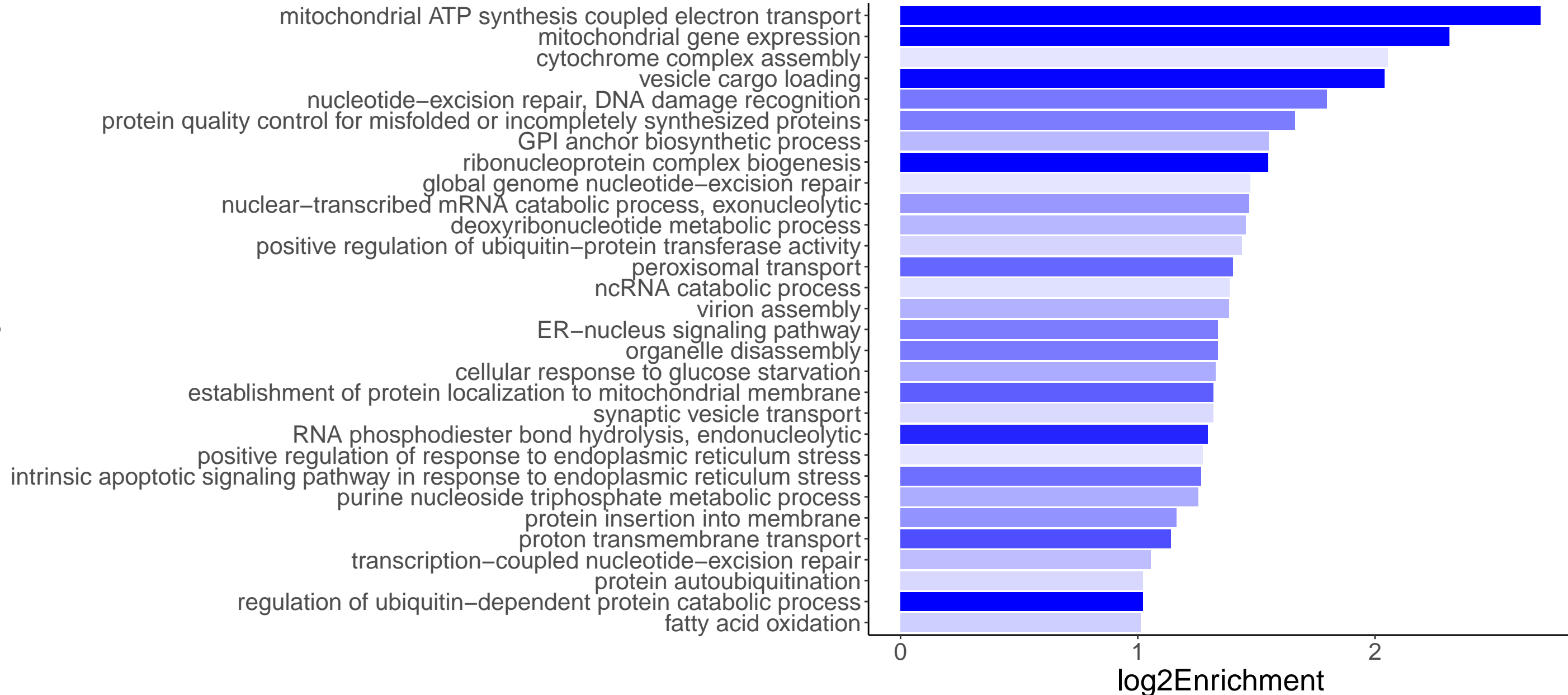


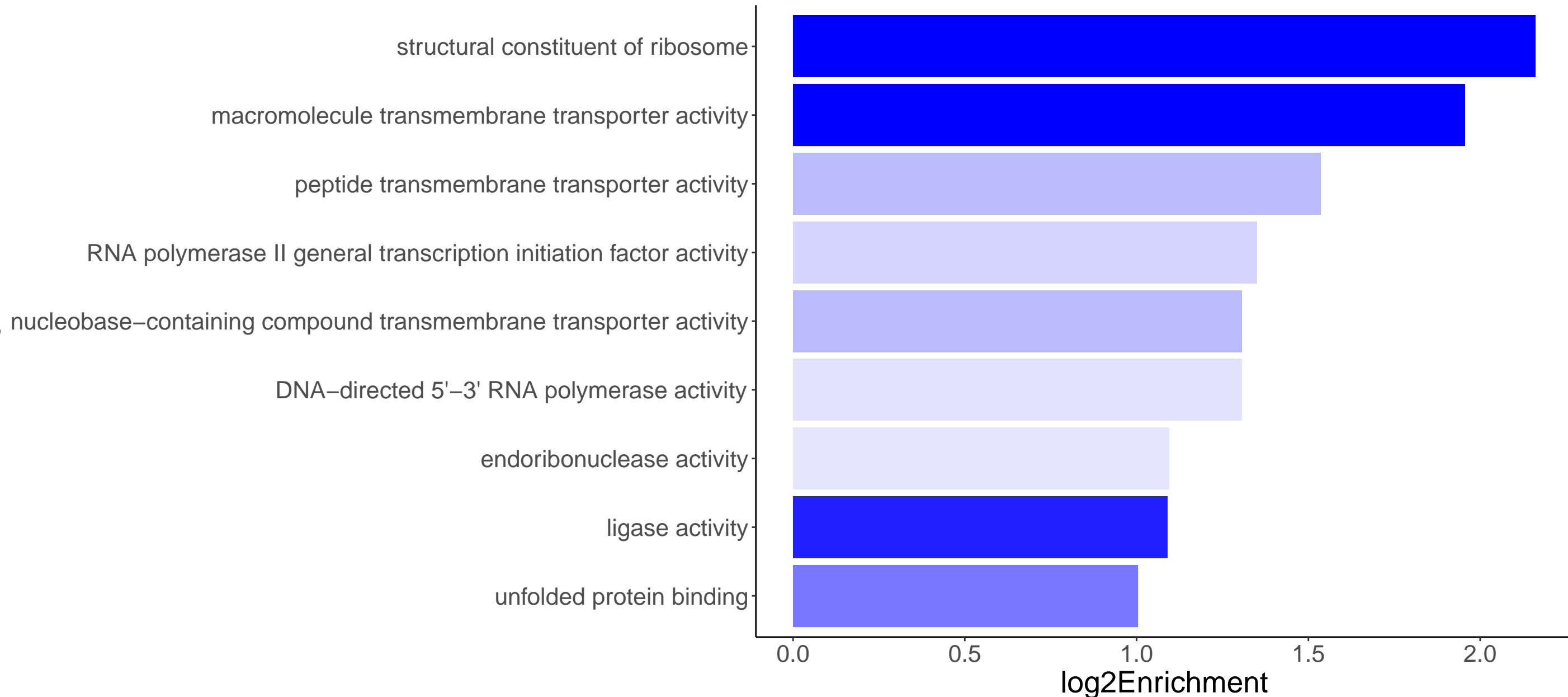
Original module 4 BP enrichment

Term



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

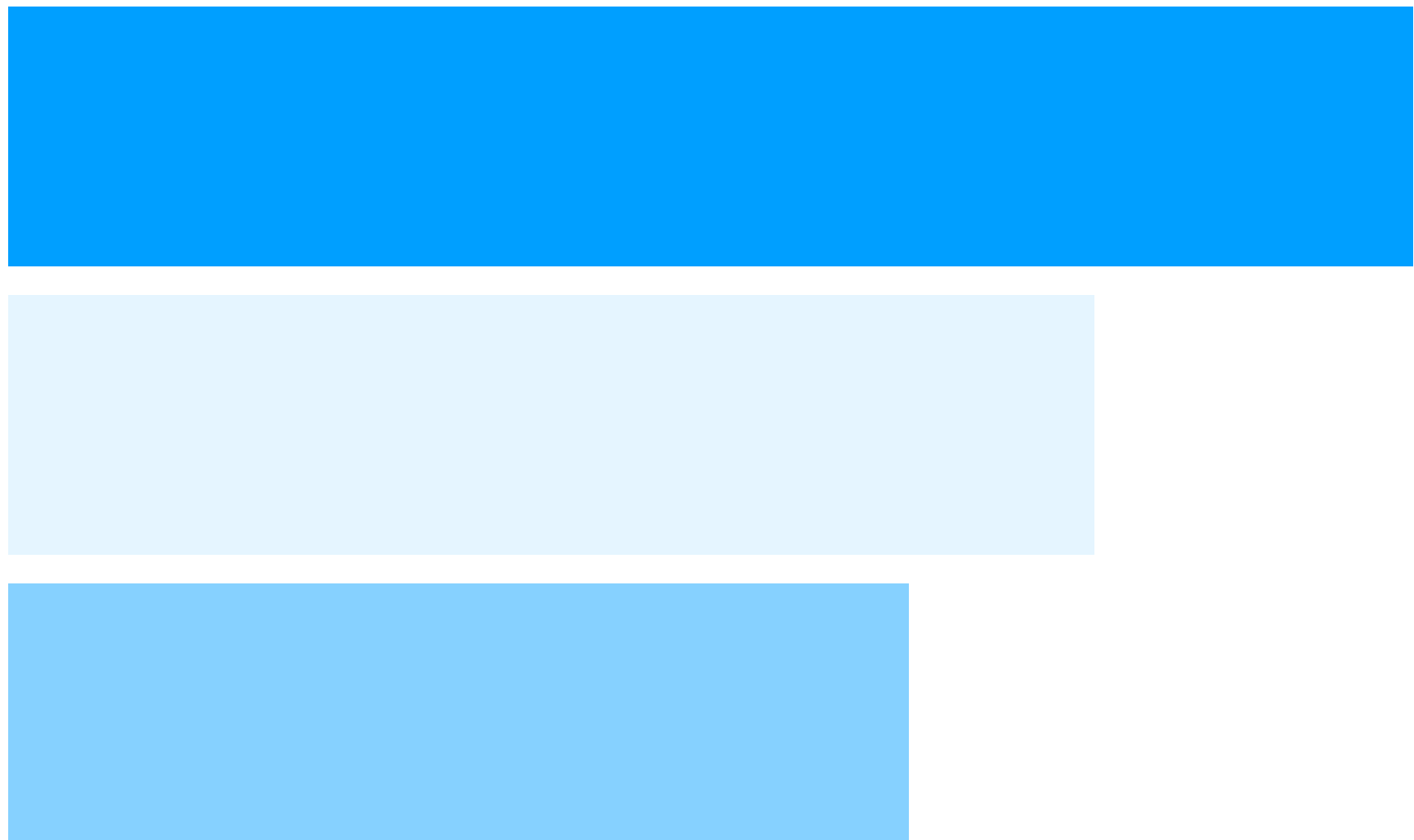
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log2Enrichment



