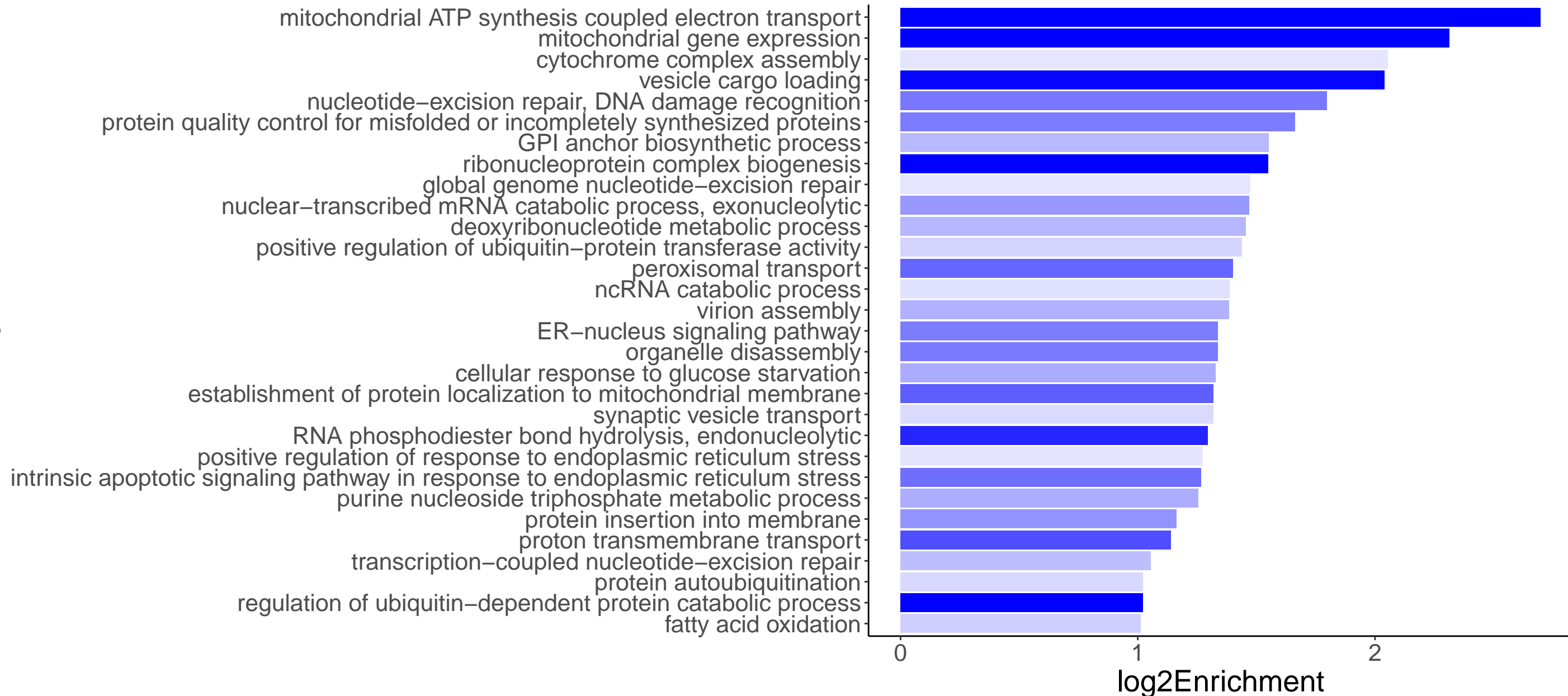
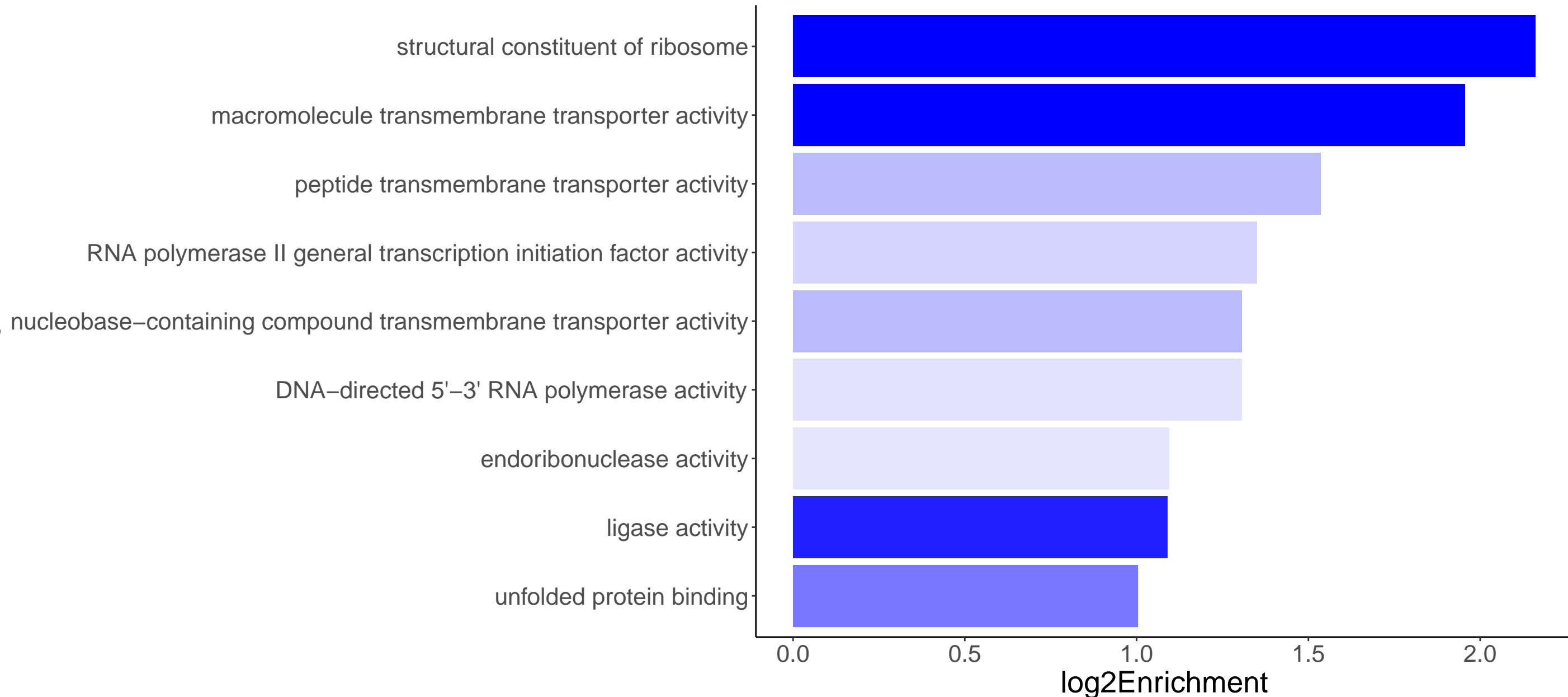


# Original module 4 BP enrichment



# Original module 4 MF enrichment

Term



# Re-clustered module 4.1 BP enrichment

Term

NAD biosynthetic process

intermediate filament cytoskeleton organization

mRNA export from nucleus

0

1

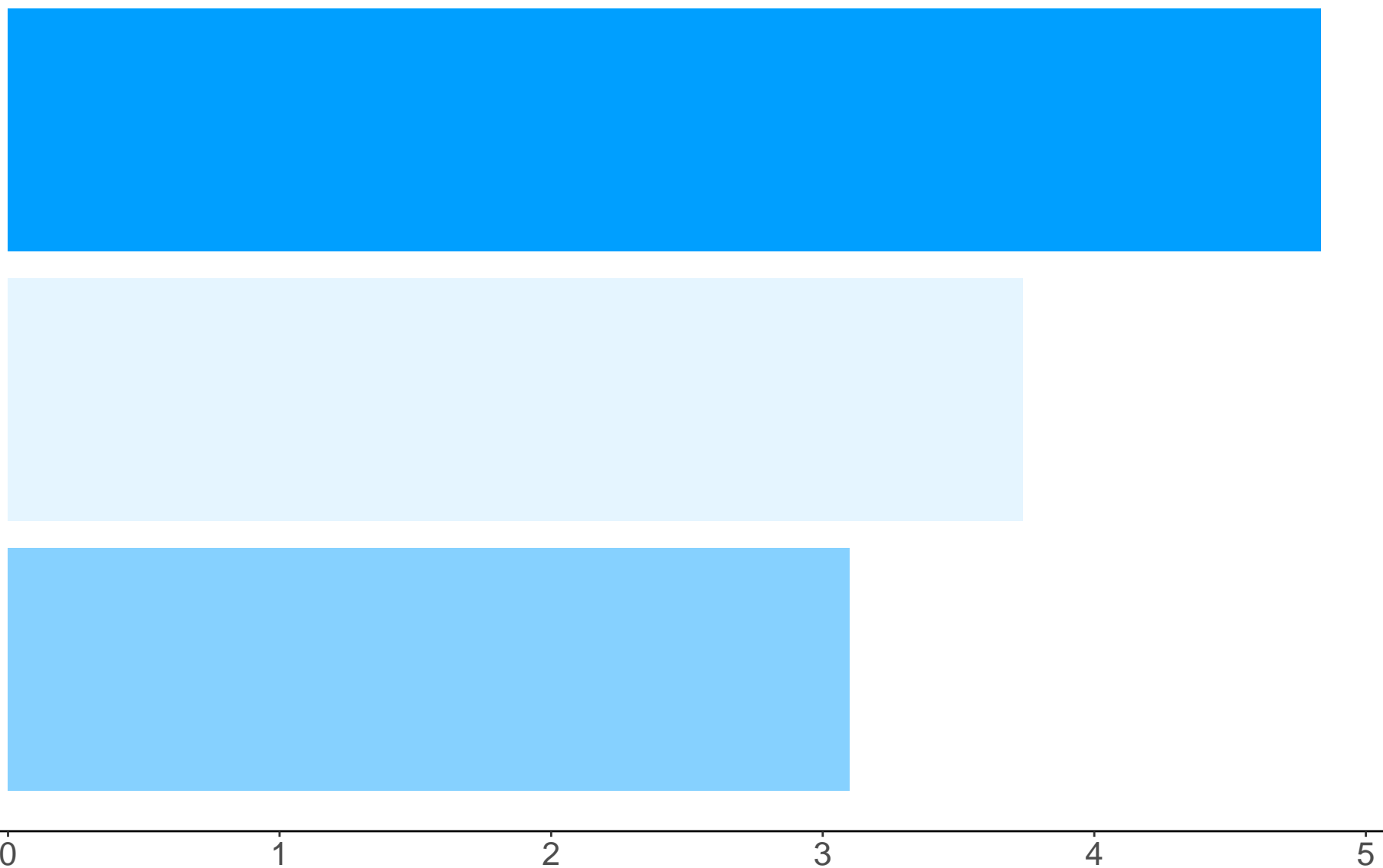
2

3

4

5

log2Enrichment



Re-clustered module 4.1 MF enrichment

Term

log2Enrichment



# Re-clustered module 4.10 BP enrichment

Term

dolichol-linked oligosaccharide biosynthetic process

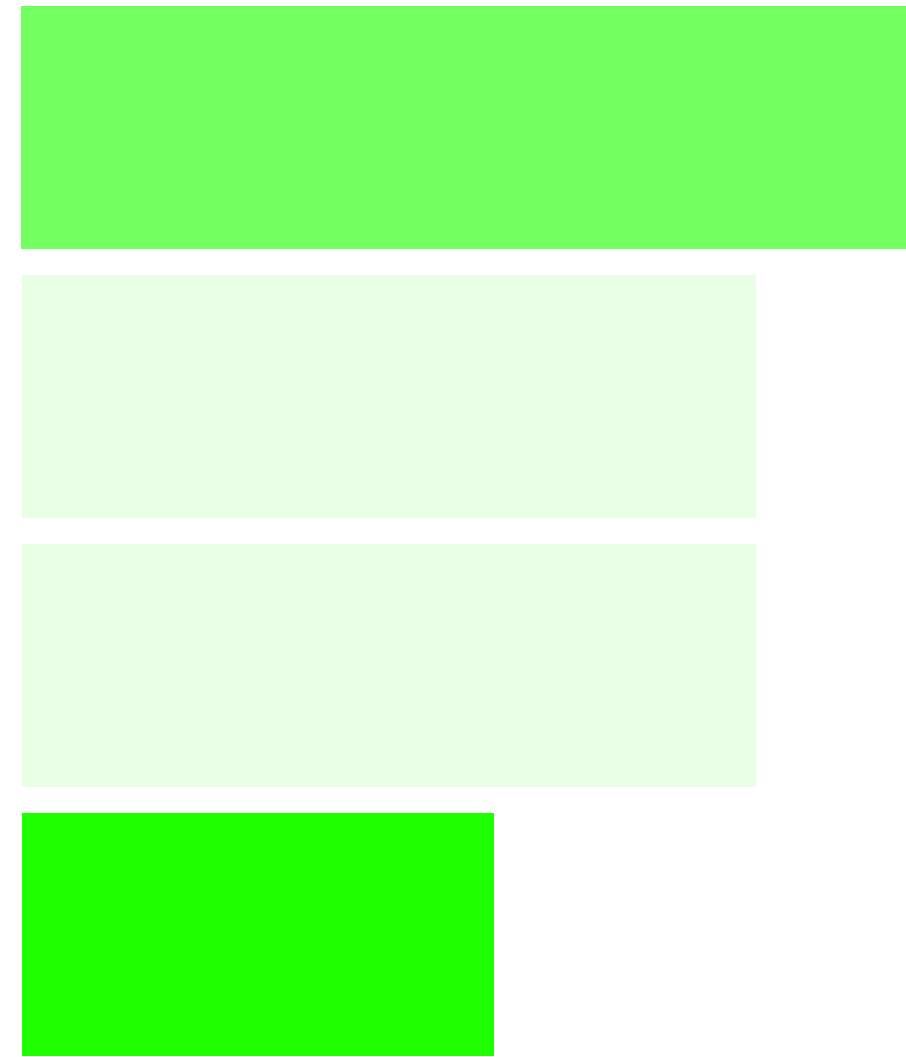
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)

