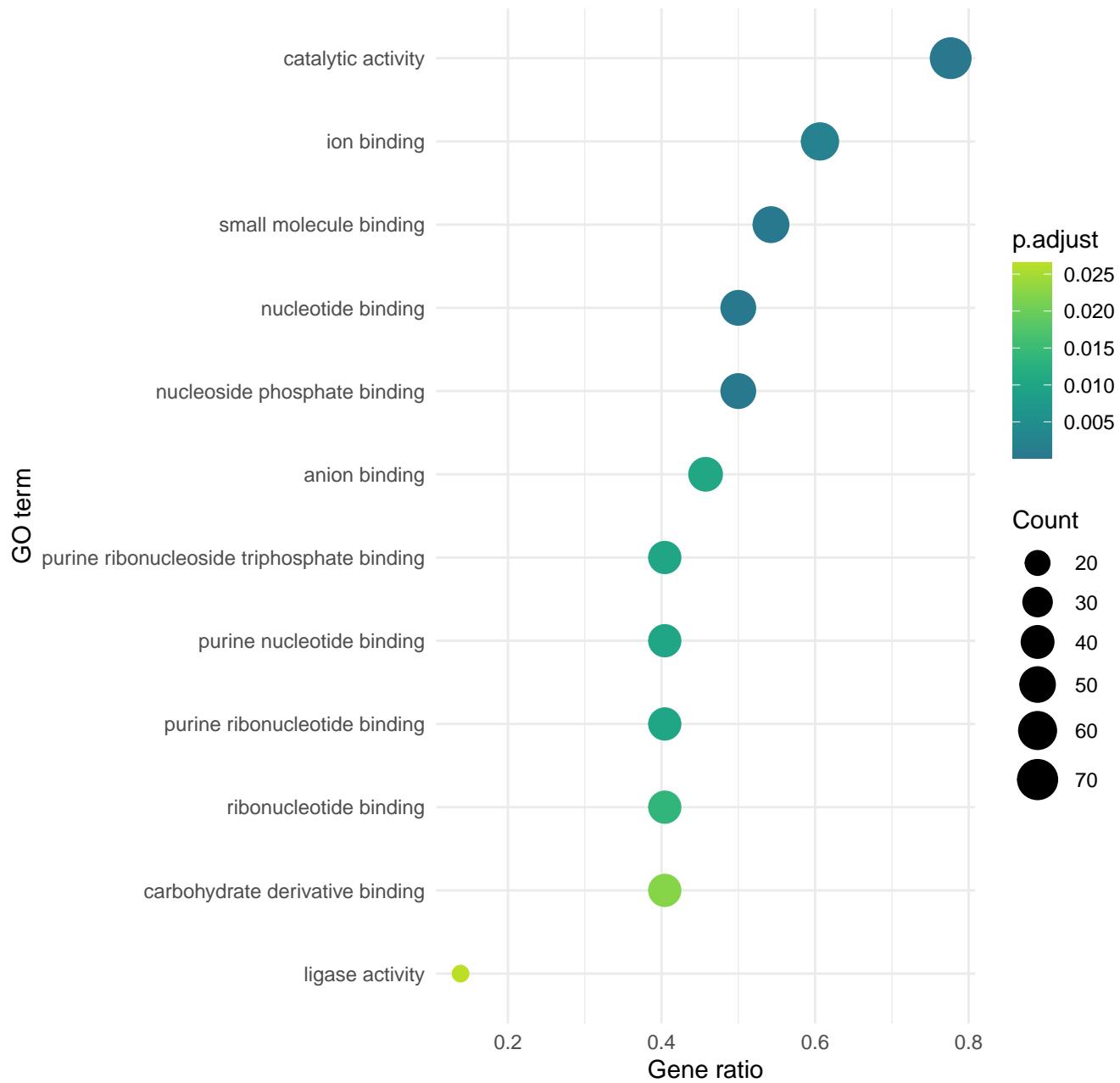
NAM7-TAP Up-regulated GO BP



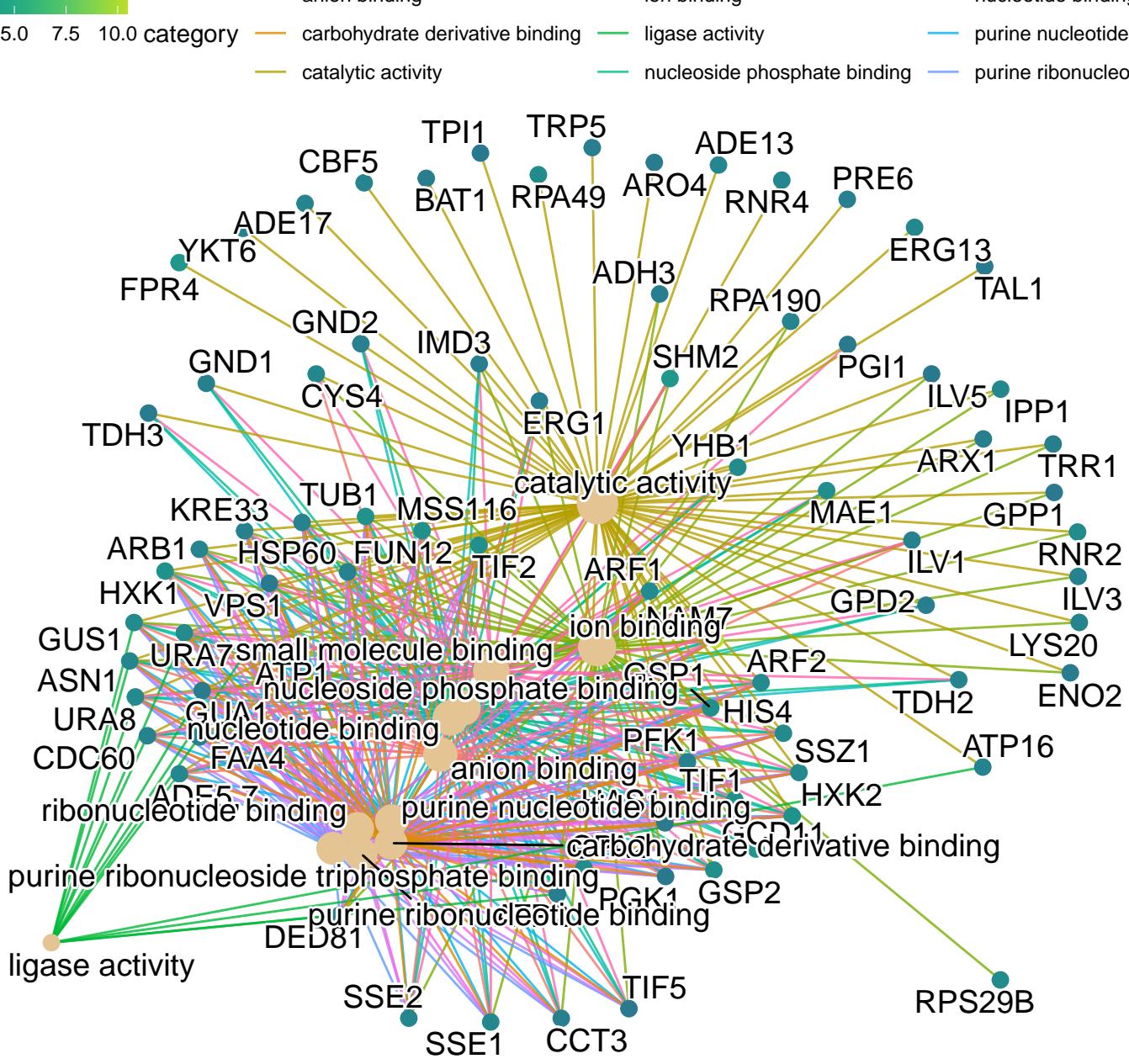
NAM7-TAP Up-regulated GO MF barplot



NAM7-TAP Up-regulated GO MF dotplot

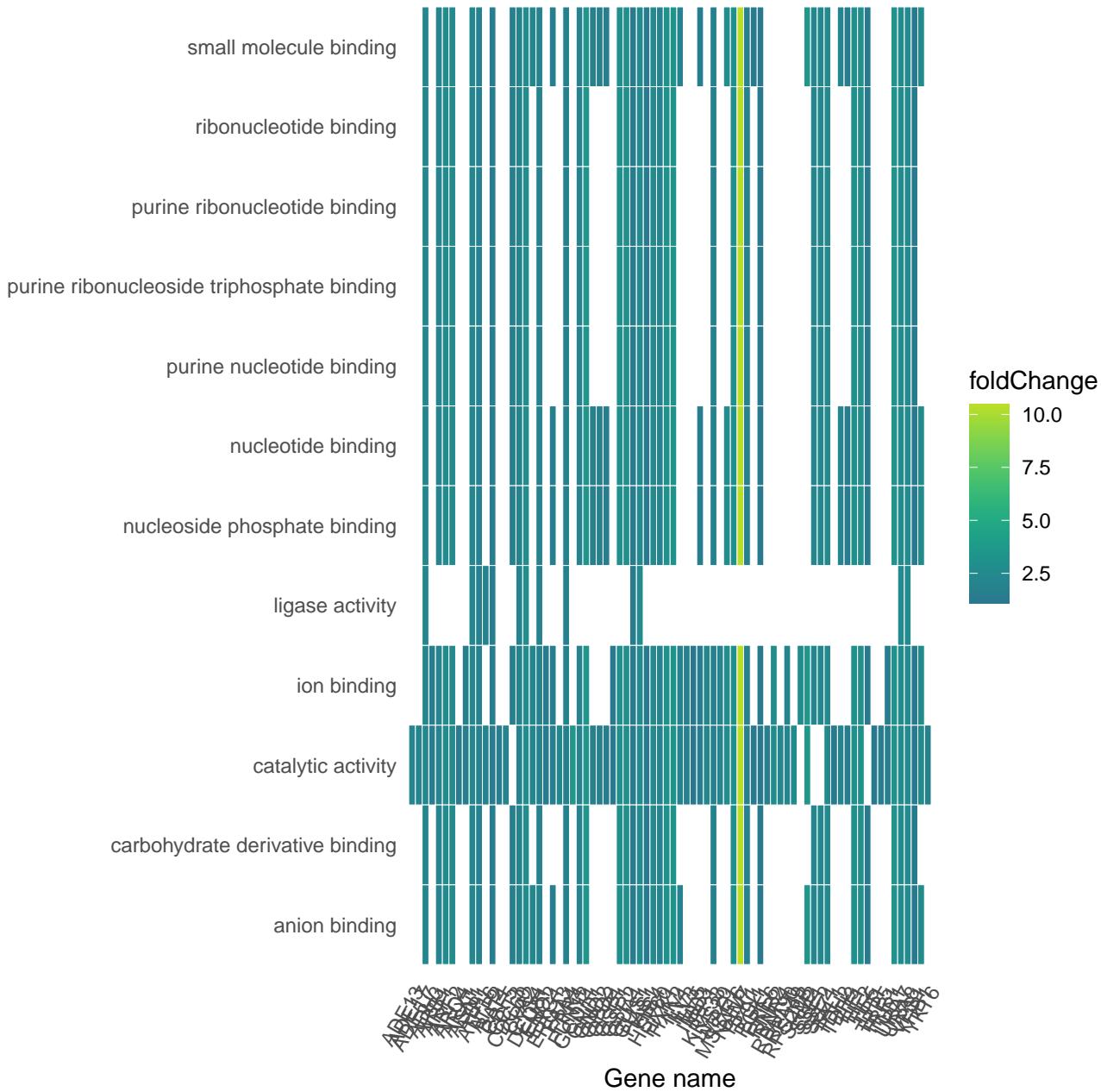


NAM7-TAP Up-regulated GO MF cnetplot

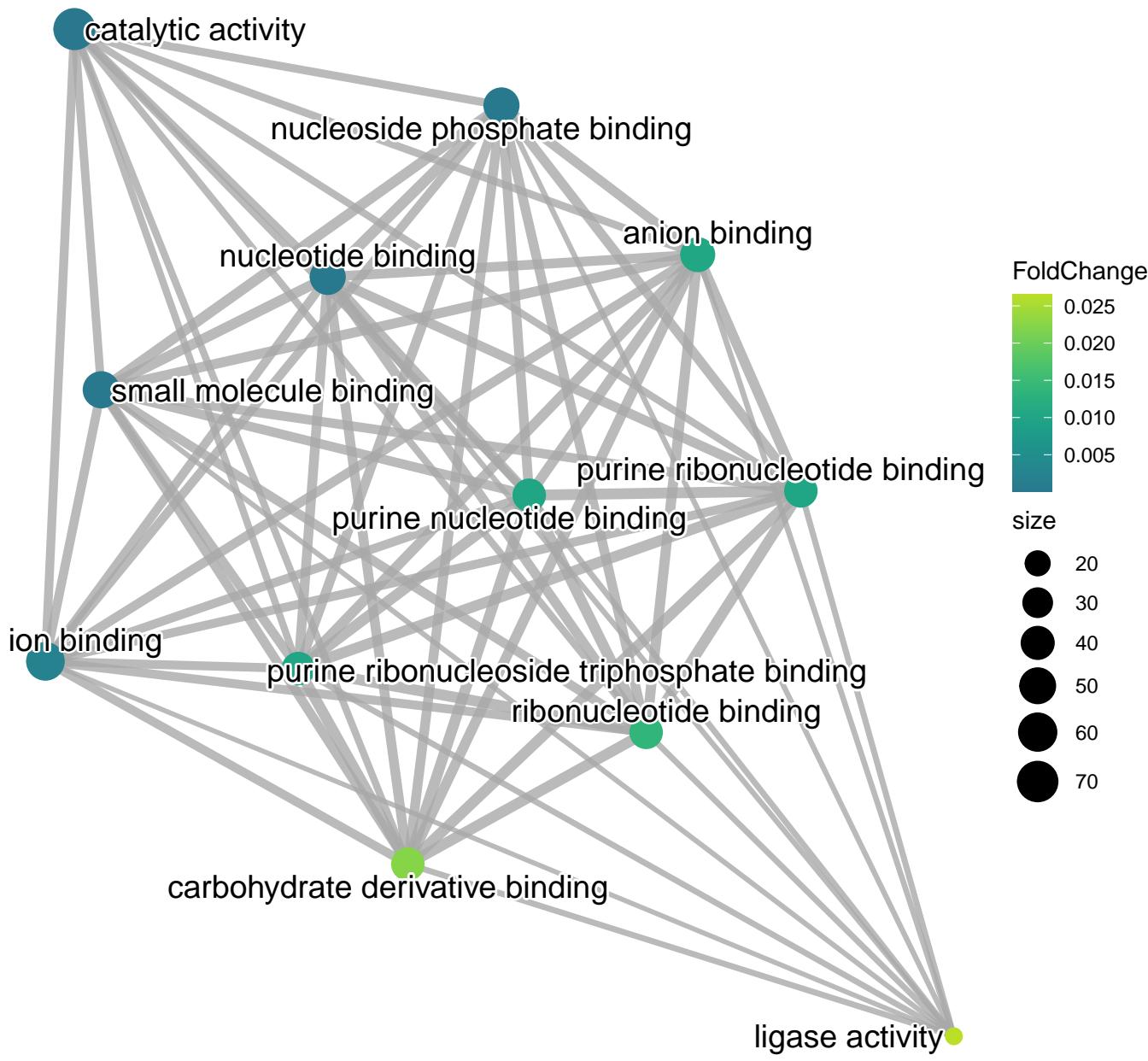


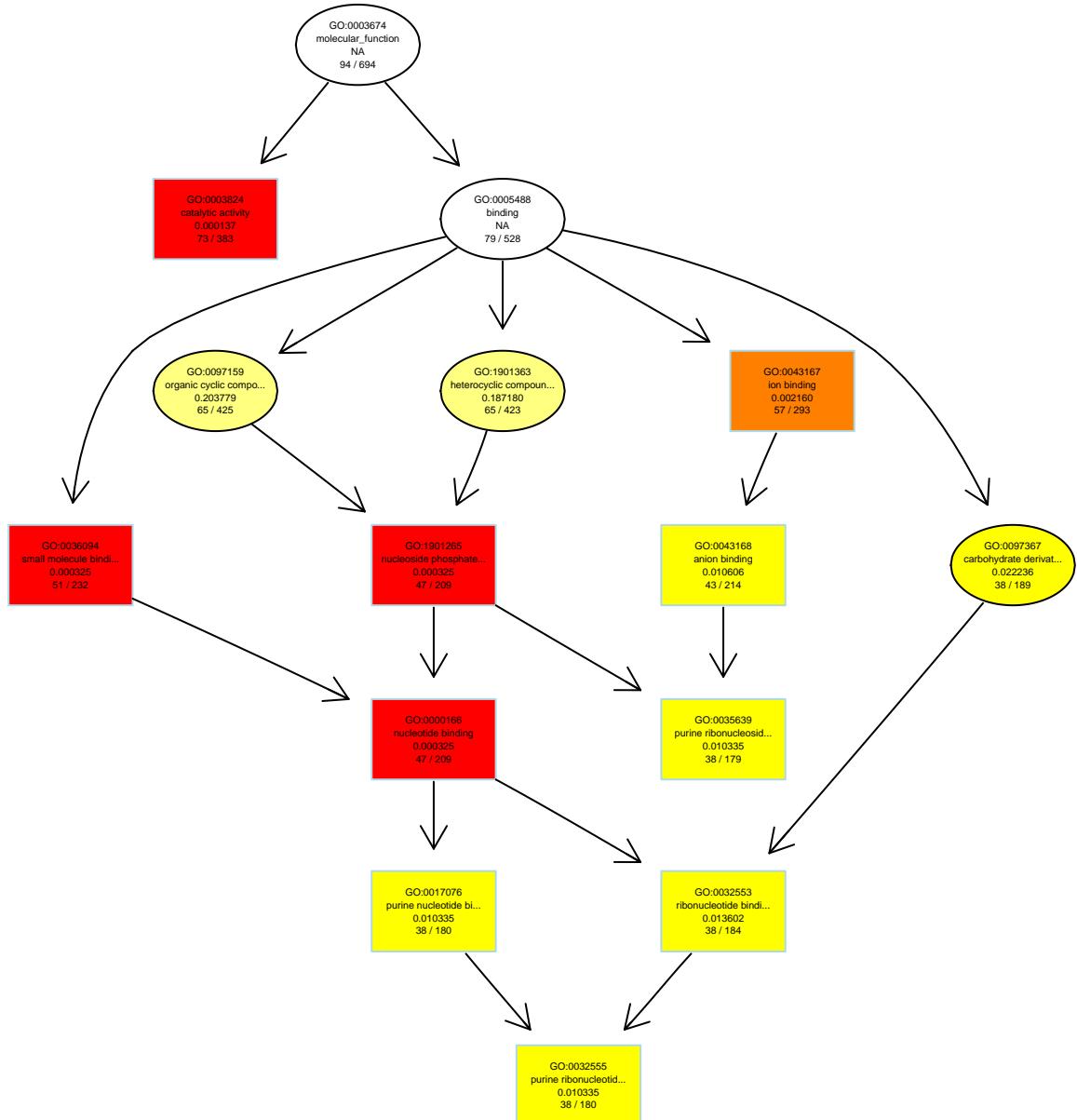
NAM7-TAP Up-regulated GO MF heatplot

GO term

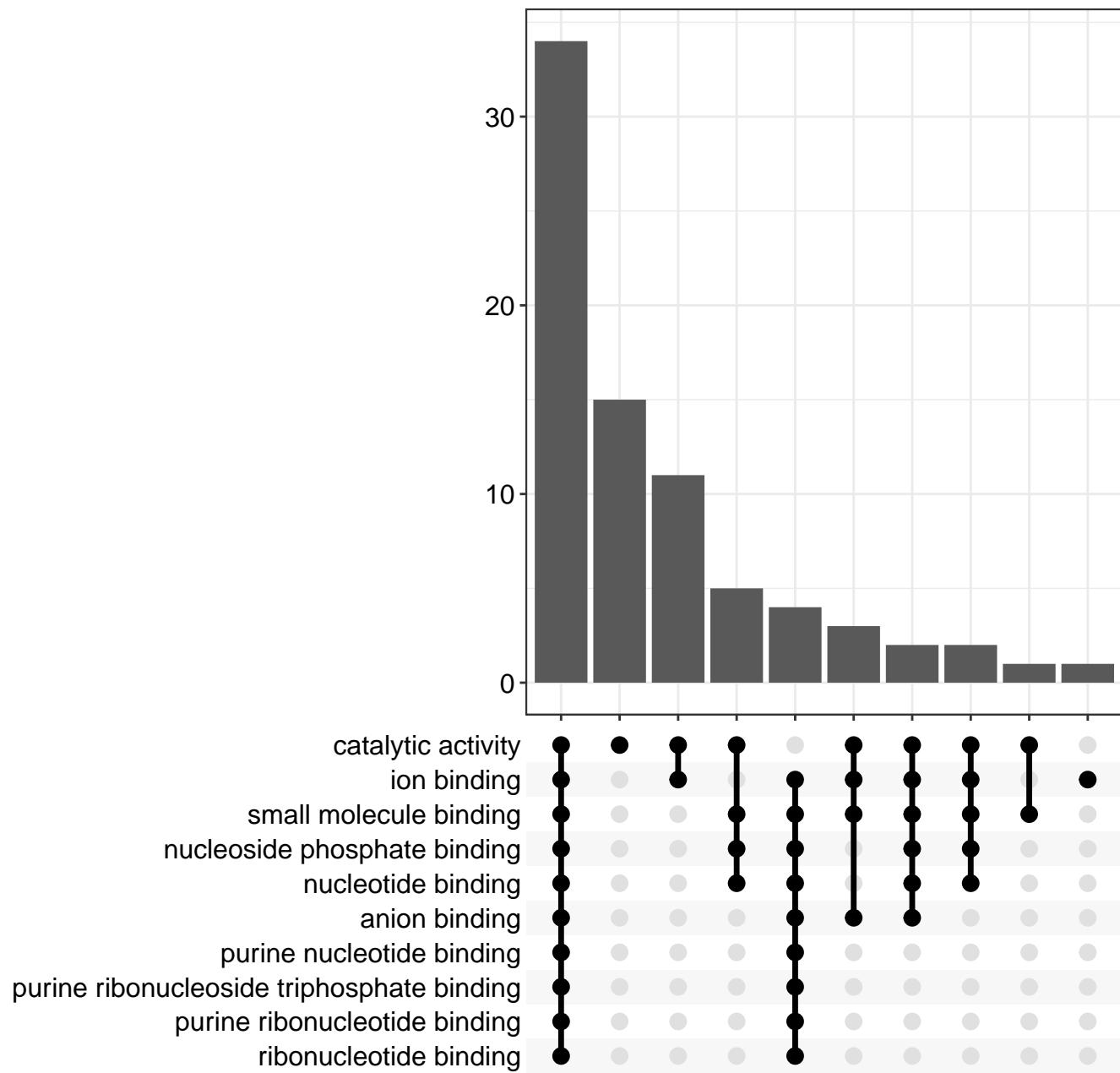


NAM7-TAP Up-regulated GO MF emapplot

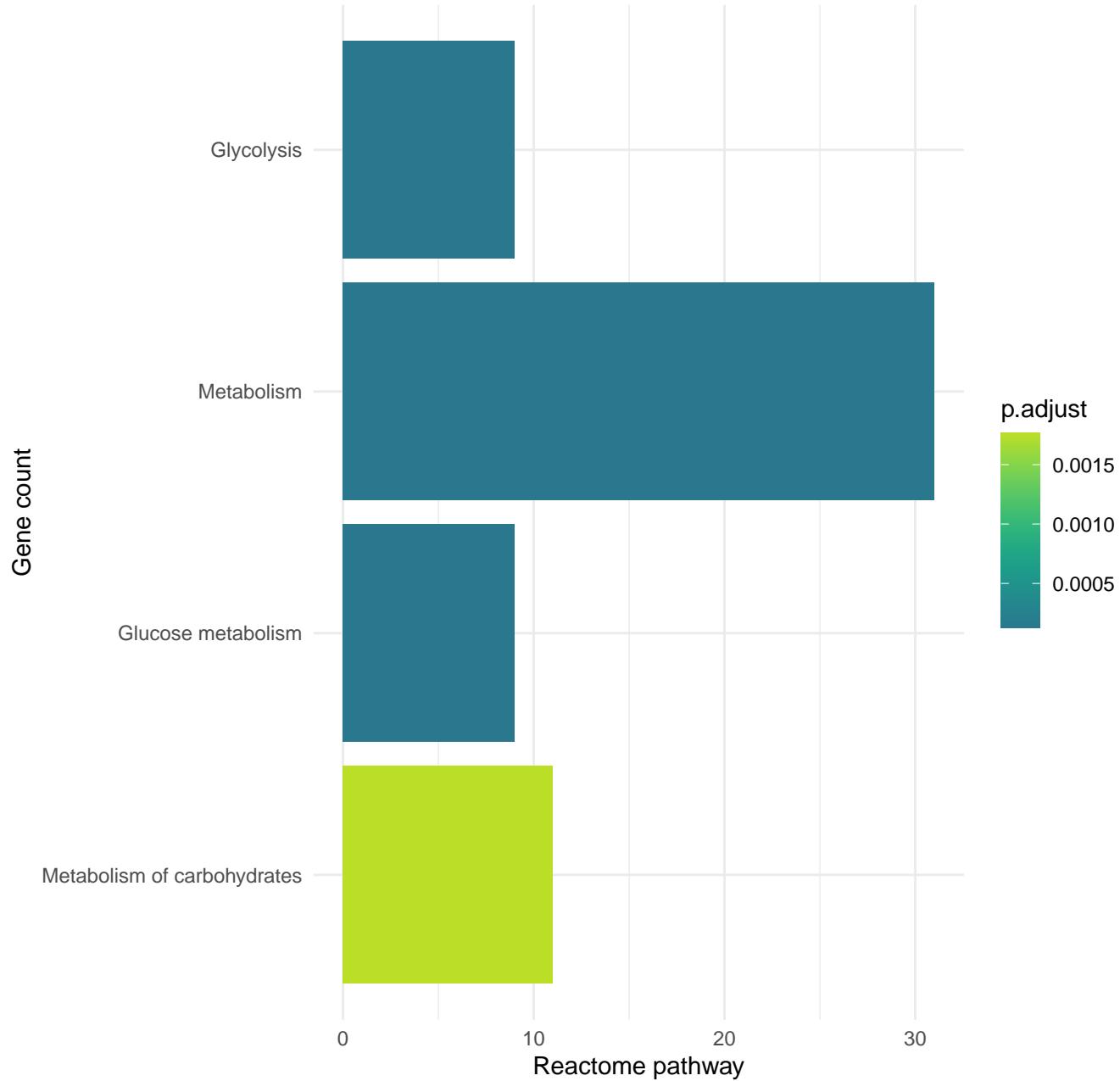




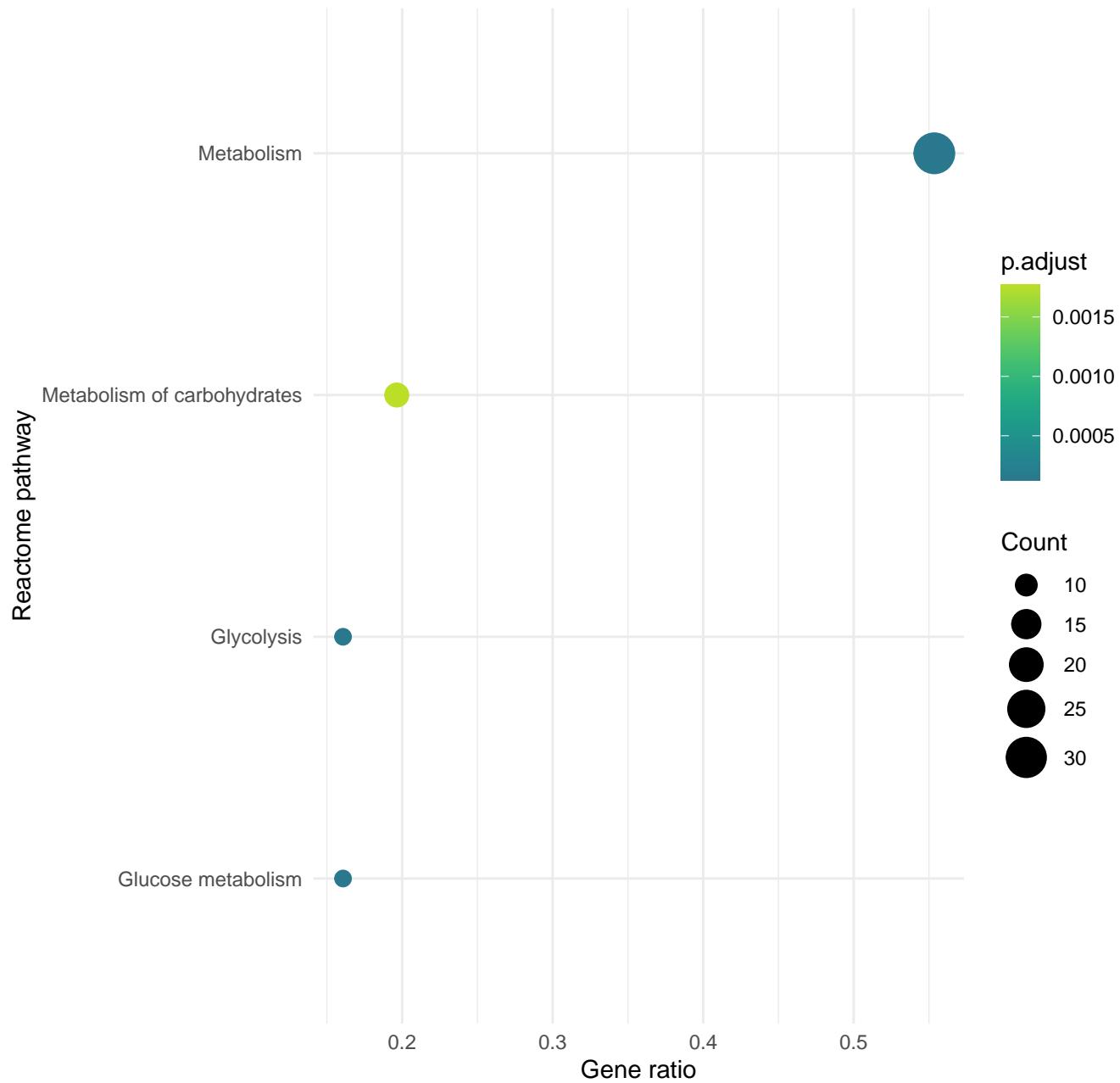
NAM7-TAP Up-regulated GO MF upsetplot



NAM7-TAP Up-regulated Reactome barplot



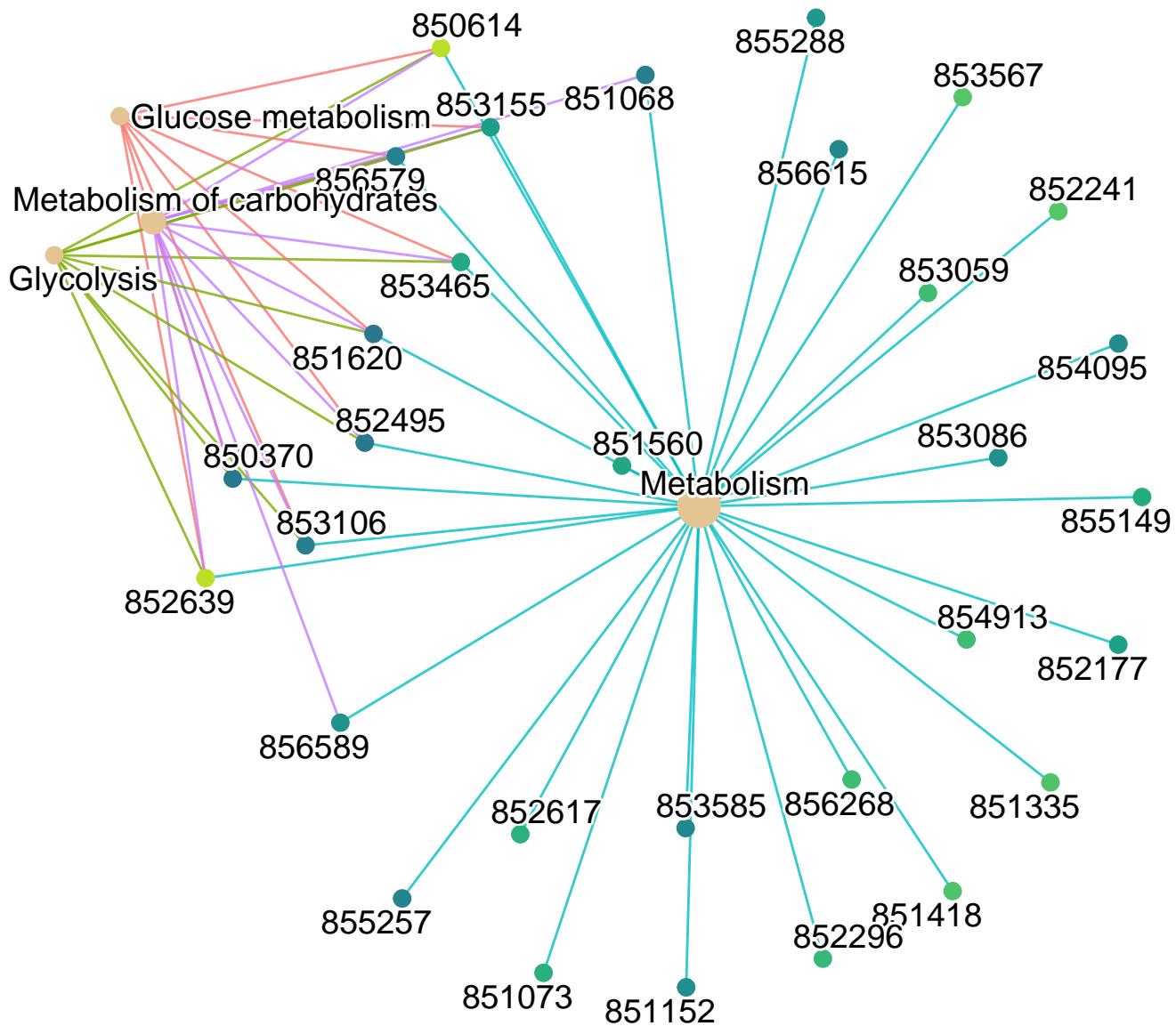
NAM7-TAP Up-regulated Reactome dotplot



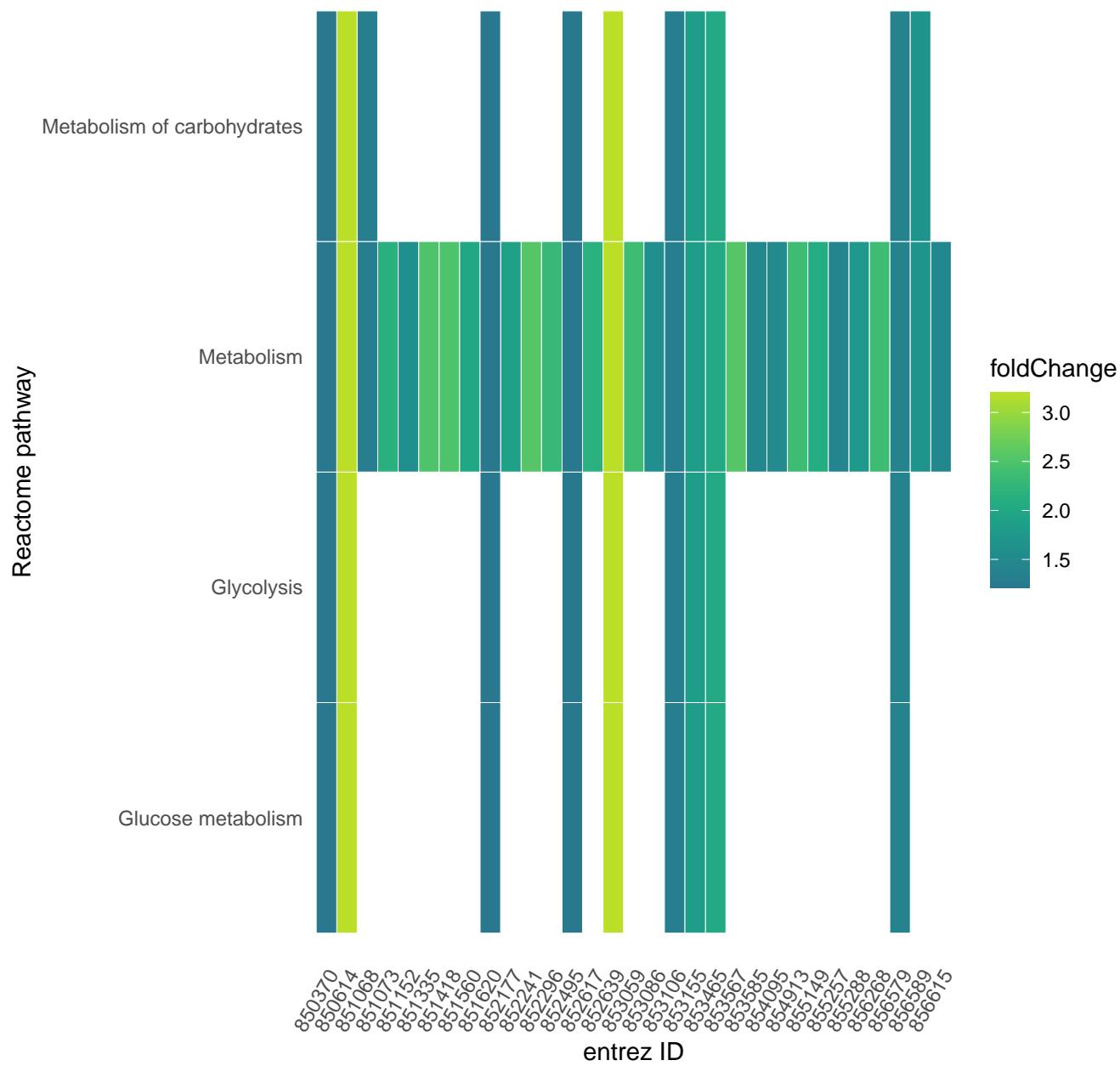
NAM7-TAP Up-regulated Reactome cnetplot

size ● 10 ● 15 ● 20 ● 25 ● 30 category

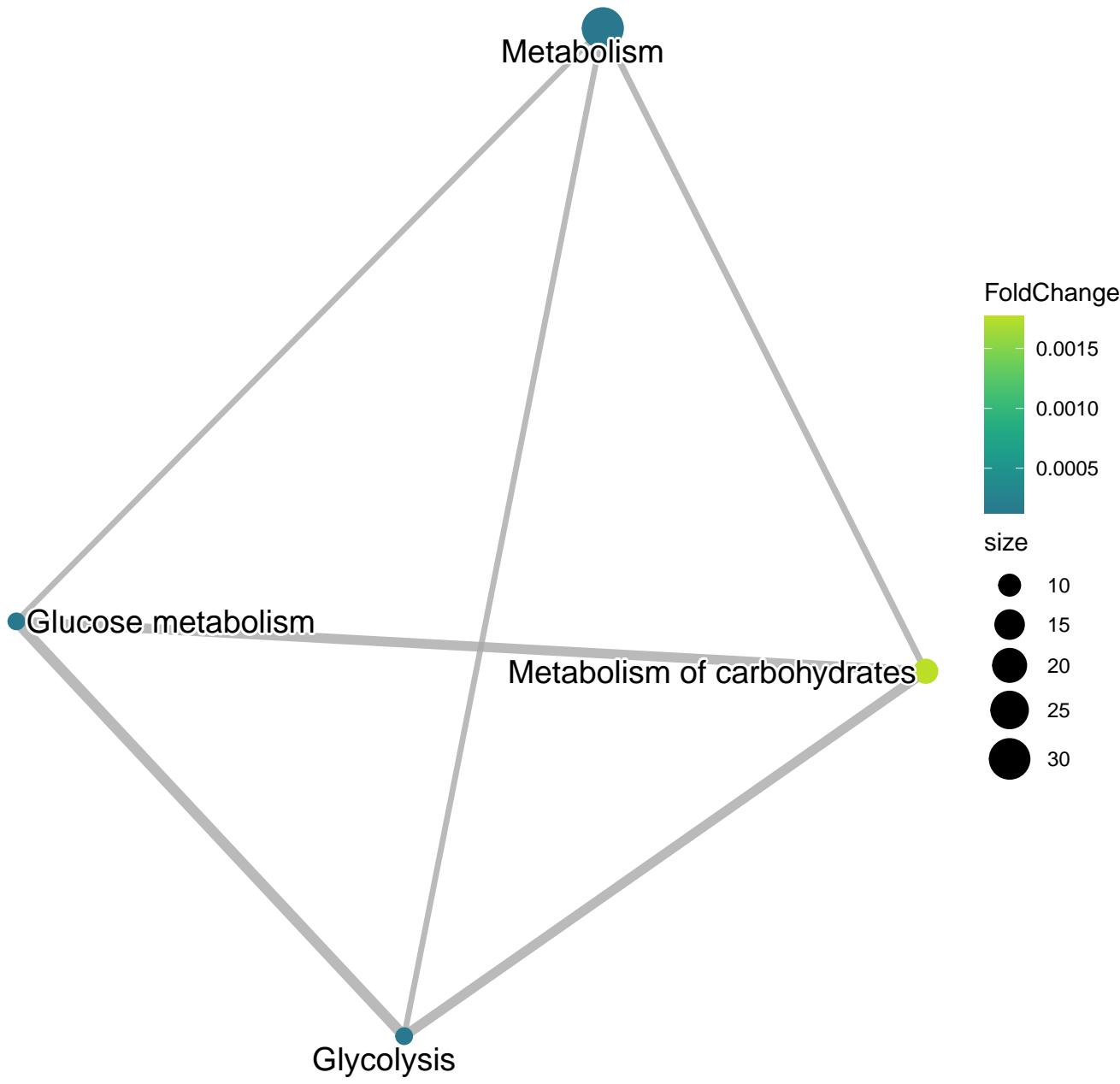
Glucose metabolism Glycolysis Metabolism



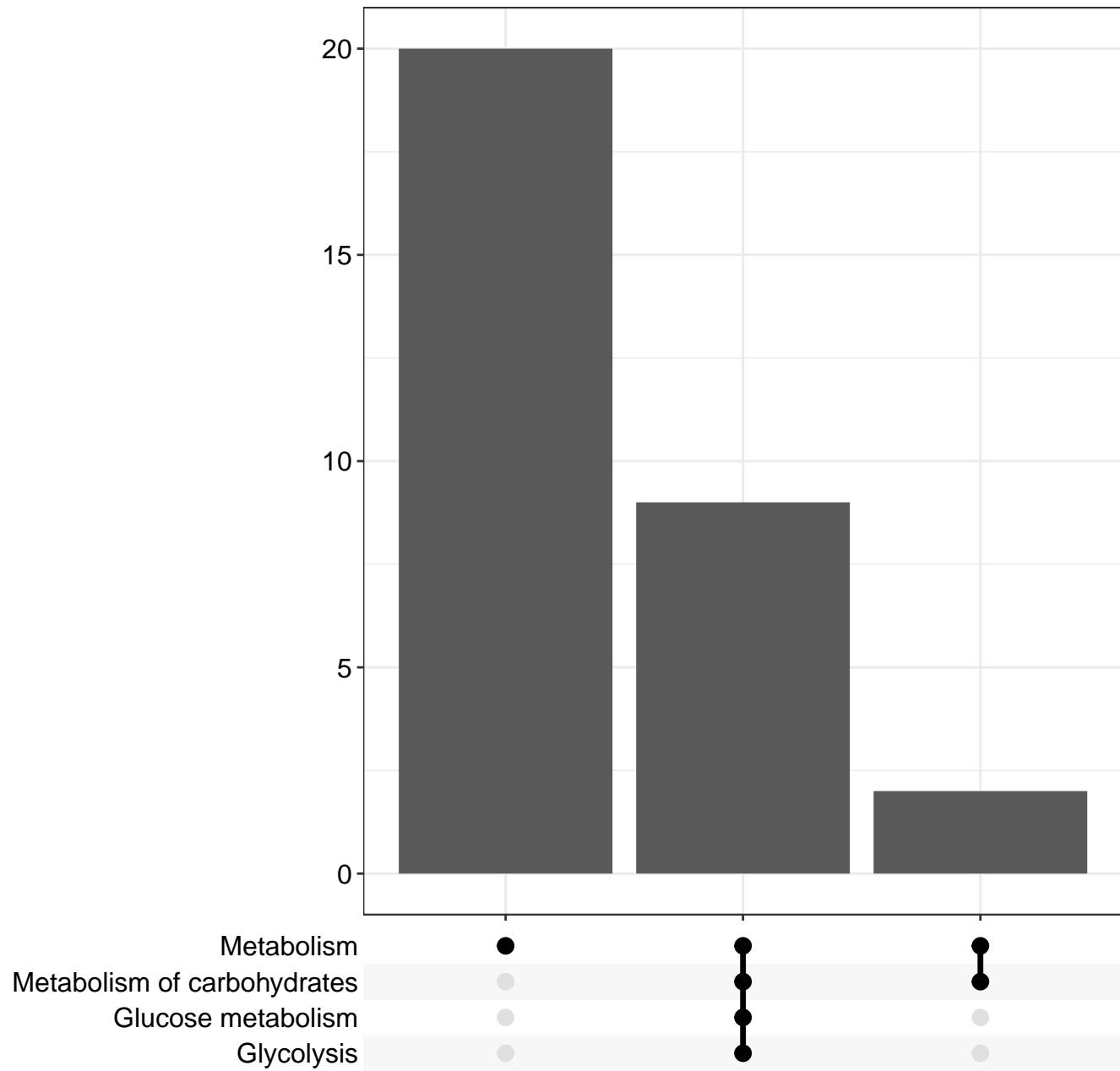
NAM7-TAP Up-regulated Reactome heatplot



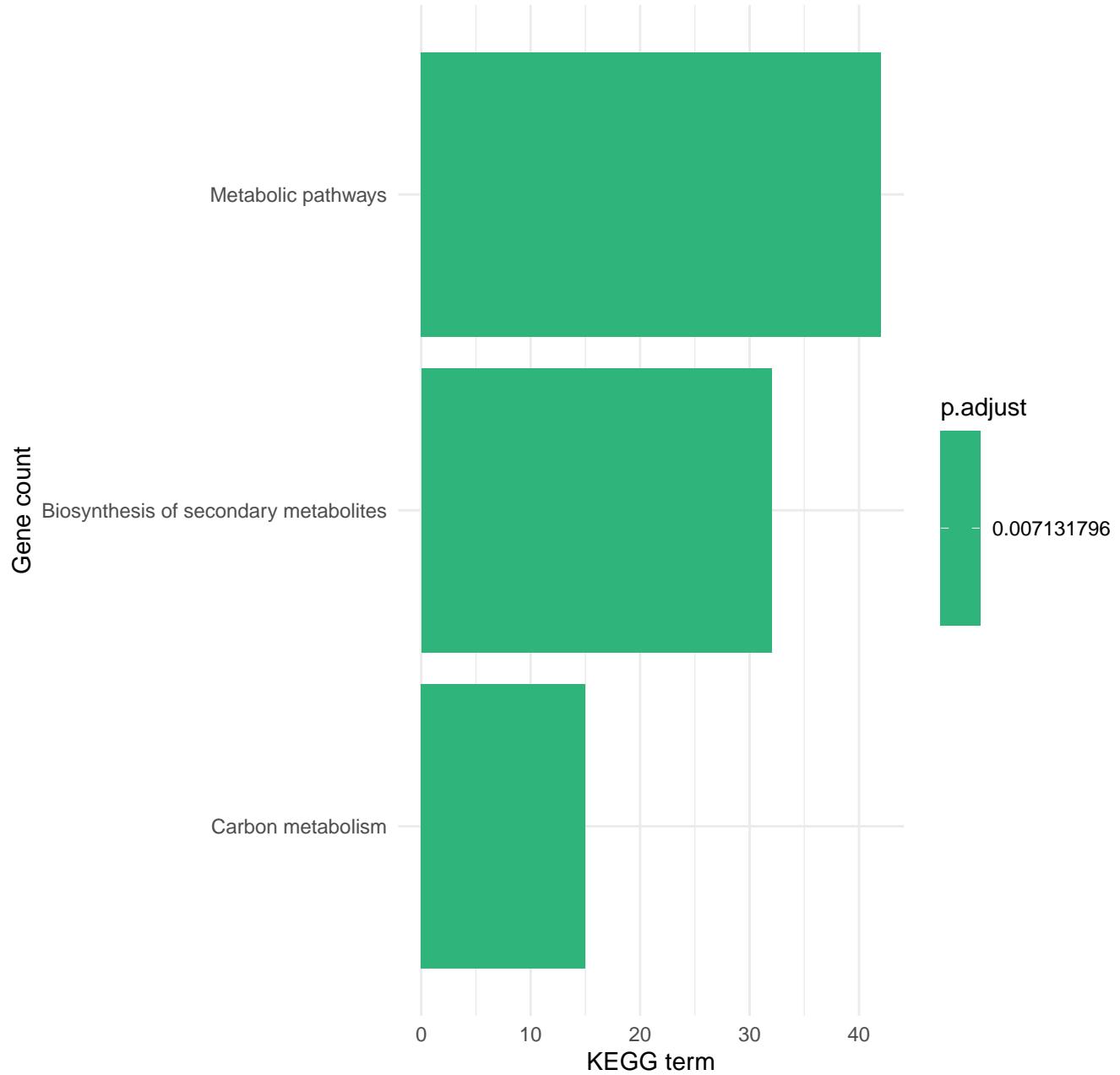
NAM7-TAP Up-regulated Reactome emappplot