Re-clustered module 4.1 MF enrichment

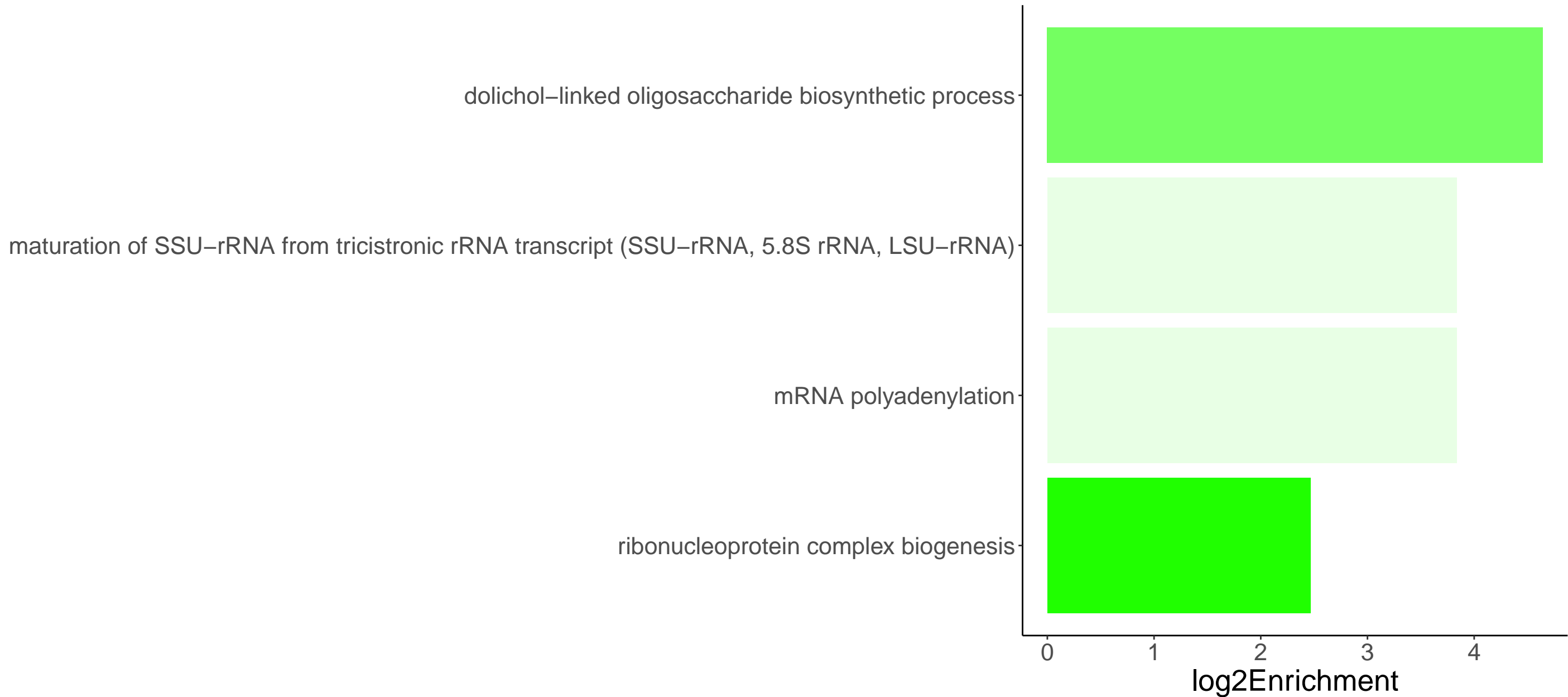
Term

log2Enrichment



Re-clustered module 4.10 BP enrichment

Term



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

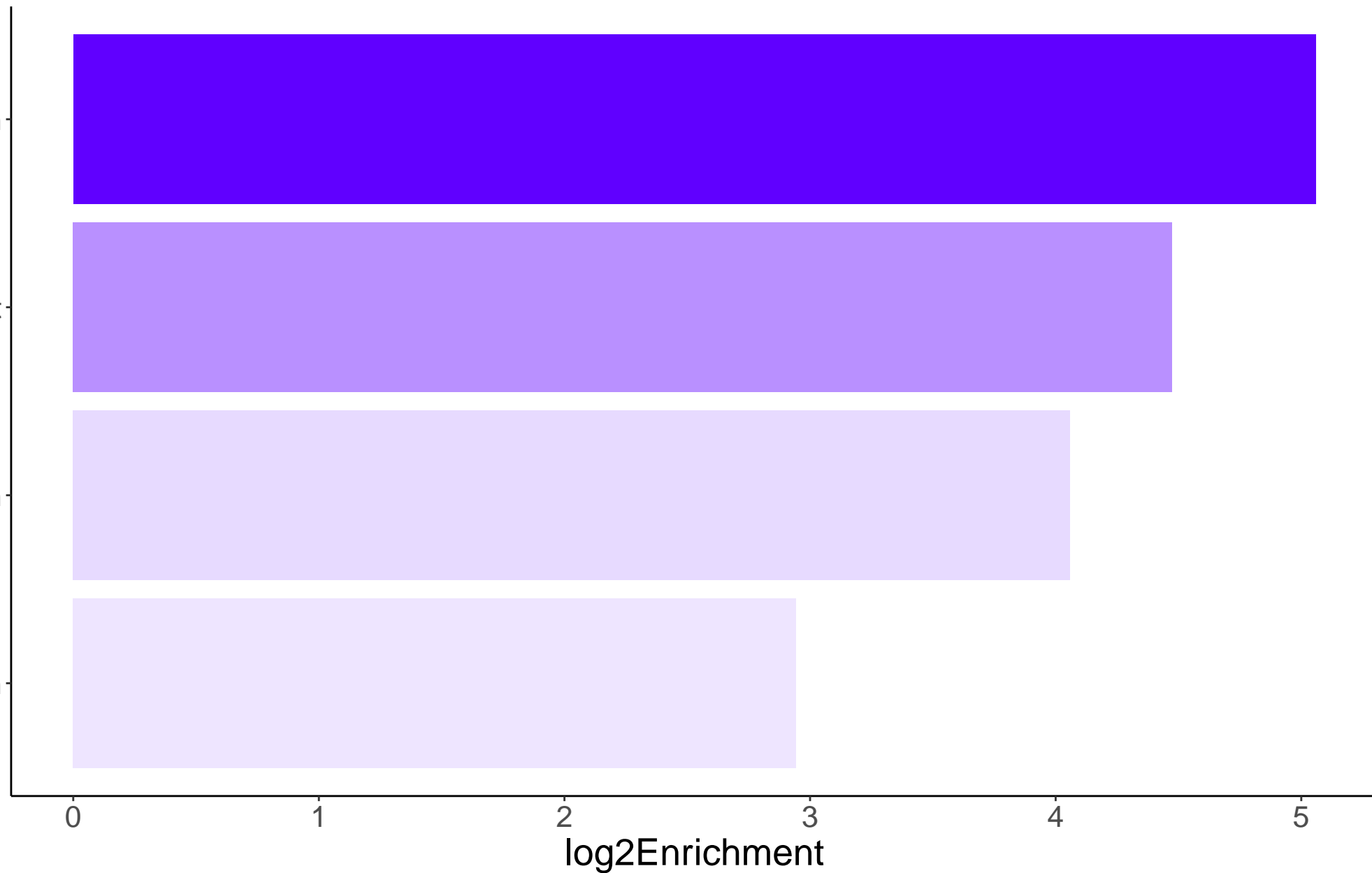
2

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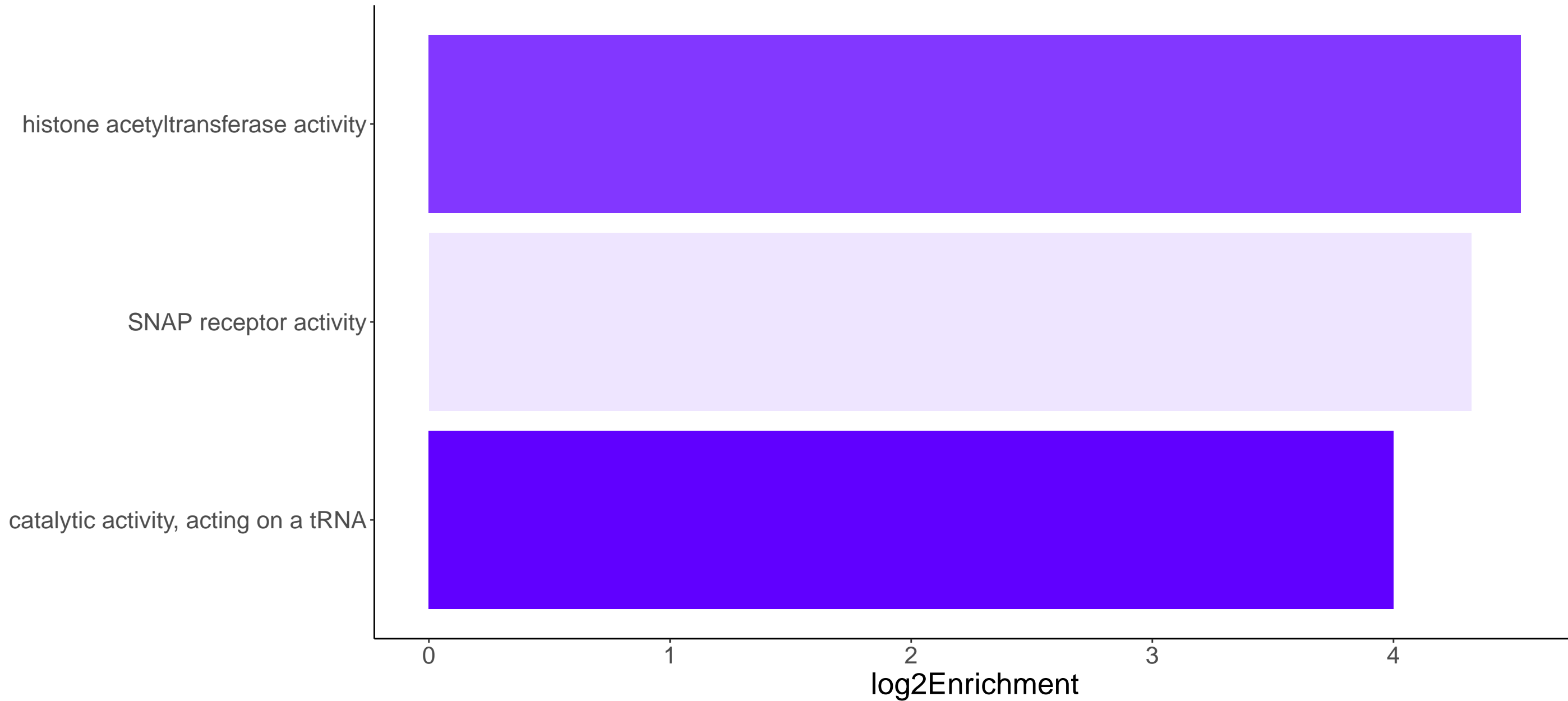
5

log2Enrichment



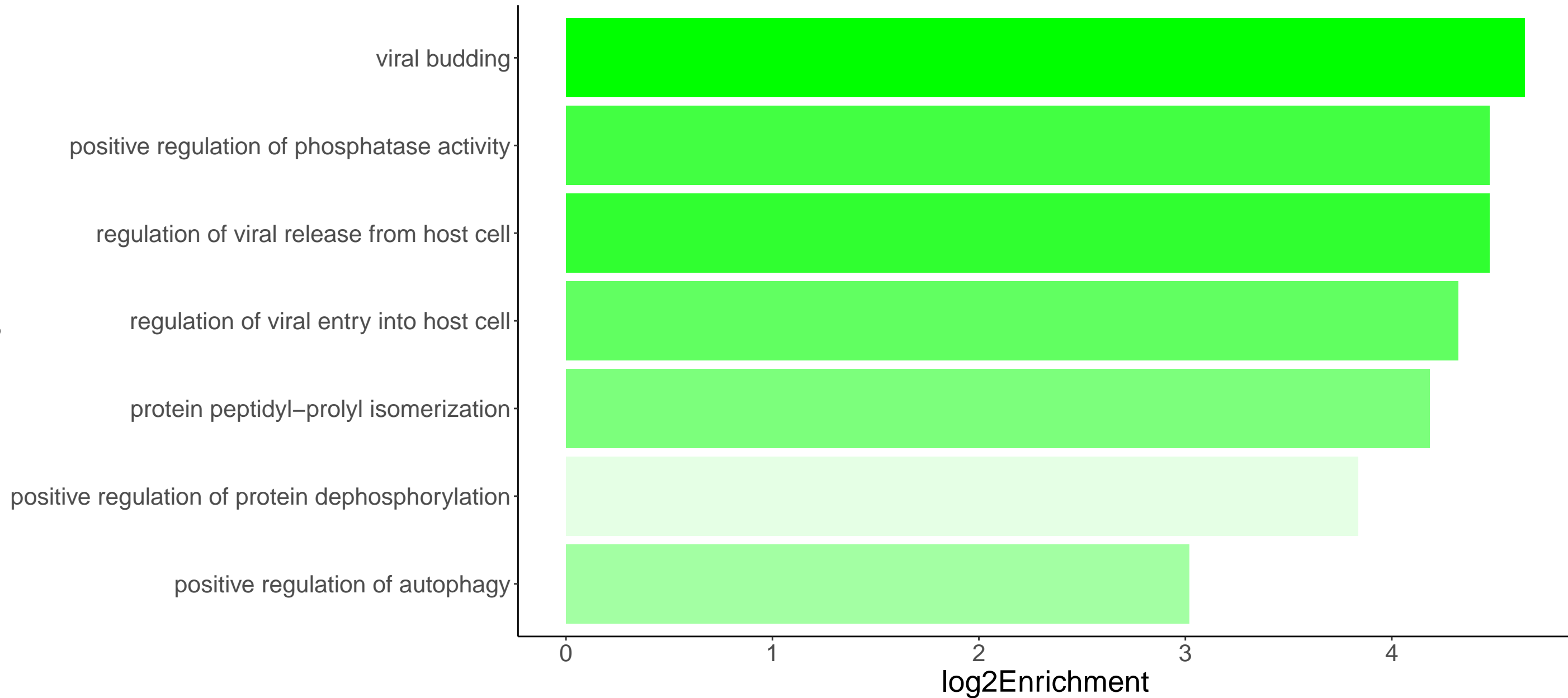
Re-clustered module 4.11 MF enrichment

Term



Re-clustered module 4.12 BP enrichment

Term



Re-clustered module 4.12 MF enrichment

Term

peptidyl-prolyl cis-trans isomerase activity

protein phosphatase binding

RNA polymerase II cis-regulatory region sequence-specific DNA binding

0

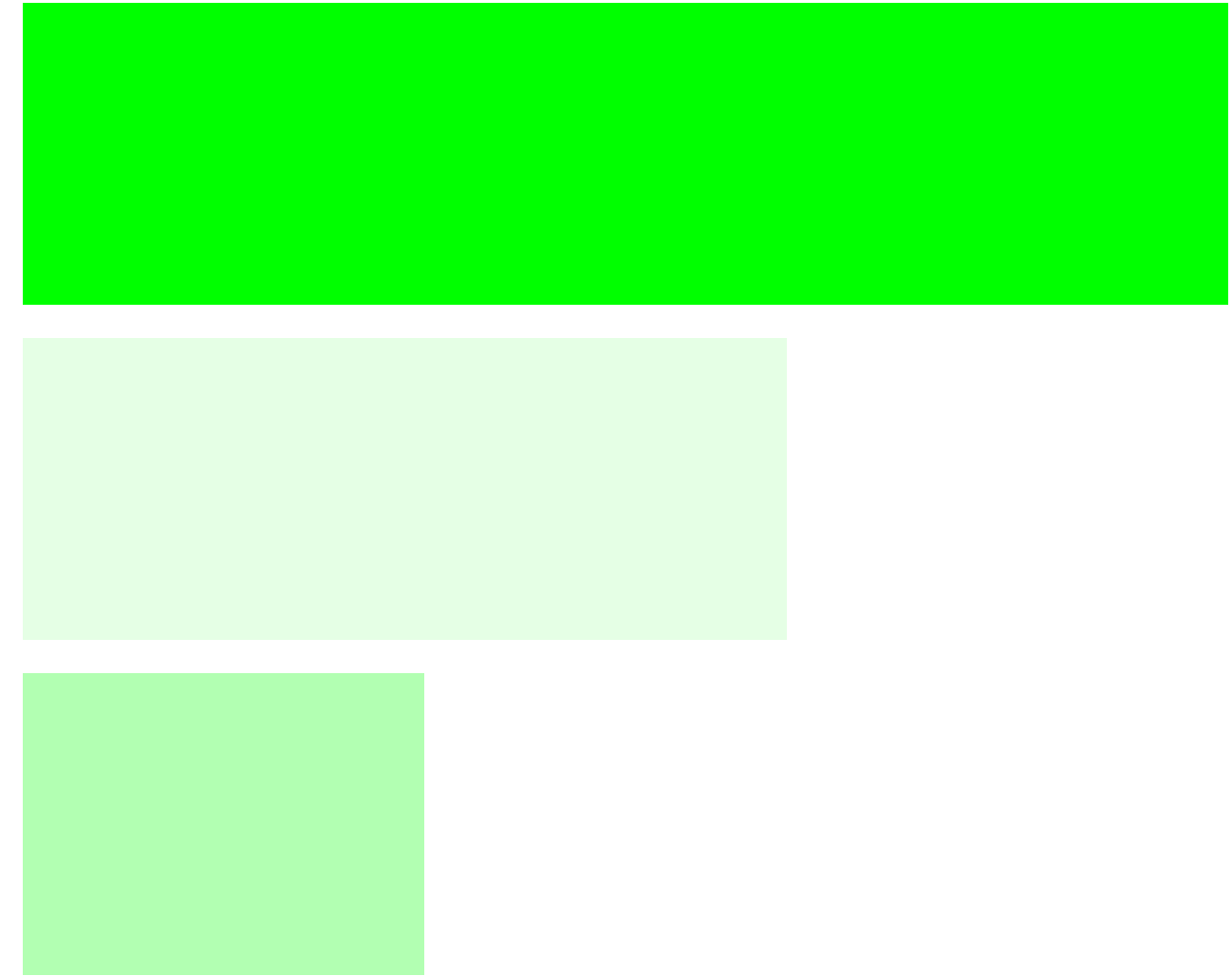
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log2Enrichment



Re-clustered module 4.13 BP enrichment

Term

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

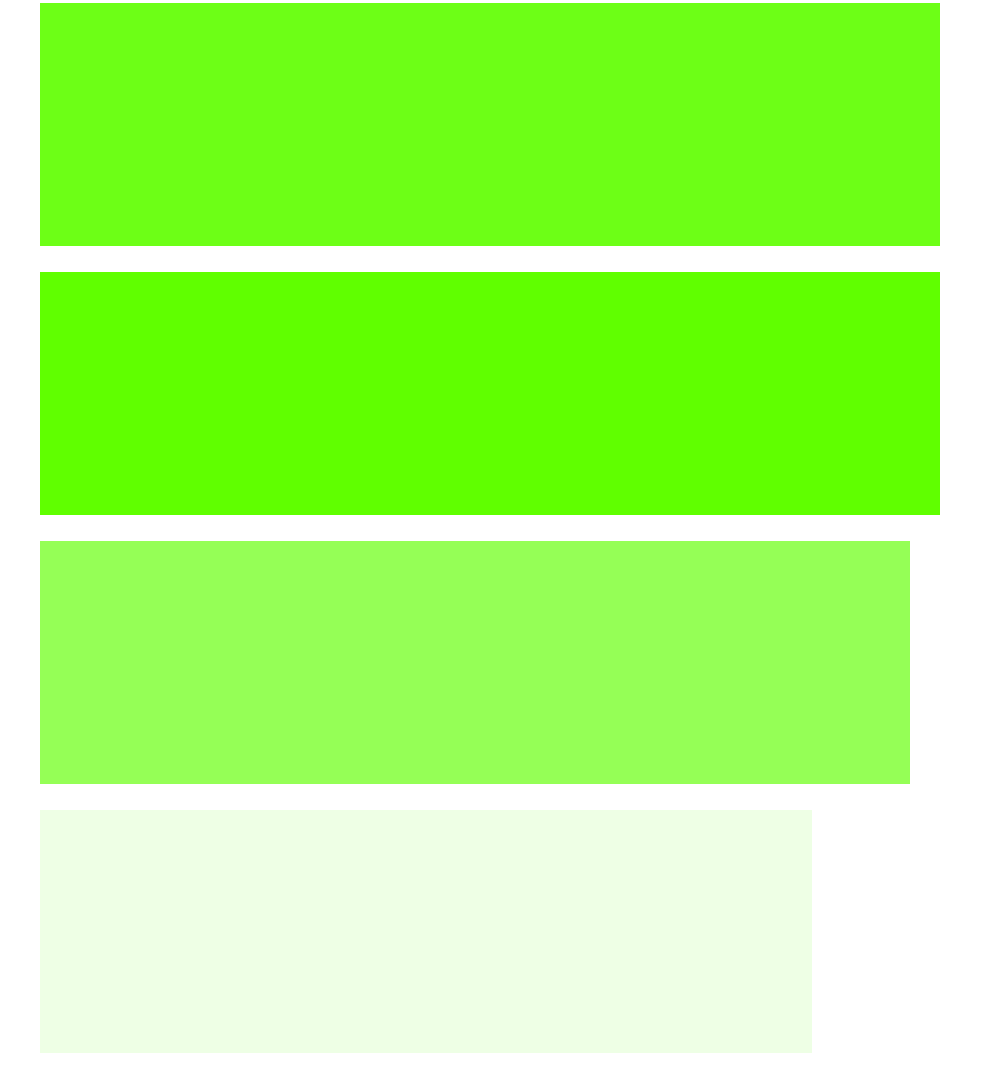
N-terminal protein amino acid modification