mRNA polyadenylation

ribonucleoprotein complex biogenesis

0 1 2 3 4

log2Enrichment



# Re-clustered module 4.10 MF enrichment

Term structural constituent of ribosome

0

1

2

3

log2Enrichment



# Re-clustered module 4.11 BP enrichment

Term

histone deubiquitination

early endosome to late endosome transport

cellular response to glucose starvation

histone acetylation

0

1

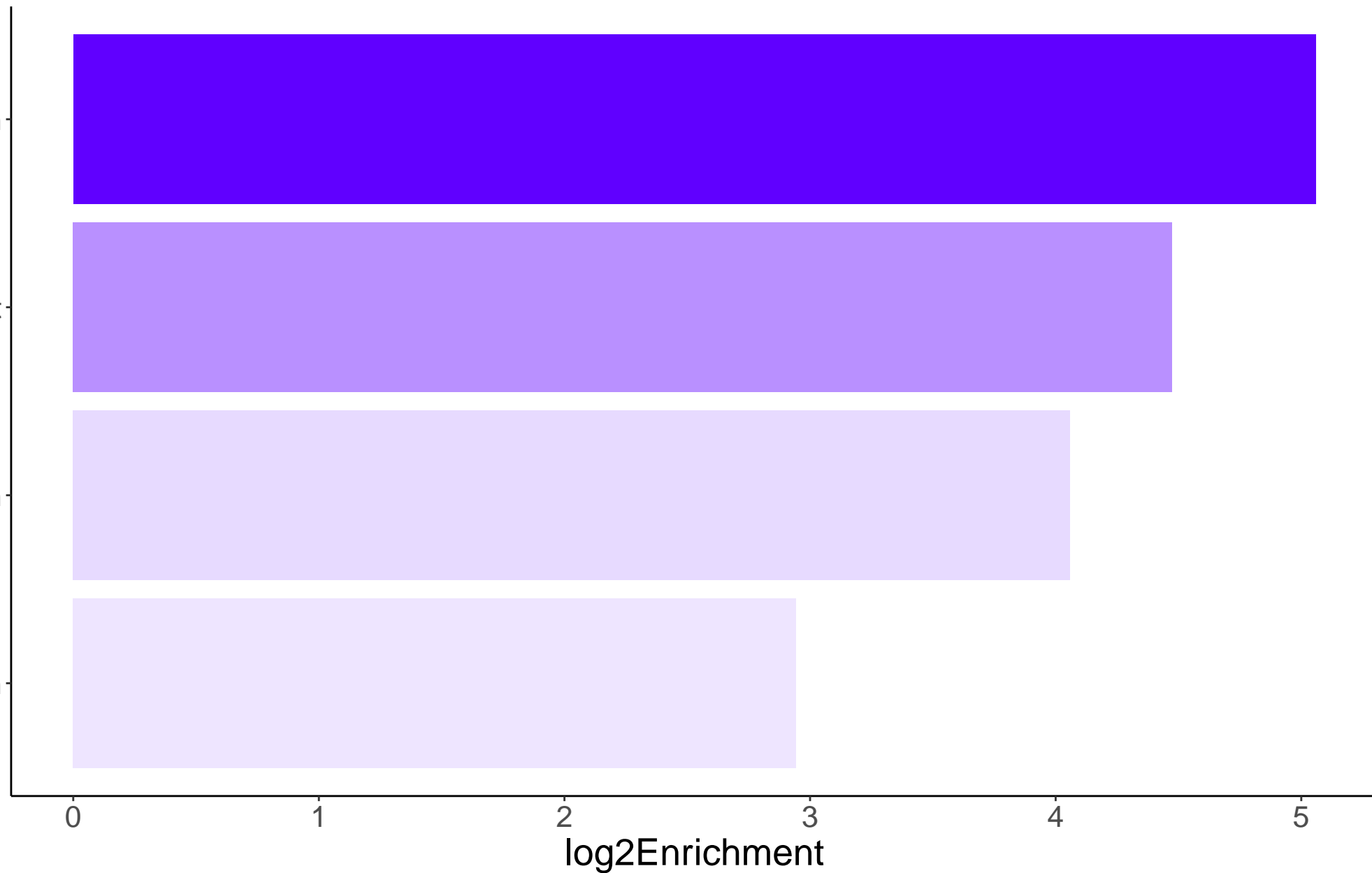
2

3

4

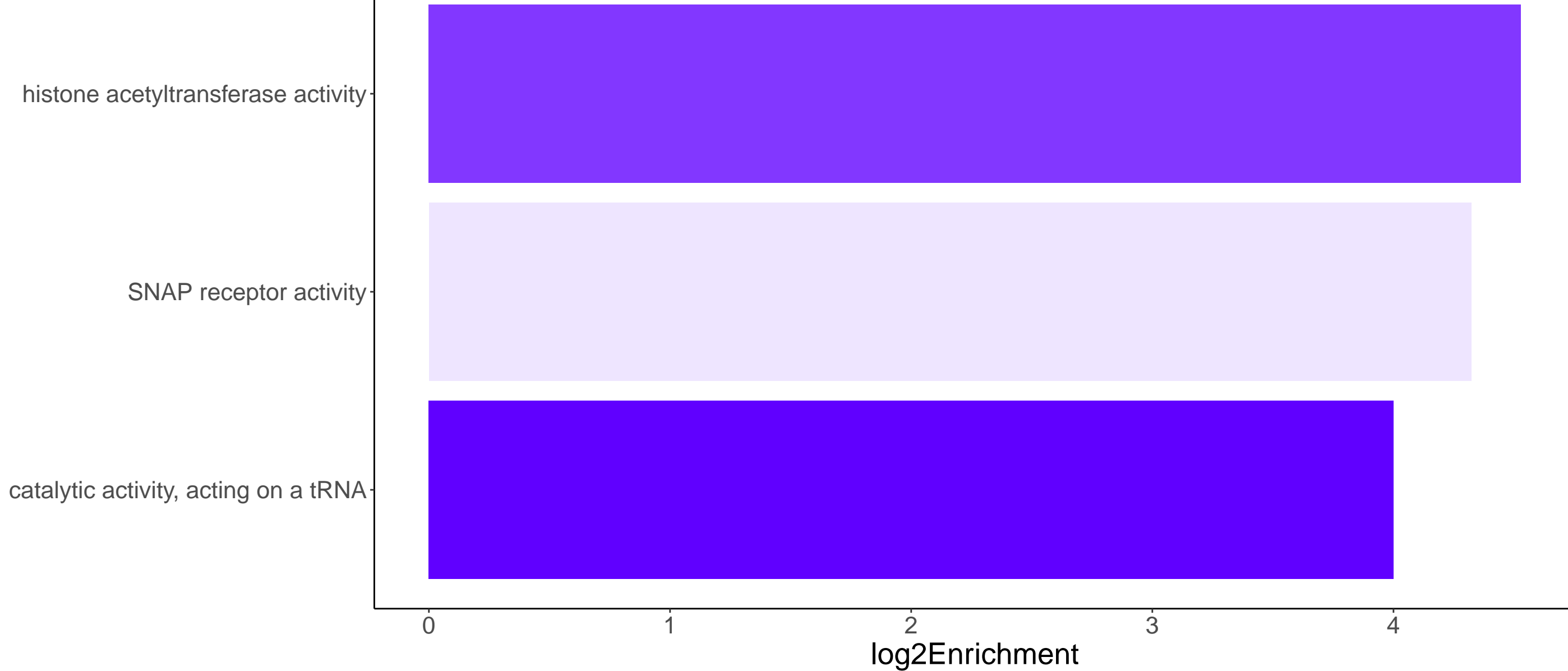
5

log2Enrichment



# Re-clustered module 4.11 MF enrichment

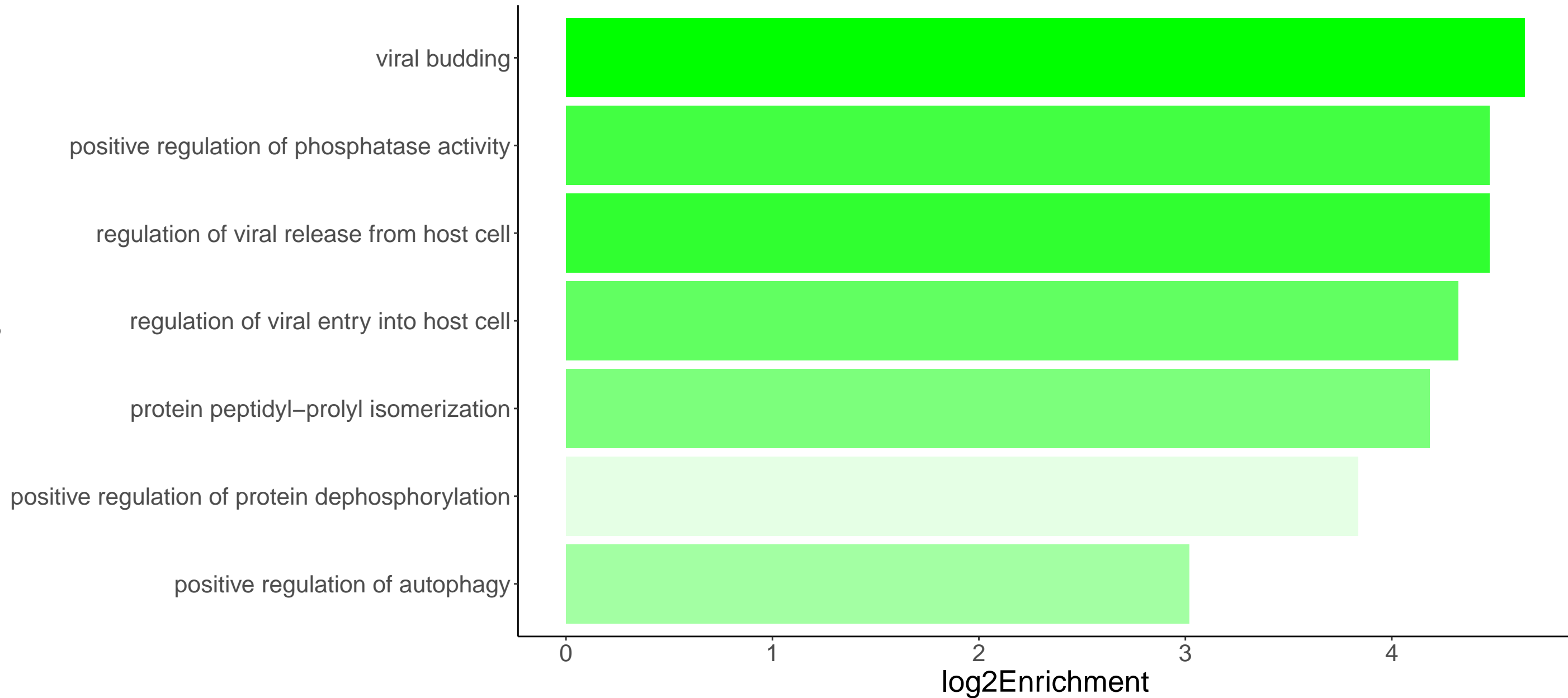
Term





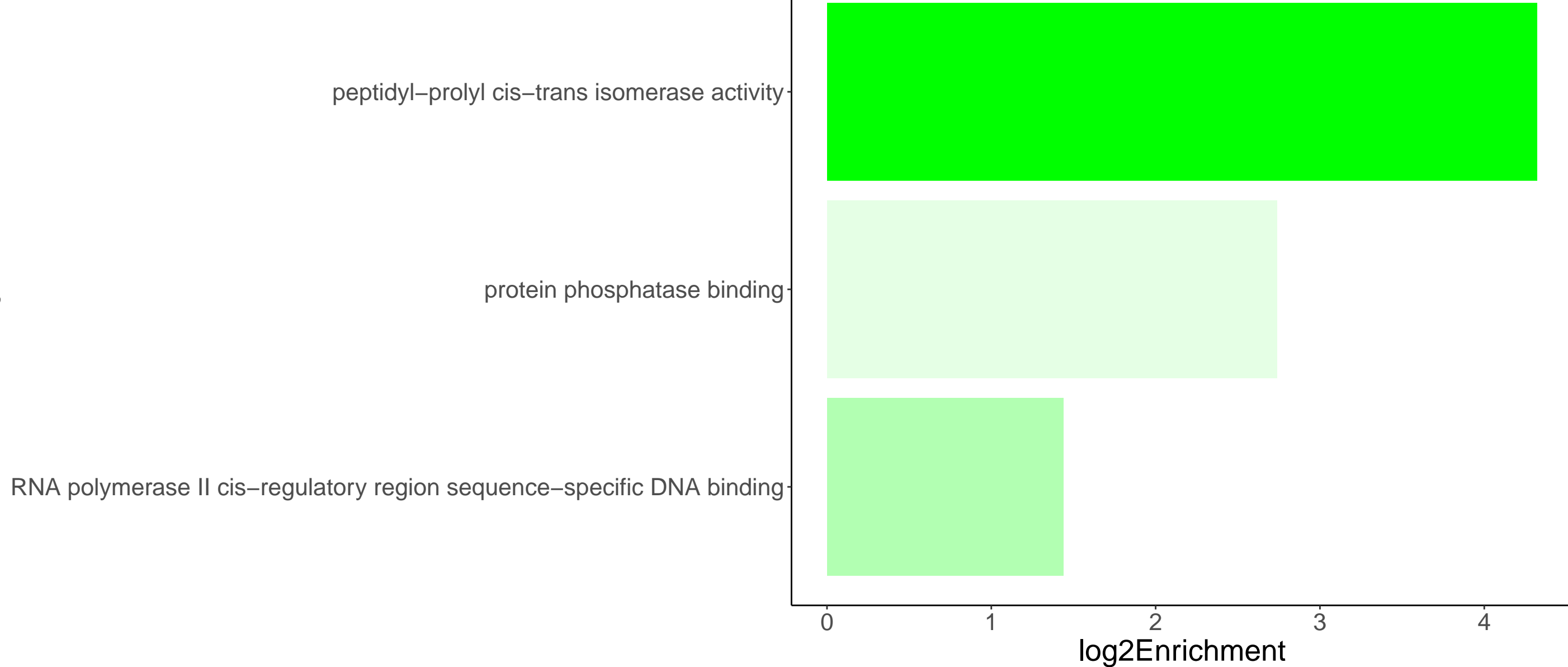
## Re-clustered module 4.12 BP enrichment

Term



# Re-clustered module 4.12 MF enrichment

Term



# Re-clustered module 4.13 BP enrichment

Term

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

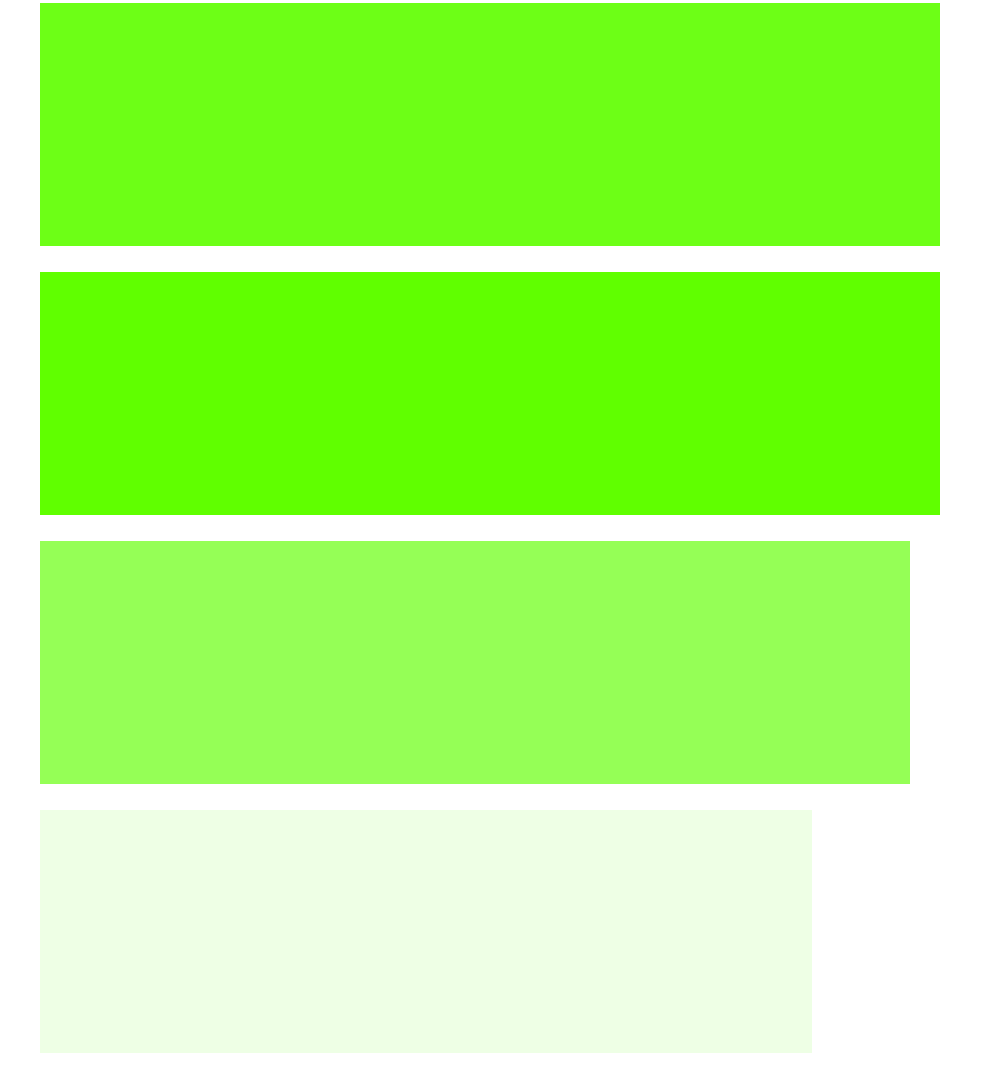
N-terminal protein amino acid modification

ncRNA catabolic process

mitochondrial RNA metabolic process

log2Enrichment

0 1 2 3 4



# Re-clustered module 4.13 MF enrichment

Term

ribonucleoprotein complex binding

ATP binding

0

1

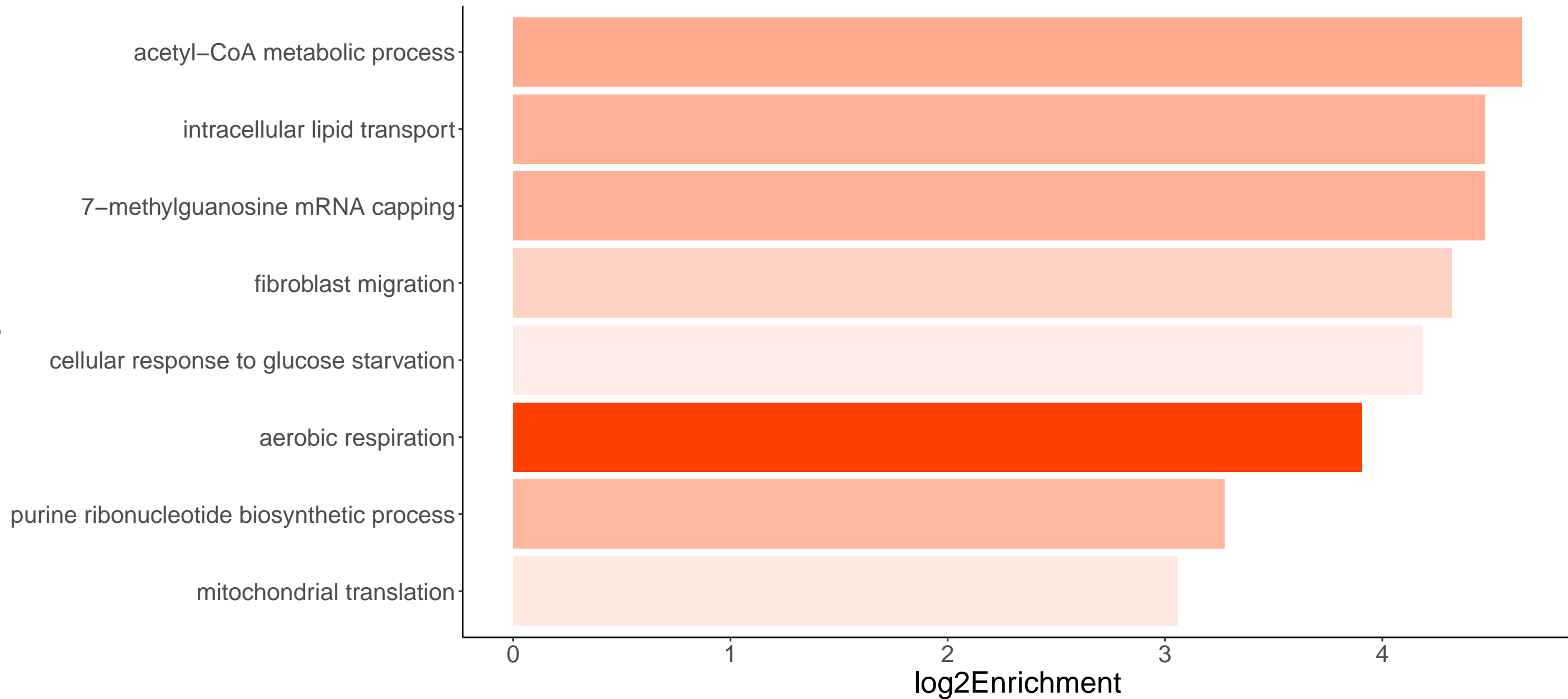
2

log2Enrichment



## Re-clustered module 4.14 BP enrichment

Term



# Re-clustered module 4.14 MF enrichment

Term

phosphotransferase activity, phosphate group as acceptor

4 iron, 4 sulfur cluster binding

NAD binding

0

1

2

3

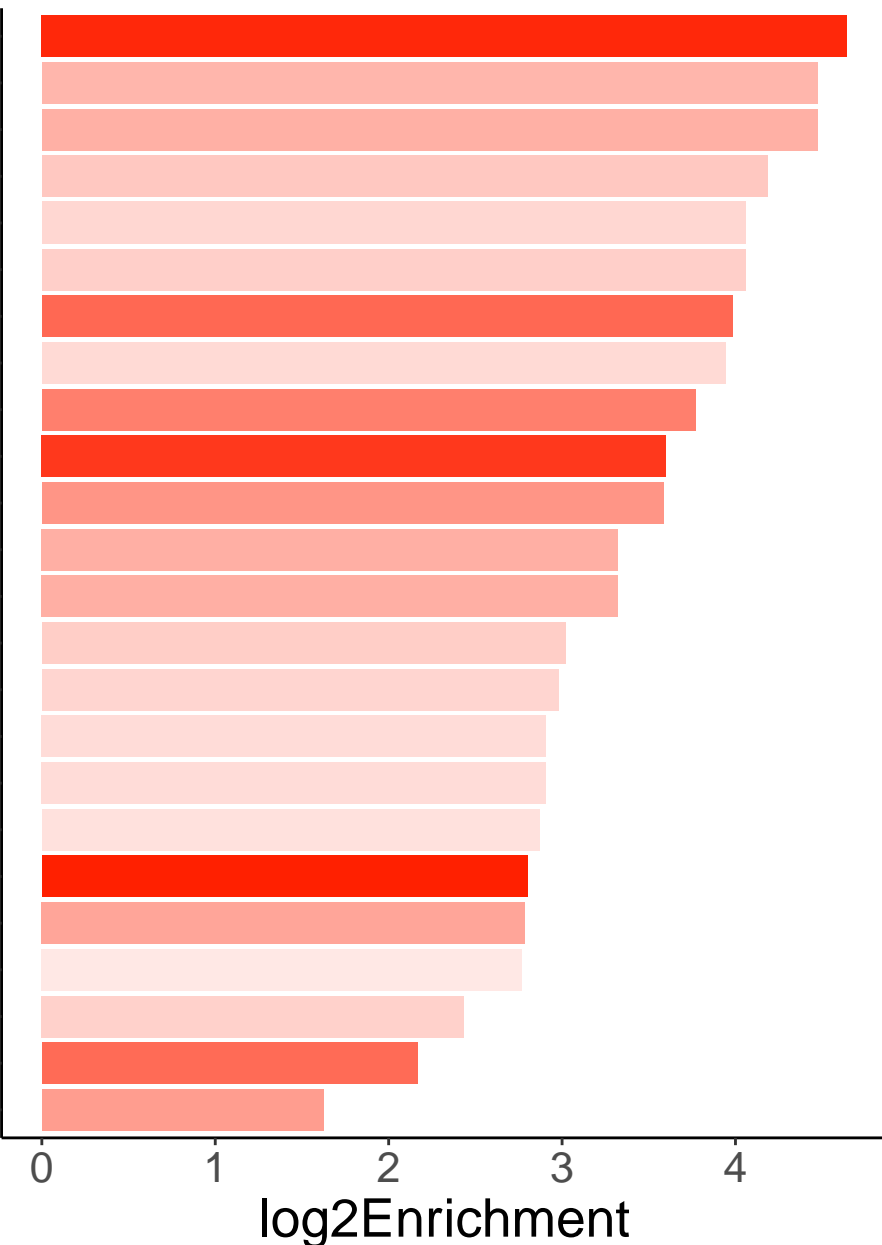
4

log2Enrichment



Term

protein transmembrane import into intracellular organelle  
 kinetochore organization  
 mitochondrial cytochrome c oxidase assembly  
 positive regulation of peptidyl–threonine phosphorylation  
 CENP–A containing nucleosome assembly  
 protein localization to chromosome, telomeric region  
 intracellular protein transmembrane transport  
 replication fork processing  
 mitochondrial respiratory chain complex I assembly  
 hematopoietic stem cell differentiation  
 regulation of cellular amino acid metabolic process  
 regulation of transcription from RNA polymerase II promoter in response to hypoxia  
 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP–dependent  
 negative regulation of DNA metabolic process  
 negative regulation of G2/M transition of mitotic cell cycle  
 interleukin–1–mediated signaling pathway  
 Wnt signaling pathway, planar cell polarity pathway  
 stimulatory C–type lectin receptor signaling pathway  
 mitochondrial transport  
 tumor necrosis factor–mediated signaling pathway  
 Fc–epsilon receptor signaling pathway  
 T cell receptor signaling pathway  
 proteasome–mediated ubiquitin–dependent protein catabolic process  
 protein ubiquitination