NAM7-TAP Up-regulated Reactome upsetplot



NAM7-TAP Up-regulated KEGG barplot



NAM7-TAP Up-regulated KEGG dotplot

KEGG term

Metabolic pathways

Count



Biosynthesis of secondary metabolites

p.adjust

0.007131796

Carbon metabolism

0.3

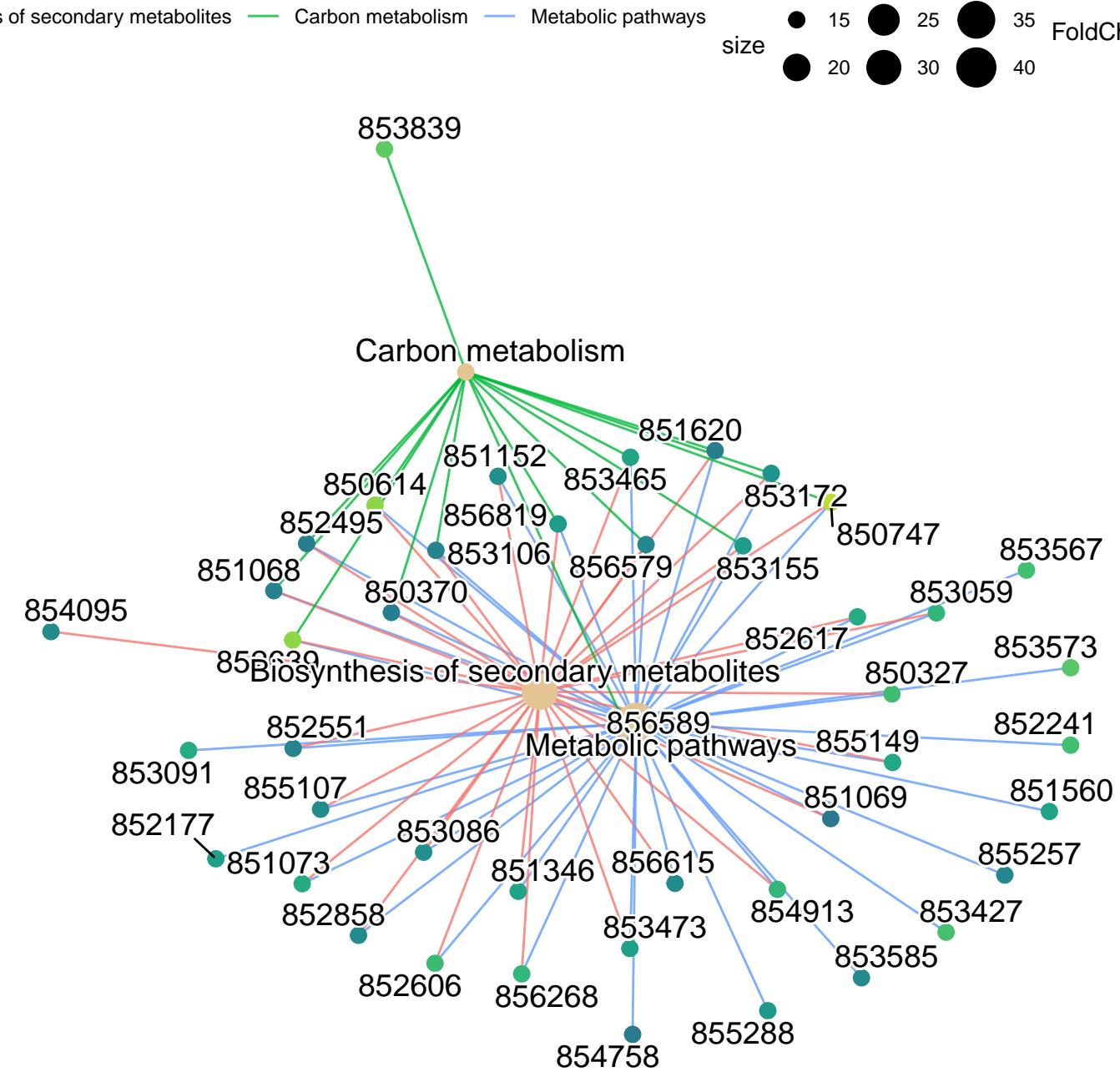
Gene ratio

0.4

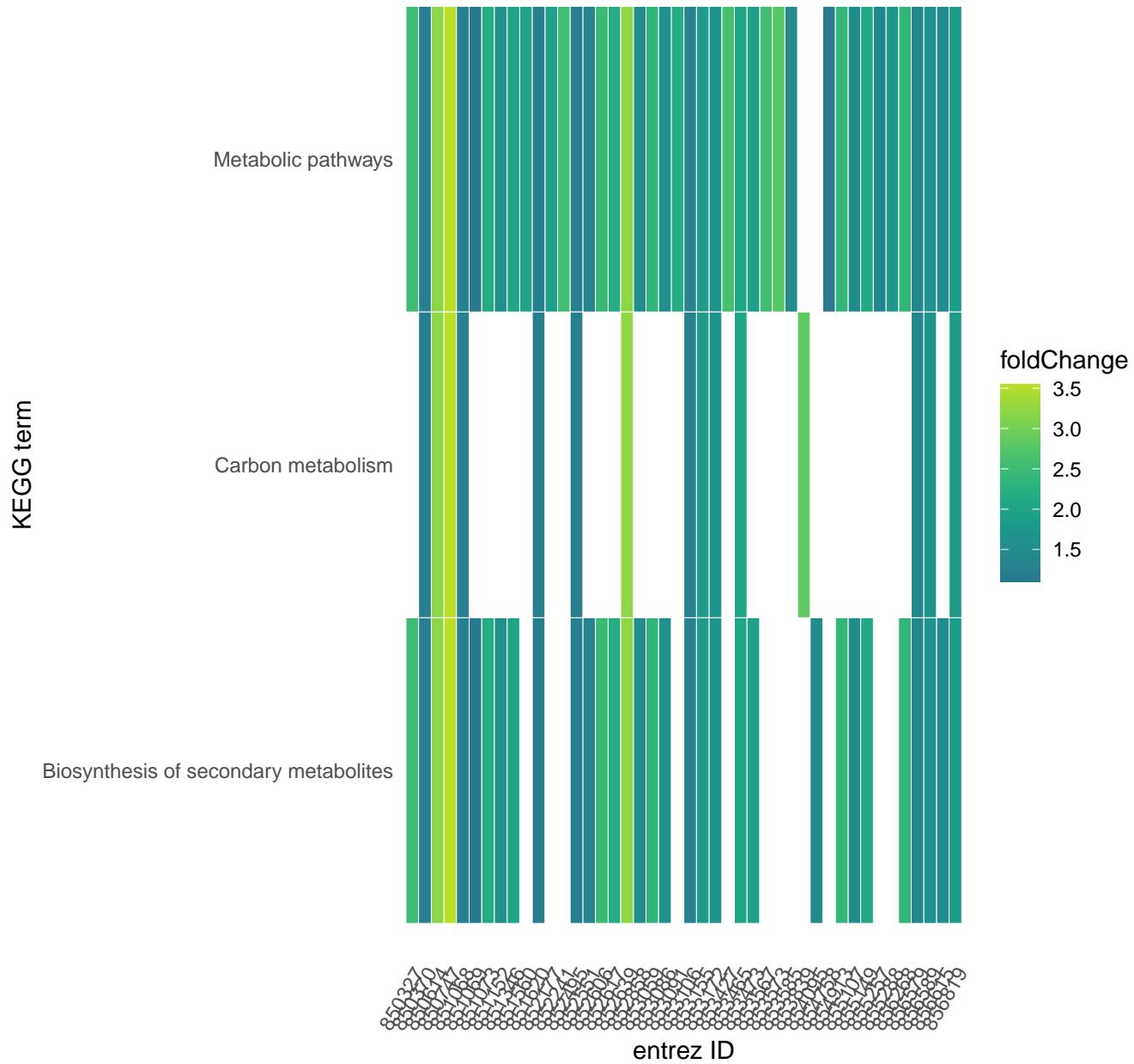
0.5

0.6

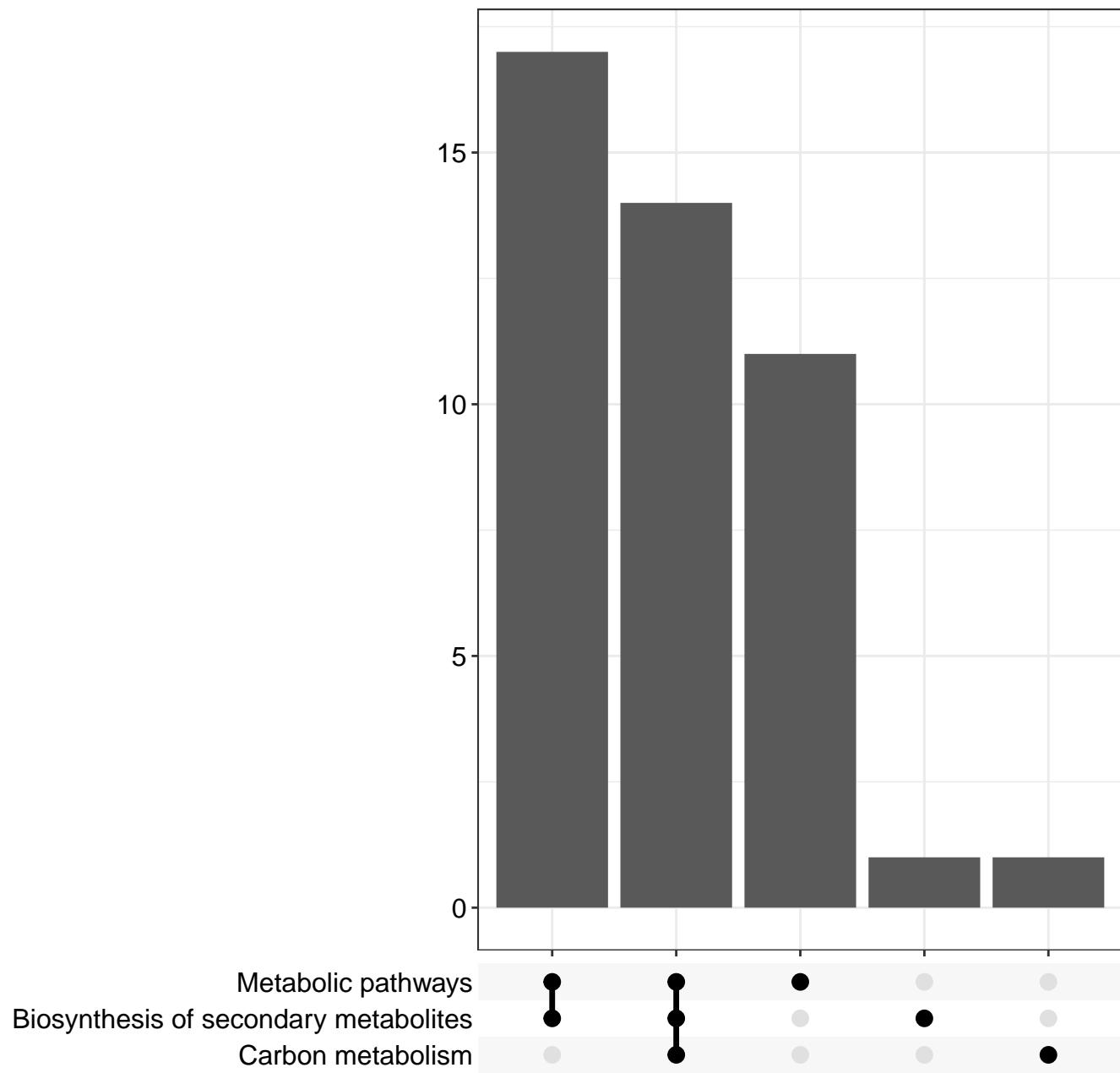
NAM7-TAP Up-regulated KEGG dotplot



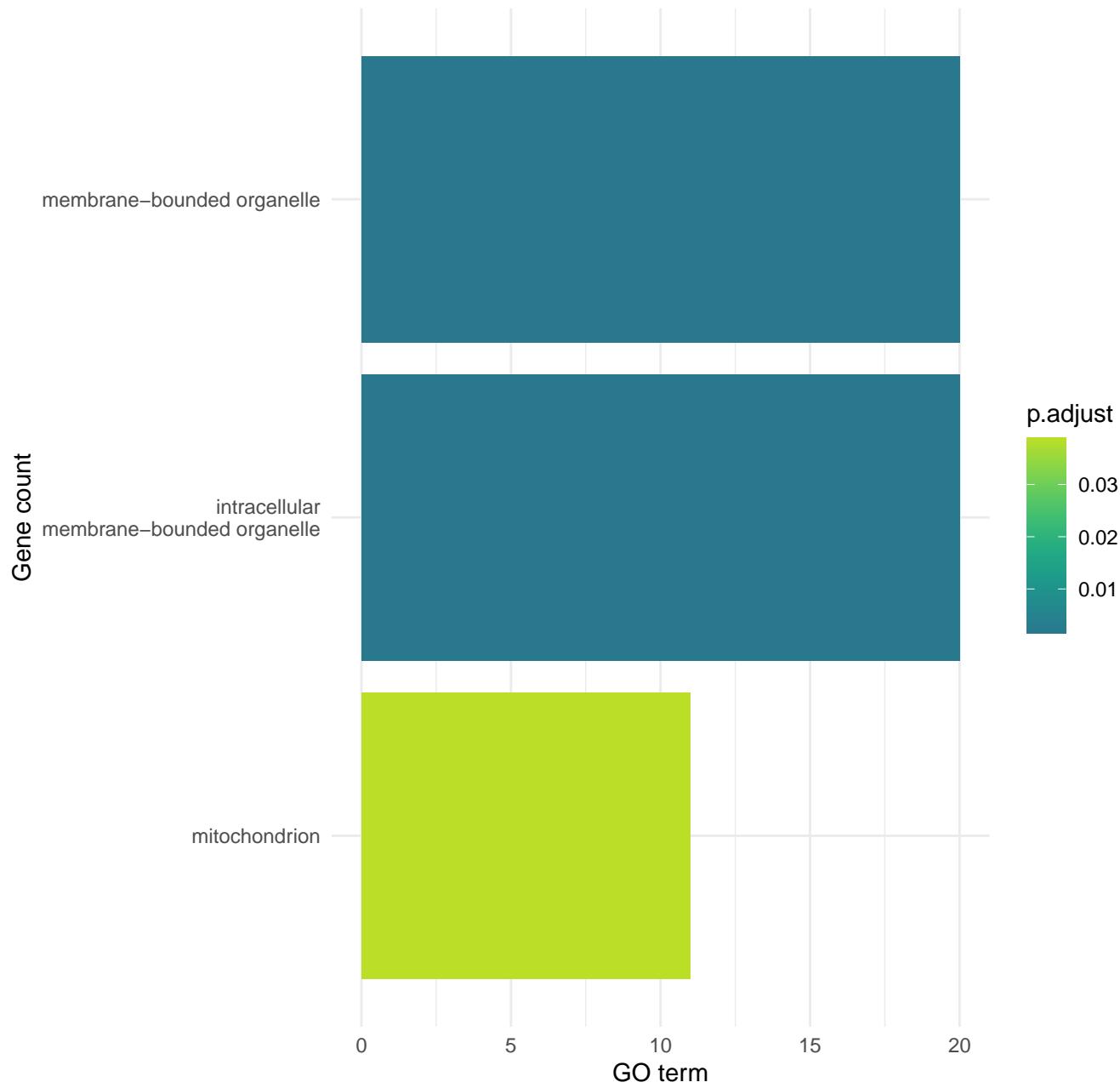
NAM7-TAP Up-regulated KEGG heatplot



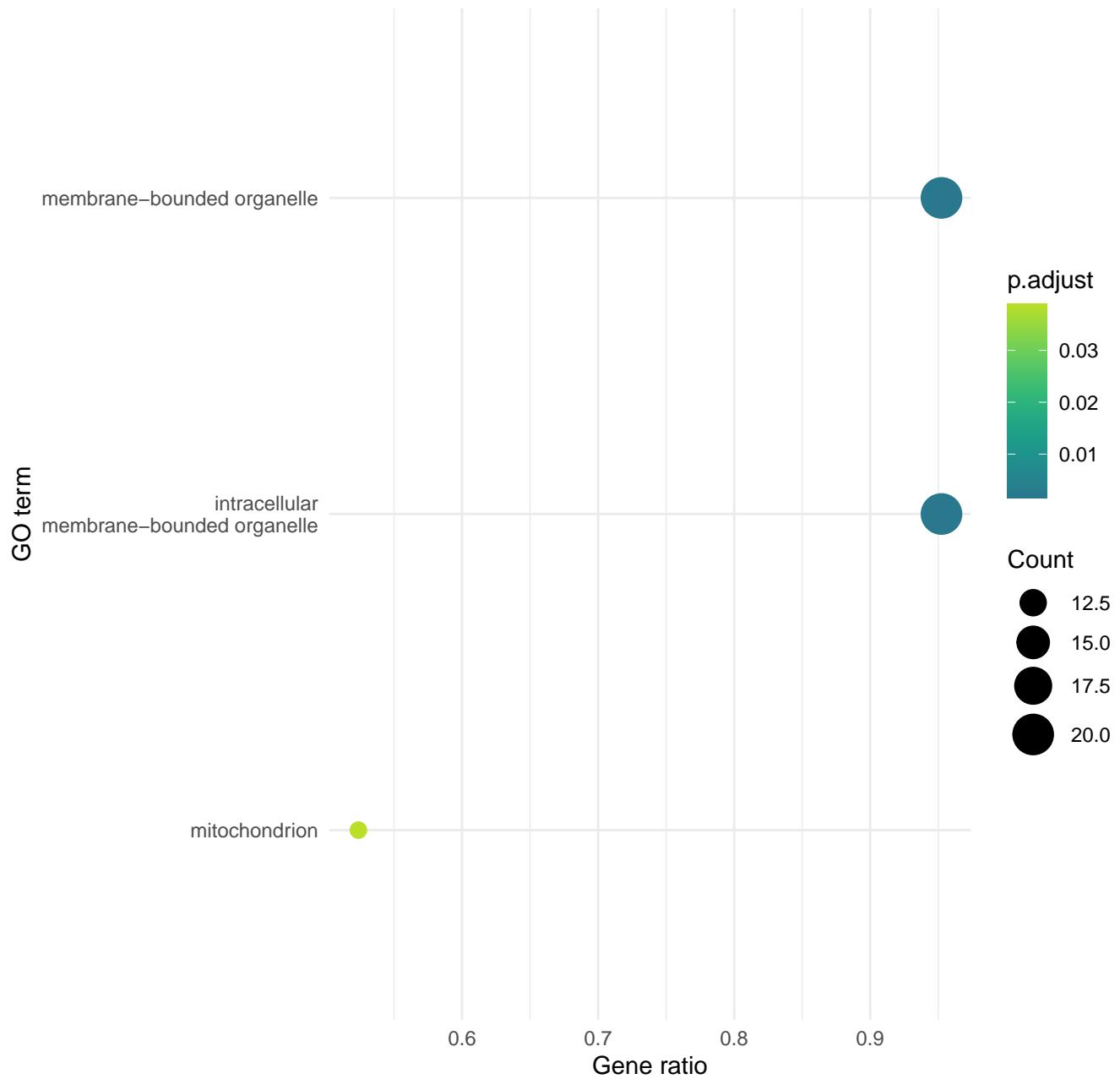
NAM7-TAP Up-regulated KEGG upsetplot



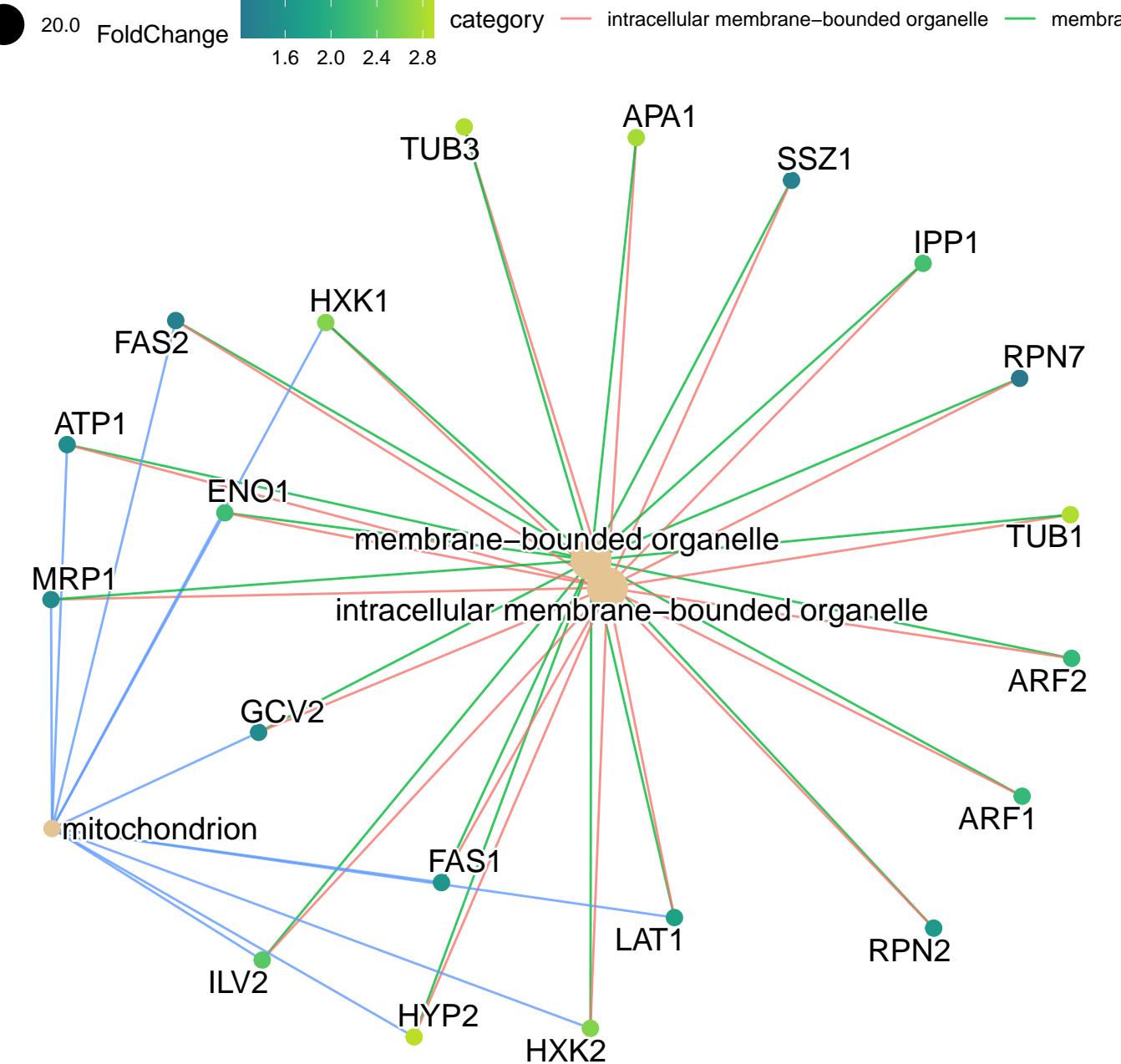
MEX67-TAP Up-regulated GO CC barplot



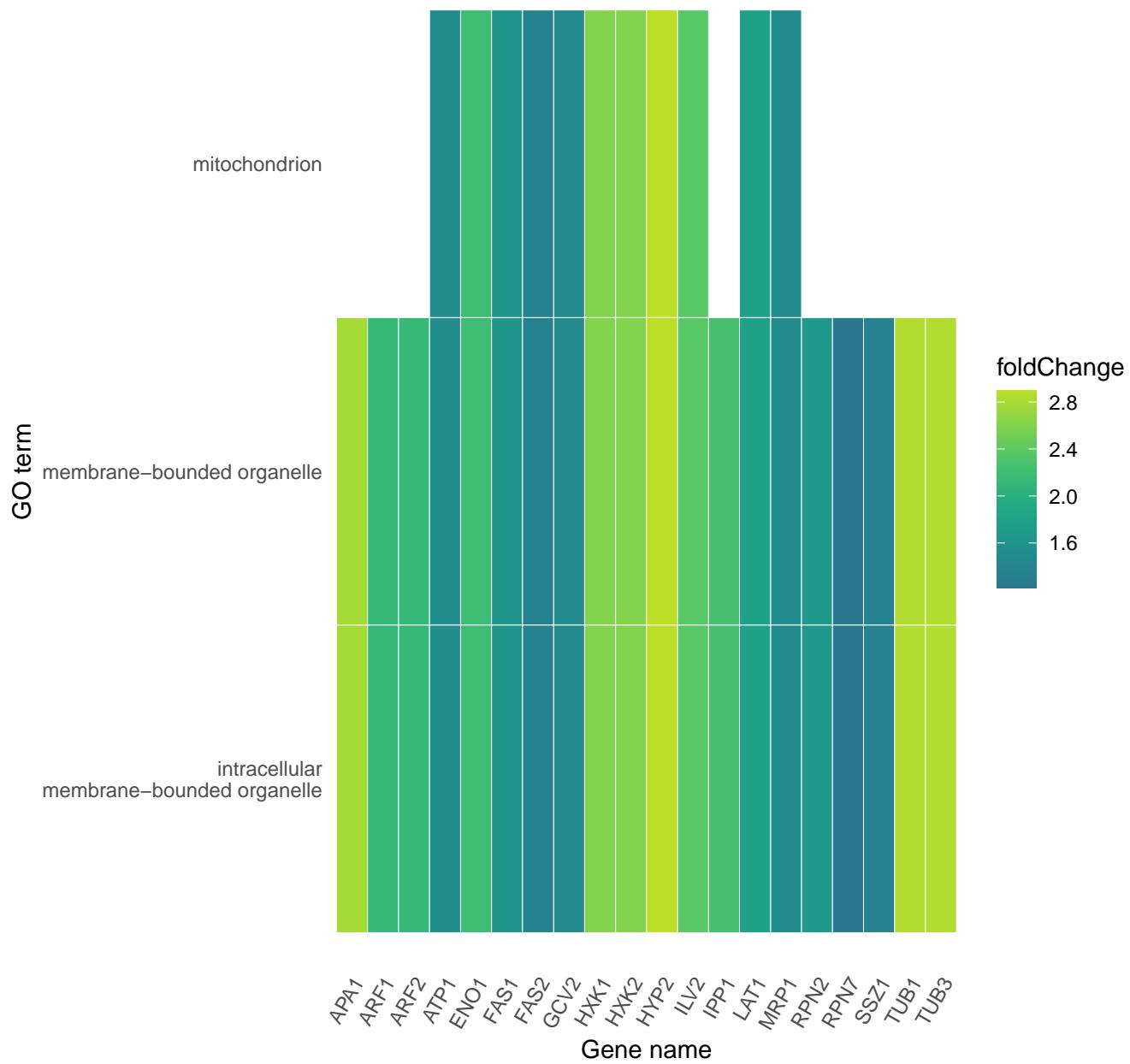
MEX67-TAP Up-regulated GO CC dotplot



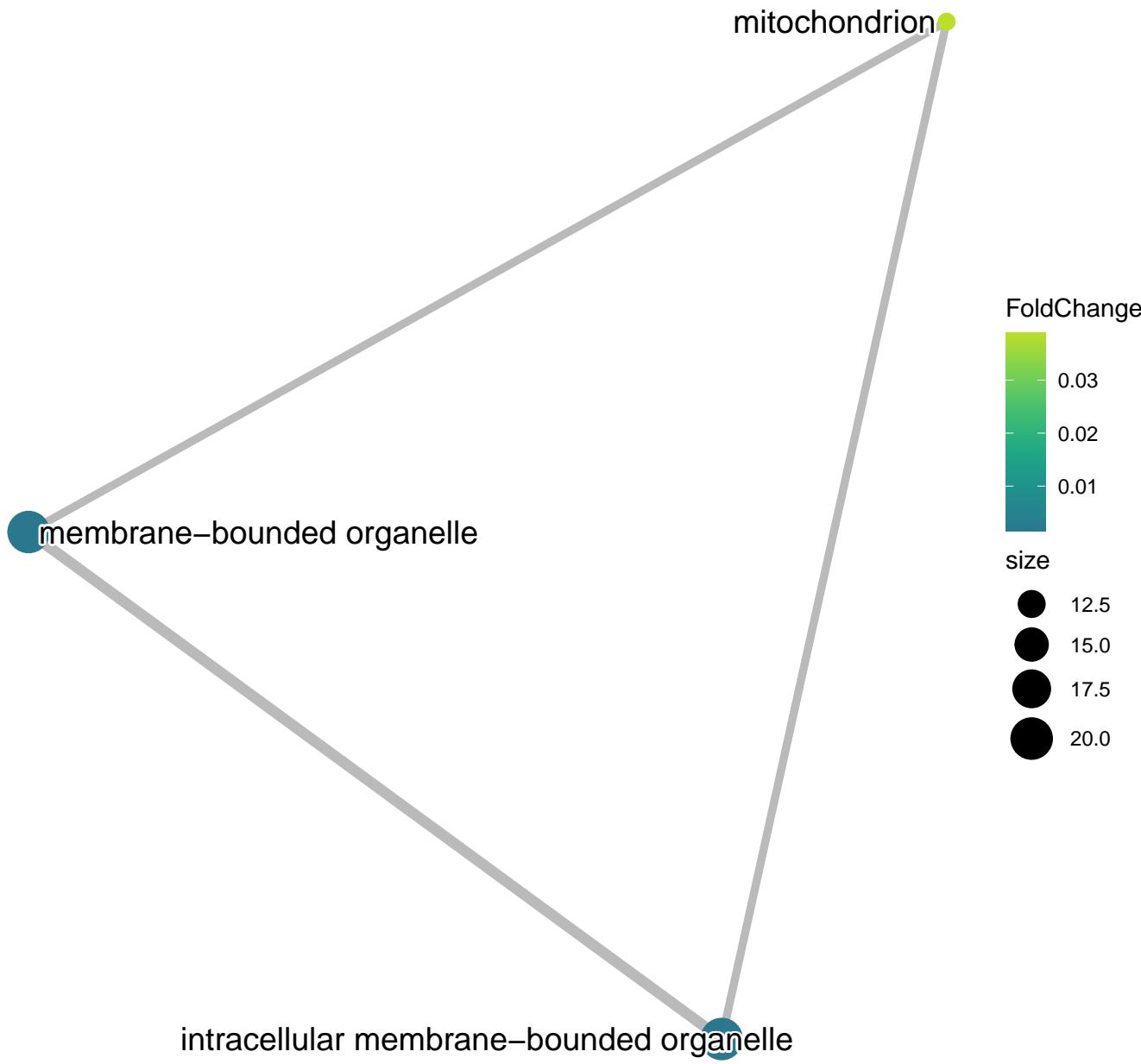
MEX67-TAP Up-regulated GO CC cnetplot

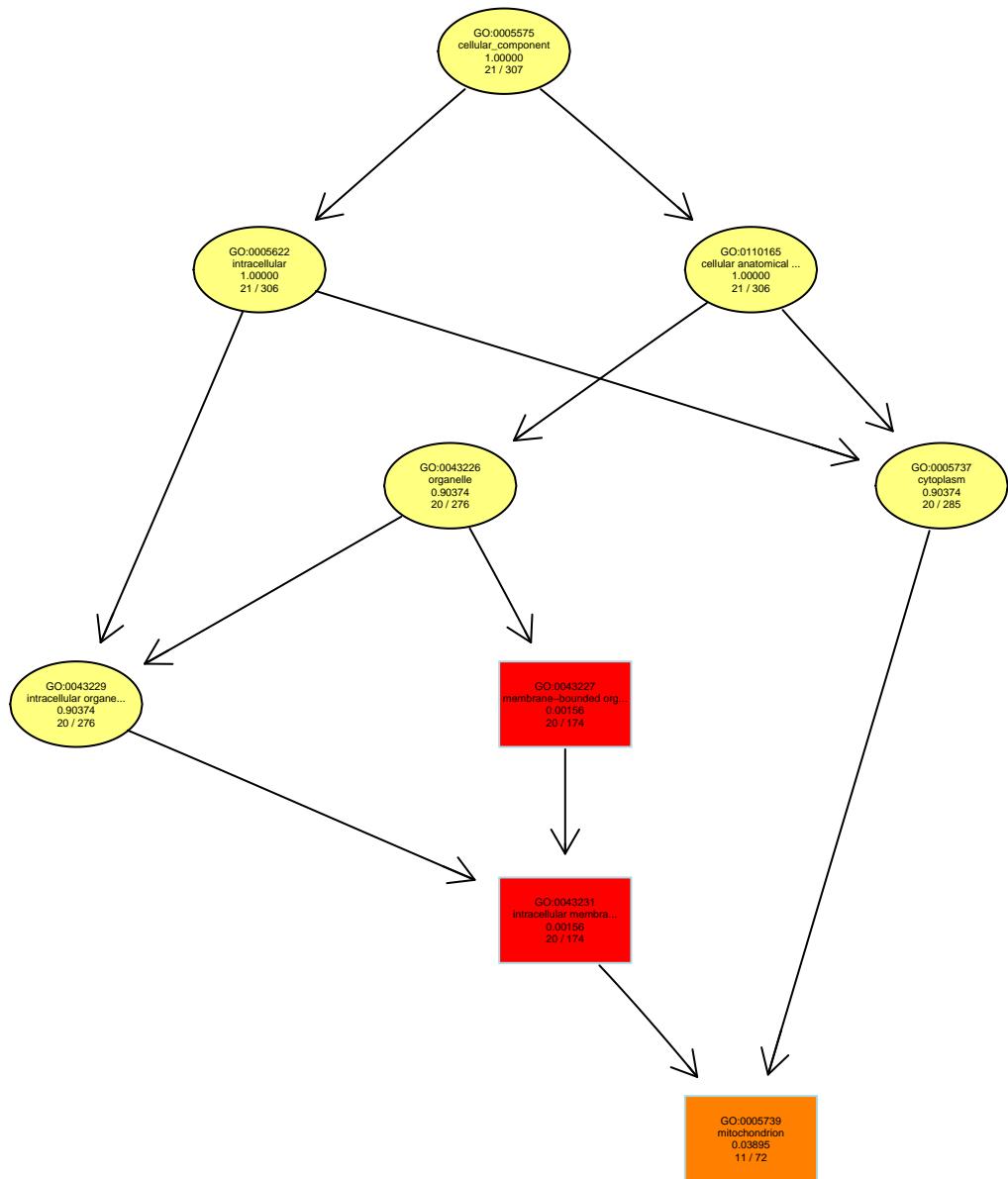


MEX67-TAP Up-regulated GO CC heatplot

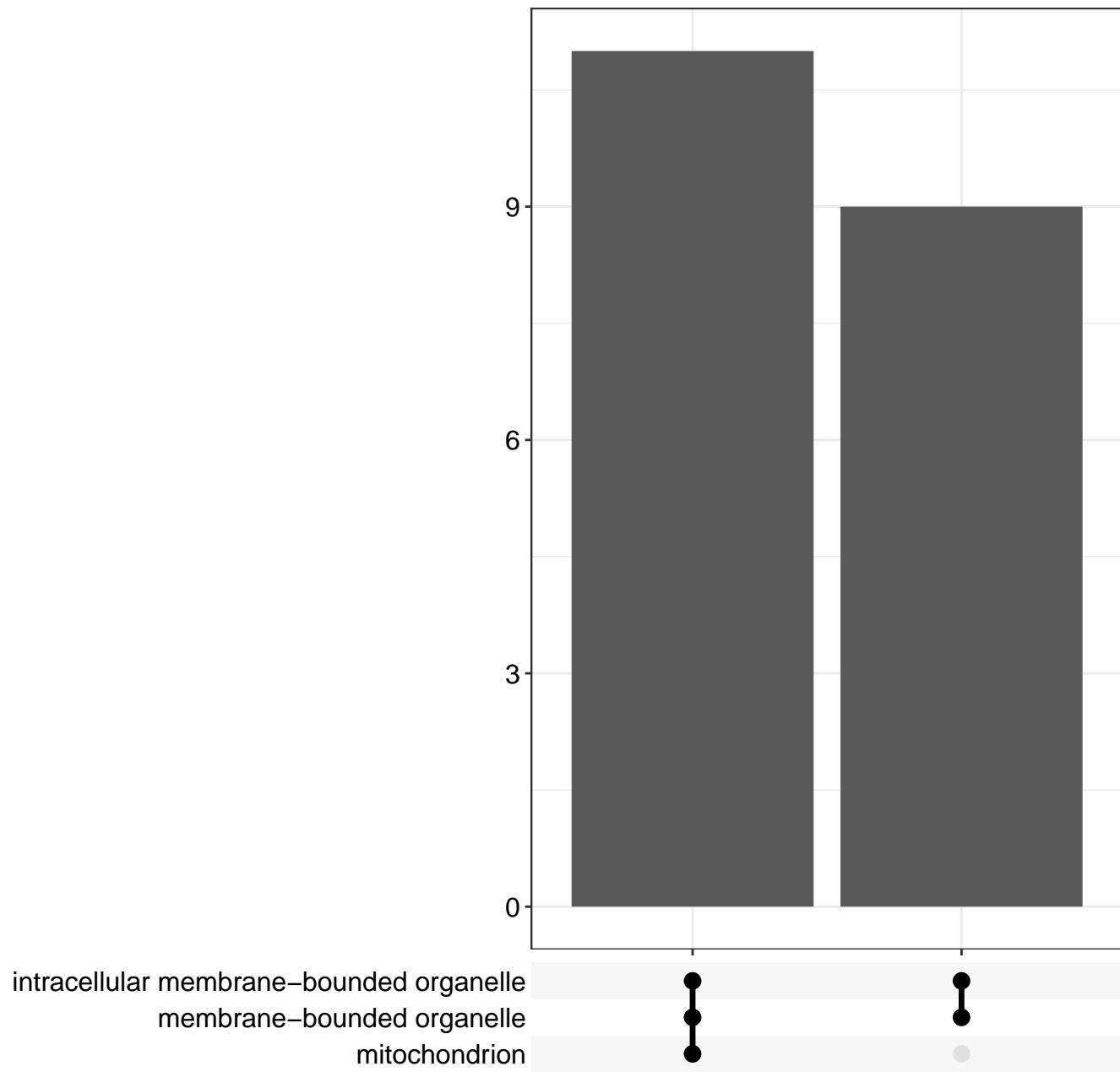


MEX67-TAP Up-regulated GO CC emapplot

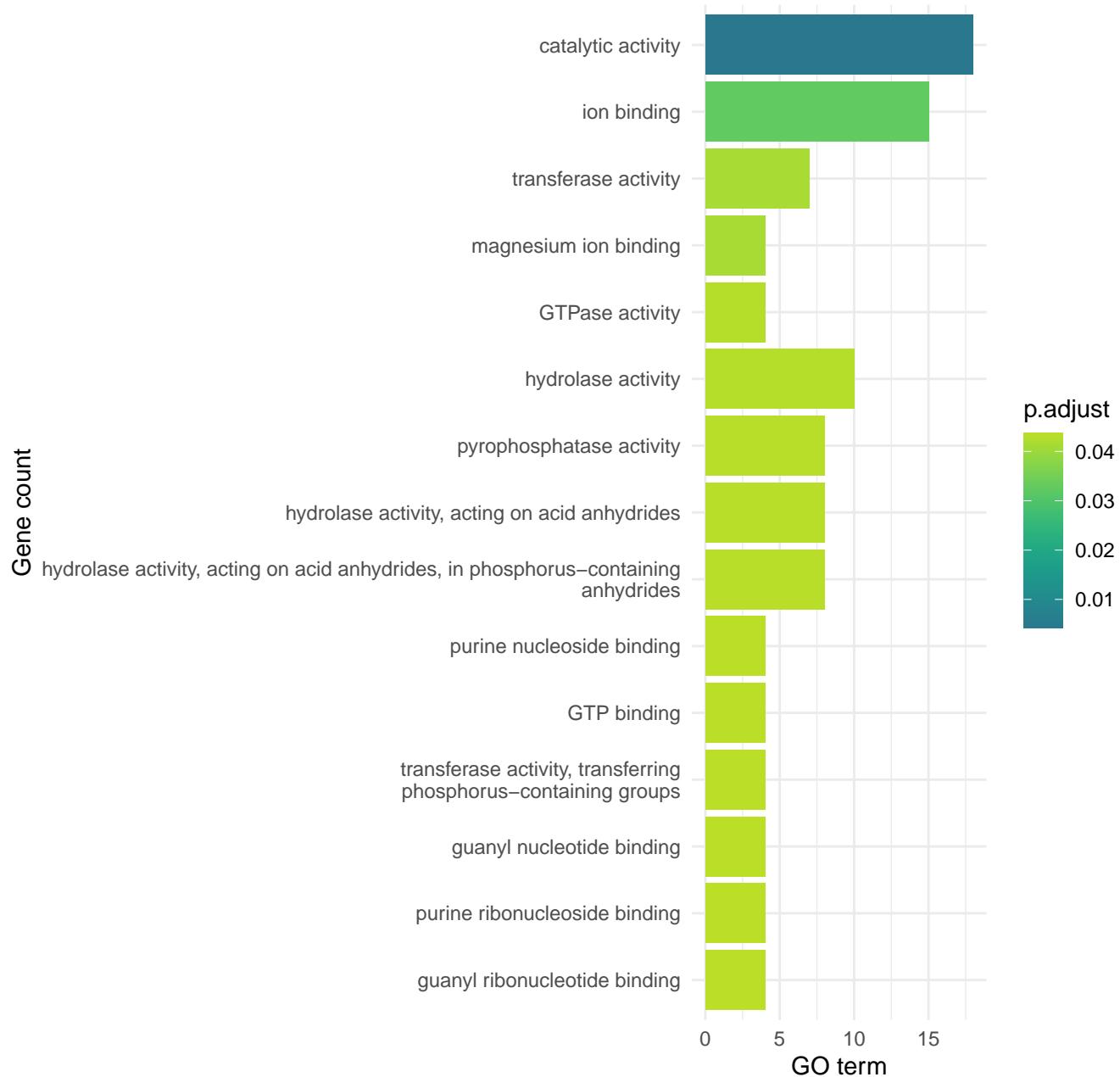




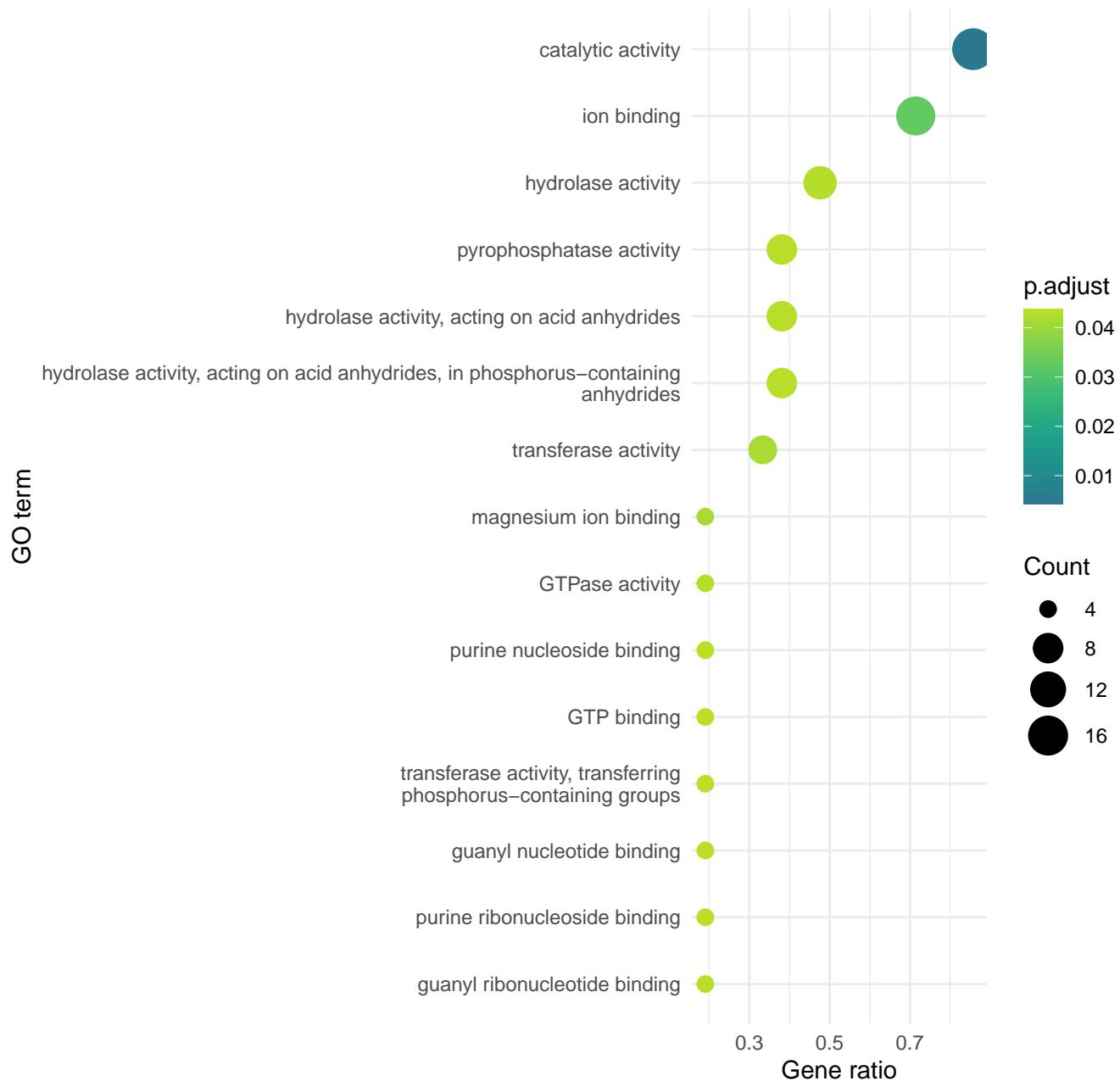
MEX67-TAP Up-regulated GO CC upsetplot



MEX67-TAP Up-regulated GO MF

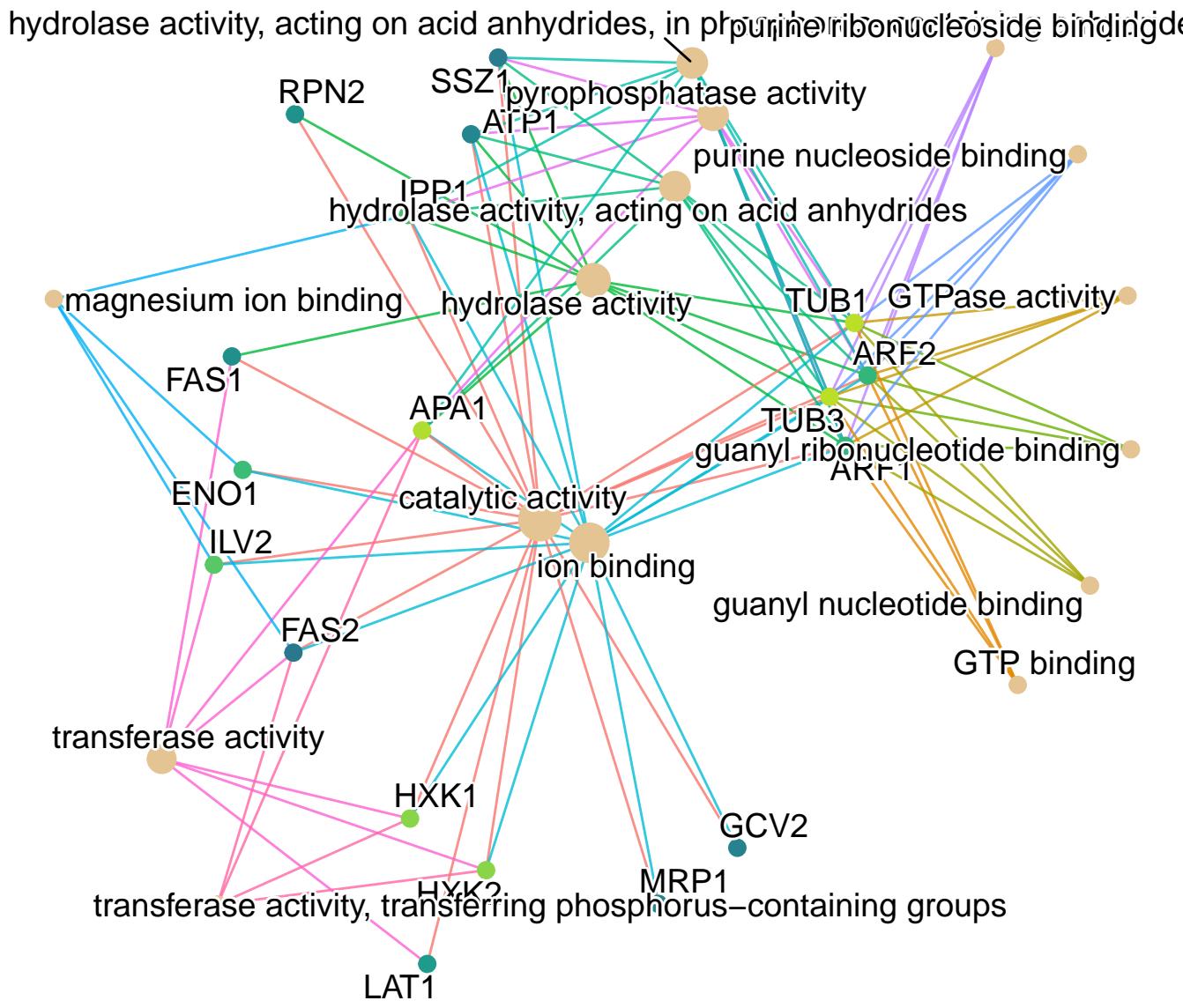


MEX67-TAP Up-regulated GO MF

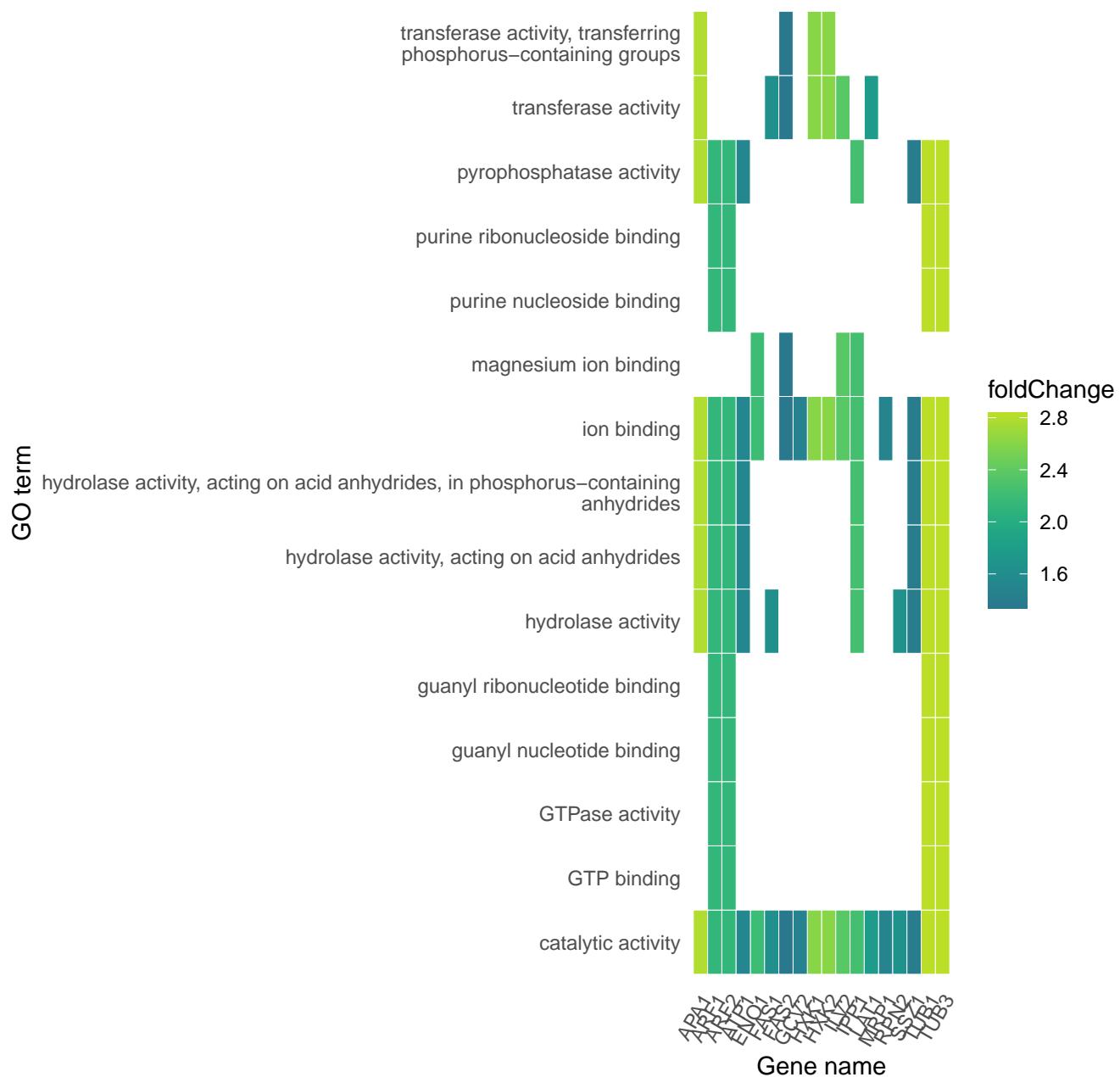


MEX67-TAP Up-regulated GO MF cnetplot

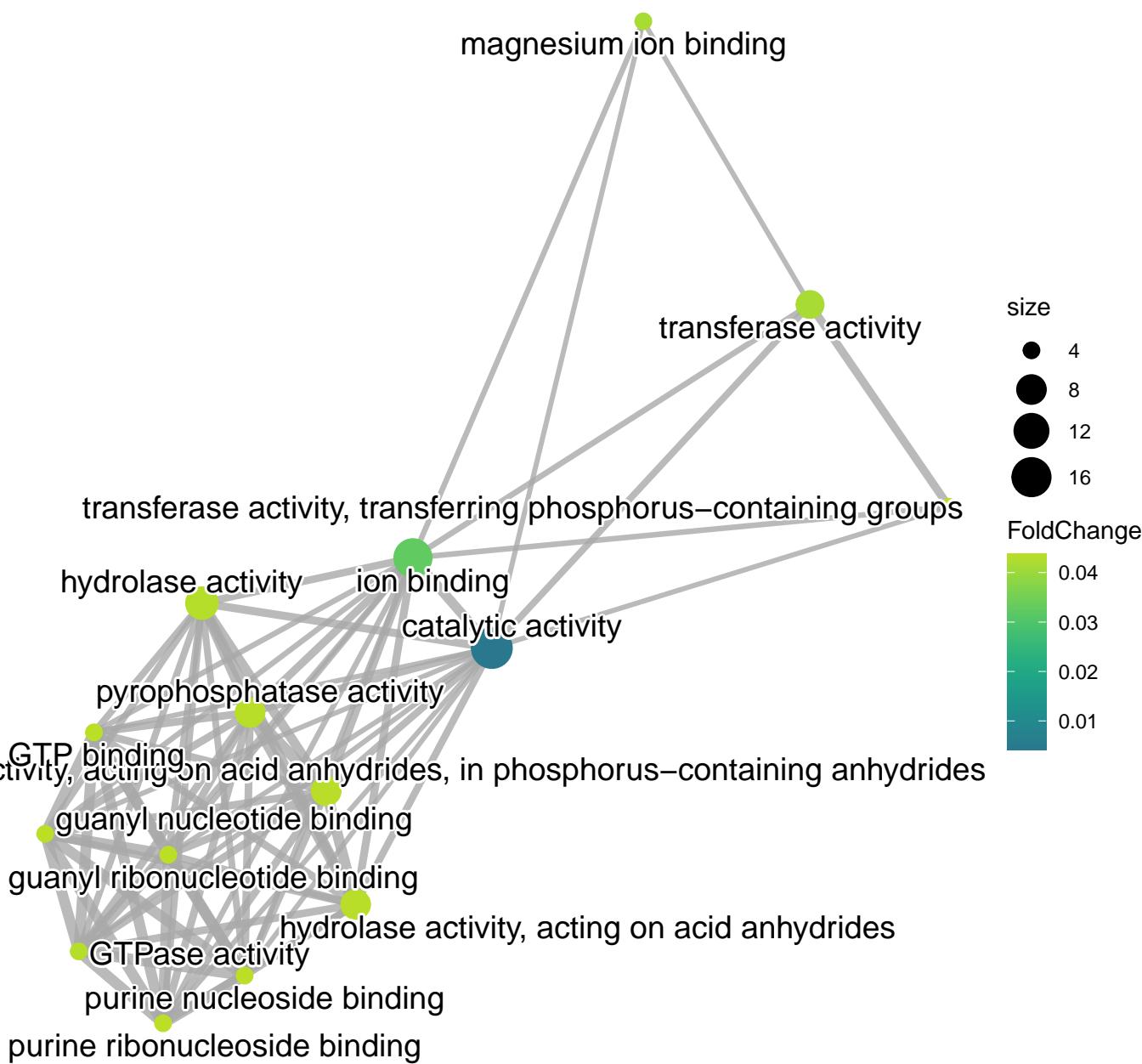
hydrides
hydrides, in phosphorus-containing anhydrides
magnesium ion binding
purine nucleoside binding
purine ribonucleoside binding
pyrophosphatase activity
transferase activity
transferase activity, transferring phosphorus-containing groups

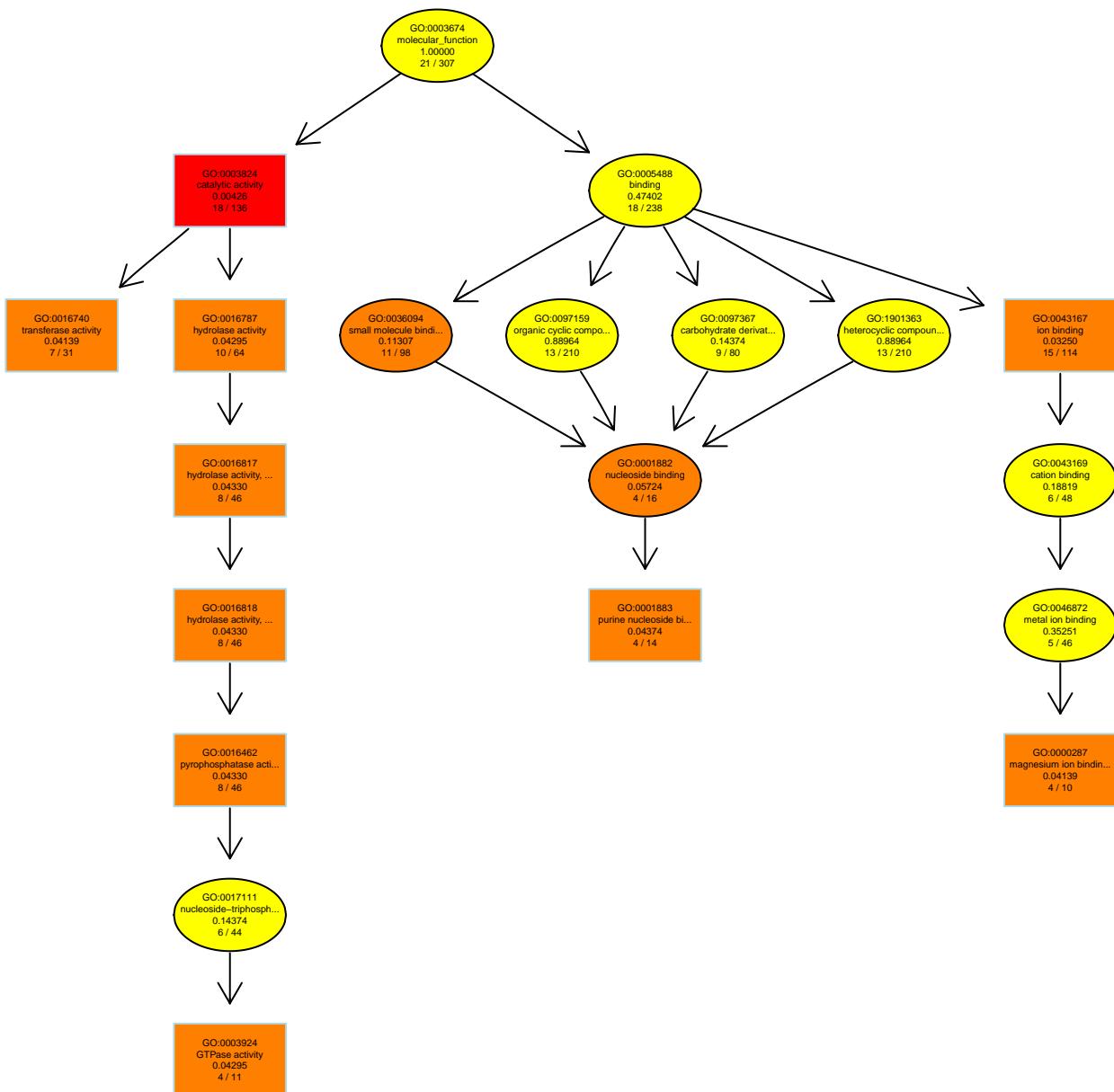


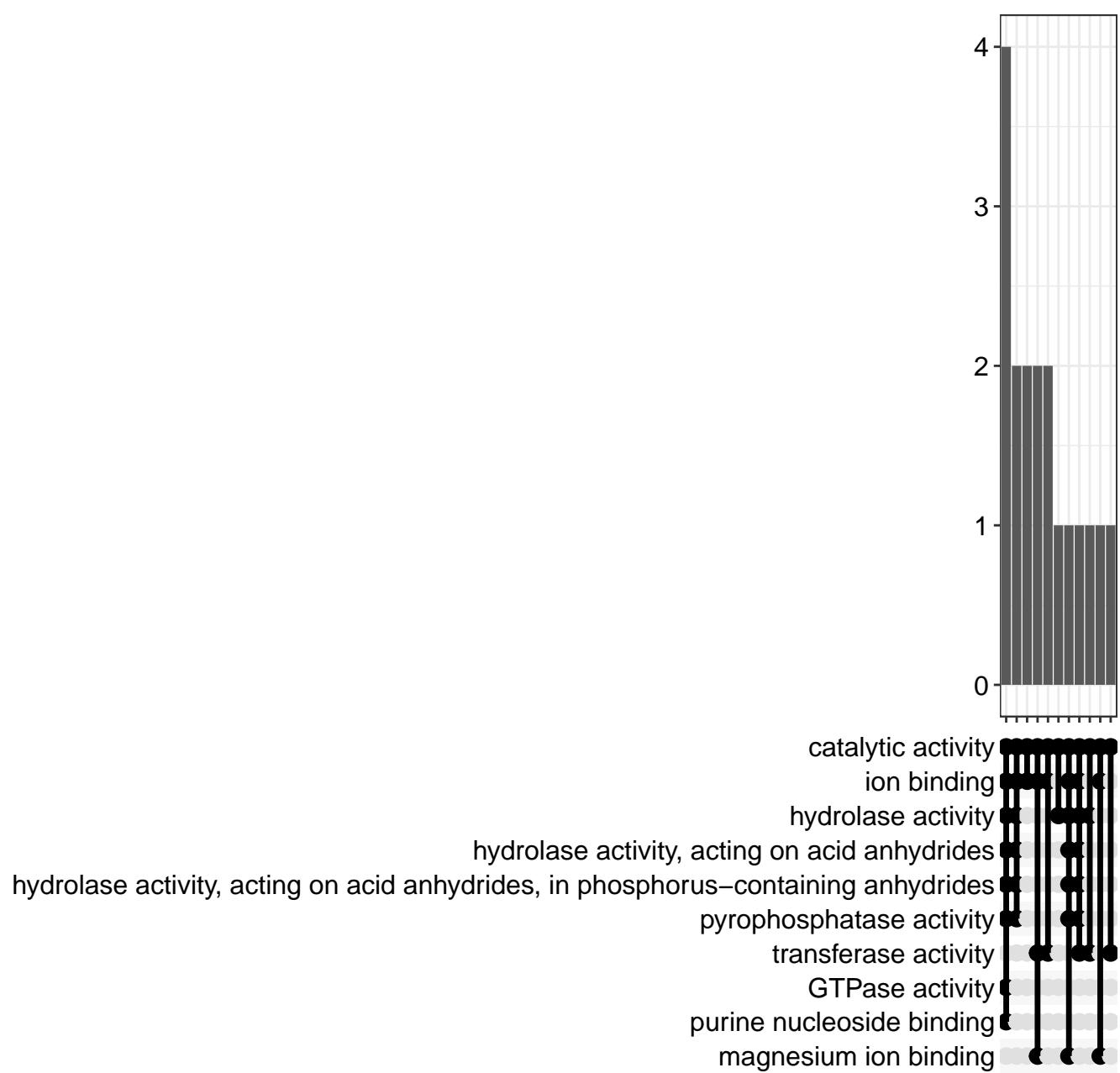
MEX67-TAP Up-regulated GO MF



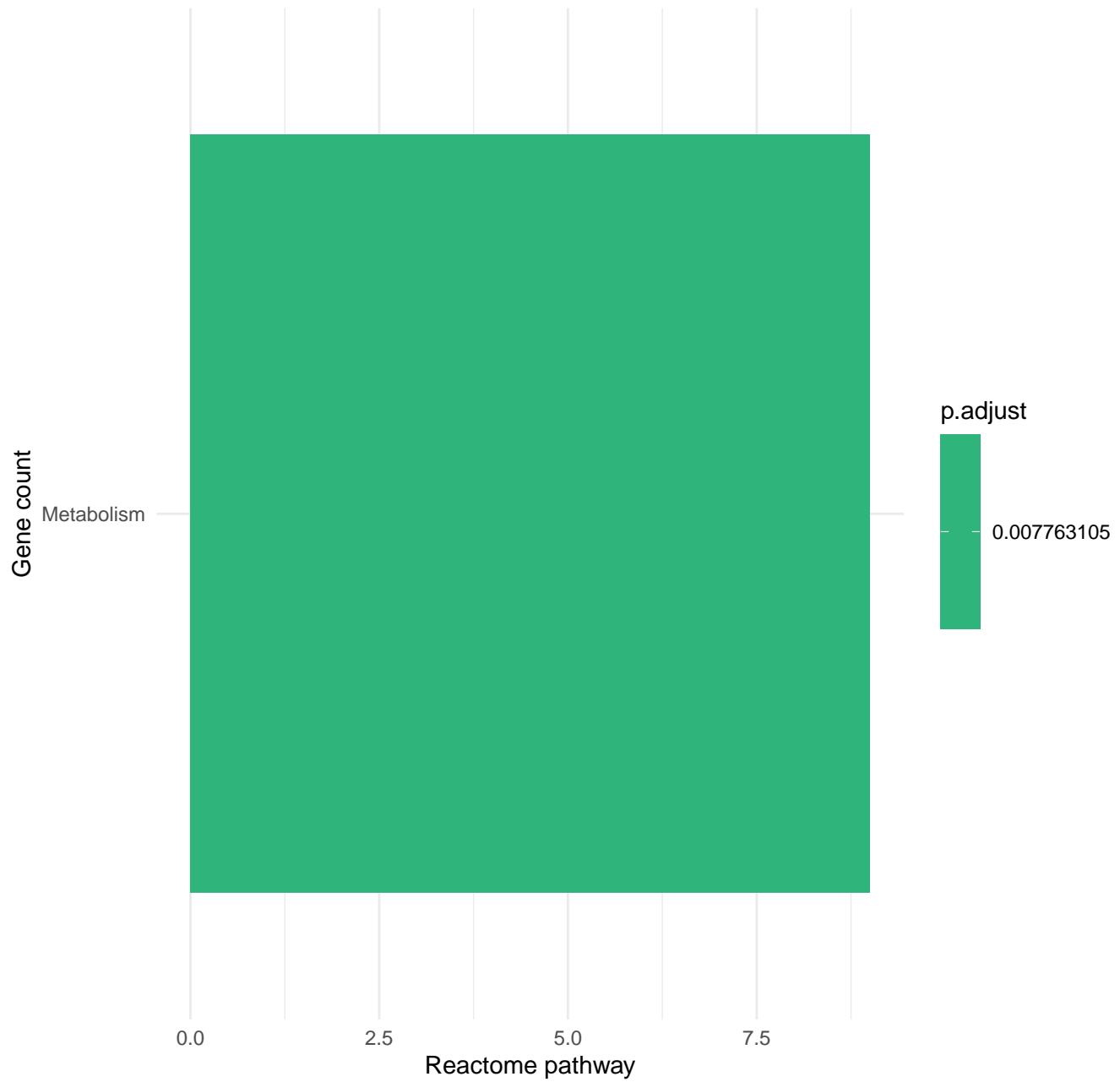
MEX67-TAP Up-regulated GO MF emapplot



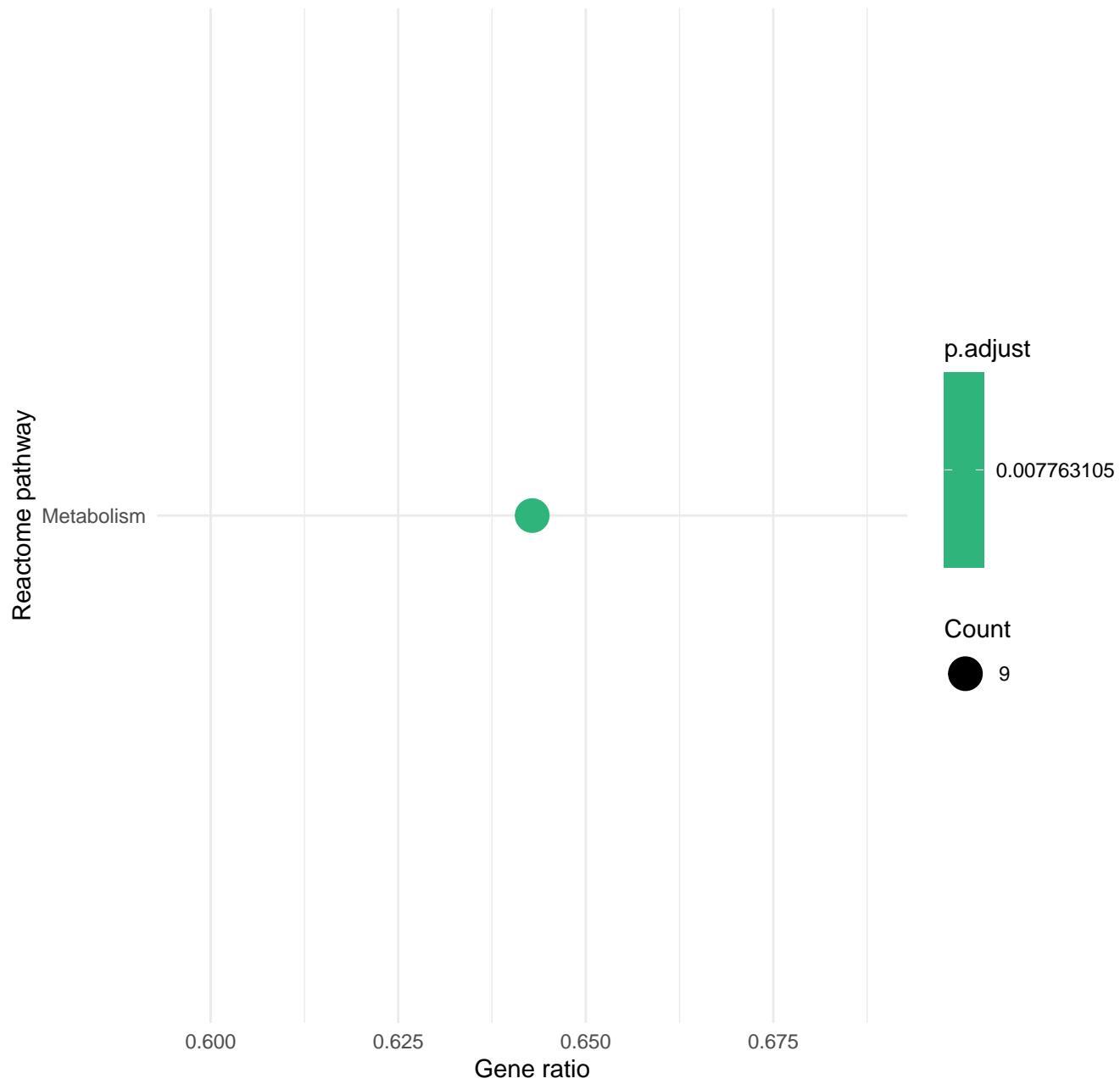




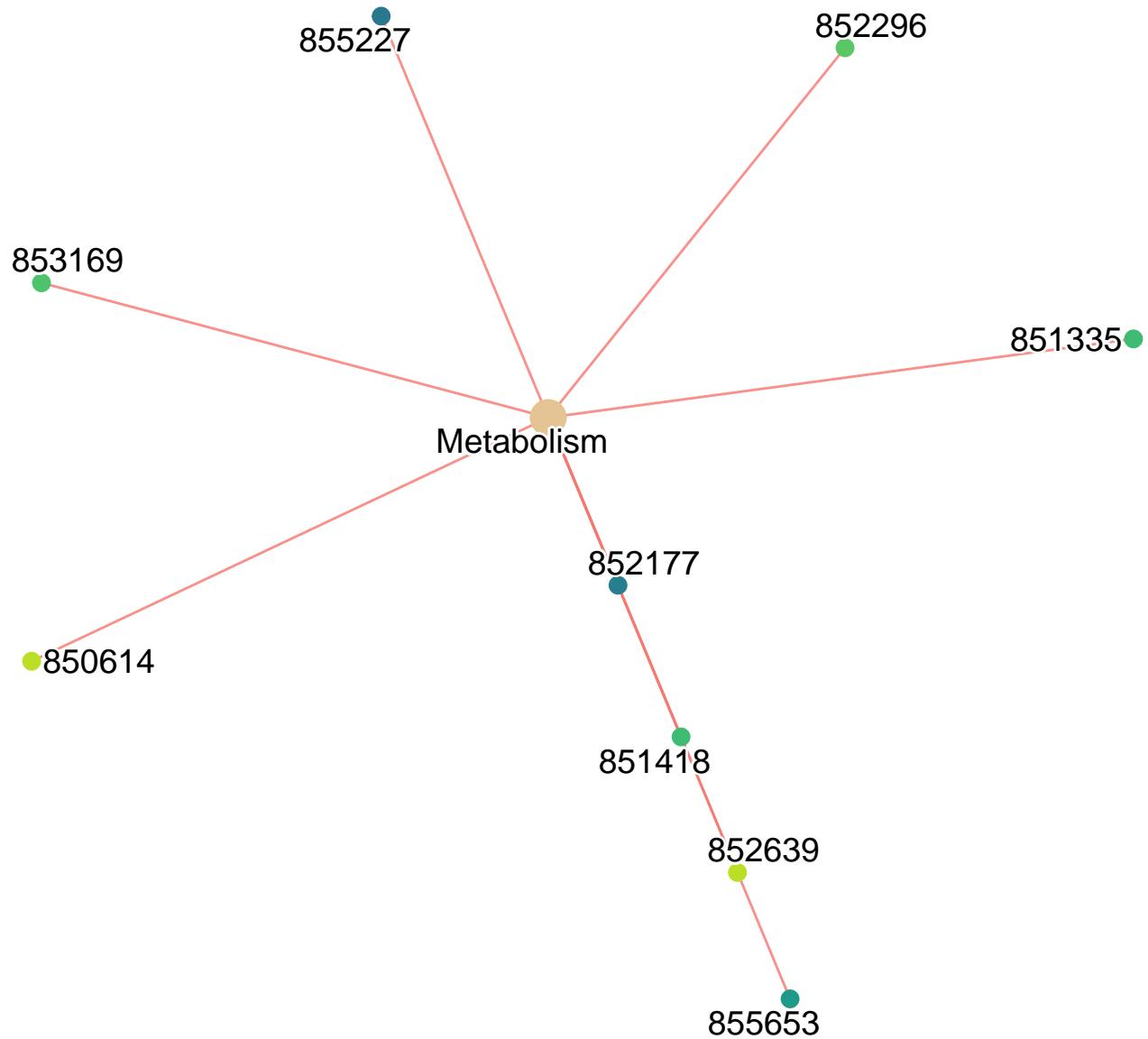
MEX67-TAP Up-regulated Reactome barplot



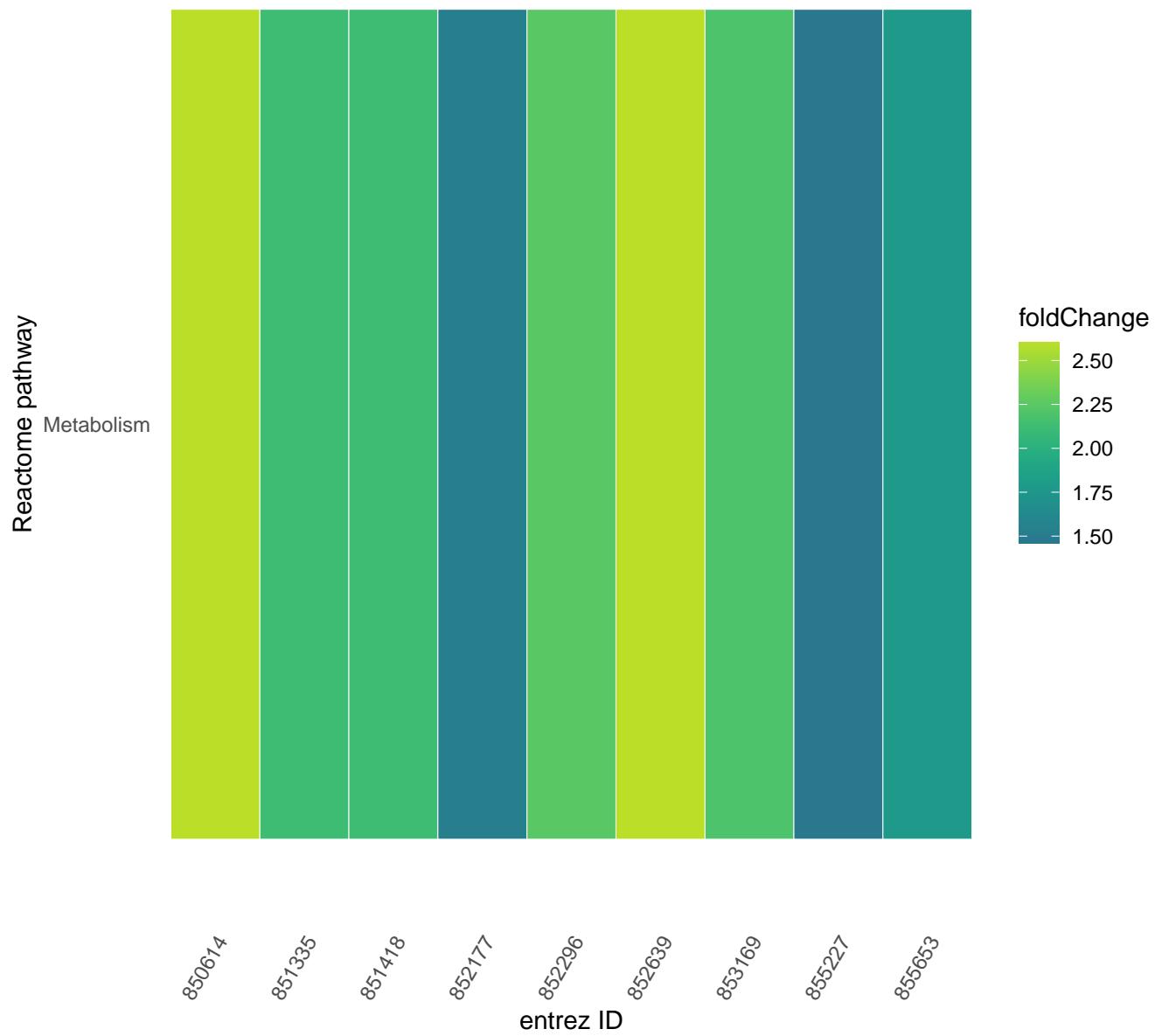
MEX67-TAP Up-regulated Reactome dotplot



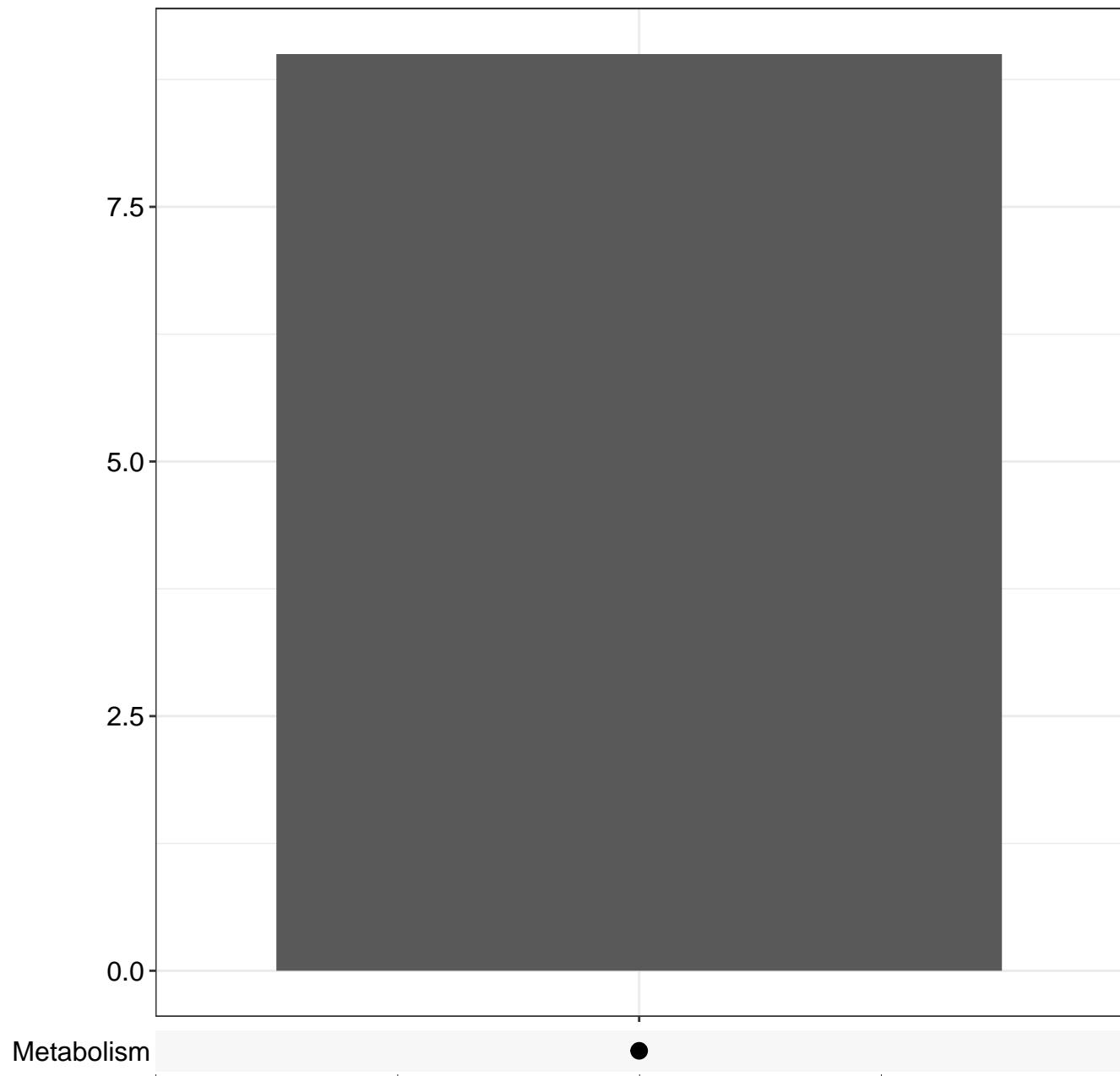
MEX67-TAP Up-regulated Reactome cnetplot



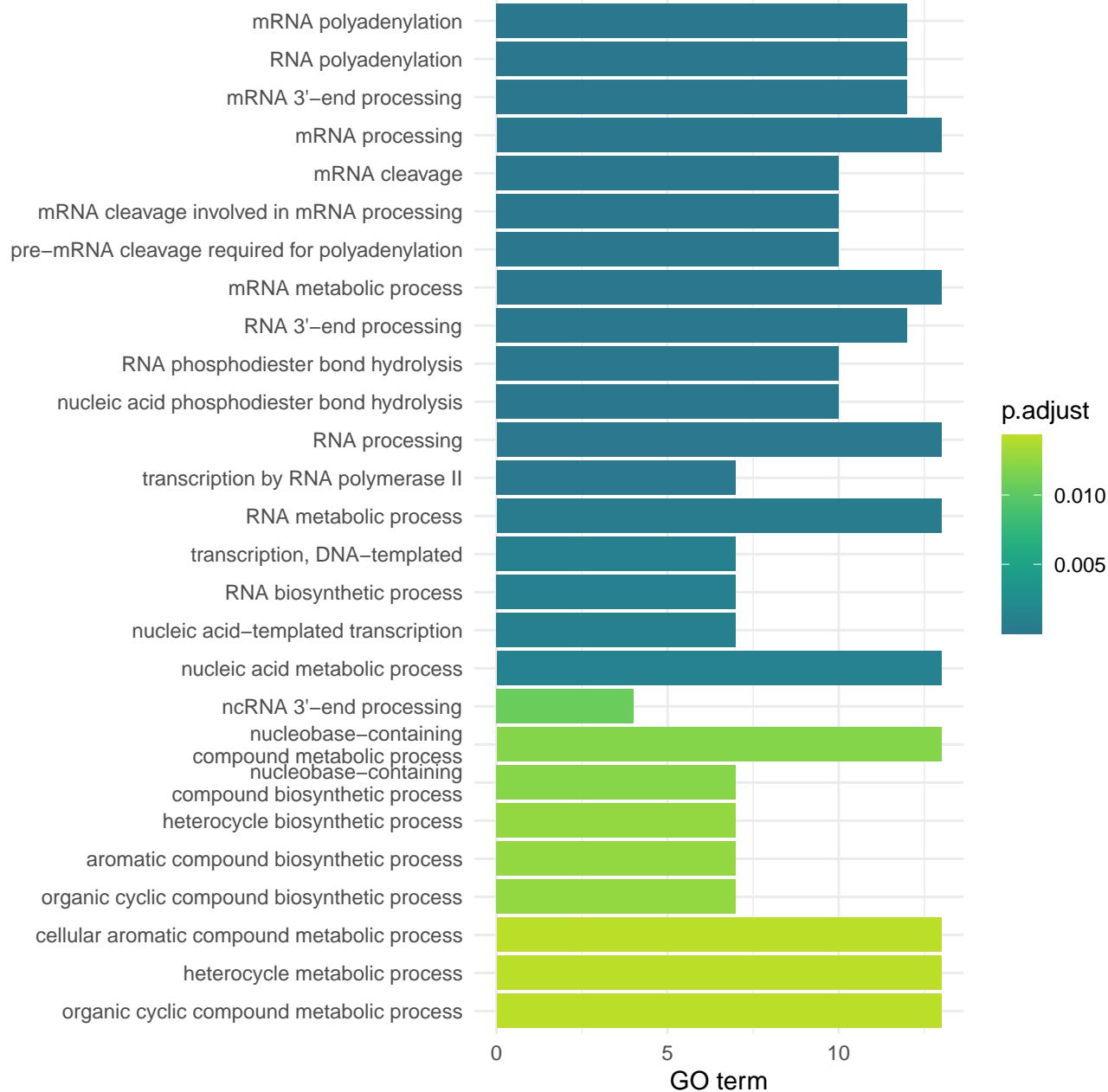
MEX67-TAP Up-regulated Reactome heatplot



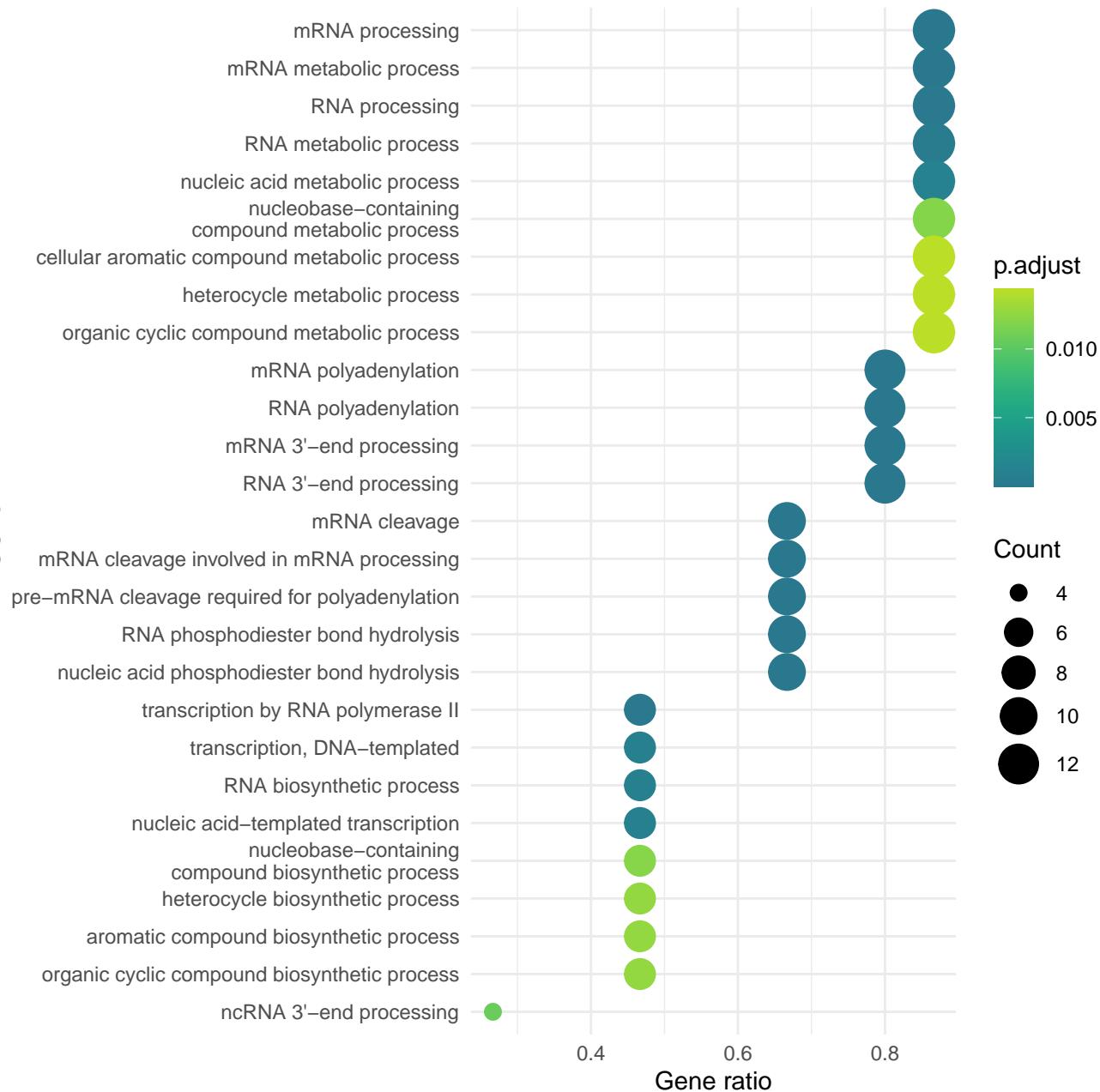
MEX67-TAP Up-regulated Reactome upsetplot



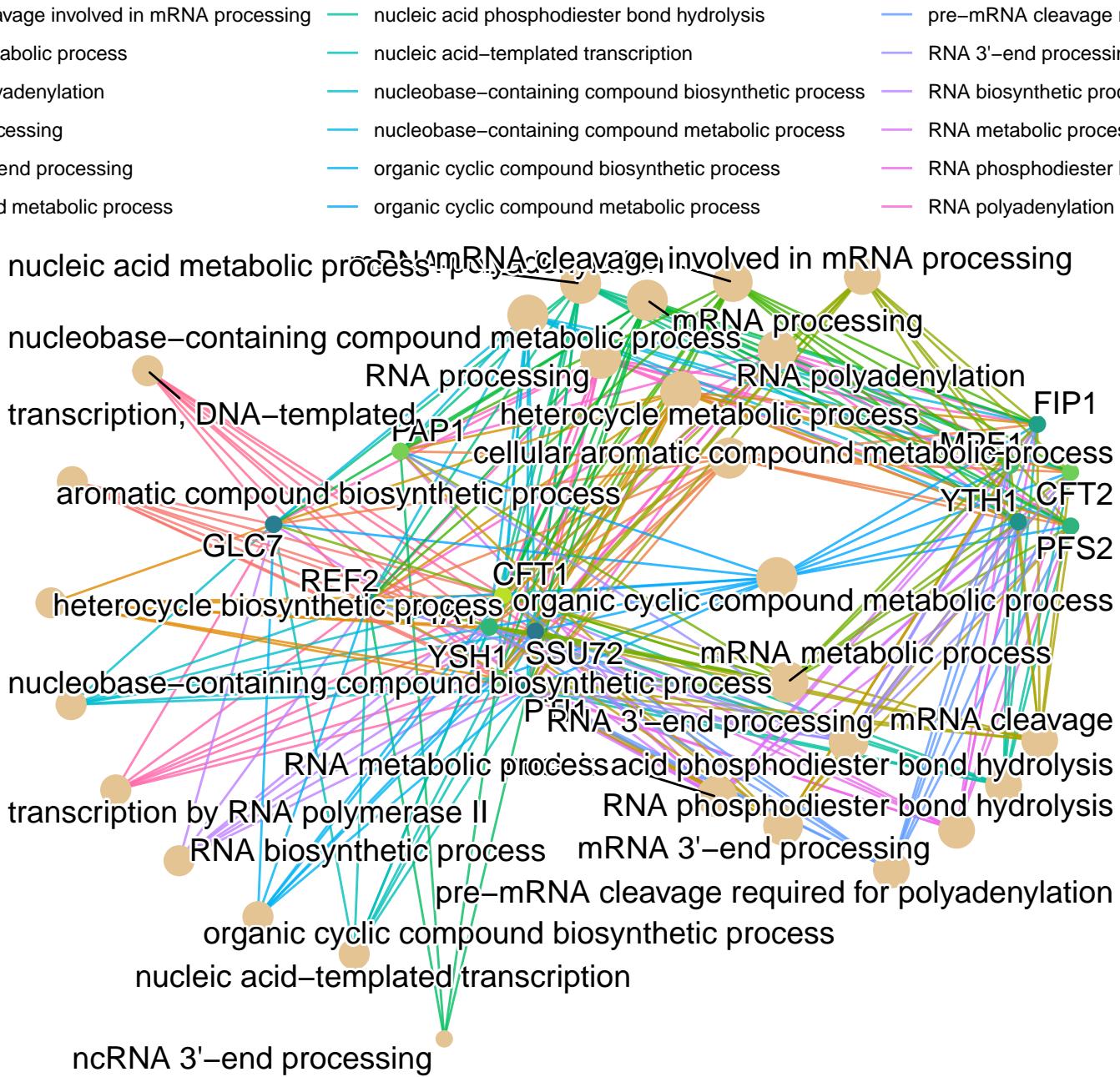
CFT1-TAP Up-regulated GO BP barplot



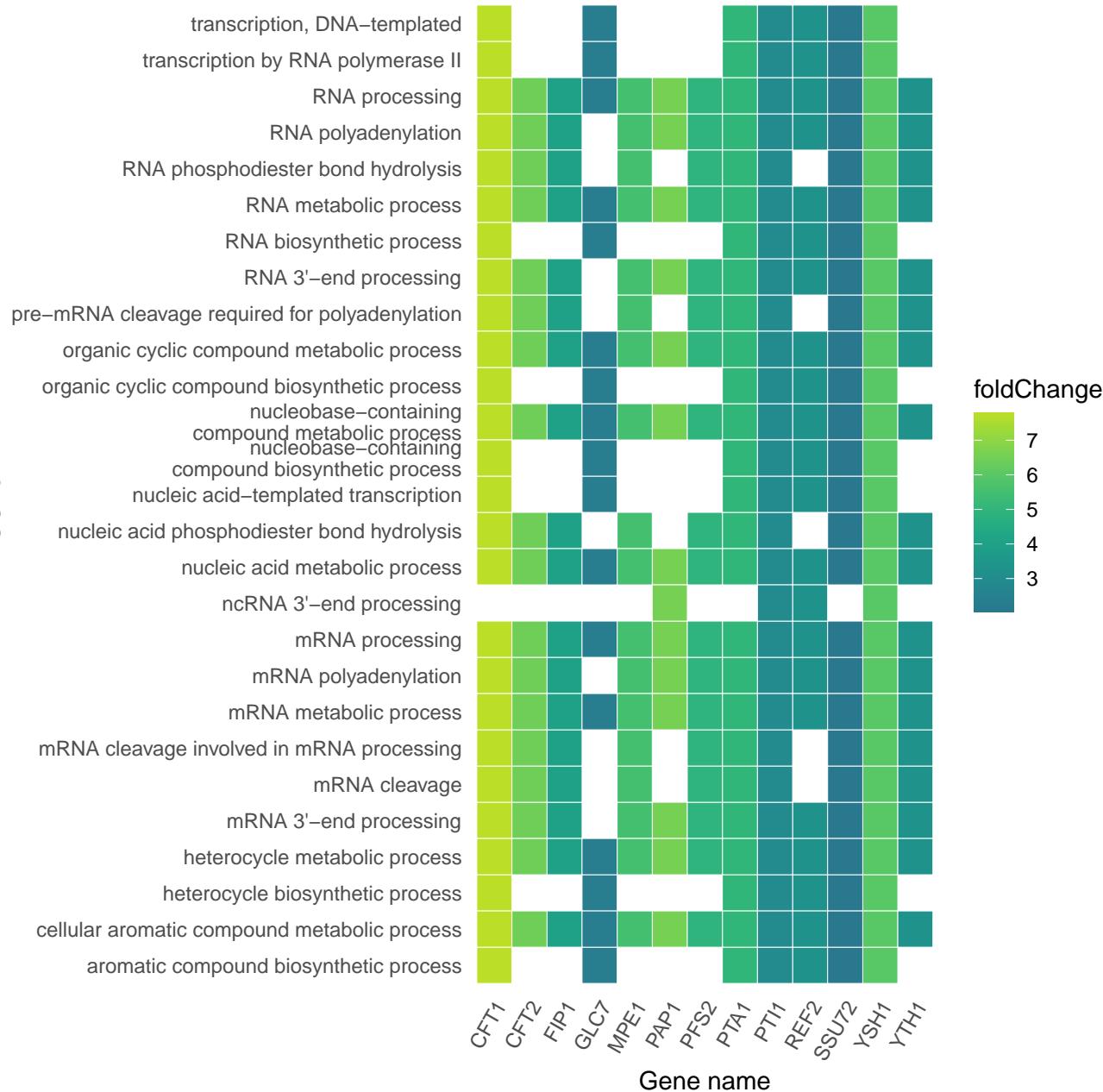
CFT1-TAP Up-regulated GO BP dotplot



CFT1-TAP Up-regulated GO BP cnetplot



CFT1-TAP Up-regulated GO BP heatplot



CFT1-TAP Up-regulated GO BP emapplot

RNA metabolic process

ncRNA 3'-end processing

nucleobase-containing compound metabolic process

nucleobase-containing compound biosynthetic process

organic cyclic compound metabolic process

nucleic acid phosphodiester bond hydrolysis

RNA biosynthetic process

cellular aromatic compound metabolic process

heterocycle metabolic process

RNA polyadenylation

organic cyclic compound biosynthetic process

phosphodiester bond hydrolysis

nucleic acid metabolic process

mRNA metabolic process

transcription, DNA-templated

mRNA cleavage

nucleic acid-templated transcription

mRNA 3'-end processing

RNA processing

mRNA cleavage involved in mRNA processing

aromatic compound biosynthetic process

mRNA processing

pre-mRNA cleavage required for polyadenylation

heterocycle biosynthetic process

transcription by RNA polymerase II

FoldChange

0.010

0.005

size

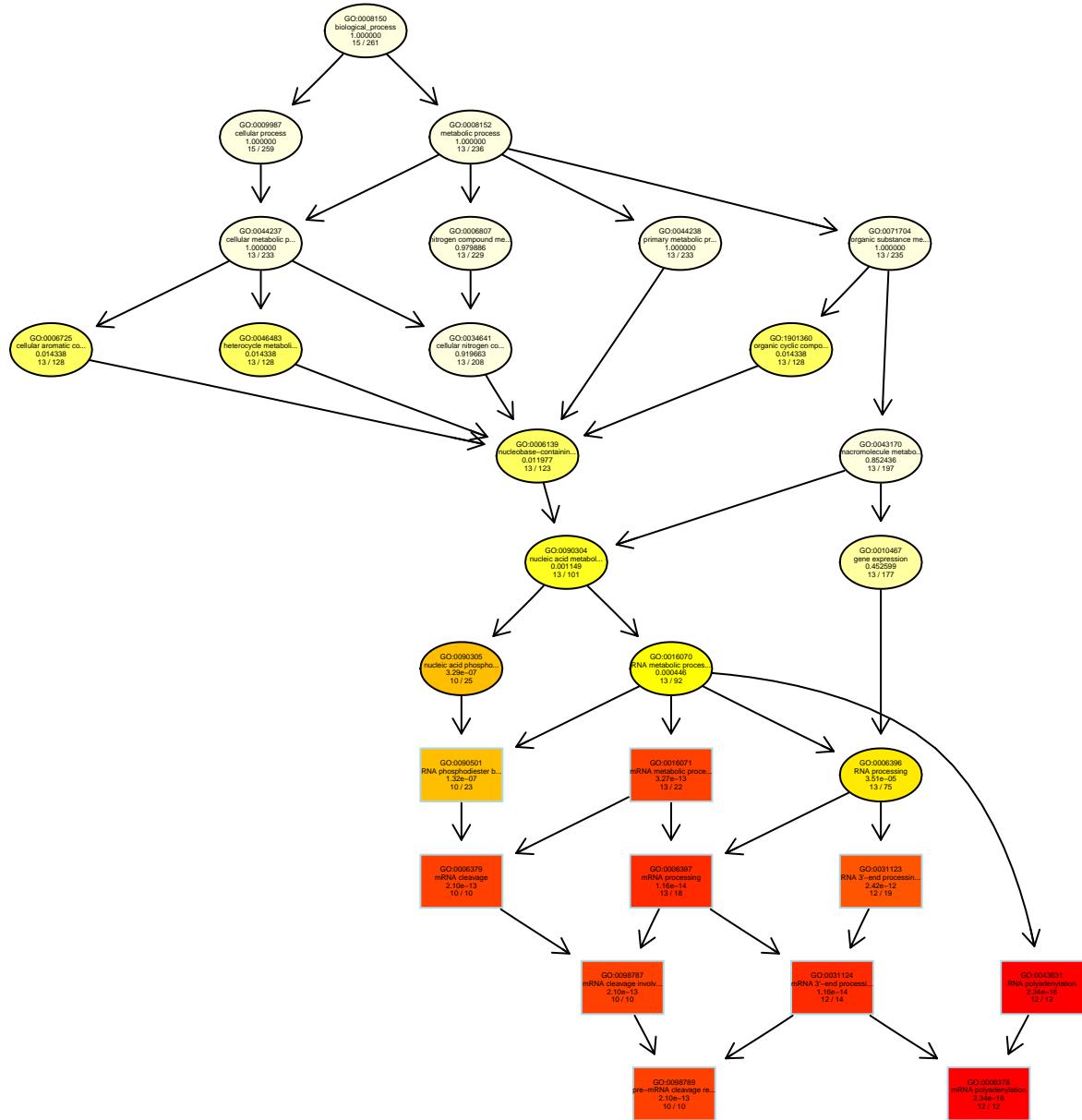
4

6

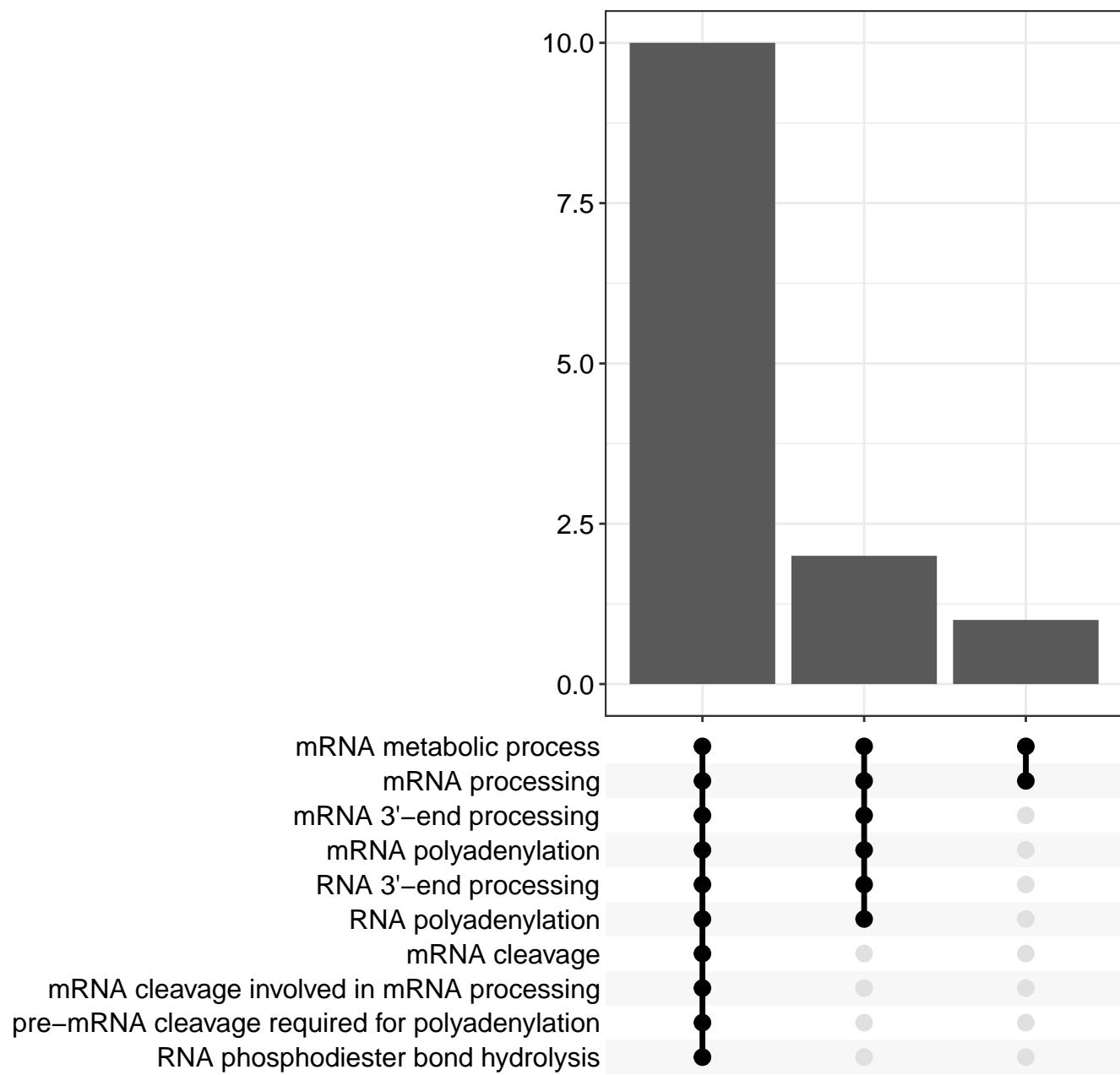
8

10

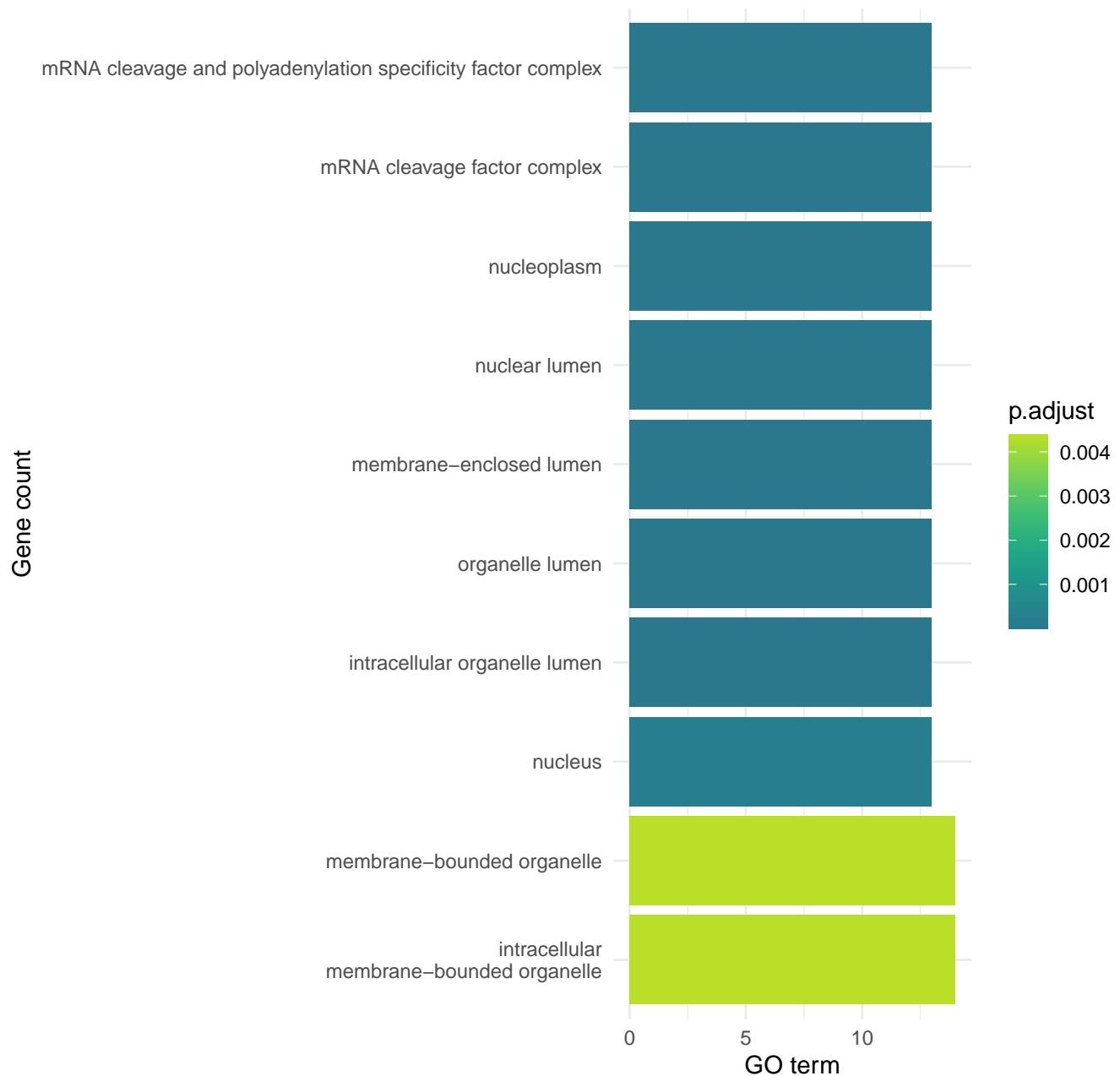
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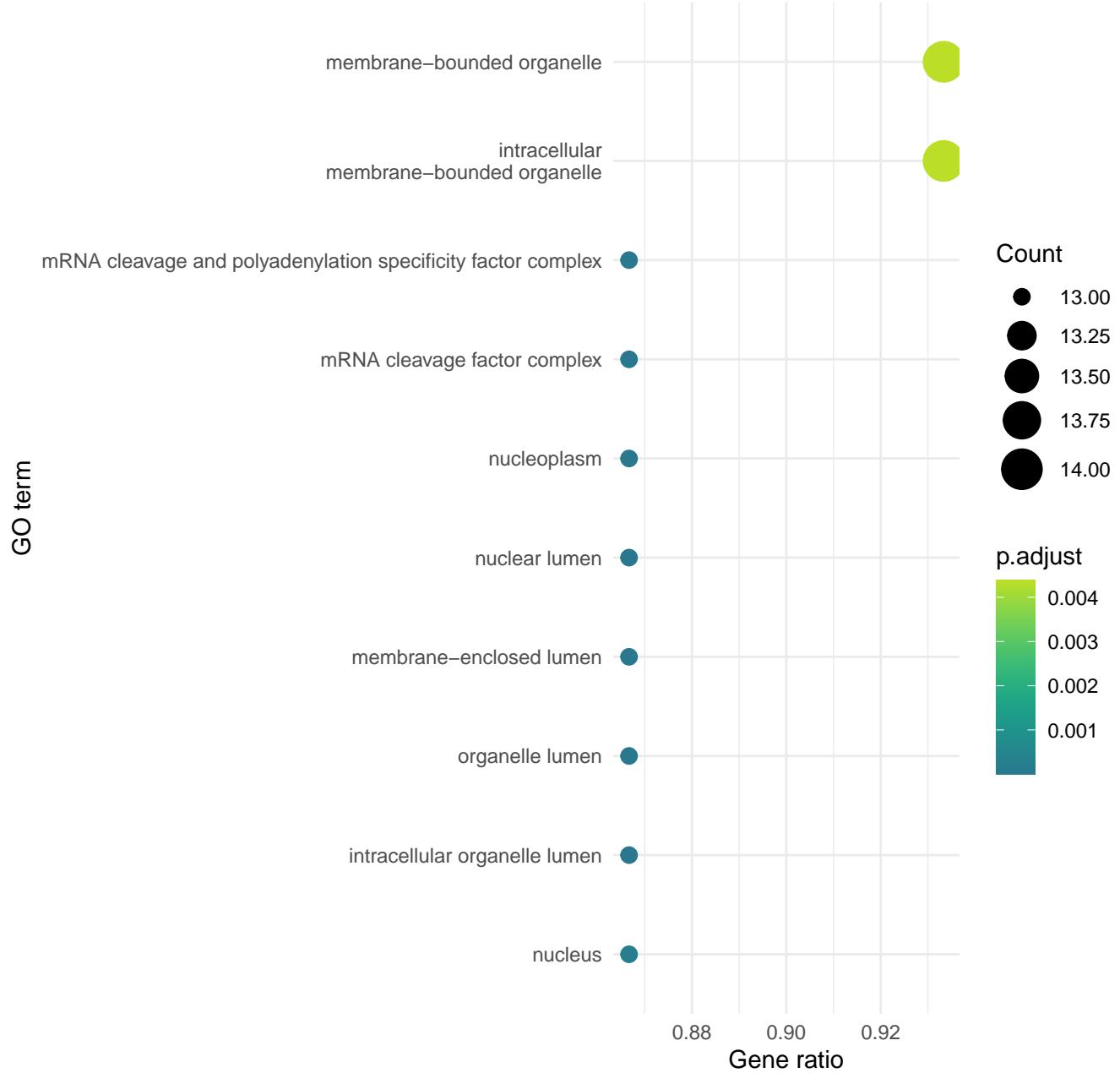
CFT1-TAP Up-regulated GO BP upsets