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

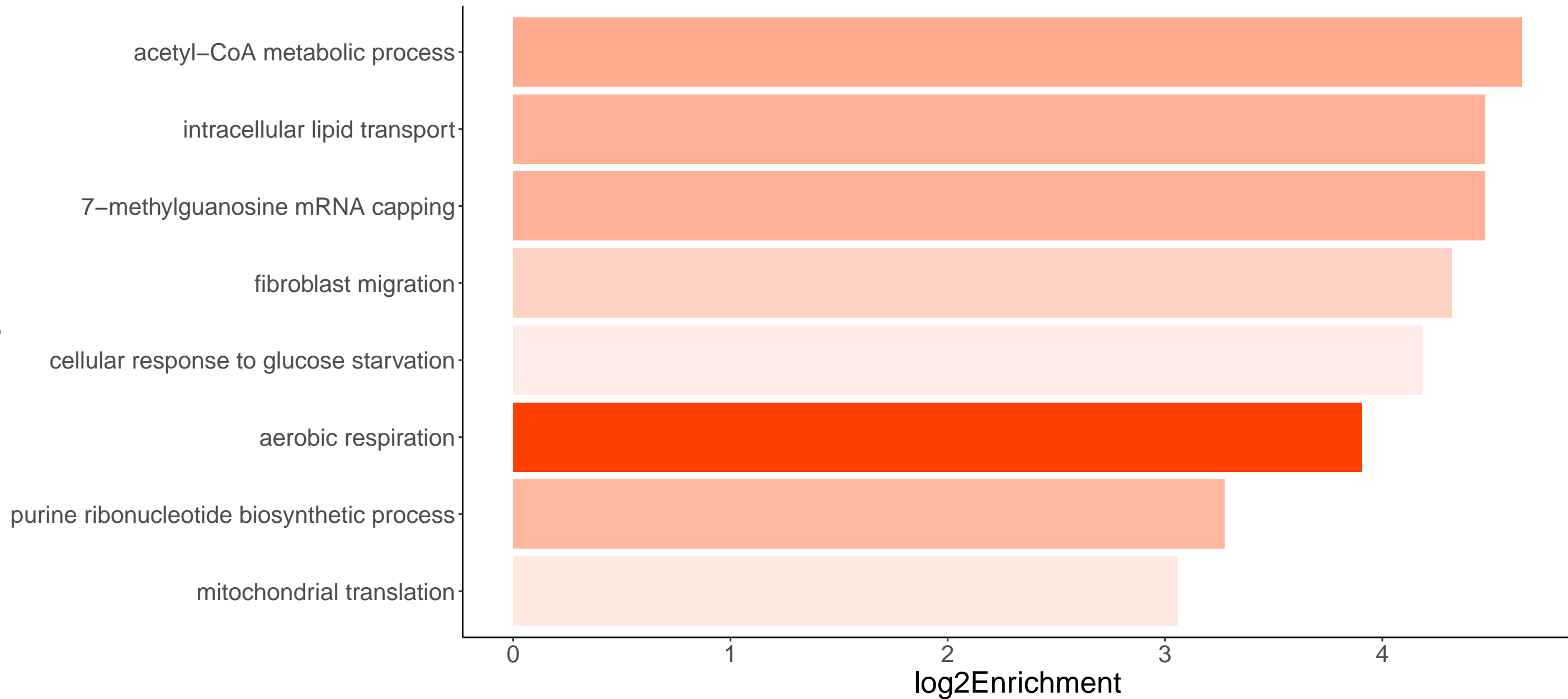
2

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

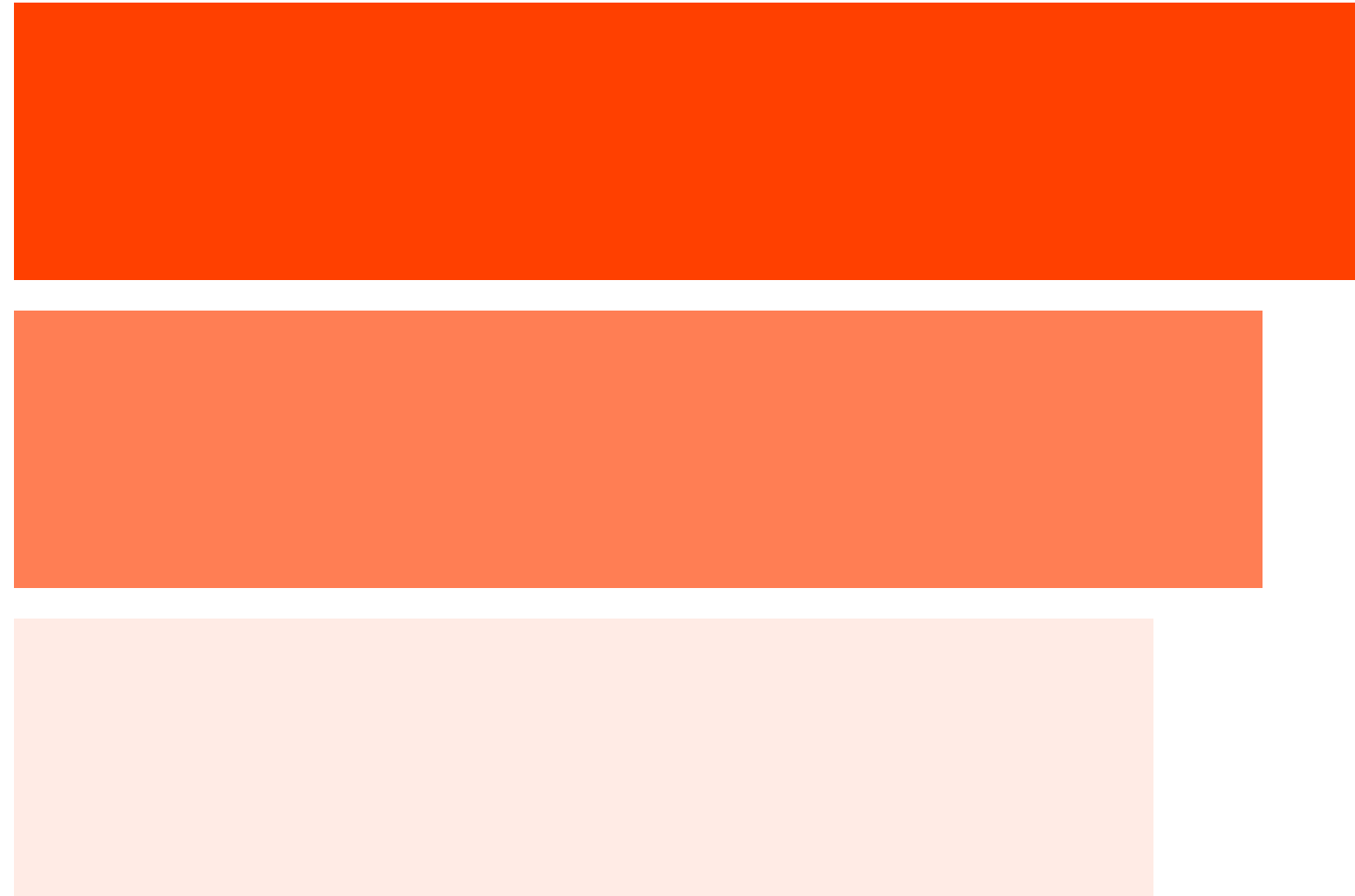
1

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

0 1 2 3 4
log2Enrichment

Re-clustered module 4.15 MF enrichment

Term

translation initiation factor activity

telomeric DNA binding

0

1

2

3

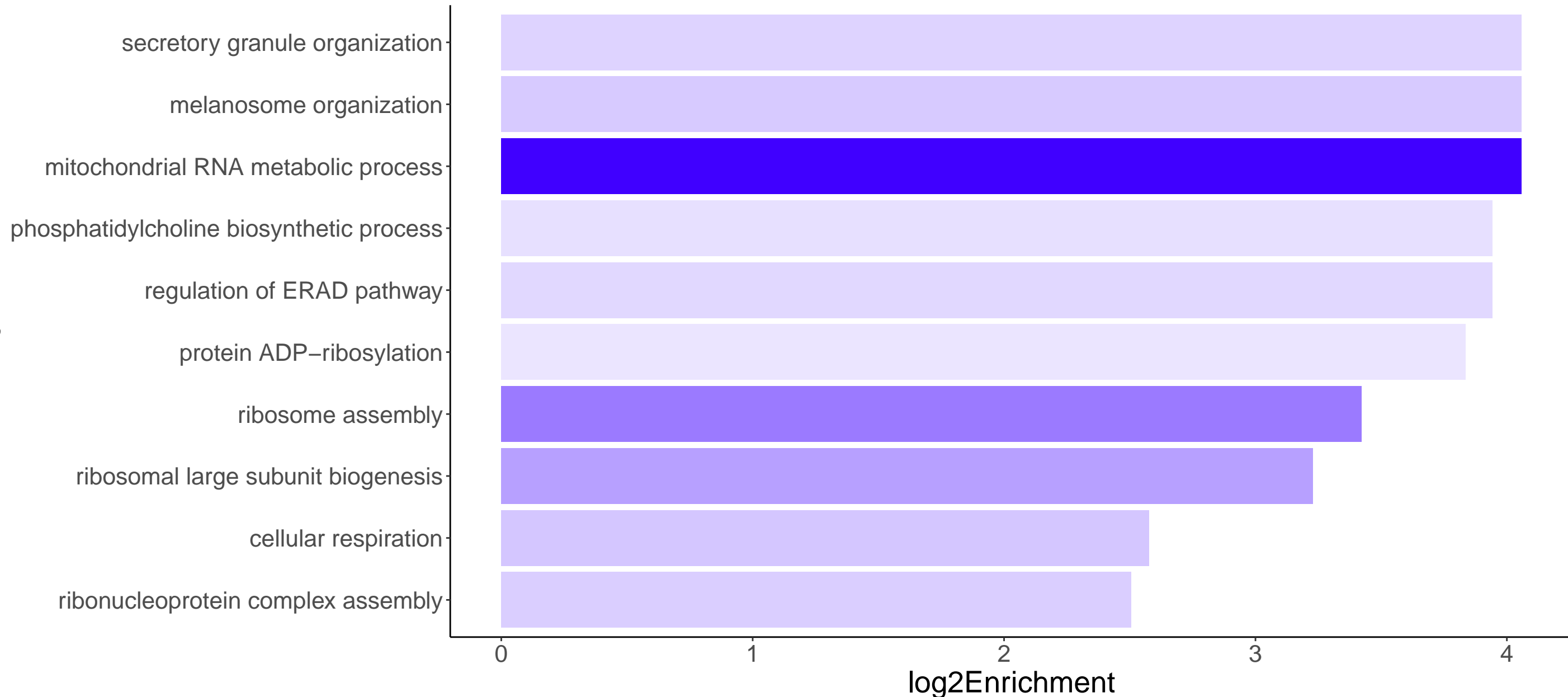
4

log2Enrichment



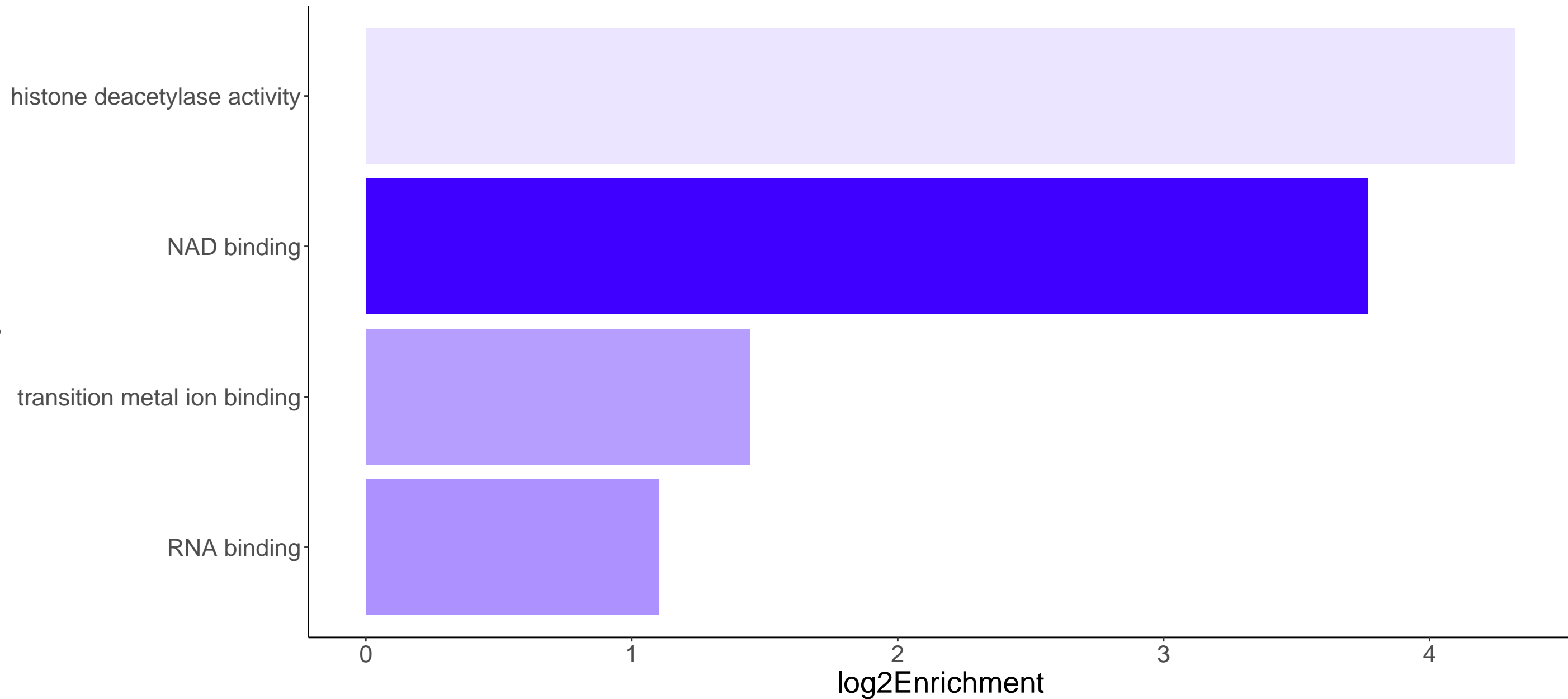
Re-clustered module 4.16 BP enrichment

Term



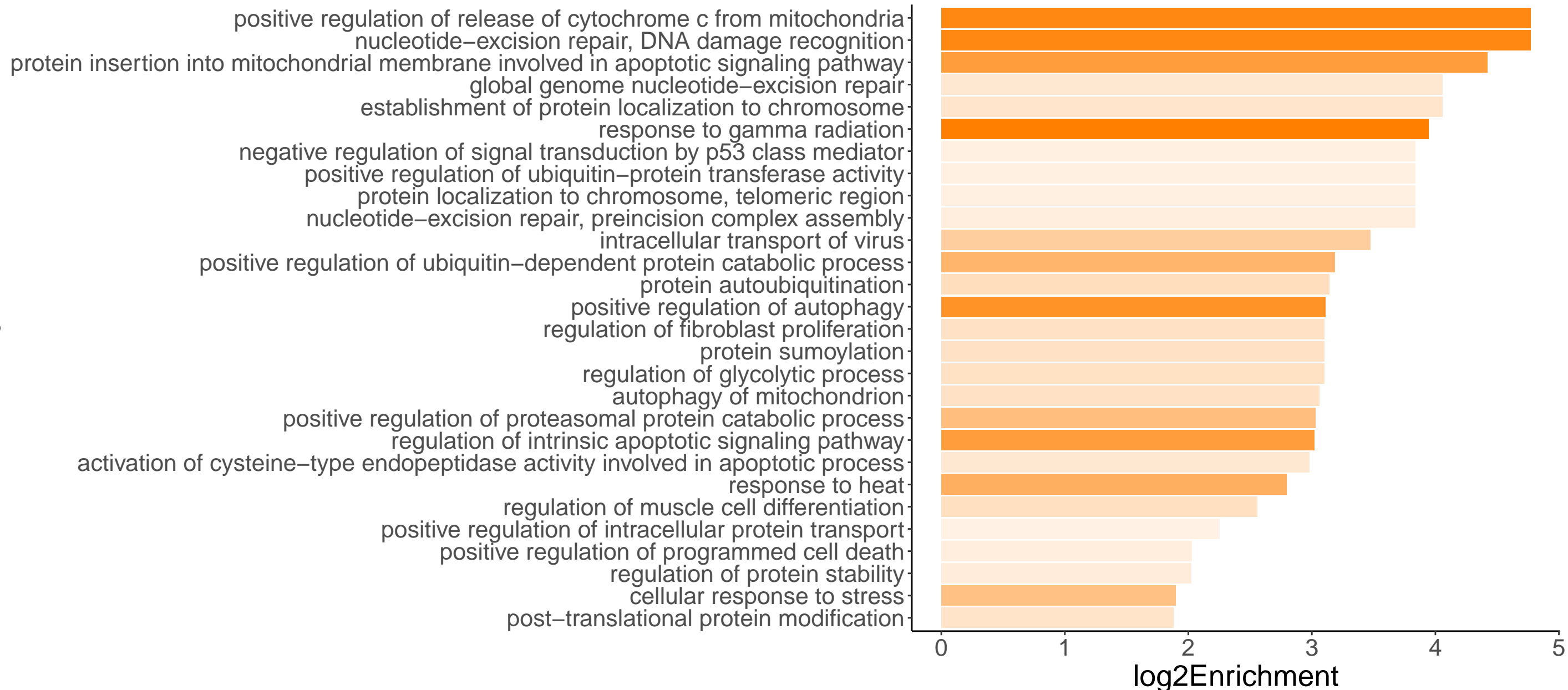
Re-clustered module 4.16 MF enrichment

Term



Re-clustered module 4.17 BP enrichment

Term



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