# Re-clustered module 4.15 MF enrichment

Term

translation initiation factor activity

telomeric DNA binding

0

1

2

3

4

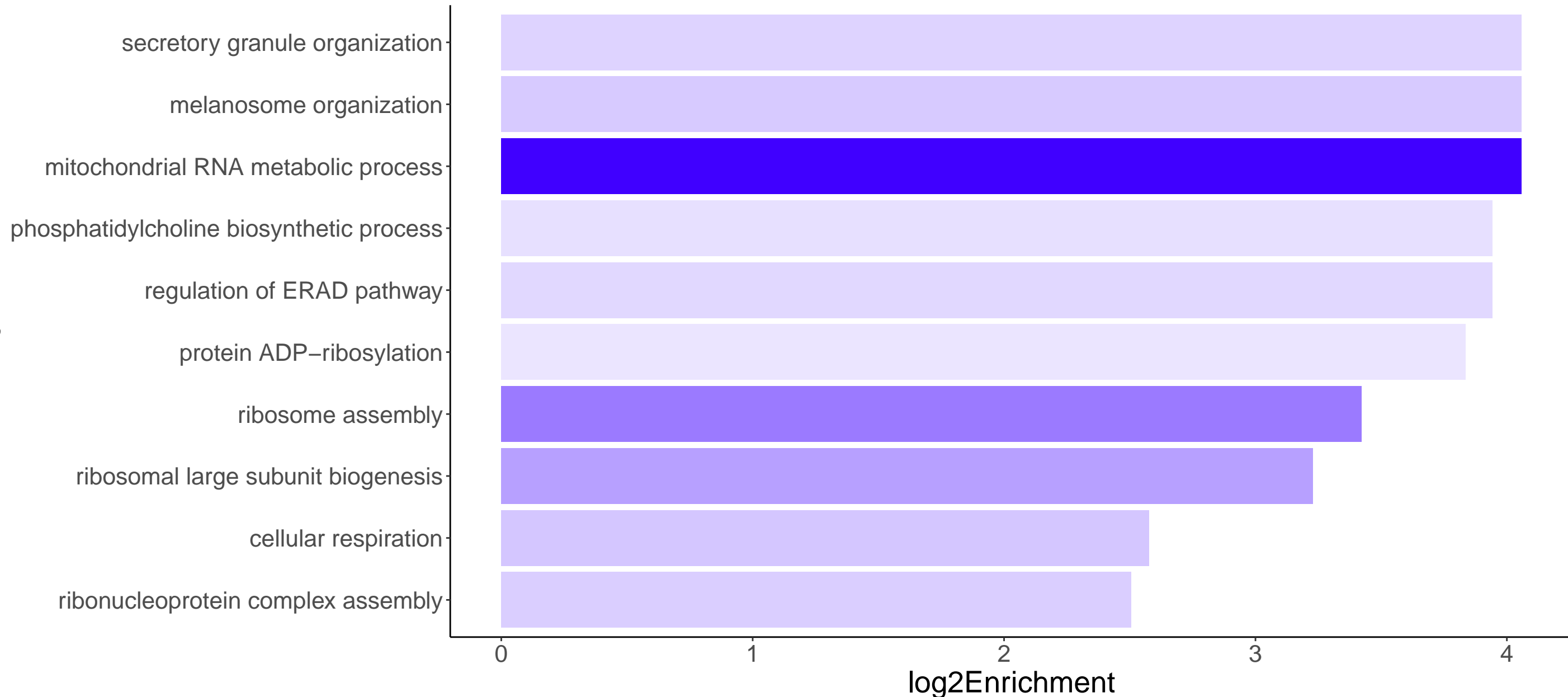
log2Enrichment





# Re-clustered module 4.16 BP enrichment

Term



# Re-clustered module 4.16 MF enrichment

Term

histone deacetylase activity

NAD binding

transition metal ion binding

RNA binding

0

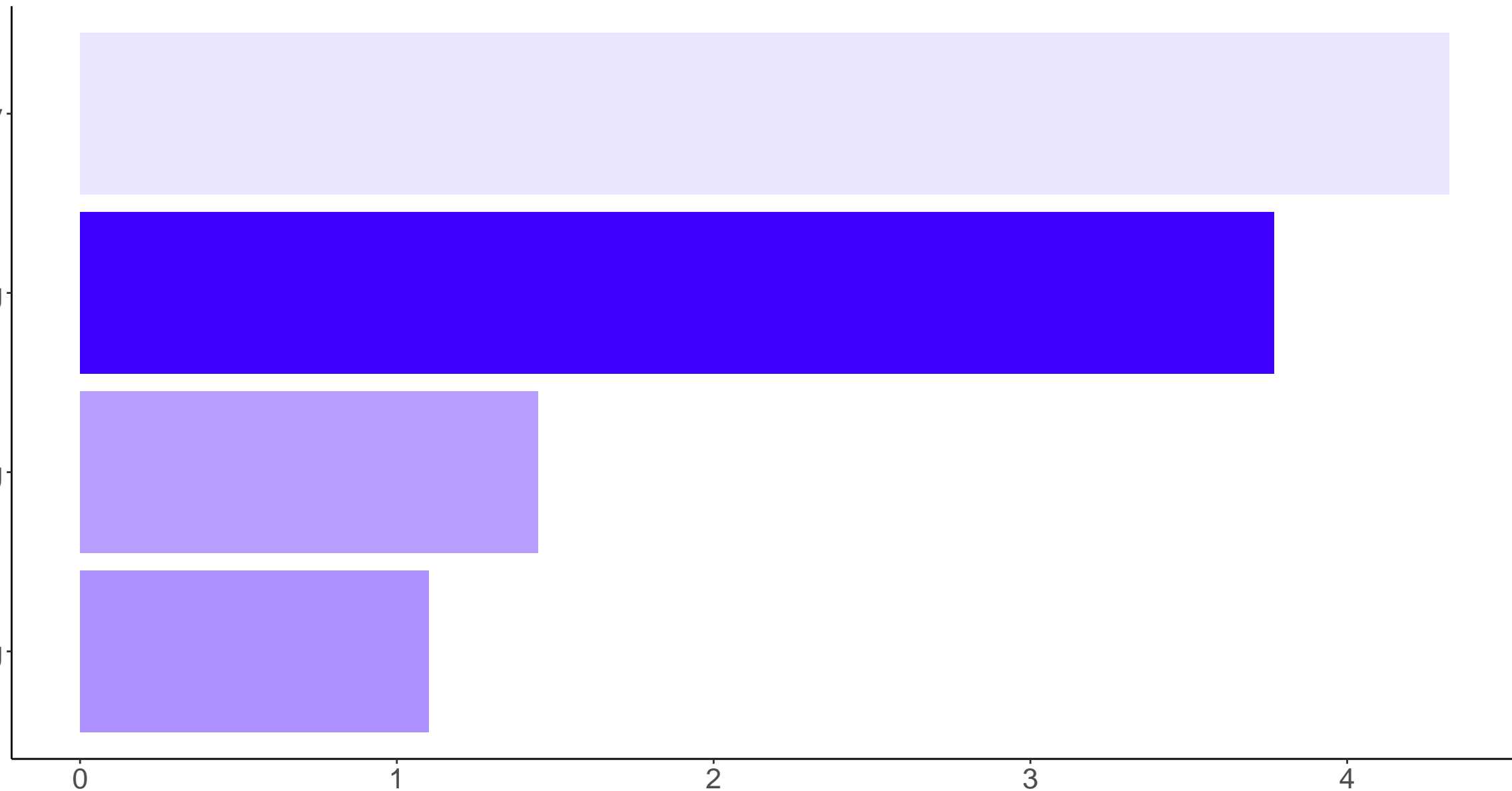
1

2

3

4

log2Enrichment





## Re-clustered module 4.17 MF enrichment

Term

phosphatidylinositol-3,5-bisphosphate binding

structural constituent of nuclear pore

DNA secondary structure binding

cyclin binding

ubiquitin binding

ubiquitin protein ligase binding

0

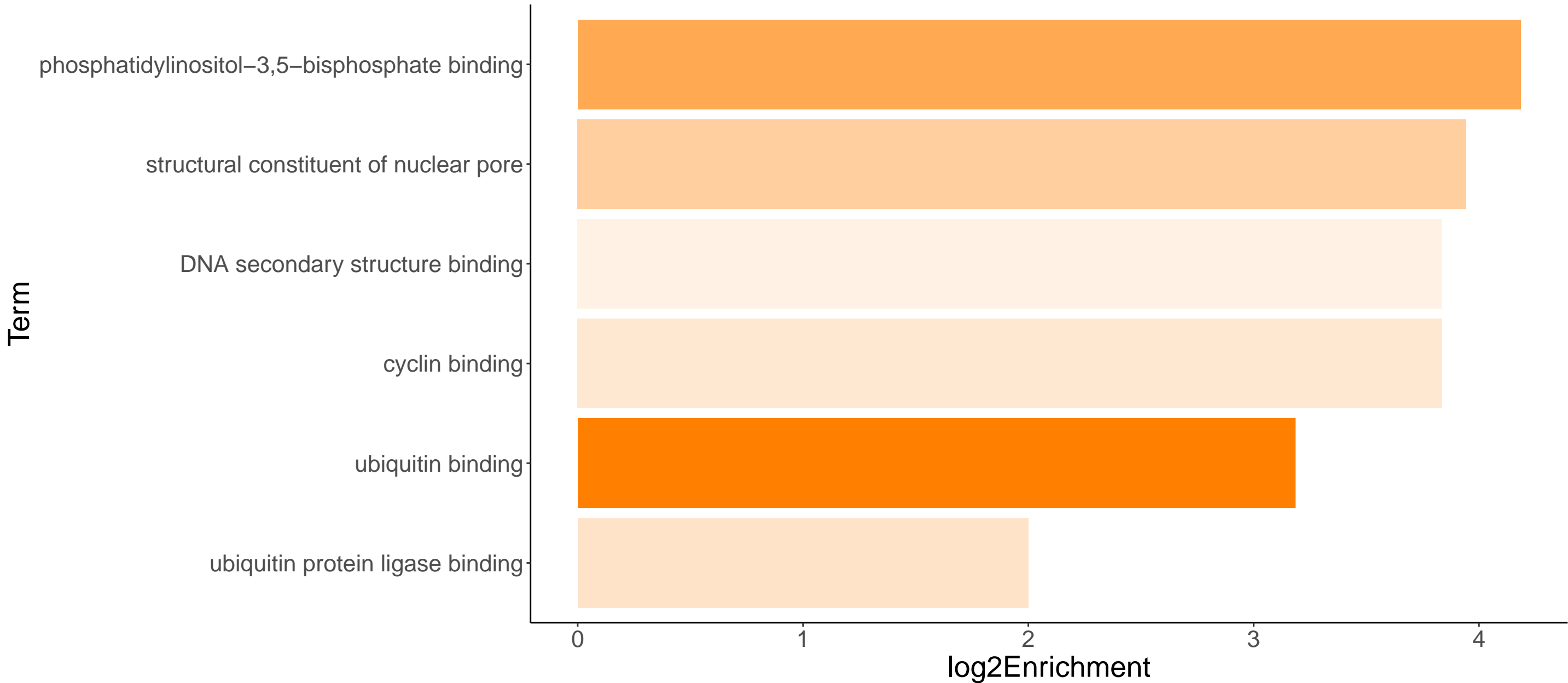
1

2

3

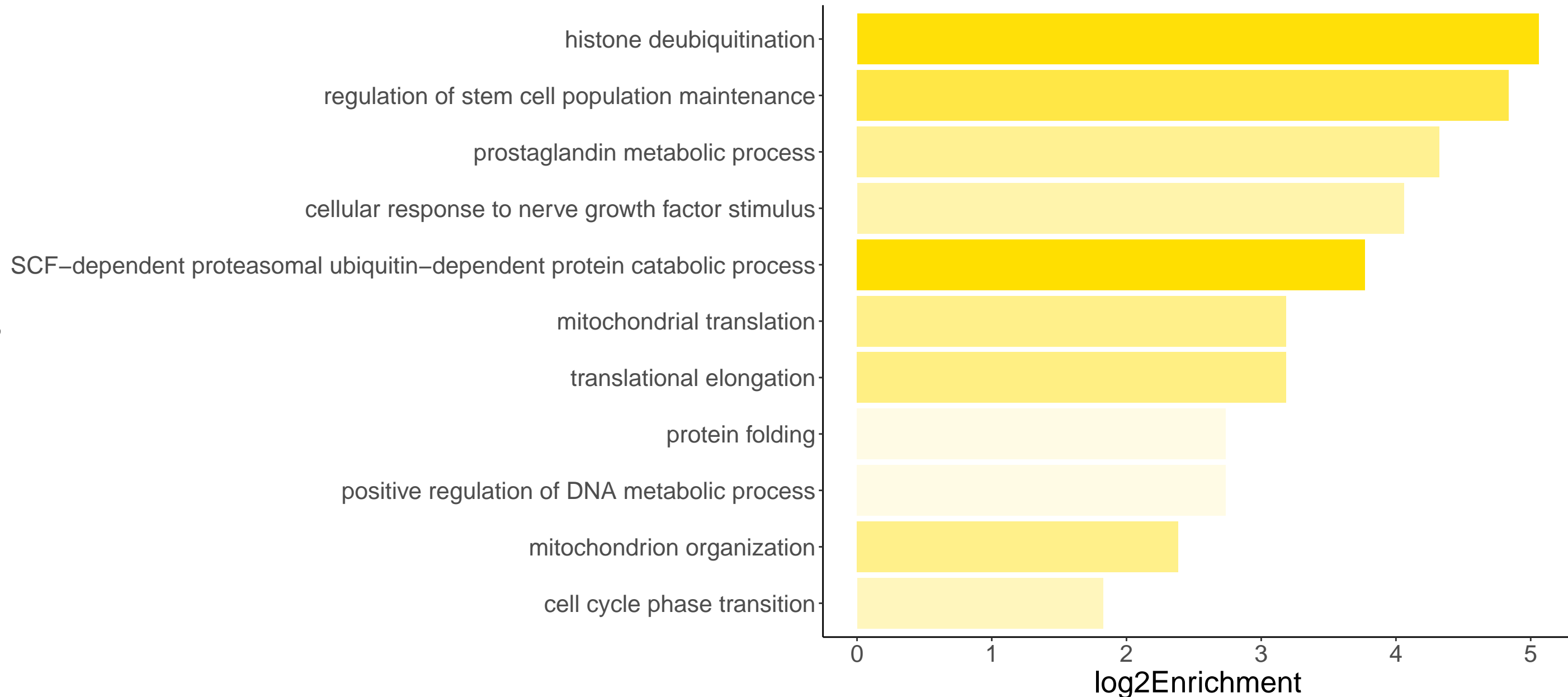
4

log2Enrichment



## Re-clustered module 4.18 BP enrichment

Term



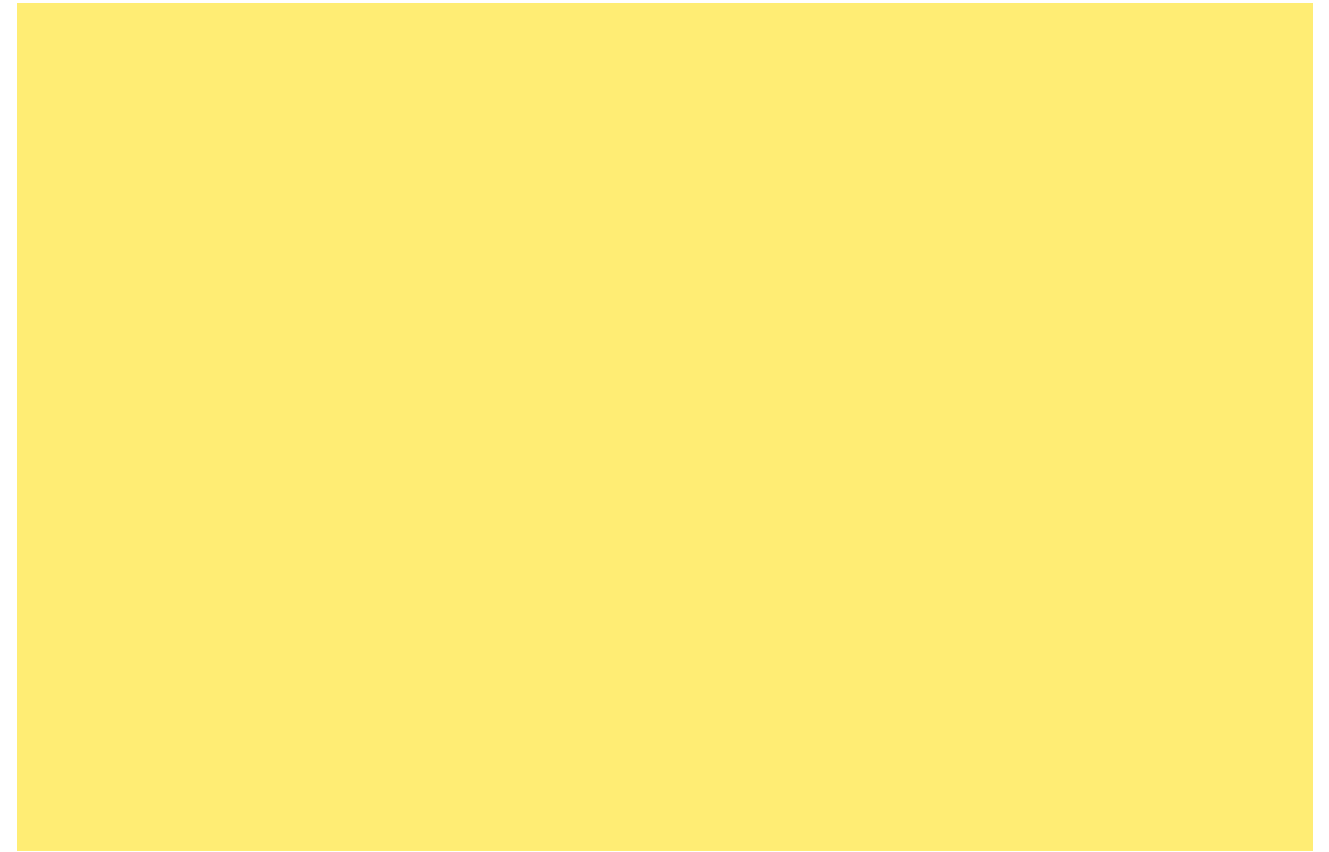
# Re-clustered module 4.18 MF enrichment

Term

DNA-binding transcription activator activity, RNA polymerase II-specific

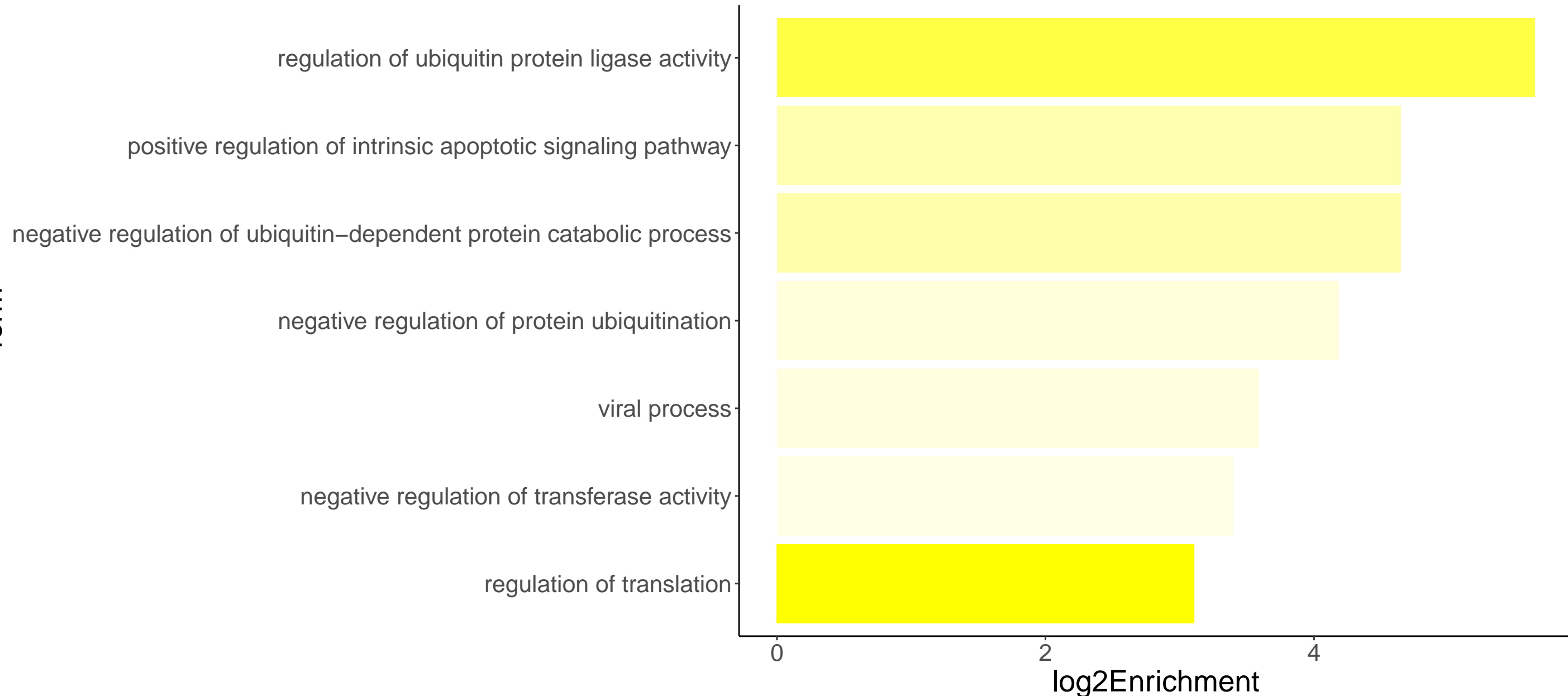
0.0 0.5 1.0 1.5 2.0

log2Enrichment



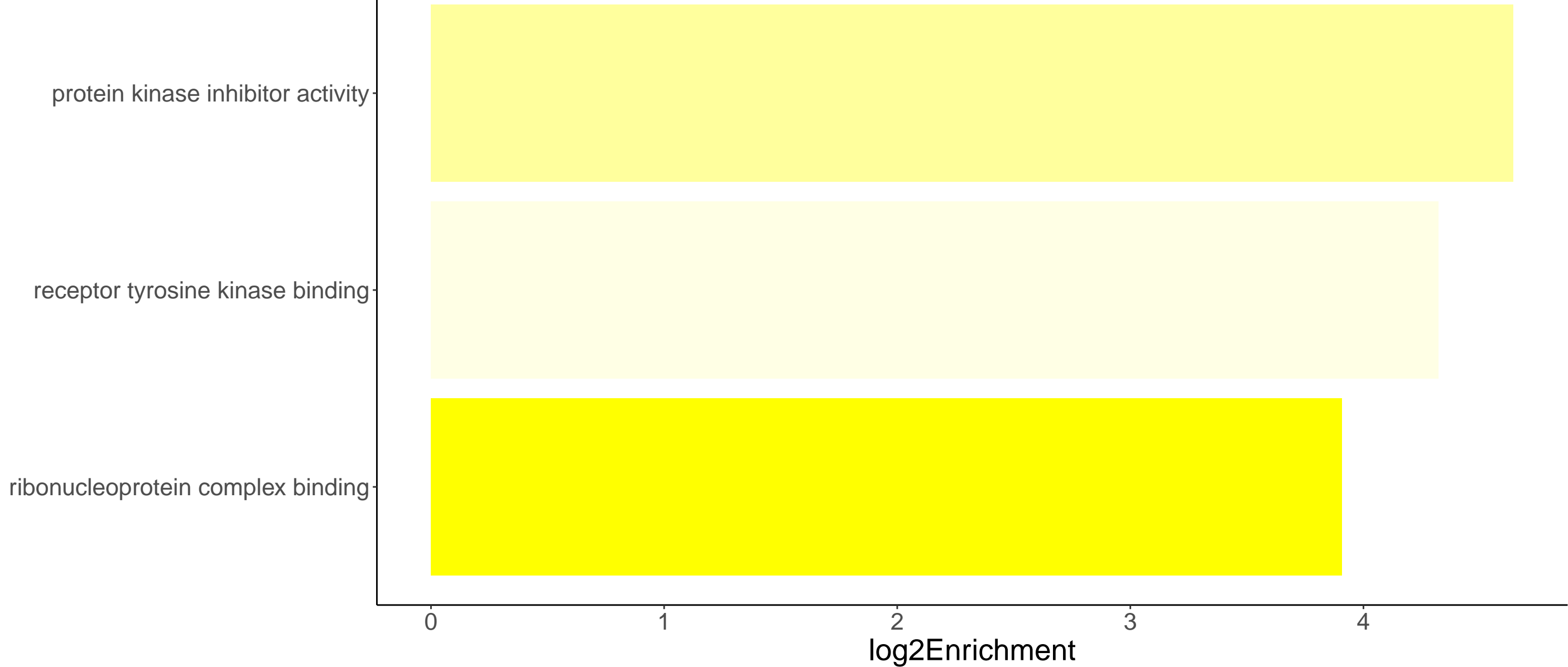
## Re-clustered module 4.19.1 BP enrichment