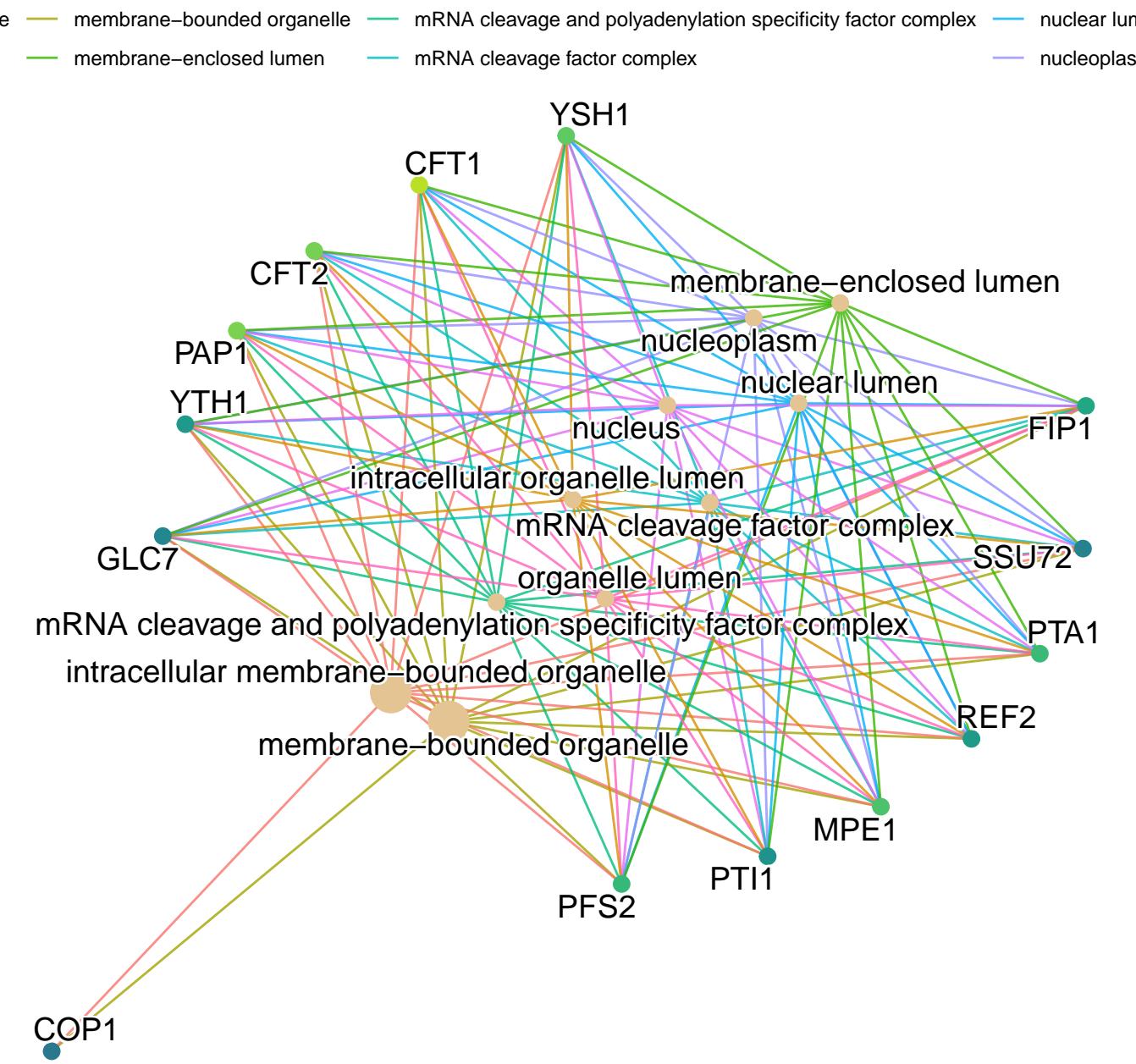
CFT1-TAP Up-regulated GO CC barplot



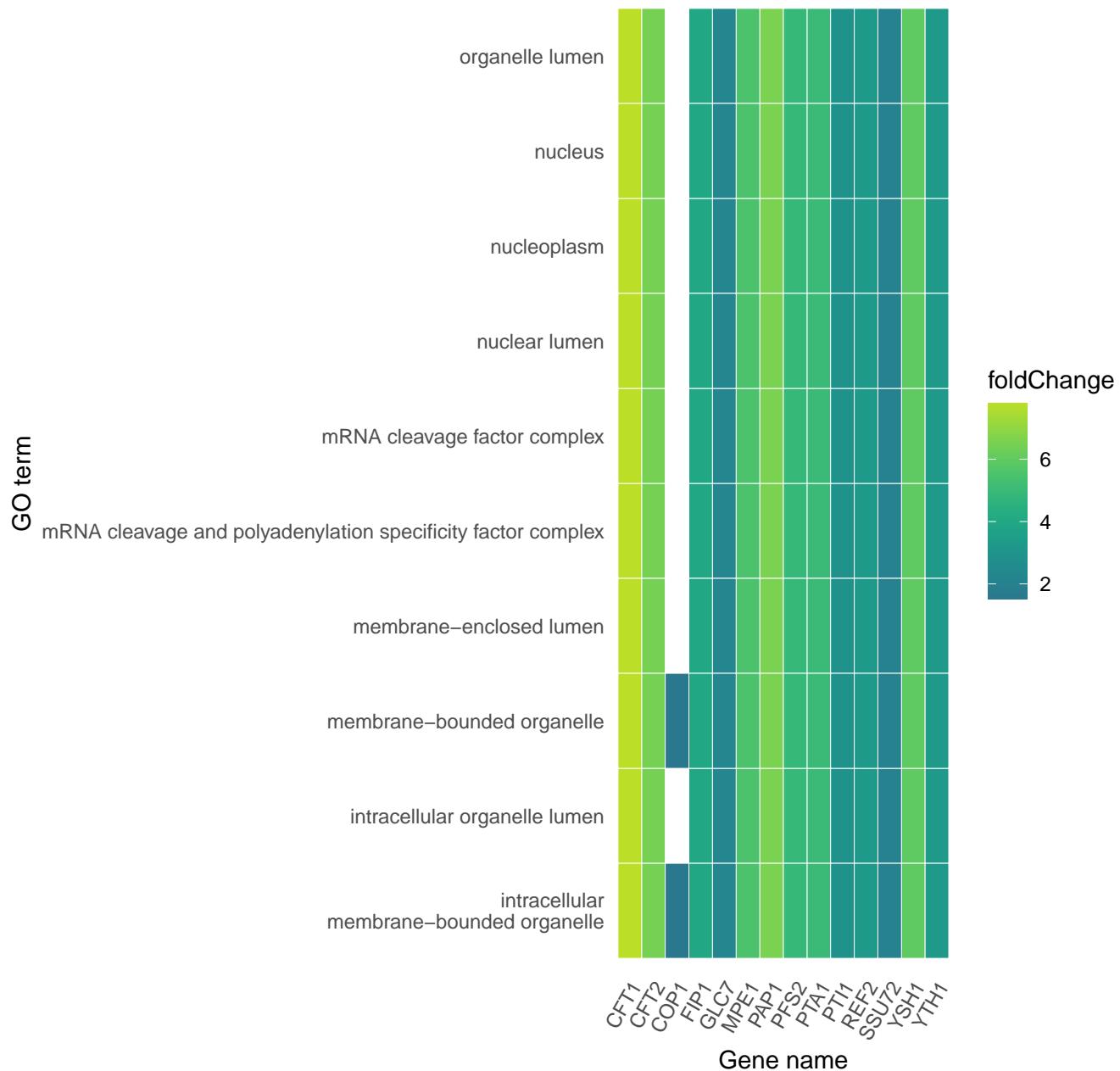
CFT1-TAP Up-regulated GO CC dotplot



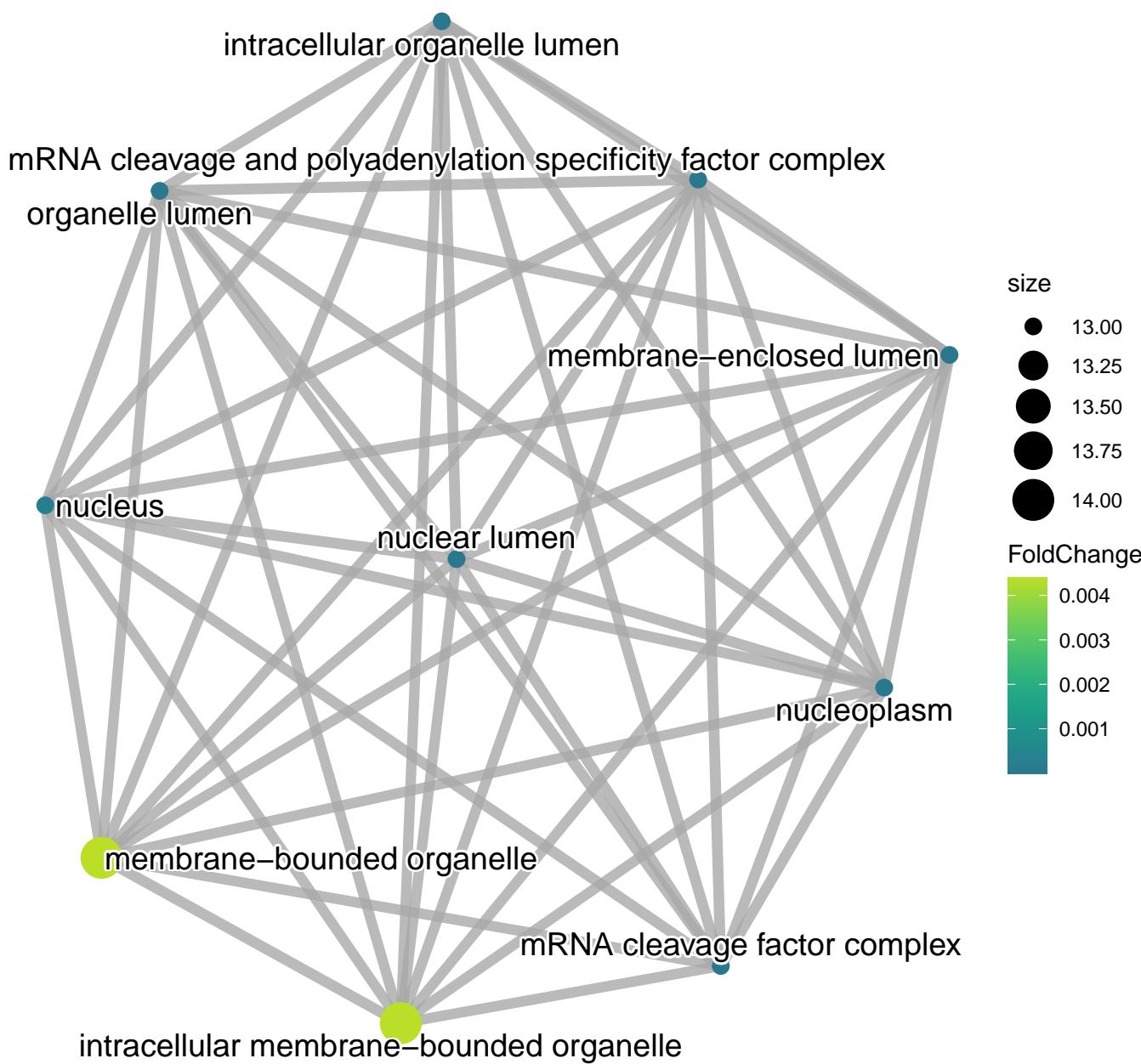
CFT1-TAP Up-regulated GO CC cnetplot

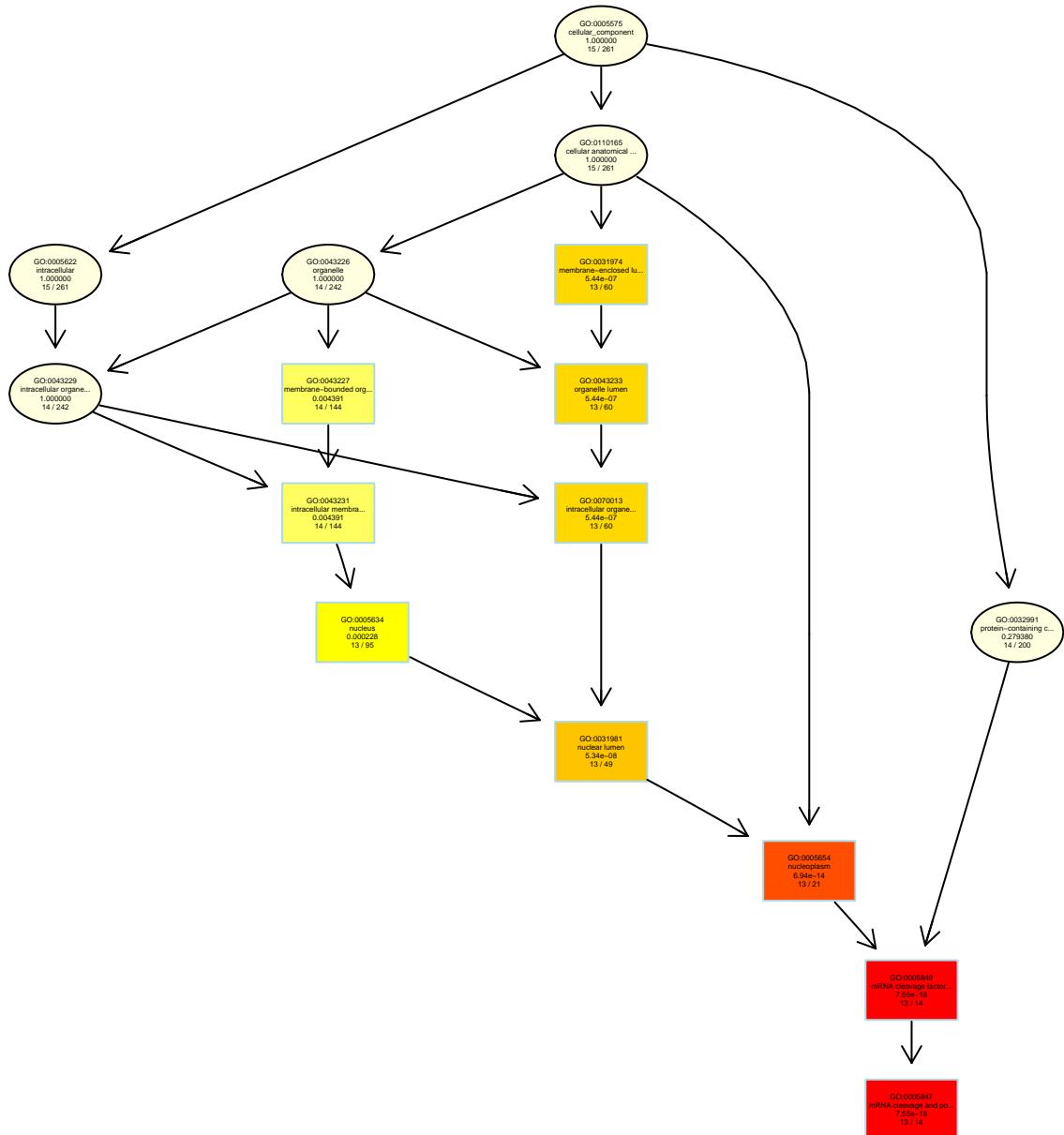


CFT1-TAP Up-regulated GO CC heatmap

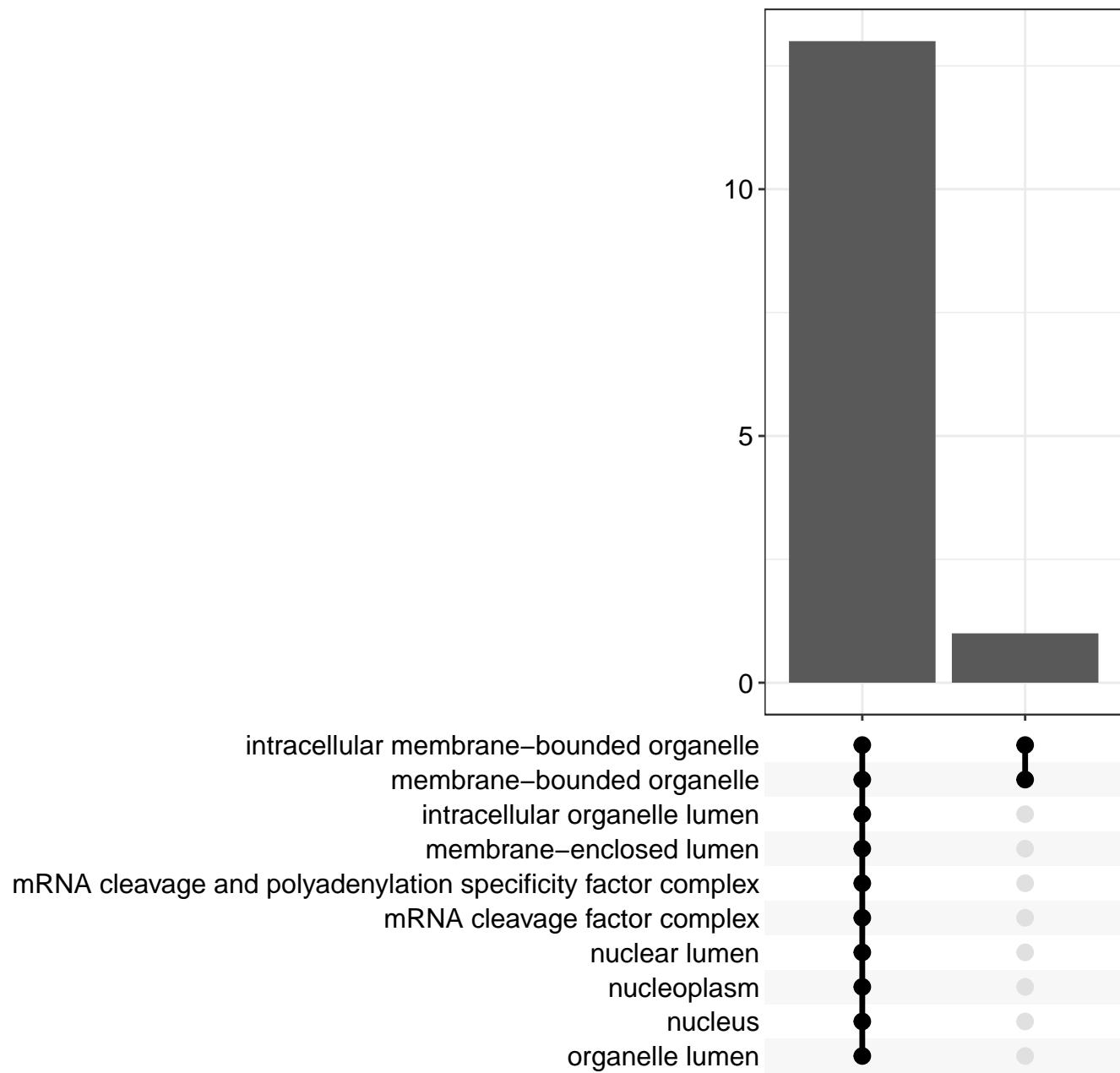


CFT1-TAP Up-regulated GO CC emapplot

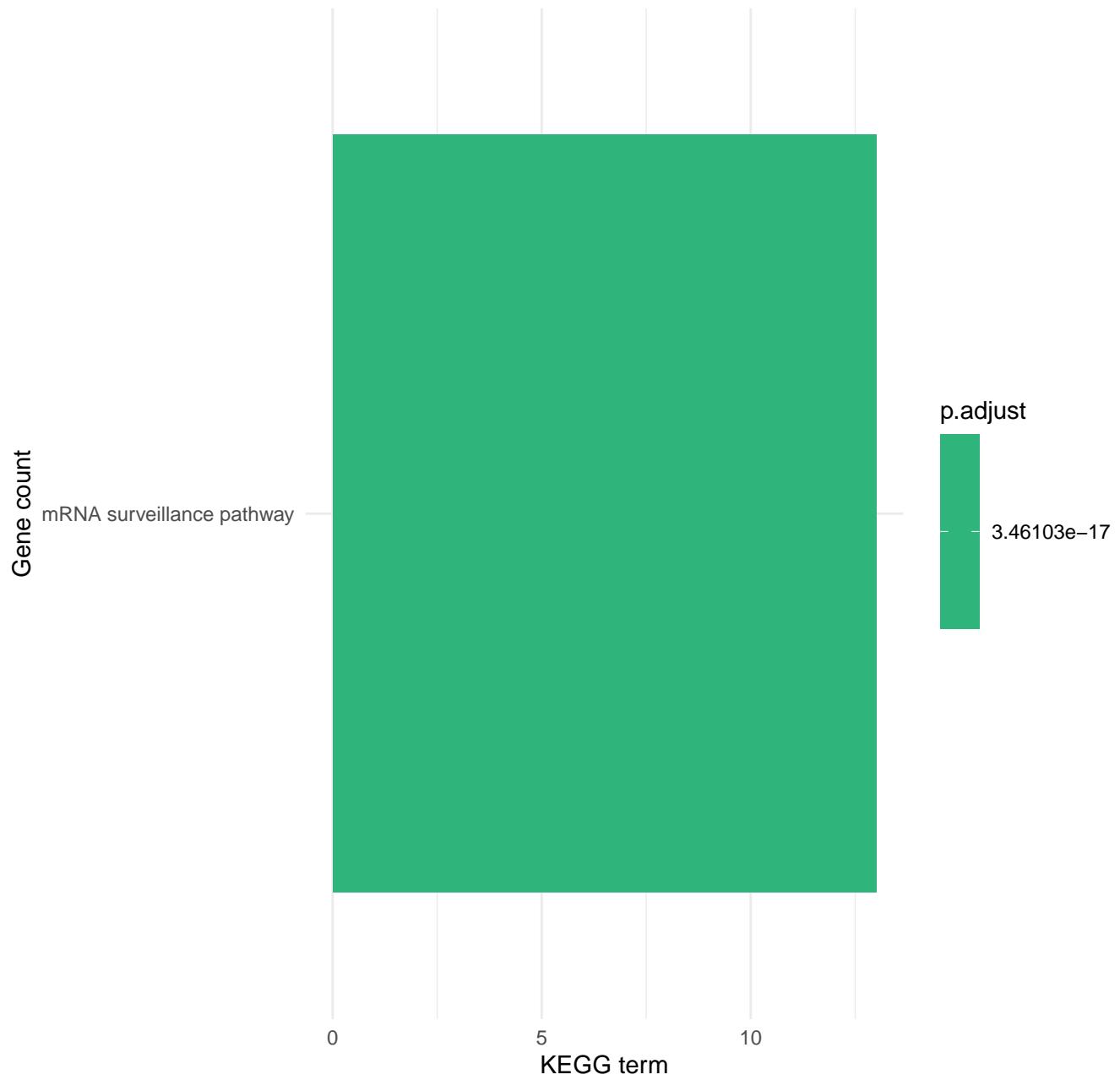




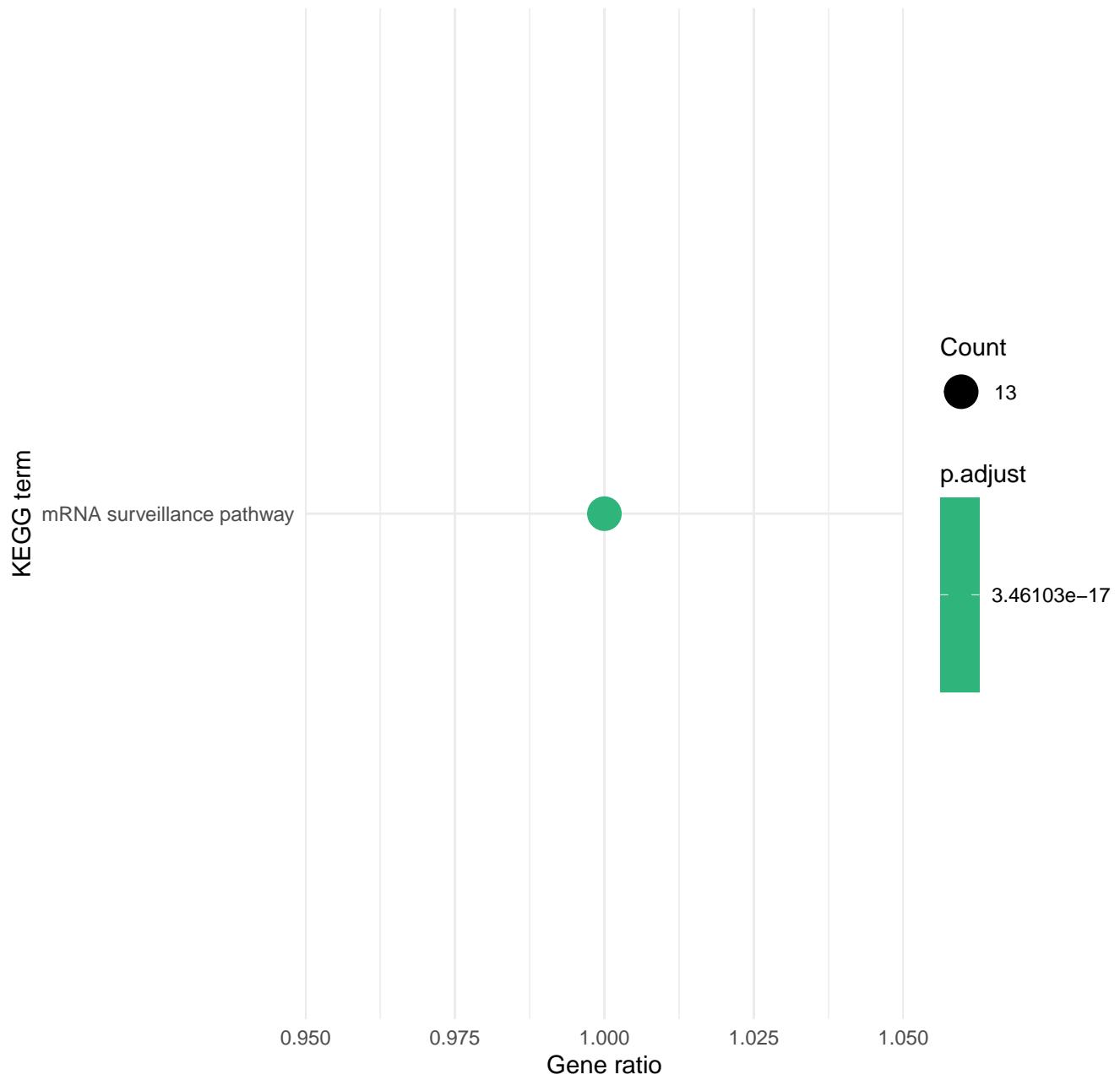
CFT1-TAP Up-regulated GO



CFT1-TAP Up-regulated KEGG barplot



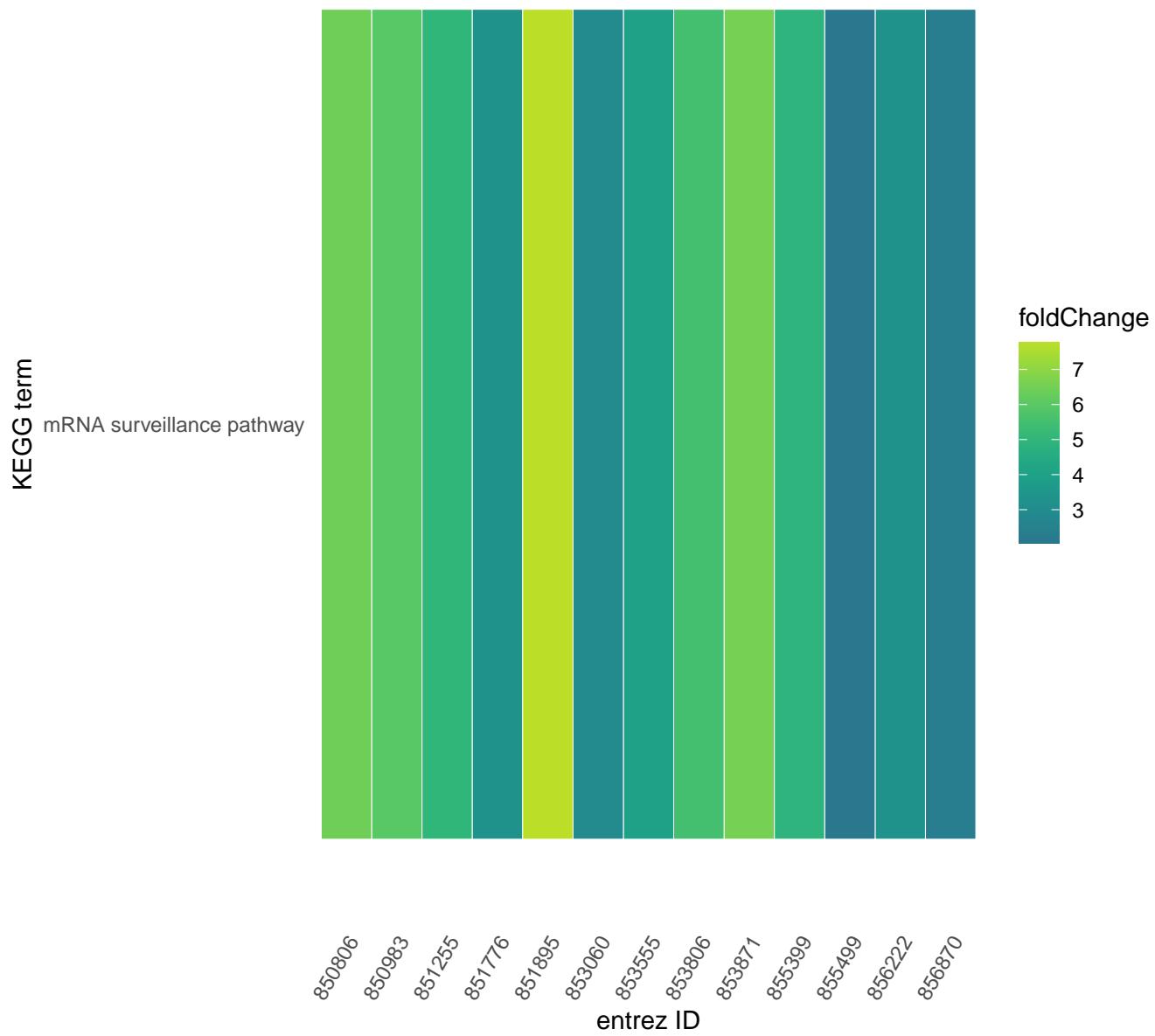
CFT1-TAP Up-regulated KEGG dotplot



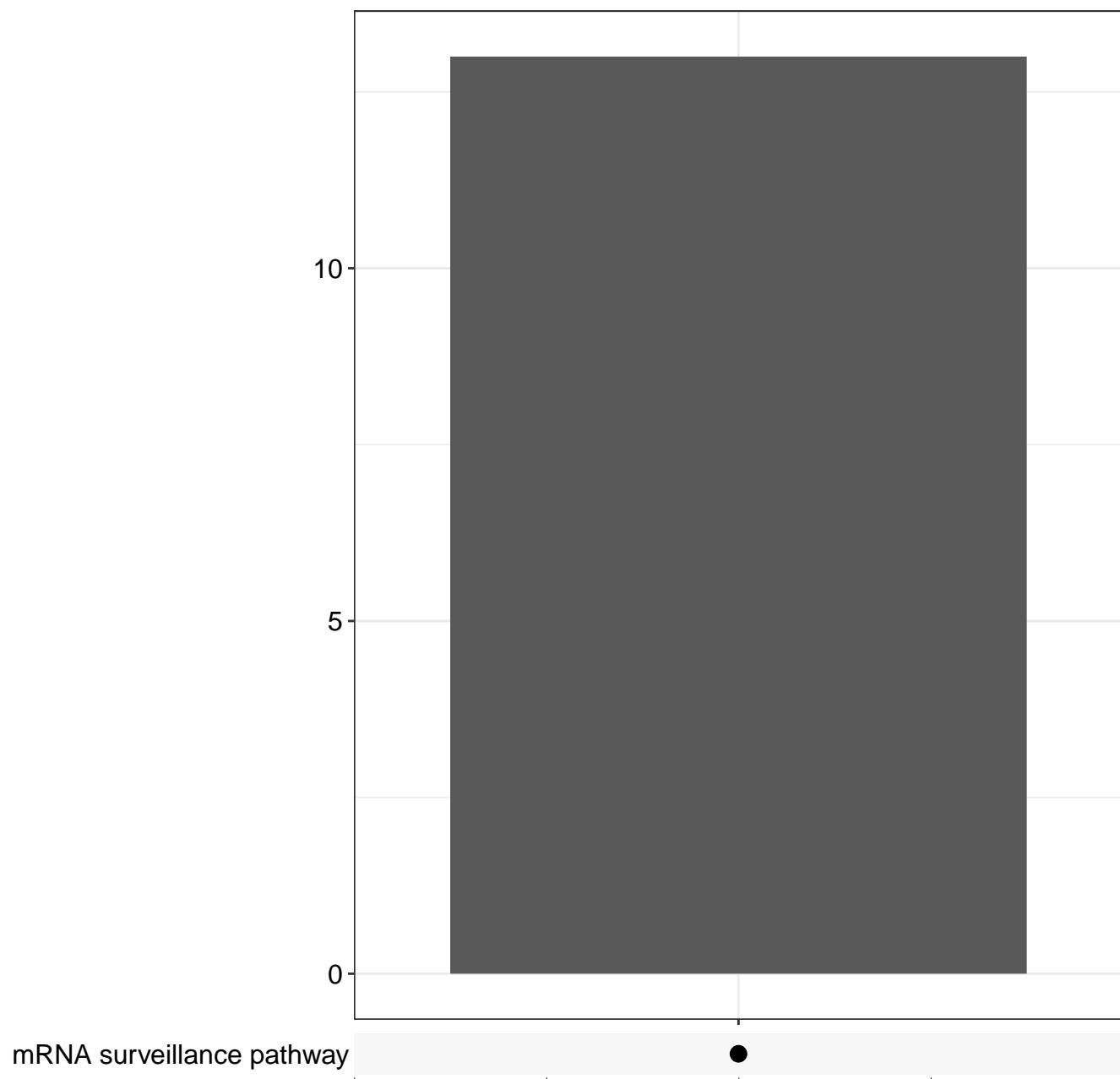
CFT1-TAP Up-regulated KEGG dotplot



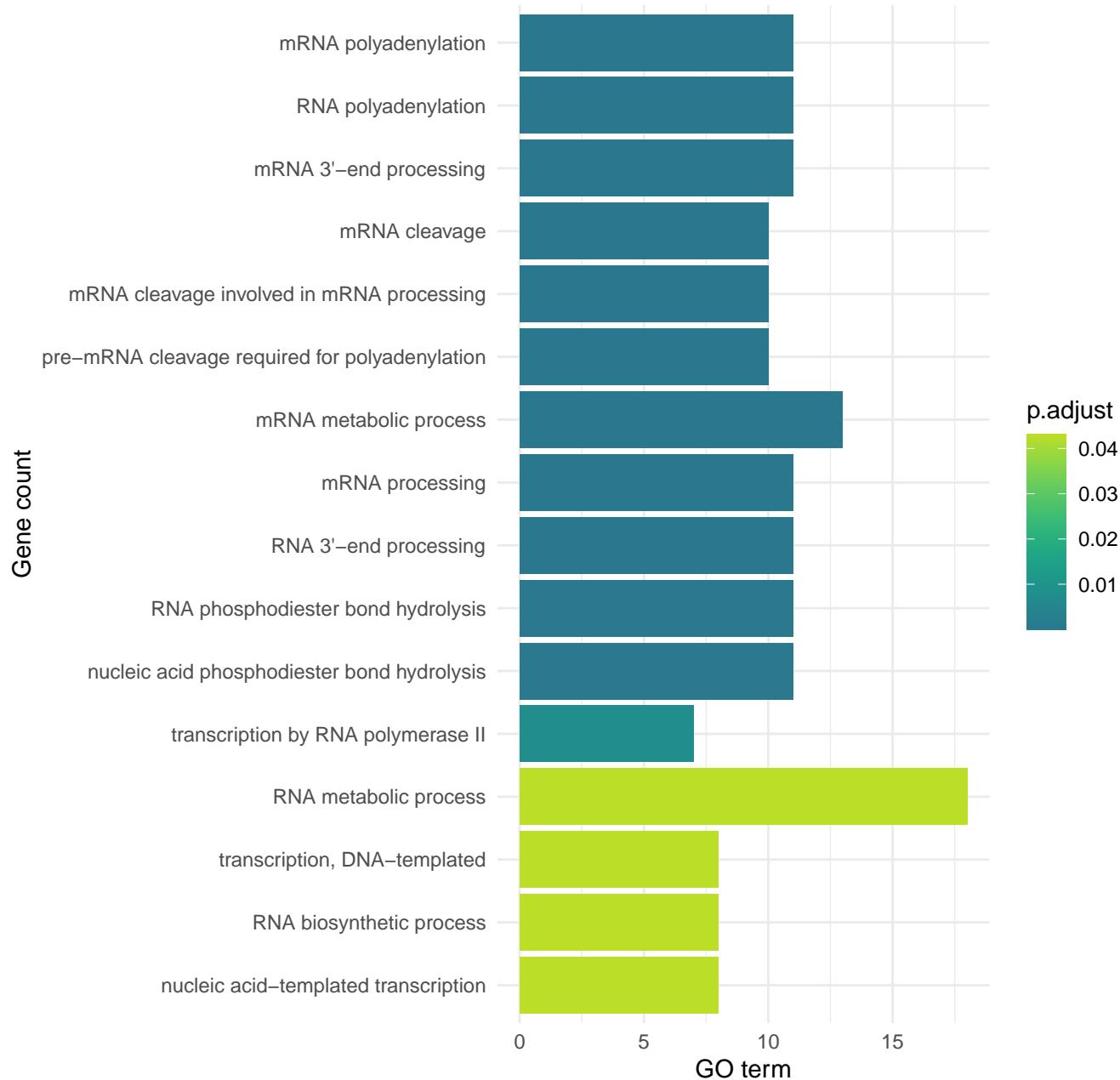
CFT1-TAP Up-regulated KEGG heatplot



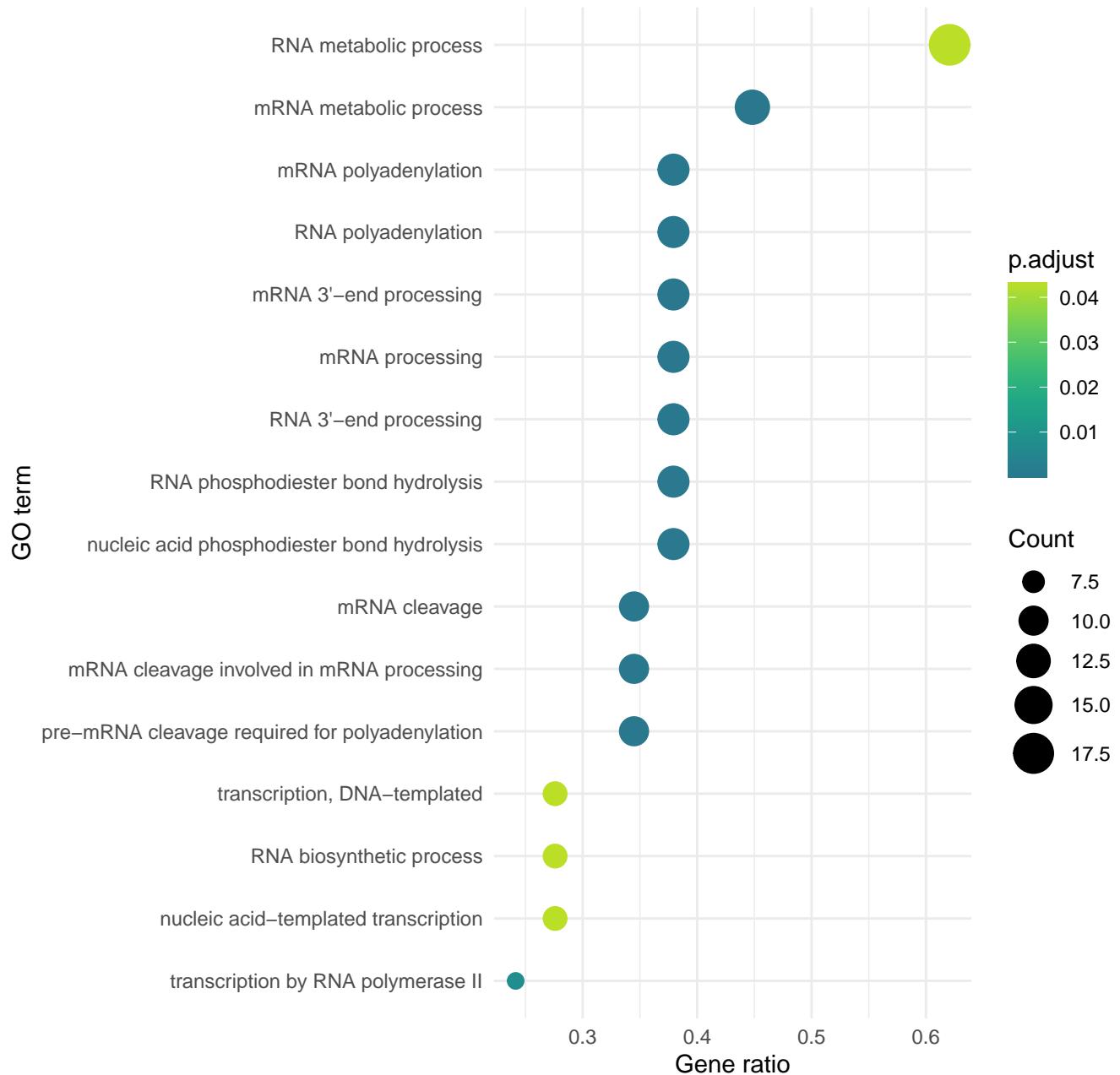
CFT1-TAP Up-regulated KEGG upsetplot



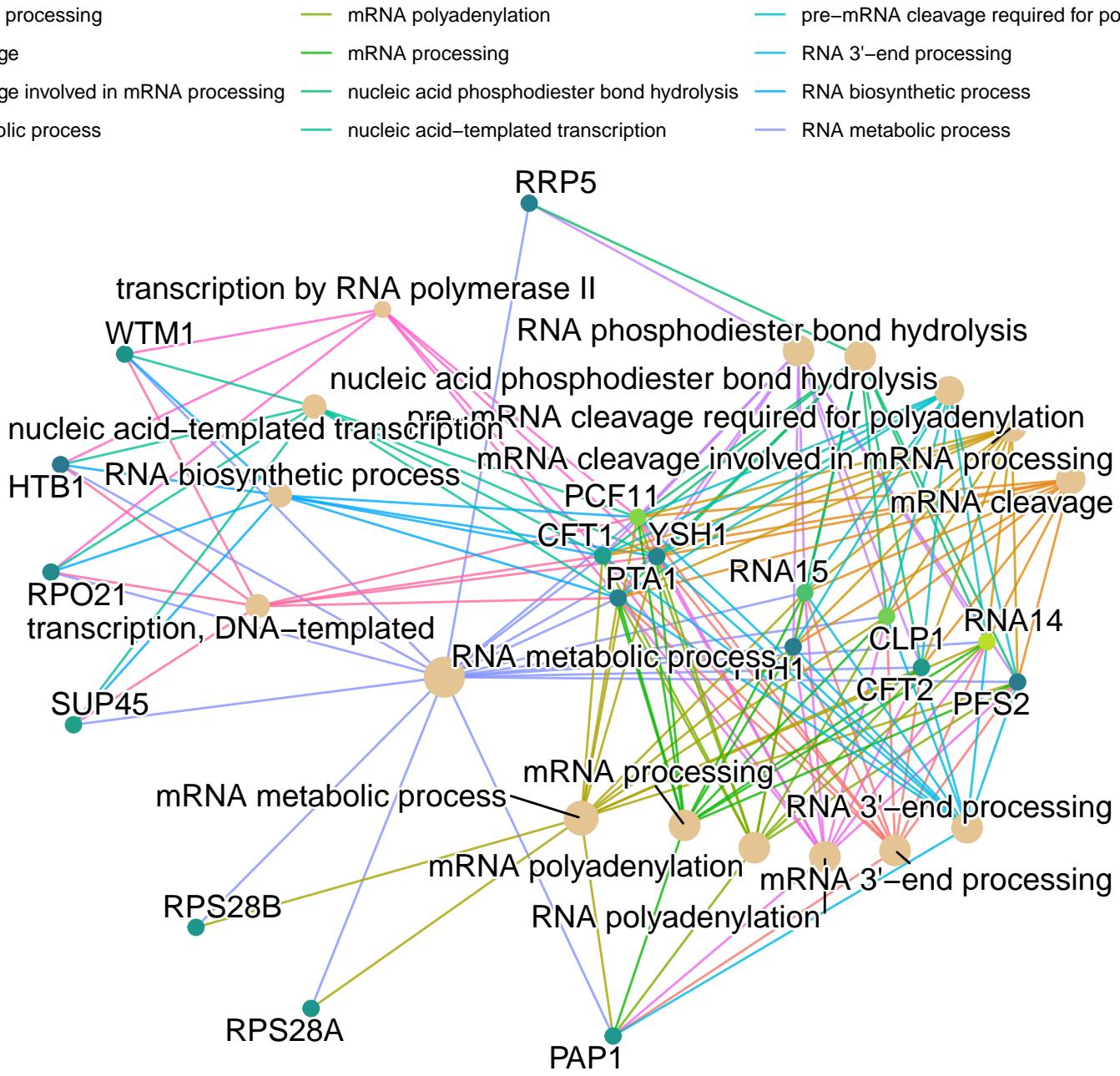
RNA14-TAP Up-regulated GO BP barplot



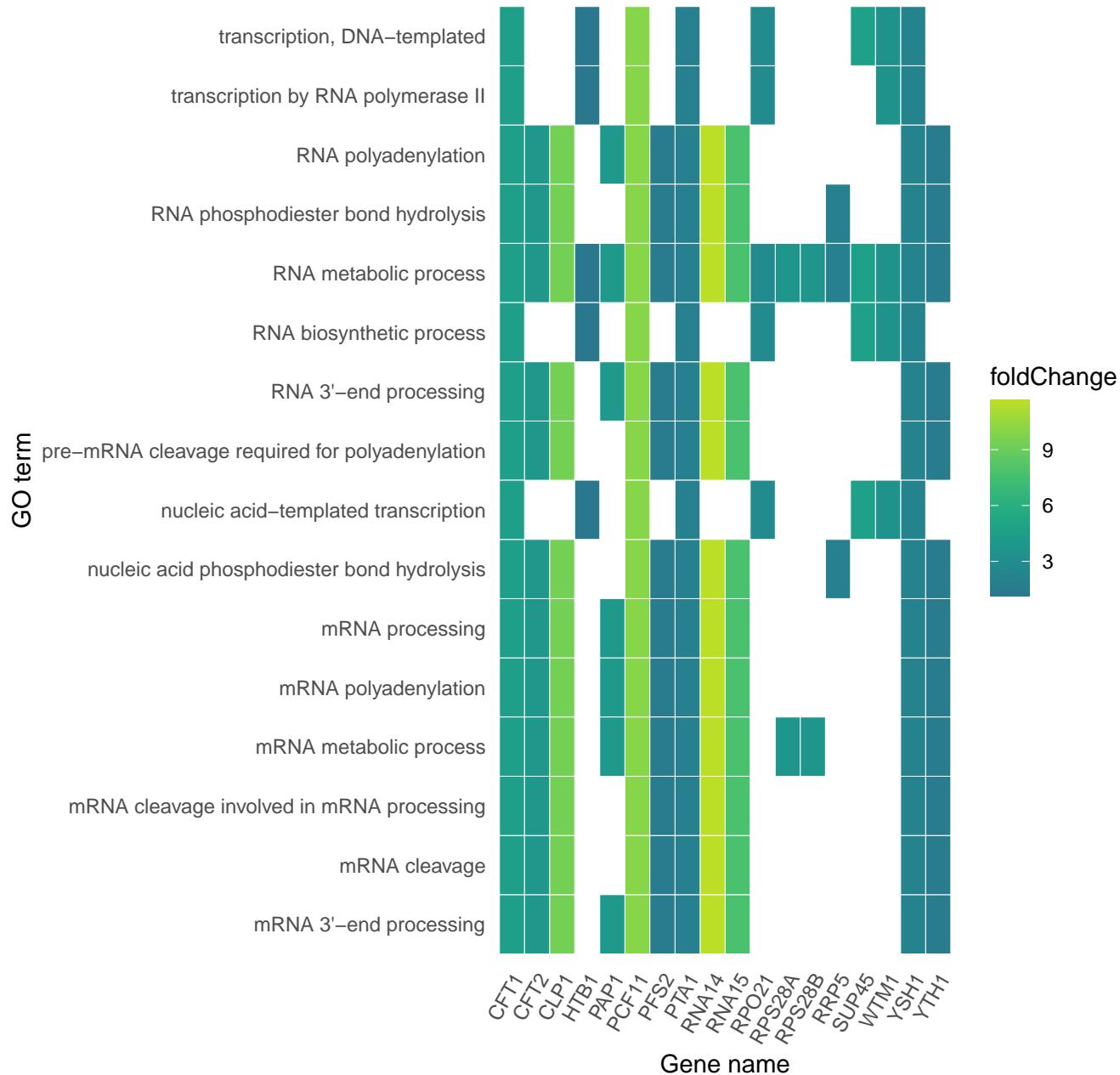
RNA14-TAP Up-regulated GO BP dotplot



RNA14-TAP Up-regulated GO BP cnetplot



RNA14–TAP Up-regulated GO BP heatplot



RNA14-TAP Up-regulated GO BP emapplot

mRNA metabolic process

RNA metabolic process

transcription by RNA polymerase II

RNA 3'-end processing

mRNA polyadenylation

RNA polyadenylation

mRNA 3'-end processing

RNA biosynthetic process

mRNA cleavage

nucleic acid-templated transcription

pre-mRNA cleavage required for polyadenylation

mRNA cleavage involved in mRNA processing

mRNA processing

transcription, DNA-templated

RNA phosphodiester bond hydrolysis

nucleic acid phosphodiester bond hydrolysis

FoldChange

0.04

0.03

0.02

0.01

size

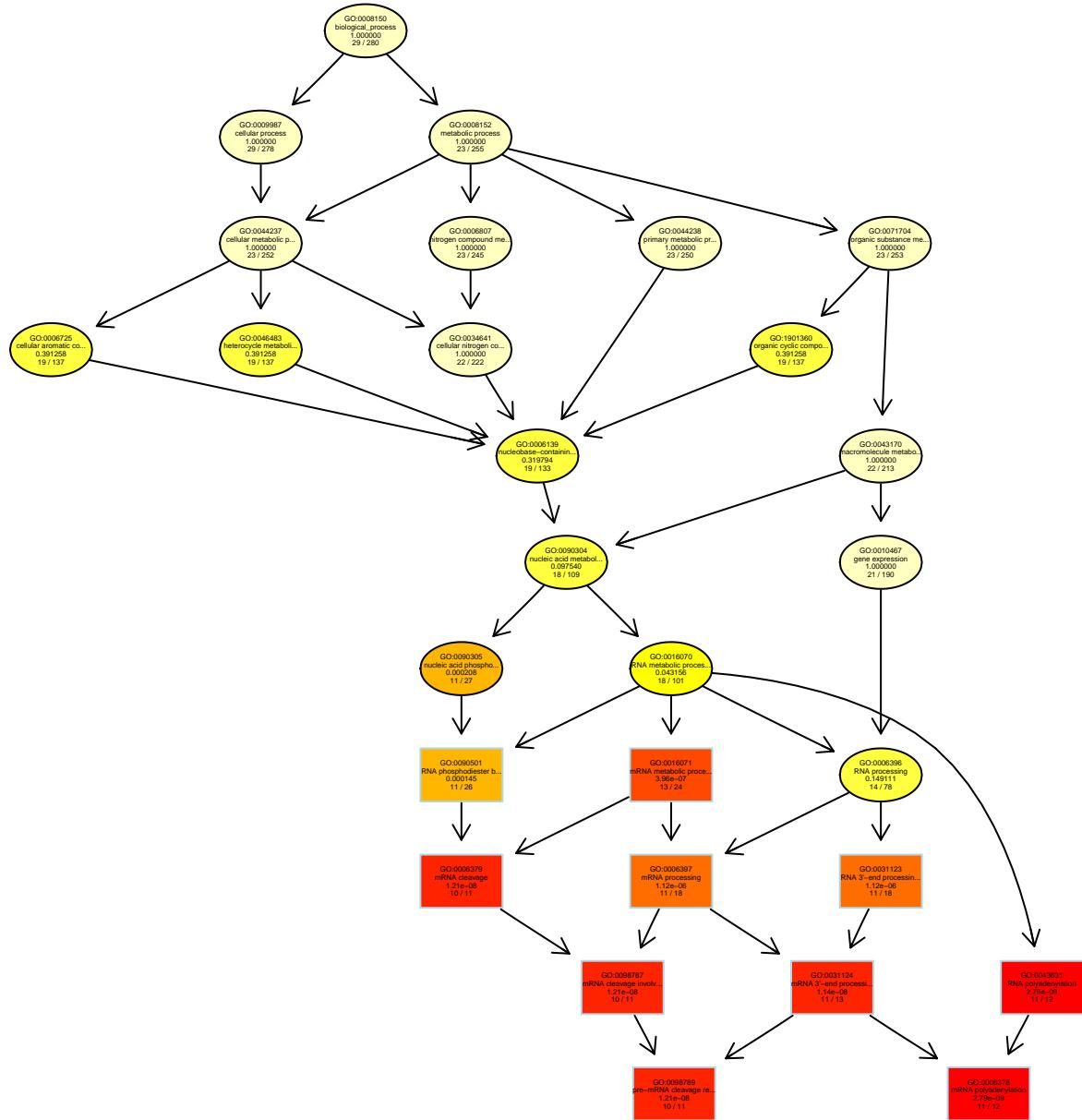
7.5

10.0

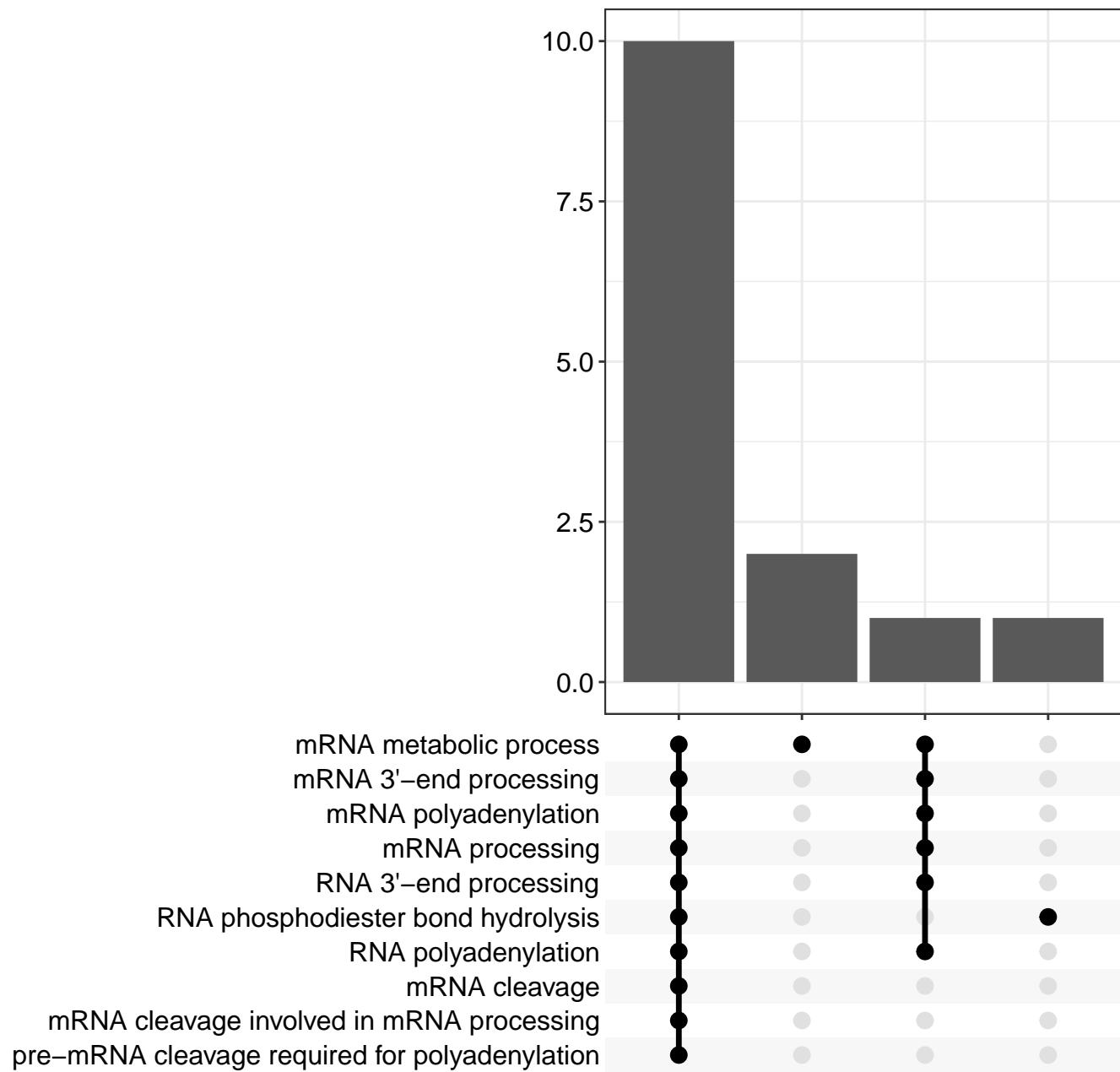
12.5

15.0

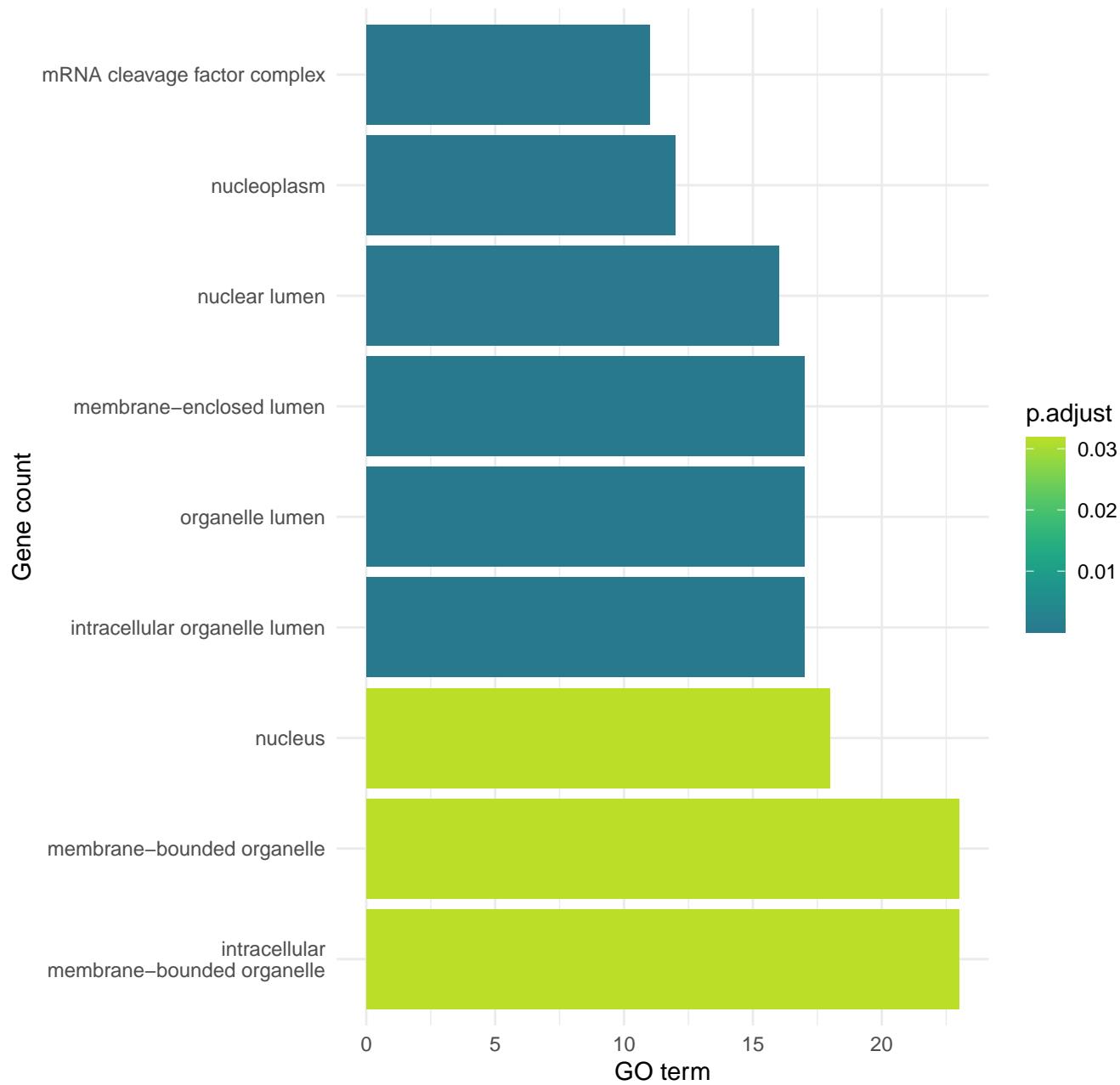
17.5



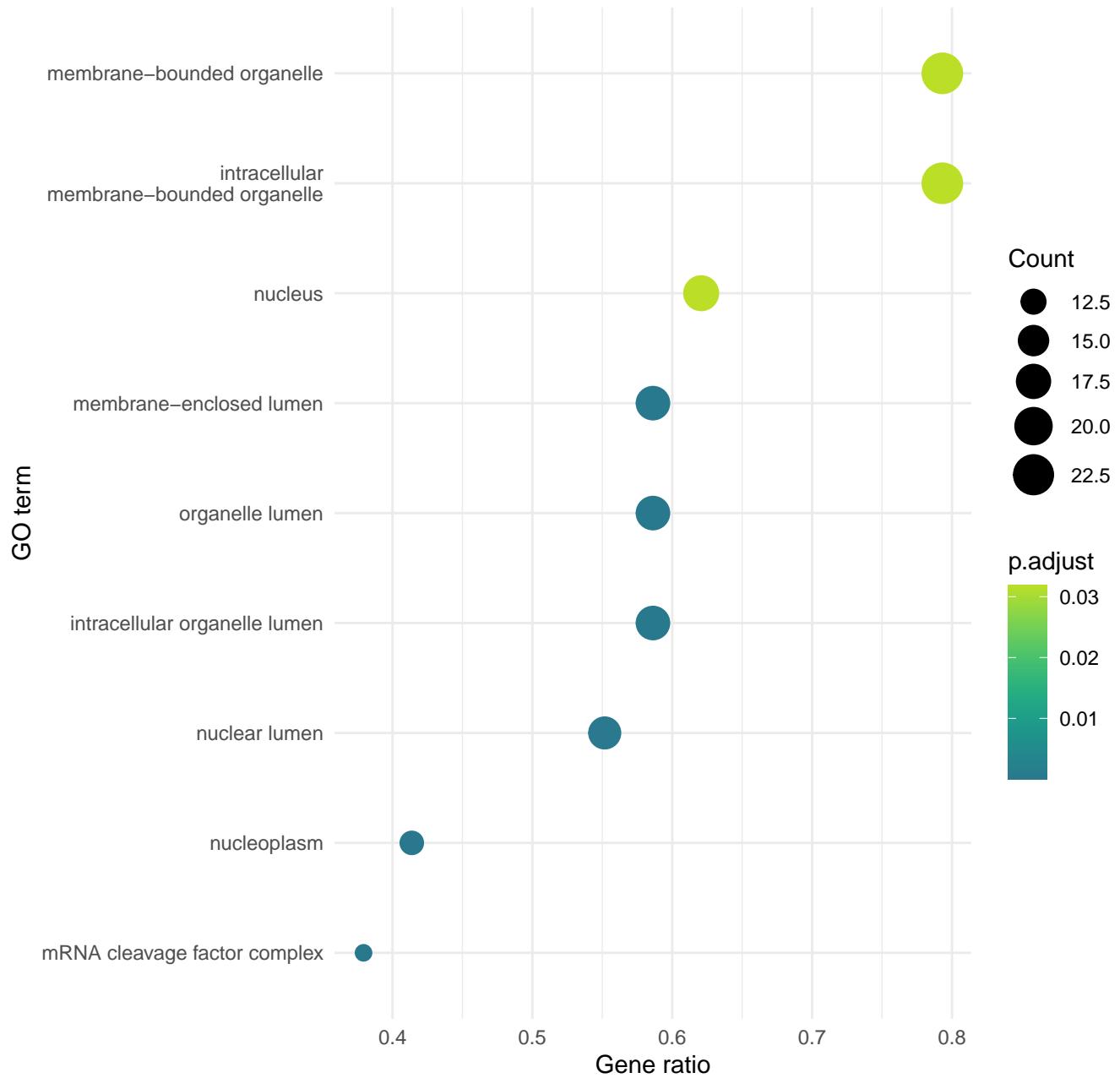
RNA14–TAP Up-regulated GO BP upset



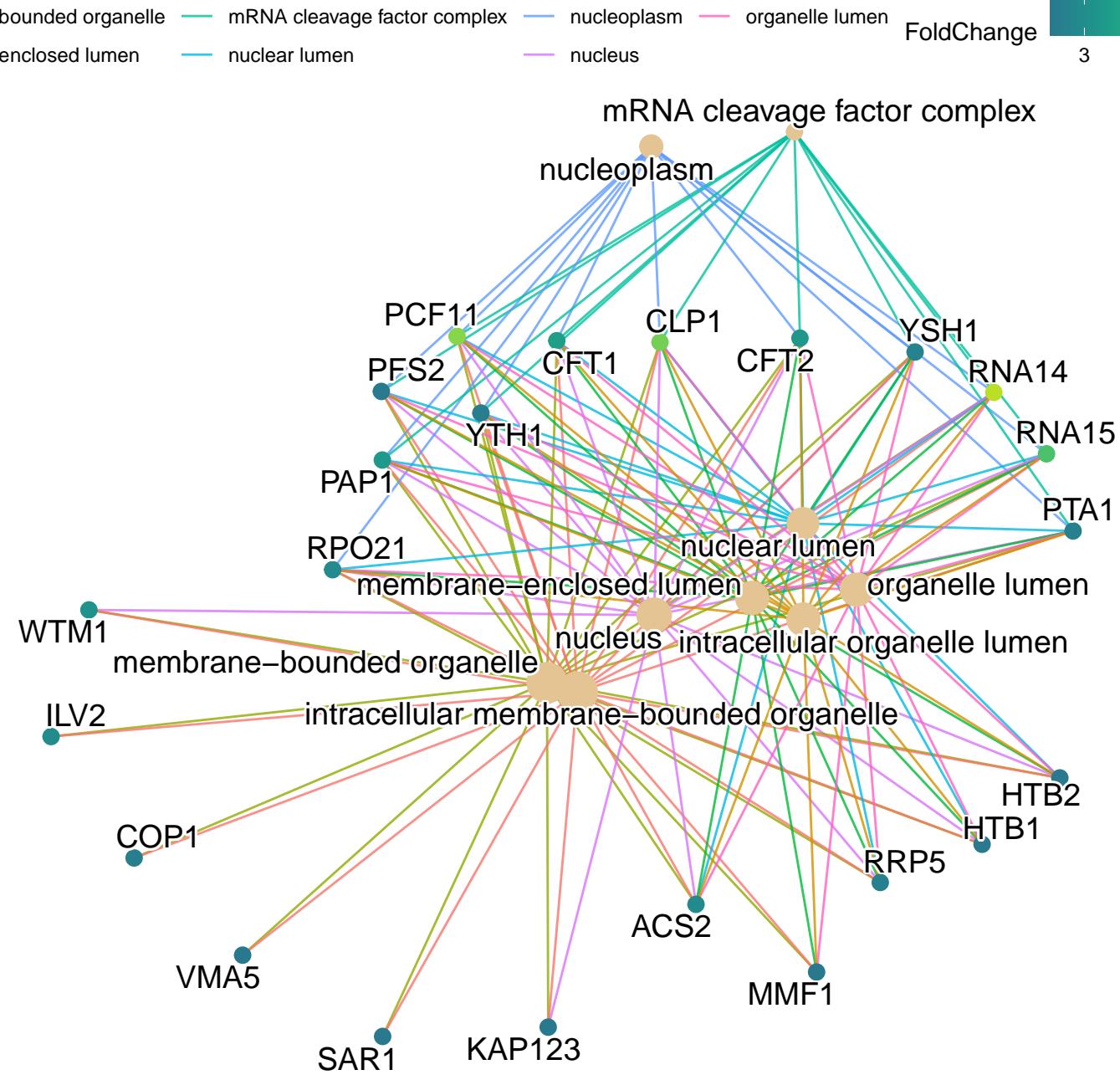
RNA14-TAP Up-regulated GO CC barplot



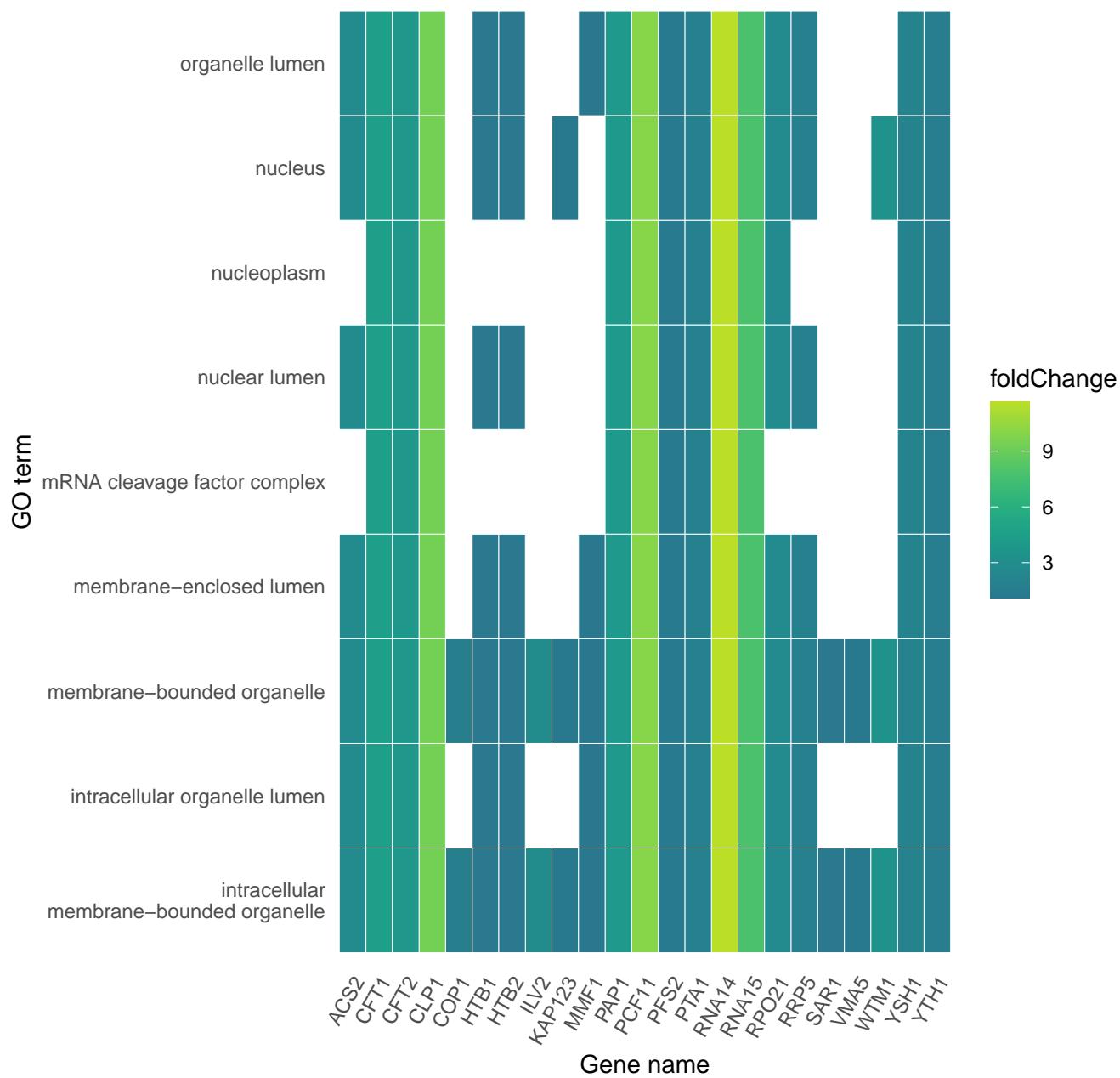
RNA14-TAP Up-regulated GO CC dotplot



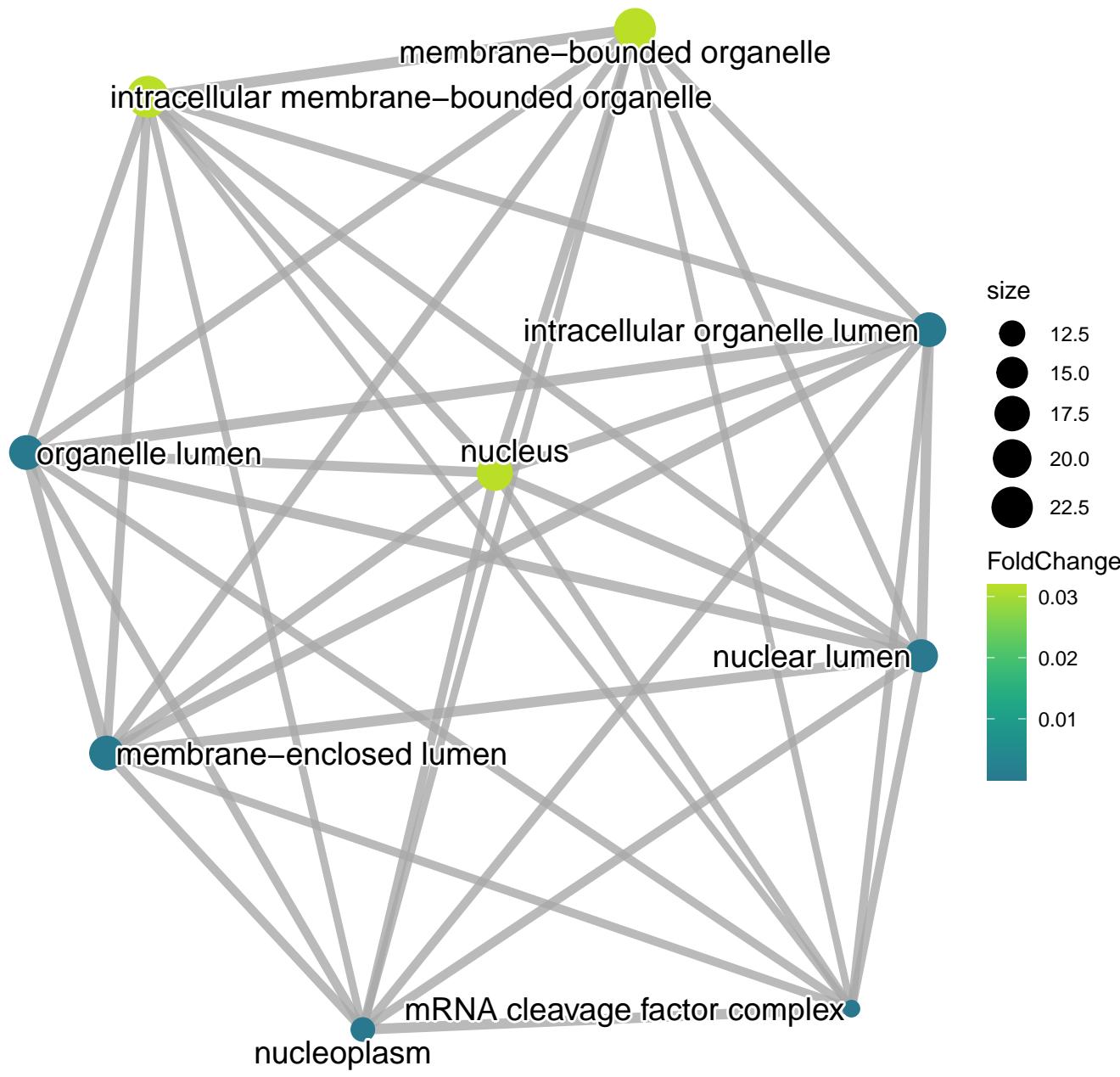
RNA14-TAP Up-regulated GO CC cnetplot

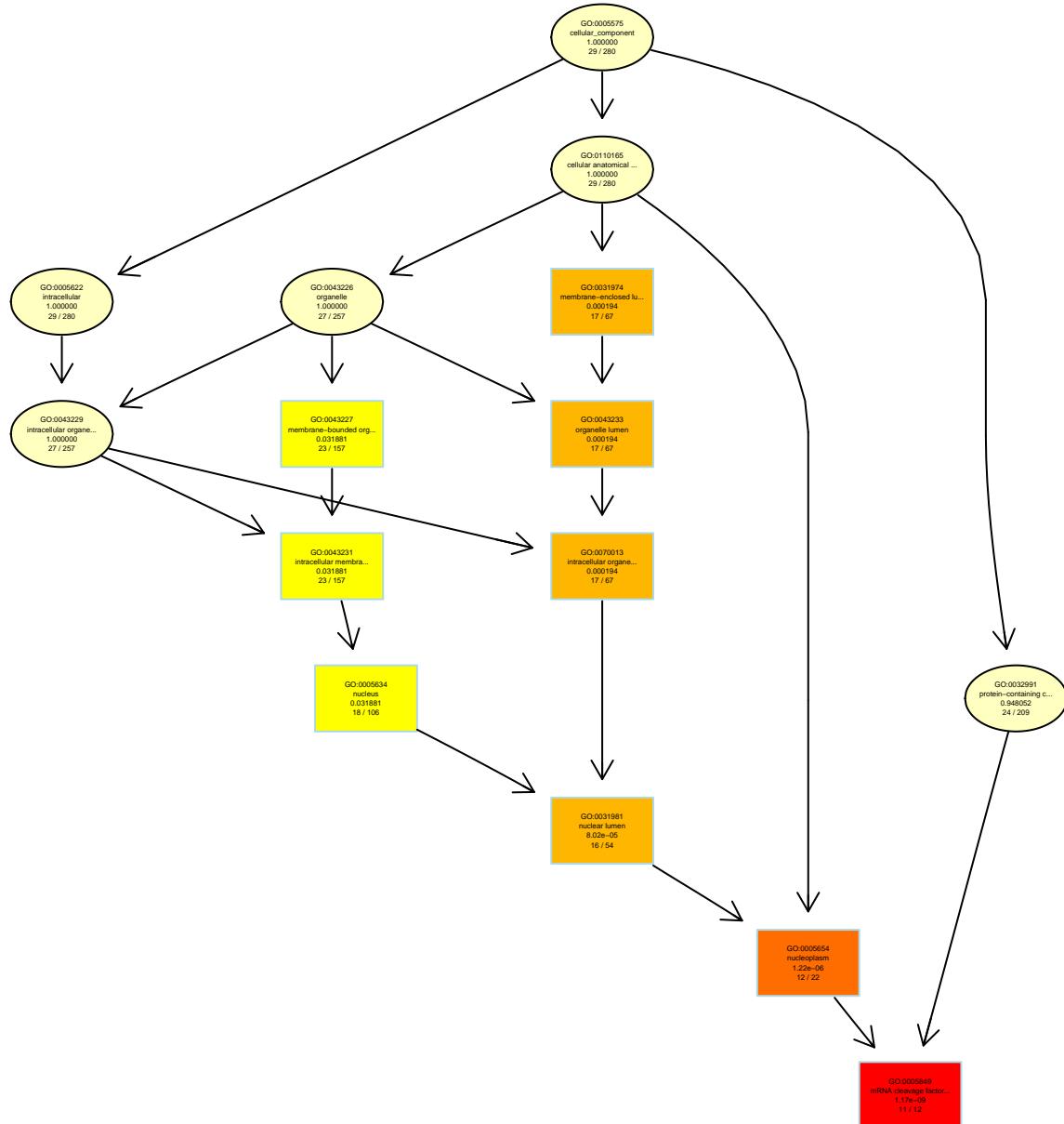


RNA14–TAP Up-regulated GO CC heatplot

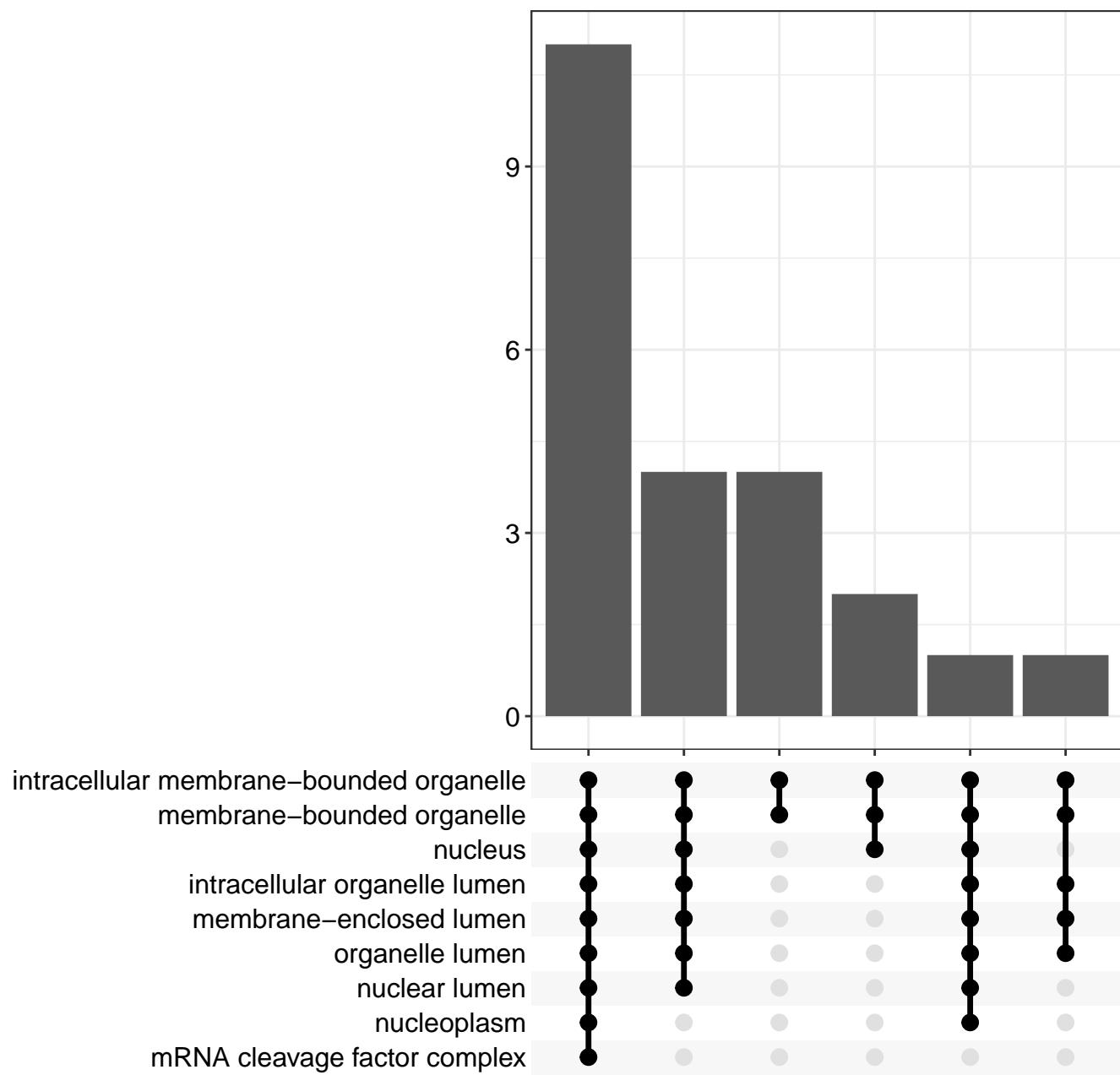


RNA14-TAP Up-regulated GO CC emapplot

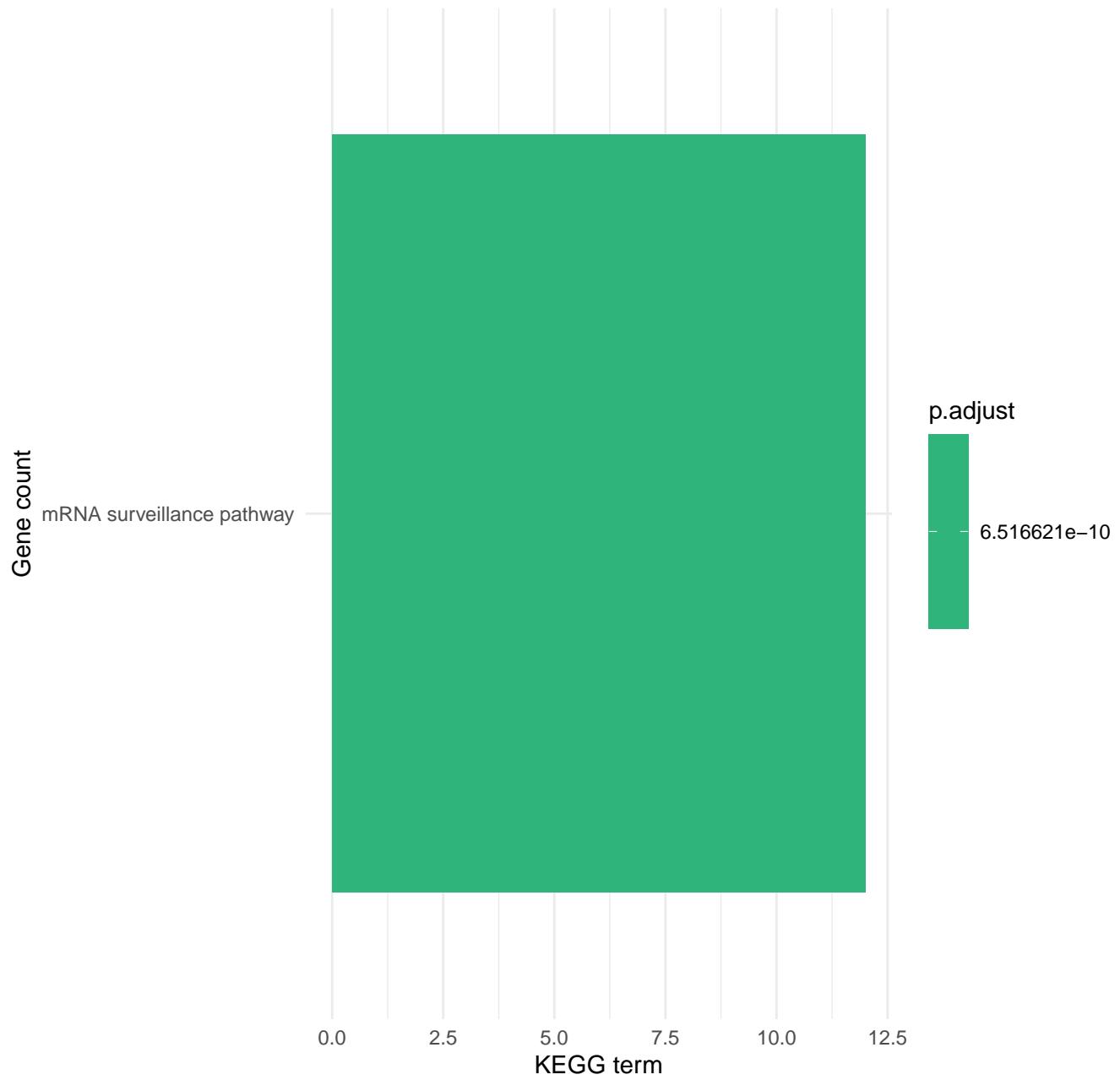




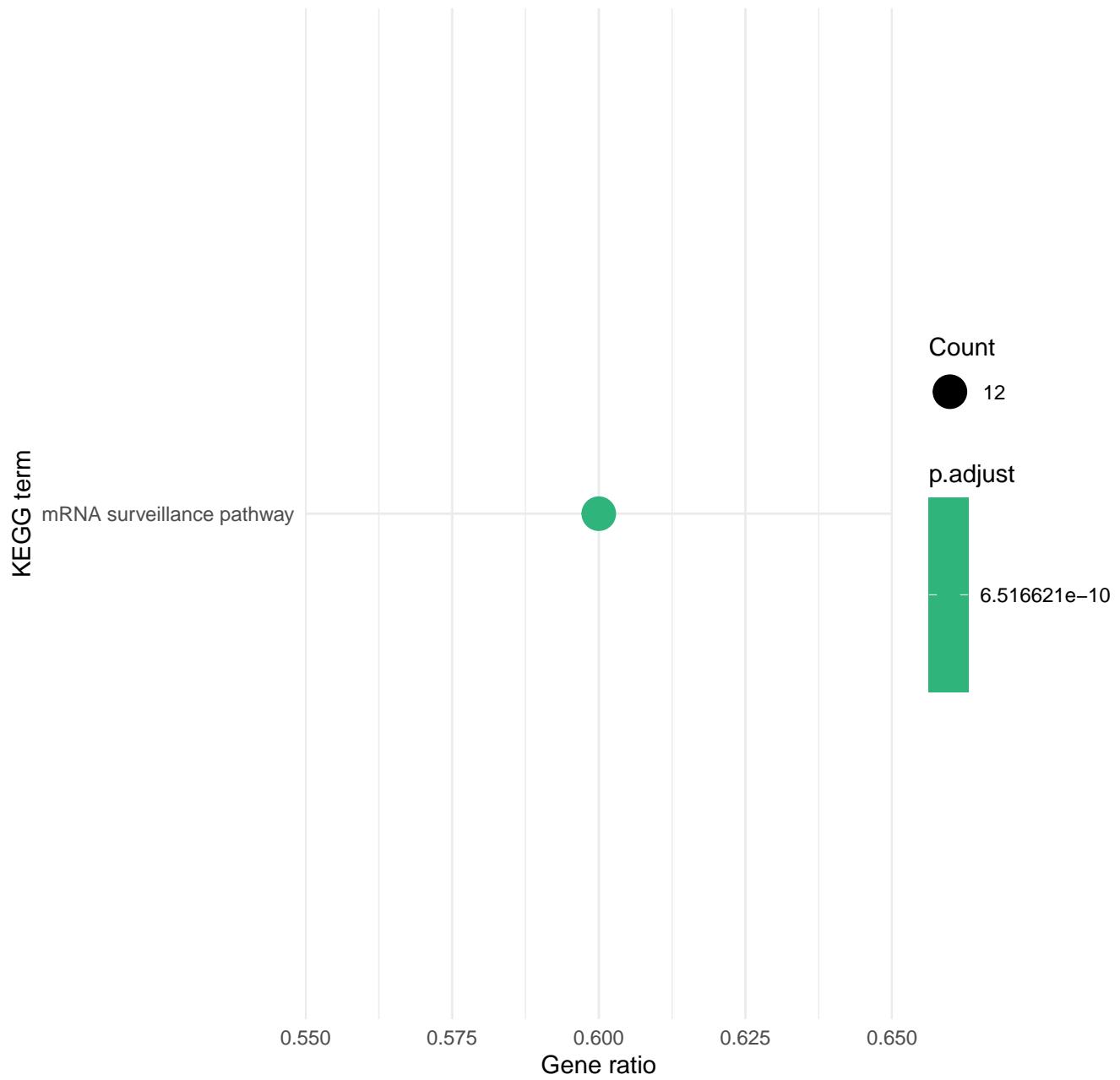
RNA14–TAP Up-regulated GO CC upsetplot



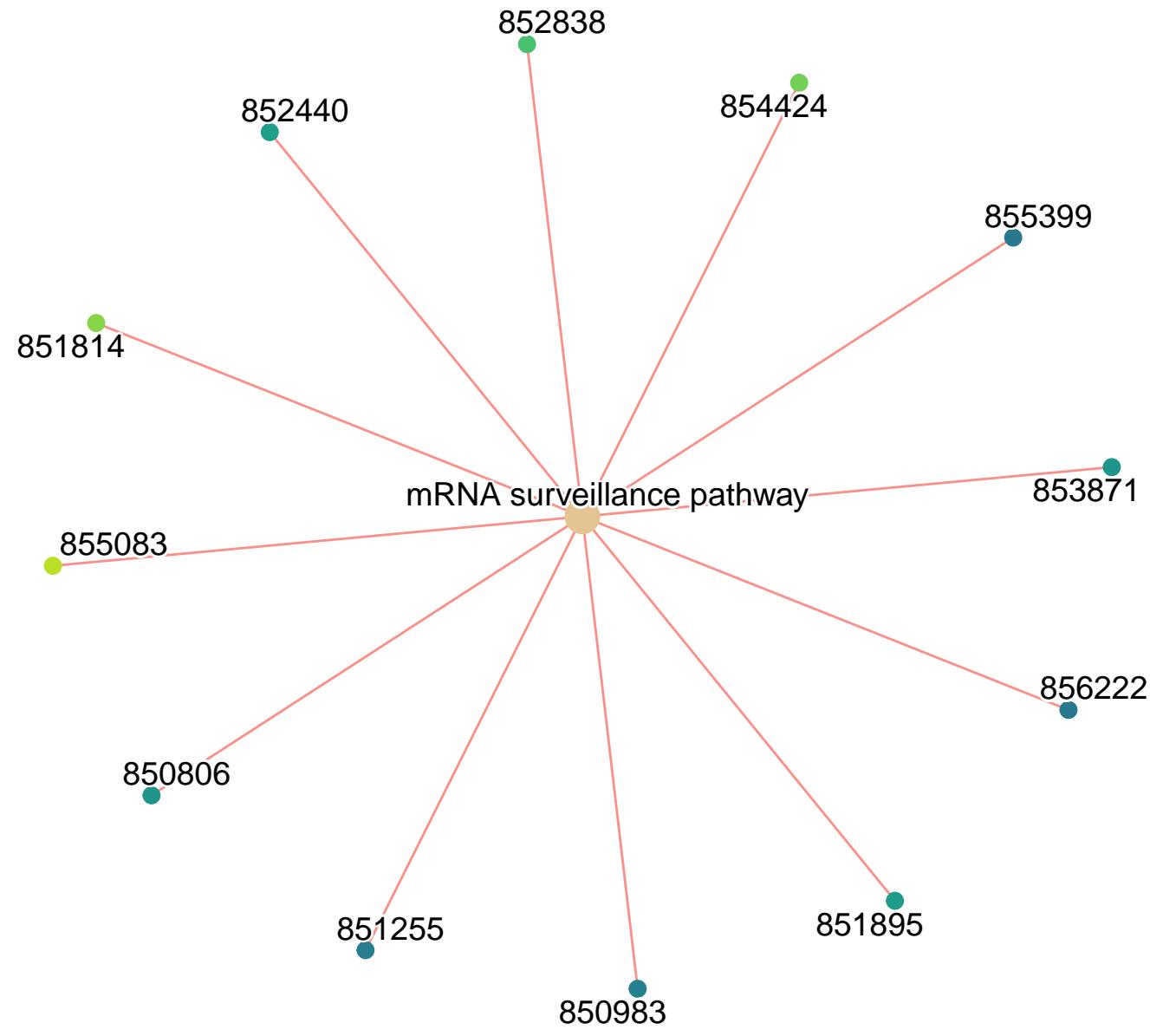
RNA14–TAP Up-regulated KEGG barplot



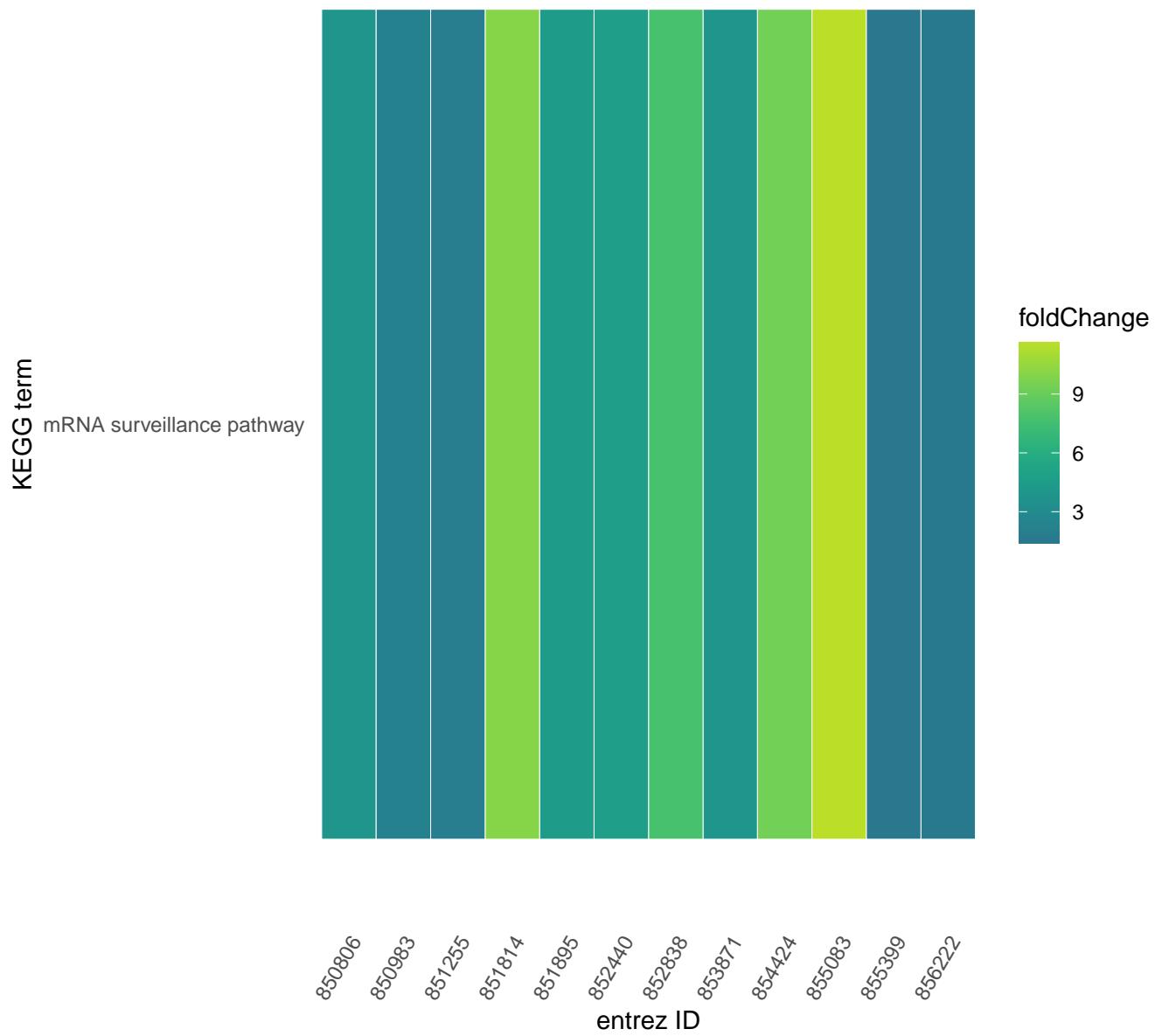
RNA14–TAP Up-regulated KEGG dotplot



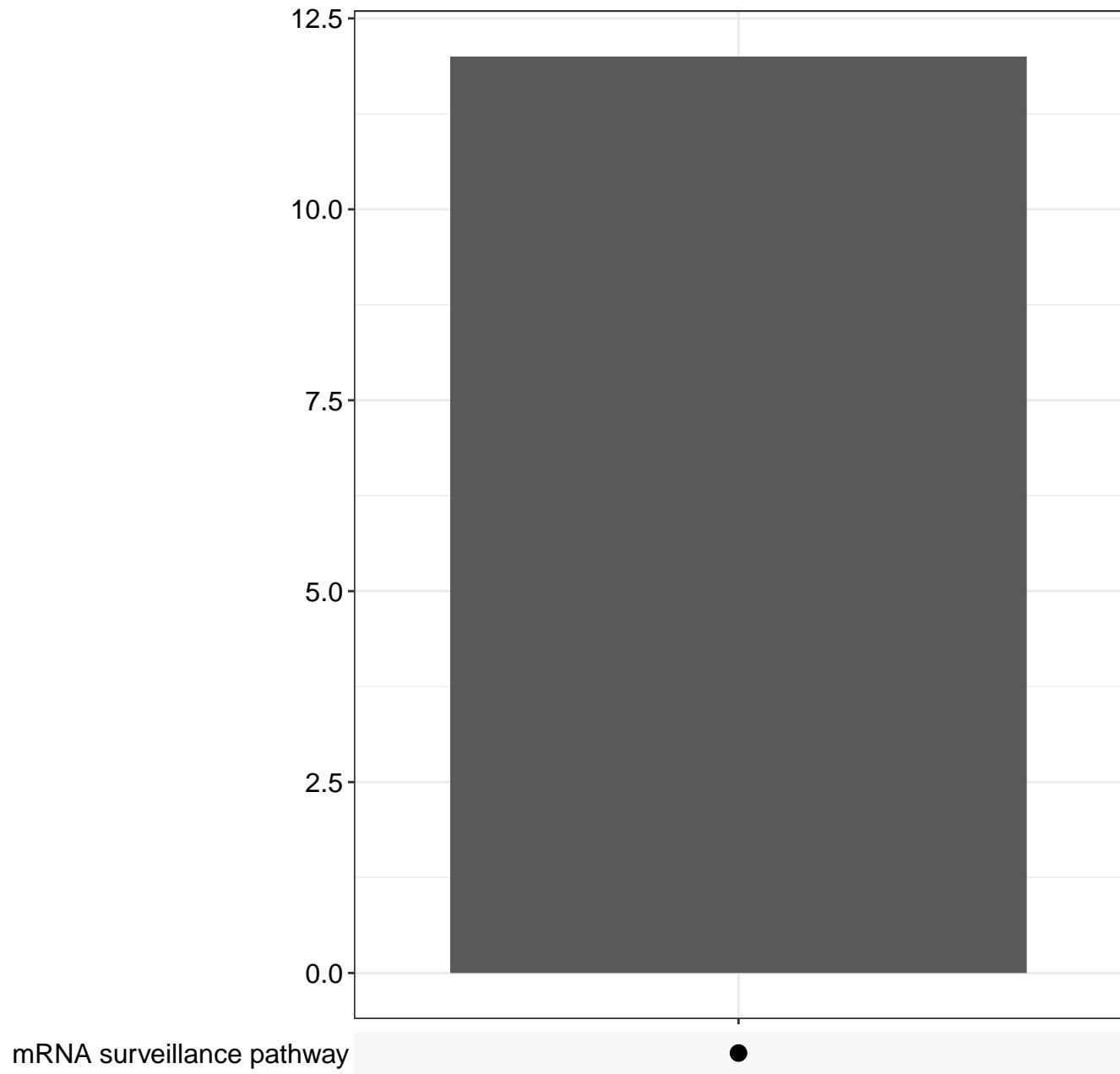
RNA14-TAP Up-regulated KEGG dotplot



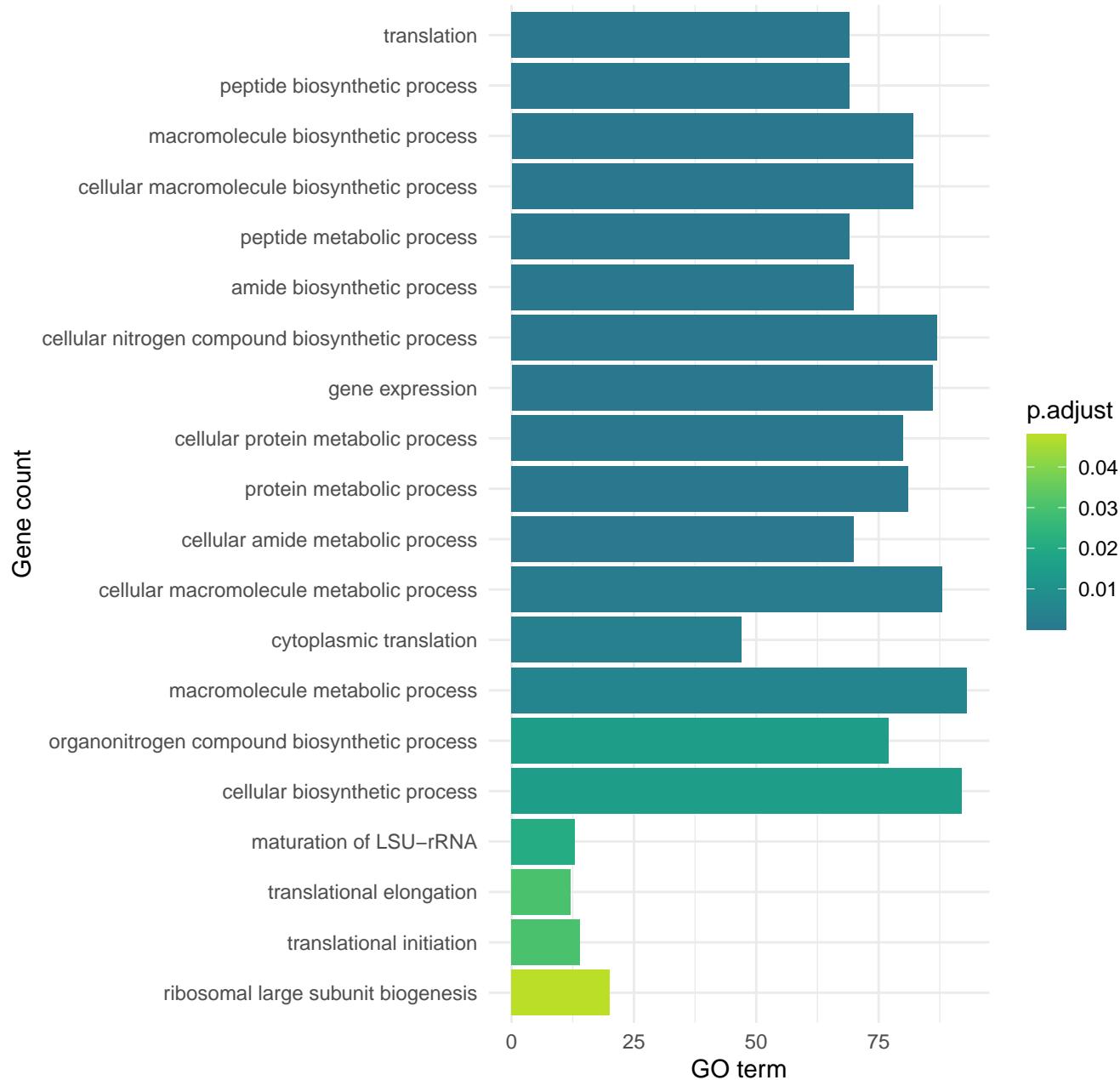
RNA14–TAP Up-regulated KEGG heatplot



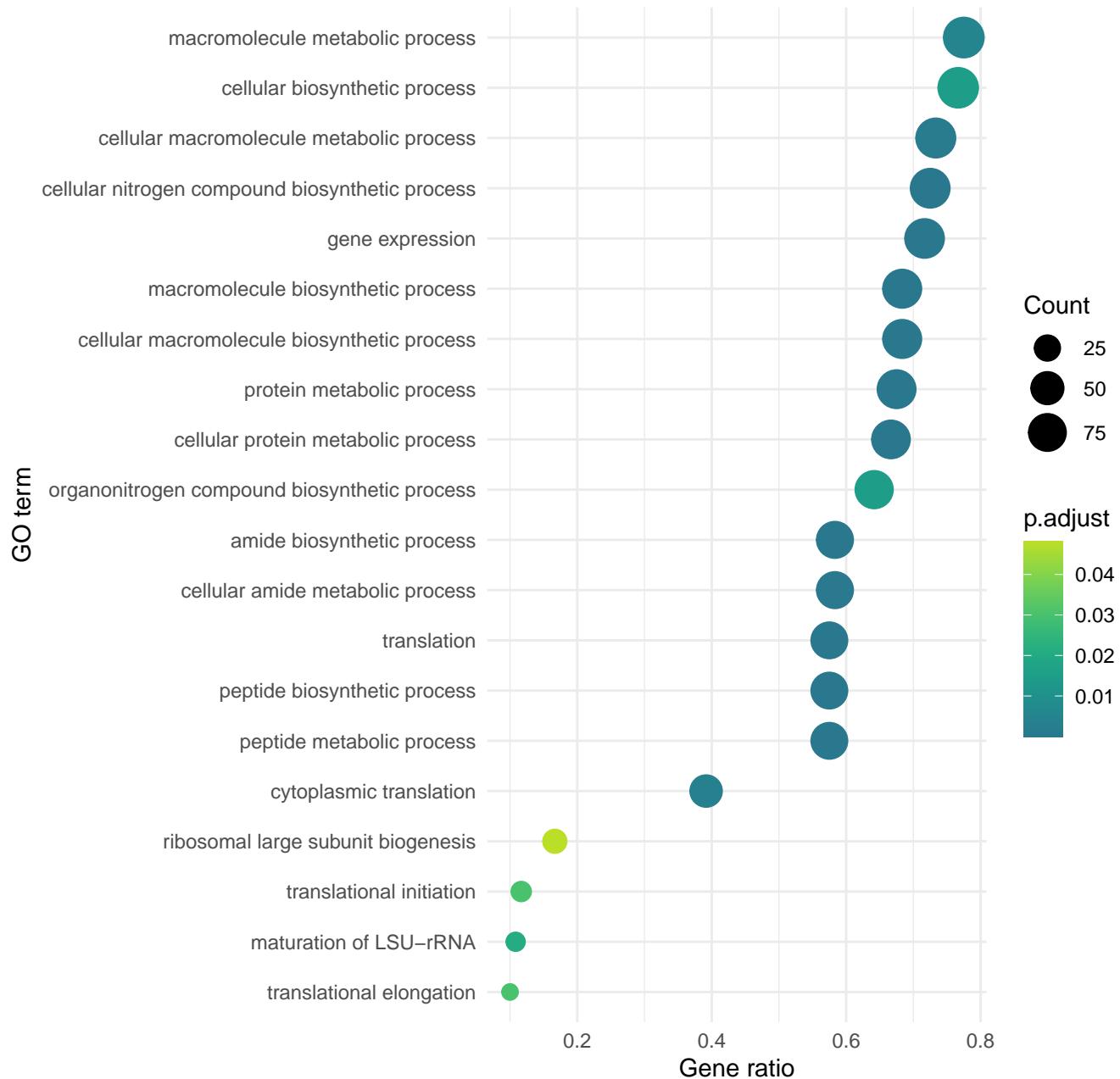
RNA14-TAP Up-regulated KEGG upsetplot



MPE1–TAP Up-regulated GO BP barplot



MPE1–TAP Up-regulated GO BP dotplot



MPE1-TAP Up-regulated GO BP cnetplot

biosynthetic process

cellular macromolecule metabolic process

gene expression

amide metabolic process

cellular nitrogen compound biosynthetic process

macromolecule biosynthetic p

osynthetic process

cellular protein metabolic process

macromolecule metabolic pro

macromolecule biosynthetic process

cytoplasmic translation

maturation of LSU-rRNA

ribosomal large subunit biogenesis
maturation of LSU-rRNA

RPL35A
RPL35B
RPL7A
RPL8B
RPS26B
RPL1A-RPL11B
RPL11A
GCN20
TEF4
organonitrogen compound biosynthetic process
YEF3
ASC1
translational elongation