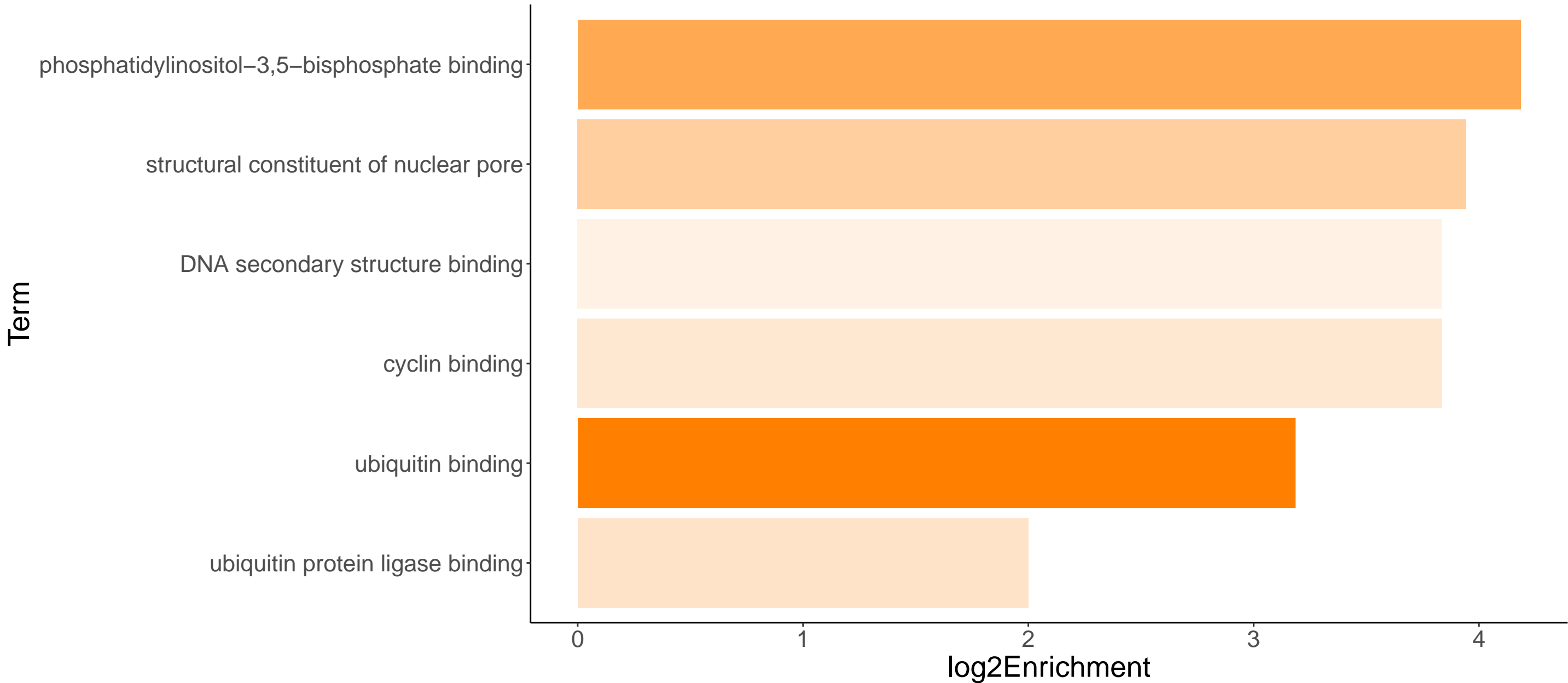
1

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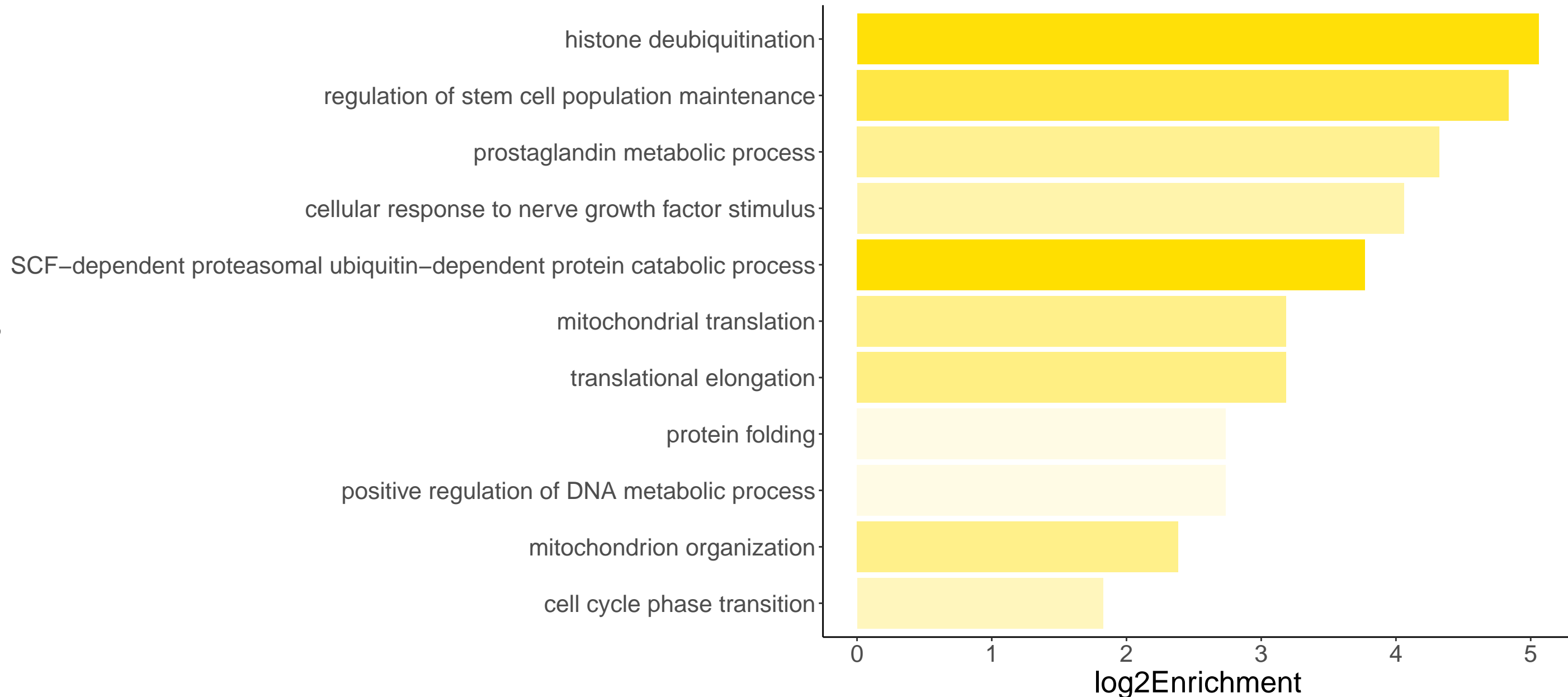
4

log2Enrichment



Re-clustered module 4.18 BP enrichment

Term



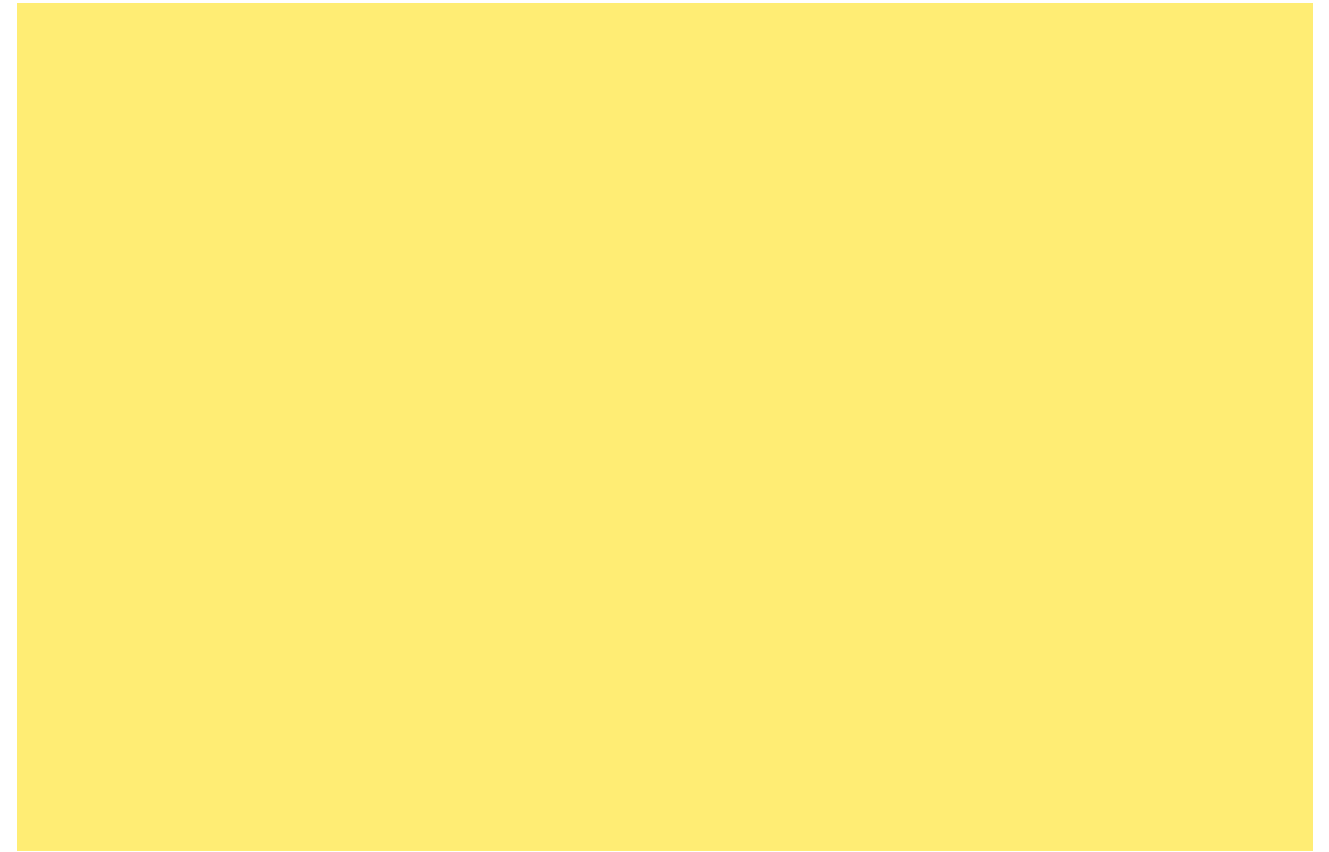
Re-clustered module 4.18 MF enrichment

Term

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

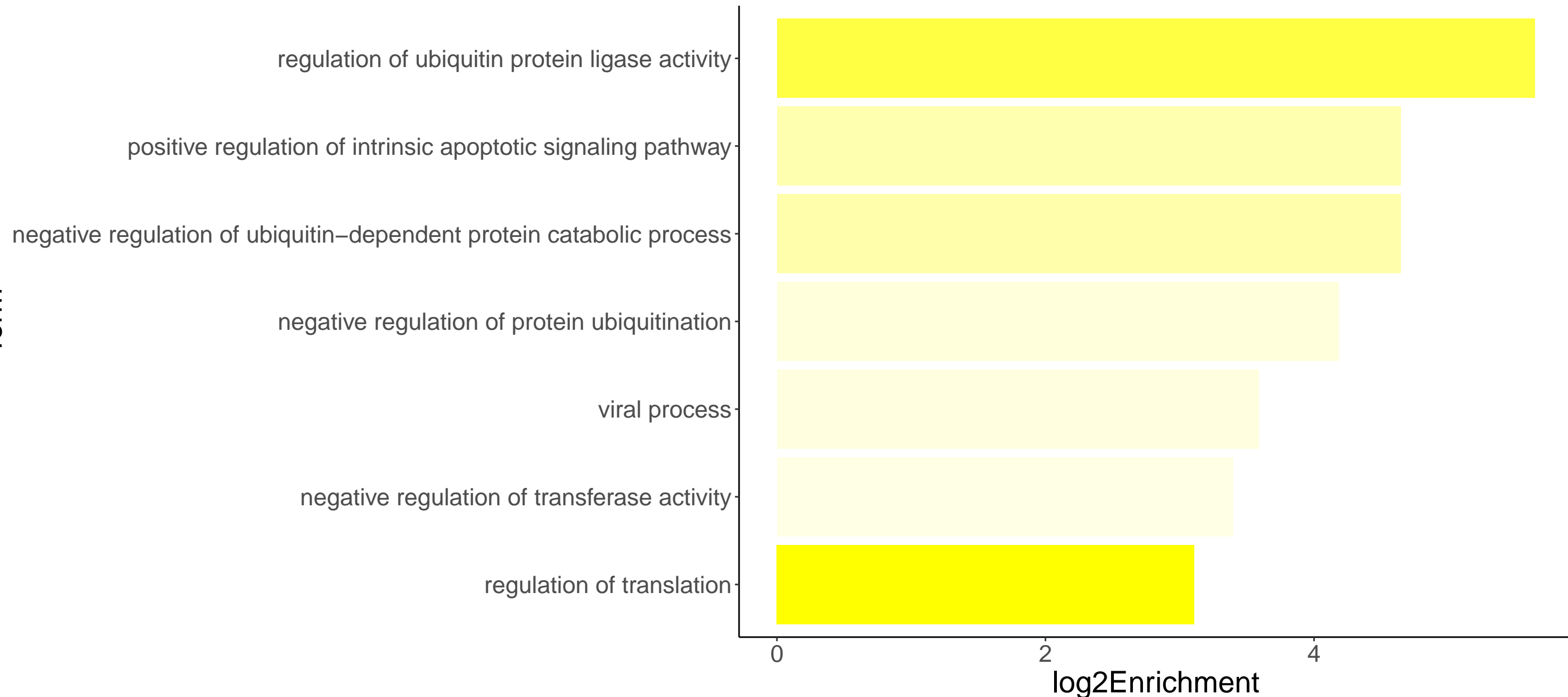
0.0 0.5 1.0 1.5 2.0

log2Enrichment



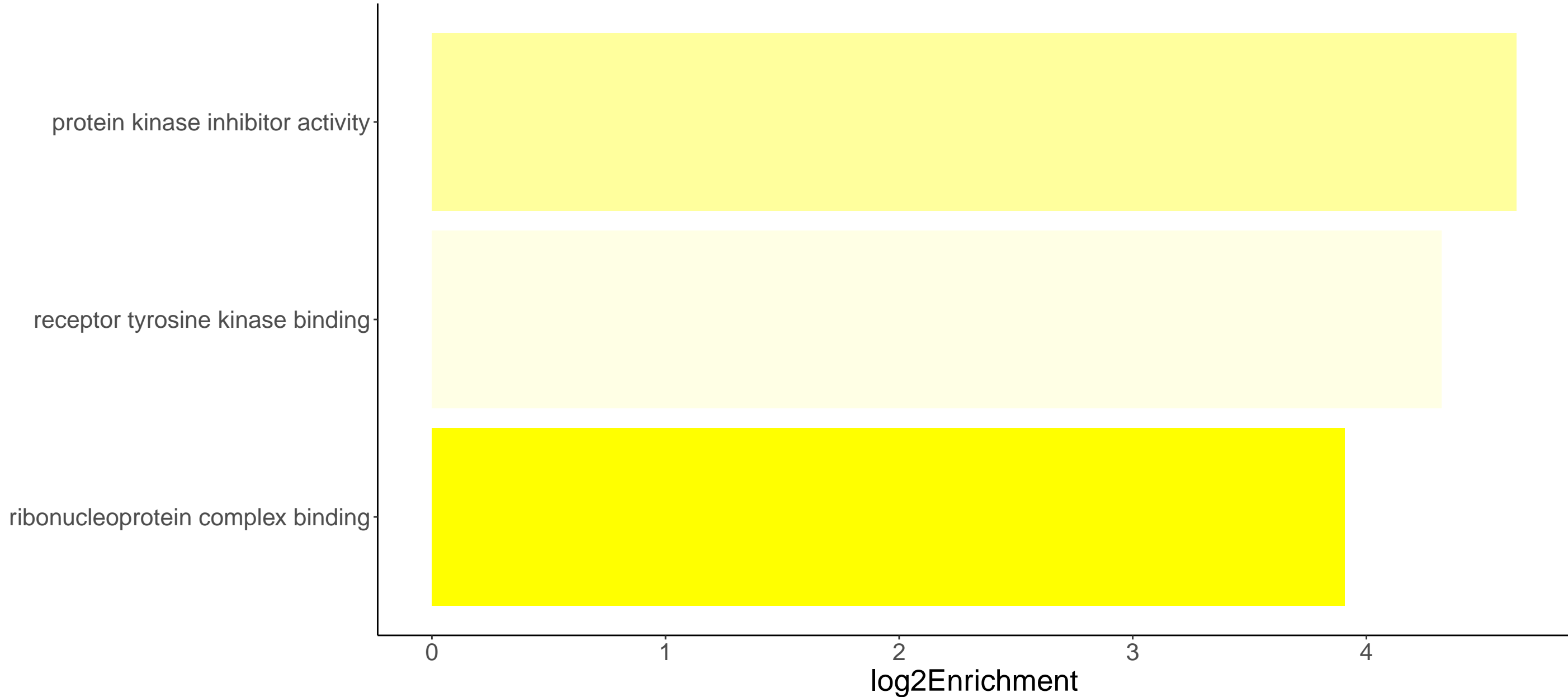
Re-clustered module 4.19.1 BP enrichment

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

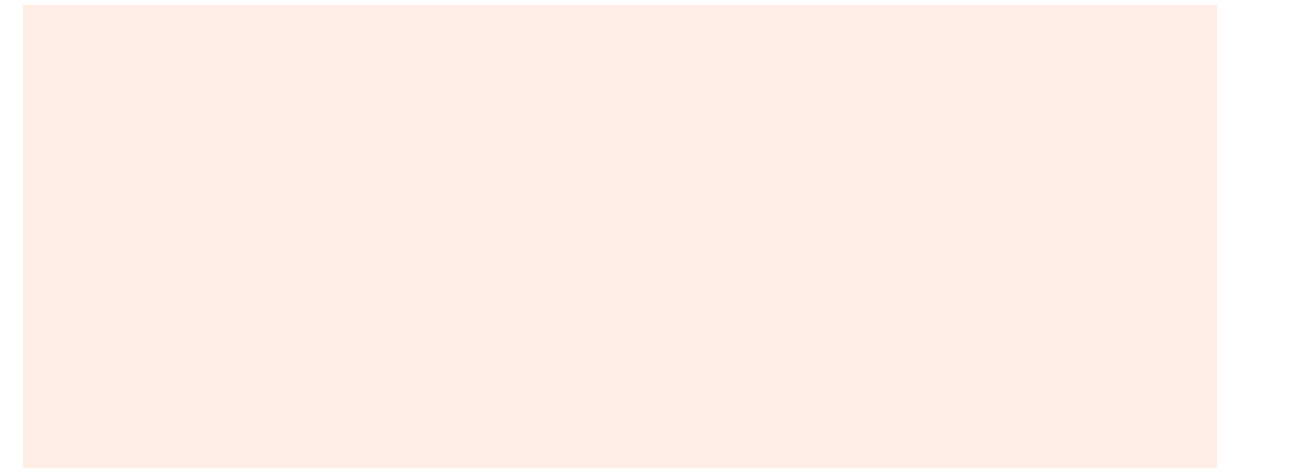
1

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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

