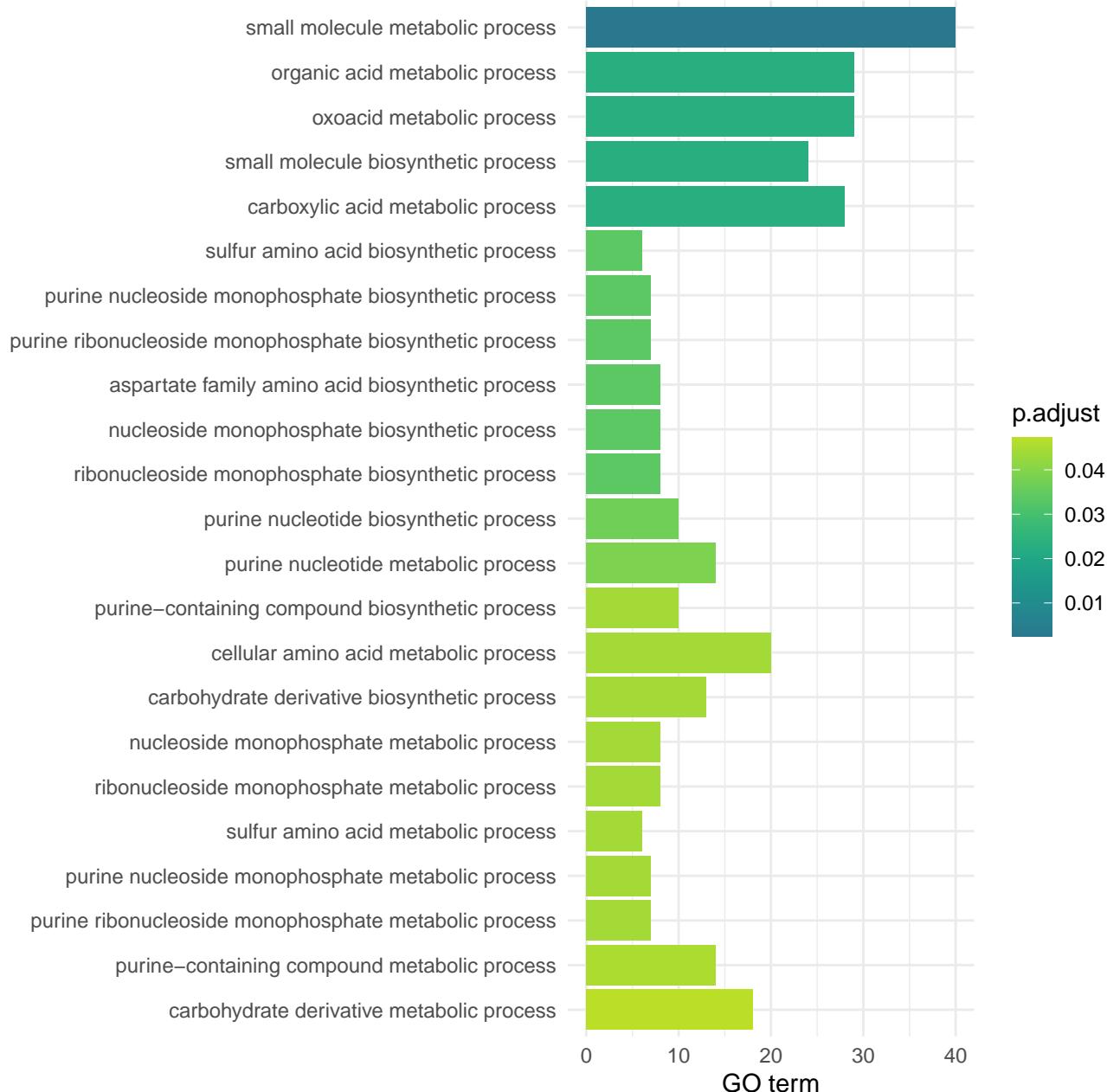
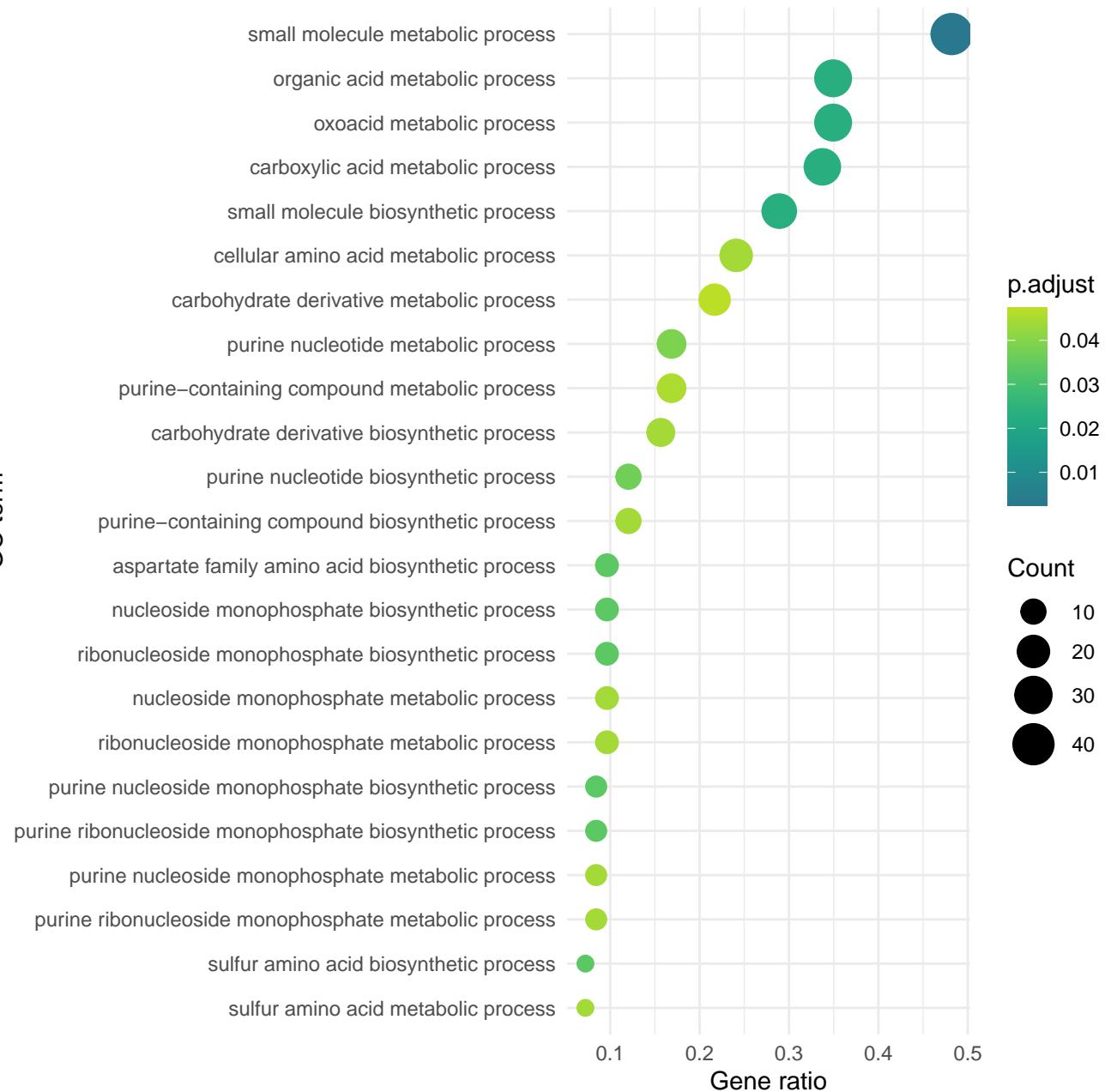


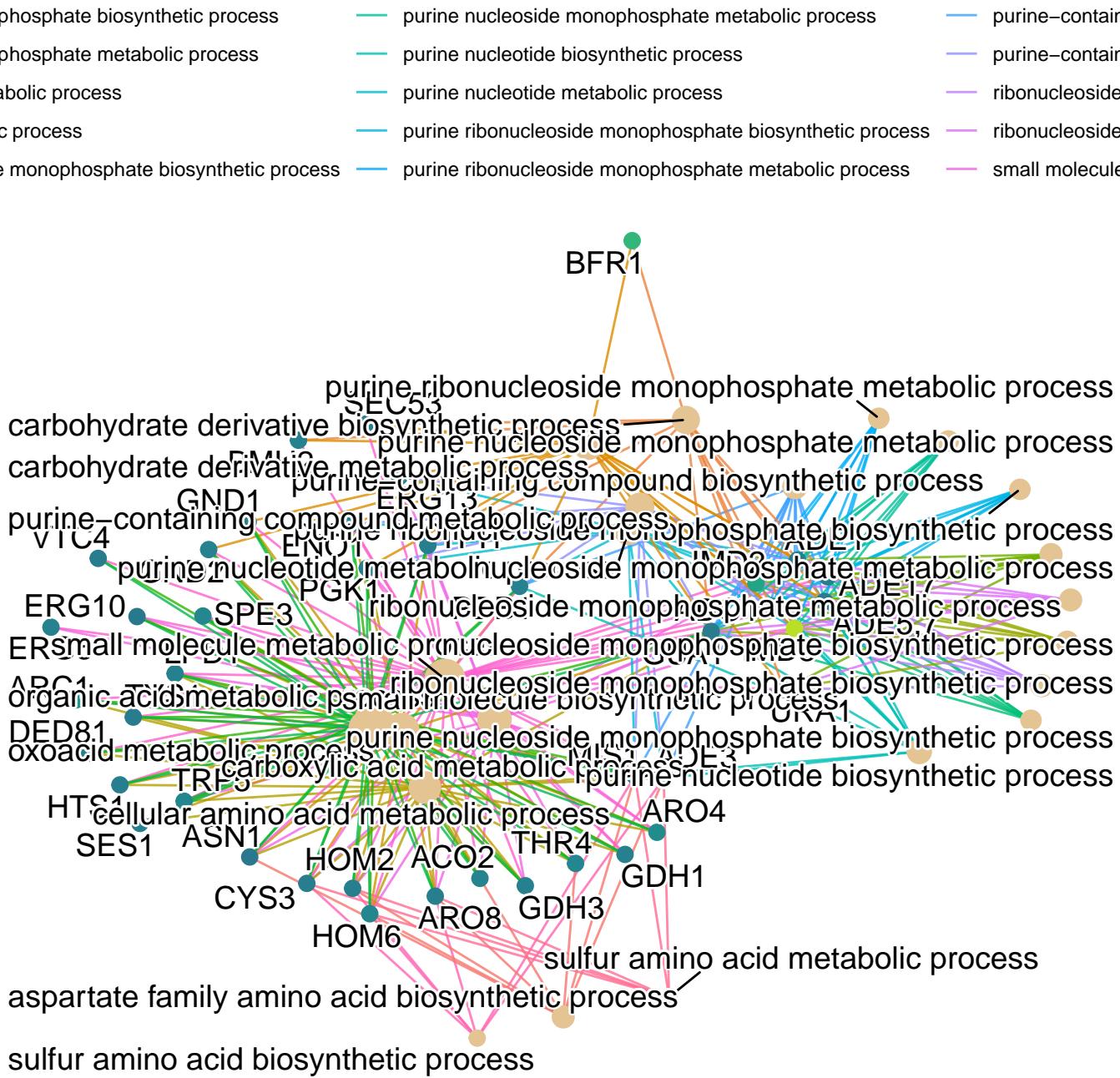
PAB1-TAP Up-regulated GO BP barplot



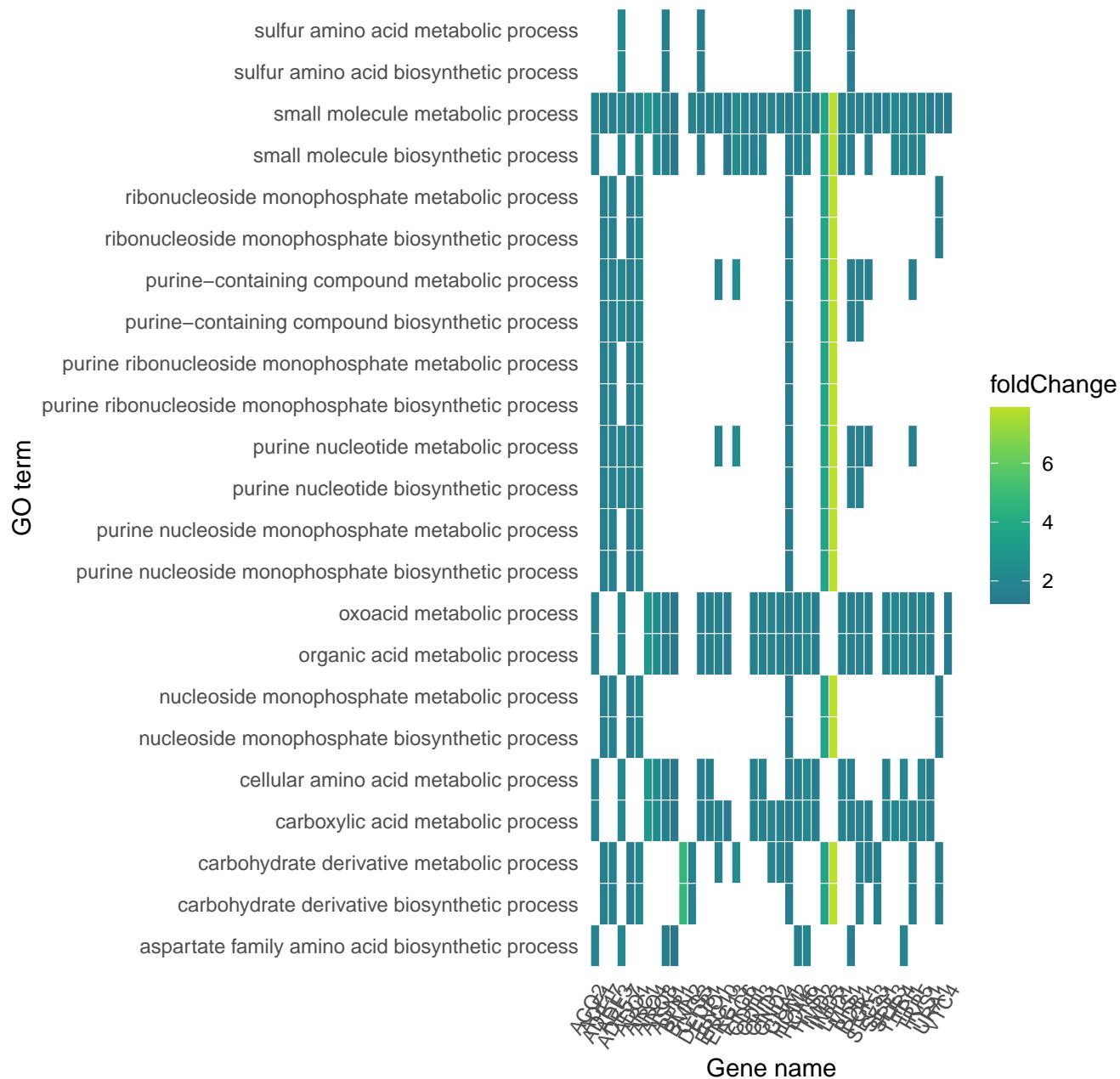
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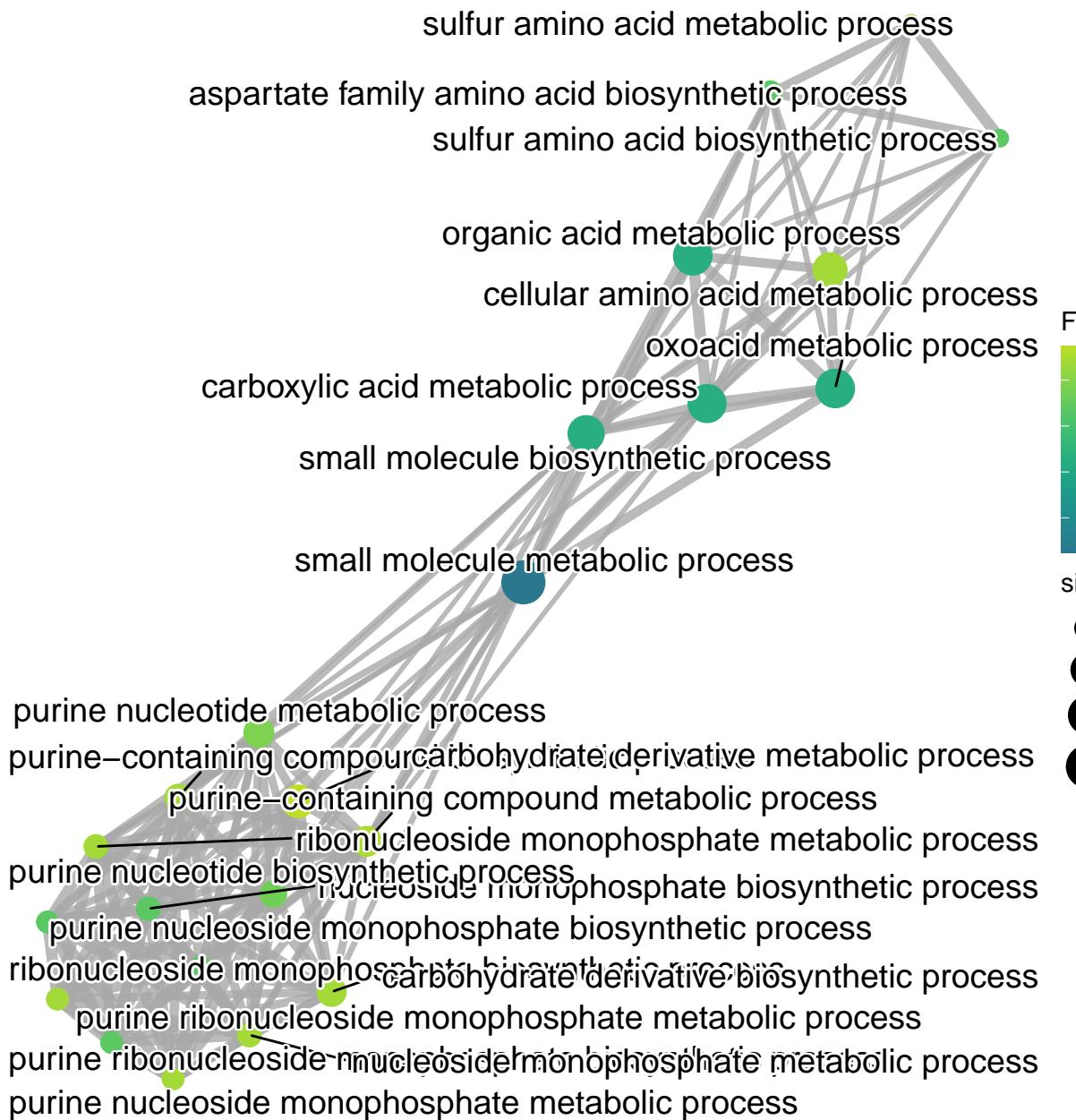
PAB1-TAP Up-regulated GO BP cnetplot

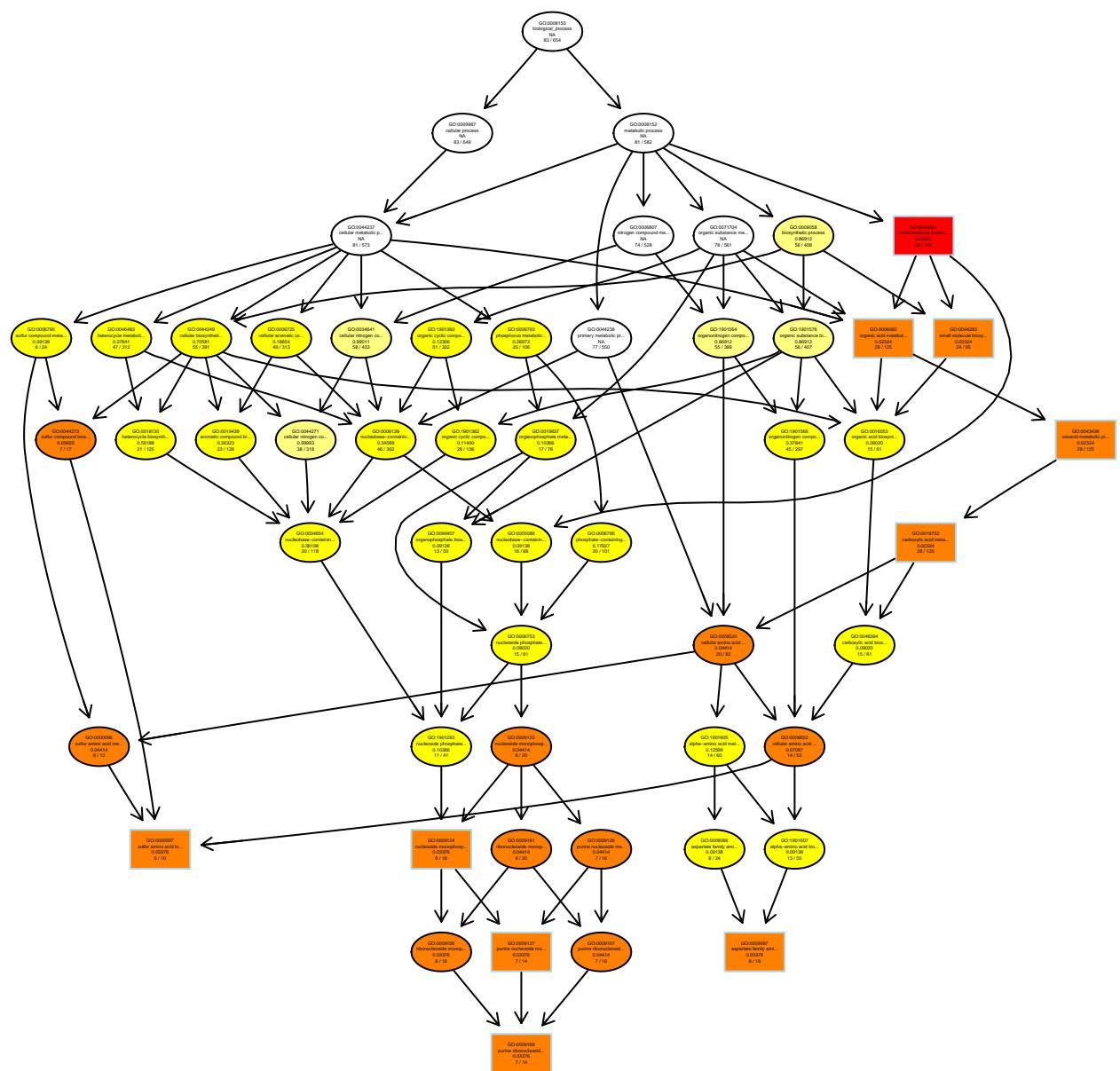


PAB1–TAP Up-regulated GO BP heatplot

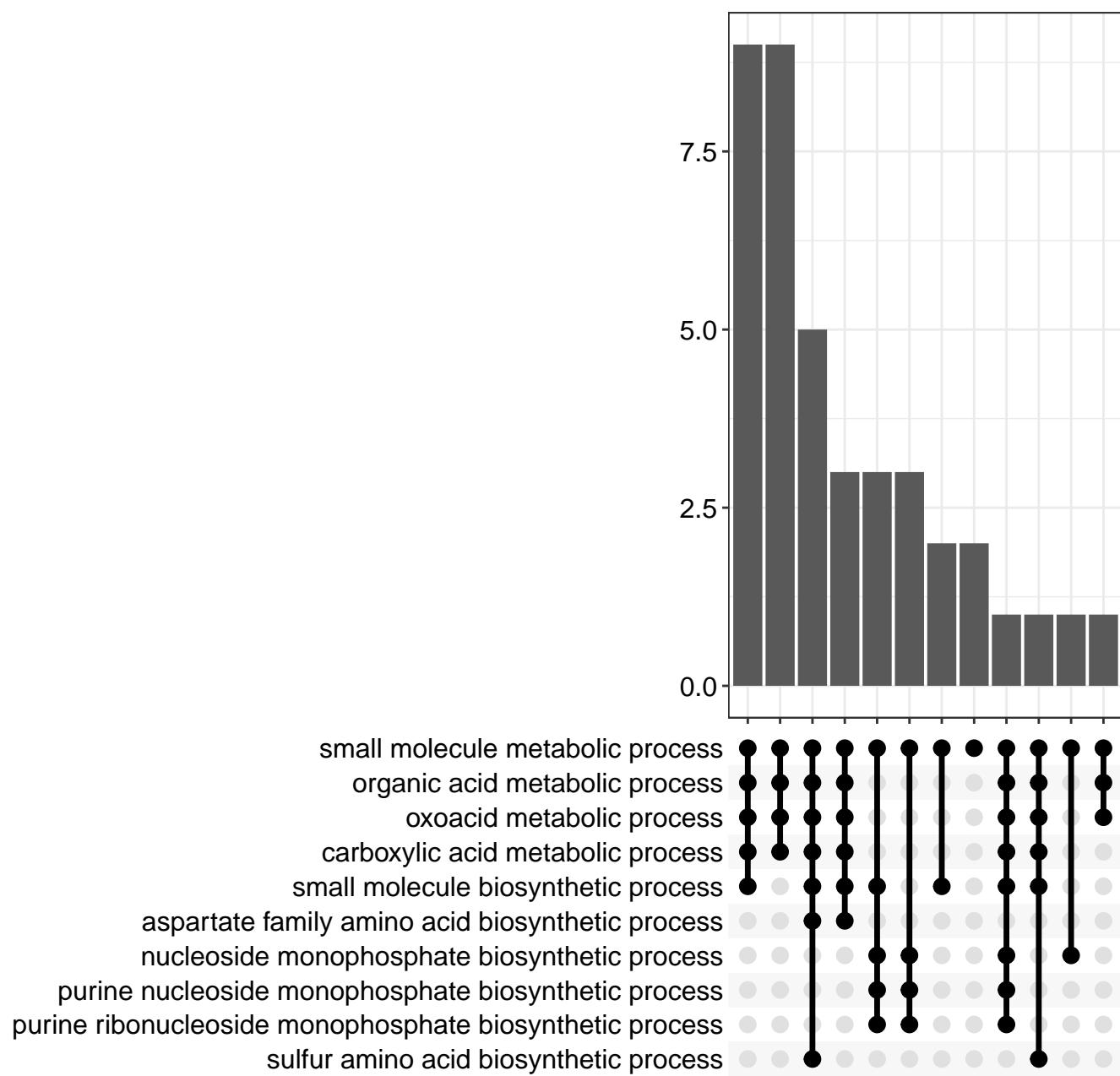


PAB1-TAP Up-regulated GO BP emapplot

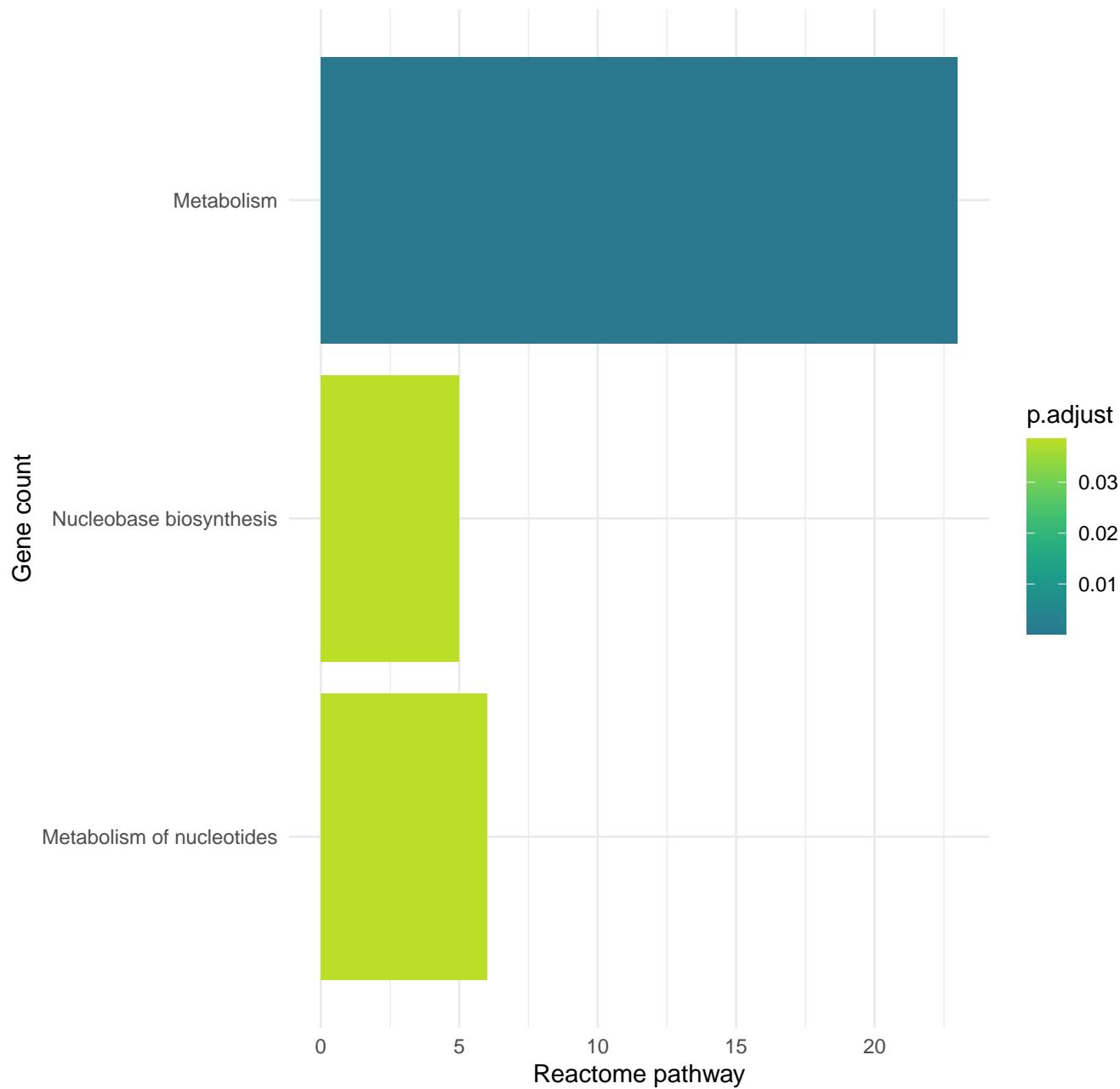




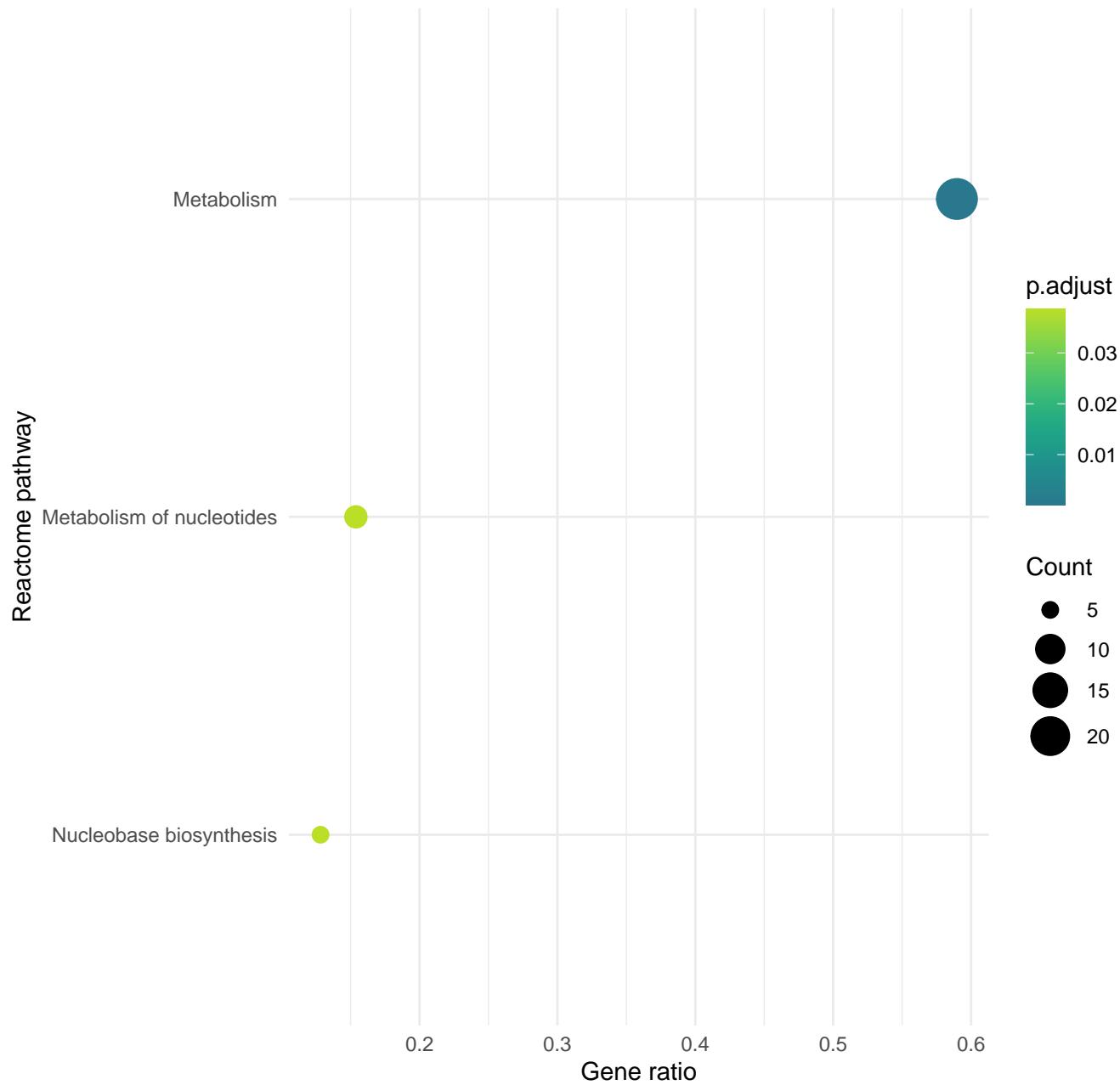
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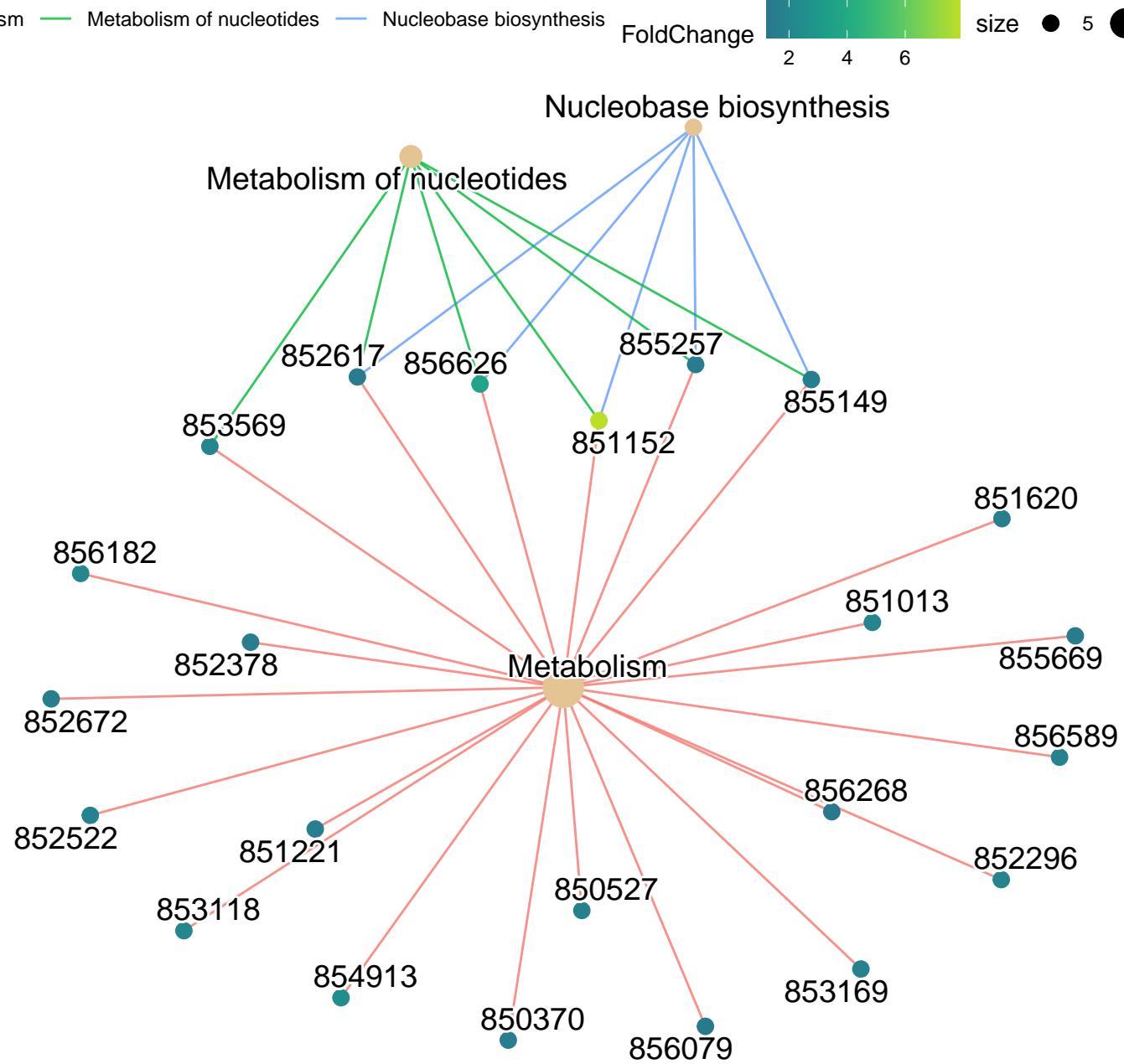
PAB1-TAP Up-regulated Reactome barplot



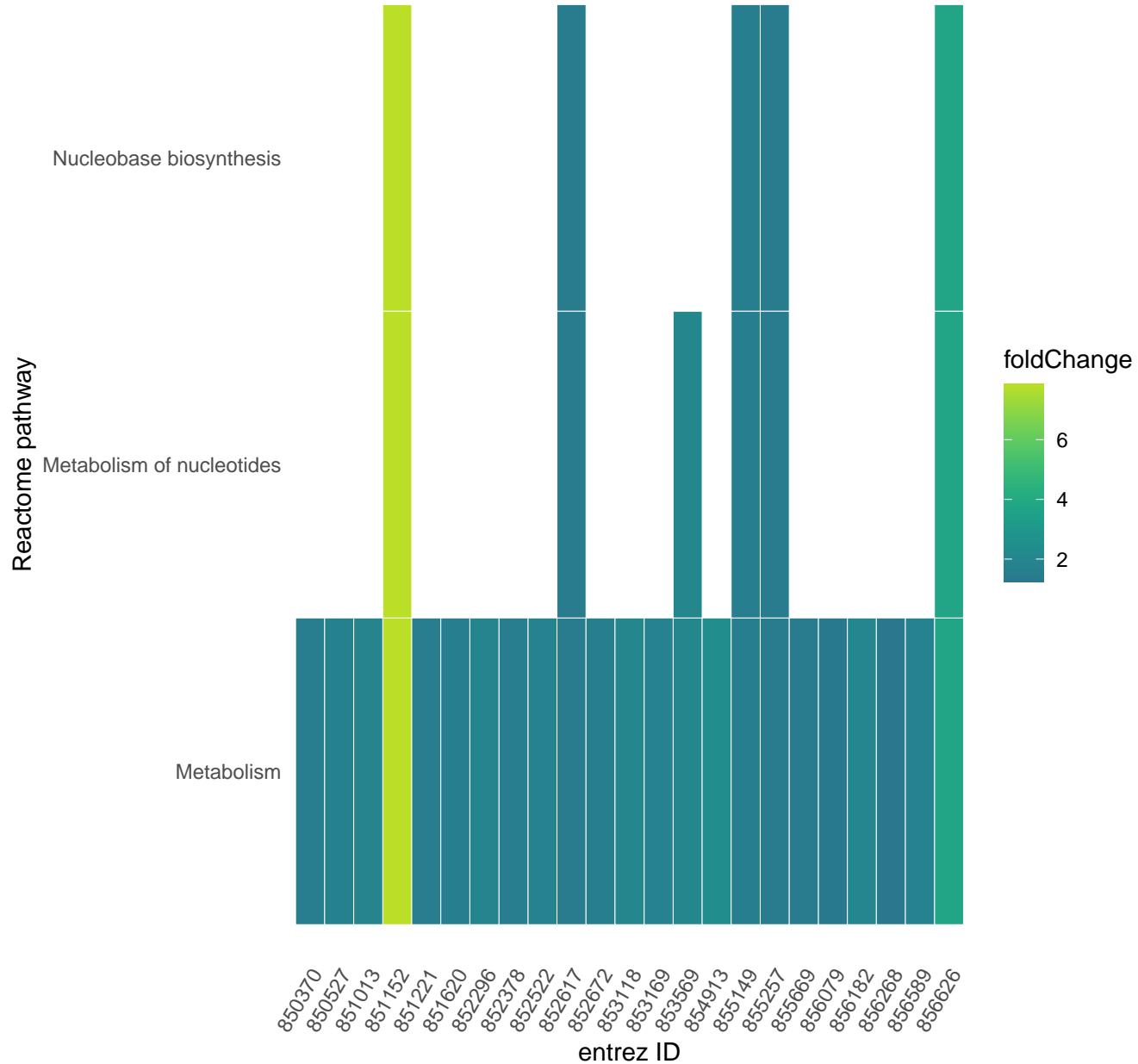
PAB1-TAP Up-regulated Reactome dotplot



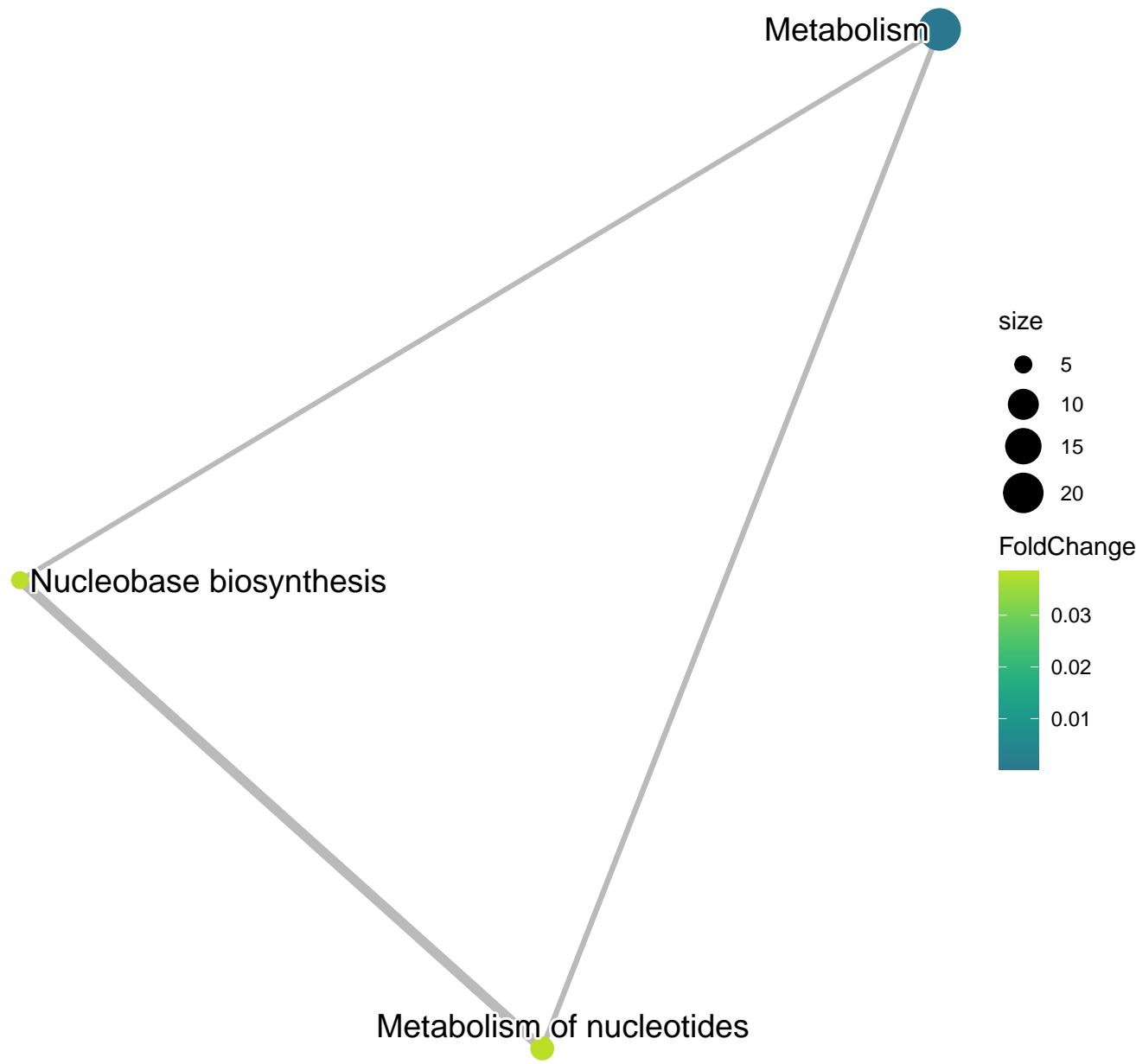
PAB1-TAP Up-regulated Reactome cnetplot



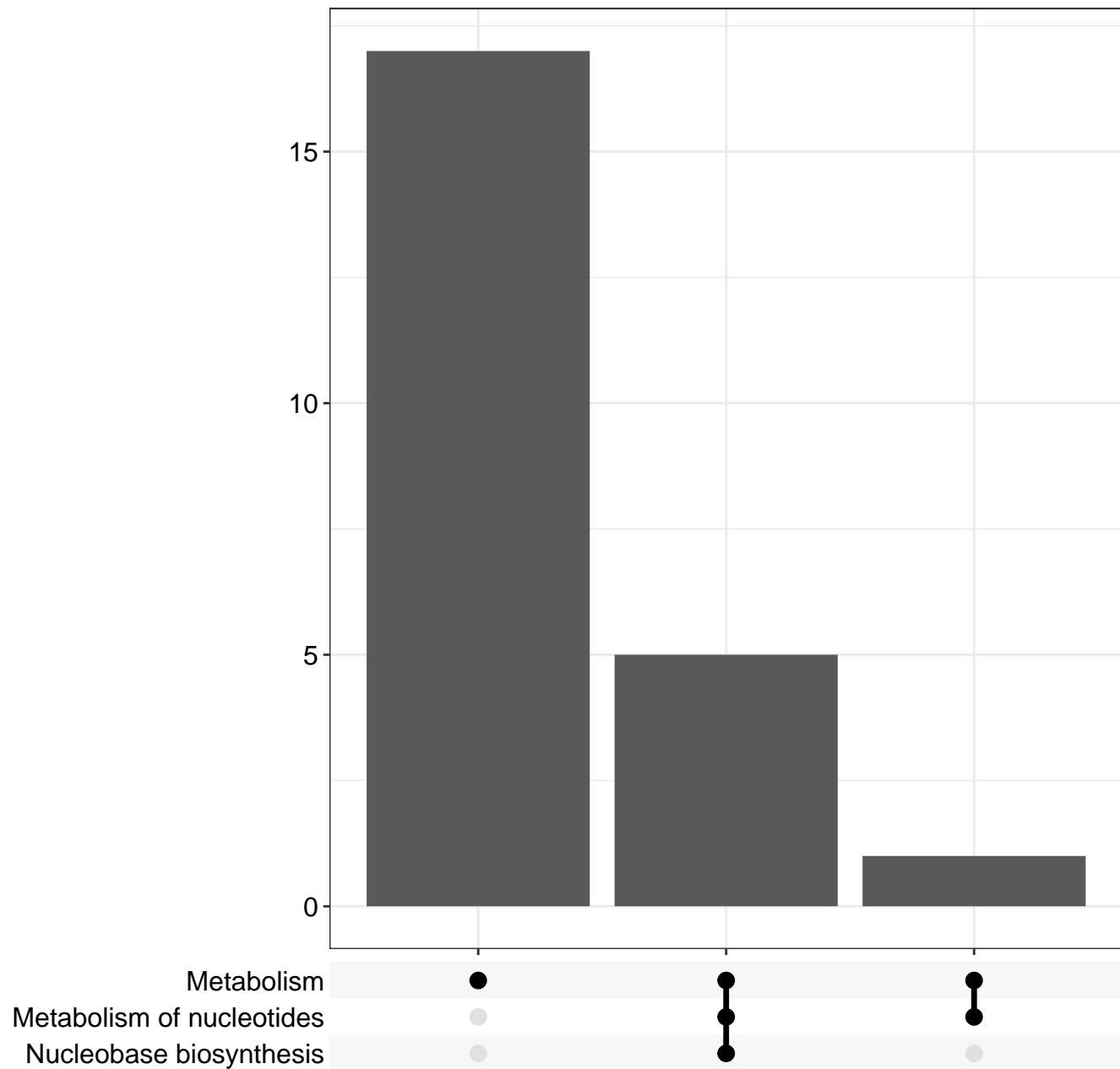
PAB1-TAP Up-regulated Reactome heatplot



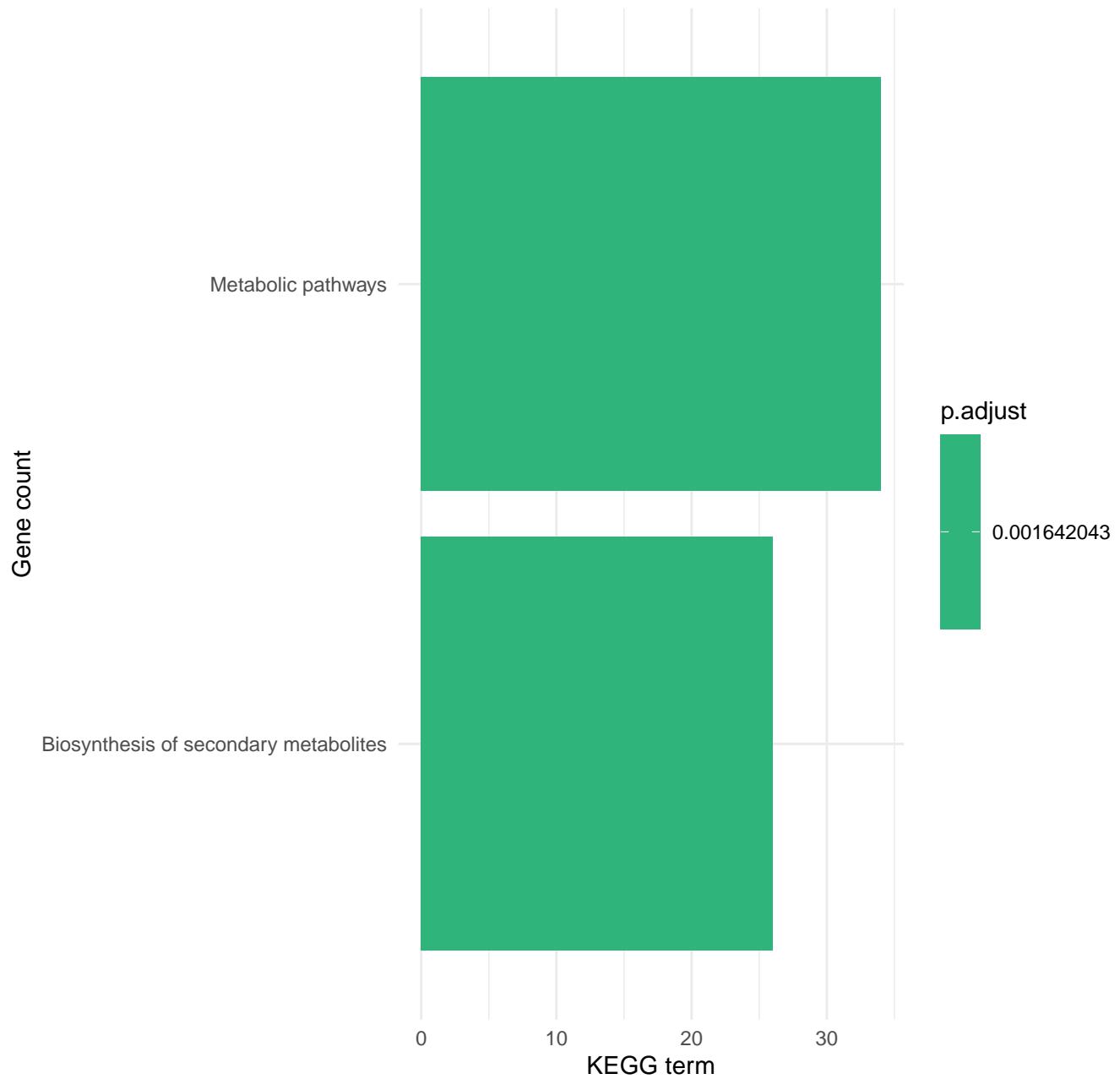
PAB1-TAP Up-regulated Reactome emapplot



PAB1-TAP Up-regulated Reactome upsetplot



PAB1-TAP Up-regulated KEGG barplot



PAB1-TAP Up-regulated KEGG dotplot

KEGG term

Metabolic pathways

Biosynthesis of secondary metabolites

0.50

0.55

0.60

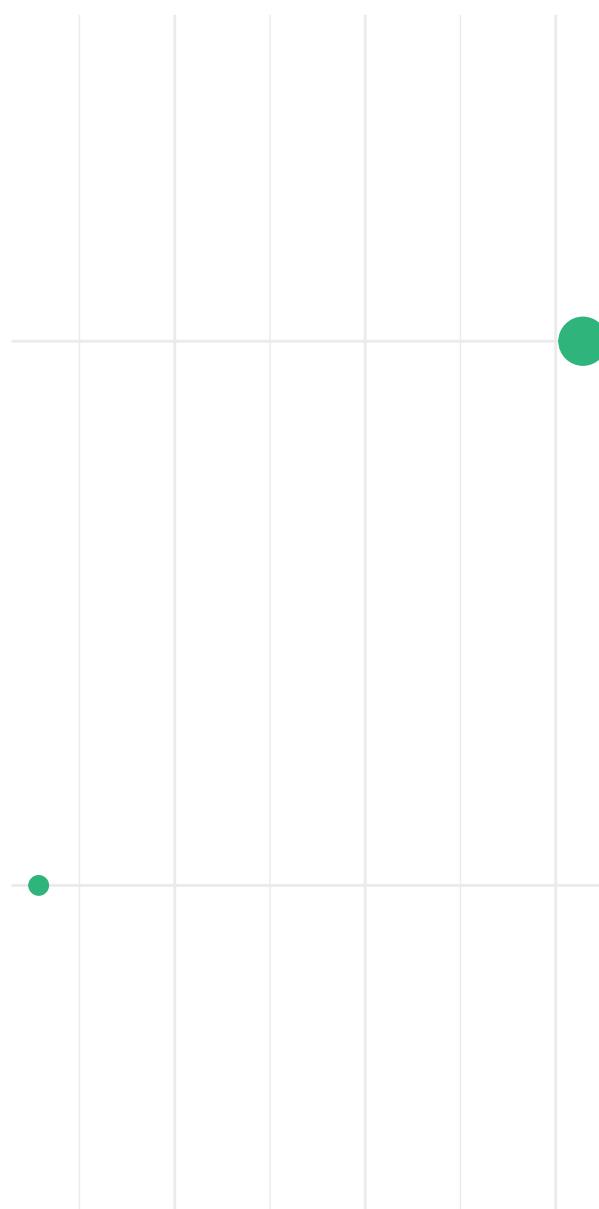
Gene ratio

Count

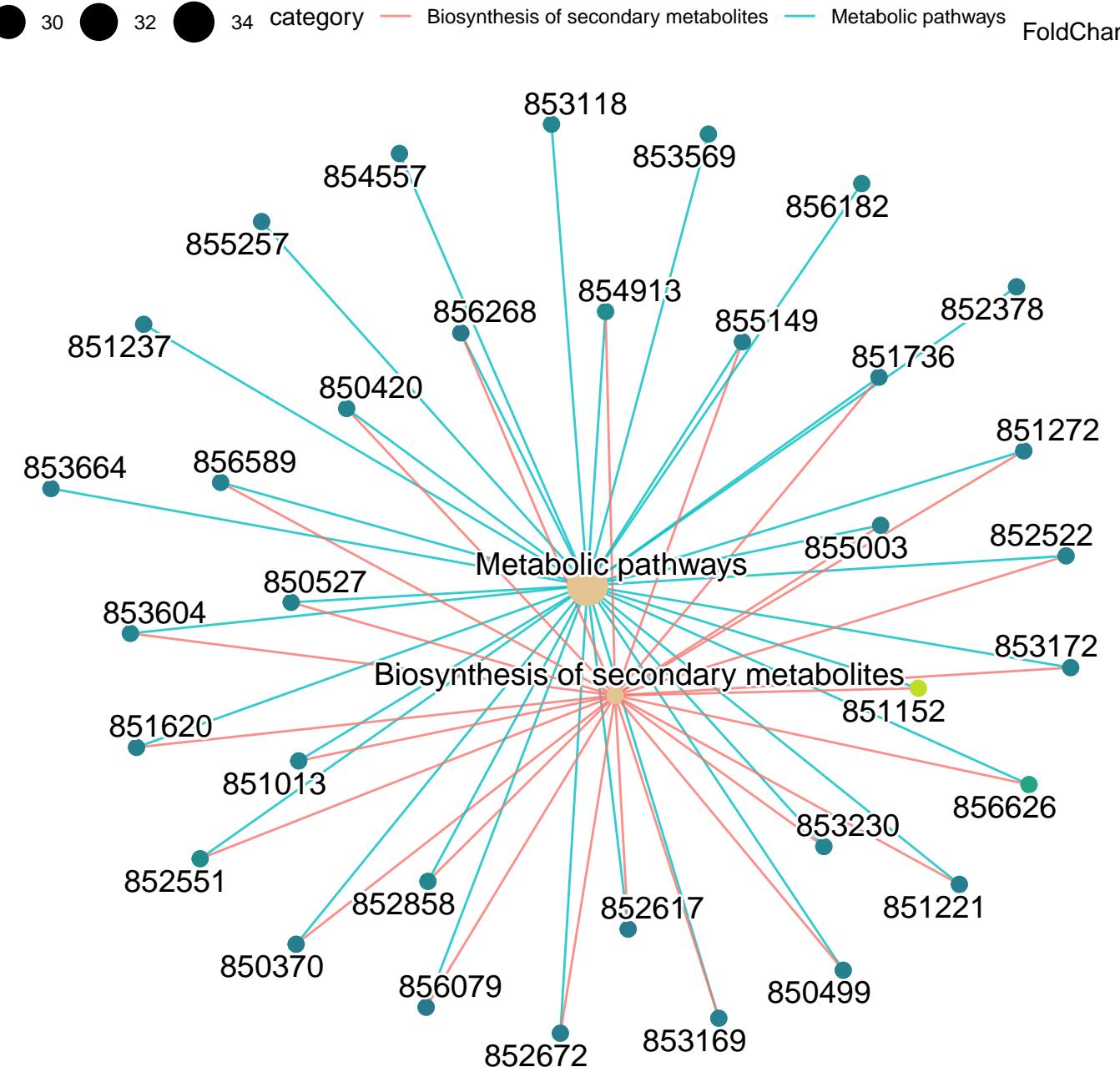
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- 28
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- 34

p.adjust

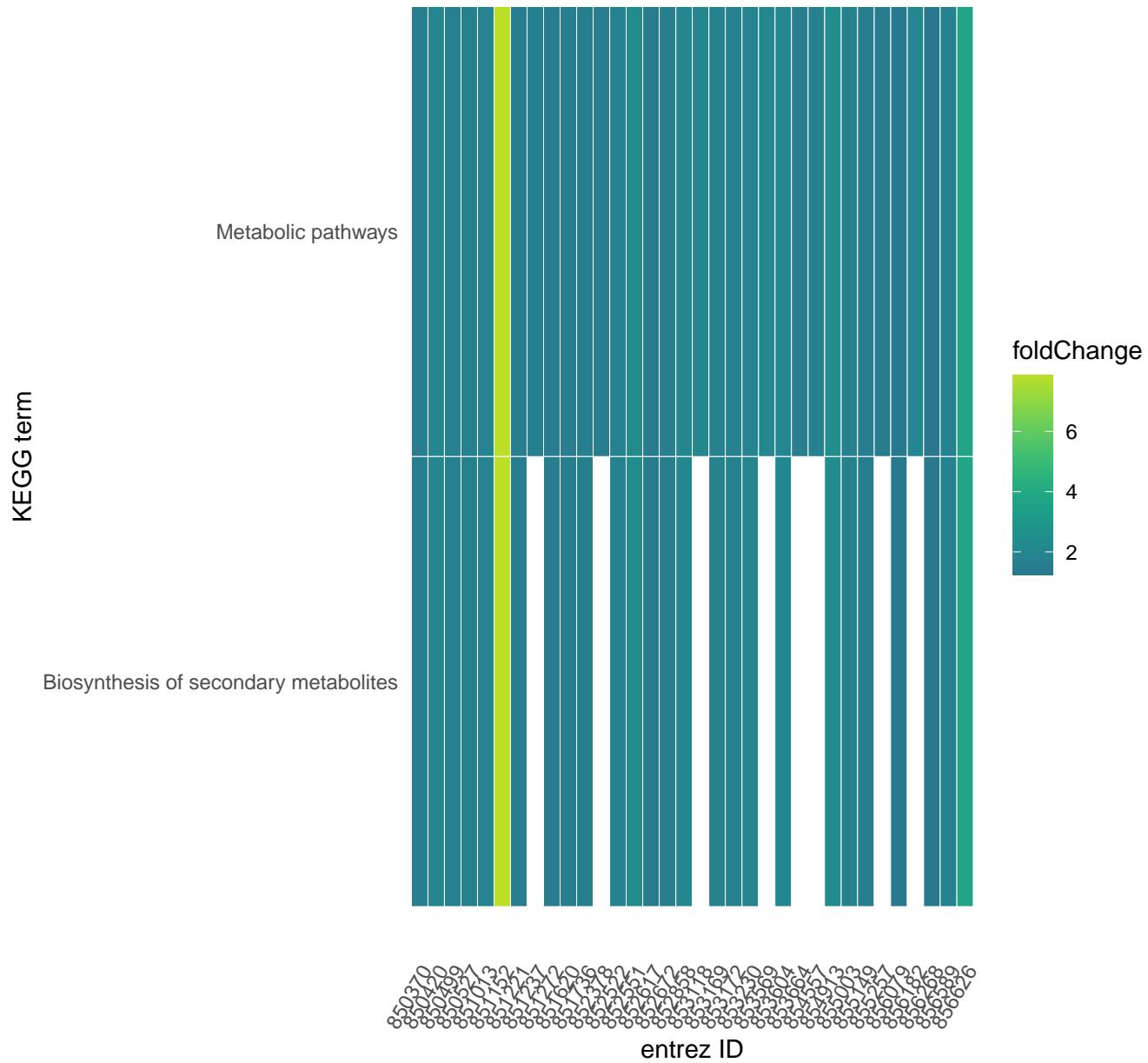
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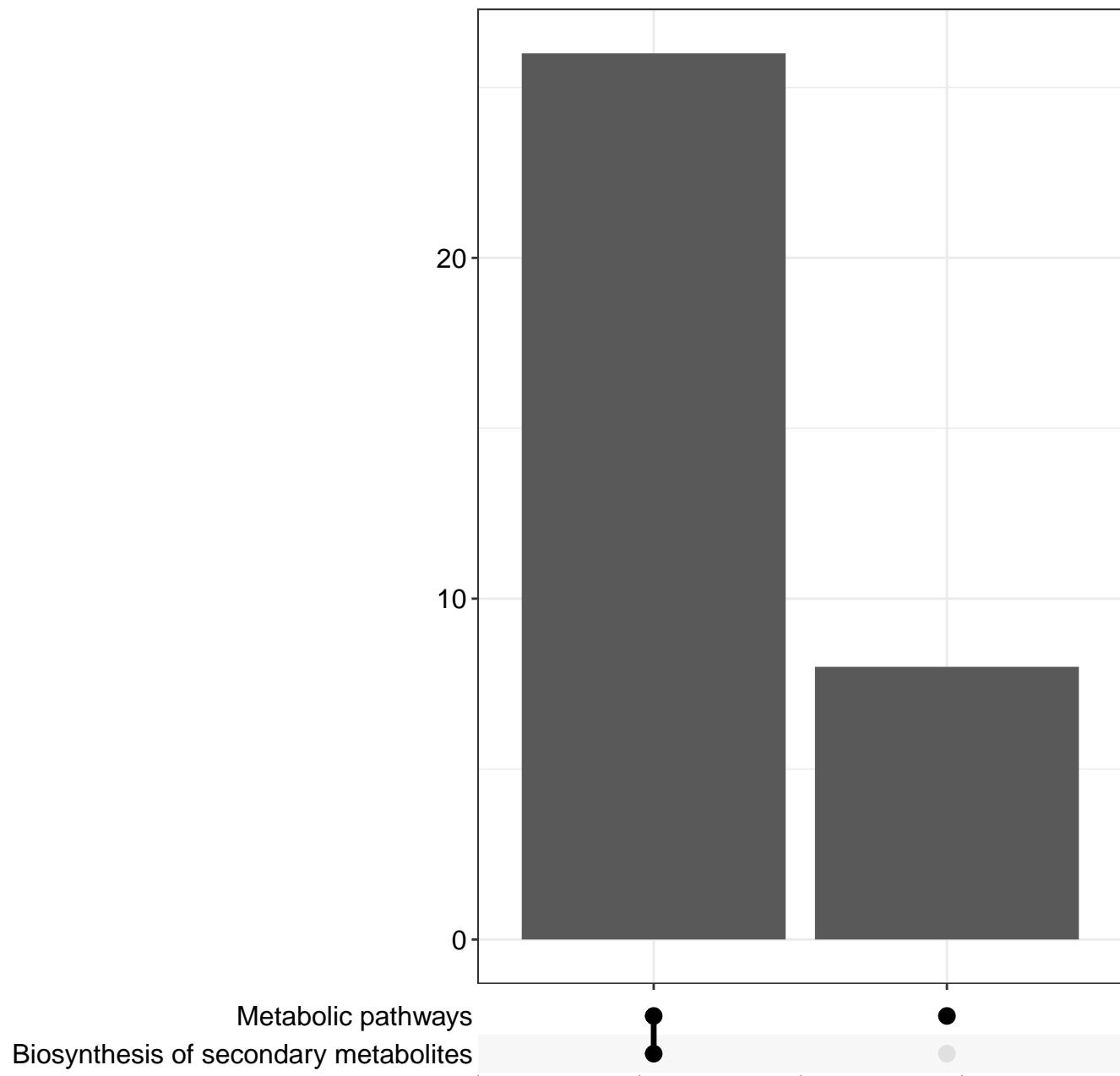
PAB1-TAP Up-regulated KEGG dotplot



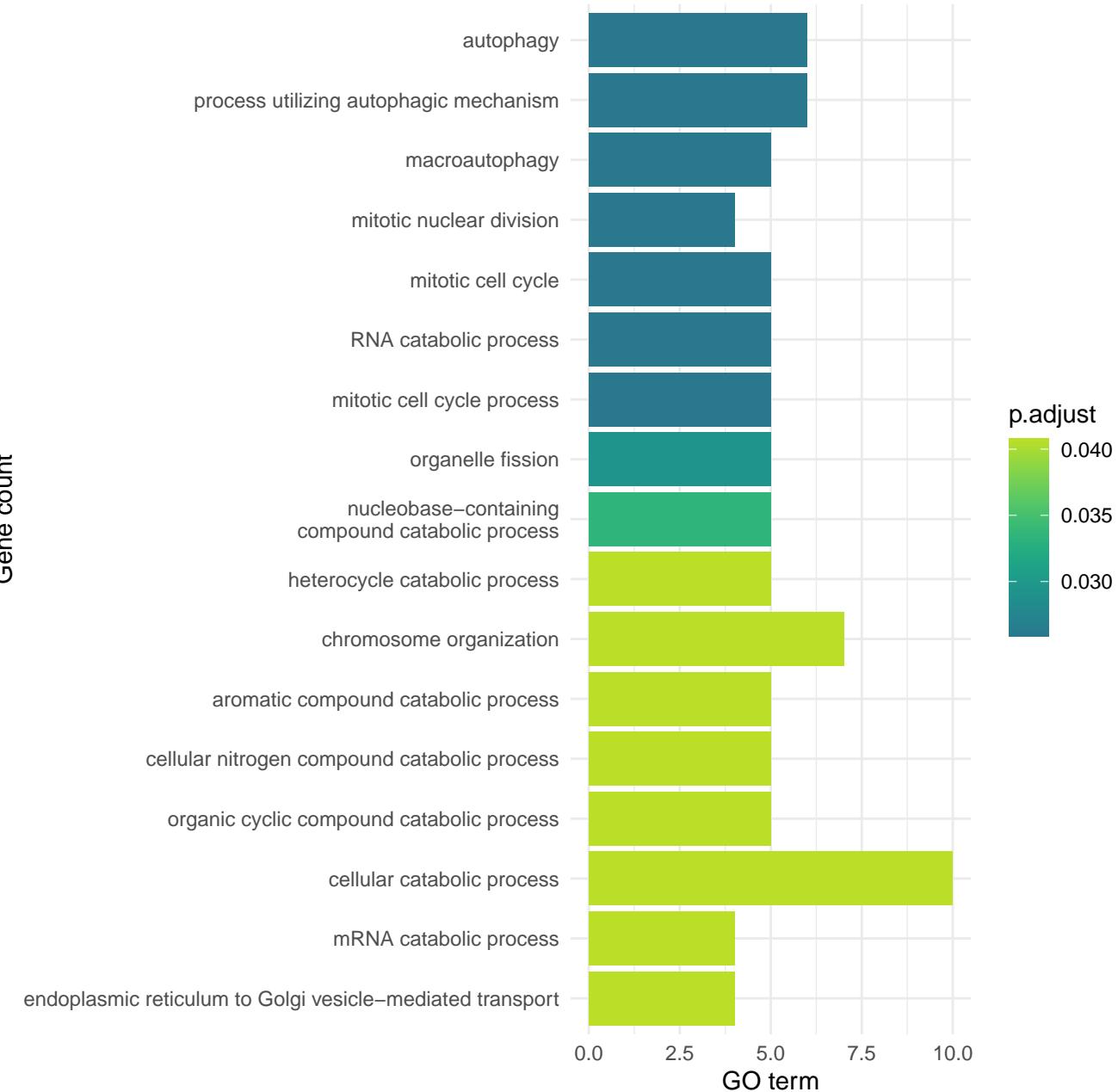
PAB1-TAP Up-regulated KEGG heatplot



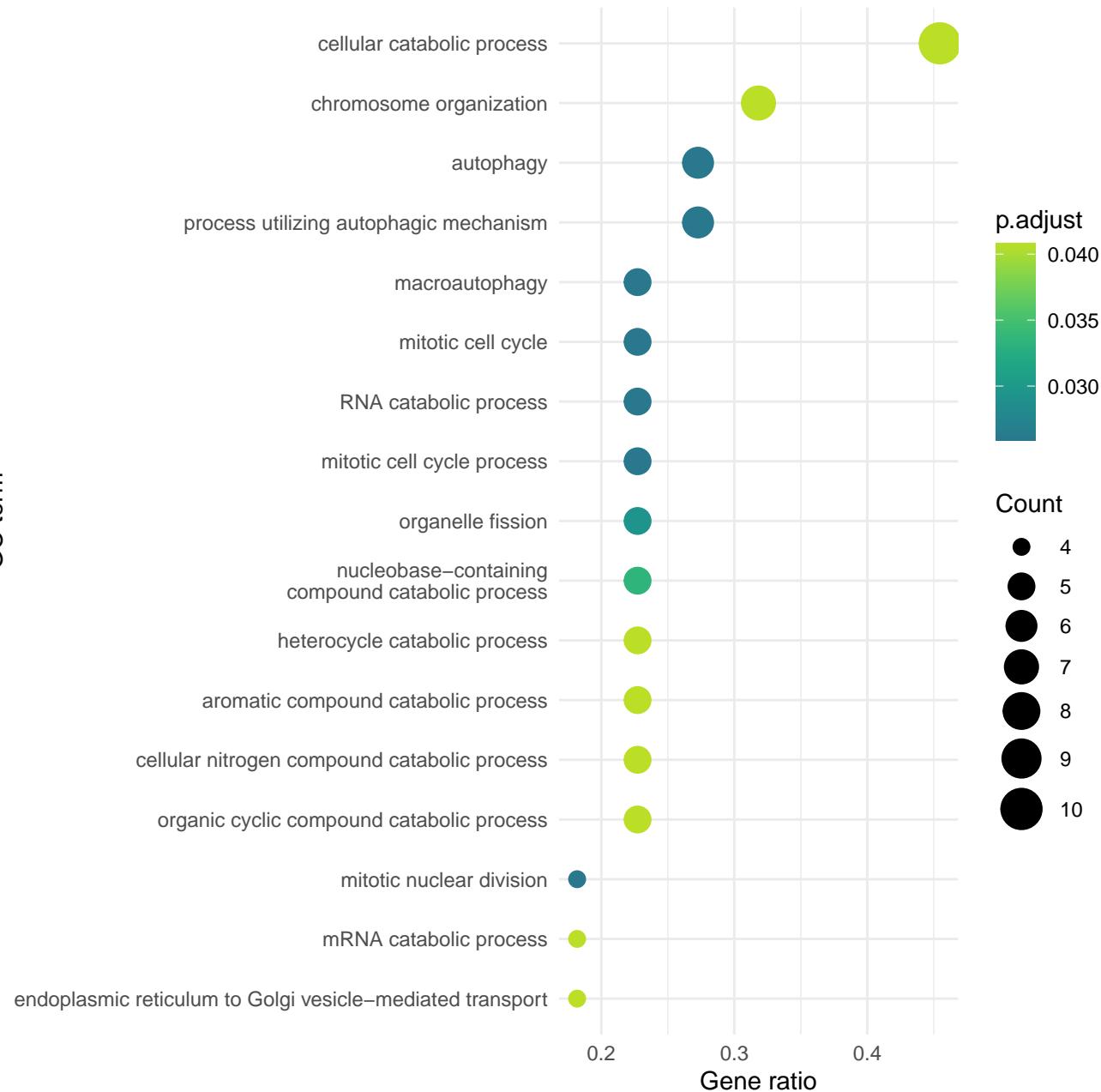
PAB1-TAP Up-regulated KEGG upsetplot



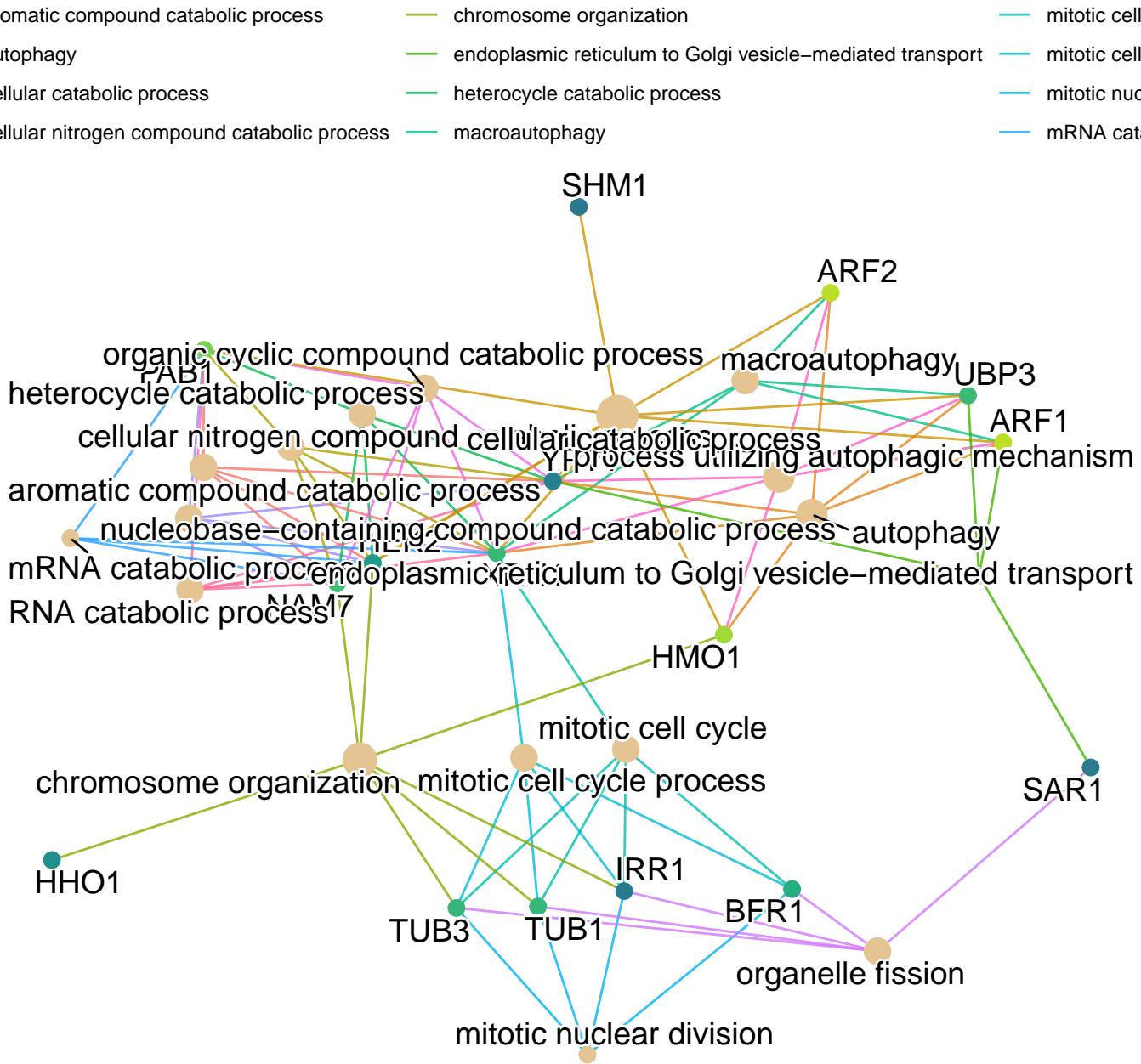
PUF3-TAP Up-regulated GO BP barplot



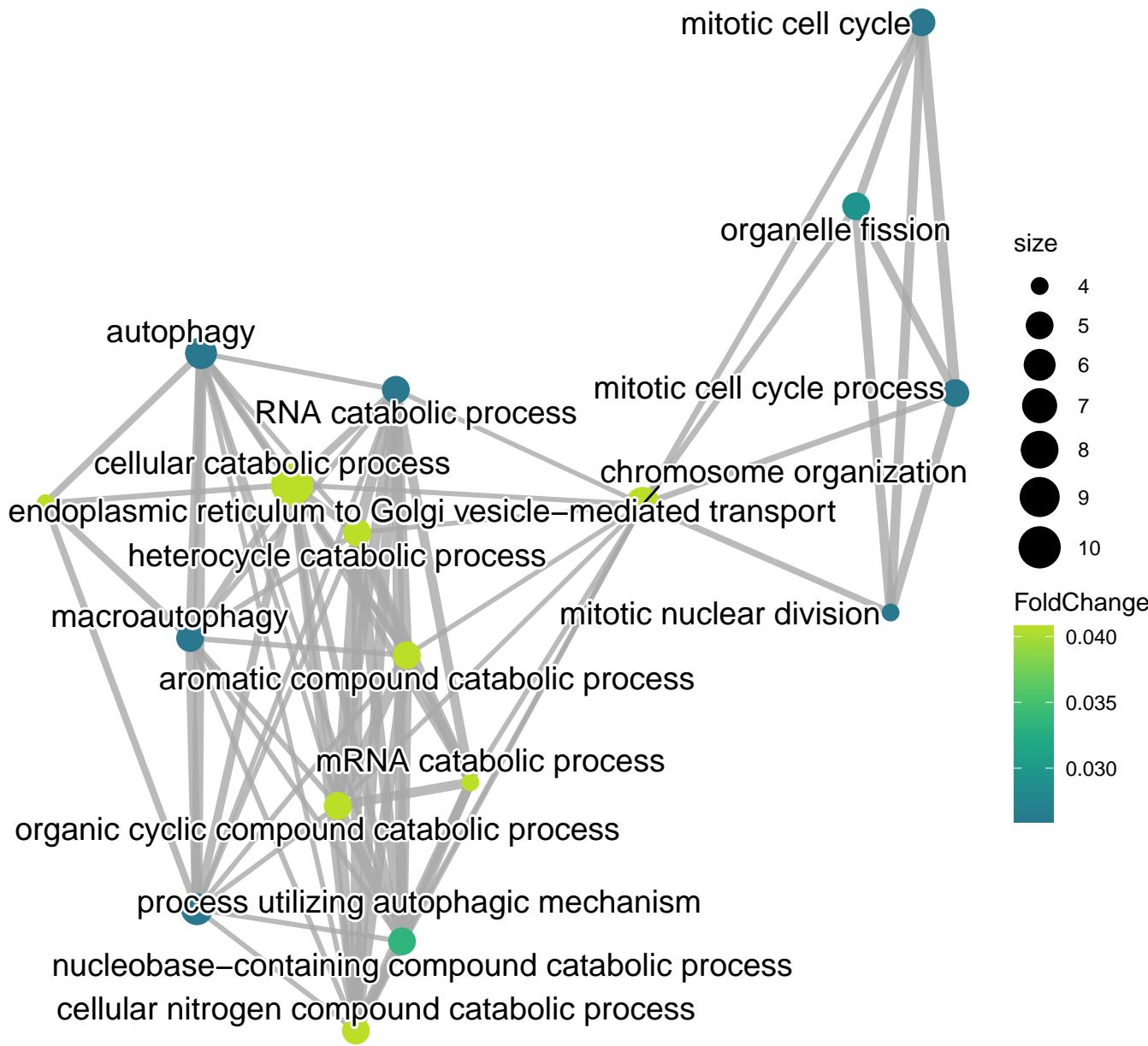
PUF3-TAP Up-regulated GO BP dotplot

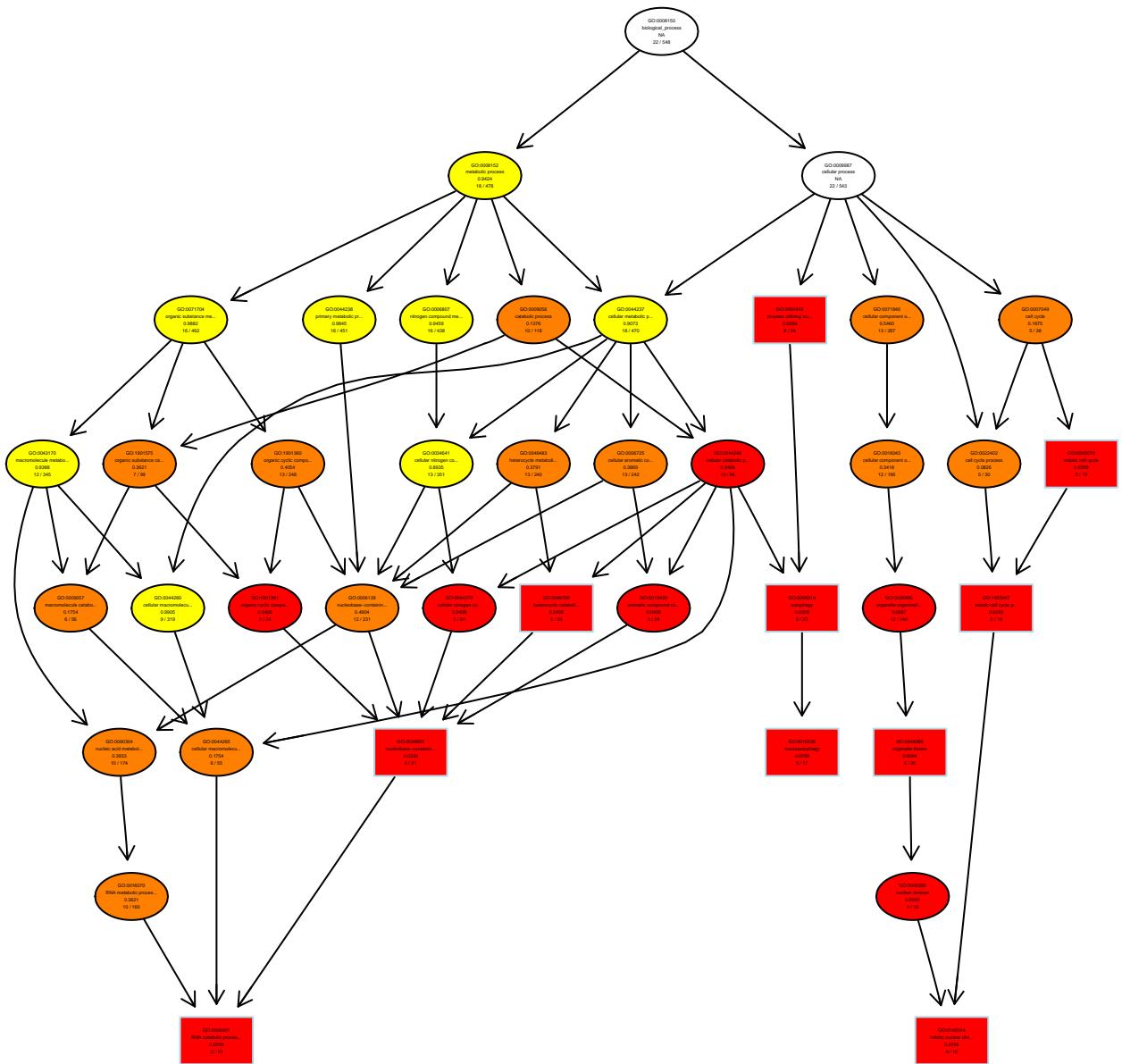


PUF3-TAP Up-regulated GO BP cnetplot

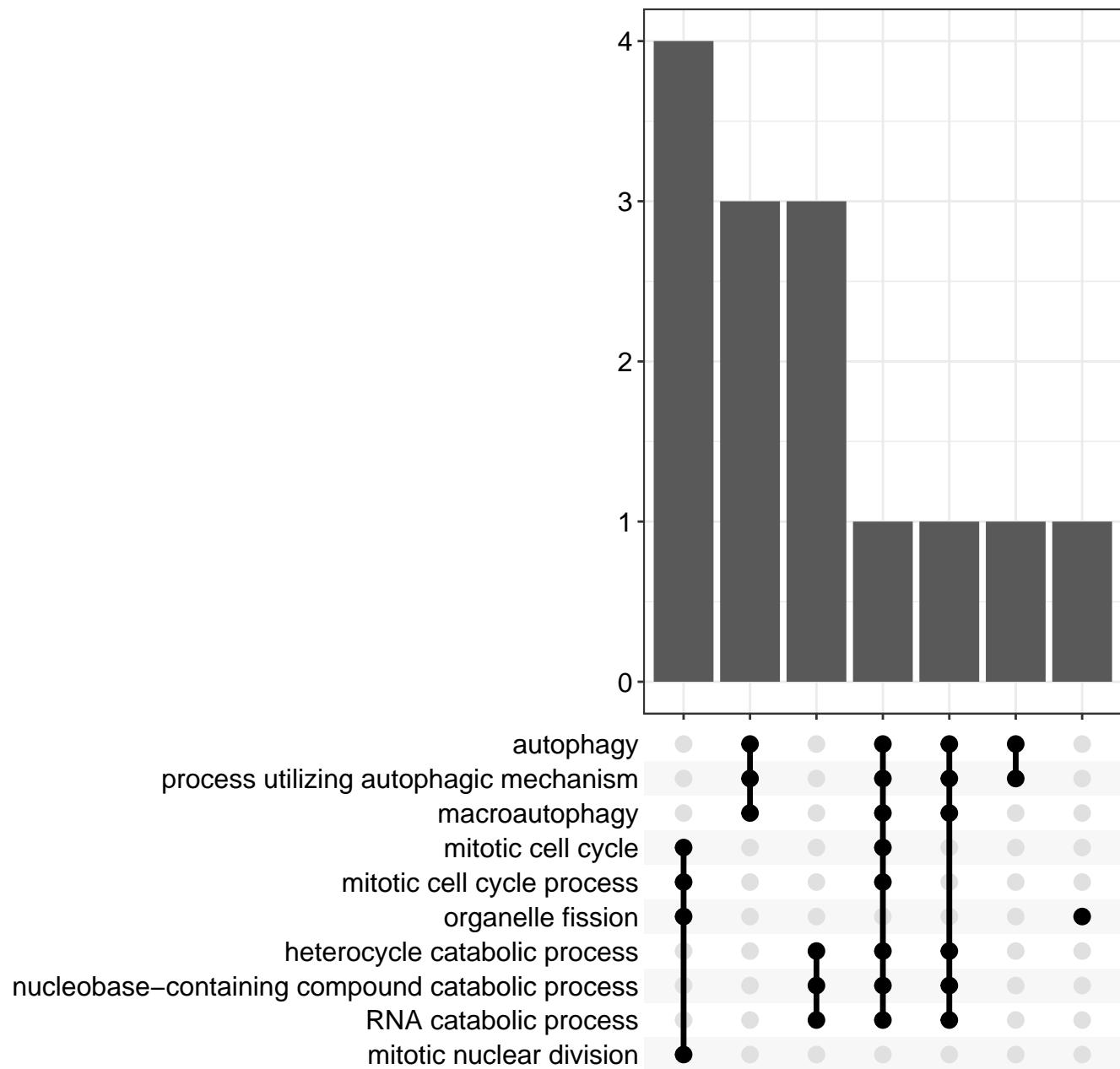


PUF3-TAP Up-regulated GO BP emapplot

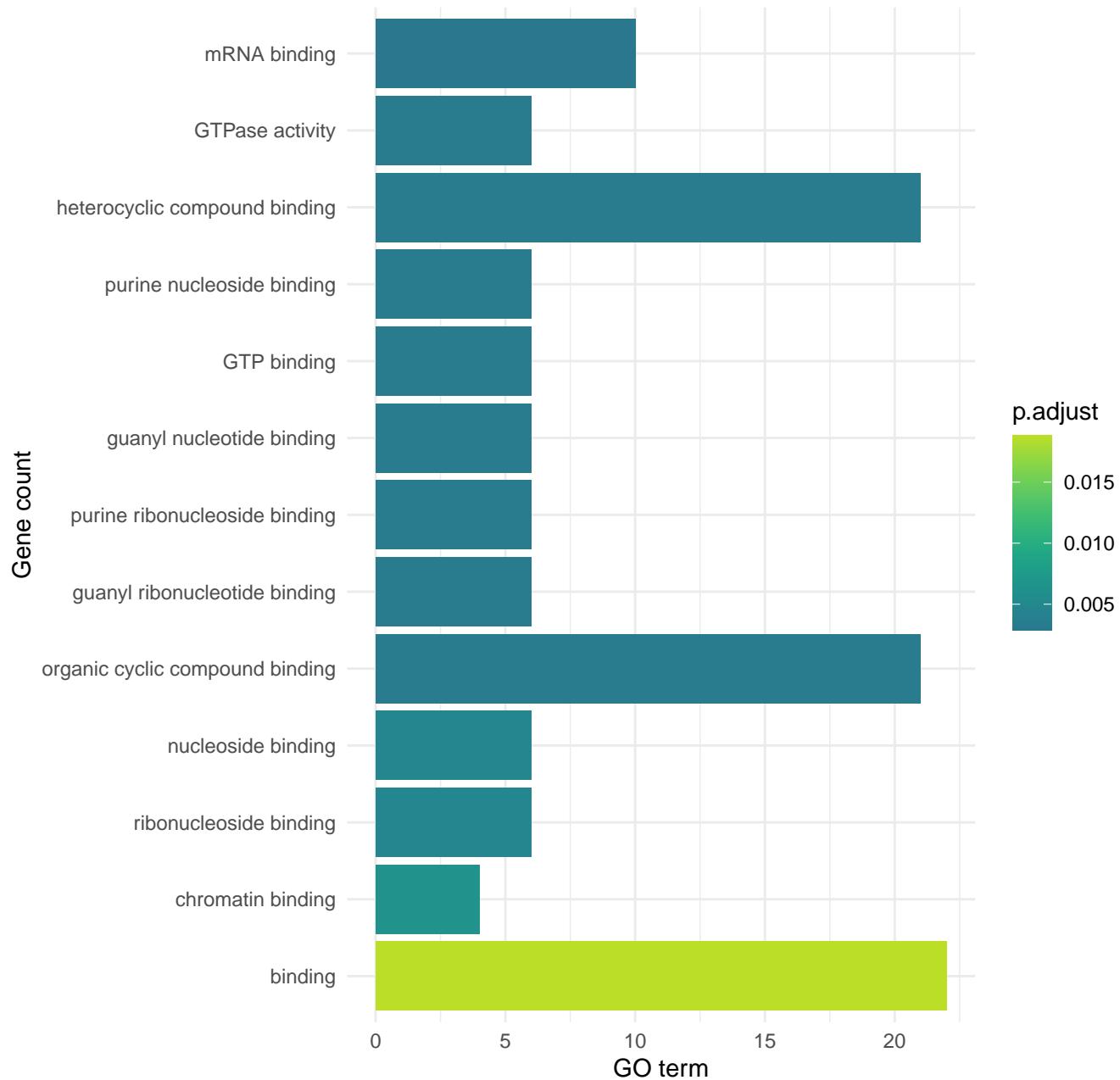




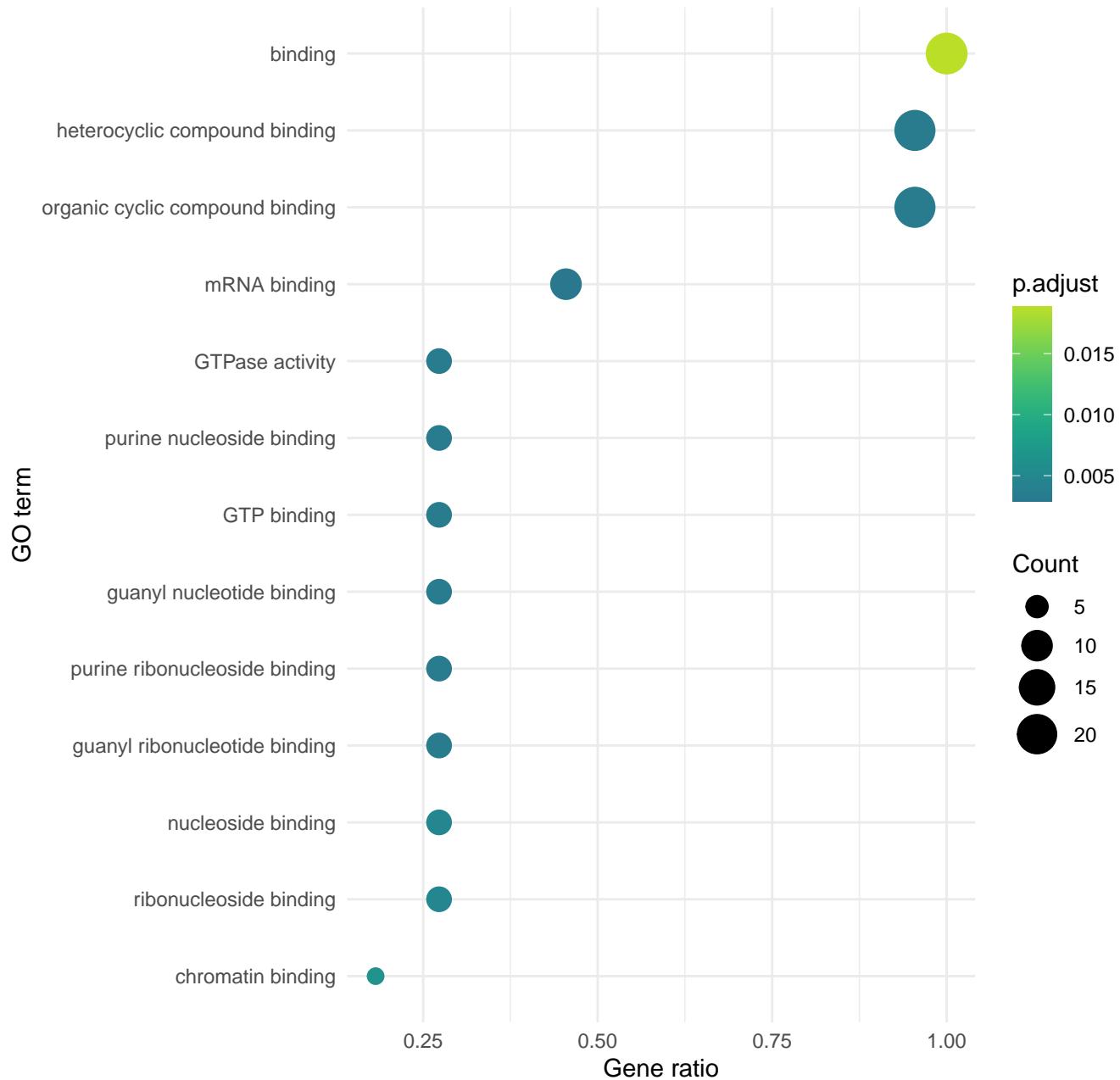
PUF3-TAP Up-regulated GO BP upse



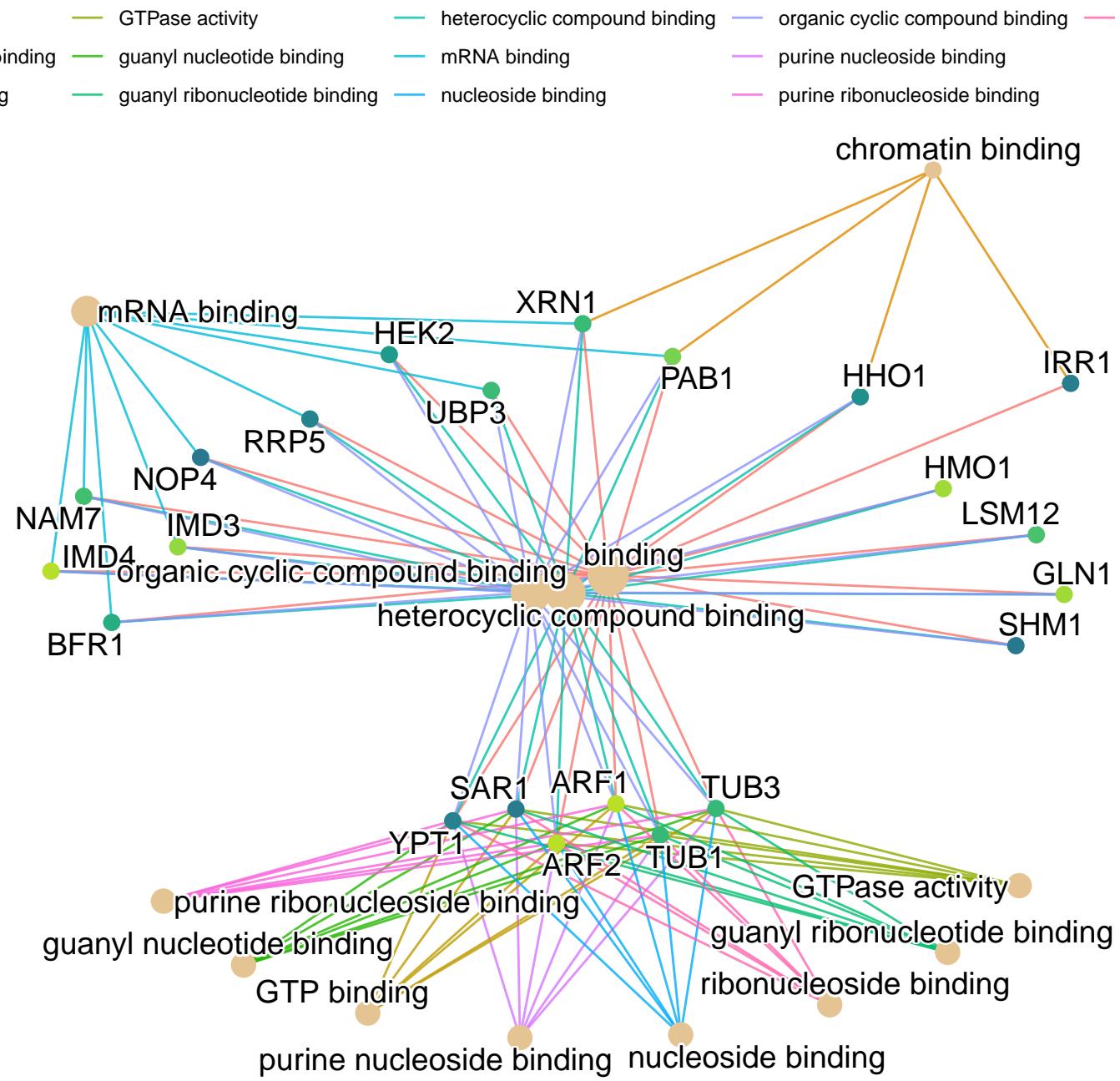
PUF3-TAP Up-regulated GO MF barplot



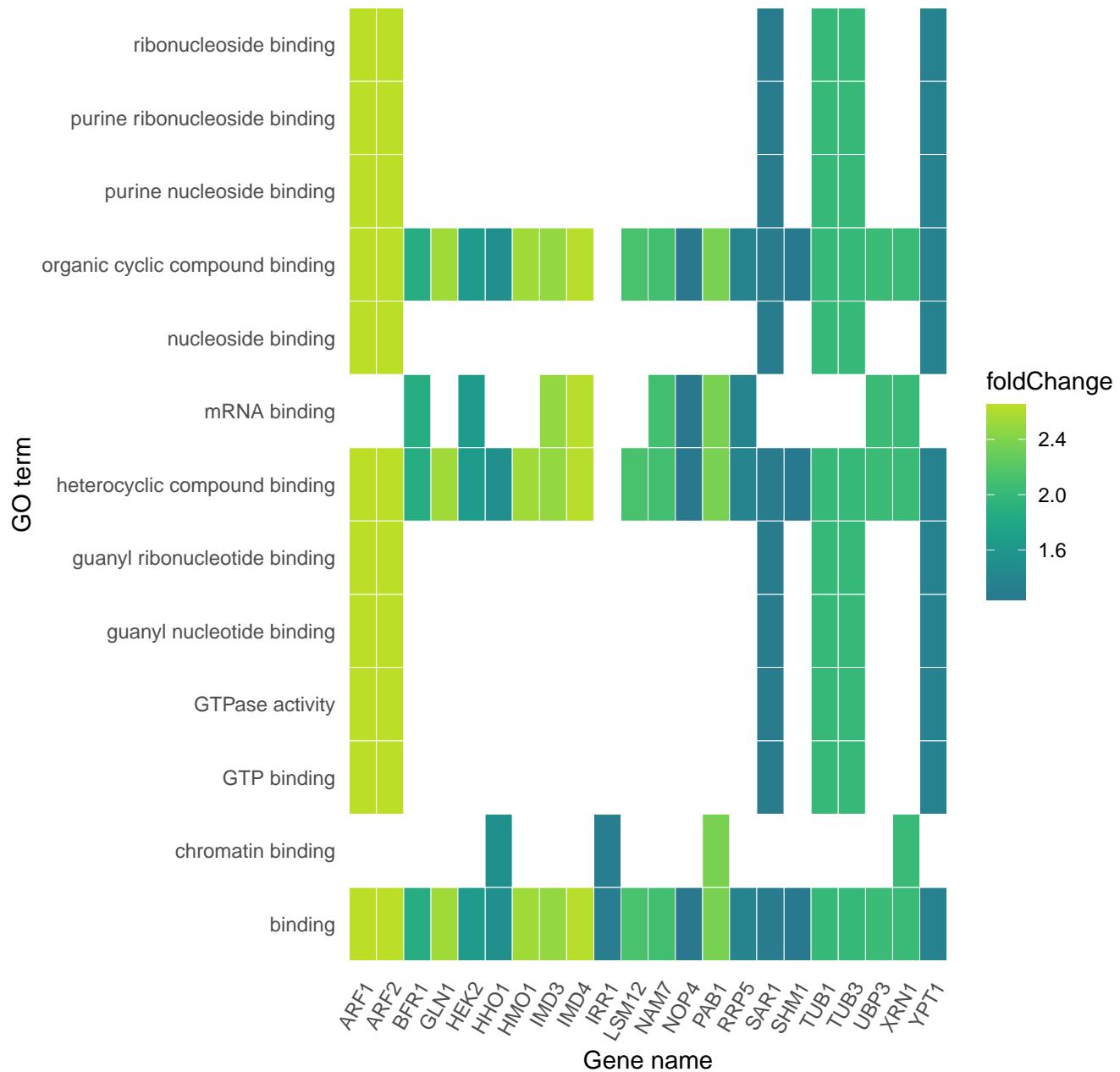
PUF3-TAP Up-regulated GO MF dotplot



PUF3-TAP Up-regulated GO MF cnetplot

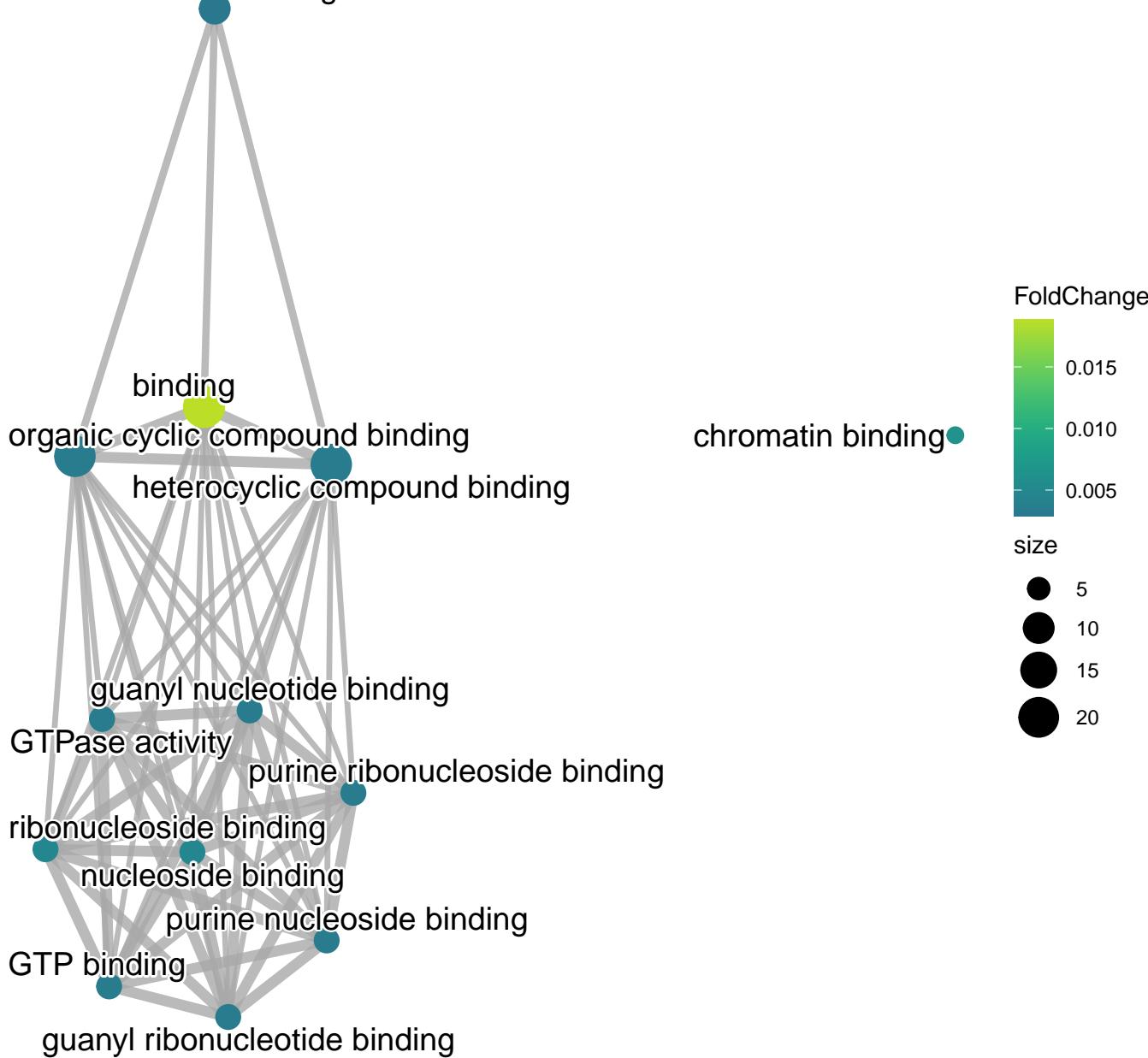


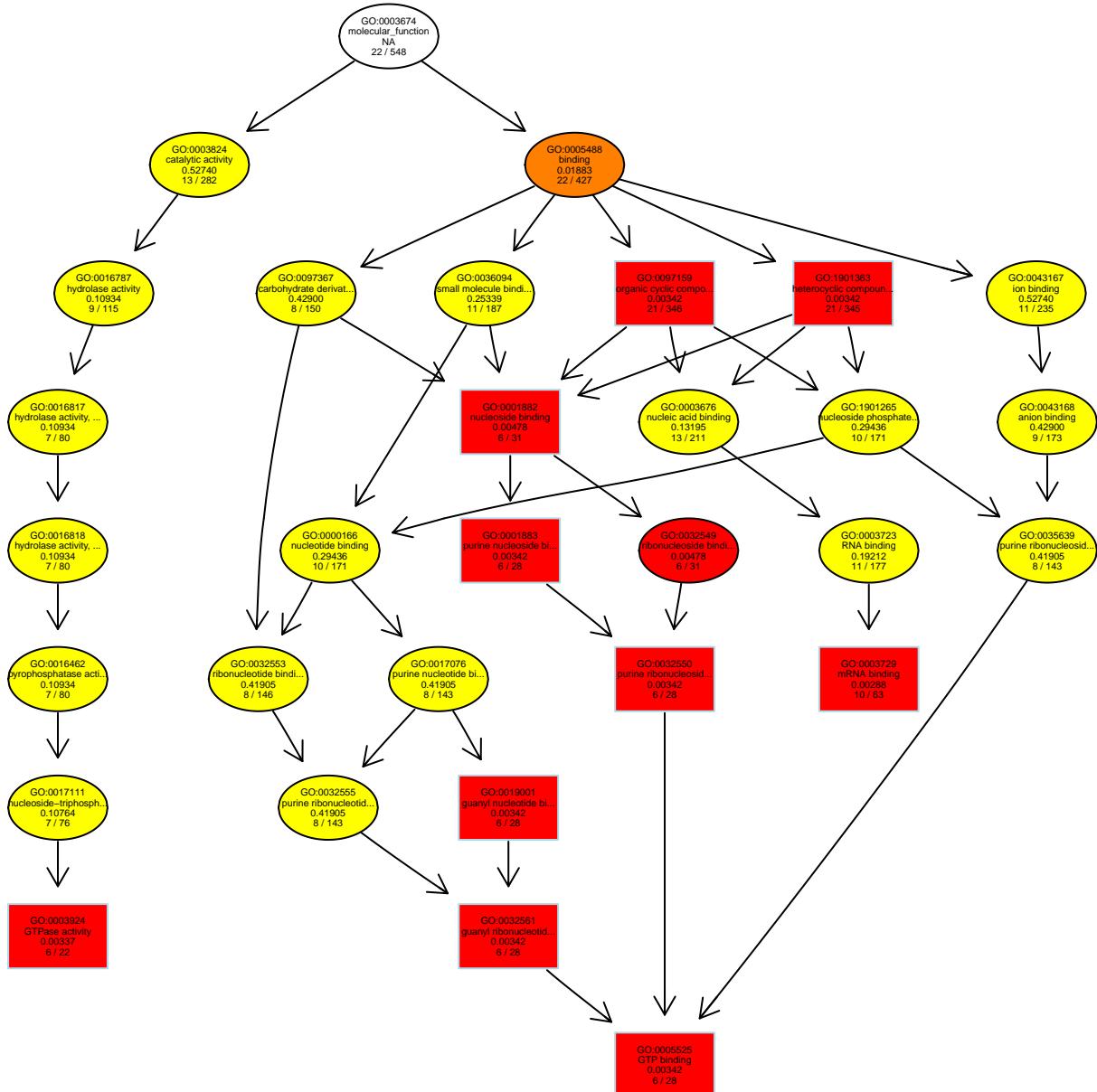
PUF3-TAP Up-regulated GO MF heatplot



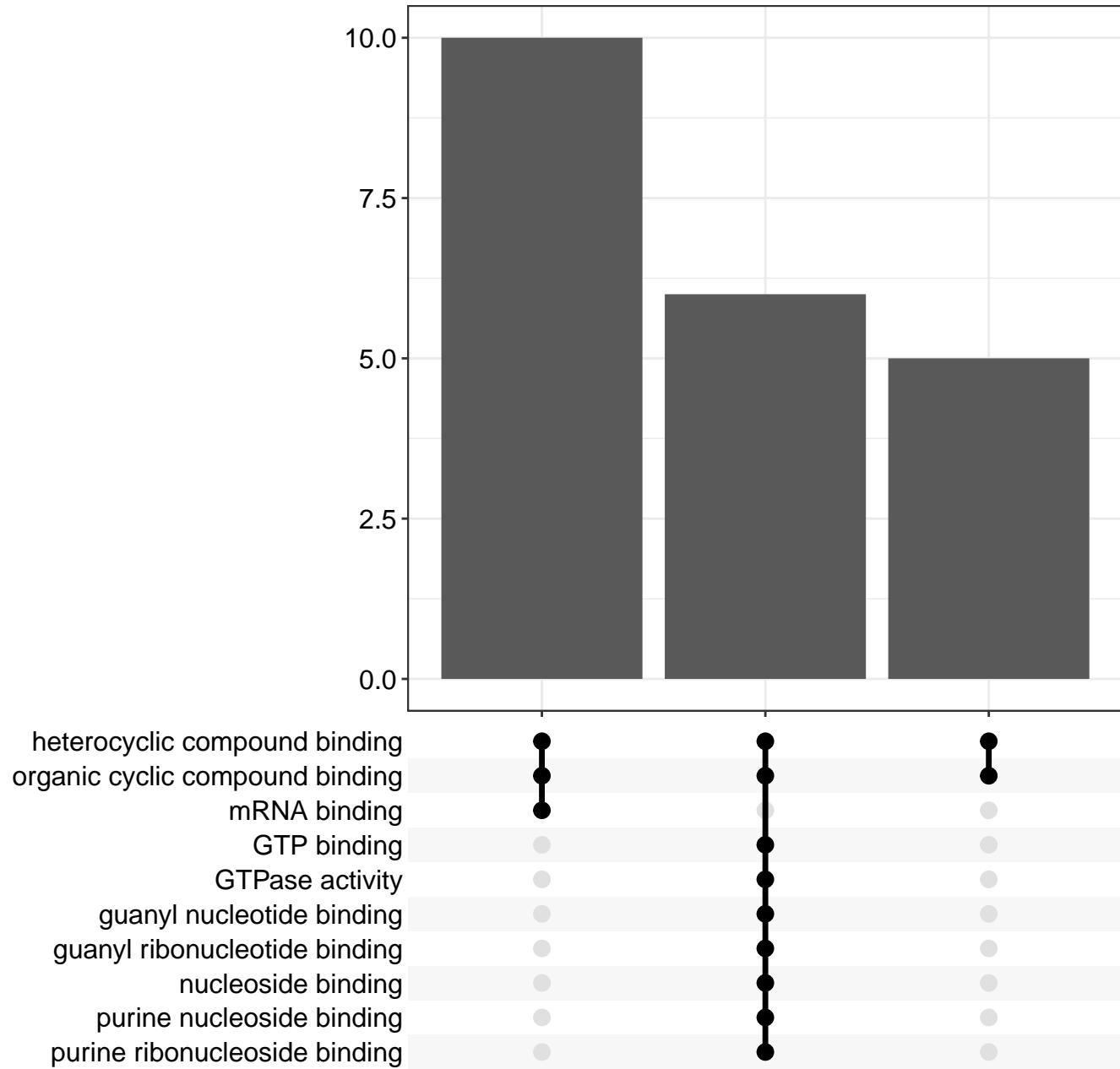
PUF3-TAP Up-regulated GO MF emapplot

mRNA binding

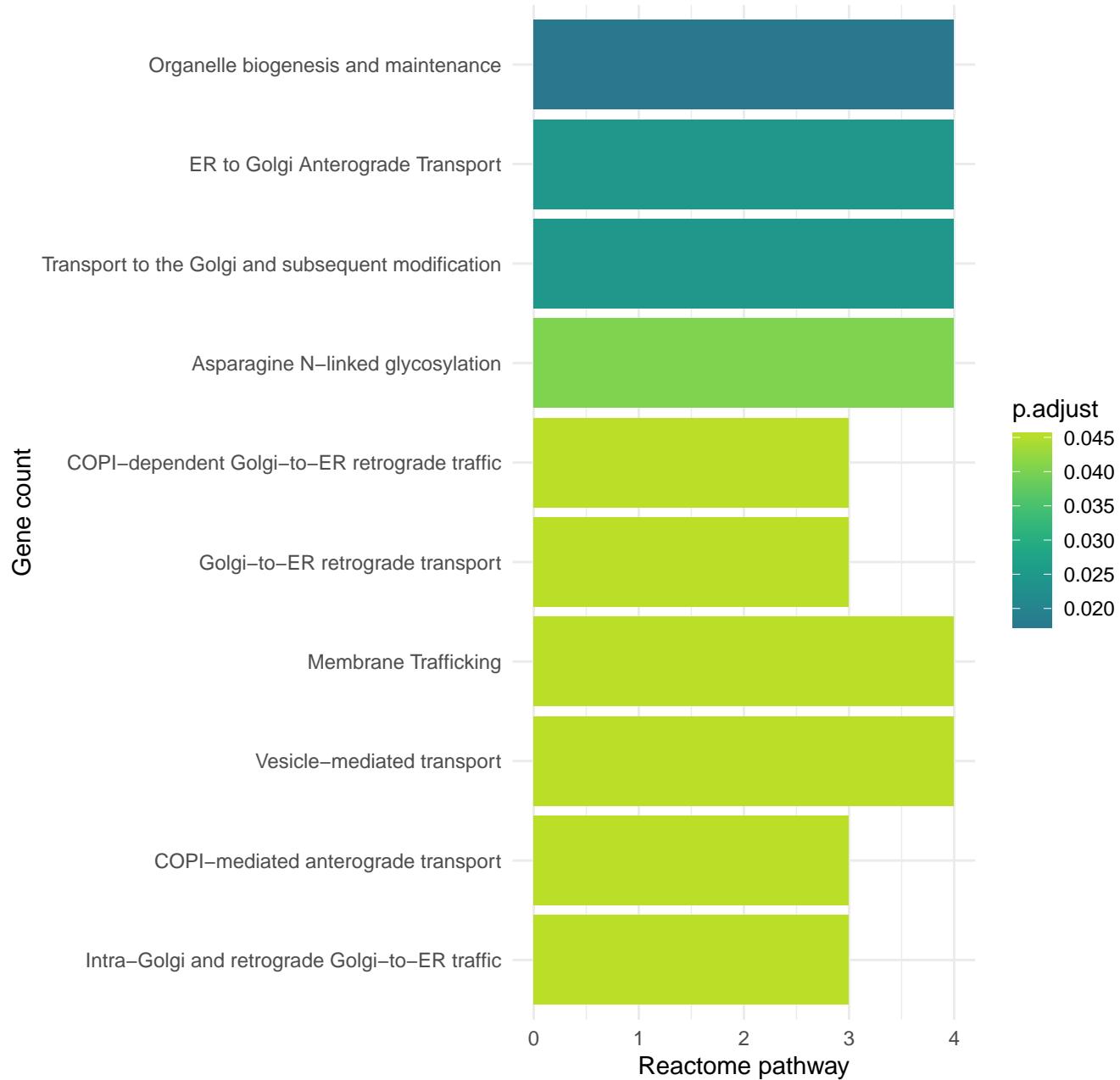




PUF3-TAP Up-regulated GO MF upsetplot

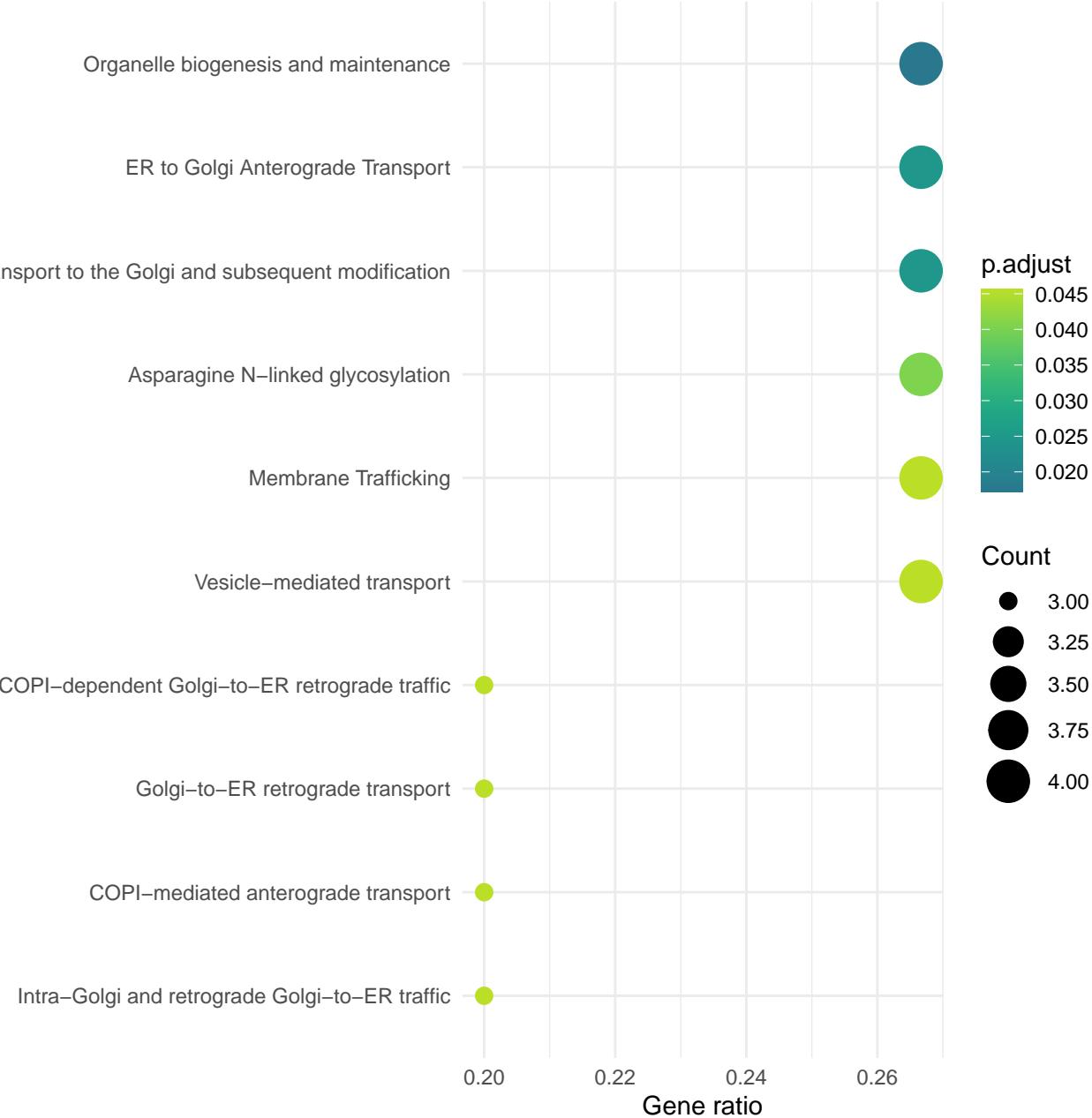


PUF3-TAP Up-regulated Reactome barplot

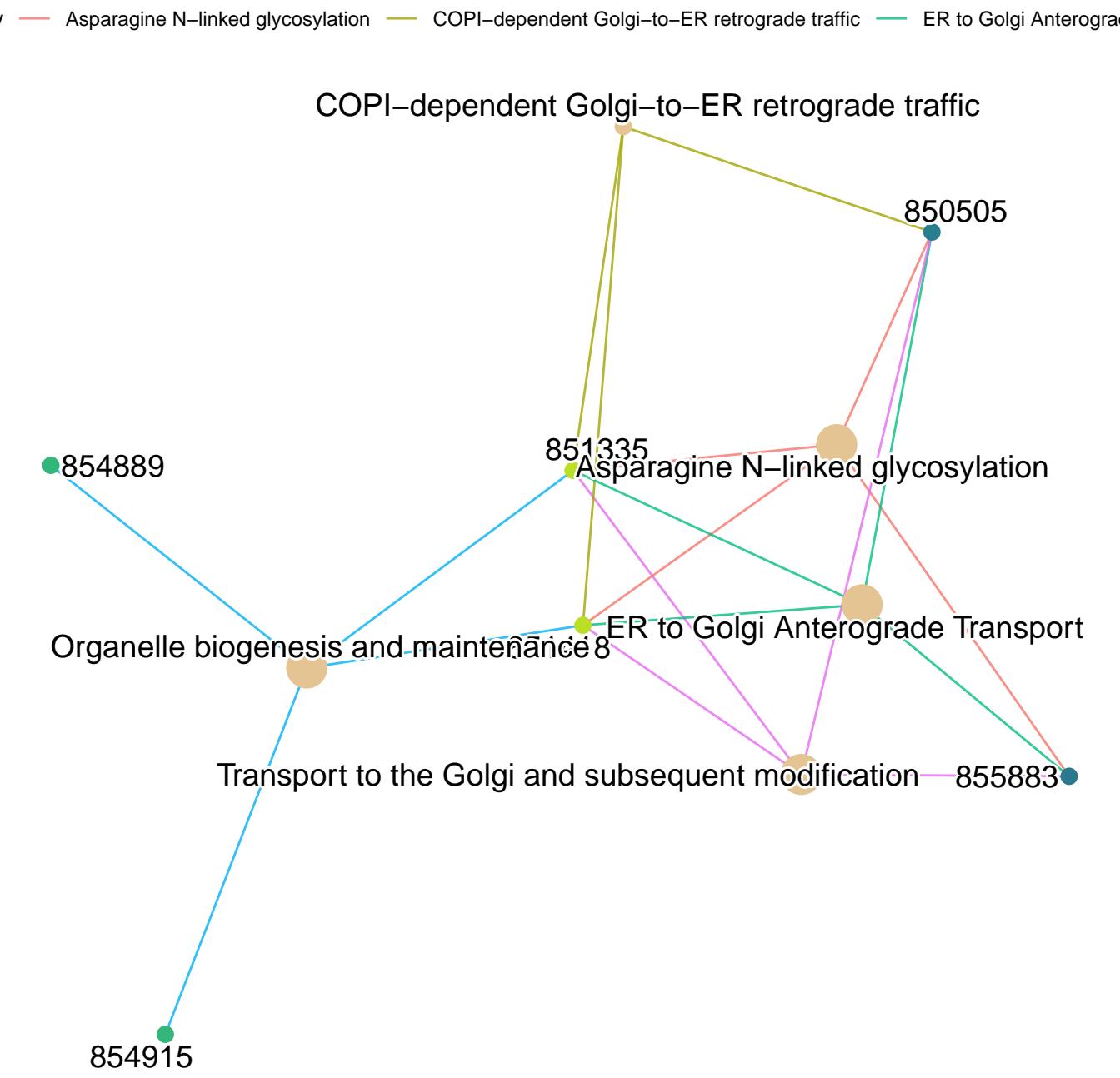


PUF3–TAP Up-regulated Reactome dotplot

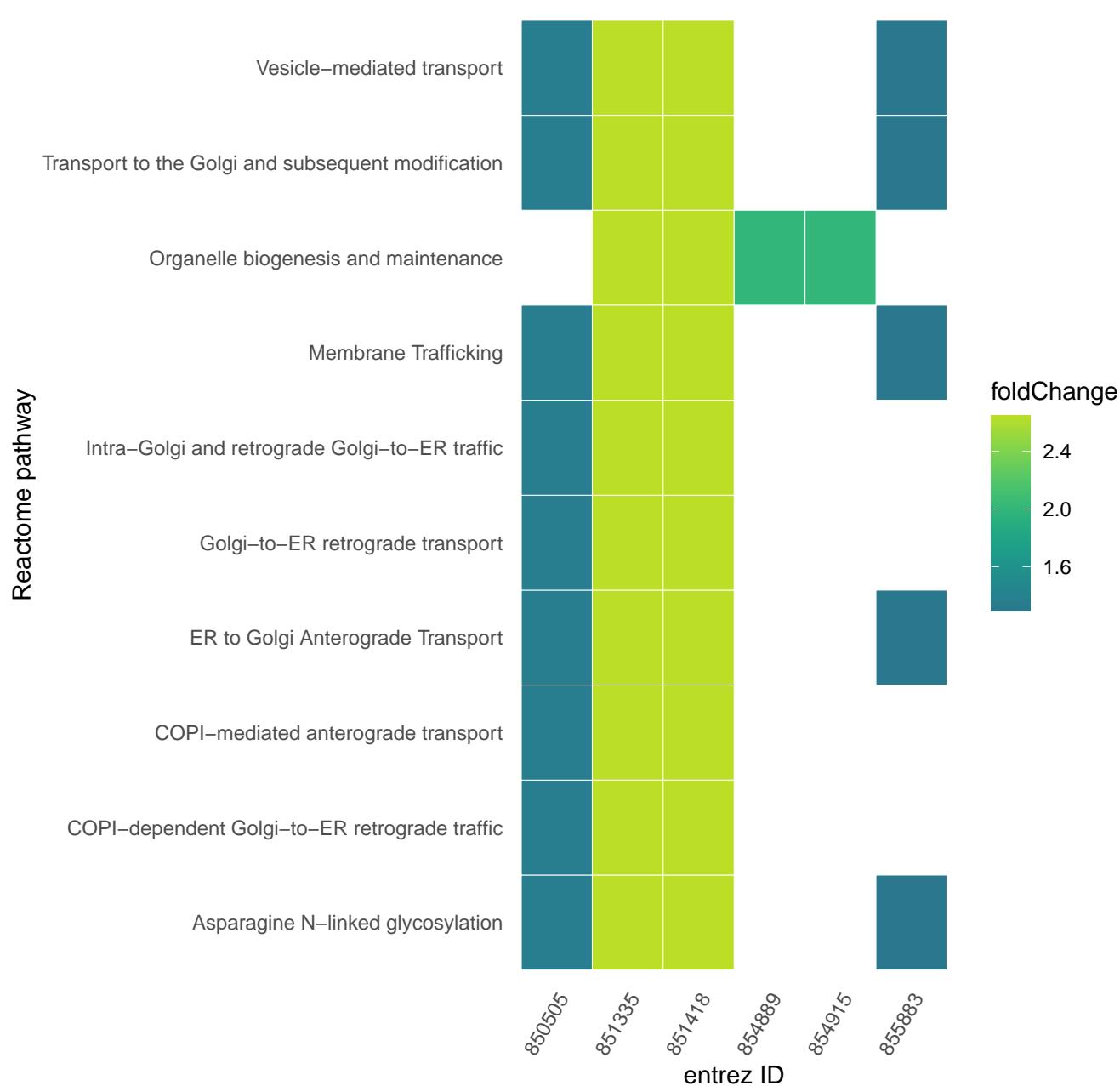
Reactome pathway



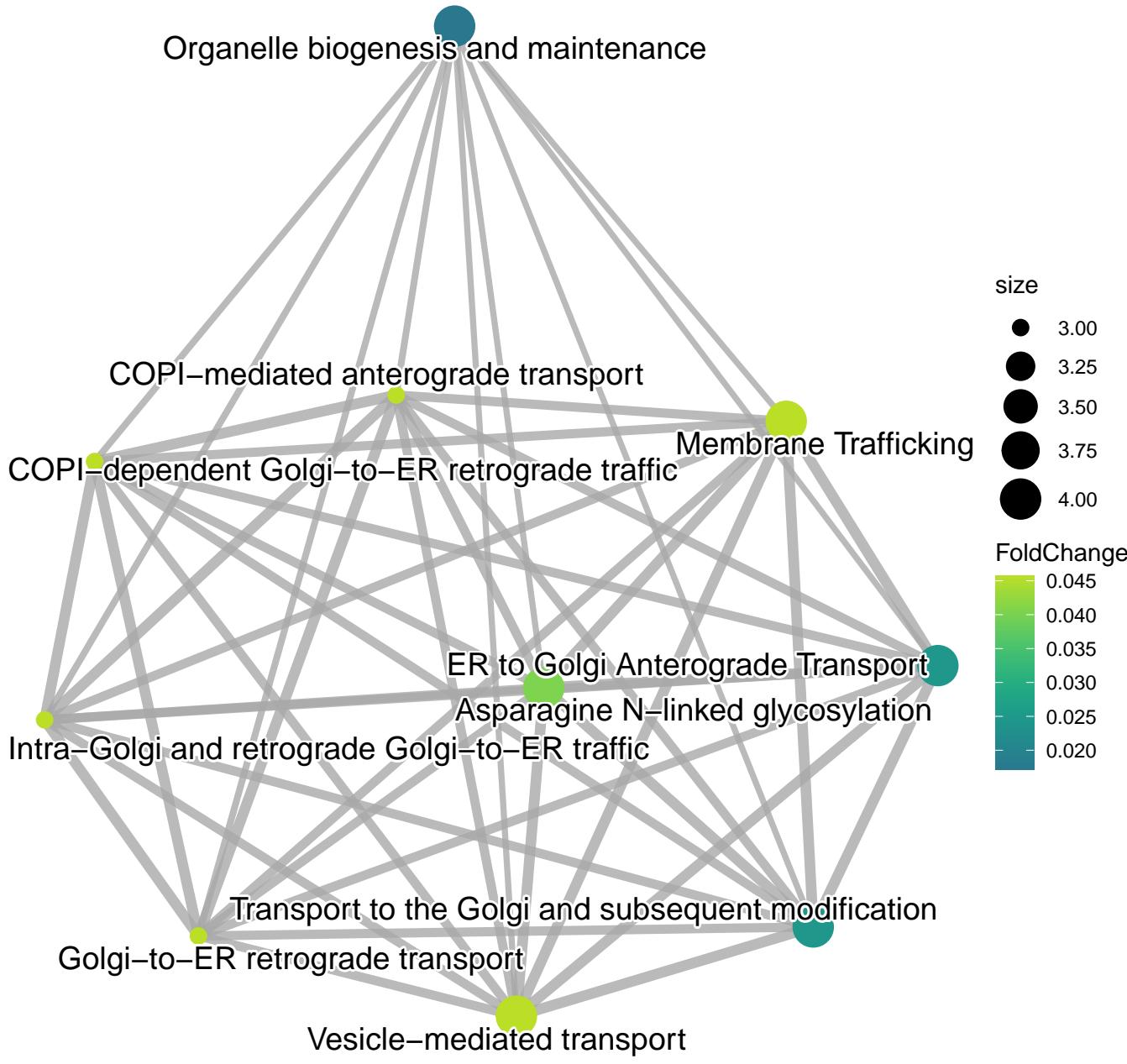
PUF3-TAP Up-regulated Reactome cnetplot



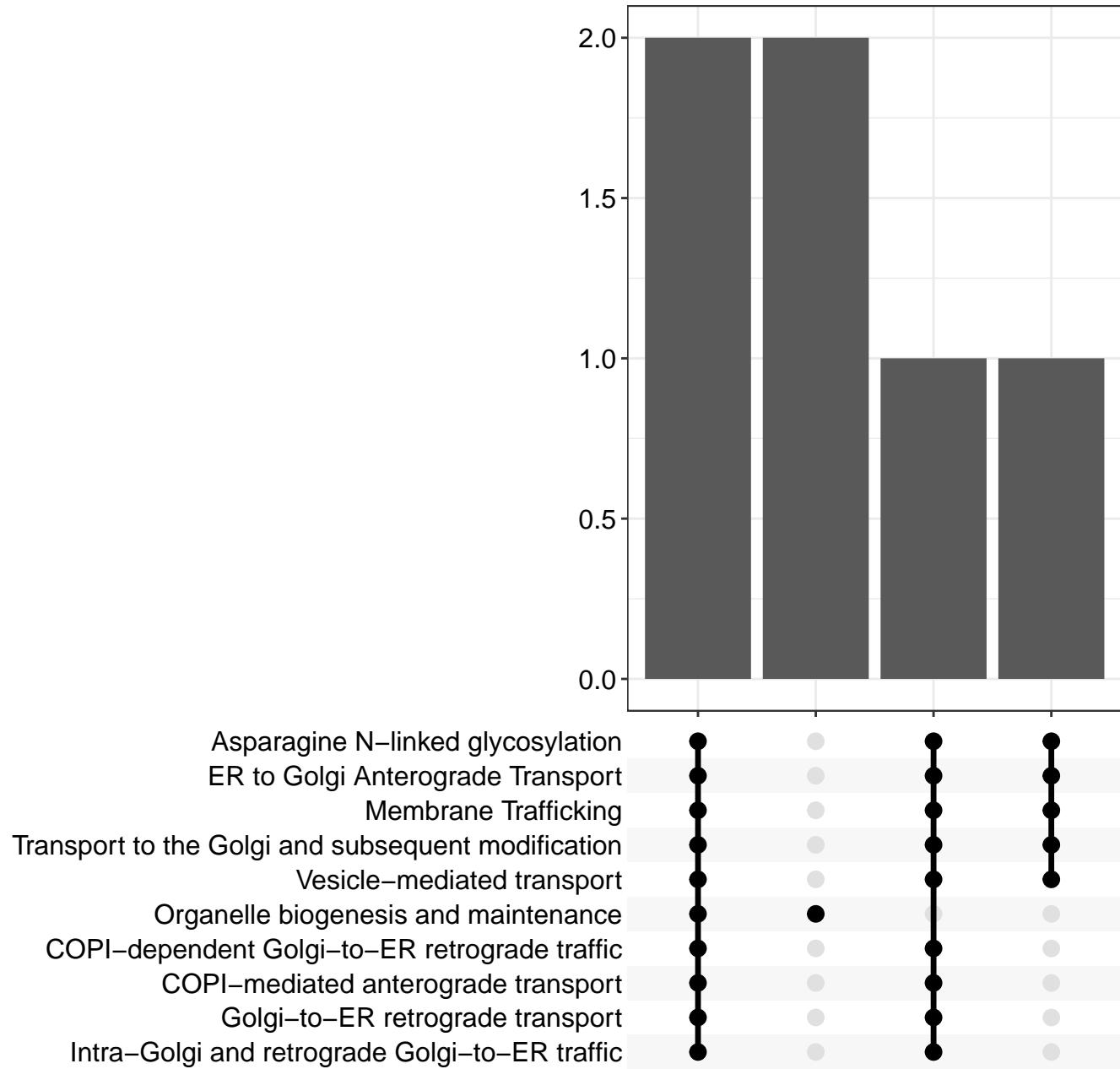
PUF3-TAP Up-regulated Reactome heatplot



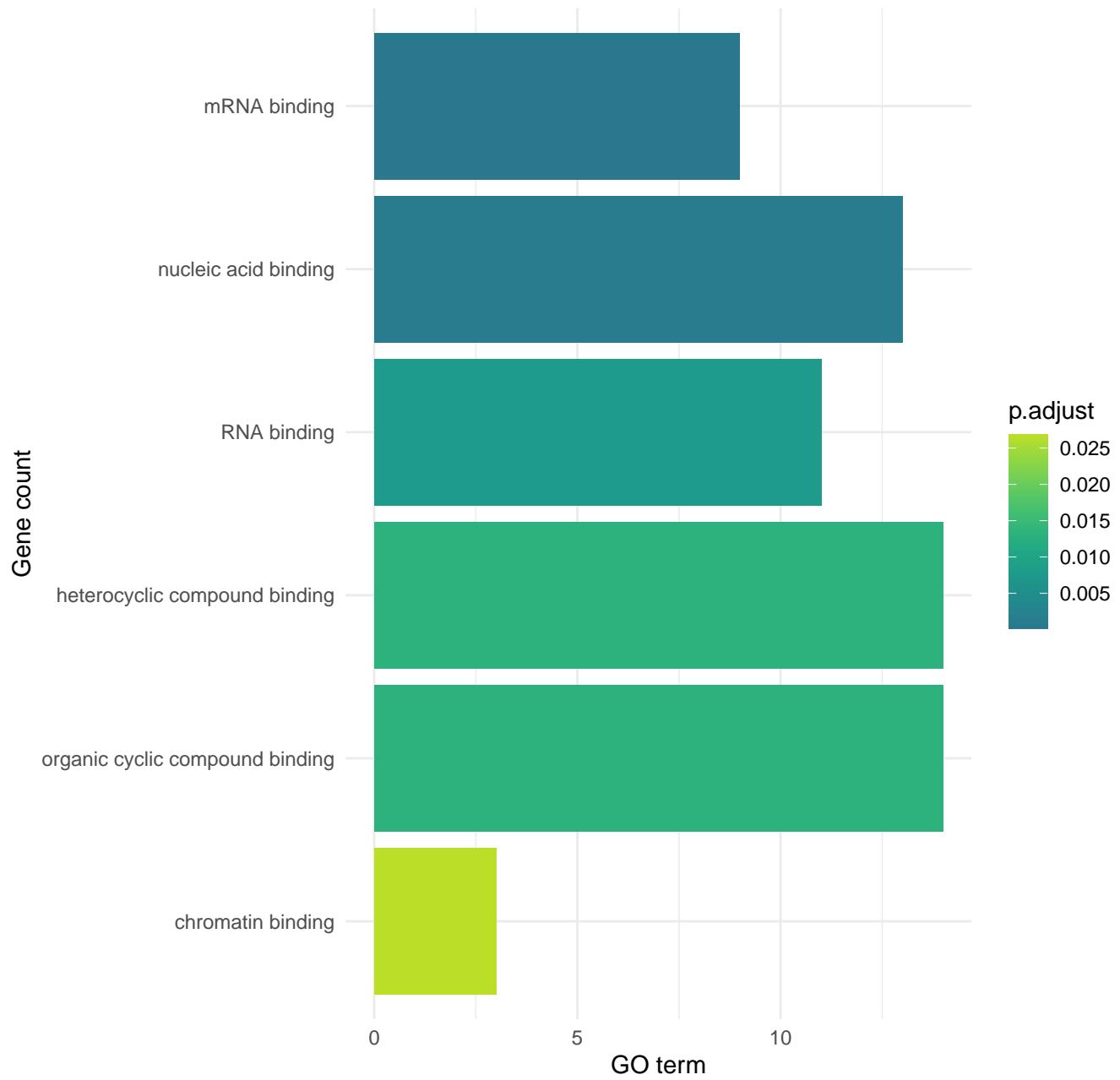
PUF3-TAP Up-regulated Reactome emapplot



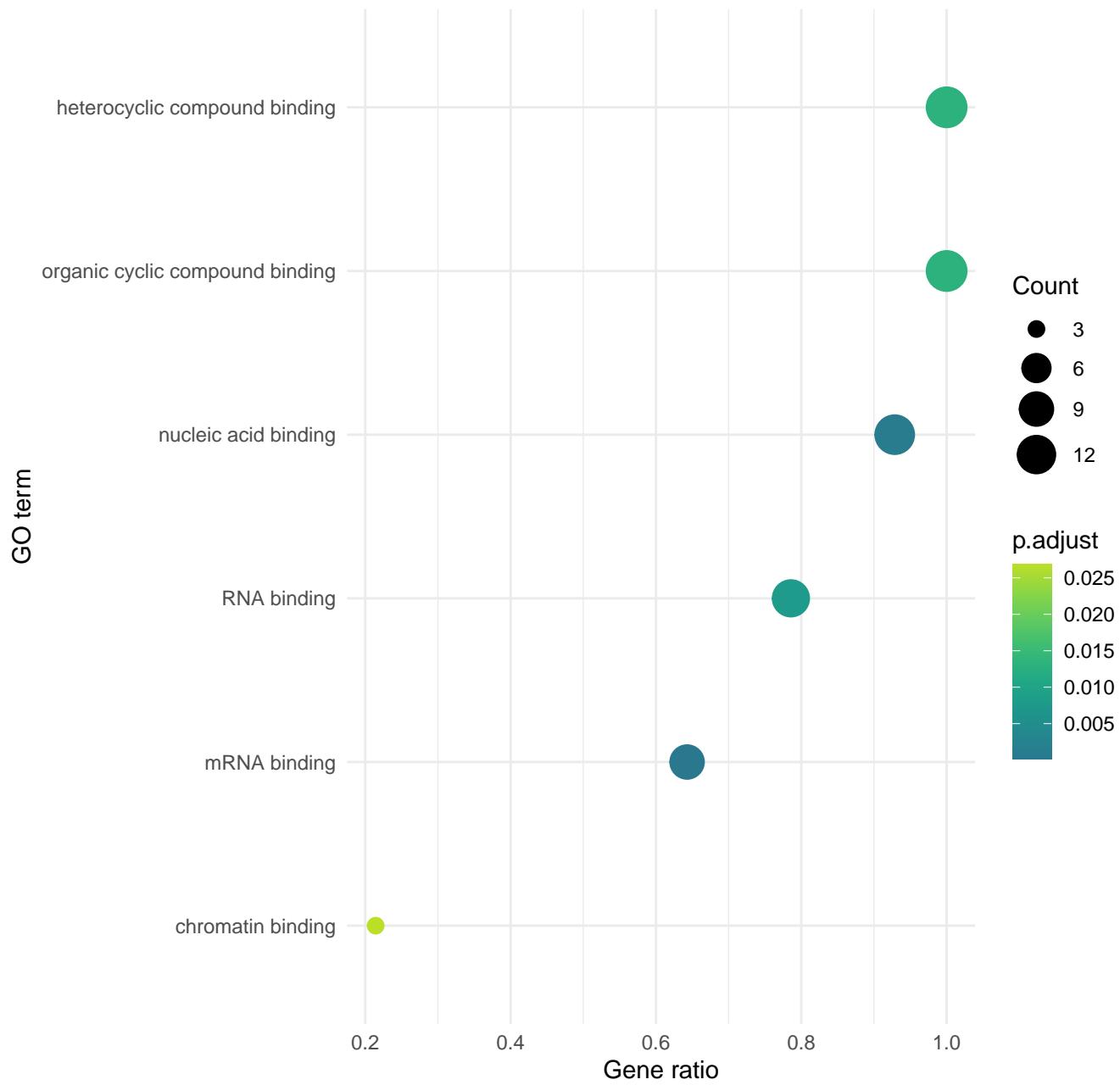
PUF3-TAP Up-regulated Reactome up



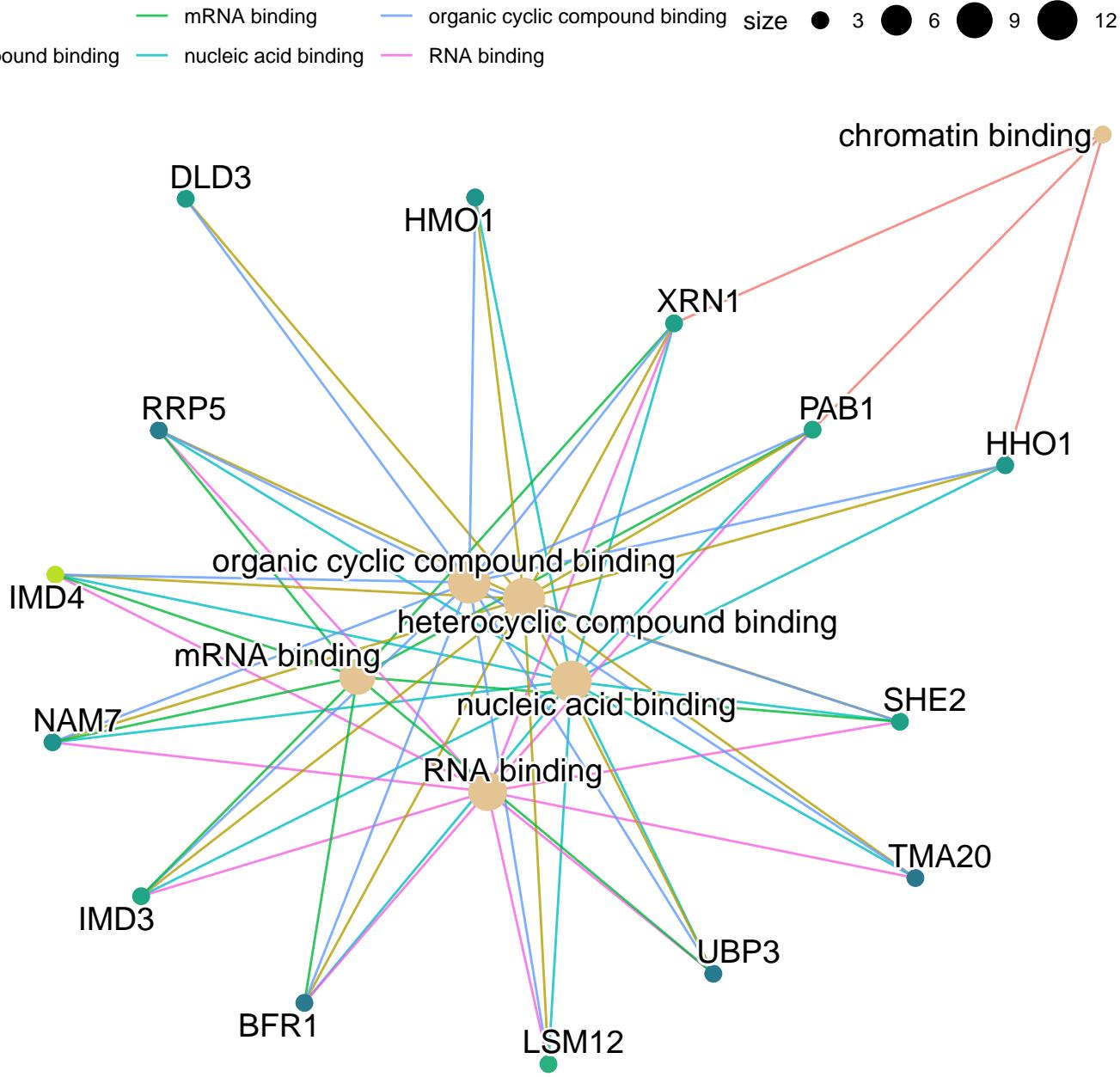
IST3–TAP Up-regulated GO MF barplot



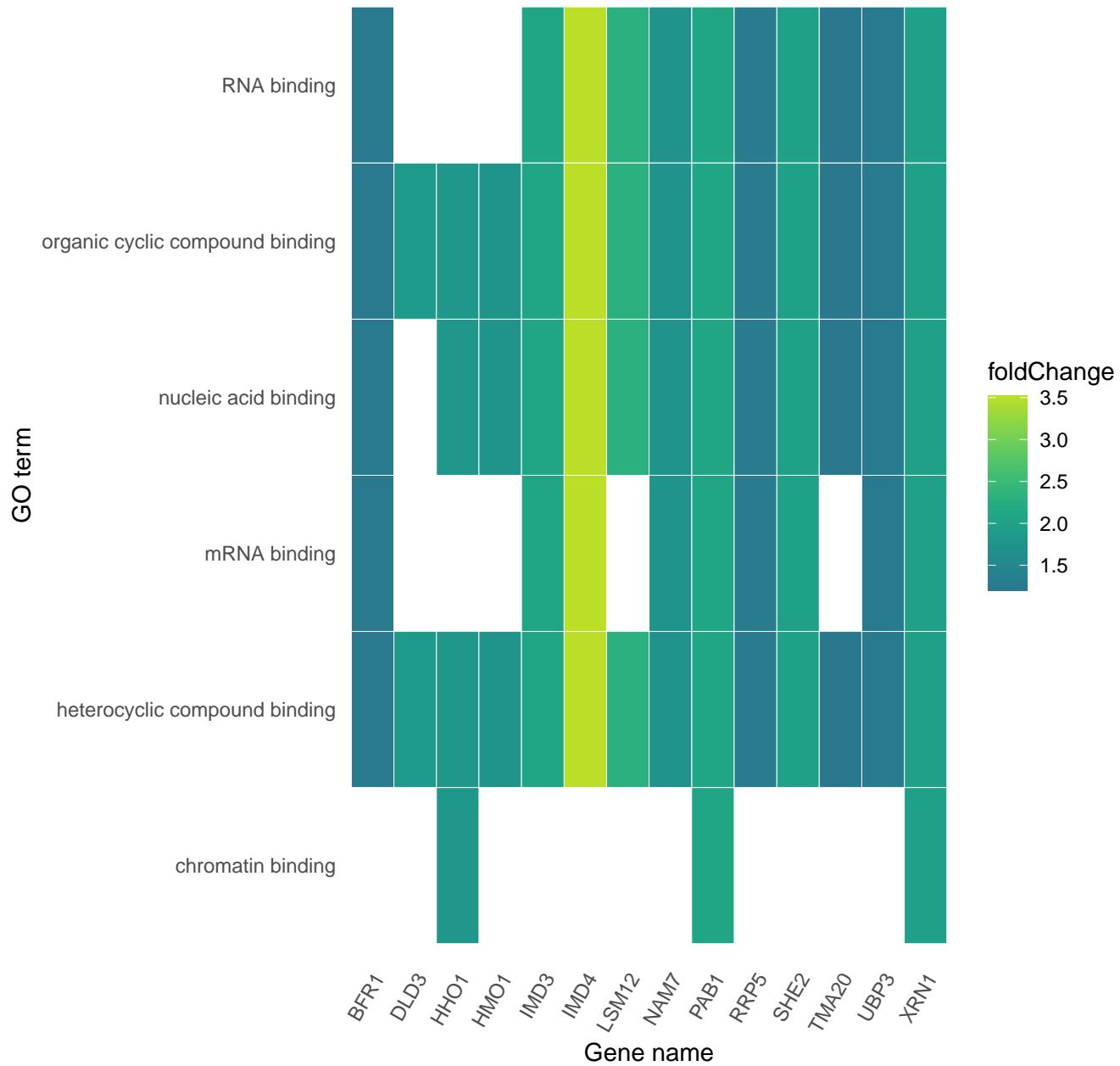
IST3–TAP Up-regulated GO MF dotplot



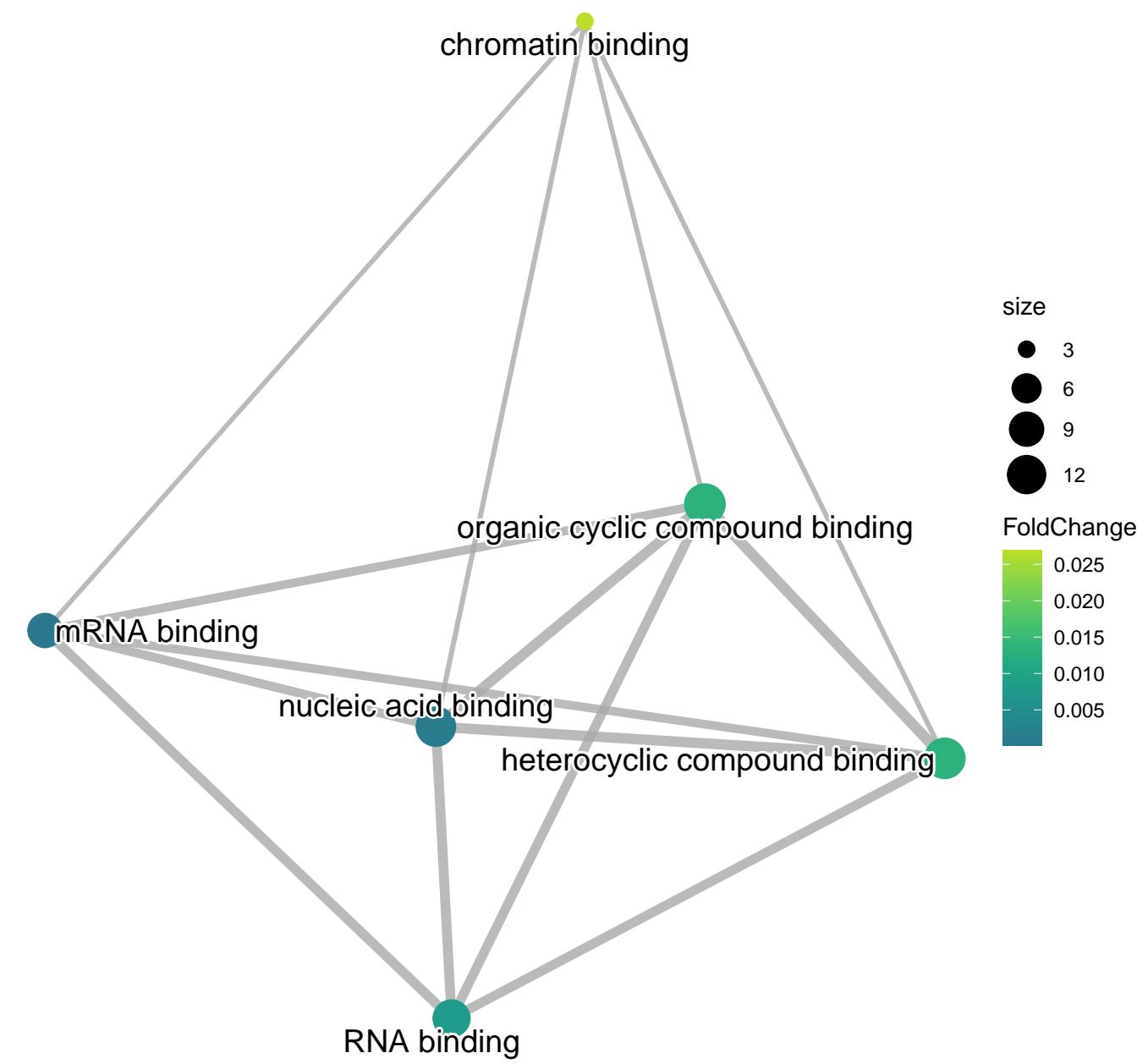
IST3-TAP Up-regulated GO MF cnetplot

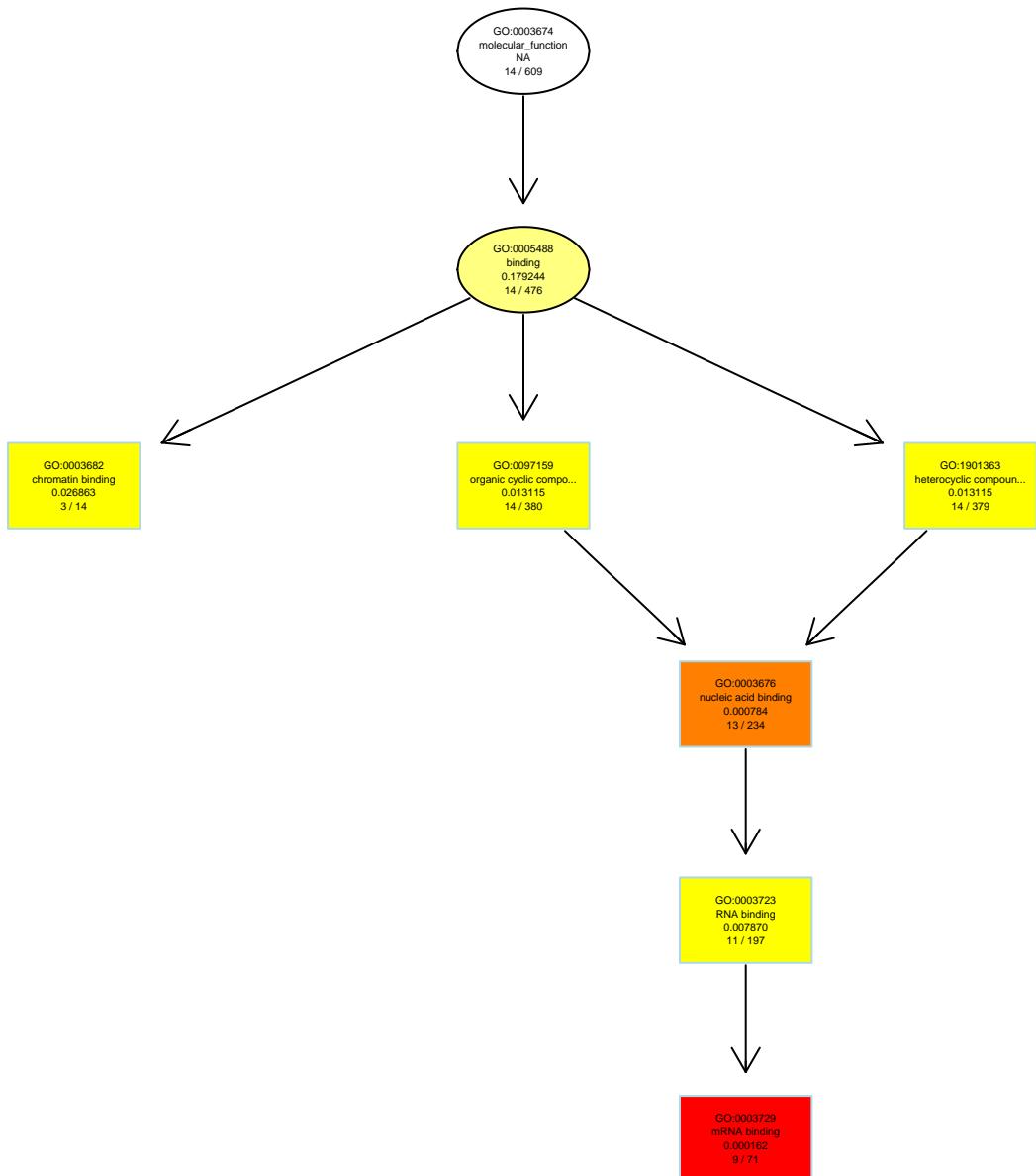


IST3-TAP Up-regulated GO MF heatplot

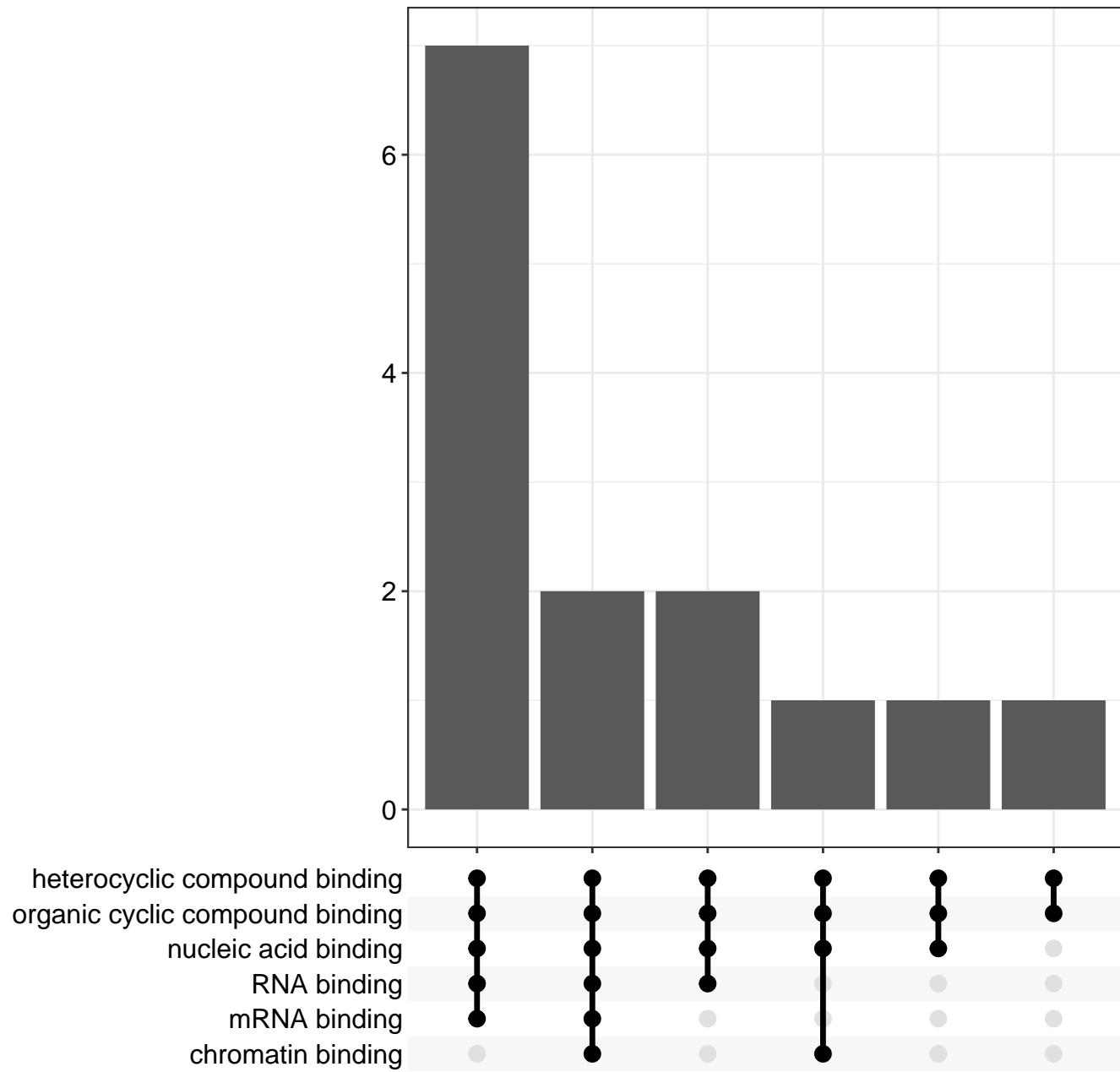


IST3-TAP Up-regulated GO MF emapplot

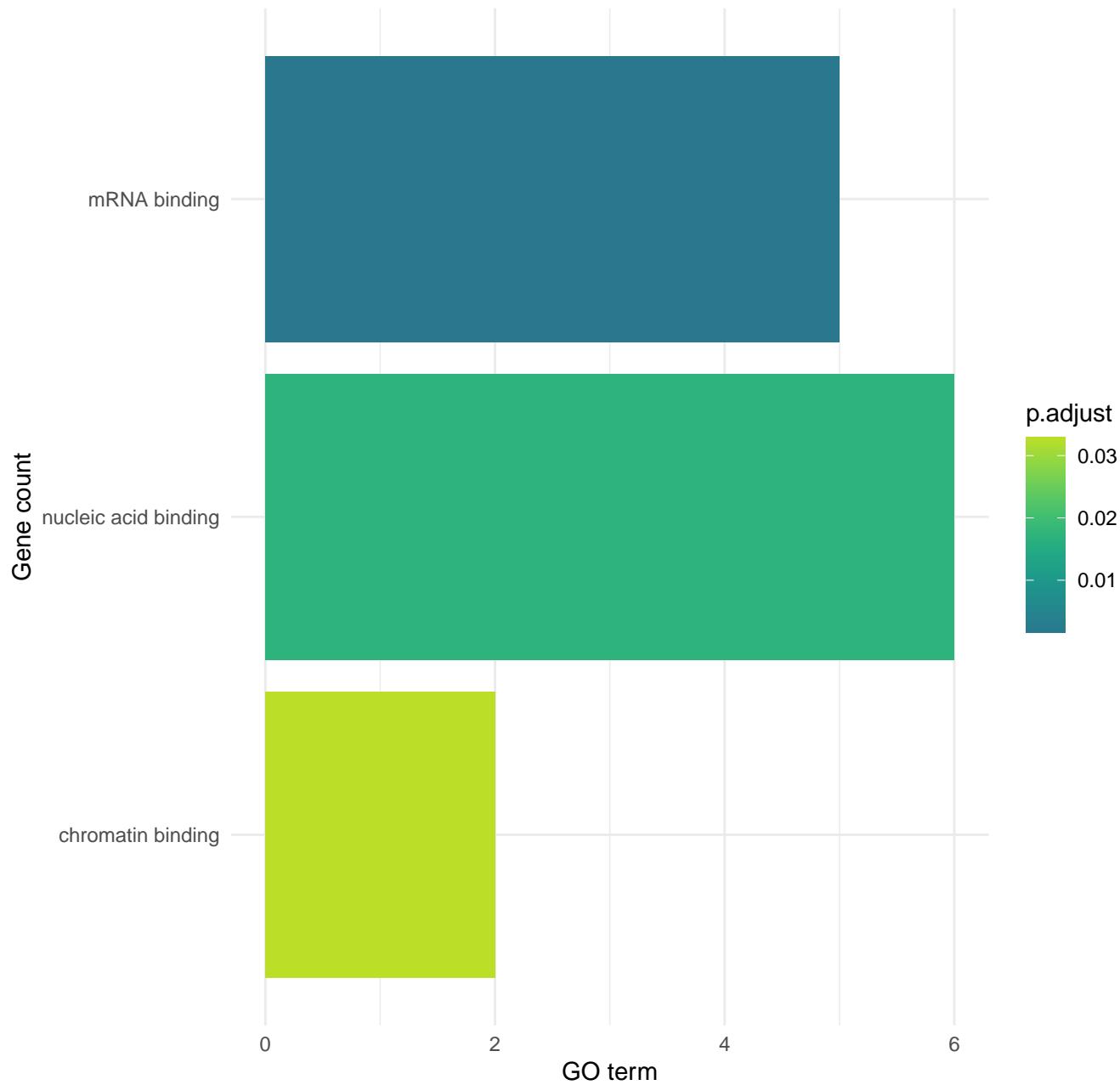




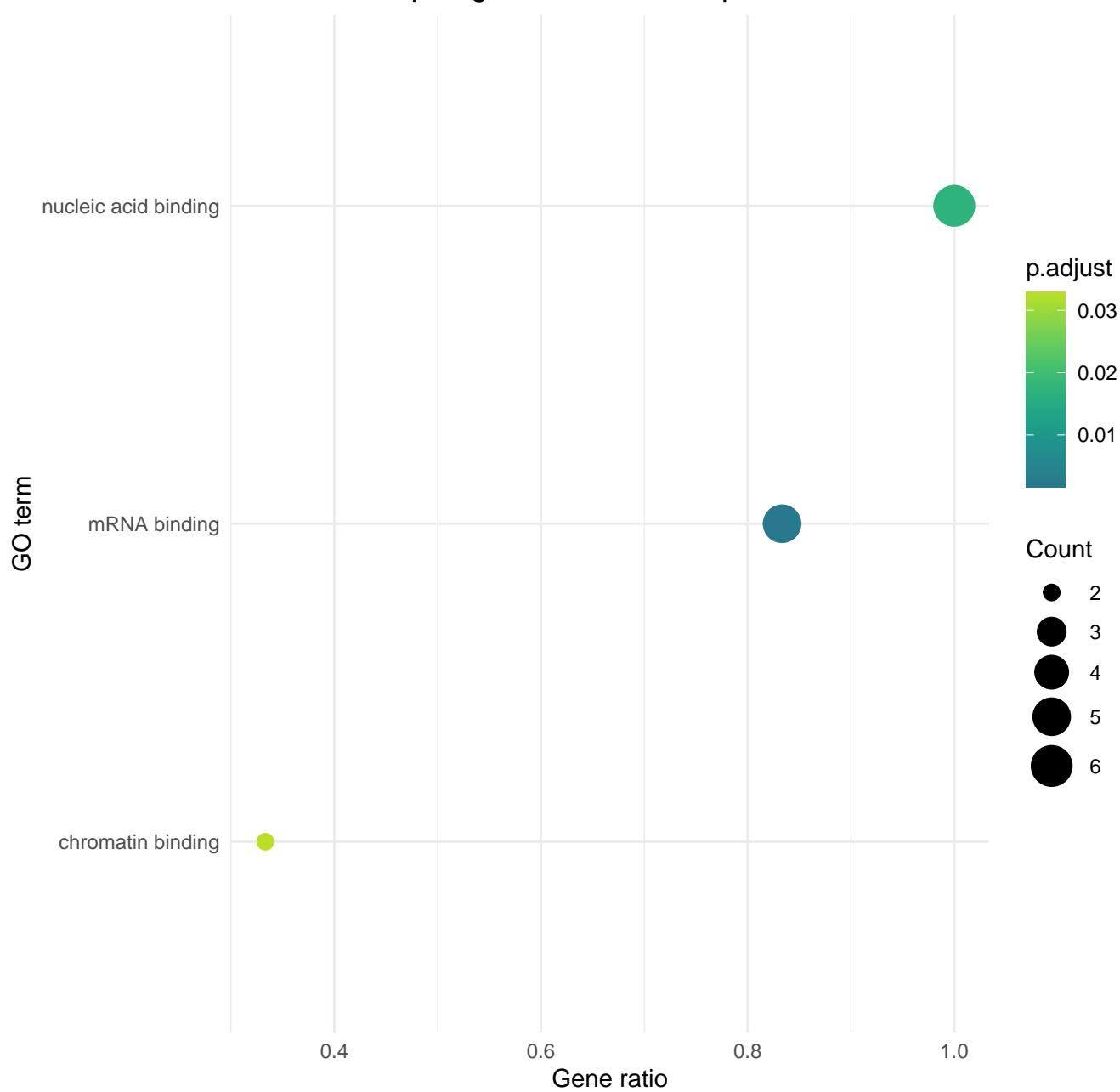
IST3-TAP Up-regulated GO MF upsetplot



NDC1-TAP Up-regulated GO MF barplot

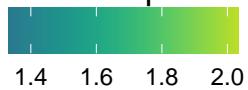


NDC1-TAP Up-regulated GO MF dotplot



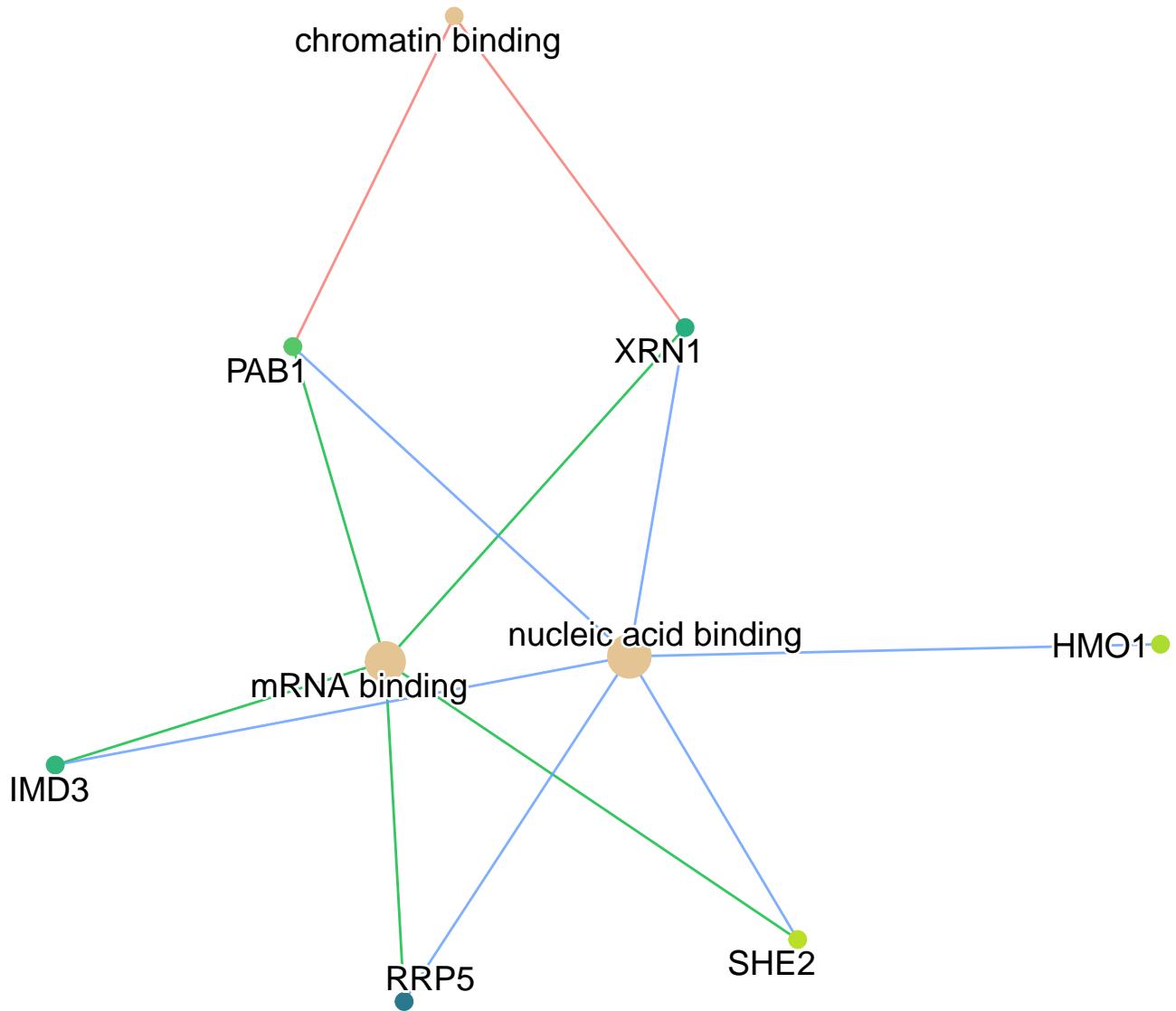
NDC1-TAP Up-regulated GO MF cnetplot

● 4 ● 5 ● 6 FoldChange

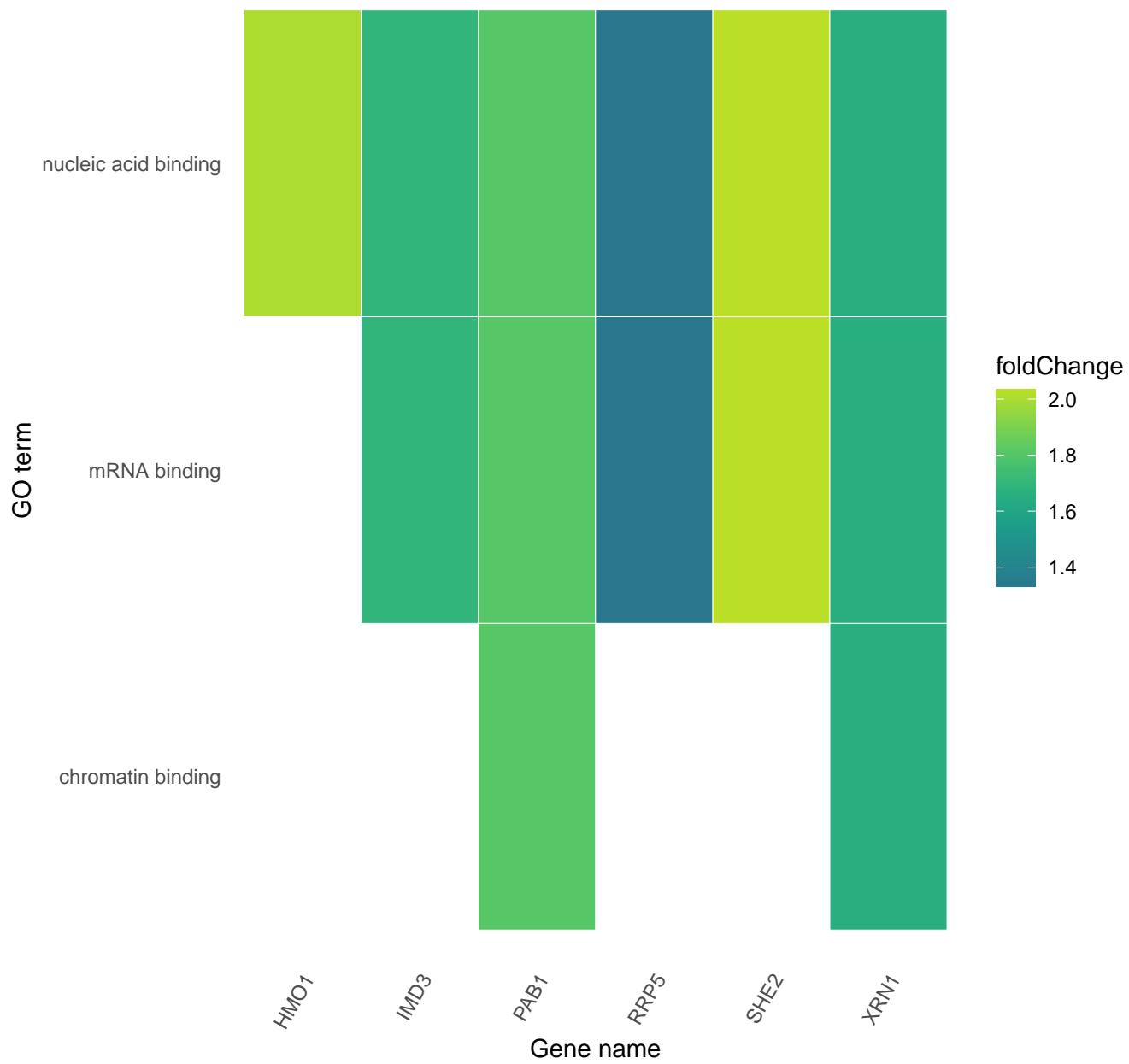


category

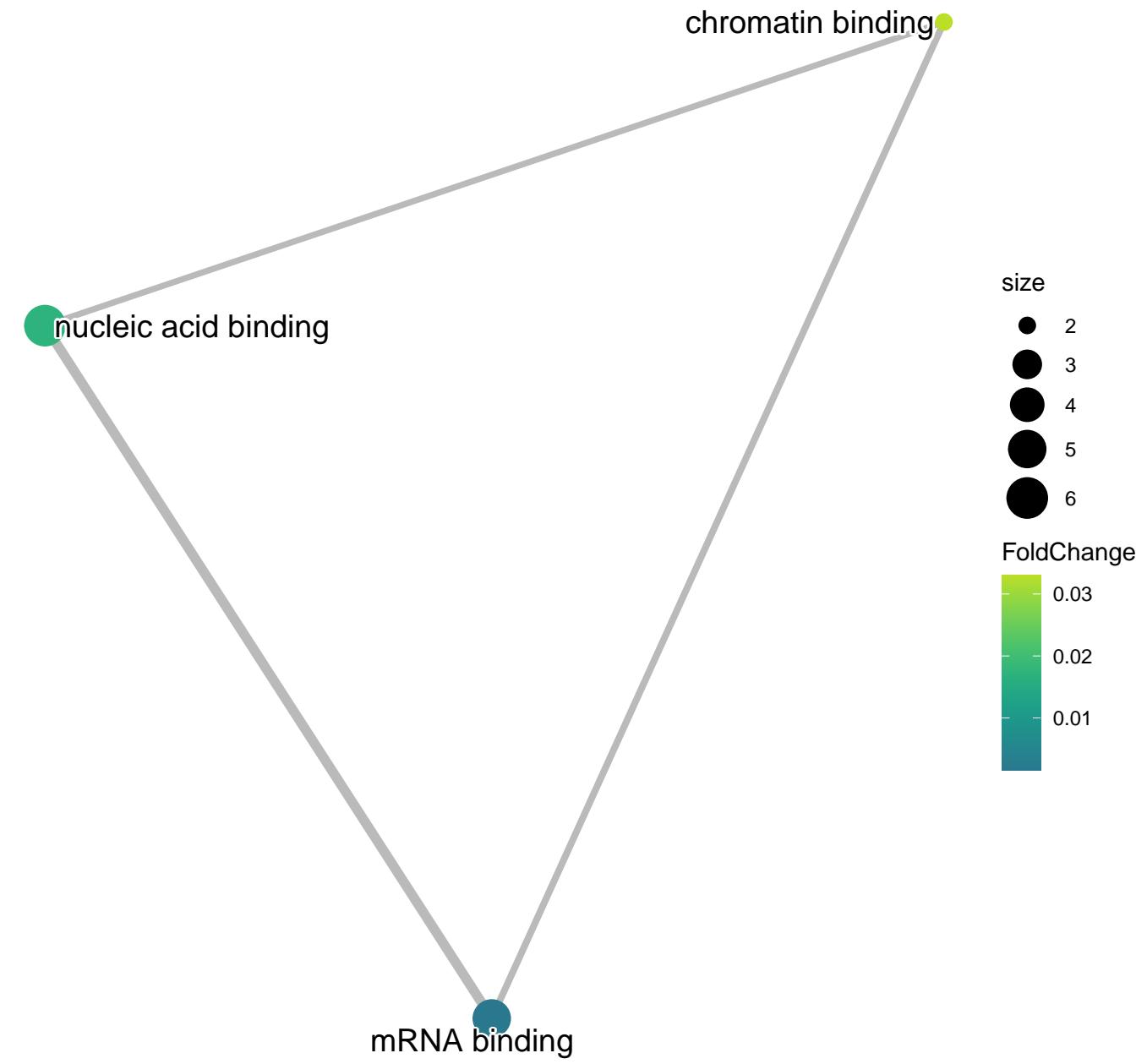
chromatin binding mRNA binding

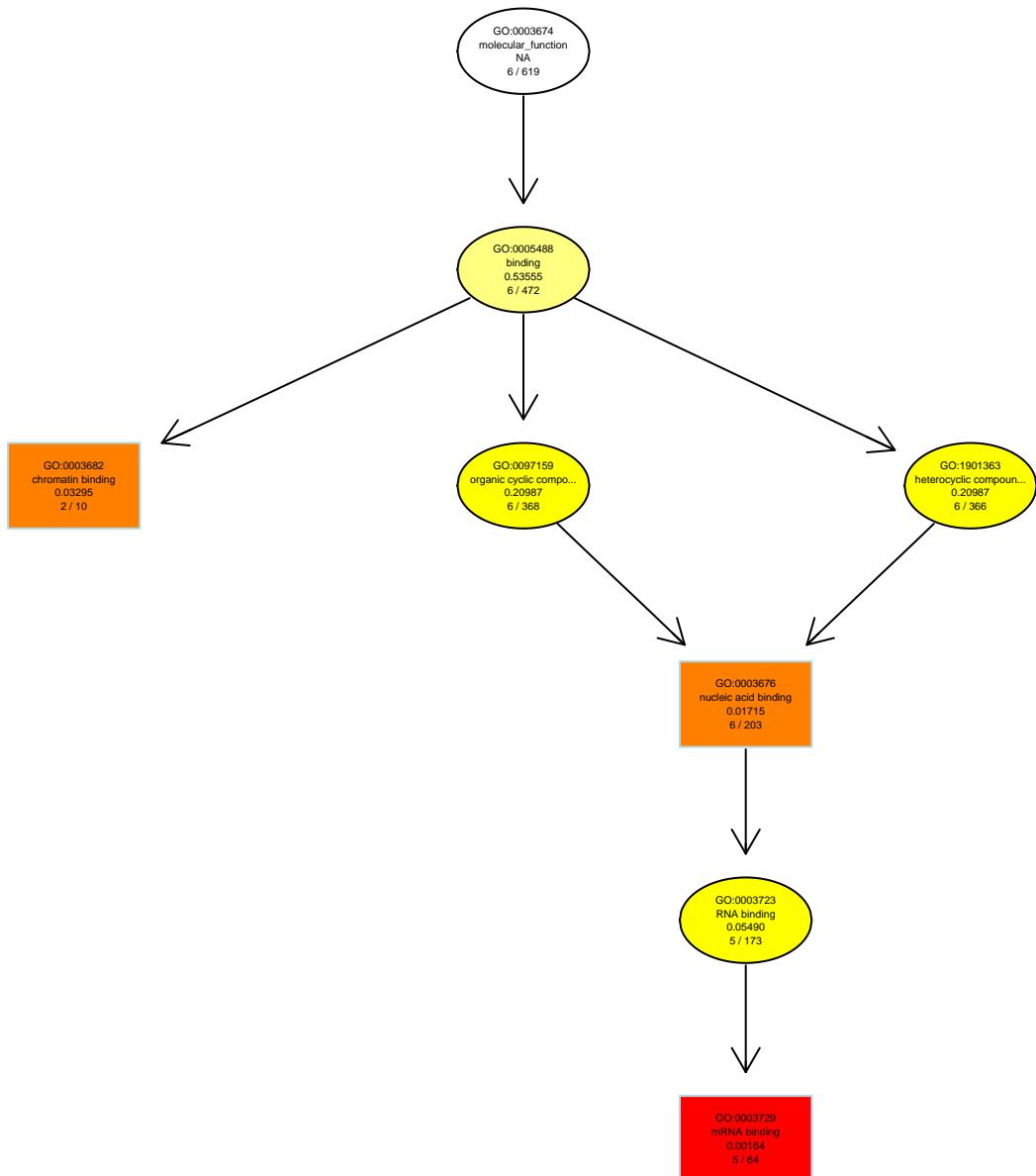


NDC1-TAP Up-regulated GO MF heatplot

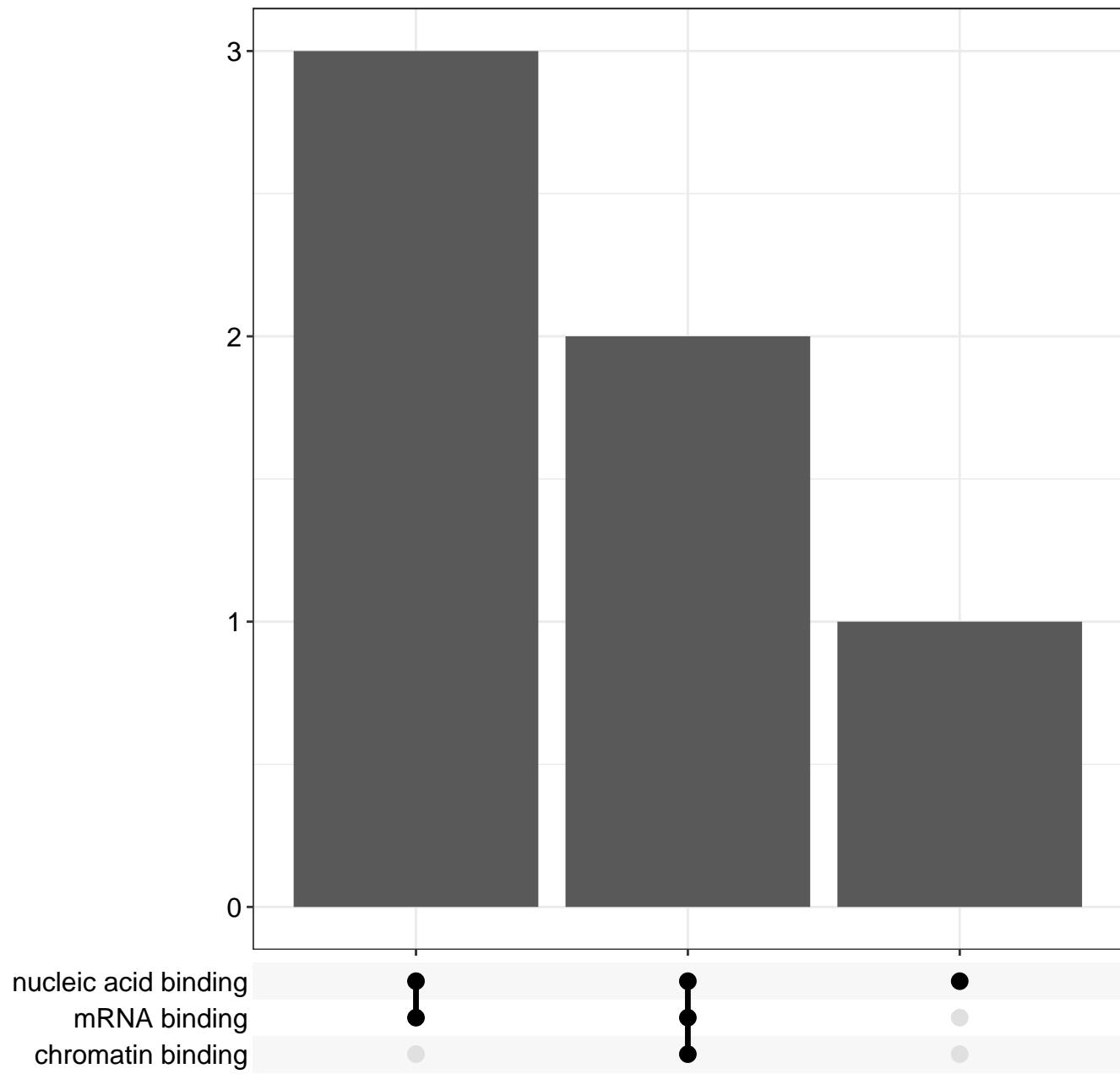


NDC1-TAP Up-regulated GO MF emapplot

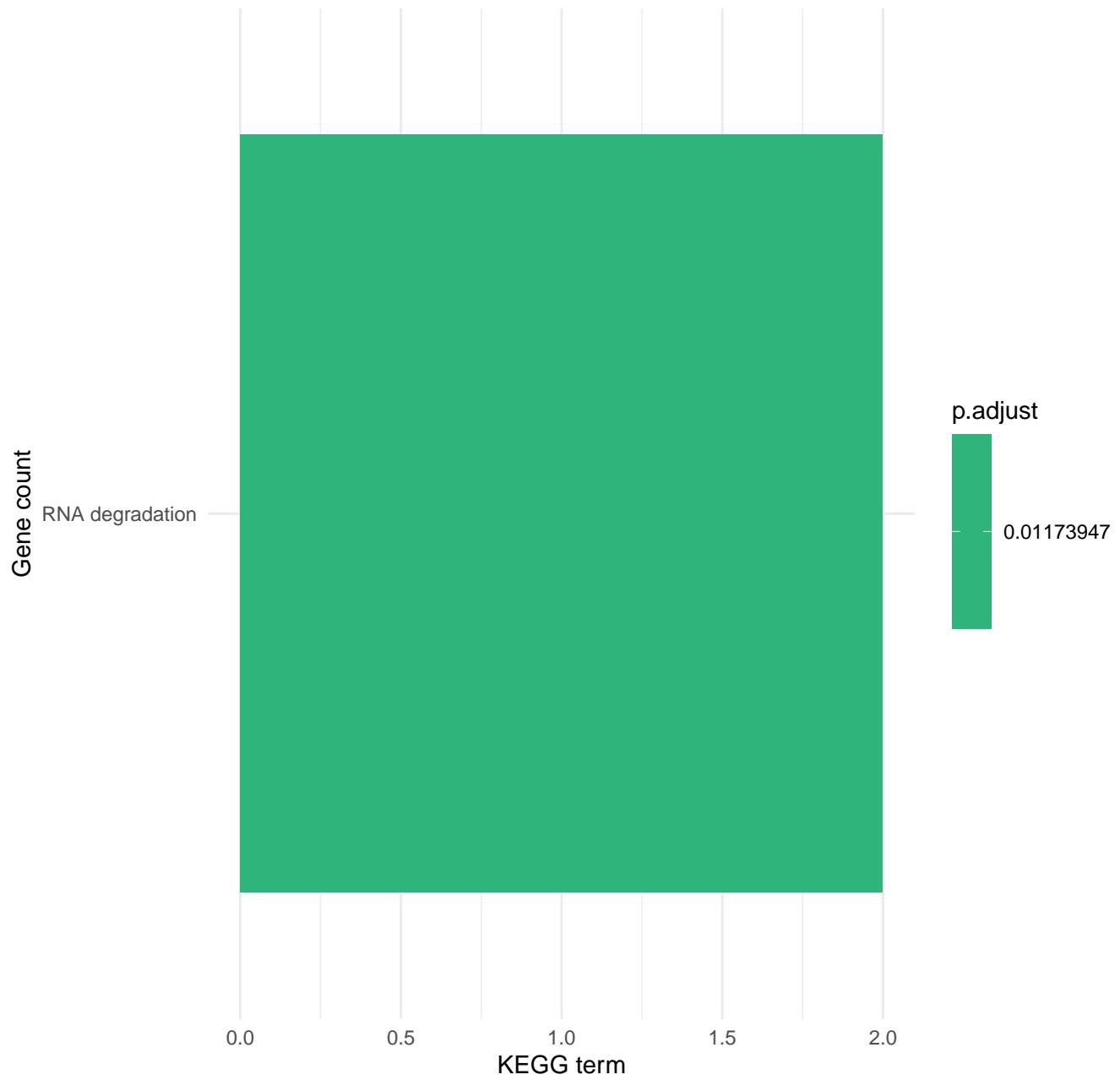




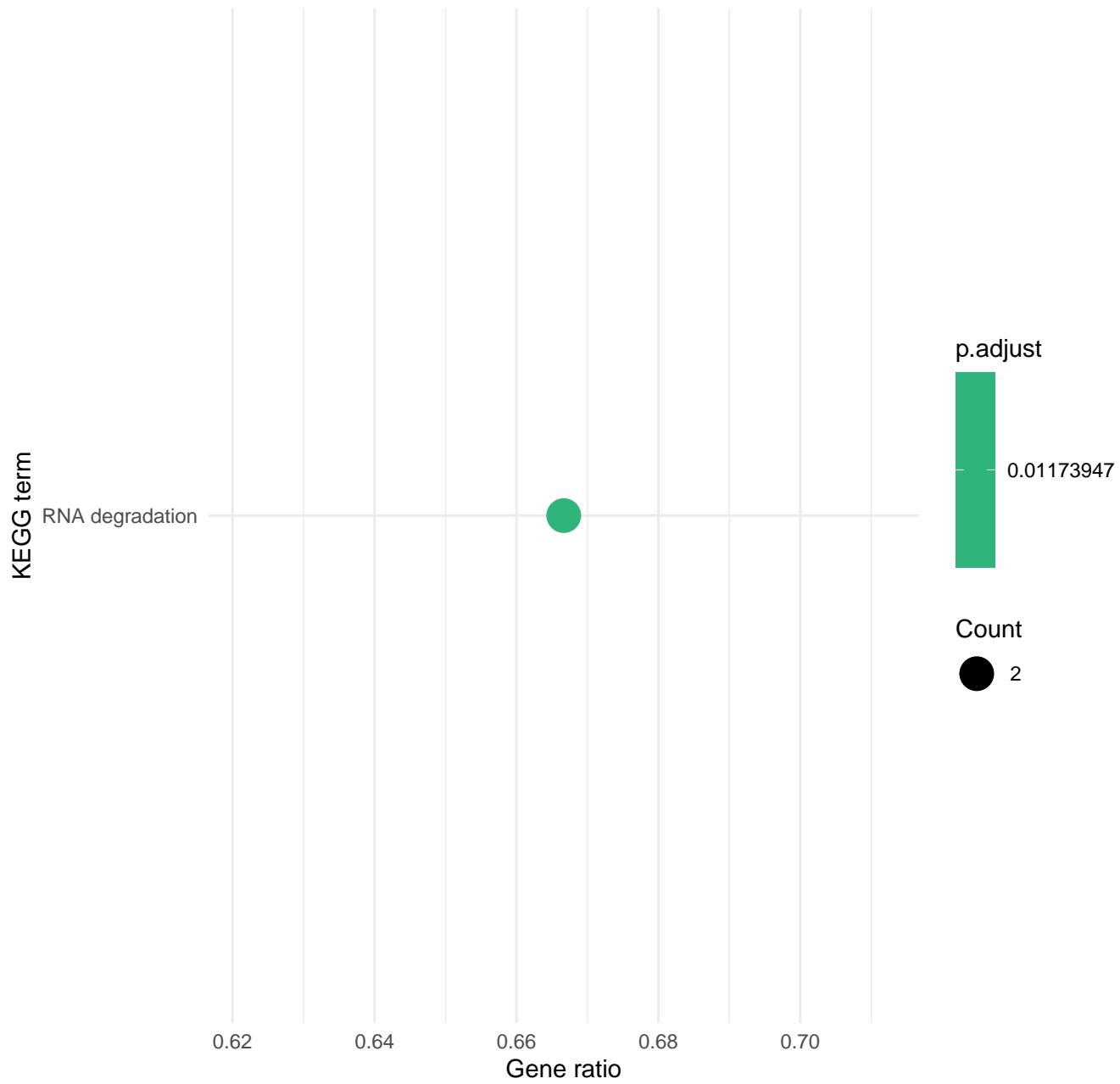
NDC1-TAP Up-regulated GO MF upsetplot



NDC1-TAP Up-regulated KEGG barplot



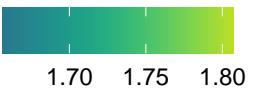
NDC1-TAP Up-regulated KEGG dotplot



NDC1-TAP Up-regulated KEGG dotplot

category RNA degradation

FoldChange



size 2

856912

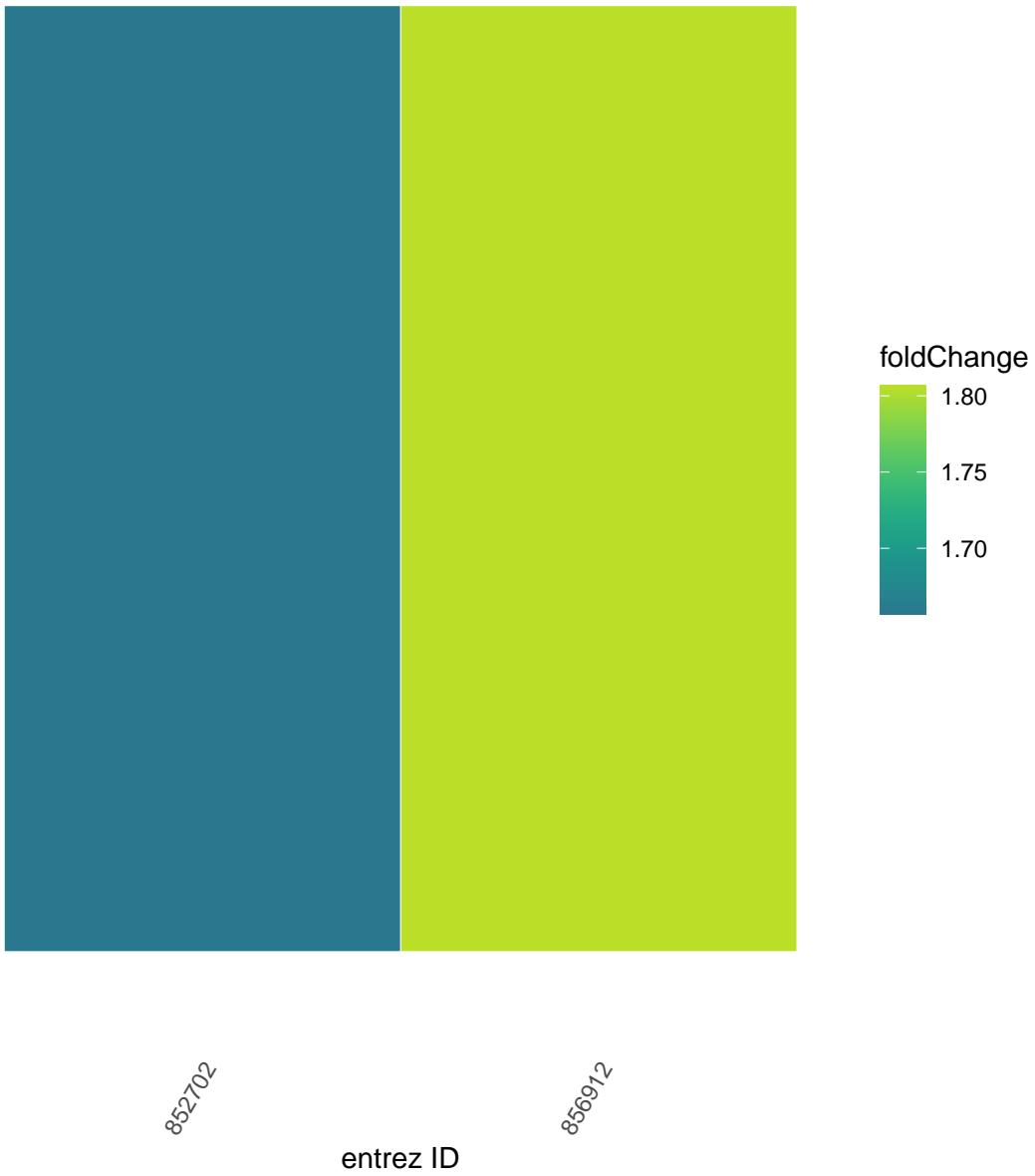
RNA degradation

852702

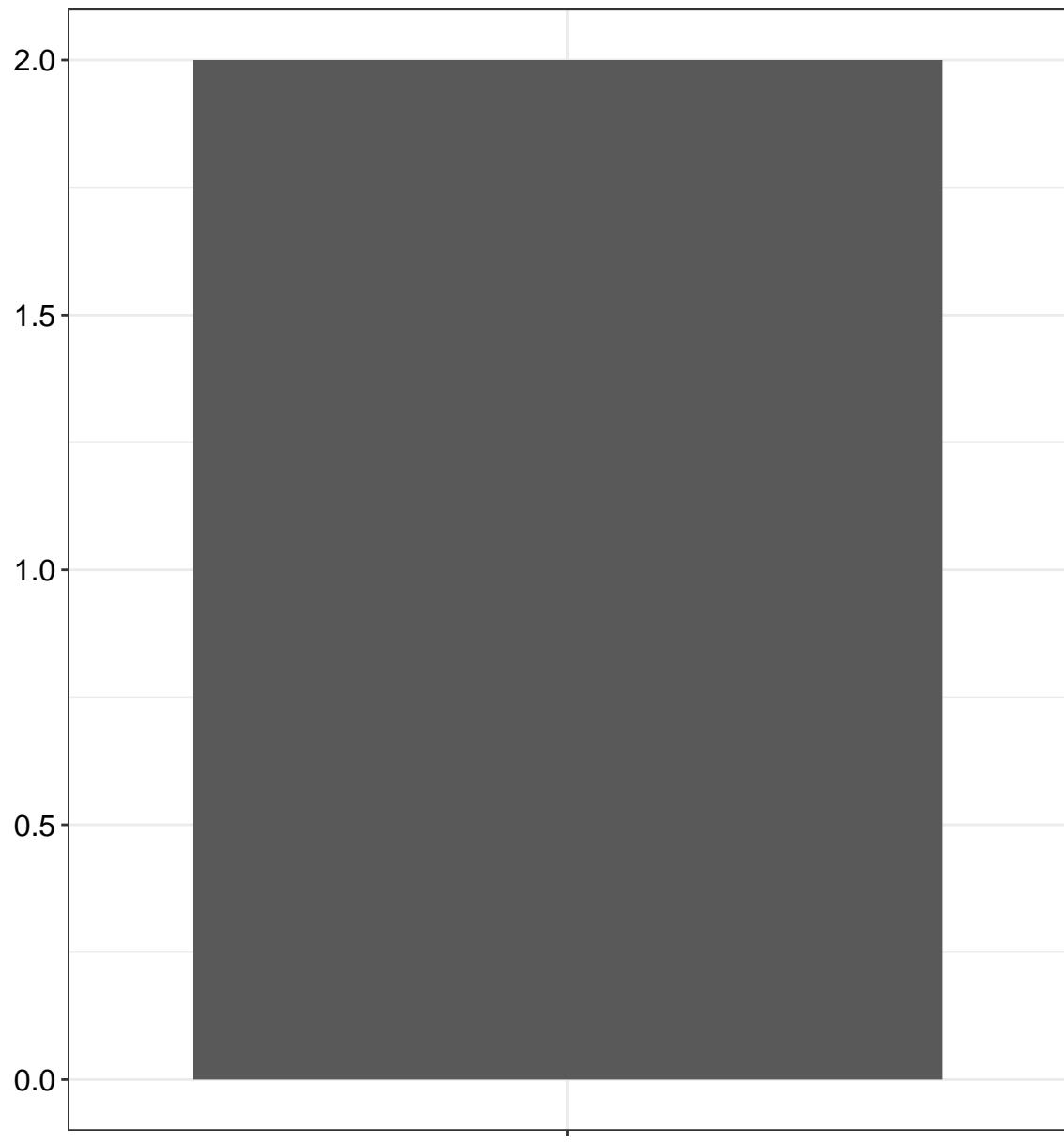
NDC1-TAP Up-regulated KEGG heatplot

KEGG term

RNA degradation

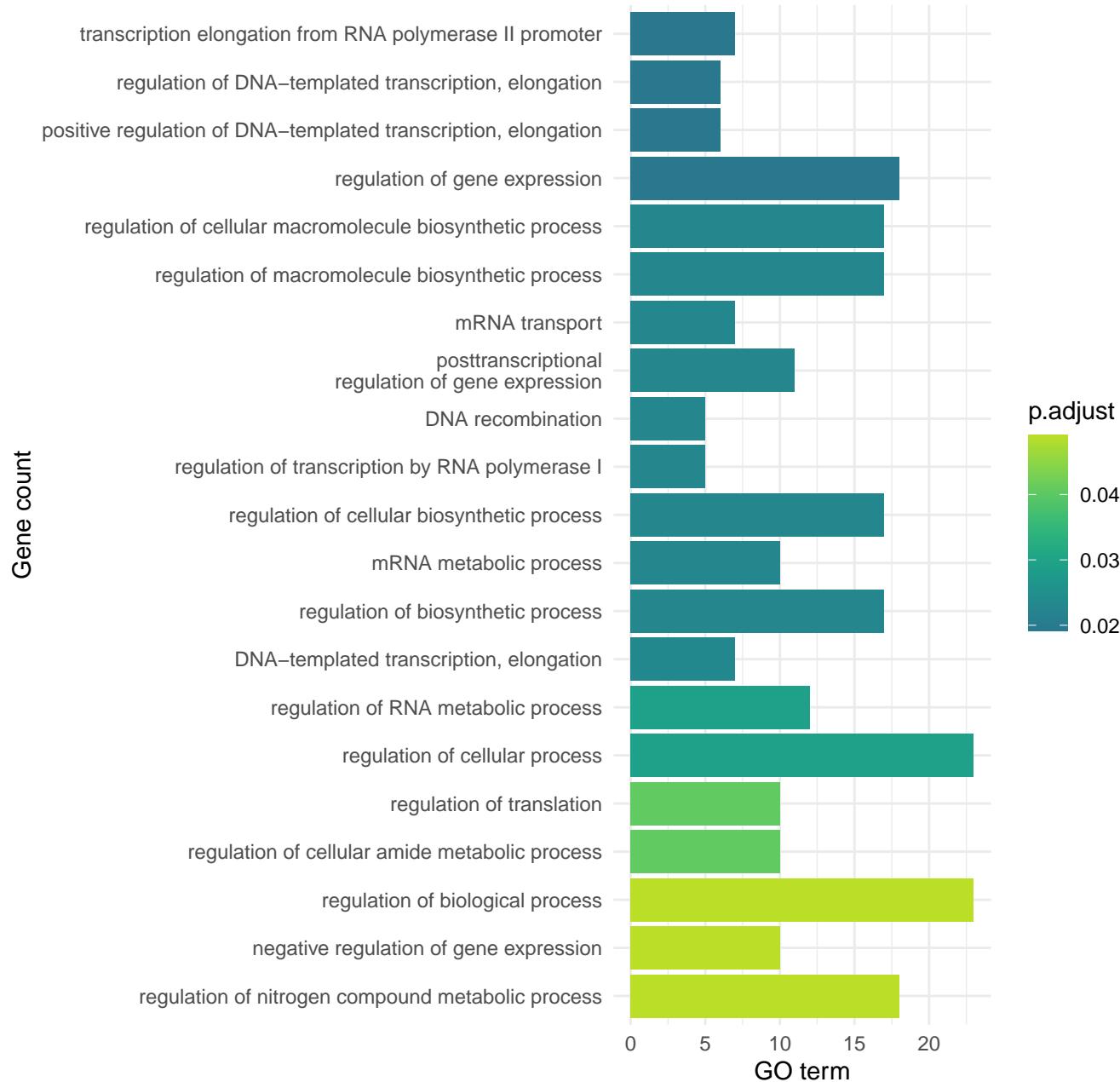


NDC1-TAP Up-regulated KEGG upsetplot

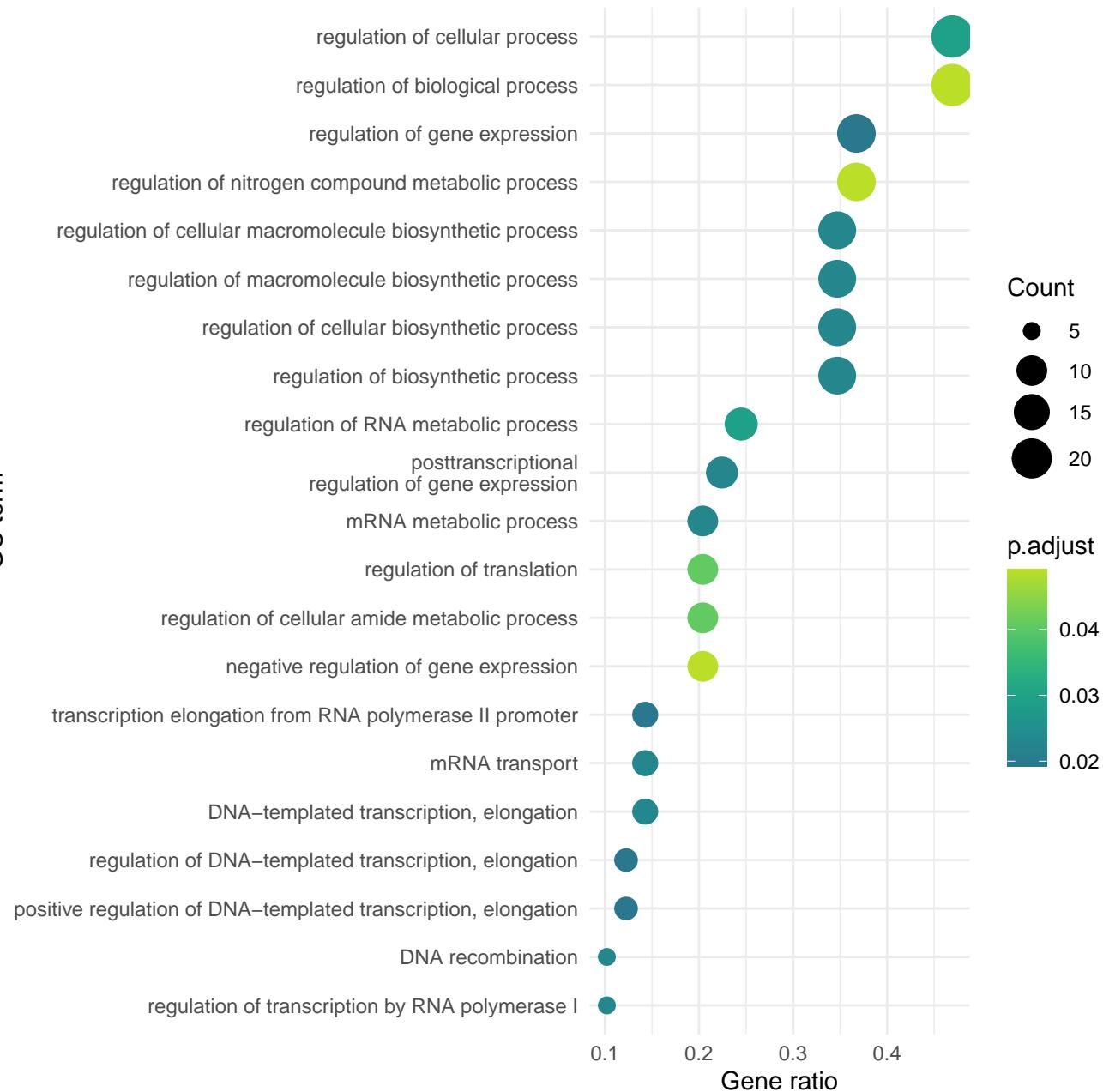


RNA degradation

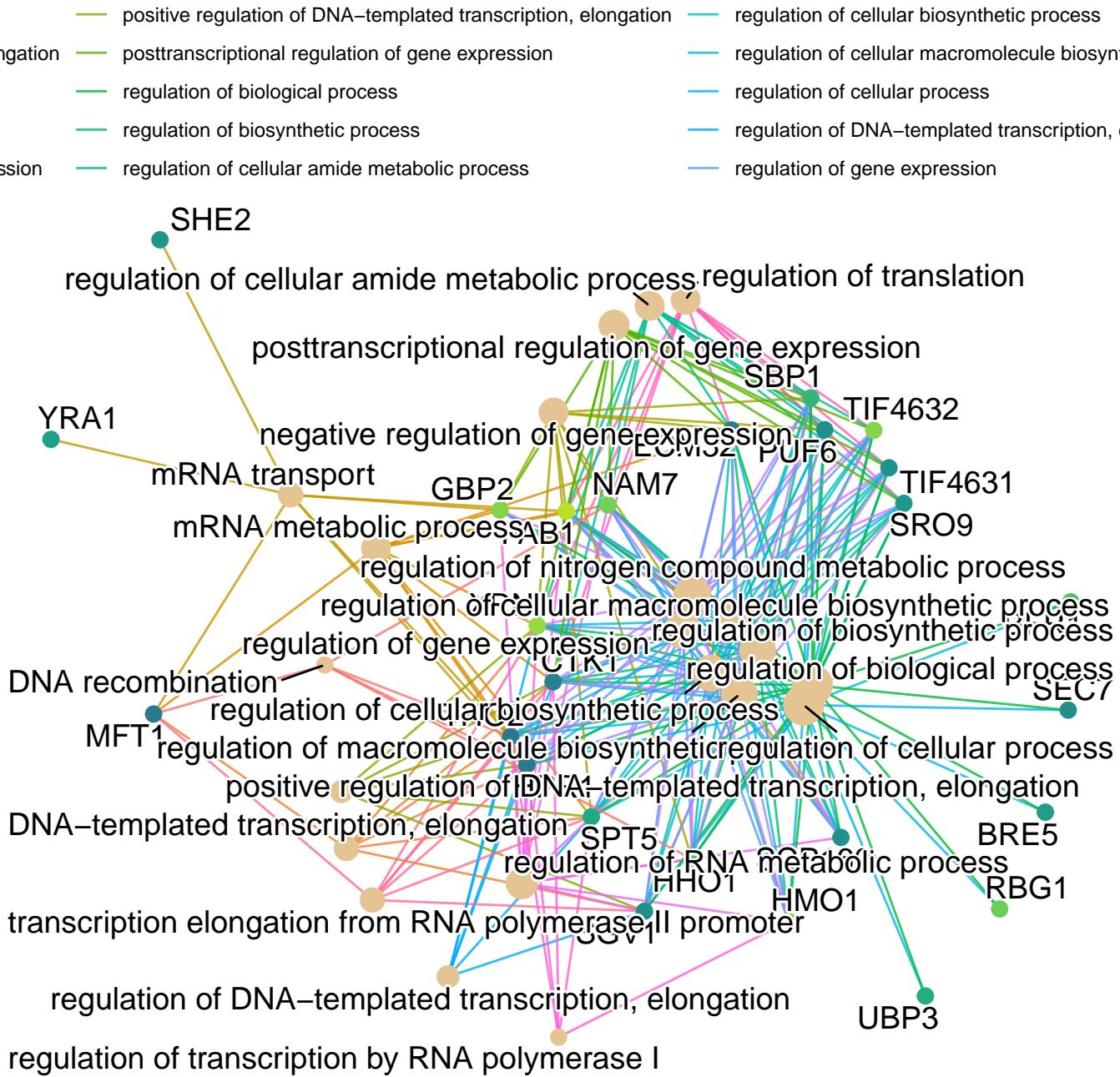
HRB1-TAP Up-regulated GO BP barplot



HRB1-TAP Up-regulated GO BP dotplot

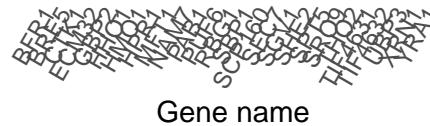
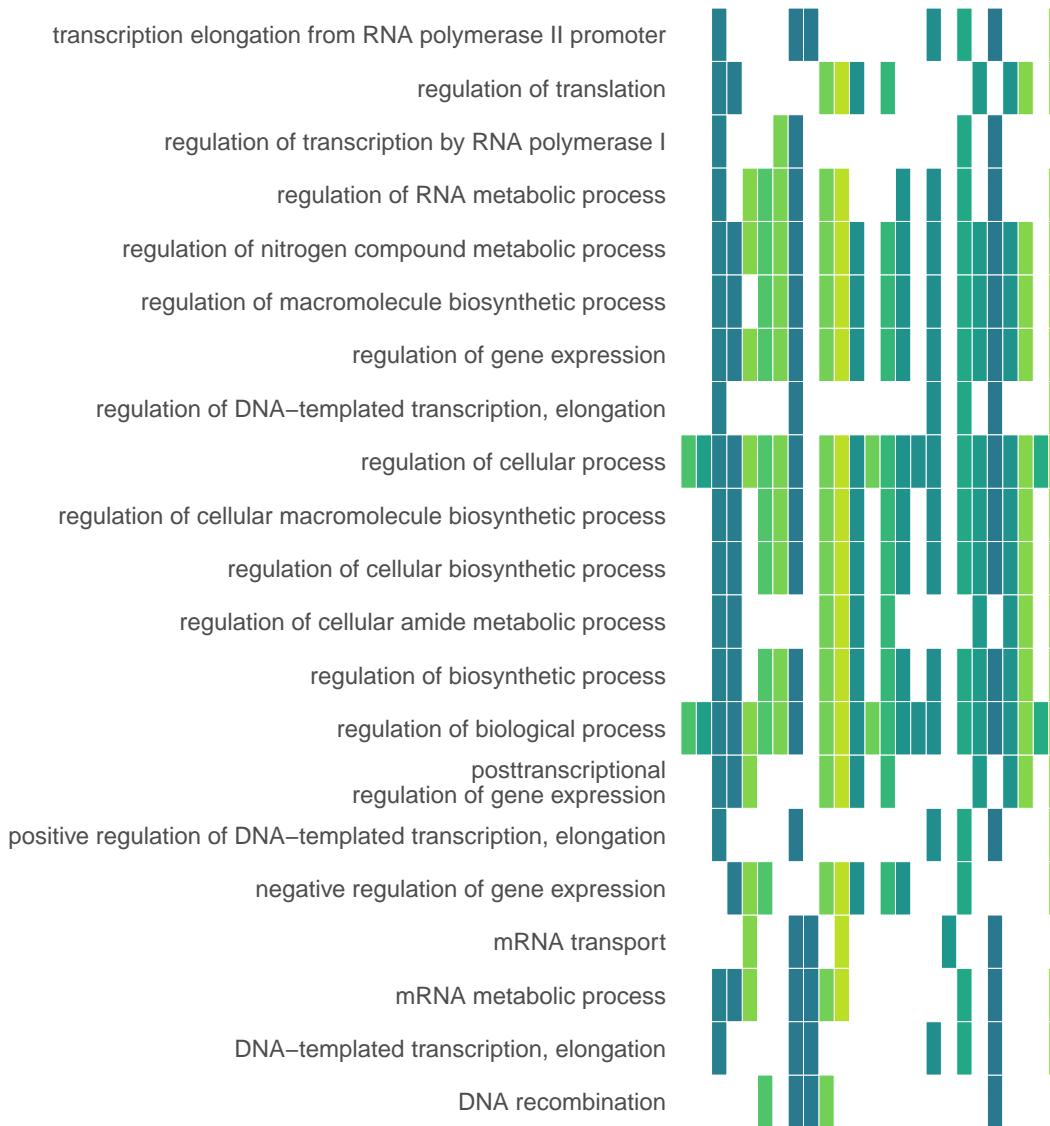


HRB1-TAP Up-regulated GO BP cnetplot

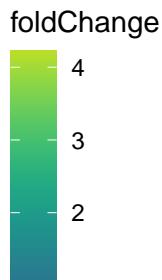


HRB1-TAP Up-regulated GO BP heatmap

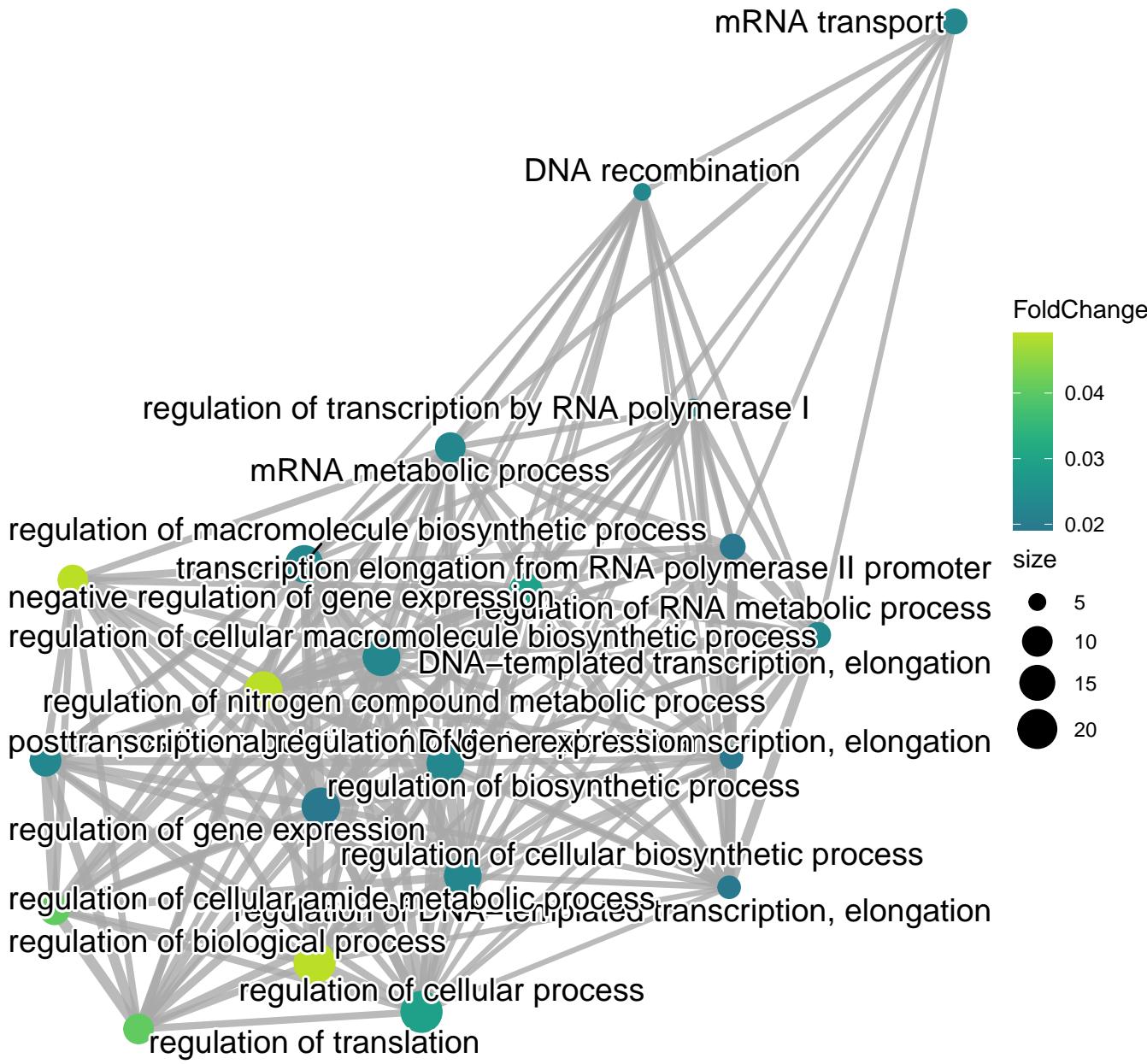
GO term

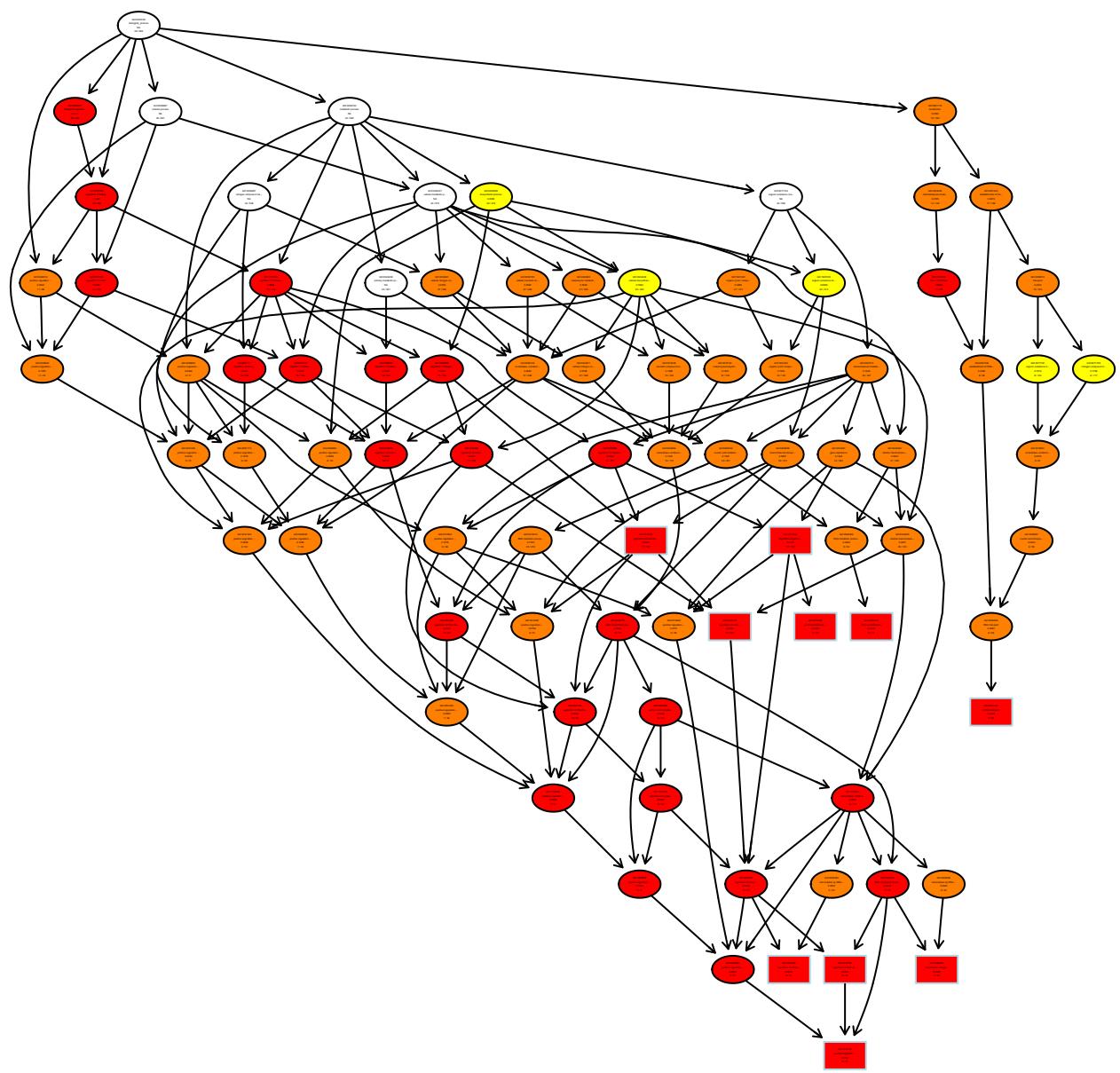


Gene name

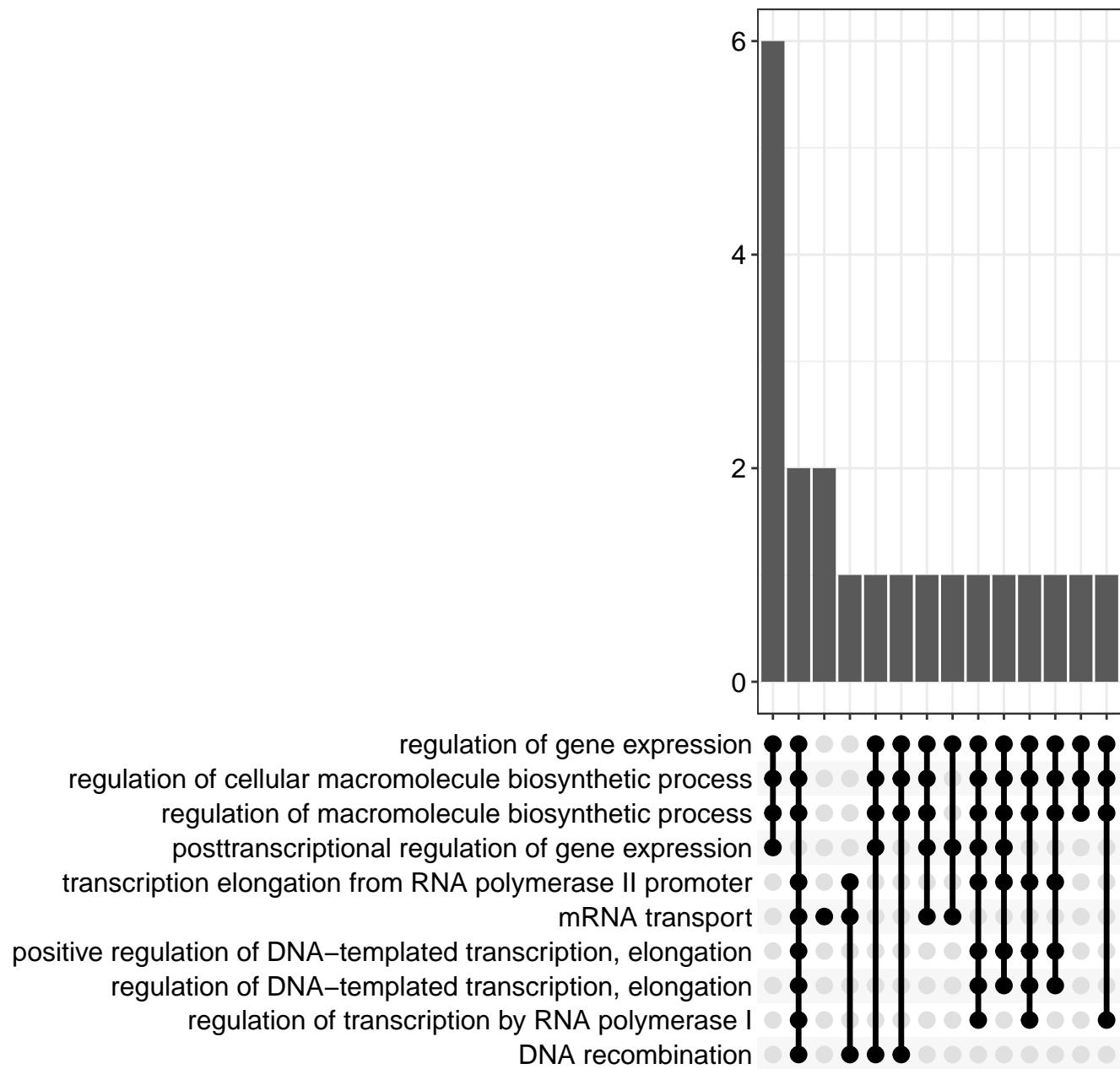


HRB1-TAP Up-regulated GO BP emapplot

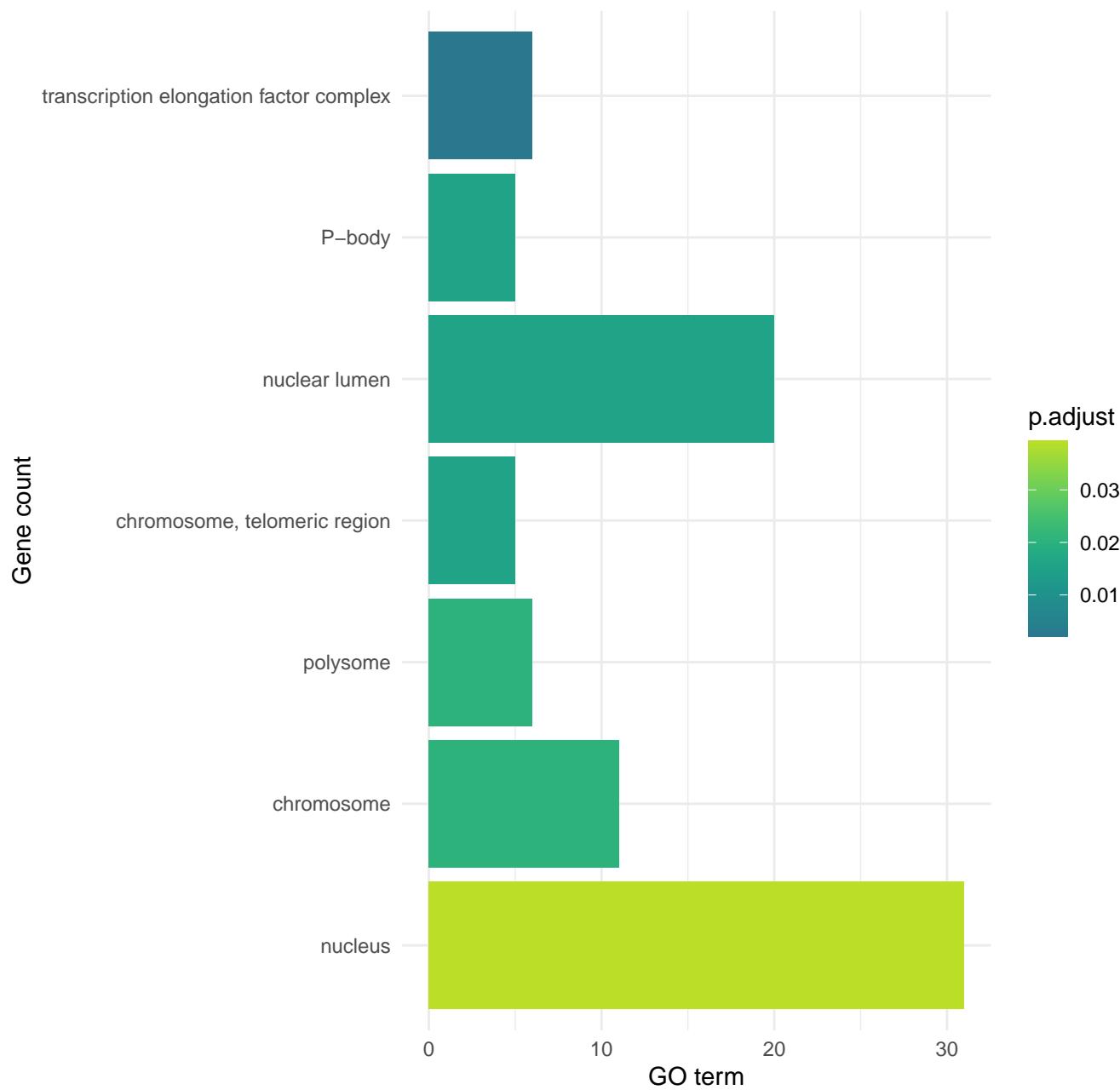




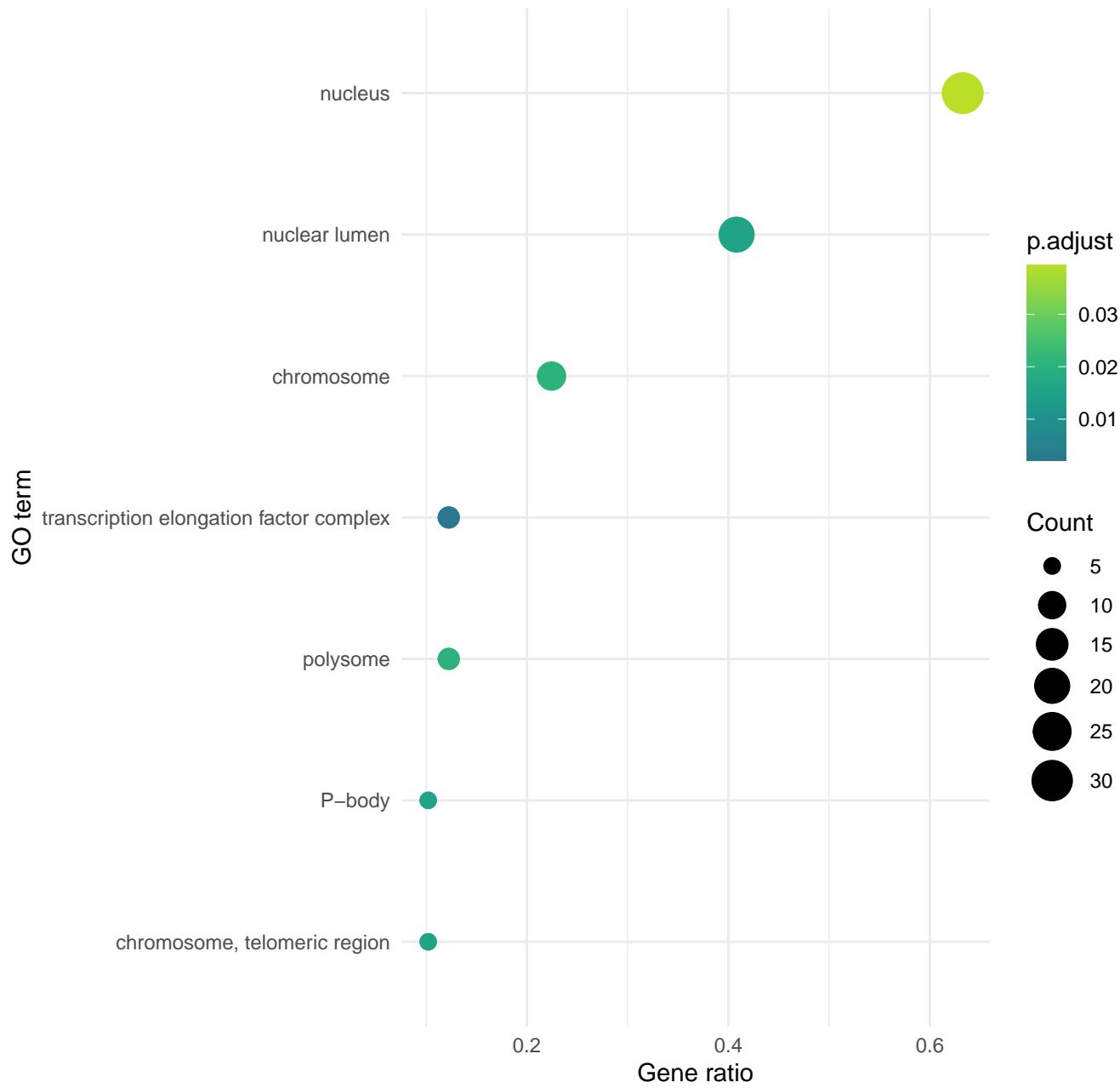
HRB1-TAP Up-regulated GO



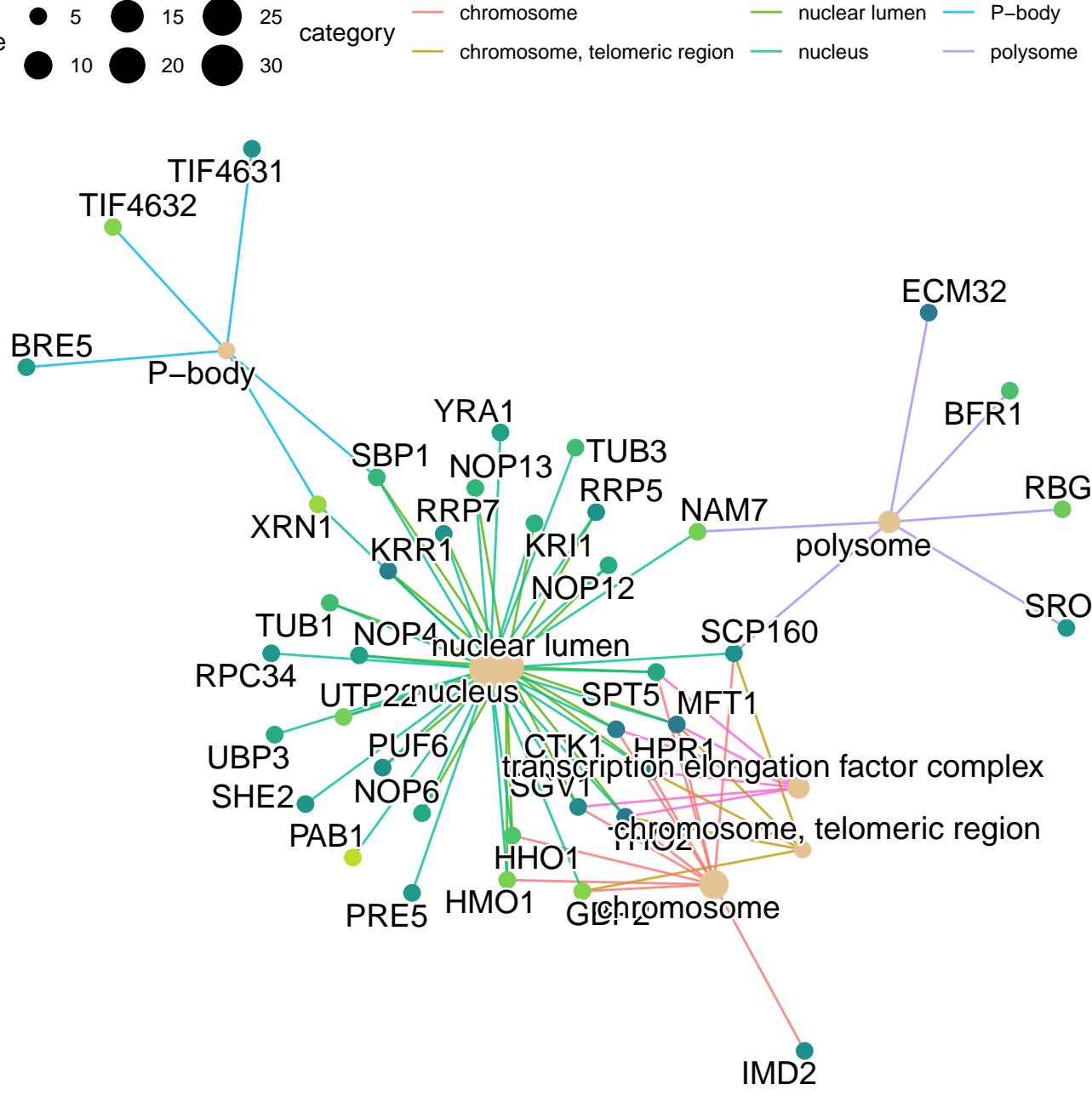
HRB1-TAP Up-regulated GO CC barplot



HRB1-TAP Up-regulated GO CC dotplot



HRB1-TAP Up-regulated GO CC cnetplot



HRB1-TAP Up-regulated GO CC heatplot

GO term

transcription elongation factor complex

polysome

P-body

nucleus

nuclear lumen

chromosome, telomeric region

chromosome

foldChange

4

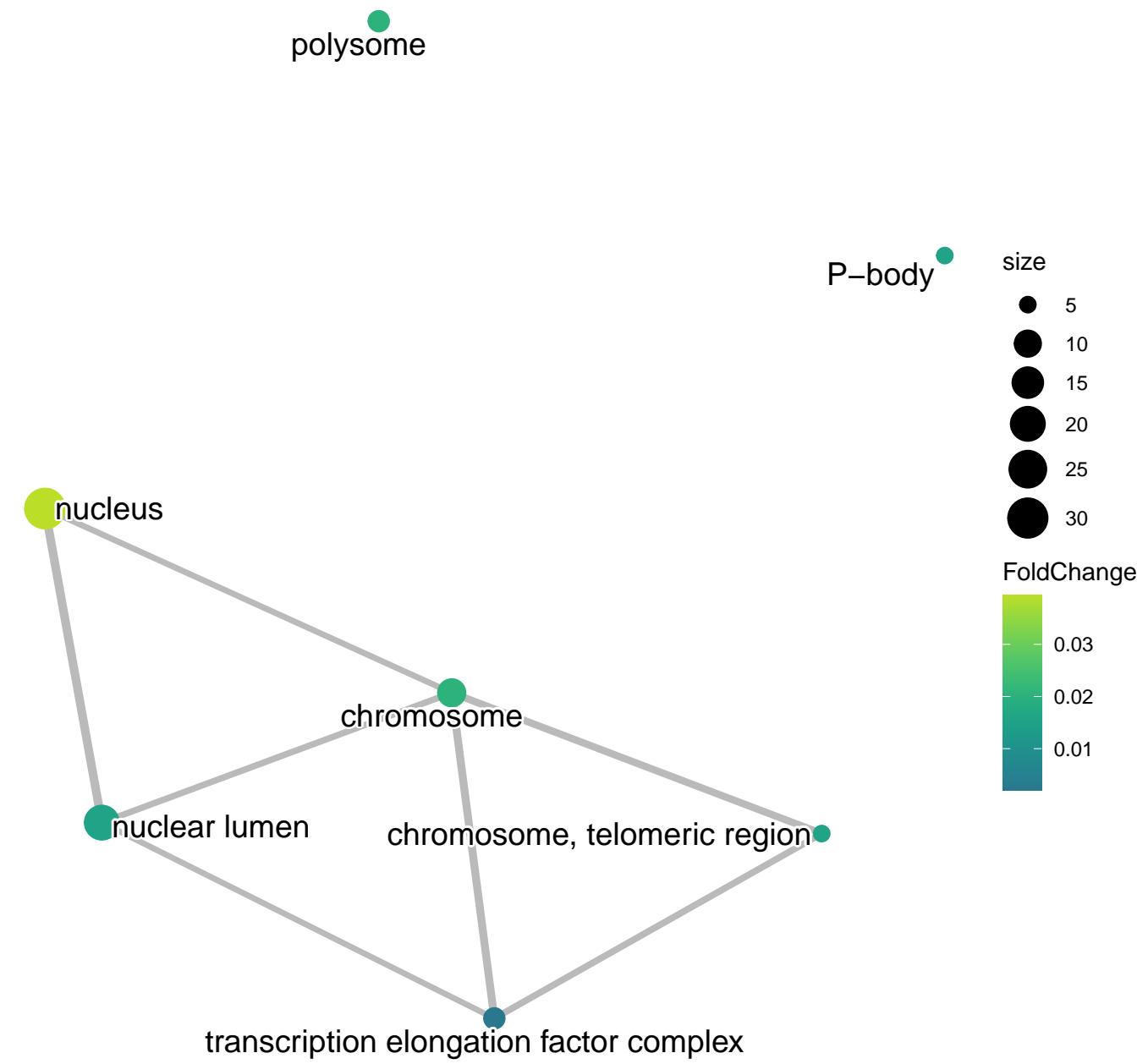
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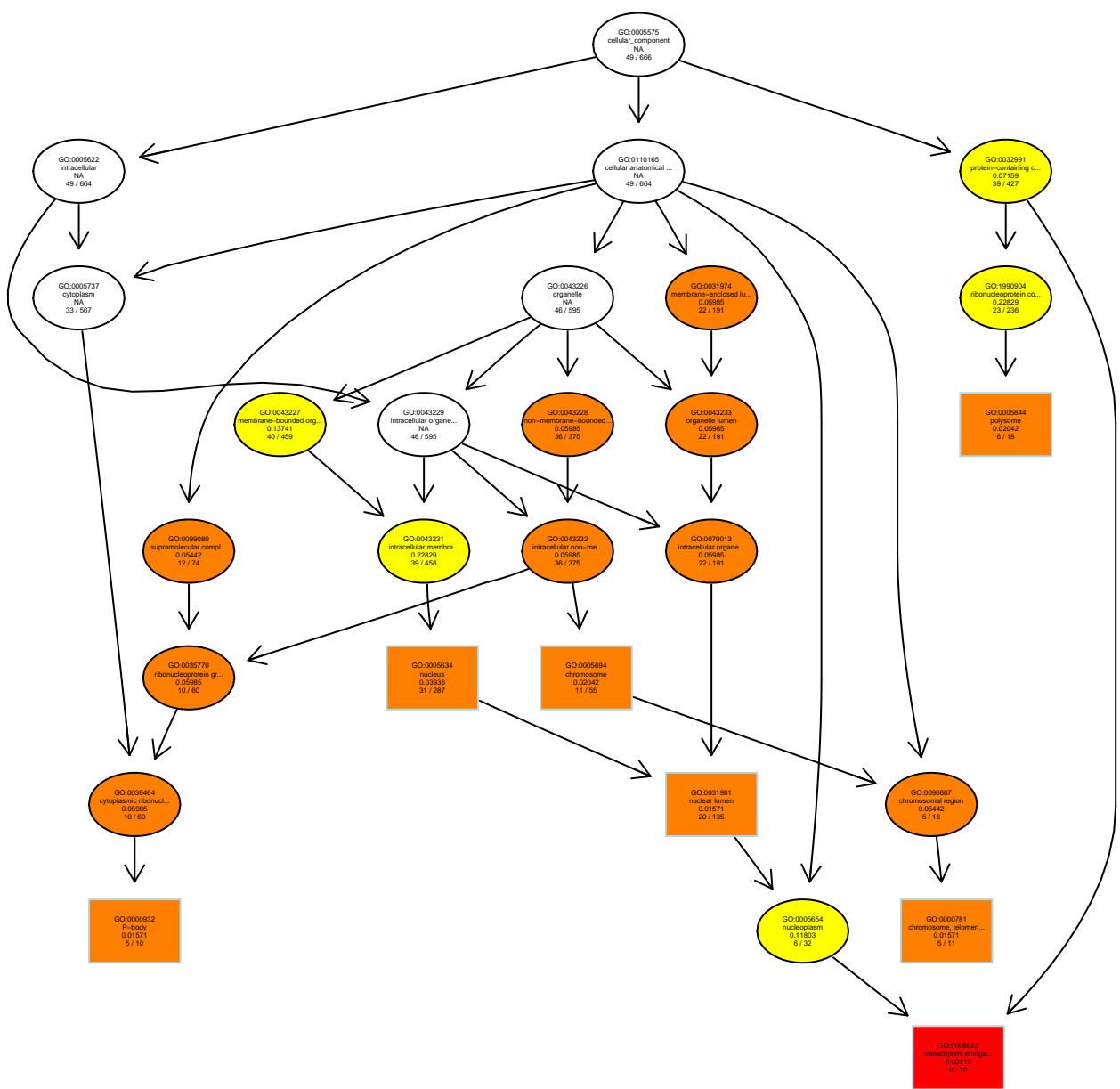
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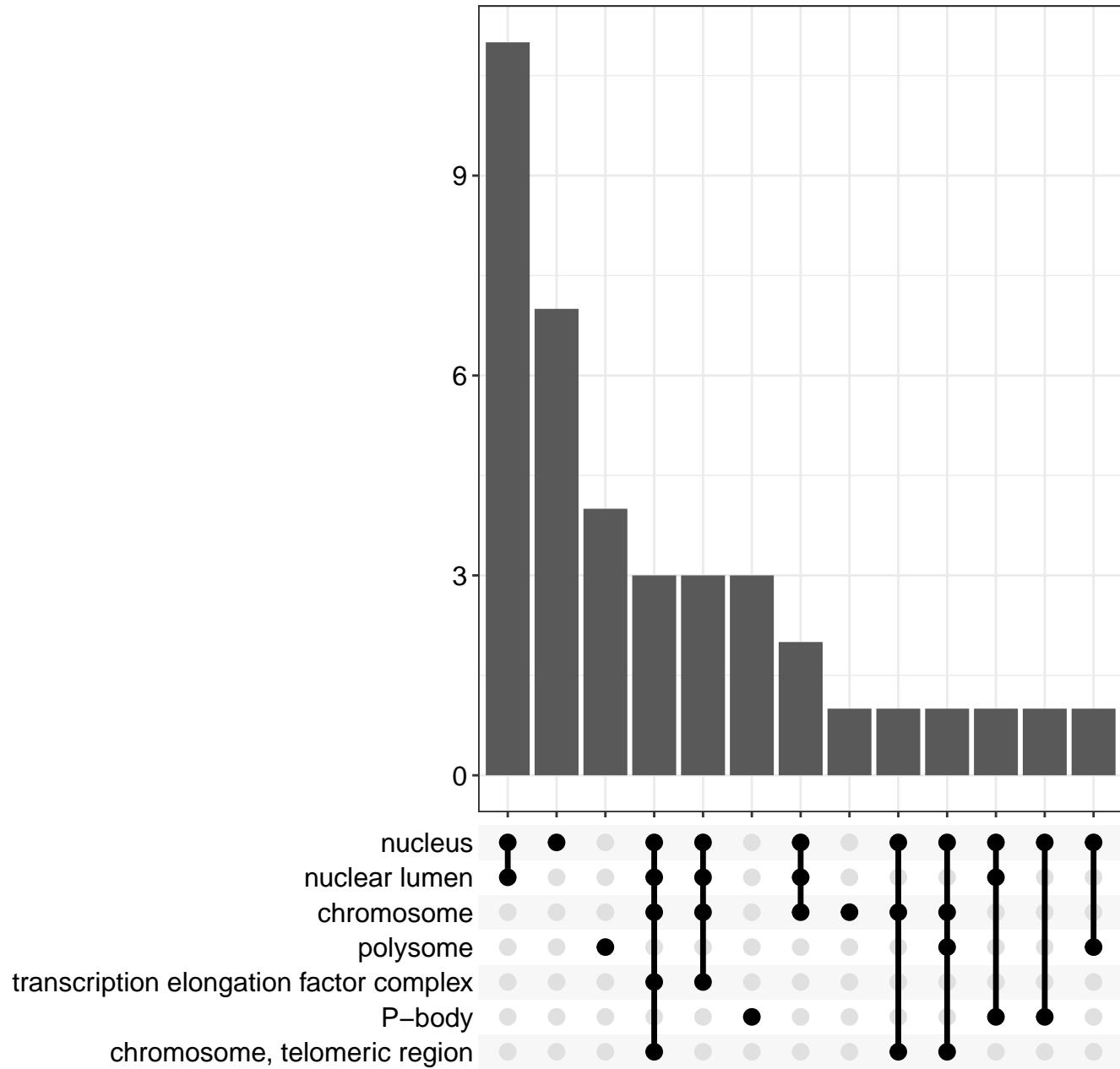
Gene name