Term



# Re-clustered module 4.19.1 MF enrichment

Term





# Re-clustered module 4.19.2 BP enrichment

Term

SRP-dependent cotranslational protein targeting to membrane

nuclear-transcribed mRNA catabolic process, nonsense-mediated decay

0

1

2

3

4

log2Enrichment



# Re-clustered module 4.19.2 MF enrichment

Term

ion channel binding

GTP binding

cadherin binding

Ras GTPase binding

0

1

2

3

4

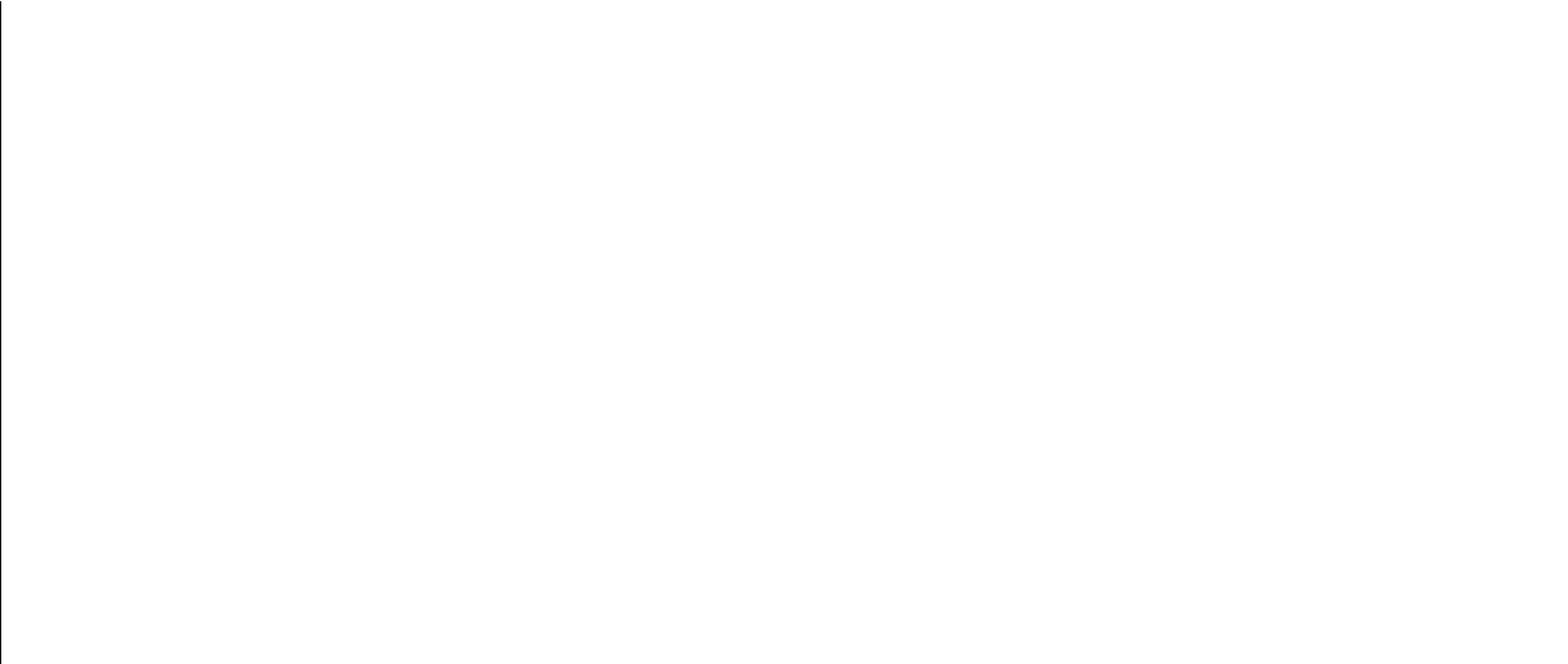
log2Enrichment



Re-clustered module 4.19.4 BP enrichment

Term

log2Enrichment



Re-clustered module 4.19.4 MF enrichment

Term

log2Enrichment



Term

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



Re-clustered module 4.19.8 MF enrichment

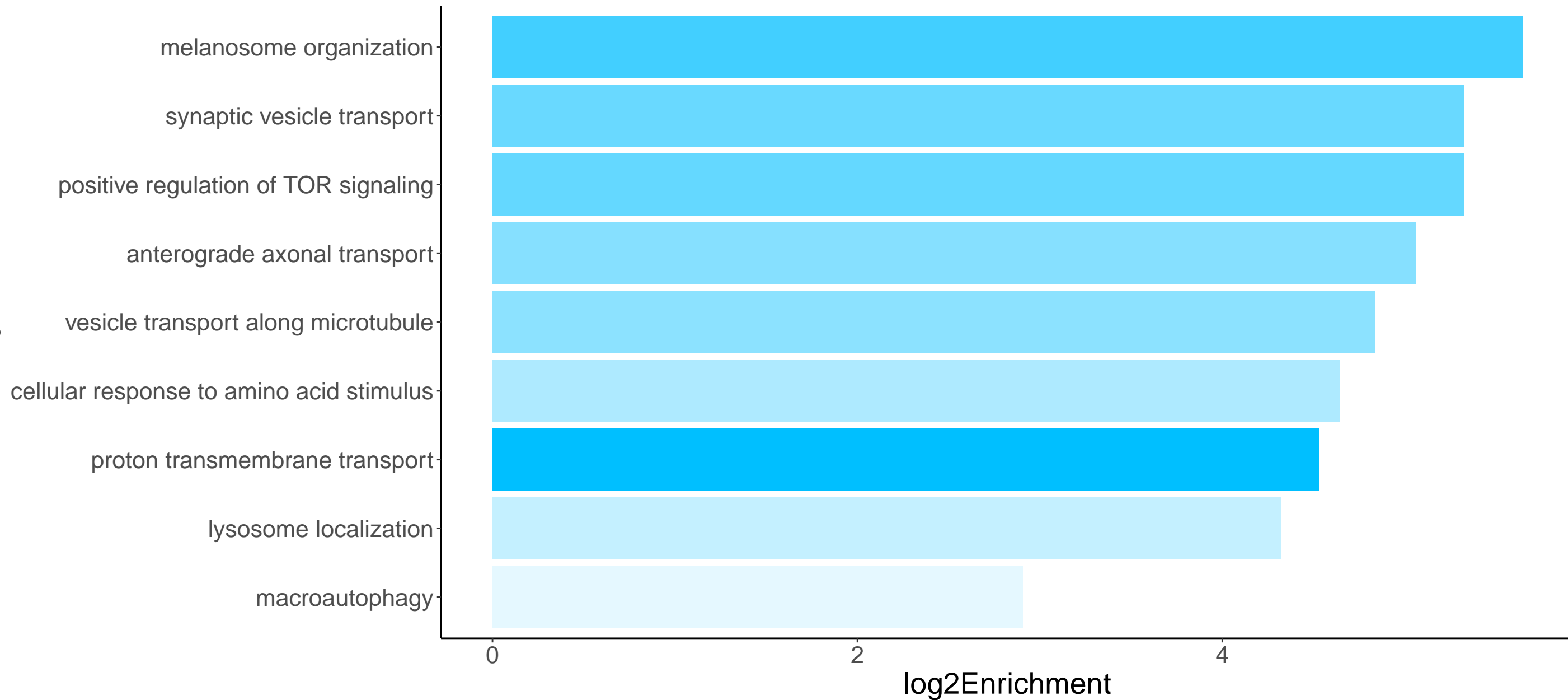
Term

log2Enrichment



## Re-clustered module 4.2.1 BP enrichment

Term



# Re-clustered module 4.2.1 MF enrichment

Term

proton transmembrane transporter activity

0

1

2

3

4

5

log2Enrichment





# Re-clustered module 4.2.12 BP enrichment

Term

positive regulation of cellular amide metabolic process

0

1

2

3

4

log2Enrichment



# Re-clustered module 4.2.12 MF enrichment

Term

RNA methyltransferase activity

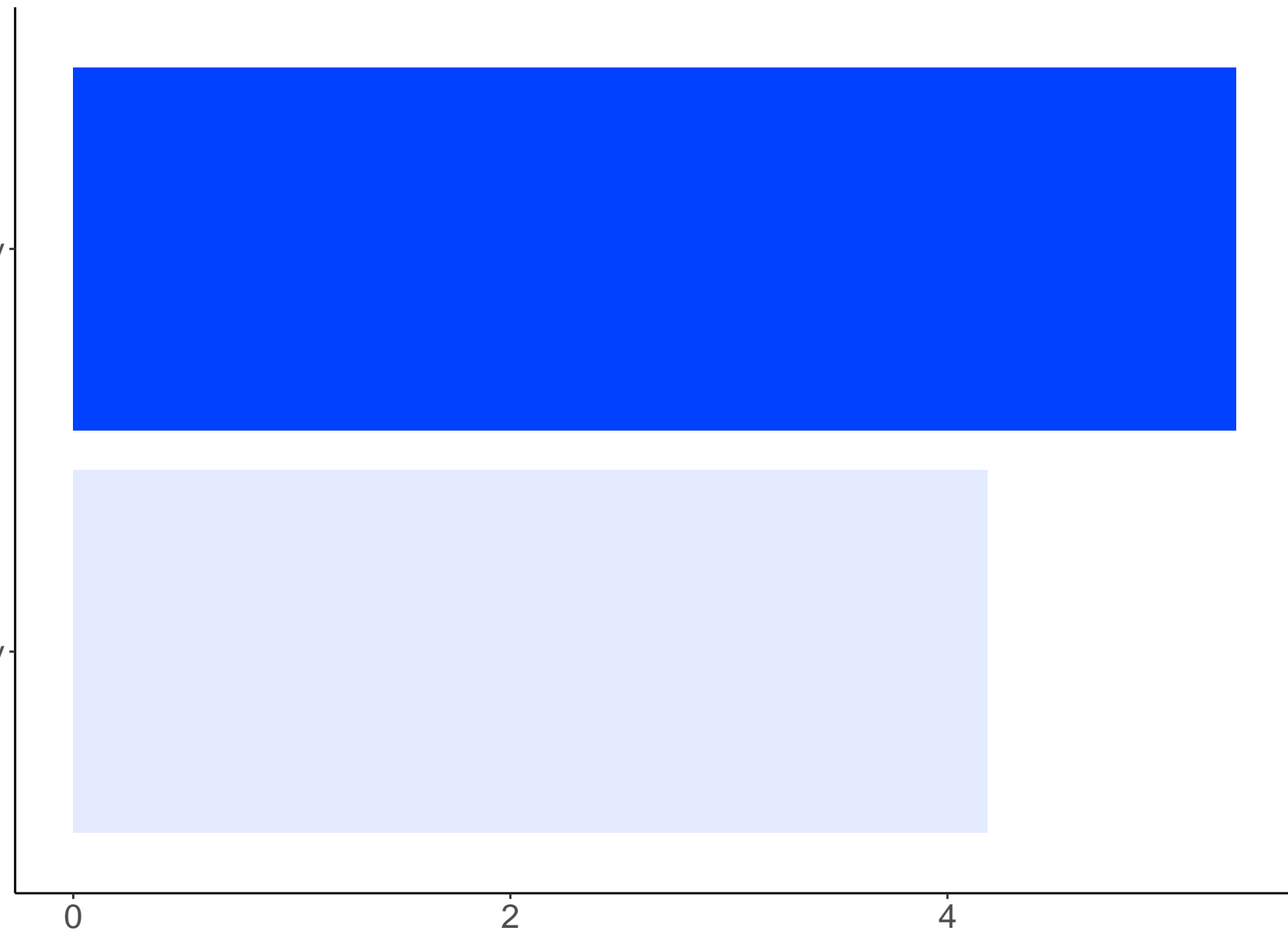
S-adenosylmethionine-dependent methyltransferase activity