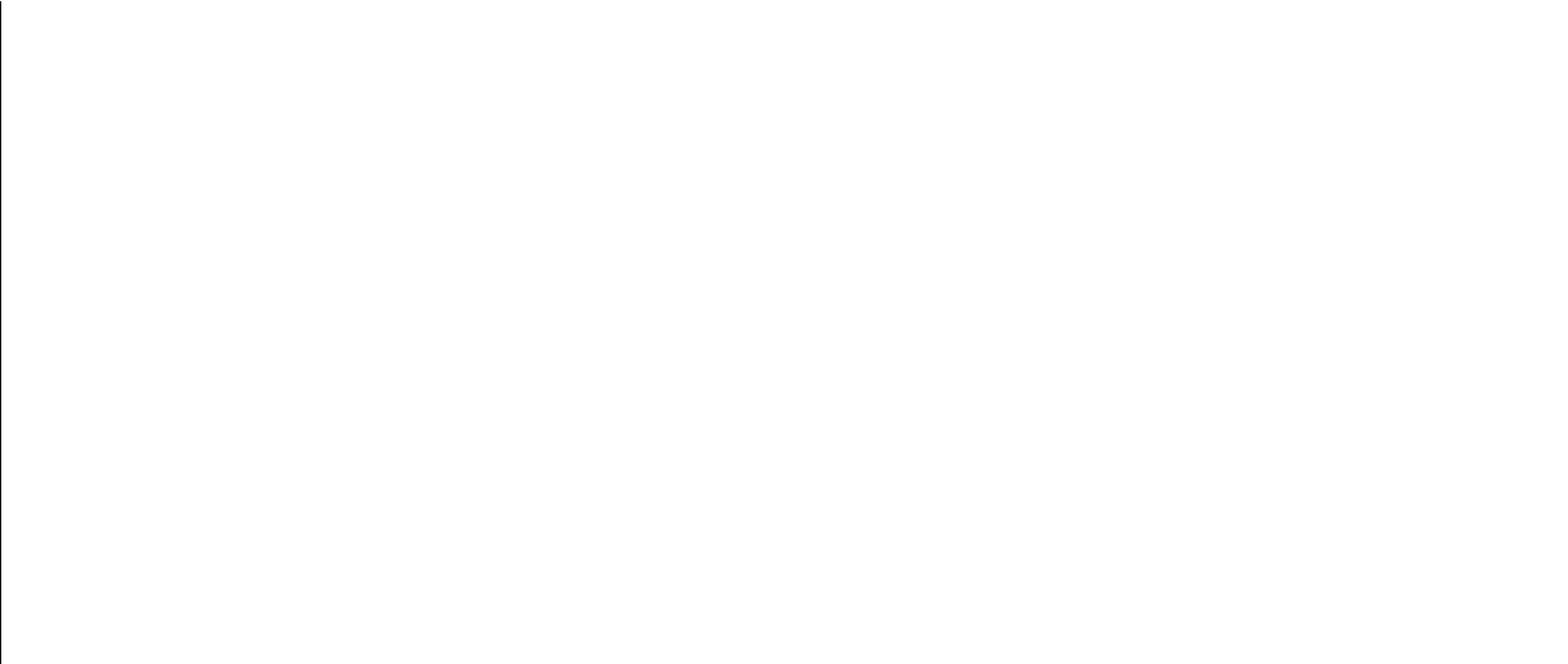
log2Enrichment



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

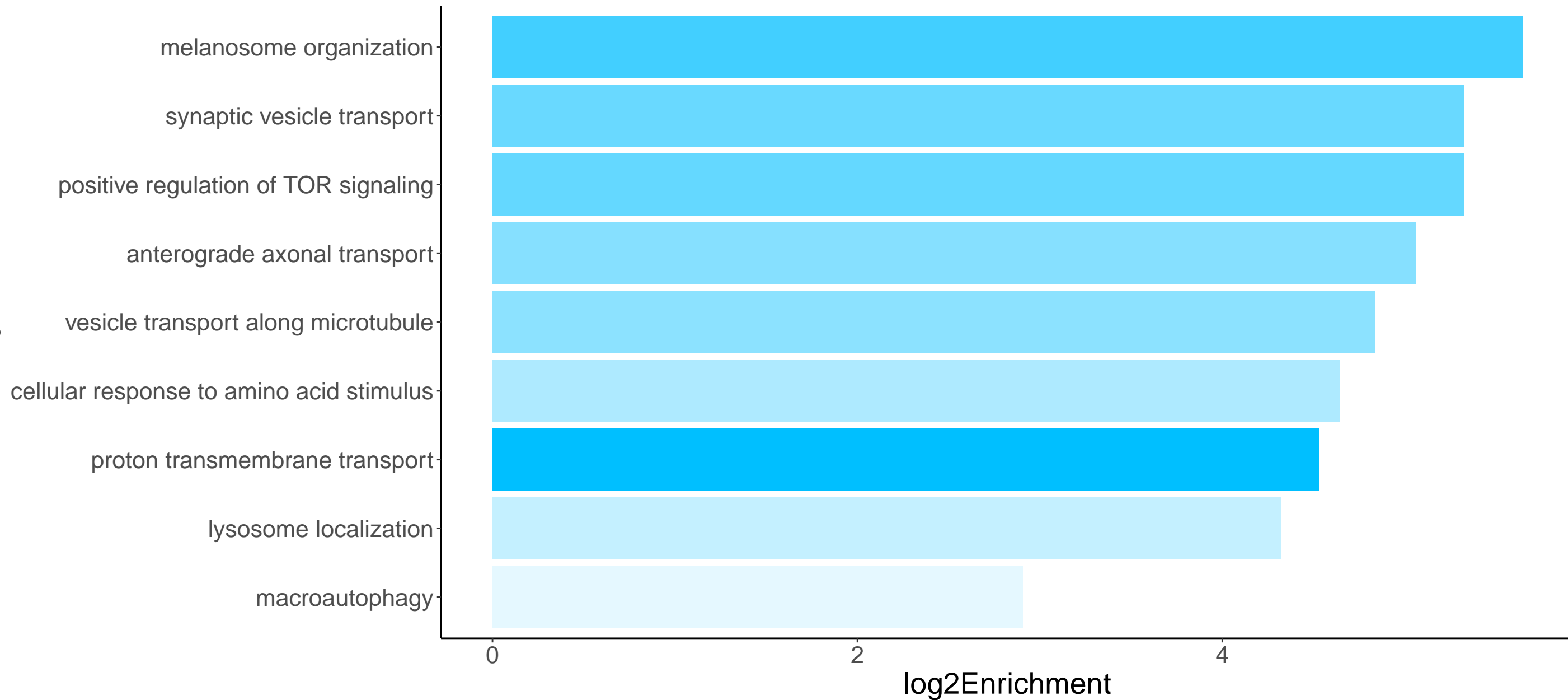
Term

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

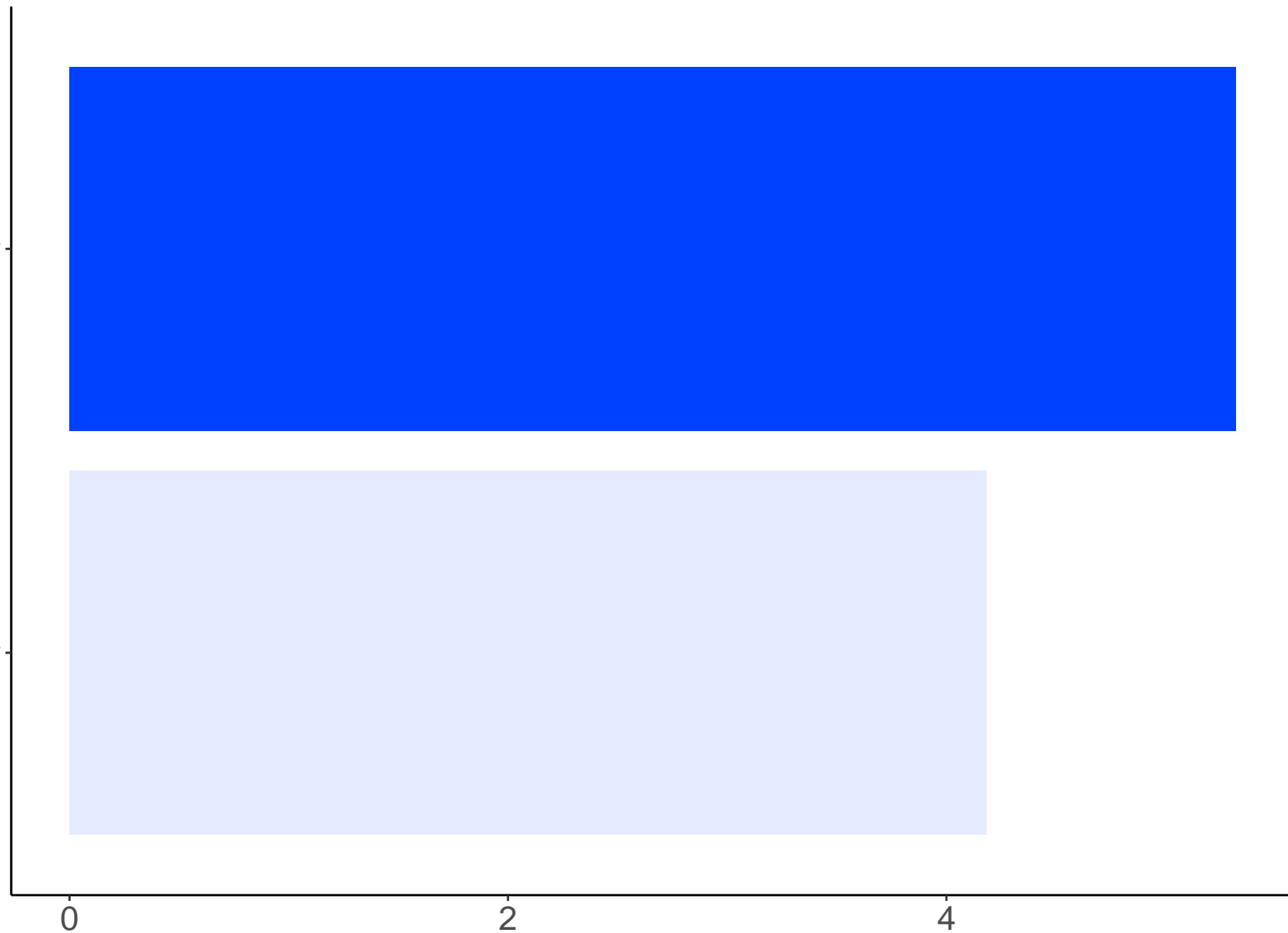
S-adenosylmethionine-dependent methyltransferase activity

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

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4

5

log2Enrichment



Re-clustered module 4.2.4 MF enrichment

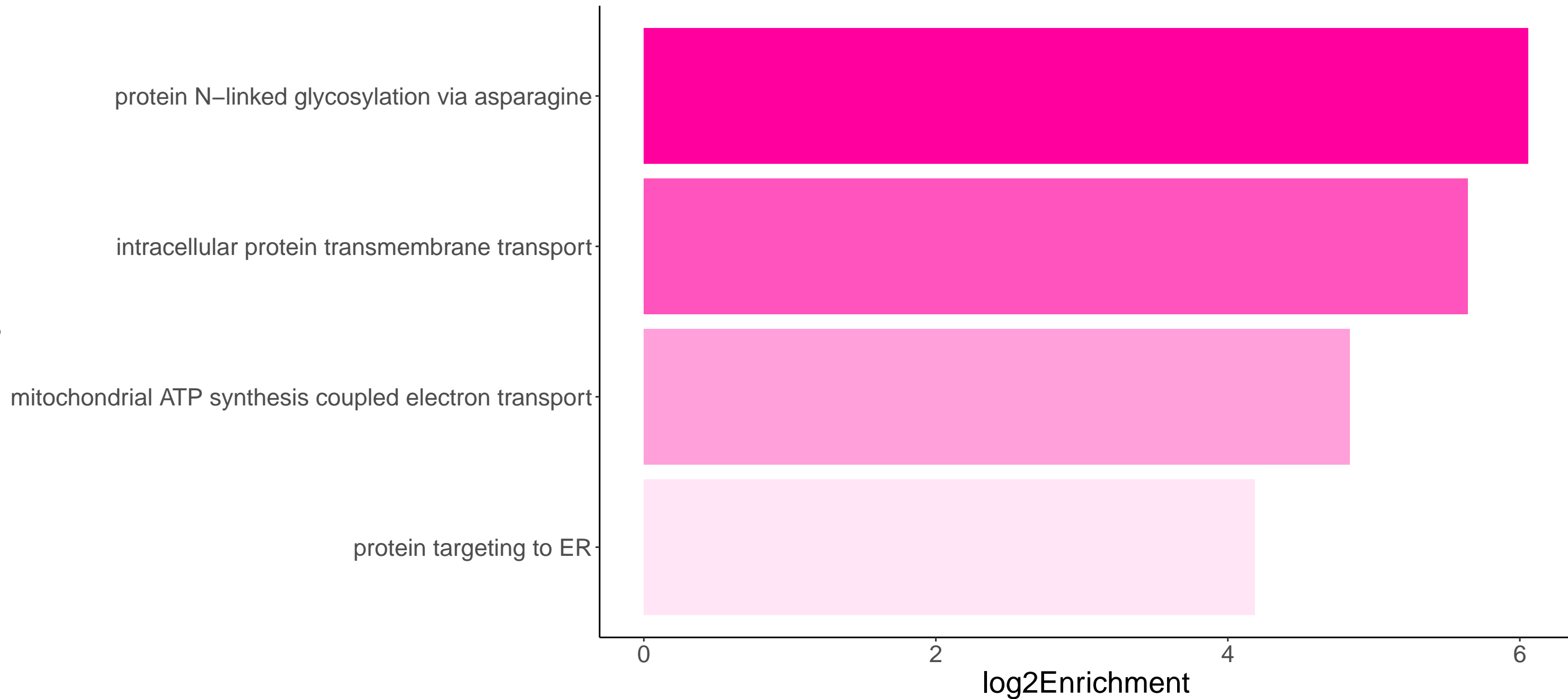
Term

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

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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

alternative mRNA splicing, via spliceosome

regulation of mRNA splicing, via spliceosome

positive regulation of canonical Wnt signaling pathway

protein deubiquitination

0

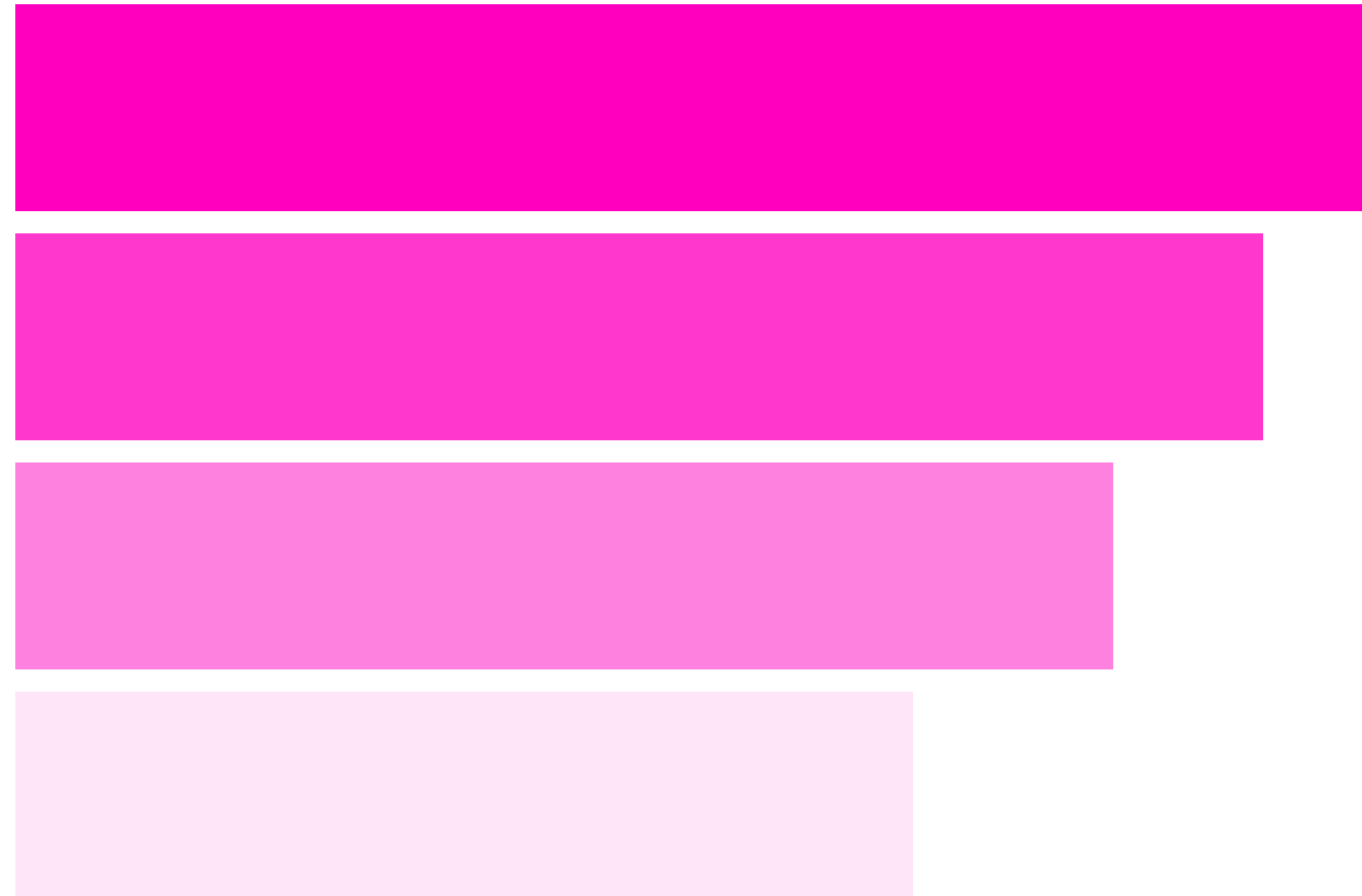
1

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log2Enrichment



Re-clustered module 4.20 MF enrichment

Term

signaling adaptor activity

0

1

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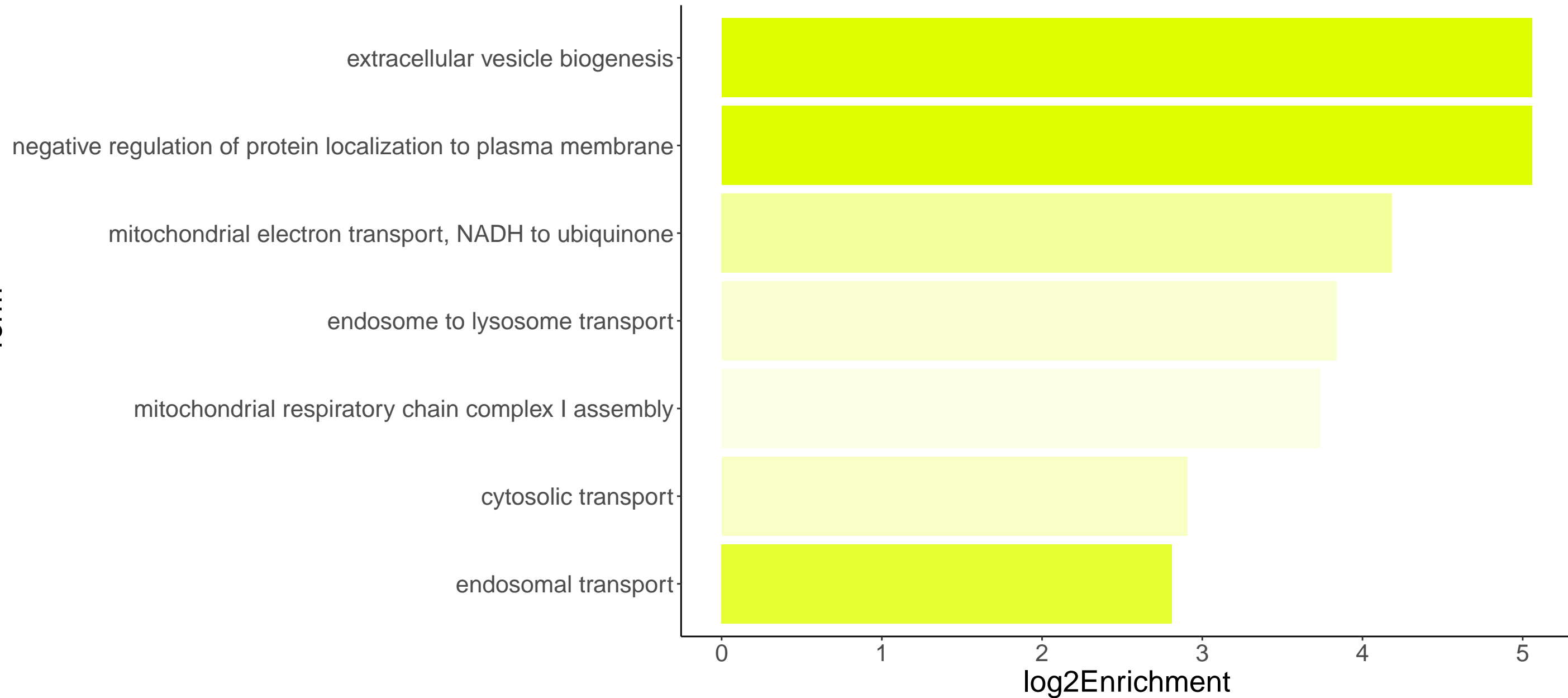
4