HRB1-TAP Up-regulated GO CC emapplot

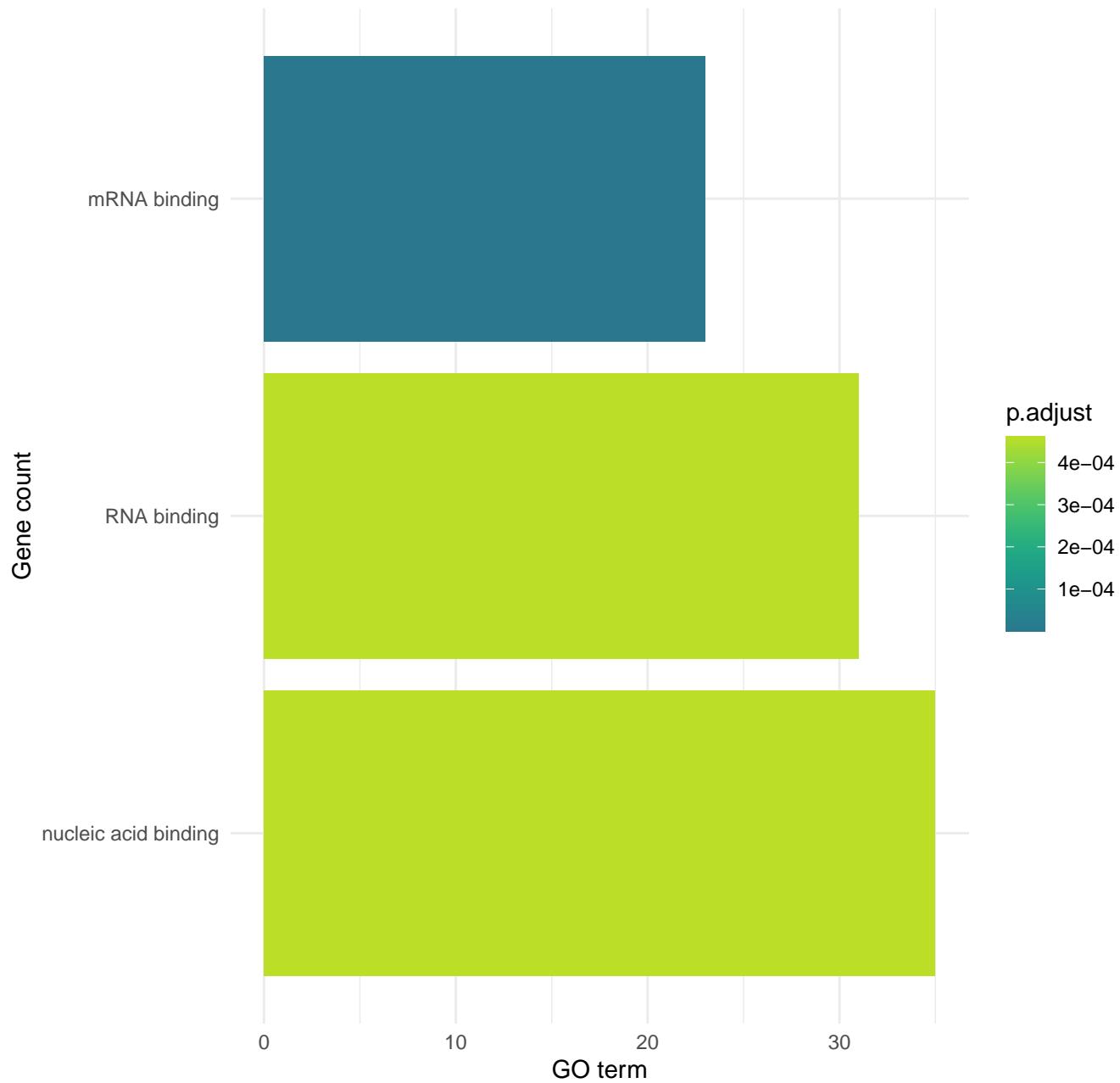




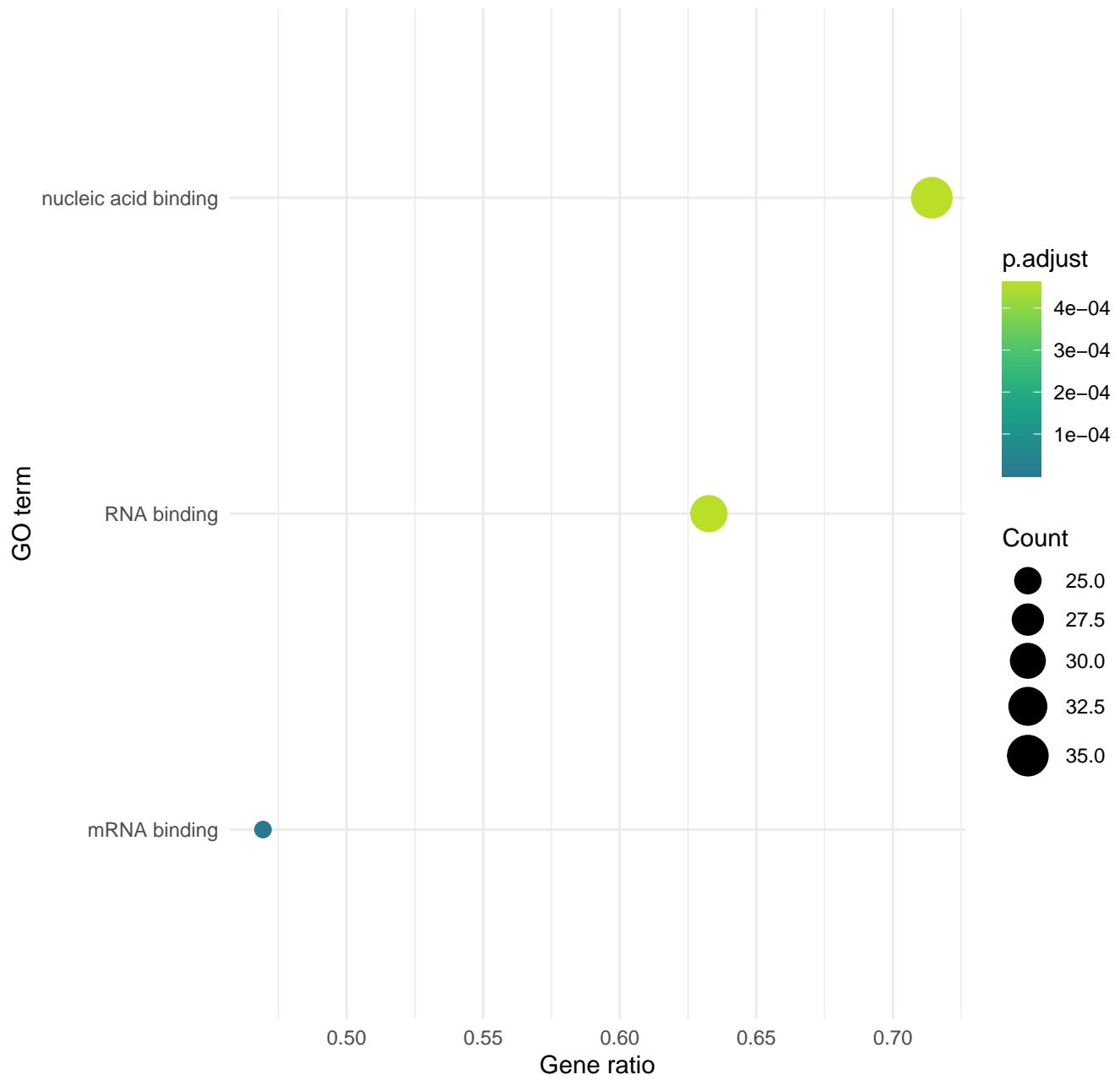
HRB1-TAP Up-regulated GO CC upsetplot



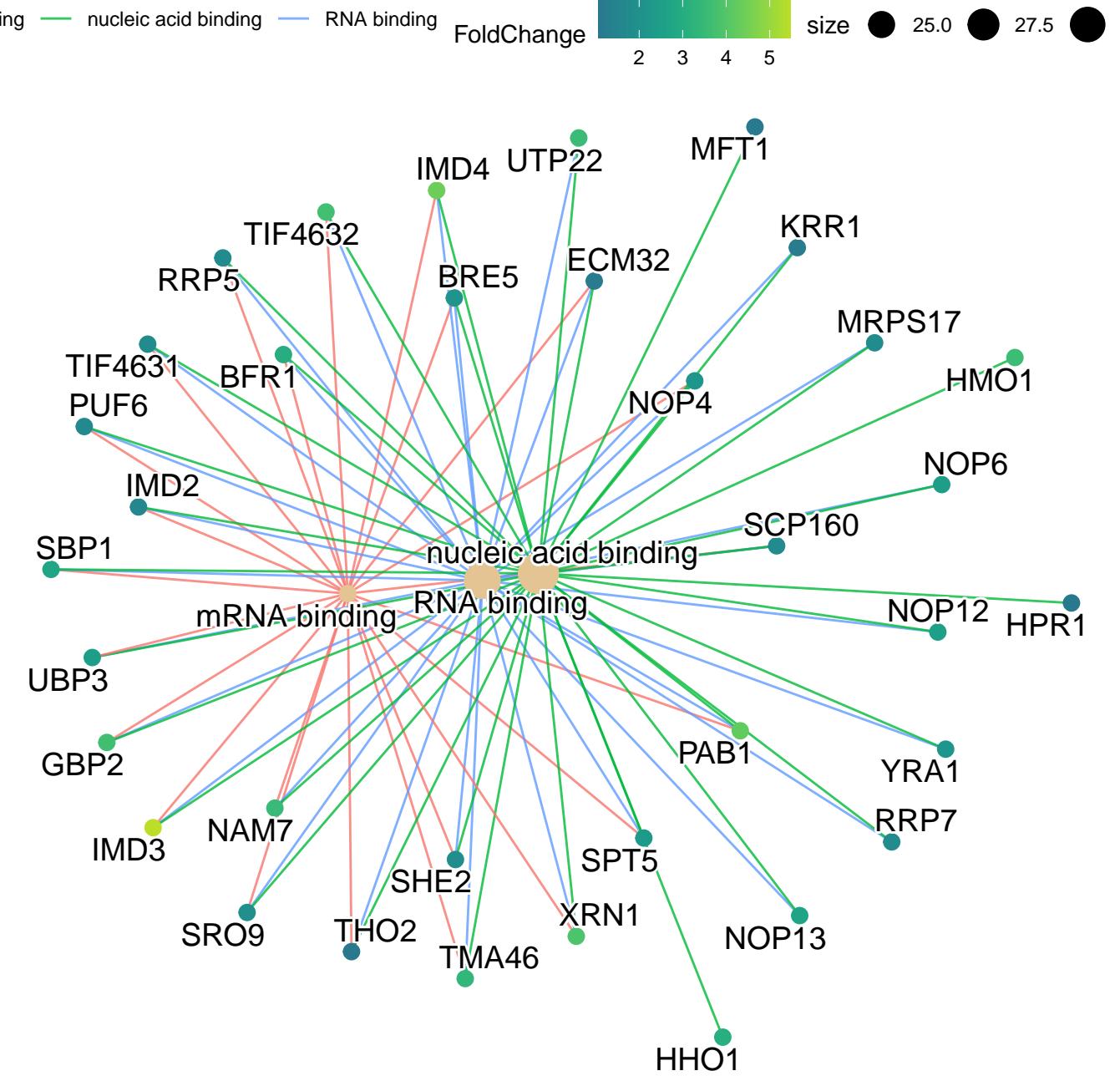
HRB1-TAP Up-regulated GO MF barplot



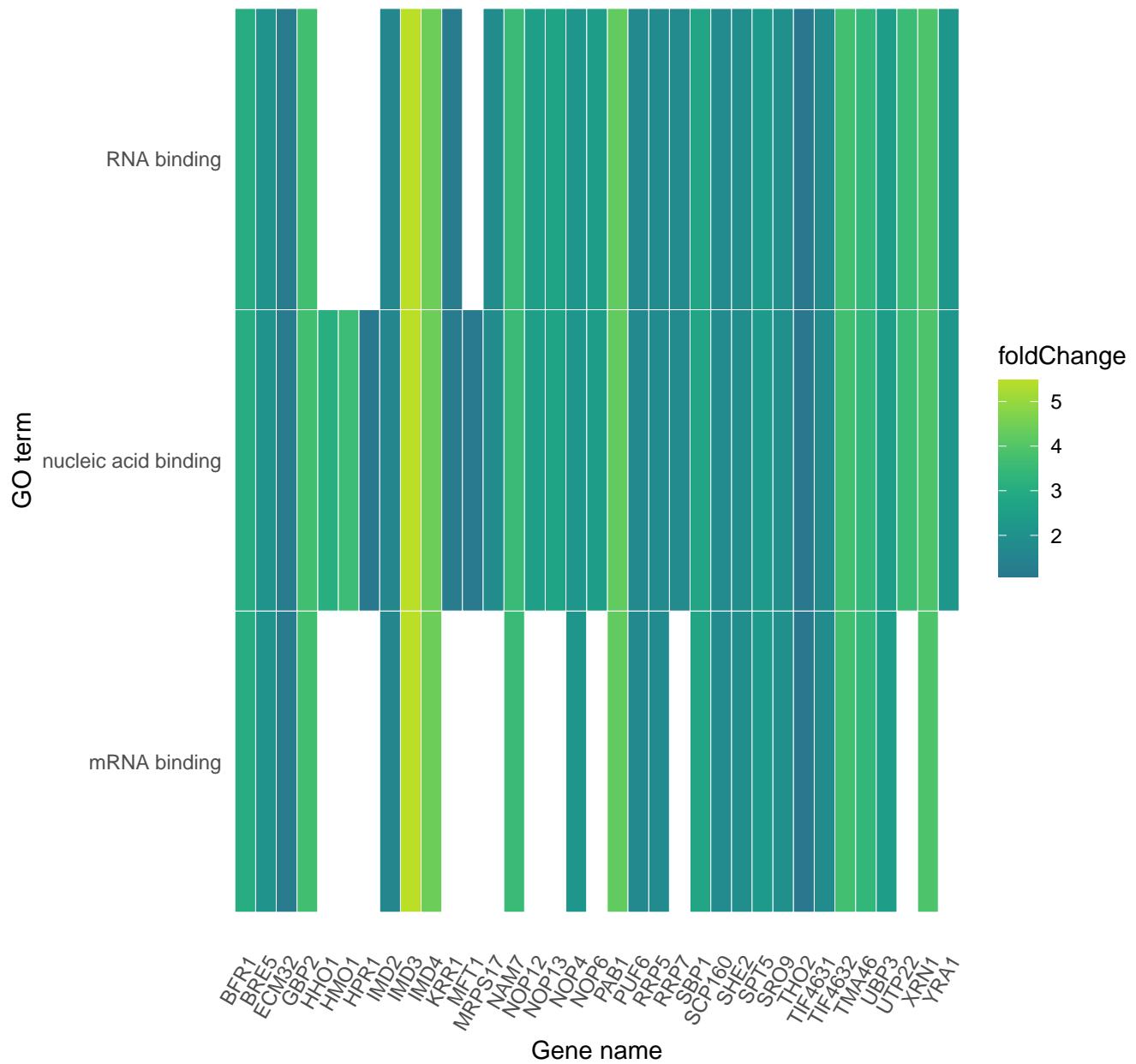
HRB1-TAP Up-regulated GO MF dotplot



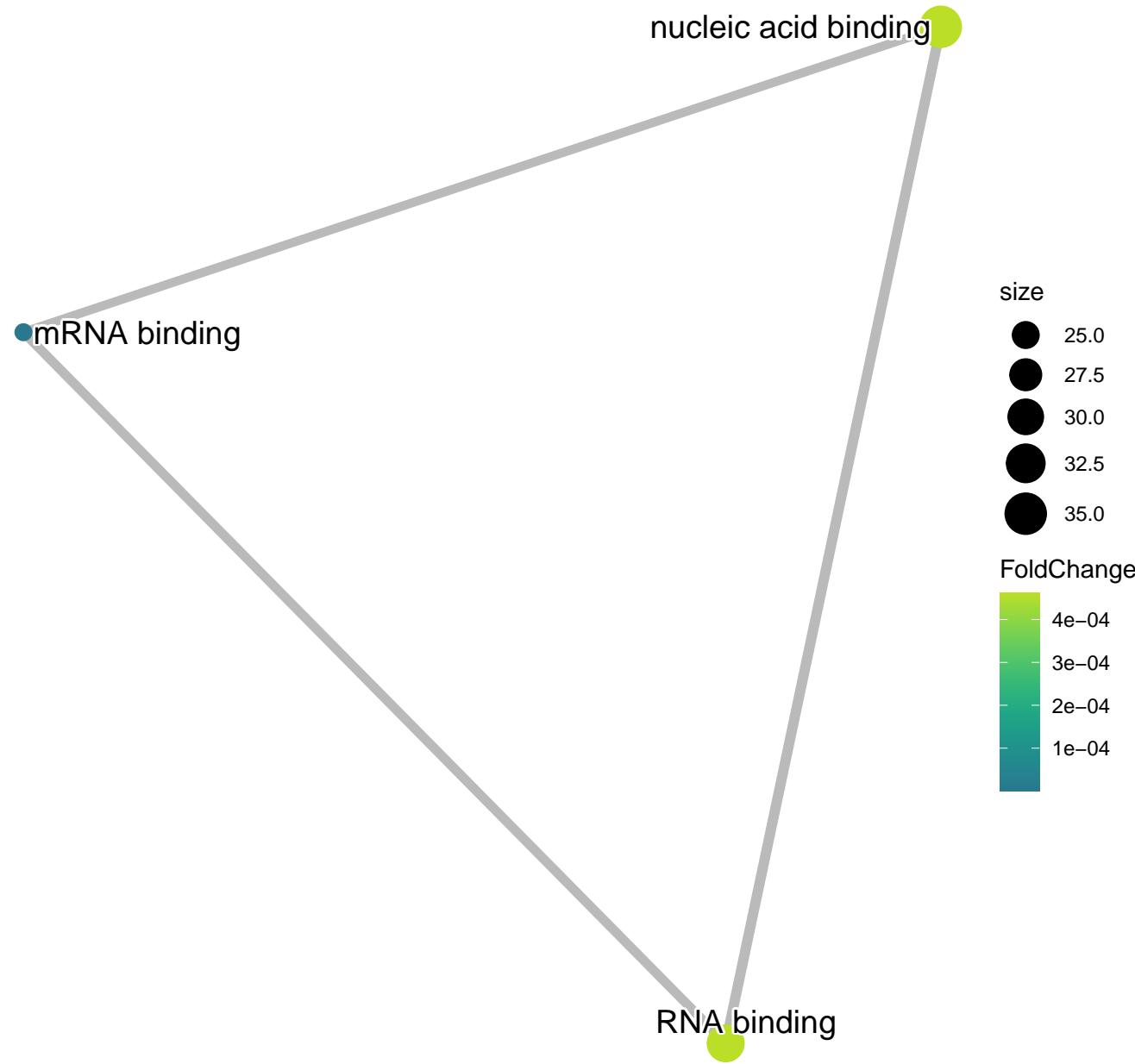
HRB1-TAP Up-regulated GO MF cnetplot

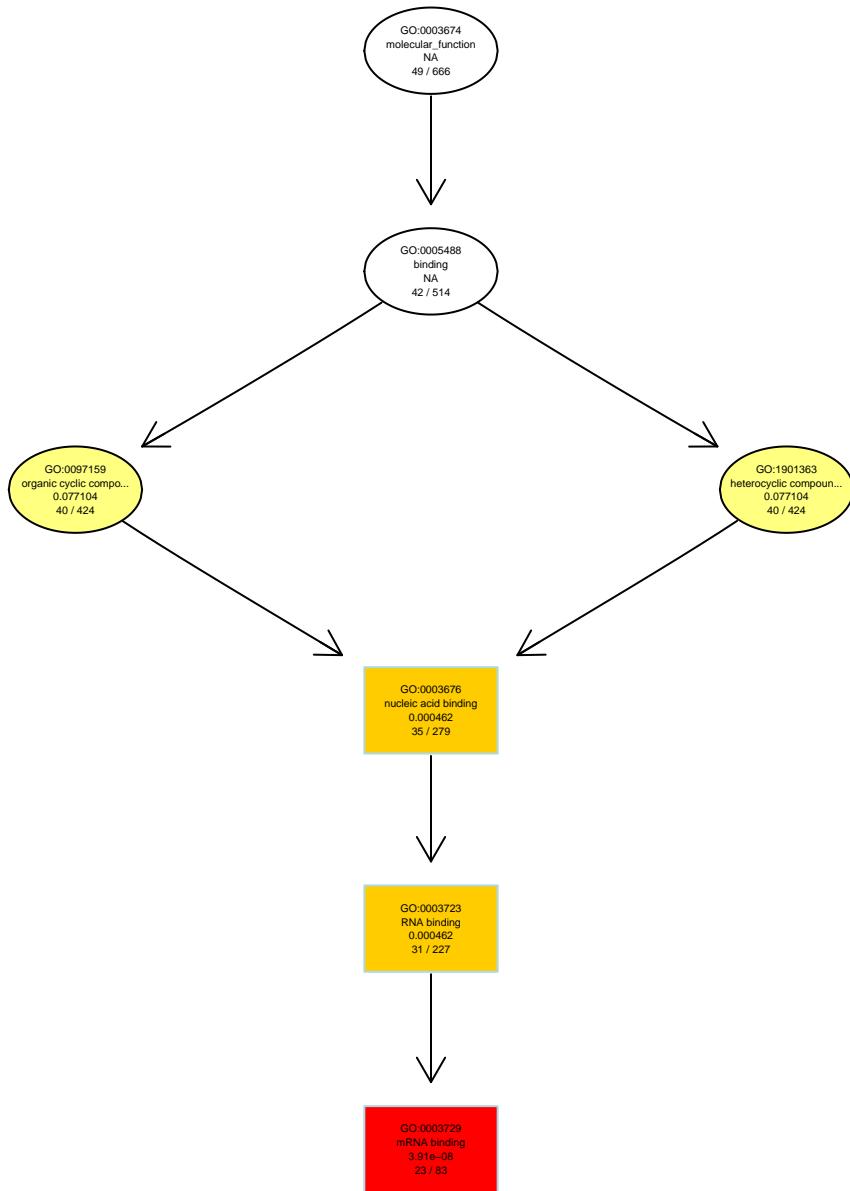


HRB1-TAP Up-regulated GO MF heatplot

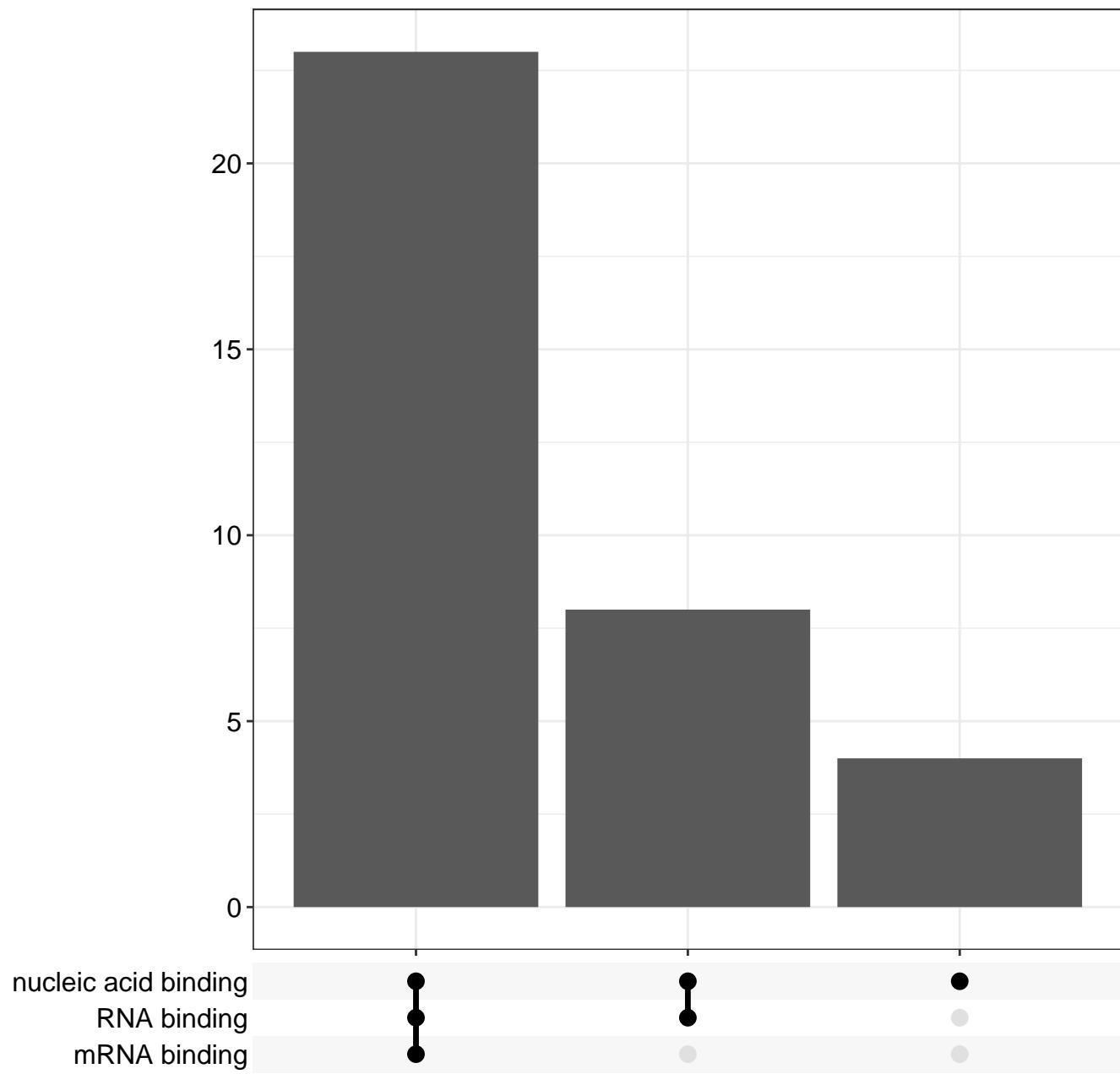


HRB1-TAP Up-regulated GO MF emapplot

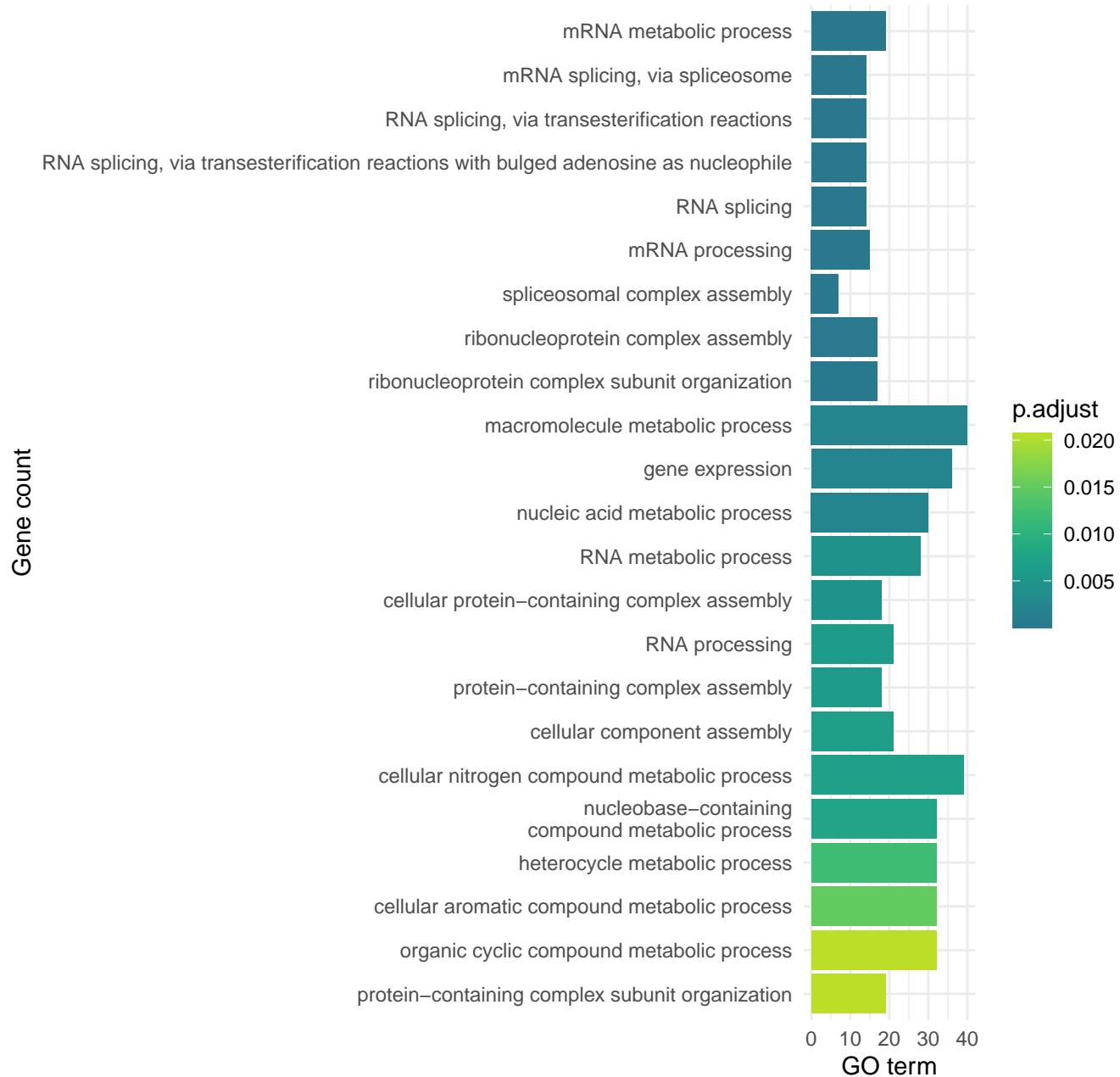




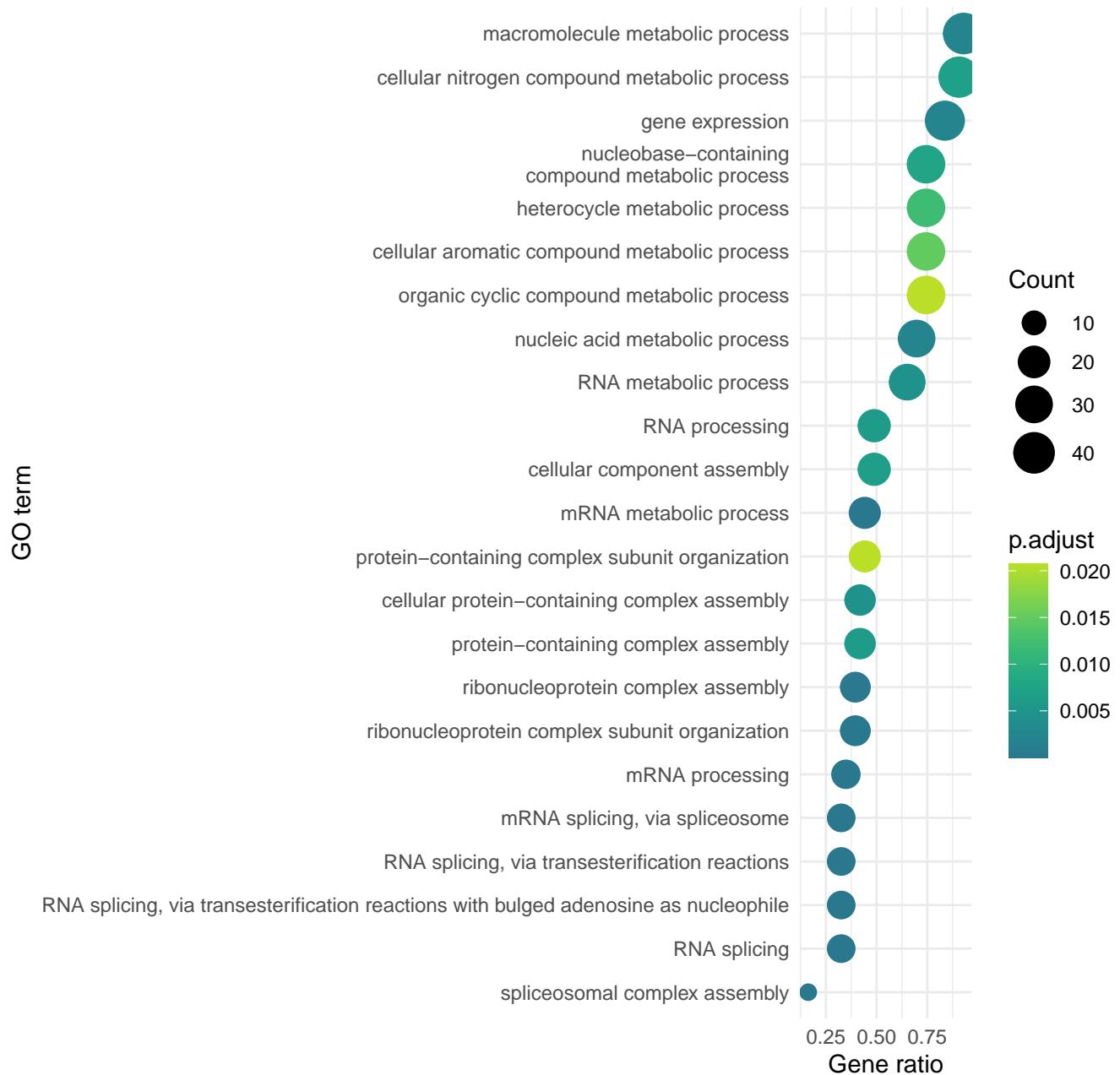
HRB1-TAP Up-regulated GO MF upsetplot



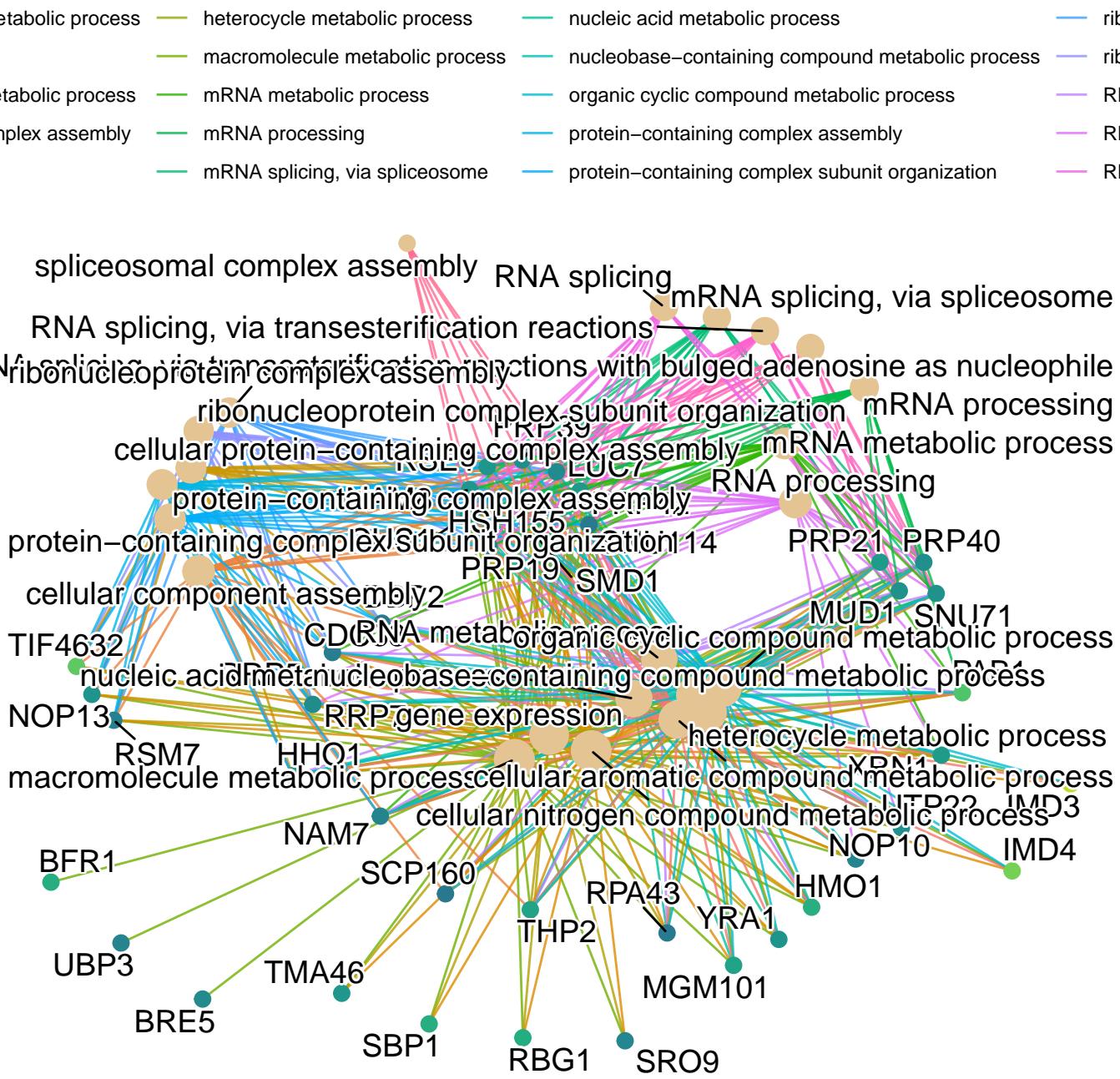
CBC2-TAP Up-regulated



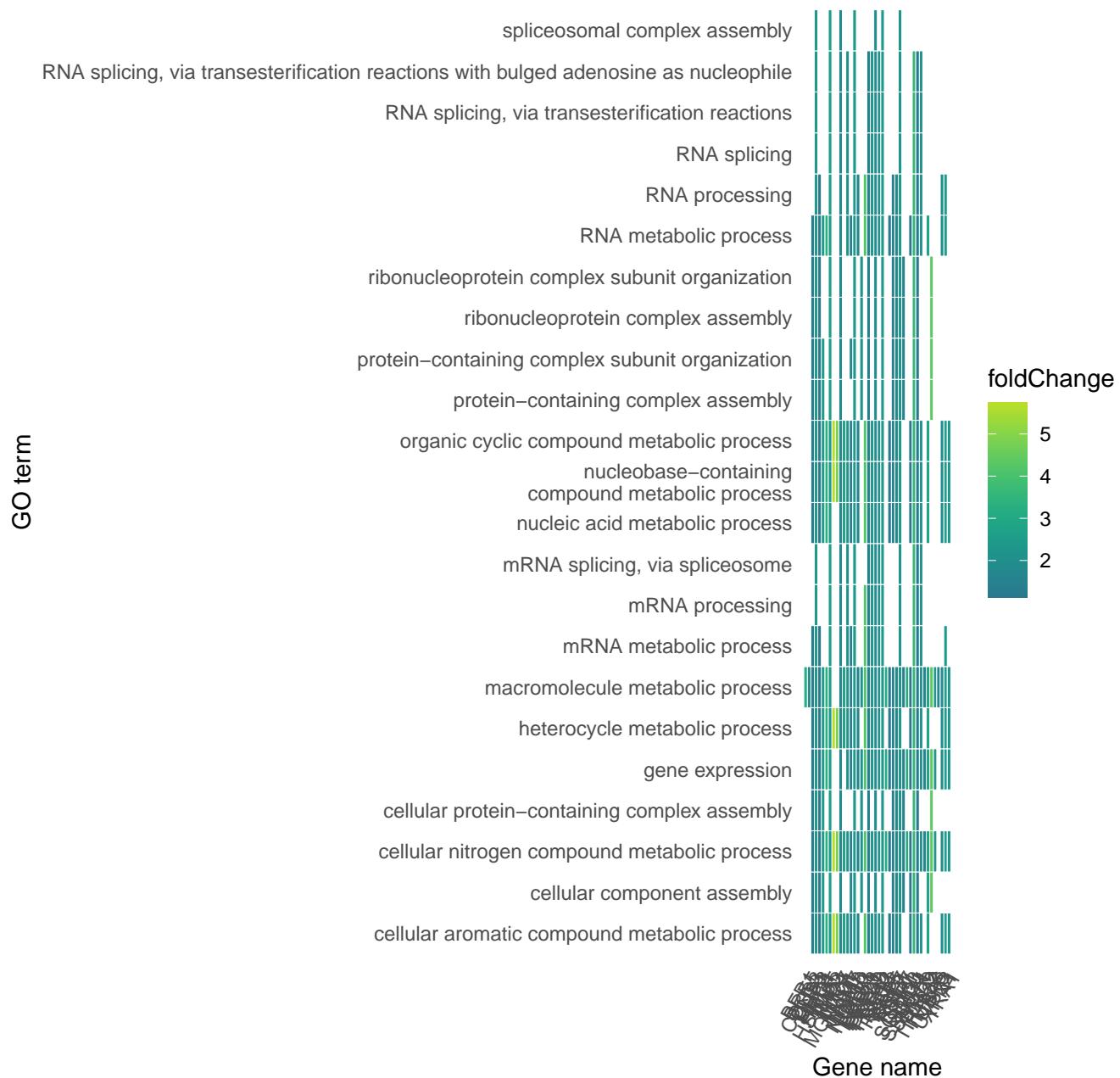
CBC2-TAP Up-regulated



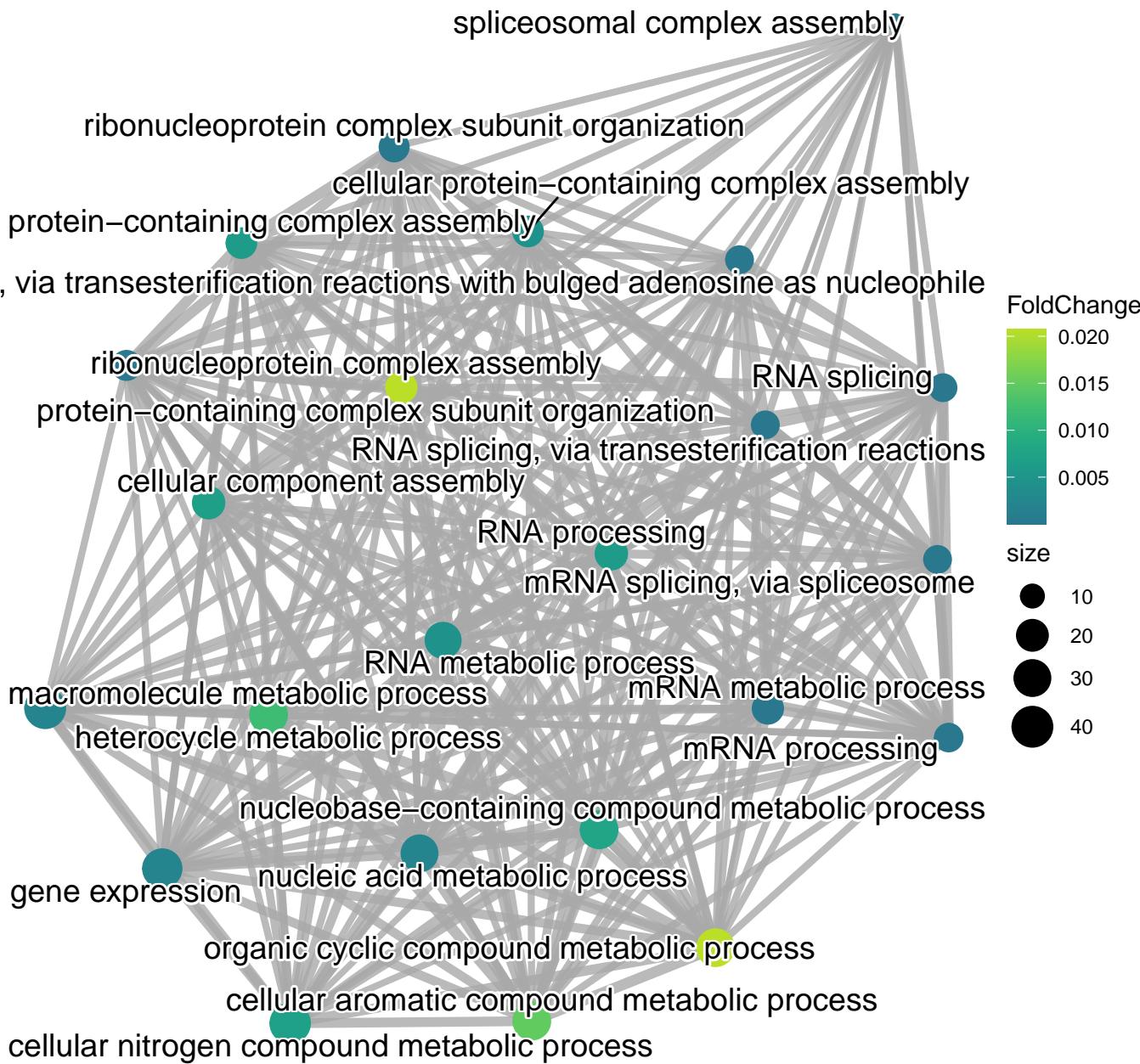
CBC2-TAP Up-regulated GO BP cnetplot

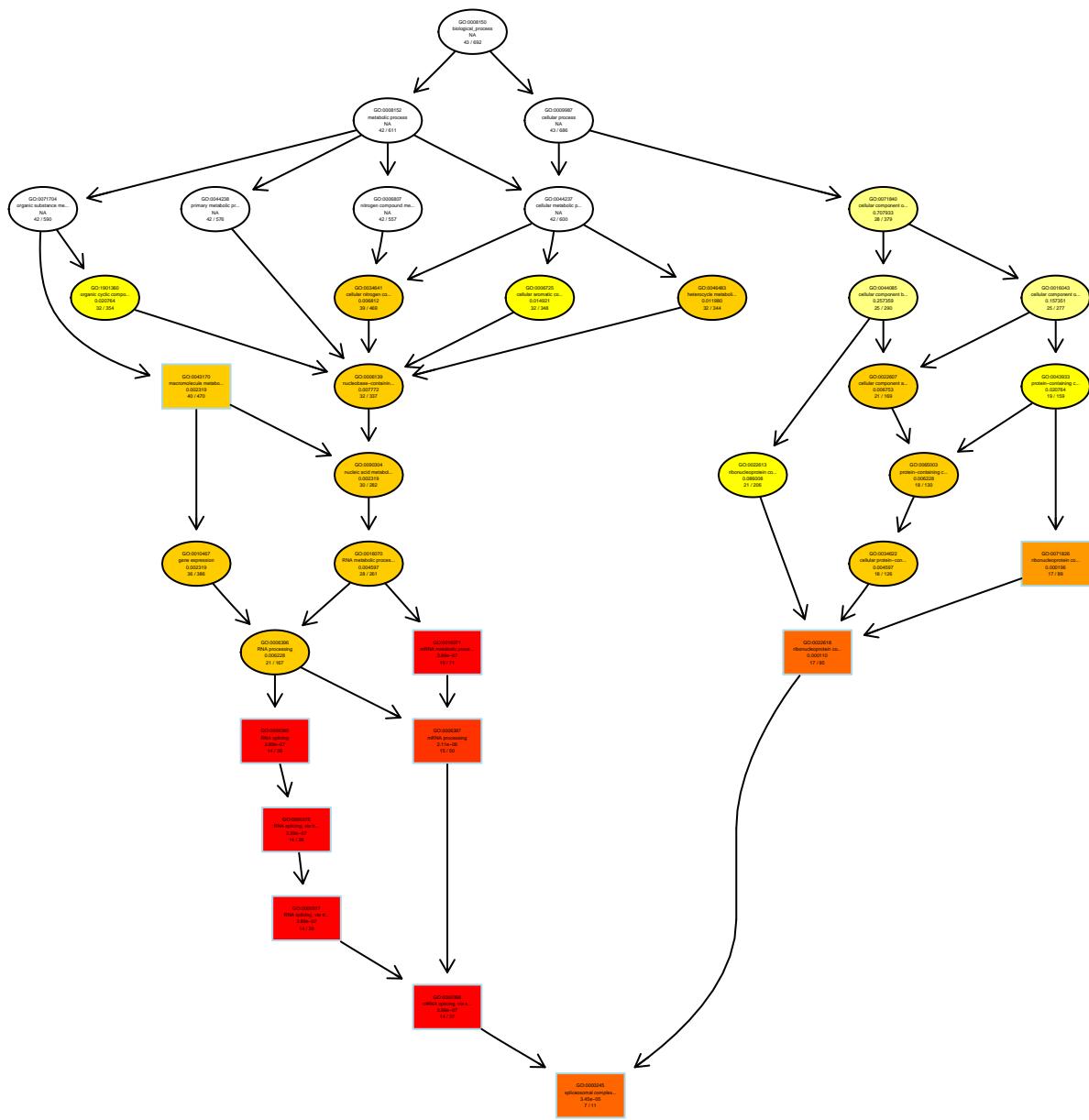


CBC2-TAP Up-regulated

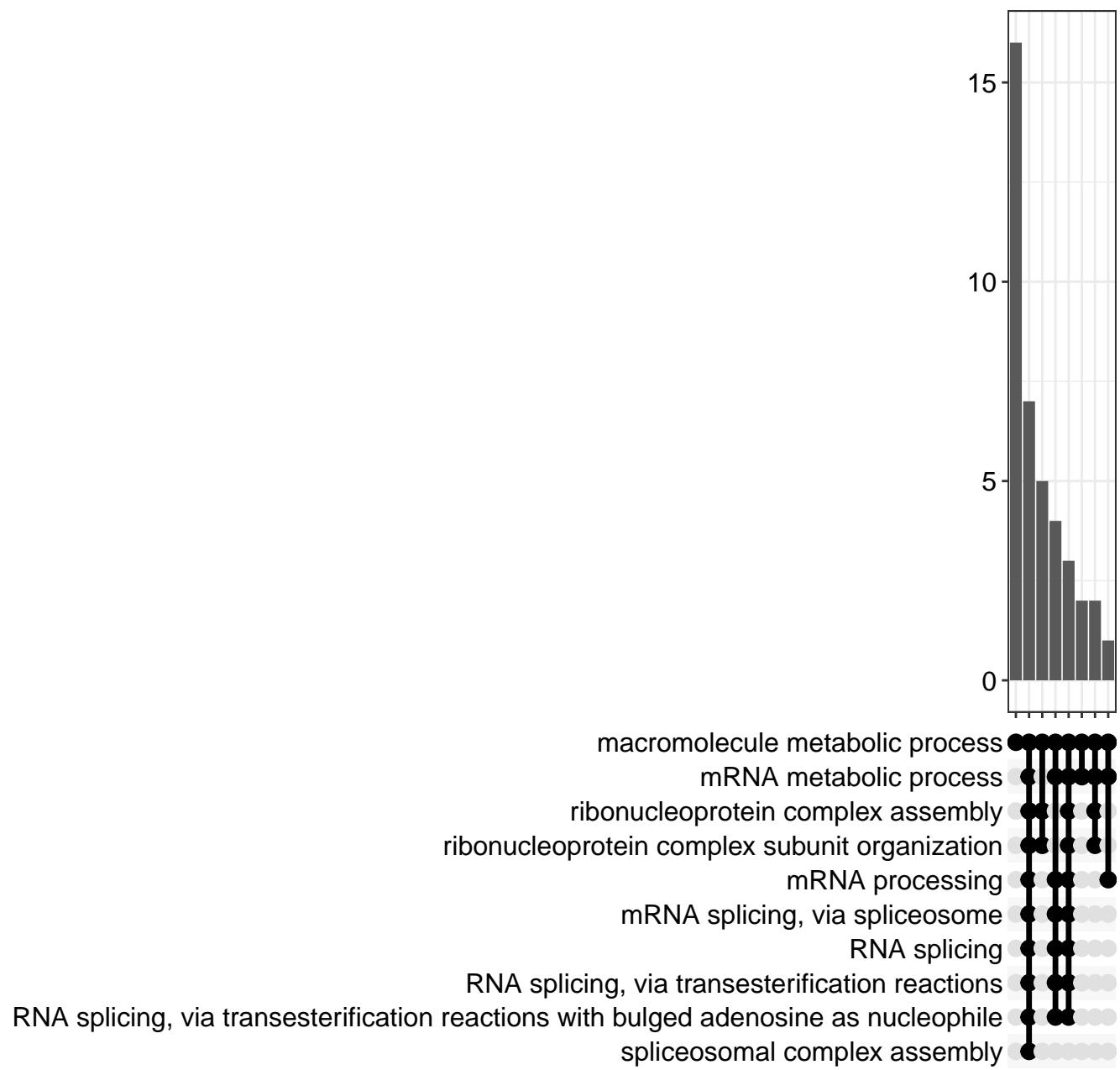


CBC2-TAP Up-regulated GO BP emapplot

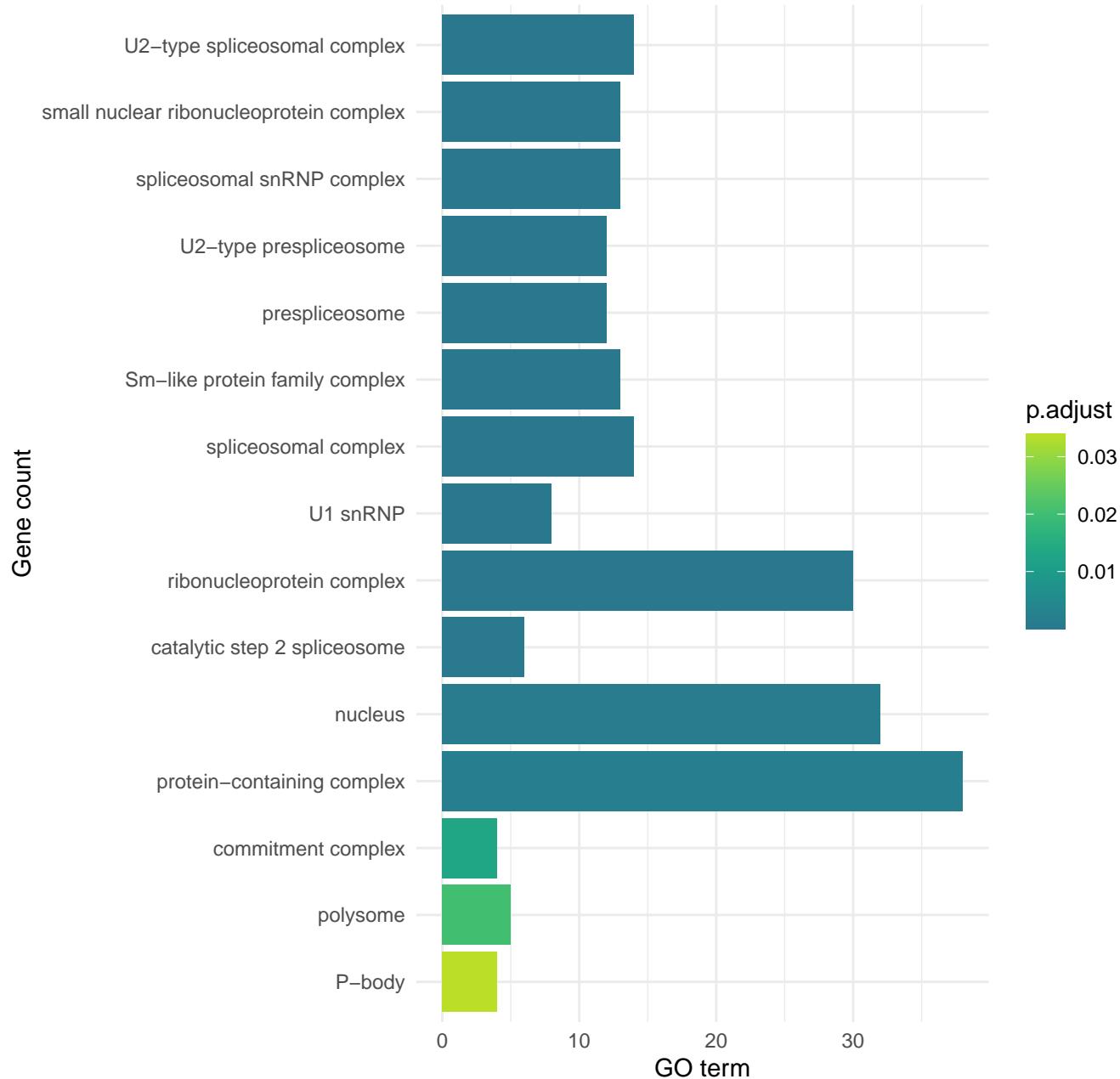




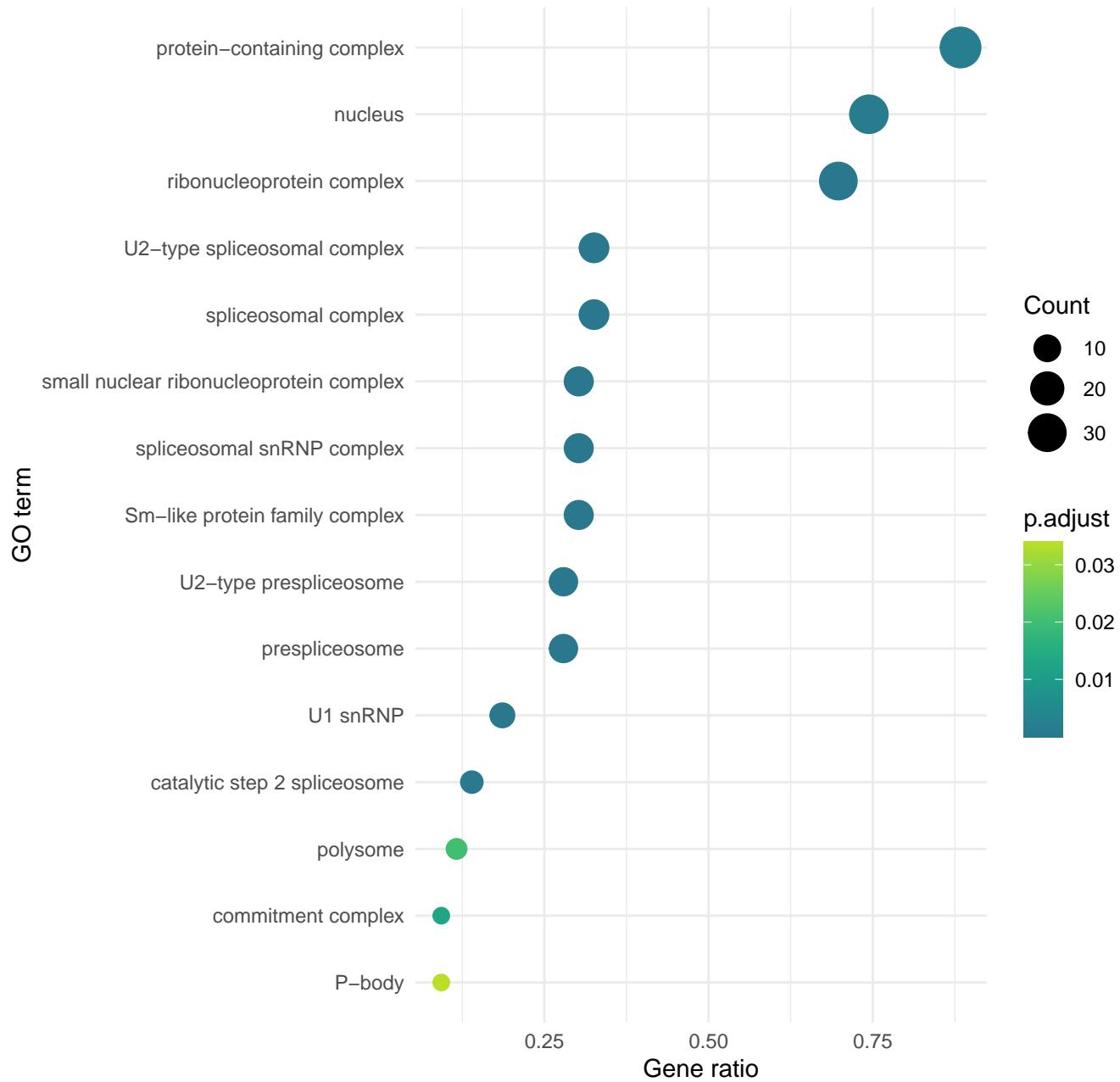
CBC2-TA



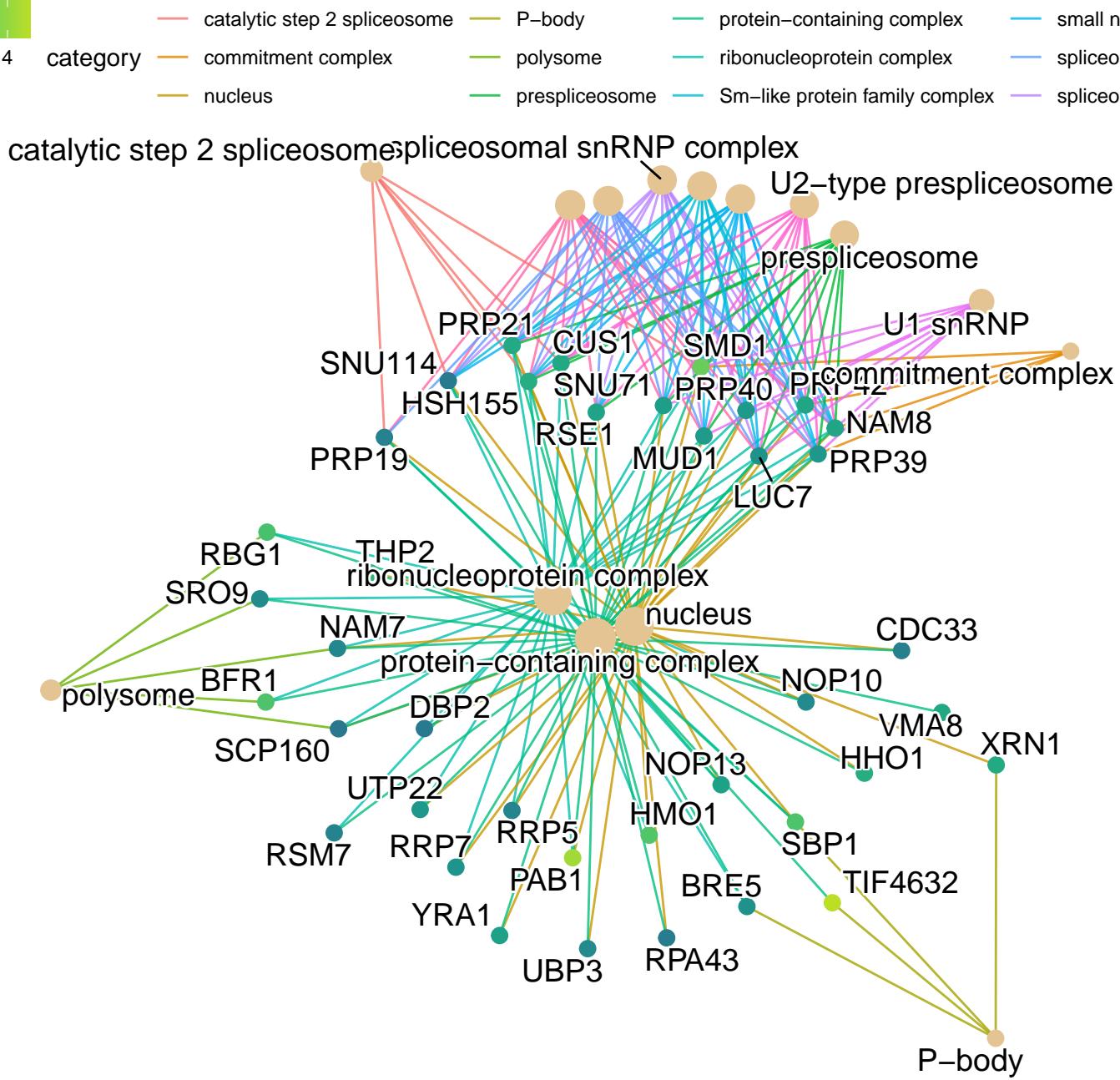
CBC2-TAP Up-regulated GO CC barplot



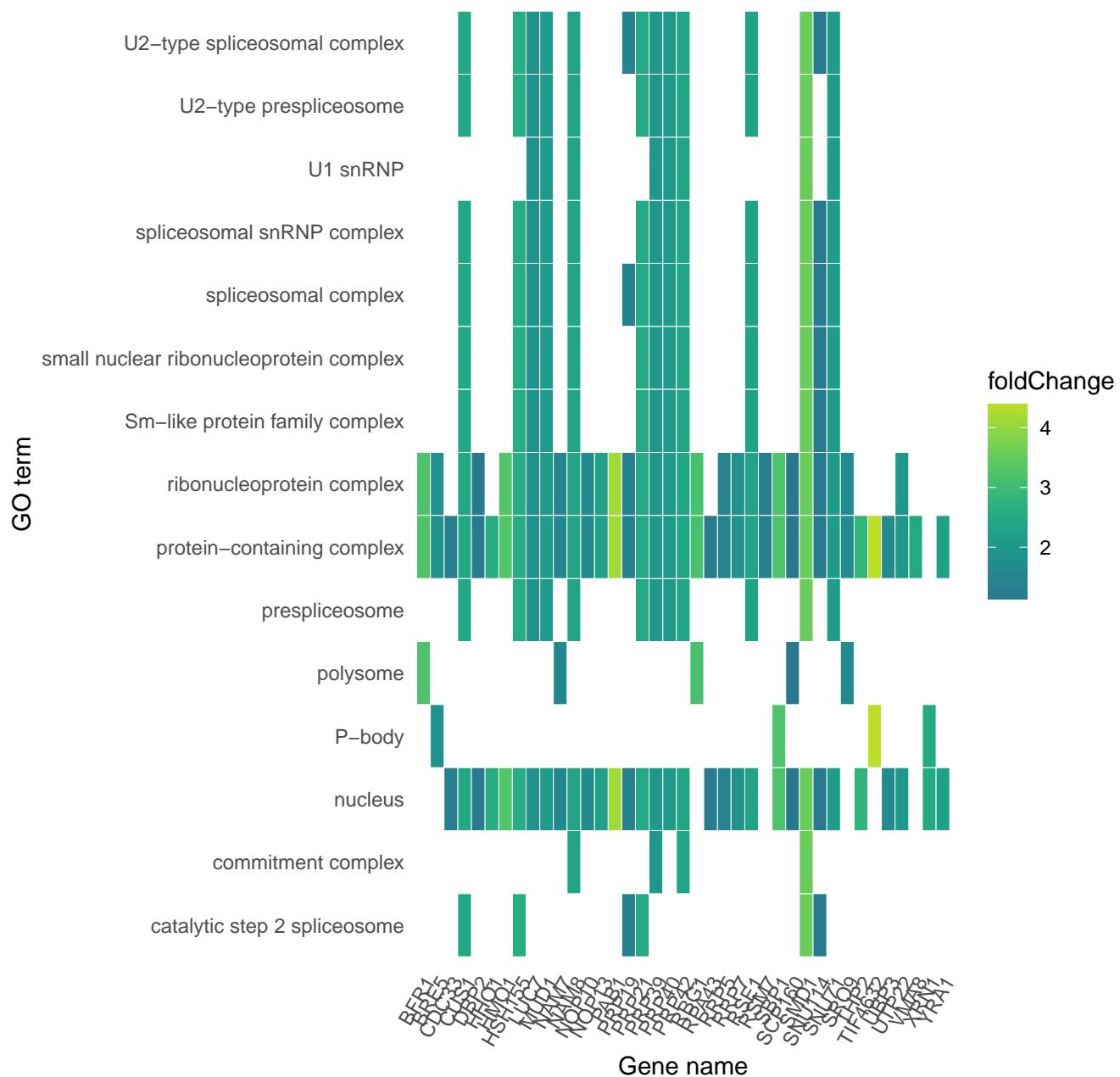
CBC2-TAP Up-regulated GO CC dotplot



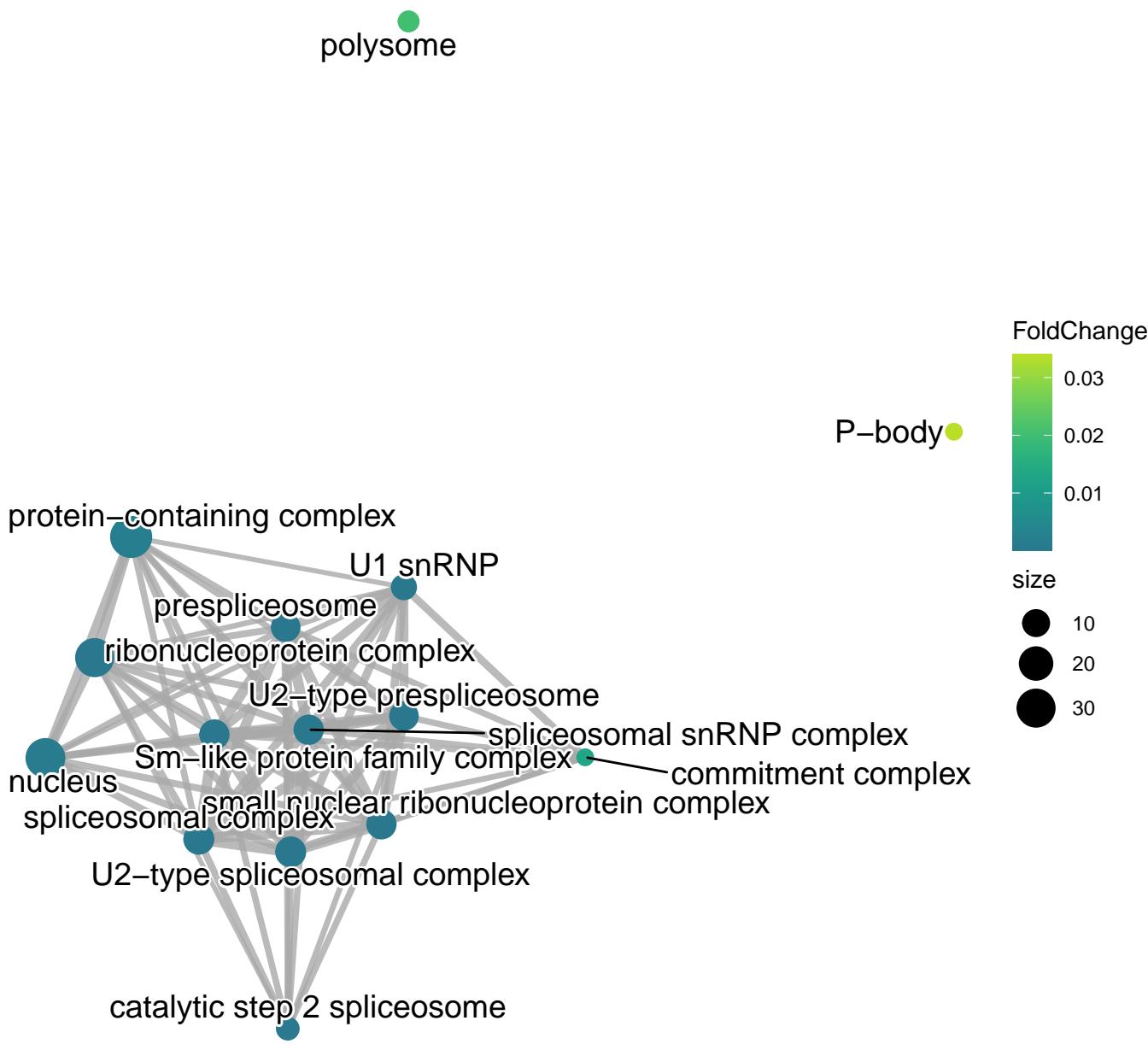
CBC2-TAP Up-regulated GO CC cnetplot

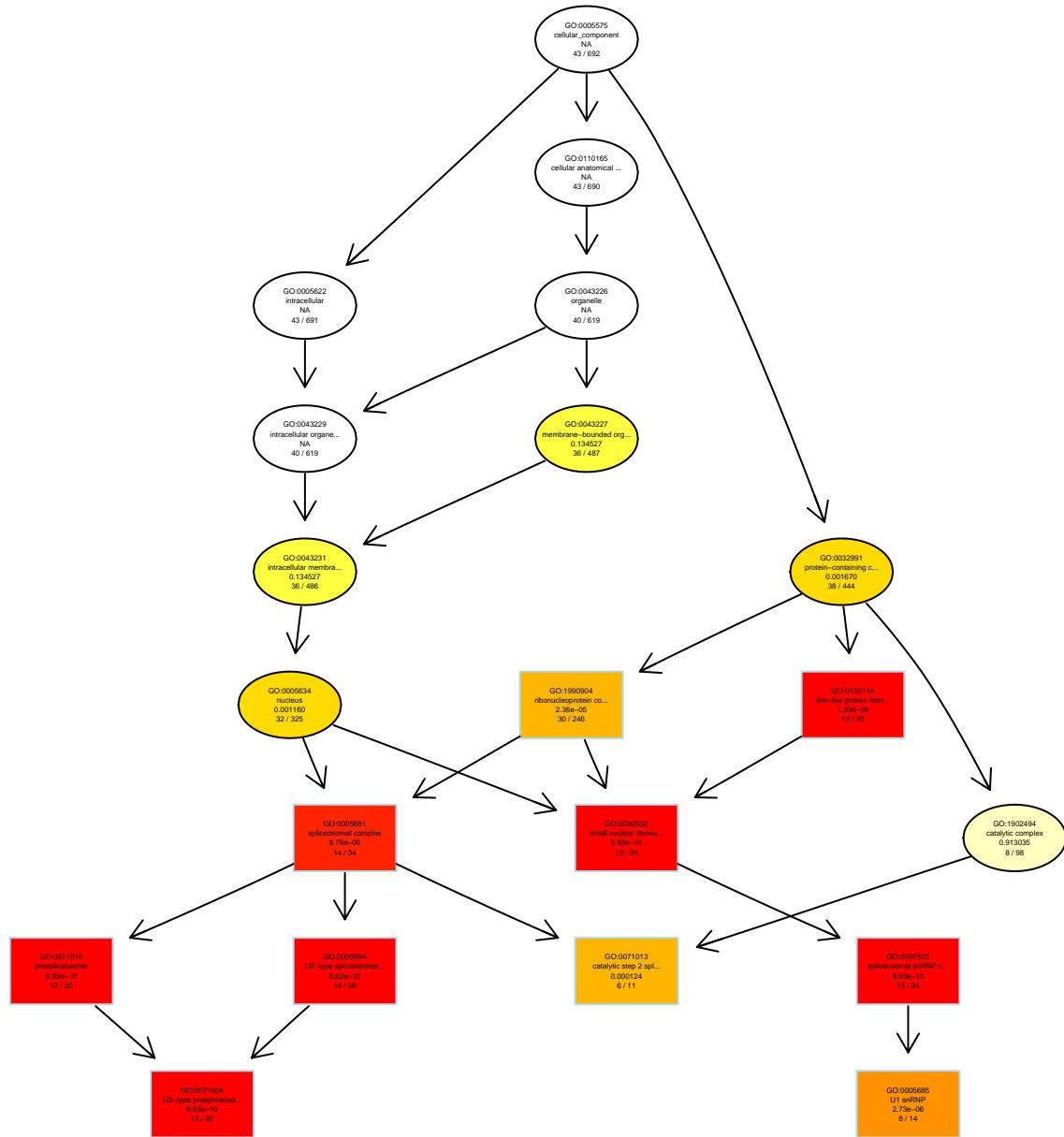


CBC2-TAP Up-regulated GO CC heatplot

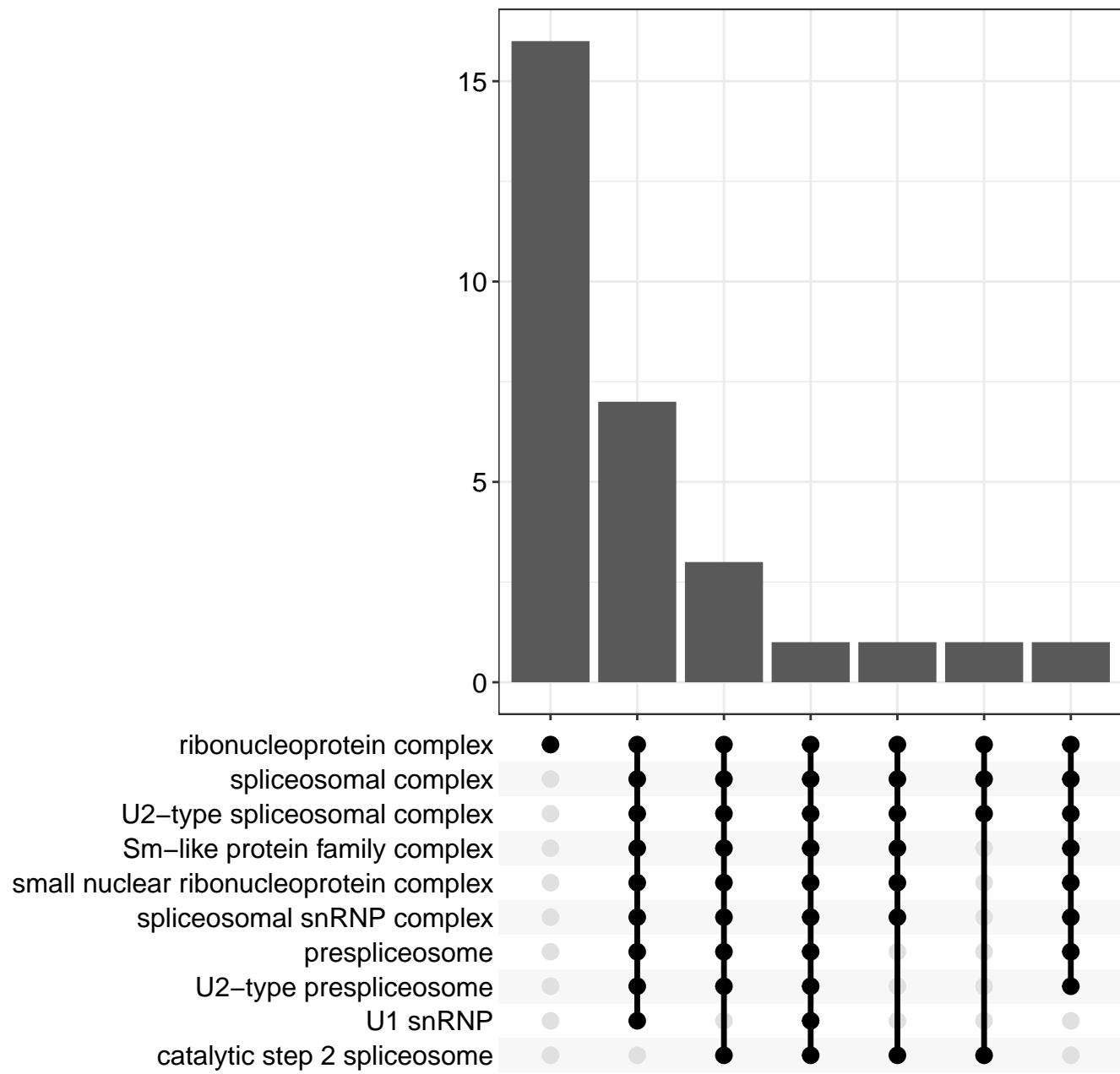


CBC2-TAP Up-regulated GO CC emapplot

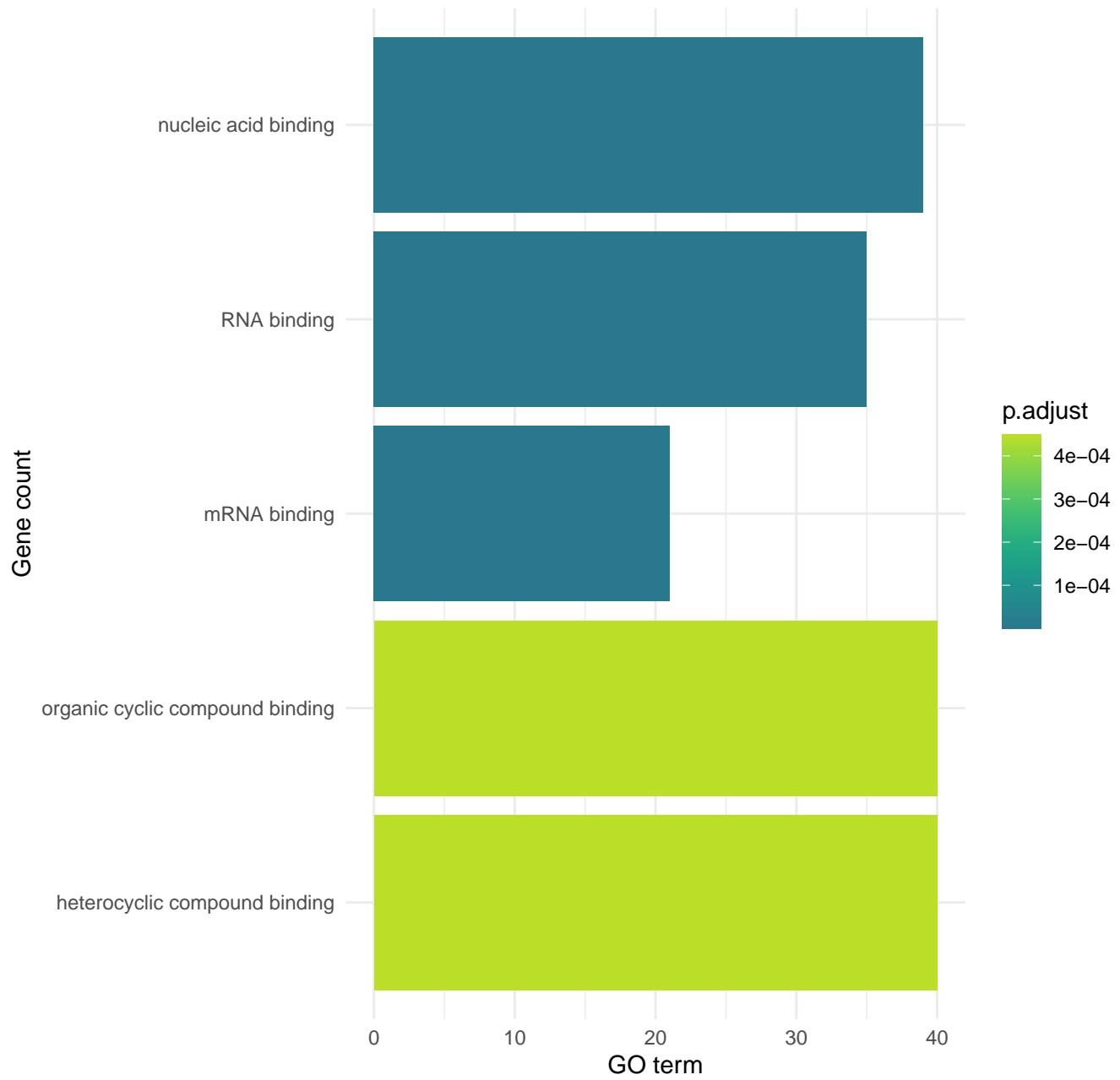




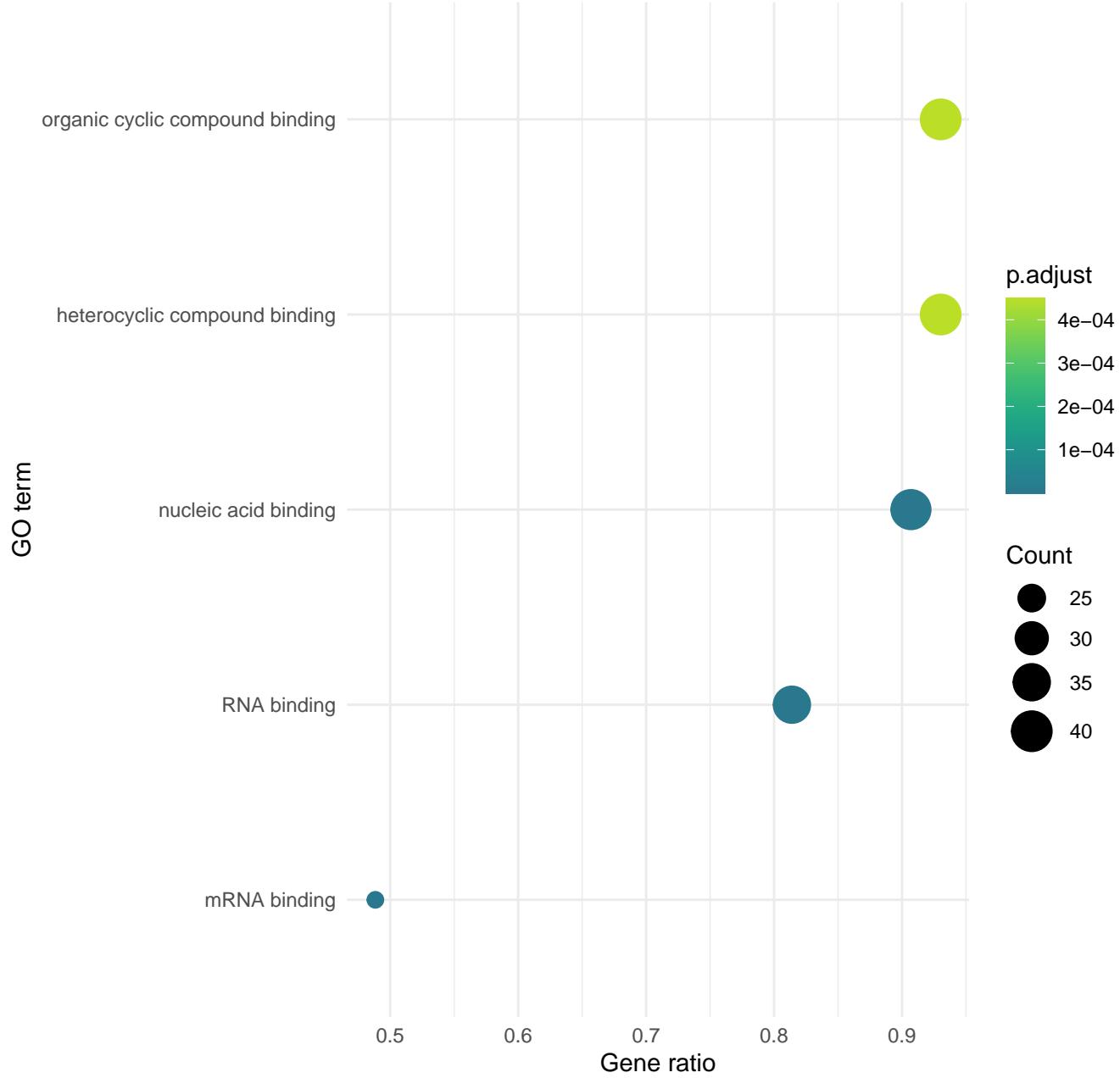
CBC2-TAP Up-regulated GO CC upsetplot



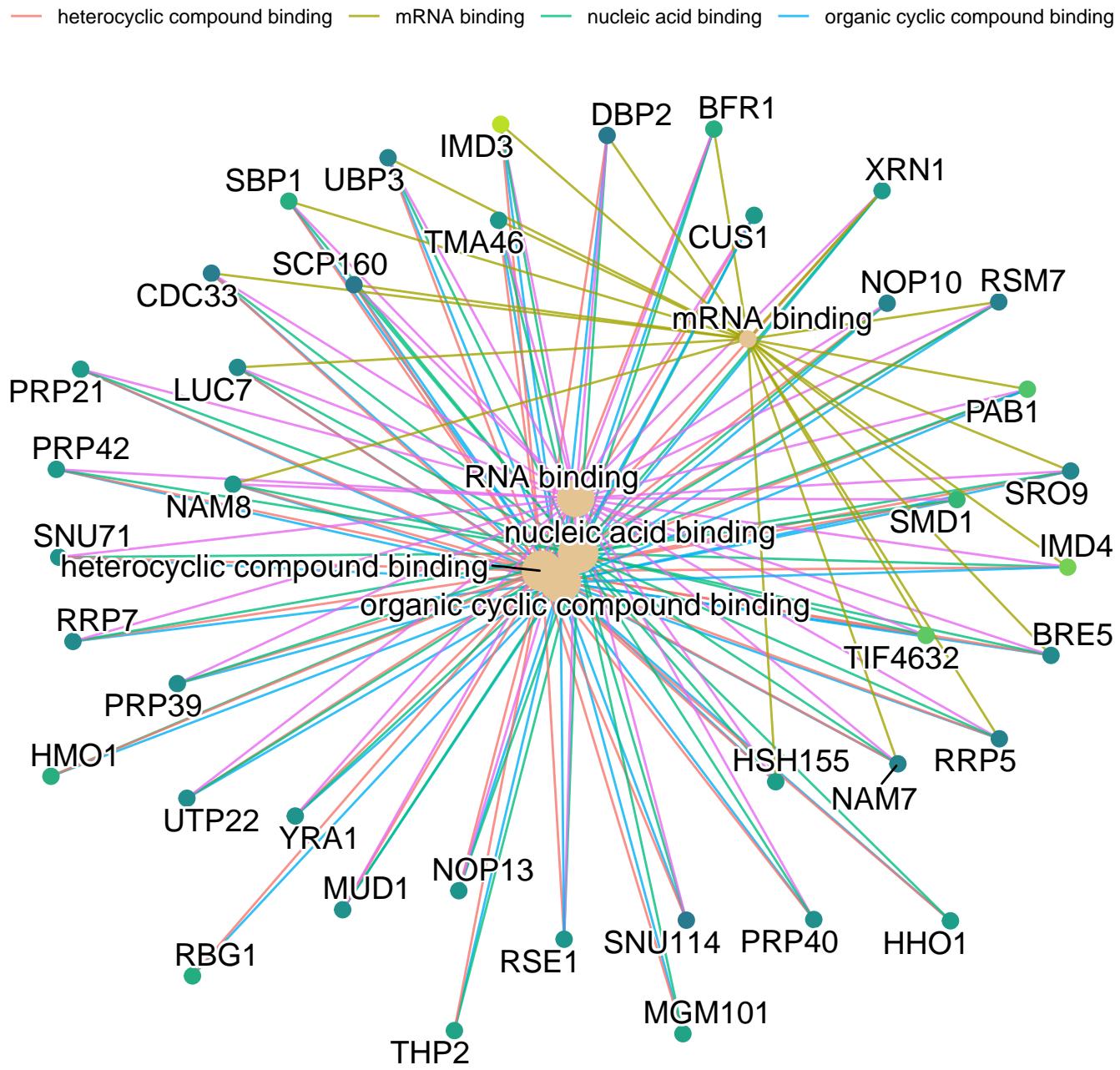
CBC2-TAP Up-regulated GO MF barplot



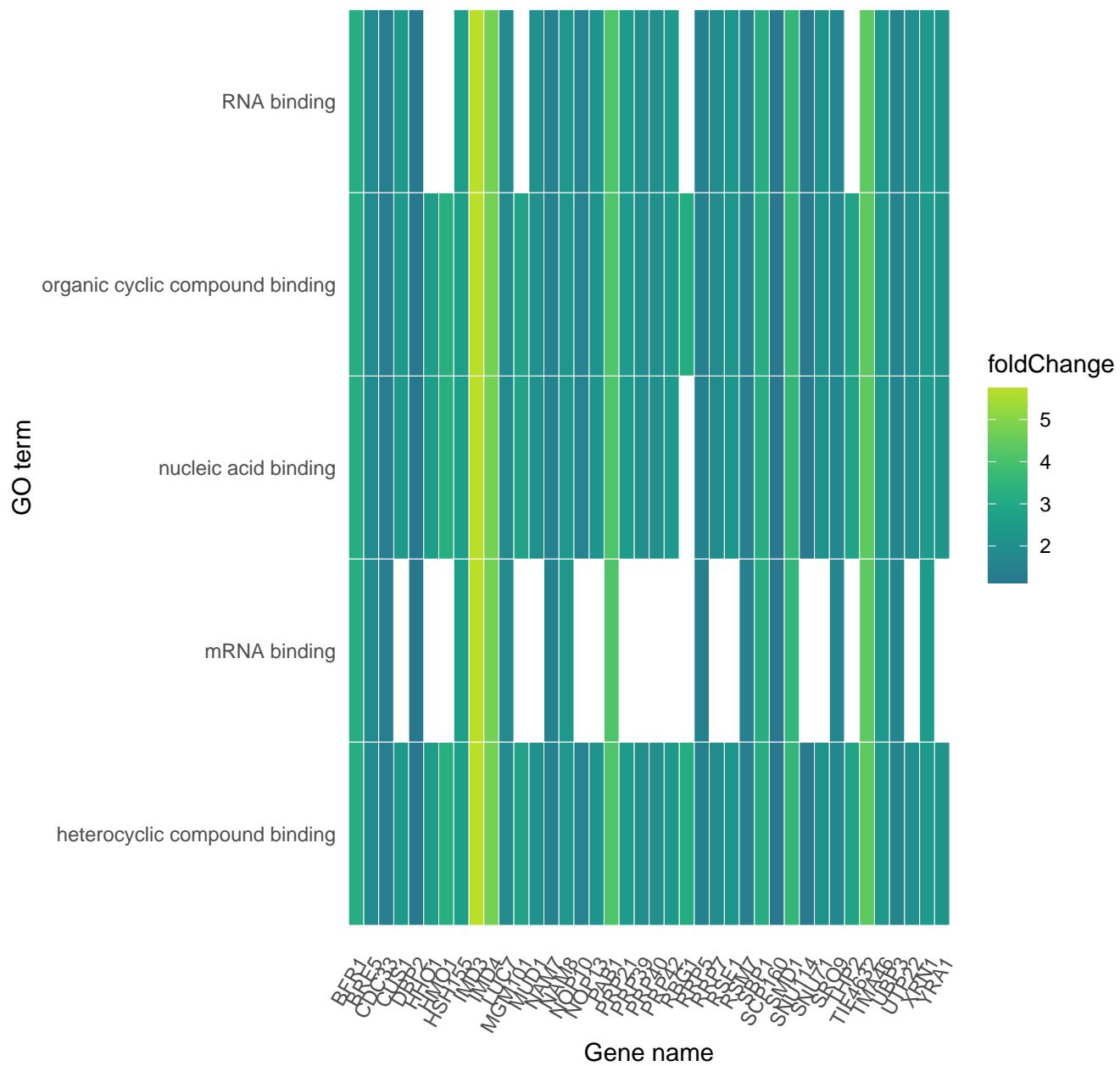
CBC2-TAP Up-regulated GO MF dotplot



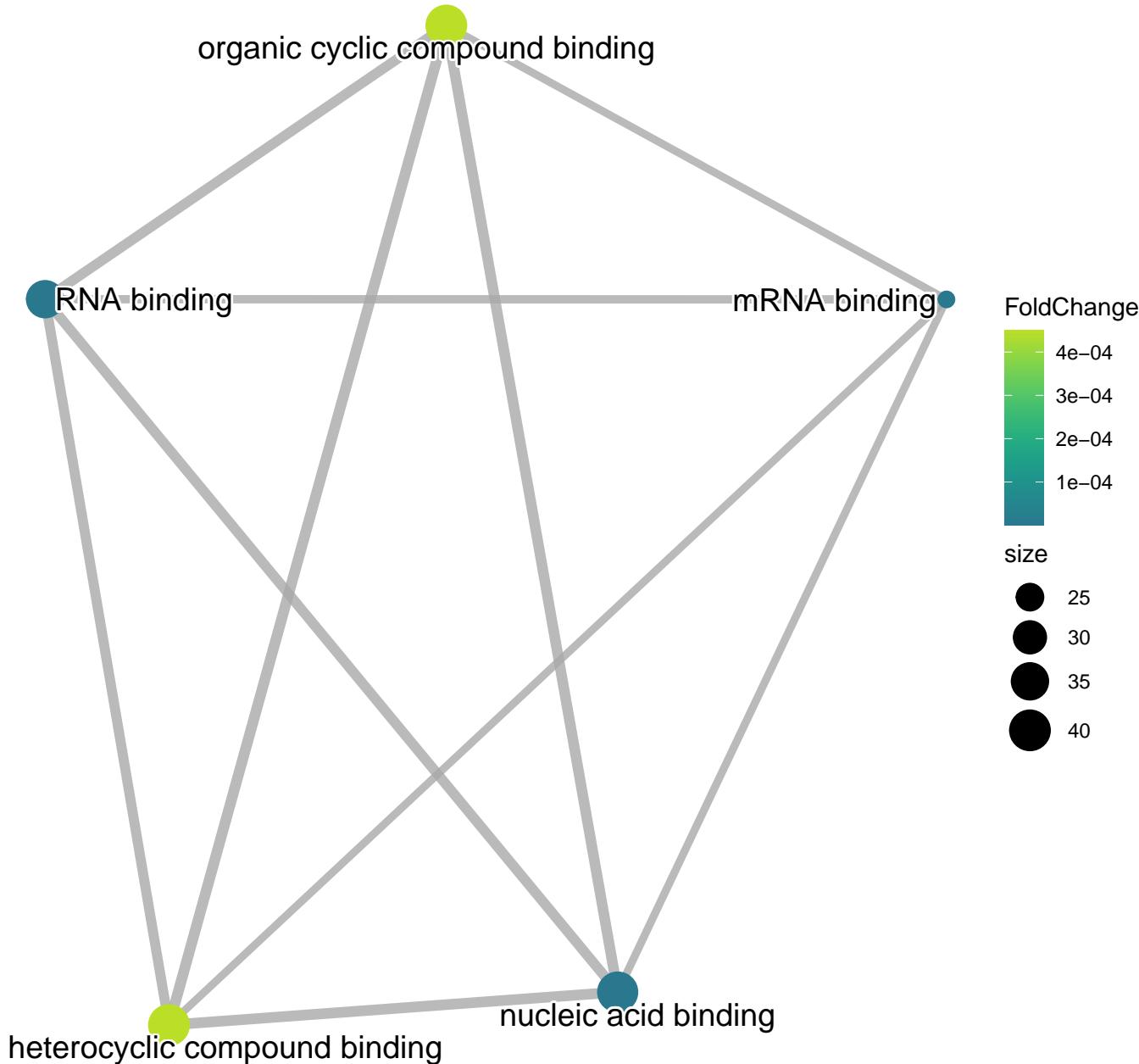
CBC2-TAP Up-regulated GO MF cnetplot

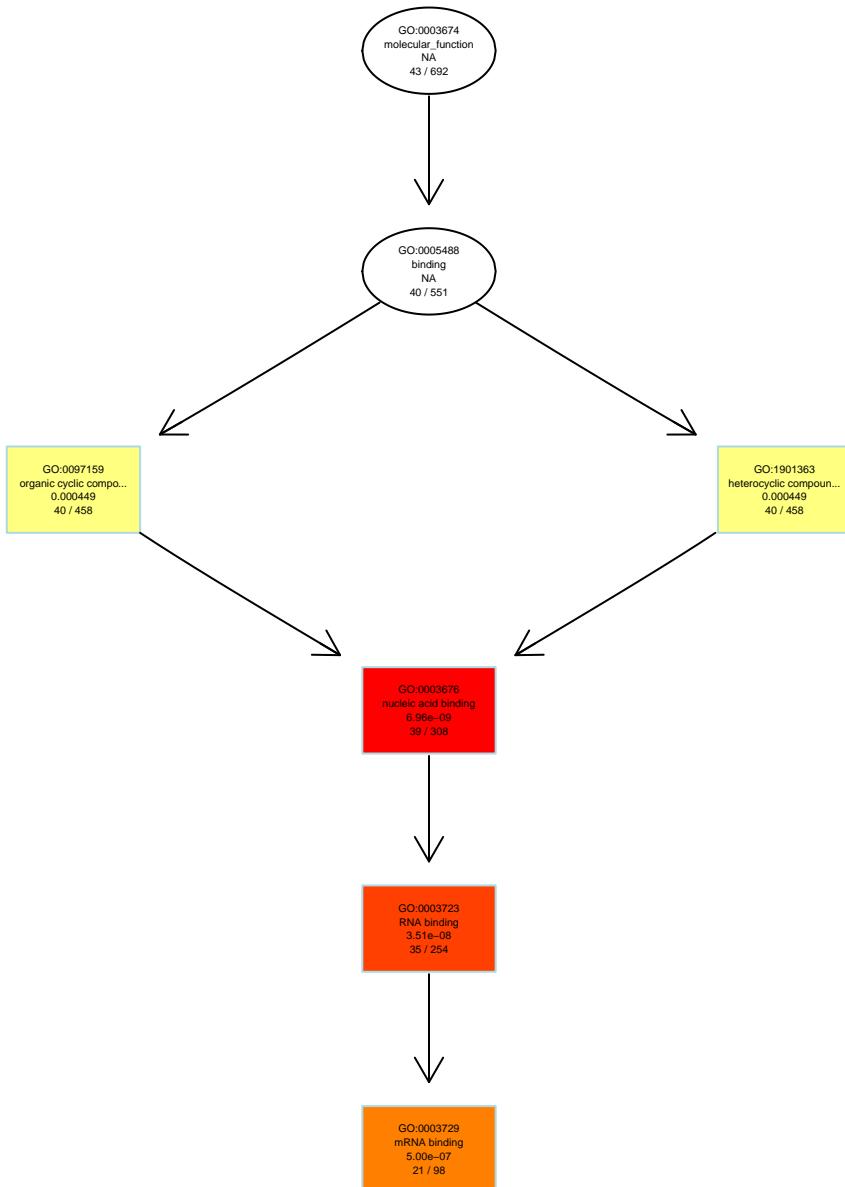


CBC2-TAP Up-regulated GO MF heatplot

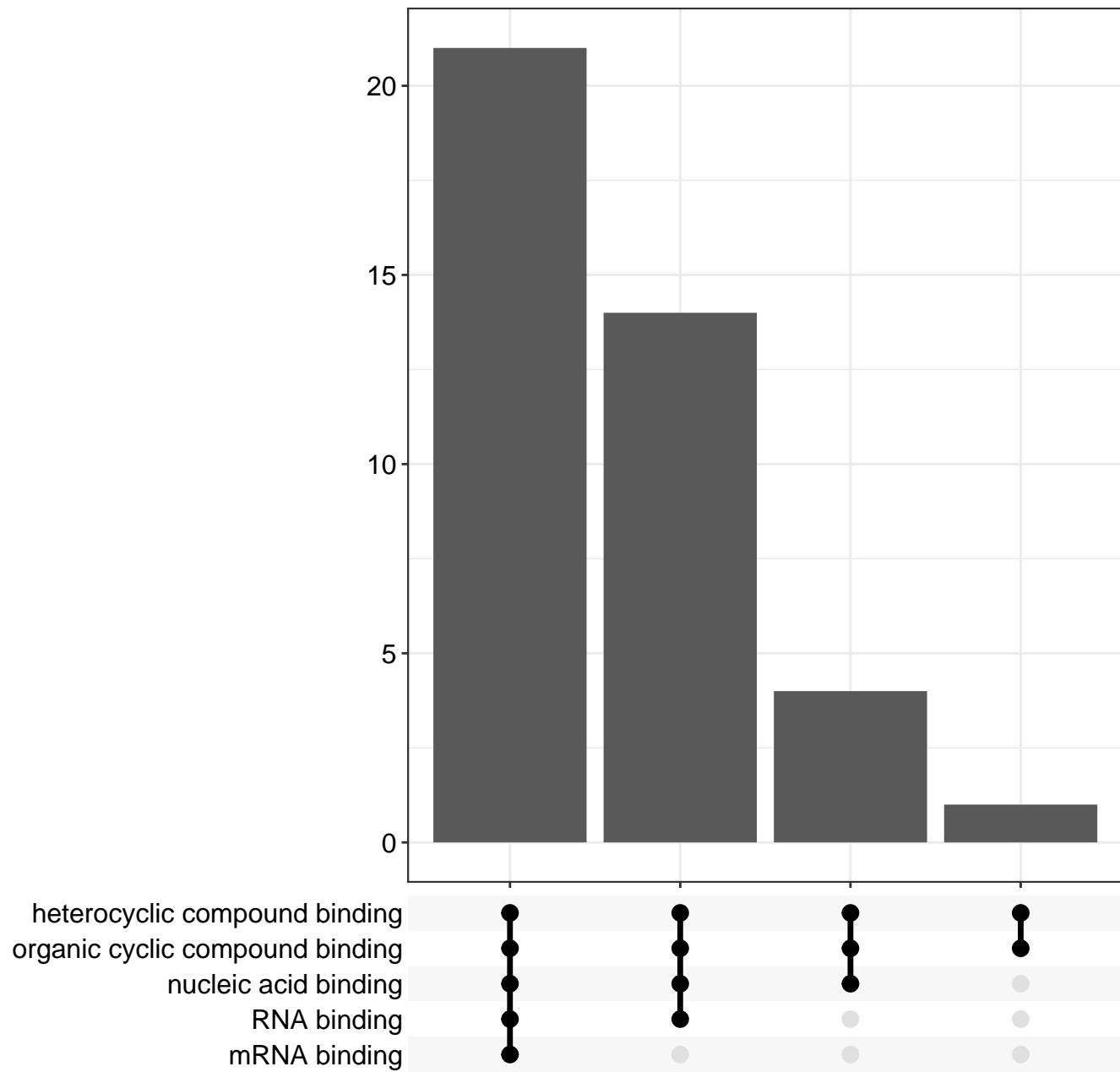


CBC2-TAP Up-regulated GO MF emapplot

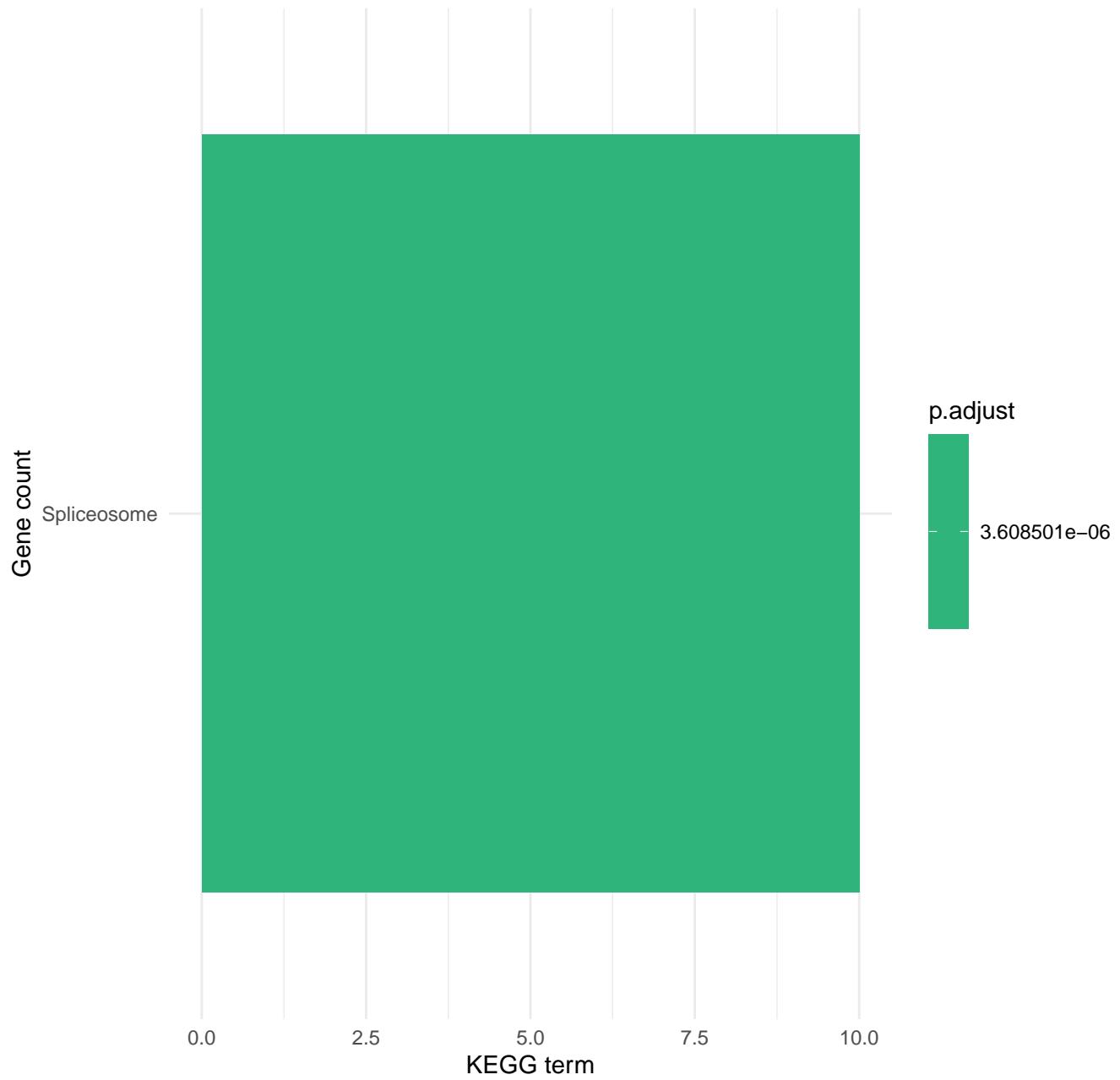




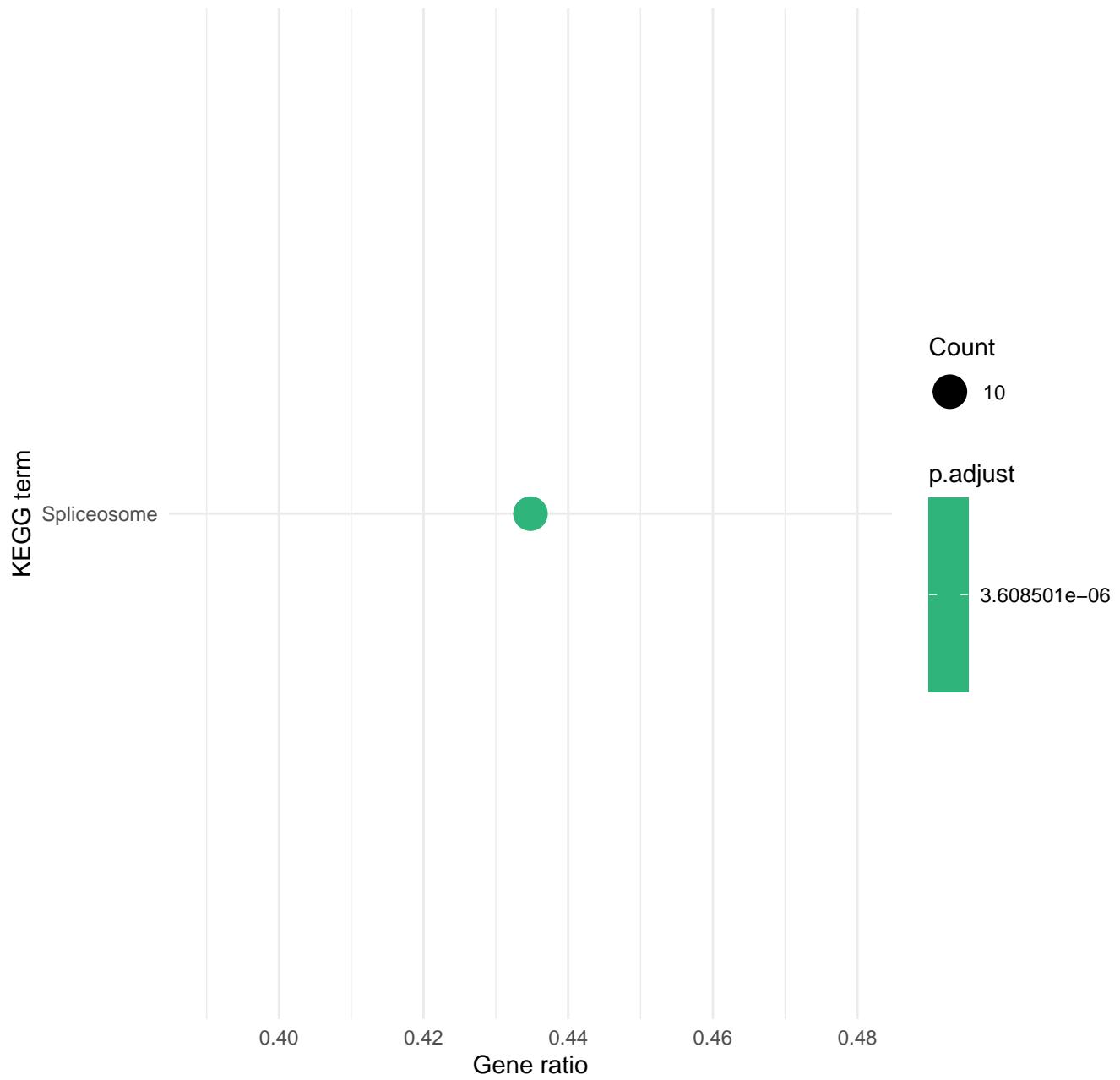
CBC2-TAP Up-regulated GO MF upsetplot



CBC2–TAP Up-regulated KEGG barplot



CBC2-TAP Up-regulated KEGG dotplot



CBC2-TAP Up-regulated KEGG dotplot

category

Spliceosome

size

FoldChange

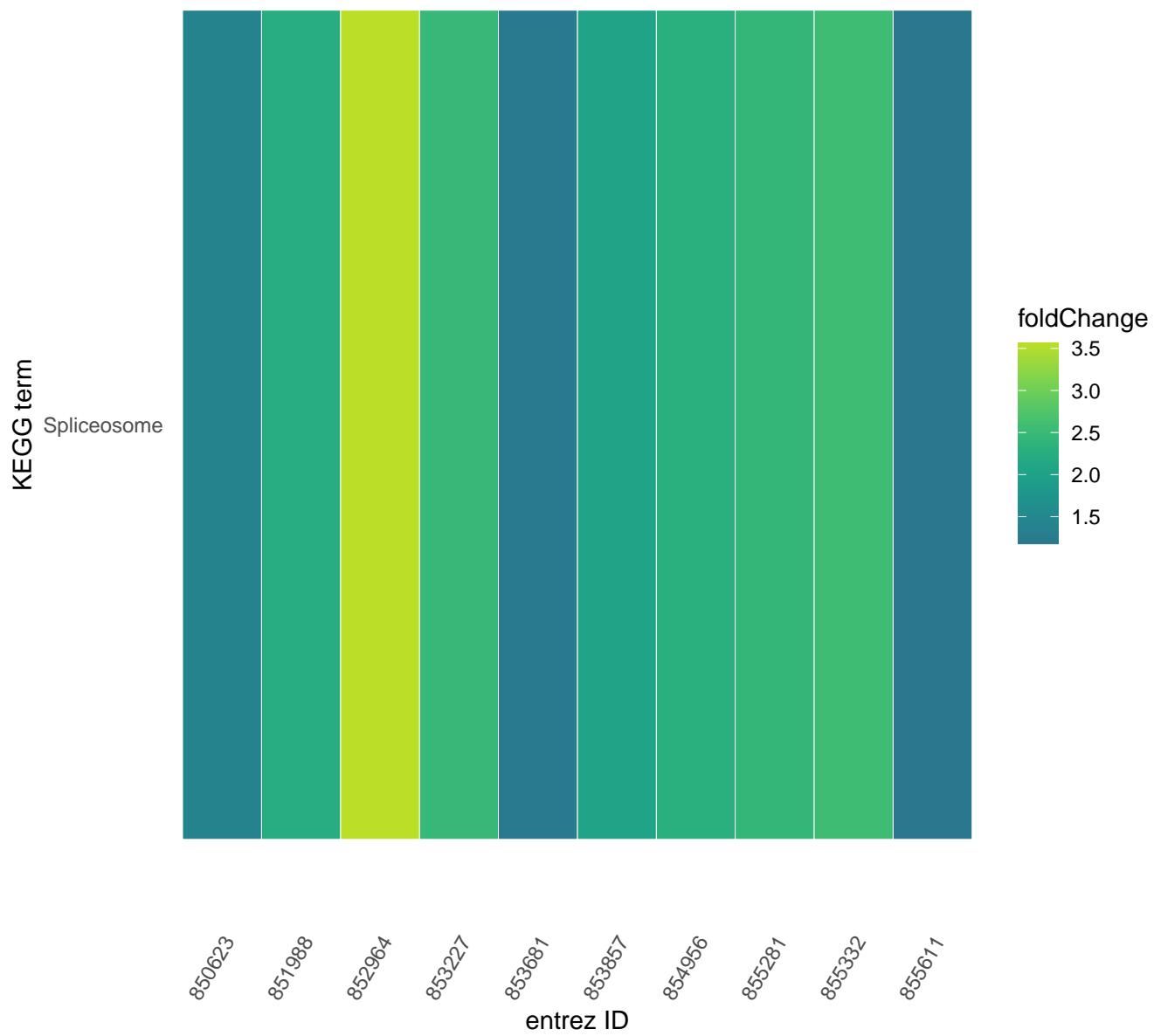
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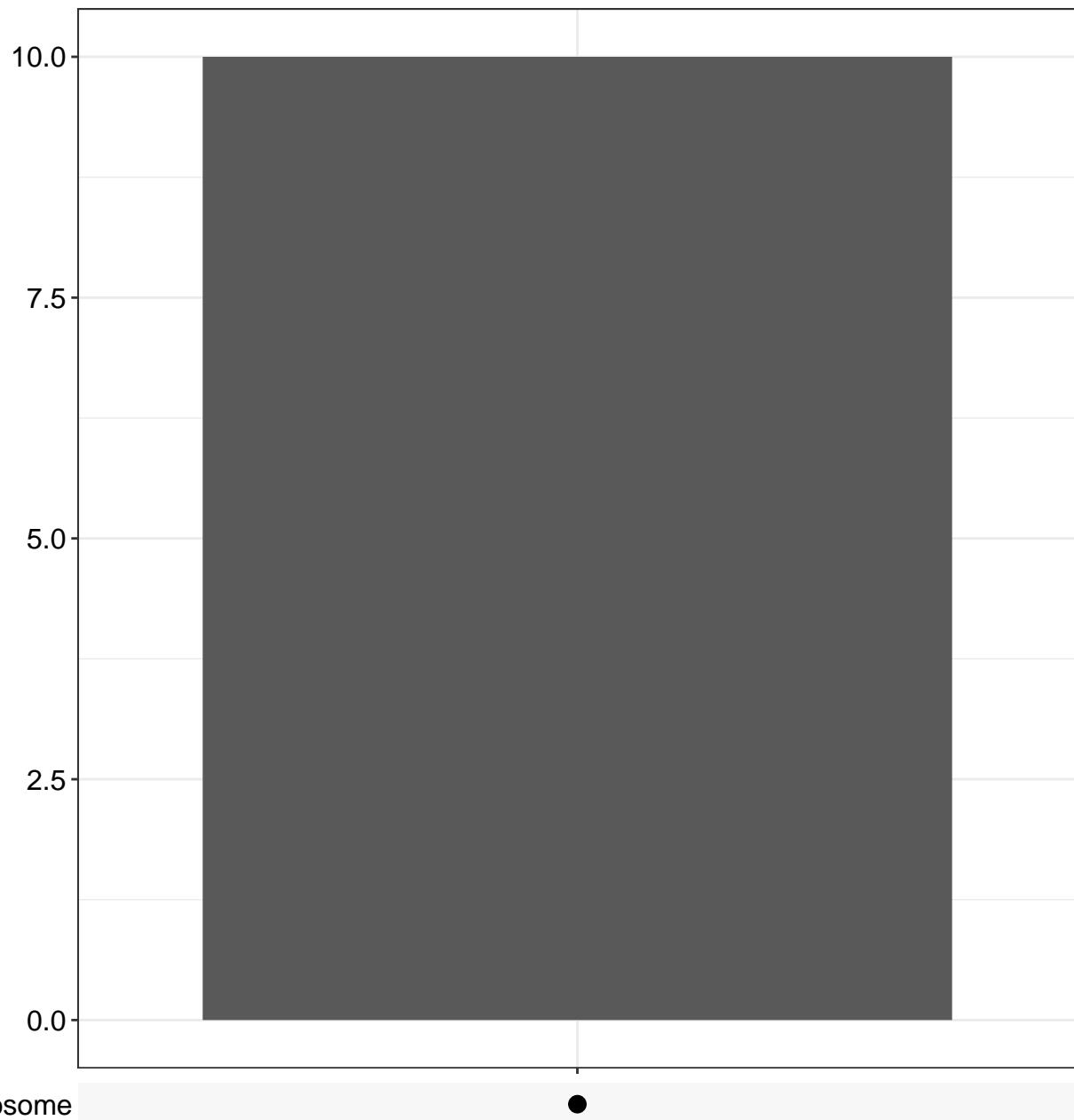
1.5 2.0 2.5 3.0 3.5



CBC2-TAP Up-regulated KEGG heatplot

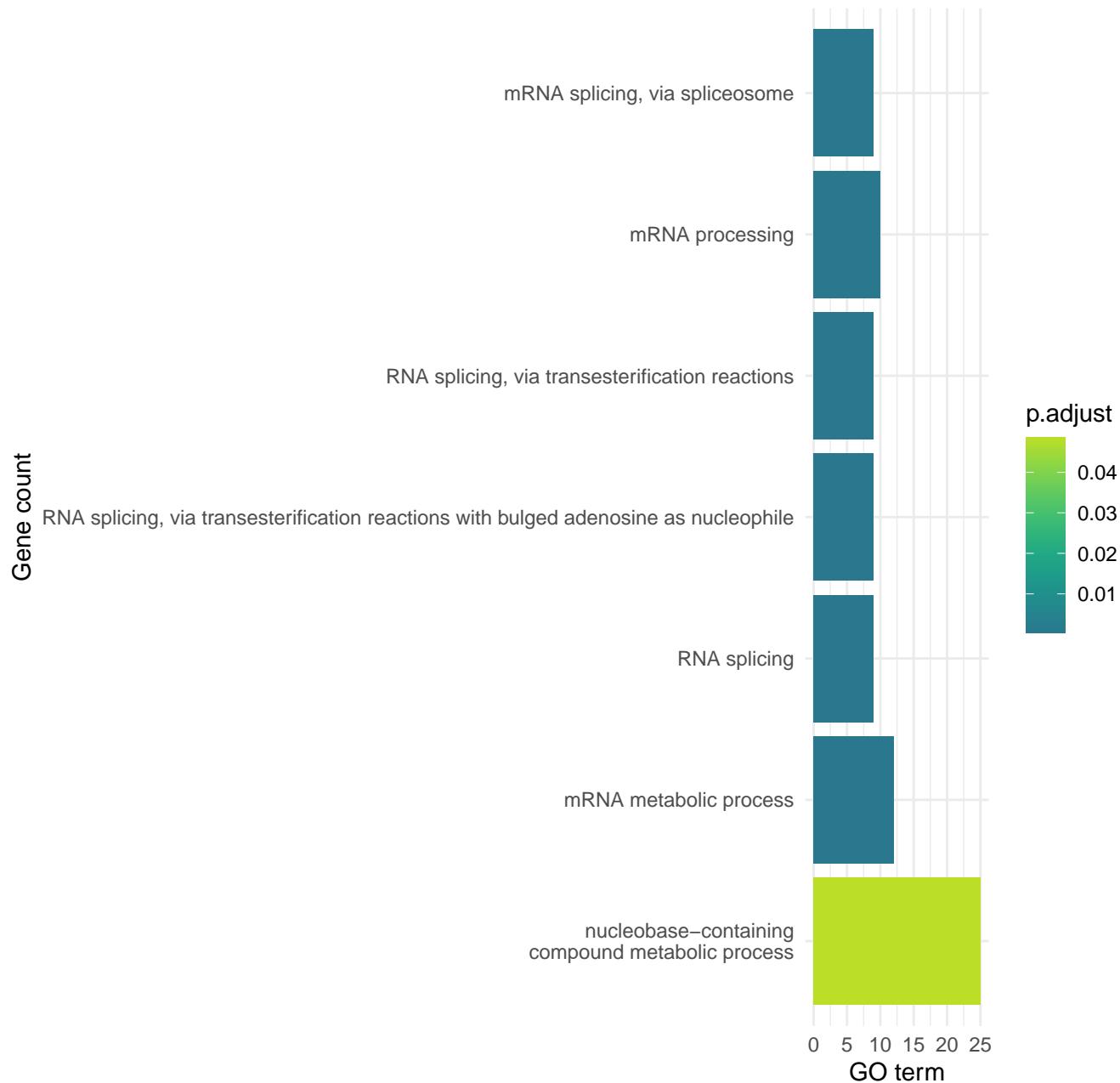


CBC2-TAP Up-regulated KEGG upsetplot

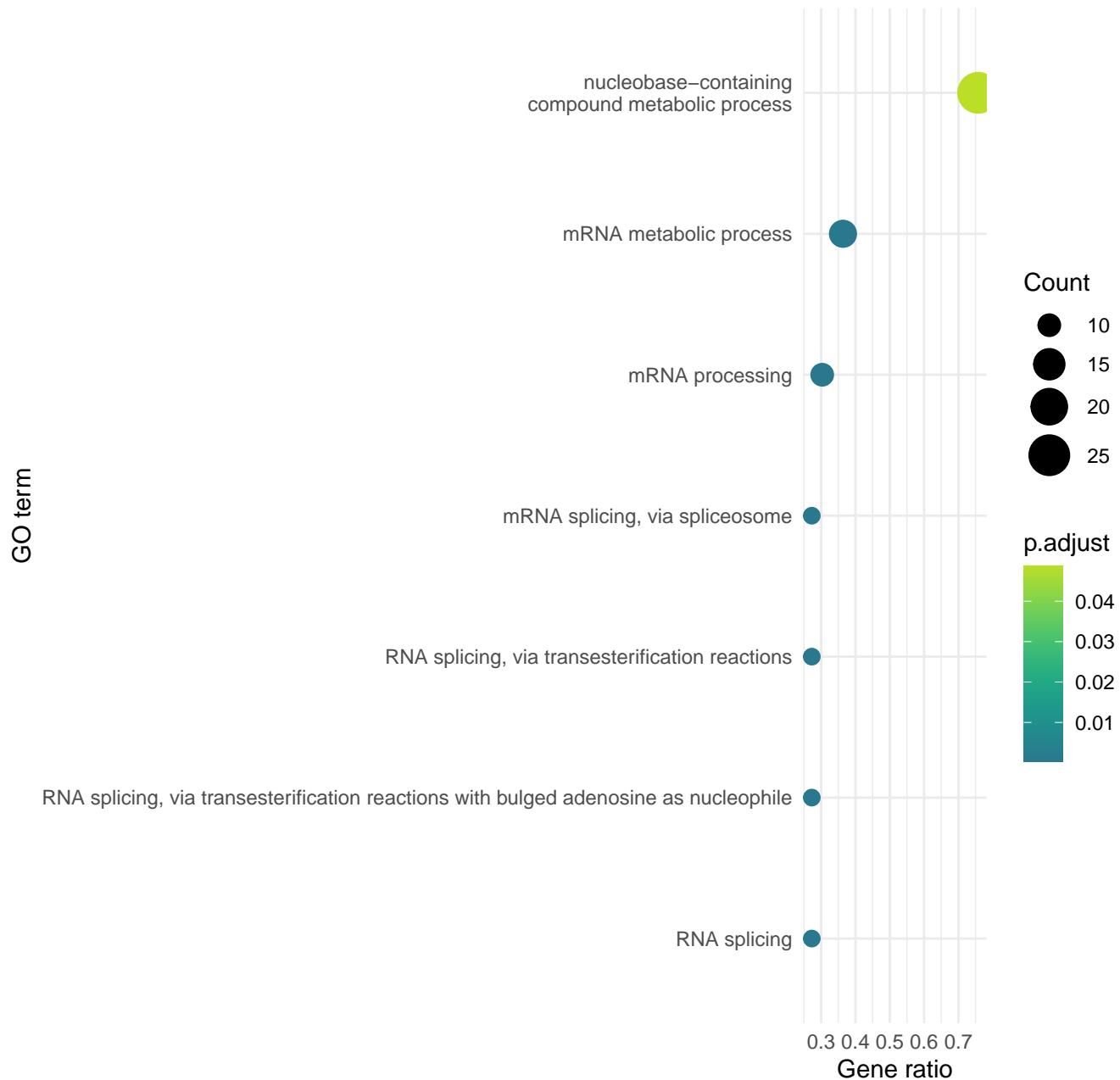


Spliceosome

MSL1-TAP Up-regulated



MSL1-TAP Up-regulated



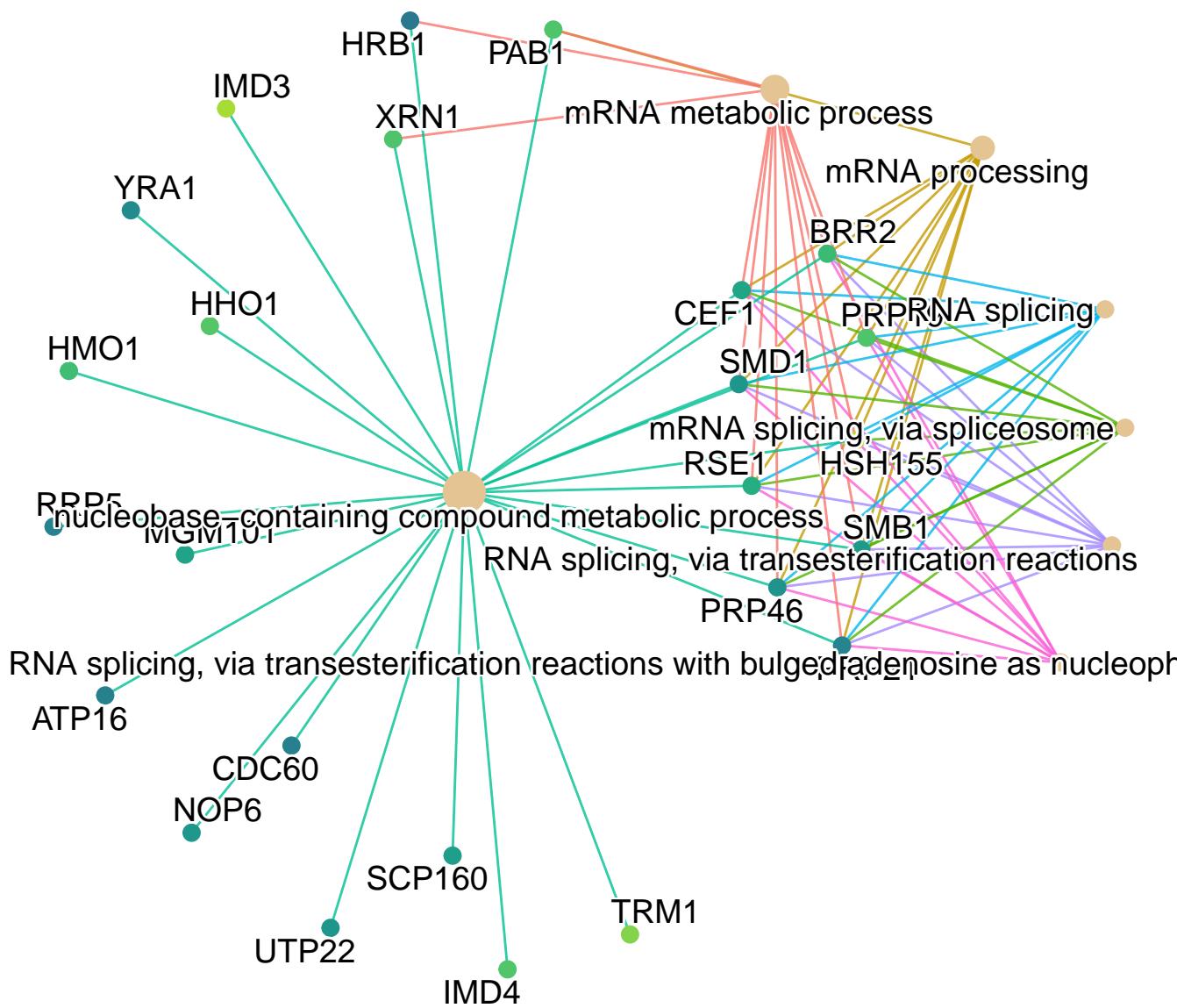
MSL1-TAP Up-regulated GO BP cnetplot

mRNA metabolic process mRNA processing

mRNA splicing, via spliceosome nucleobase-containing compound metabolic process

RNA splicing

RNA splicing, via transesterification reactions



MSL1-TAP Up-regulated

GO term

RNA splicing, via transesterification reactions with bulged adenosine as nucleophile

RNA splicing, via transesterification reactions

RNA splicing

nucleobase-containing compound metabolic process

mRNA splicing, via spliceosome

mRNA processing

mRNA metabolic process

foldChange

4

3

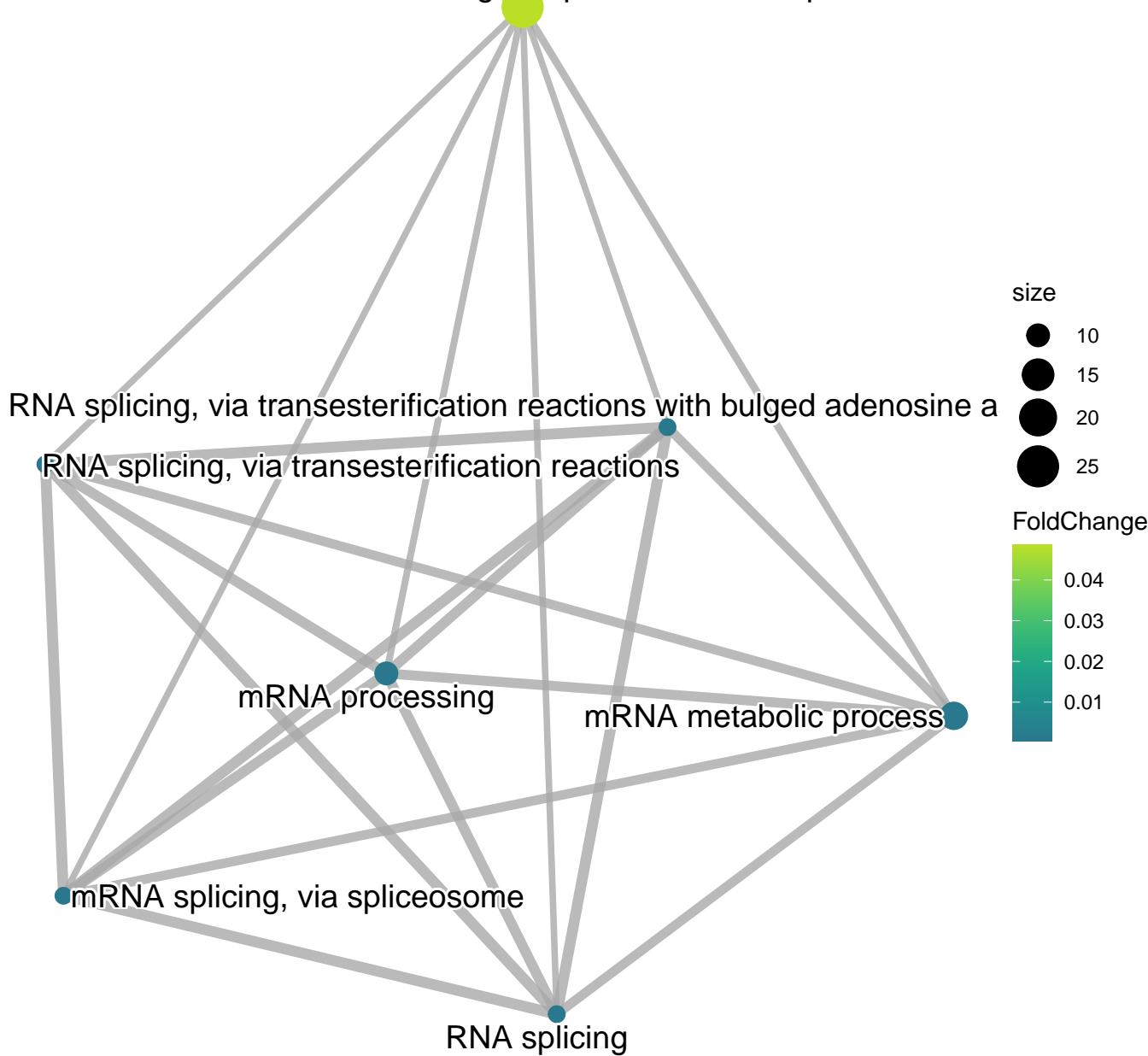
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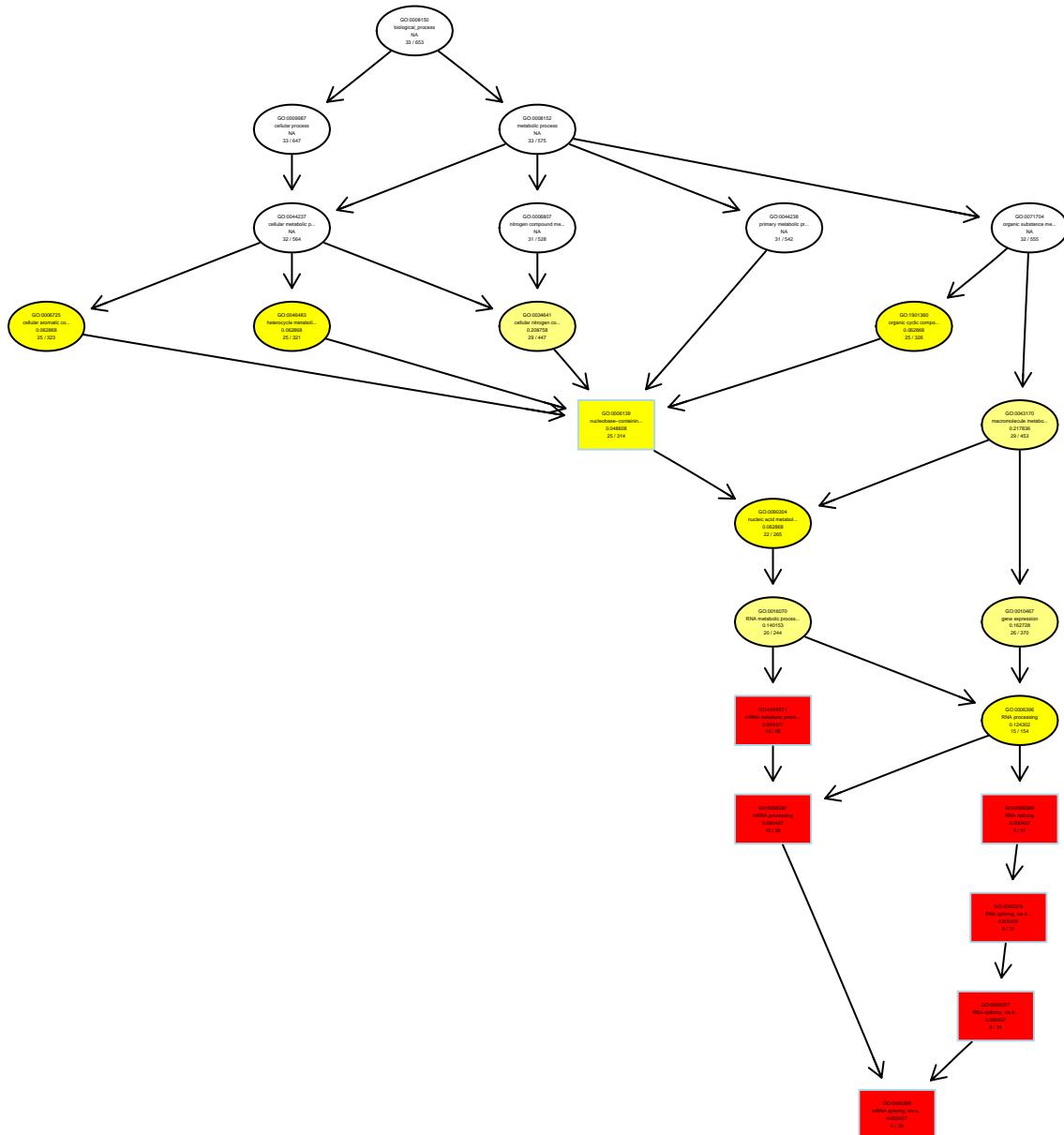


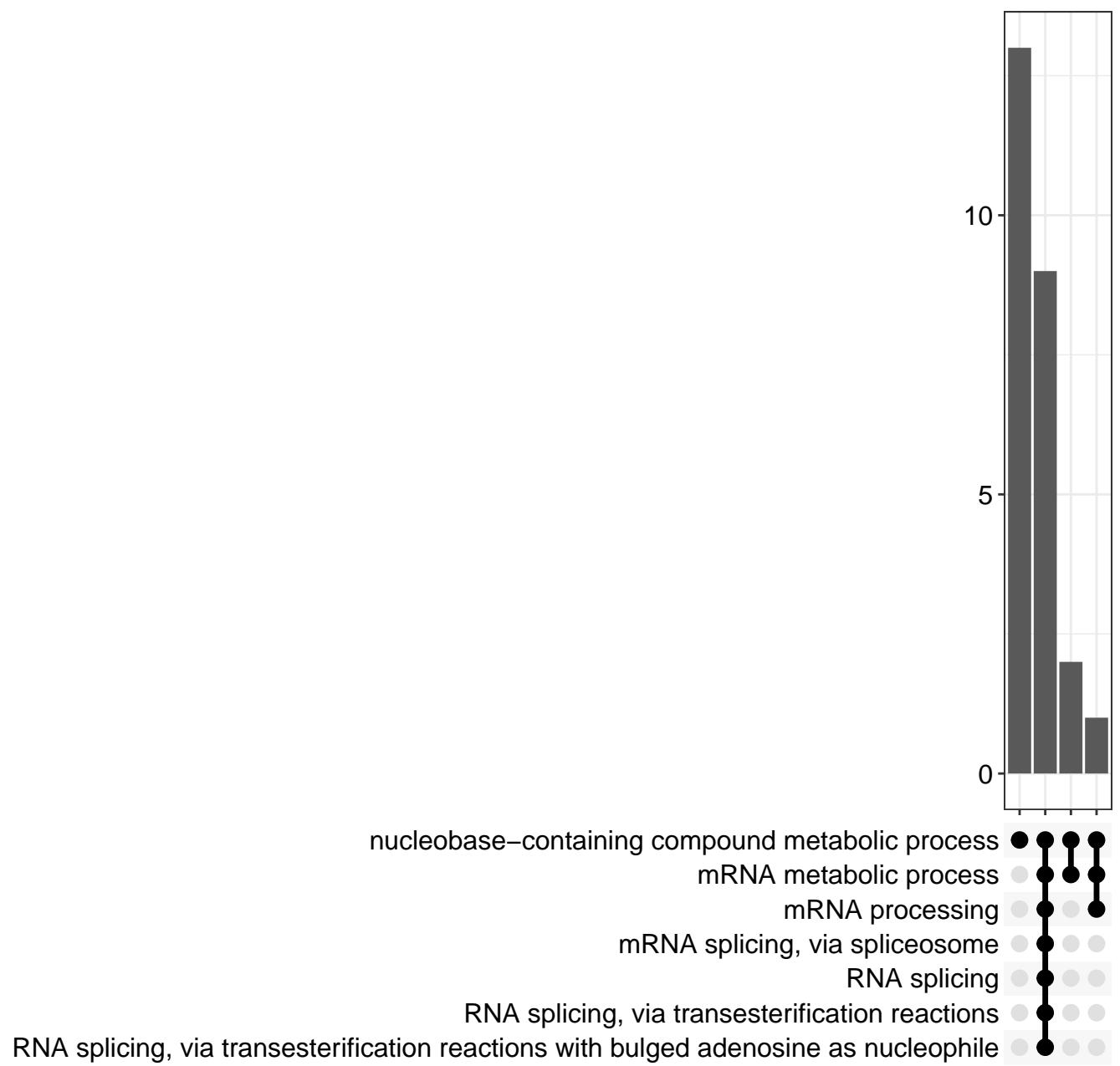
Gene name

MSL1-TAP Up-regulated GO BP emapplot

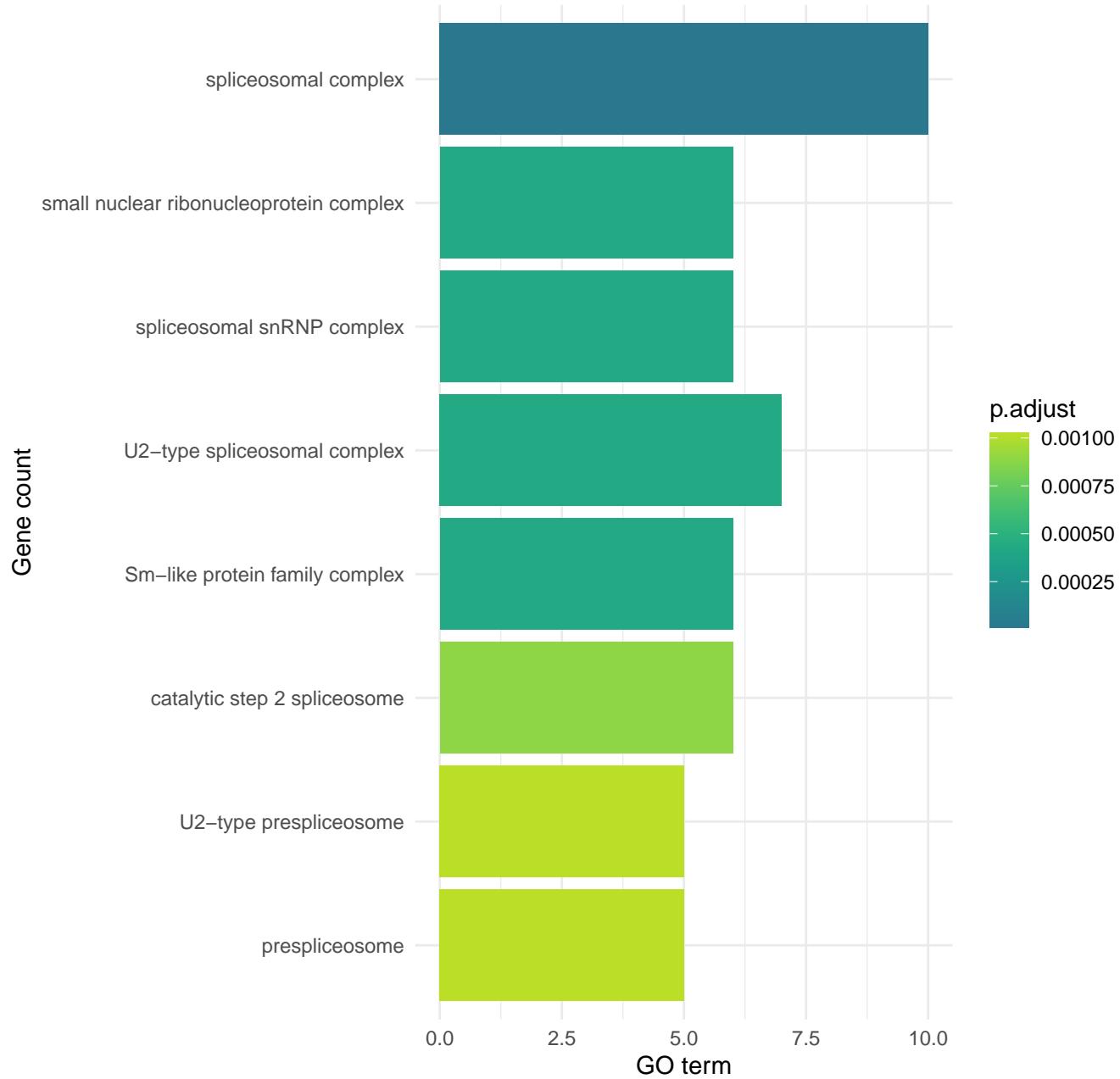
nucleobase-containing compound metabolic process



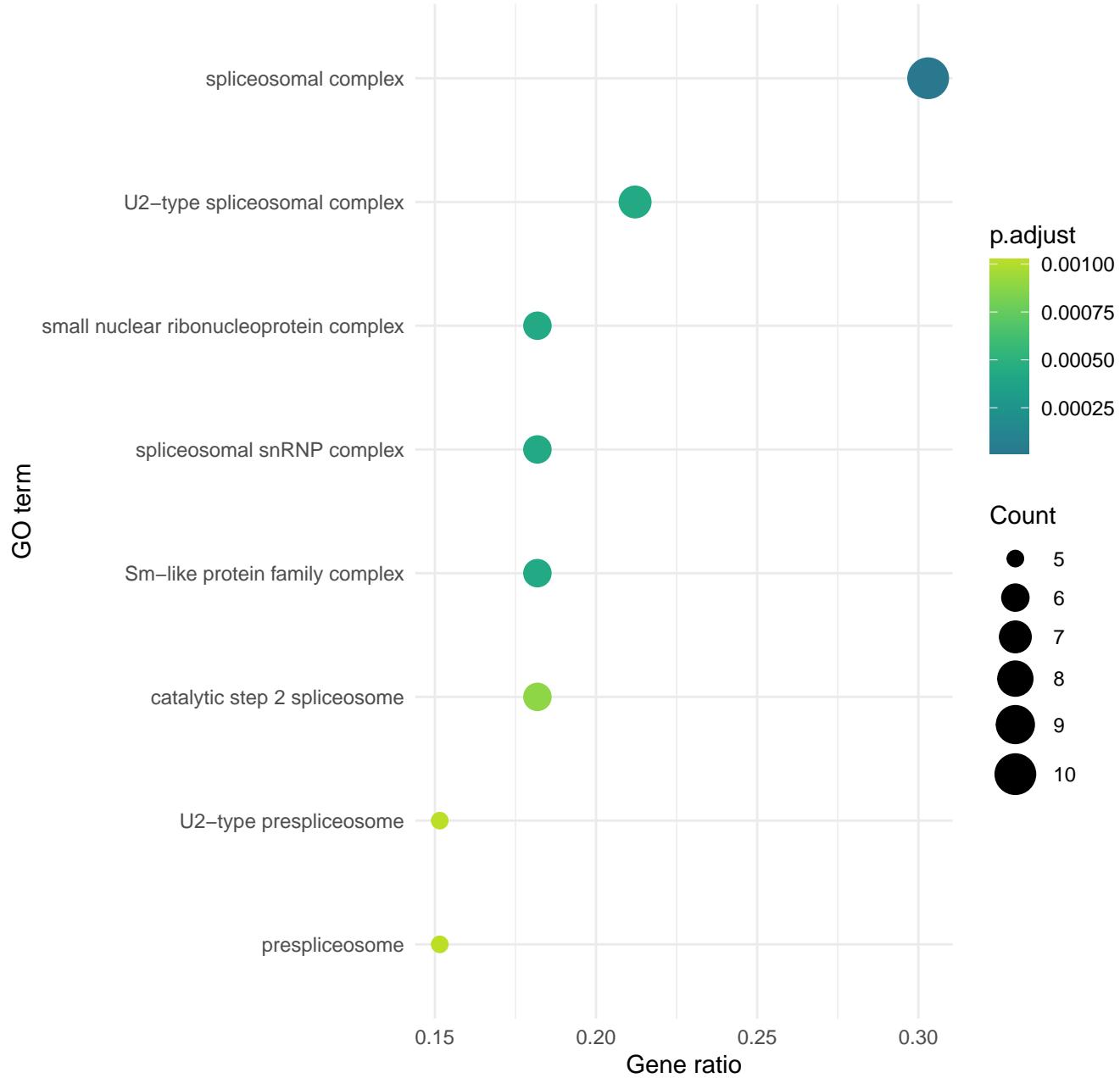




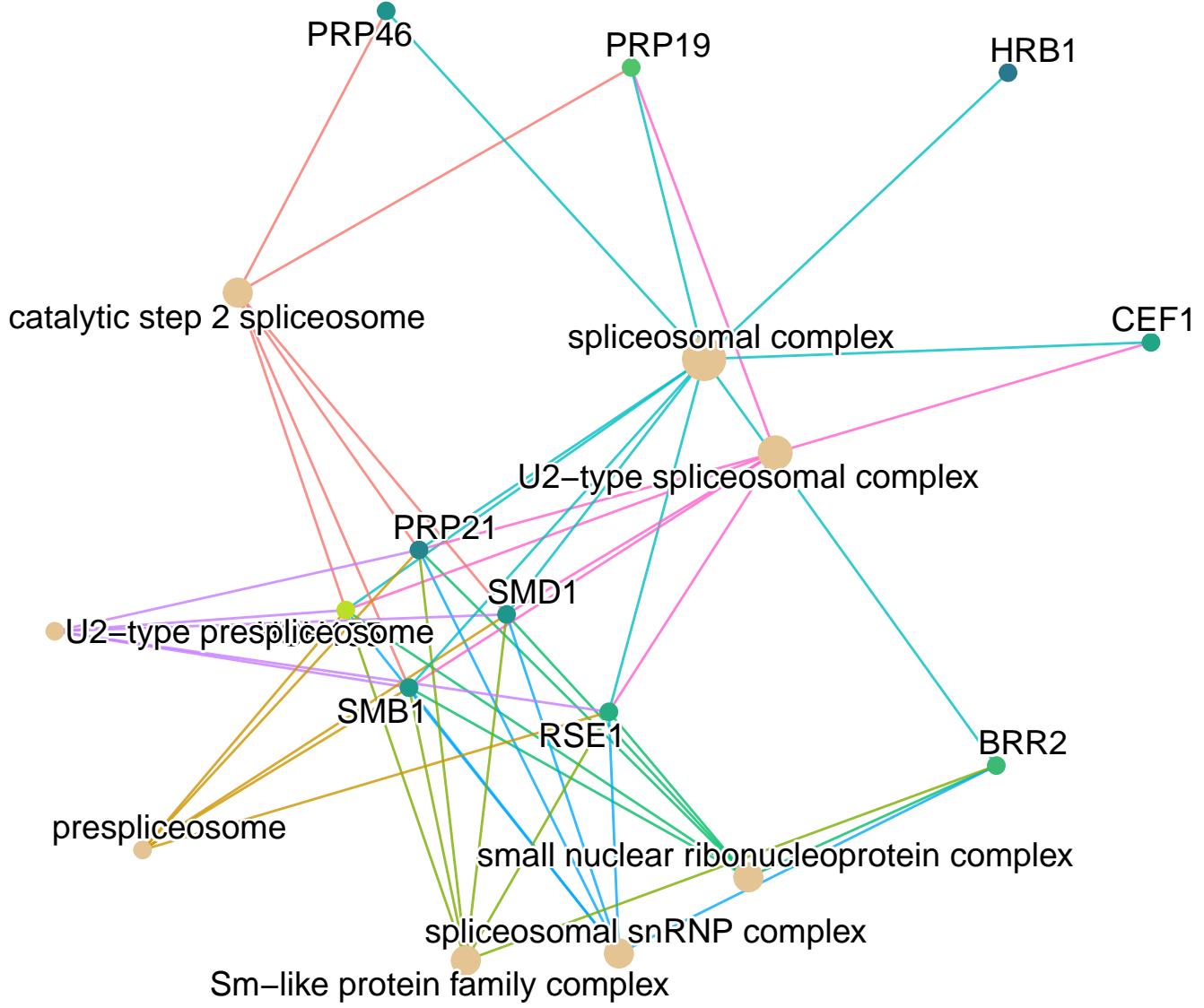
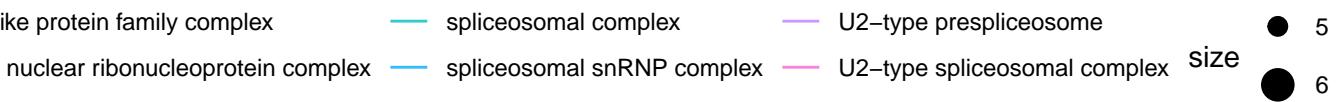
MSL1-TAP Up-regulated GO CC barplot



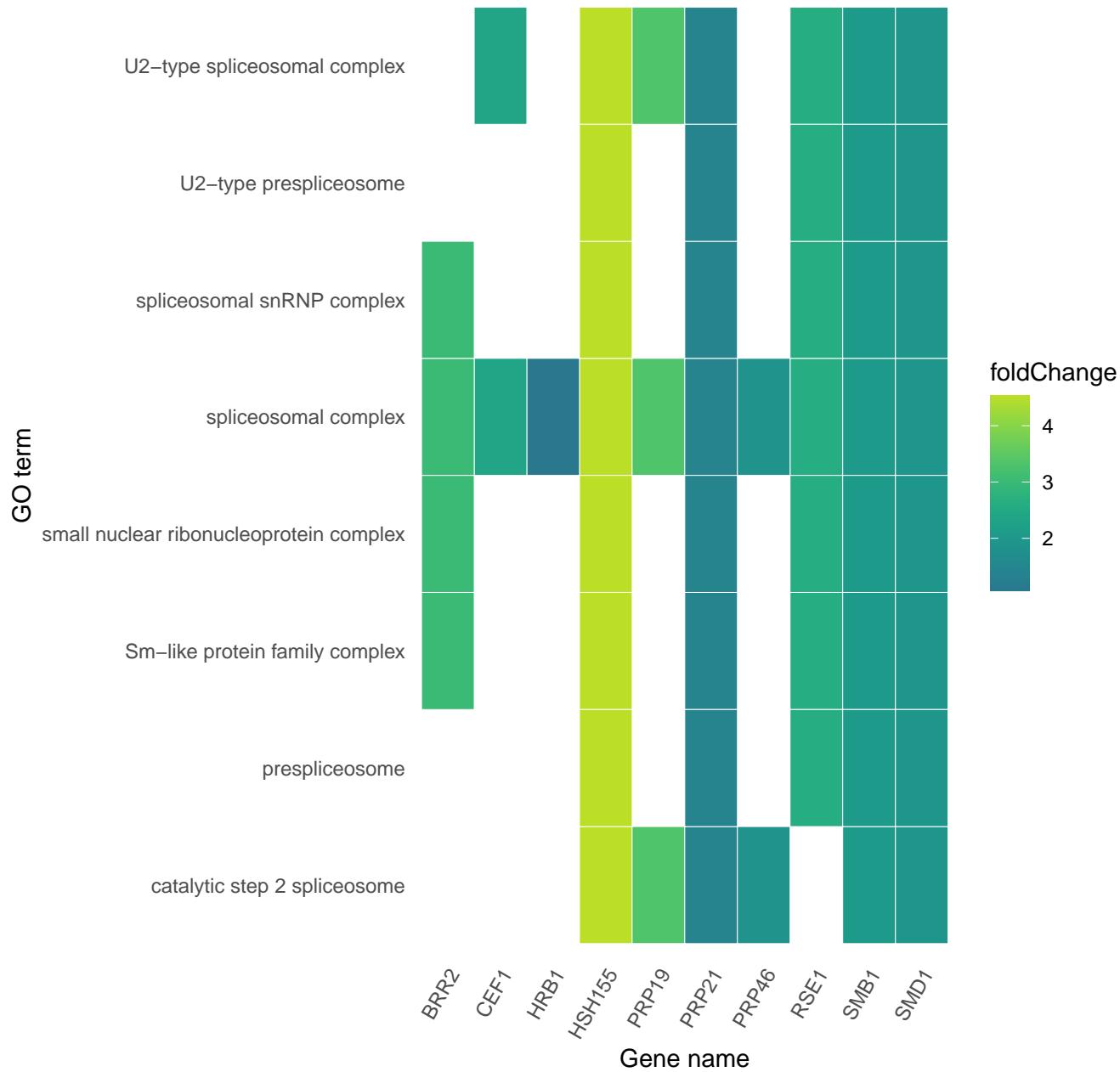
MSL1-TAP Up-regulated GO CC dotplot



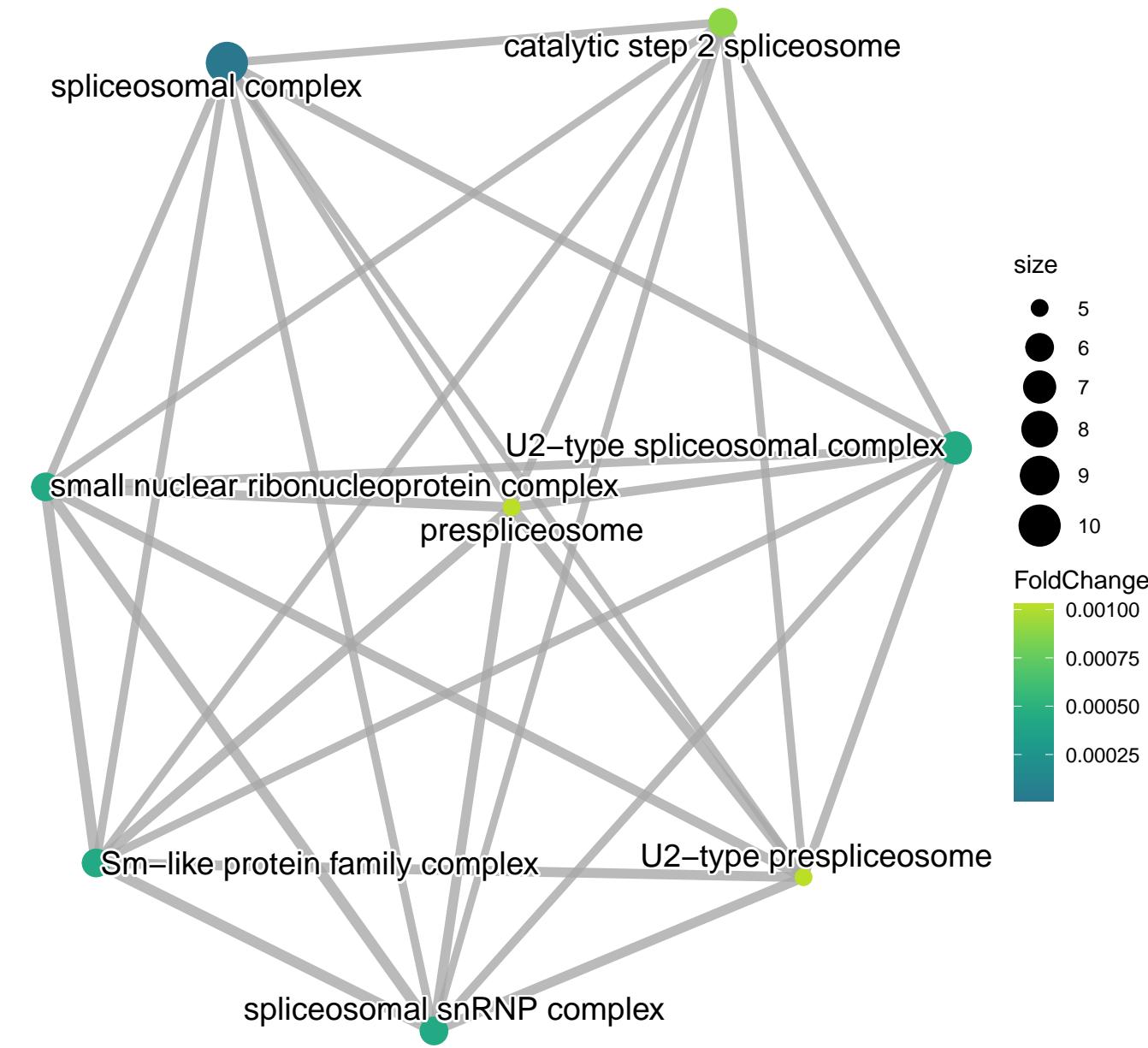
MSL1-TAP Up-regulated GO CC cnetplot

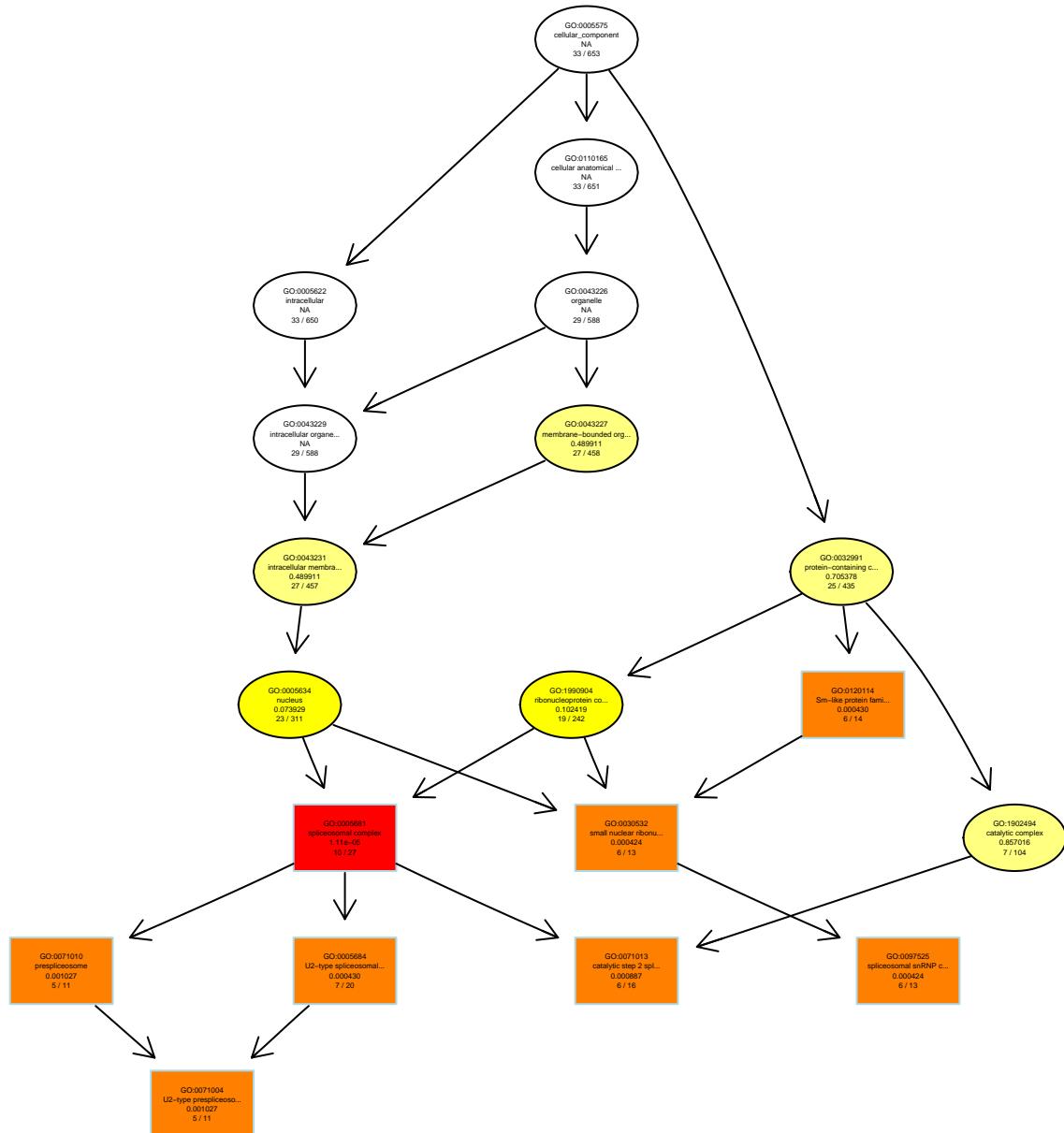


MSL1-TAP Up-regulated GO CC heatplot

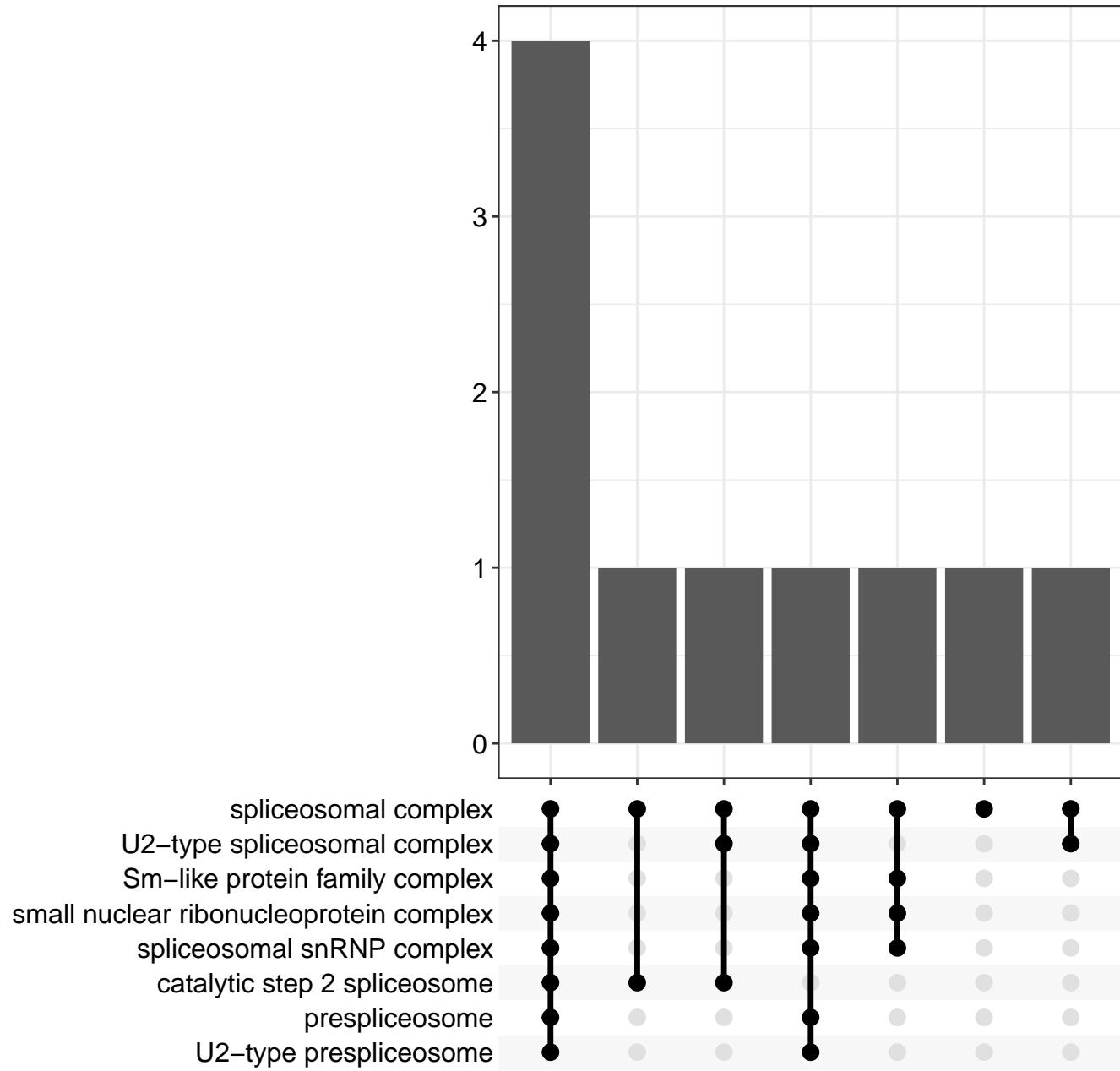


MSL1-TAP Up-regulated GO CC emapplot

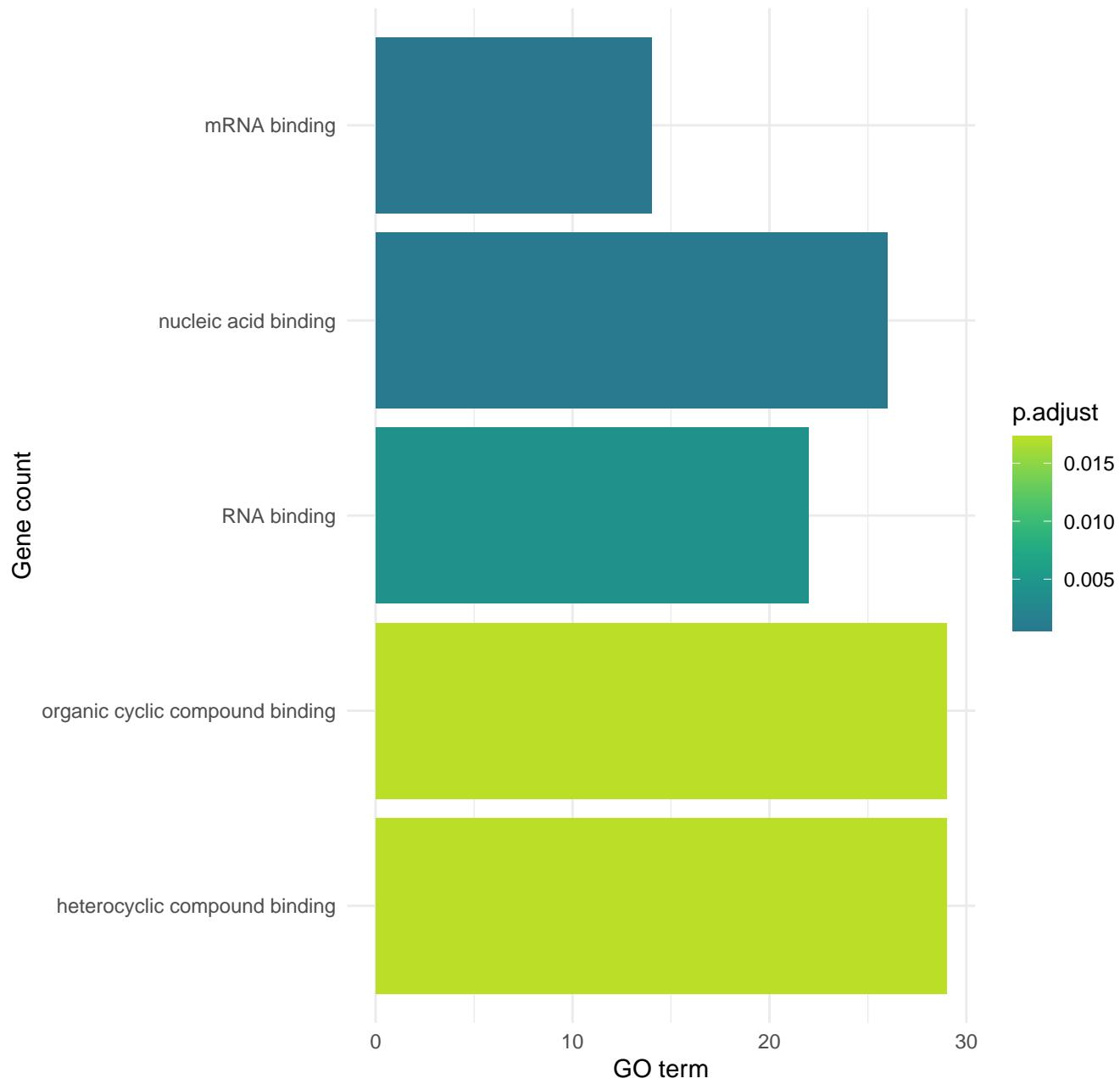




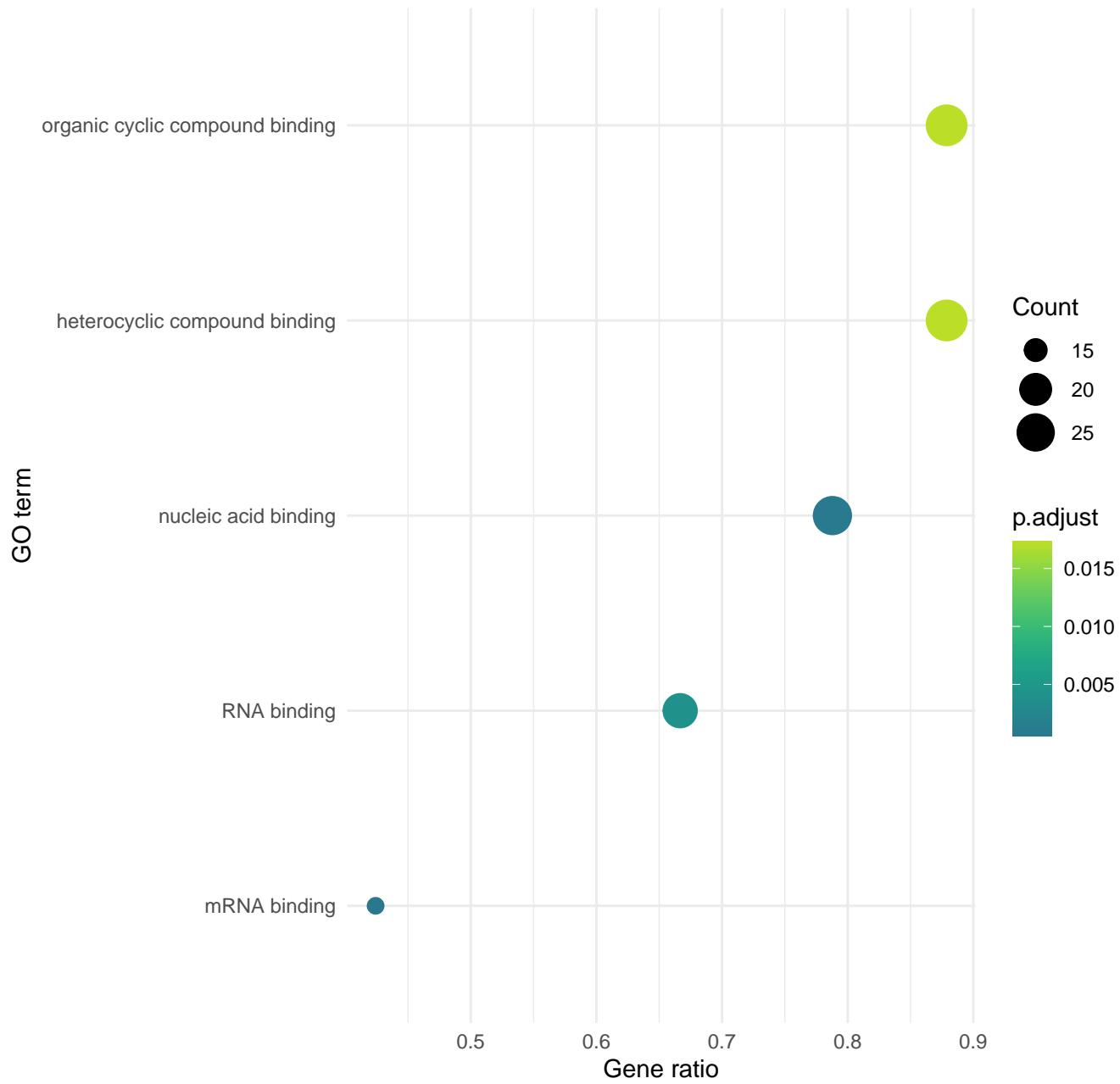
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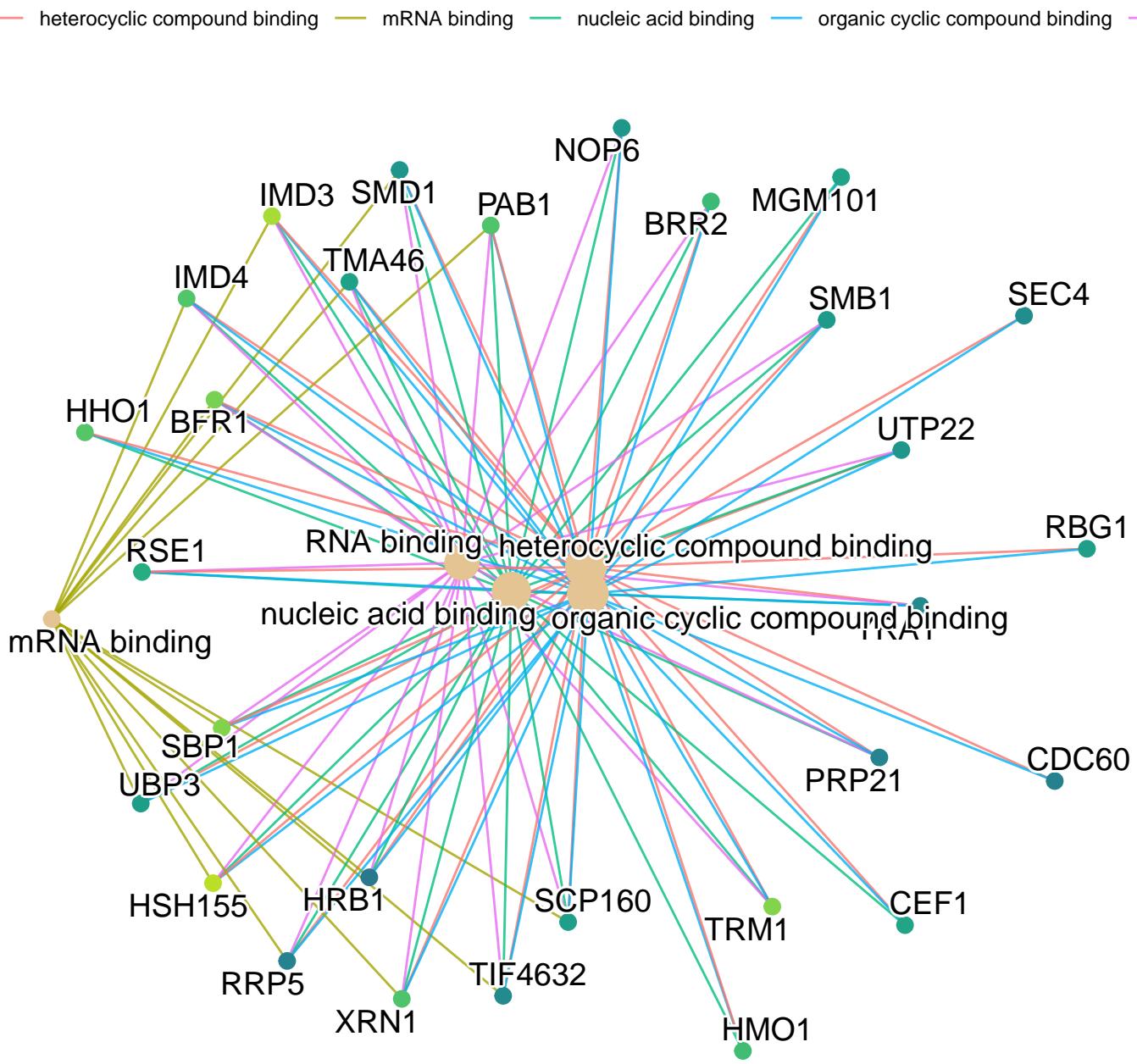
MSL1-TAP Up-regulated GO MF barplot



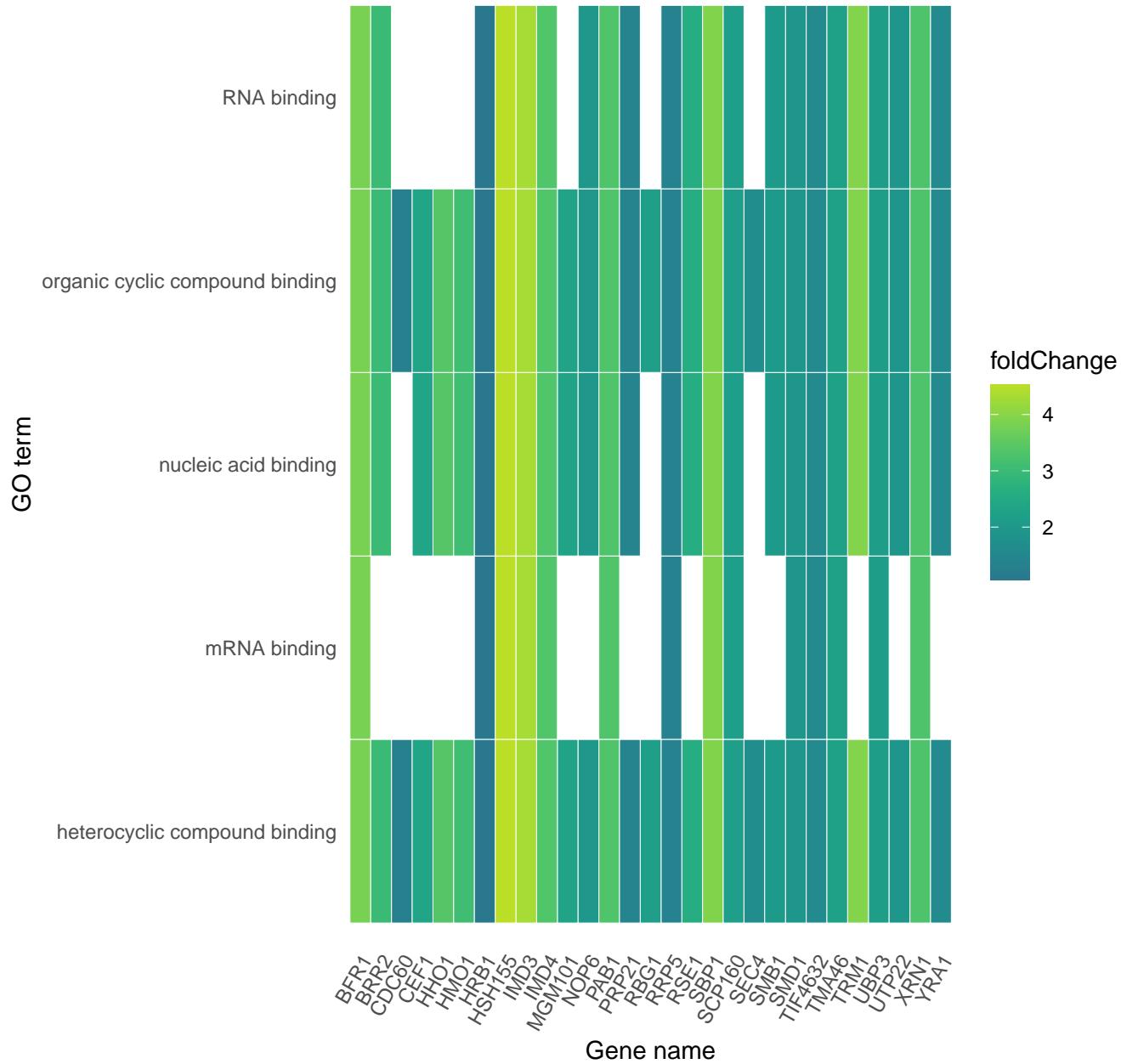
MSL1-TAP Up-regulated GO MF dotplot



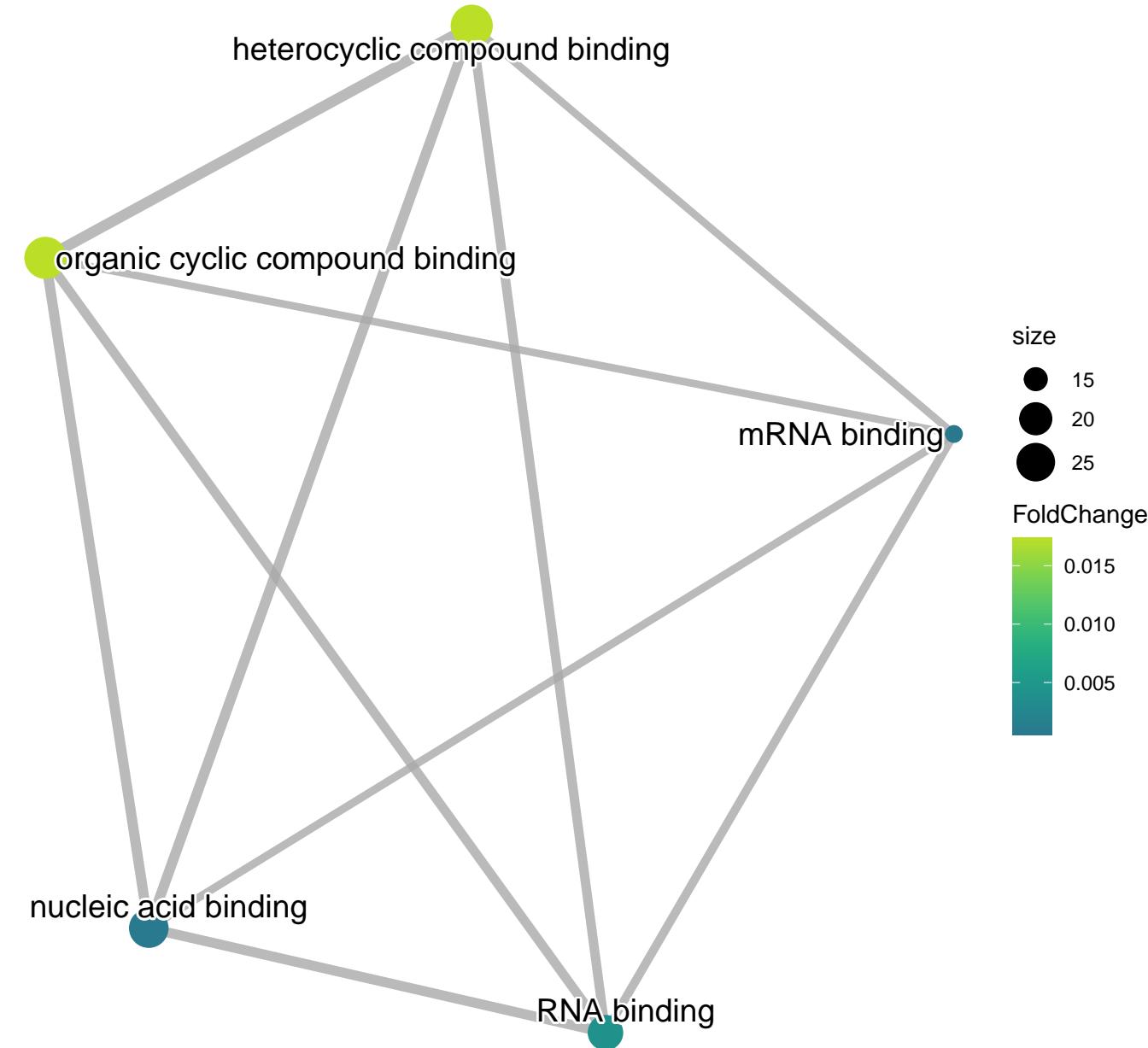
MSL1-TAP Up-regulated GO MF cnetplot

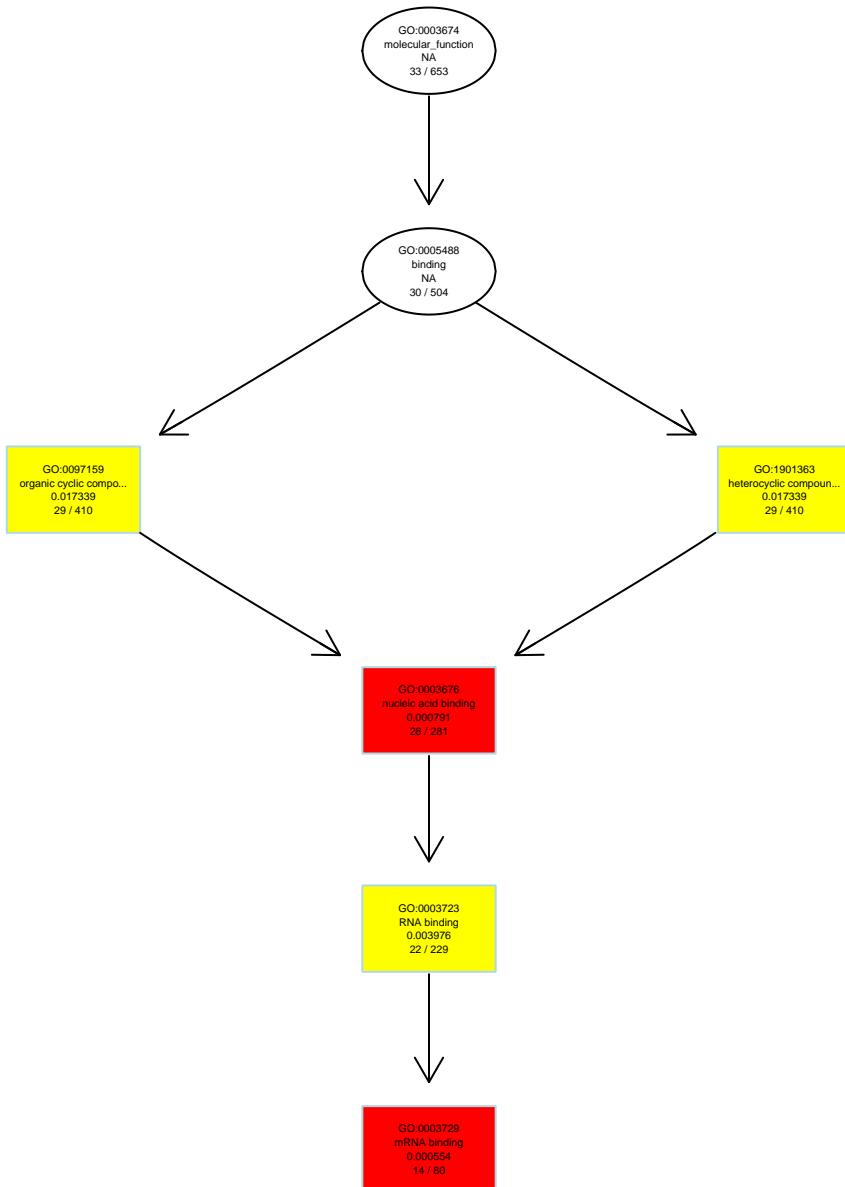


MSL1-TAP Up-regulated GO MF heatplot

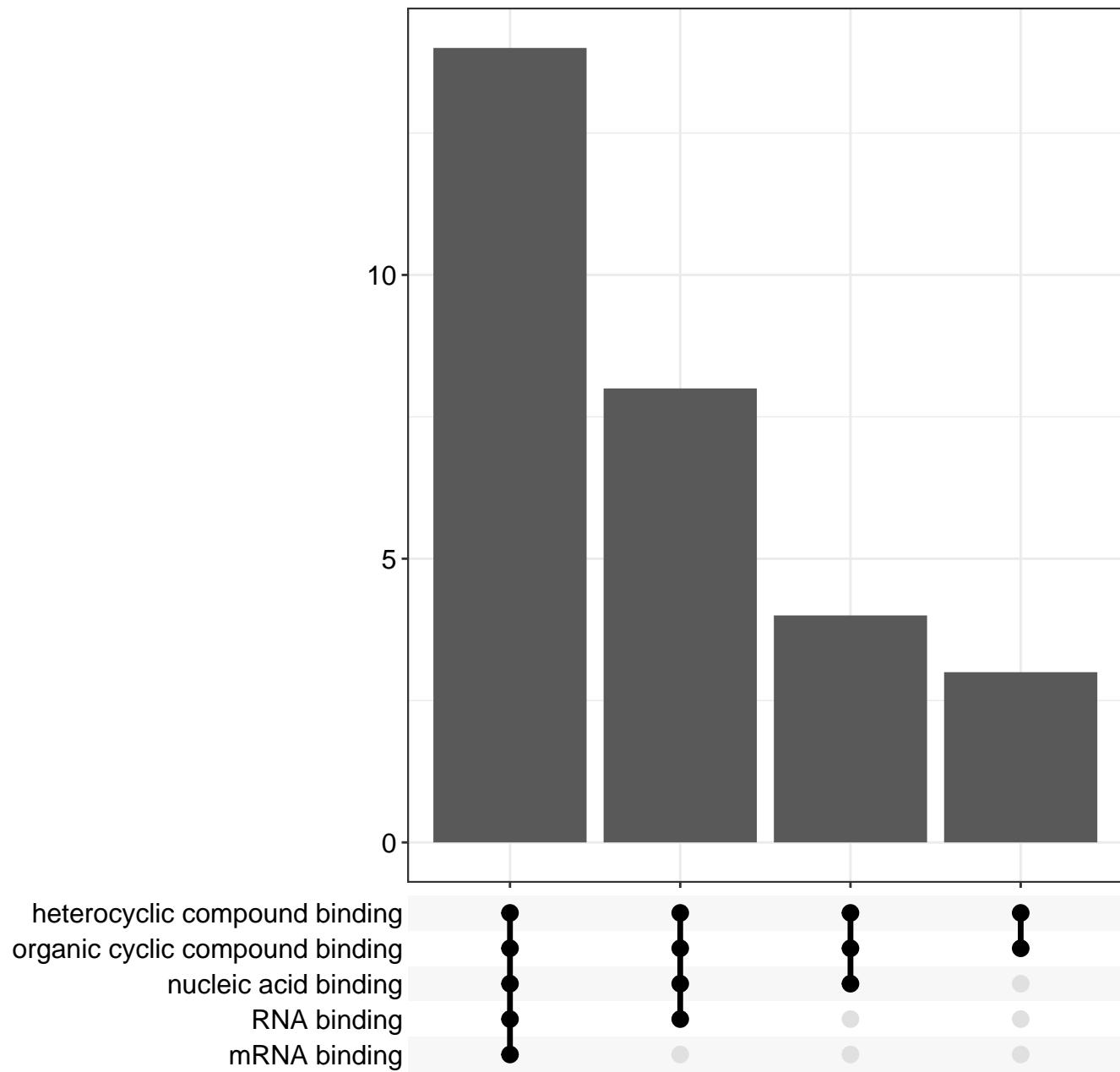


MSL1-TAP Up-regulated GO MF emapplot

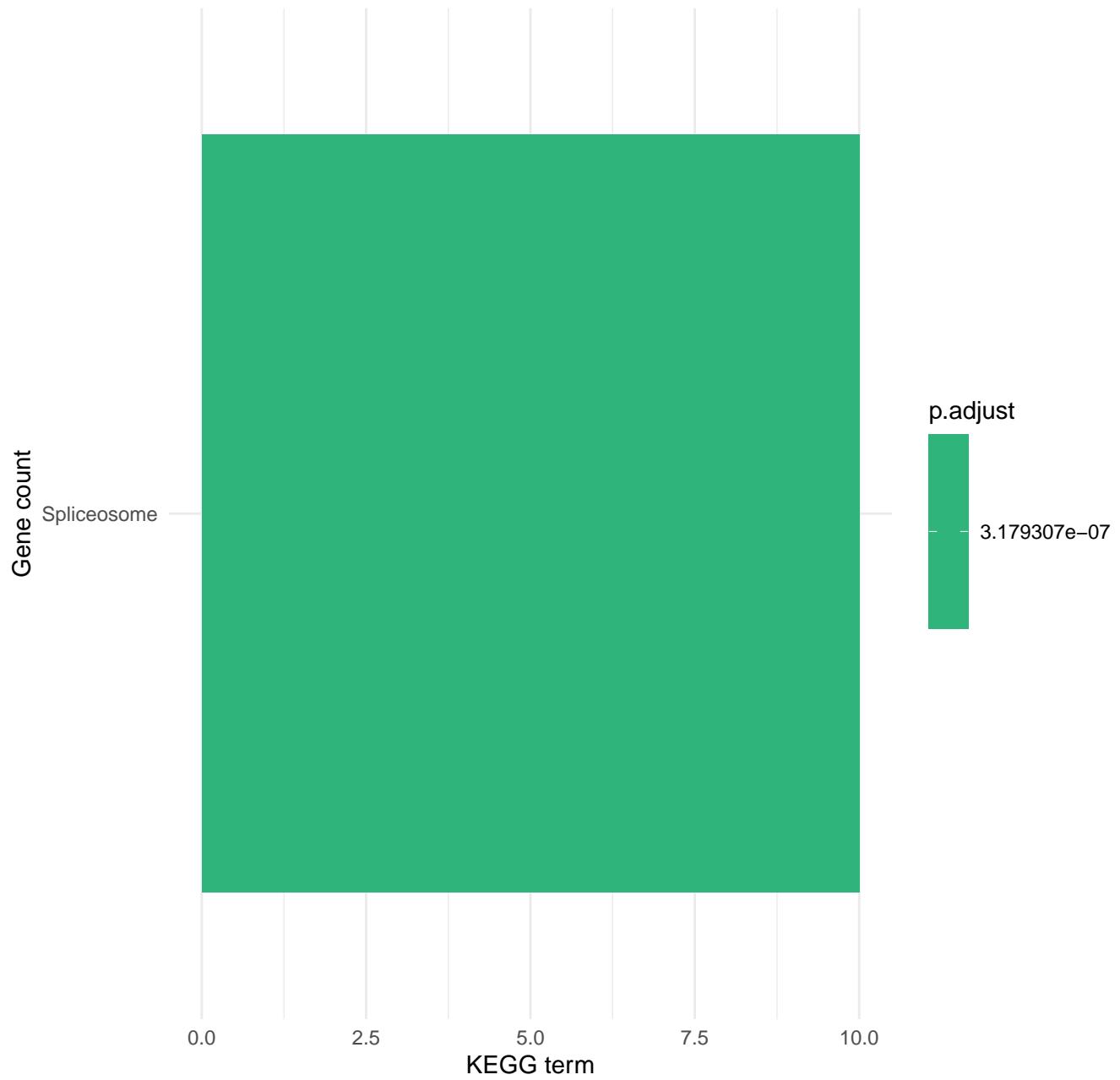




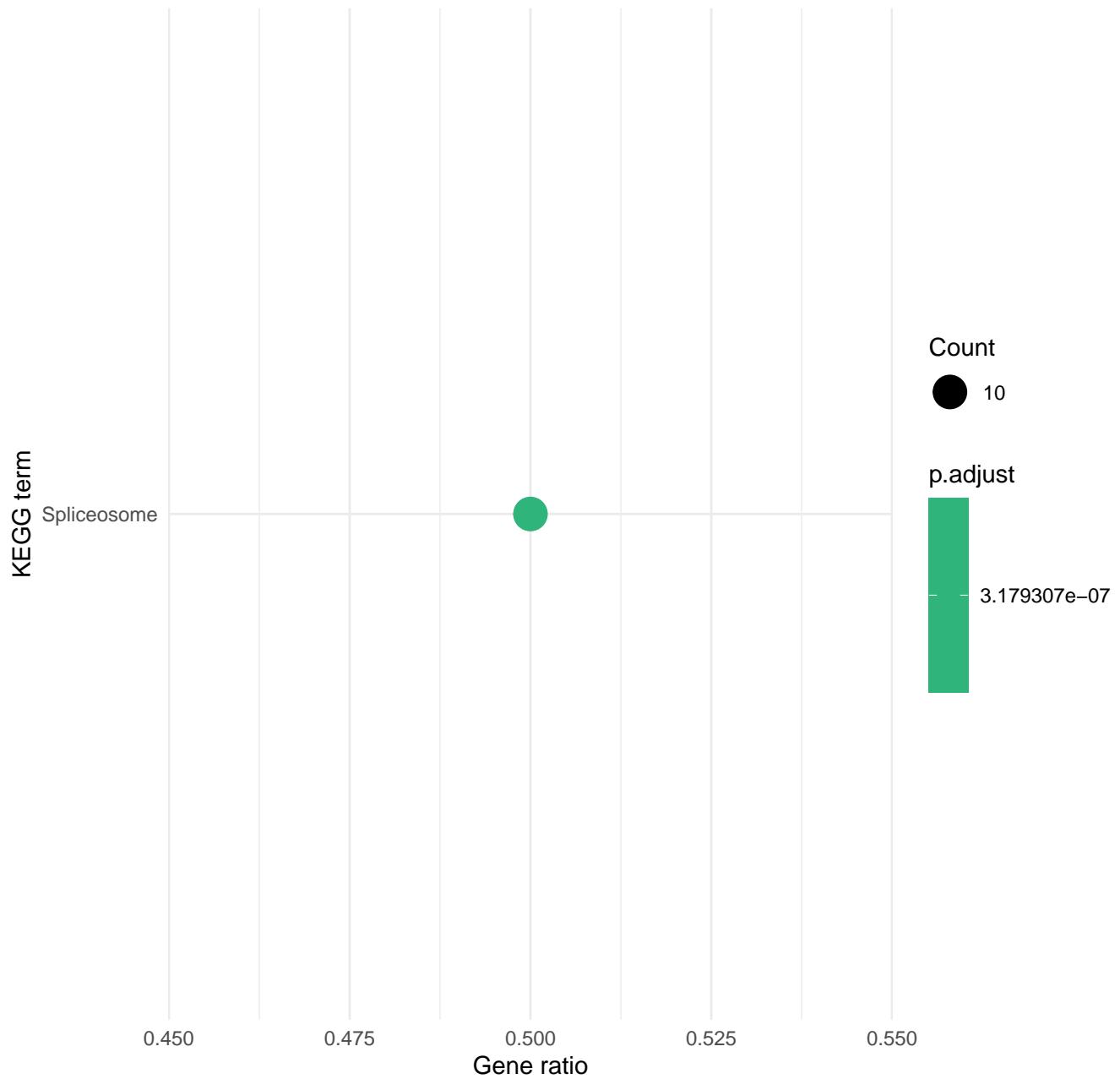
MSL1-TAP Up-regulated GO MF upsetplot



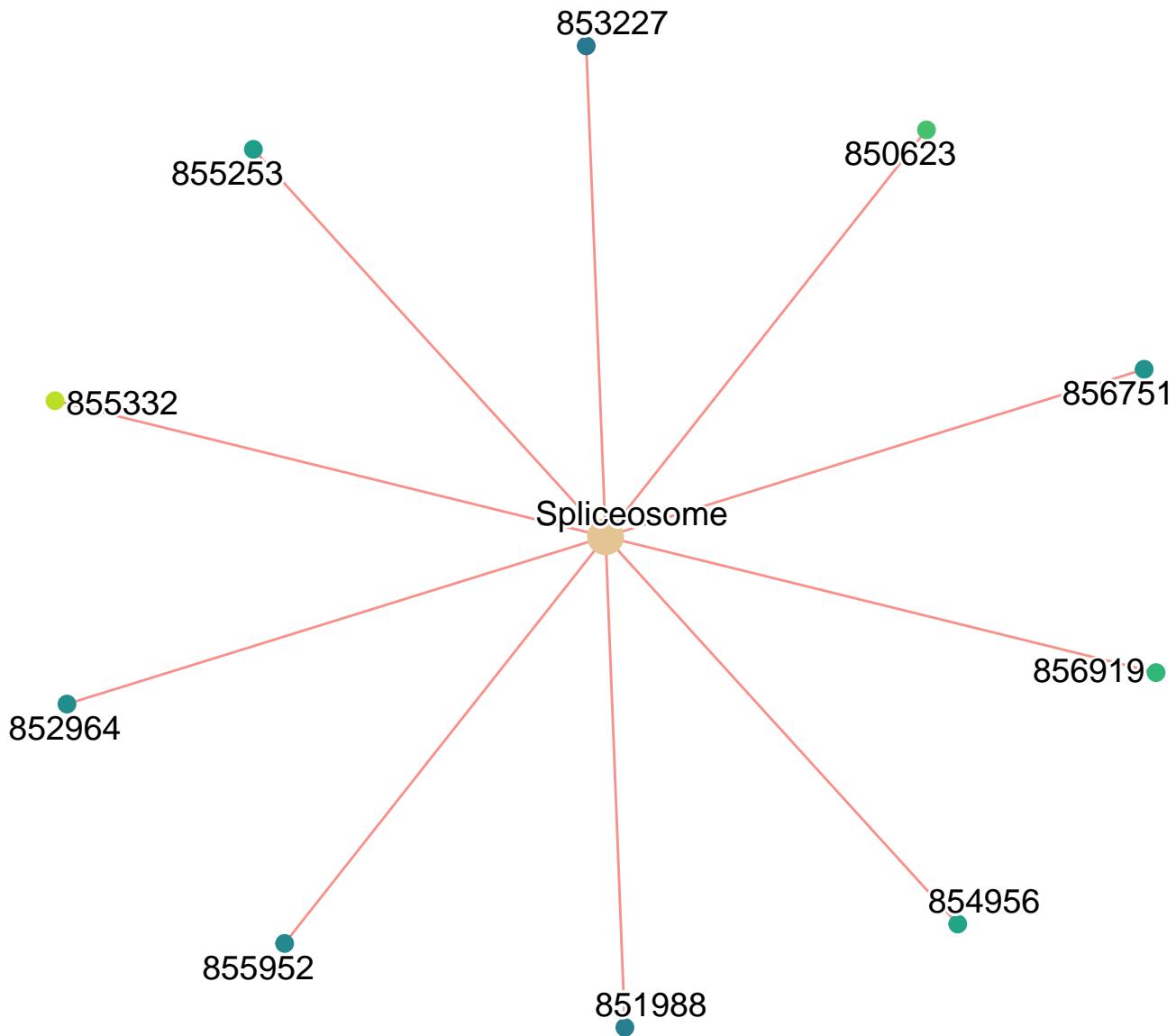
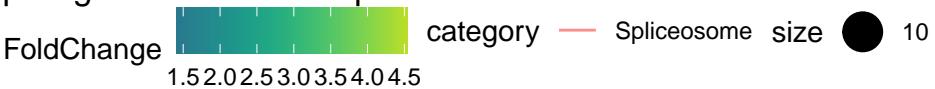
MSL1-TAP Up-regulated KEGG barplot



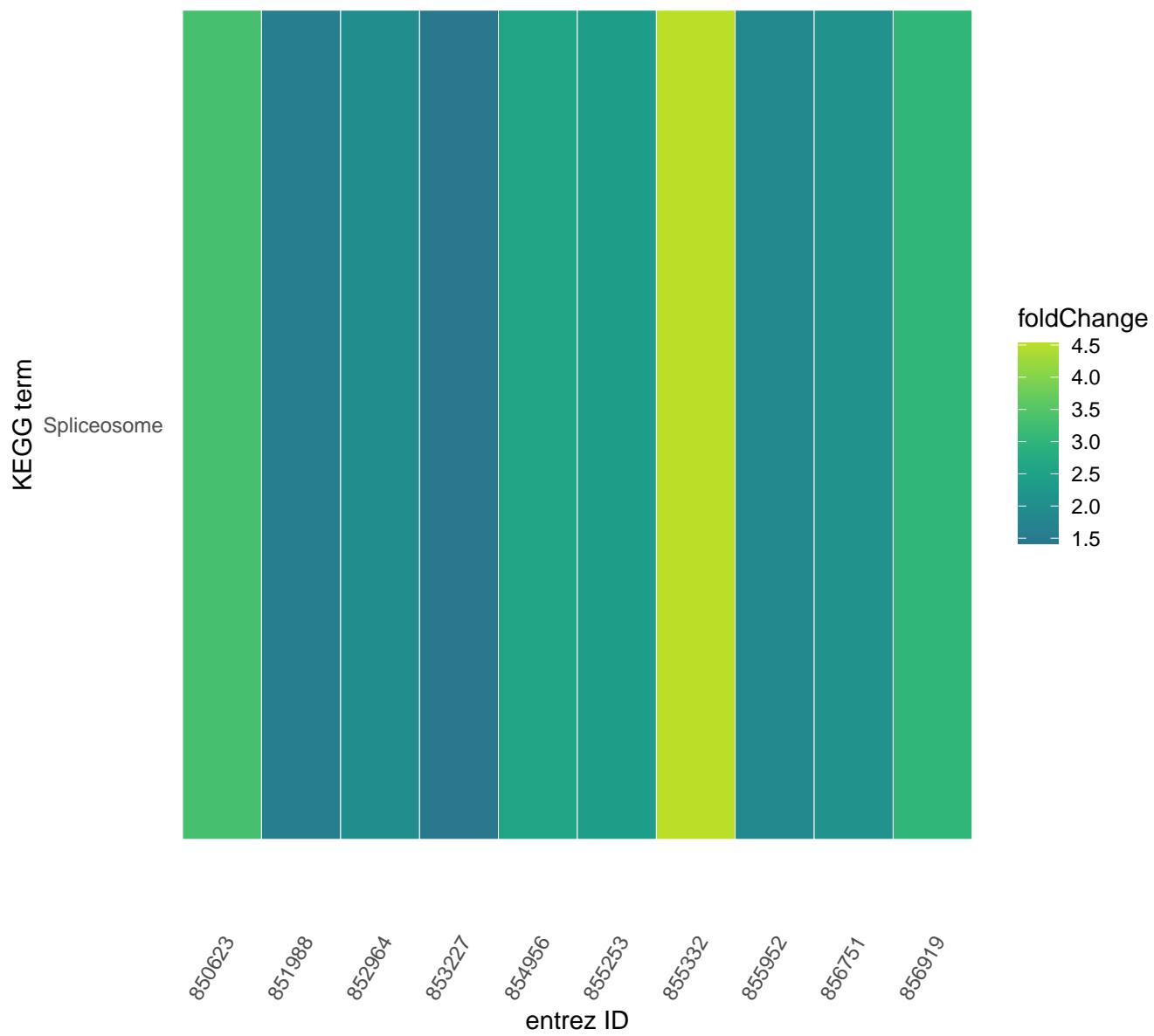
MSL1-TAP Up-regulated KEGG dotplot



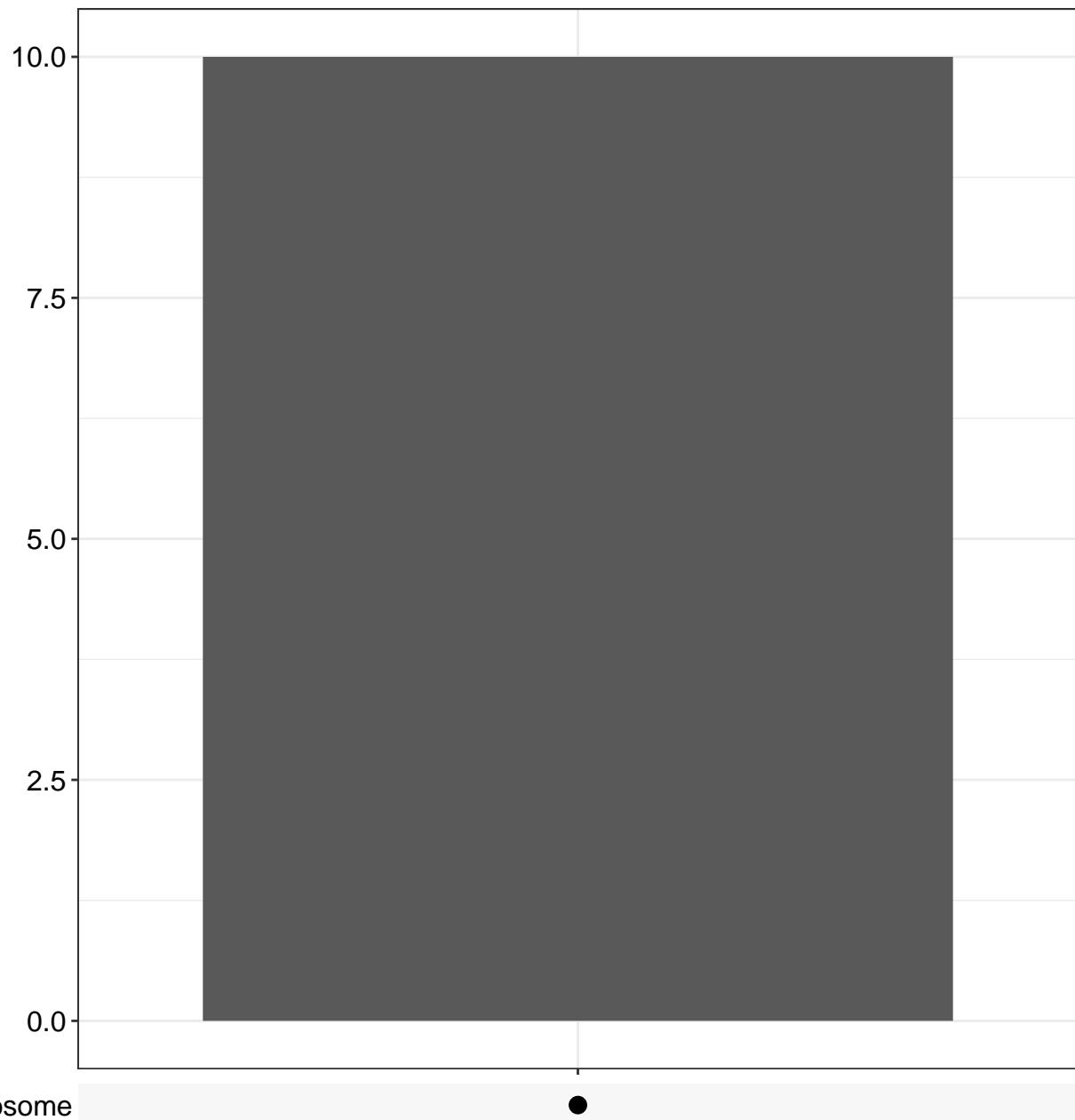
MSL1-TAP Up-regulated KEGG dotplot



MSL1-TAP Up-regulated KEGG heatplot

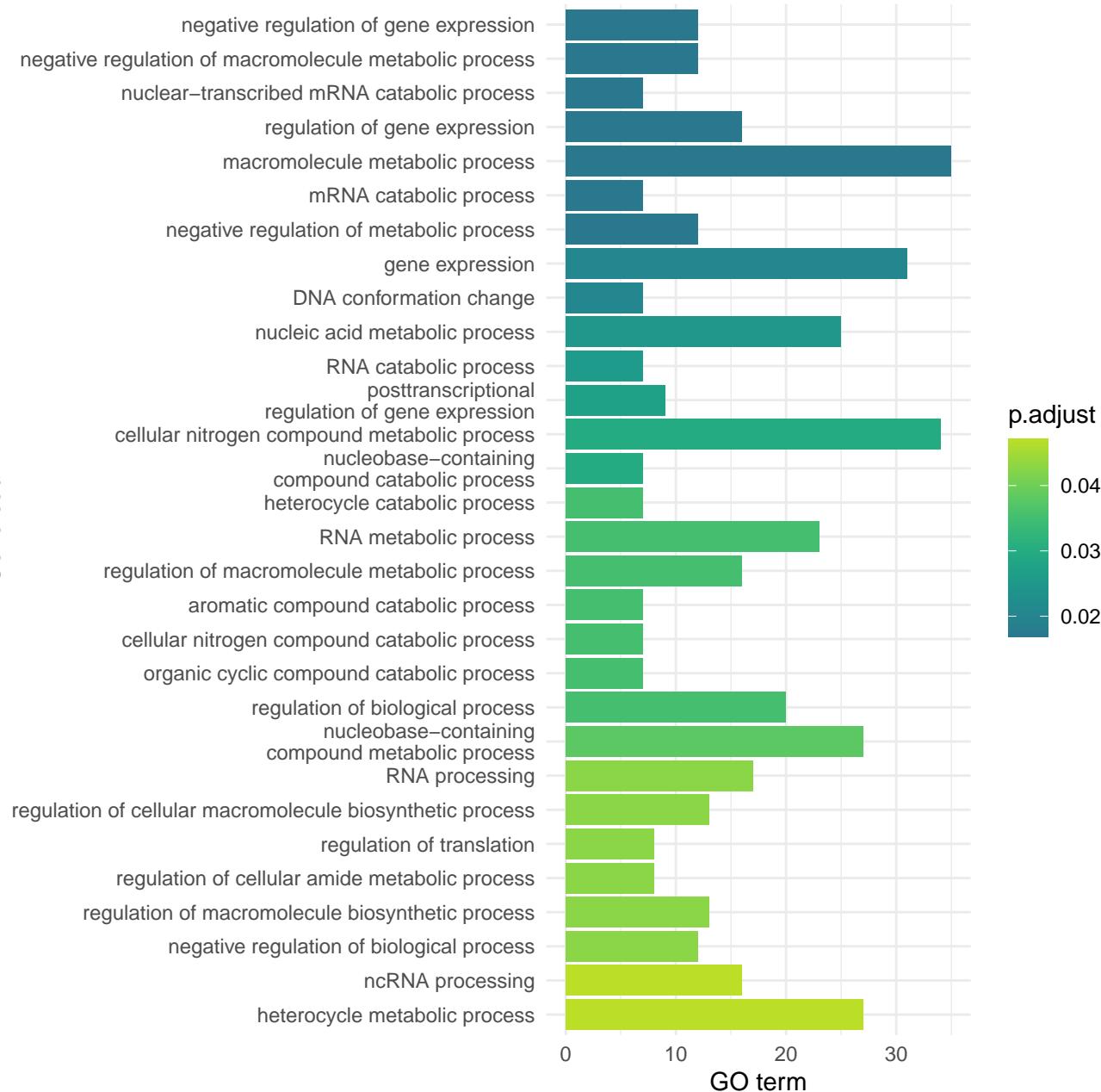


MSL1-TAP Up-regulated KEGG upsetplot

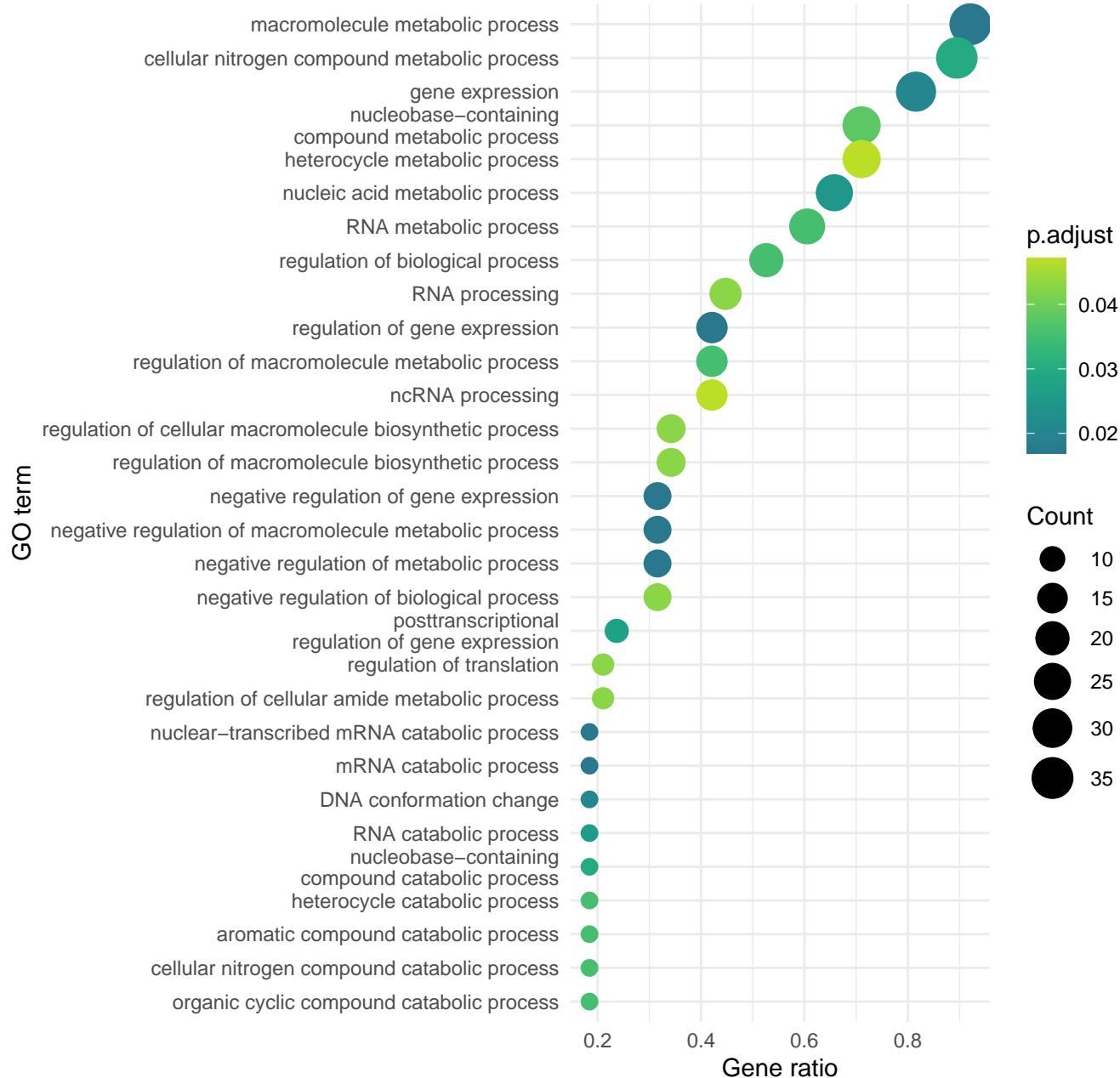


Spliceosome

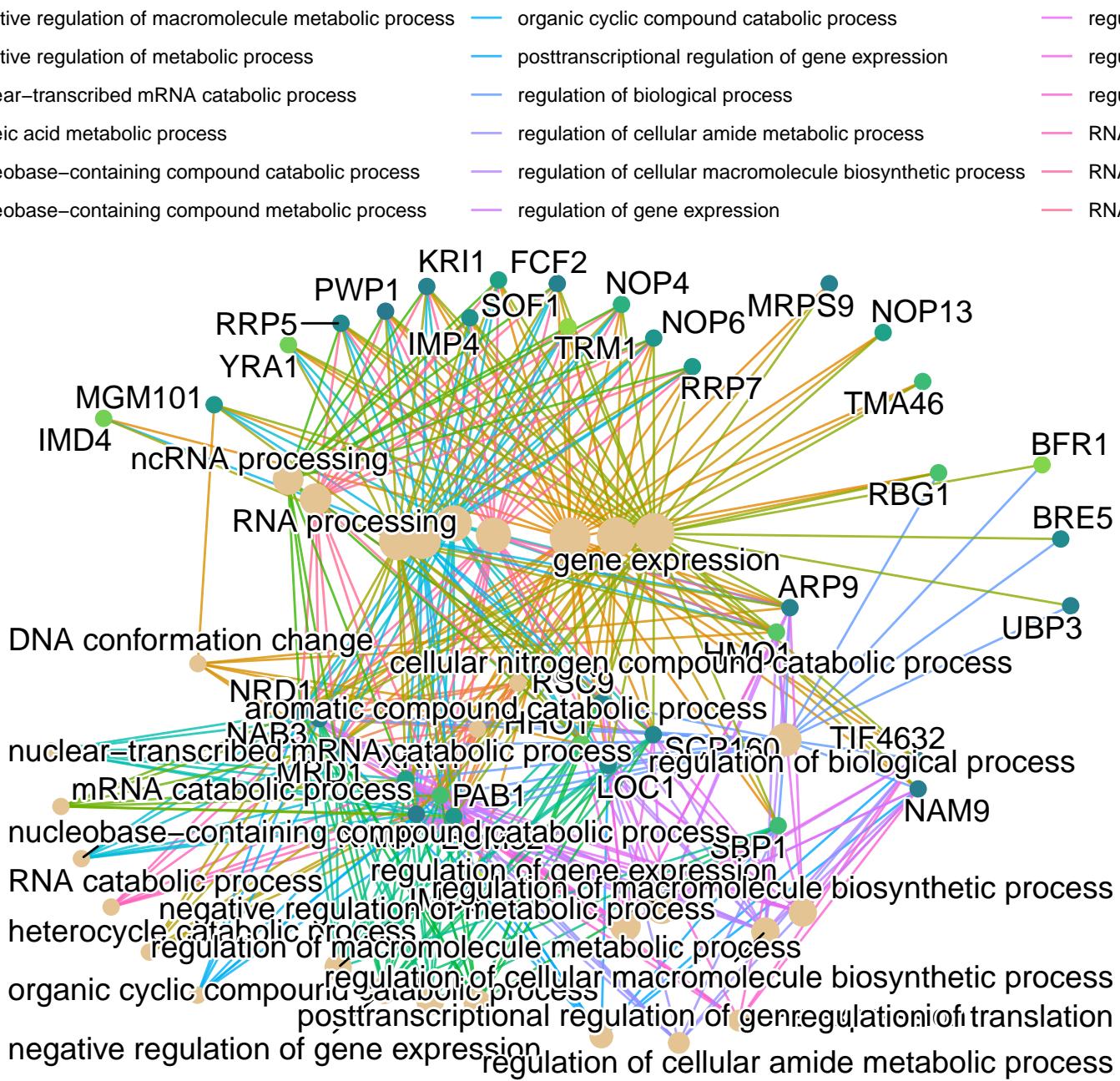
MTR4-TAP Up-regulated GO BP barplot



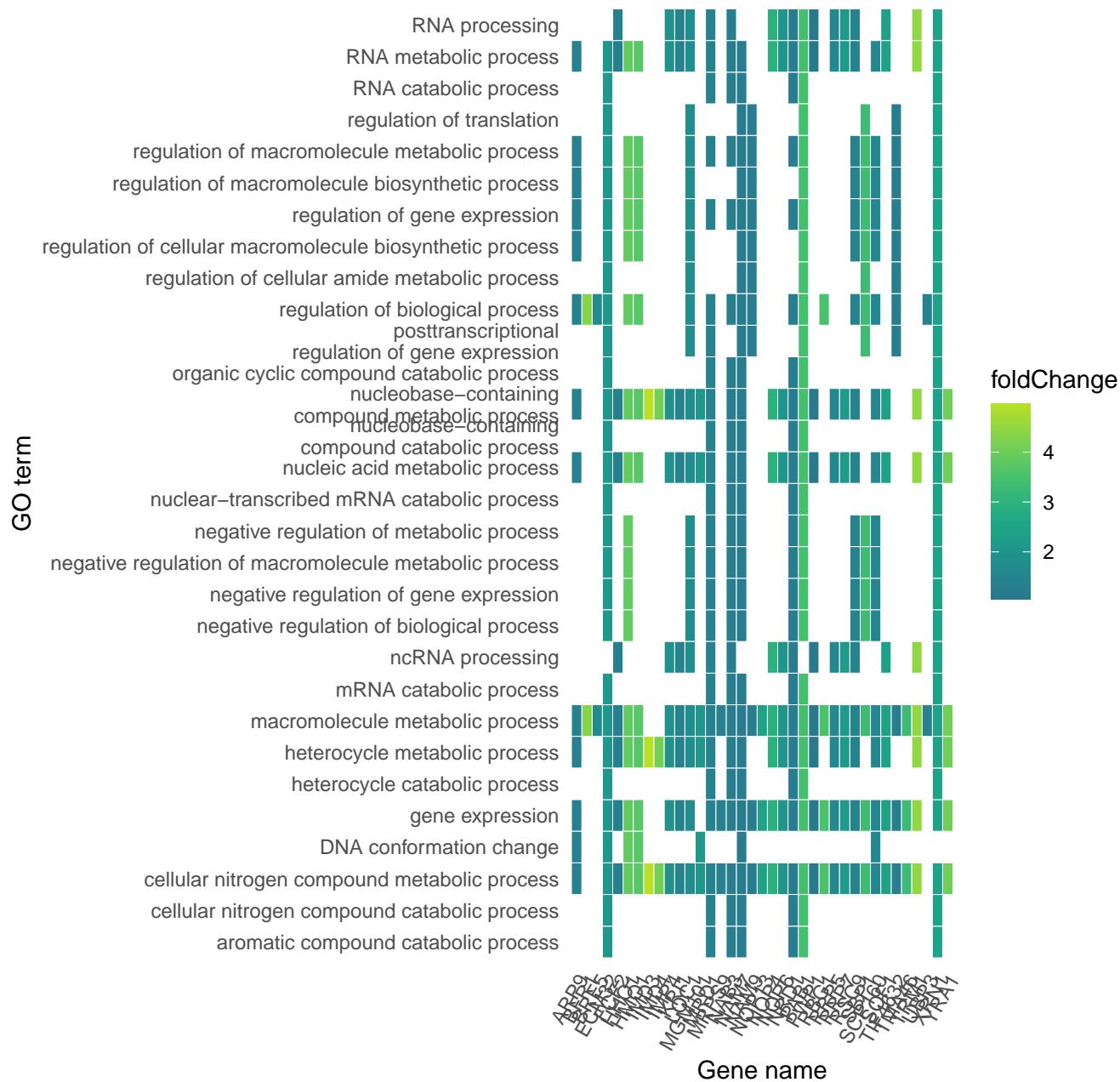
MTR4-TAP Up-regulated GO BP dotplot



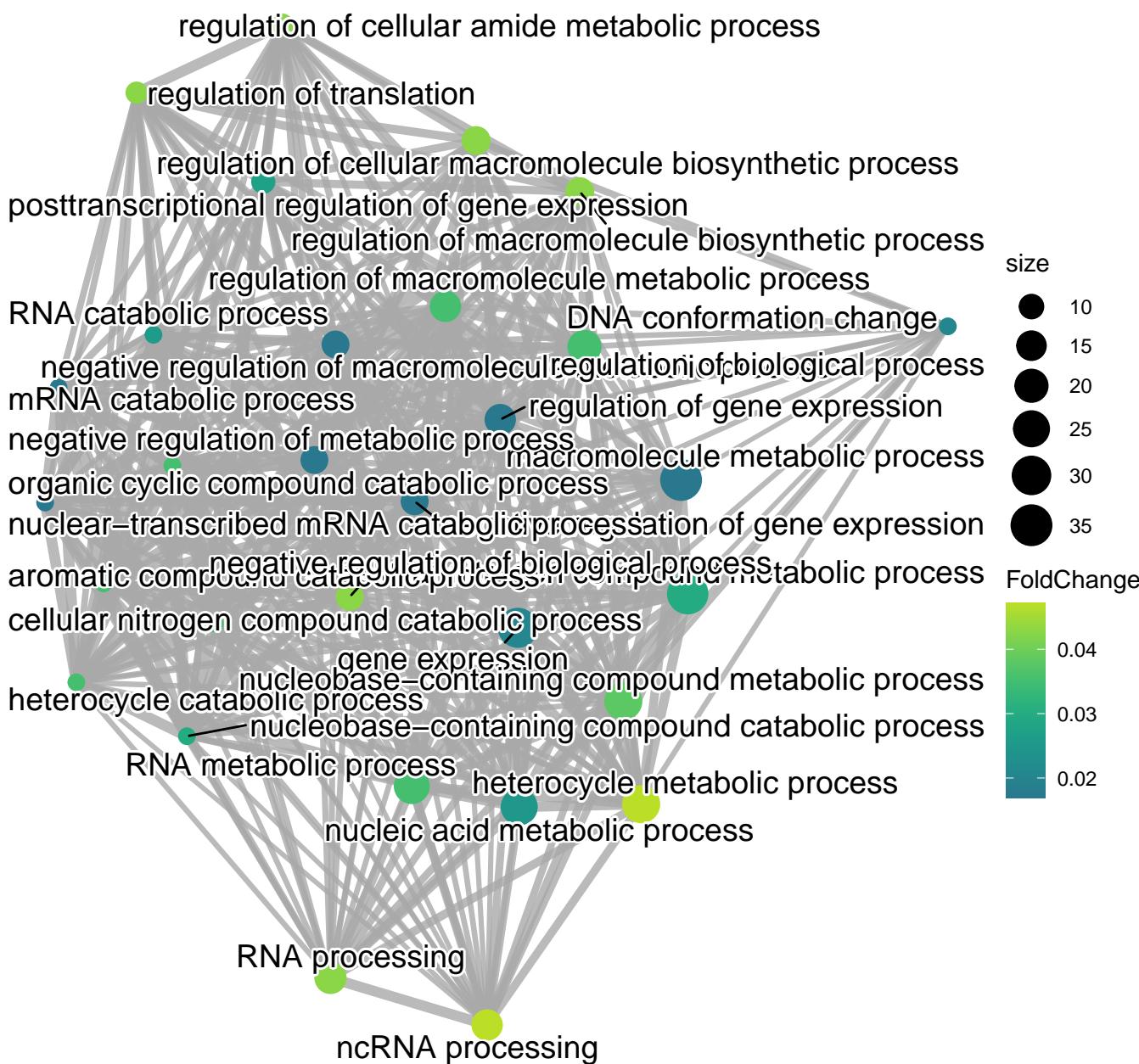
MTR4-TAP Up-regulated GO BP cnetplot

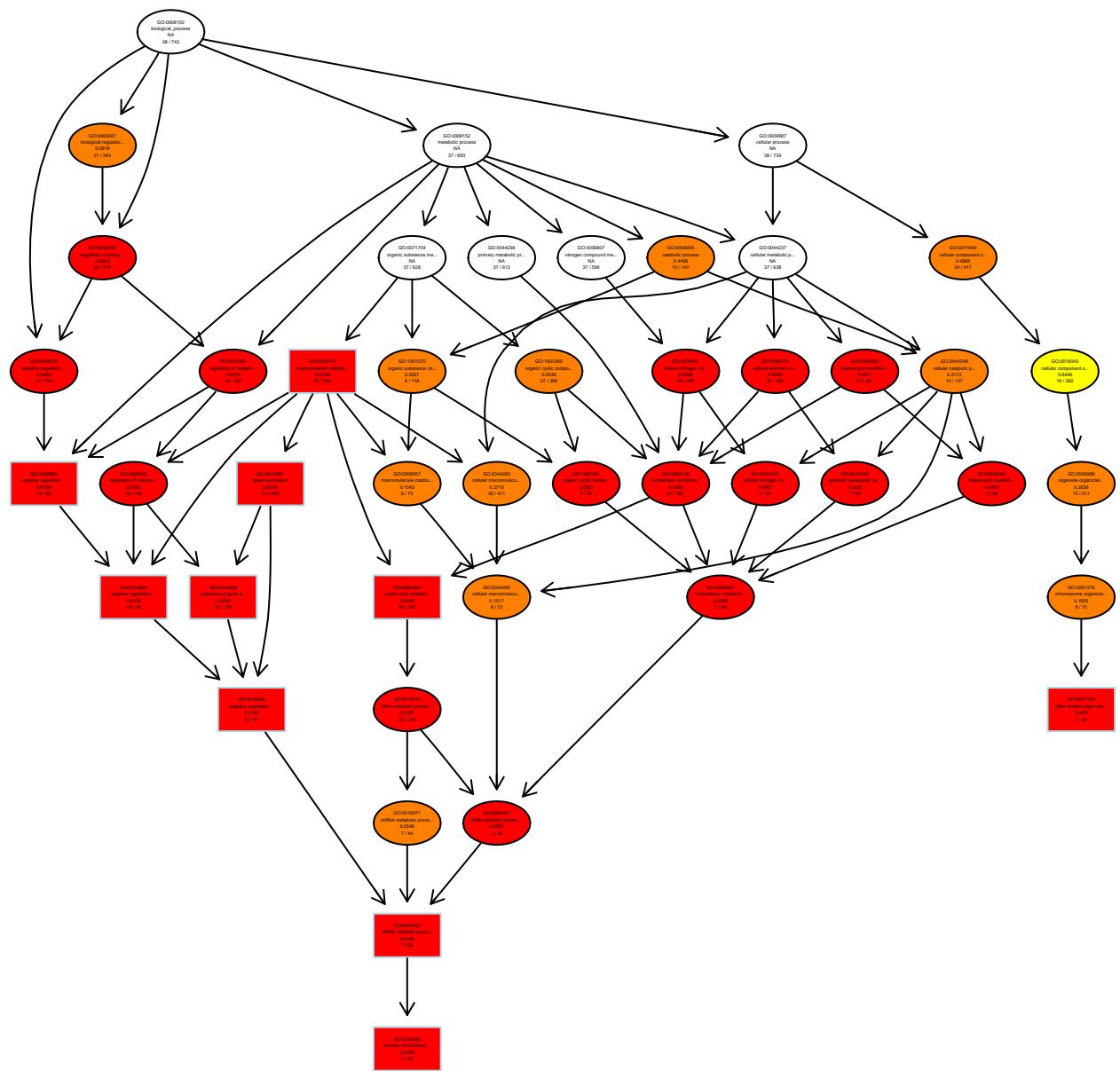


MTR4-TAP Up-regulated GO BP heatplot

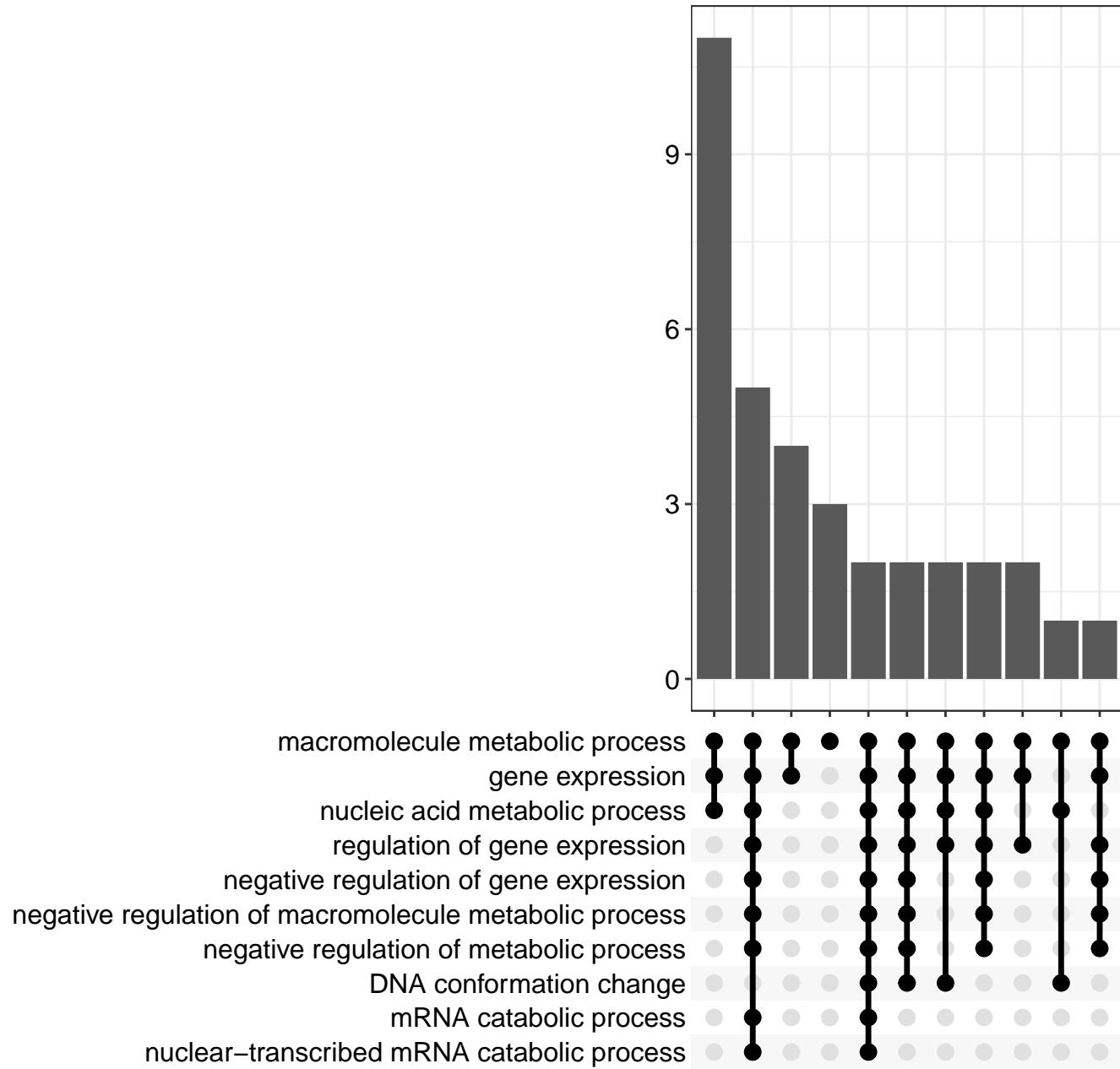


MTR4-TAP Up-regulated GO BP emapplot

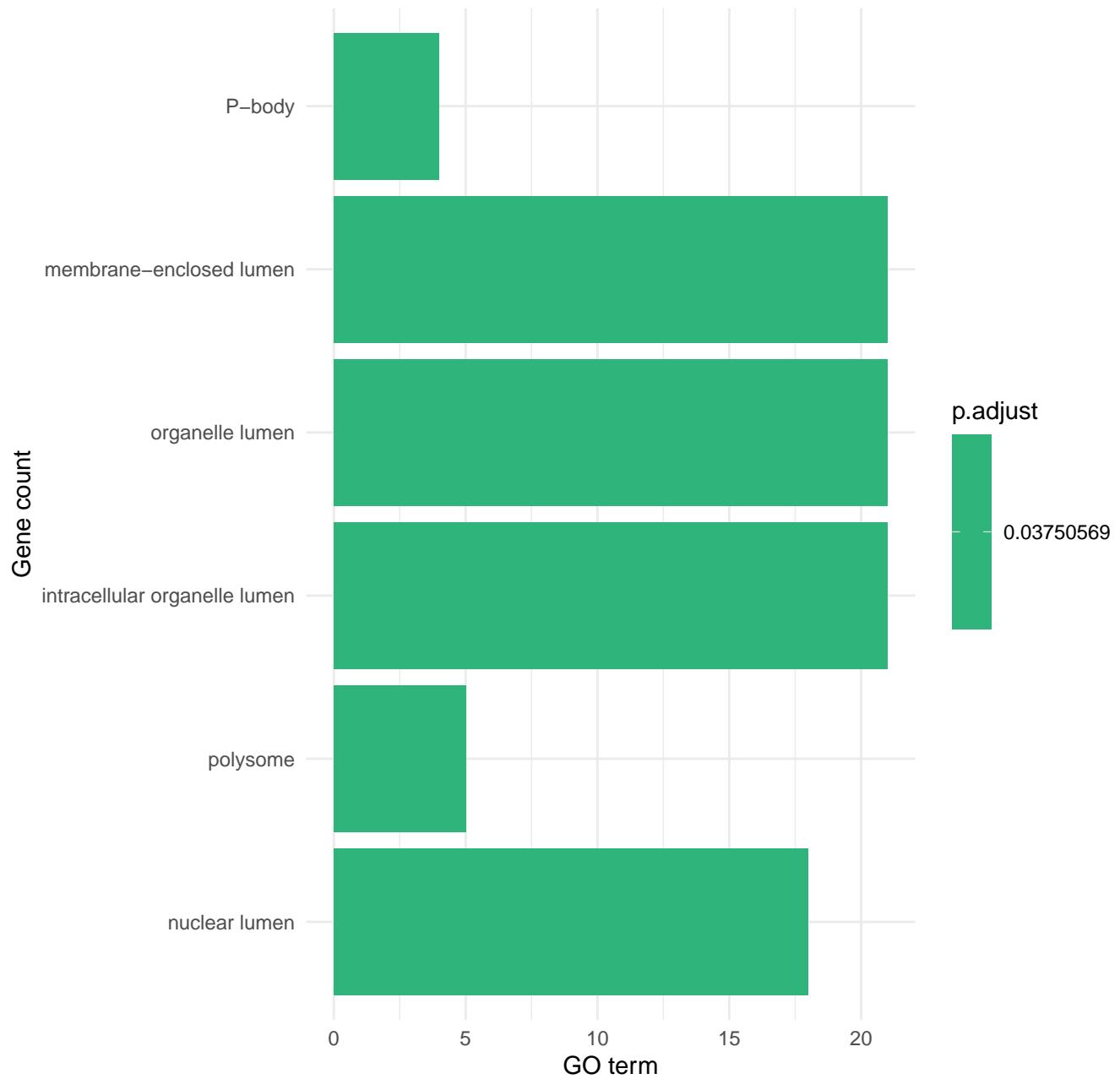




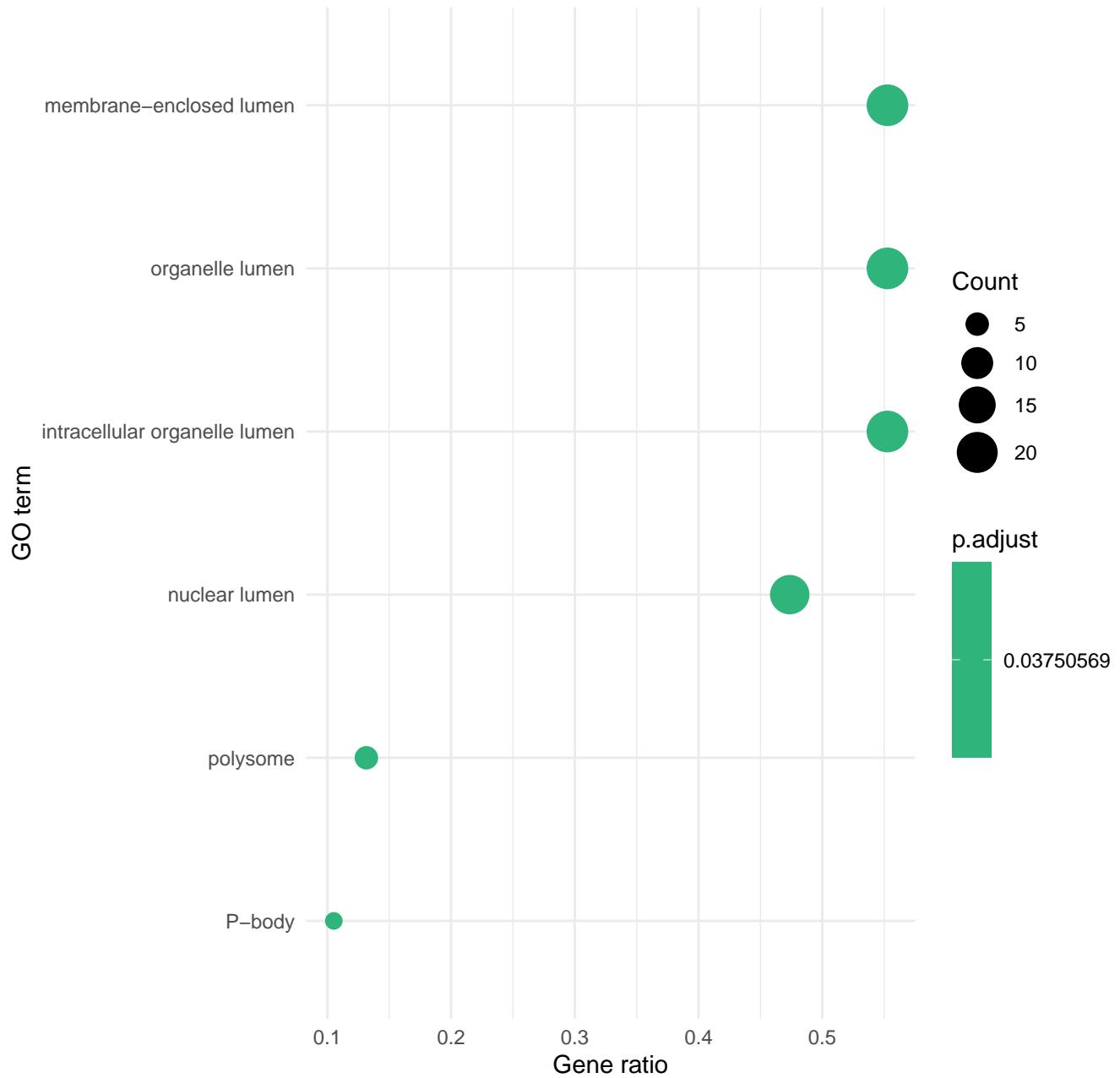
MTR4-TAP Up-regulated GO BP



MTR4-TAP Up-regulated GO CC barplot

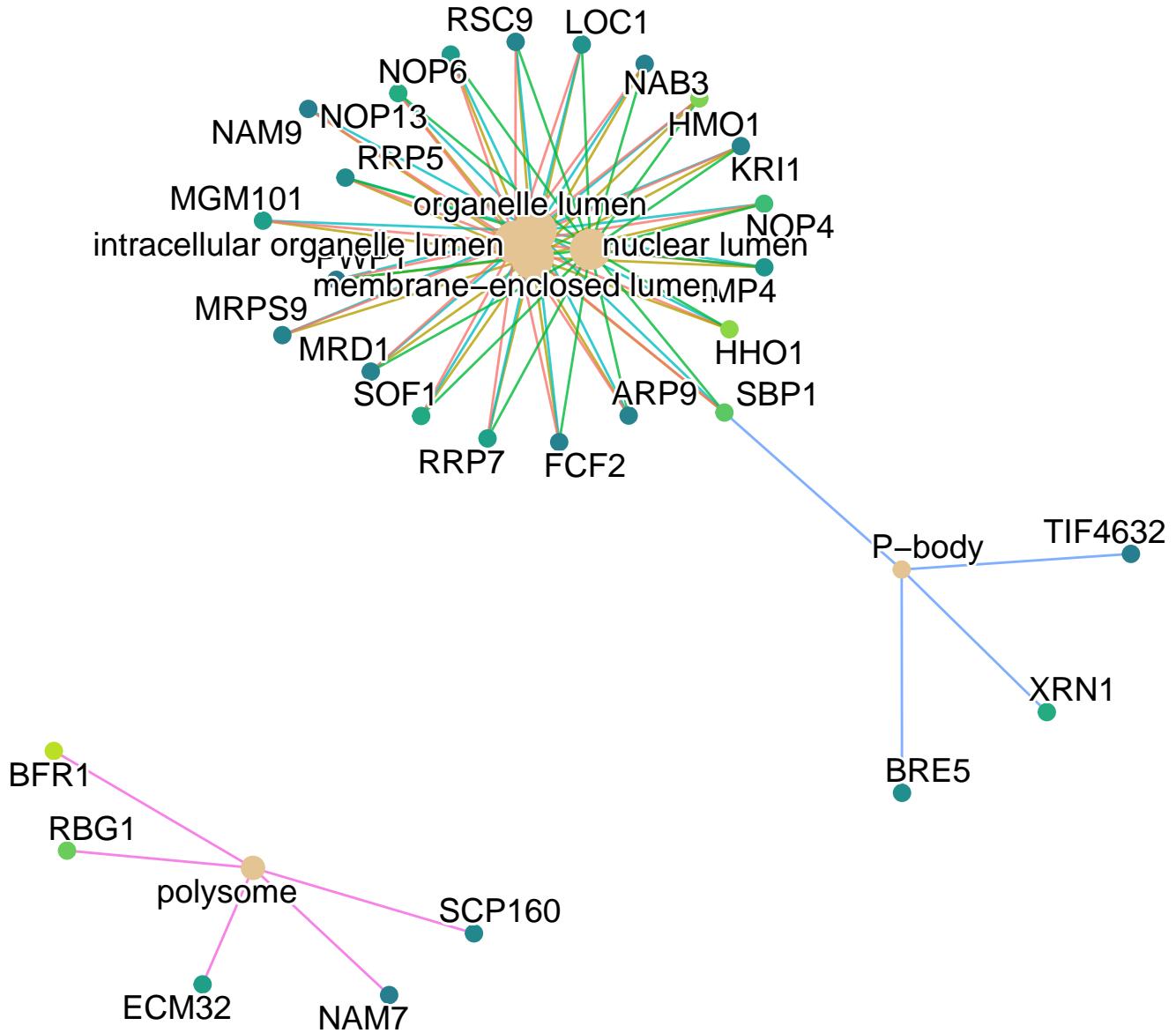


MTR4–TAP Up-regulated GO CC dotplot

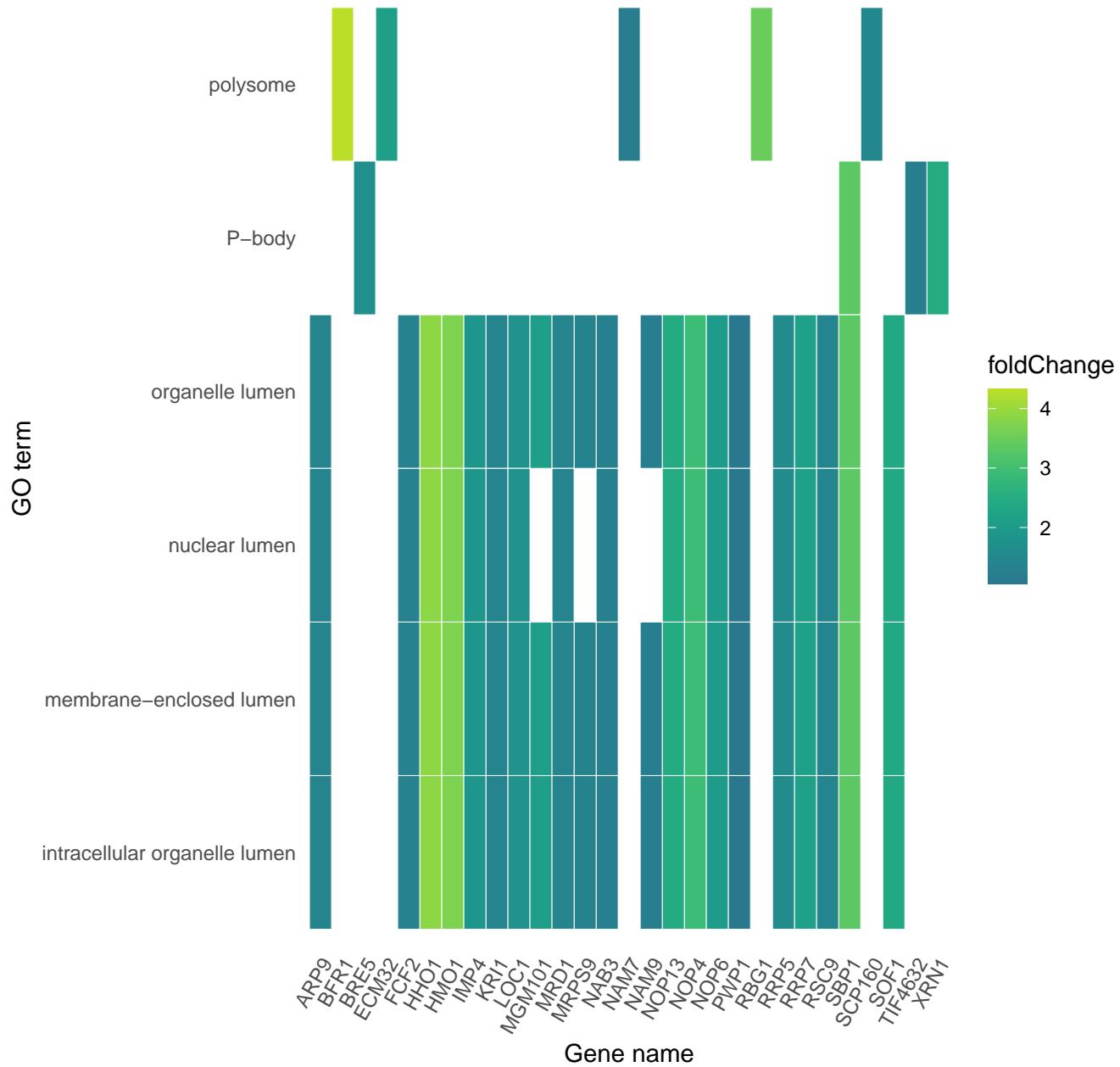


MTR4-TAP Up-regulated GO CC cnetplot

cellular organelle lumen green nuclear lumen blue P-body
membrane-enclosed lumen cyan organelle lumen pink polysome



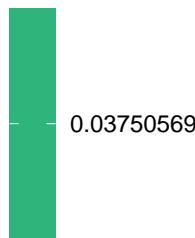
MTR4–TAP Up-regulated GO CC heatplot



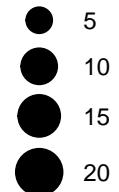
MTR4-TAP Up-regulated GO CC emapplot

P-body

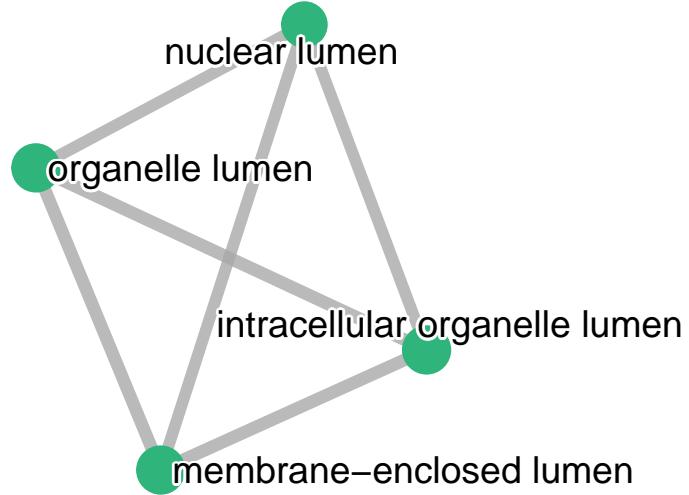
FoldChange

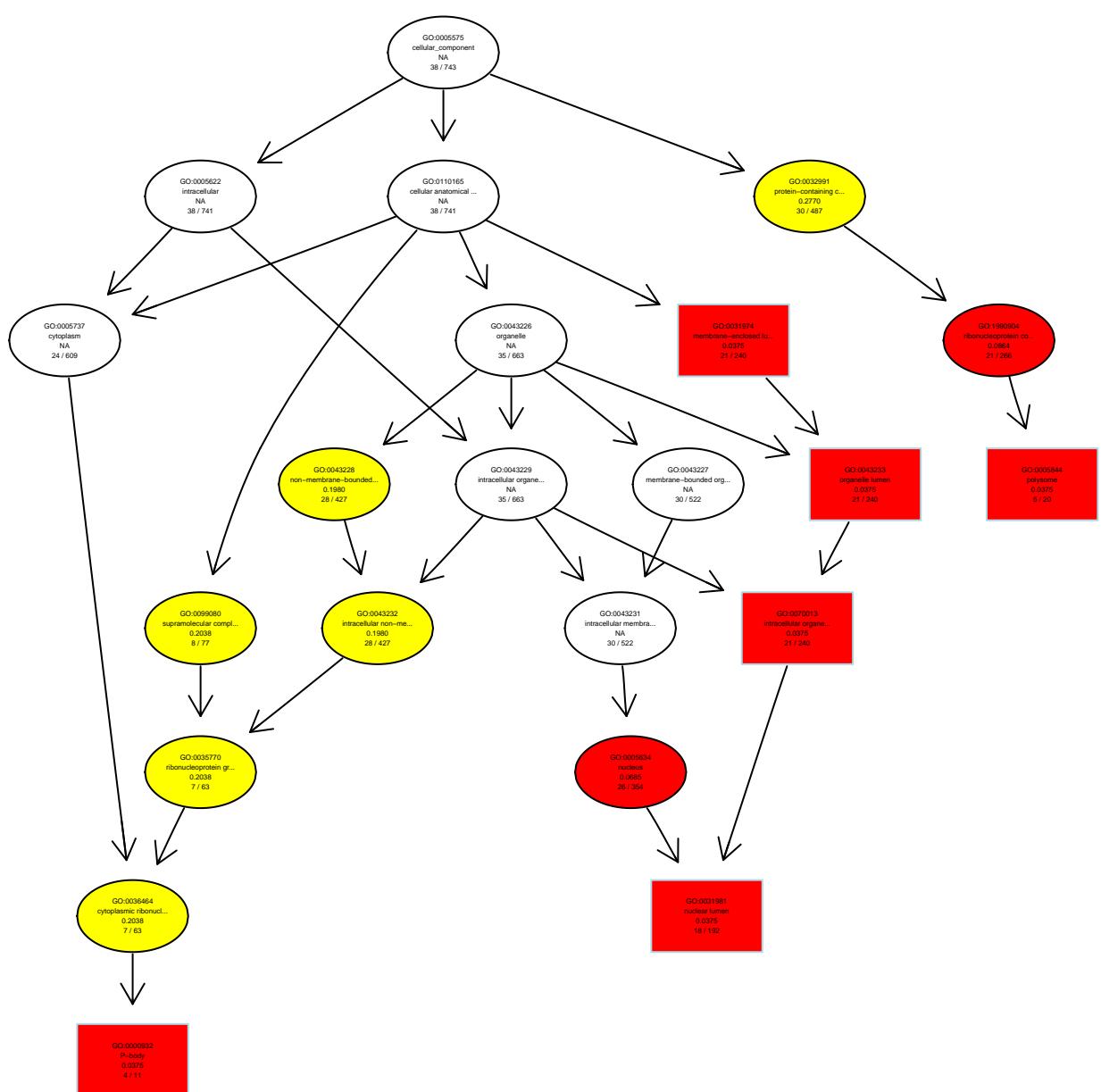


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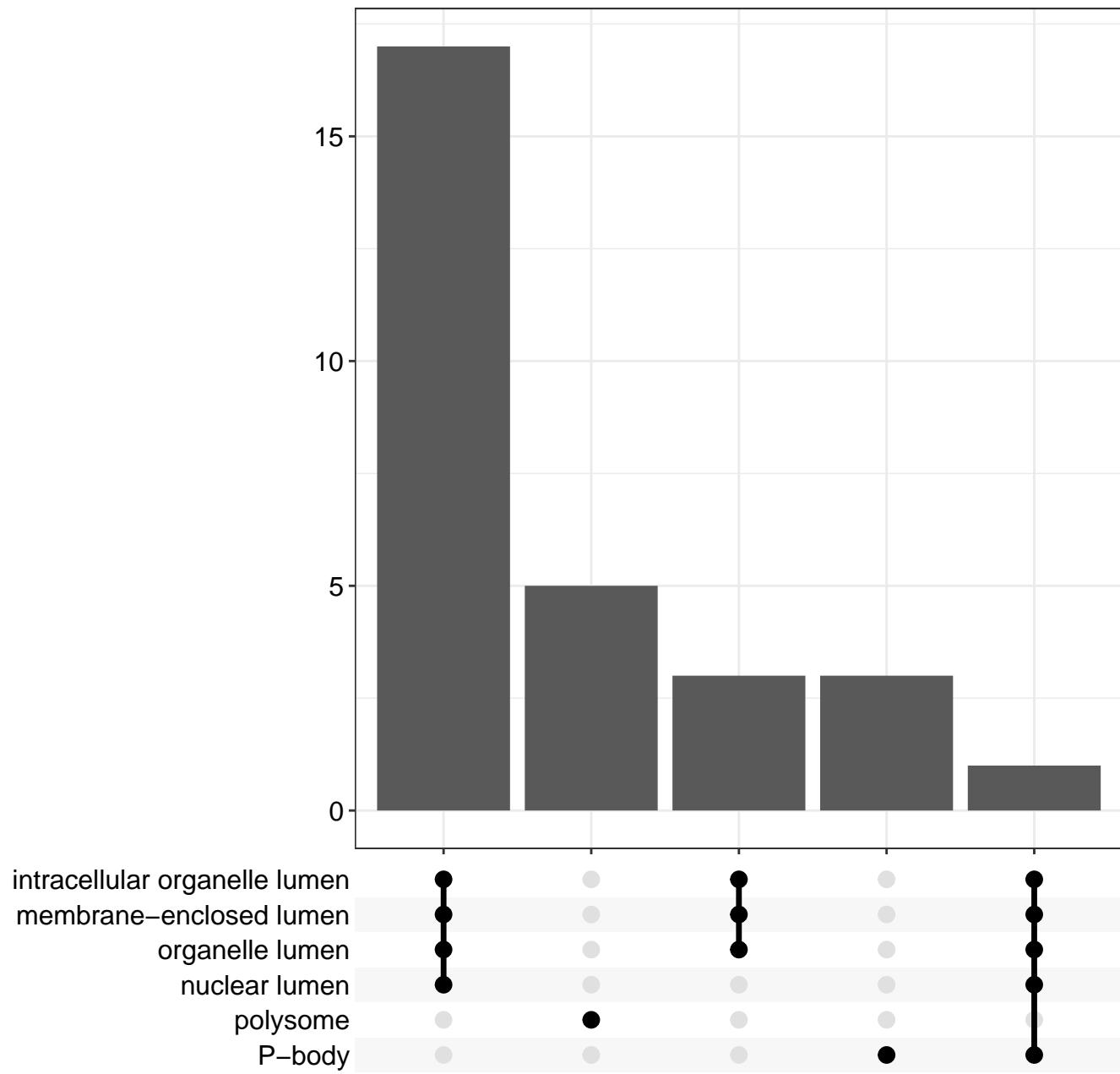


polysome

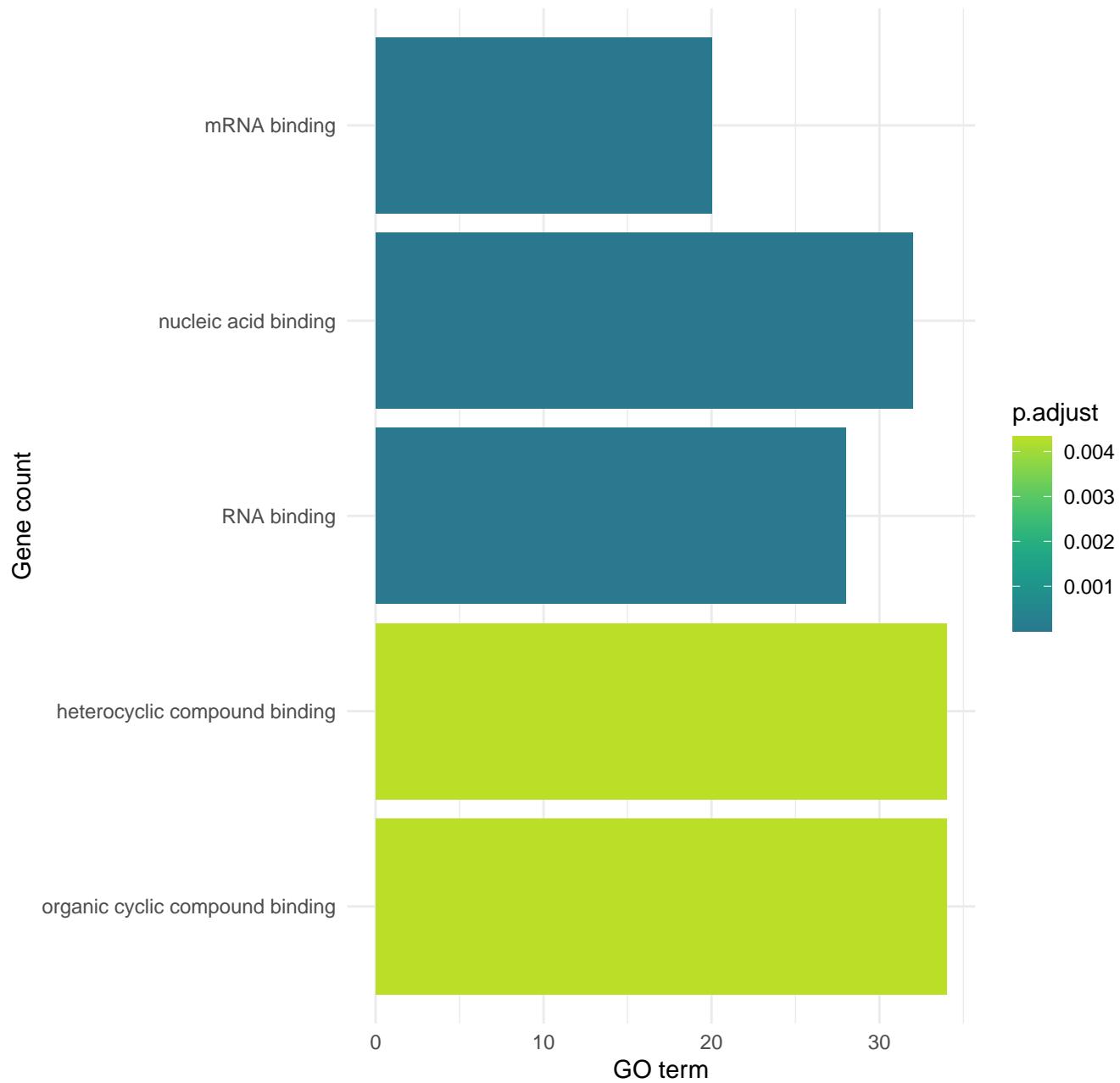




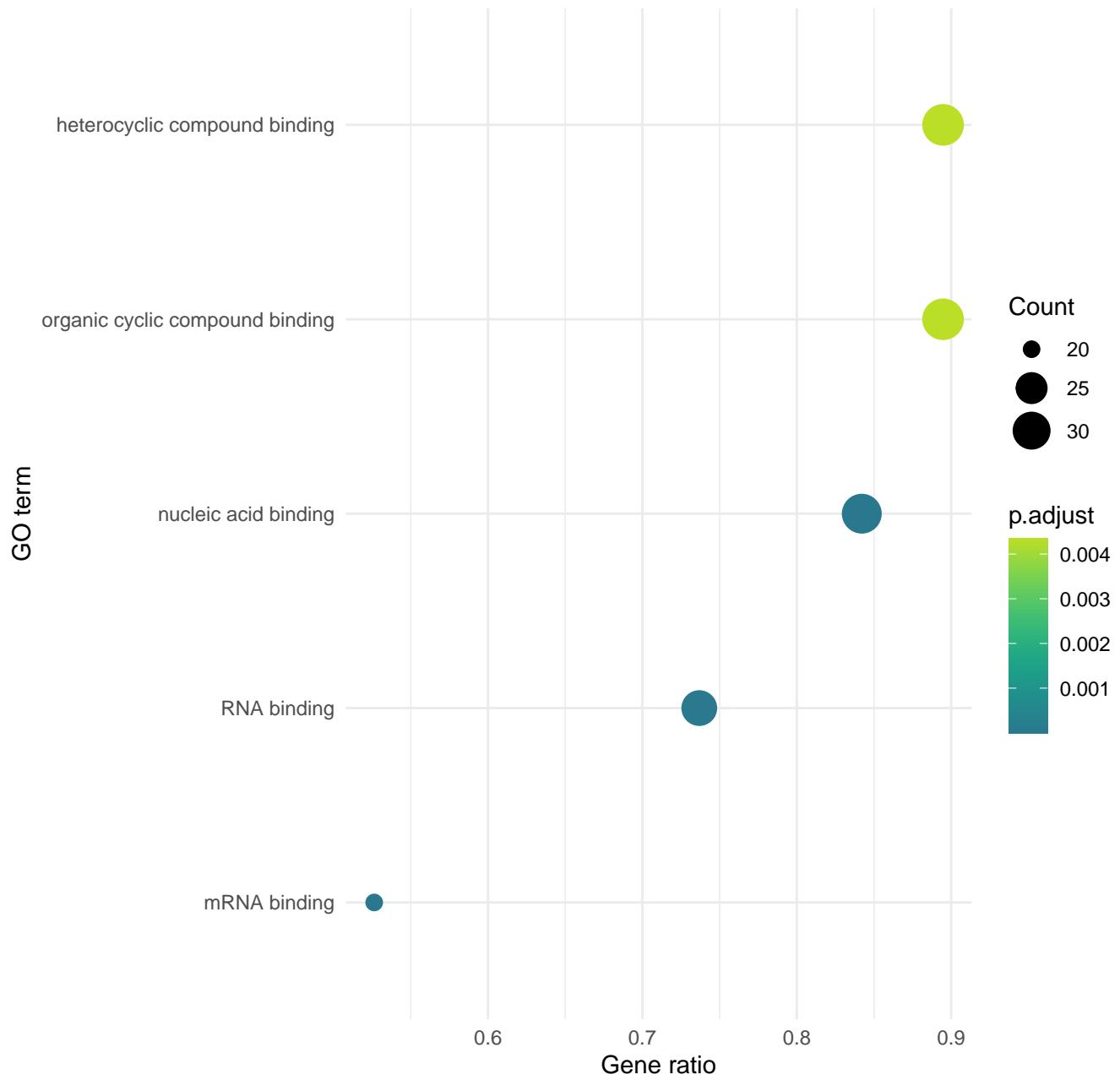
MTR4-TAP Up-regulated GO CC upsetplot



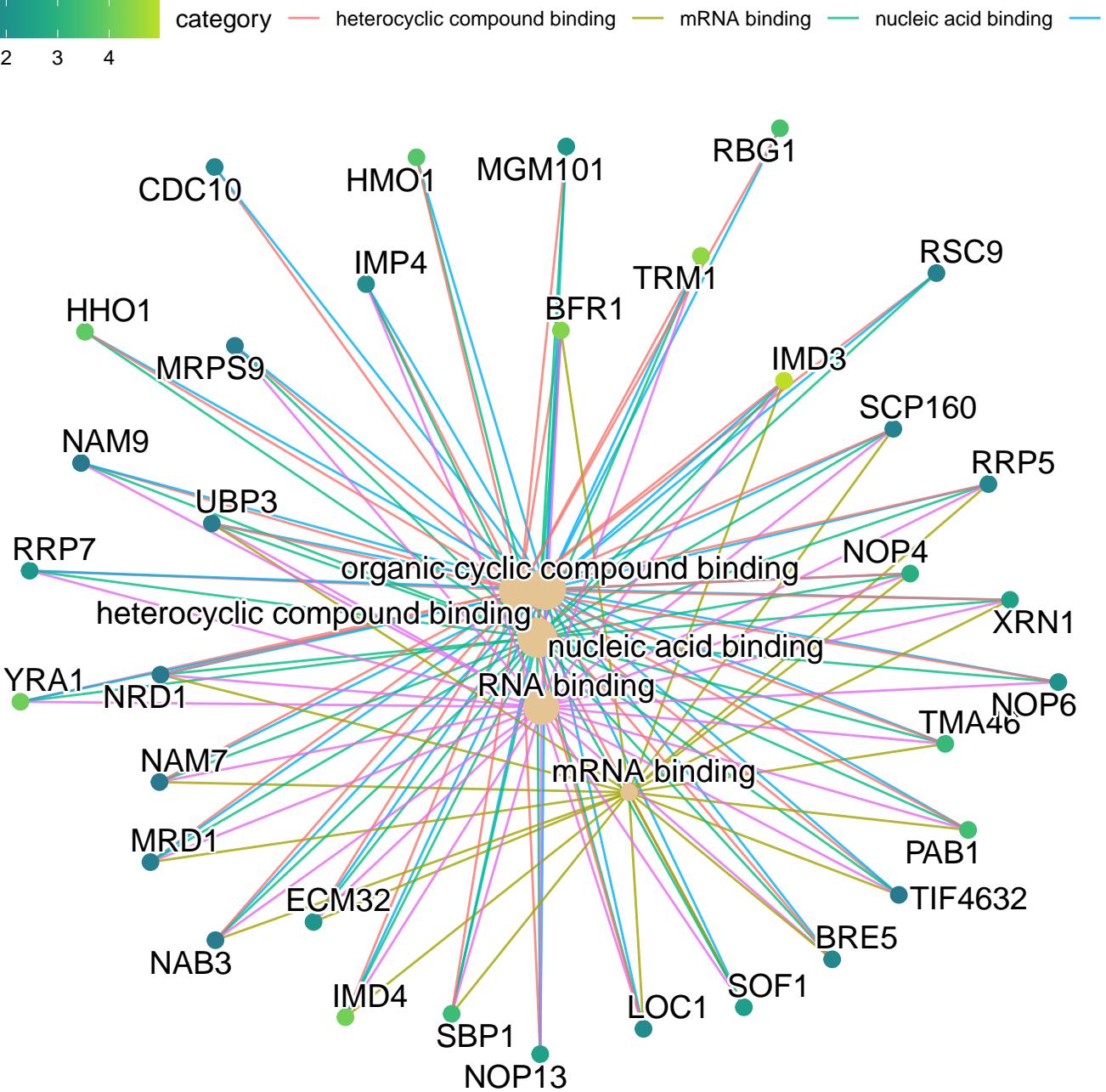
MTR4-TAP Up-regulated GO MF barplot



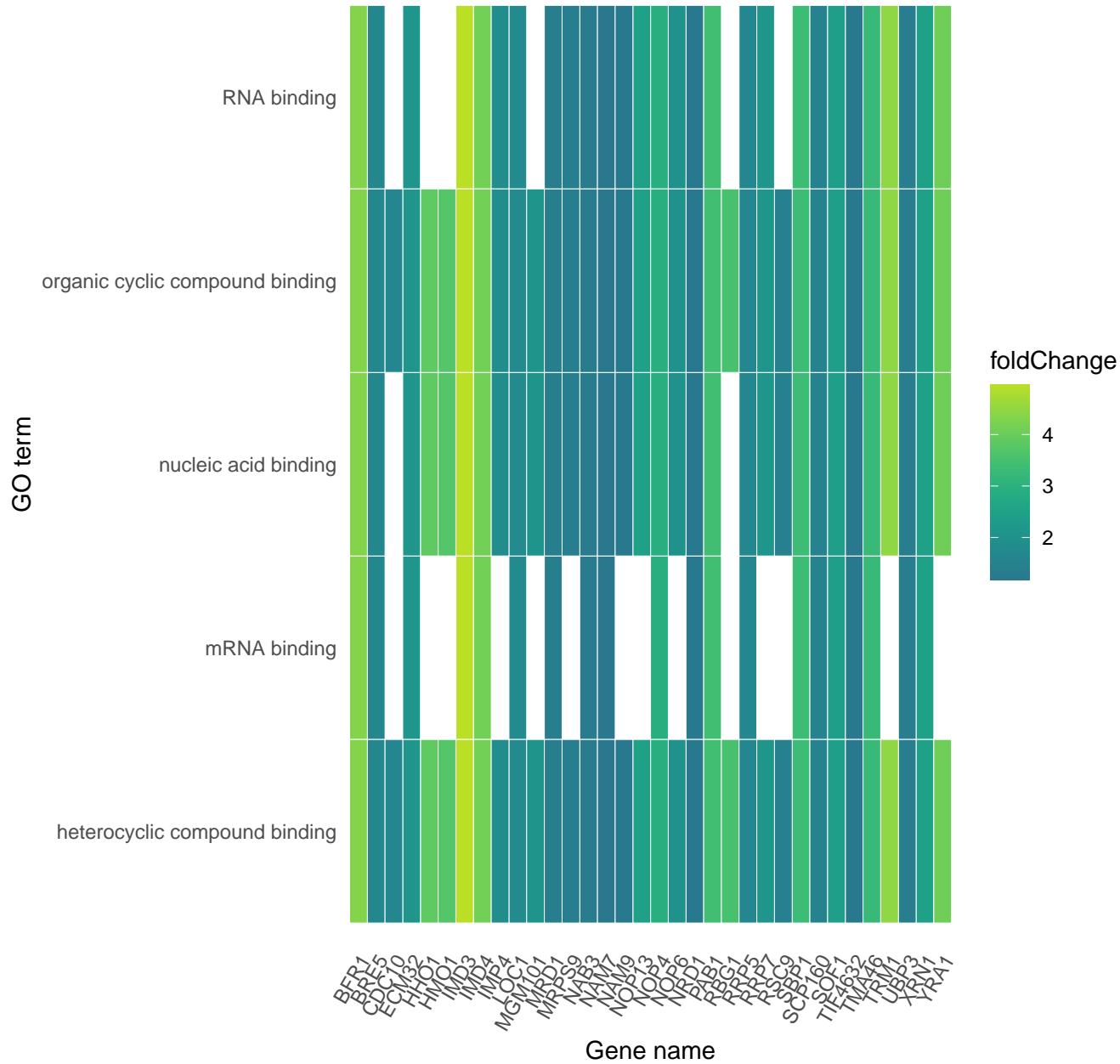
MTR4-TAP Up-regulated GO MF dotplot



MTR4-TAP Up-regulated GO MF cnetplot

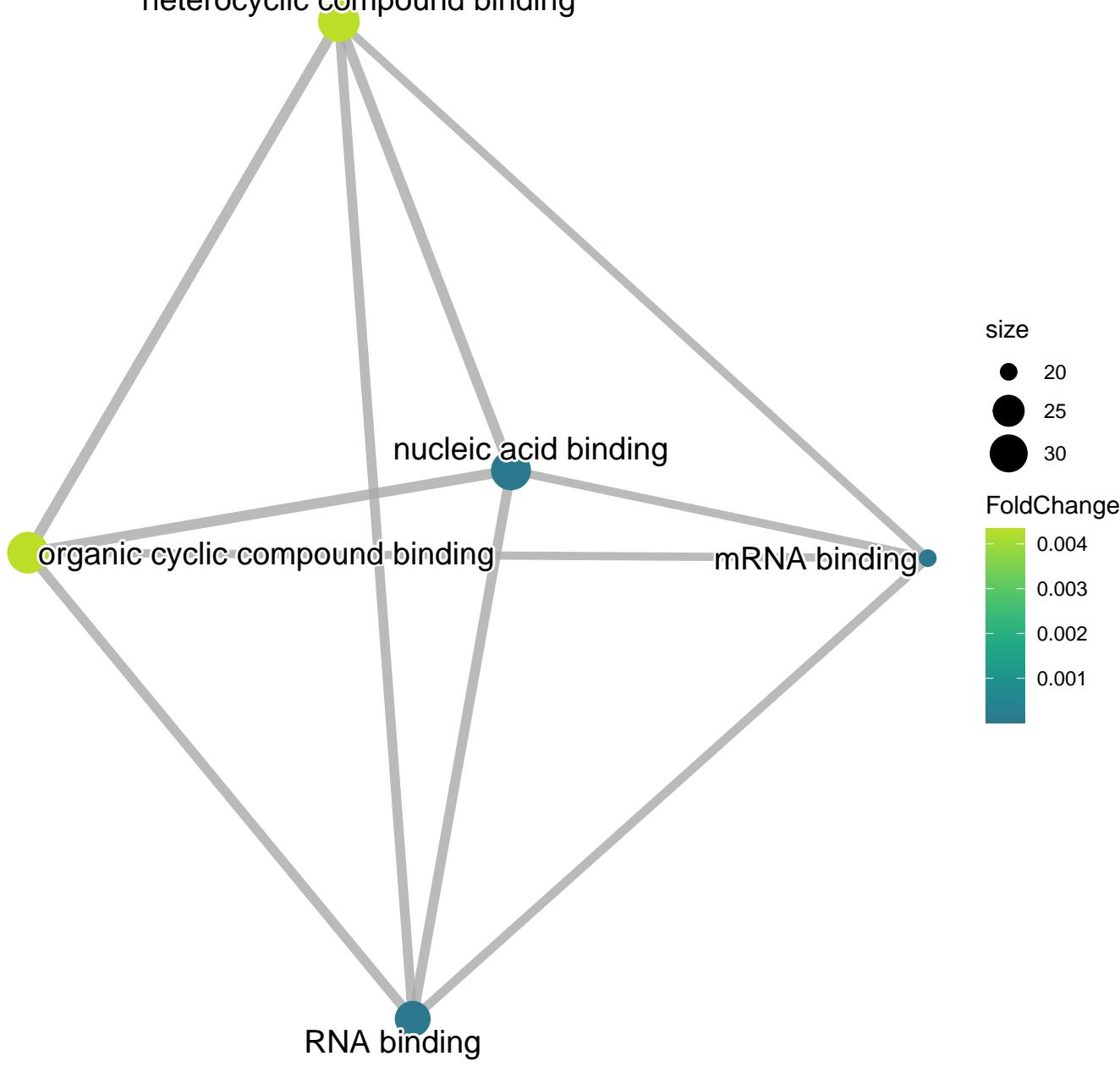


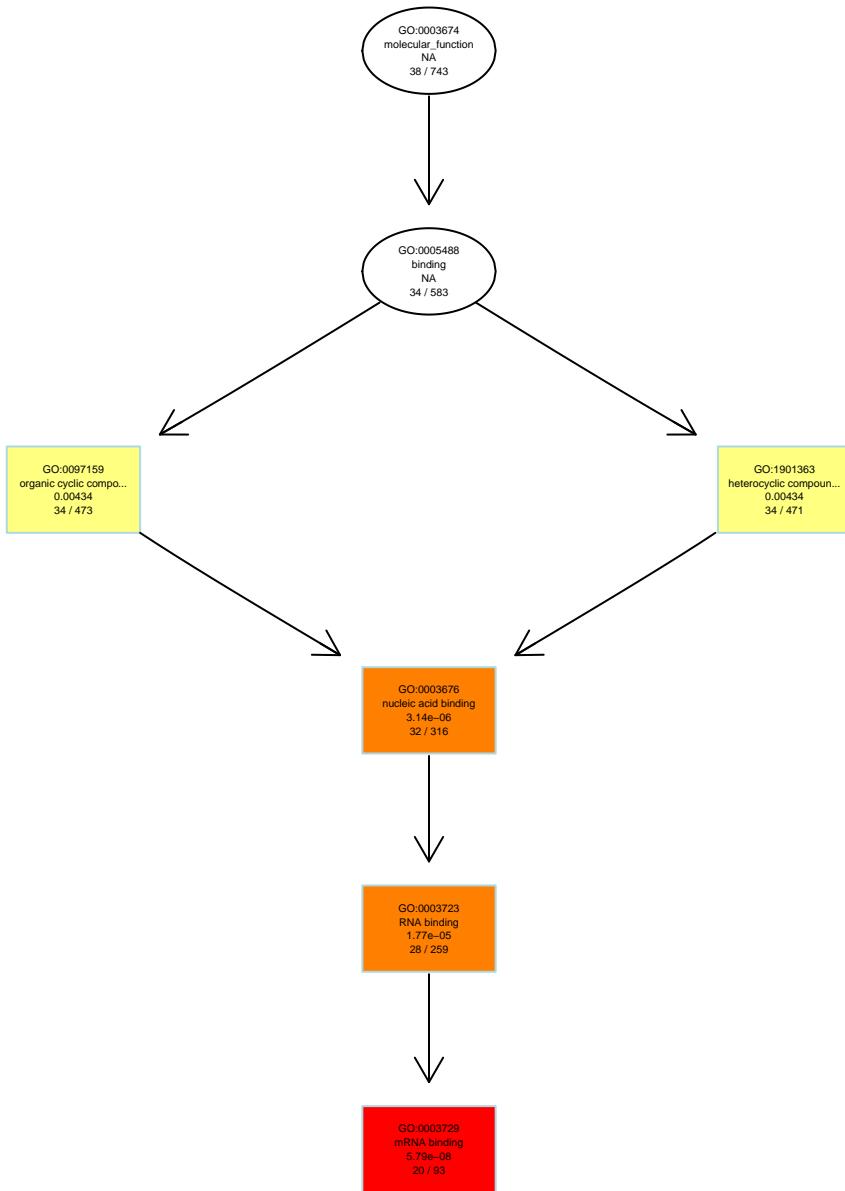
MTR4-TAP Up-regulated GO MF heatplot



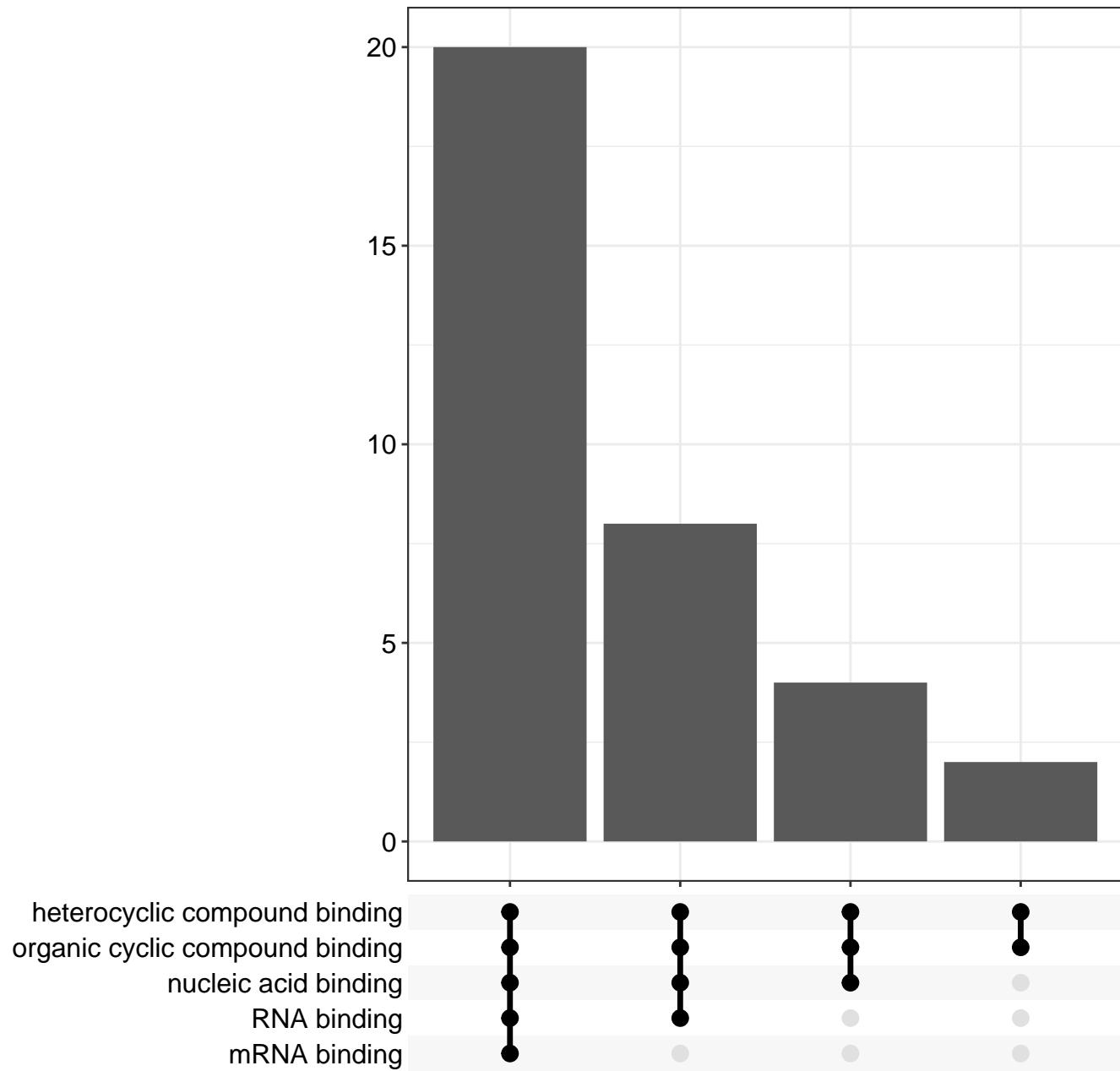
MTR4-TAP Up-regulated GO MF emapplot

heterocyclic compound binding

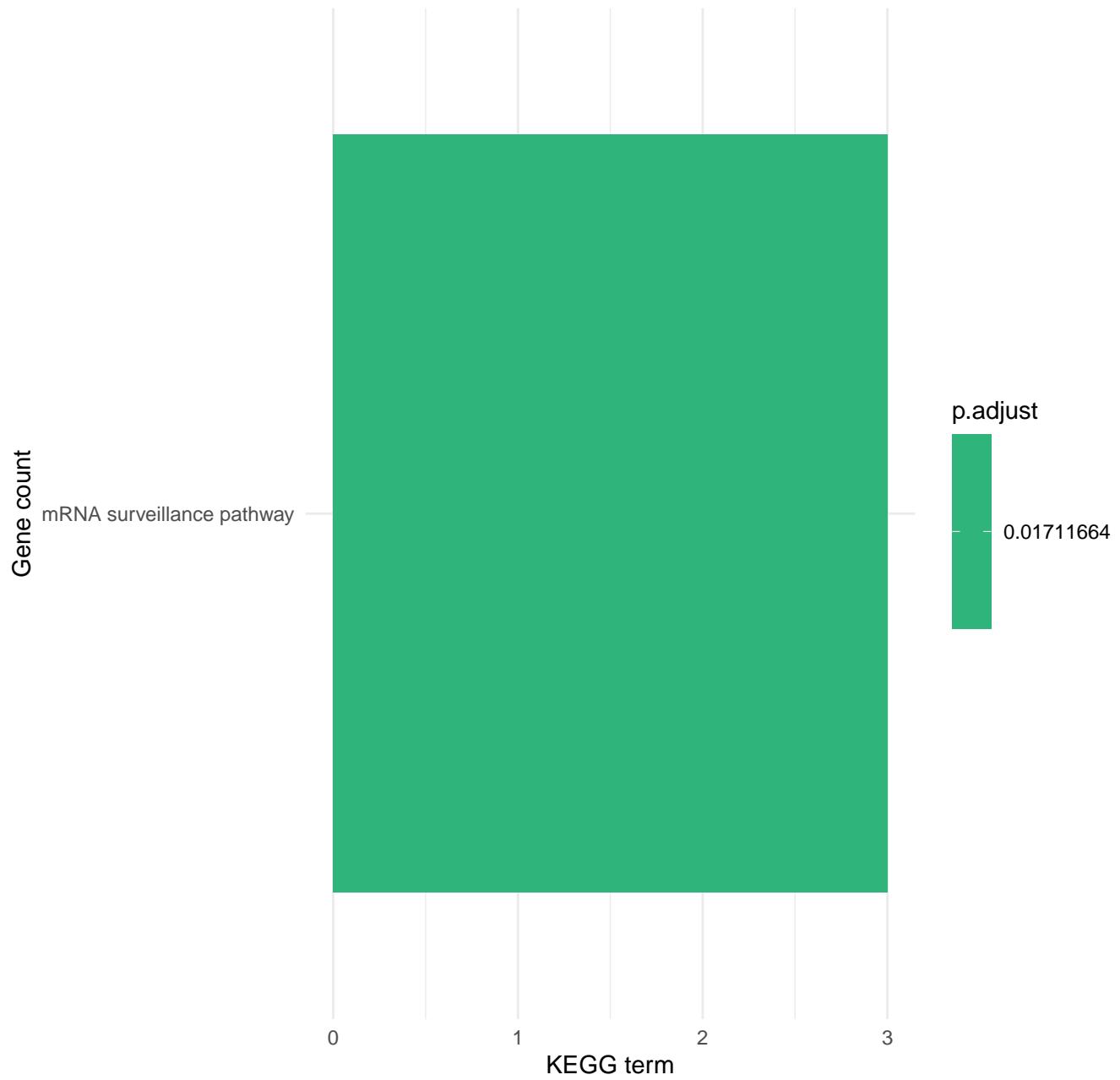




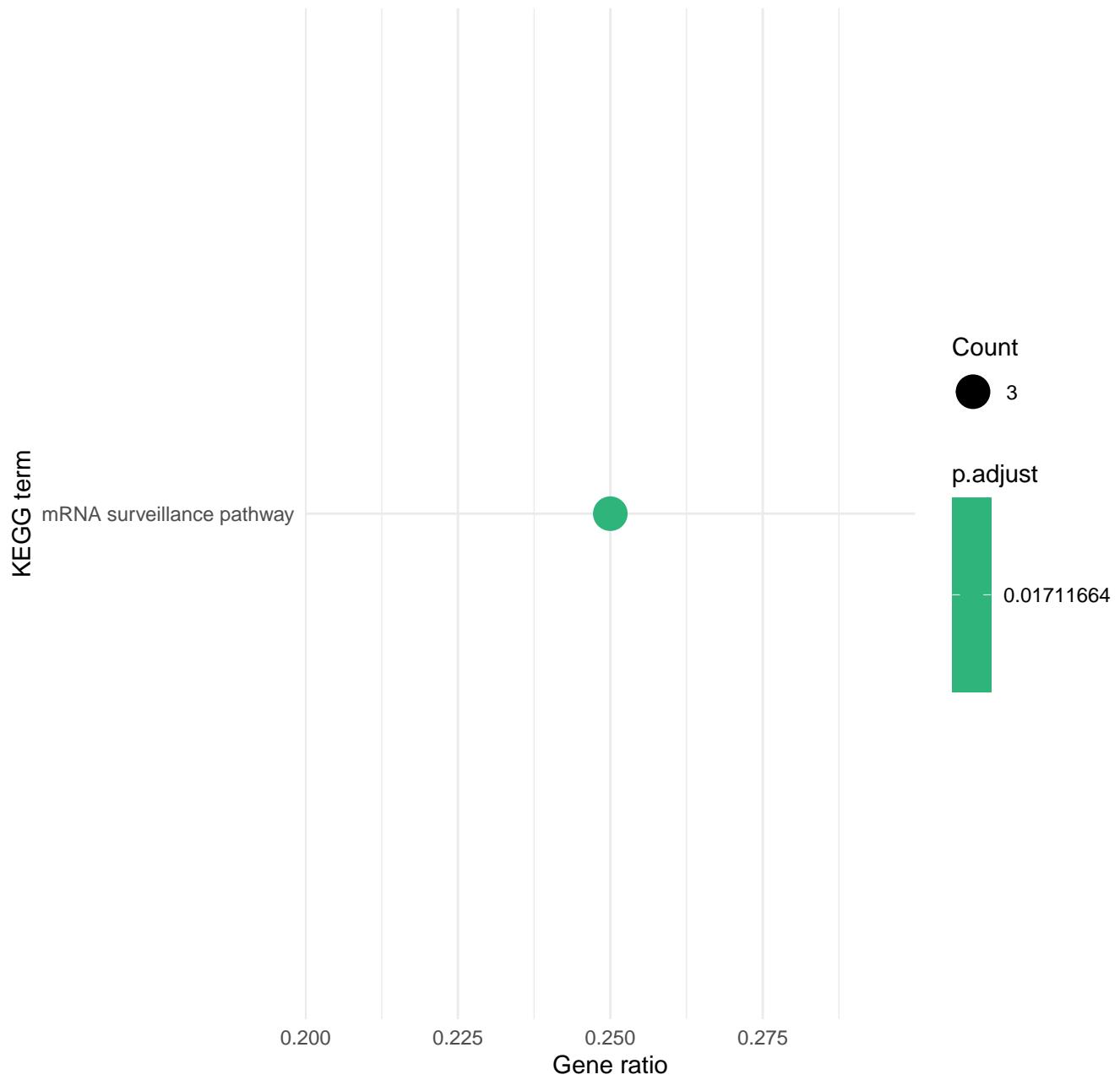
MTR4-TAP Up-regulated GO MF upsetplot



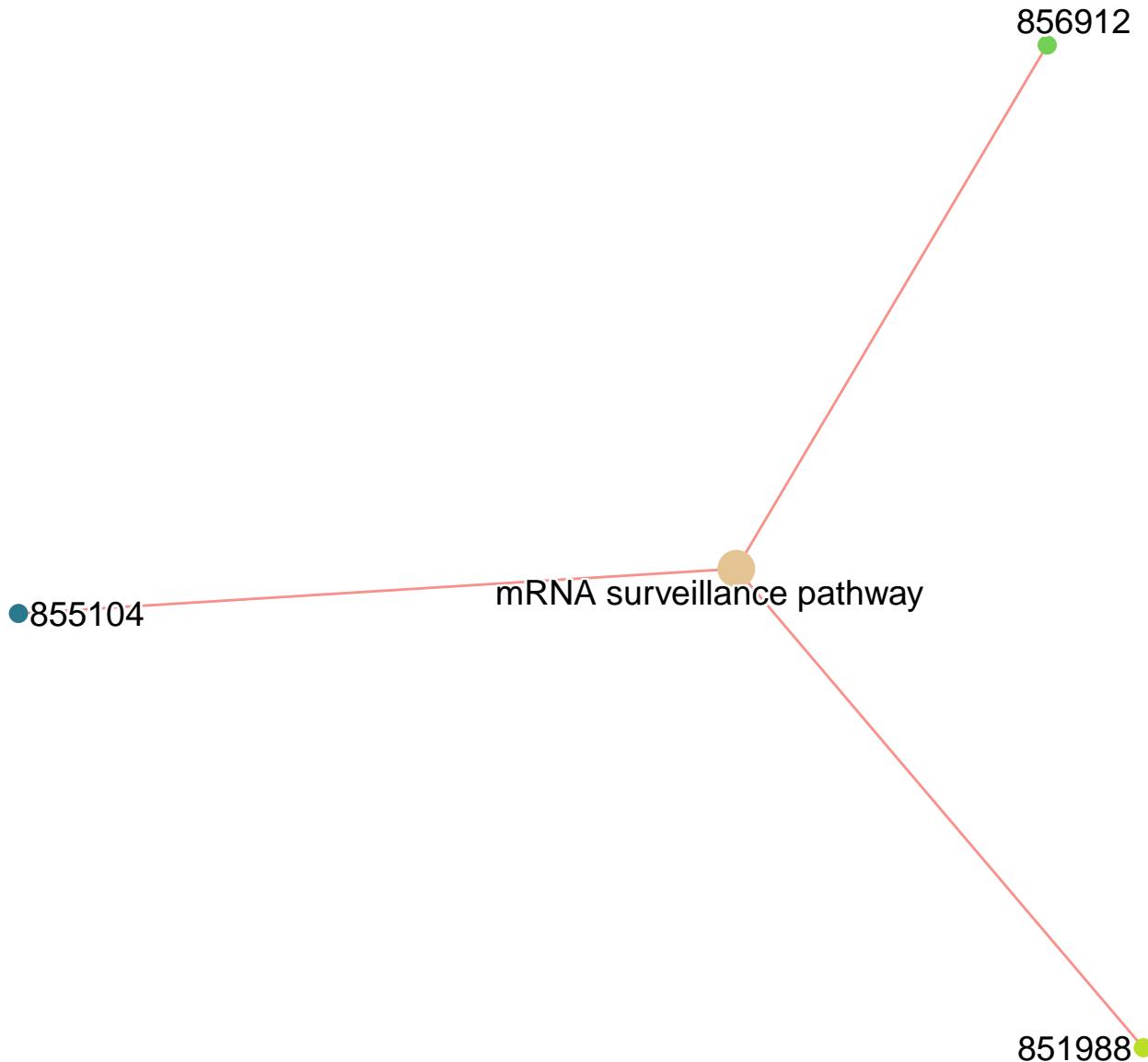
MTR4–TAP Up-regulated KEGG barplot



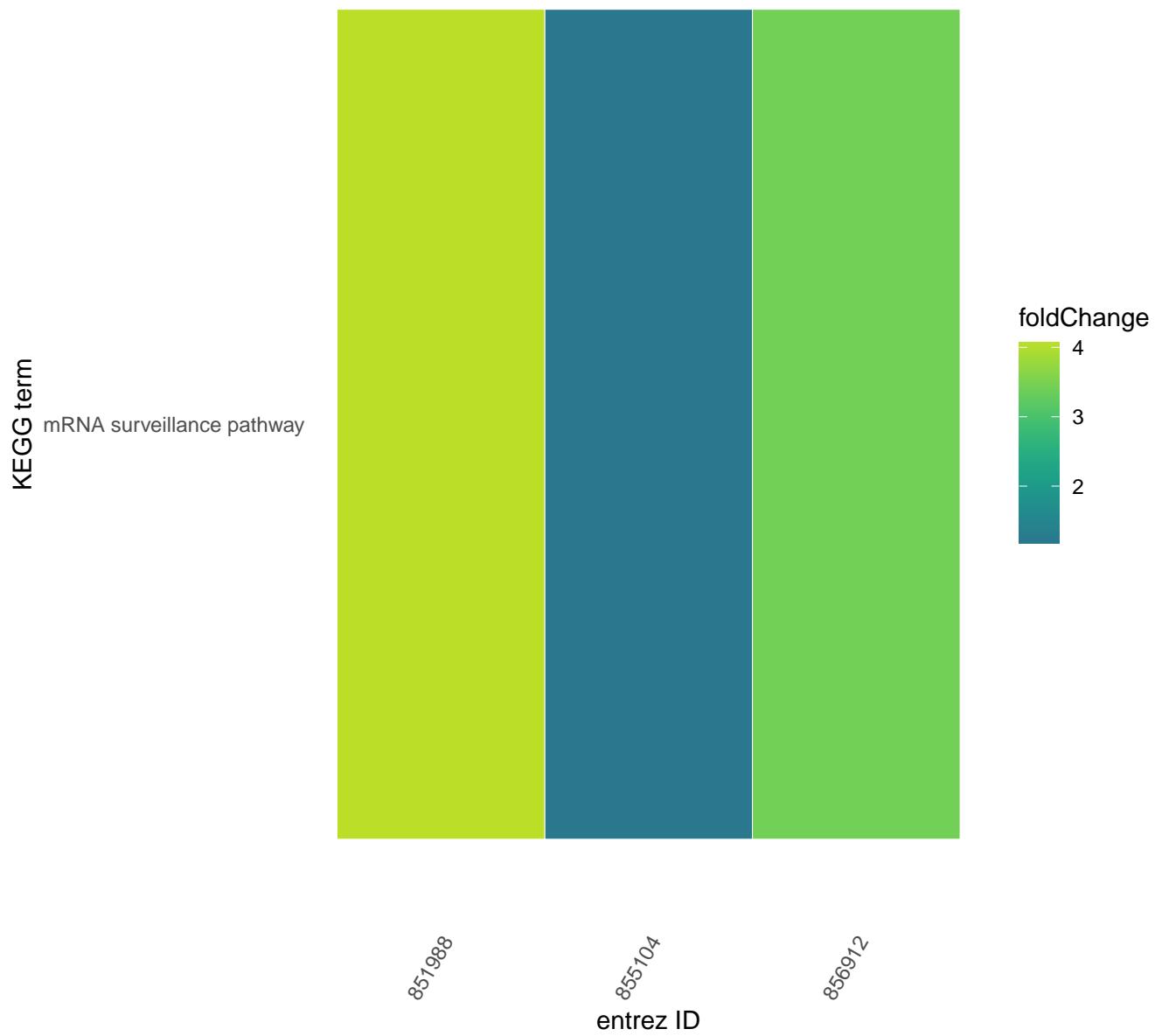
MTR4–TAP Up-regulated KEGG dotplot



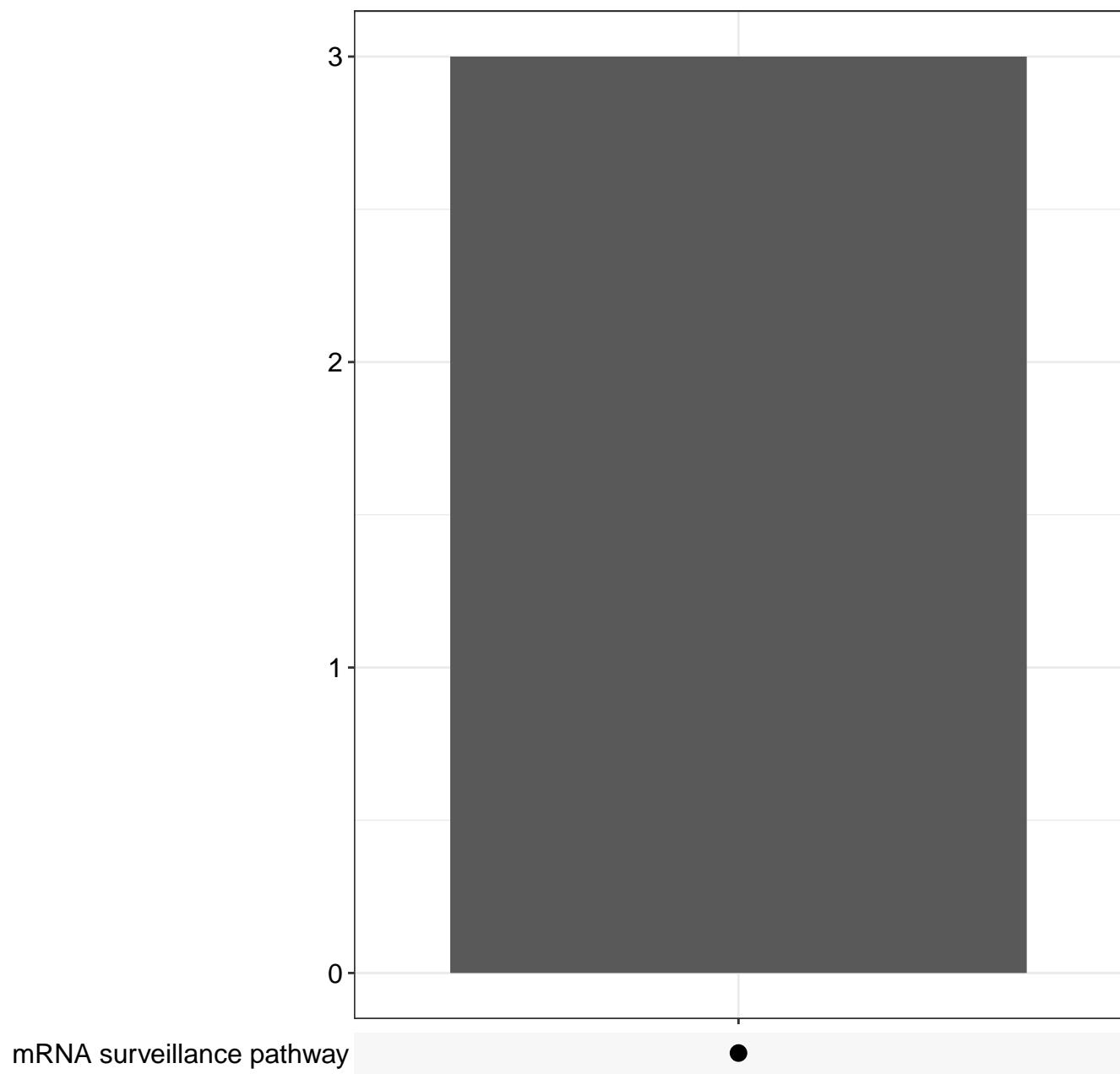
MTR4-TAP Up-regulated KEGG dotplot



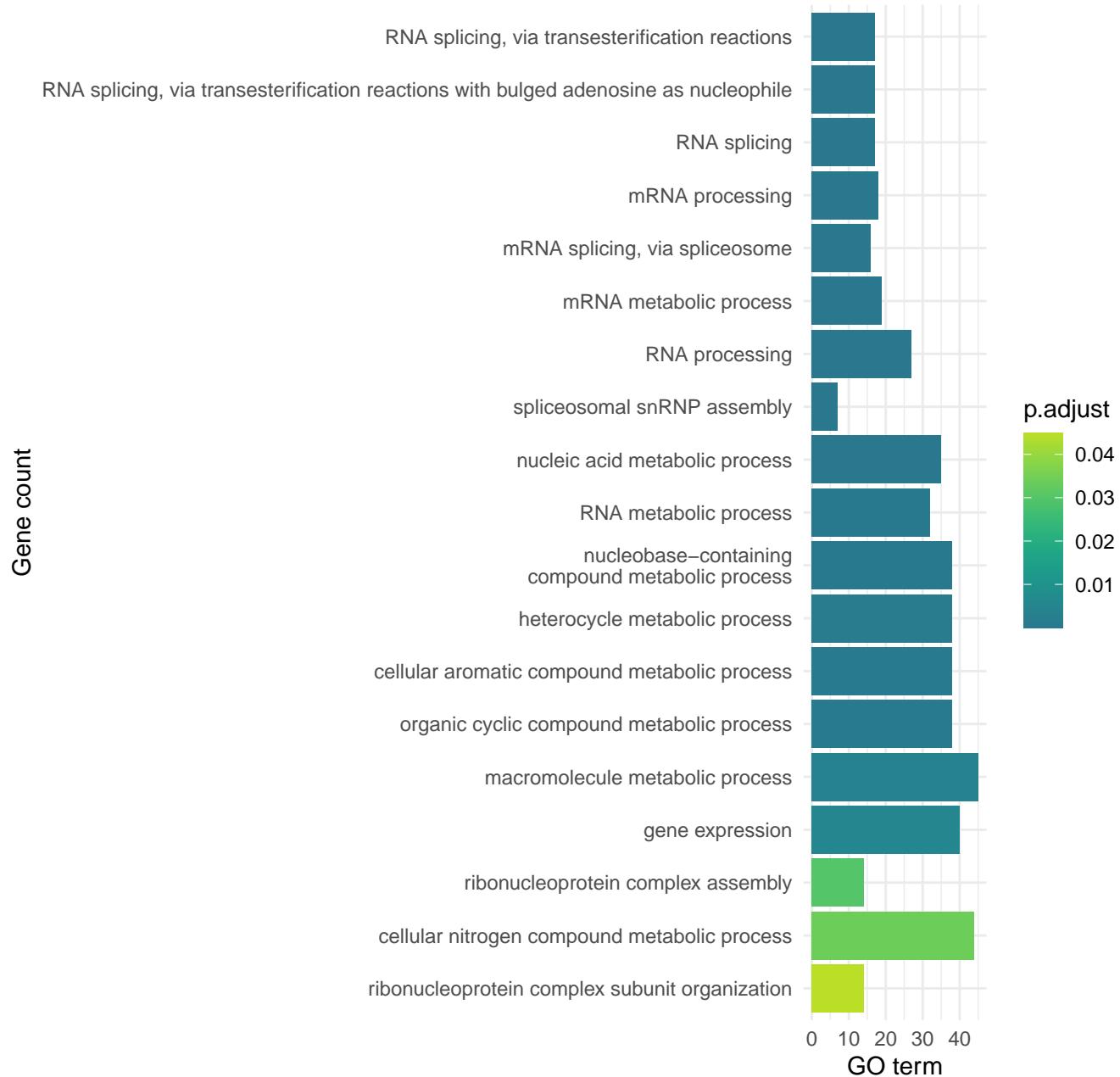
MTR4–TAP Up-regulated KEGG heatplot



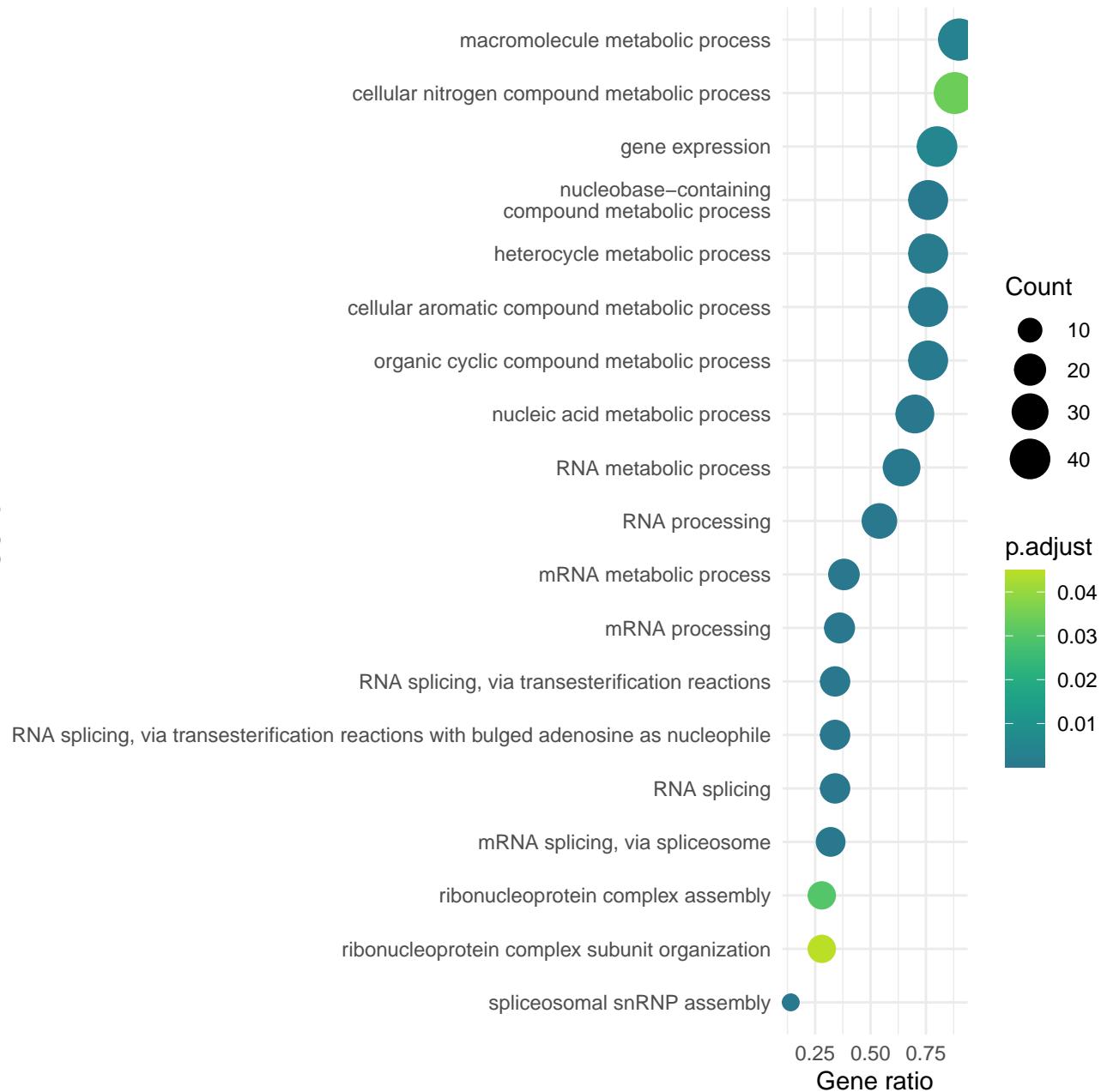
MTR4-TAP Up-regulated KEGG upsetplot



LSM2-TAP Up-regulated



LSM2-TAP Up-regulated



LSM2-TAP Up-regulated GO BP cnetplot

ic process — nucleic acid metabolic process

— ribonucleoprotein complex subunit organization

Nucleic acid metabolism processes

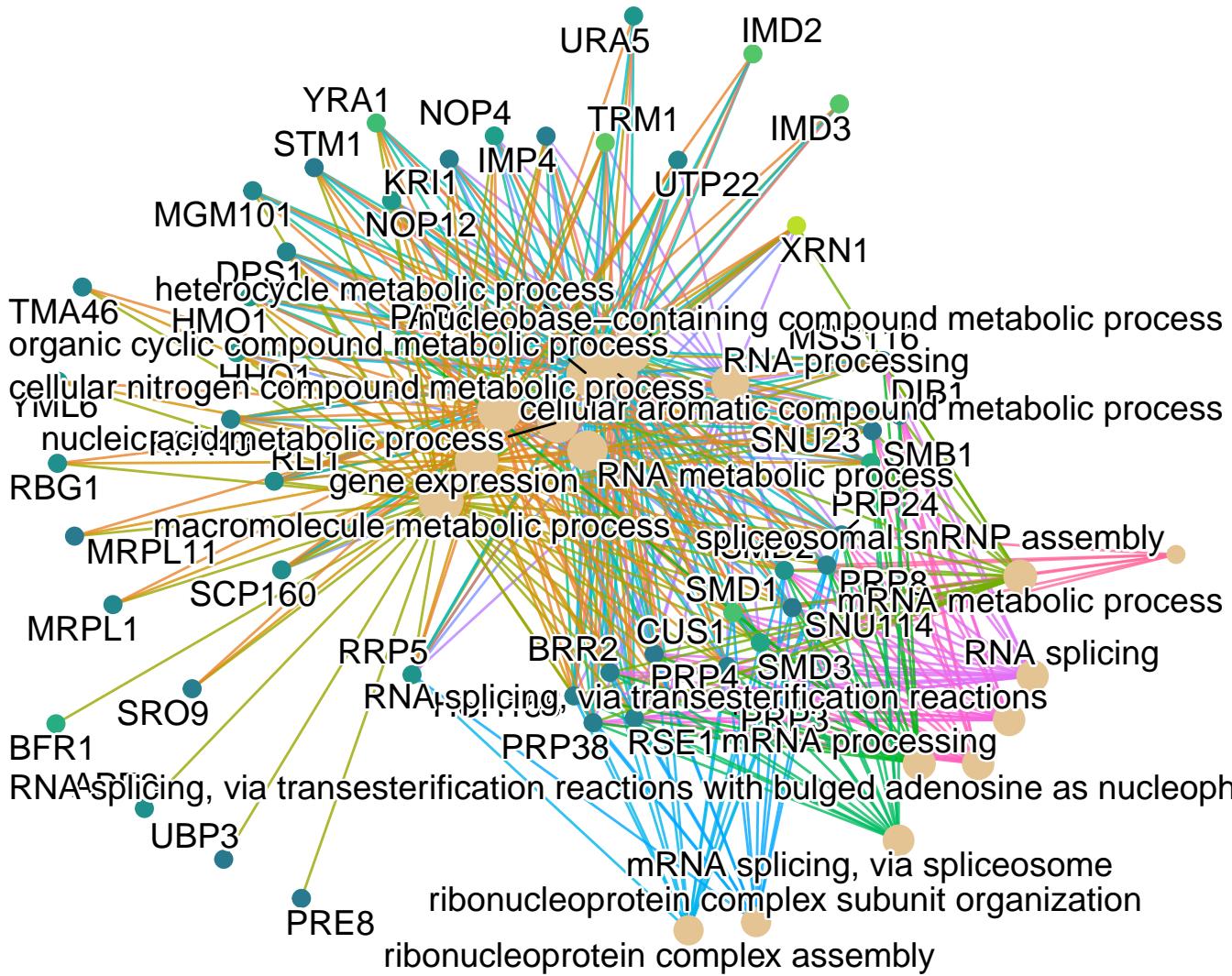
Ribonucleoprotein complex

— nucleobase-containing compound metabolism

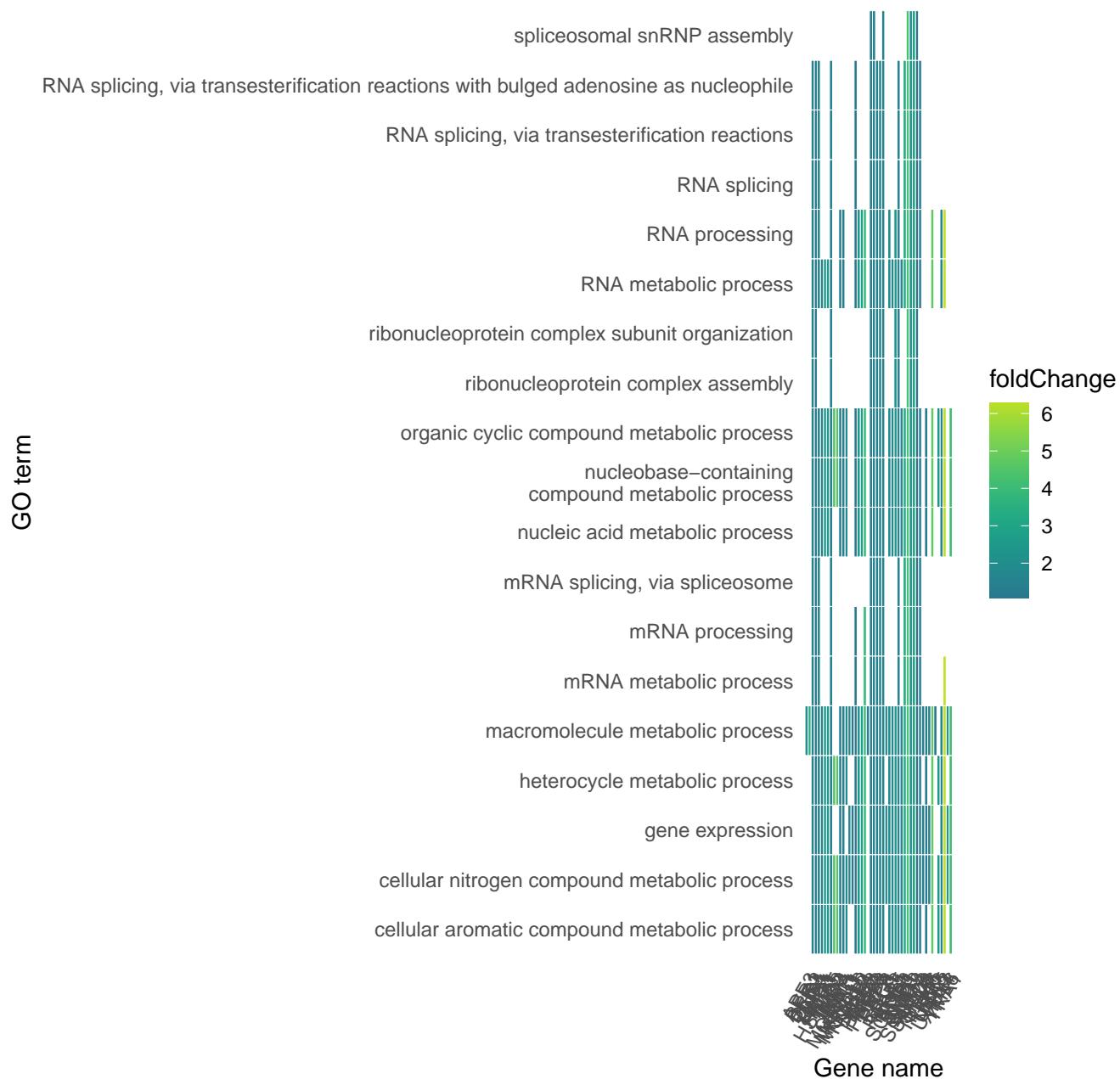
— RNA metabolic p

organic cyclic compound metabolic pathway

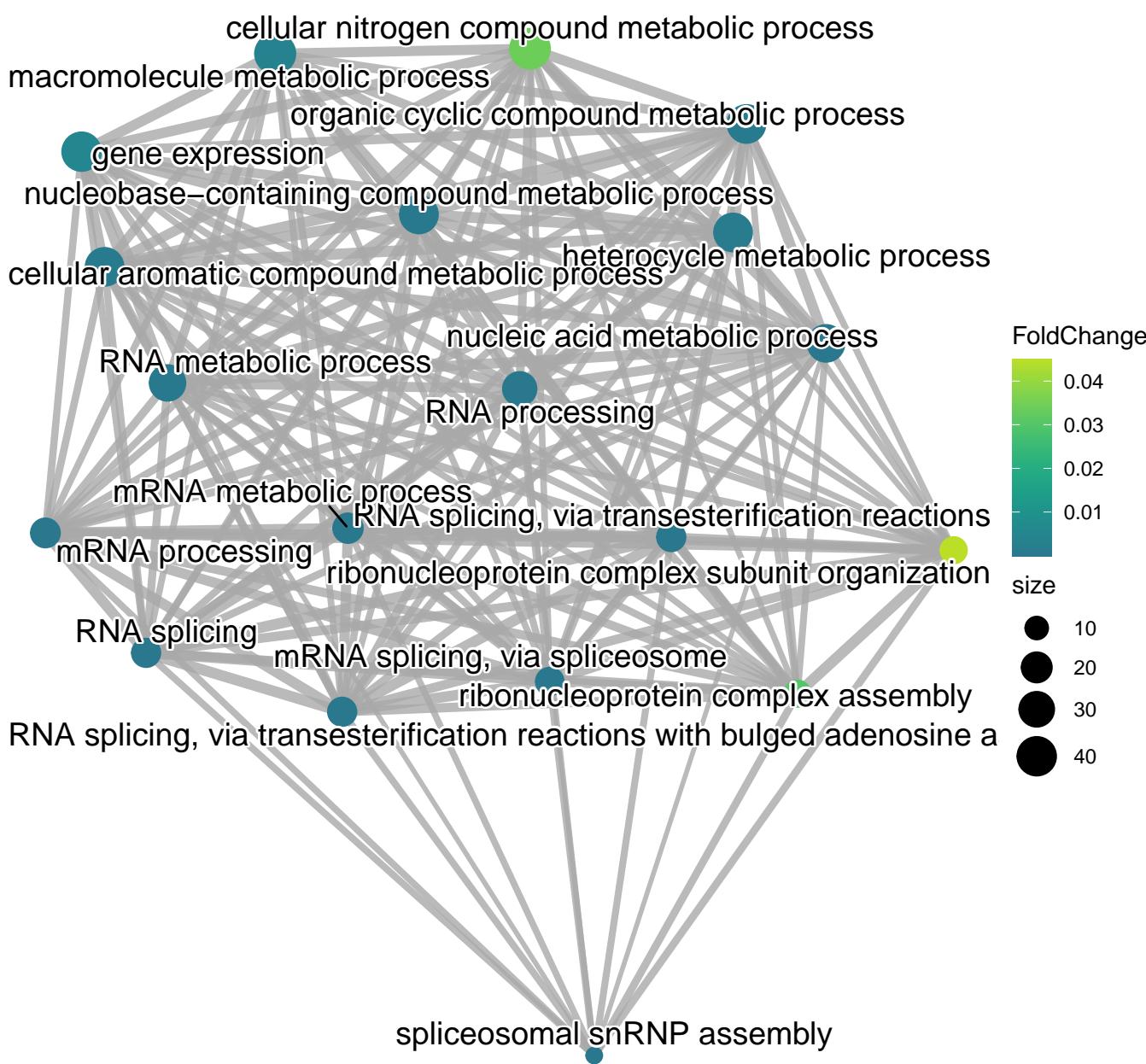
RNA metabolism

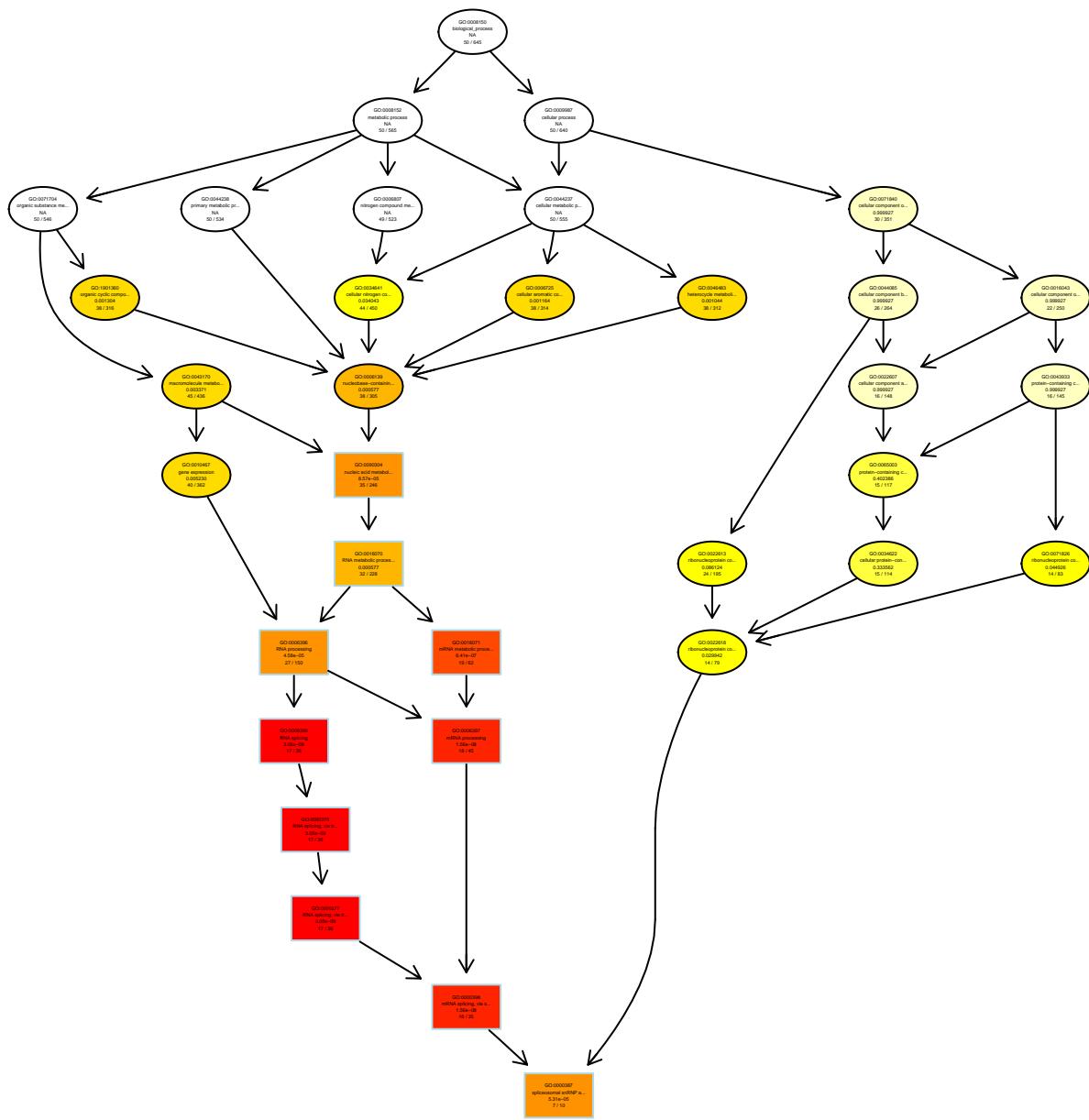


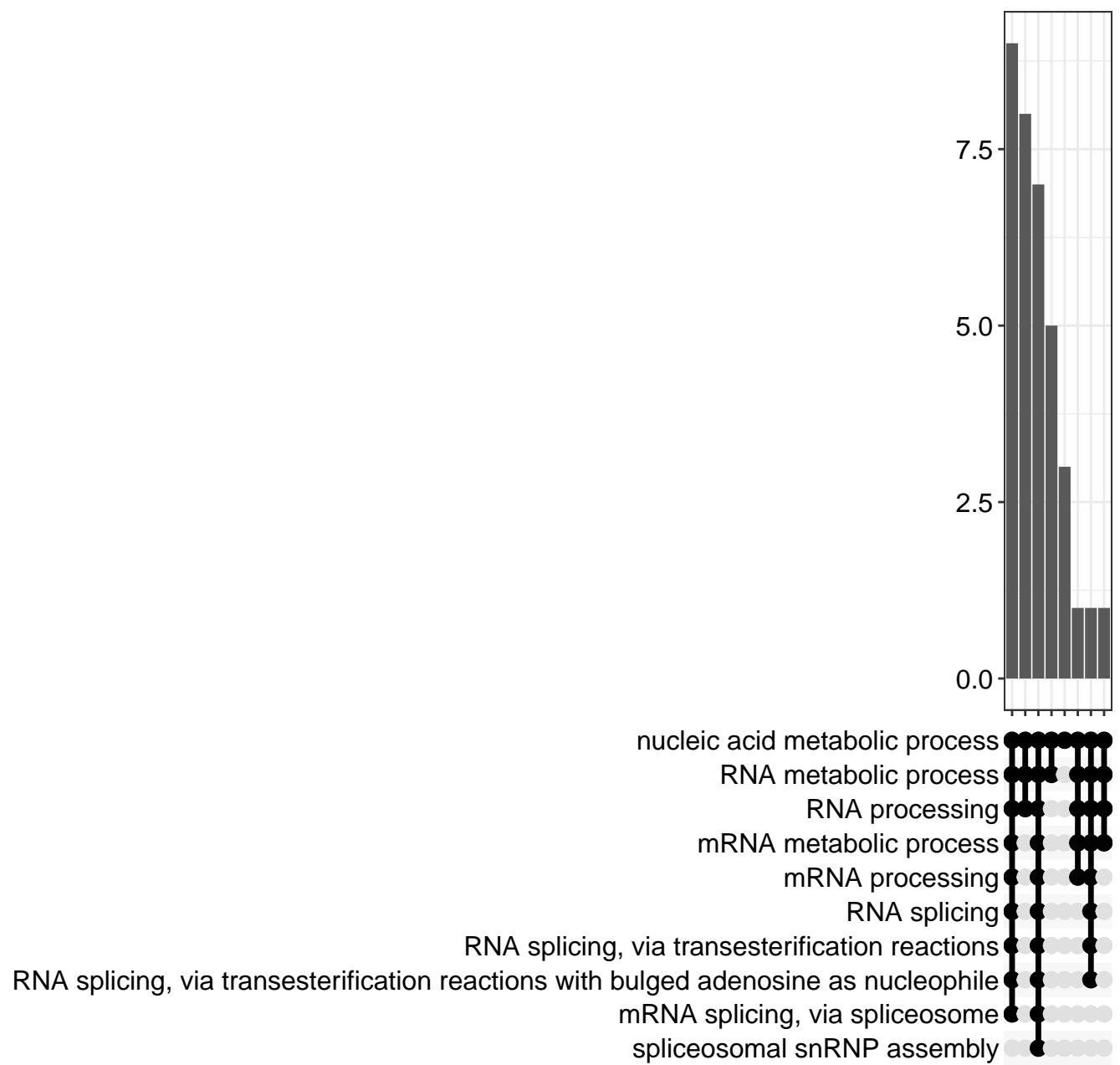
LSM2-TAP Up-regulated



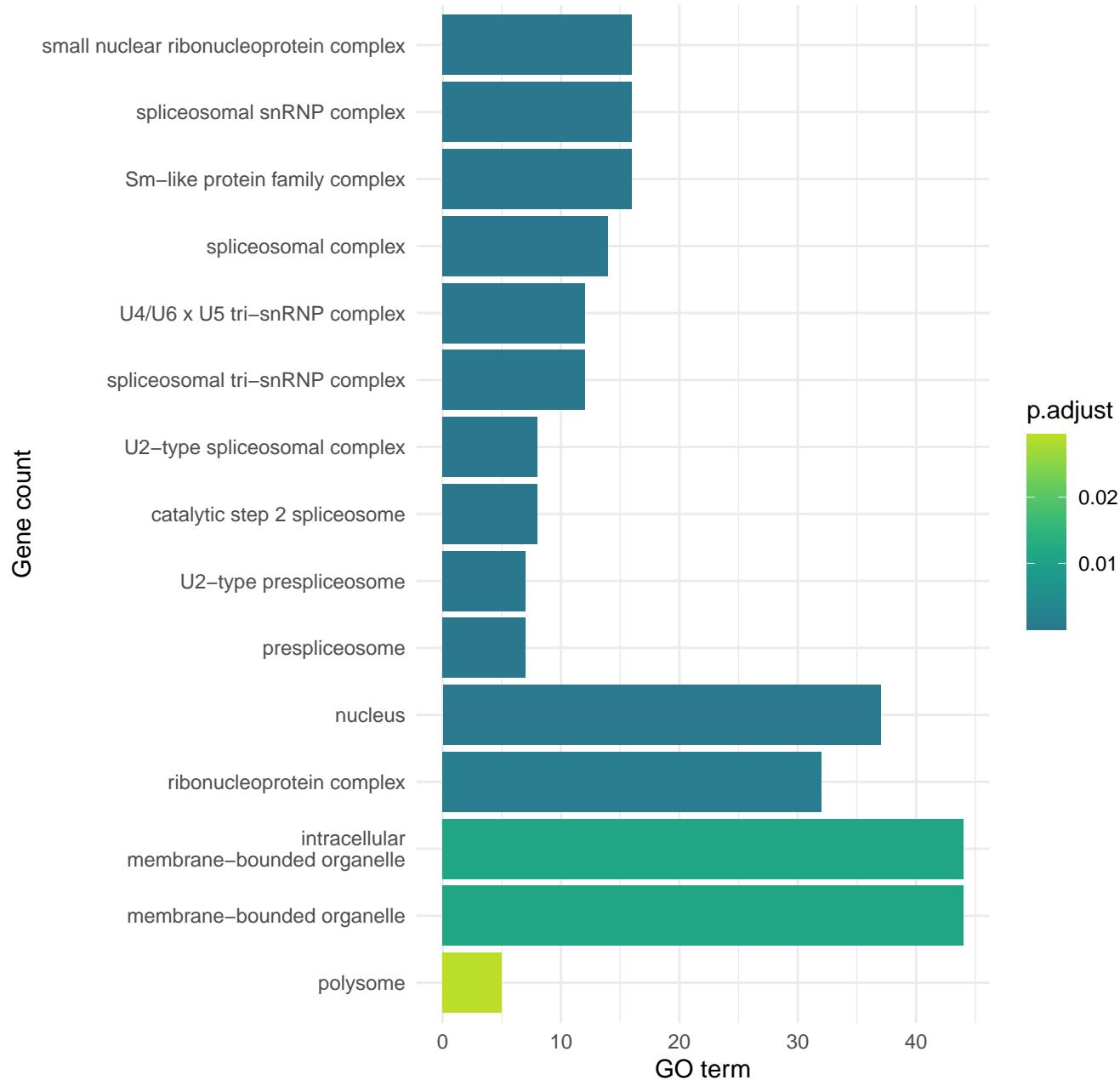
LSM2-TAP Up-regulated GO BP emapplot



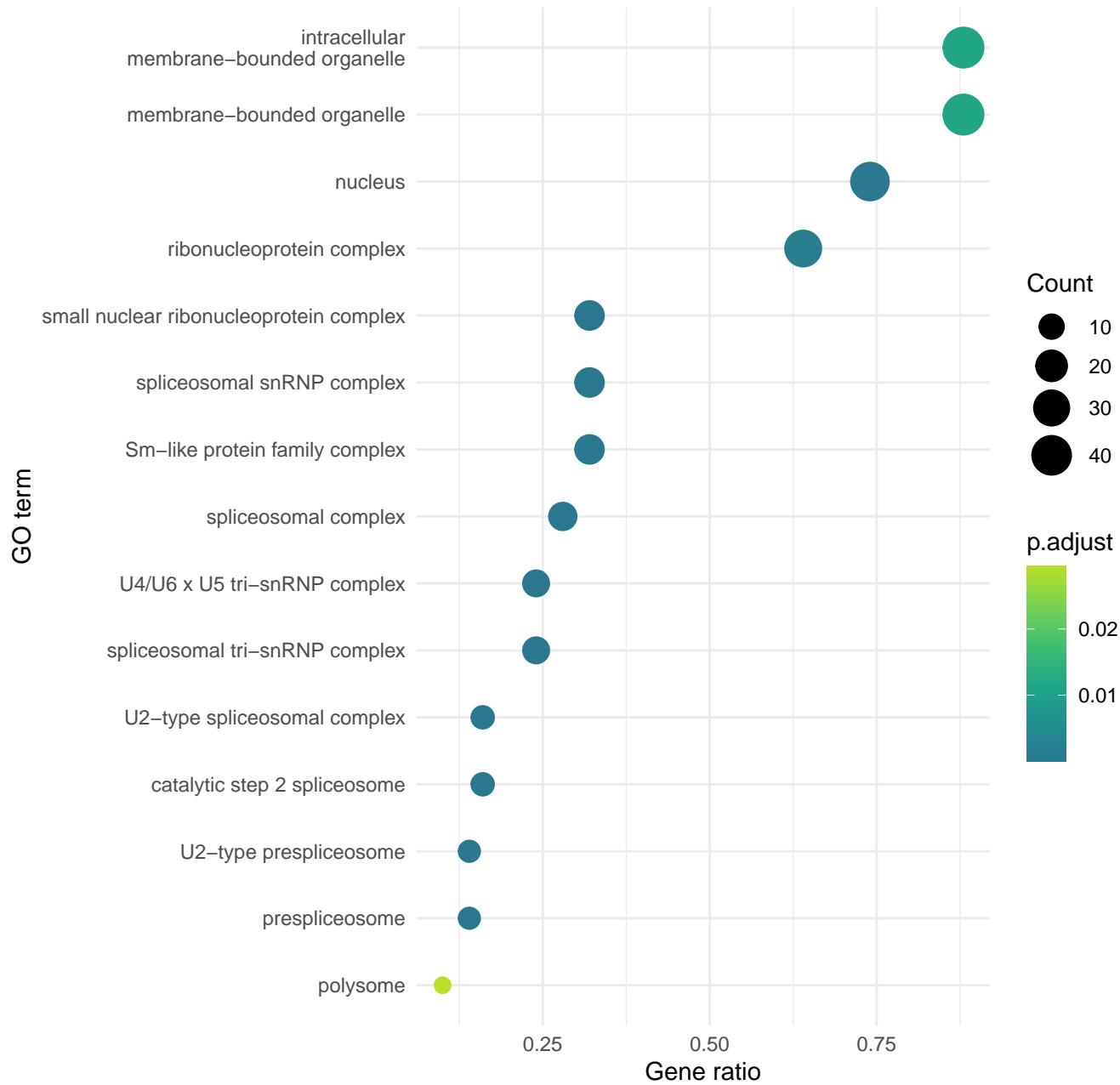




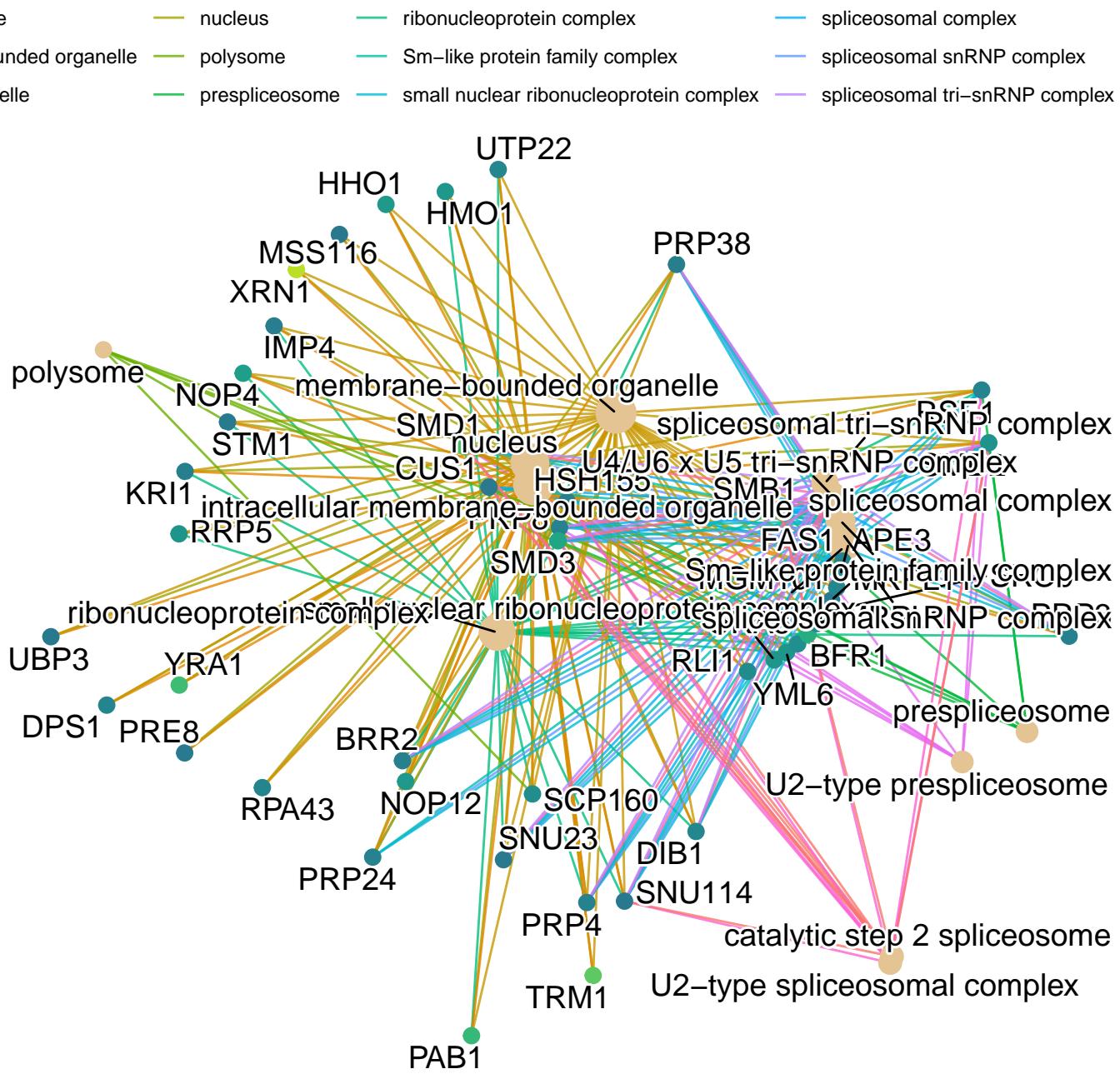
LSM2-TAP Up-regulated GO CC barplot



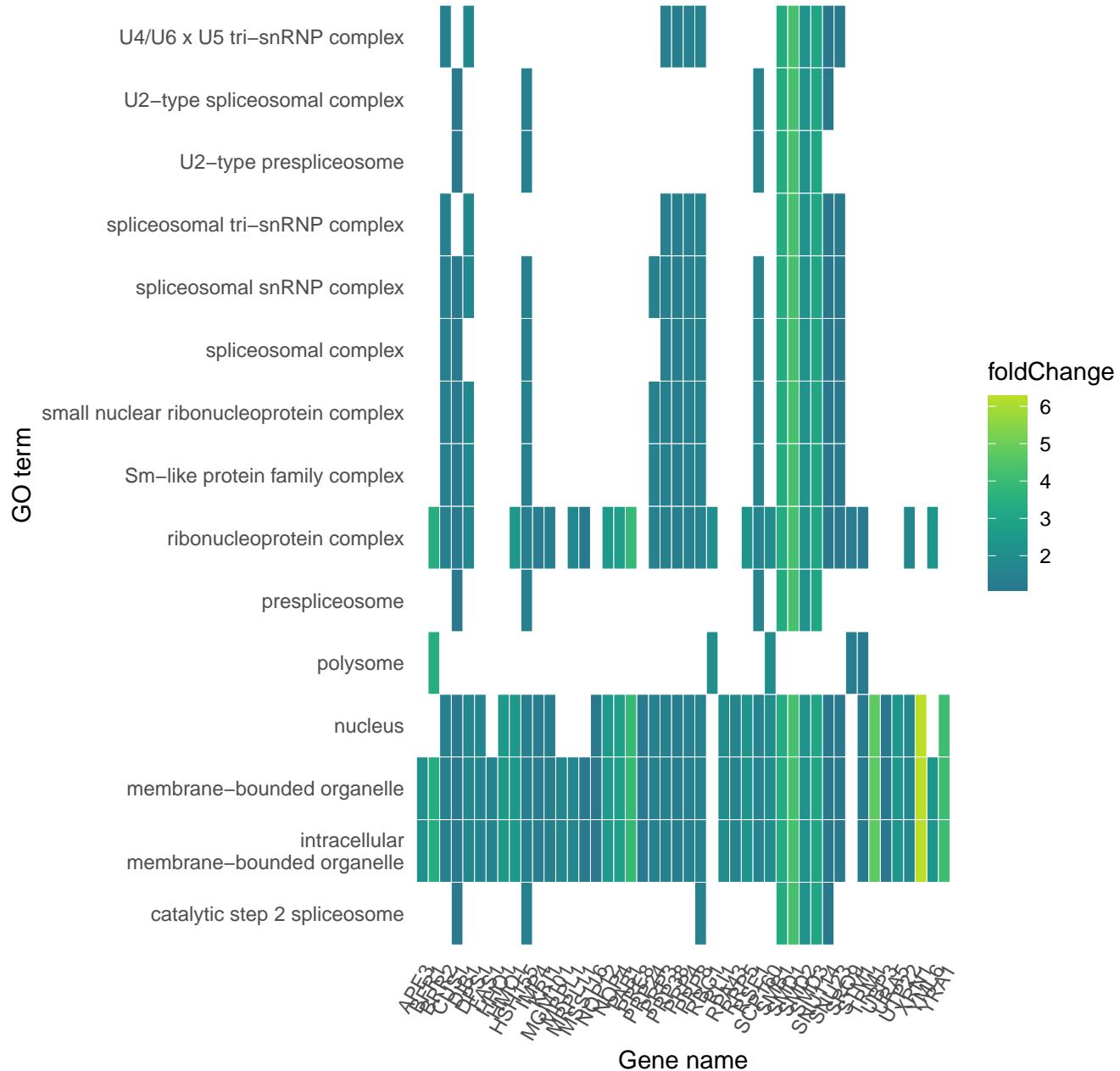
LSM2-TAP Up-regulated GO CC dotplot



LSM2-TAP Up-regulated GO CC cnetplot

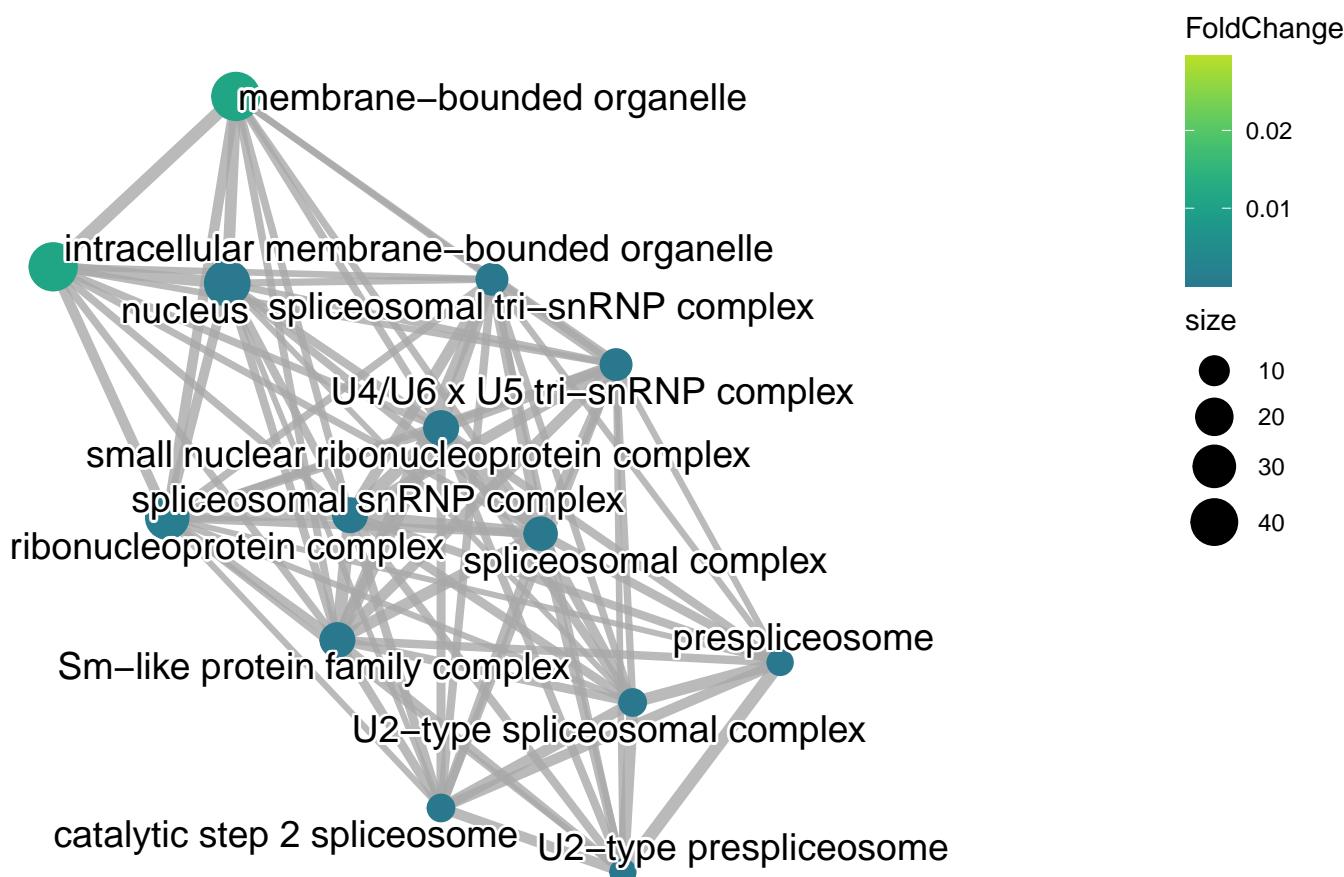


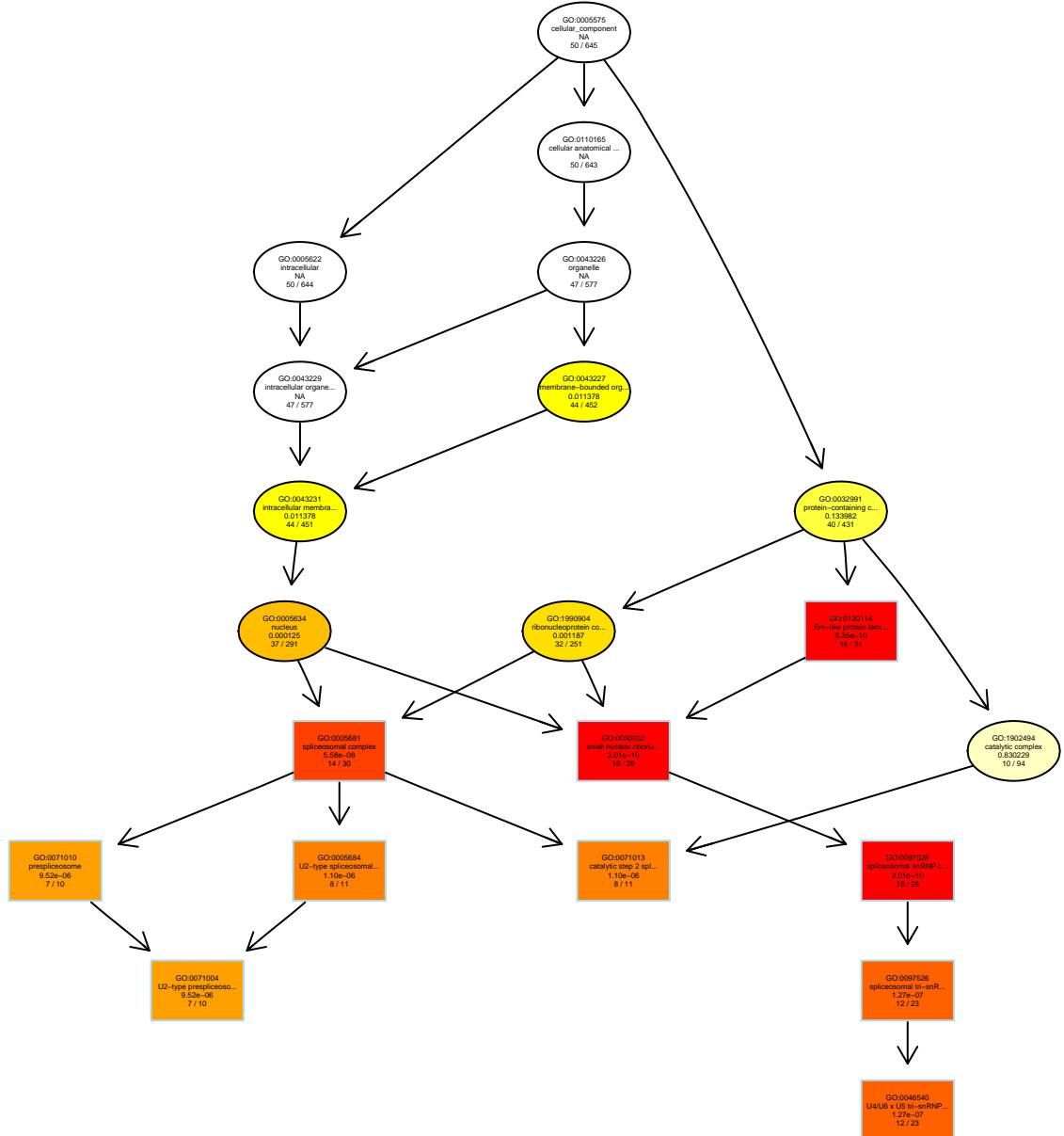
LSM2-TAP Up-regulated GO CC heatplot



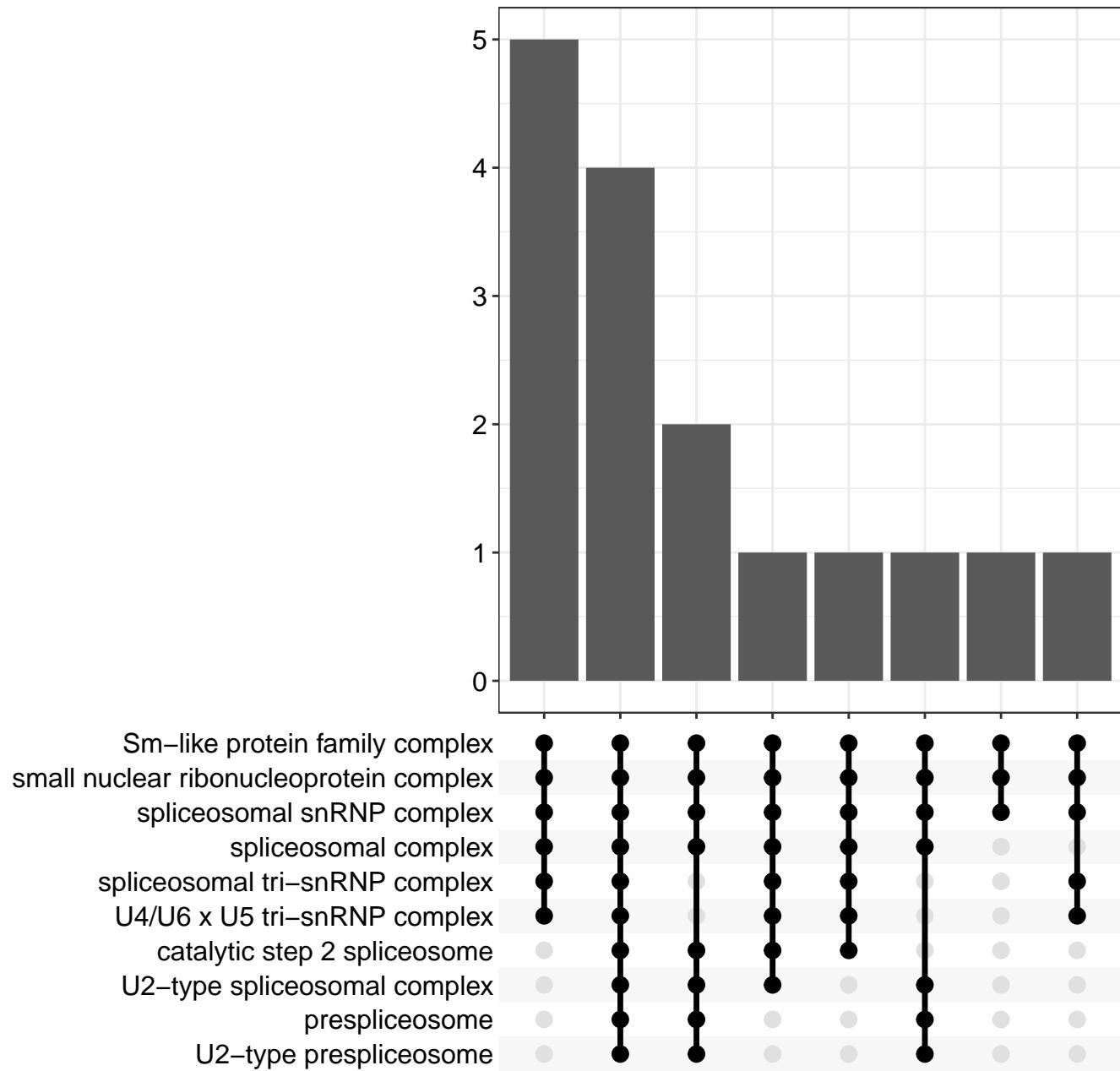
LSM2-TAP Up-regulated GO CC emapplot

polysome

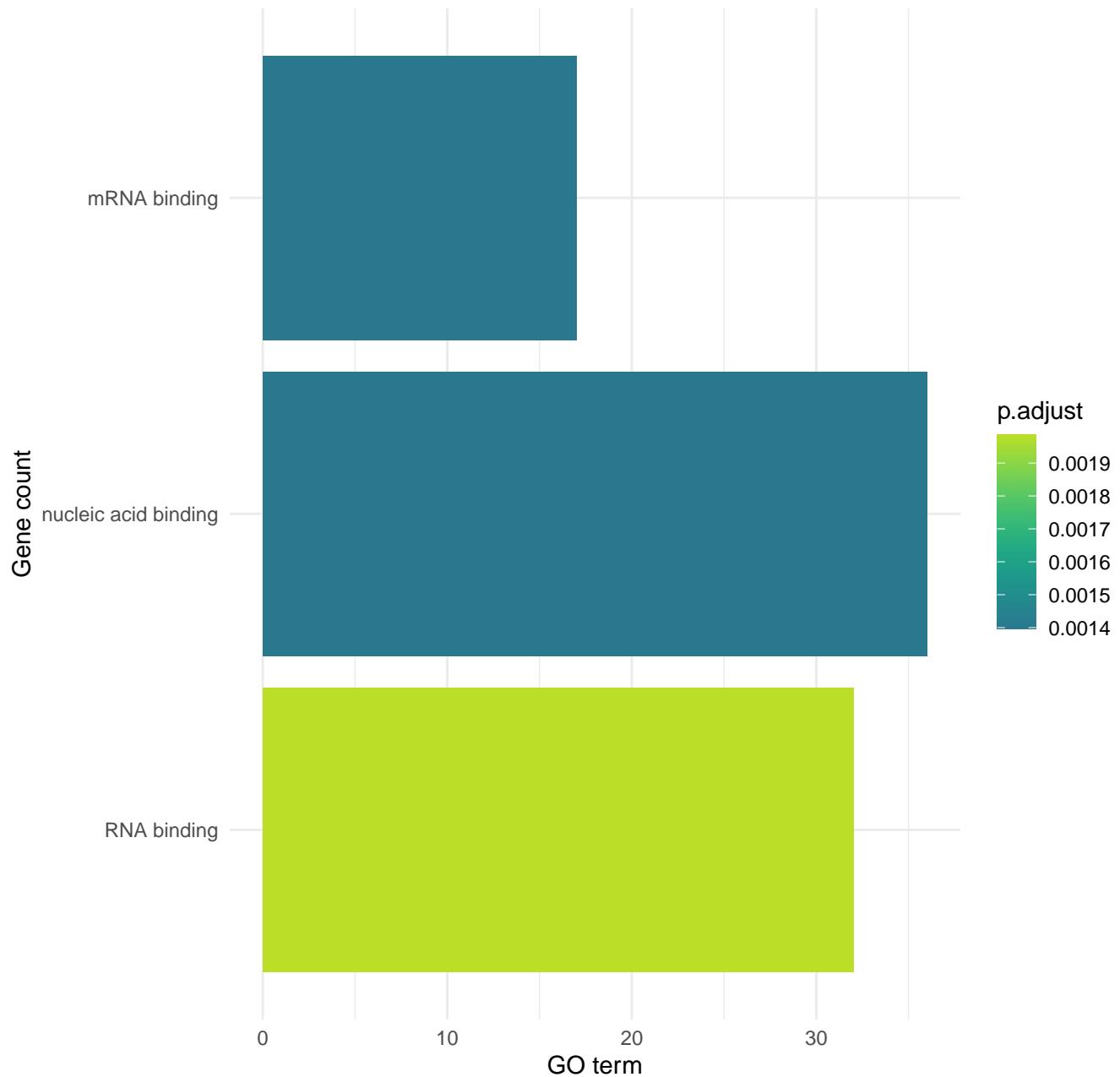




LSM2-TAP Up-regulated GO CC upsetplot



LSM2-TAP Up-regulated GO MF barplot



LSM2-TAP Up-regulated GO MF dotplot

GO term

nucleic acid binding

RNA binding

mRNA binding

0.4

0.5

0.6

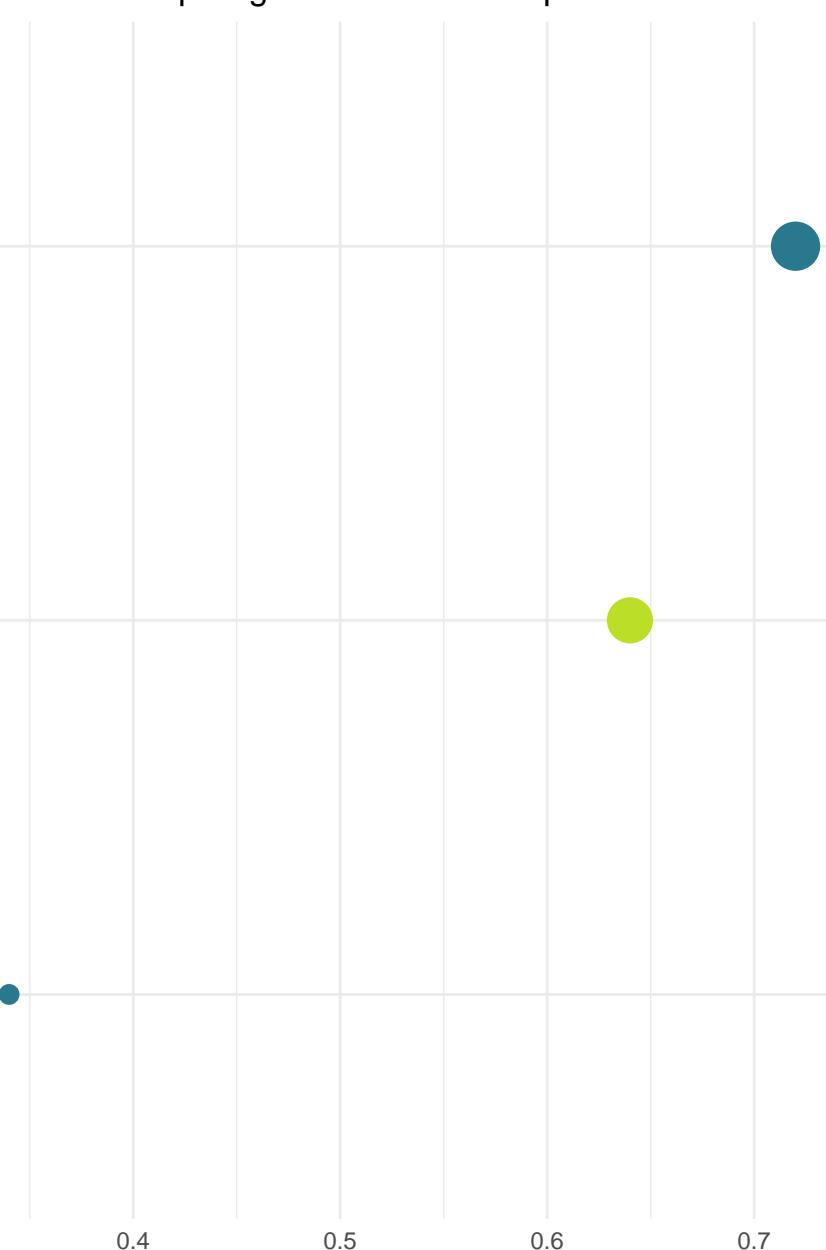
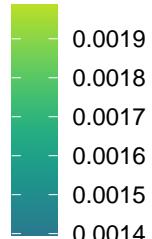
0.7