0

2

4

log2Enrichment



## Re-clustered module 4.2.2 BP enrichment

Term

establishment of protein localization to mitochondrion

0

1

2

3

4

log2Enrichment



# Re-clustered module 4.2.2 MF enrichment

Term

oxidoreductase activity, acting on NAD(P)H

0

2

4

6

log2Enrichment



Re-clustered module 4.2.3 BP enrichment

Term

log2Enrichment



# Re-clustered module 4.2.3 MF enrichment

Term

rRNA binding

chaperone binding

0

1

2

3

4

log2Enrichment



# Re-clustered module 4.2.4 BP enrichment

Term

mitochondrial respiratory chain complex assembly

0

1

2

3

4

5

log2Enrichment



Re-clustered module 4.2.4 MF enrichment

Term

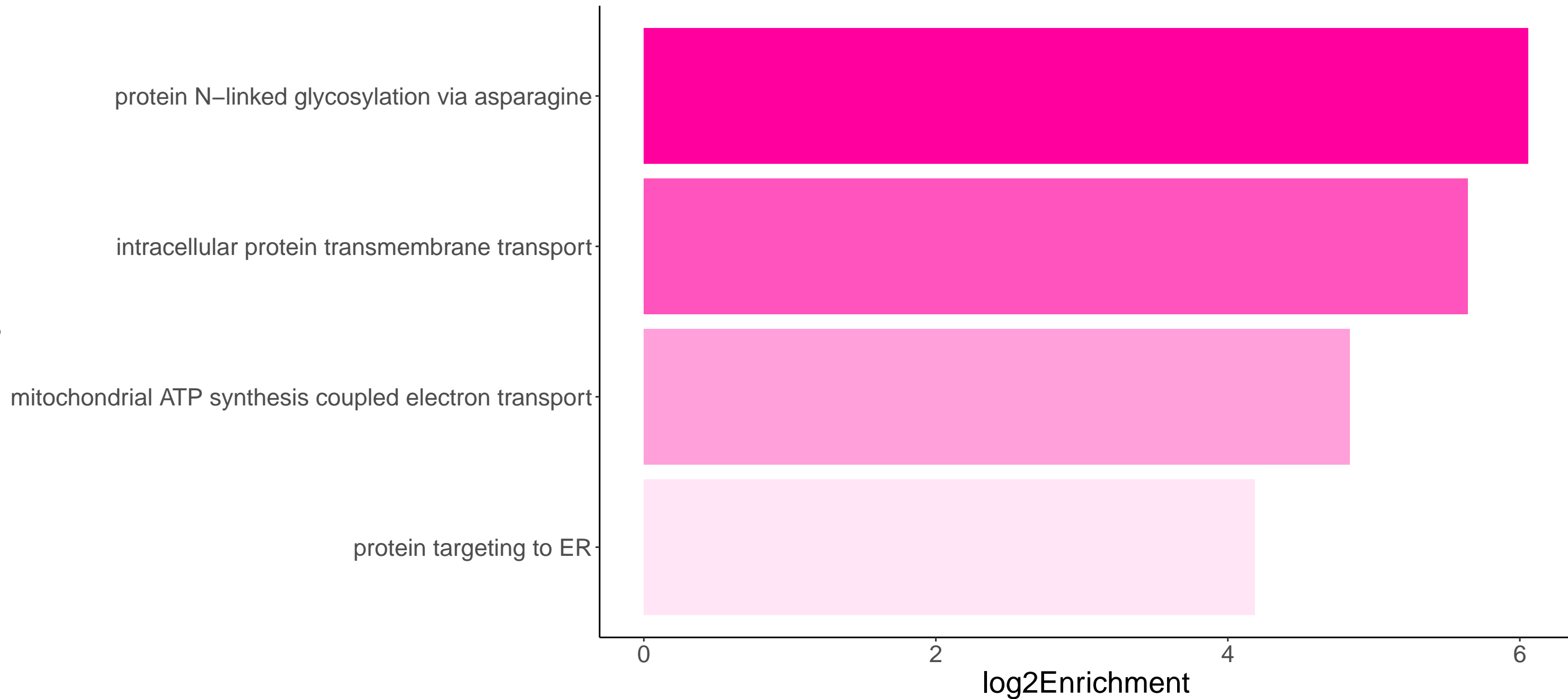
log2Enrichment





## Re-clustered module 4.2.7 BP enrichment

Term



Re-clustered module 4.2.7 MF enrichment

Term

log2Enrichment



# Re-clustered module 4.2.9 BP enrichment

Term

proton transmembrane transport

0

1

2

3

4

5

log2Enrichment



# Re-clustered module 4.2.9 MF enrichment

Term

NADH dehydrogenase (ubiquinone) activity

proton transmembrane transporter activity

0

2

4

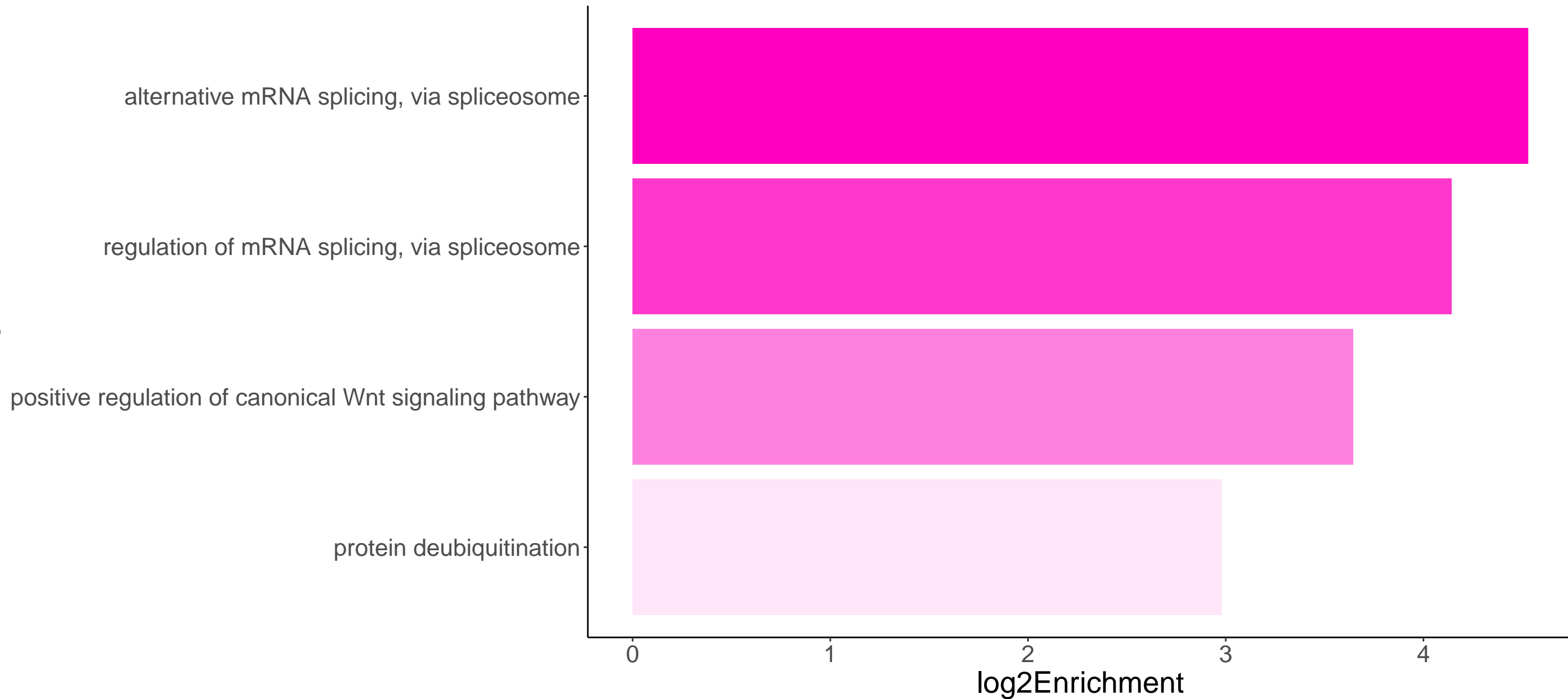
6

log2Enrichment



## Re-clustered module 4.20 BP enrichment

Term



# Re-clustered module 4.20 MF enrichment

Term

signaling adaptor activity

0

1

2

3

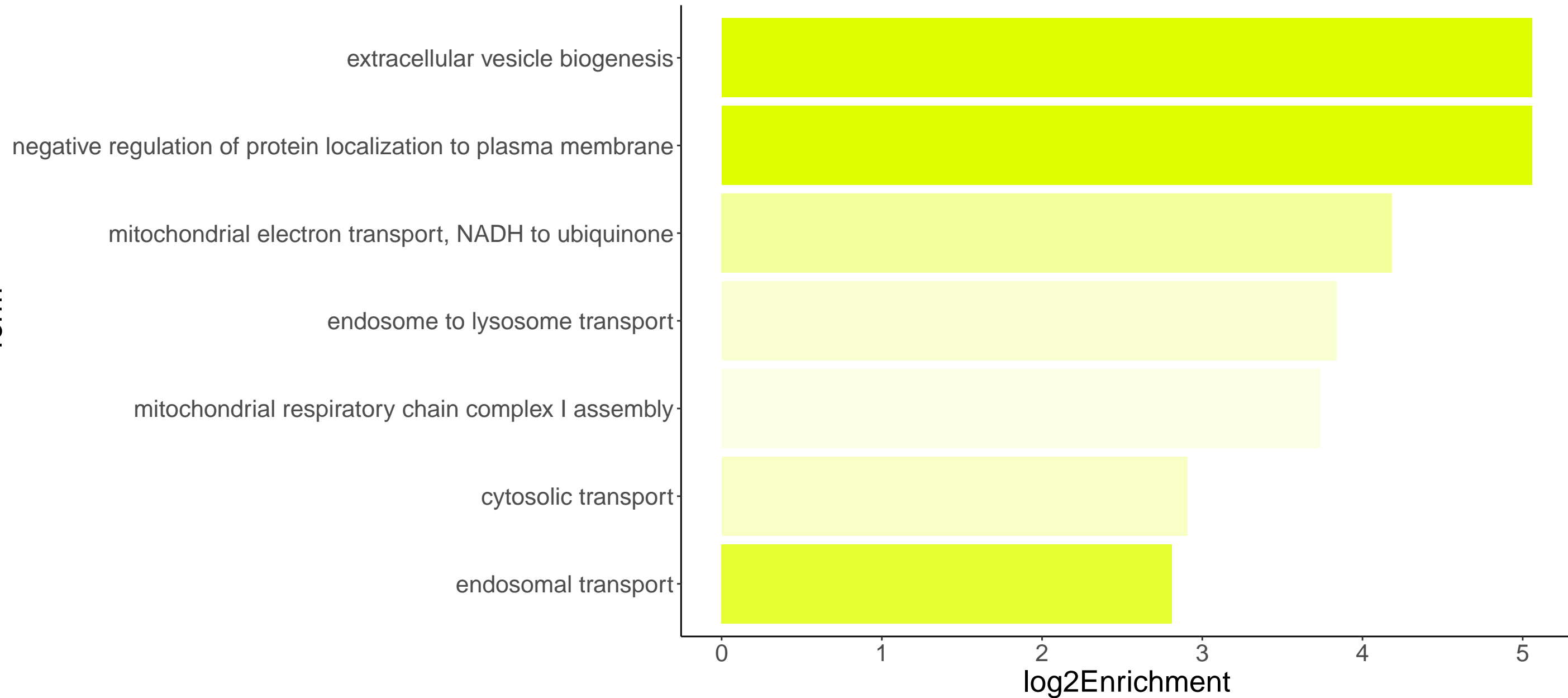
4

log2Enrichment



## Re-clustered module 4.21 BP enrichment

Term



Re-clustered module 4.21 MF enrichment

Term

log2Enrichment





## Re-clustered module 4.22 BP enrichment

Term

tRNA aminoacylation for protein translation

vesicle transport along microtubule

protein targeting to peroxisome

protein transmembrane transport

mitochondrial translation

0

1

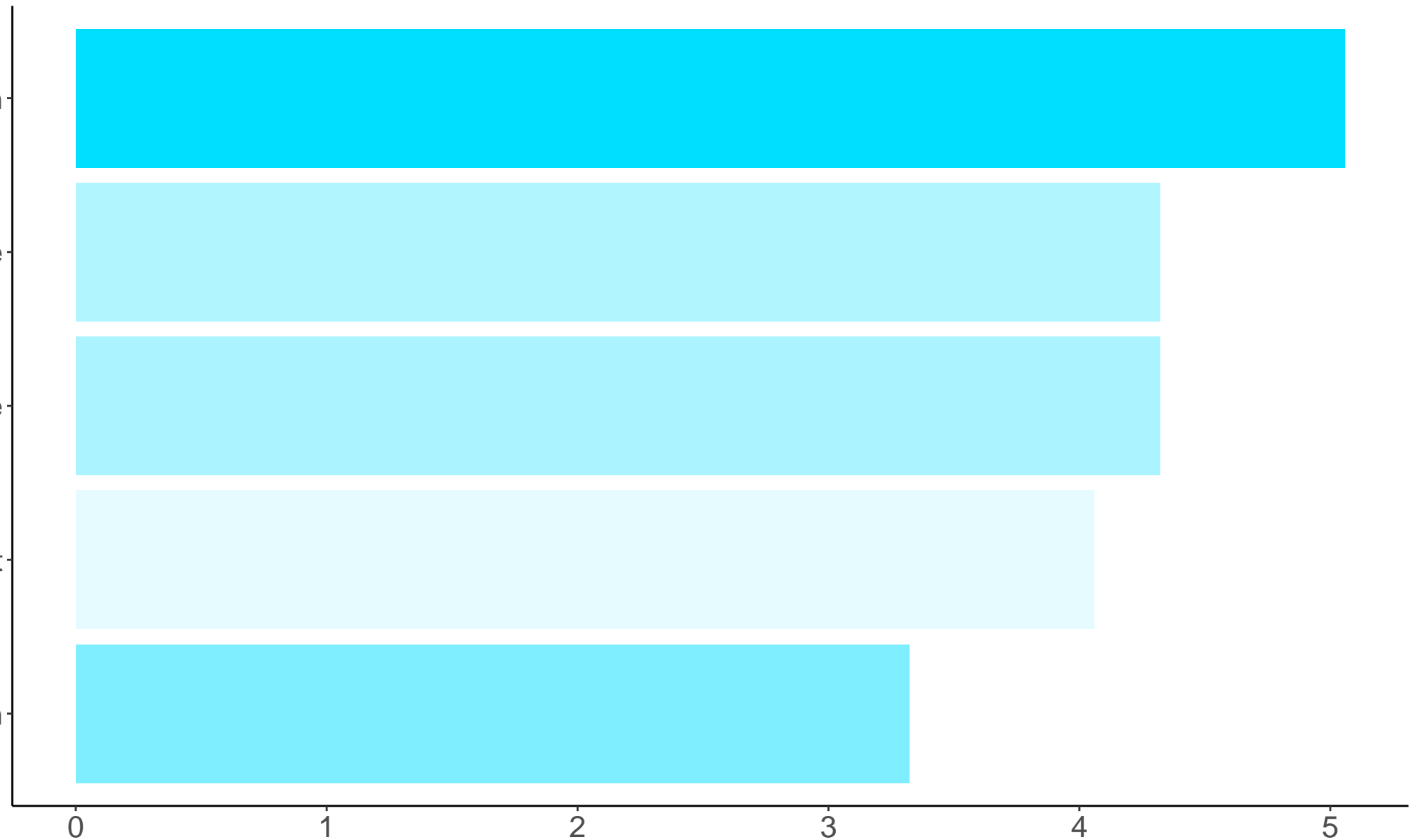
2

3

4

5

log2Enrichment



## Re-clustered module 4.22 MF enrichment

Term

macromolecule transmembrane transporter activity

tRNA binding

myosin binding

catalytic activity, acting on a tRNA