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

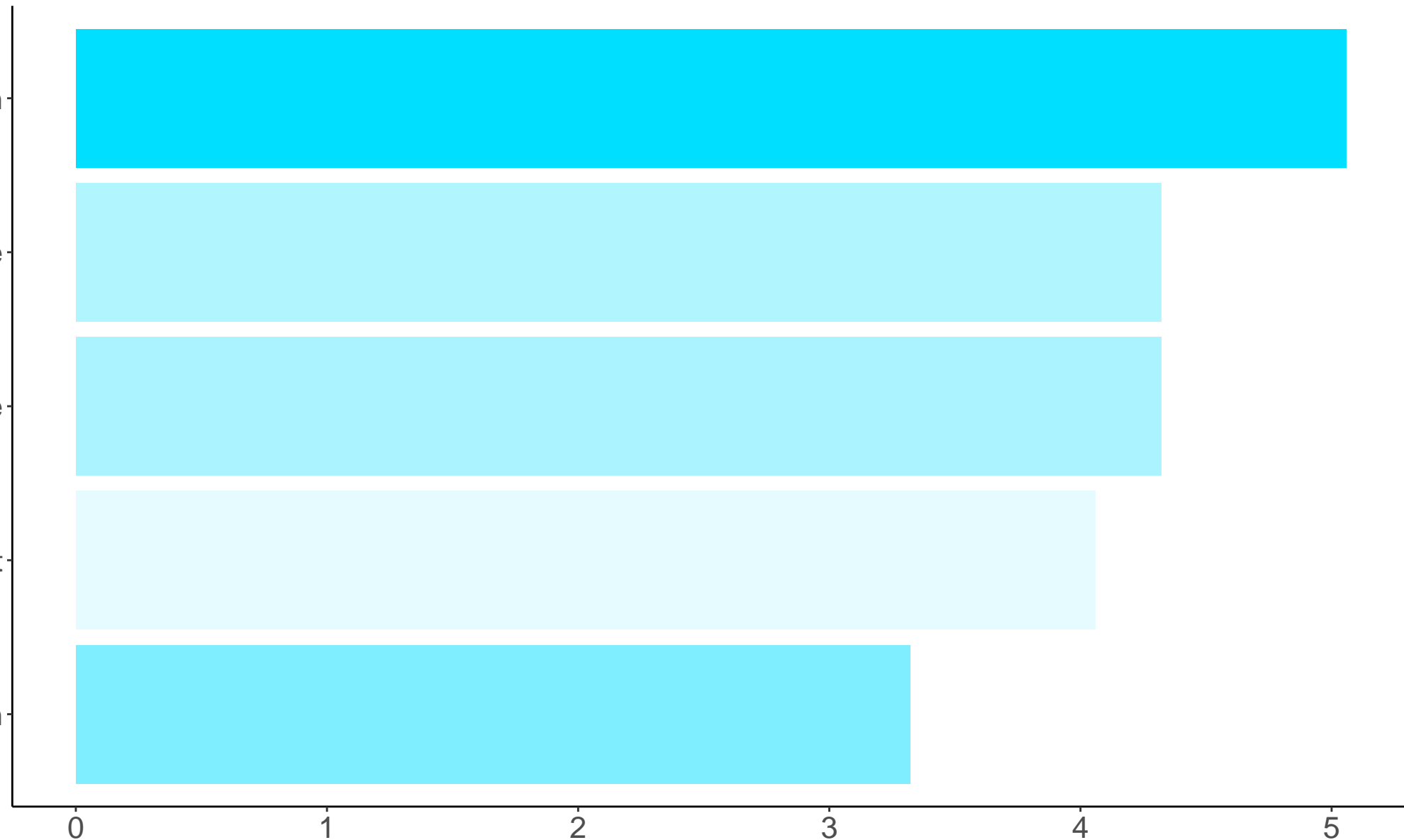
2

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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

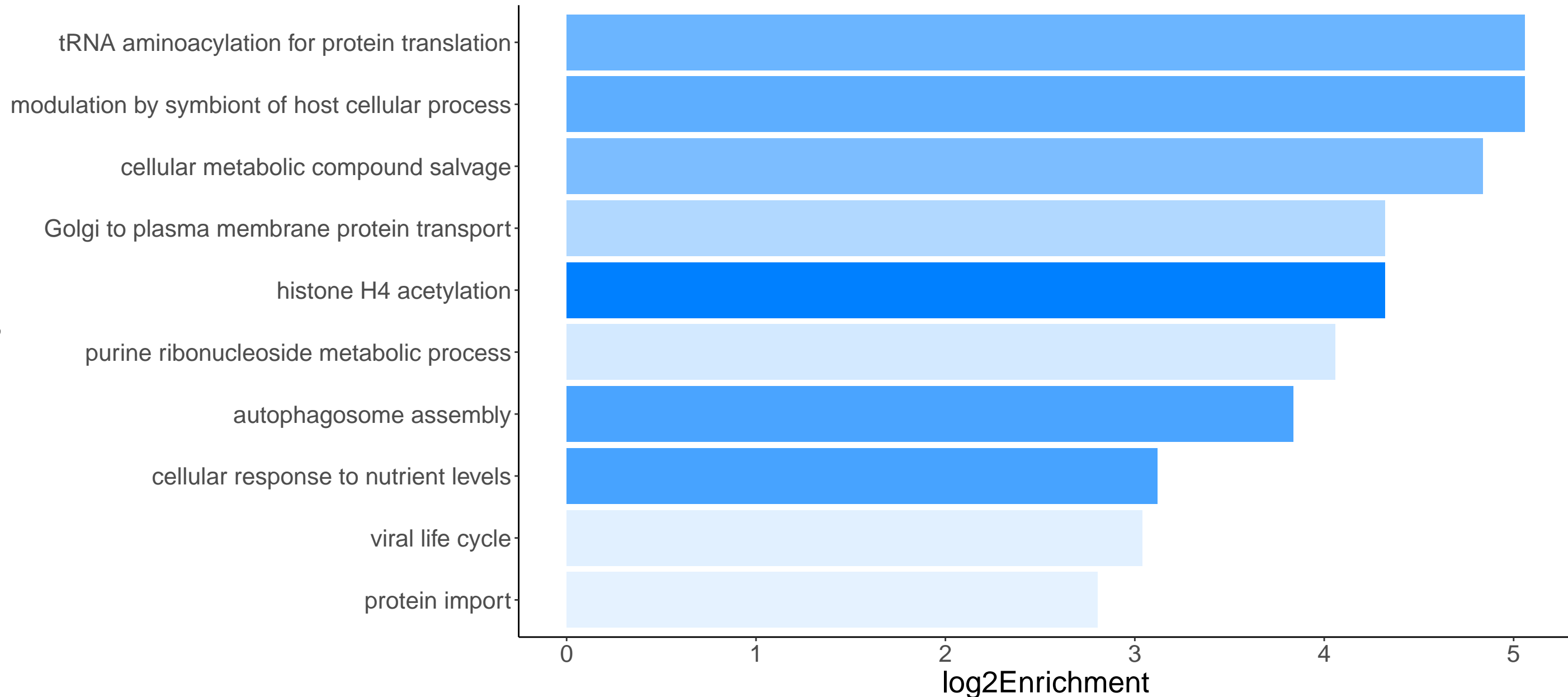
4

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

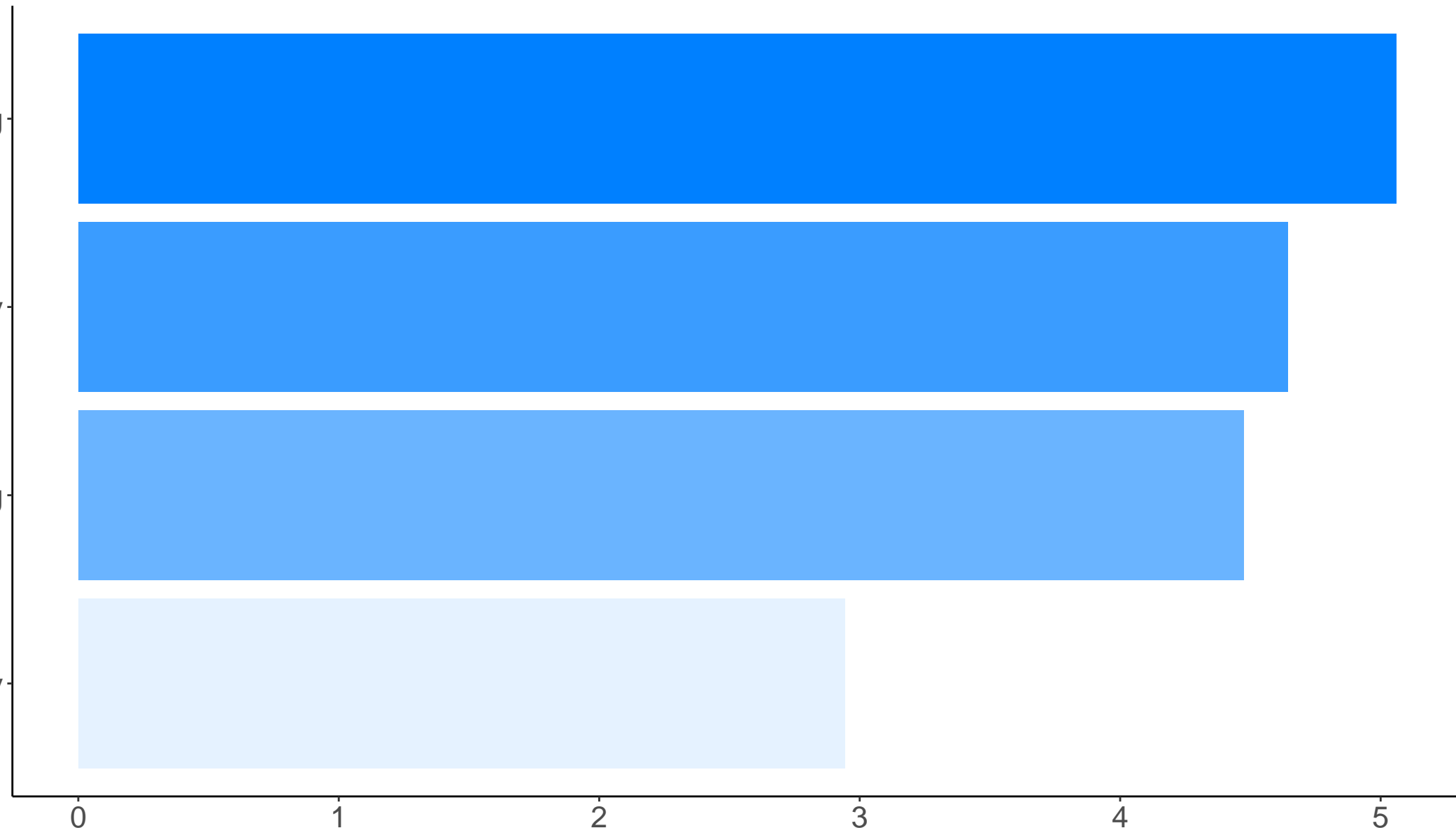
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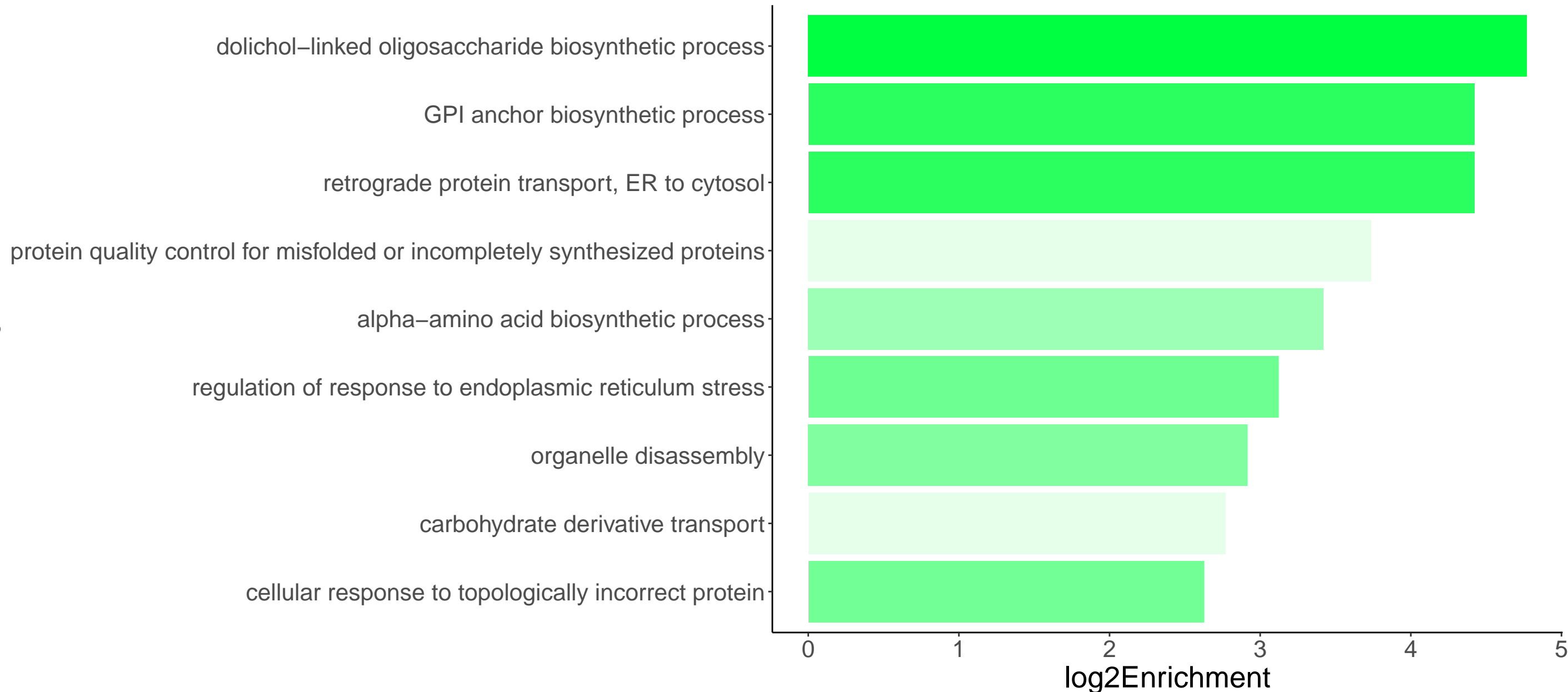
5