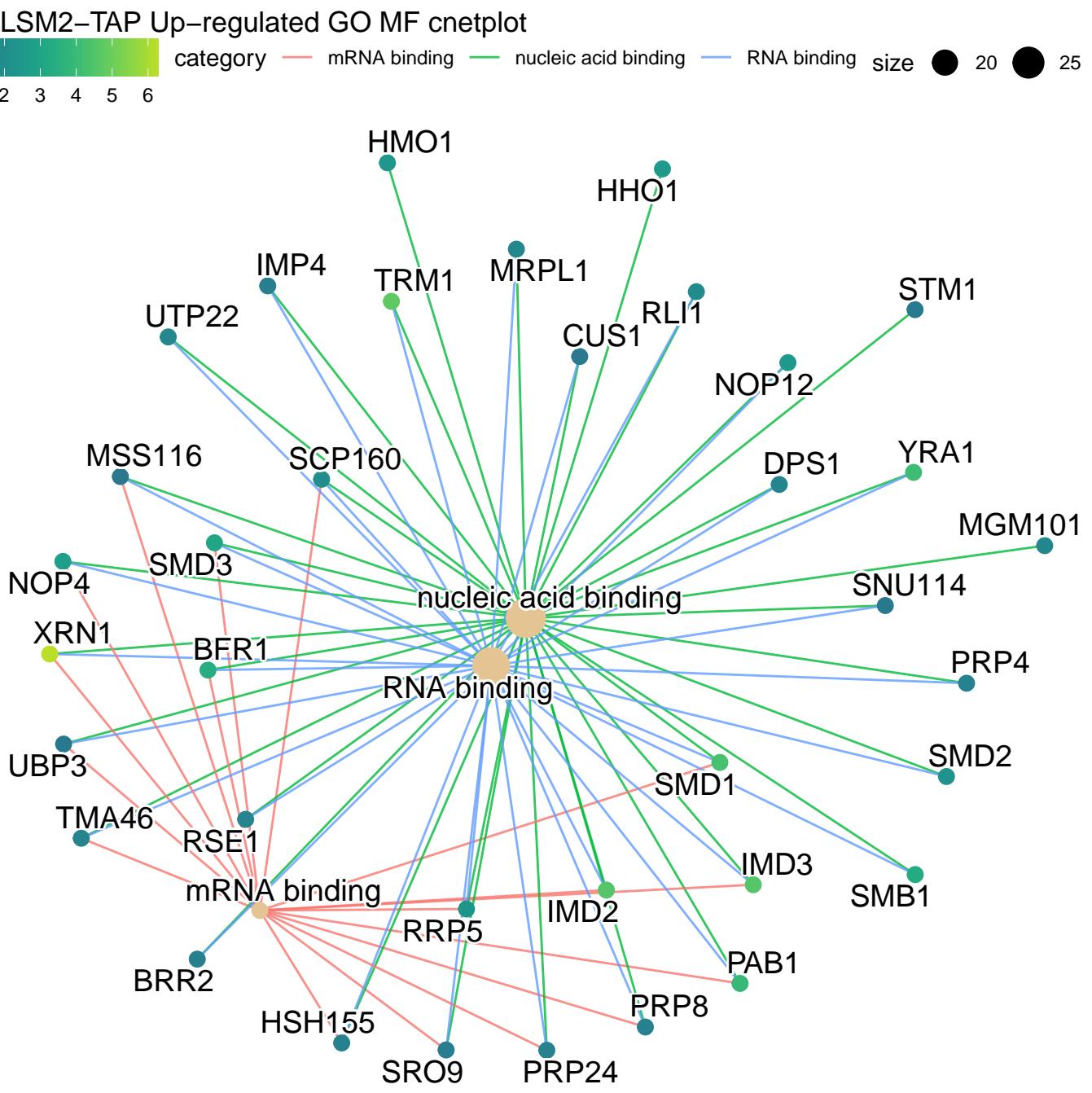
Gene ratio

Count

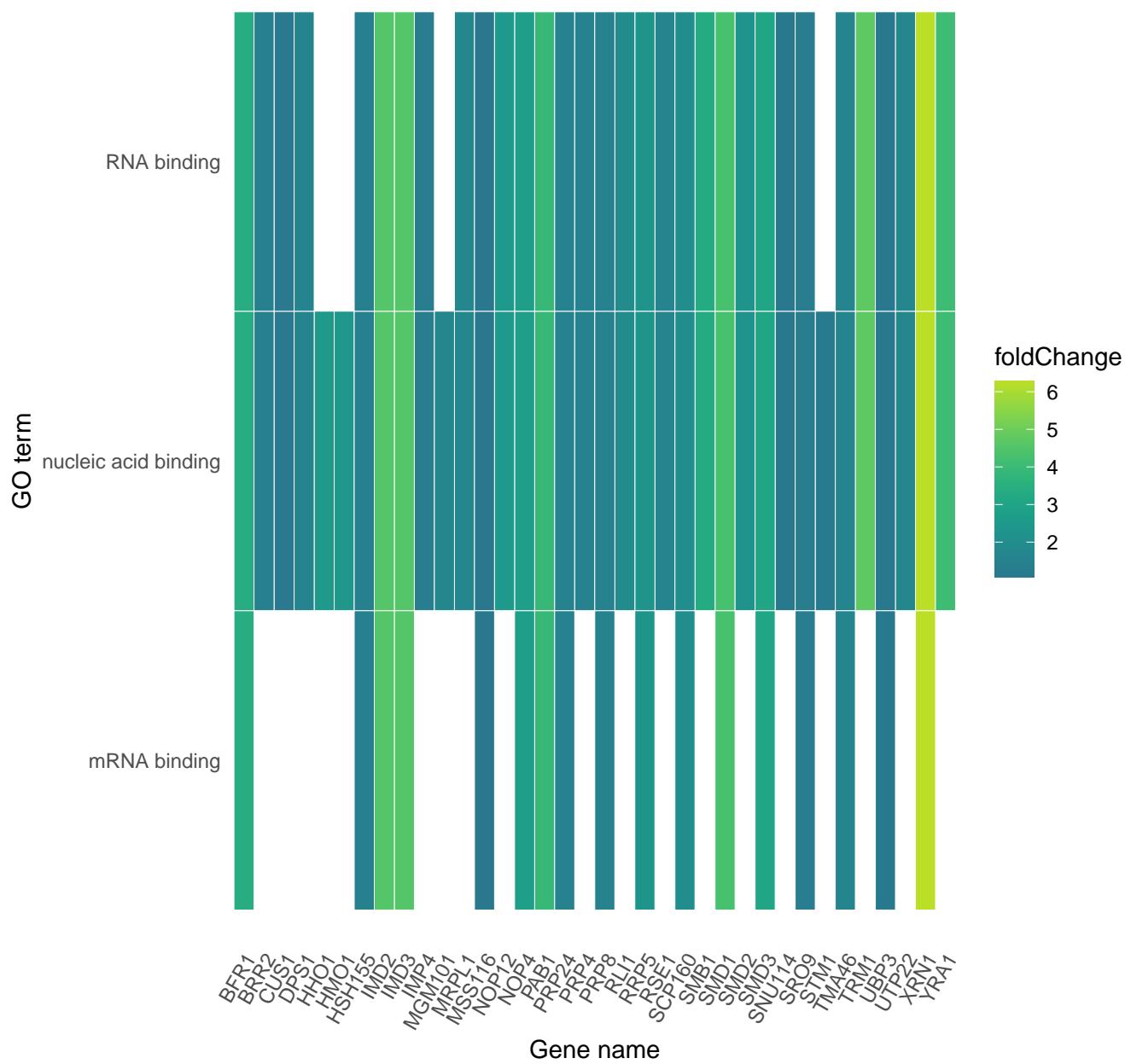
- 20
- 25
- 30
- 35

p.adjust

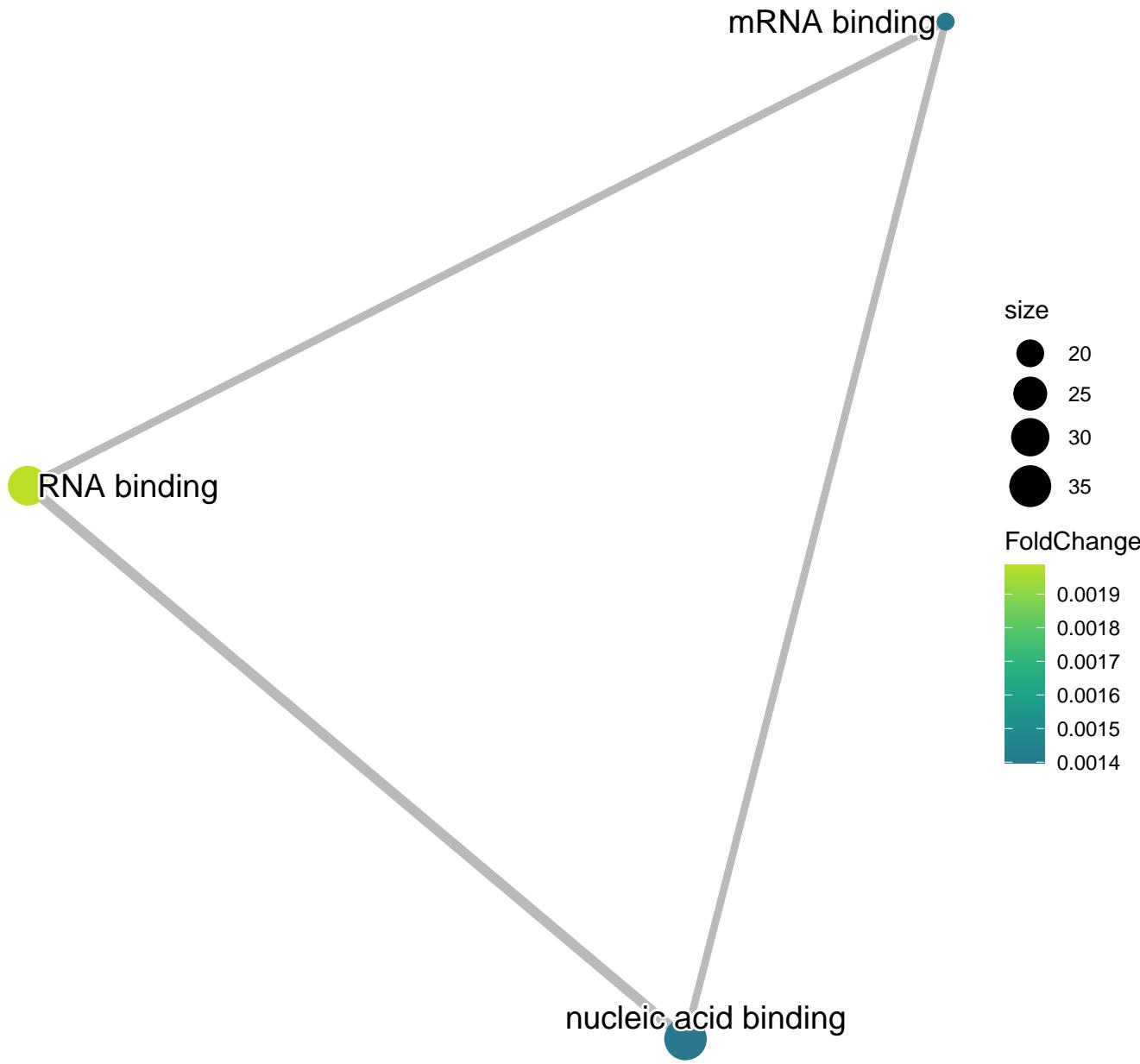


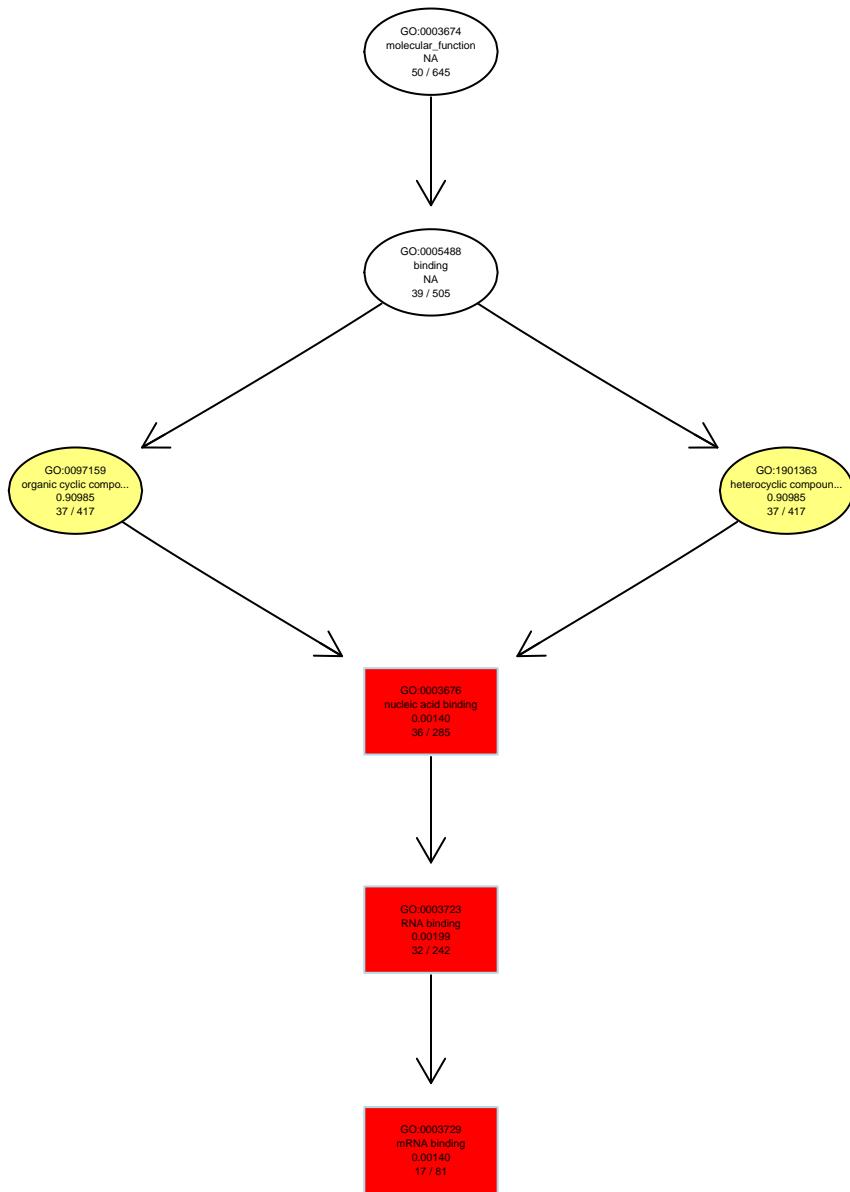


LSM2-TAP Up-regulated GO MF heatplot

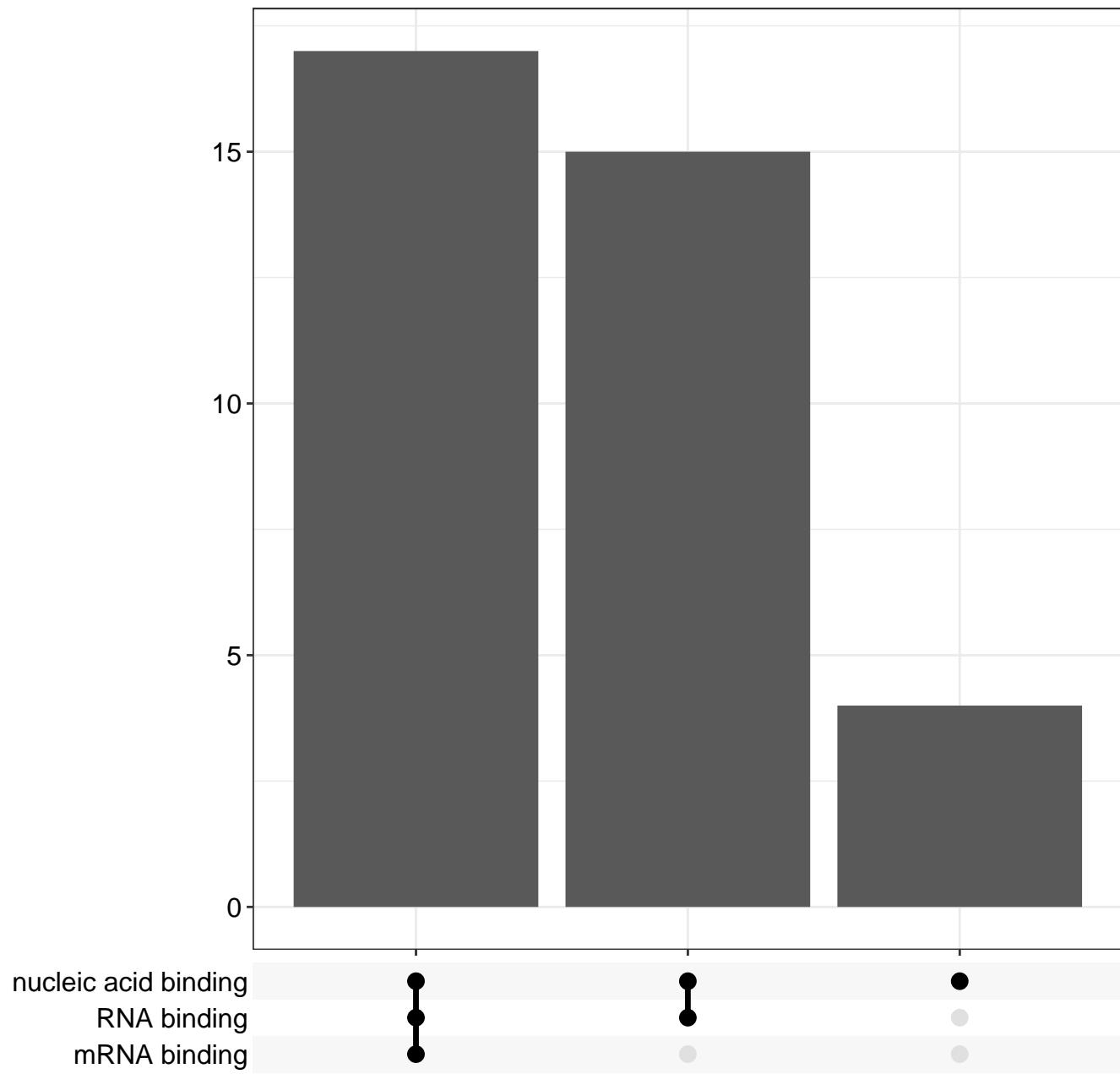


LSM2-TAP Up-regulated GO MF emapplot

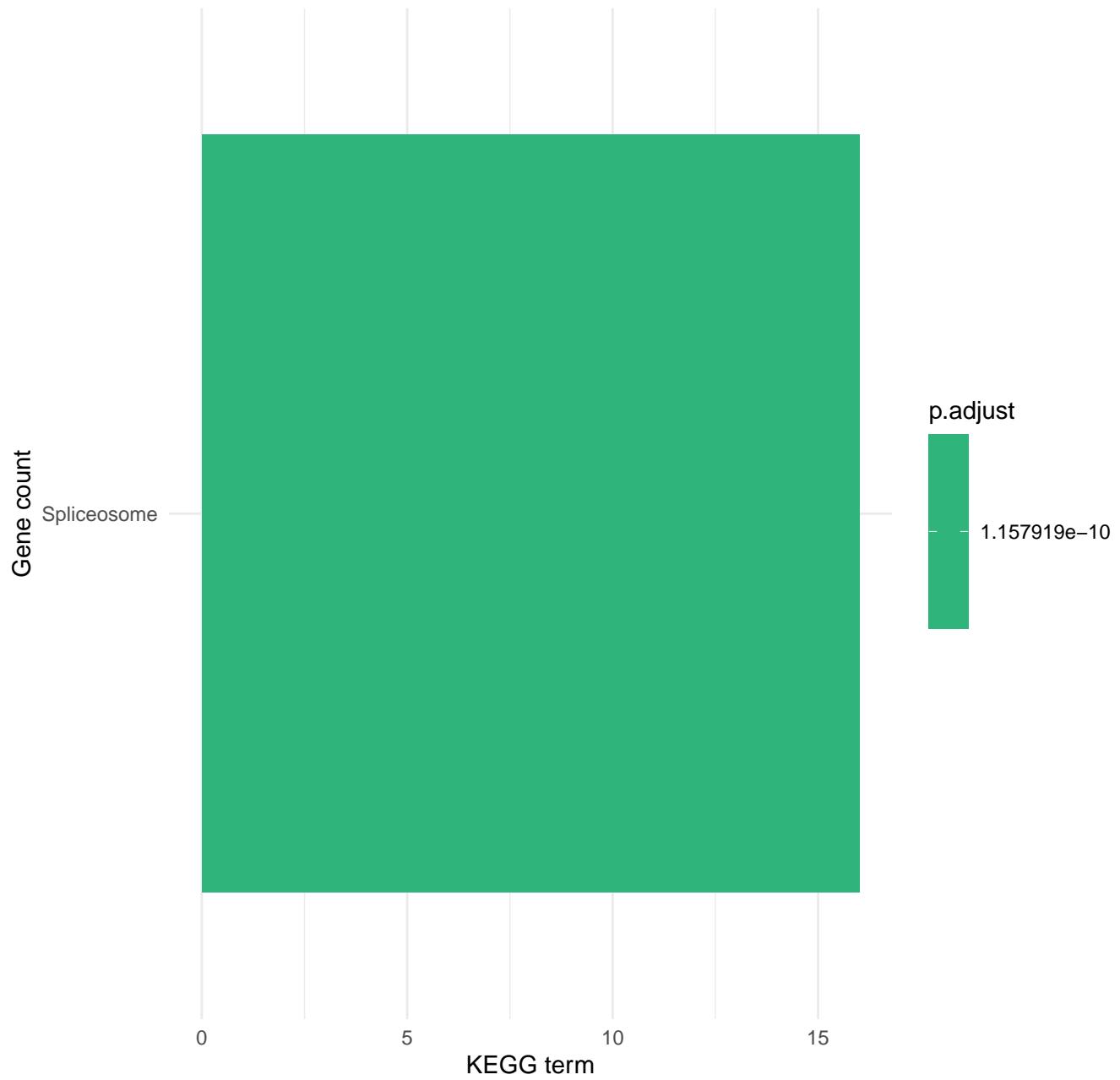




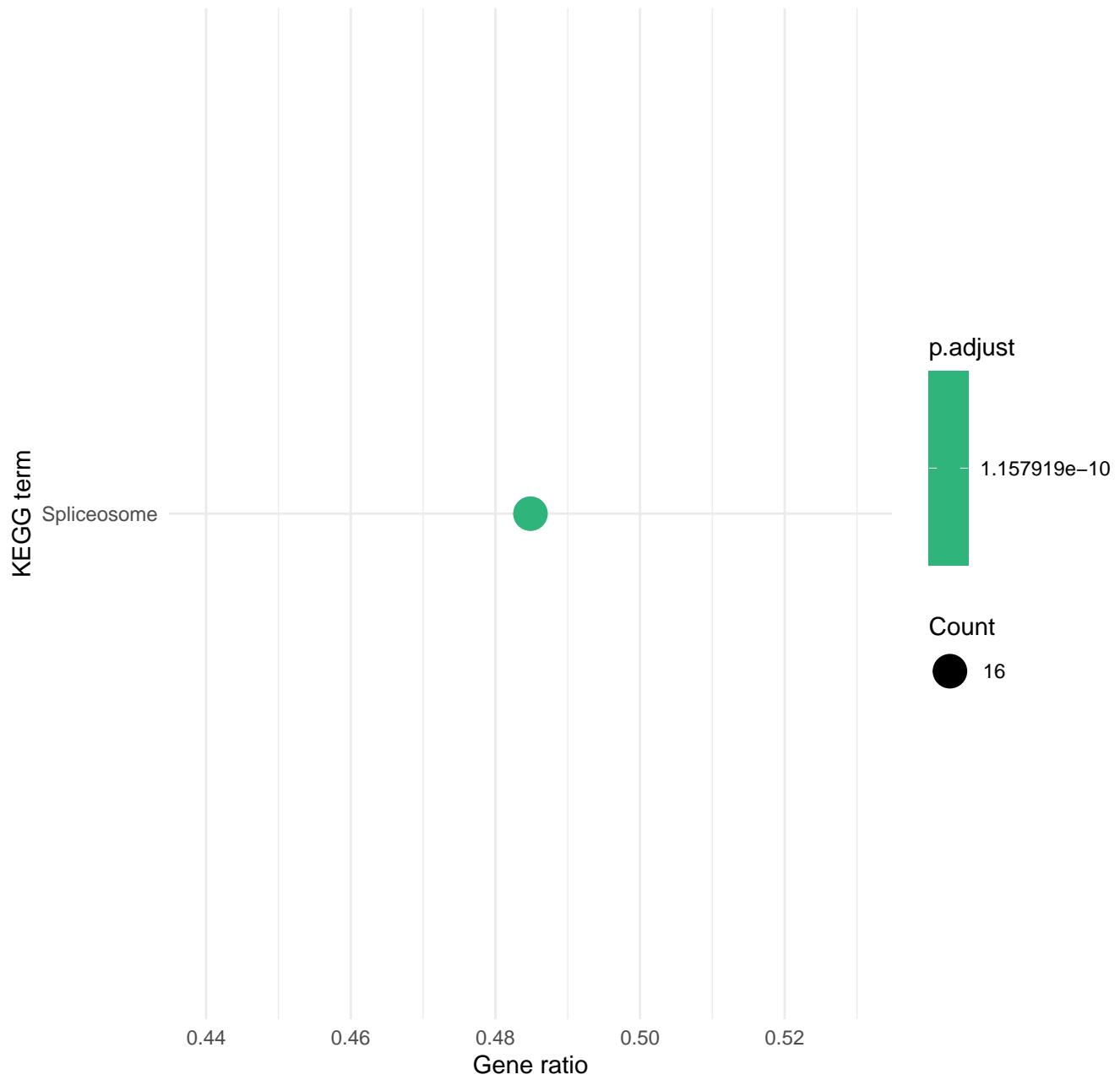
LSM2-TAP Up-regulated GO MF upsetplot



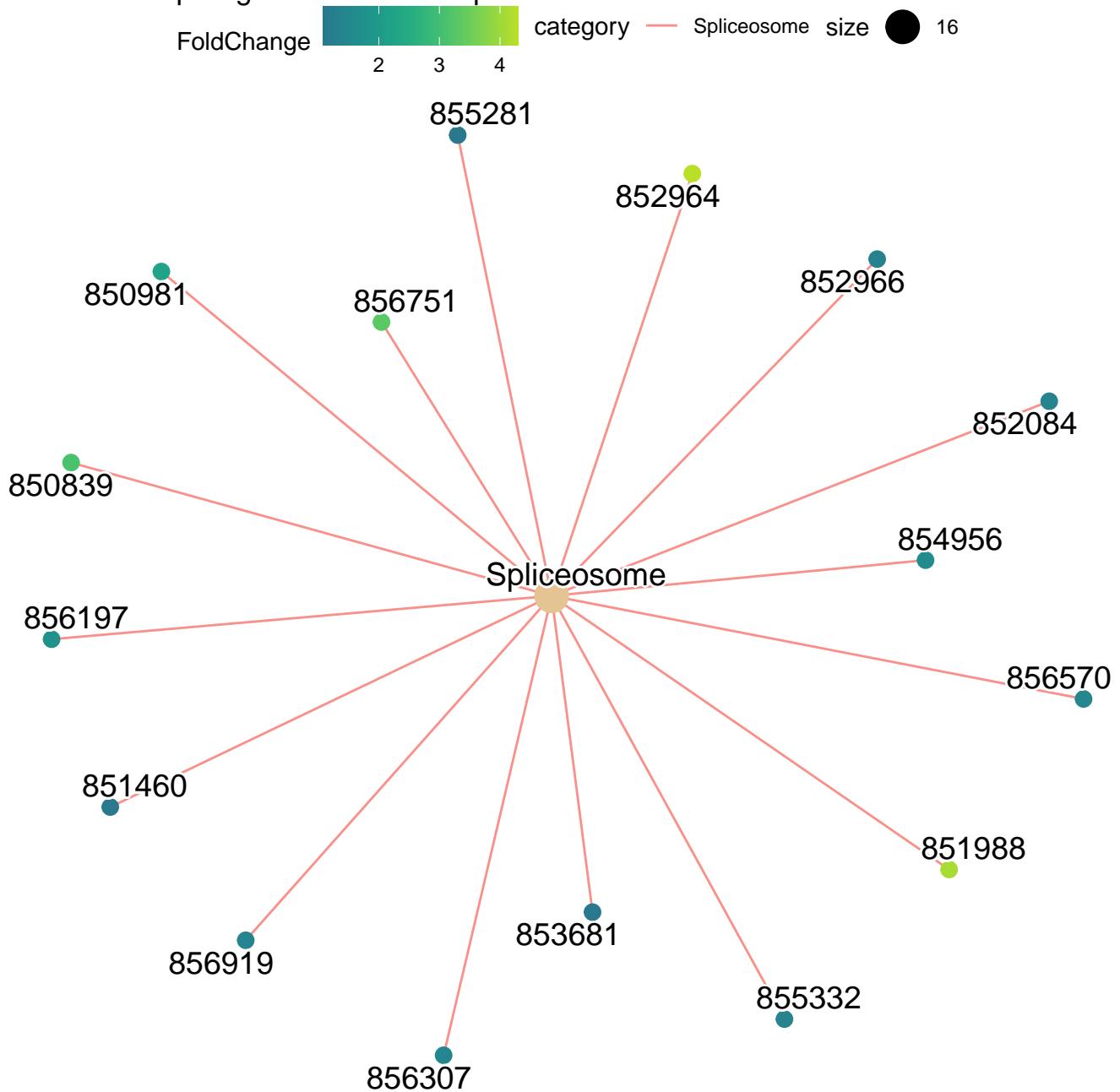
LSM2-TAP Up-regulated KEGG barplot



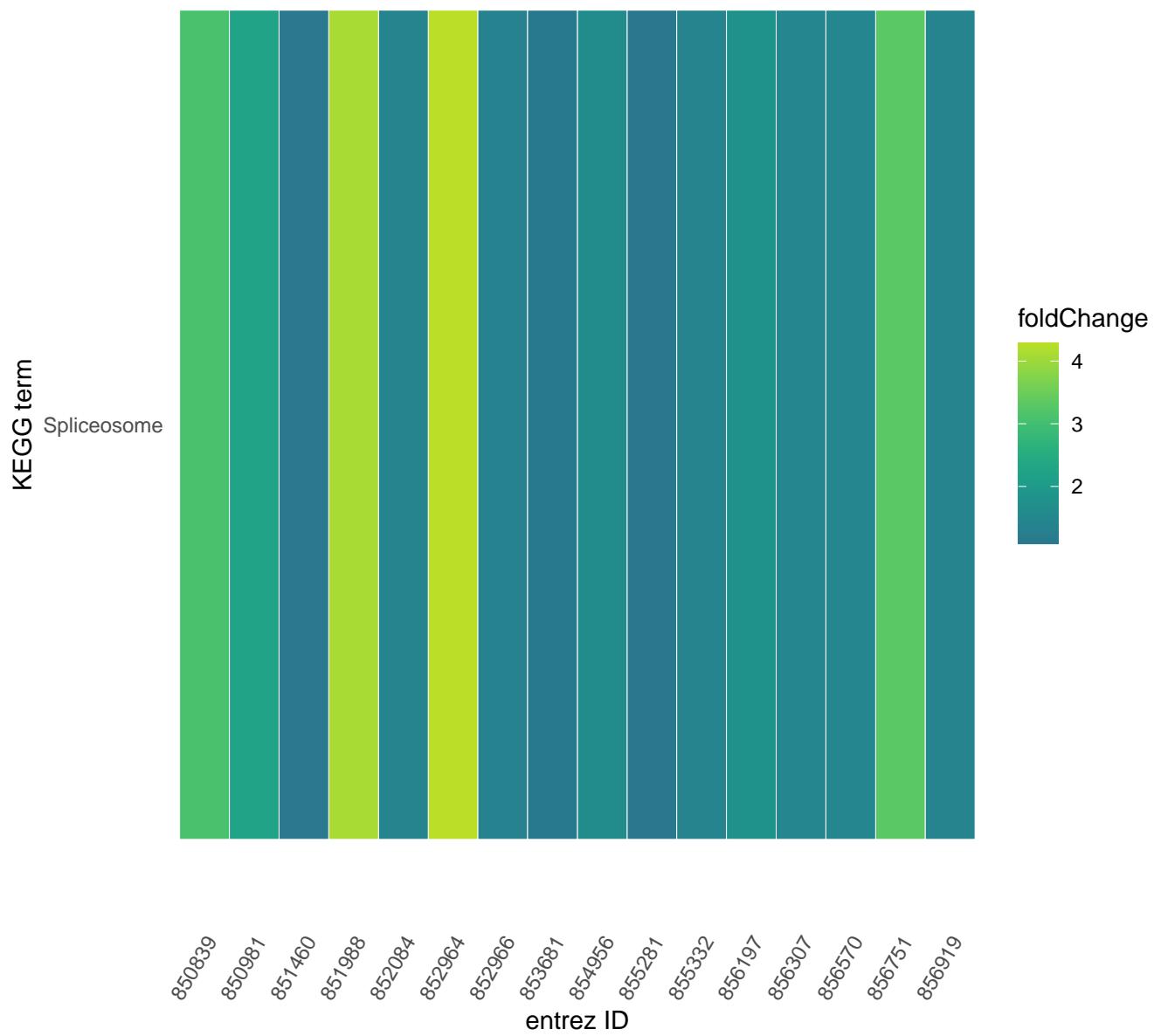
LSM2-TAP Up-regulated KEGG dotplot



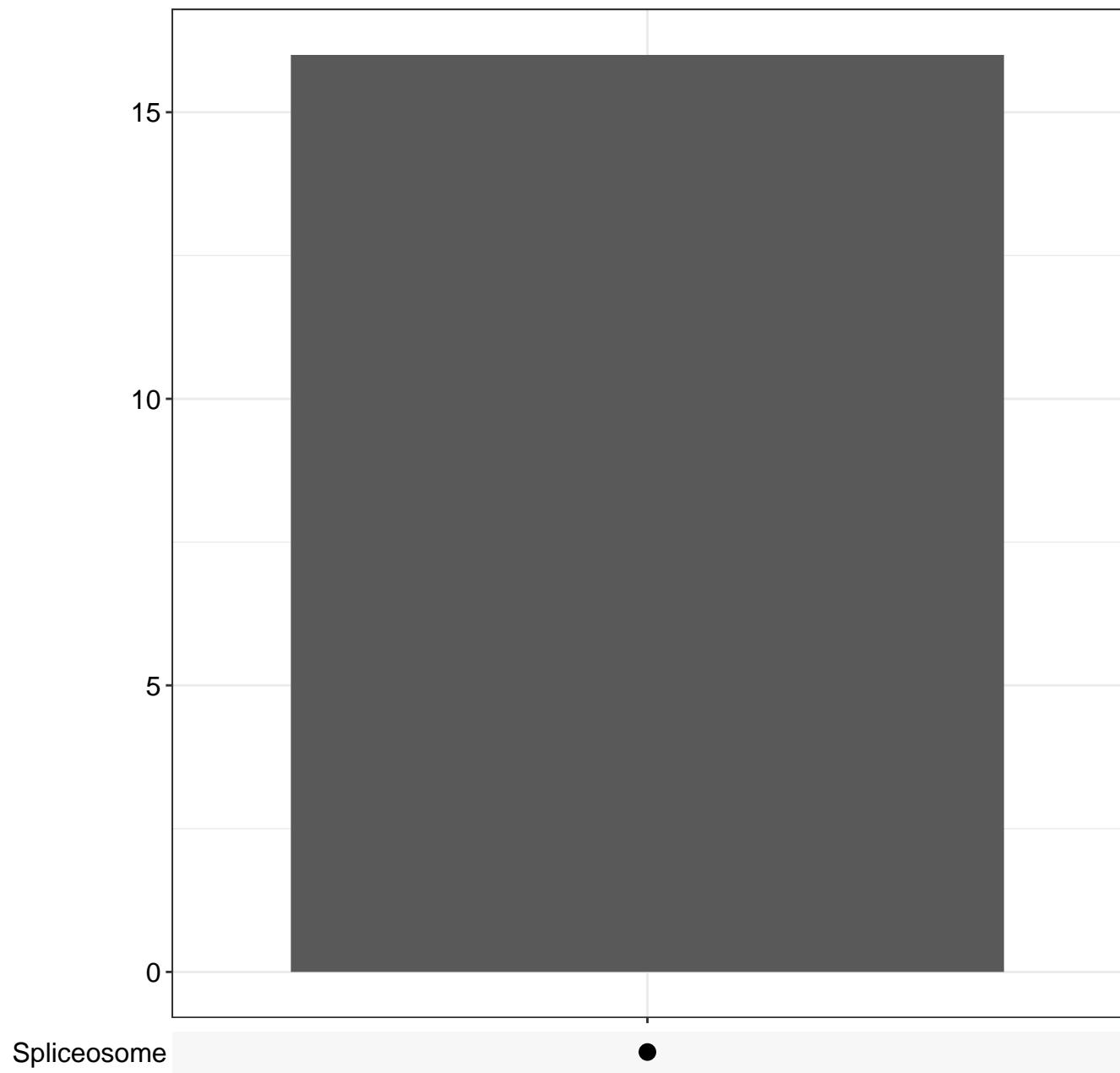
LSM2-TAP Up-regulated KEGG dotplot



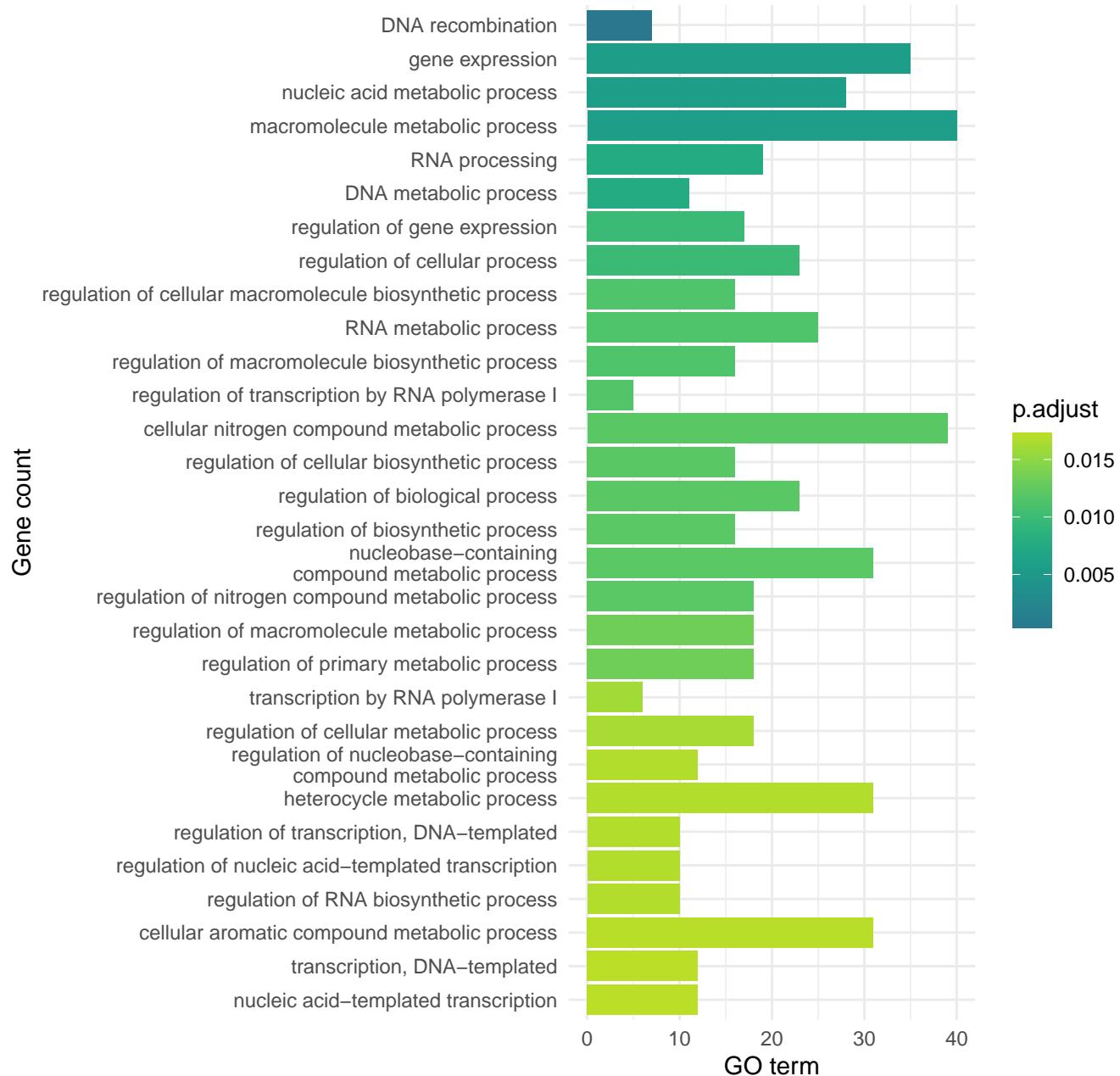
LSM2-TAP Up-regulated KEGG heatplot



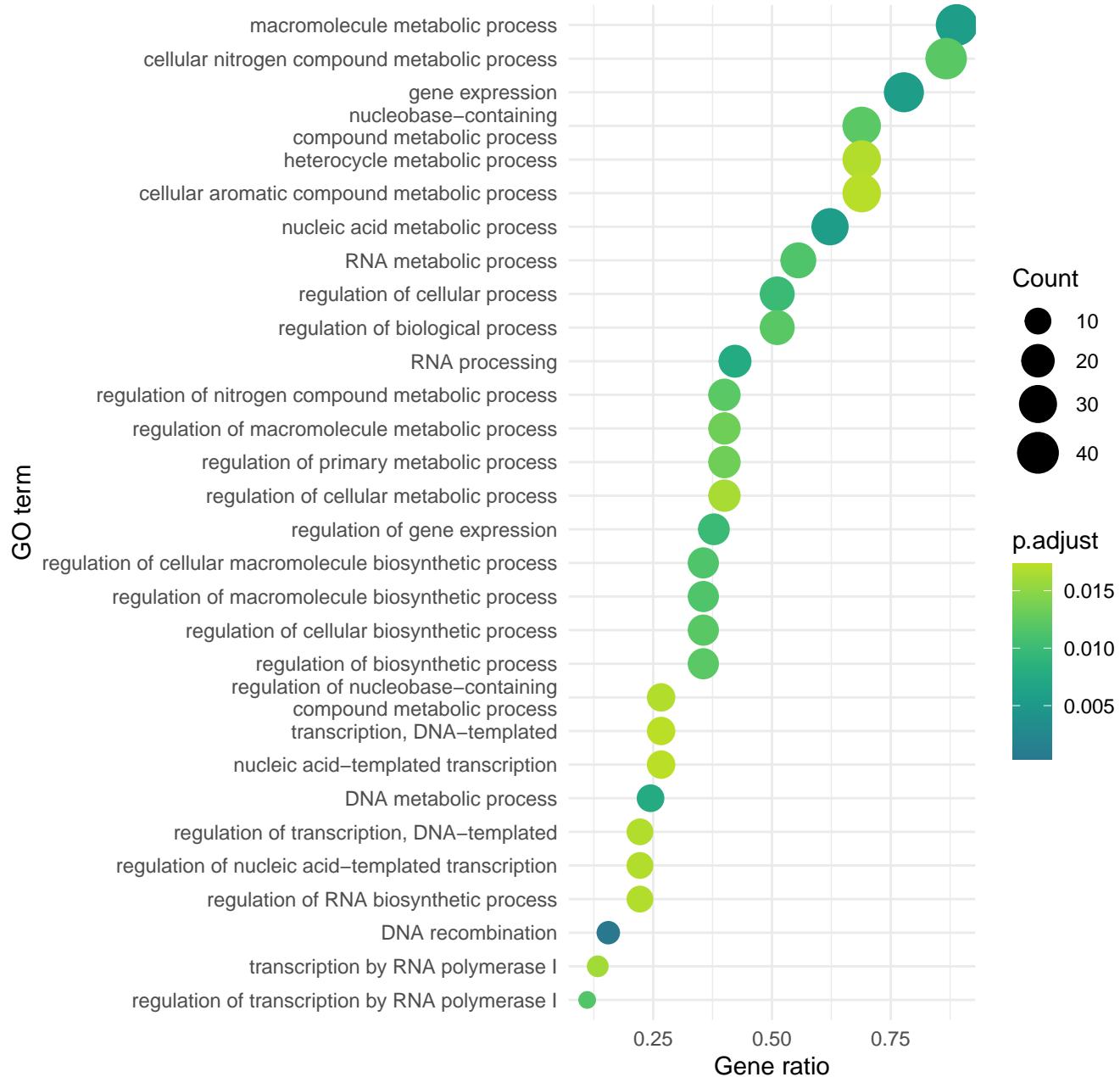
LSM2-TAP Up-regulated KEGG upsetplot



GBP2-TAP Up-regulated GO BP barplot



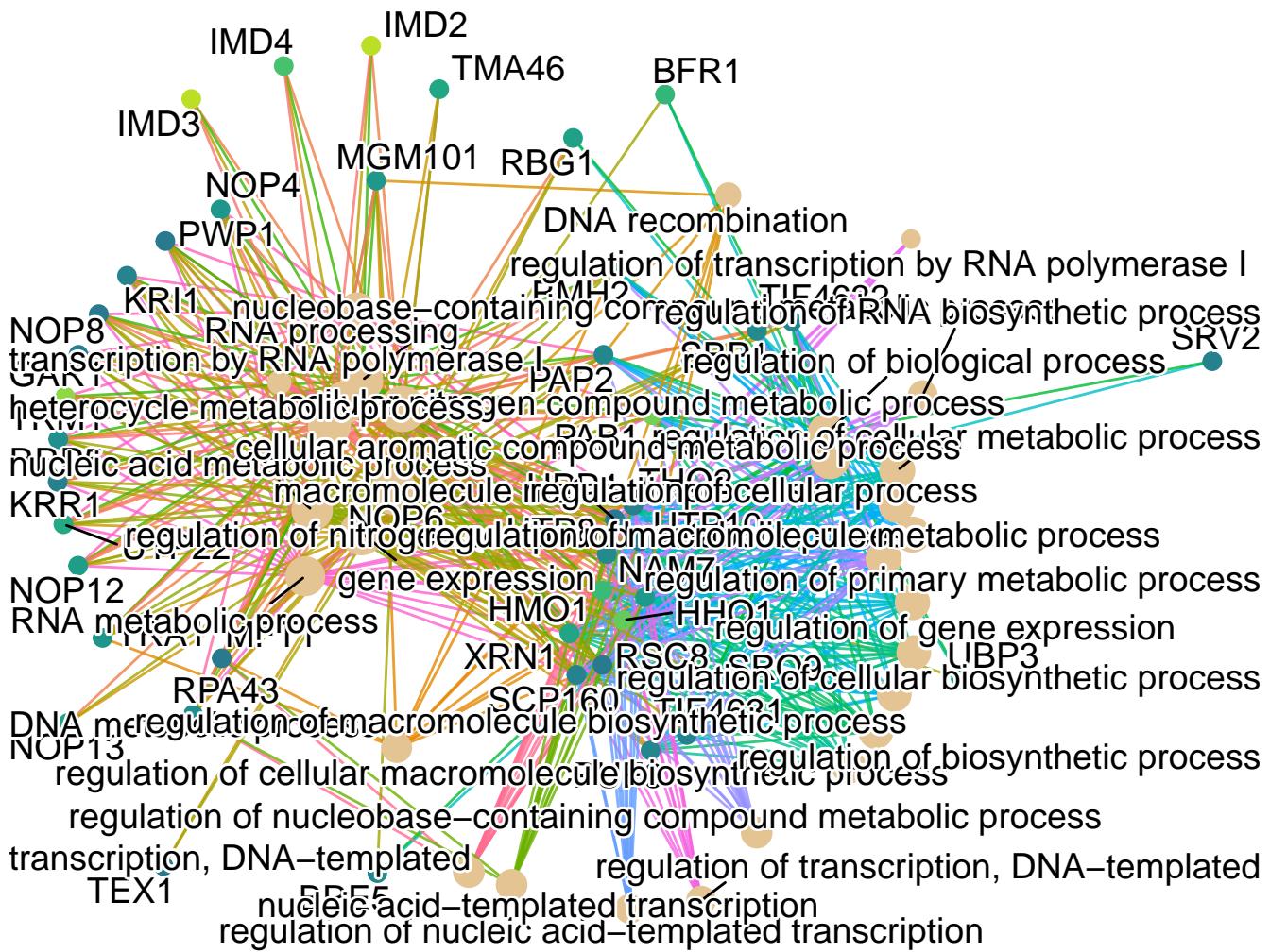
GBP2-TAP Up-regulated GO BP dotplot



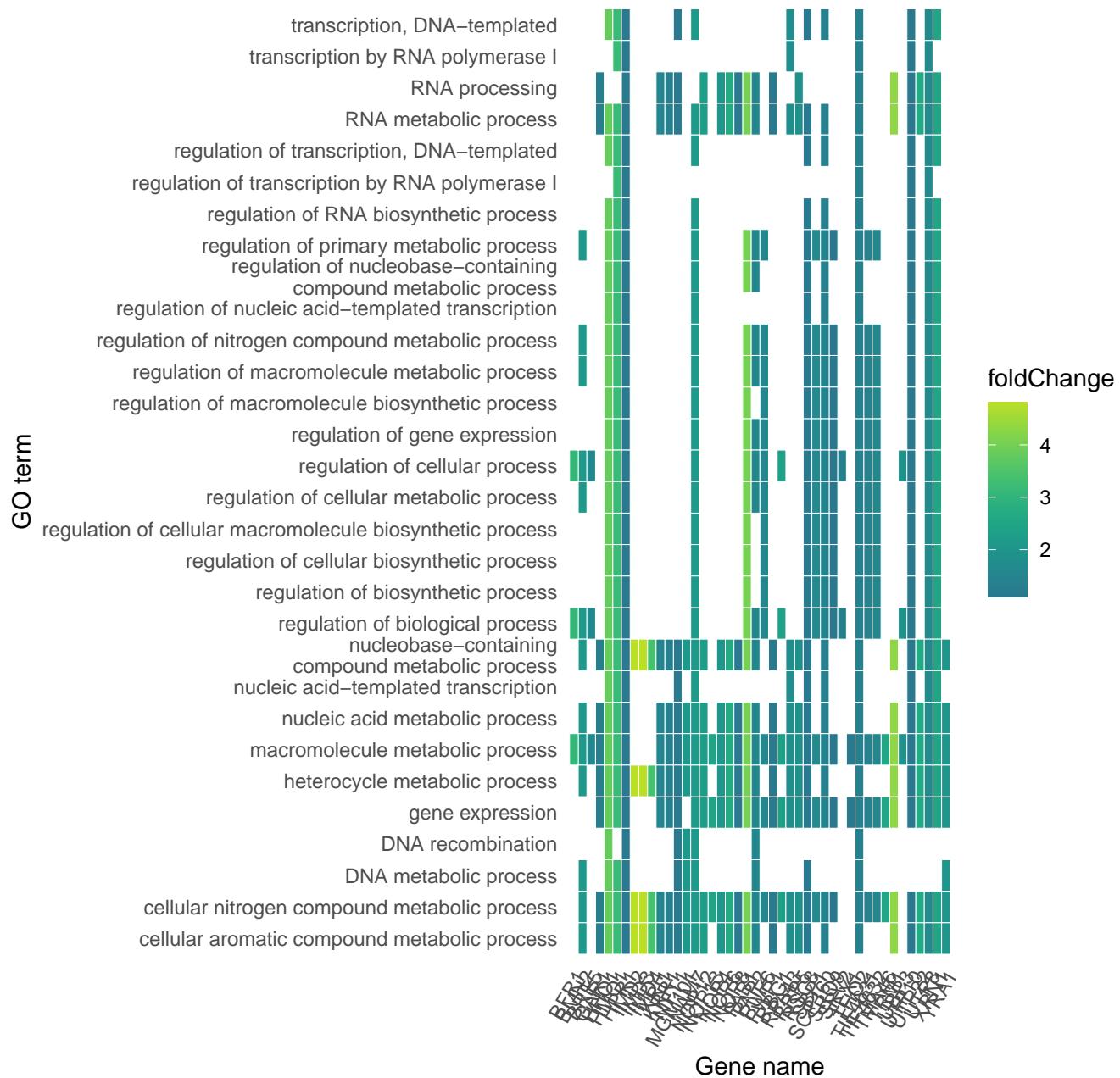
GBP2-TAP Up-regulated GO BP cnetplot

bolic process macromolecule metabolic process
bolic process nucleic acid metabolic process
bolic process nucleic acid-templated transcription
bolic process nucleobase-containing compound metabolic process
regulation of biological process regulation of biosynthetic process

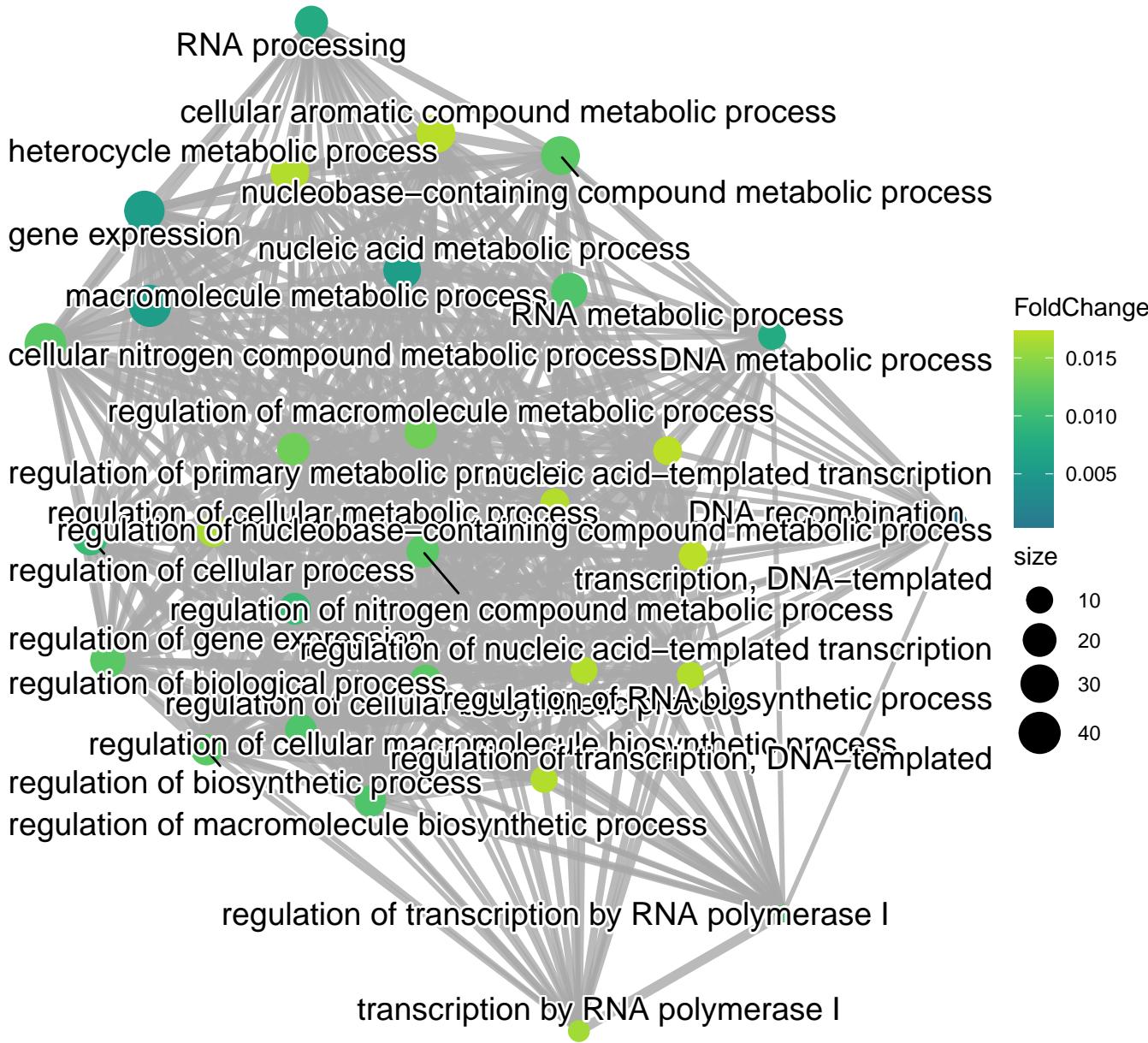
regulation of cellular biosynthetic process
regulation of cellular macromolecule biosynthe
regulation of cellular metabolic process
regulation of cellular process
regulation of gene expression
regulation of macromolecule biosynthetic proce

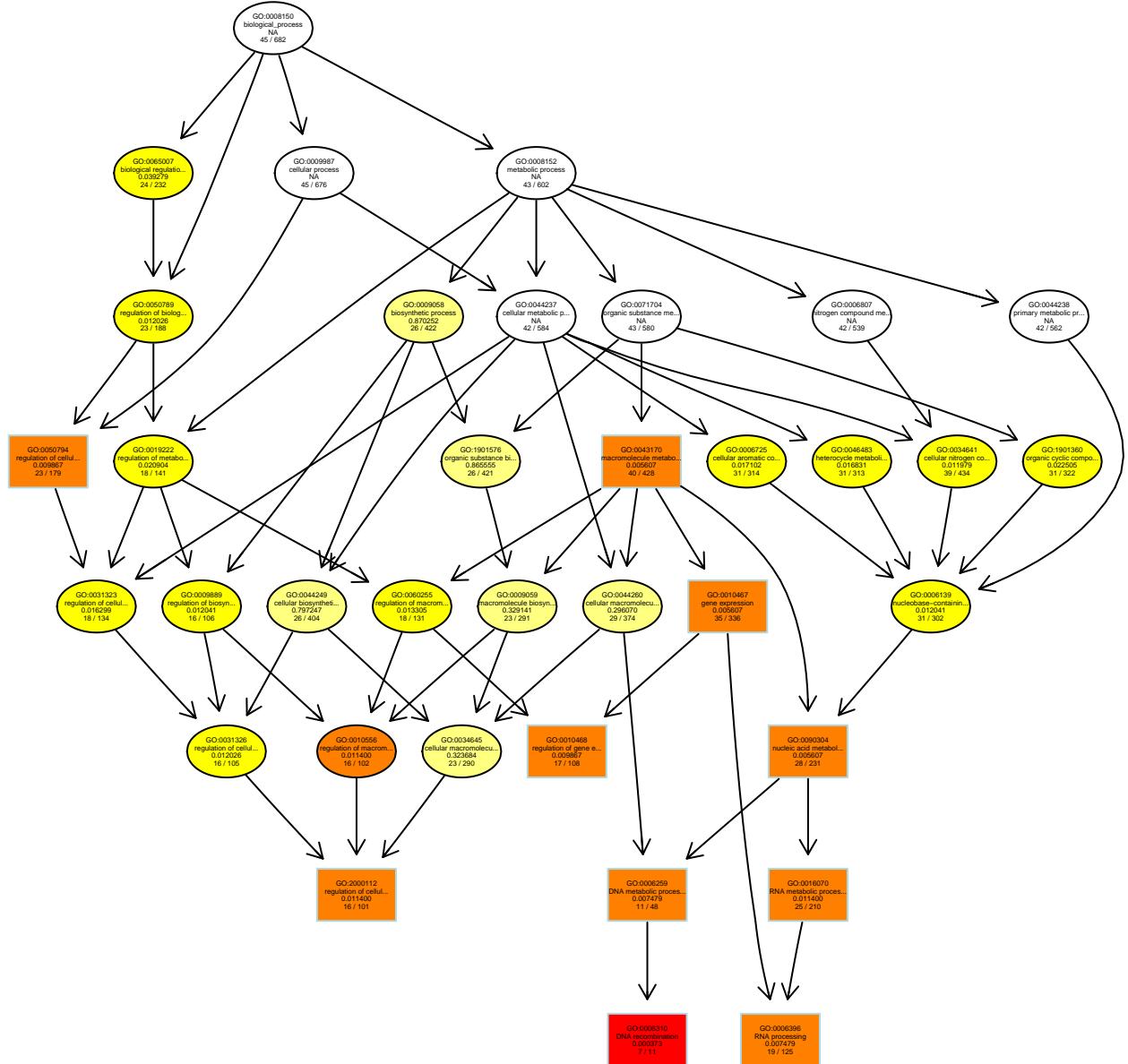


GBP2-TAP Up-regulated GO BP heatplot

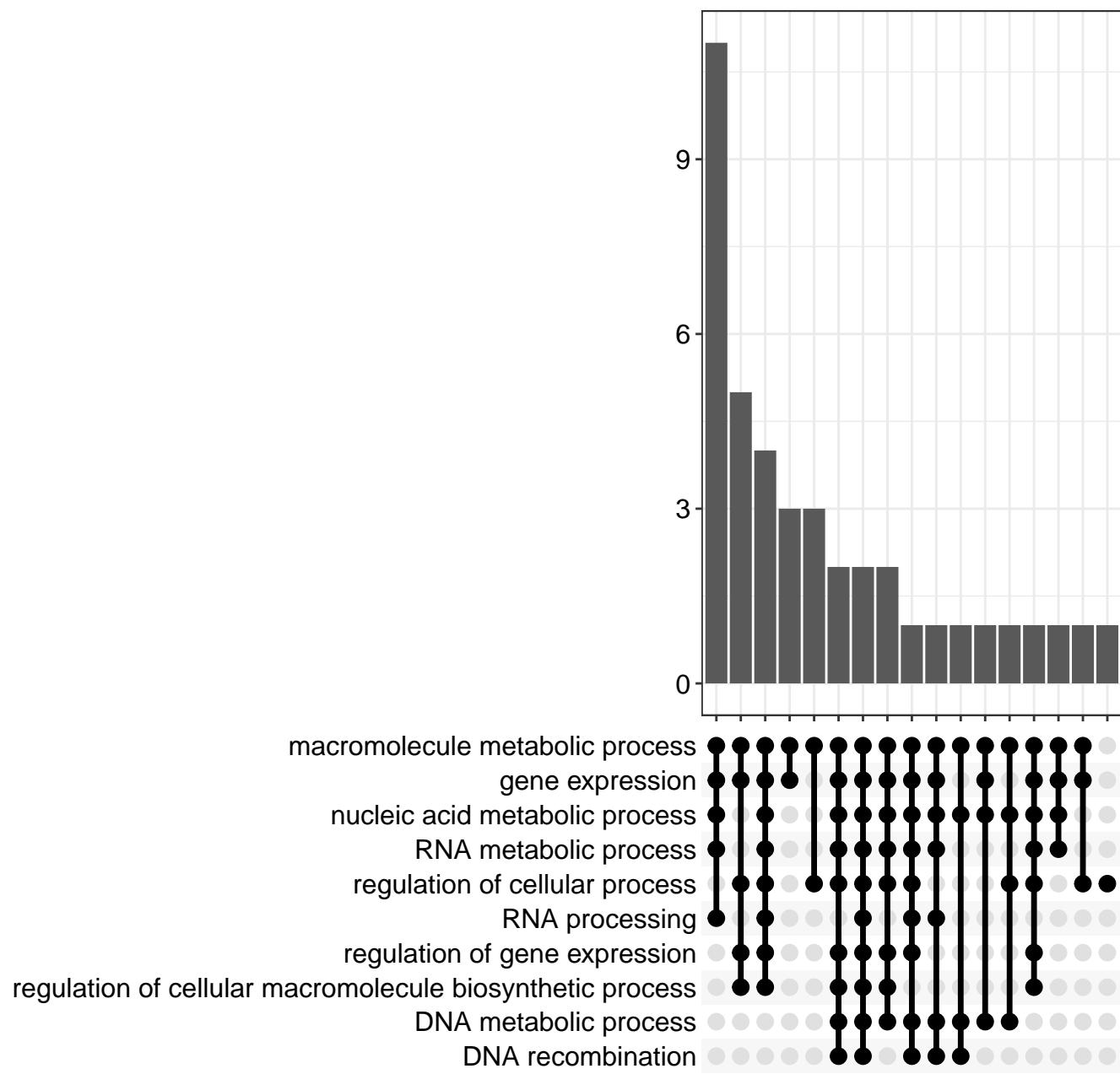


GBP2-TAP Up-regulated GO BP emapplot

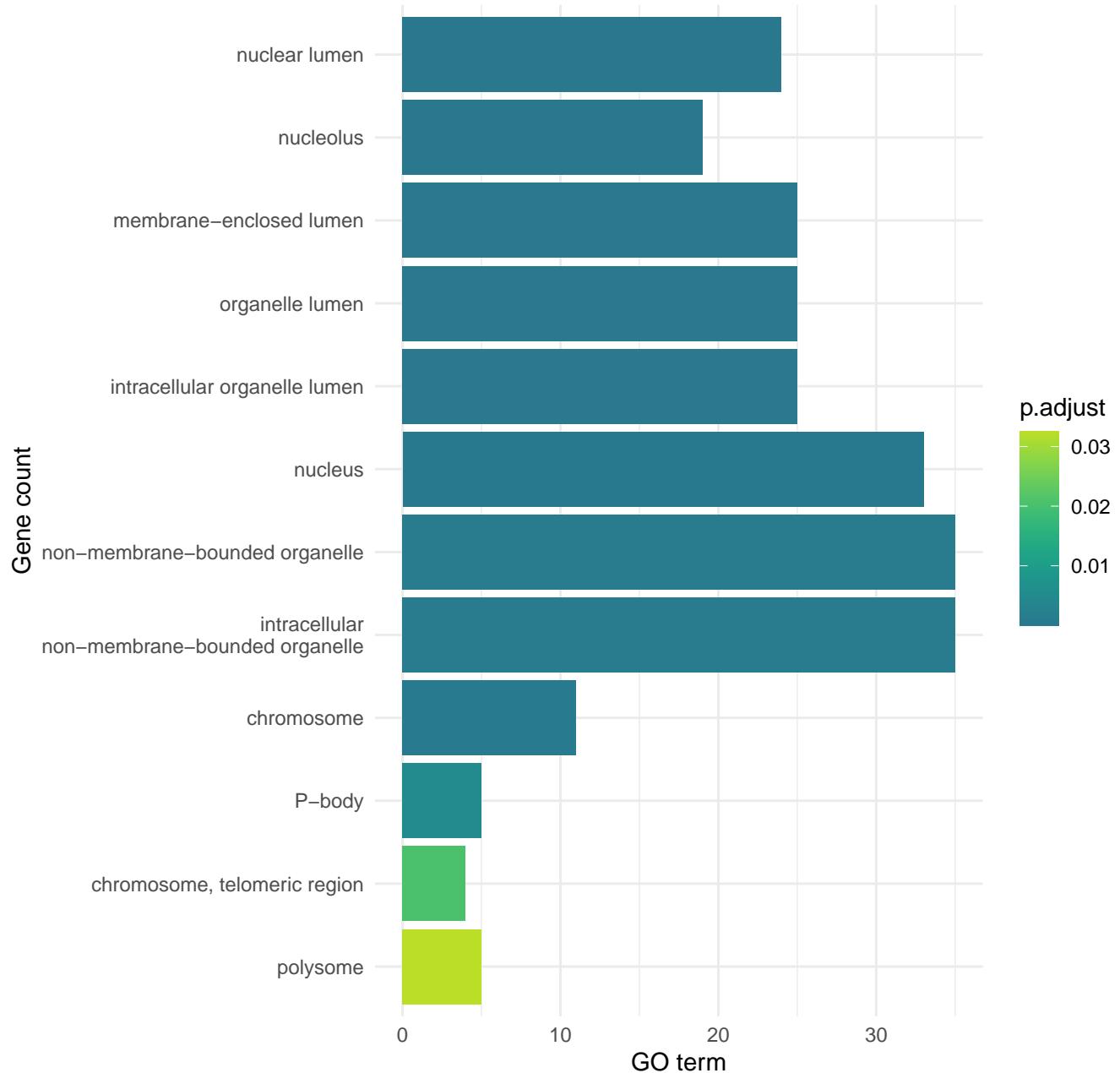




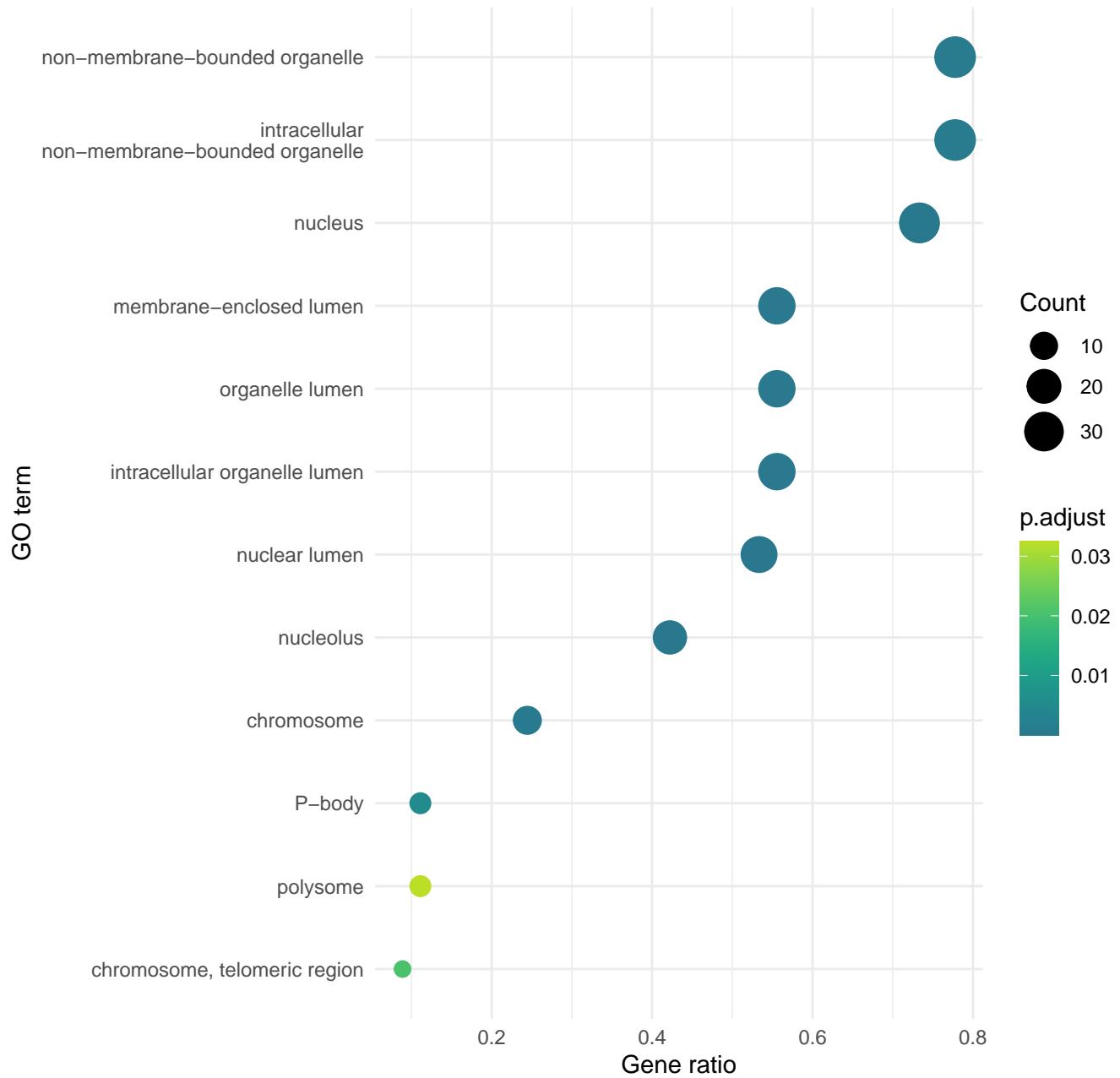
GBP2-TAP Up-regulated GO BP



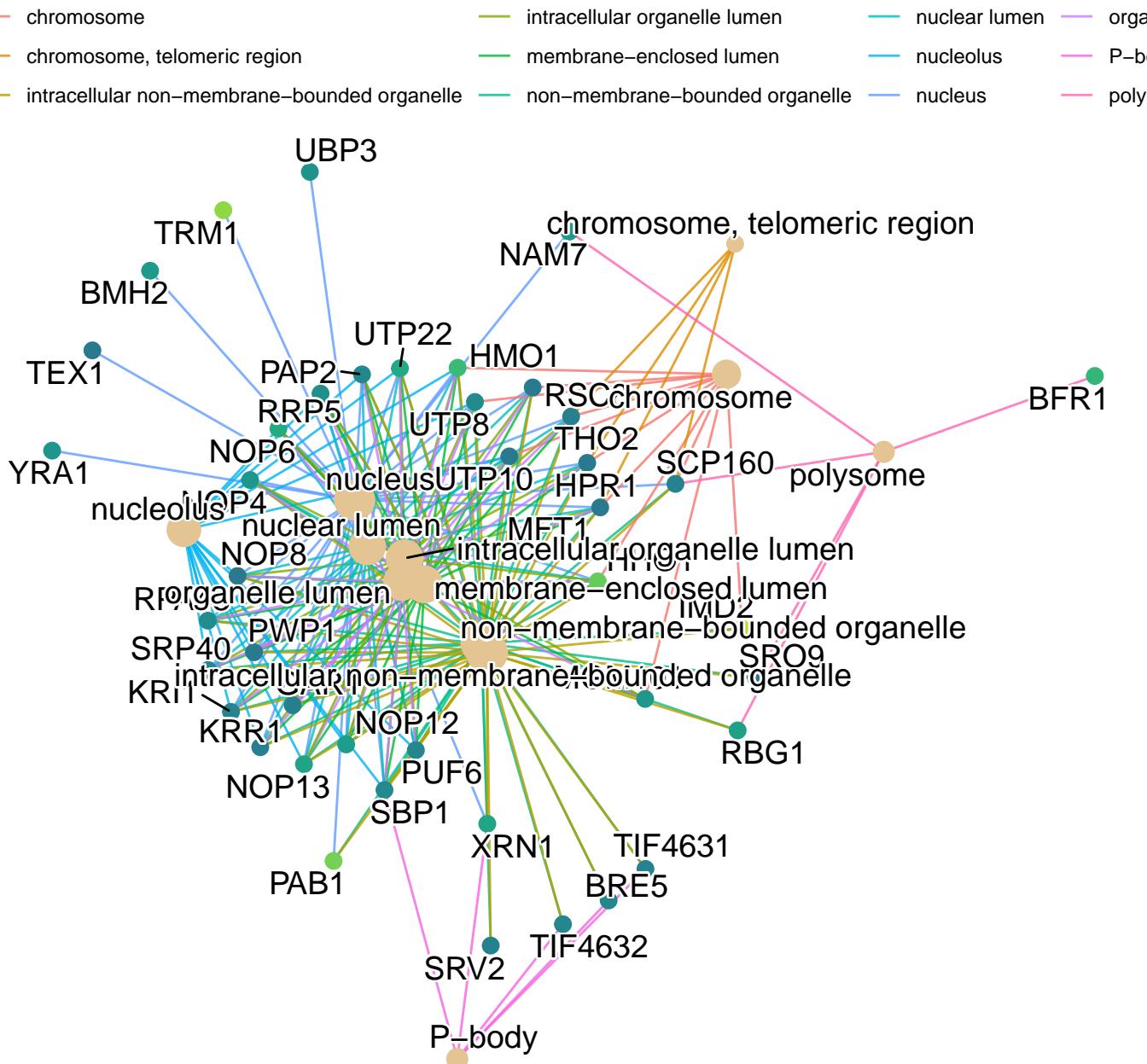
GBP2-TAP Up-regulated GO CC barplot



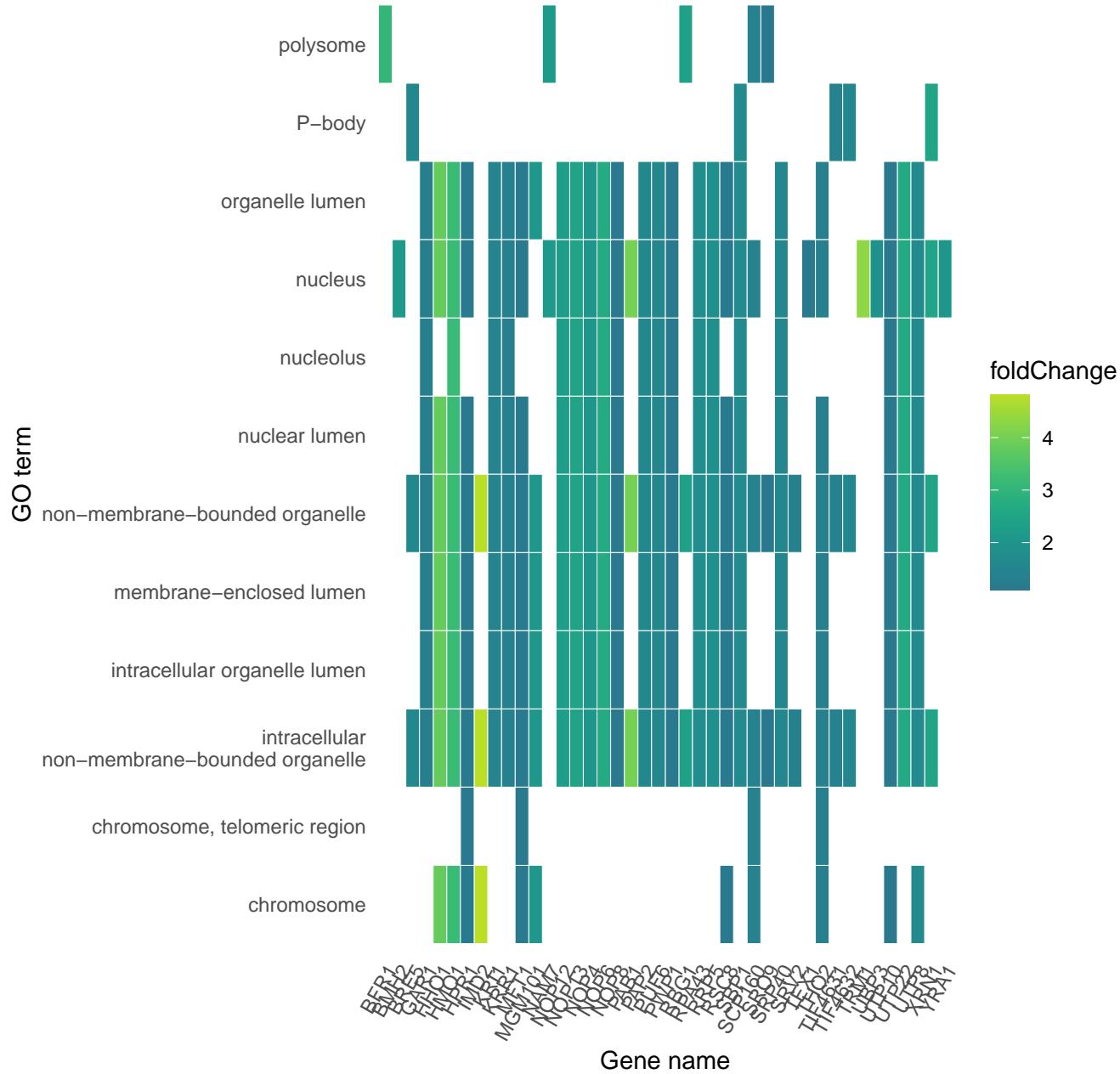
GBP2-TAP Up-regulated GO CC dotplot



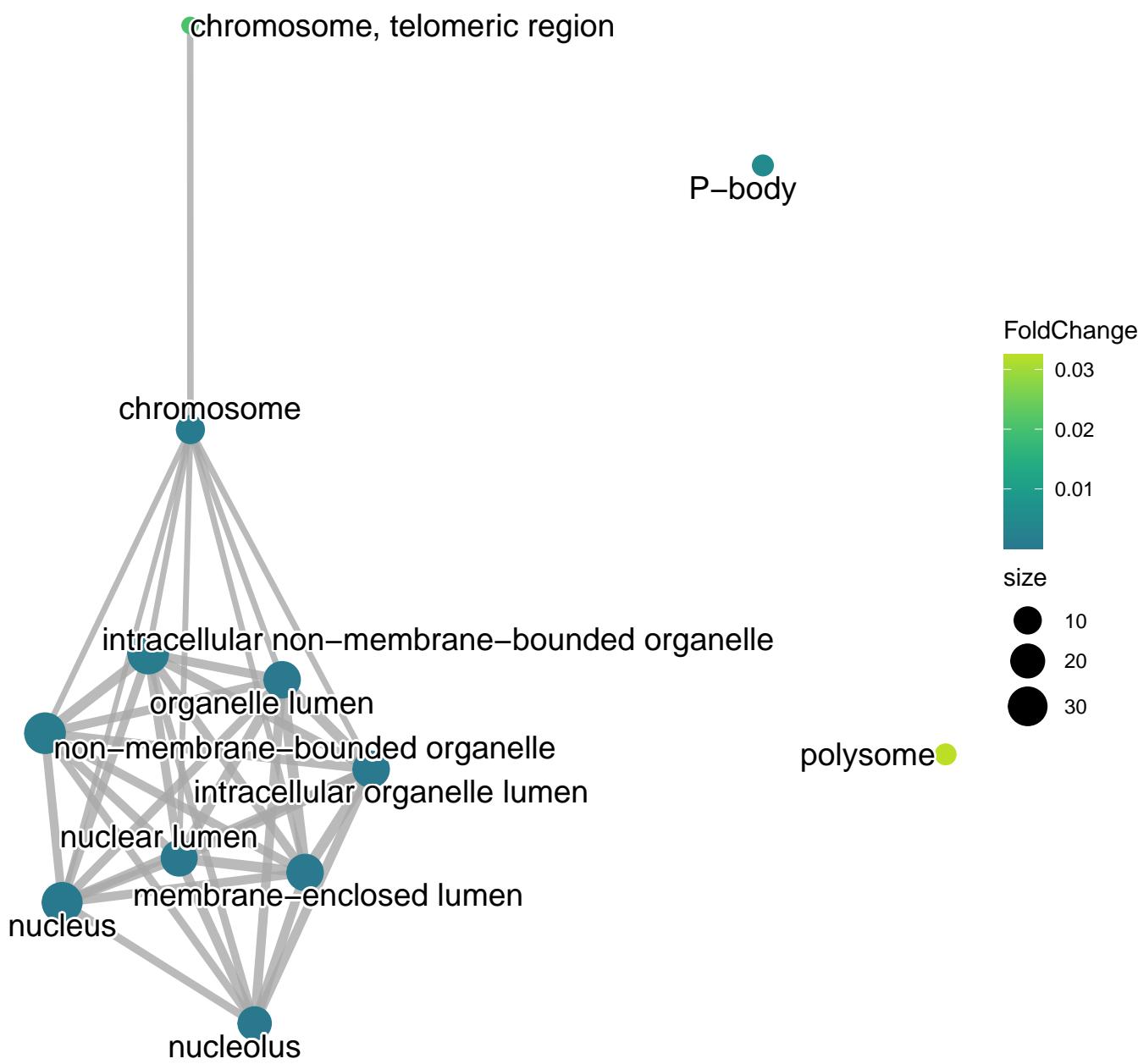
GBP2-TAP Up-regulated GO CC cnetplot

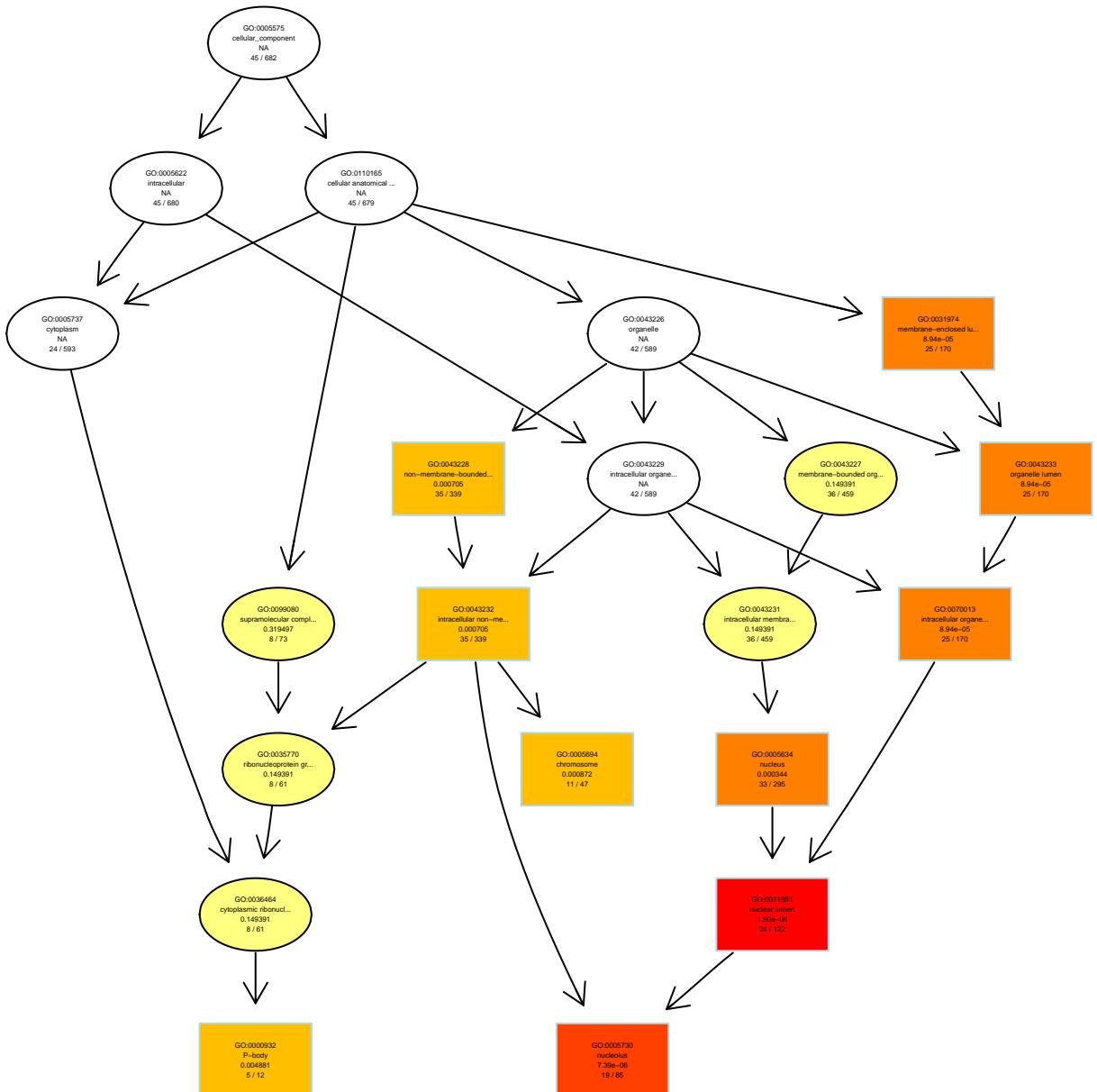


GBP2-TAP Up-regulated GO CC heatplot

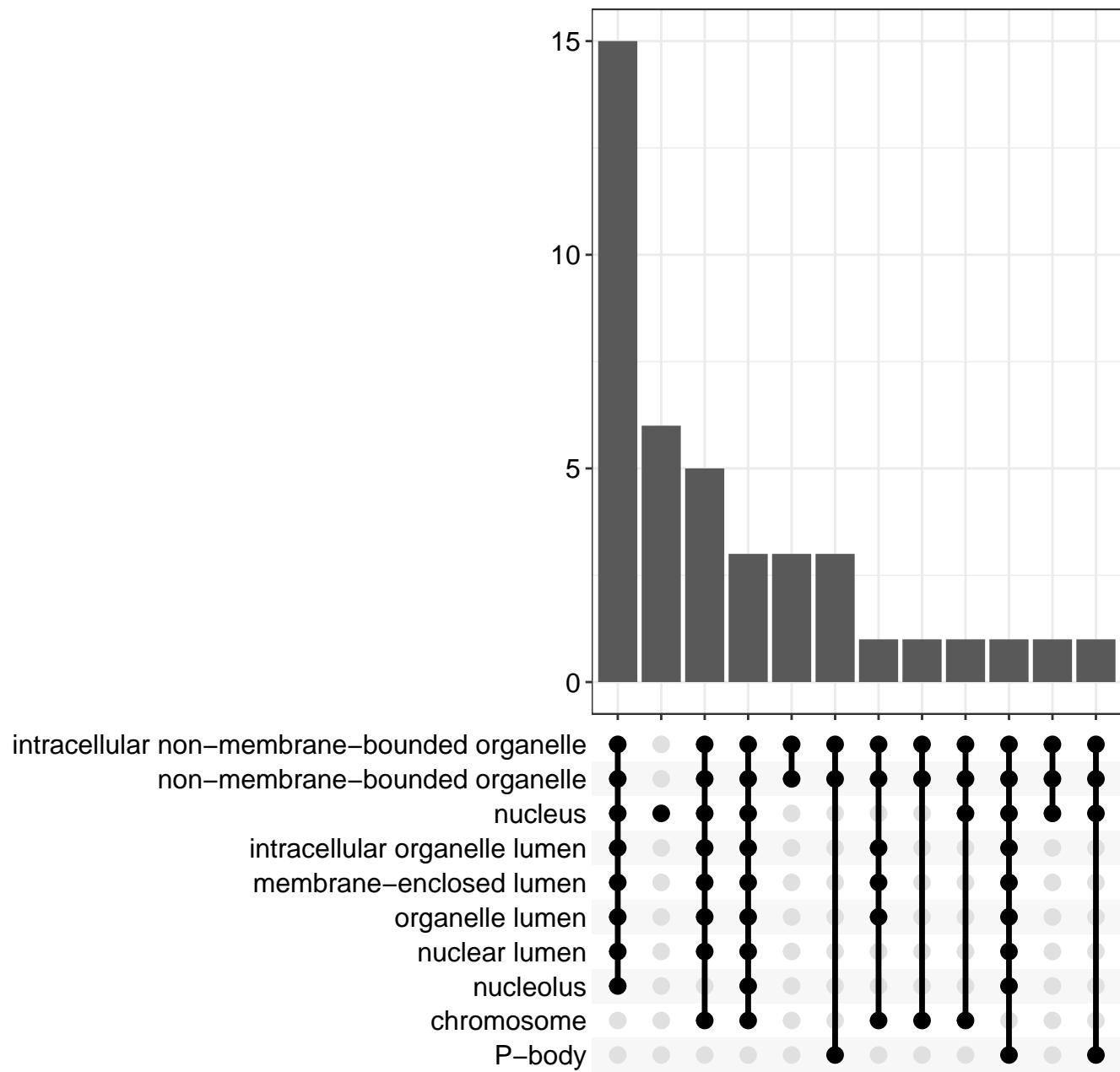


GBP2-TAP Up-regulated GO CC emapplot

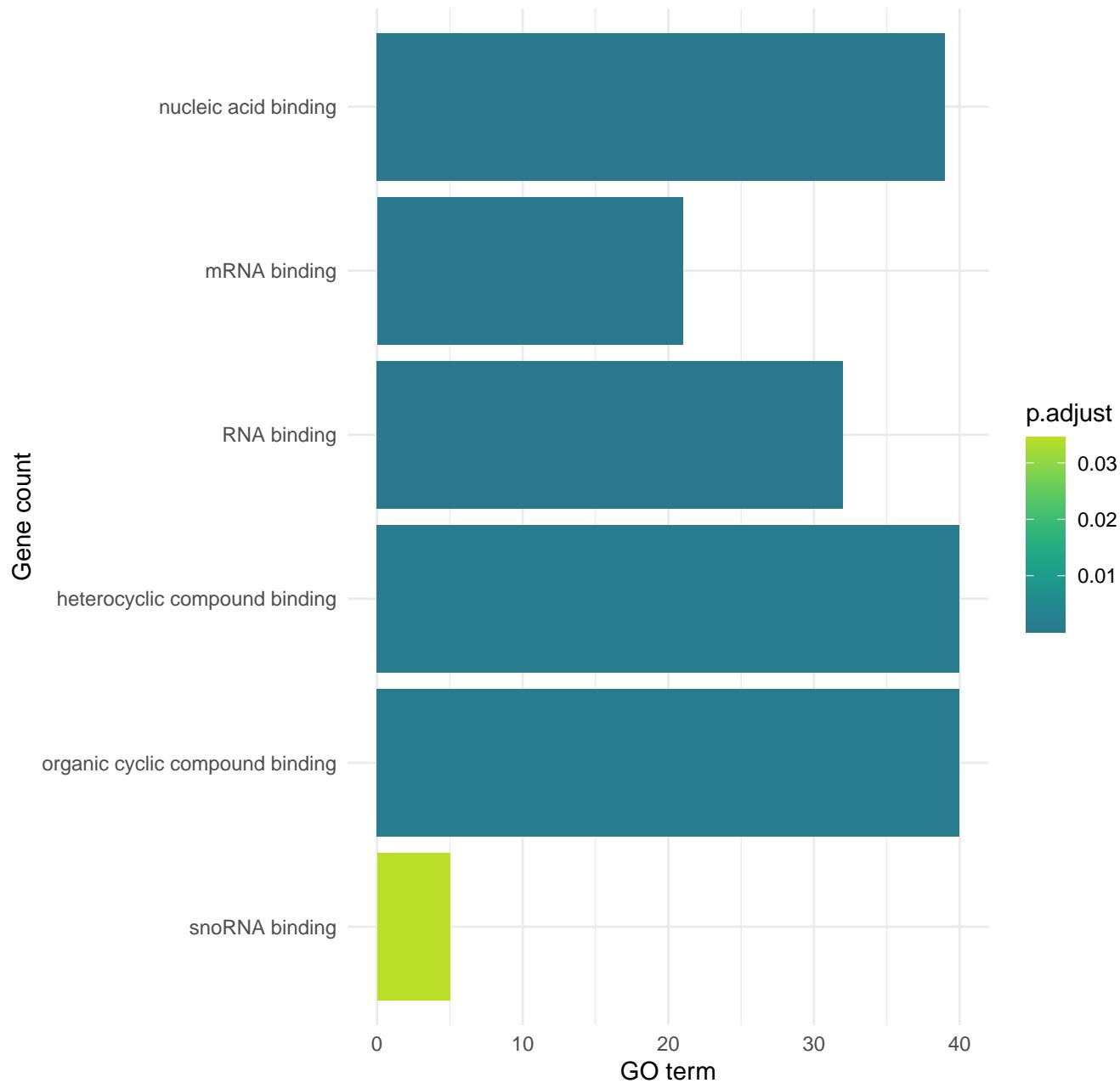




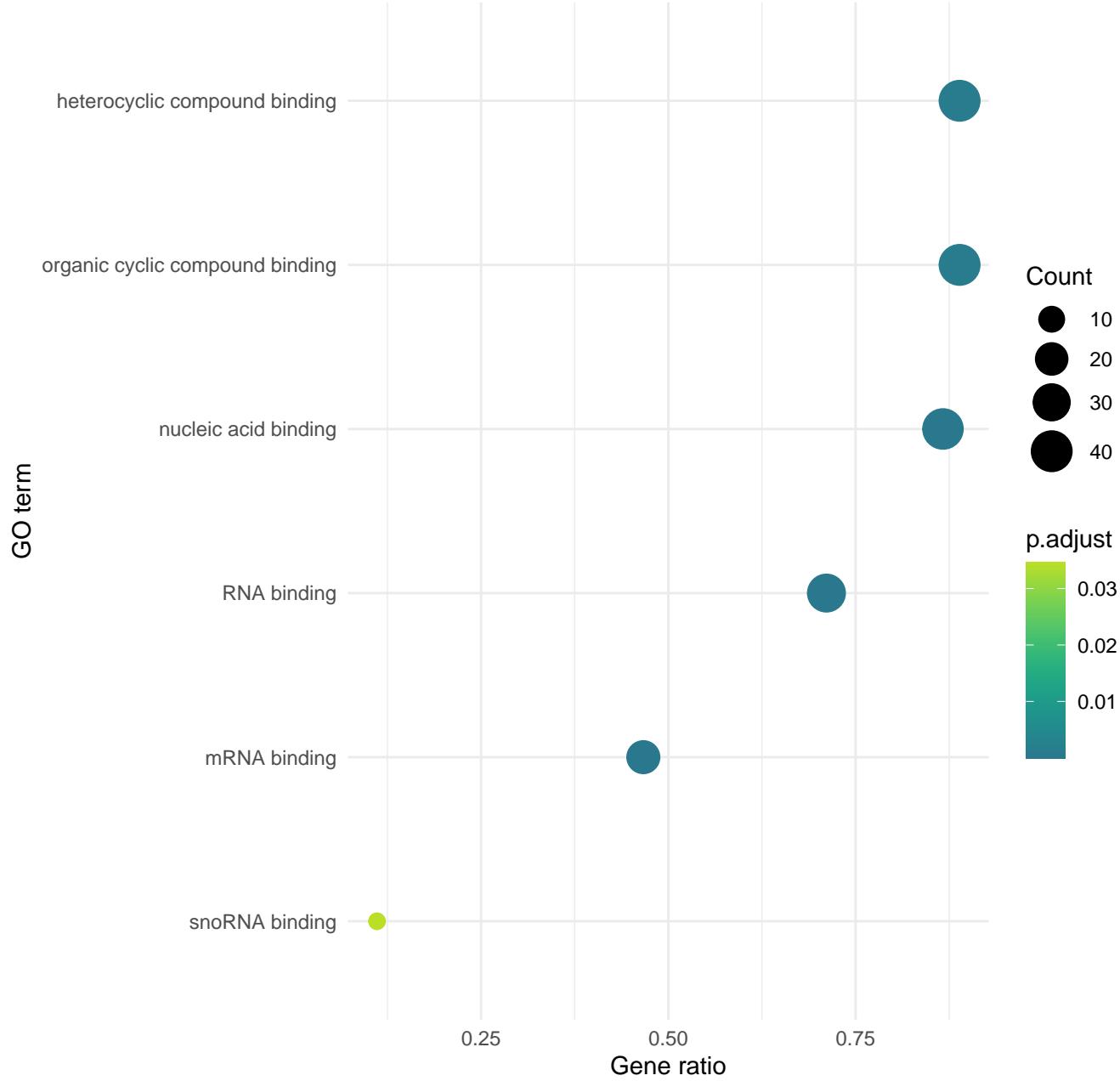
GBP2-TAP Up-regulated GO CC upset



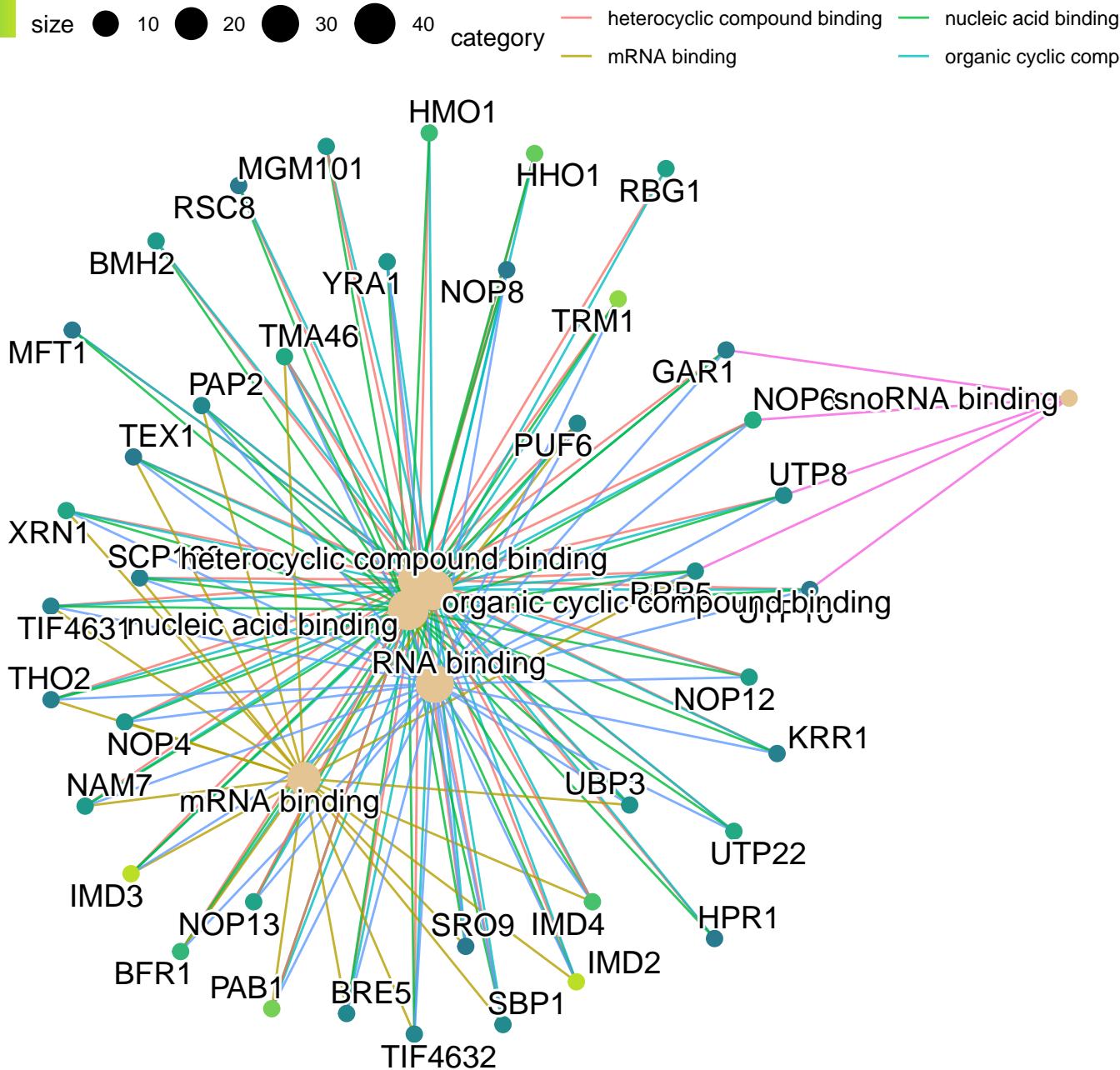
GBP2-TAP Up-regulated GO MF barplot



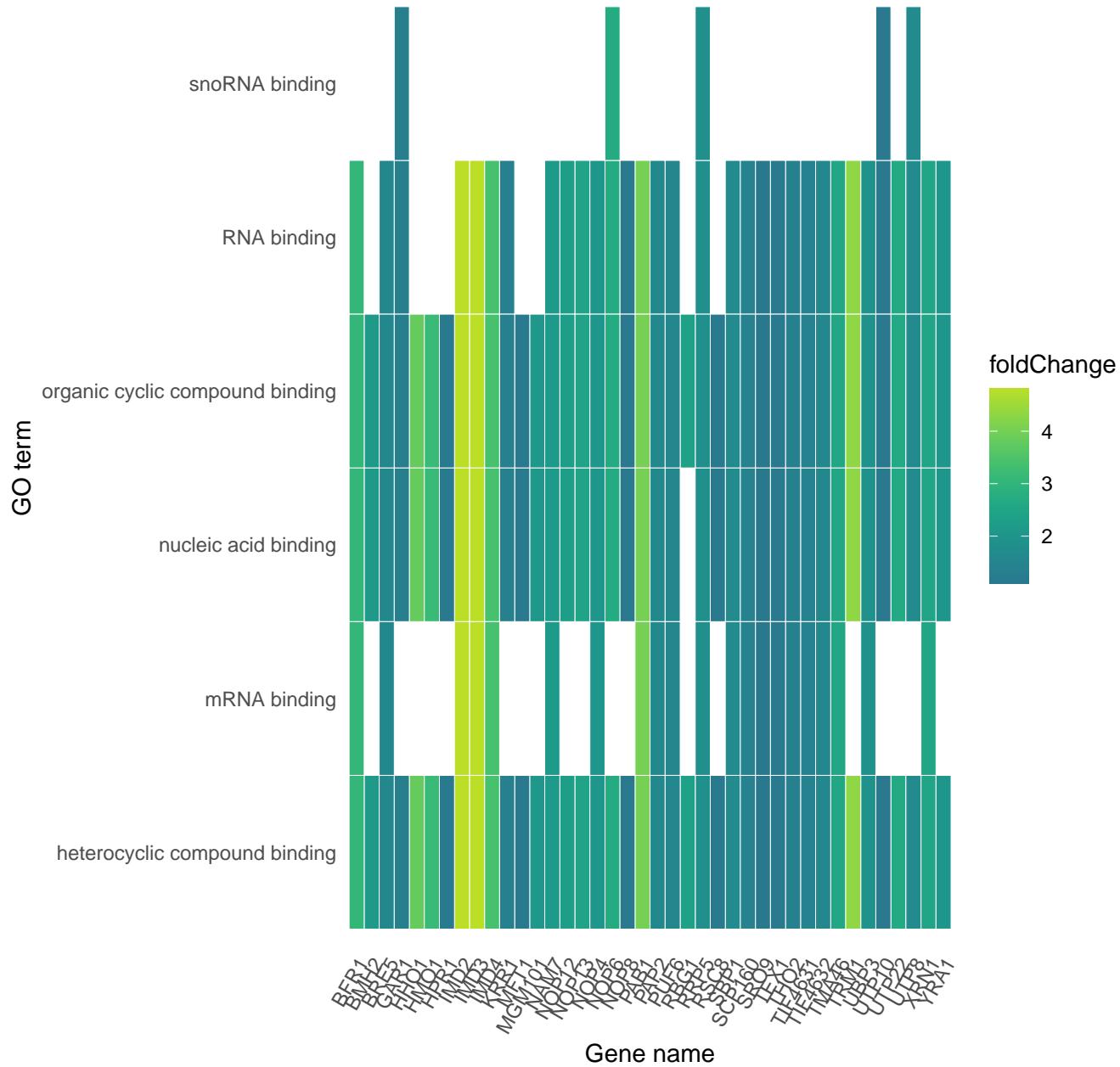
GBP2-TAP Up-regulated GO MF dotplot



GBP2-TAP Up-regulated GO MF cnetplot



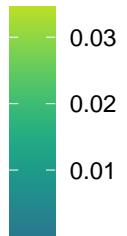
GBP2-TAP Up-regulated GO MF heatplot



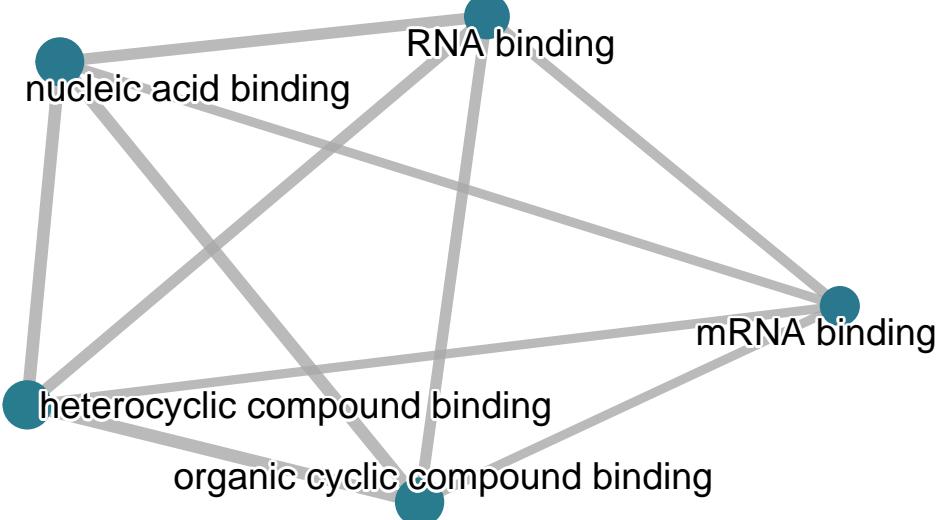
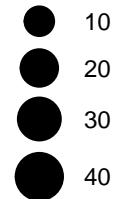
GBP2-TAP Up-regulated GO MF emapplot

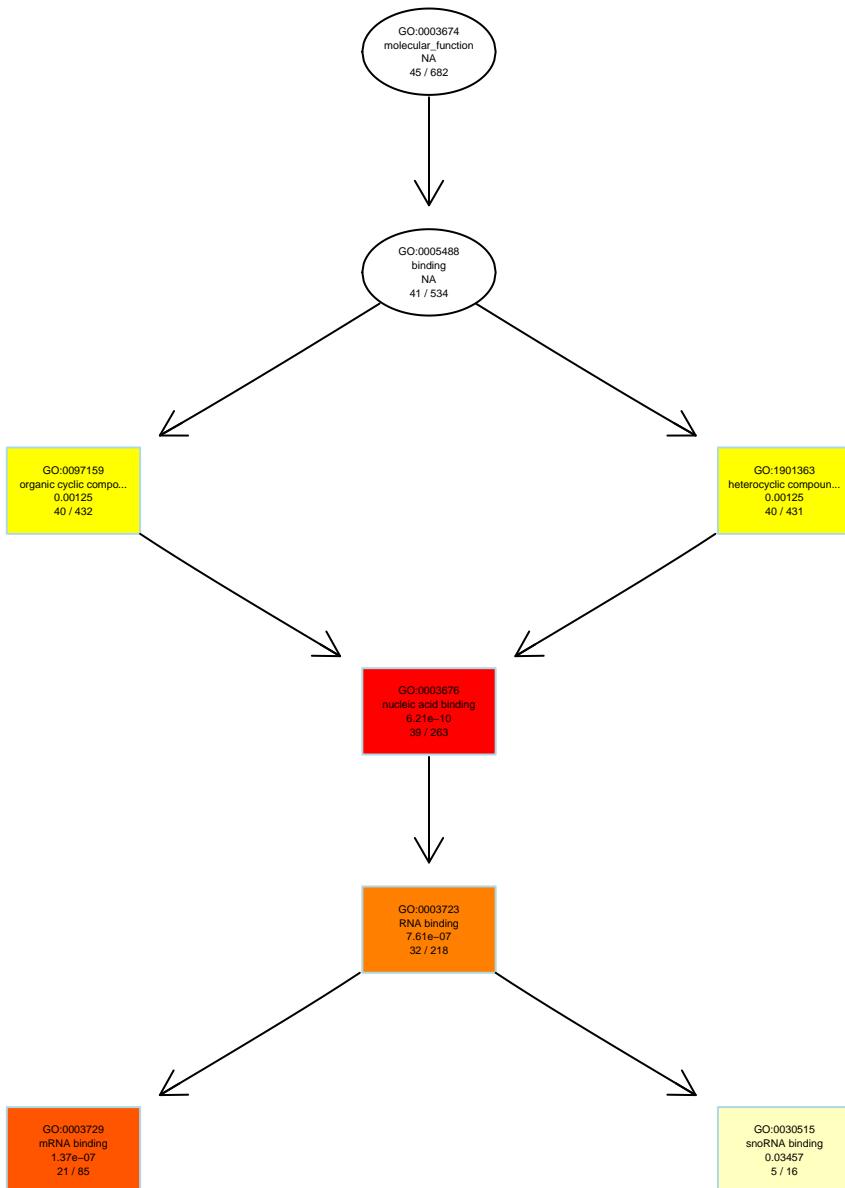
snoRNA binding ●

FoldChange

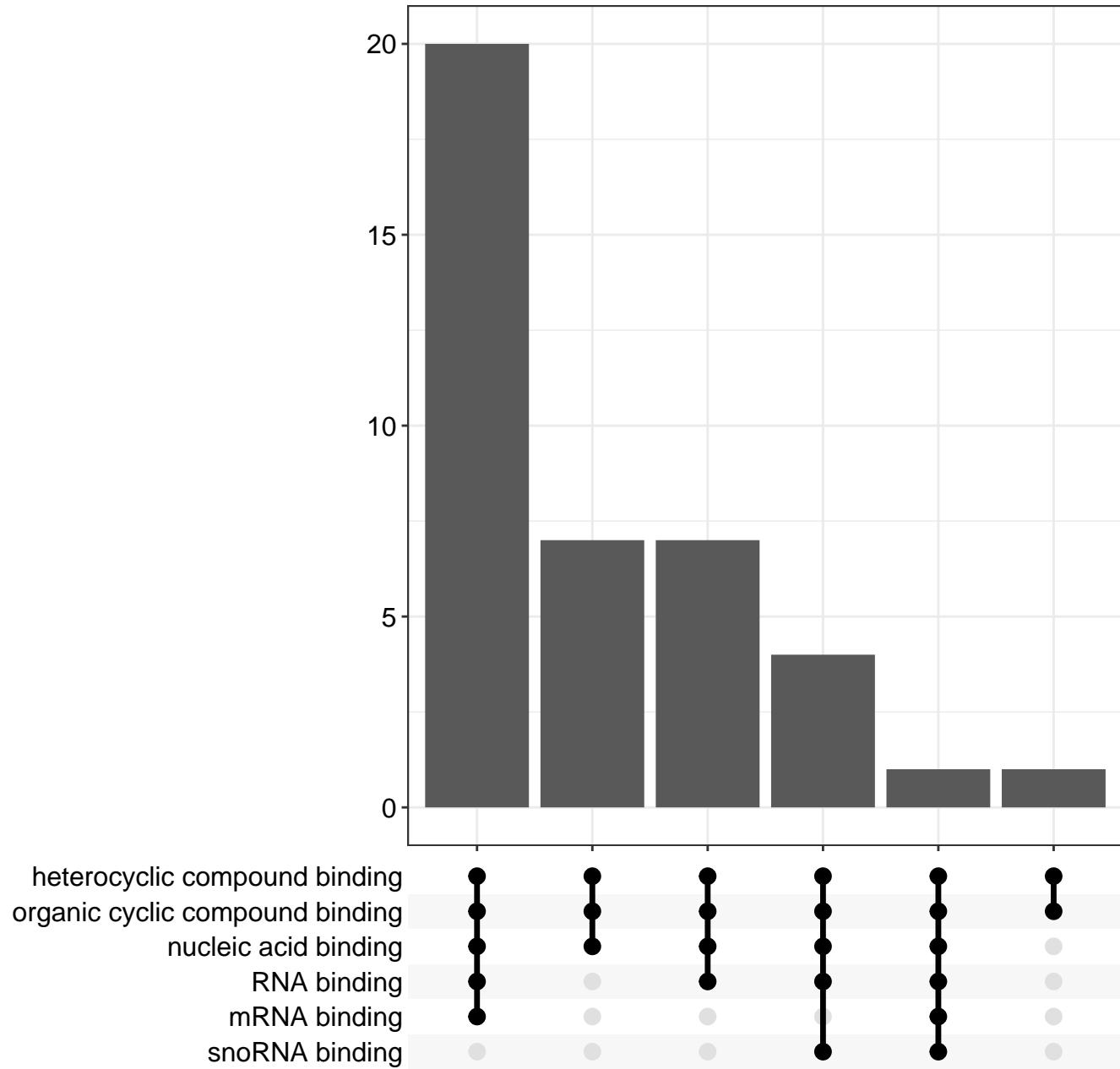


size

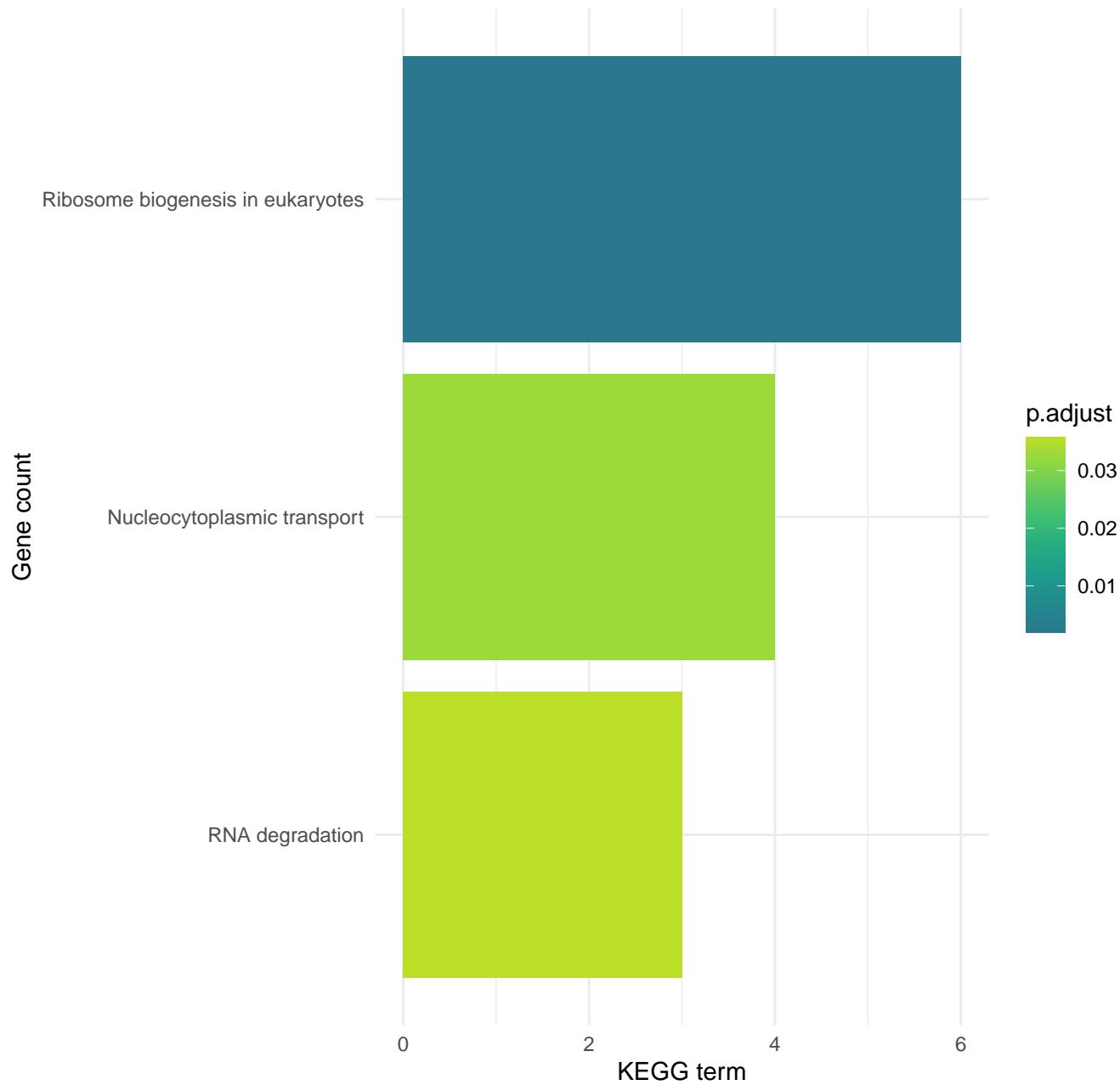




GBP2-TAP Up-regulated GO MF upsetplot



GBP2-TAP Up-regulated KEGG barplot



GBP2-TAP Up-regulated KEGG dotplot

KEGG term

Ribosome biogenesis in eukaryotes

3.5

p.adjust



Nucleocytoplasmic transport

0.21

Count



RNA degradation

0.15

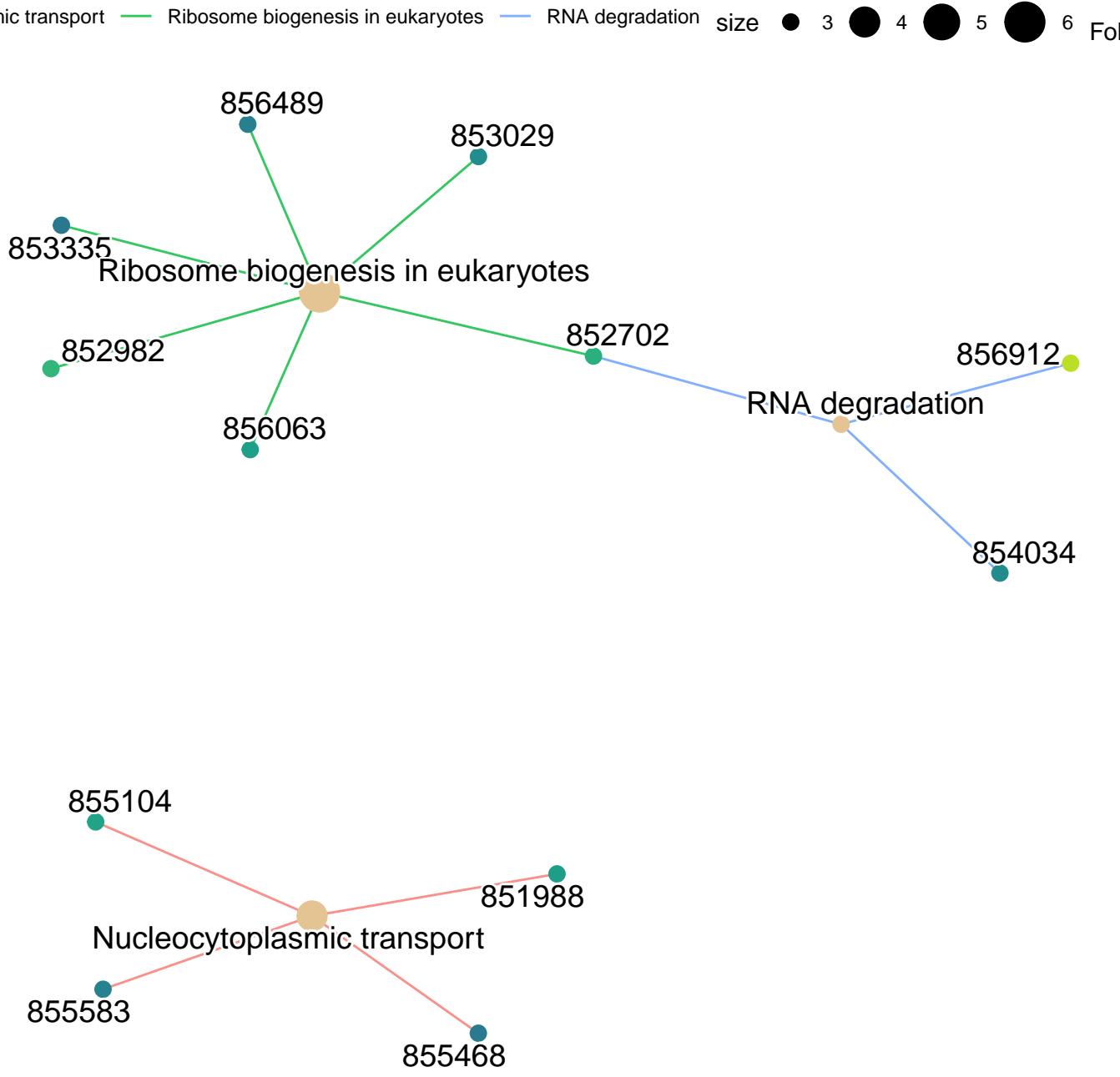
0.20

0.25

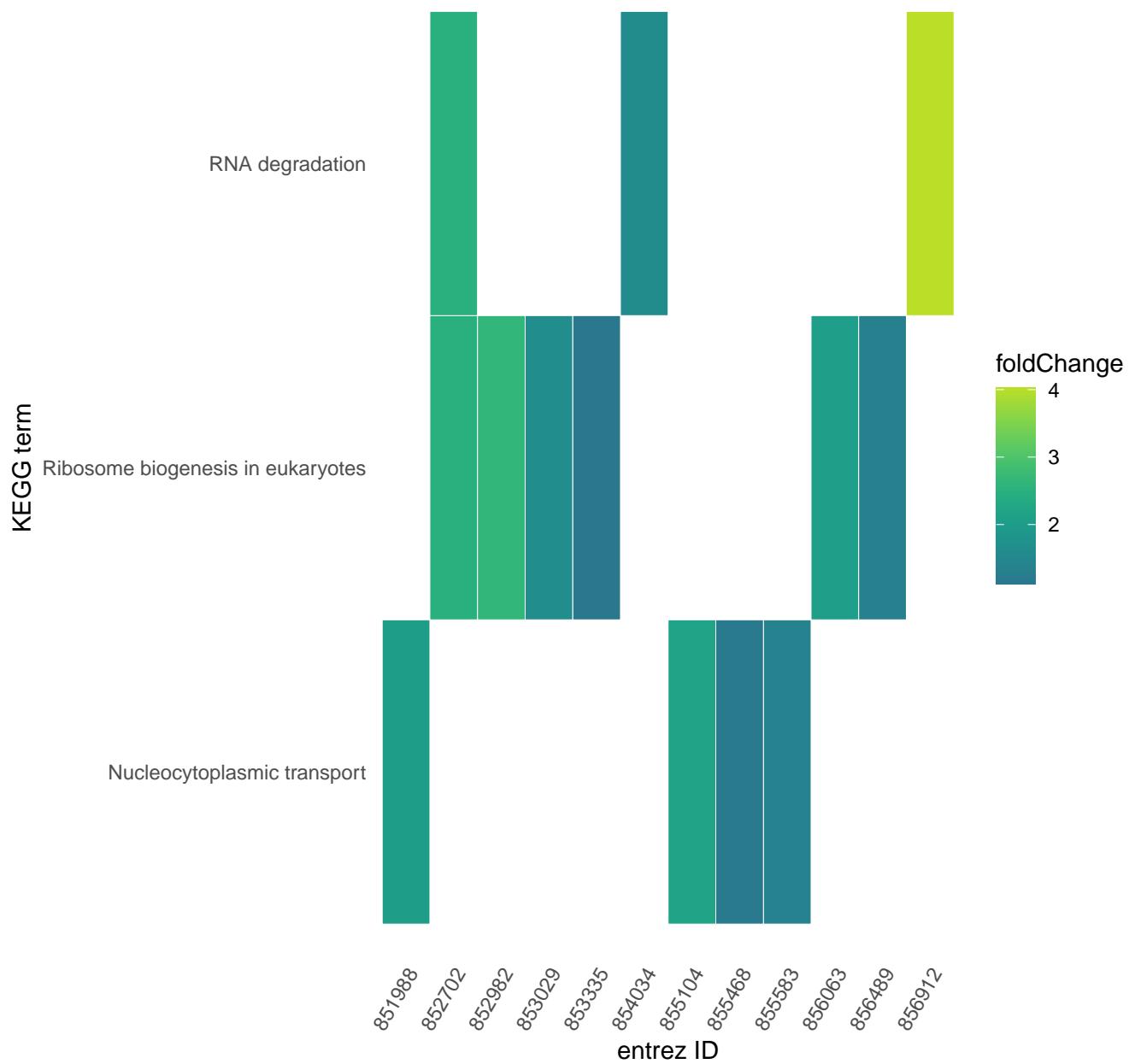
0.30

Gene ratio

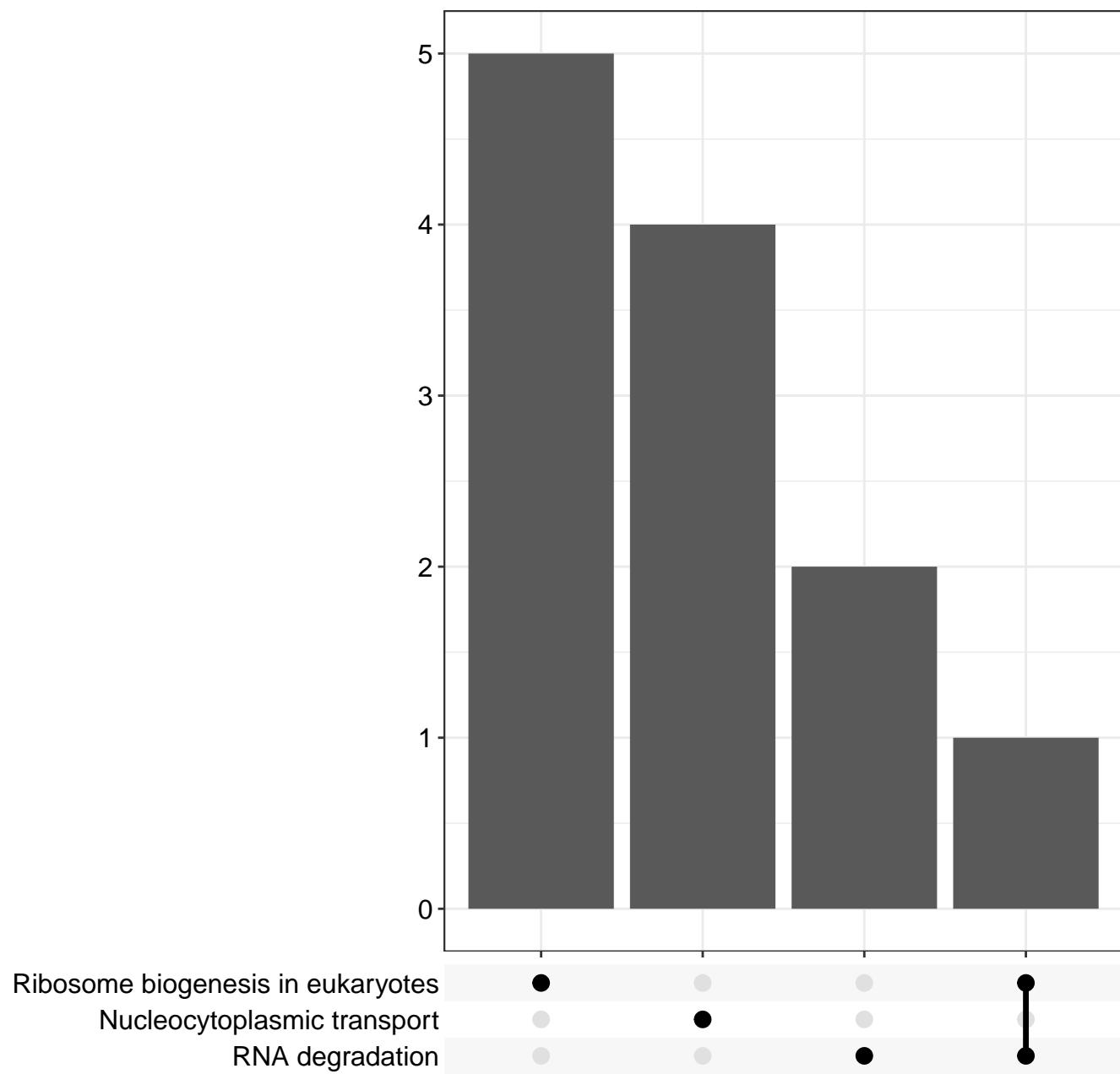
GBP2-TAP Up-regulated KEGG dotplot



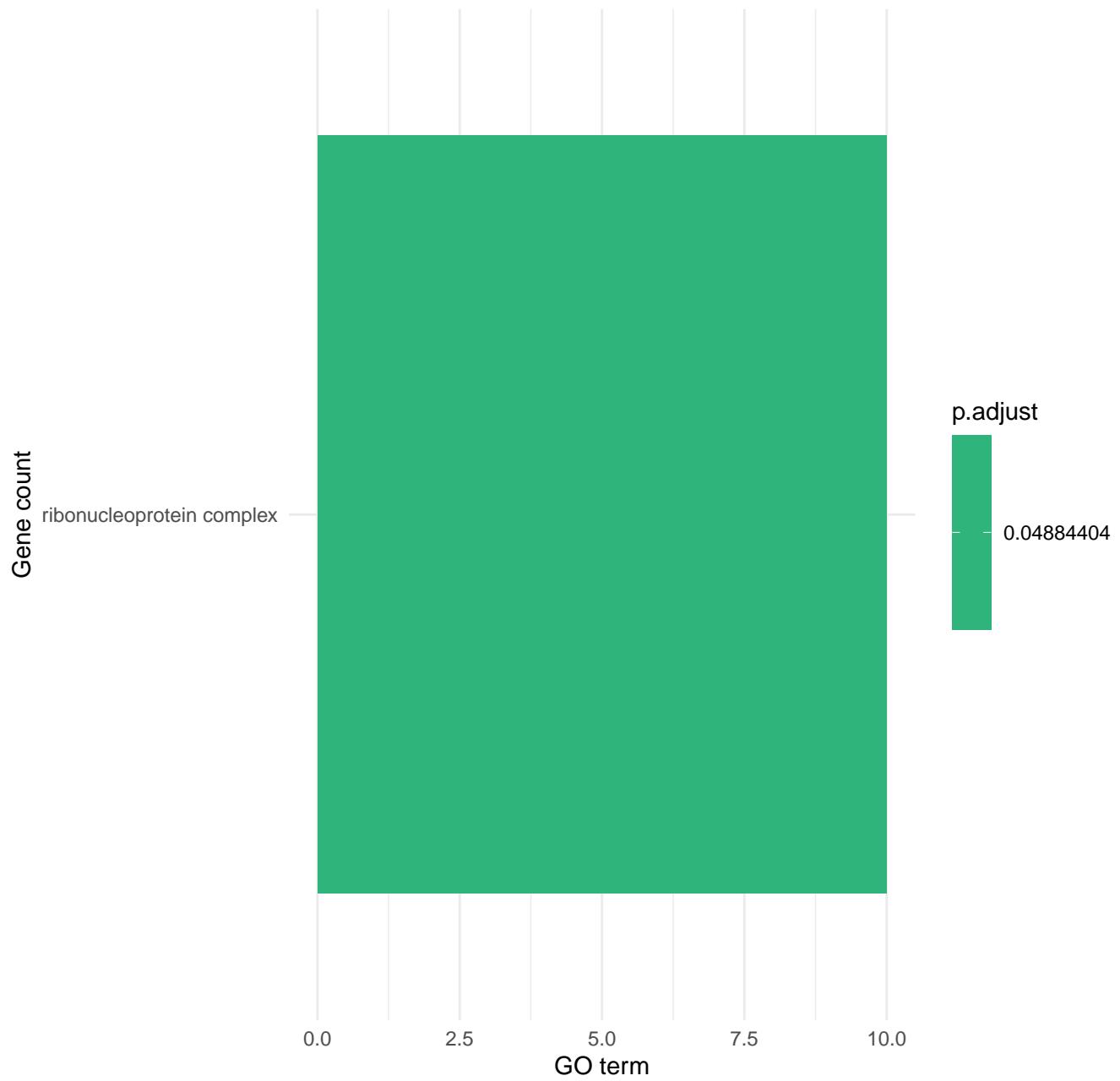
GBP2-TAP Up-regulated KEGG heatplot



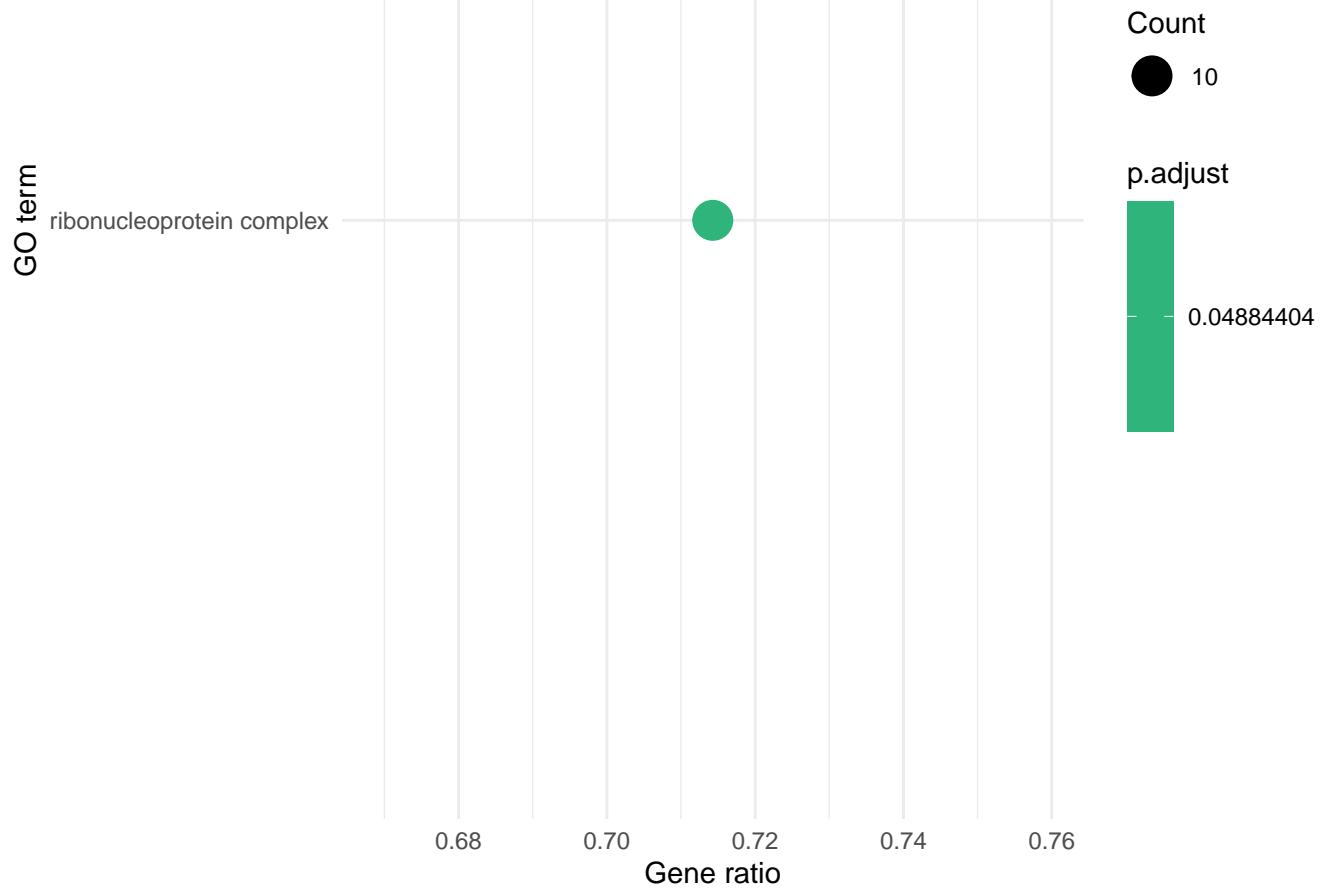
GBP2-TAP Up-regulated KEGG upsetplot



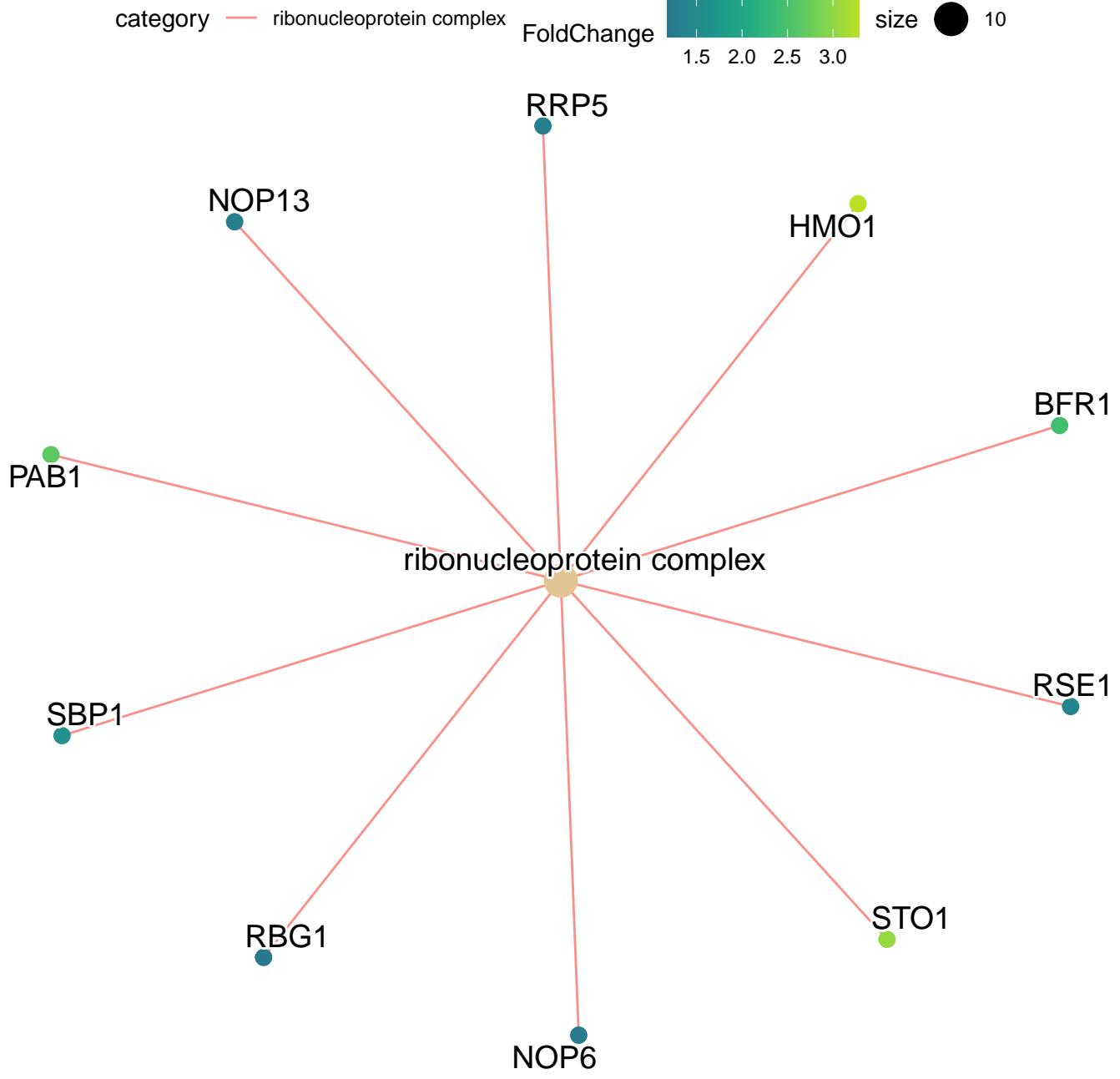
SNP1-TAP Up-regulated GO CC barplot



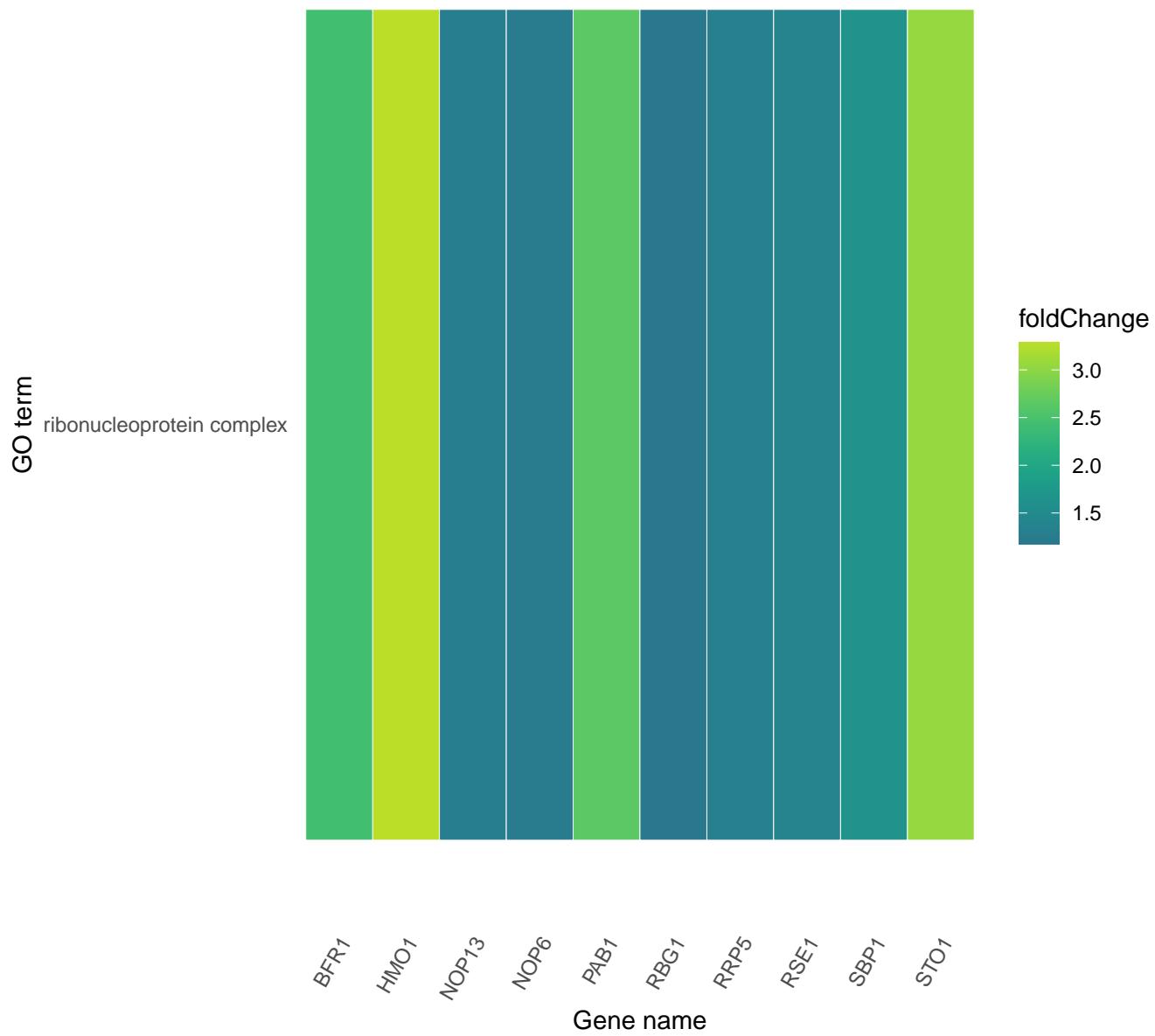
SNP1-TAP Up-regulated GO CC dotplot



SNP1-TAP Up-regulated GO CC cnetplot



SNP1-TAP Up-regulated GO CC heatplot



GO:0005575
cellular_component
NA
14 / 745

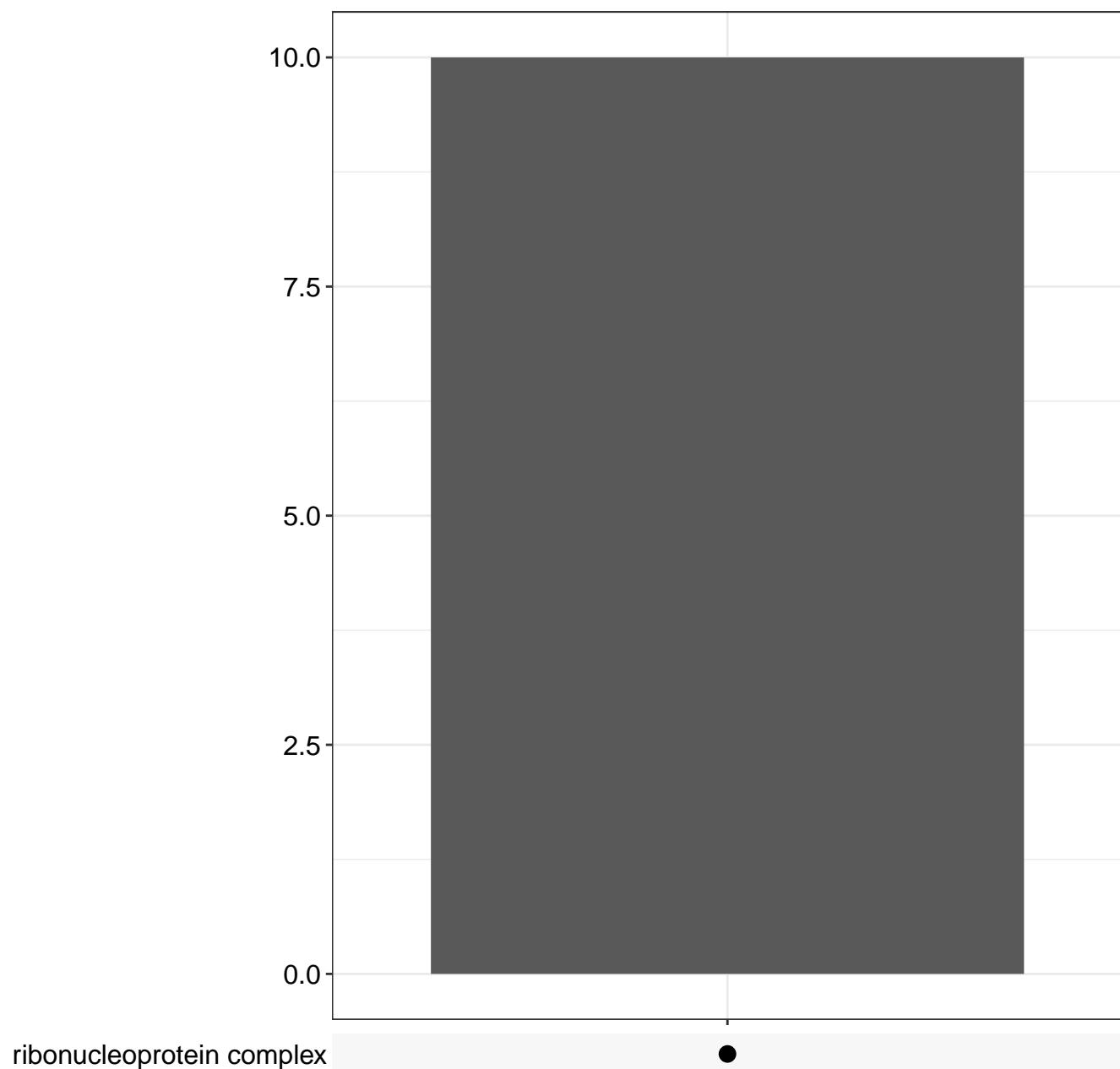


GO:0032991
protein-containing c...
0.3177
11 / 423

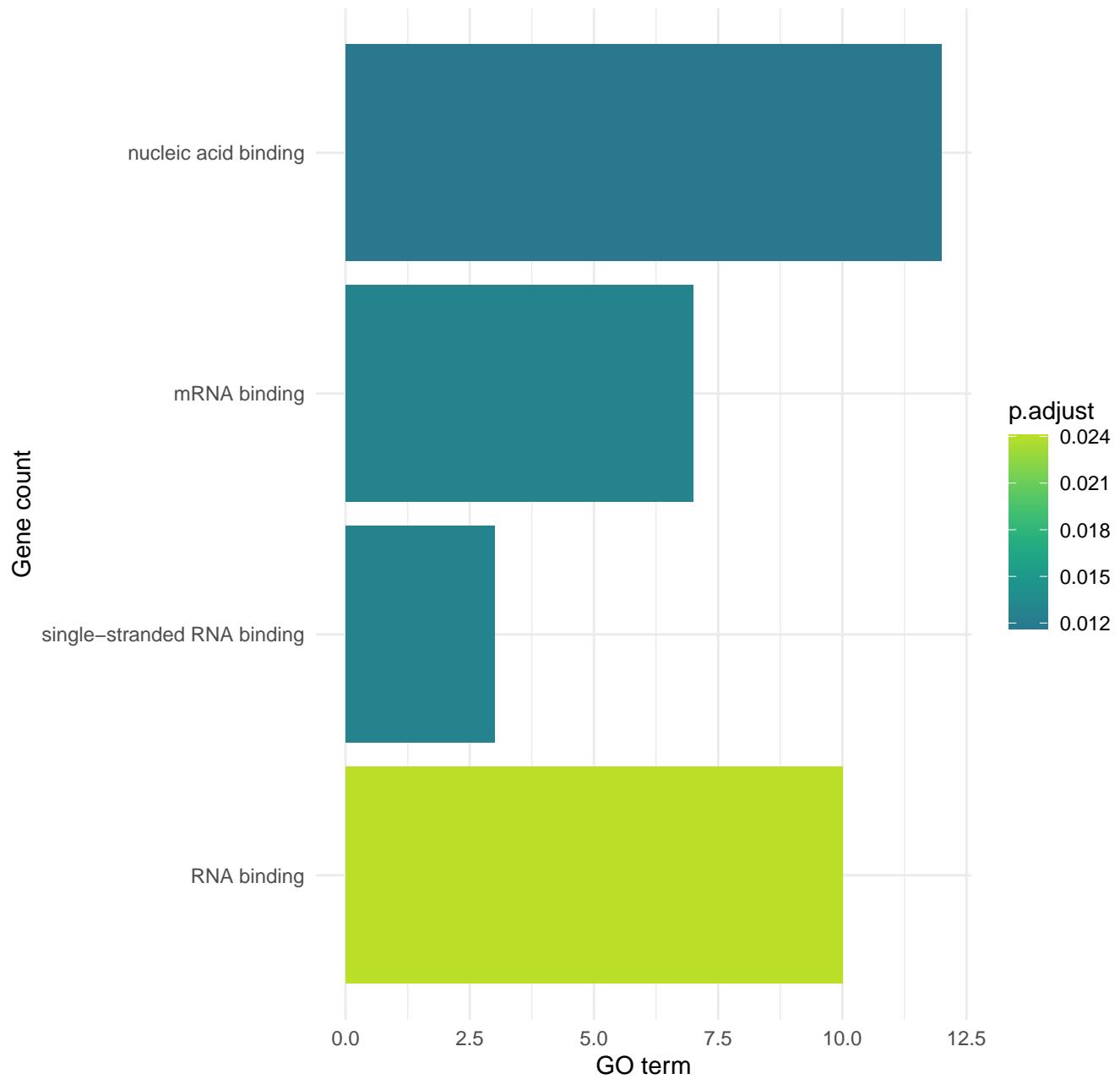


GO:1990904
ribonucleoprotein co...
0.0488
10 / 210

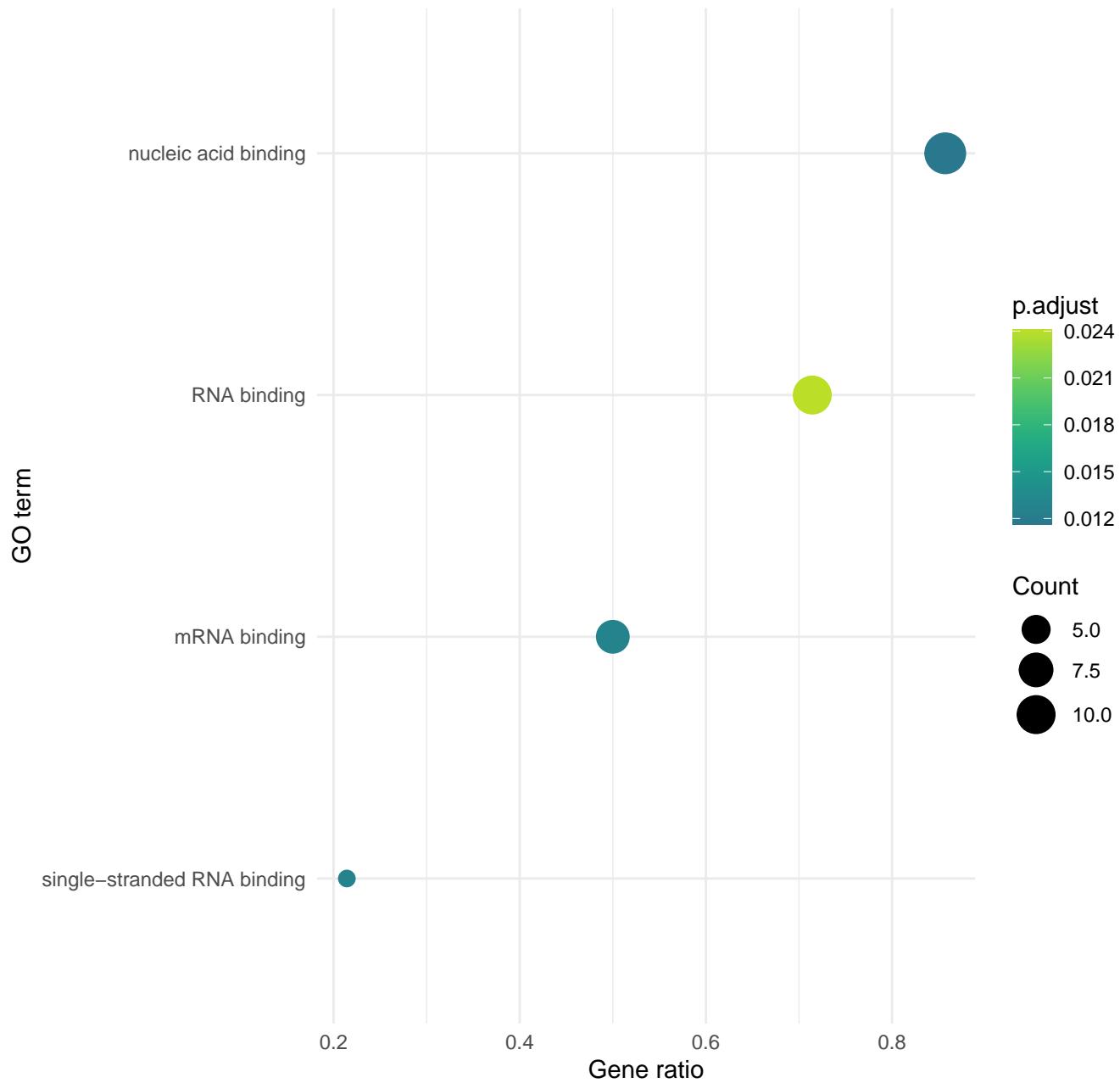
SNP1-TAP Up-regulated GO CC upsetplot



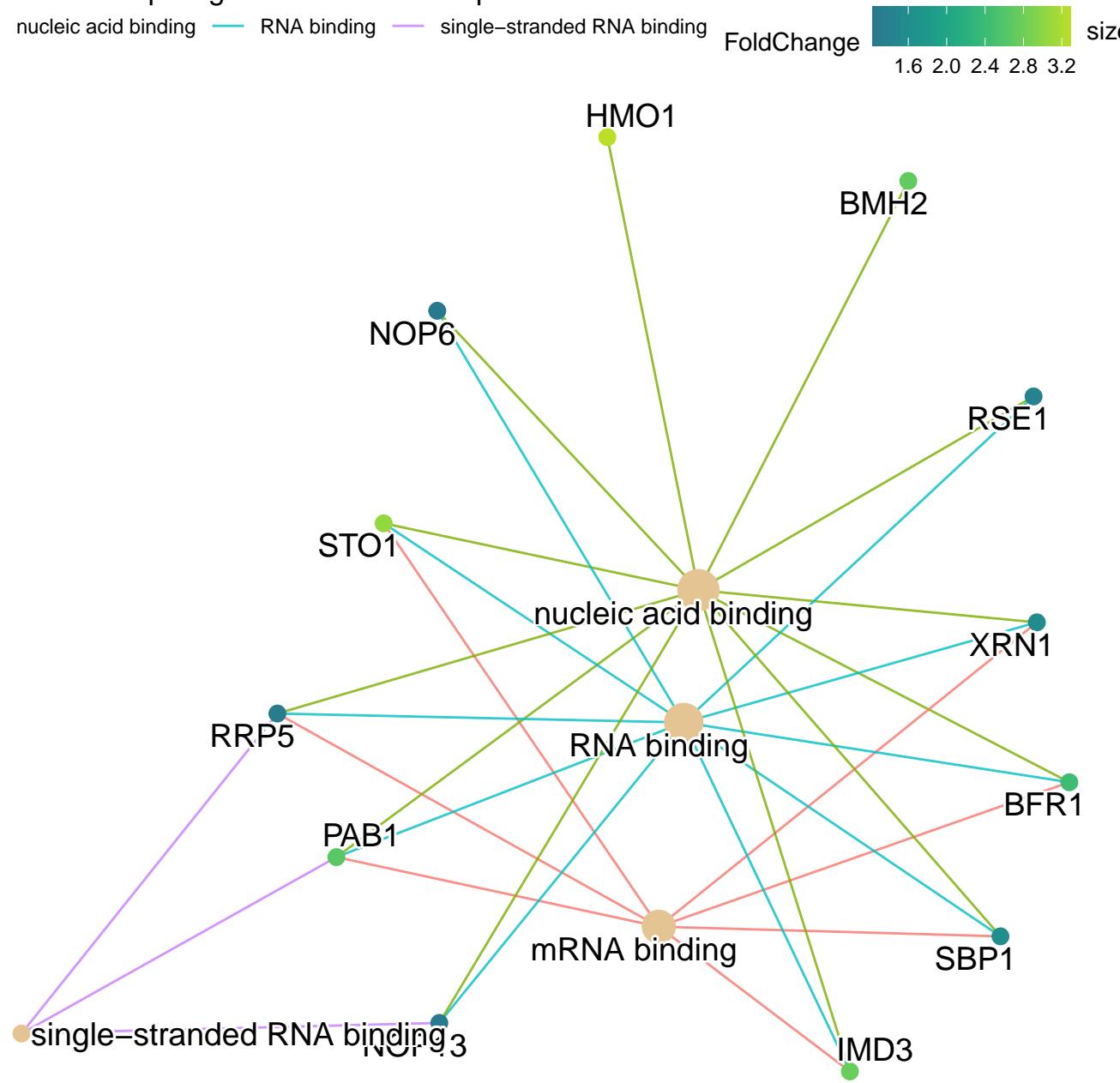
SNP1-TAP Up-regulated GO MF barplot



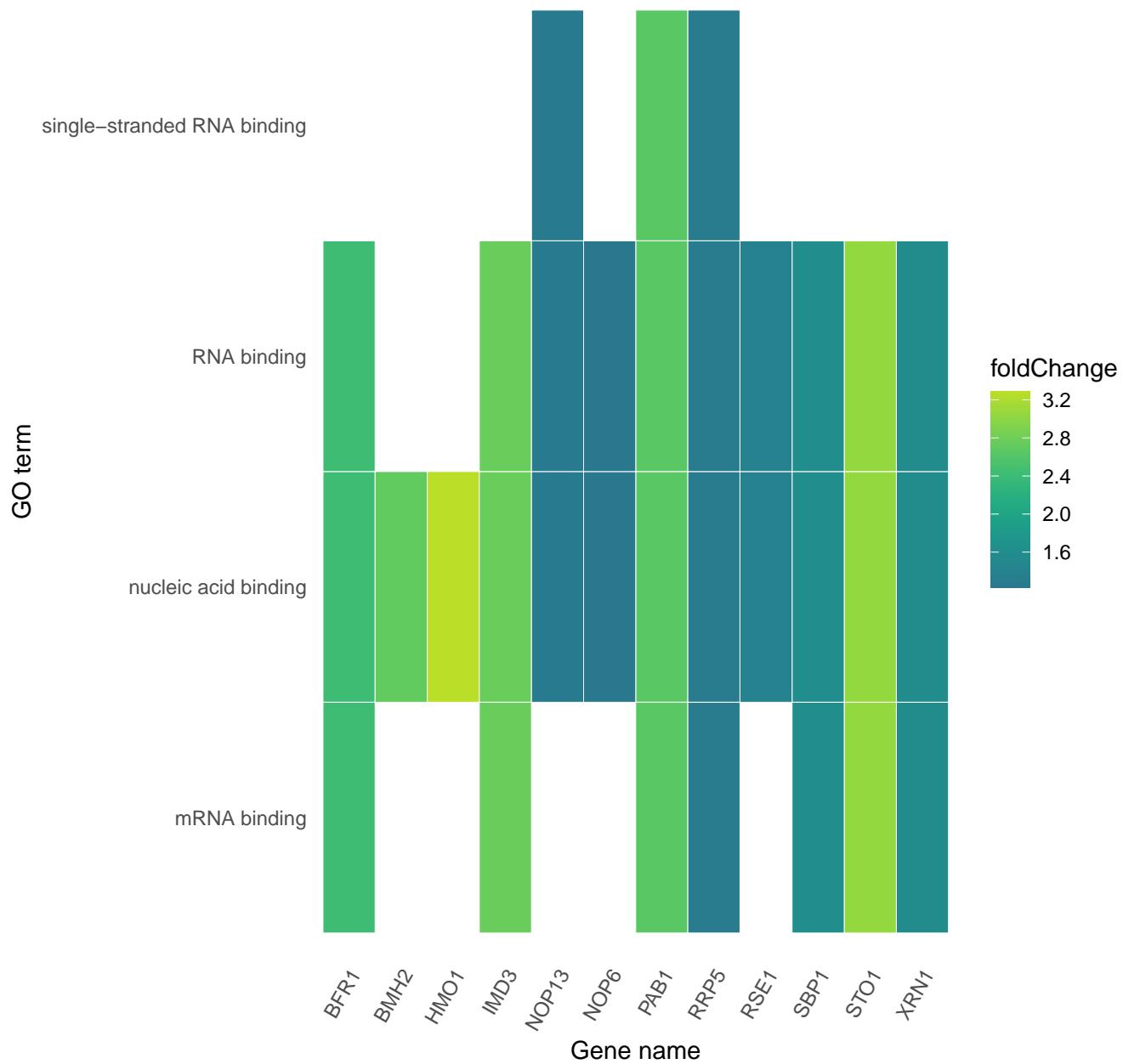
SNP1-TAP Up-regulated GO MF dotplot



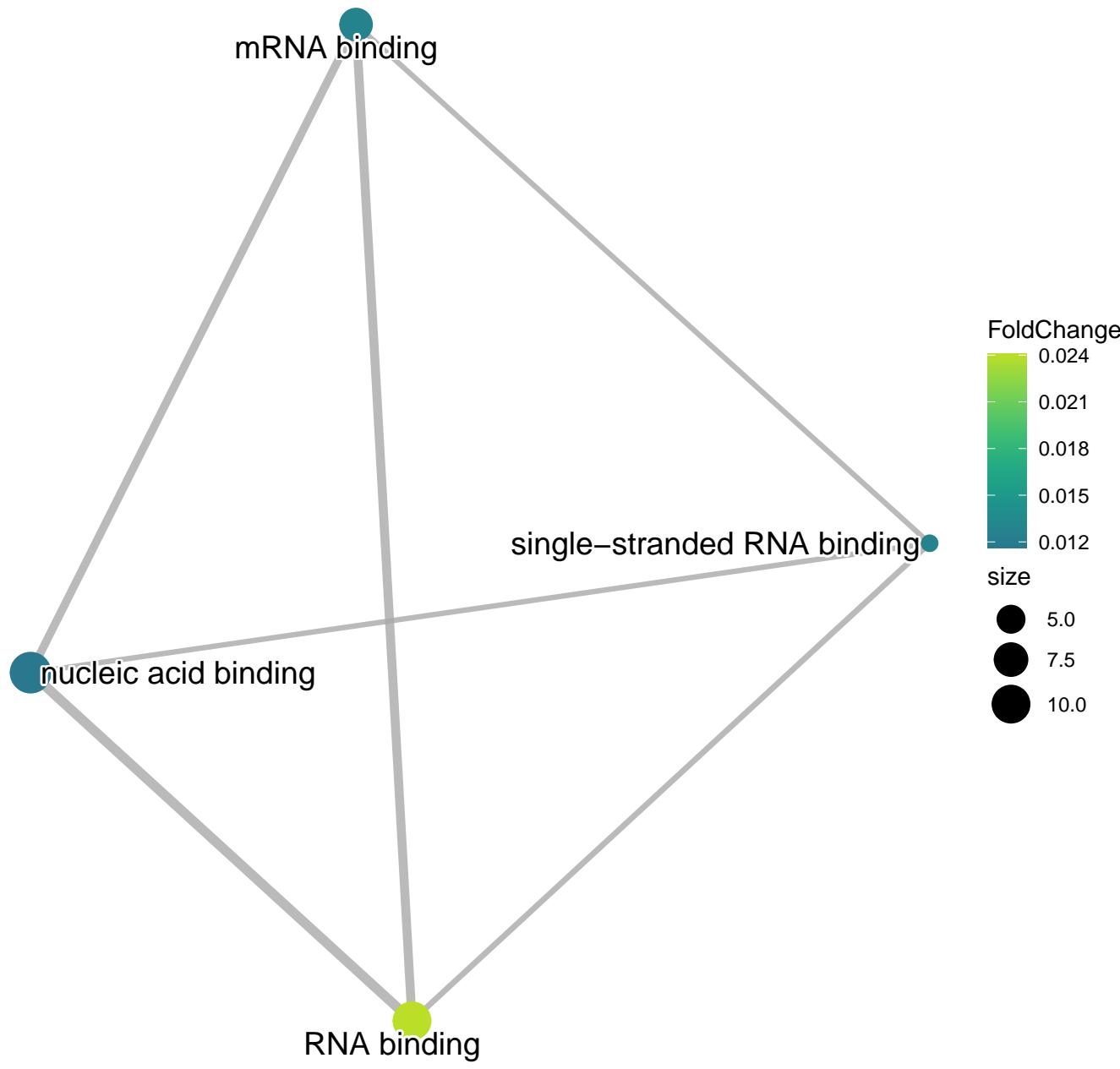
SNP1-TAP Up-regulated GO MF cnetplot

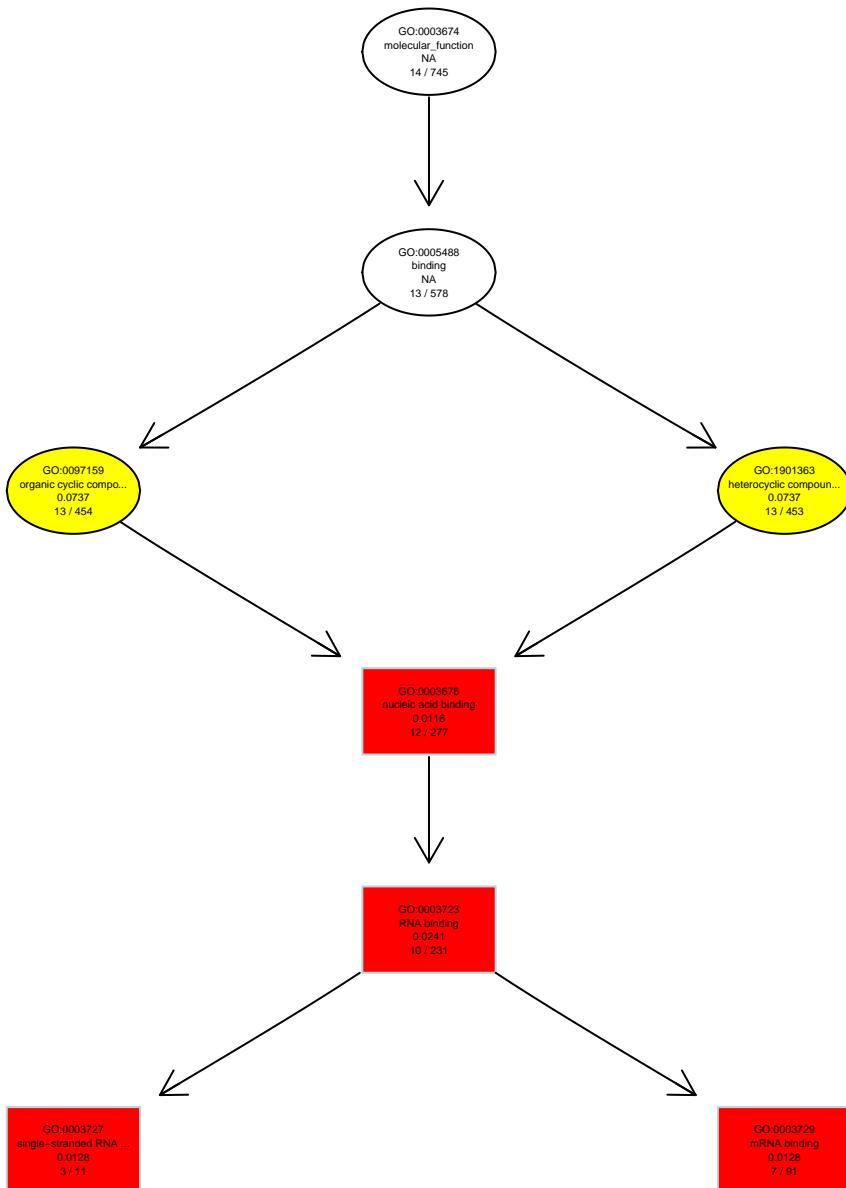


SNP1-TAP Up-regulated GO MF heatplot

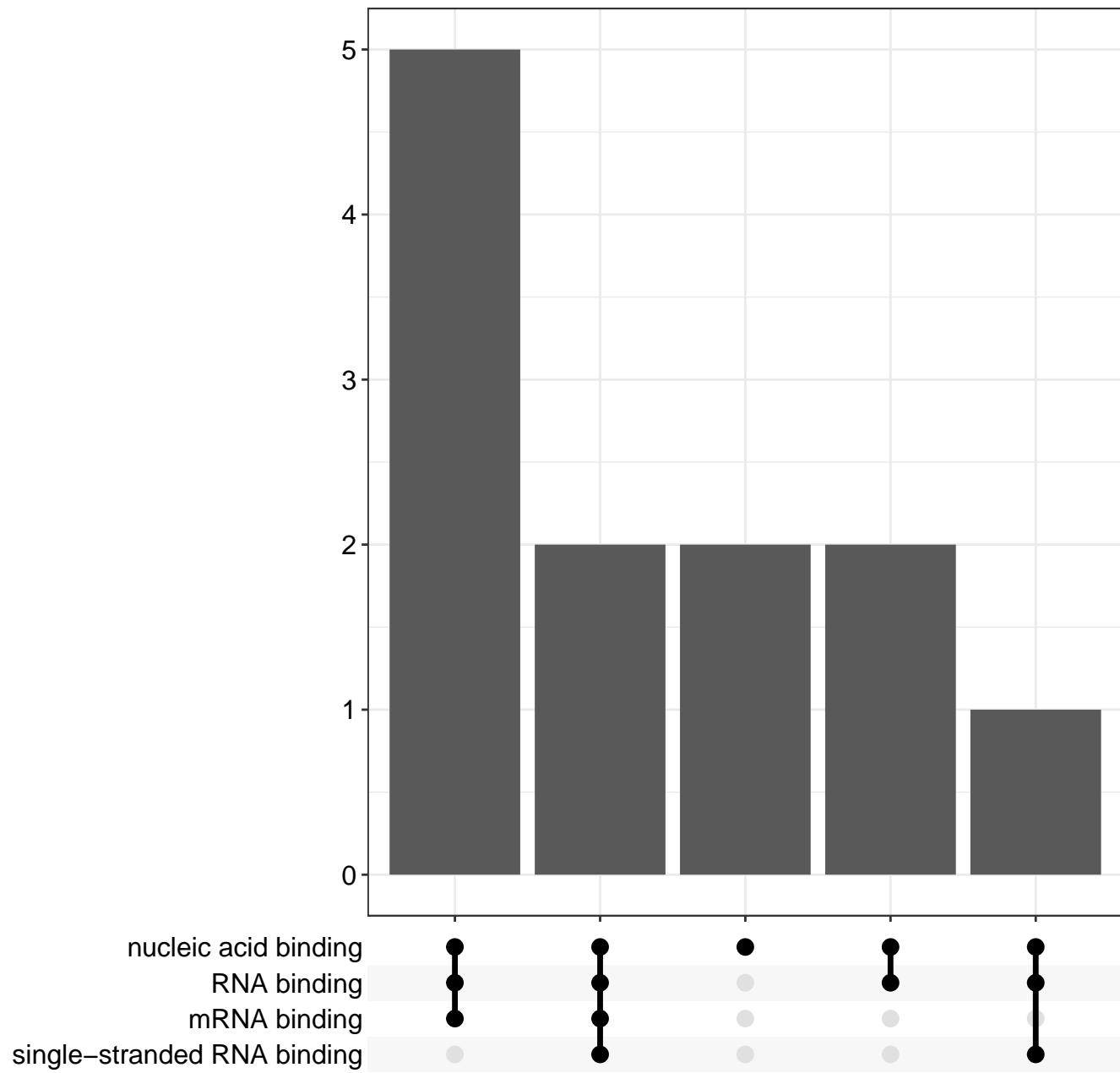


SNP1-TAP Up-regulated GO MF emapplot

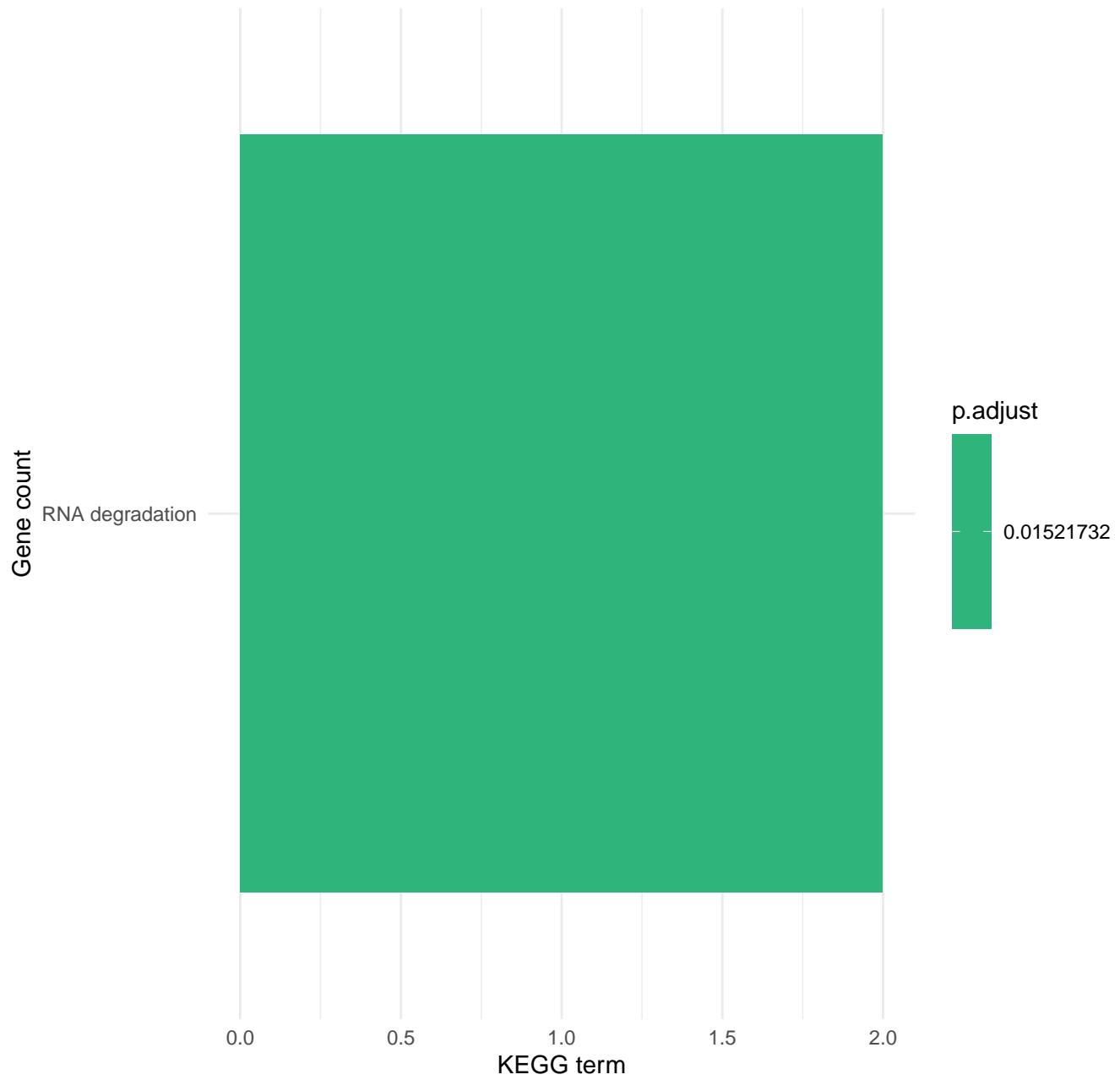




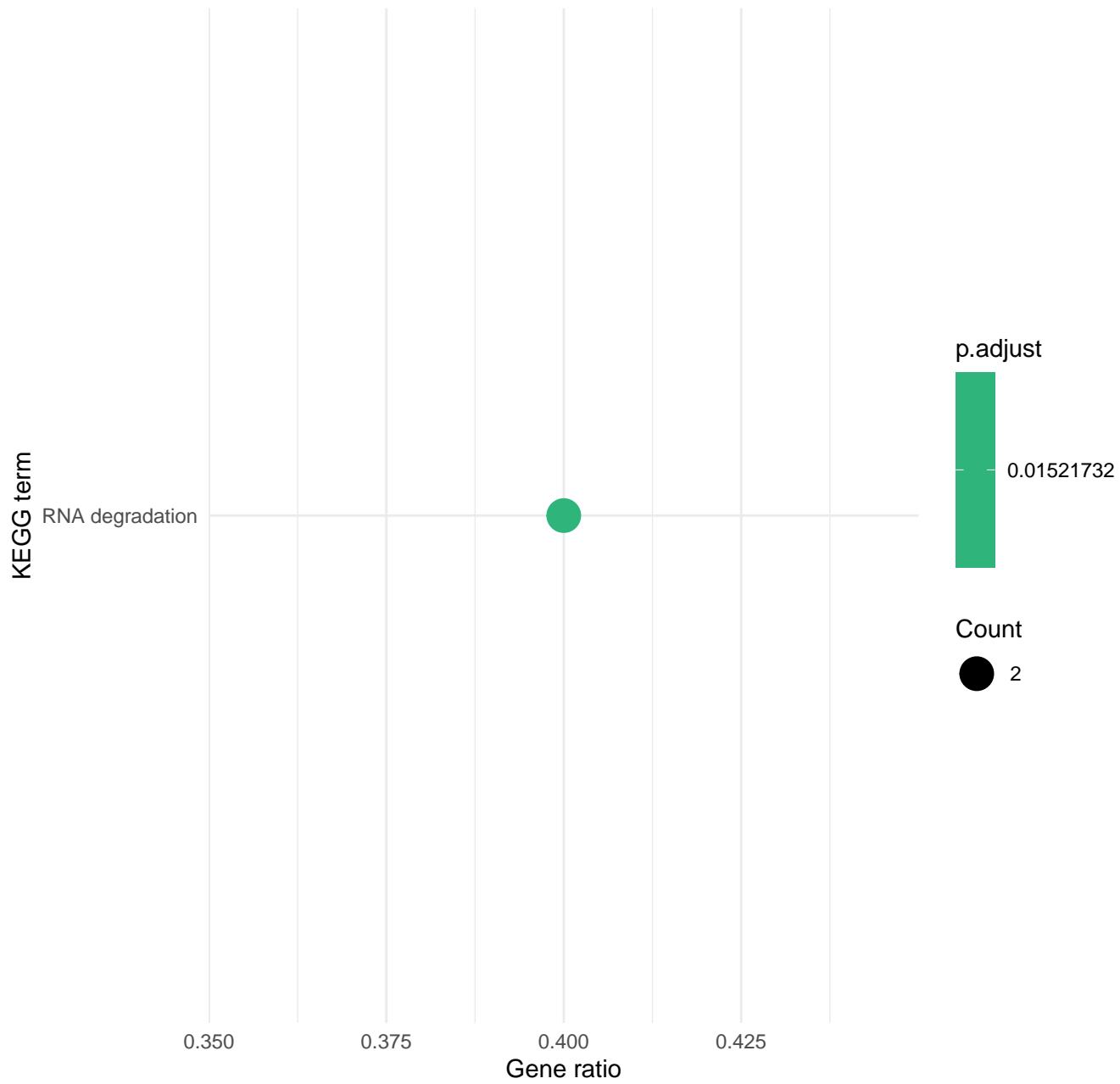
SNP1-TAP Up-regulated GO MF upsetplot



RPO21-TAP Up-regulated KEGG barplot



RPO21-TAP Up-regulated KEGG dotplot



RPO21-TAP Up-regulated KEGG dotplot

category RNA degradation

FoldChange



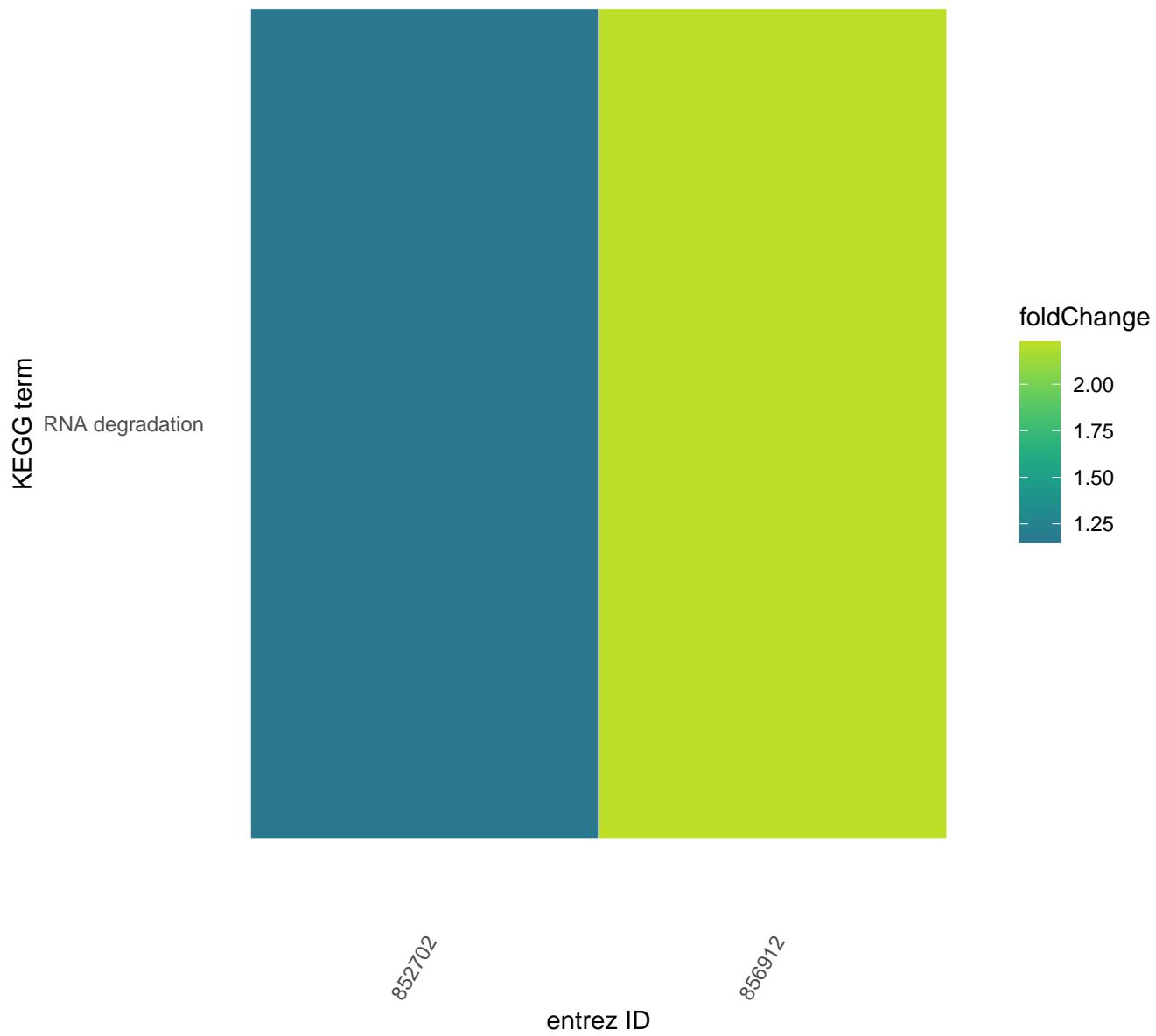
size 2

852702

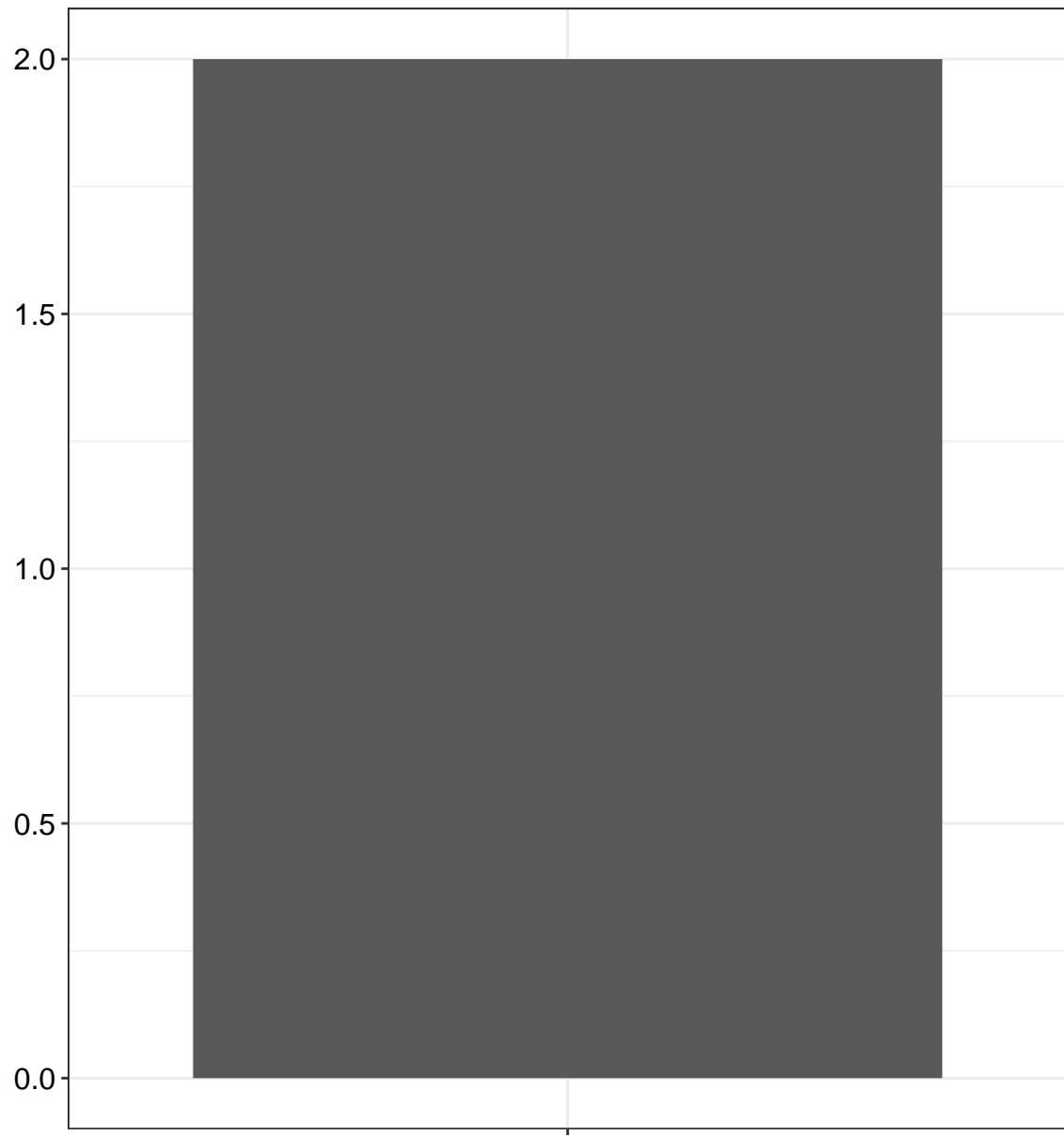
RNA degradation

856912

RPO21-TAP Up-regulated KEGG heatplot



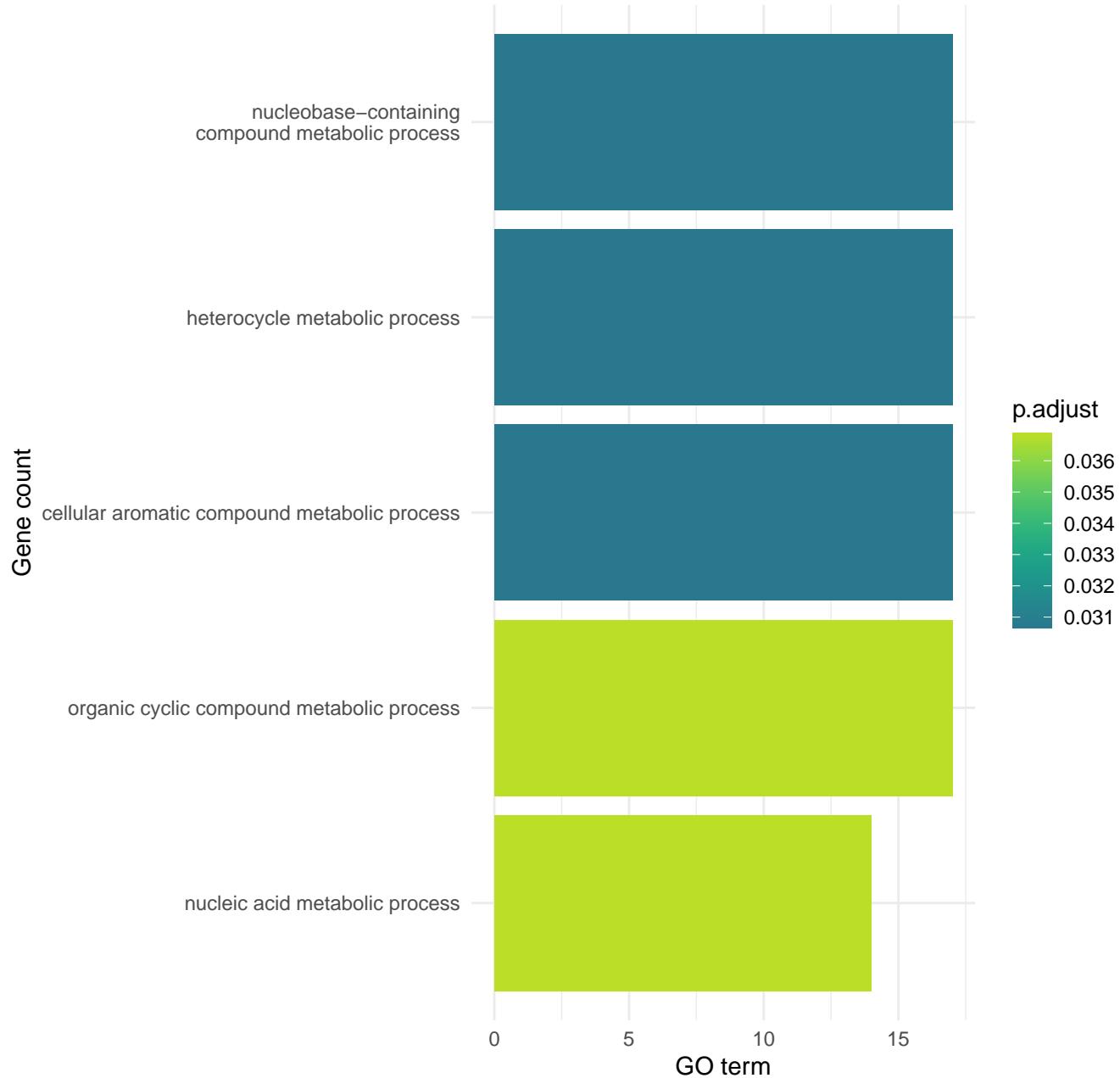
RPO21-TAP Up-regulated KEGG upsetplot



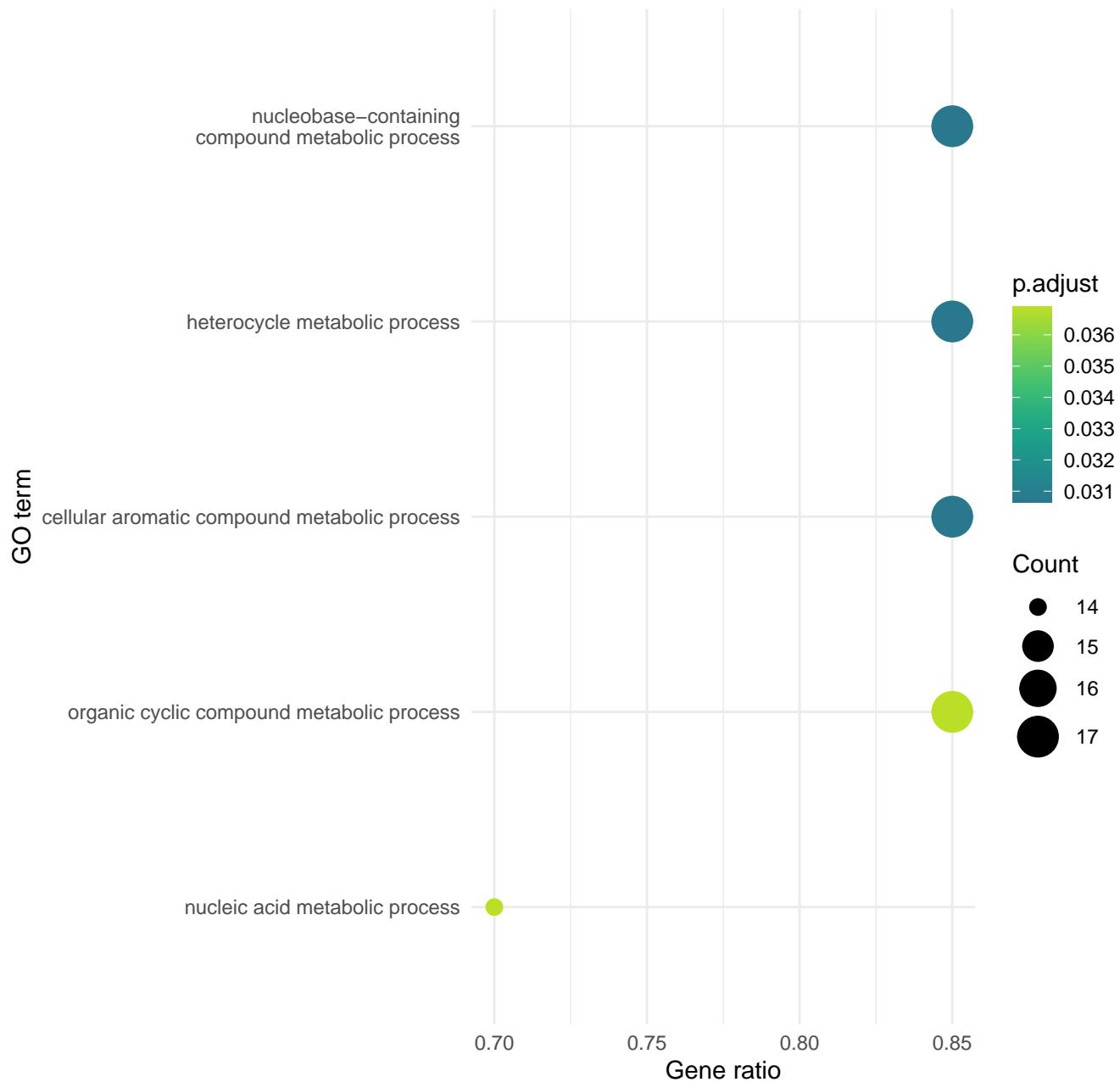
RNA degradation

●

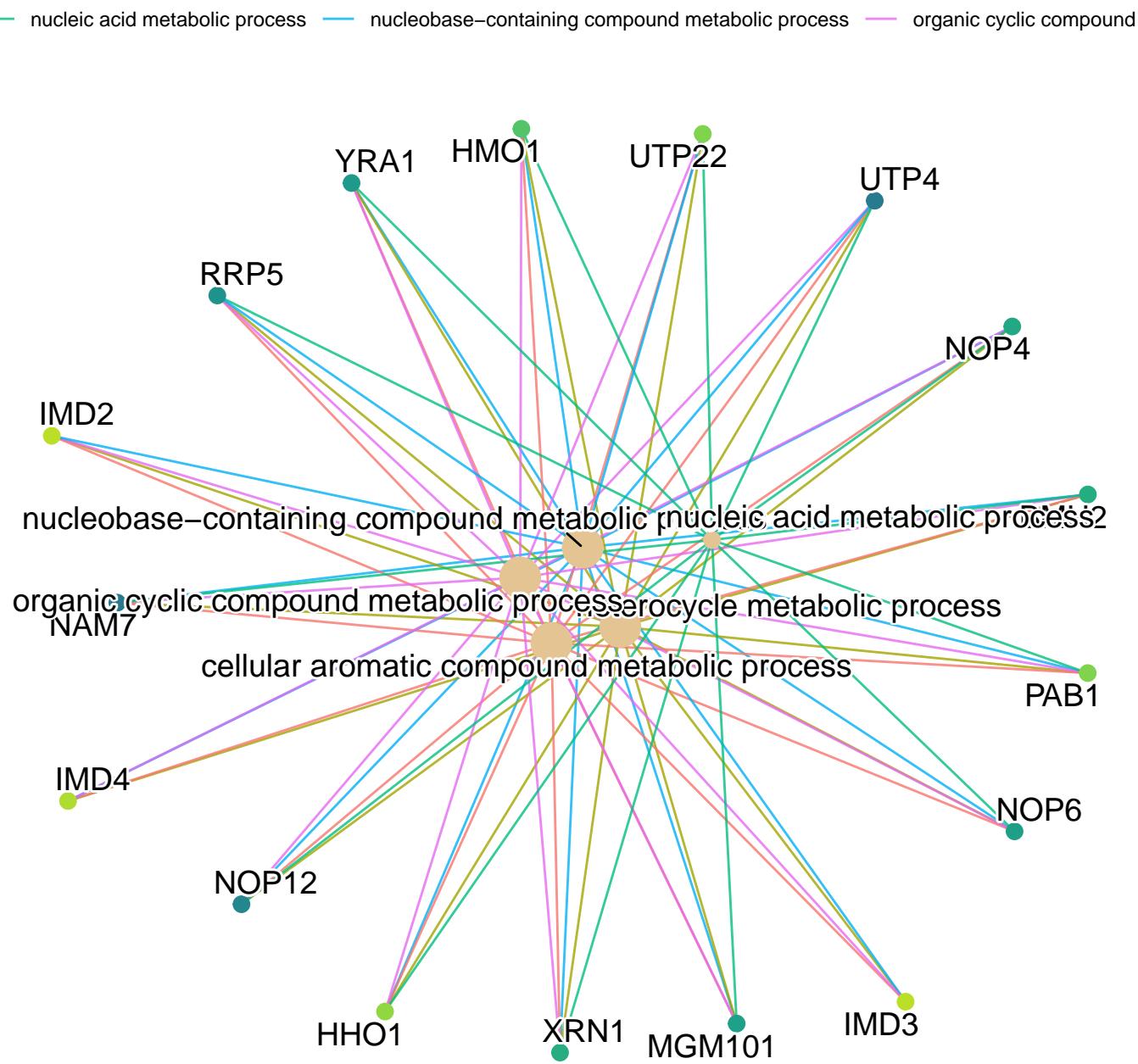
HSH49-TAP Up-regulated GO BP barplot



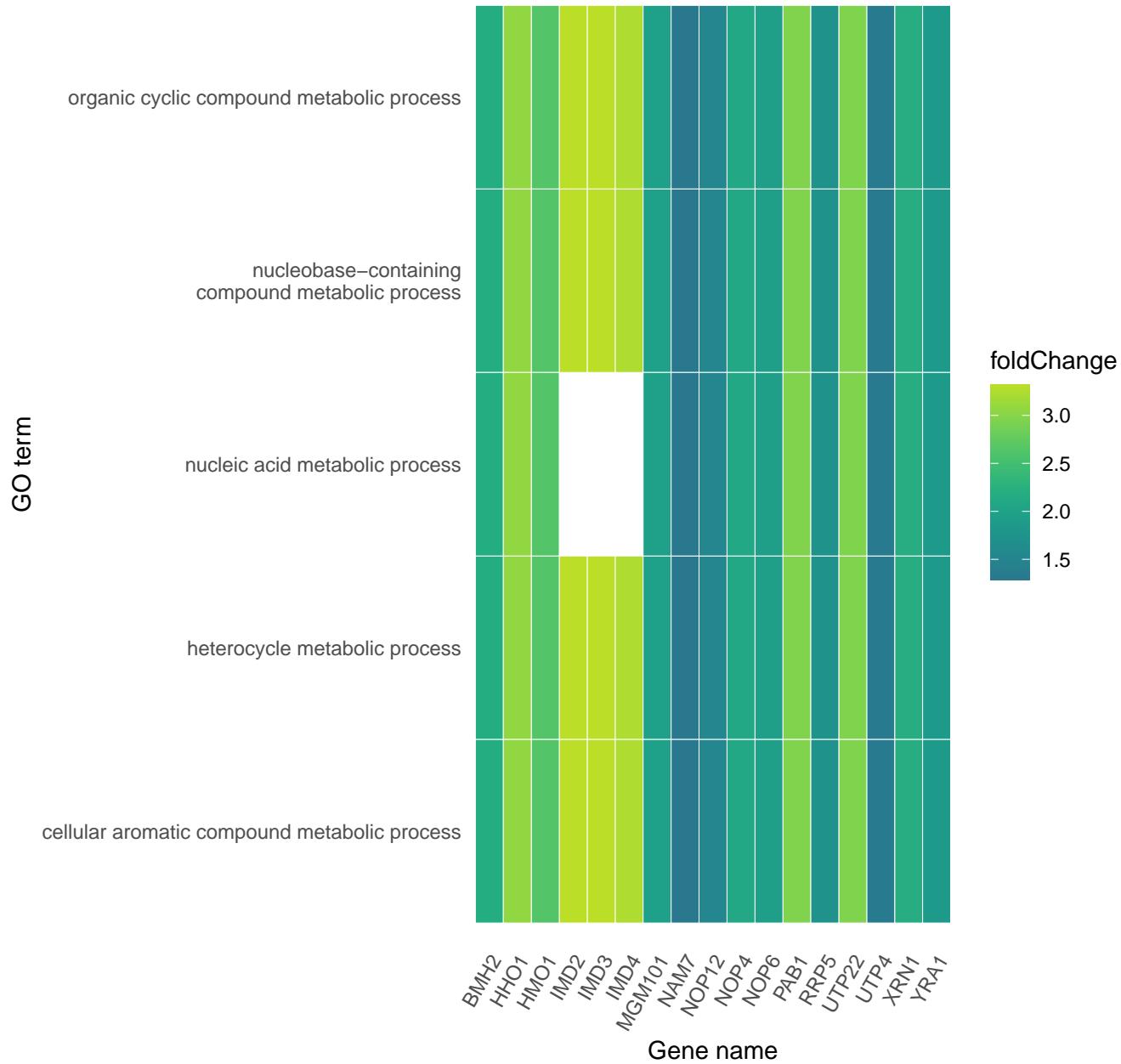
HSH49–TAP Up-regulated GO BP dotplot



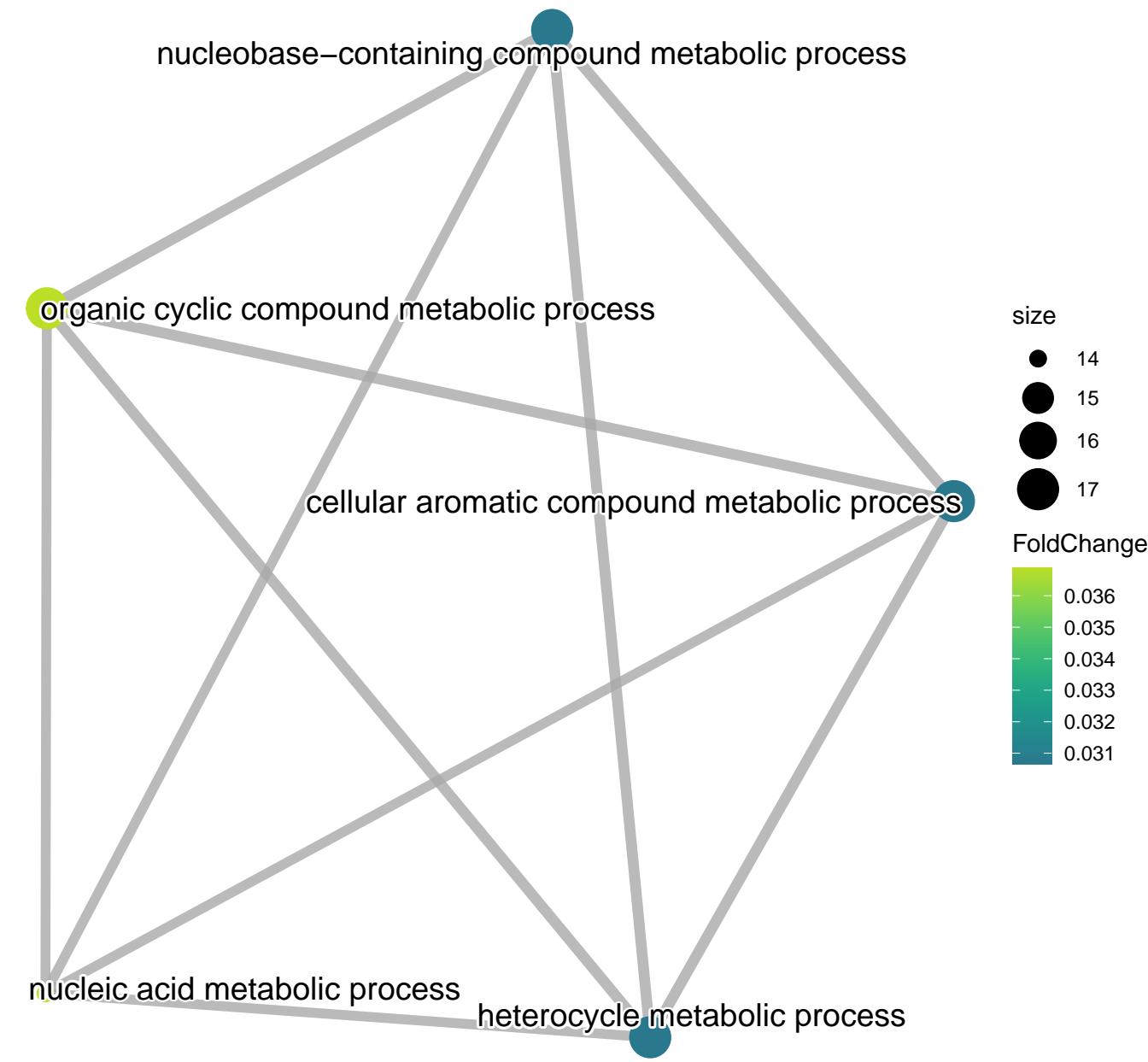
HSH49-TAP Up-regulated GO BP cnetplot

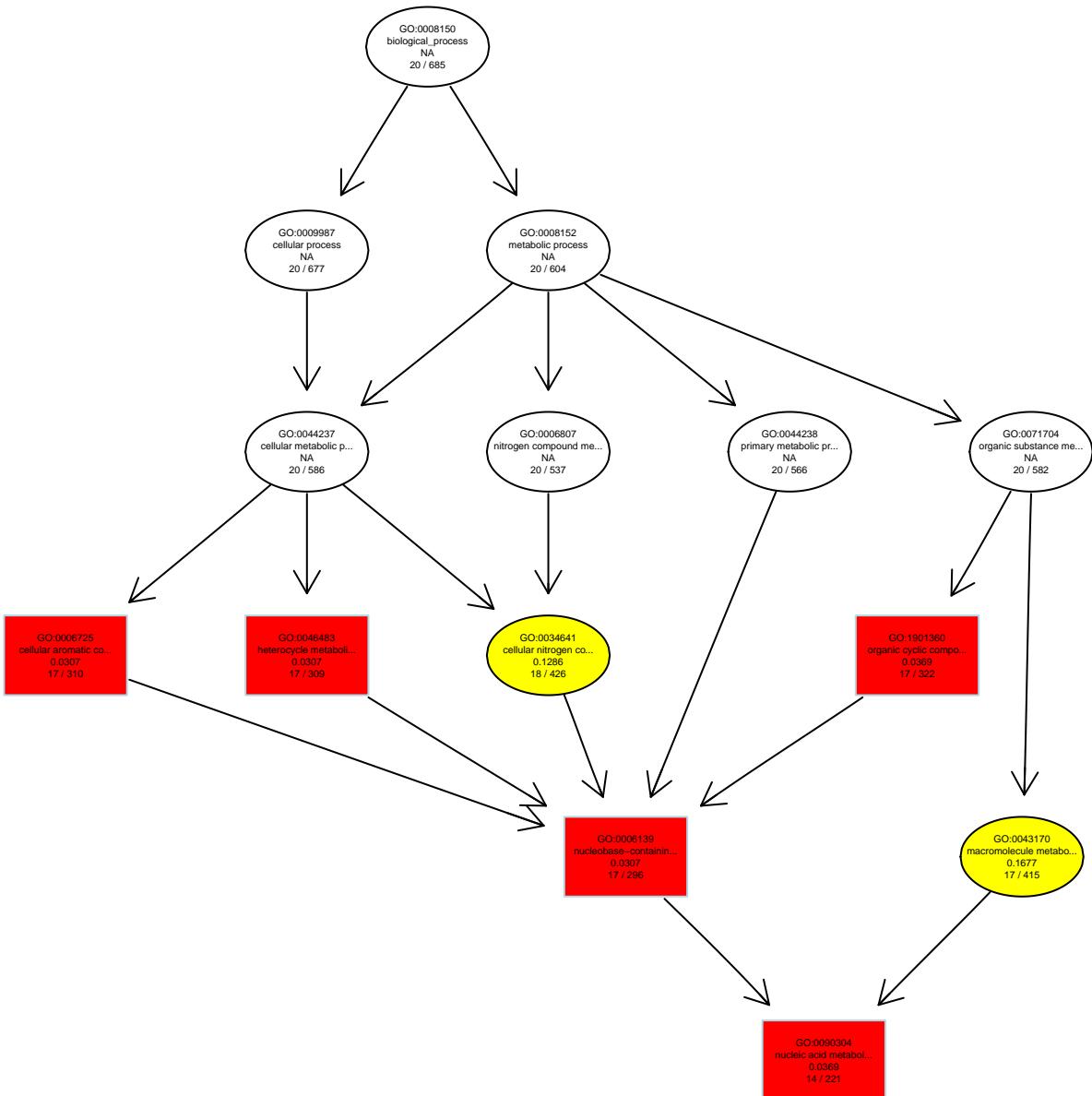


HSH49-TAP Up-regulated GO BP heatplot

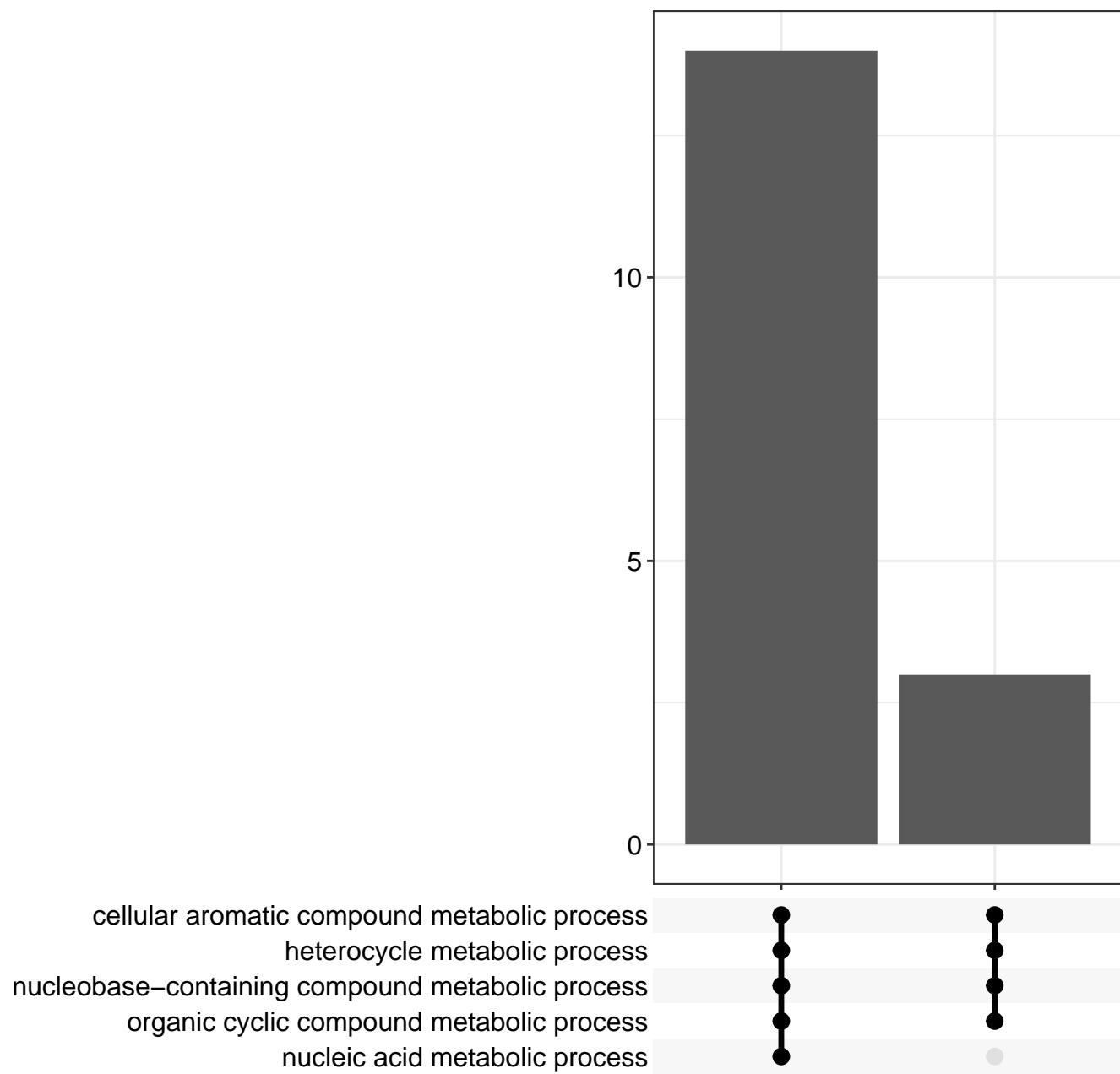


HSH49-TAP Up-regulated GO BP emapplot

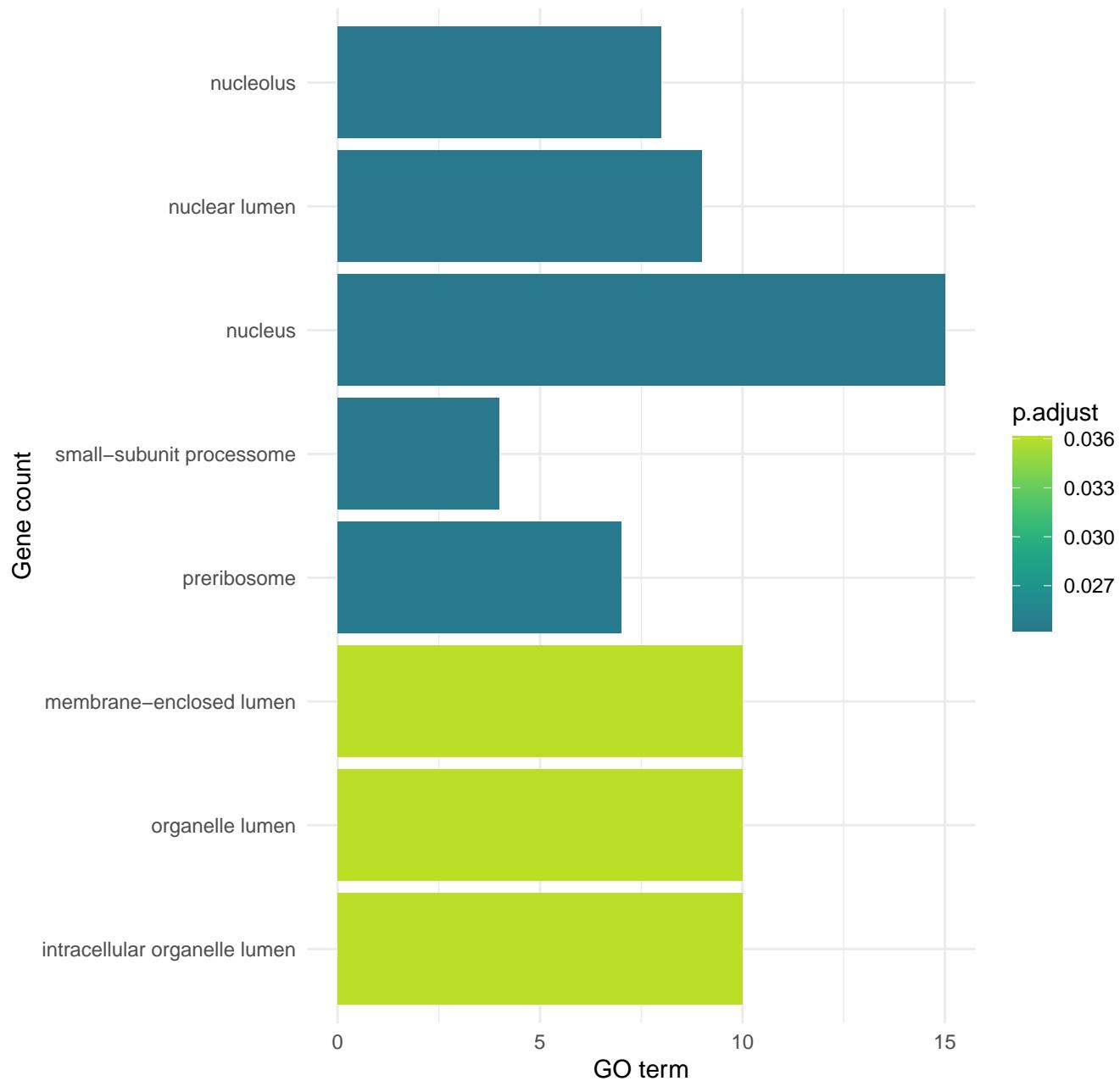




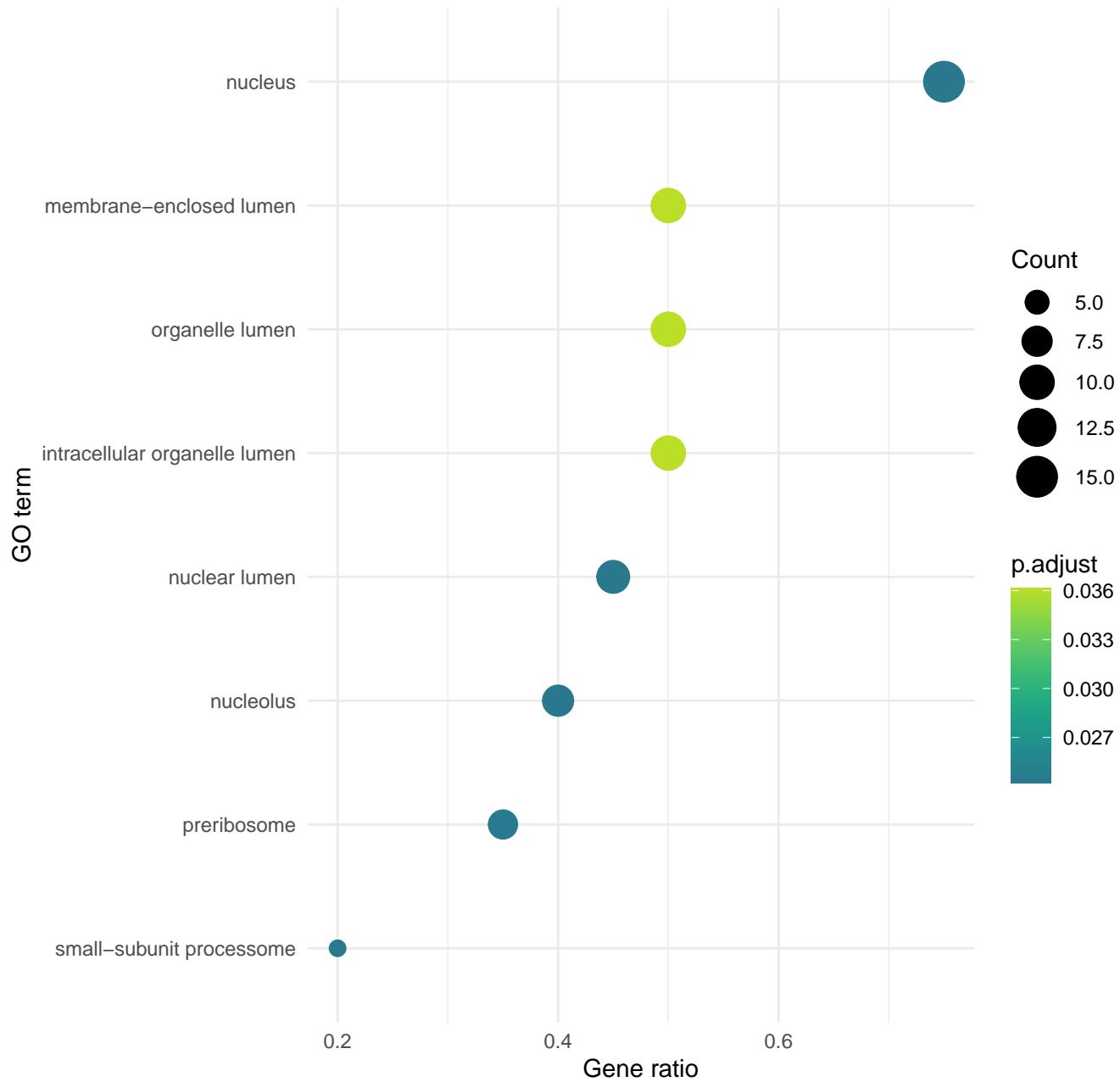
HSH49-TAP Up-regulated GO BP up



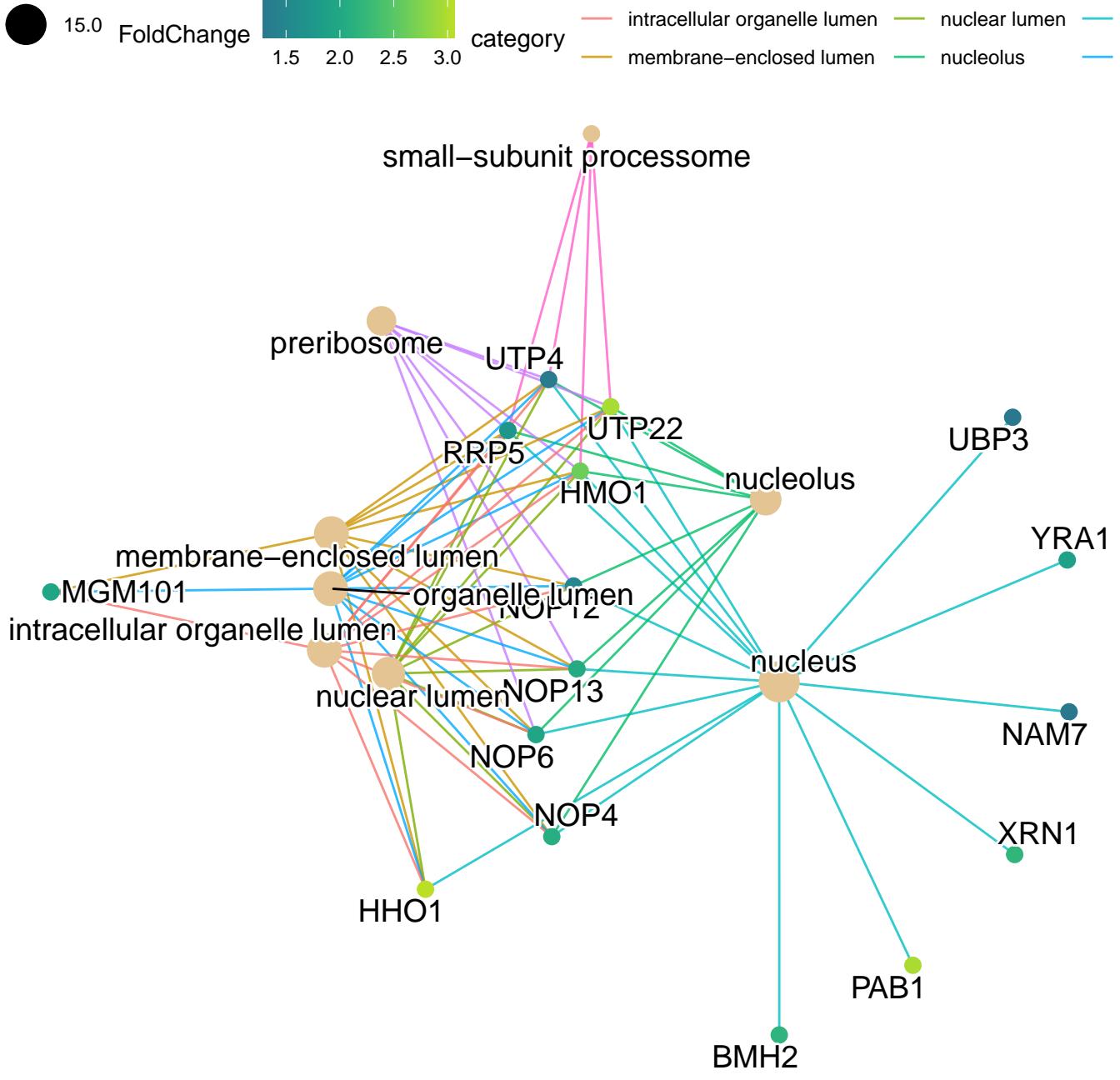
HSH49-TAP Up-regulated GO CC barplot



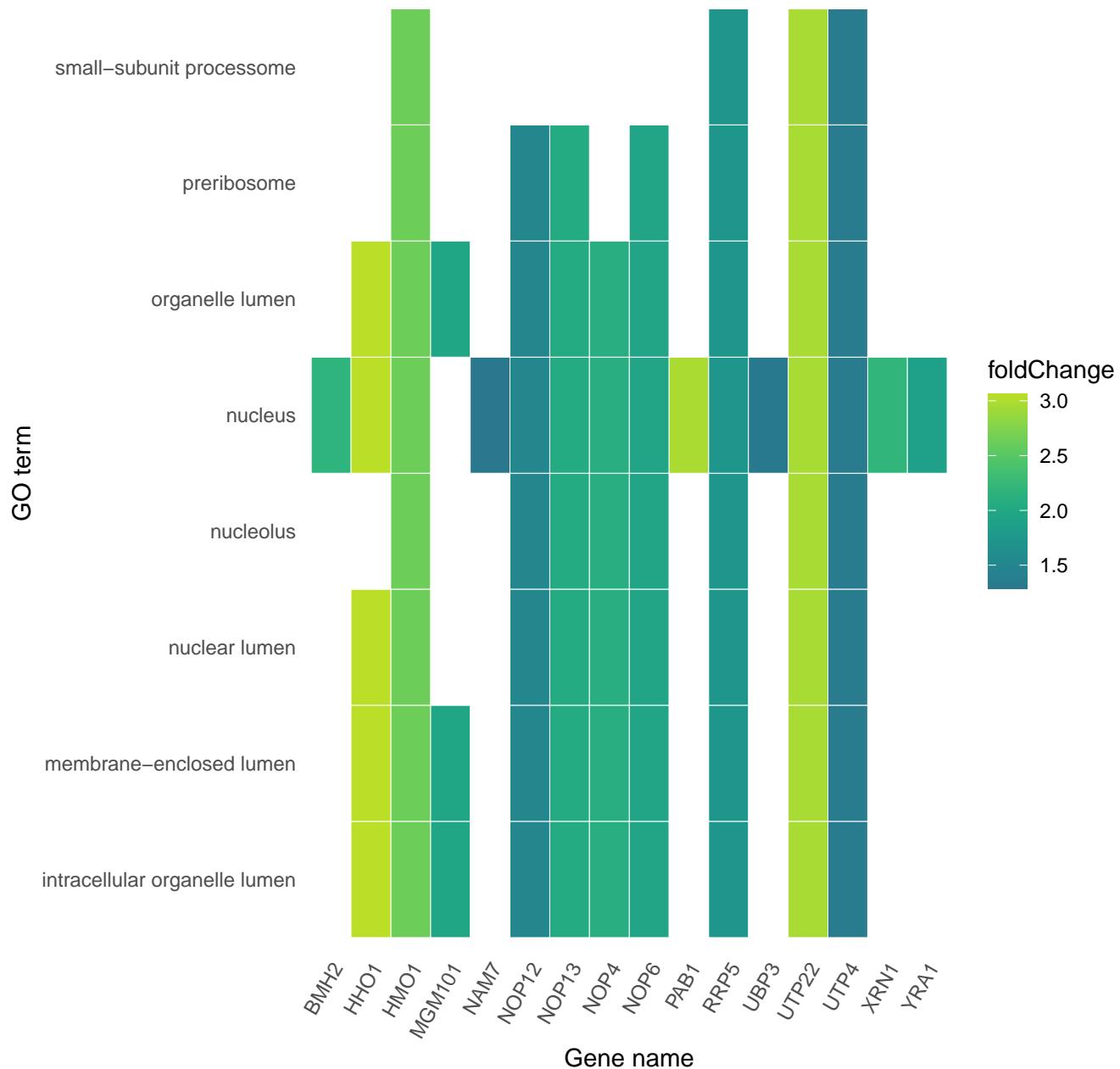
HSH49–TAP Up-regulated GO CC dotplot



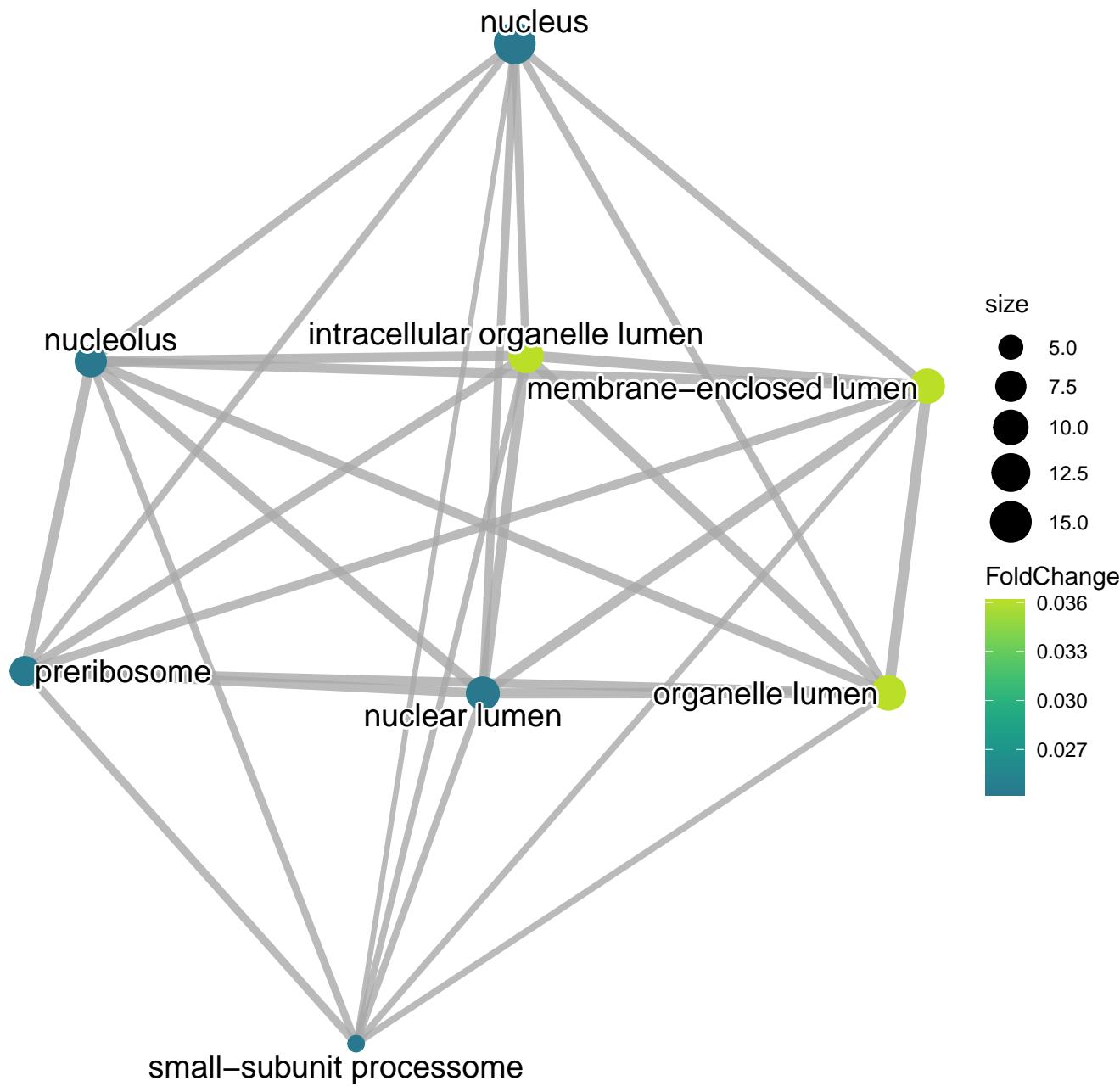
HSH49-TAP Up-regulated GO CC cnetplot

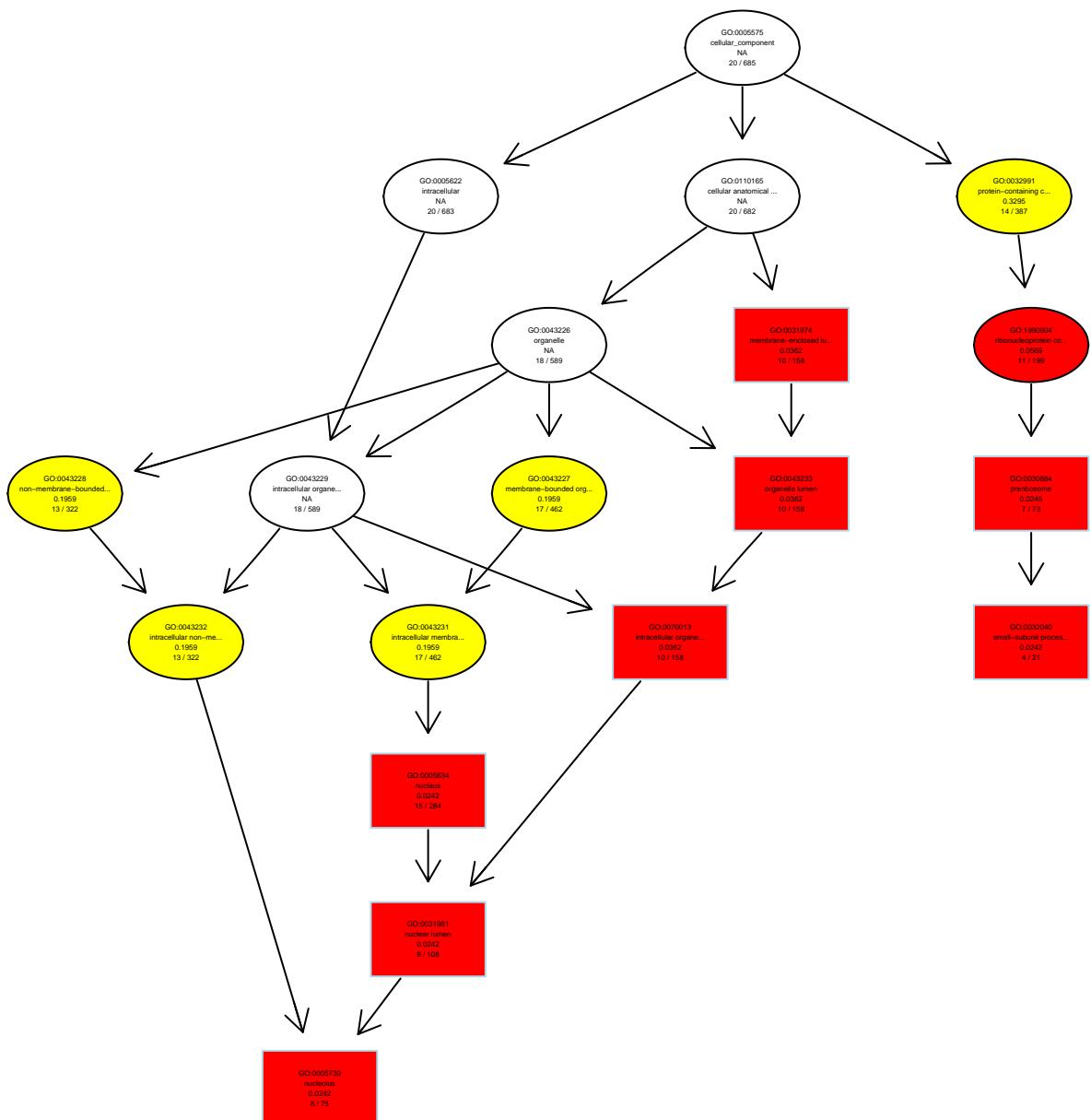


HSH49-TAP Up-regulated GO CC heatplot

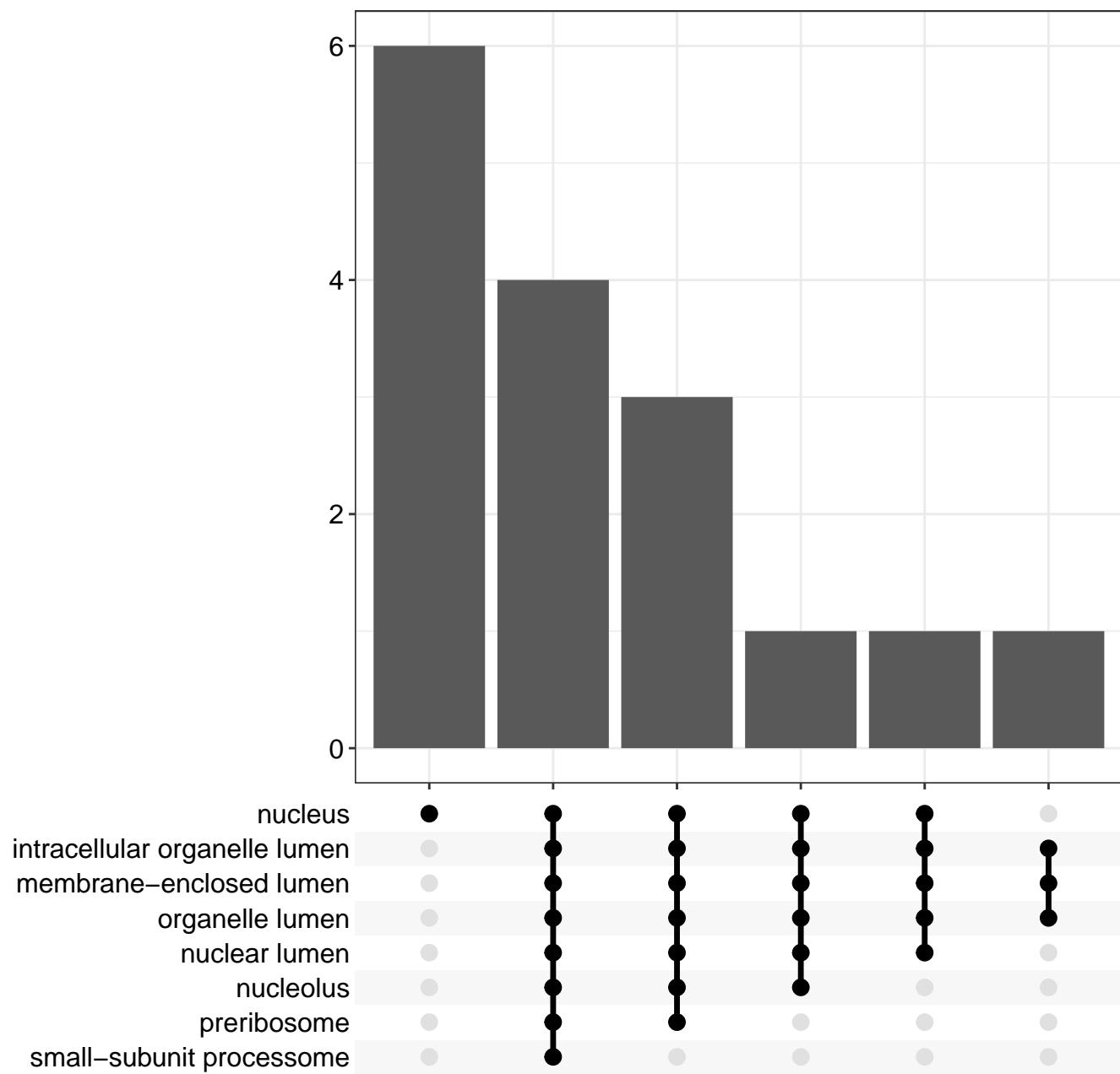


HSH49-TAP Up-regulated GO CC emapplot

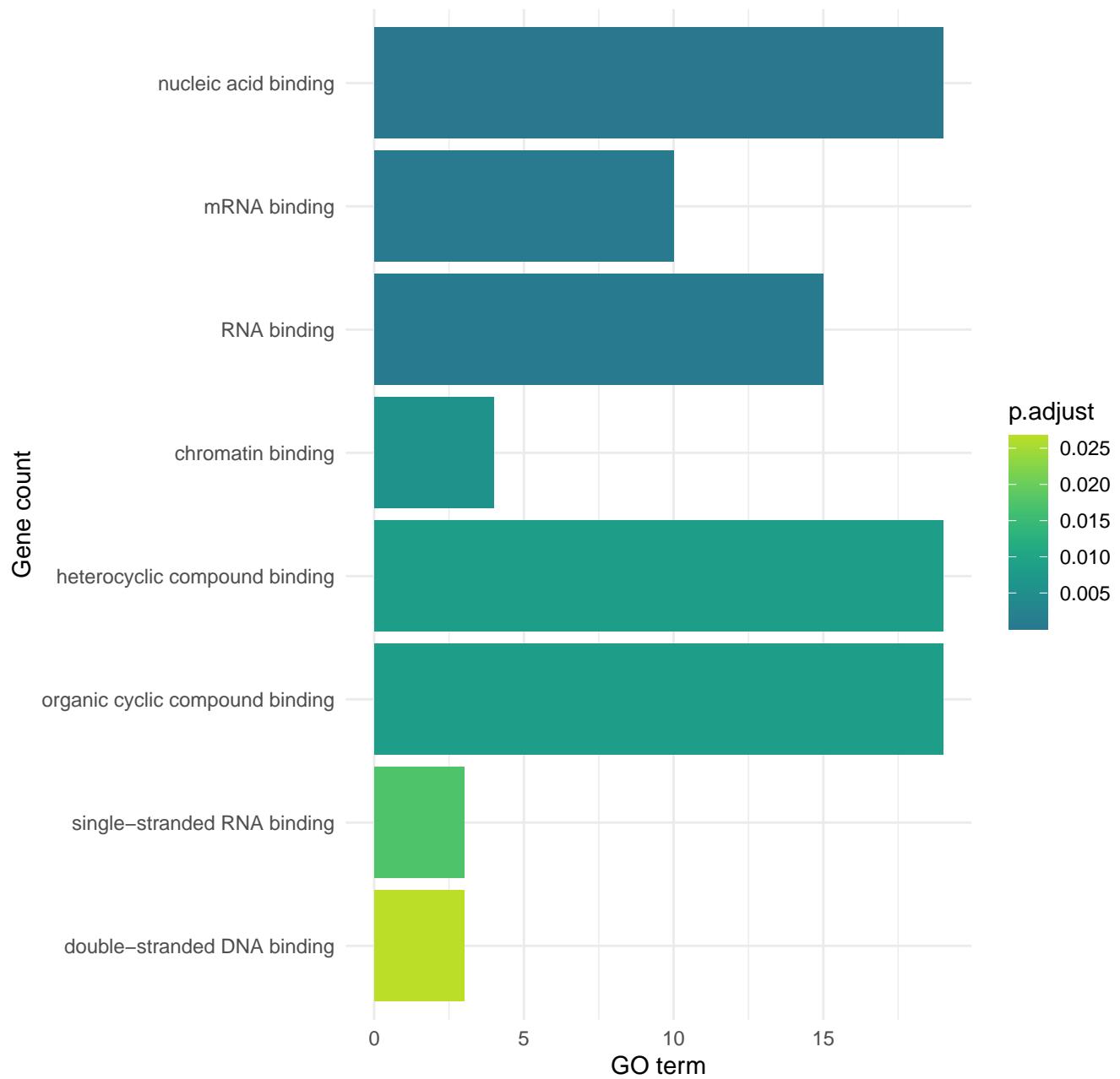




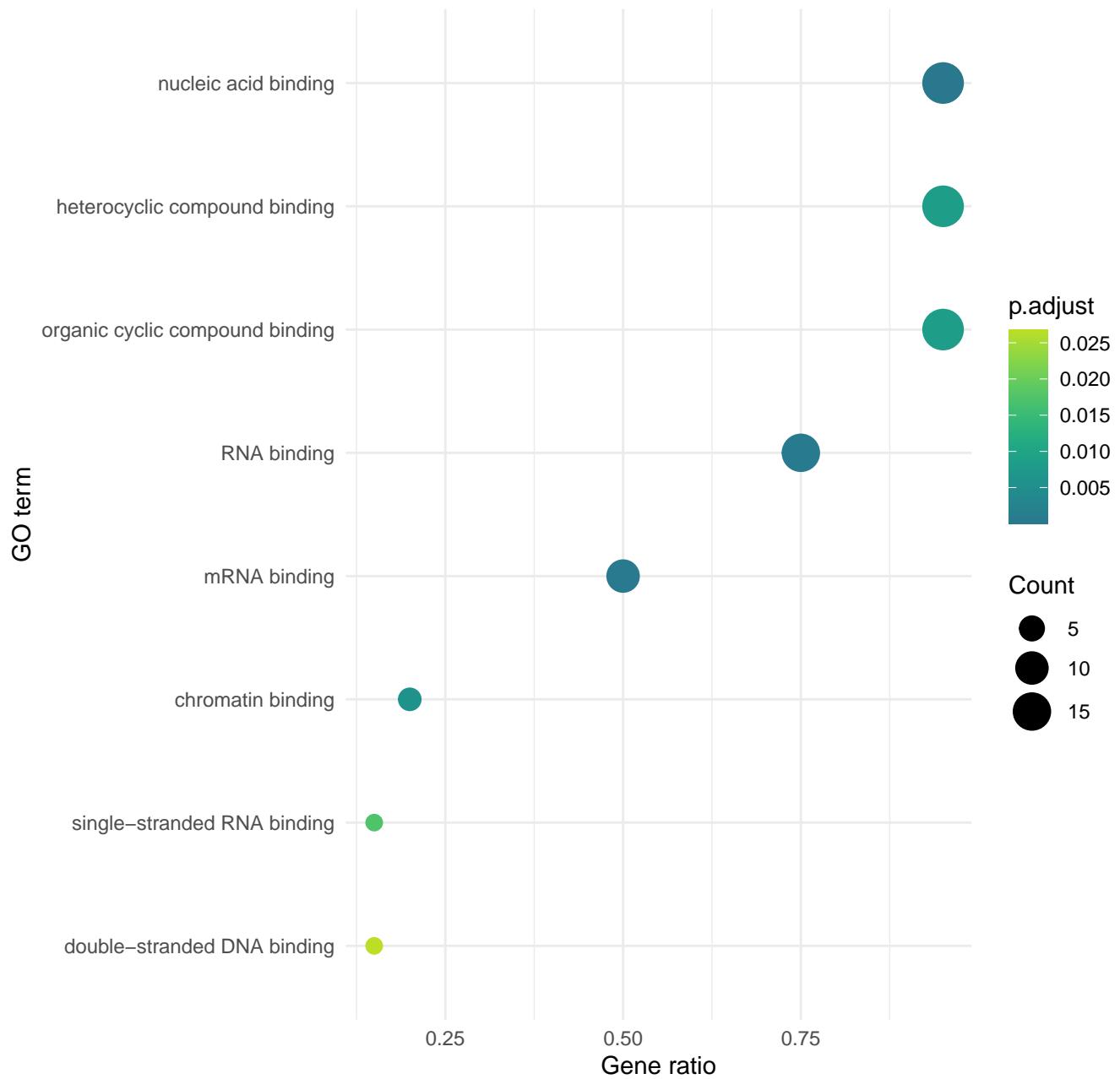
HSH49-TAP Up-regulated GO CC upsetplot



HSH49-TAP Up-regulated GO MF barplot



HSH49-TAP Up-regulated GO MF dotplot



HSH49-TAP Up-regulated GO MF cnetplot

chromatin binding

heterocyclic compound binding

nucleic acid binding

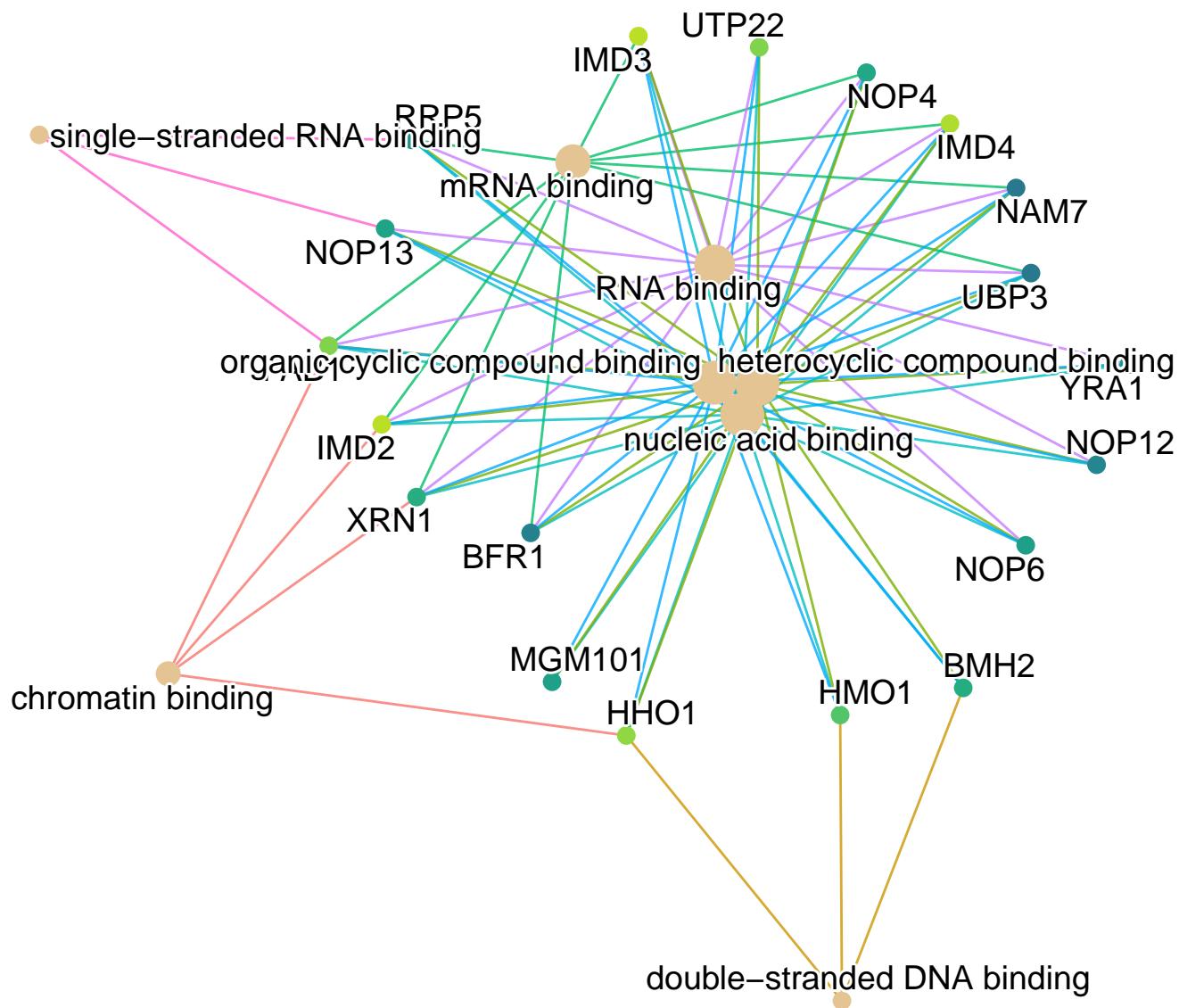
RNA binding

double-stranded DNA binding

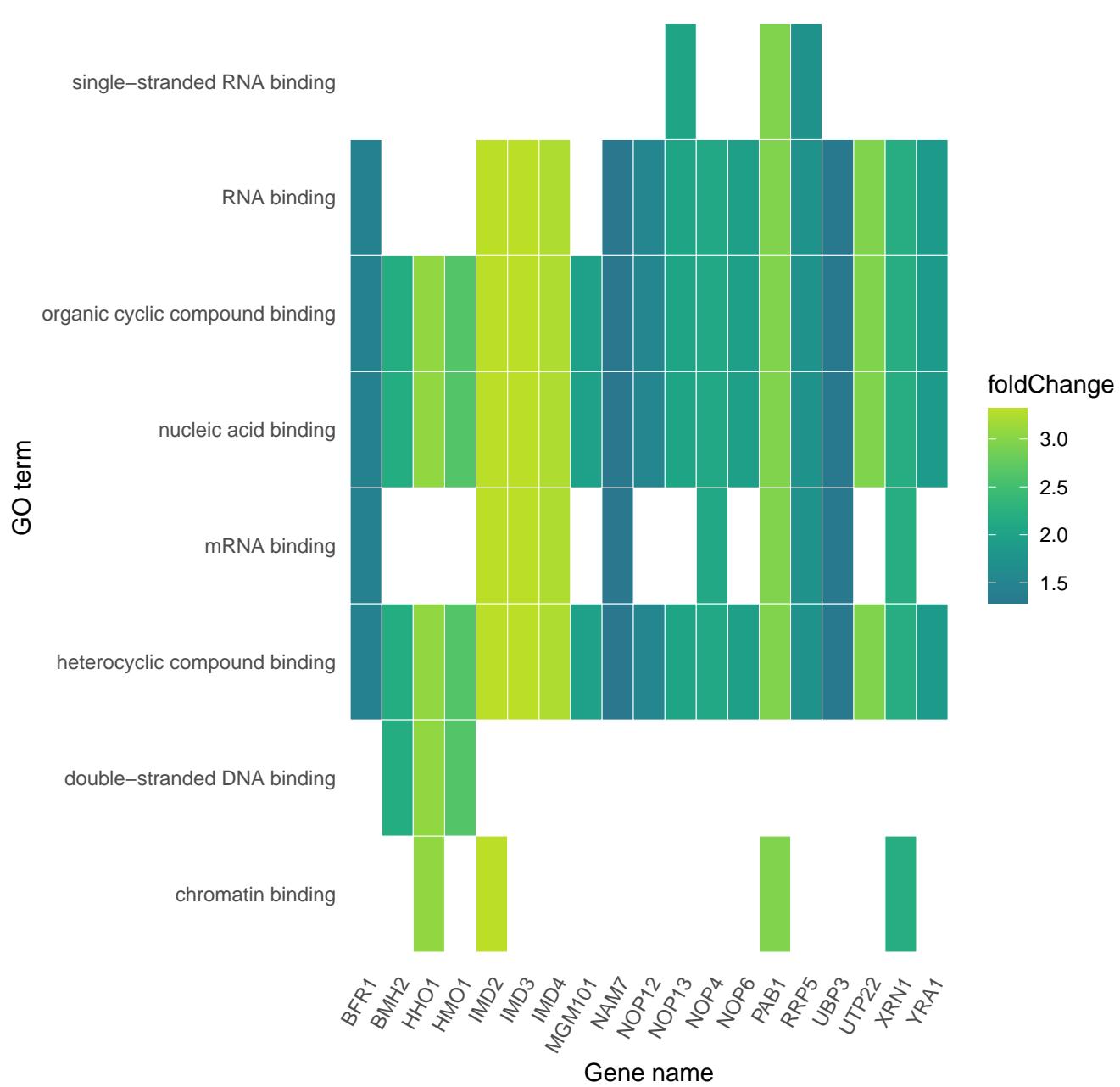
mRNA binding

organic cyclic compound binding

single-stranded

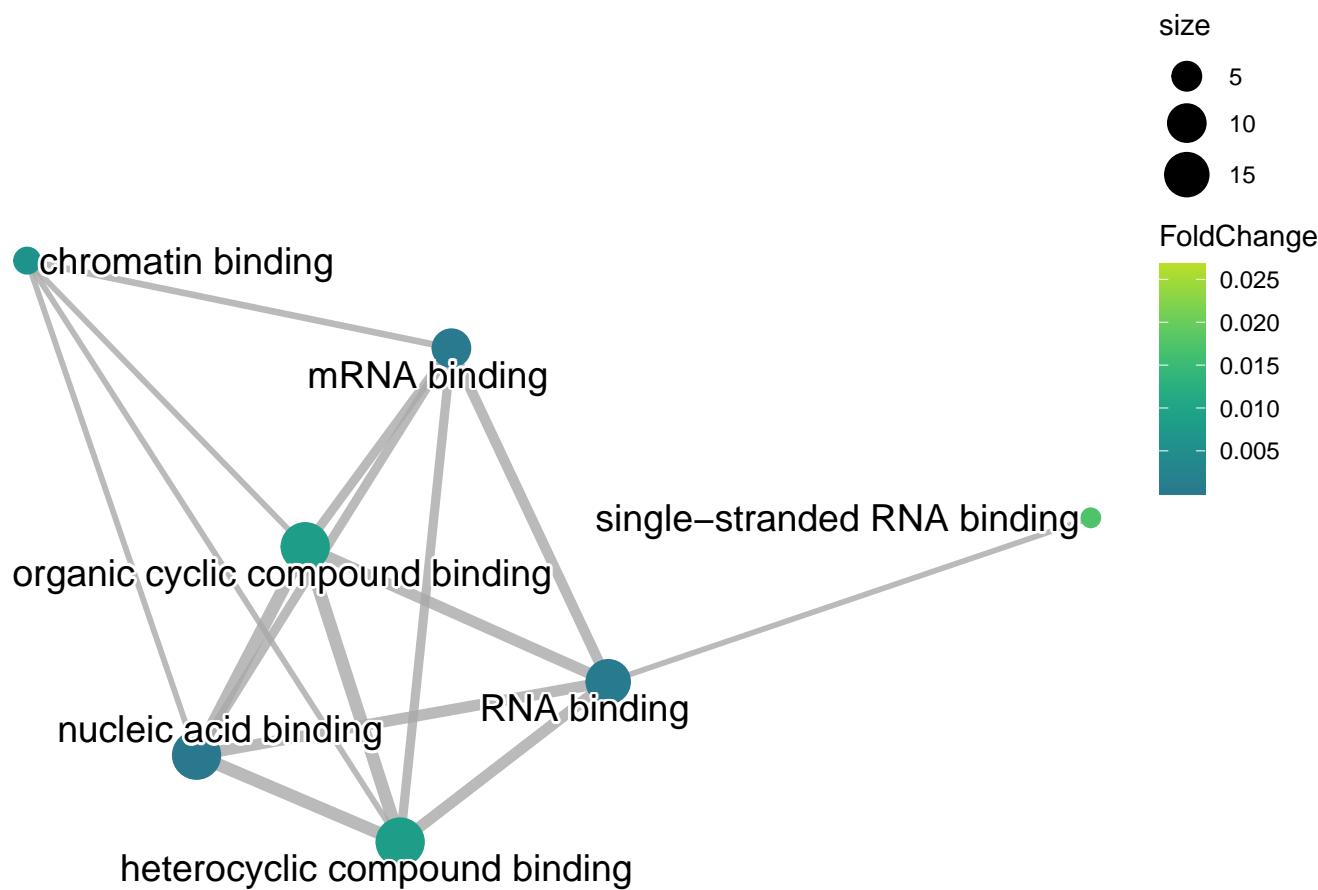


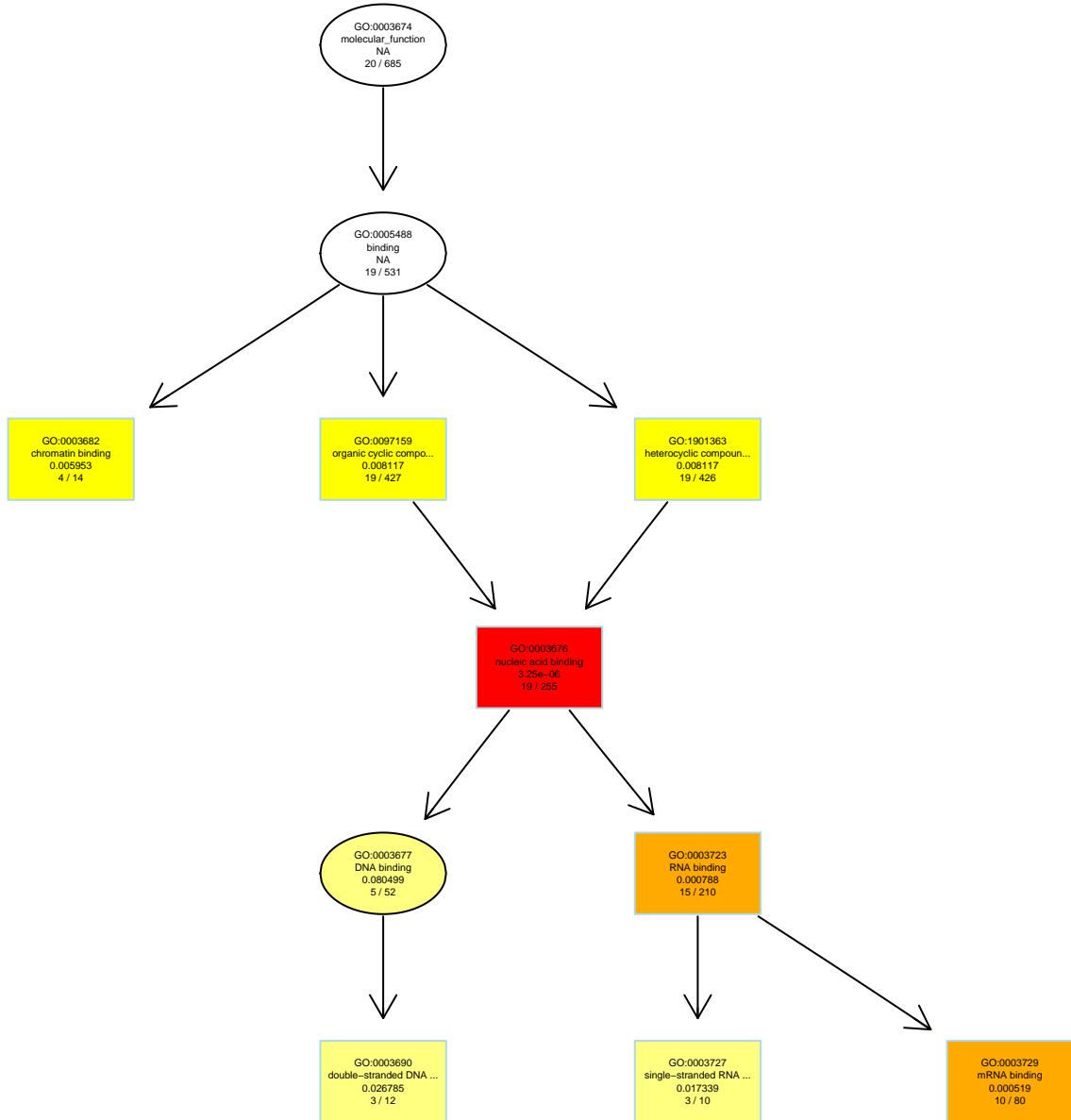
HSH49-TAP Up-regulated GO MF heatplot



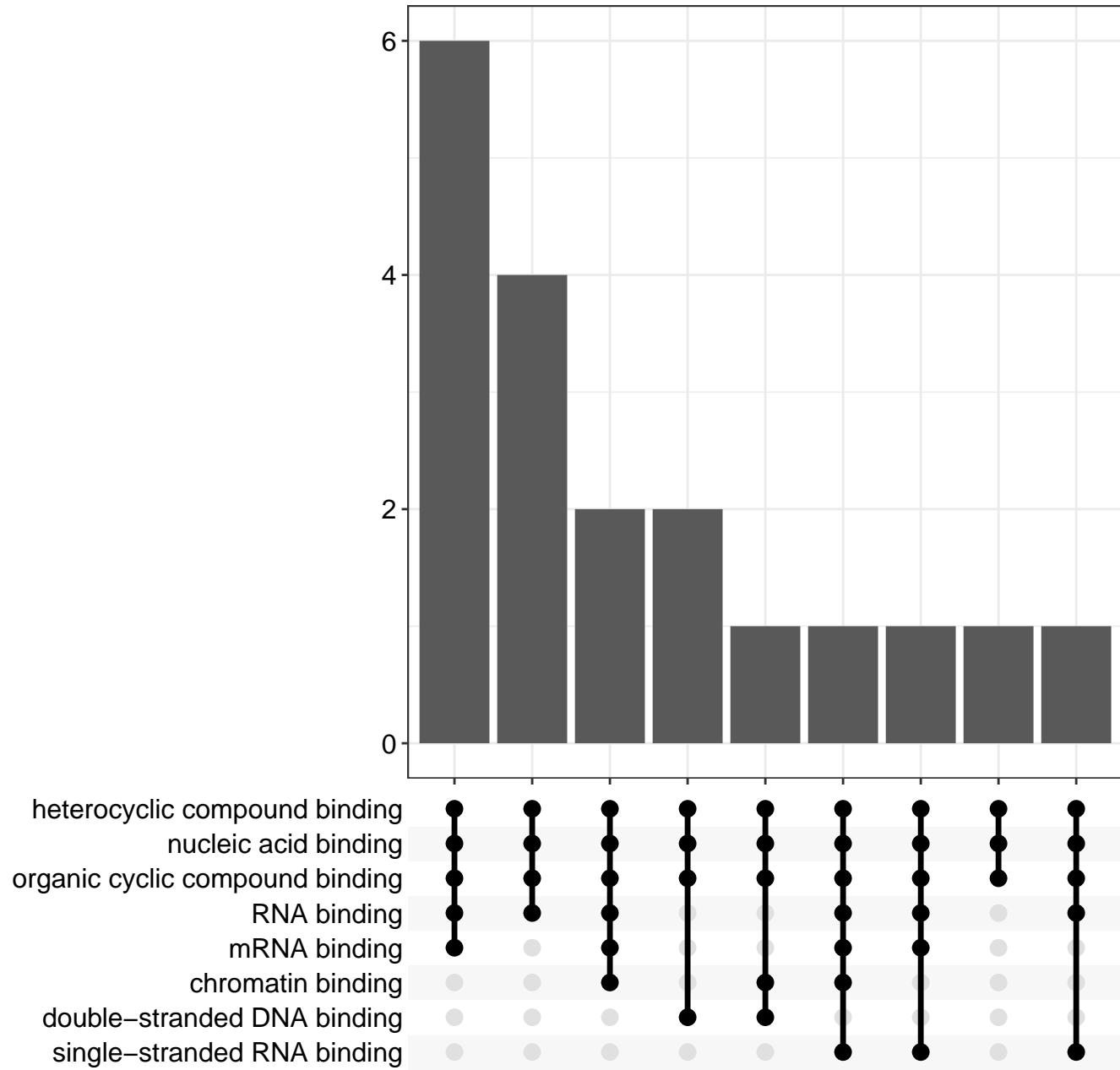
HSH49-TAP Up-regulated GO MF emapplot

double-stranded DNA binding

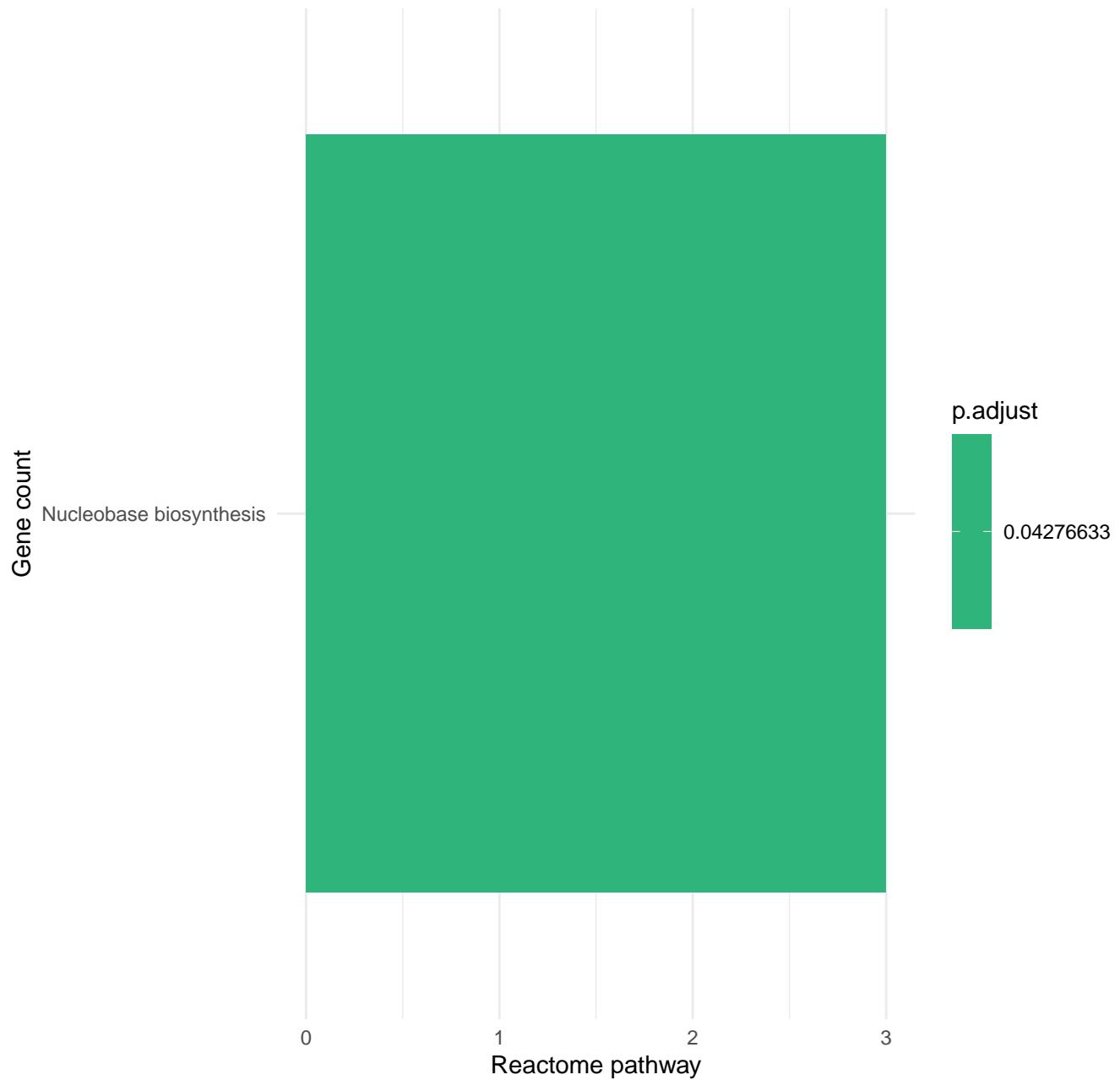




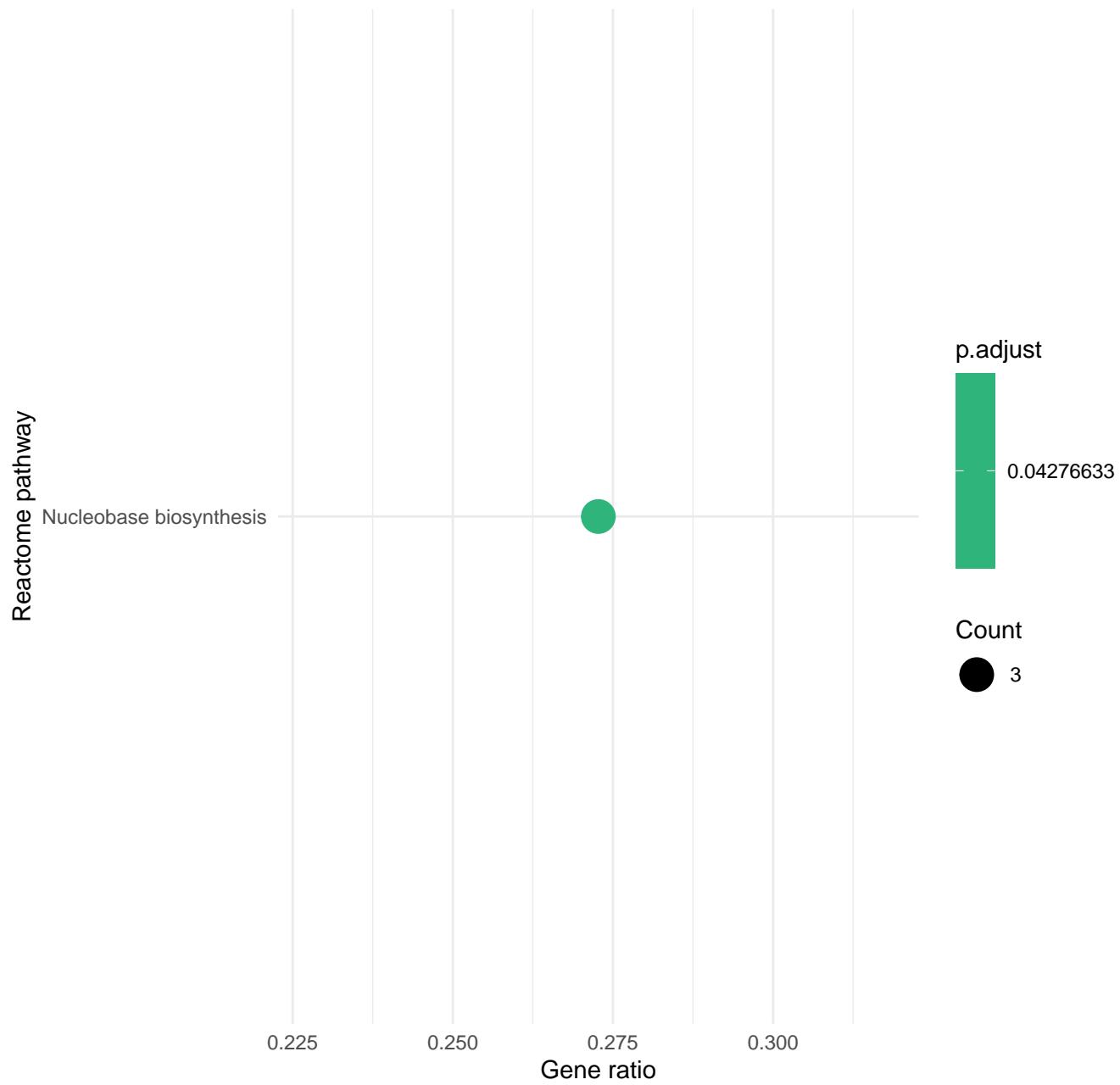
HSH49-TAP Up-regulated GO MF upsetplot



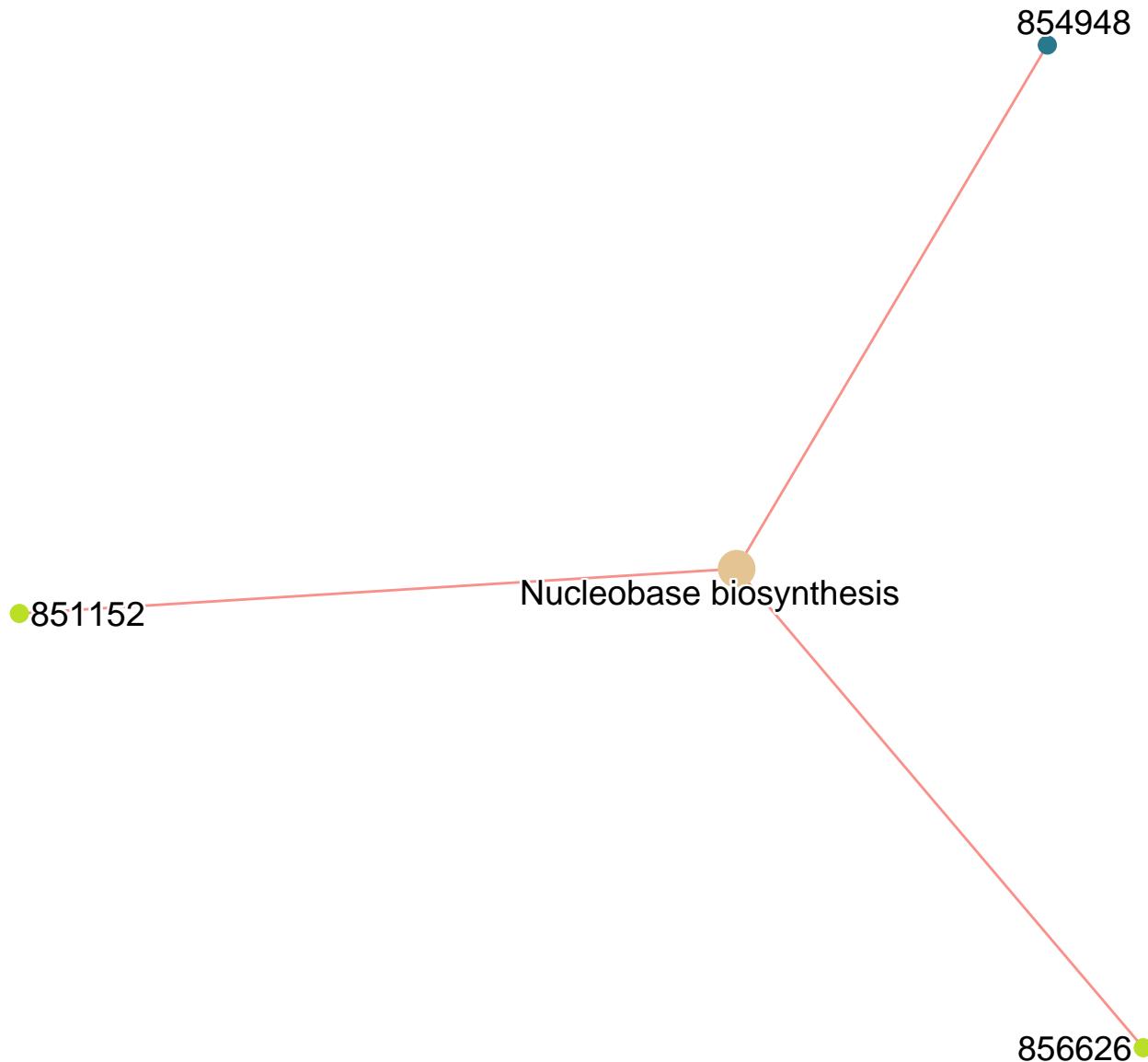
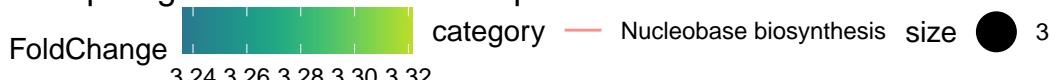
HSH49-TAP Up-regulated Reactome barplot



HSH49–TAP Up-regulated Reactome dotplot



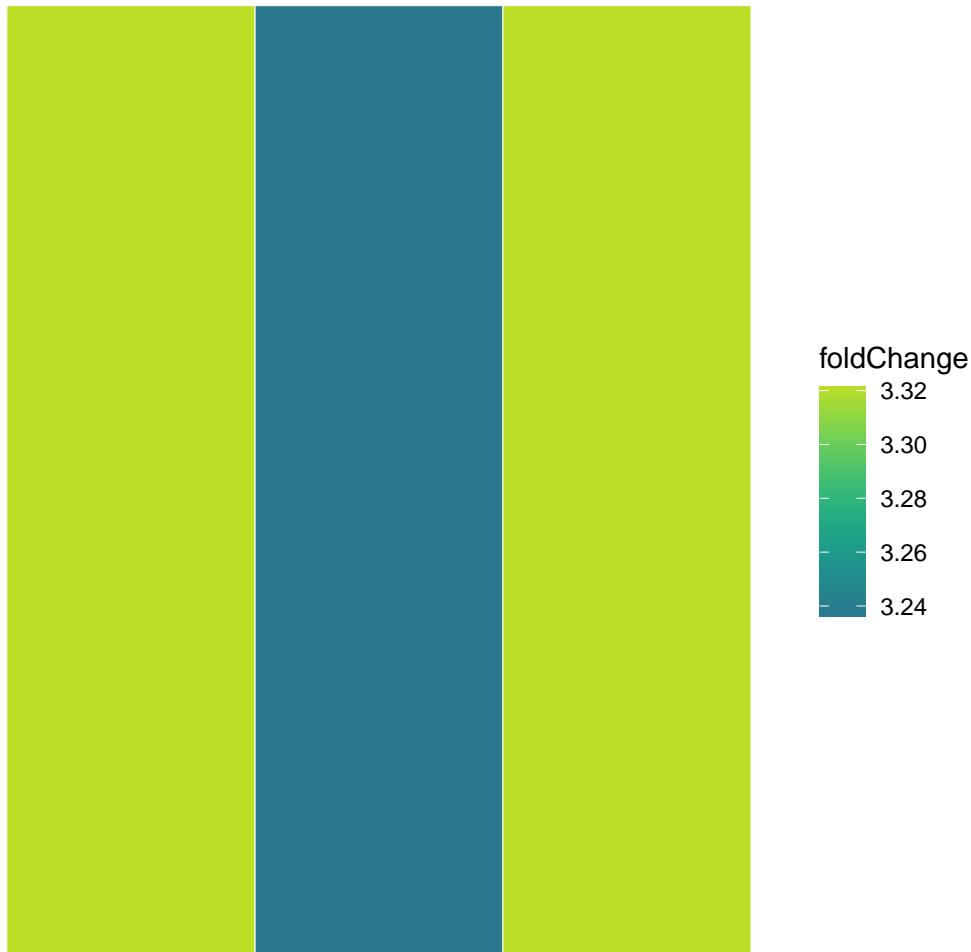
HSH49-TAP Up-regulated Reactome cnetplot



HSH49–TAP Up-regulated Reactome heatplot

Reactome pathway

Nucleobase biosynthesis



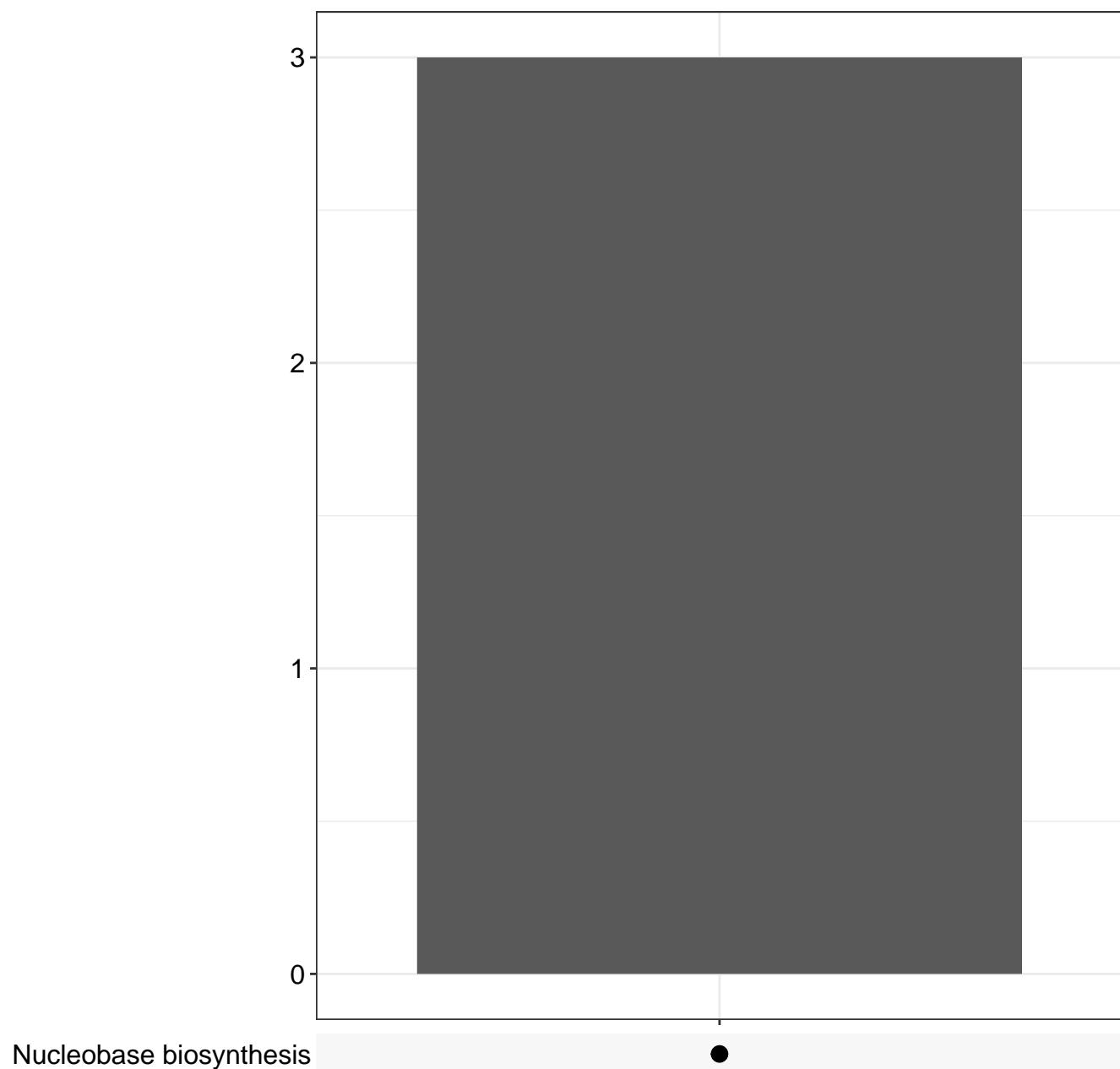
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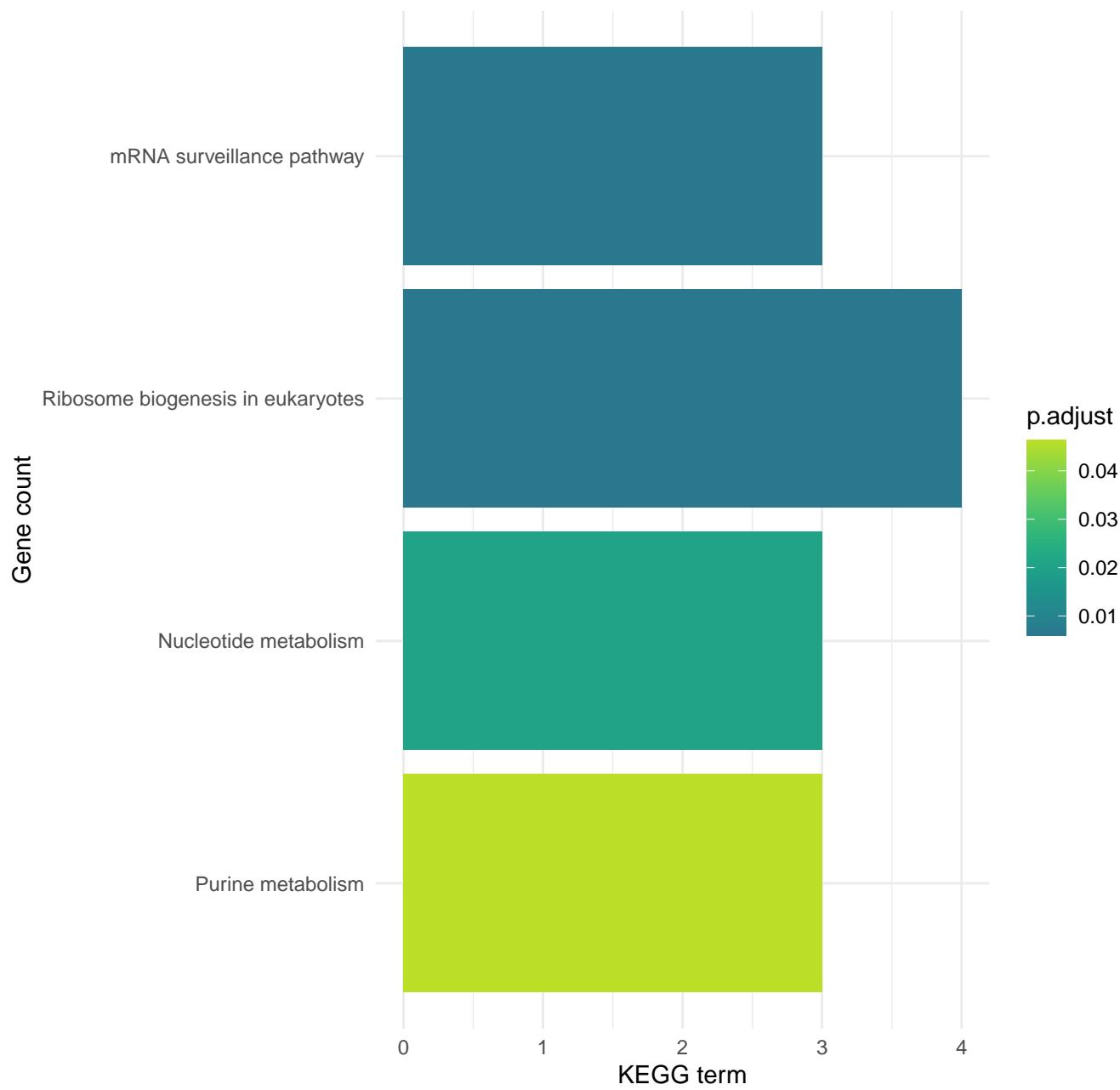
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entrez ID

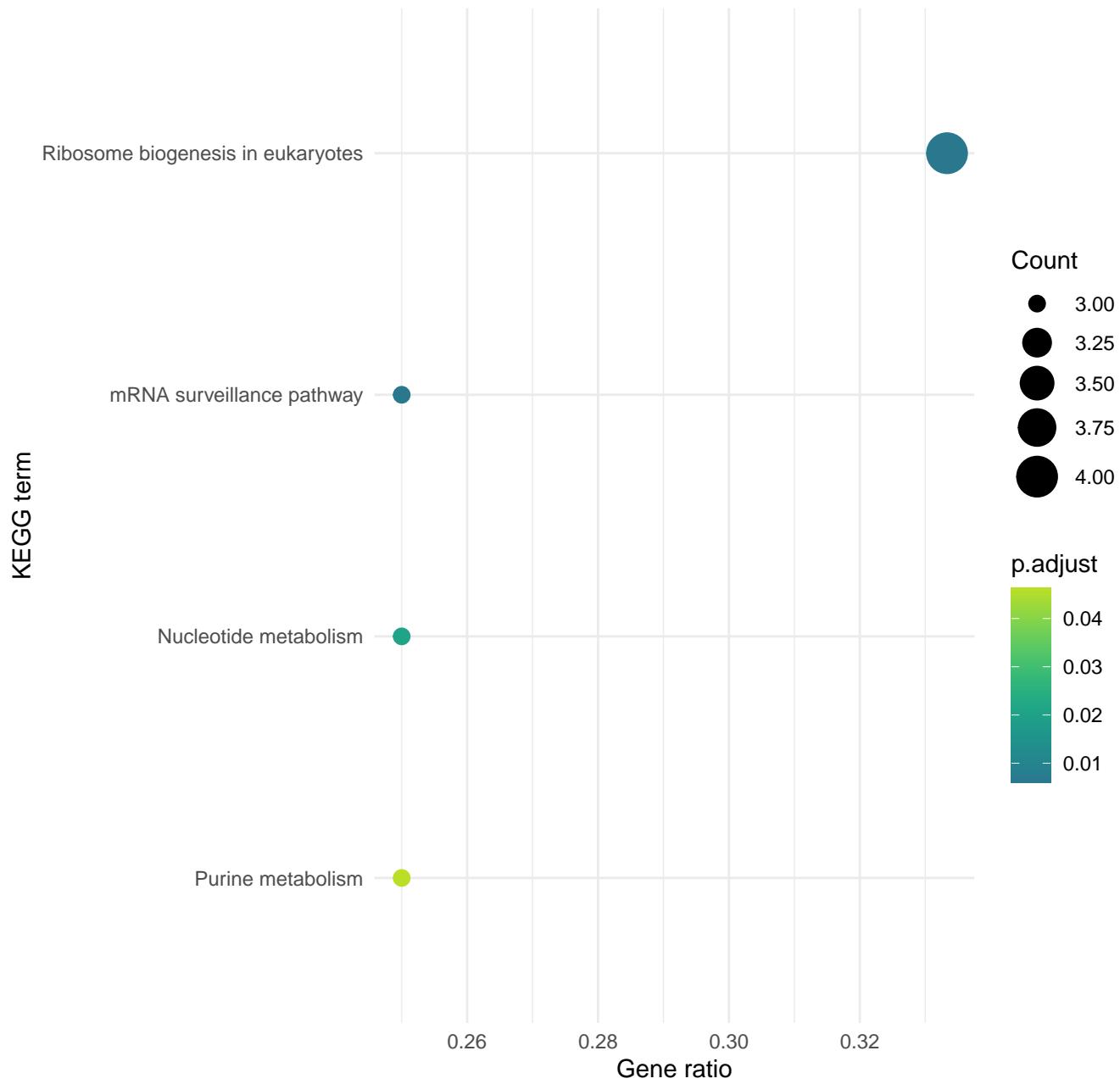
HSH49–TAP Up-regulated Reactome upsetplot