CHA1

ACC1
ATP2

ERG6

ADE6

TRP5

PRS3

SEC14

ERG11

ERG1

UTP10

VAS-MBF1

RAD52

GCD2

HOG1

PAB1

DYS1

PRE9

GAR1

UBP3

translational initiation

RPN7

RPN1

RLI1

NIP1

TIF5

SIS1

CDC33

FUN12

SUJ2

GCD6

SCP160

NEW1

RVB1

SPT16

NPL3

UPF3A

UPF3B

DEF1

TIF4631

RPL3

PRT1

RPS1AGCD11

SUP45

RPL1B

TIF34

SCC1

UPF3B

UPF3A

UPF3B

UPF3A

UPF3B

UPF3A

UPF3B

UPF3A

NUG1

HSP60

RPL35A

RPL35B

RPL8A

RPL1B

RPL27A

RPL5

RPL11A

RPL1A

TEF1

ZUO1

RPP2A

RPL13B

RPS15

RBG2

RPL27B

RPL27B

DBP3

DBP5

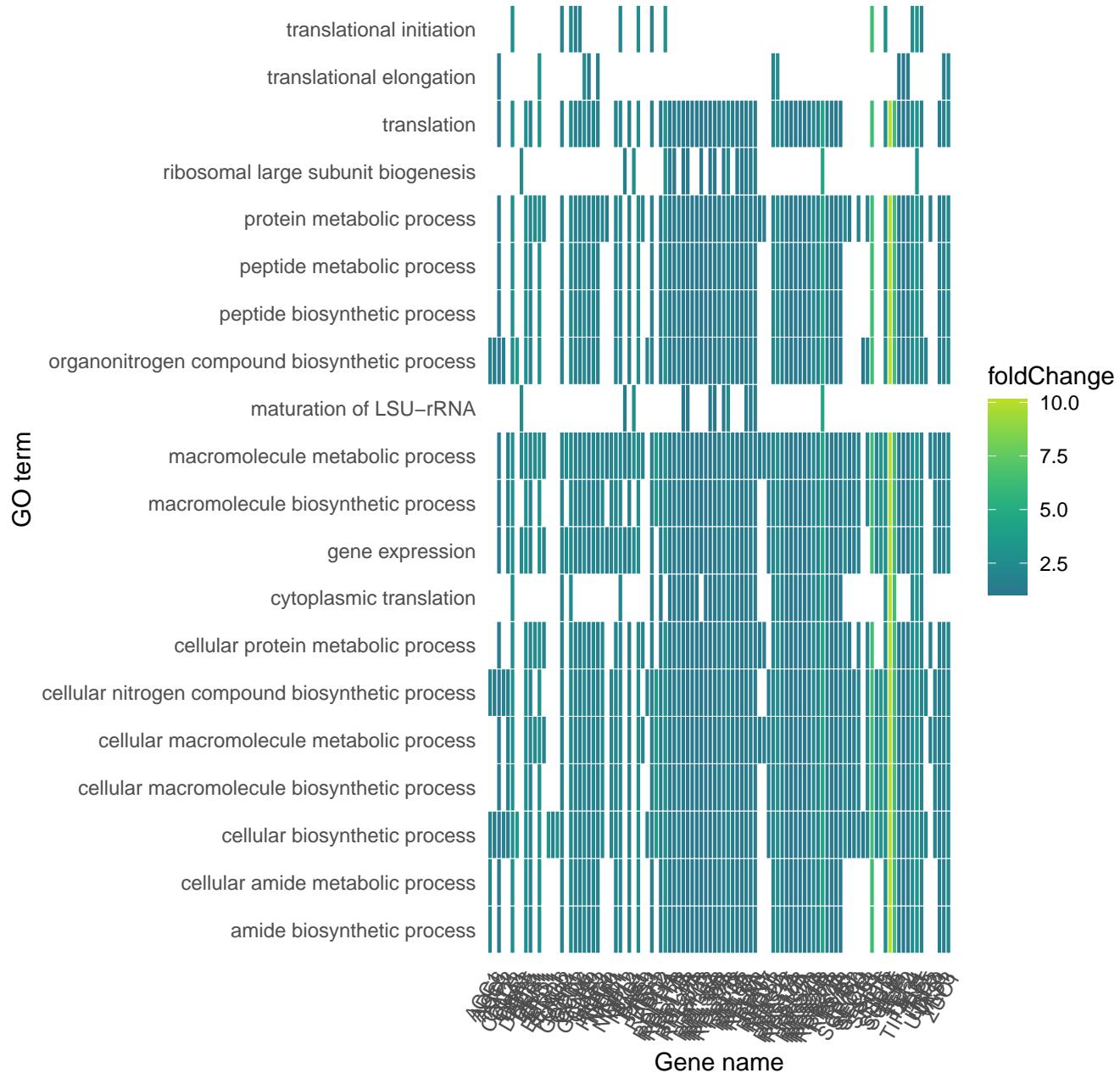
DED81

RPS20

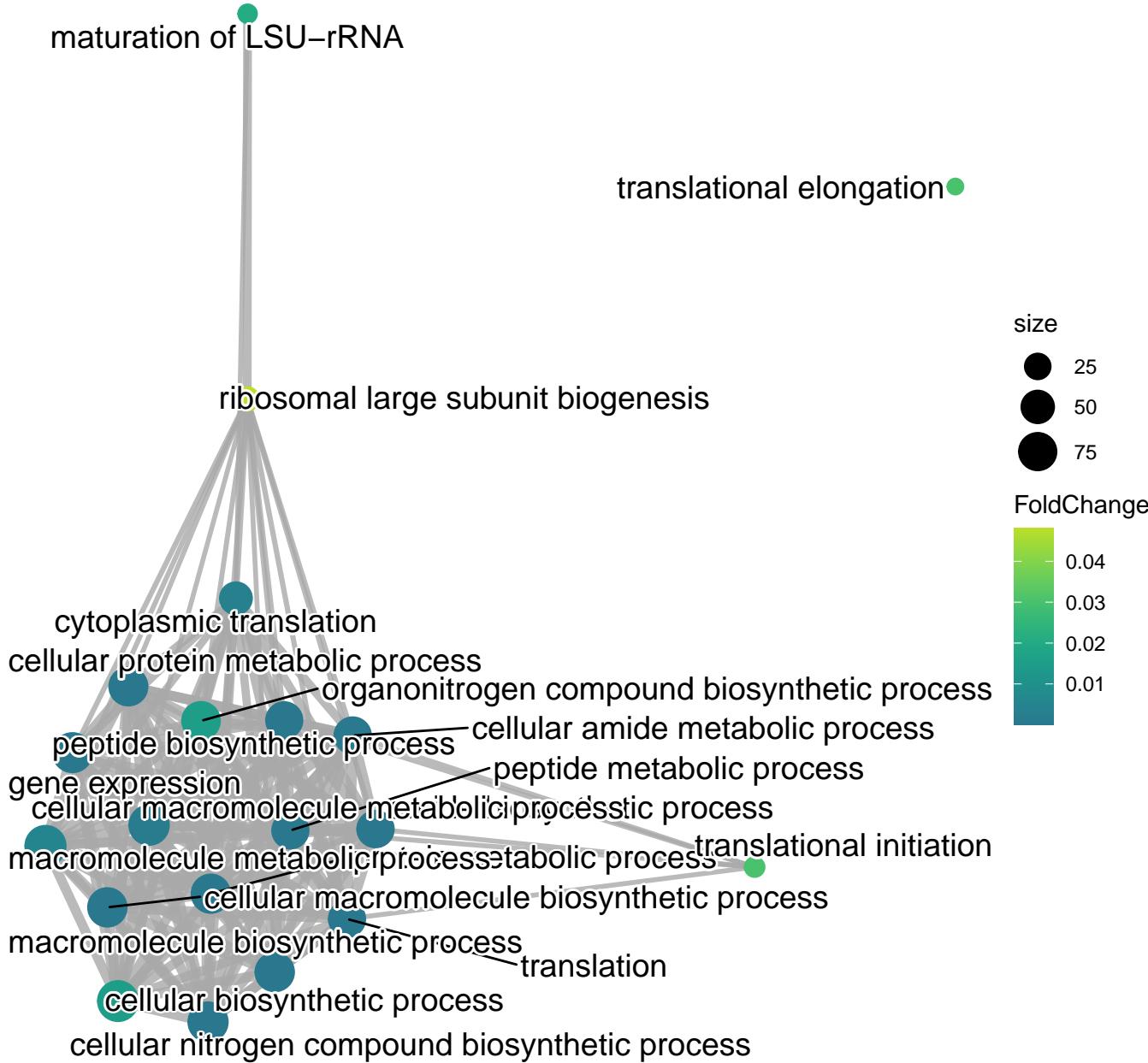
RPL27B

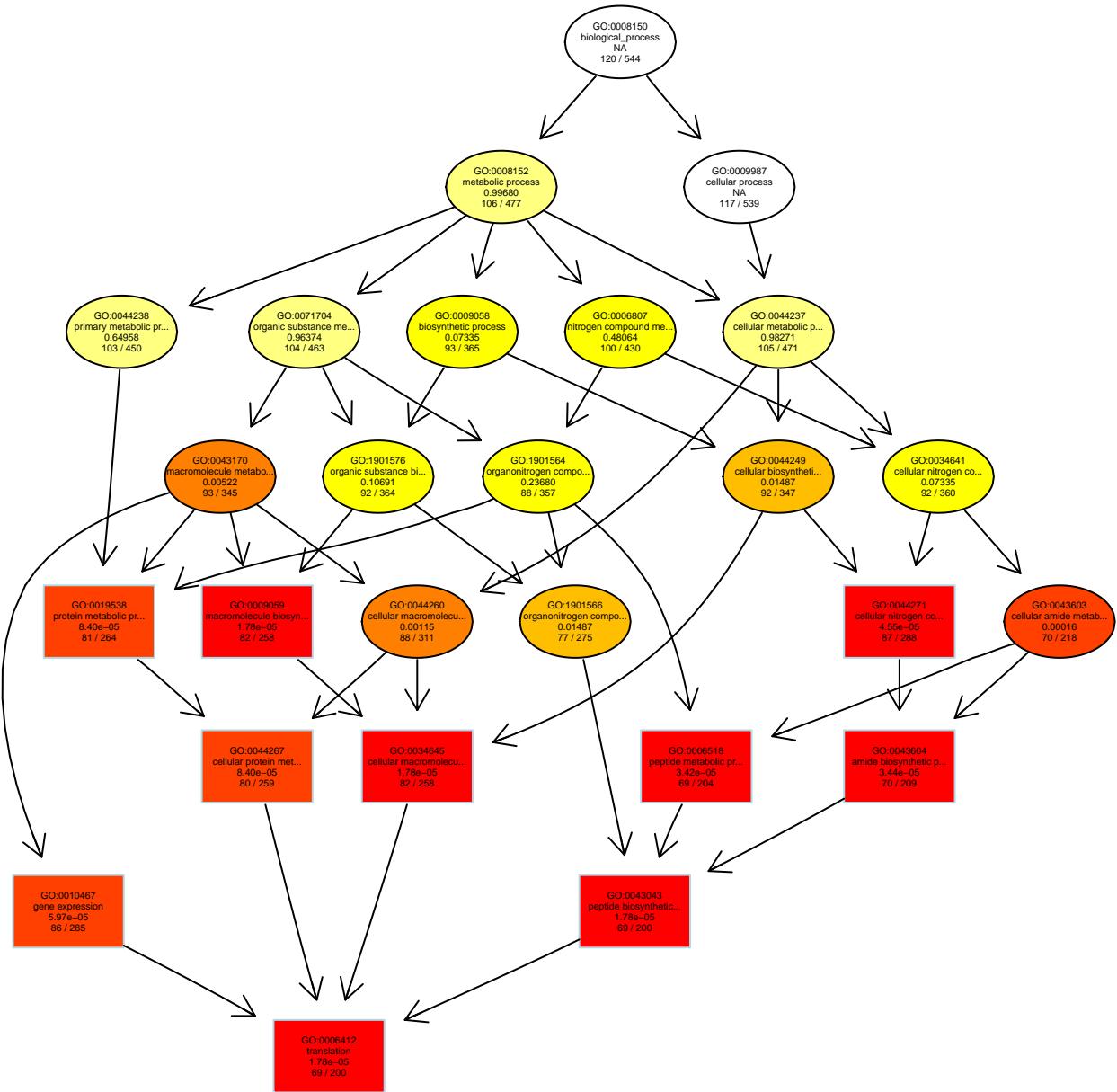
RPS21B

MPE1-TAP Up-regulated GO BP heatplot

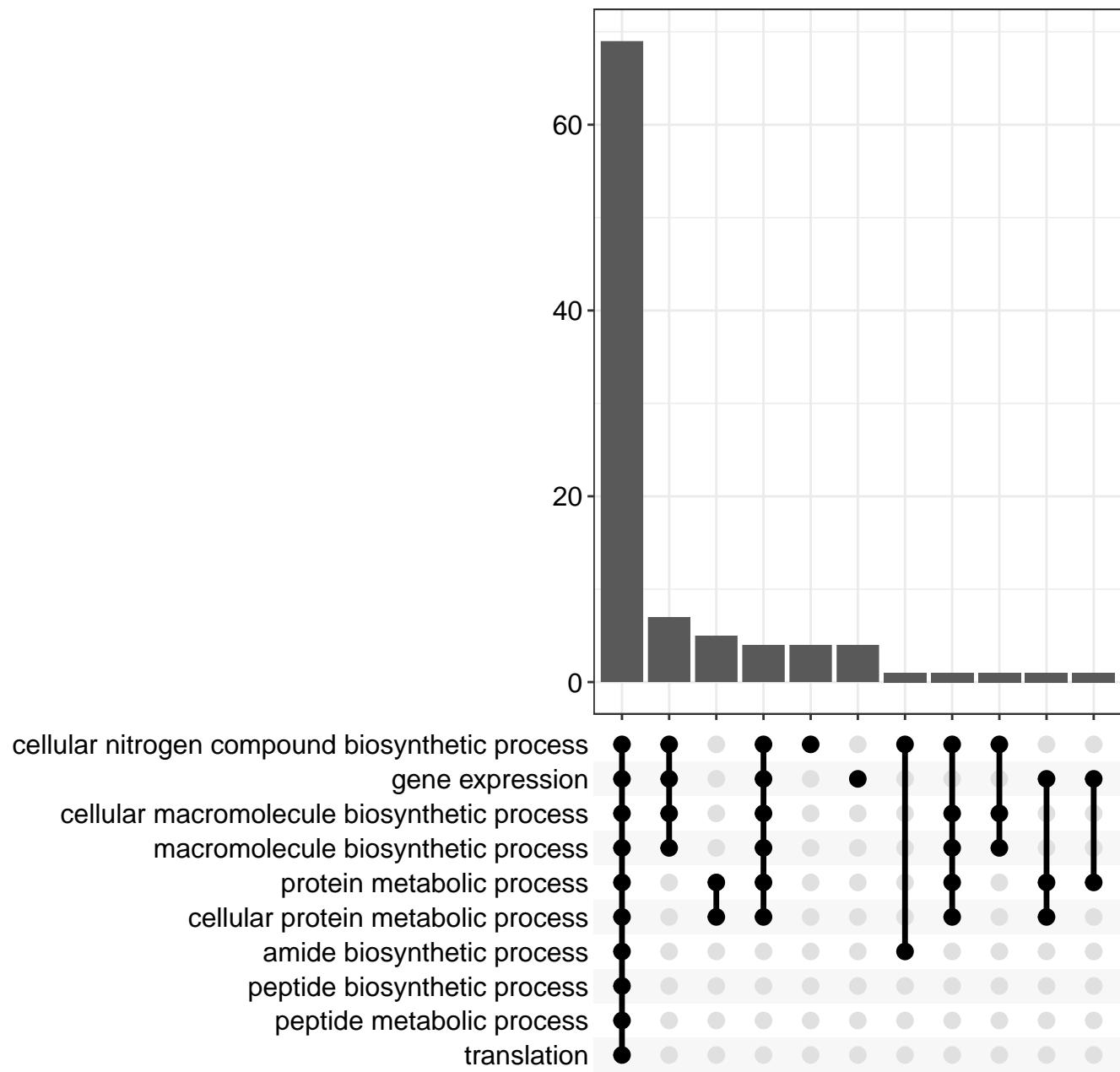


MPE1-TAP Up-regulated GO BP emapplot

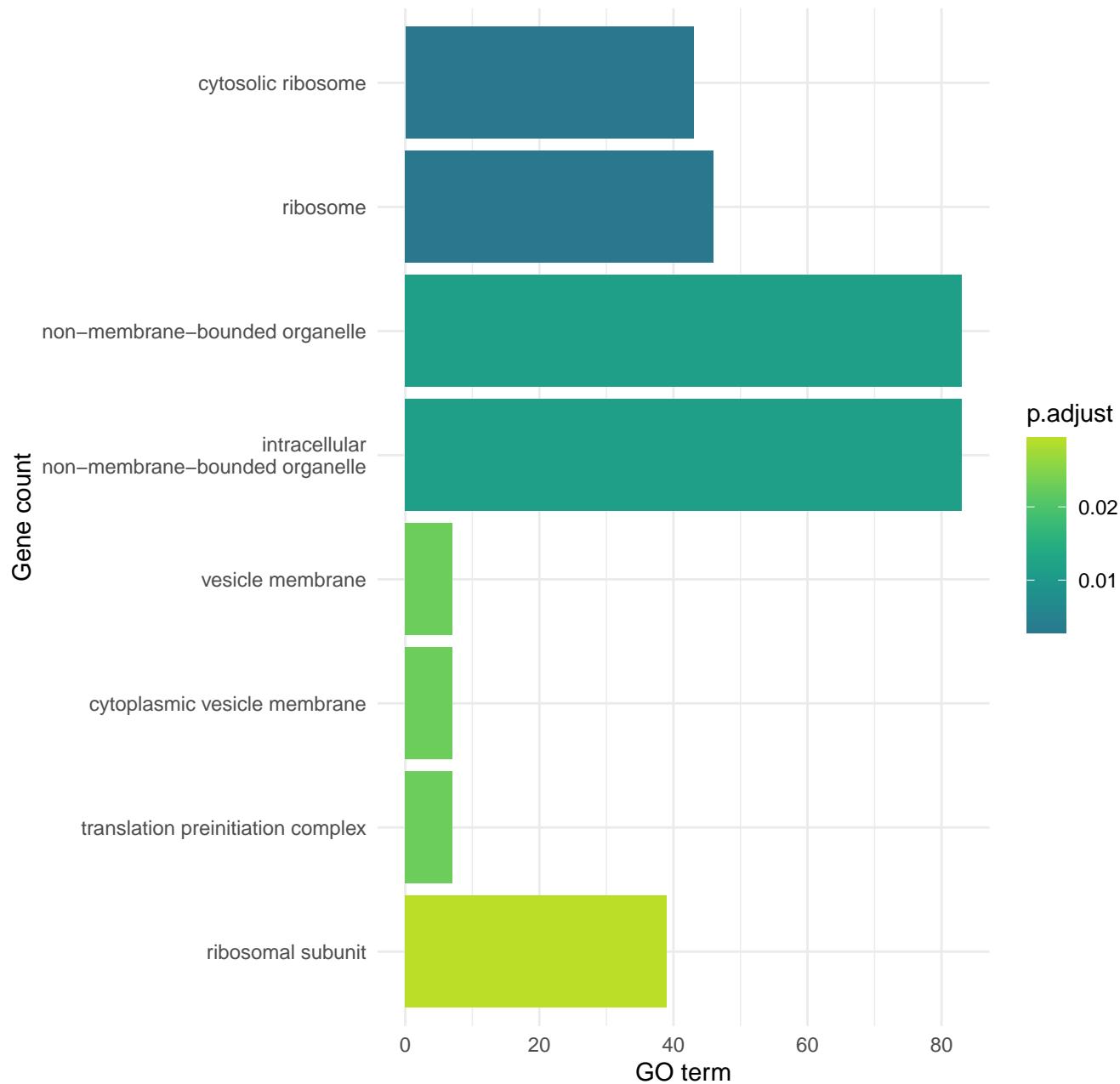




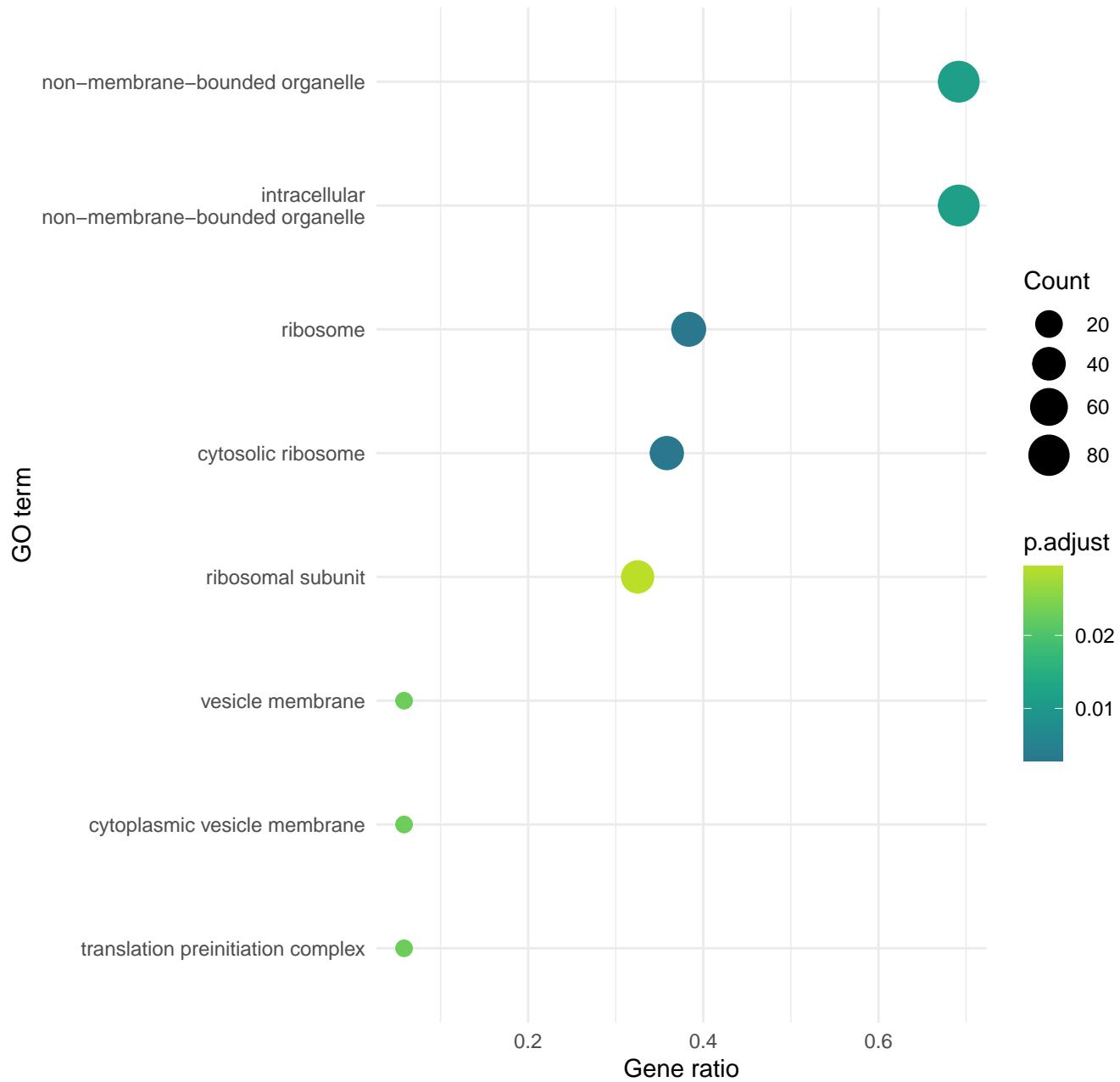
MPE1-TAP Up-regulated GO BP upsetplot



MPE1-TAP Up-regulated GO CC barplot



MPE1-TAP Up-regulated GO CC dotplot

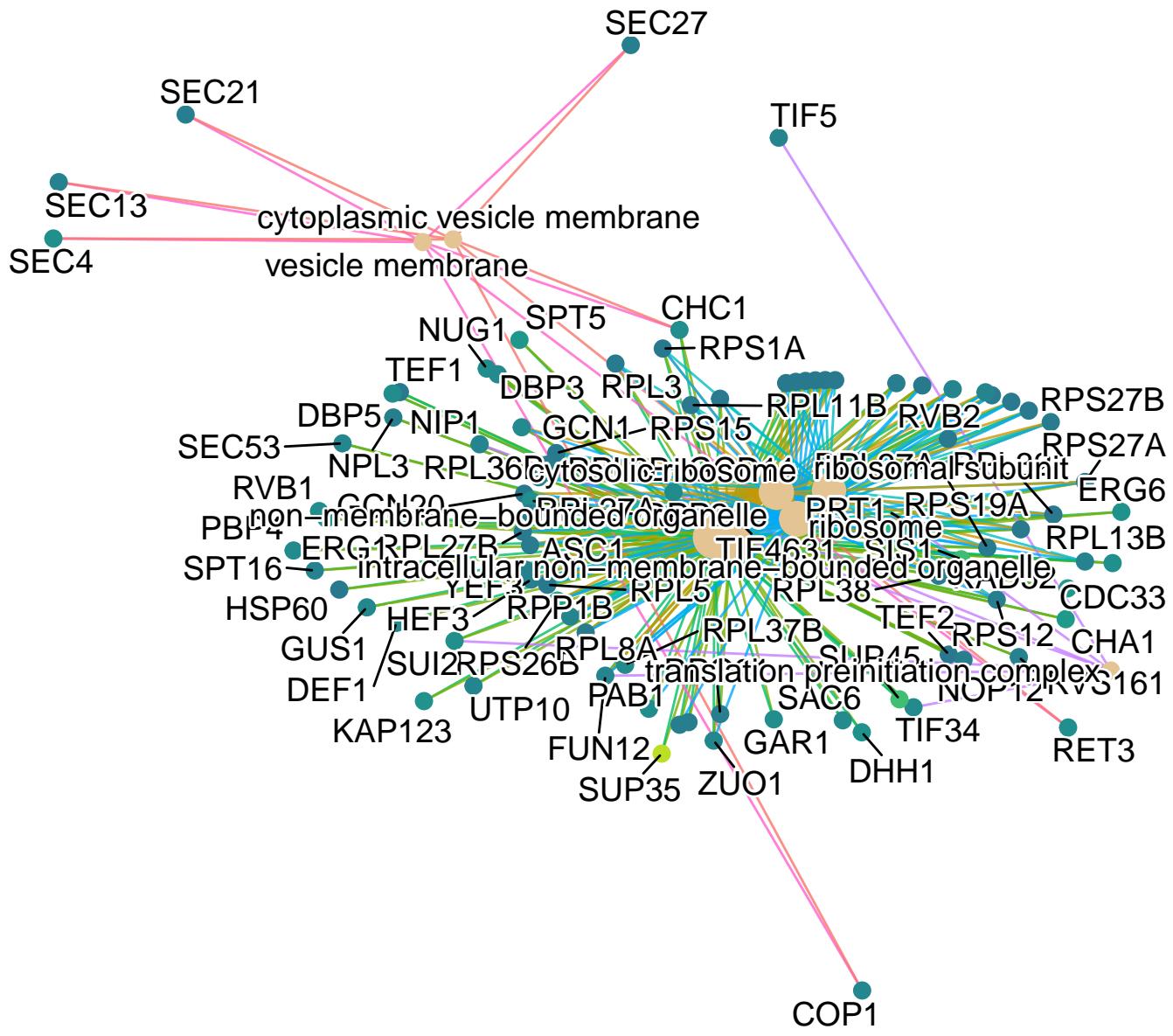


MPE1-TAP Up-regulated GO CC cnetplot

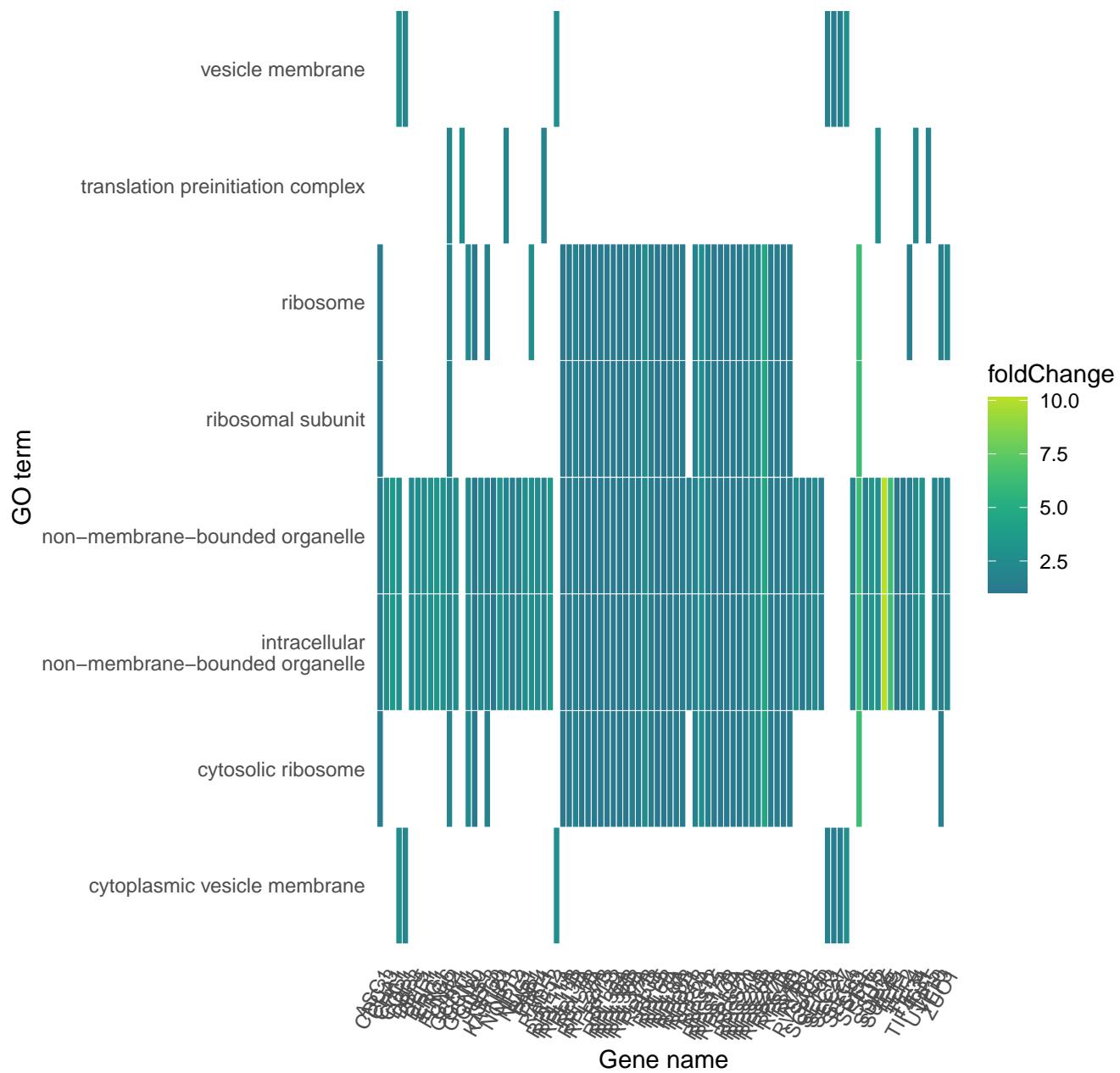
ular non-membrane-bound
membrane-bounded organelle

— ribosomal subunit — translation preinitiation complex
— ribosome — vesicle membrane

FoldChange 2.5



MPE1-TAP Up-regulated GO CC heatplot

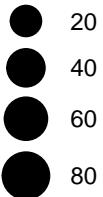


MPE1-TAP Up-regulated GO CC emapplot

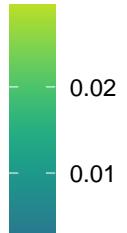
cytoplasmic vesicle membrane

vesicle membrane

size



FoldChange



translation preinitiation complex

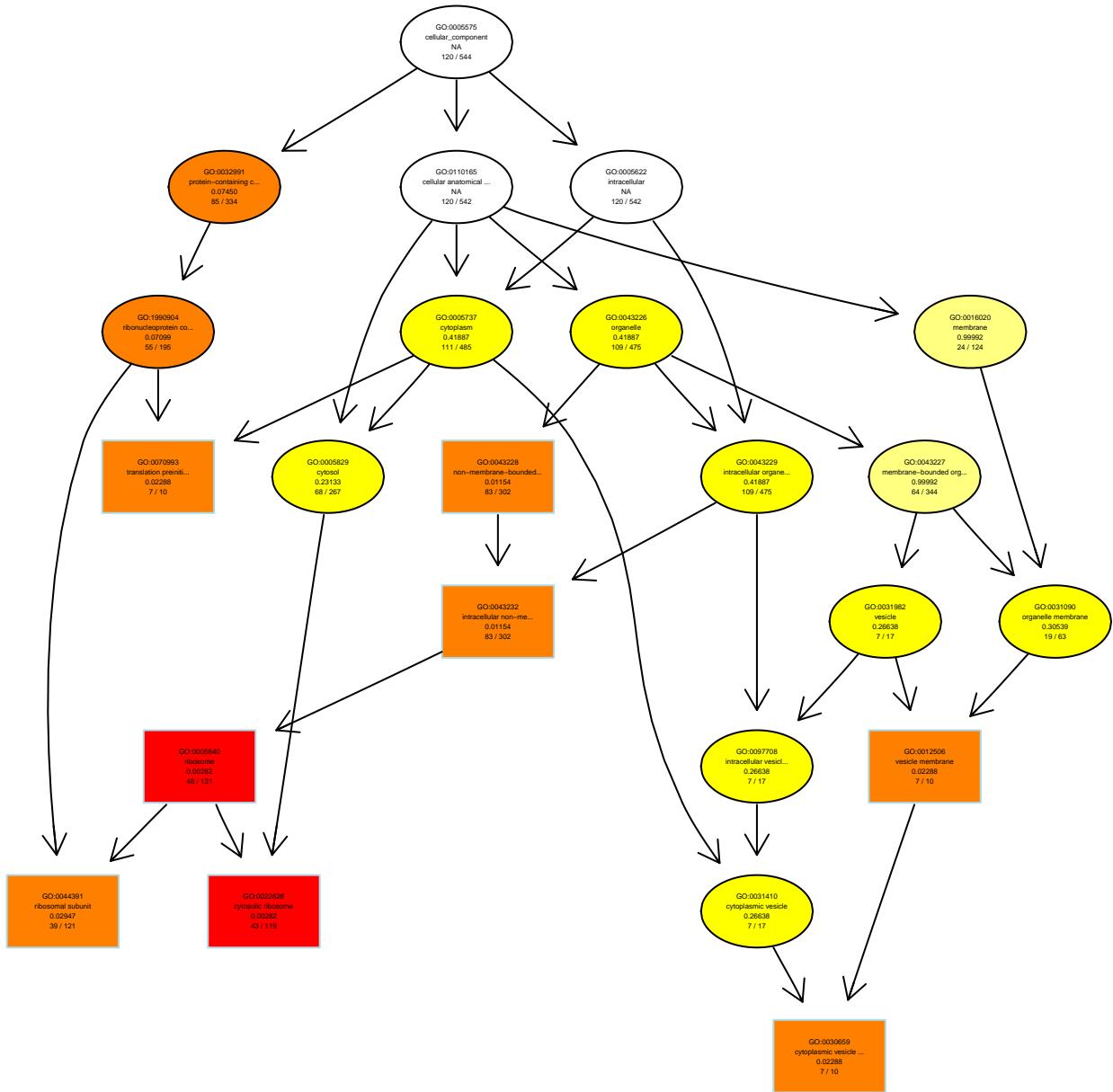
intracellular non-membrane-bounded organelle

non-membrane-bounded organelle

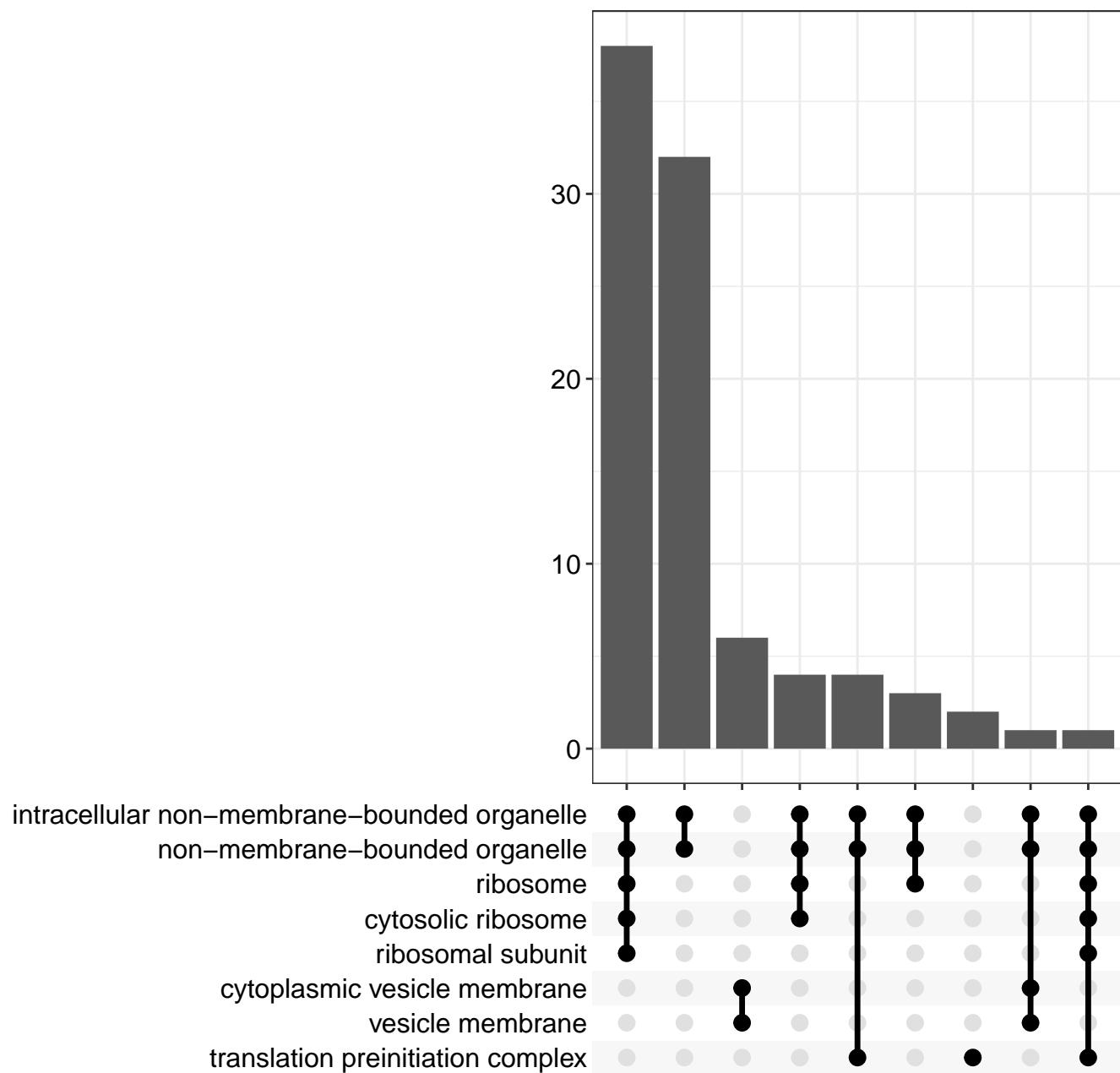
ribosome

ribosomal subunit

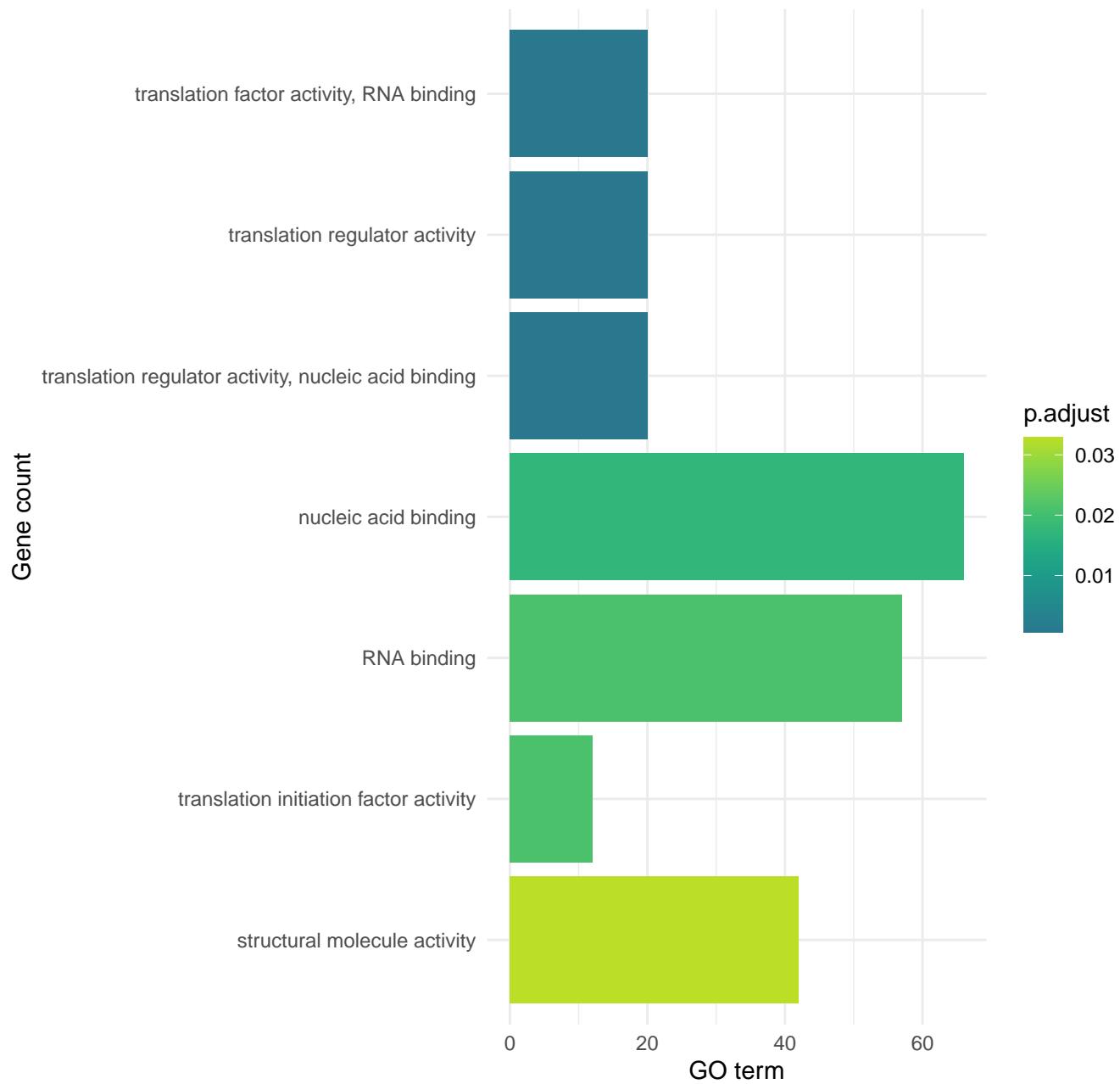
cytosolic ribosome



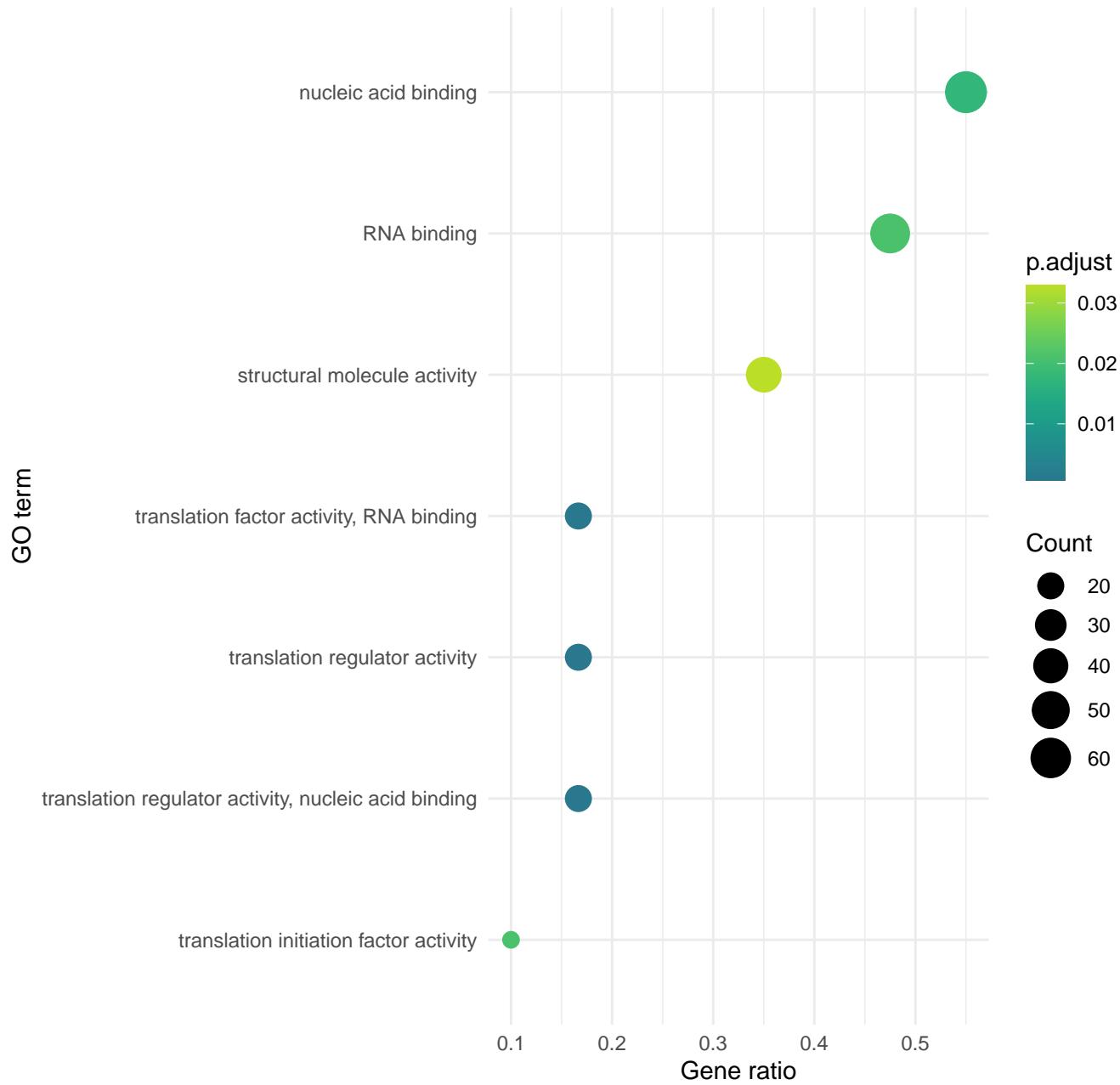
MPE1-TAP Up-regulated GO CC upsetpl



MPE1-TAP Up-regulated GO MF barplot



MPE1–TAP Up-regulated GO MF dotplot



MPE1-TAP Up-regulated GO MF cnetplot

nucleic acid binding

- structural molecule activity

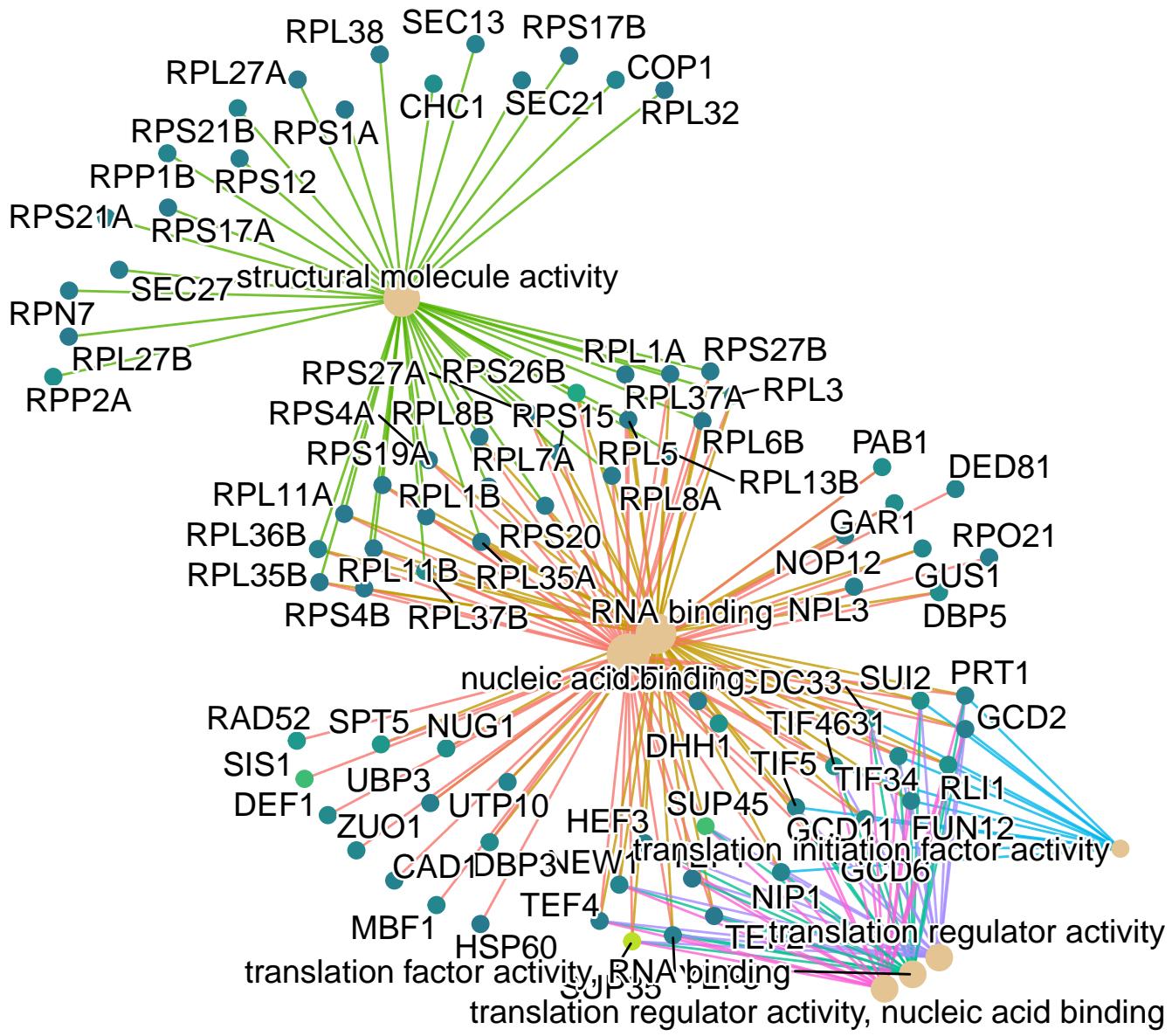
— translation initiation factor activity

— translation reg

RNA binding

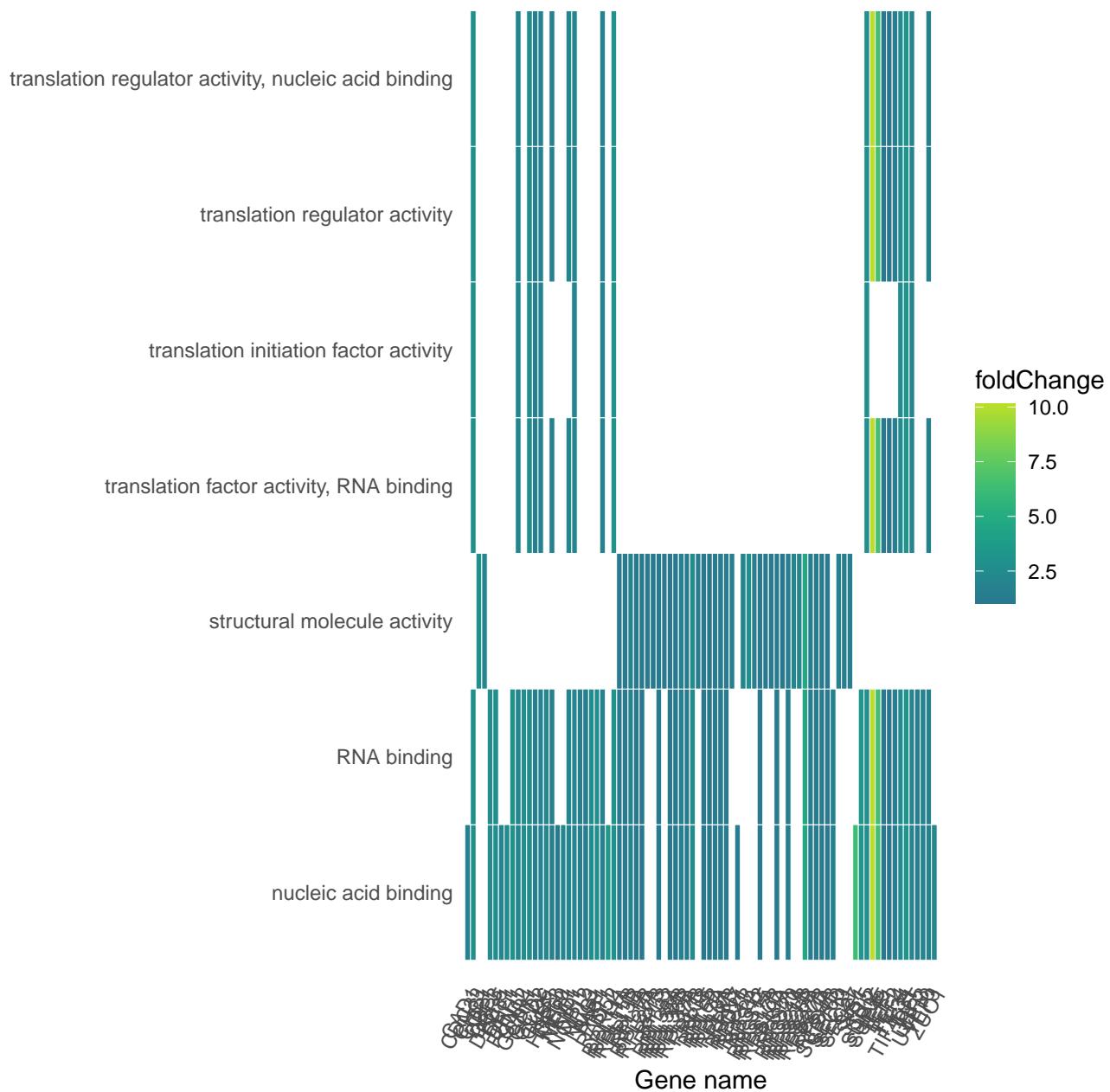
— translation factor activity, RNA binding

— translation regulator activity

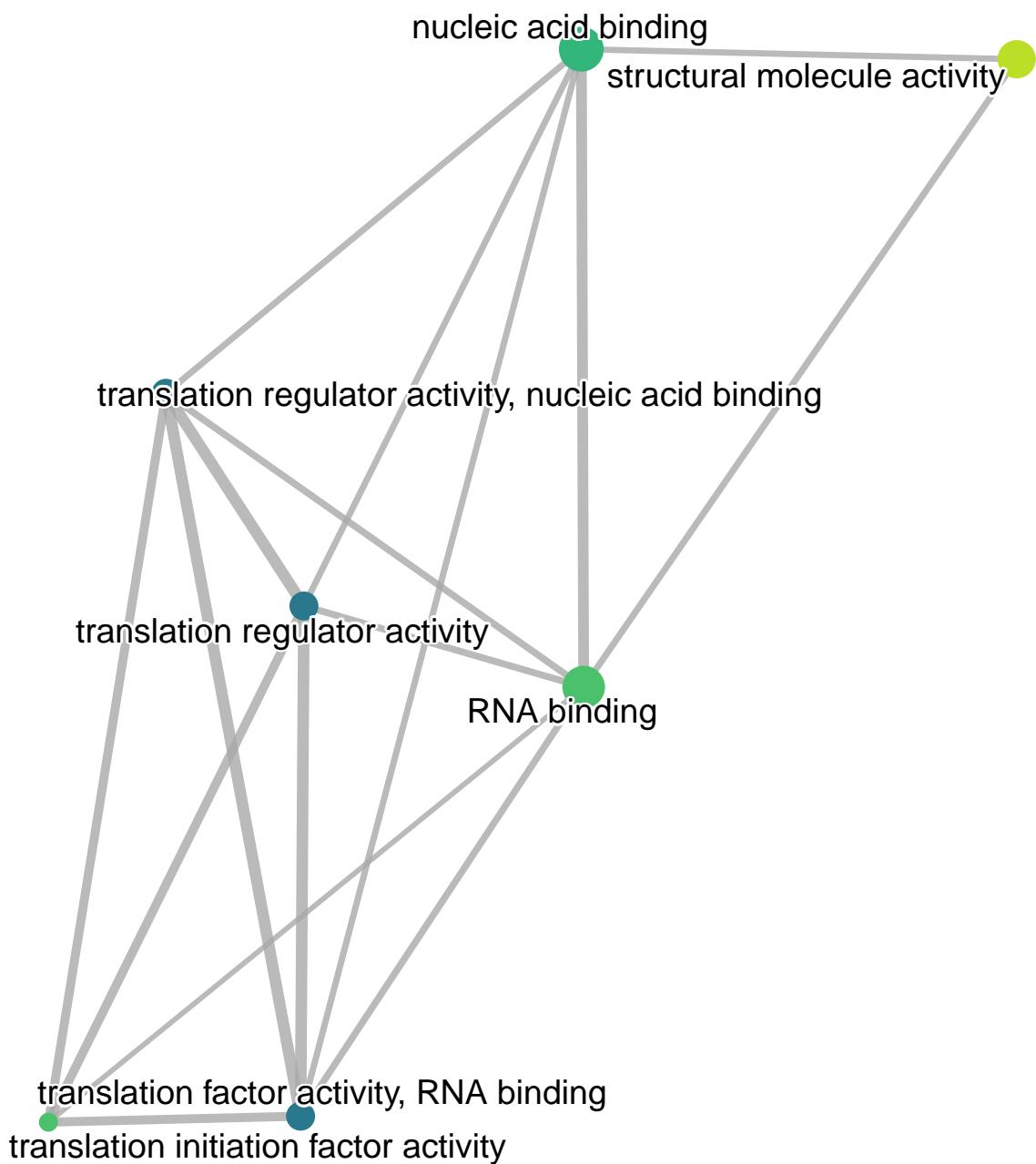


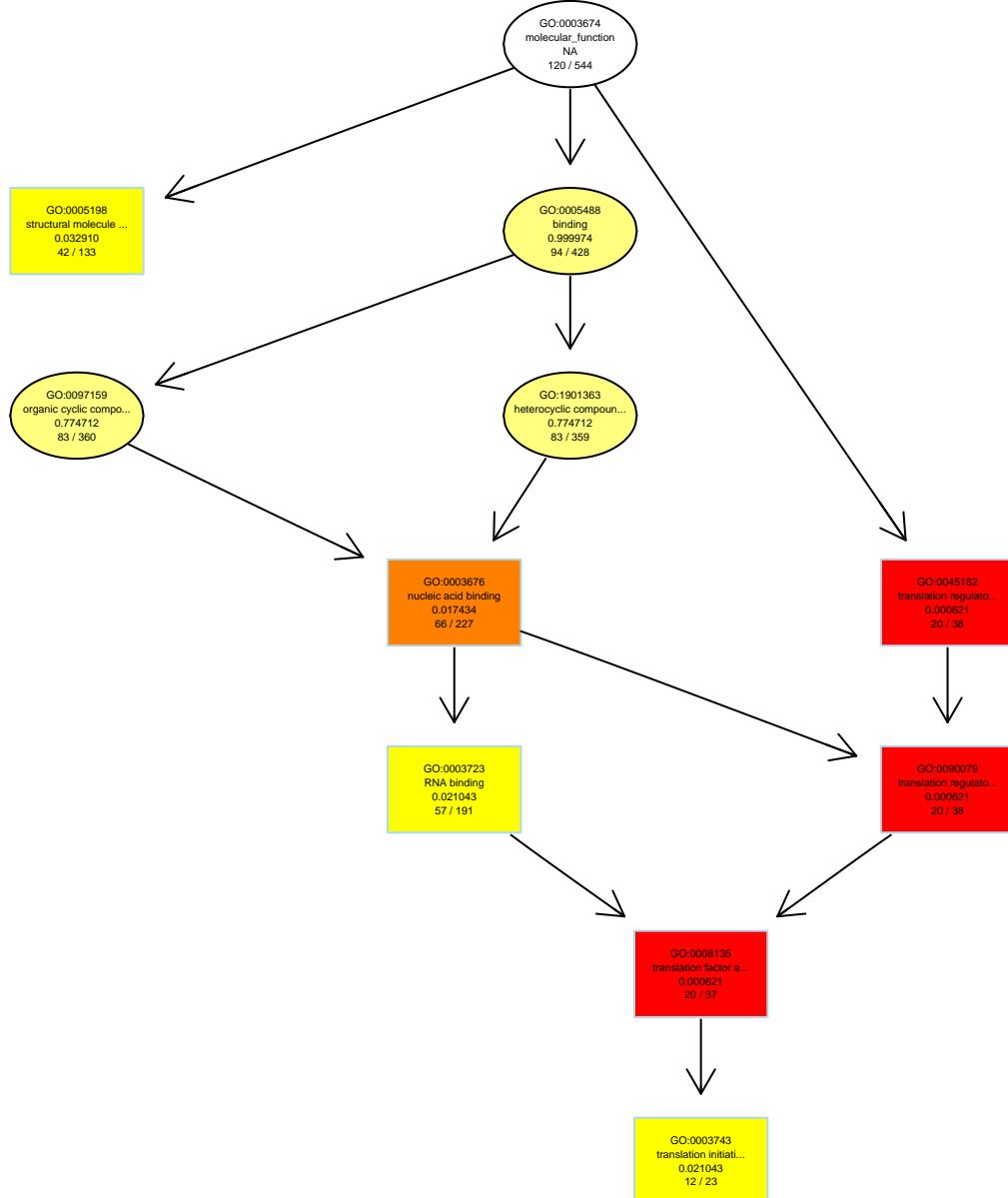
MPE1-TAP Up-regulated GO MF heatplot

GO term

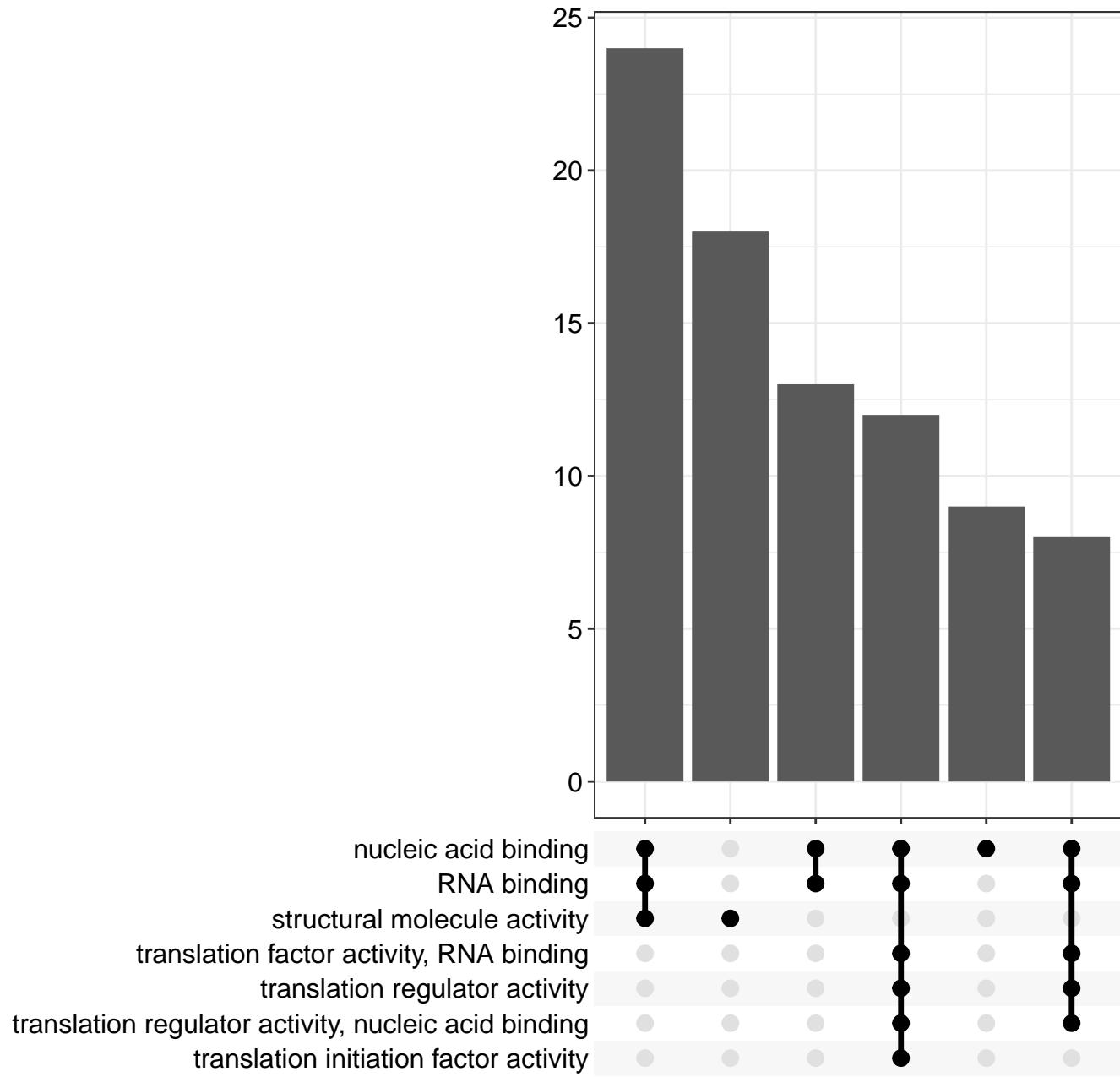


MPE1-TAP Up-regulated GO MF emapplot



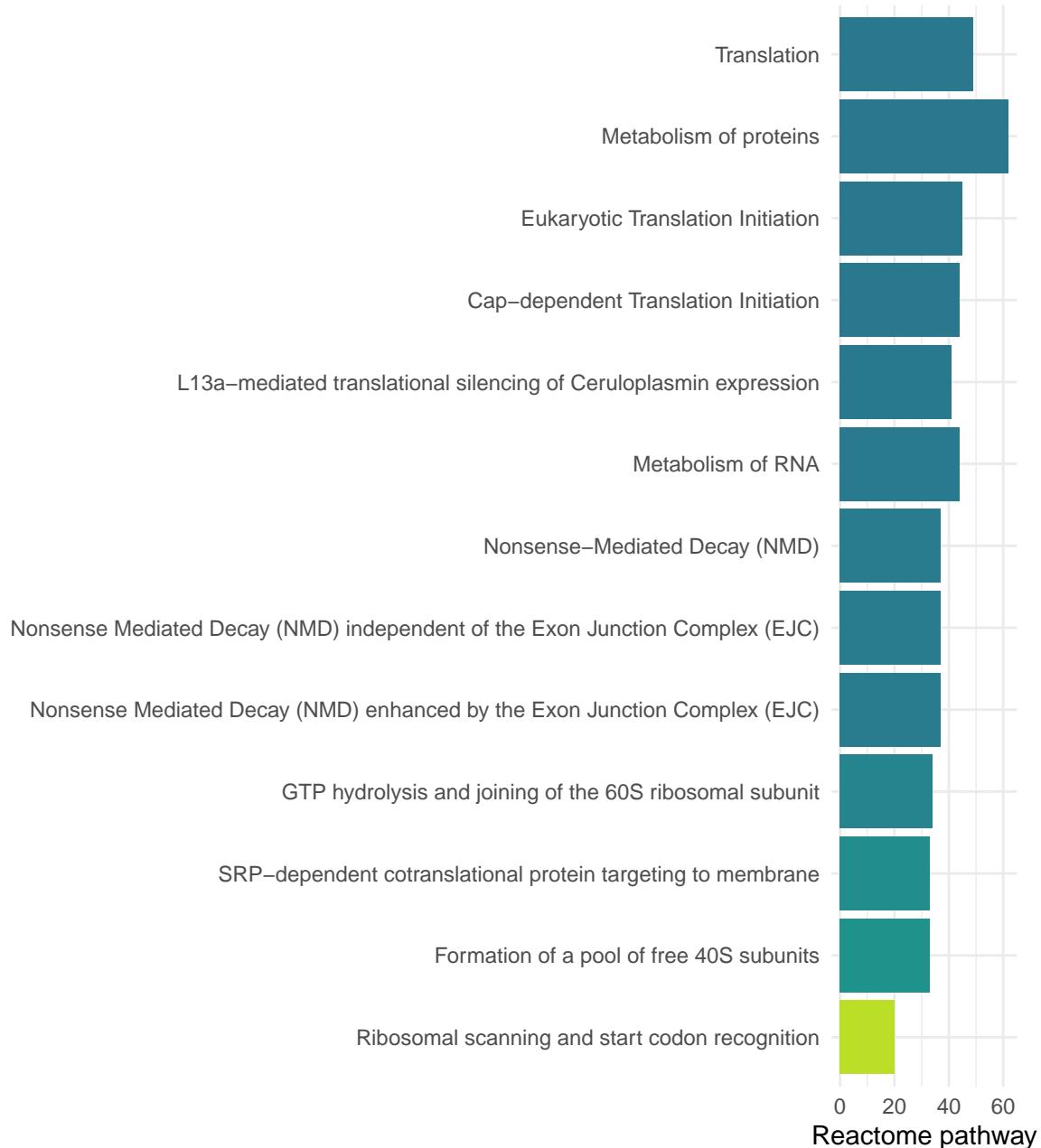


MPE1-TAP Up-regulated GO MF upsetpl



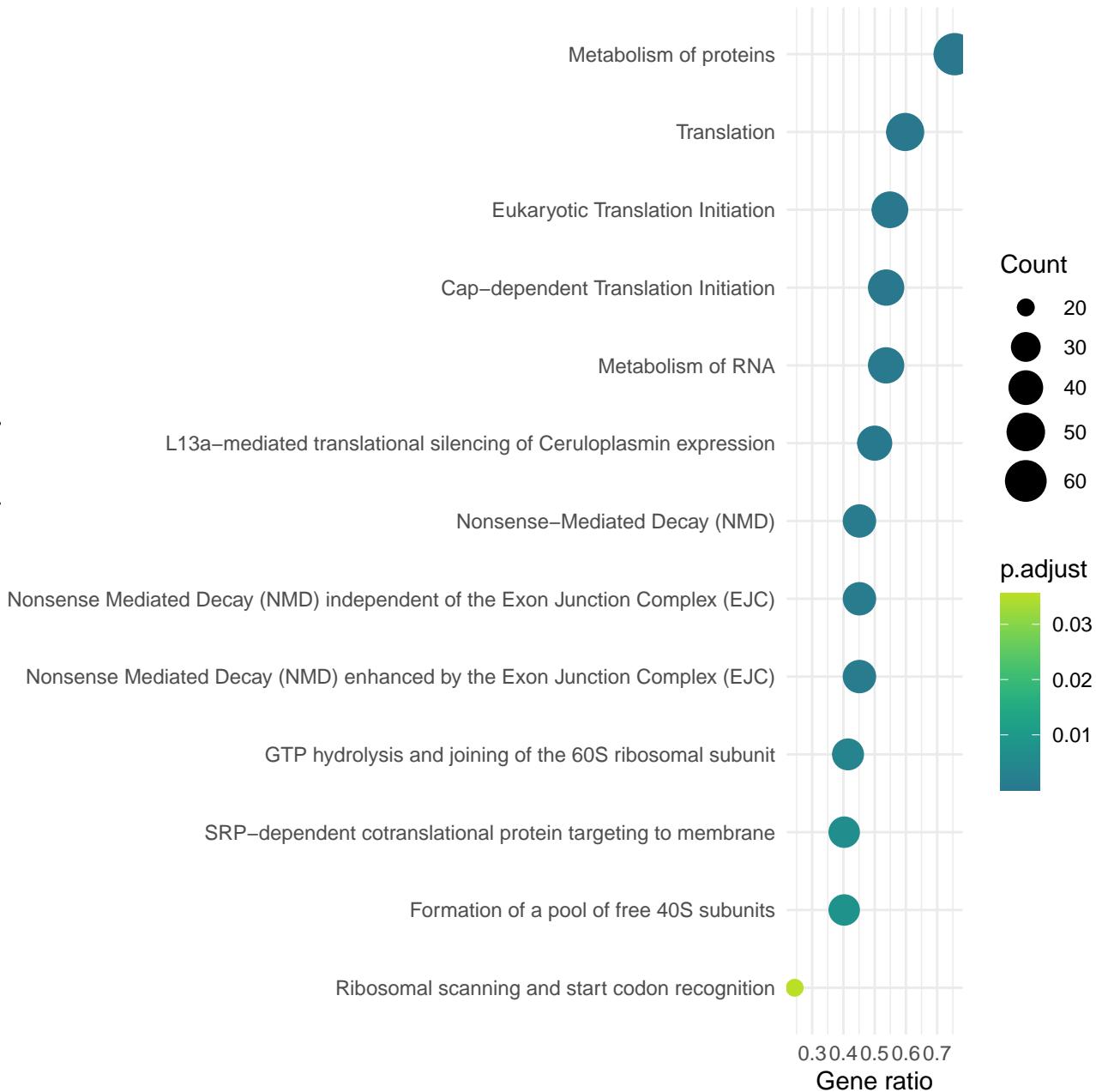
MPE1-TAP Up-regulated

Gene count



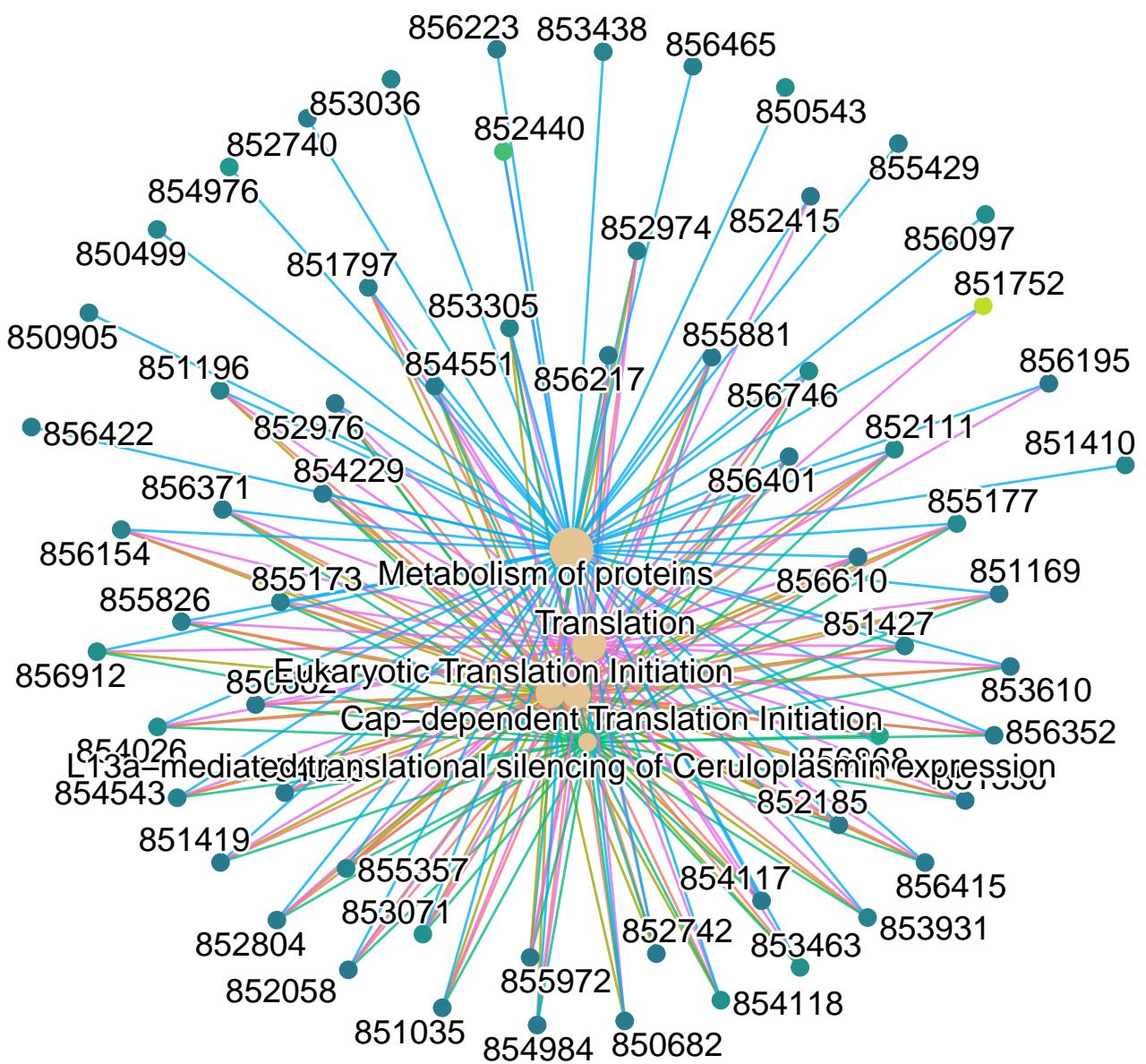
MPE1-TAP Up-regulated

Reactome pathway



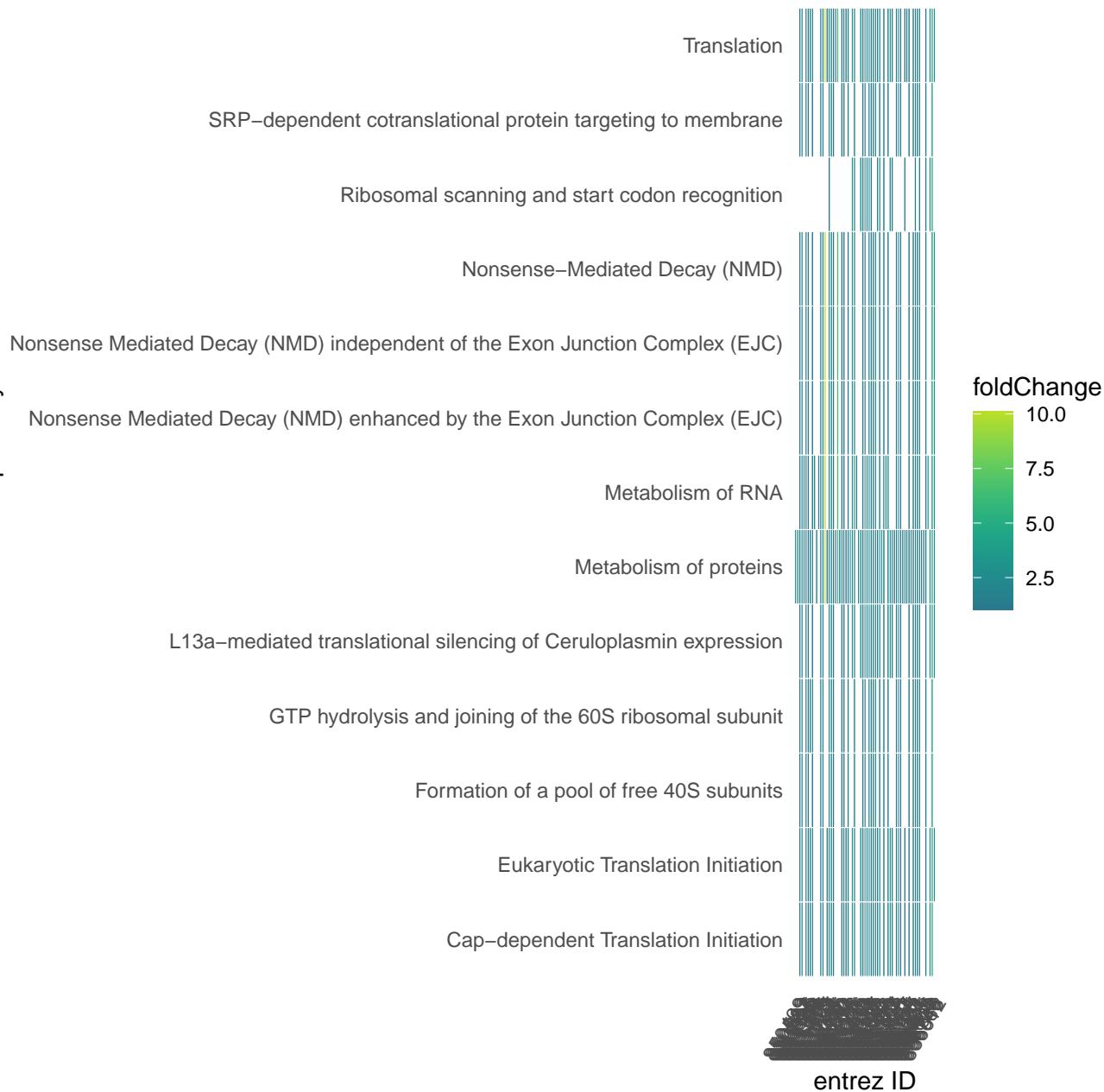
MPE1–TAP Up-regulated Reactome cnetplot

category — Cap-dependent Translation Initiation — Eukaryotic Translation Initiation — L13a-mediated translational