log2Enrichment



Re-clustered module 4.24 BP enrichment

Term



Re-clustered module 4.24 MF enrichment

Term

O-methyltransferase activity

0

1

2

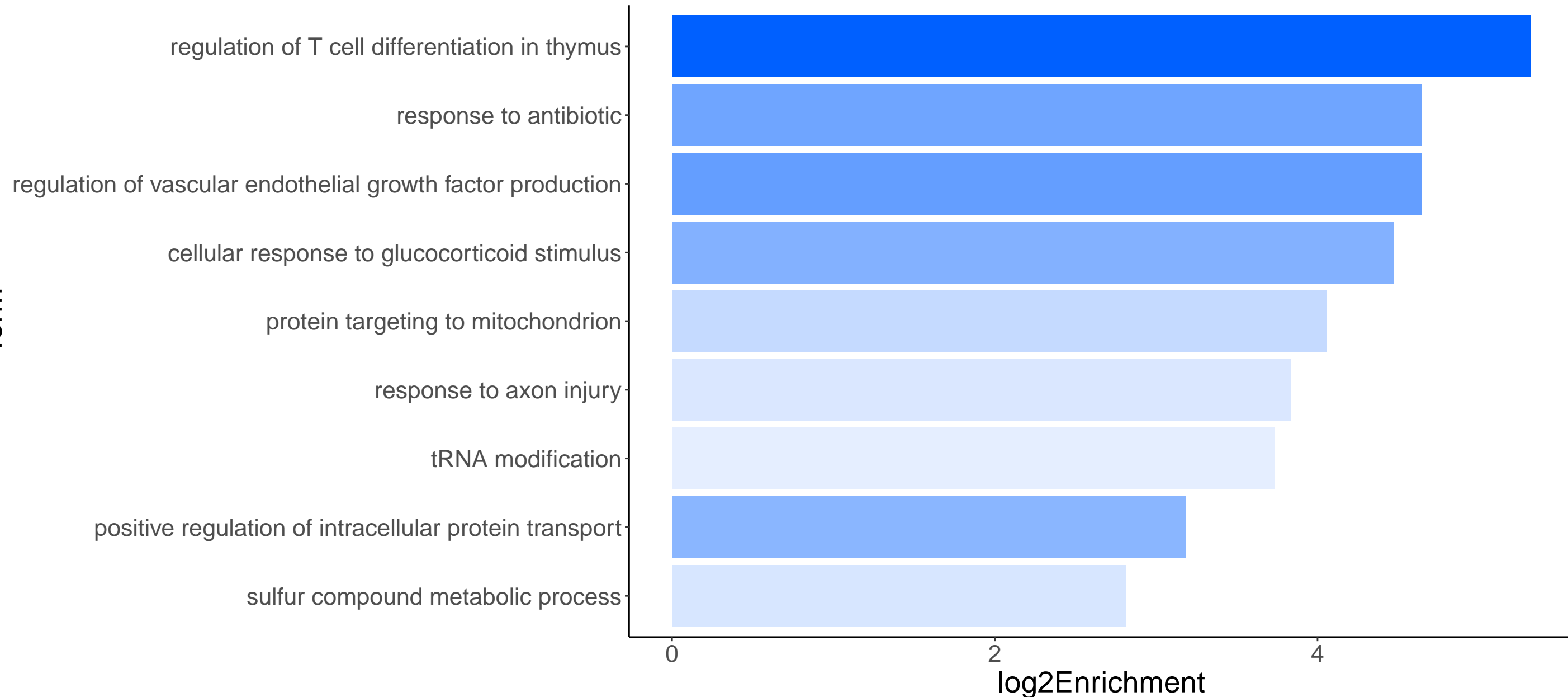
3

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

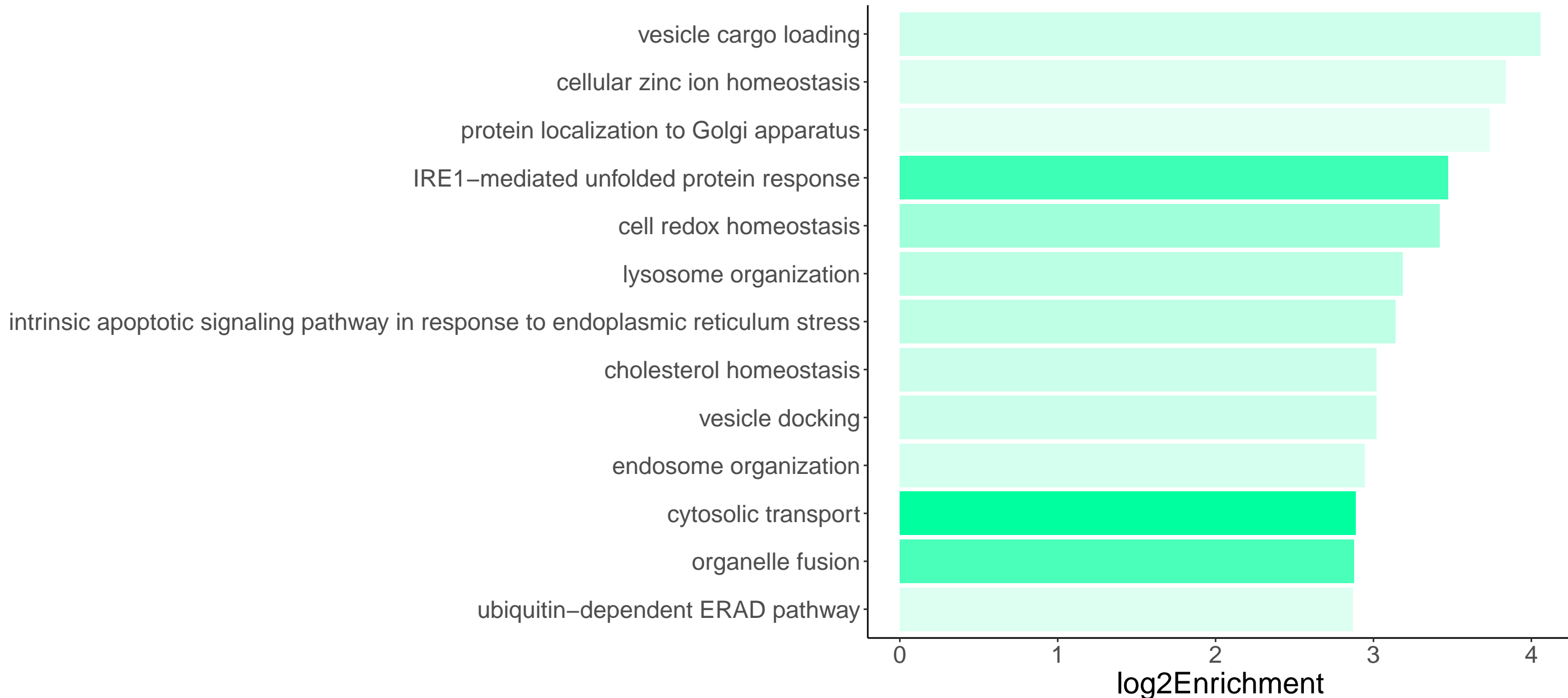
4

log2Enrichment



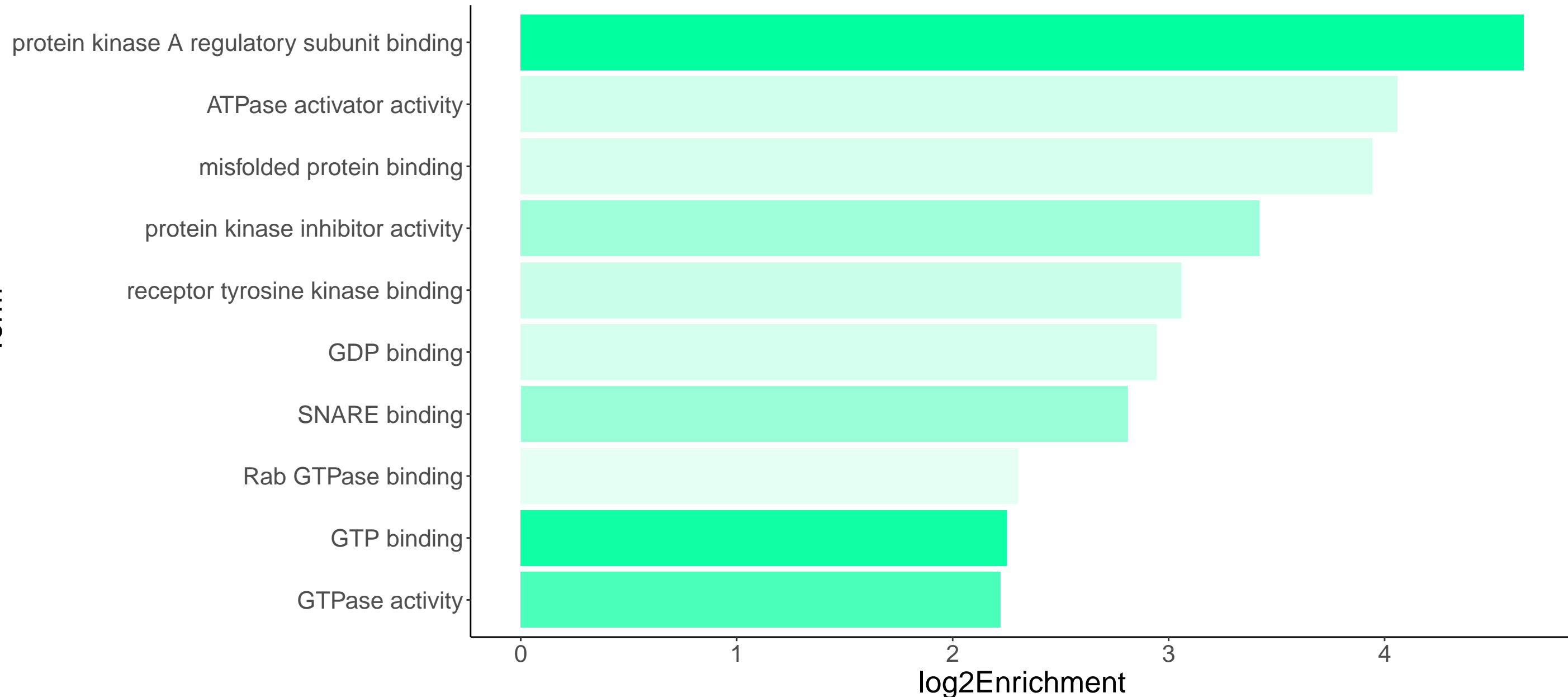
Re-clustered module 4.26 BP enrichment

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

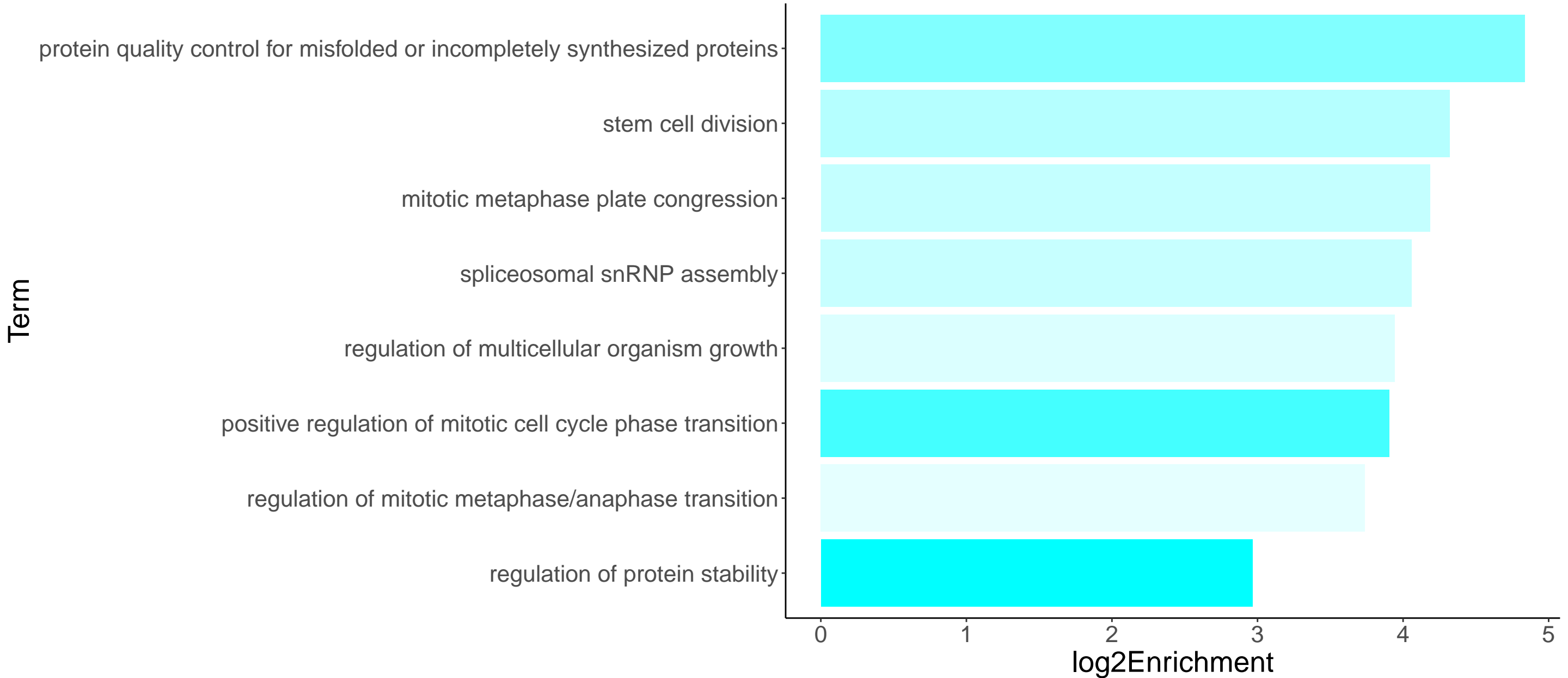
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log2Enrichment



Re-clustered module 4.27 MF enrichment

Term

RNA polymerase II activating transcription factor binding

catalytic activity, acting on DNA

helicase activity

0

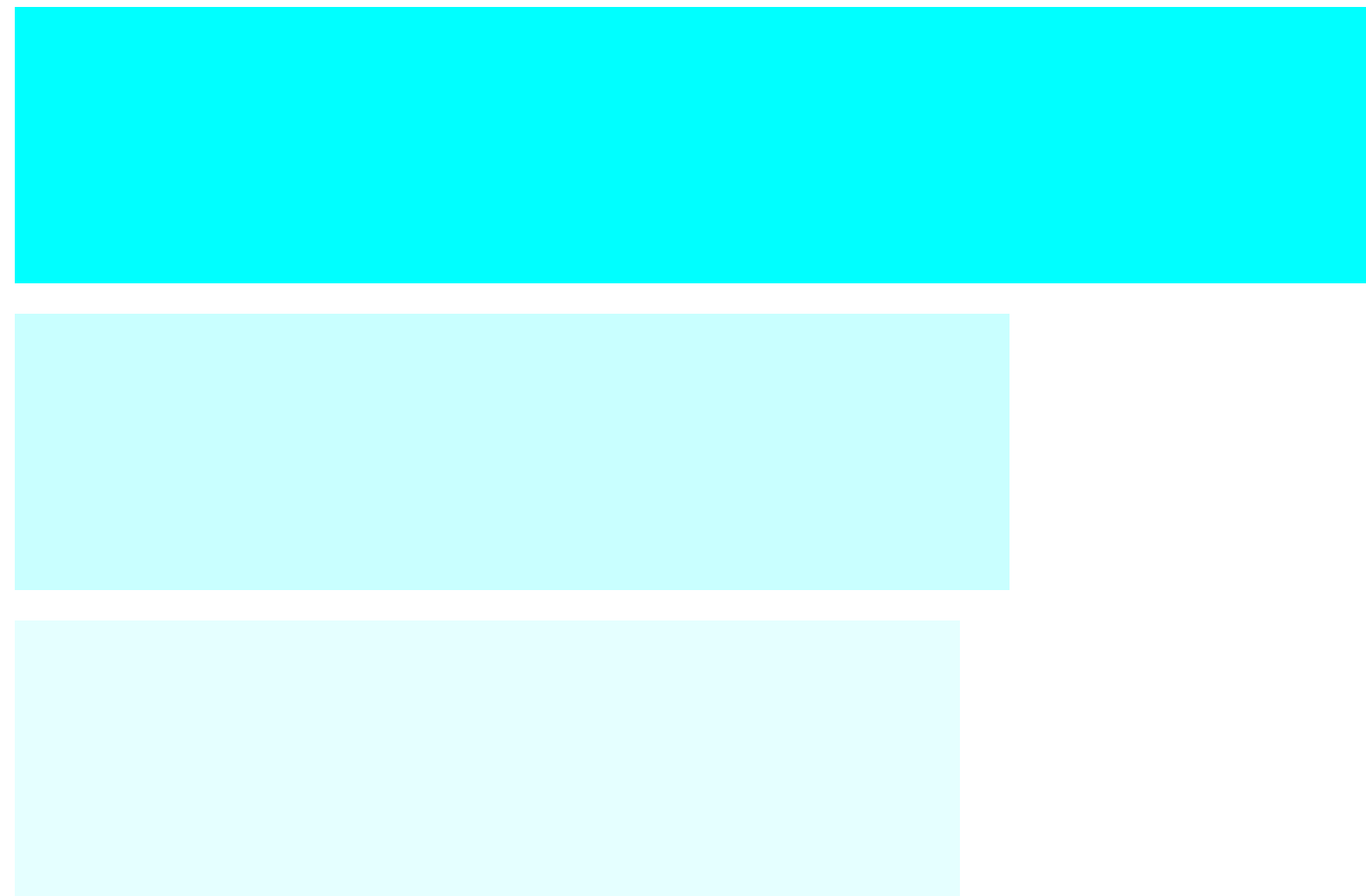
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log2Enrichment