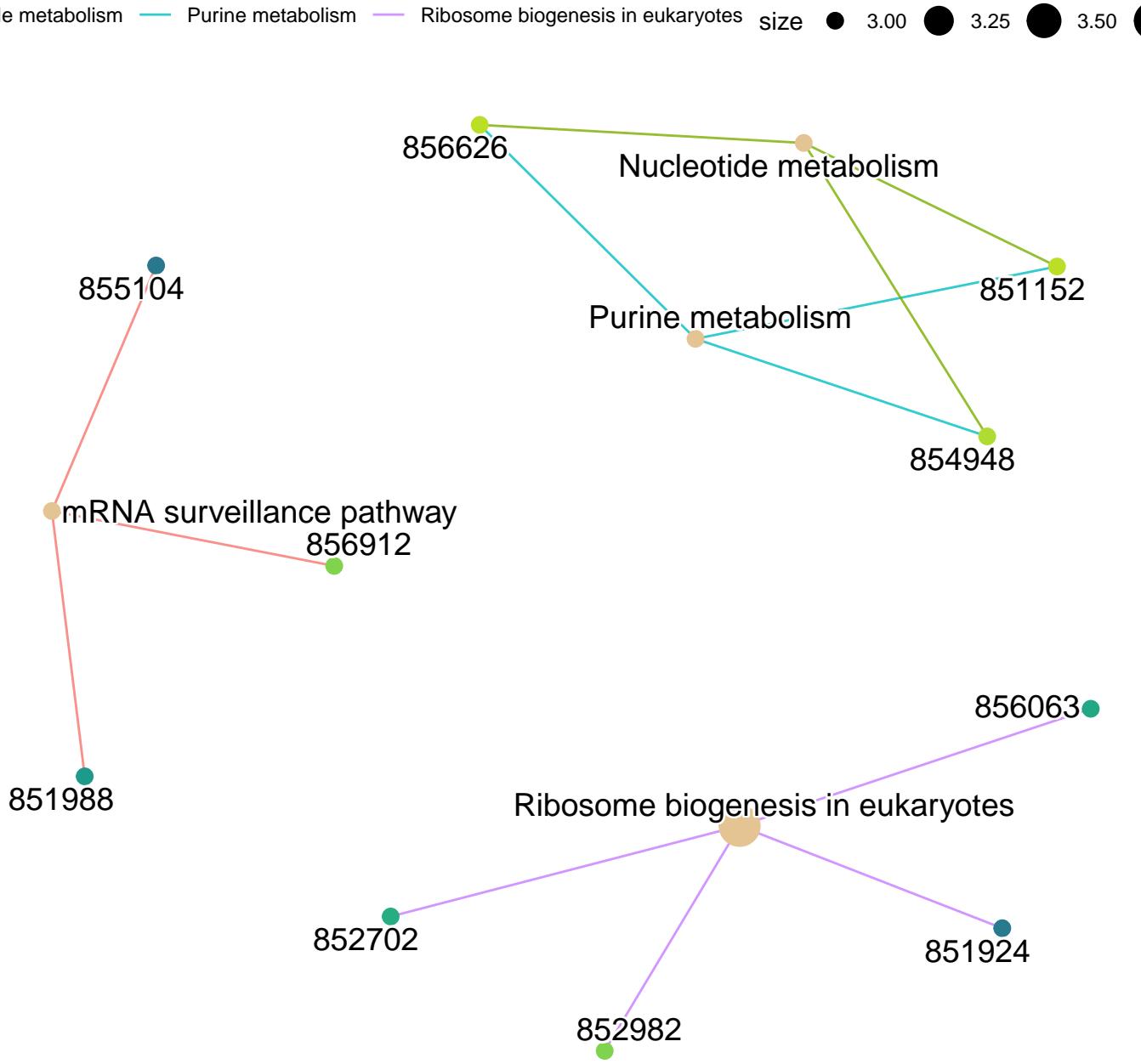
HSH49-TAP Up-regulated KEGG barplot



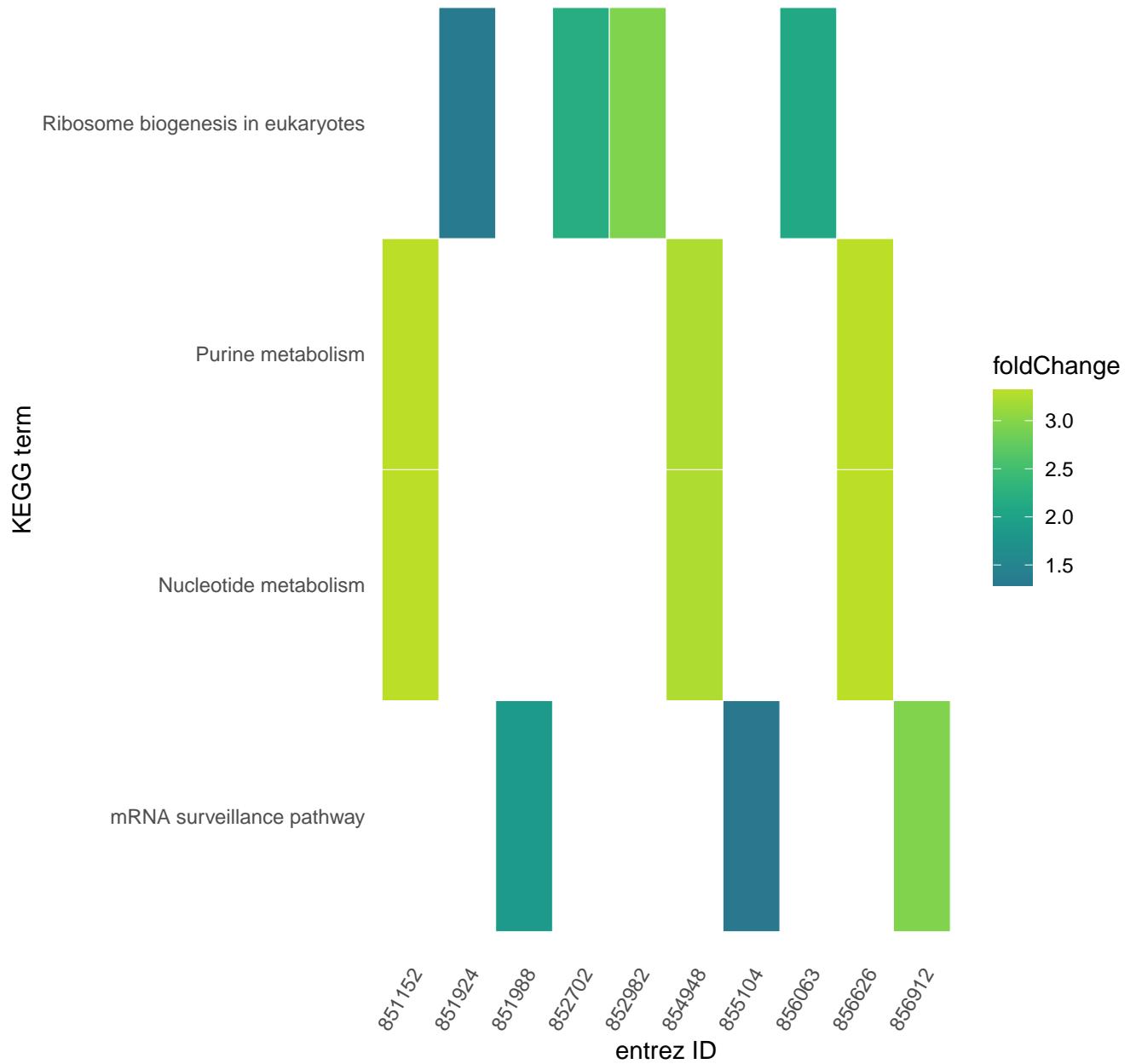
HSH49-TAP Up-regulated KEGG dotplot



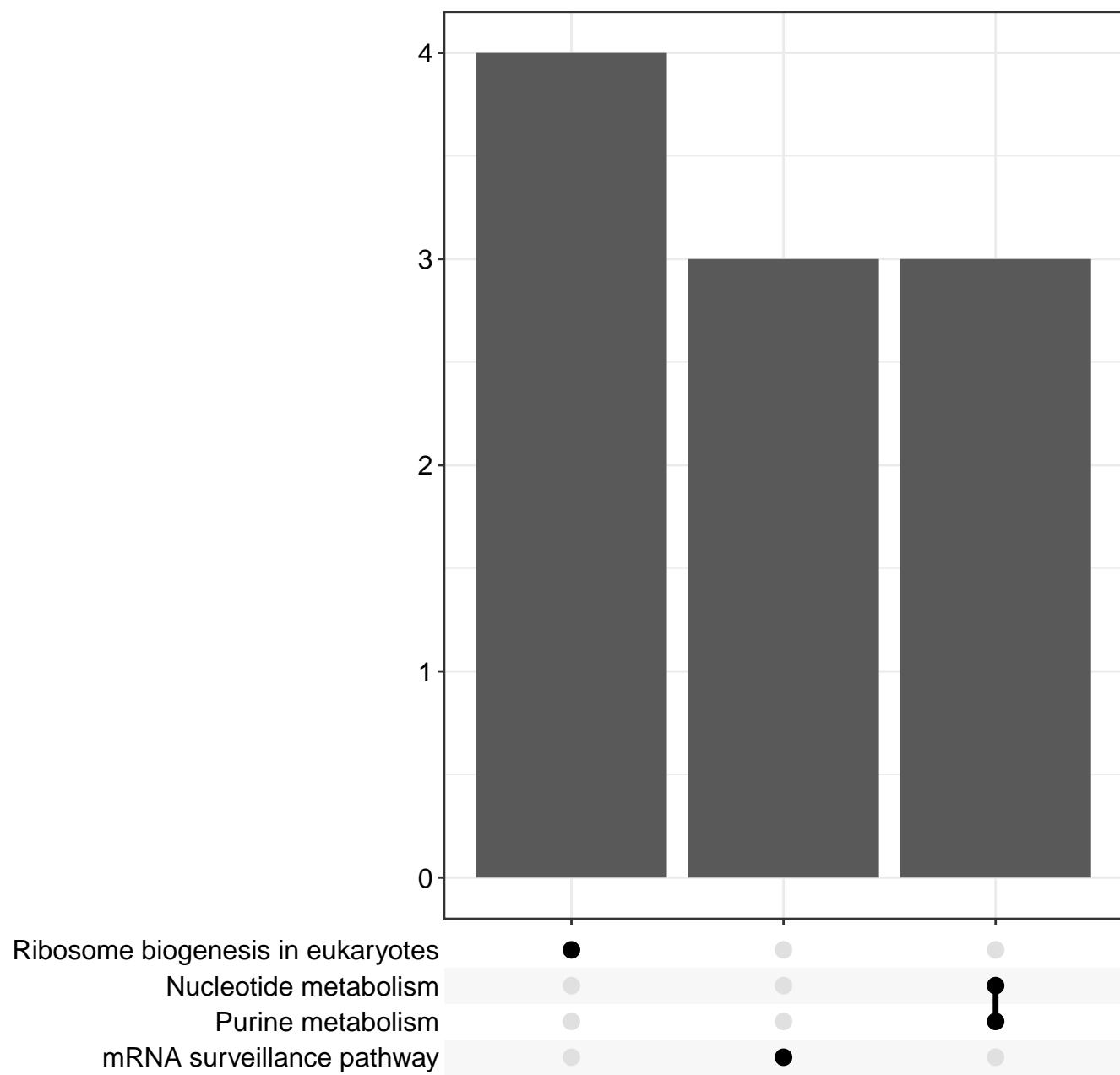
HSH49-TAP Up-regulated KEGG dotplot



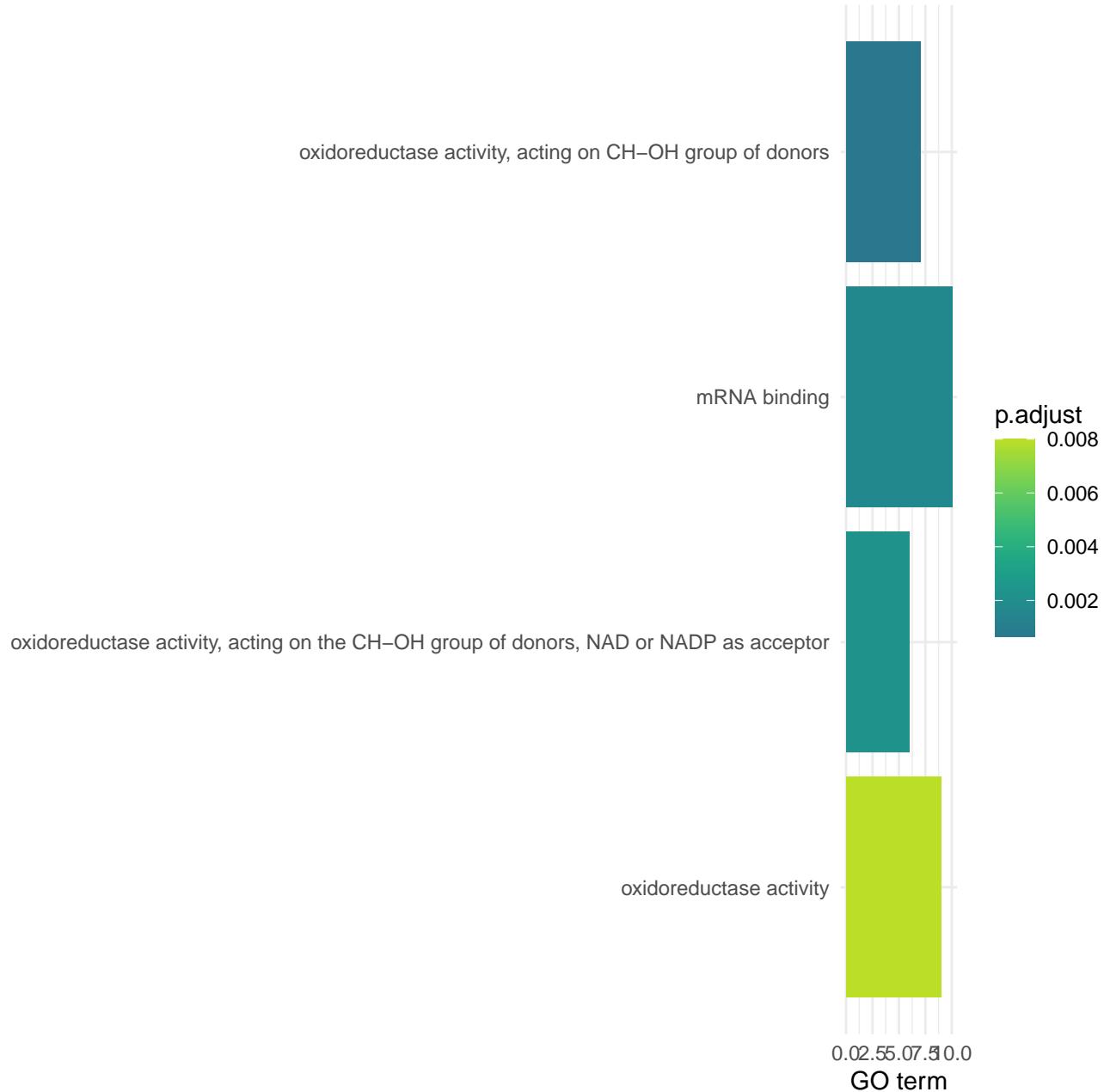
HSH49-TAP Up-regulated KEGG heatplot

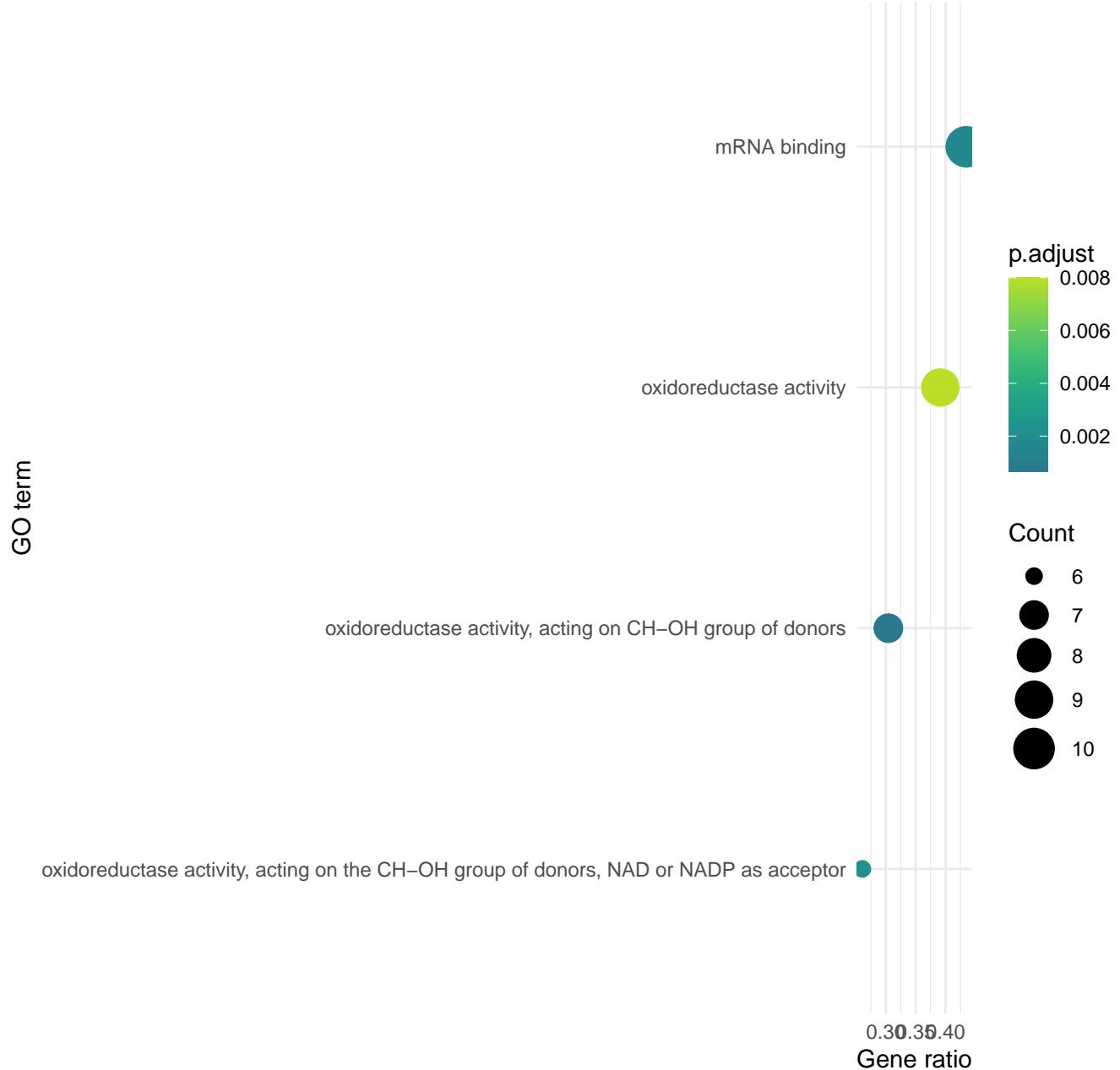


HSH49-TAP Up-regulated KEGG upsetplot



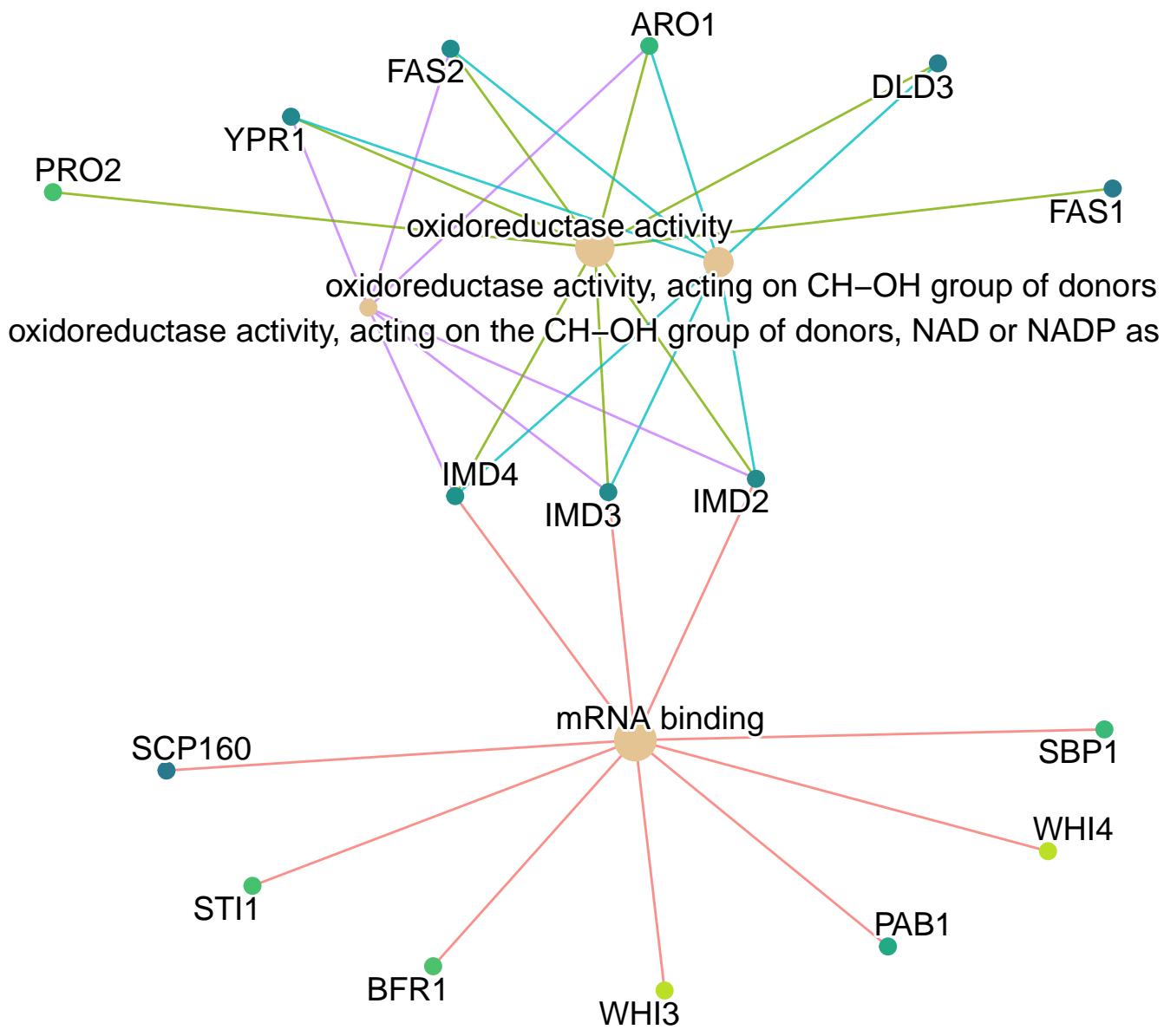
Gene count

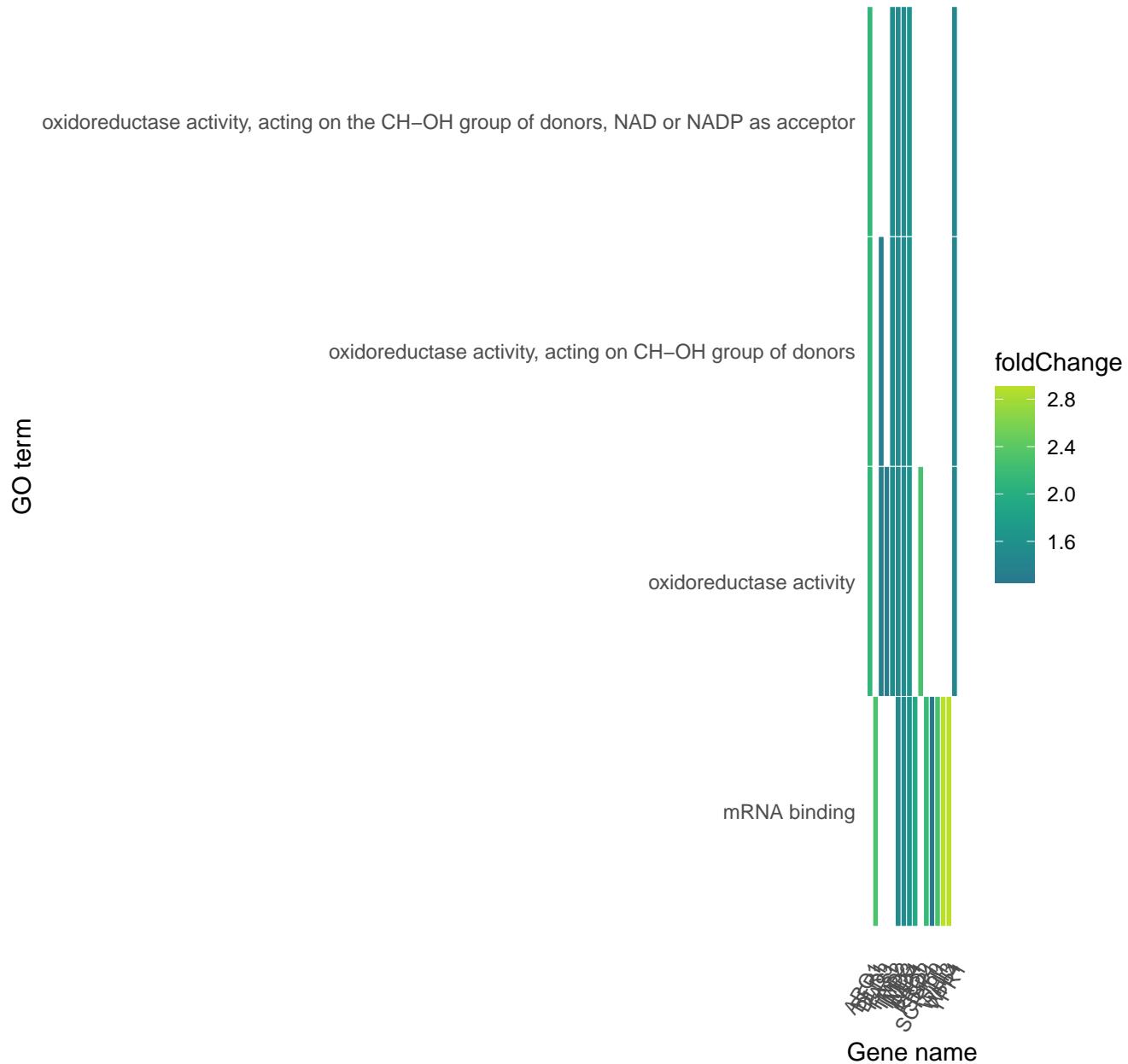




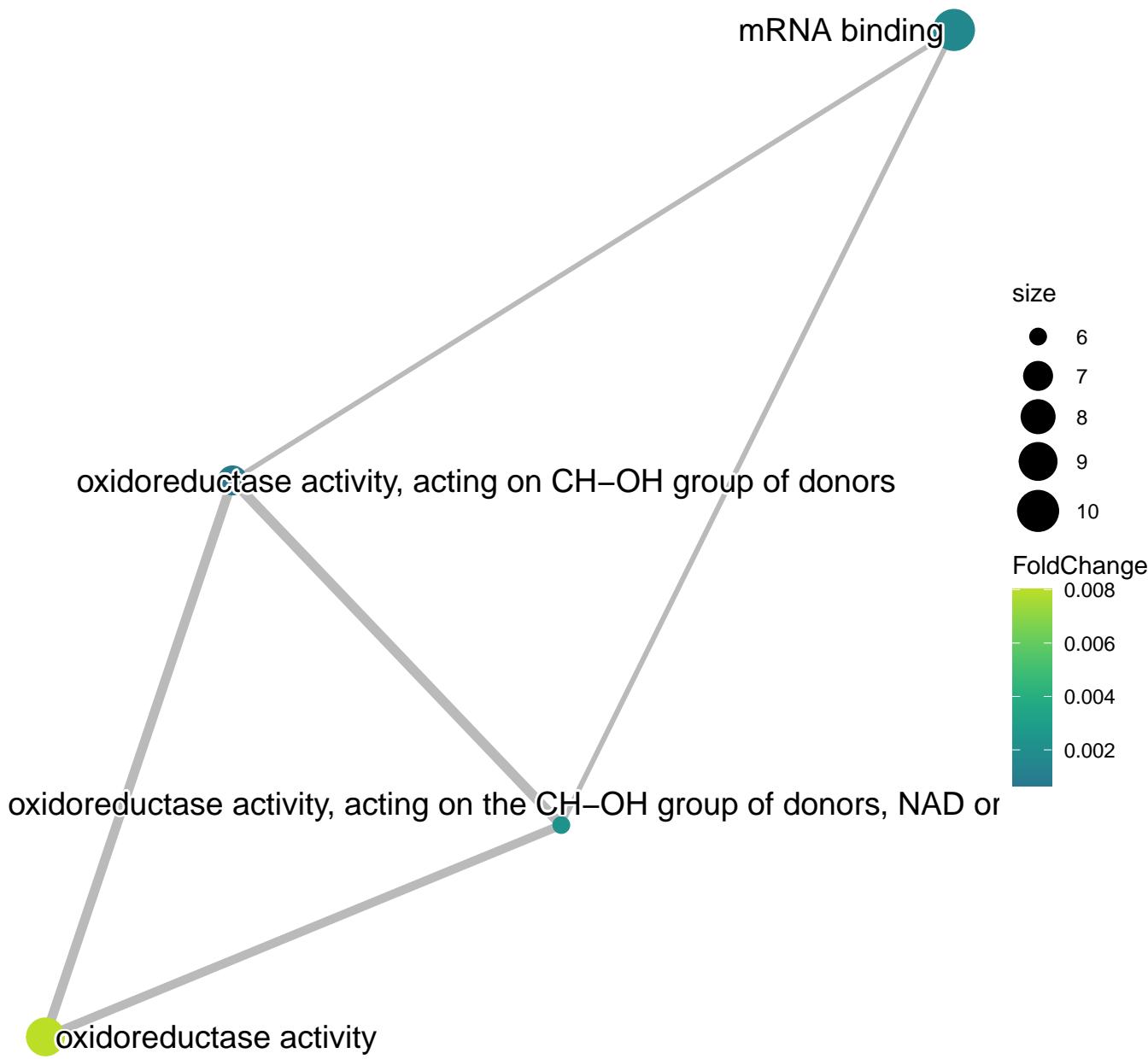
RPB7-TAP Up-regulated GO MF cnetplot

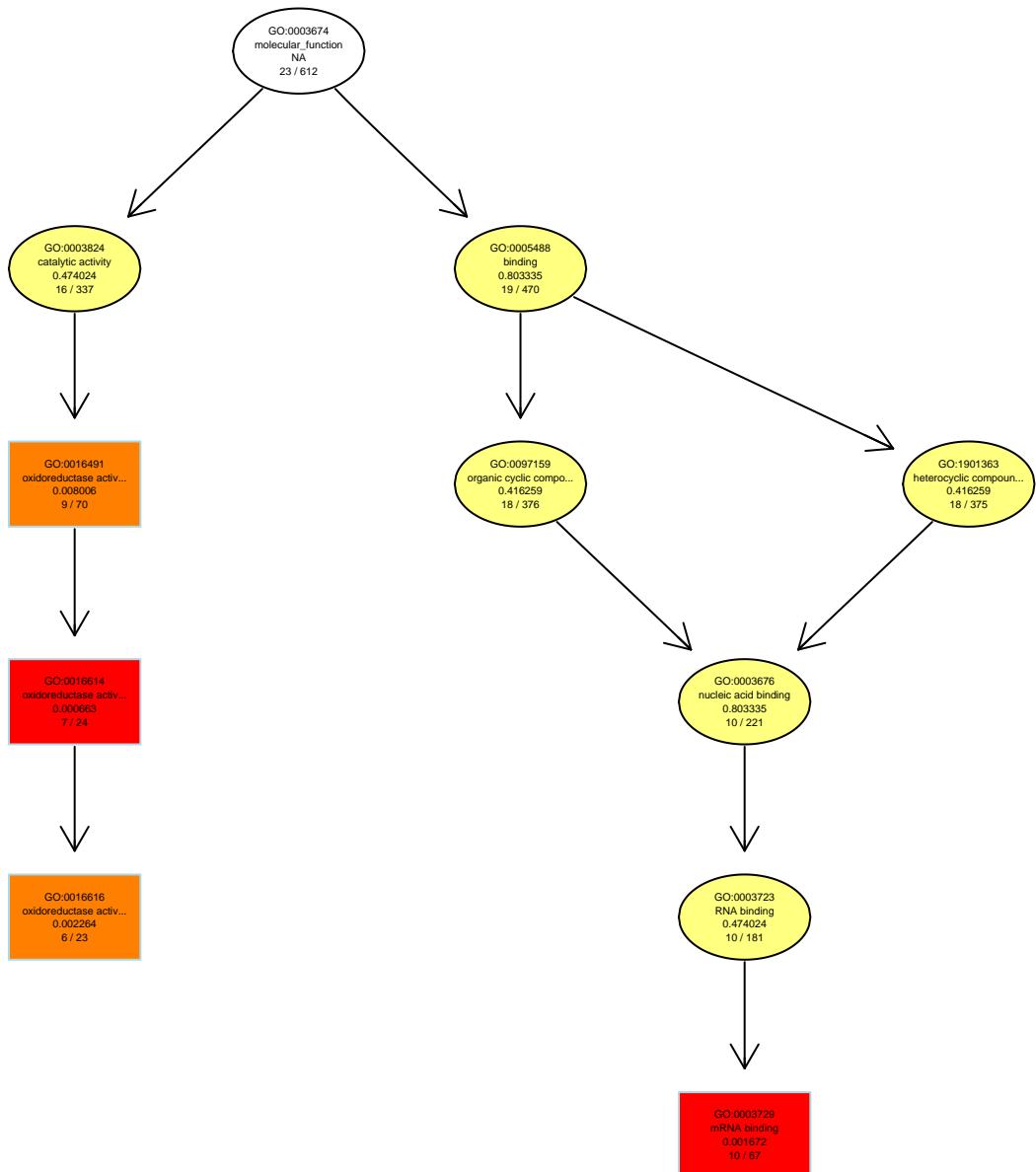
acting on CH-OH group of donors — oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor





RPB7-TAP Up-regulated GO MF emapplot





RPI

6

4

2

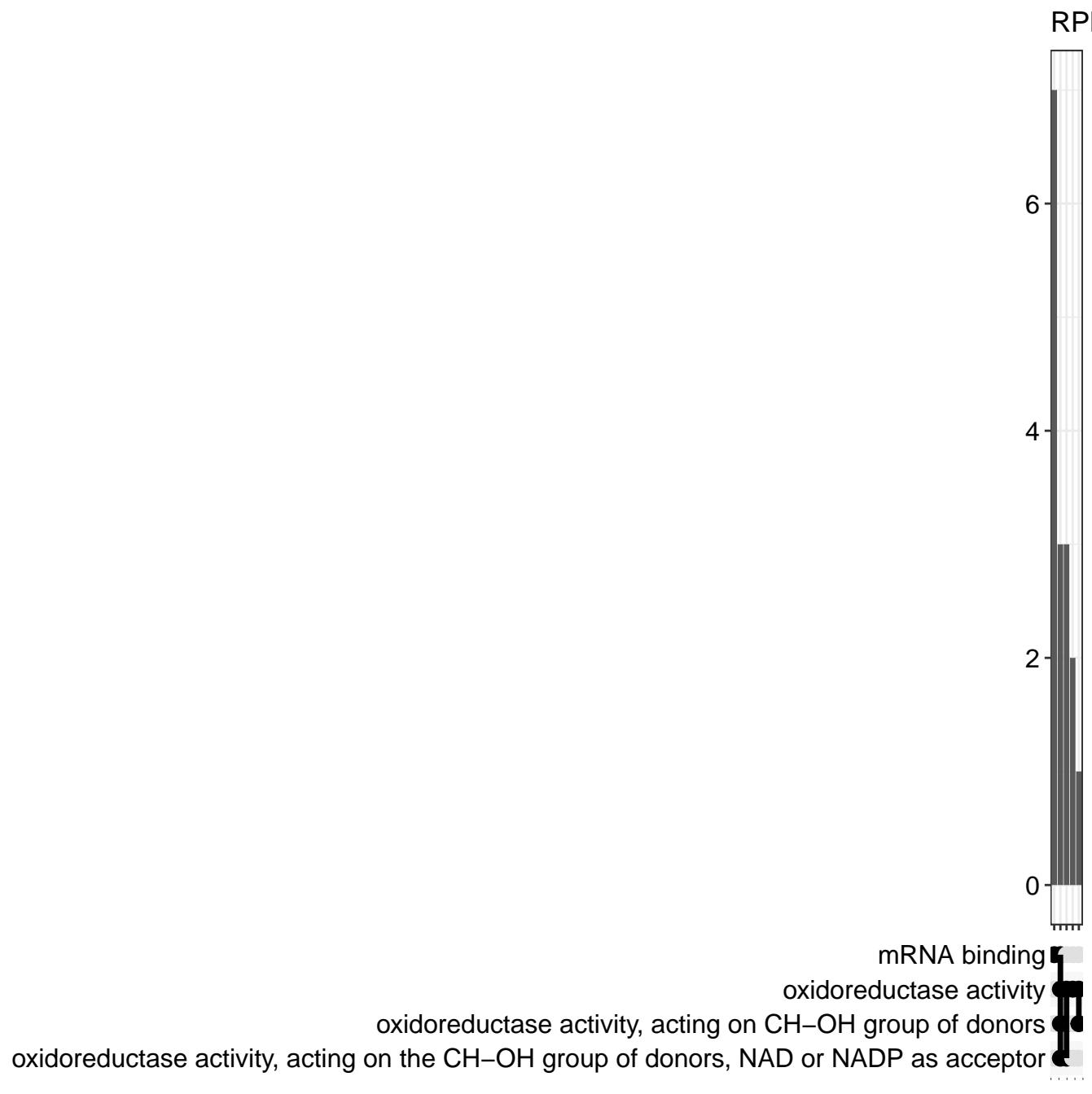
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mRNA binding

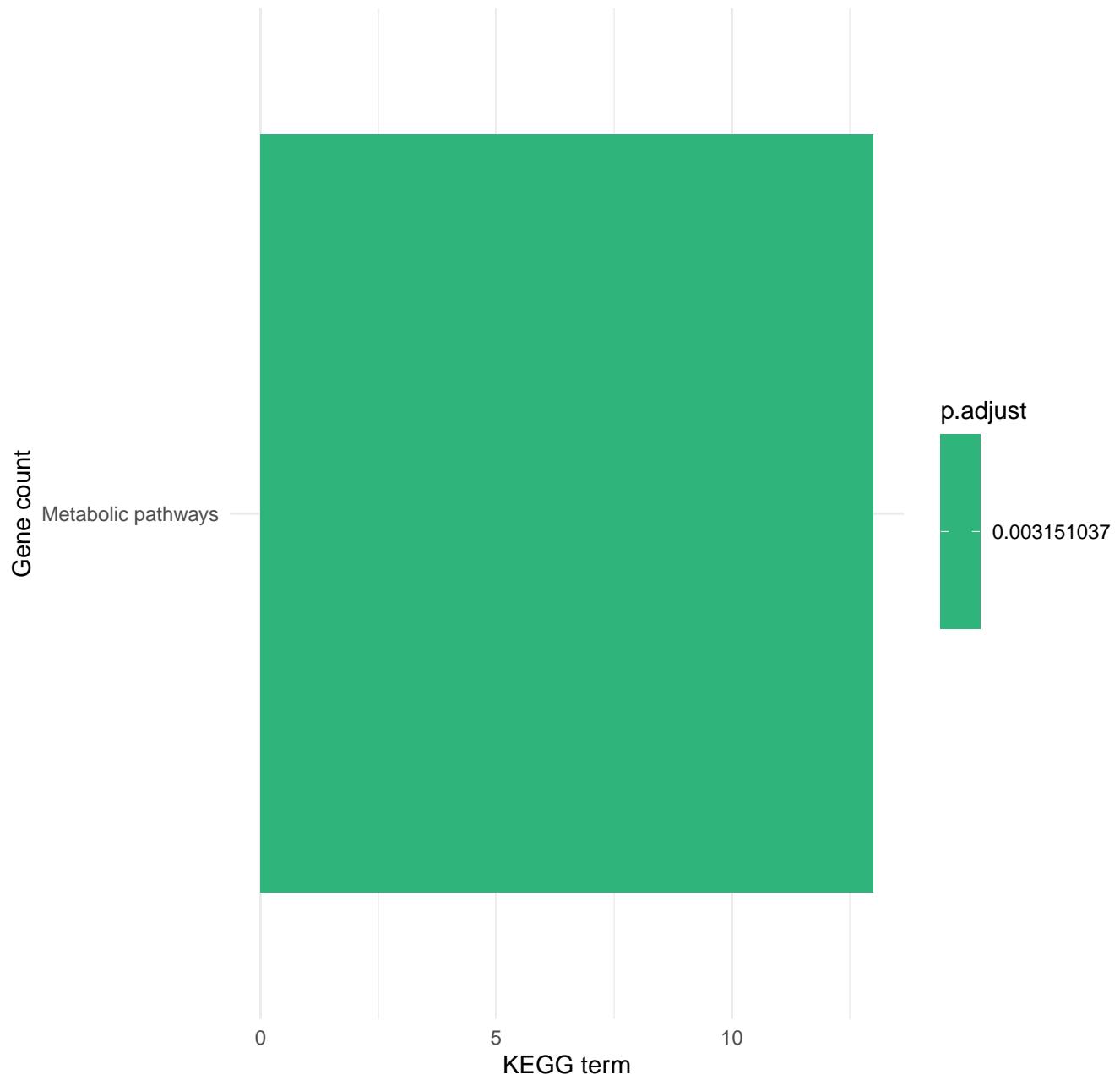
oxidoreductase activity

oxidoreductase activity, acting on CH-OH group of donors

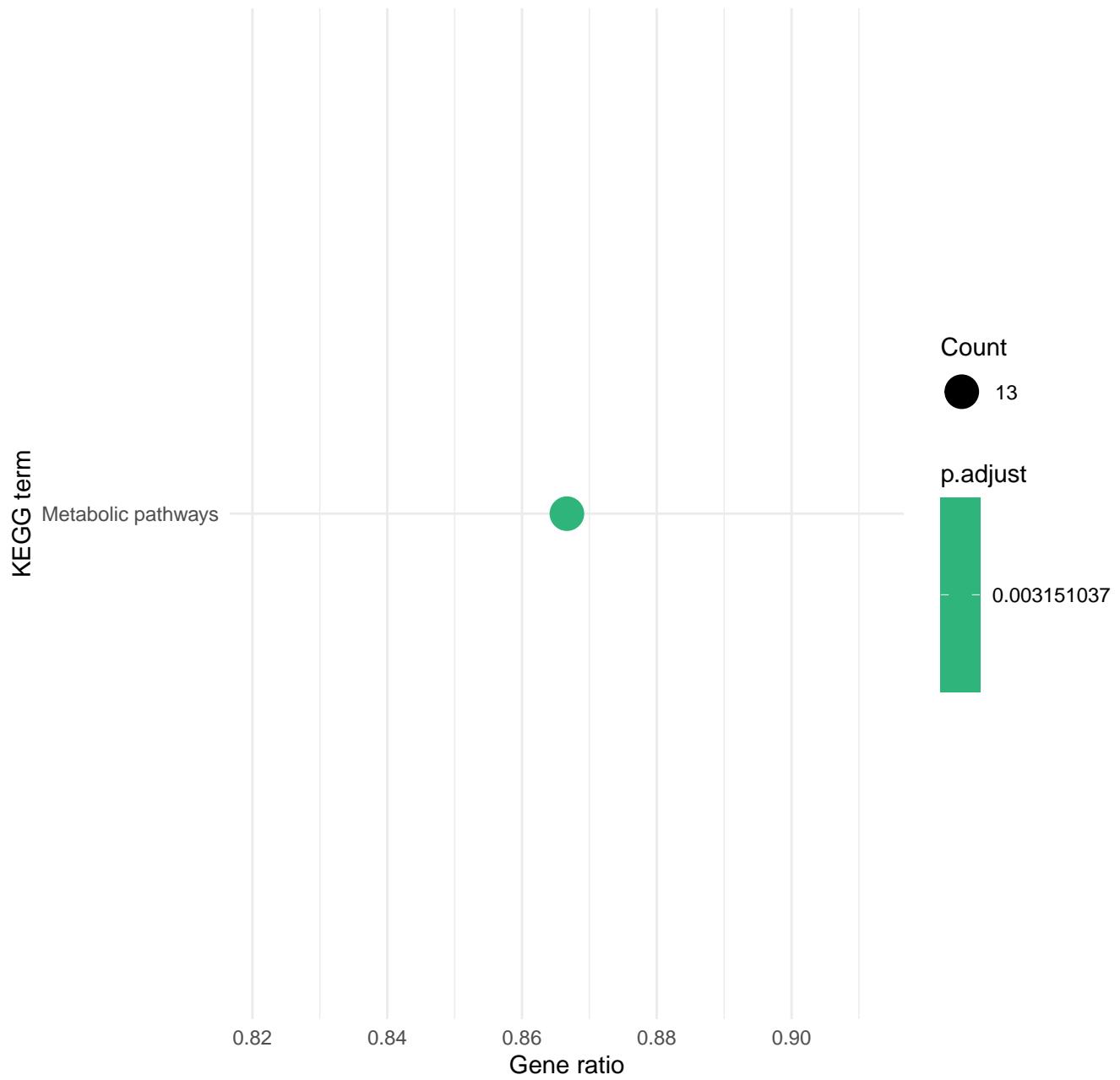
oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor



RPB7-TAP Up-regulated KEGG barplot



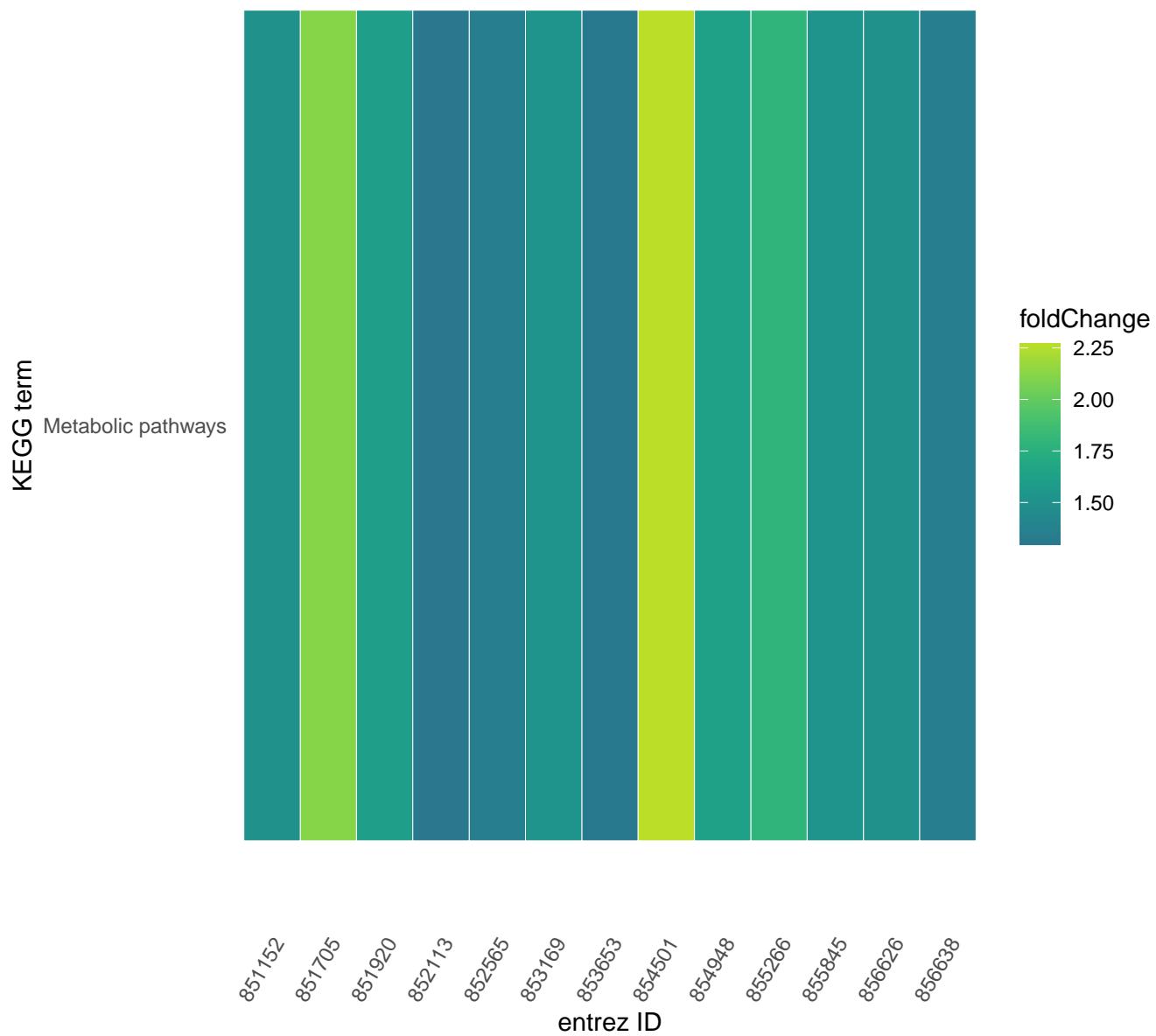
RPB7-TAP Up-regulated KEGG dotplot



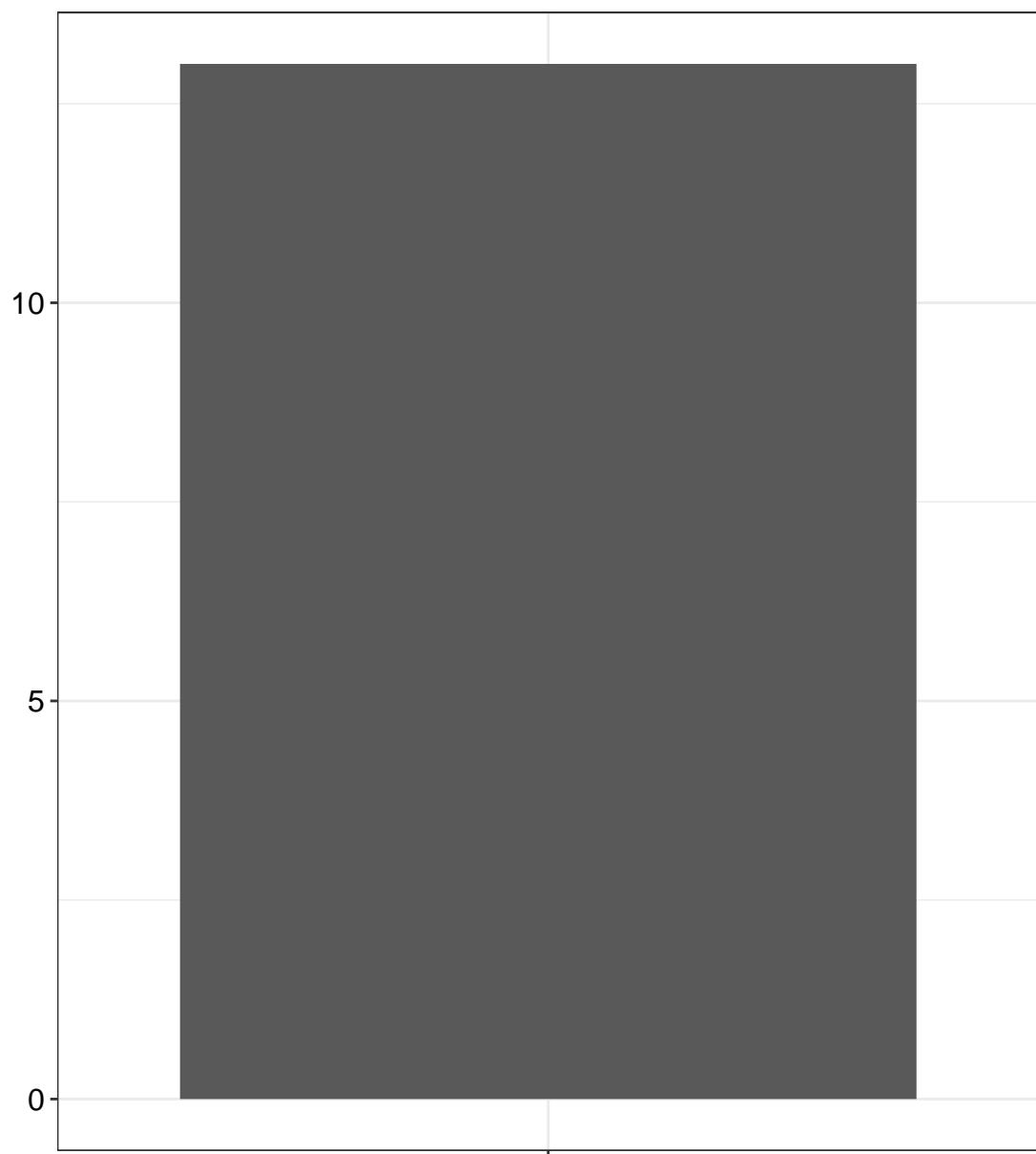
RPB7-TAP Up-regulated KEGG dotplot



RPB7-TAP Up-regulated KEGG heatplot

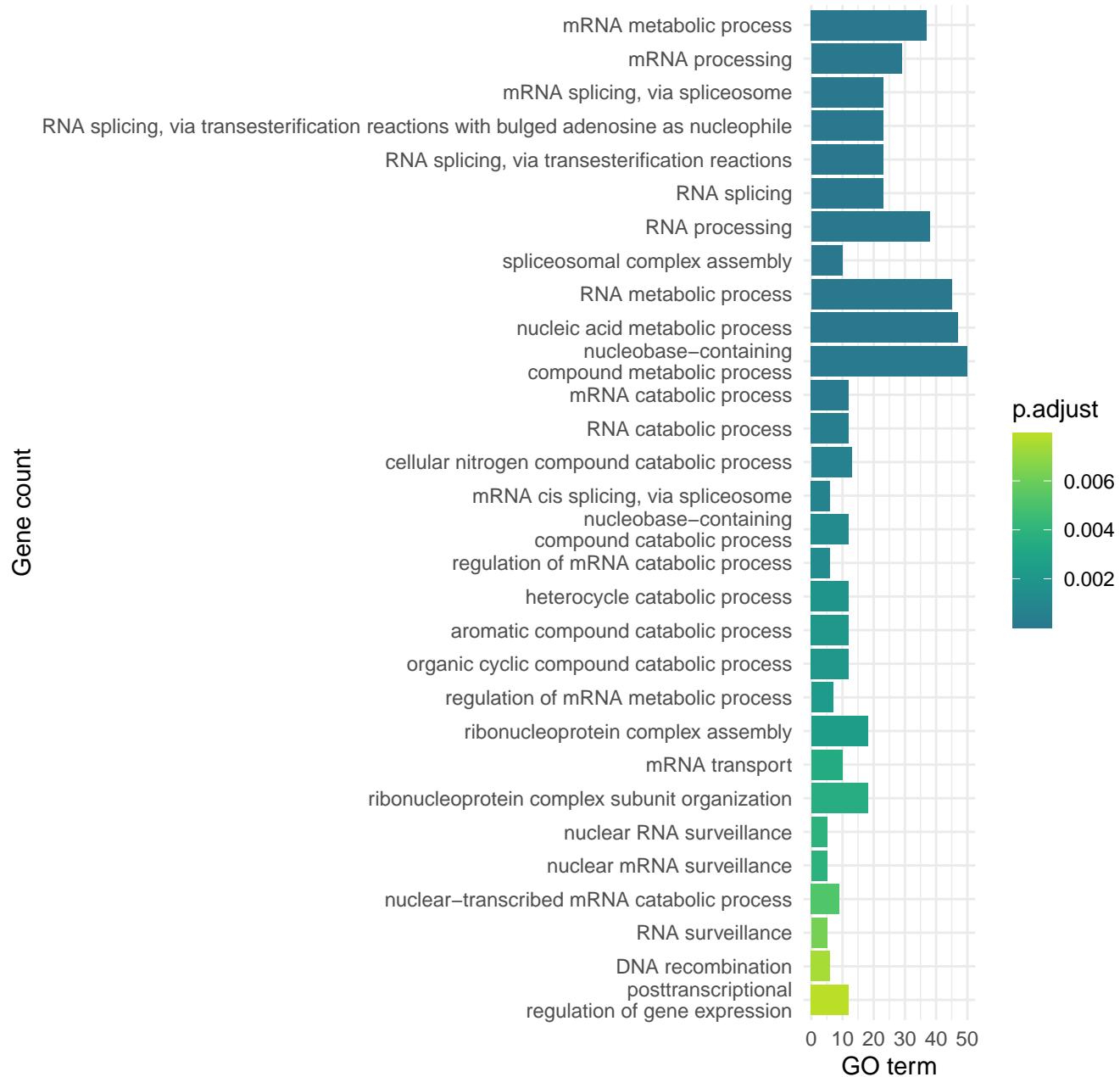


RPB7-TAP Up-regulated KEGG upsetplot

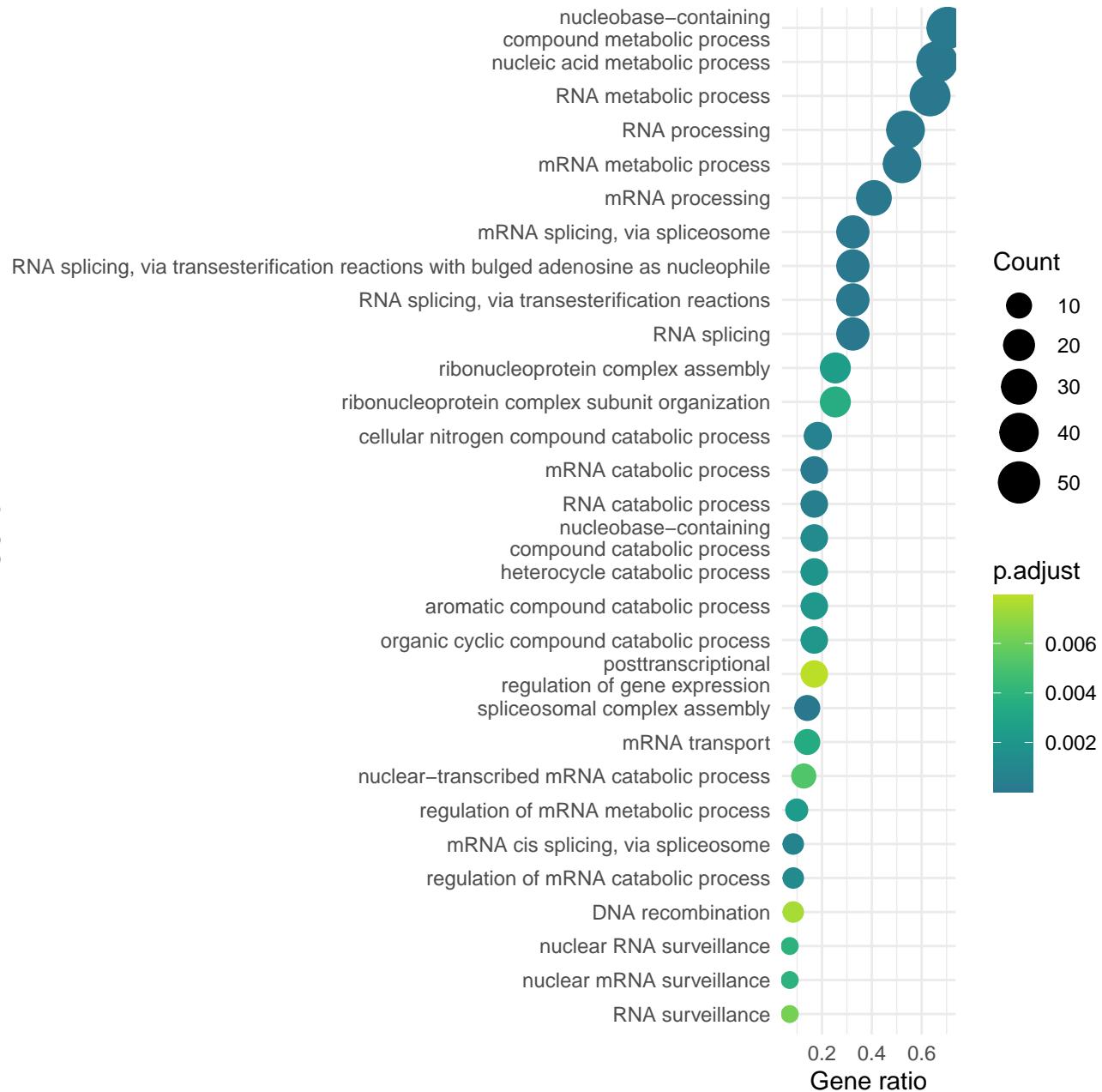


Metabolic pathways

STO1-TAP Up-regulated

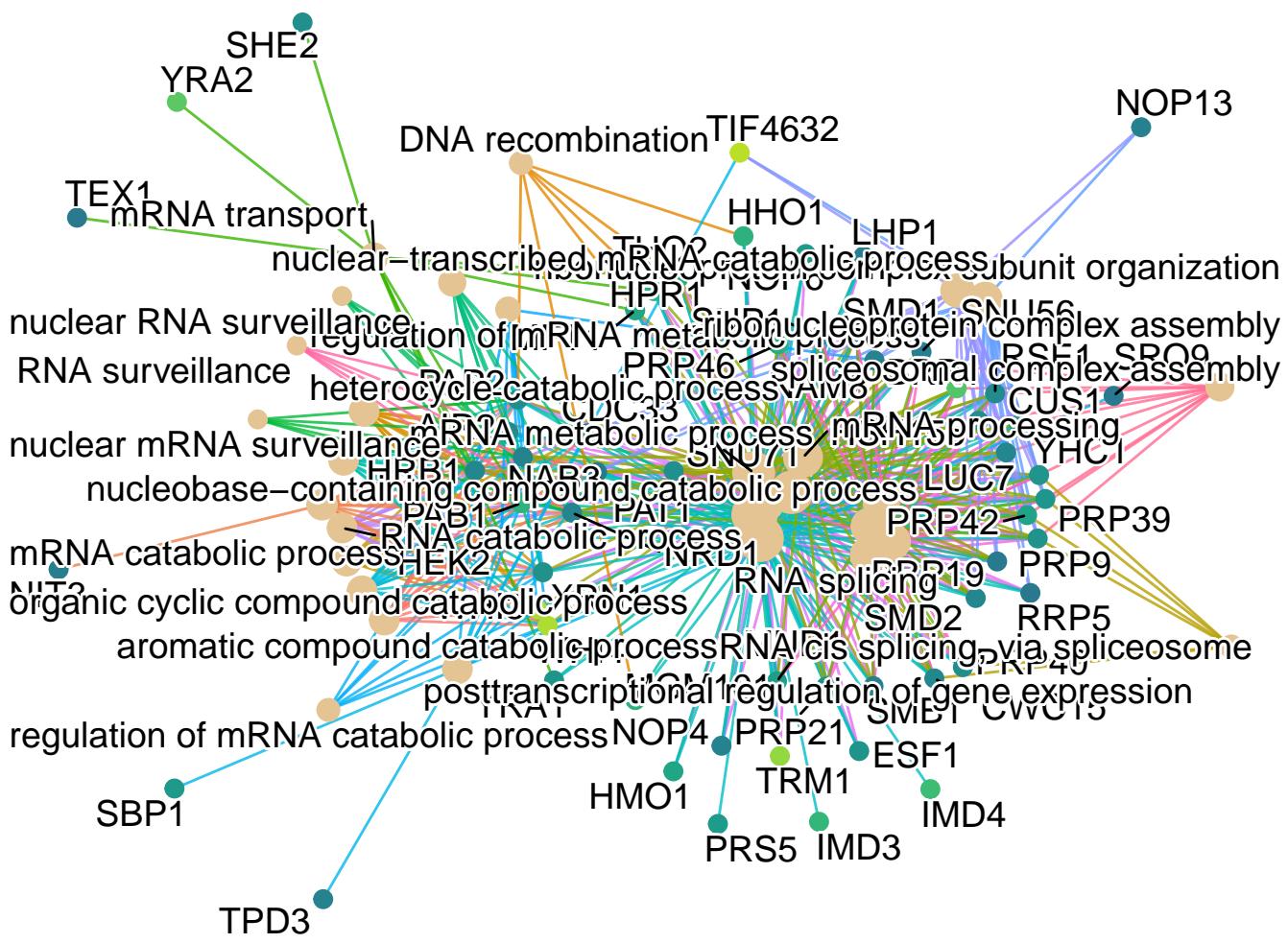


STO1-TAP Up-regulated

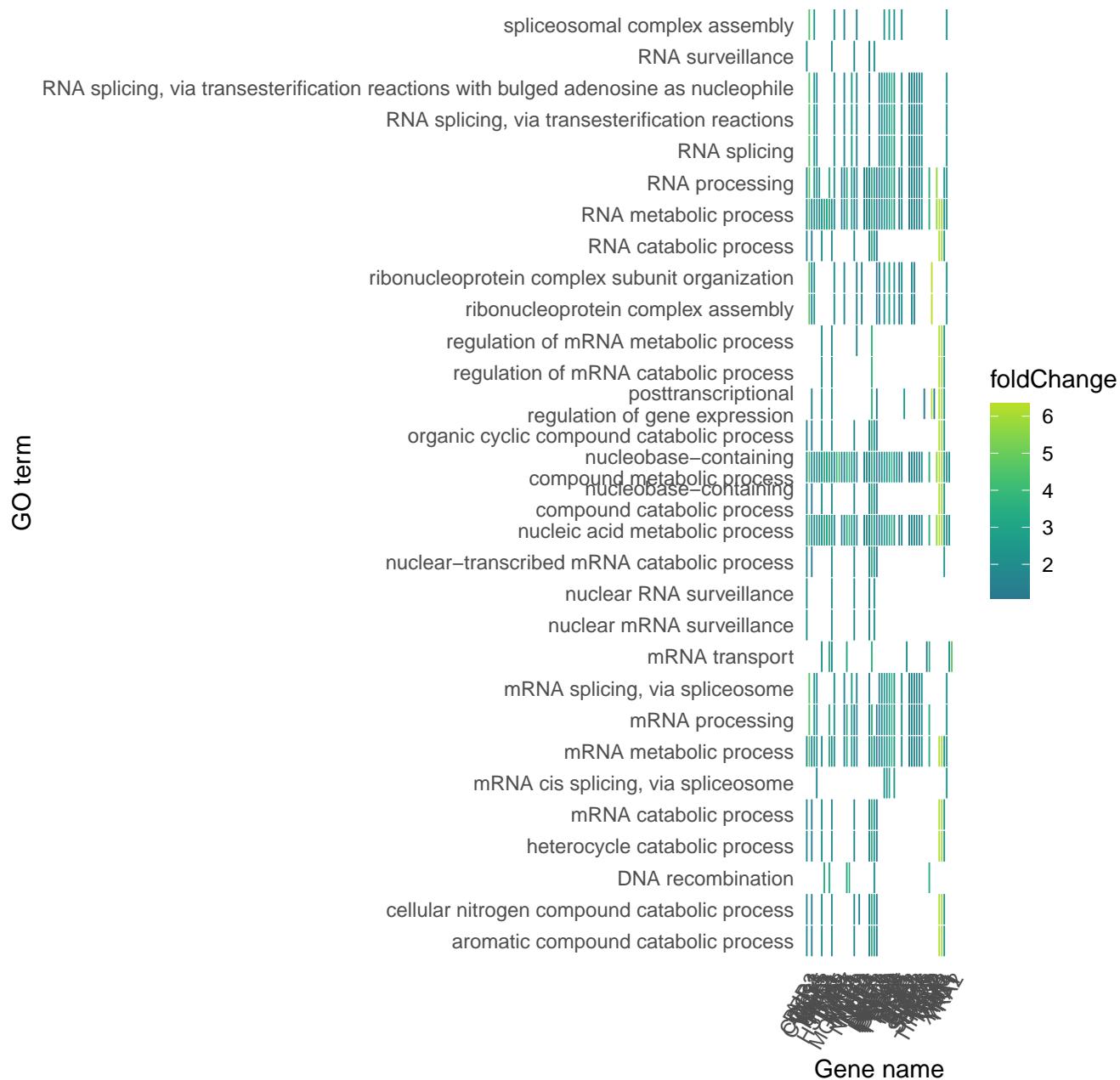


STO1-TAP Up-regulated GO BP cnetplot

abolic process	mRNA metabolic process	nuclear-transcribed mRNA catabolic process	
nd catabolic process	mRNA processing	nucleic acid metabolic process	
	mRNA splicing, via spliceosome	nucleobase-containing compound catabolic process	
cess	mRNA transport	nucleobase-containing compound metabolic process	
s	nuclear mRNA surveillance	organic cyclic compound catabolic process	
spliceosome	nuclear RNA surveillance	posttranscriptional regulation of gene expression	

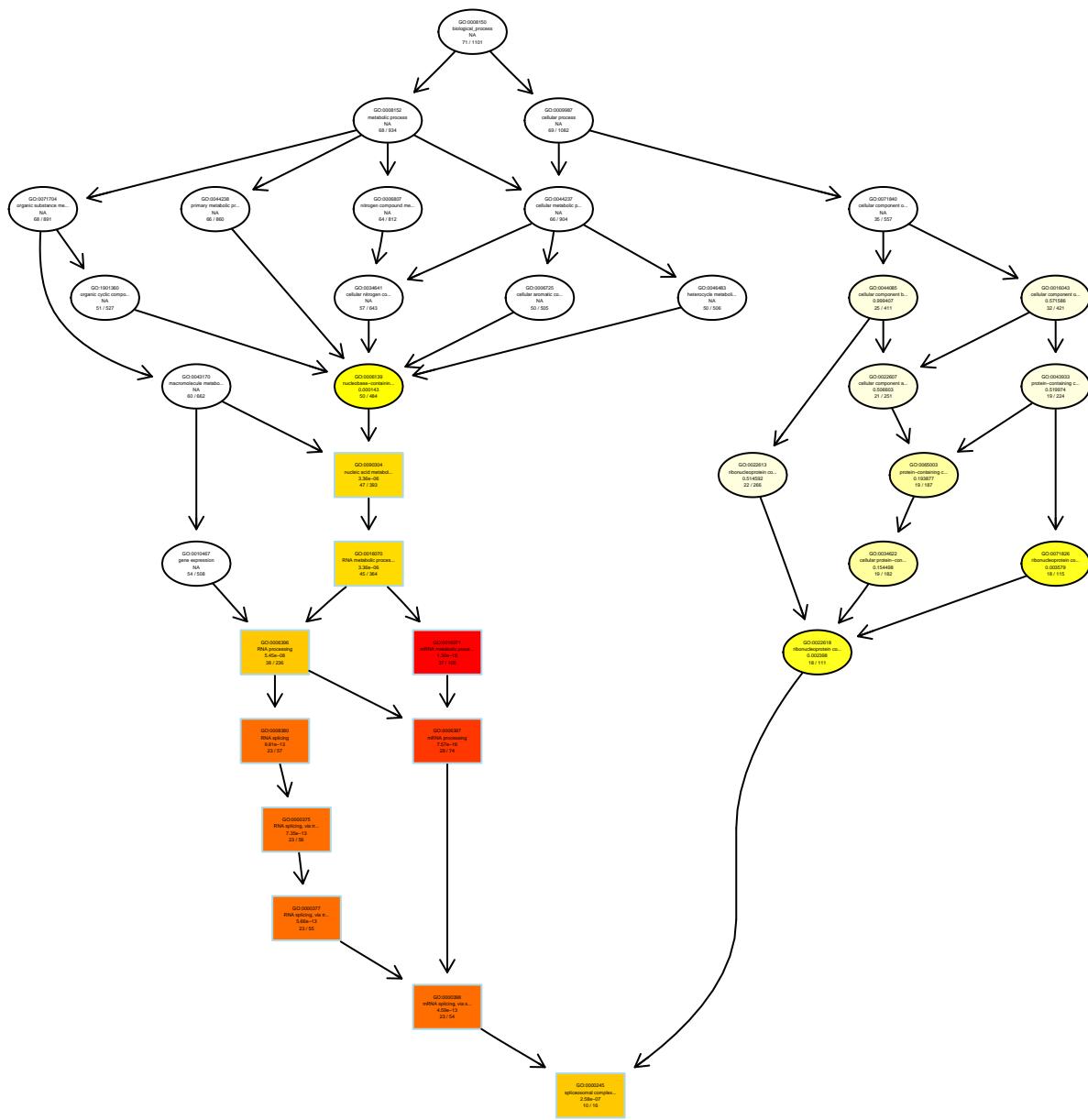


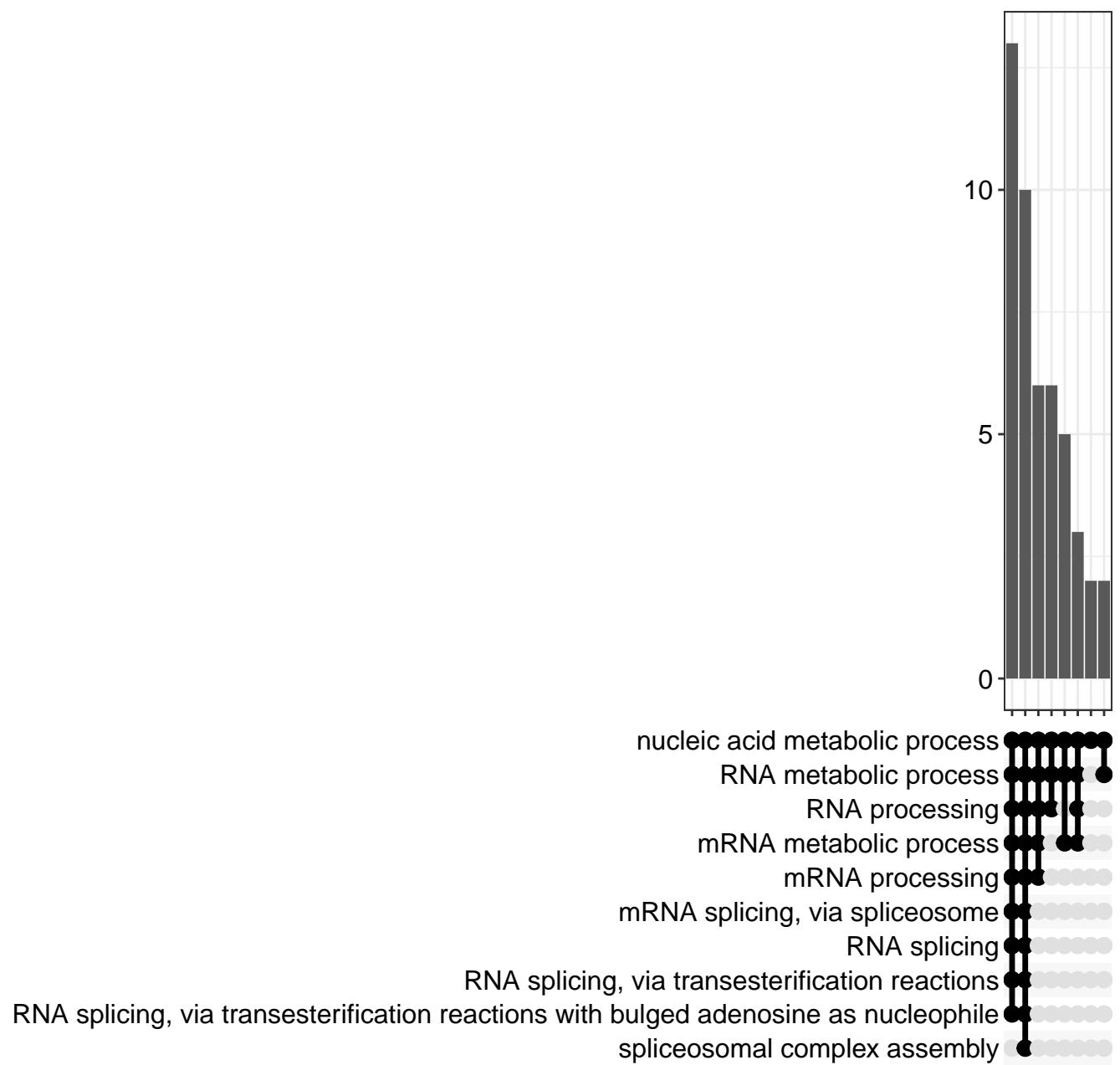
STO1-TAP Up-regulated



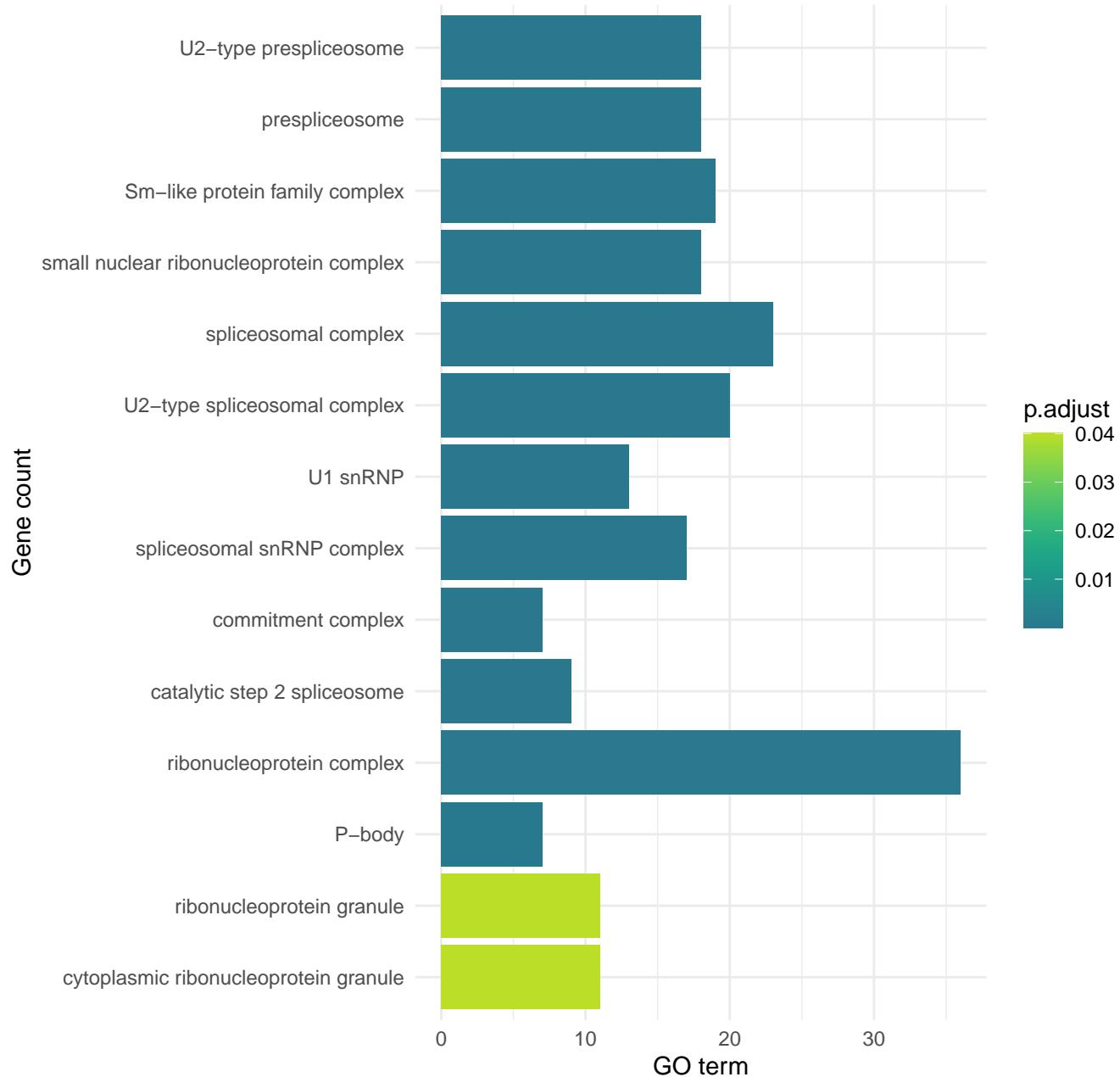
STO1-TAP Up-regulated GO BP emapplot



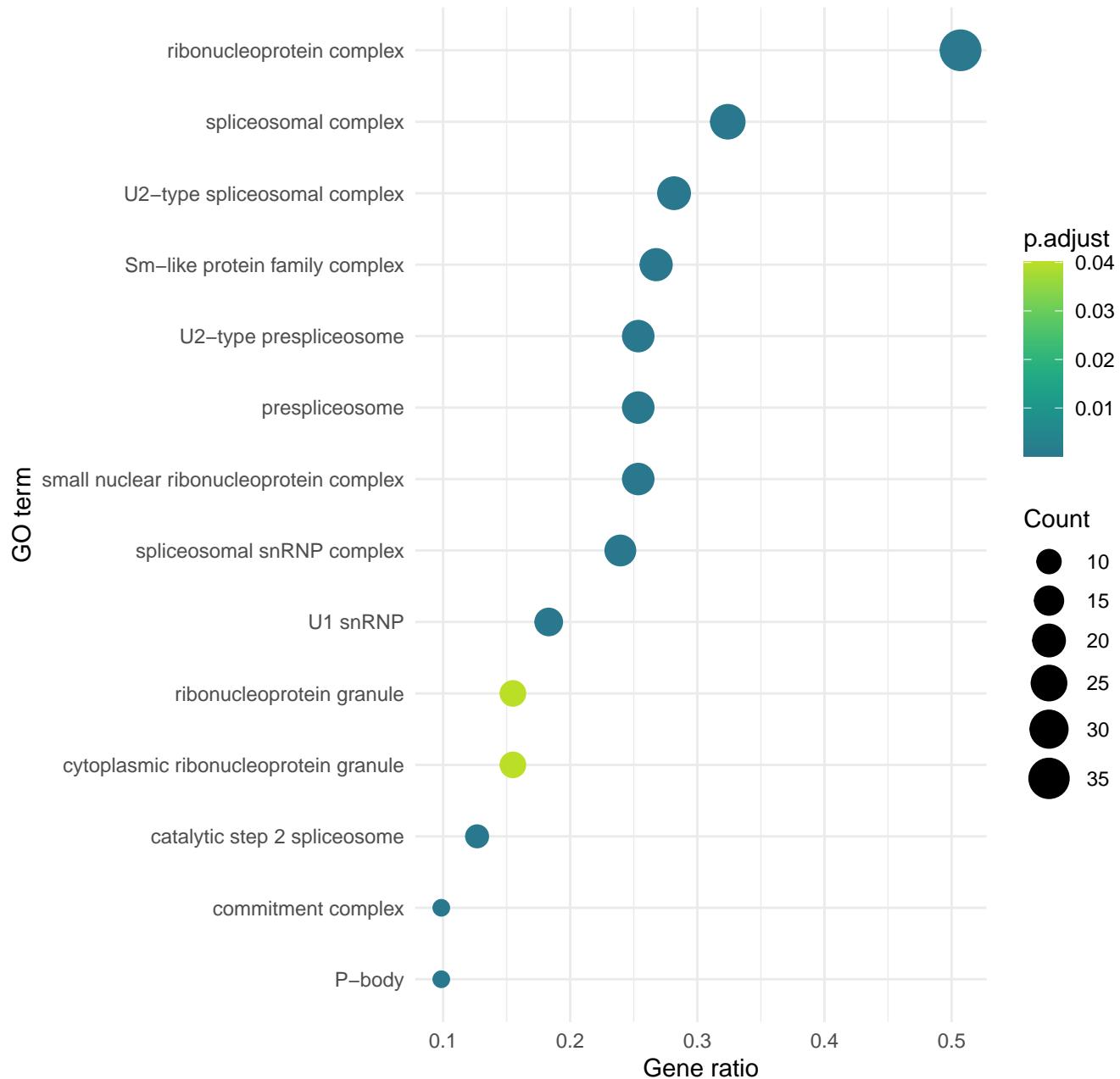




STO1-TAP Up-regulated GO CC barplot

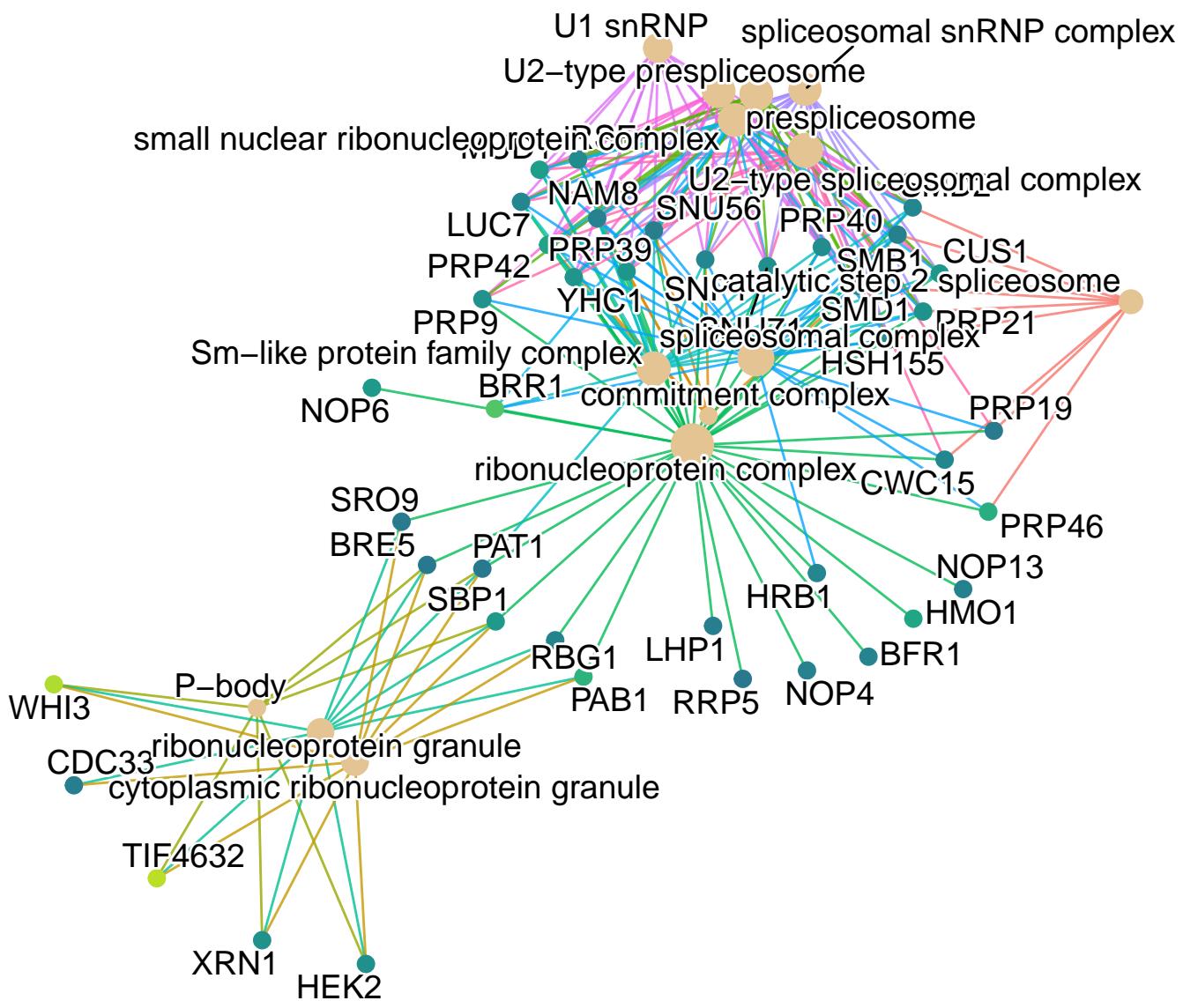


STO1-TAP Up-regulated GO CC dotplot

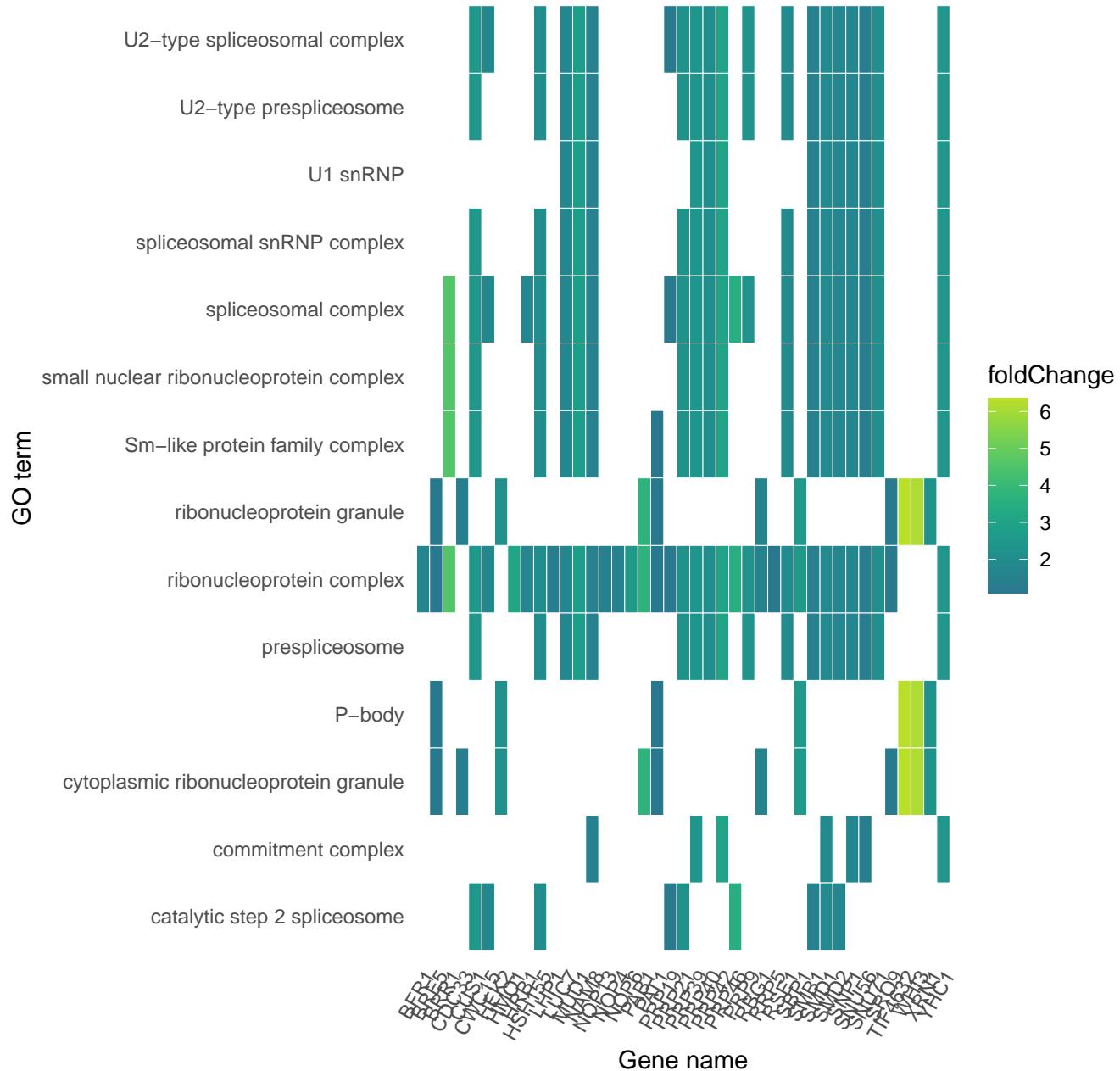


STO1-TAP Up-regulated GO CC cnetplot

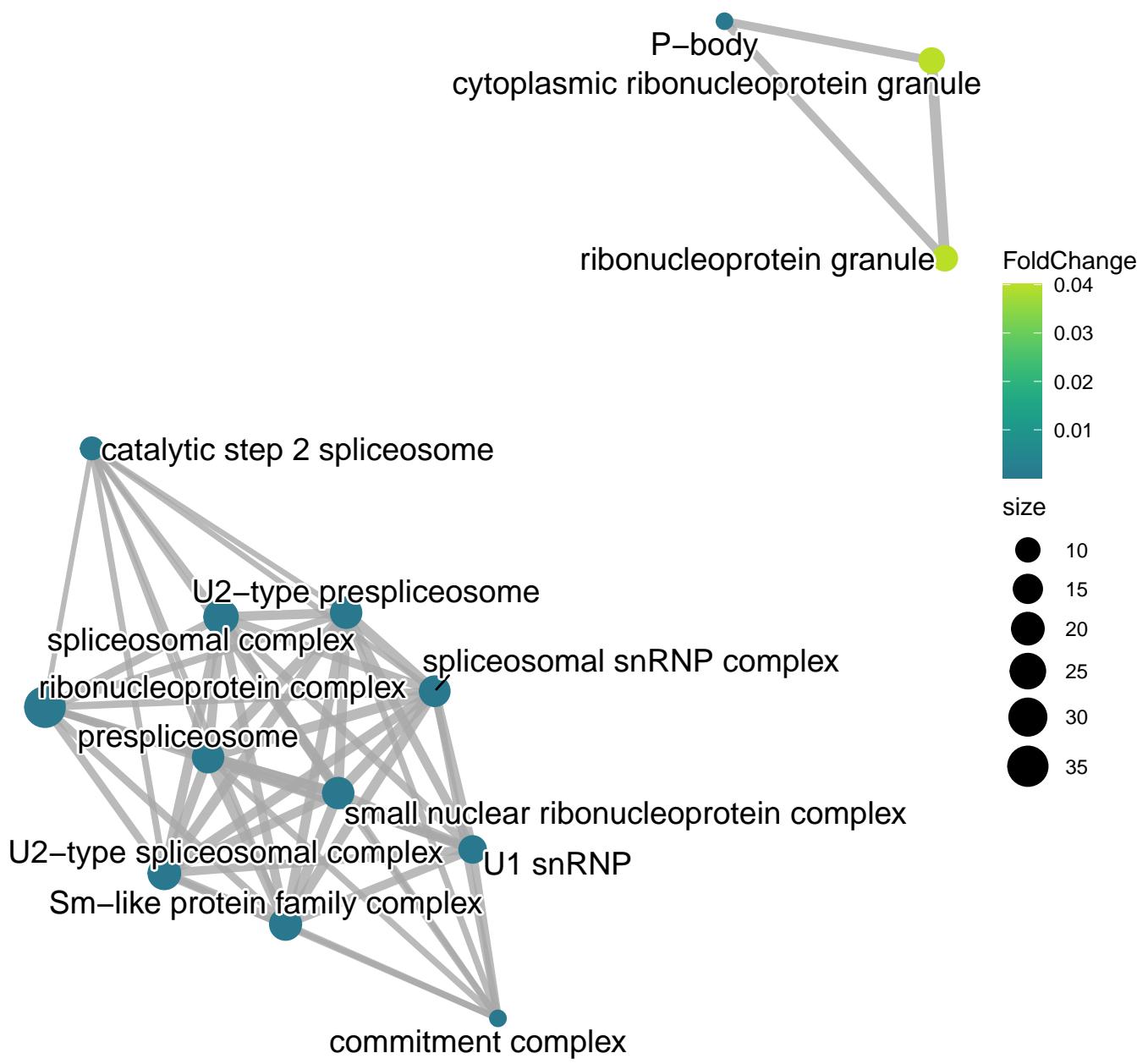
— ribonucleoprotein granule
 — Sm-like protein family complex
 — complex
 — small nuclear ribonucleoprotein complex
 — U1 snRNP
 — spliceosomal complex
 — spliceosomal snRNP complex
 — U2-type presspliceosome
 — U2-type spliceosomal complex
 — prespliceosome
 — spliceosomal snRNP complex
 — U2-type spliceosomal complex
 — prespliceosome
 — catalytic step 2 spliceosome
 — spliceosomal complex
 — commitment complex
 — ribonucleoprotein complex
 — P-body
 — cytoplasmic ribonucleoprotein granule

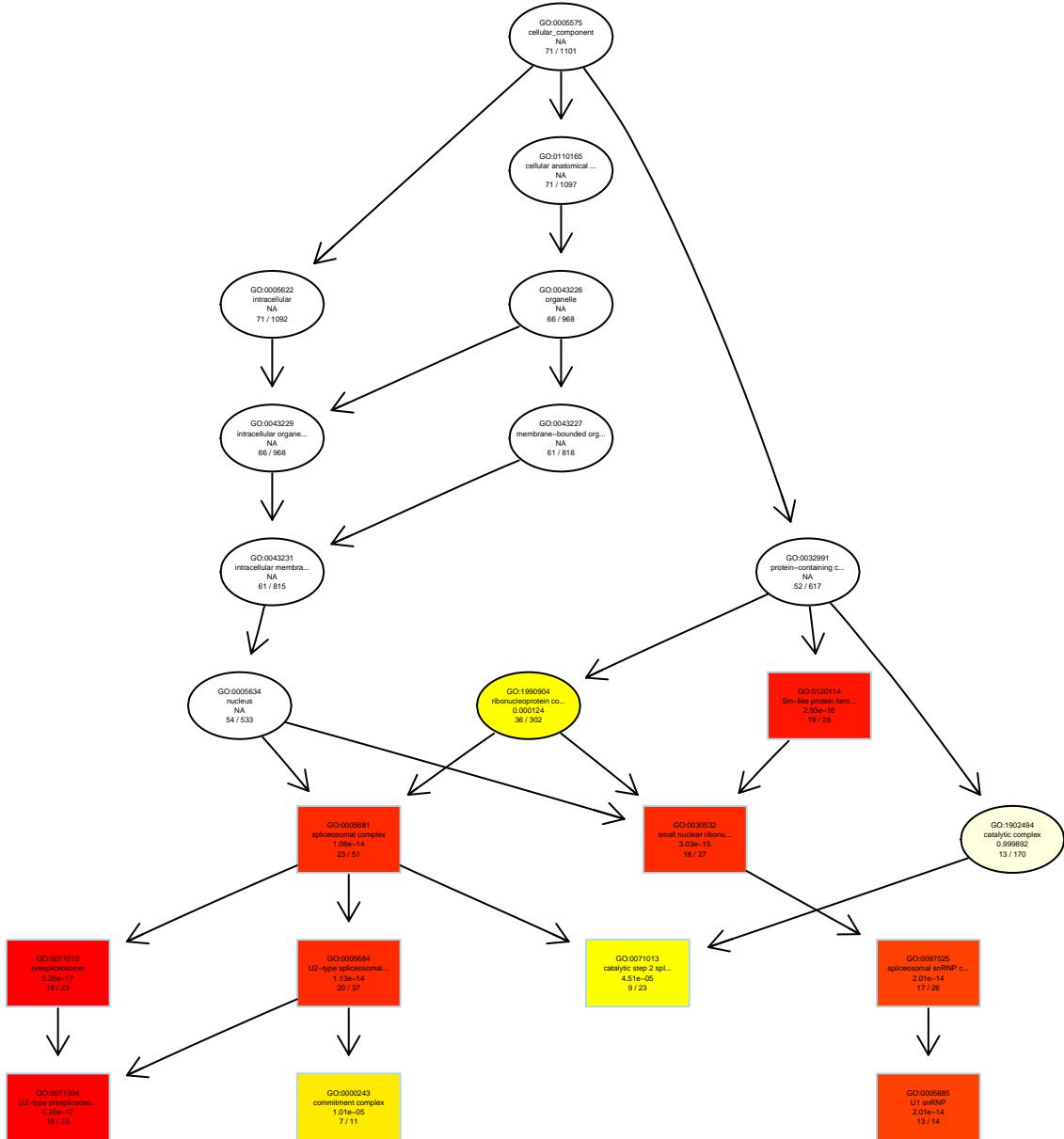


STO1-TAP Up-regulated GO CC heatplot

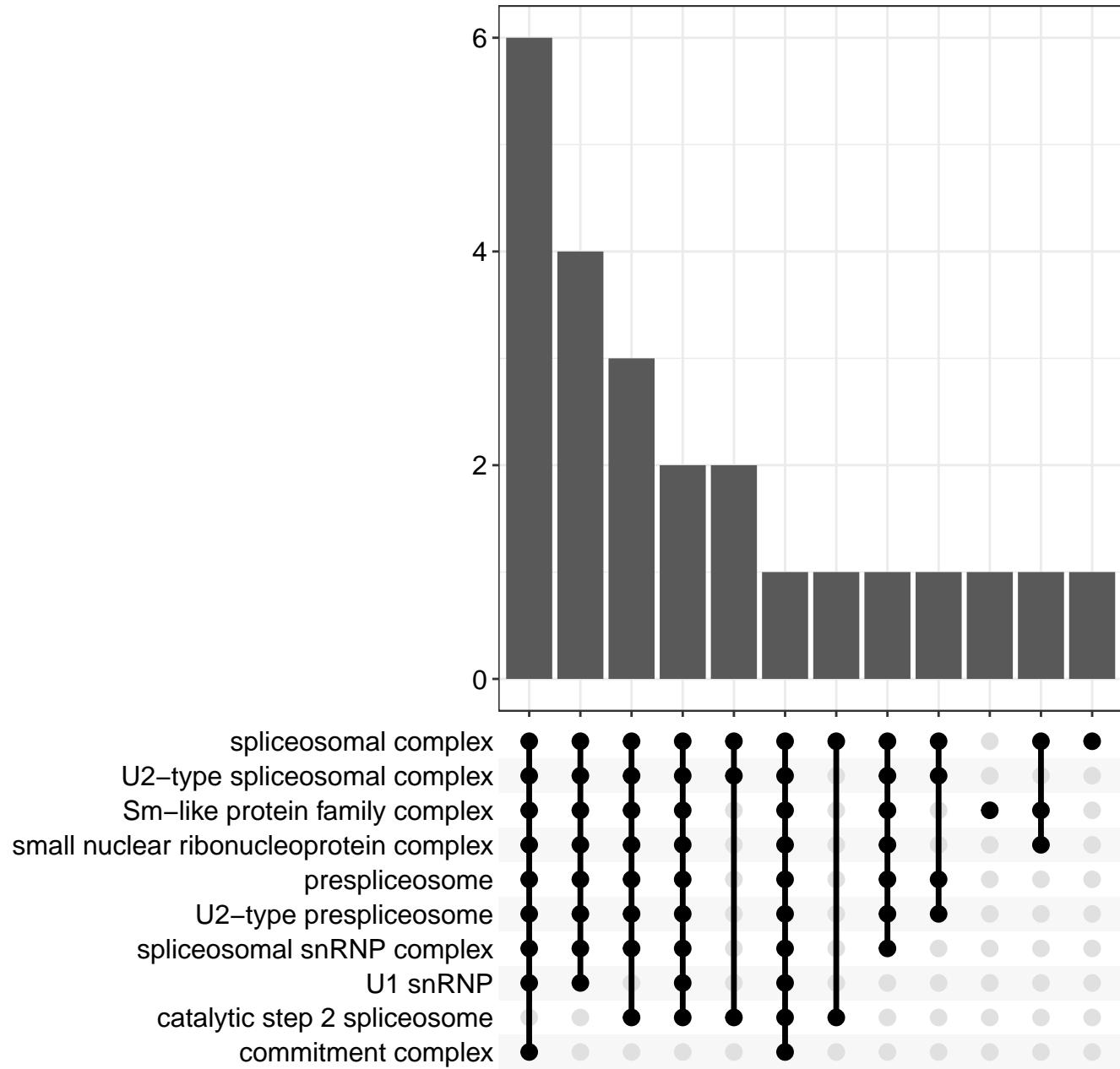


STO1-TAP Up-regulated GO CC emapplot

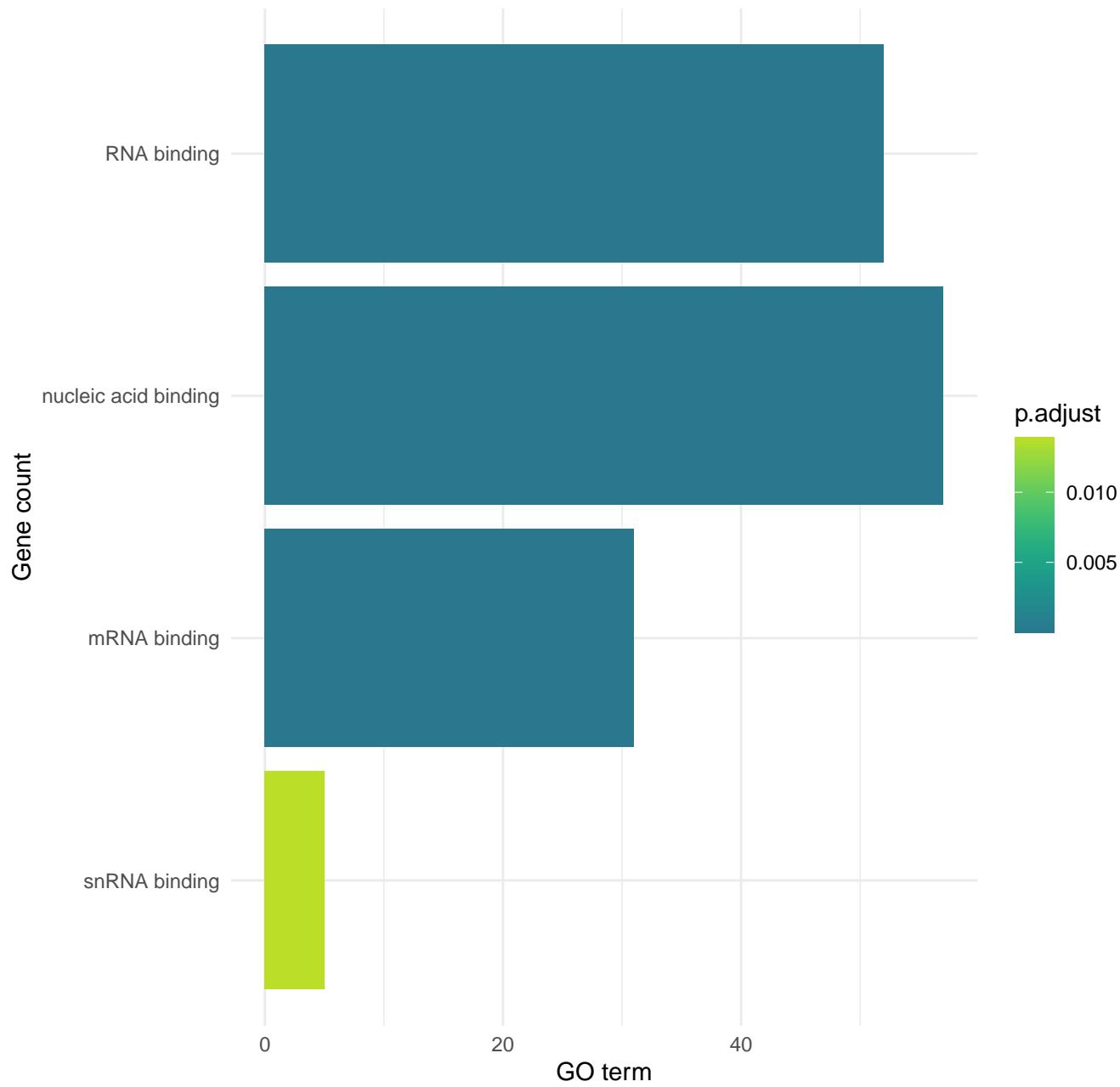




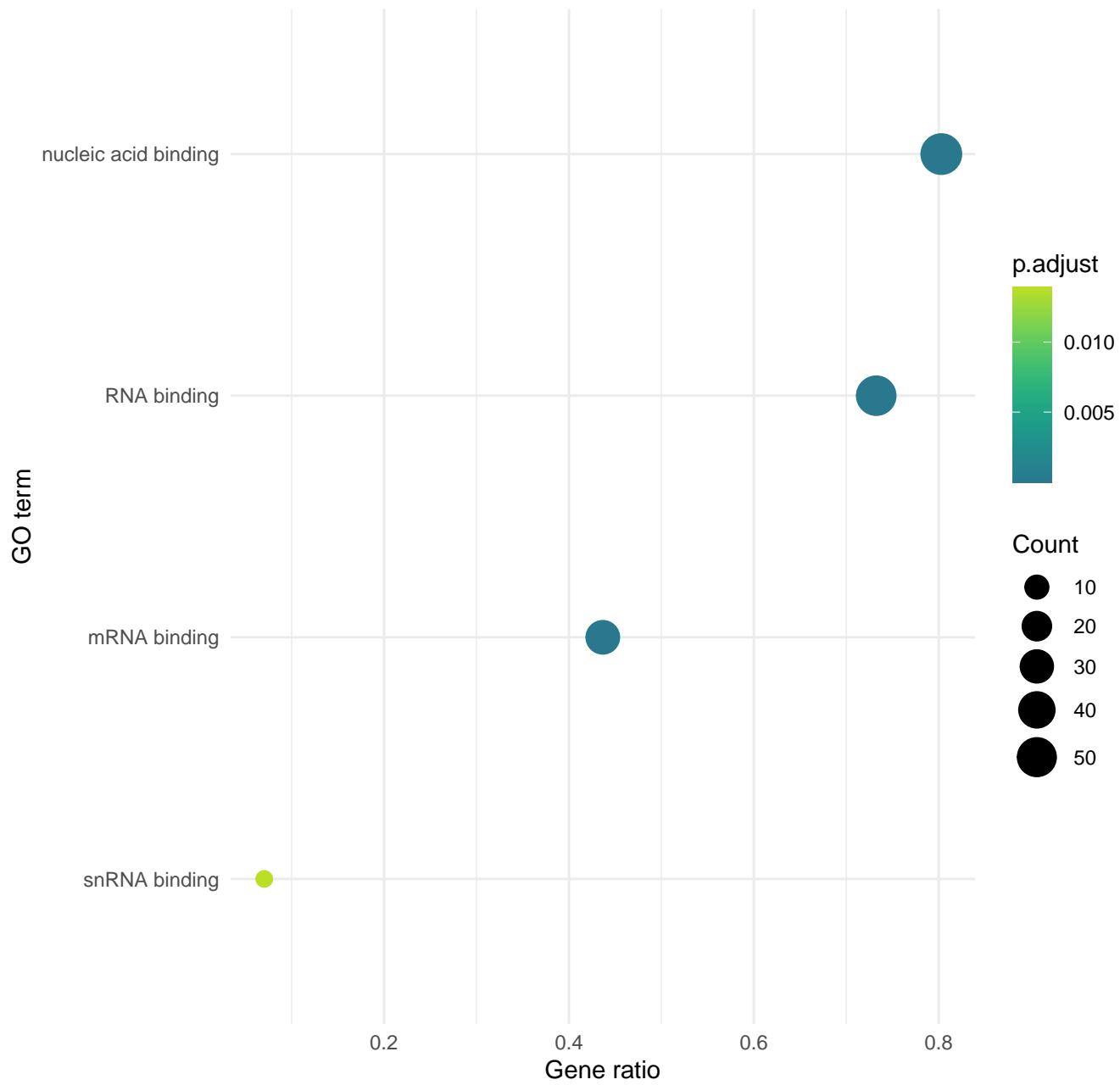
STO1-TAP Up-regulated GO CC upsetplot



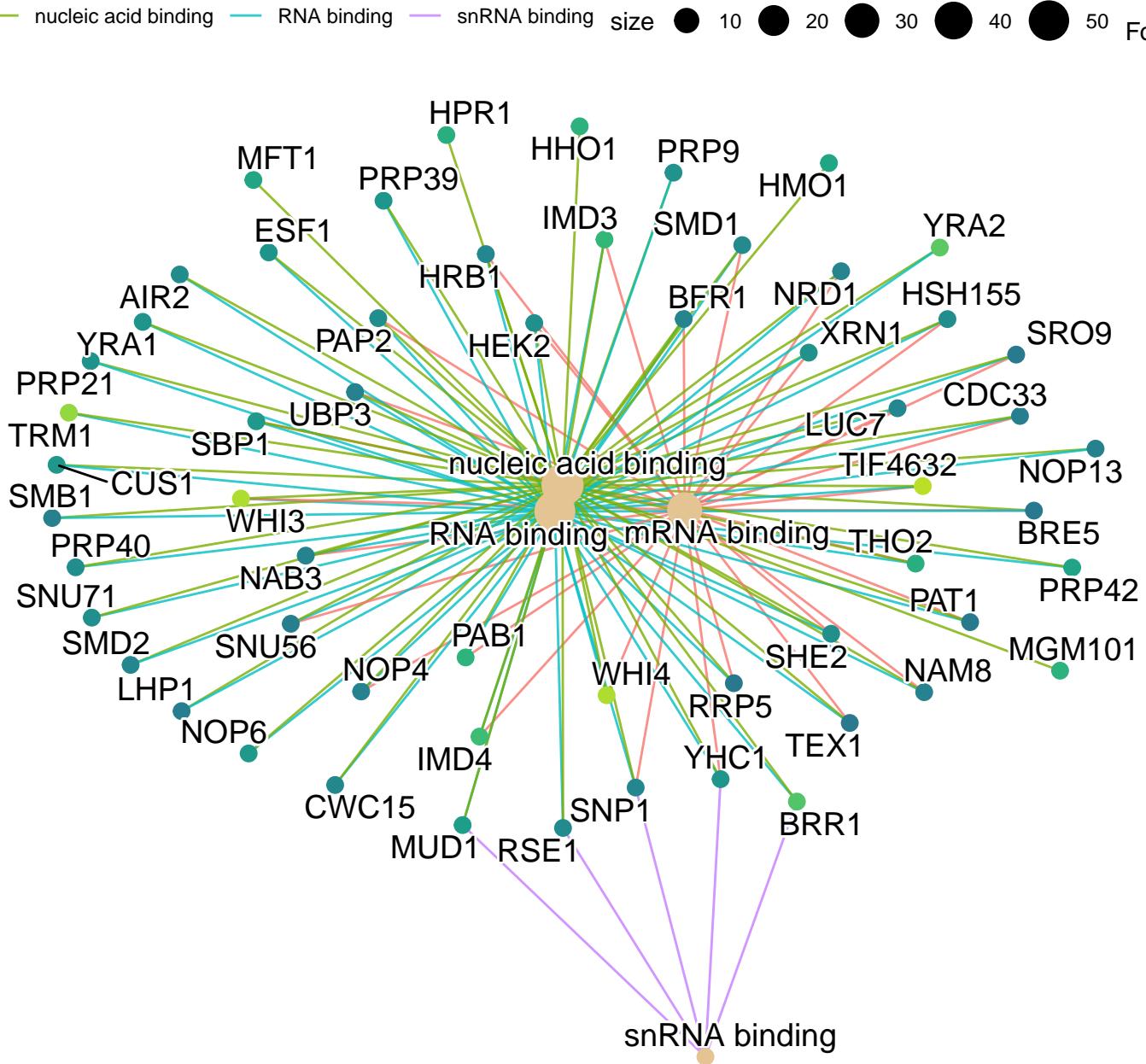
STO1-TAP Up-regulated GO MF barplot



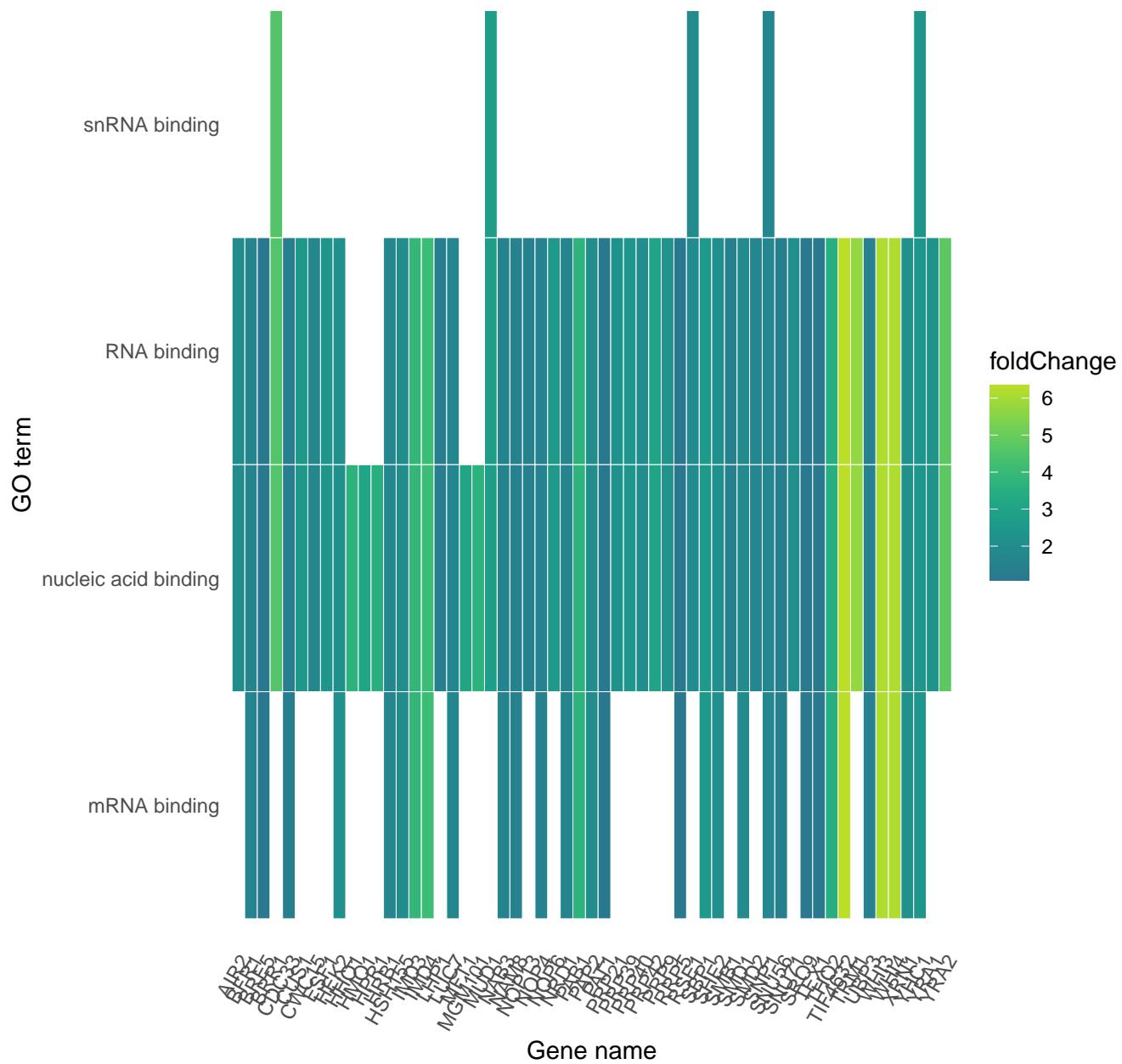
STO1-TAP Up-regulated GO MF dotplot



STO1-TAP Up-regulated GO MF cnetplot



STO1-TAP Up-regulated GO MF heatplot



STO1-TAP Up-regulated GO MF emapplot

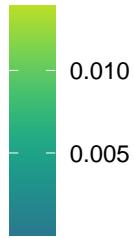
snRNA binding

mRNA binding

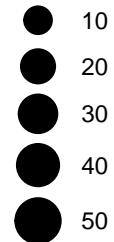
RNA binding

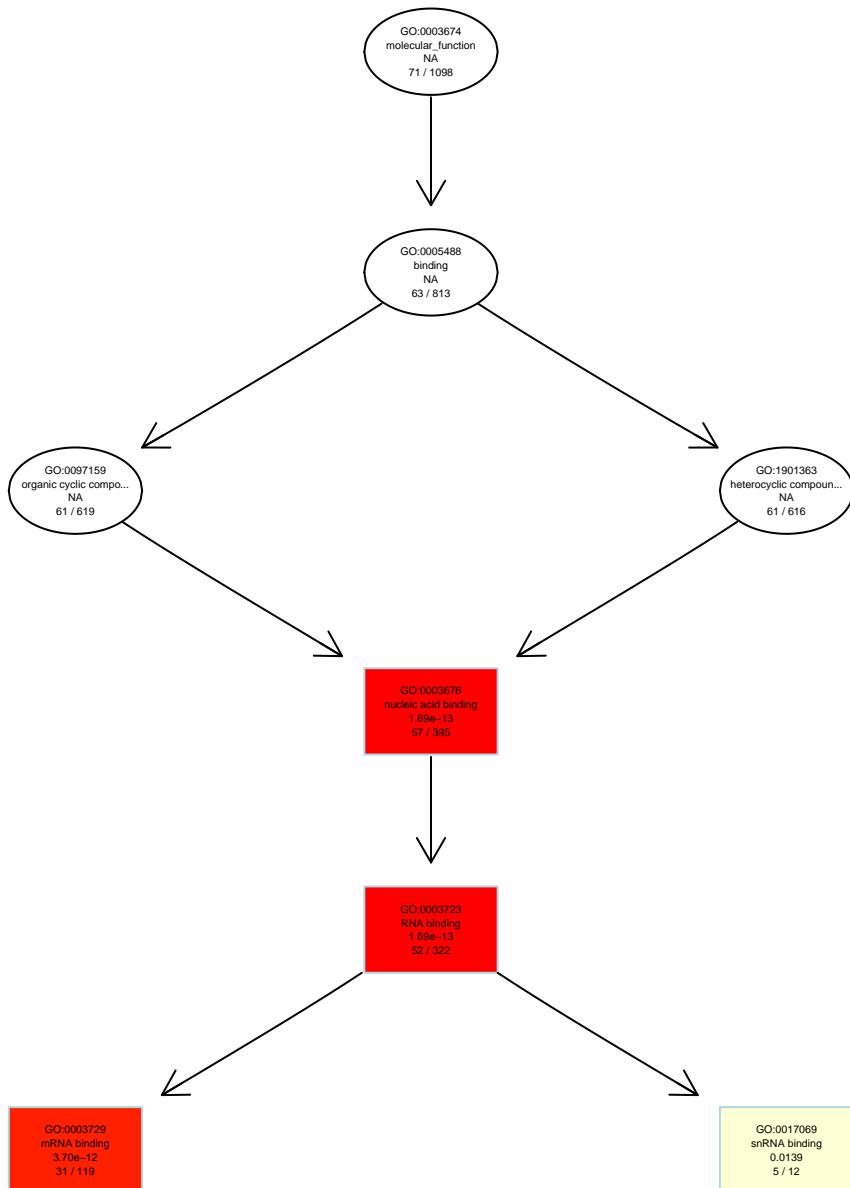
nucleic acid binding

FoldChange

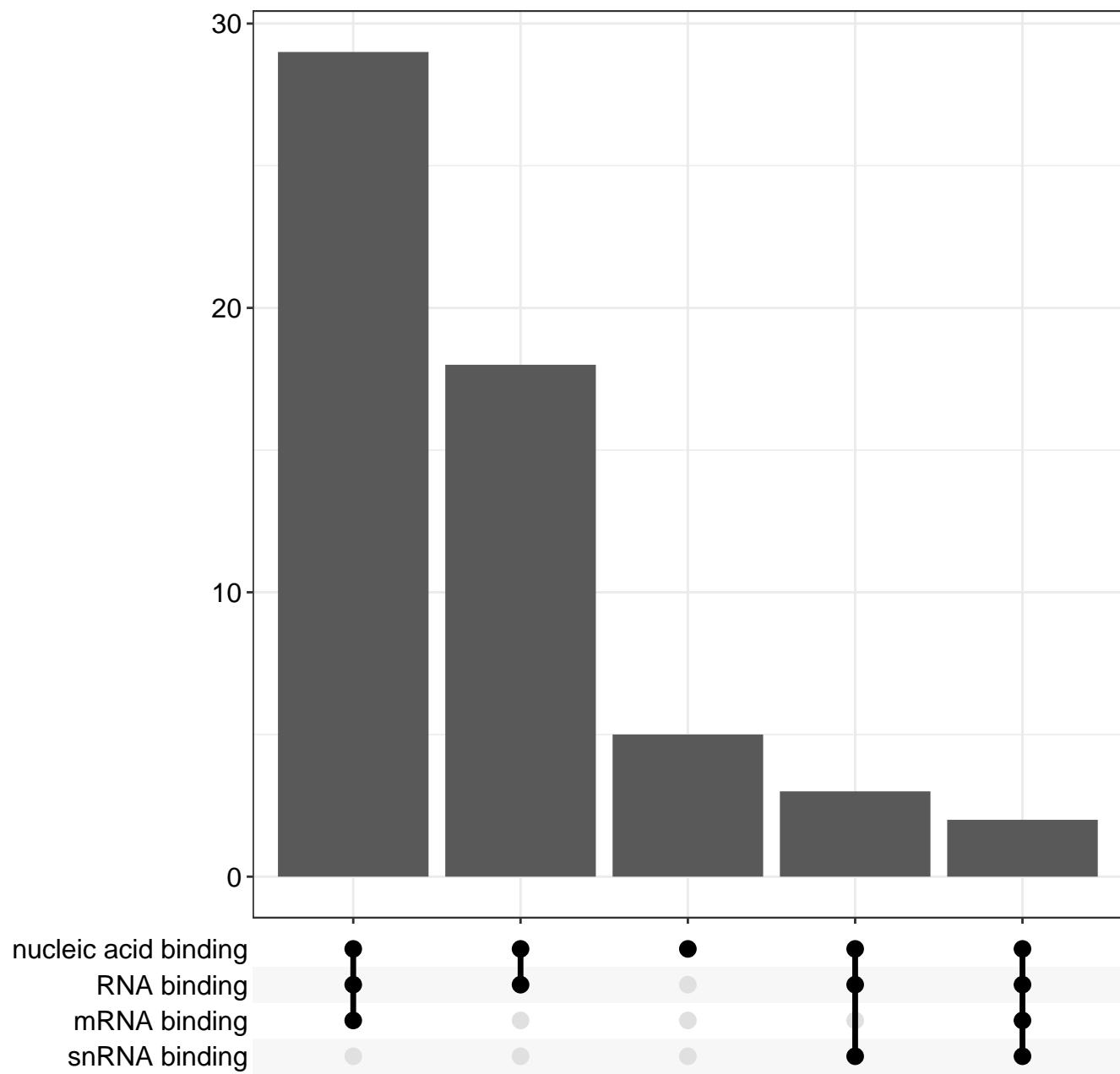


size

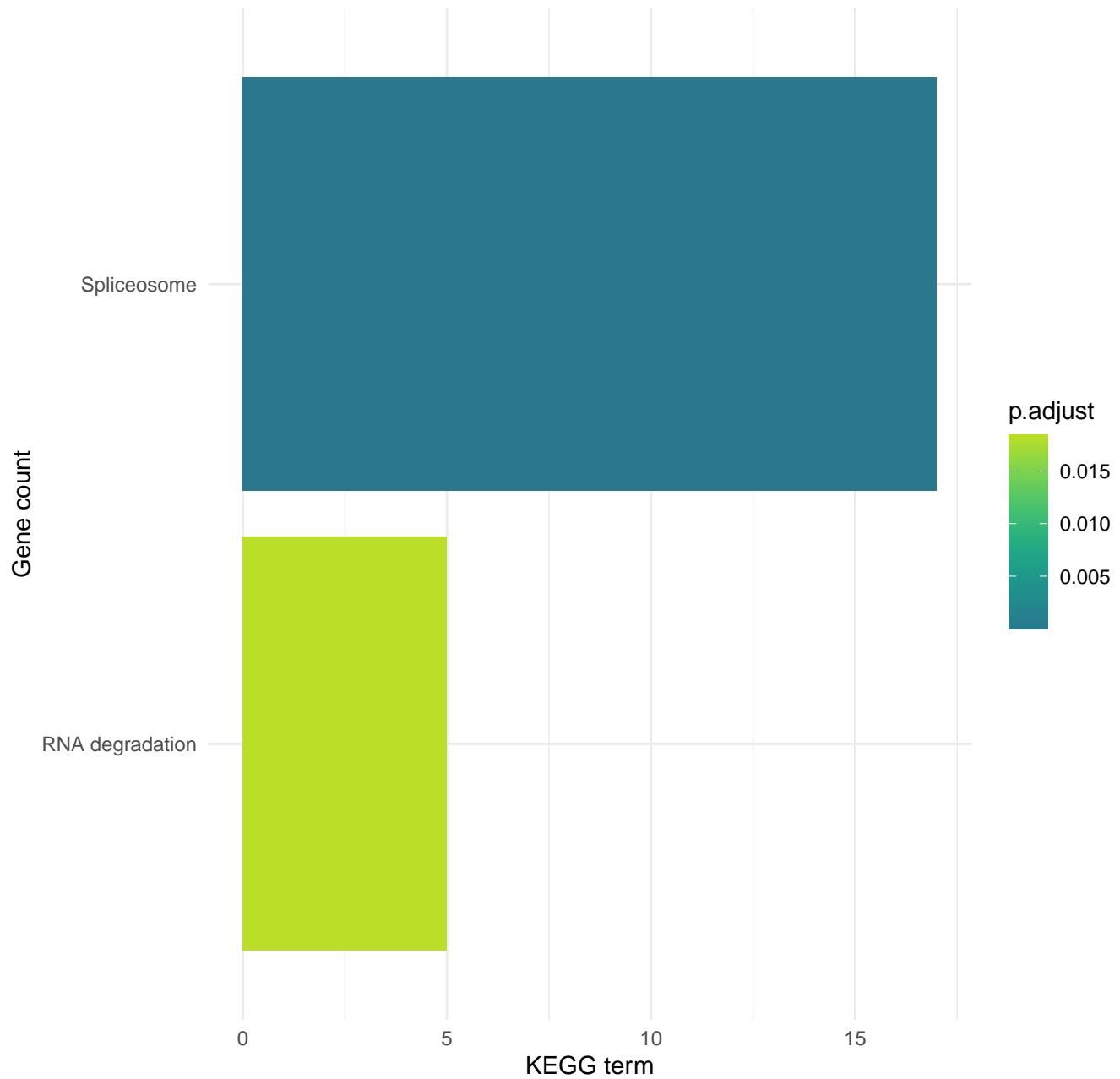




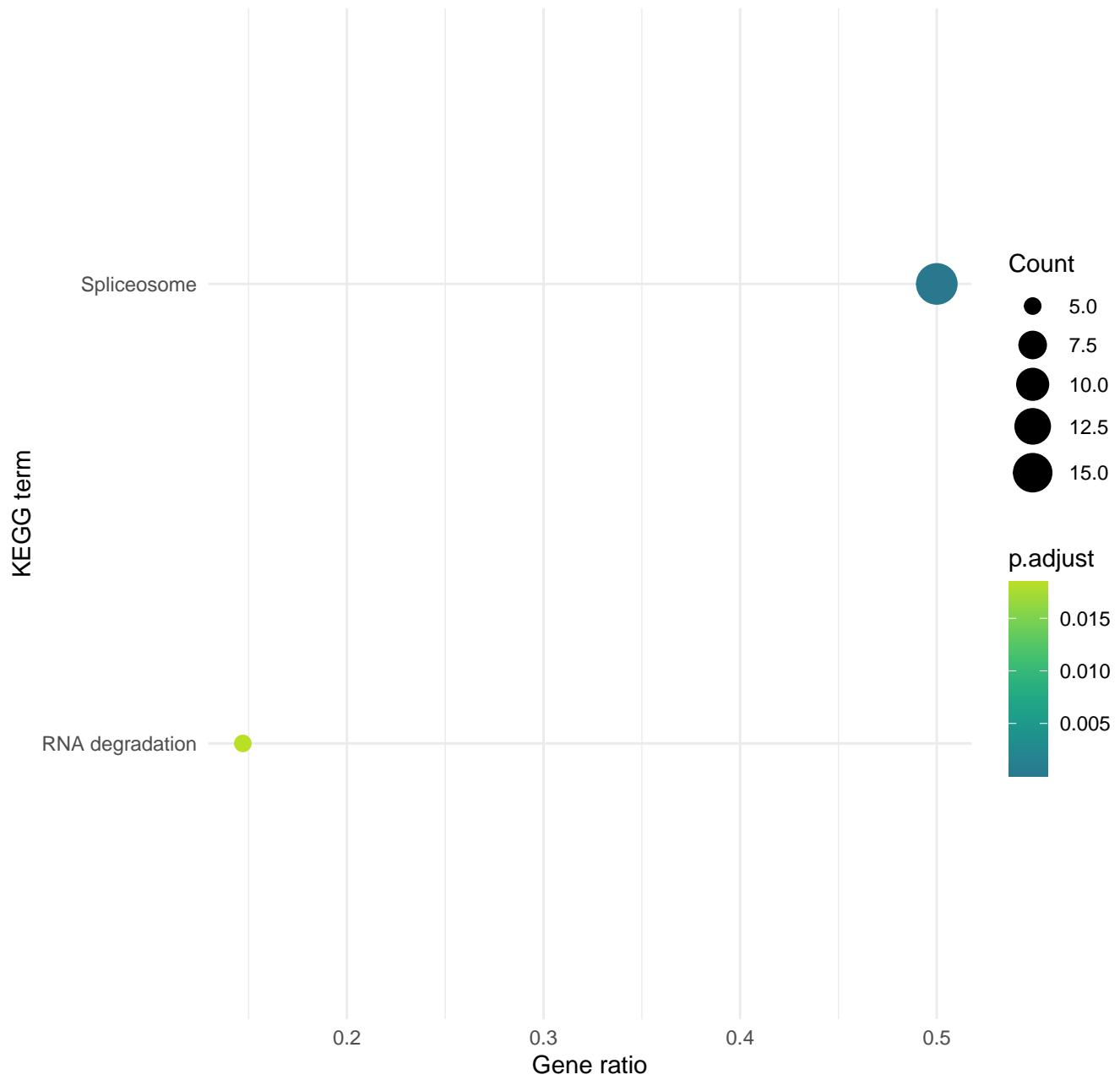
STO1-TAP Up-regulated GO MF upsetplot



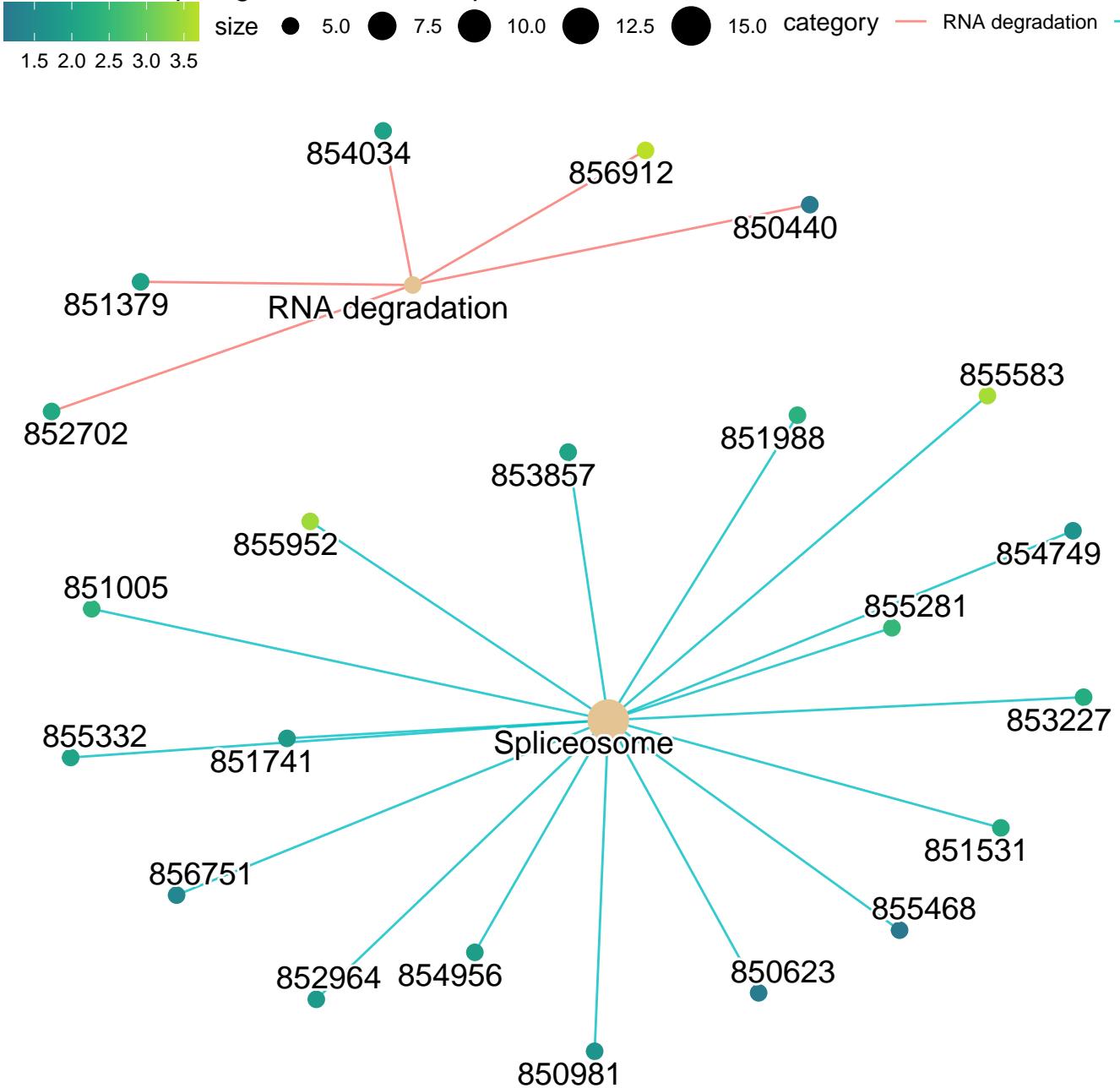
STO1-TAP Up-regulated KEGG barplot



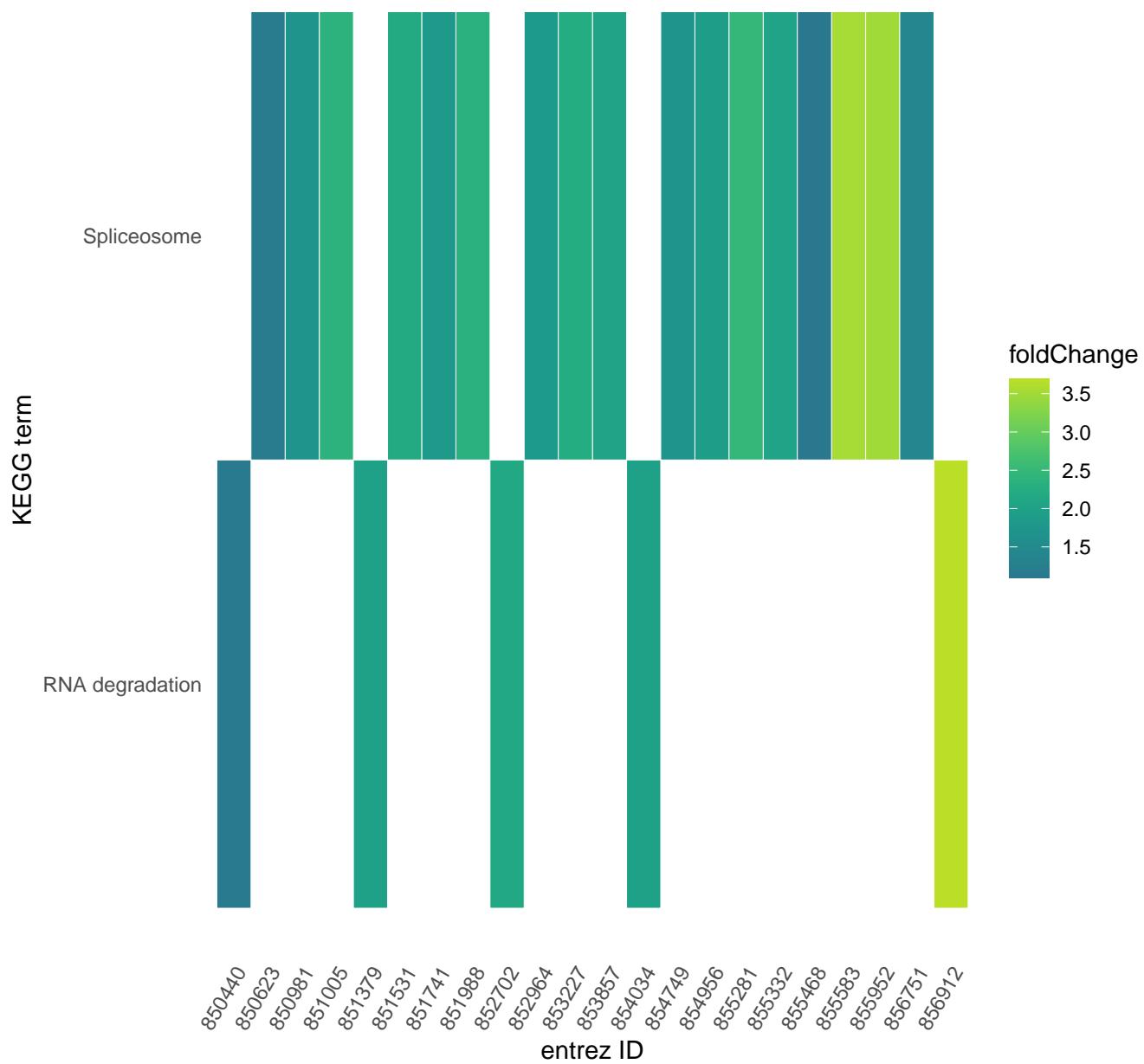
STO1-TAP Up-regulated KEGG dotplot



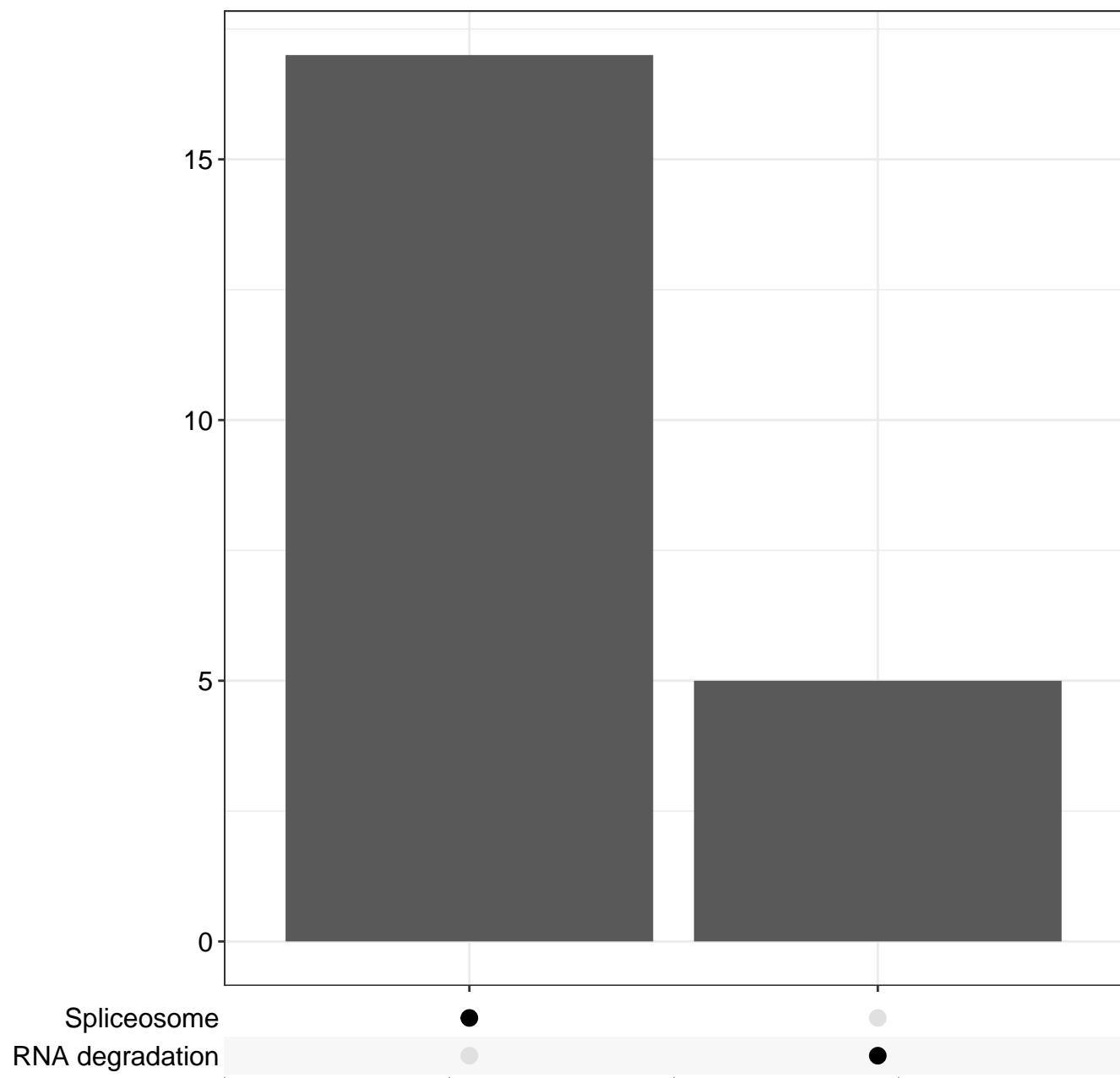
STO1-TAP Up-regulated KEGG dotplot



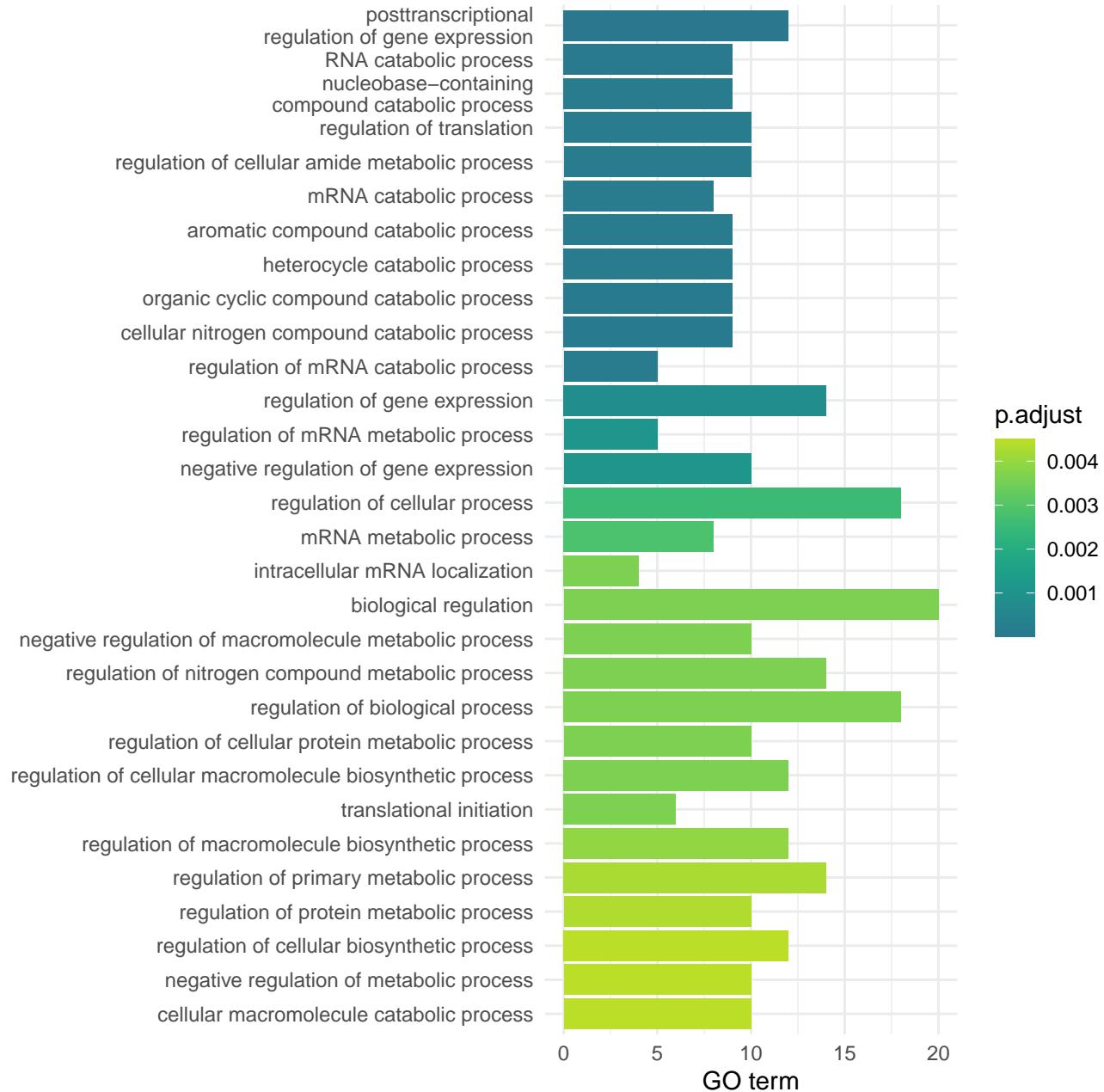
STO1-TAP Up-regulated KEGG heatplot



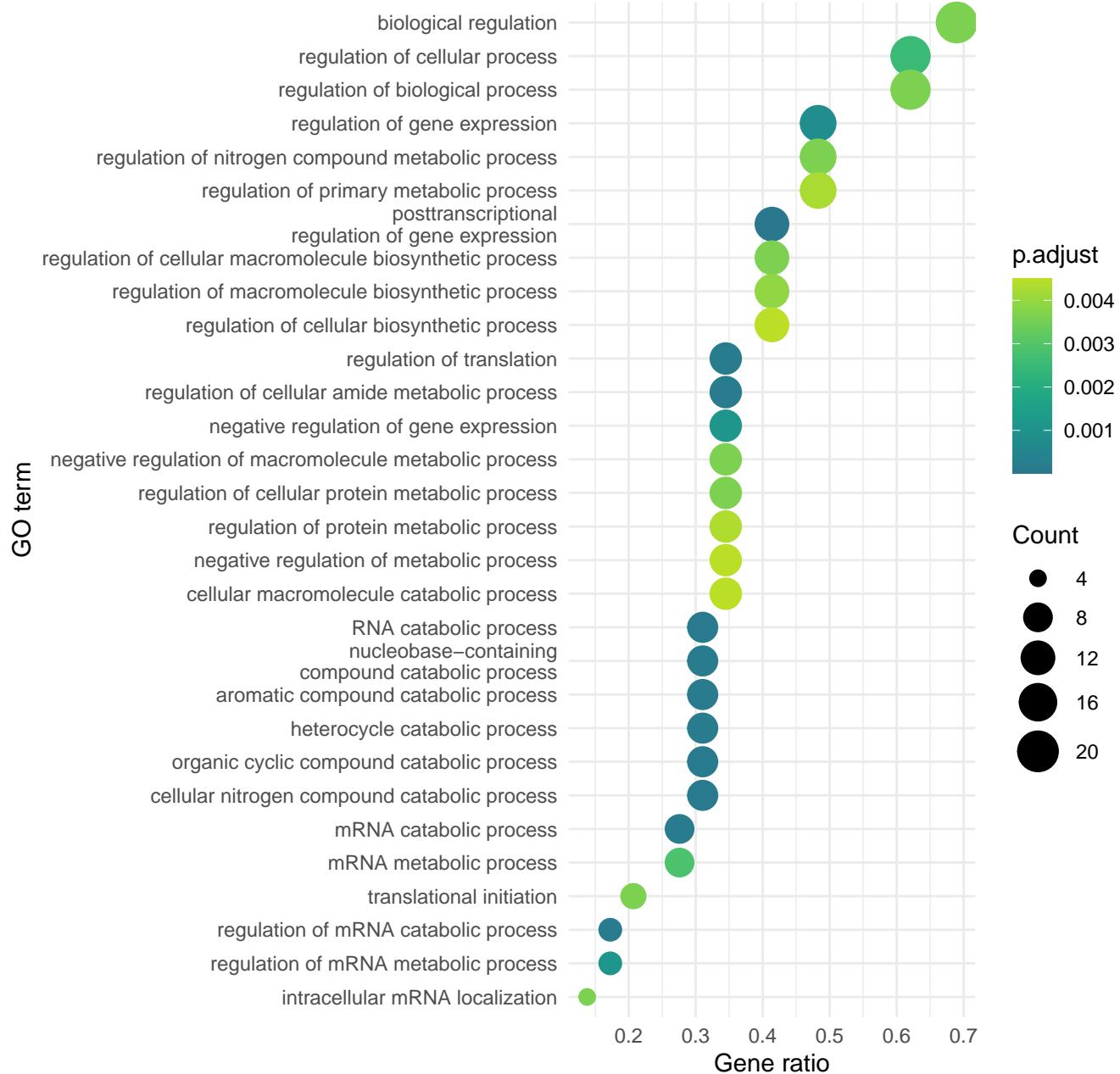
STO1-TAP Up-regulated KEGG upsetplot



SGN1-TAP Up-regulated GO BP barplot

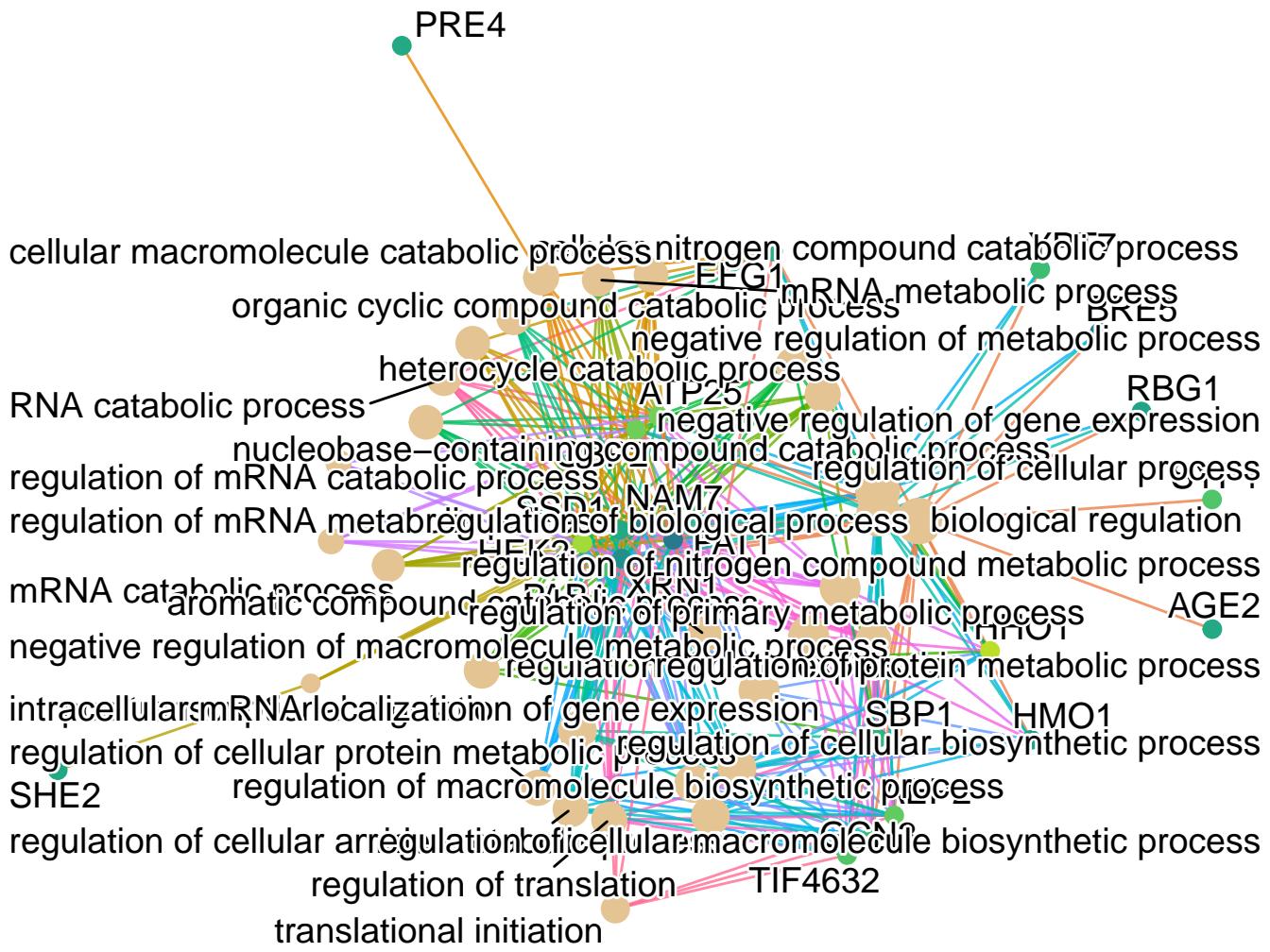


SGN1-TAP Up-regulated GO BP dotplot

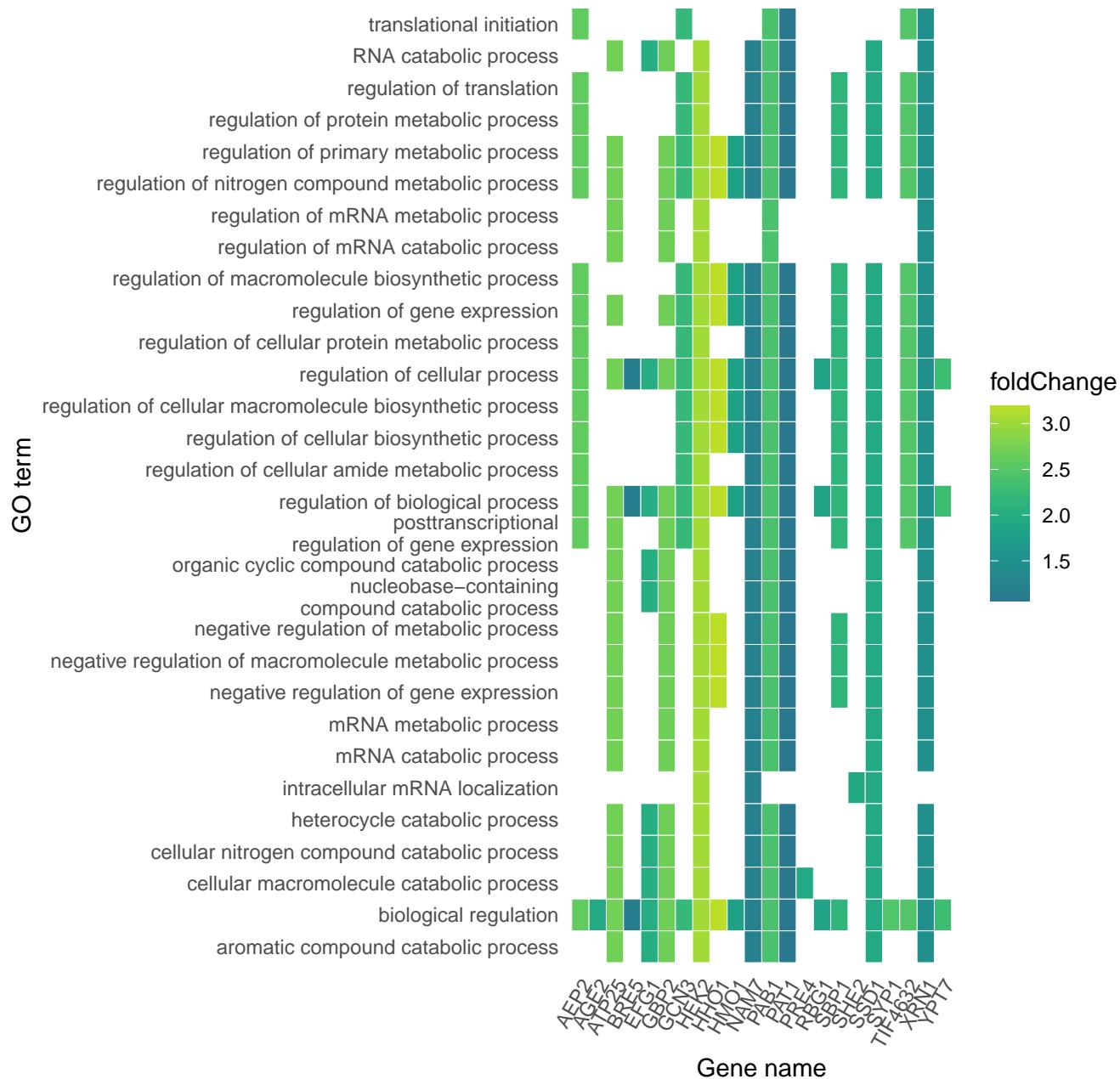


SGN1-TAP Up-regulated GO BP cnetplot

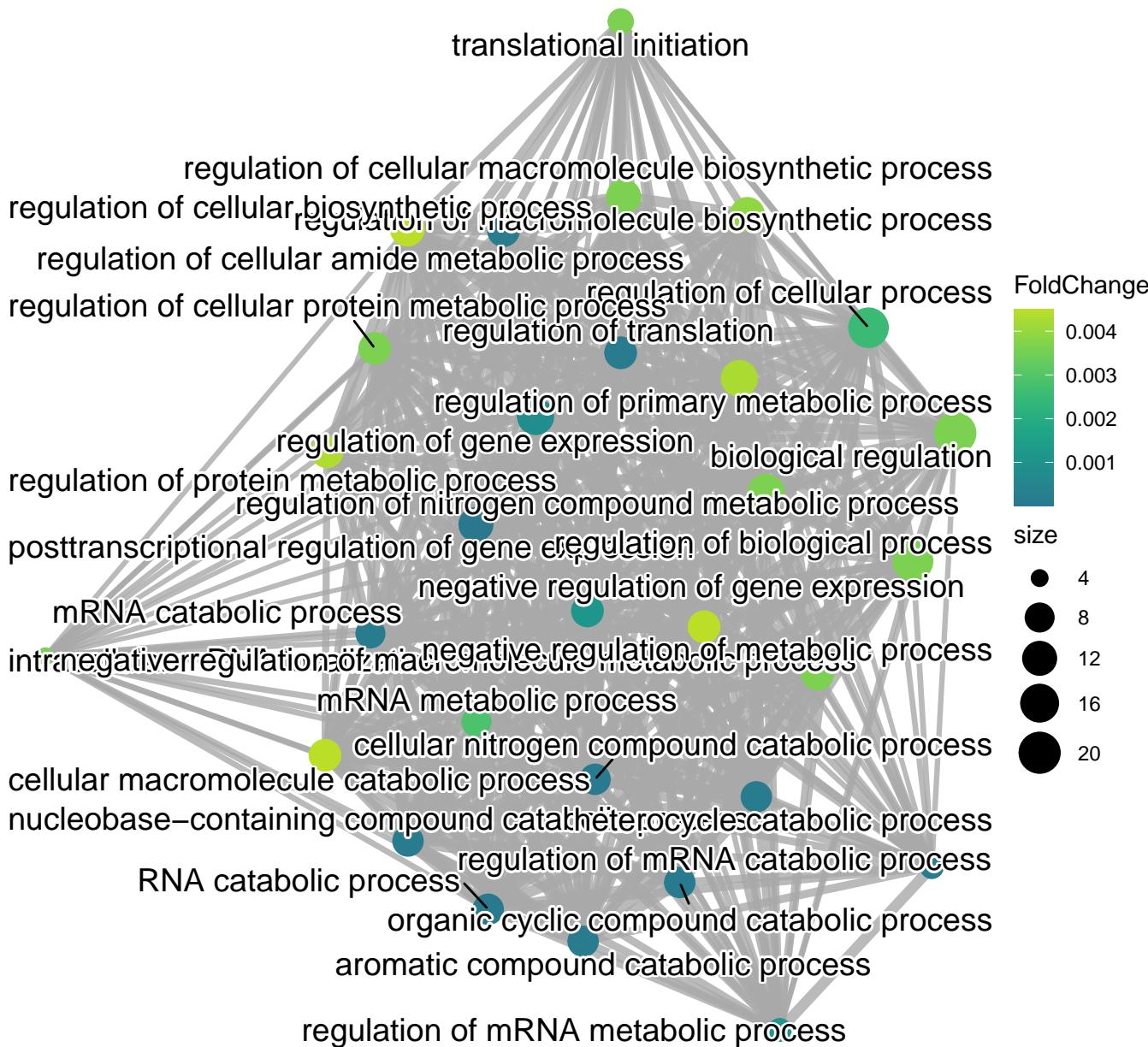
- organic cyclic compound catabolic process
 - posttranscriptional regulation of gene expression
 - regulation of biological process
 - regulation of cellular amide metabolic process
 - regulation of cellular biosynthetic process
 - regulation of cellular macromolecule biosynthetic process
 - regulation of cellular process
 - regulation of cellular protein metabolic process
 - regulation of gene expression
 - regulation of macromolecule catabolic process
 - regulation of mRNA catabolic process
 - regulation of mRNA metabolism

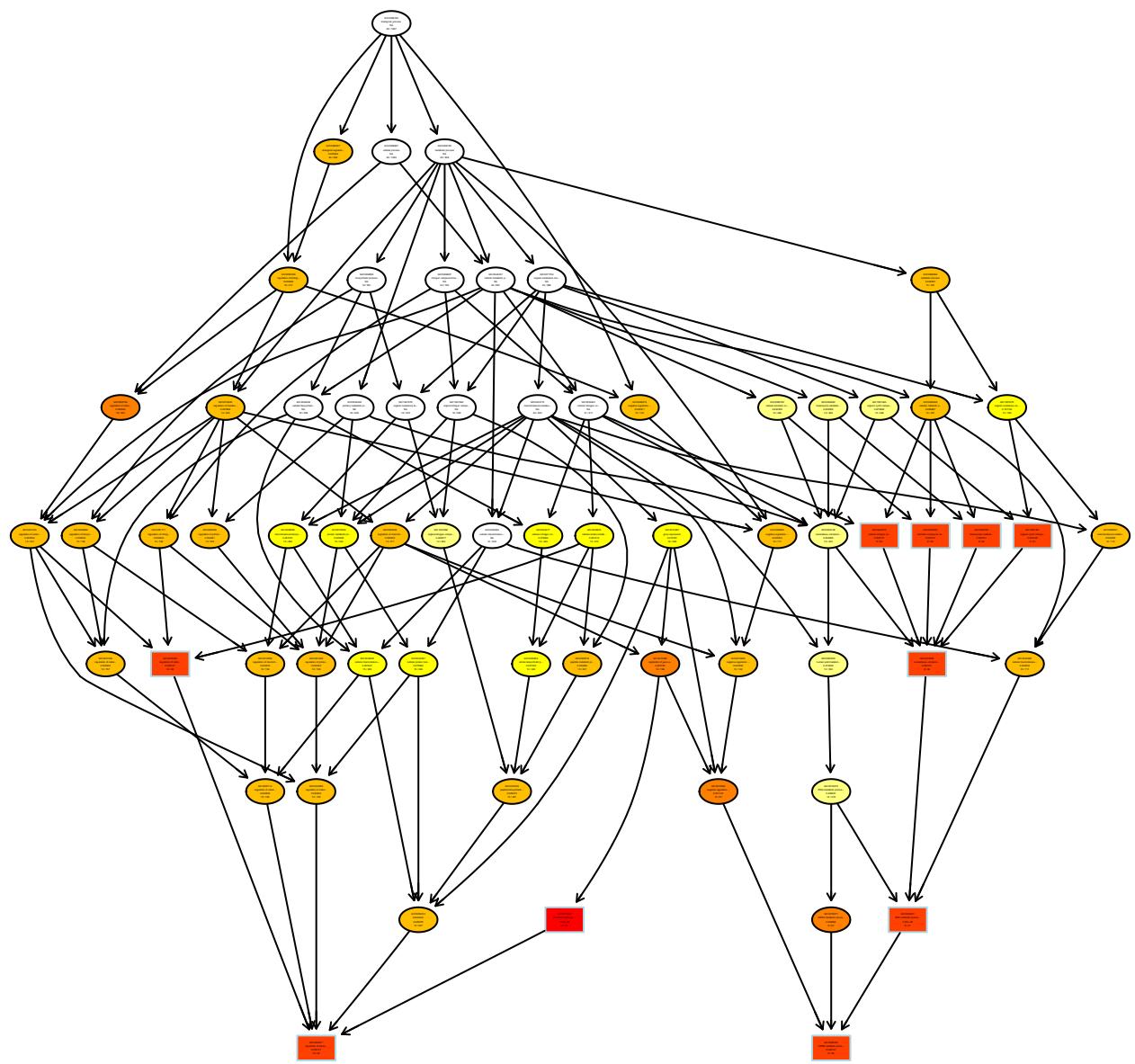


SGN1-TAP Up-regulated GO BP heatplot

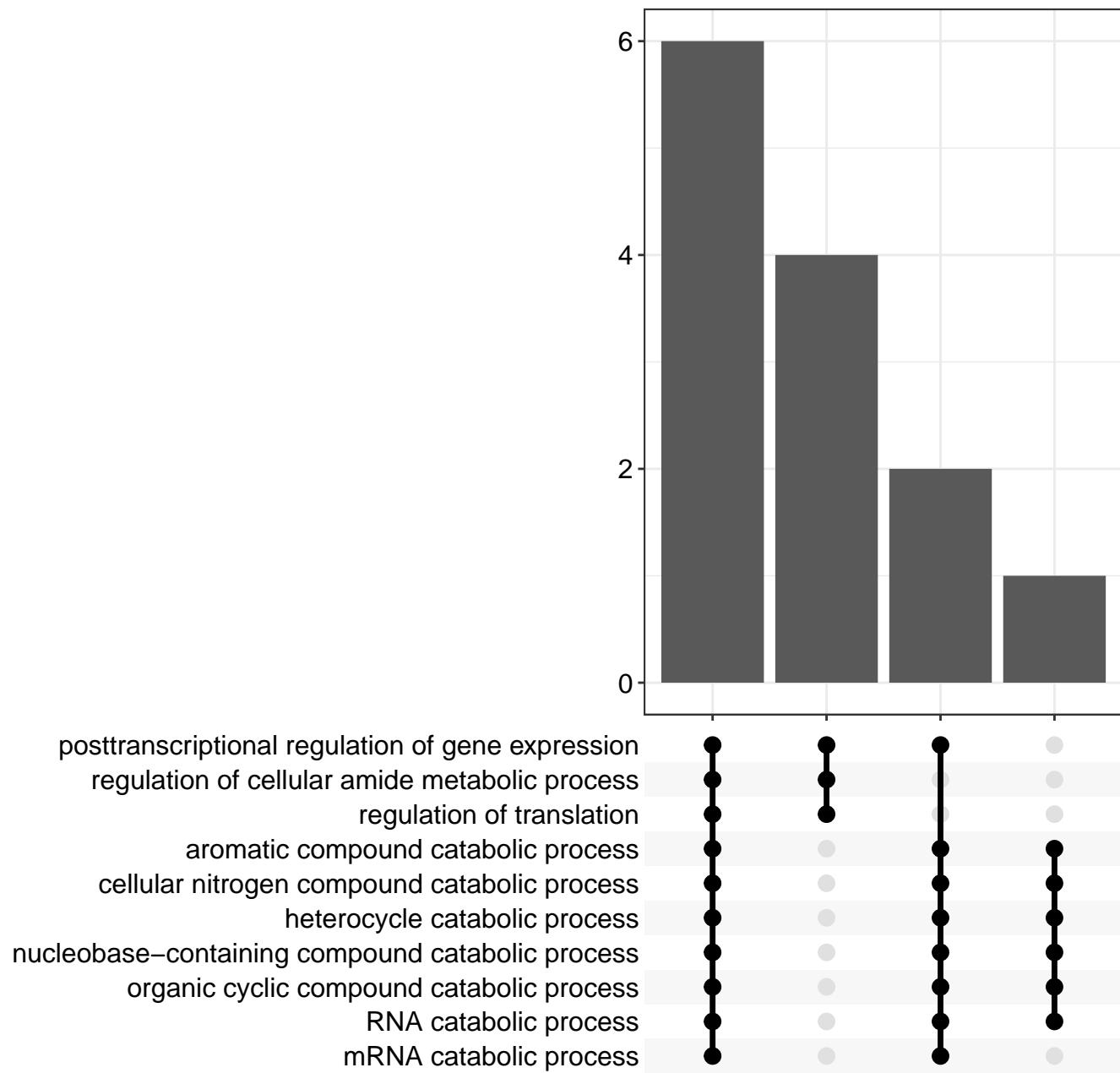


SGN1-TAP Up-regulated GO BP emapplot

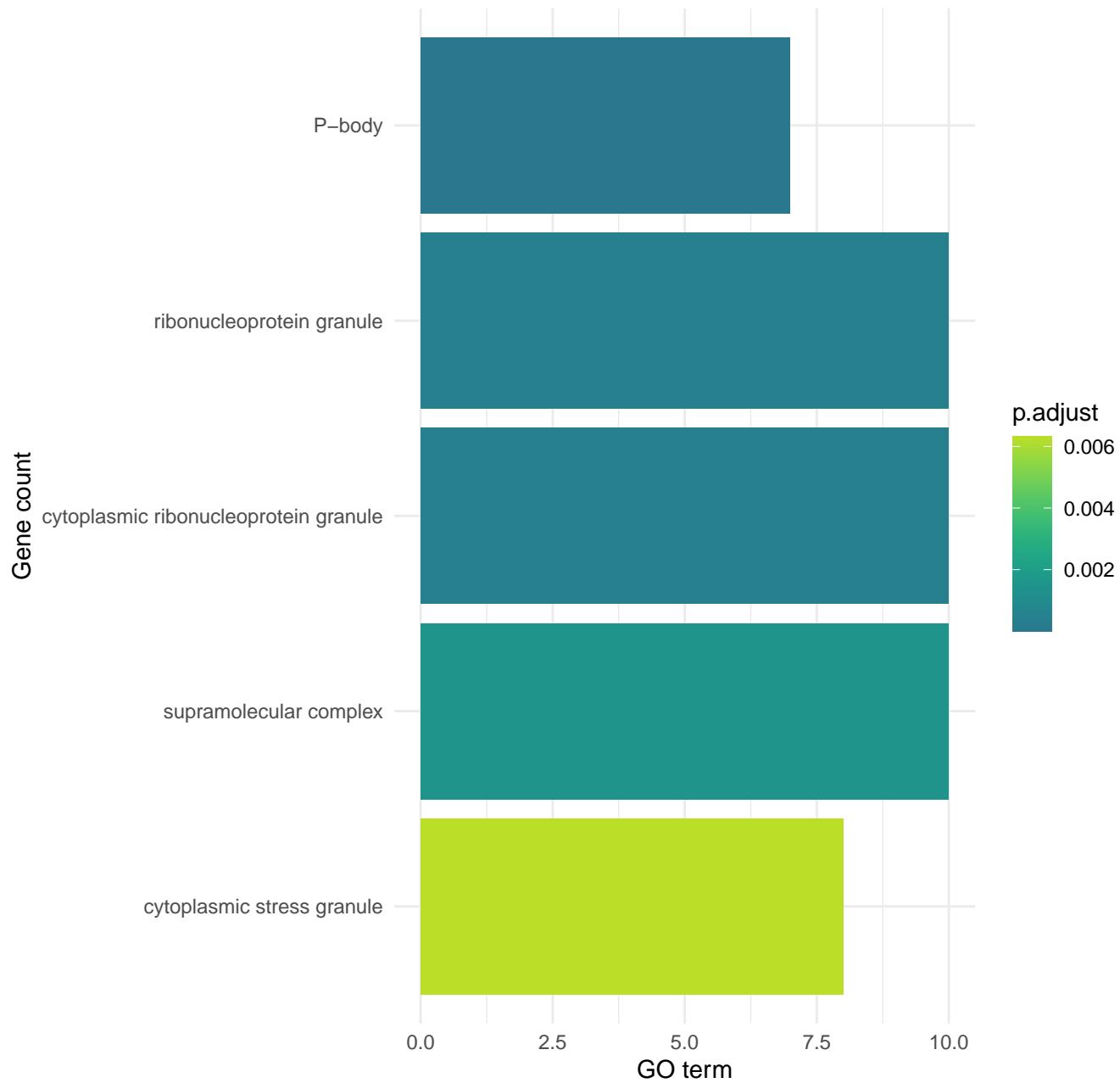




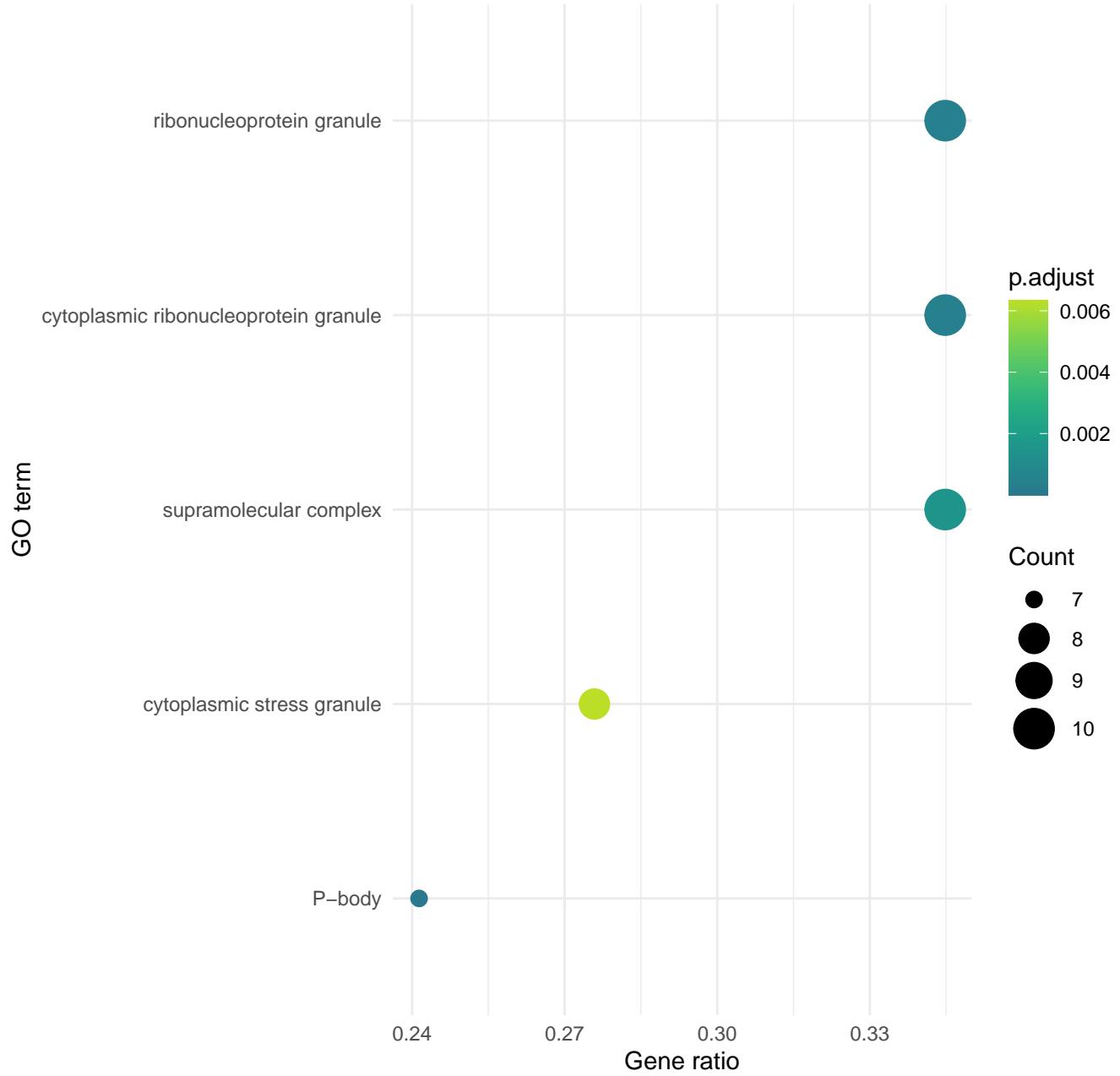
SGN1-TAP Up-regulated GO BP ups



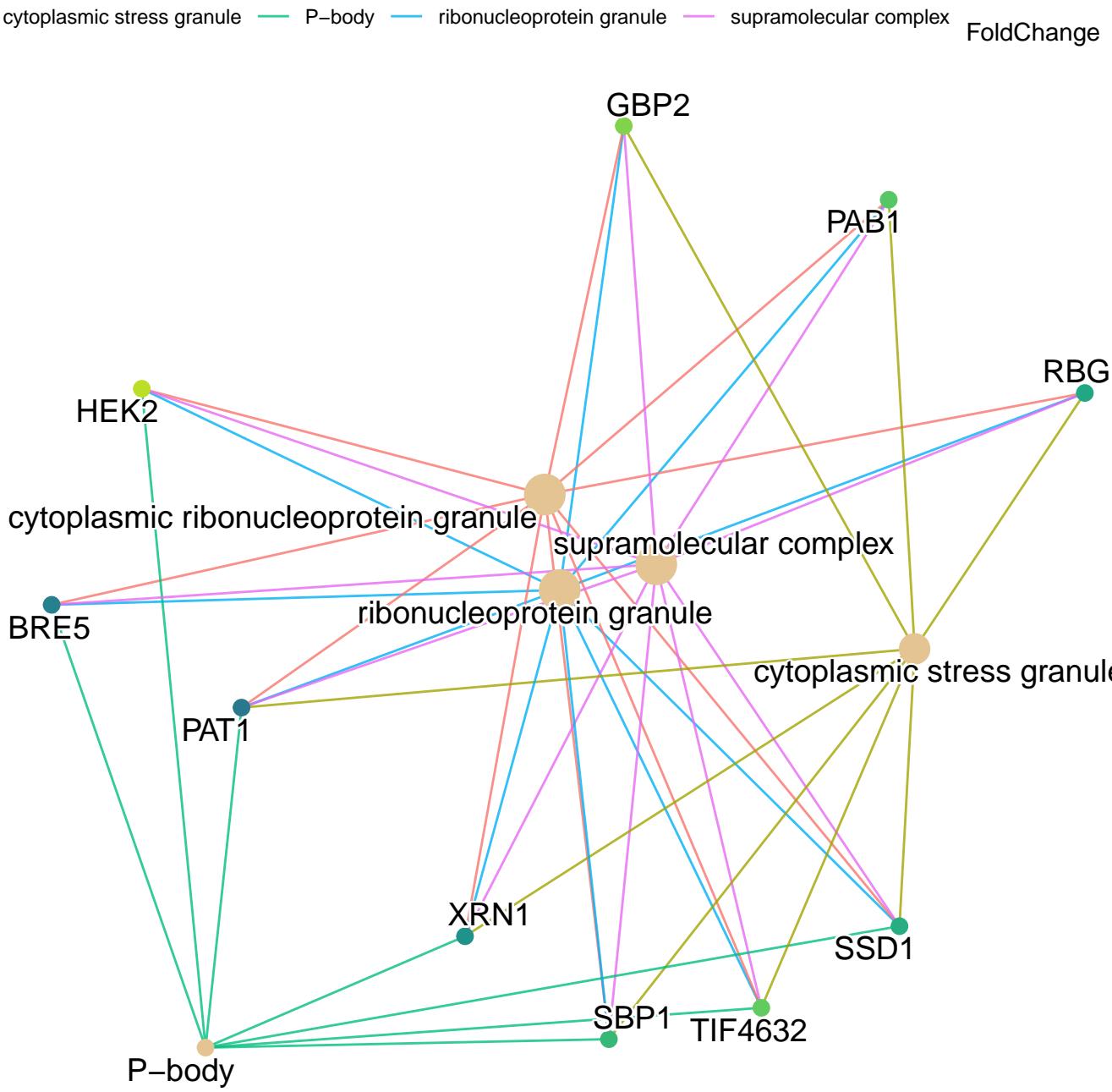
SGN1-TAP Up-regulated GO CC barplot



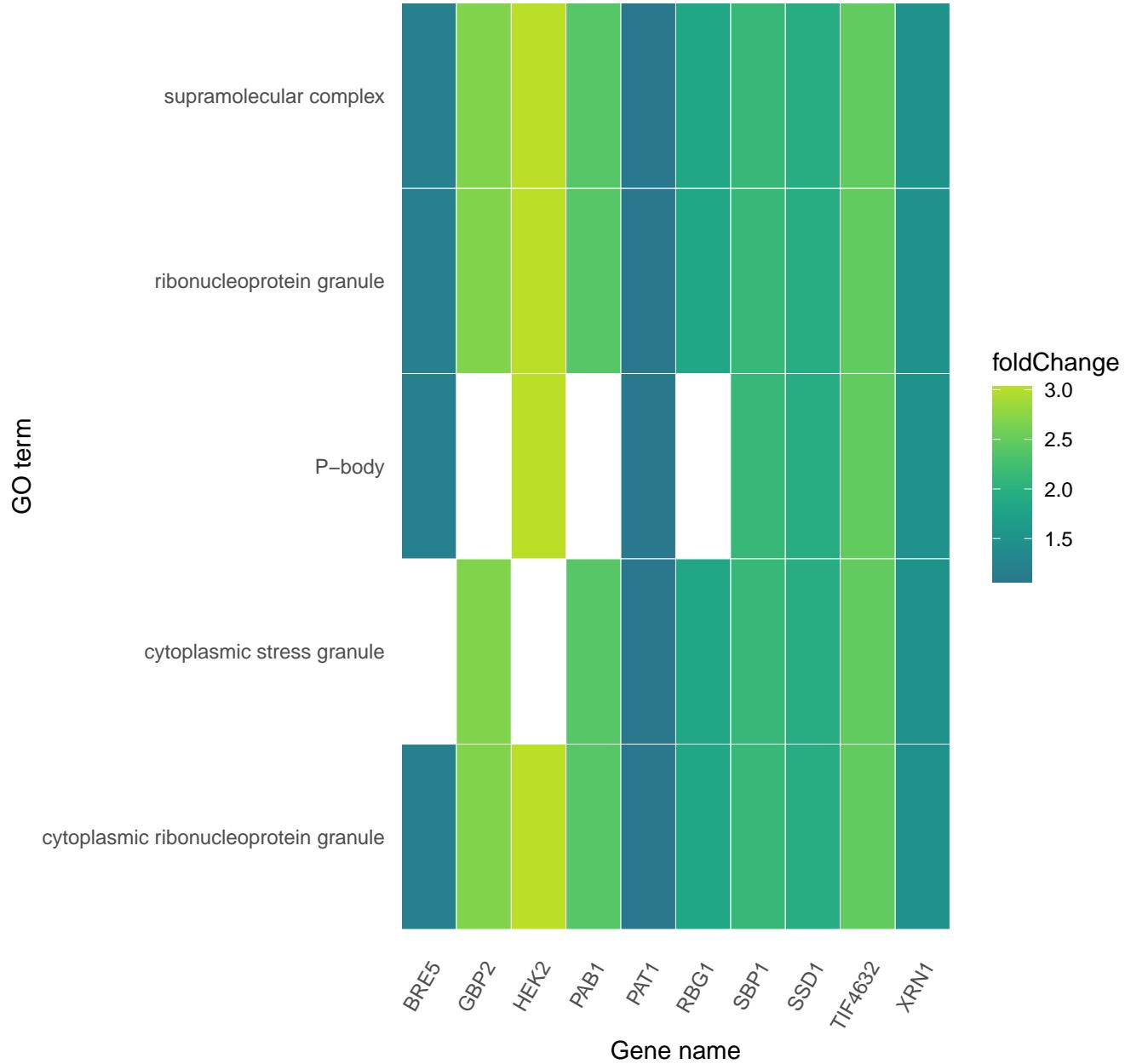
SGN1-TAP Up-regulated GO CC dotplot



SGN1-TAP Up-regulated GO CC cnetplot

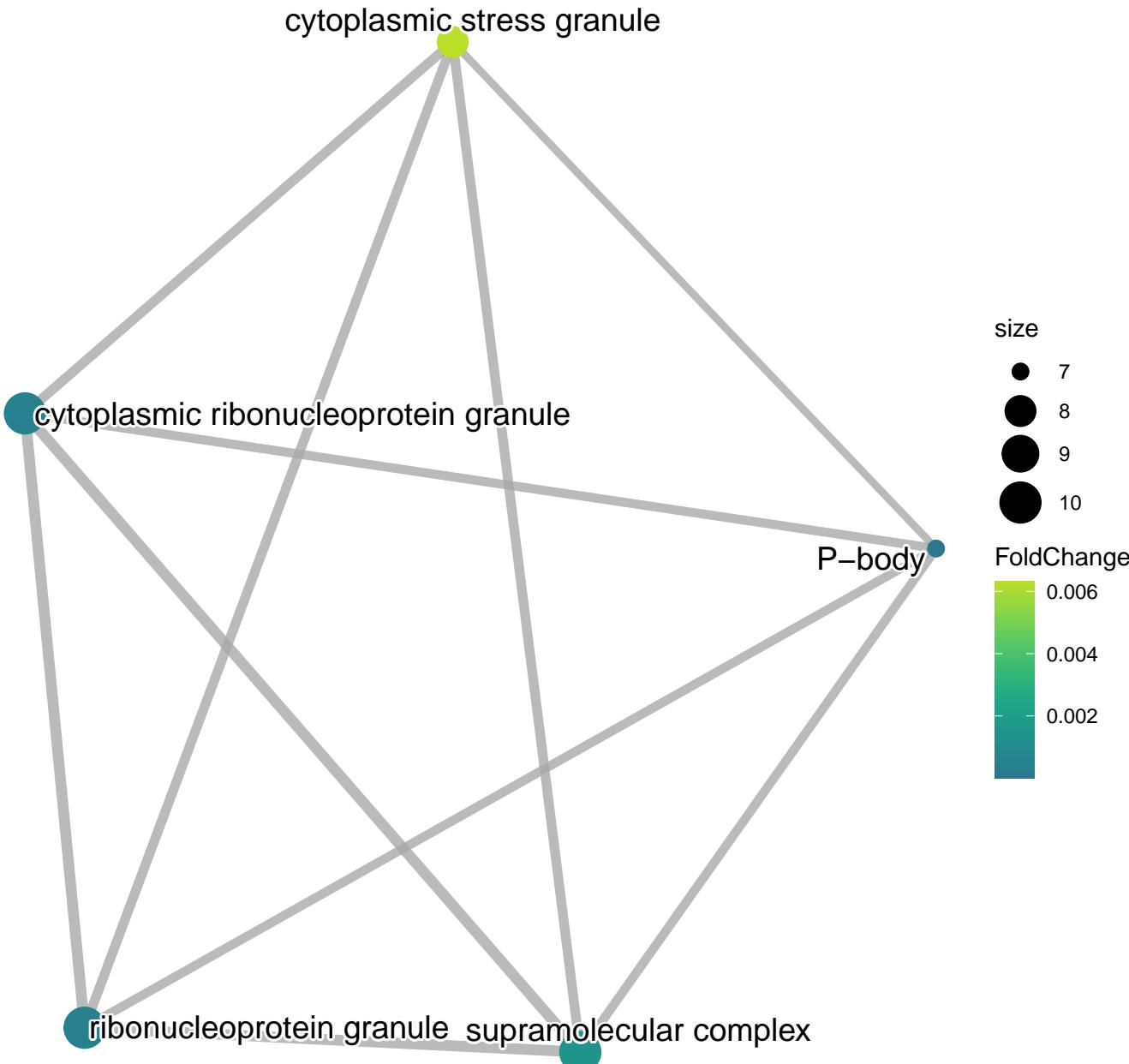


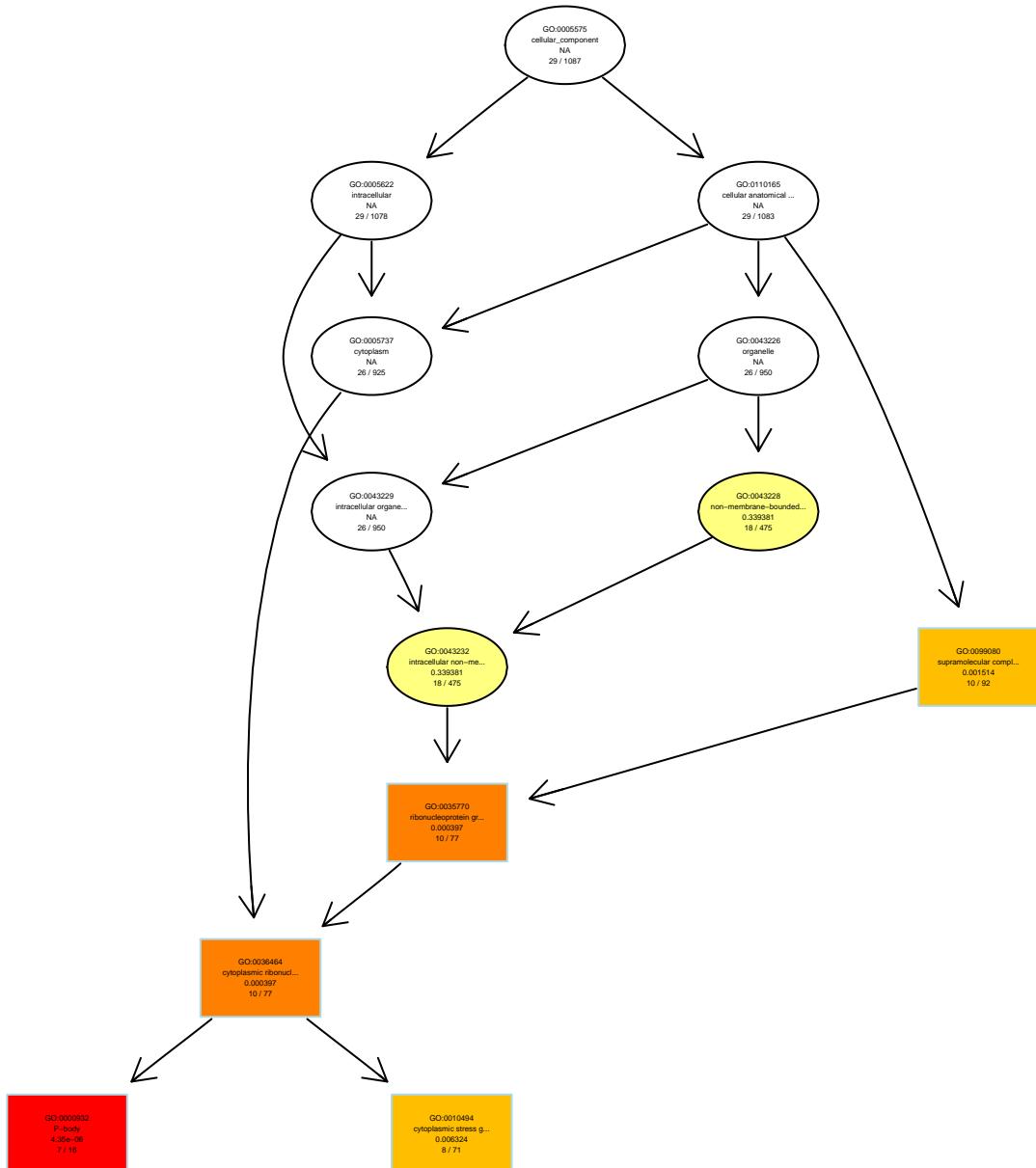
SGN1-TAP Up-regulated GO CC heatplot



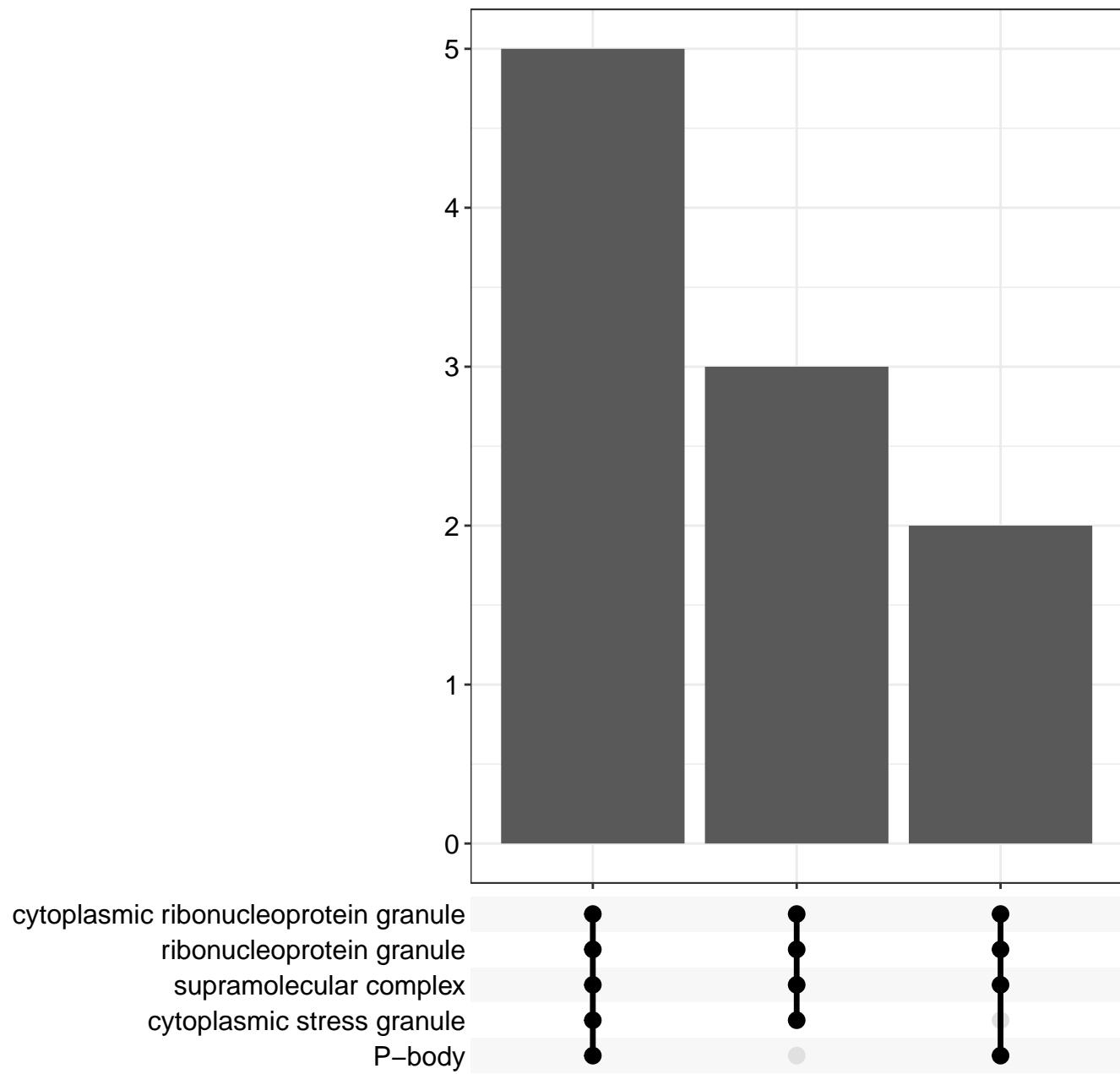
SGN1-TAP Up-regulated GO CC emapplot

cytoplasmic stress granule

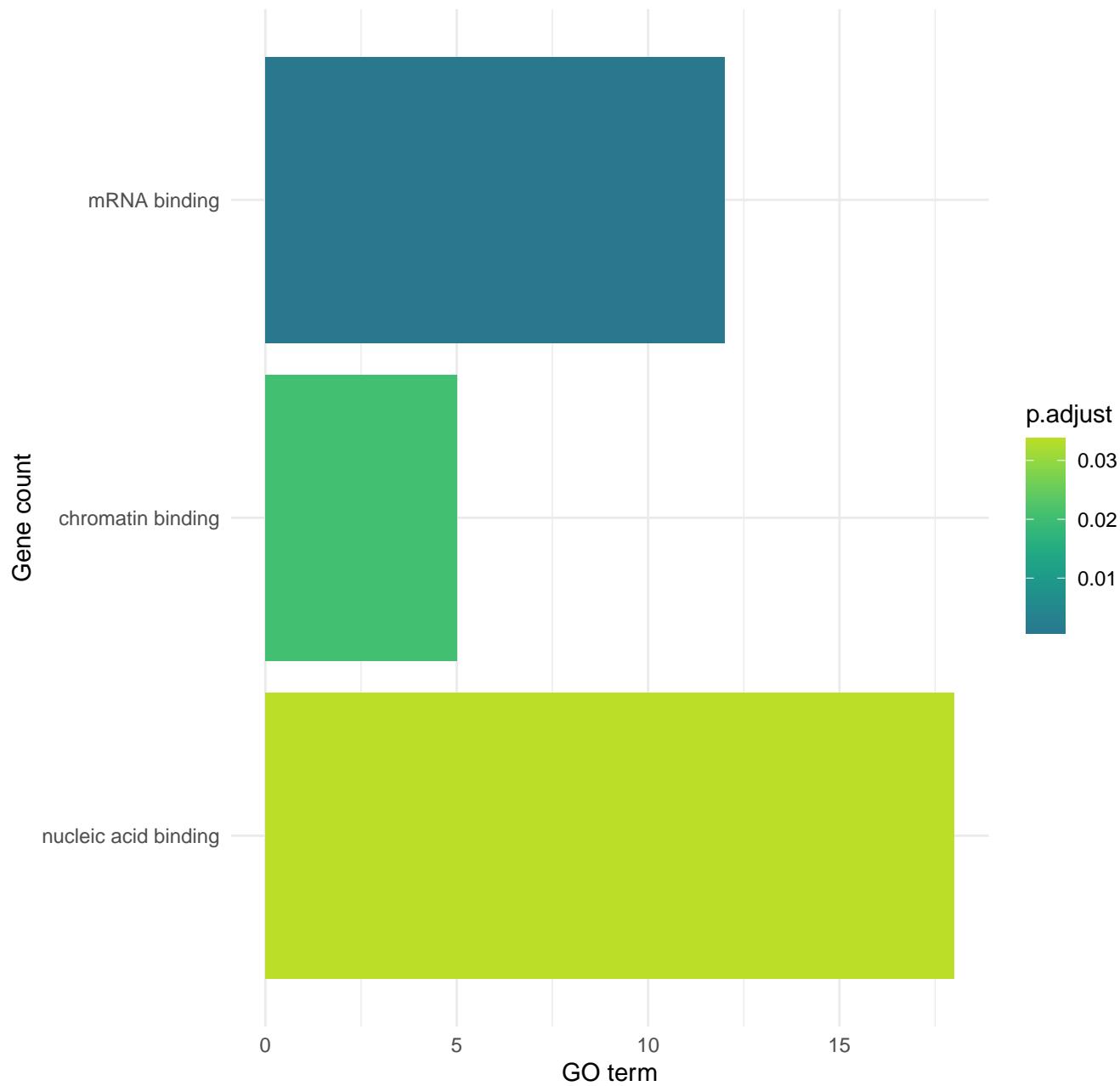




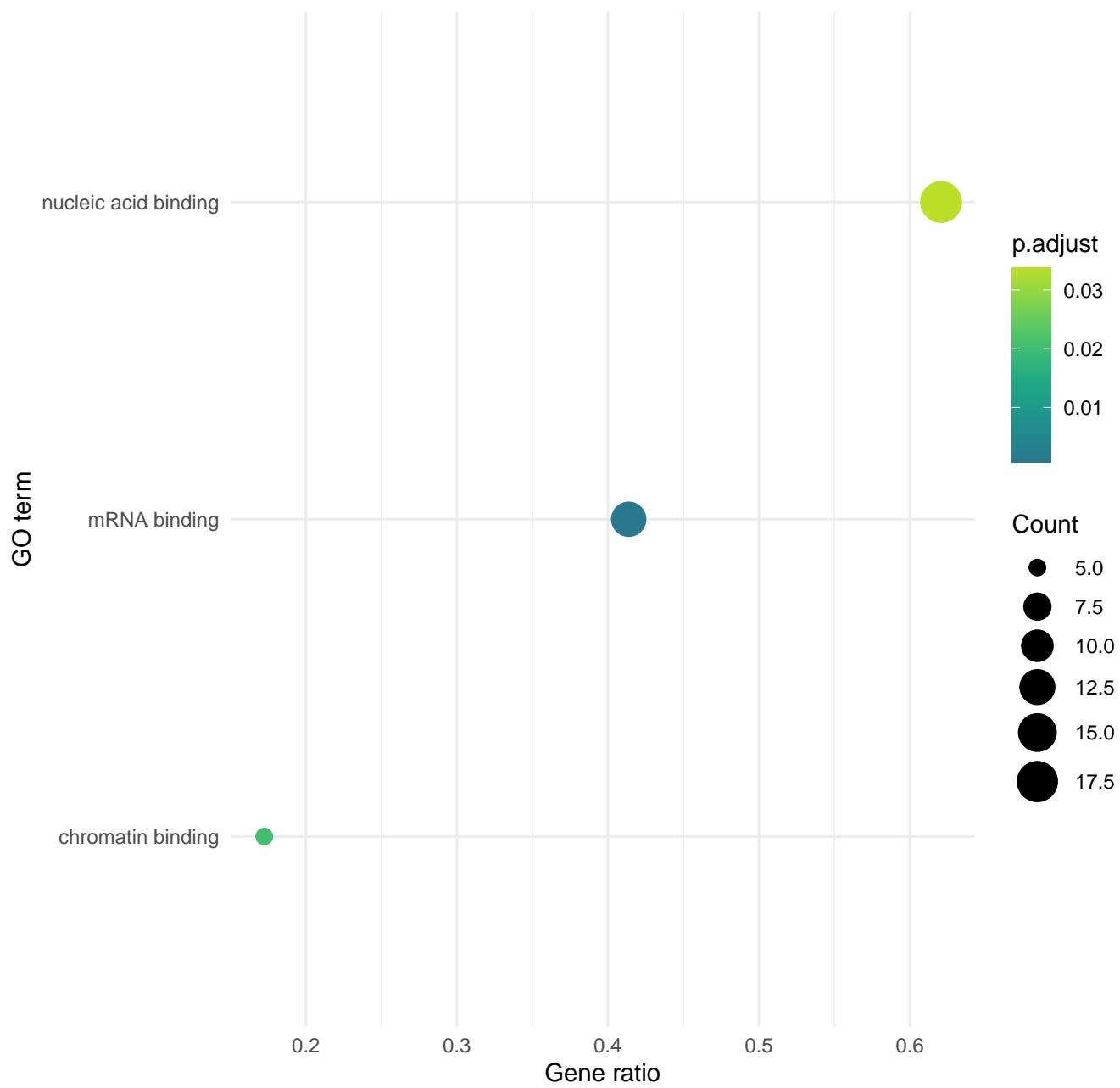
SGN1-TAP Up-regulated GO CC upsetplot



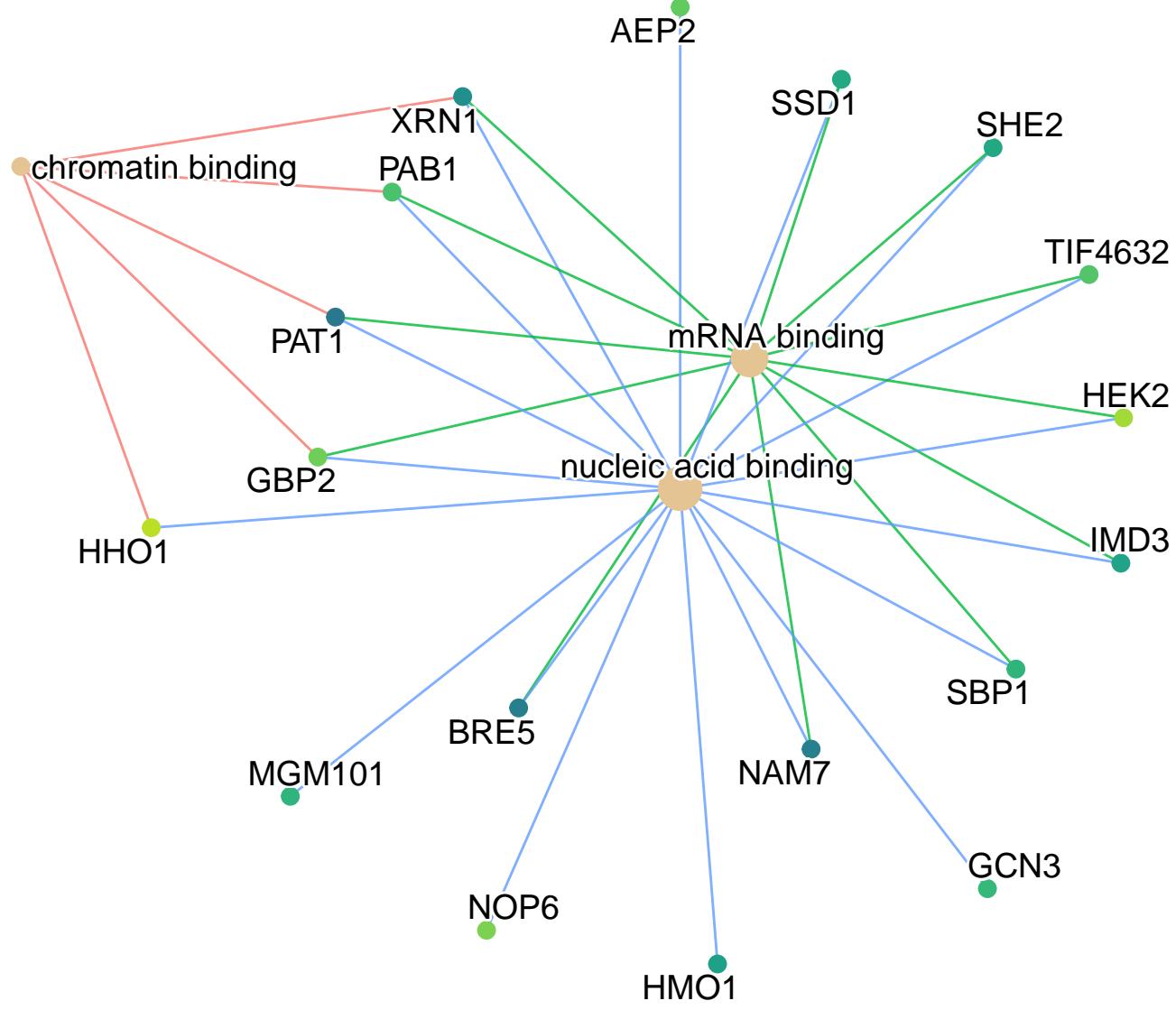
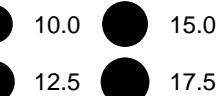
SGN1-TAP Up-regulated GO MF barplot



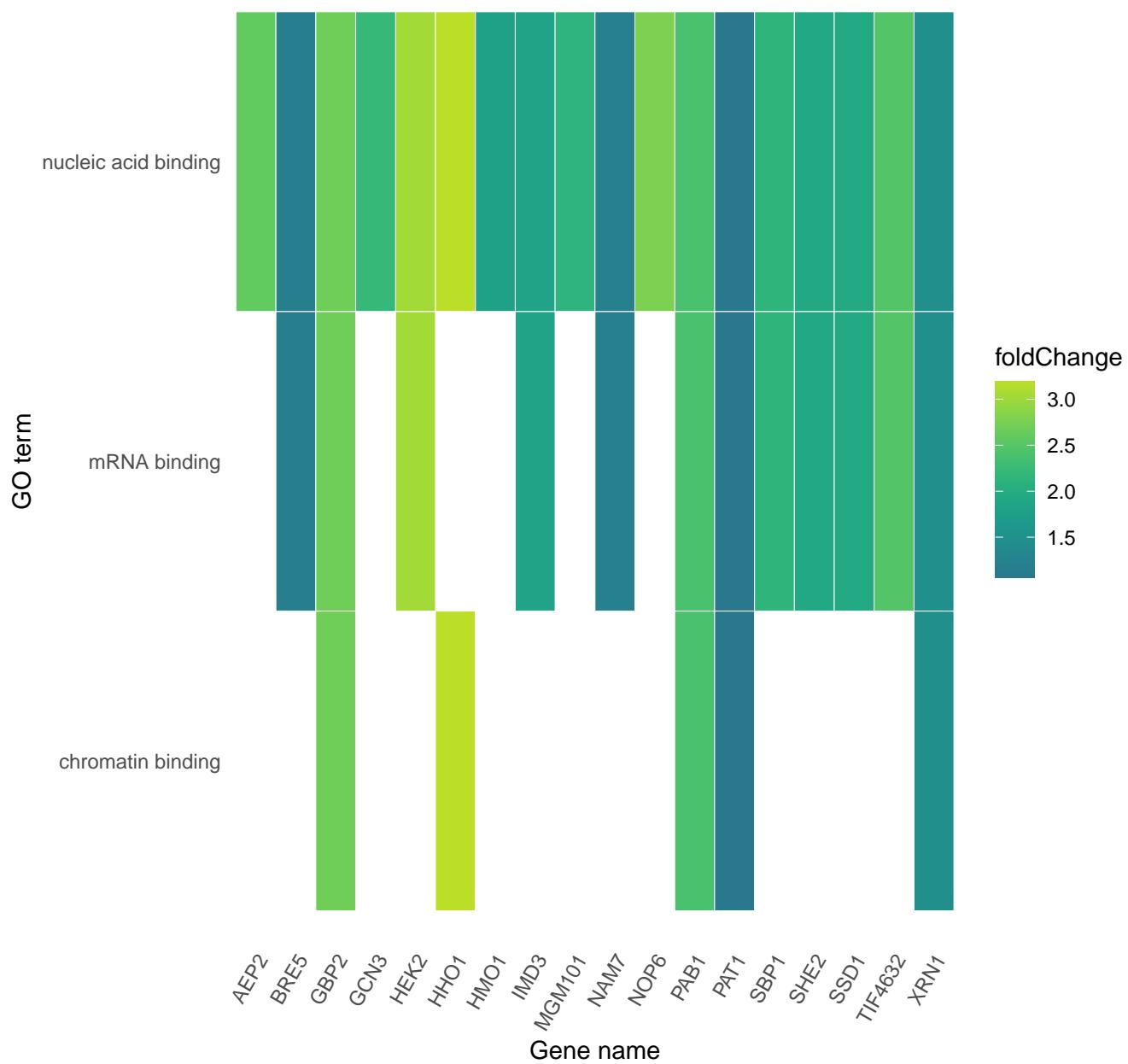
SGN1-TAP Up-regulated GO MF dotplot



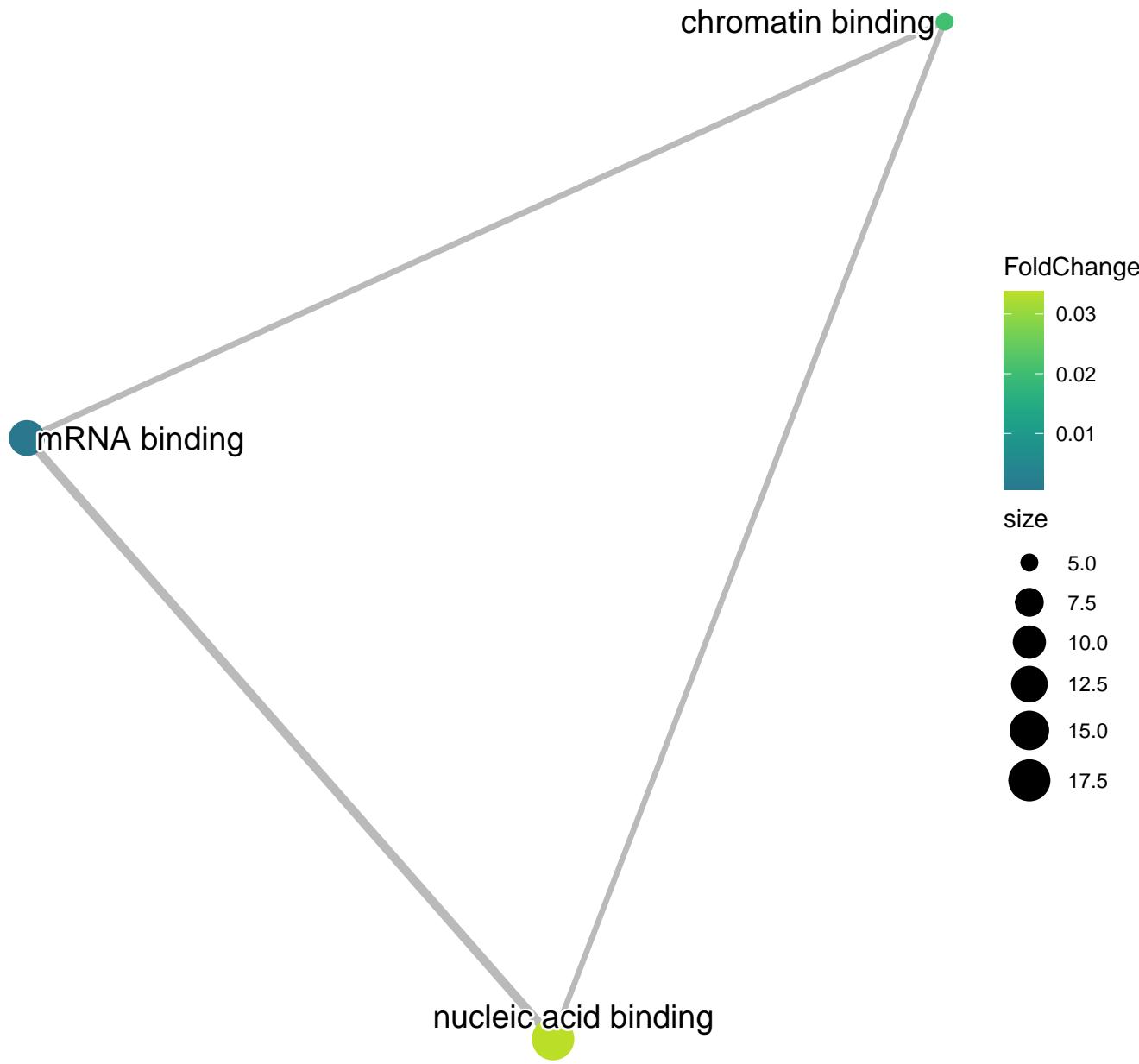
SGN1-TAP Up-regulated GO MF cnetplot

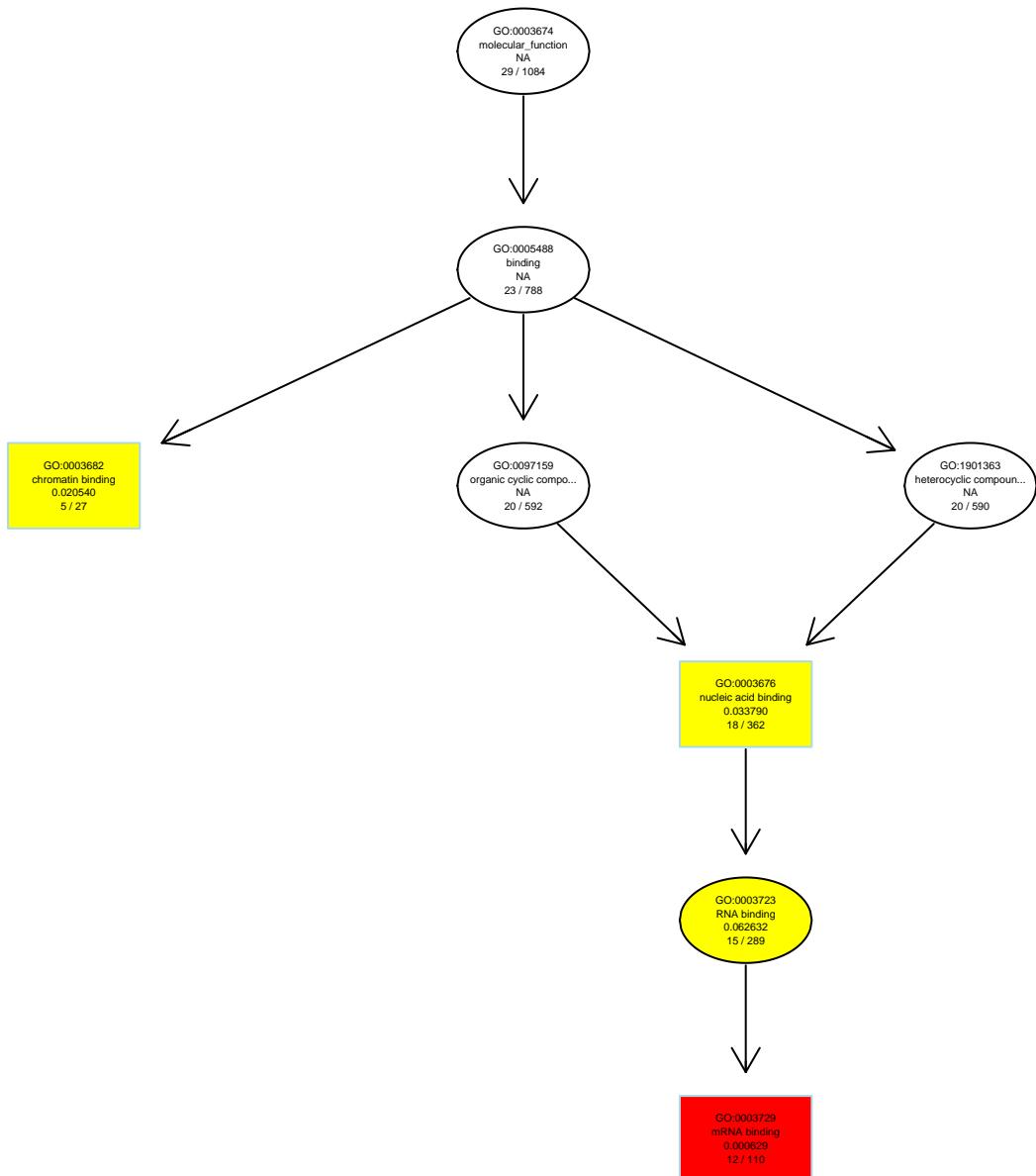


SGN1-TAP Up-regulated GO MF heatplot

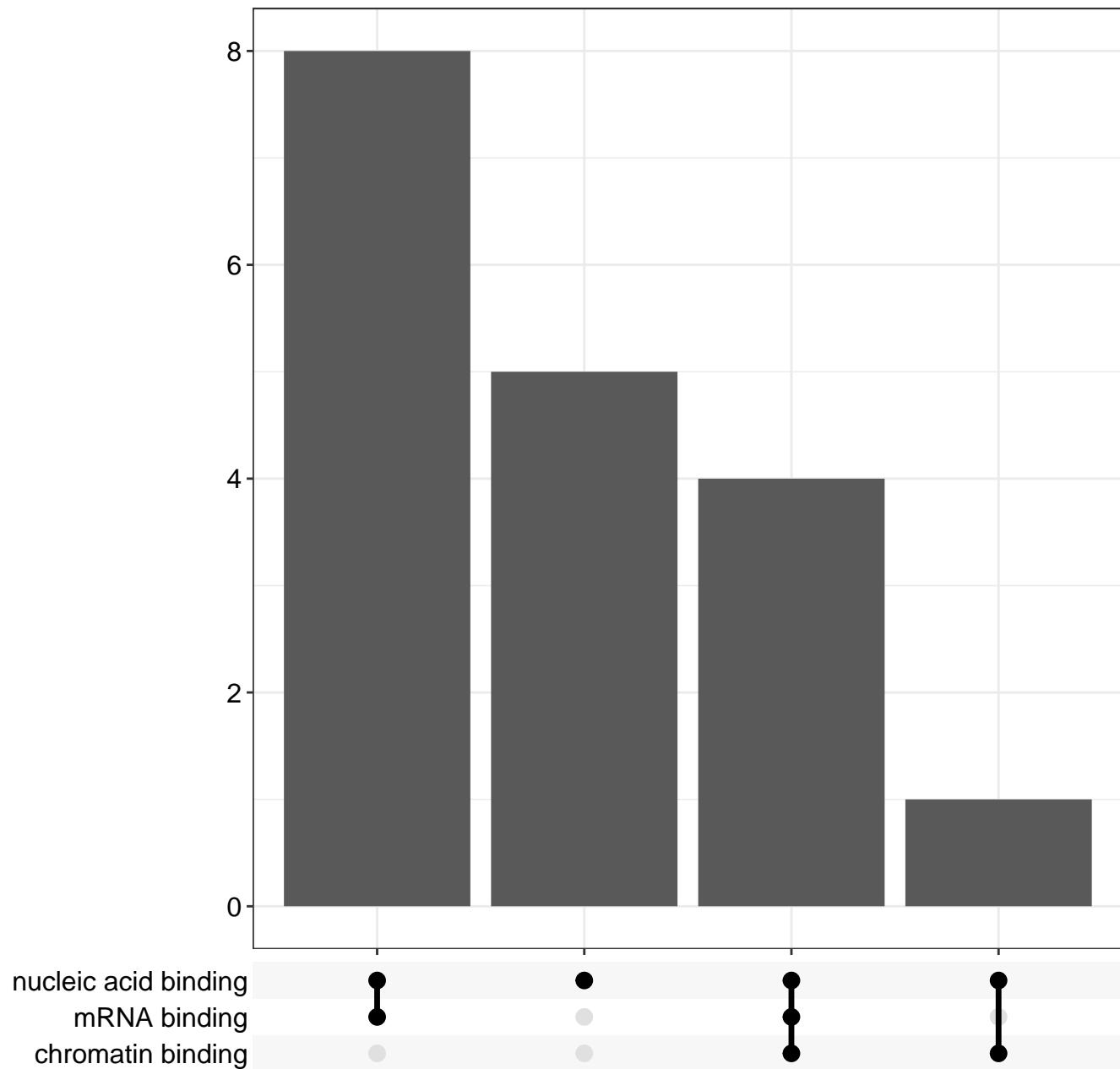


SGN1-TAP Up-regulated GO MF emapplot

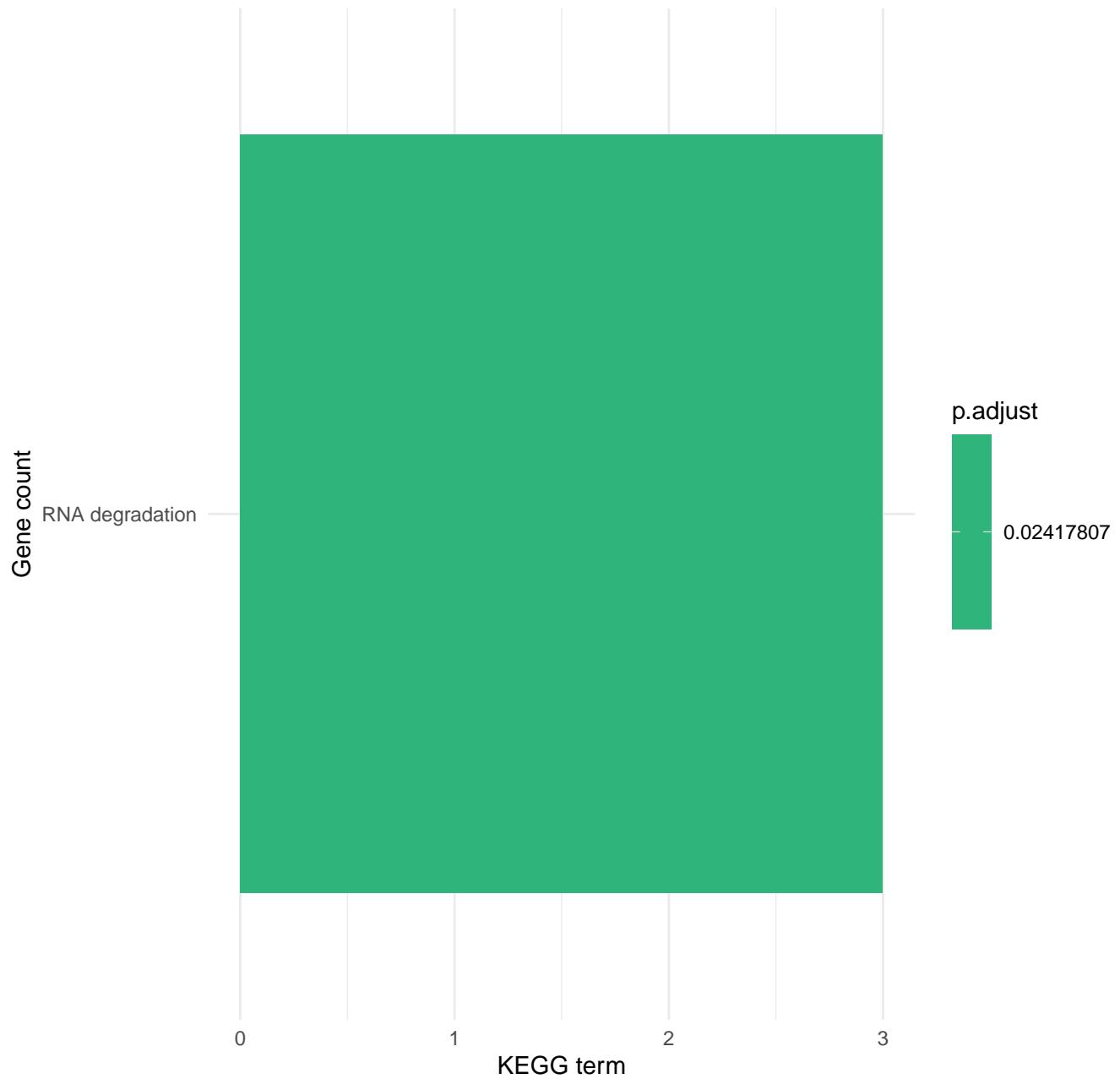




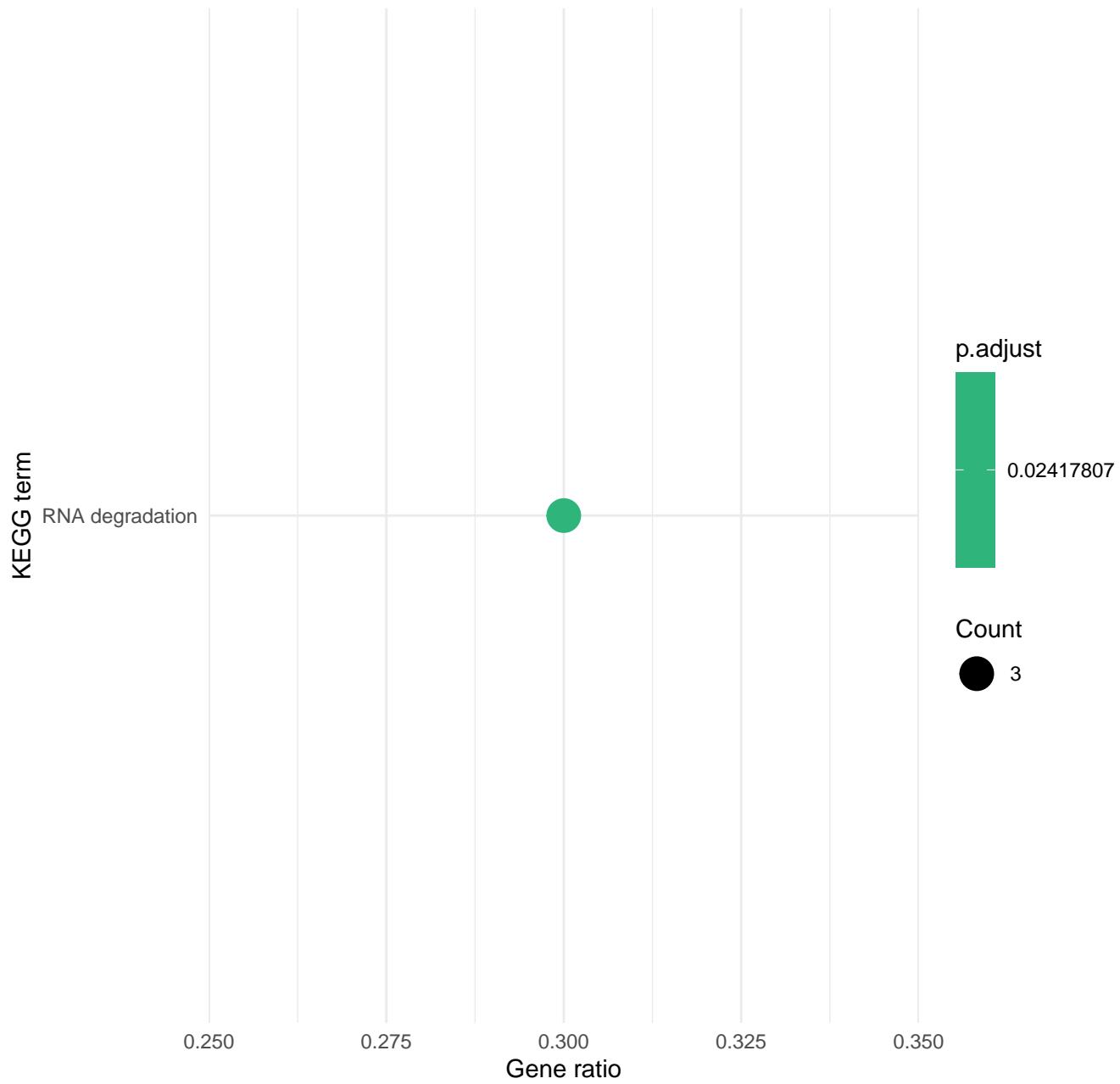
SGN1-TAP Up-regulated GO MF upsetplot



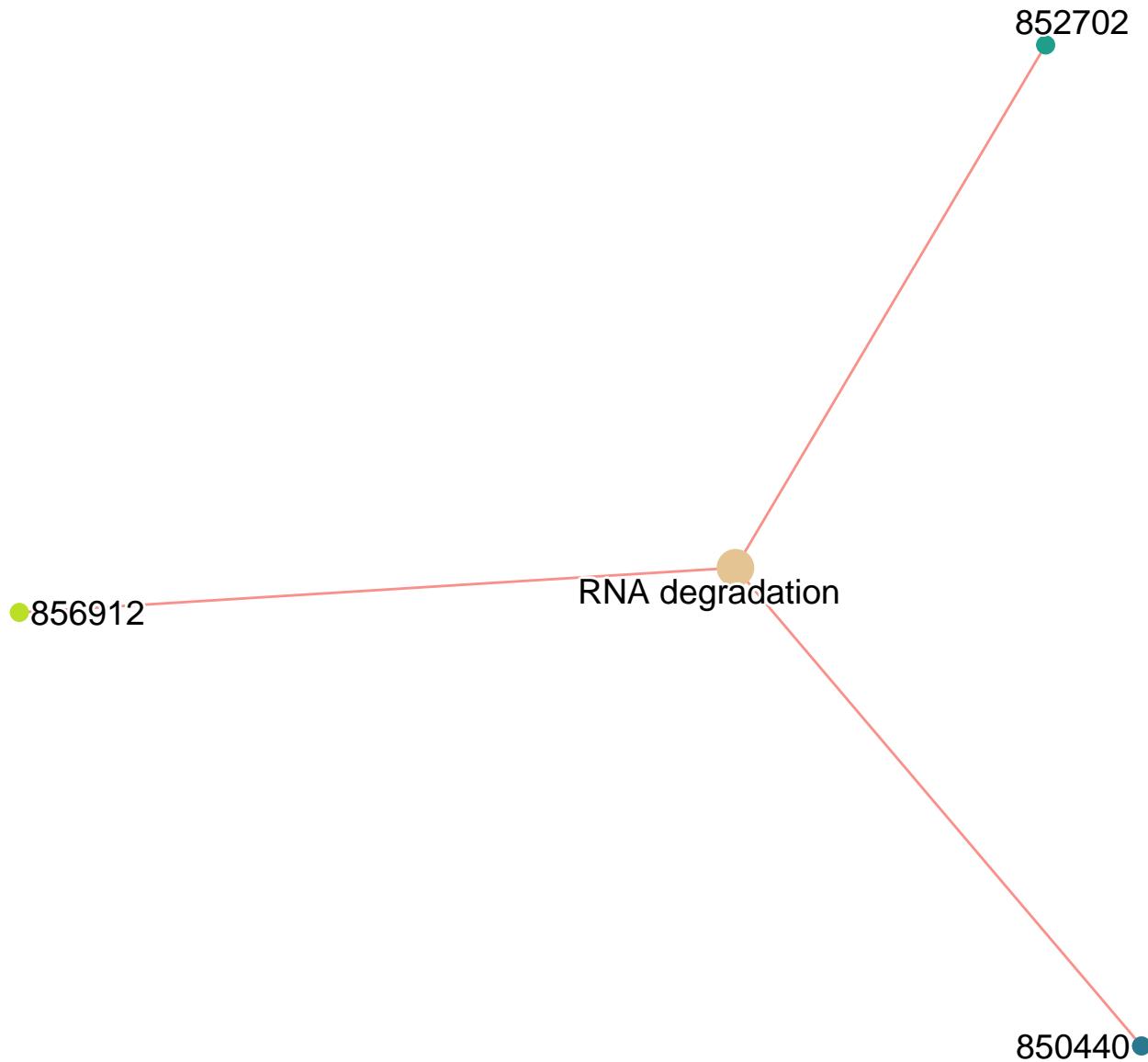
SGN1-TAP Up-regulated KEGG barplot



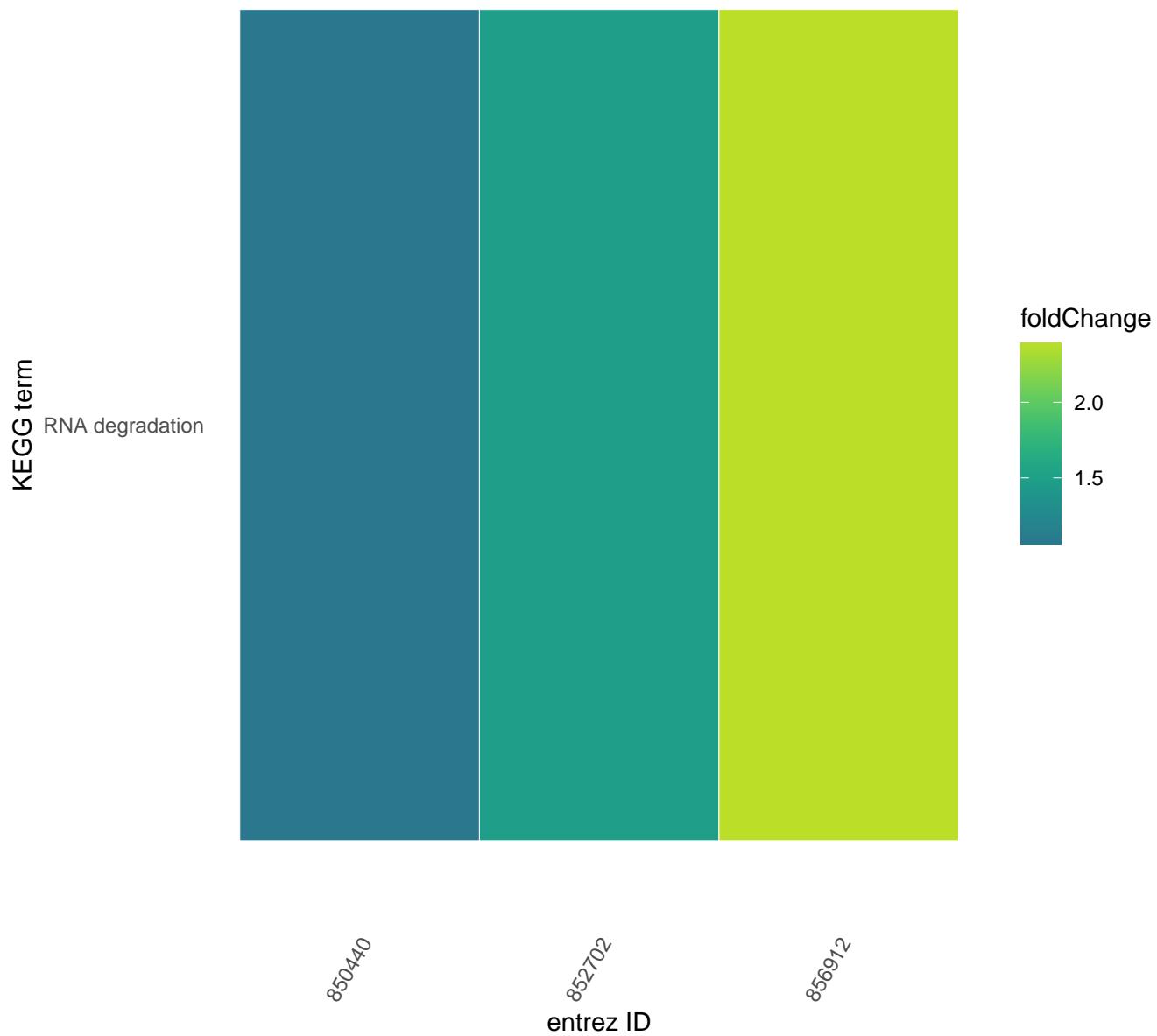
SGN1-TAP Up-regulated KEGG dotplot



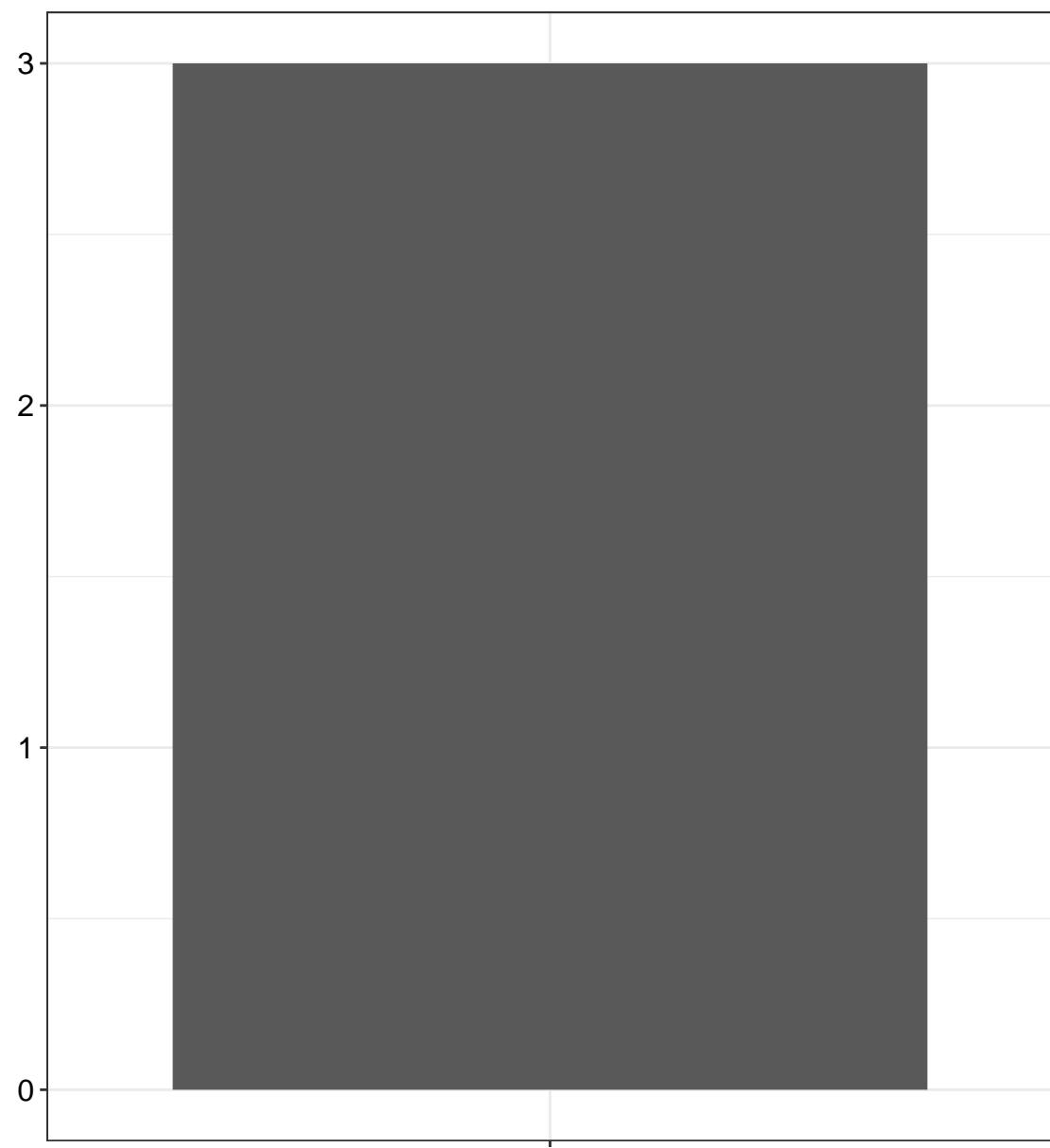
SGN1-TAP Up-regulated KEGG dotplot



SGN1-TAP Up-regulated KEGG heatplot



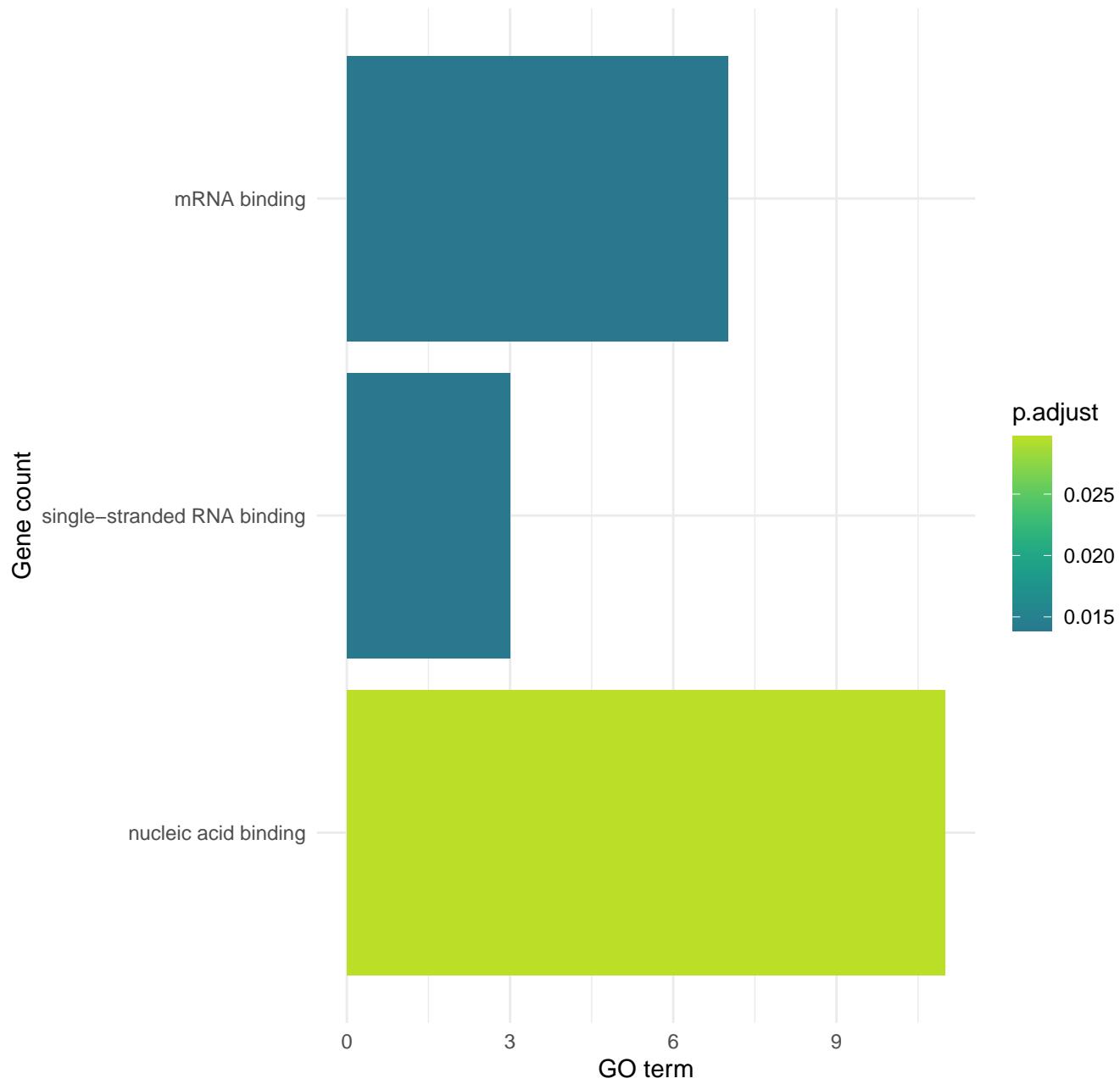
SGN1-TAP Up-regulated KEGG upsetplot



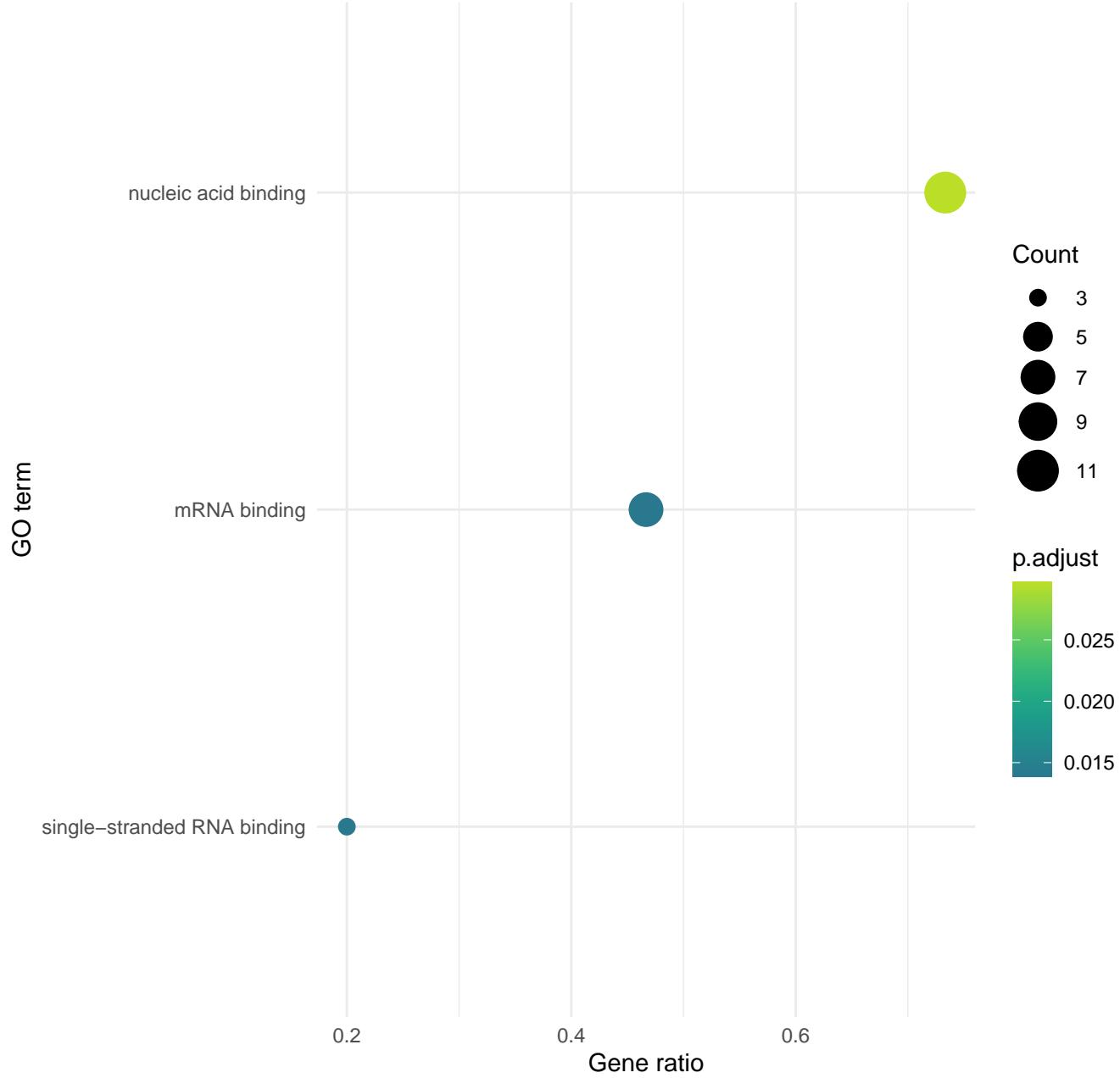
RNA degradation



MIP6–TAP Up-regulated GO MF barplot



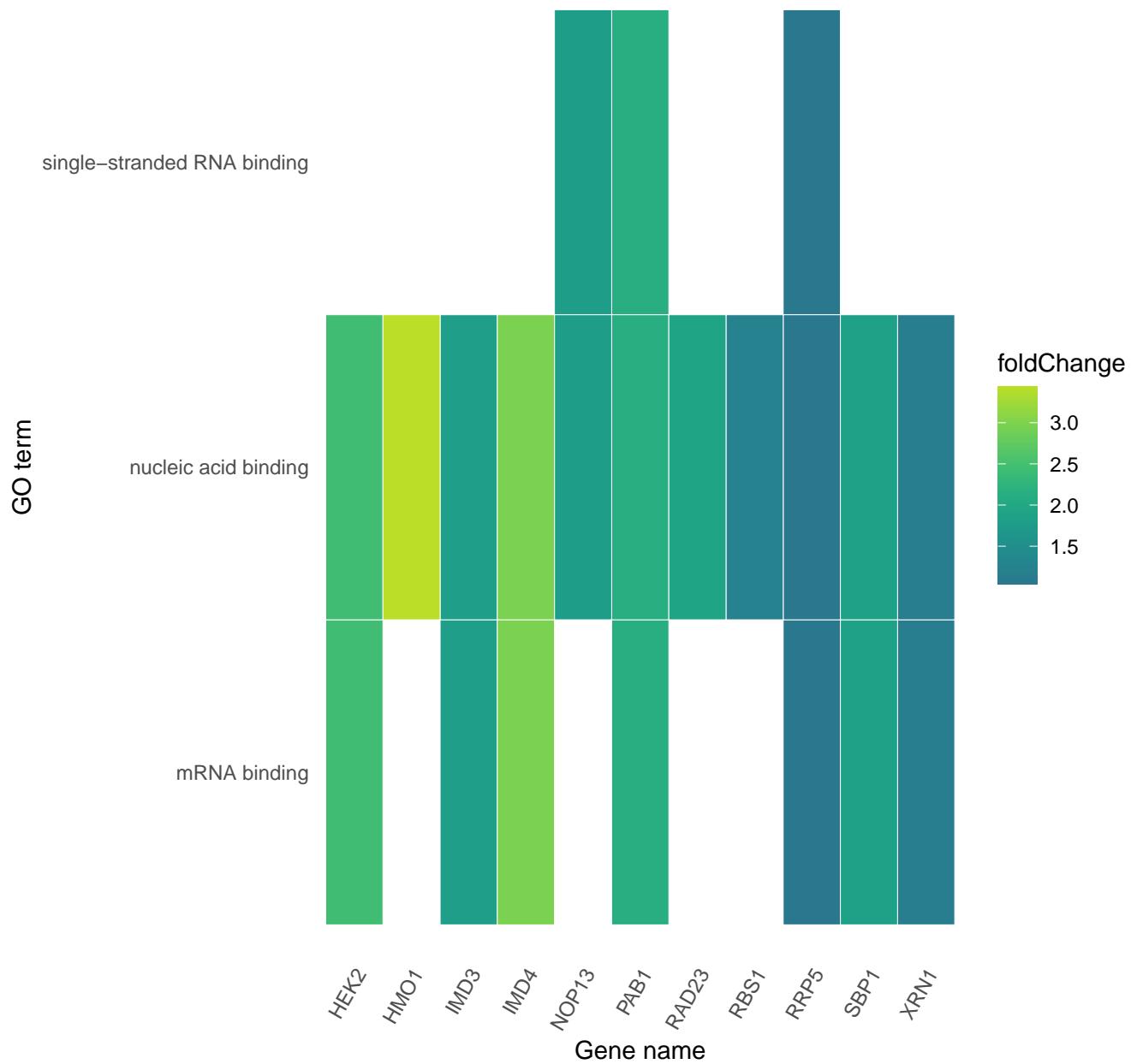
MIP6–TAP Up-regulated GO MF dotplot



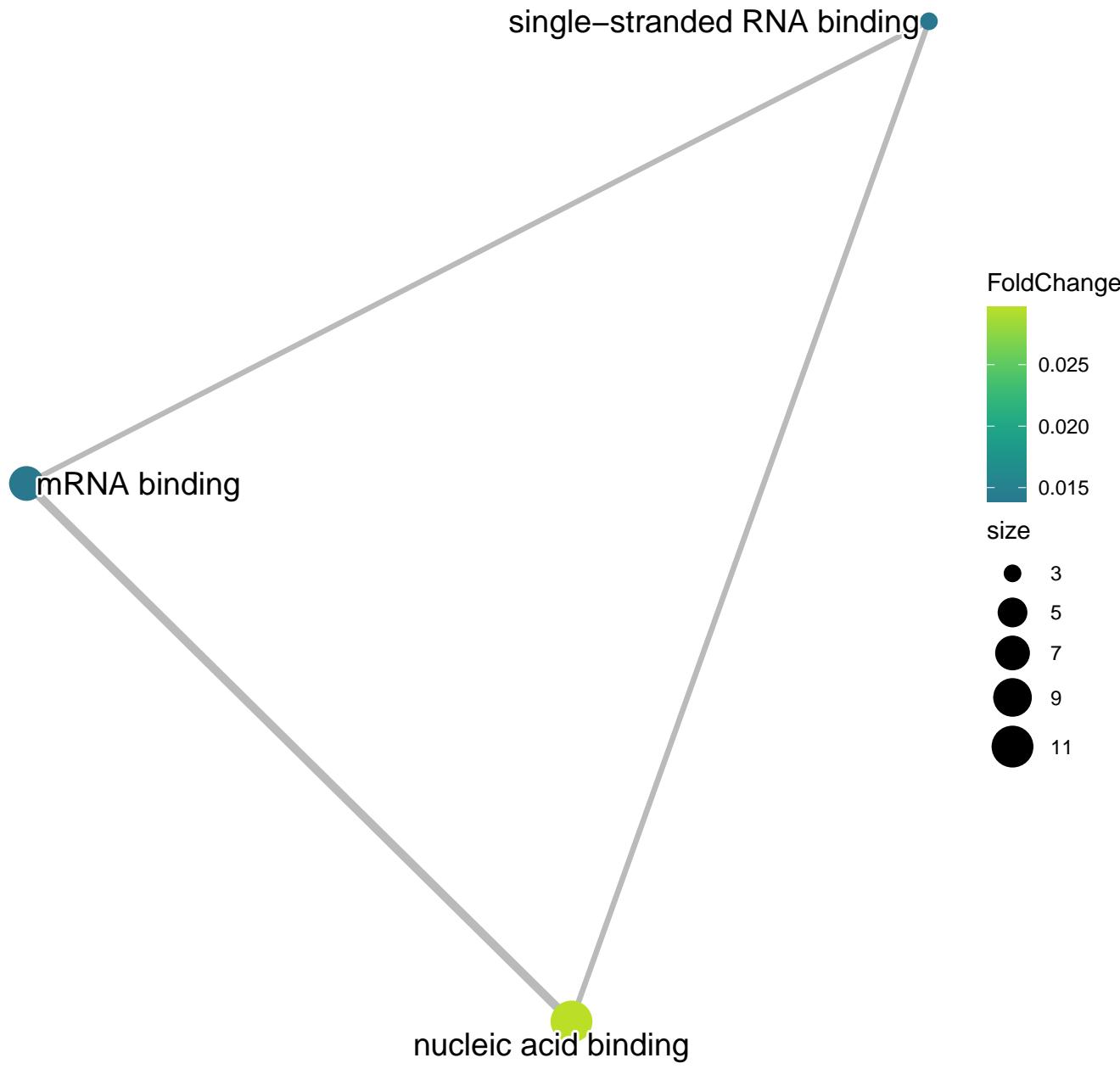
MIP6-TAP Up-regulated GO MF cnetplot

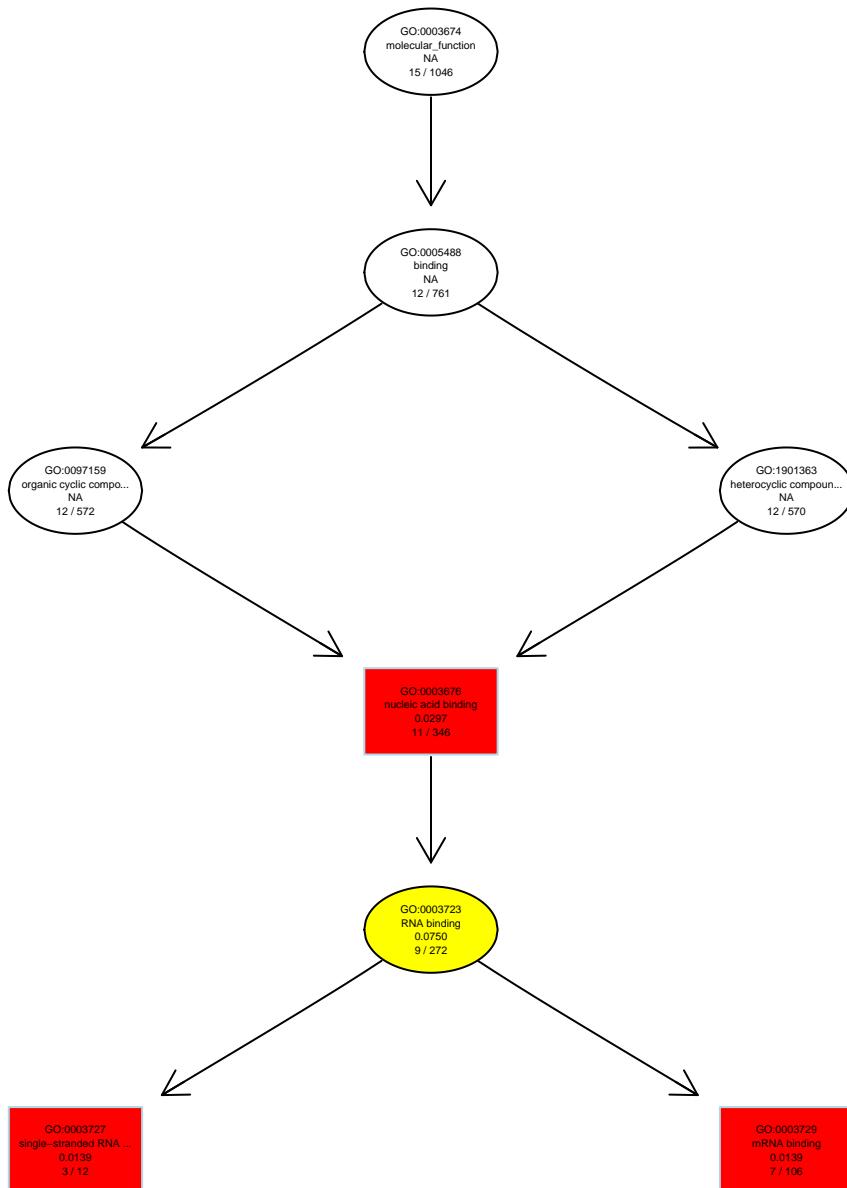


MIP6-TAP Up-regulated GO MF heatplot

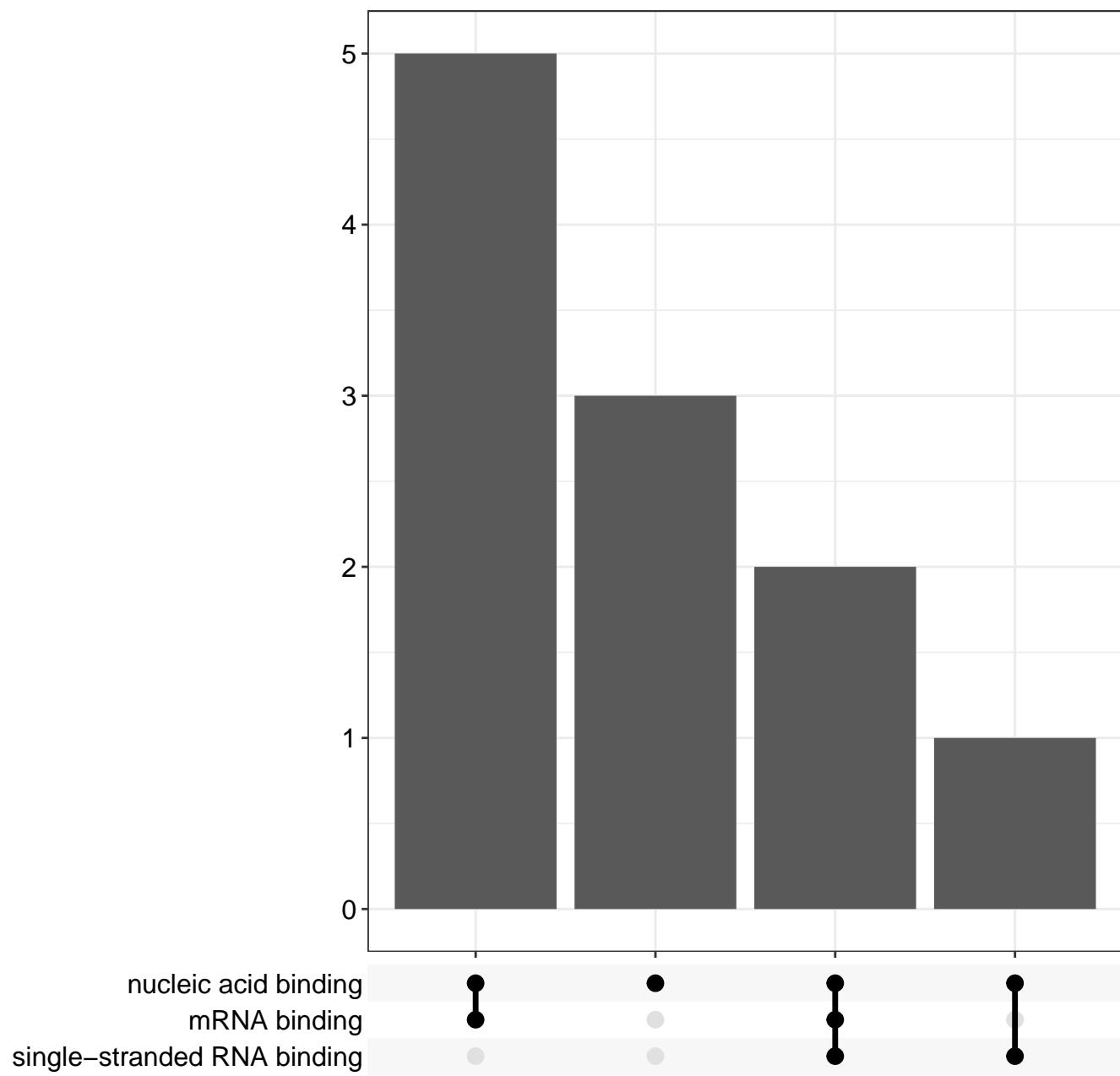


MIP6-TAP Up-regulated GO MF emapplot

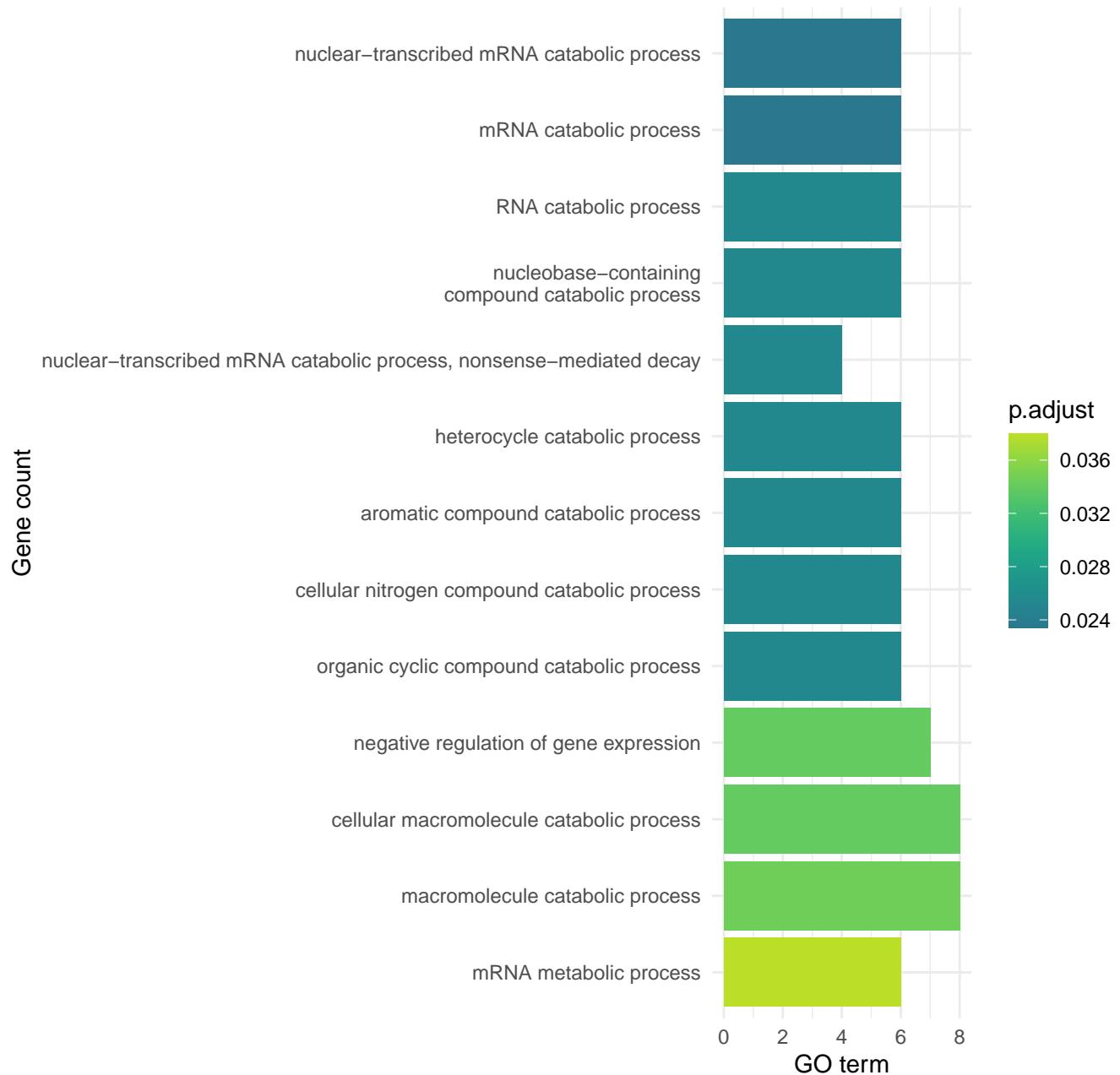




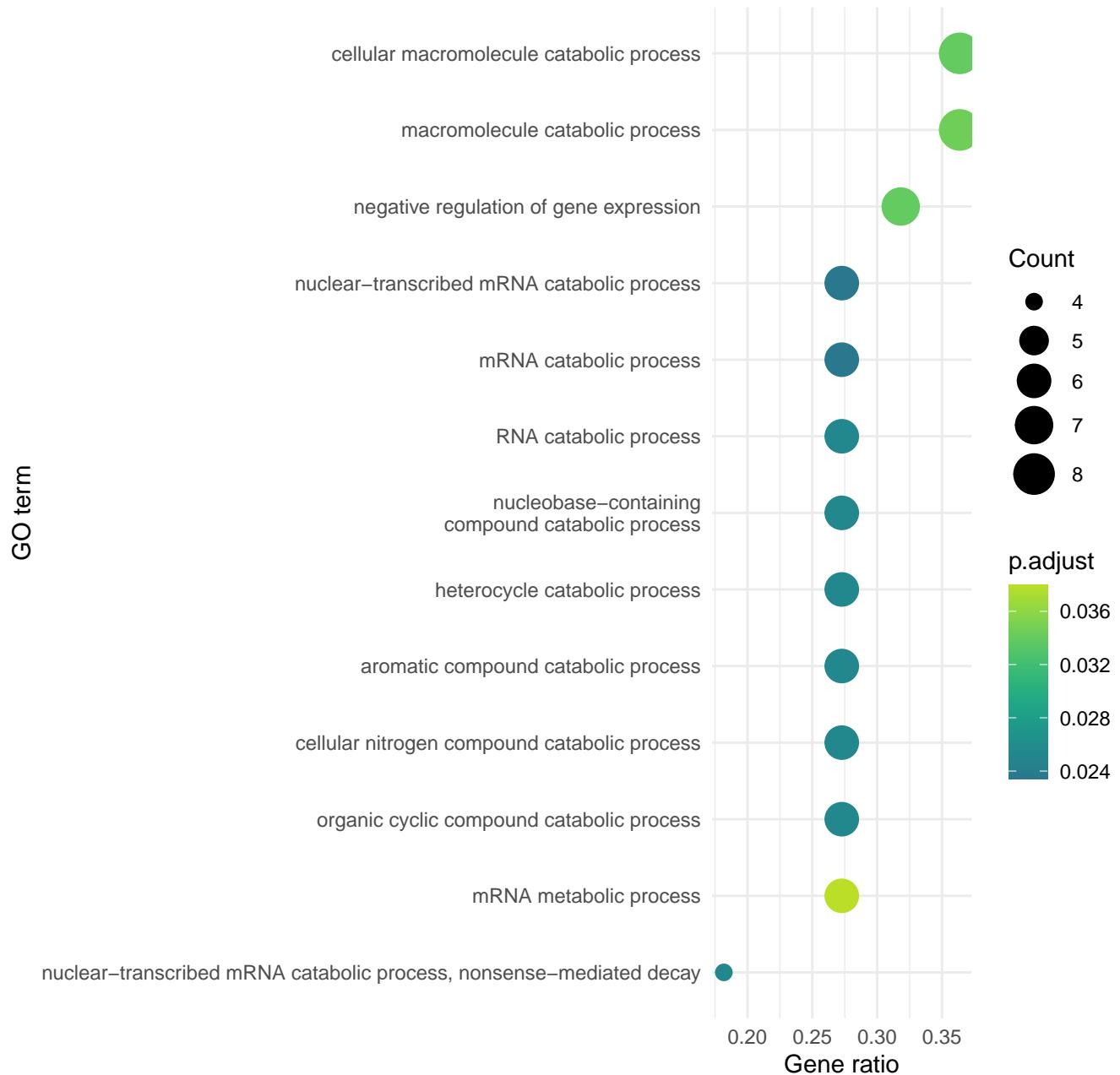
MIP6–TAP Up-regulated GO MF upsetplot



DCP2-TAP Up-regulated GO BP

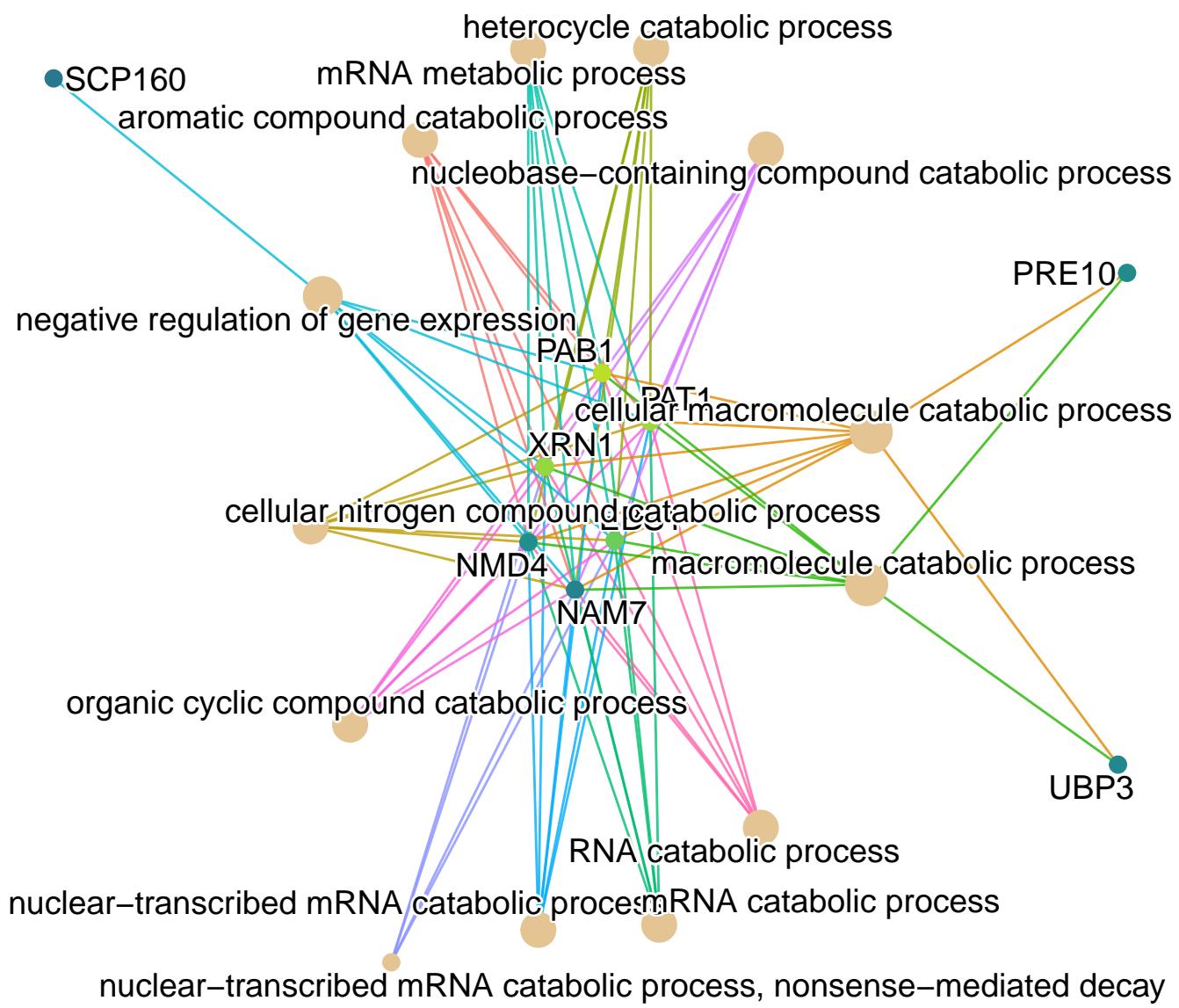


DCP2-TAP Up-regulated GO BP

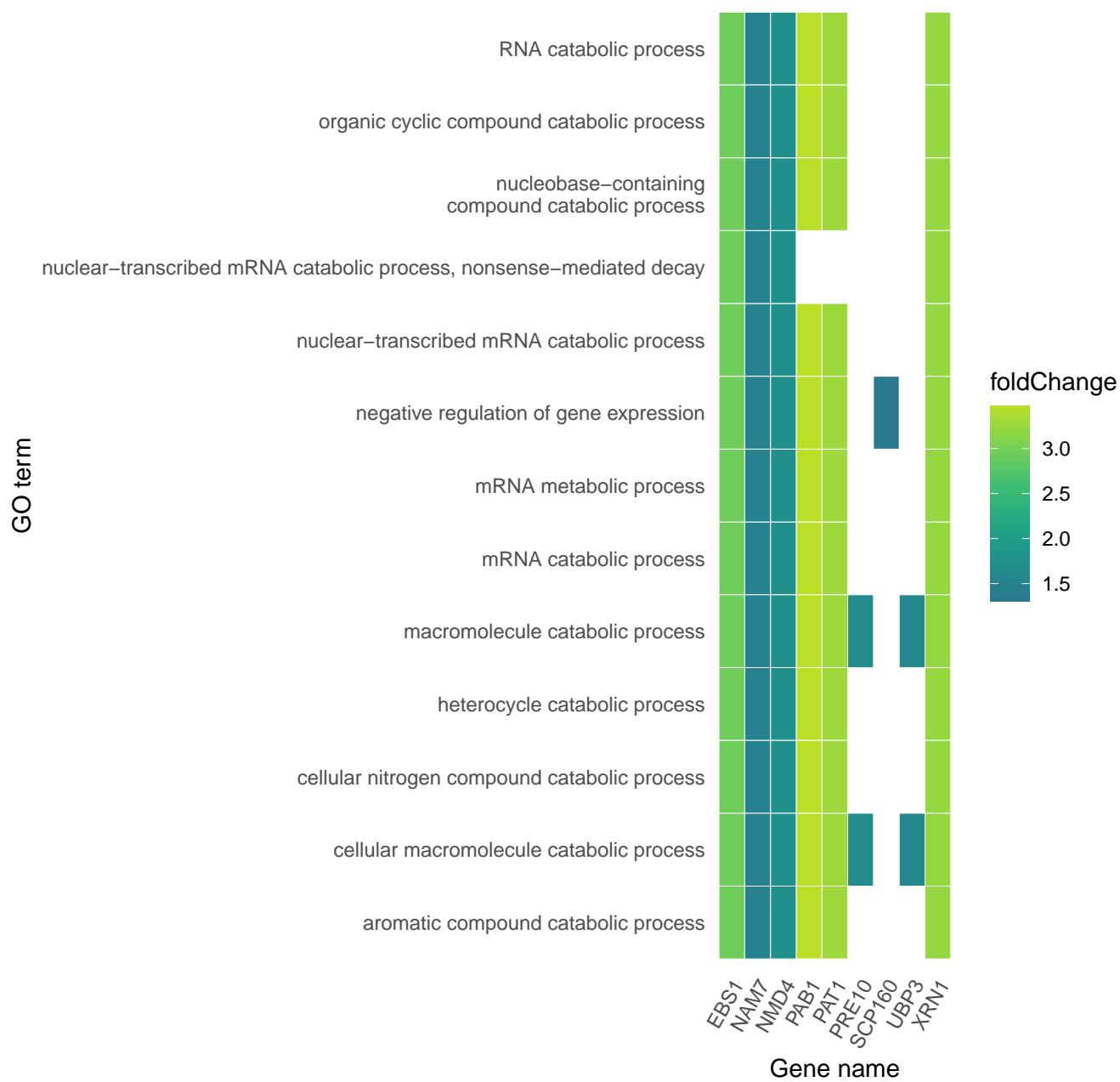


DCP2-TAP Up-regulated GO BP cnetplot

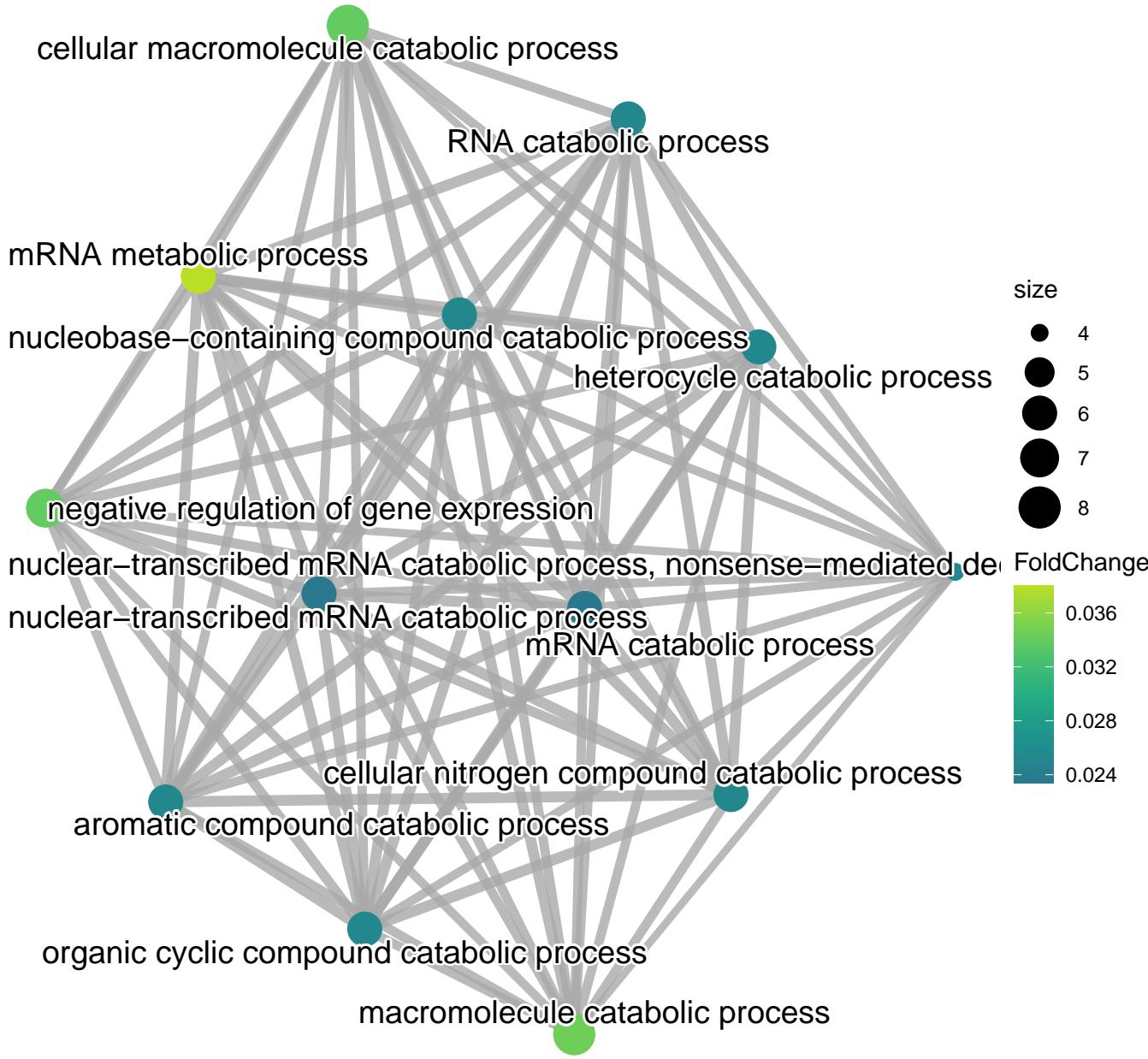
ocycle catabolic process mRNA metabolic process nuclear-transcribed mRNA catabolic pr
omolecule catabolic process negative regulation of gene expression nucleobase-containing compound cata
A catabolic process nuclear-transcribed mRNA catabolic process organic cyclic compound catabolic pro

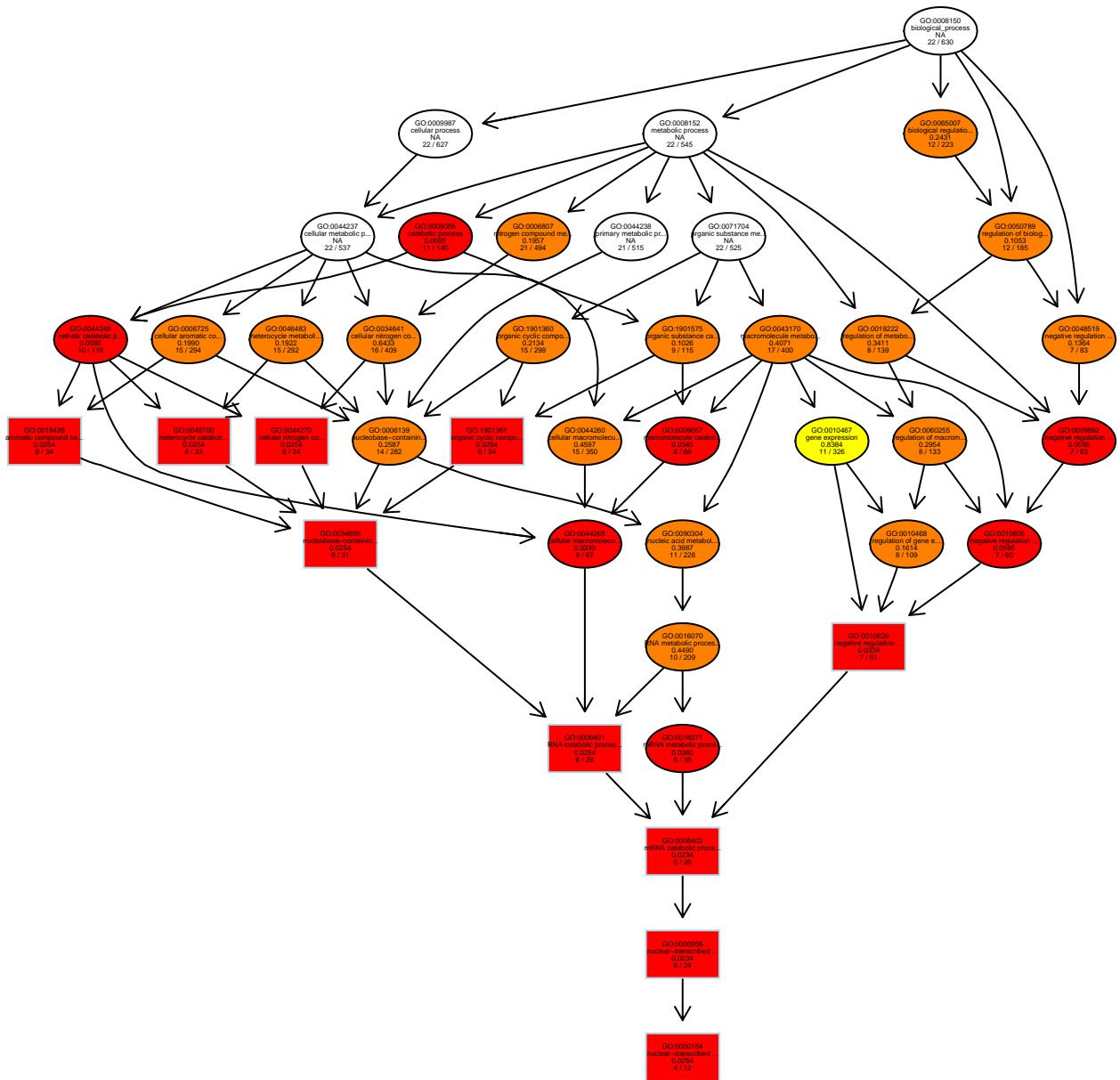


DCP2-TAP Up-regulated GO BP

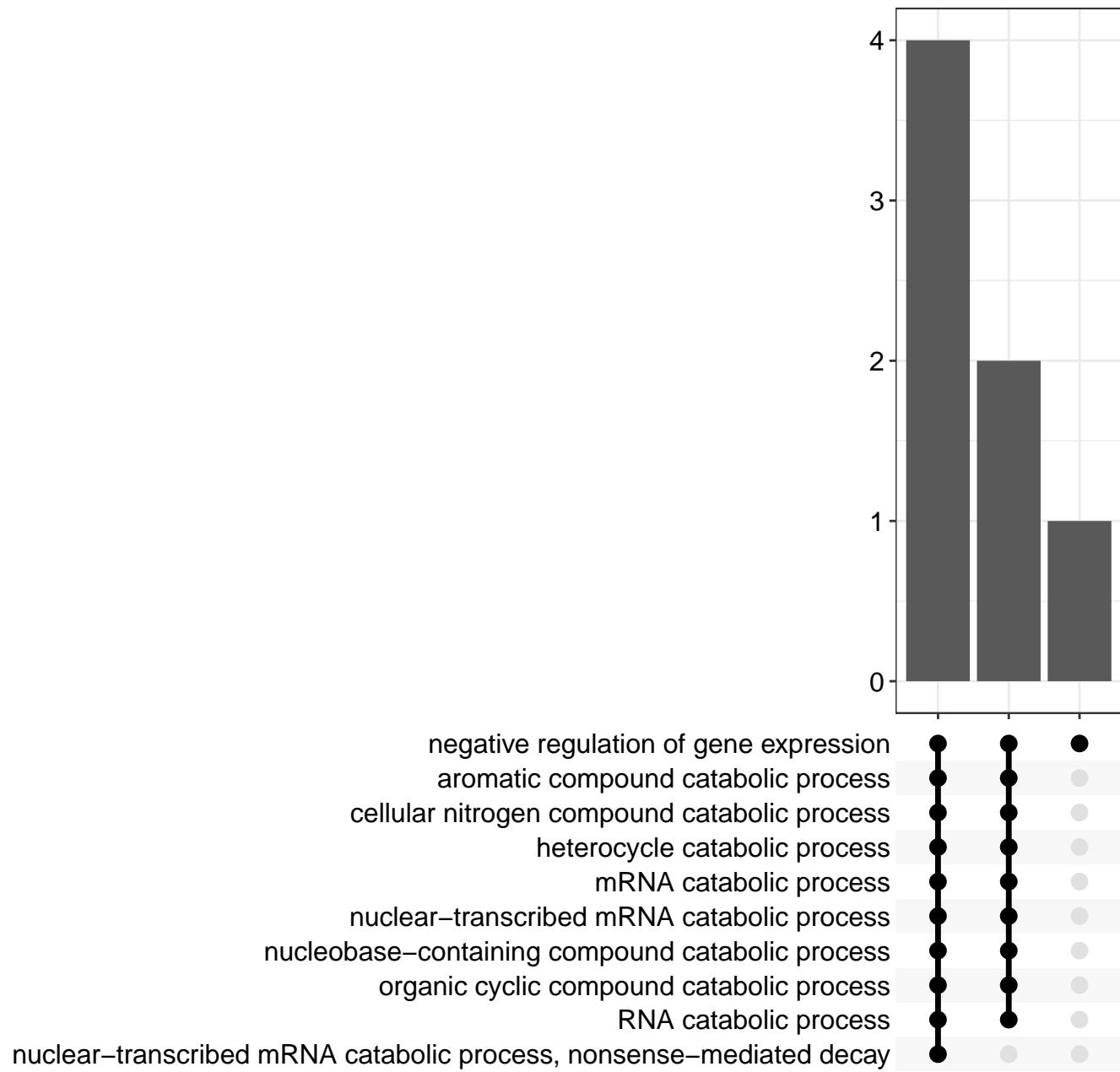


DCP2-TAP Up-regulated GO BP emapplot

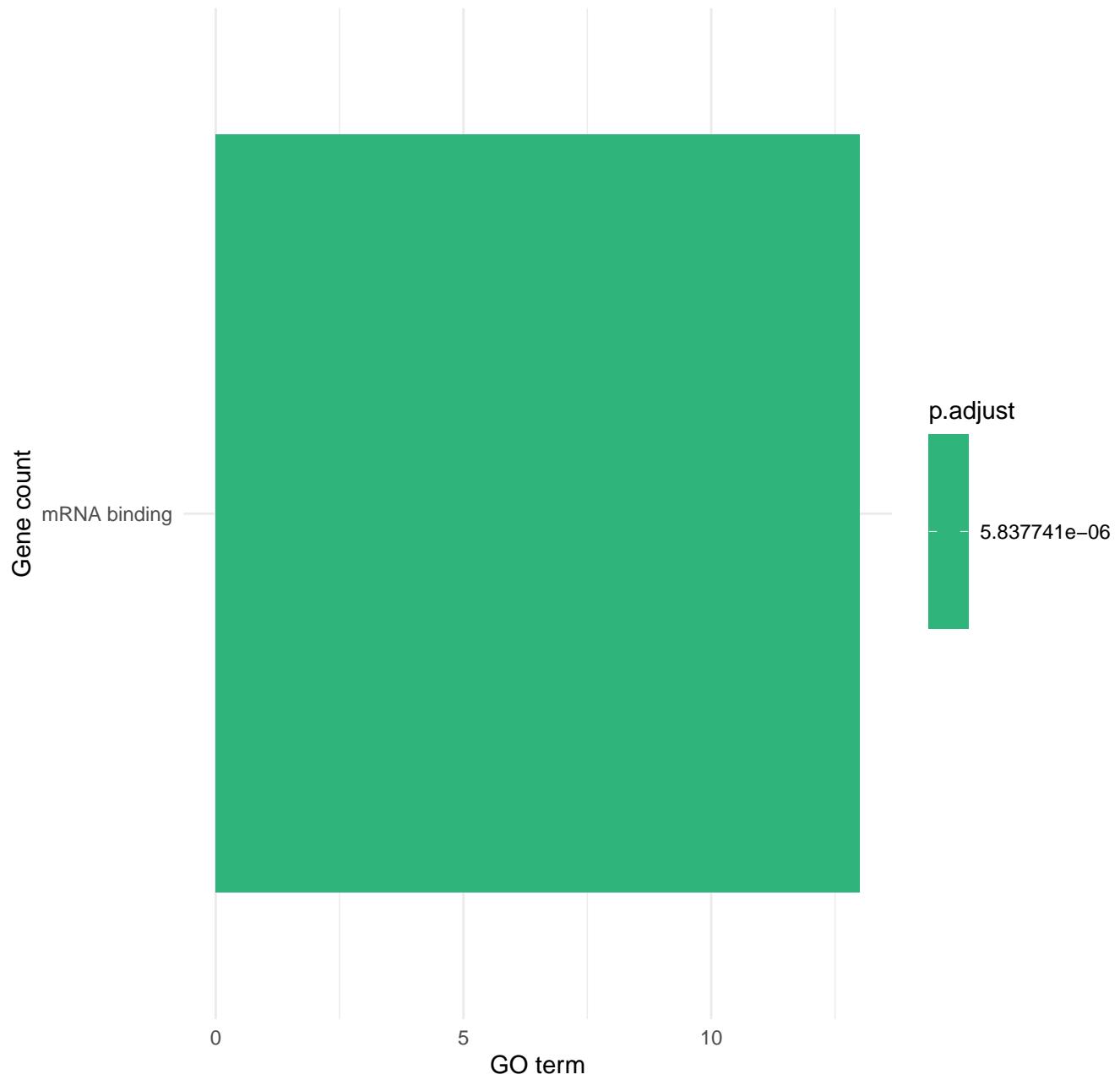




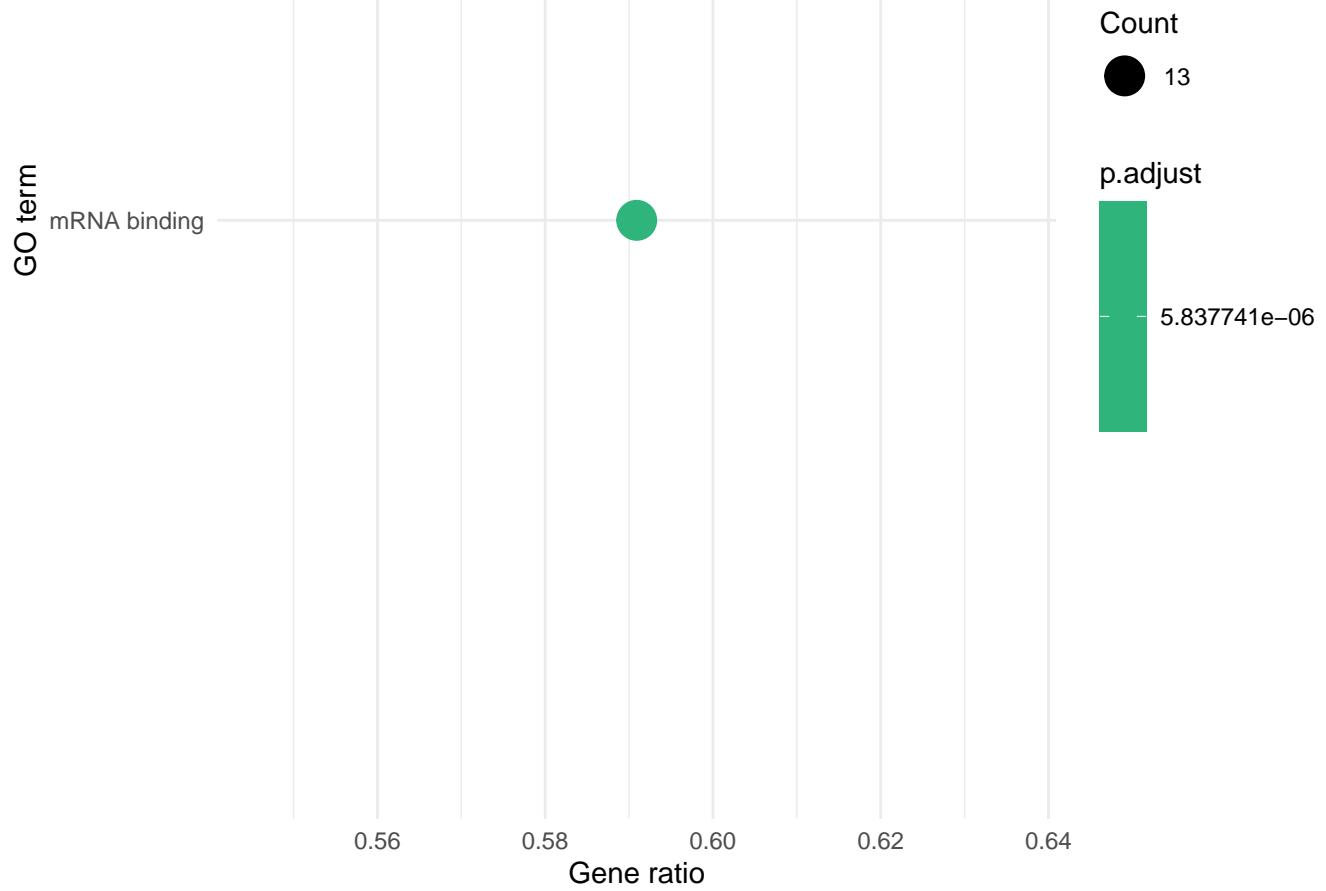
DCP2-TAP Up-re



DCP2-TAP Up-regulated GO MF barplot



DCP2-TAP Up-regulated GO MF dotplot



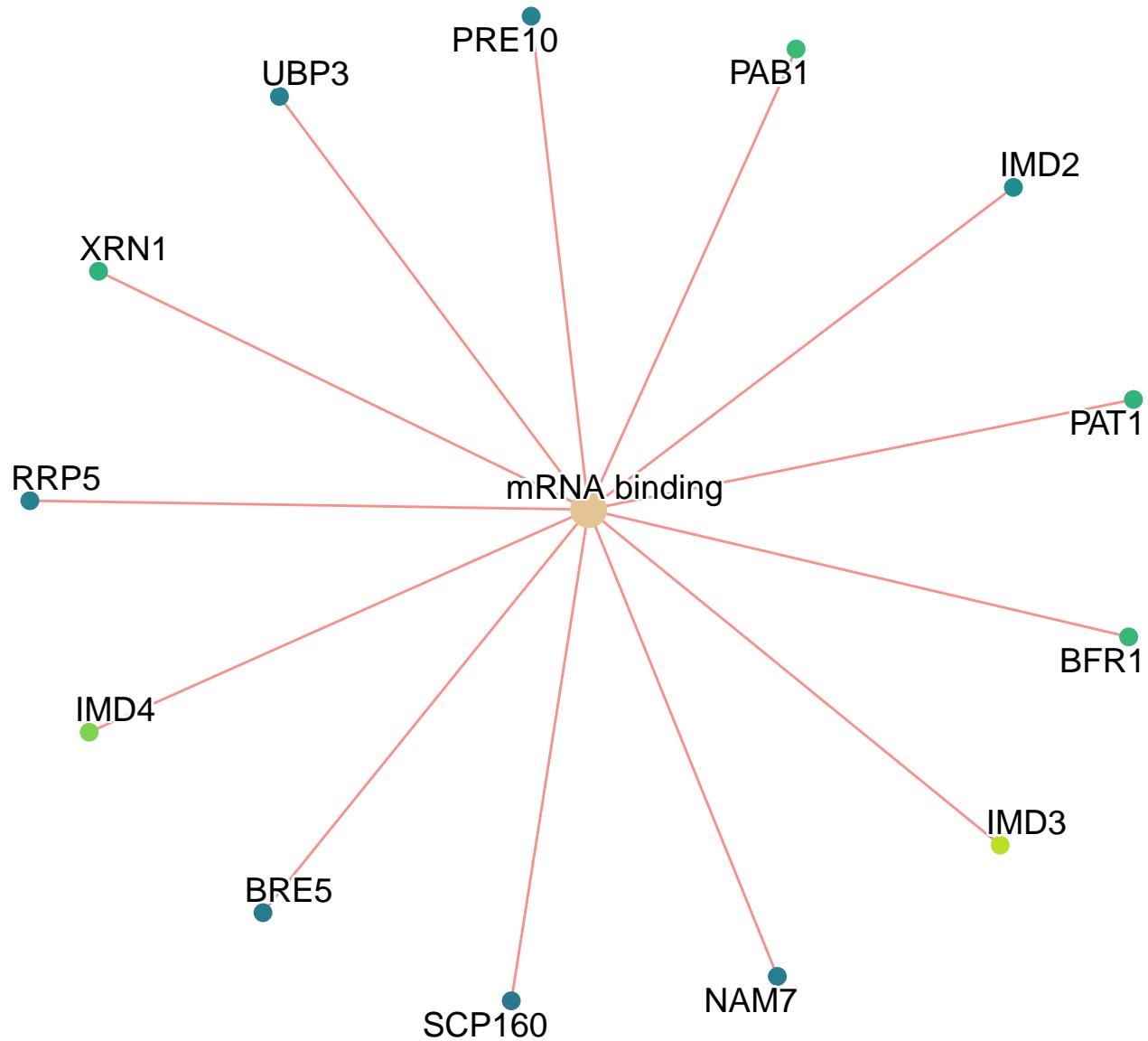
DCP2-TAP Up-regulated GO MF cnetplot

category mRNA binding

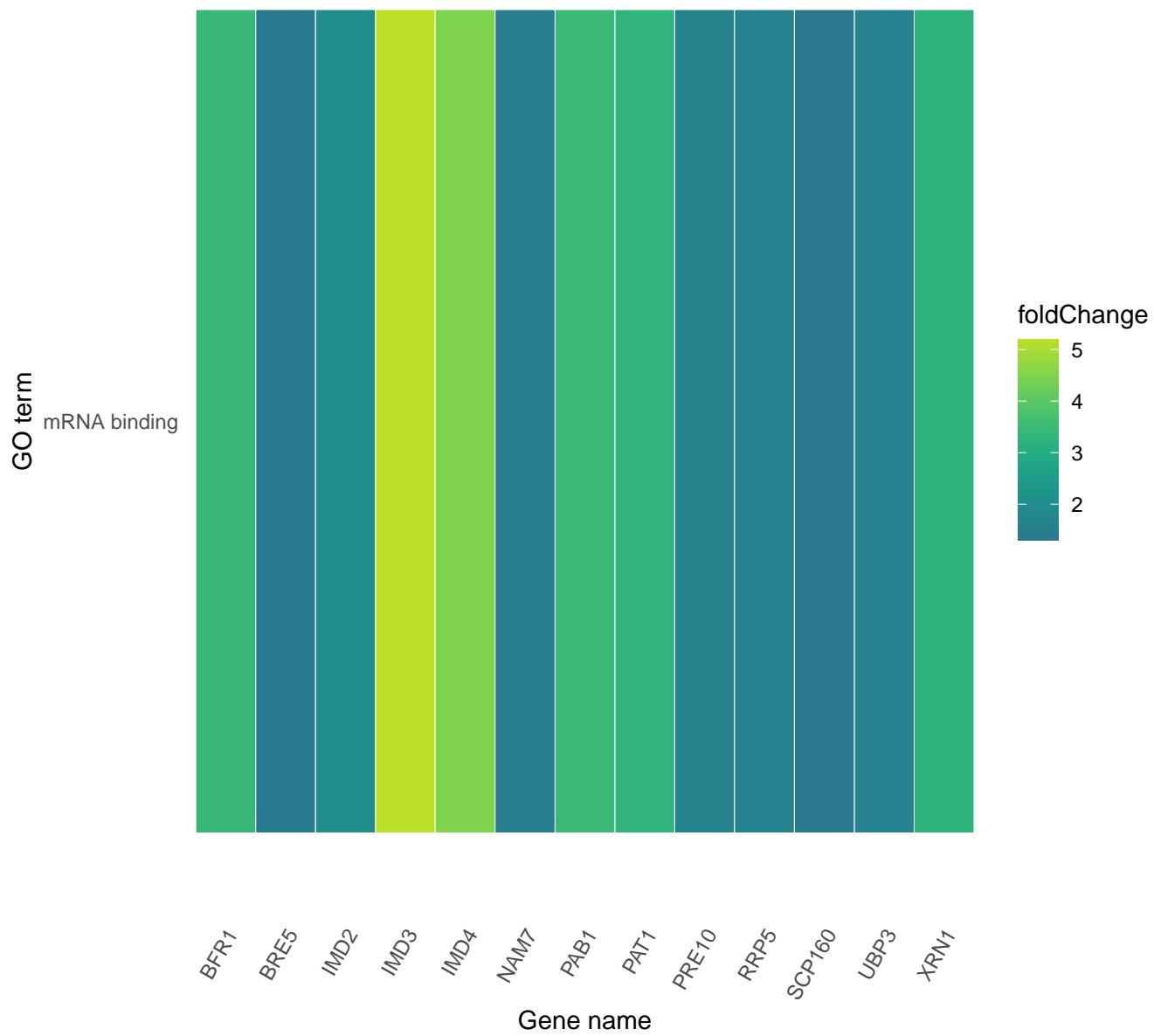
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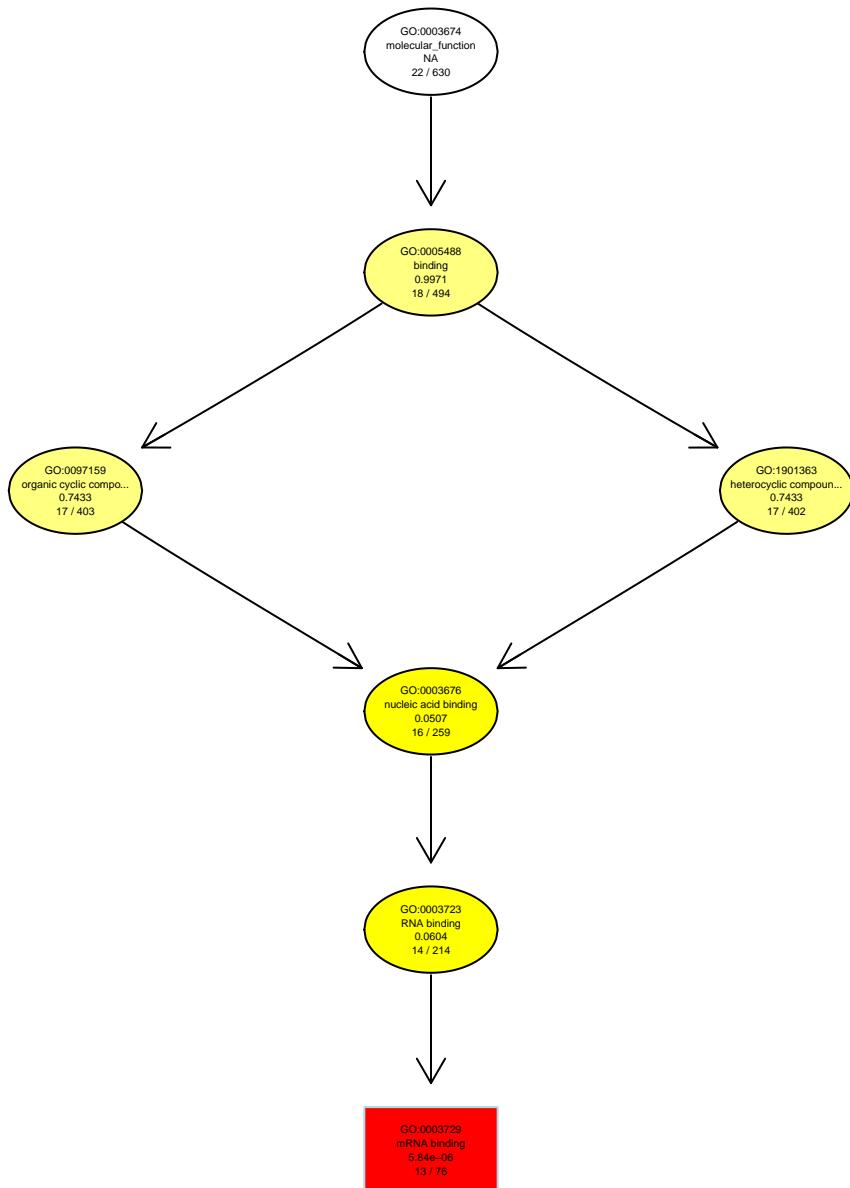


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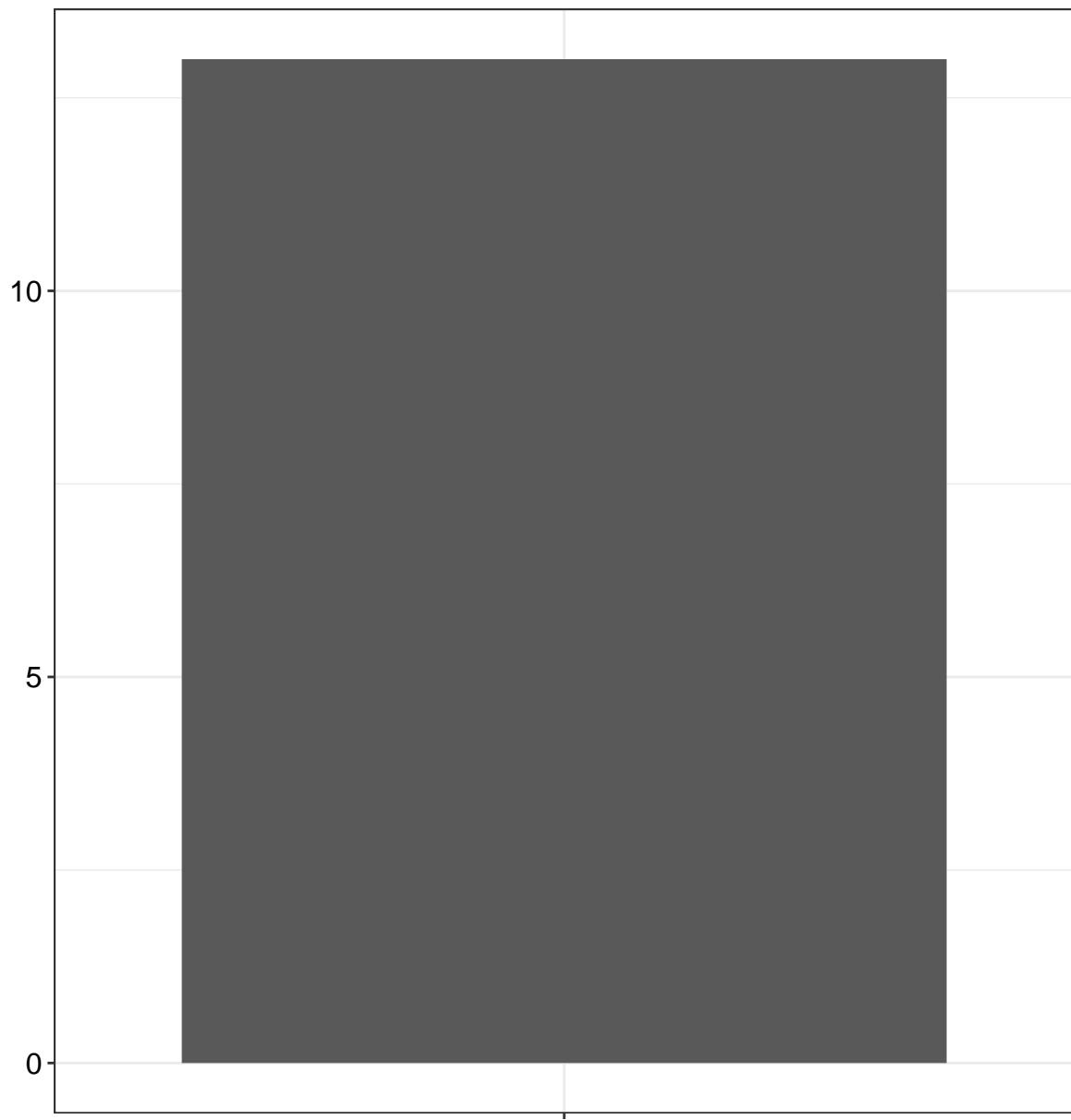