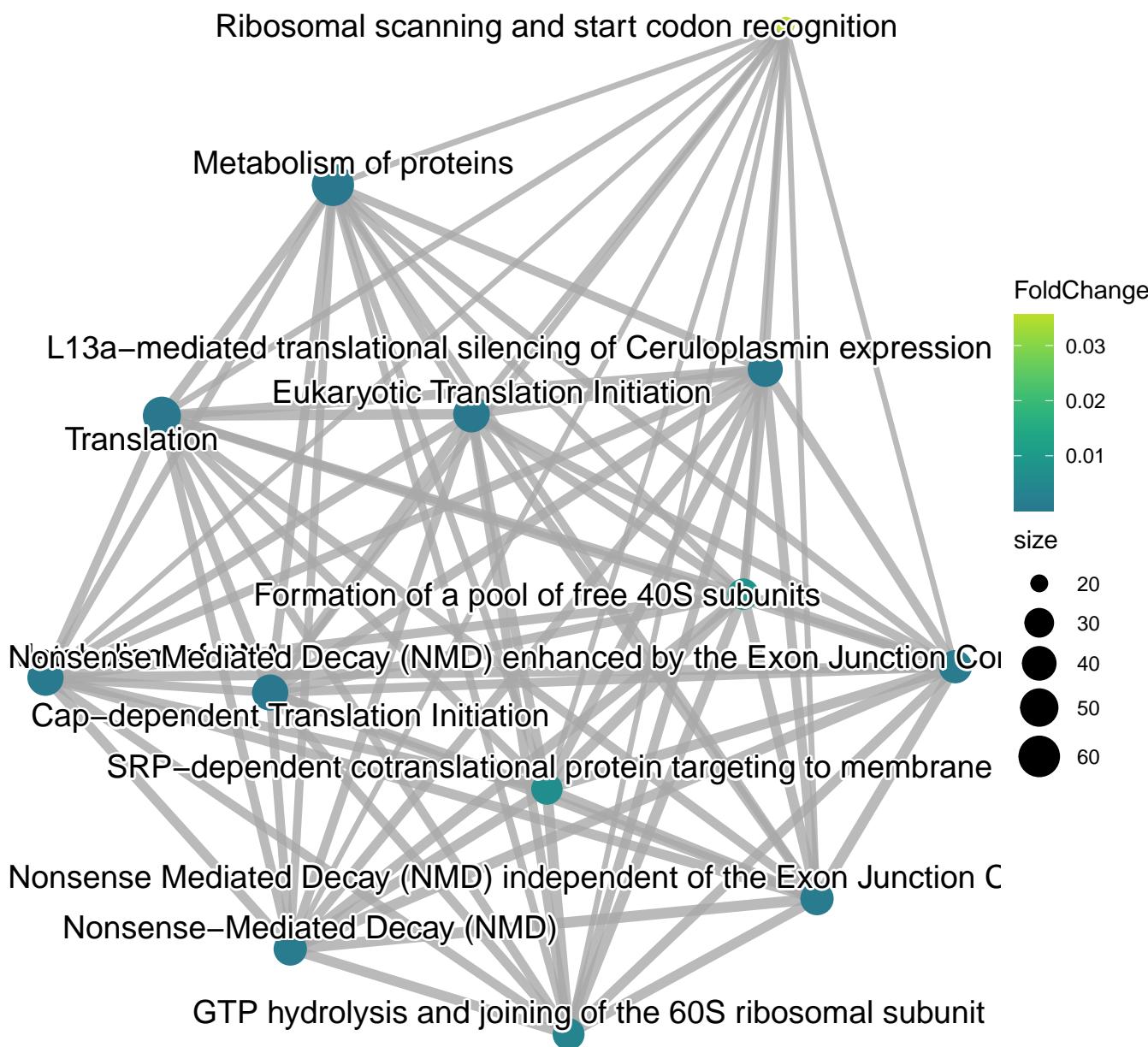


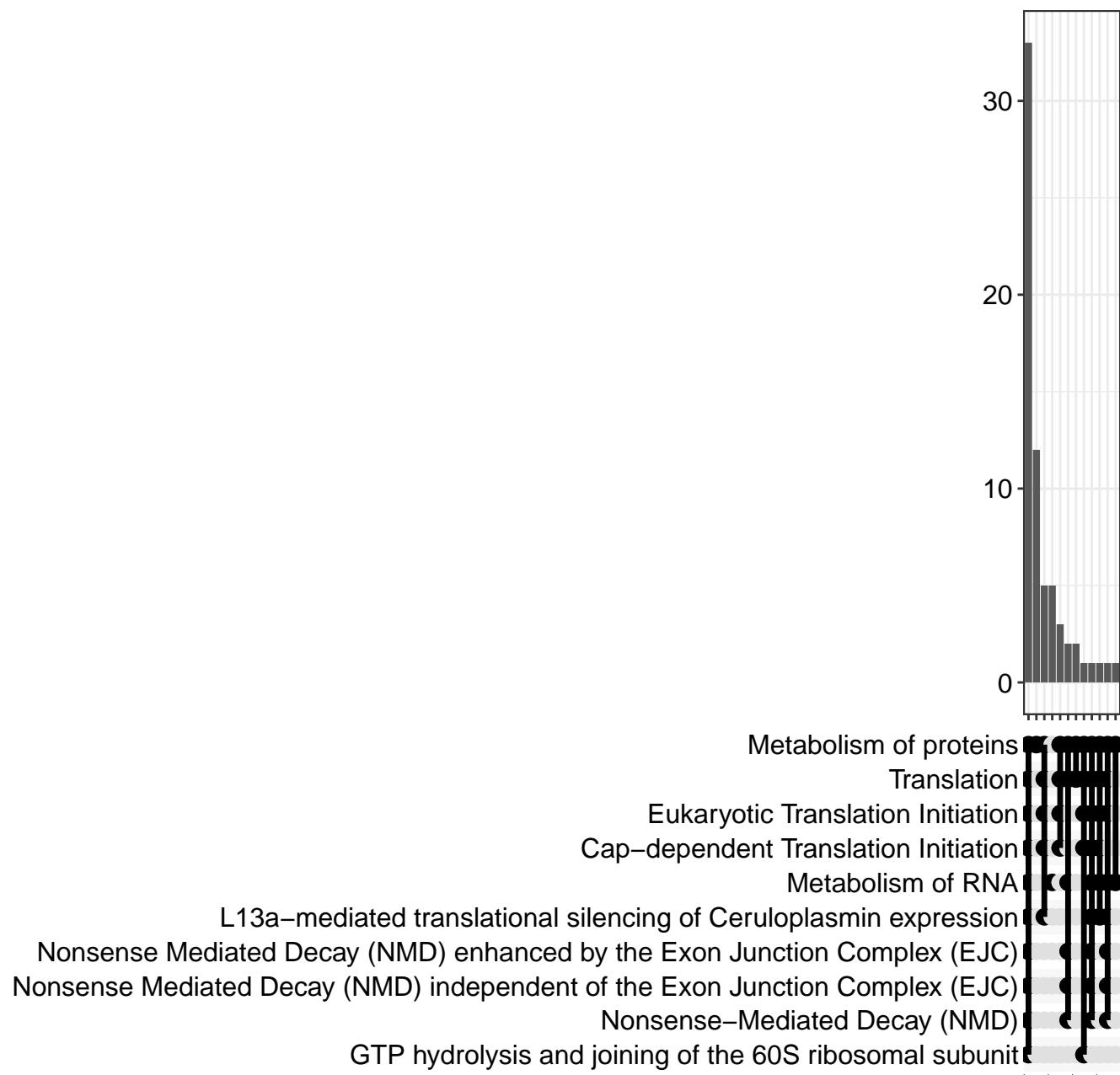
MPE1-TAP Up-regulated

Reactome pathway

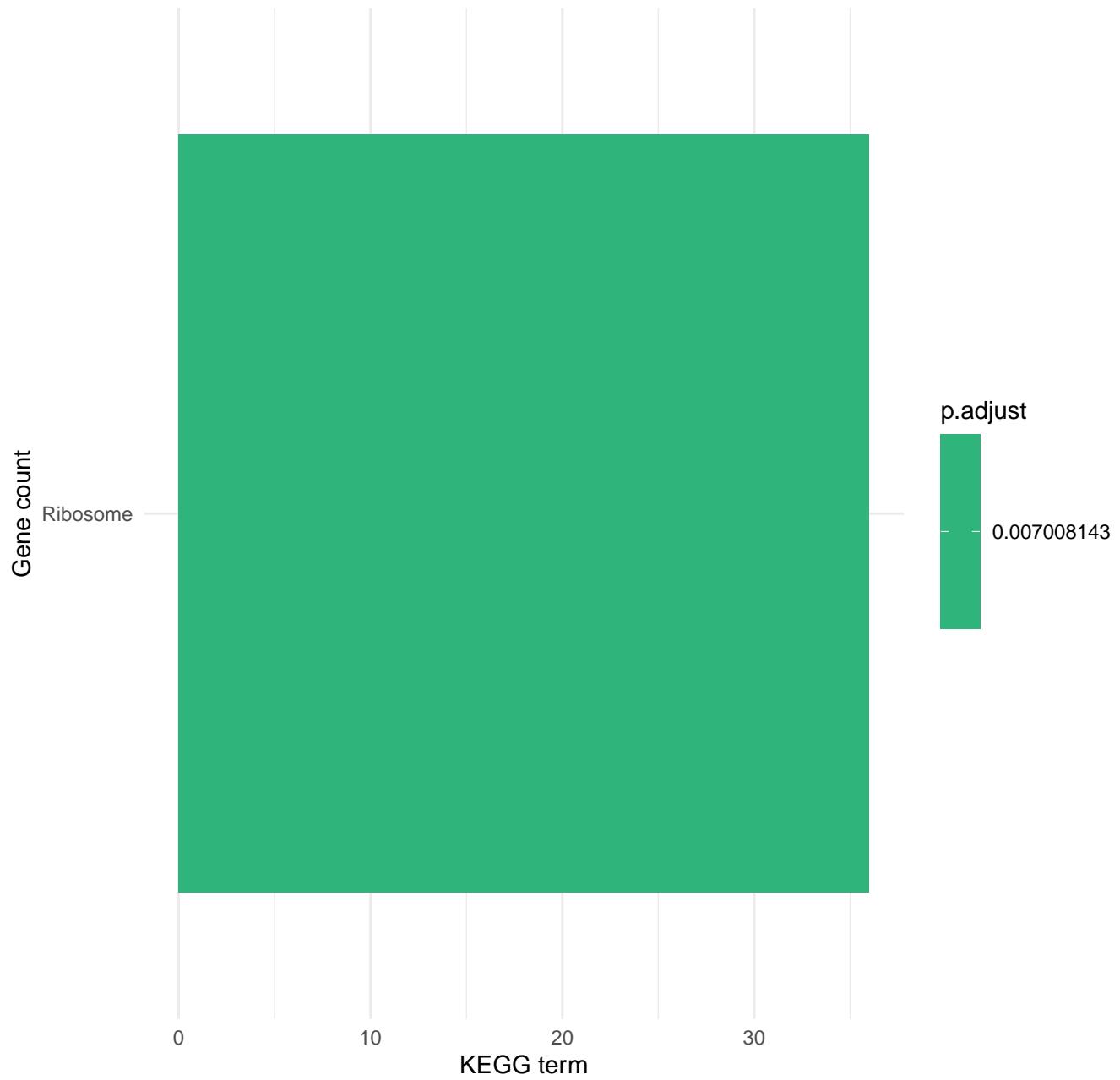


MPE1-TAP Up-regulated Reactome emapplot

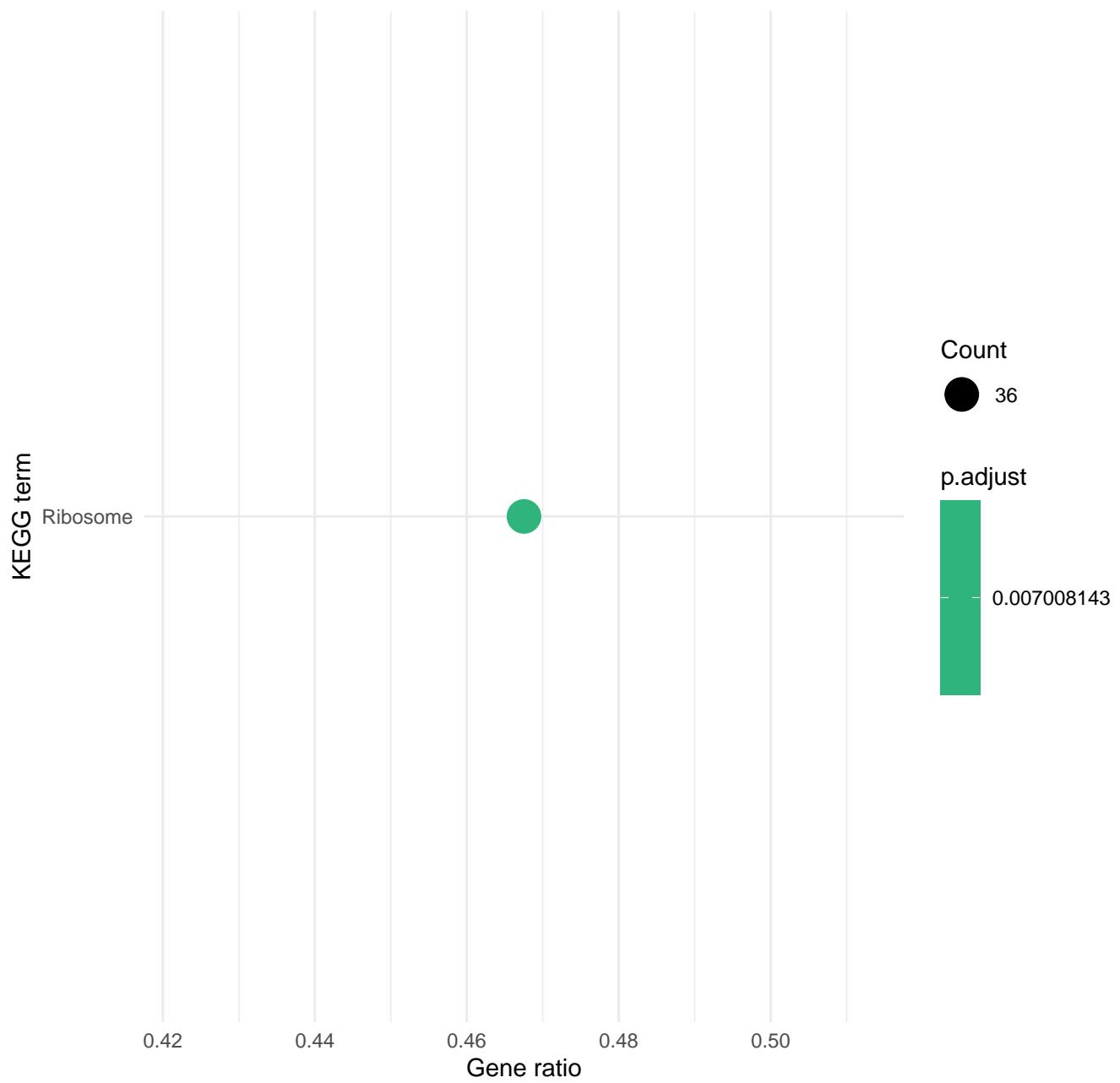




MPE1-TAP Up-regulated KEGG barplot



MPE1-TAP Up-regulated KEGG dotplot



MPE1-TAP Up-regulated KEGG dotplot

size

36

category

Ribosome

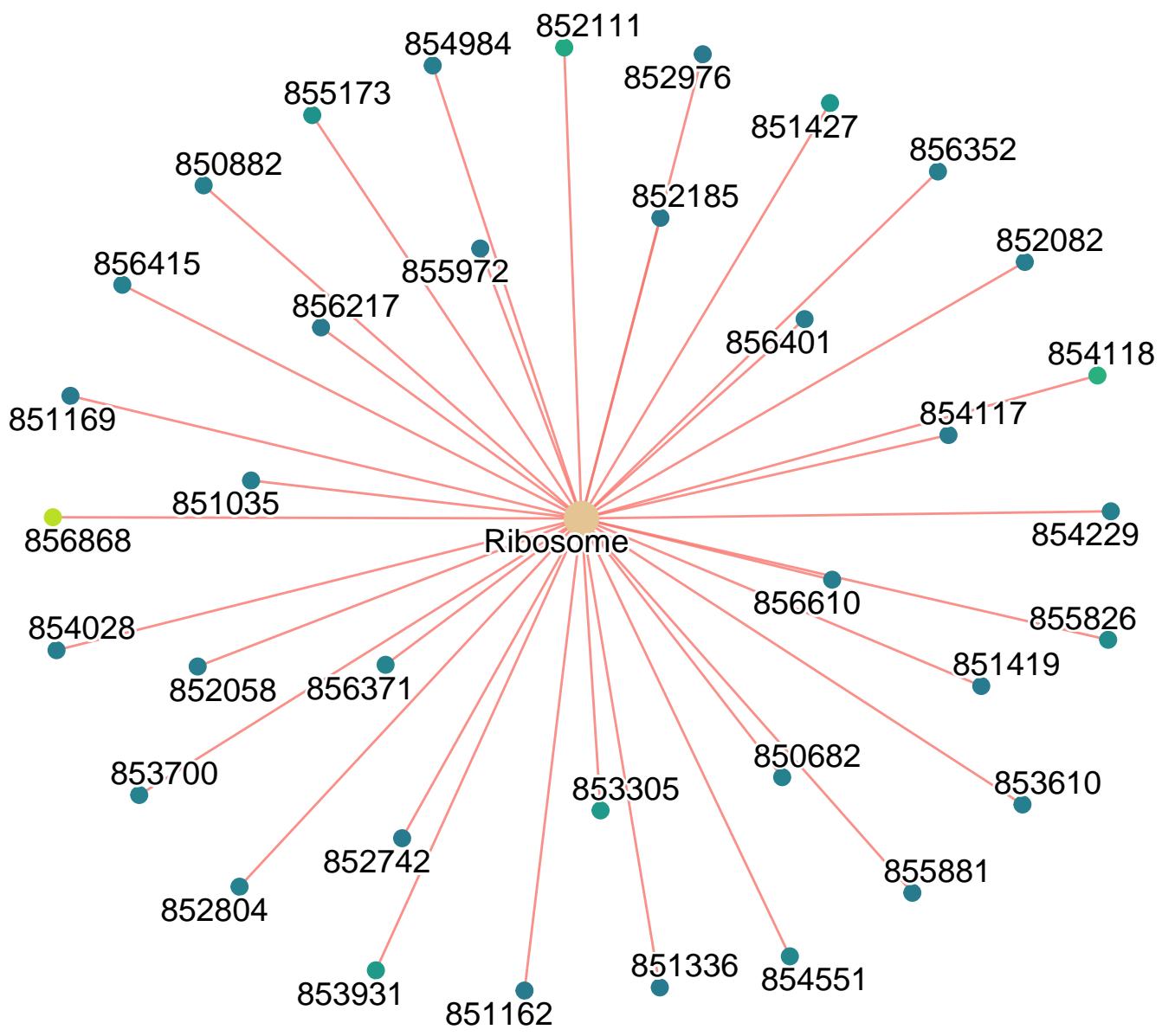
FoldChange



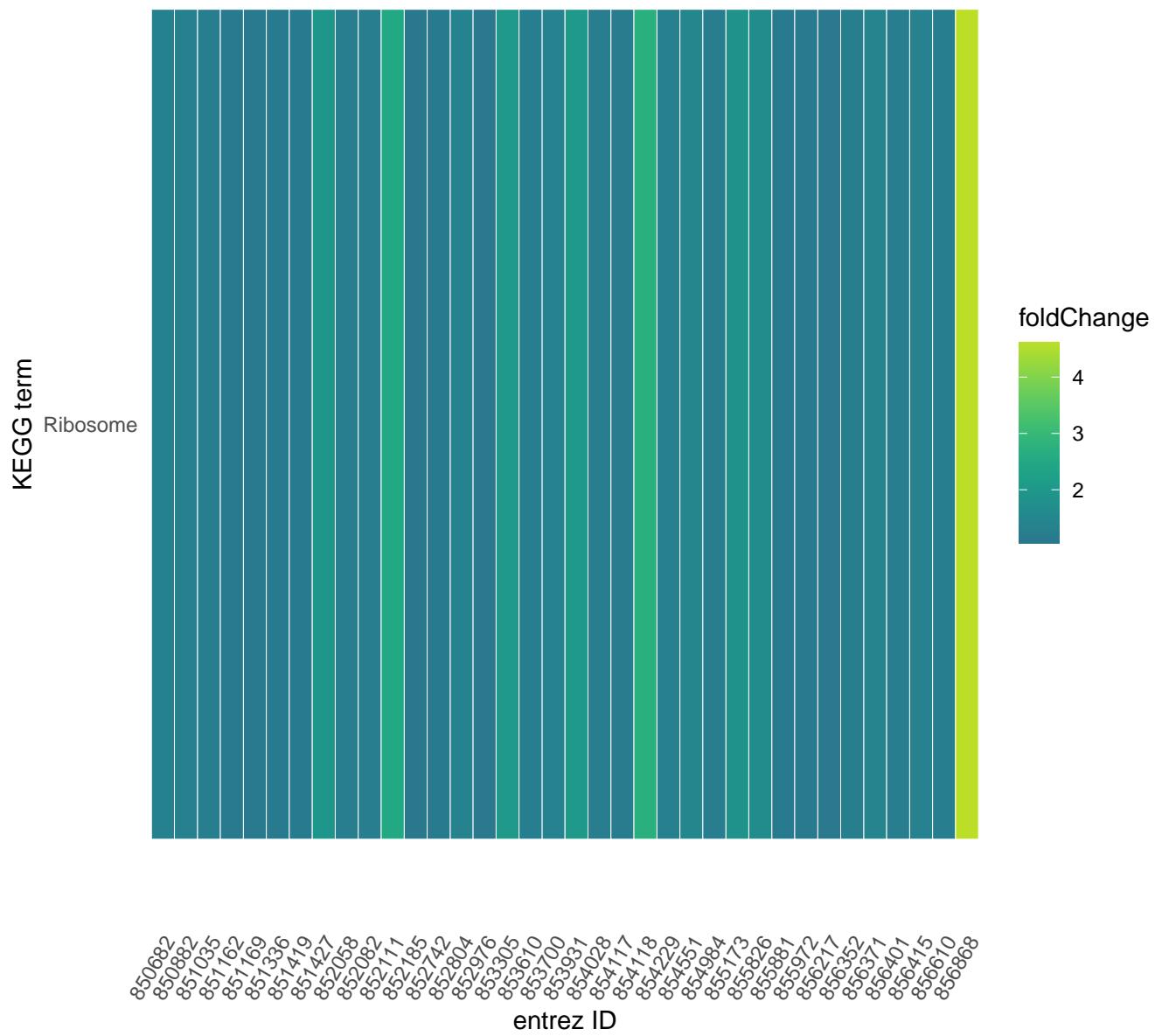
2

3

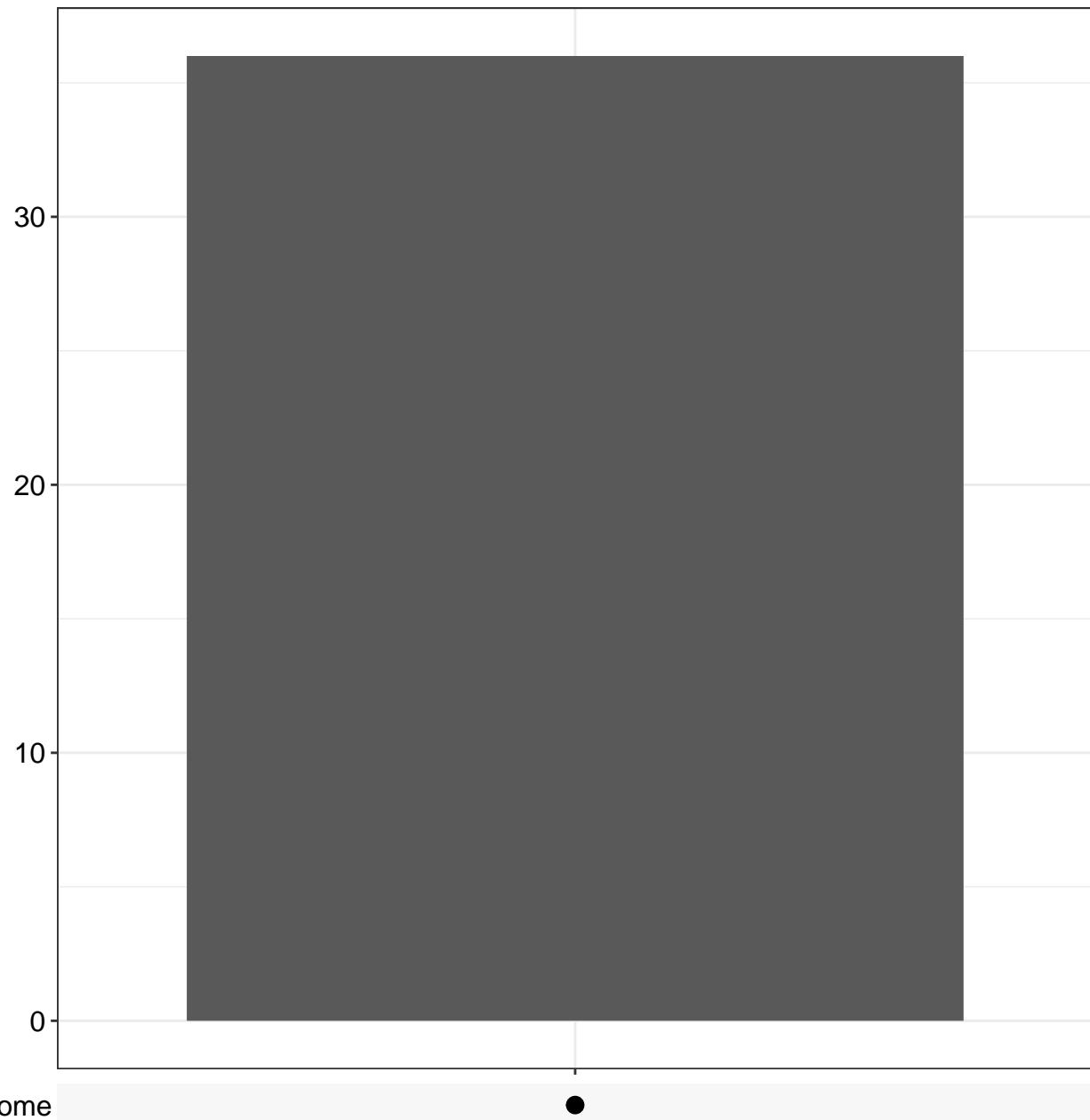
4



MPE1-TAP Up-regulated KEGG heatplot

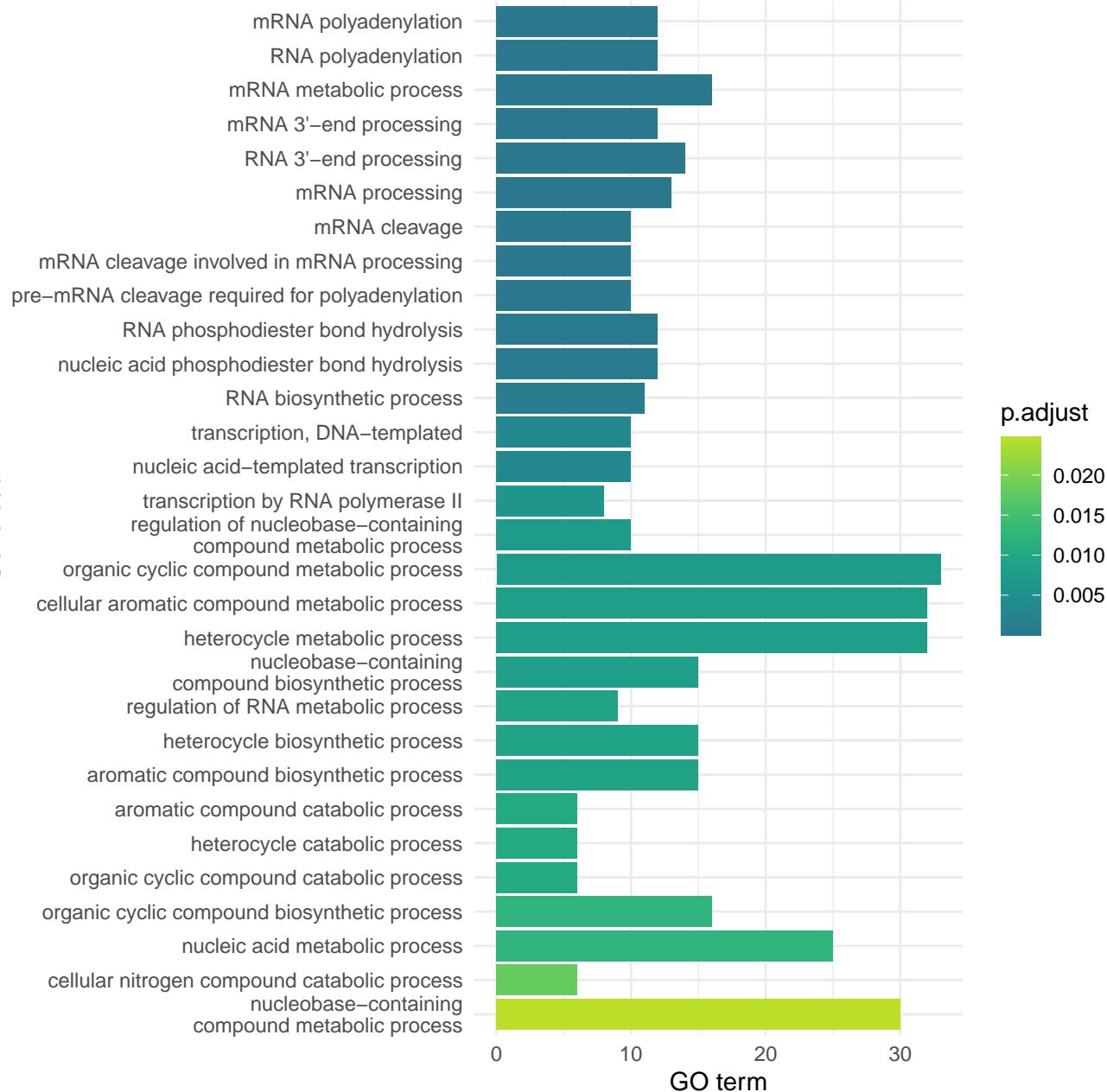


MPE1-TAP Up-regulated KEGG upsetplot

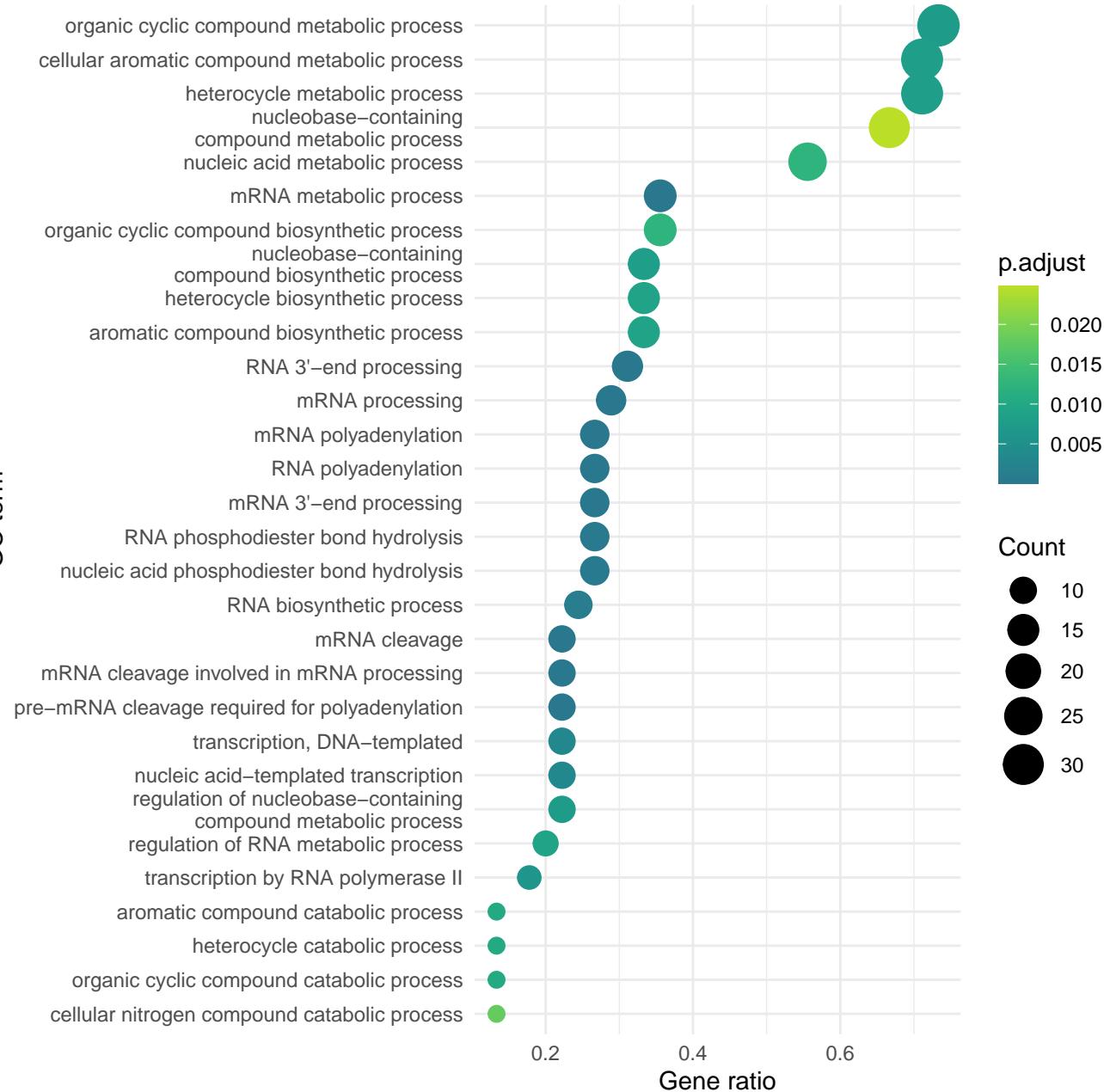


Ribosome

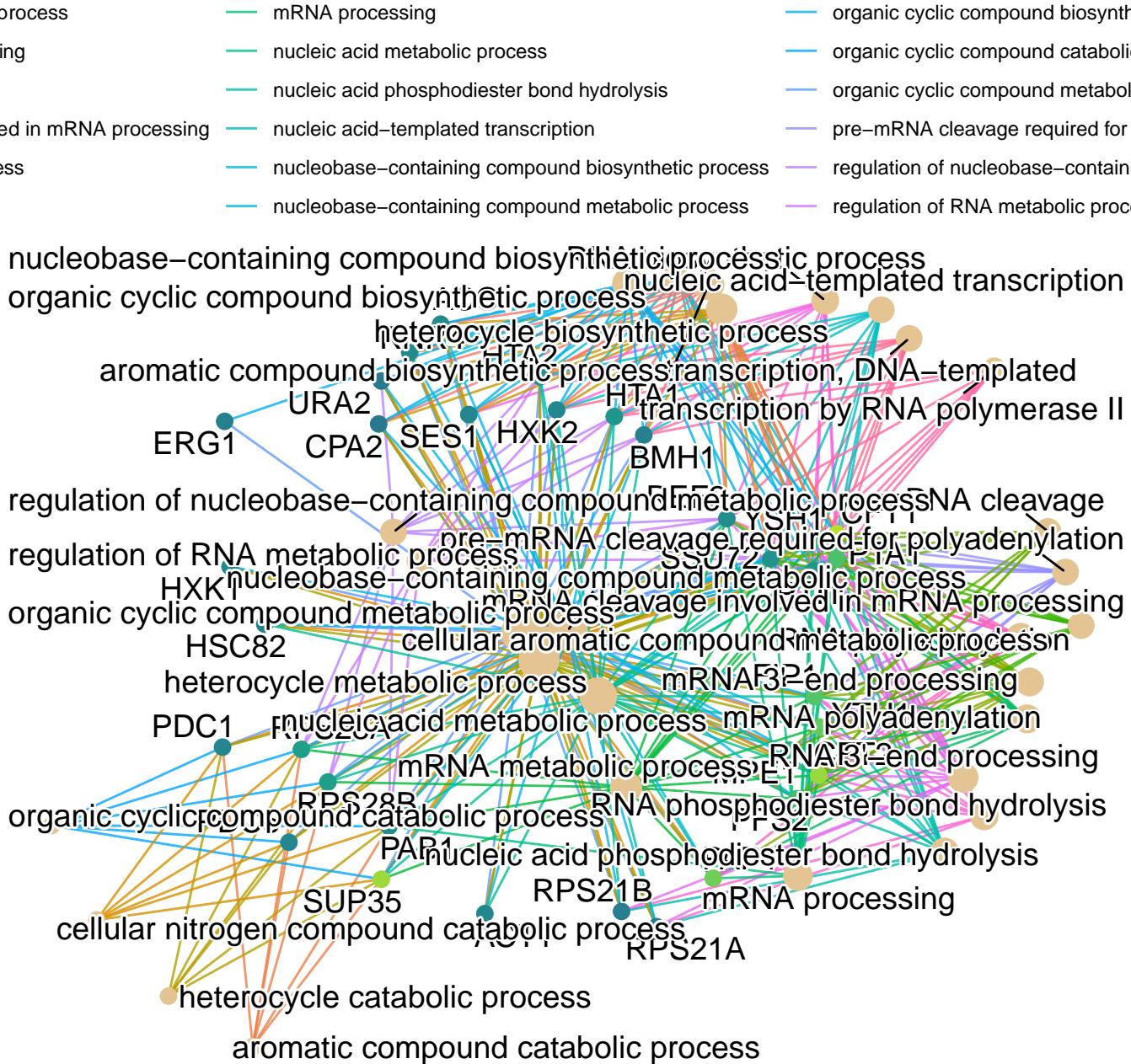
SUP35-TAP Up-regulated GO BP barplot



SUP35-TAP Up-regulated GO BP dotplot



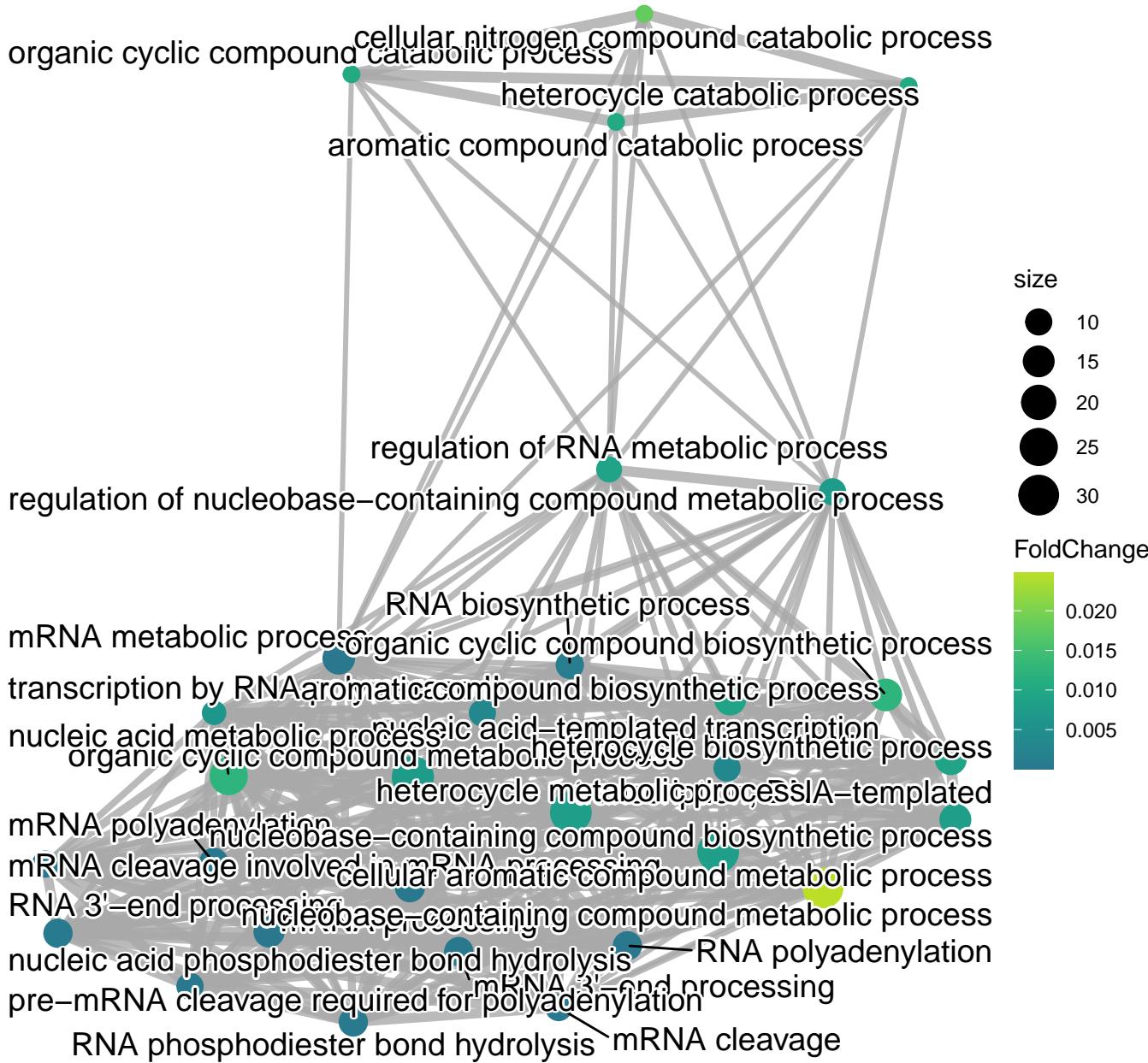
SUP35-TAP Up-regulated GO BP cnetplot

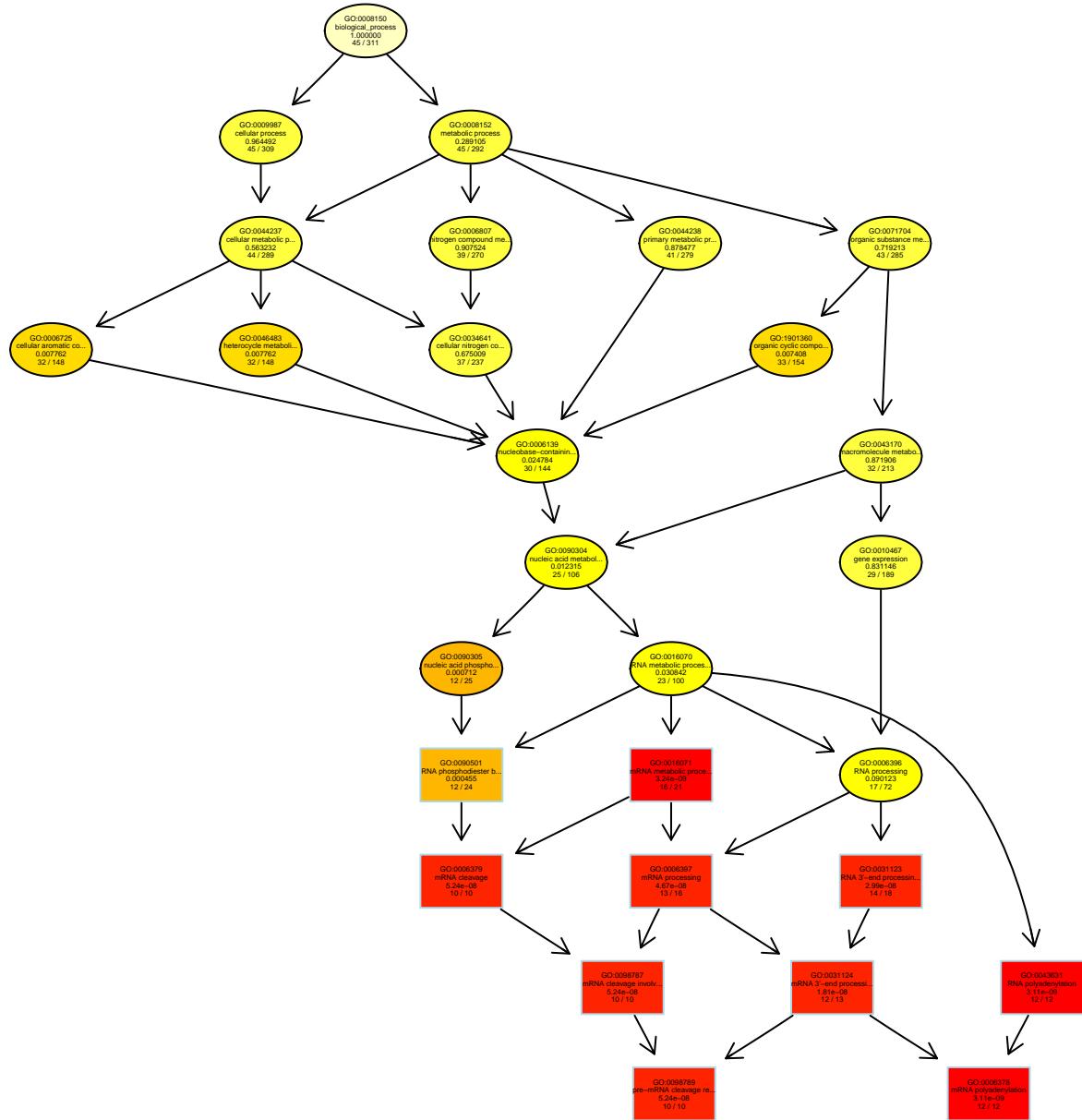


SUP35-TAP Up-regulated GO BP heatplot

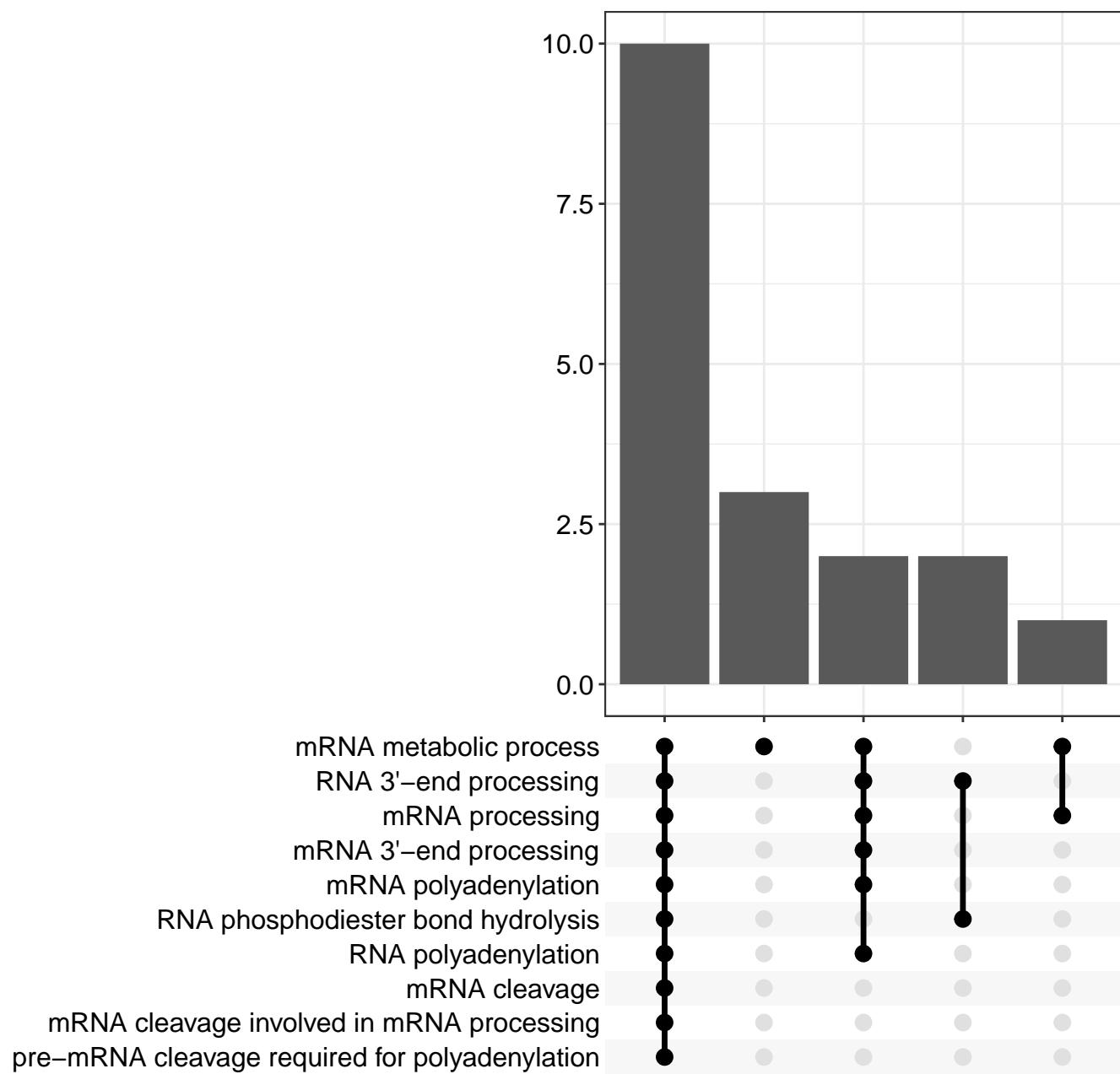


SUP35-TAP Up-regulated GO BP emapplot

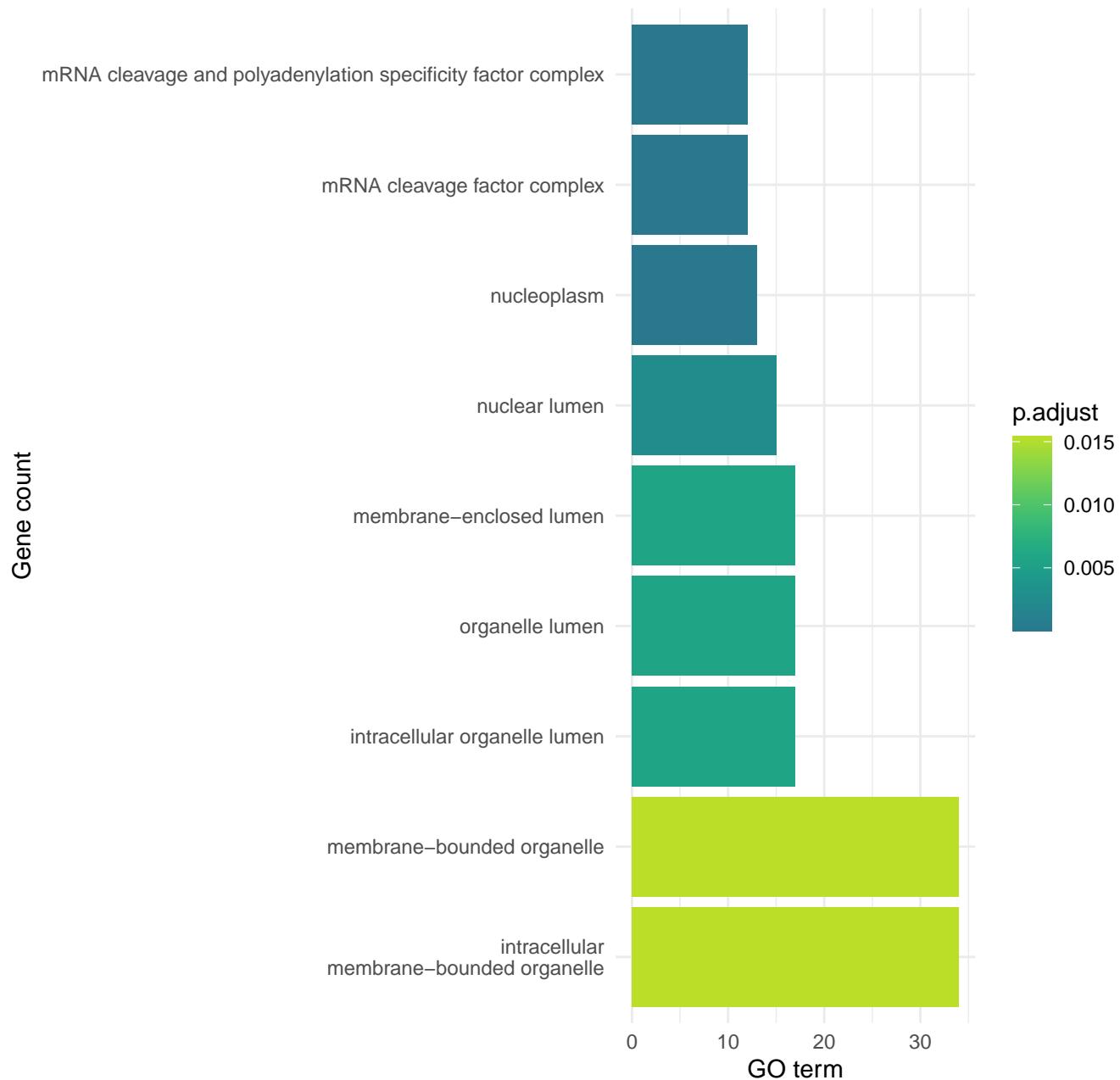




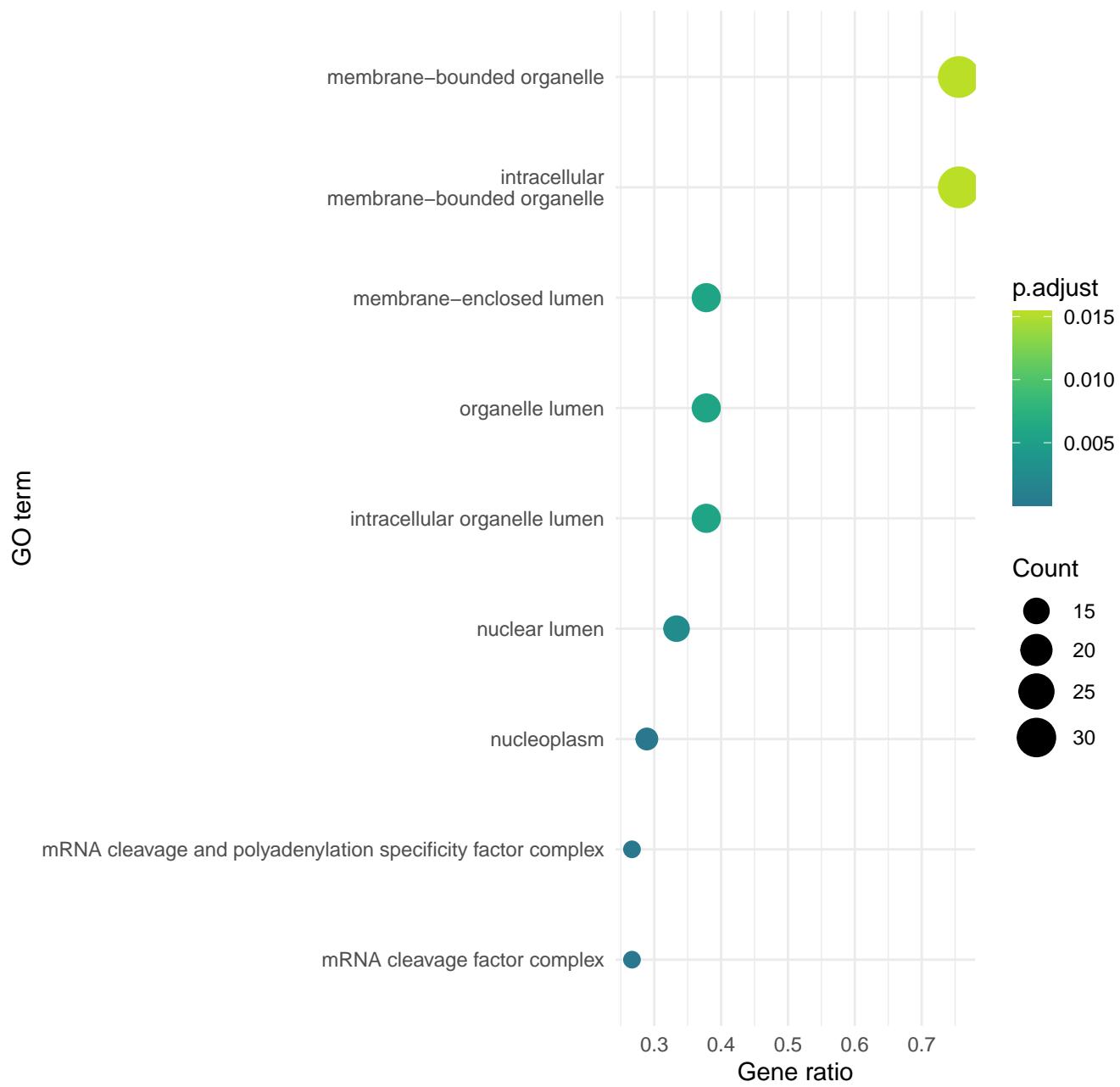
SUP35-TAP Up-regulated GO BP upset



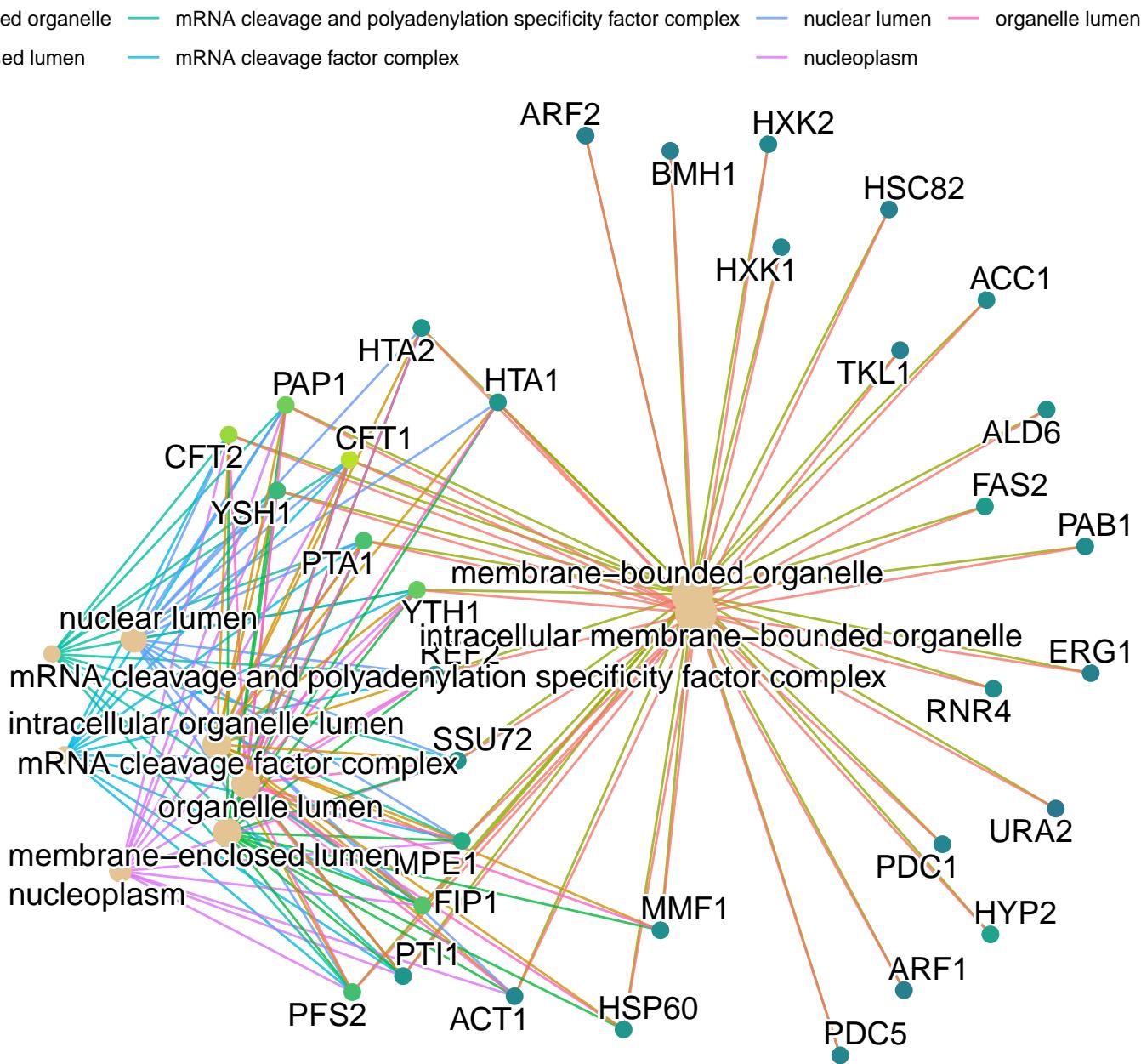
SUP35-TAP Up-regulated GO CC barp



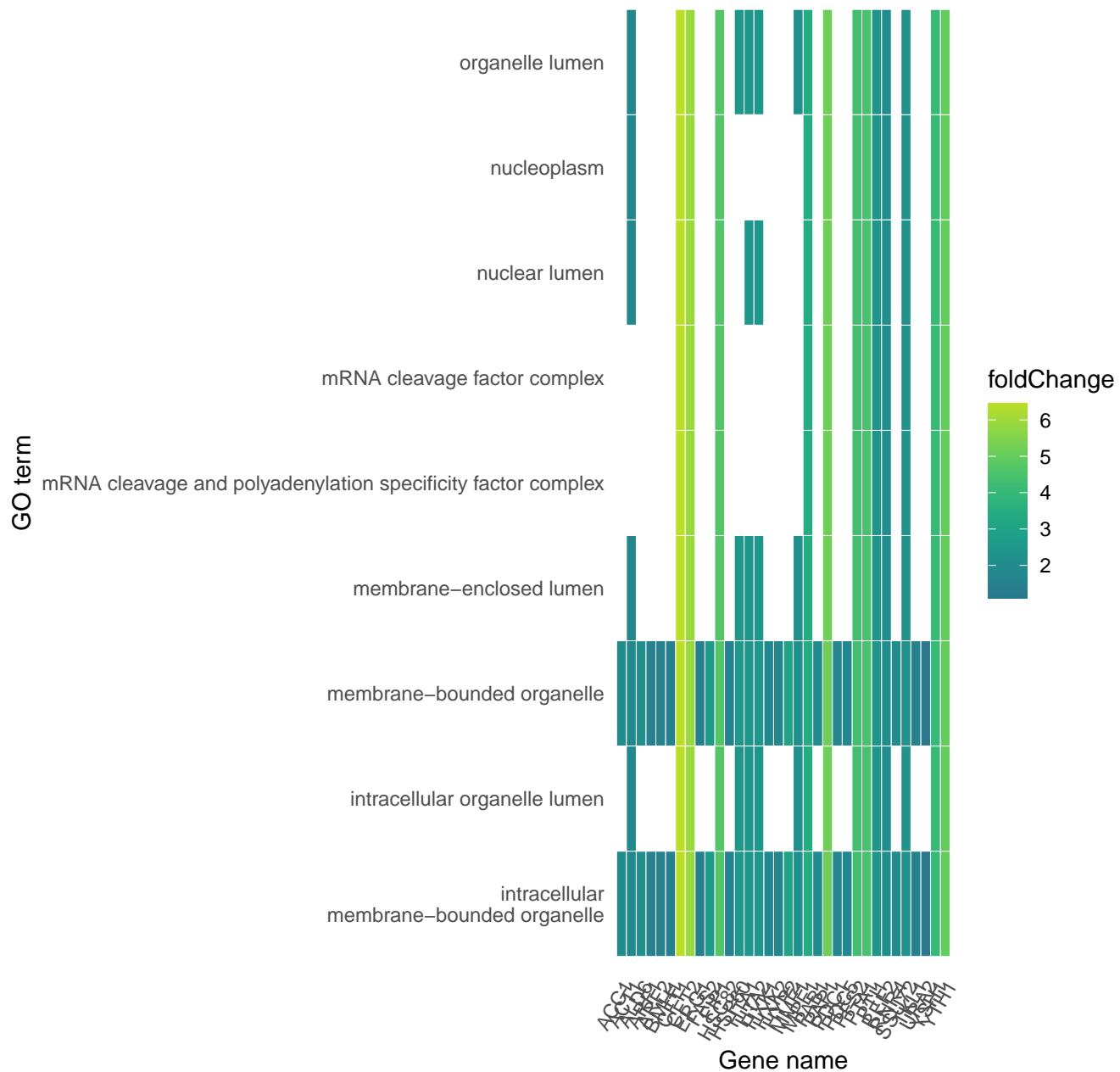
SUP35-TAP Up-regulated GO CC dotplot



SUP35-TAP Up-regulated GO CC cnetplot

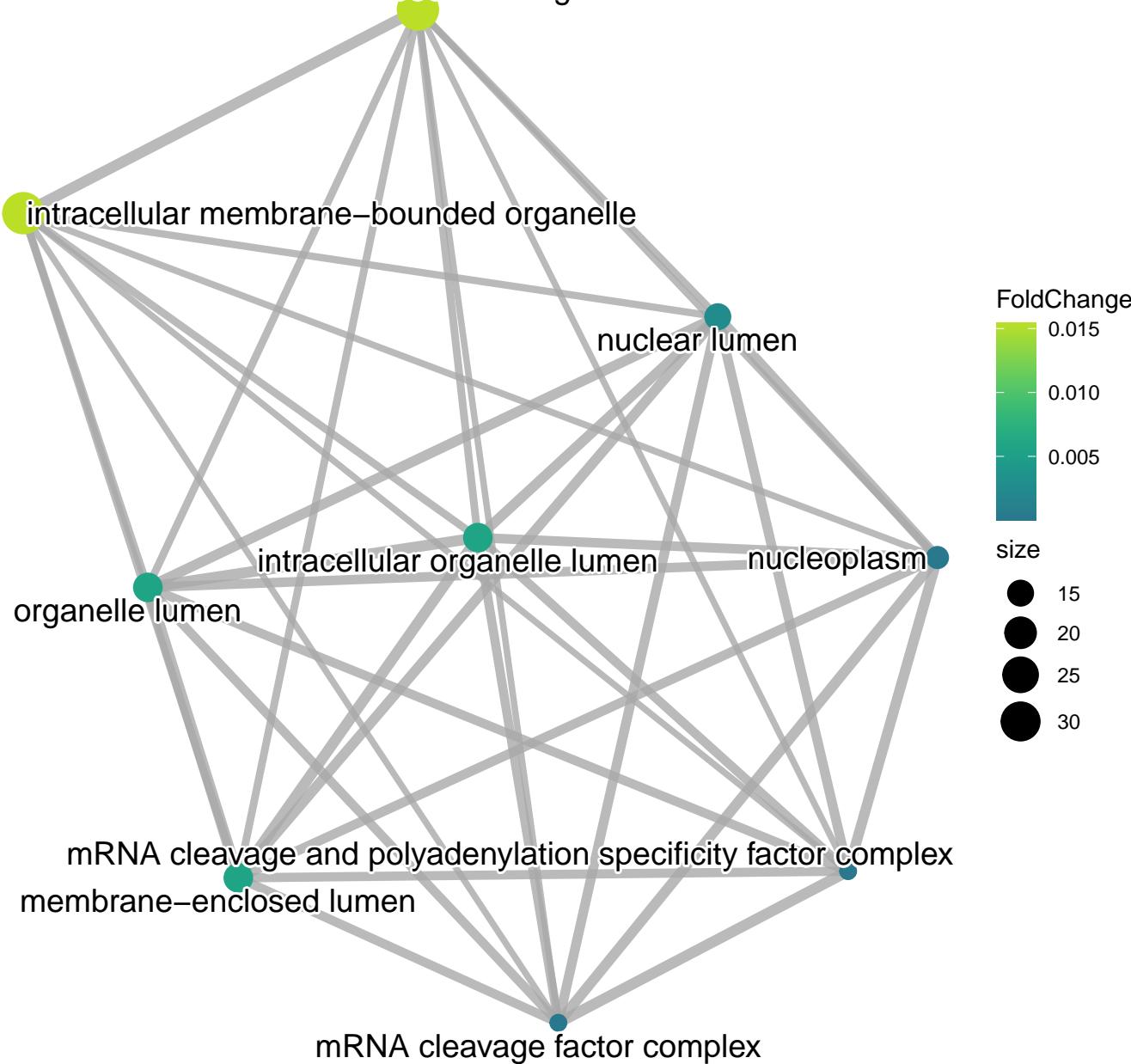


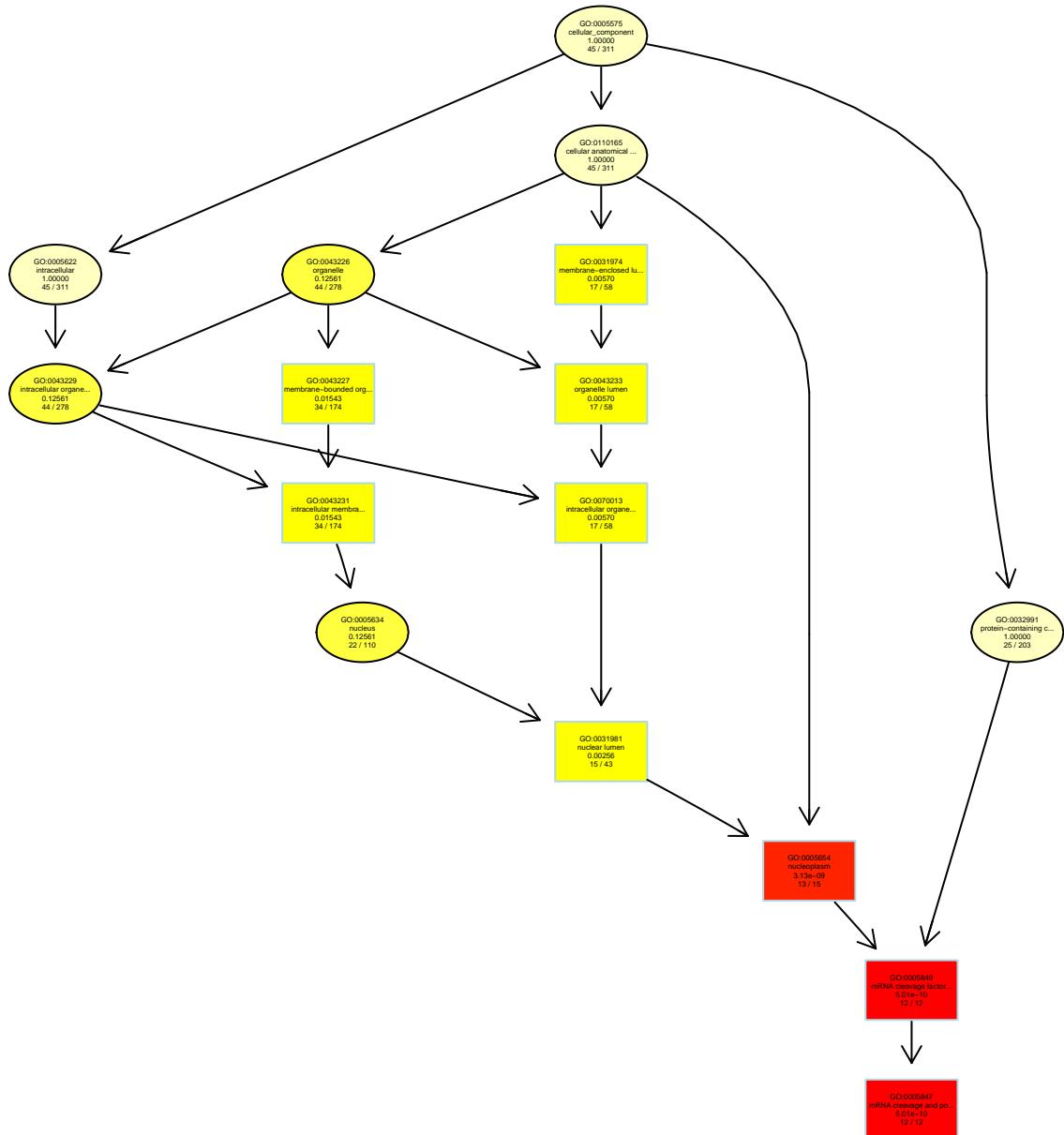
SUP35-TAP Up-regulated GO CC heatmap

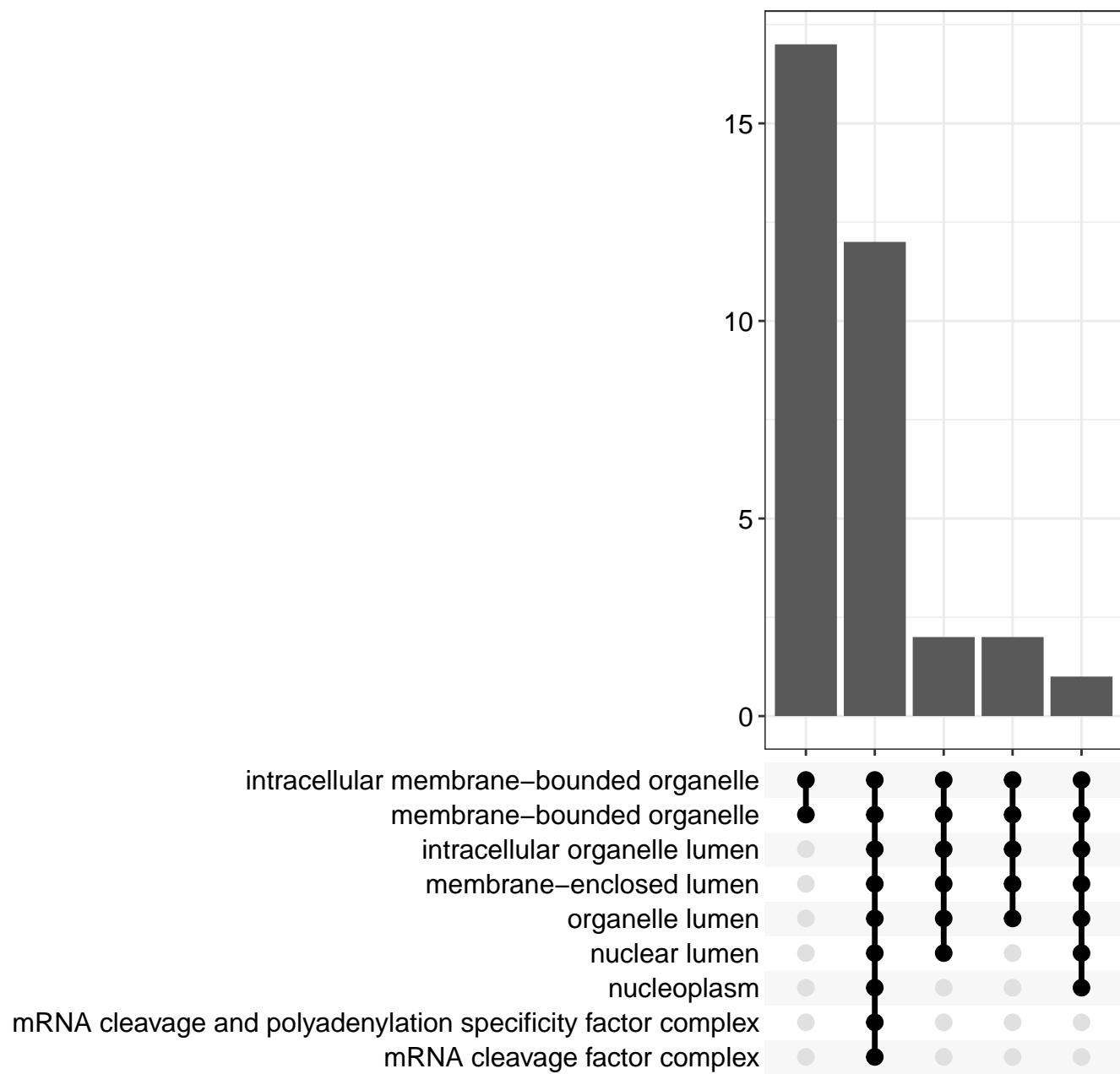


SUP35-TAP Up-regulated GO CC emapplot

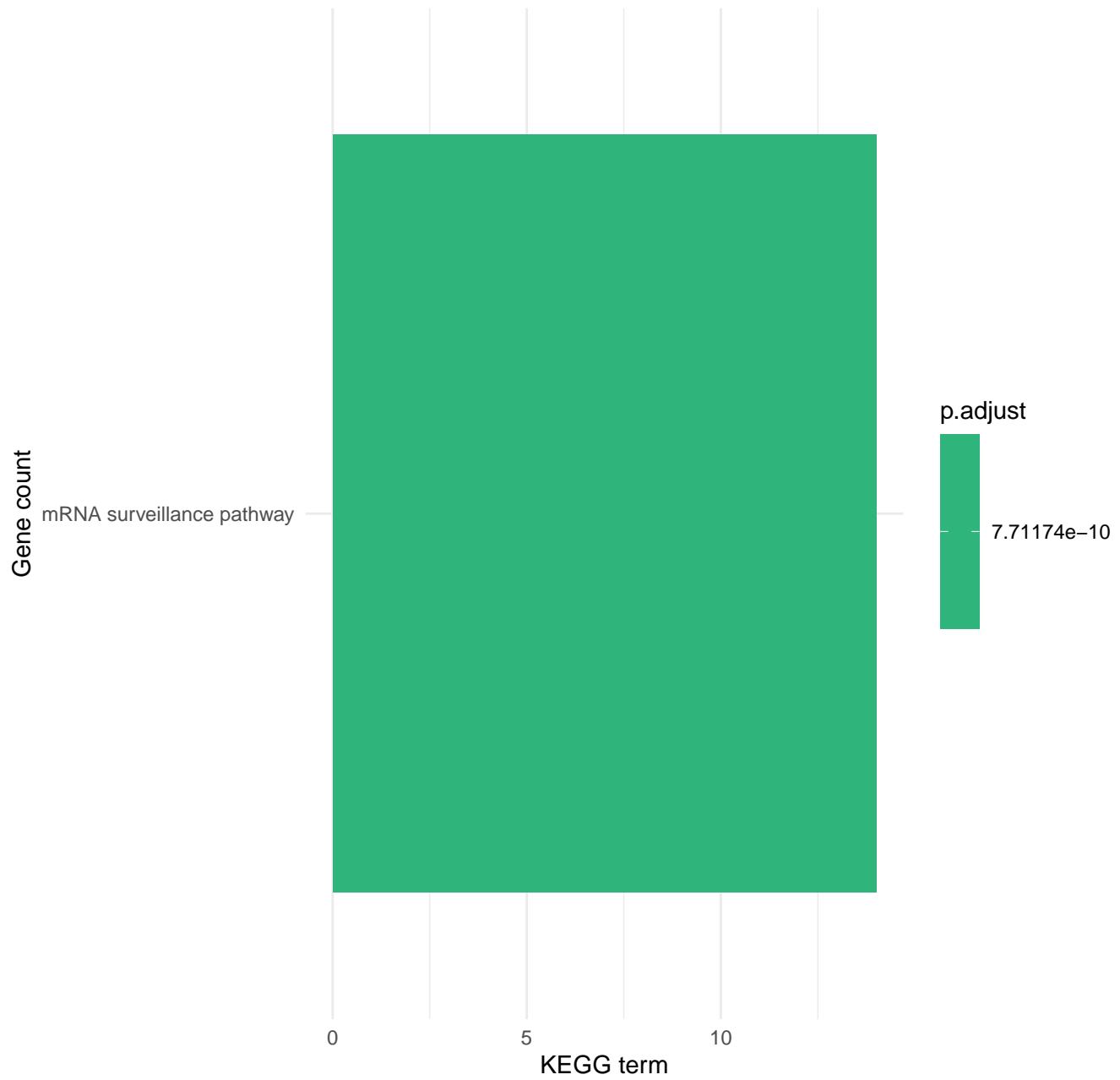
membrane–bounded organelle



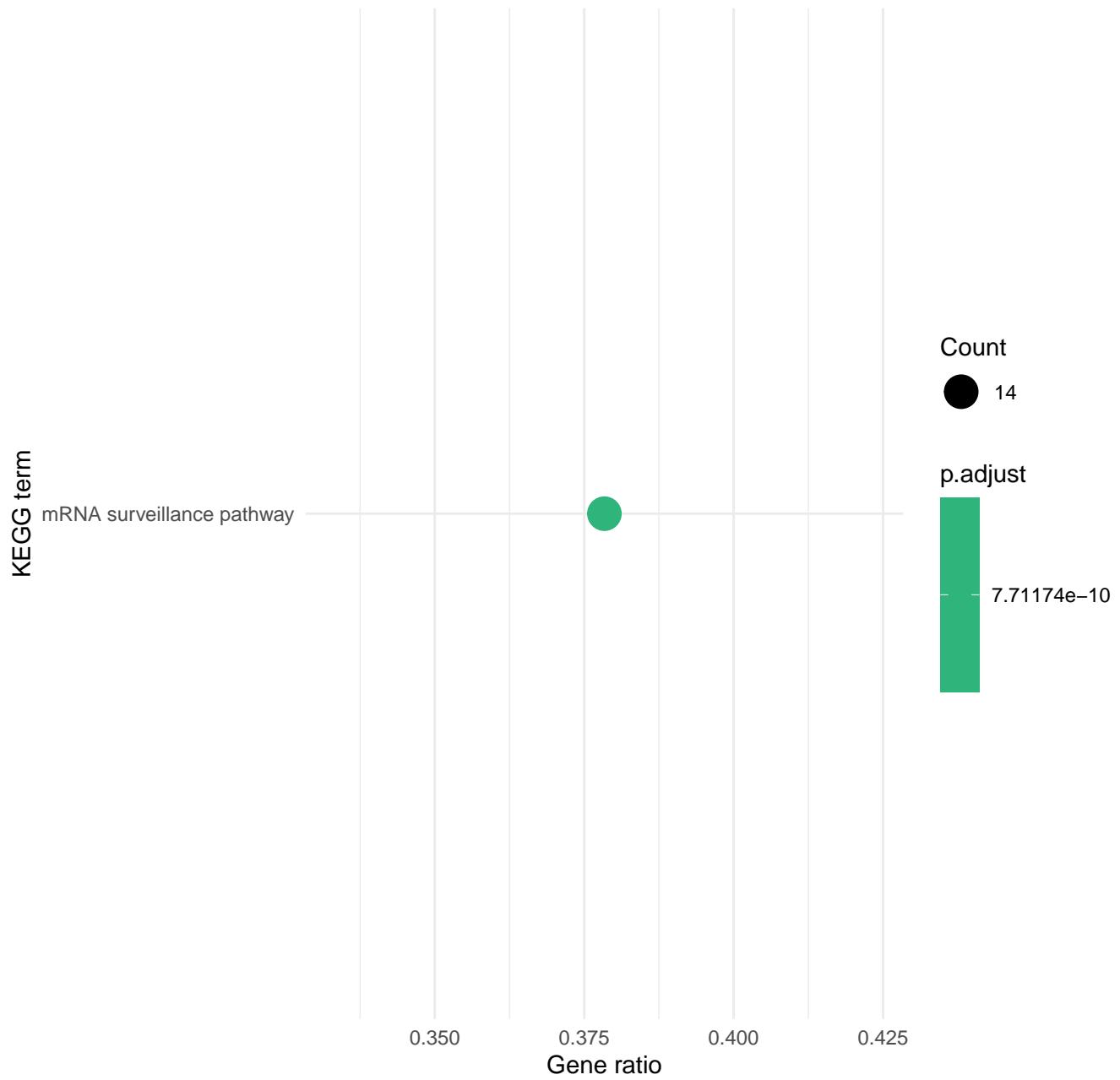




SUP35-TAP Up-regulated KEGG barplot



SUP35-TAP Up-regulated KEGG dotplot



SUP35-TAP Up-regulated KEGG dotplot

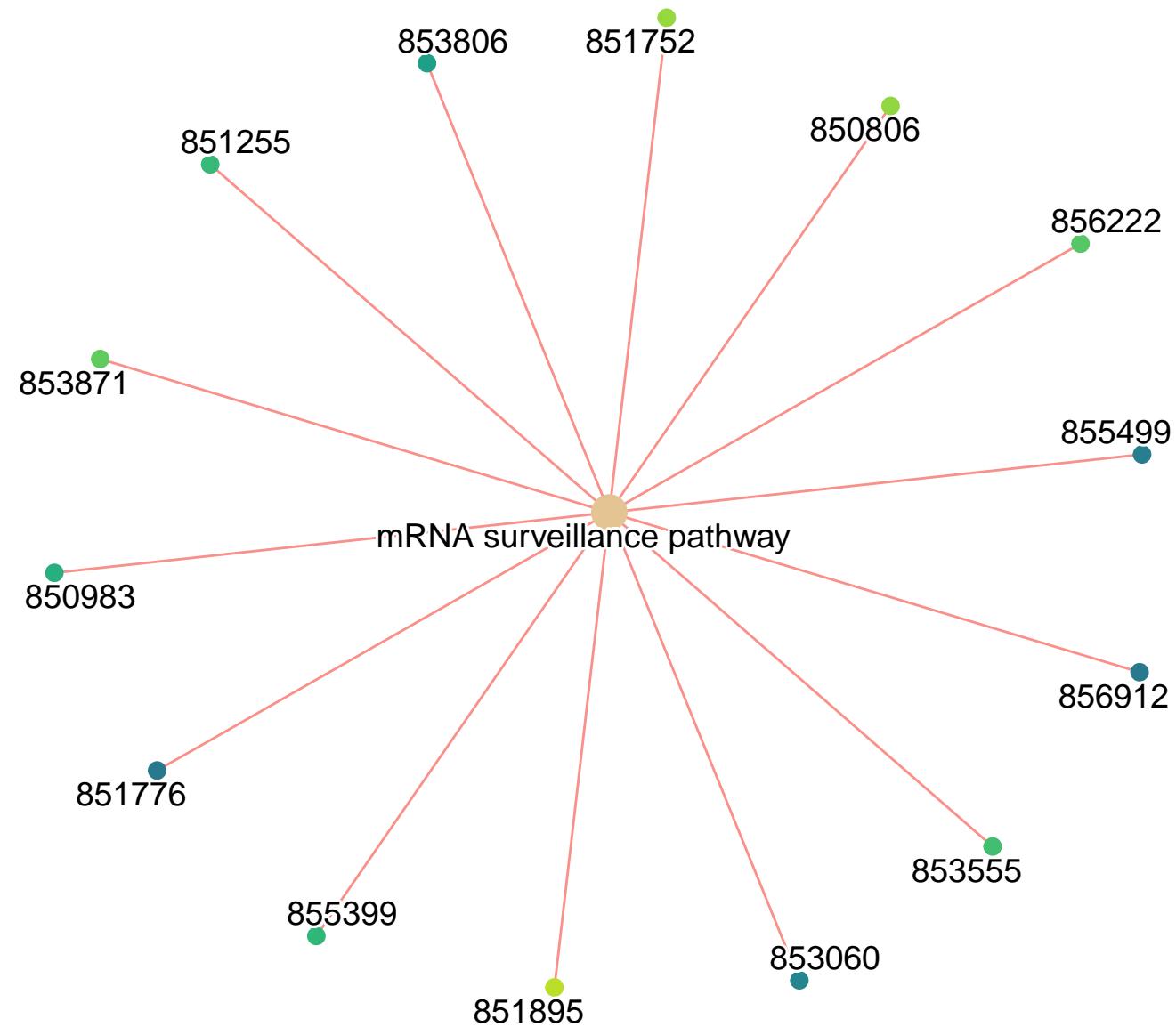
size