protein serine/threonine phosphatase activity

protein phosphatase binding

0

2

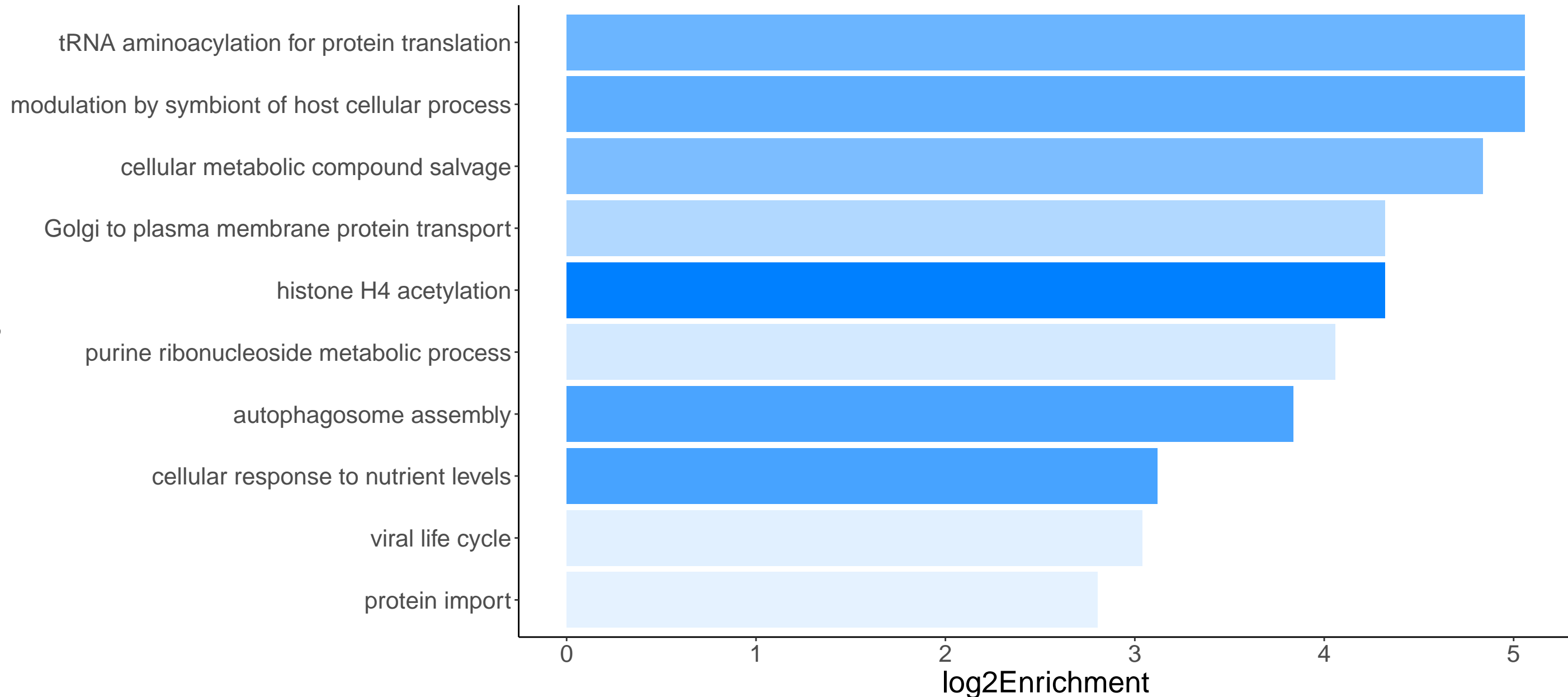
4

log2Enrichment



## Re-clustered module 4.23 BP enrichment

Term



## Re-clustered module 4.23 MF enrichment

Term

nuclear localization sequence binding

nucleocytoplasmic carrier activity

Ran GTPase binding

helicase activity

0

1

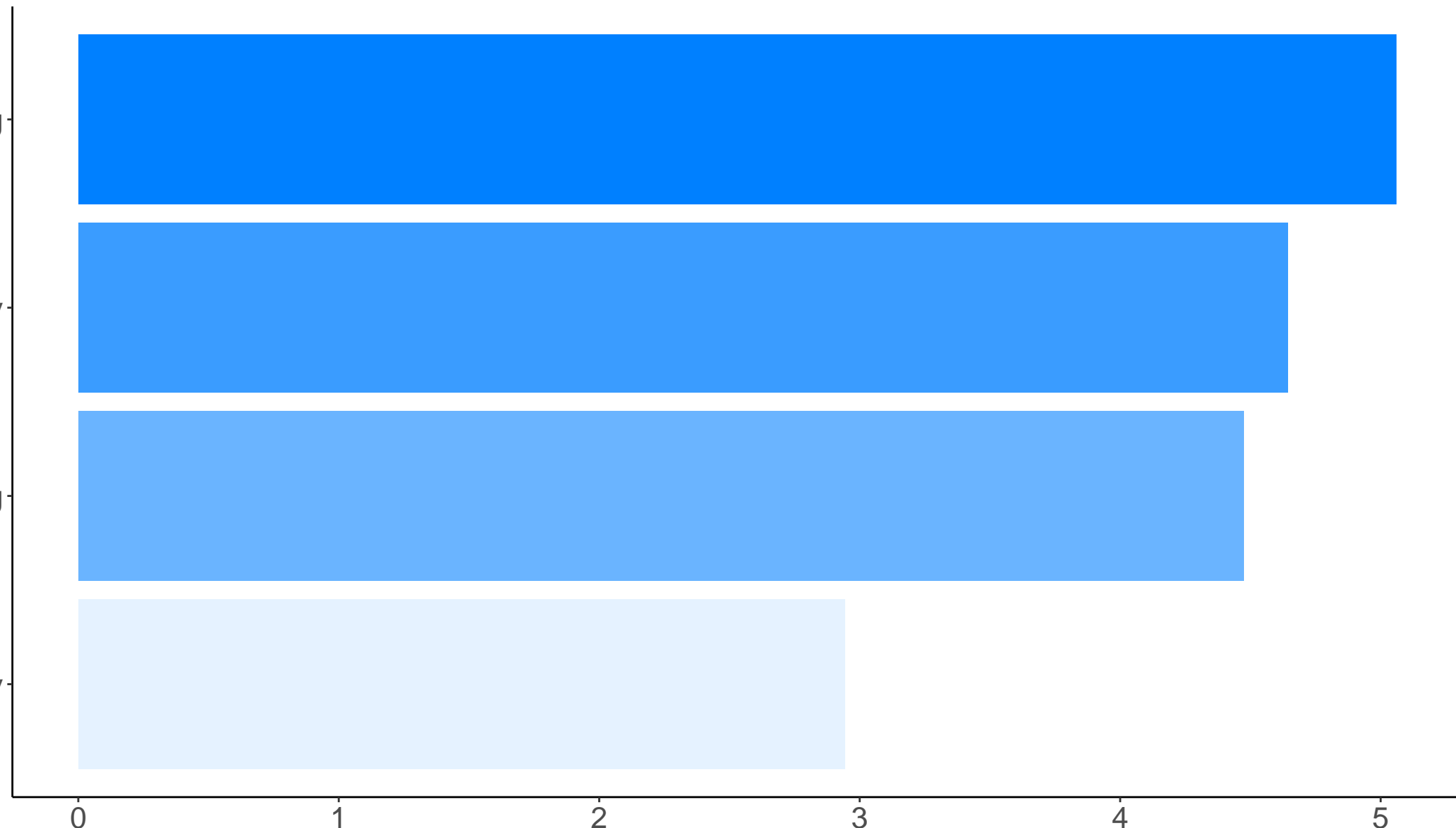
2

3

4

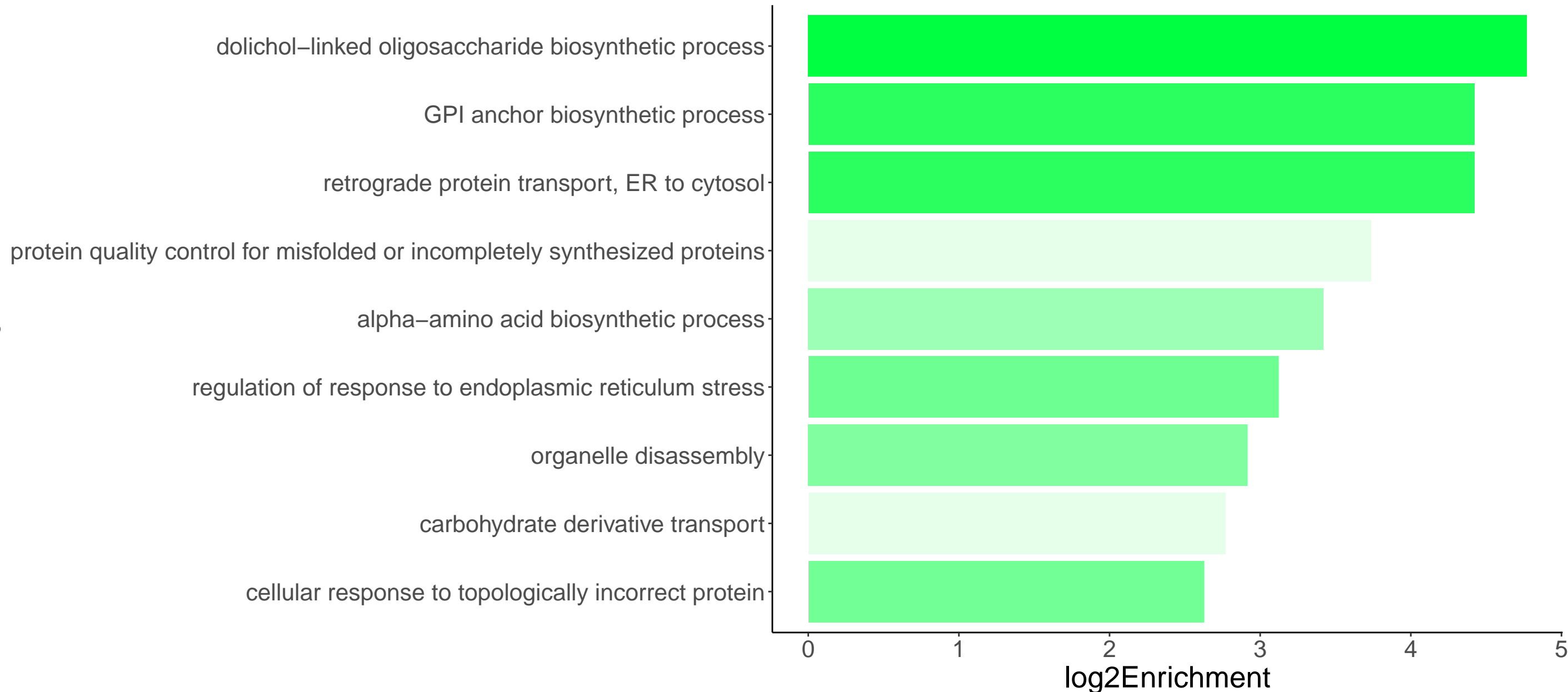
5

log2Enrichment



## Re-clustered module 4.24 BP enrichment

Term



# Re-clustered module 4.24 MF enrichment

Term

O-methyltransferase activity

0

1

2

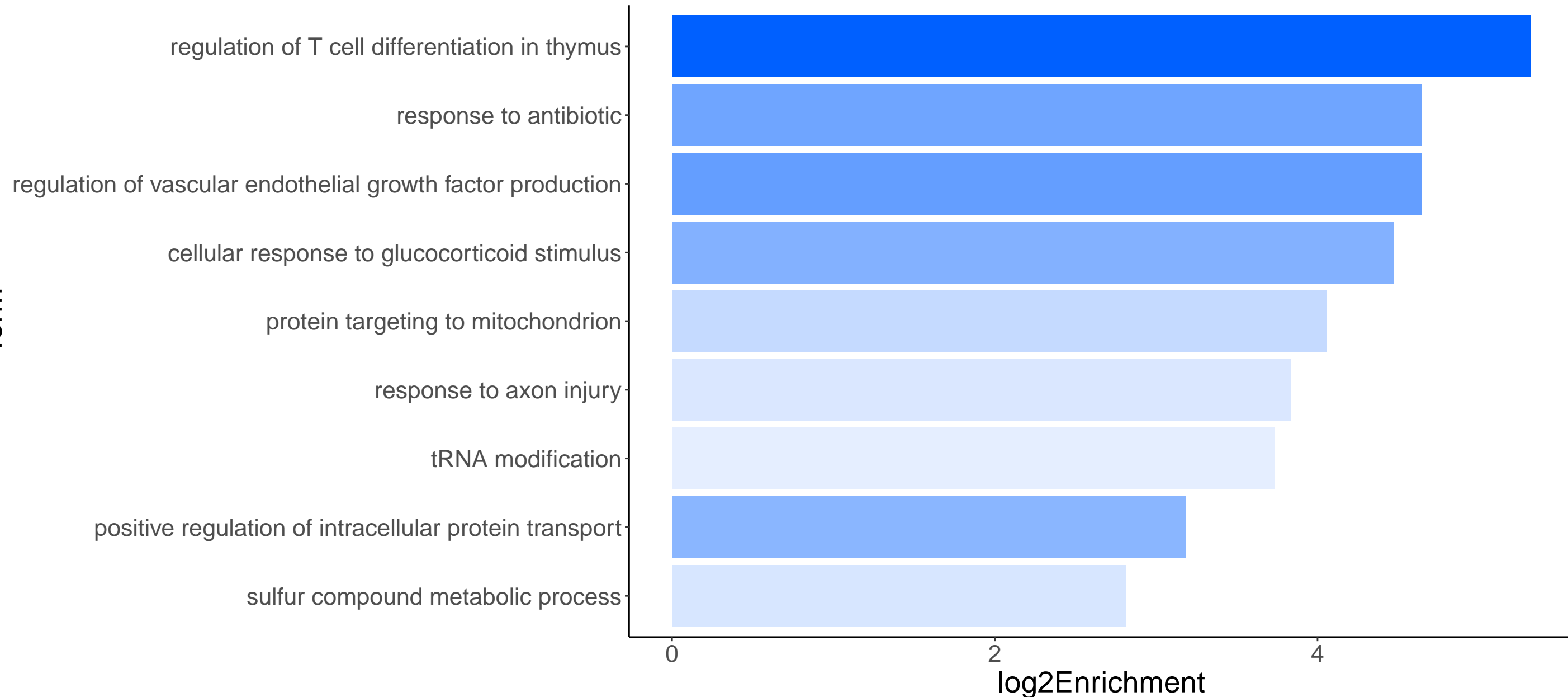
3

4

log2Enrichment



## Re-clustered module 4.25 BP enrichment



# Re-clustered module 4.25 MF enrichment

Term

iron-sulfur cluster binding

0

1

2

3

4

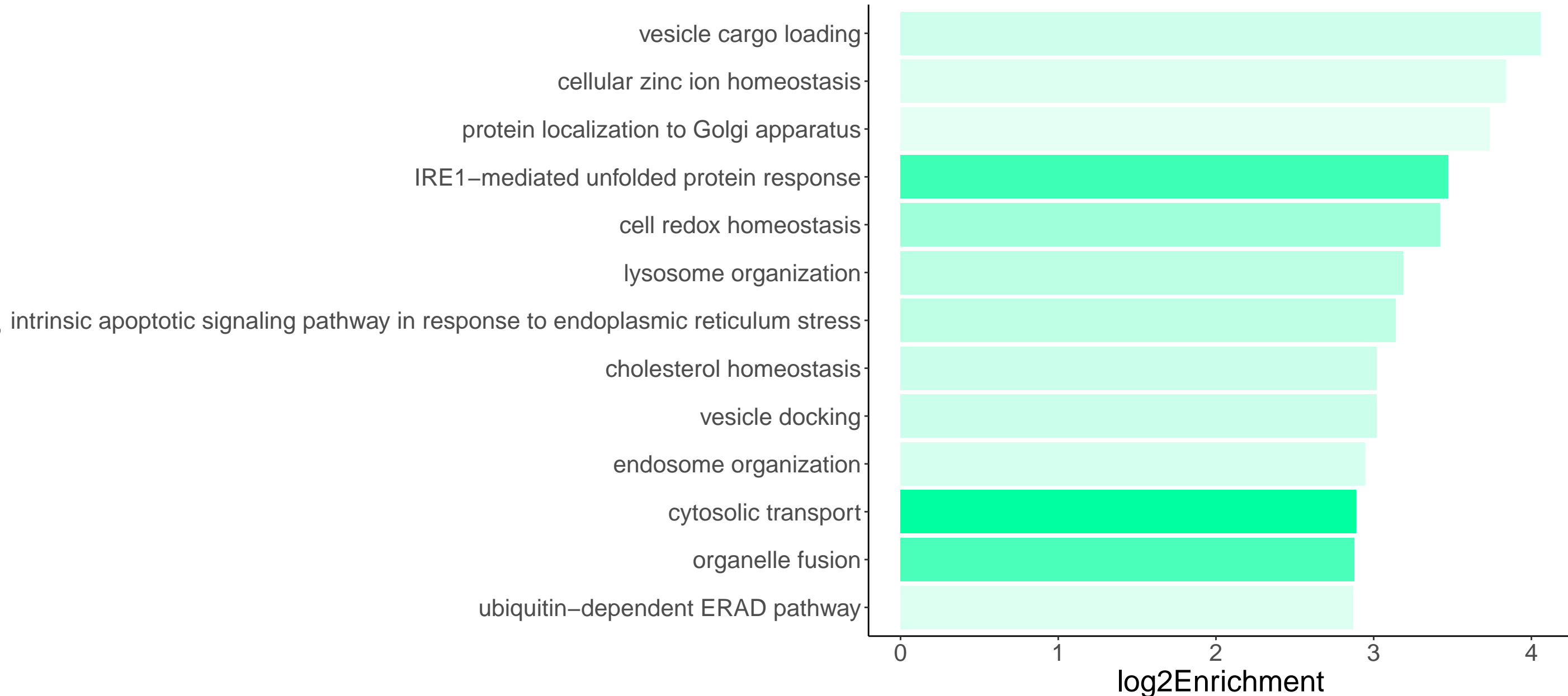
log2Enrichment





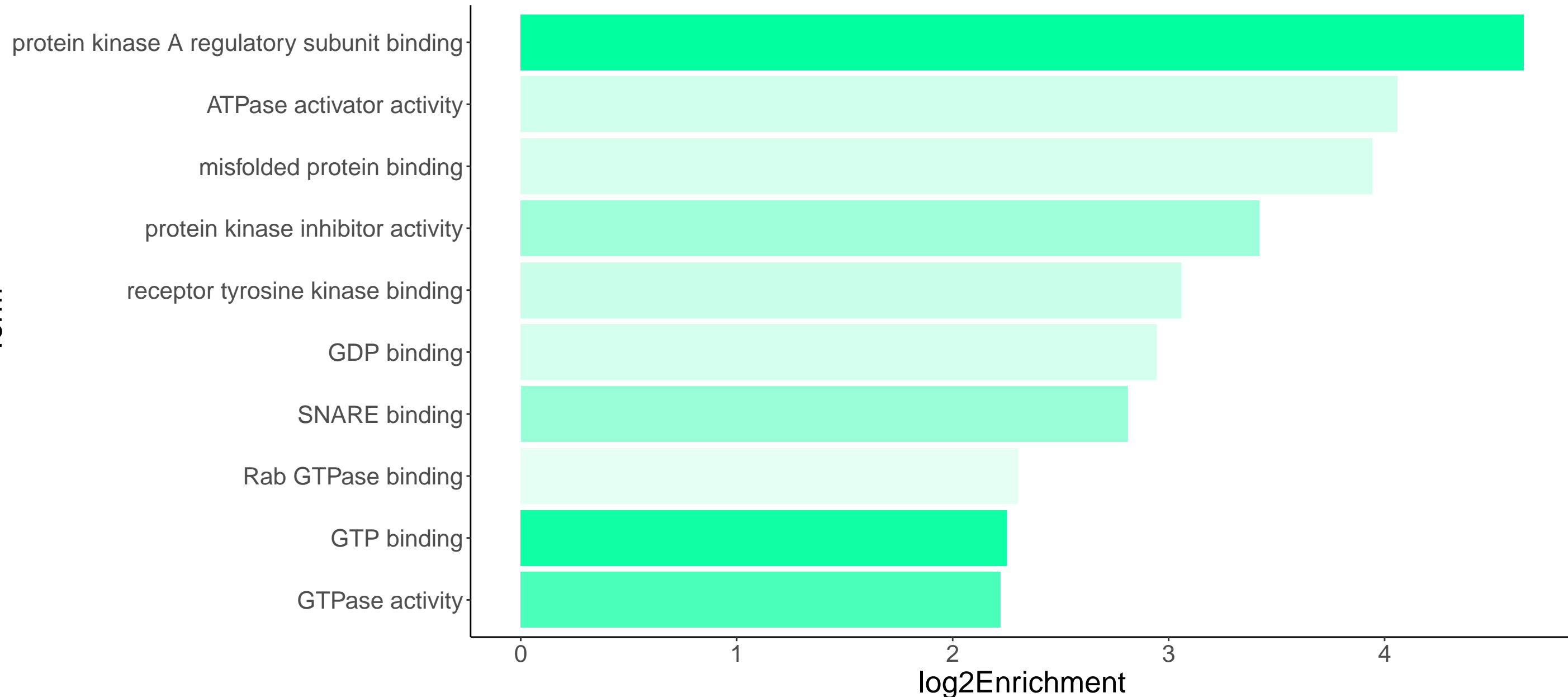
# Re-clustered module 4.26 BP enrichment

Term



## Re-clustered module 4.26 MF enrichment

Term



## Re-clustered module 4.27 BP enrichment

Term

protein quality control for misfolded or incompletely synthesized proteins

stem cell division

mitotic metaphase plate congression

spliceosomal snRNP assembly

regulation of multicellular organism growth

positive regulation of mitotic cell cycle phase transition

regulation of mitotic metaphase/anaphase transition

regulation of protein stability

0

1

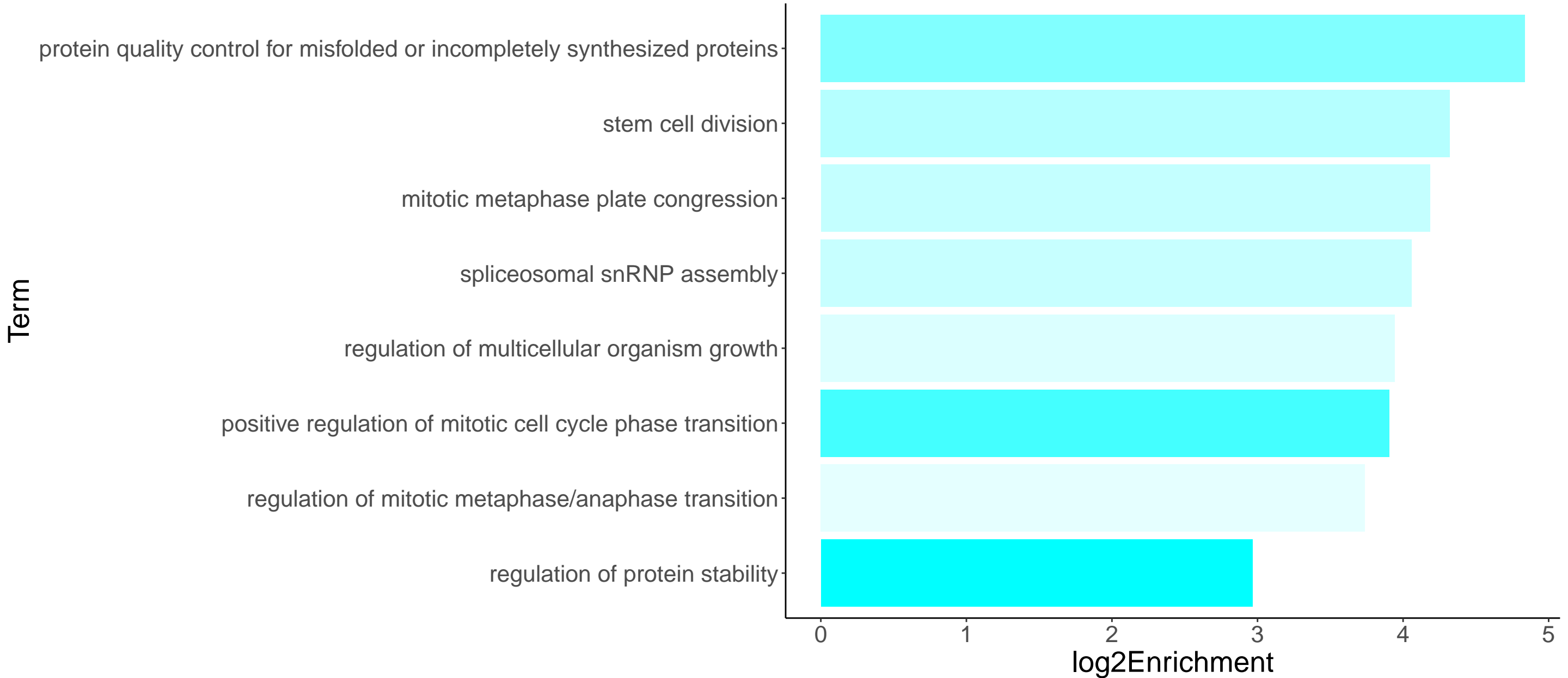
2

3

4

5

log2Enrichment



# Re-clustered module 4.27 MF enrichment

Term

RNA polymerase II activating transcription factor binding

catalytic activity, acting on DNA

helicase activity

0

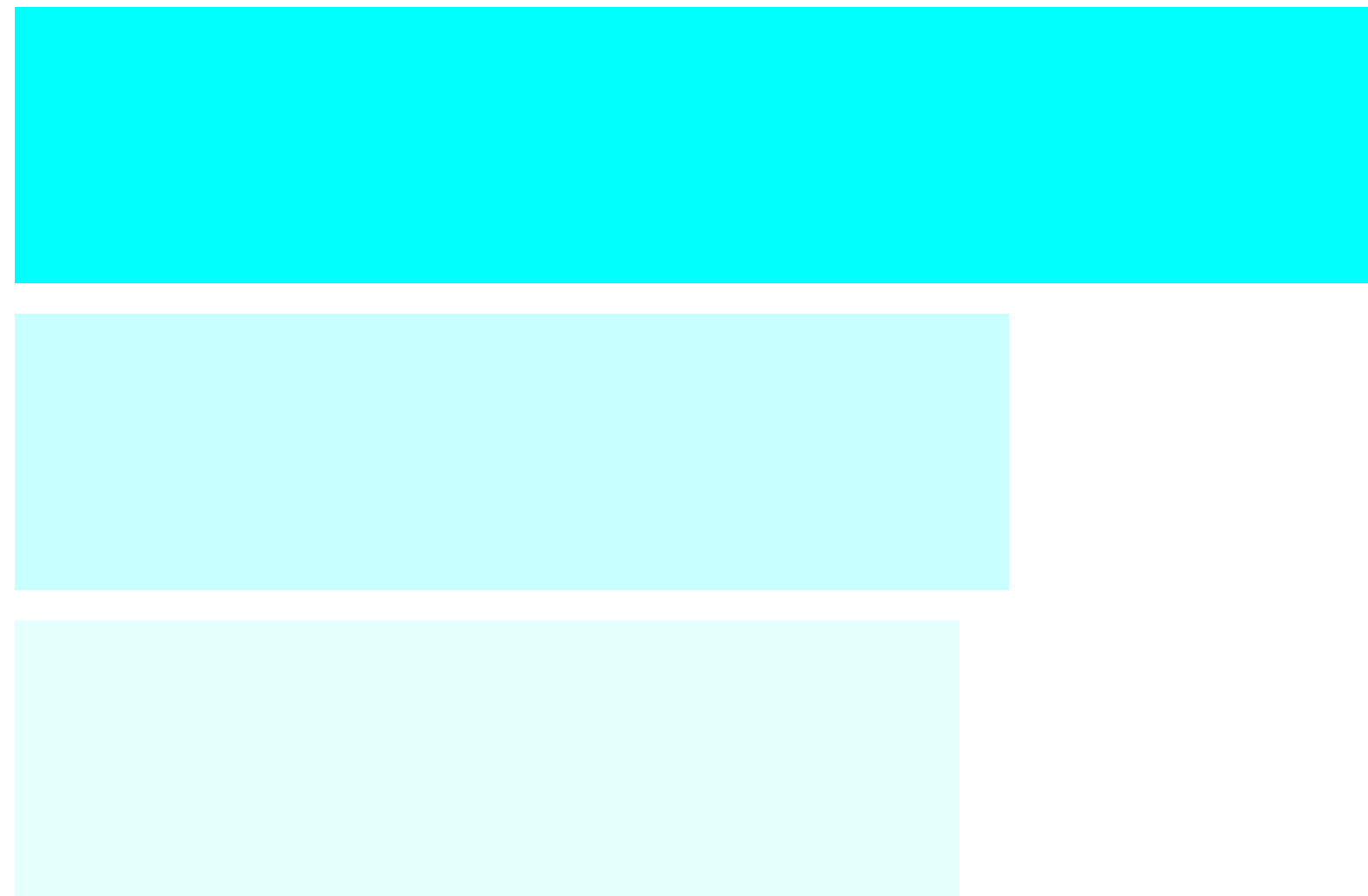
1

2

3

4

log2Enrichment



# Re-clustered module 4.28 BP enrichment

Term

vesicle cargo loading

vesicle coating

retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum

antigen processing and presentation of exogenous peptide antigen via MHC class II