DCP2-TAP Up-regulated GO MF heatplot



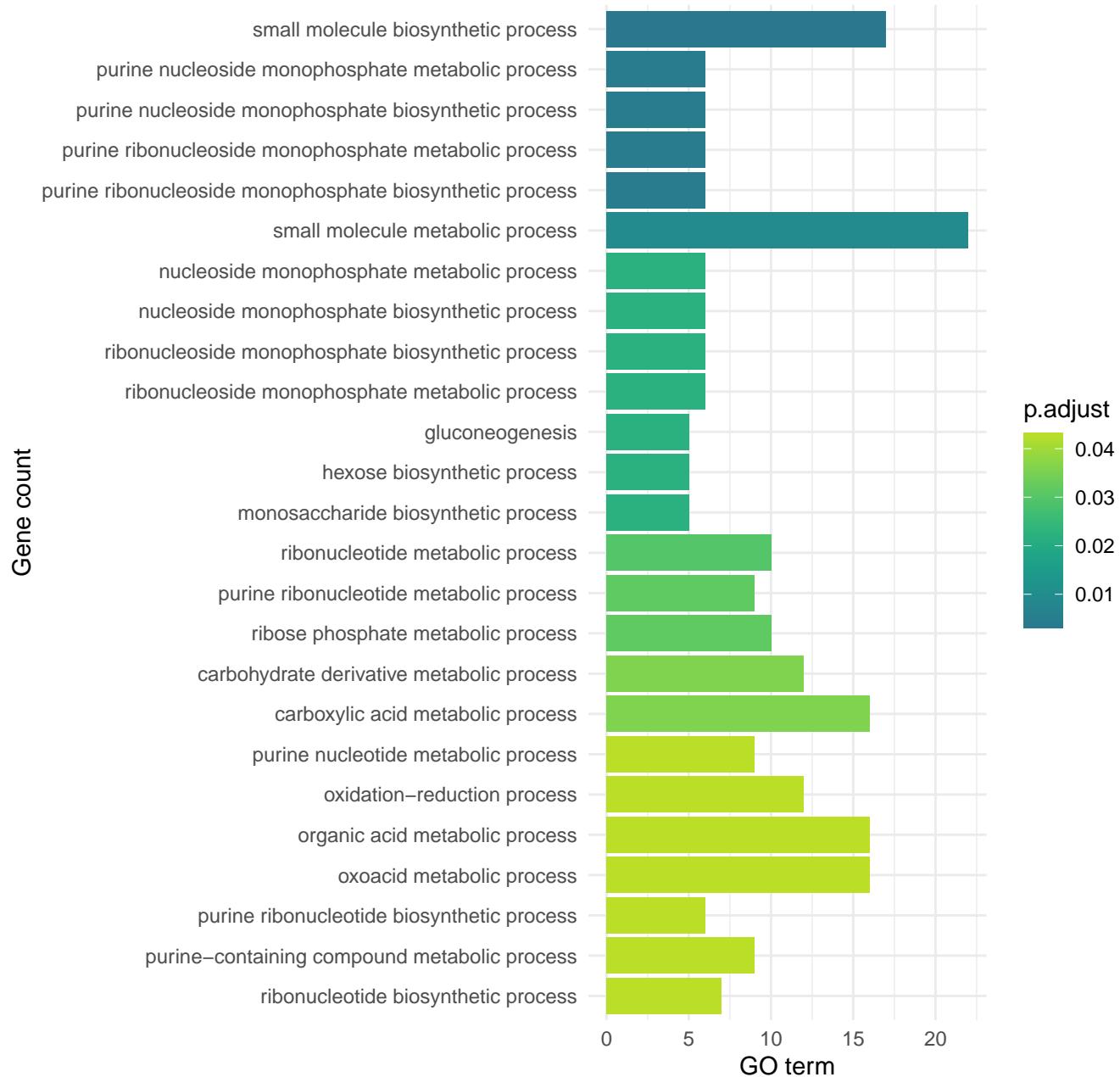


DCP2-TAP Up-regulated GO MF upsetplot

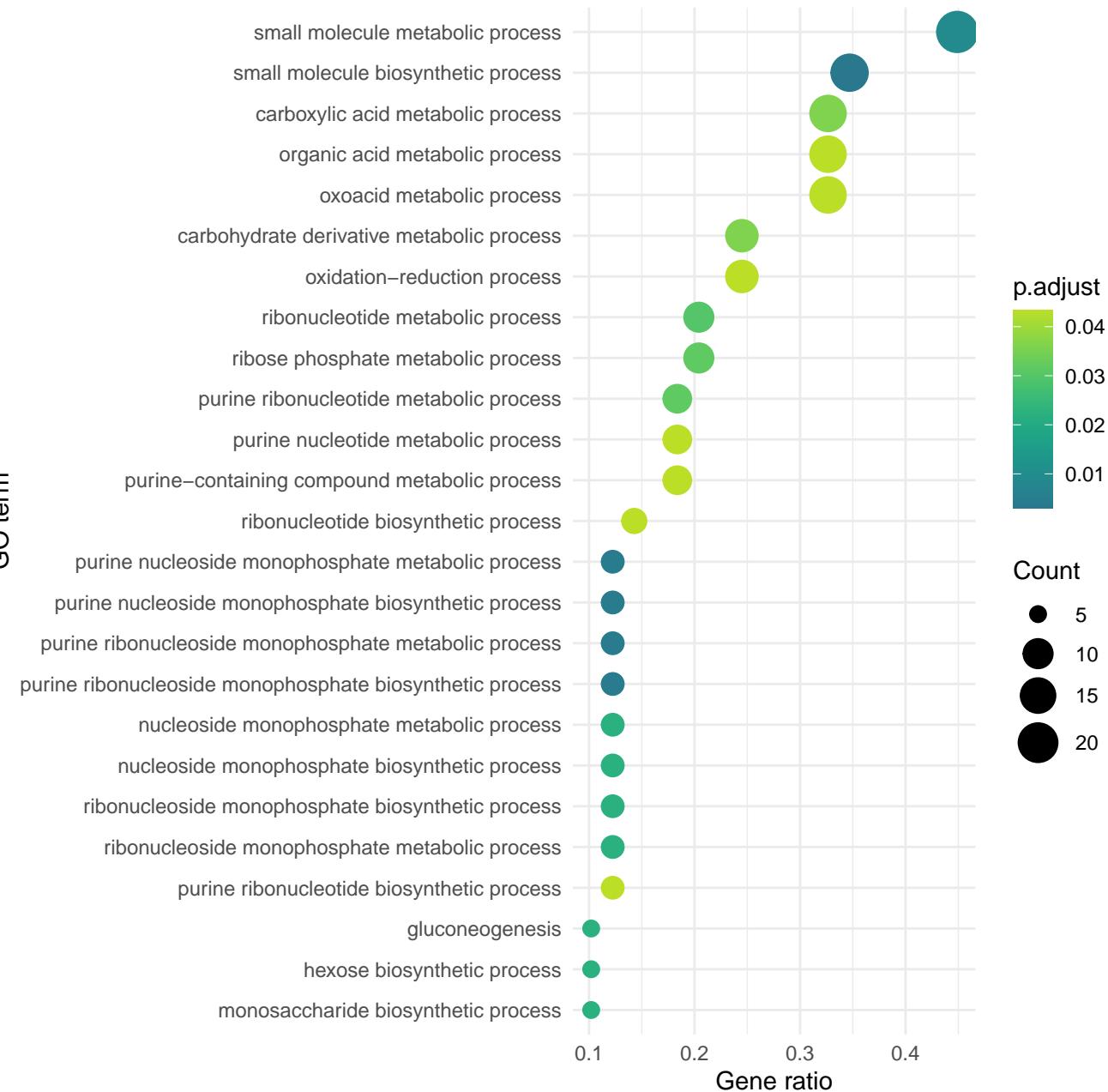


mRNA binding

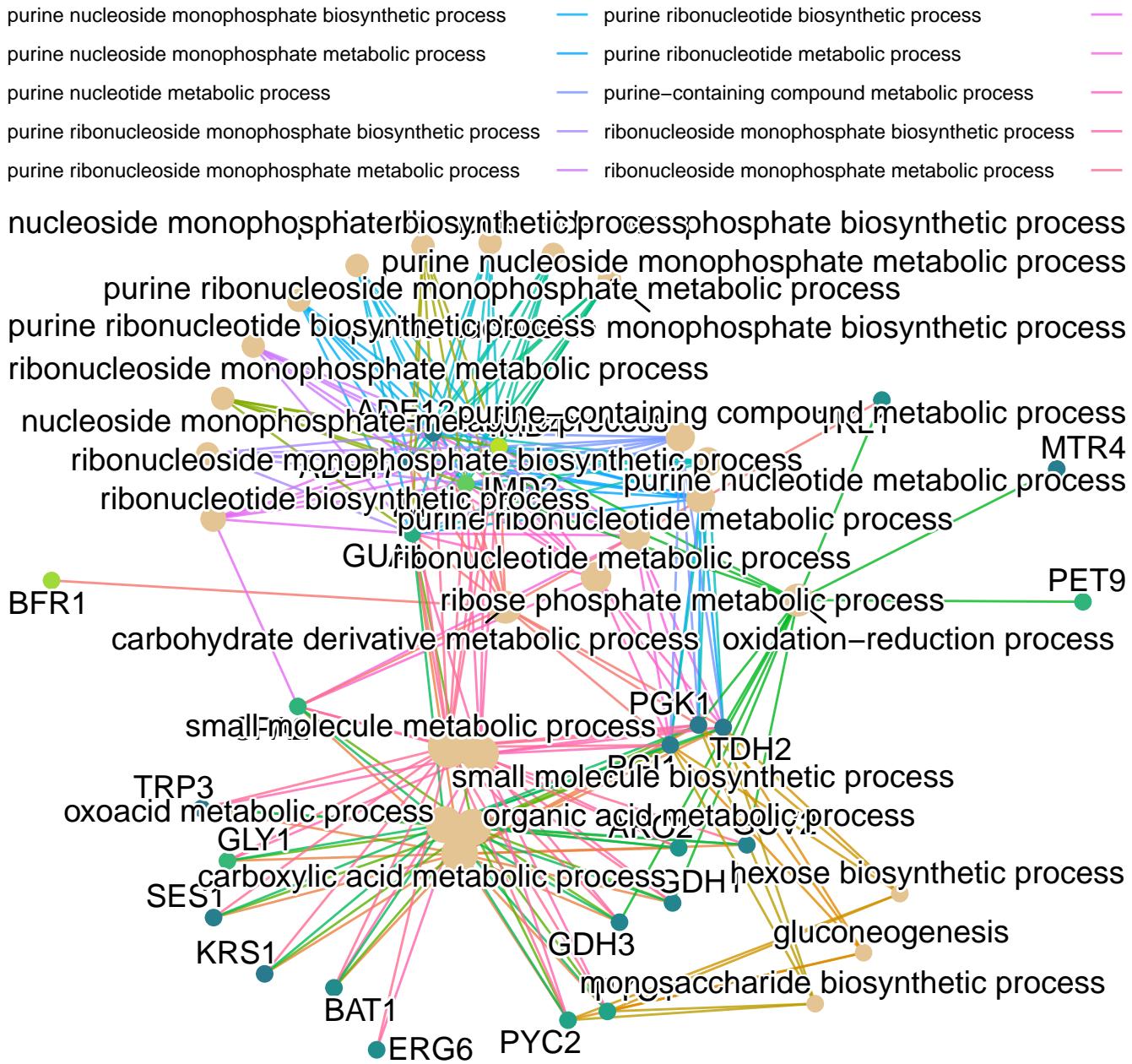
RRP40-TAP Up-regulated GO BP barplot



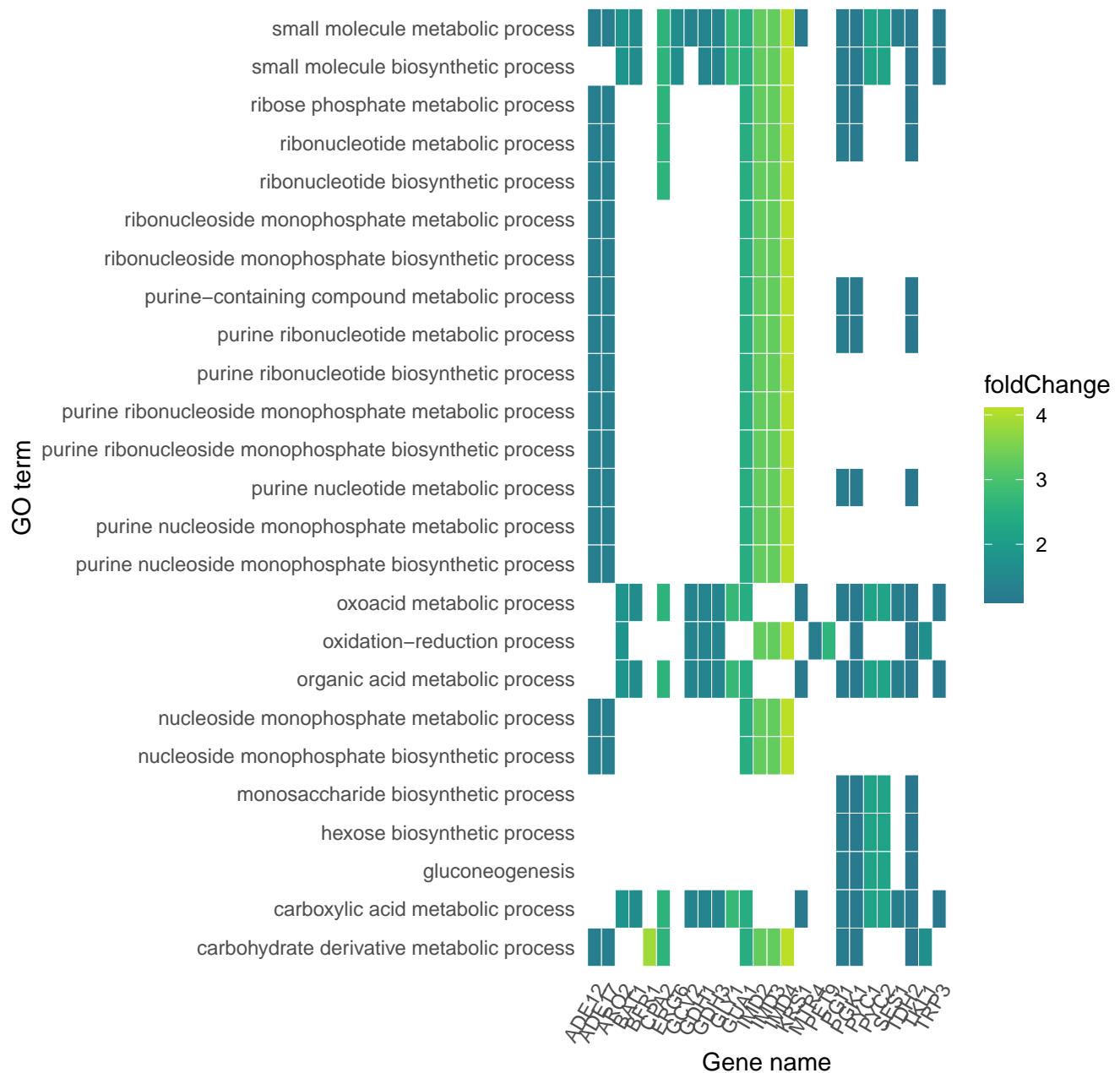
RRP40-TAP Up-regulated GO BP dotplot



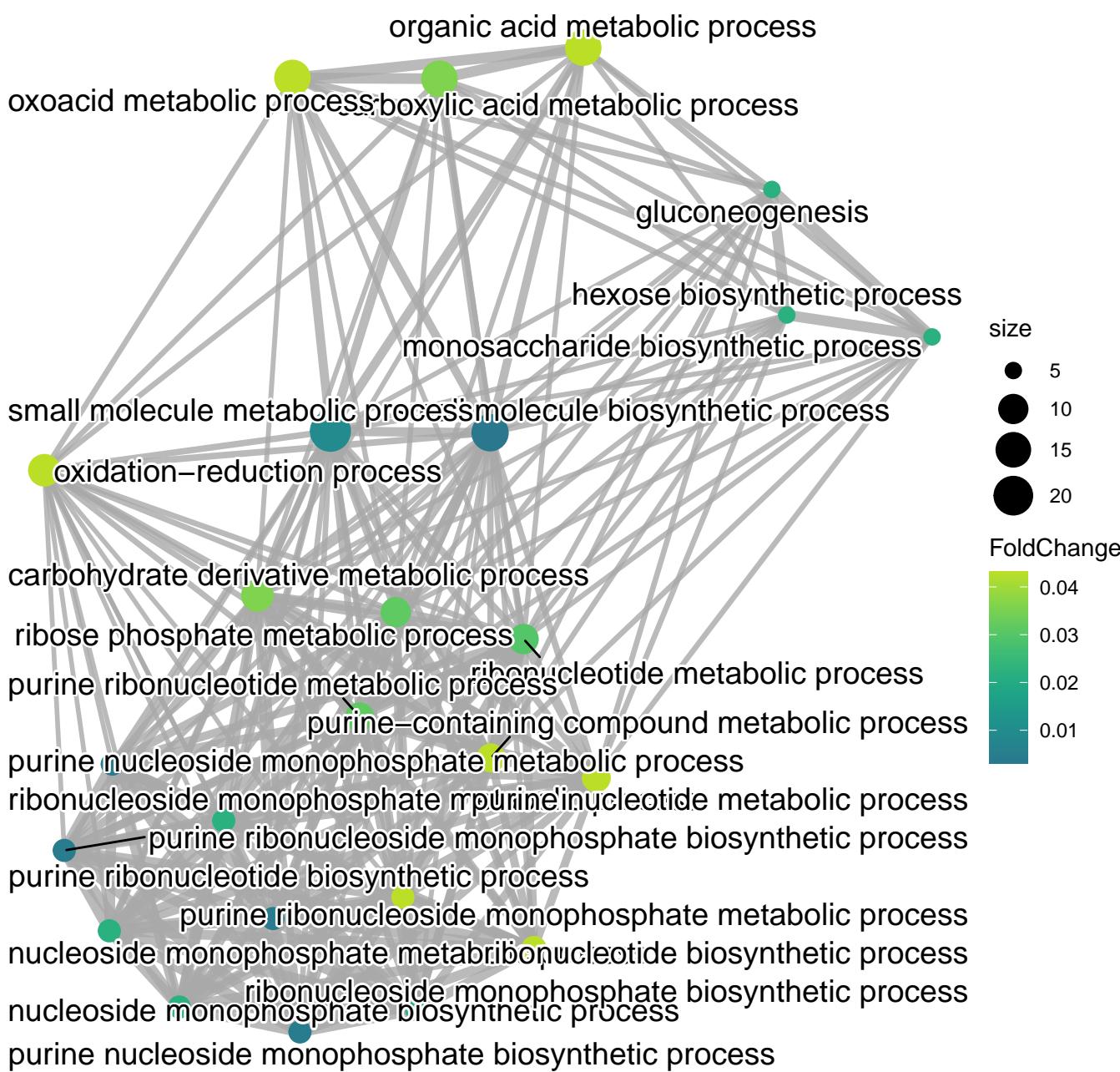
RRP40-TAP Up-regulated GO BP cnetplot

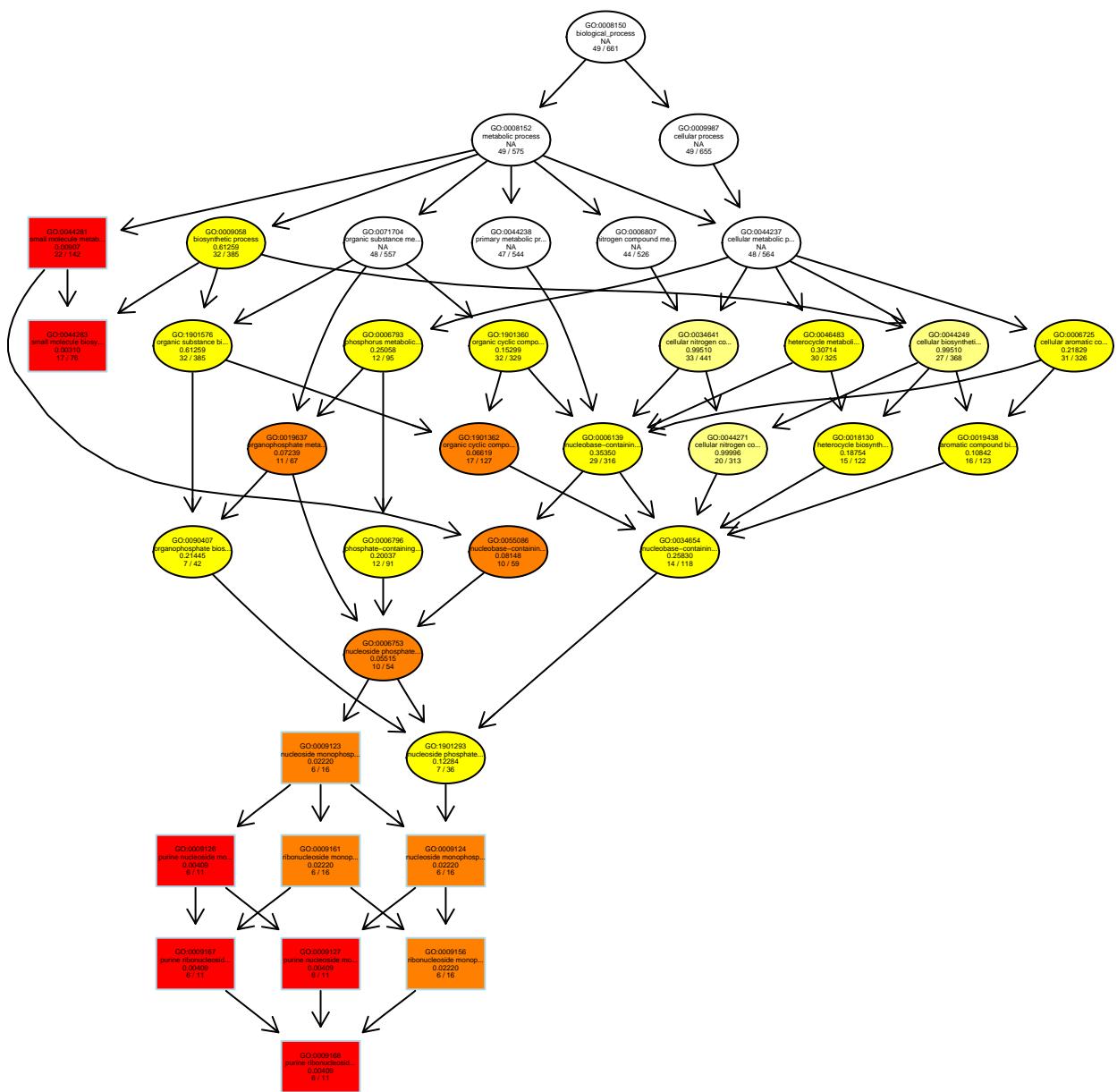


RRP40-TAP Up-regulated GO BP heatplo

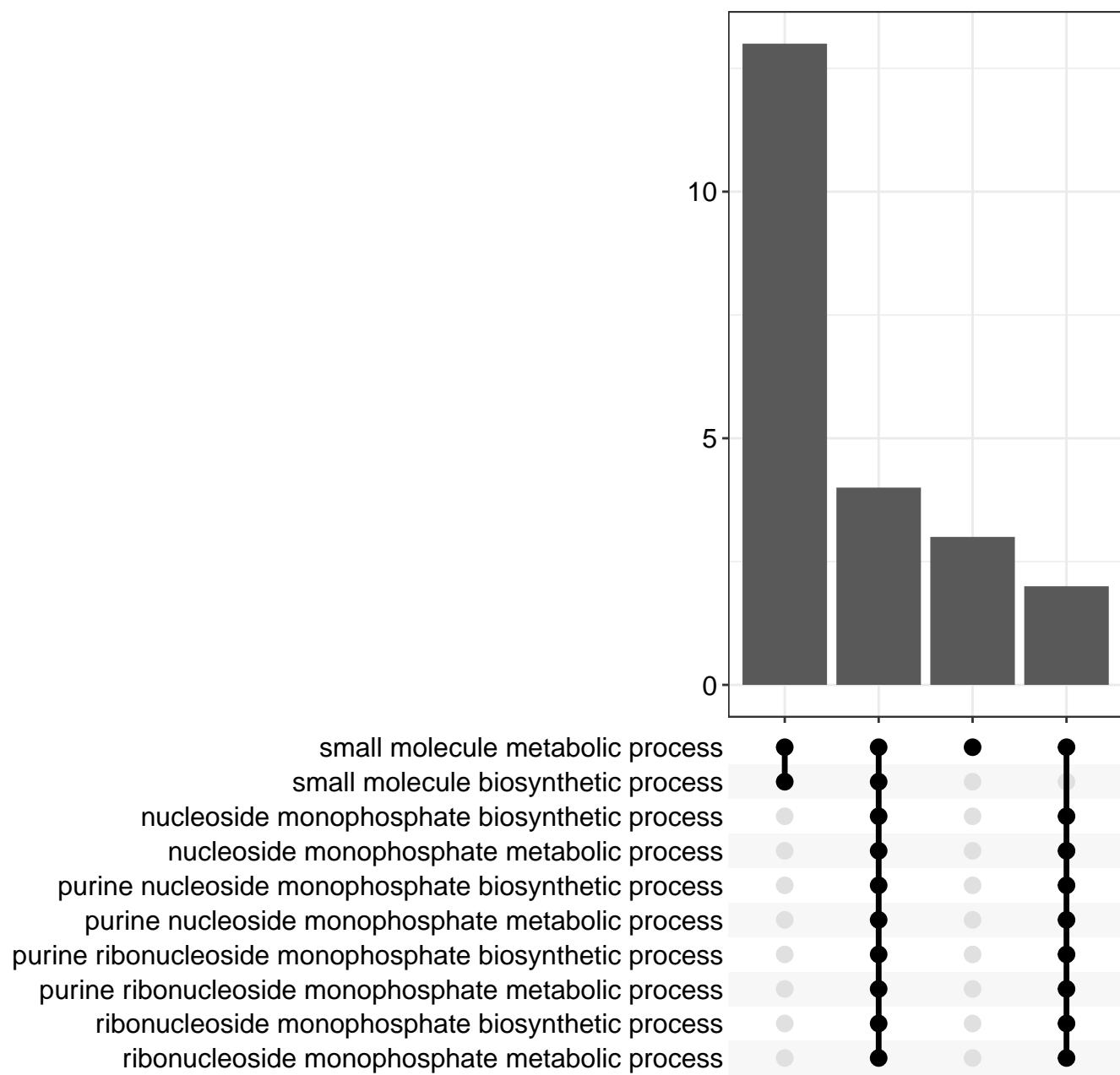


RRP40-TAP Up-regulated GO BP emapplot

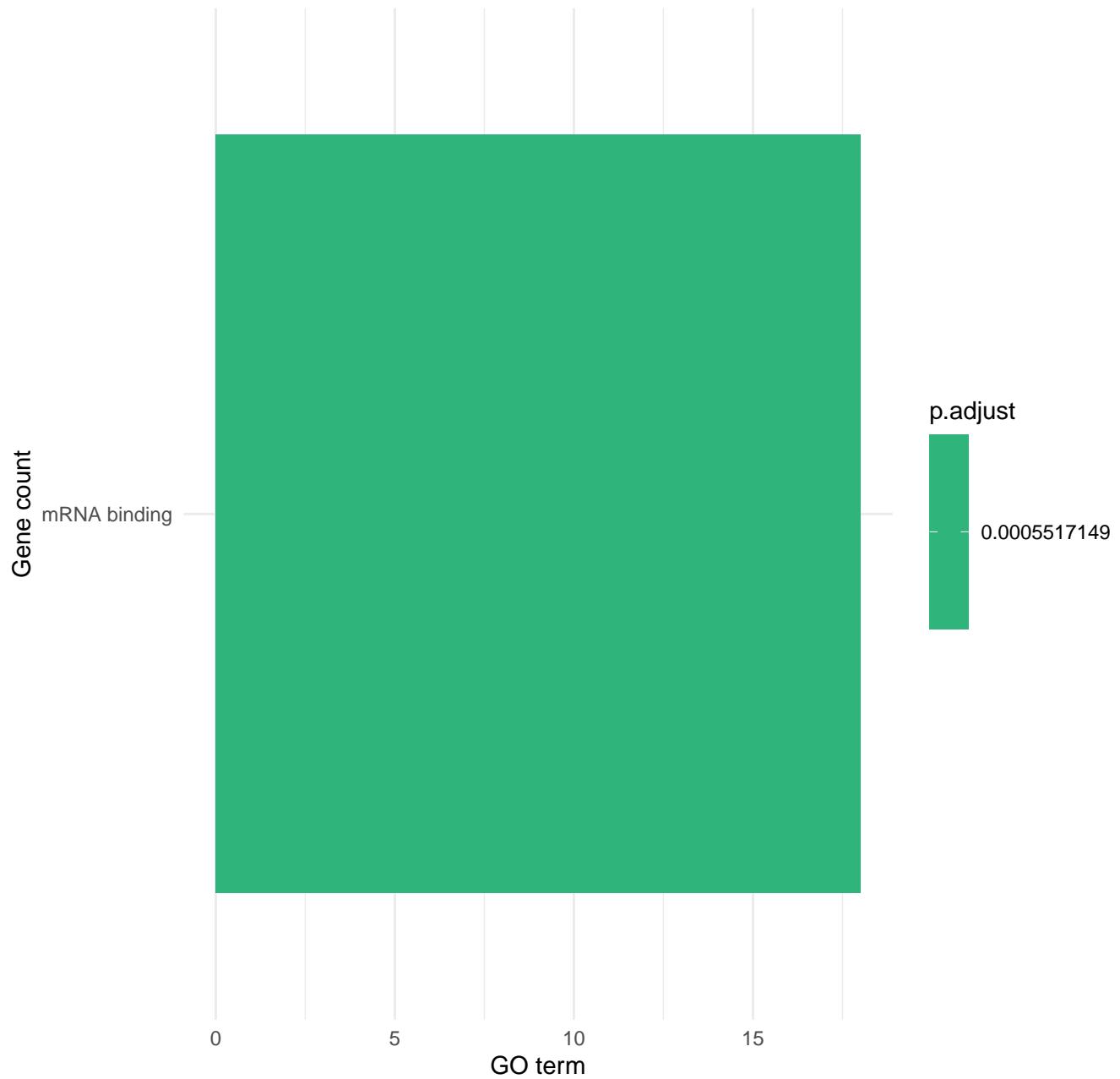




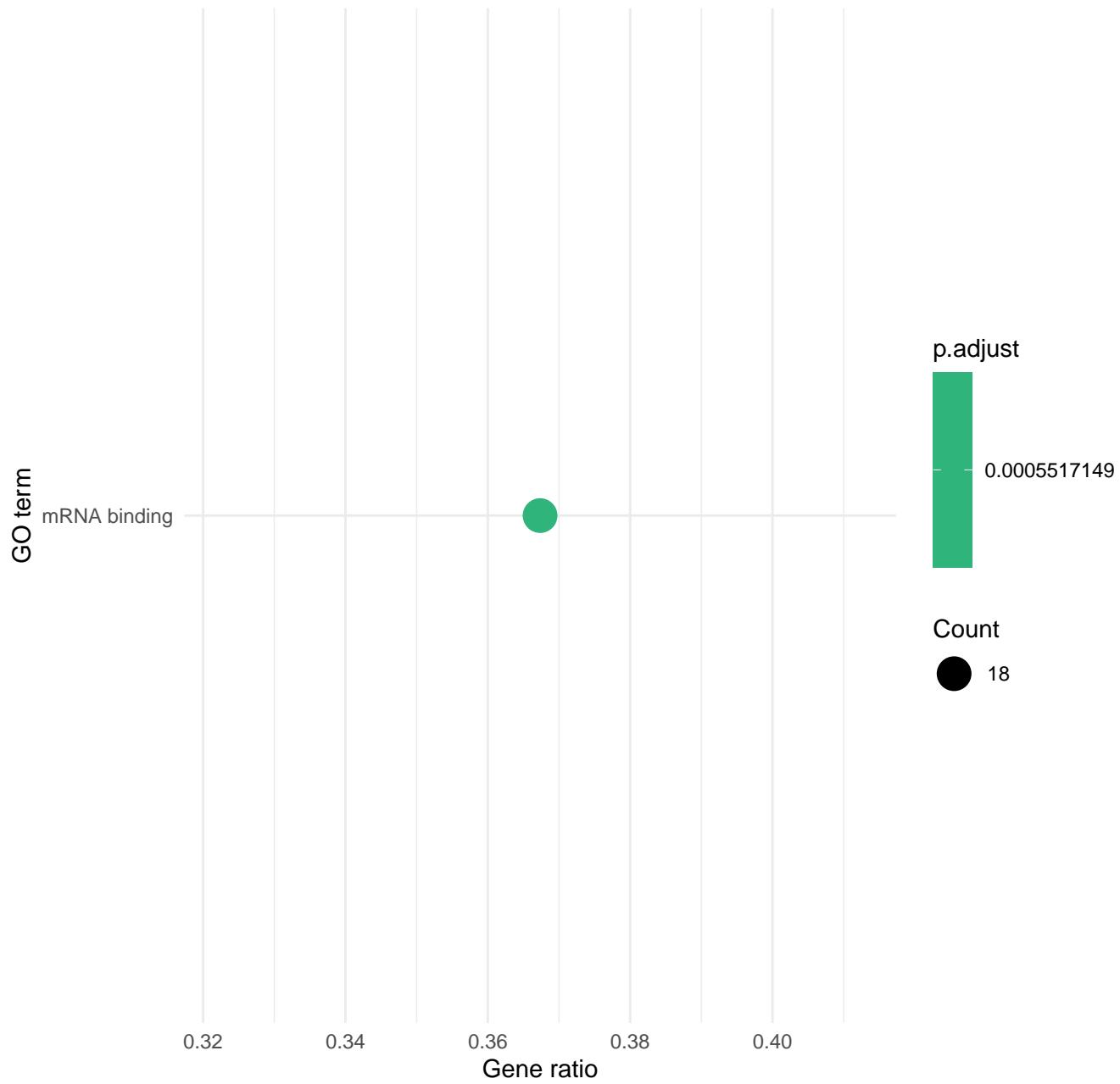
RRP40-TAP Up-regulated GO



RRP40–TAP Up-regulated GO MF barplot



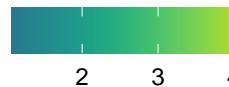
RRP40–TAP Up-regulated GO MF dotplot



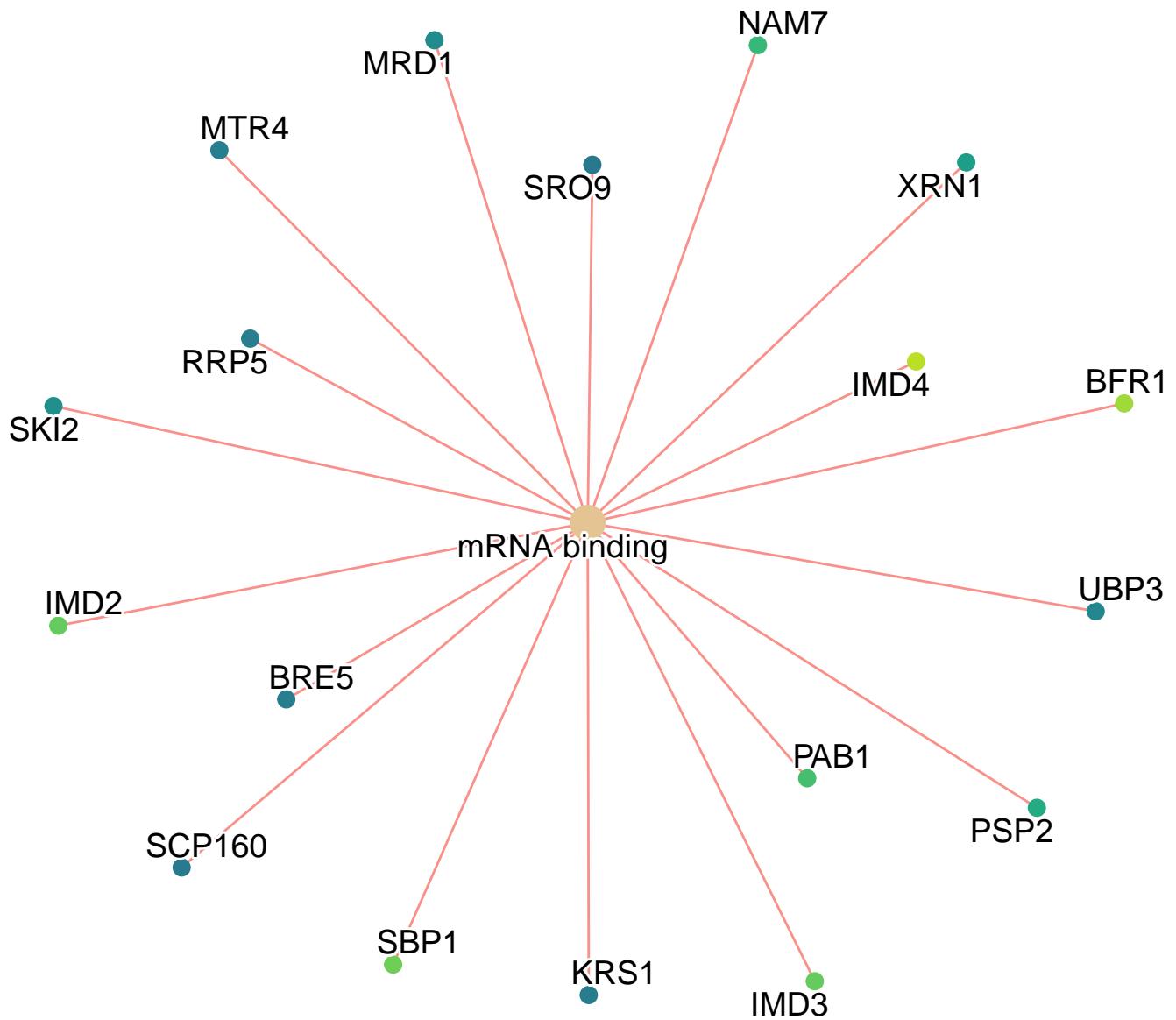
RRP40-TAP Up-regulated GO MF cnetplot

category mRNA binding

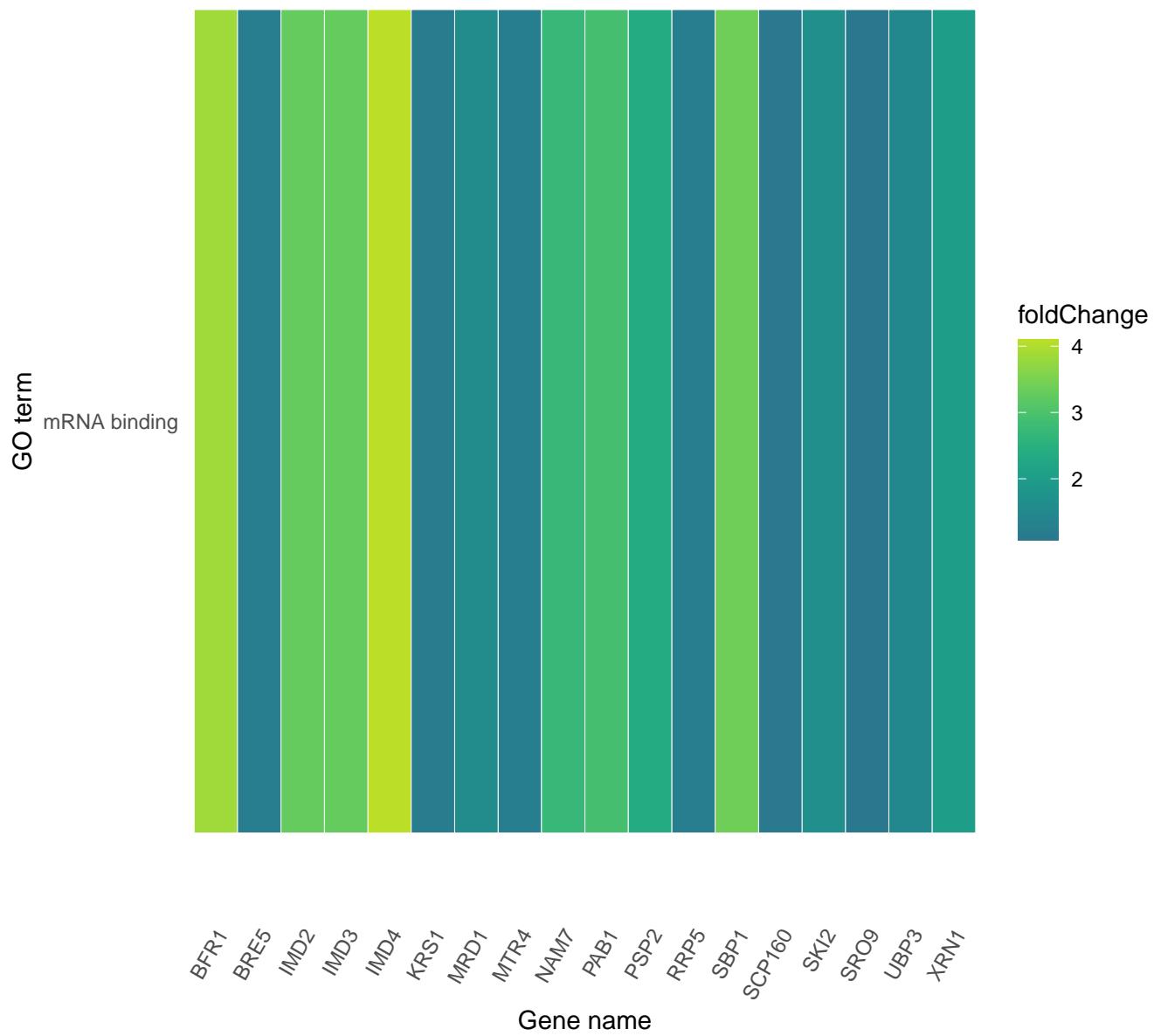
FoldChange

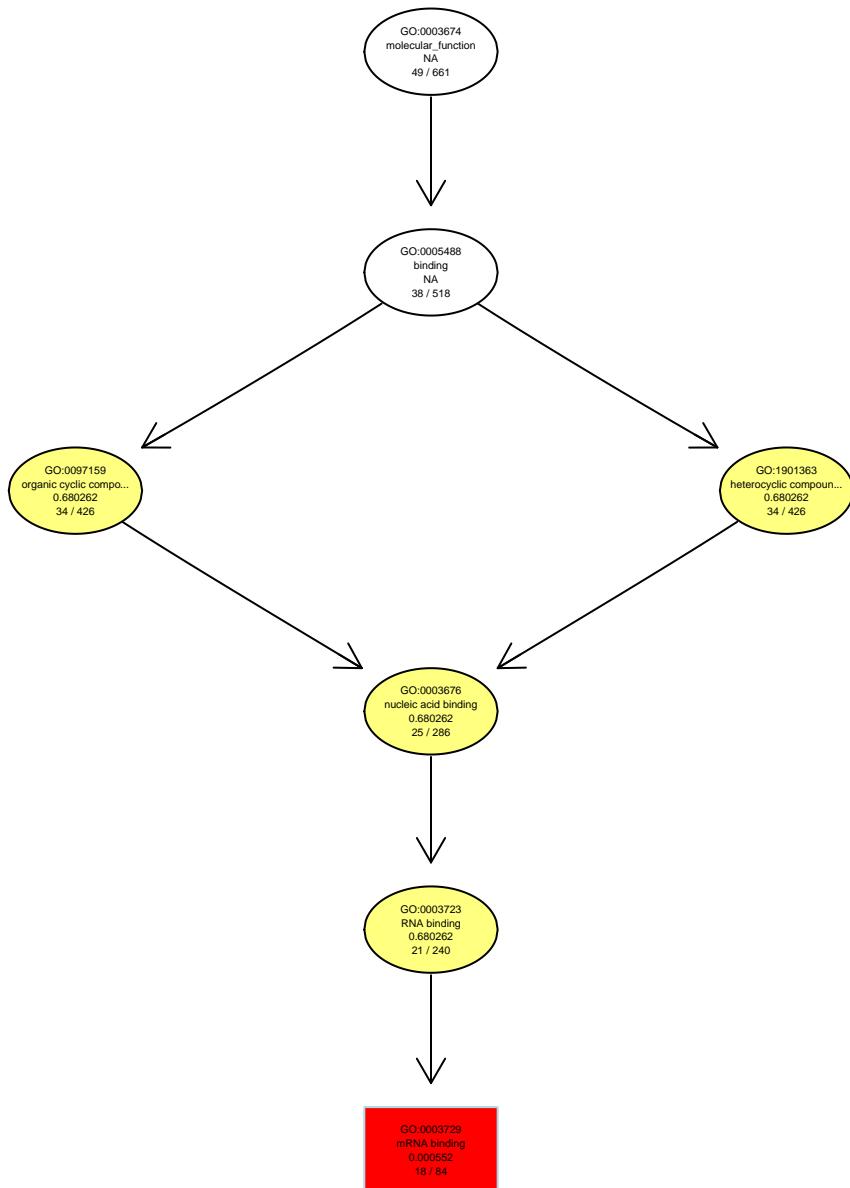


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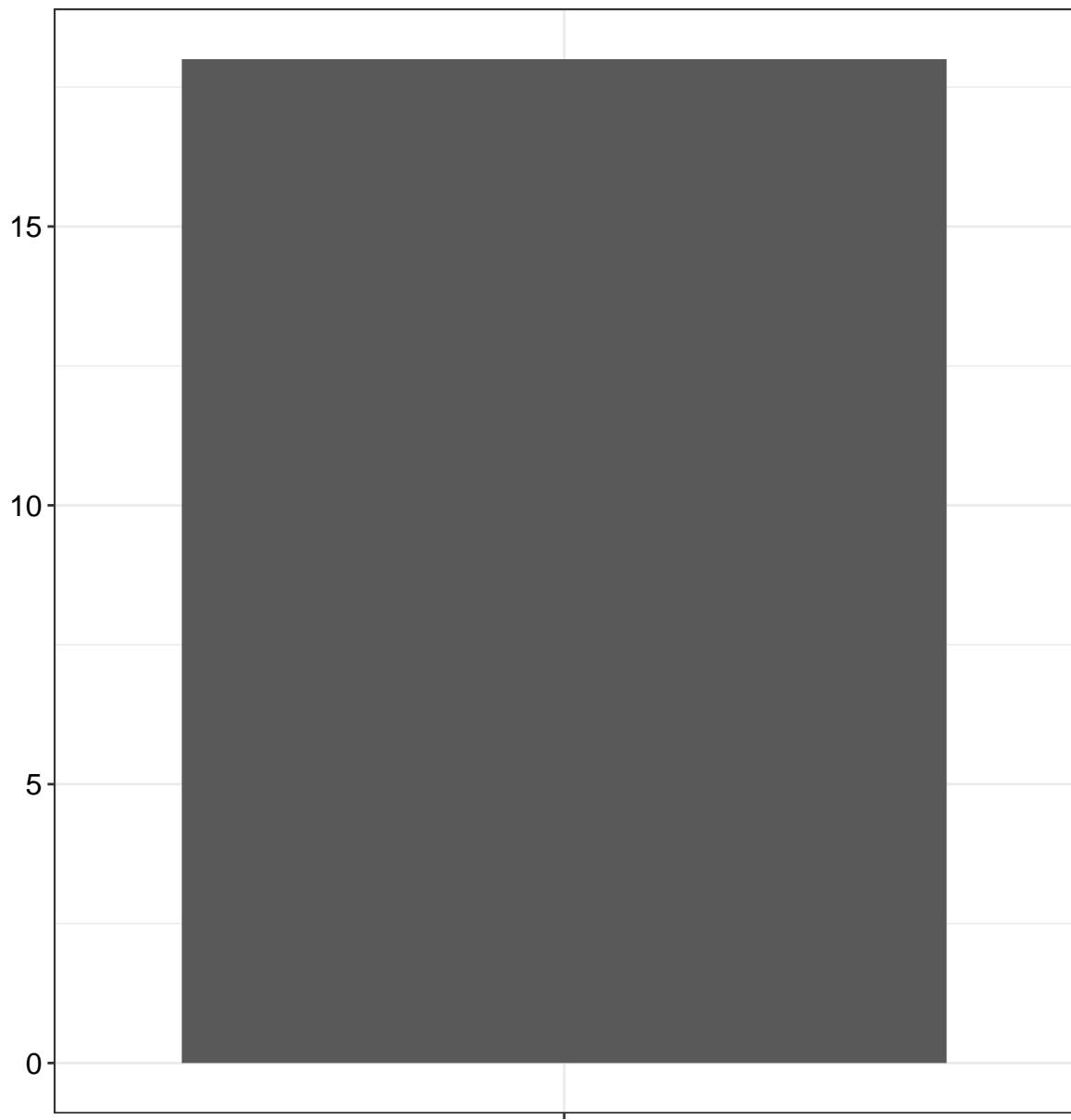


RRP40–TAP Up-regulated GO MF heatplot





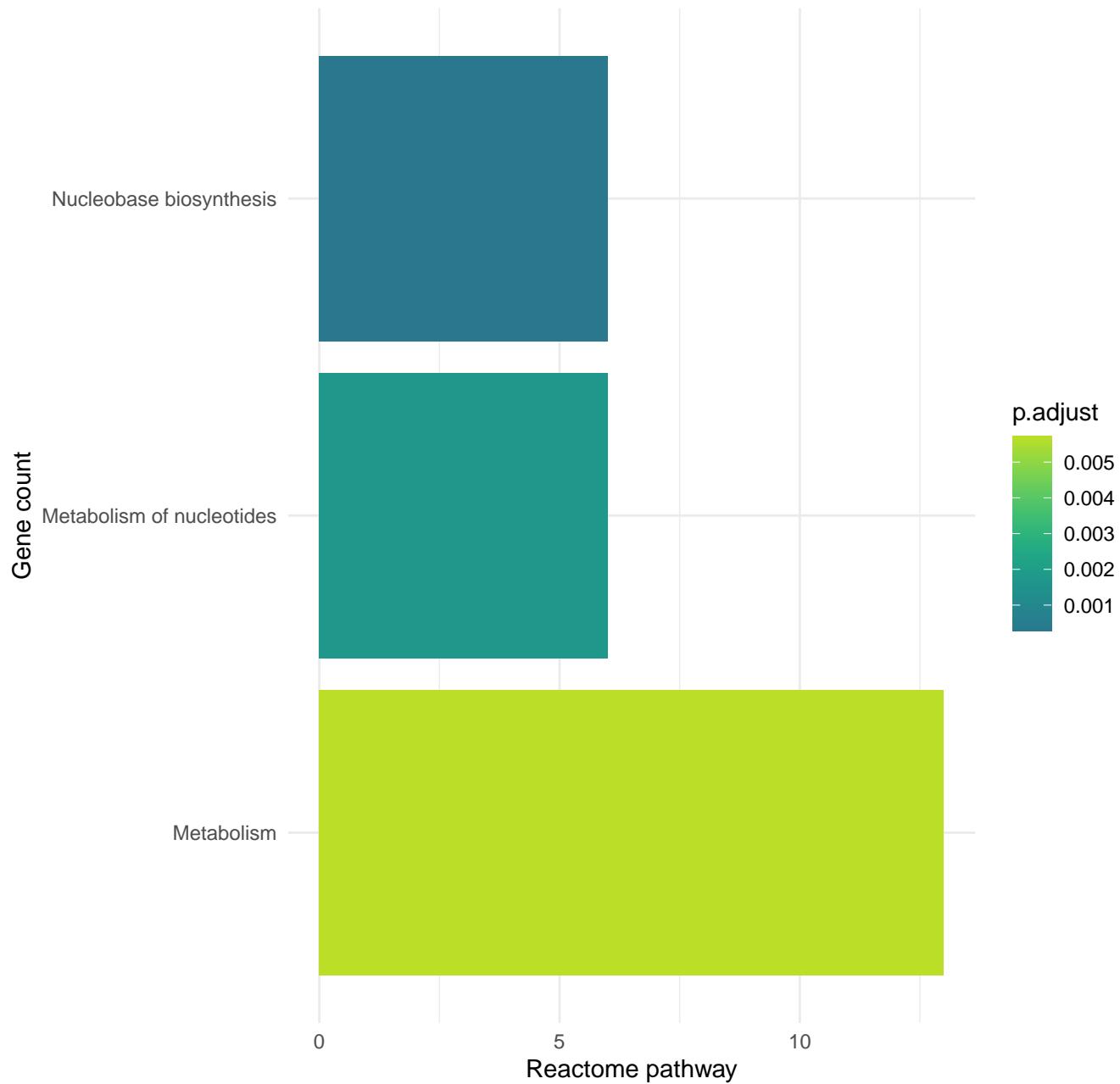
RRP40–TAP Up-regulated GO MF upsetplot



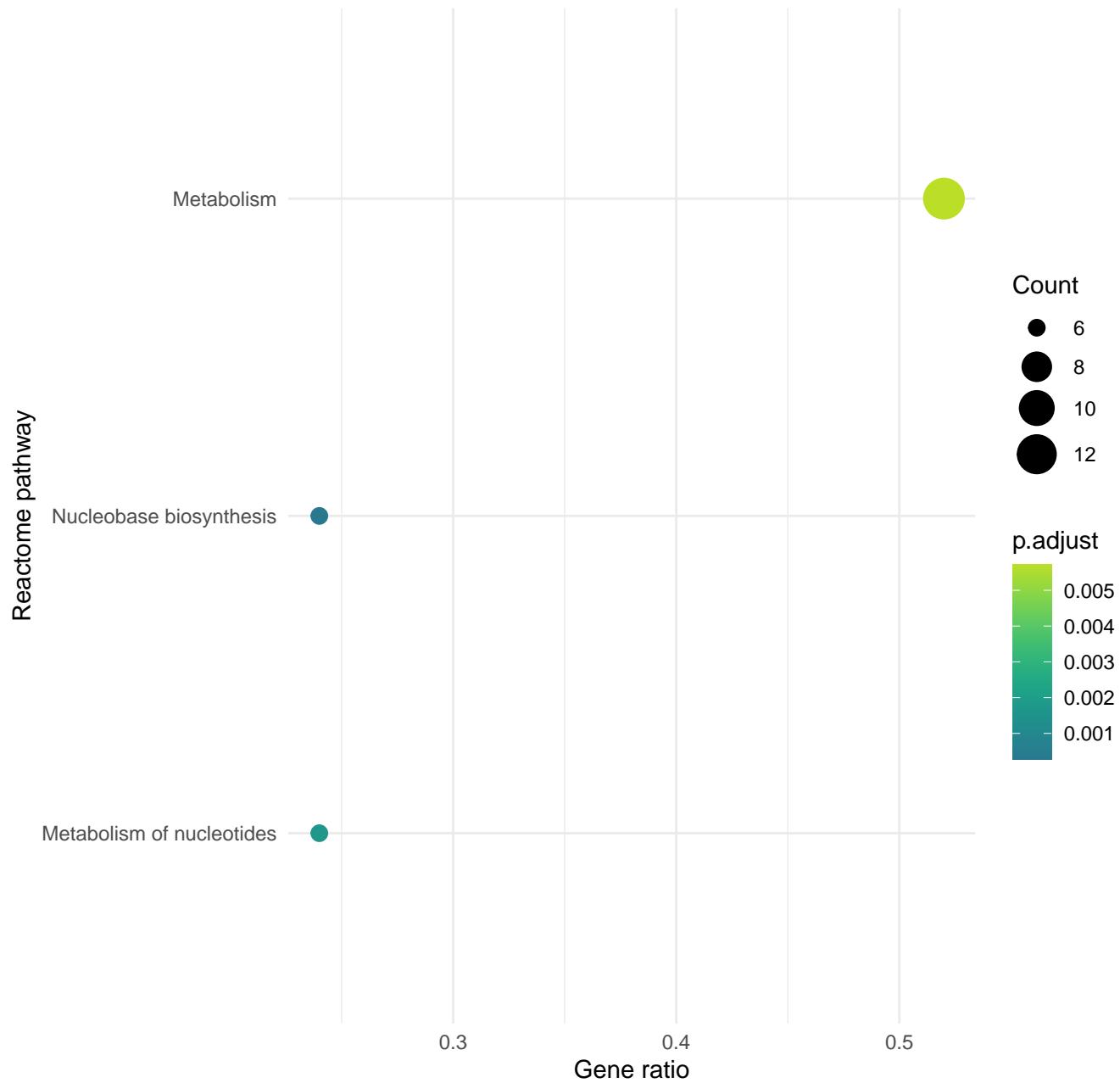
mRNA binding

●

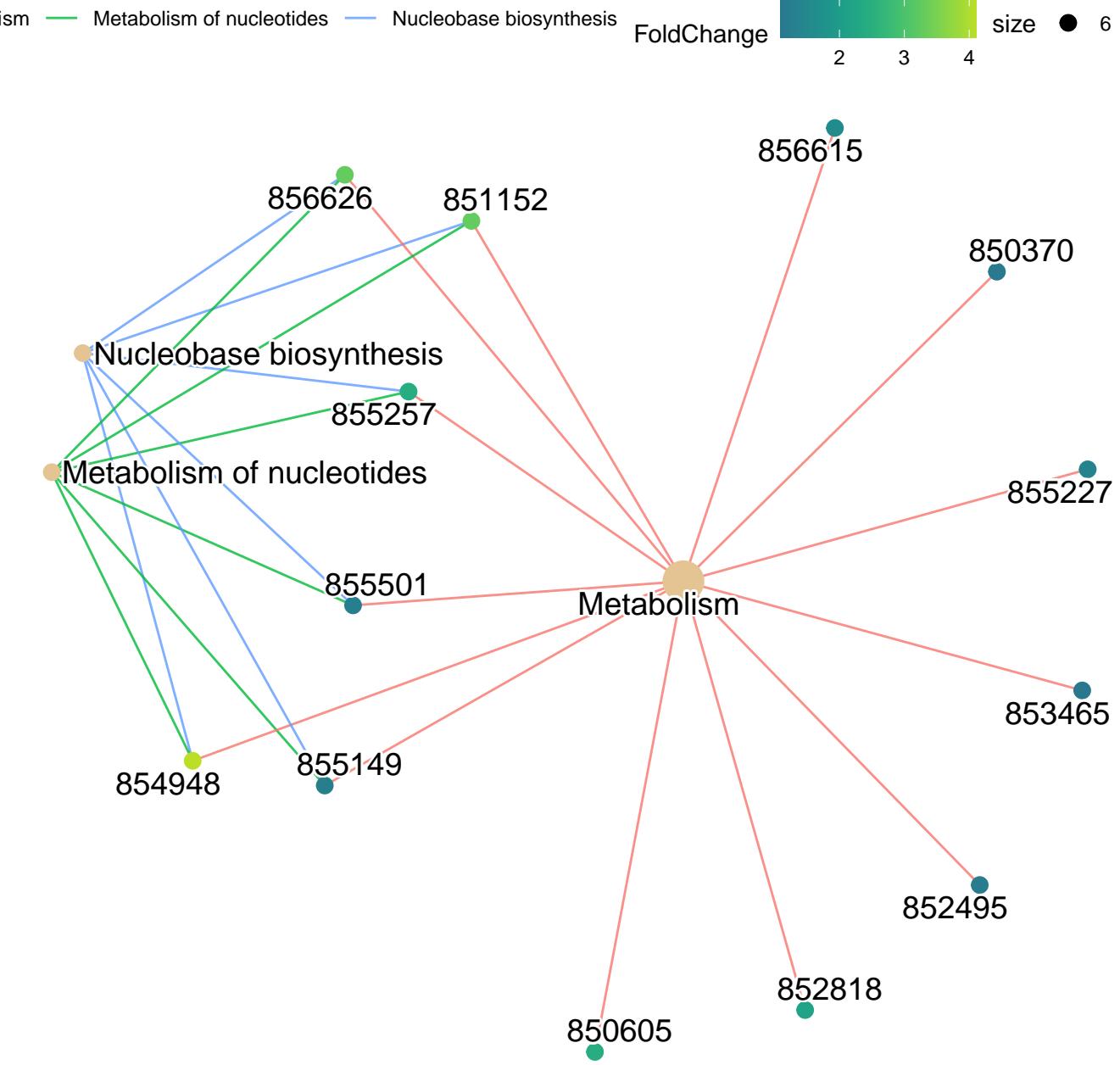
RRP40-TAP Up-regulated Reactome barplot



RRP40–TAP Up-regulated Reactome dotplot



RRP40-TAP Up-regulated Reactome cnetplot



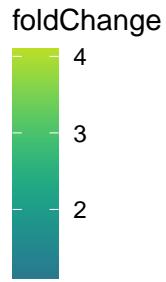
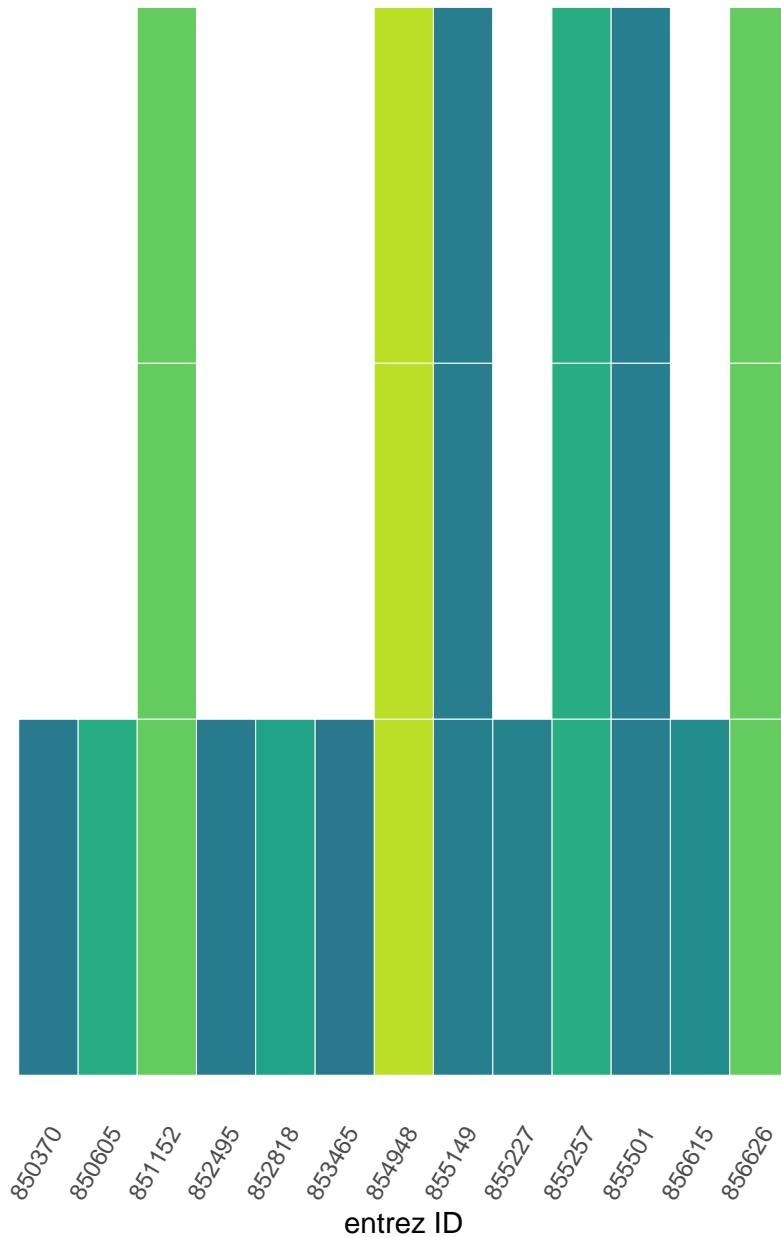
RRP40-TAP Up-regulated Reactome heatplot

Reactome pathway

Nucleobase biosynthesis

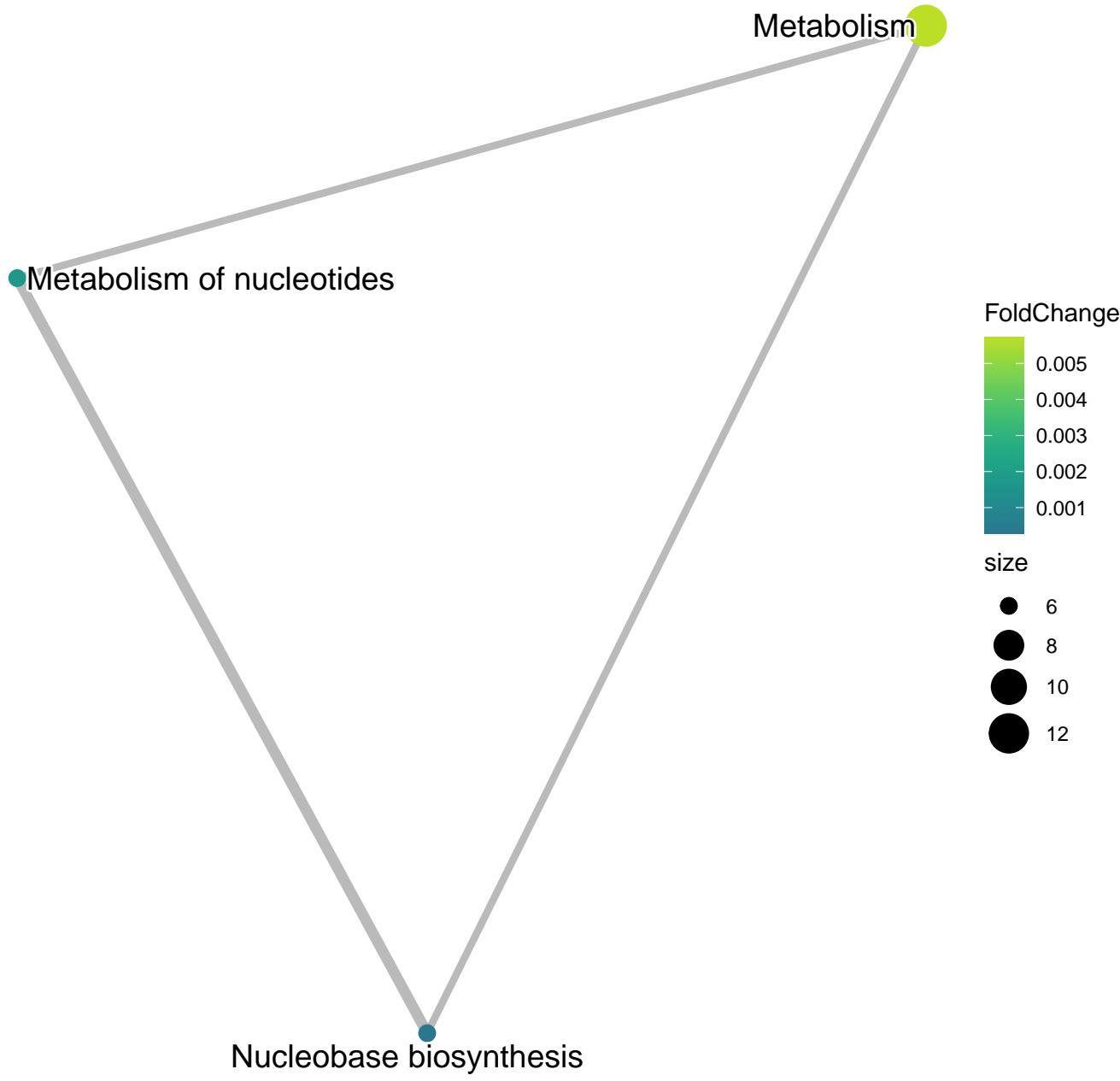
Metabolism of nucleotides

Metabolism

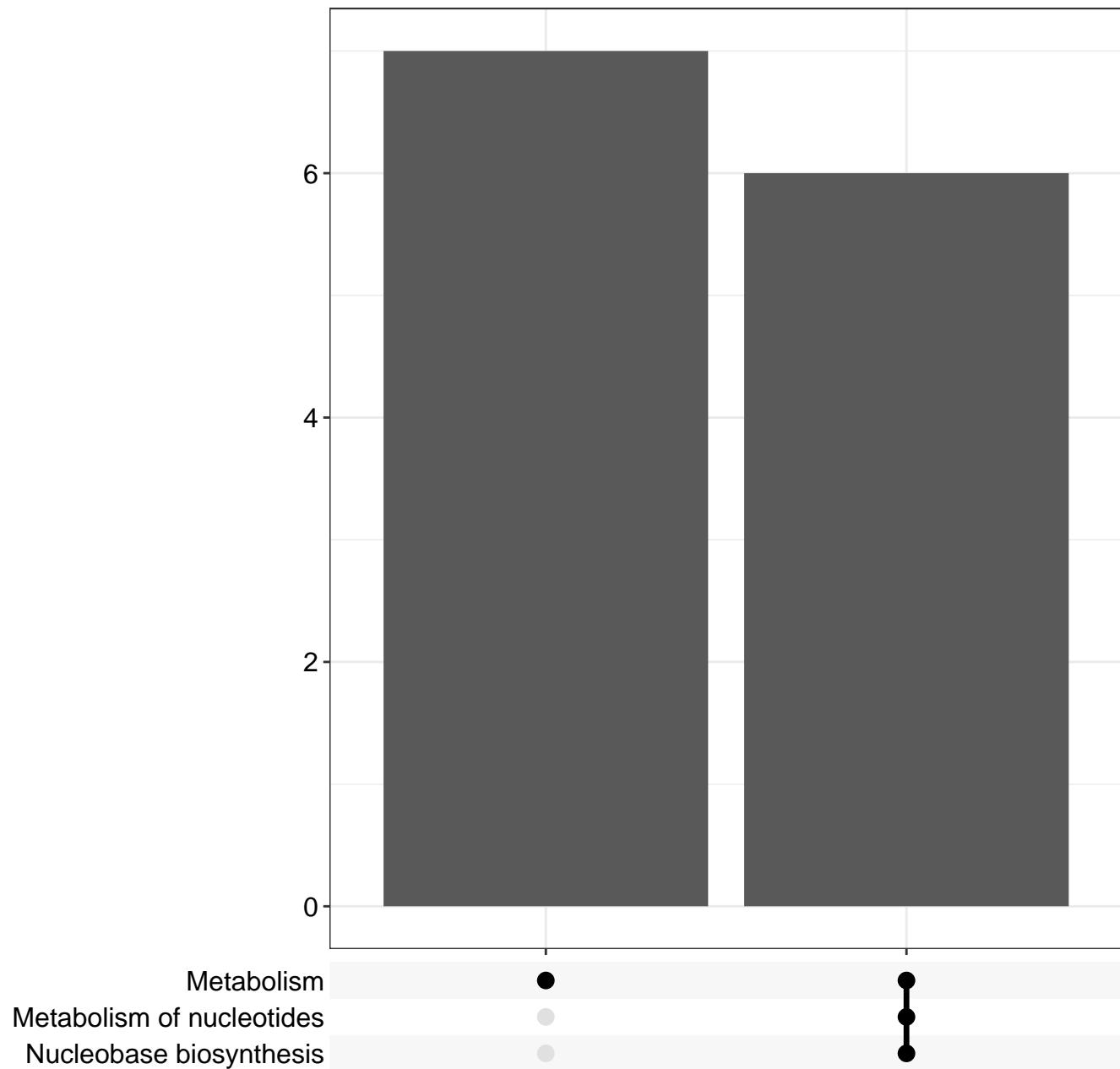


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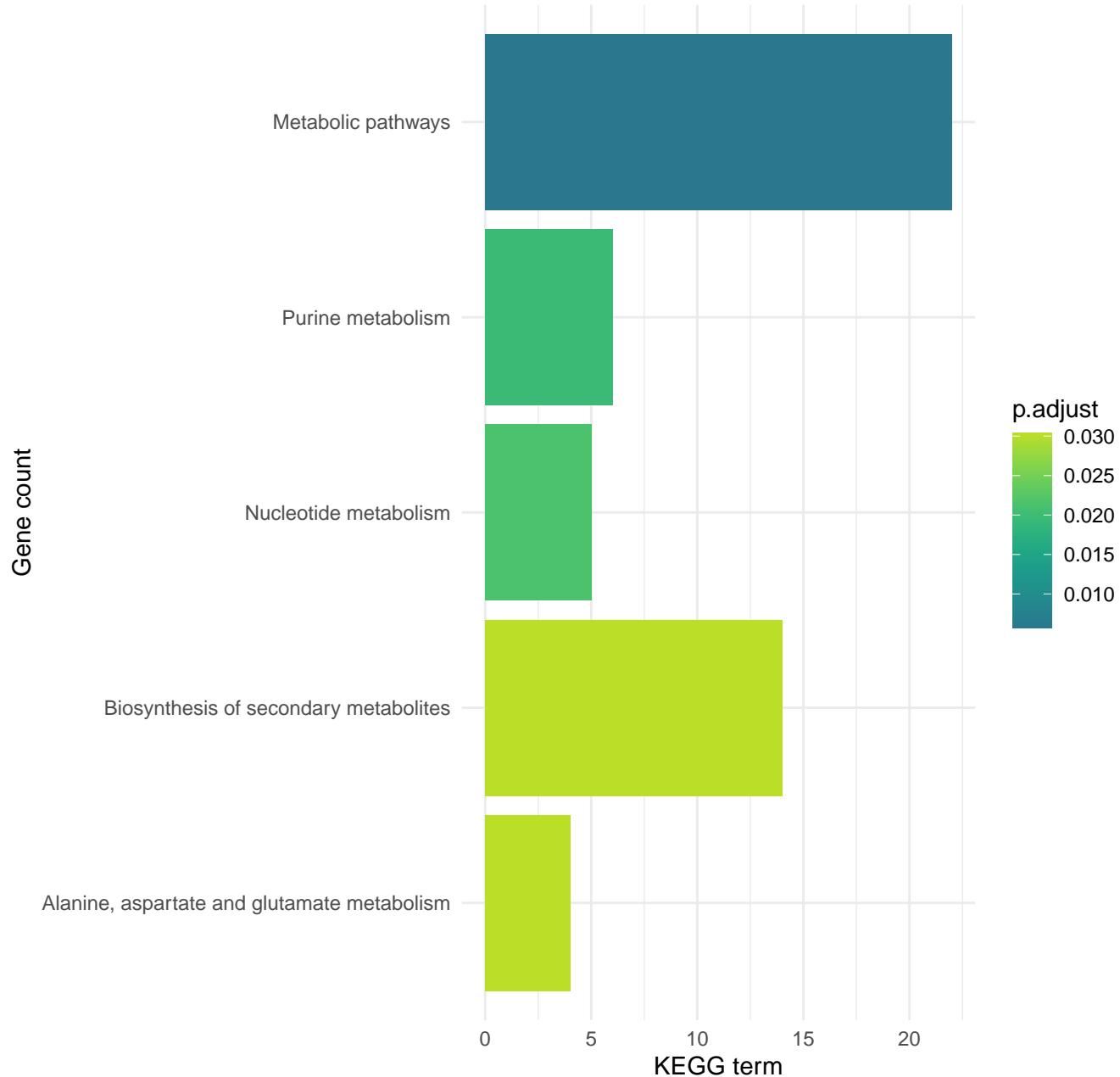
RRP40-TAP Up-regulated Reactome emapplot



RRP40-TAP Up-regulated Reactome upsetplot

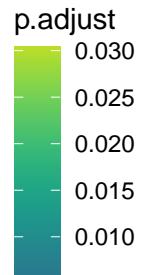
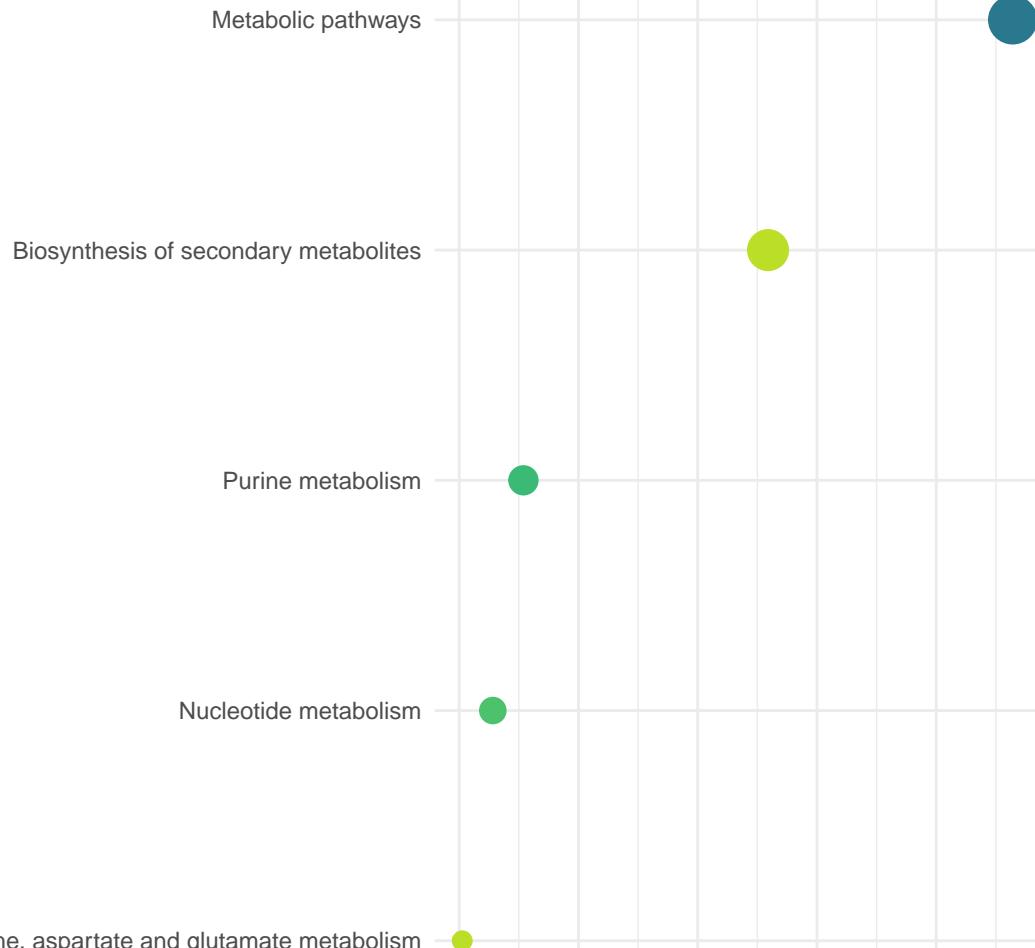


RRP40-TAP Up-regulated KEGG barplot



RRP40–TAP Up-regulated KEGG dotplot

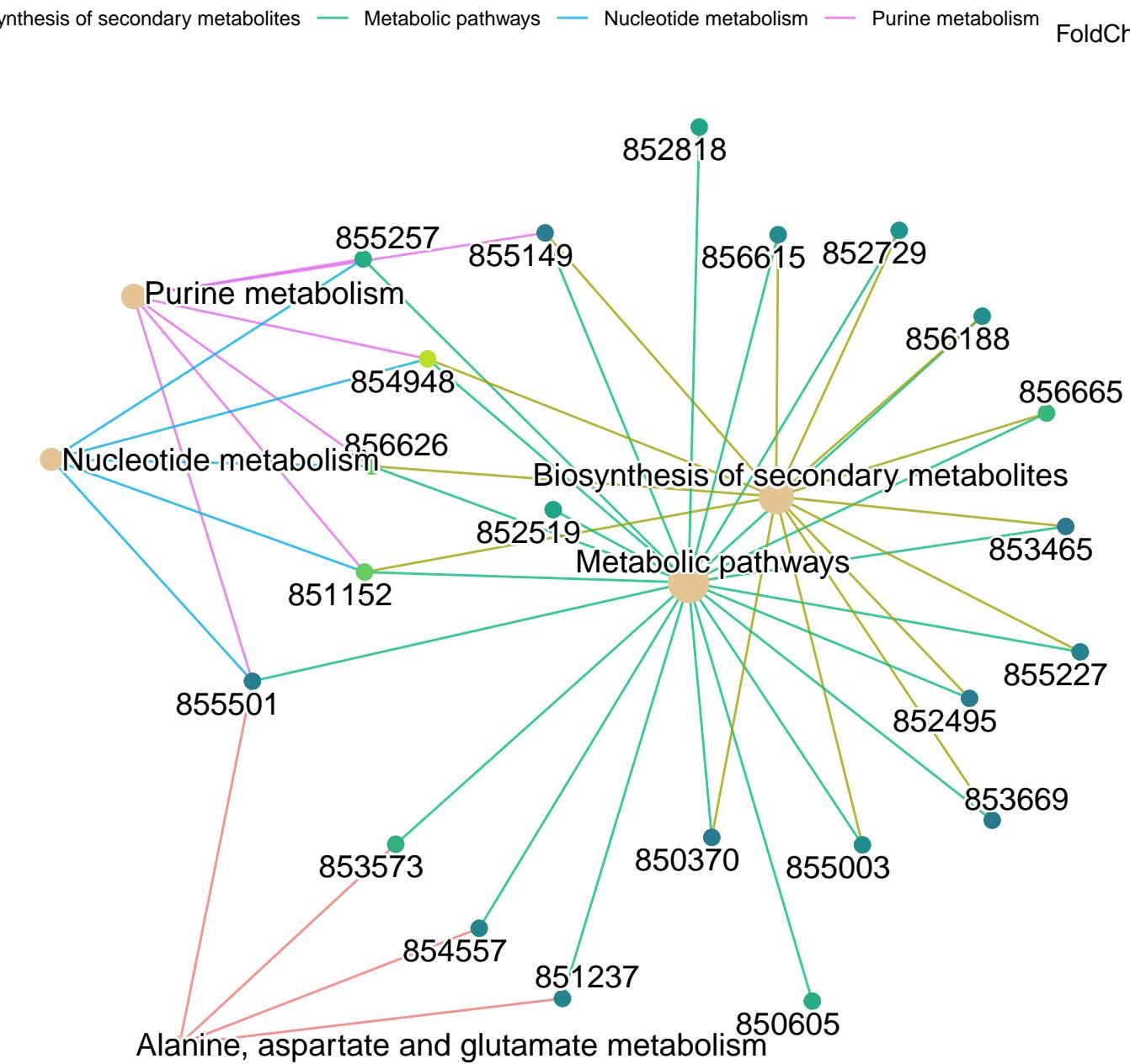
KEGG term



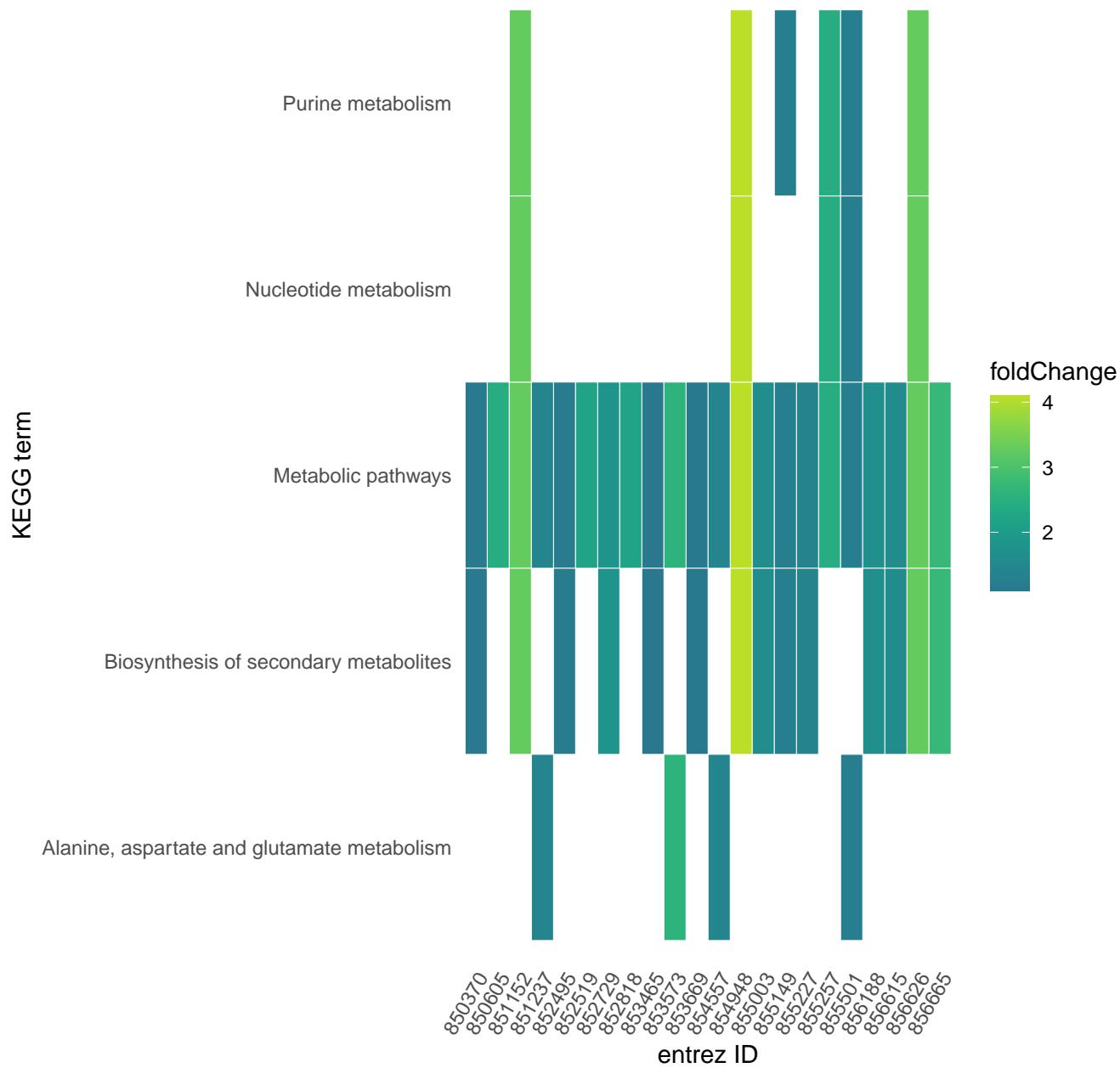
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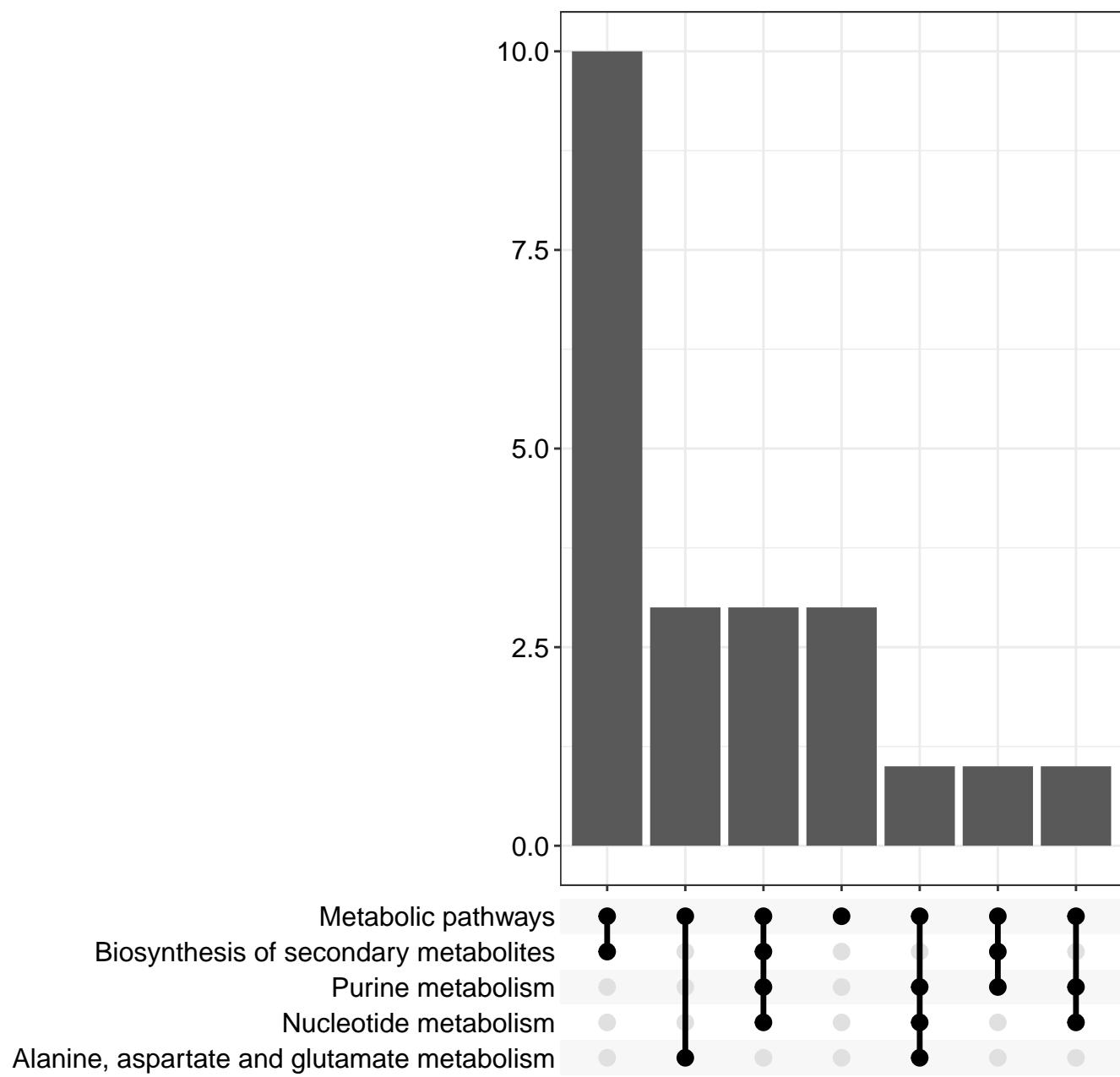
RRP40-TAP Up-regulated KEGG dotplot



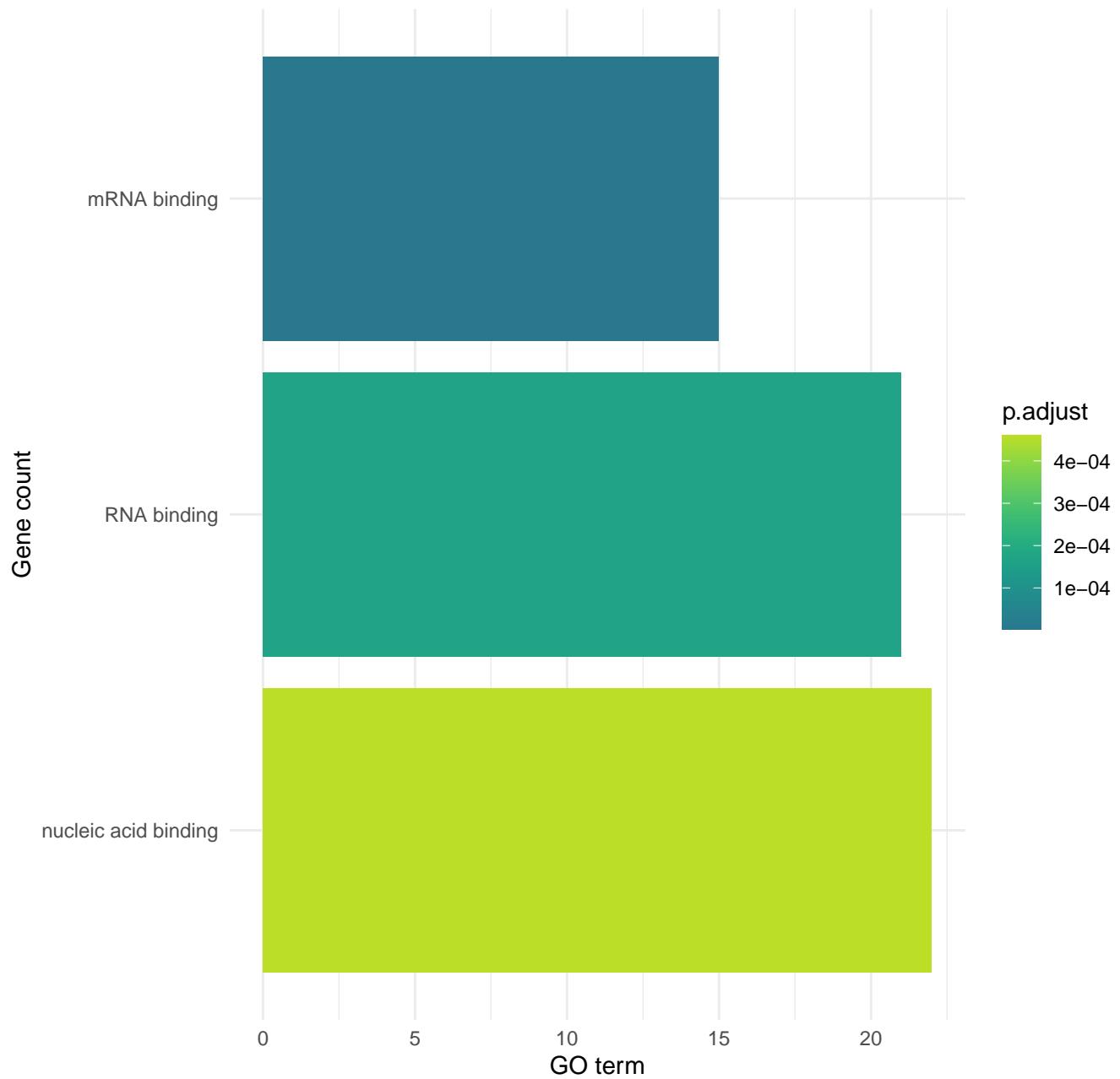
RRP40-TAP Up-regulated KEGG heatplot



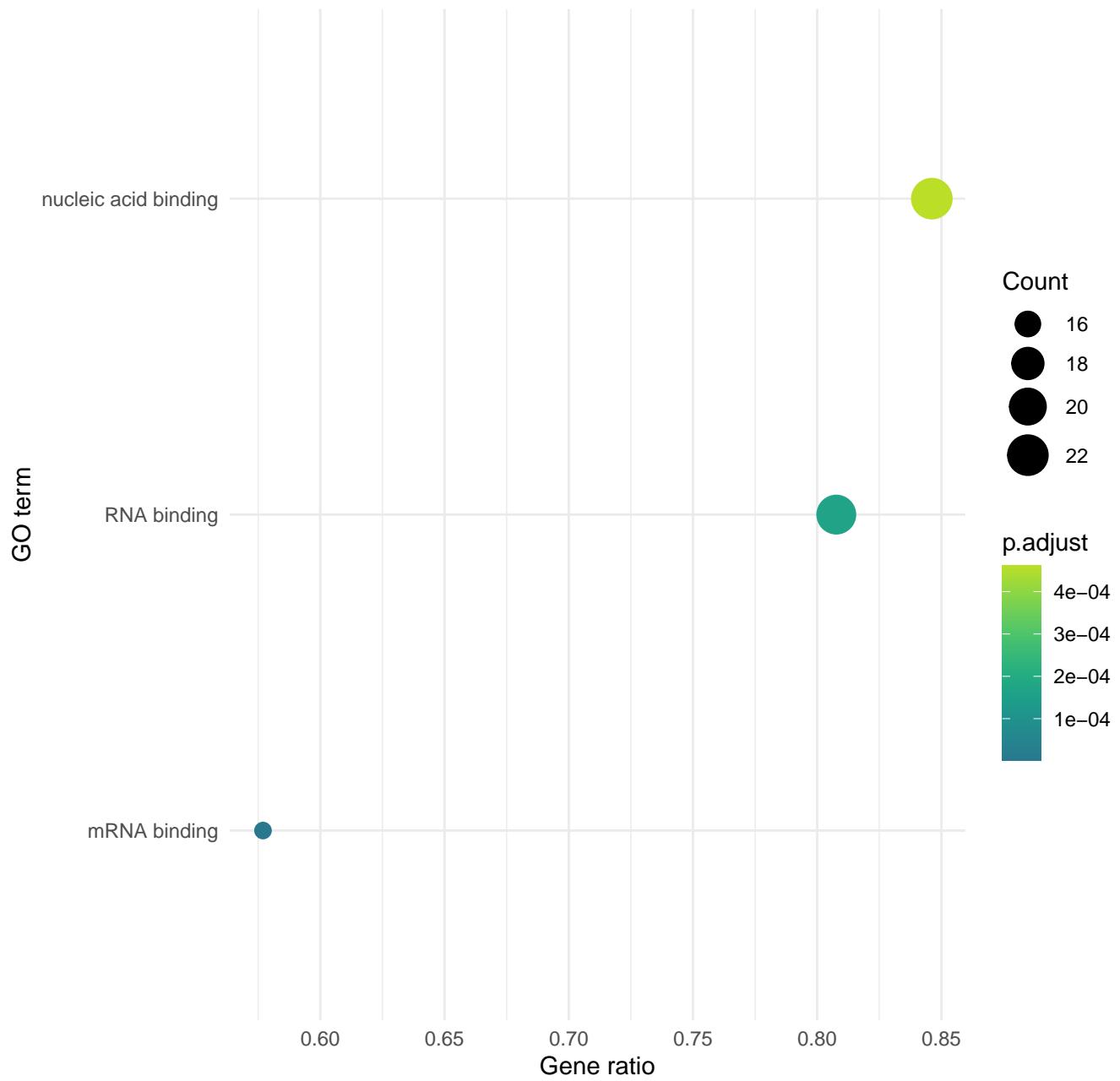
RRP40-TAP Up-regulated KEGG upsetplot



SKI2-TAP Up-regulated GO MF barplot



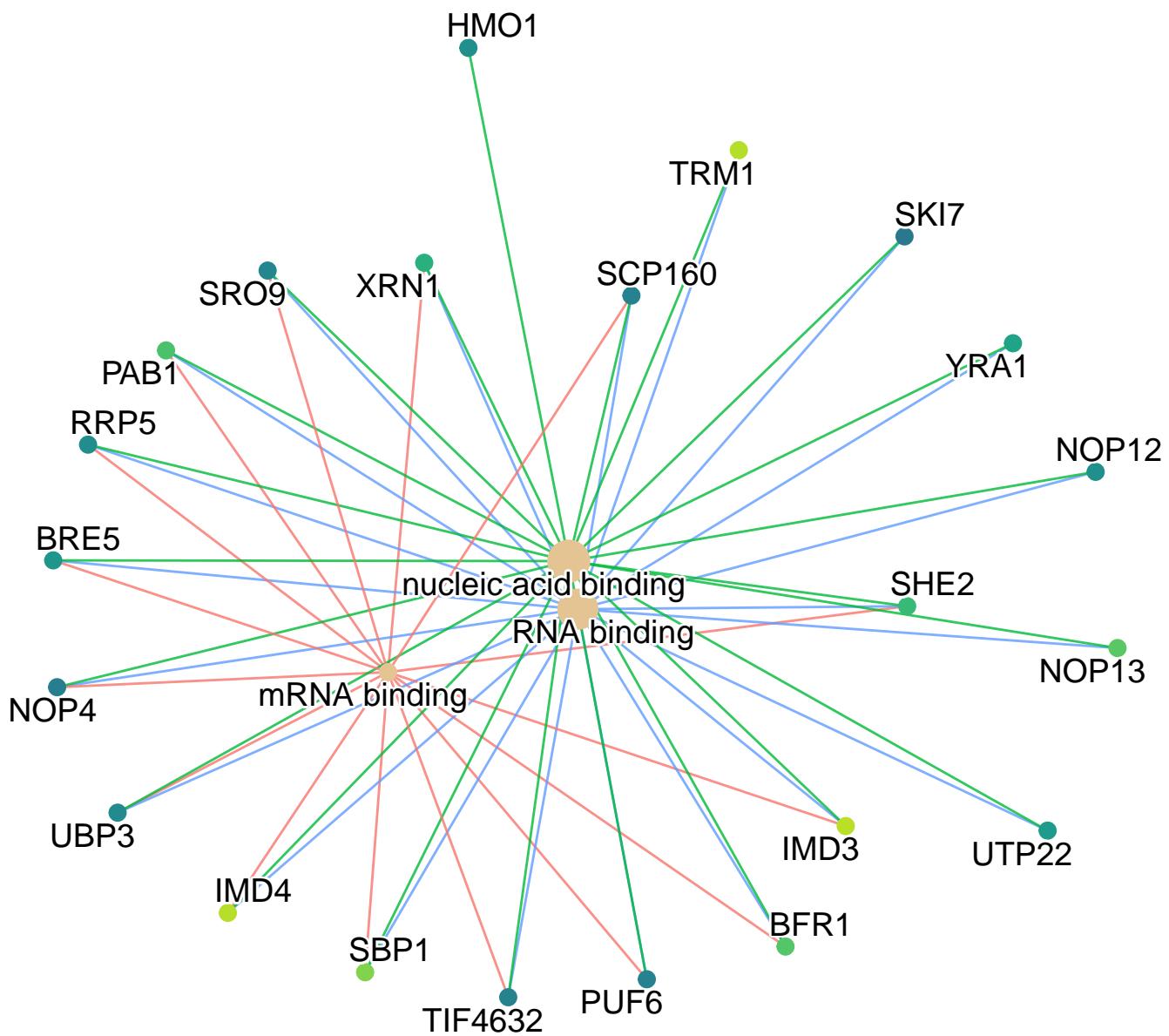
SKI2-TAP Up-regulated GO MF dotplot



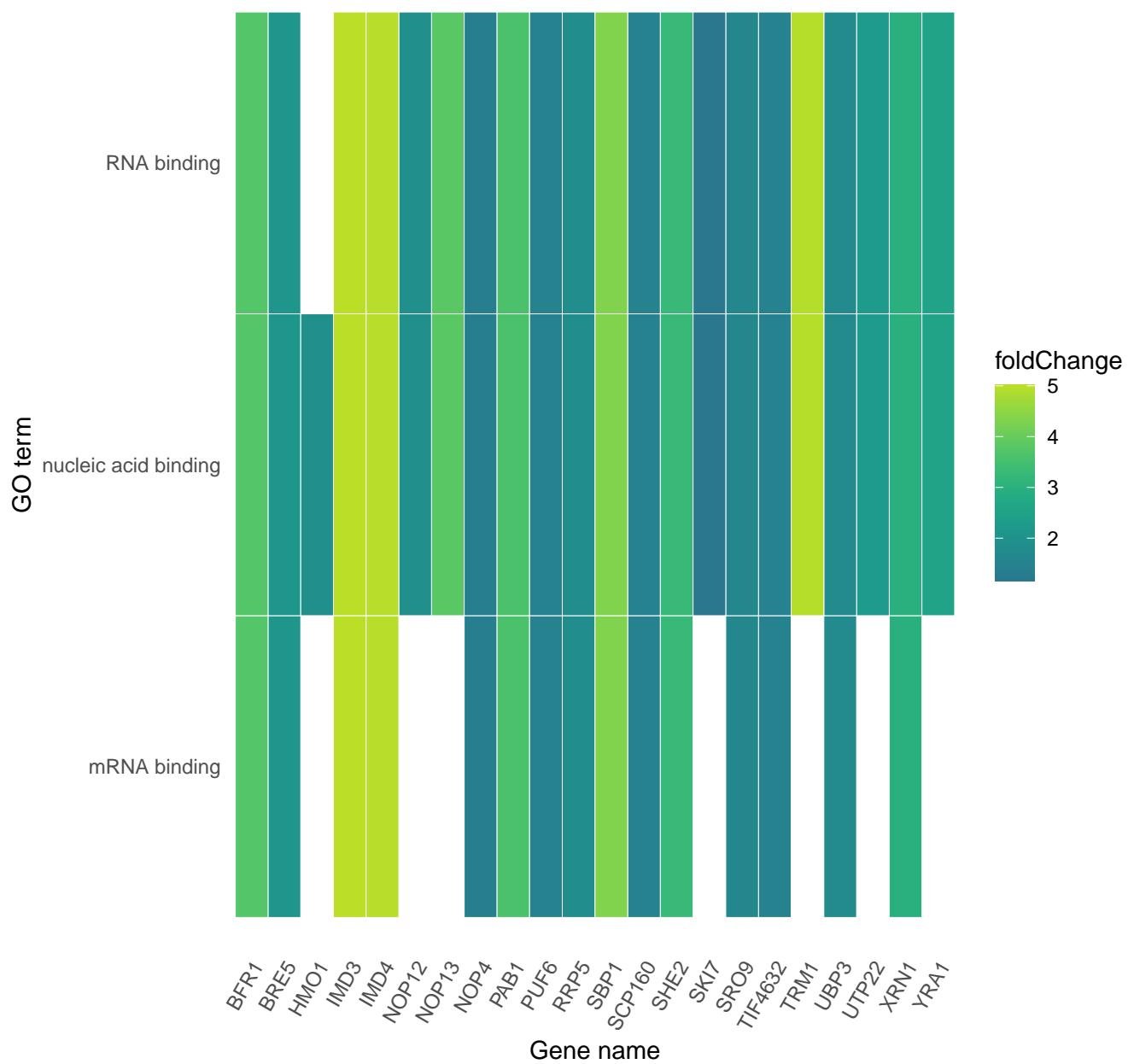
SKI2-TAP Up-regulated GO MF cnetplot

RNA binding — nucleic acid binding — RNA binding

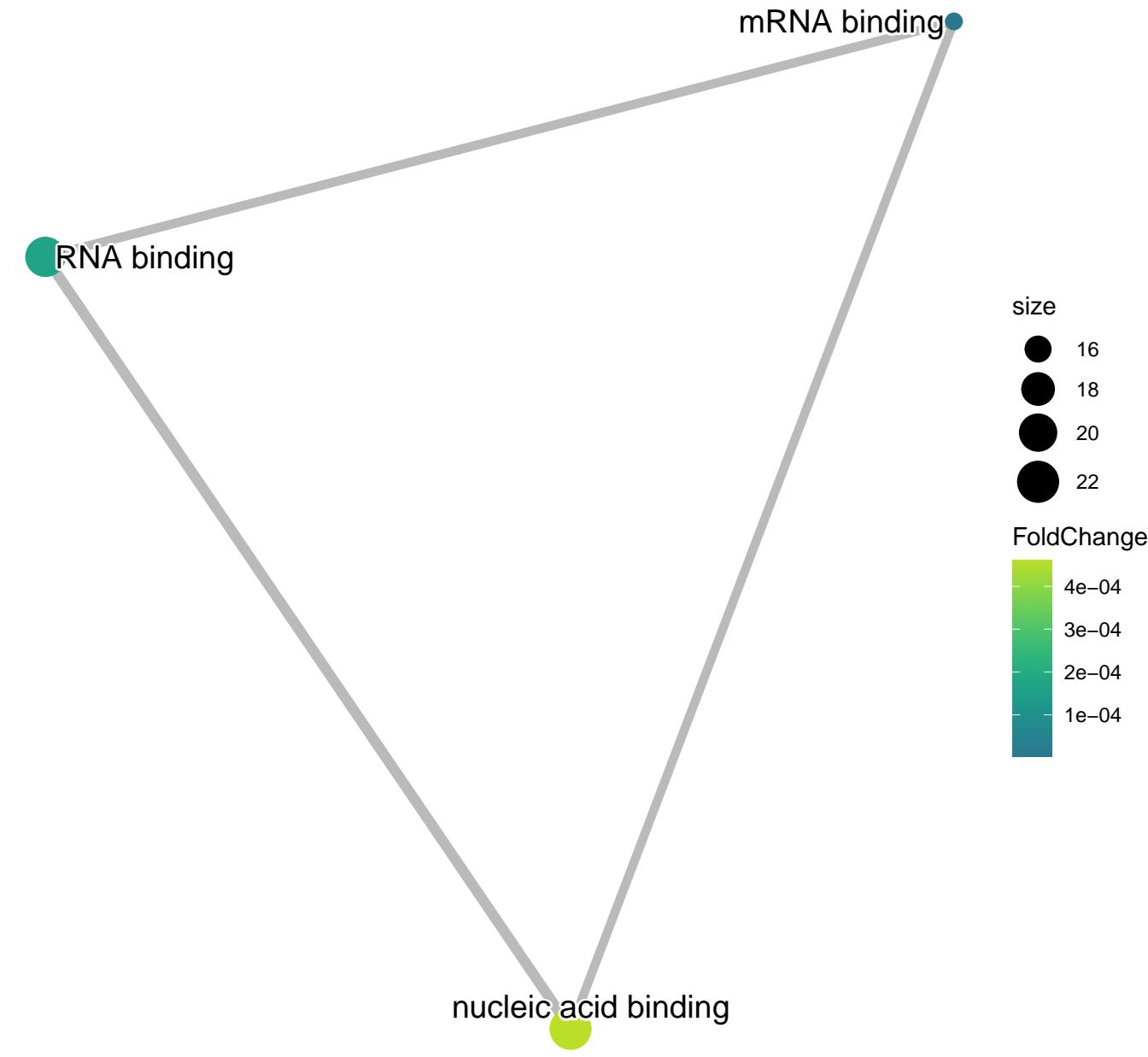
FoldChange

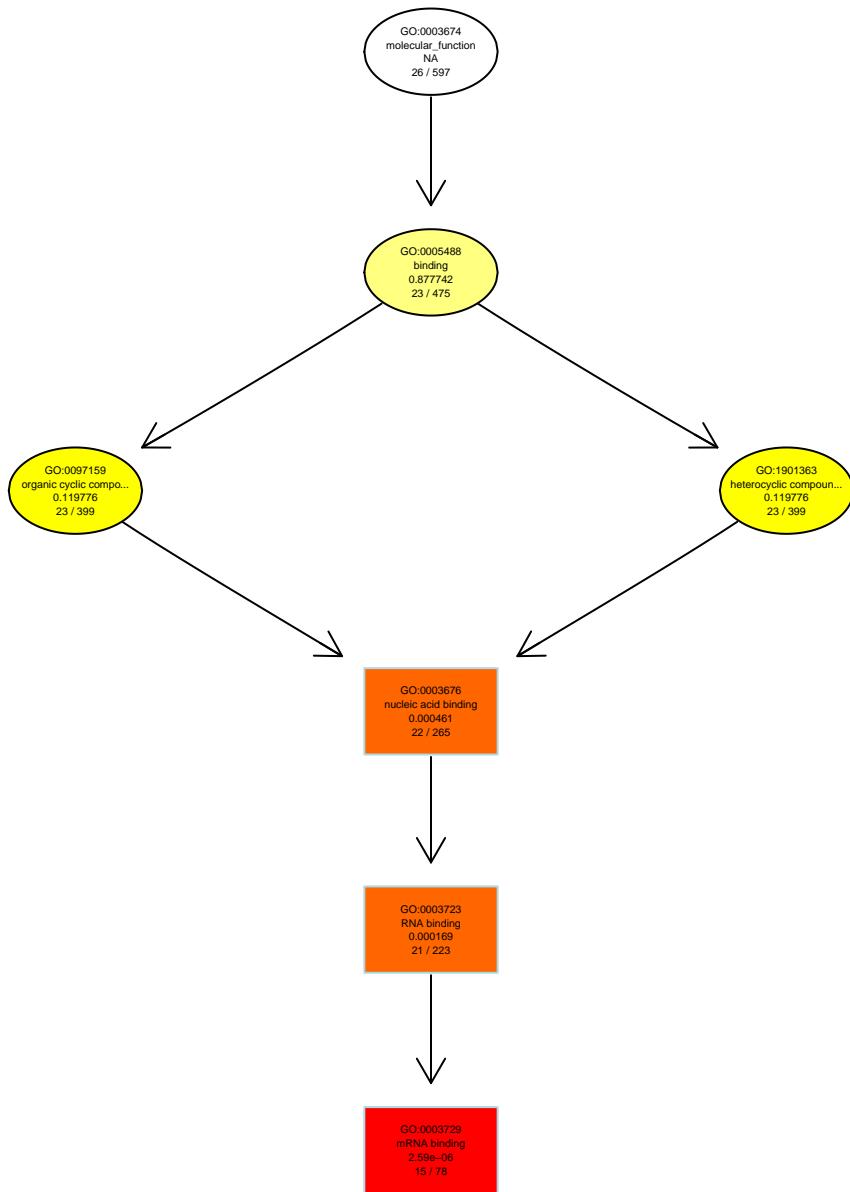


SKI2-TAP Up-regulated GO MF heatplot

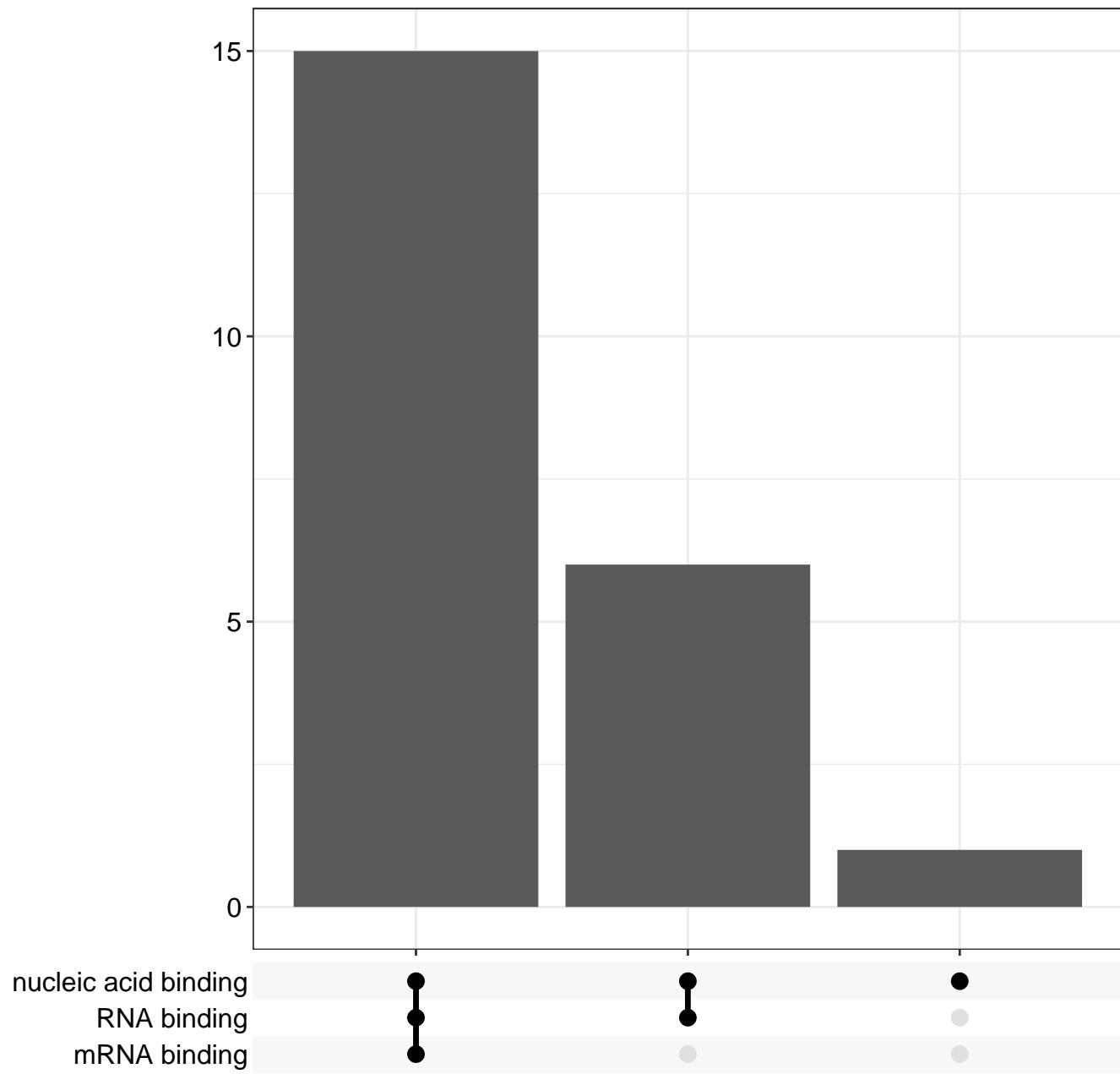


SKI2-TAP Up-regulated GO MF emapplot



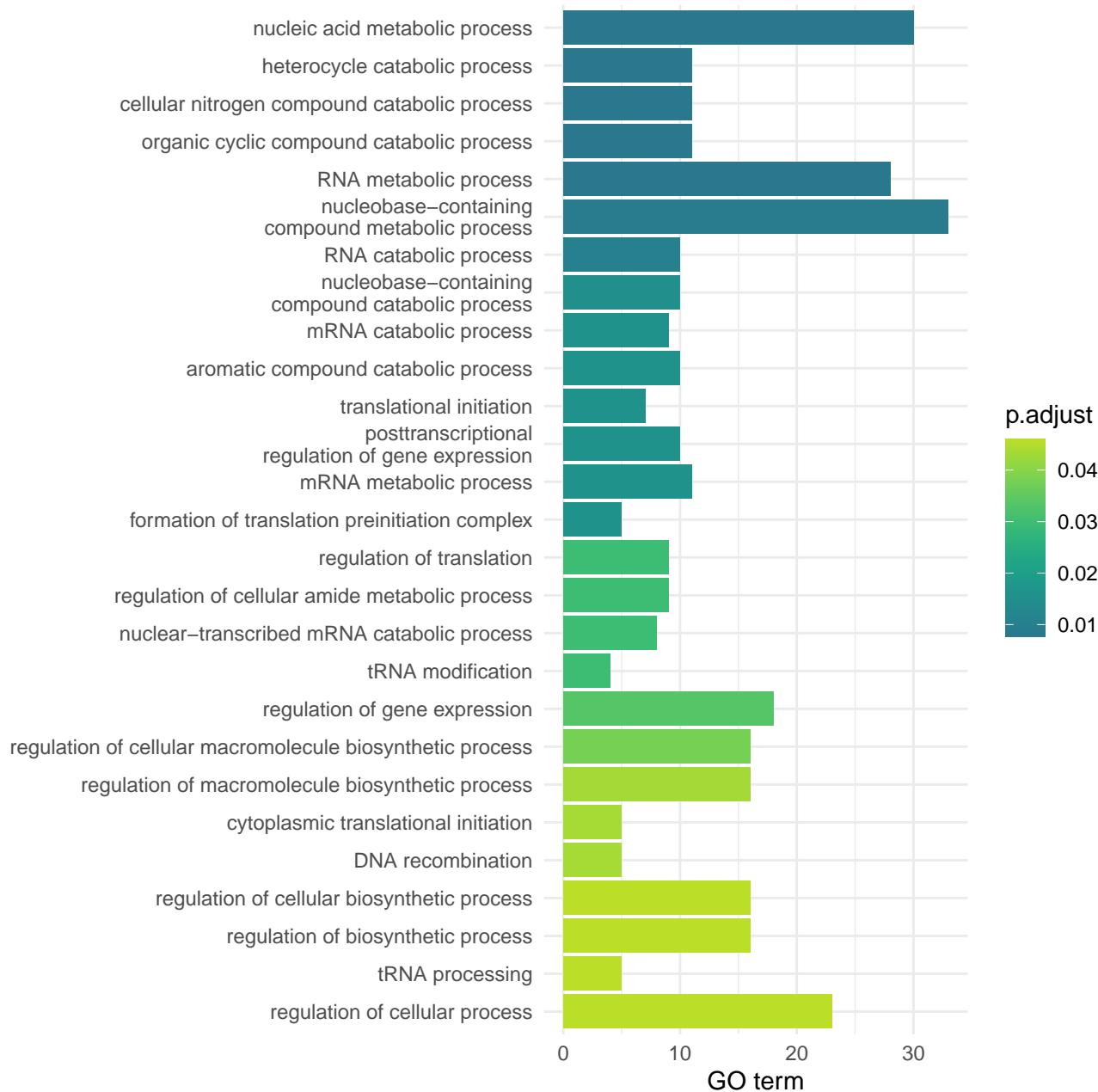


SKI2-TAP Up-regulated GO MF upsetplot

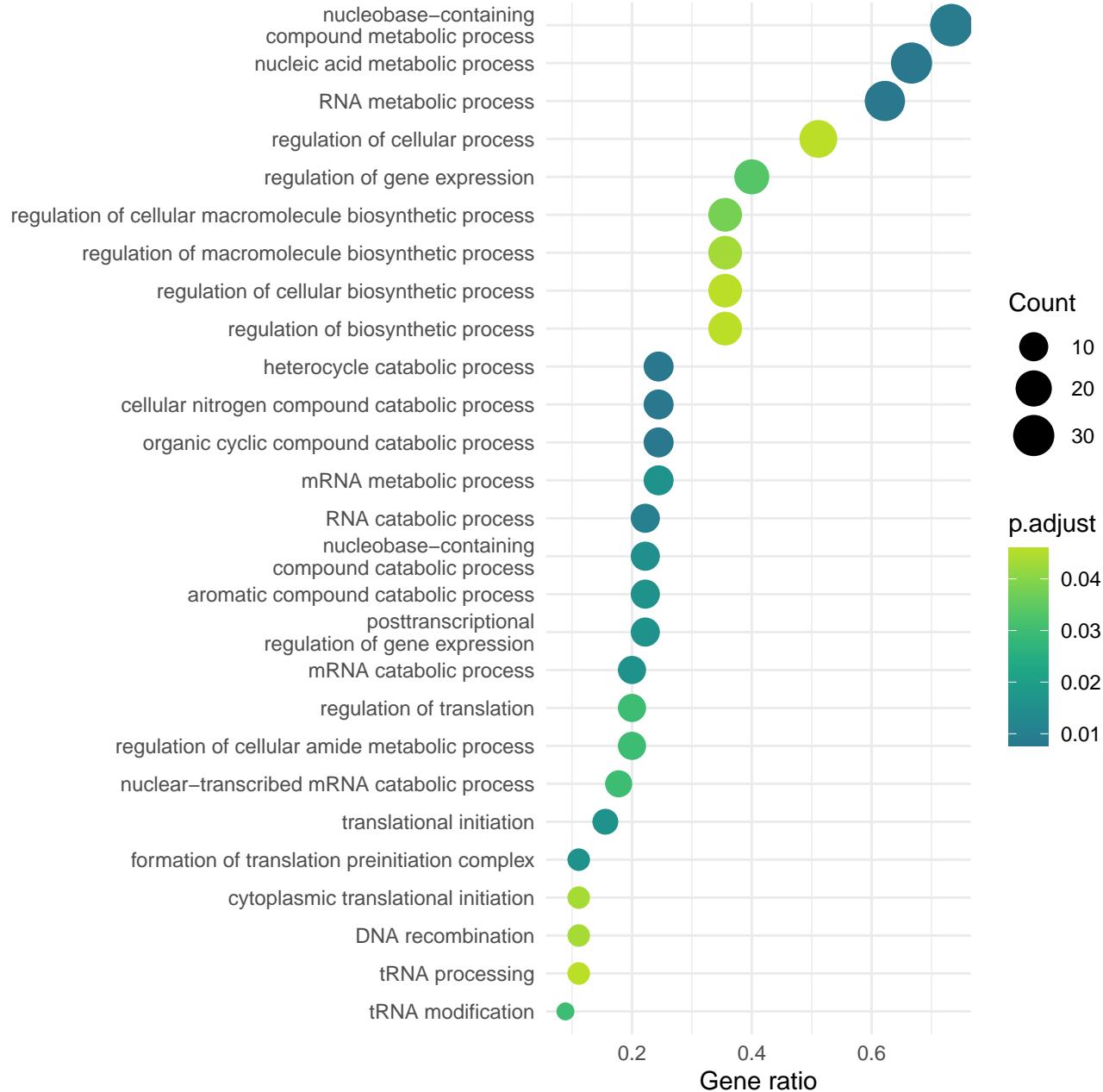


DHH1-TAP Up-regulated GO BP barplot

Gene count



DHH1–TAP Up-regulated GO BP dotplot



DHH1-TAP Up-regulated GO BP cnetplot

ound catabolic process

mRNA catabolic process

compound catabolic process

mRNA metabolic process

translational initiation

— nuclear-transcribed mRNA catabolic process

ion

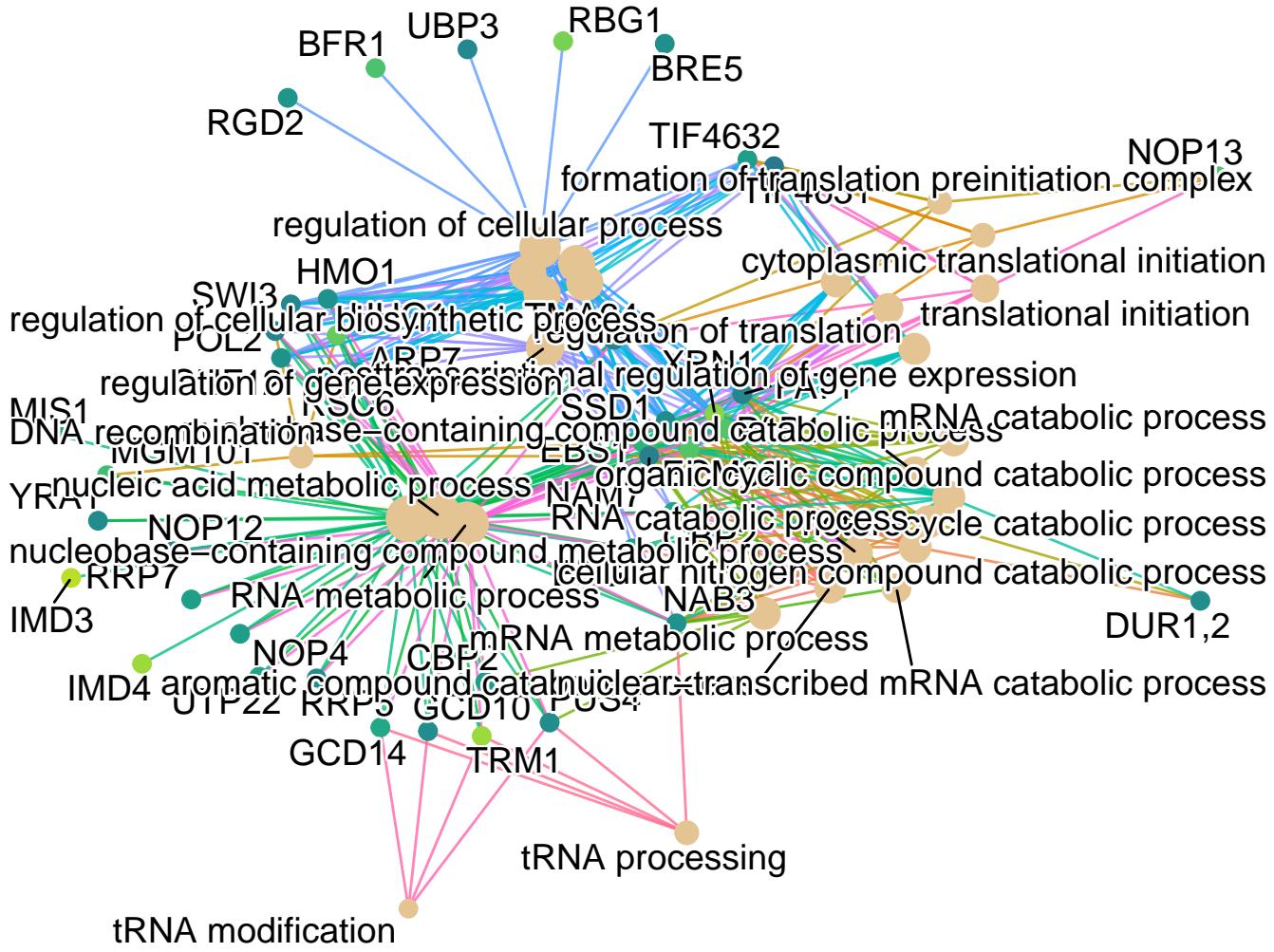
— nucleic acid metabolic process

translation preinitiation complex

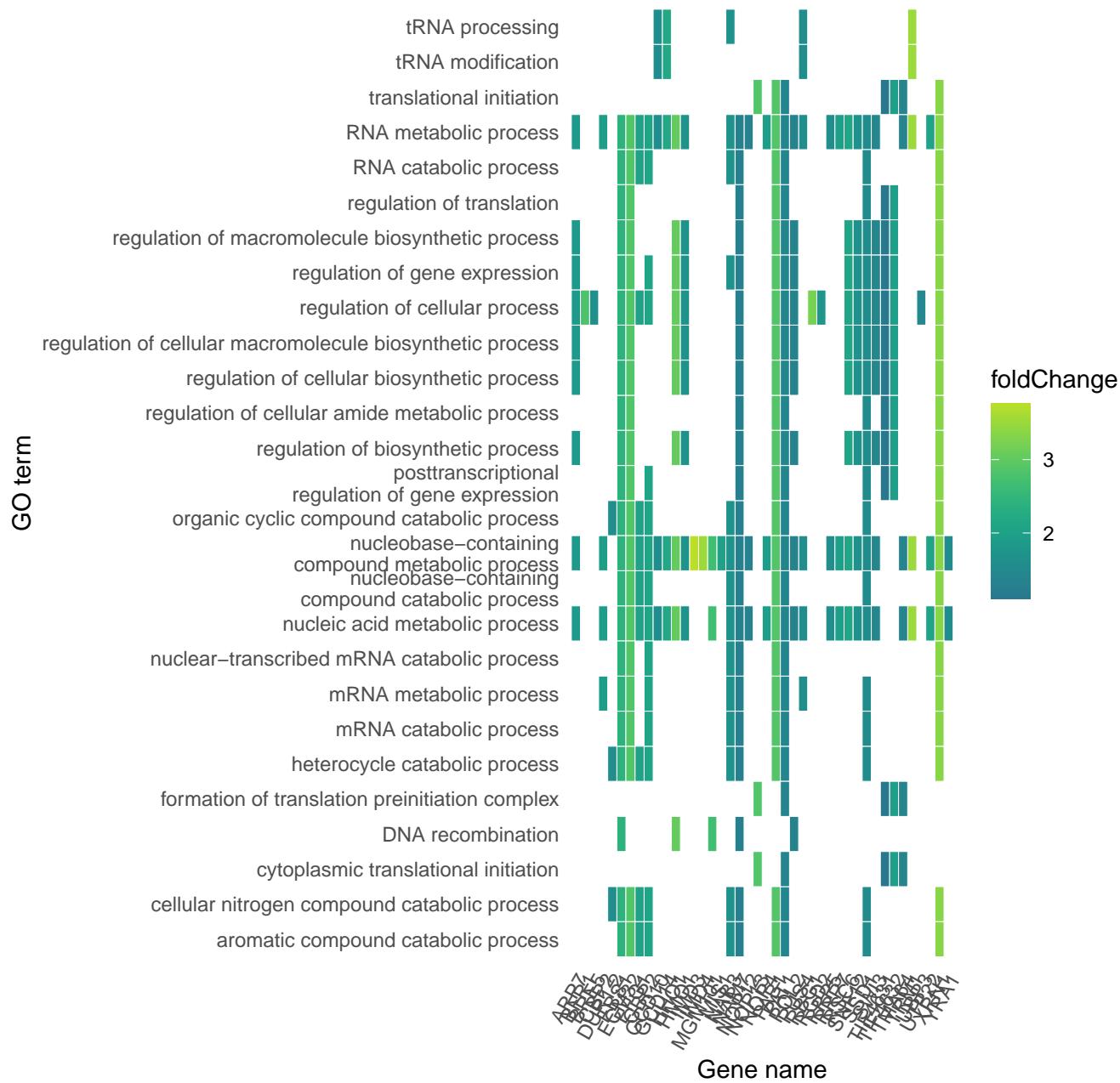
— nucleobase-containing compound catabolic process

bolic process

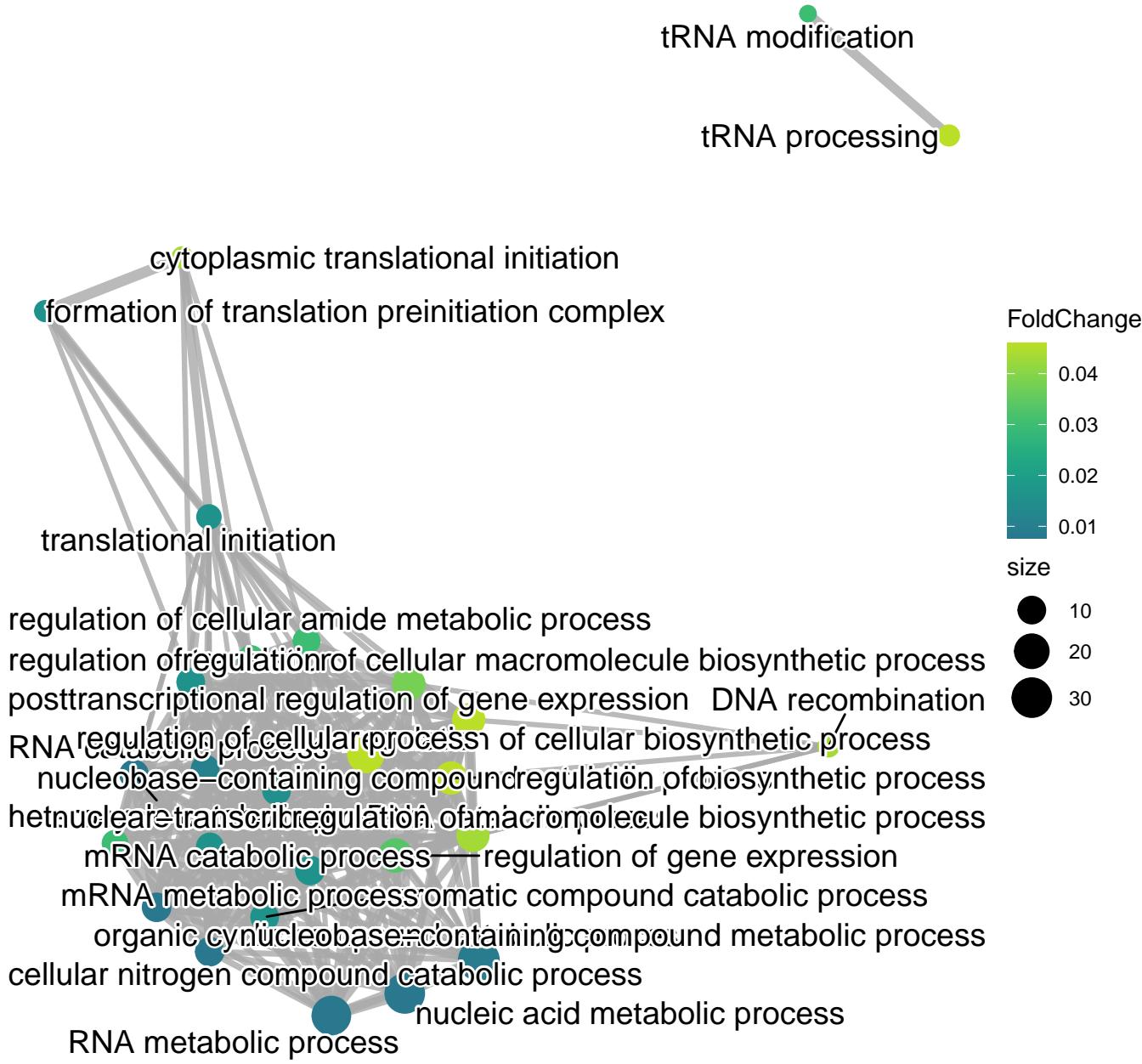
— nucleobase-containing compound metabolic process

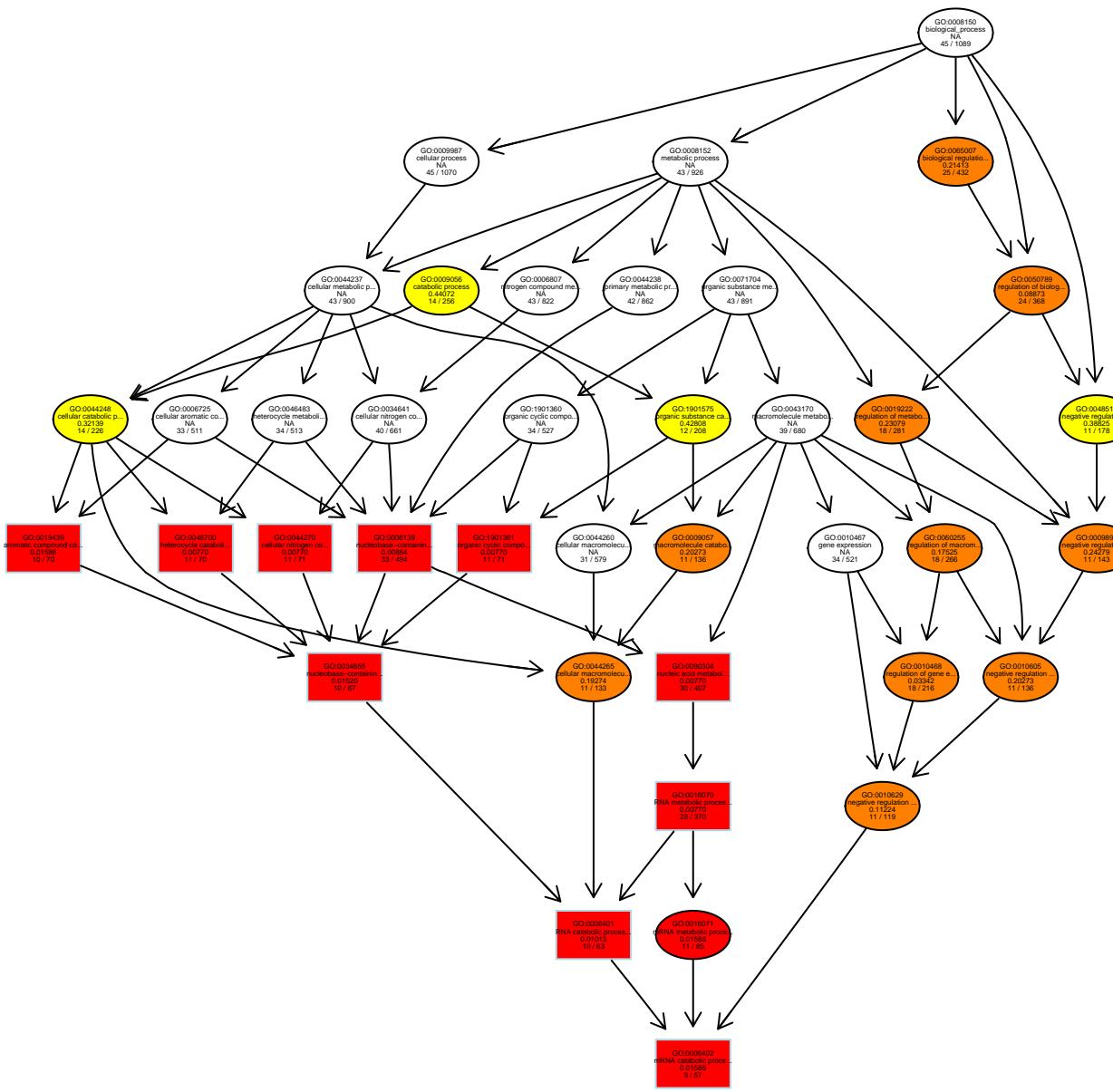


DHH1-TAP Up-regulated GO BP heatplot

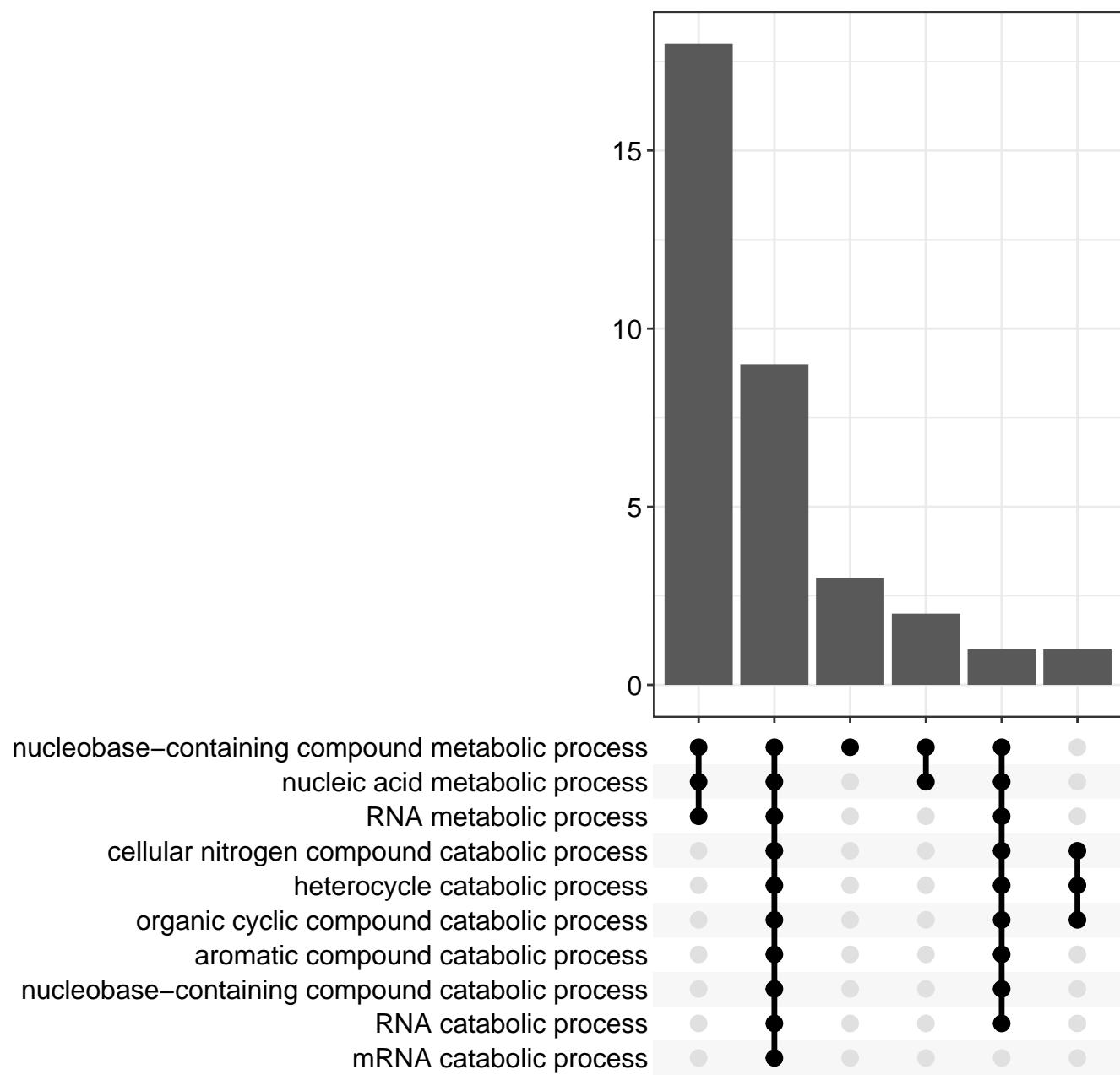


DHH1-TAP Up-regulated GO BP emapplot

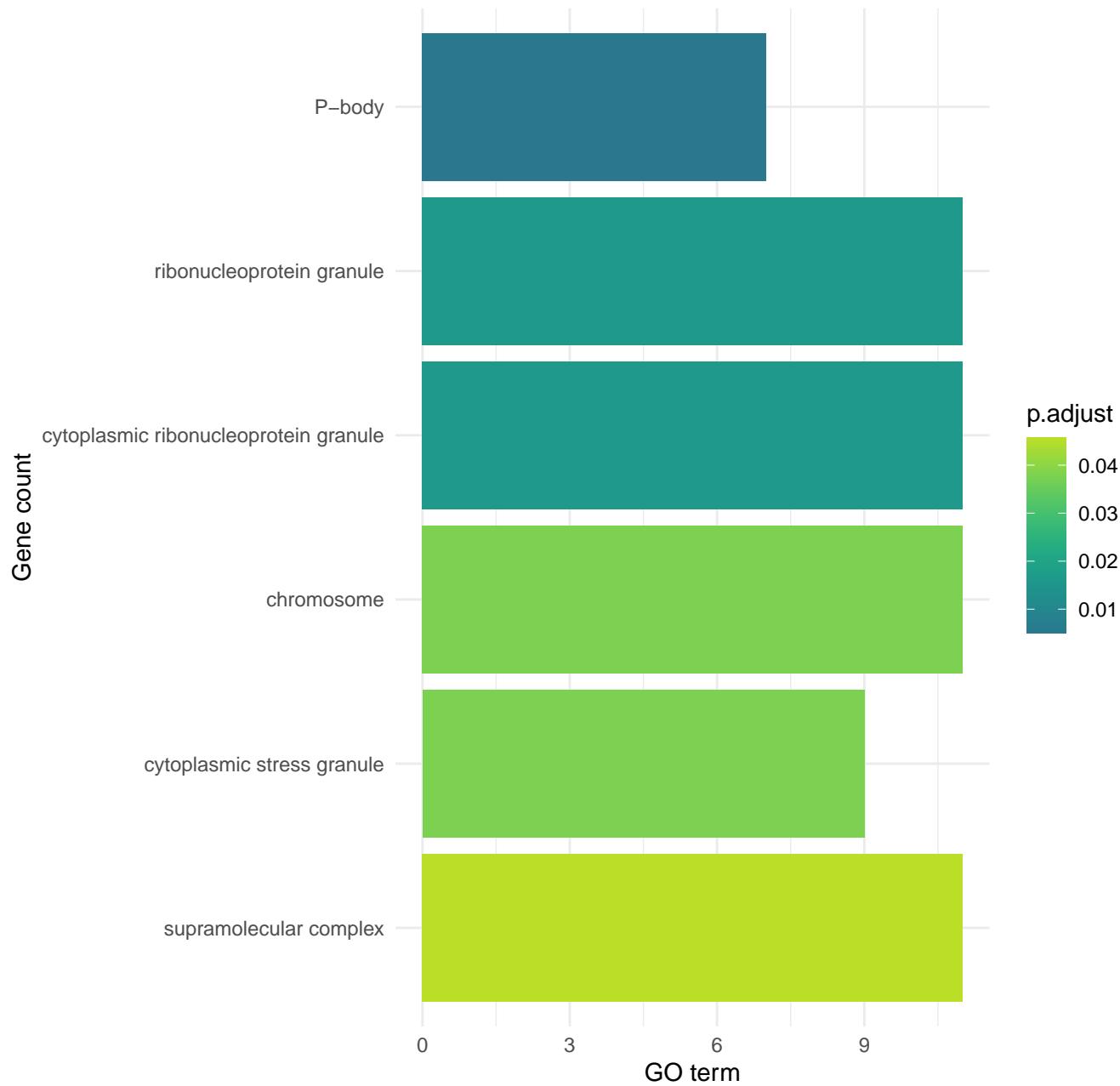




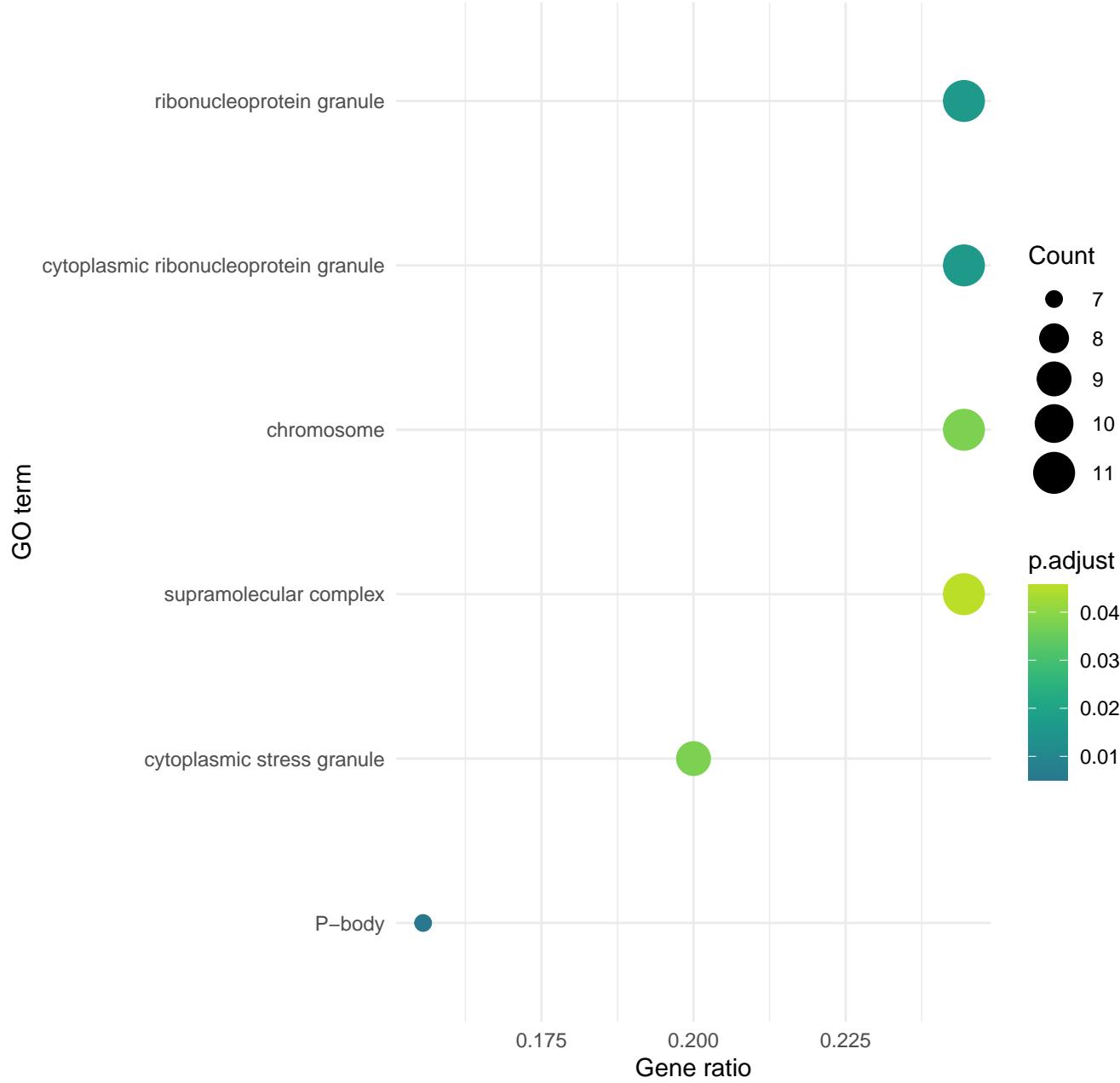
DHH1-TAP Up-regulated GO BP up



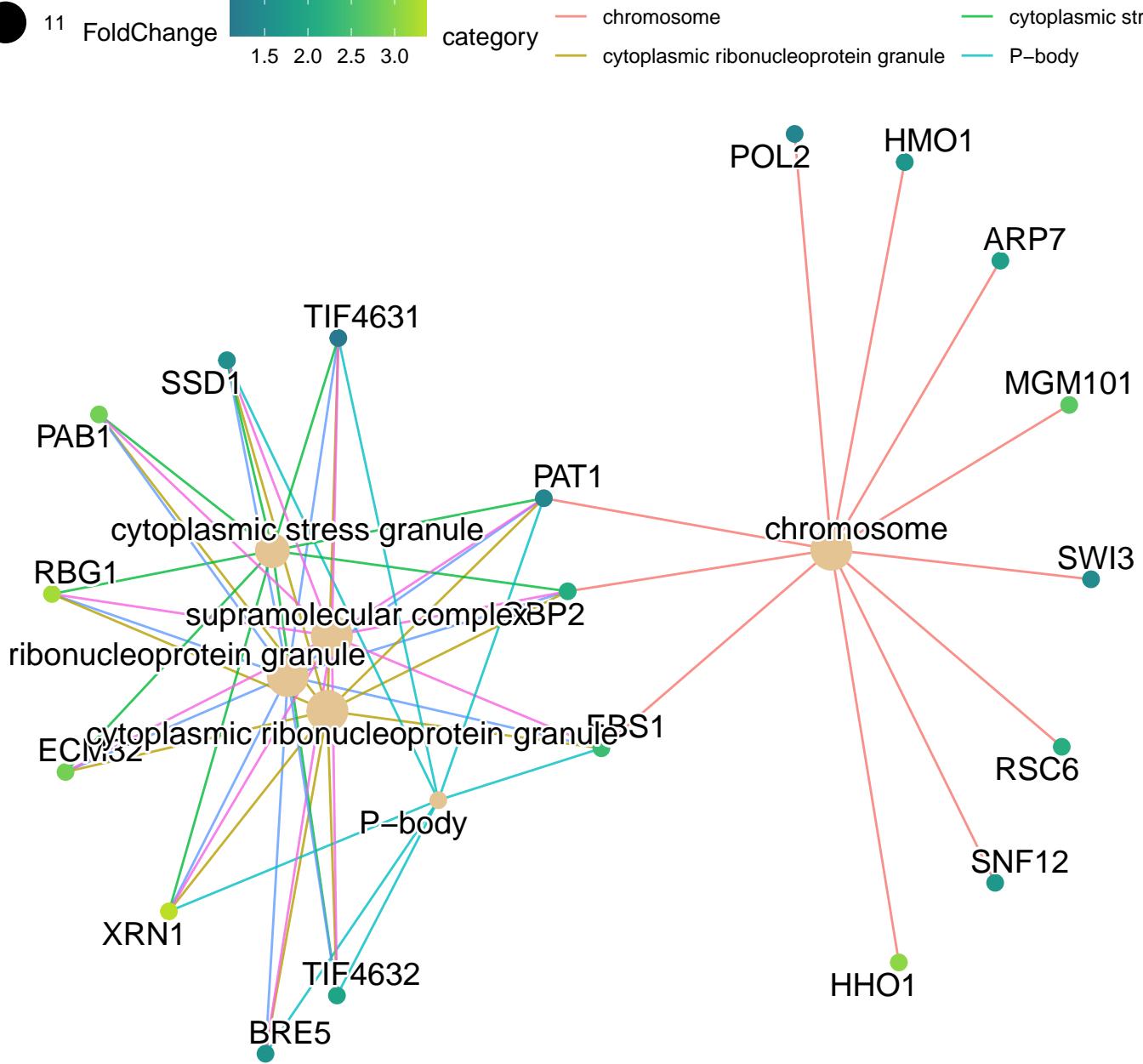
DHH1-TAP Up-regulated GO CC barplot



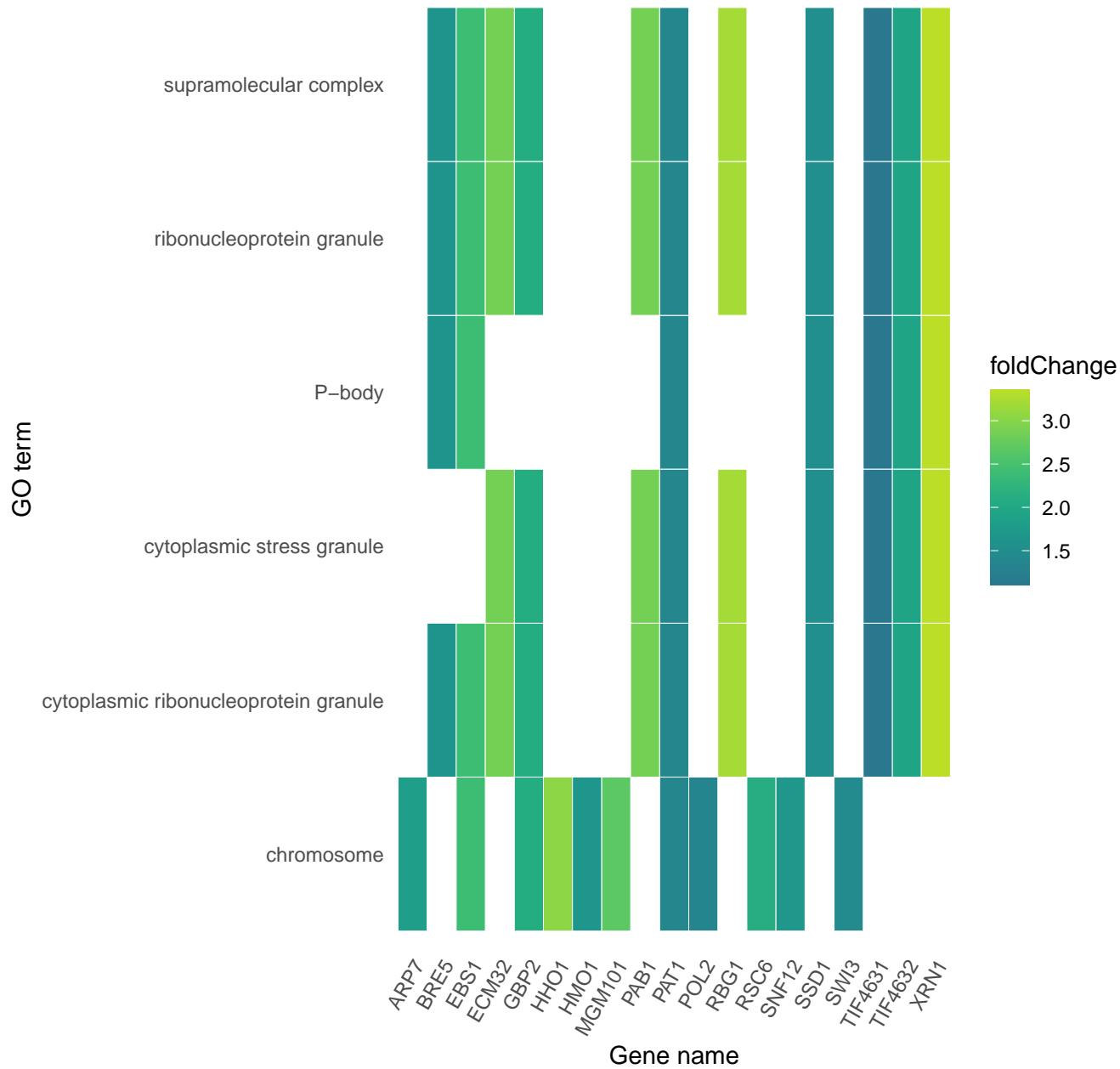
DHH1-TAP Up-regulated GO CC dotplot



DHH1-TAP Up-regulated GO CC cnetplot



DHH1-TAP Up-regulated GO CC heatplot



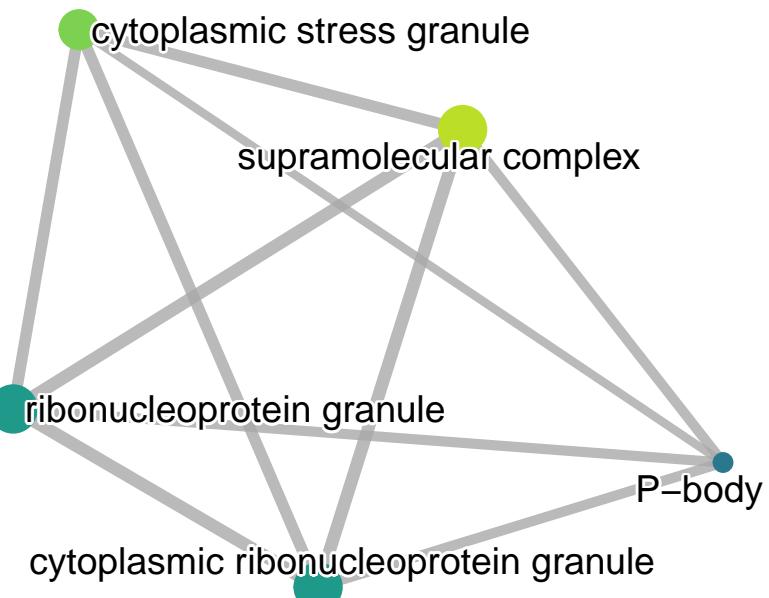
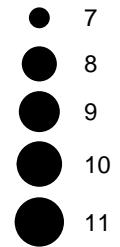
DHH1-TAP Up-regulated GO CC emapplot

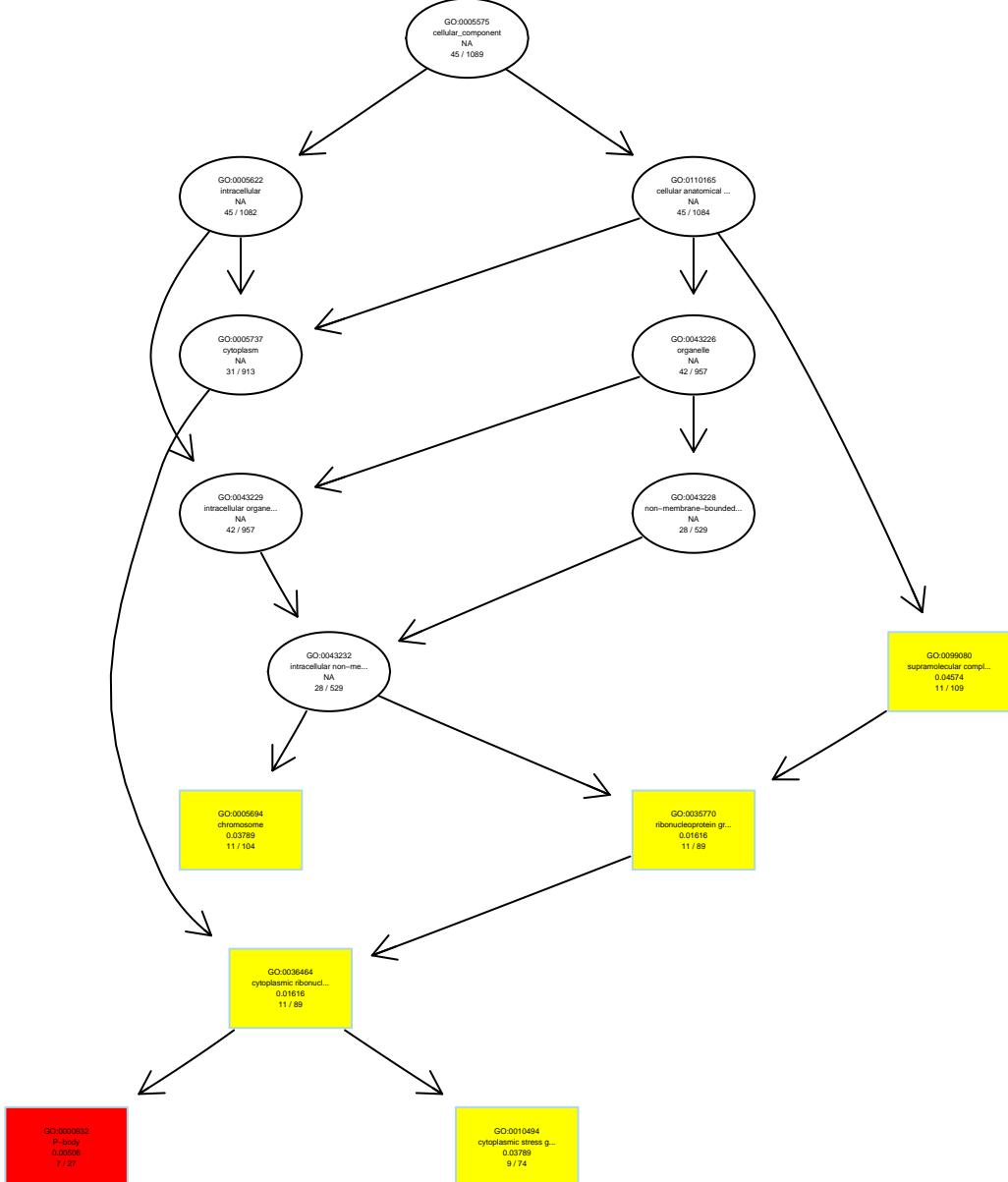
chromosome

FoldChange

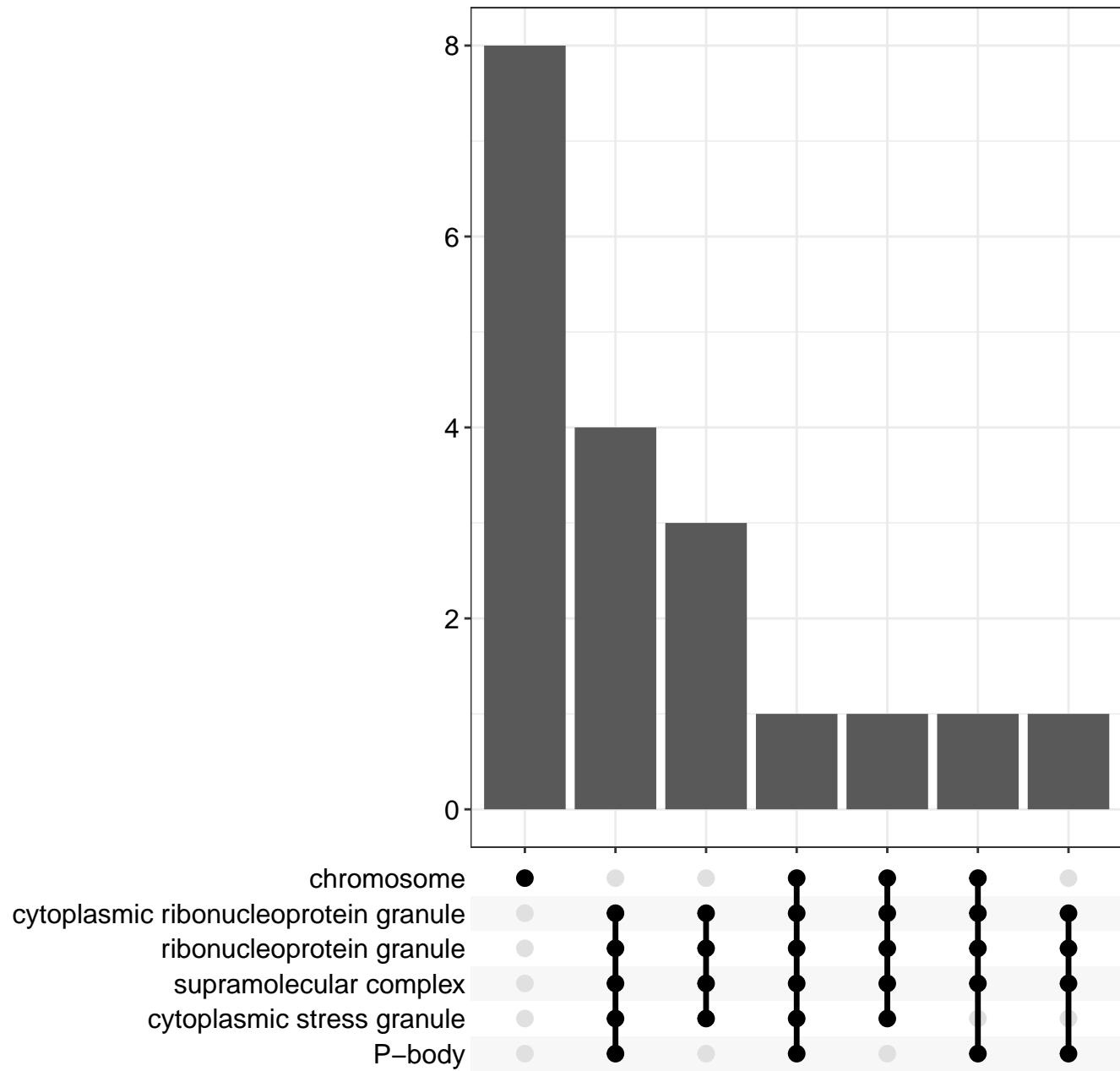


size

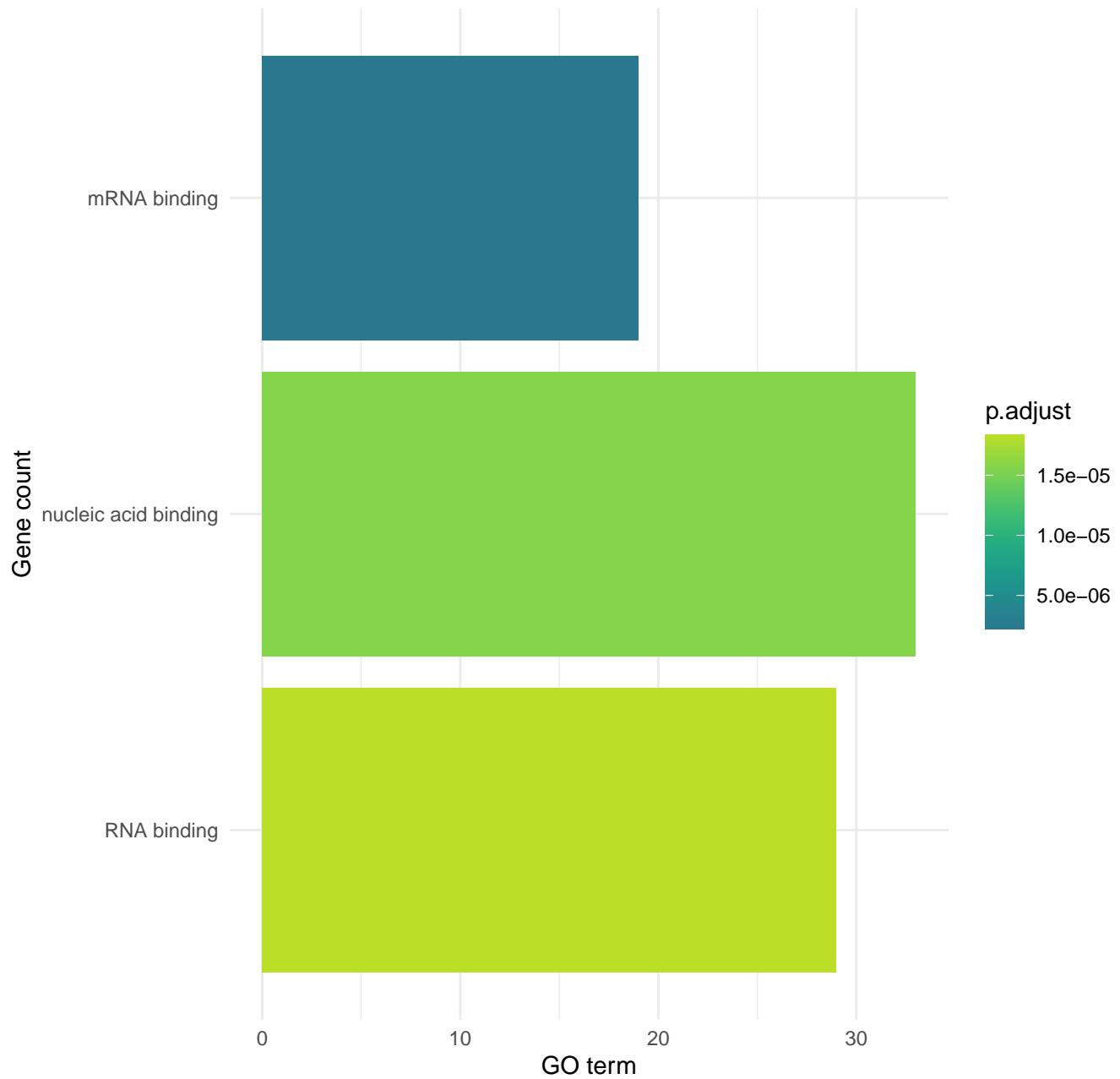




DHH1-TAP Up-regulated GO CC upsetplot



DHH1-TAP Up-regulated GO MF barplot



DHH1-TAP Up-regulated GO MF dotplot

GO term

nucleic acid binding

RNA binding

mRNA binding

0.5

0.6

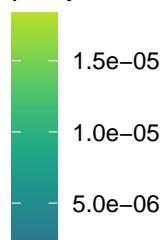
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Gene ratio

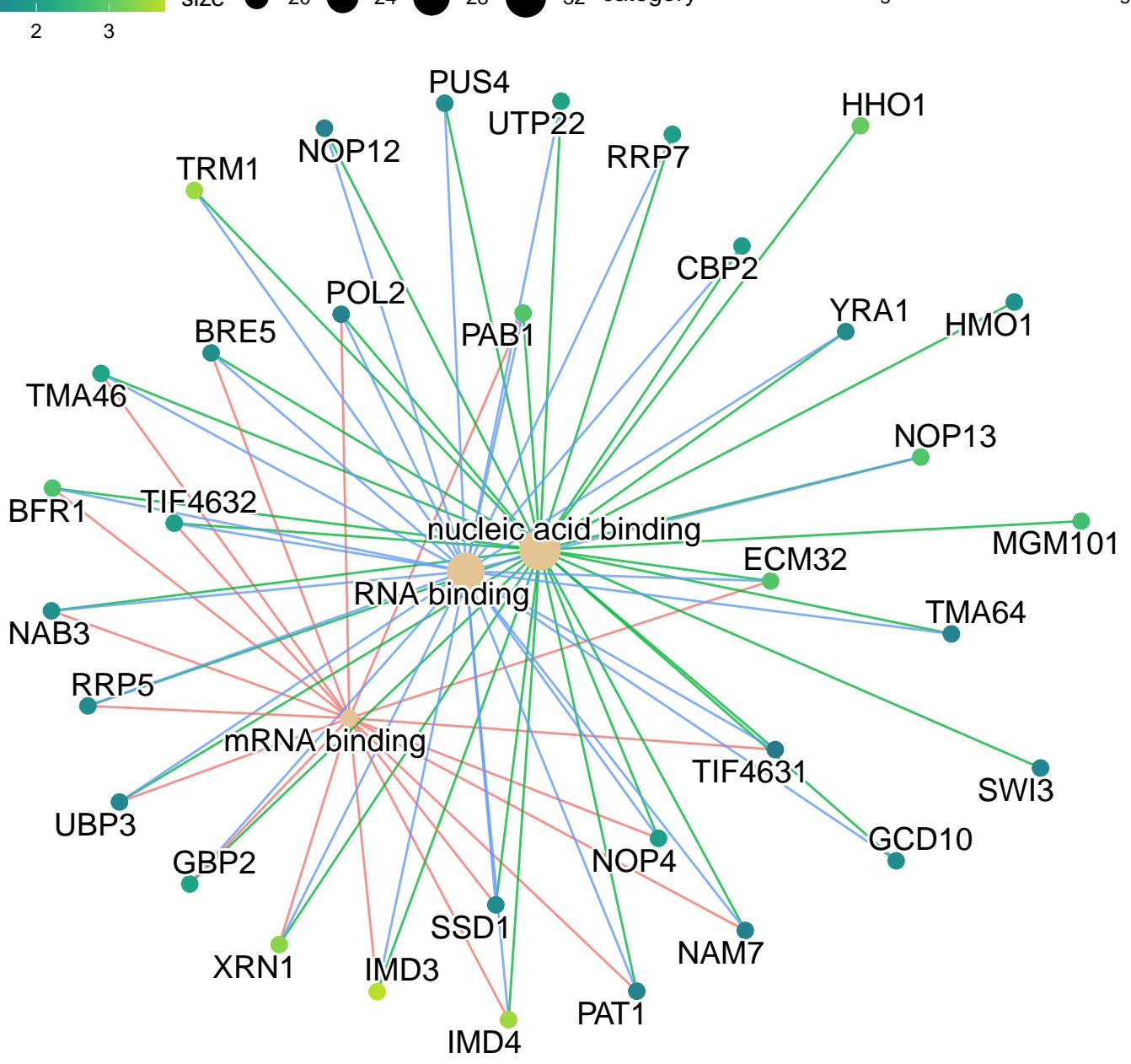
Count

- 20
- 24
- 28
- 32

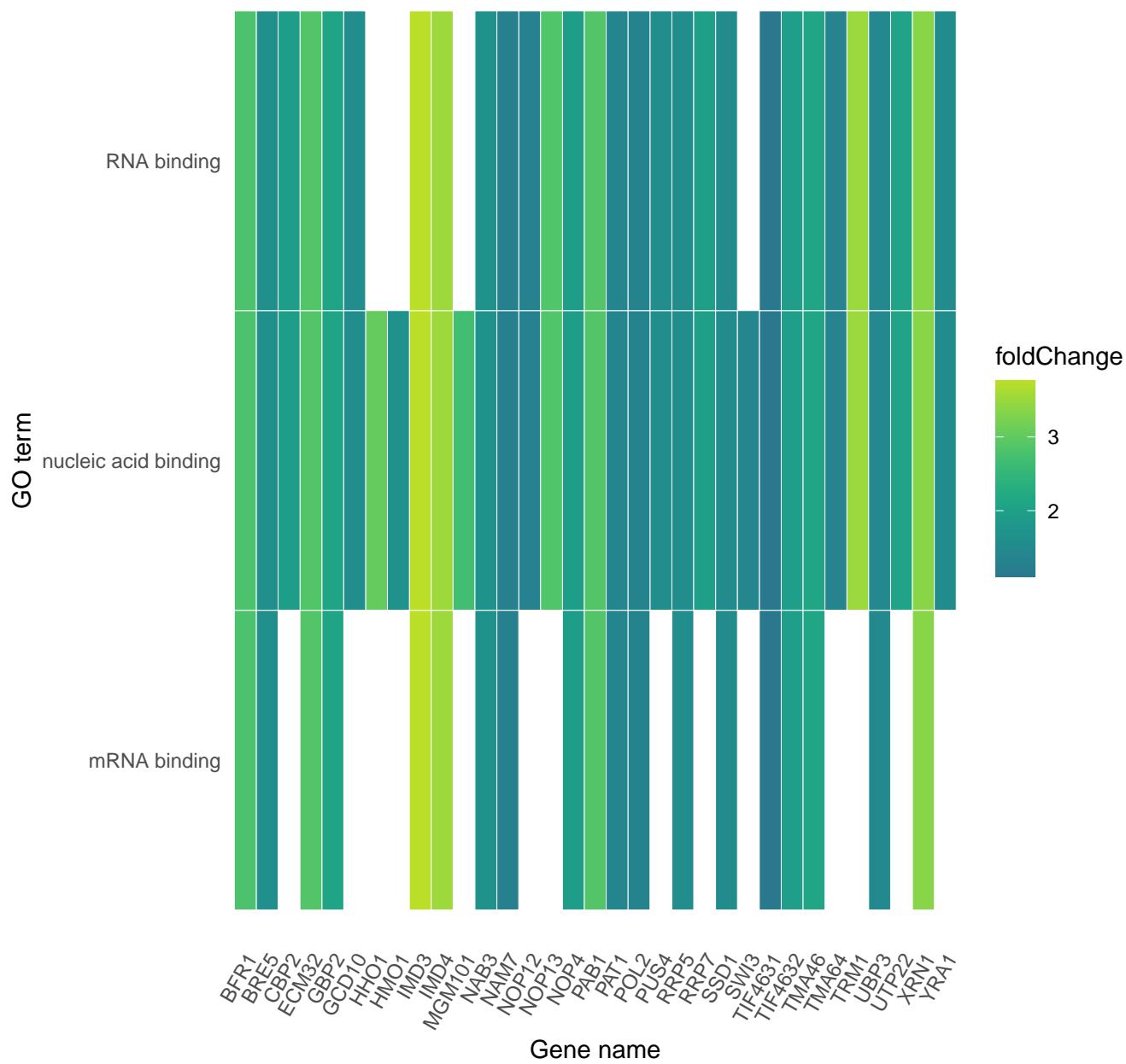
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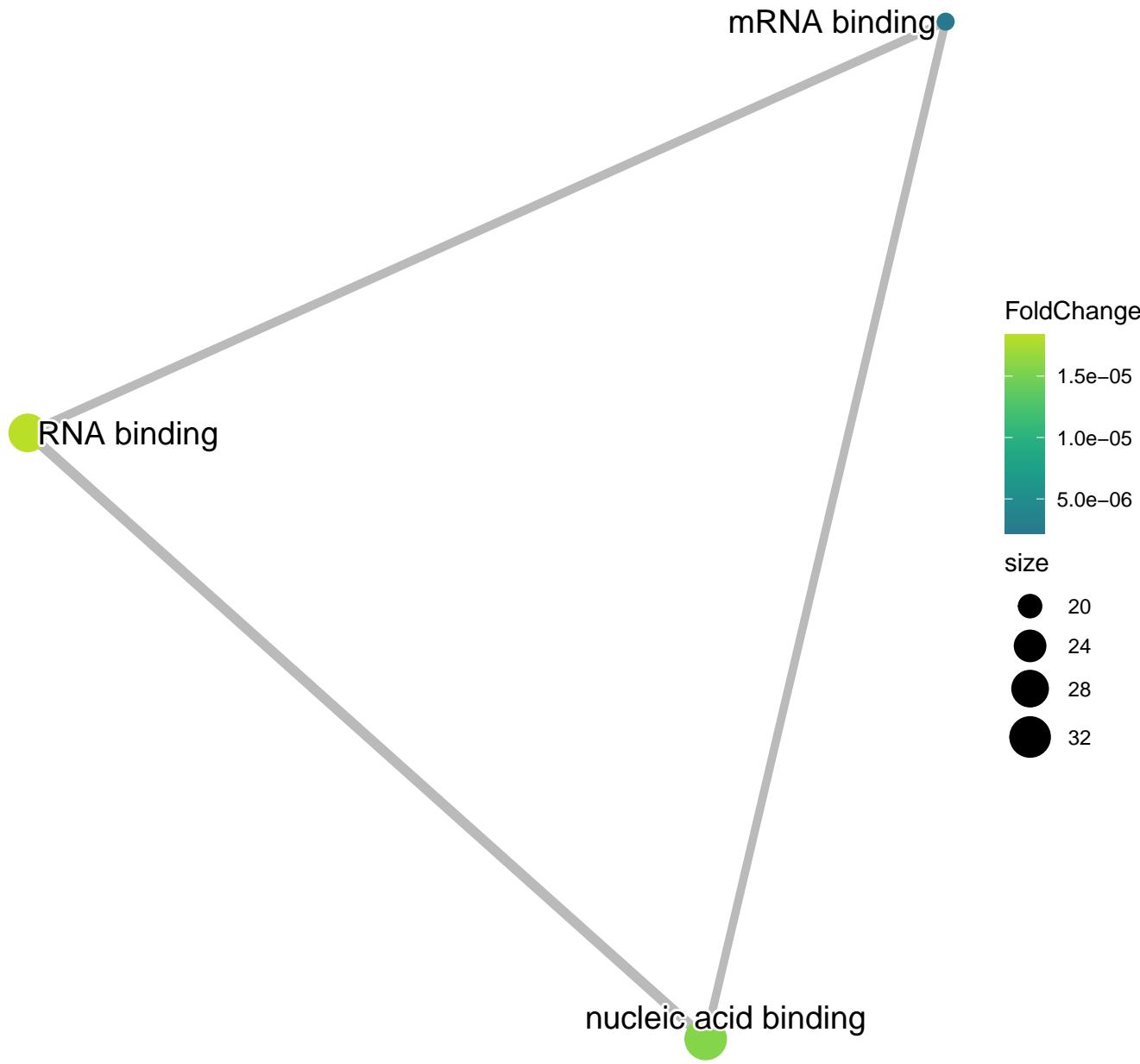
DHH1-TAP Up-regulated GO MF cnetplot

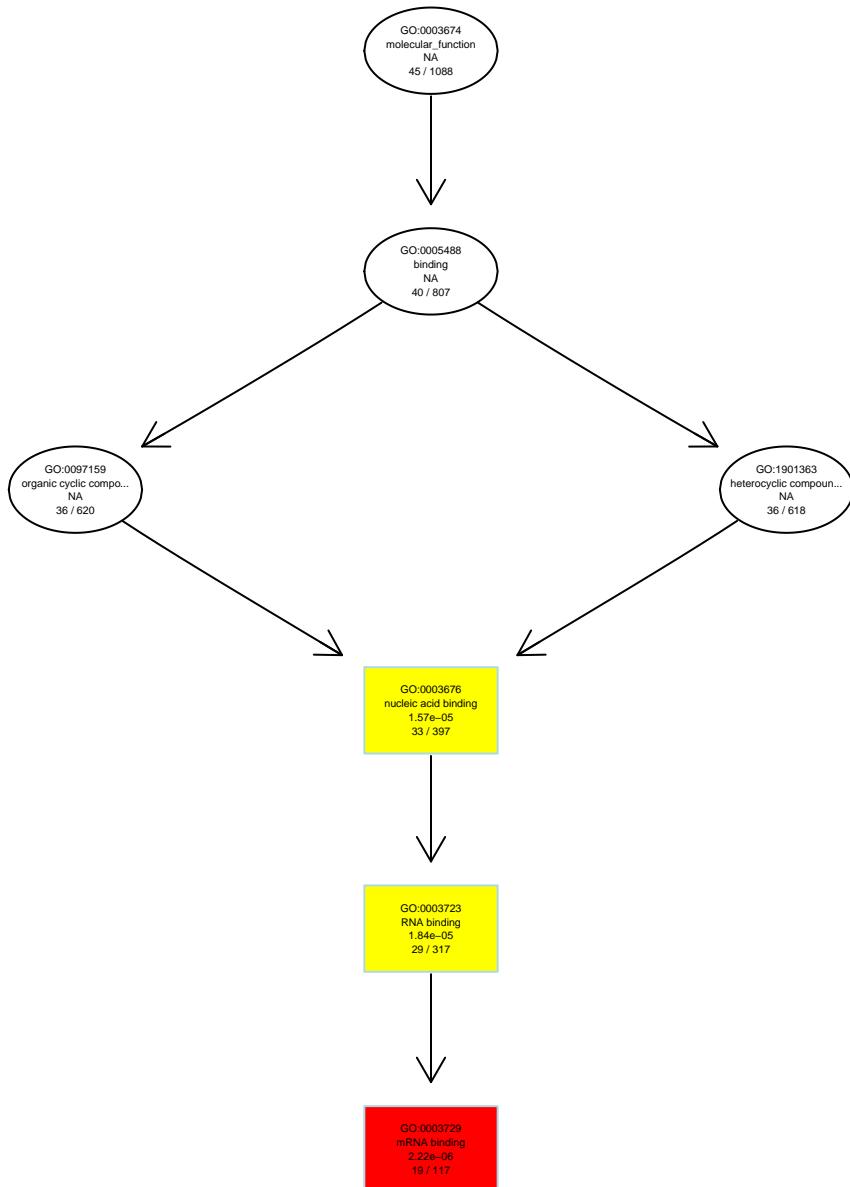


DHH1-TAP Up-regulated GO MF heatplot

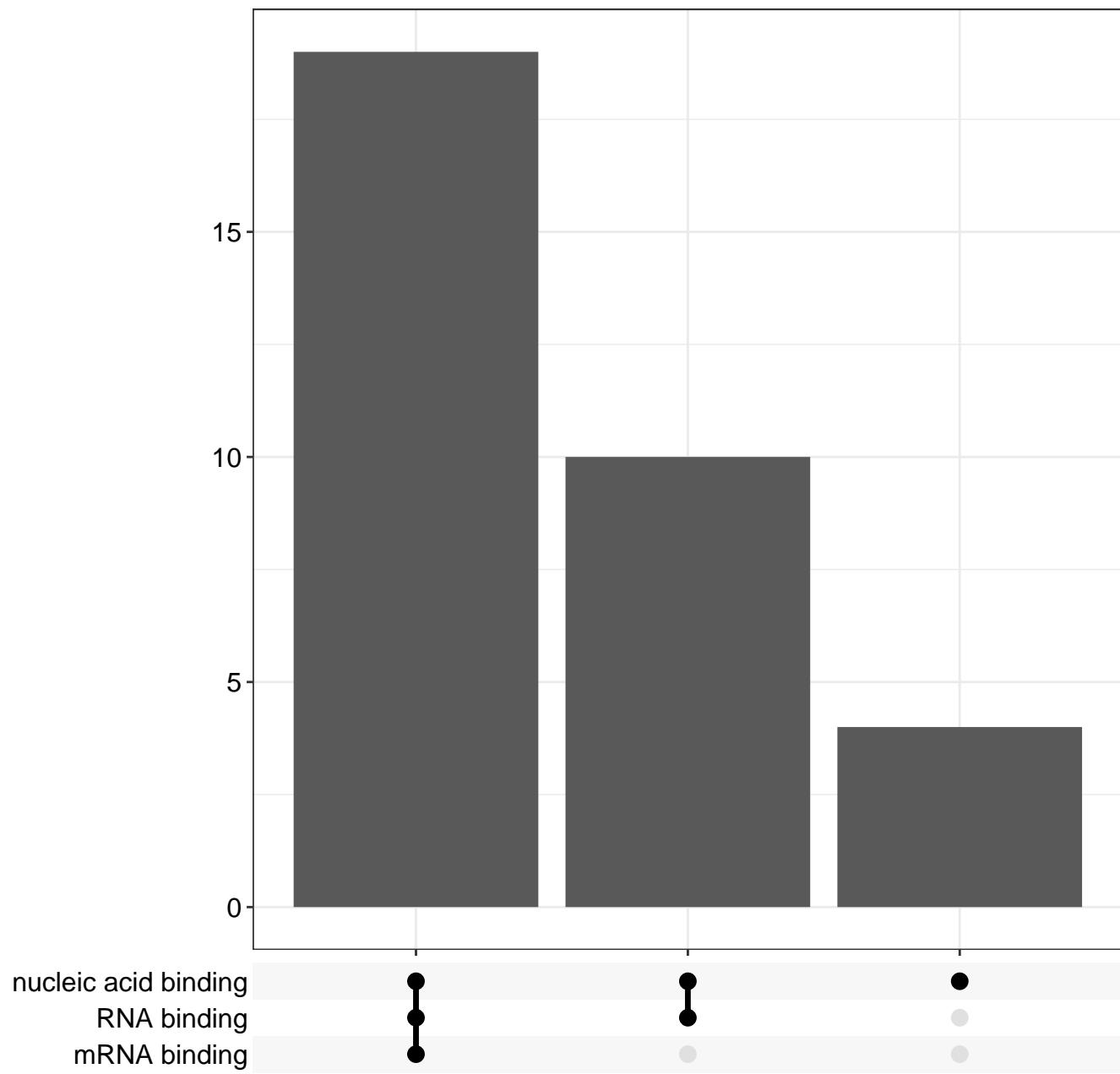


DHH1-TAP Up-regulated GO MF emapplot

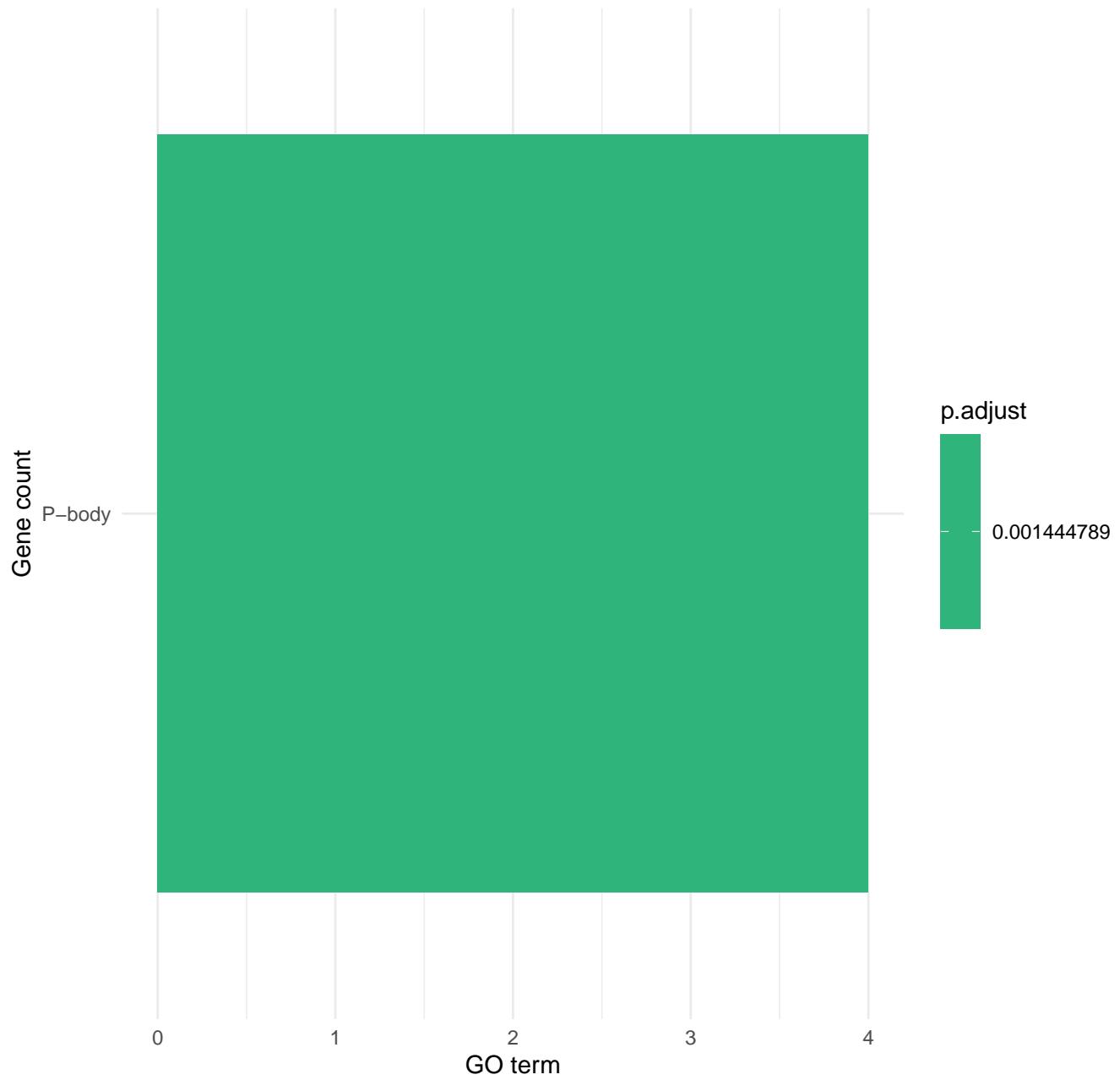




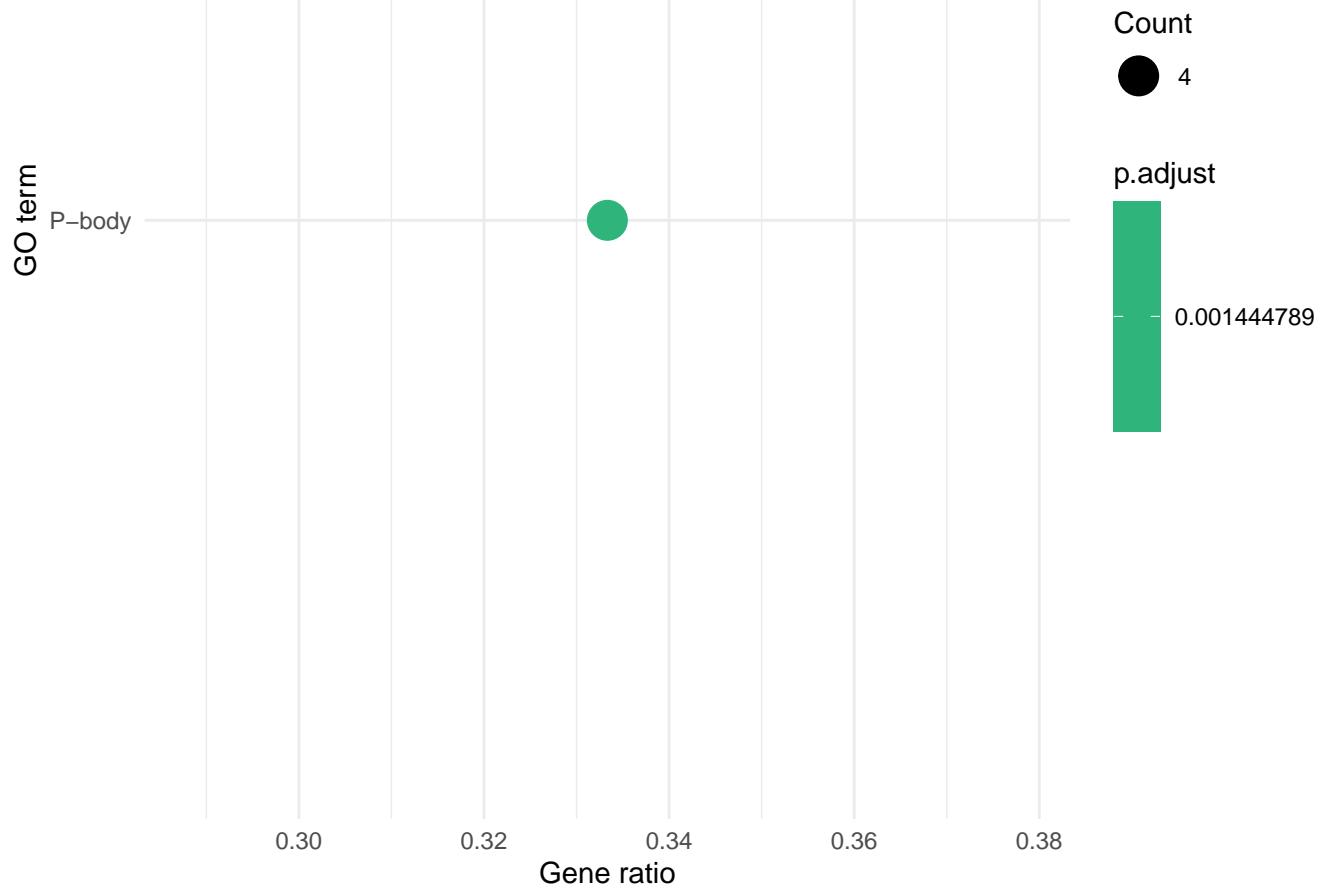
DHH1-TAP Up-regulated GO MF upsetplot



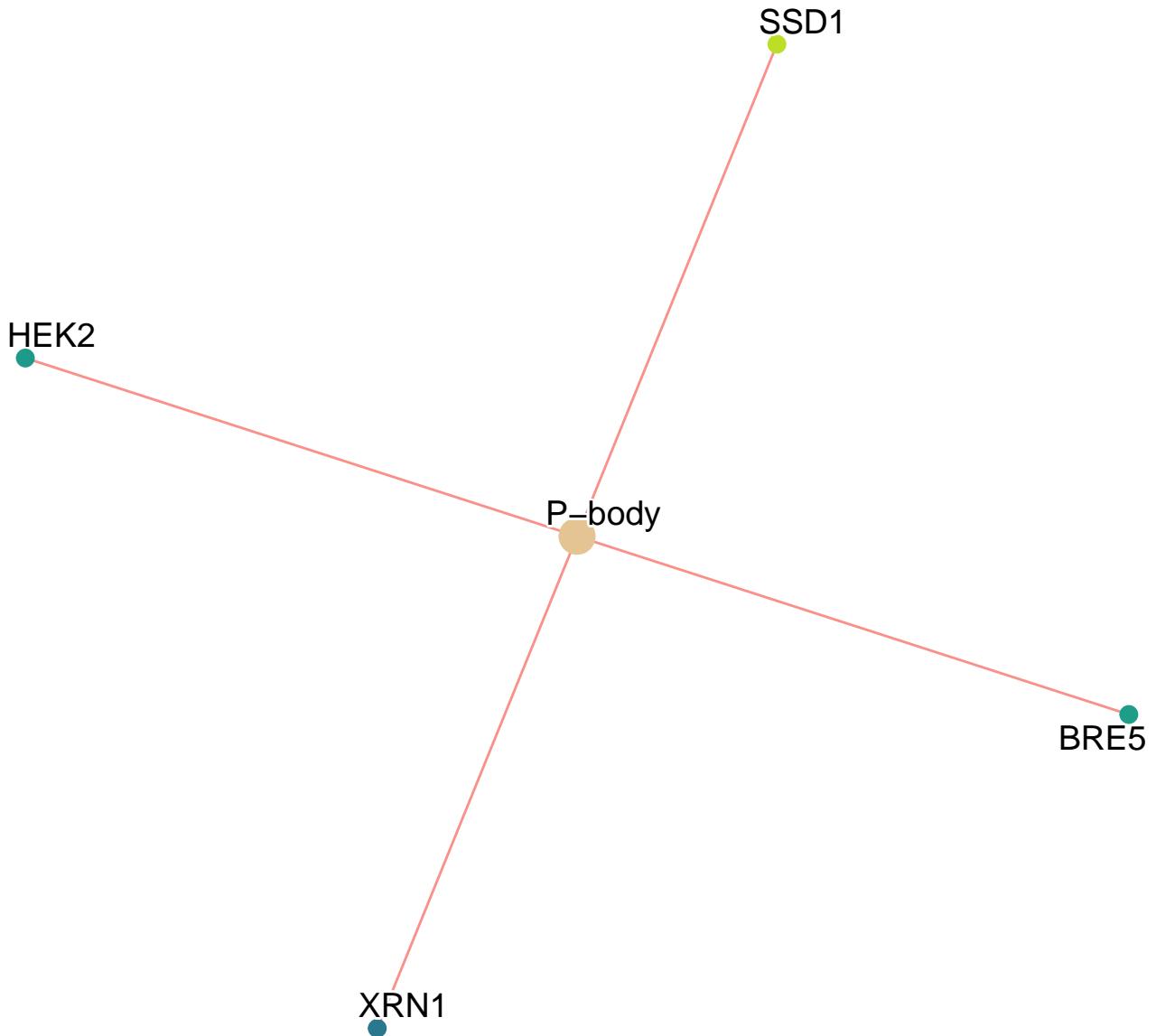
DIS3–TAP Up-regulated GO CC barplot



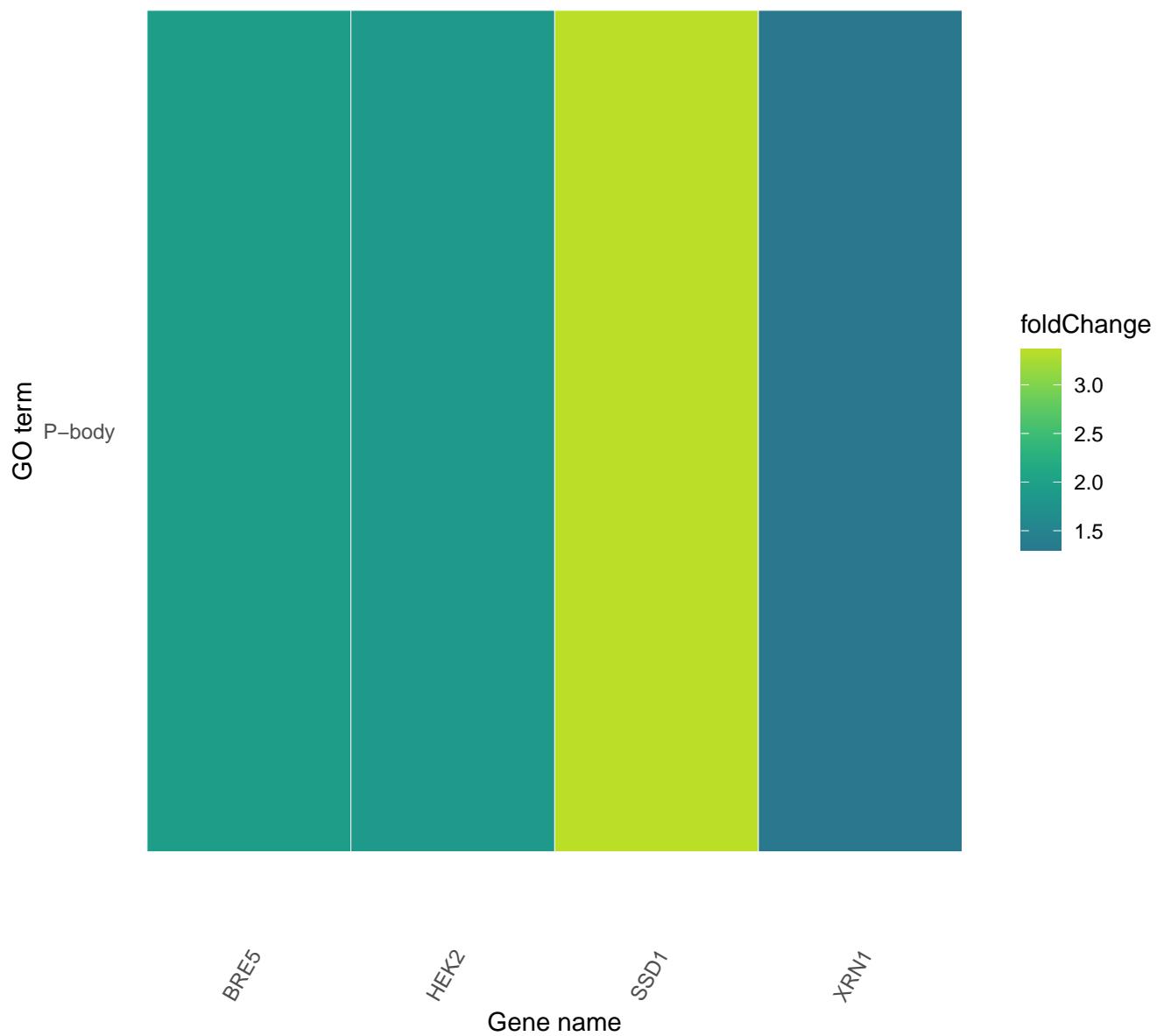
DIS3-TAP Up-regulated GO CC dotplot

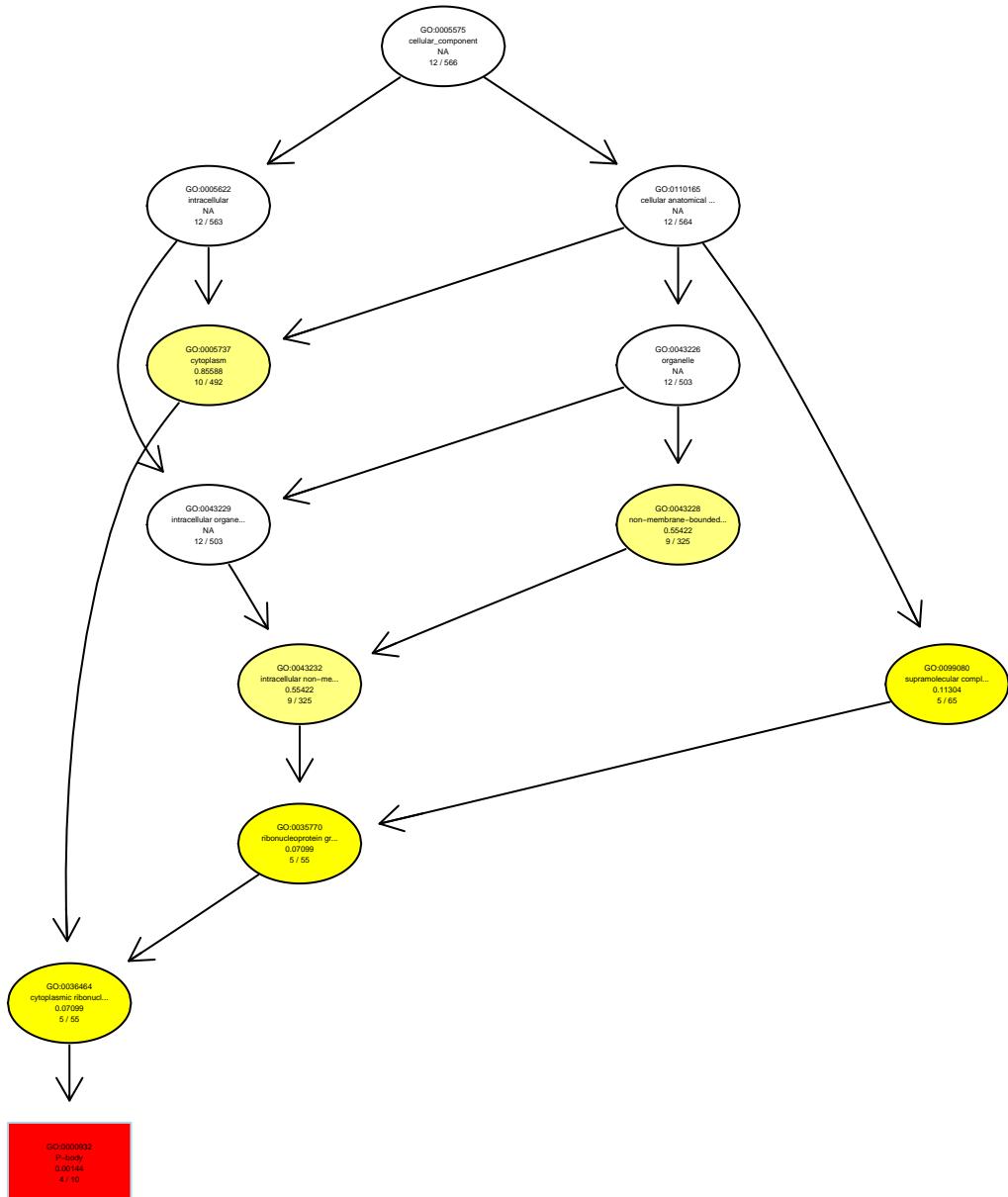


DIS3-TAP Up-regulated GO CC cnetplot

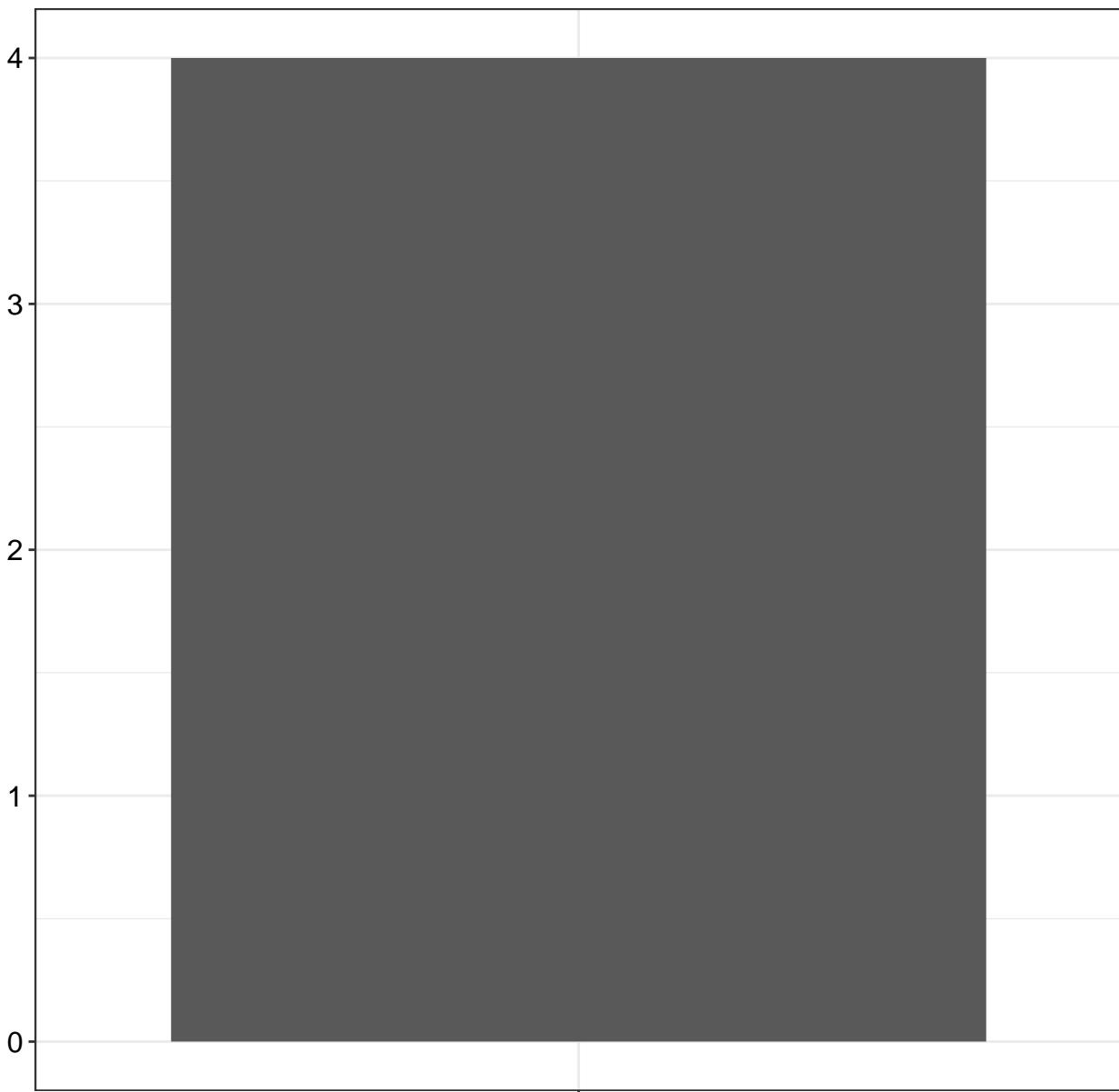


DIS3-TAP Up-regulated GO CC heatplot





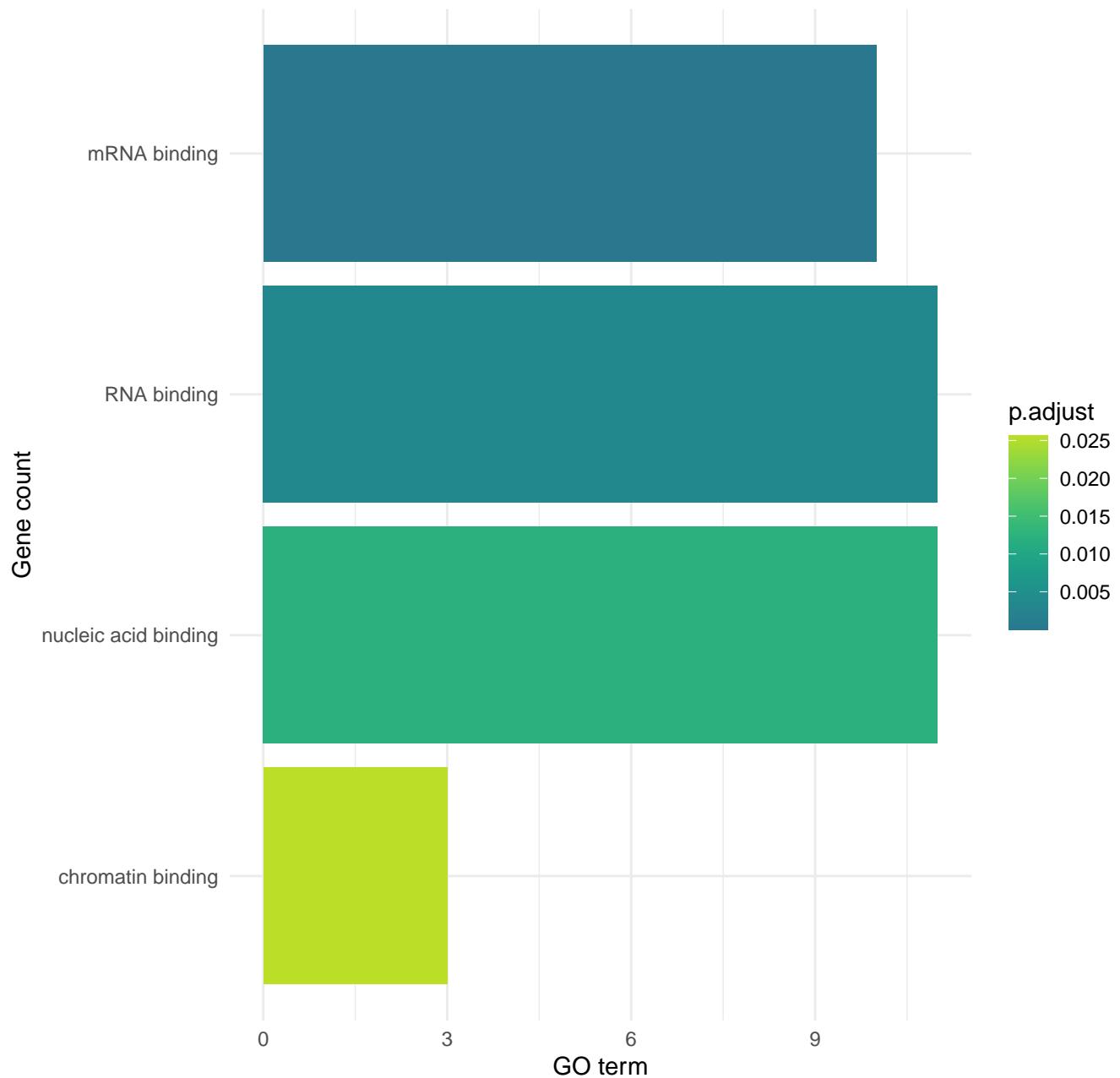
DIS3-TAP Up-regulated GO CC upsetplot



P-body

●

DIS3-TAP Up-regulated GO MF barplot



DIS3-TAP Up-regulated GO MF dotplot

GO term

RNA binding

nucleic acid binding

mRNA binding

chromatin binding

0.4

0.6

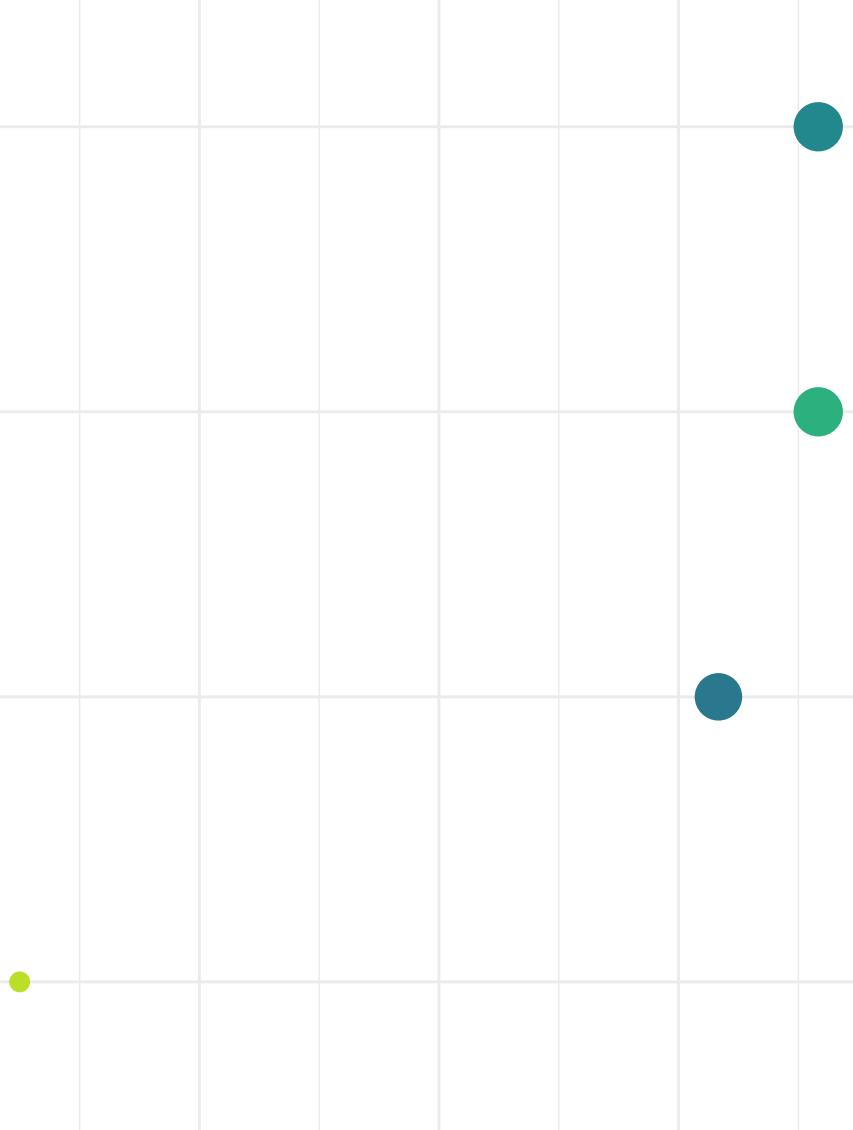
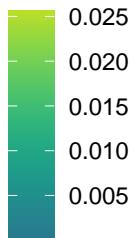
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Gene ratio

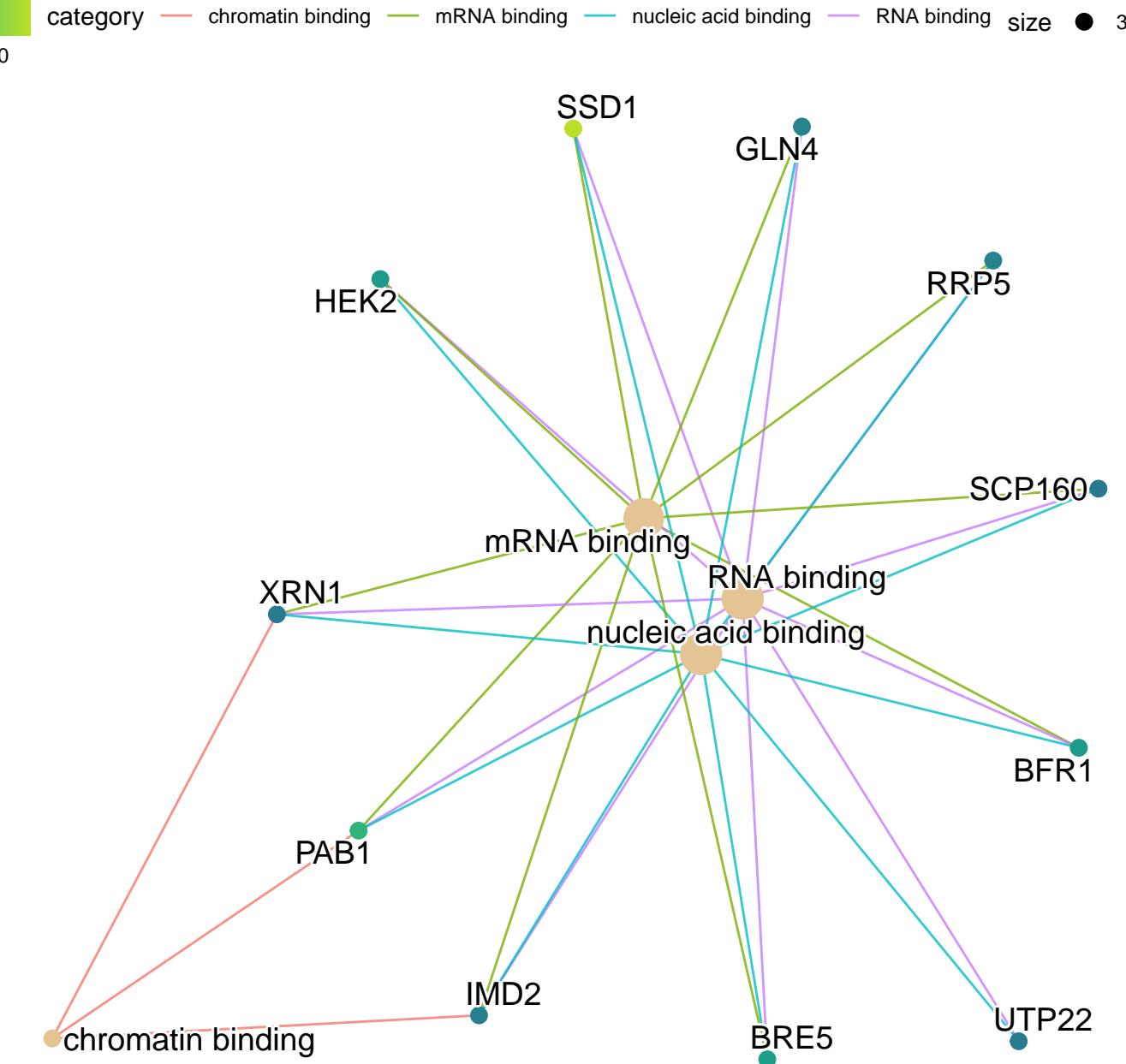
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- 5
- 7
- 9
- 11

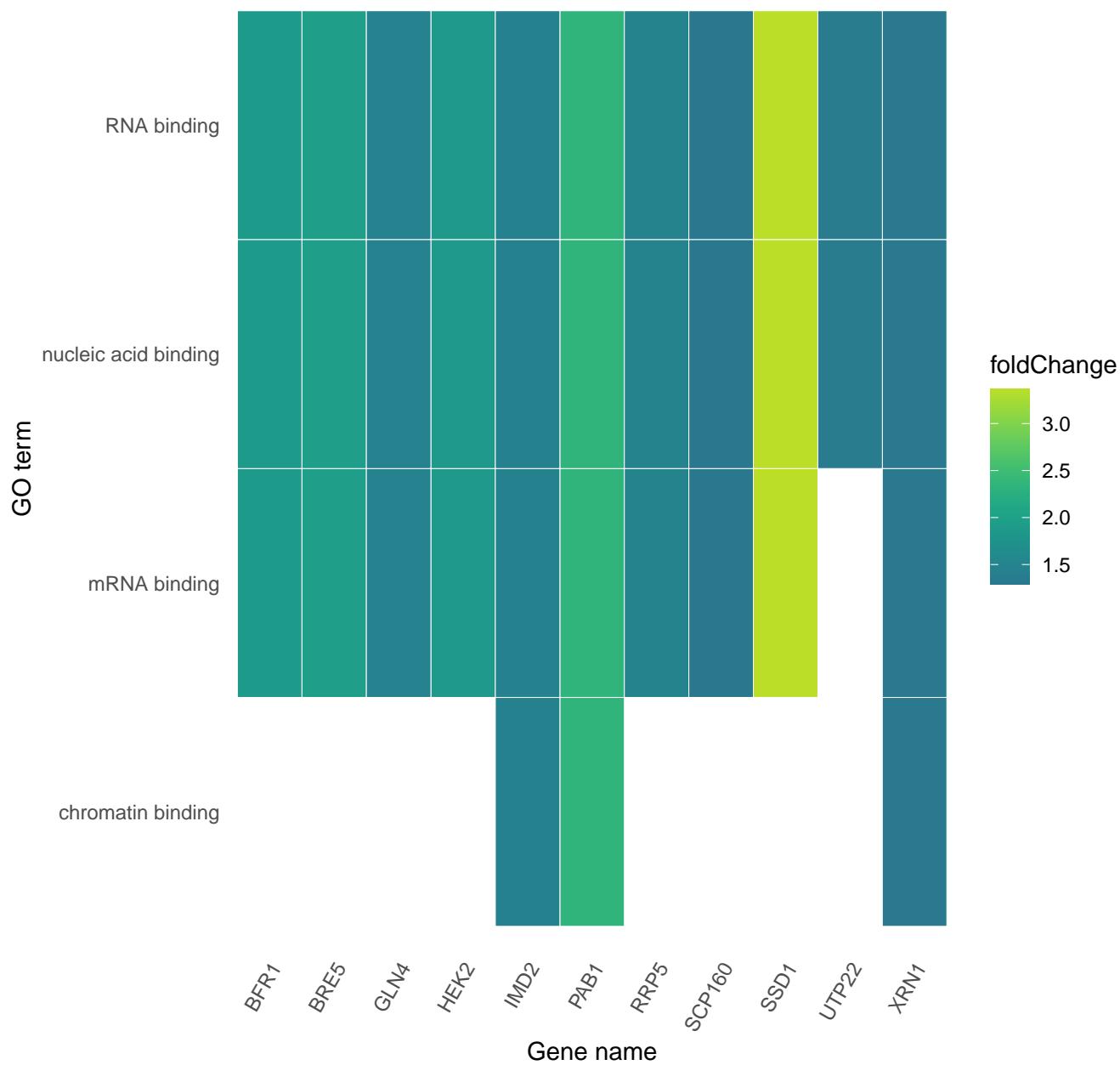
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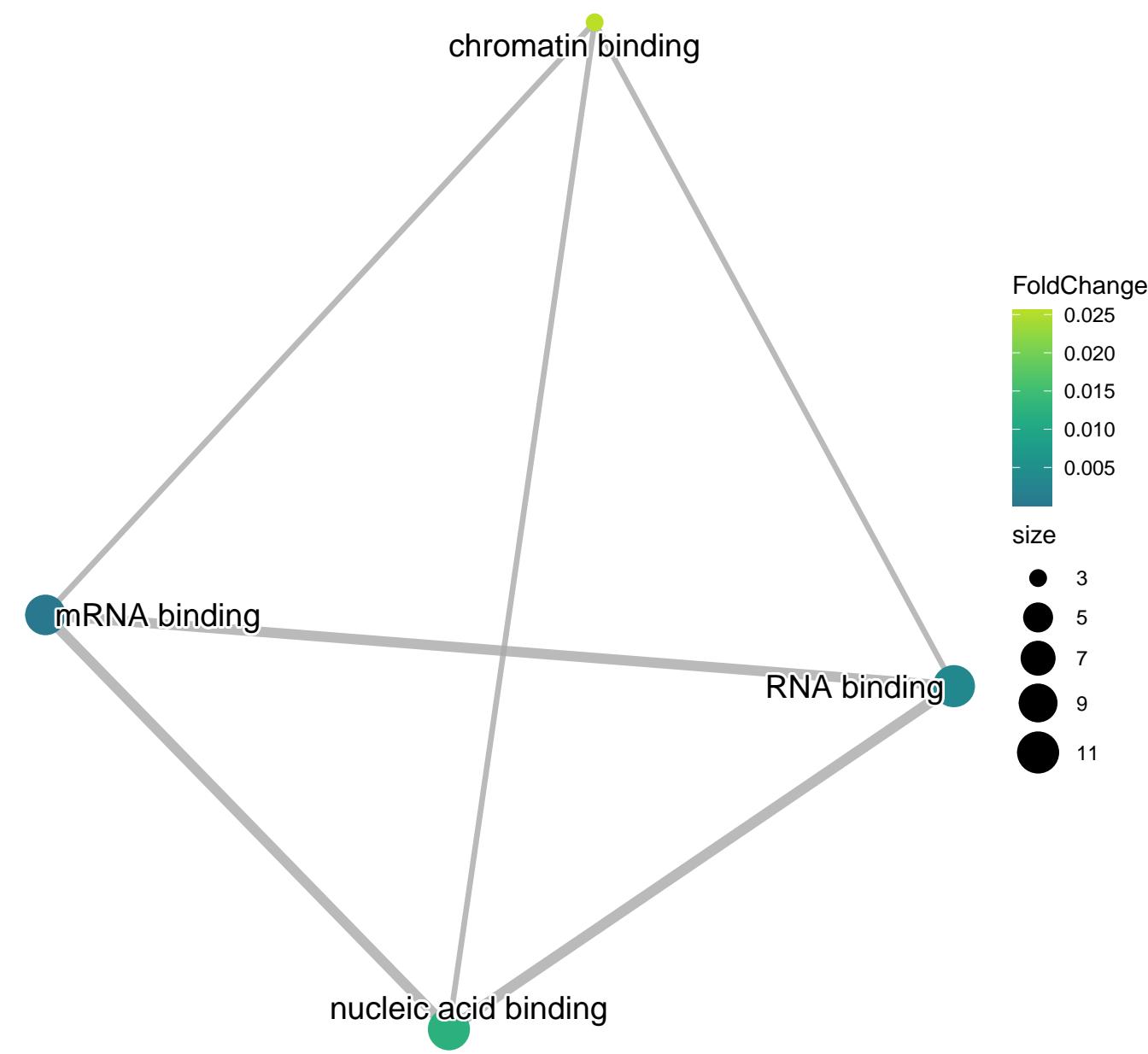
DIS3-TAP Up-regulated GO MF cnetplot

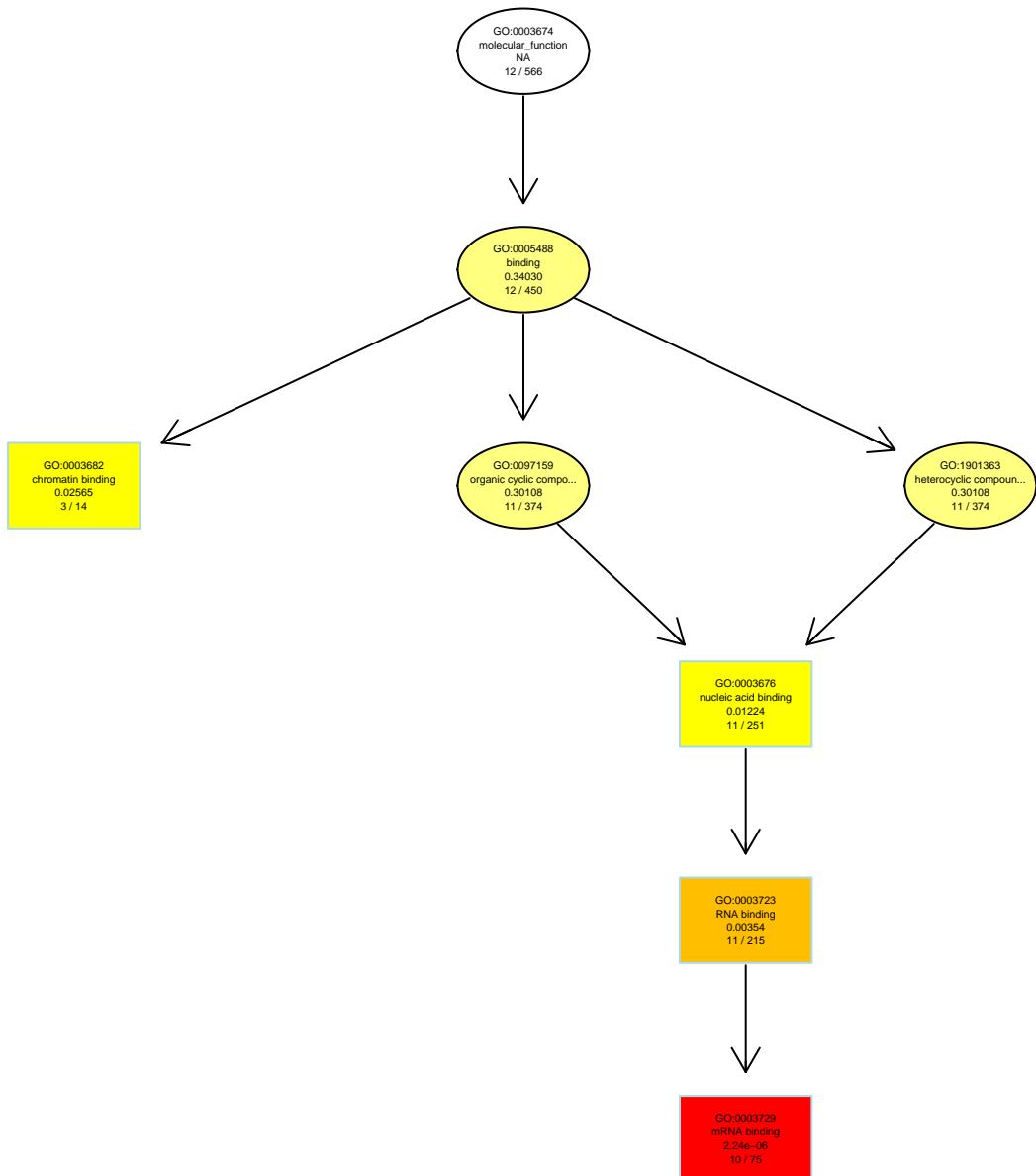


DIS3-TAP Up-regulated GO MF heatplot

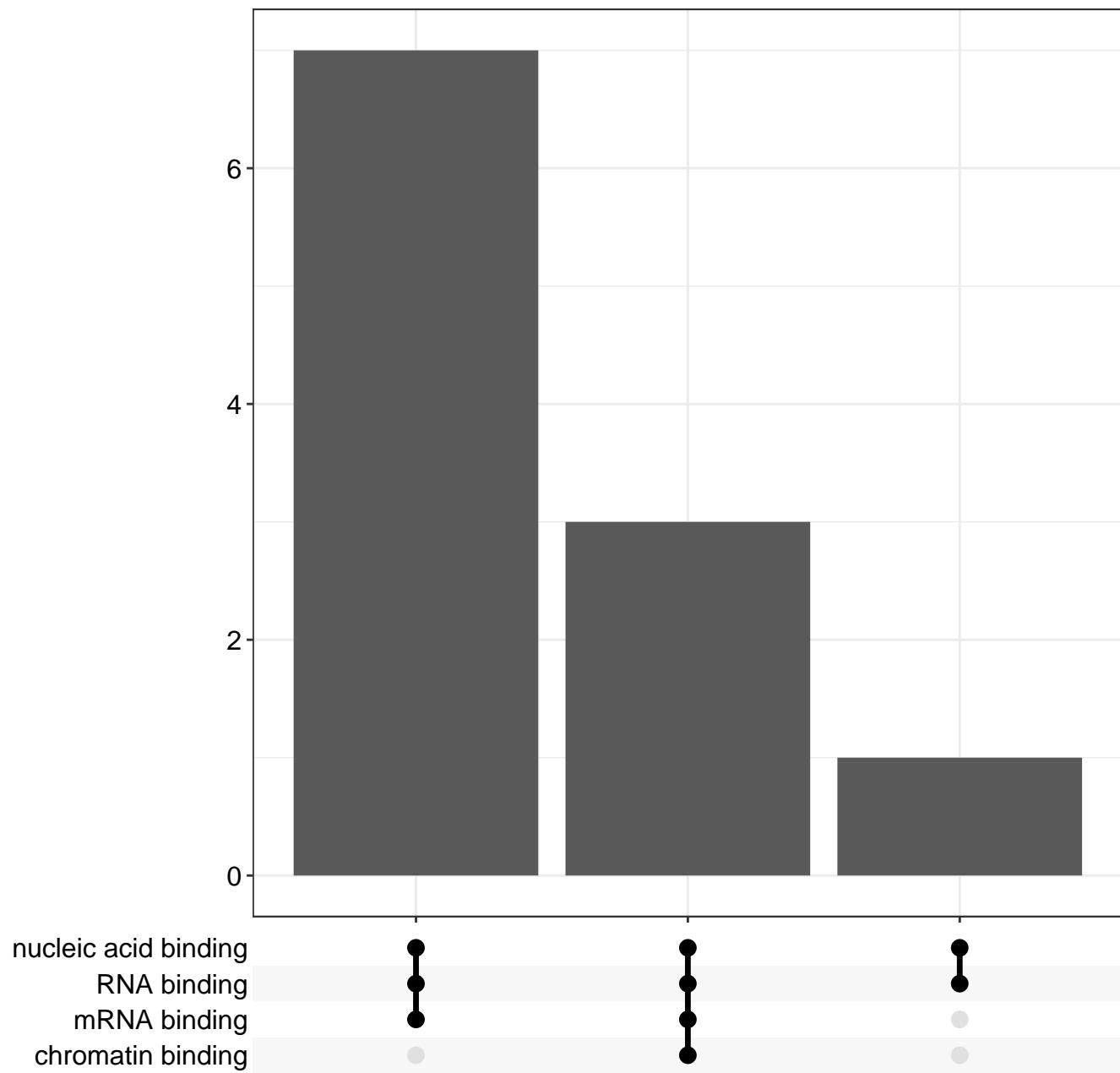


DIS3-TAP Up-regulated GO MF emapplot

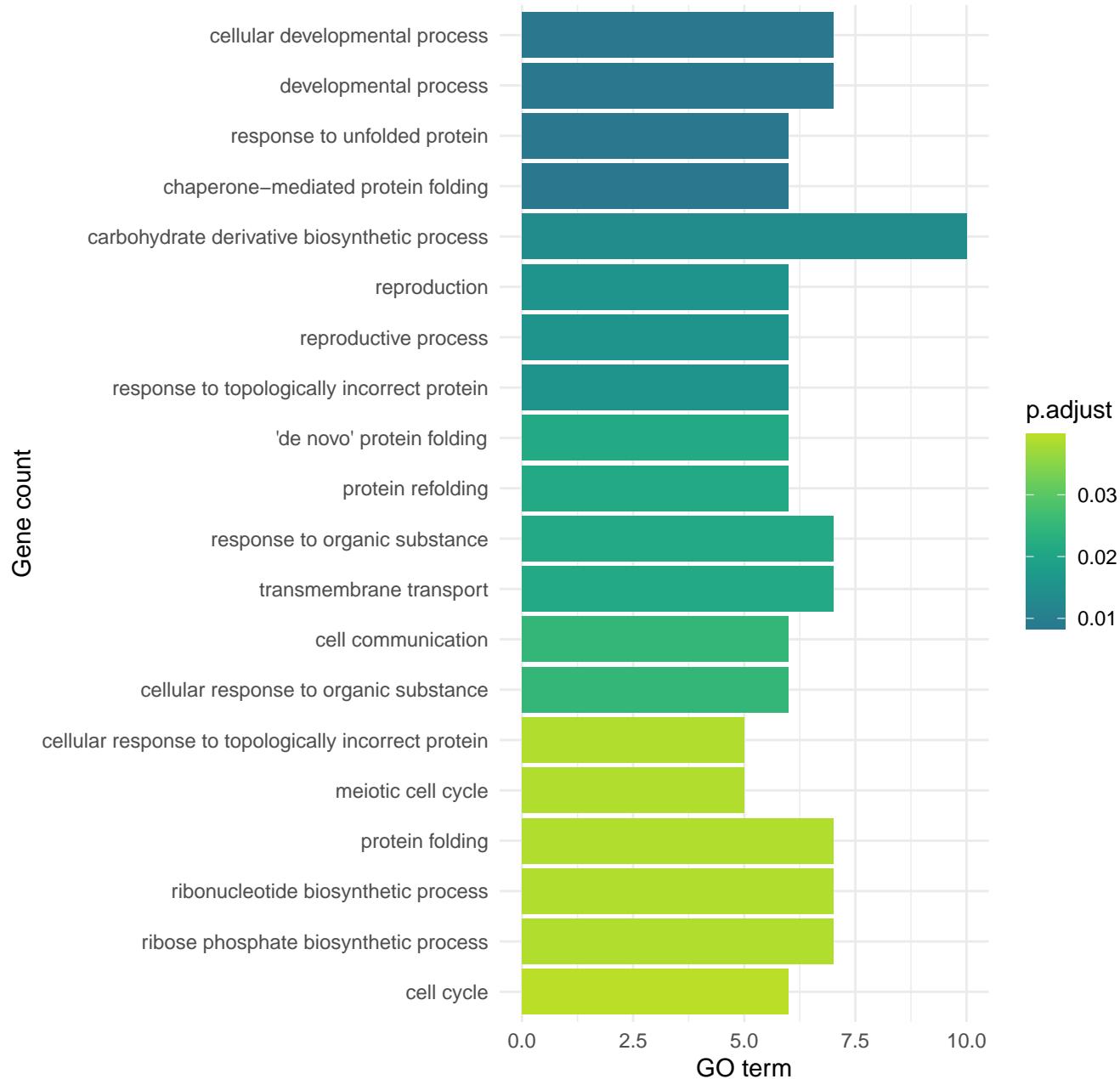




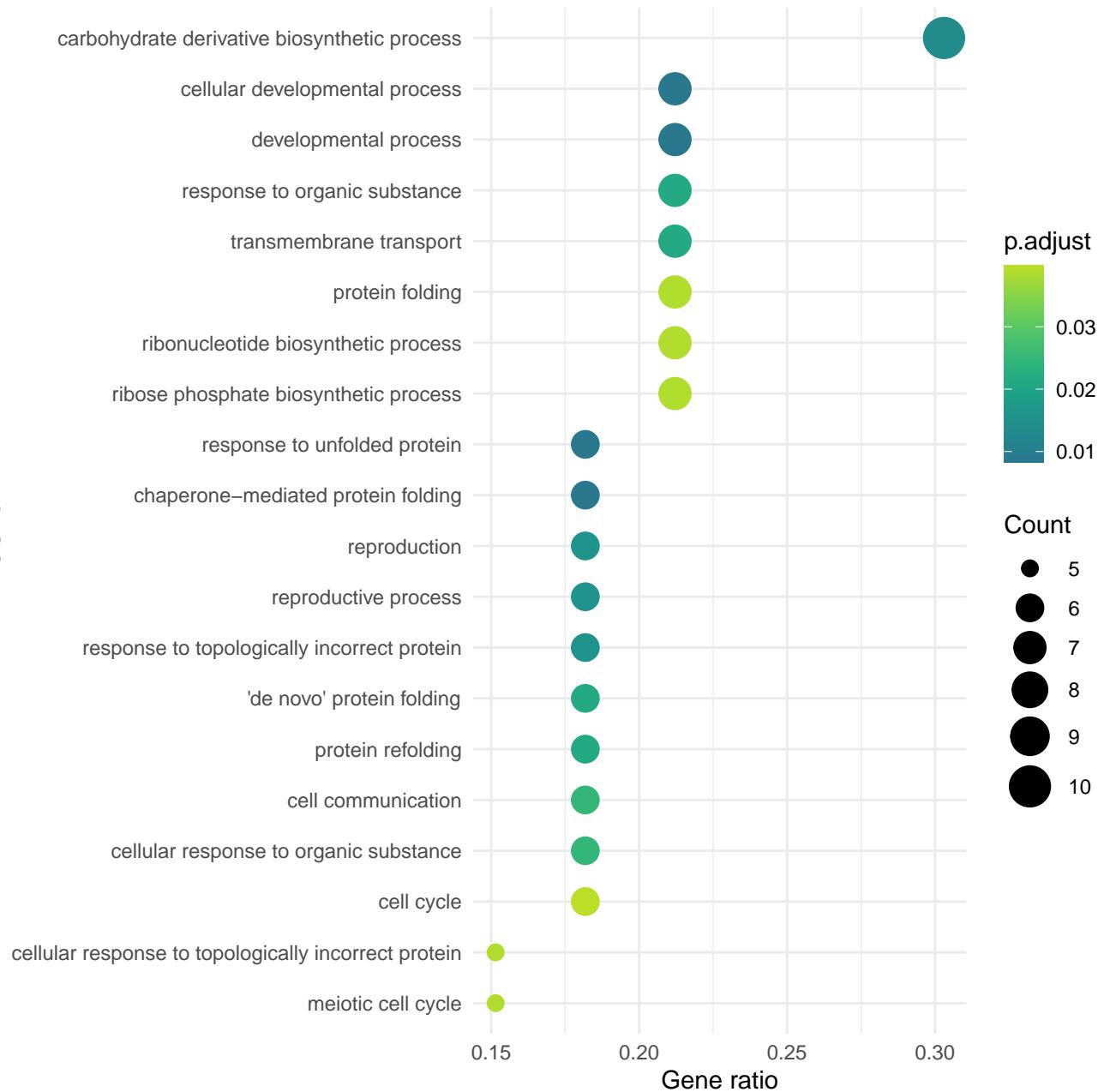
DIS3-TAP Up-regulated GO MF upsetplot



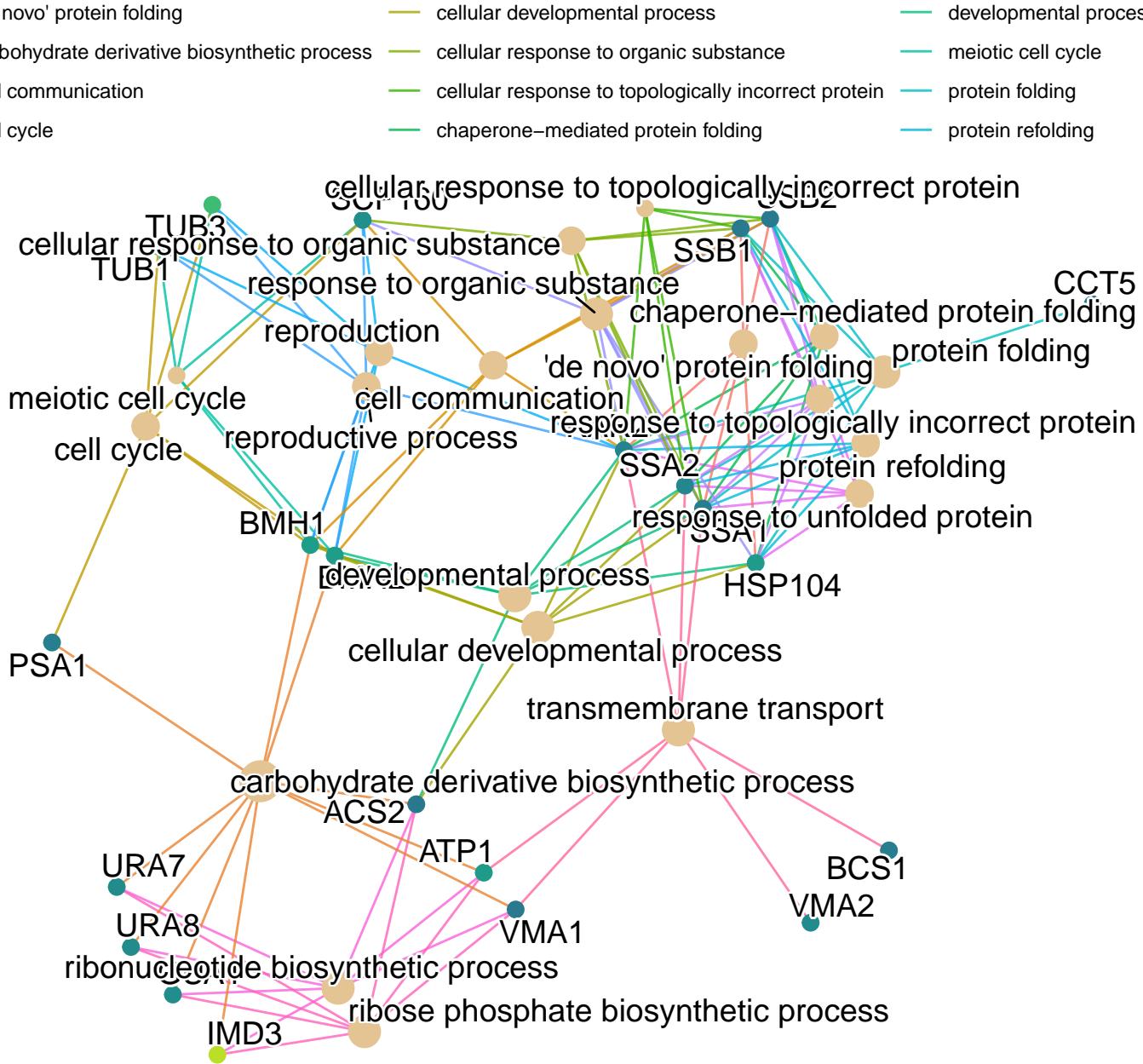
FAL1-TAP Up-regulated GO BP barplot



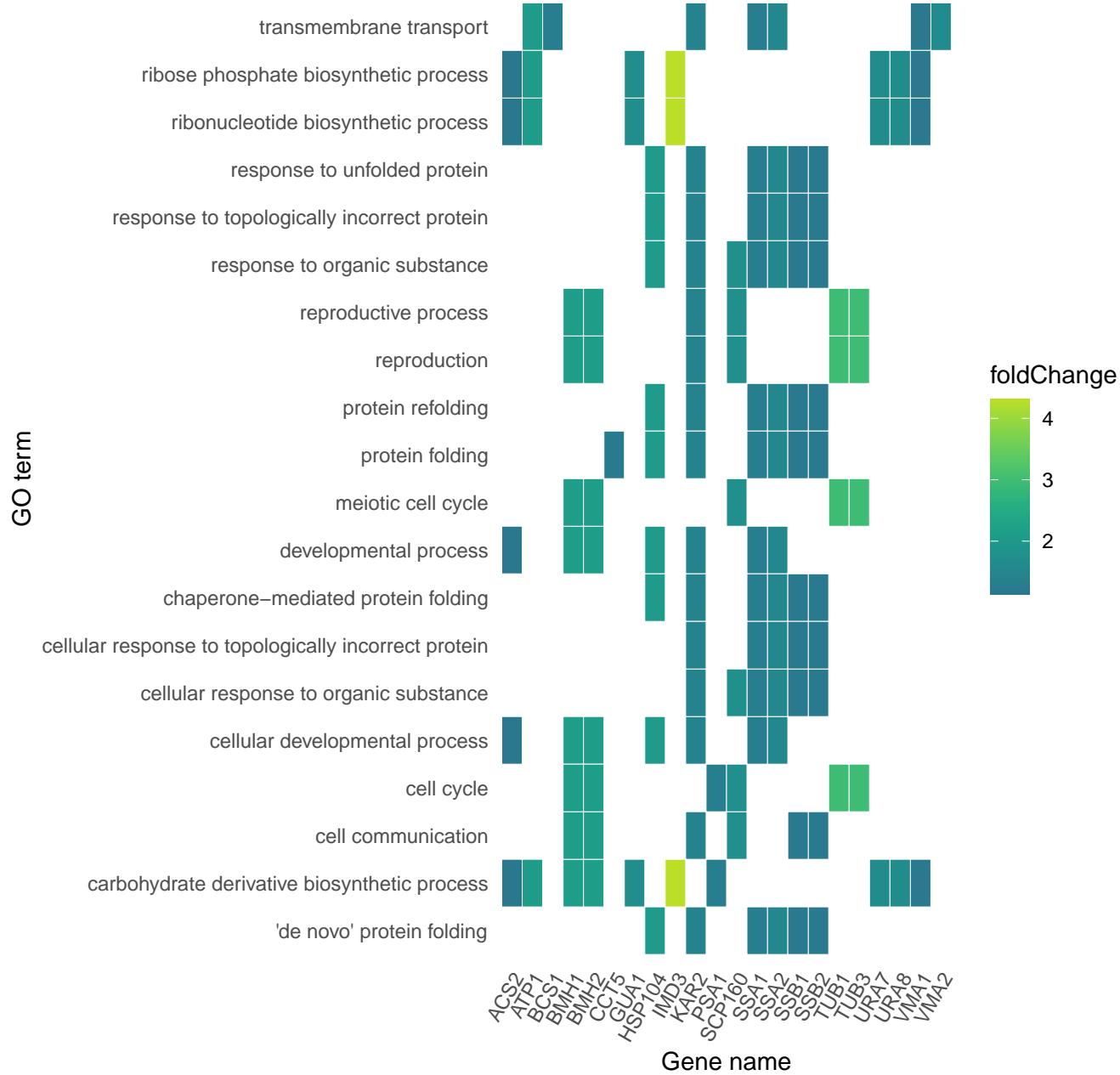
FAL1-TAP Up-regulated GO BP dotplot



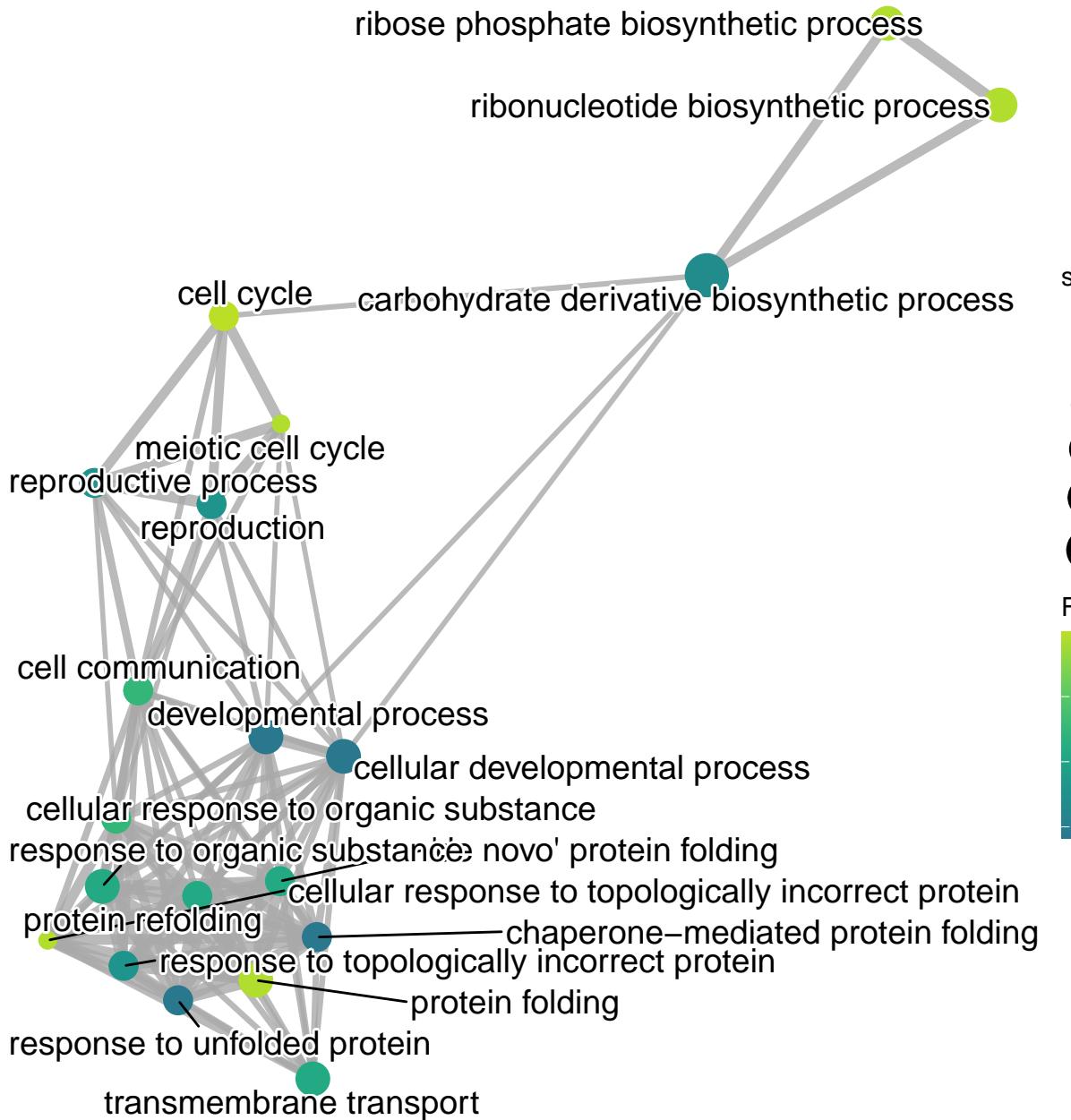
FAL1-TAP Up-regulated GO BP cnetplot



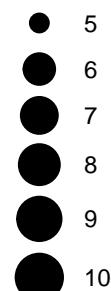
FAL1-TAP Up-regulated GO BP heatplot



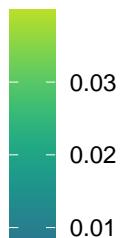
FAL1-TAP Up-regulated GO BP emapplot

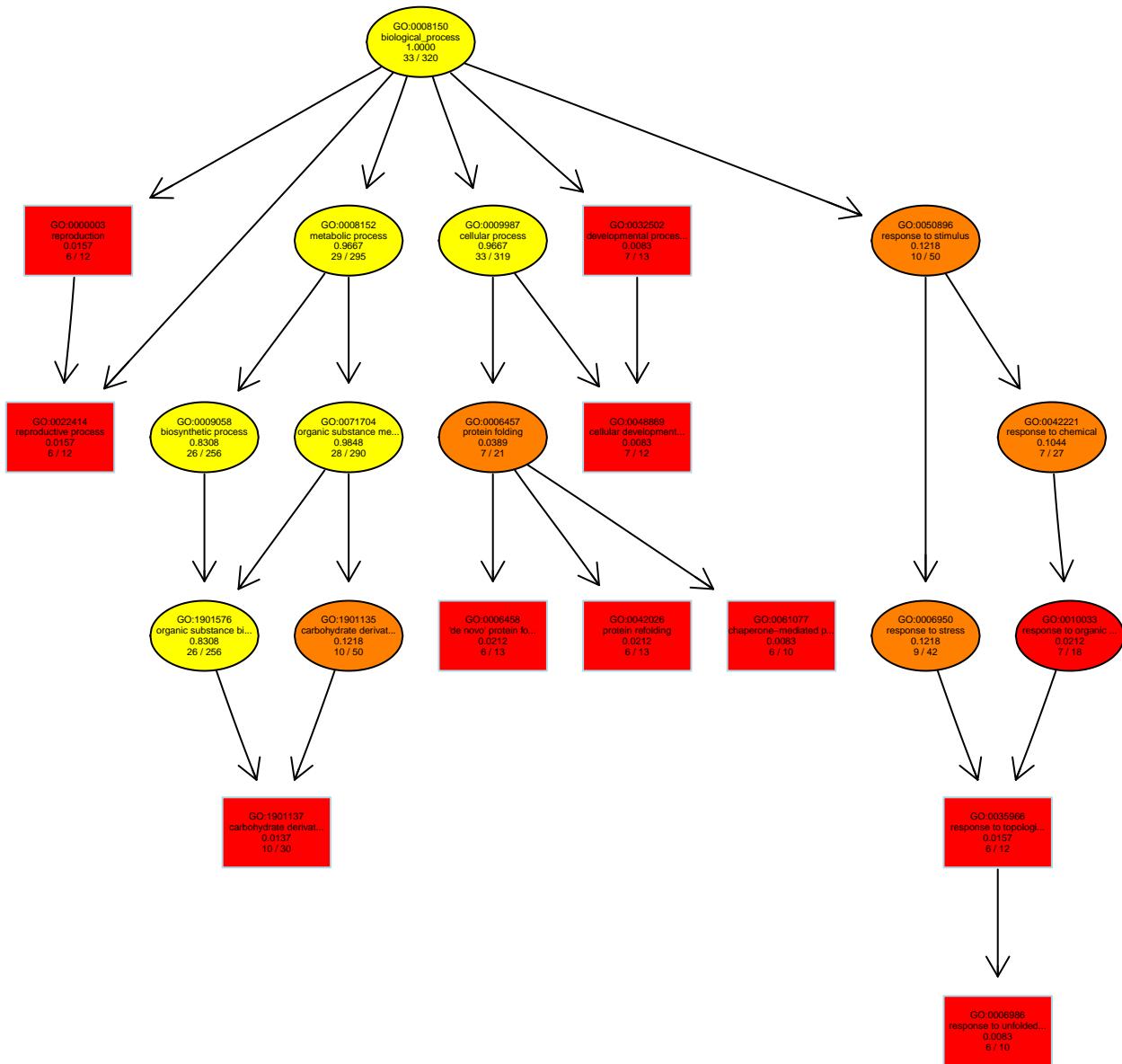


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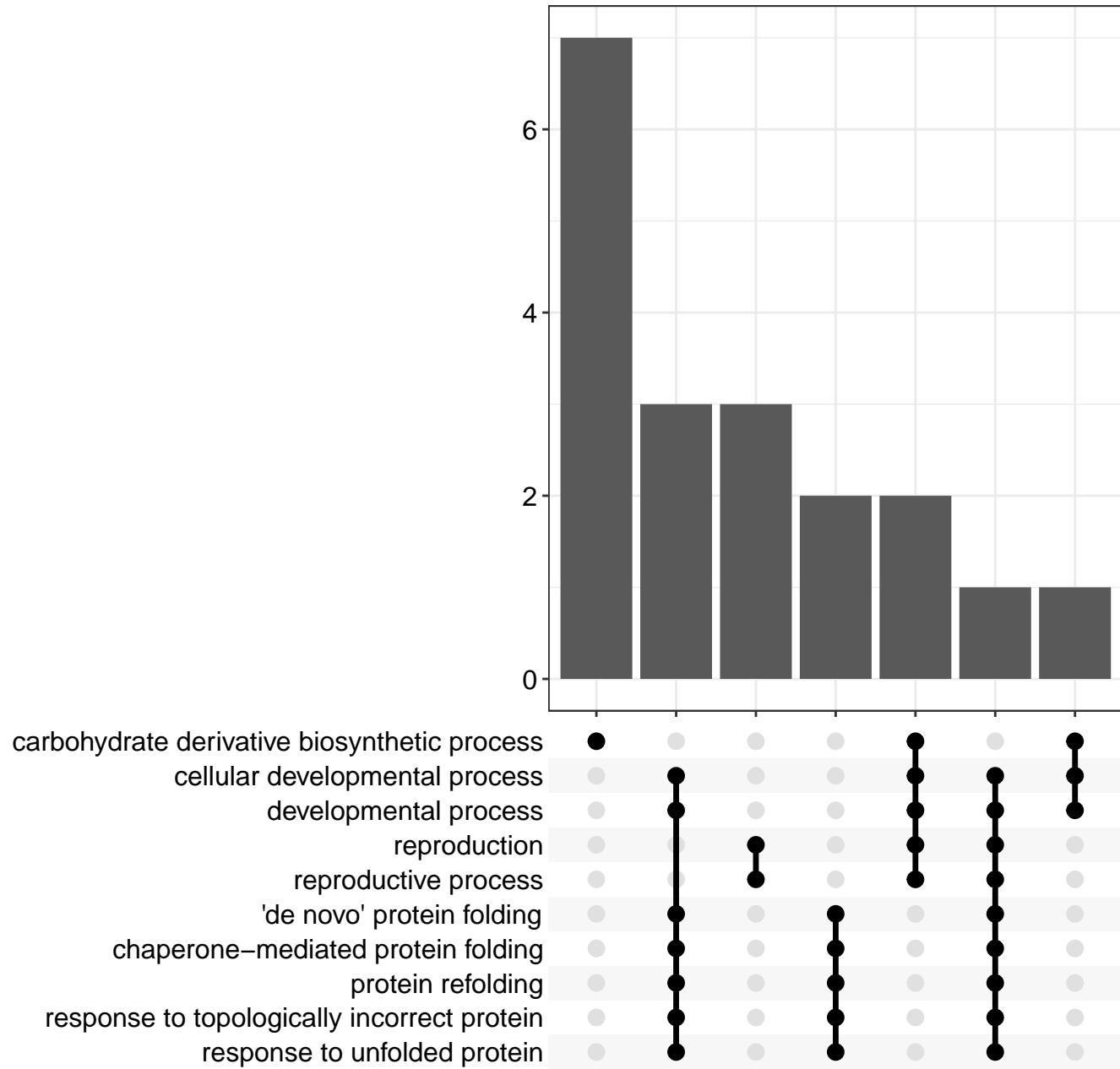


FoldChange

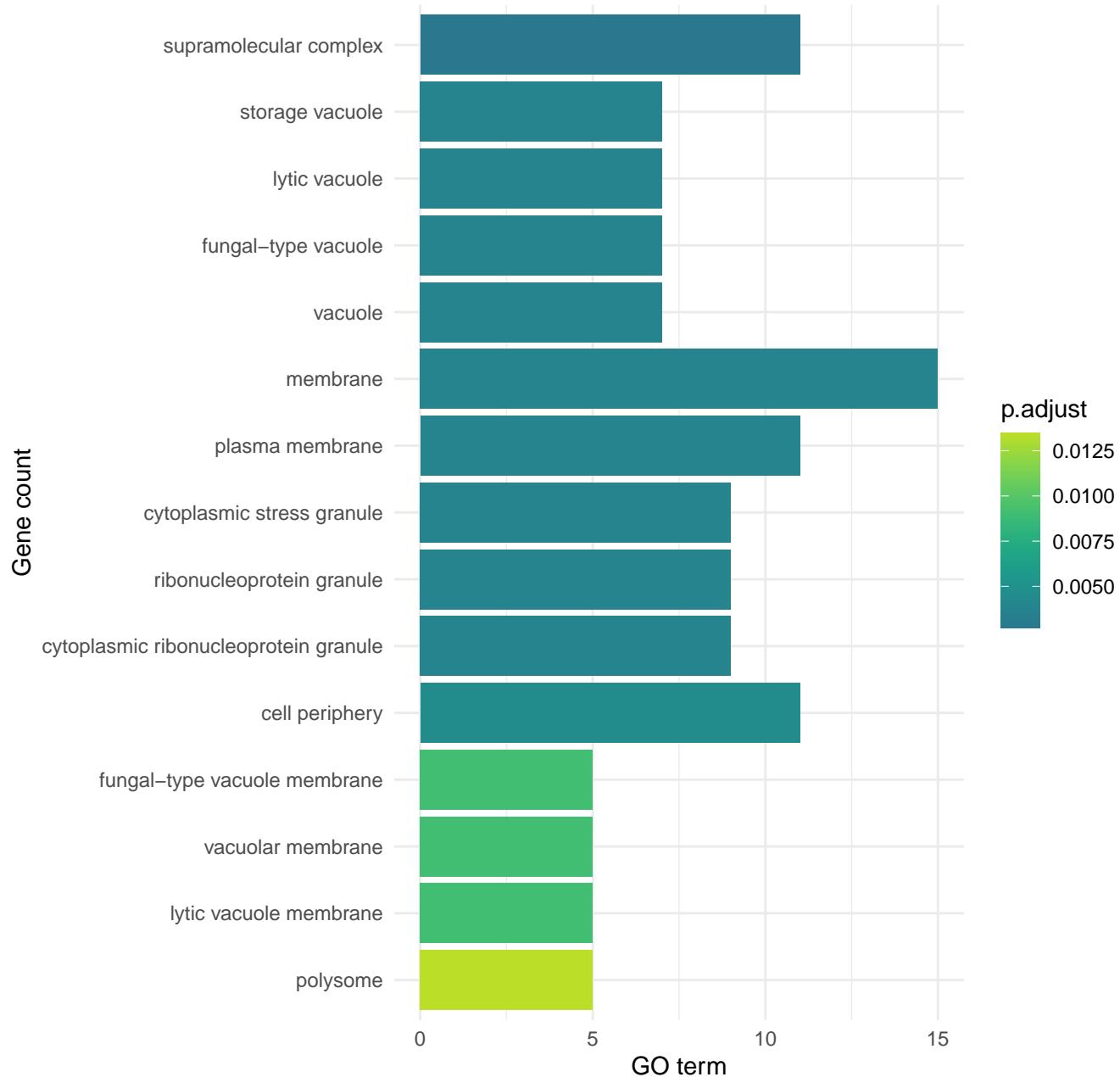




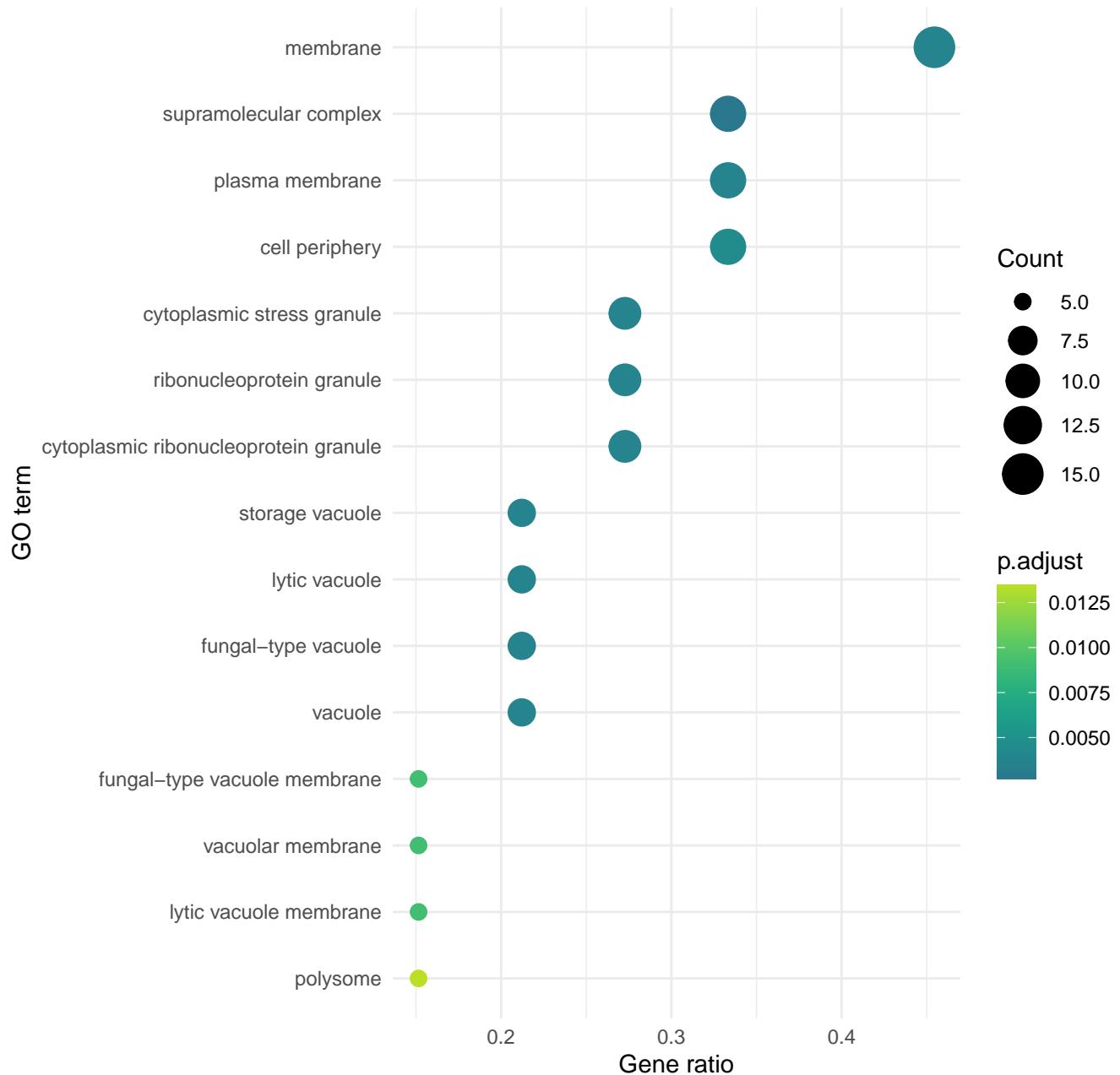
FAL1-TAP Up-regulated GO BP upsetplot



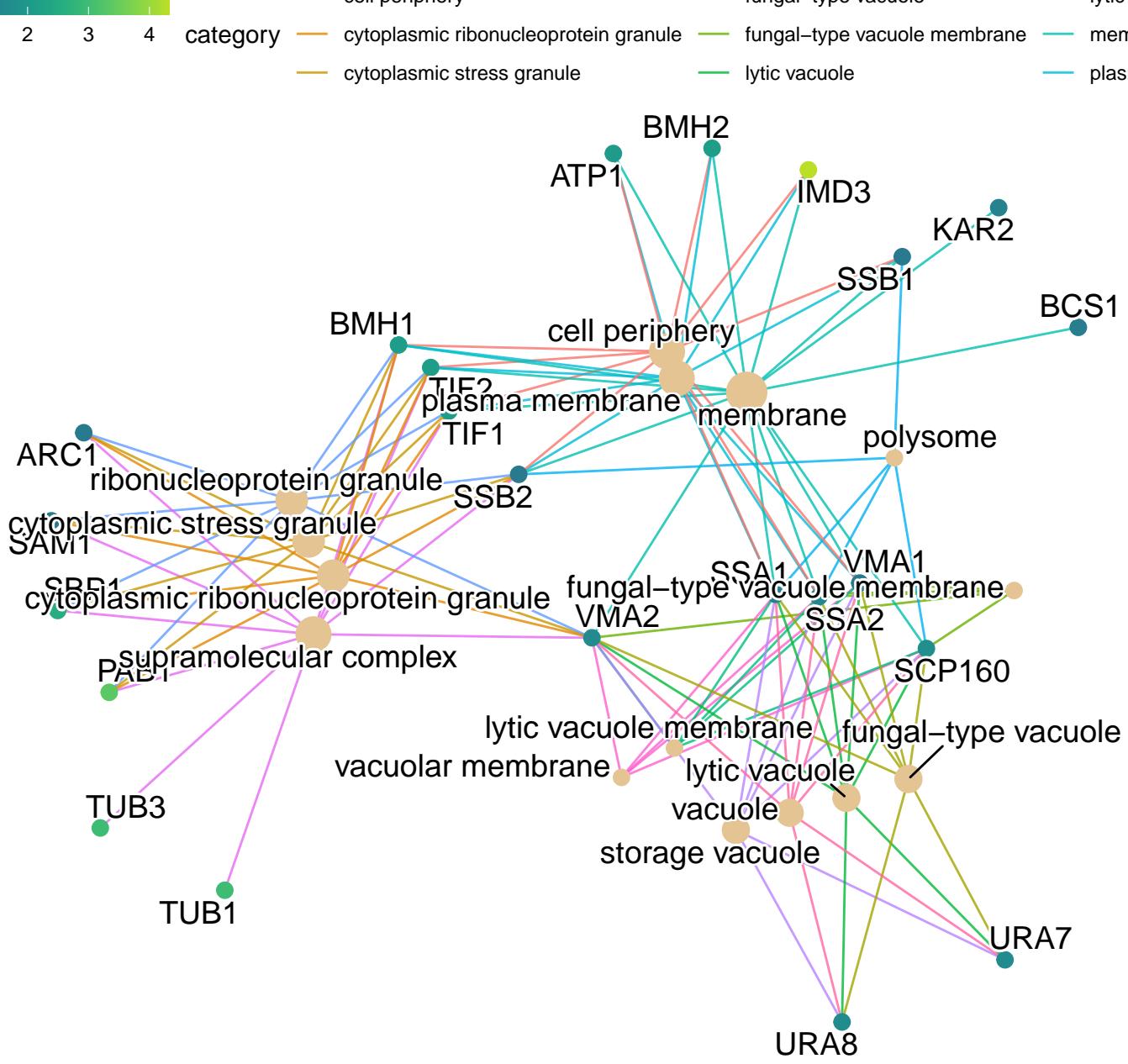
FAL1-TAP Up-regulated GO CC barplot



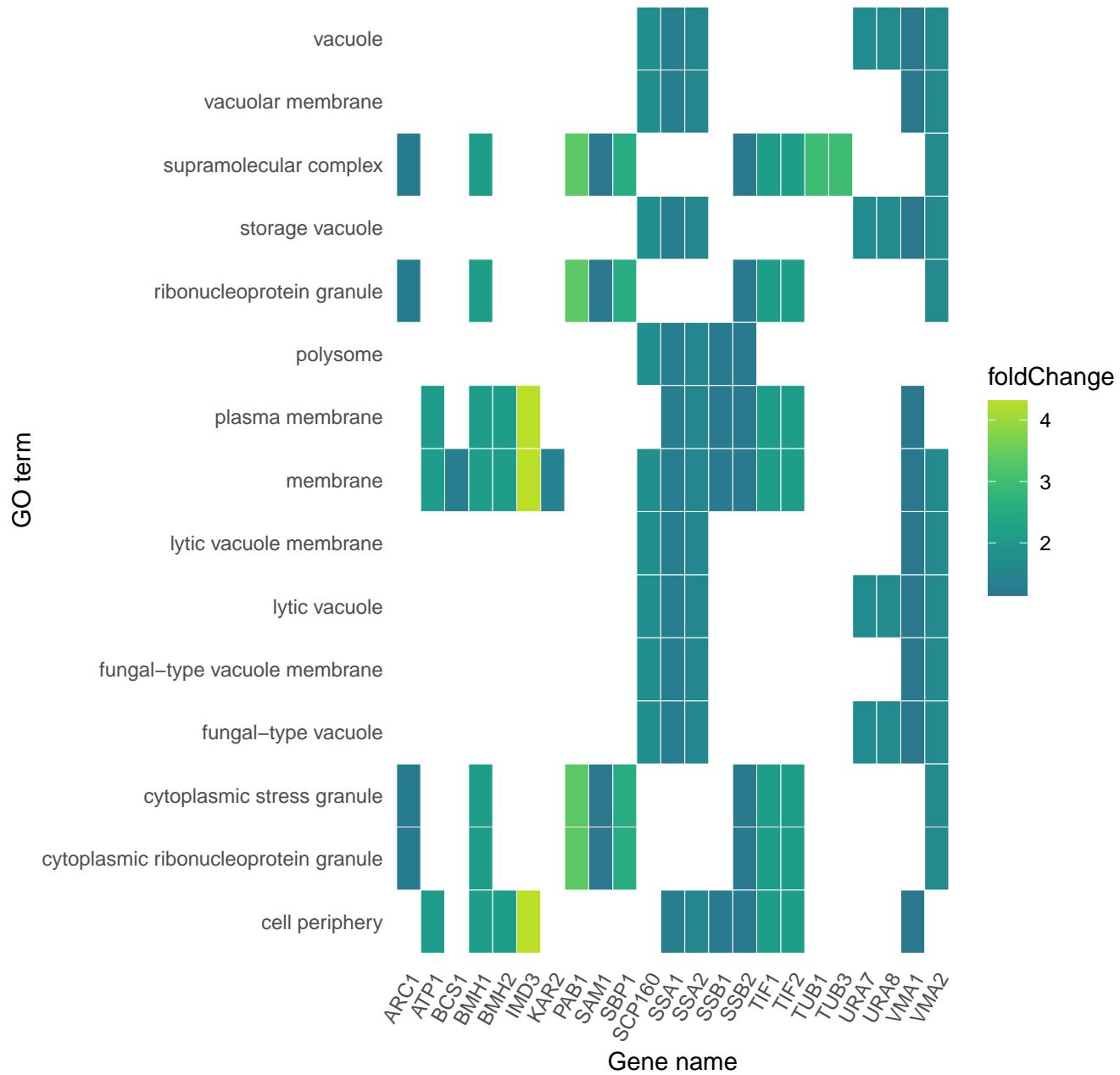
FAL1-TAP Up-regulated GO CC dotplot



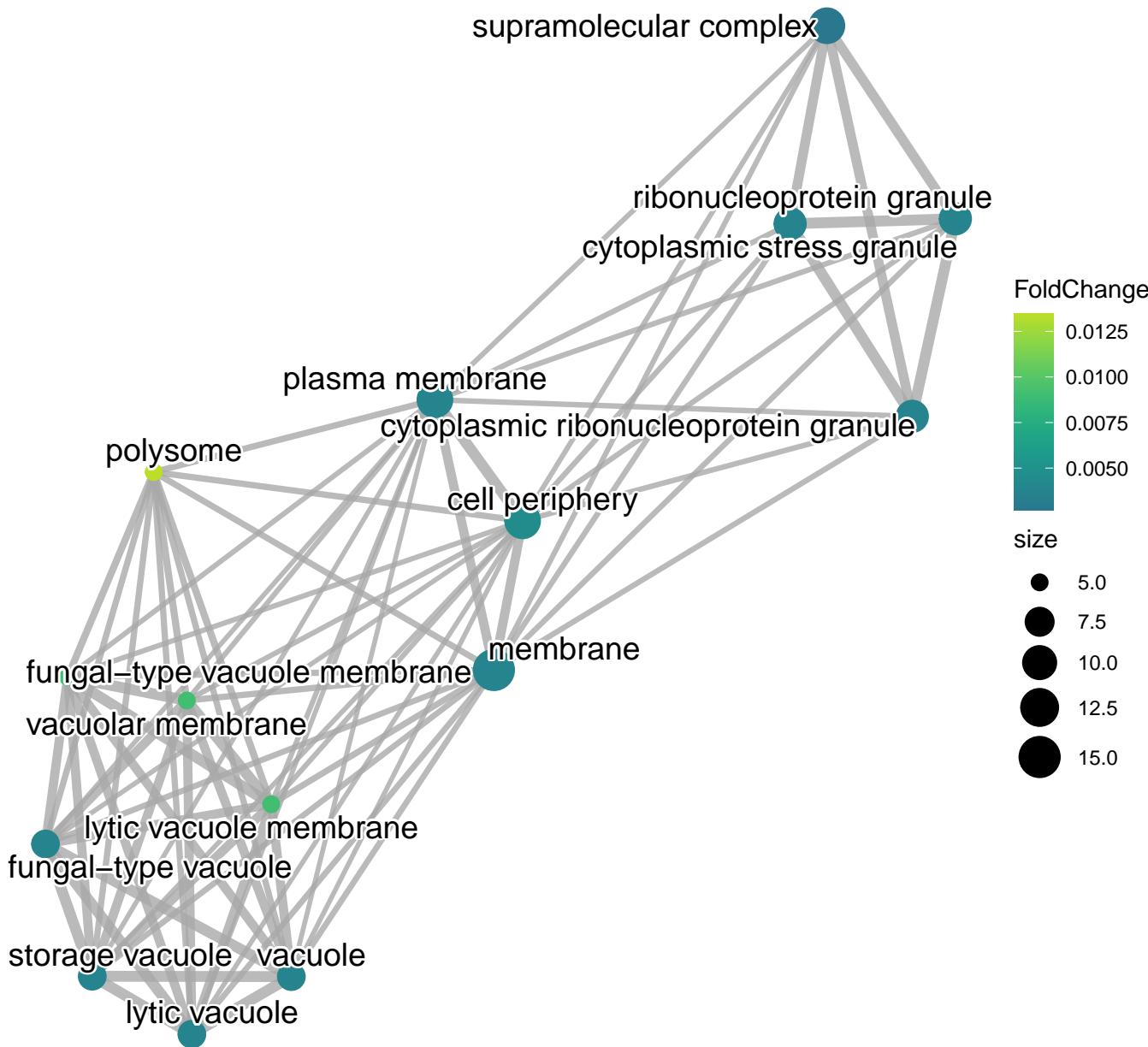
FAL1-TAP Up-regulated GO CC cnetplot

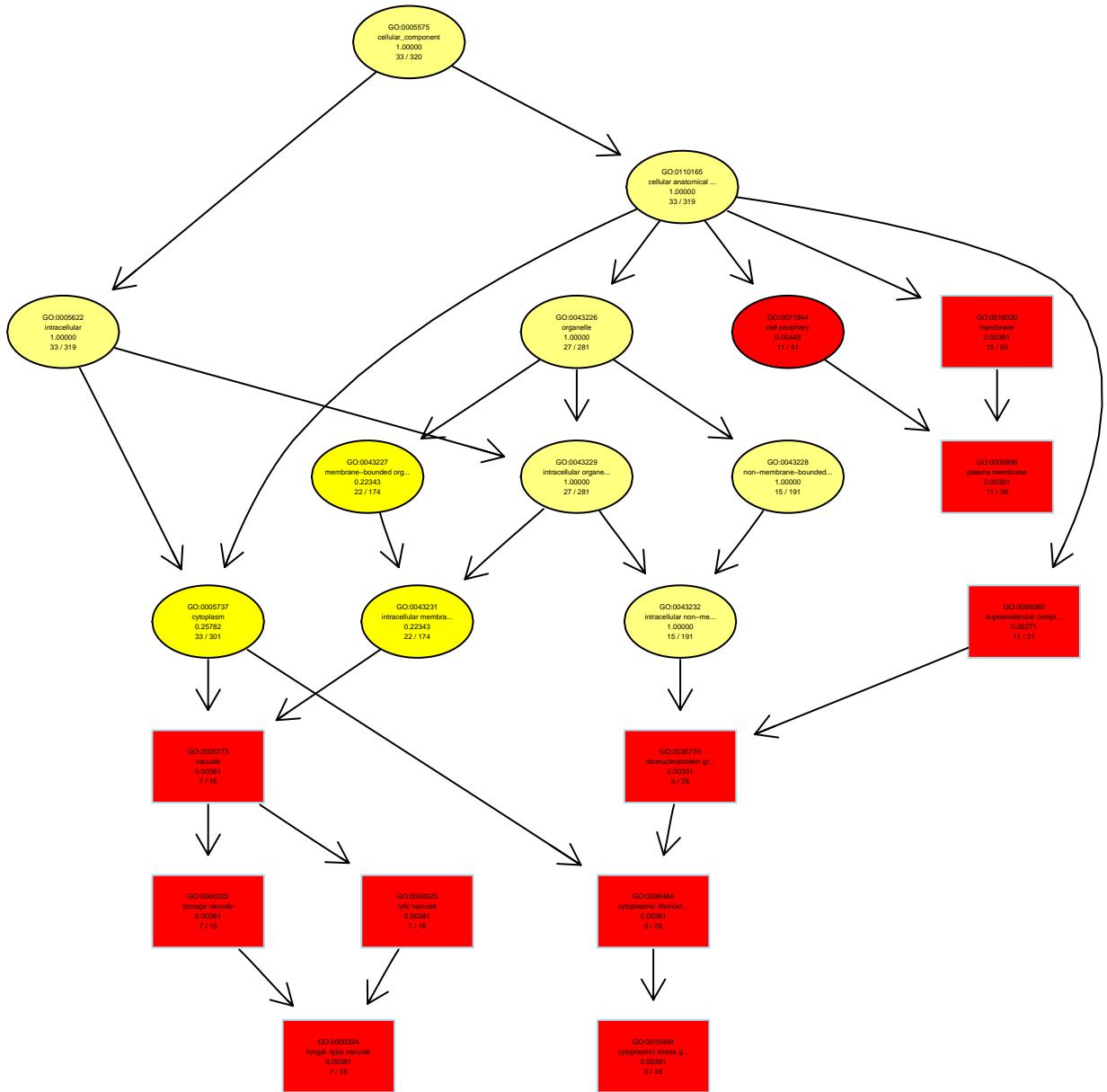


FAL1-TAP Up-regulated GO CC heatplot

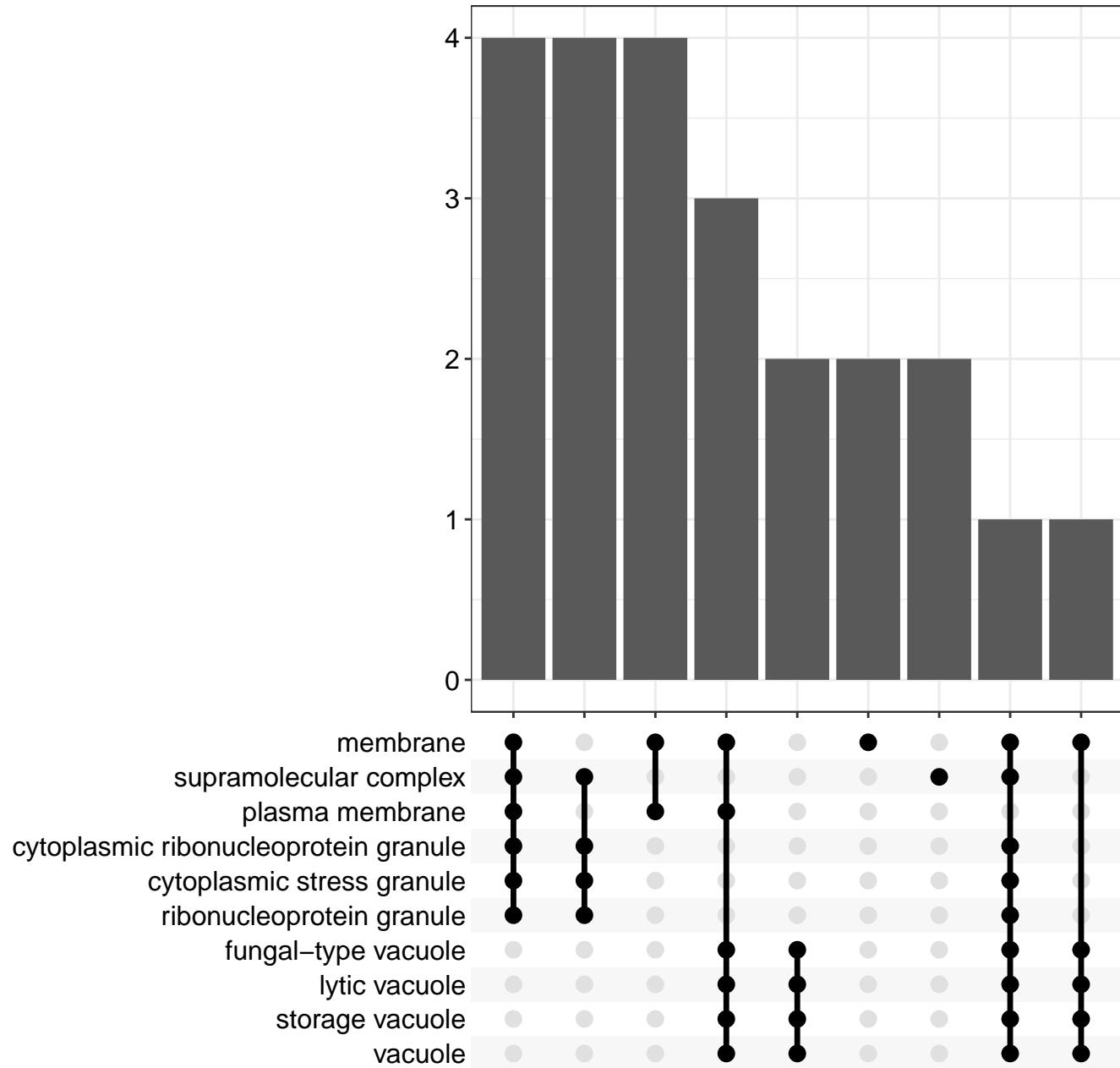


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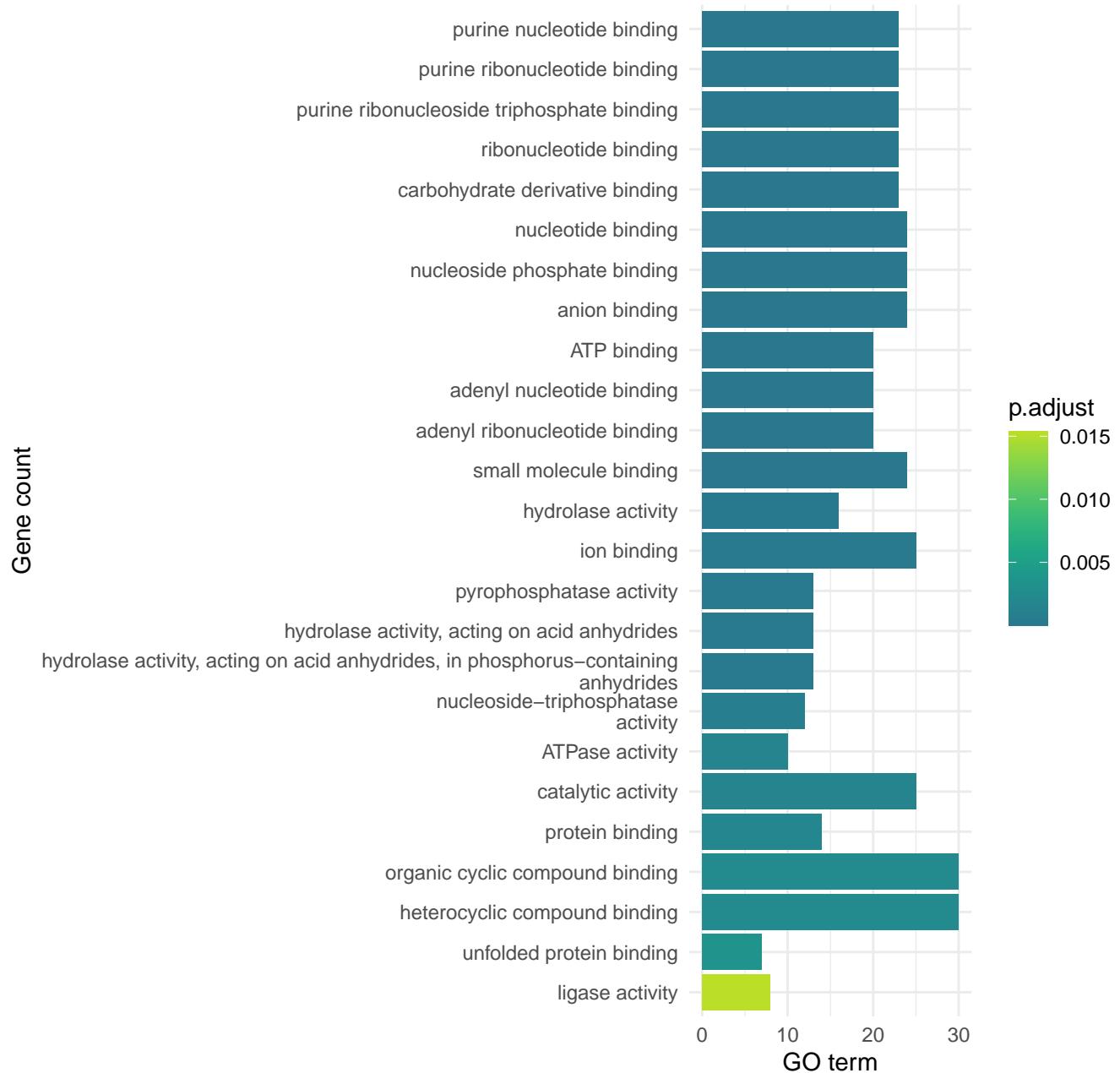




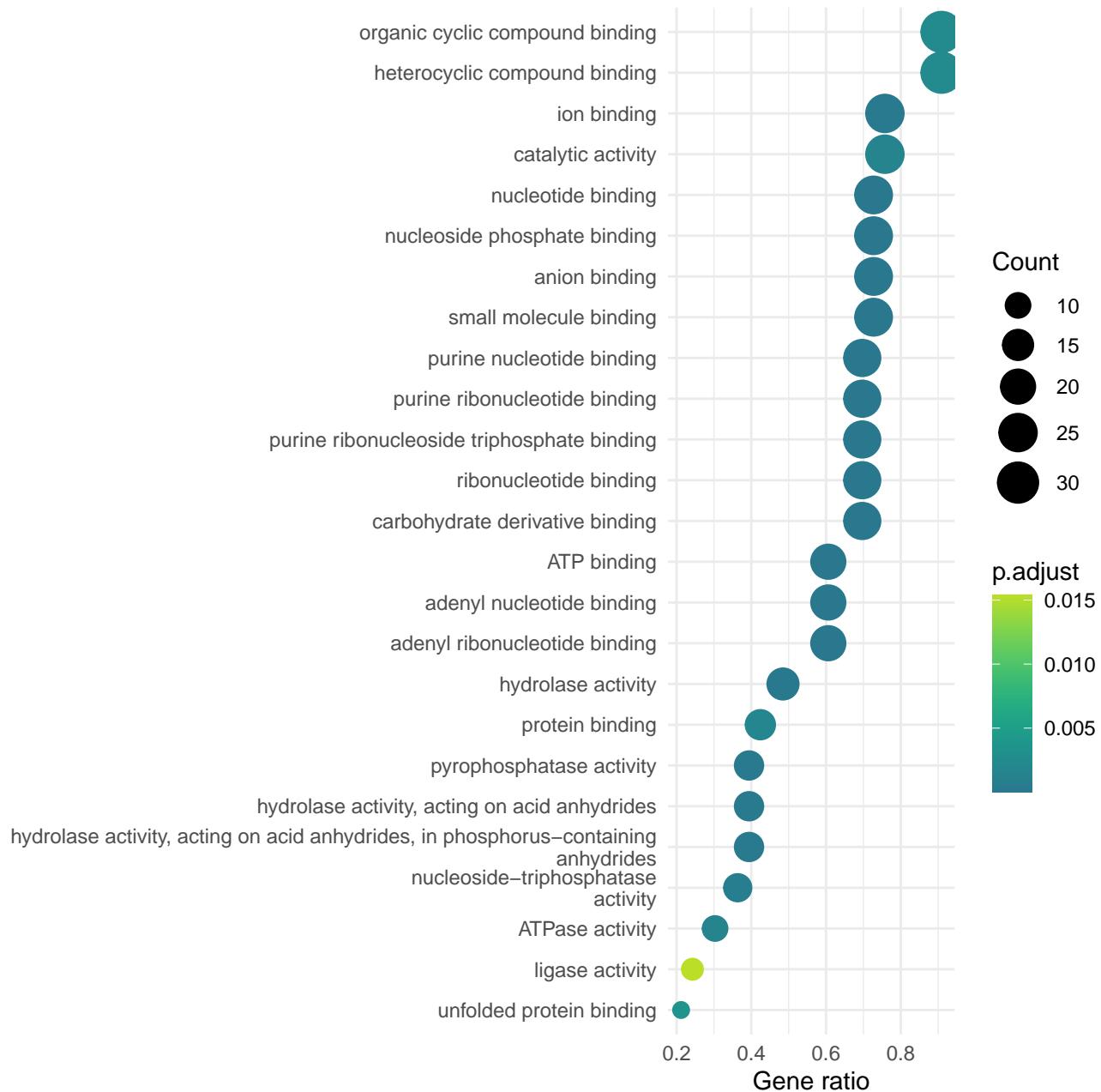
FAL1-TAP Up-regulated GO CC upsetplot



FAL1-TAP Up-regulated GO MF b



FAL1-TAP Up-regulated GO MF c



FAL1-TAP Up-regulated GO MF cnetplot

y, acting on acid anhydrides, in phosphorus-containing anhydrides

For more information about the study, please contact Dr. John D. Cawley at (609) 258-4626 or via email at jdcawley@princeton.edu.