● 14

FoldChange

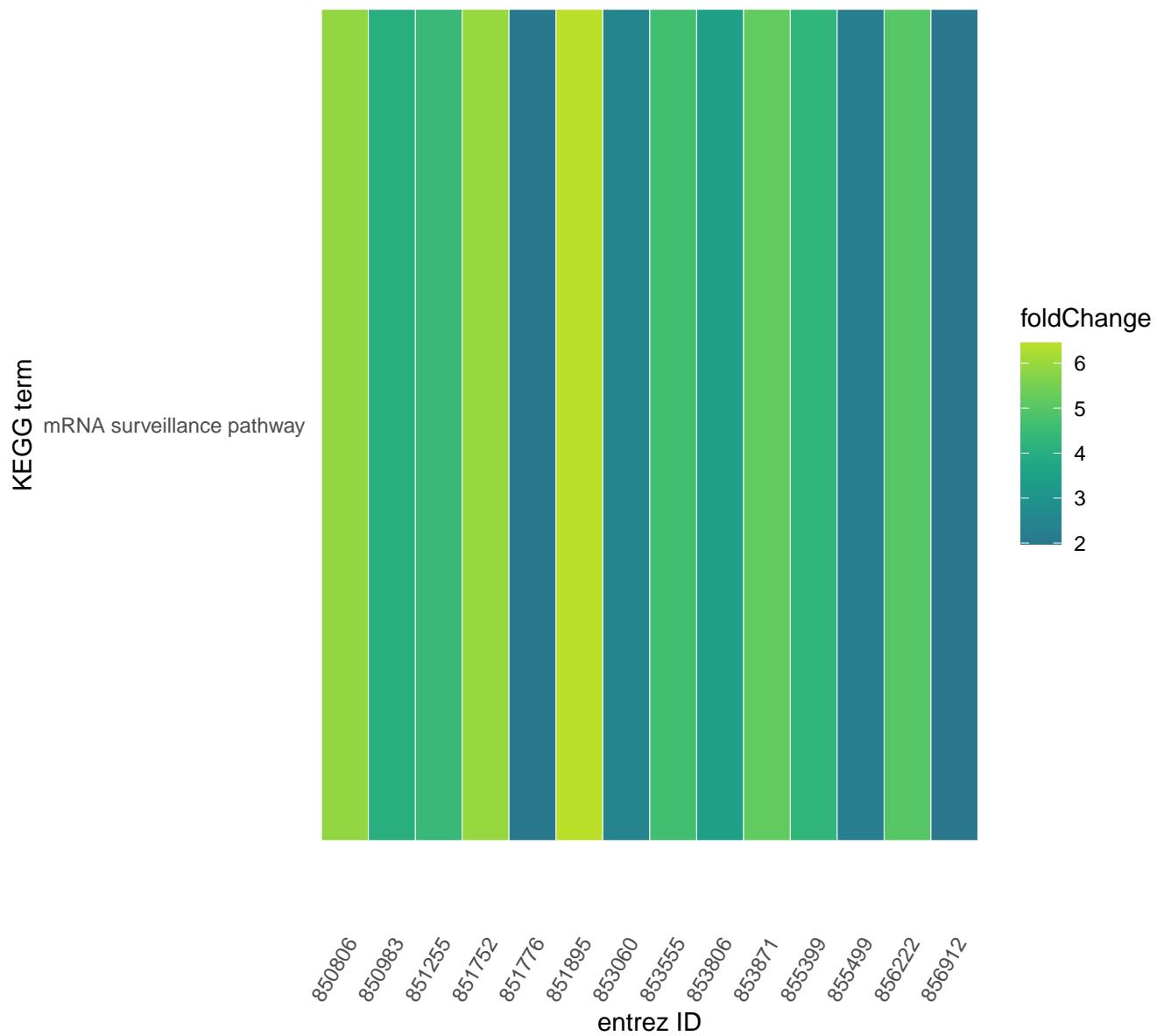


category

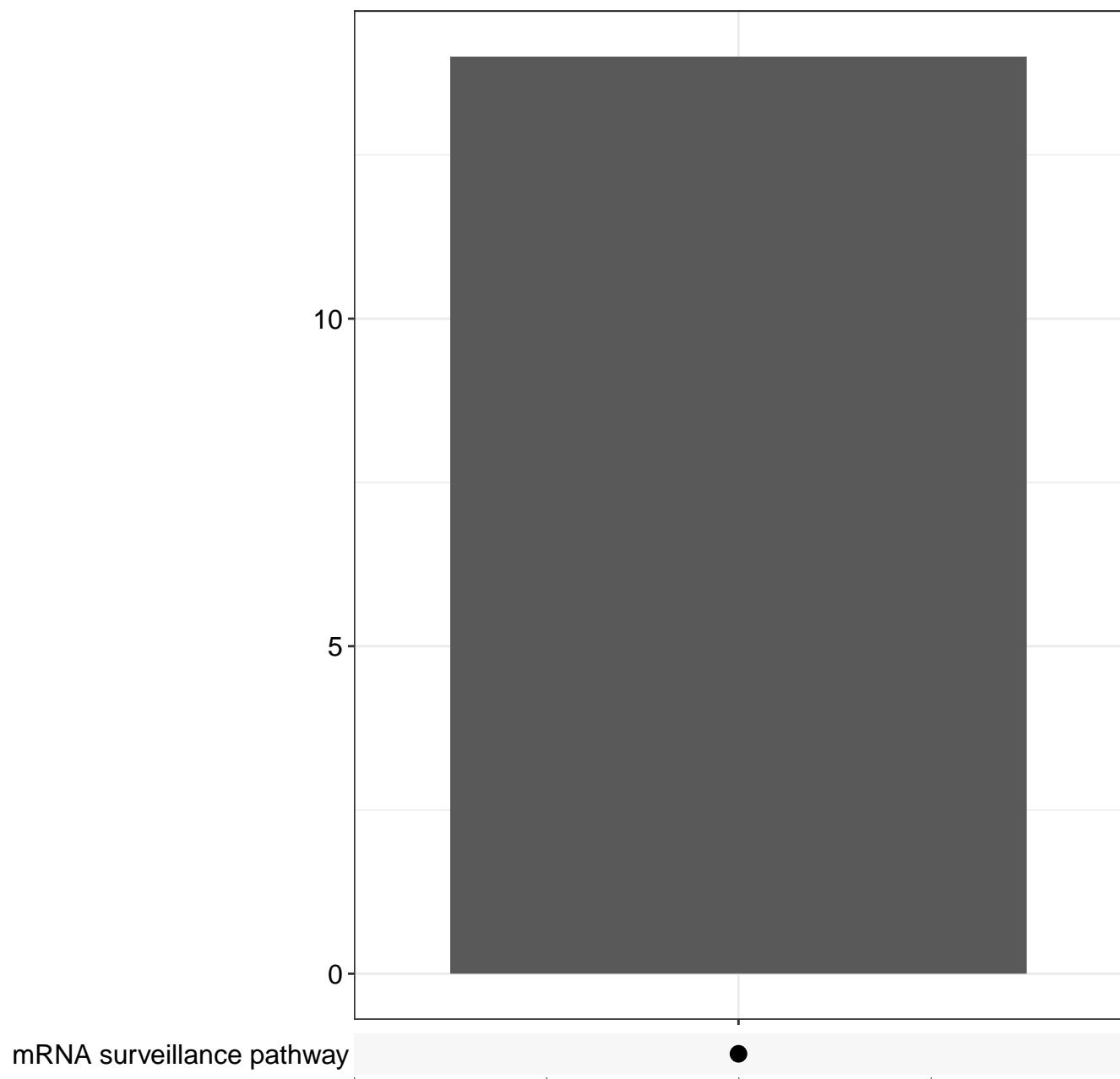
mRNA surveillance pathway



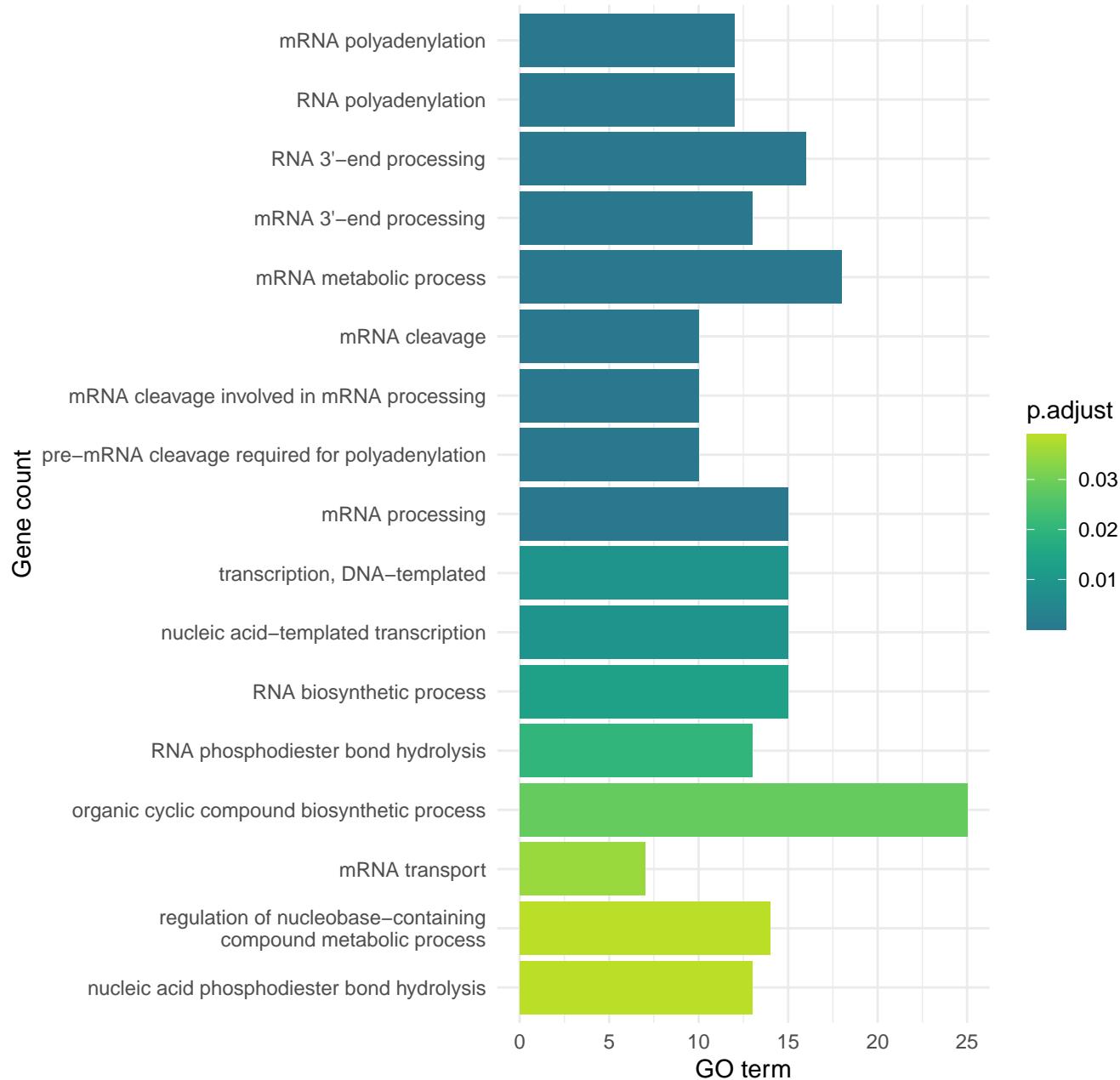
SUP35-TAP Up-regulated KEGG heatmap



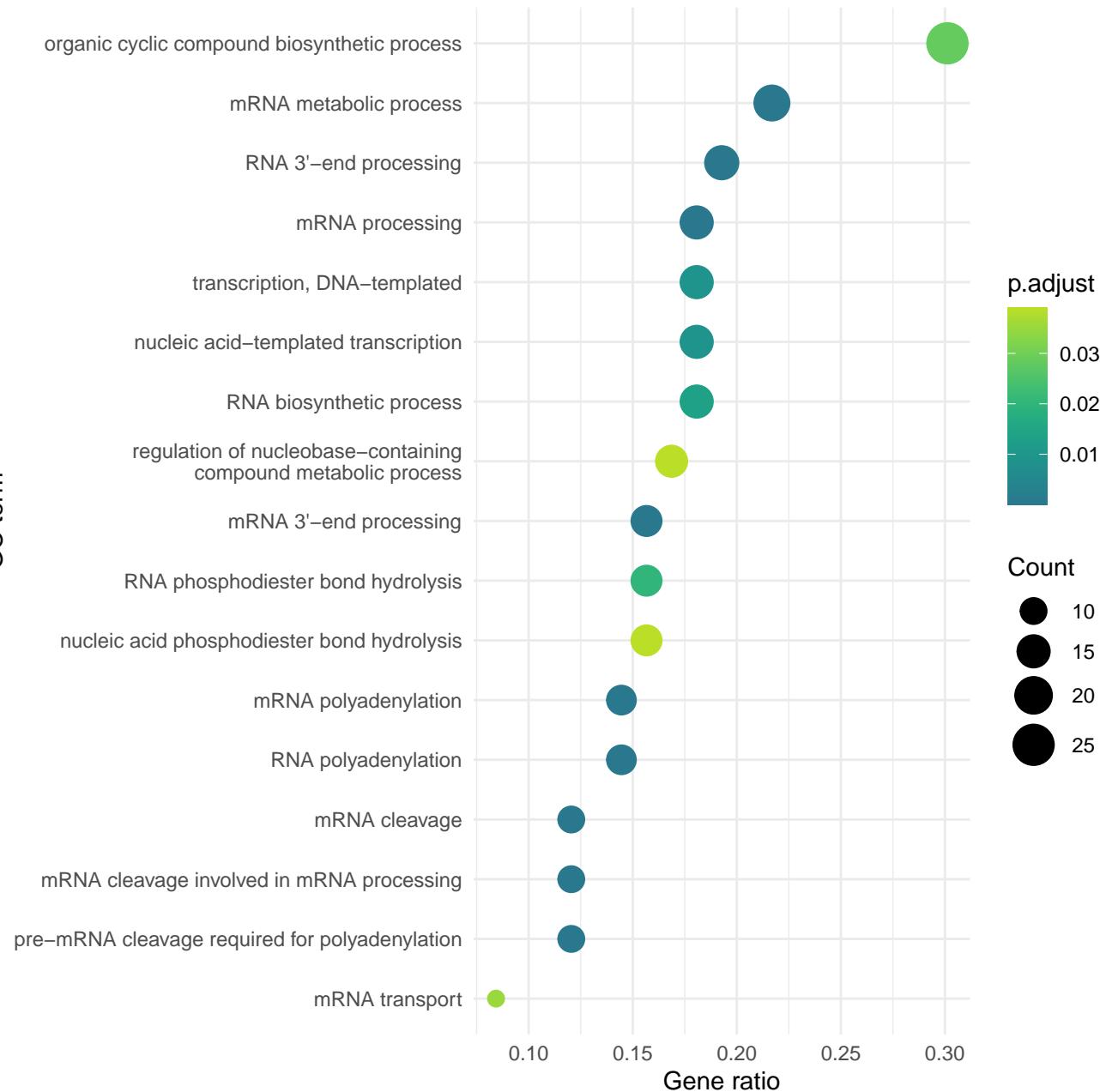
SUP35-TAP Up-regulated KEGG upsetplot



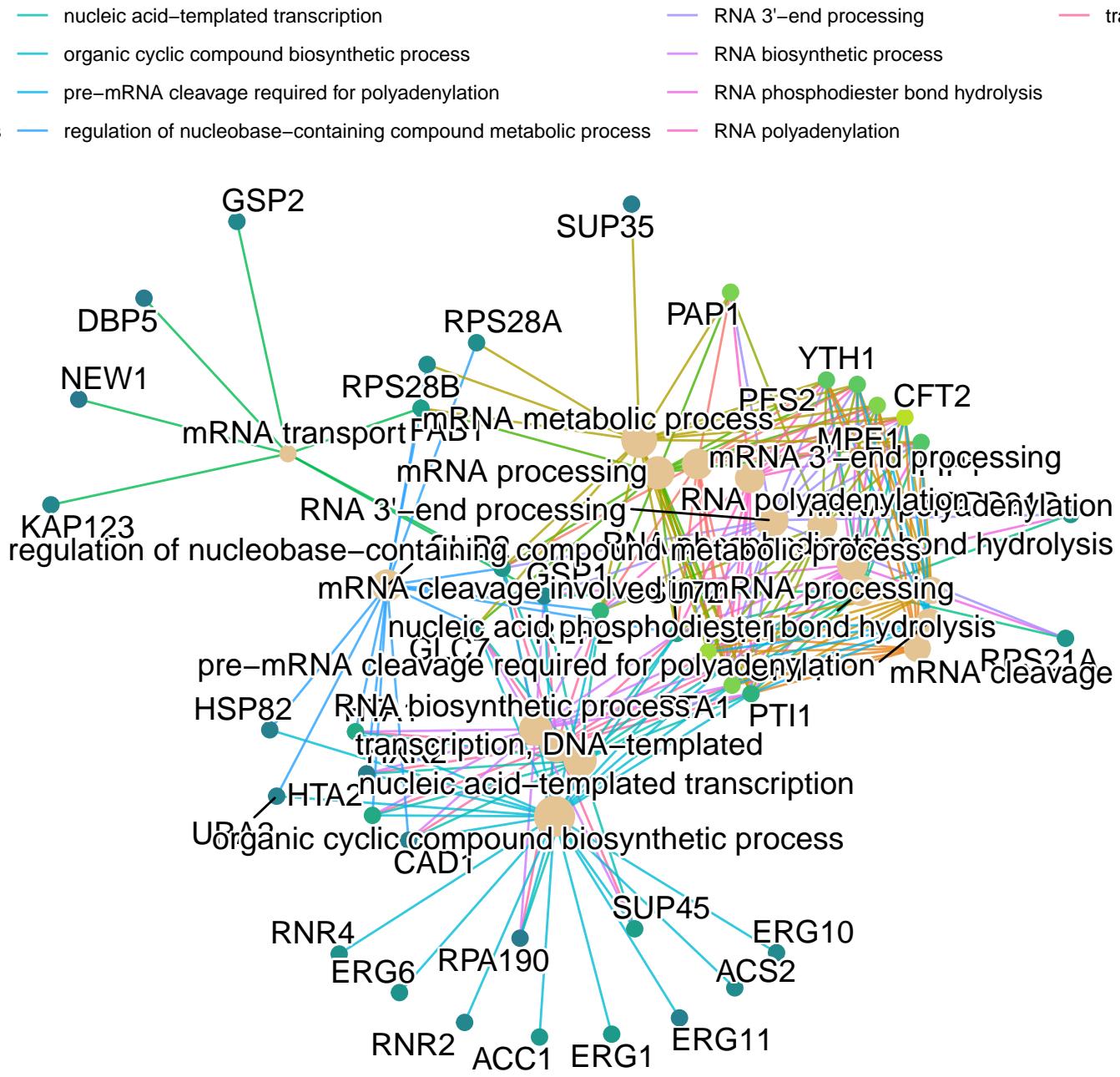
HBS1-TAP Up-regulated GO BP barplot



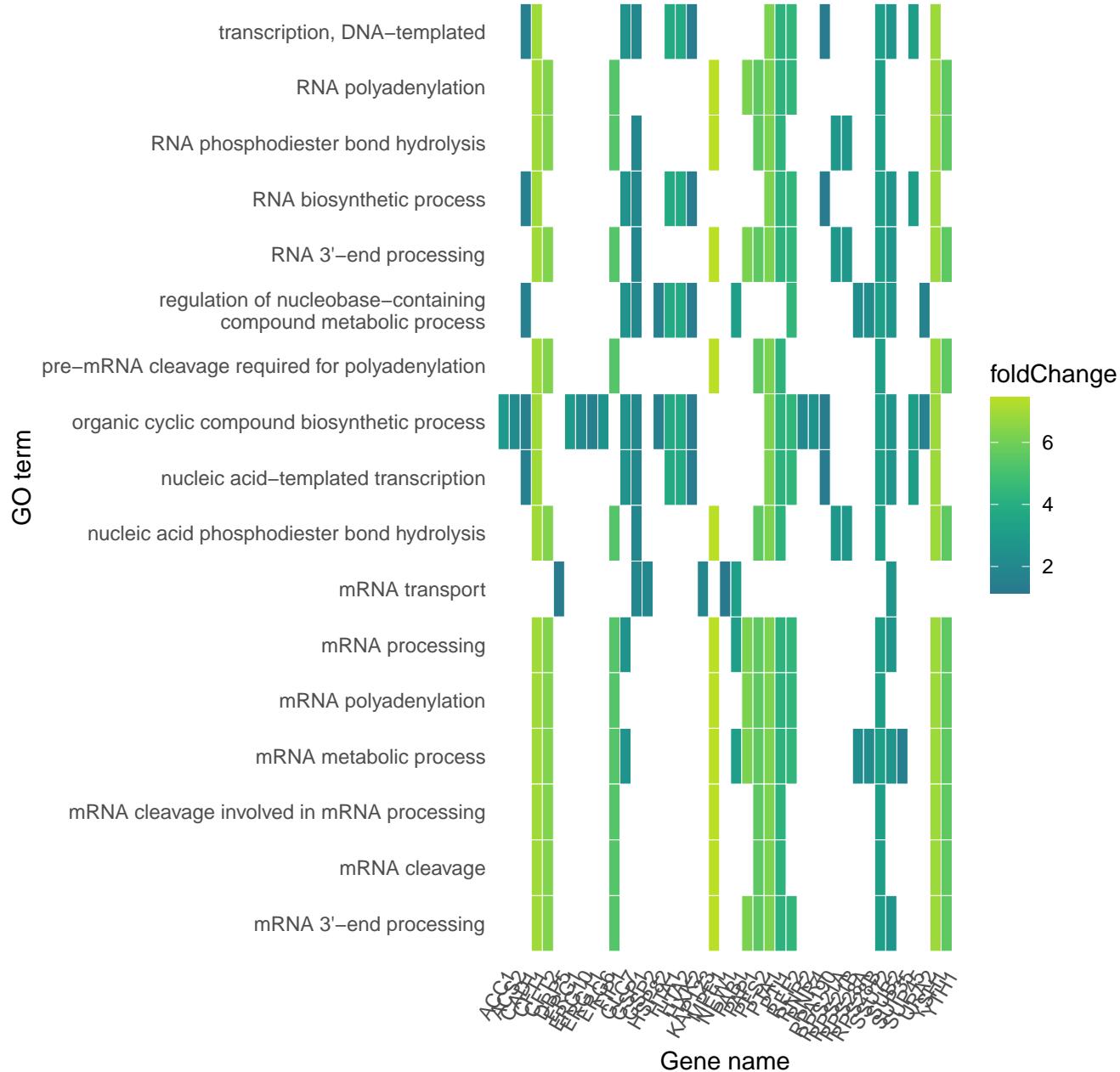
HBS1-TAP Up-regulated GO BP dotplot



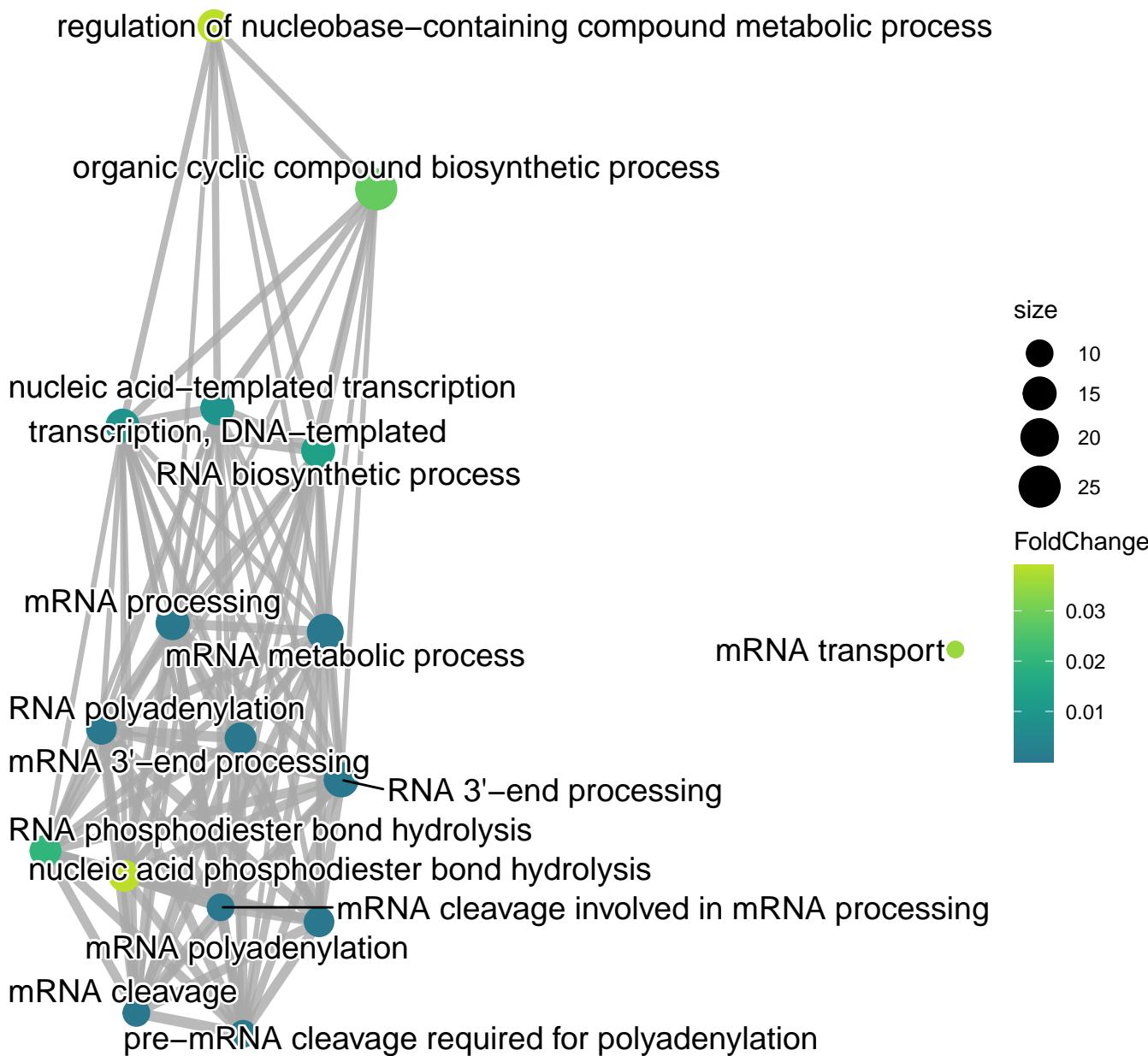
HBS1-TAP Up-regulated GO BP cnetplot

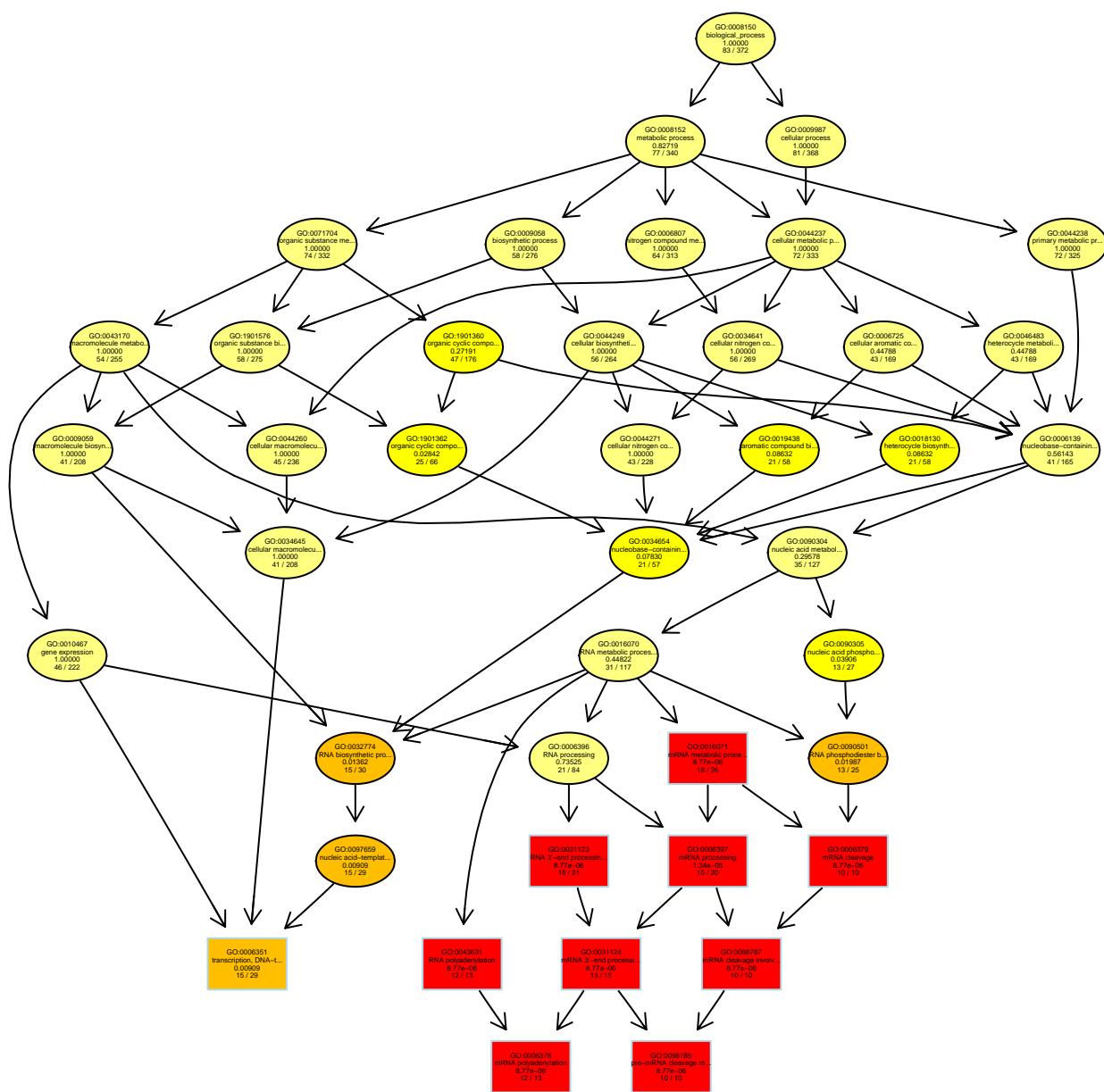


HBS1-TAP Up-regulated GO BP heatplot

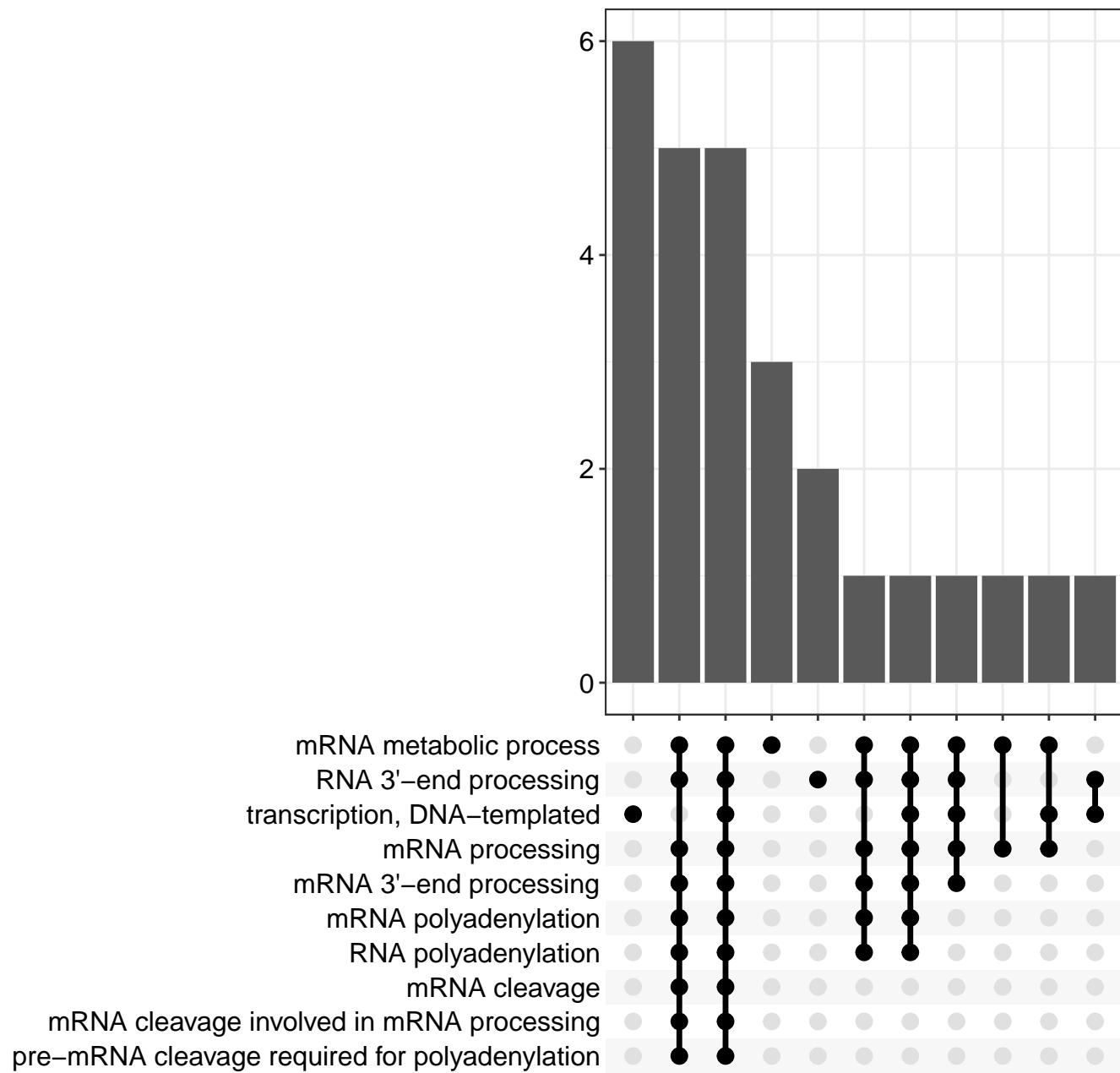


HBS1-TAP Up-regulated GO BP emapplot

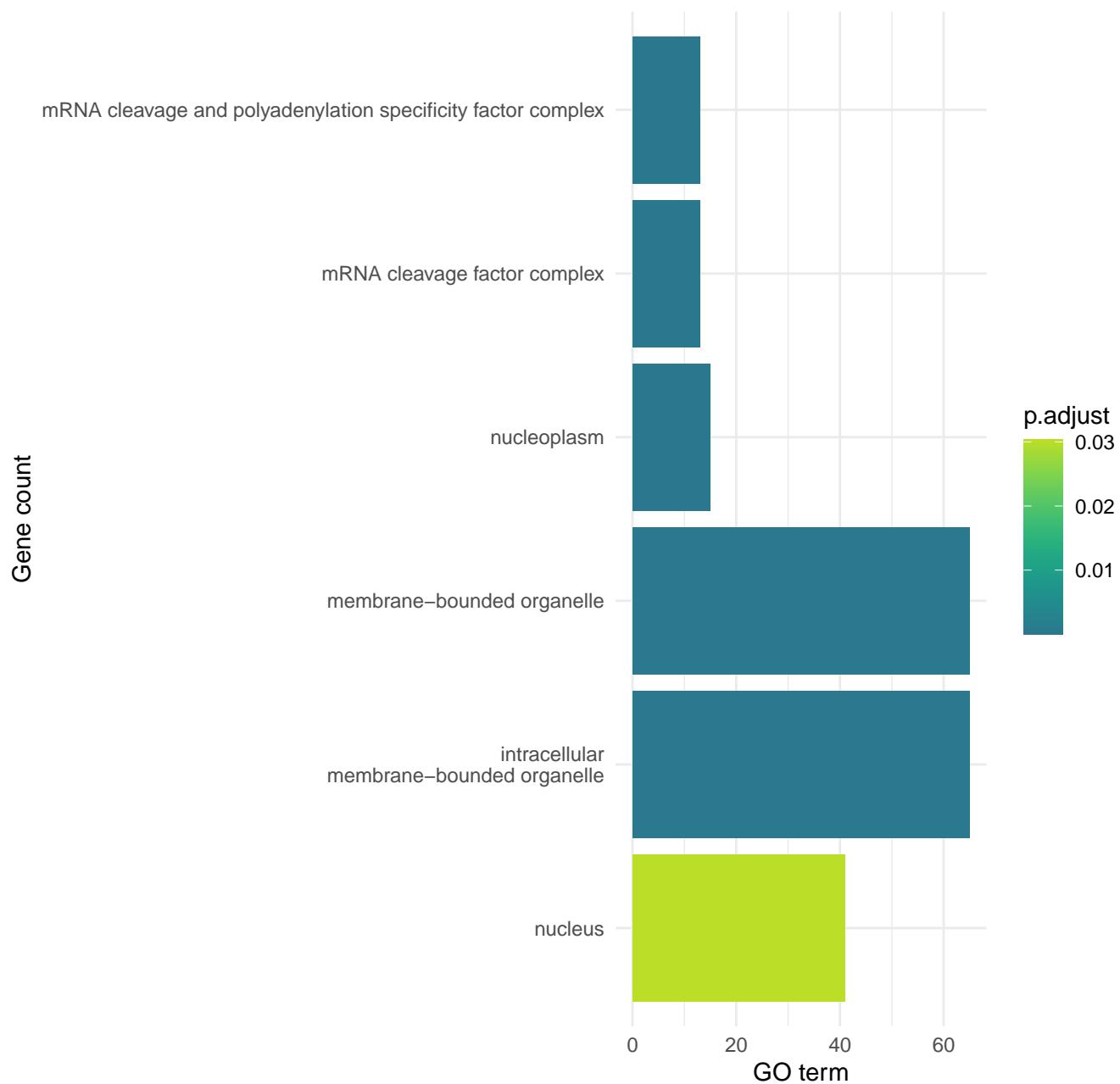




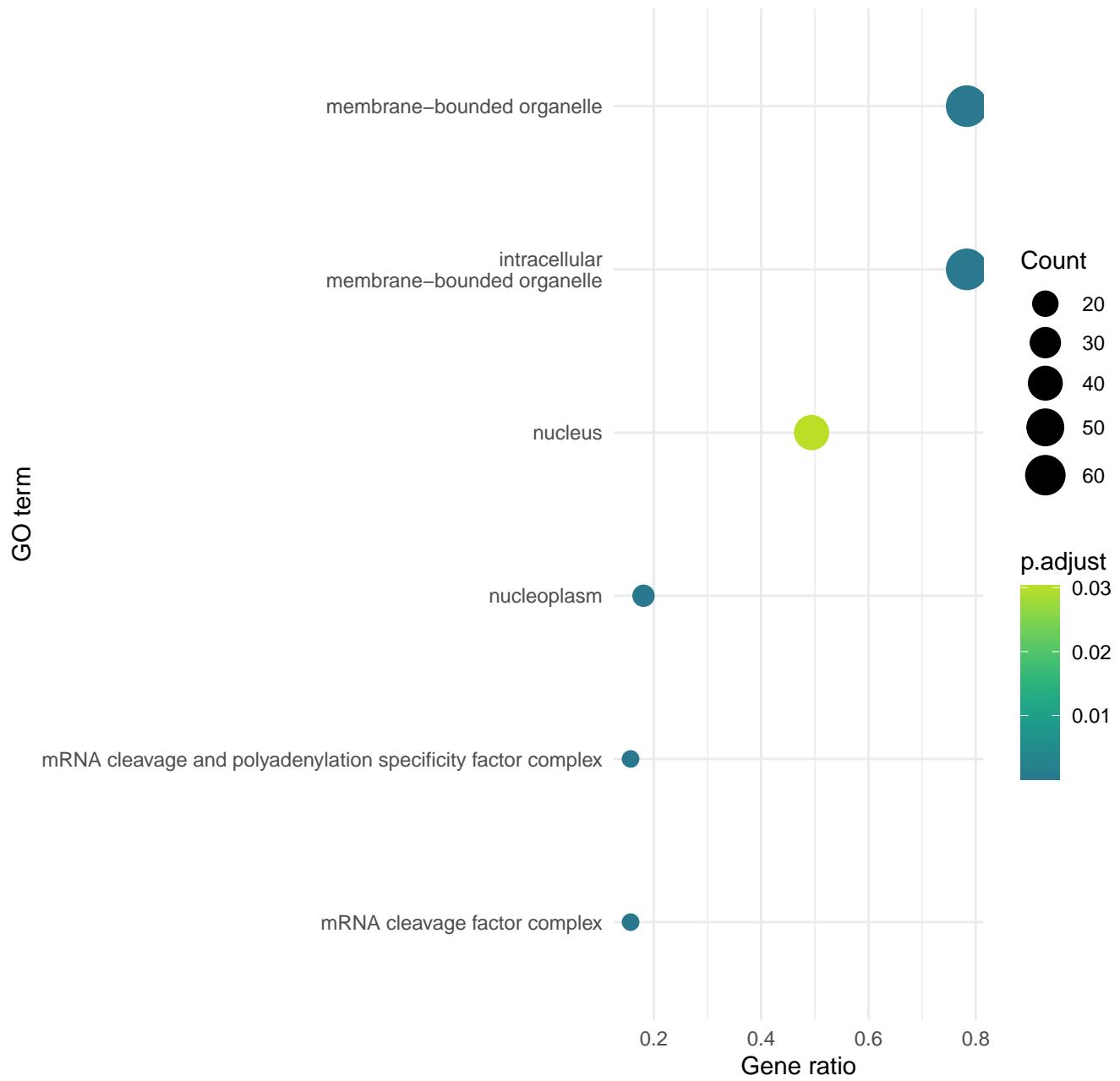
HBS1-TAP Up-regulated GO BP upsetp



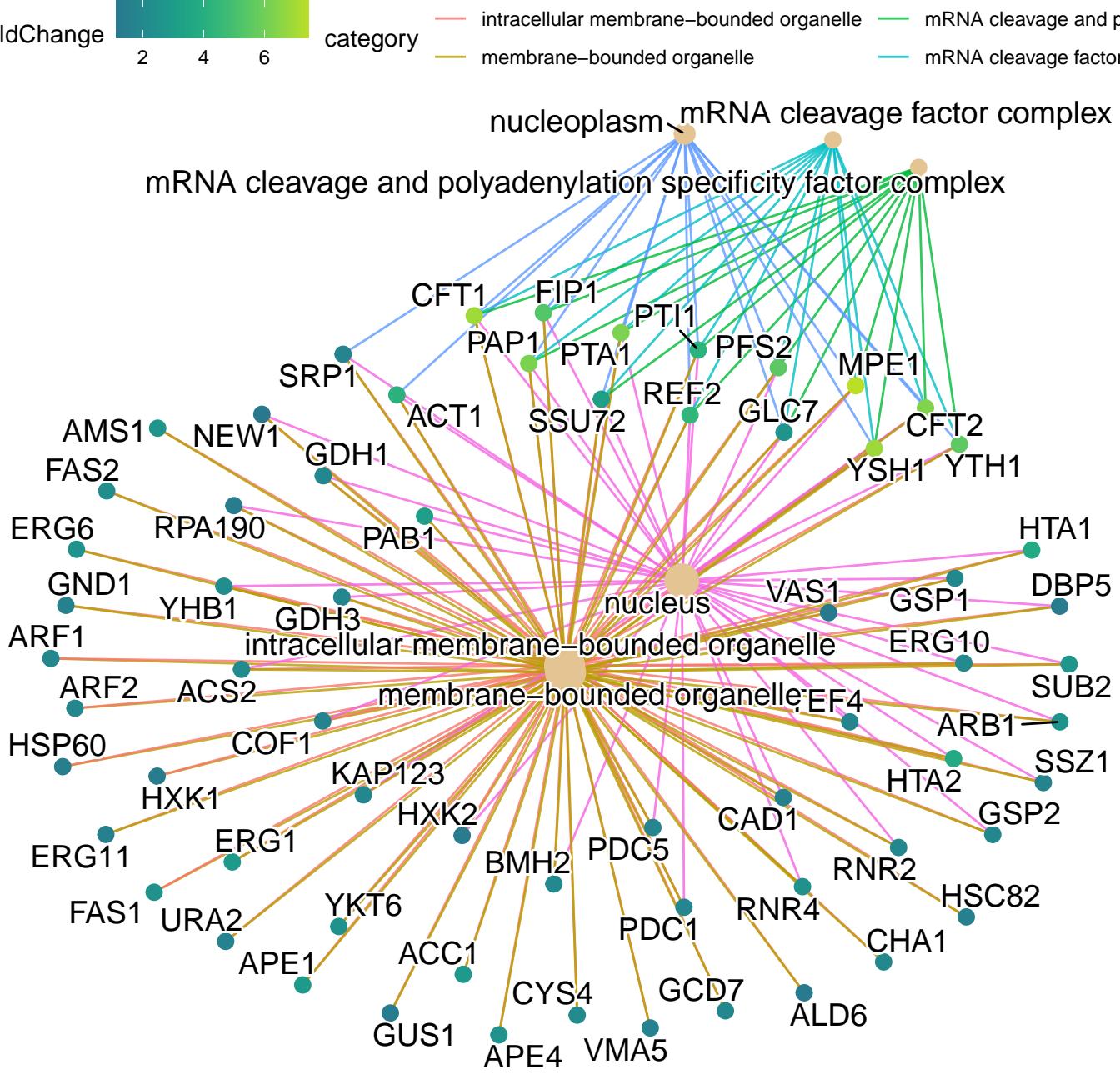
HBS1-TAP Up-regulated GO CC barplot



HBS1-TAP Up-regulated GO CC dotplot

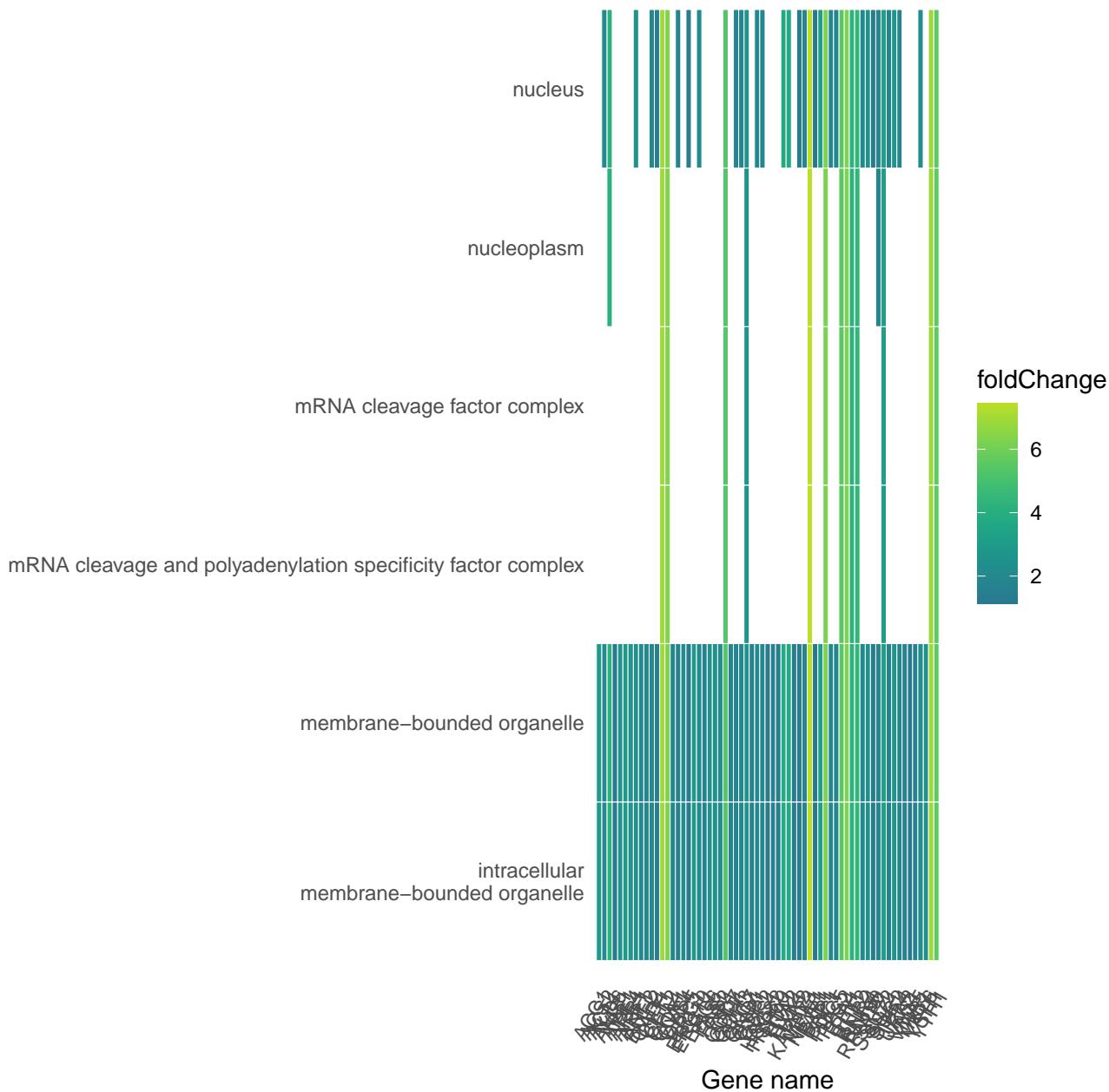


HBS1-TAP Up-regulated GO CC cnetplot



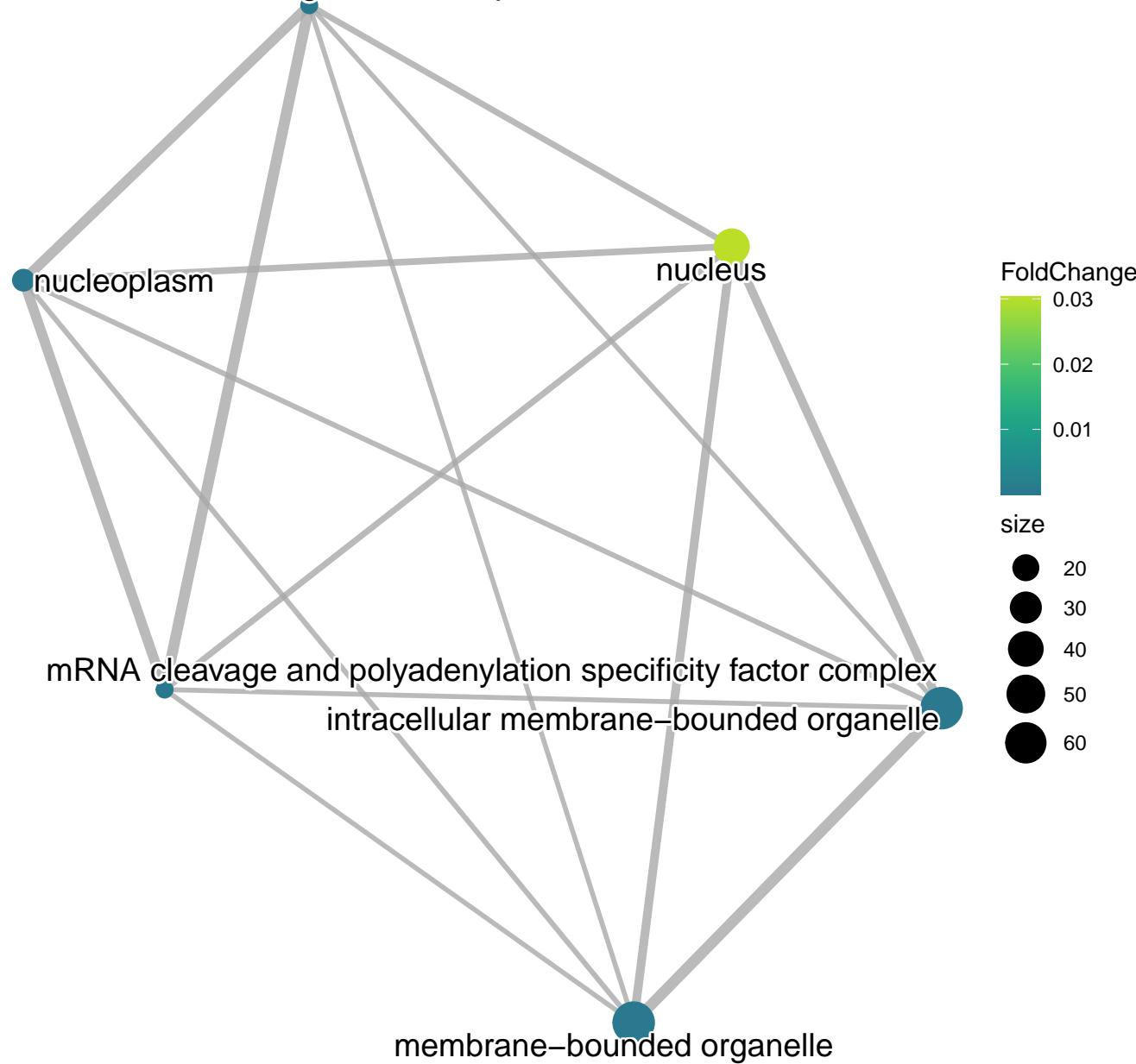
HBS1-TAP Up-regulated GO CC heatmap

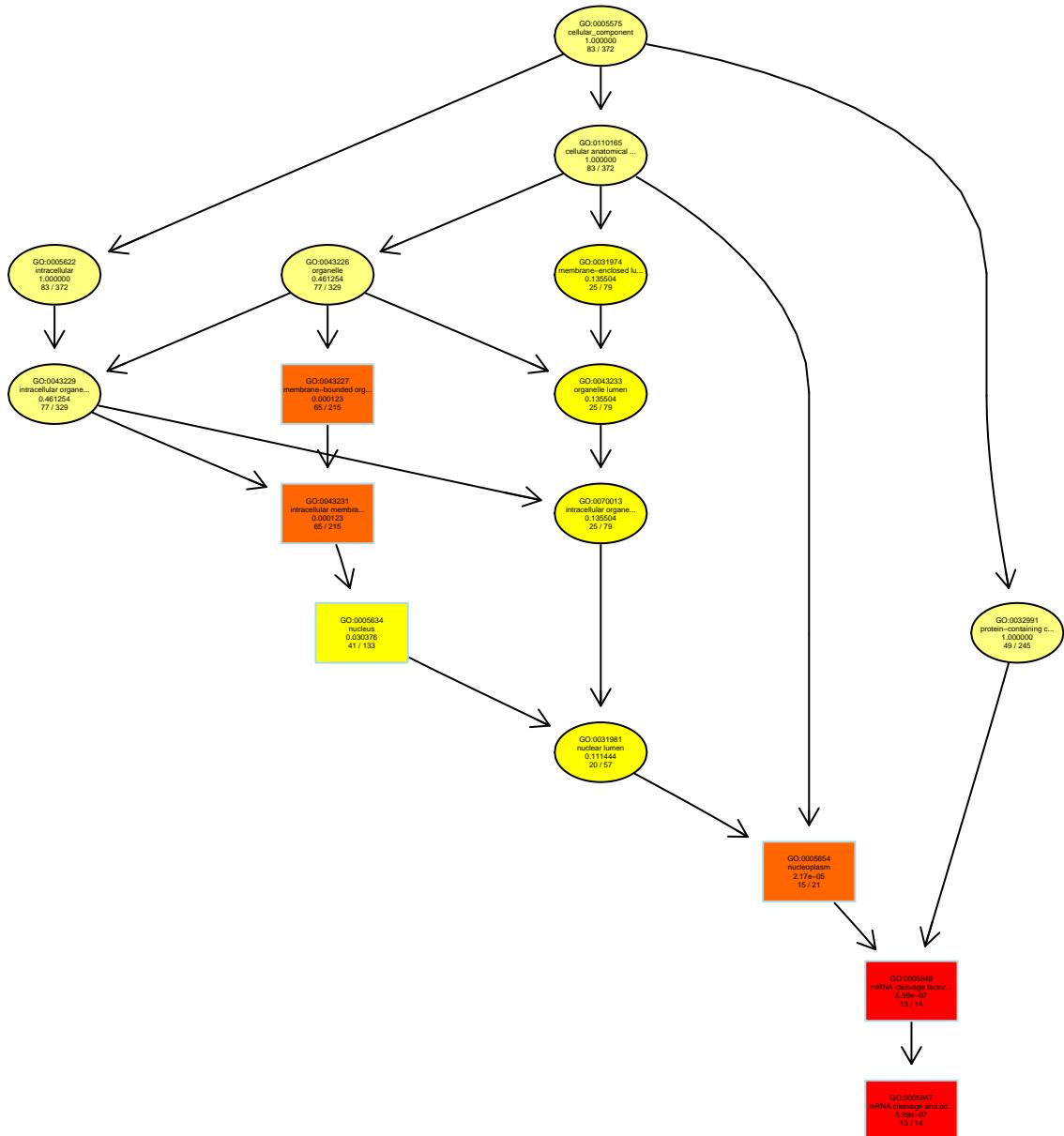
GO term

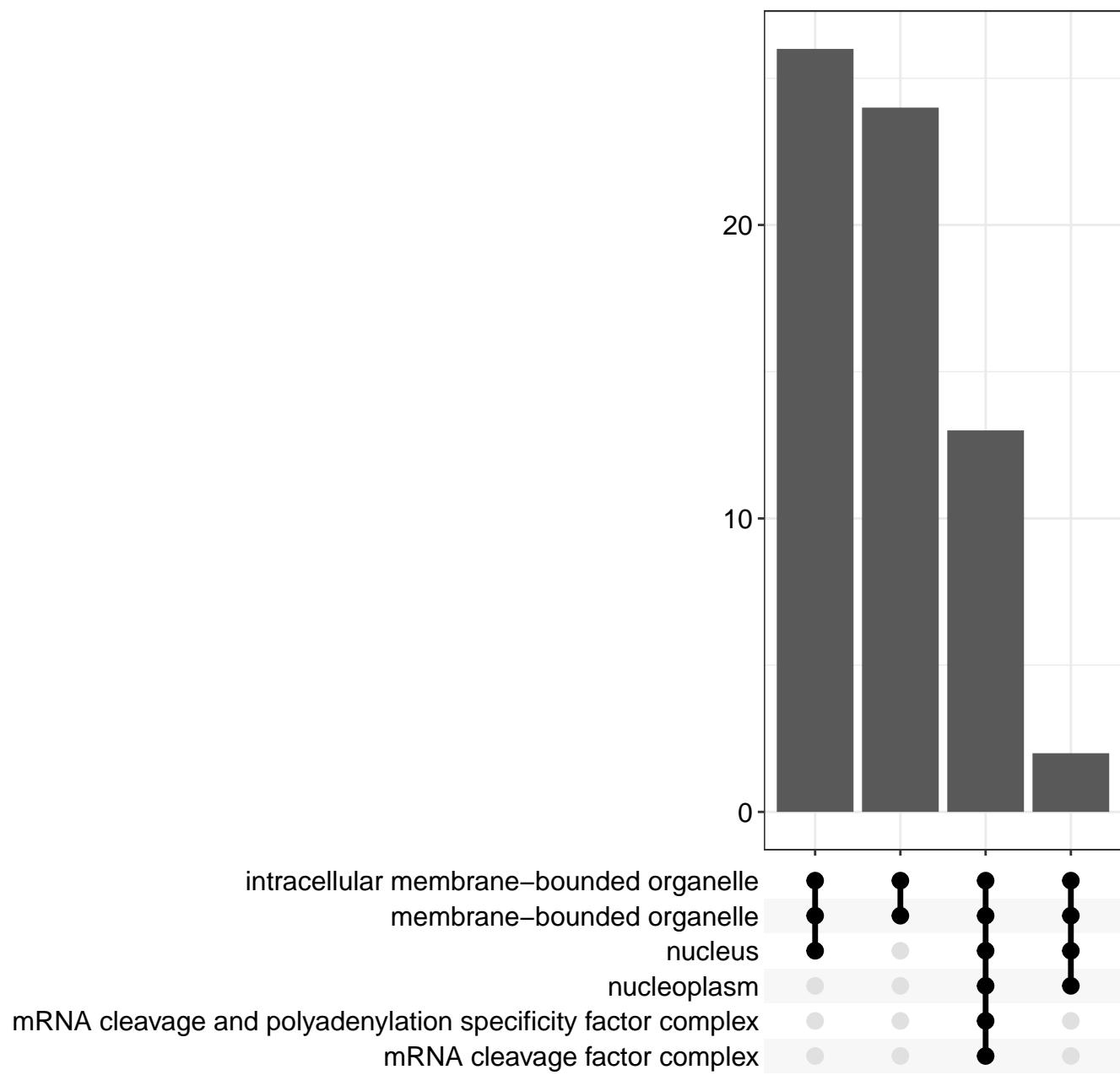


HBS1-TAP Up-regulated GO CC emapplot

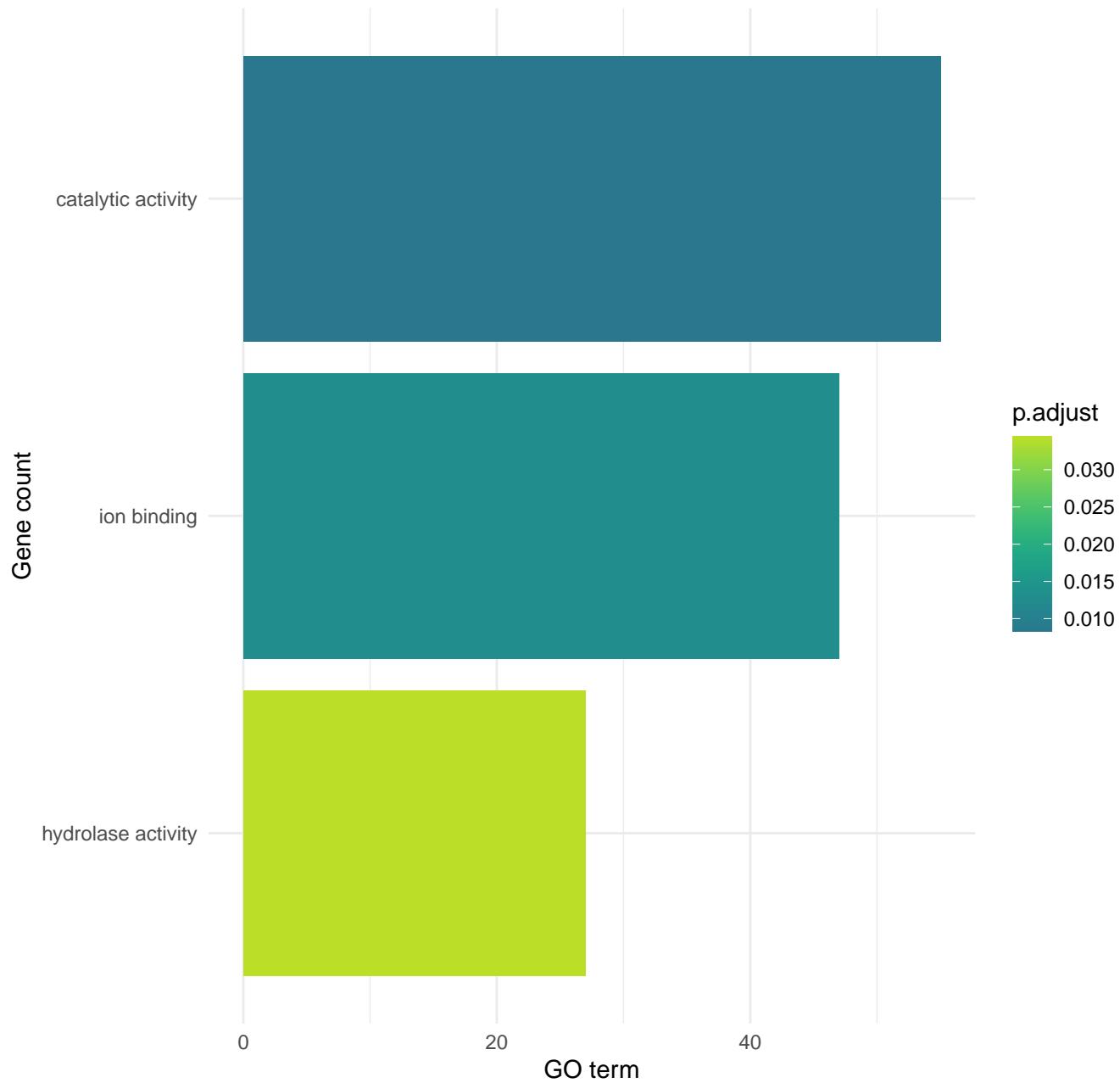
mRNA cleavage factor complex



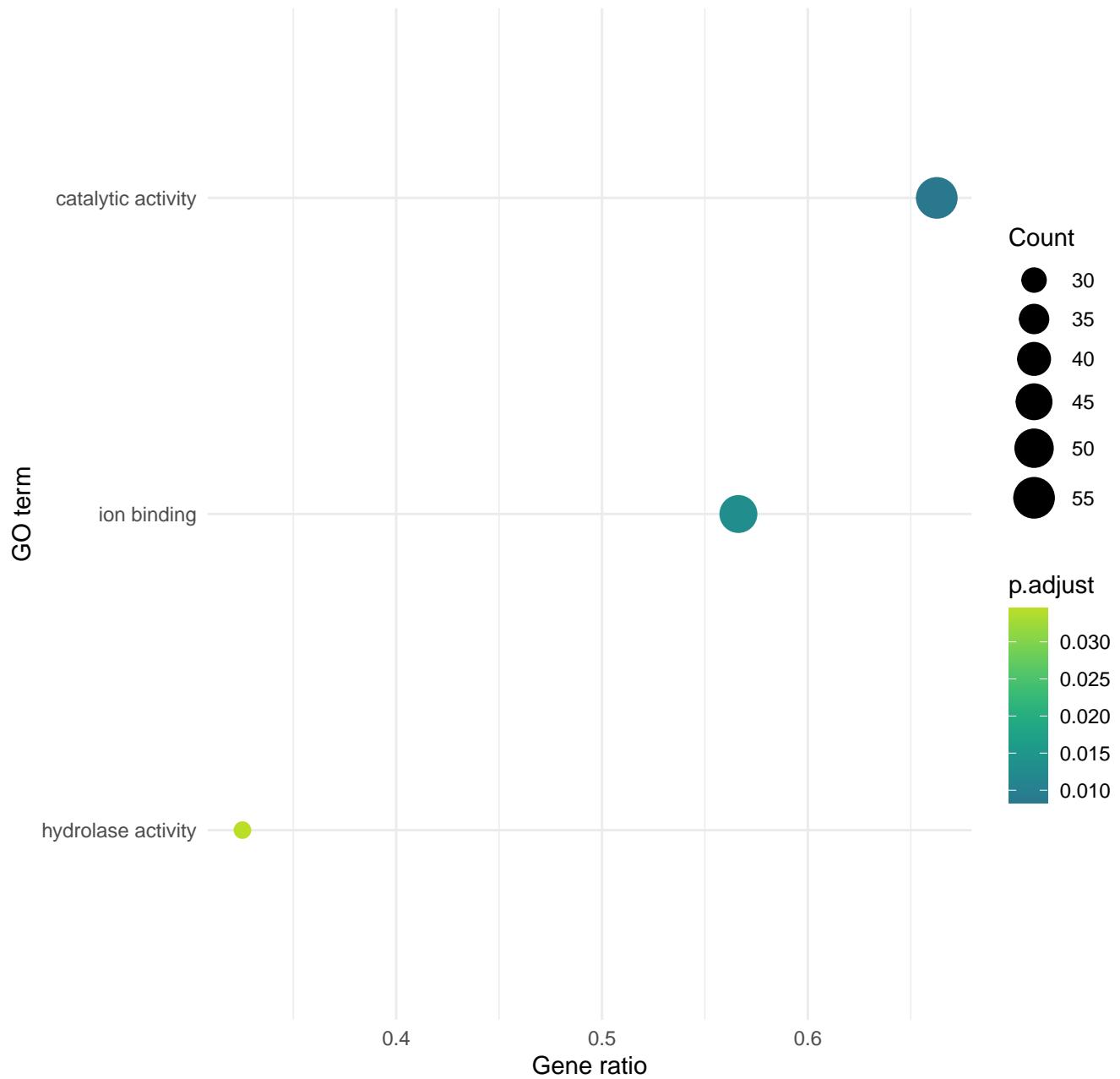




HBS1-TAP Up-regulated GO MF barplot



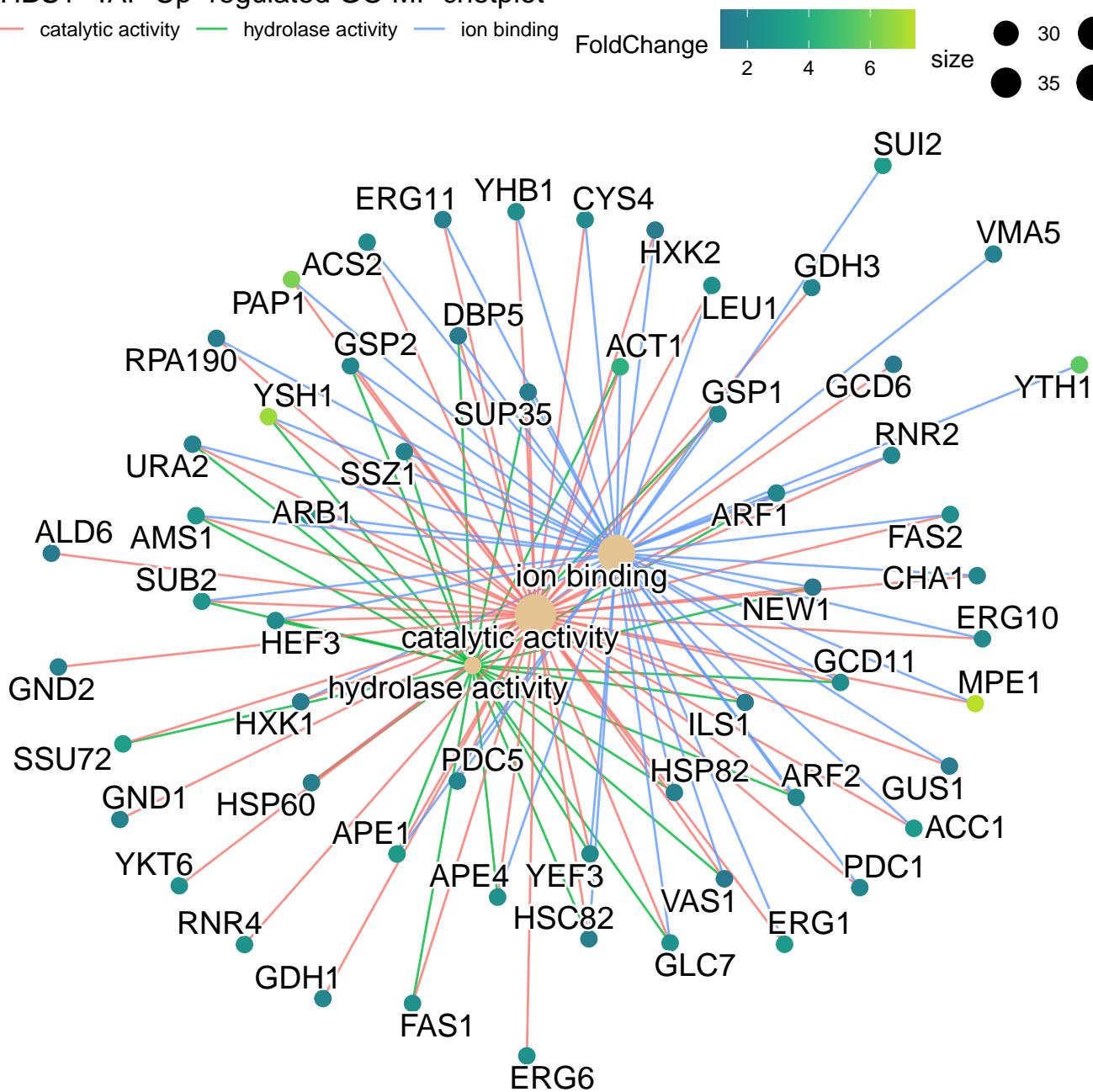
HBS1-TAP Up-regulated GO MF dotplot



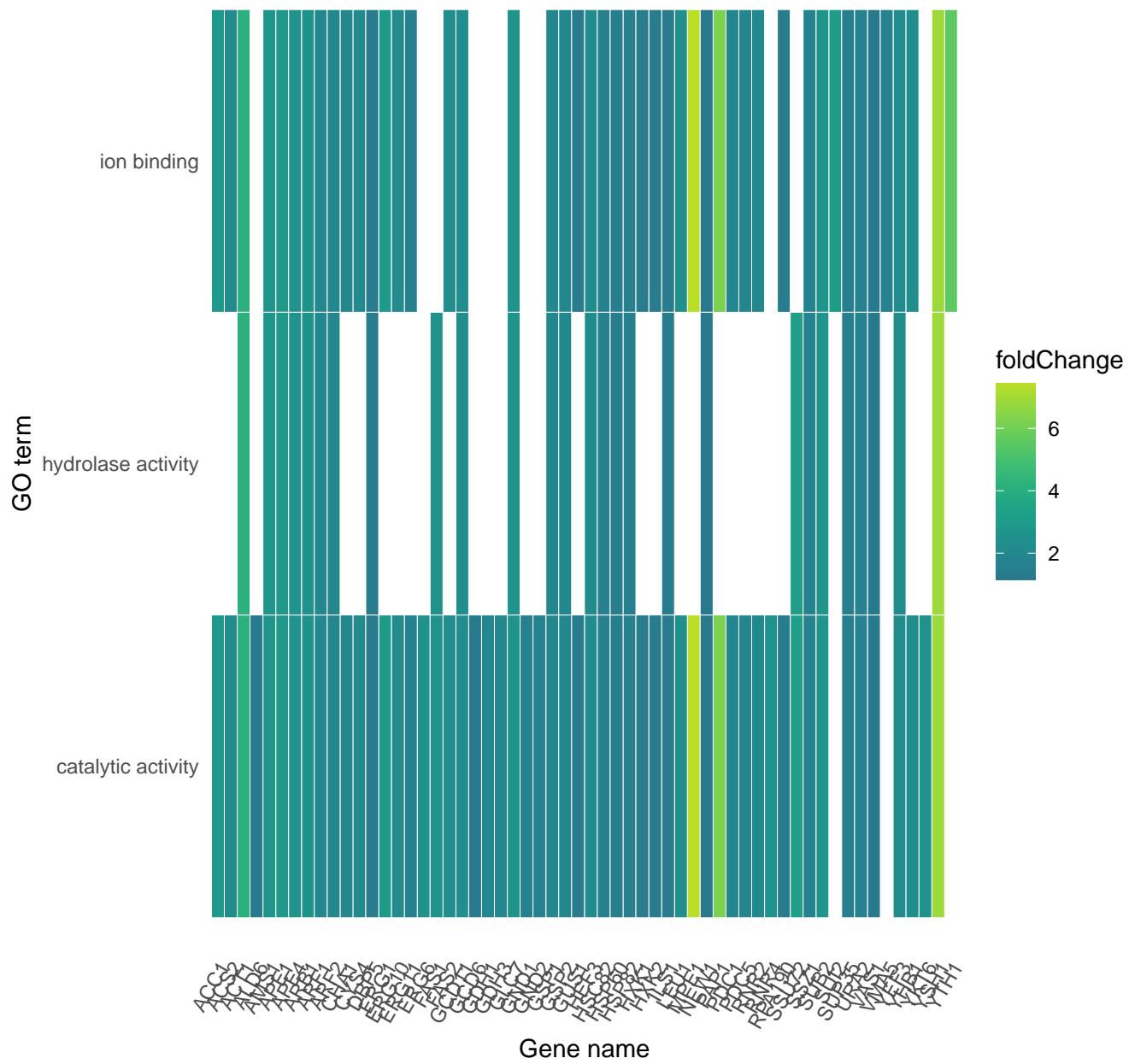
HBS1-TAP Up-regulated GO MF cnetplot

catalytic activity — hydrolase activity — ion binding

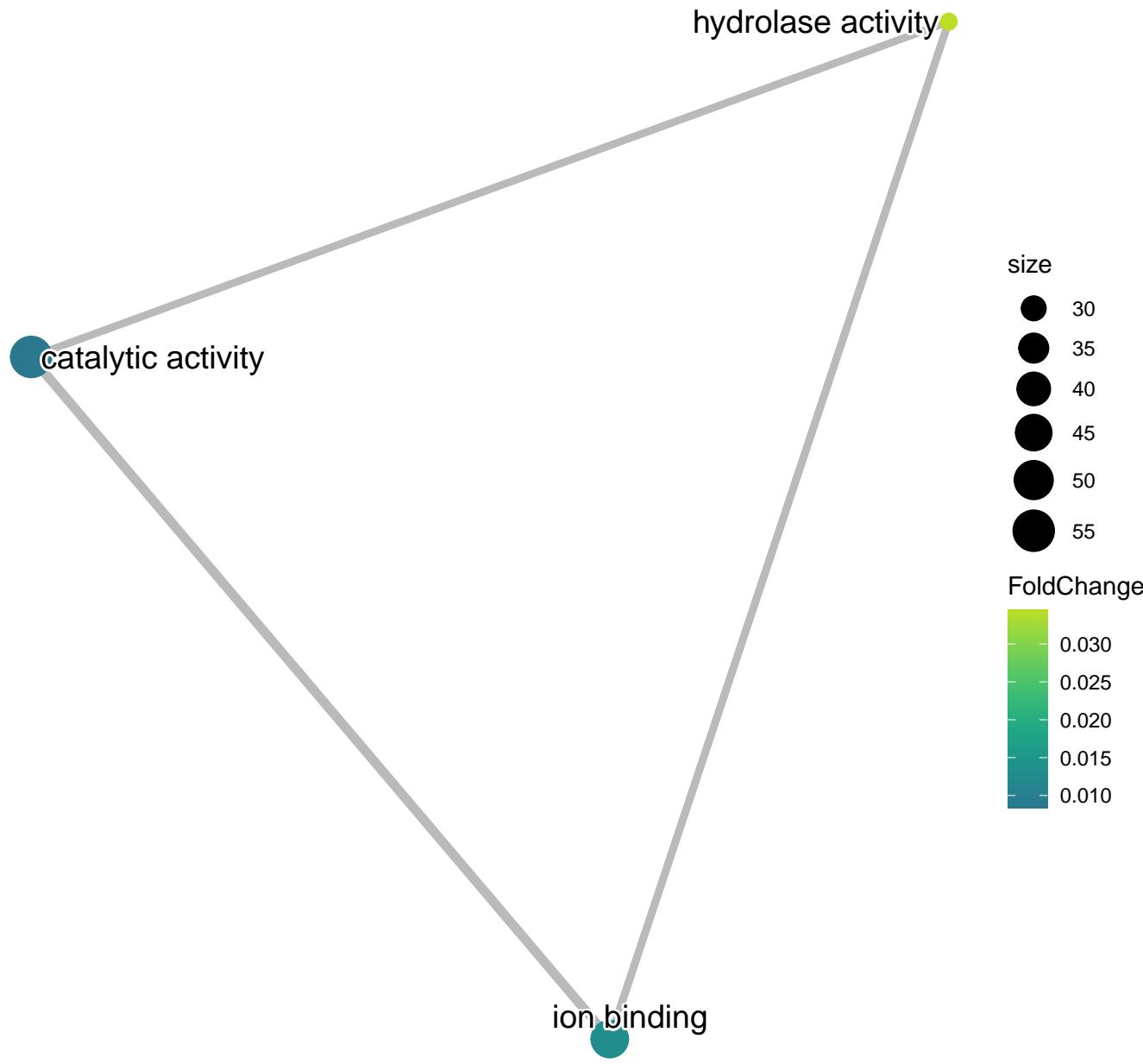
FoldCha

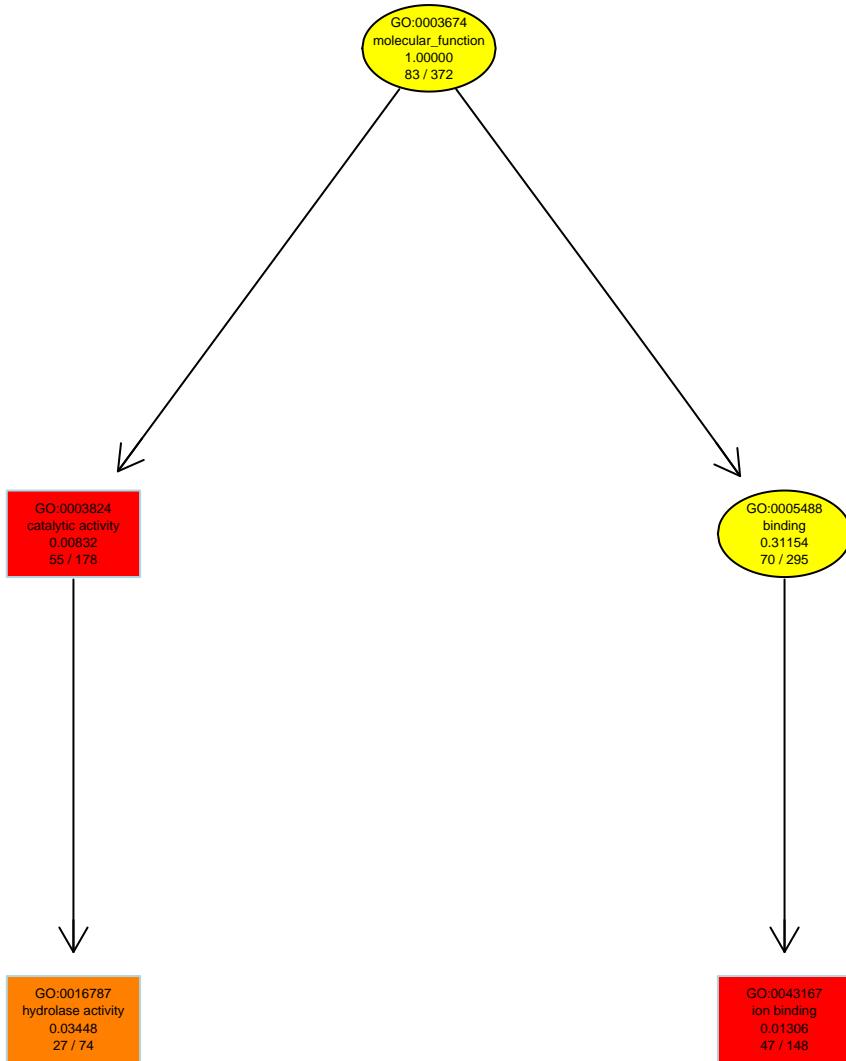


HBS1-TAP Up-regulated GO MF heatplot

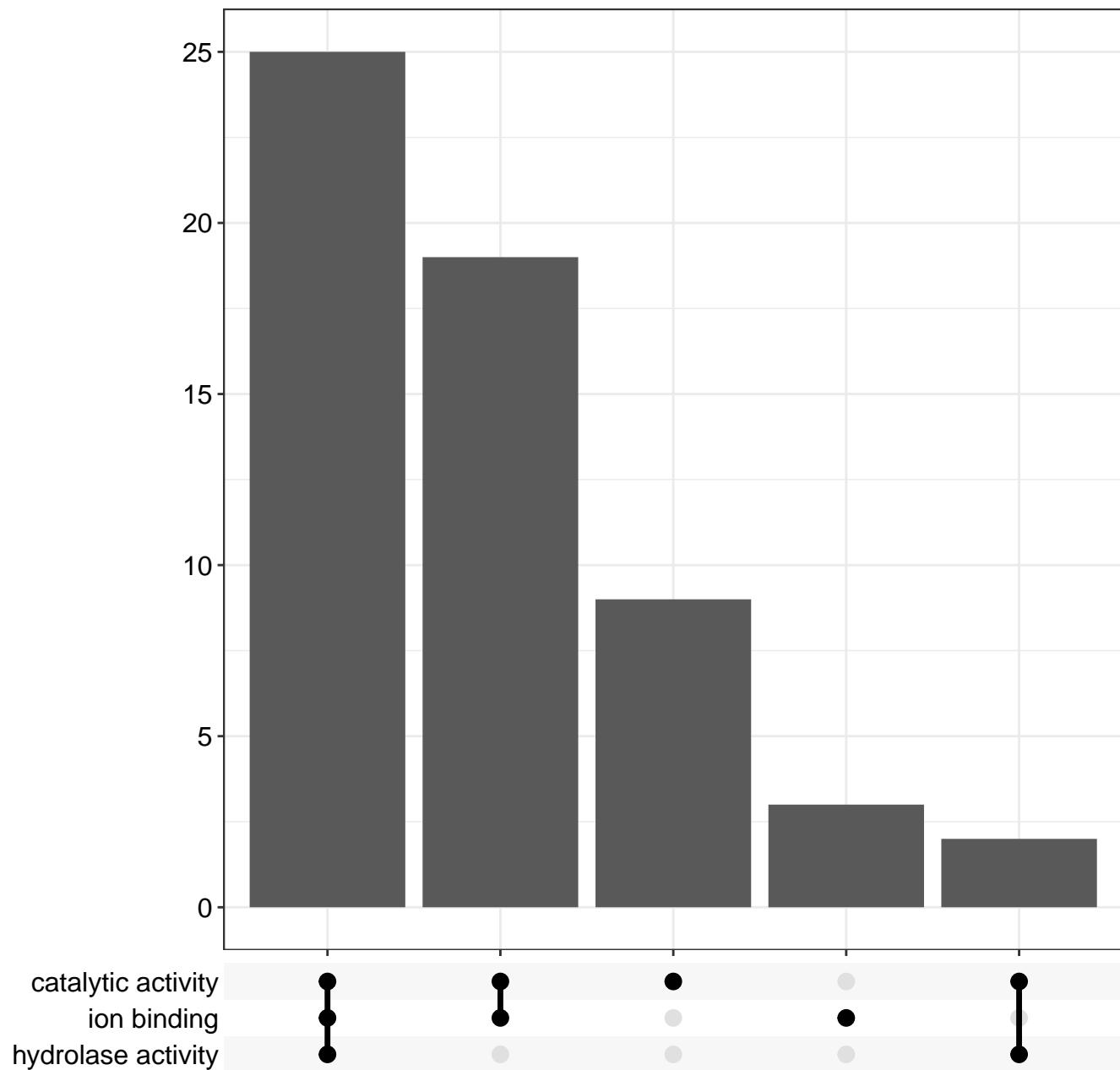


HBS1-TAP Up-regulated GO MF emapplot

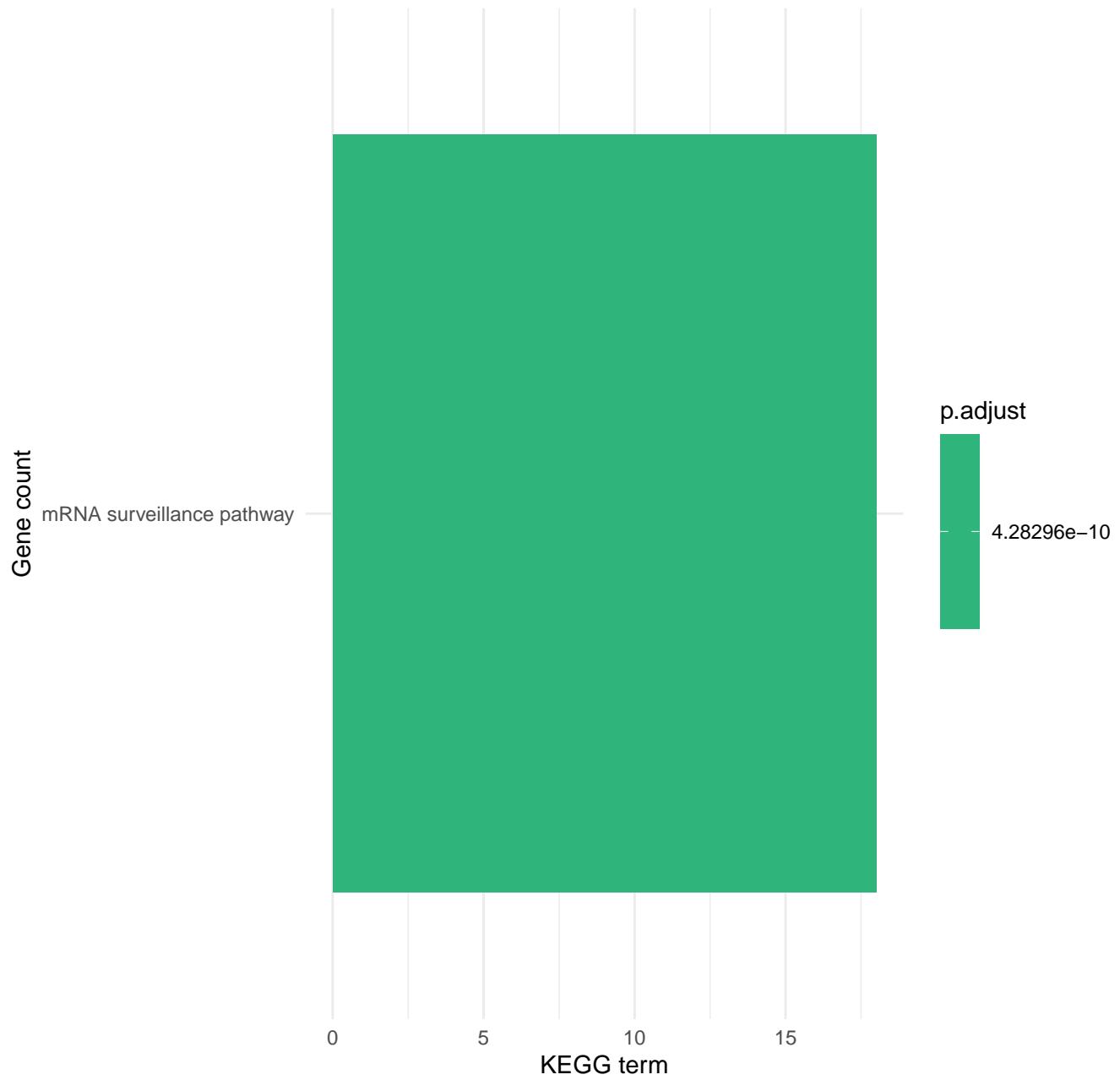