translational elongation

endoplasmic reticulum to Golgi vesicle-mediated transport

nucleus organization

mitochondrion organization

0

1

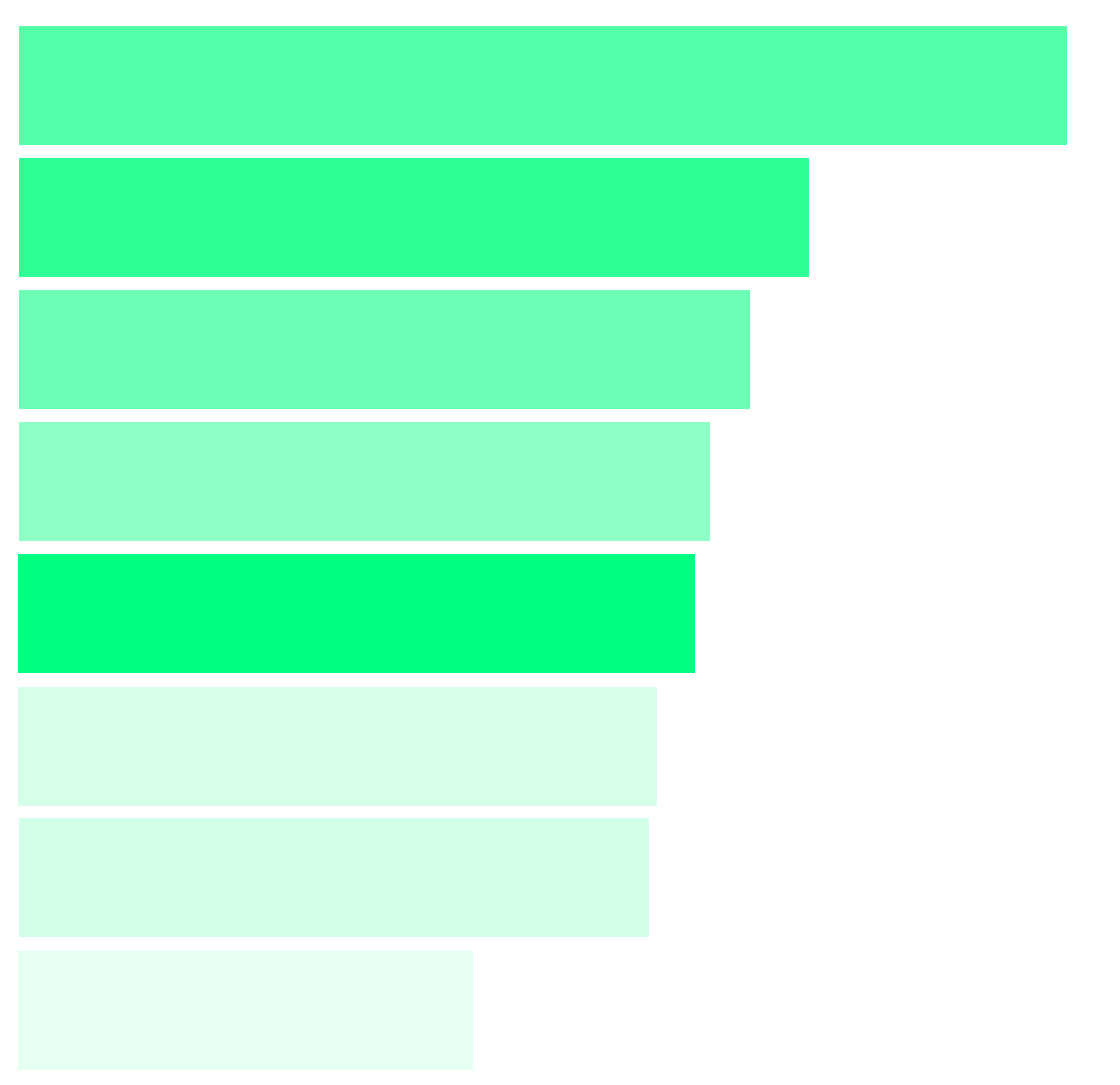
2

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4

5

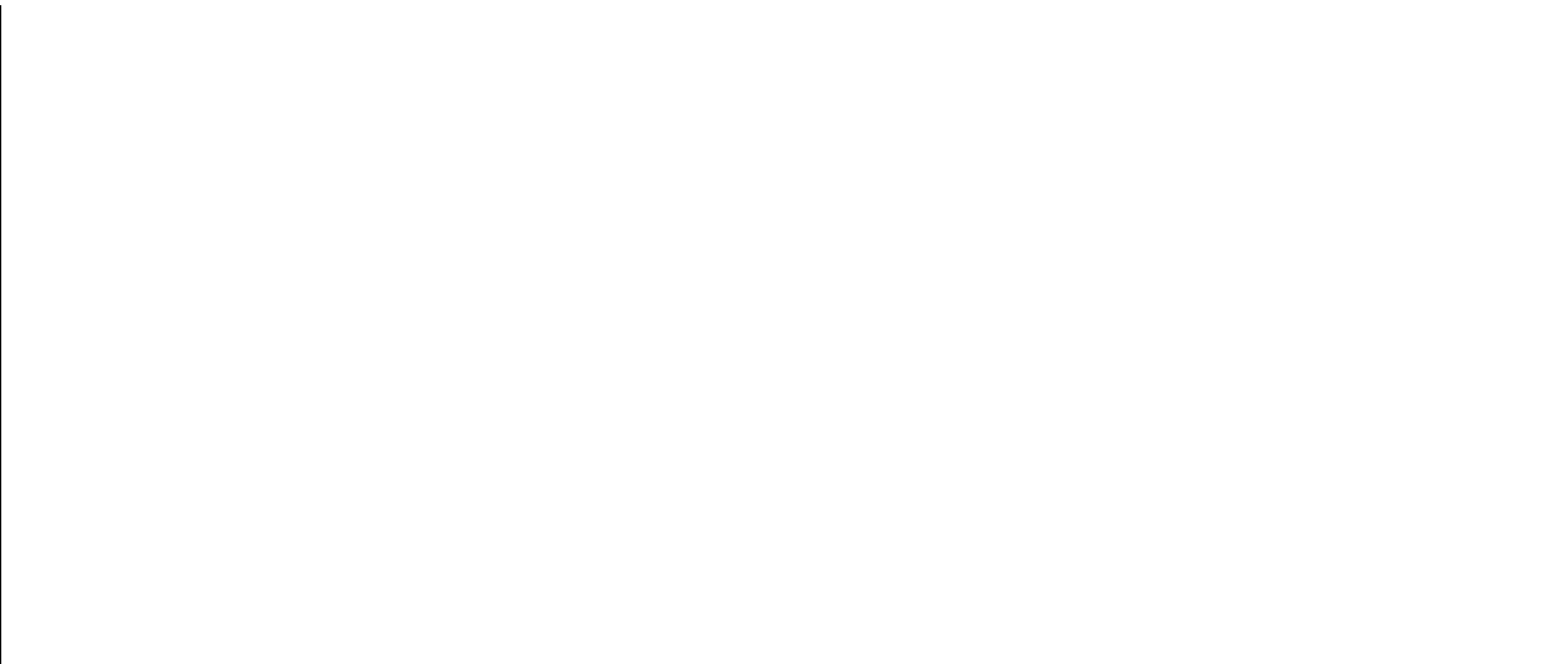
log2Enrichment



Re-clustered module 4.28 MF enrichment

Term

log2Enrichment



## Re-clustered module 4.29 BP enrichment

Term

regulation of endoplasmic reticulum unfolded protein response

face morphogenesis

positive regulation of response to endoplasmic reticulum stress

Golgi to plasma membrane protein transport

endoplasmic reticulum organization

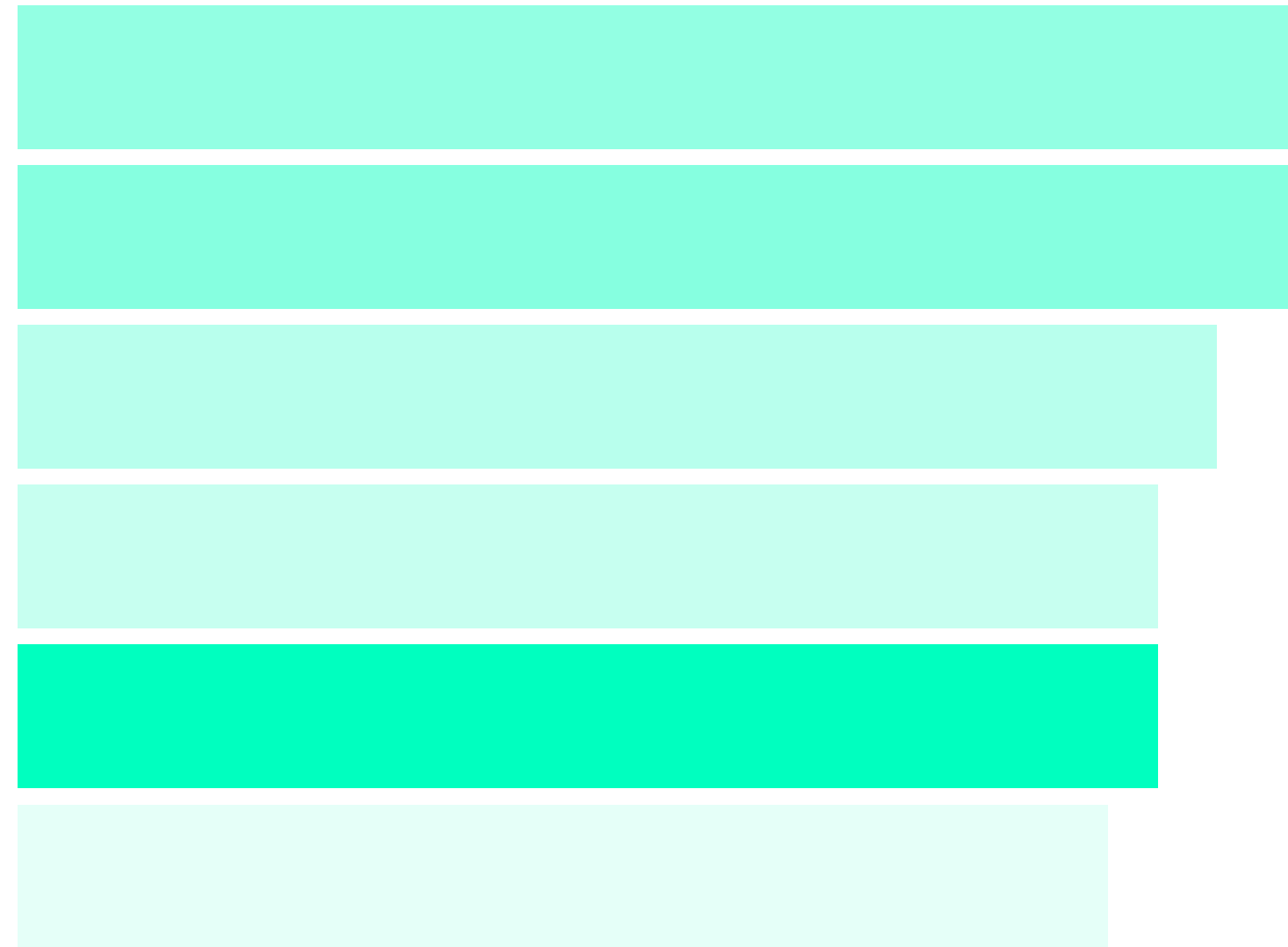
ER-nucleus signaling pathway

0

2

4

log2Enrichment



# Re-clustered module 4.29 MF enrichment

Term

ubiquitin protein ligase binding

0

1

2

3

log2Enrichment





# Re-clustered module 4.3 BP enrichment

Term

transcription by RNA polymerase III

cellular response to glucocorticoid stimulus

mitochondrial translation

translational elongation

0

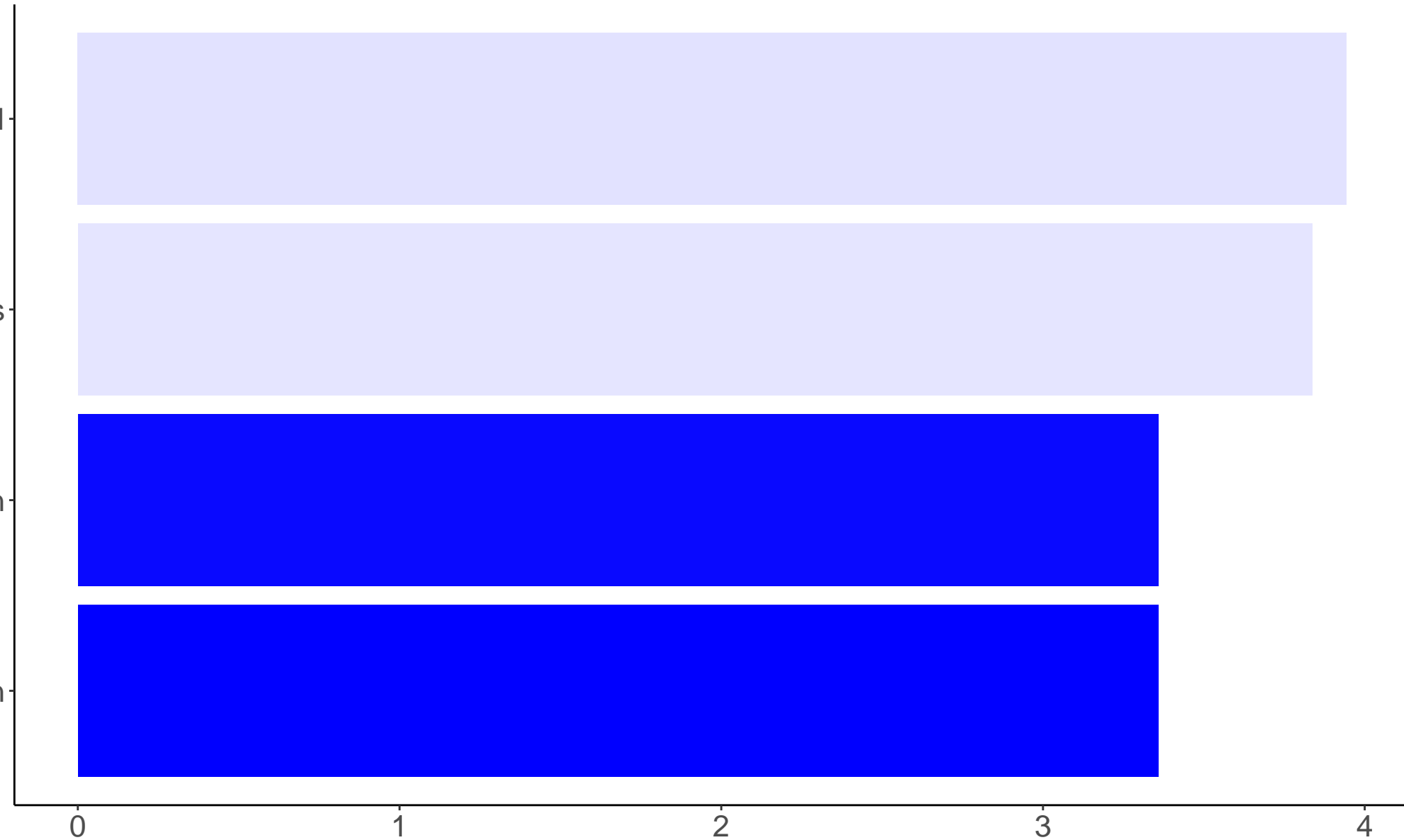
1

2

3

4

log2Enrichment



# Re-clustered module 4.3 MF enrichment

Term

lysine-acetylated histone binding

DNA-directed 5'-3' RNA polymerase activity

0

1

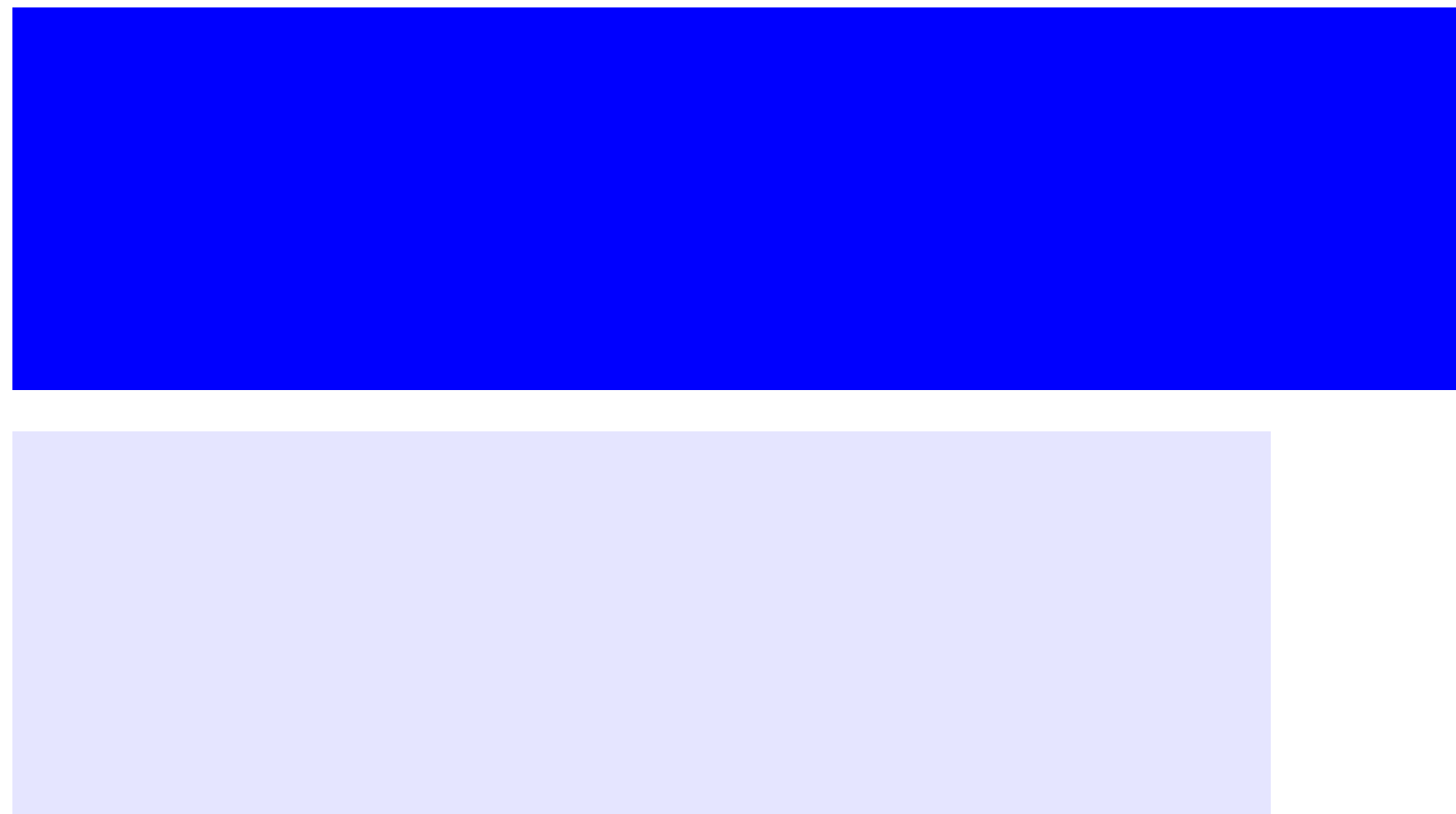
2

3

4

5

log2Enrichment



# Re-clustered module 4.4 BP enrichment

Term

syncytium formation by plasma membrane fusion

RNA phosphodiester bond hydrolysis, exonucleolytic

0

1

2

3

4

log2Enrichment



# Re-clustered module 4.4 MF enrichment

Term

telomeric DNA binding

3'-5' exonuclease activity

signal sequence binding

nucleic acid binding

0

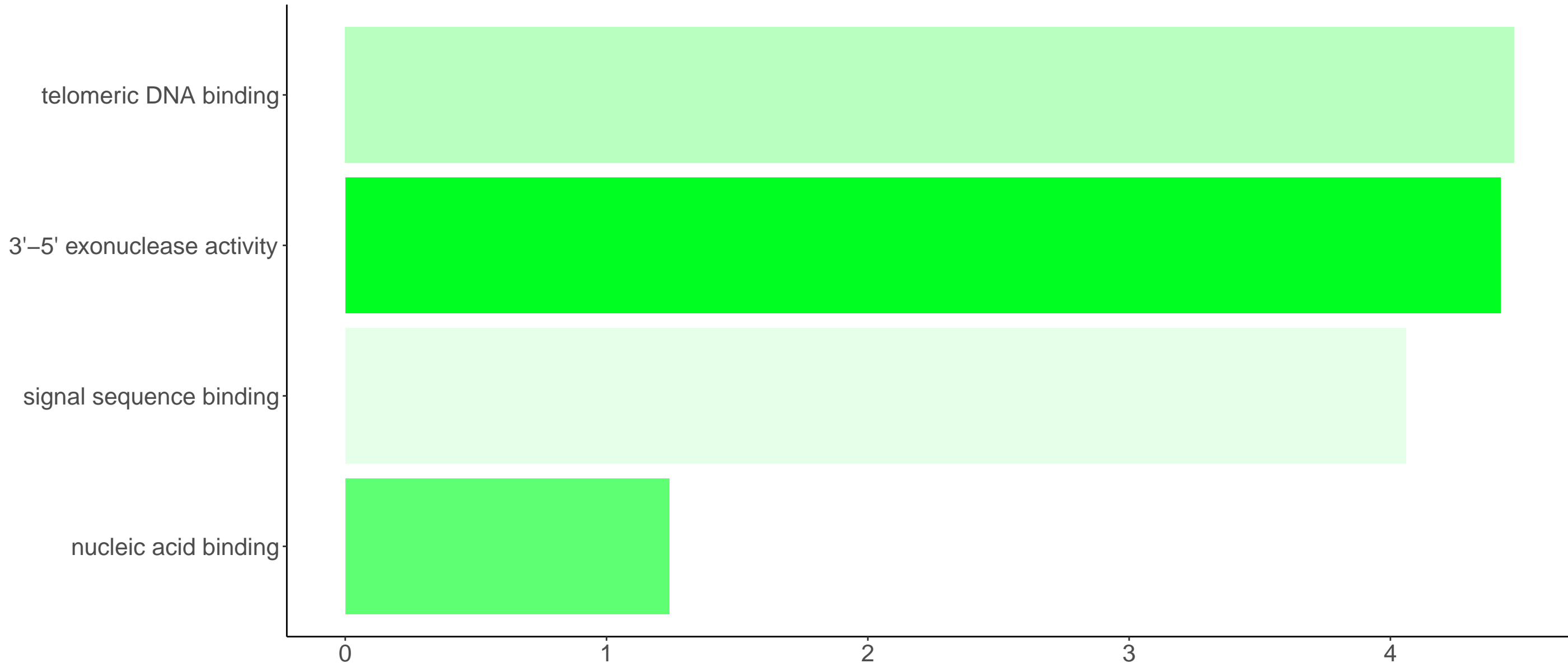
1

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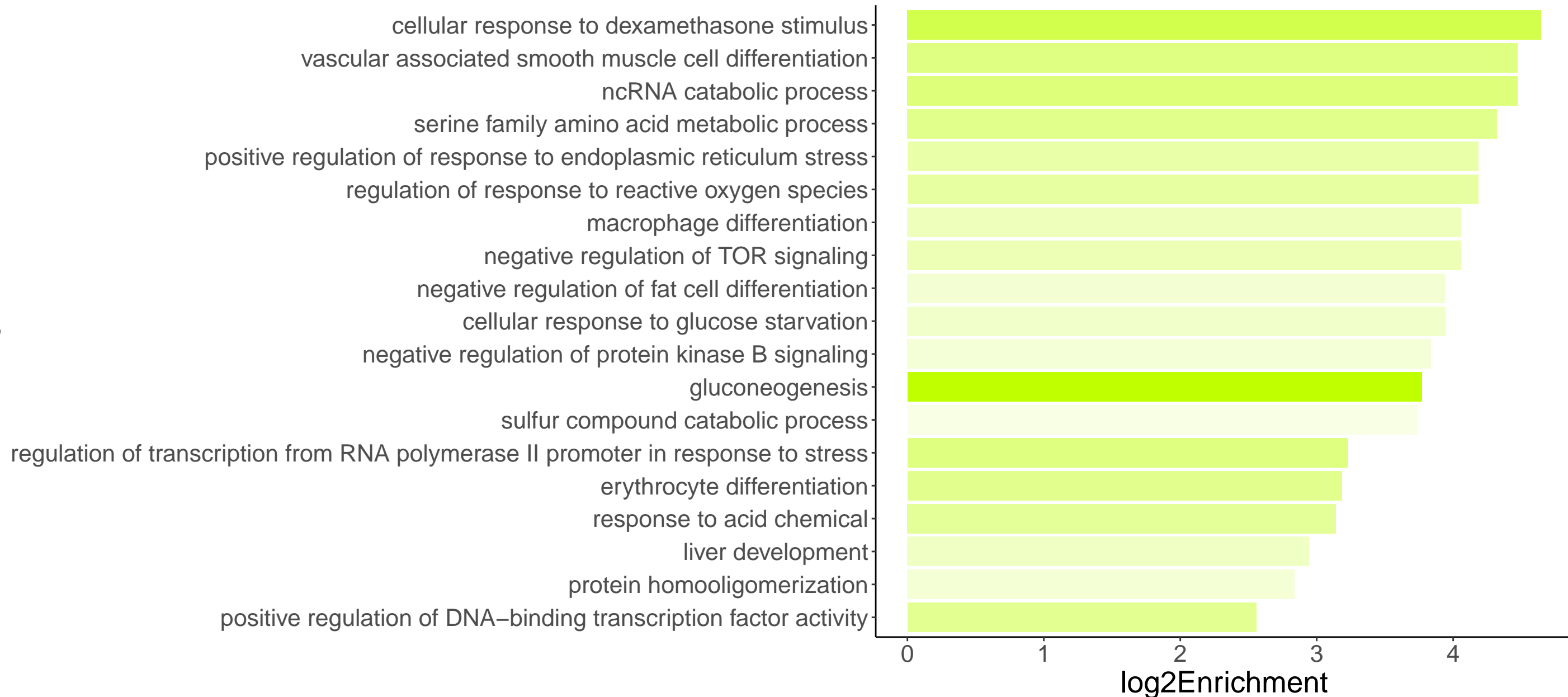
4