Phosphate binding

Phosphatase activity

respiratory activity

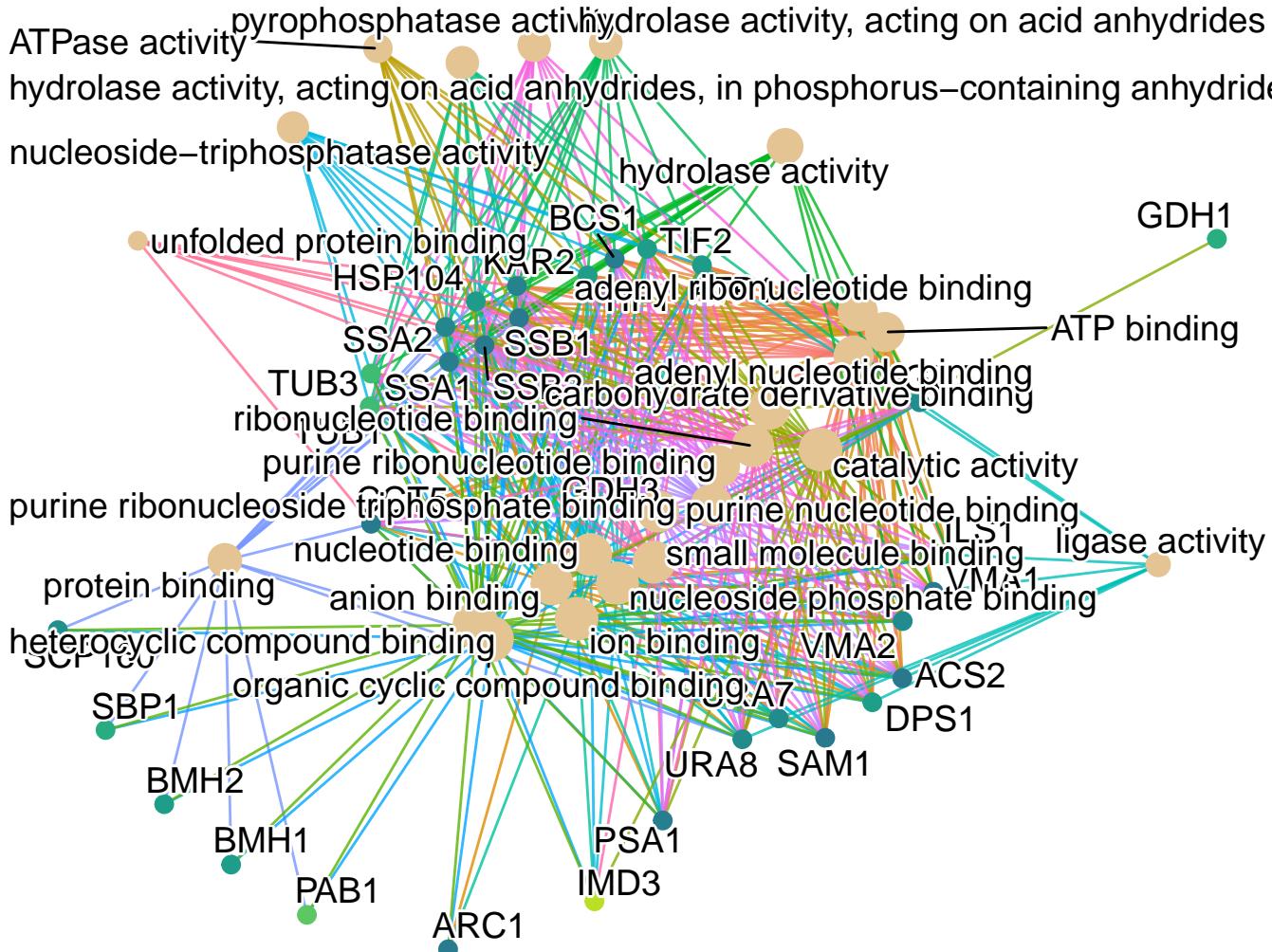
— nucleotide binding

— organic cyclic compound binding

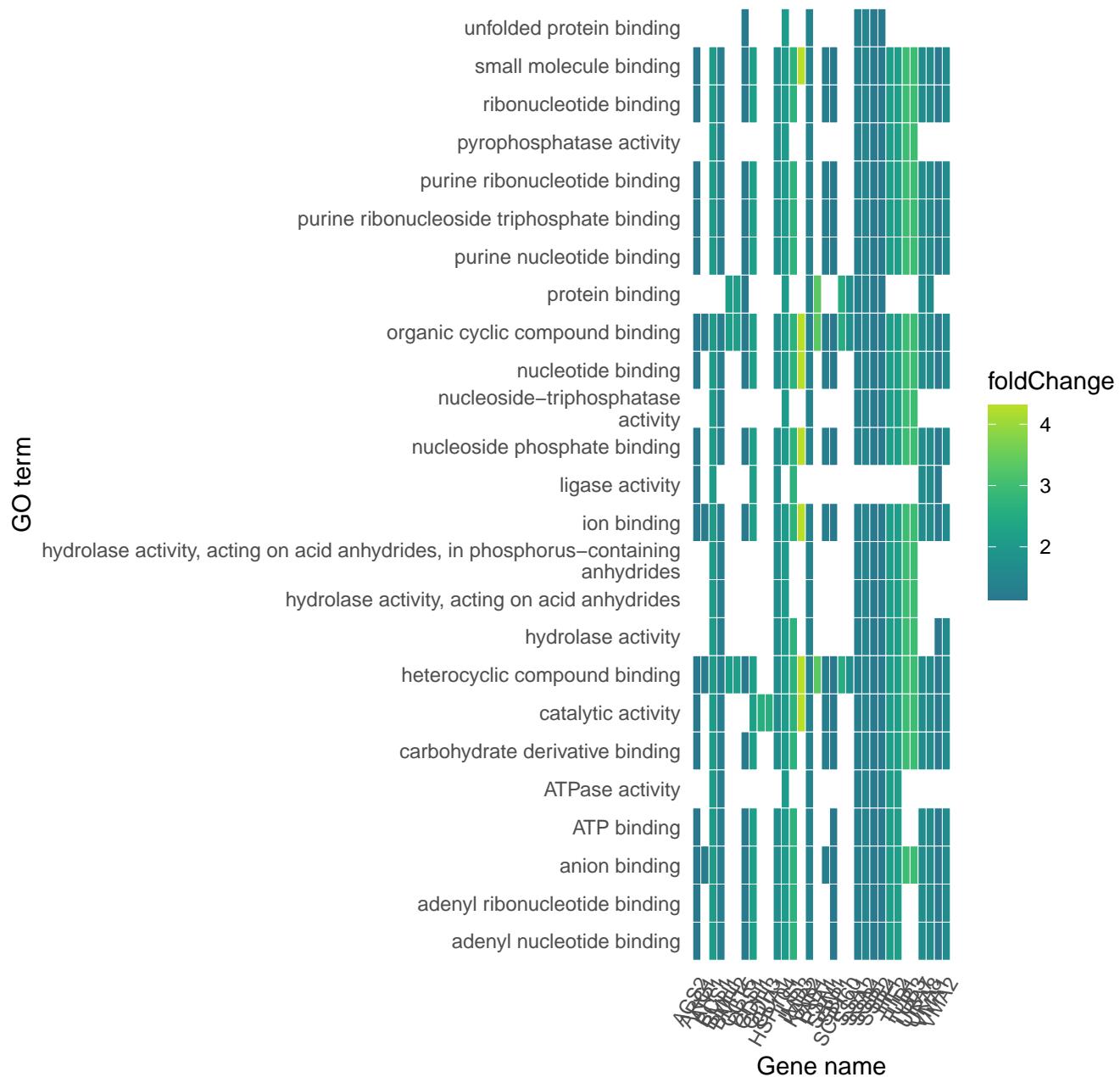
— protein binding

REFERENCES AND NOTES

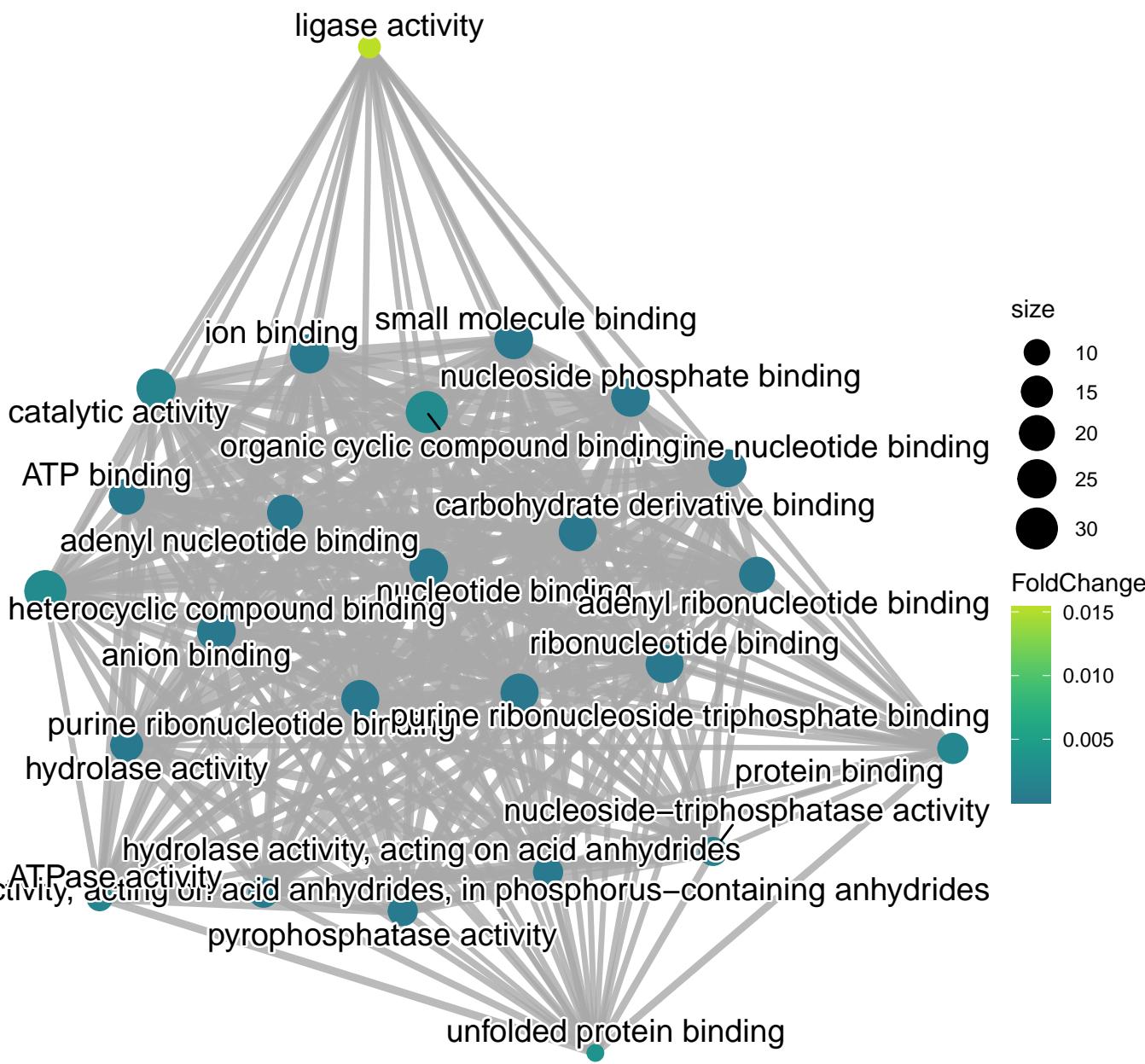
purine ribonucleoside triphosphate binding

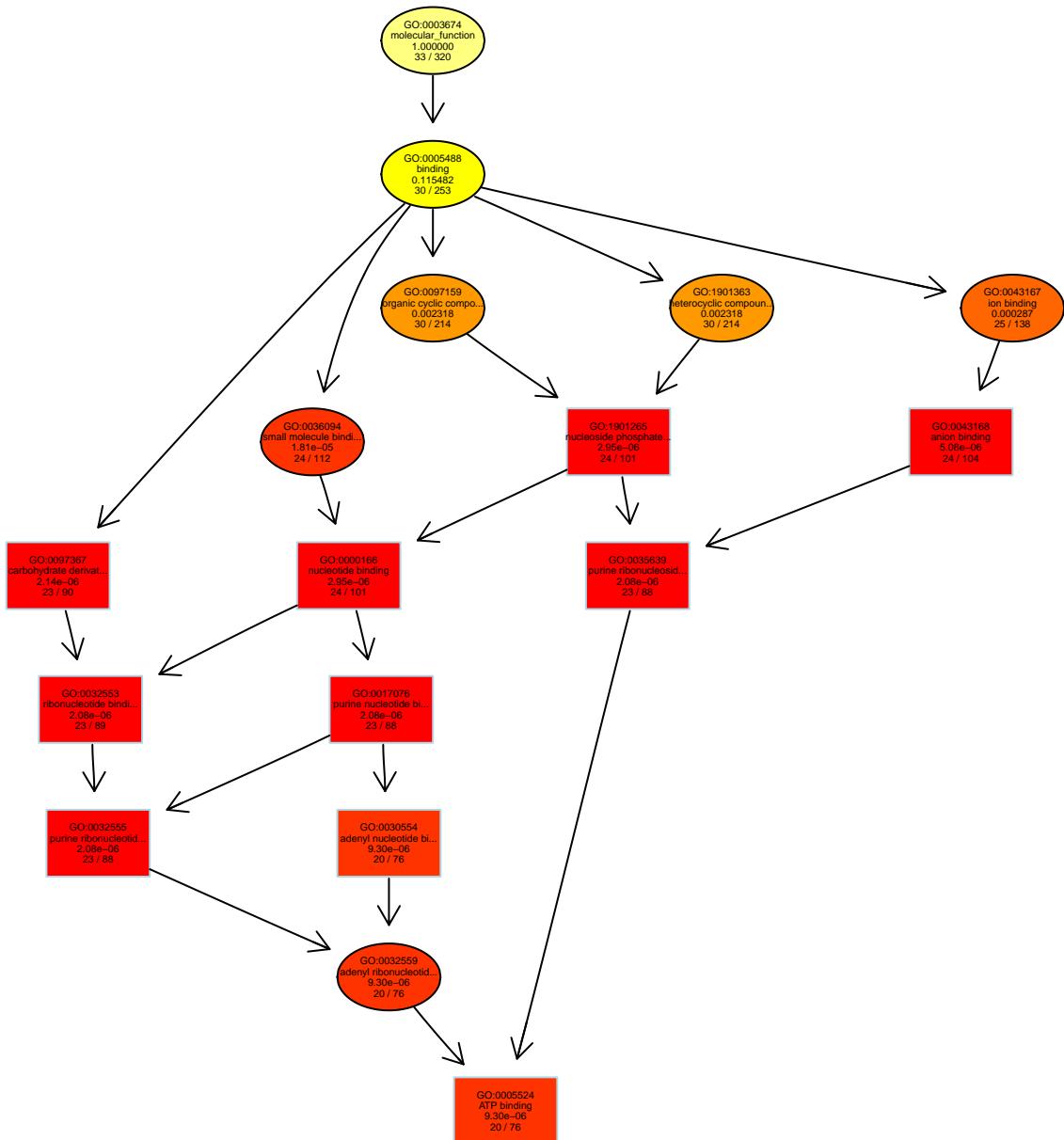


FAL1-TAP Up-regulated GO MF h

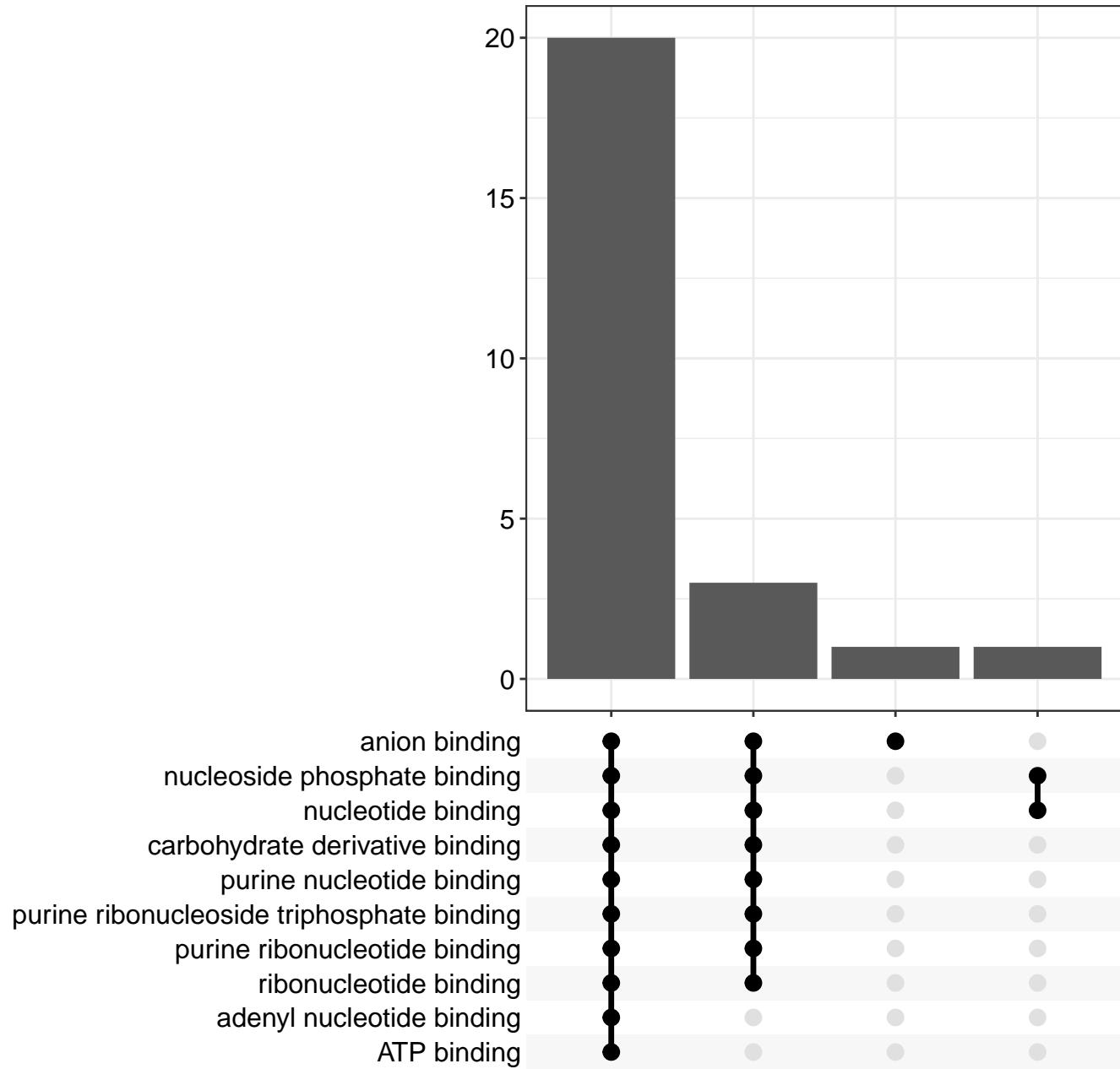


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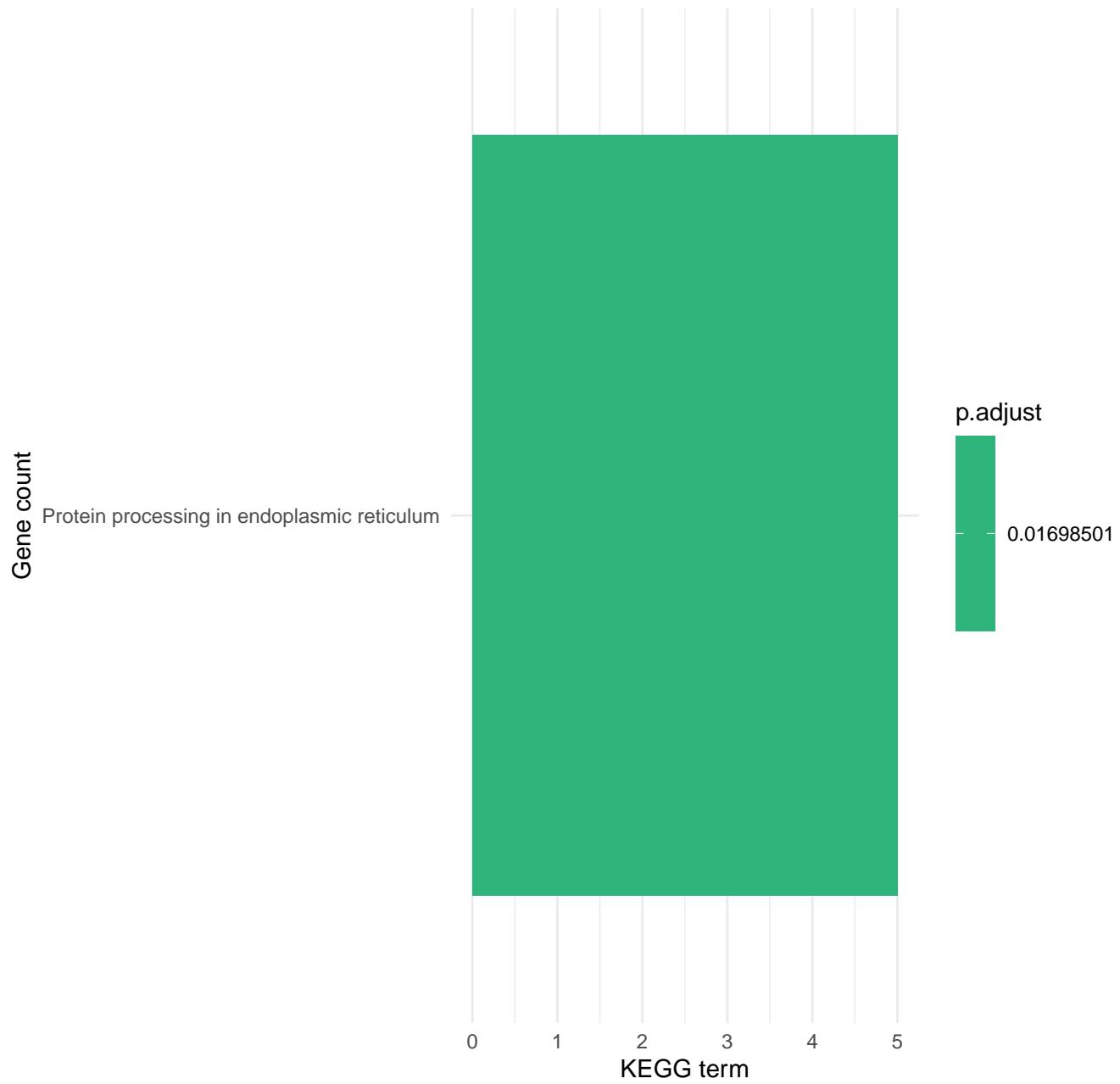




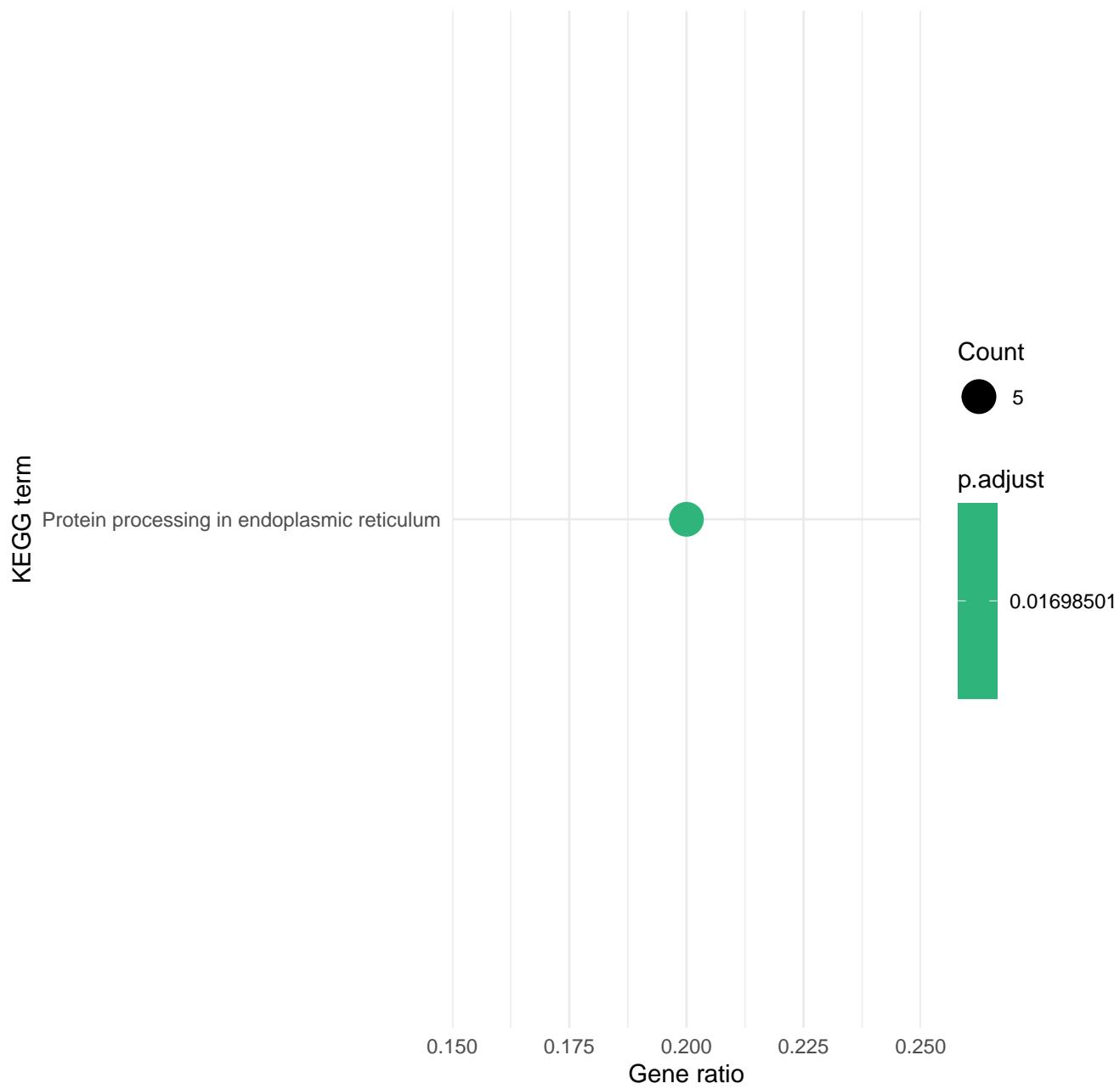
FAL1-TAP Up-regulated GO MF upsetplot



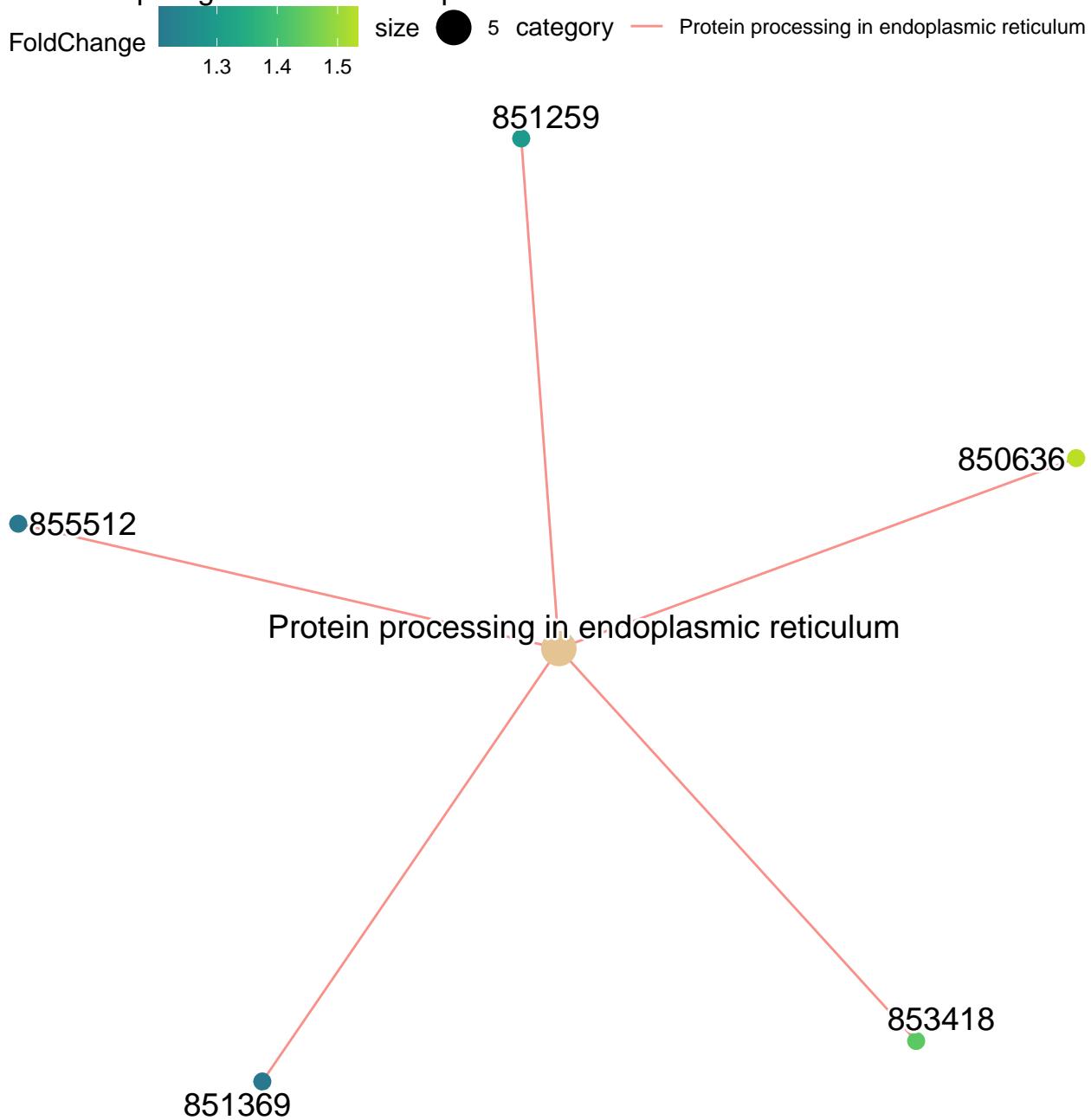
FAL1-TAP Up-regulated KEGG barplot



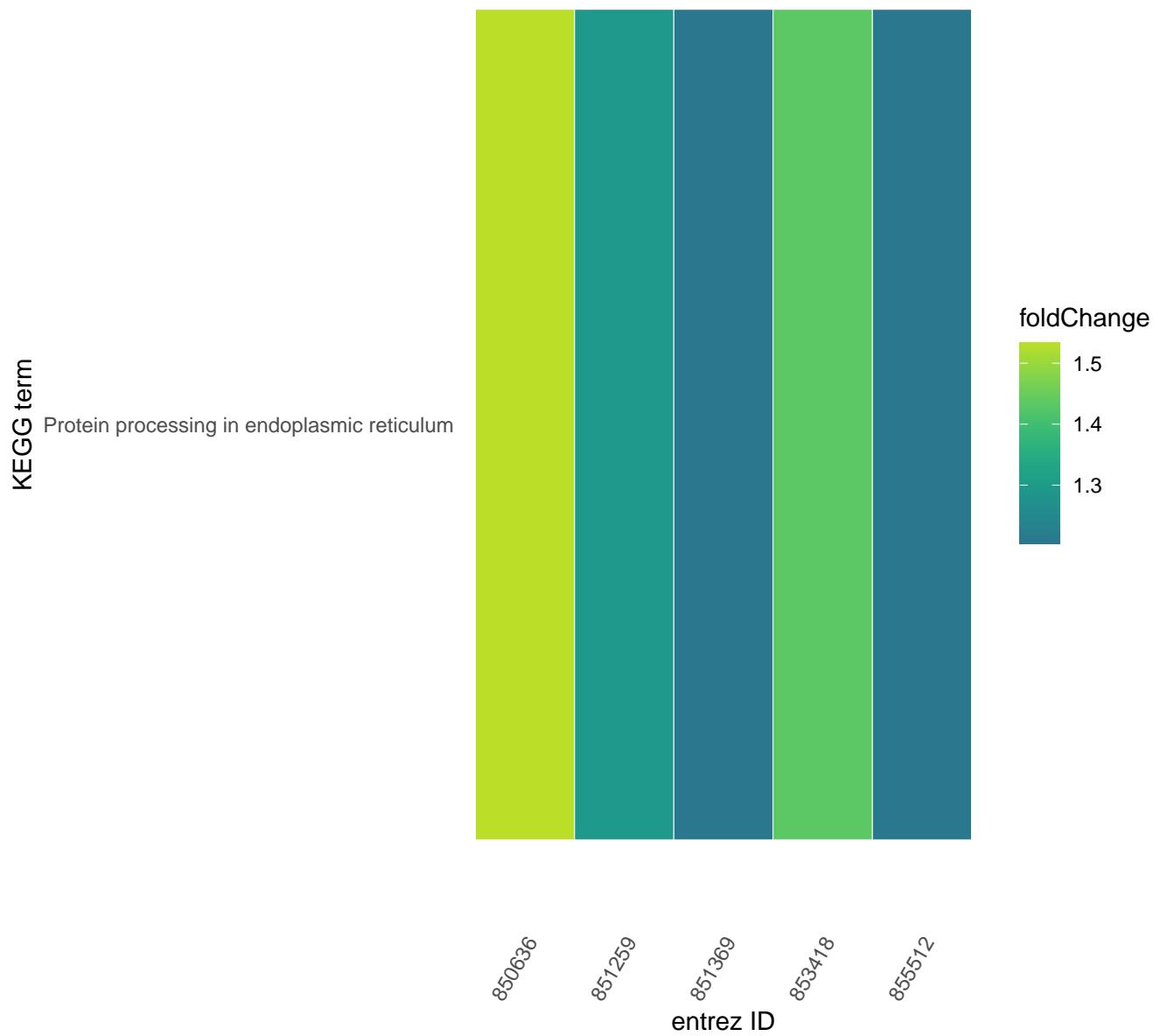
FAL1-TAP Up-regulated KEGG dotplot



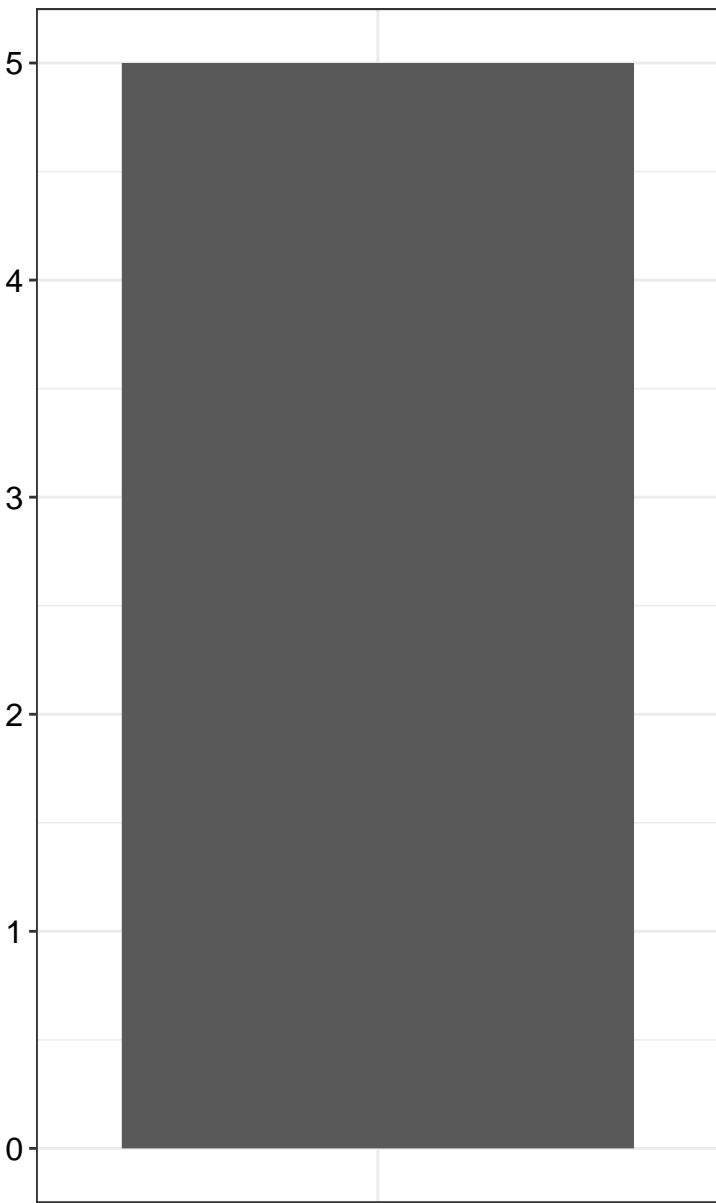
FAL1-TAP Up-regulated KEGG dotplot



FAL1-TAP Up-regulated KEGG heatplot



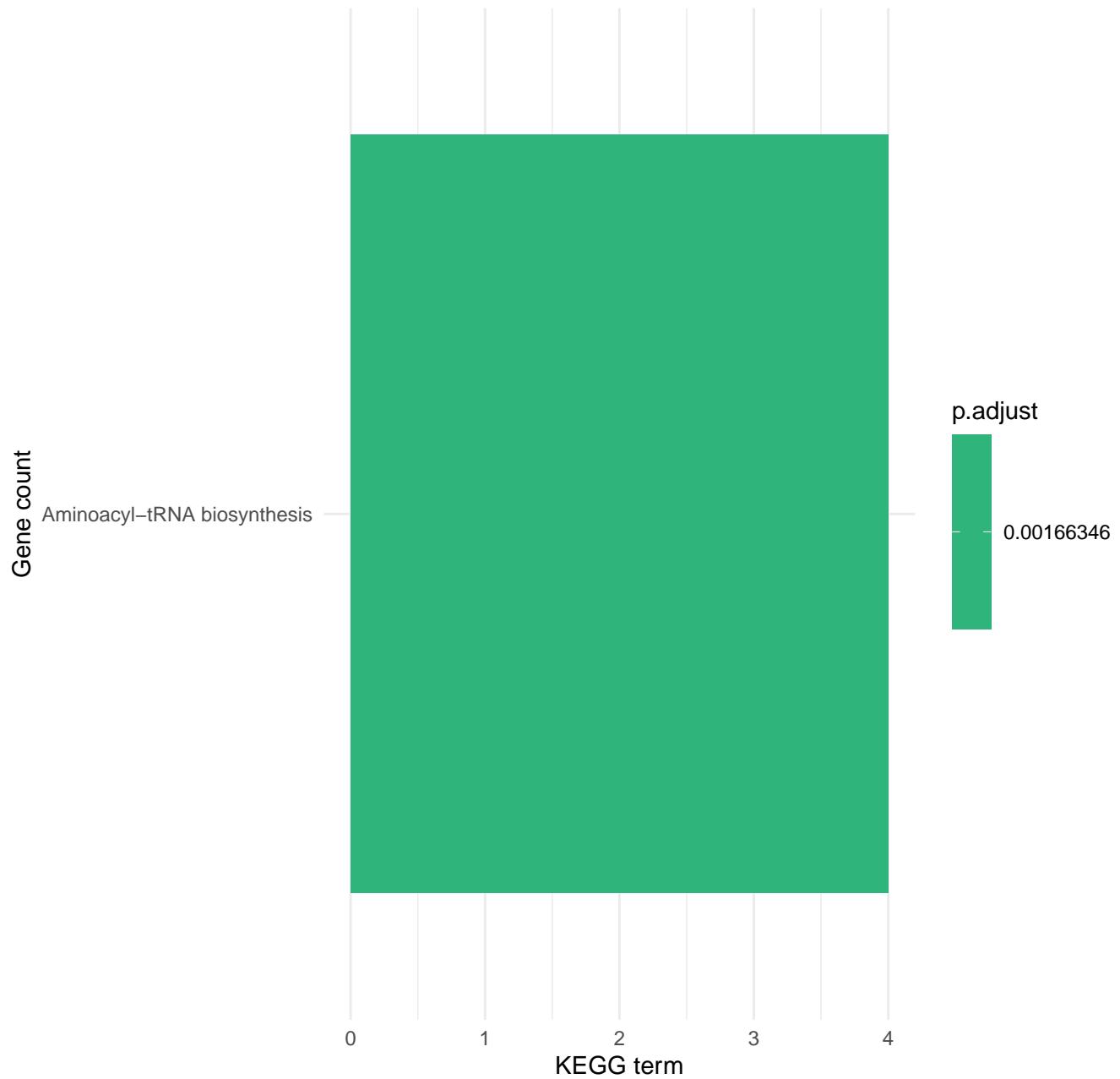
FAL1-TAP Up-regulated KEGG upsetplot



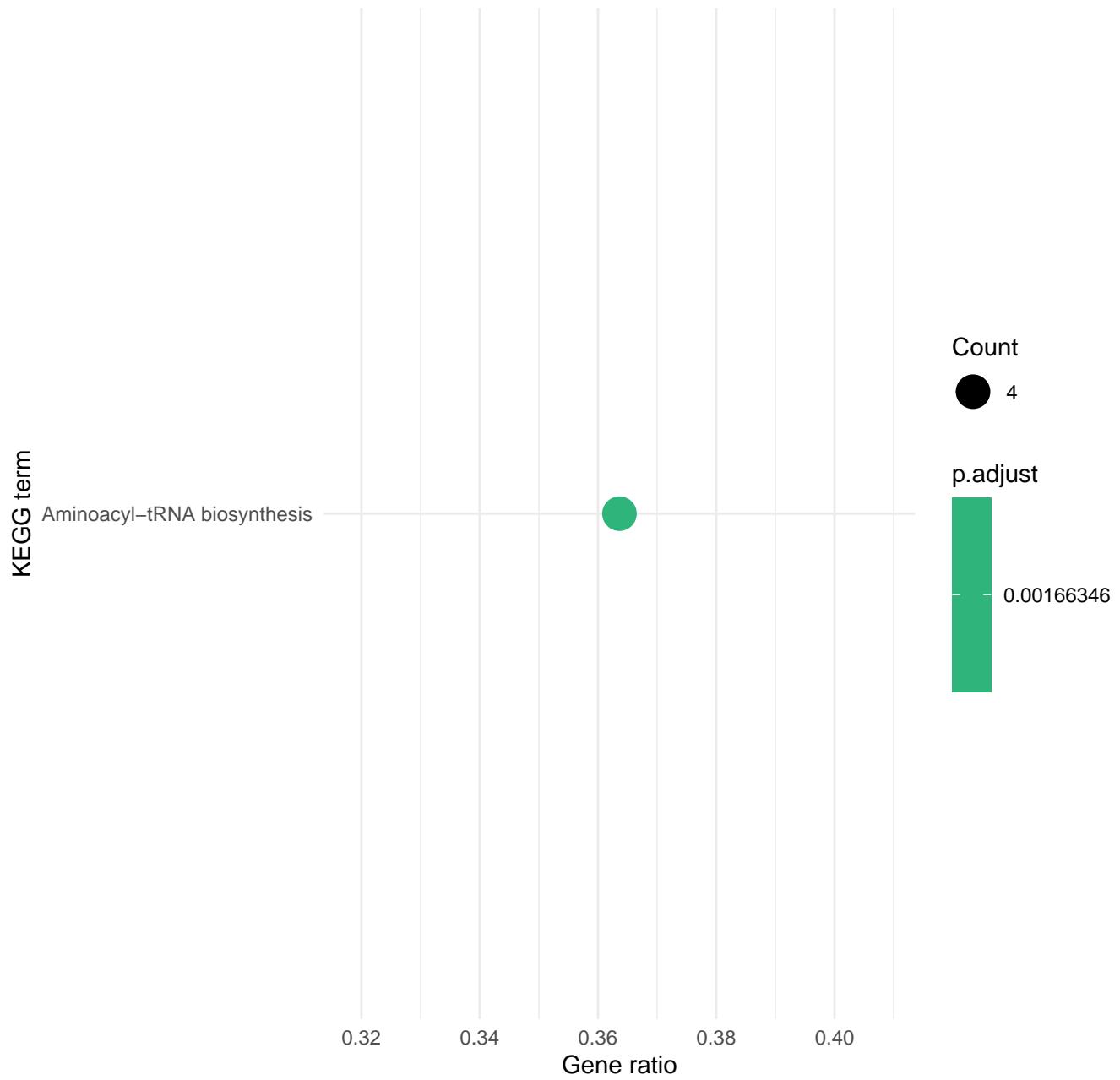
Protein processing in endoplasmic reticulum



NMD2-TAP Up-regulated KEGG barplot



NMD2-TAP Up-regulated KEGG dotplot



NMD2-TAP Up-regulated KEGG dotplot

size



4

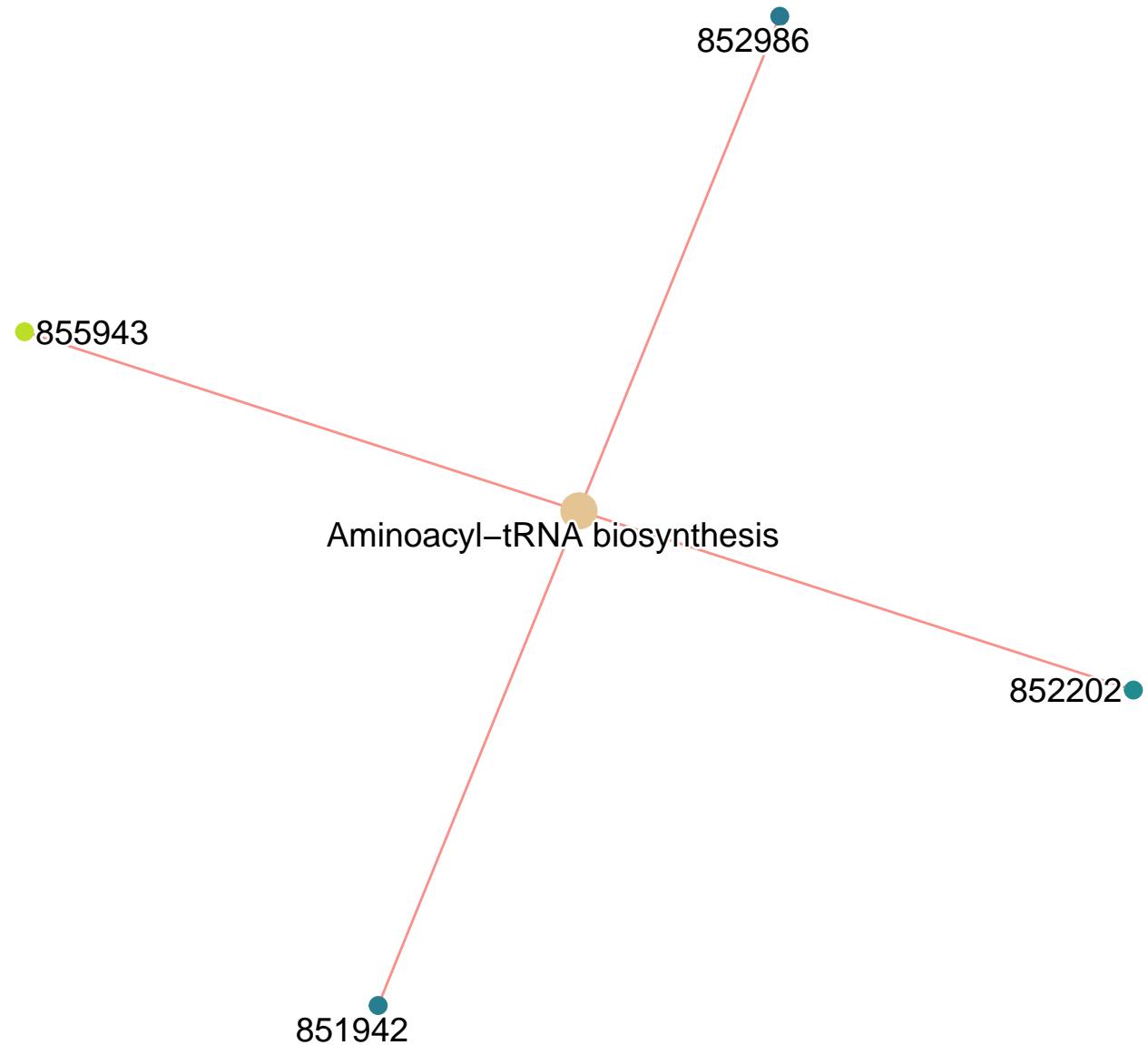
category

Aminoacyl-tRNA biosynthesis

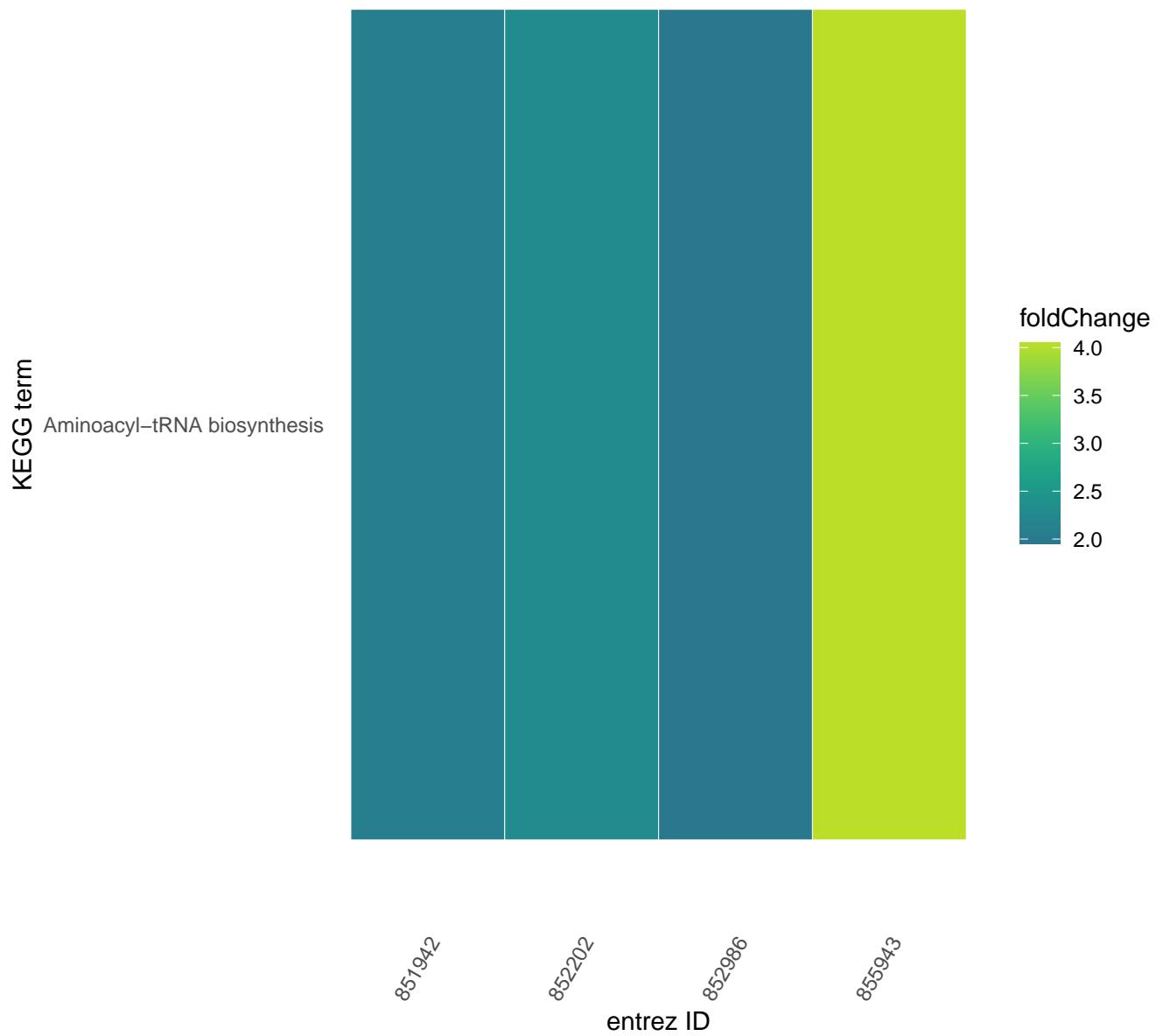
FoldChange



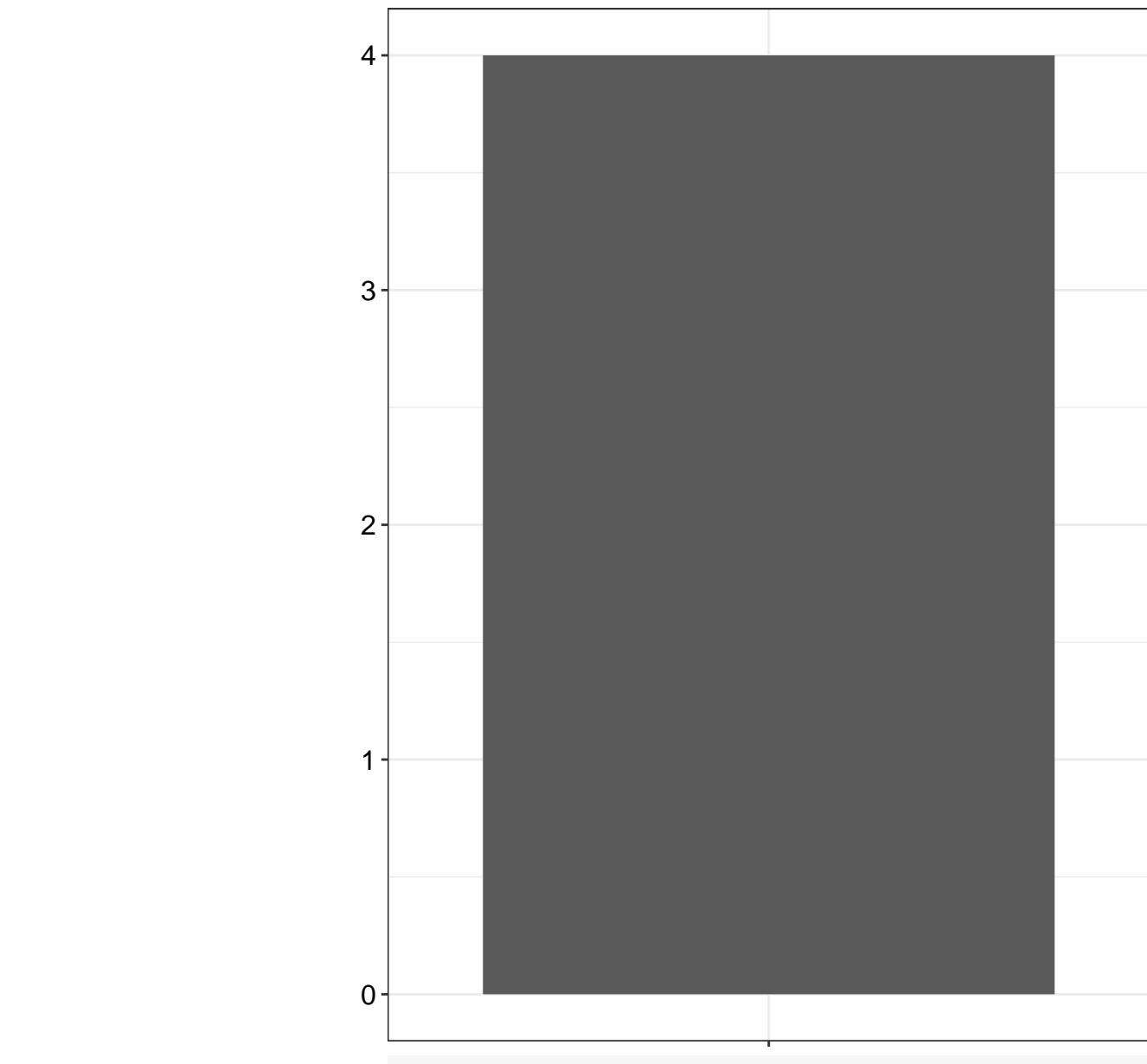
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NMD2-TAP Up-regulated KEGG heatplot



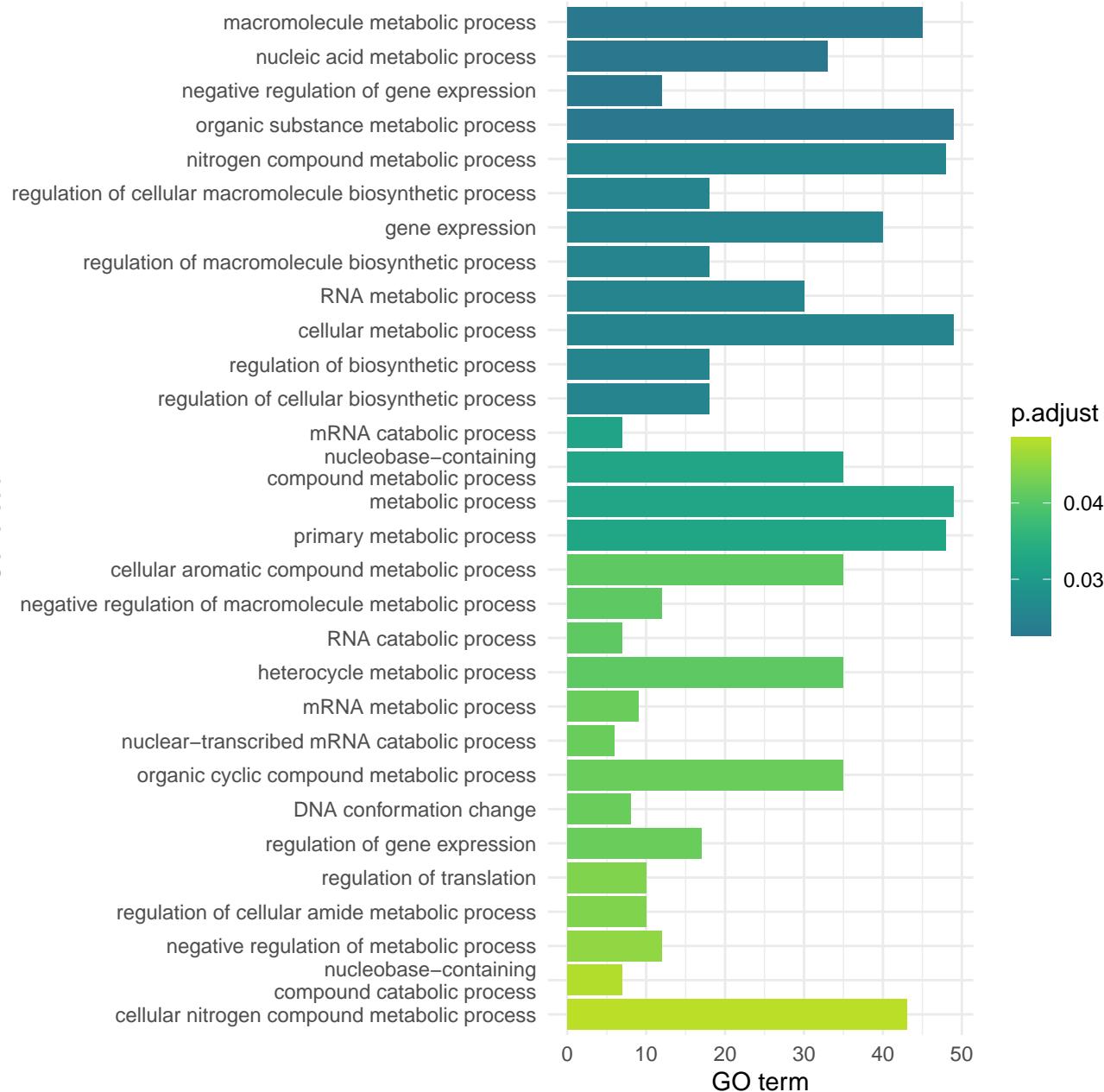
NMD2-TAP Up-regulated KEGG upsetplot



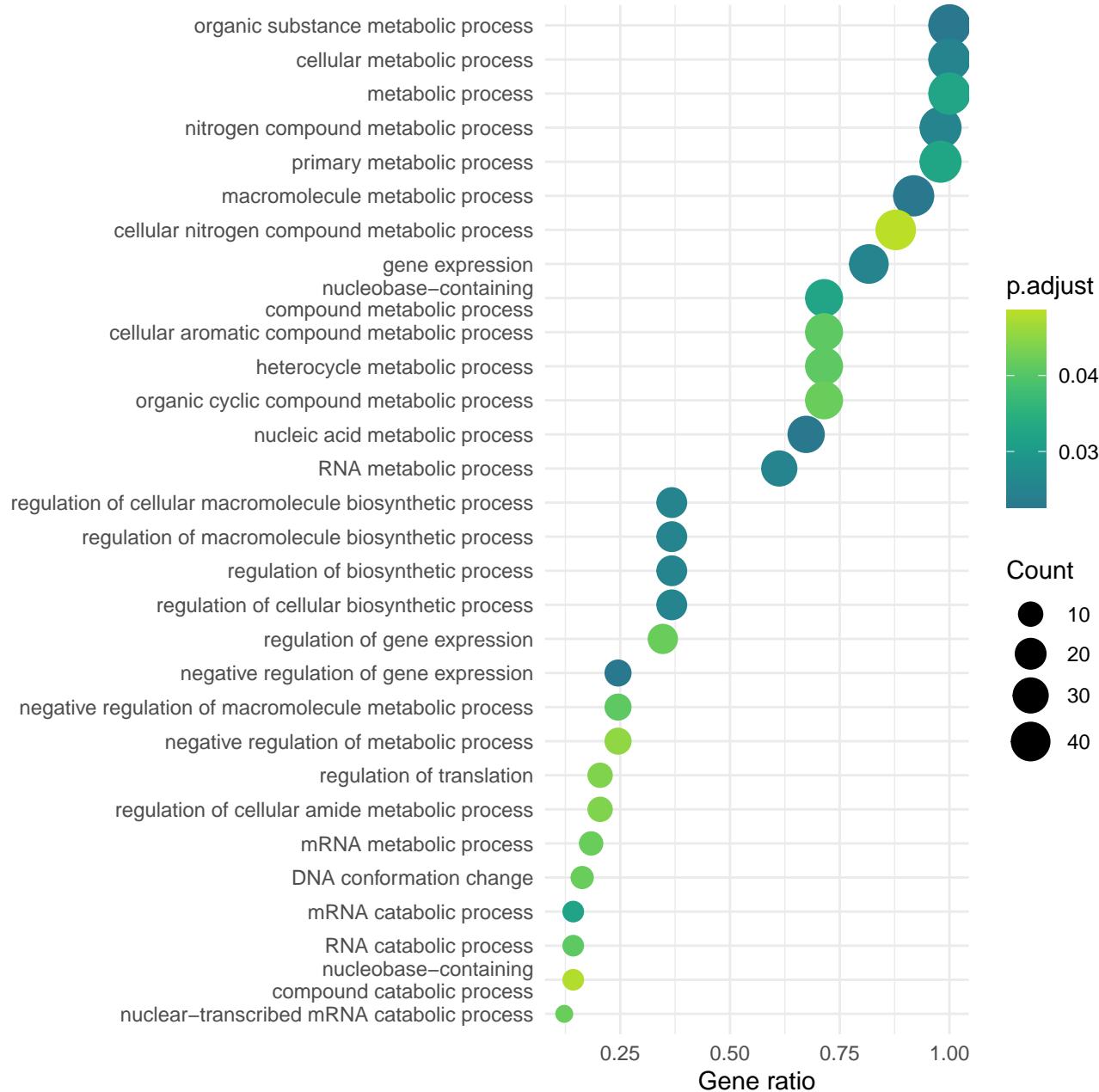
Aminoacyl-tRNA biosynthesis

●

TIF4631-TAP Up-regulated GO BP barplot



TIF4631-TAP Up-regulated GO BP dotplot



TIF4631-TAP Up-regulated GO BP cnetplot

metabolic process — macromolecule metabolic process

— metabolic process

metabolic process — mRNA catabolic process

mRNA metabolic process

— negative regulation of gene expression

negative regulation of macromolecule metabolic process

— negative regulation of metabolic process

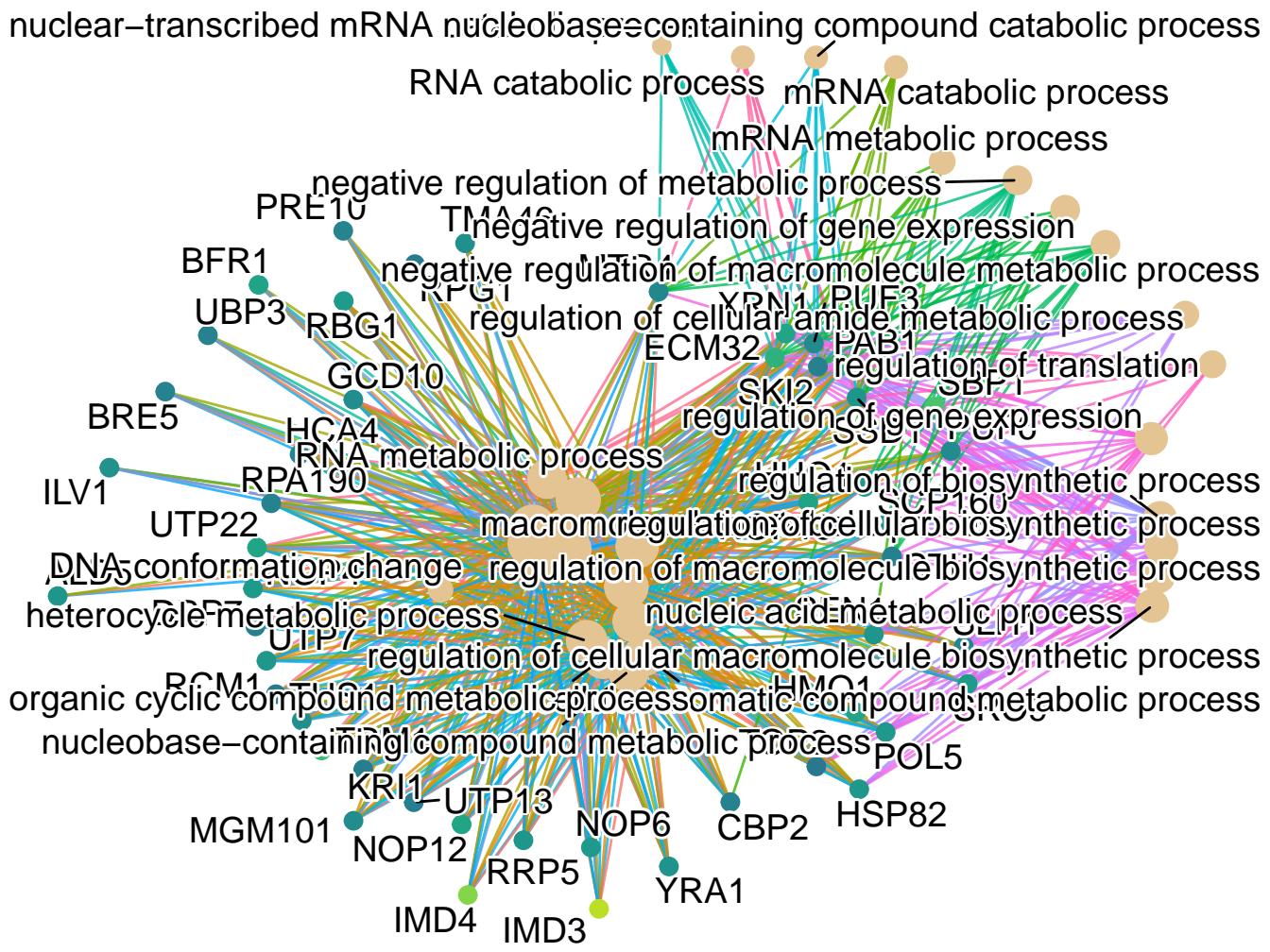
— nitrogen compound metabolic process

— nuclear-transcribed mRNA catabolic pathway

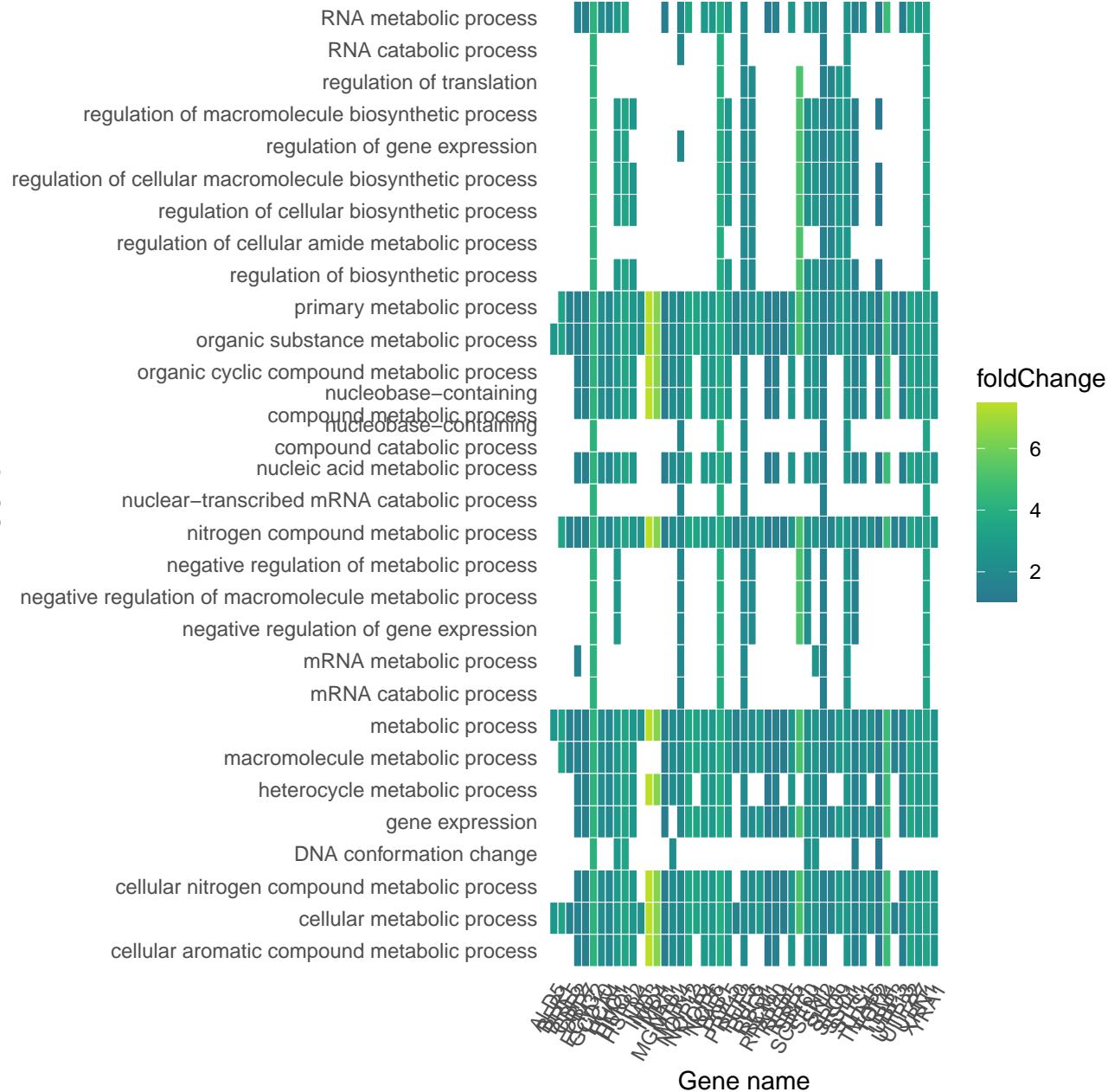
— nucleic acid metabolic process

— nucleobase-containing compound cat

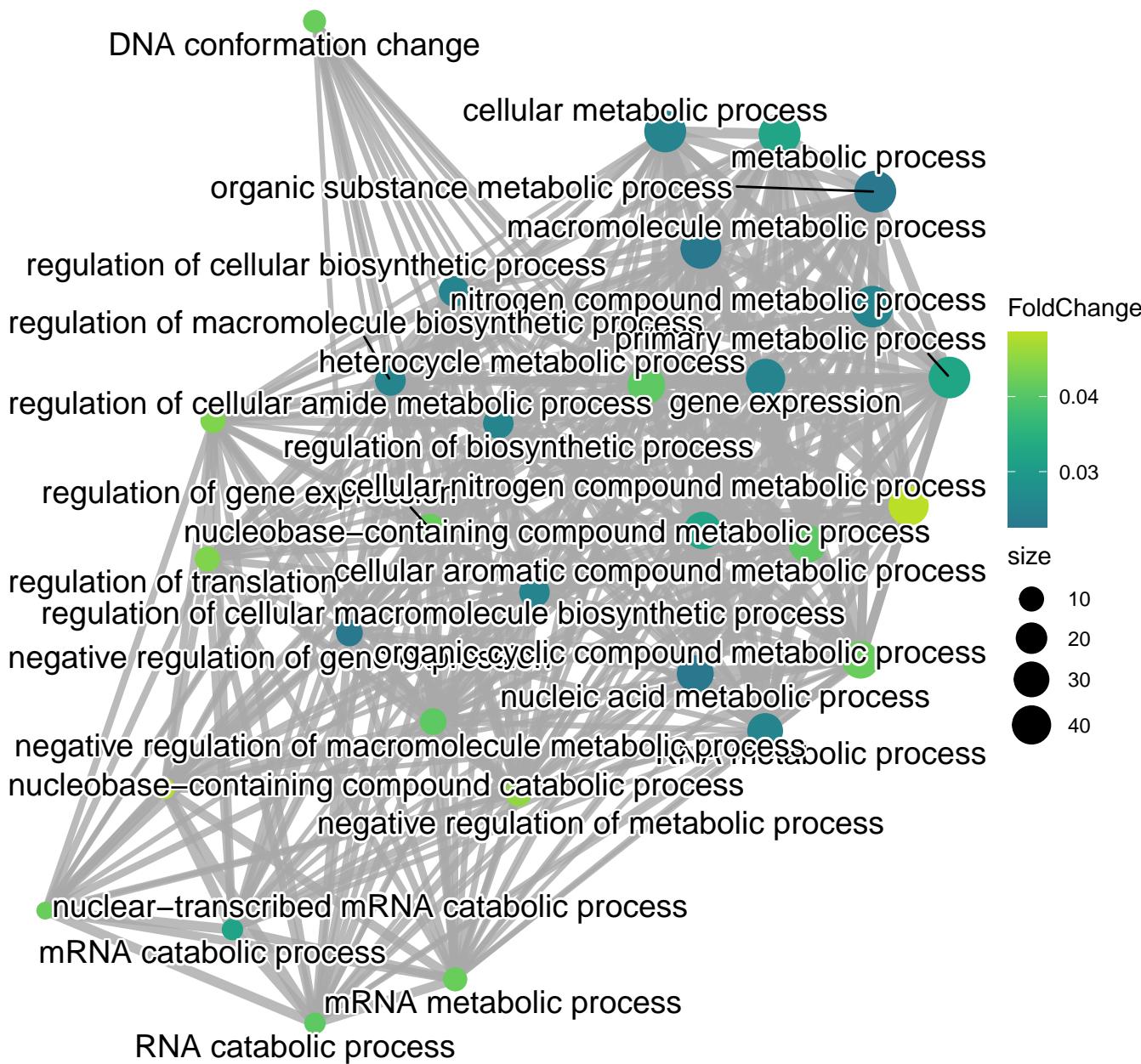
— nucleobase-containing compound me

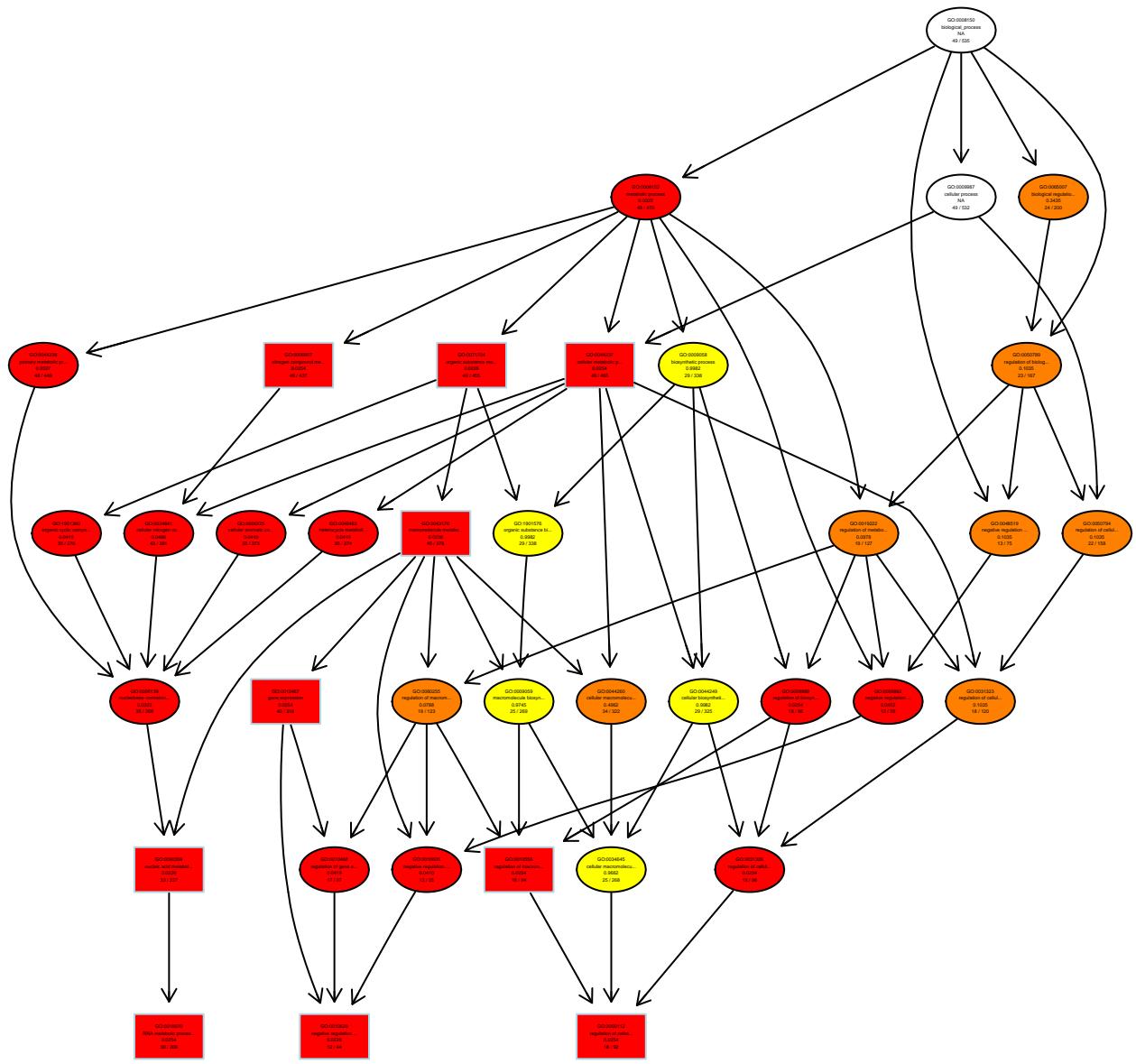


TIF4631-TAP Up-regulated GO BP heatplot

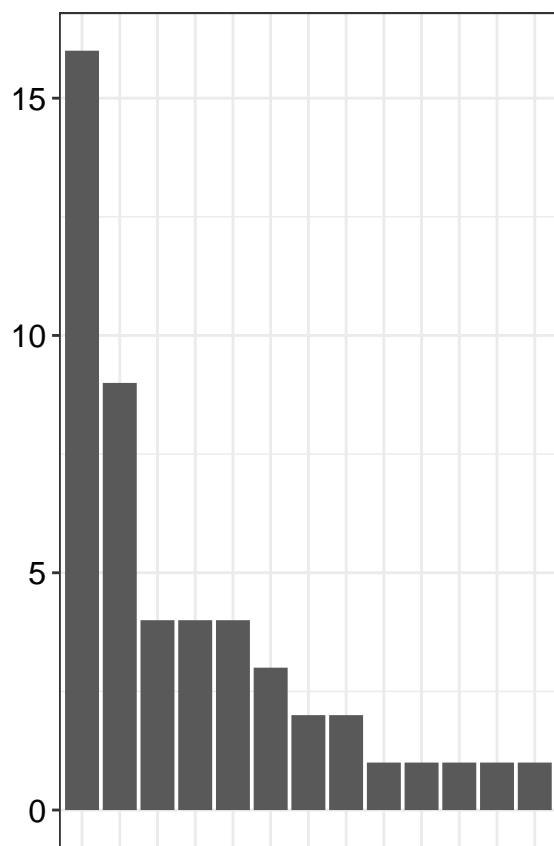


TIF4631-TAP Up-regulated GO BP emapplot





TIF4631–TAP Up-regulated GO Biological Processes



cellular metabolic process

organic substance metabolic process

nitrogen compound metabolic process

macromolecule metabolic process

gene expression

nucleic acid metabolic process

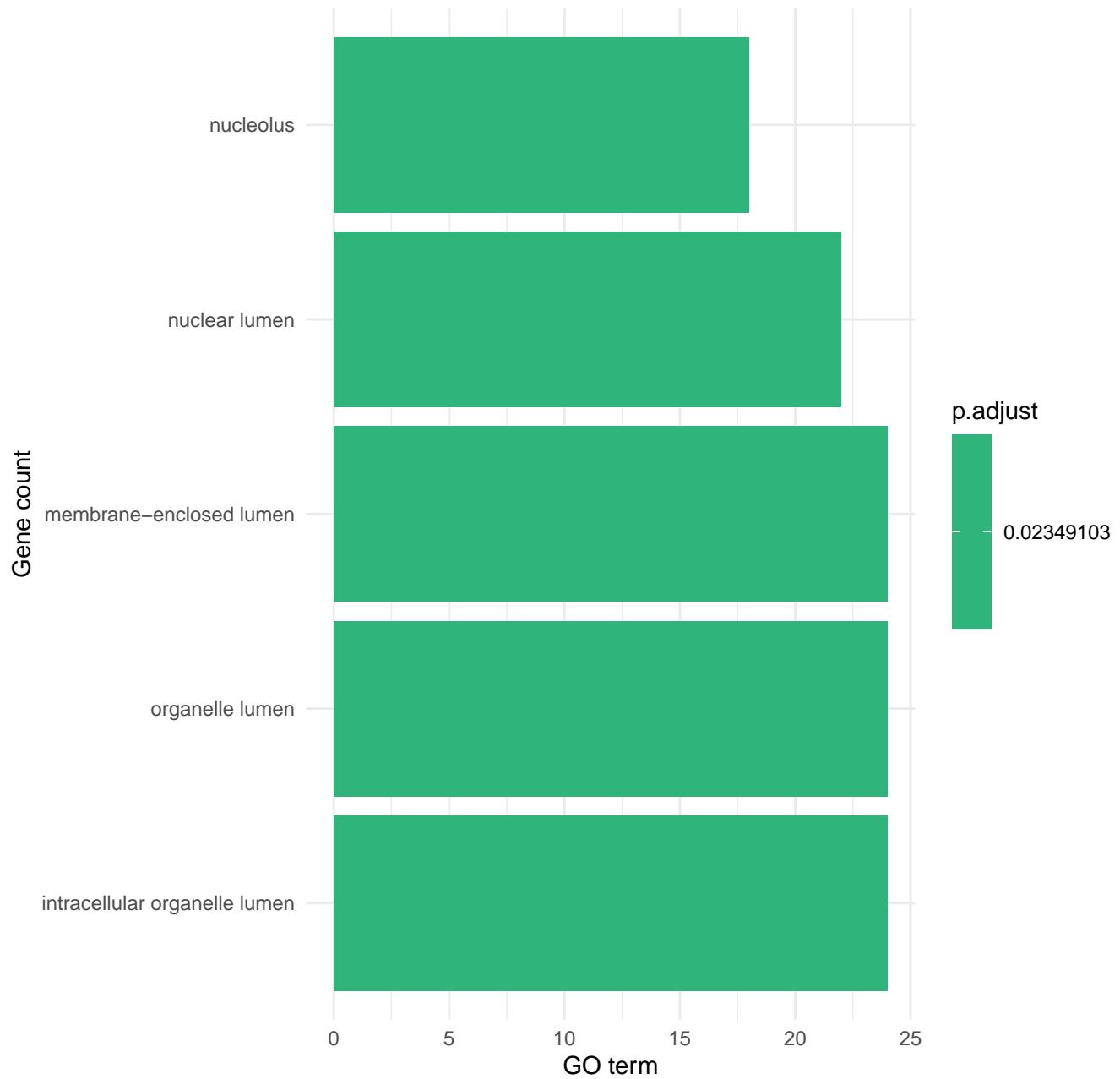
RNA metabolic process

regulation of cellular macromolecule biosynthetic process

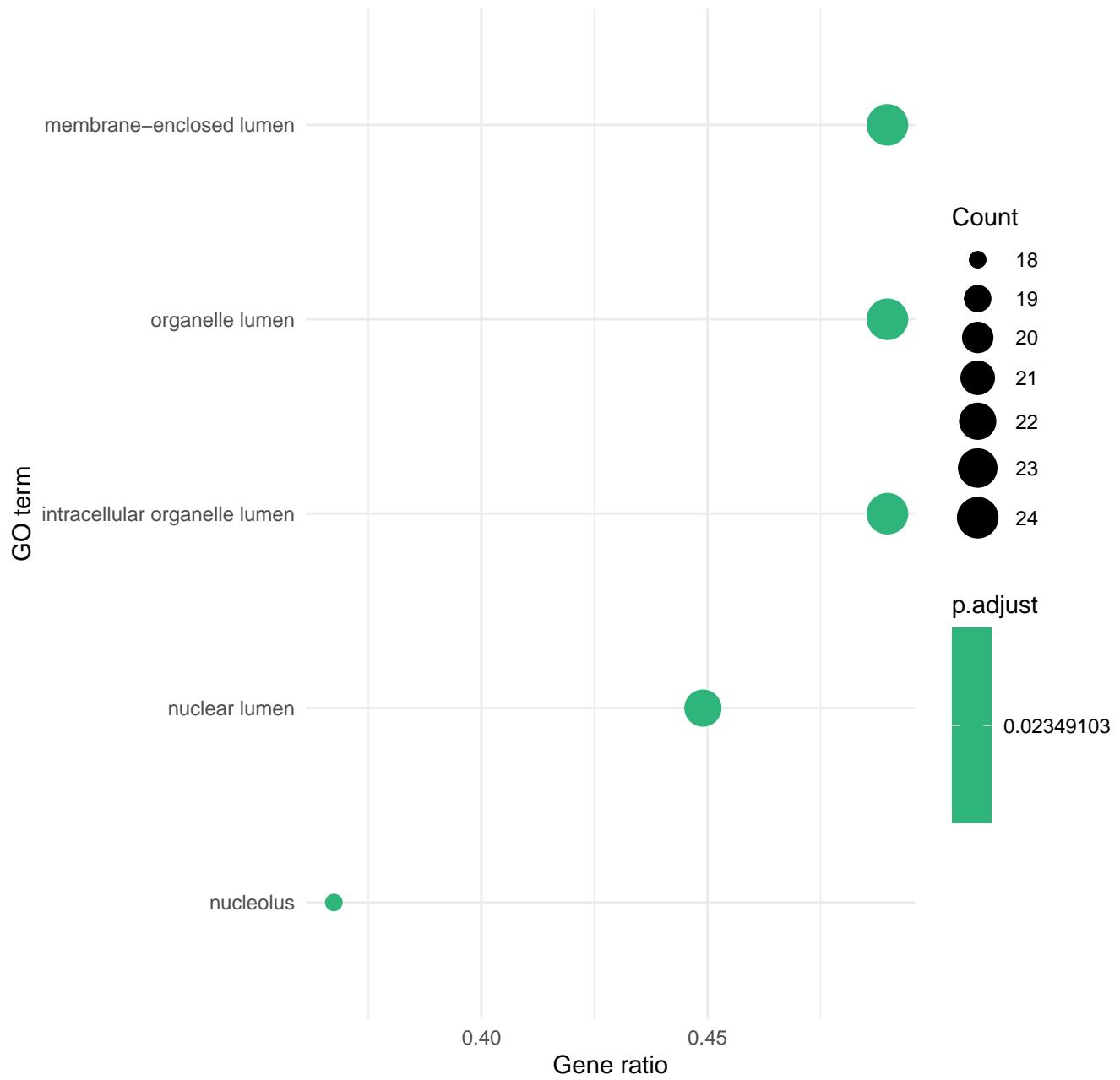
regulation of macromolecule biosynthetic process

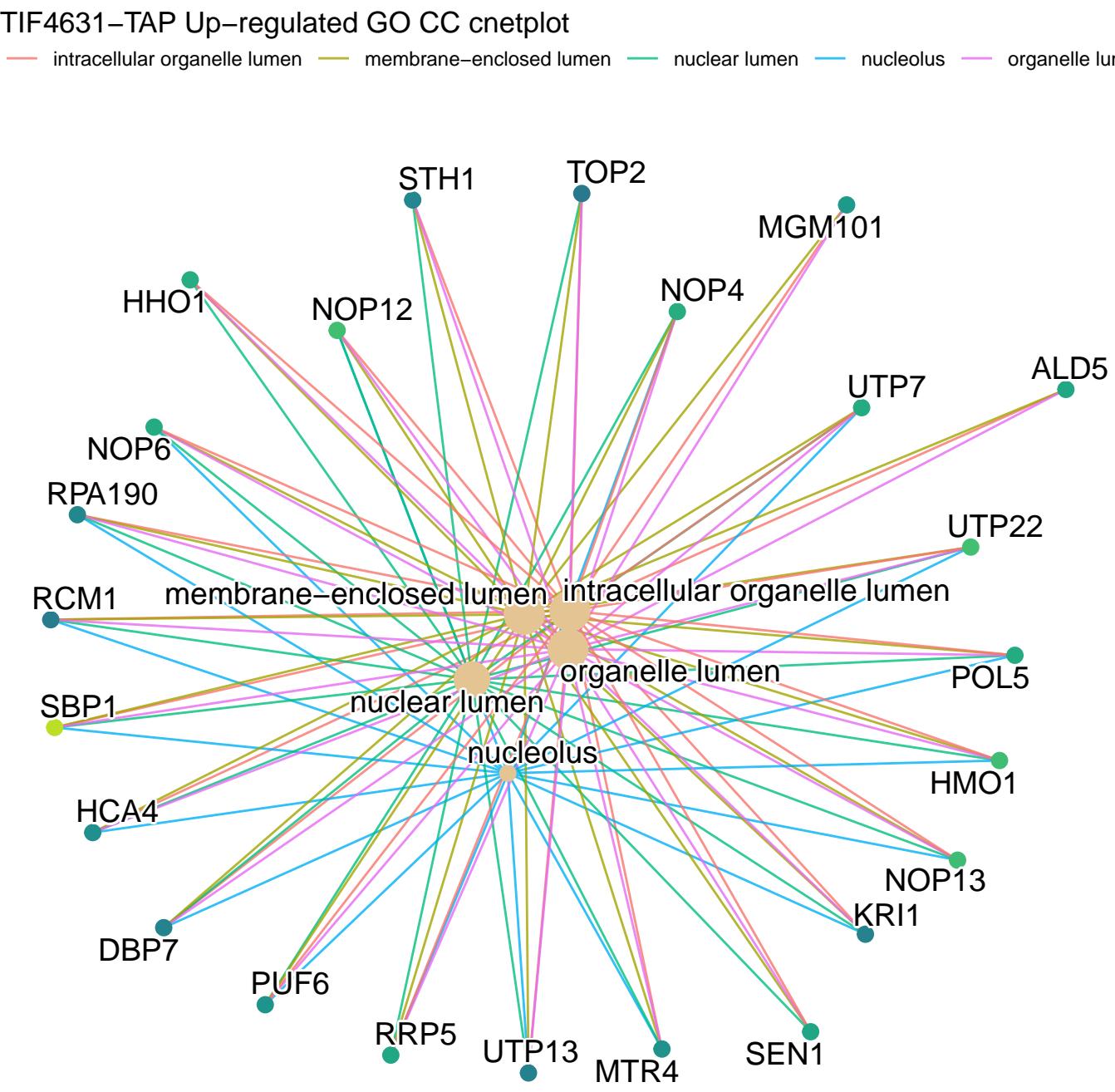
negative regulation of gene expression

TIF4631–TAP Up-regulated GO CC barplot

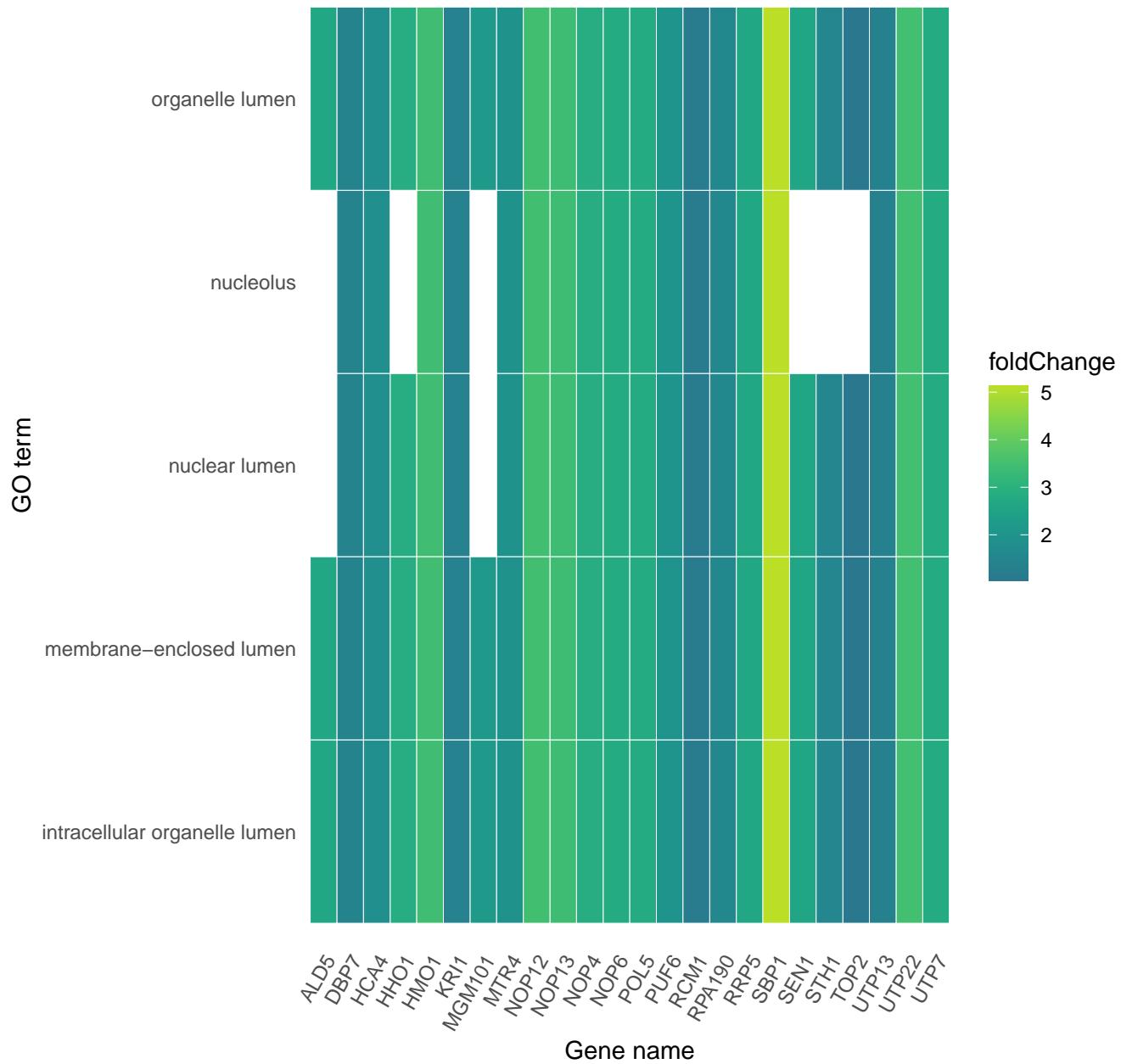


TIF4631-TAP Up-regulated GO CC dotplot

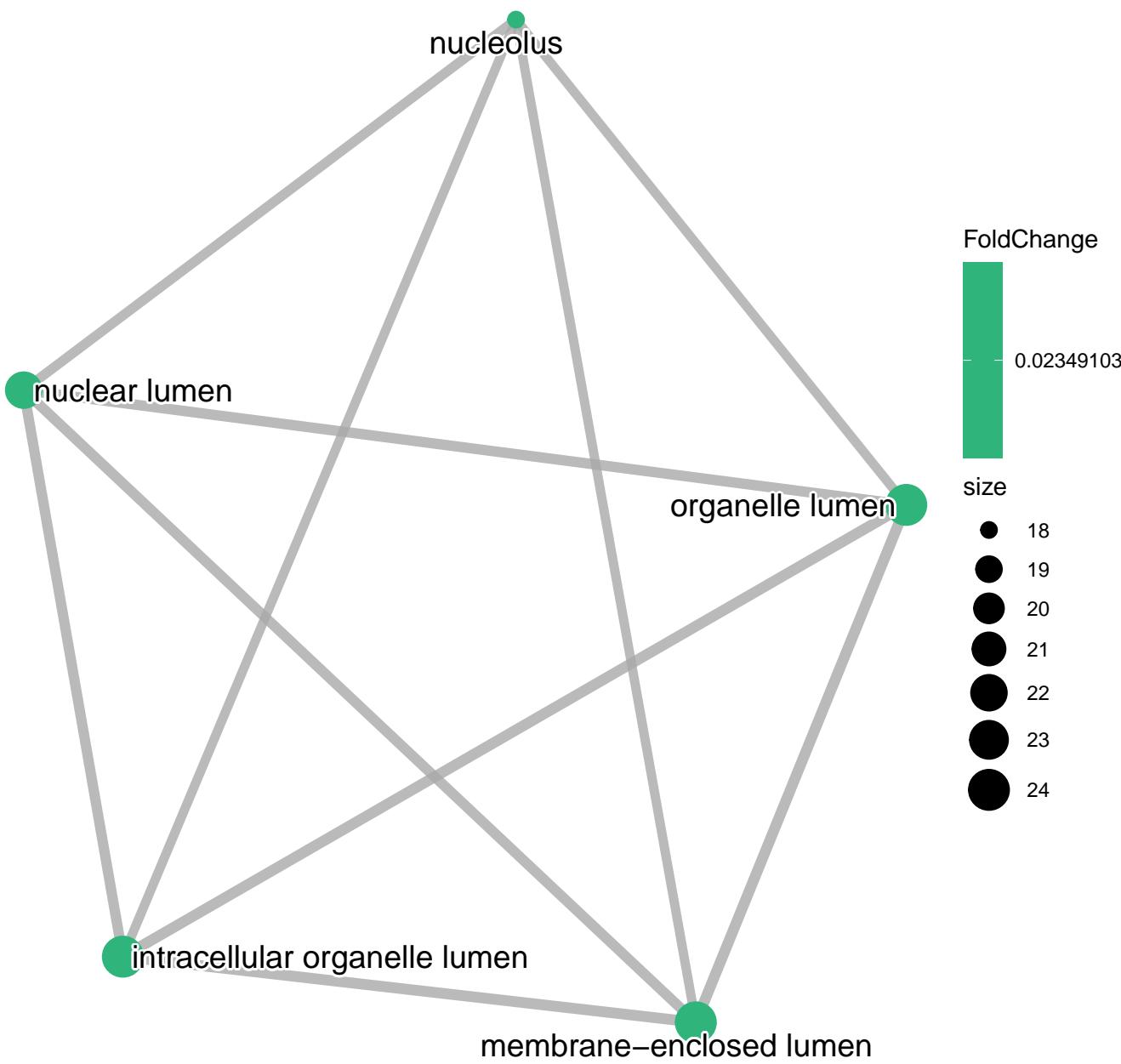


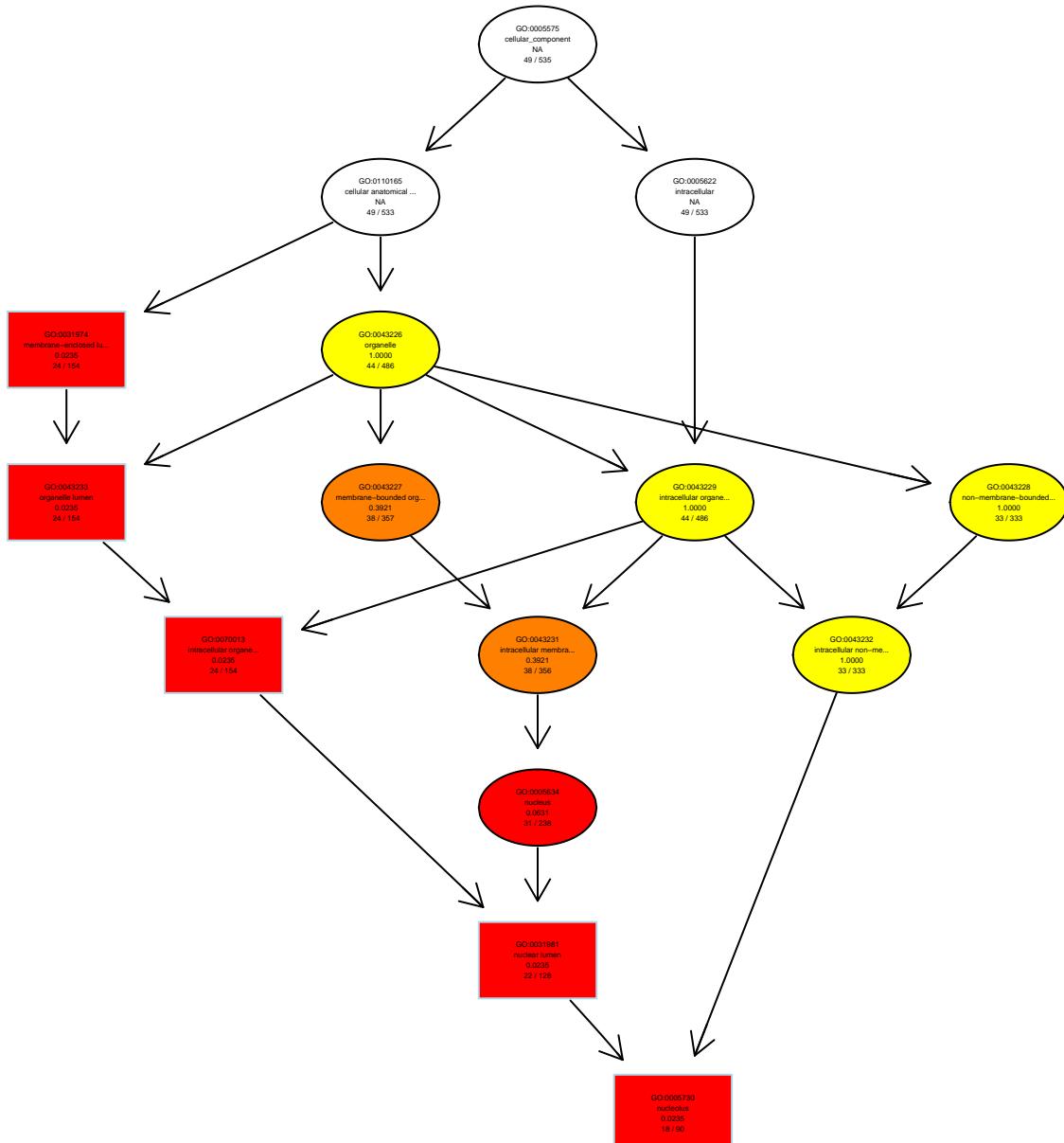


TIF4631-TAP Up-regulated GO CC heatplot

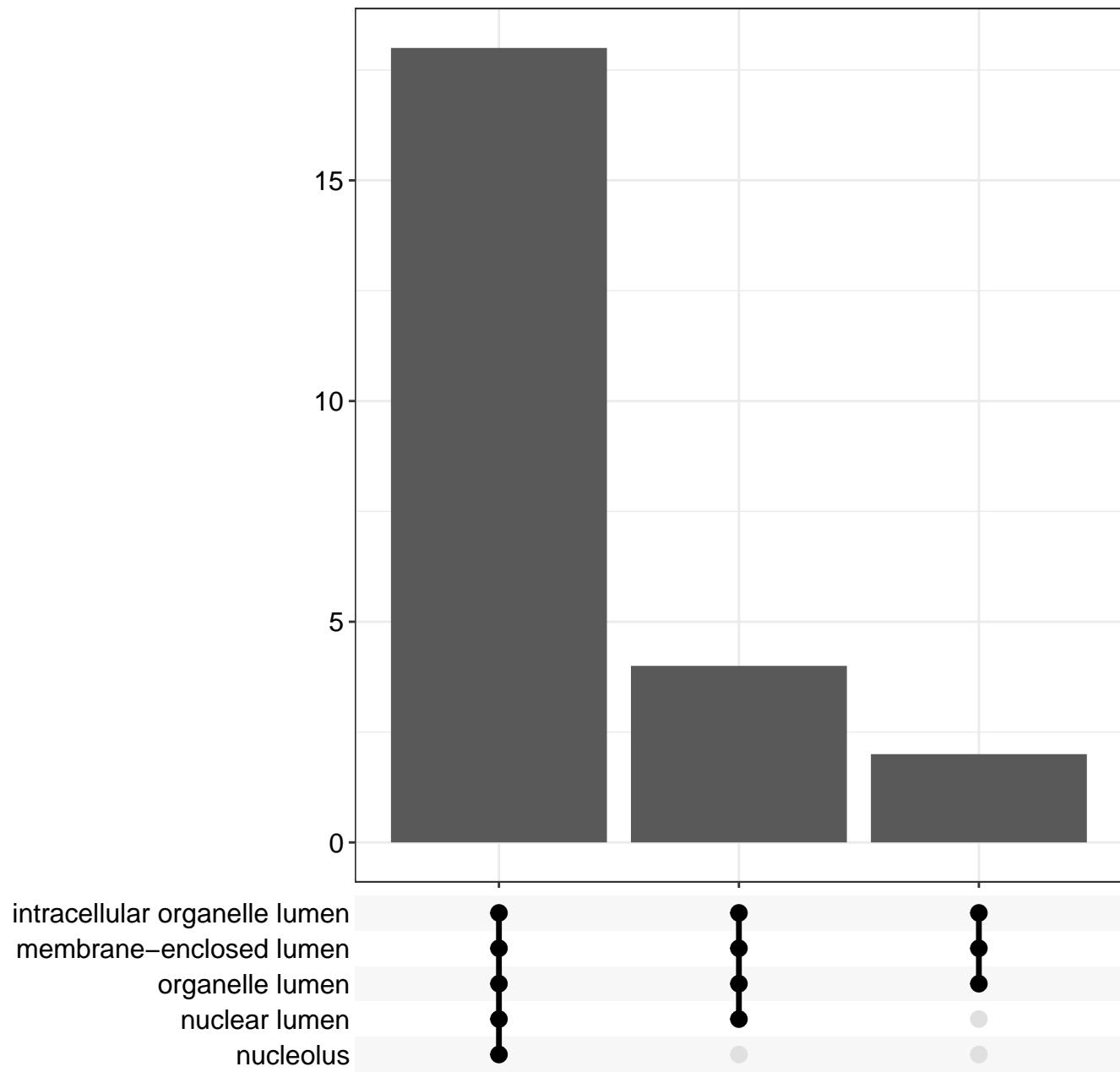


TIF4631-TAP Up-regulated GO CC emapplot

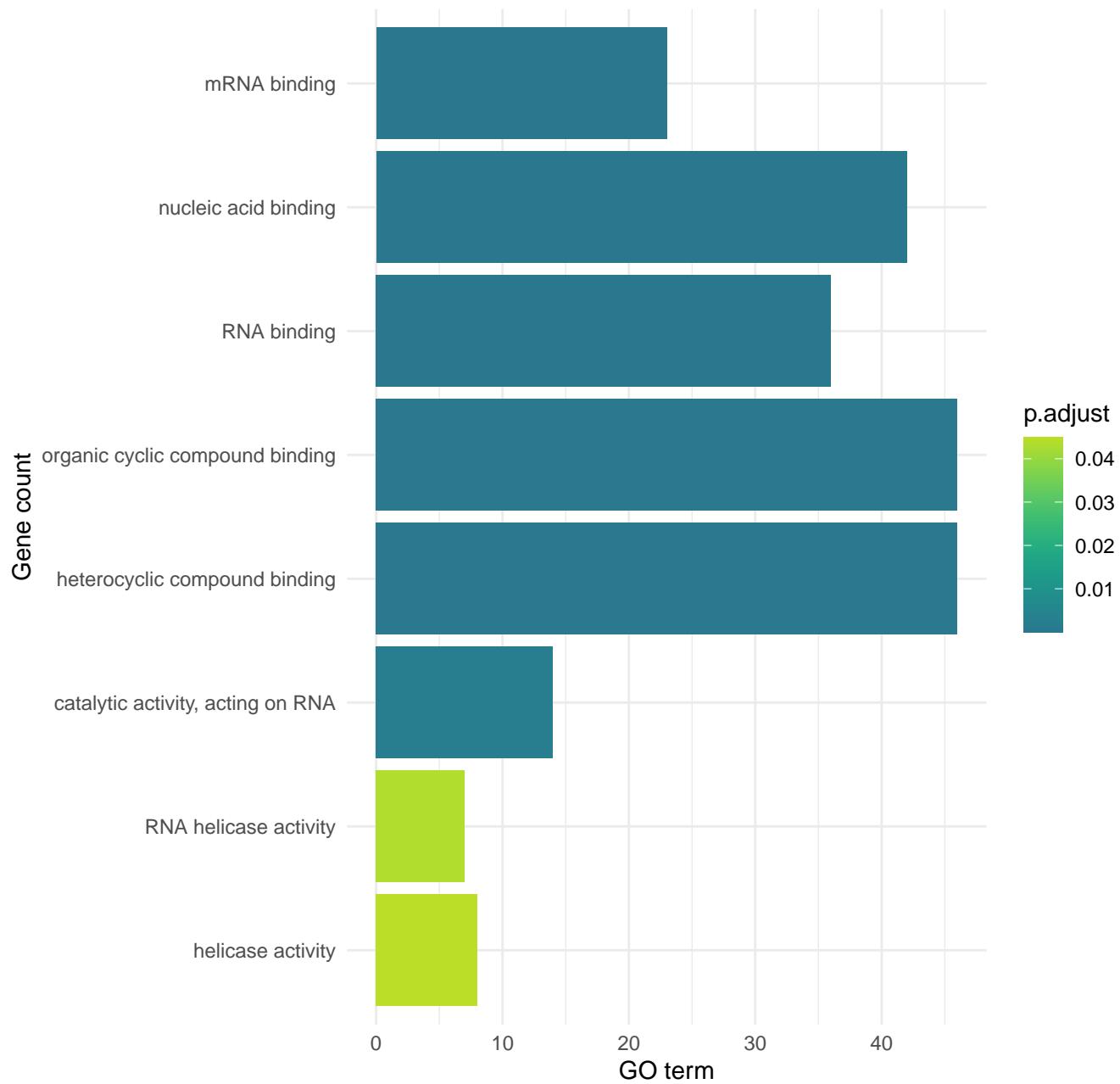




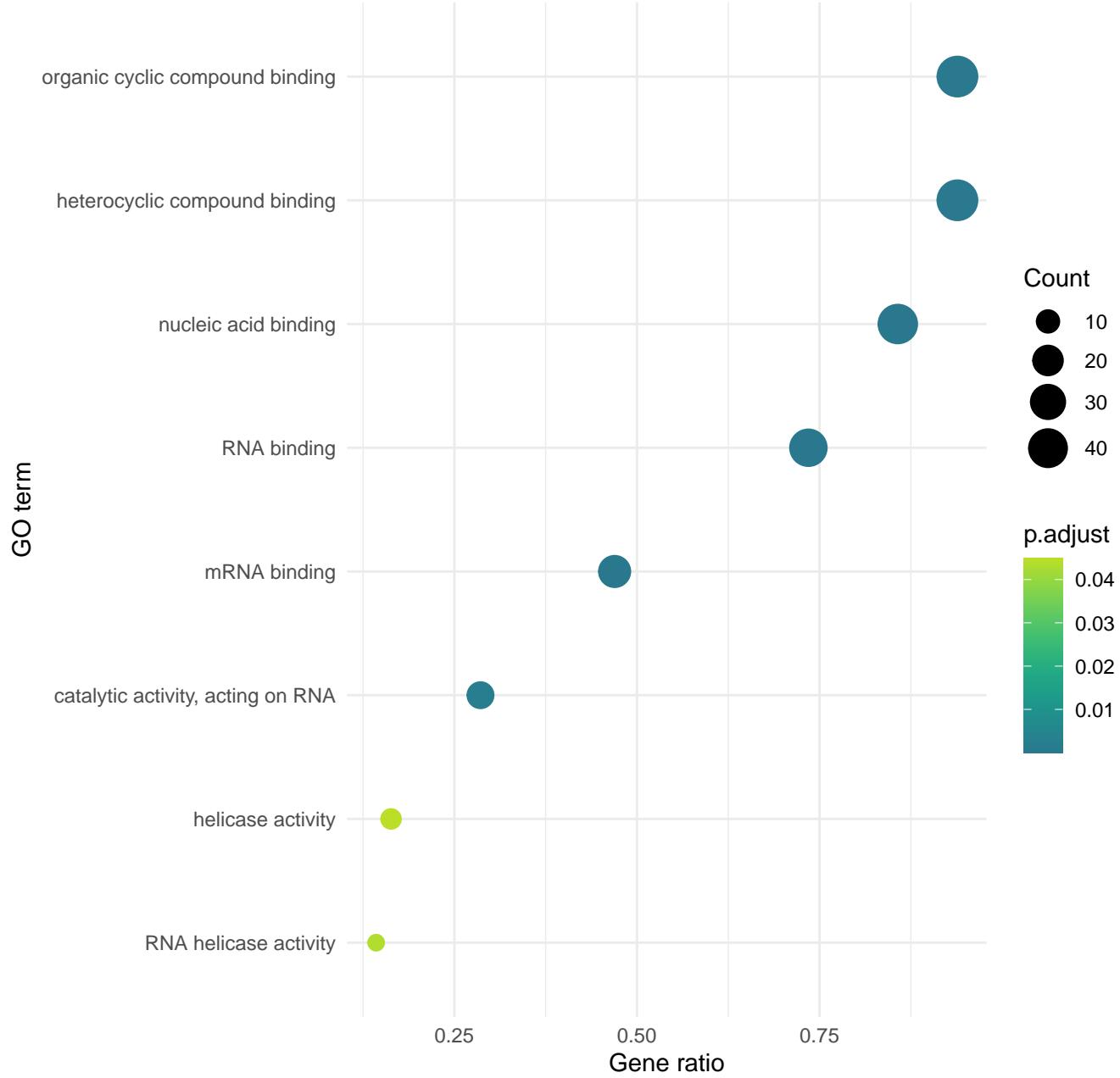
TIF4631-TAP Up-regulated GO CC upsetplot



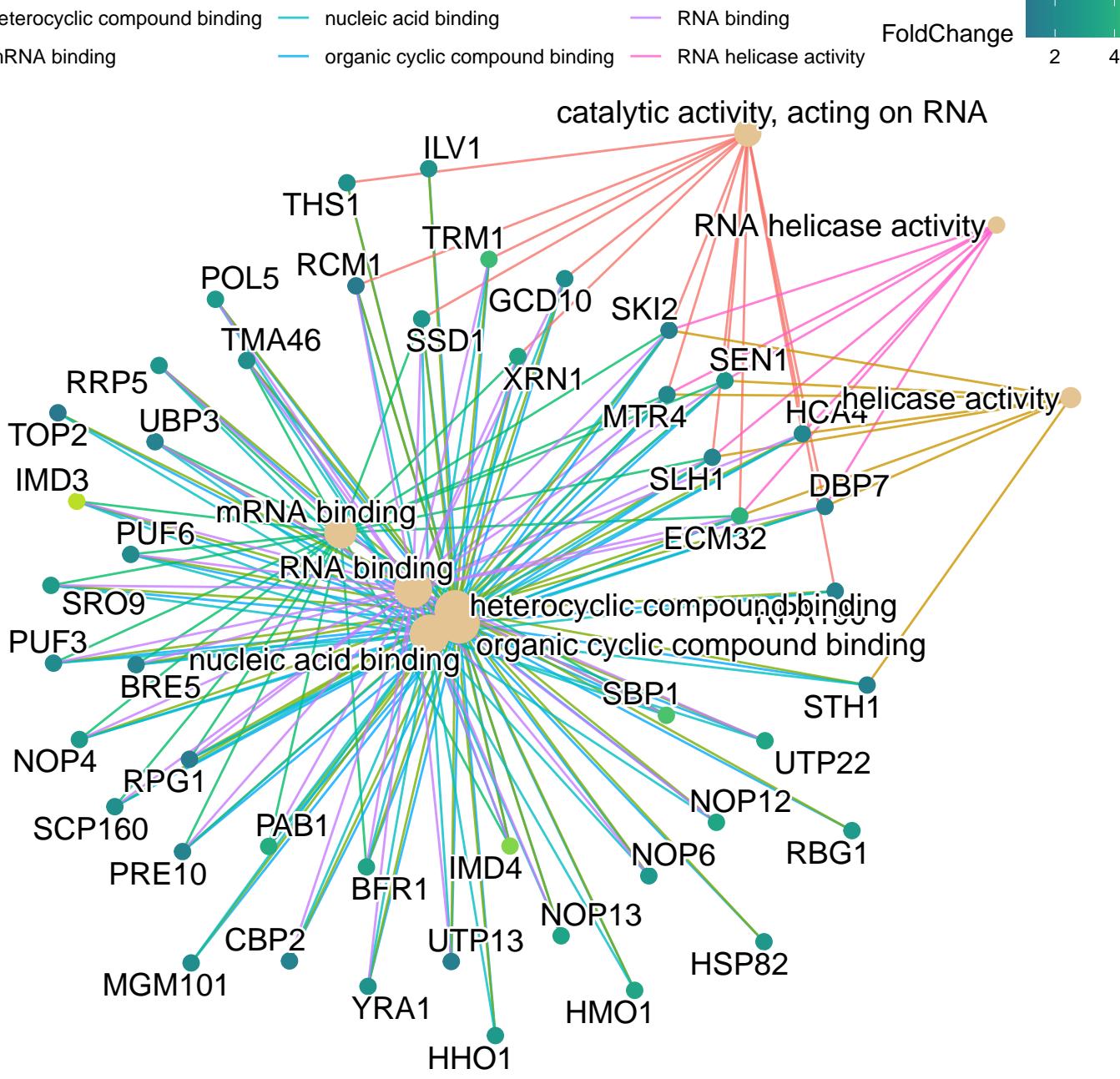
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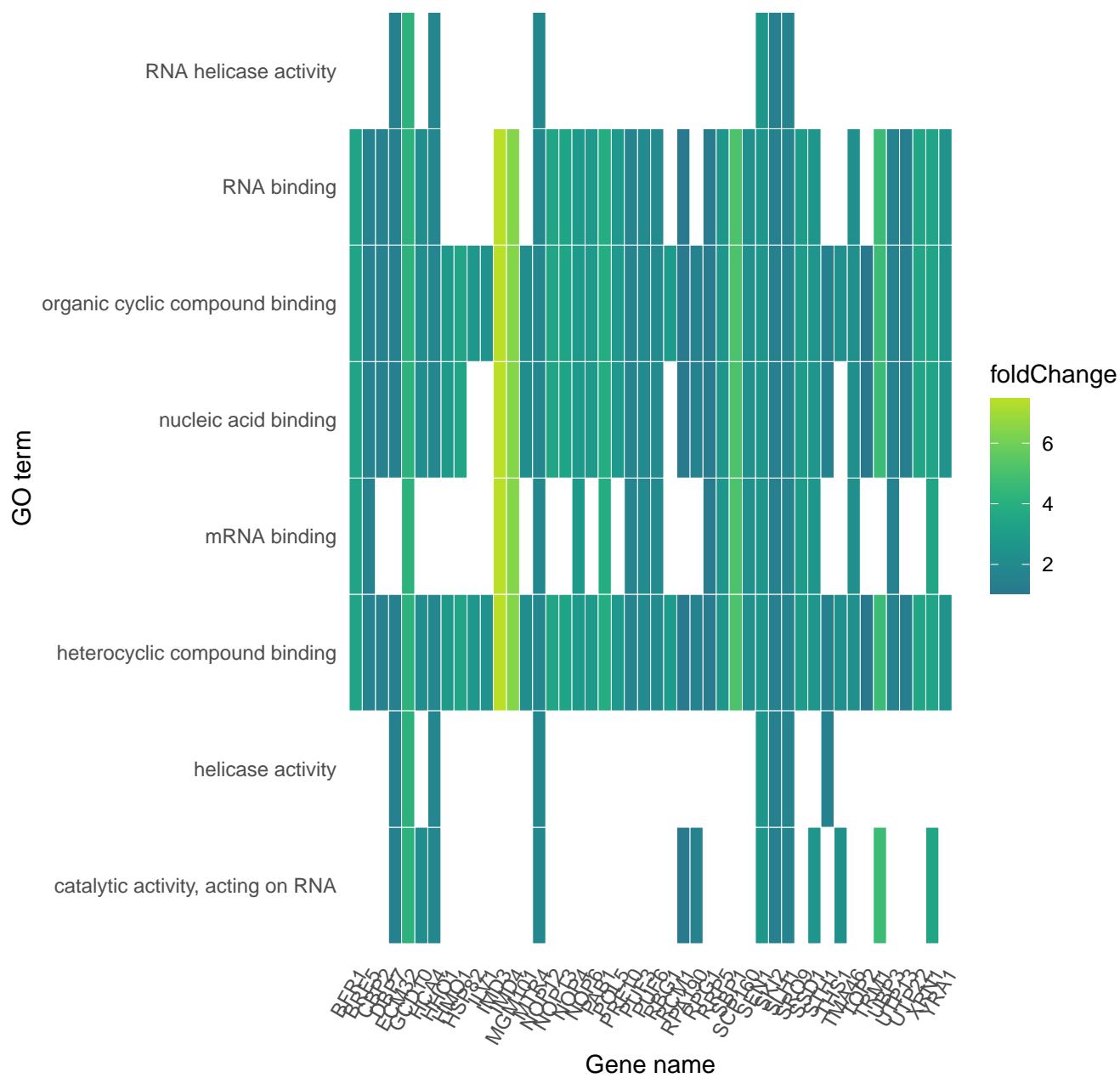
TIF4631-TAP Up-regulated GO MF dotplot



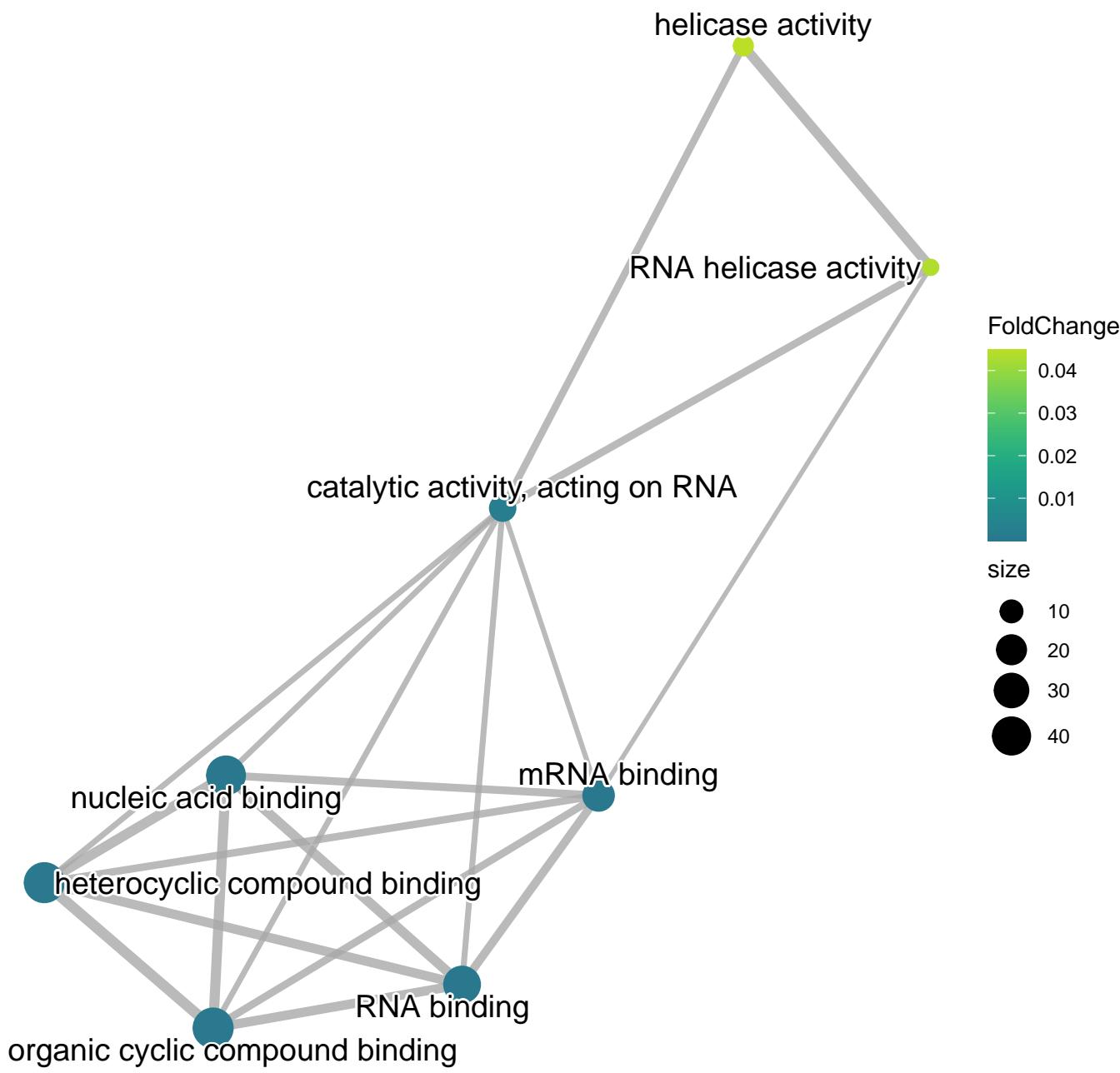
TIF4631-TAP Up-regulated GO MF cnetplot

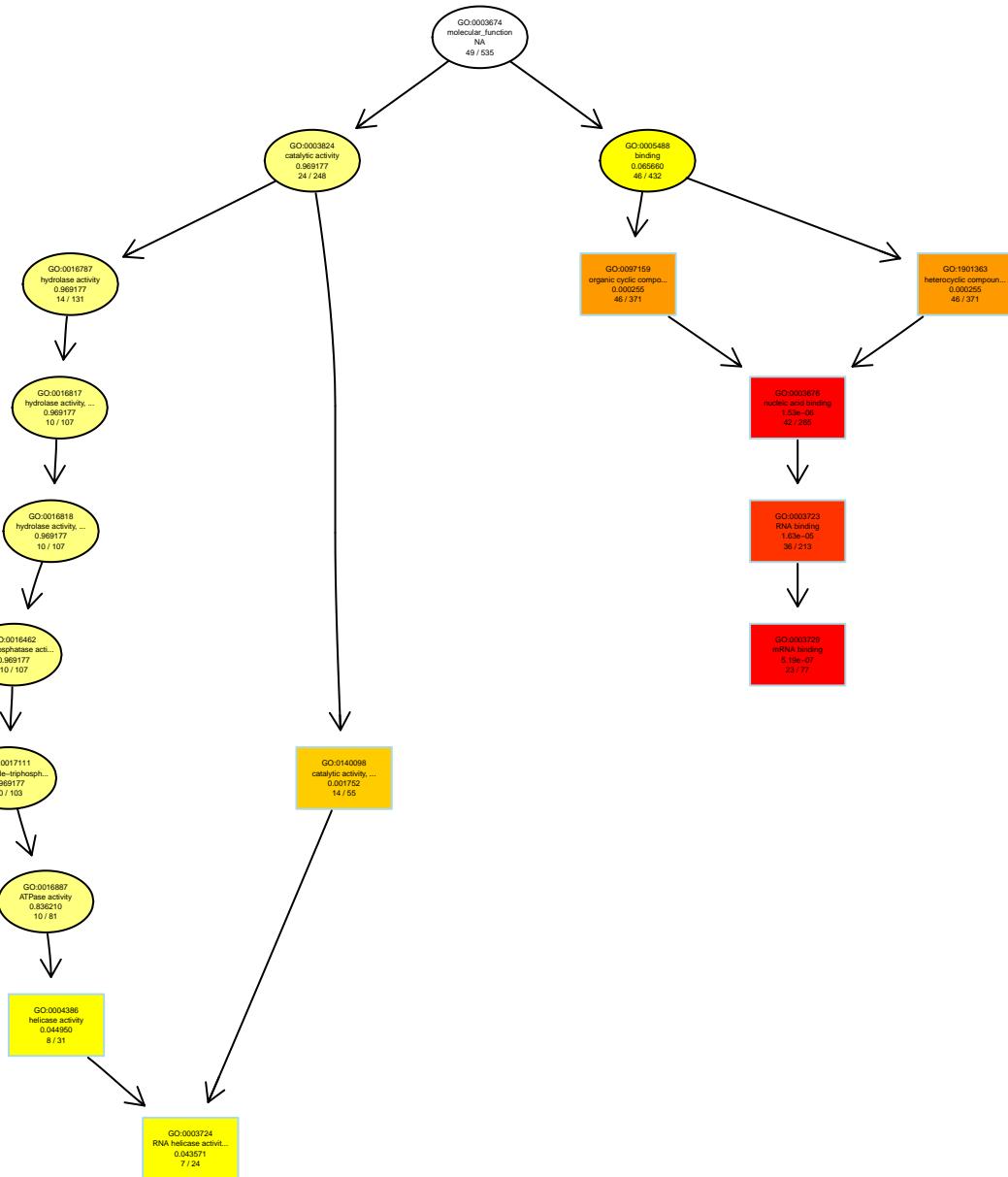


TIF4631-TAP Up-regulated GO MF heatplot

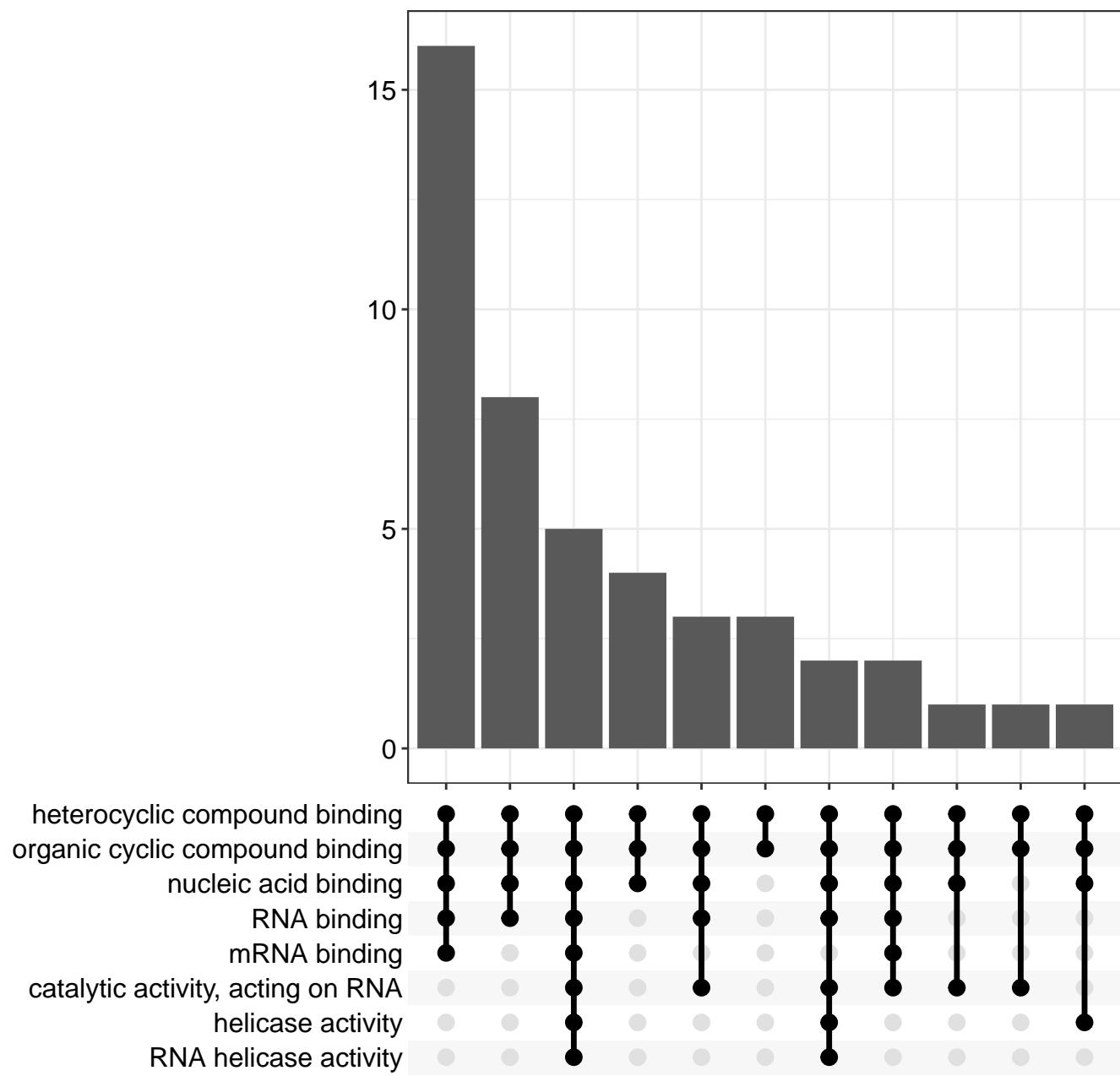


TIF4631-TAP Up-regulated GO MF emapplot

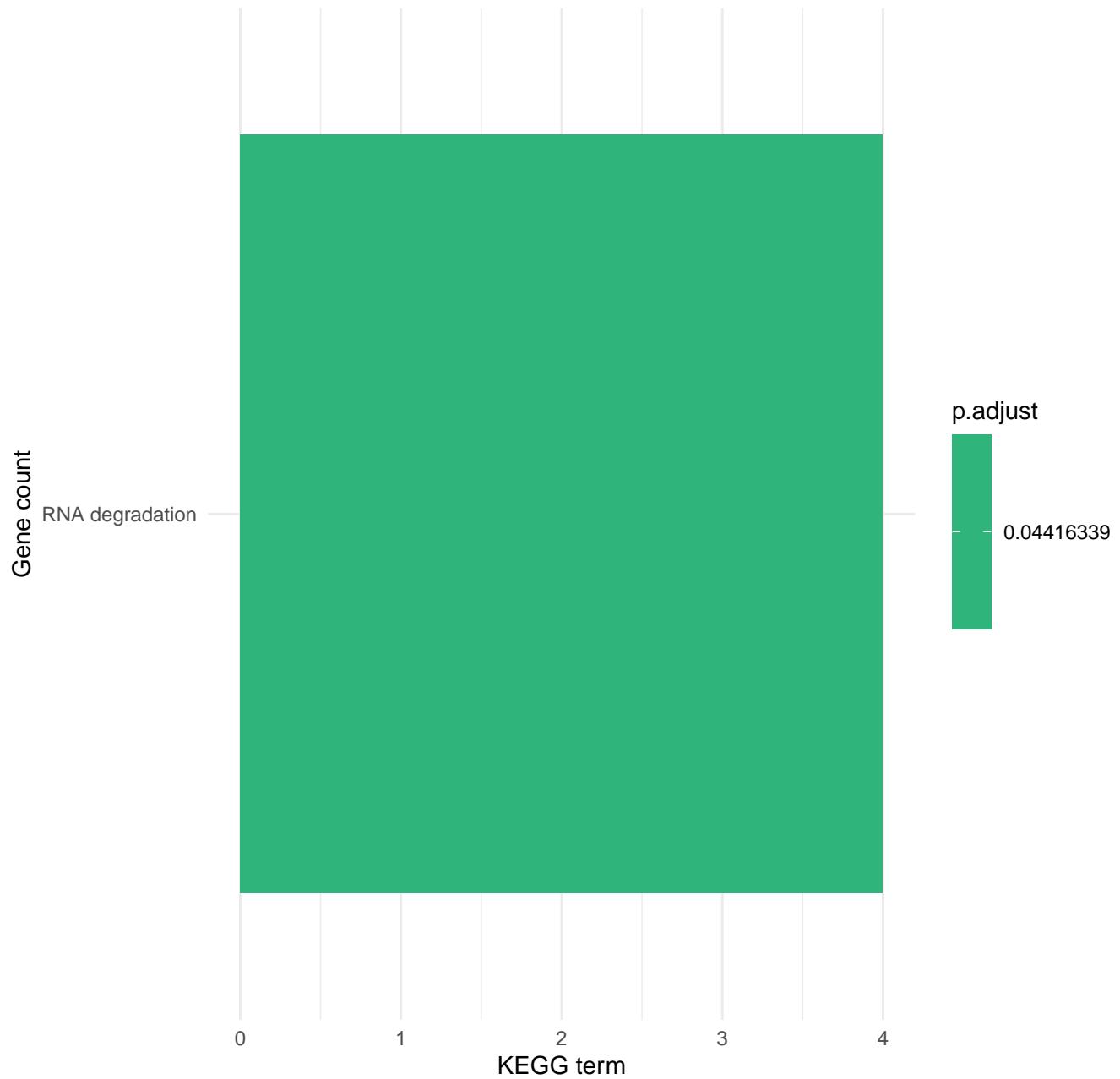




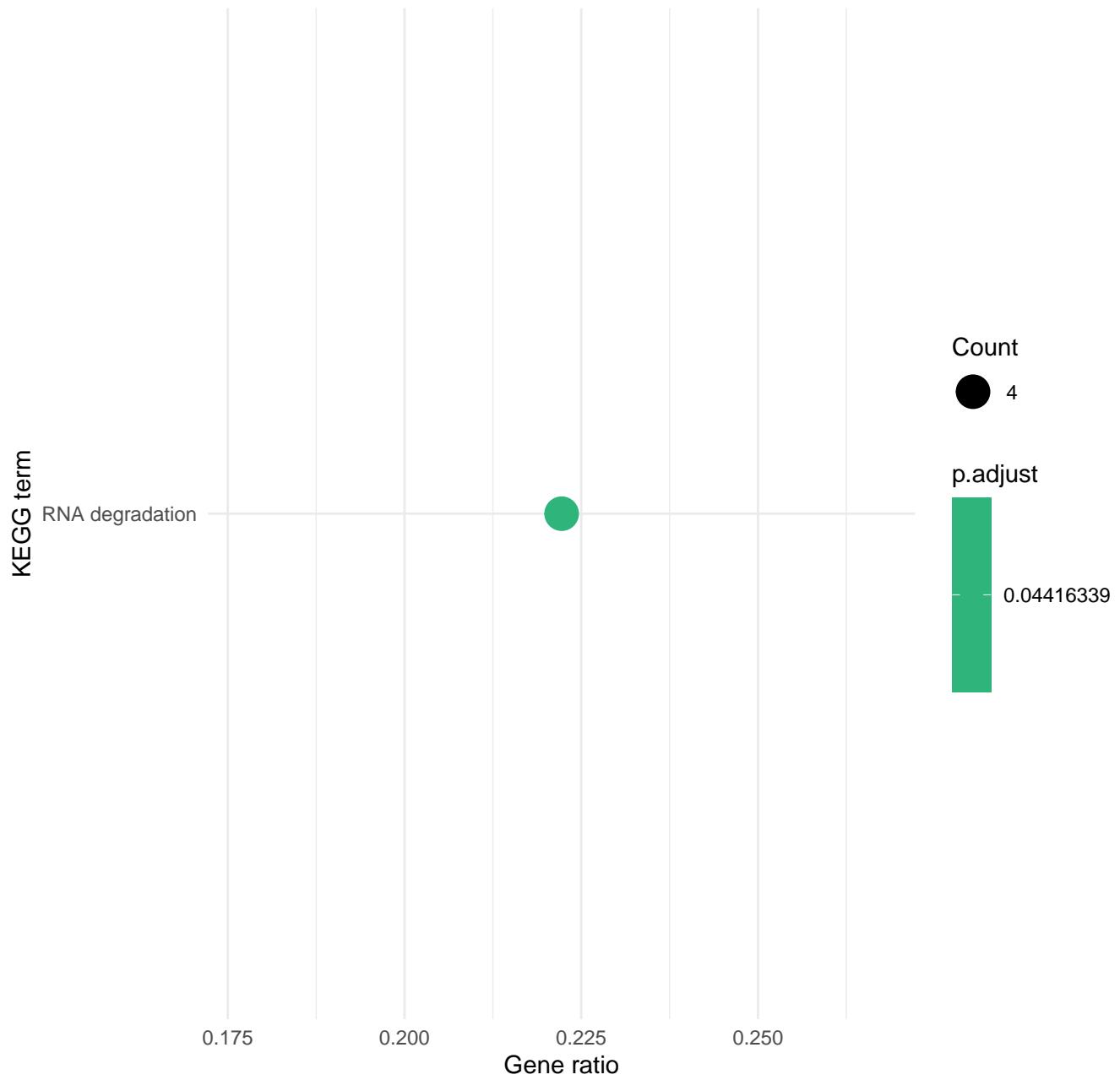
TIF4631-TAP Up-regulated GO MF upsetplot



TIF4631–TAP Up-regulated KEGG barplot



TIF4631–TAP Up-regulated KEGG dotplot



TIF4631-TAP Up-regulated KEGG dotplot

category

RNA degradation

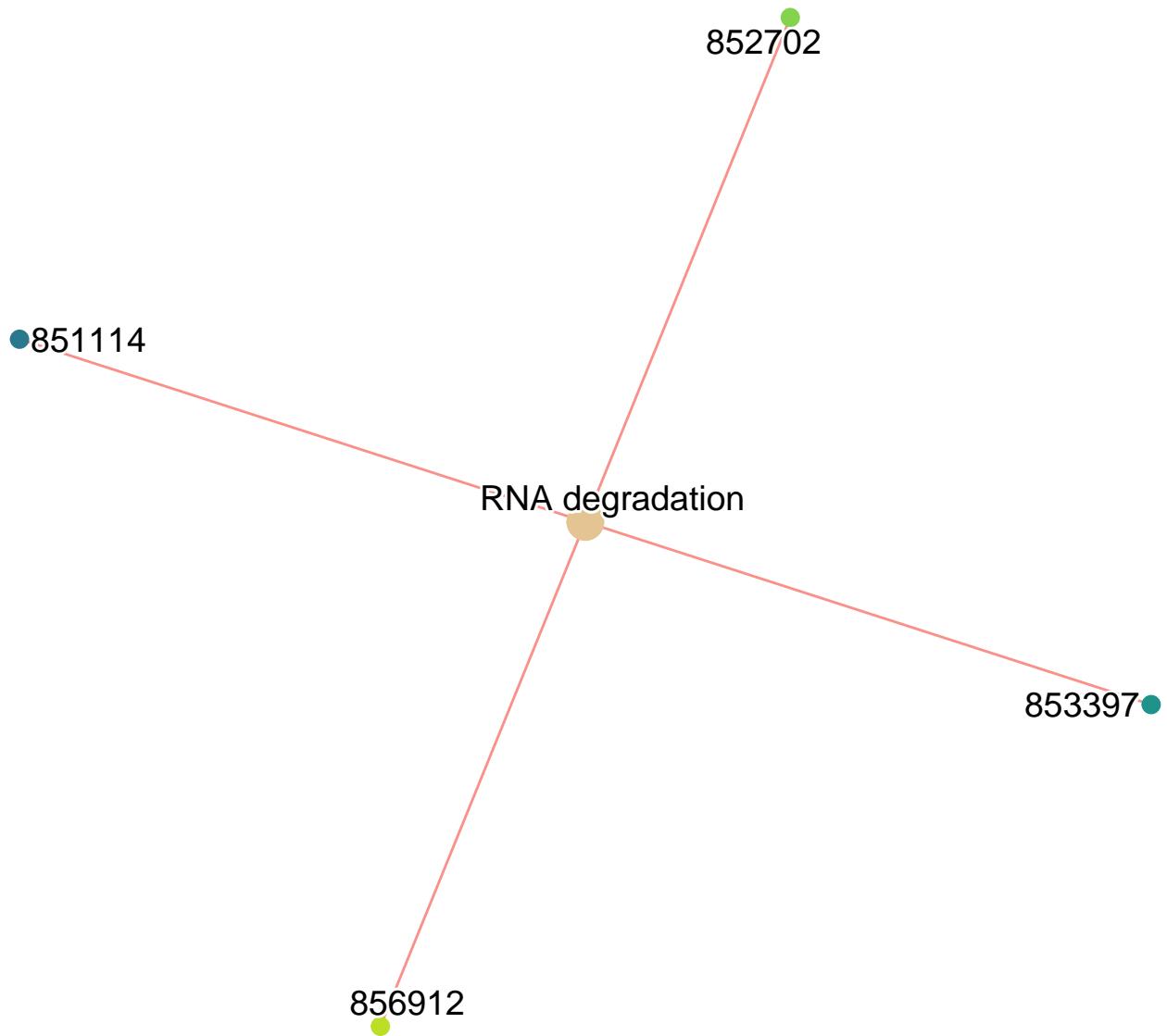
size

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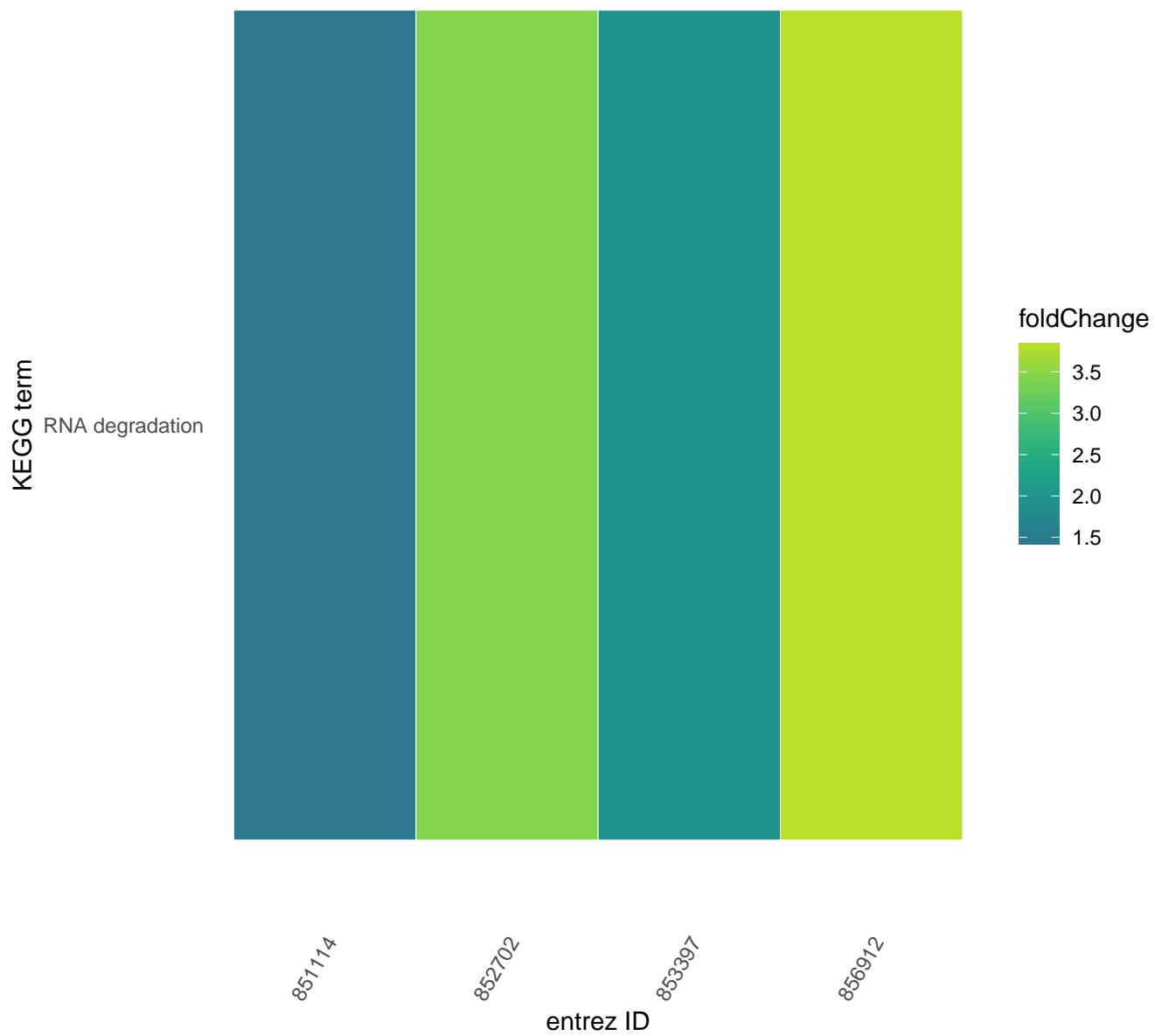
FoldChange



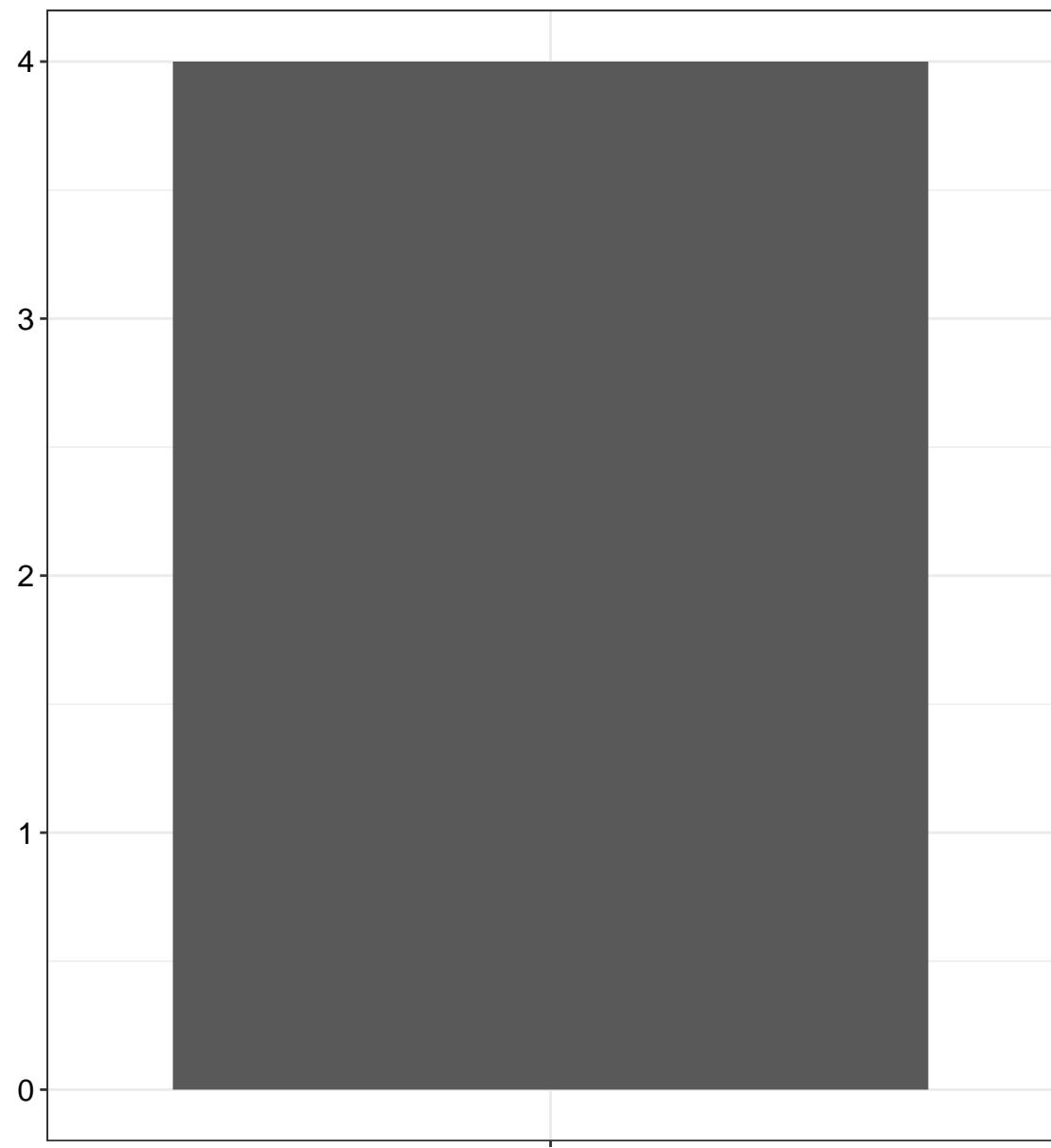
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TIF4631–TAP Up-regulated KEGG heatplot

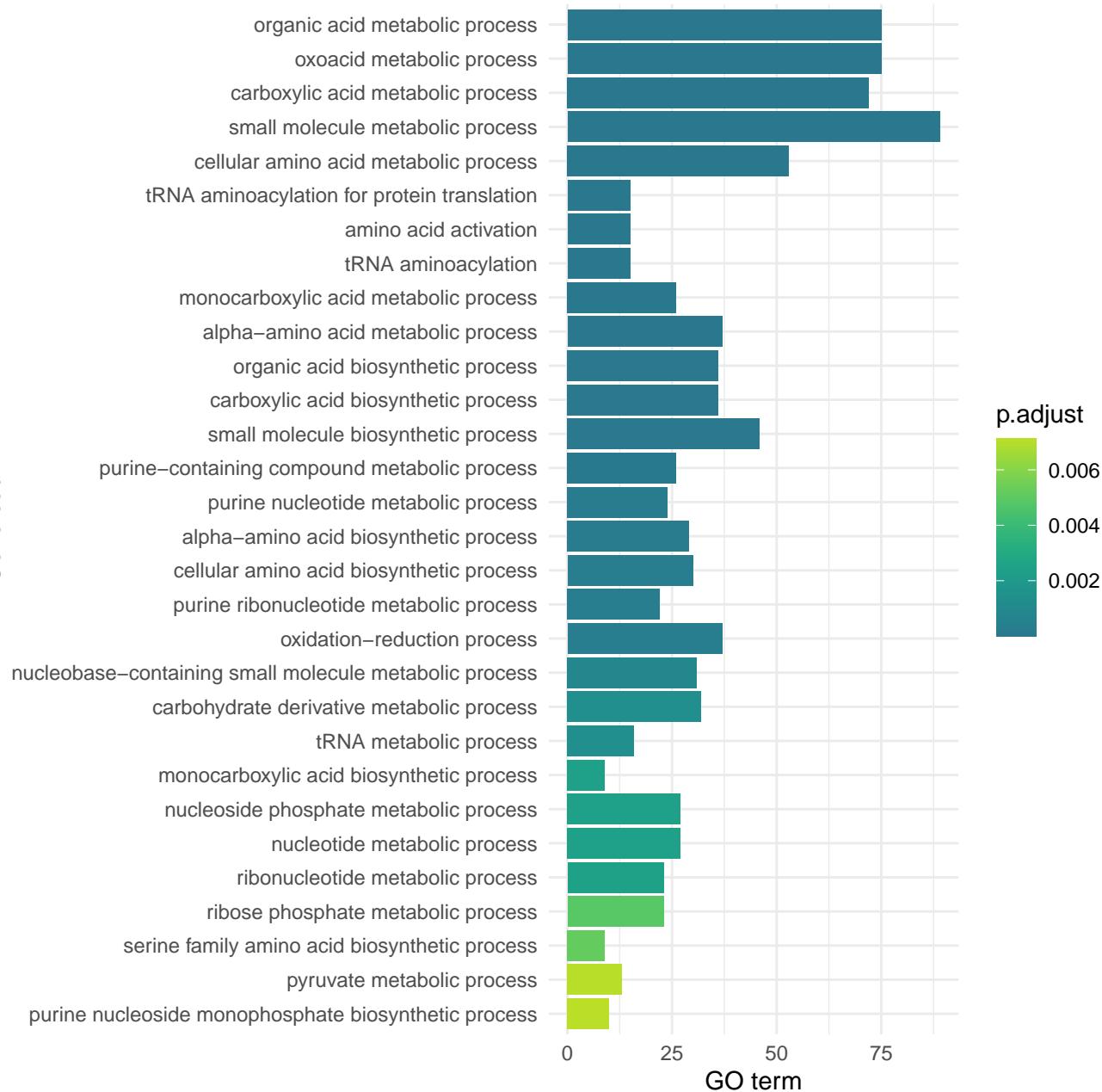


TIF4631-TAP Up-regulated KEGG upsetplot

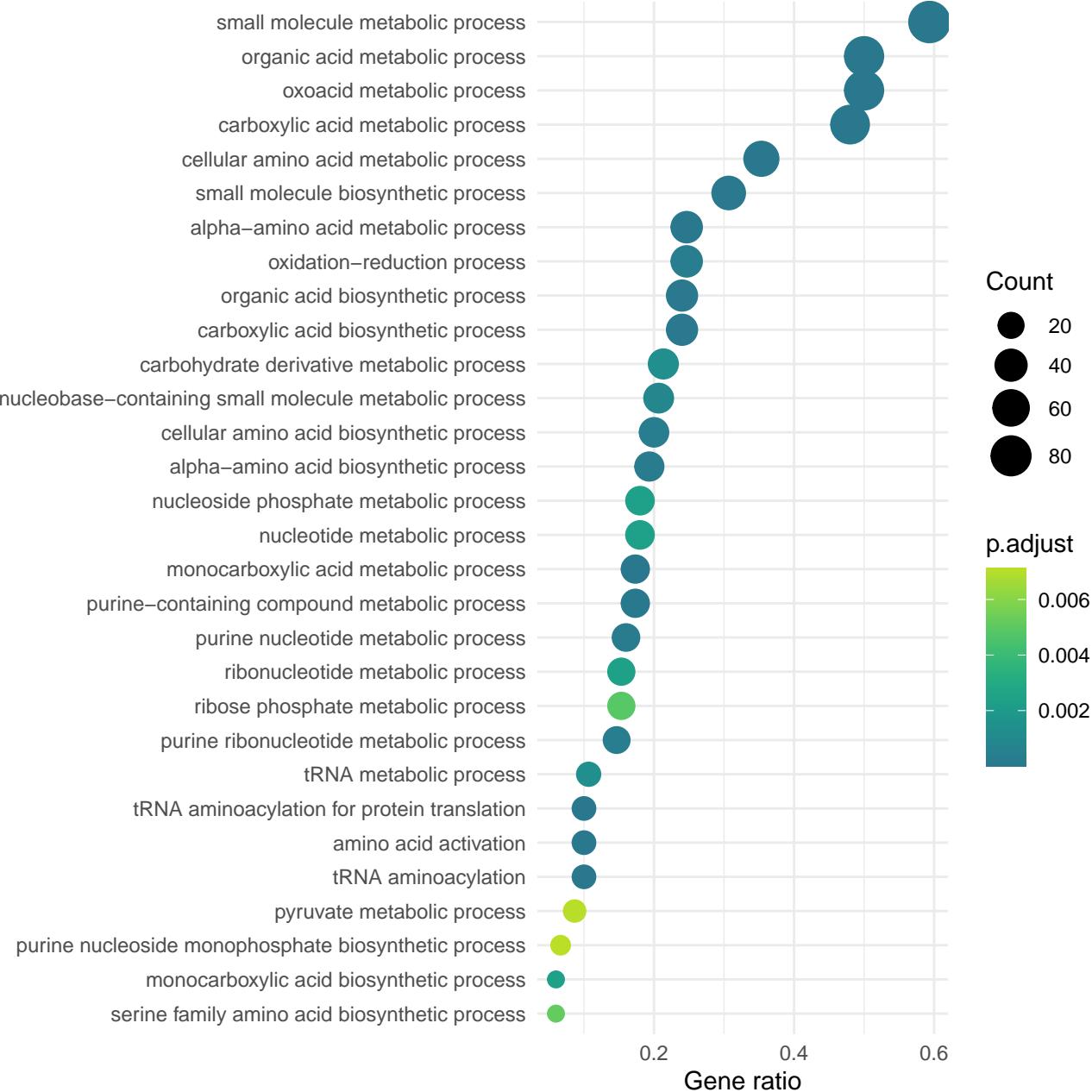


RNA degradation

NAM7-TAP Up-regulated GO BP barplot

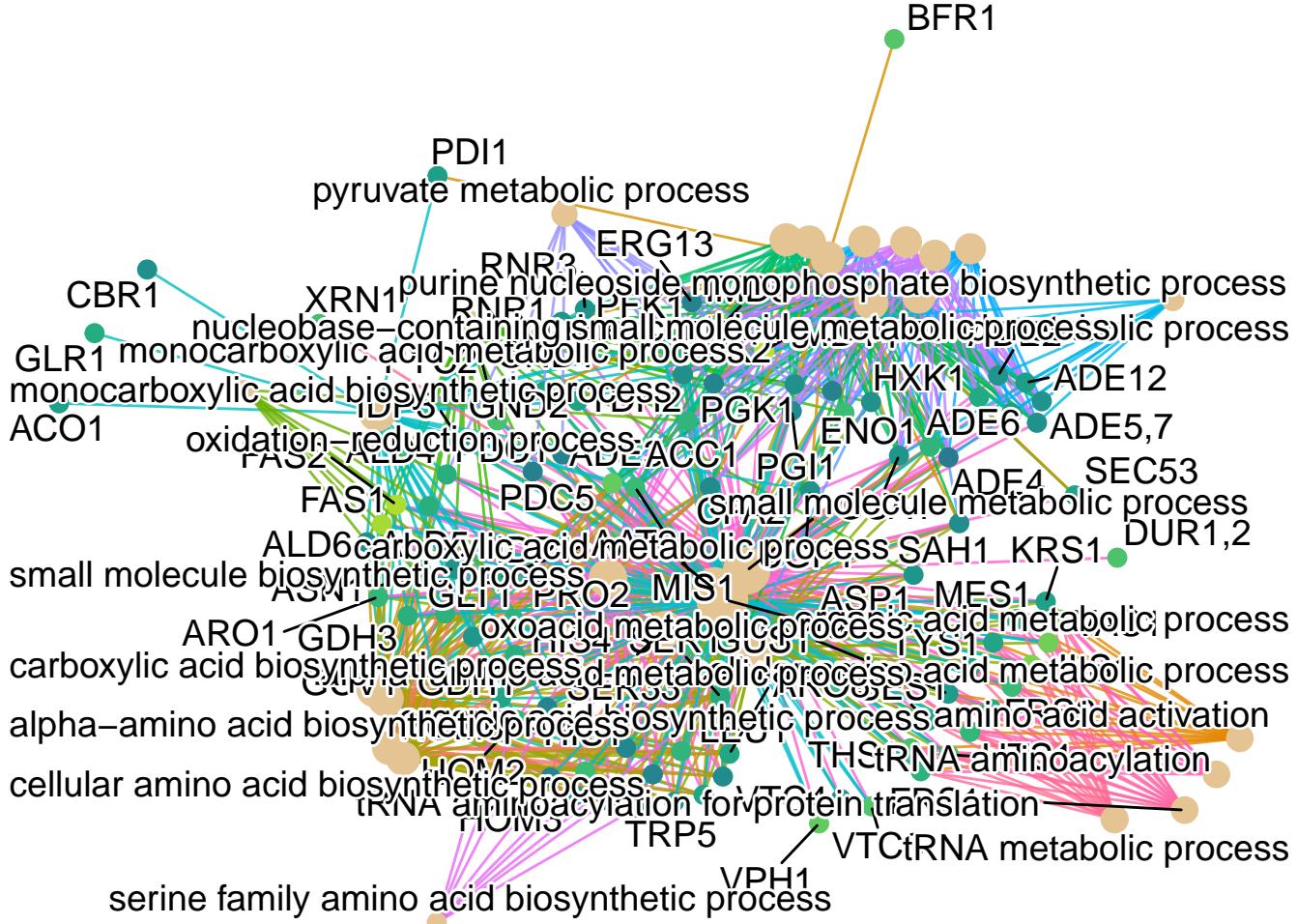


NAM7-TAP Up-regulated GO BP dotplot

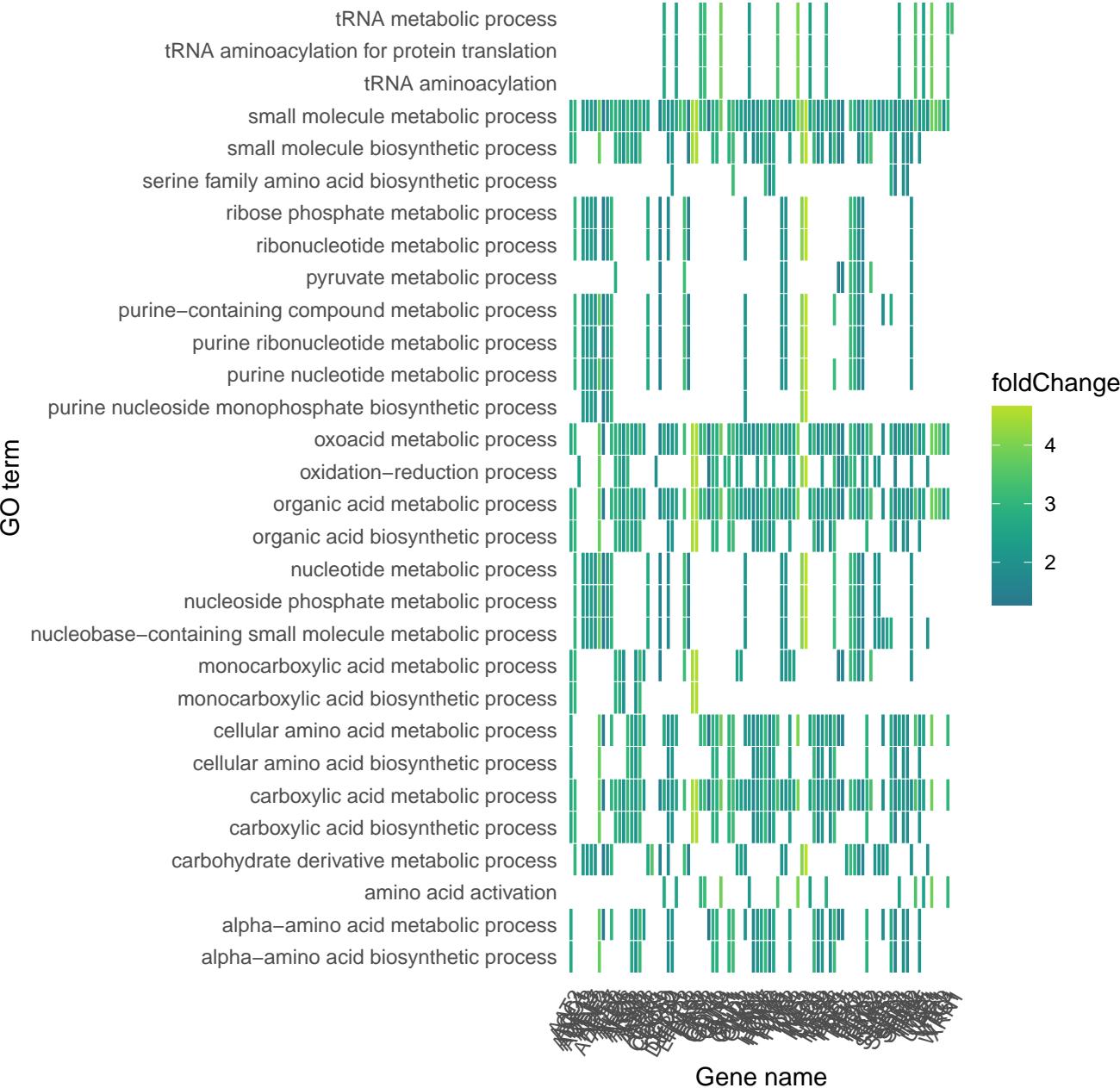


NAM7-TAP Up-regulated GO BP cnetplot

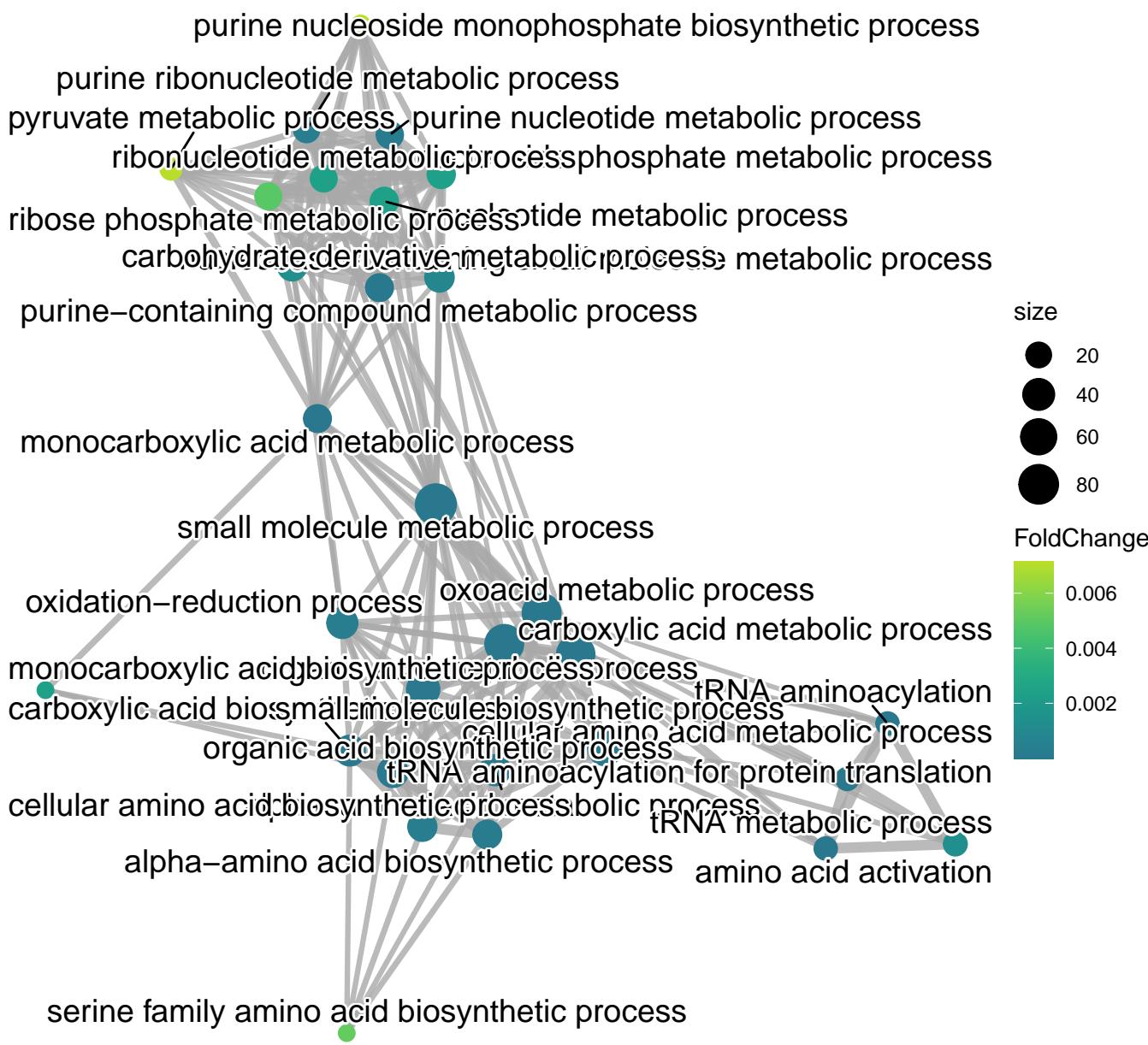
- | | | | | | |
|--|-------------|--|-------------|----------------------------------|-------------|
| nucleotide metabolic process | dark blue | purine nucleotide metabolic process | light blue | serine metabolic process | pink |
| organic acid biosynthetic process | light blue | purine ribonucleotide metabolic process | medium blue | small molecule metabolic process | light green |
| organic acid metabolic process | medium blue | purine-containing compound metabolic process | teal | tRNA metabolic process | pink |
| oxidation–reduction process | teal | pyruvate metabolic process | purple | tRNA processing | light green |
| oxoacid metabolic process | purple | ribonucleotide metabolic process | pink | | |
| purine nucleoside monophosphate biosynthetic process | light green | ribose phosphate metabolic process | light green | | |

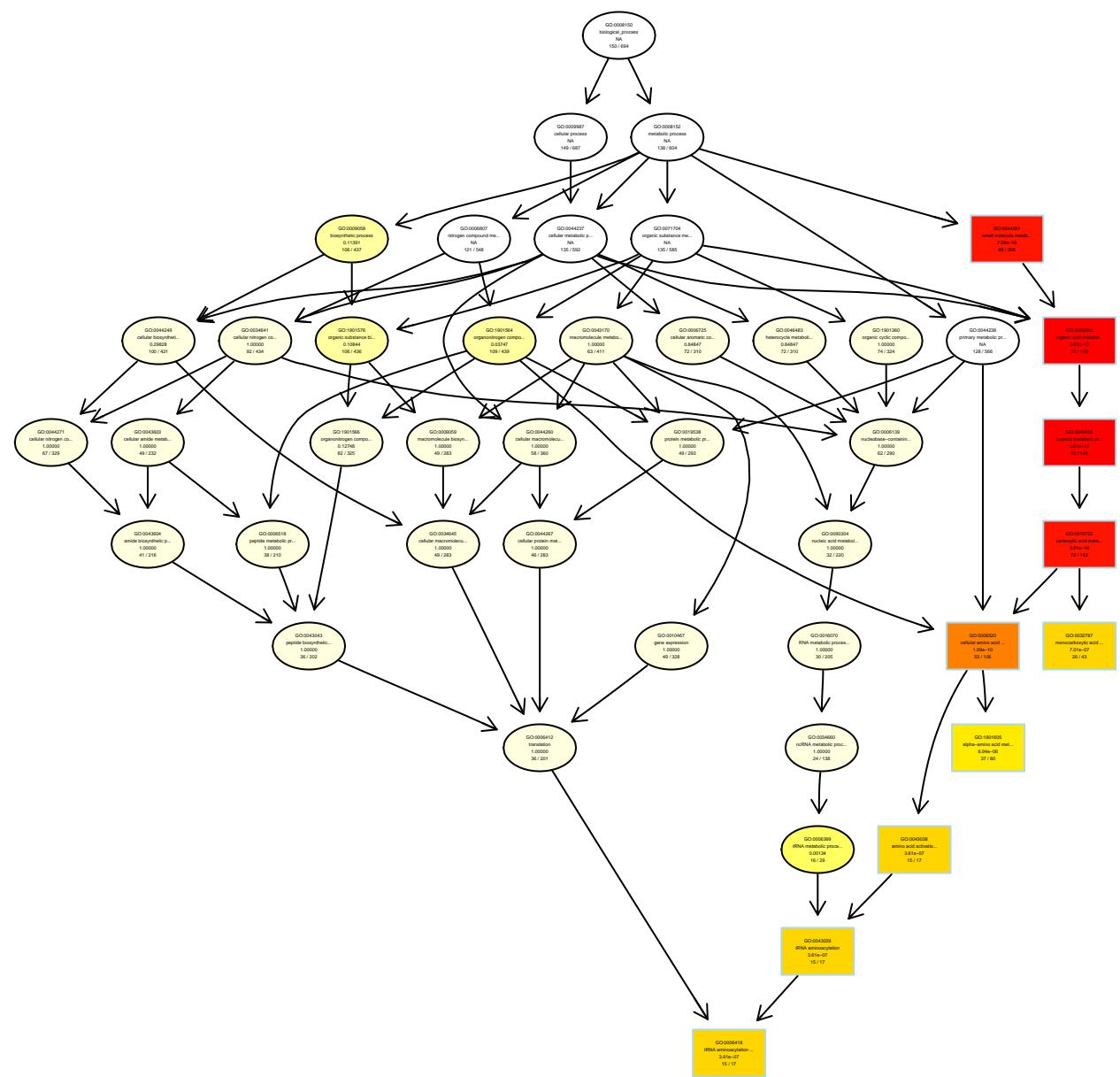


NAM7-TAP Up-regulated GO BP heatplot

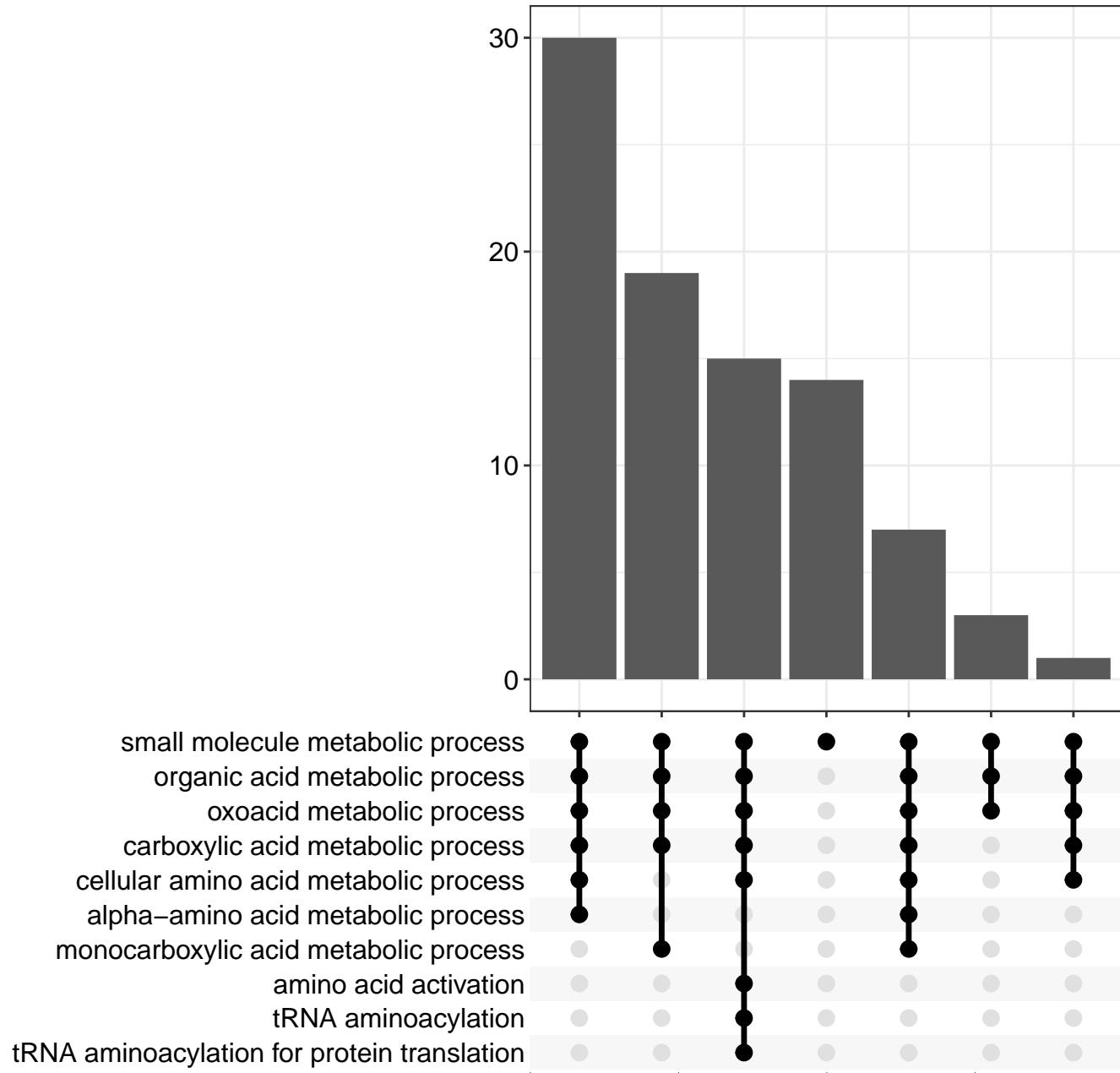


NAM7-TAP Up-regulated GO BP emapplot

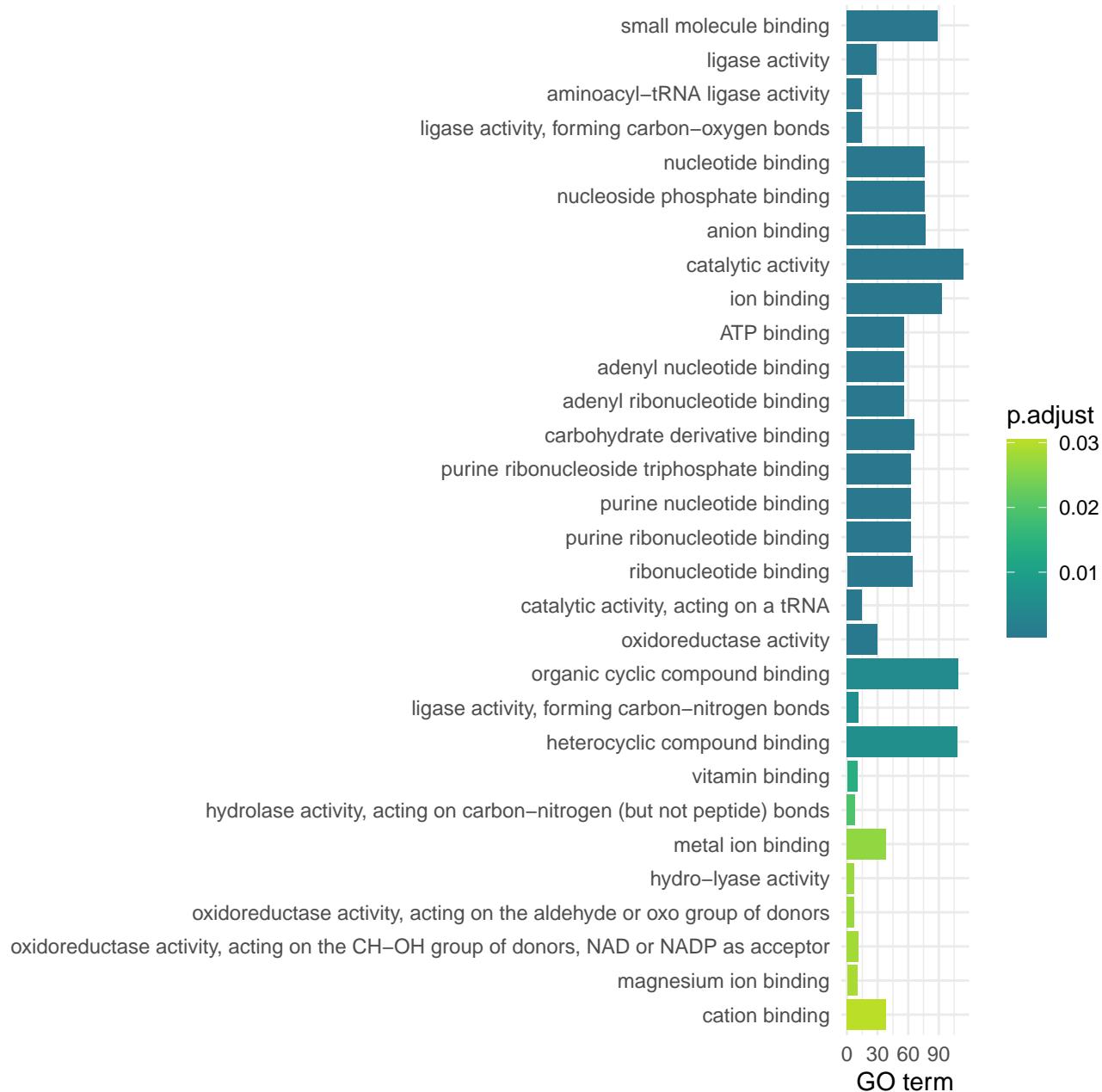




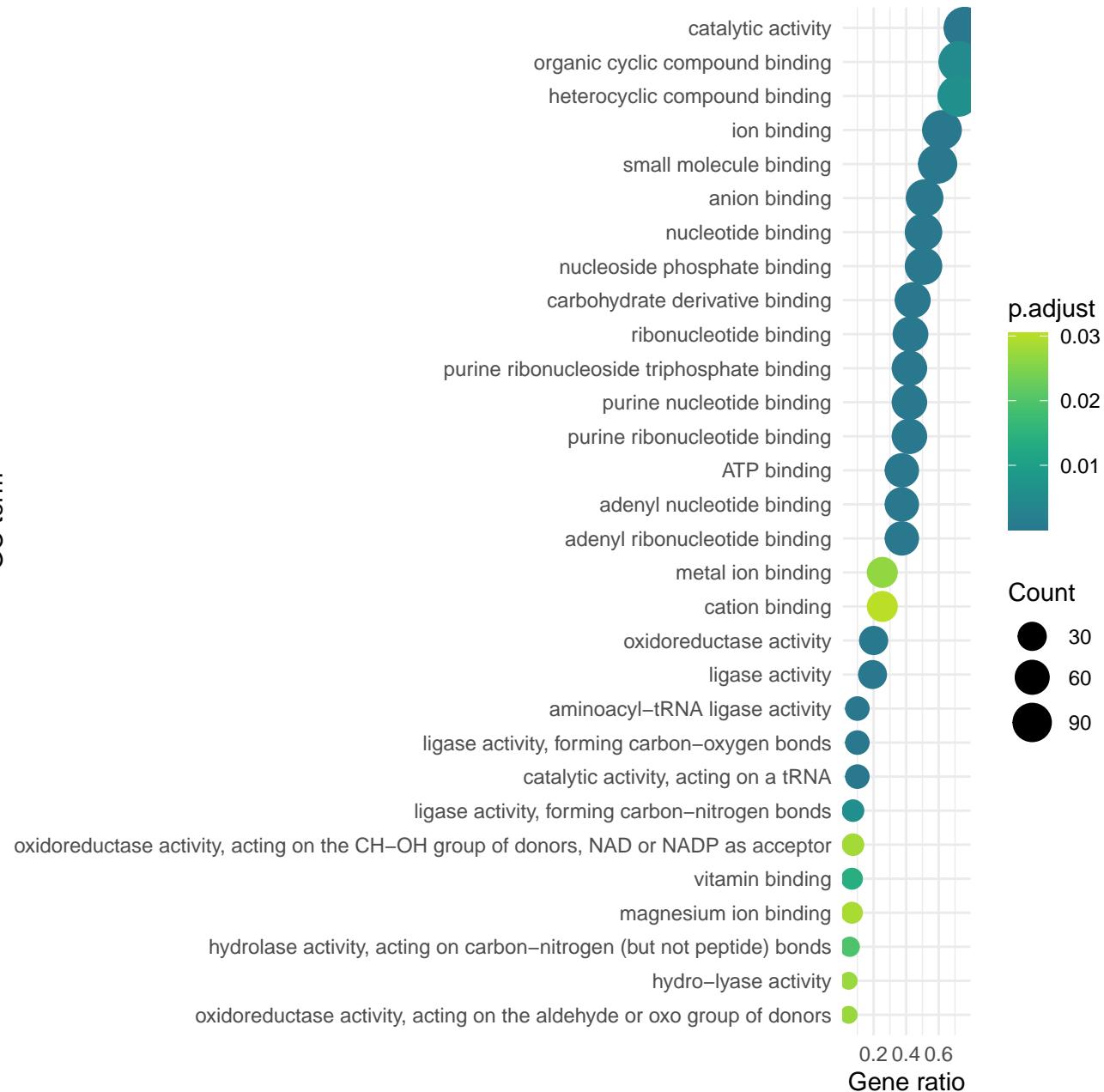
NAM7-TAP Up-regulated GO BP upsetplot



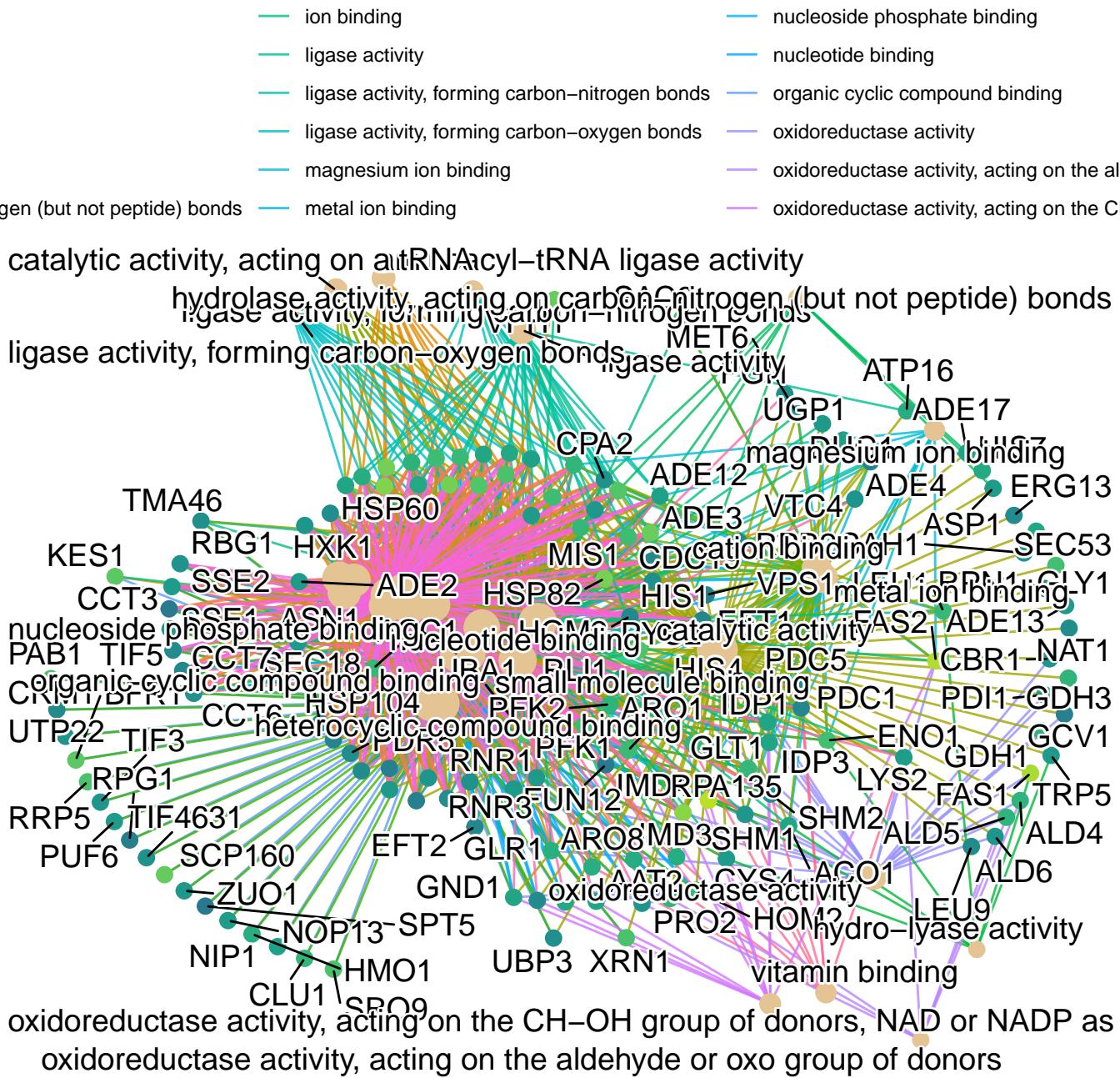
NAM7-TAP Up-regulated



NAM7-TAP Up-regul

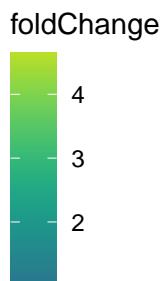


NAM7-TAP Up-regulated GO MF cnetplot



GO term

vitamin binding
 small molecule binding
 ribonucleotide binding
 purine ribonucleotide binding
 purine ribonucleoside triphosphate binding
 purine nucleotide binding
 oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
 oxidoreductase activity, acting on the aldehyde or oxo group of donors
 oxidoreductase activity
 organic cyclic compound binding
 nucleotide binding
 nucleoside phosphate binding
 metal ion binding
 magnesium ion binding
 ligase activity, forming carbon-oxygen bonds
 ligase activity, forming carbon-nitrogen bonds
 ligase activity
 ion binding
 hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
 hydro-lyase activity
 heterocyclic compound binding
 cation binding
 catalytic activity, acting on a tRNA
 catalytic activity
 carbohydrate derivative binding
 ATP binding
 anion binding
 aminoacyl-tRNA ligase activity
 adenyl ribonucleotide binding
 adenyl nucleotide binding



Gene name

NAM7-TAP Up-regulated GO MF emapplot

hydrolase activity, acting on carbon–nitrogen (but not peptide) bonds

hydro-lyase activity

ligase activity, forming carbon–nitrogen bonds

vitamin binding

activity, acting on the CH–OH group of donors, NAD or NADP as acceptor

ligase activity, forming carbon–oxygen bonds

NA ligase activity

ligase activity

purine ribonucleoside triphosphate oxidoreductase activity

catalytic activity, acting on a tRNA

nucleotide binding

carbohydrate derivative binding

oxidoreductase activity, acting on the aldehyde or oxo group of donors

adenyl nucleotide binding

nucleoside phosphate binding

ATP binding

purine ribonucleotide binding-catalytic activity

ribonucleotide binding-small molecule binding

purine nucleotide binding ion binding

anion binding

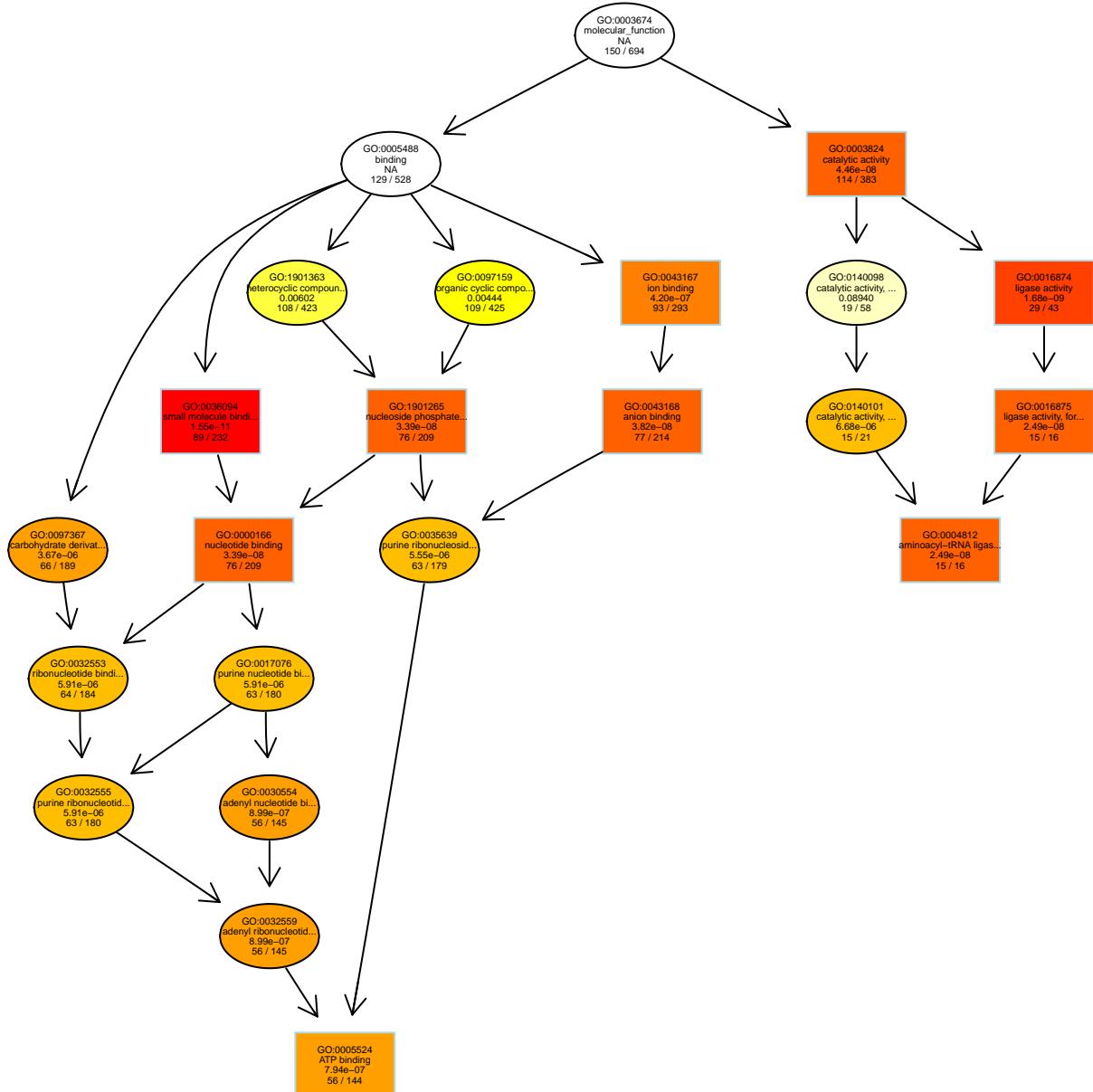
heterocyclic compound binding

organic cyclic compound binding metal ion binding

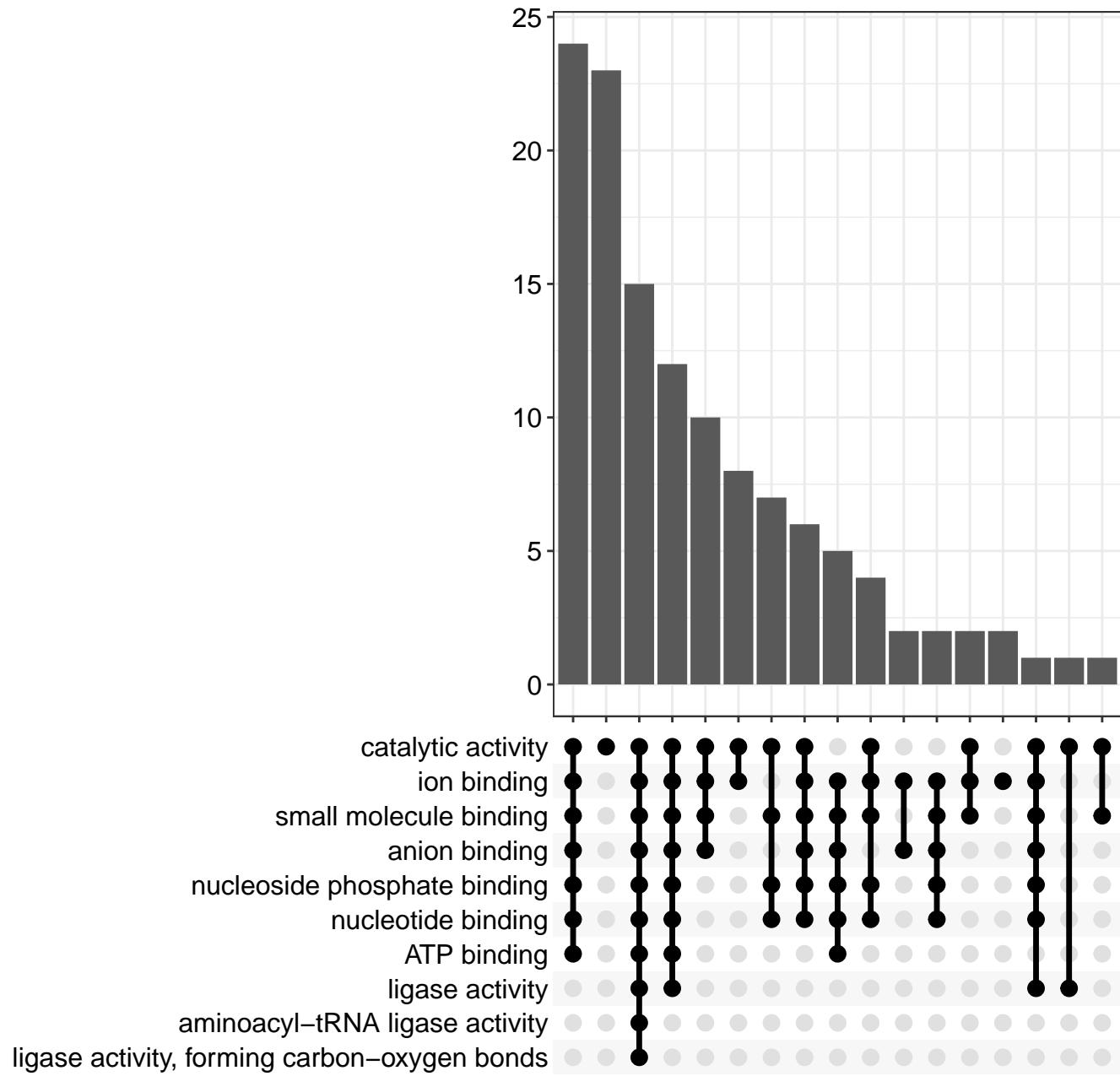
cation binding

magnesium ion binding

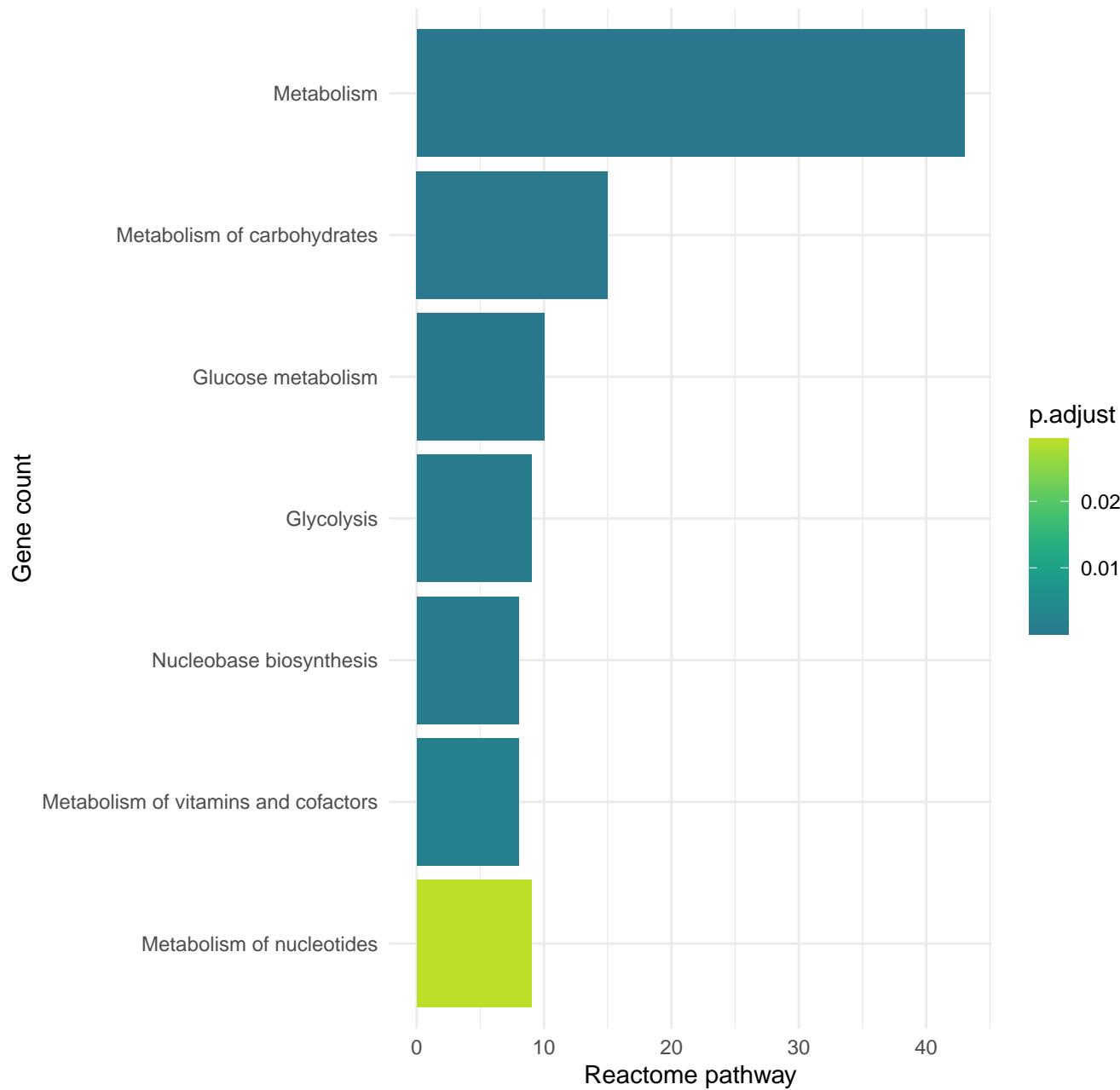




NAM7-TAP Up-regulated GO MF upsetplot



NAM7-TAP Up-regulated Reactome barplot



NAM7-TAP Up-regulated Reactome dotplot

Reactome pathway

Metabolism

Metabolism of carbohydrates

Glucose metabolism

Glycolysis

Metabolism of nucleotides

Nucleobase biosynthesis

Metabolism of vitamins and cofactors

0.1

0.2

0.3

0.4

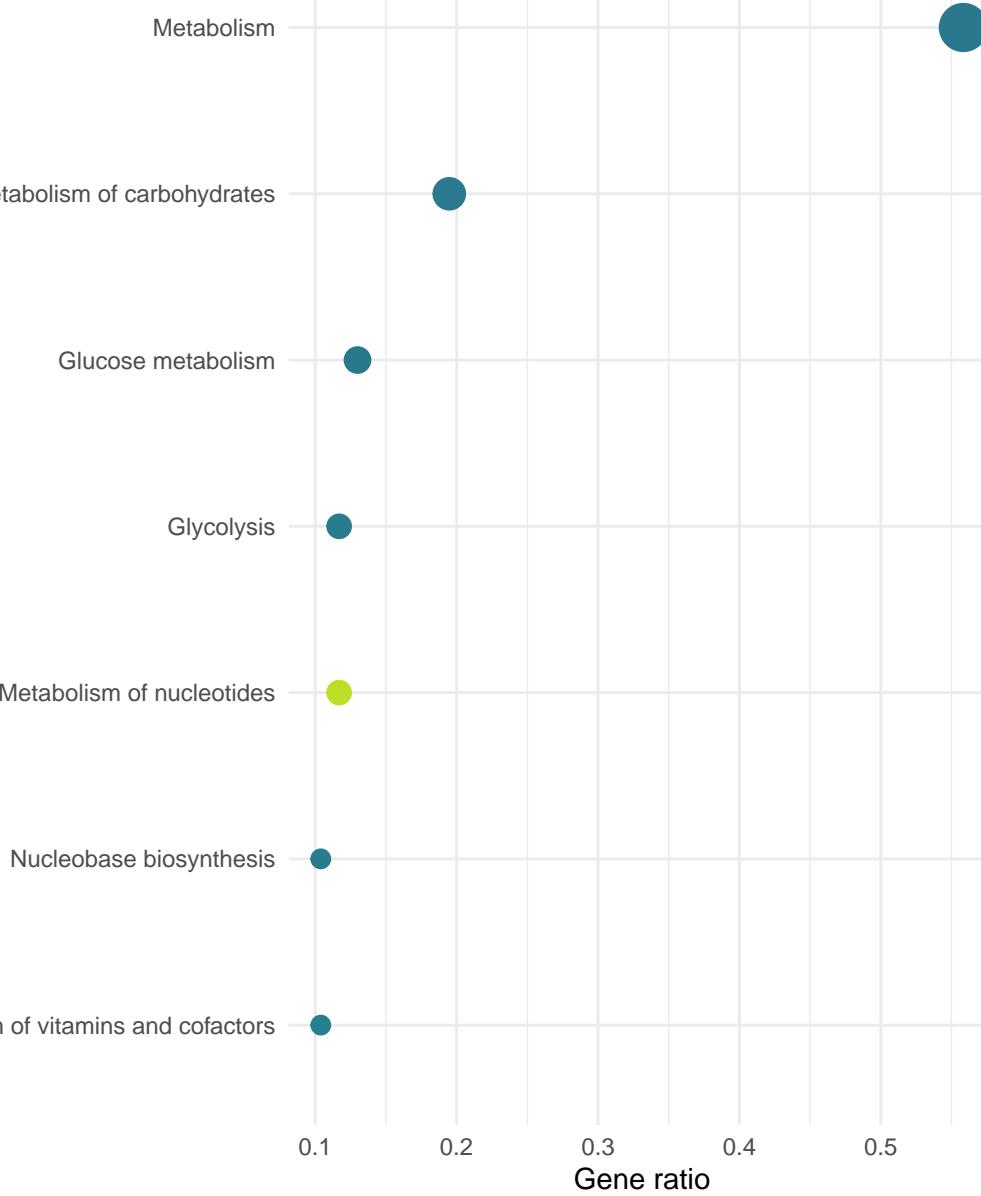
0.5

Gene ratio

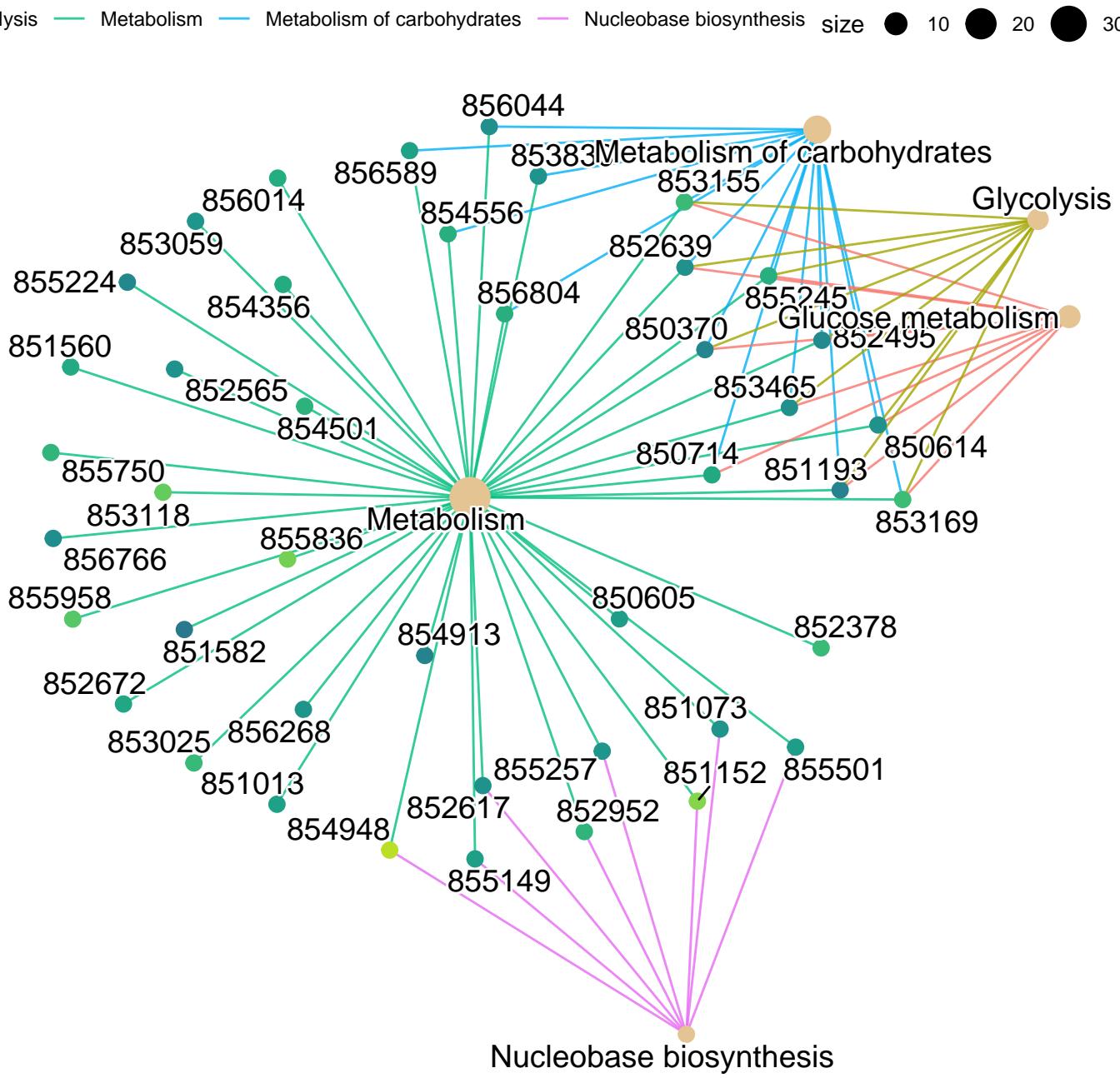
Count



p.adjust

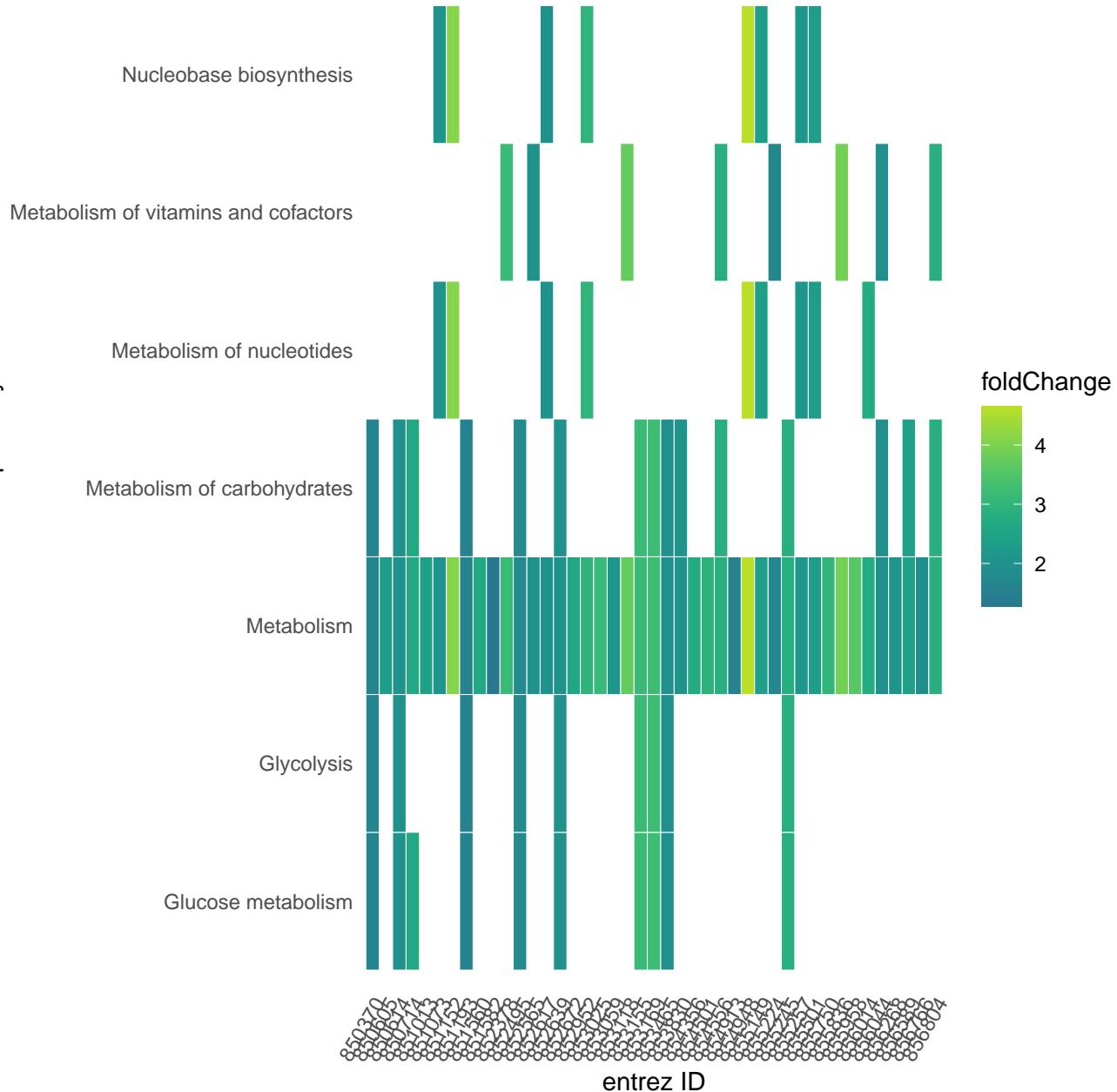


NAM7-TAP Up-regulated Reactome cnetplot



NAM7-TAP Up-regulated Reactome heatplot

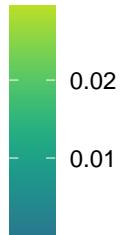
Reactome pathway



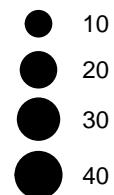
NAM7-TAP Up-regulated Reactome emappplot

Metabolism of vitamins and cofactors

FoldChange



size



Nucleobase biosynthesis

Glycolysis

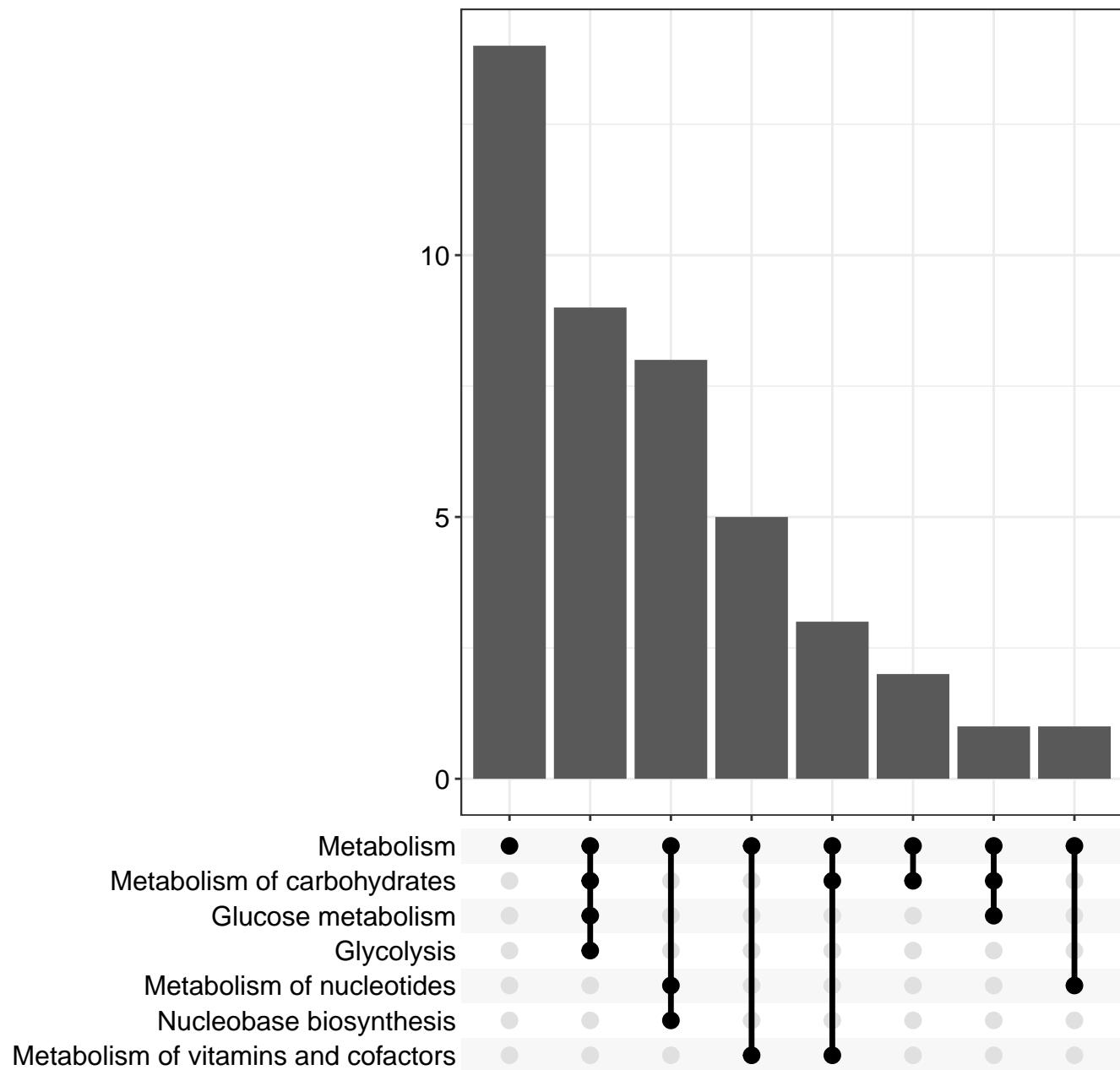
Glucose metabolism

Metabolism of carbohydrates

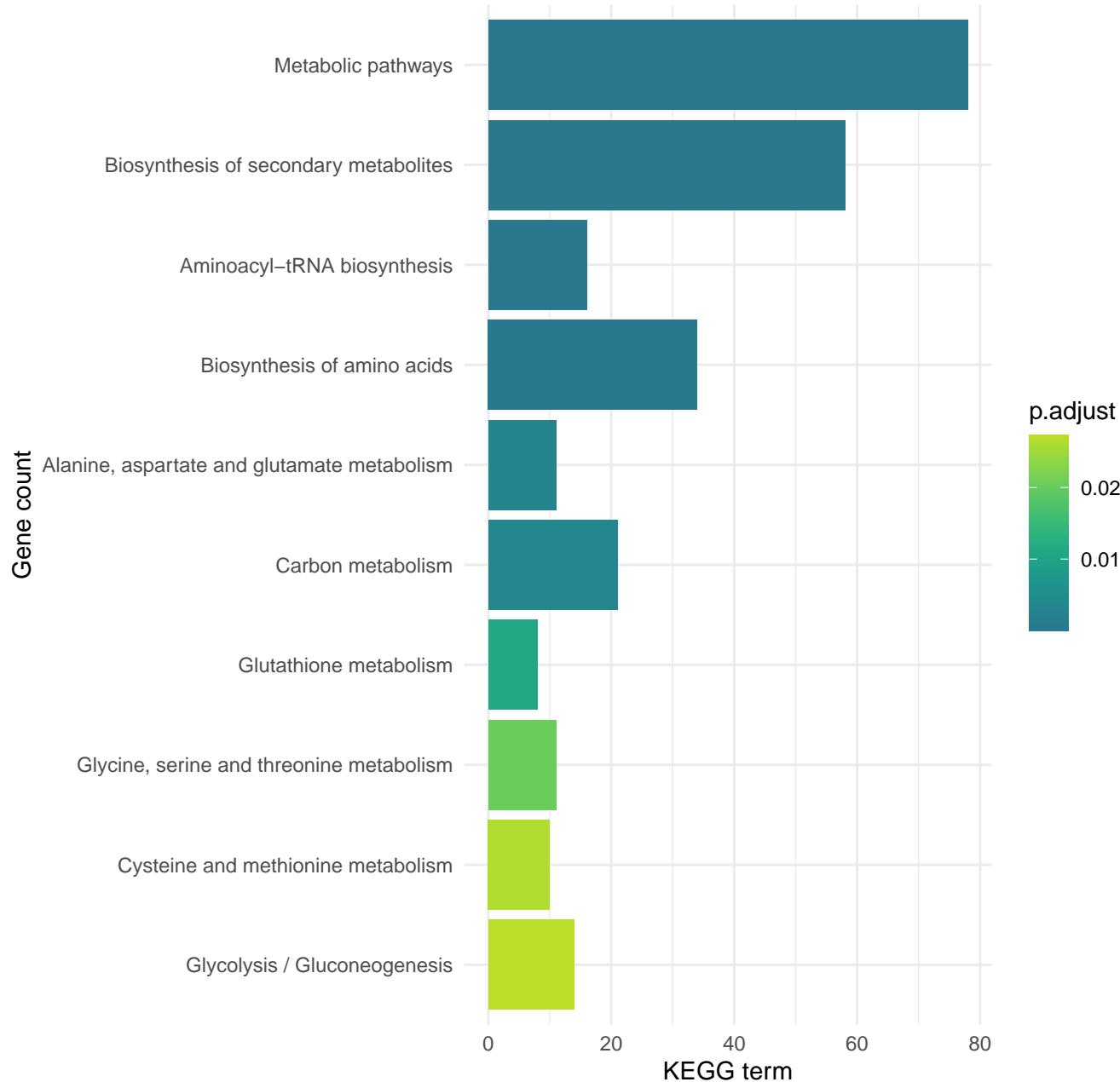
Metabolism

Metabolism of nucleotides

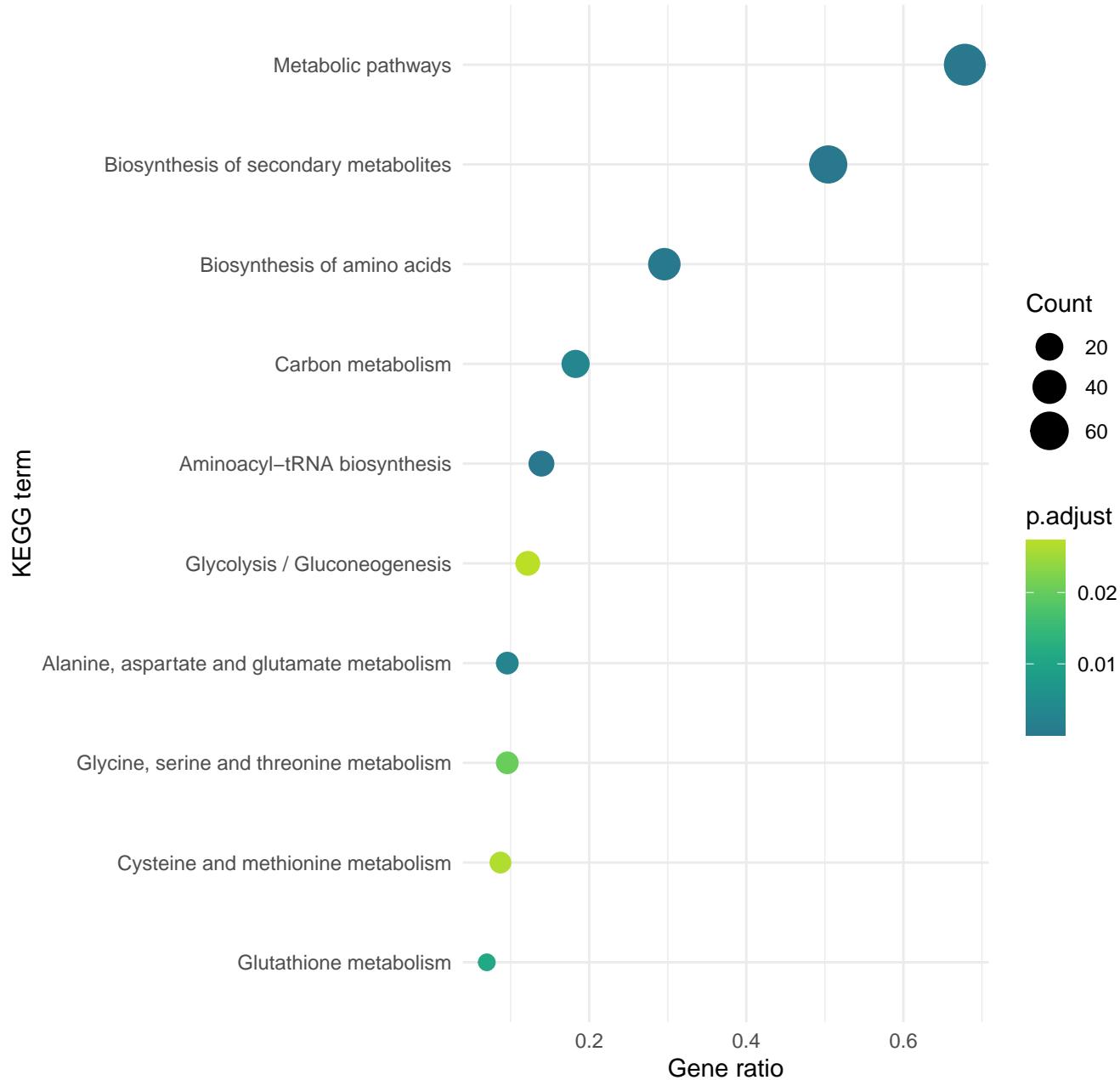
NAM7-TAP Up-regulated Reactome upsetplot