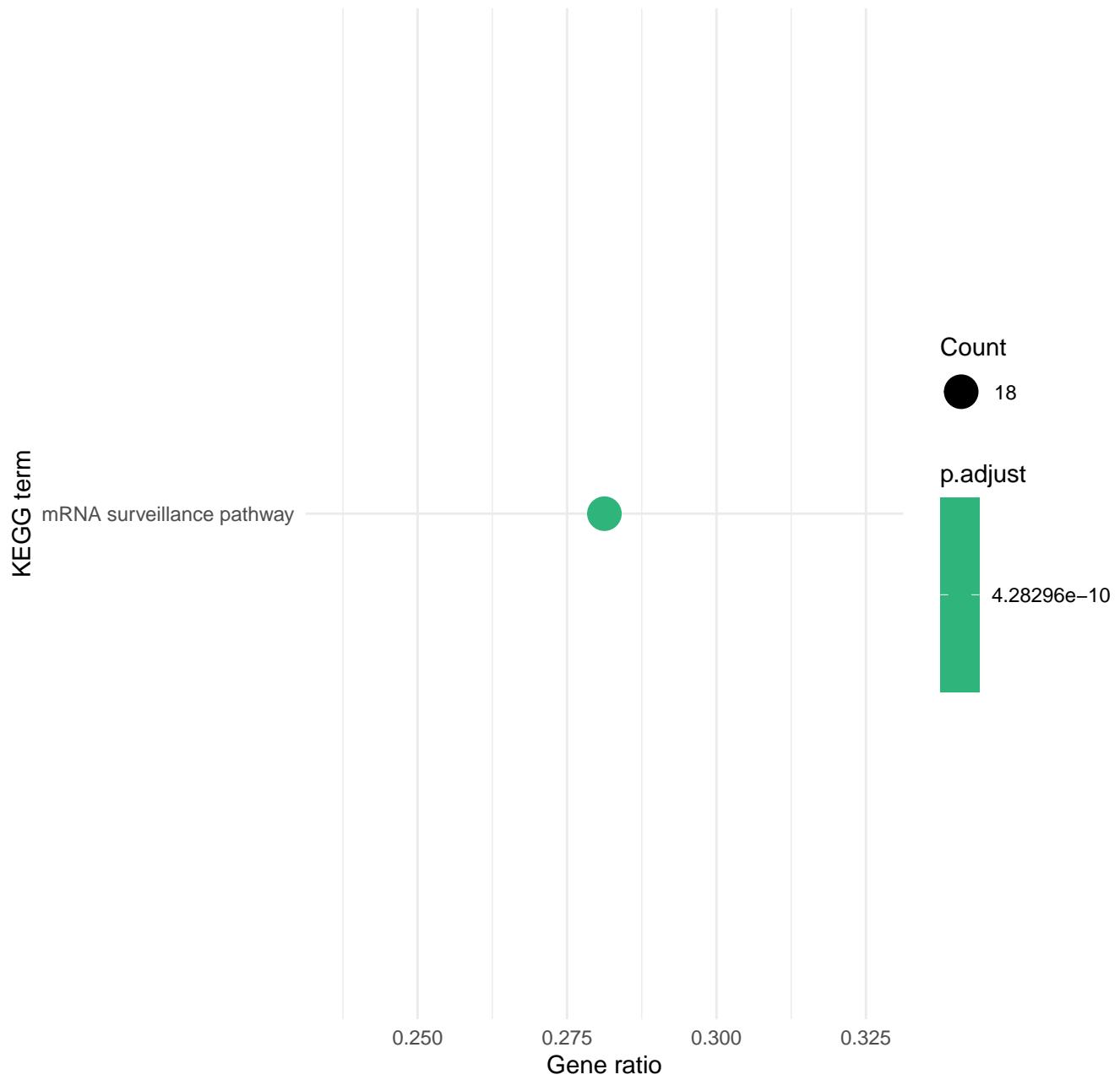
HBS1-TAP Up-regulated GO MF upsetplot



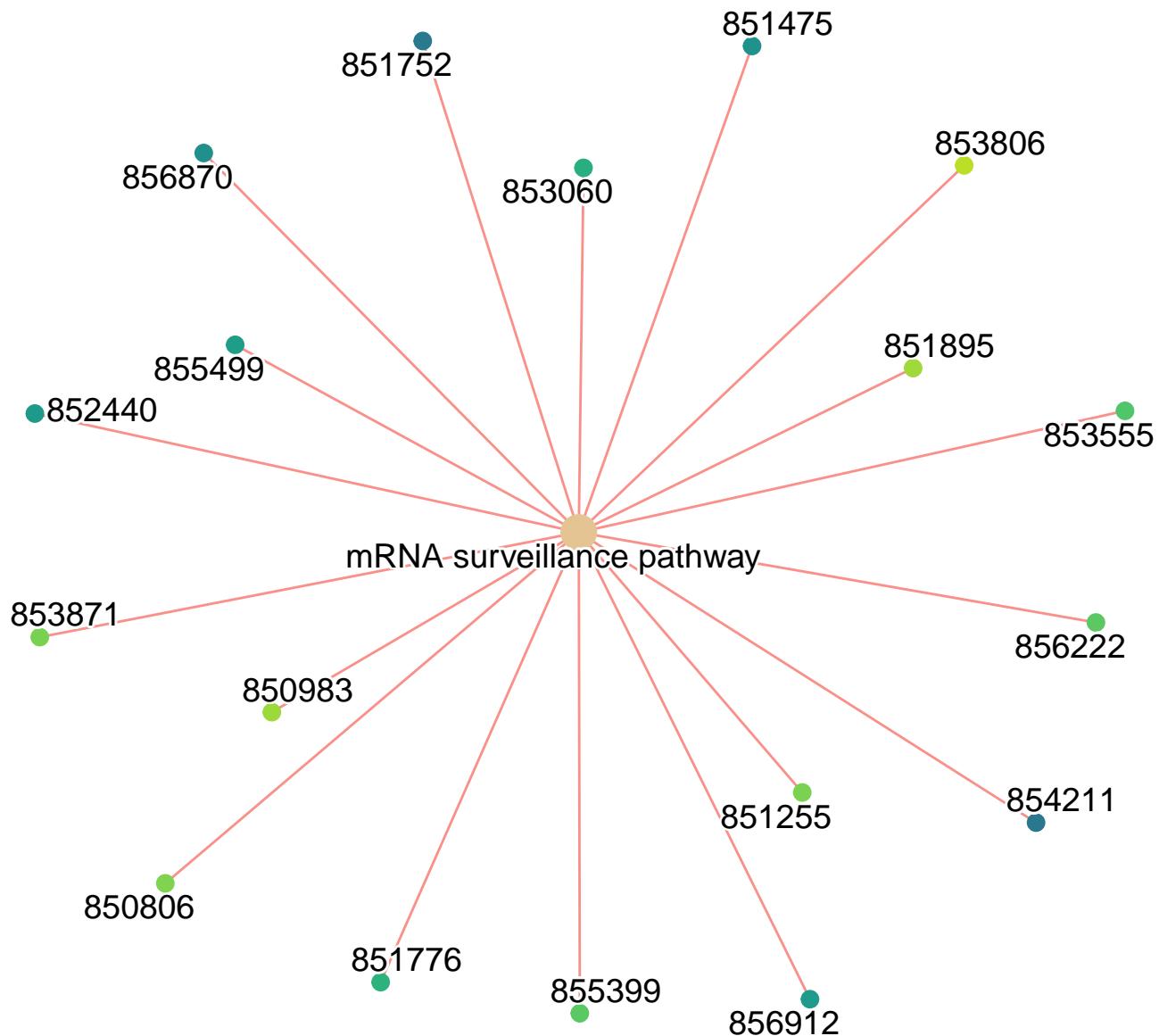
HBS1-TAP Up-regulated KEGG barplot



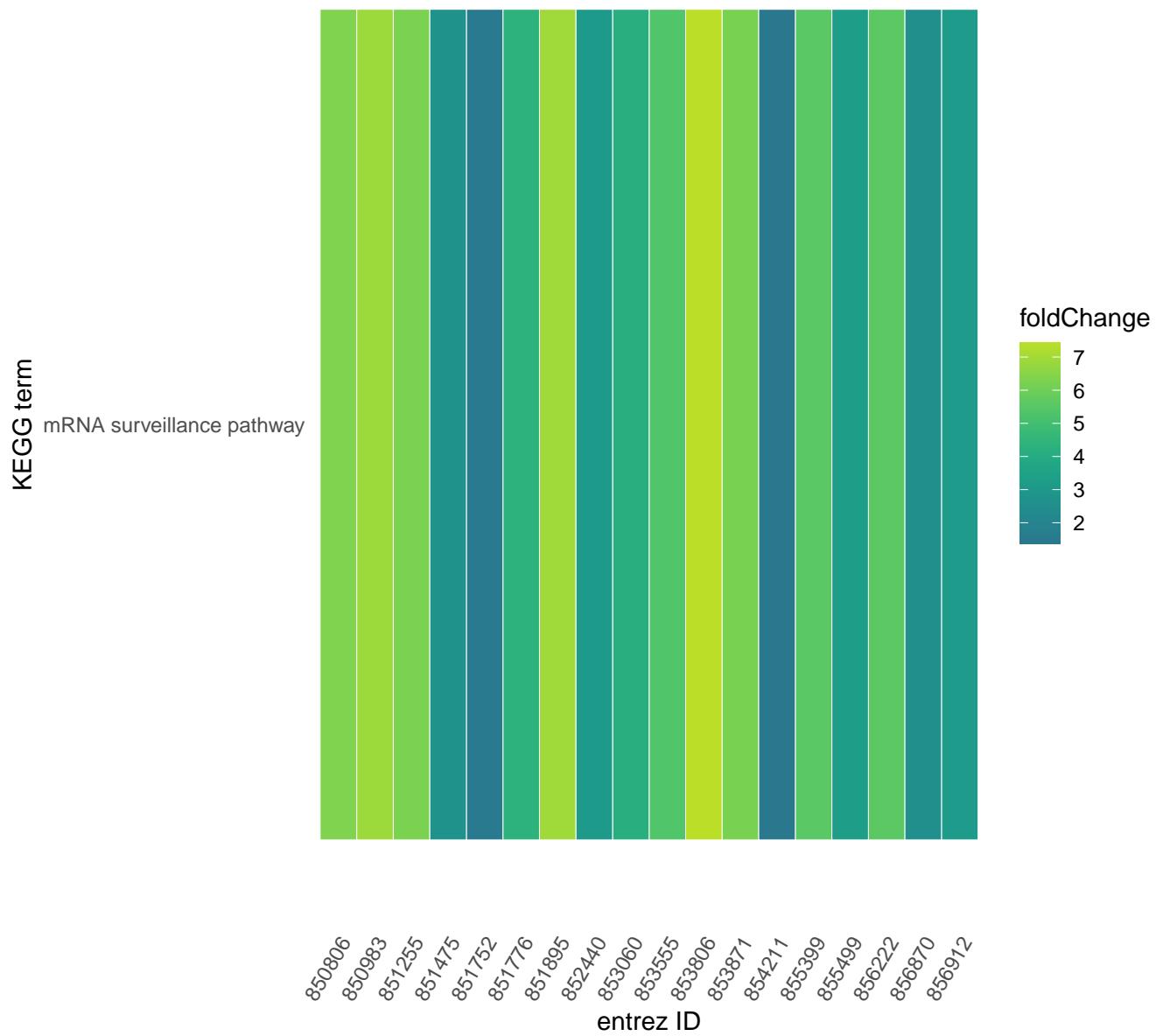
HBS1-TAP Up-regulated KEGG dotplot



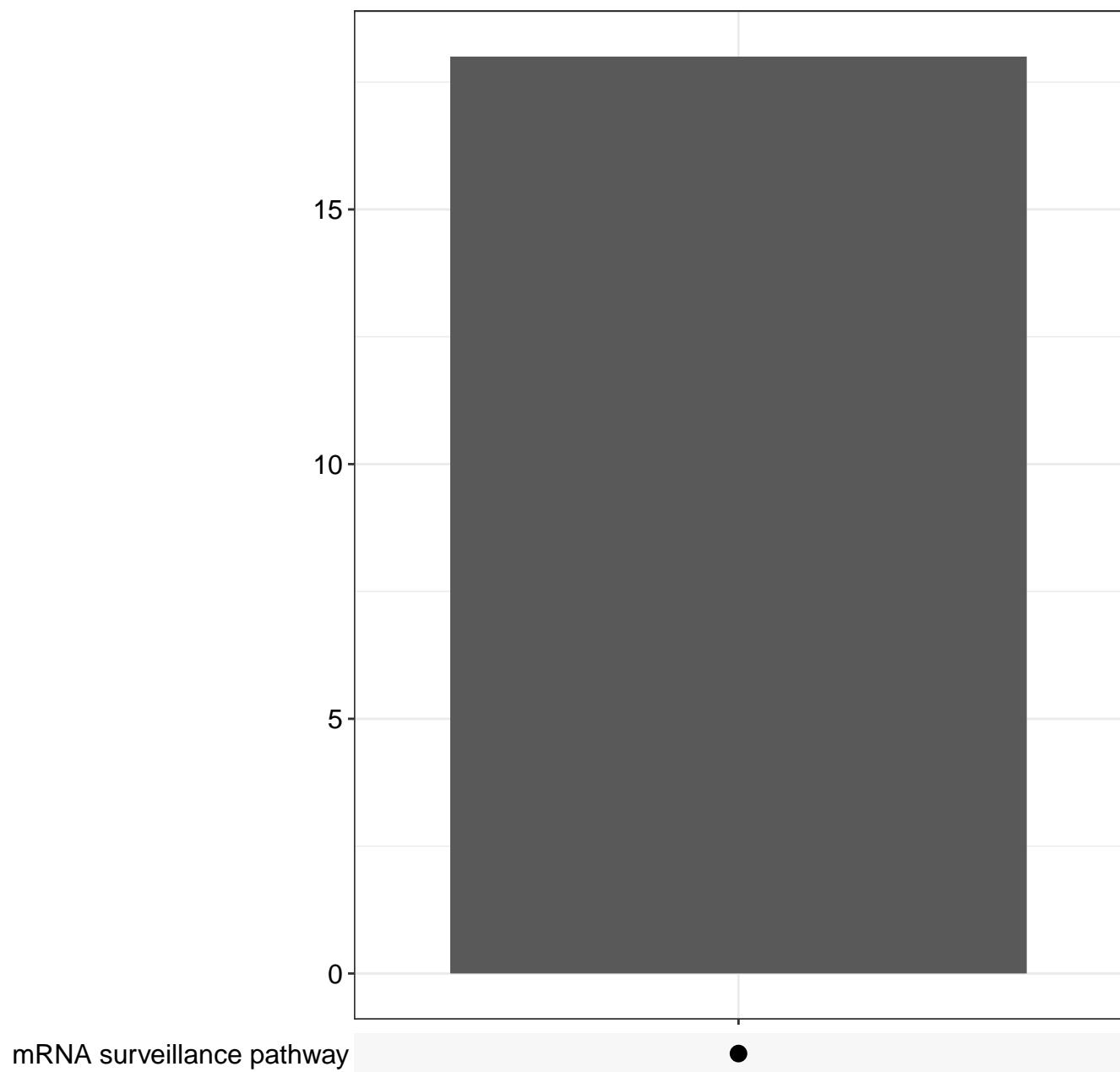
HBS1-TAP Up-regulated KEGG dotplot



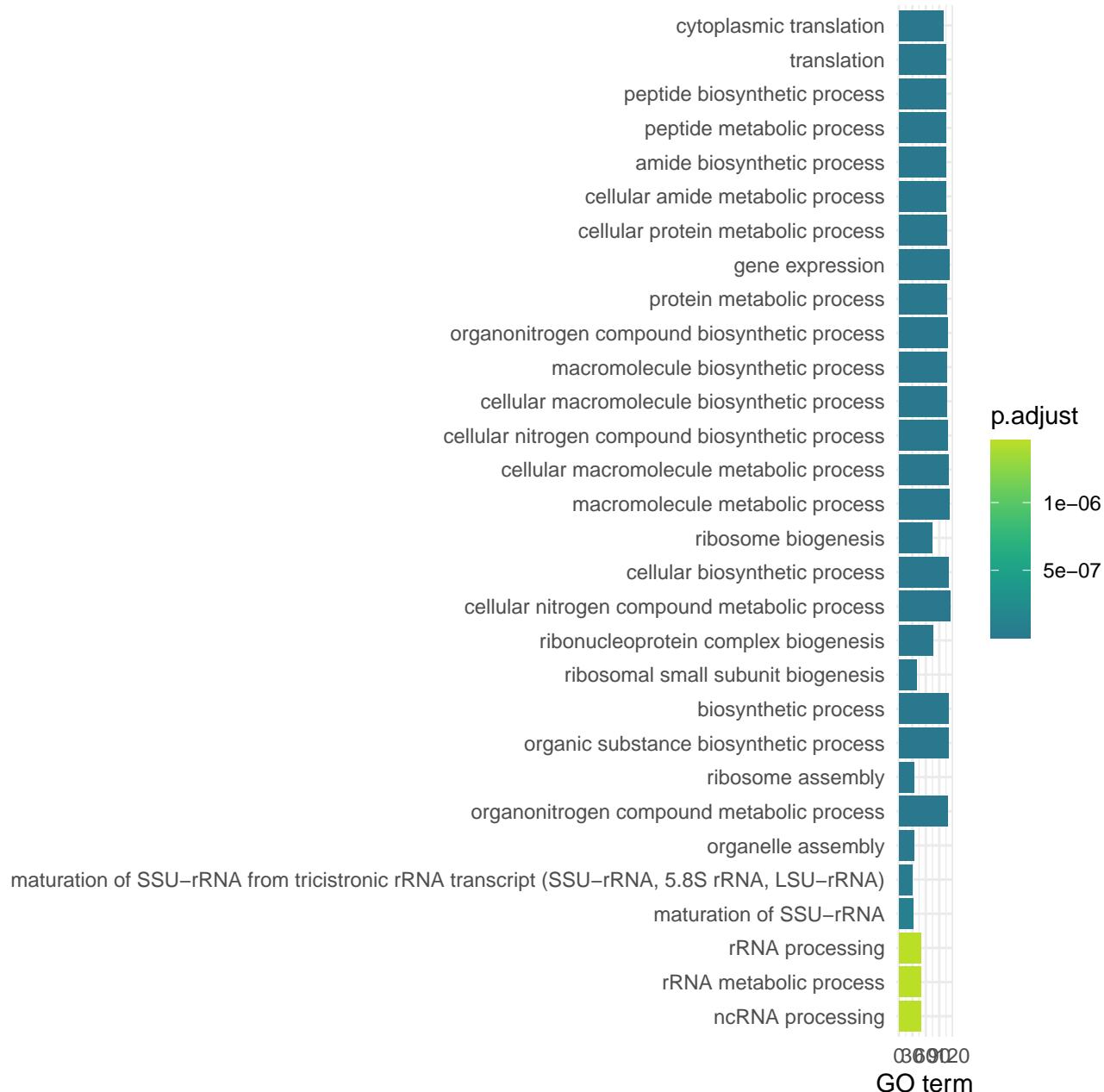
HBS1-TAP Up-regulated KEGG heatmap



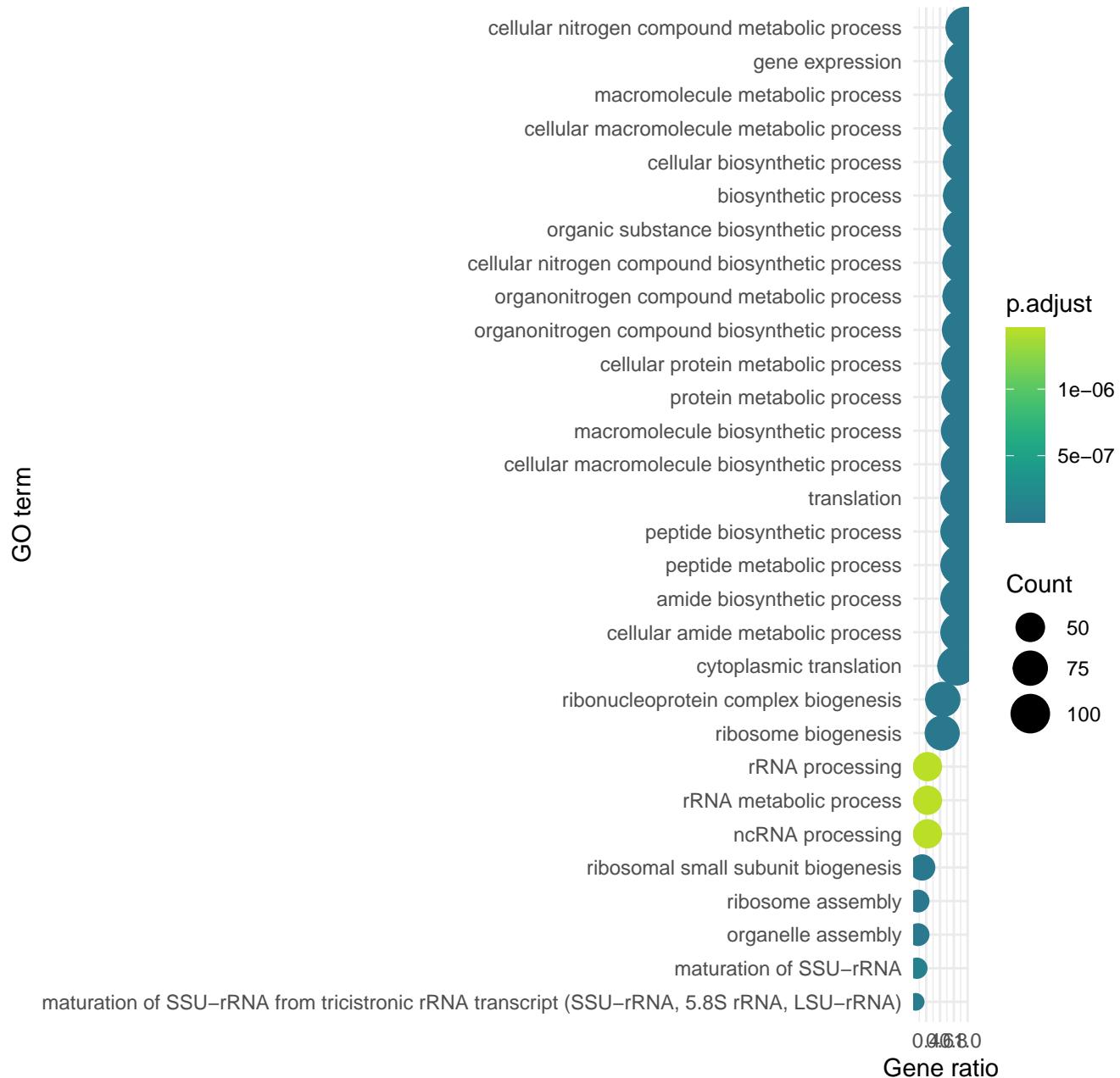
HBS1-TAP Up-regulated KEGG upsetplot



MUD2-TAP Up-

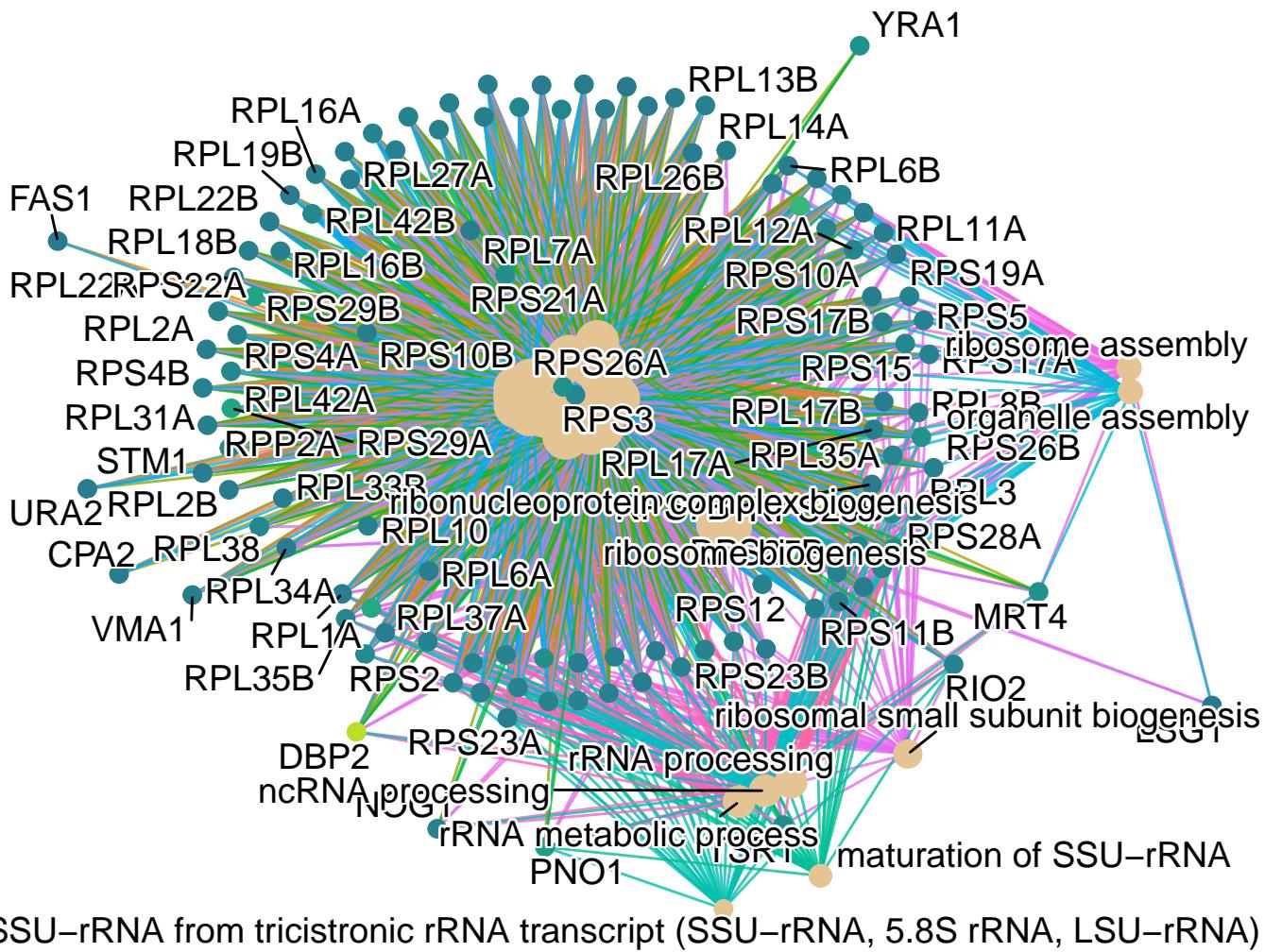


MUD2-TAP Up-

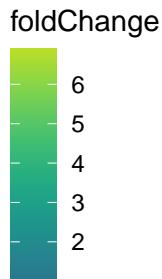
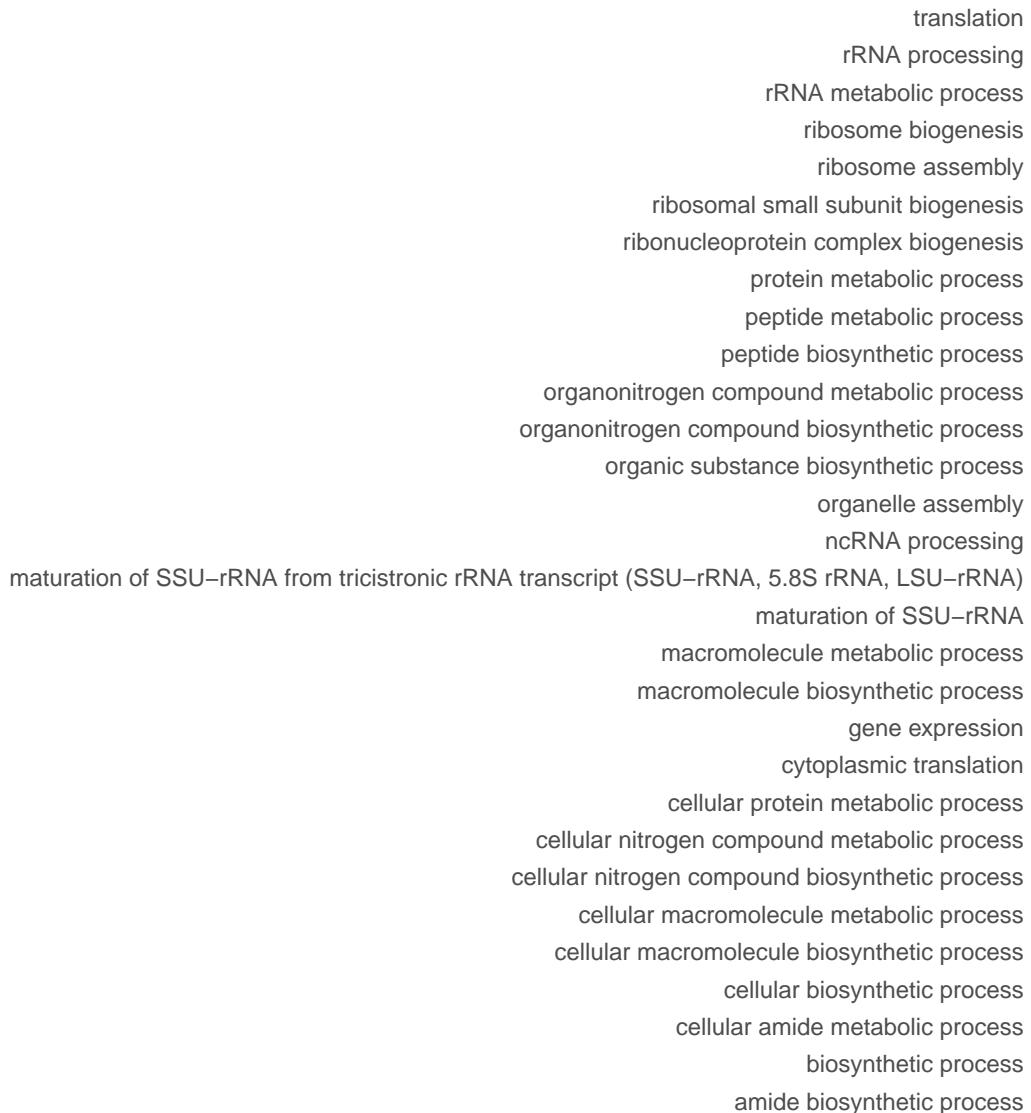


MUD2-TAP Up-regulated GO BP cnetplot

and biosynthetic process — macromolecule metabolic process
and metabolic process — maturation of SSU-rRNA
process — ncRNA processing
process — organelle assembly
etic process — organic substance biosynthetic process



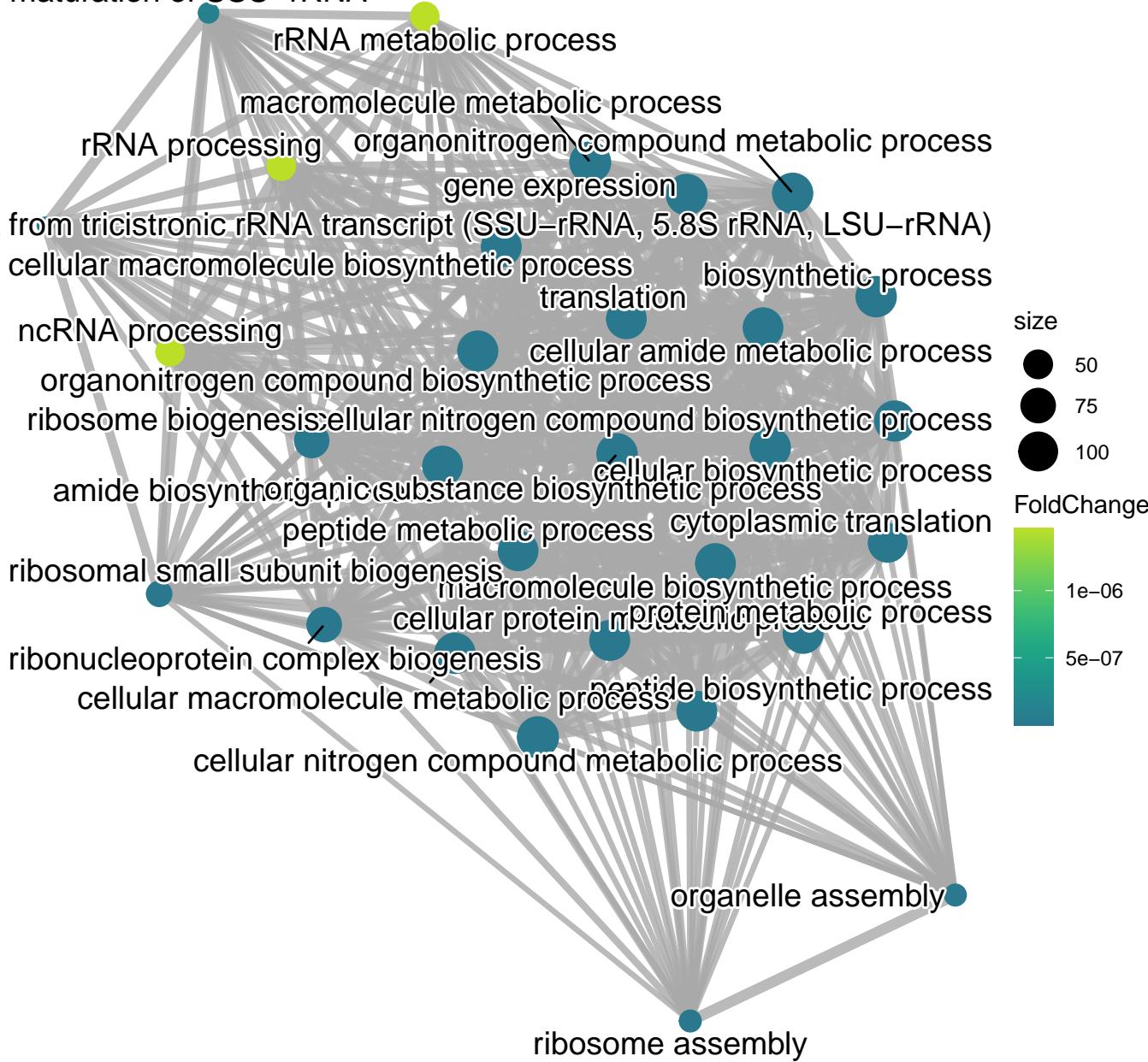
GO term

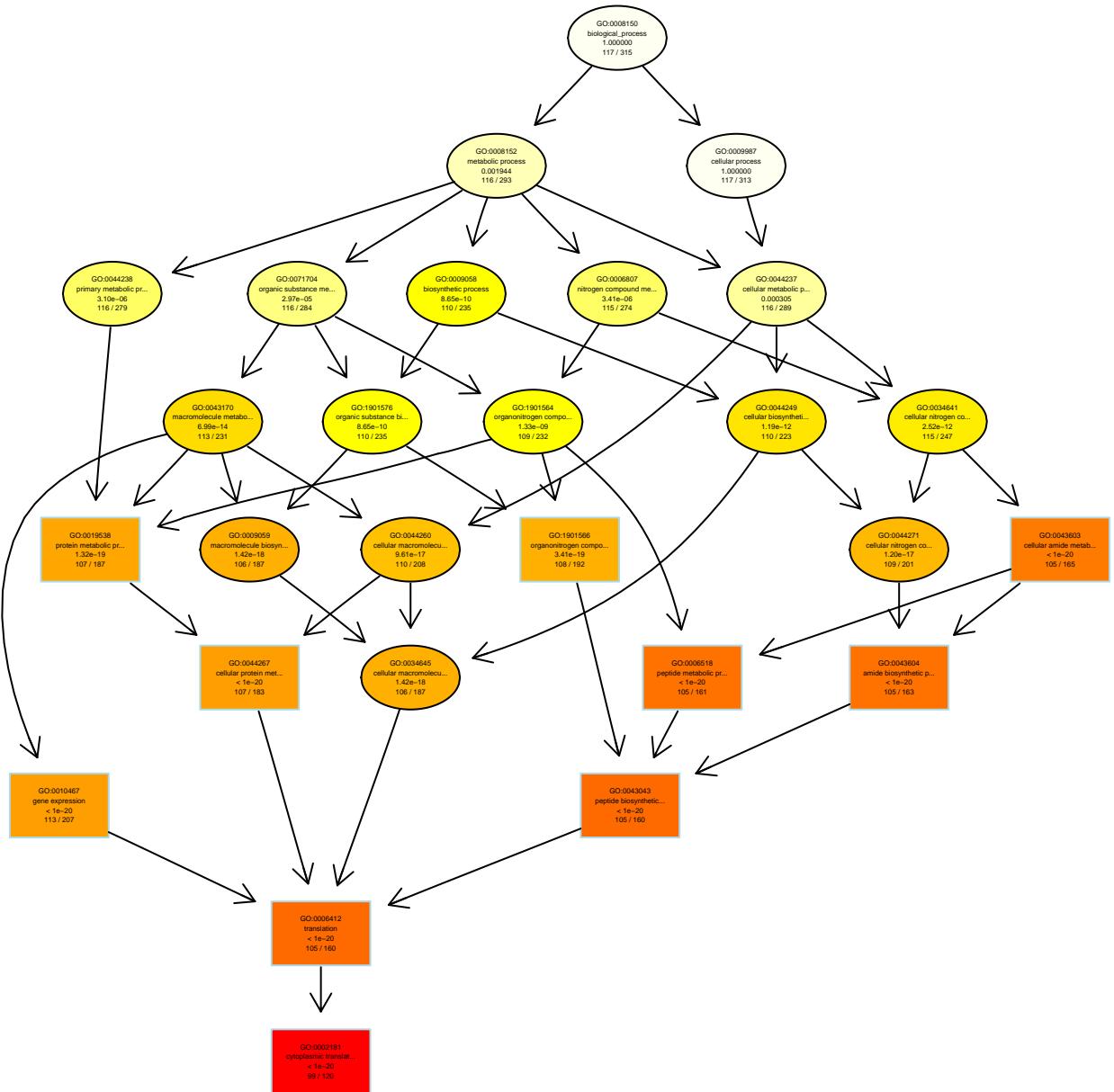


Gene name

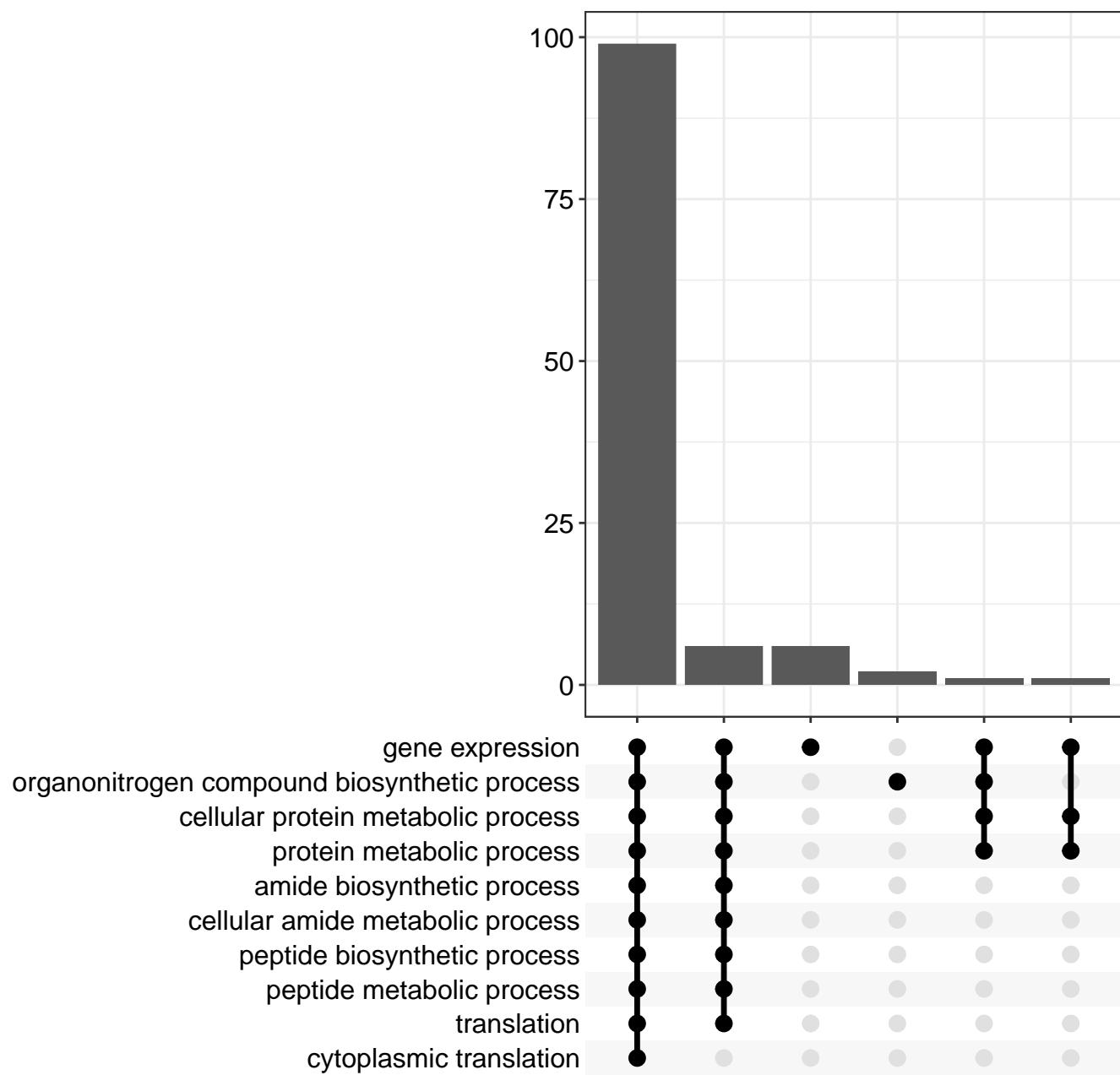
MUD2-TAP Up-regulated GO BP emapplot

maturation of SSU-rRNA

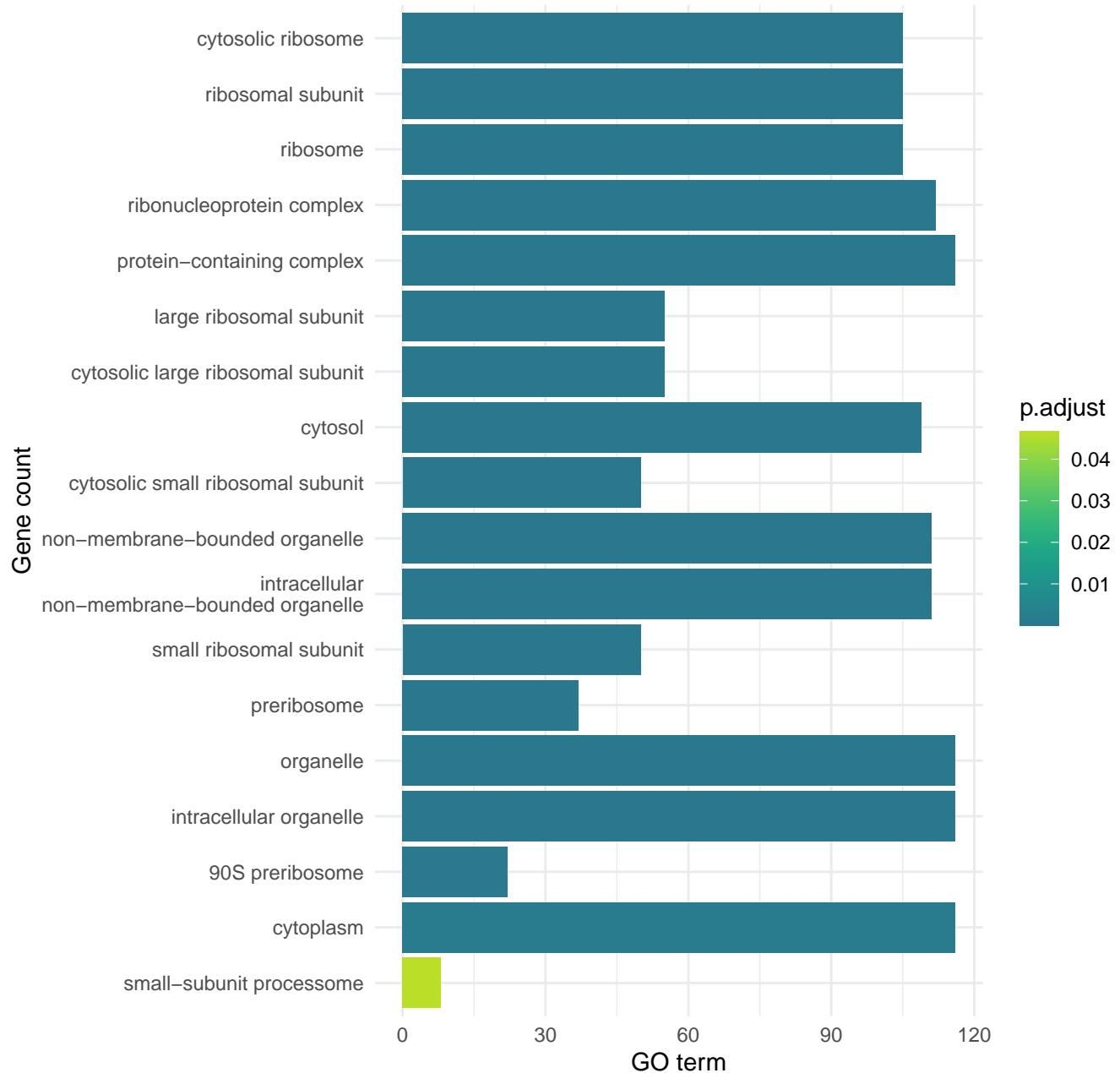




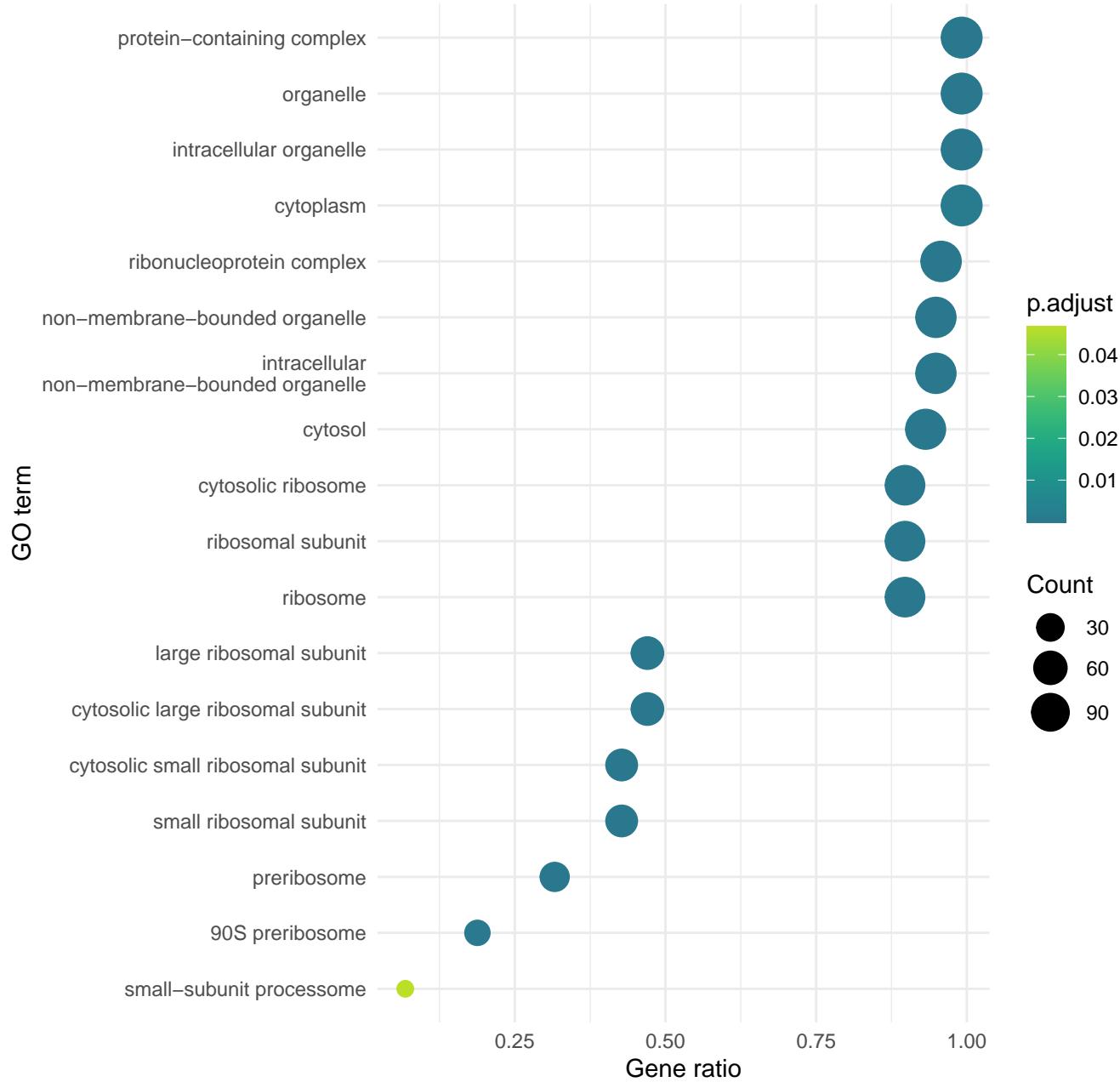
MUD2-TAP Up-regulated GO BP upsetplot



MUD2-TAP Up-regulated GO CC barplot



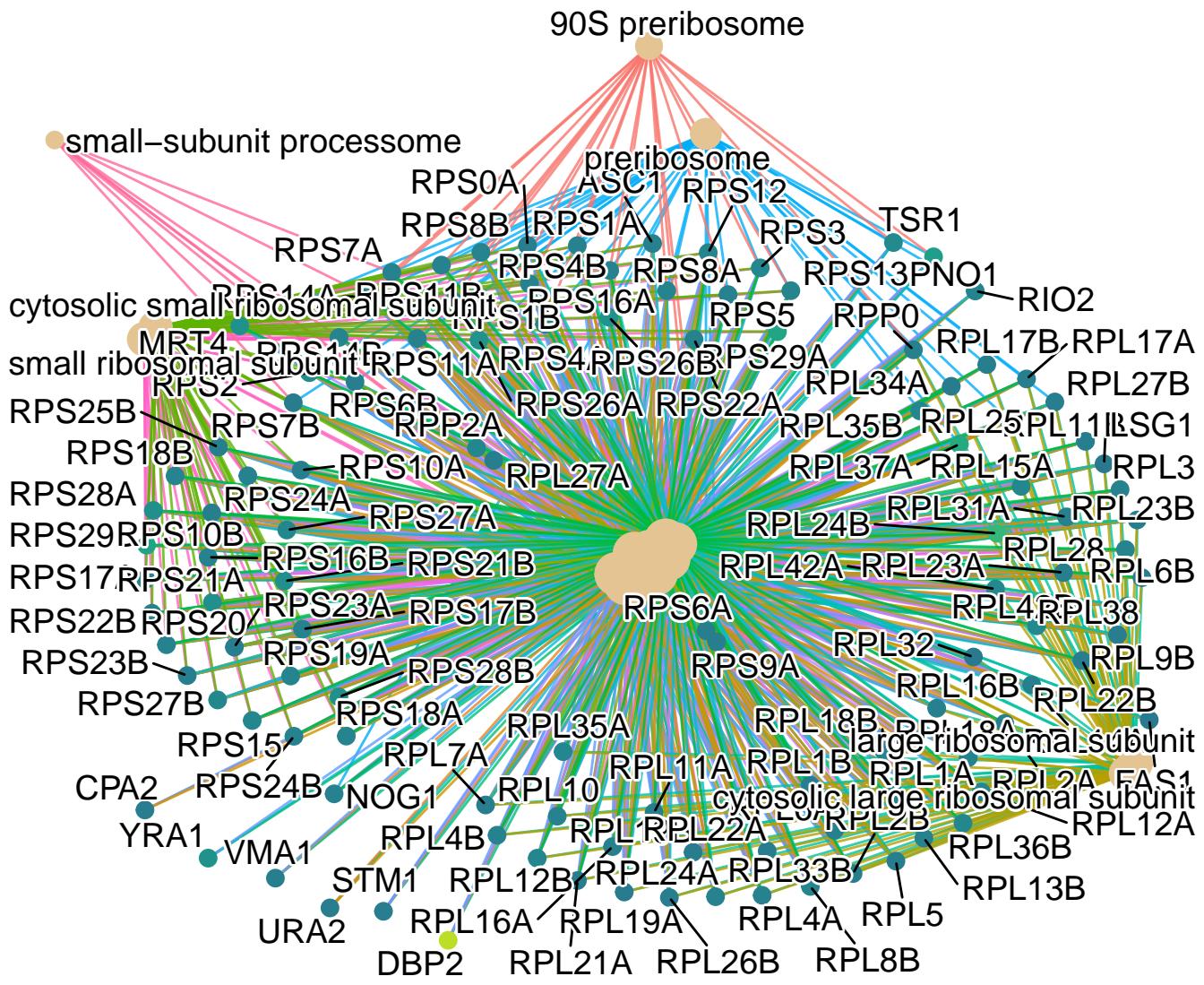
MUD2-TAP Up-regulated GO CC dotplot



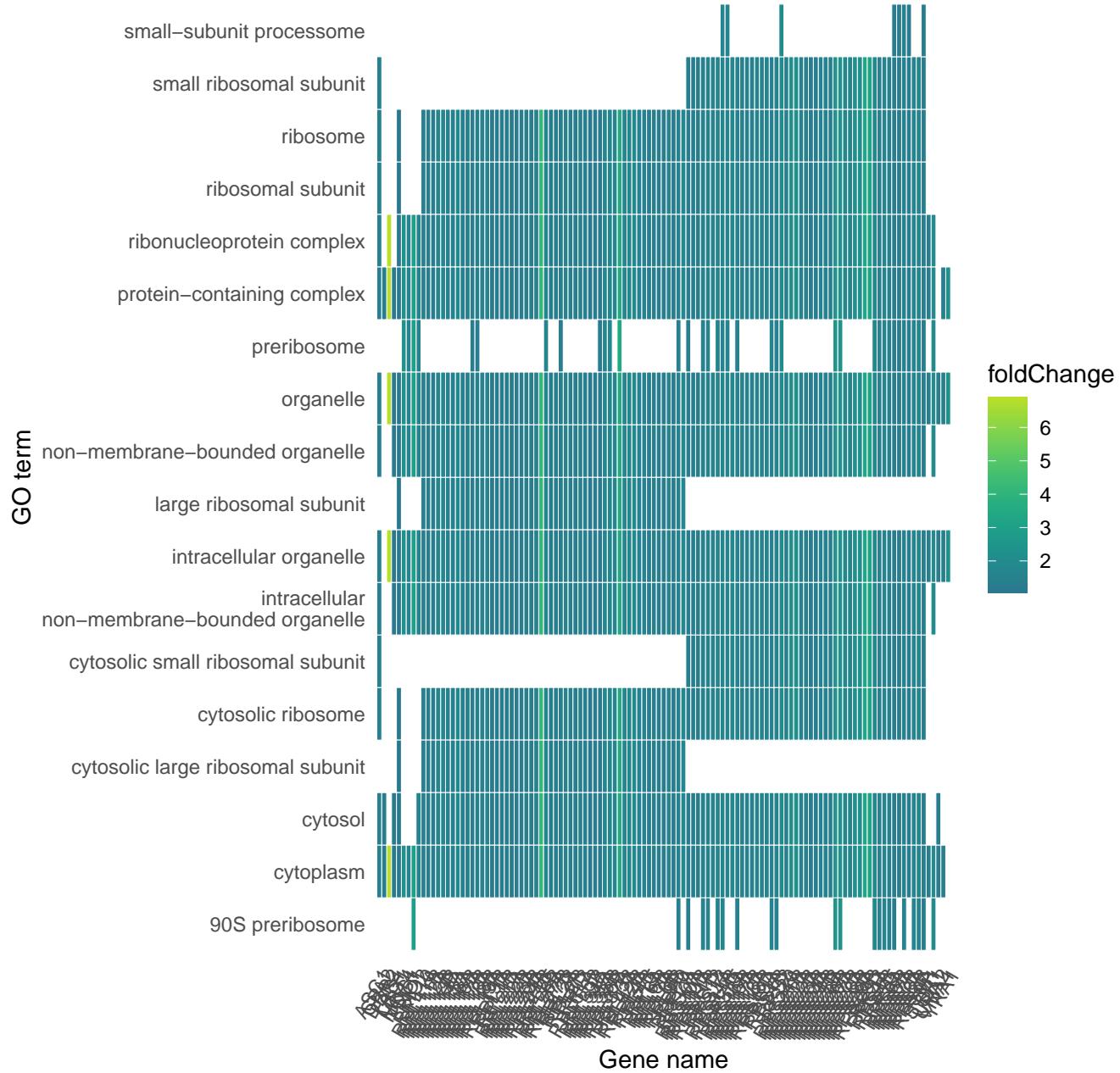
MUD2-TAP Up-regulated GO CC cnetplot

or

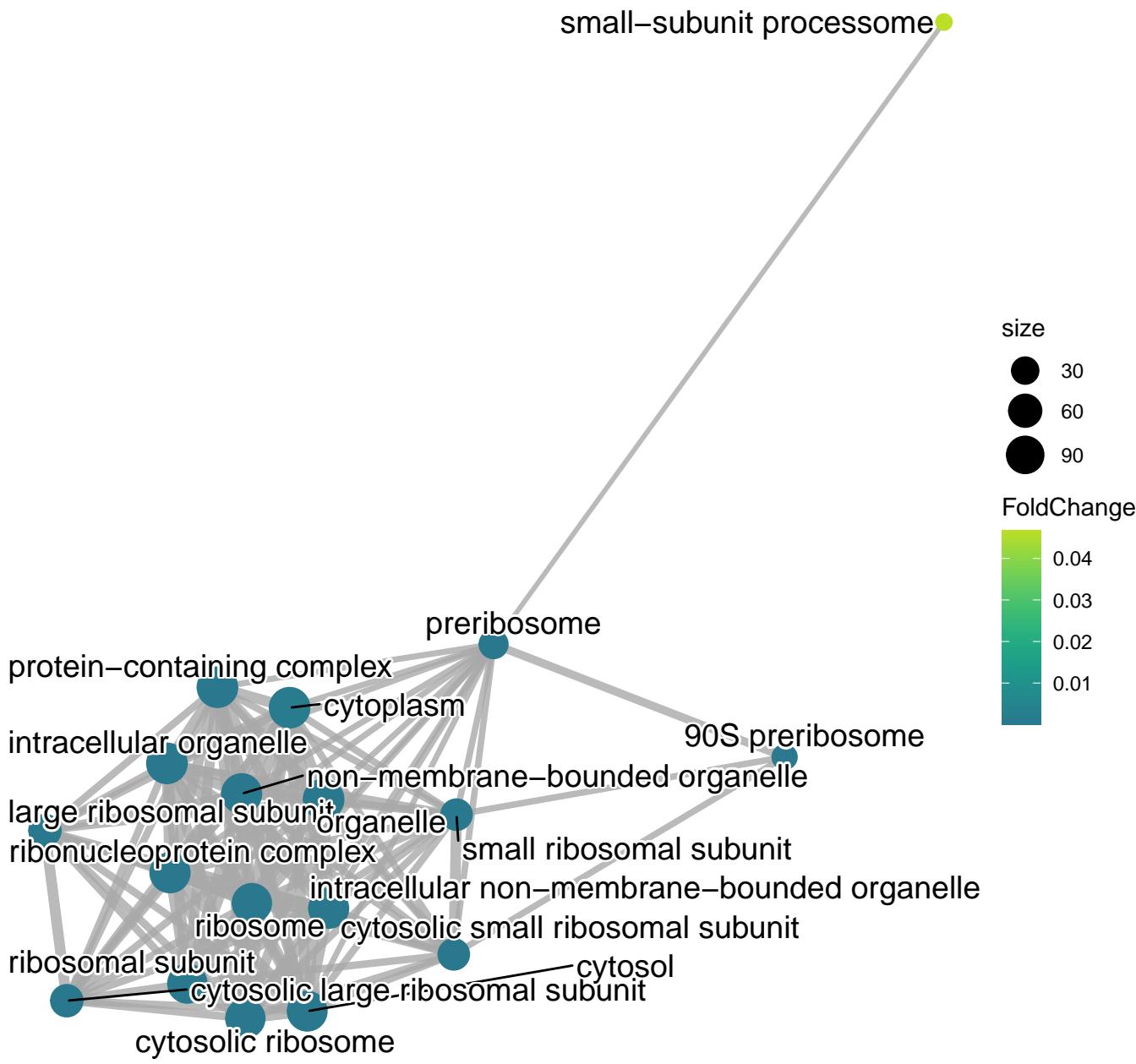
- | | | | | | |
|---|-----------------------------------|---|--|---|-------------------------|
| — | 90S preribosome | — | cytosolic ribosome | — | large ribosomal subunit |
| — | cytoplasm | — | cytosolic small ribosomal subunit | — | non-membrane-bound |
| — | cytosol | — | intracellular non-membrane-bound organelle | — | organelle |
| — | cytosolic large ribosomal subunit | — | intracellular organelle | — | preribosome |