log2Enrichment



# Re-clustered module 4.5 BP enrichment

Term



# Re-clustered module 4.5 MF enrichment

Term

gamma-tubulin binding

pyridoxal phosphate binding

protein-lysine N-methyltransferase activity

identical protein binding

0

1

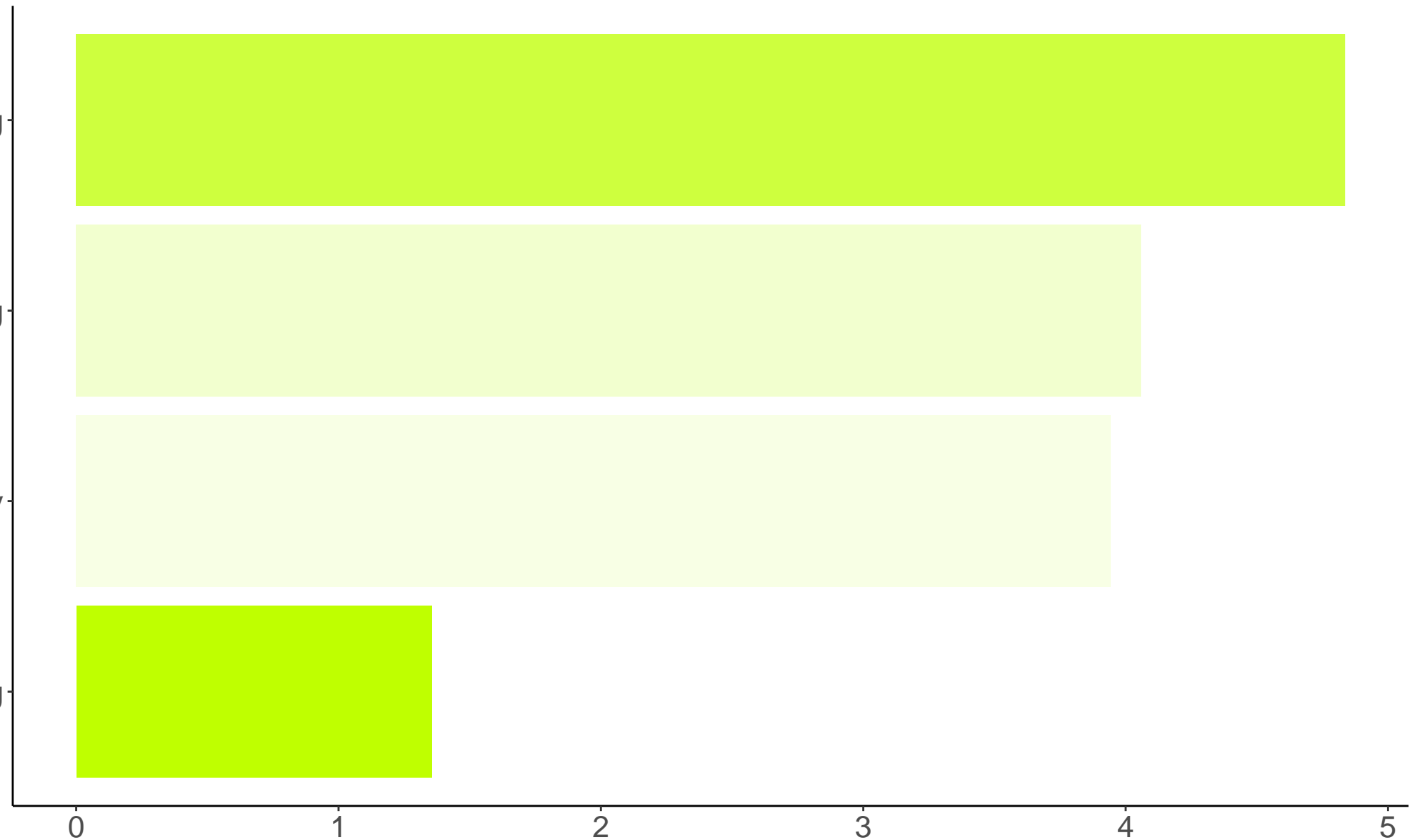
2

3

4

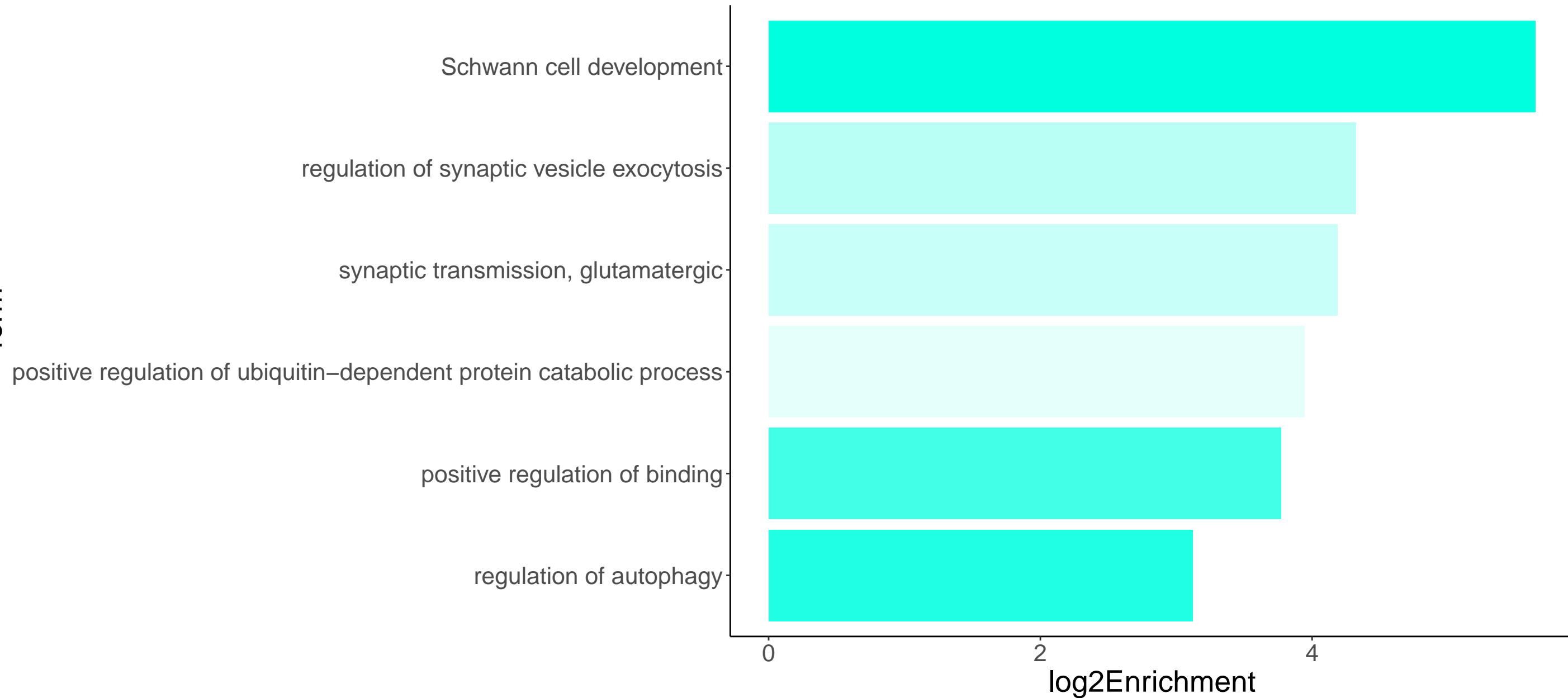
5

log2Enrichment



## Re-clustered module 4.6 BP enrichment

Term



Re-clustered module 4.6 MF enrichment

Term

log2Enrichment





# Re-clustered module 4.7 BP enrichment

Term

intracellular lipid transport

peroxisomal transport

fatty acid transport

mitochondrial translation

mitochondrial transport

0

1

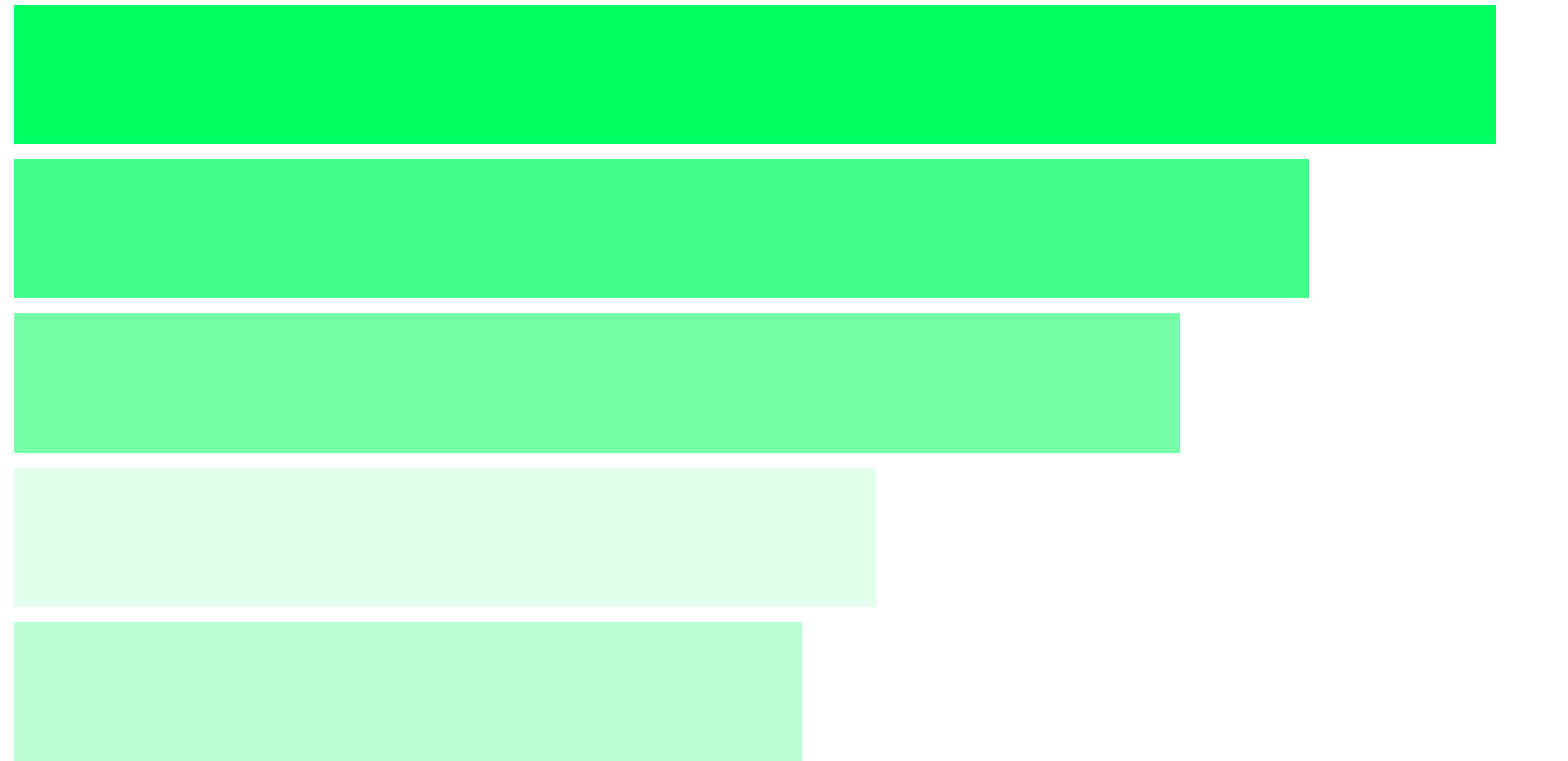
2

3

4

5

log2Enrichment



# Re-clustered module 4.7 MF enrichment

Term

pyridoxal phosphate binding

transferase activity, transferring acyl groups other than amino-acyl groups

0

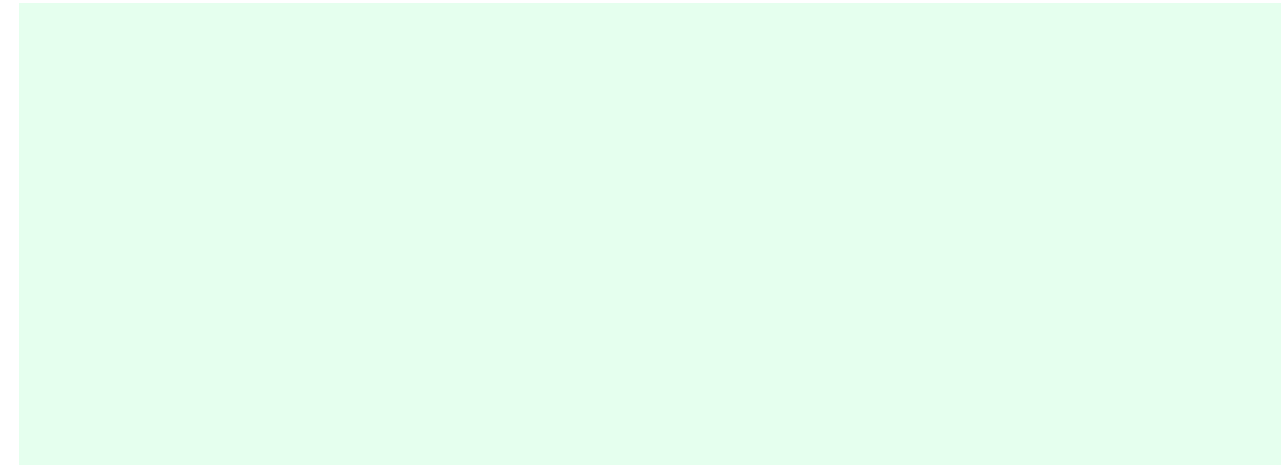
1

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3

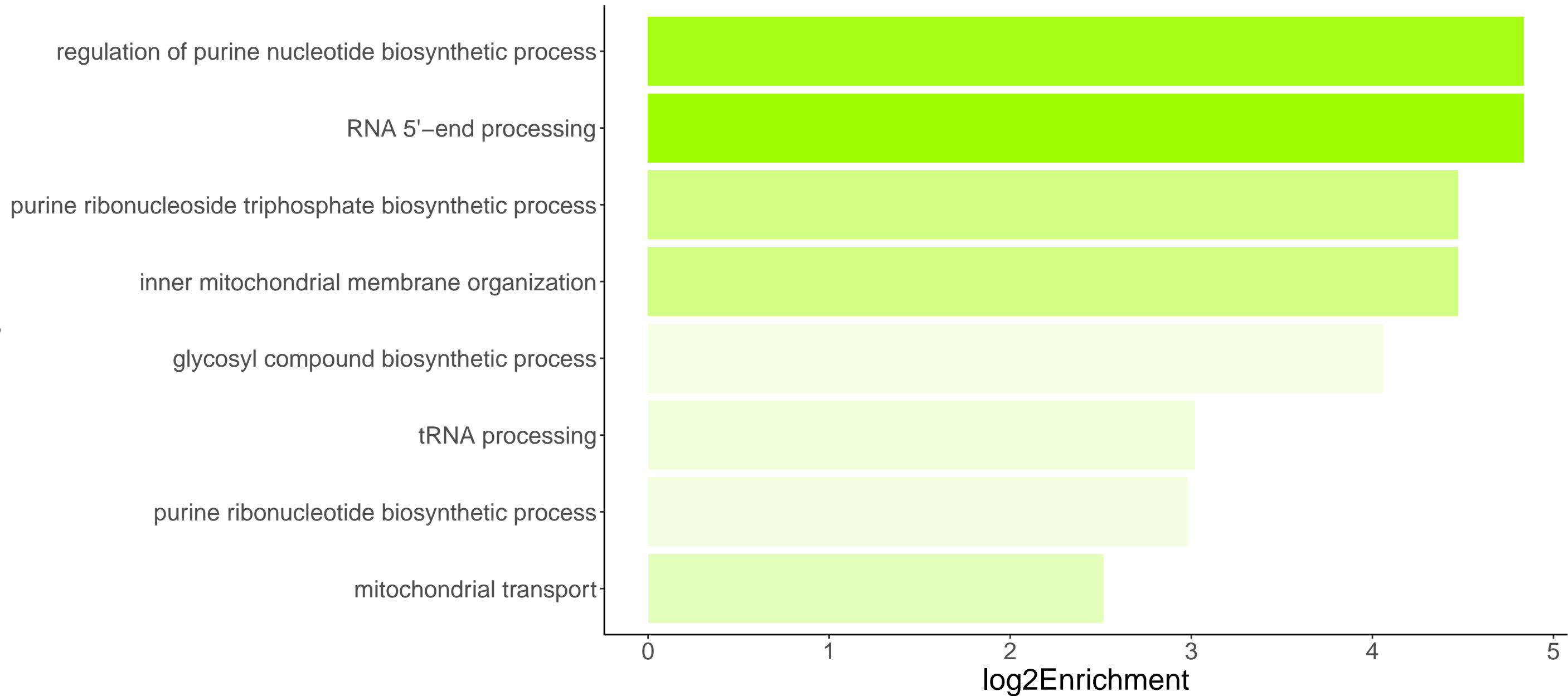
4

log2Enrichment



## Re-clustered module 4.8 BP enrichment

Term



# Re-clustered module 4.8 MF enrichment

Term

O-acyltransferase activity

iron-sulfur cluster binding

catalytic activity, acting on a tRNA

heat shock protein binding

0

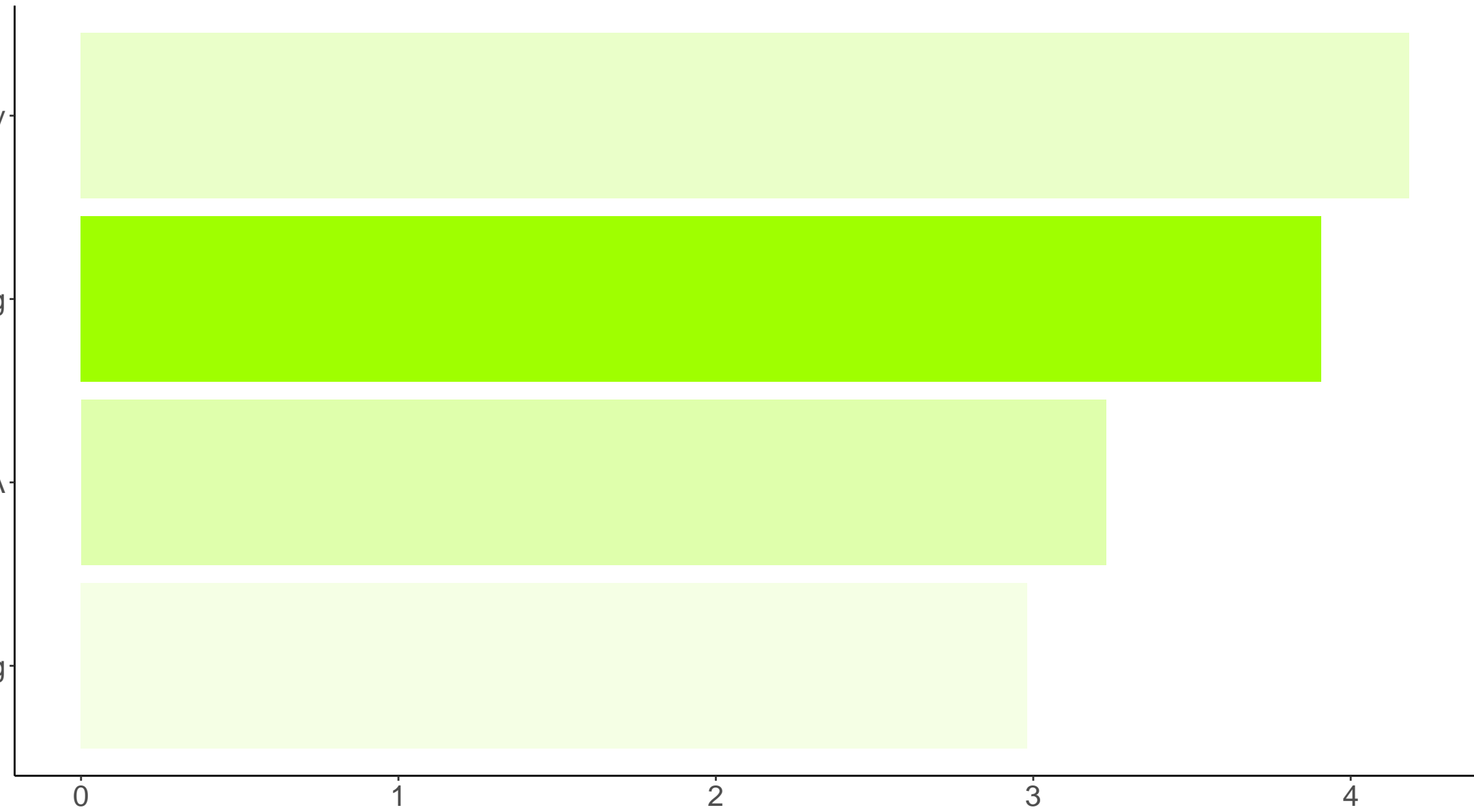
1

2

3

4

log2Enrichment



## Re-clustered module 4.9 BP enrichment

Term



## Re-clustered module 4.9 MF enrichment

Term