NAM7-TAP Up-regulated KEGG barplot



NAM7-TAP Up-regulated KEGG dotplot



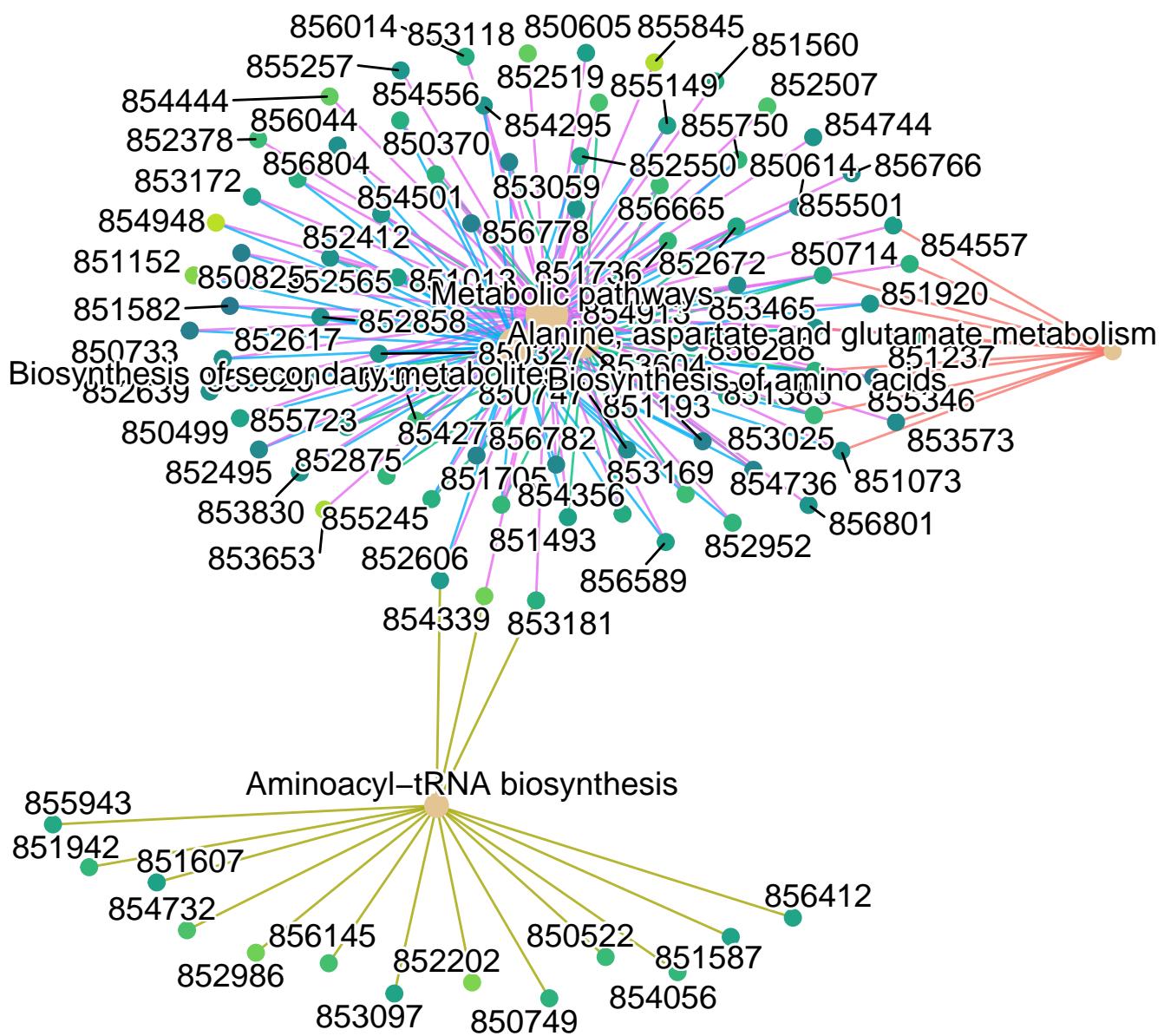
NAM7-TAP Up-regulated KEGG dotplot

Lutamate metabolism

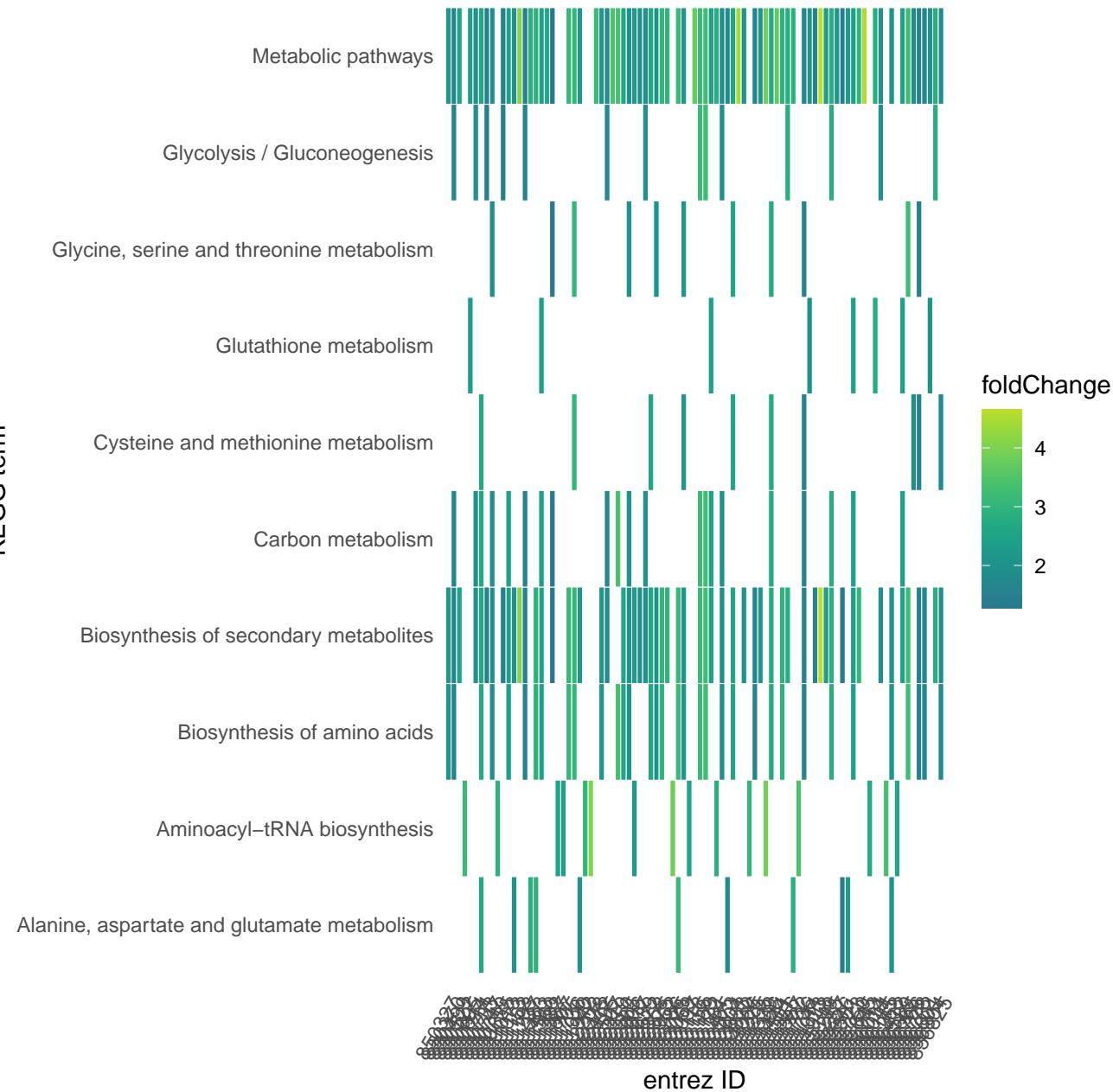
Aminoacyl-tRNA biosynthesis

Biosynthesis of amino acids

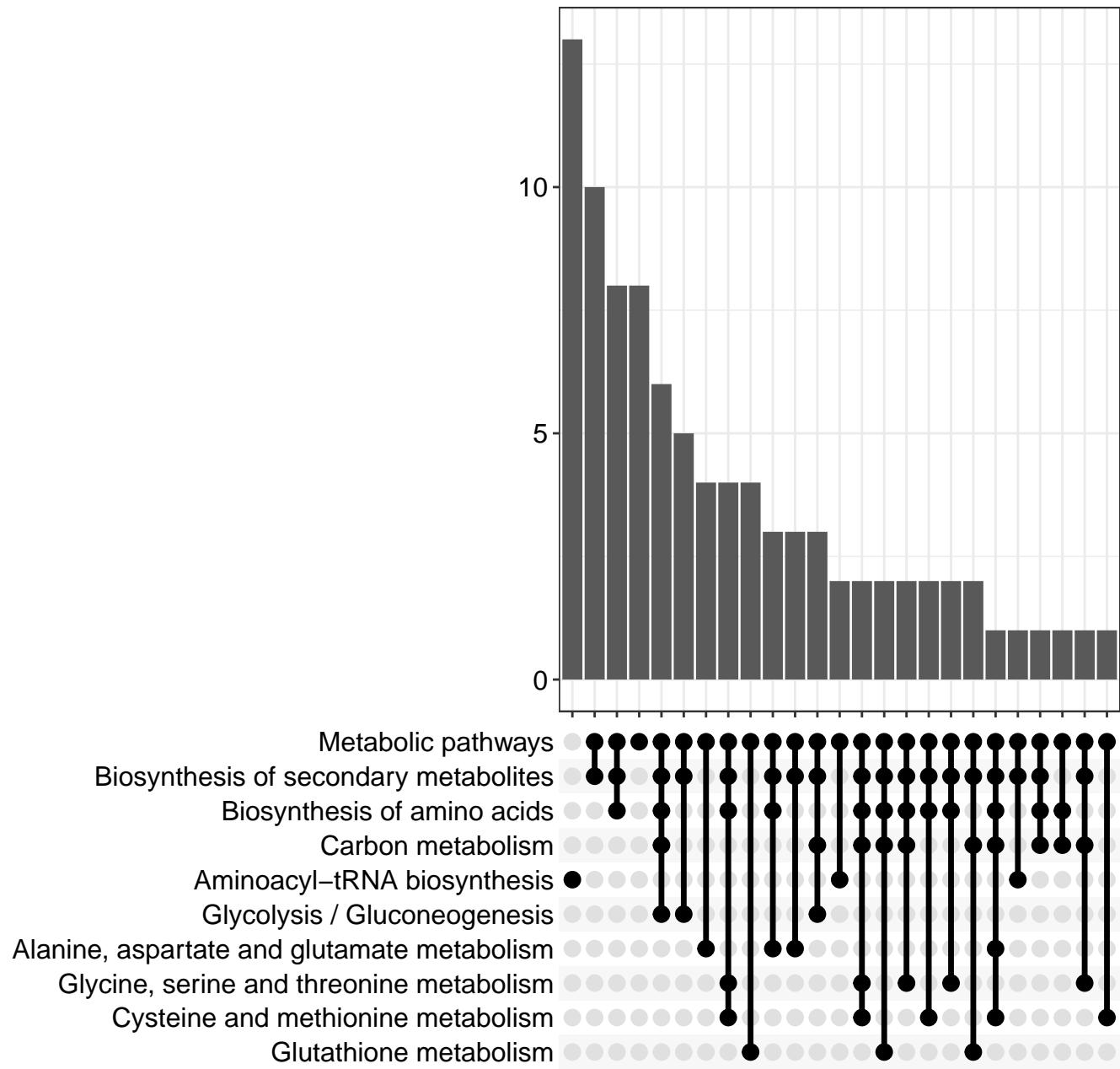
Biosynthesis of secondary



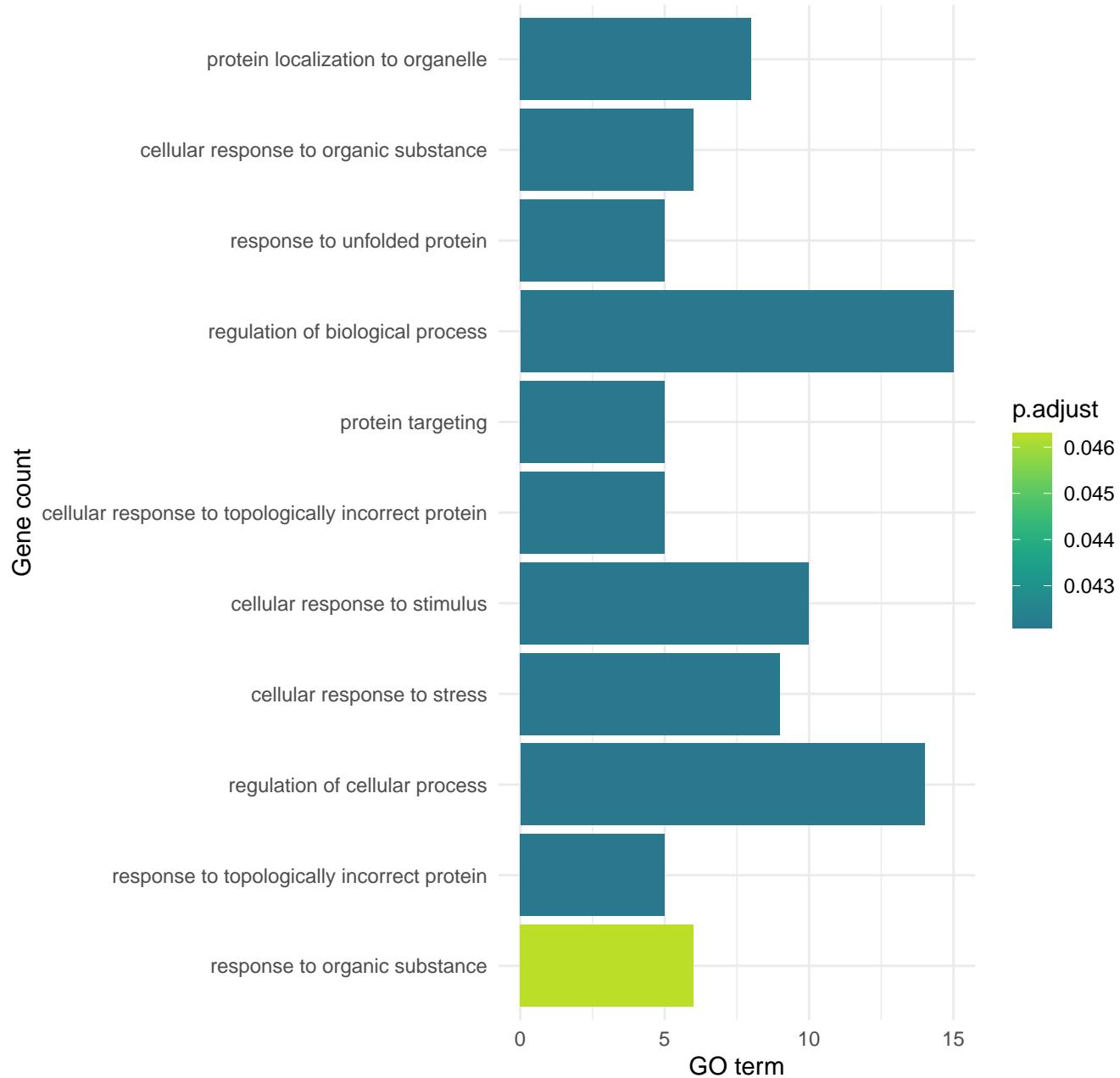
NAM7-TAP Up-regulated KEGG heatplot



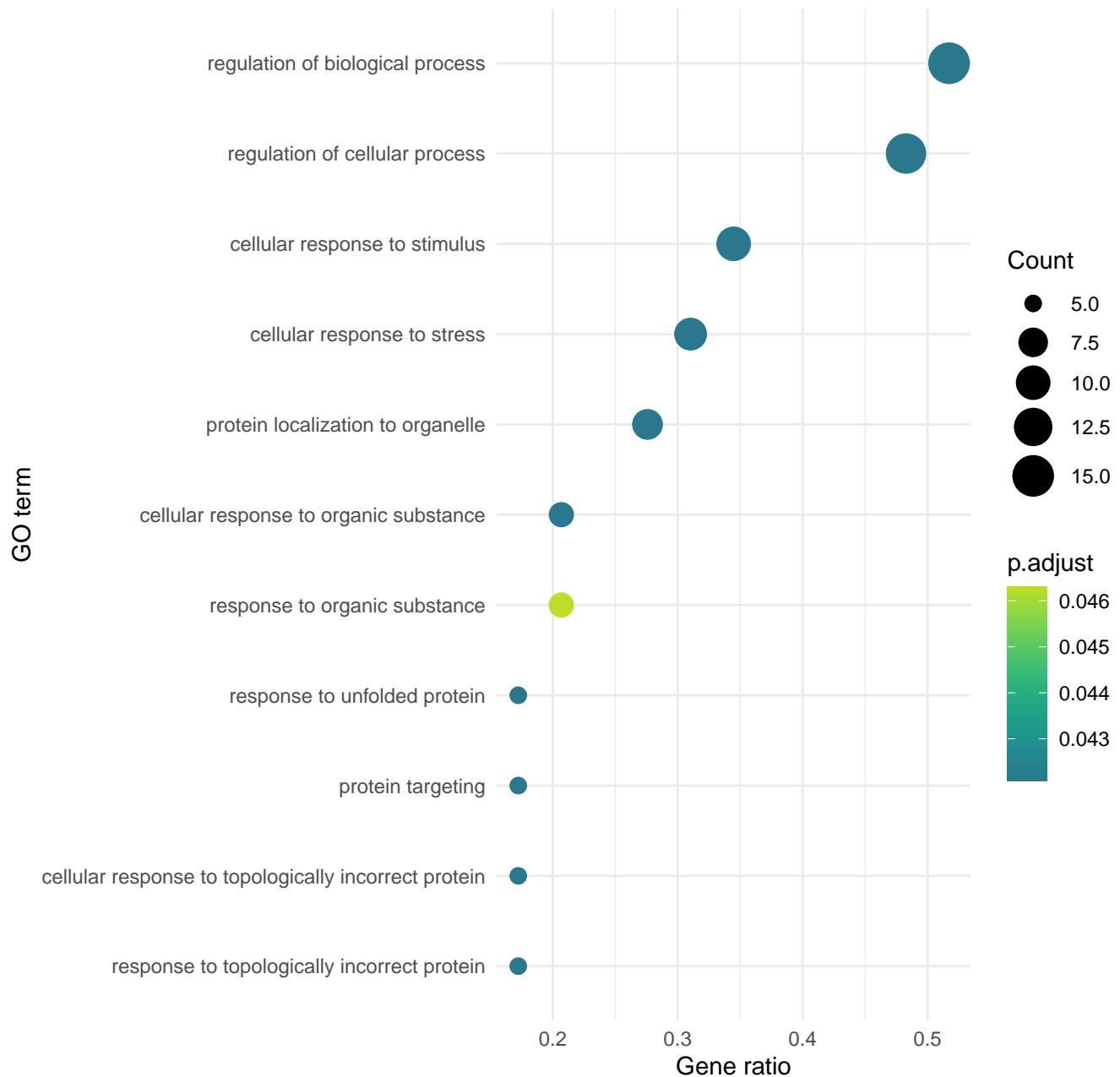
NAM7-TAP Up-regulated KEGG upsetplot



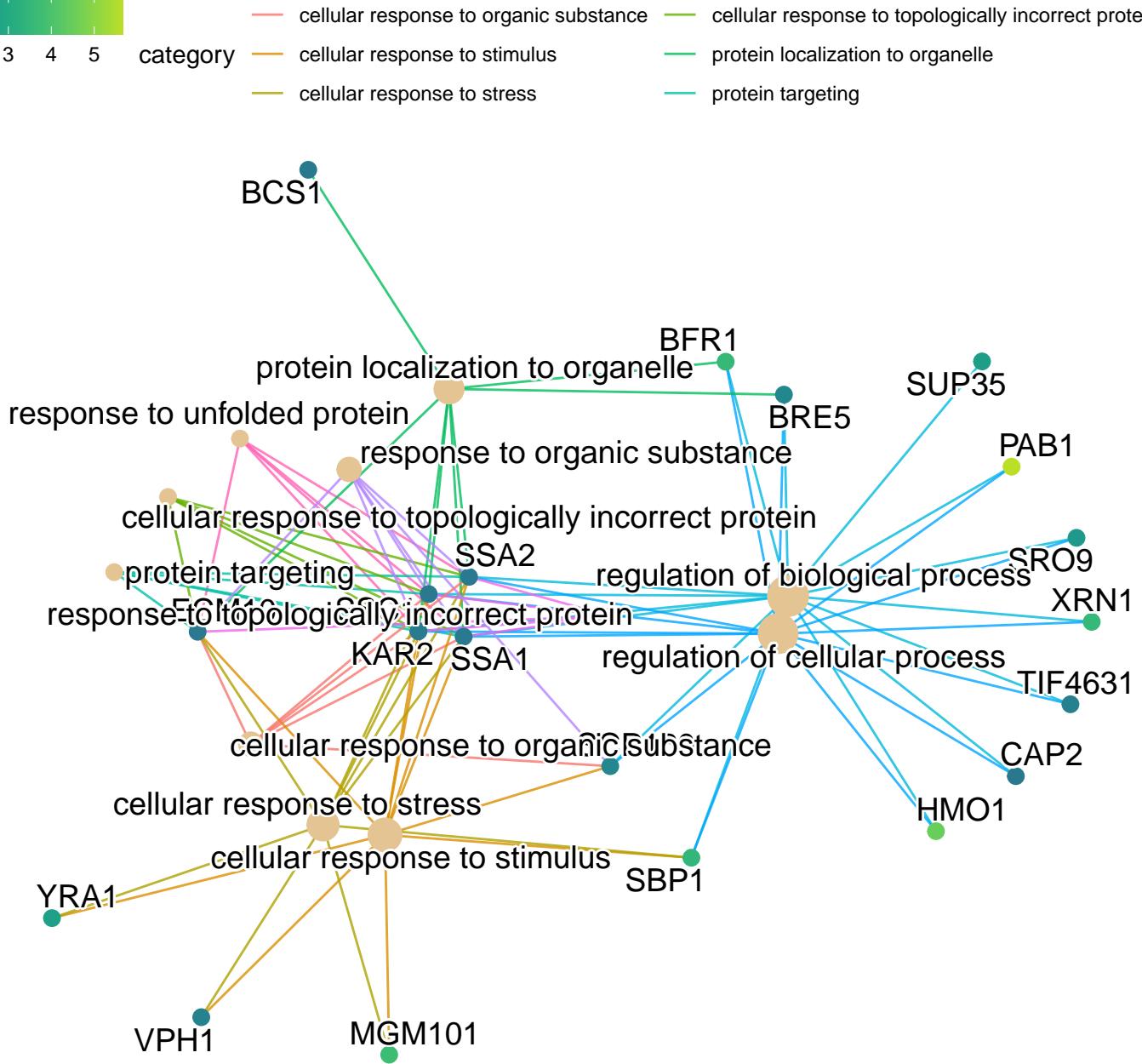
SUB2-TAP Up-regulated GO BP barplot



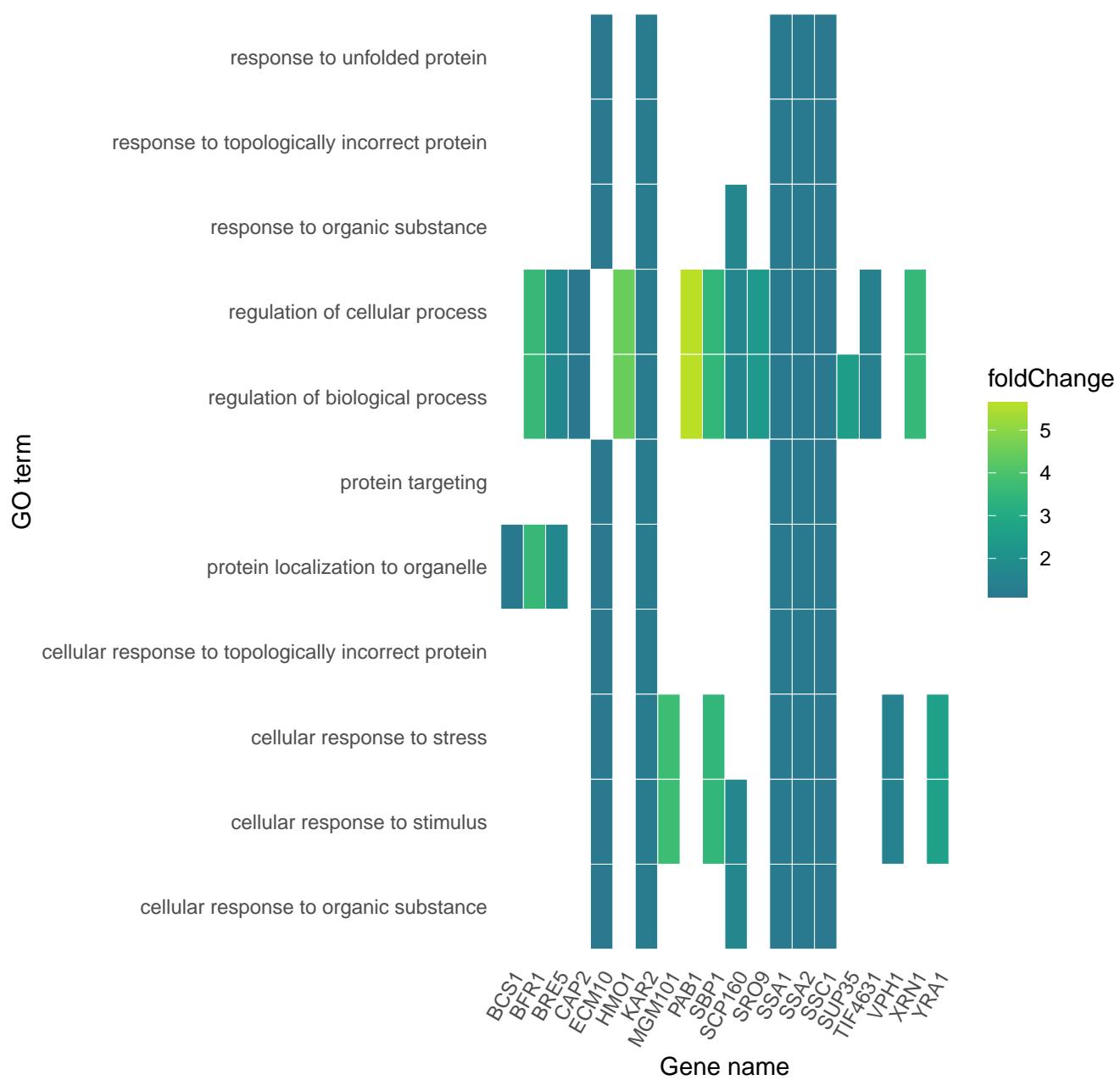
SUB2-TAP Up-regulated GO BP dotplot



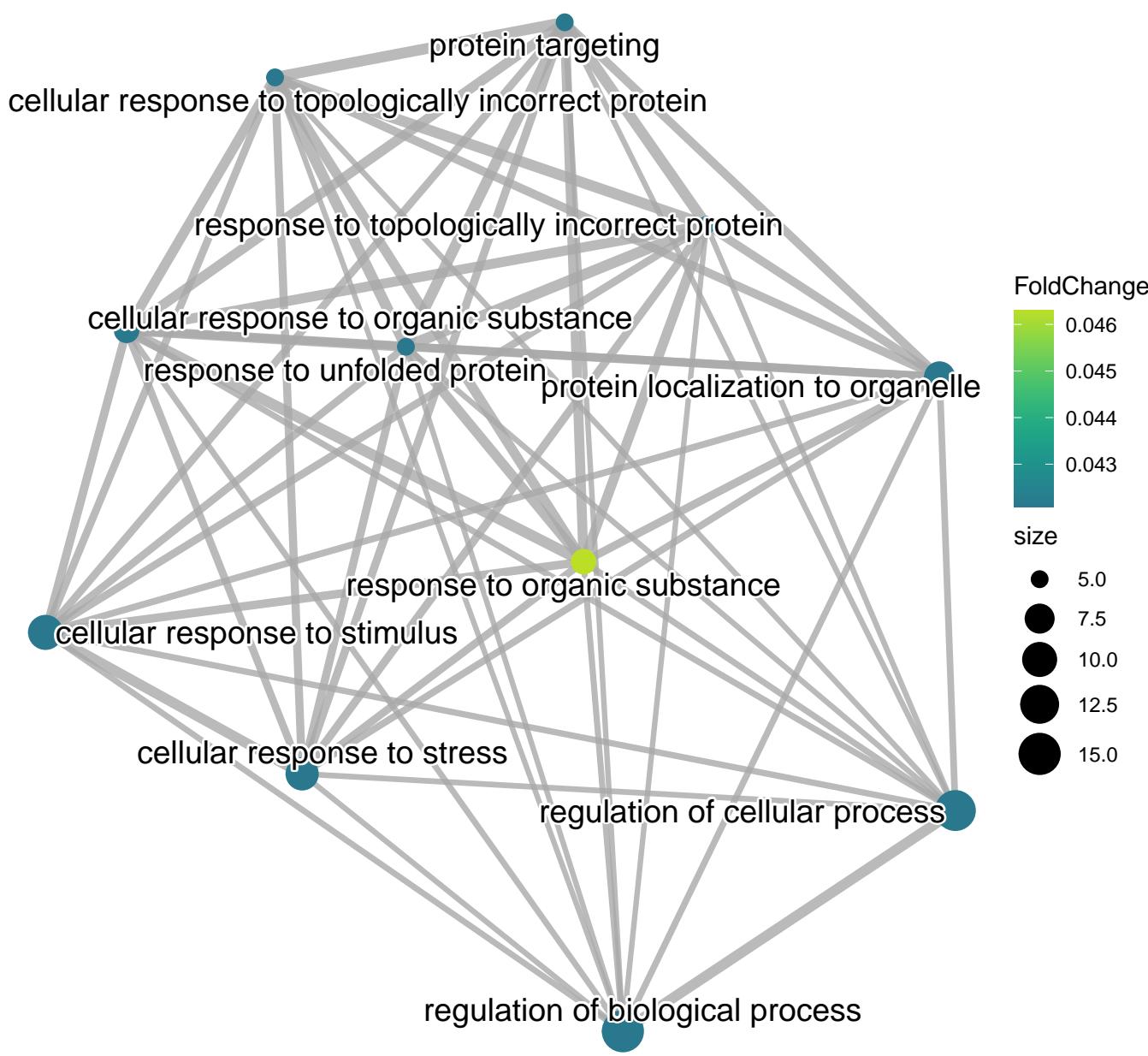
SUB2-TAP Up-regulated GO BP cnetplot

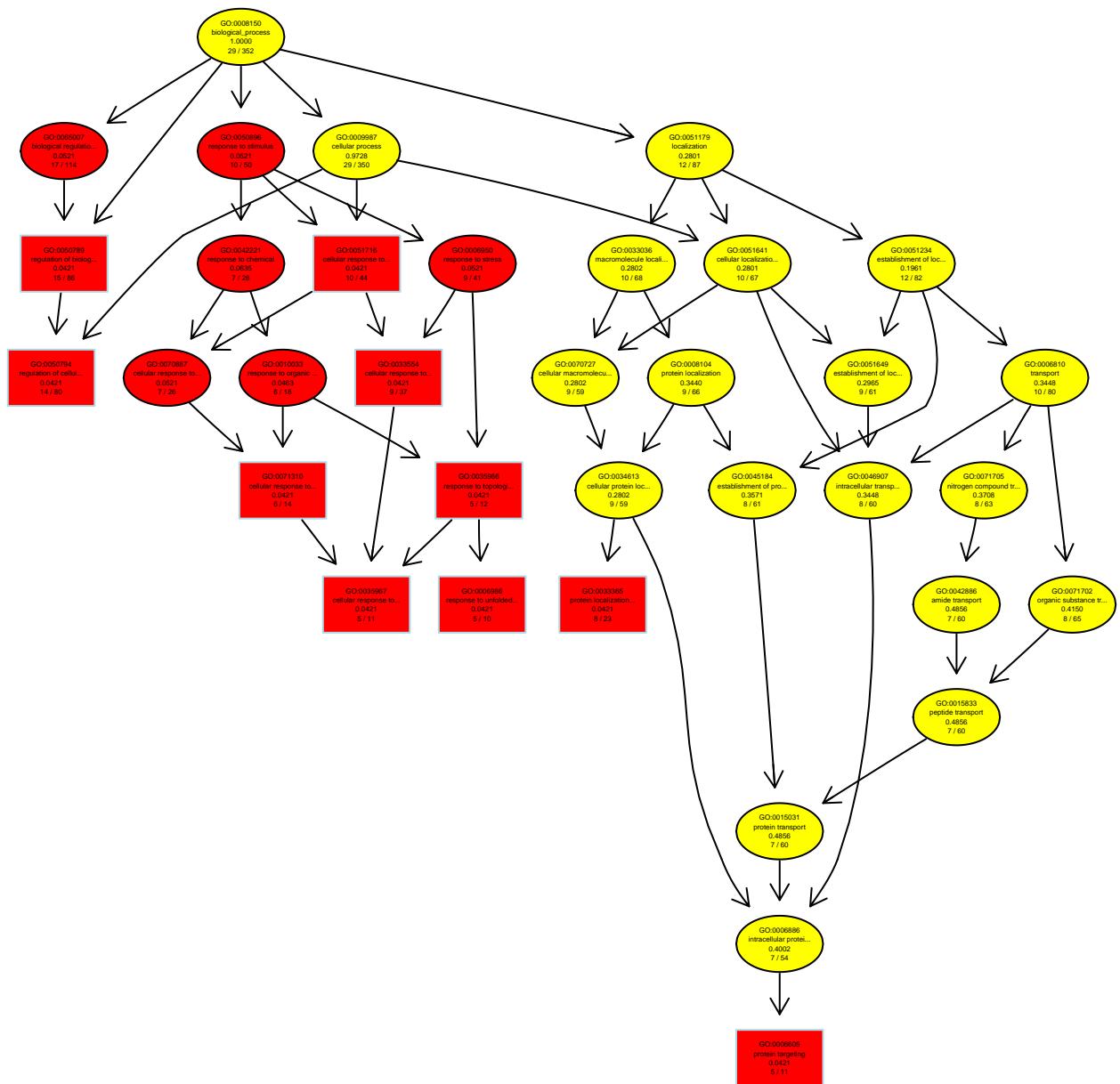


SUB2-TAP Up-regulated GO BP heatplot

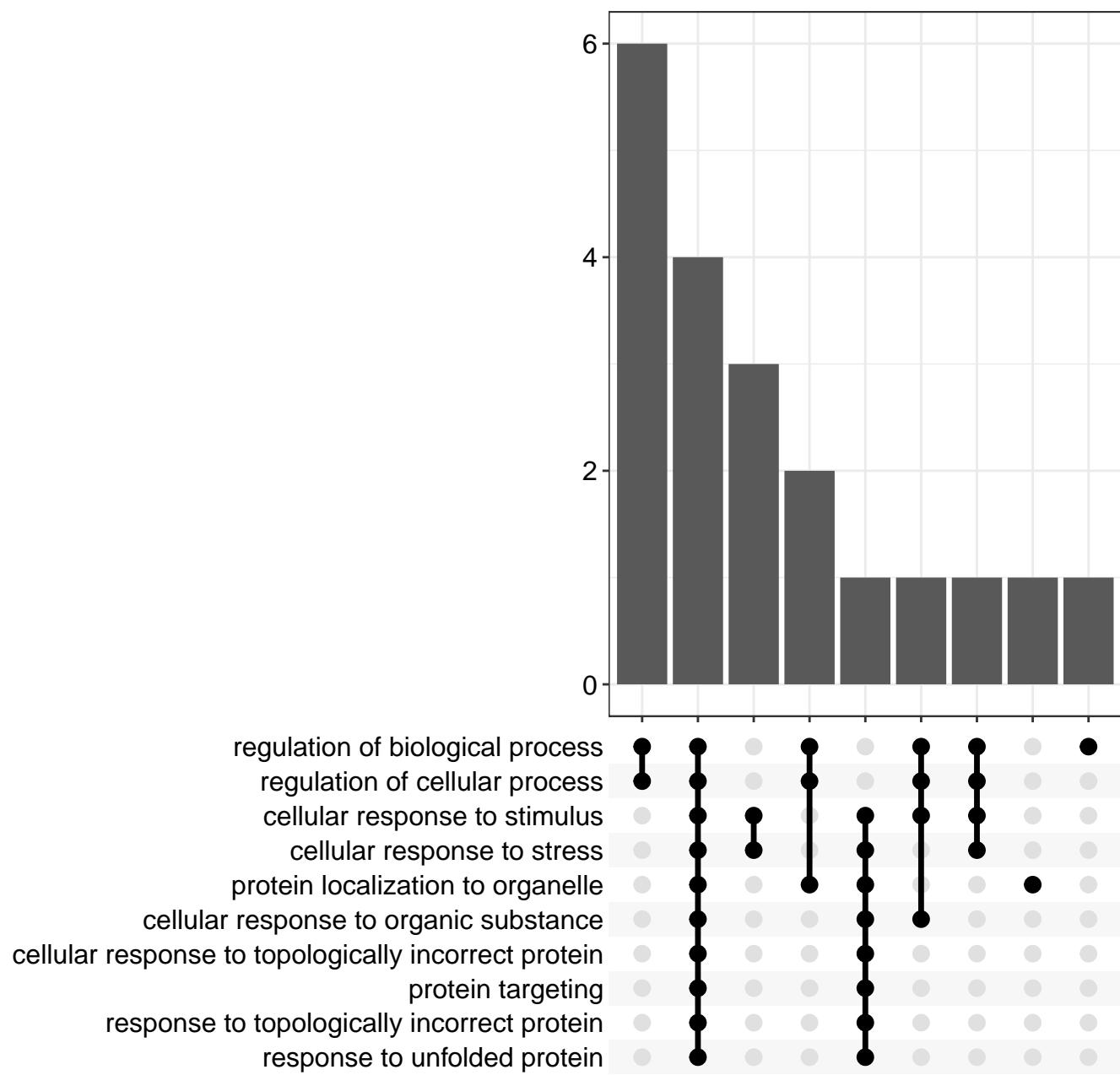


SUB2-TAP Up-regulated GO BP emapplot

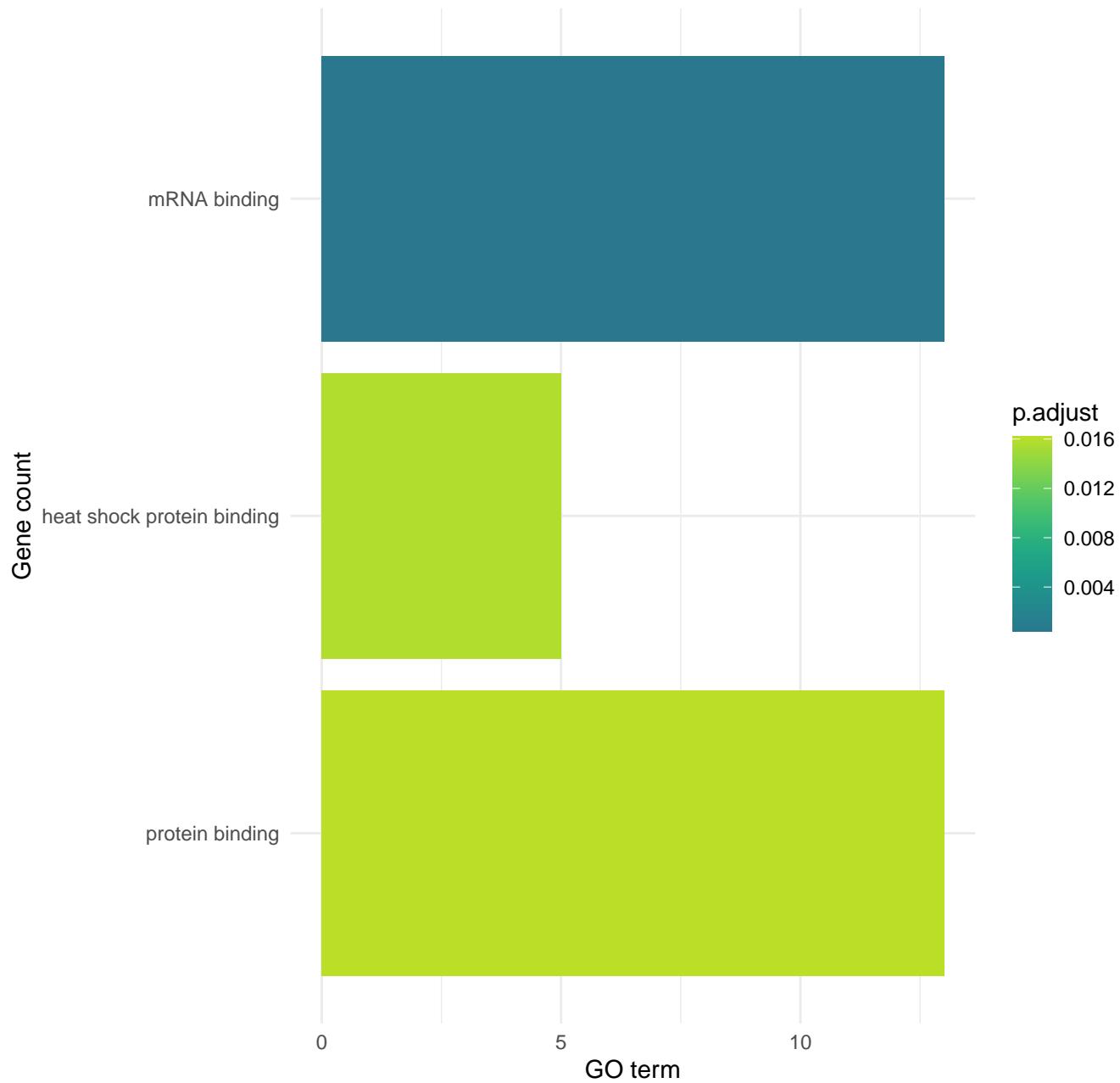




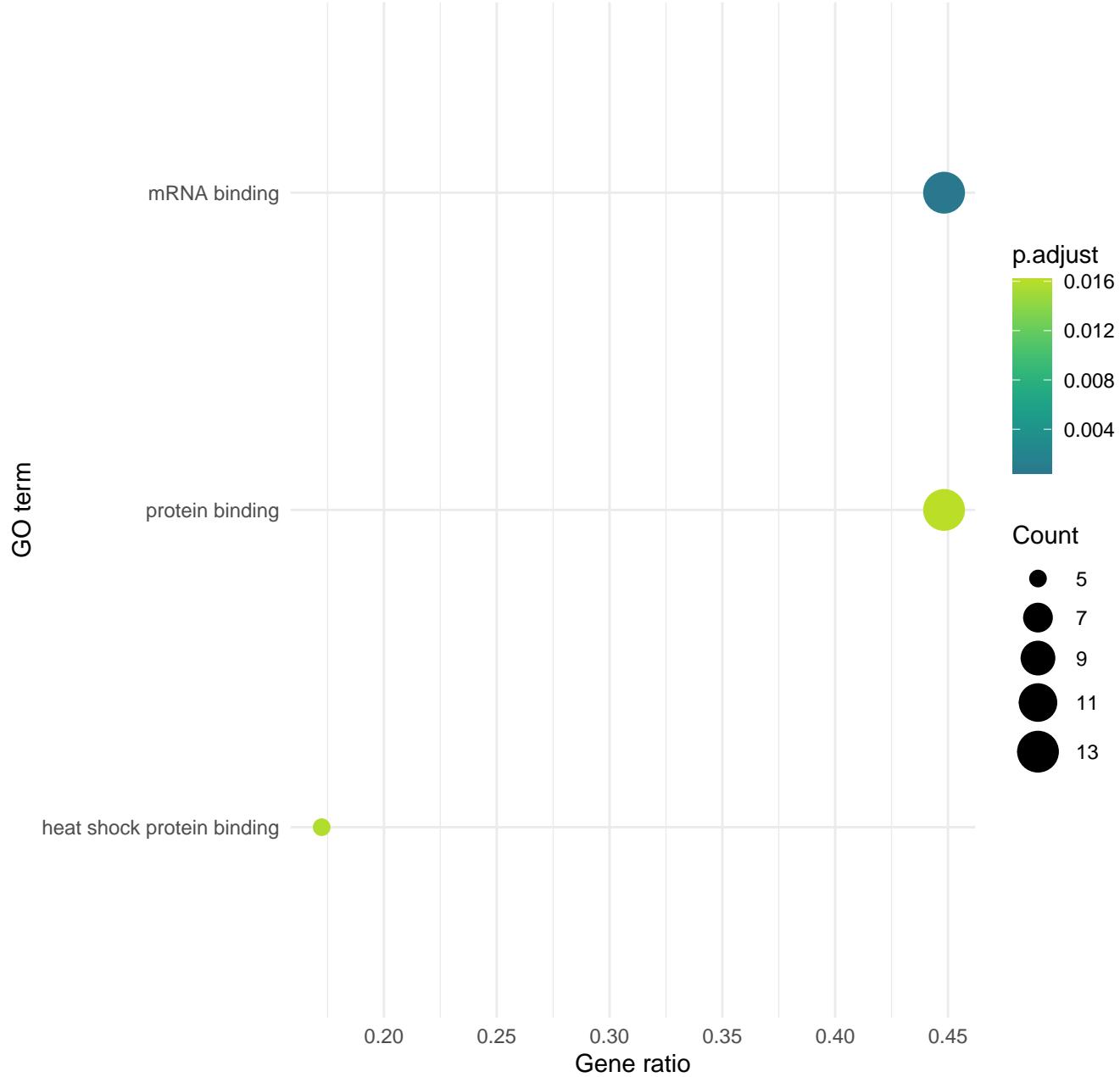
SUB2-TAP Up-regulated GO BP upsets



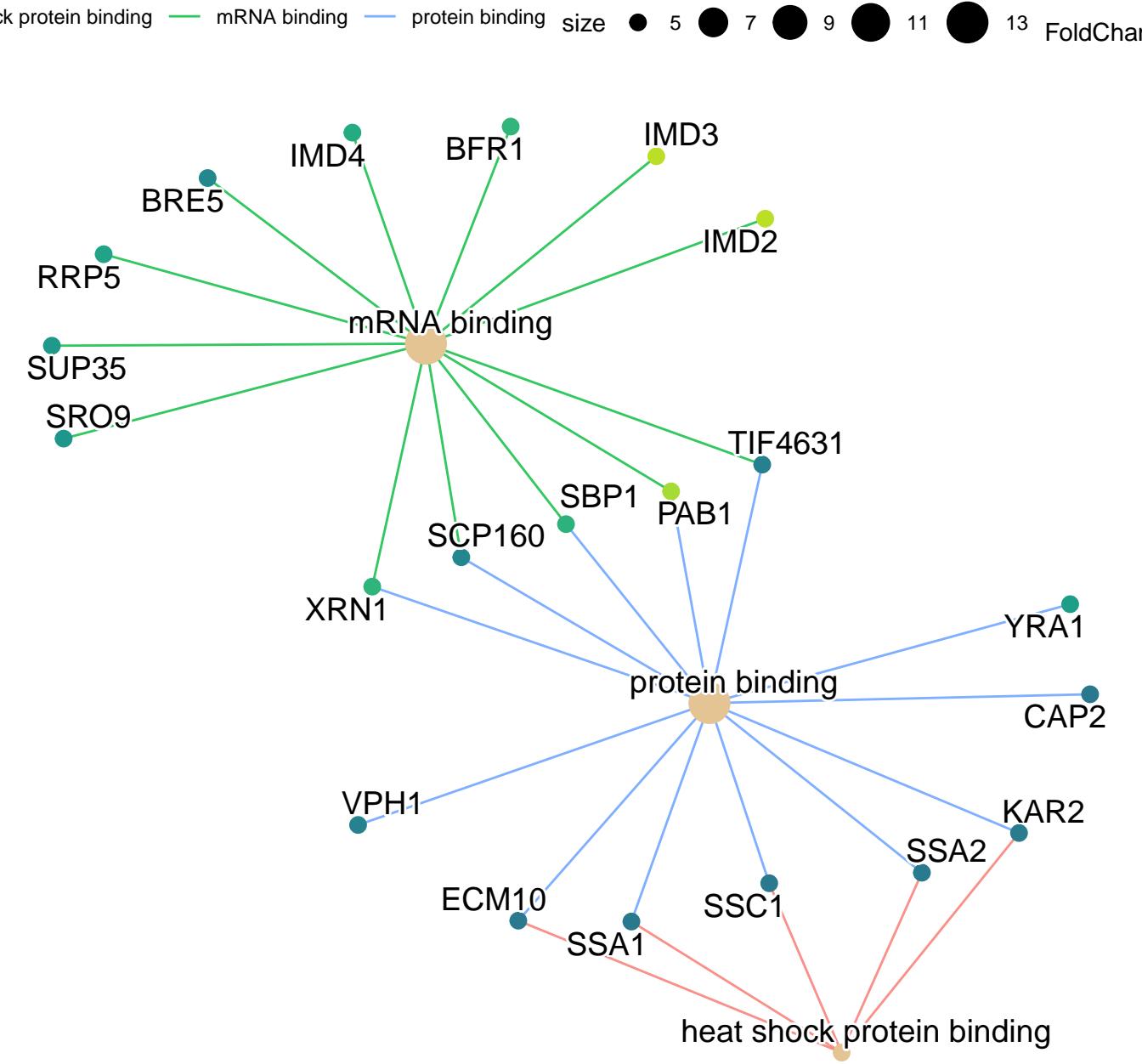
SUB2-TAP Up-regulated GO MF barplot



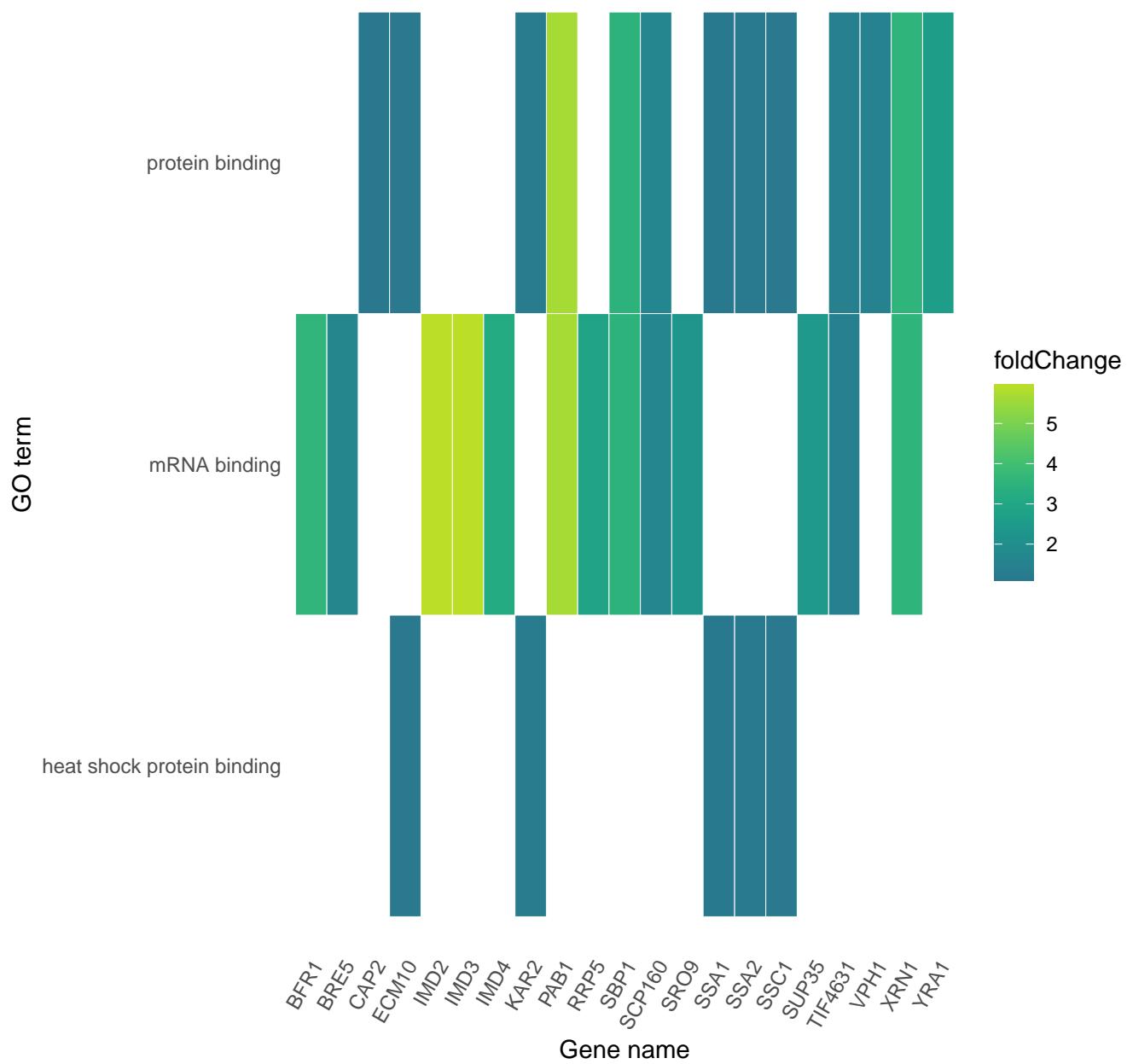
SUB2-TAP Up-regulated GO MF dotplot



SUB2-TAP Up-regulated GO MF cnetplot



SUB2-TAP Up-regulated GO MF heatplot



SUB2-TAP Up-regulated GO MF emapplot

protein binding

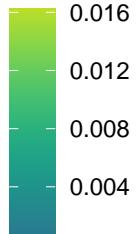
heat shock protein binding

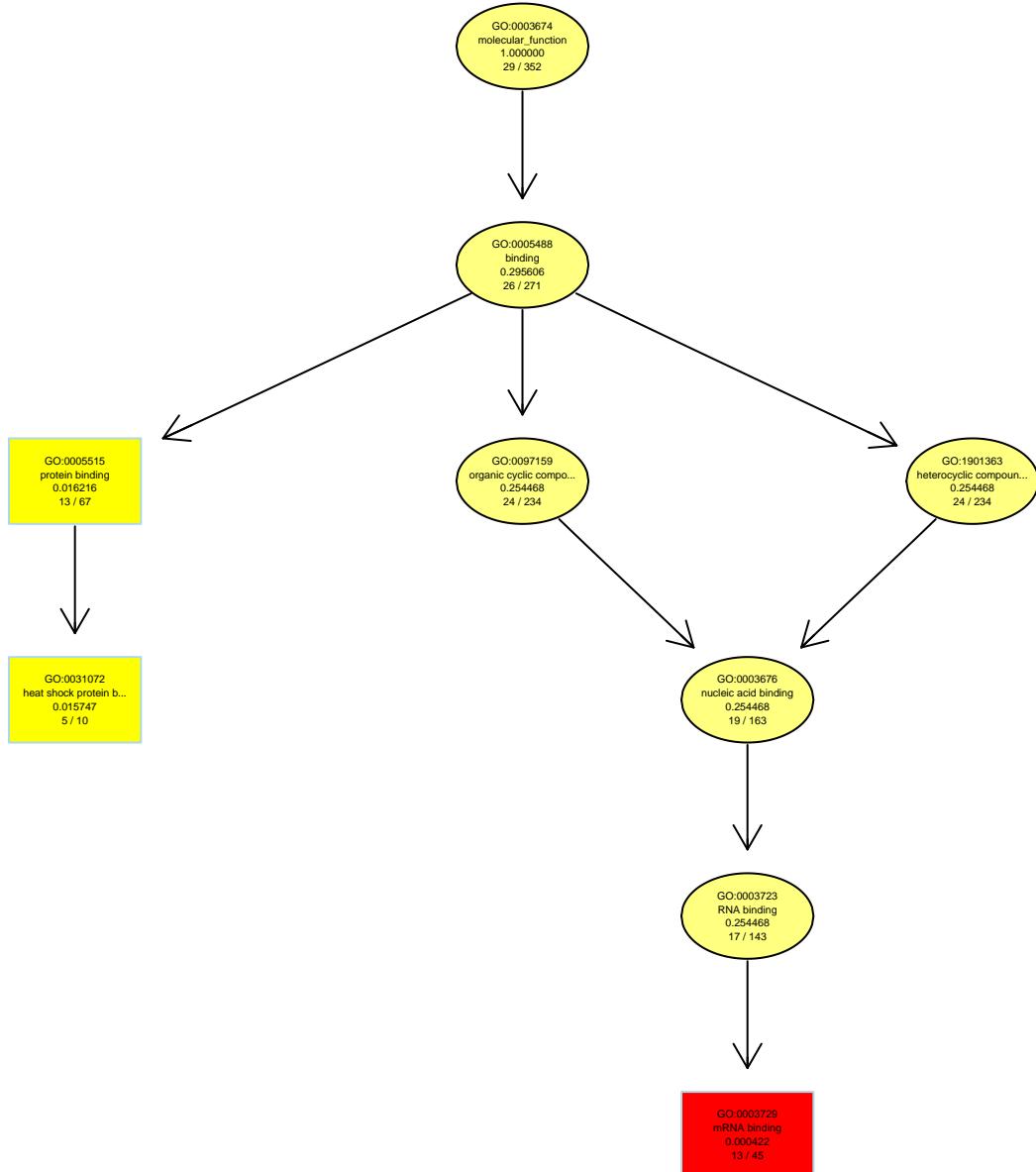
mRNA binding

size

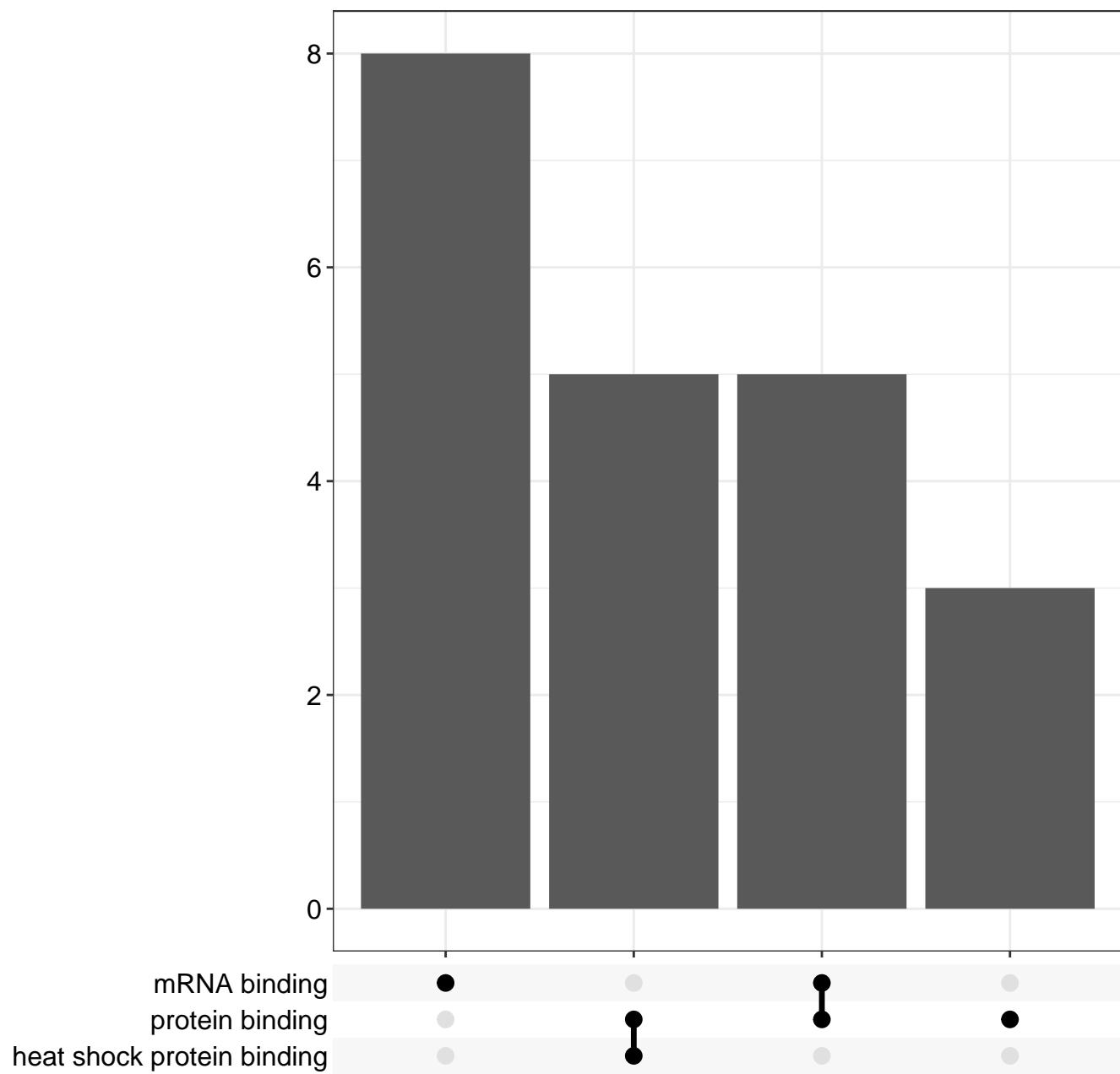
- 5
- 7
- 9
- 11
- 13

FoldChange

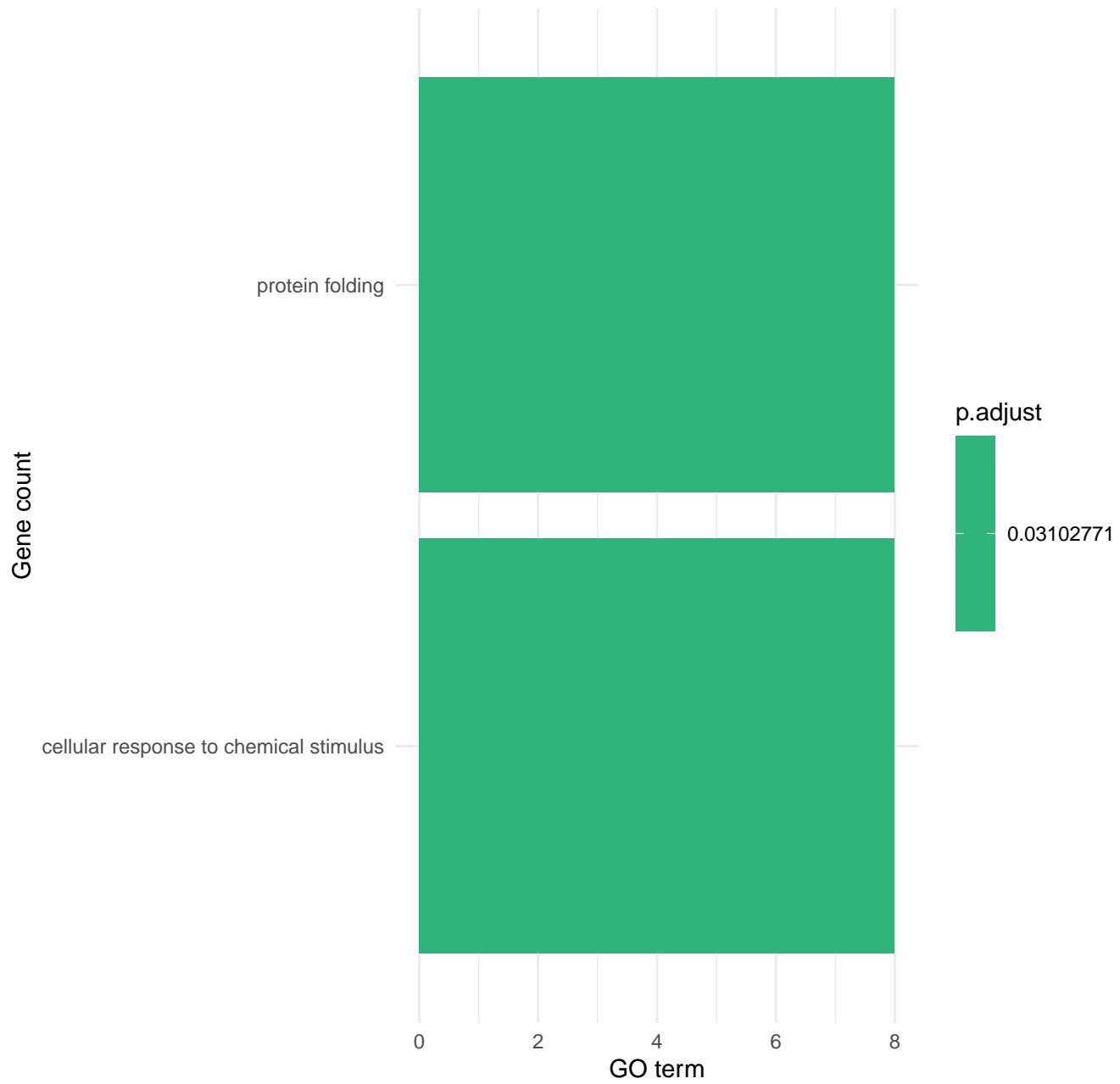




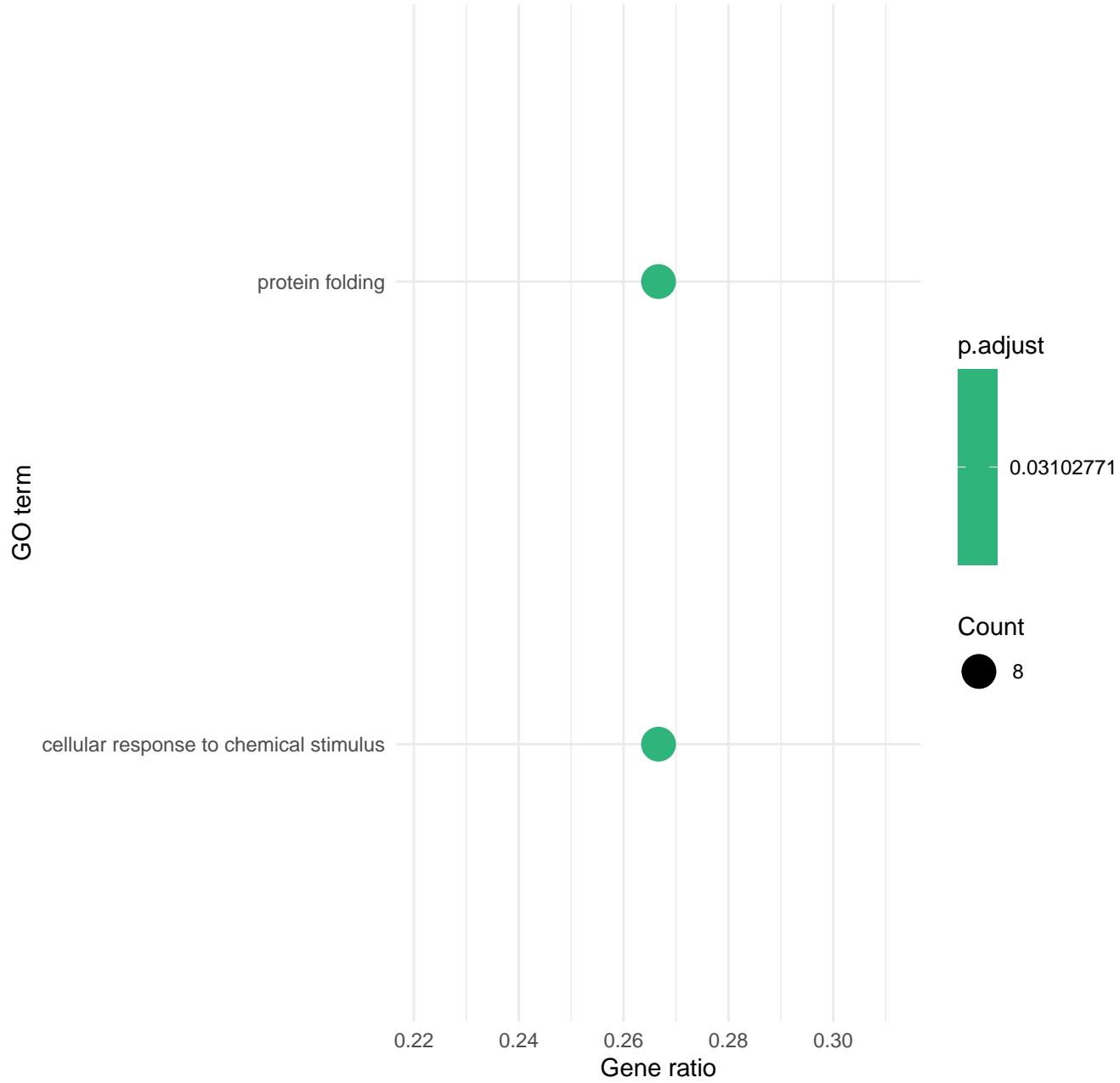
SUB2-TAP Up-regulated GO MF upsetplot



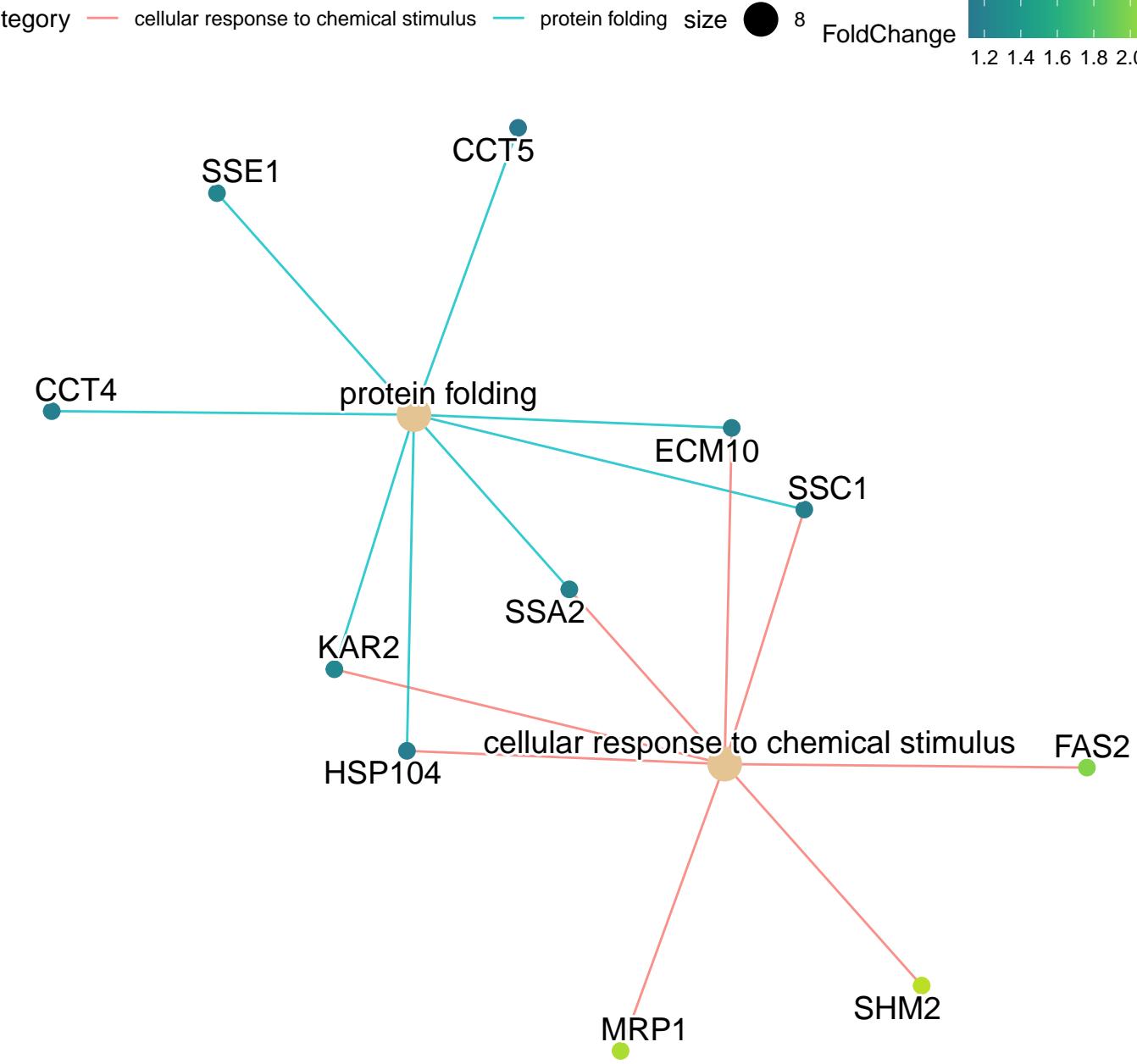
CFT1-TAP Up-regulated GO BP barplot



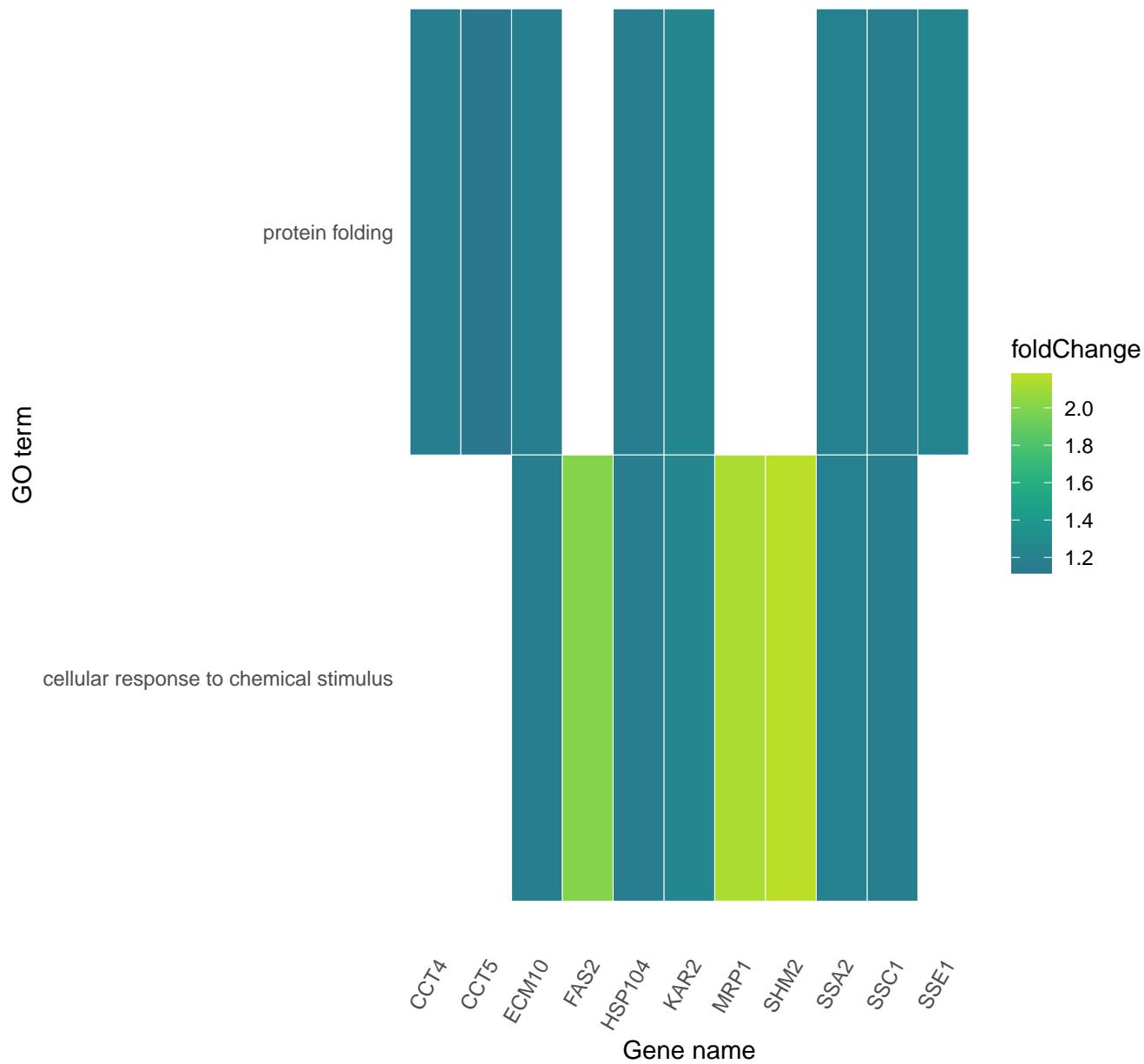
CFT1–TAP Up-regulated GO BP dotplot



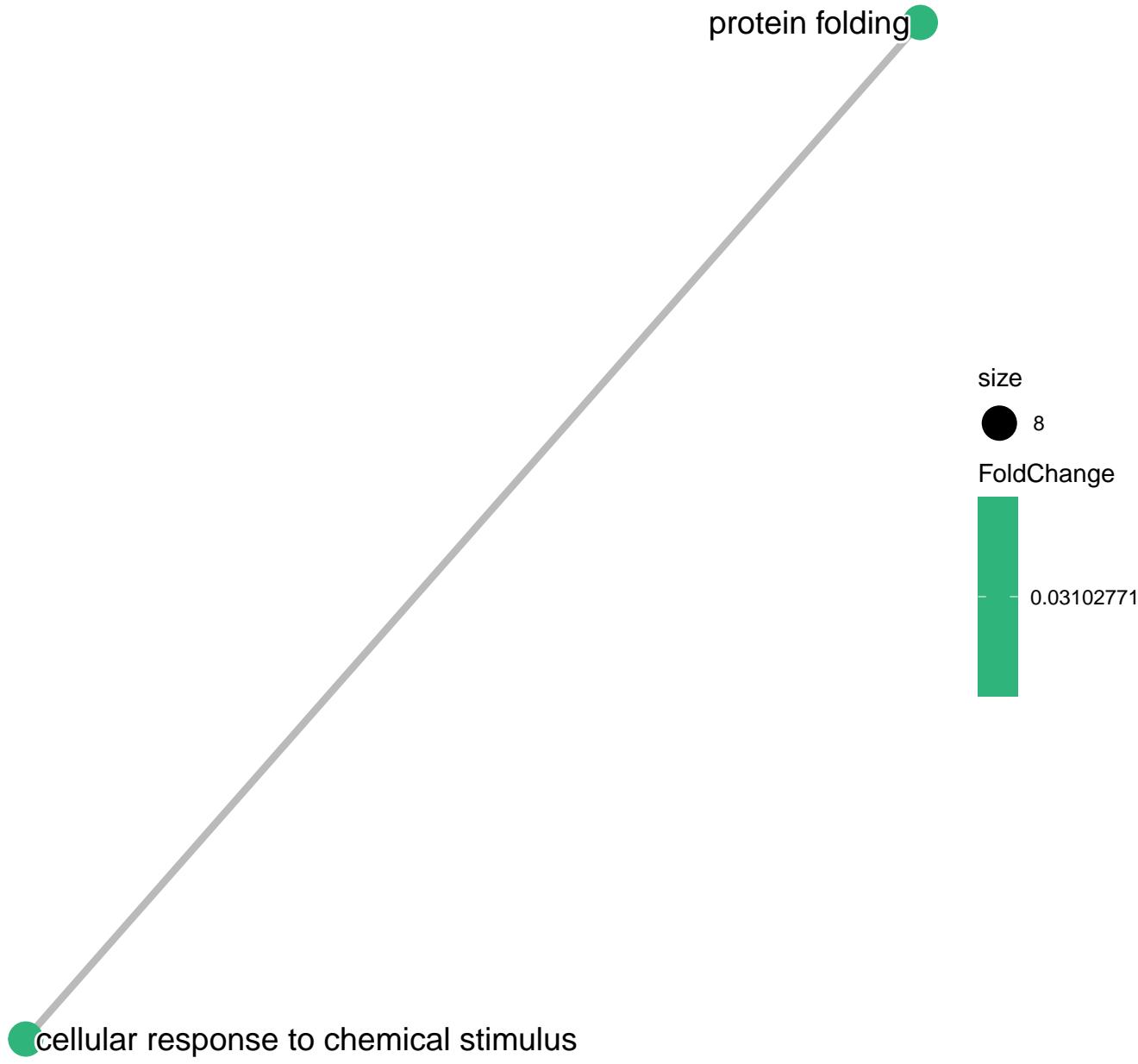
CFT1-TAP Up-regulated GO BP cnetplot

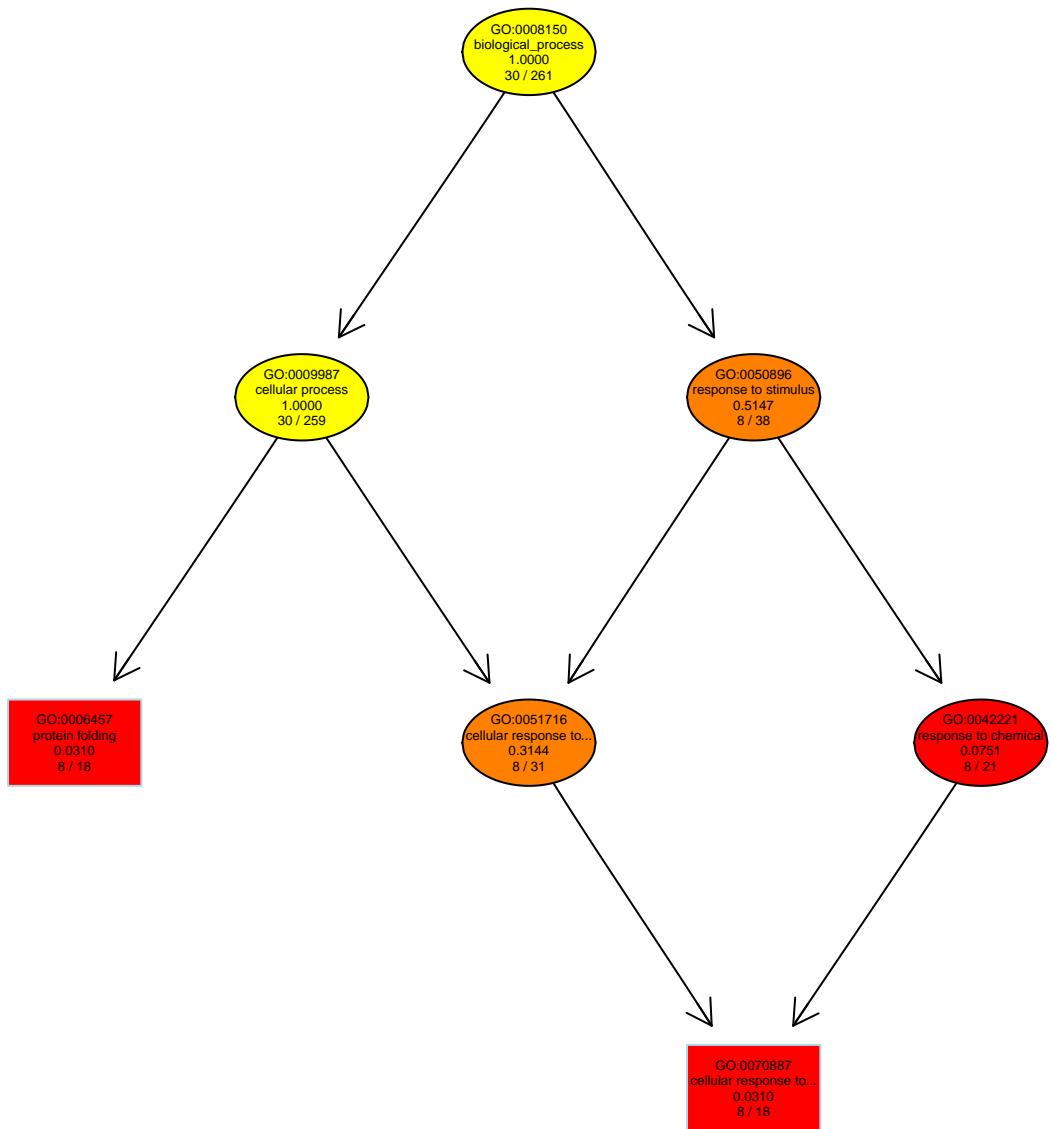


CFT1-TAP Up-regulated GO BP heatplot

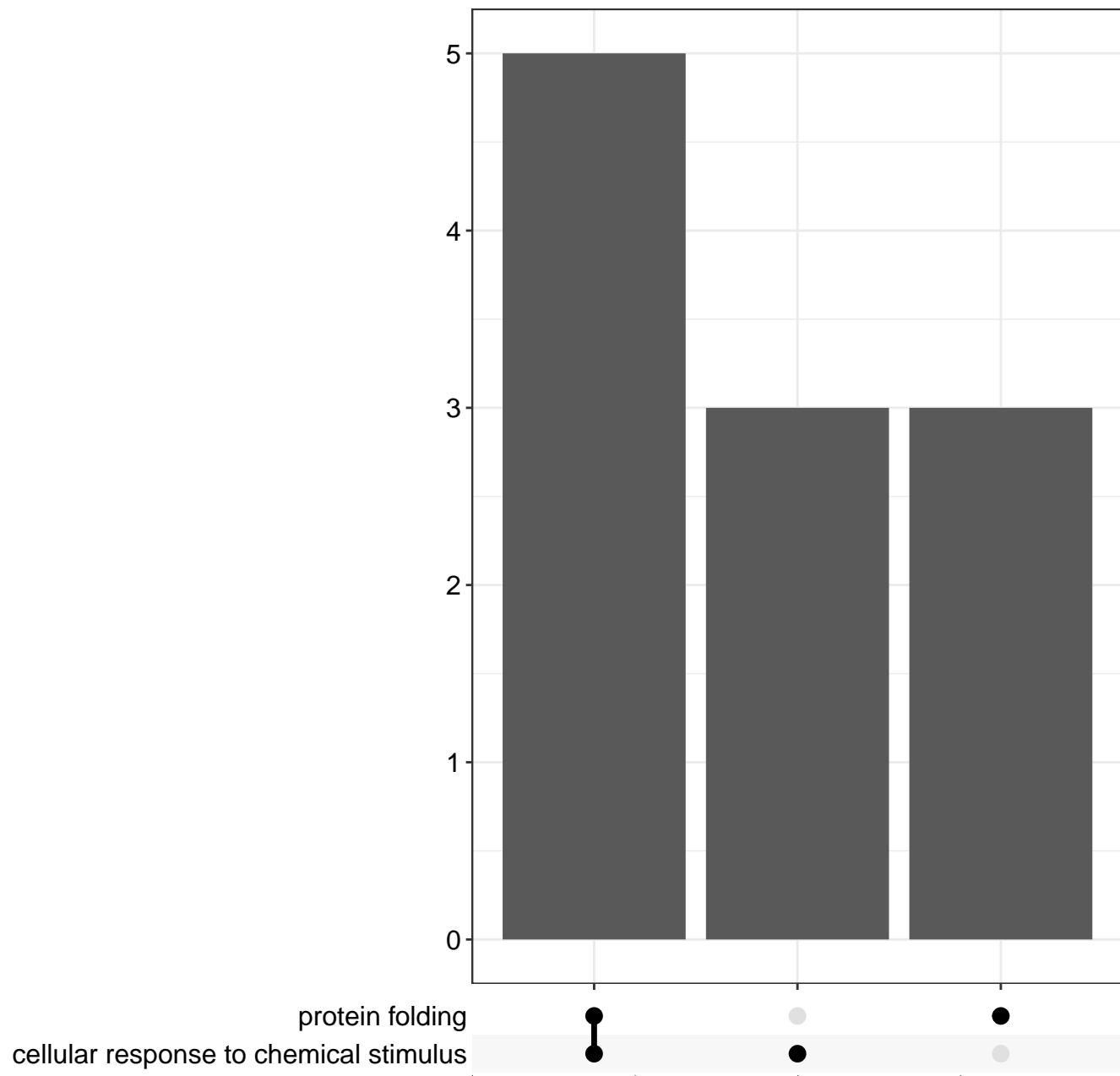


CFT1-TAP Up-regulated GO BP emapplot

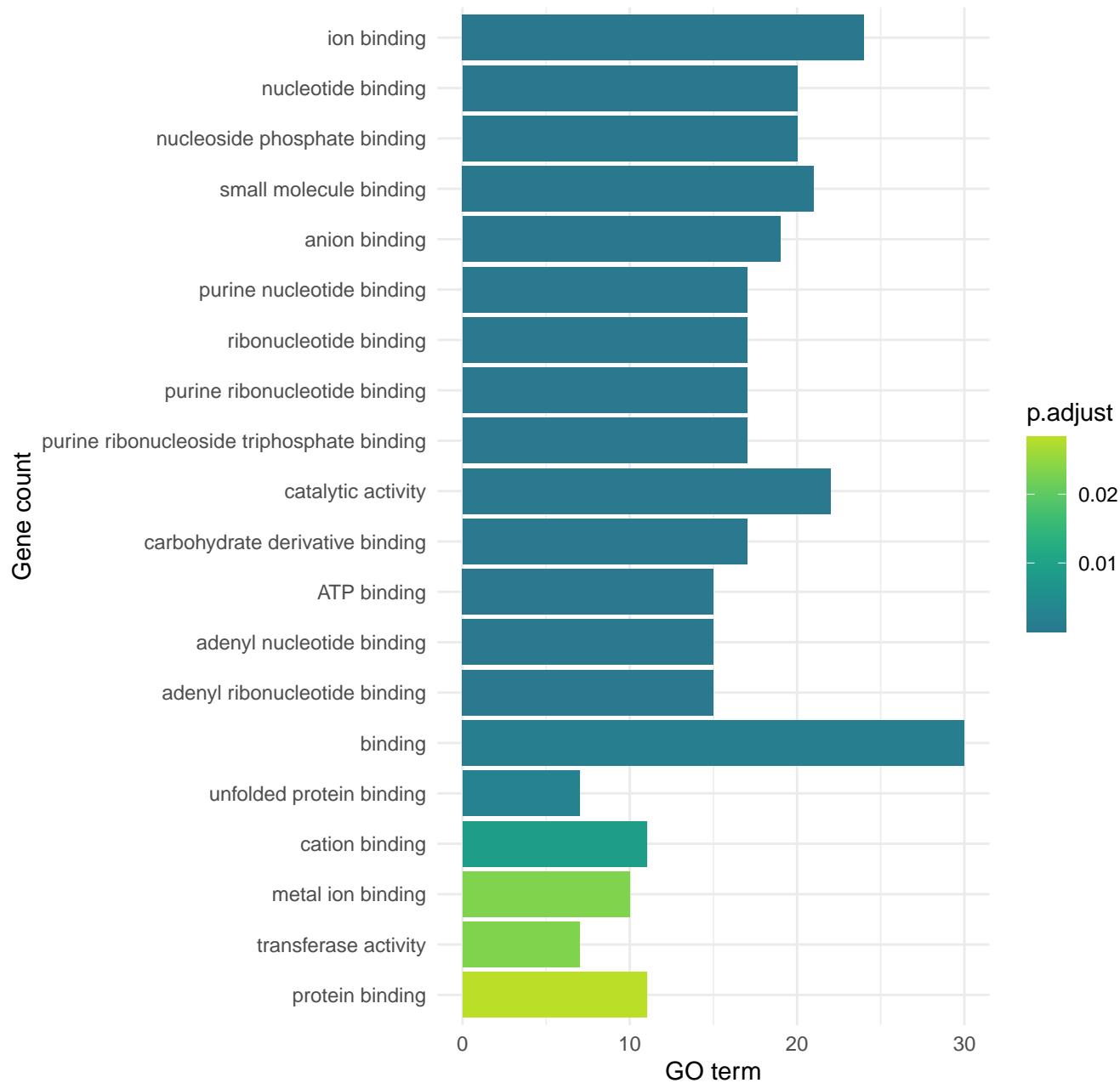




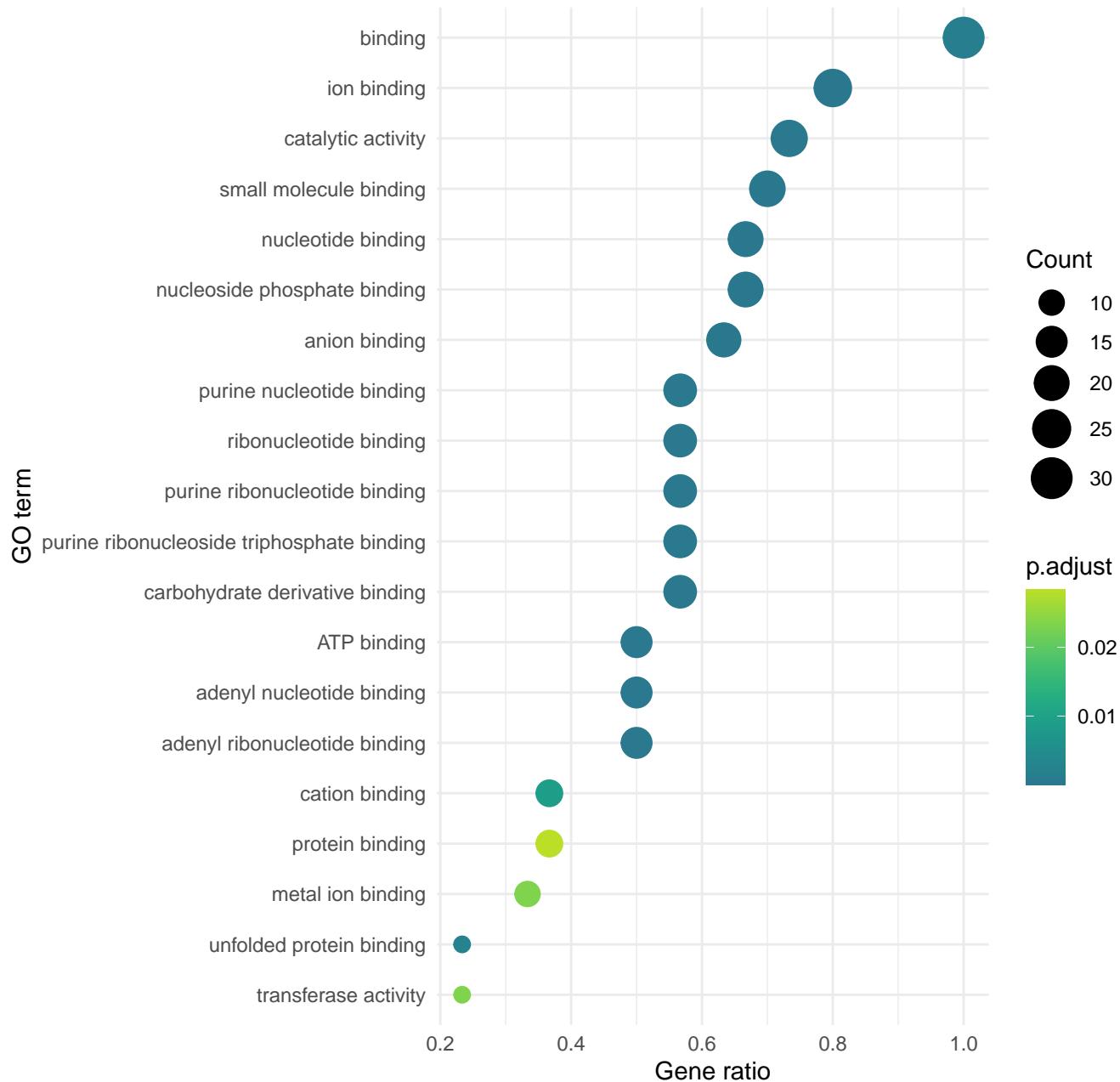
CFT1-TAP Up-regulated GO BP upsetplot



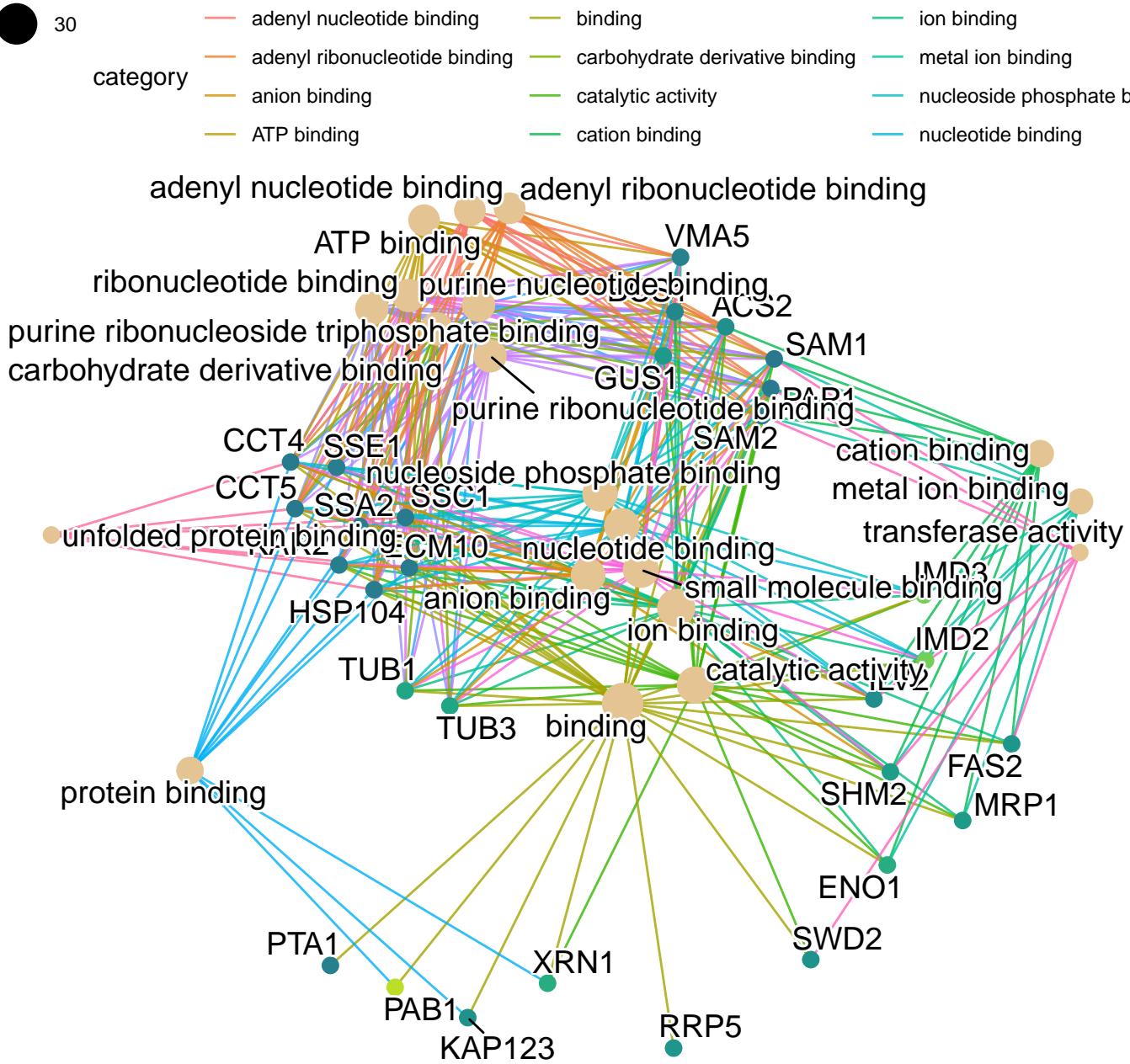
CFT1-TAP Up-regulated GO MF barplot



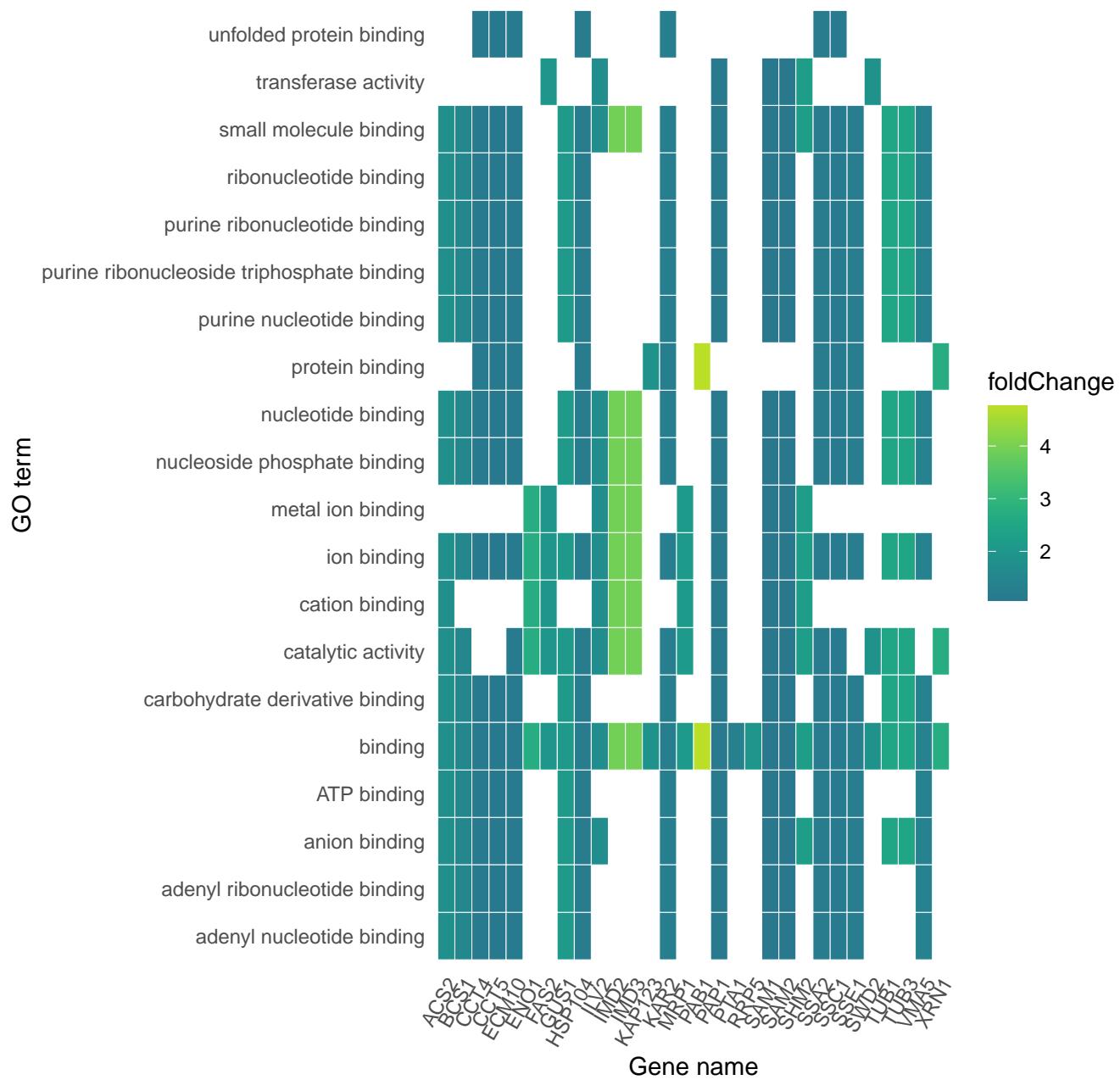
CFT1-TAP Up-regulated GO MF dotplot



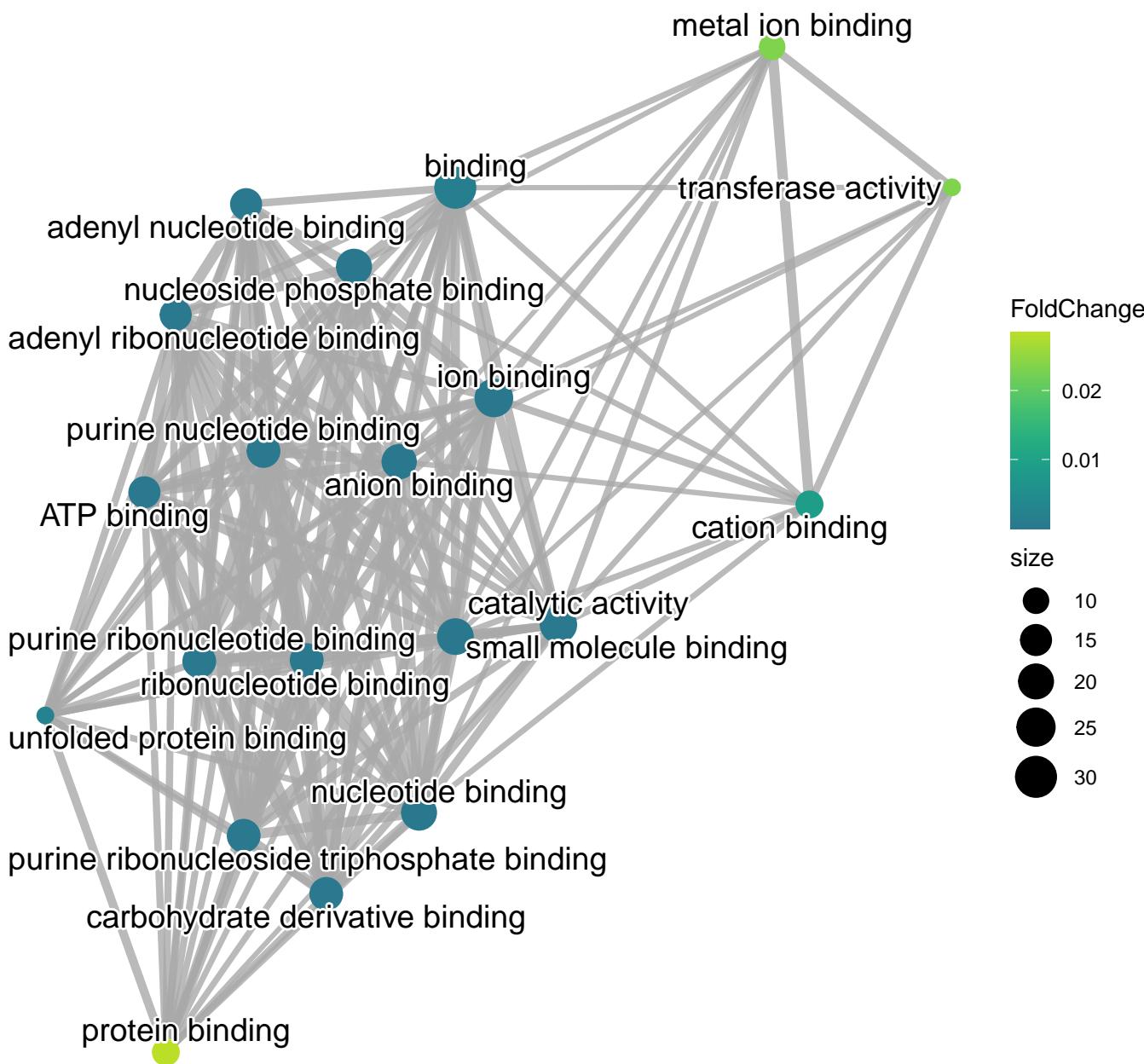
CFT1-TAP Up-regulated GO MF cnetplot

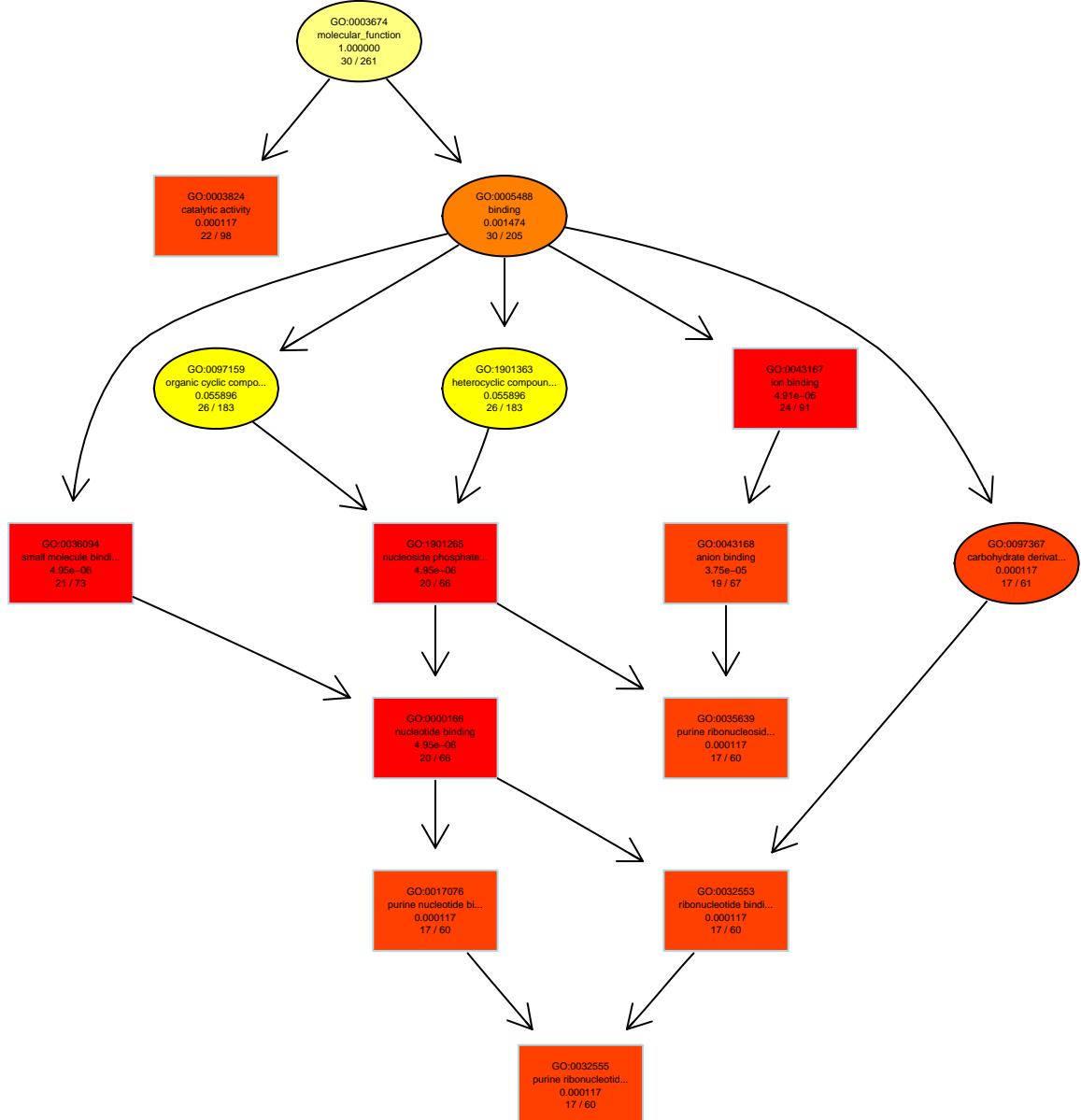


CFT1-TAP Up-regulated GO MF heatplot

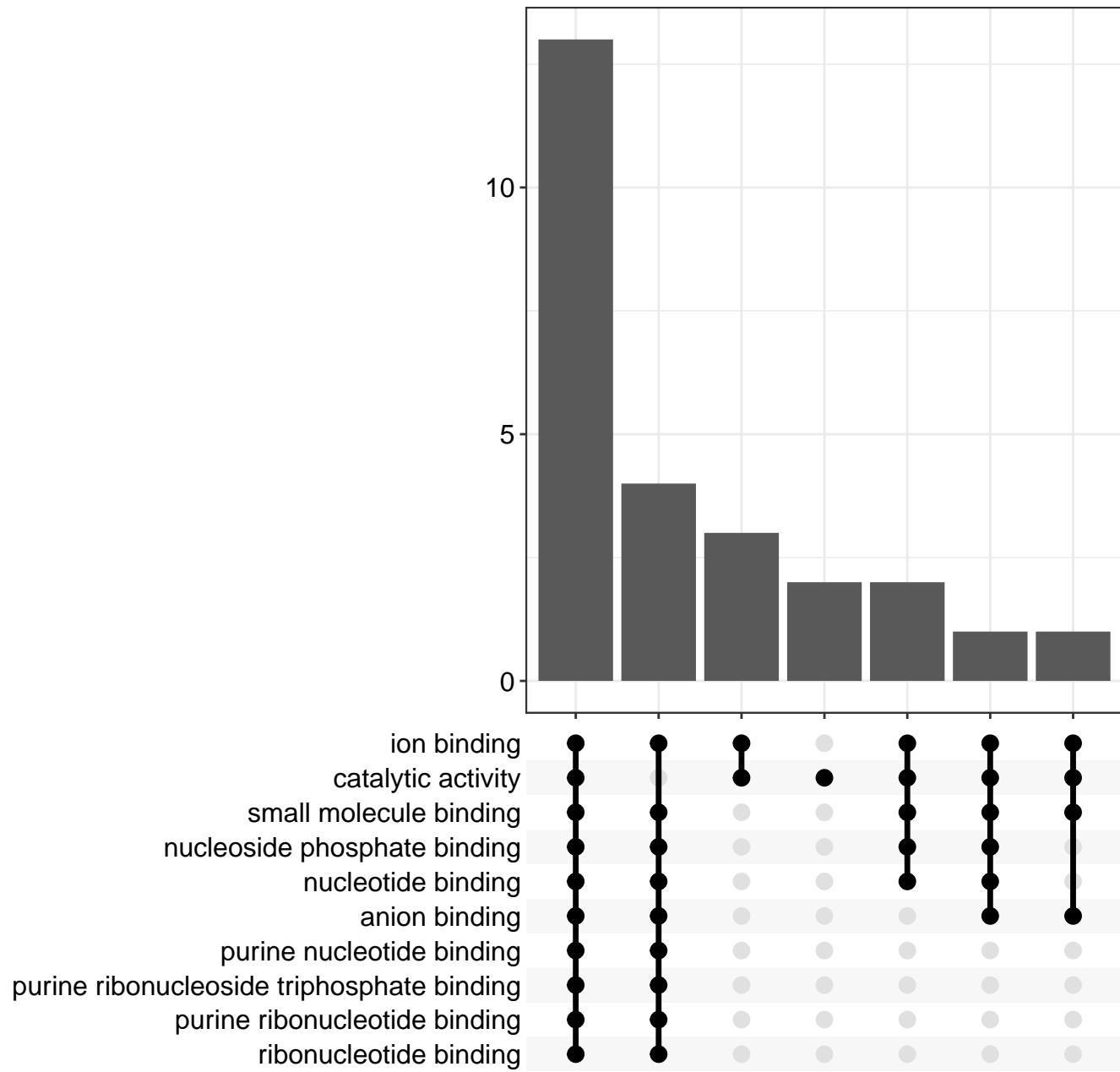


CFT1-TAP Up-regulated GO MF emapplot

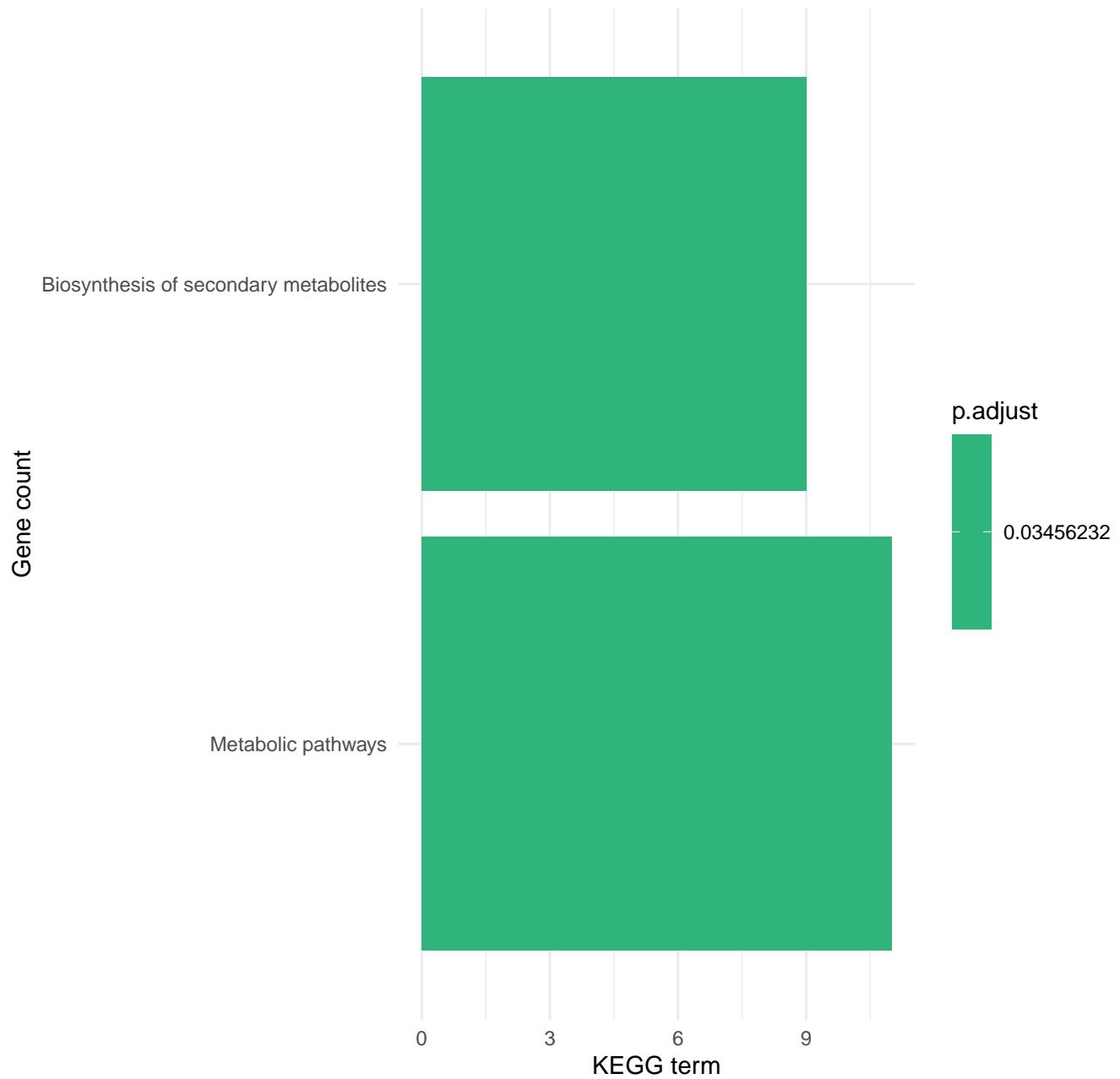




CFT1-TAP Up-regulated GO MF upsetplot



CFT1–TAP Up-regulated KEGG barplot



CFT1–TAP Up-regulated KEGG dotplot

KEGG term

Metabolic pathways

Biosynthesis of secondary metabolites

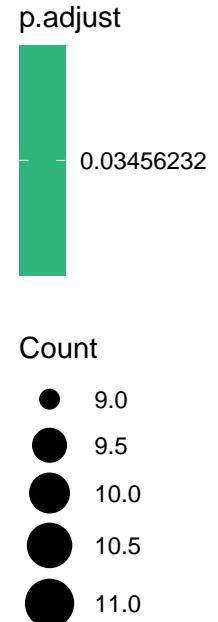
0.36

0.38

0.40

0.42

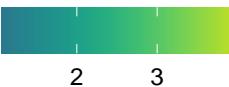
Gene ratio



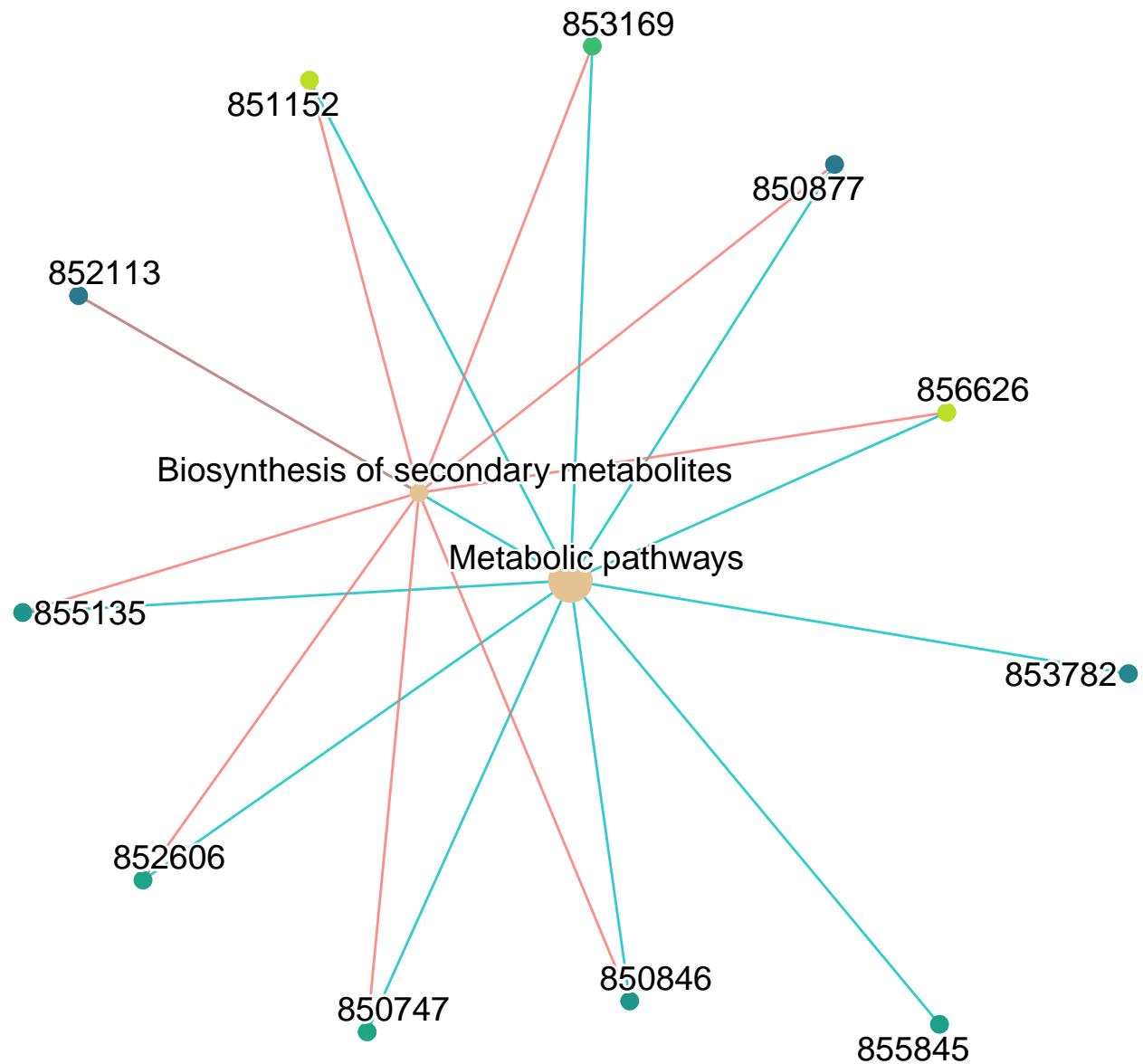
CFT1-TAP Up-regulated KEGG dotplot

of secondary metabolites Metabolic pathways

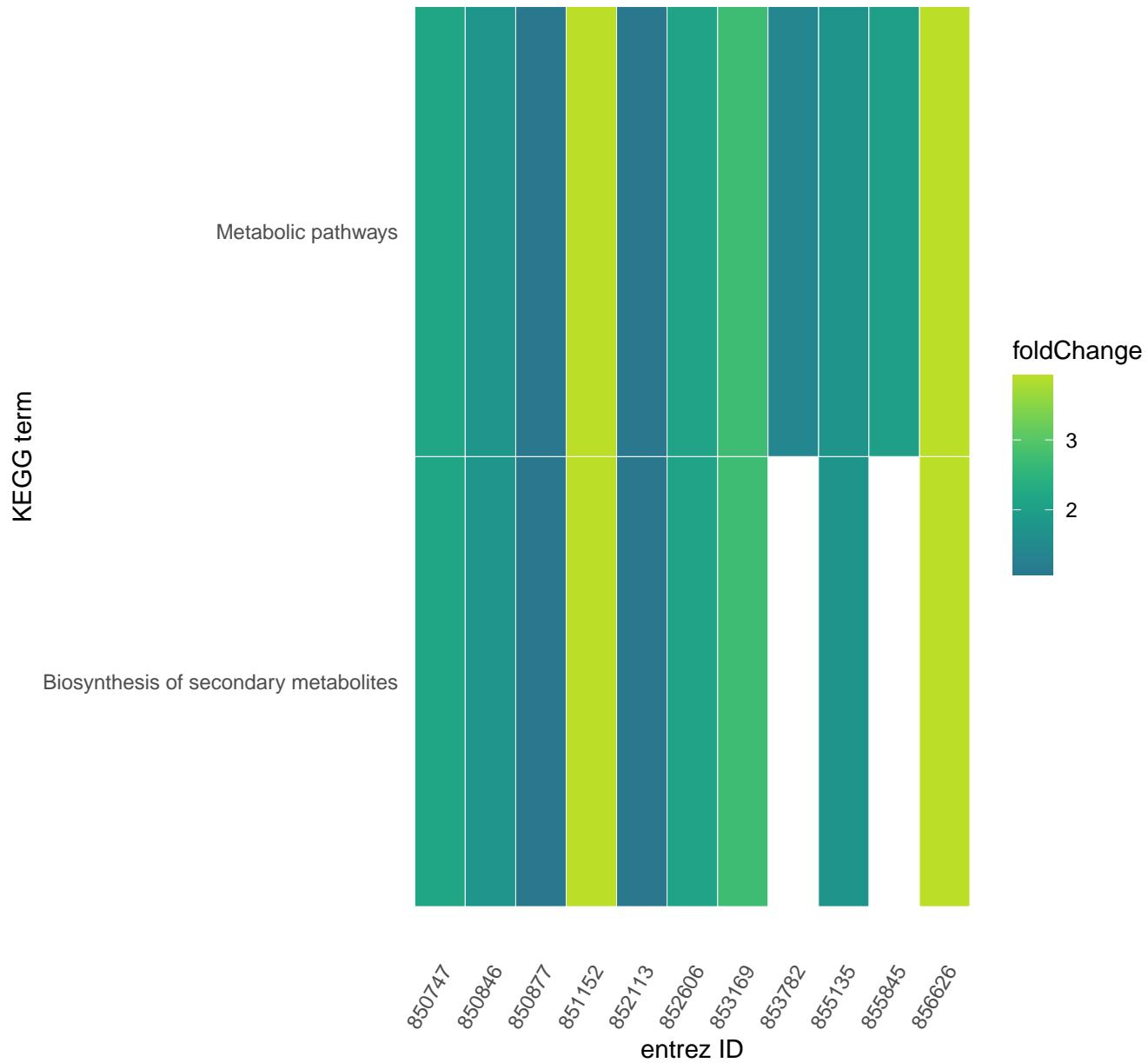
FoldChange



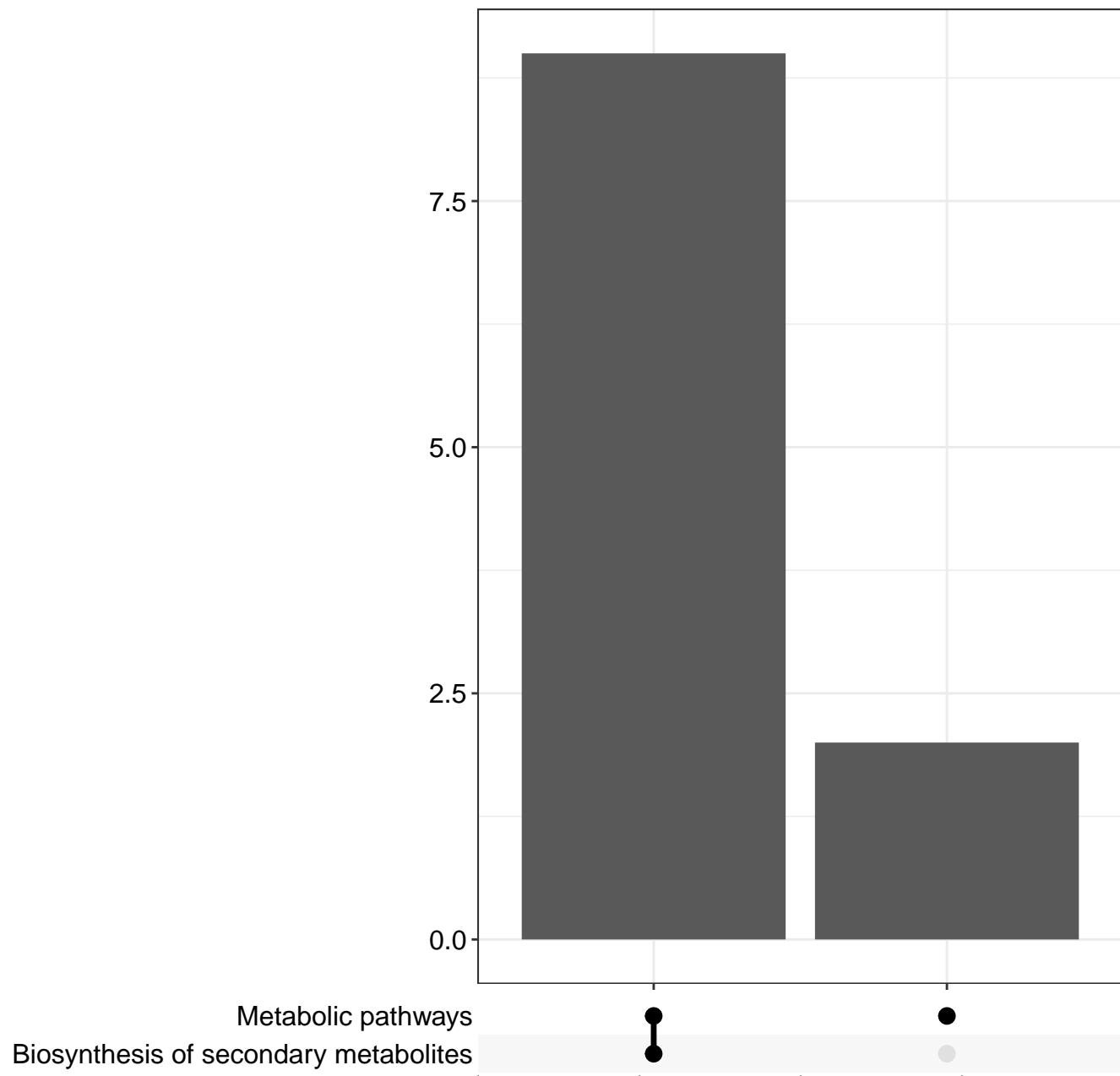
size ● 9.0 ● 9.5 ● 9.8



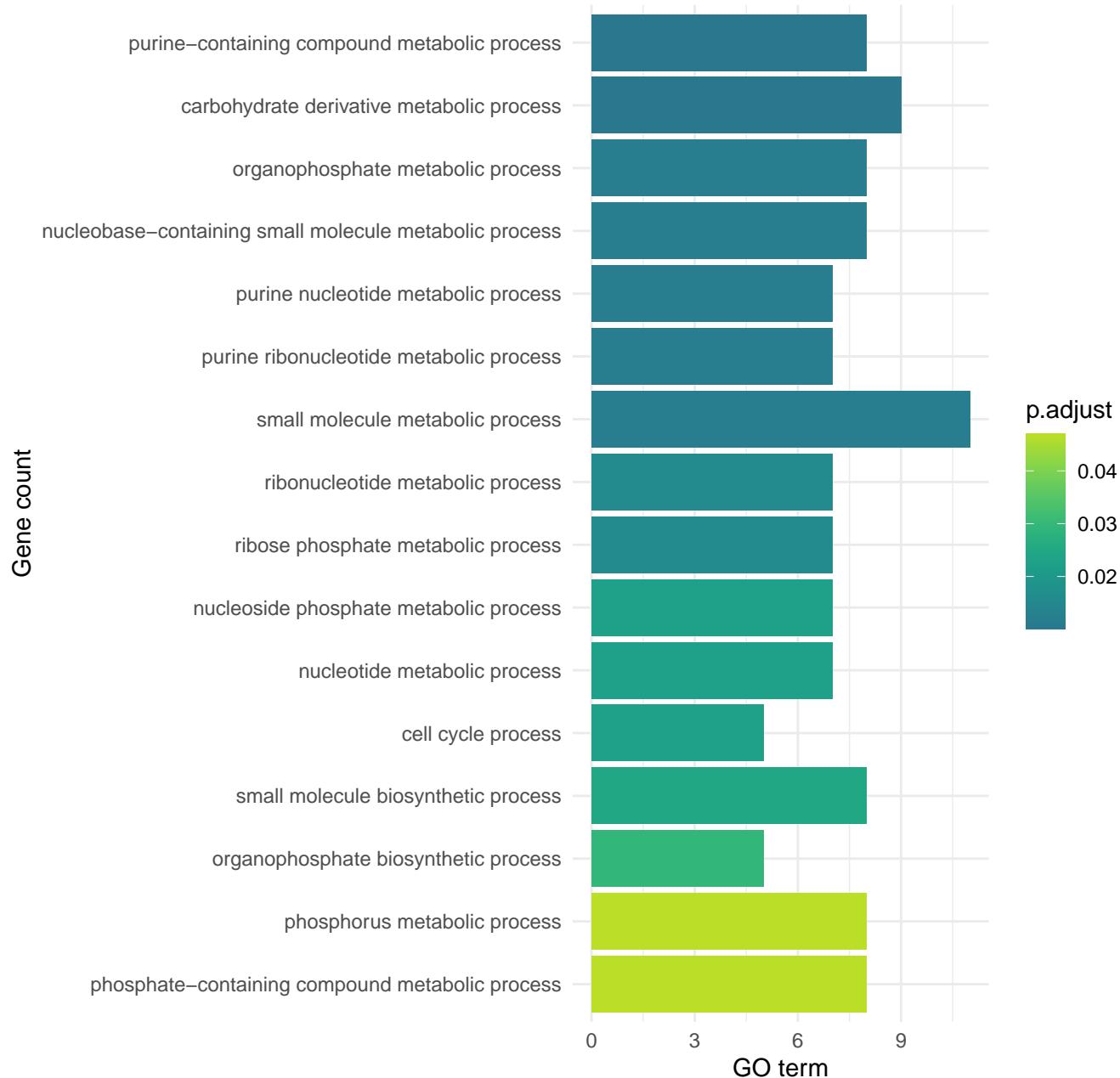
CFT1–TAP Up-regulated KEGG heatplot



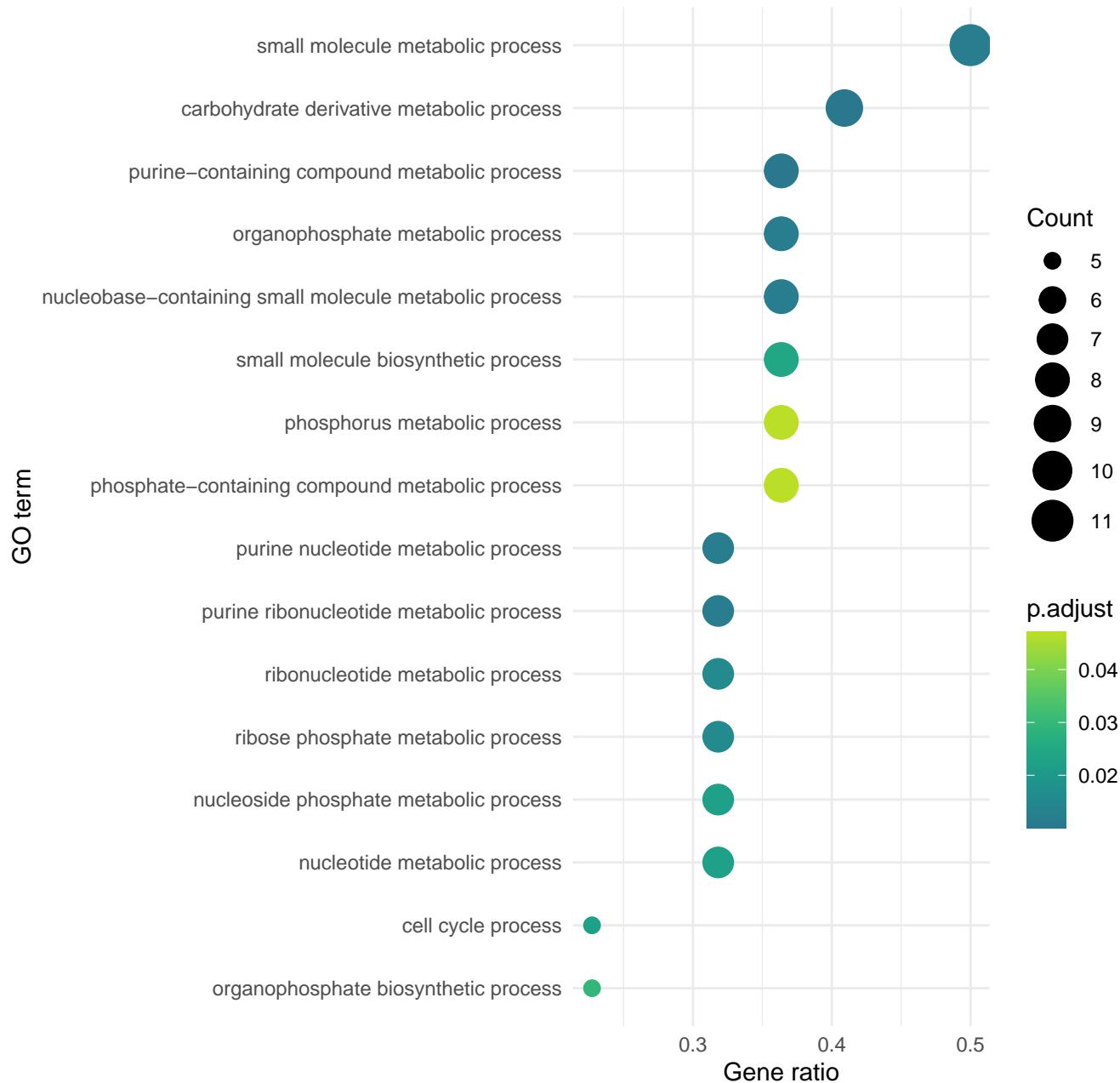
CFT1-TAP Up-regulated KEGG upsetplot



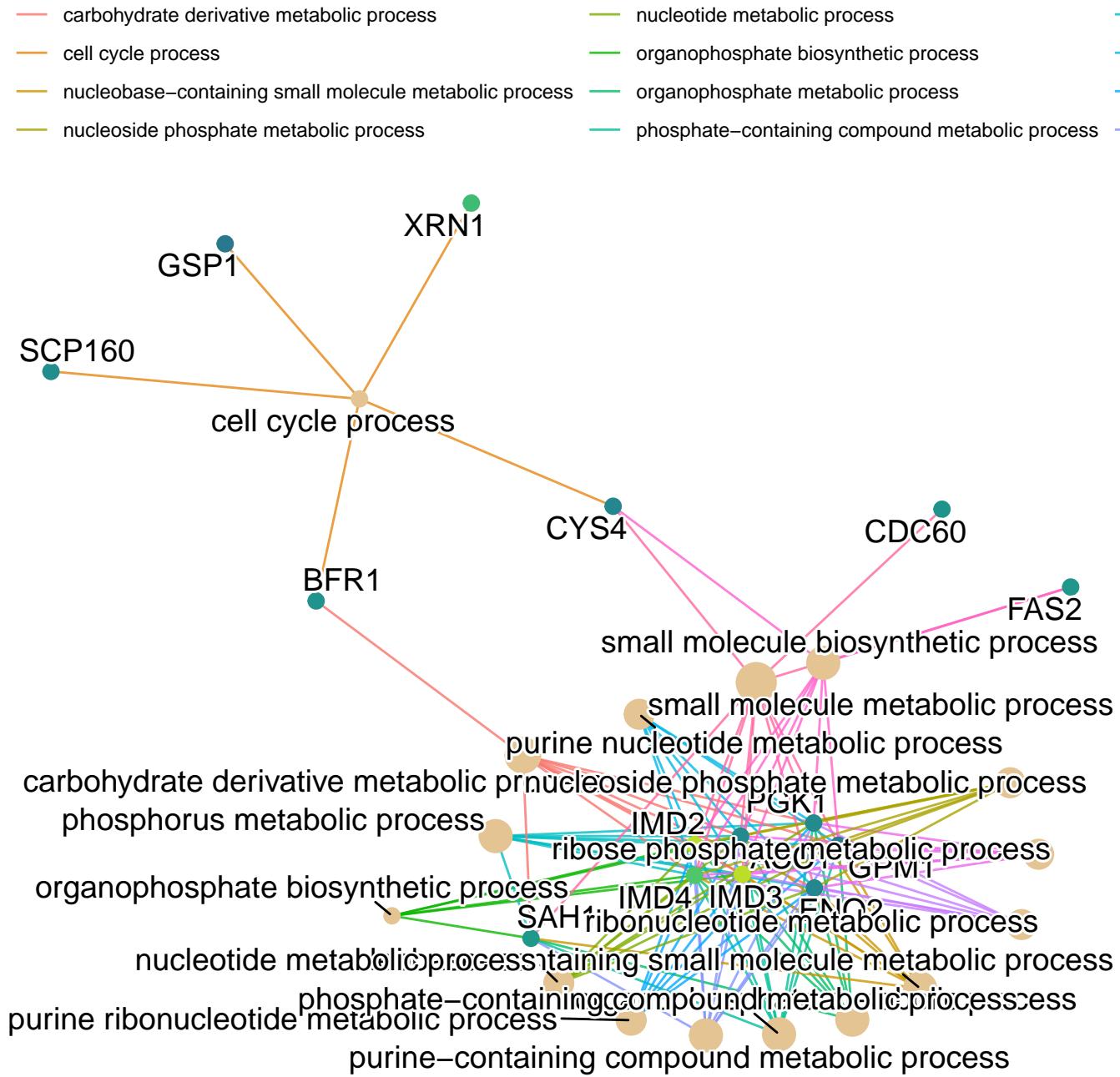
RNA14–TAP Up-regulated GO BP barplot



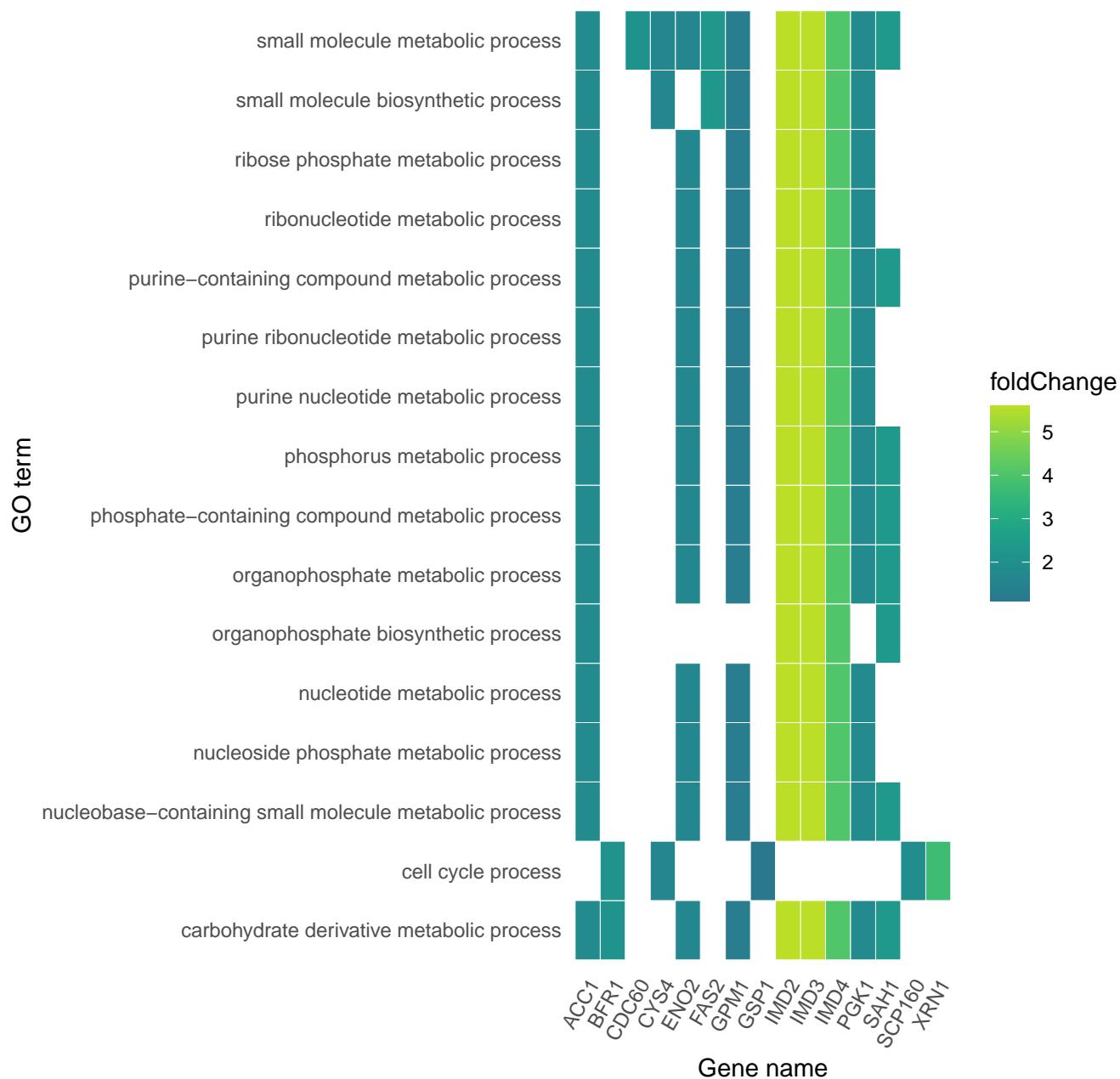
RNA14-TAP Up-regulated GO BP dotplot



RNA14-TAP Up-regulated GO BP cnetplot

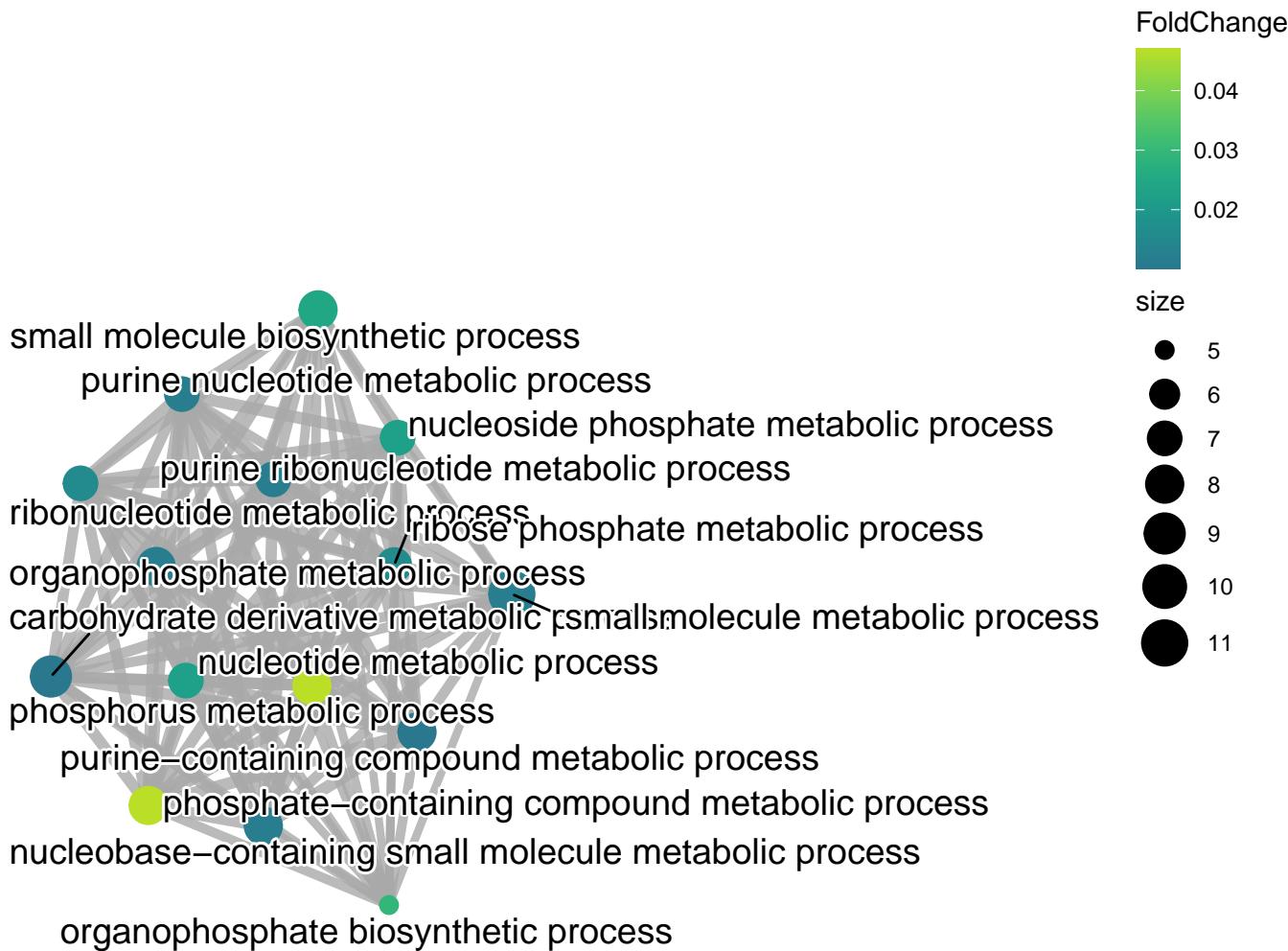


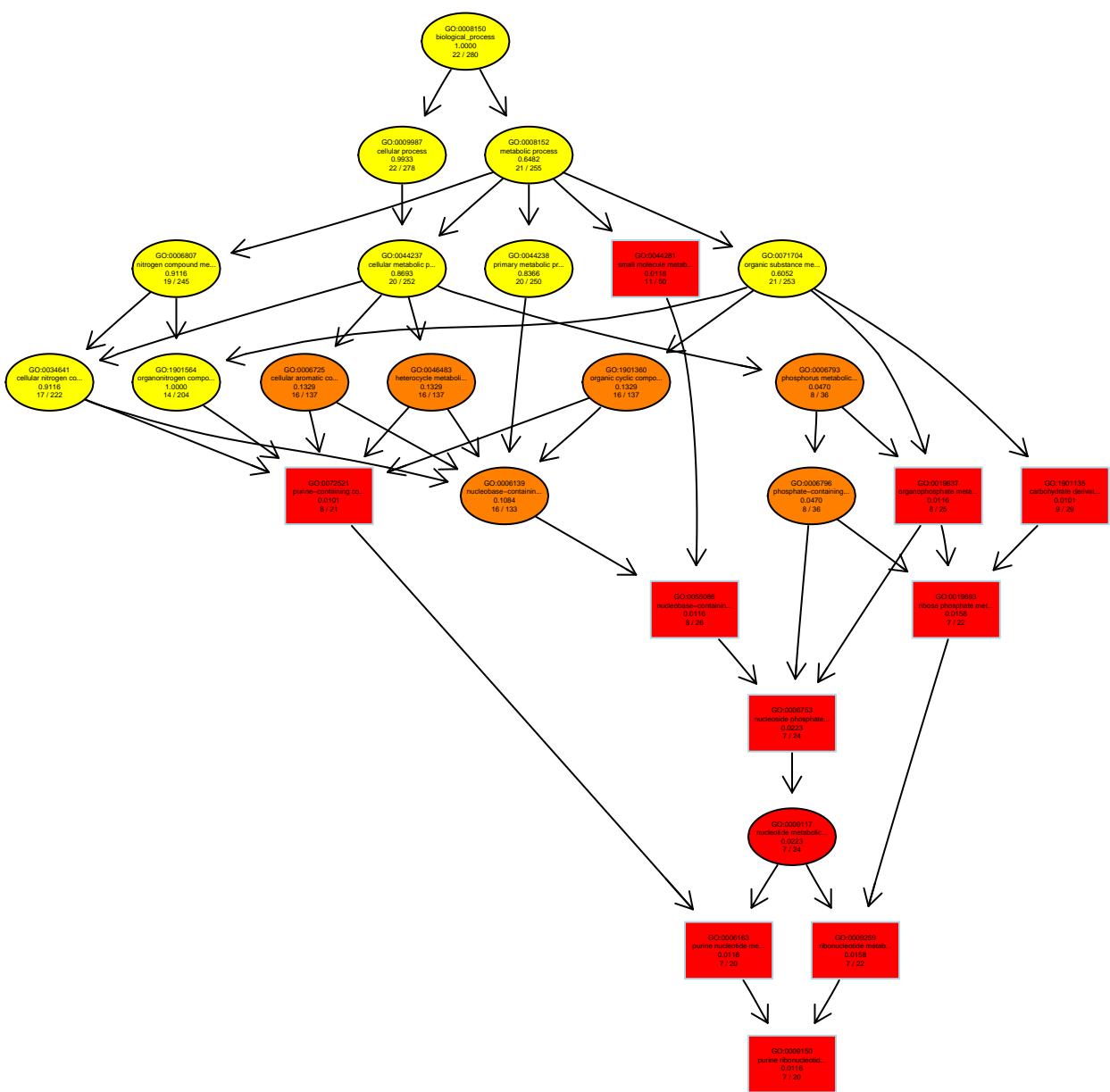
RNA14-TAP Up-regulated GO BP heatplot



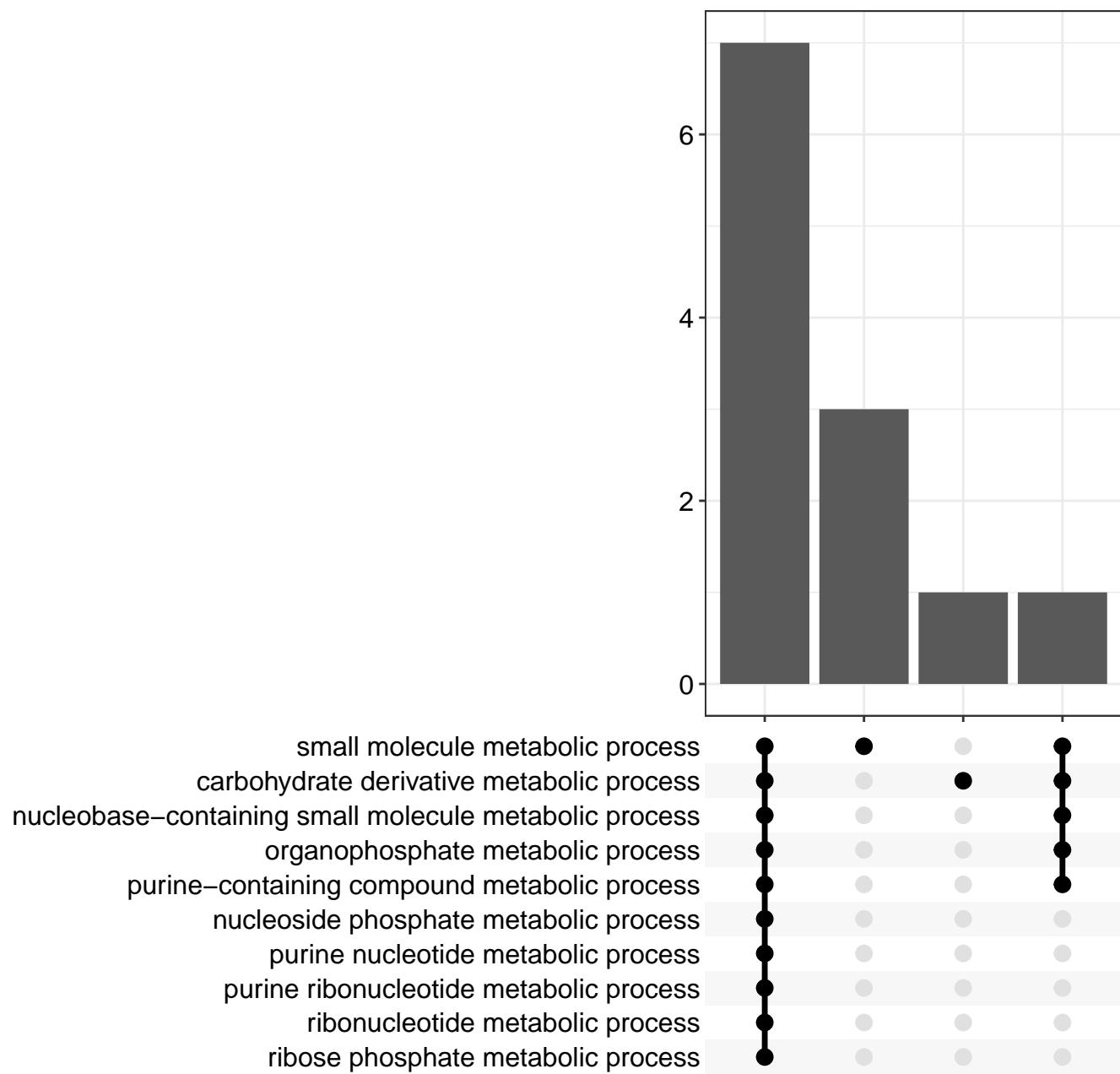
RNA14-TAP Up-regulated GO BP emapplot

cell cycle process

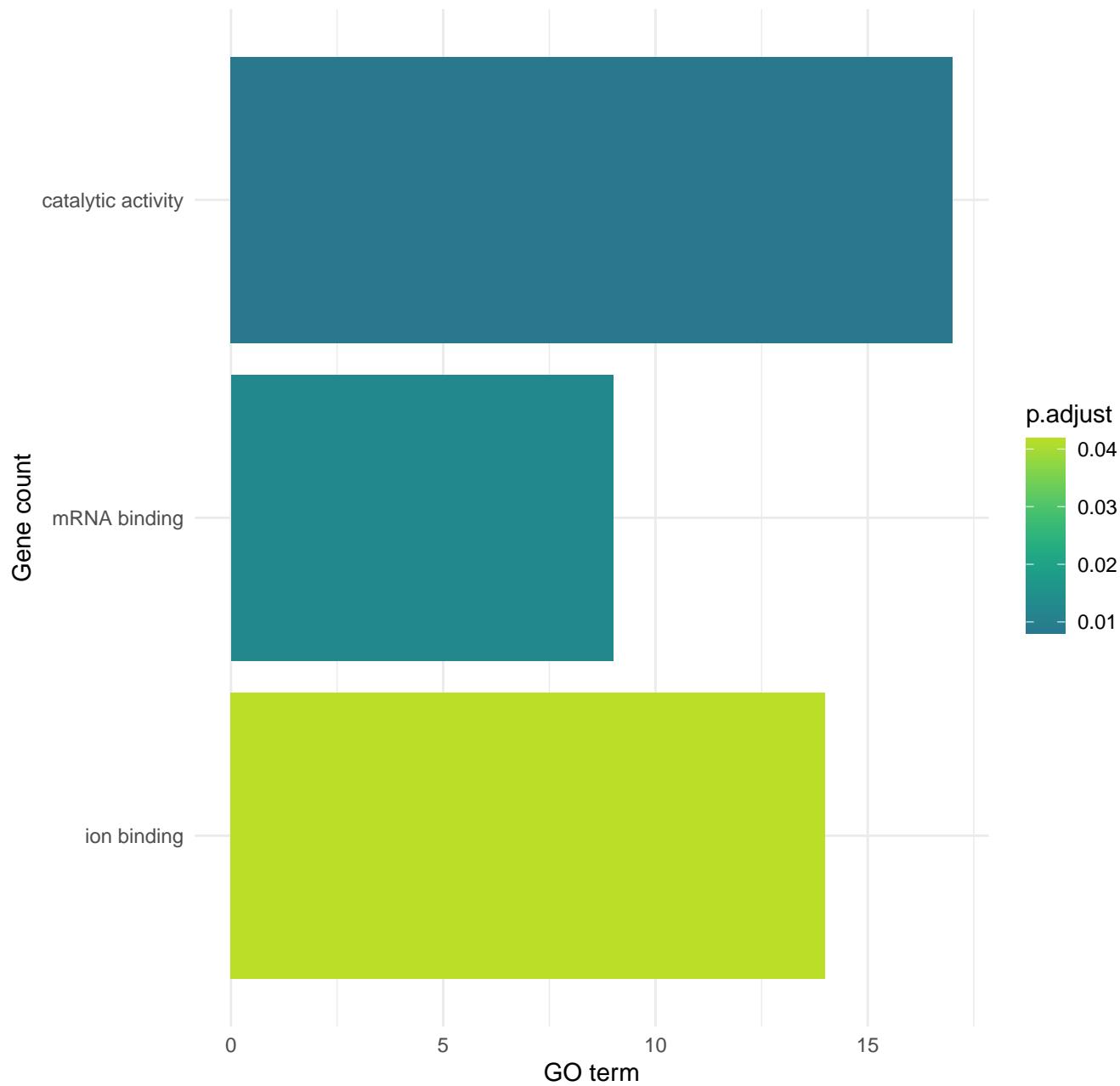




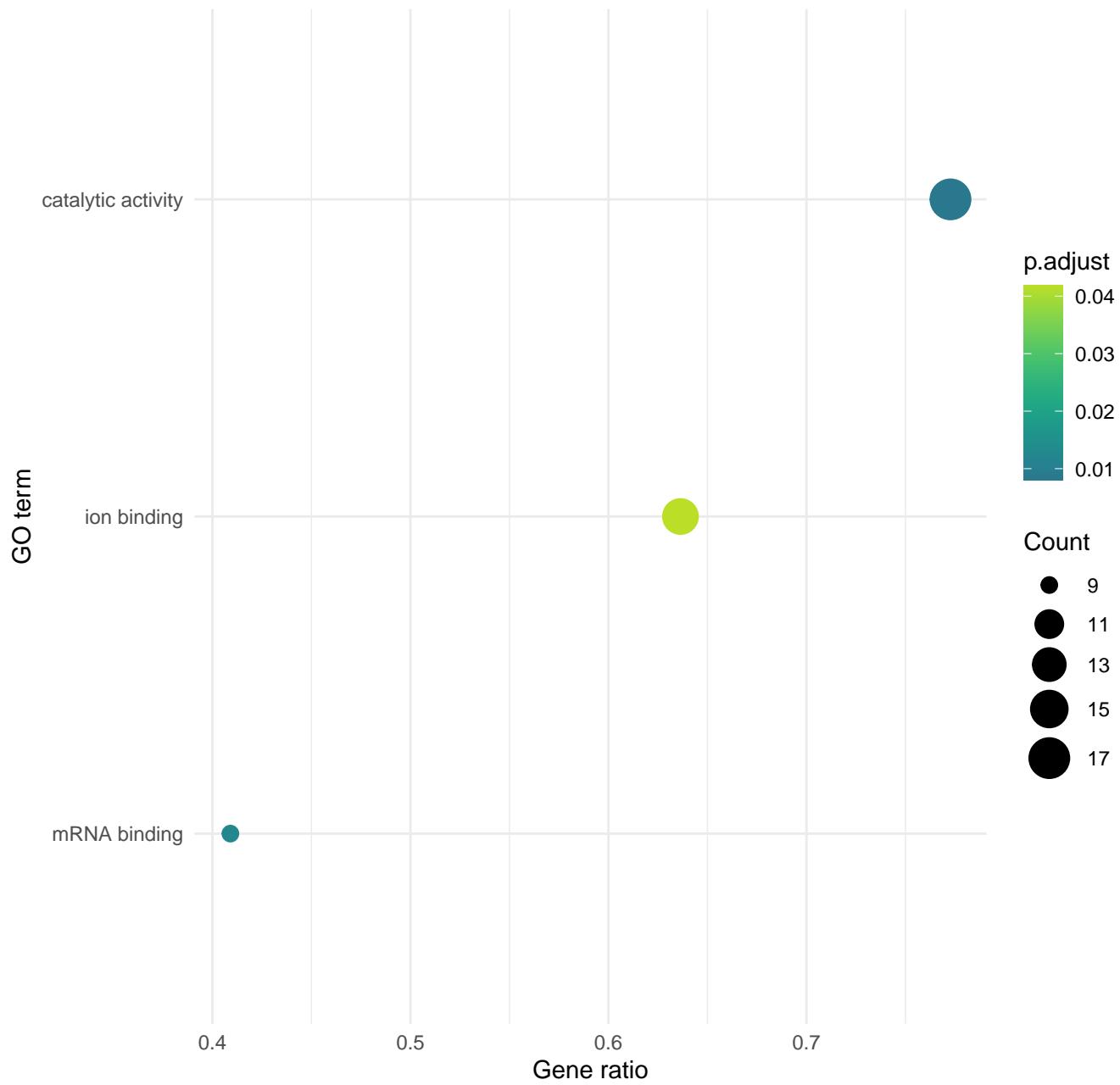
RNA14-TAP Up-regulated GO B



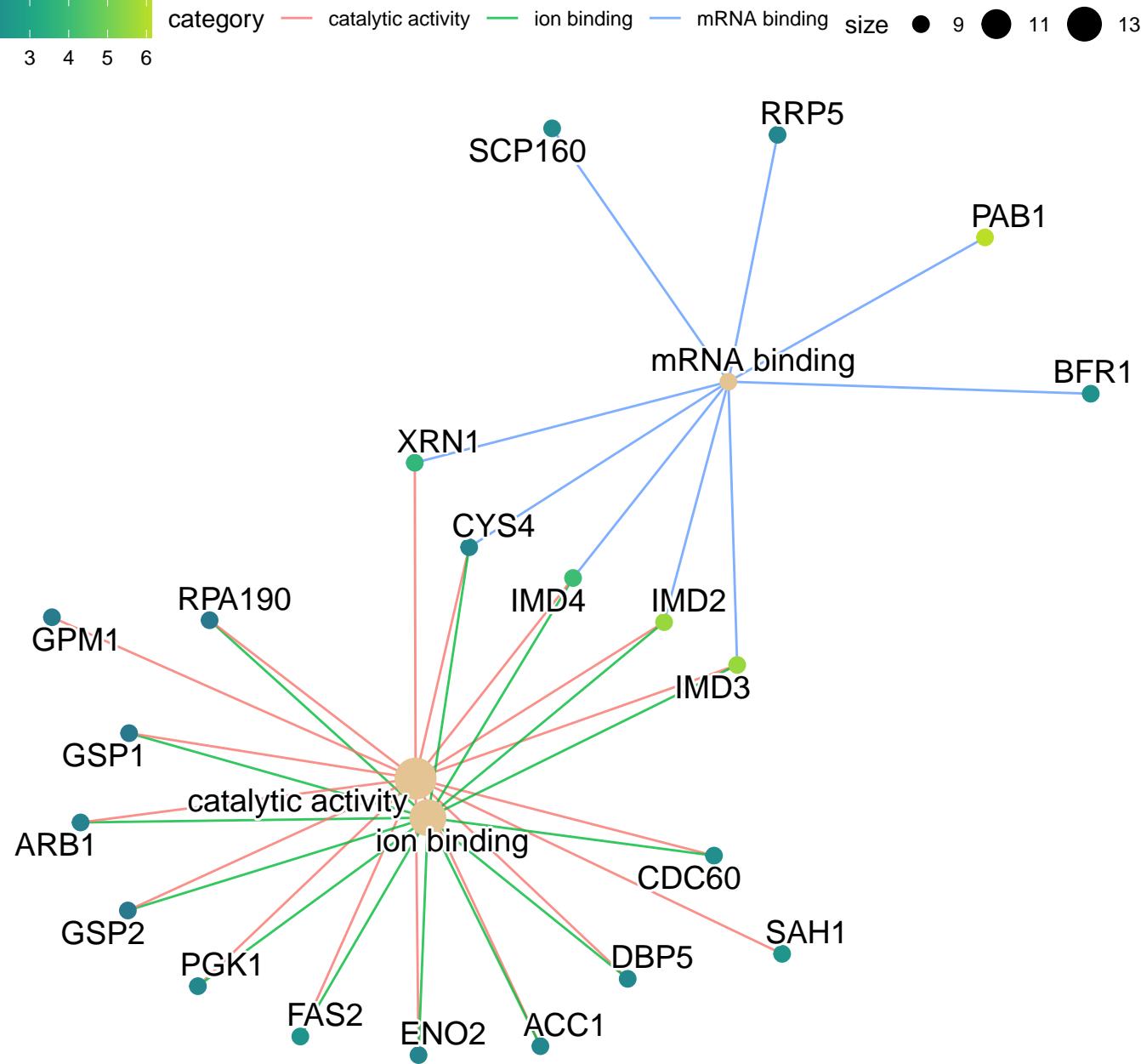
RNA14-TAP Up-regulated GO MF barplot



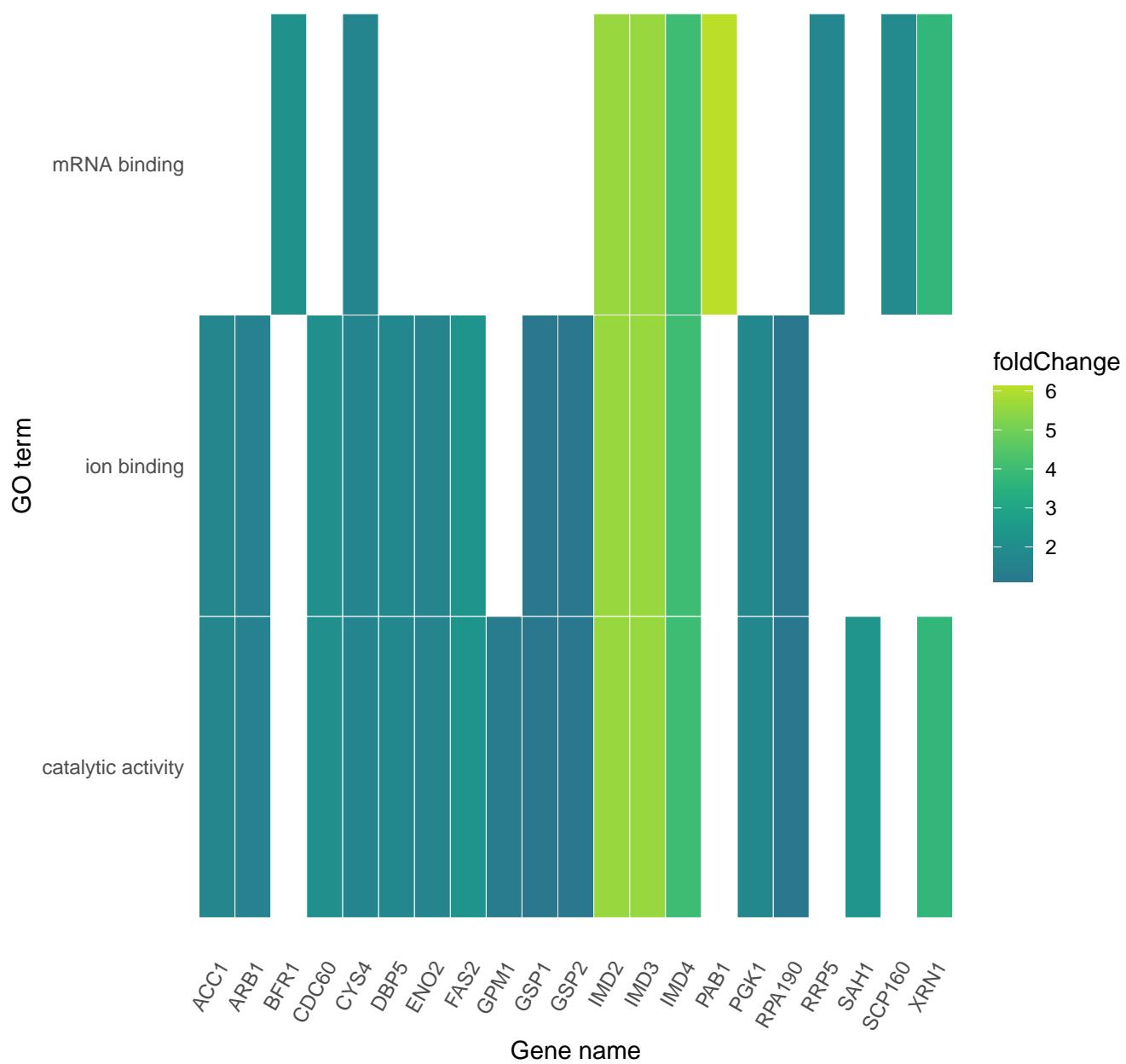
RNA14-TAP Up-regulated GO MF dotplot



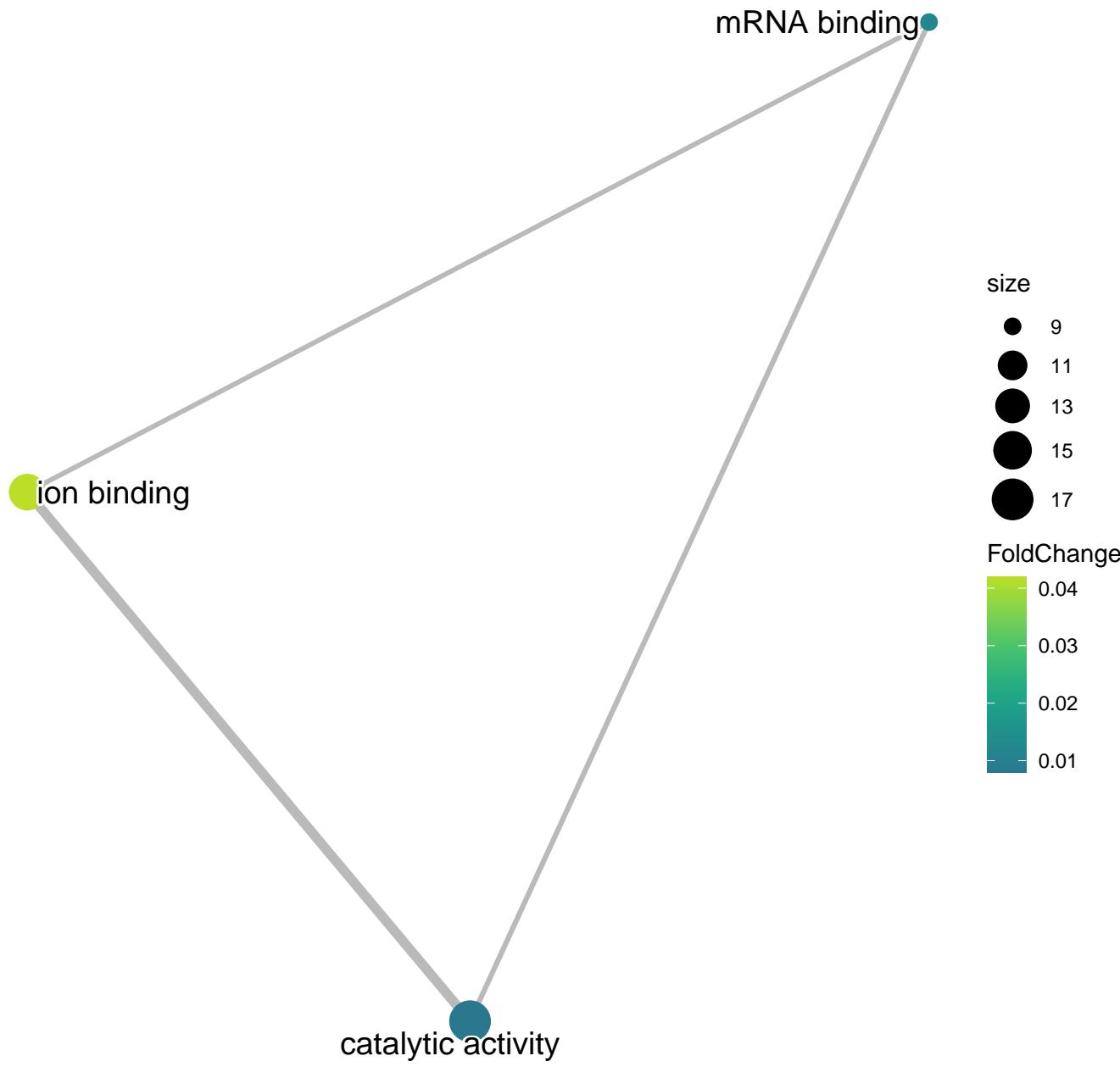
RNA14-TAP Up-regulated GO MF cnetplot

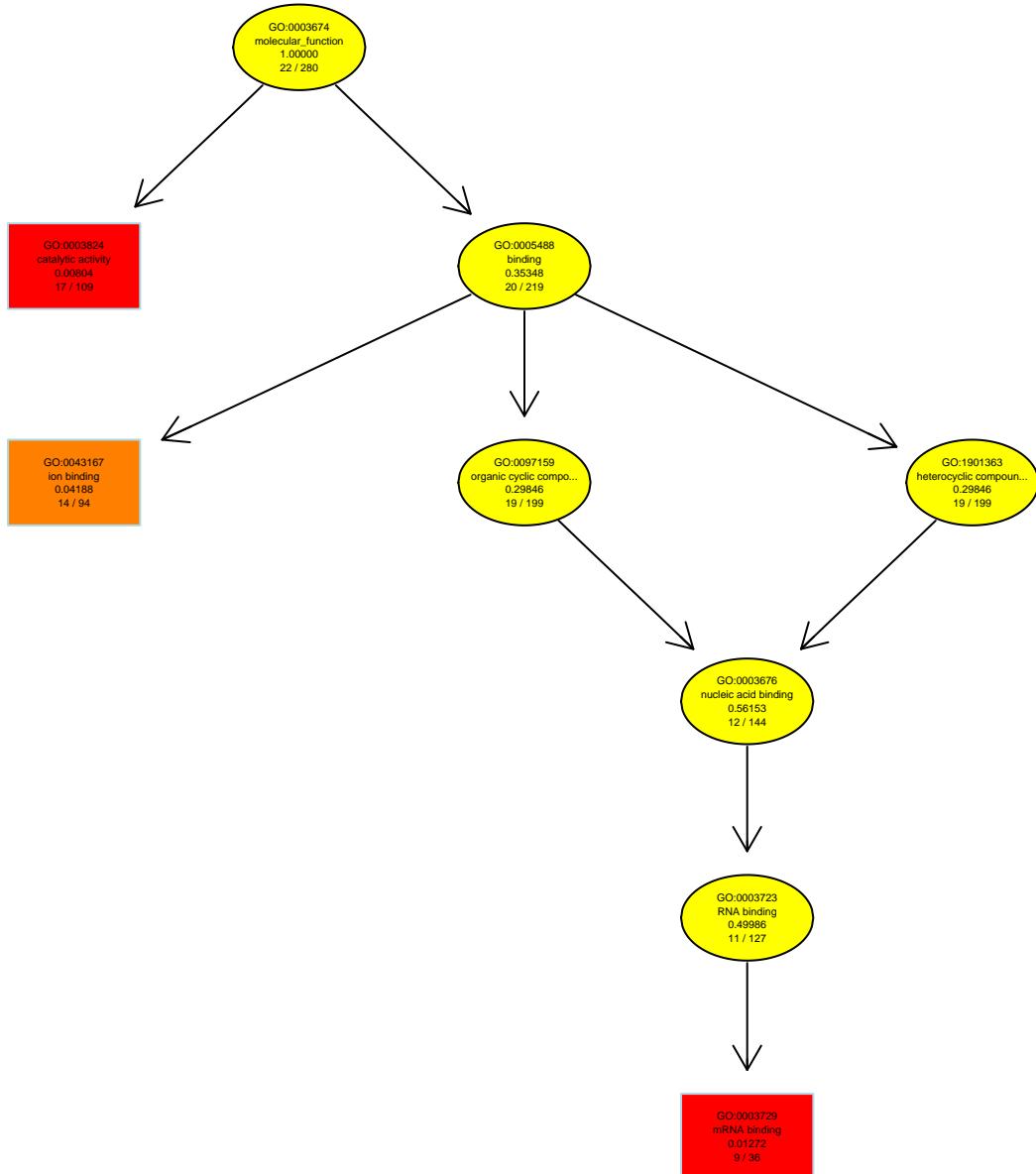


RNA14-TAP Up-regulated GO MF heatplot

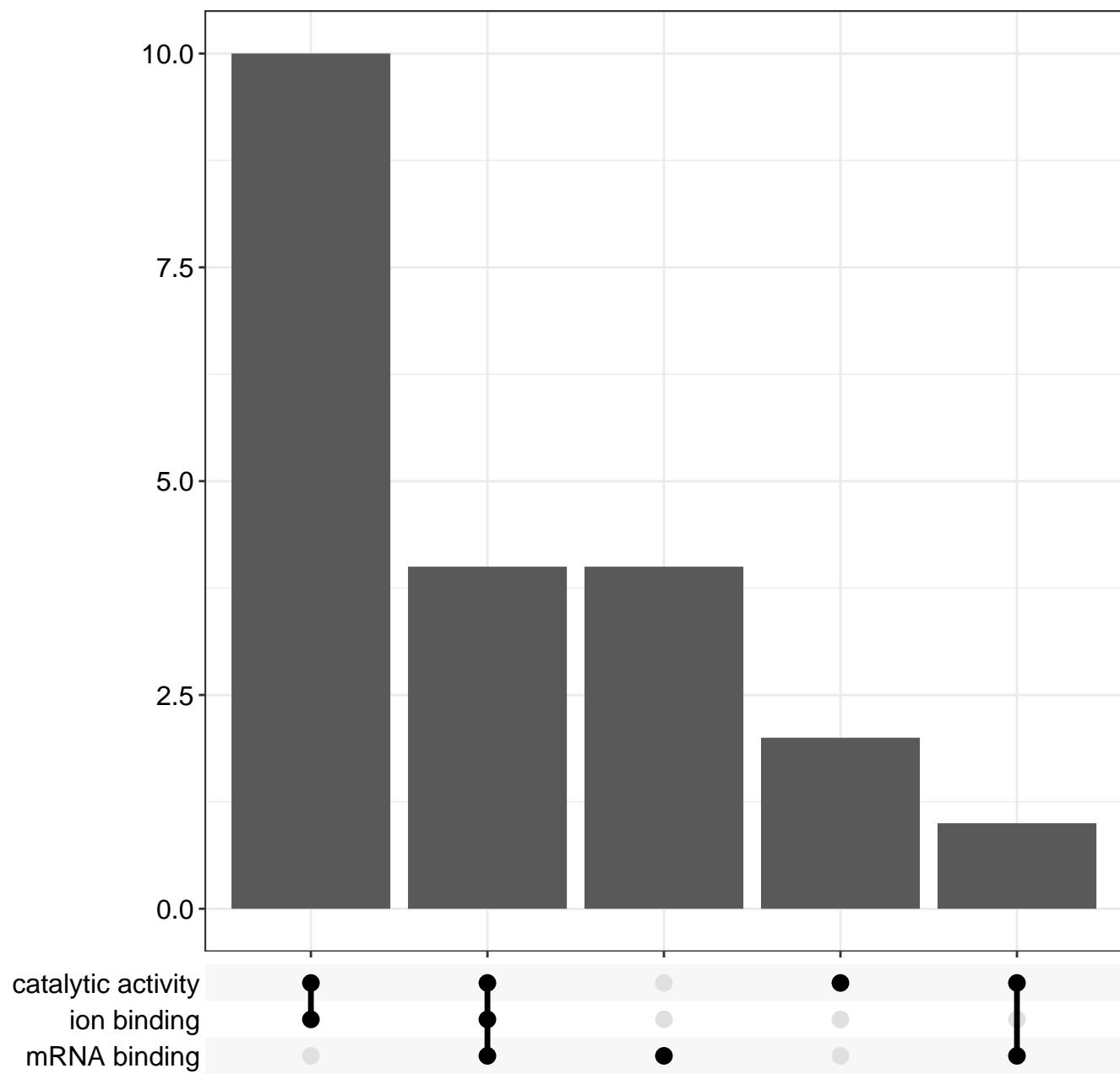


RNA14-TAP Up-regulated GO MF emapplot





RNA14-TAP Up-regulated GO MF upsetplot



RNA14-TAP Up-regulated Reactome barplot

Gene count

Metabolism

0

2

4

6

8

Reactome pathway

p.adjust

0.001625637



RNA14-TAP Up-regulated Reactome dotplot

Reactome pathway

Metabolism

0.58

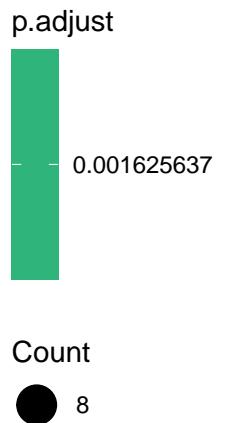
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0.62

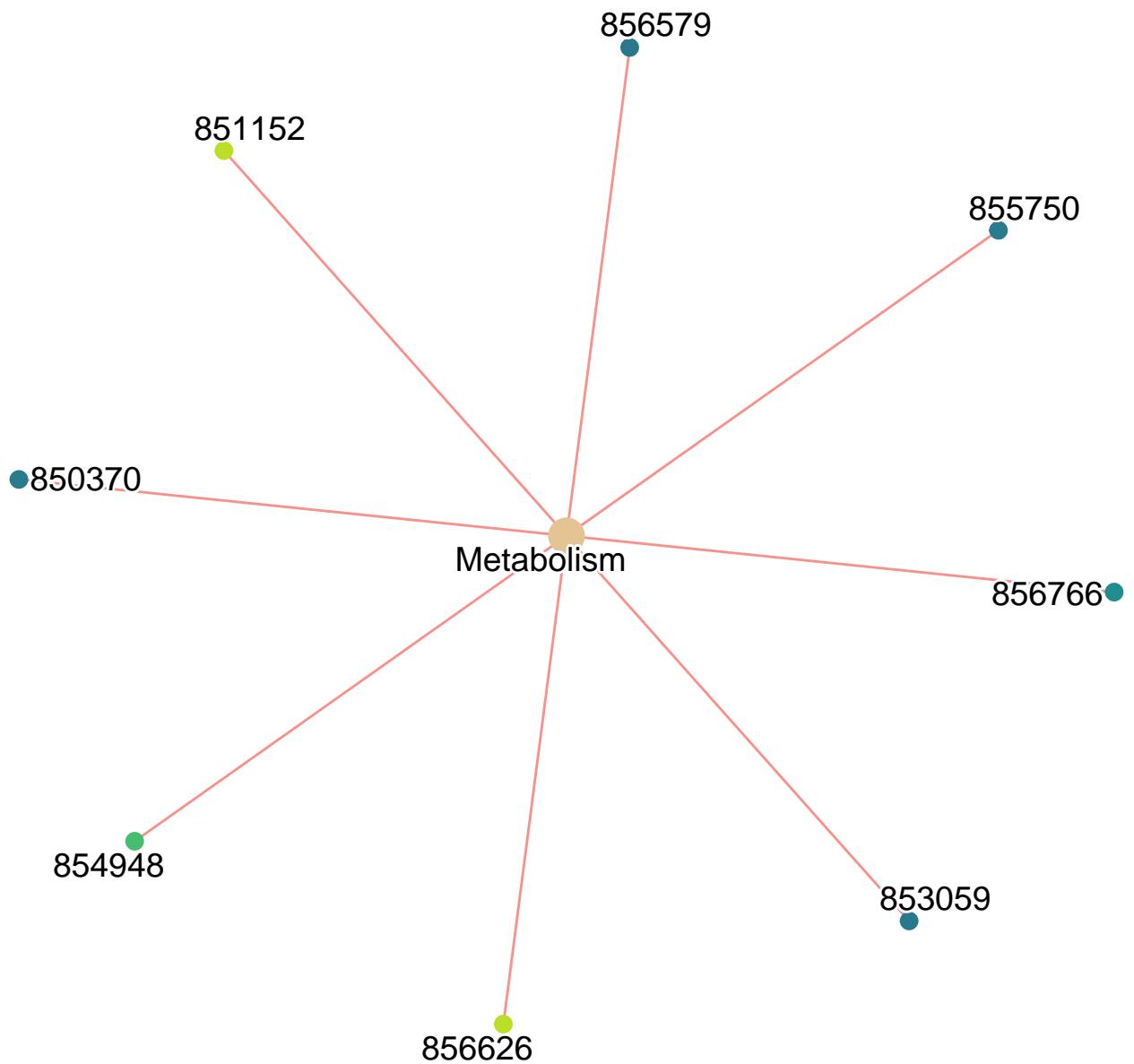
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0.66

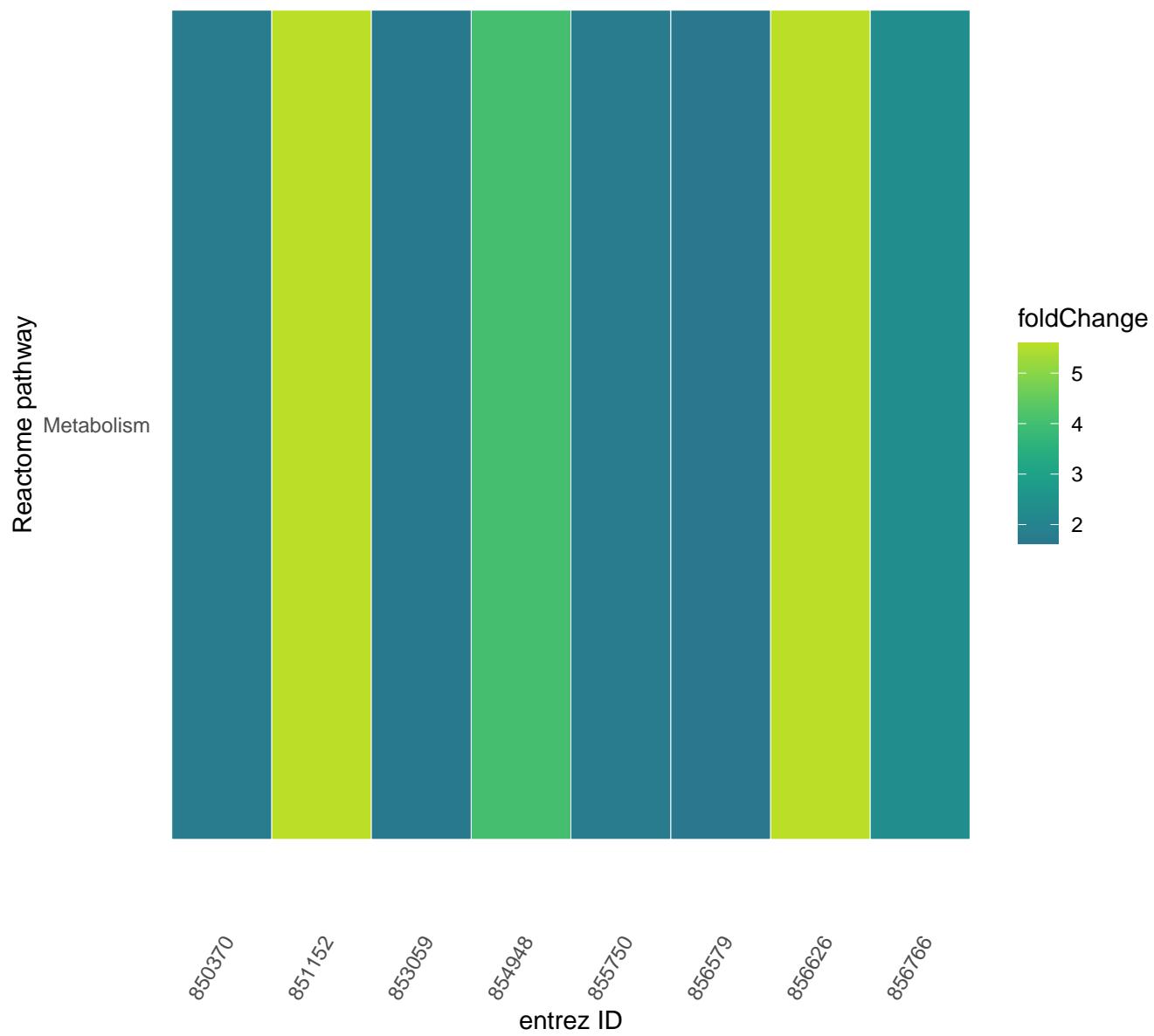
Gene ratio



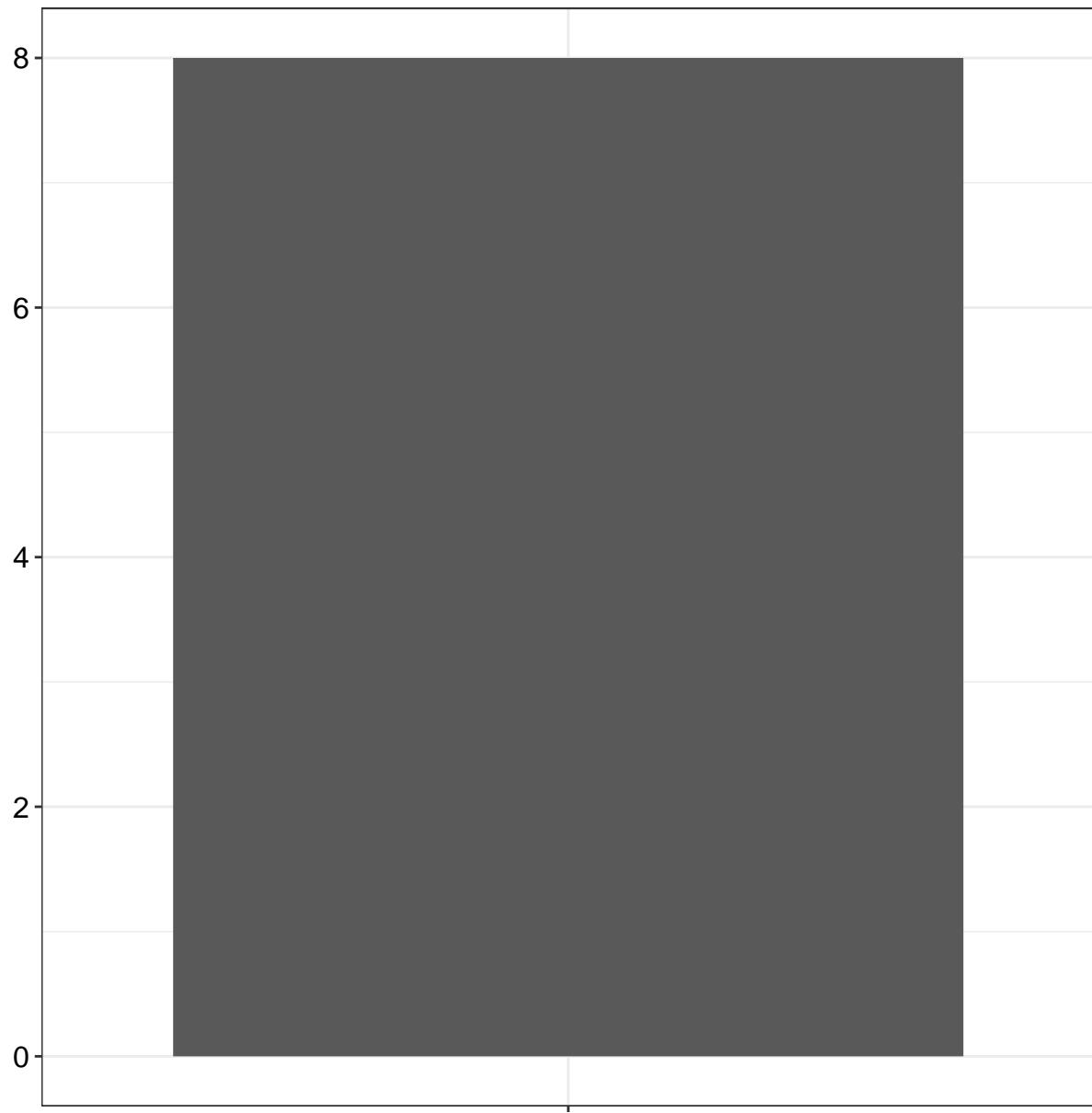
RNA14-TAP Up-regulated Reactome cnetplot



RNA14-TAP Up-regulated Reactome heatmap

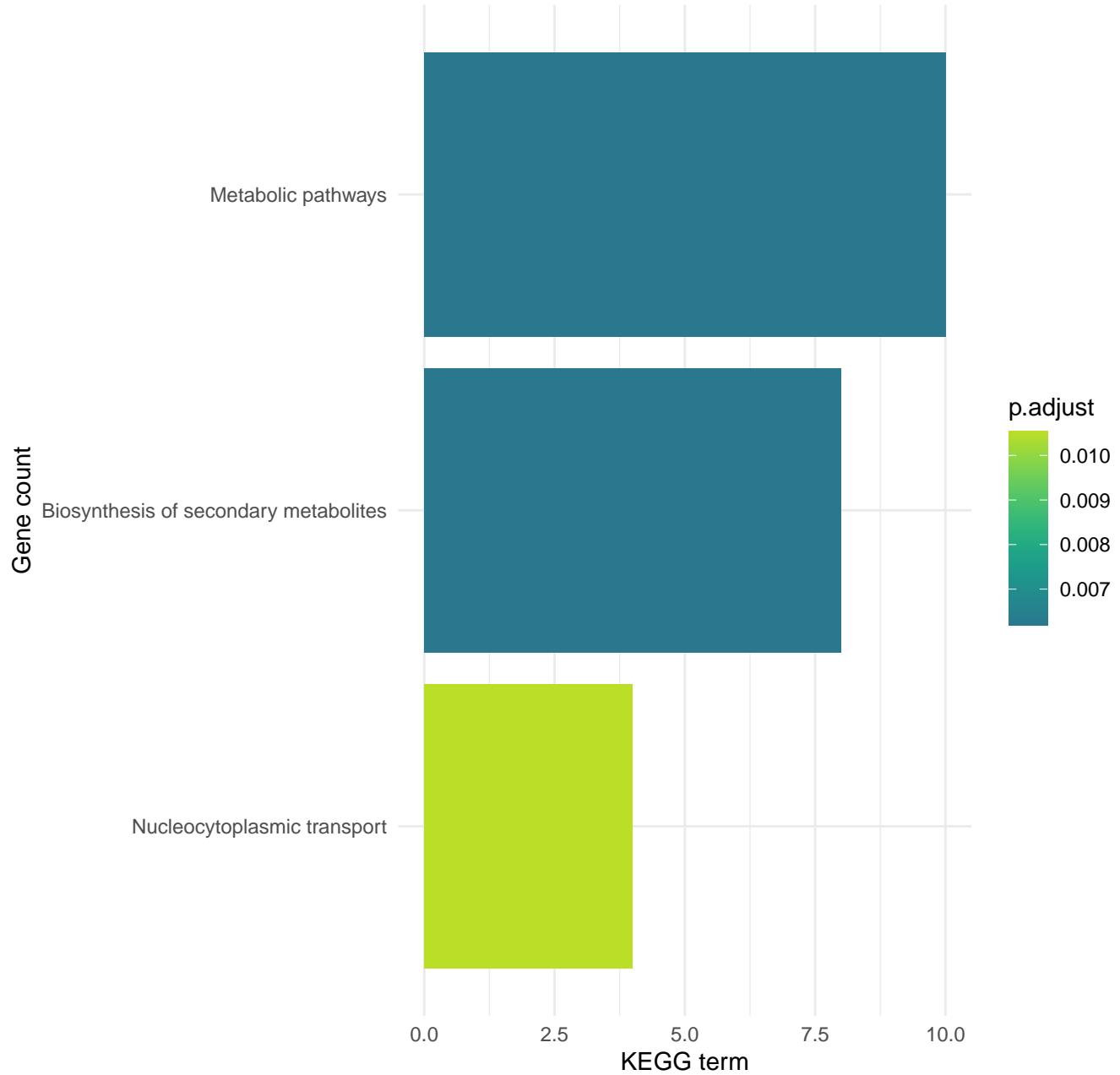


RNA14-TAP Up-regulated Reactome upsetplot



Metabolism

RNA14-TAP Up-regulated KEGG barplot

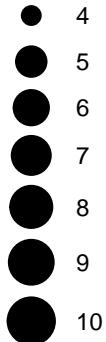


RNA14-TAP Up-regulated KEGG dotplot

KEGG term

Metabolic pathways

Count



Biosynthesis of secondary metabolites

p.adjust



Nucleocytoplasmic transport

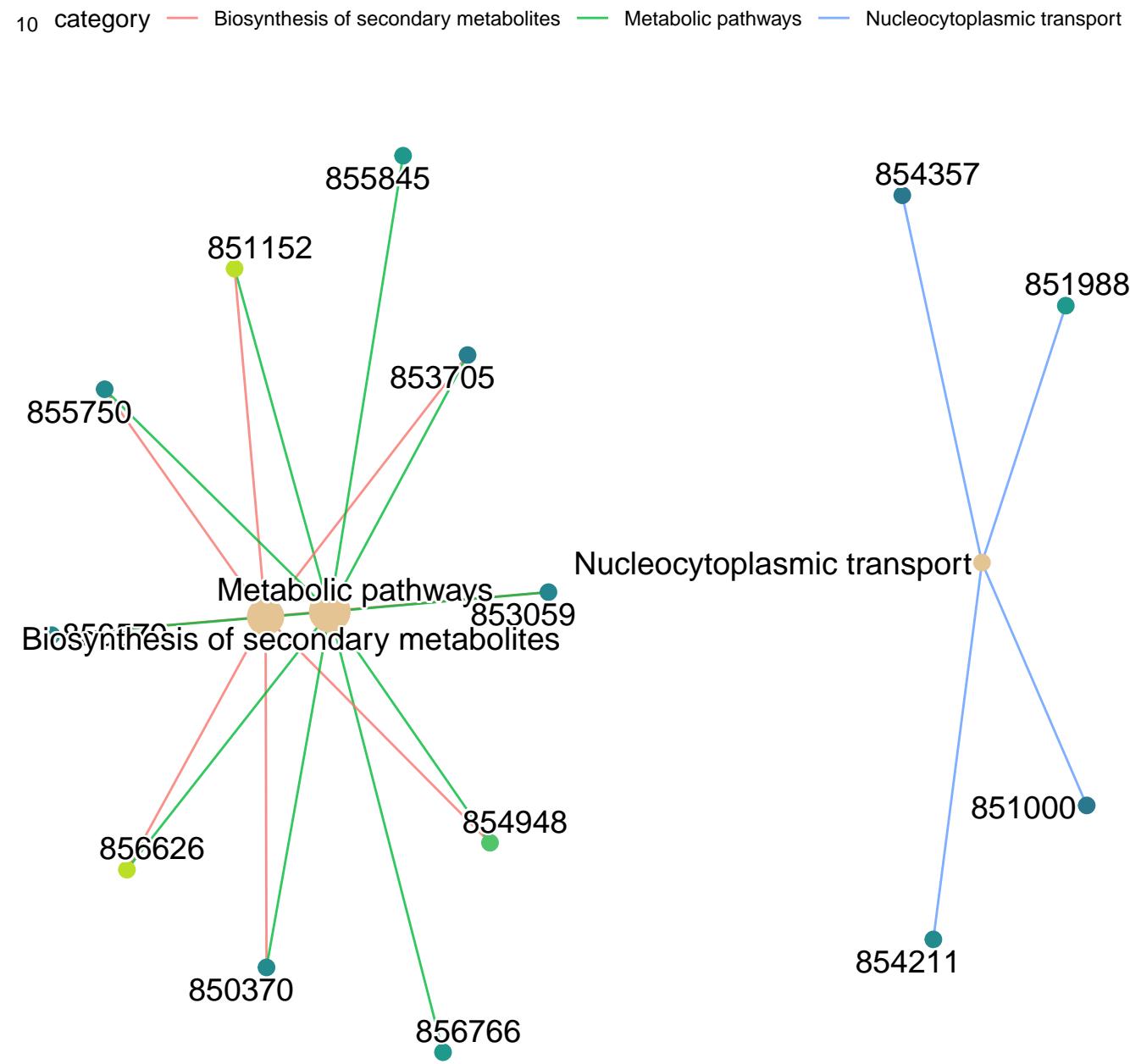
0.3

0.4

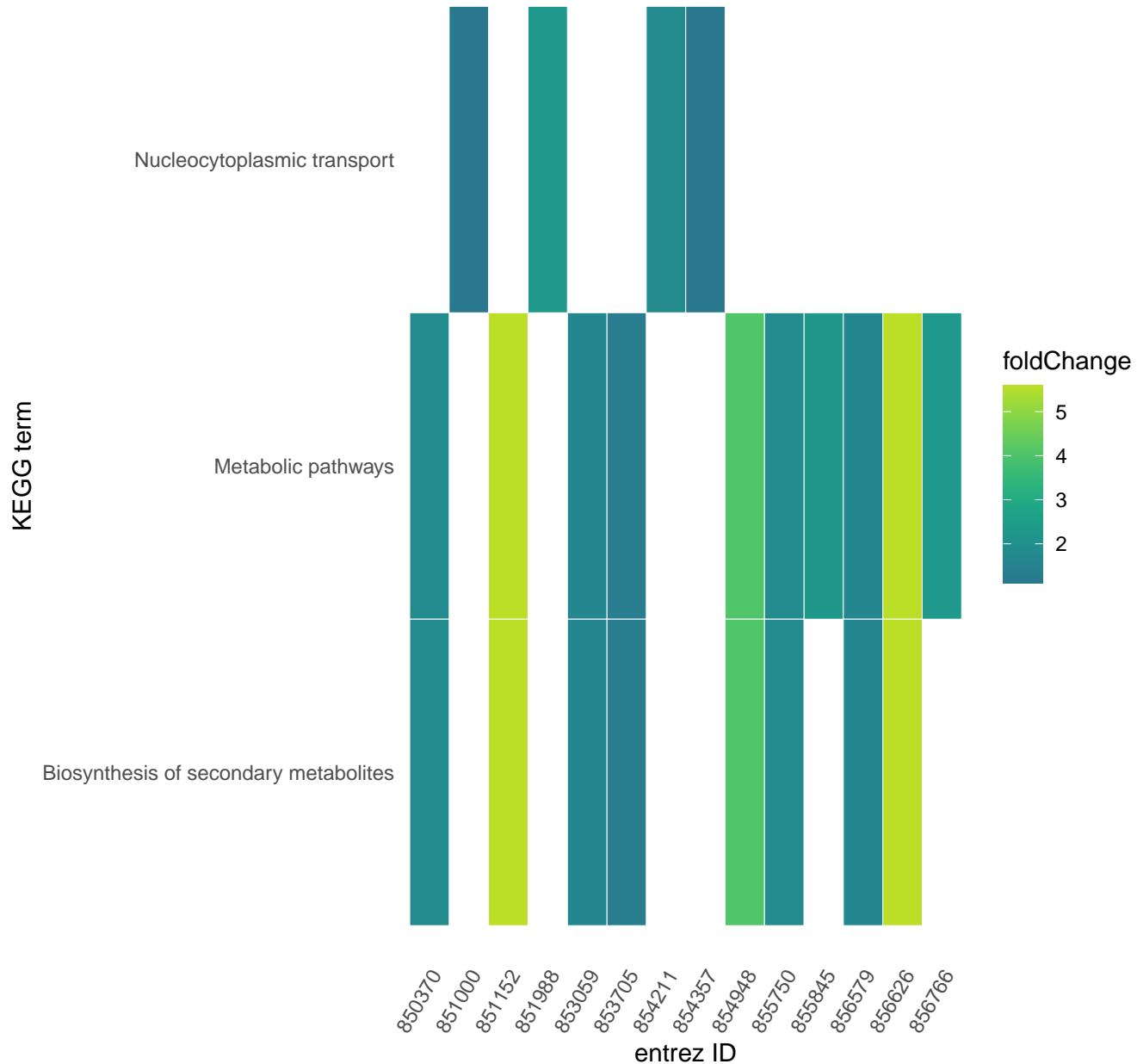
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Gene ratio

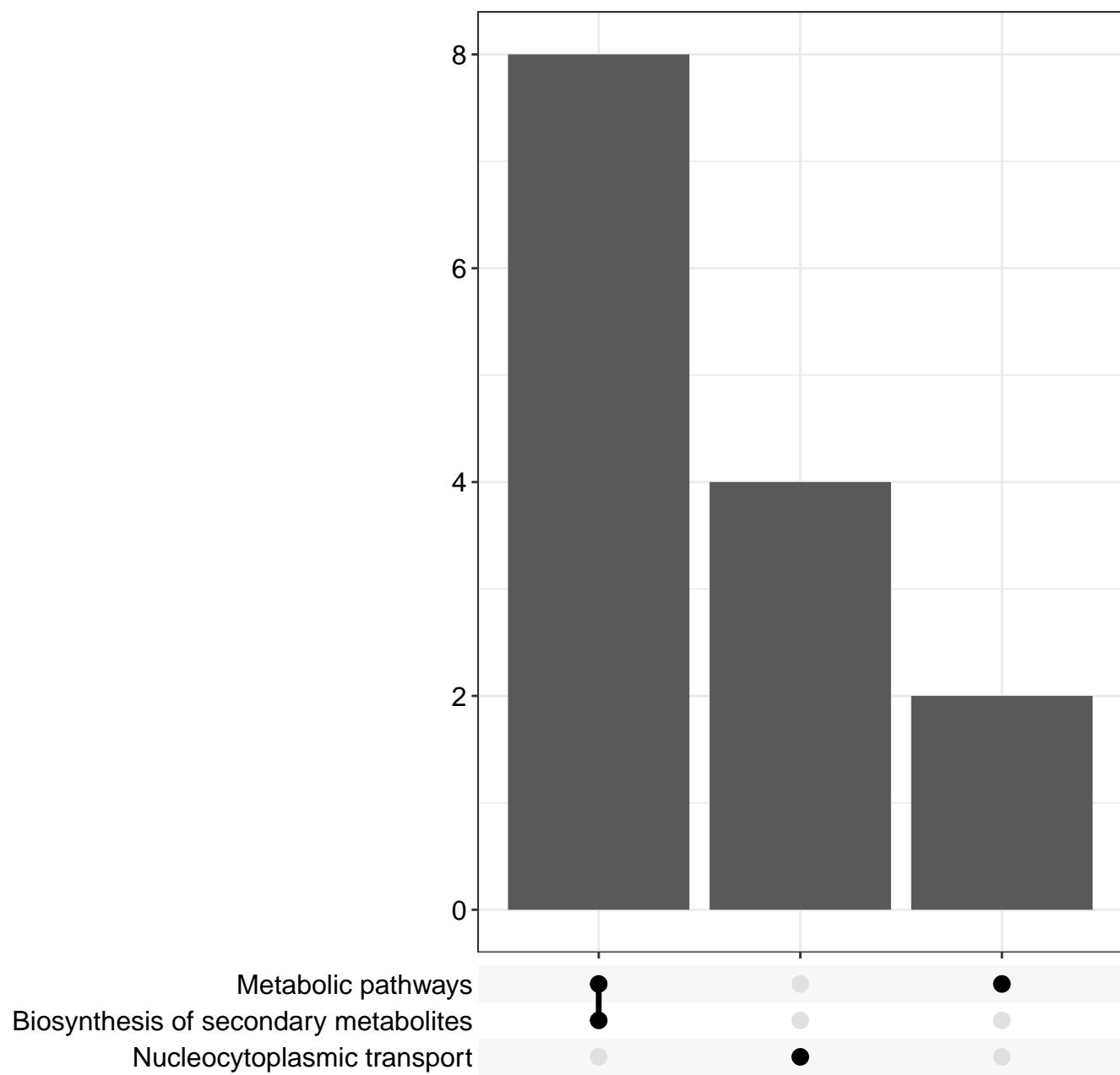
RNA14-TAP Up-regulated KEGG dotplot



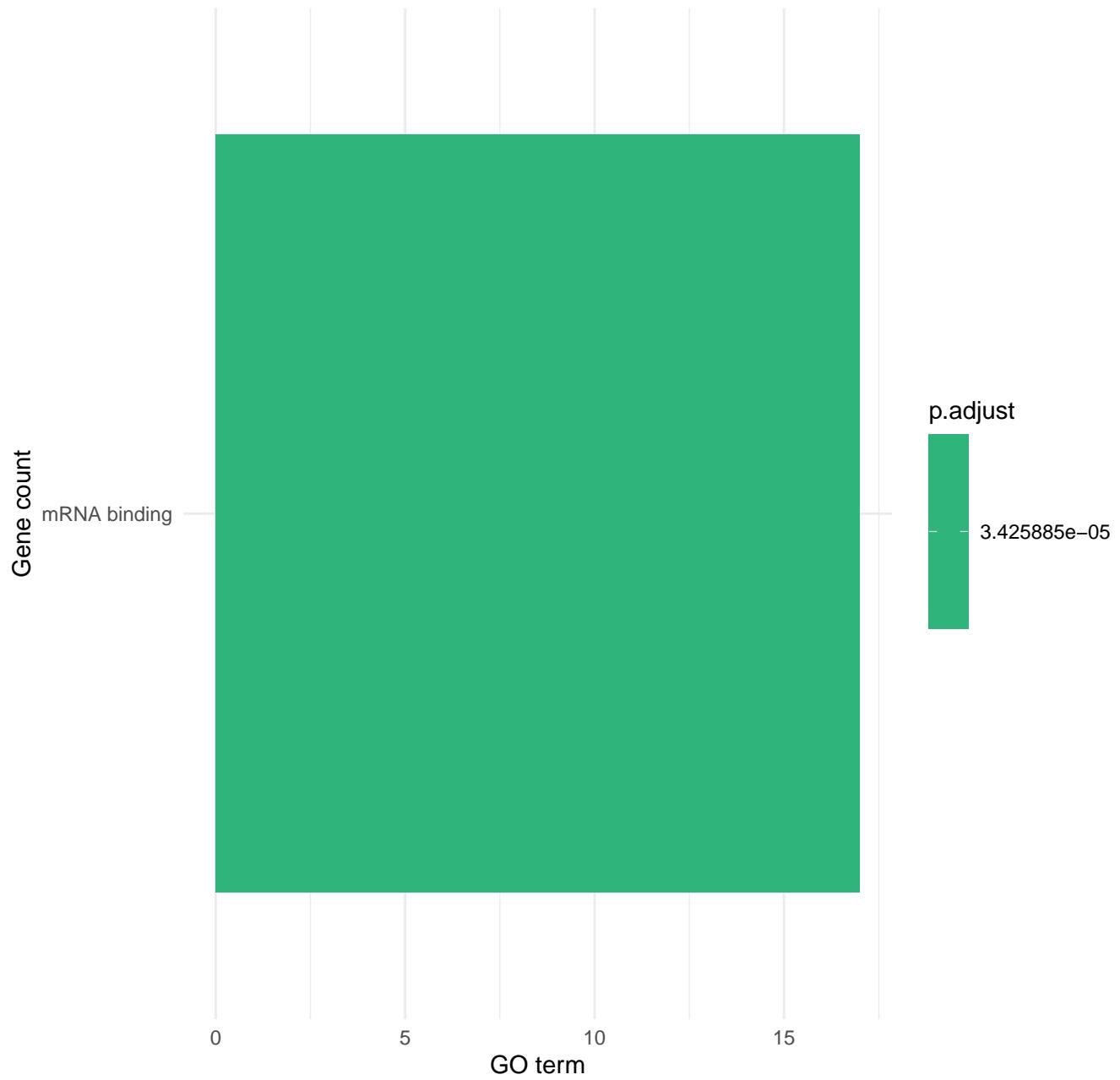
RNA14-TAP Up-regulated KEGG heatplot



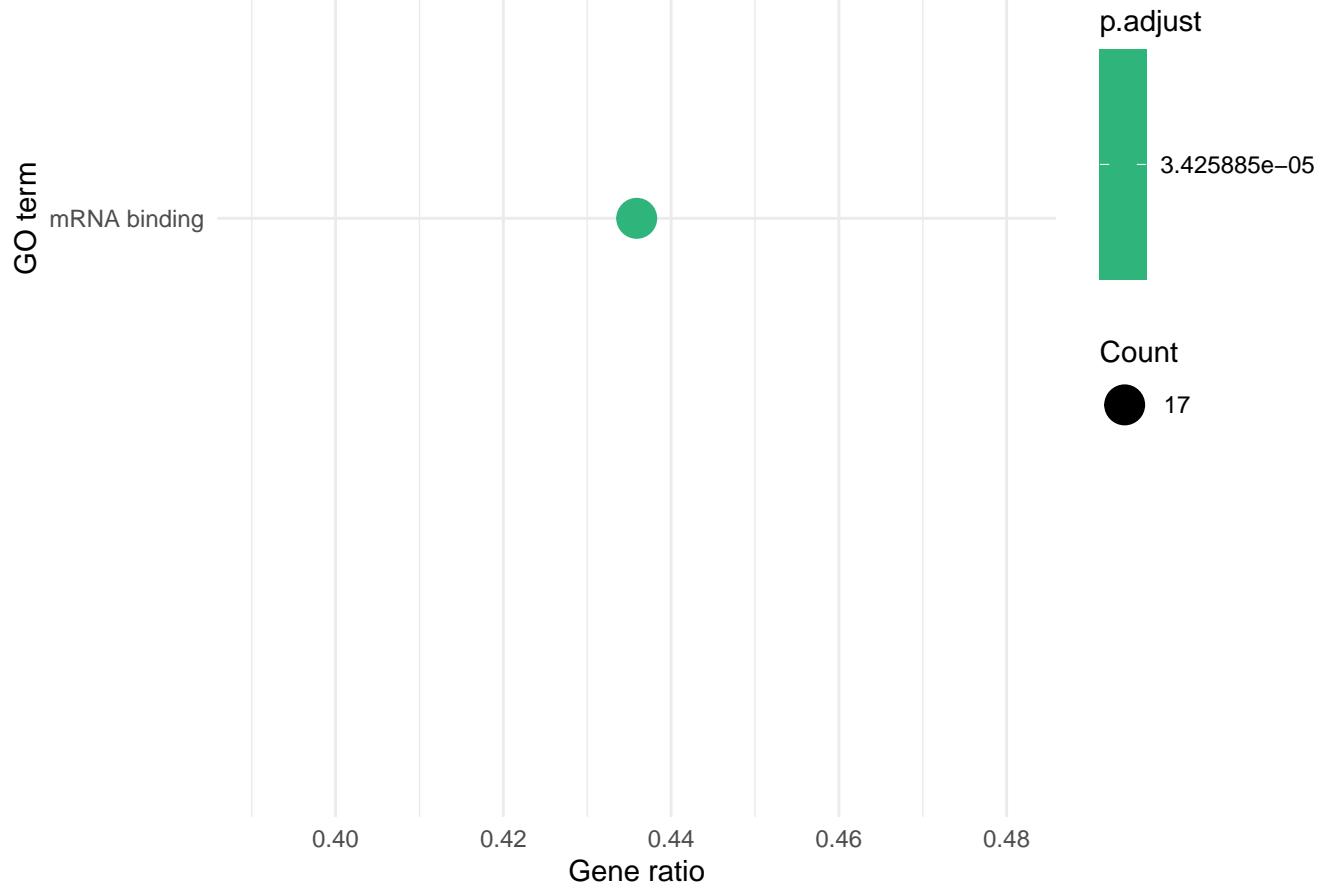
RNA14-TAP Up-regulated KEGG upsetplot



MPE1-TAP Up-regulated GO MF barplot



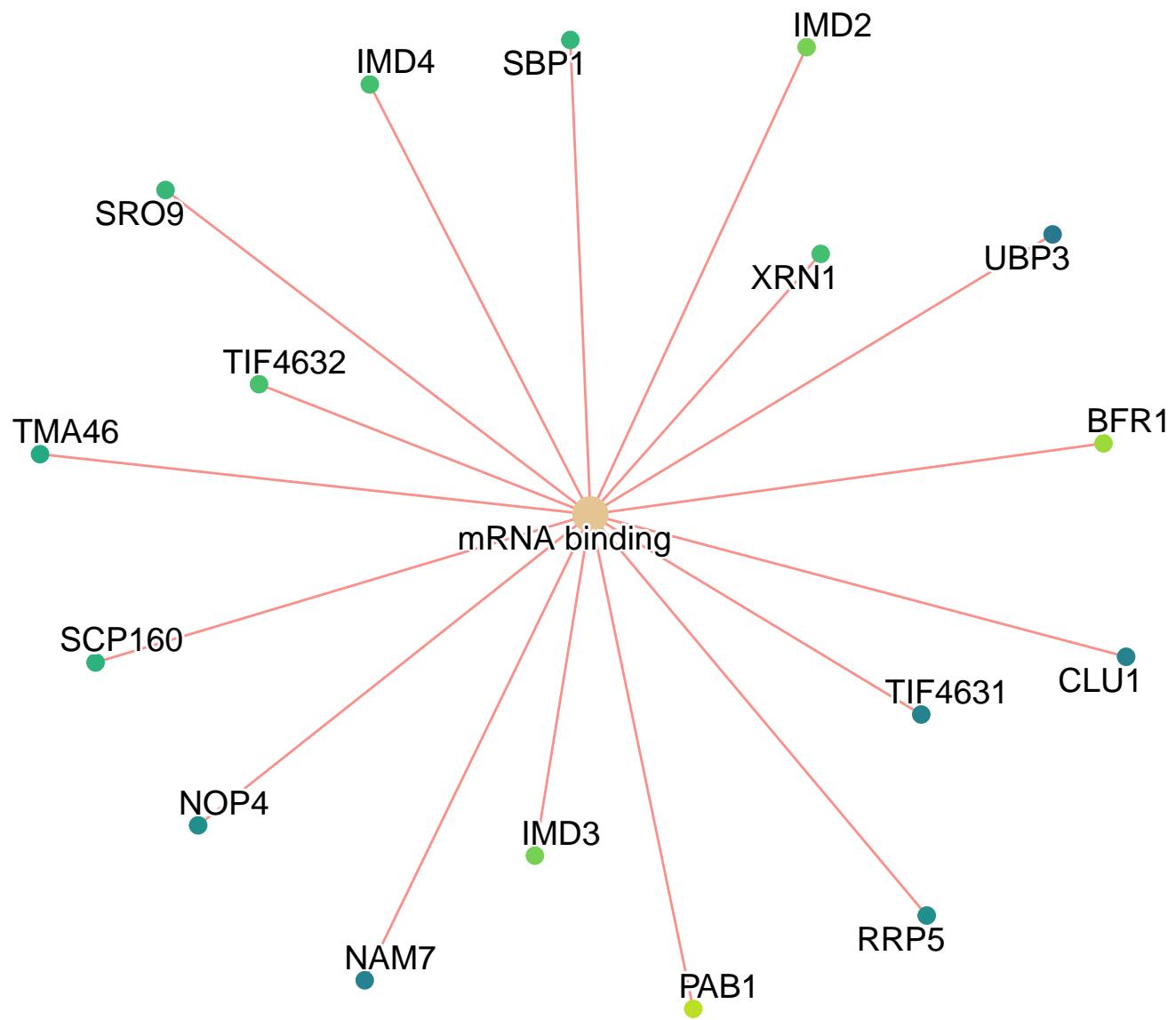
MPE1-TAP Up-regulated GO MF dotplot



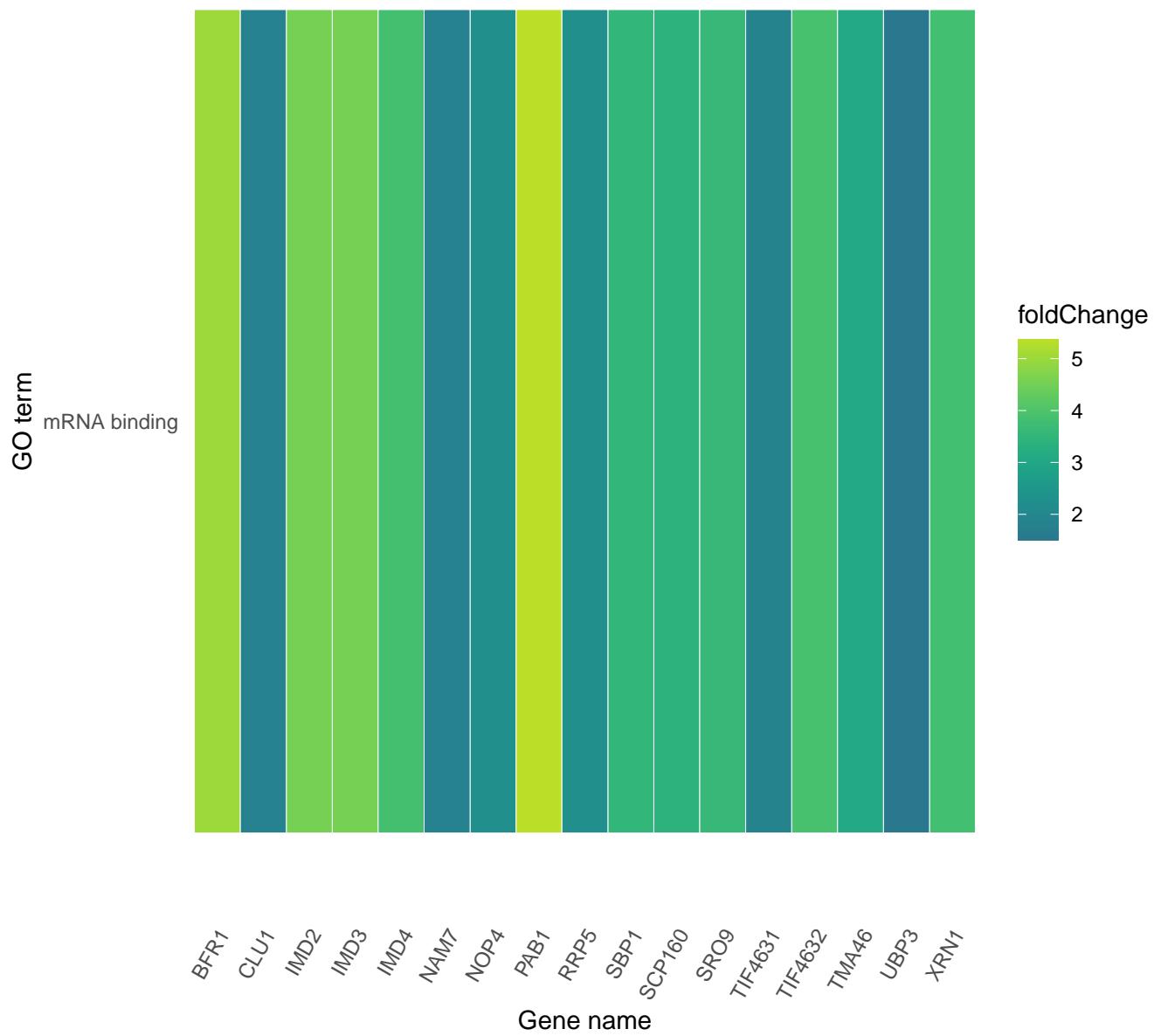
MPE1-TAP Up-regulated GO MF cnetplot

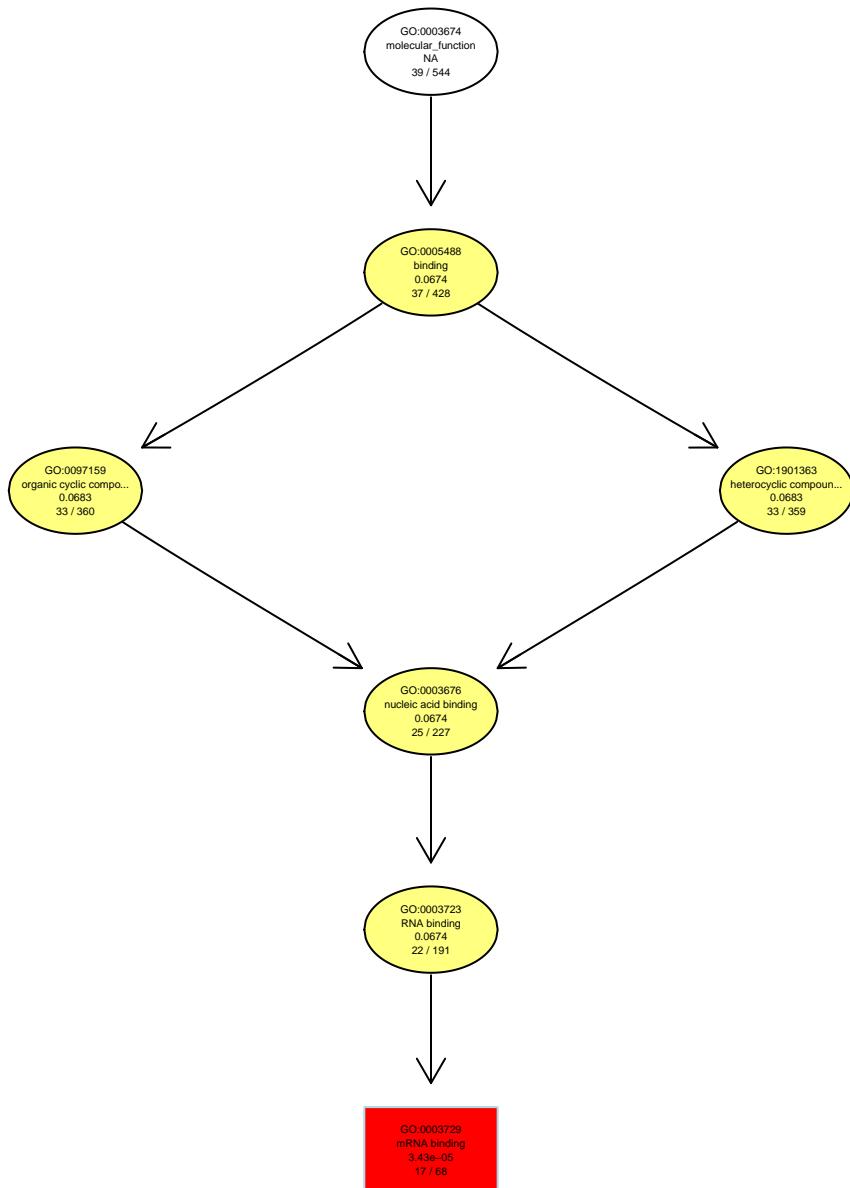
size ● 17 category

FoldChange

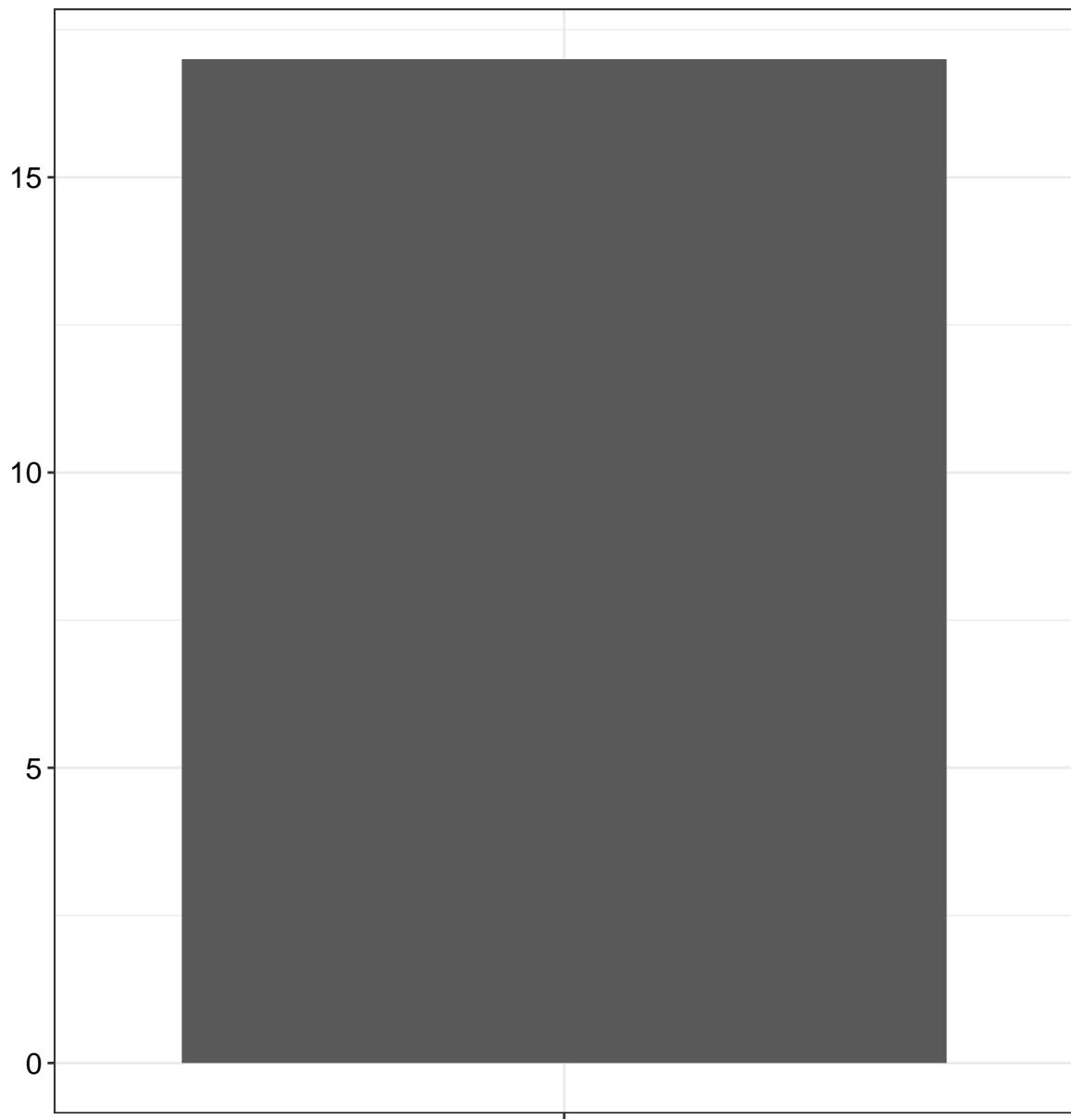


MPE1-TAP Up-regulated GO MF heatplot



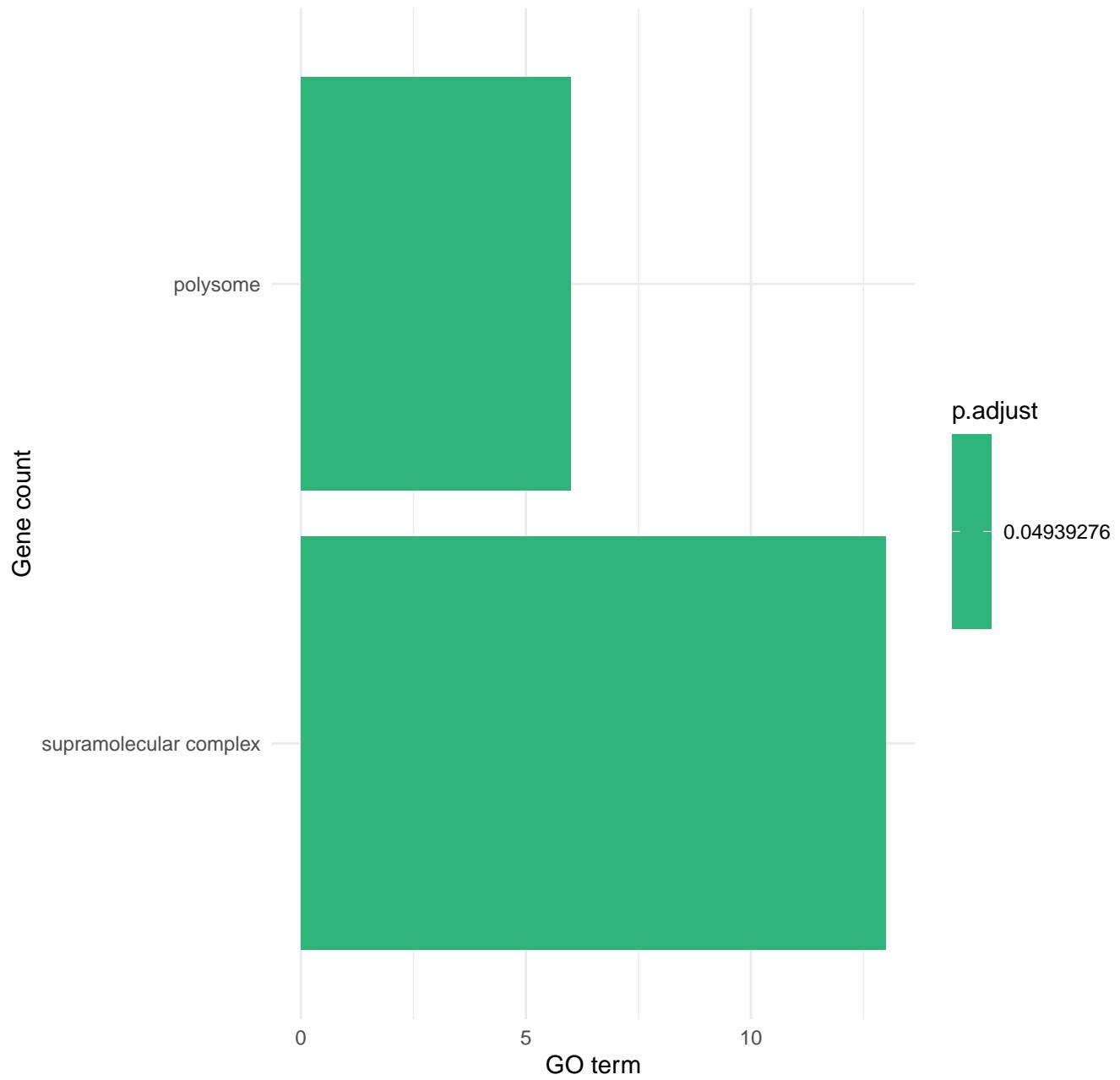


MPE1-TAP Up-regulated GO MF upsetplot

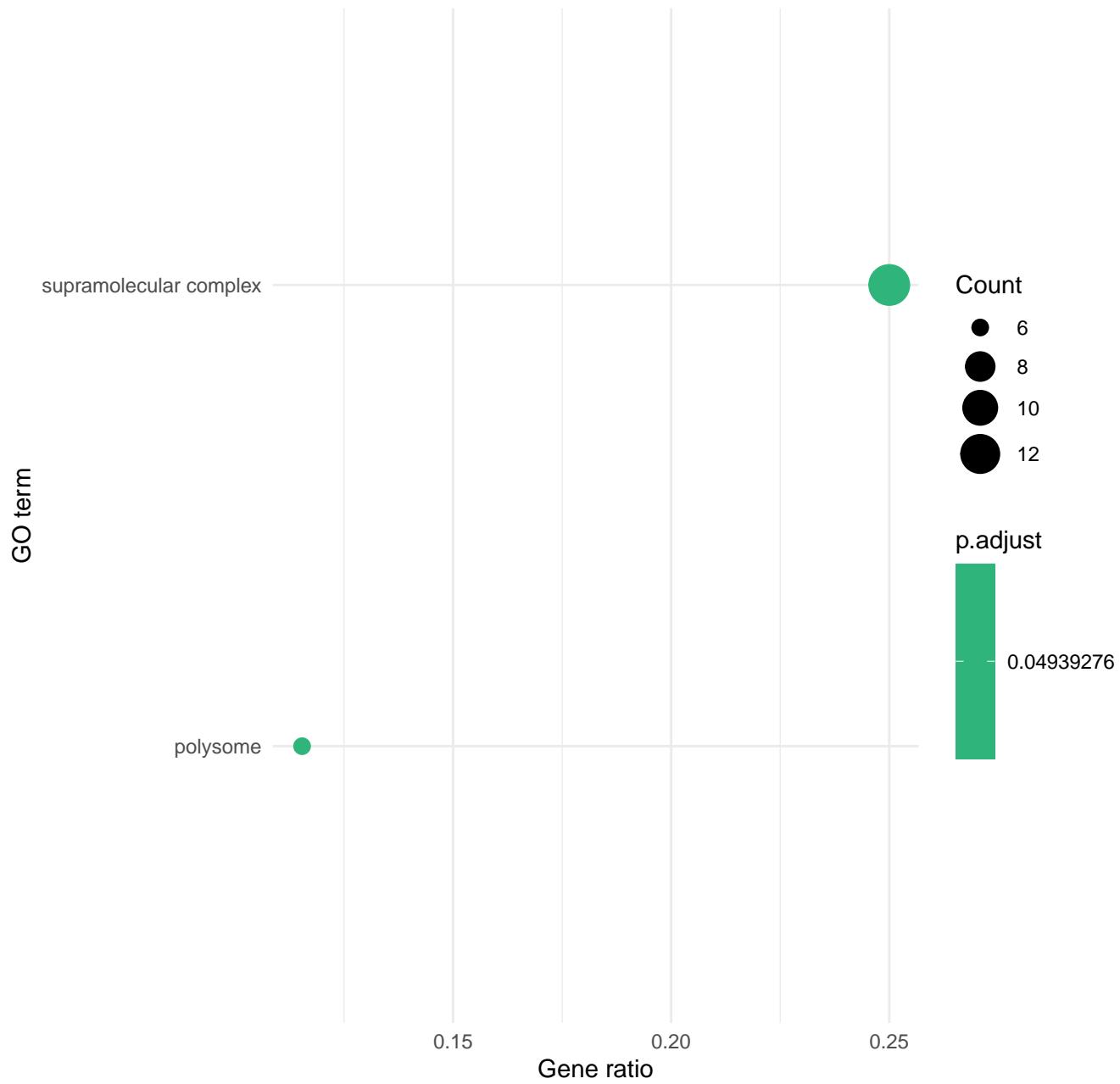


mRNA binding

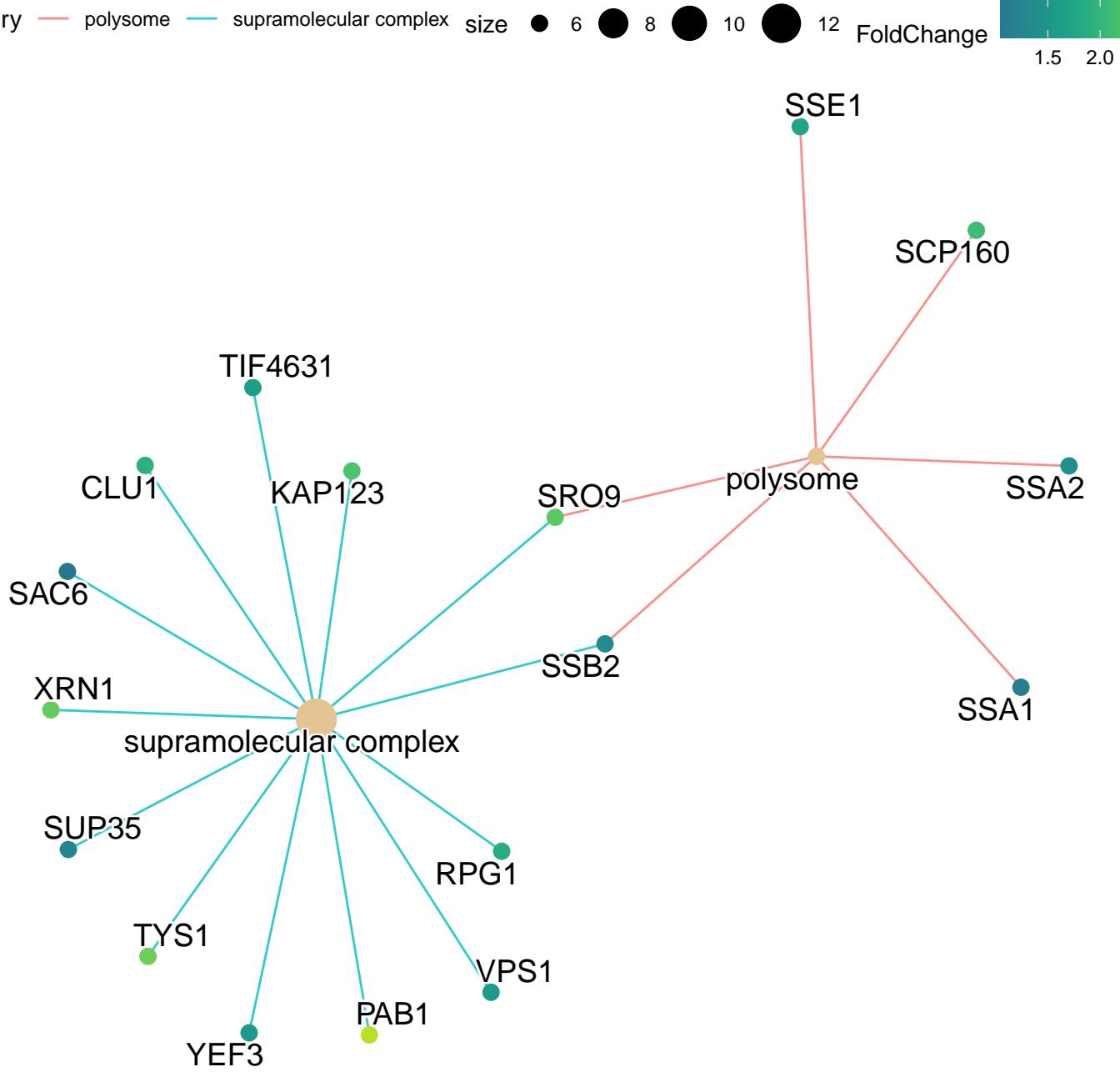
GLC7-TAP Up-regulated GO CC barplot



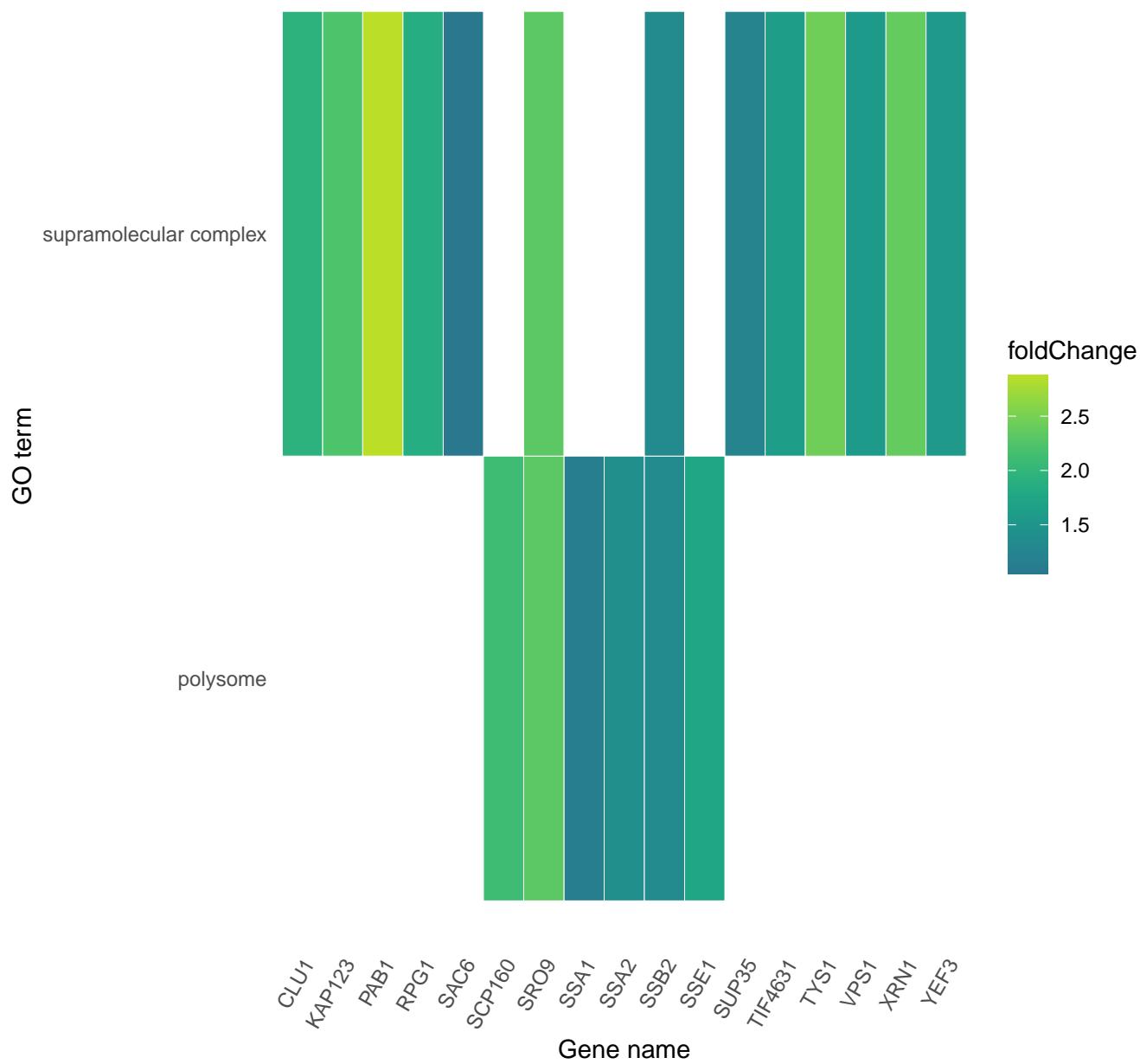
GLC7-TAP Up-regulated GO CC dotplot



GLC7-TAP Up-regulated GO CC cnetplot



GLC7-TAP Up-regulated GO CC heatplot



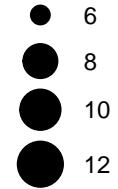
GLC7-TAP Up-regulated GO CC emapplot

supramolecular complex

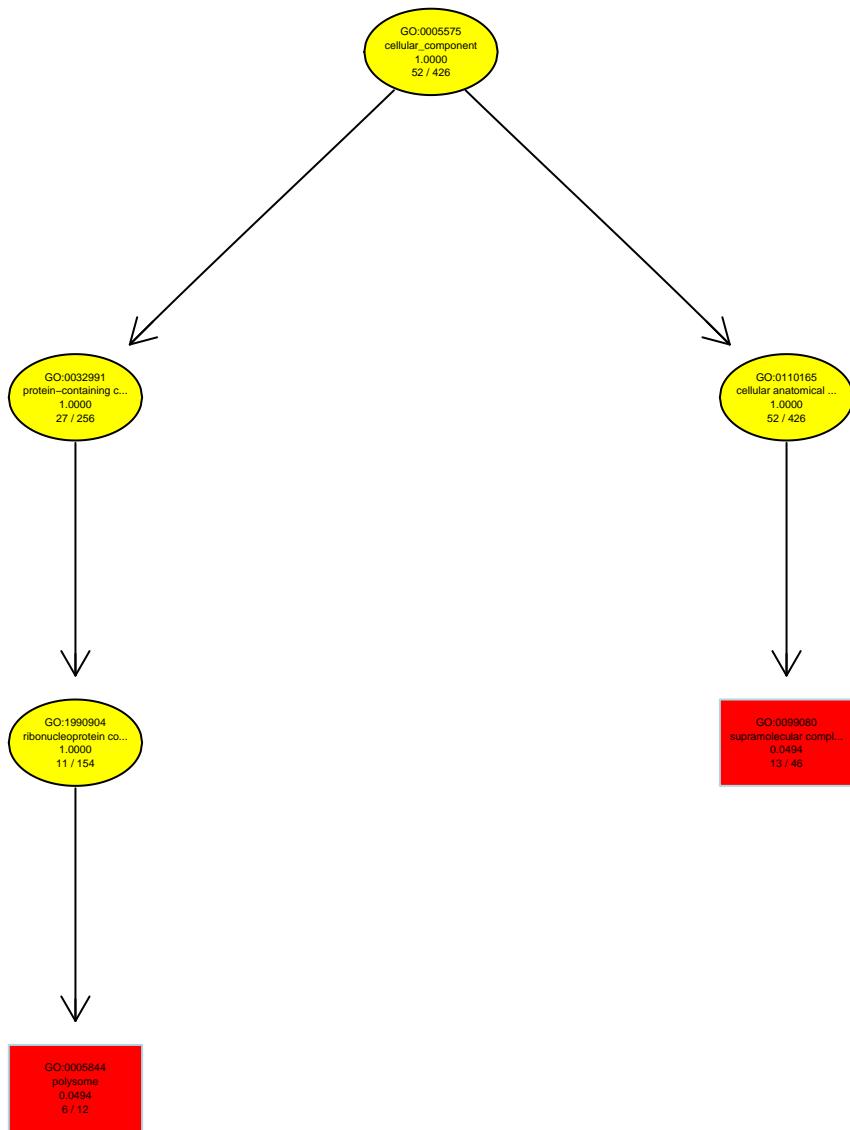
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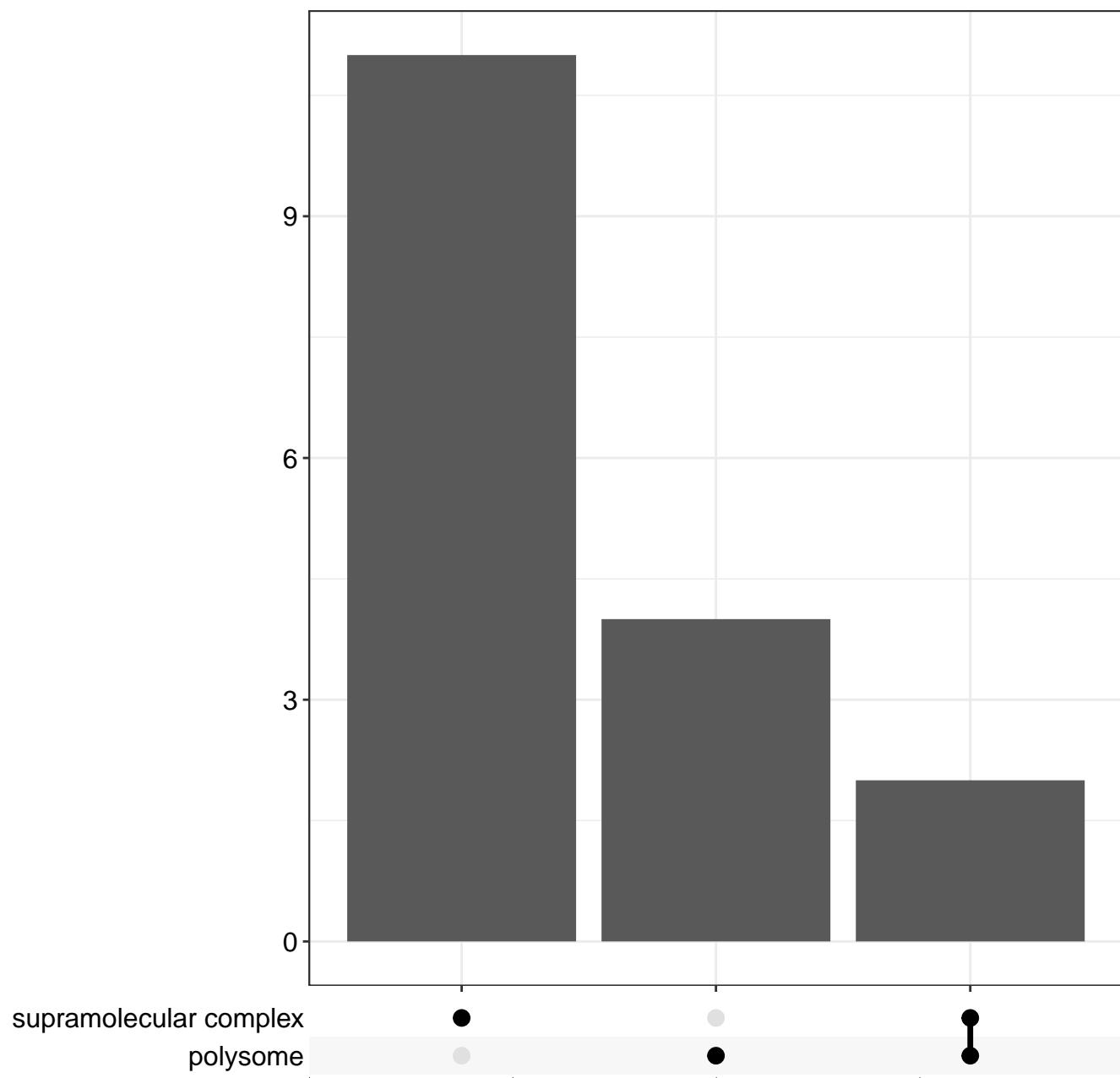
size



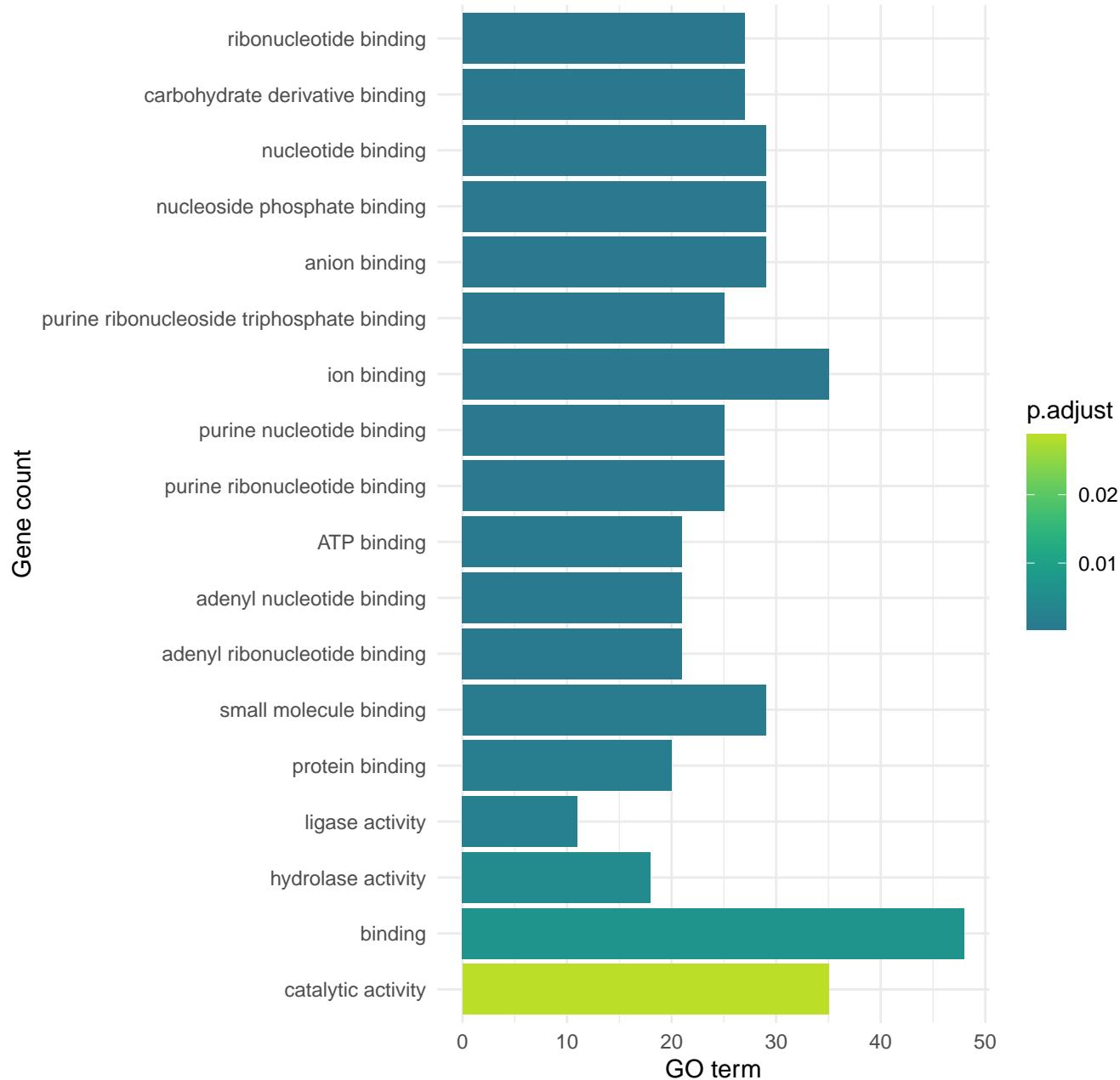
polysome



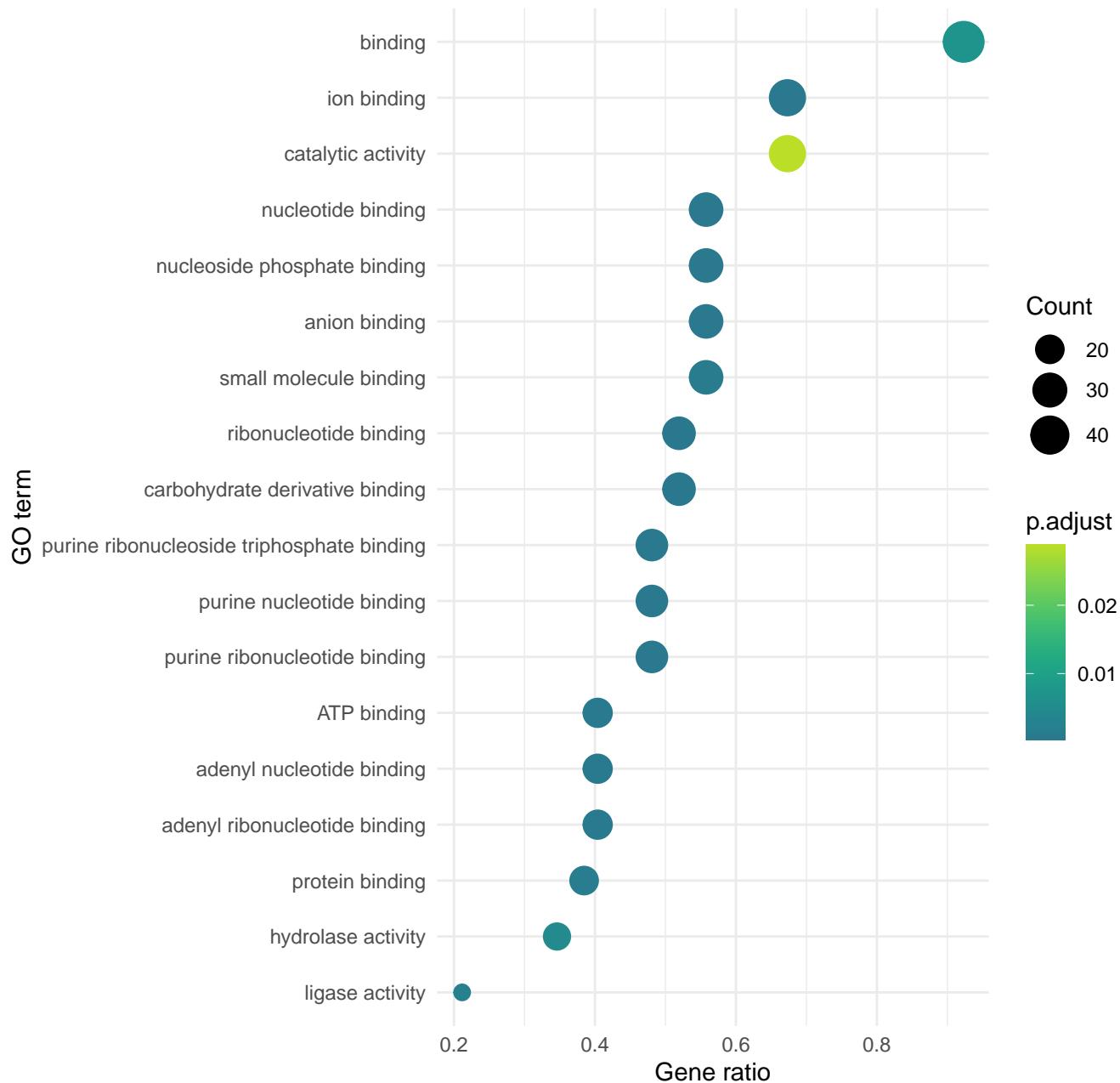
GLC7-TAP Up-regulated GO CC upsetplot



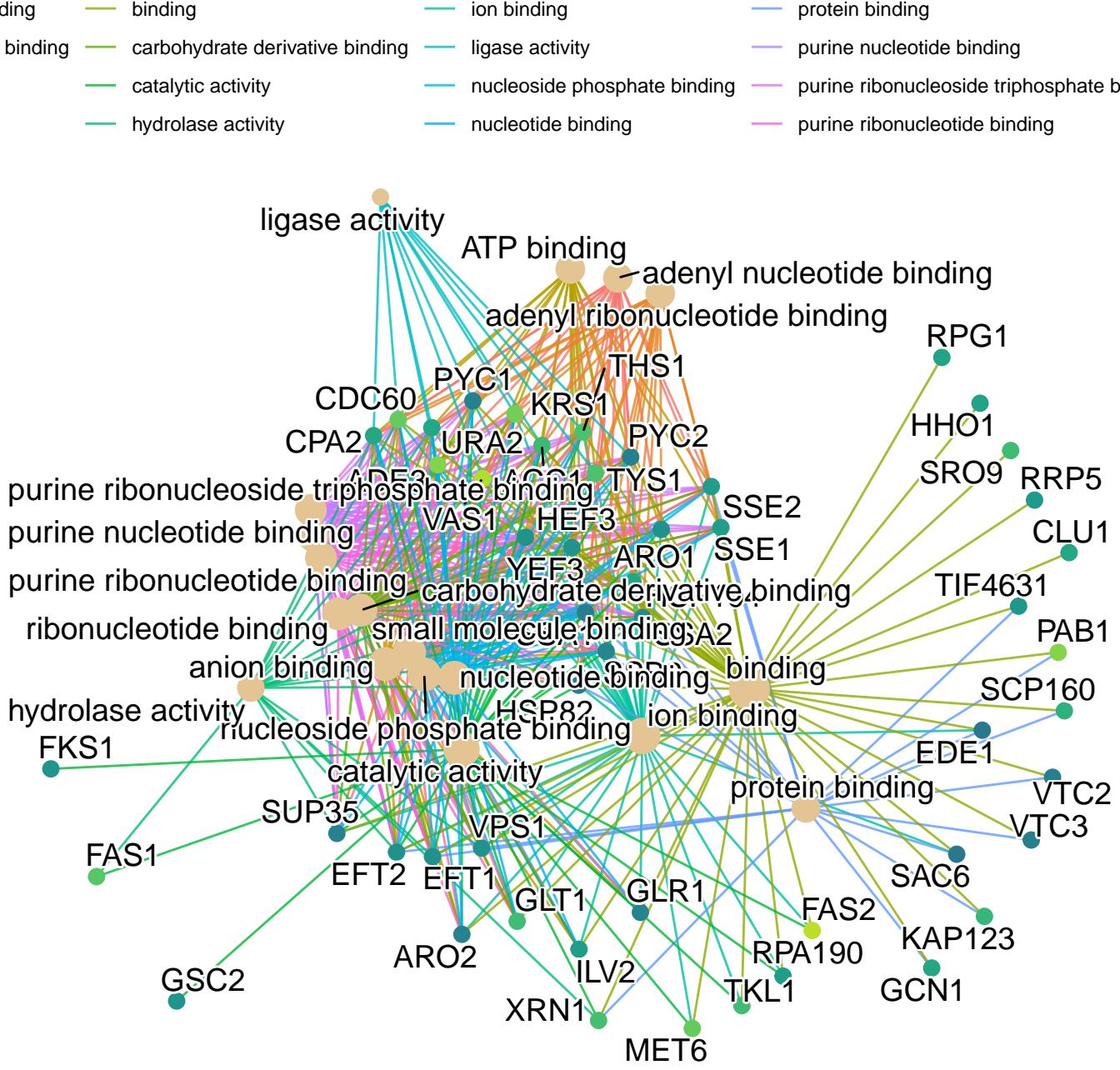
GLC7-TAP Up-regulated GO MF barplot



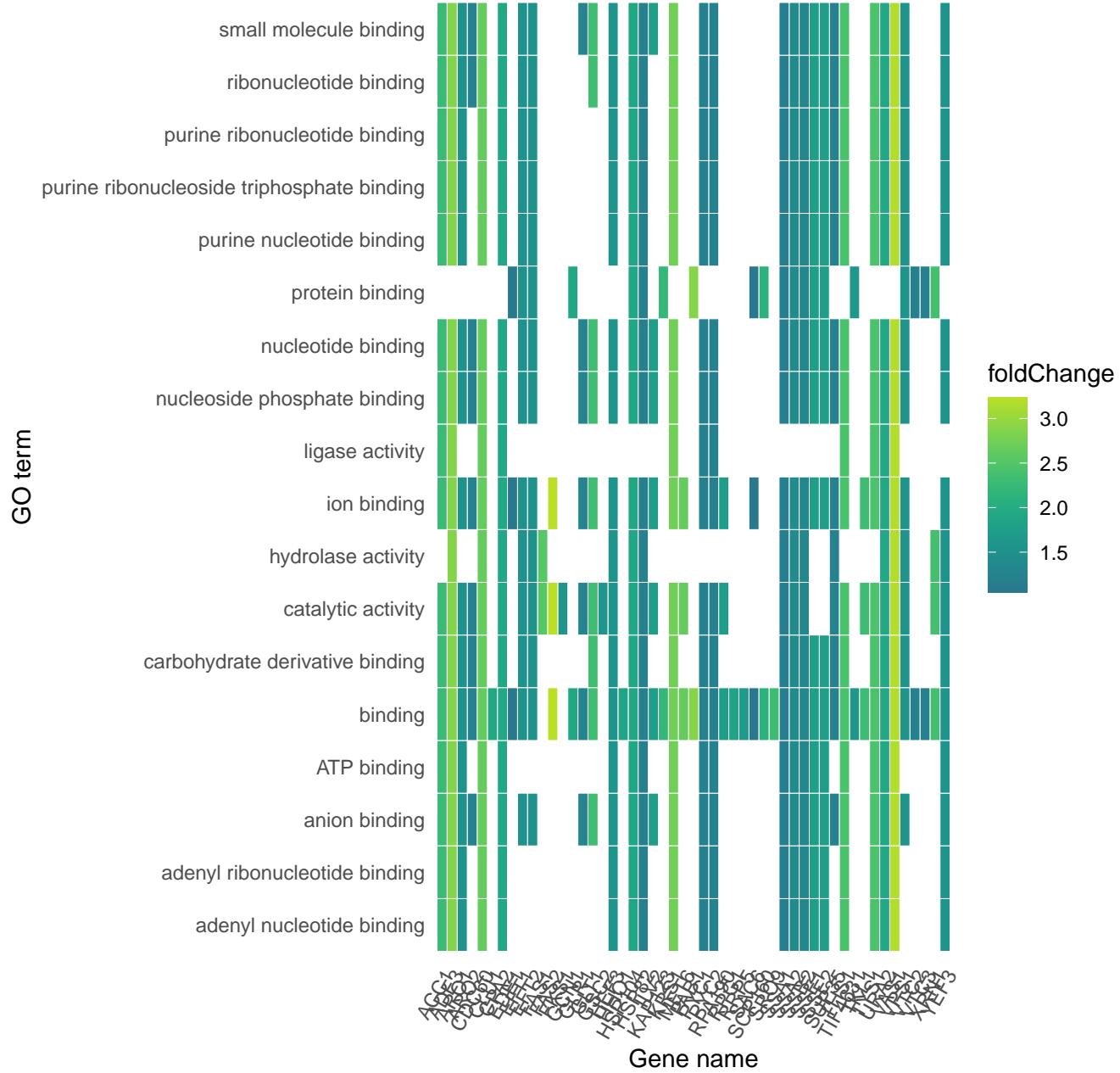
GLC7-TAP Up-regulated GO MF dotplot



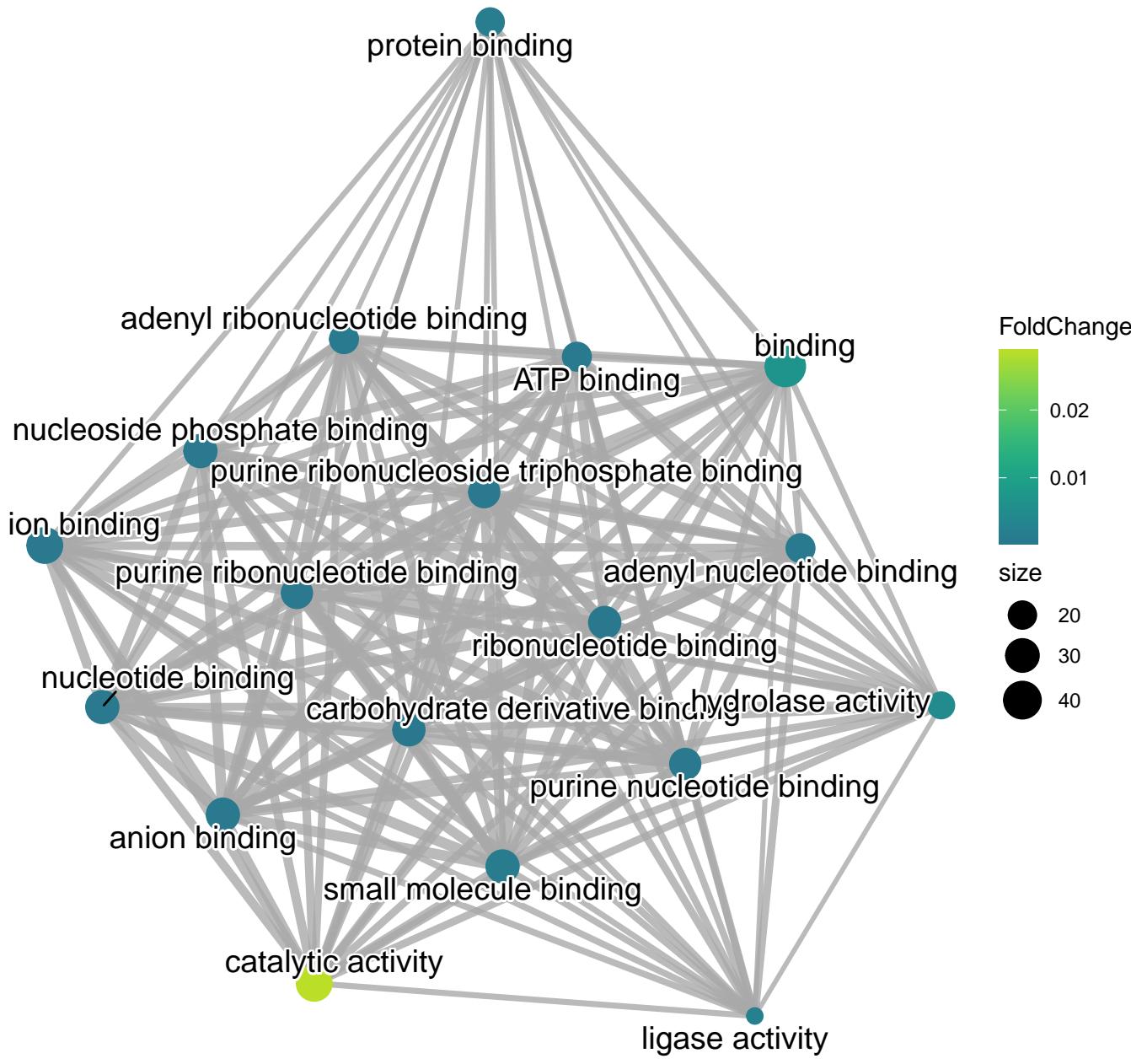
GLC7-TAP Up-regulated GO MF cnetplot

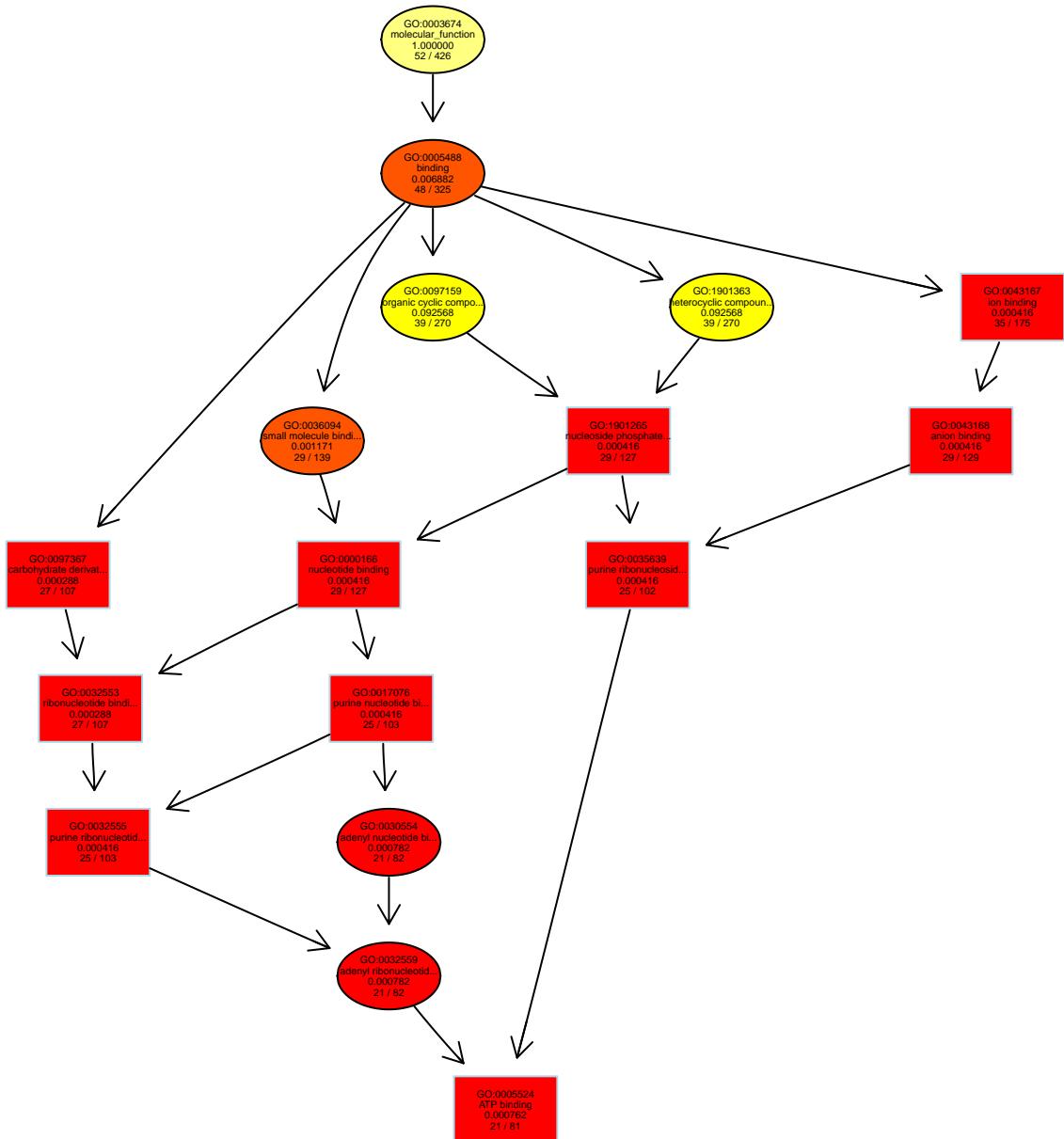


GLC7-TAP Up-regulated GO MF heatplot

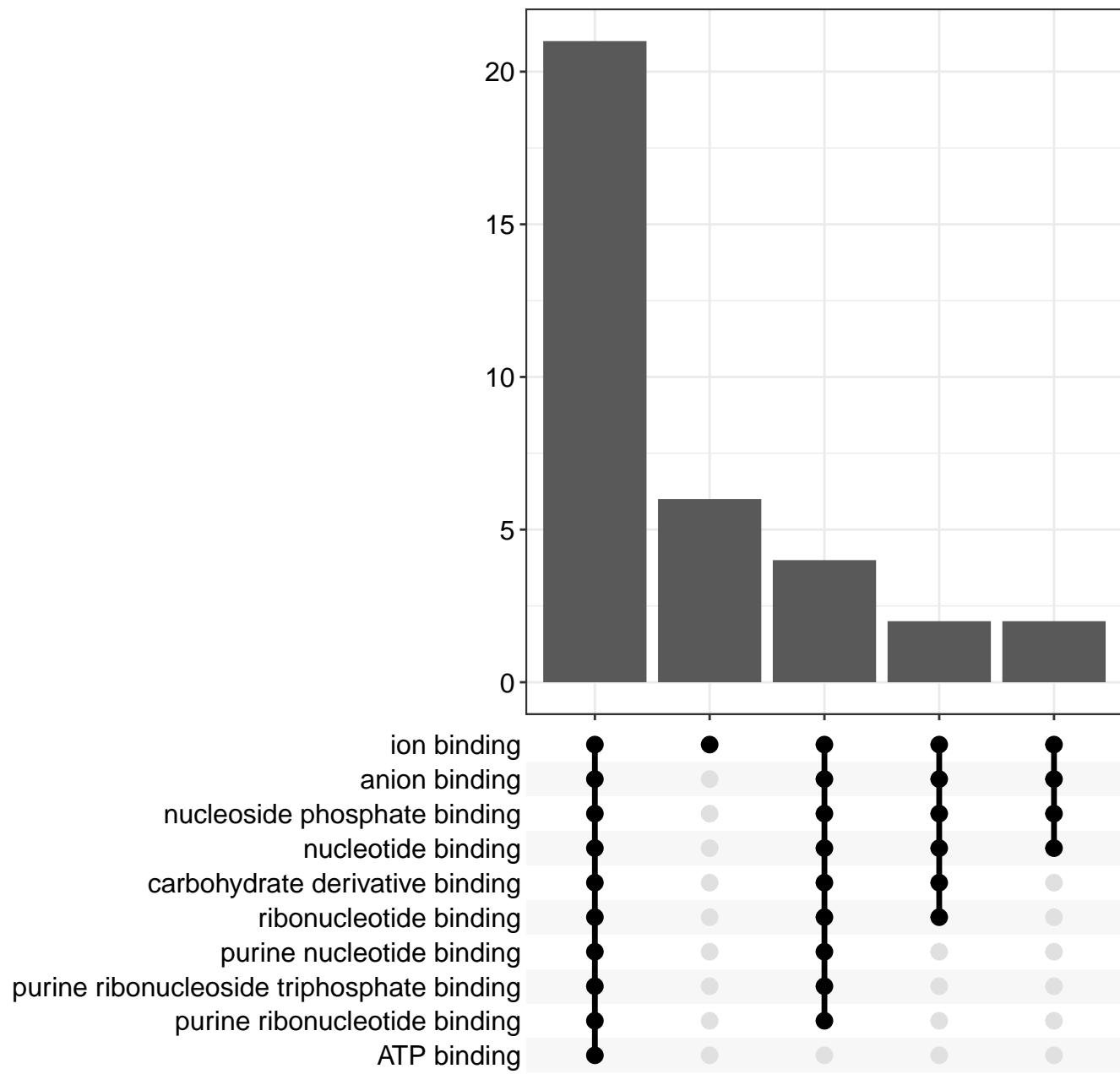


GLC7-TAP Up-regulated GO MF emapplot

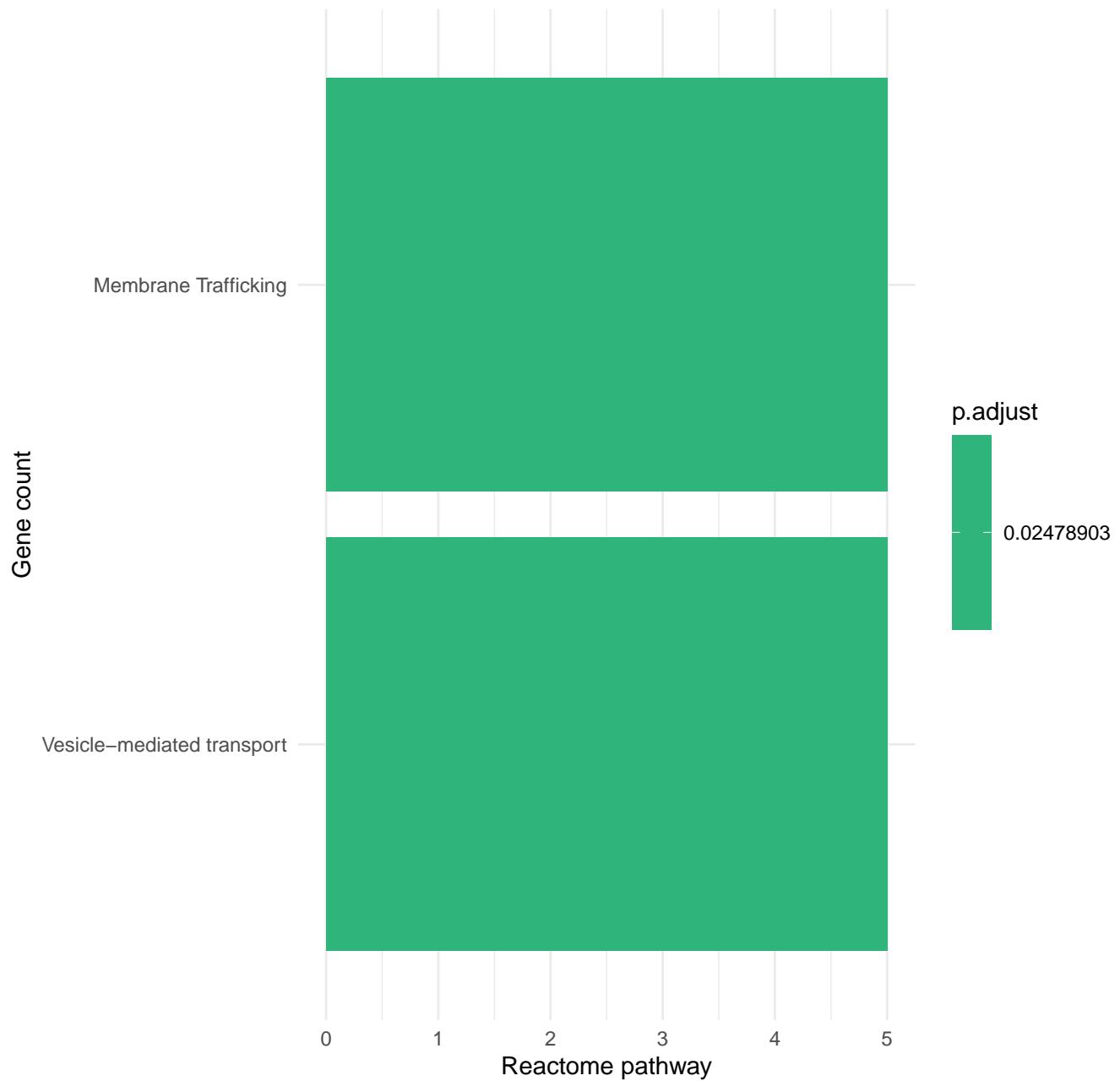




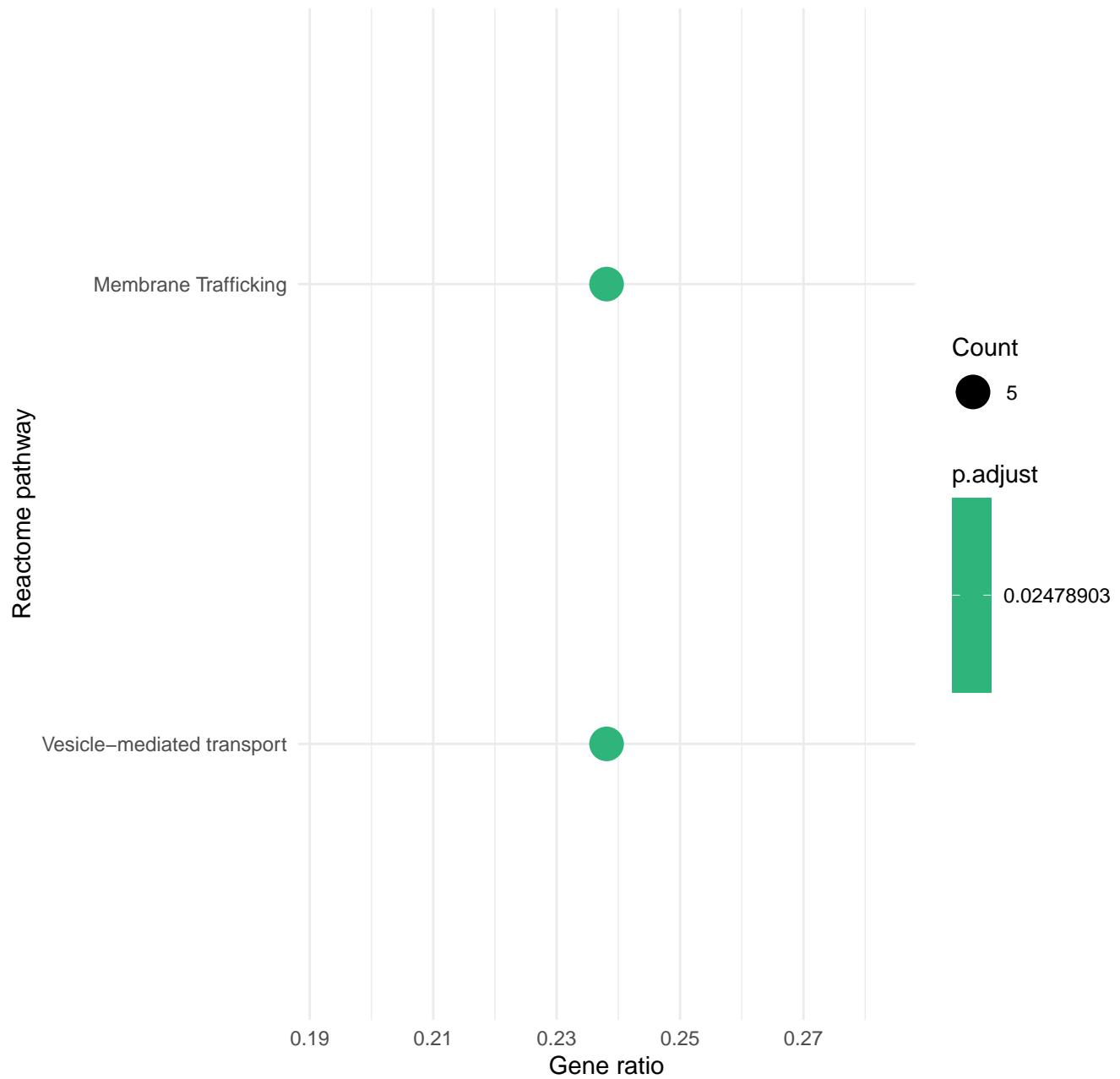
GLC7-TAP Up-regulated GO MF upsetplot



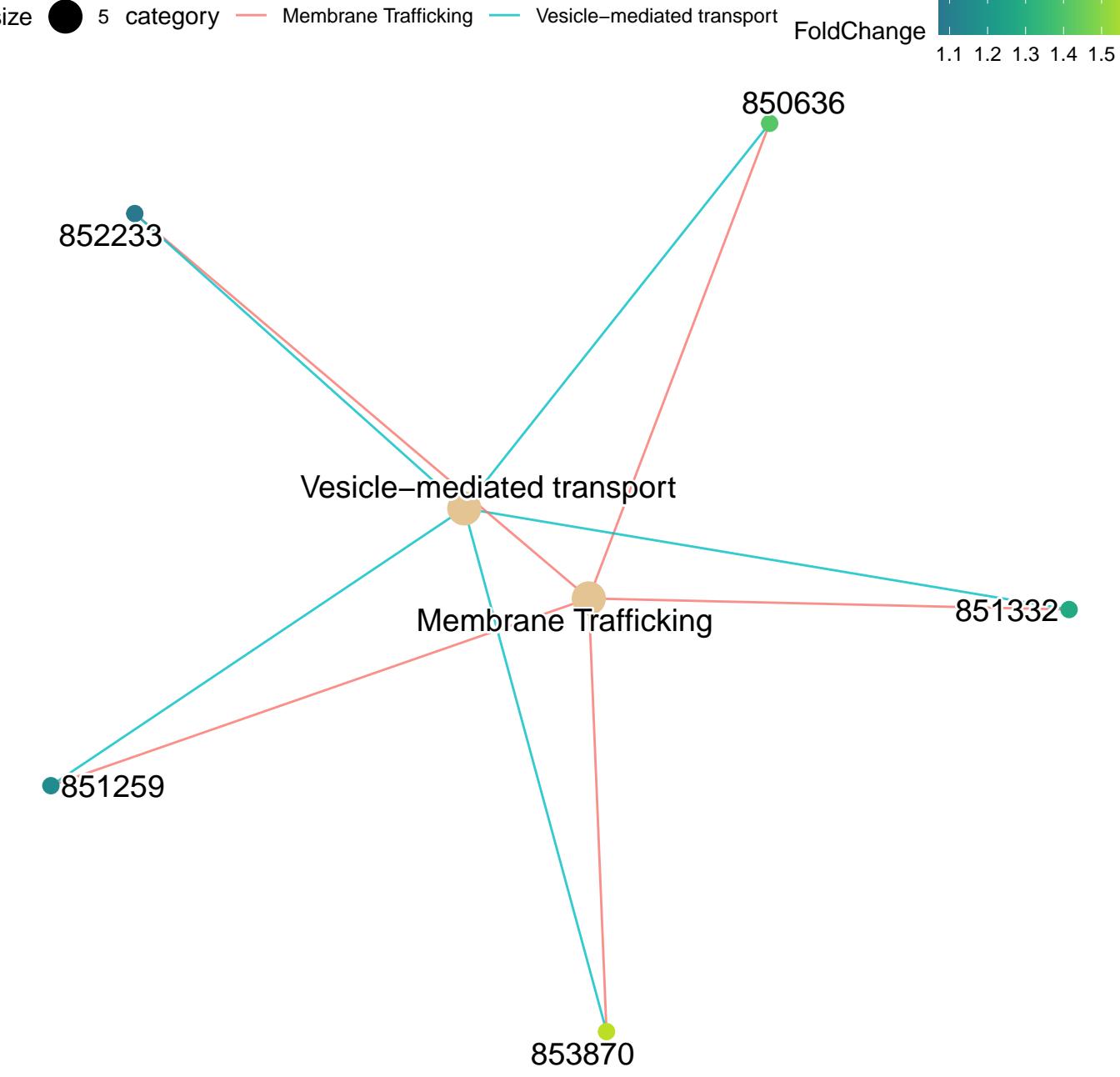
GLC7-TAP Up-regulated Reactome barplot



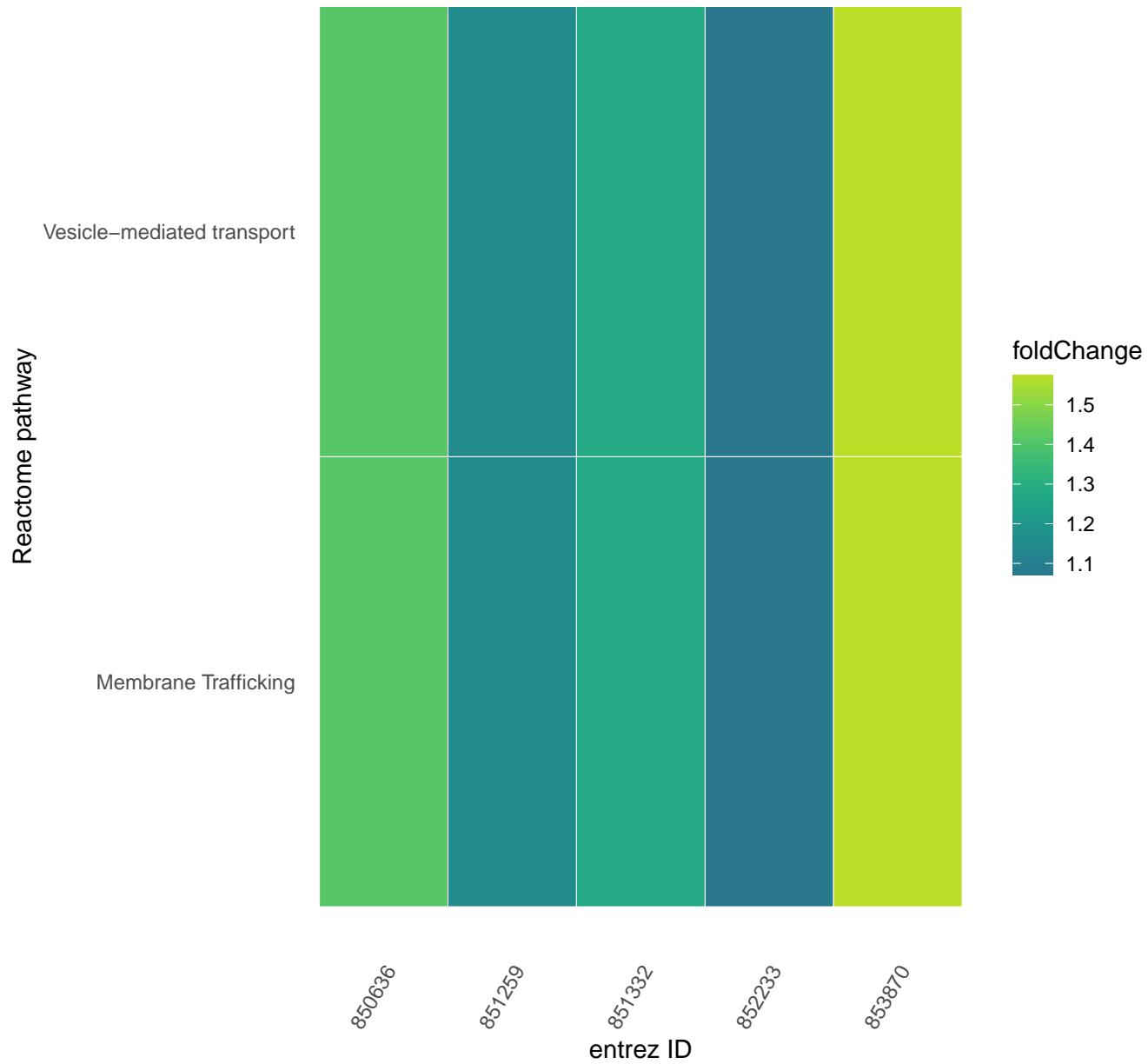
GLC7-TAP Up-regulated Reactome dotplot



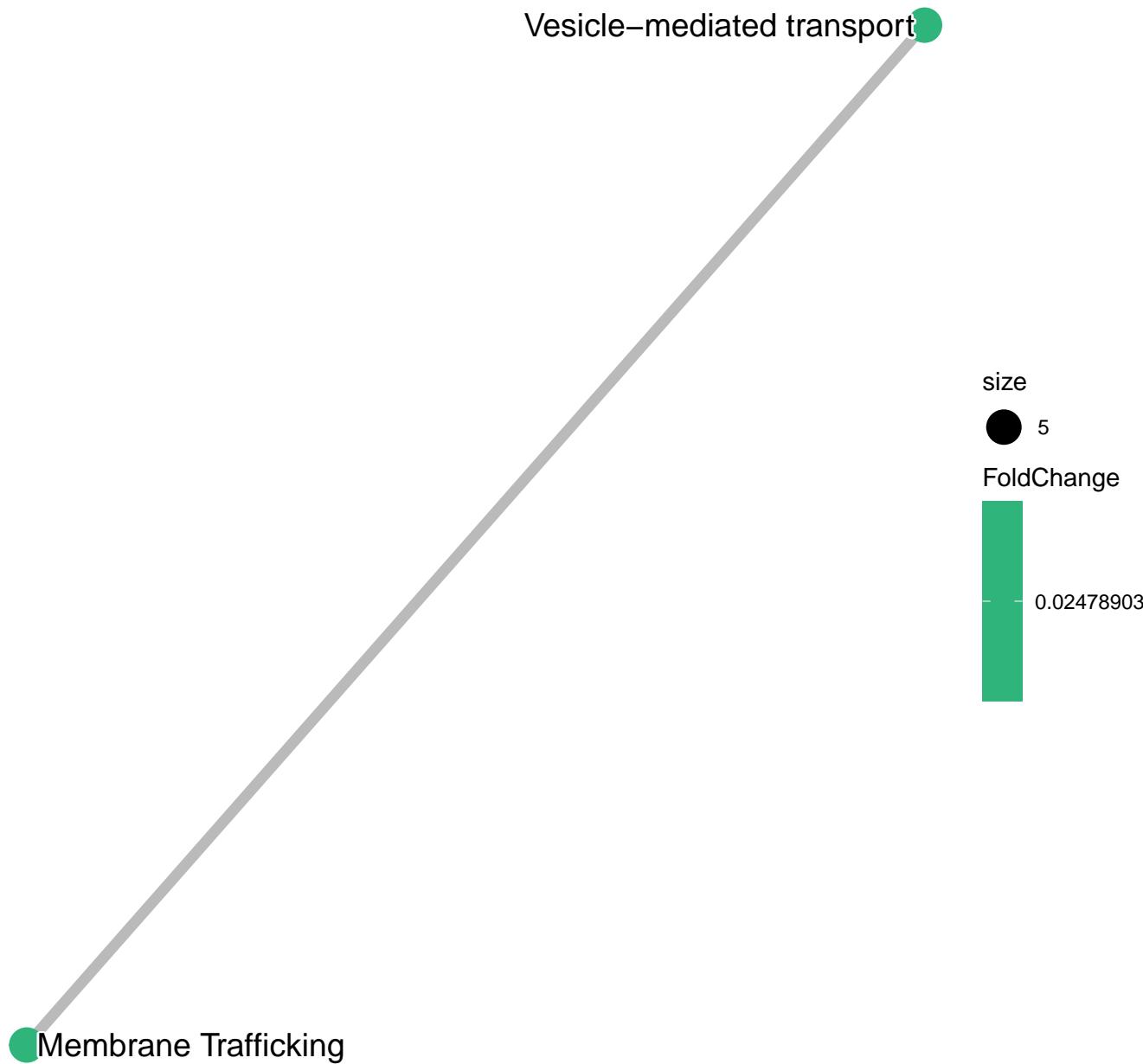
GLC7-TAP Up-regulated Reactome cnetplot



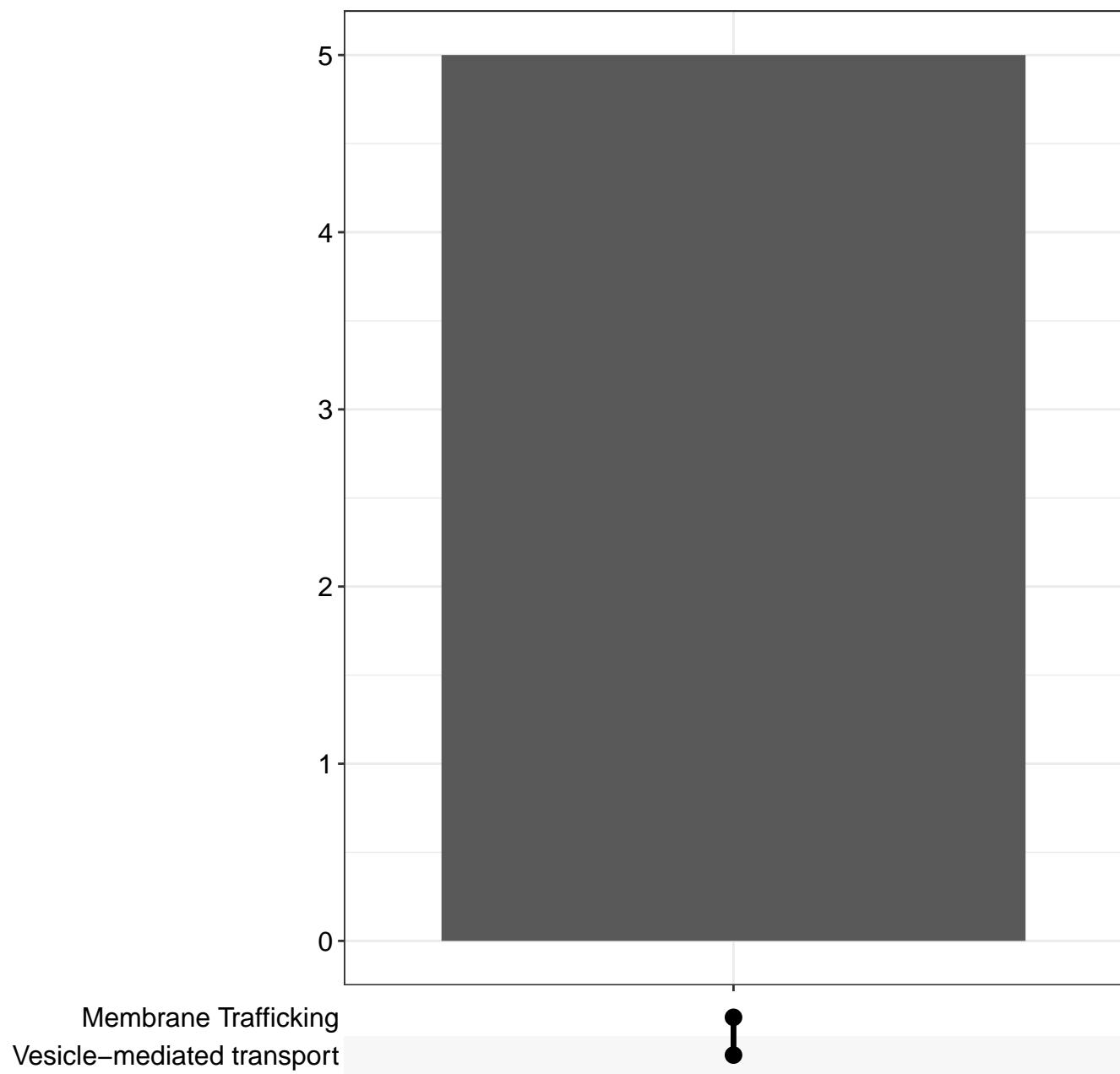
GLC7-TAP Up-regulated Reactome heatplot



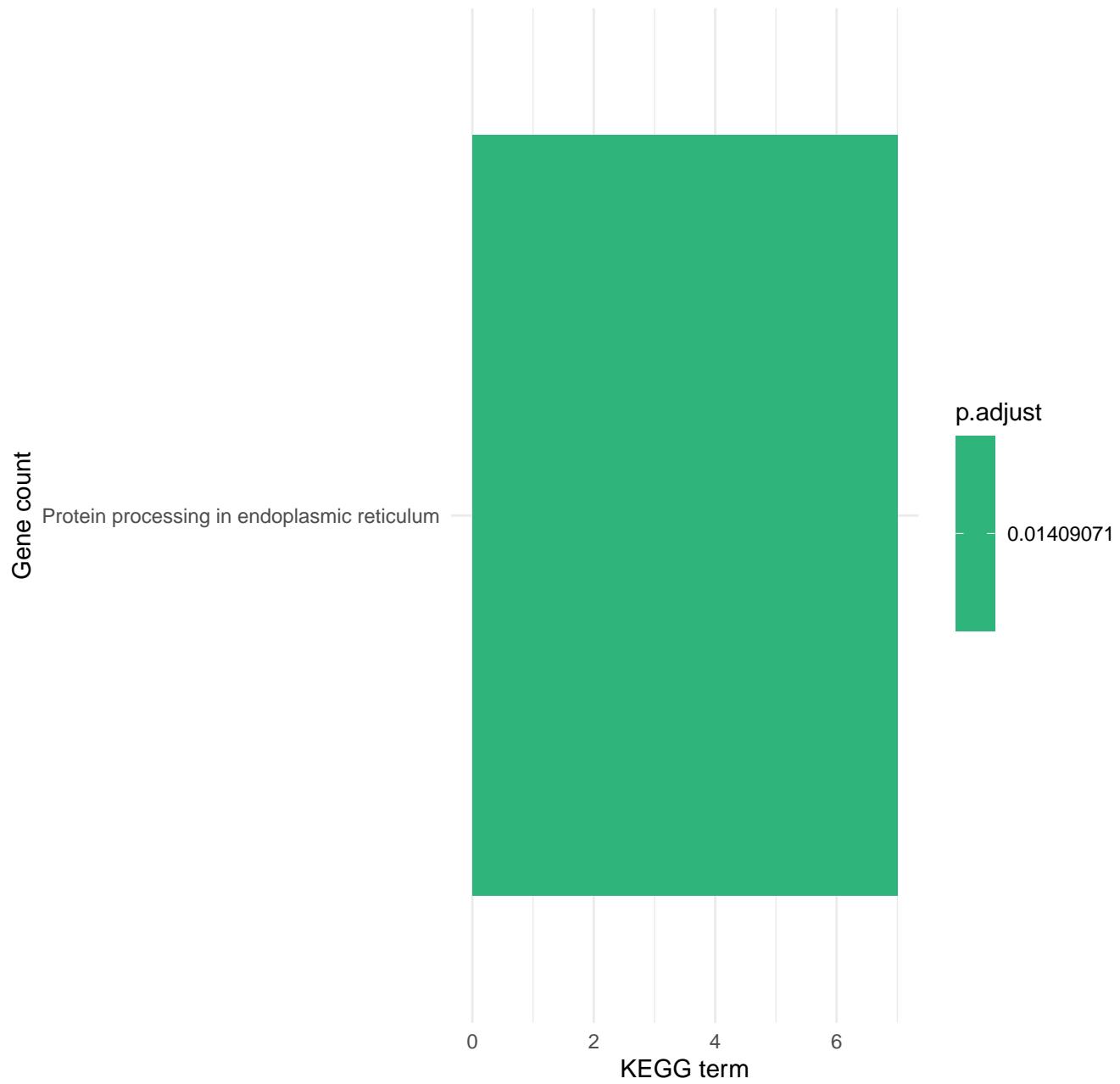
GLC7-TAP Up-regulated Reactome emapplot



GLC7-TAP Up-regulated Reactome upsetplot



GLC7-TAP Up-regulated KEGG barplot



GLC7-TAP Up-regulated KEGG dotplot

KEGG term

Protein processing in endoplasmic reticulum

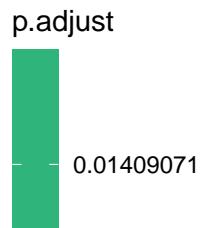
0.150

0.175

0.200

0.225

Gene ratio

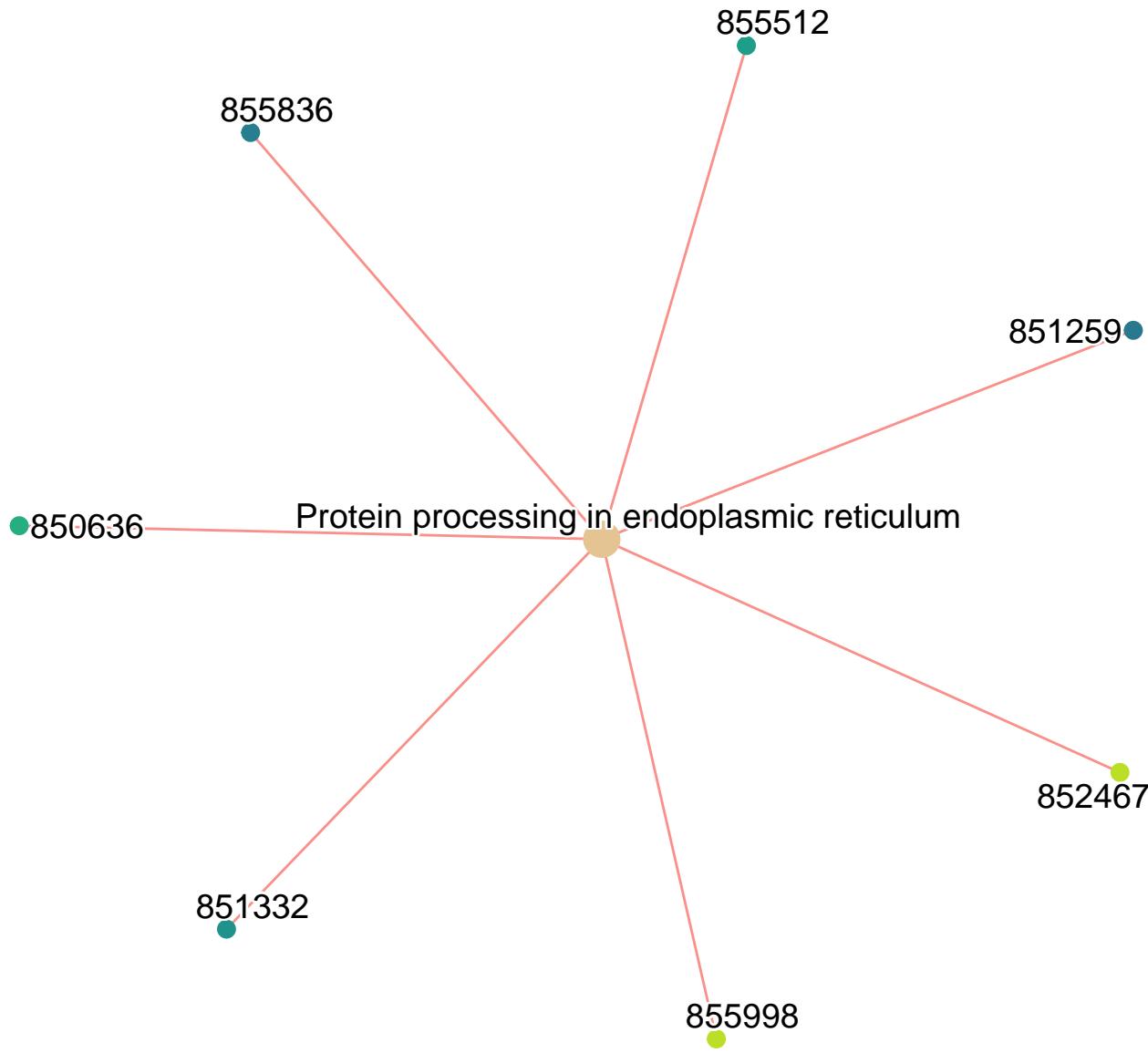


0.198

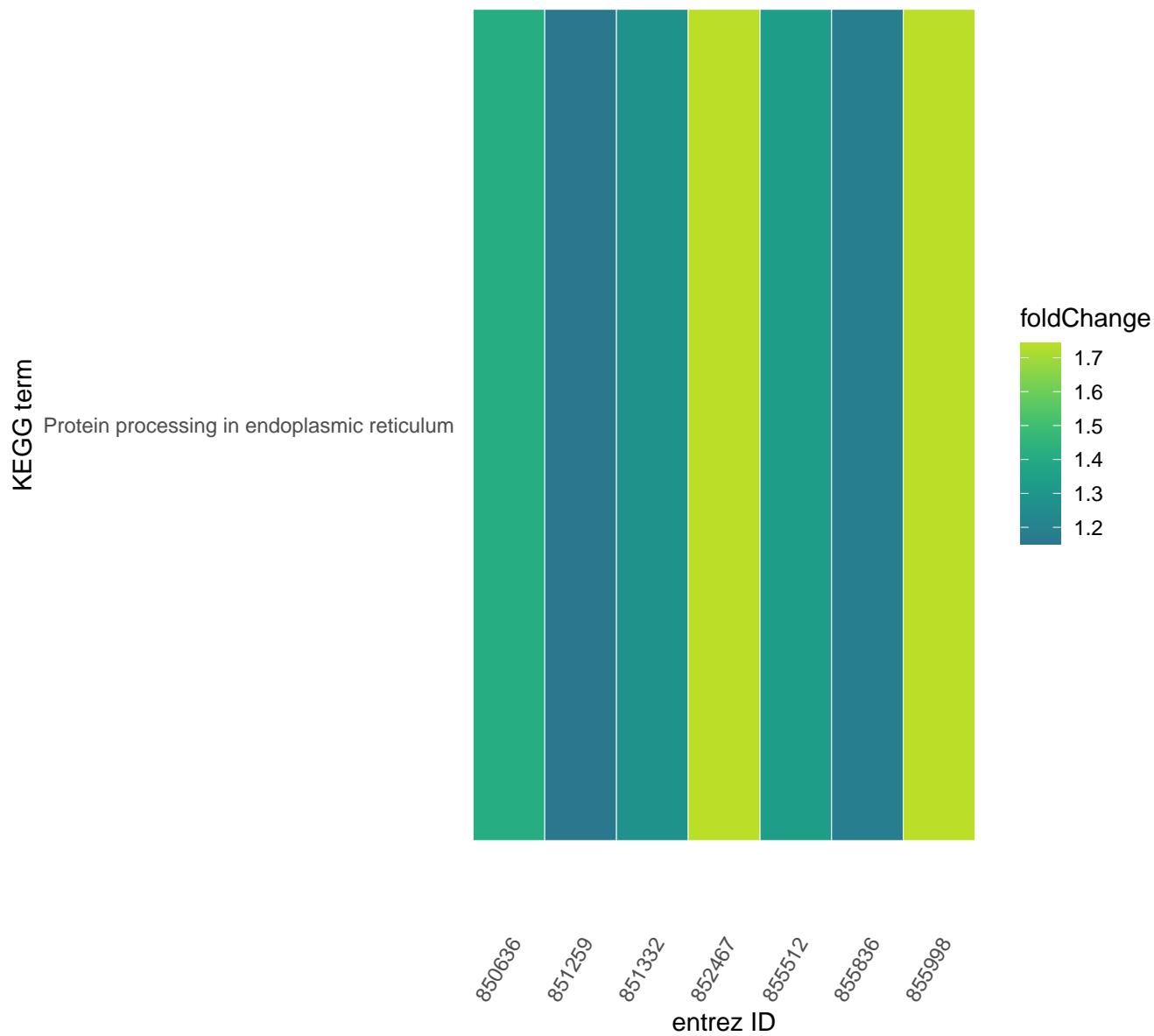
GLC7-TAP Up-regulated KEGG dotplot



size ● 7 category — Protein processing in endoplasmic reticulum



GLC7-TAP Up-regulated KEGG heatplot



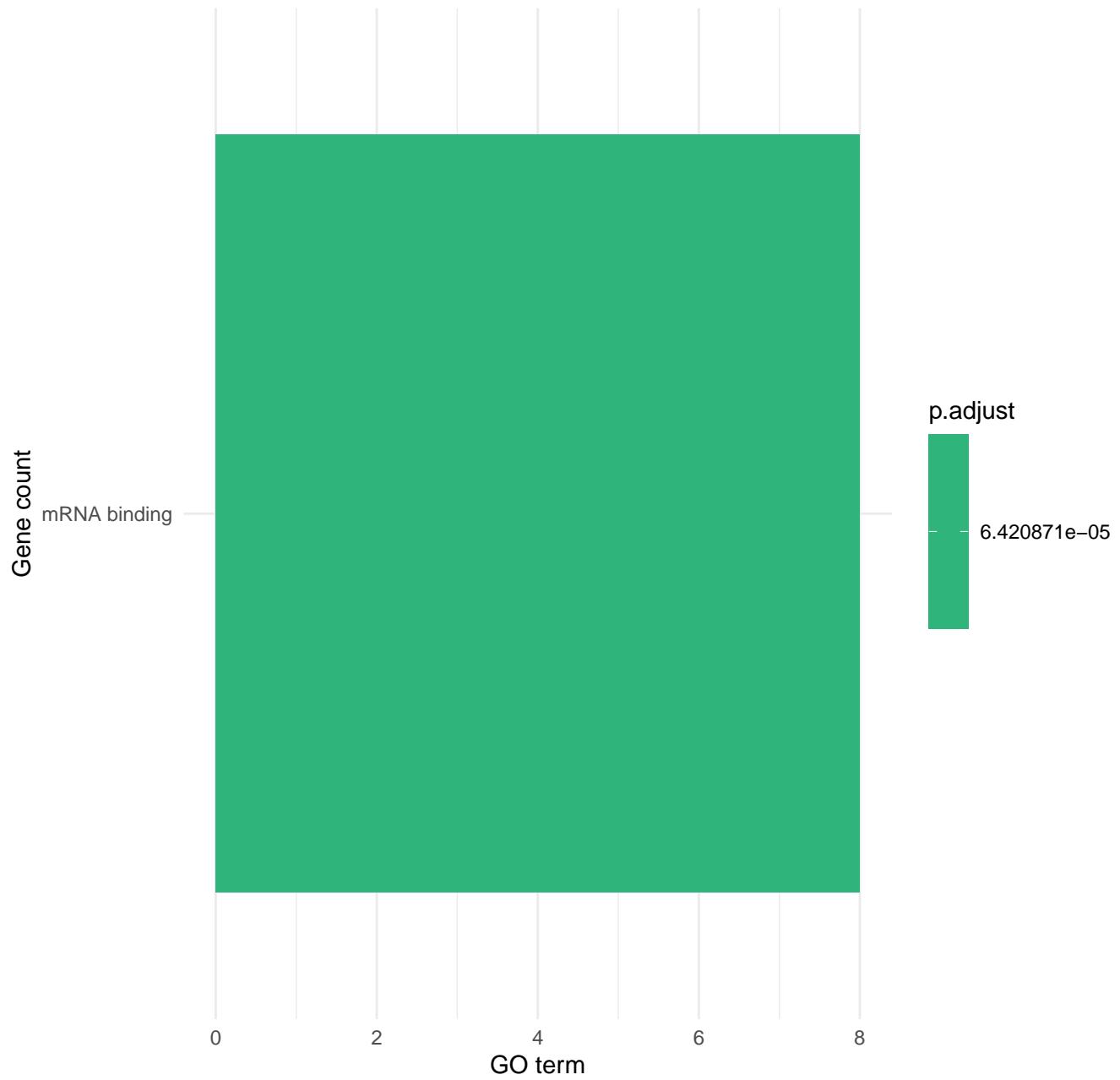
GLC7-TAP Up-regulated KEGG upsetplot



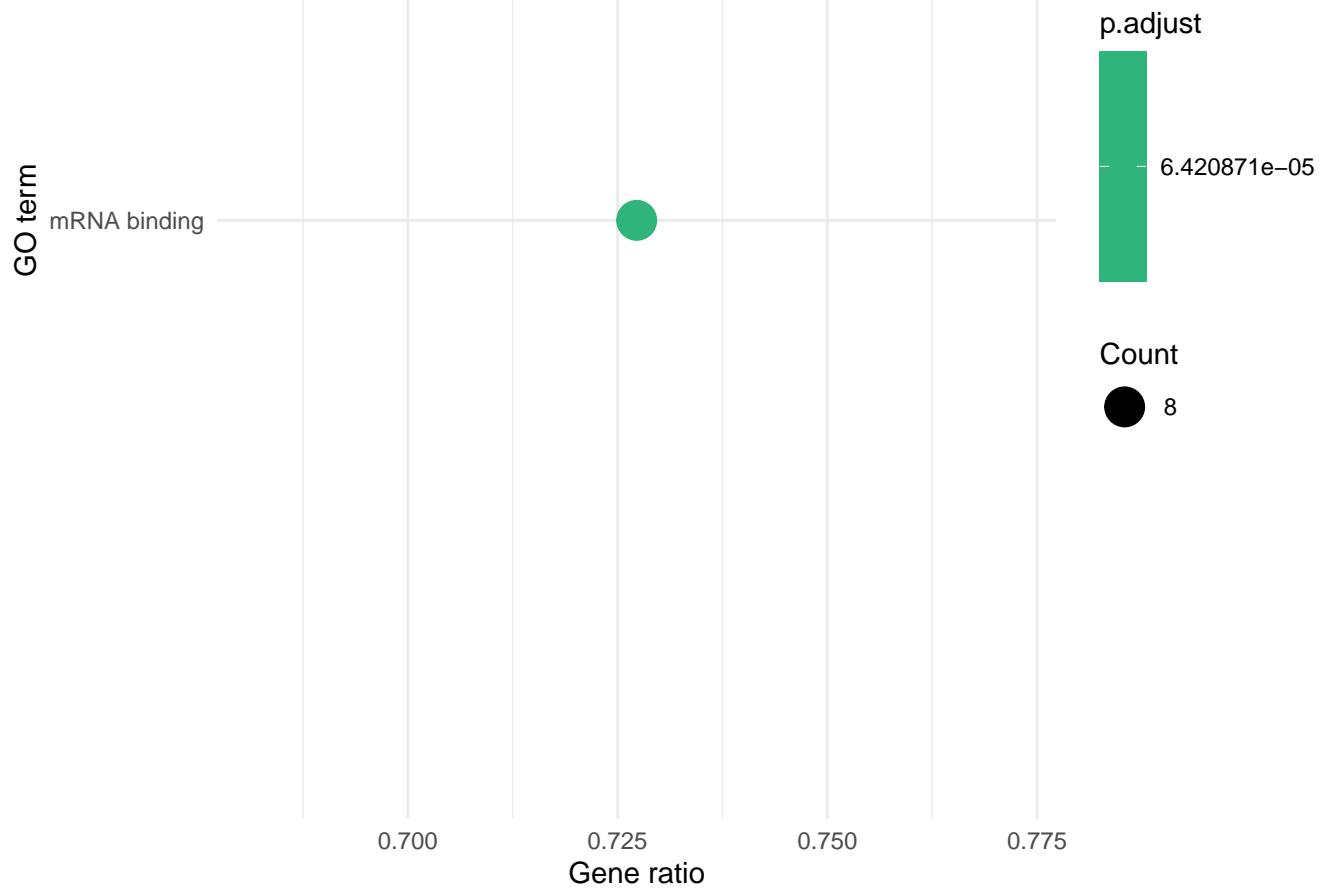
Protein processing in endoplasmic reticulum



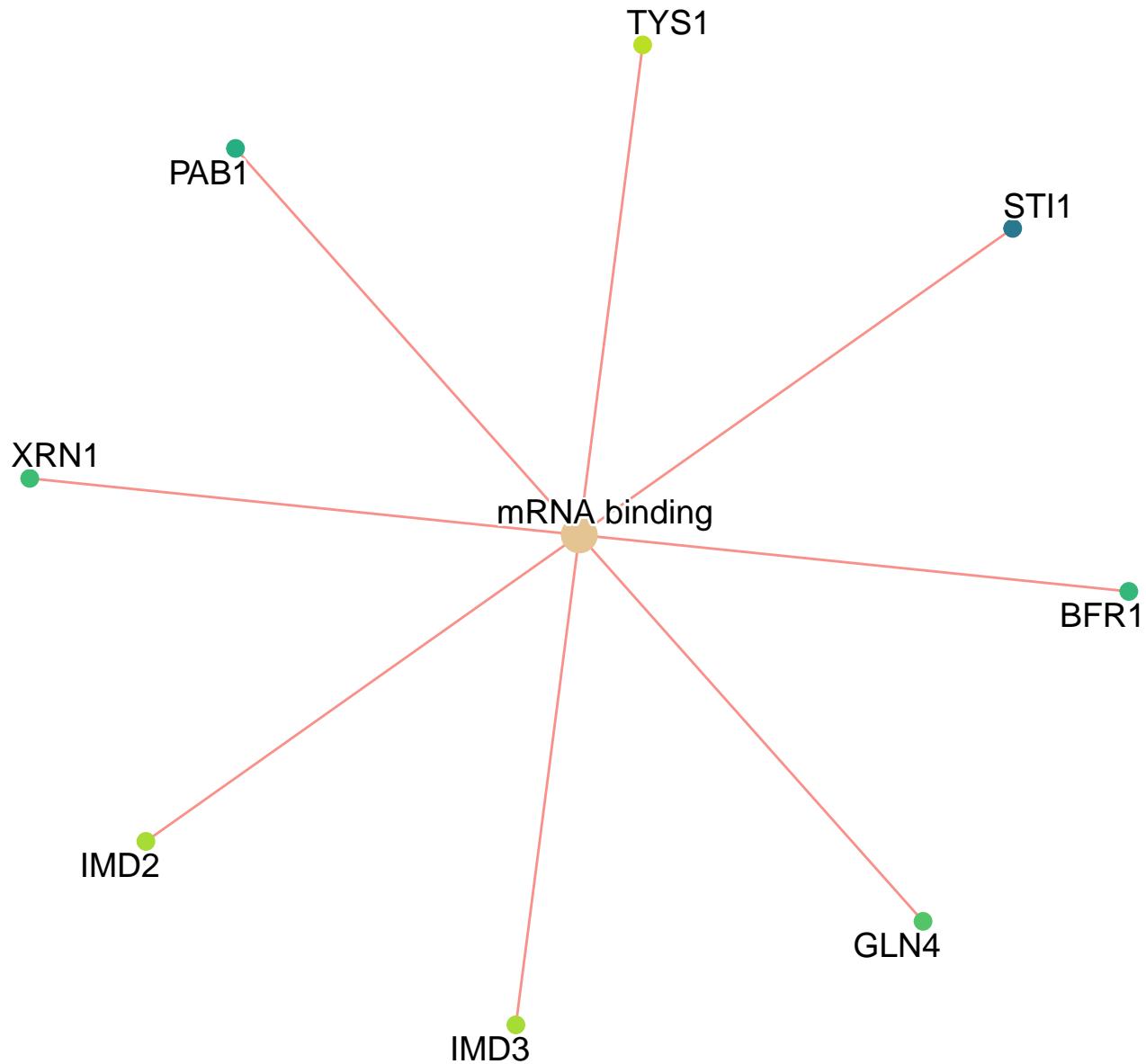
SUP35-TAP Up-regulated GO MF barplot



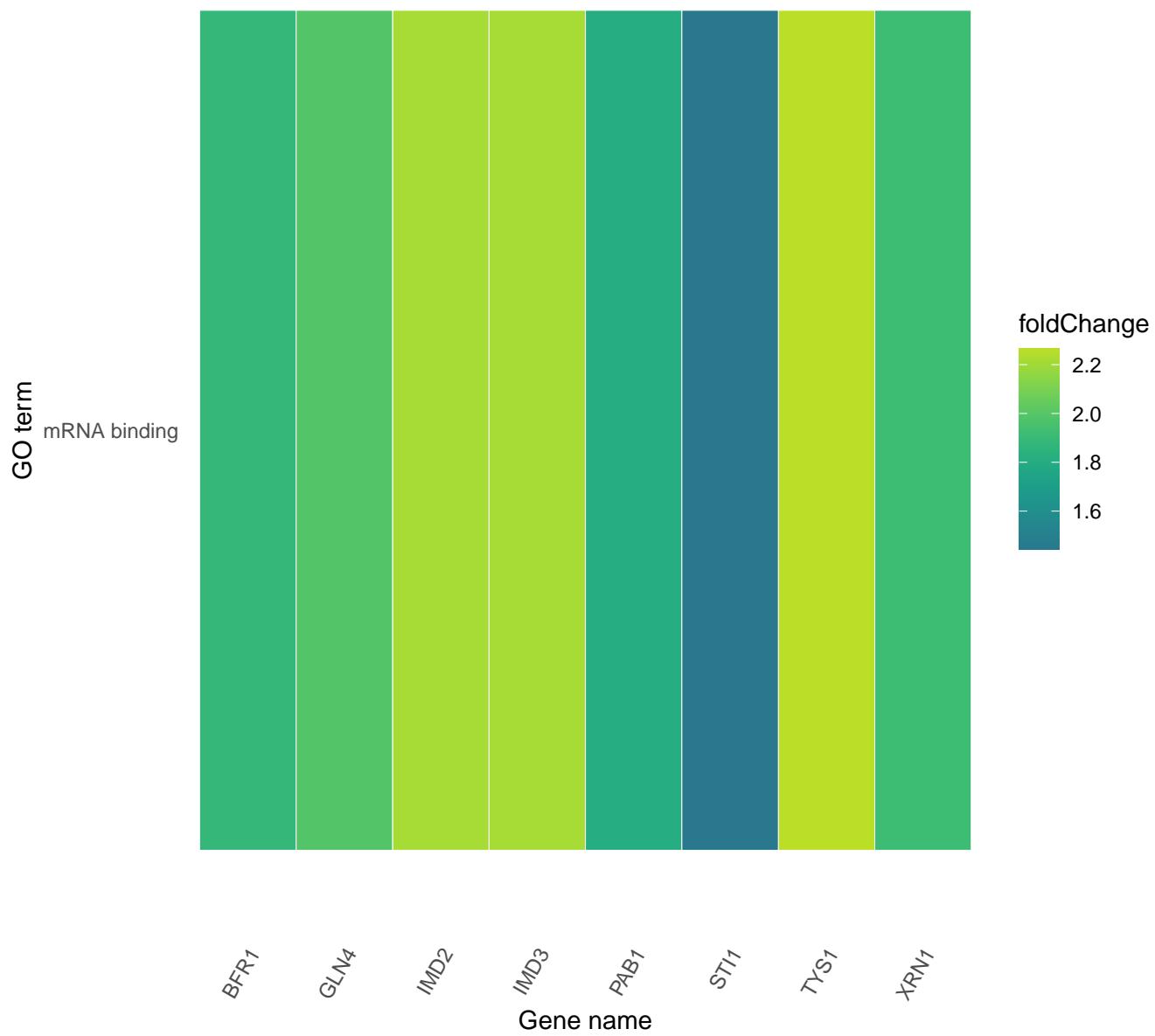
SUP35-TAP Up-regulated GO MF dotplot

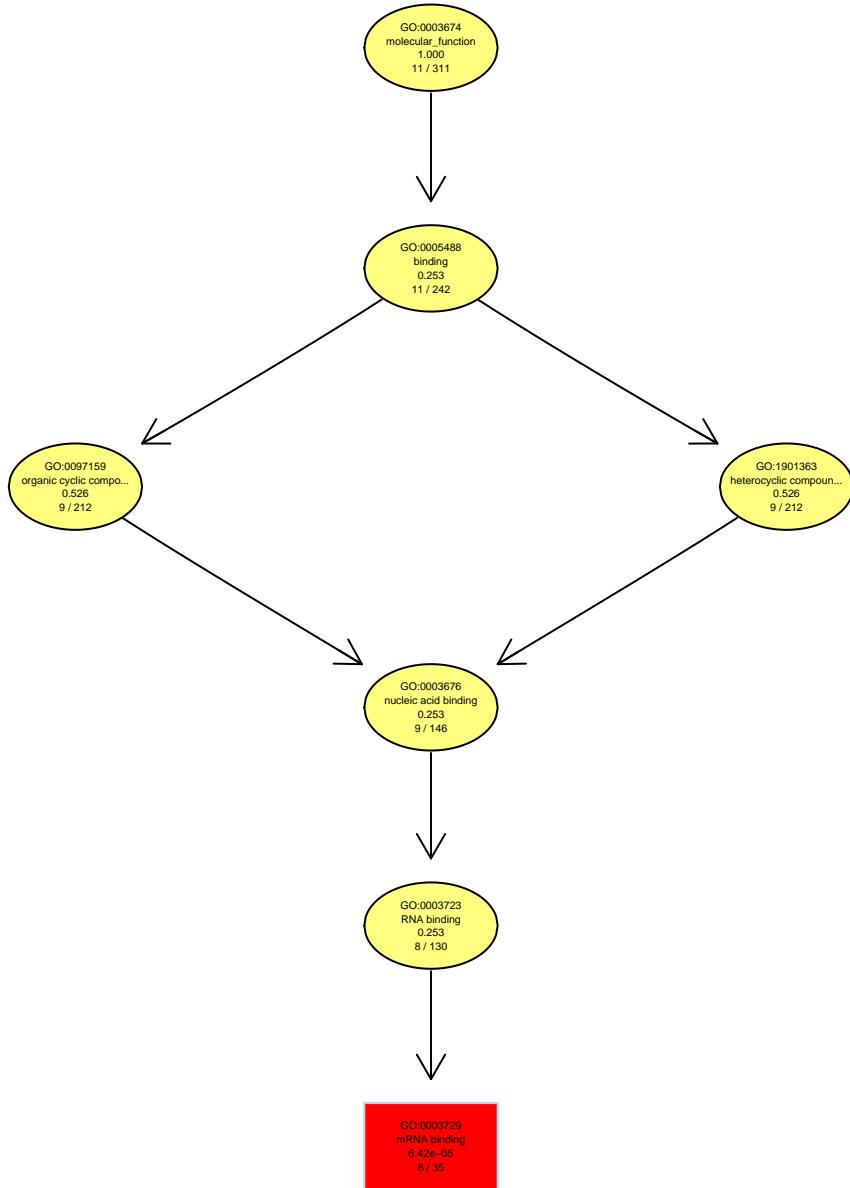


SUP35-TAP Up-regulated GO MF cnetplot

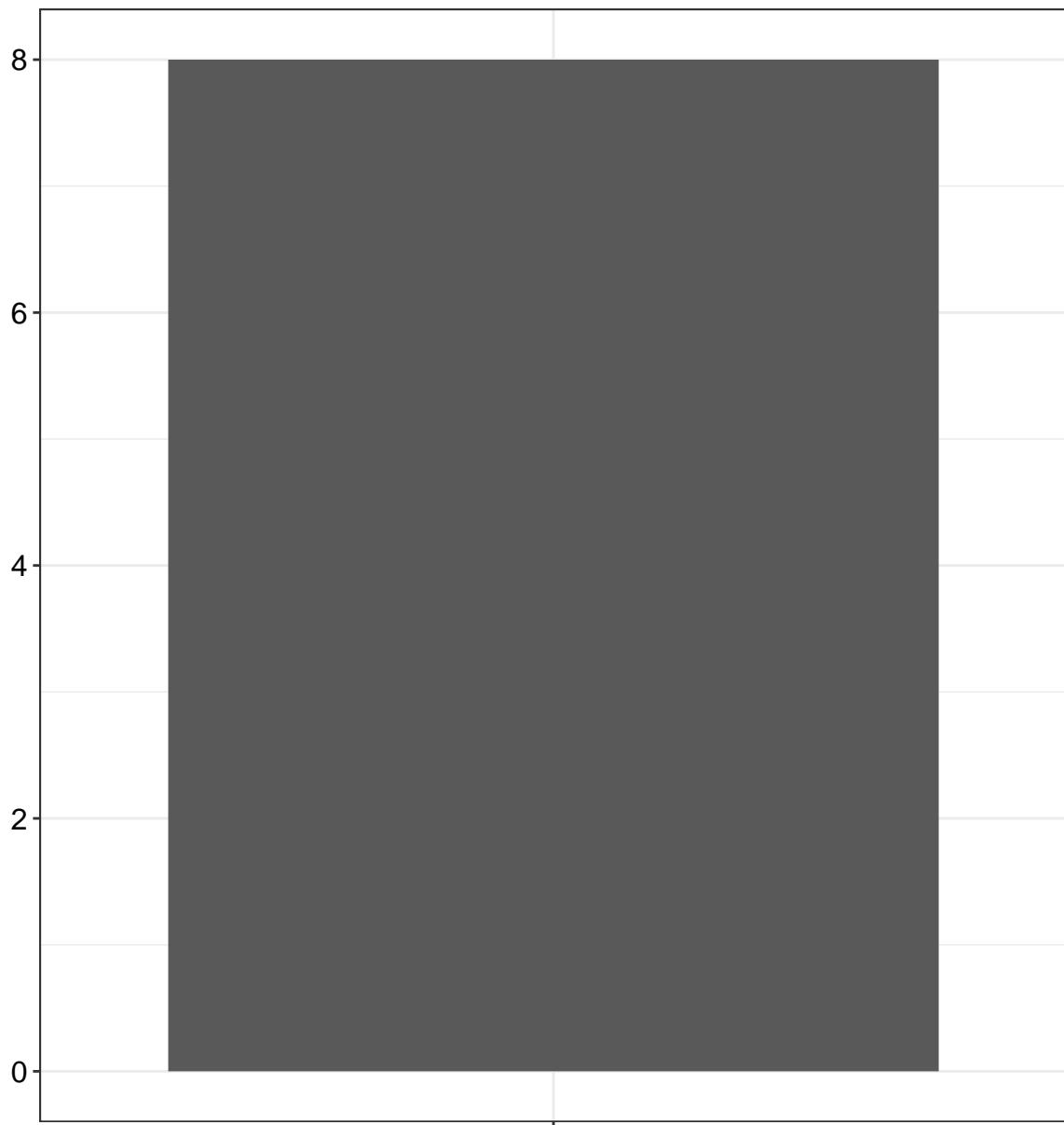


SUP35-TAP Up-regulated GO MF heatplot



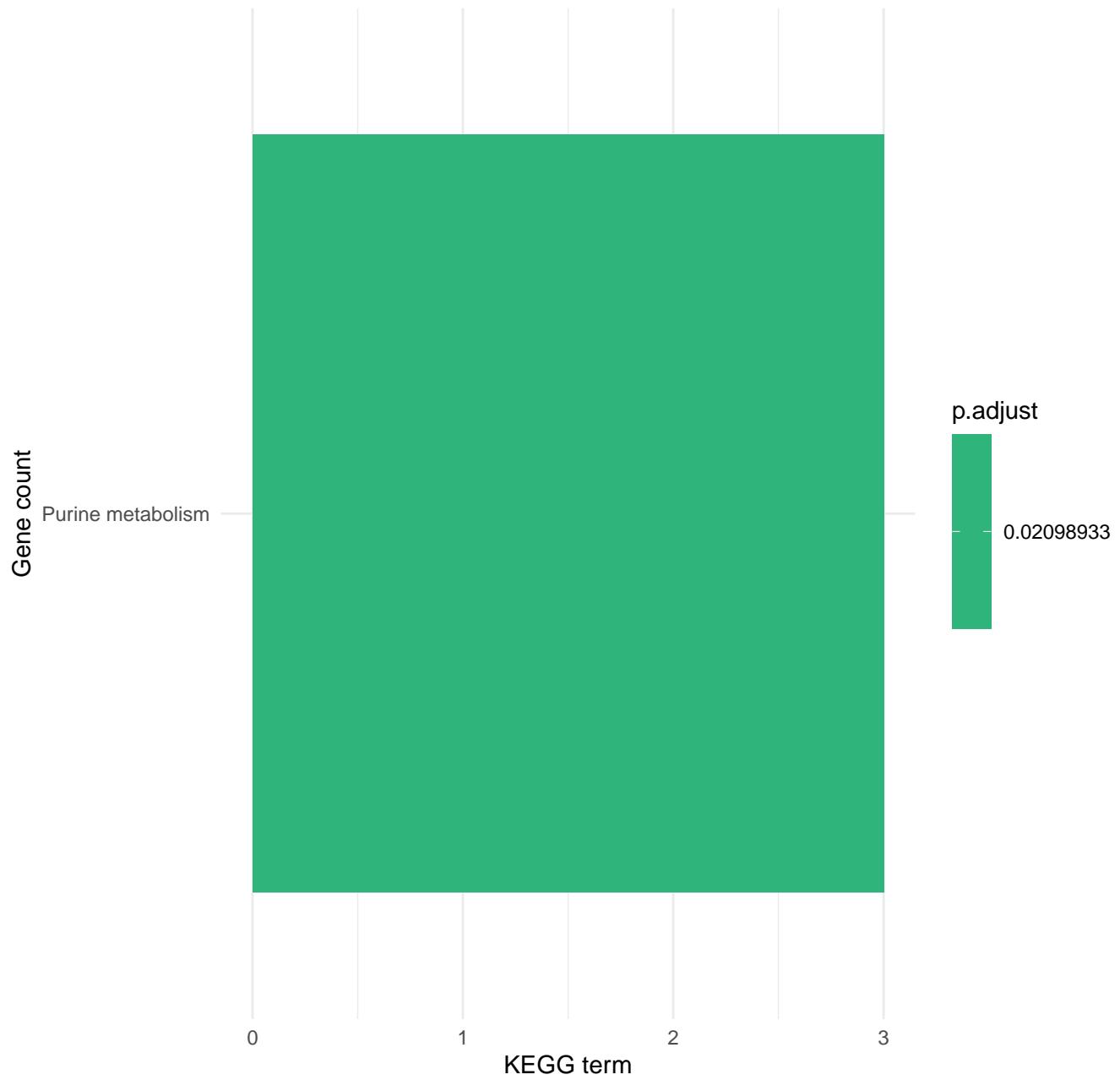


SUP35-TAP Up-regulated GO MF upsetplot

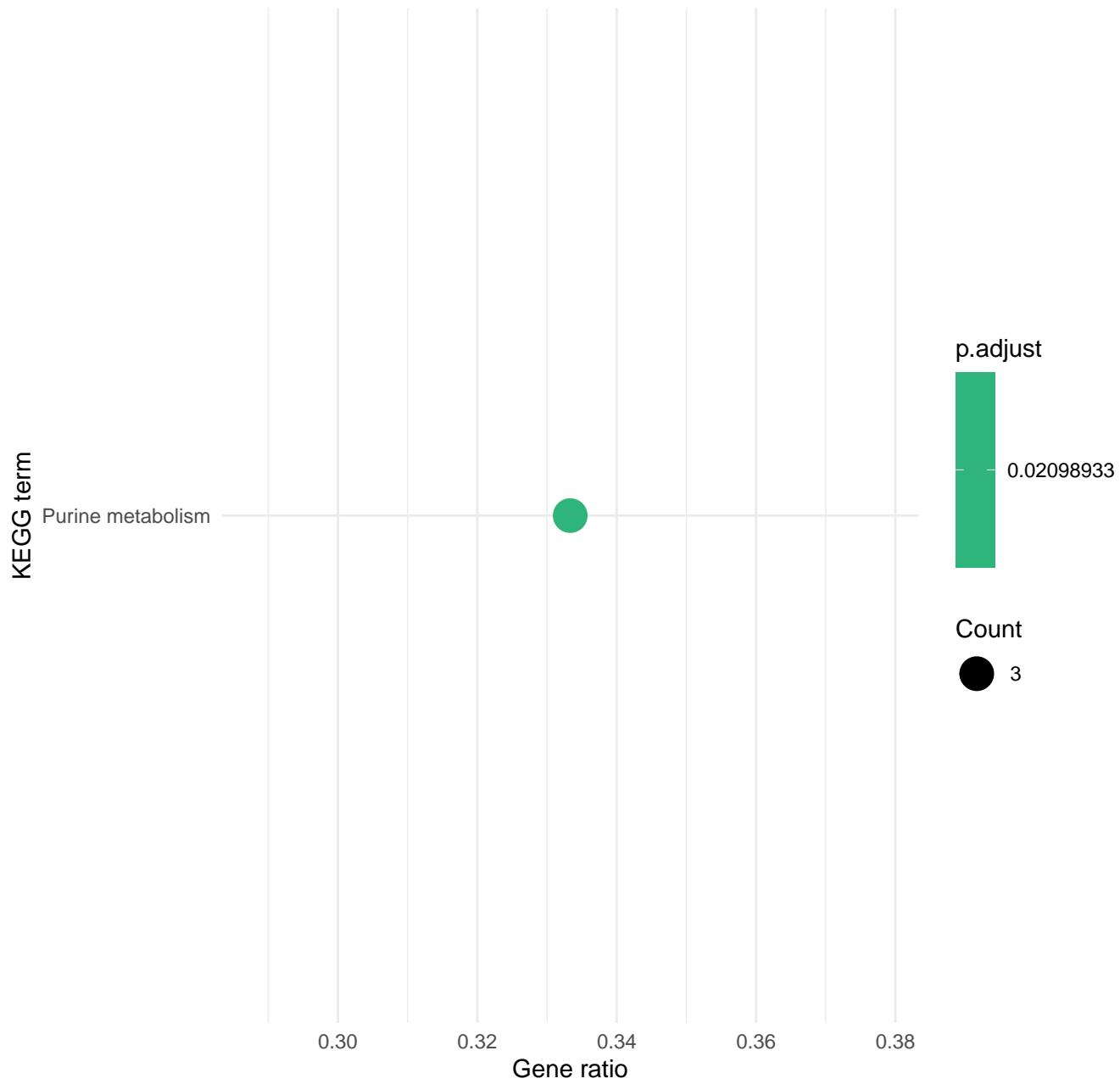


mRNA binding

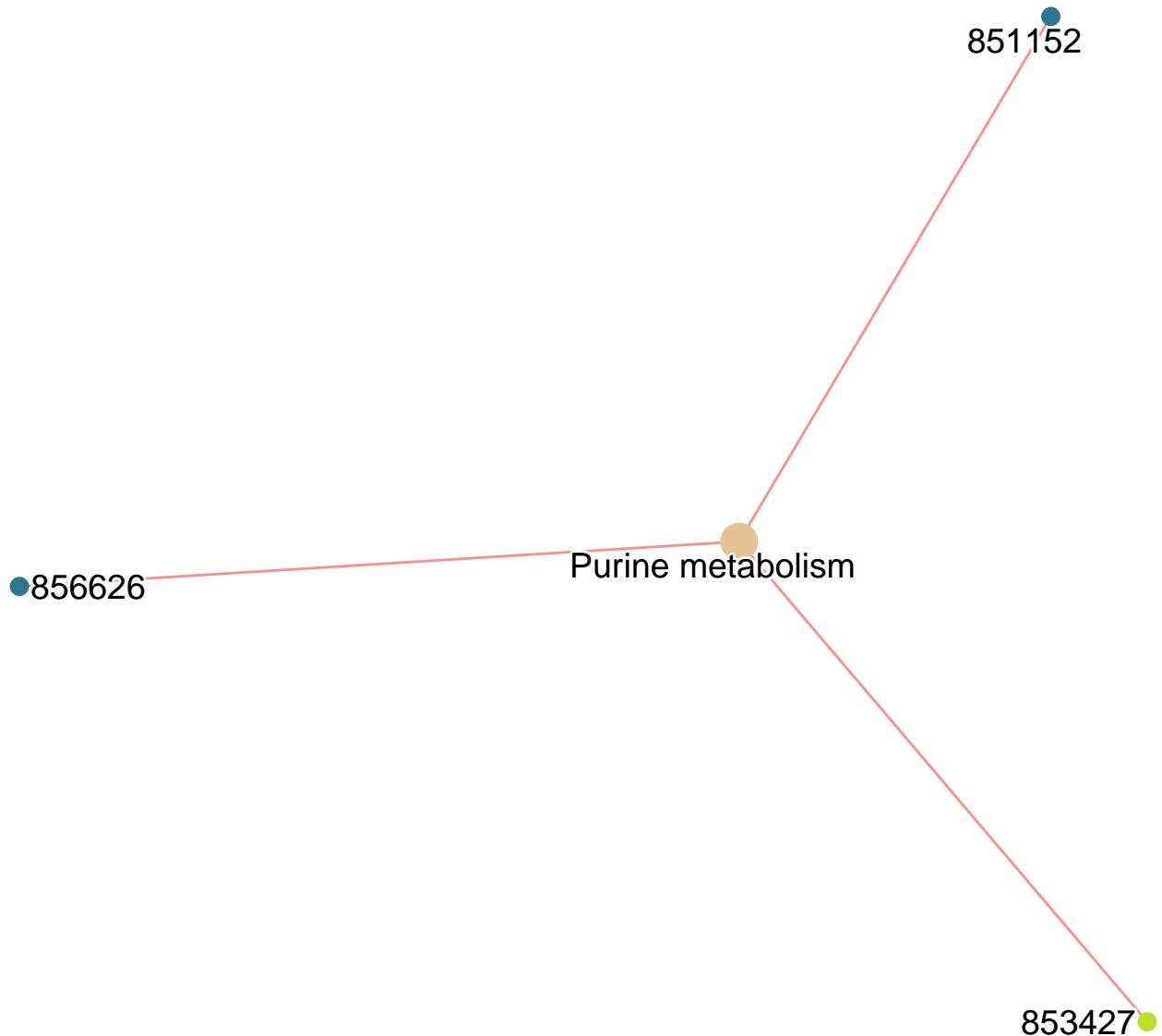
SUP35-TAP Up-regulated KEGG barplot



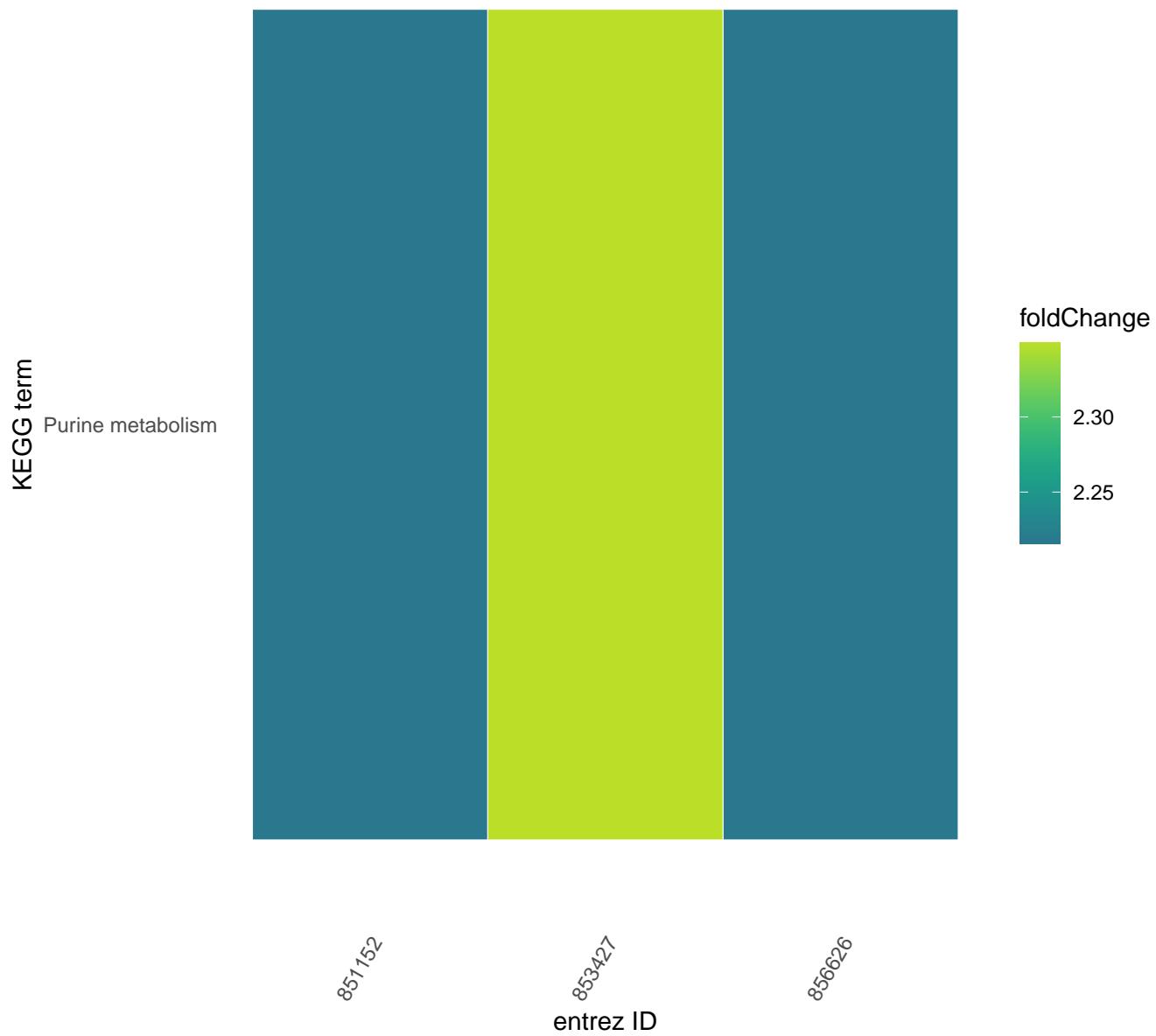
SUP35-TAP Up-regulated KEGG dotplot



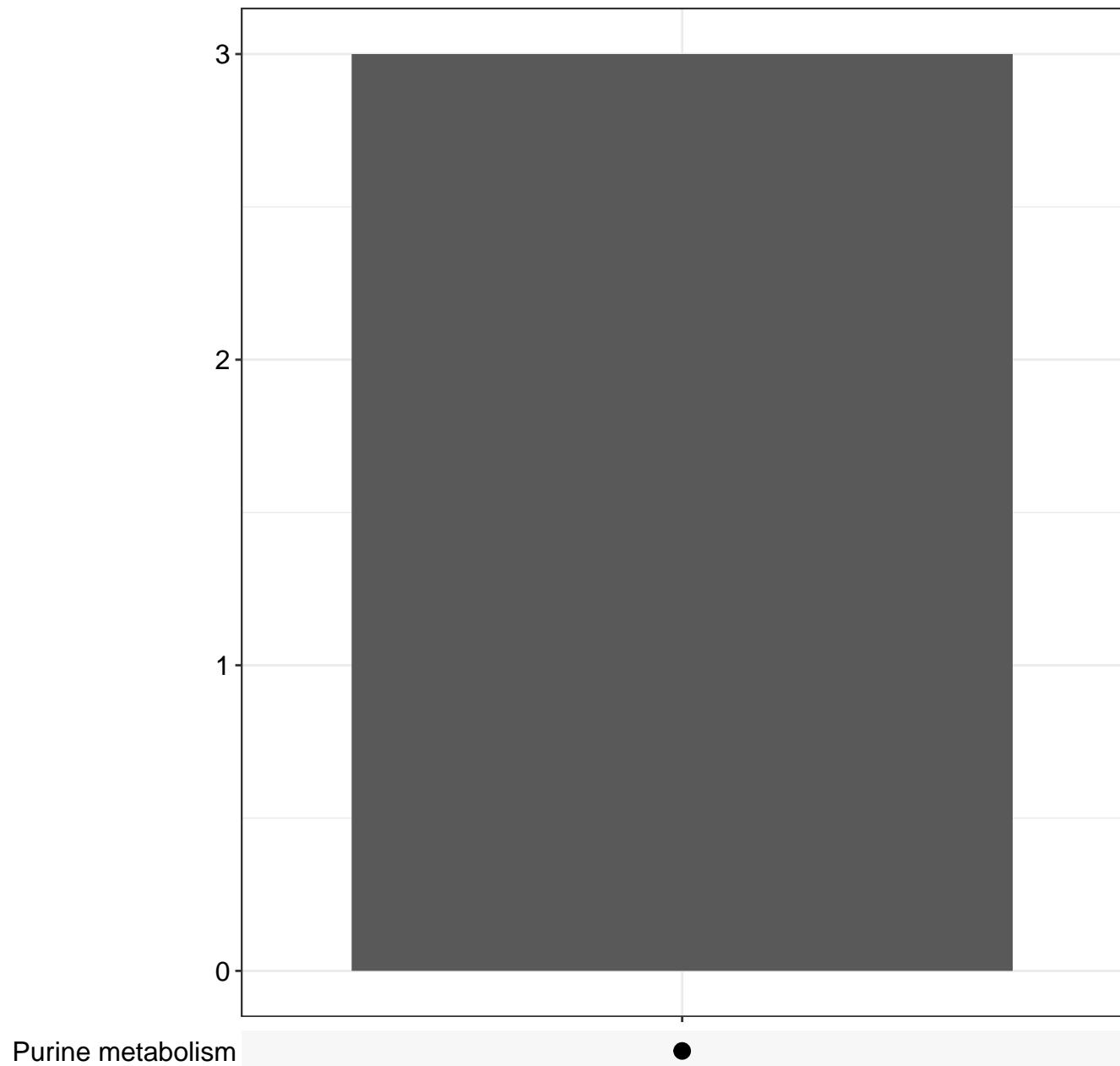
SUP35-TAP Up-regulated KEGG dotplot



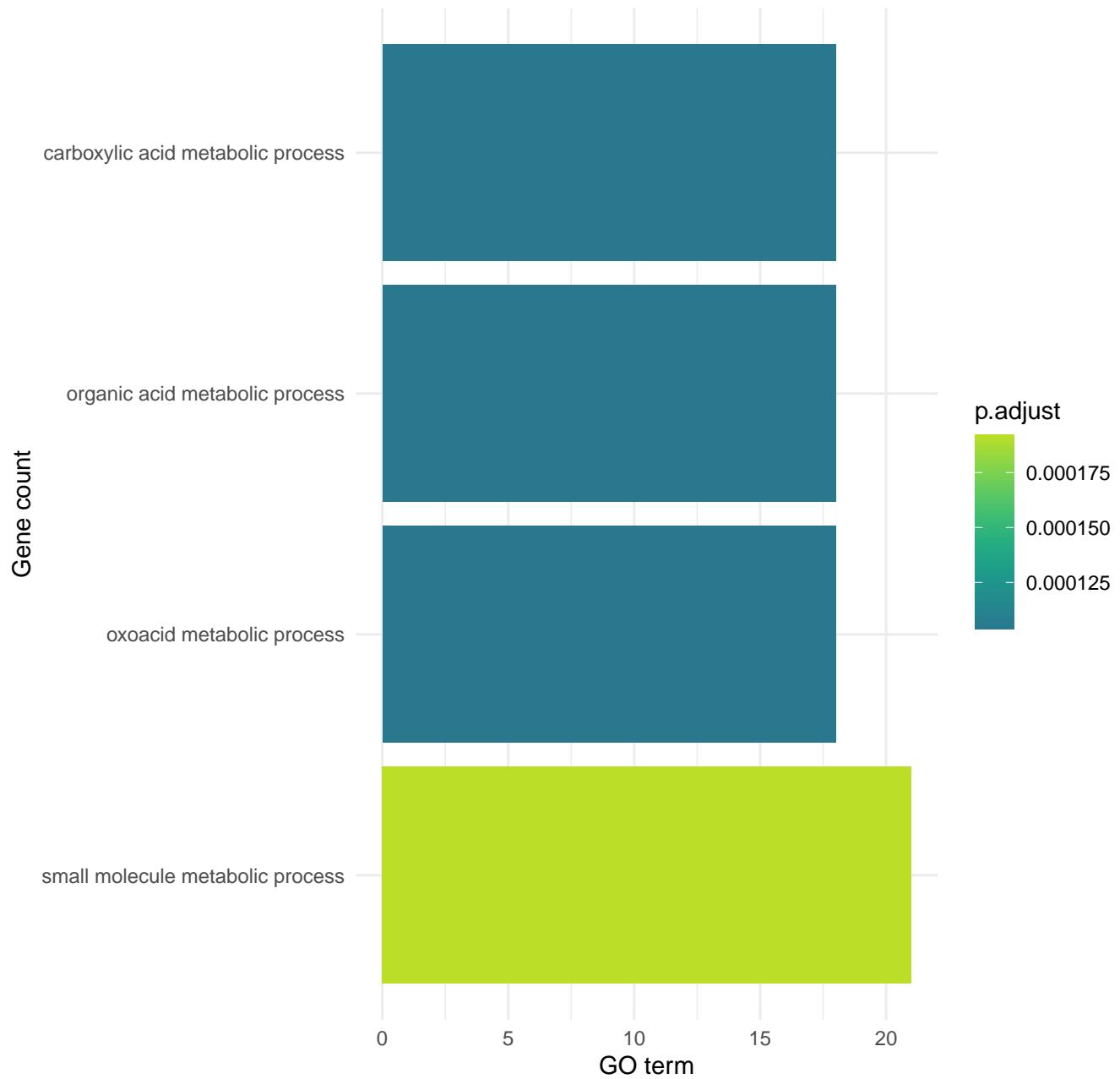
SUP35-TAP Up-regulated KEGG heatplot



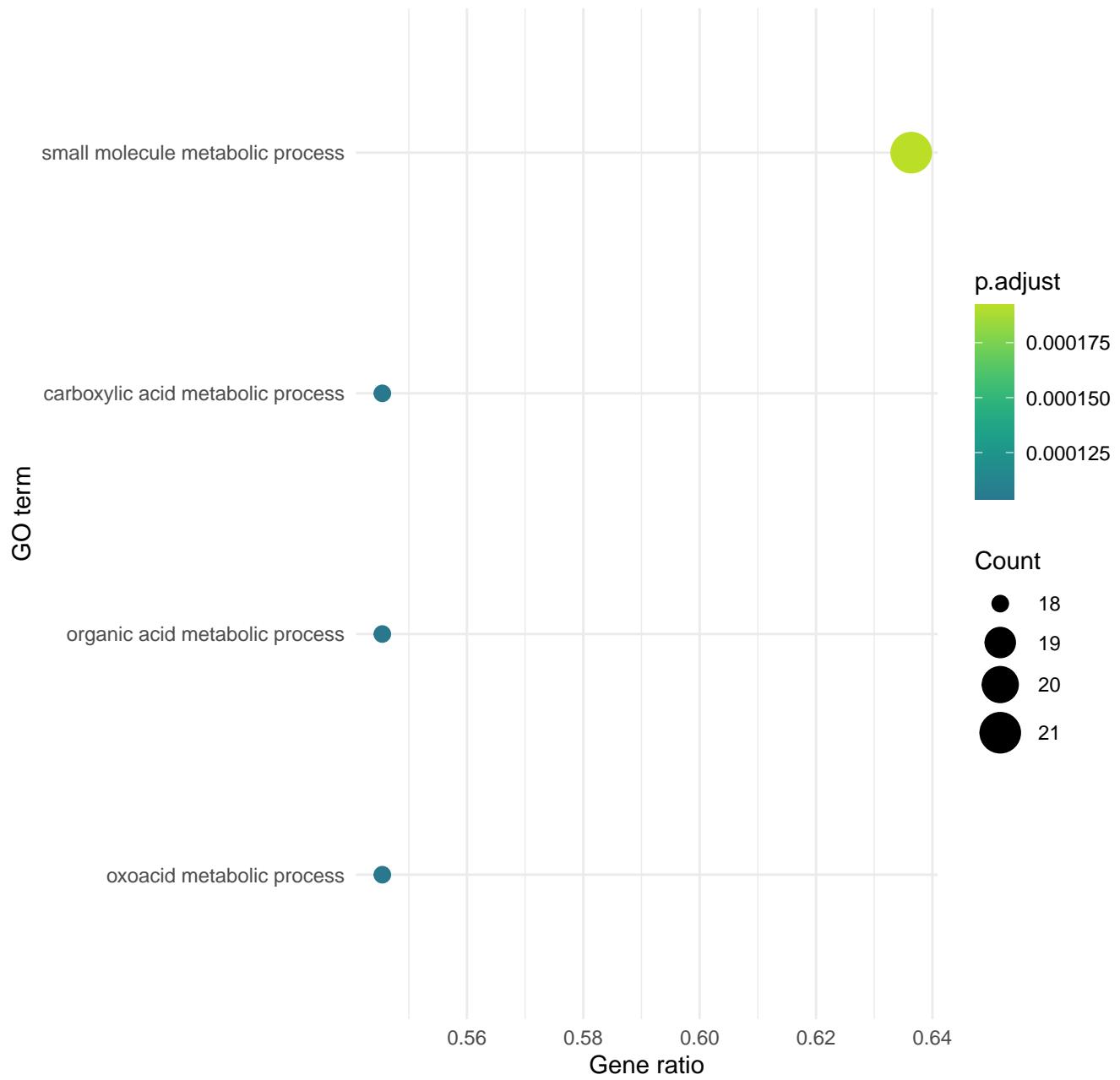
SUP35-TAP Up-regulated KEGG upsetplot



HBS1-TAP Up-regulated GO BP barplot



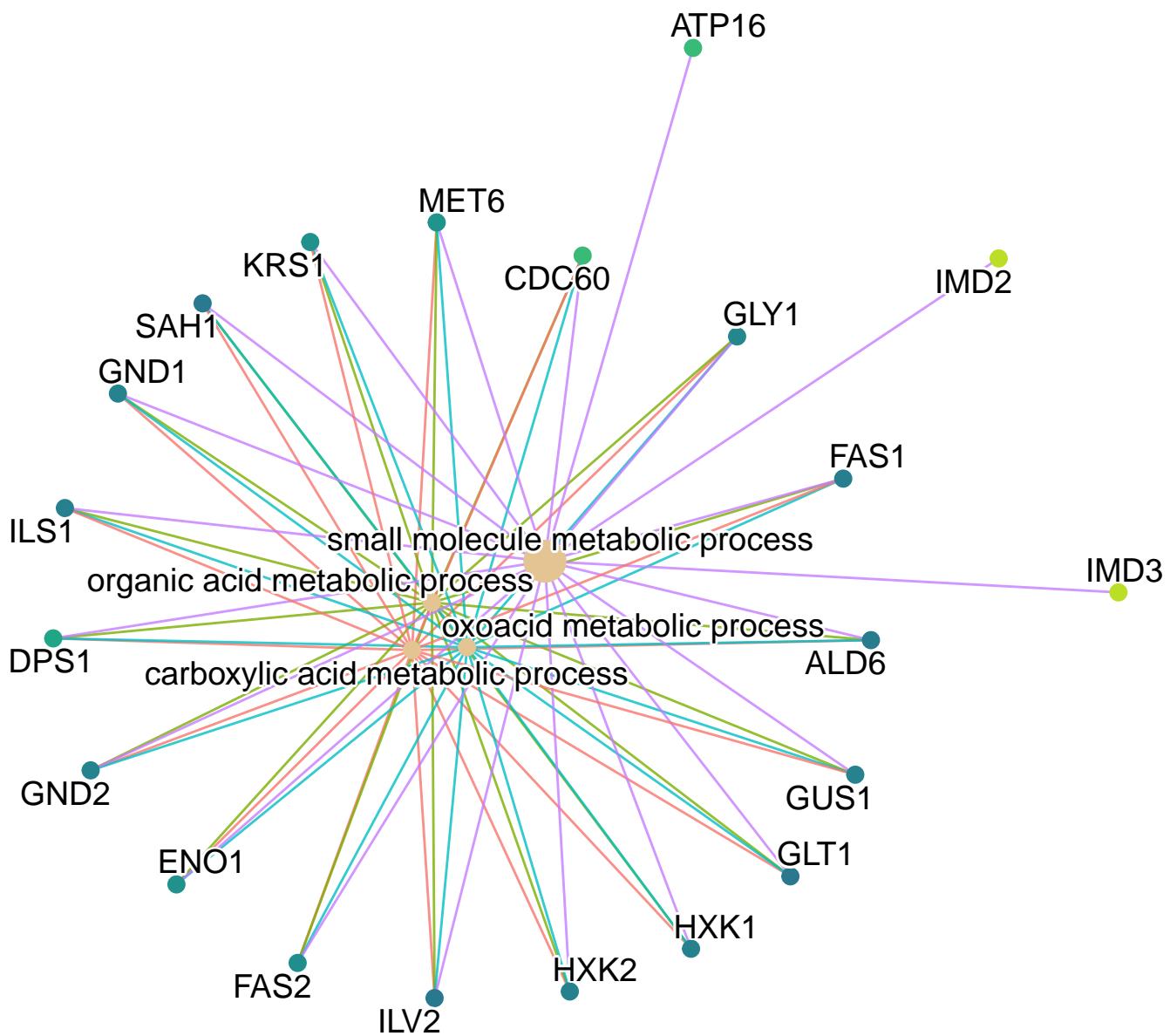
HBS1-TAP Up-regulated GO BP dotplot



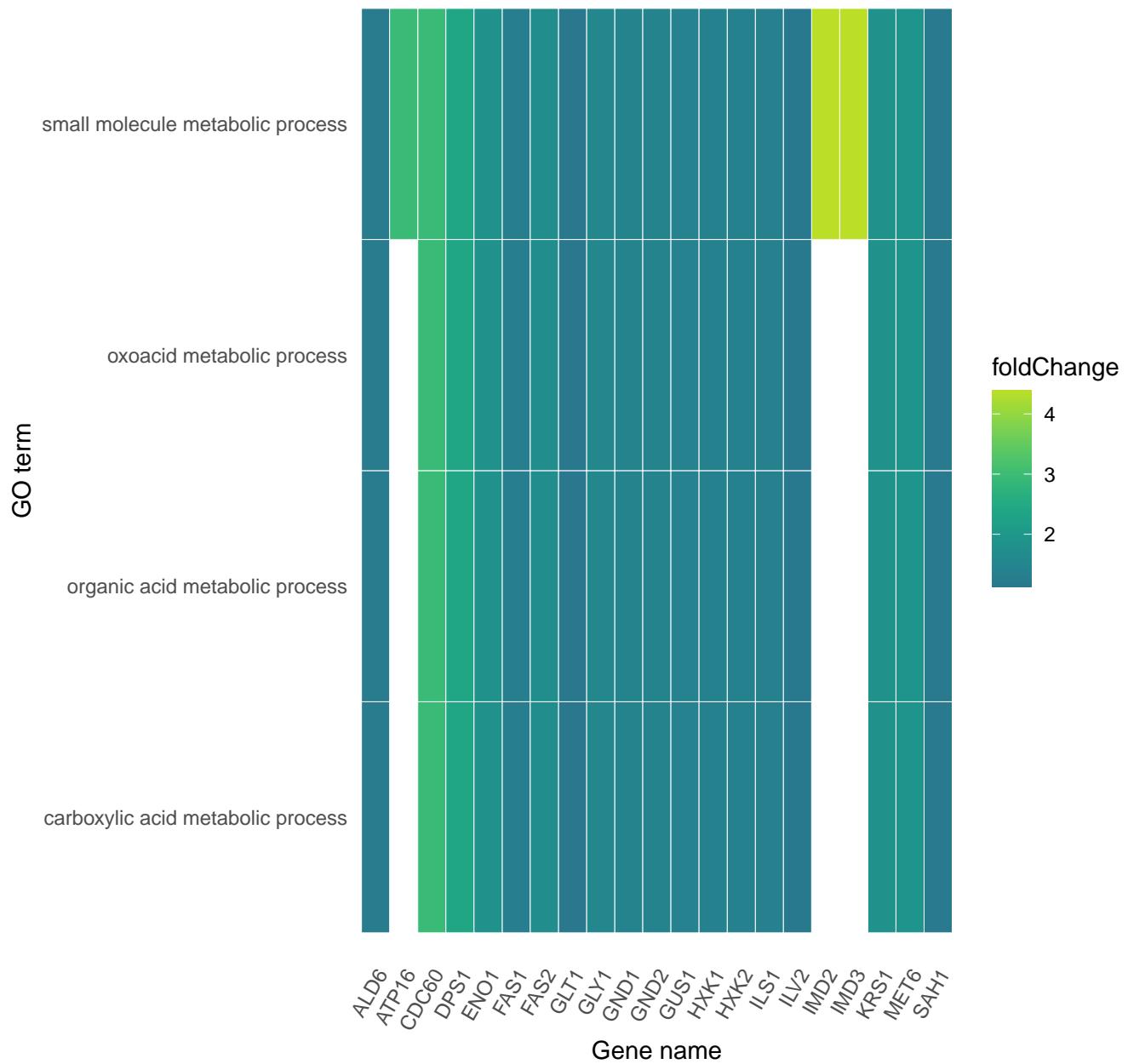
HBS1-TAP Up-regulated GO BP cnetplot

oxalic acid metabolic process organic acid metabolic process oxoacid metabolic process

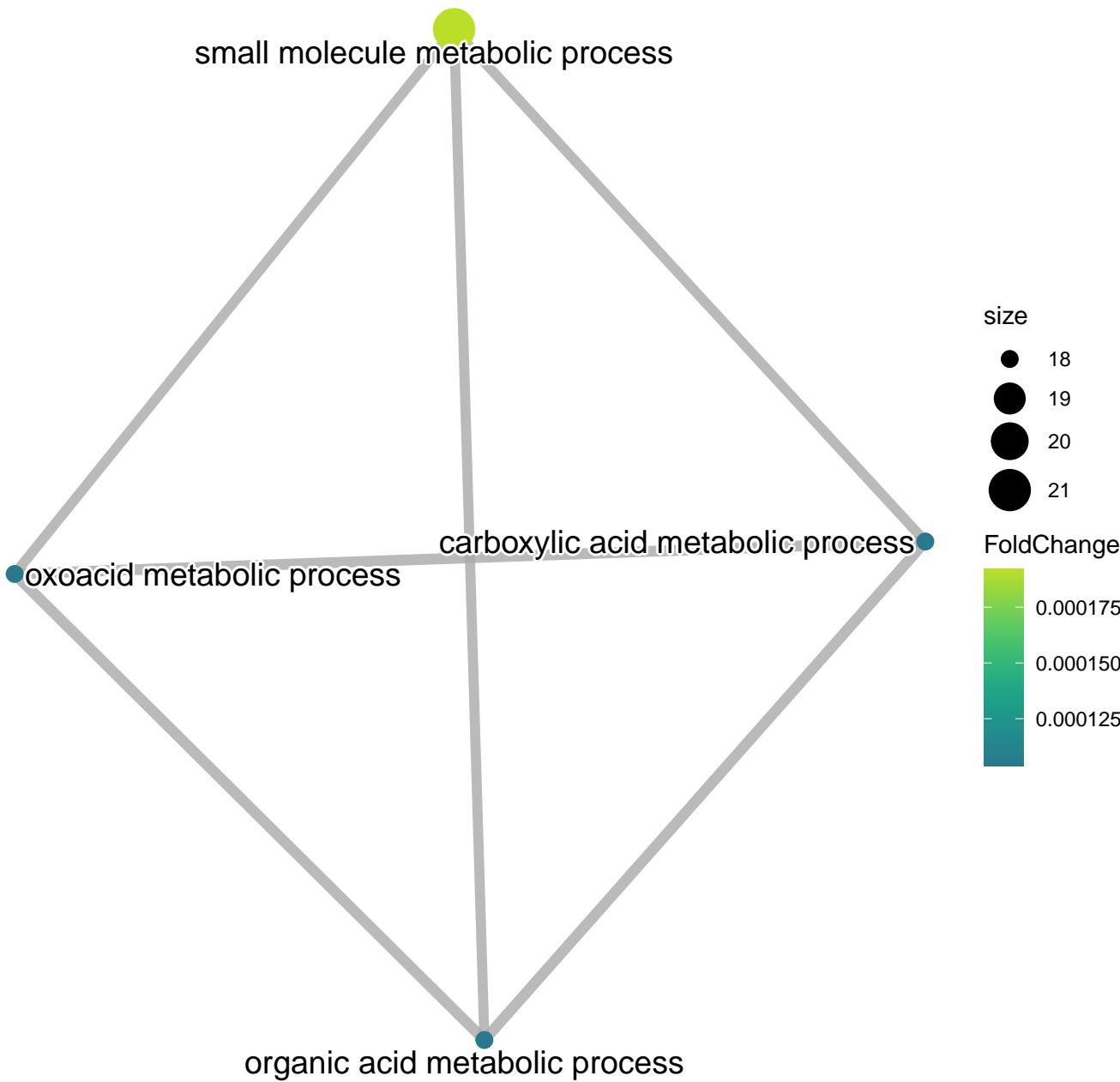
small molecule metabolic process

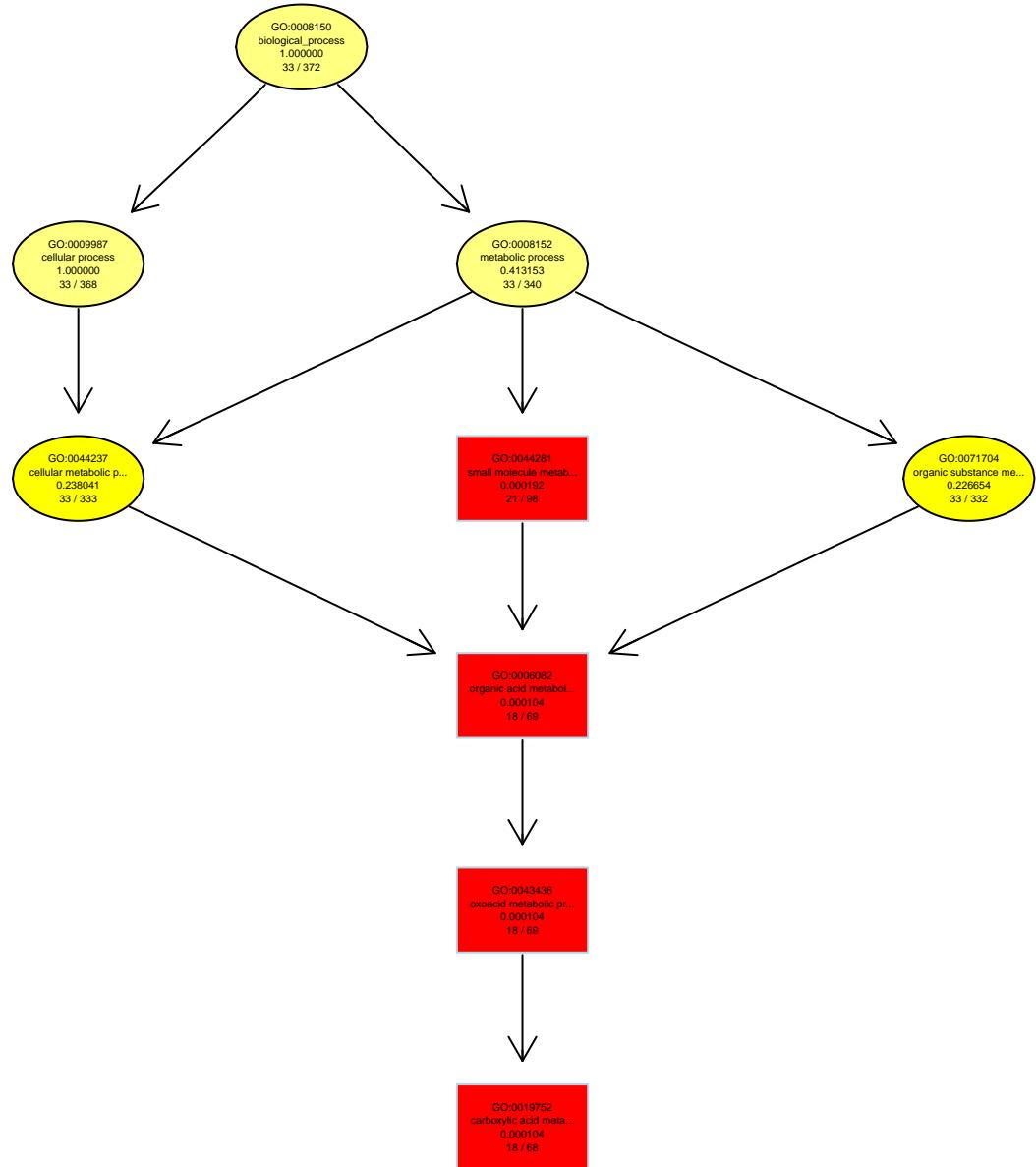


HBS1–TAP Up-regulated GO BP heatplot

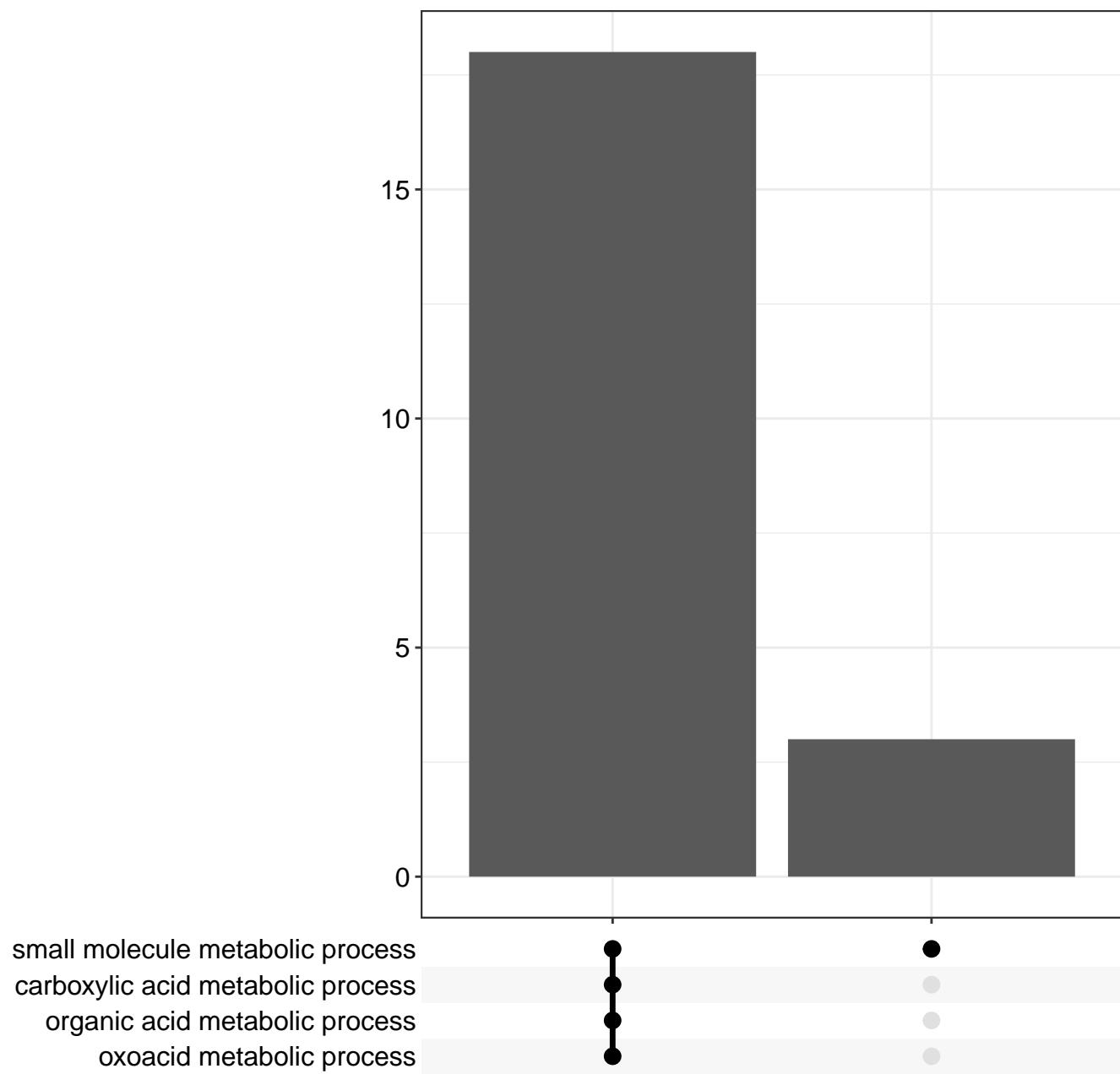


HBS1-TAP Up-regulated GO BP emapplot

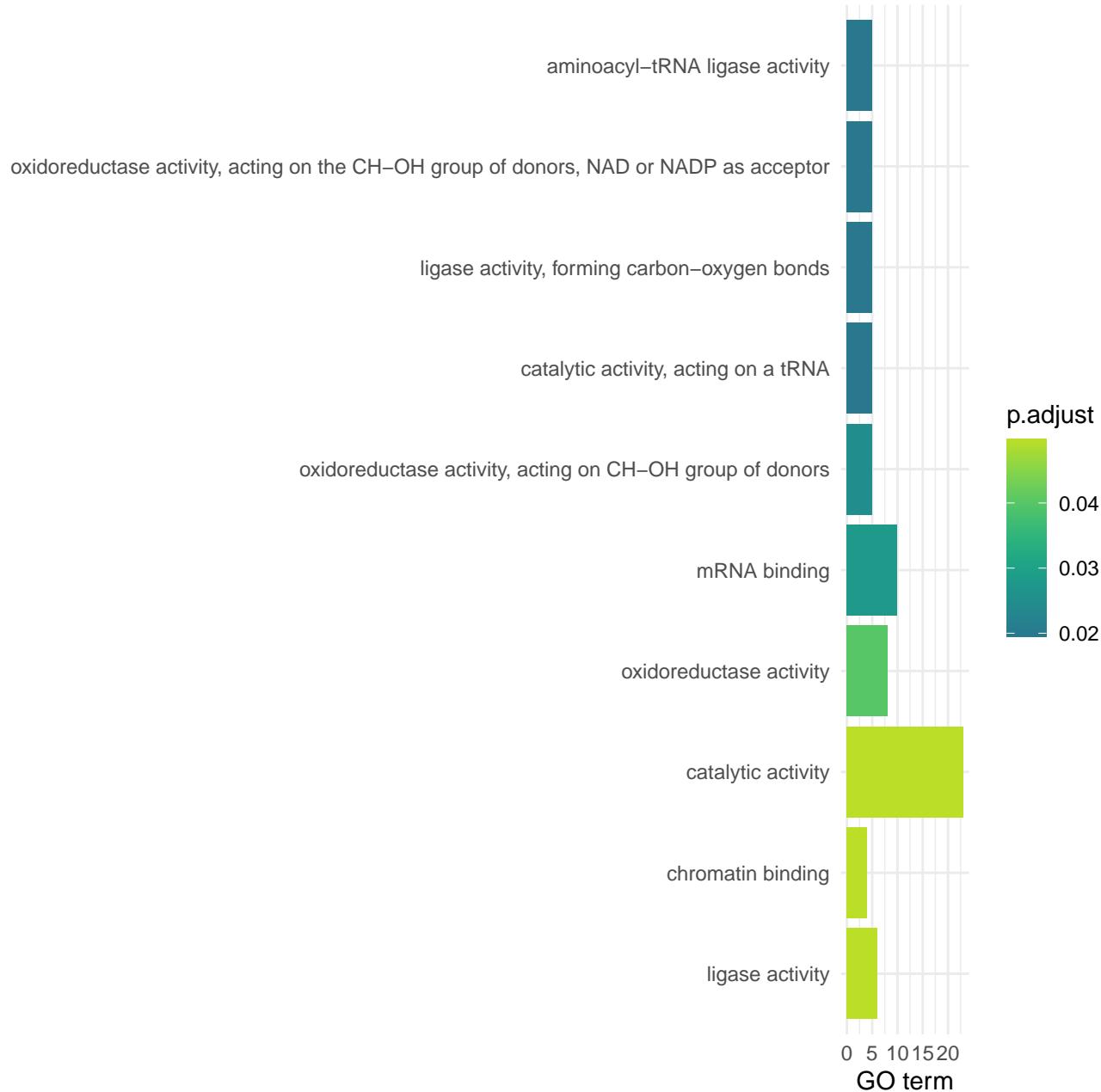




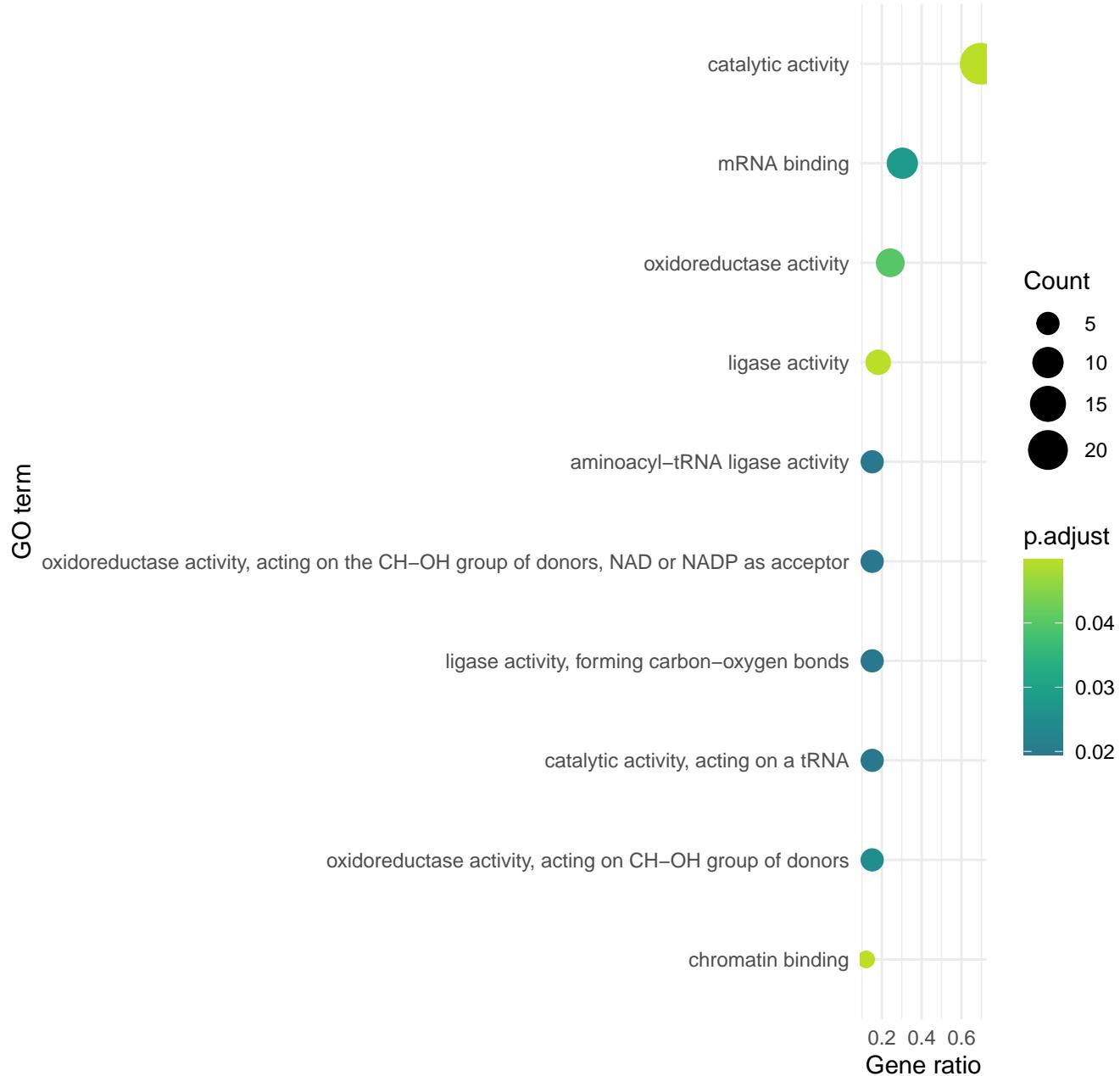
HBS1-TAP Up-regulated GO BP upsetplot



Gene count



HBS1-TAP Up-regulation



HBS1-TAP Up-regulated GO MF cnetplot

tRNA
activity

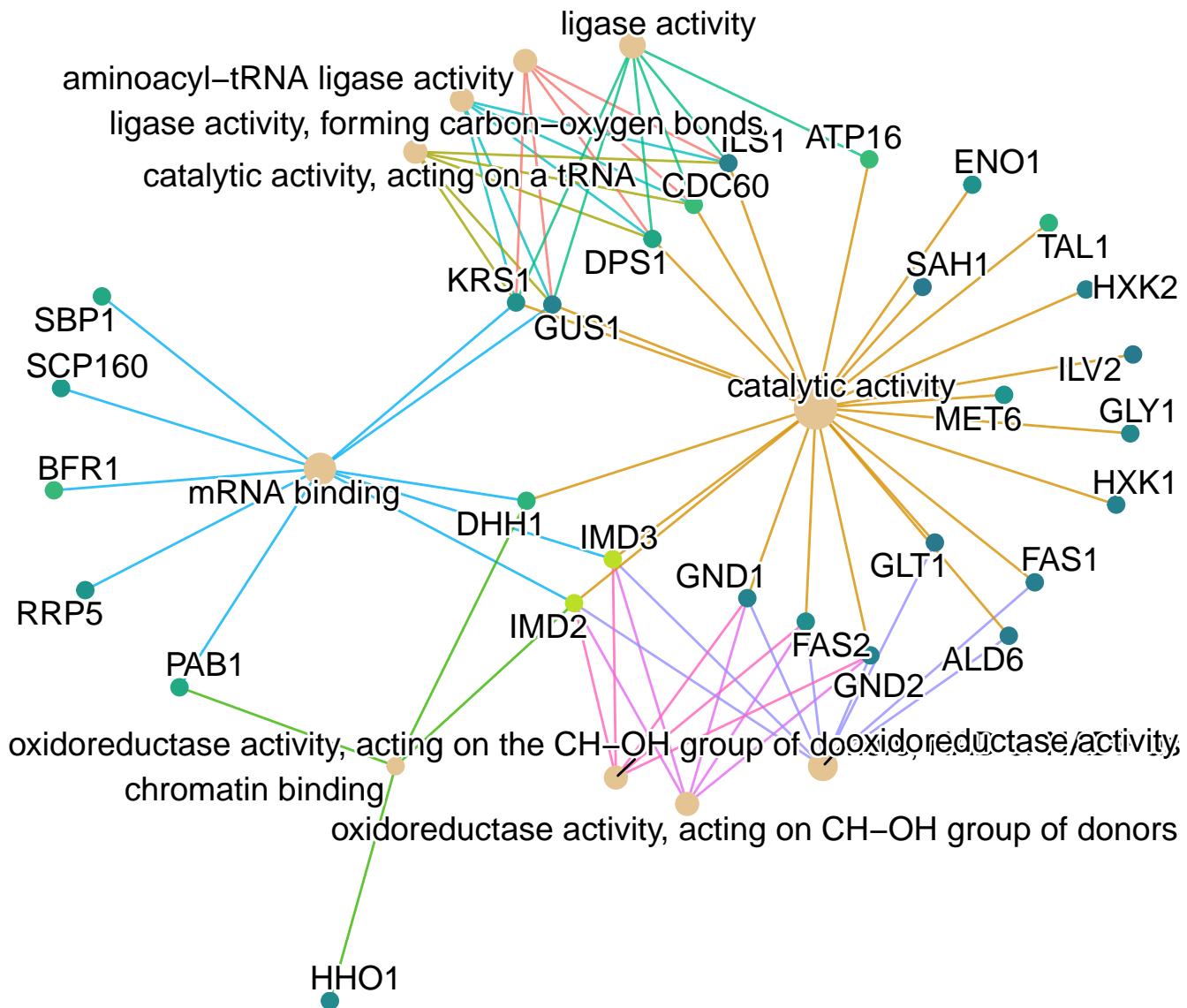
ty — catalytic activity, acting on a tRNA