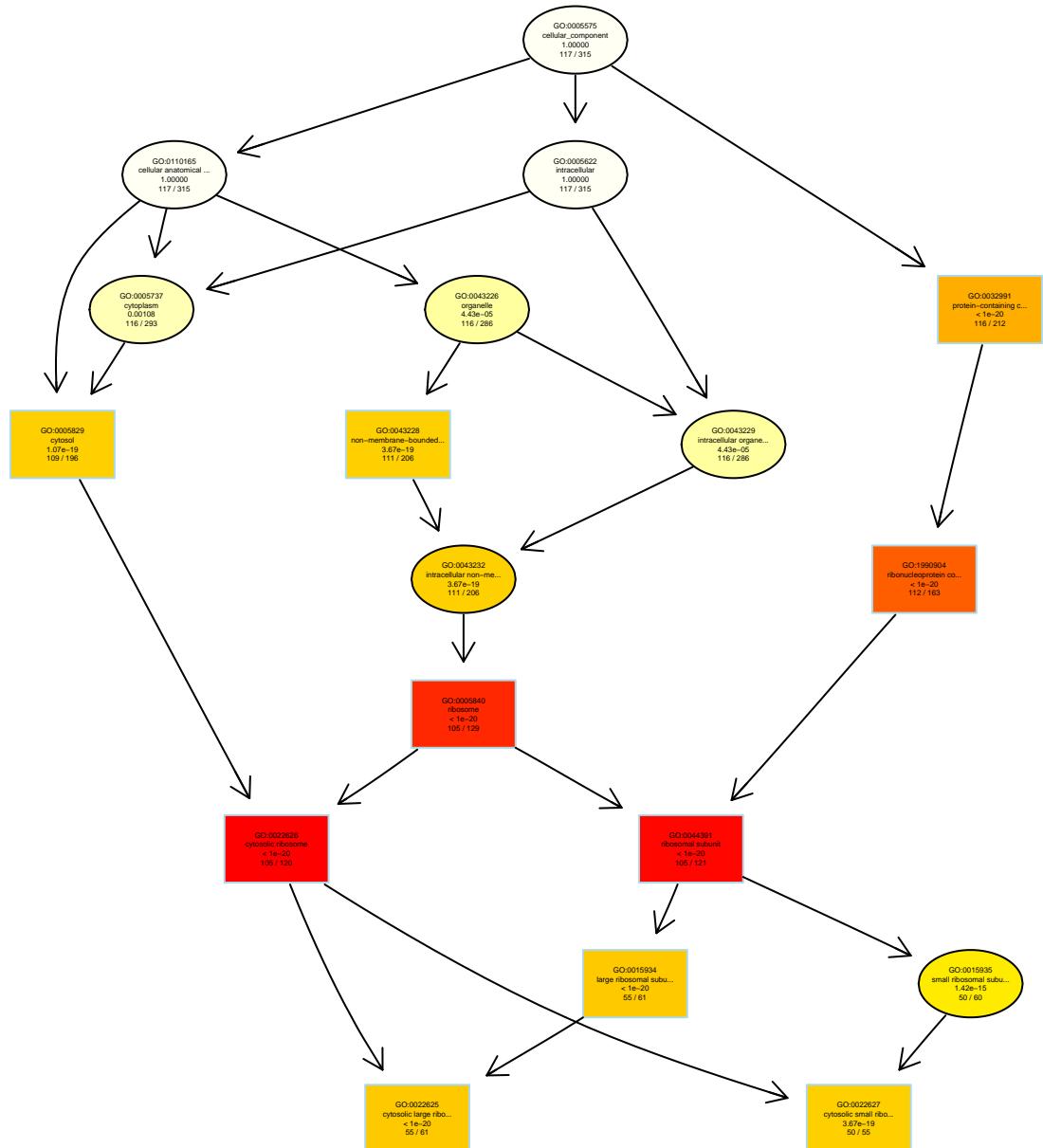


MUD2-TAP Up-regulated GO CC heatplot

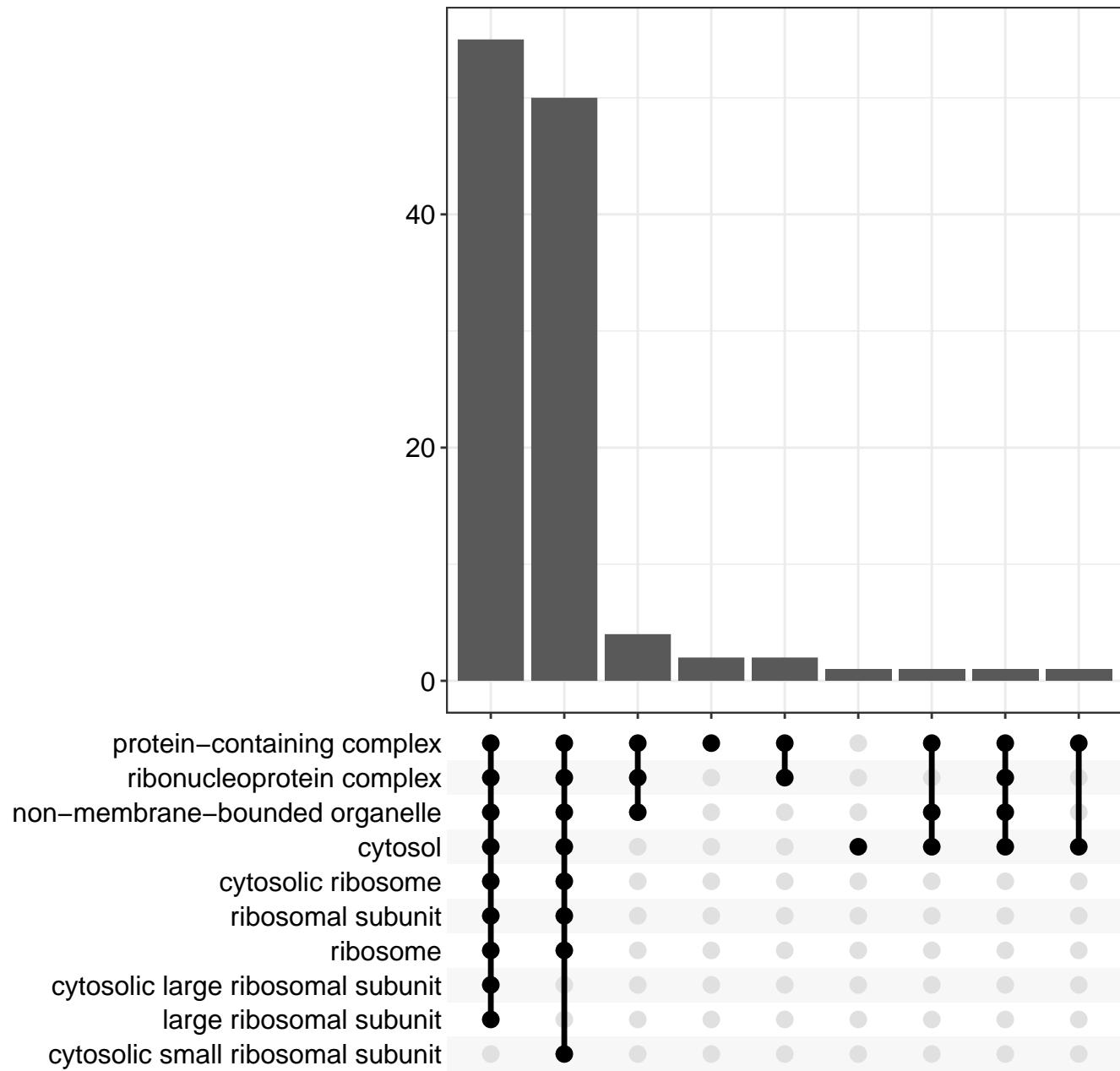


MUD2-TAP Up-regulated GO CC emapplot

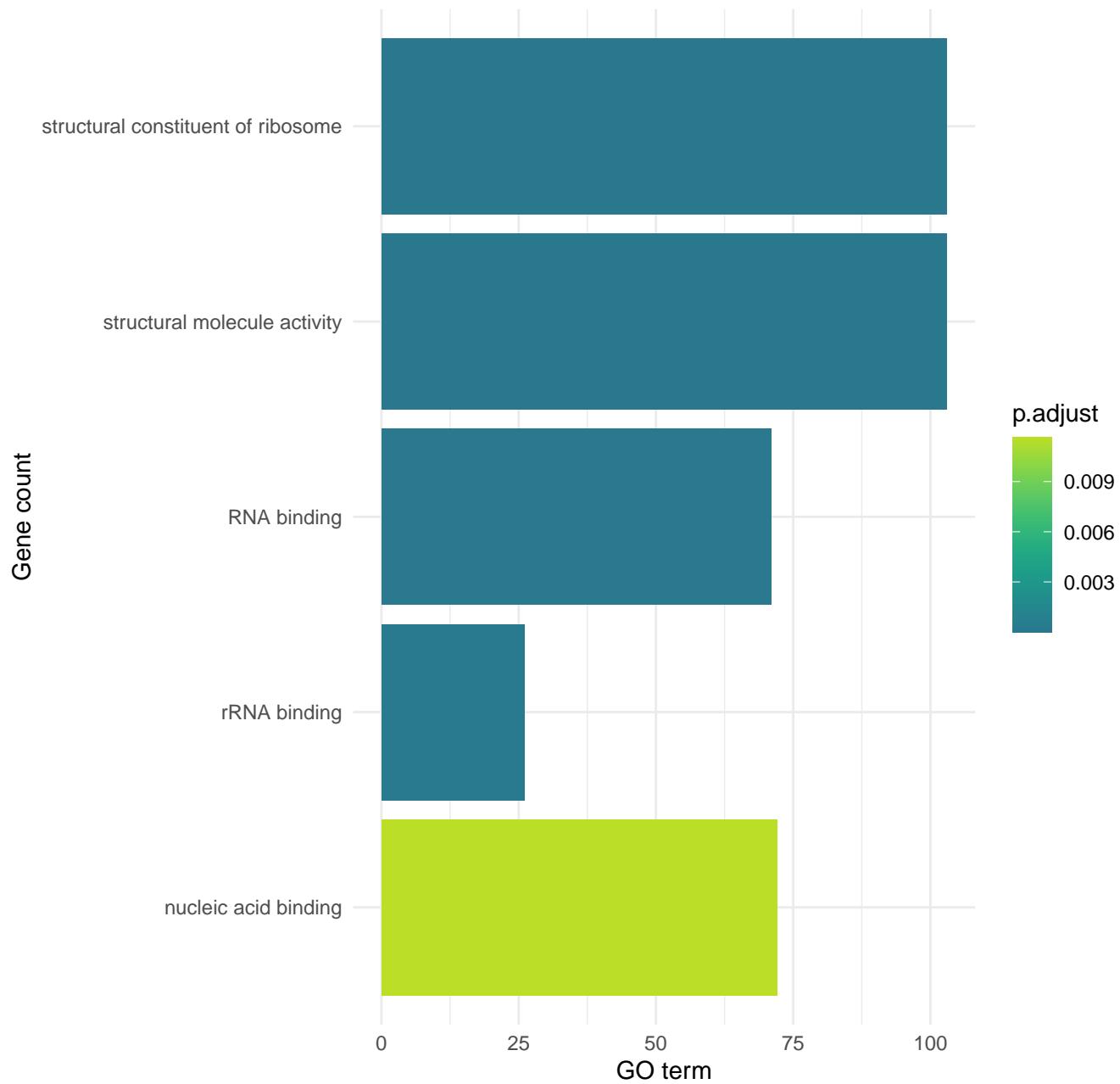




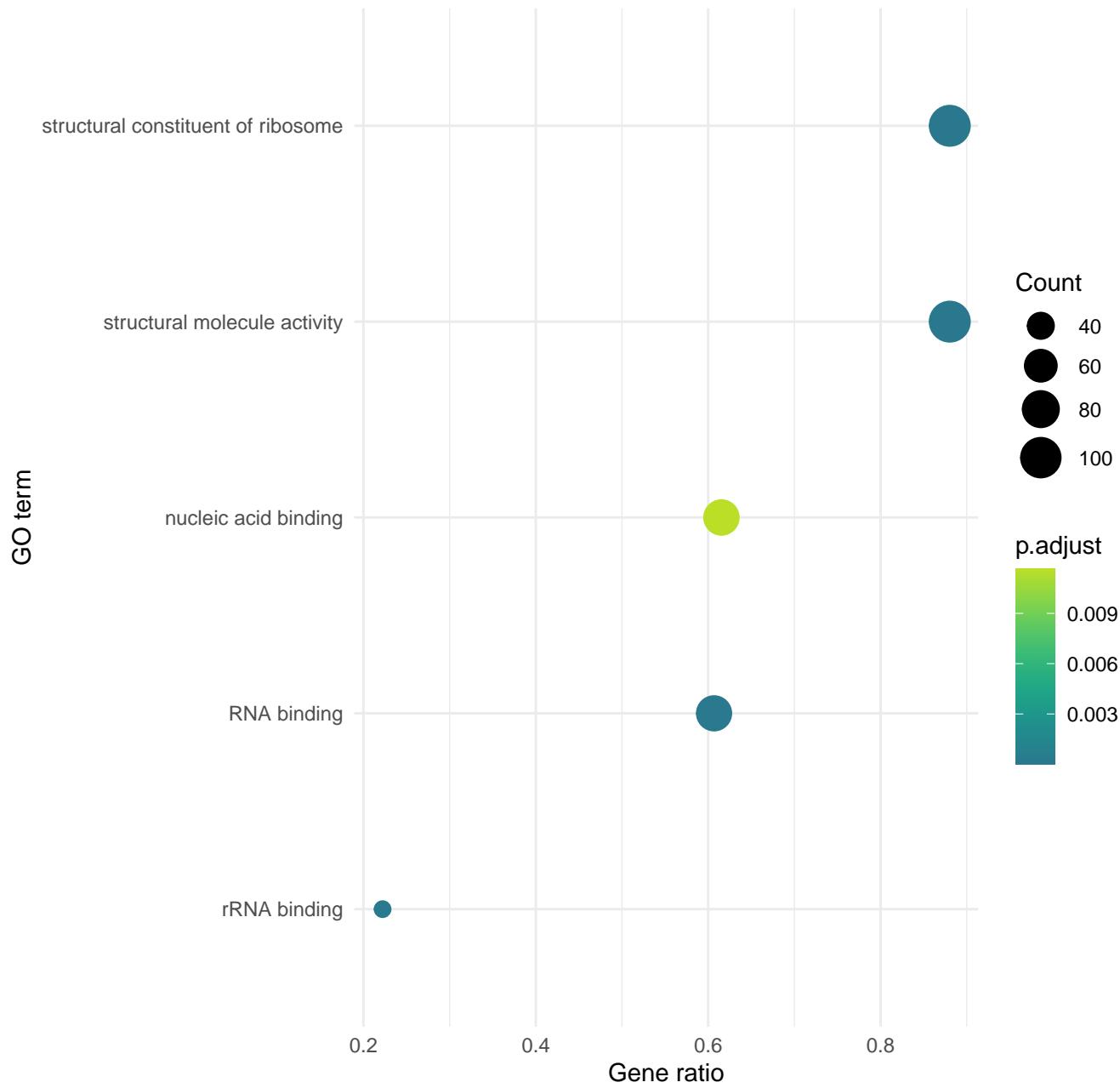
MUD2-TAP Up-regulated GO CC upsetplot



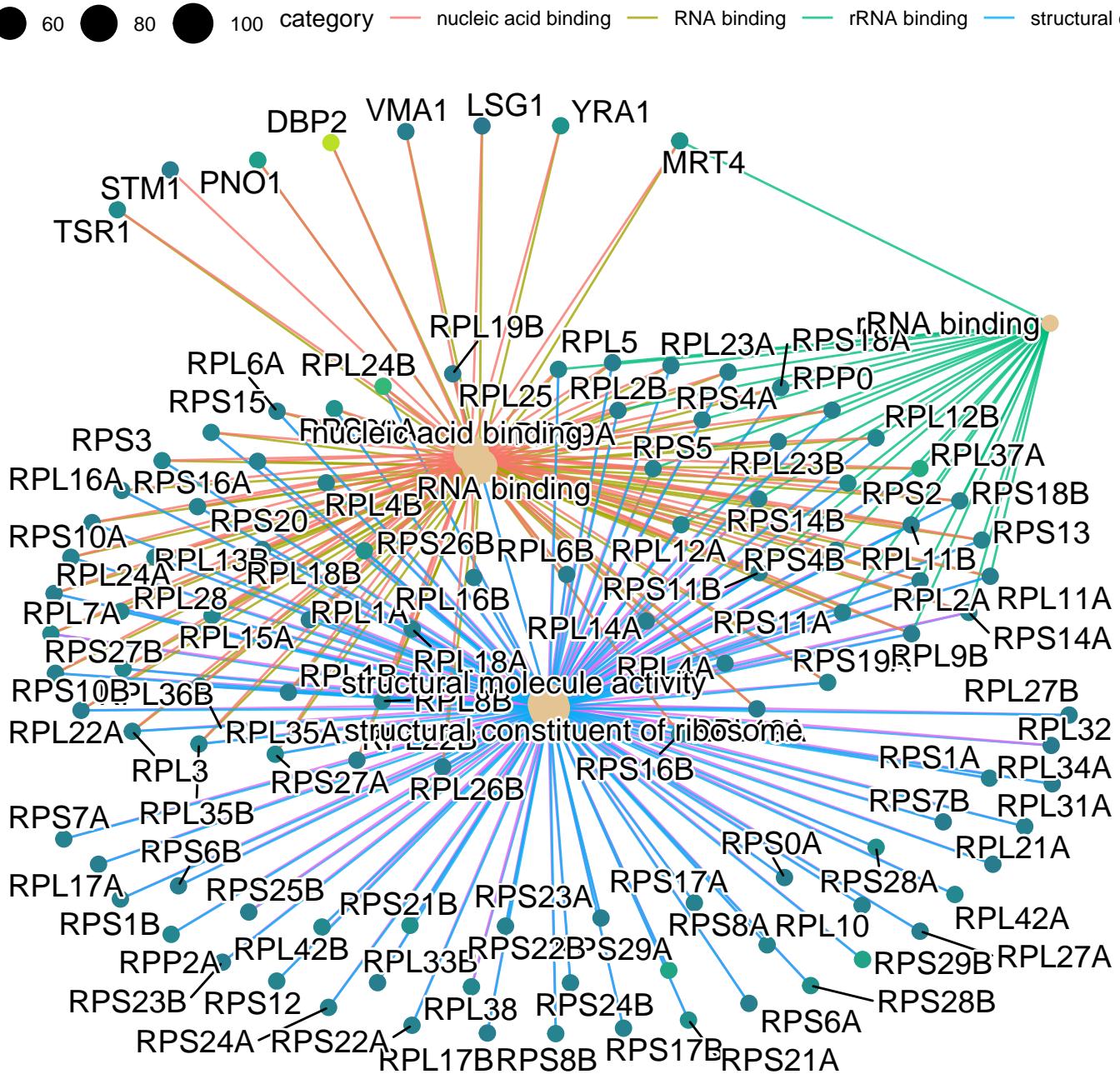
MUD2-TAP Up-regulated GO MF barplot



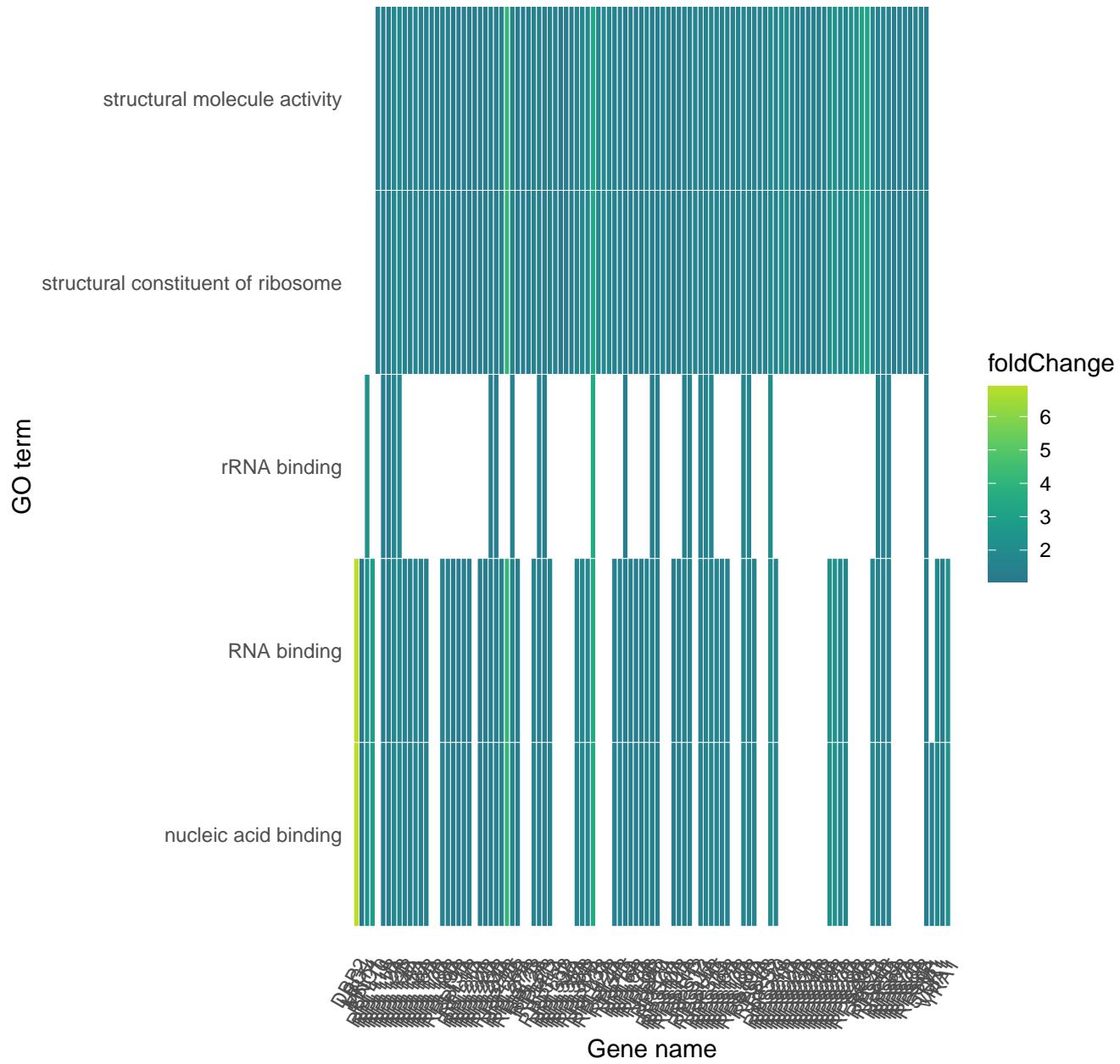
MUD2-TAP Up-regulated GO MF dotplot



MUD2-TAP Up-regulated GO MF cnetplot

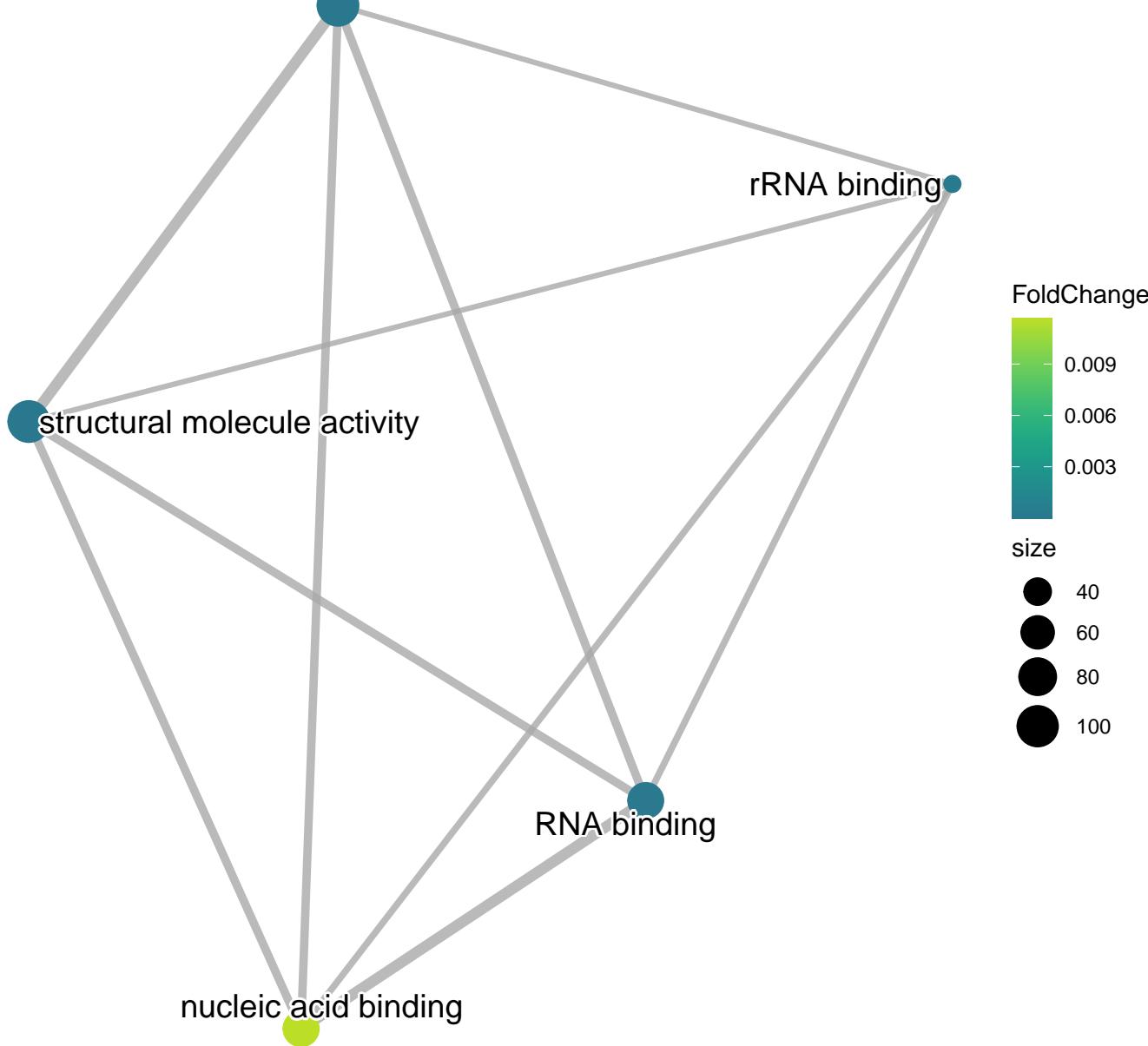


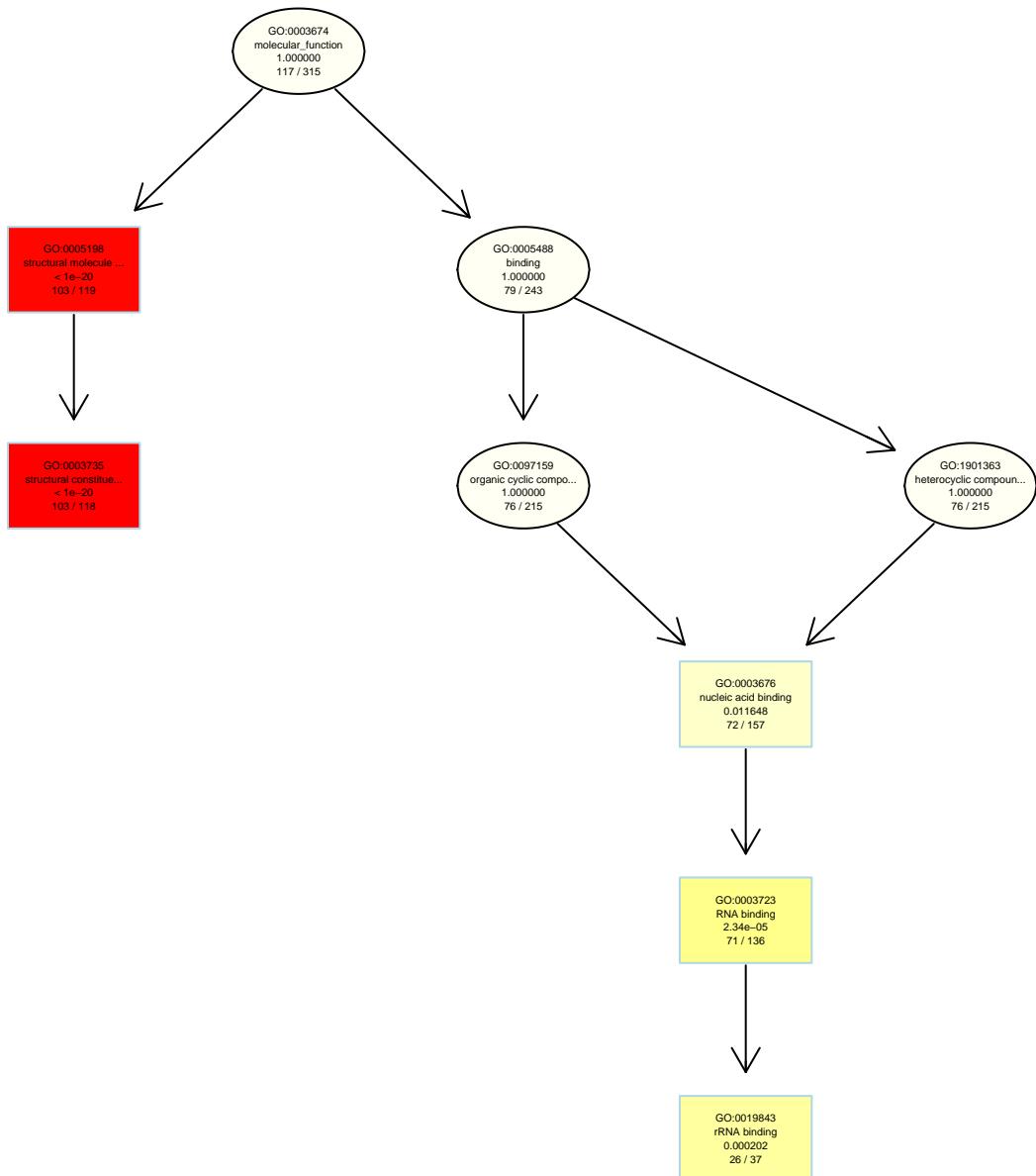
MUD2-TAP Up-regulated GO MF heatplot



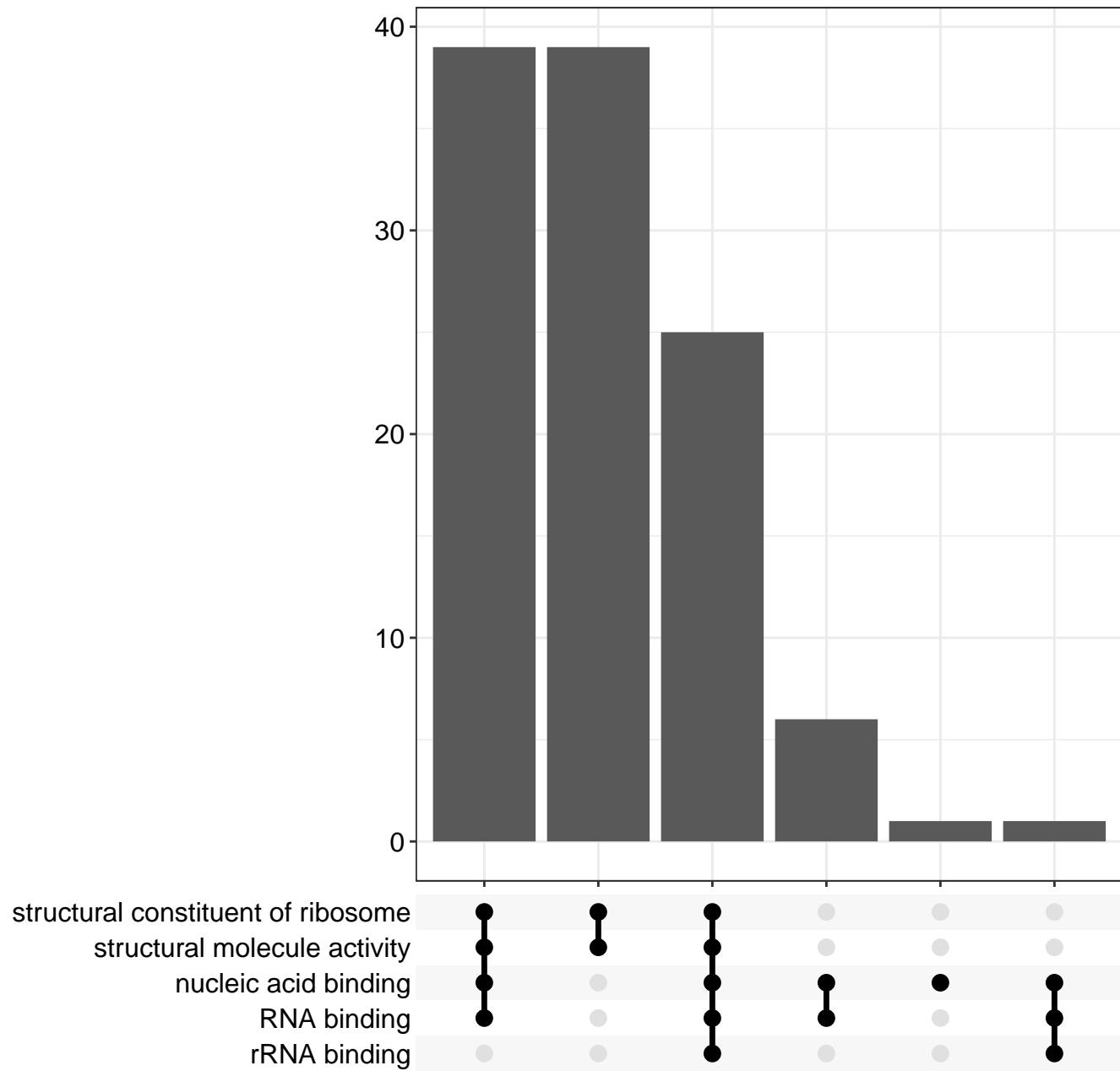
MUD2-TAP Up-regulated GO MF emapplot

structural constituent of ribosome

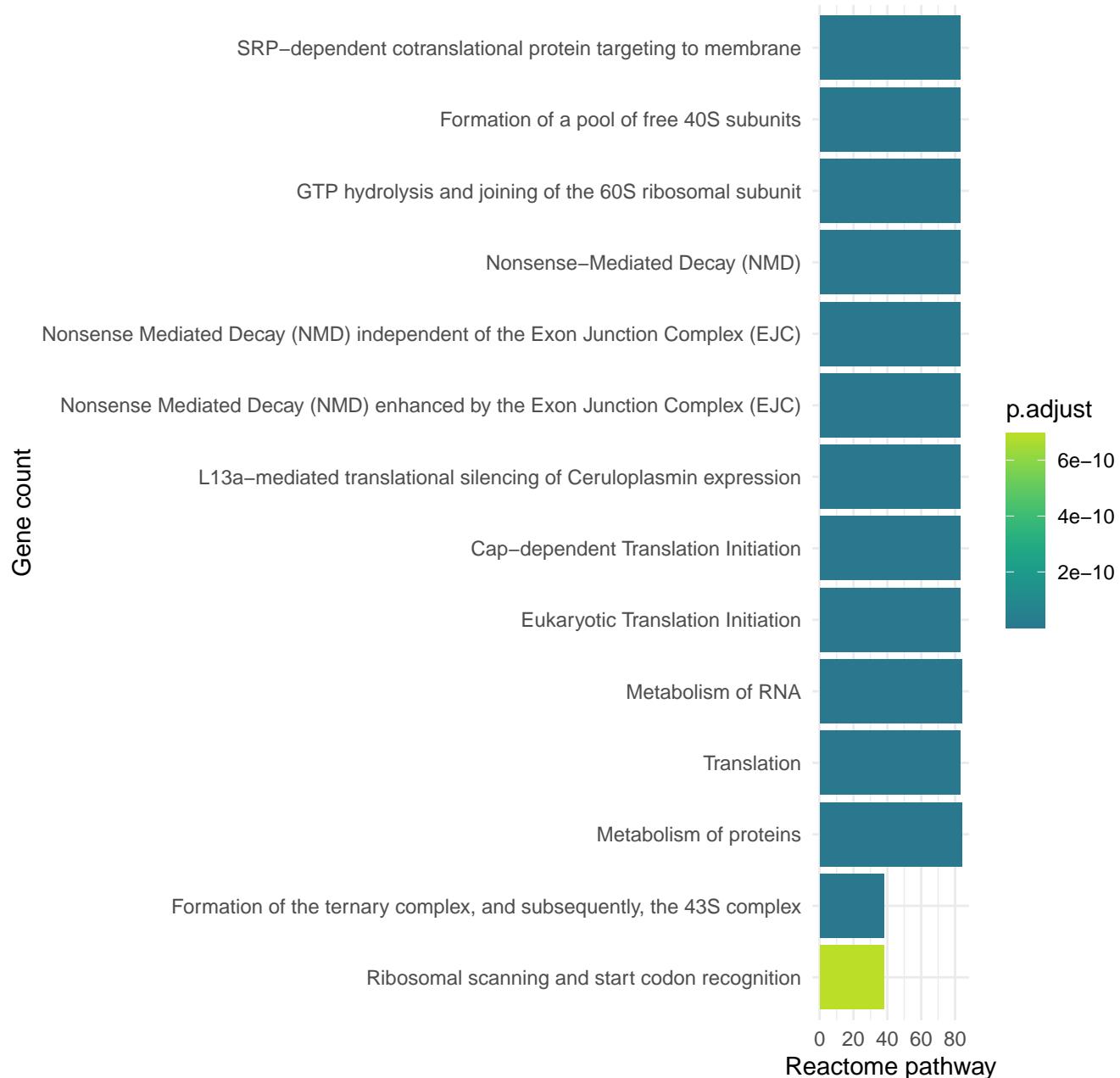




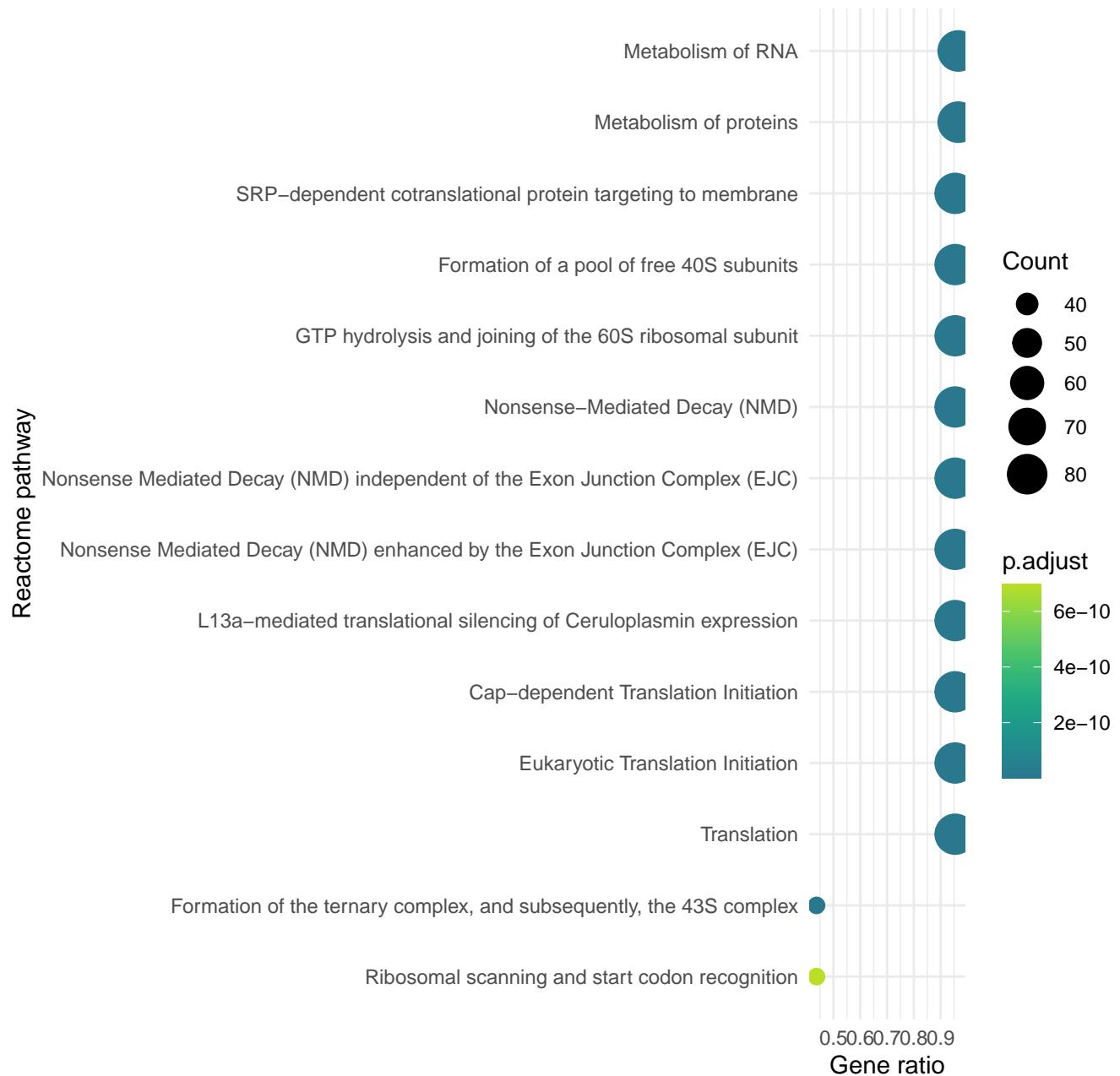
MUD2-TAP Up-regulated GO MF upsetplot



MUD2-TAP Up-regulated

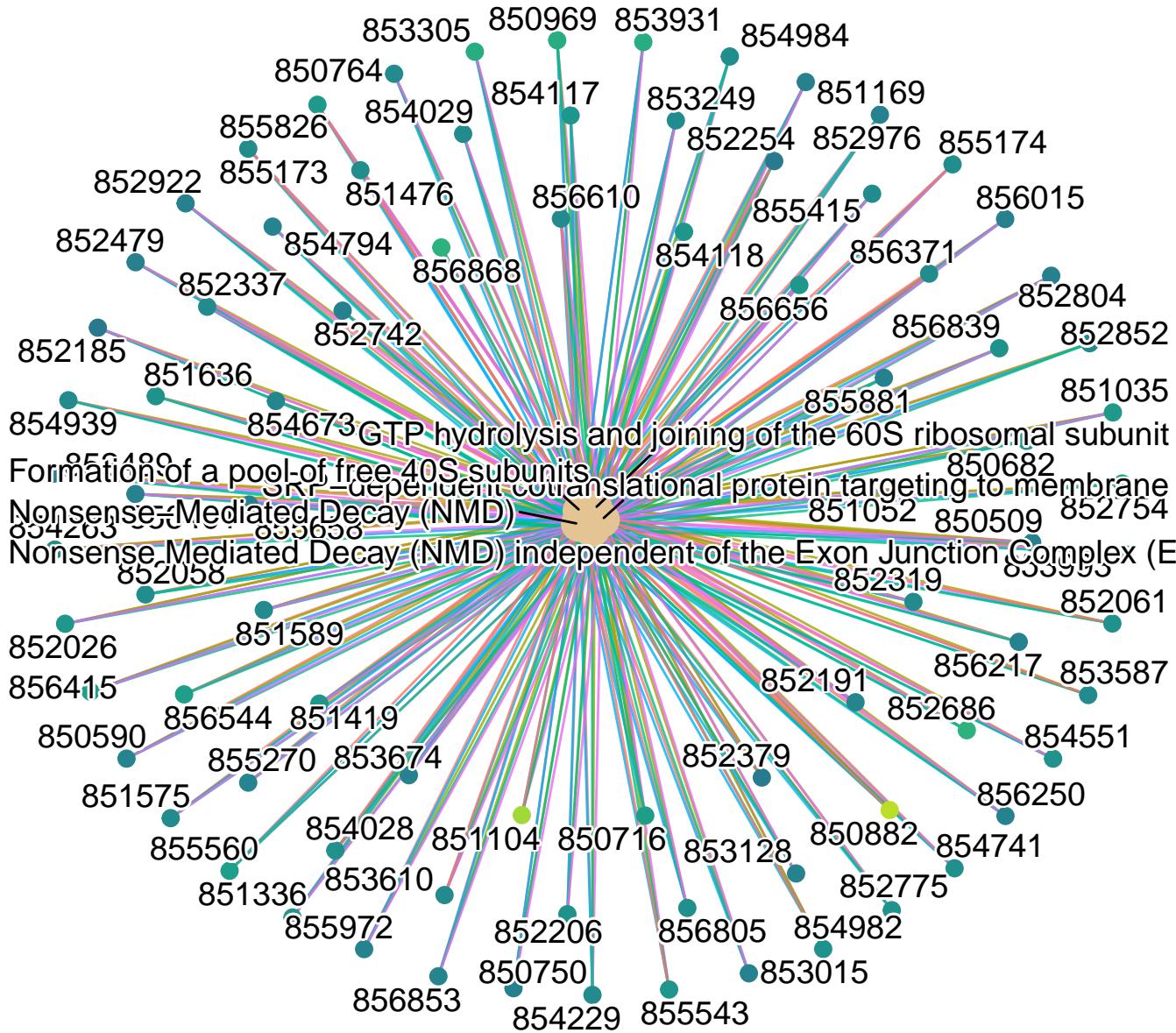


MUD2-TAP Up-regulated



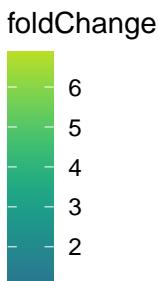
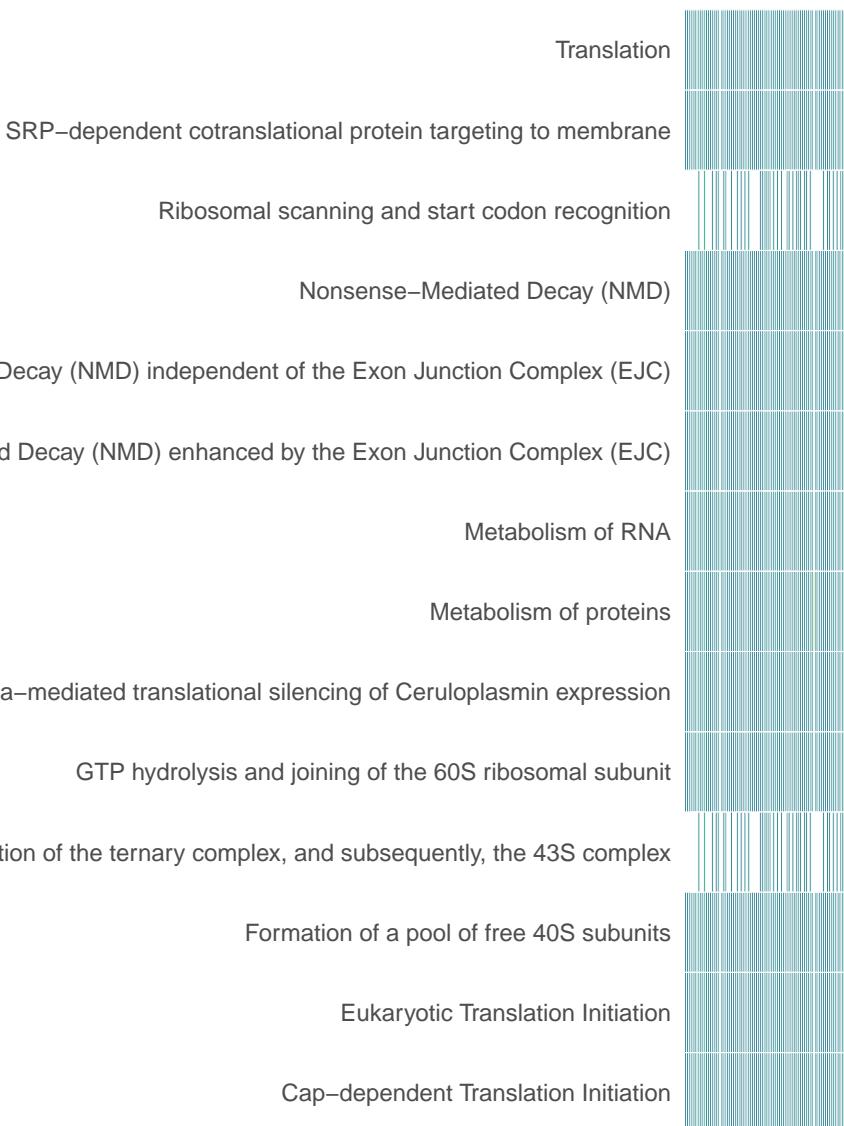
MUD2-TAP Up-regulated Reactome cnetplot

hydrolysis and joining of the 60S ribosomal subunit — Nonsense Mediated Decay (NMD) independent of the Exon Junction



MUD2-TAP Up-regulated

Reactome pathway



MUD2-TAP Up-regulated Reactome emapplot

Formation of the ternary complex, and subsequently, the 43S complex

GTP hydrolysis and joining of the 60S ribosomal subunit

L13a-mediated translational silencing of Ceruloplasmin expression

Metabolism of RNA

Eukaryotic Translation Initiation

Nonsense-Mediated Decay (NMD)

Ribosomal scanning and start codon recognition

Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)

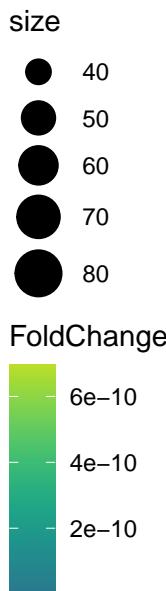
SRP-dependent cotranslational protein targeting to membrane

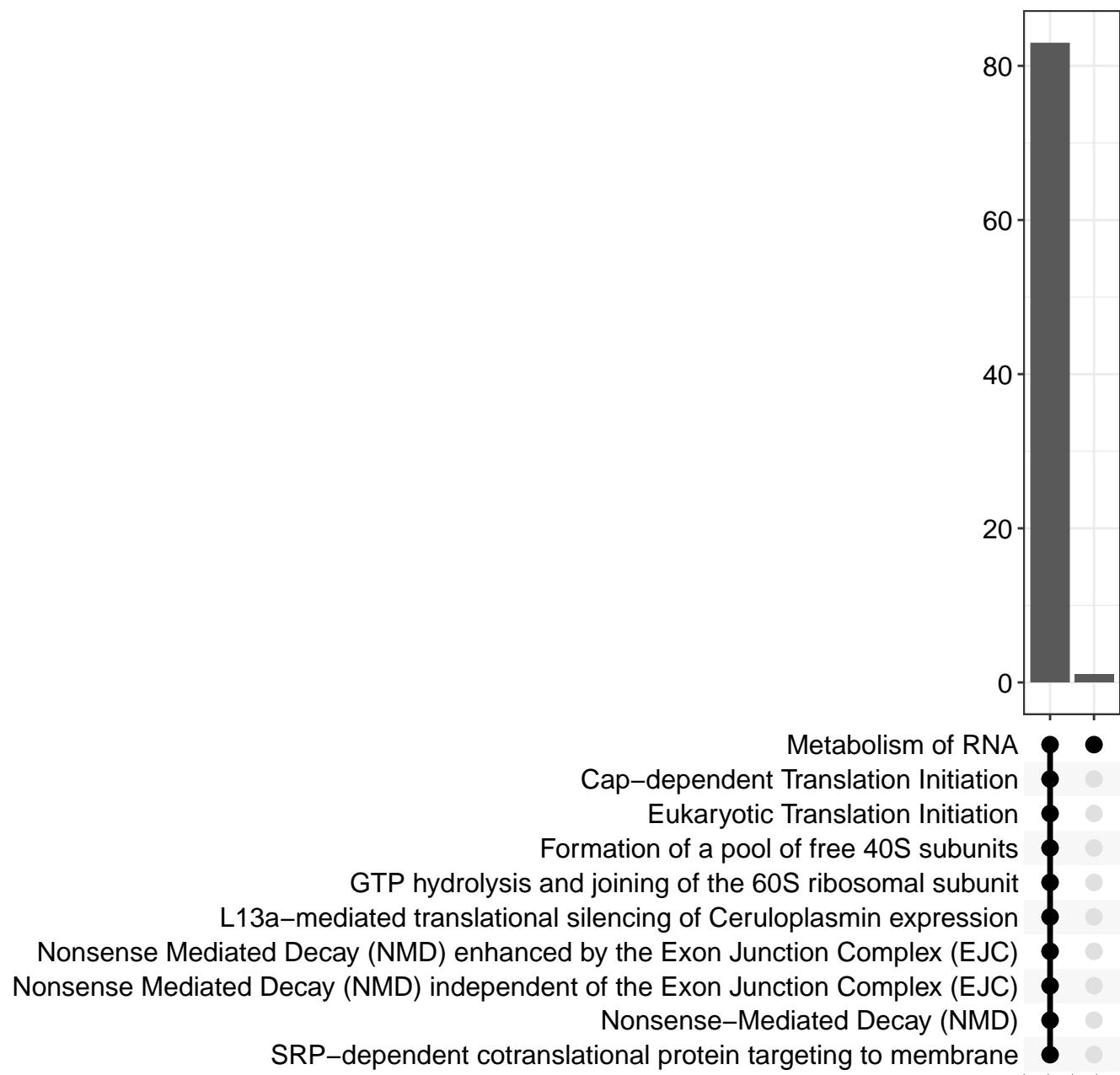
Formation of a pool of free 40S subunits

Cap-dependent Translation Initiation

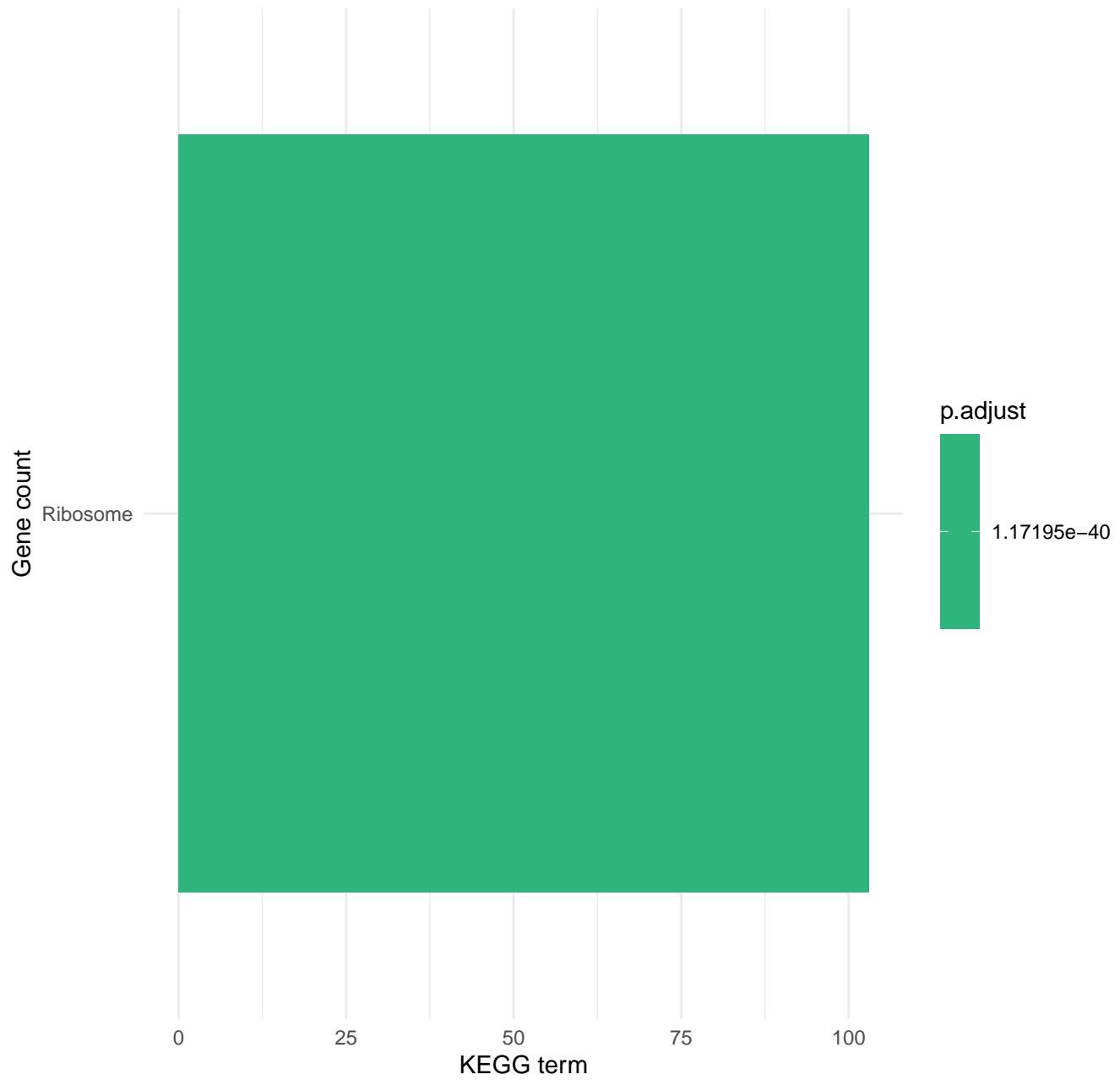
Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)

Metabolism of proteins Translation

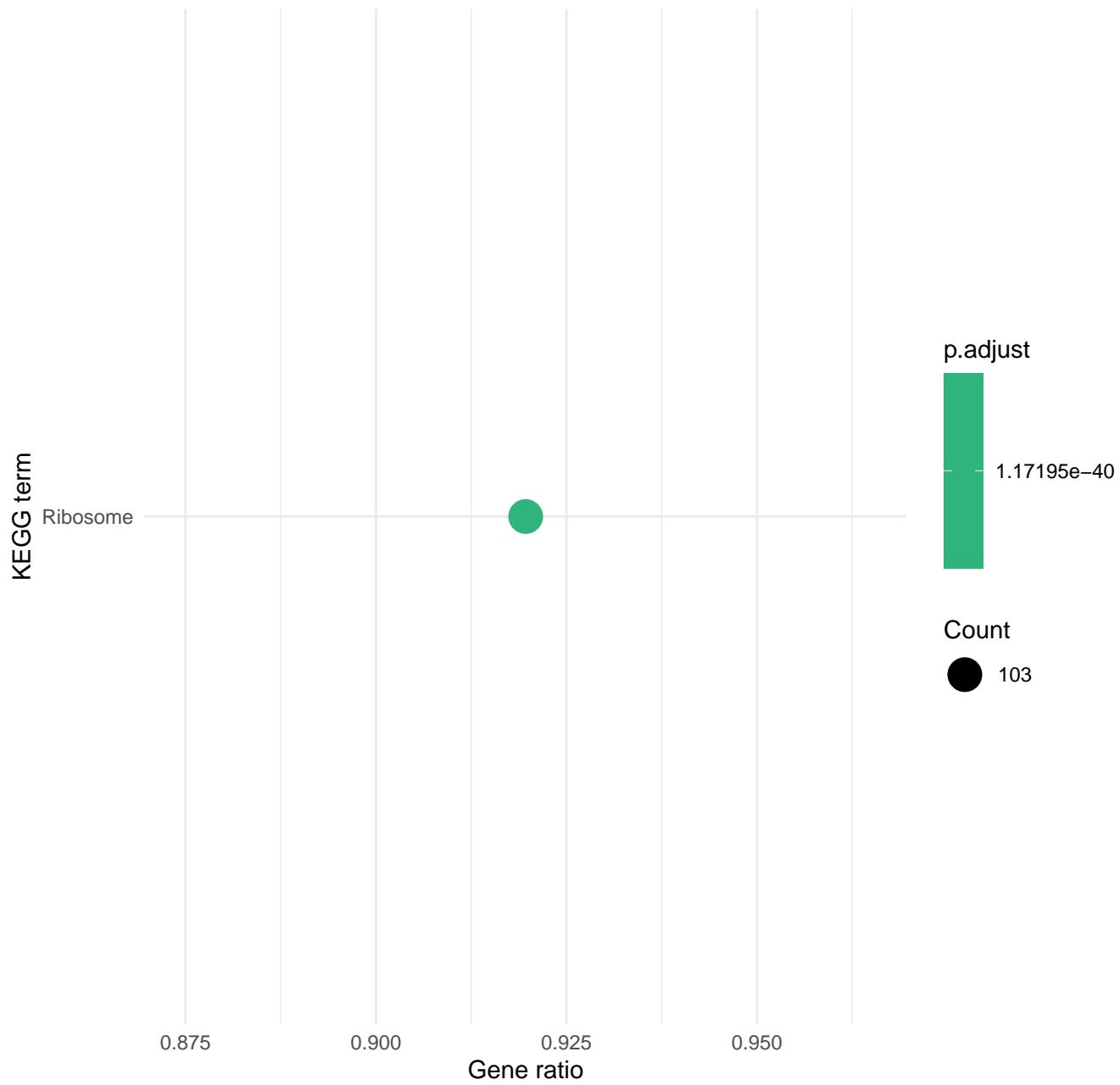




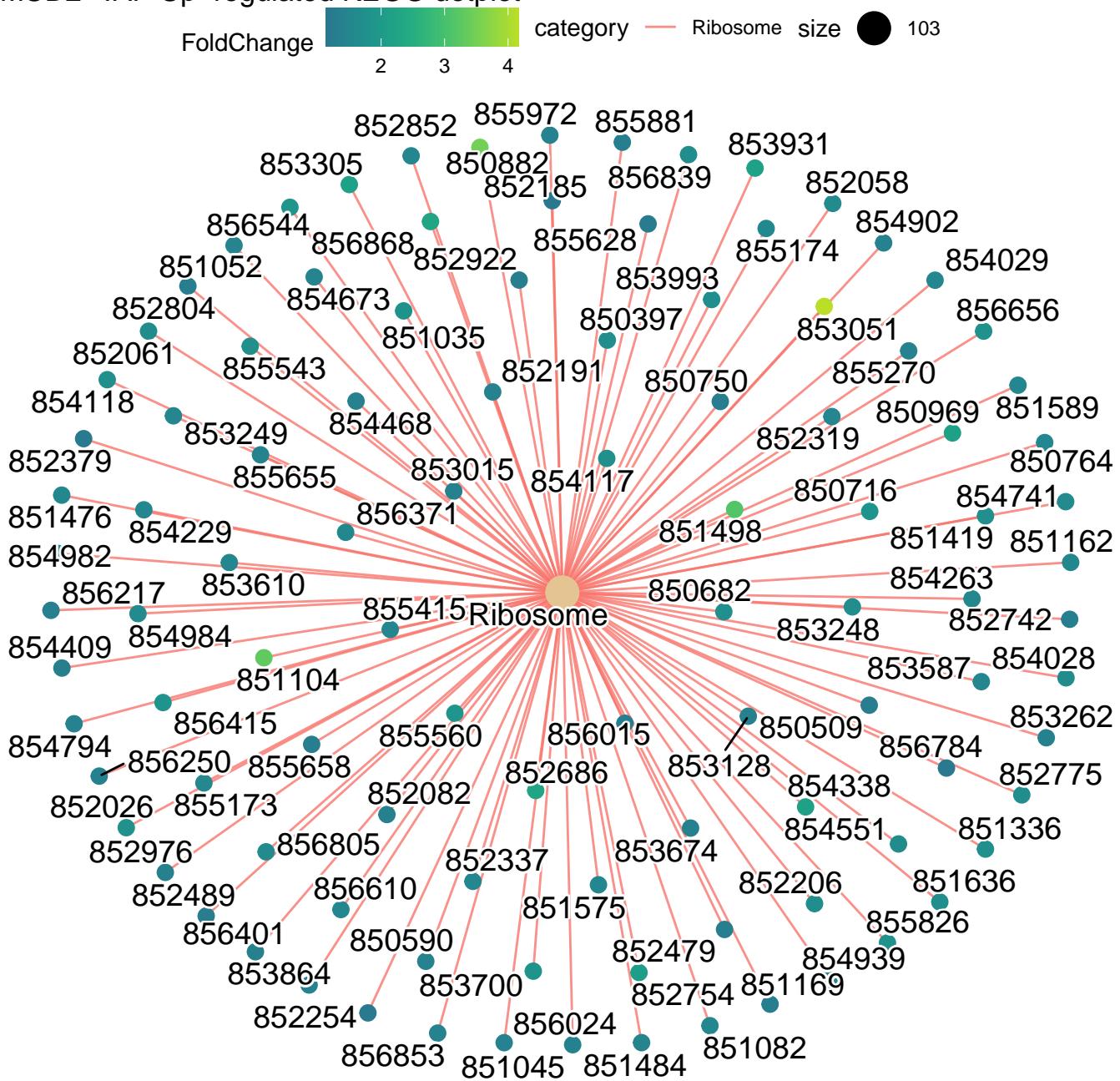
MUD2-TAP Up-regulated KEGG barplot



MUD2-TAP Up-regulated KEGG dotplot



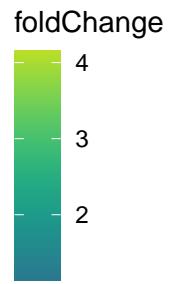
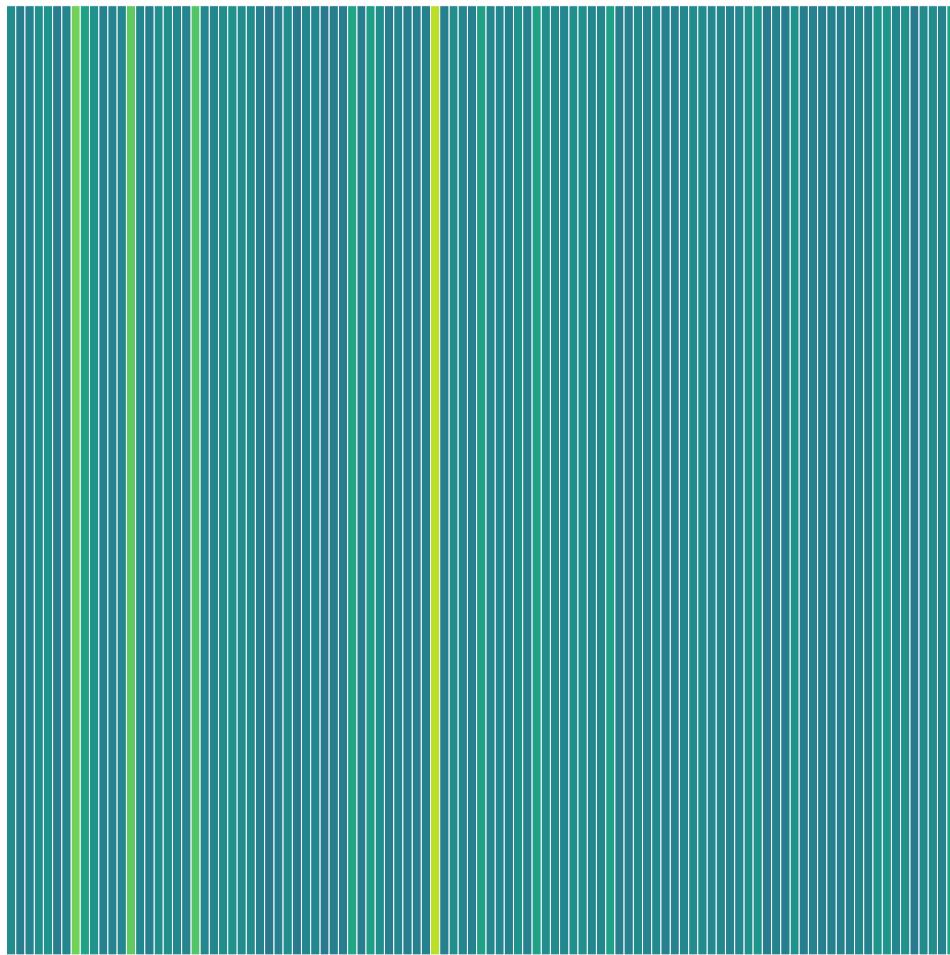
MUD2-TAP Up-regulated KEGG dotplot



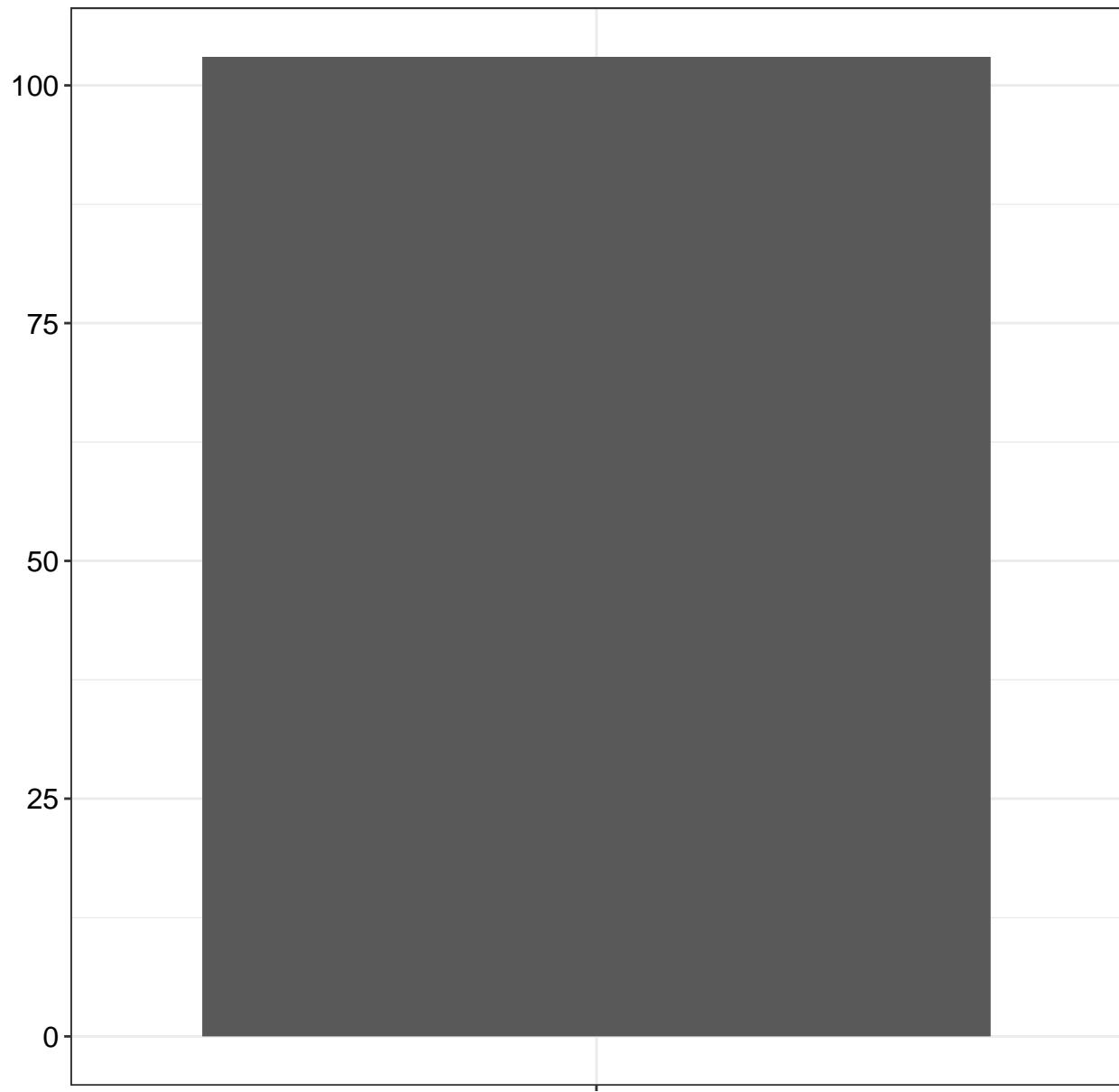
MUD2-TAP Up-regulated KEGG heatplot

KEGG term

Ribosome

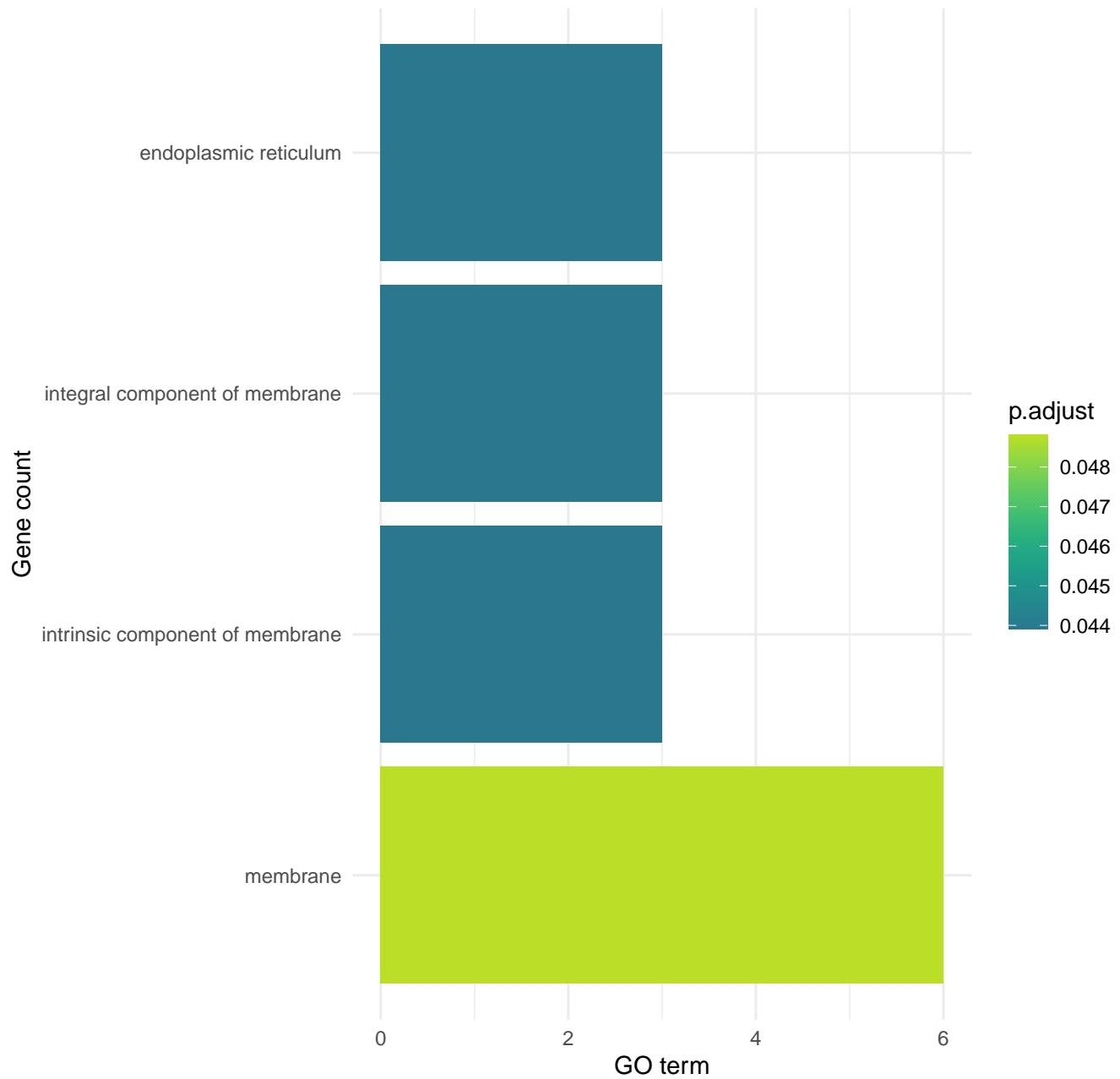


MUD2-TAP Up-regulated KEGG upsetplot

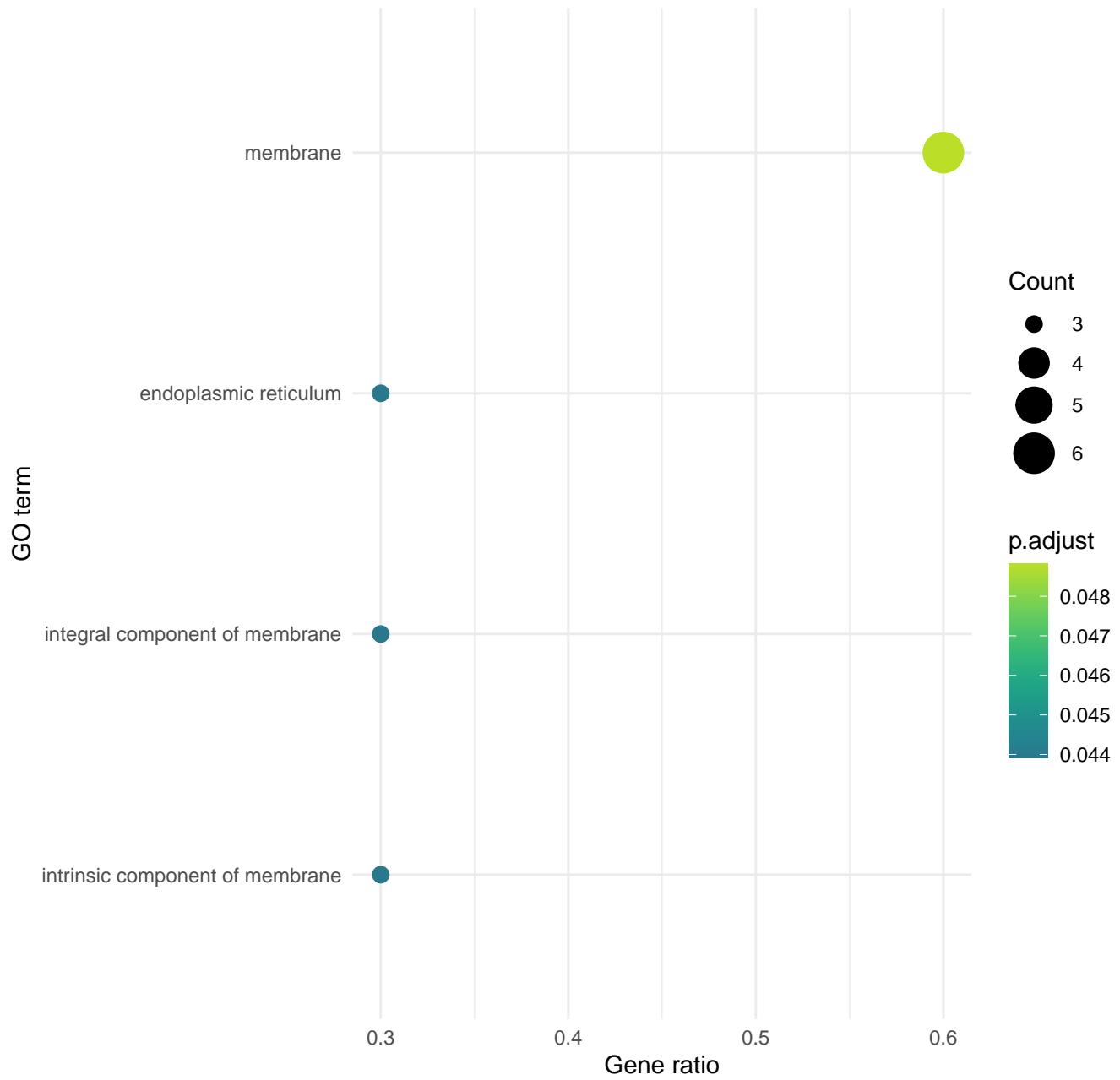


Ribosome

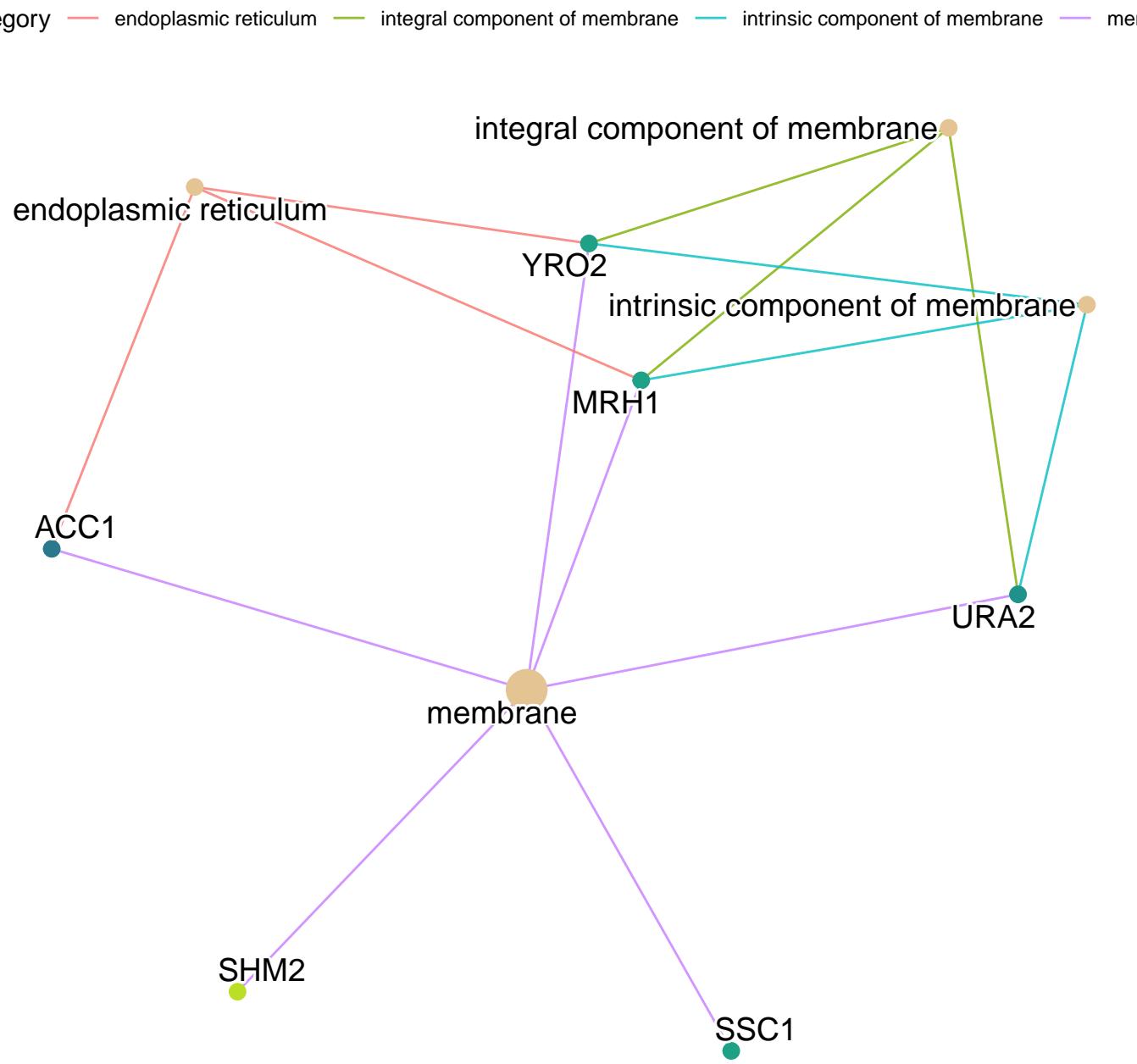
PRP22-TAP Up-regulated GO CC barplot



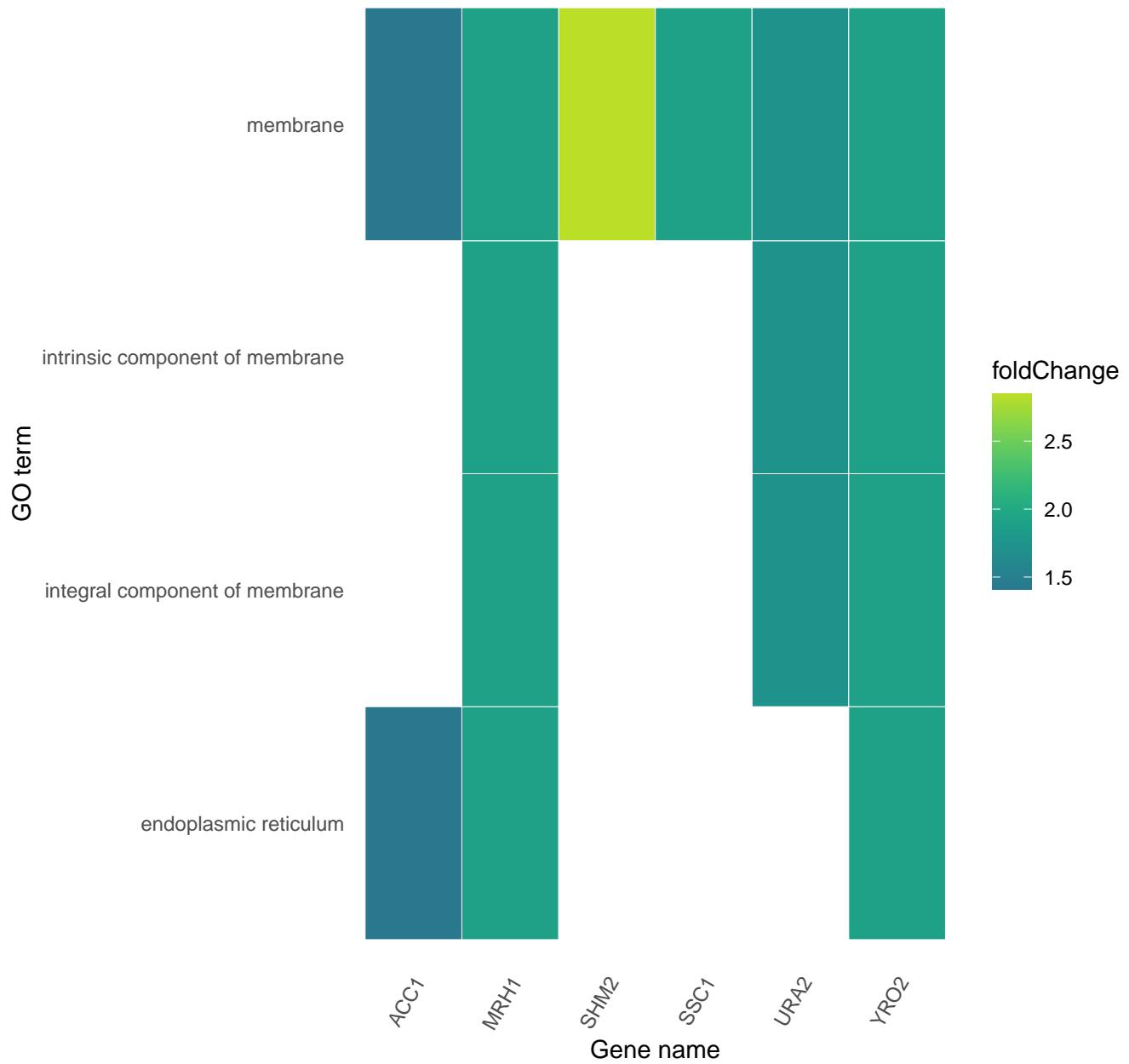
PRP22-TAP Up-regulated GO CC dotplot



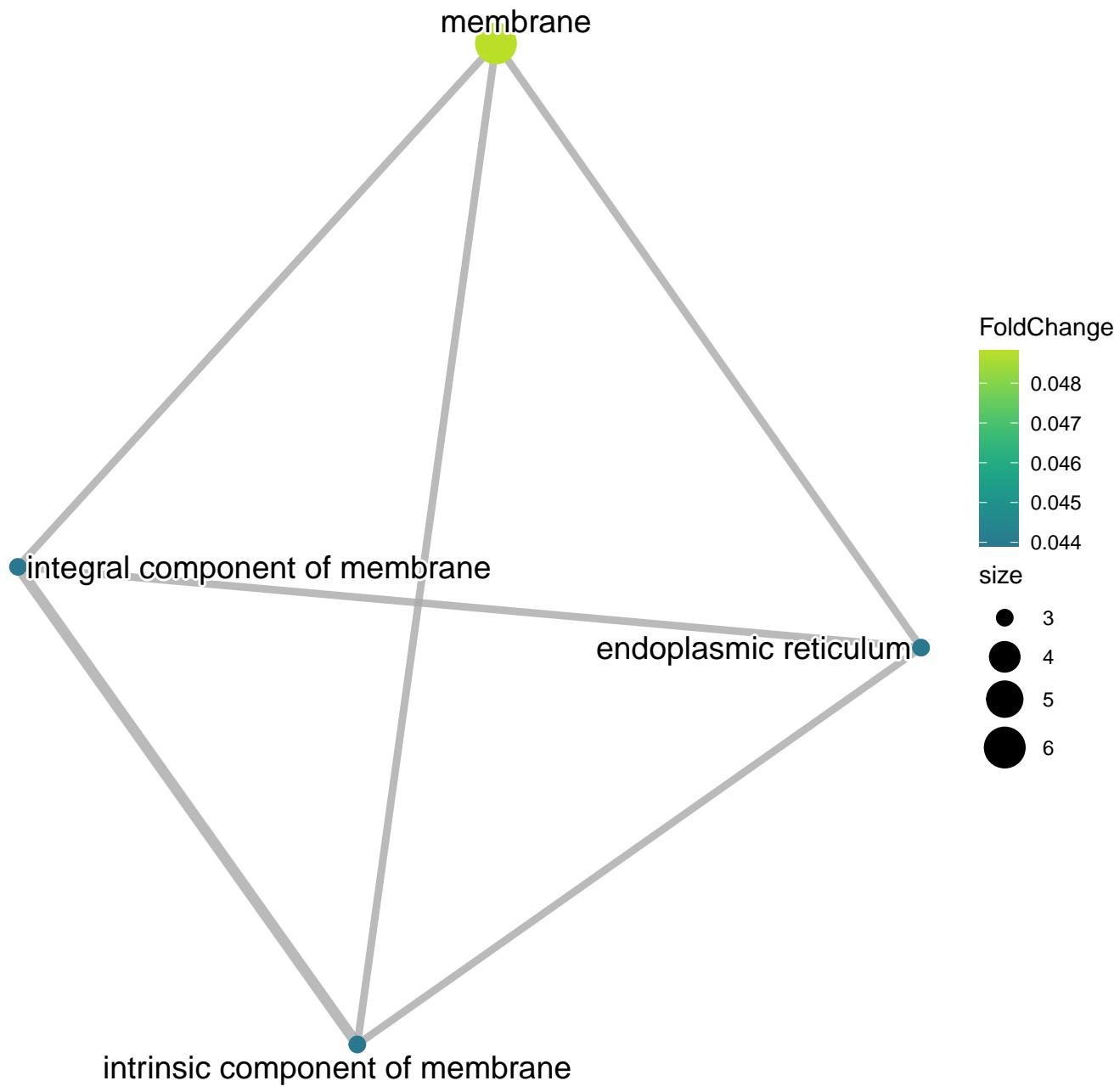
PRP22-TAP Up-regulated GO CC cnetplot

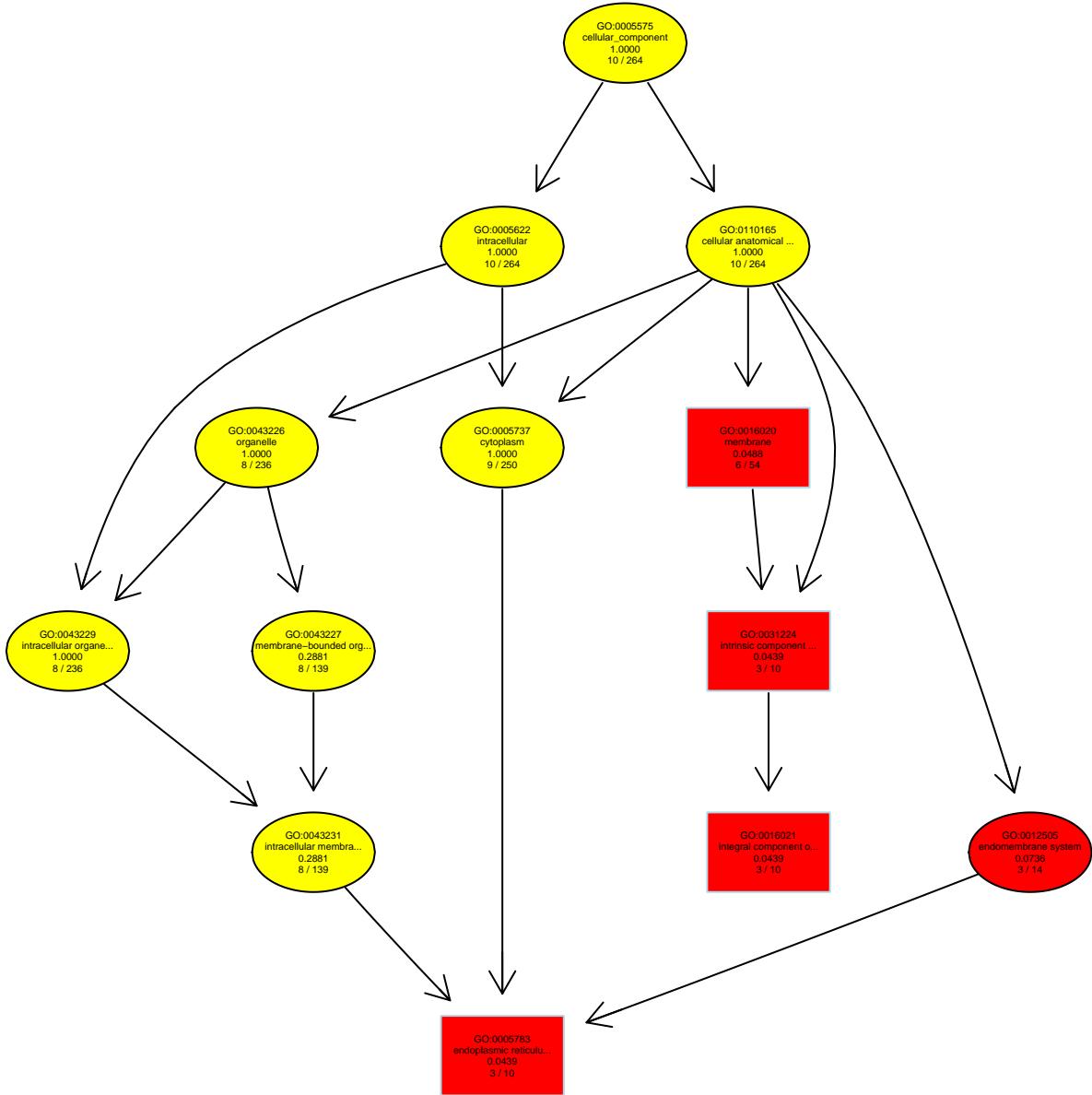


PRP22-TAP Up-regulated GO CC heatplot

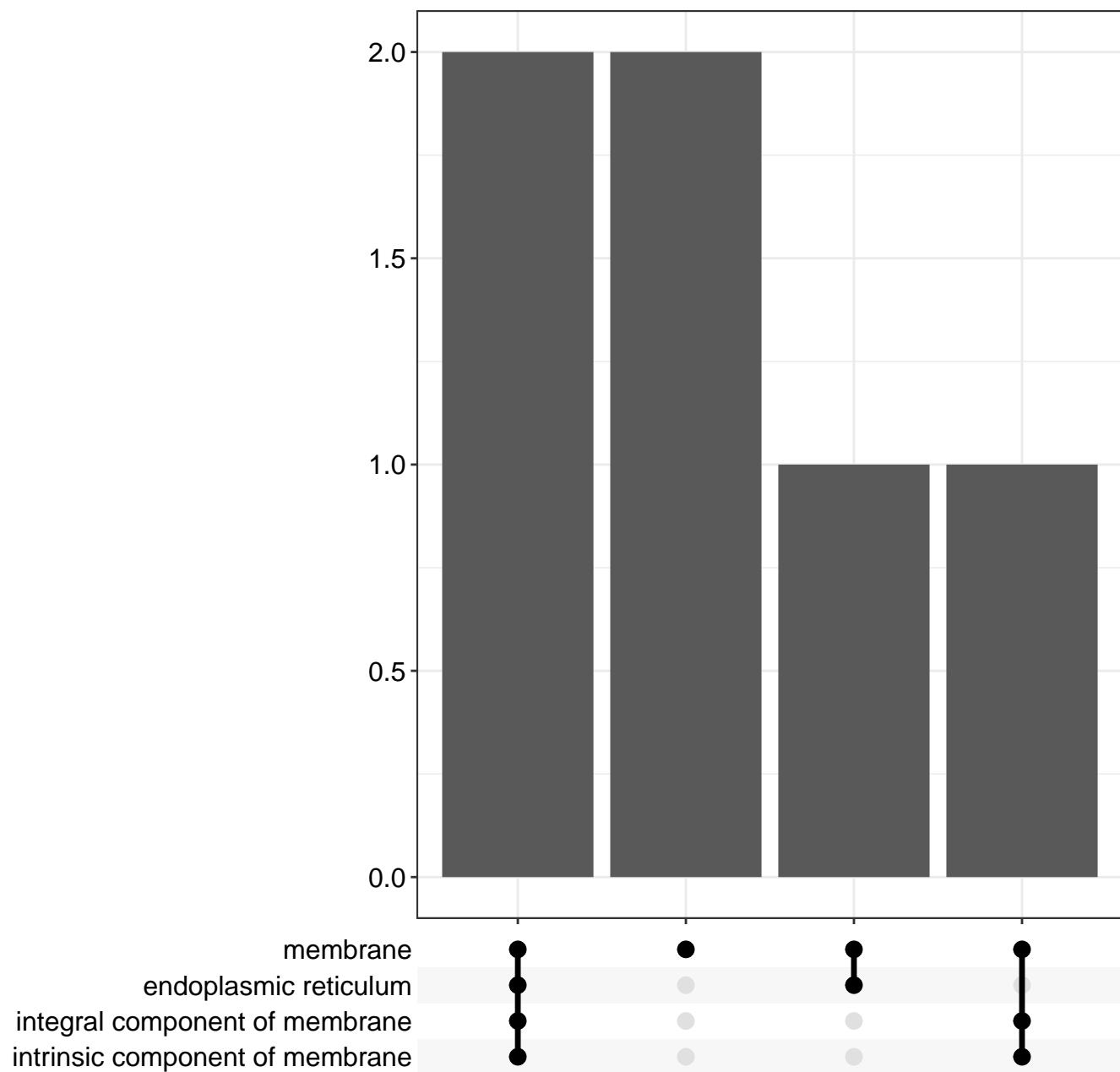


PRP22-TAP Up-regulated GO CC emapplot

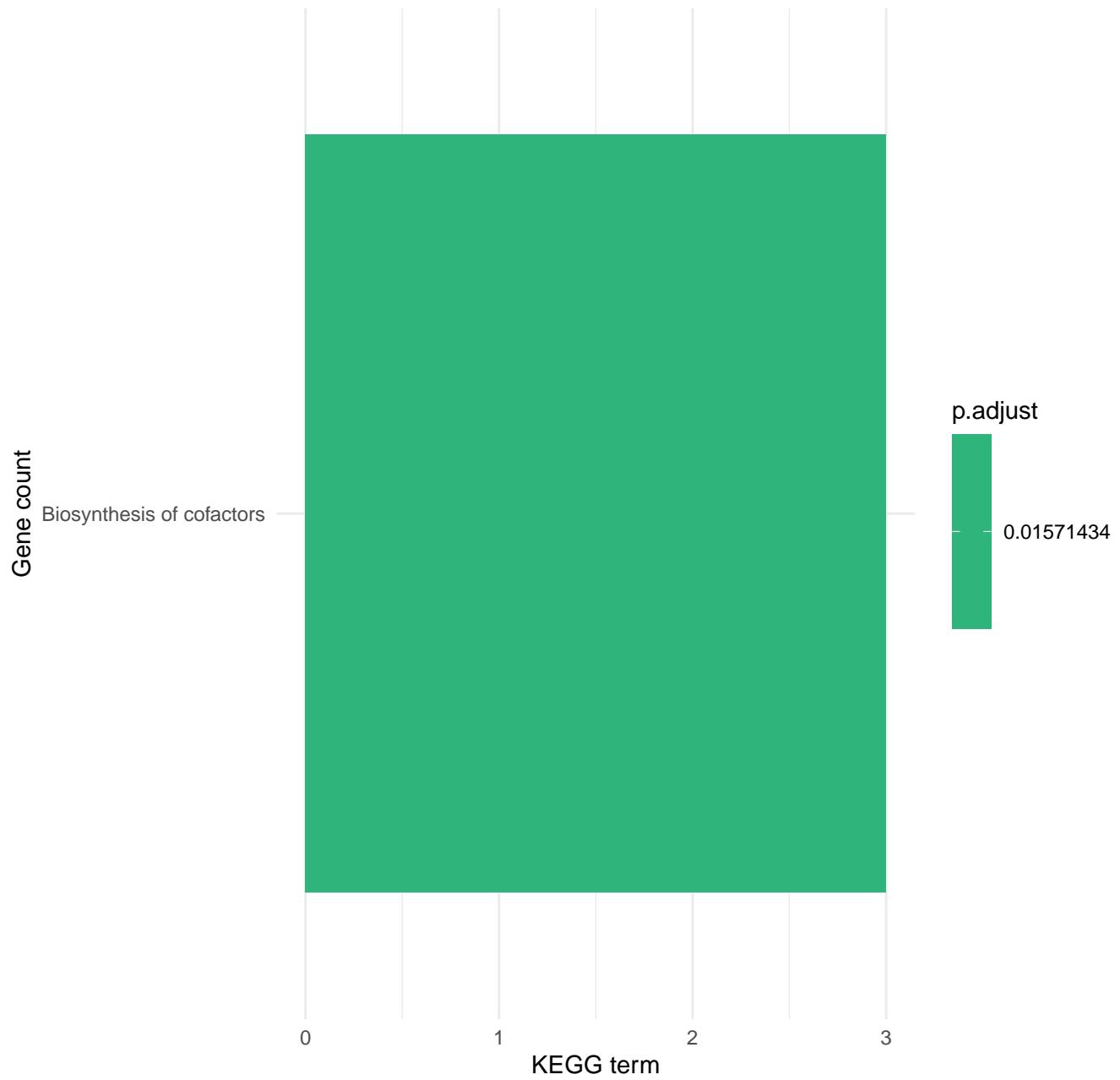




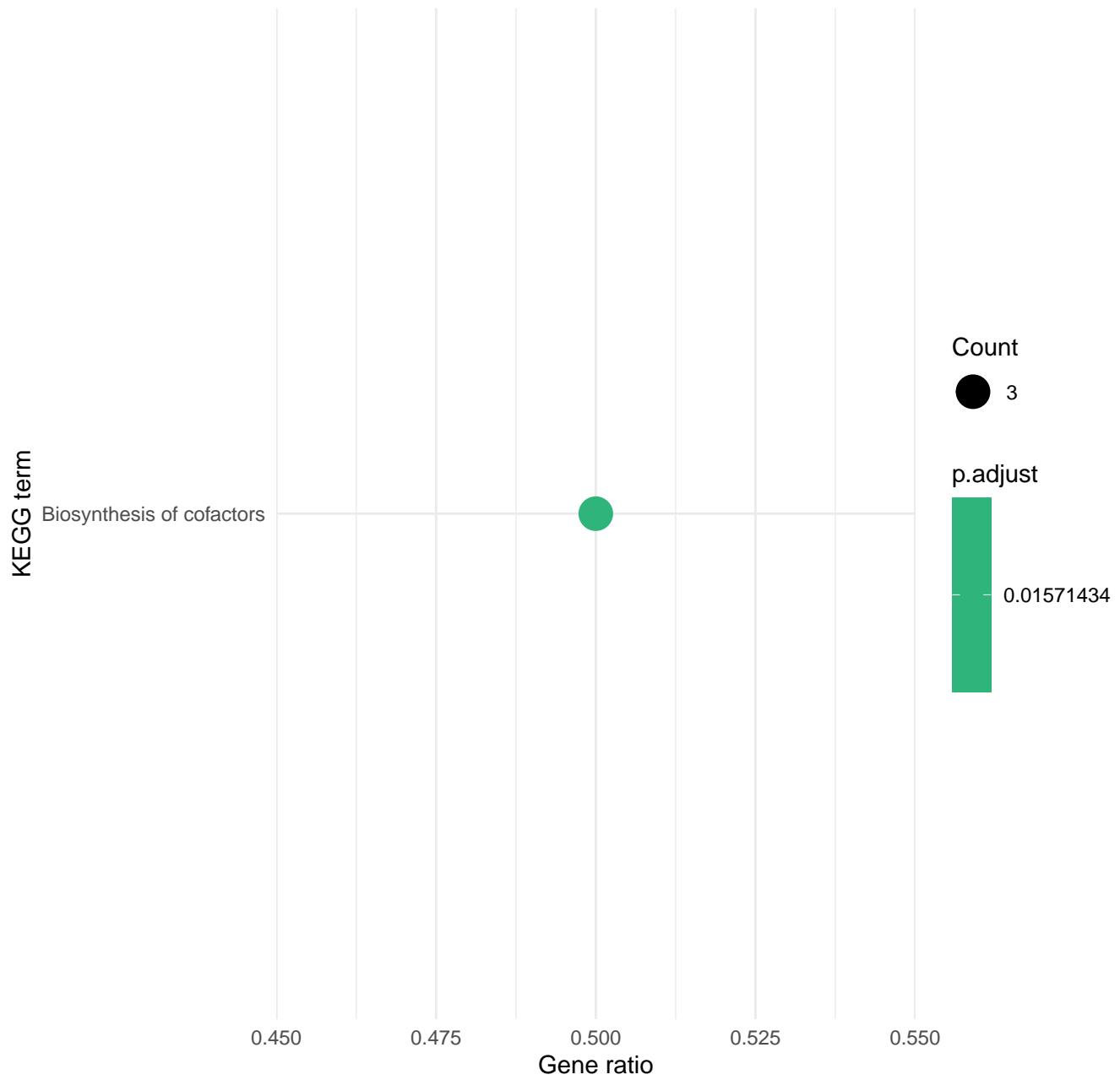
PRP22-TAP Up-regulated GO CC upsetplot



PRP22-TAP Up-regulated KEGG barplot



PRP22-TAP Up-regulated KEGG dotplot



PRP22-TAP Up-regulated KEGG dotplot

size



3

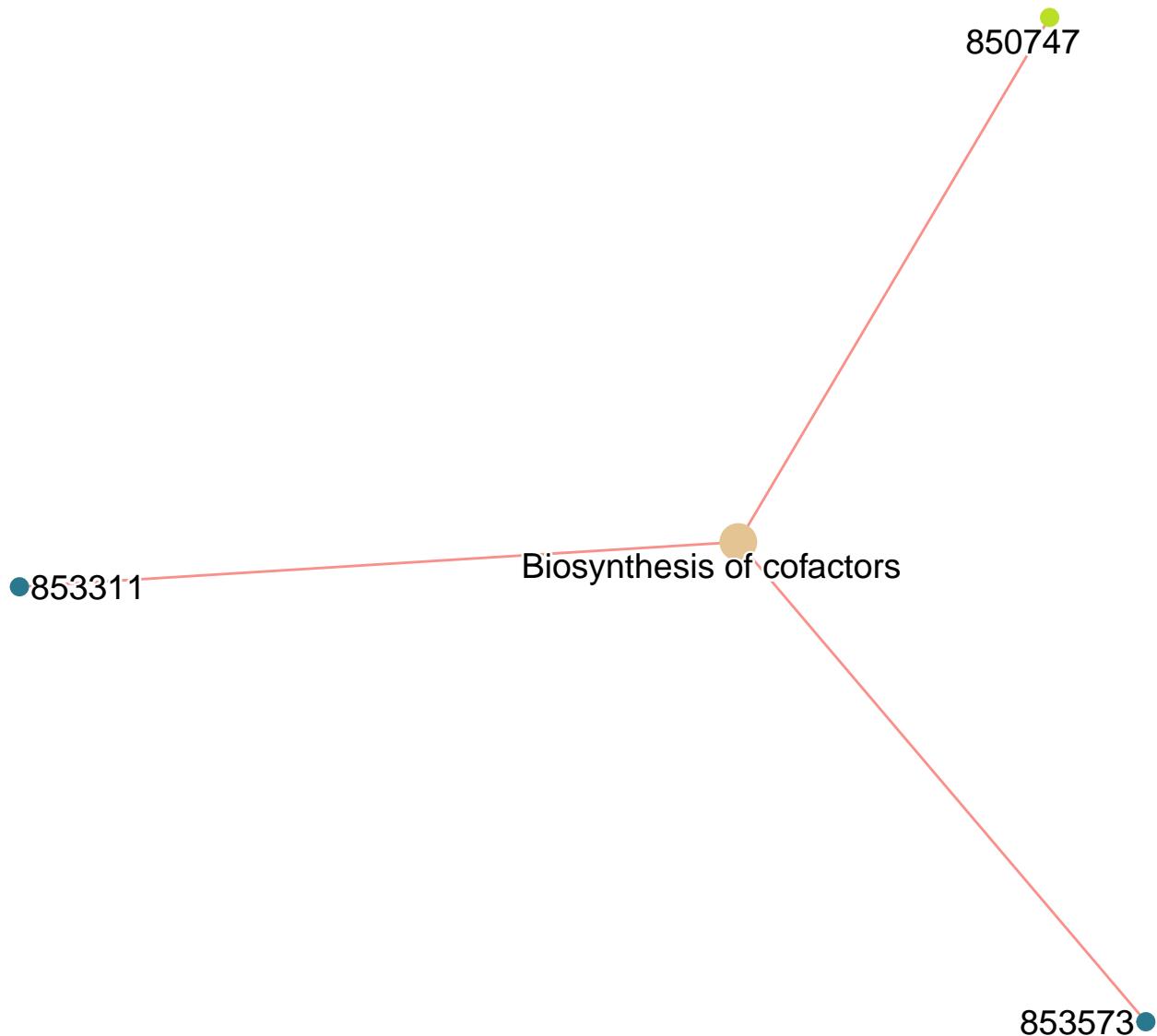
category

Biosynthesis of cofactors

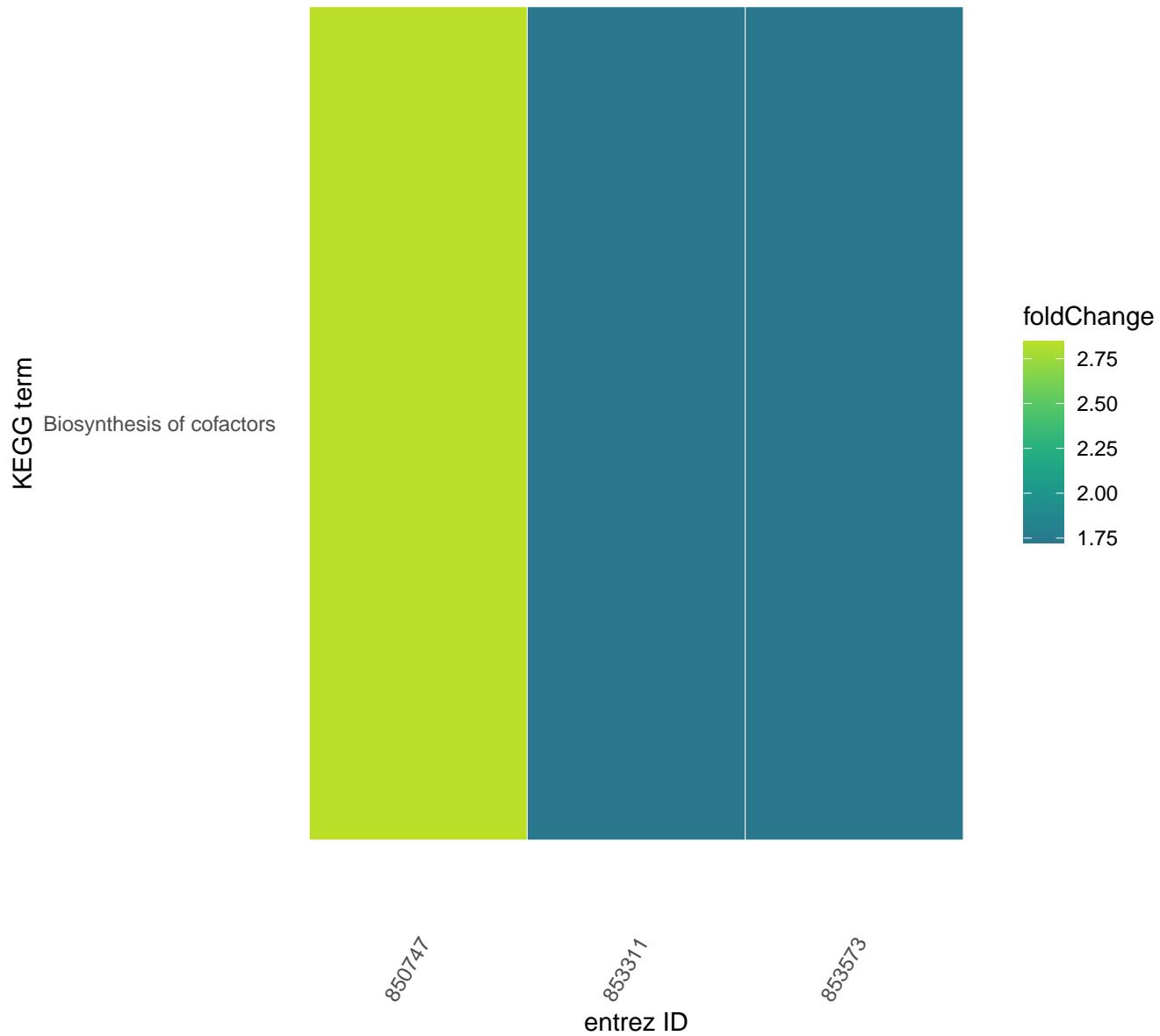
FoldChange



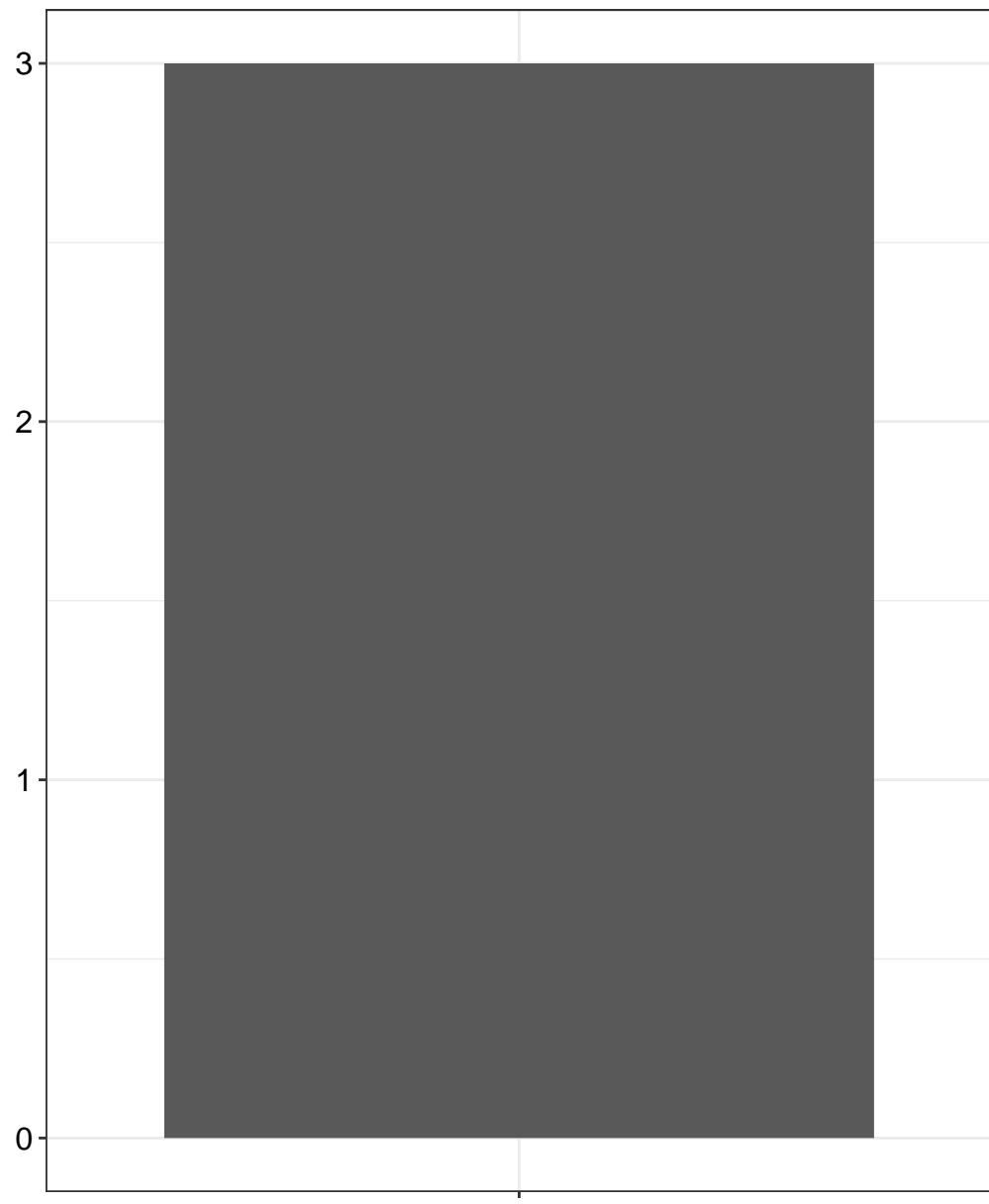
1.75 2.00 2.25 2.50 2.75



PRP22-TAP Up-regulated KEGG heatplot



PRP22-TAP Up-regulated KEGG upsetplot



Biosynthesis of cofactors