— chromatin binding

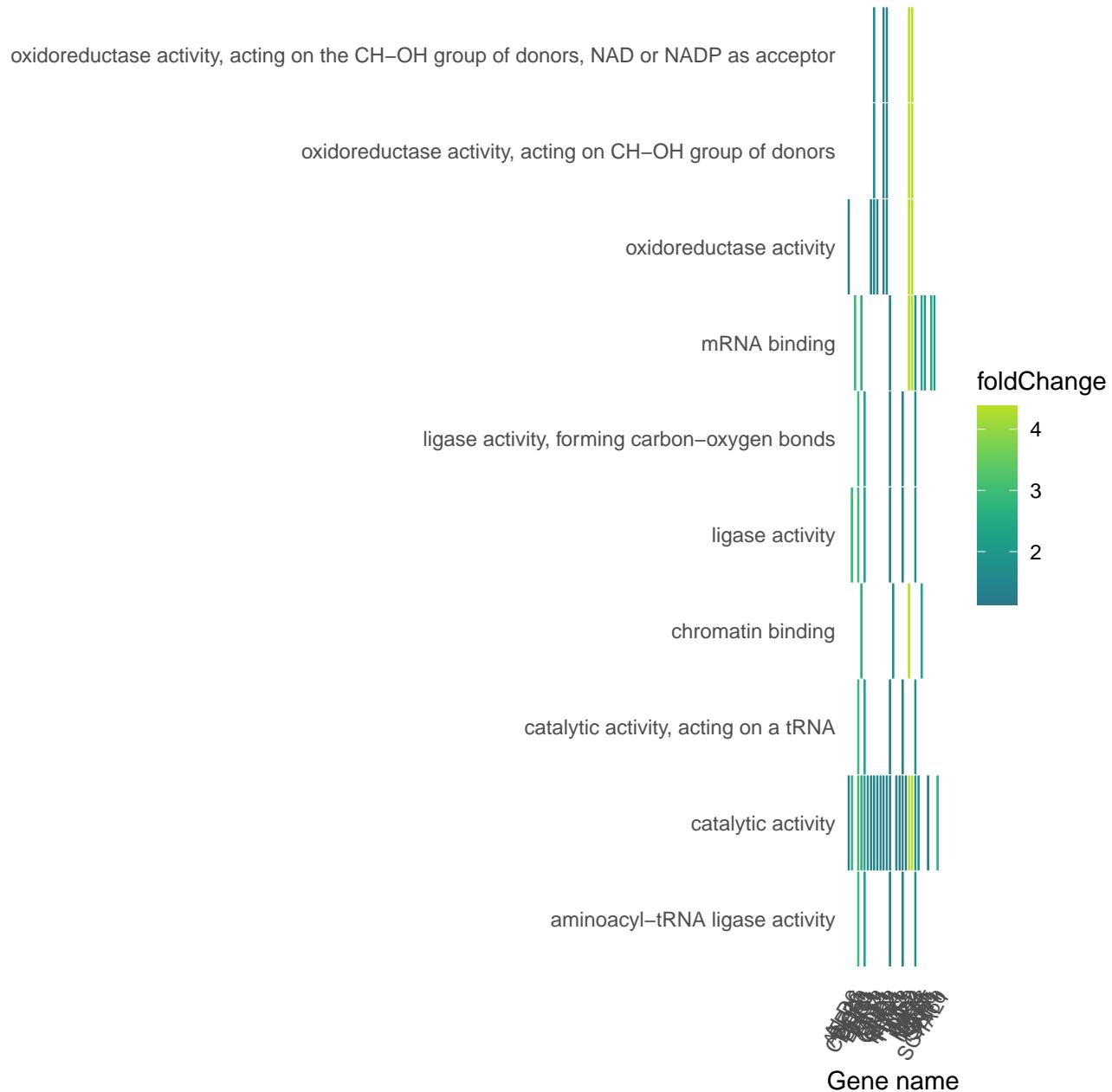
A — ligase activity

— ligase activity, forming carbon–oxygen bonds

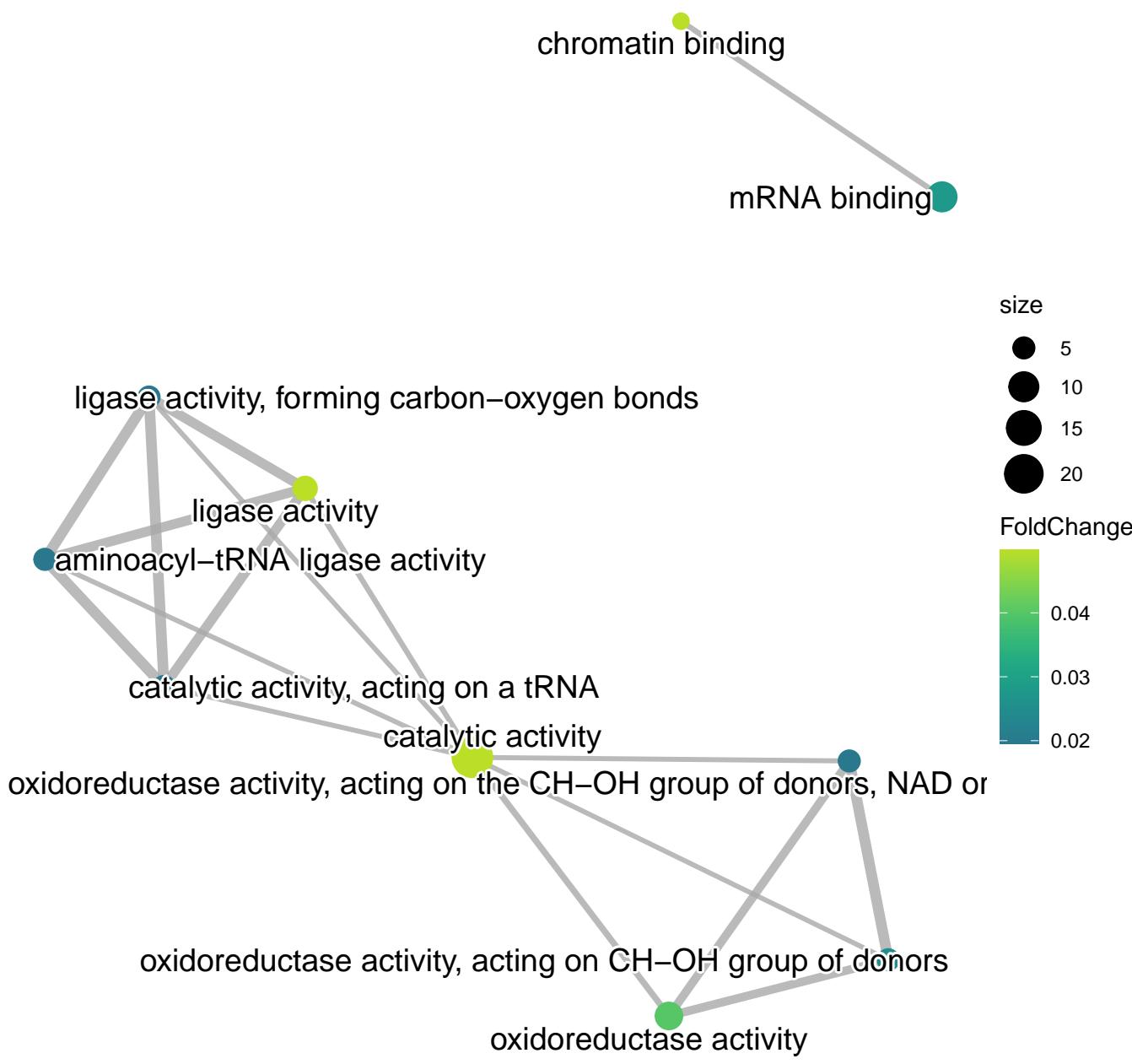
— mRNA

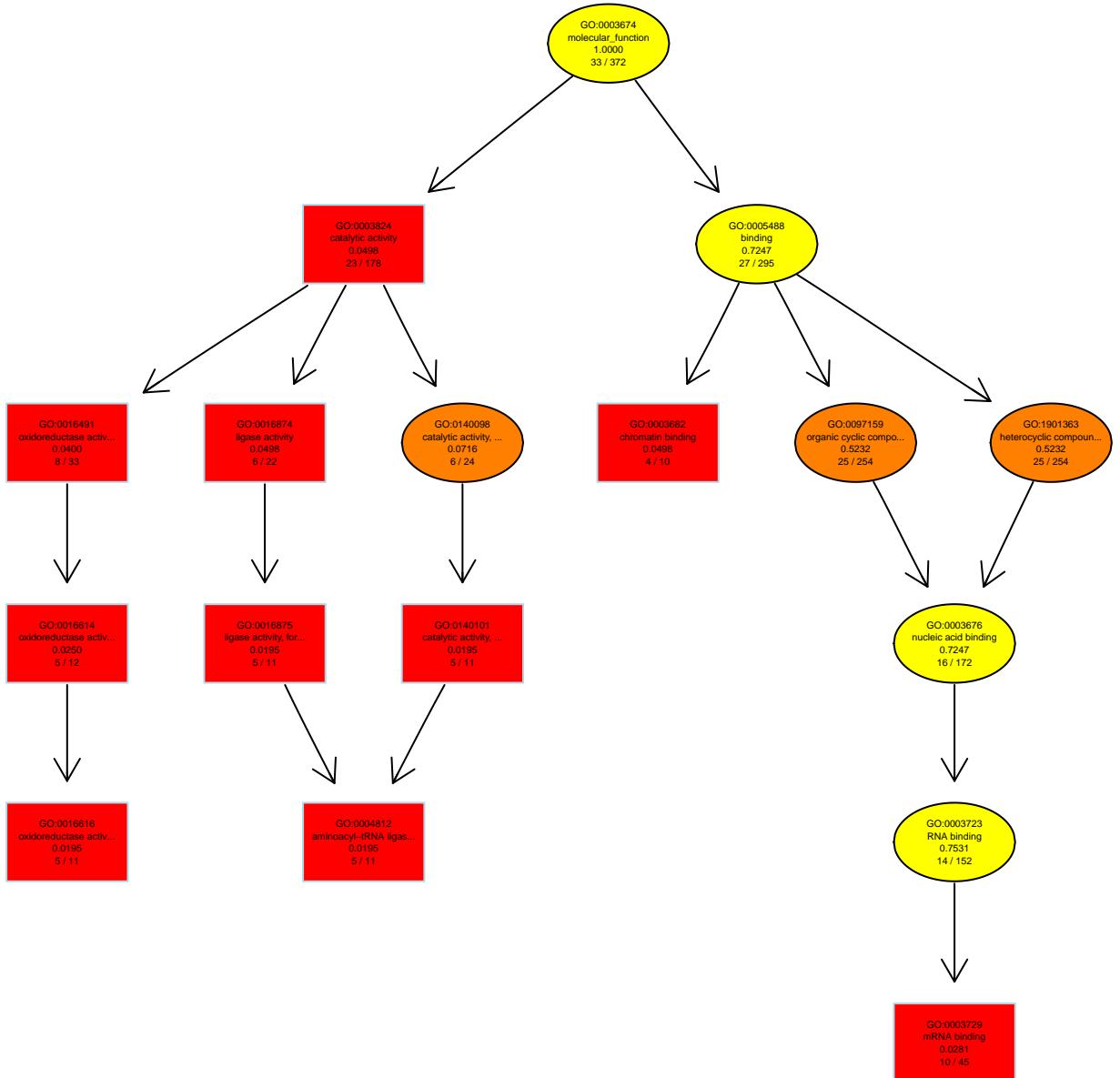


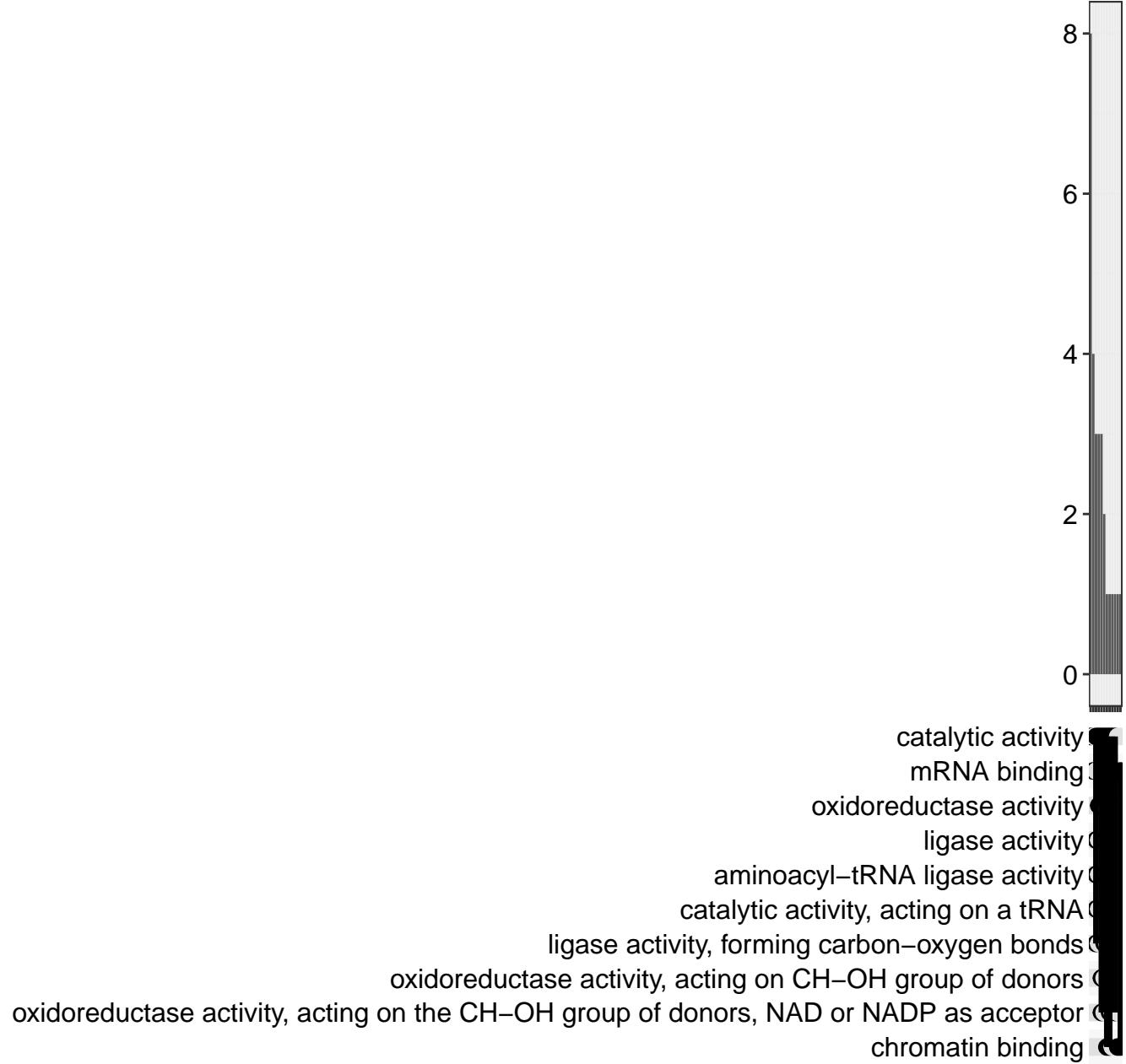
GO term



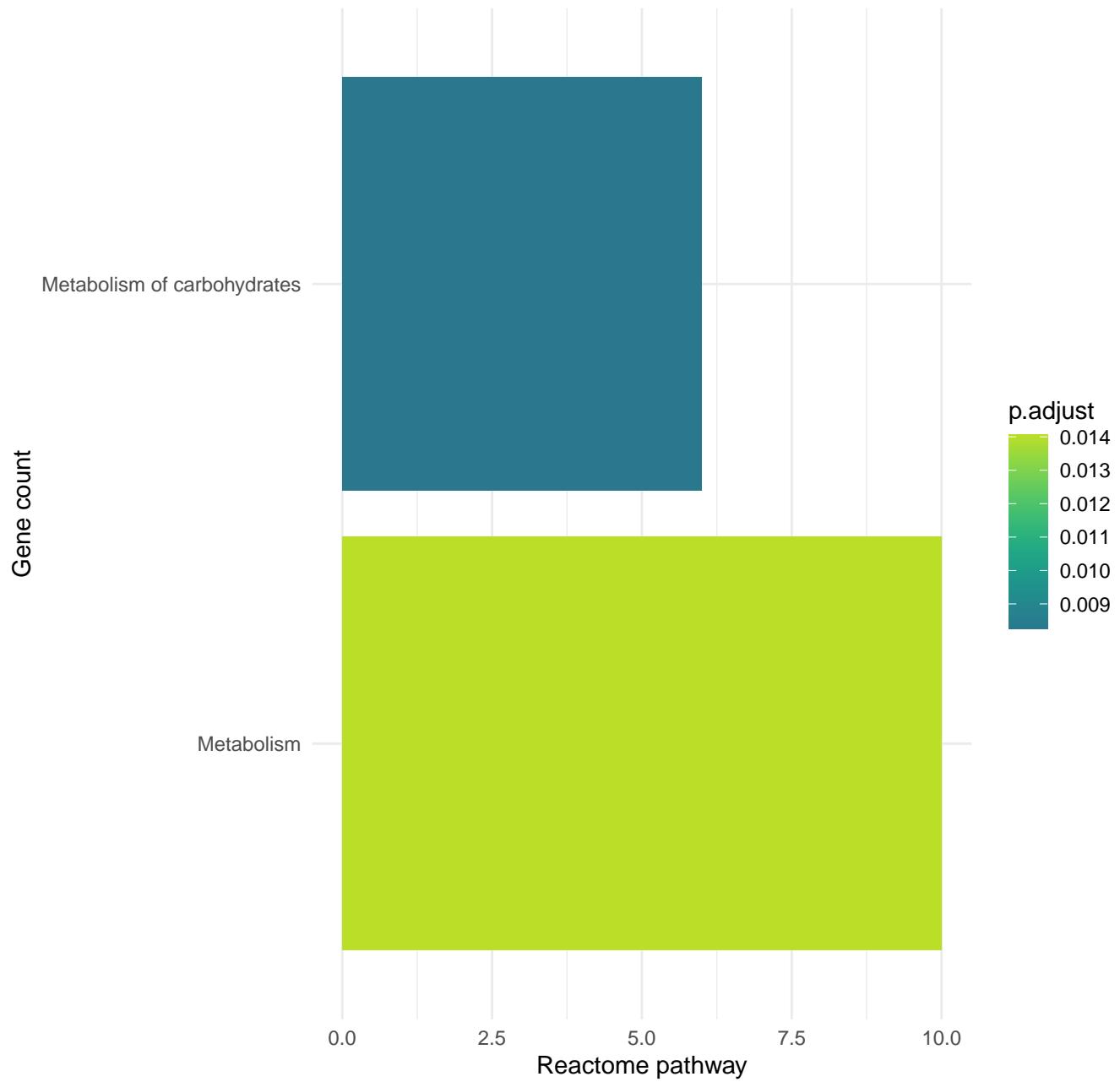
HBS1-TAP Up-regulated GO MF emapplot







HBS1-TAP Up-regulated Reactome barplot



HBS1-TAP Up-regulated Reactome dotplot

Reactome pathway

Metabolism

Metabolism of carbohydrates

0.35

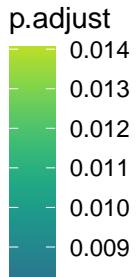
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0.45

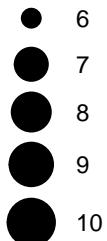
0.50

0.55

Gene ratio



Count



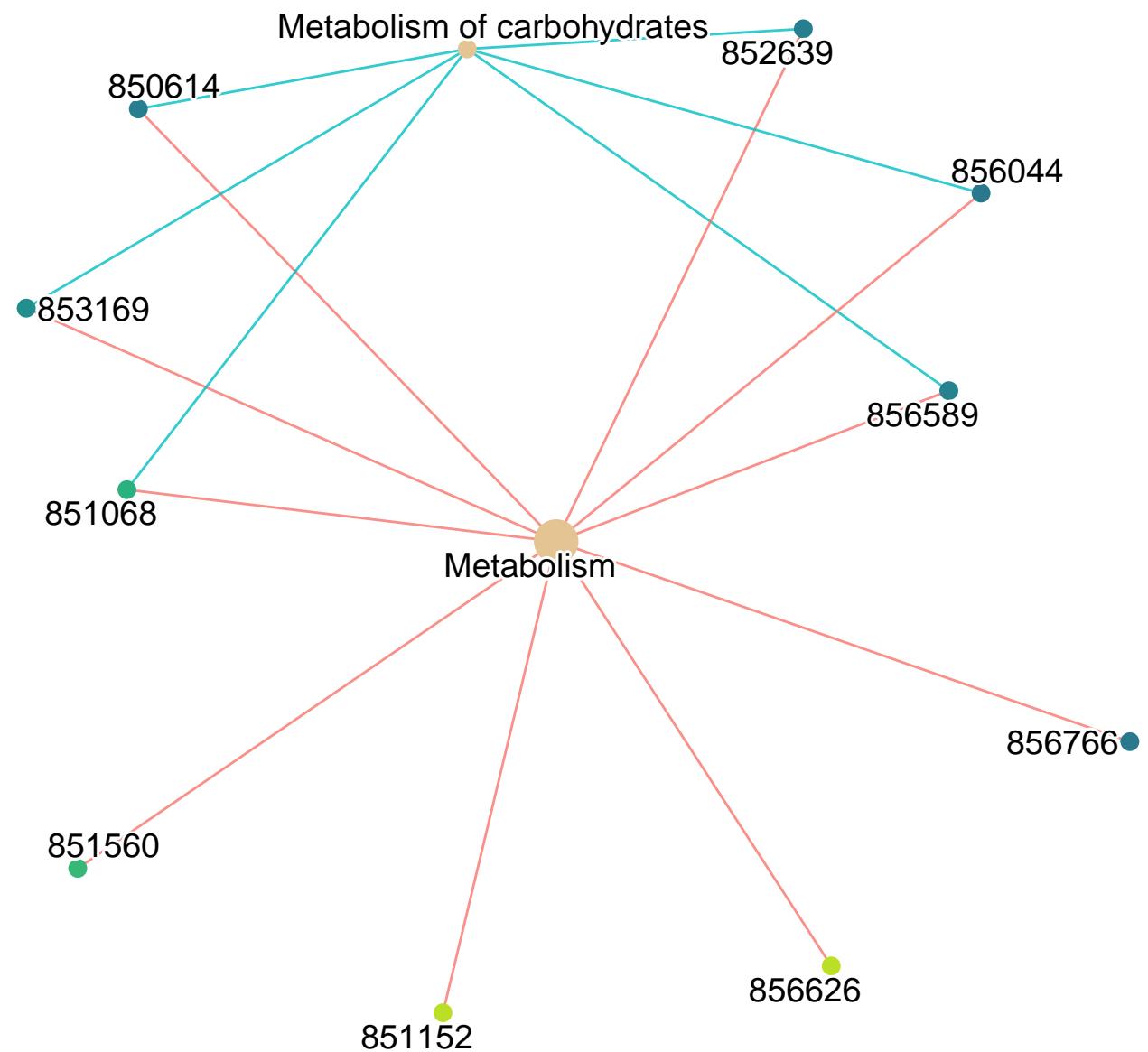
HBS1-TAP Up-regulated Reactome cnetplot

- Metabolism Metabolism of carbohydrates

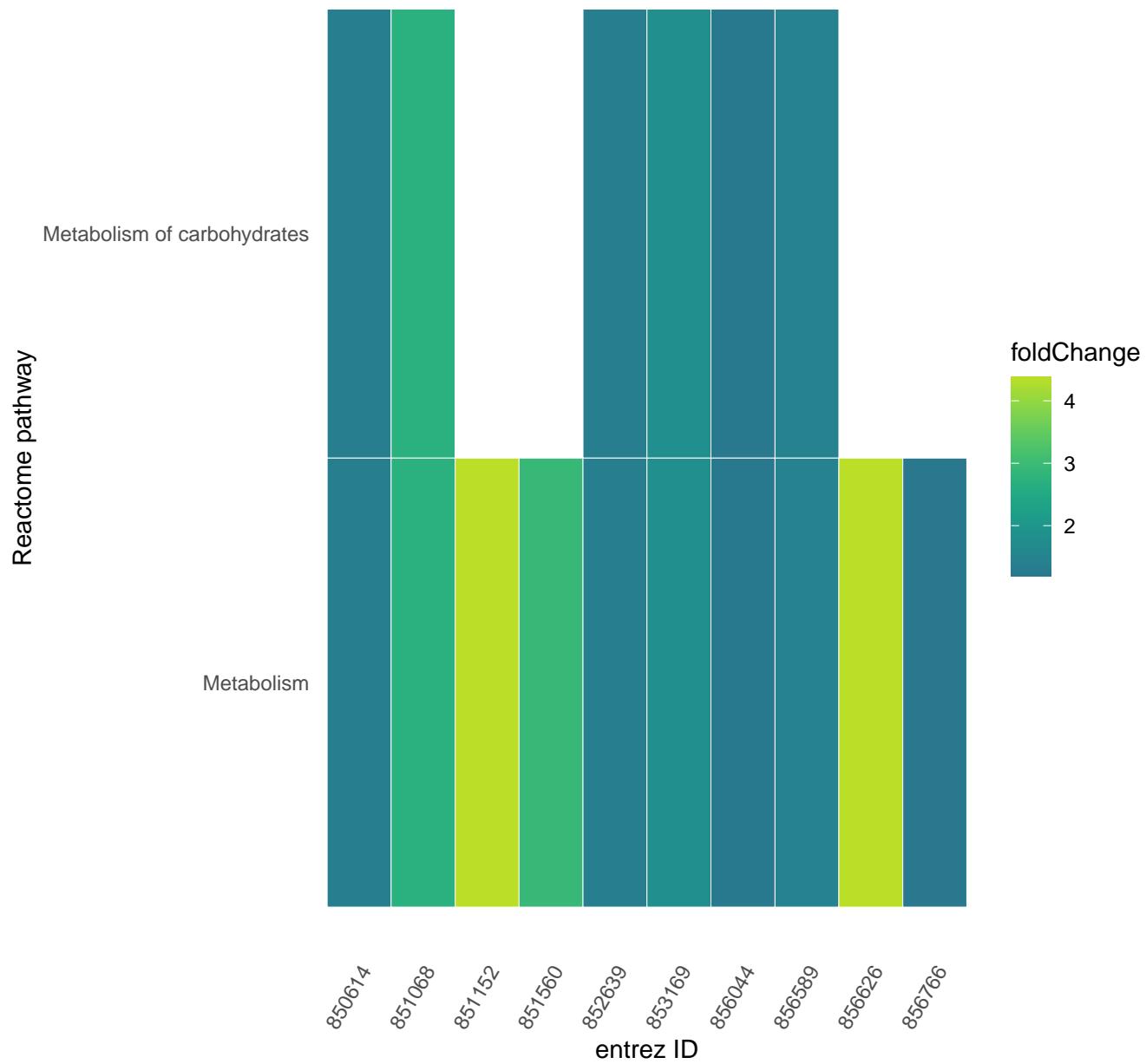
FoldChange



size

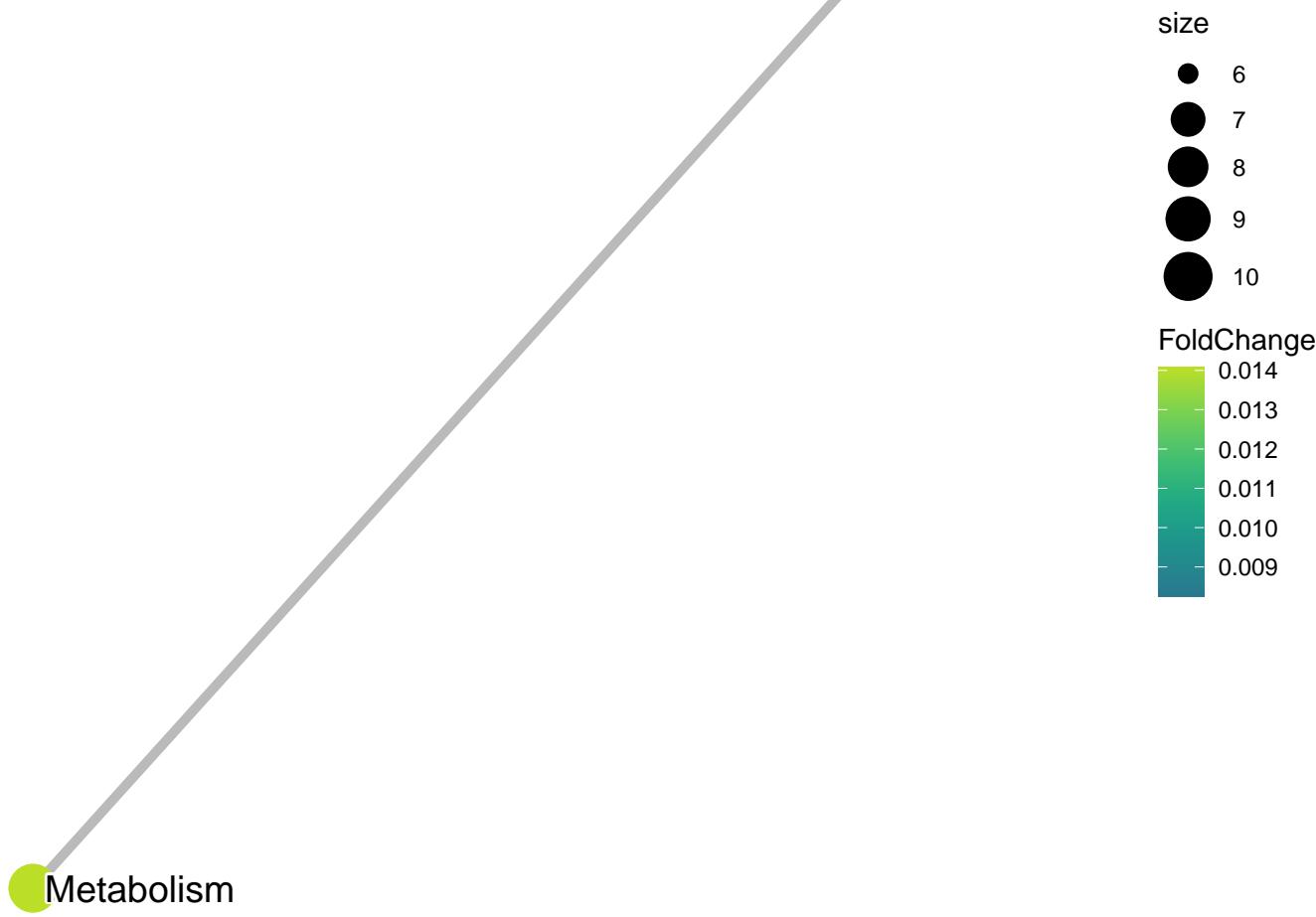


HBS1-TAP Up-regulated Reactome heatplot

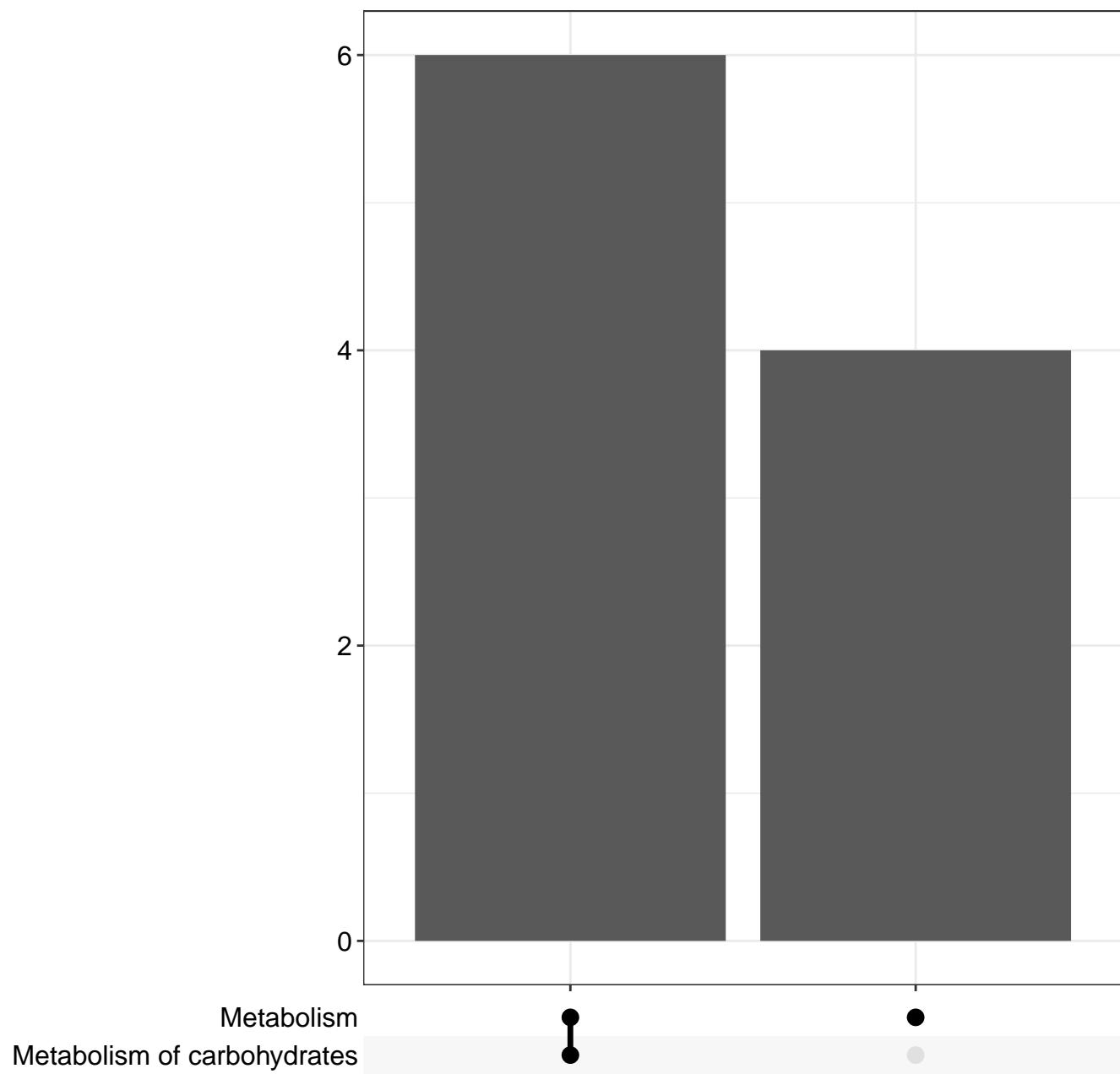


HBS1-TAP Up-regulated Reactome emapplot

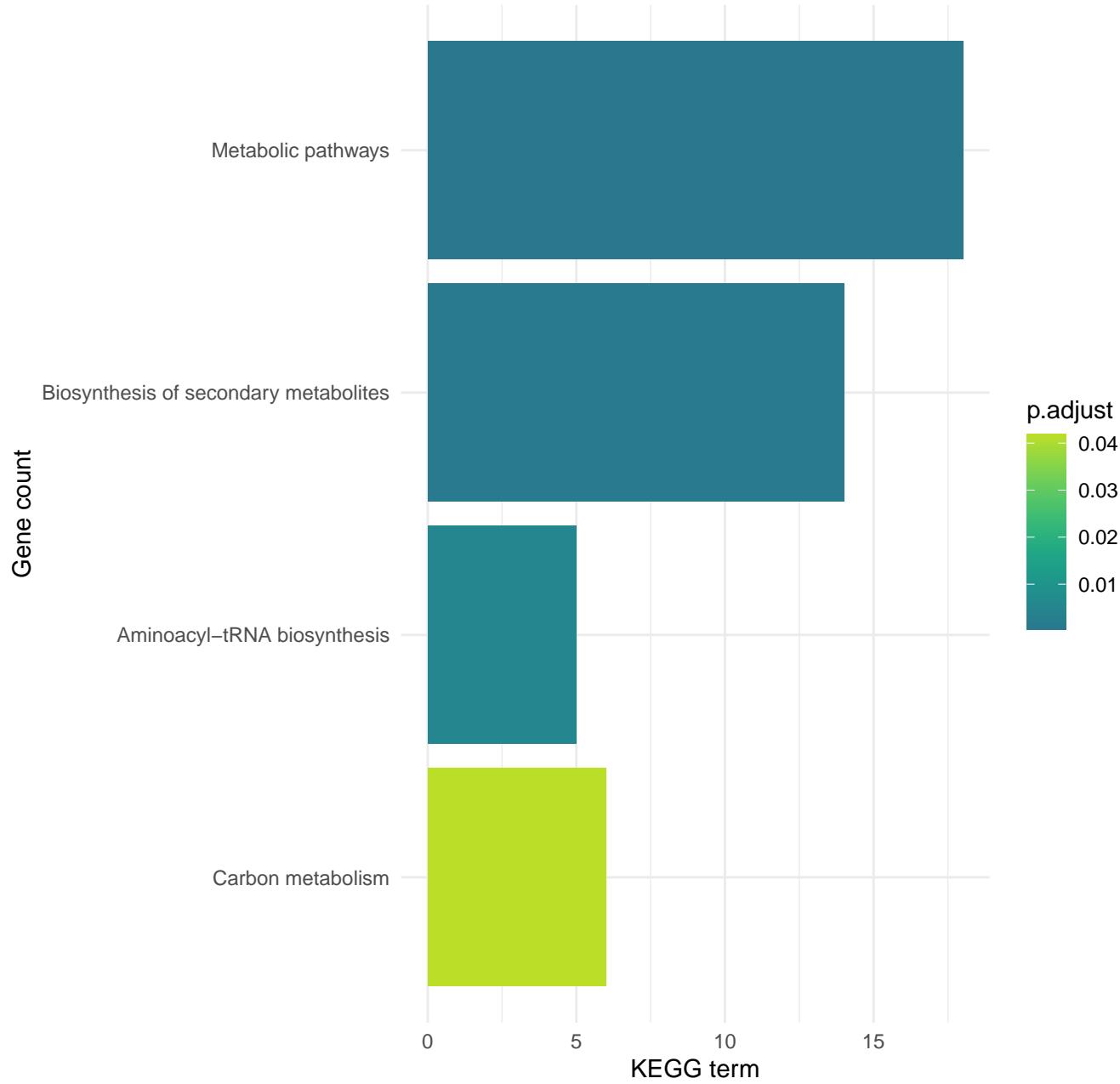
Metabolism of carbohydrates



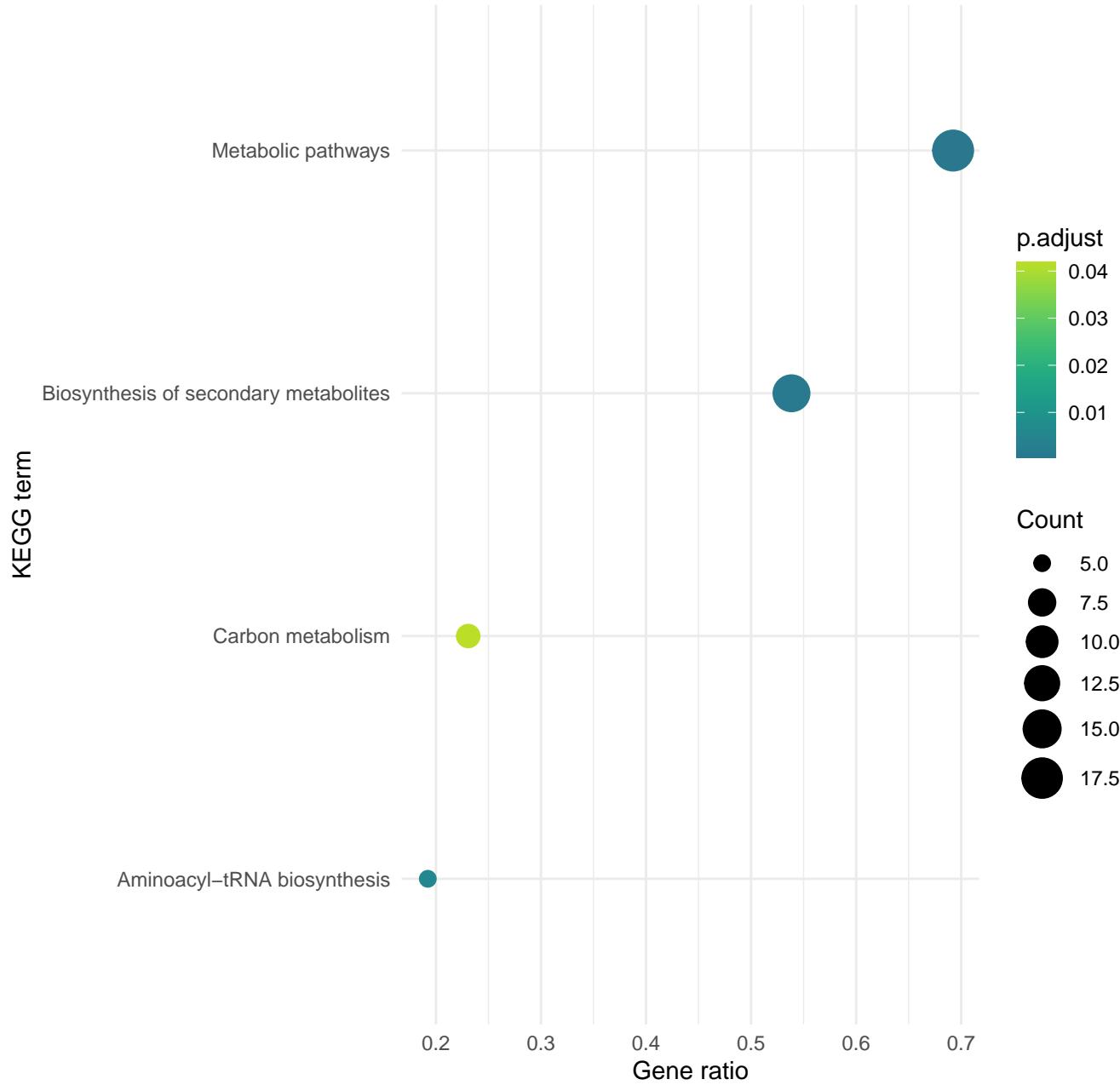
HBS1-TAP Up-regulated Reactome upsetplot



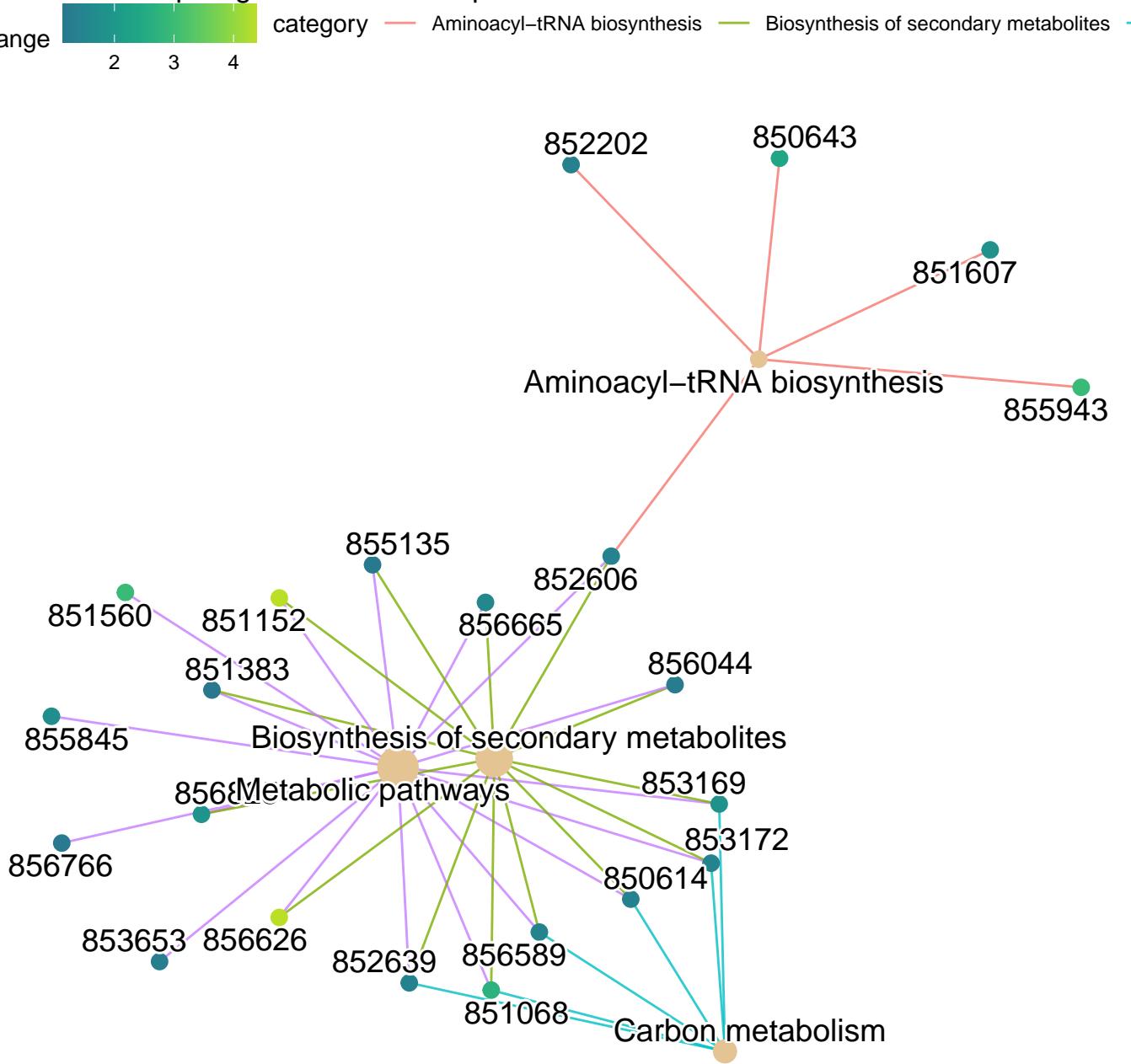
HBS1-TAP Up-regulated KEGG barplot



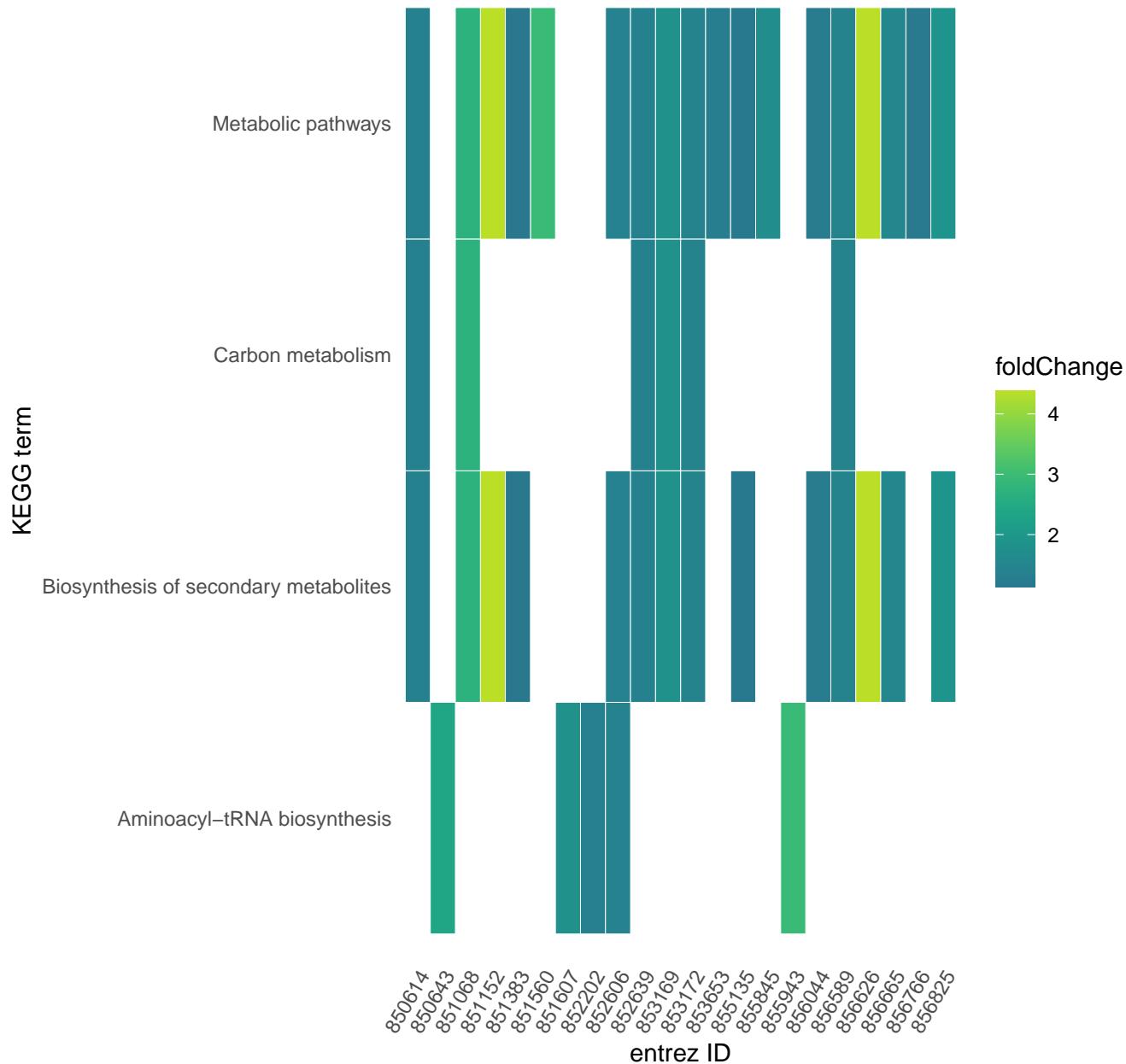
HBS1-TAP Up-regulated KEGG dotplot



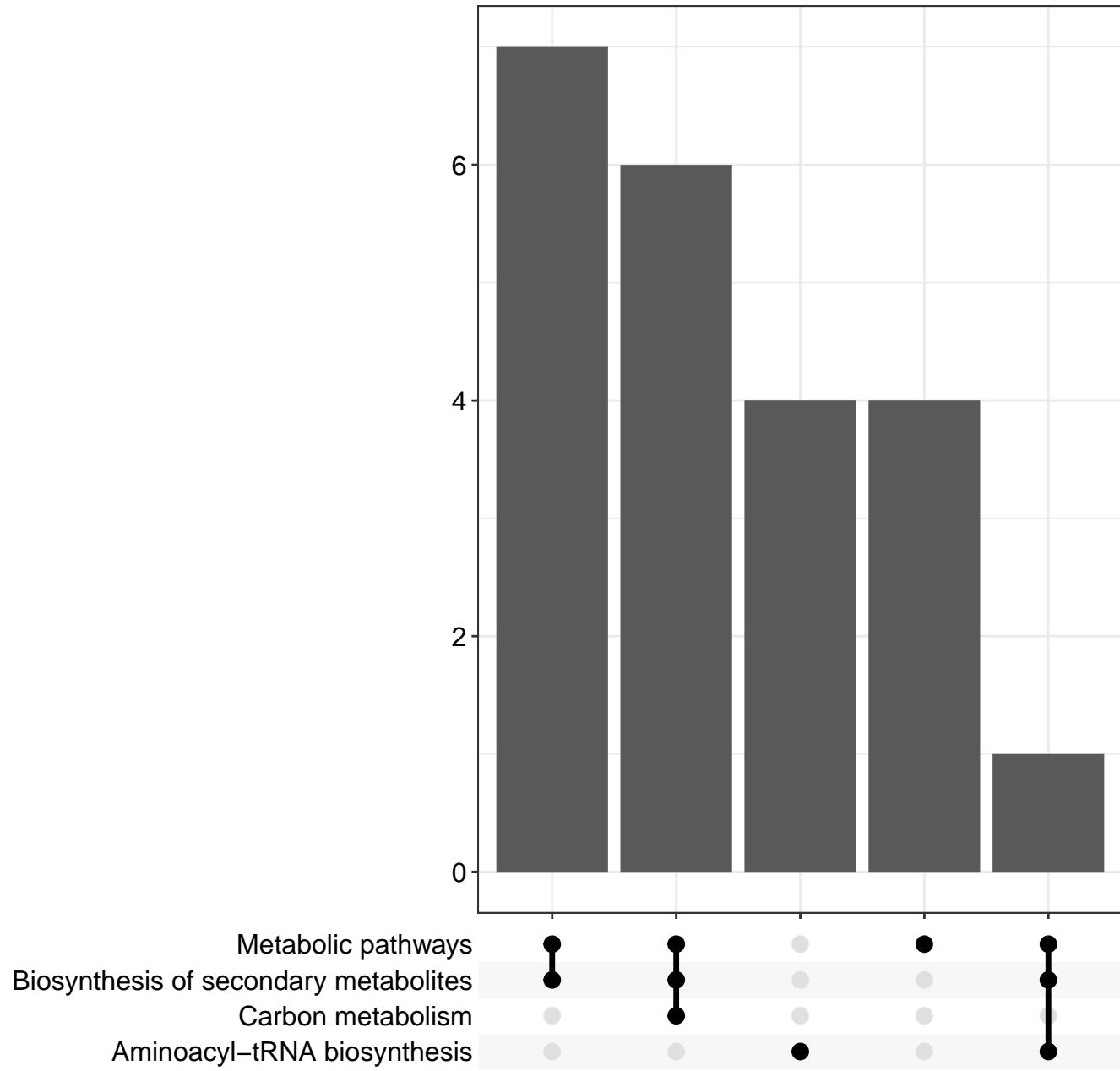
HBS1-TAP Up-regulated KEGG dotplot



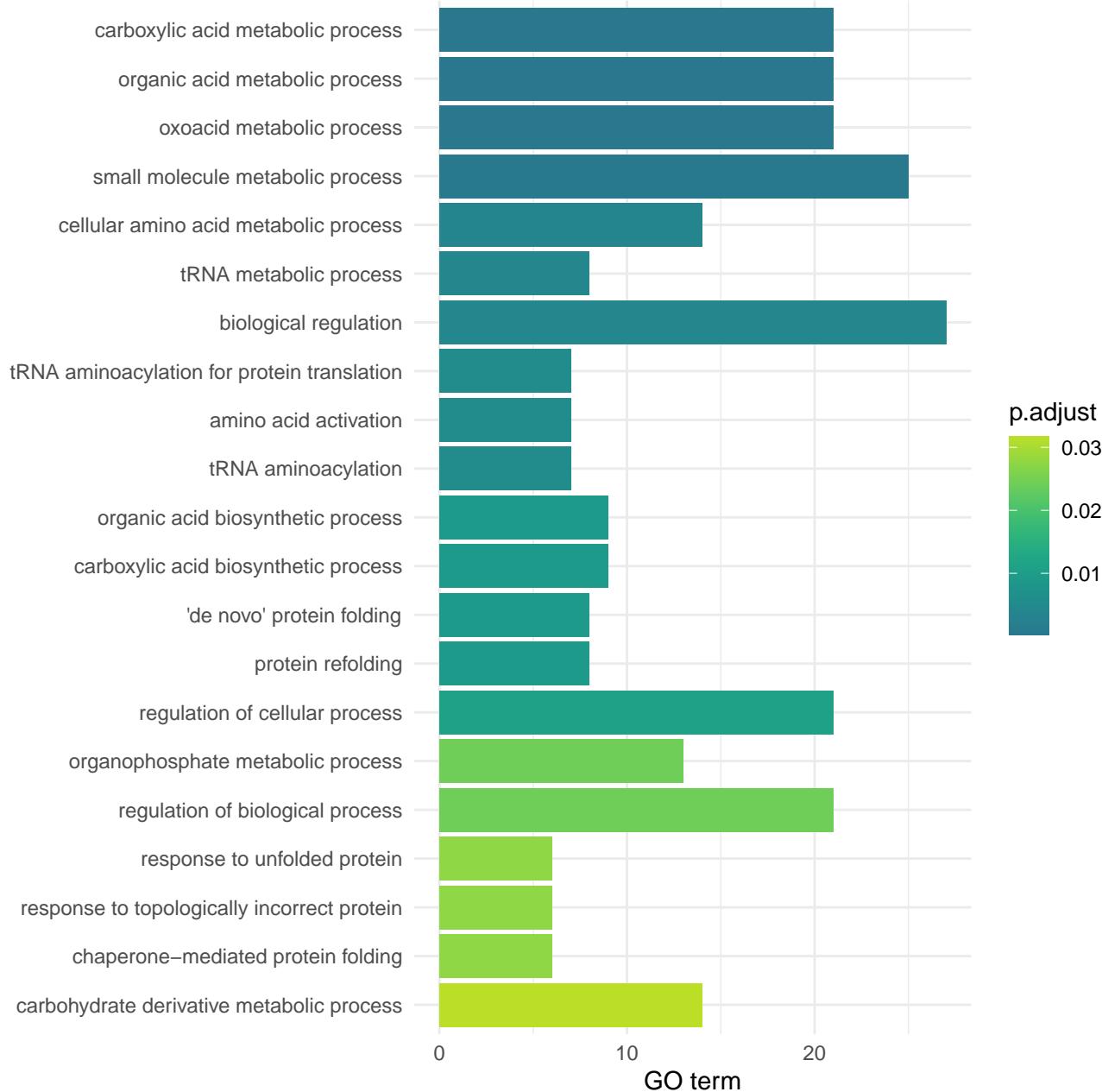
HBS1-TAP Up-regulated KEGG heatplot



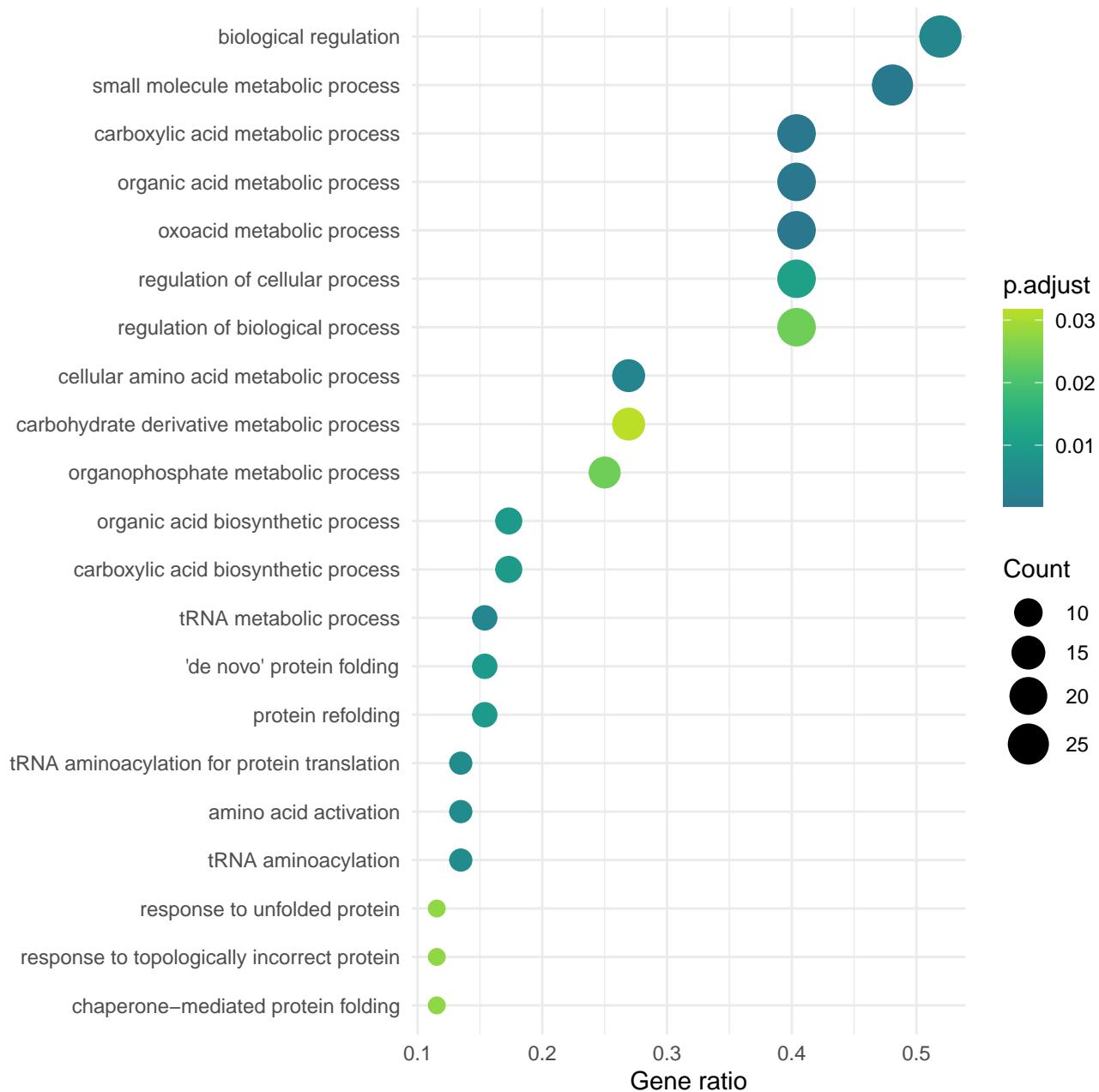
HBS1-TAP Up-regulated KEGG upsetplot



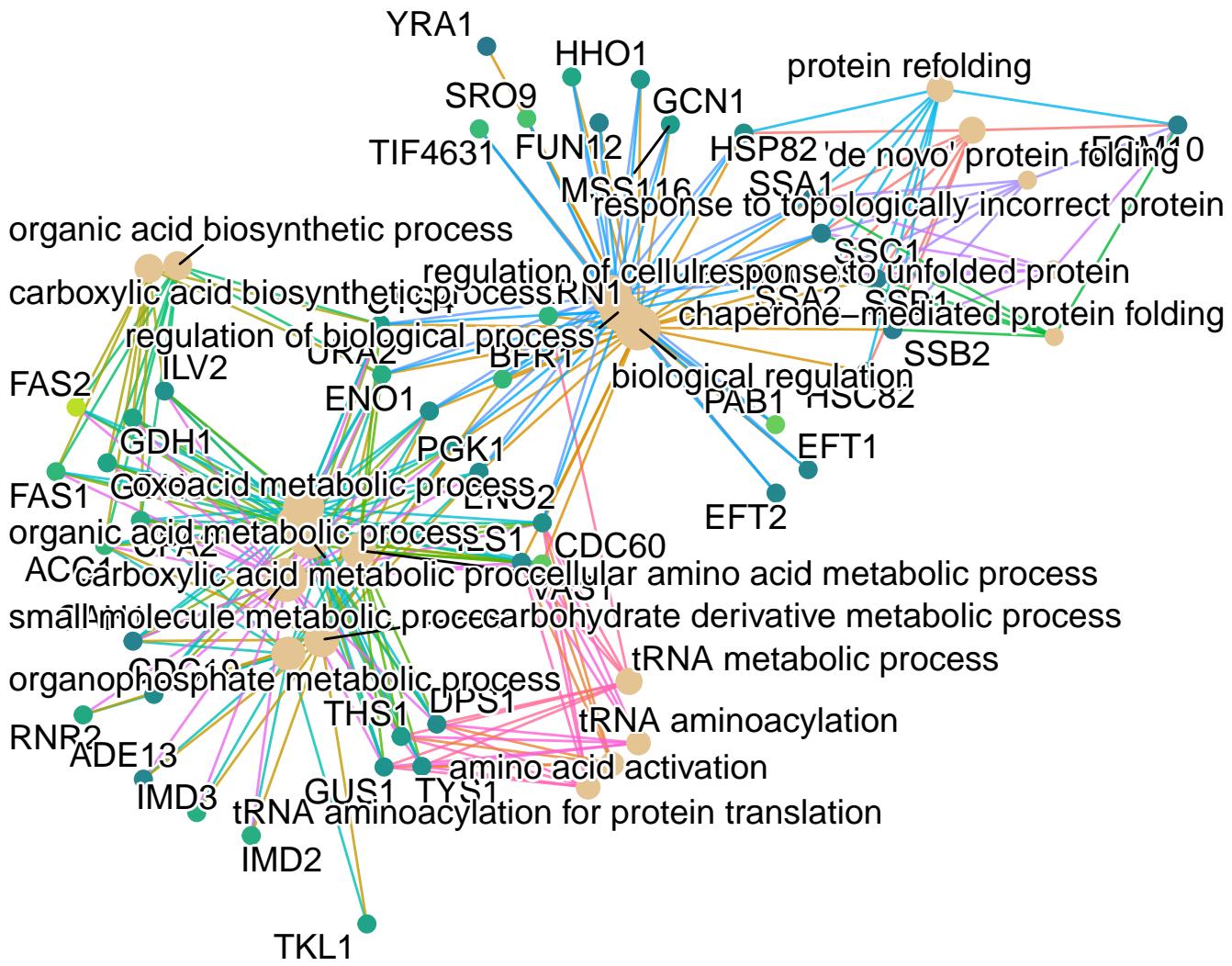
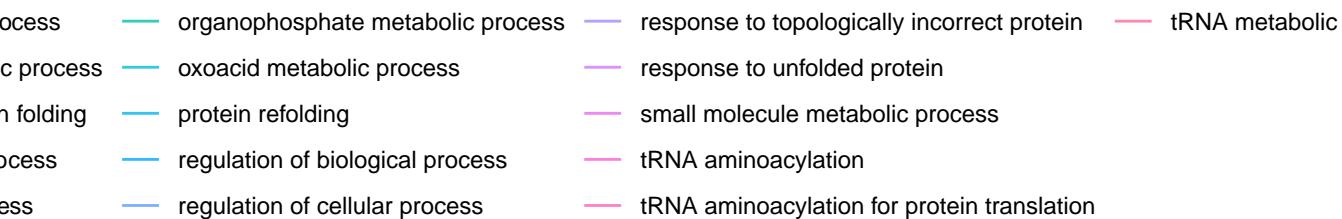
MUD2-TAP Up-regulated GO BP barplot



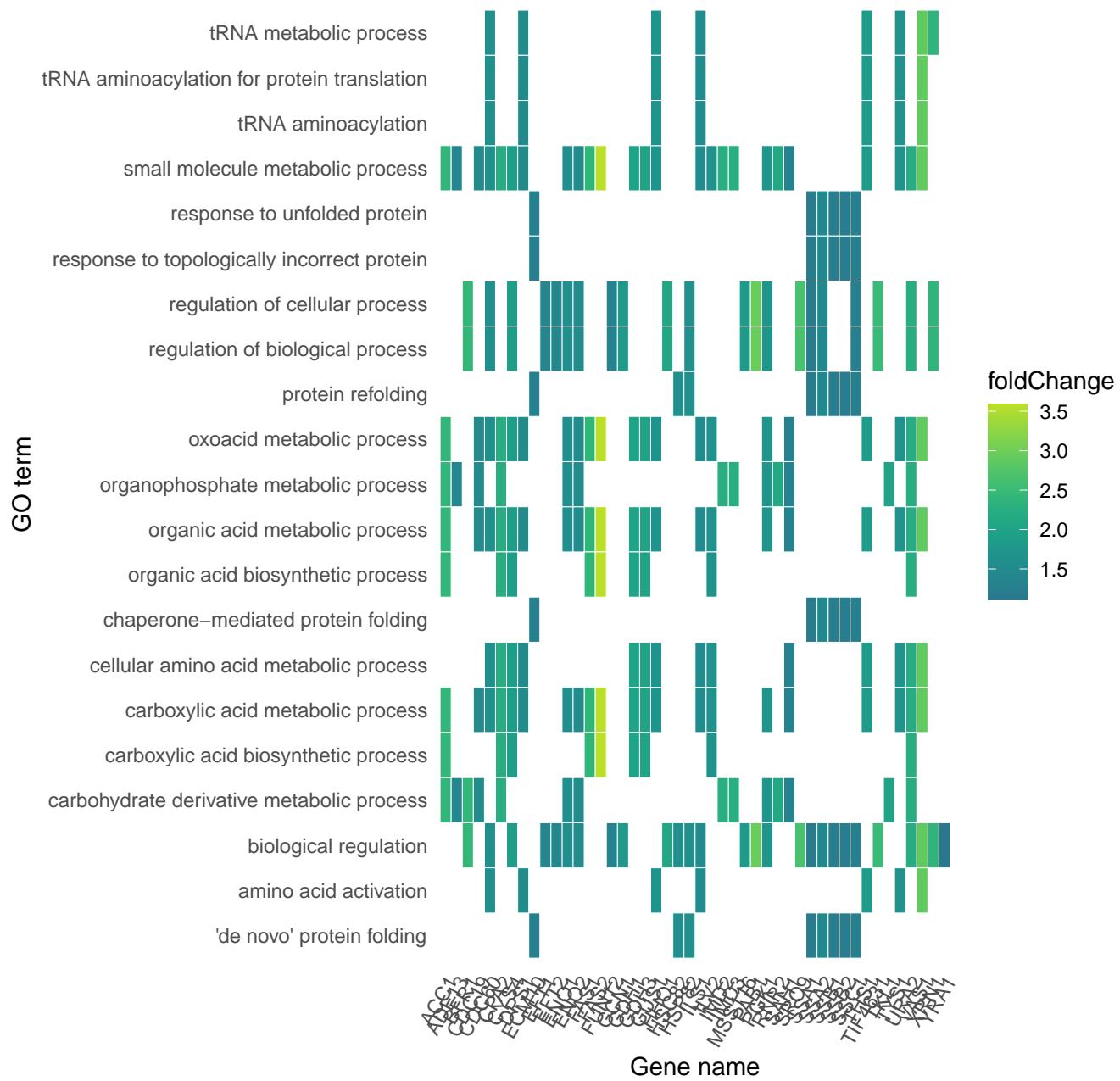
MUD2-TAP Up-regulated GO BP dotplot



MUD2-TAP Up-regulated GO BP cnetplot



MUD2-TAP Up-regulated GO BP heatplot



MUD2-TAP Up-regulated GO BP emapplot

response to unfolded protein

response to topologically incorrect protein

chaperone-mediated protein folding

protein refolding

'de novo' protein folding

size

10

15

20

25

regulation of cellular process

biological regulation

regulation of biological process

FoldChange

0.03

0.02

0.01

tRNA metabolic process

organic acid metabolic process

oxoacid

match

hialic

acid

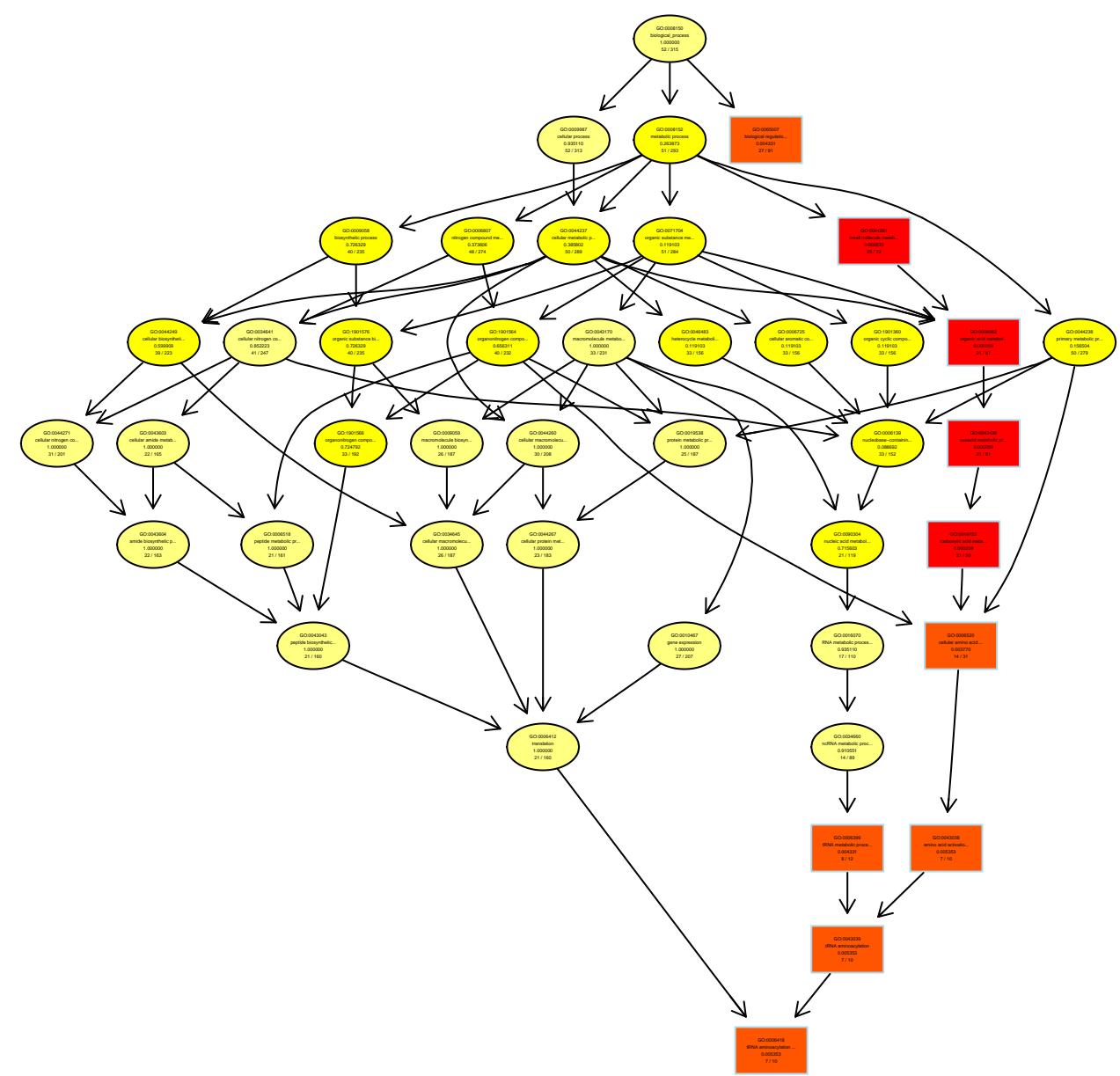
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va

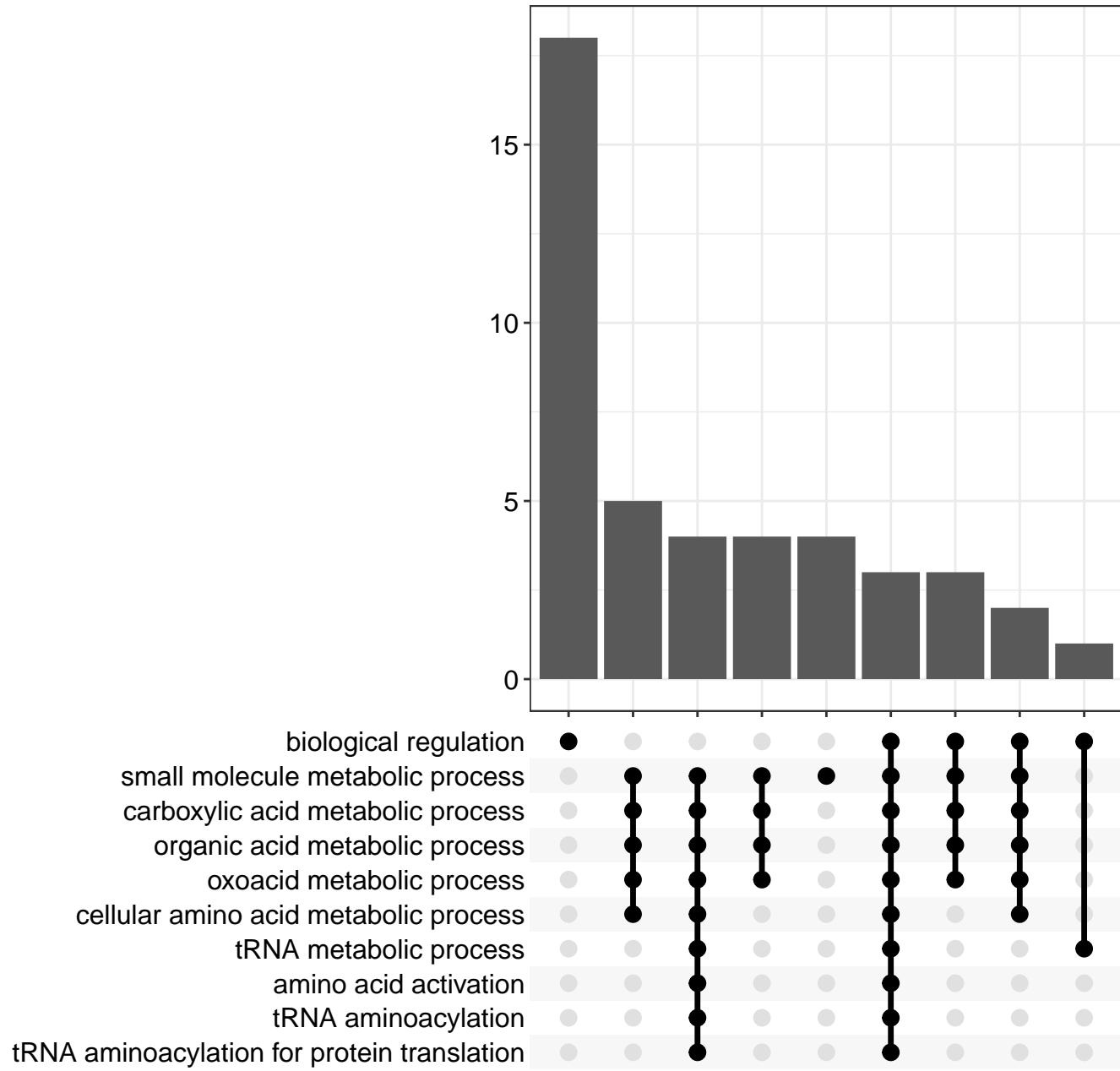
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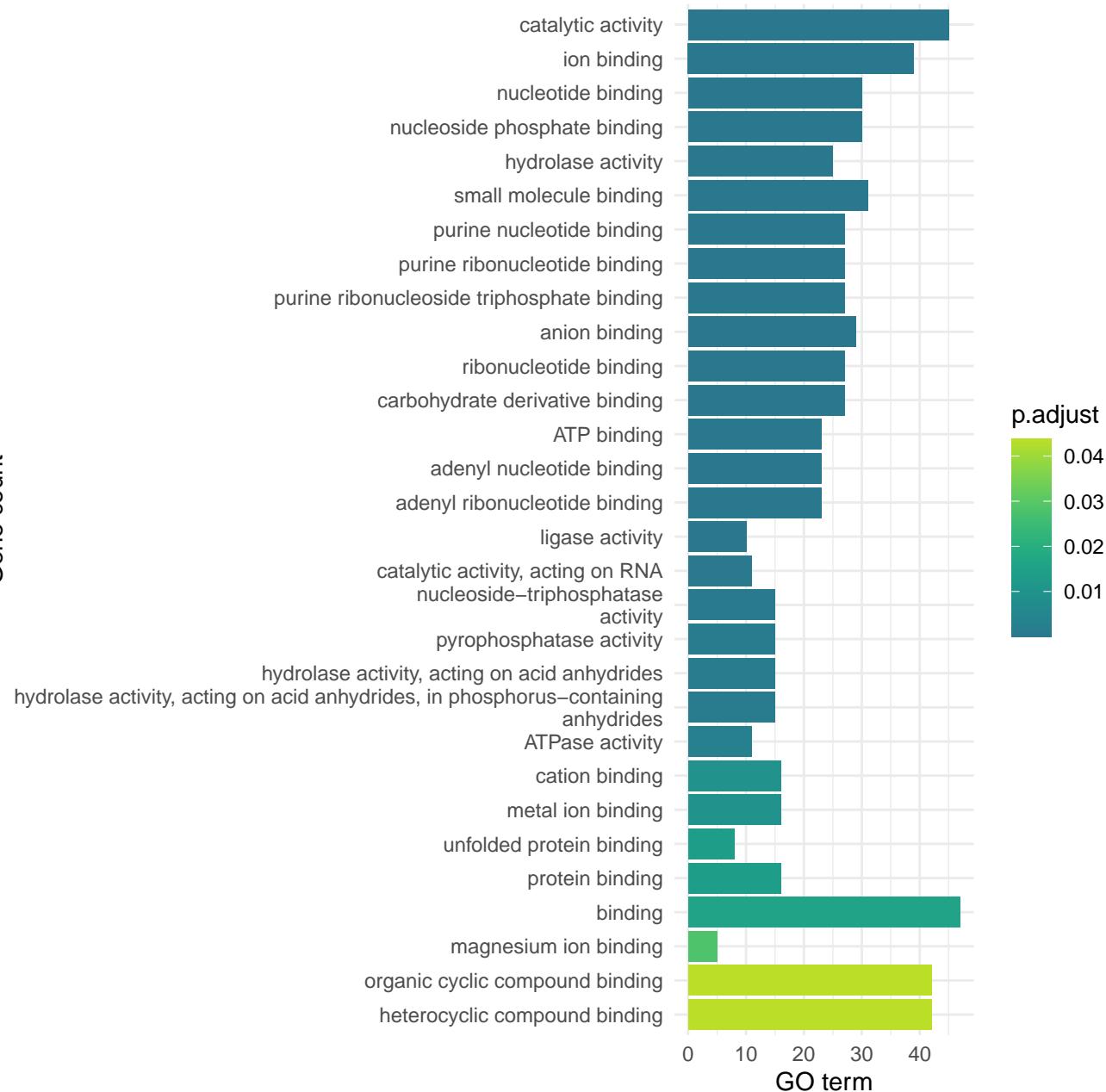
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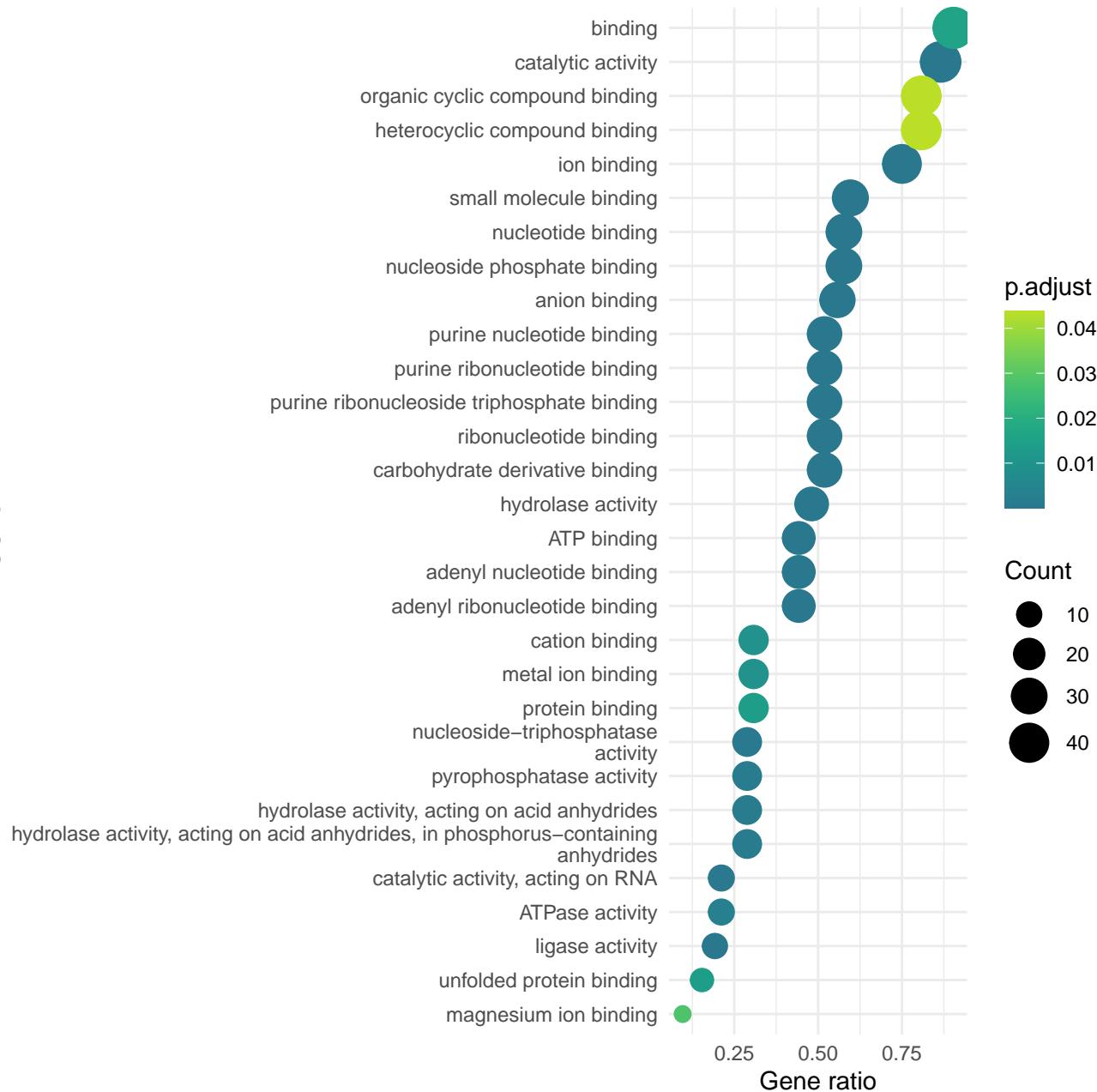
MUD2-TAP Up-regulated GO BP upsetplot



MUD2-TAP Up-regulated GO MF

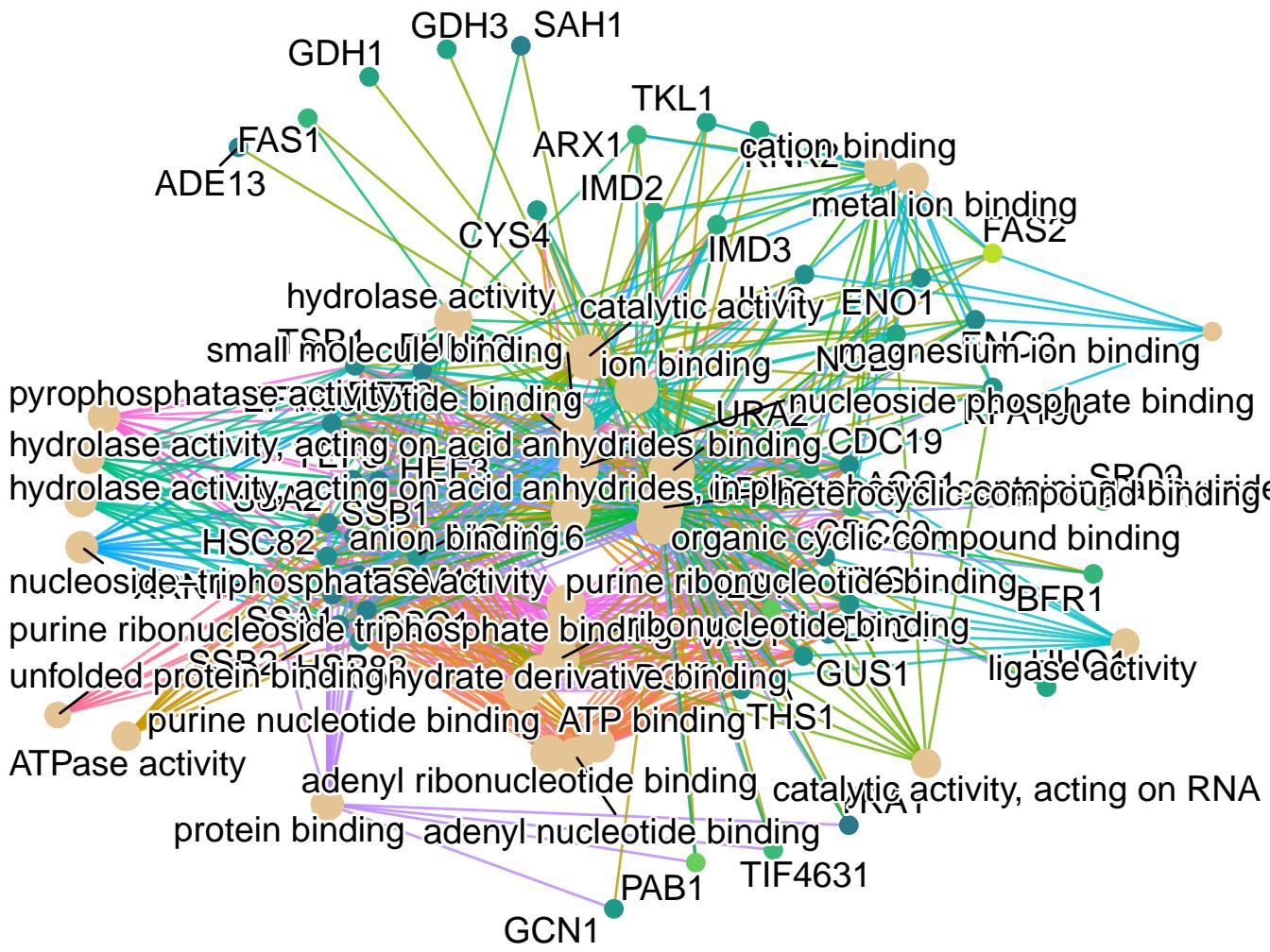


MUD2-TAP Up-regulated GO MF

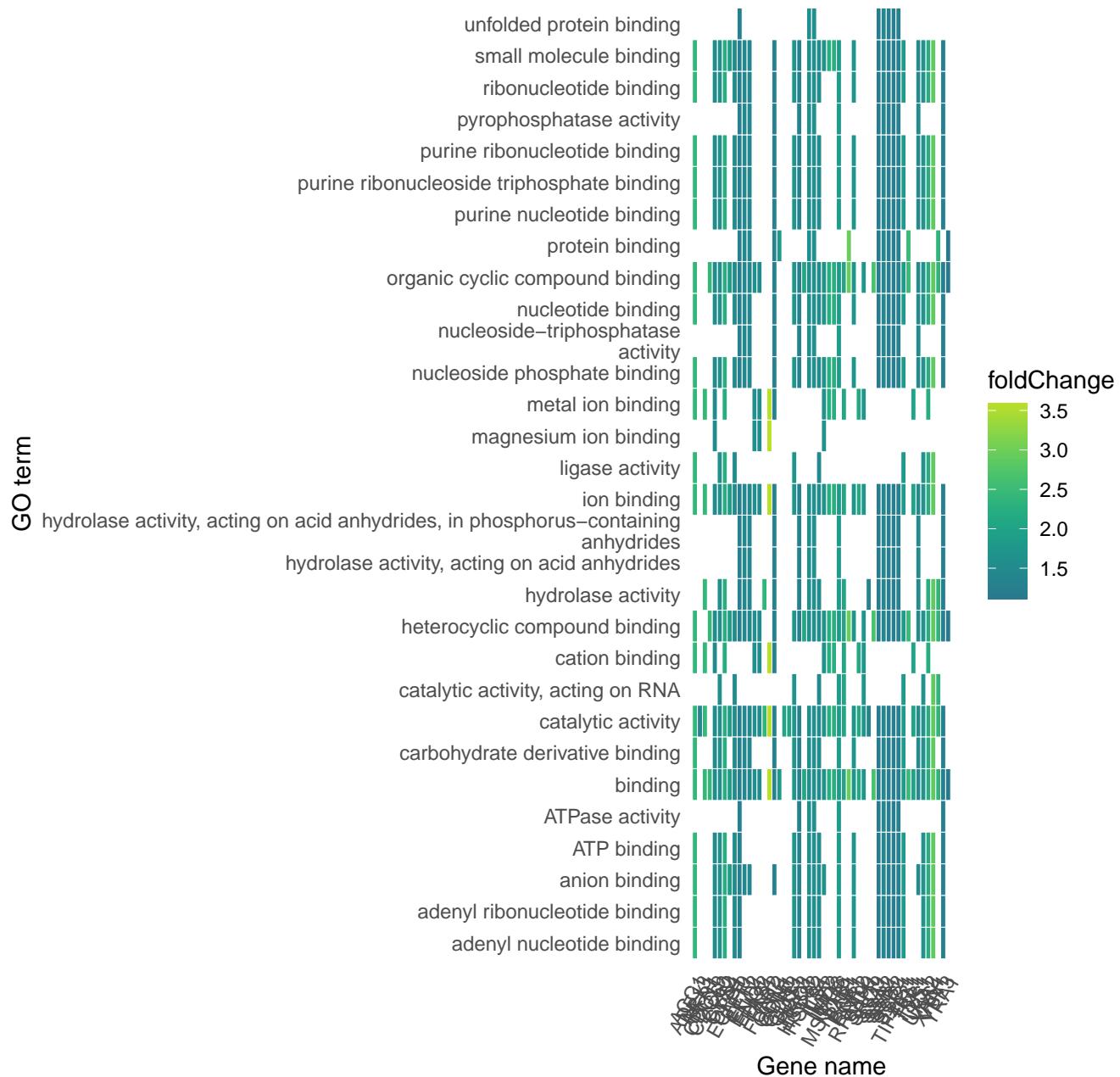


MUD2-TAP Up-regulated GO MF cnetplot

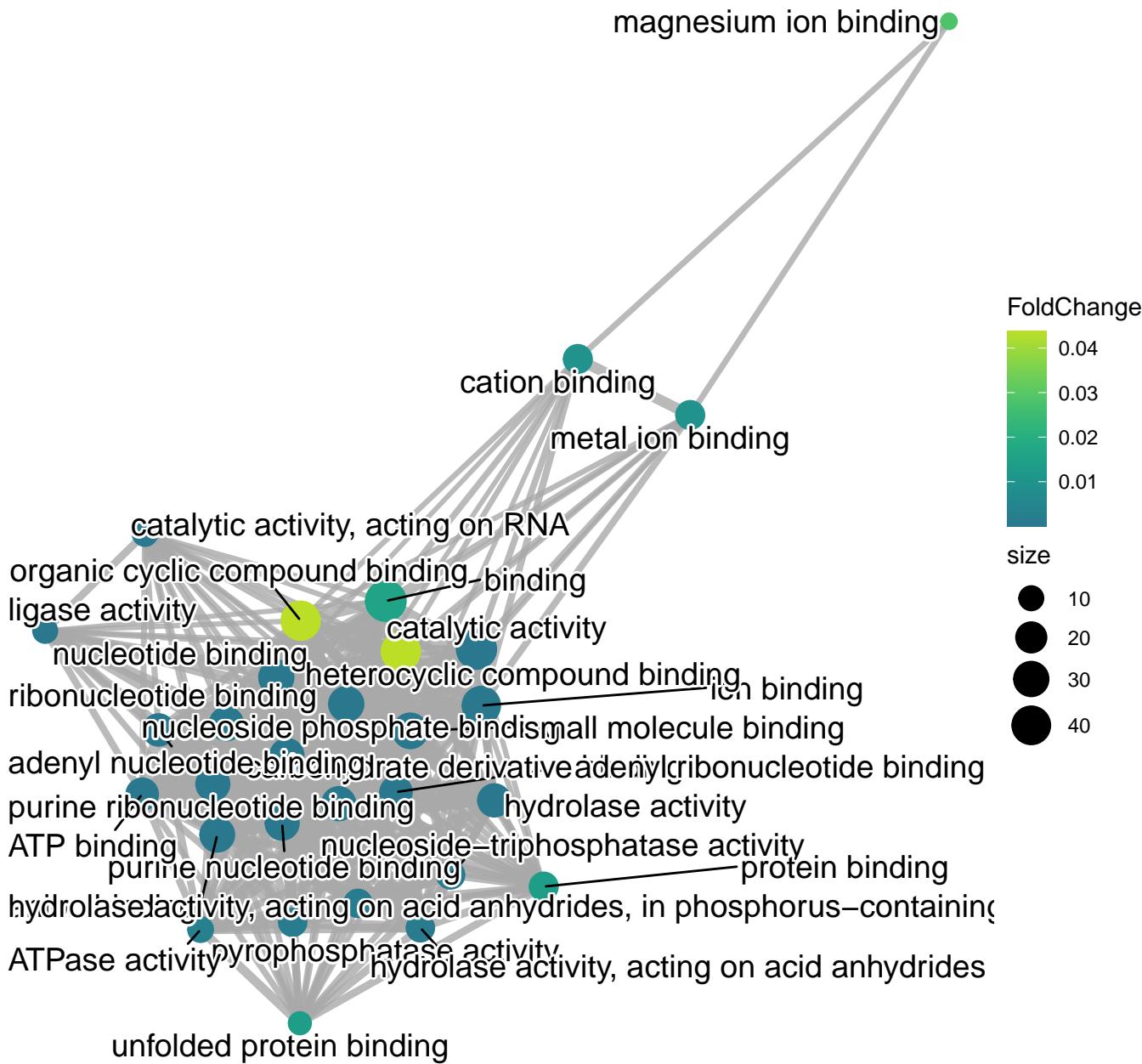
- hydrolase activity, acting on acid anhydrides
- hydrolase activity, acting on acid anhydrides
- ion binding
- ligase activity
- magnesium ion binding
- metal ion binding

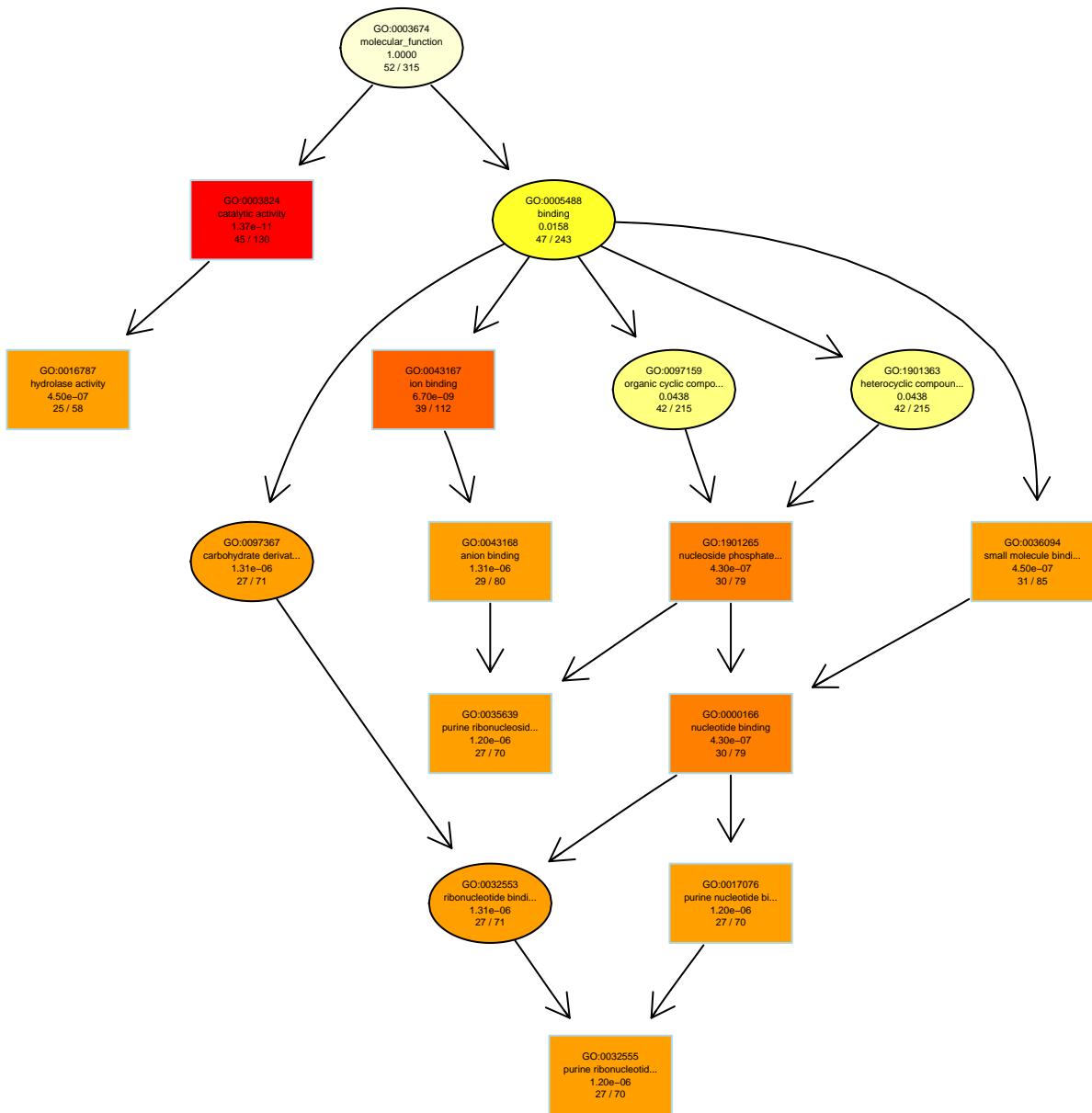


MUD2-TAP Up-regulated GO MF

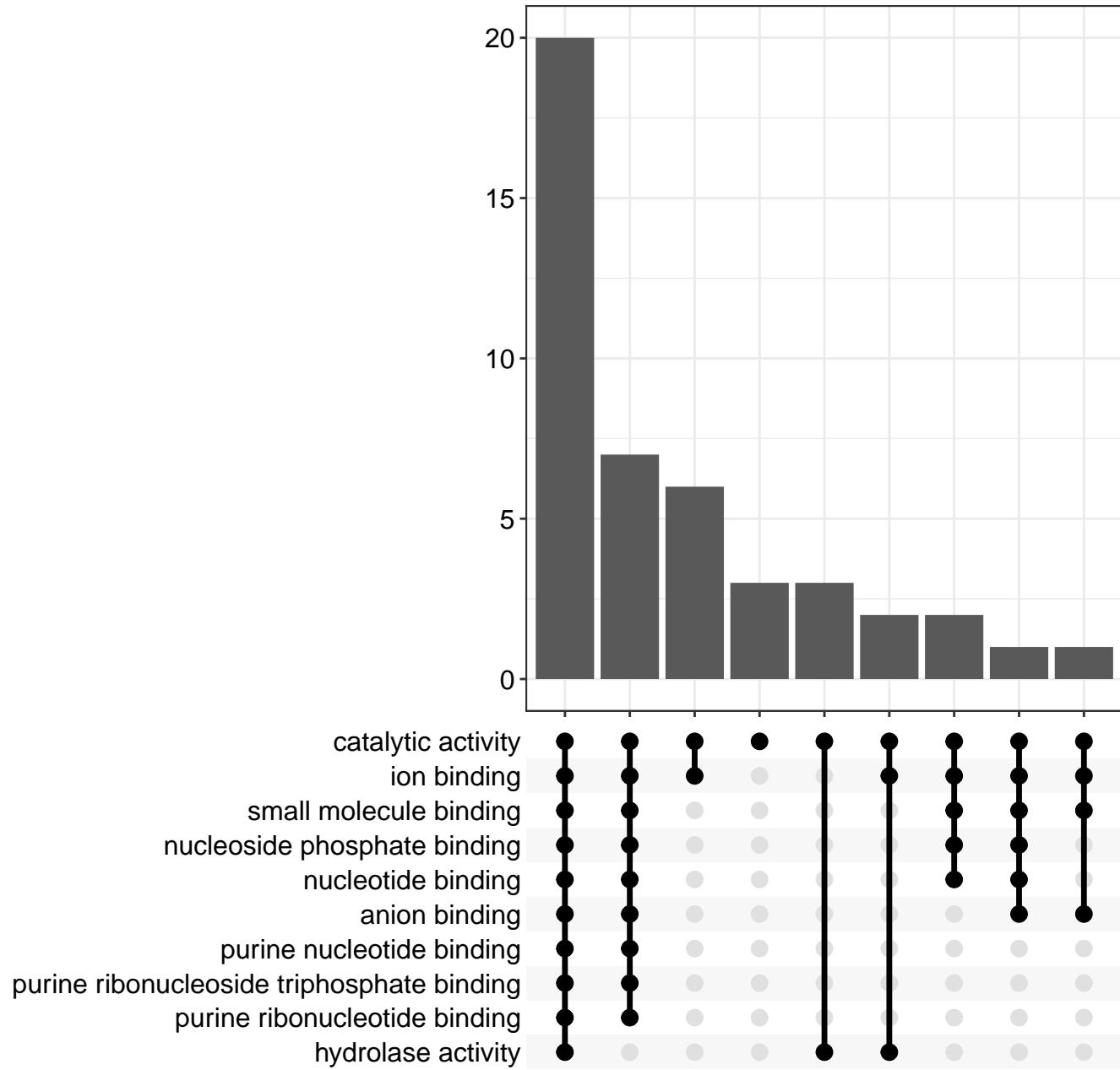


MUD2-TAP Up-regulated GO MF emapplot

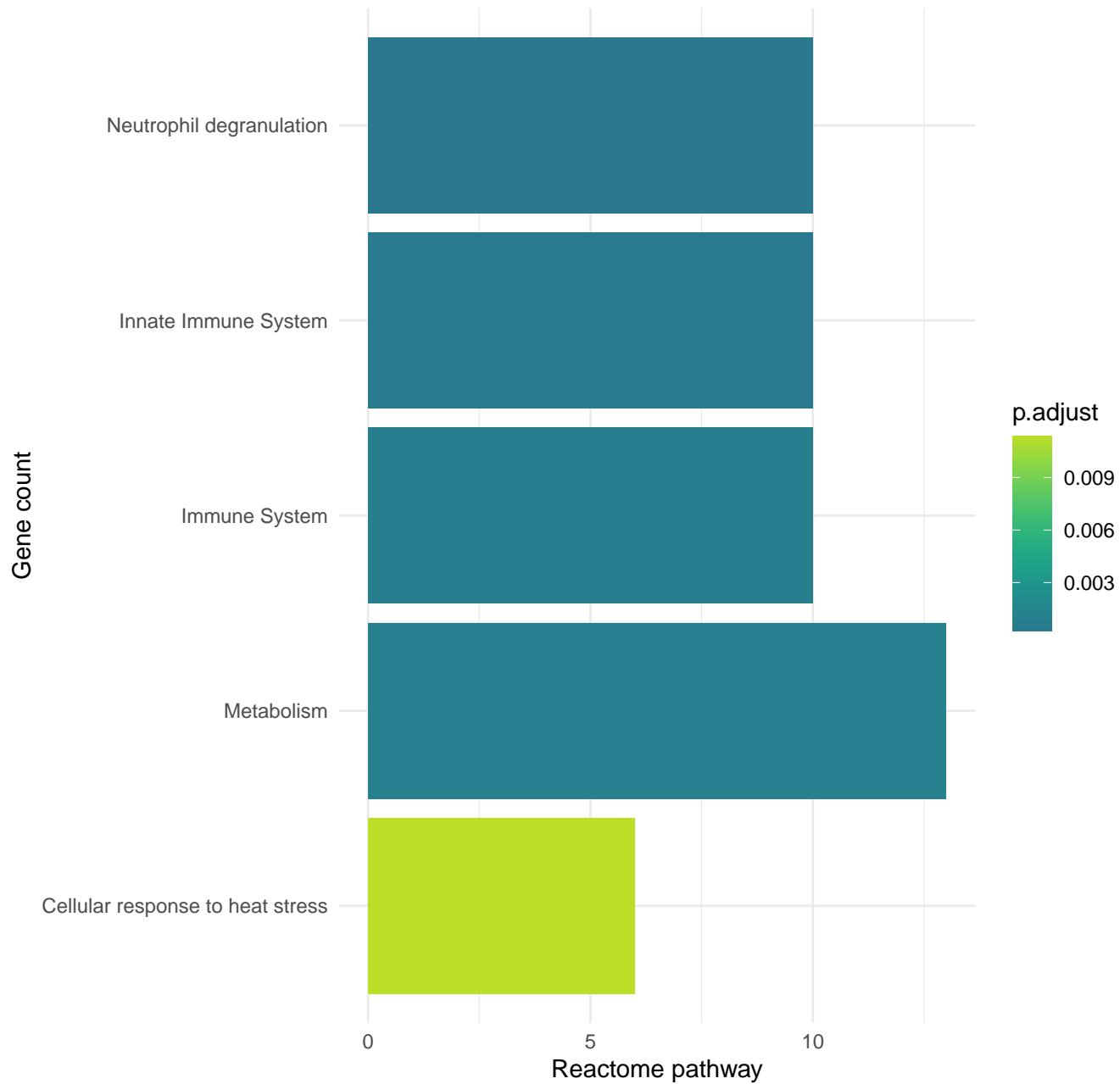




MUD2-TAP Up-regulated GO MF upsetplot



MUD2-TAP Up-regulated Reactome barplot



MUD2-TAP Up-regulated Reactome dotplot

Reactome pathway

Metabolism

Neutrophil degranulation

Innate Immune System

Immune System

Cellular response to heat stress

0.3

0.4

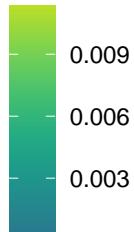
0.5

Gene ratio

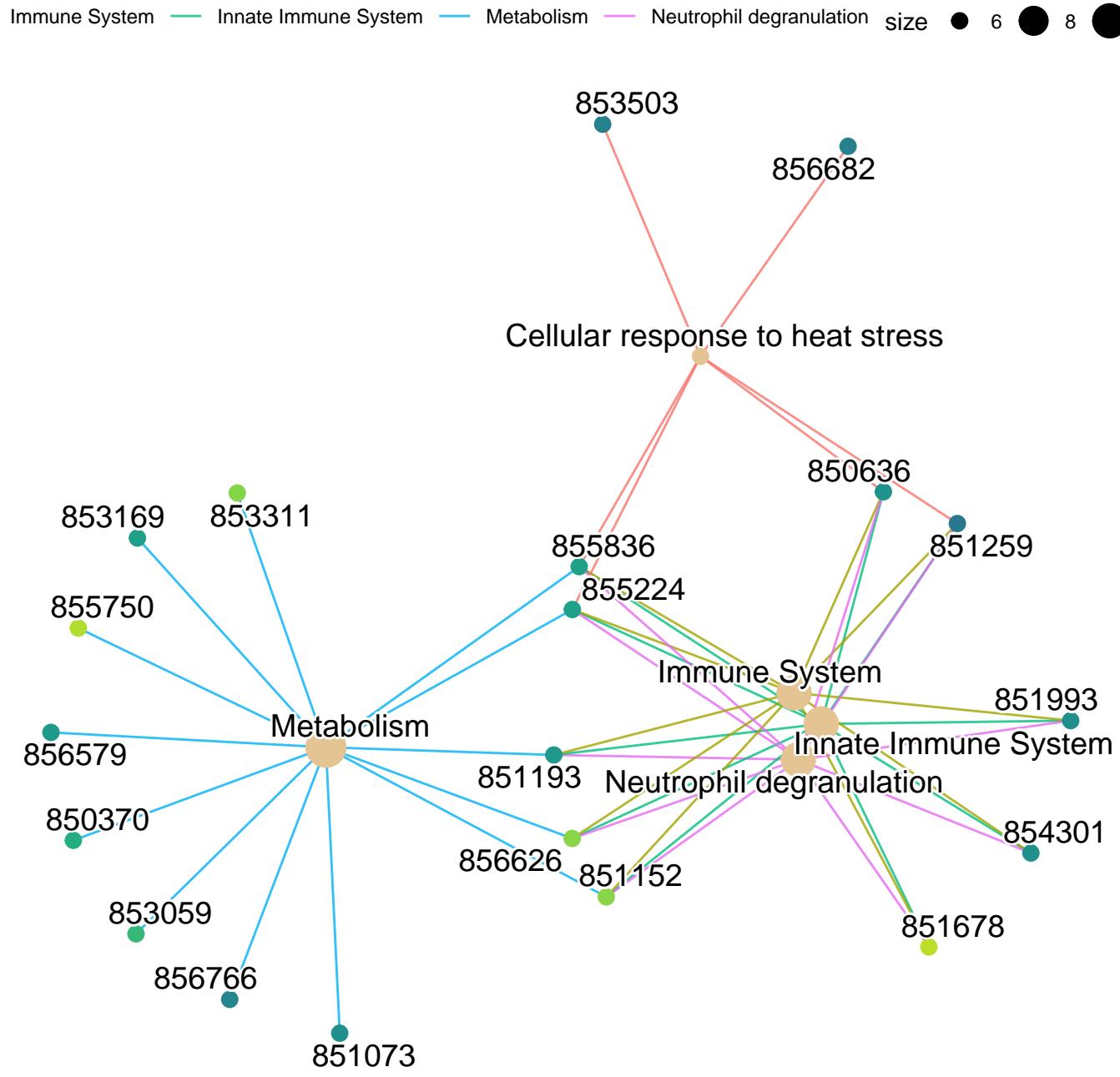
Count

- 6
- 8
- 10
- 12

p.adjust



MUD2-TAP Up-regulated Reactome cnetplot



MUD2-TAP Up-regulated Reactome heatplot

Reactome pathway

Neutrophil degranulation

Metabolism

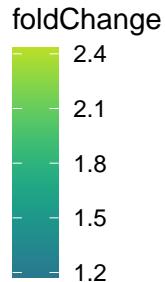
Innate Immune System

Immune System

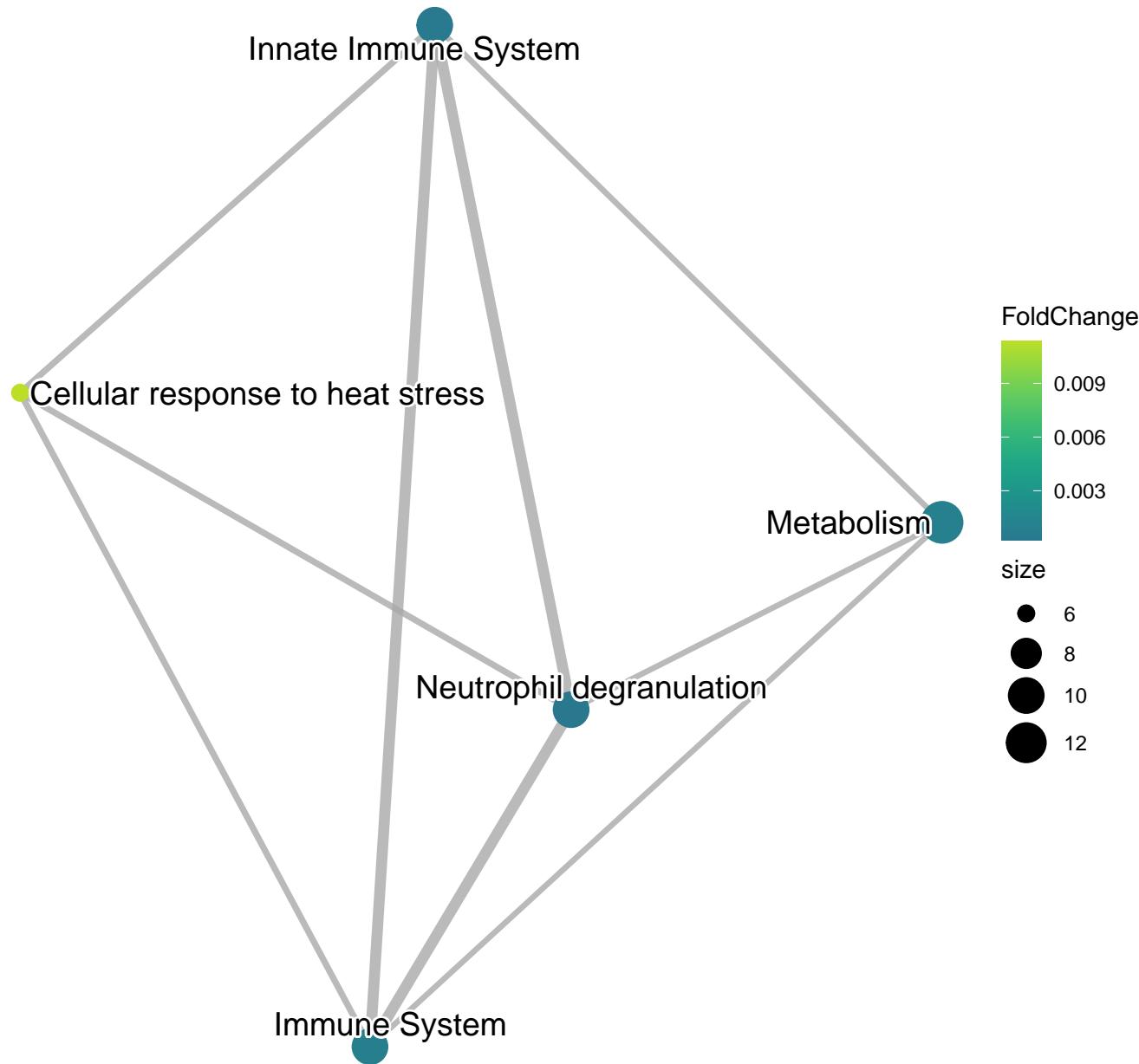
Cellular response to heat stress

850370
850636
851073
851152
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851259
851678
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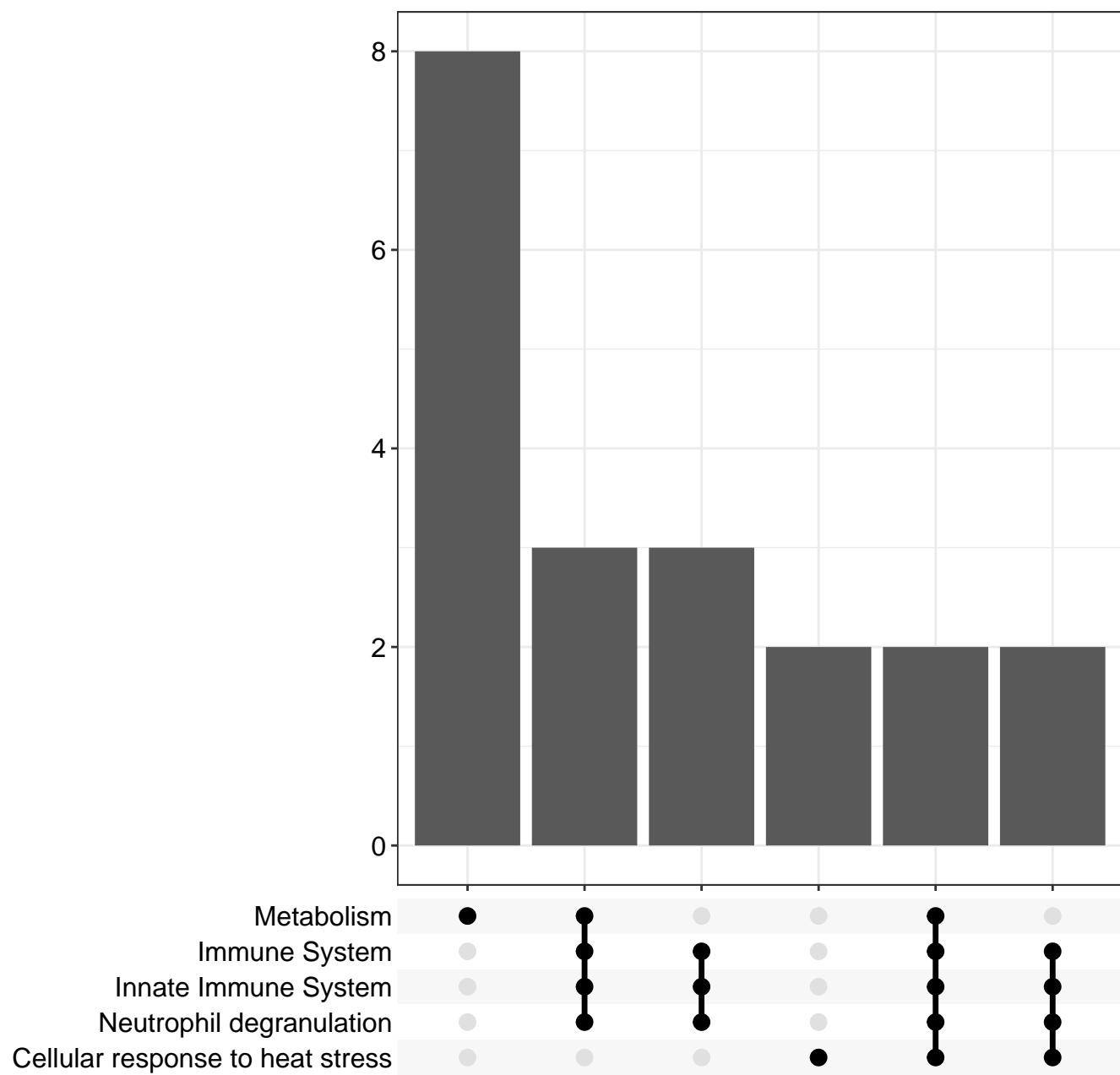
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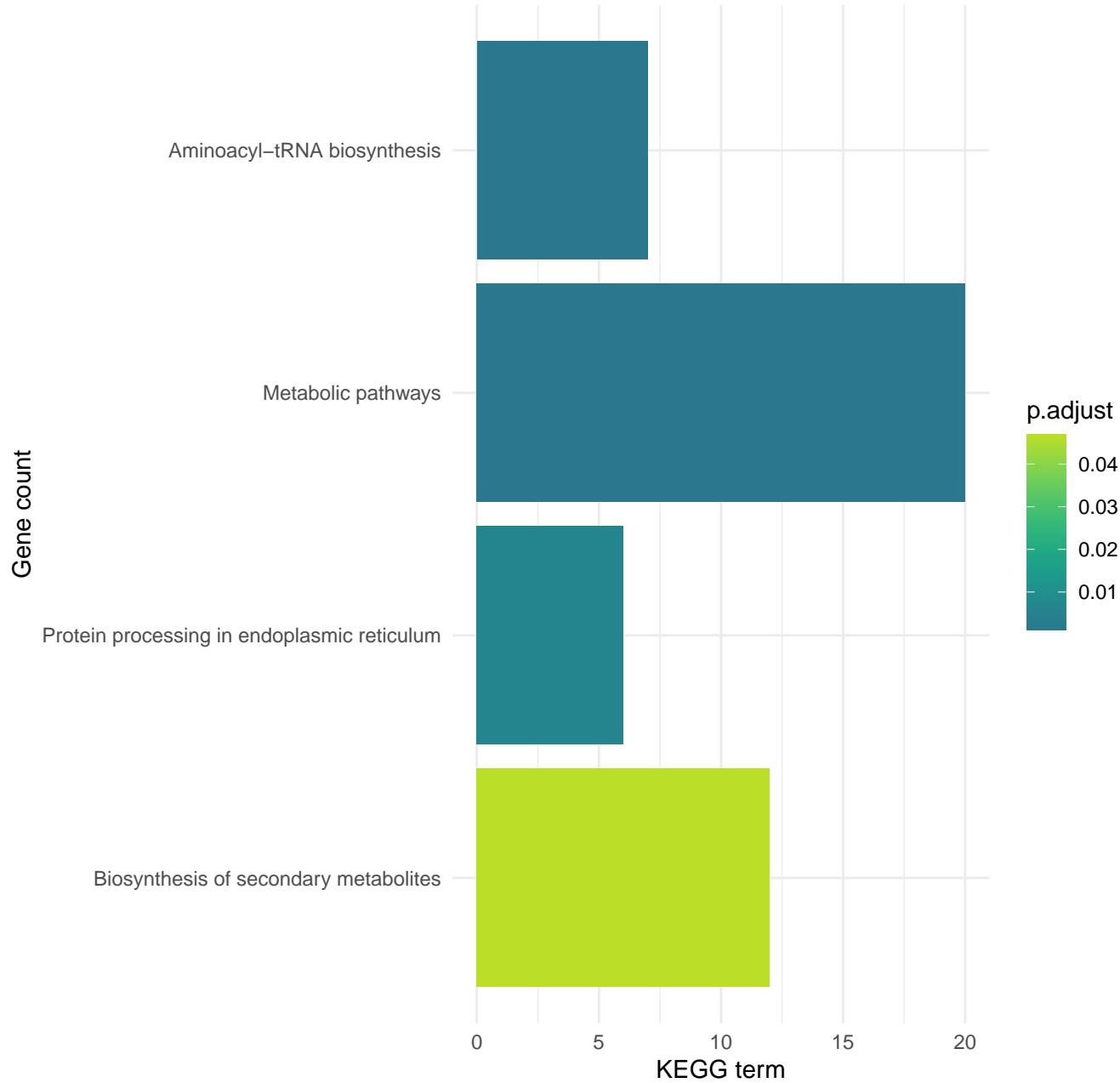
MUD2-TAP Up-regulated Reactome emapplot



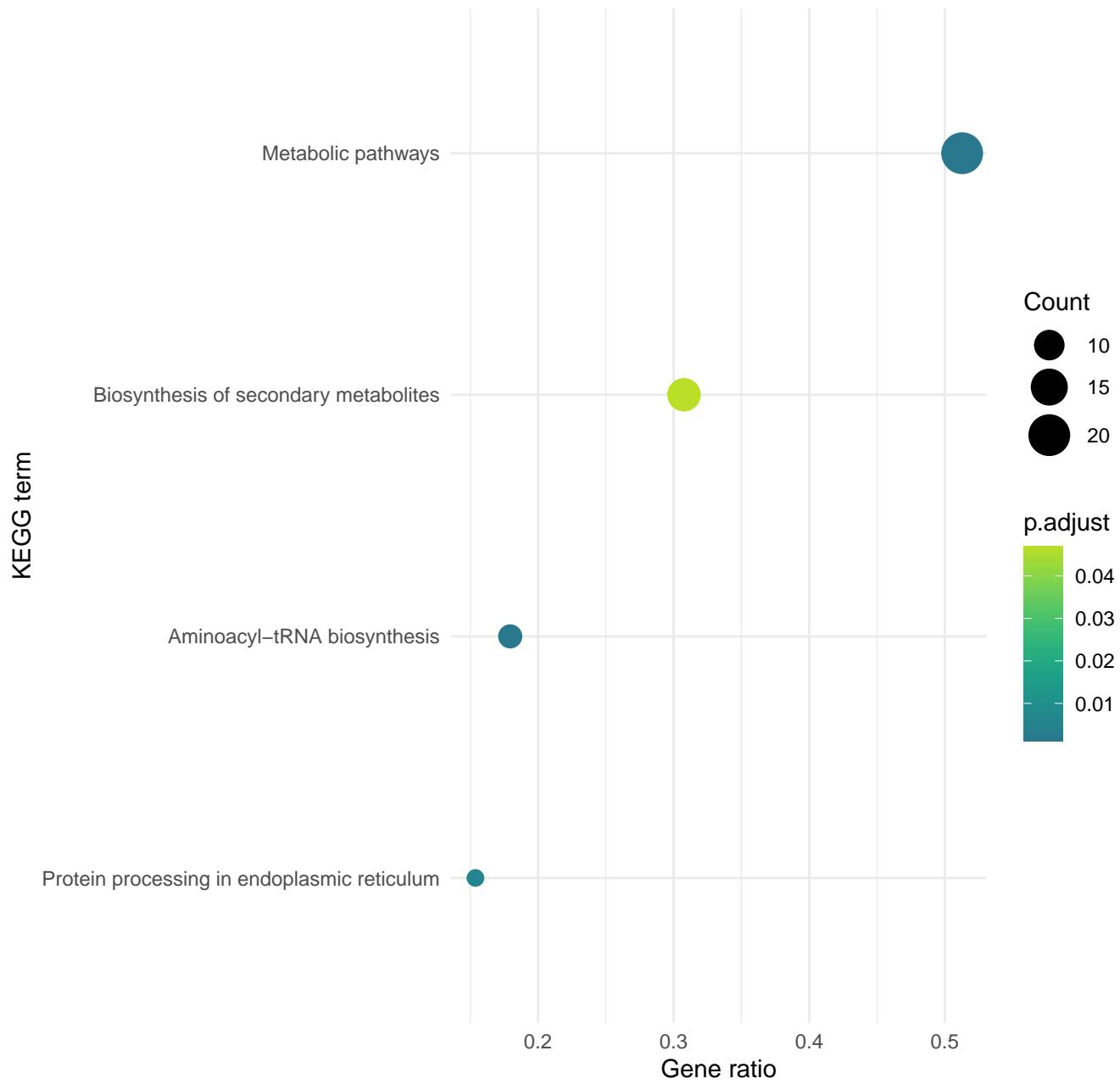
MUD2-TAP Up-regulated Reactome upsetplot



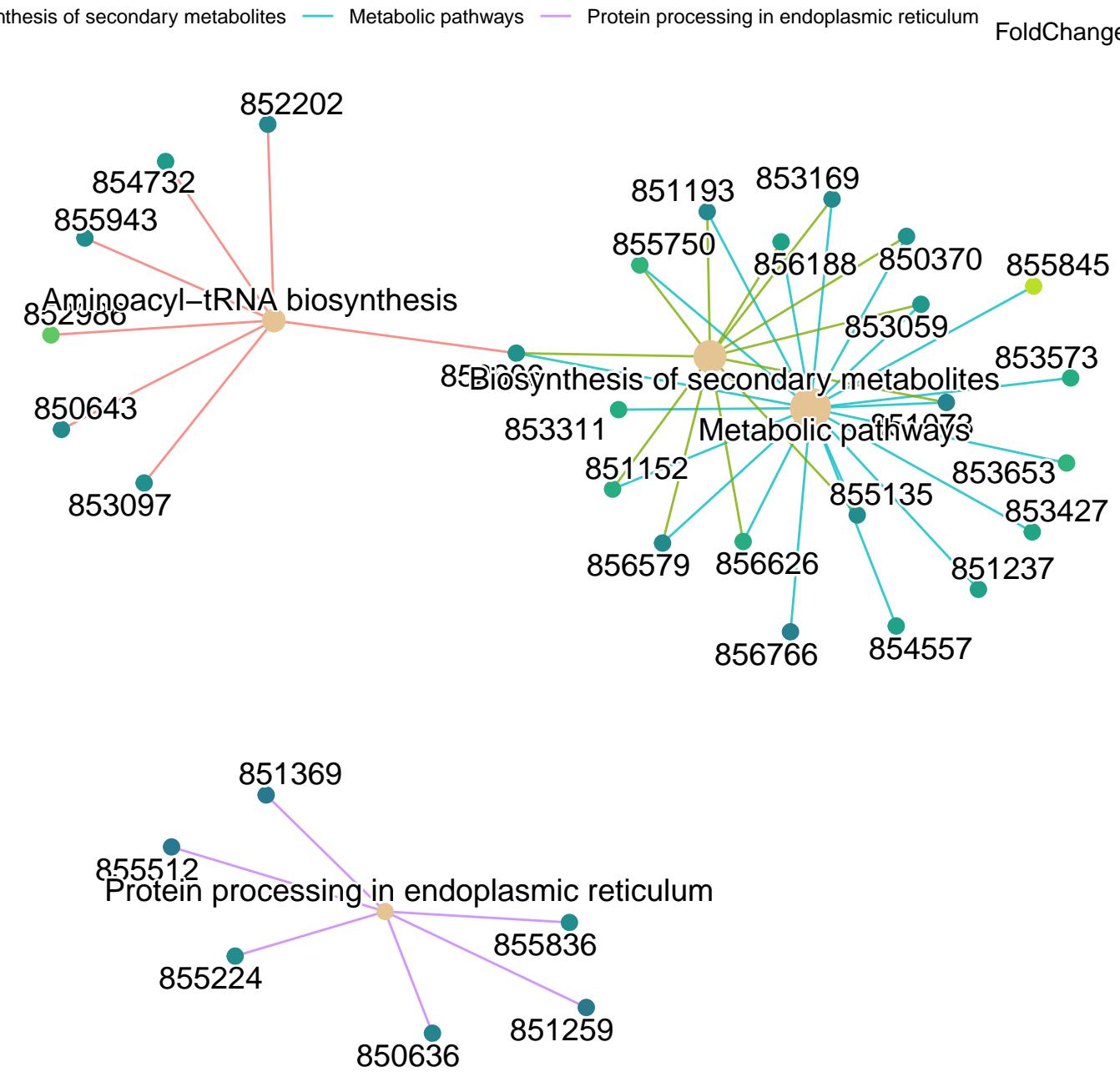
MUD2-TAP Up-regulated KEGG barplot



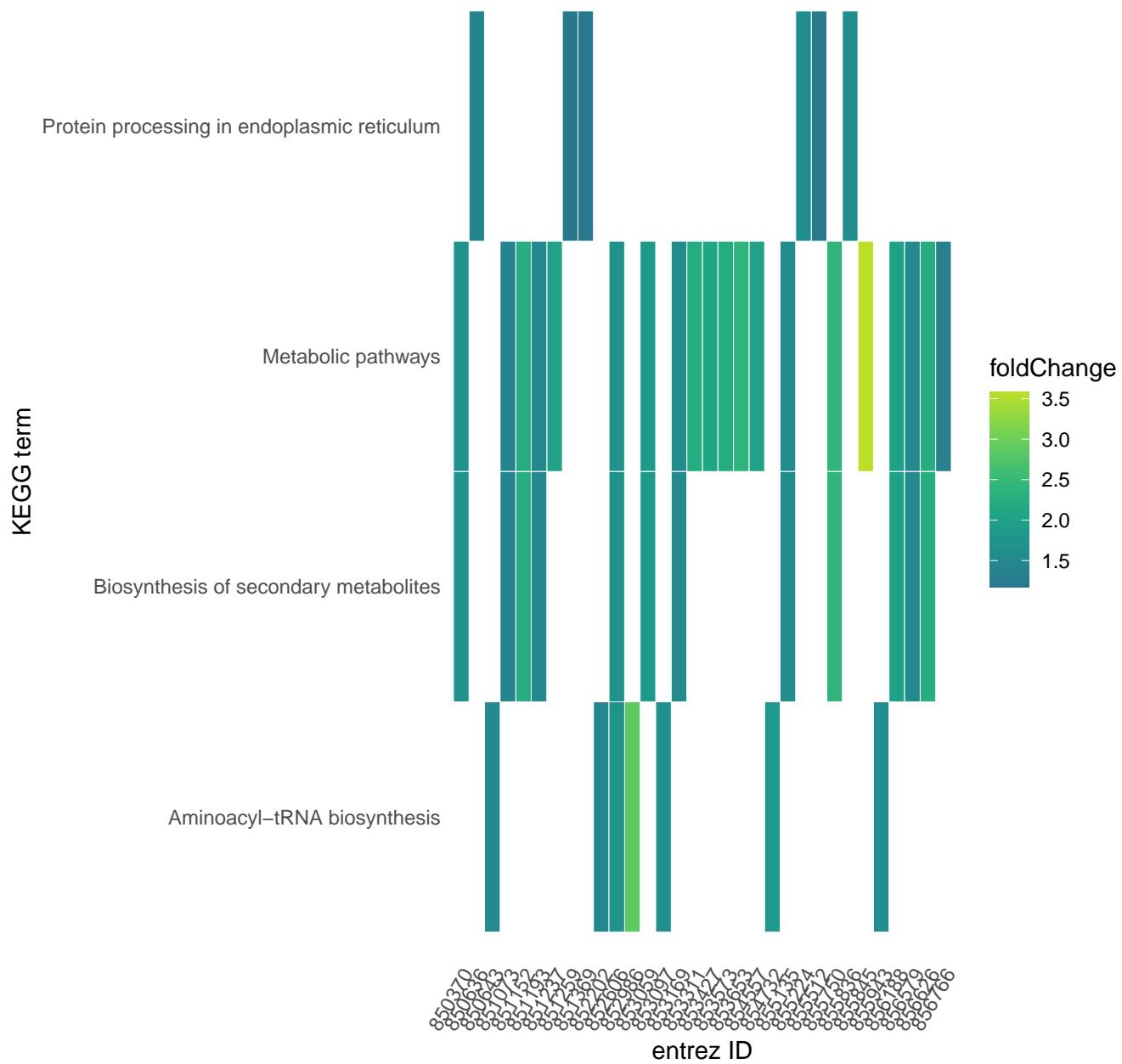
MUD2-TAP Up-regulated KEGG dotplot



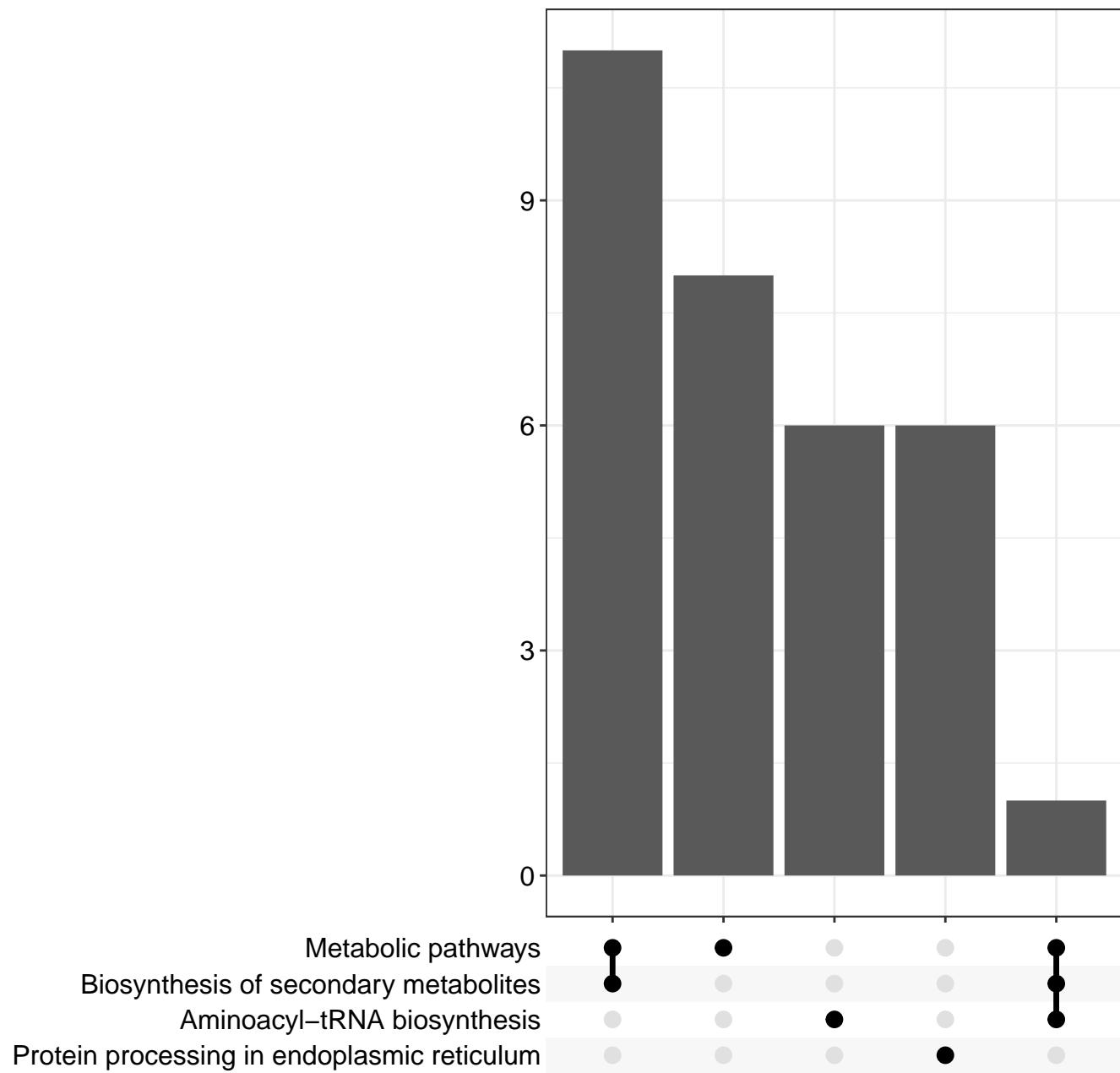
MUD2-TAP Up-regulated KEGG dotplot



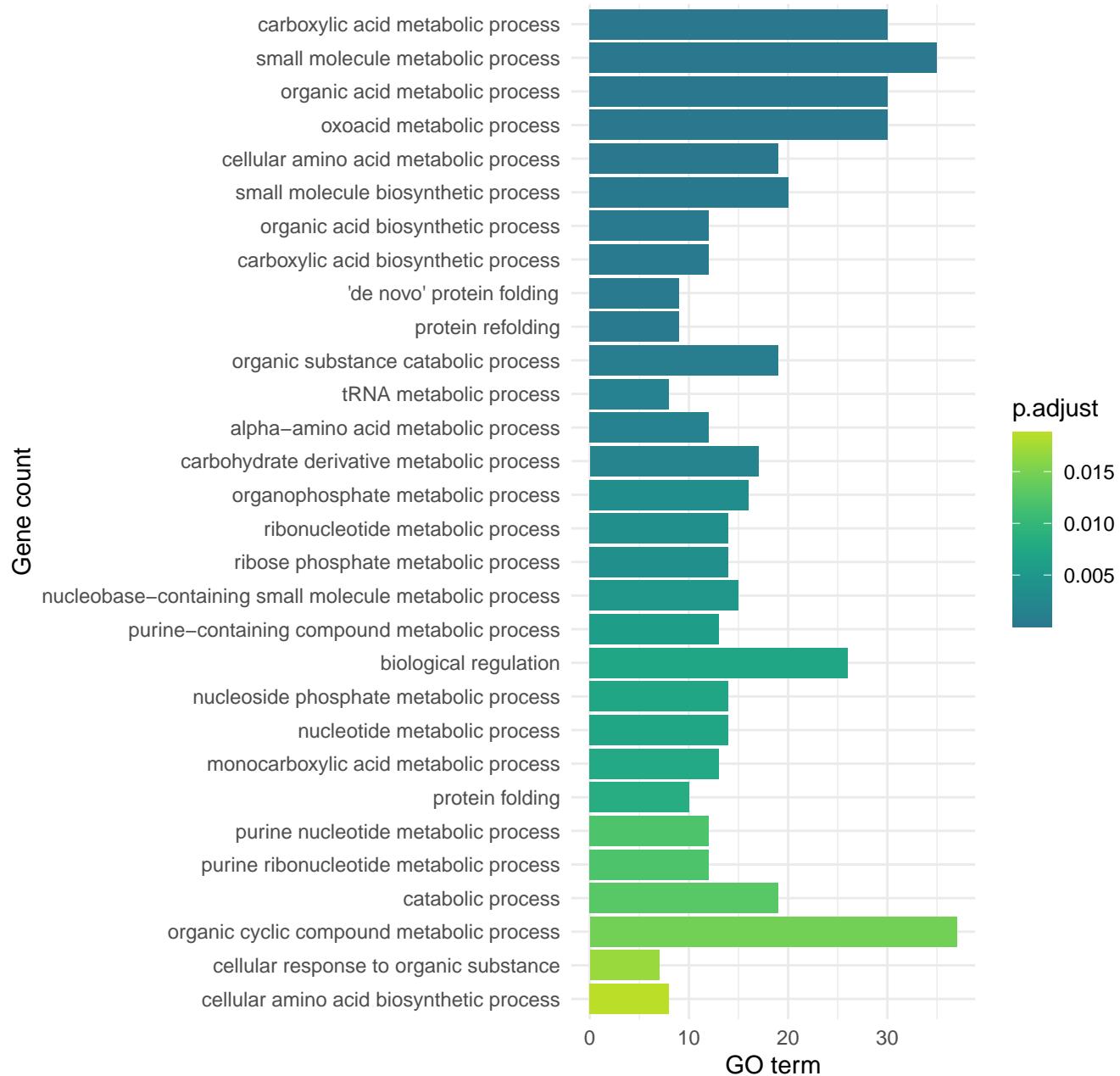
MUD2-TAP Up-regulated KEGG heatplot



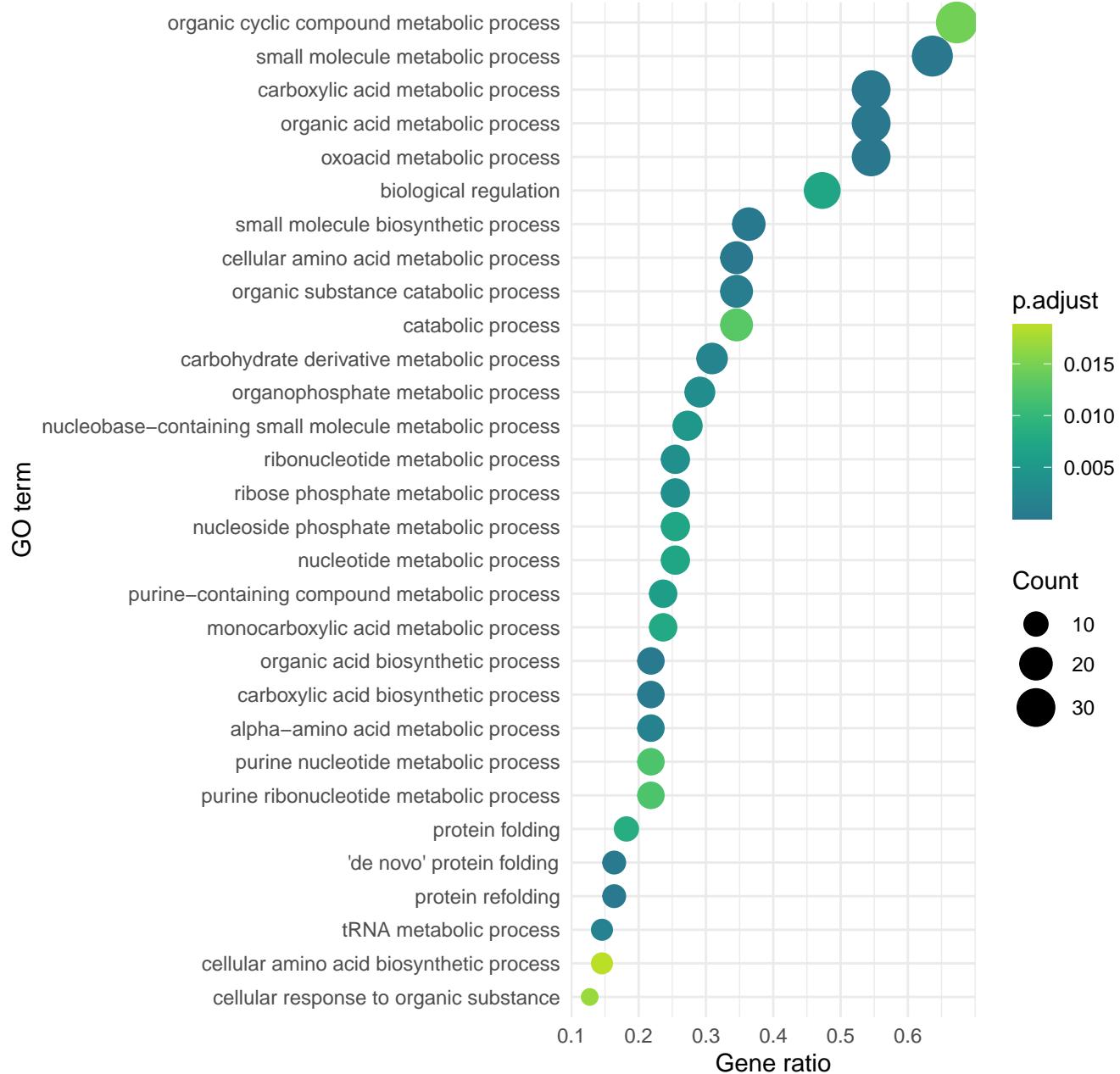
MUD2-TAP Up-regulated KEGG upsetplot



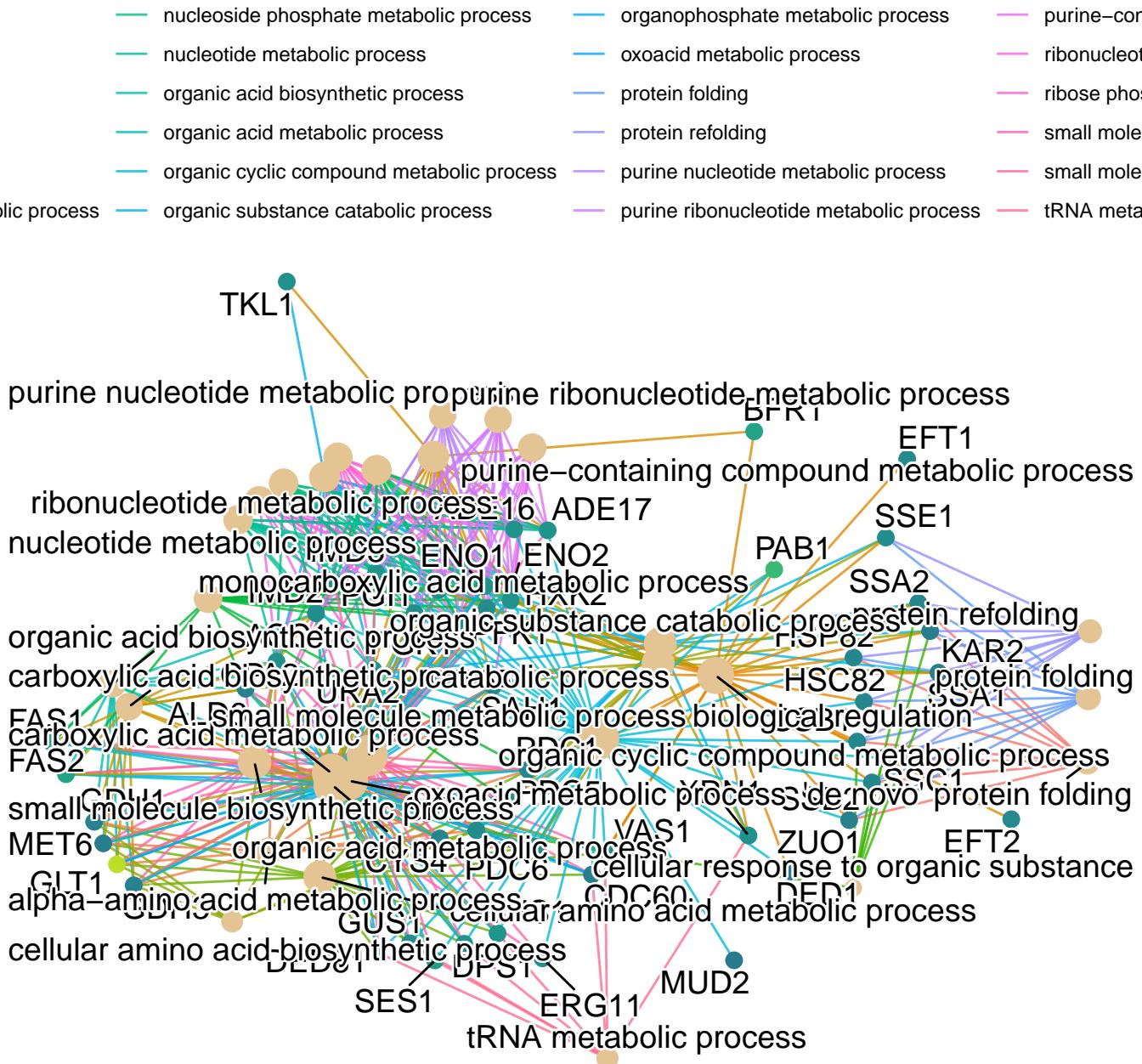
PRP22-TAP Up-regulated GO BP barplot



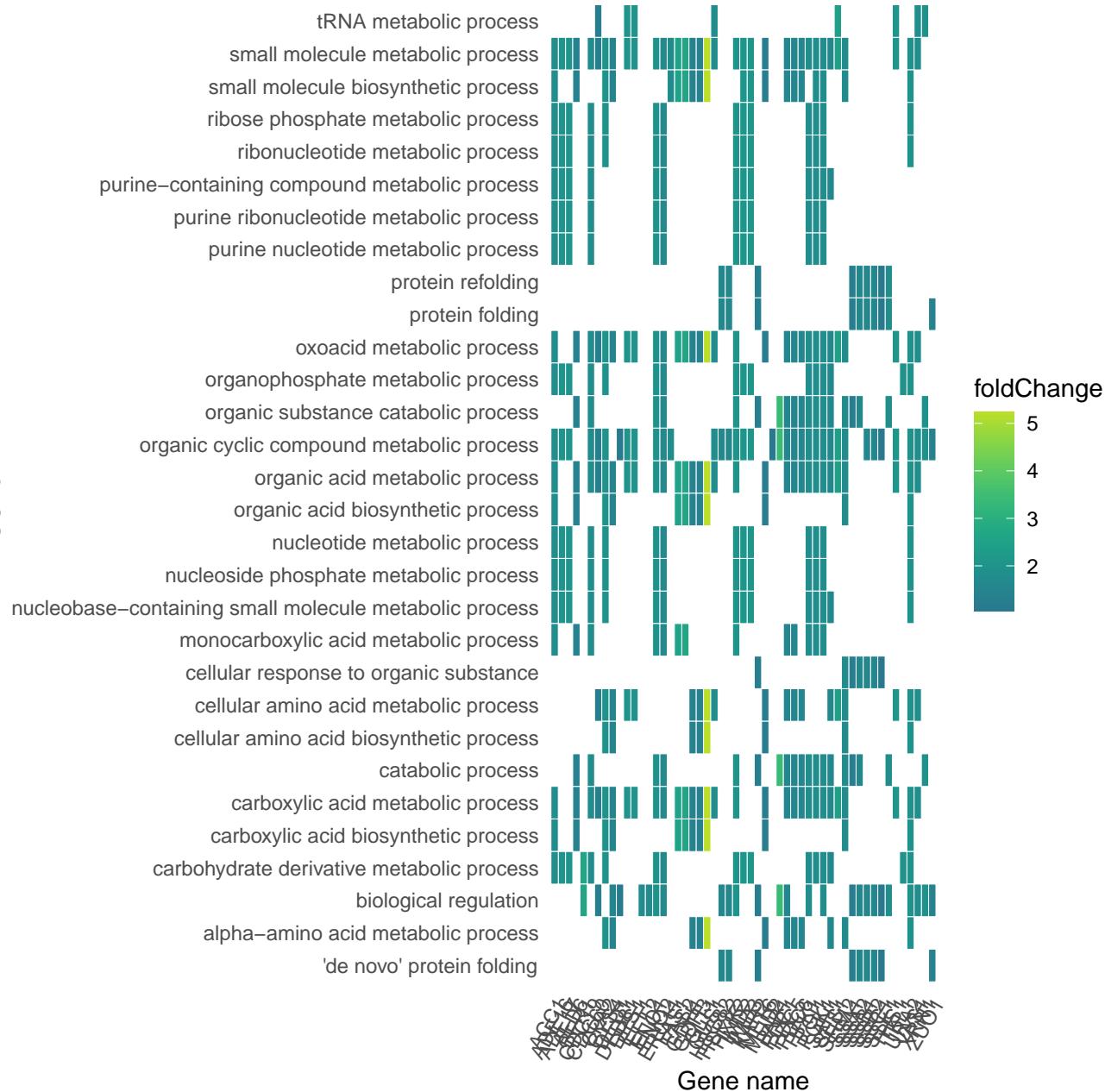
PRP22-TAP Up-regulated GO BP dotplot



PRP22-TAP Up-regulated GO BP cnetplot



PRP22-TAP Up-regulated GO BP heatplot



PRP22-TAP Up-regulated GO BP emapplot

purine nucleotide metabolic process

purine ribonucleotide metabolic process

nucleoside phosphate metabolic process

nucleotide metabolic process containing small molecule metabolic process

ribose phosphate-containing compound metabolic process

ribonucleotide metabolic process

carbohydrate derivative metabolic process

organophosphate metabolic process

catabolic process

monocarboxylic acid metabolic process catabolic process

small molecule metabolic process

oxoacid metabolic process organic cyclic compound metabolic process

small molecule biosynthetic process

carboxylic acid metabolic process

organic acid metabolic process

alpha-amino acid metabolic process

organic acid biosynthetic process

cellular amino acid metabolic process cellular response to organic substance

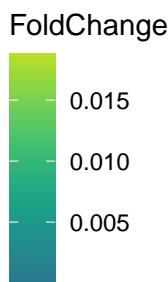
cellular amino acid biosynthetic process

carboxylic acid biosynthetic process

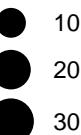
'de novo' protein folding
biological regulation

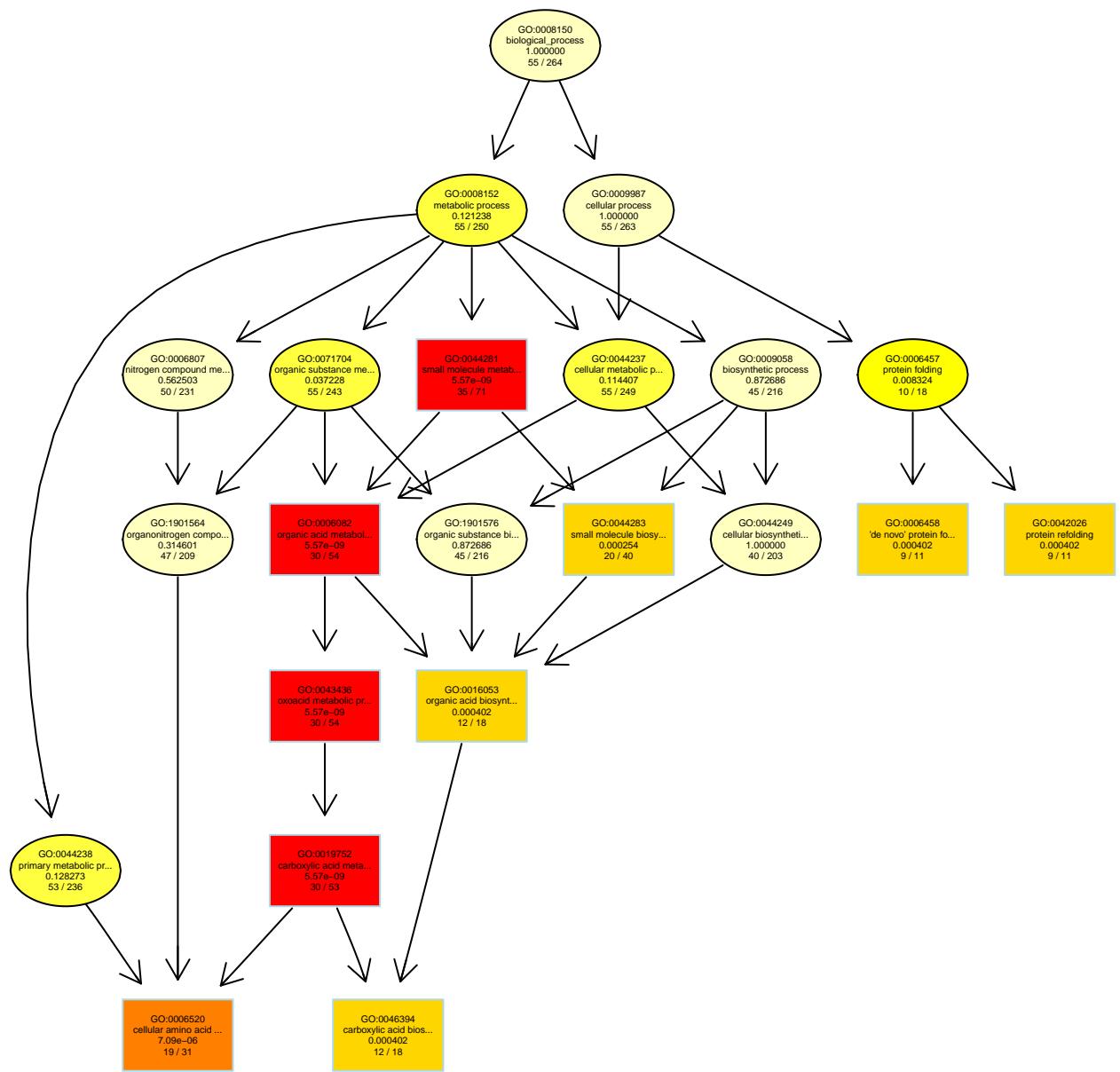
protein folding
protein refolding

tRNA metabolic process

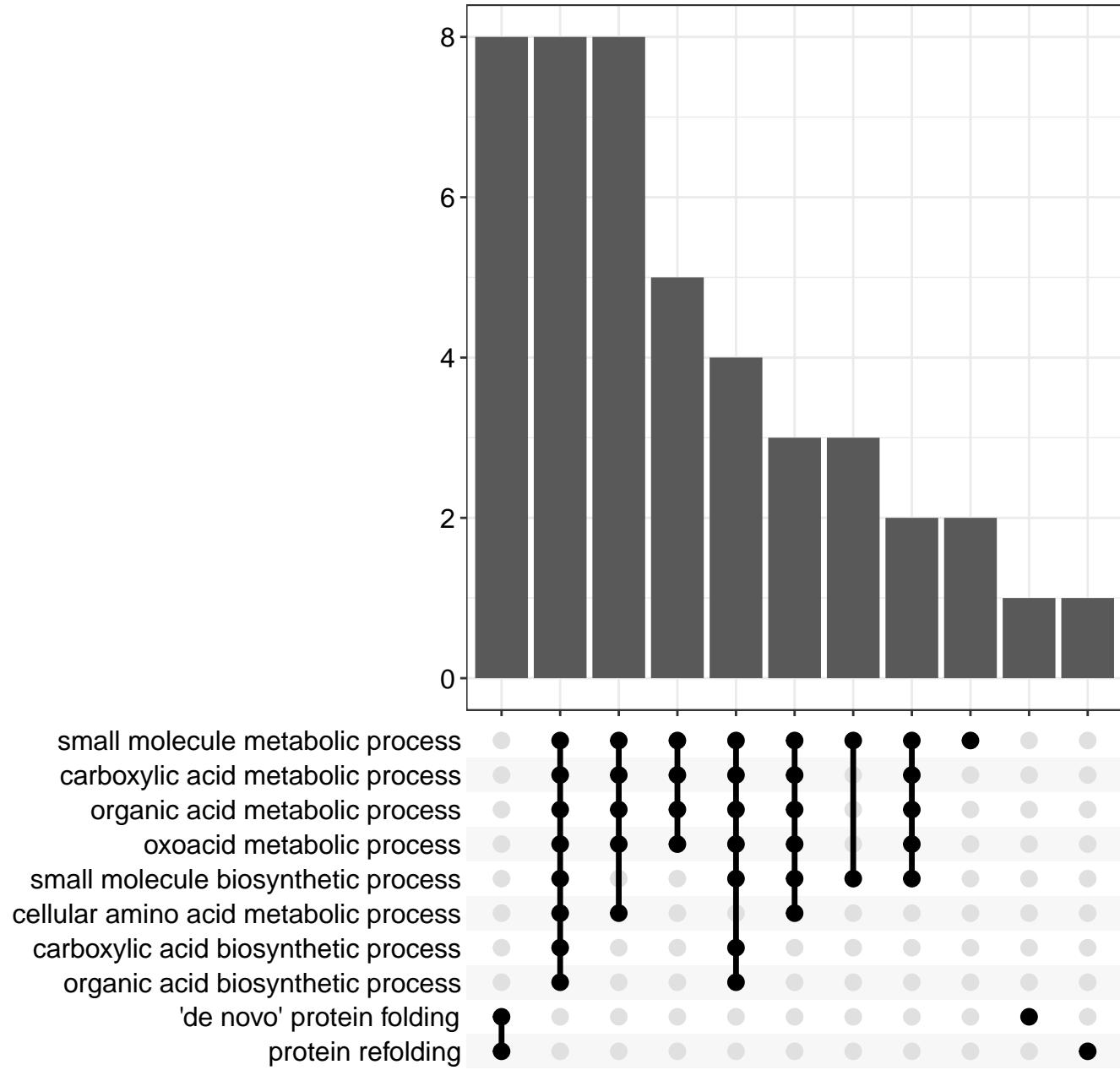


size

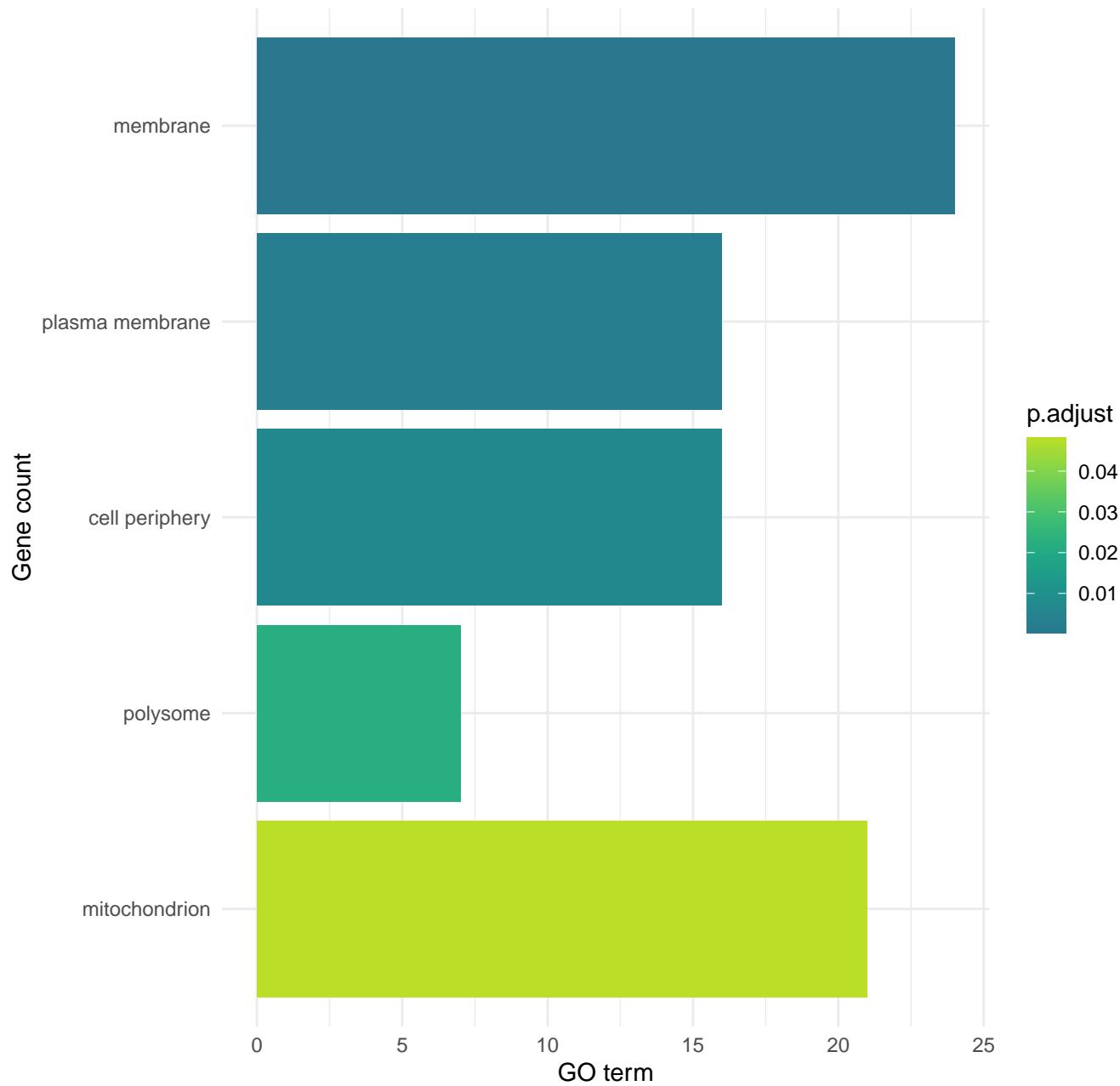




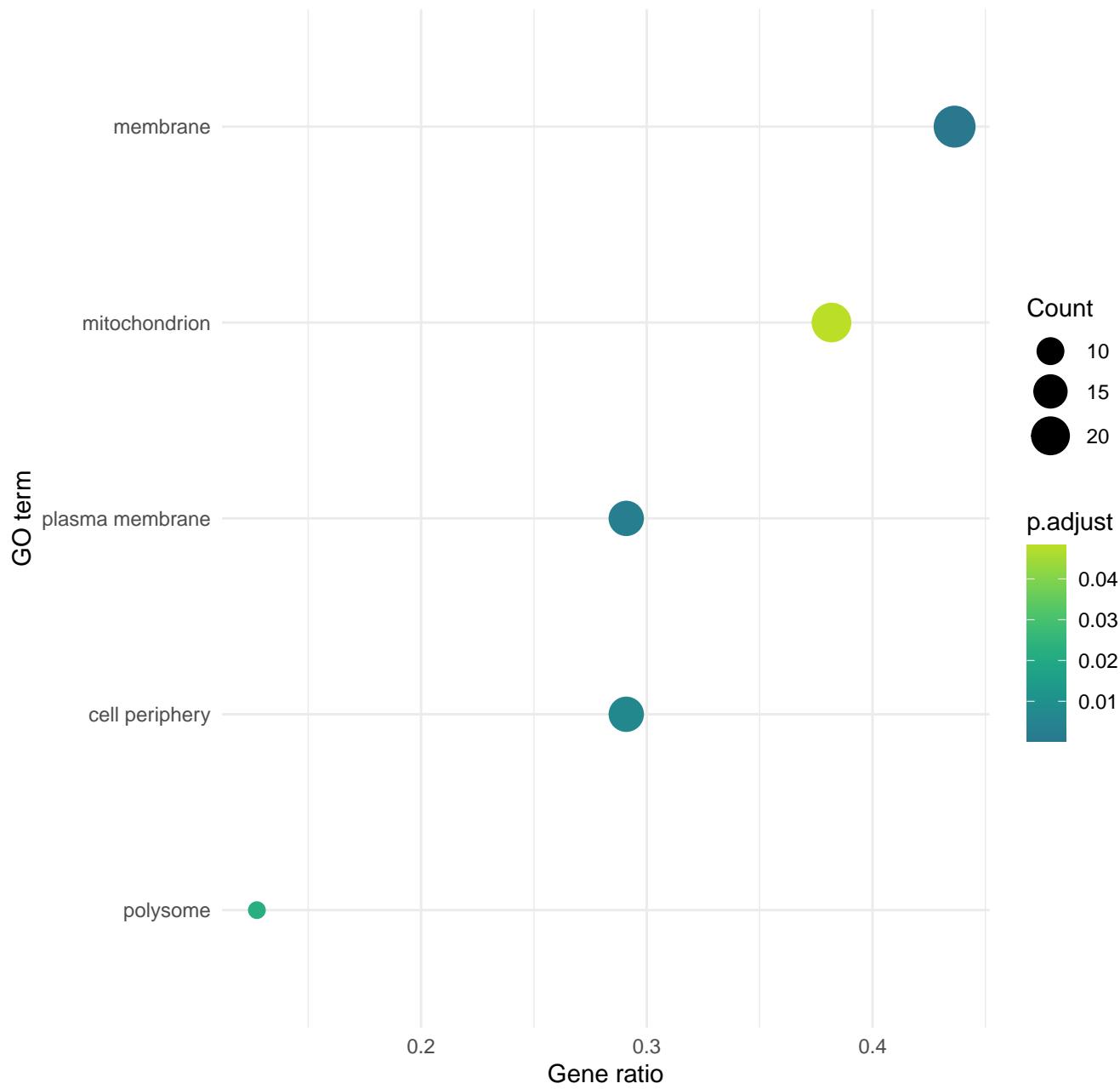
PRP22-TAP Up-regulated GO BP upsetplot



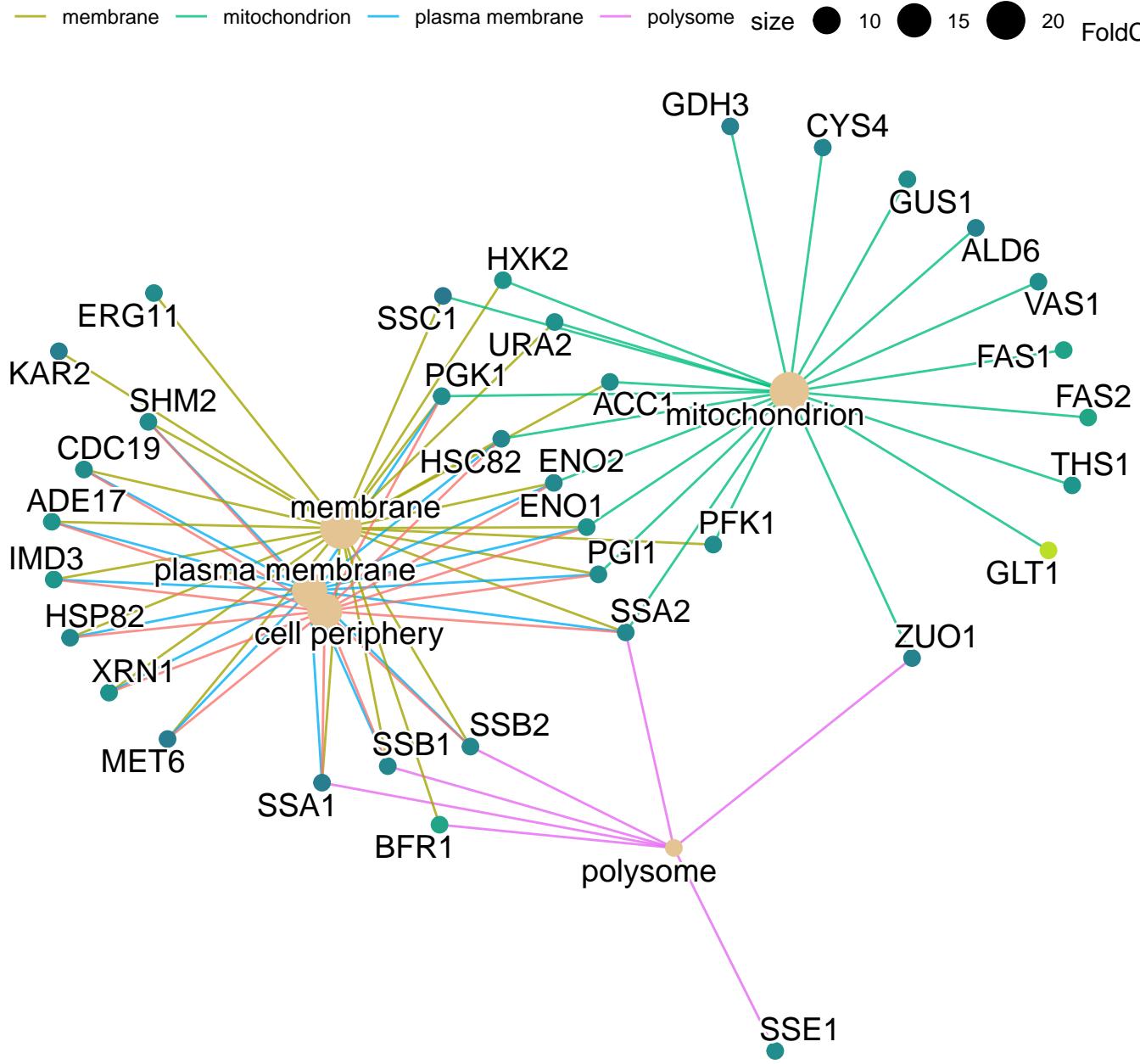
PRP22-TAP Up-regulated GO CC barplot



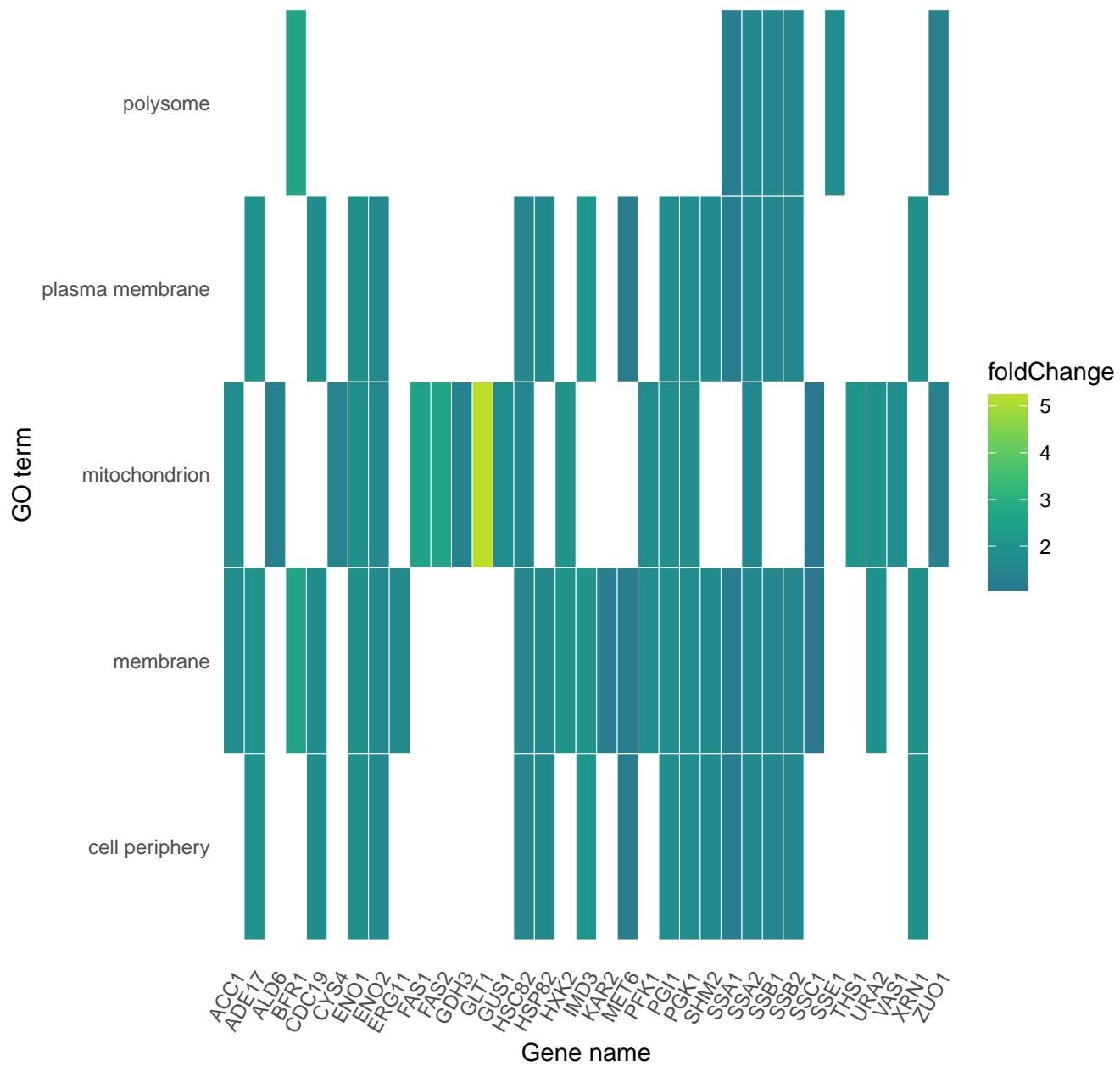
PRP22-TAP Up-regulated GO CC dotplot



PRP22-TAP Up-regulated GO CC cnetplot



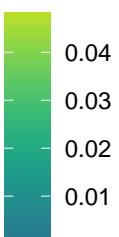
PRP22-TAP Up-regulated GO CC heatplot



PRP22-TAP Up-regulated GO CC emapplot

mitochondrion

FoldChange

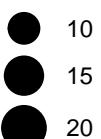


membrane

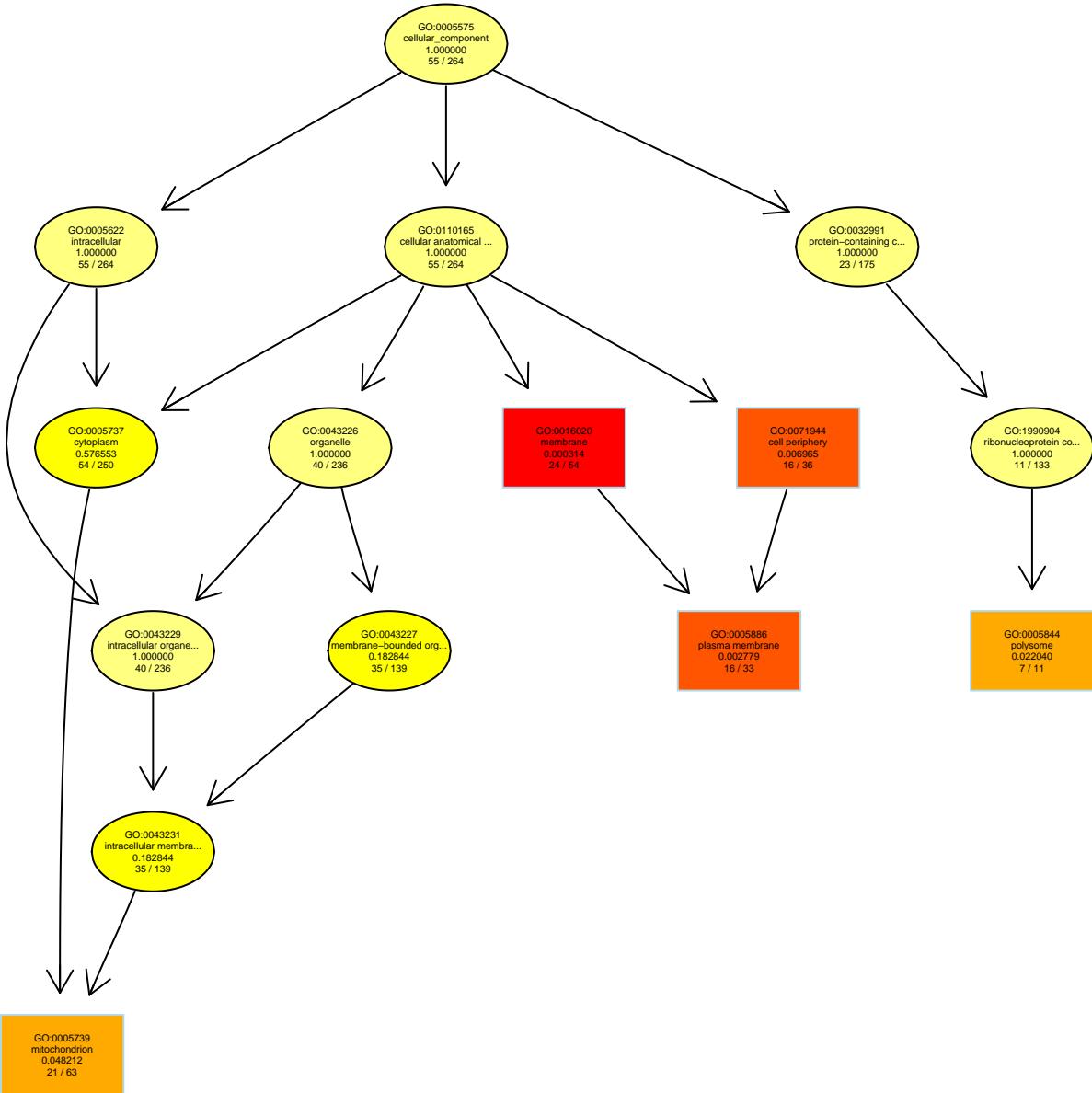
plasma membrane

cell periphery

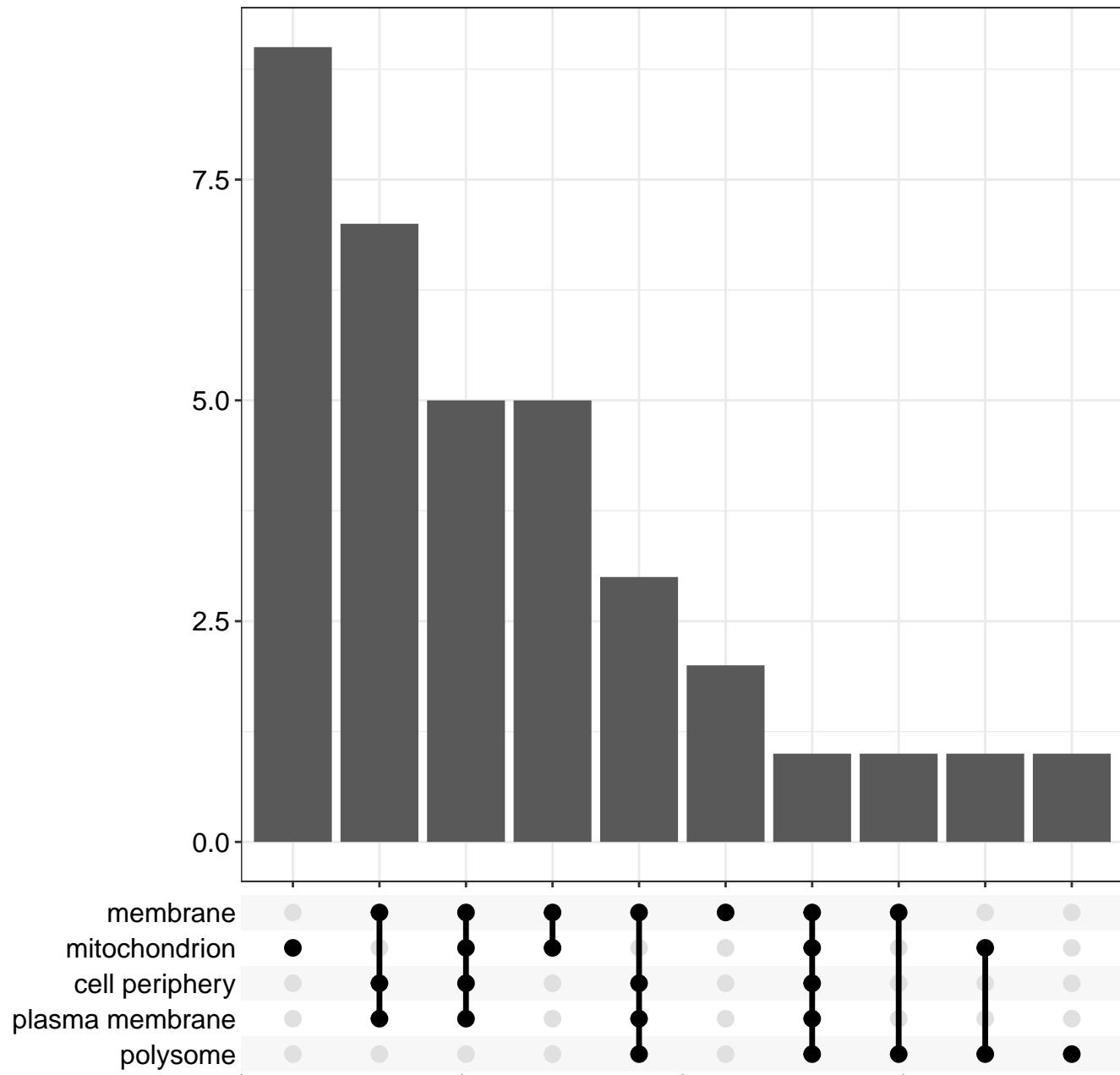
size



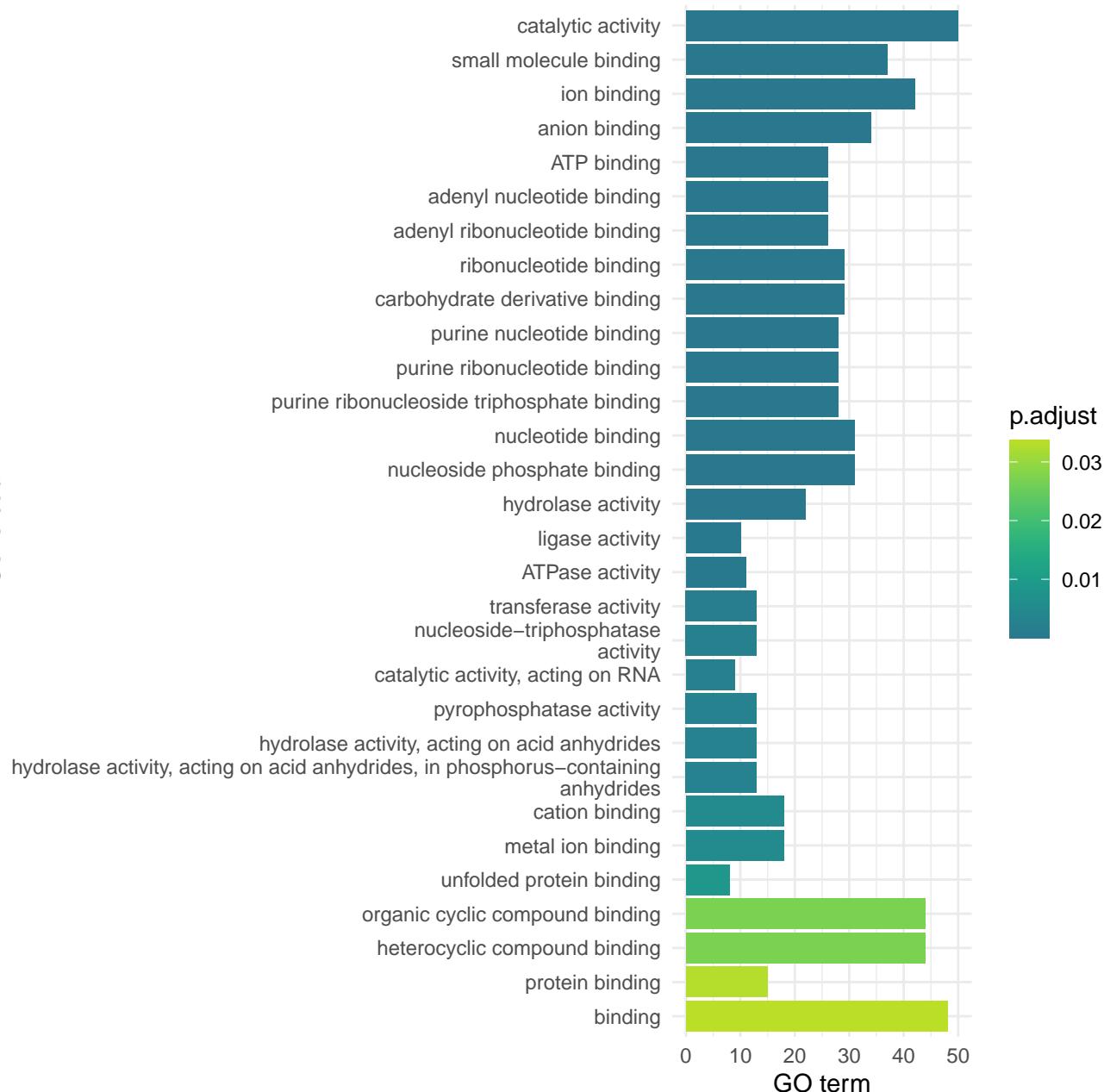
polysome



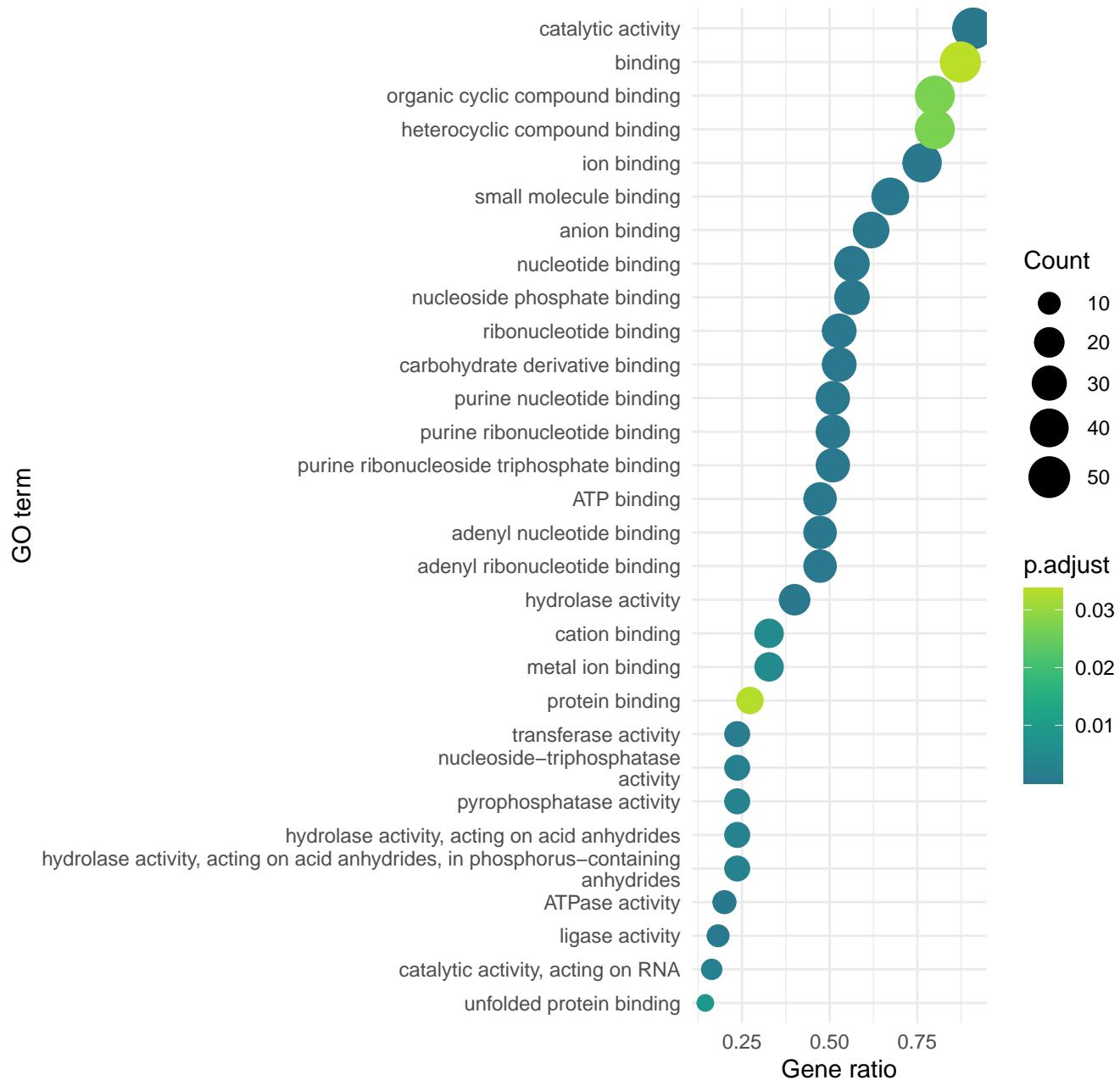
PRP22-TAP Up-regulated GO CC upsetplot



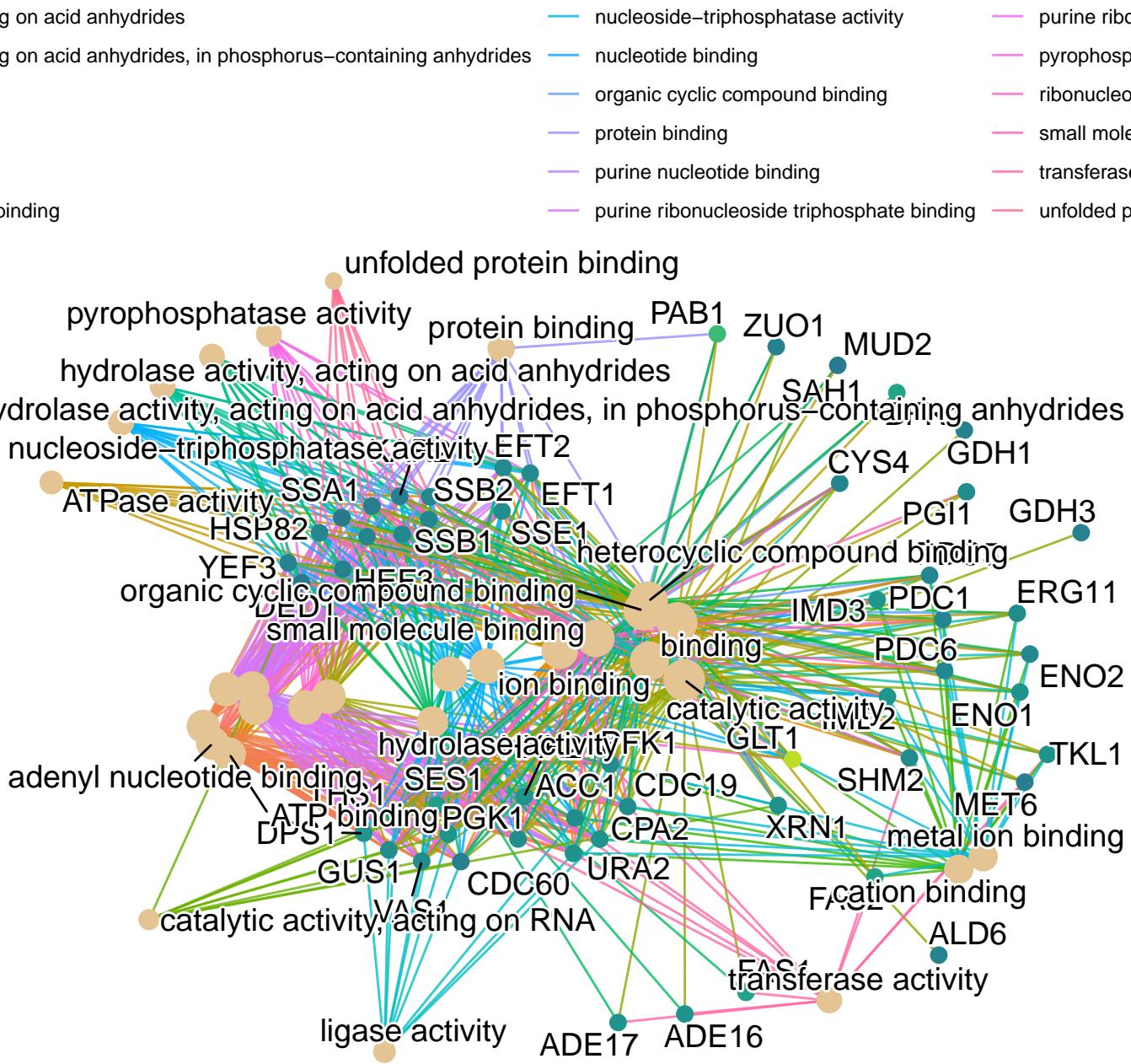
PRP22-TAP Up-regulated GO MF



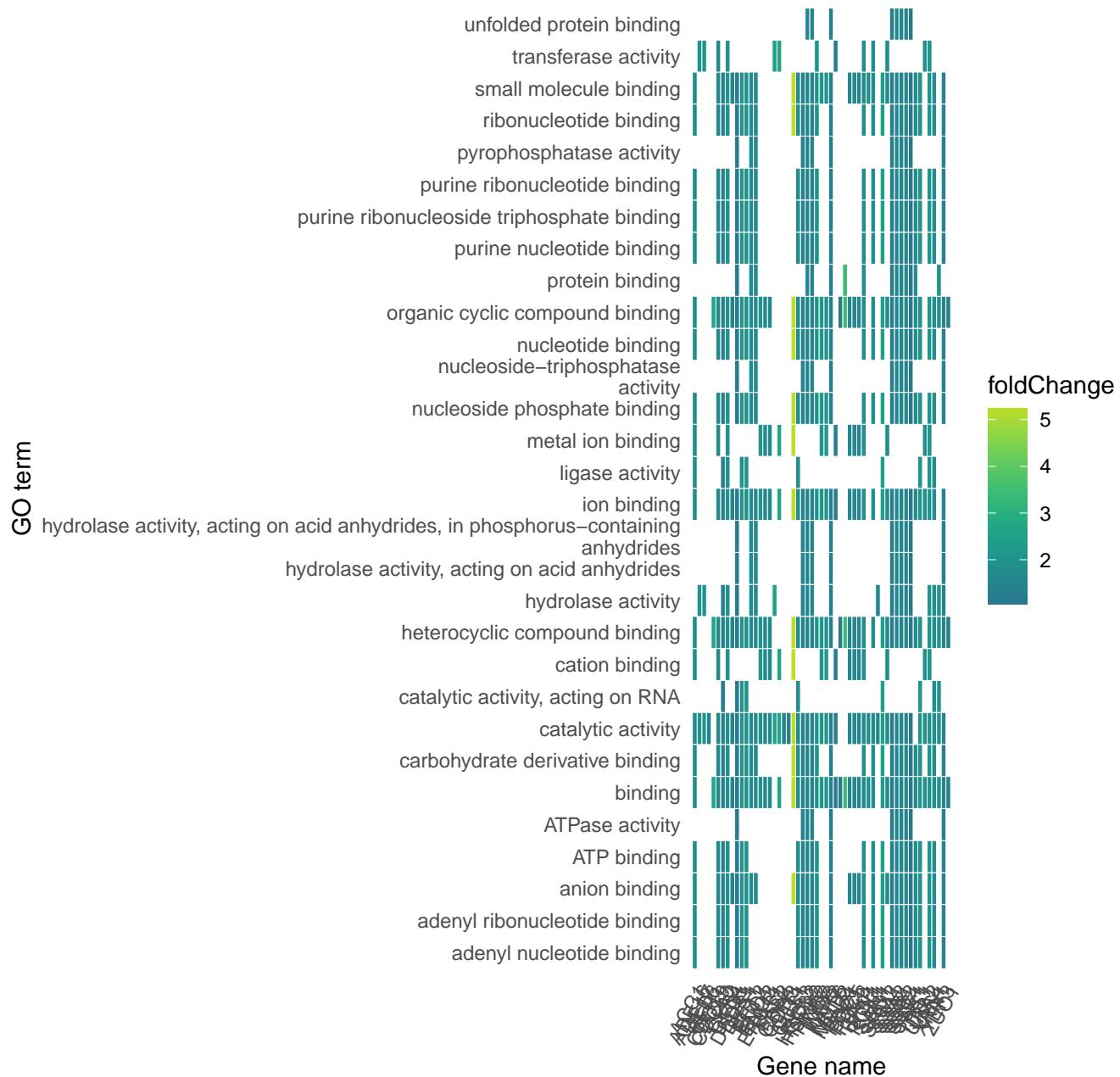
PRP22-TAP Up-regulated GO MF



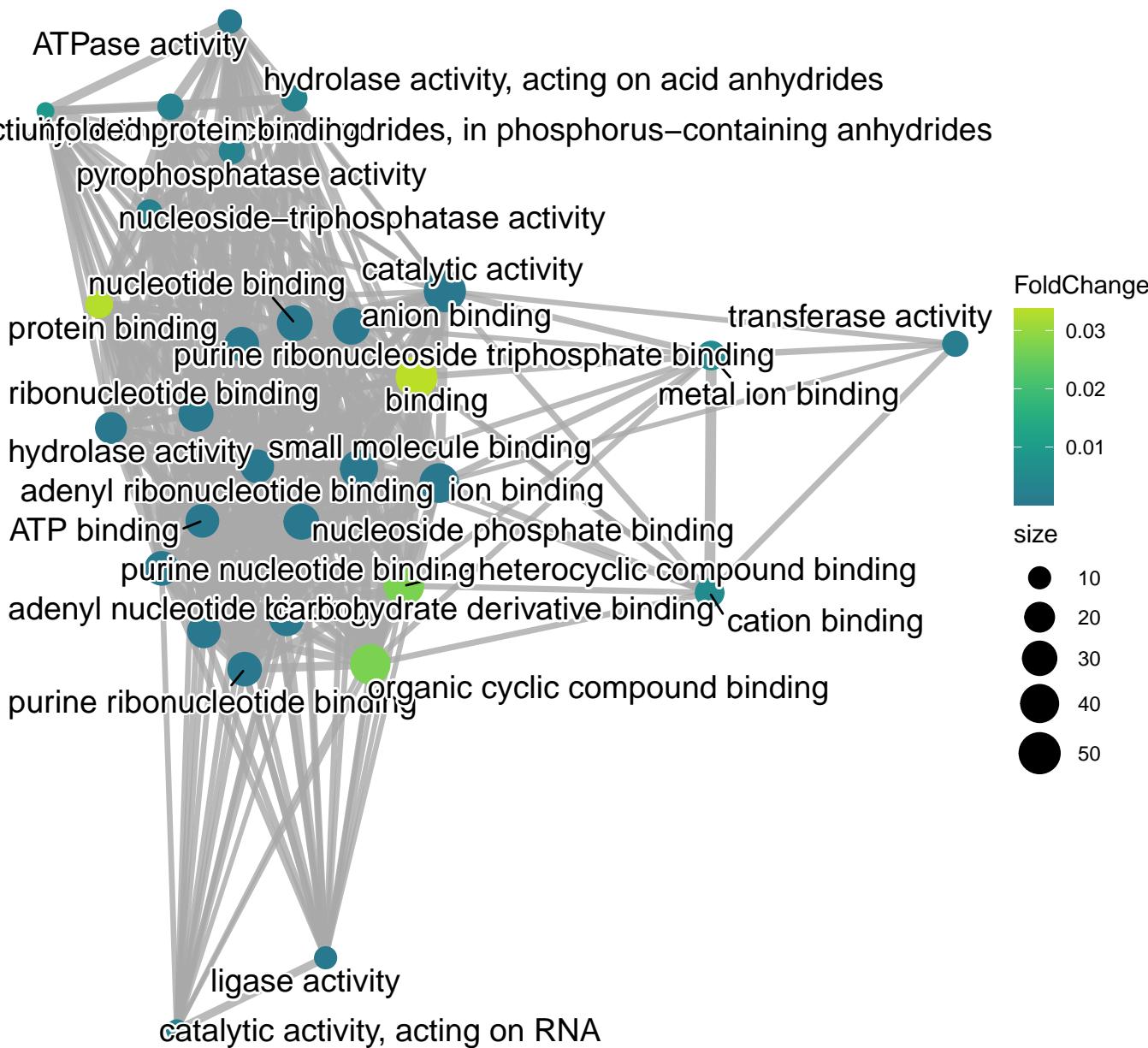
PRP22-TAP Up-regulated GO MF cnetplot

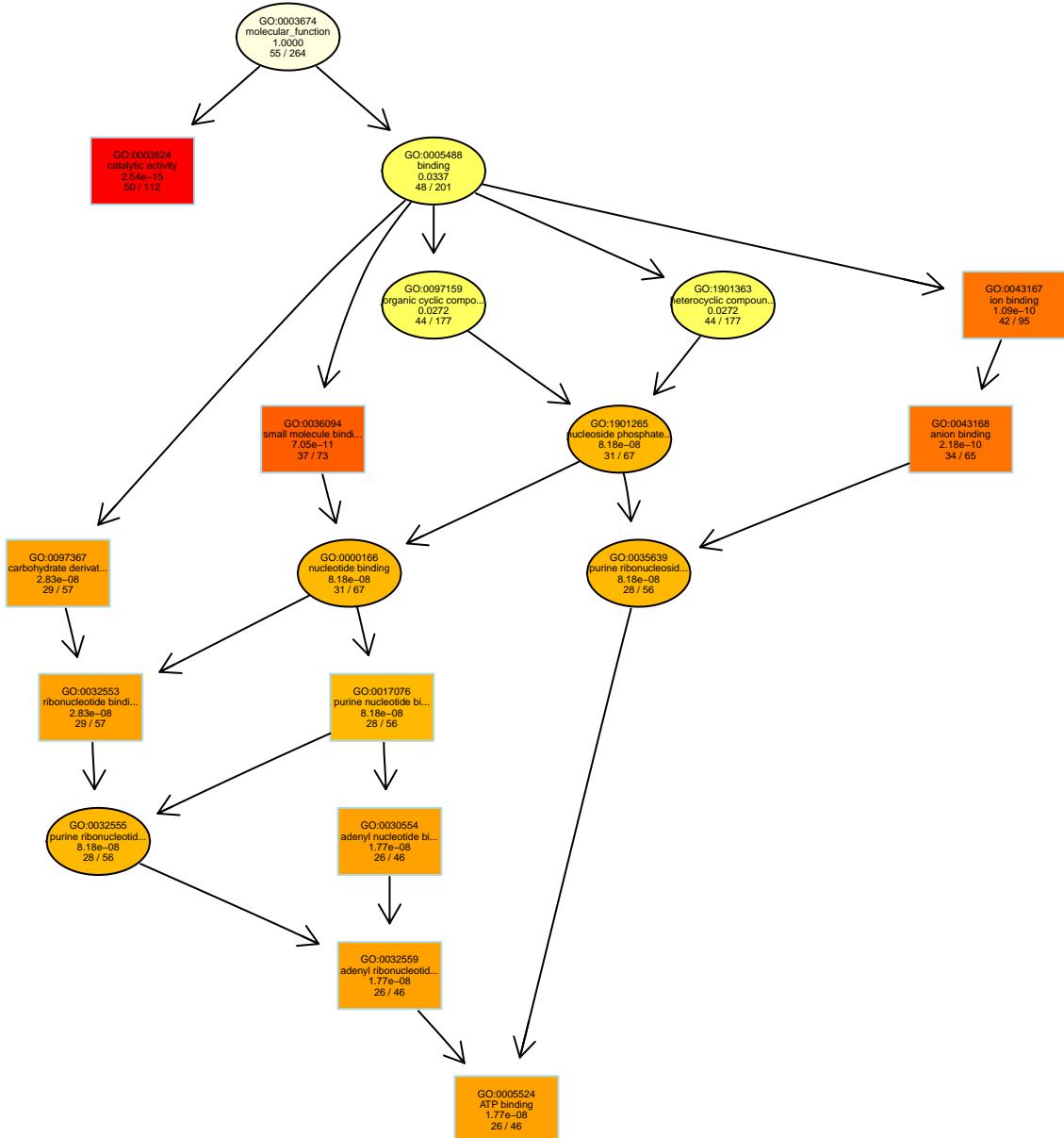


PRP22-TAP Up-regulated GO MF

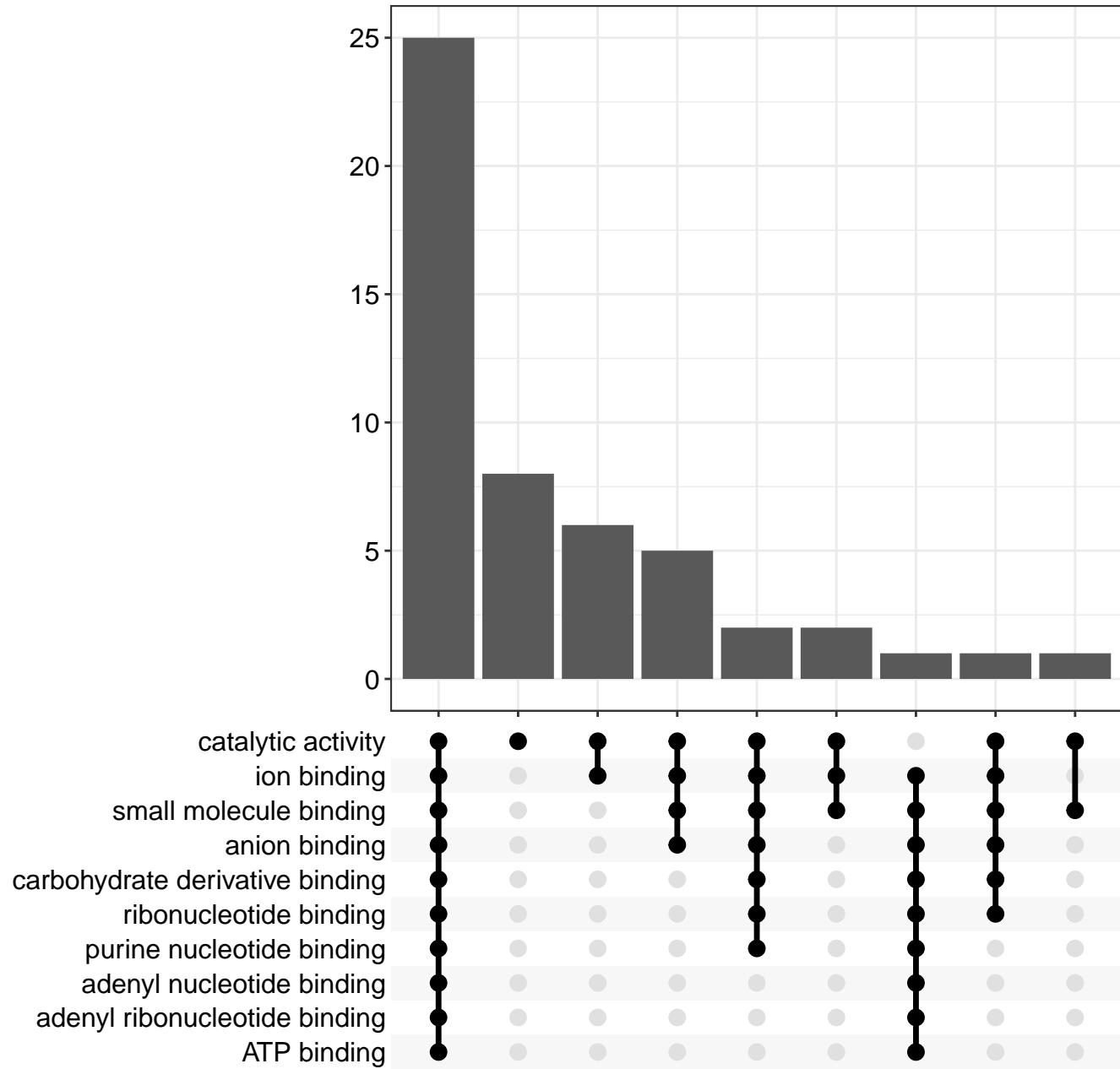


PRP22-TAP Up-regulated GO MF emapplot

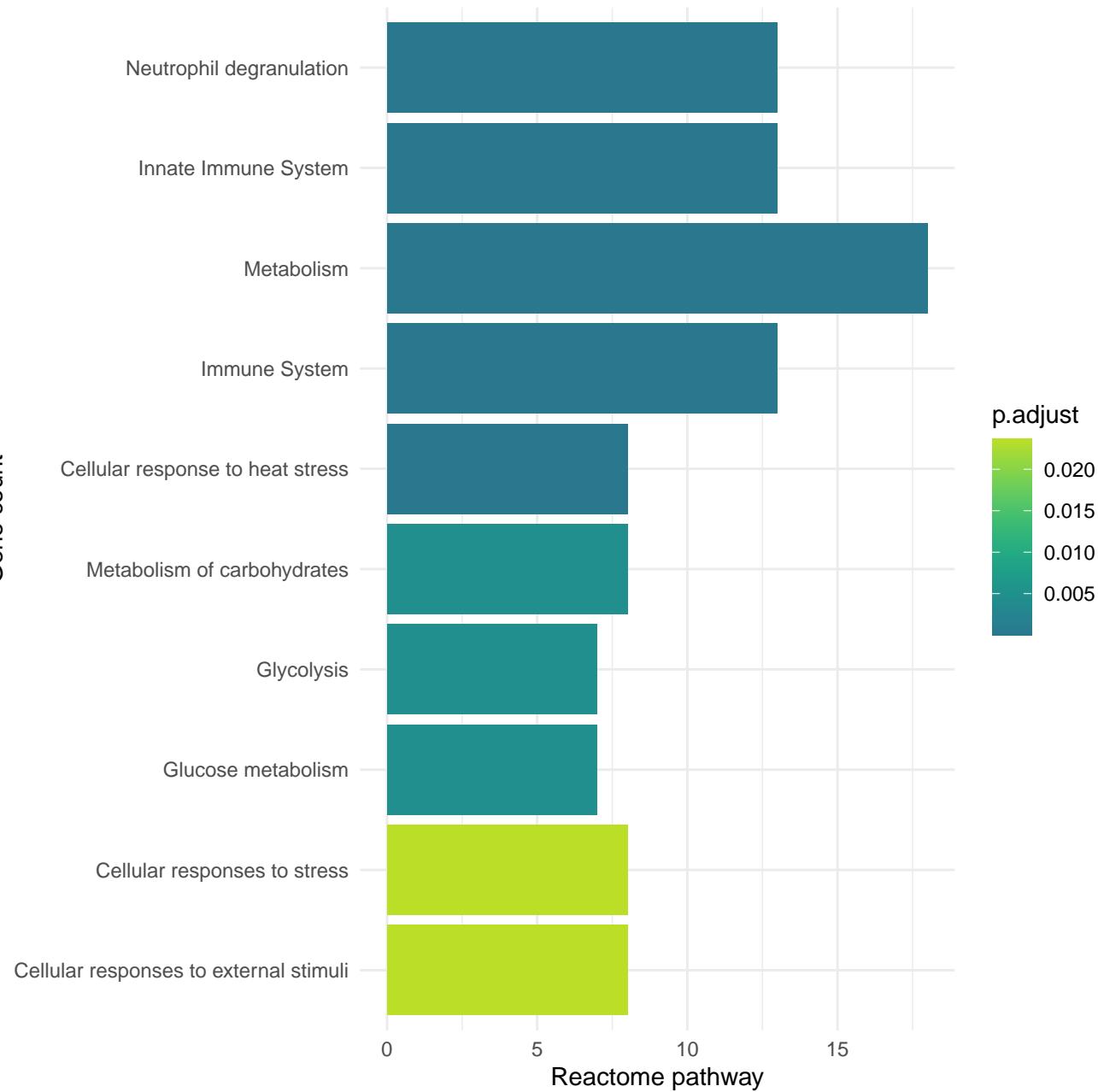




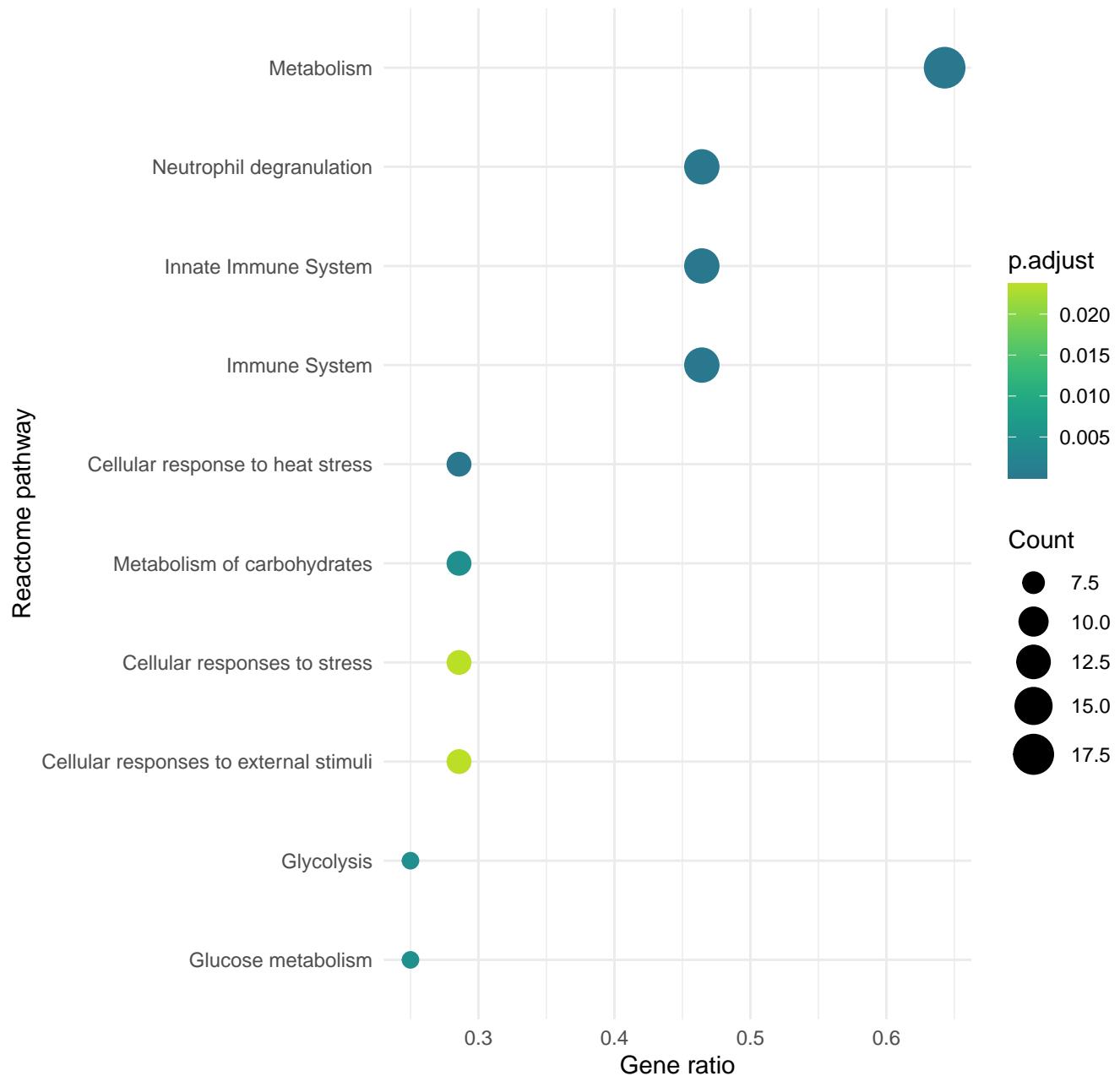
PRP22-TAP Up-regulated GO MF upsetplot



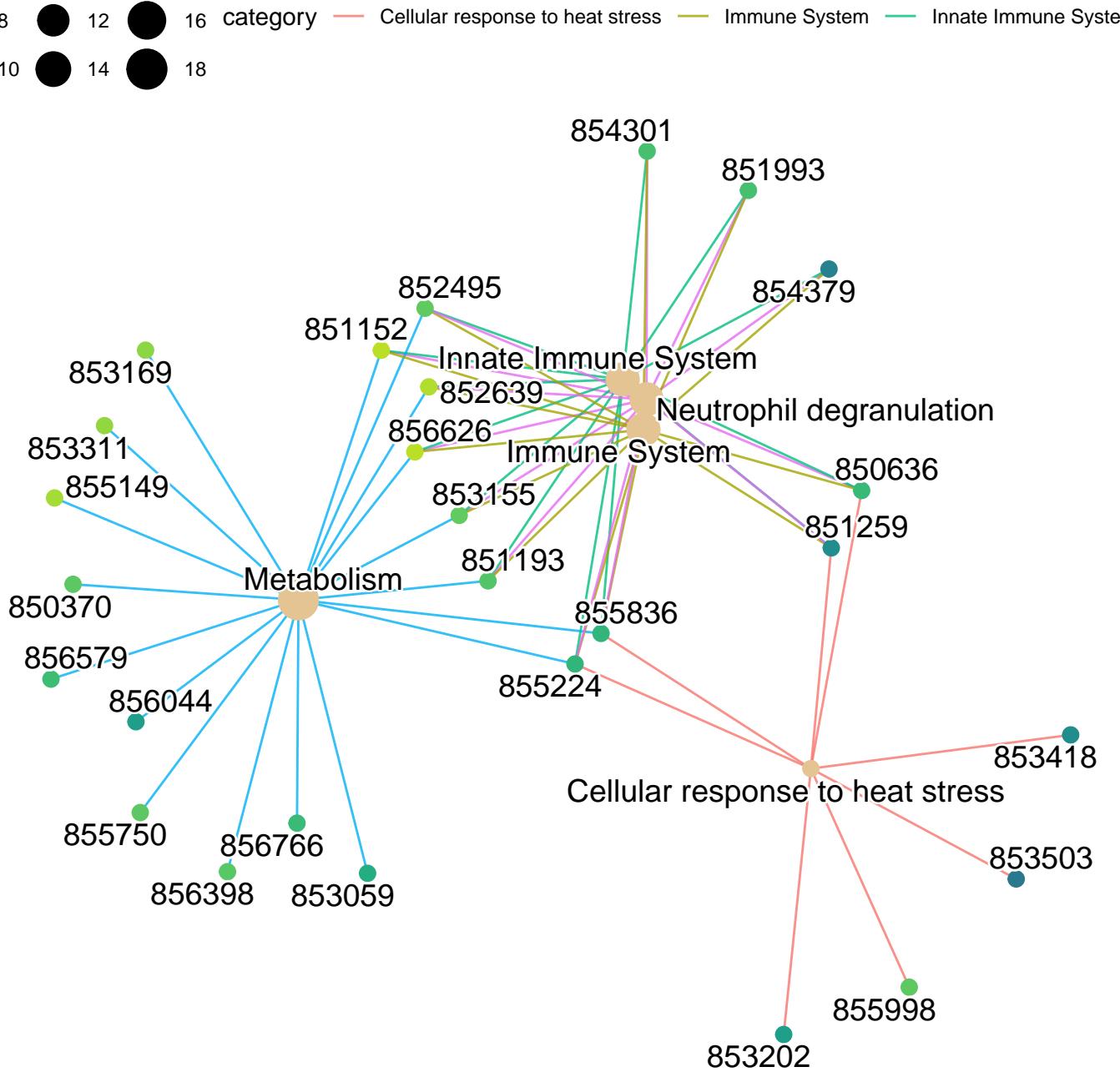
PRP22-TAP Up-regulated Reactome barplot



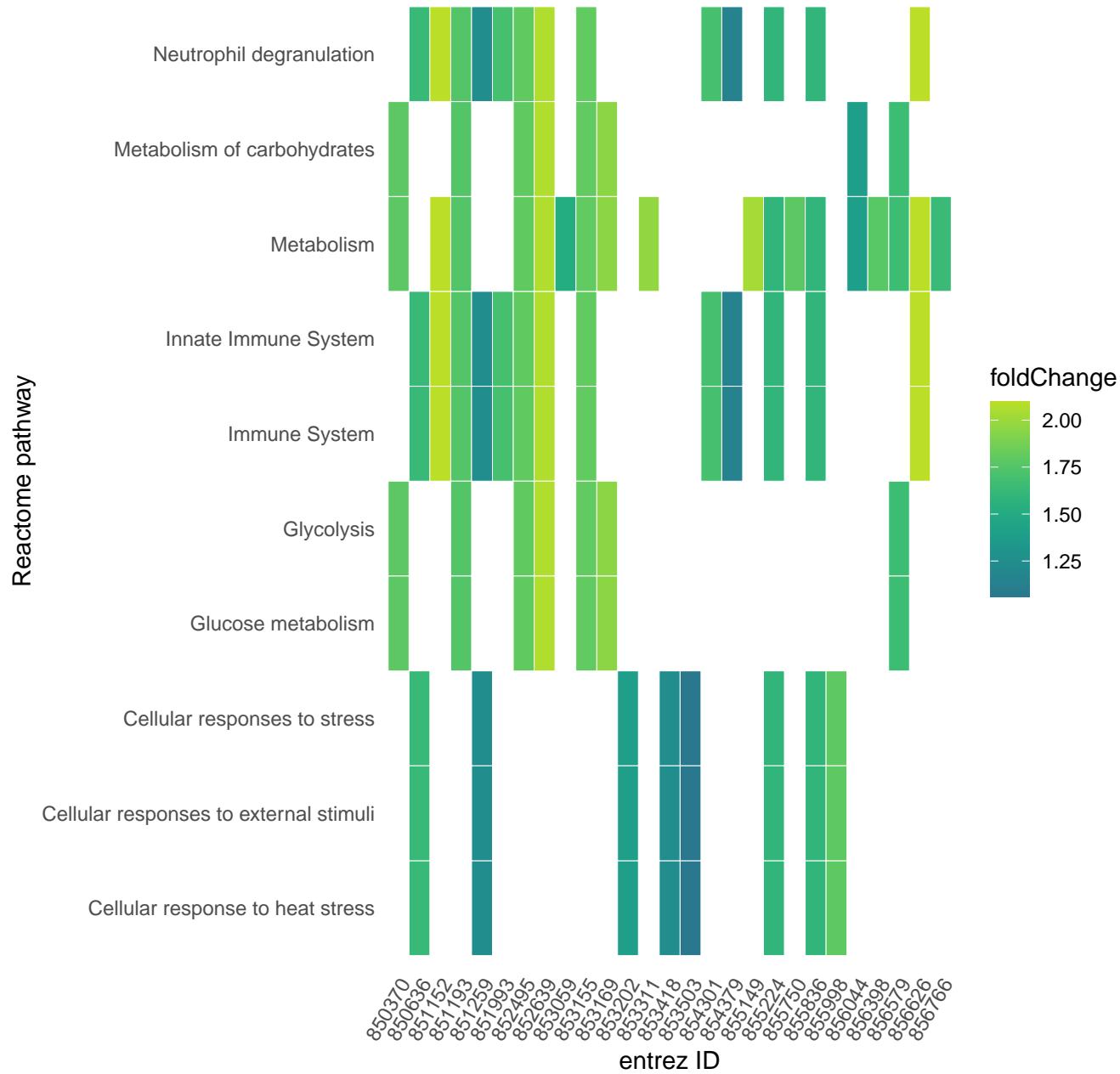
PRP22-TAP Up-regulated Reactome dotplot



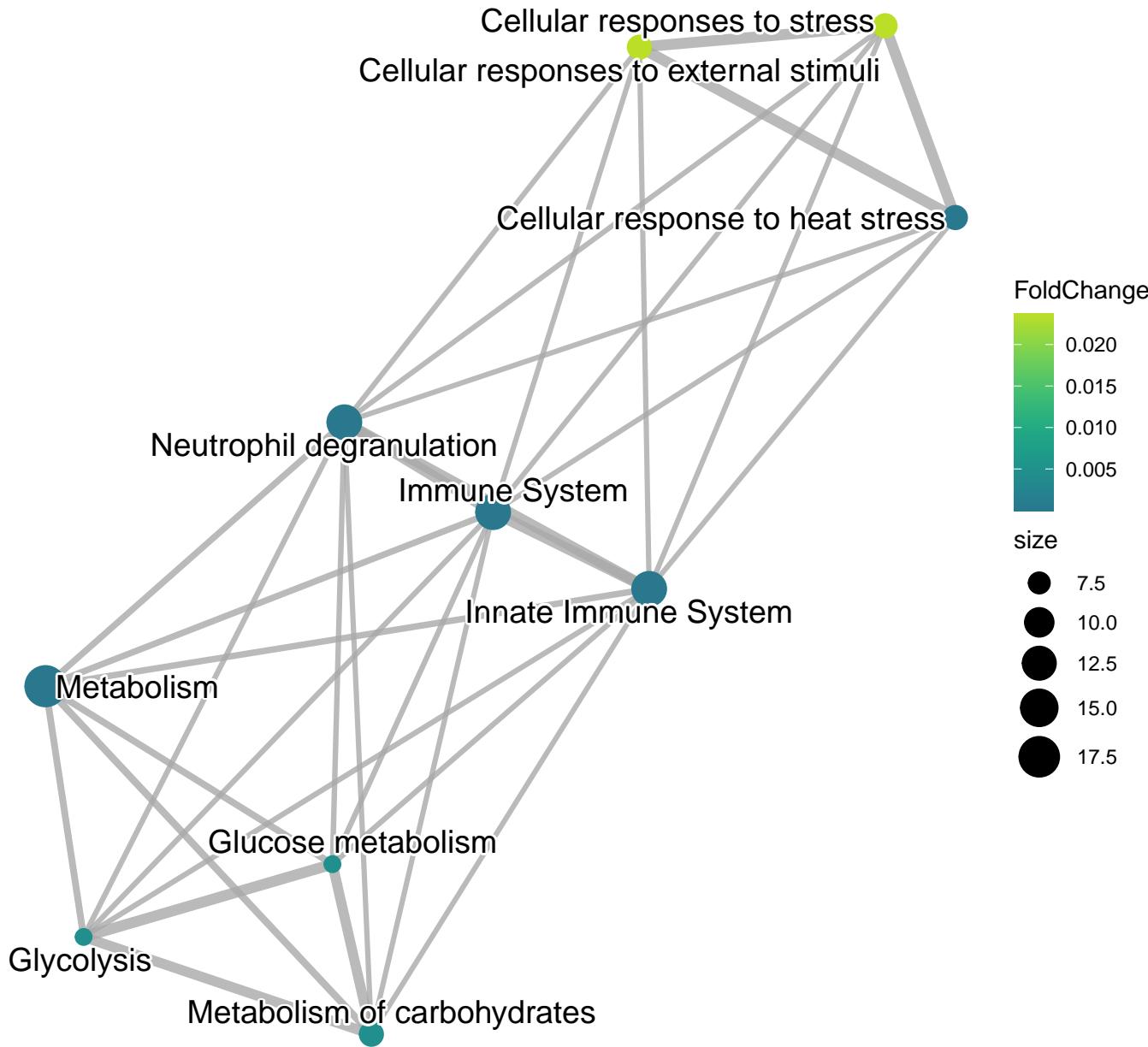
PRP22-TAP Up-regulated Reactome cnetplot



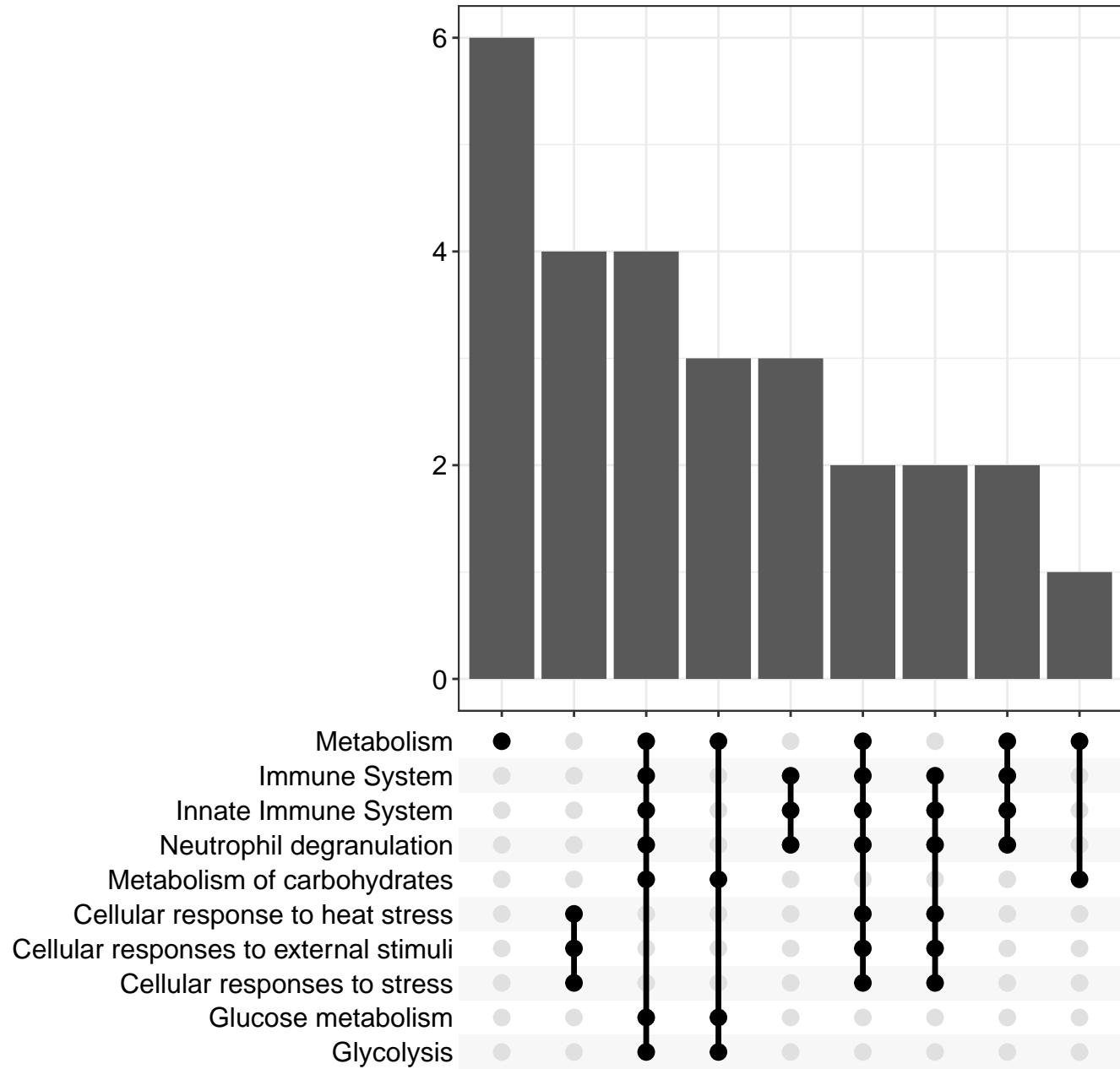
PRP22-TAP Up-regulated Reactome heatplot



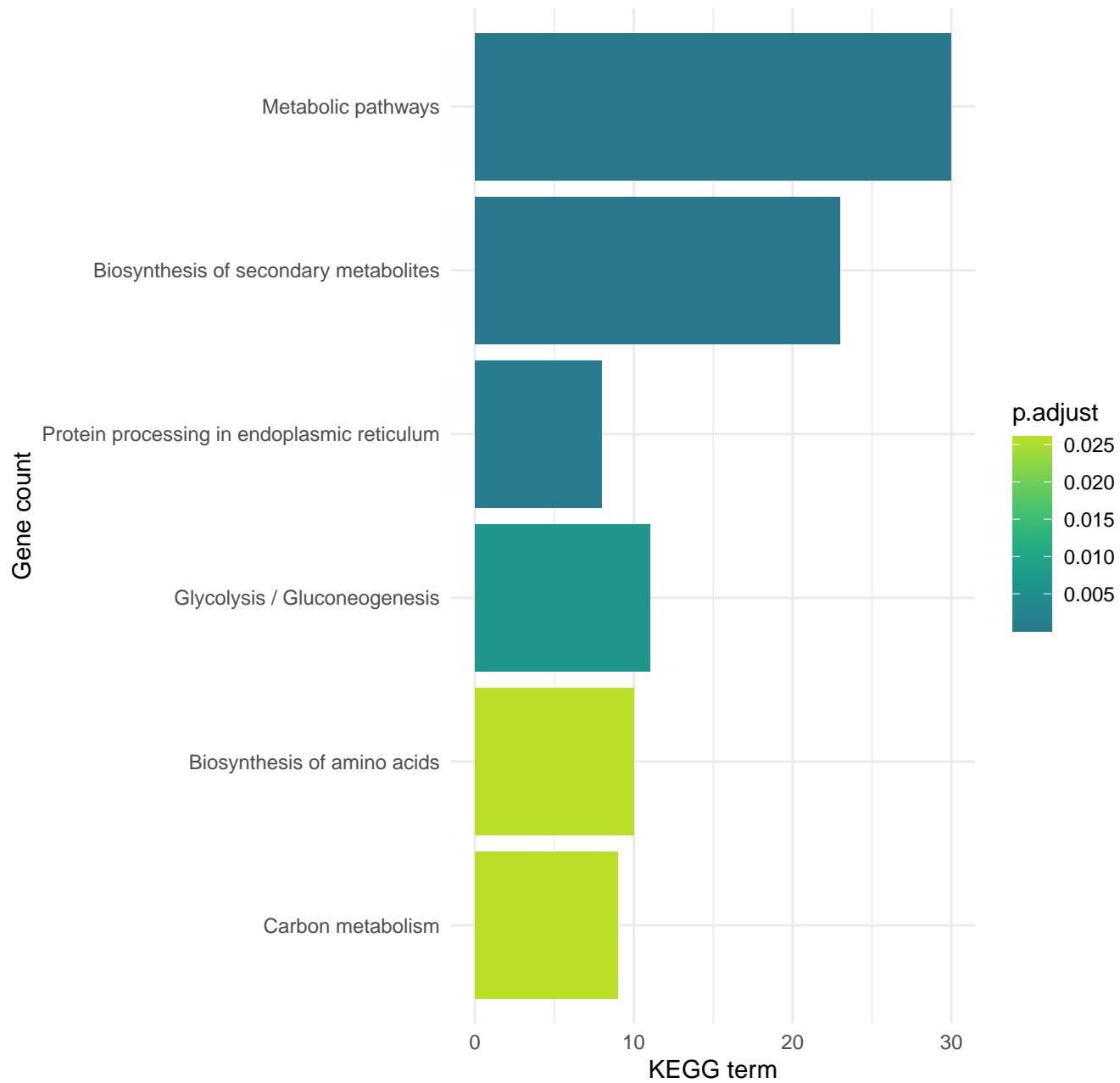
PRP22-TAP Up-regulated Reactome emapplot



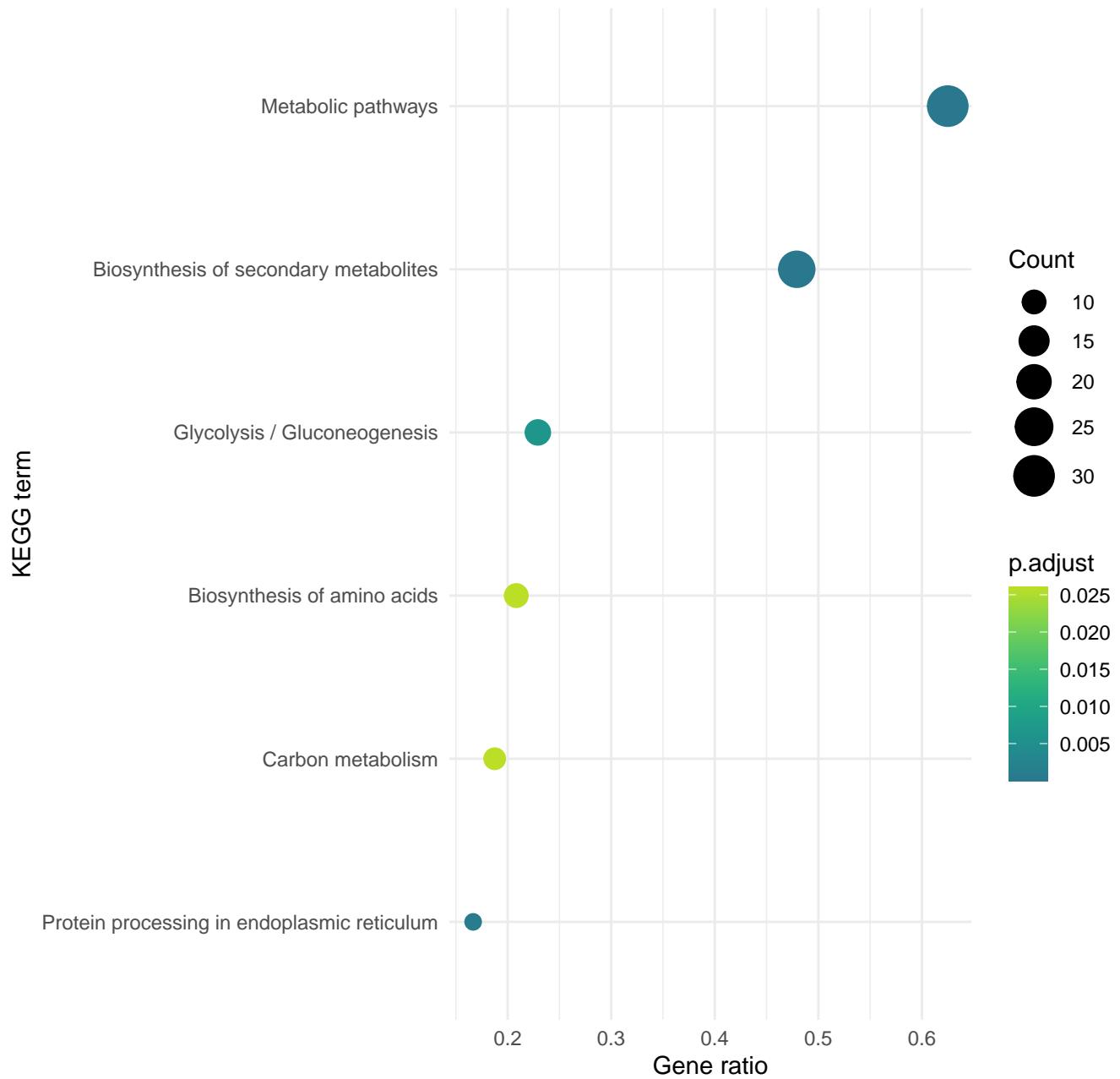
PRP22-TAP Up-regulated Reactome upsetplot



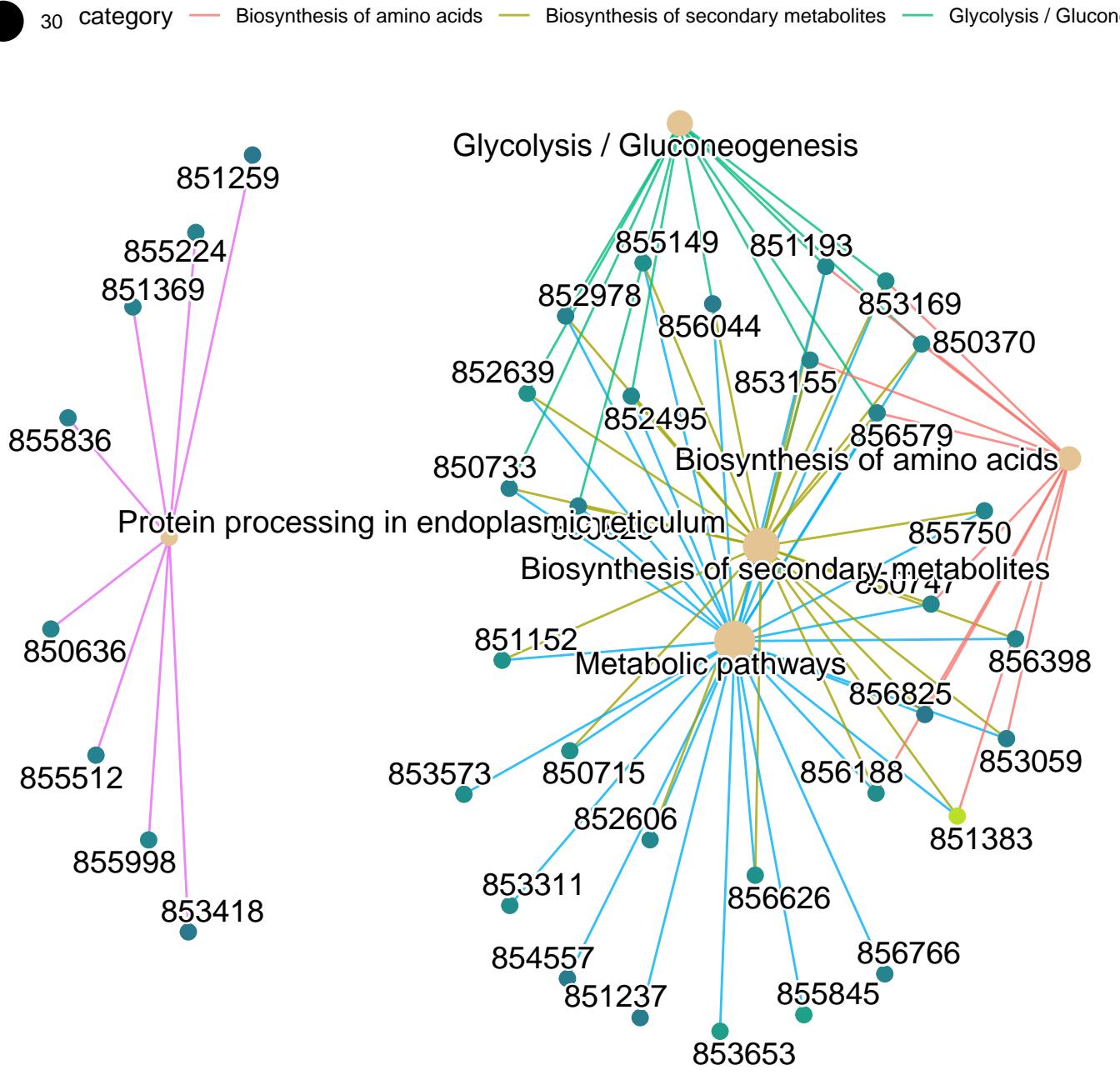
PRP22-TAP Up-regulated KEGG barplot



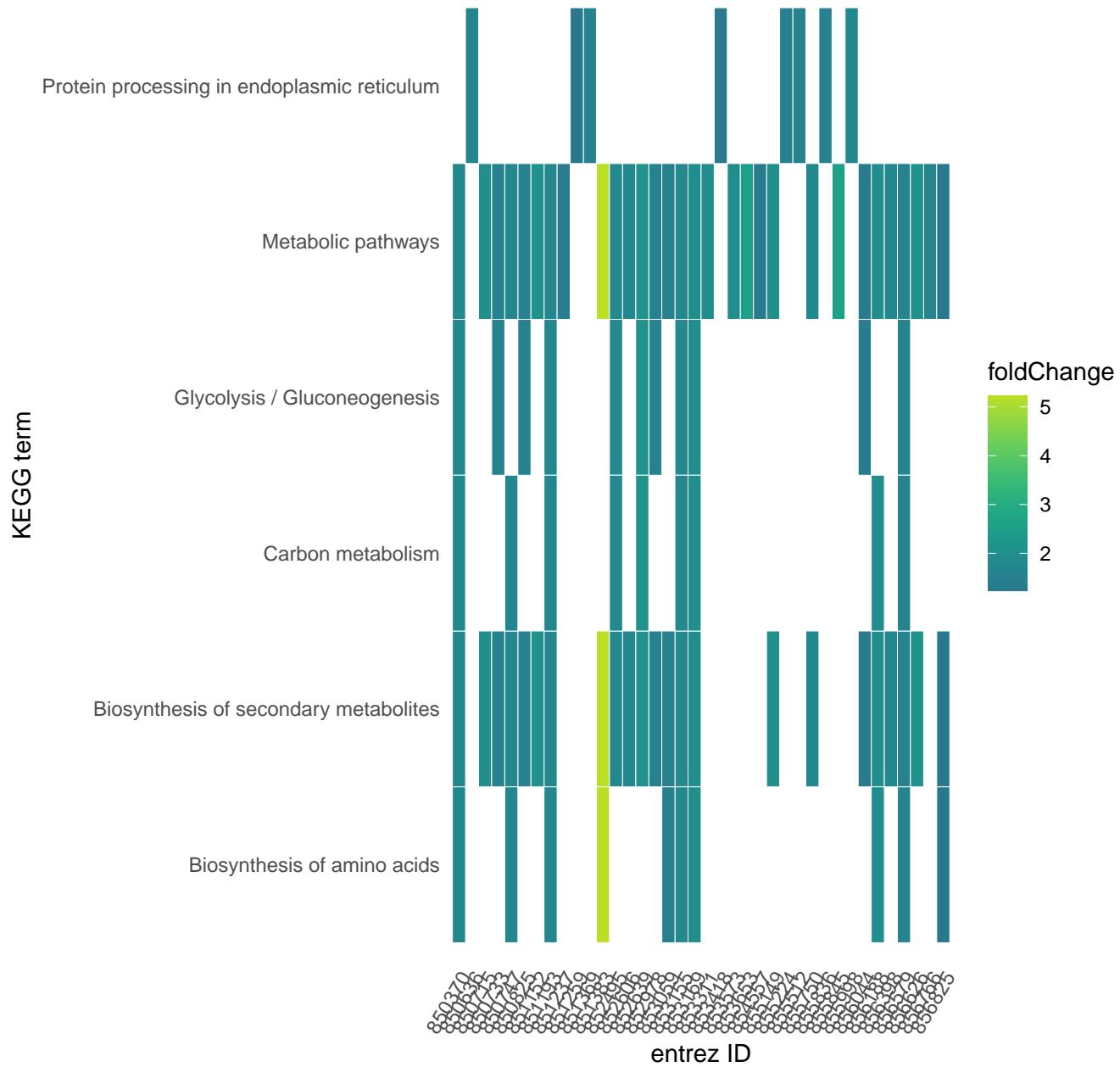
PRP22-TAP Up-regulated KEGG dotplot



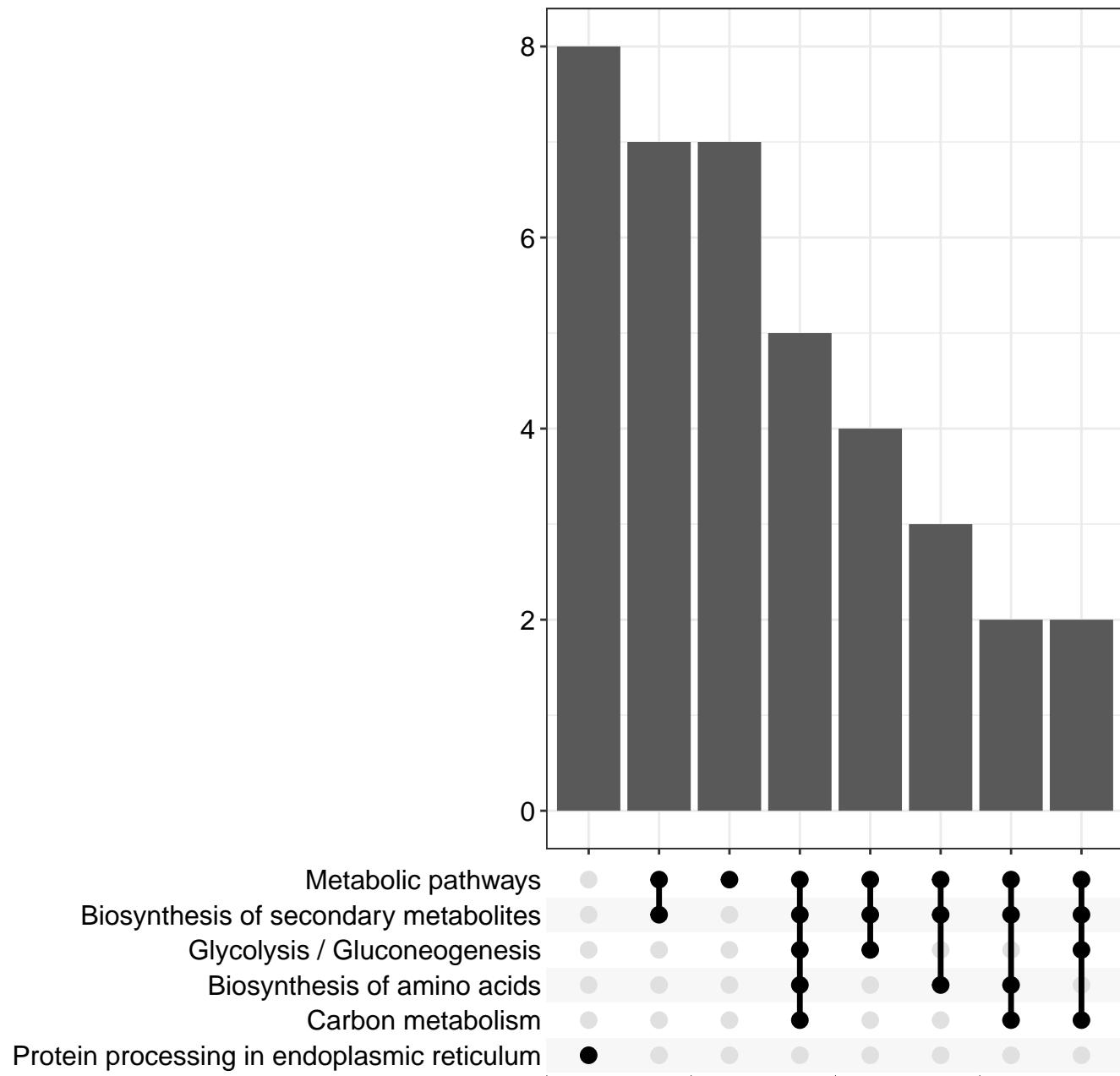
PRP22-TAP Up-regulated KEGG dotplot



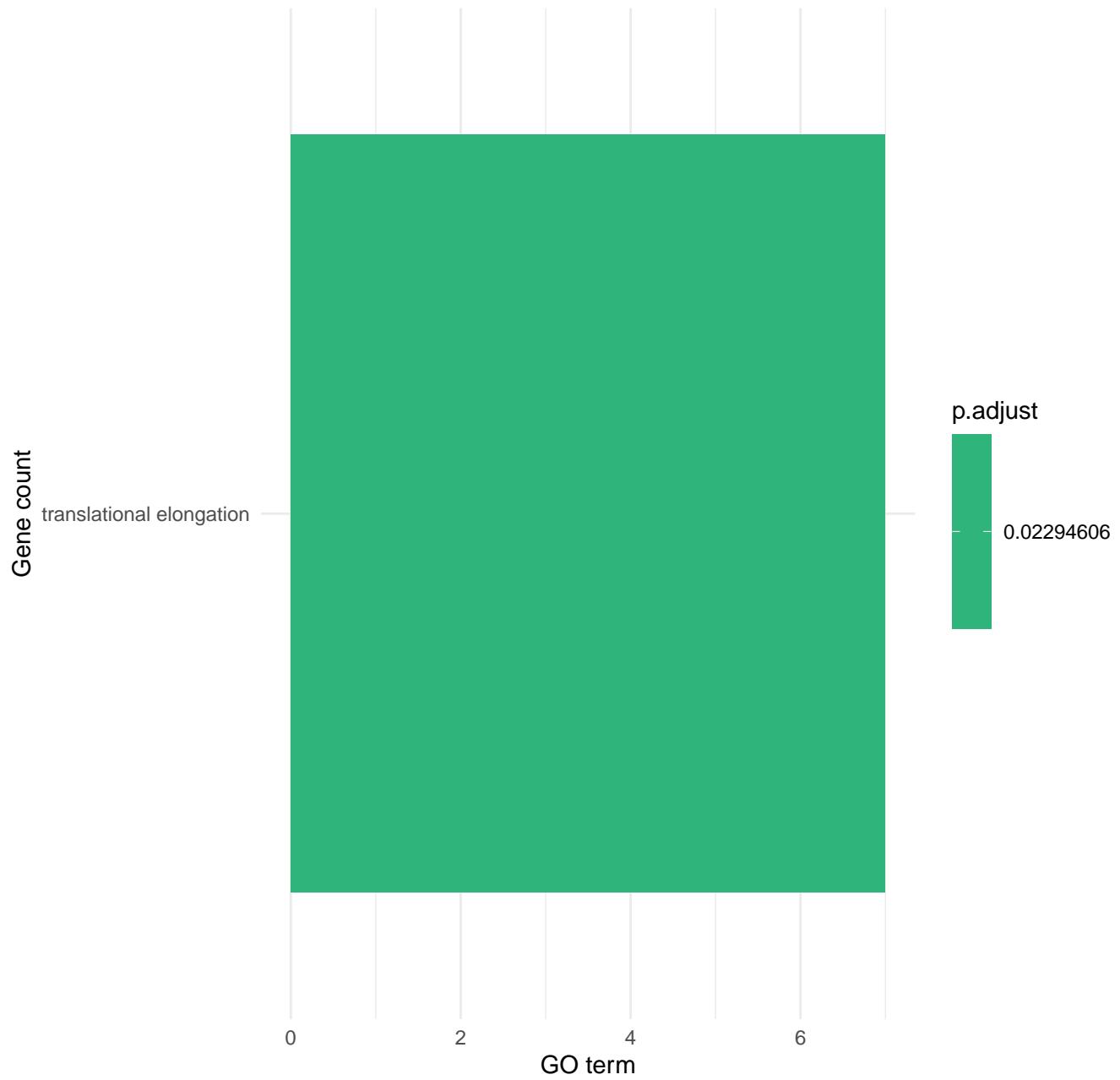
PRP22-TAP Up-regulated KEGG heatplot



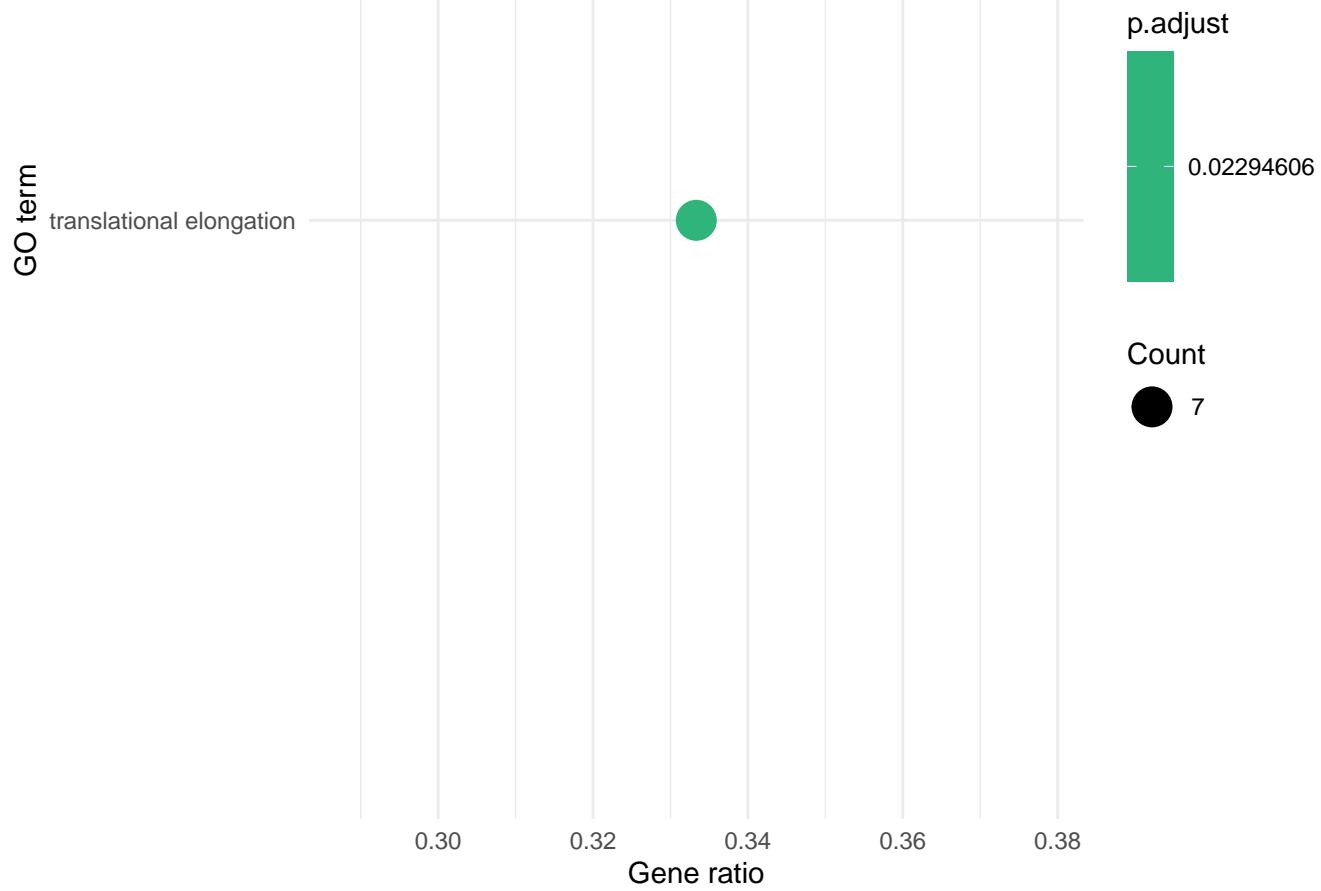
PRP22-TAP Up-regulated KEGG upsetplot



DBP2-TAP Up-regulated GO BP barplot



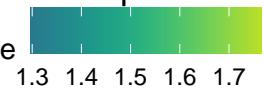
DBP2-TAP Up-regulated GO BP dotplot



DBP2-TAP Up-regulated GO BP cnetplot

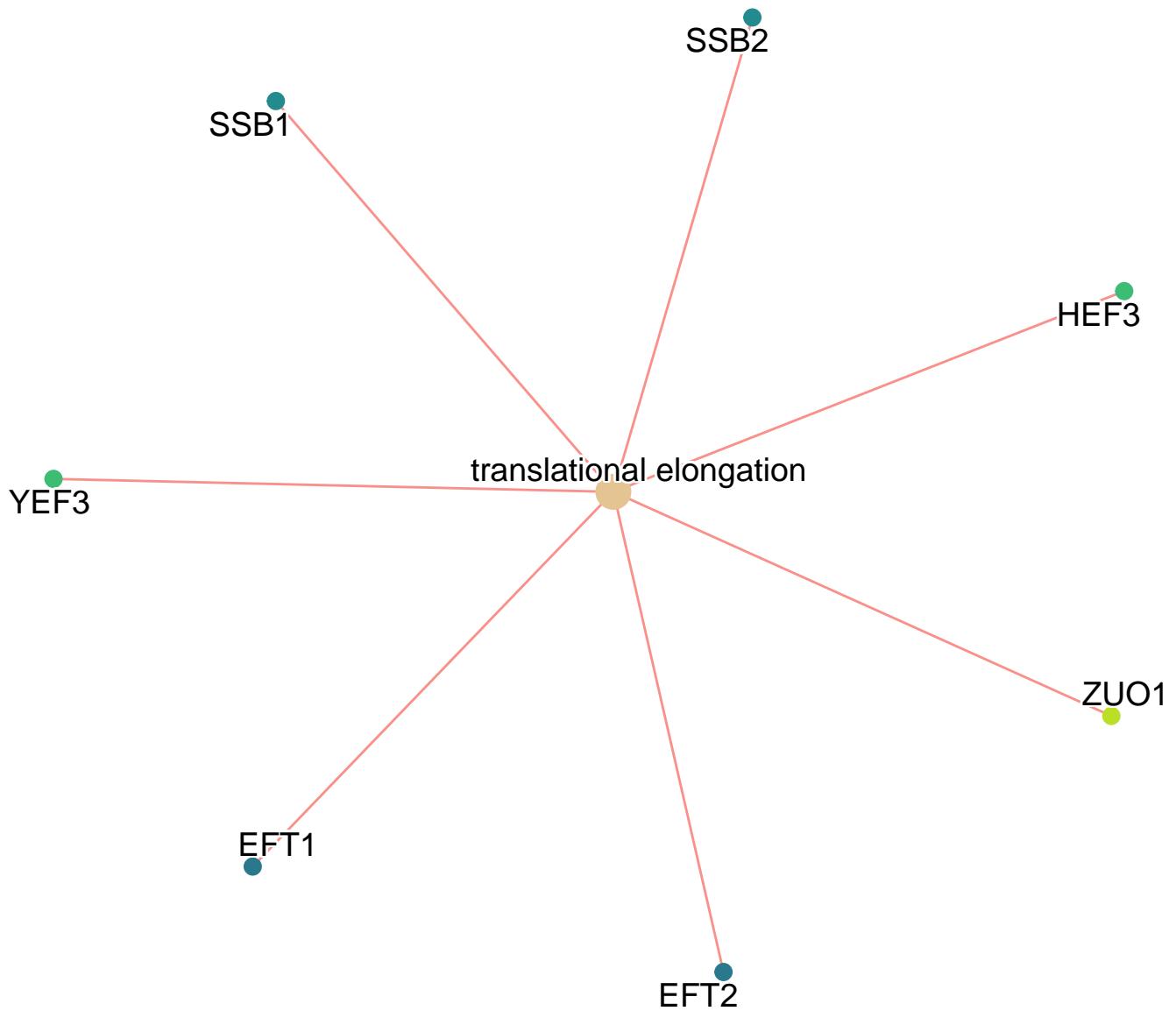
size
7

FoldChange

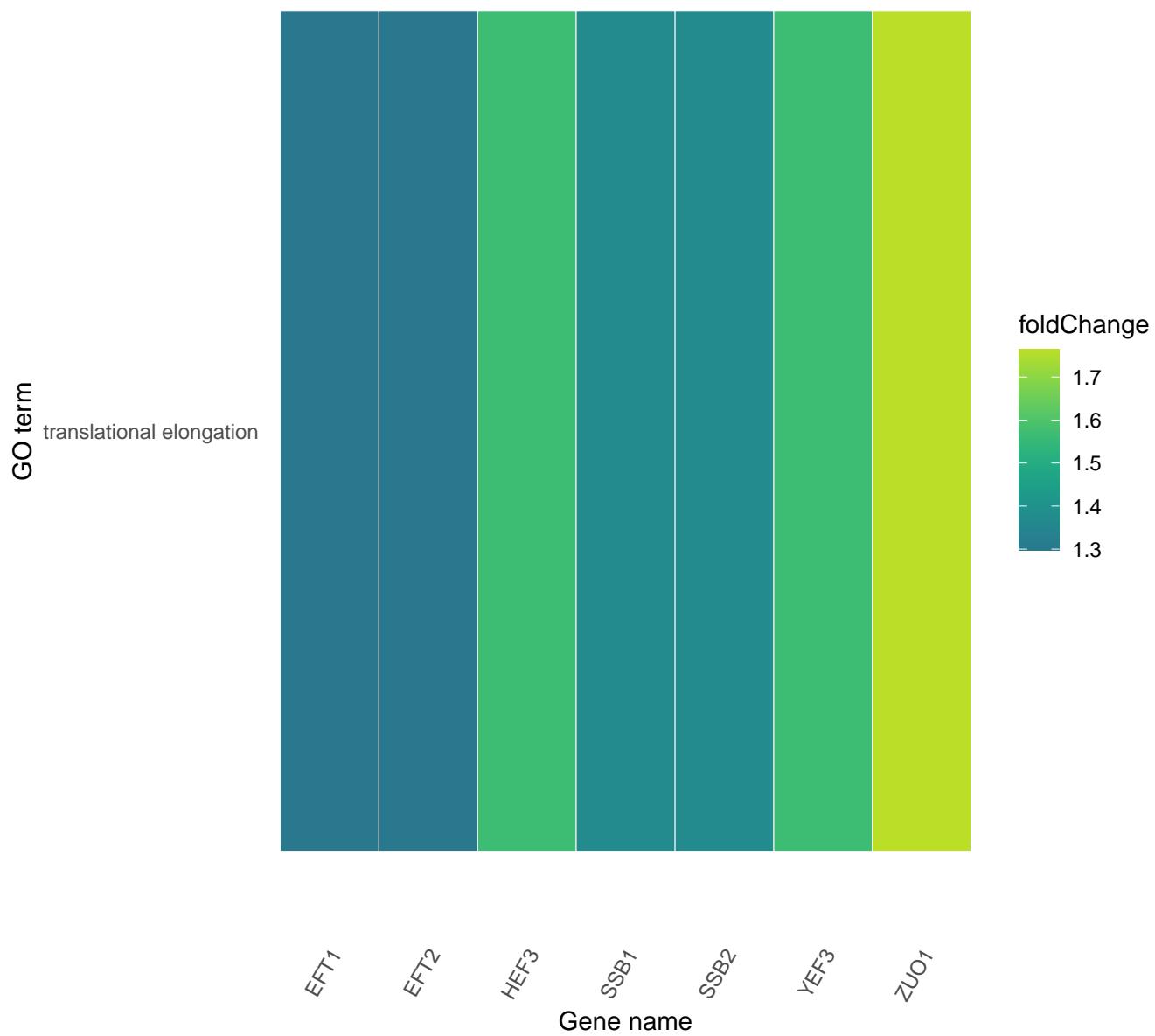


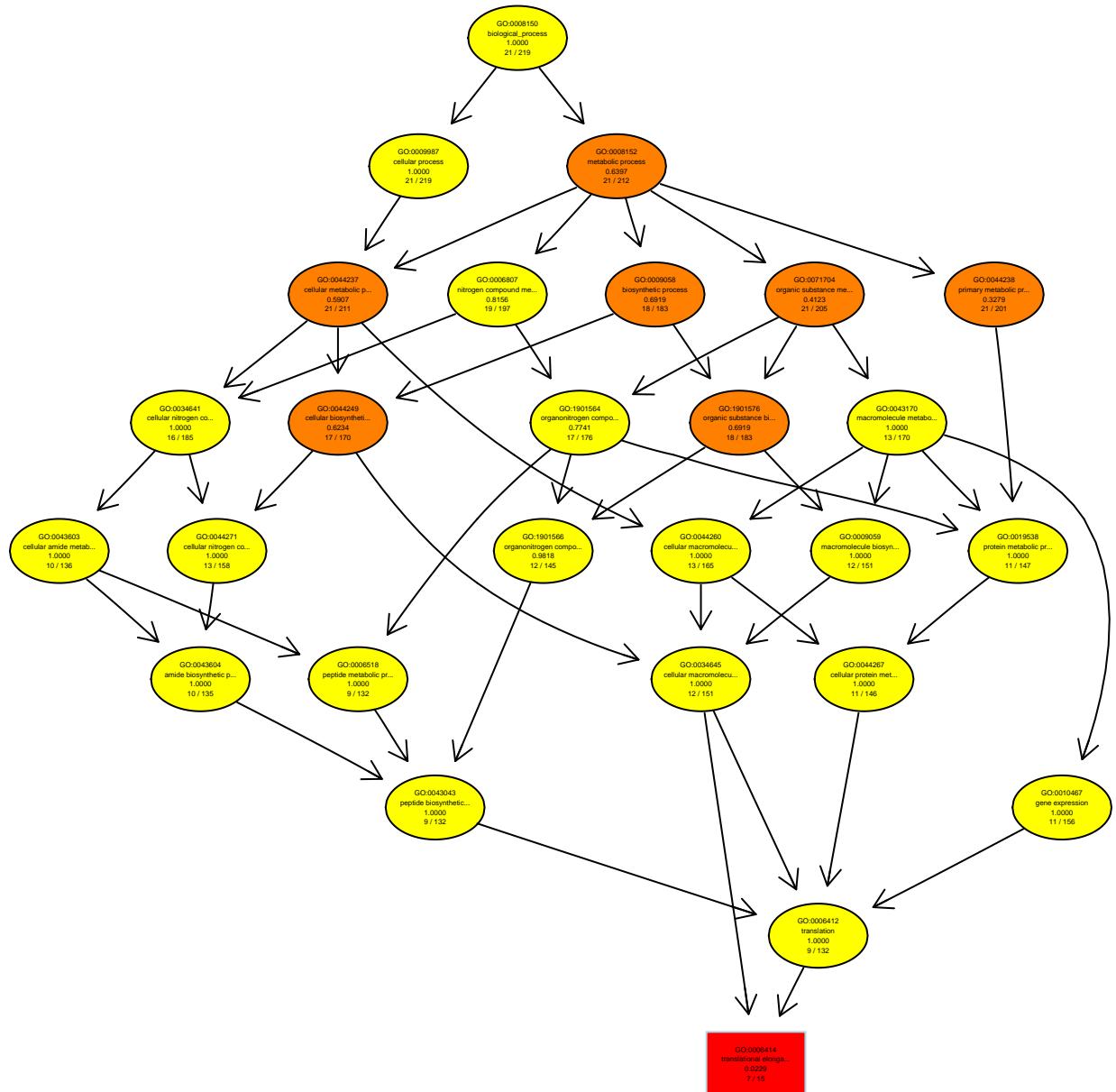
category

translational elongation

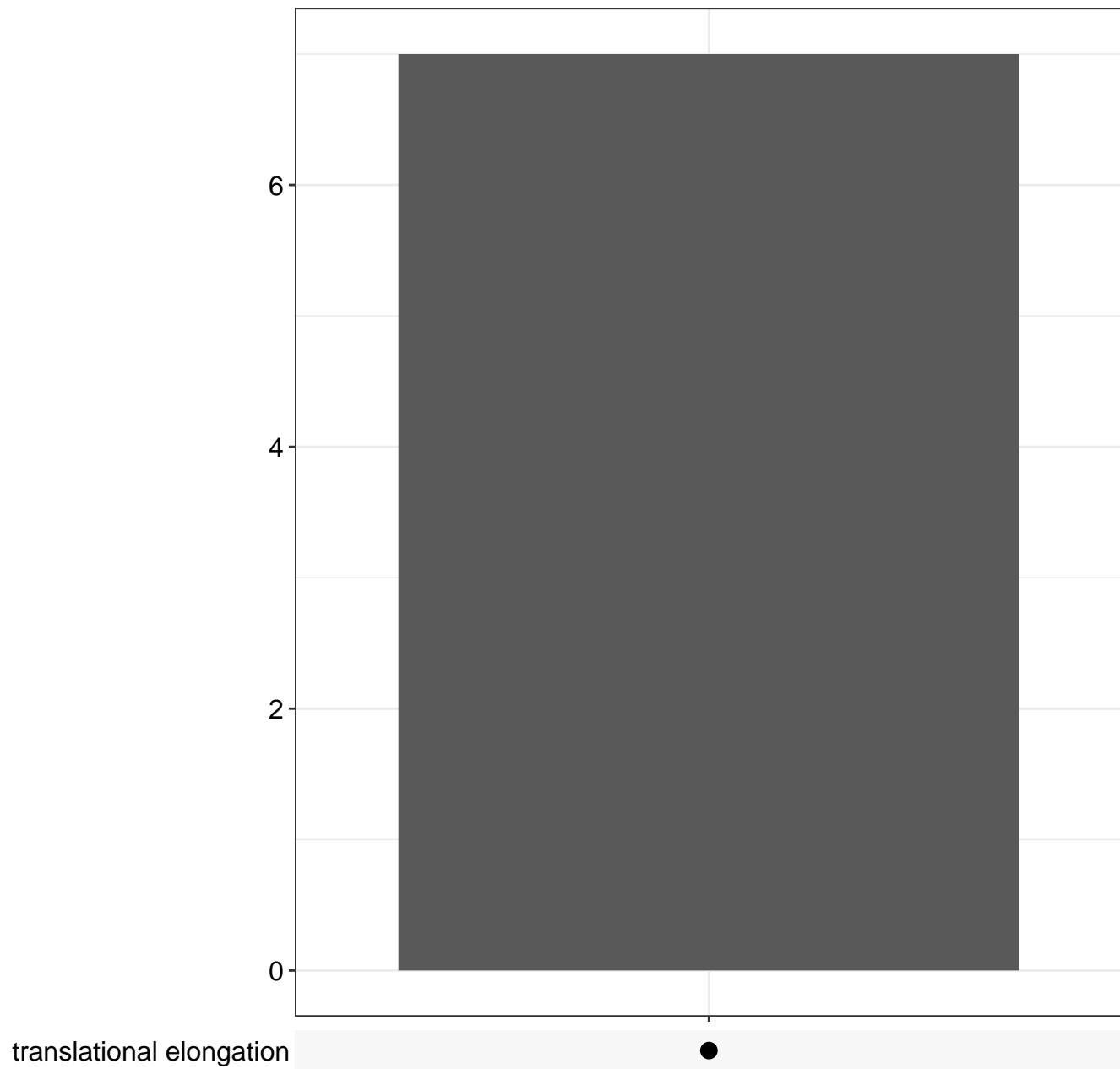


DBP2-TAP Up-regulated GO BP heatplot

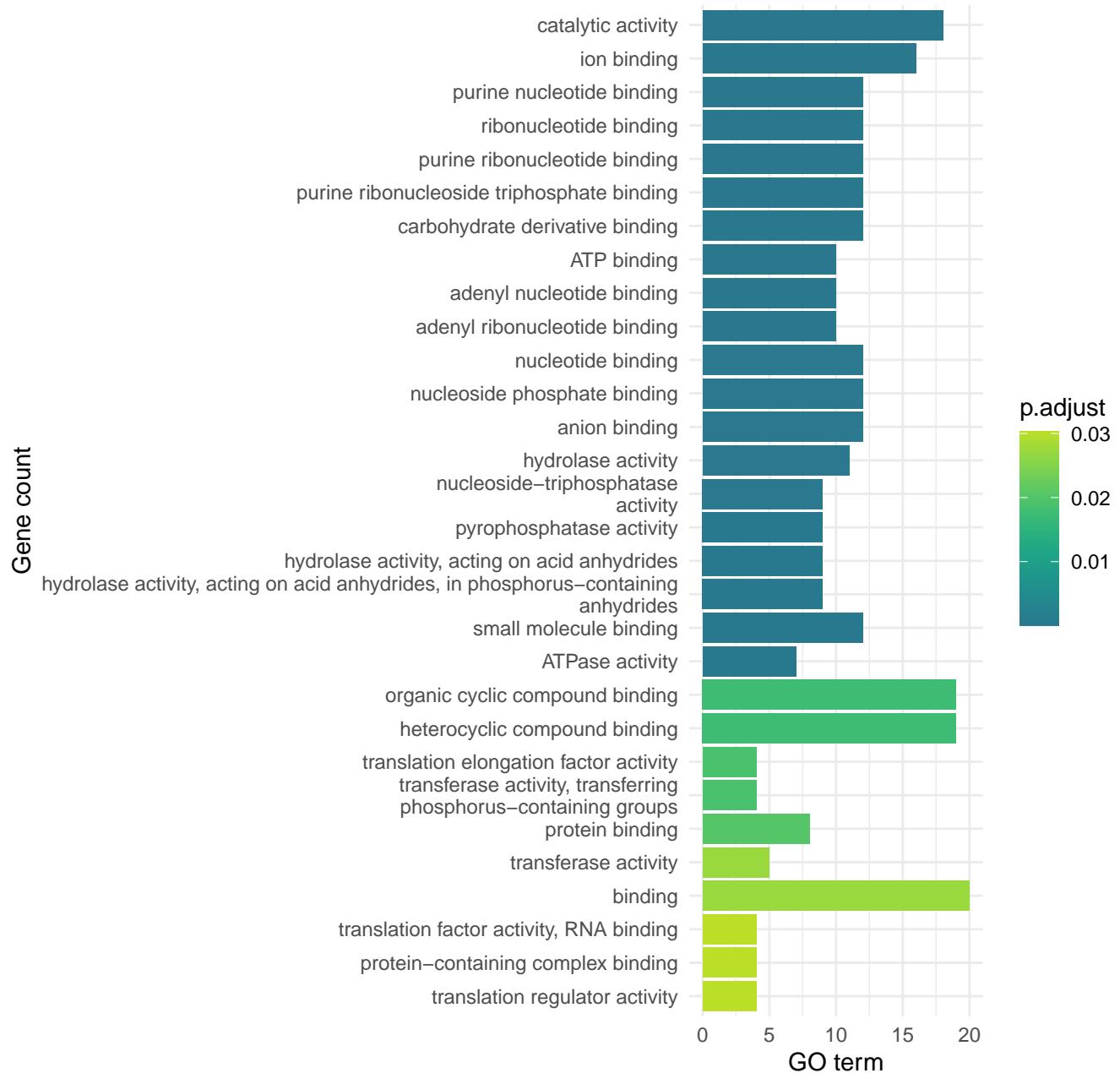




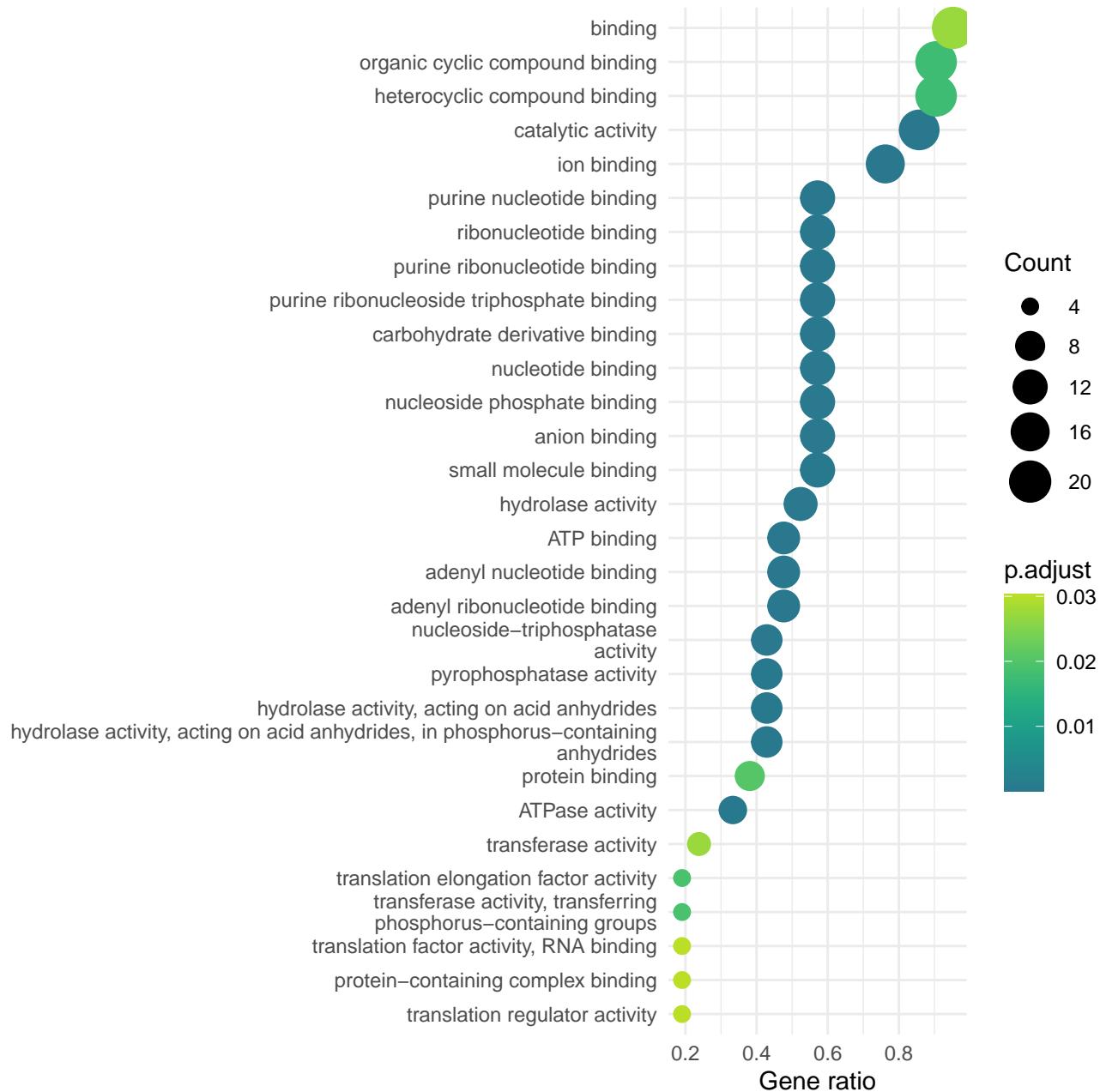
DBP2-TAP Up-regulated GO BP upsetplot



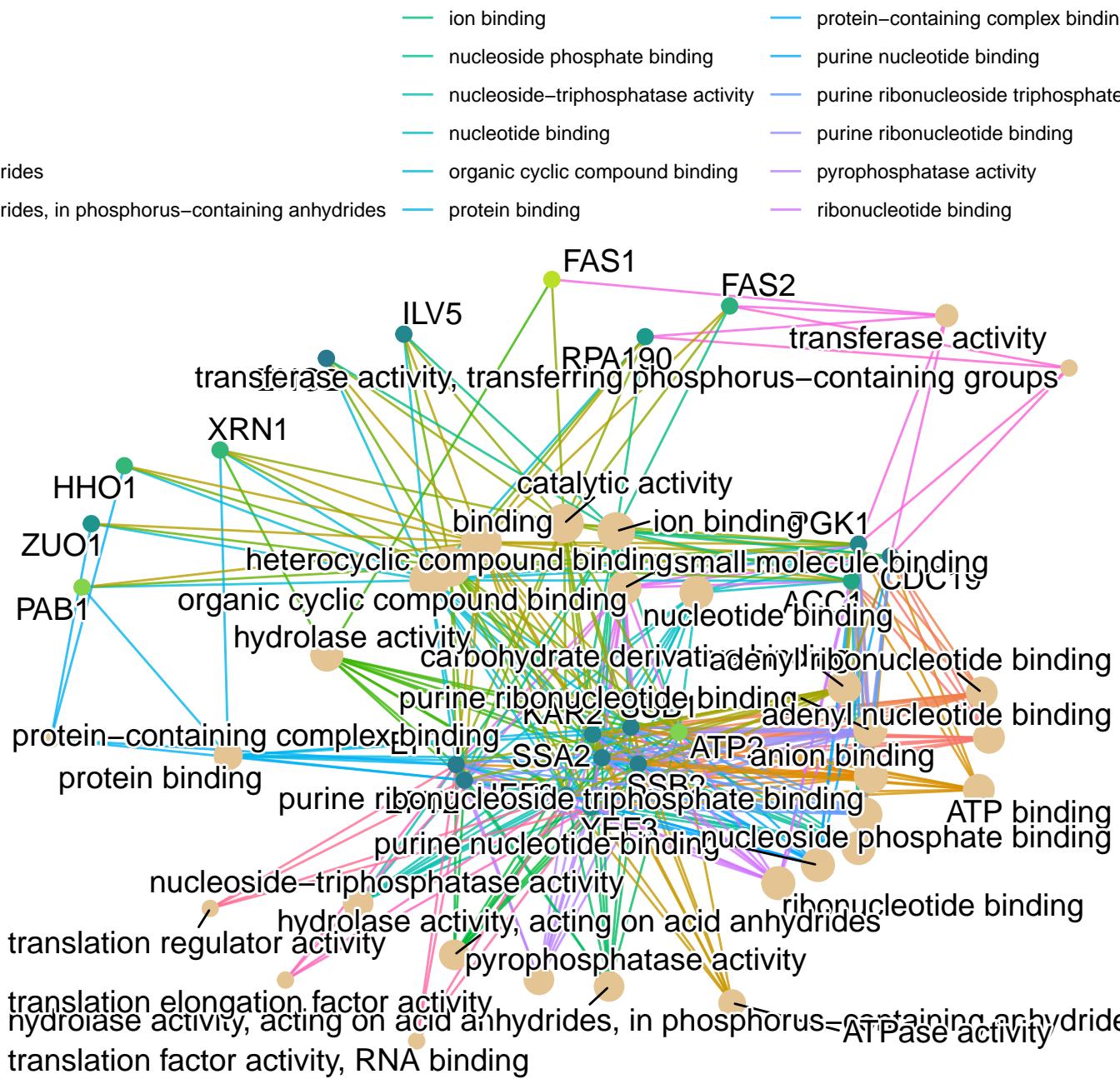
DBP2-TAP Up-regulated GO MF



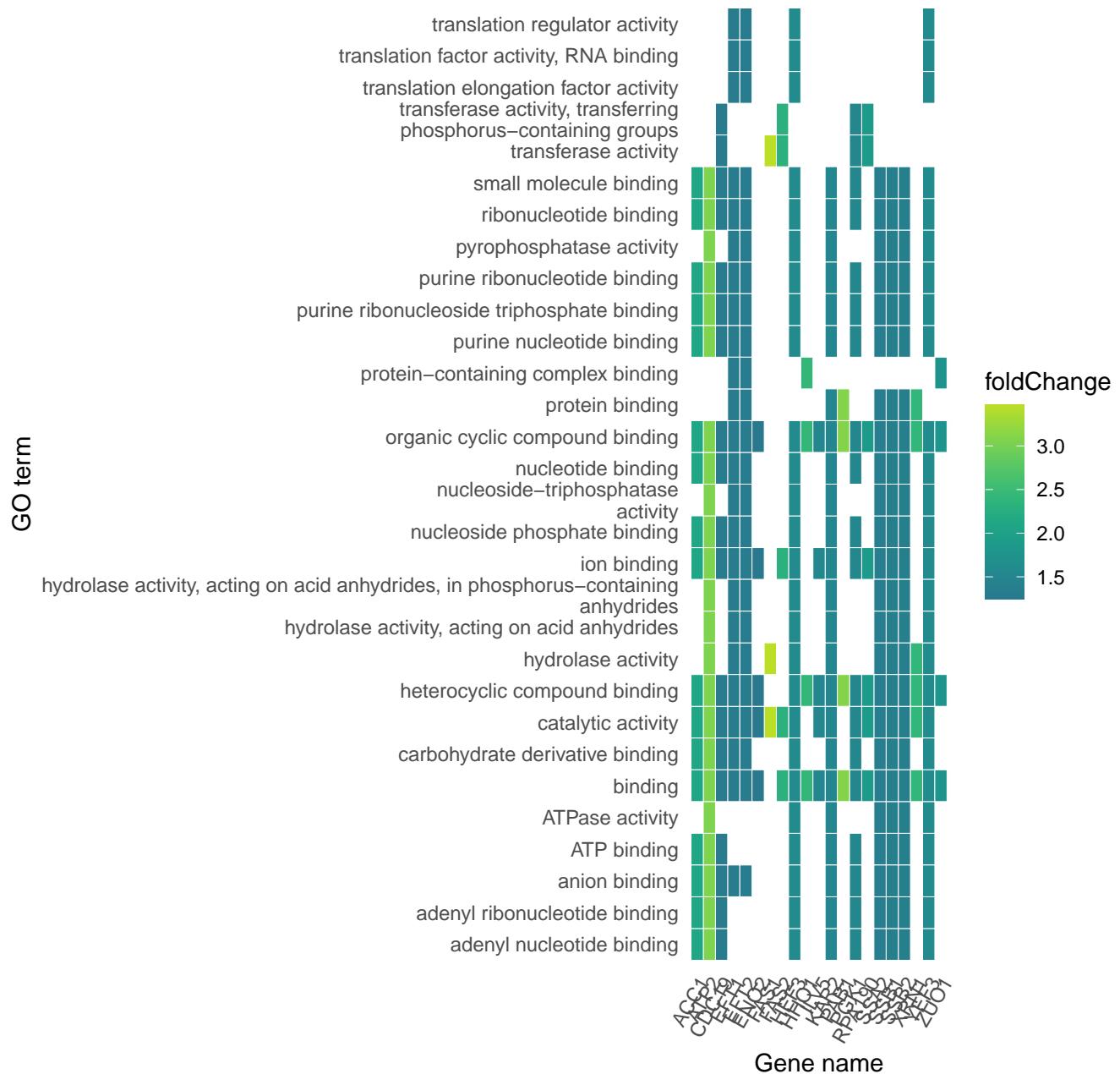
DBP2-TAP Up-regulated GO MF



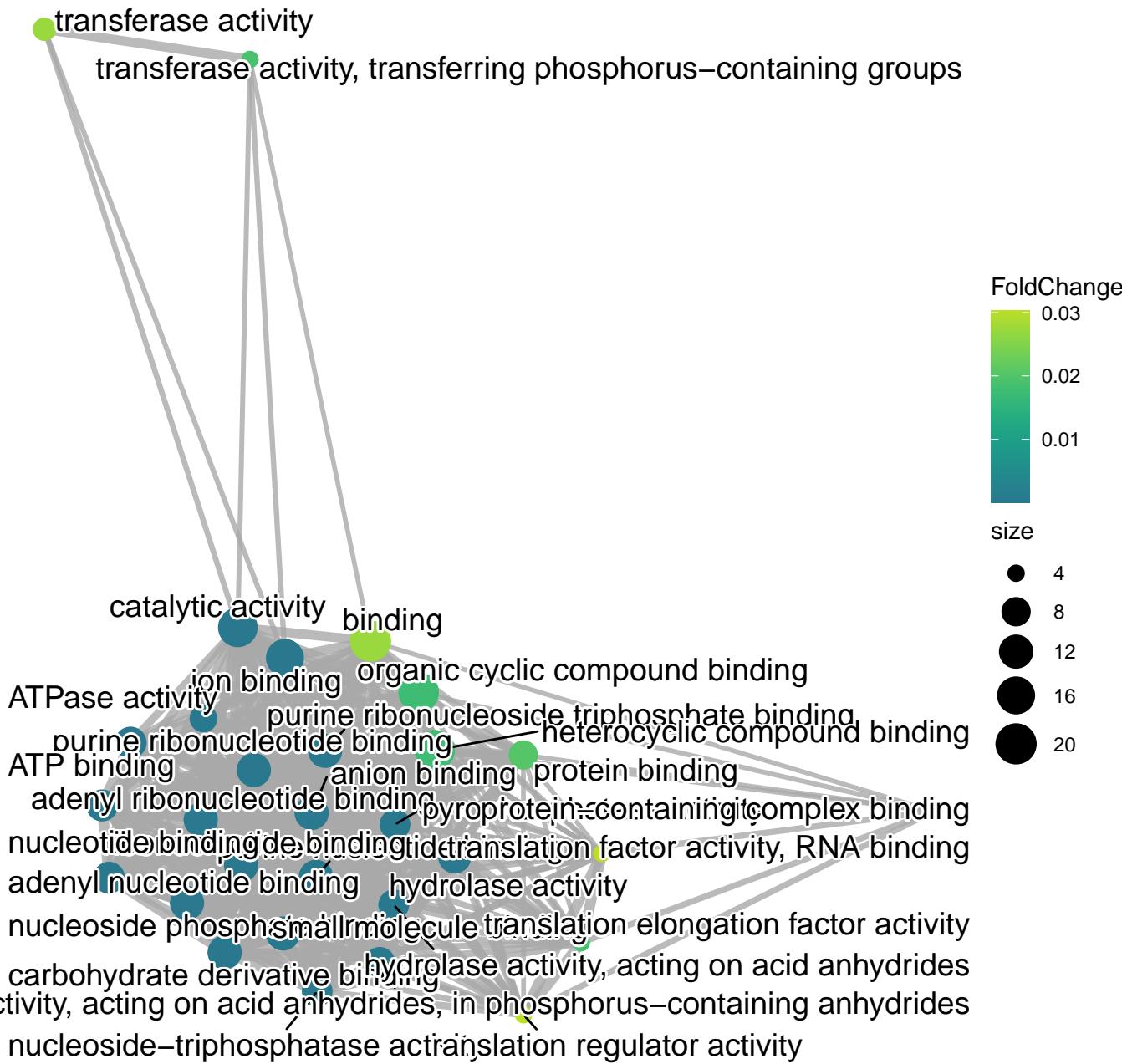
DBP2-TAP Up-regulated GO MF cnetplot

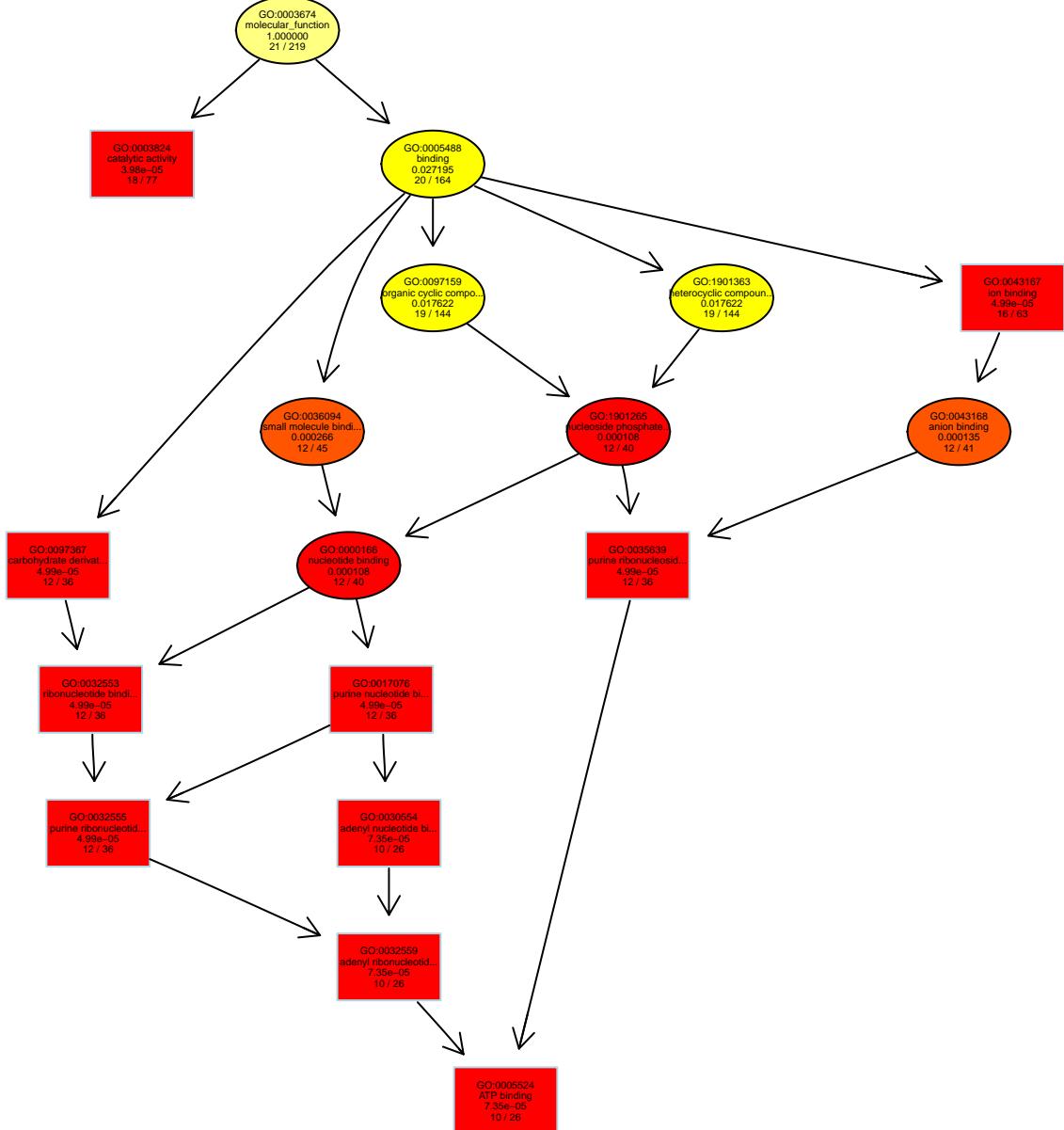


DBP2-TAP Up-regulated GO MF

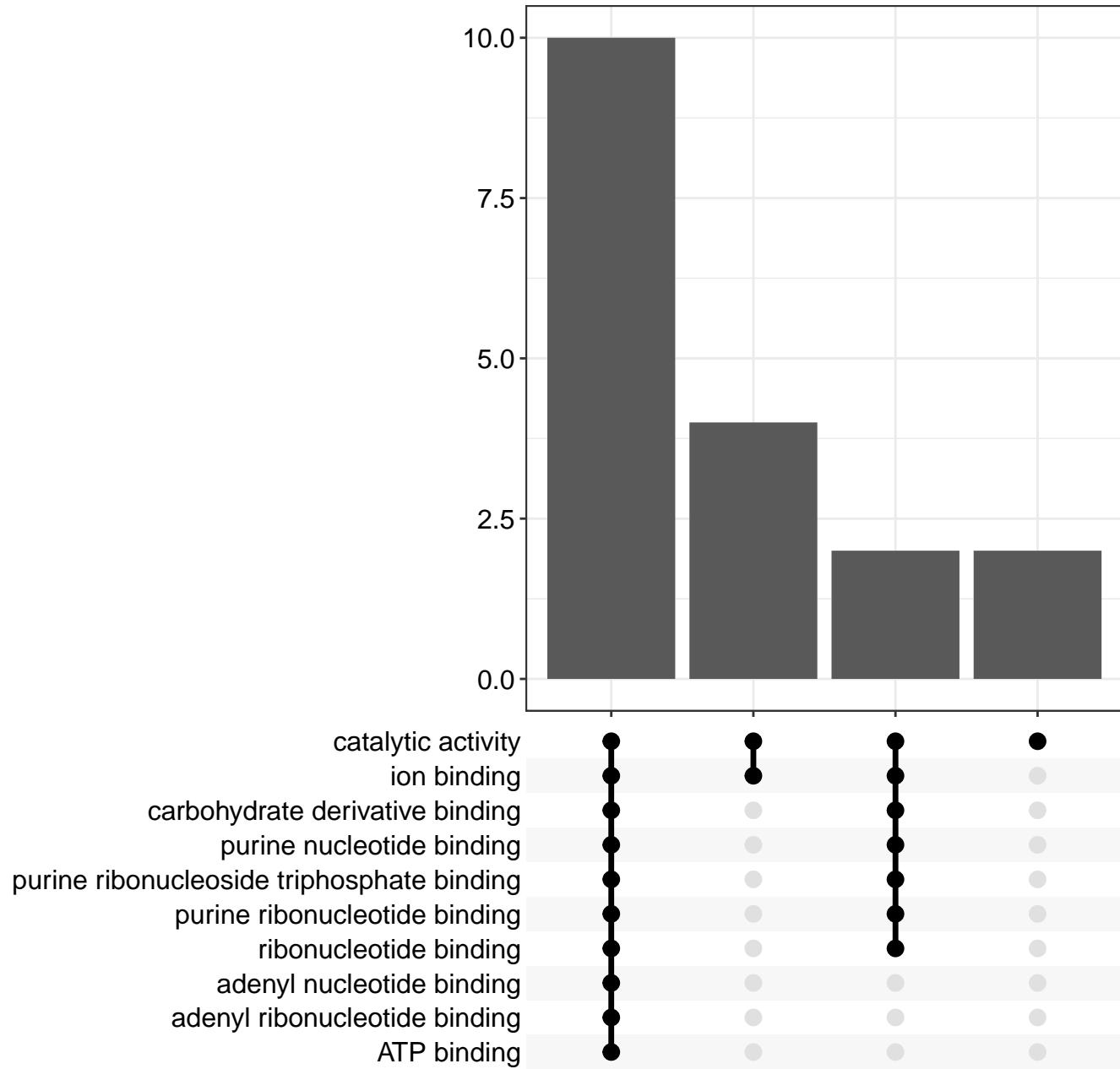


DBP2-TAP Up-regulated GO MF emapplot

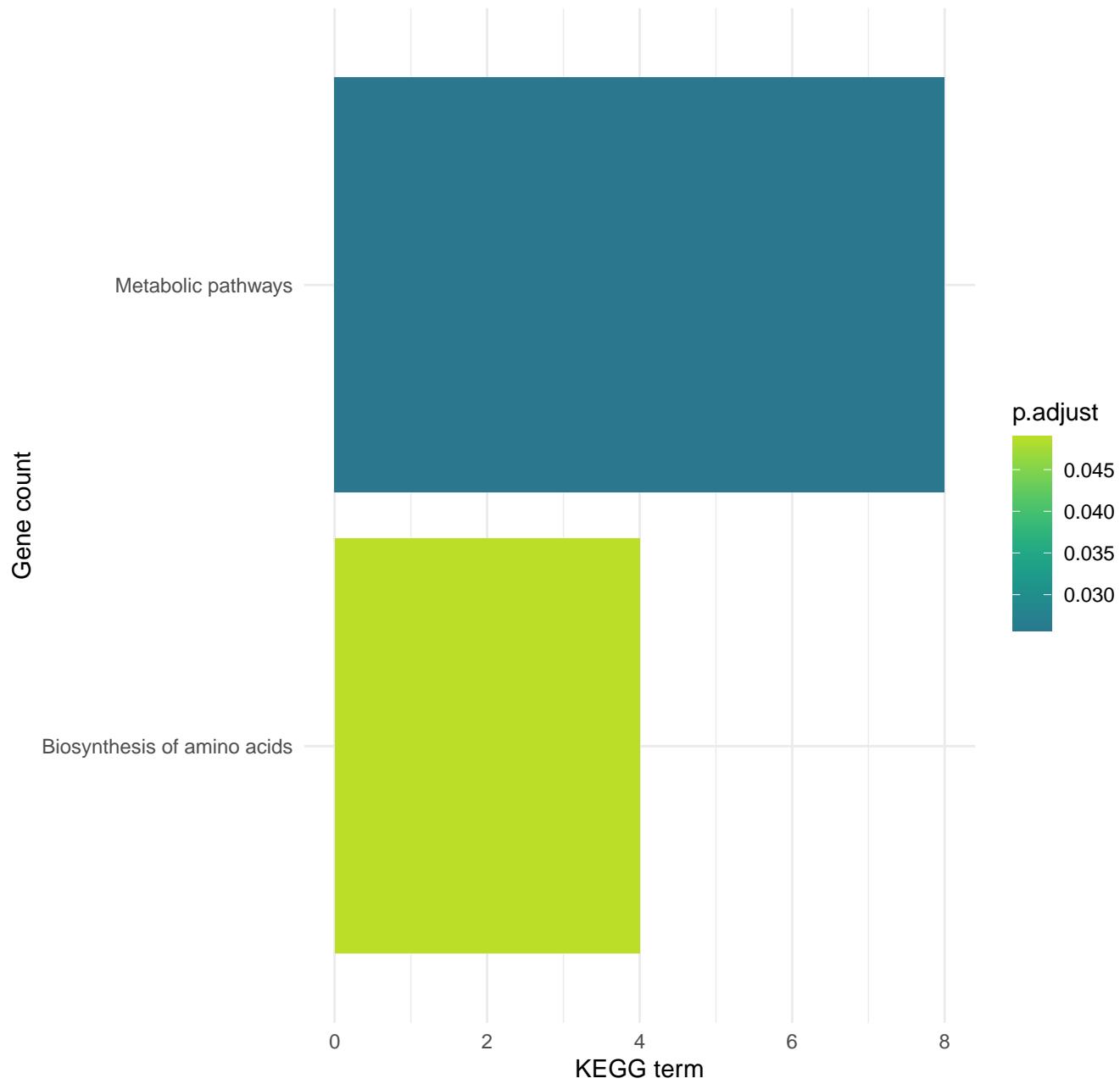




DBP2-TAP Up-regulated GO MF upsetplot



DBP2-TAP Up-regulated KEGG barplot

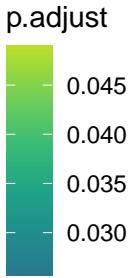


DBP2-TAP Up-regulated KEGG dotplot

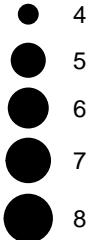
KEGG term

Metabolic pathways

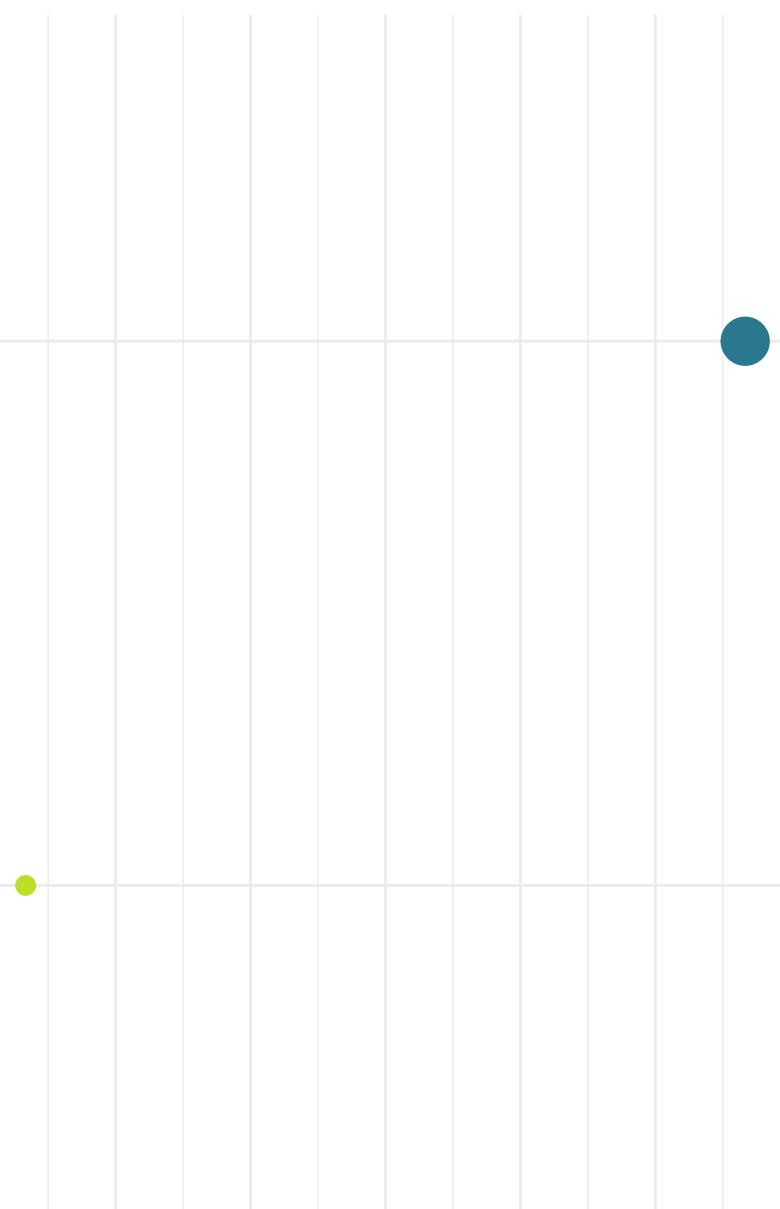
Biosynthesis of amino acids



Count



Gene ratio



DBP2-TAP Up-regulated KEGG dotplot



Biosynthesis of amino acids

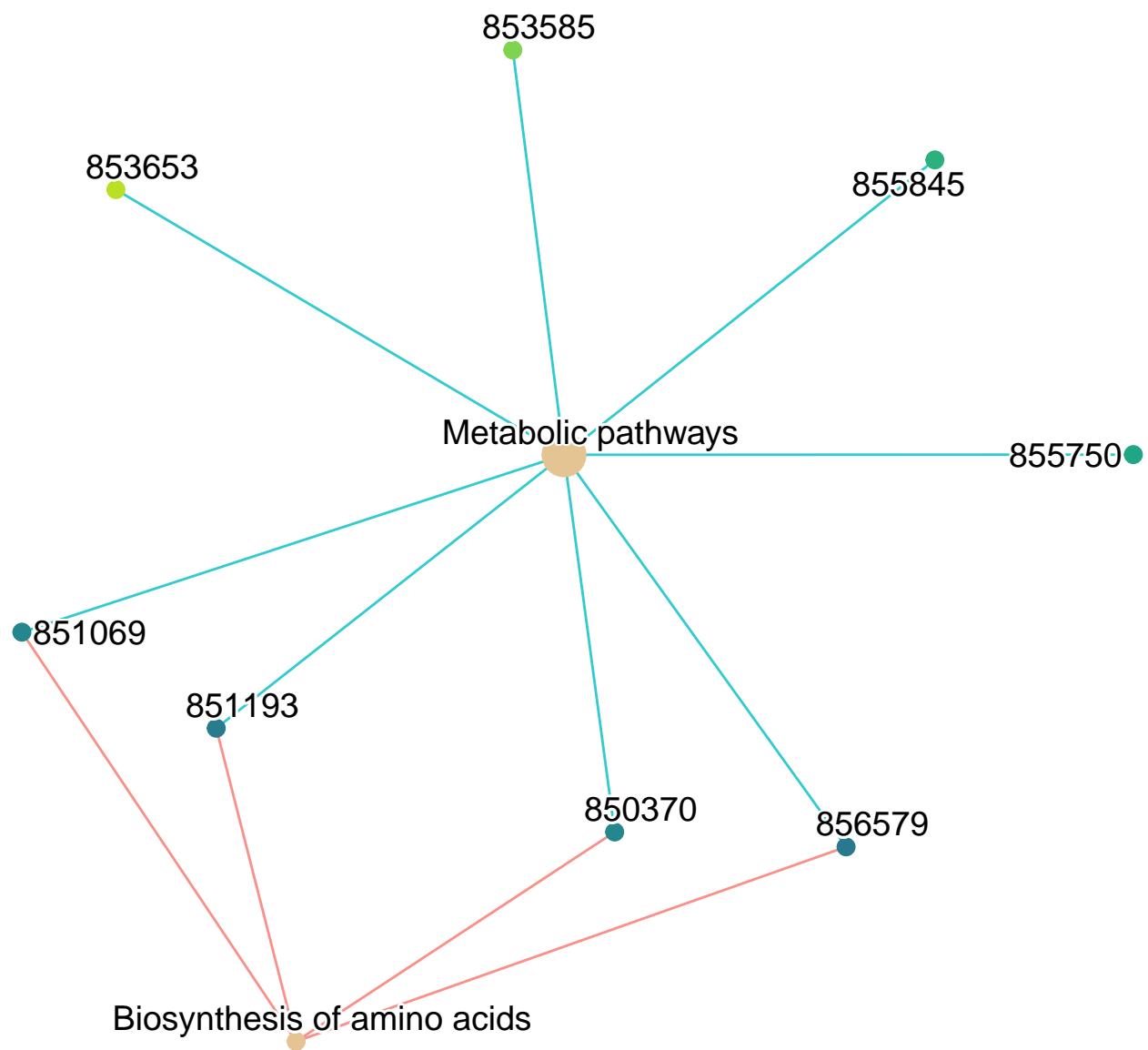
Metabolic pathways

size

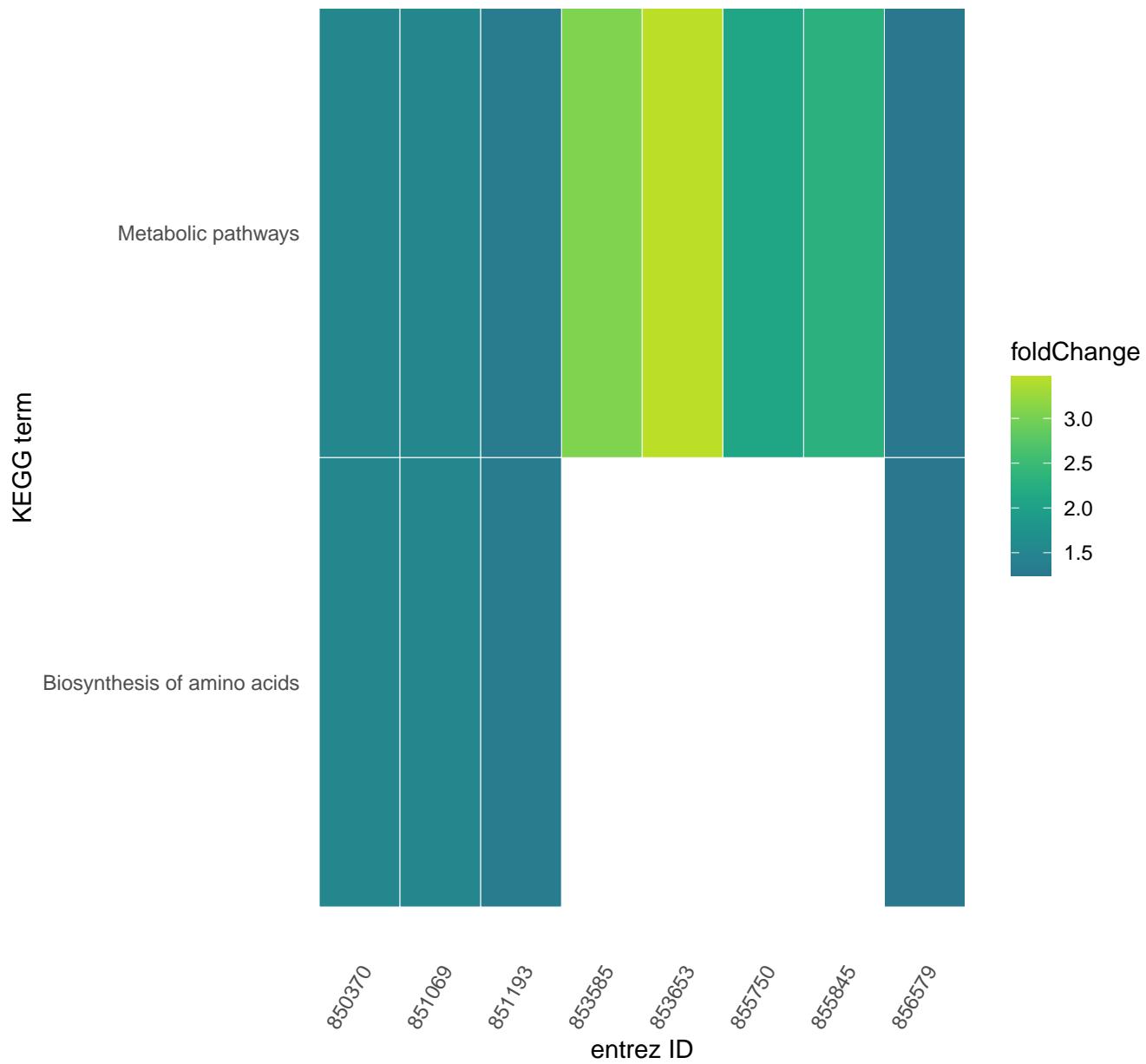
4

5

6



DBP2-TAP Up-regulated KEGG heatplot



DBP2-TAP Up-regulated KEGG upsetplot