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

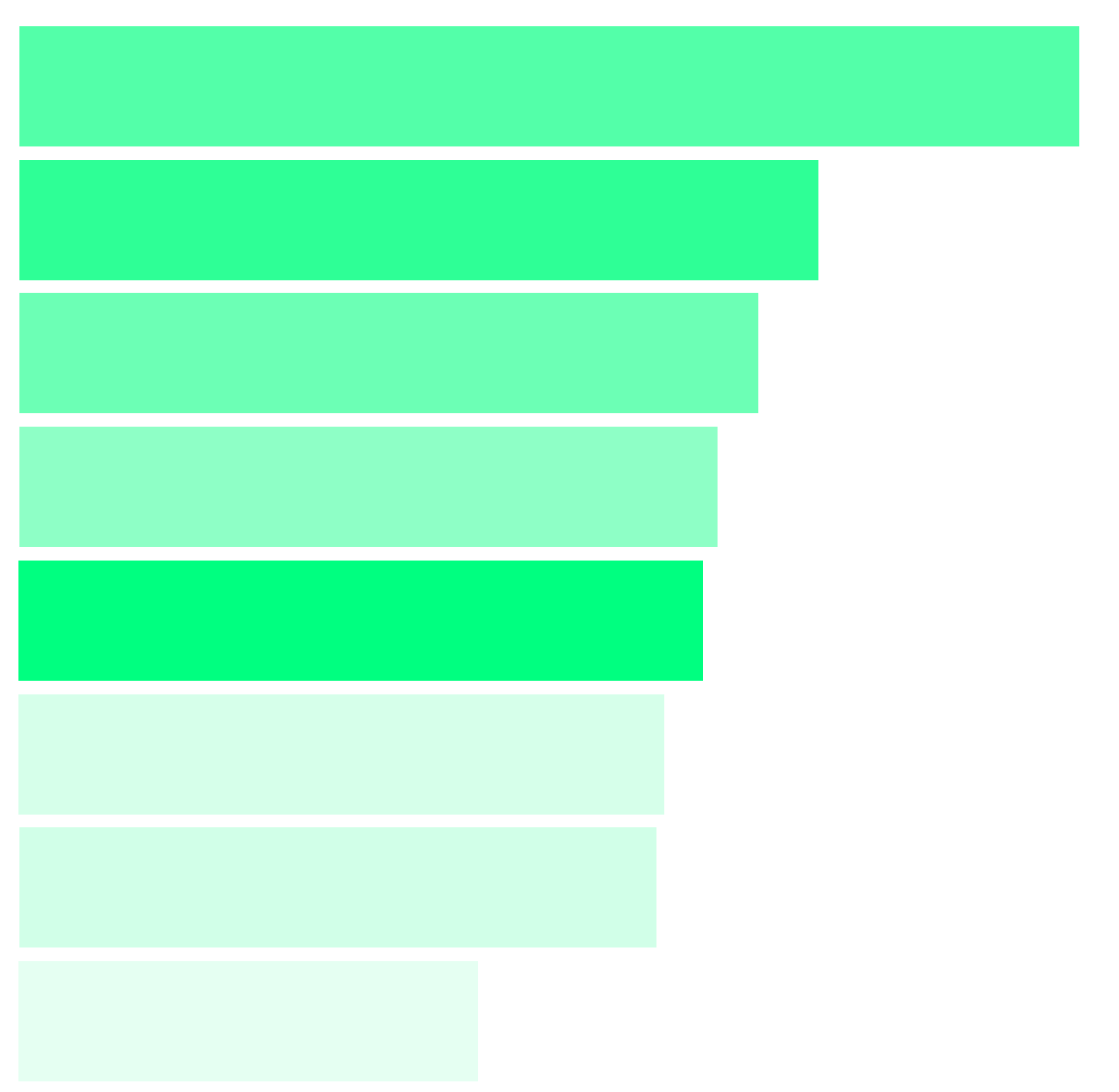
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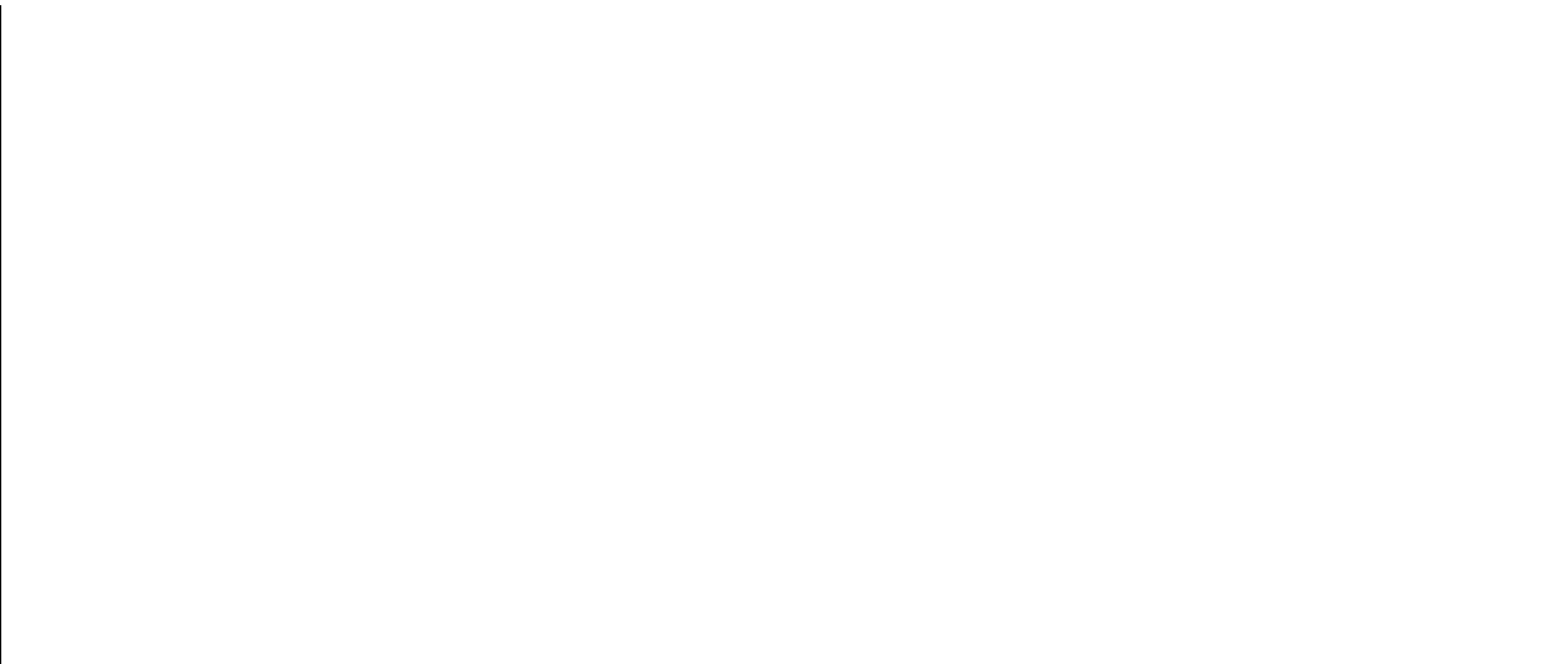
log2Enrichment



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

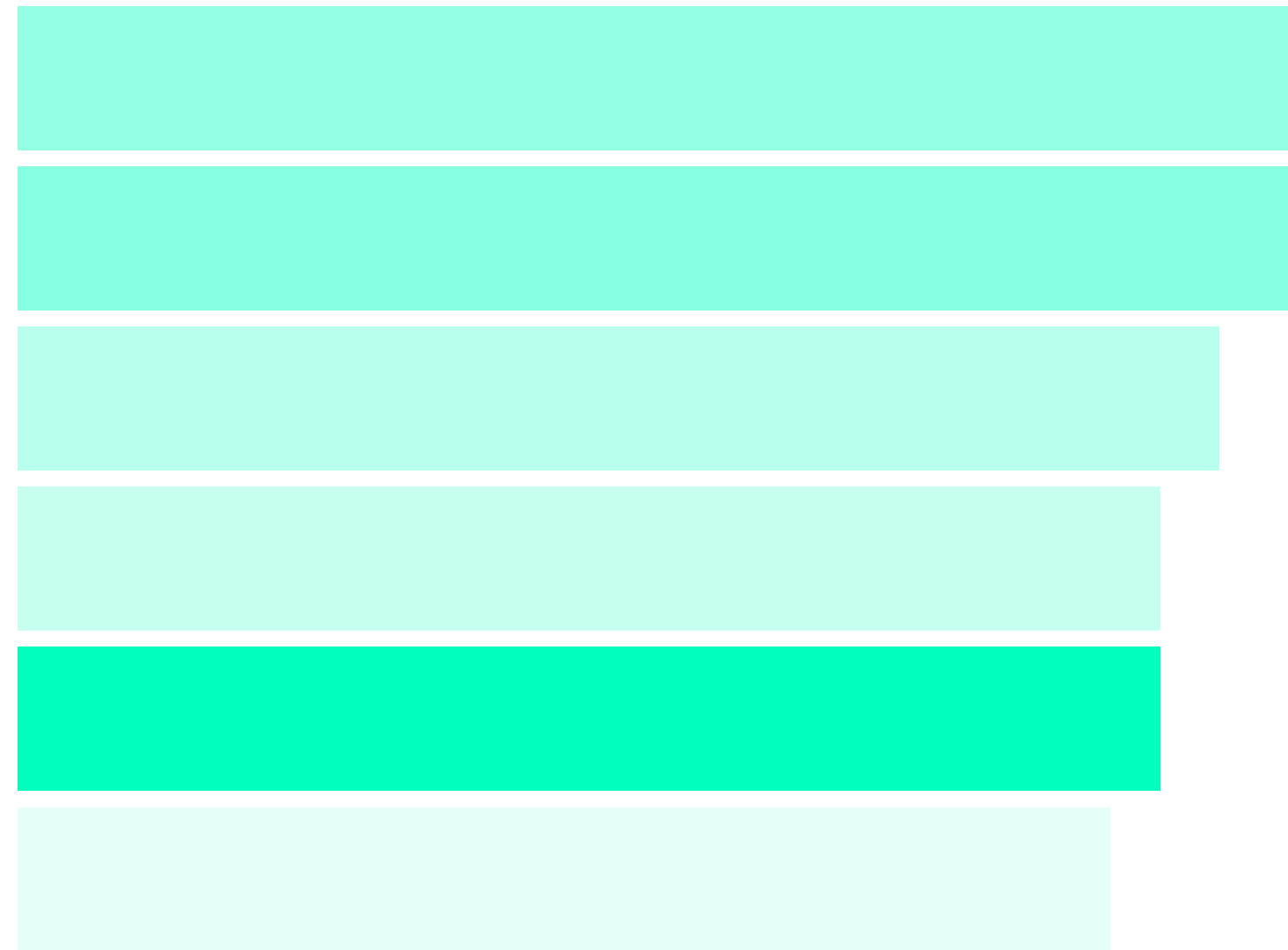
ER-nucleus signaling pathway

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

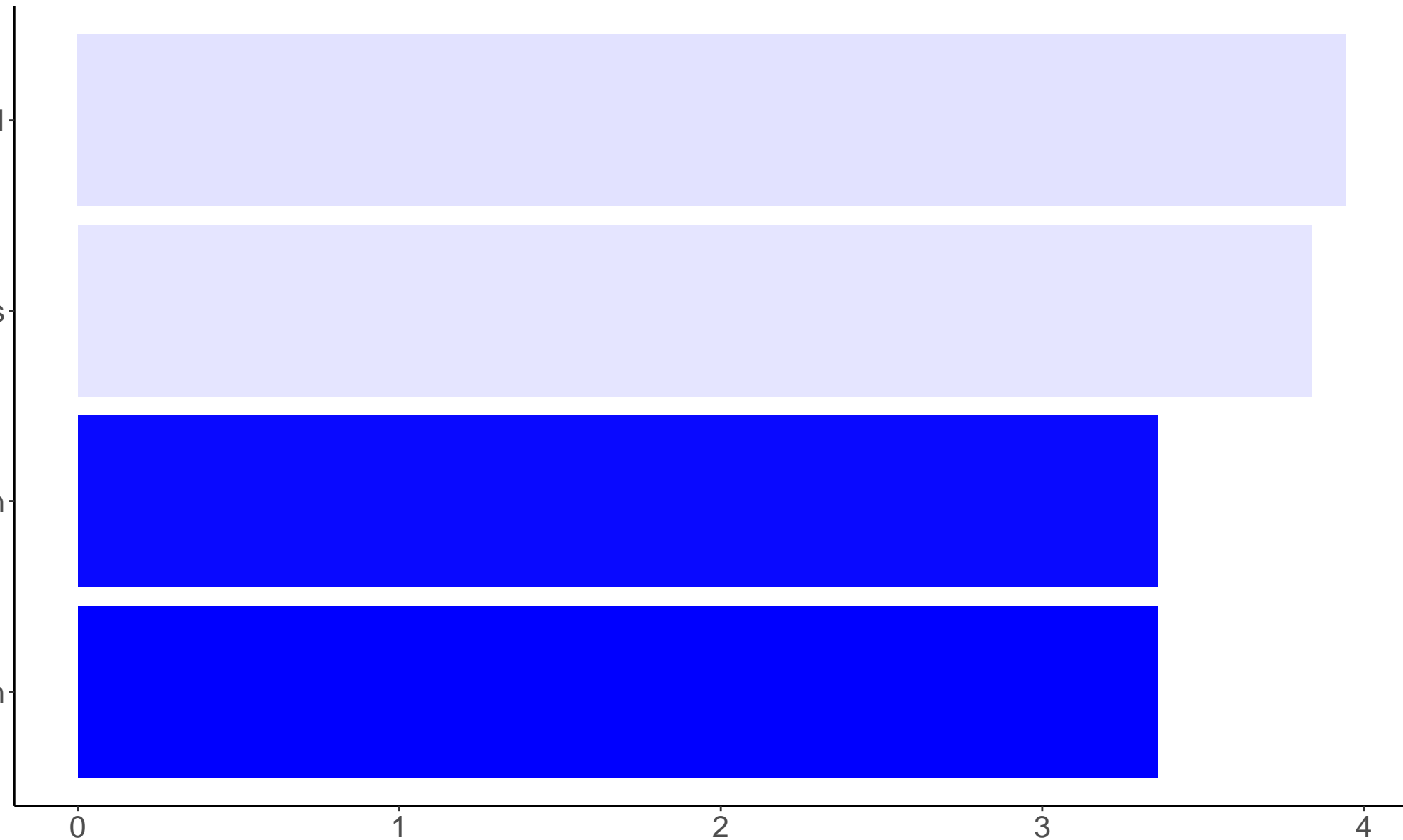
1

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log2Enrichment



Re-clustered module 4.3 MF enrichment

Term

lysine-acetylated histone binding

DNA-directed 5'-3' RNA polymerase activity

0

1

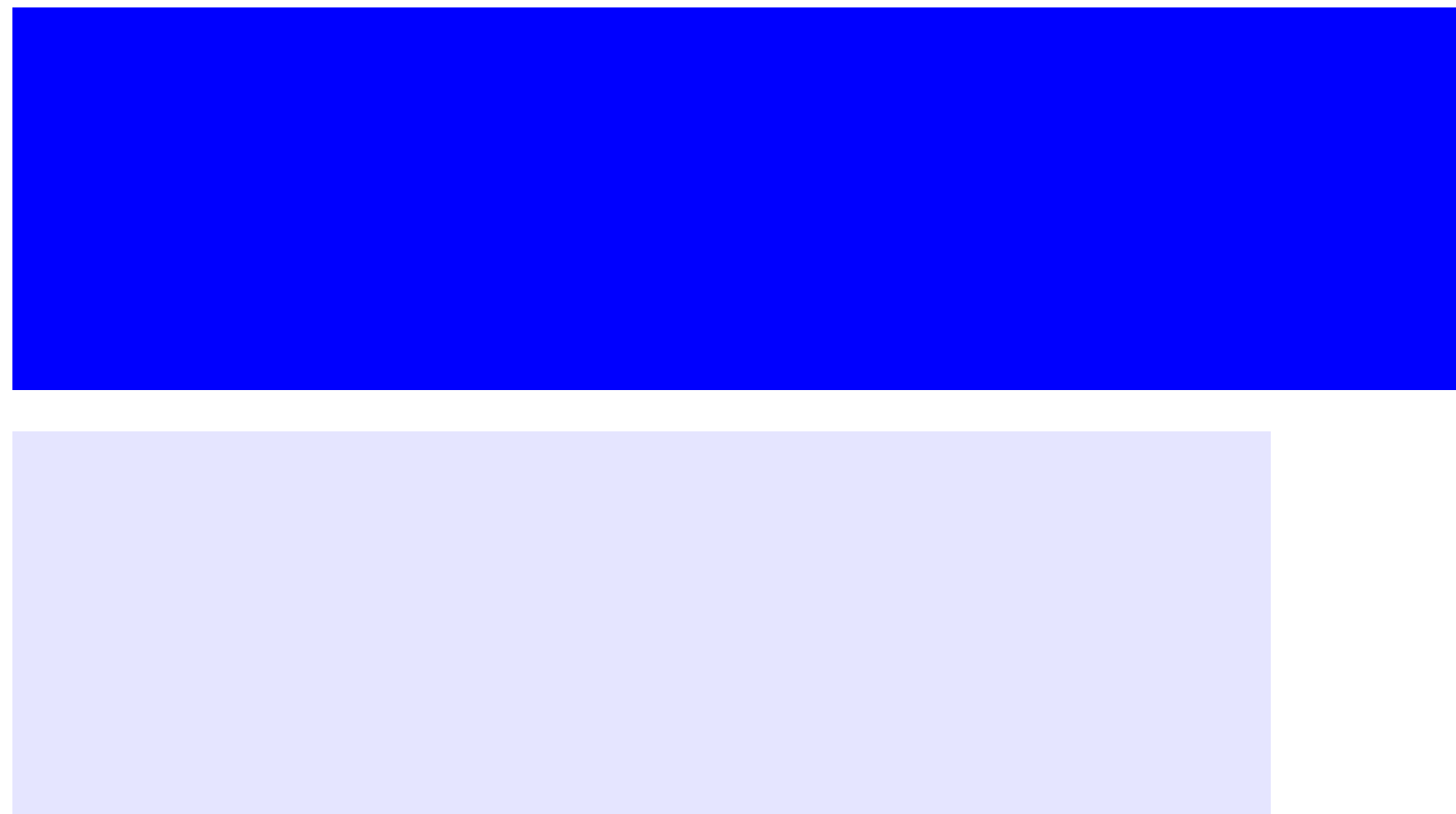
2

3

4

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log2Enrichment



Re-clustered module 4.4 BP enrichment

Term

syncytium formation by plasma membrane fusion

RNA phosphodiester bond hydrolysis, exonucleolytic

0

1

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log2Enrichment



Re-clustered module 4.4 MF enrichment

Term

telomeric DNA binding

3'-5' exonuclease activity

signal sequence binding

nucleic acid binding

0

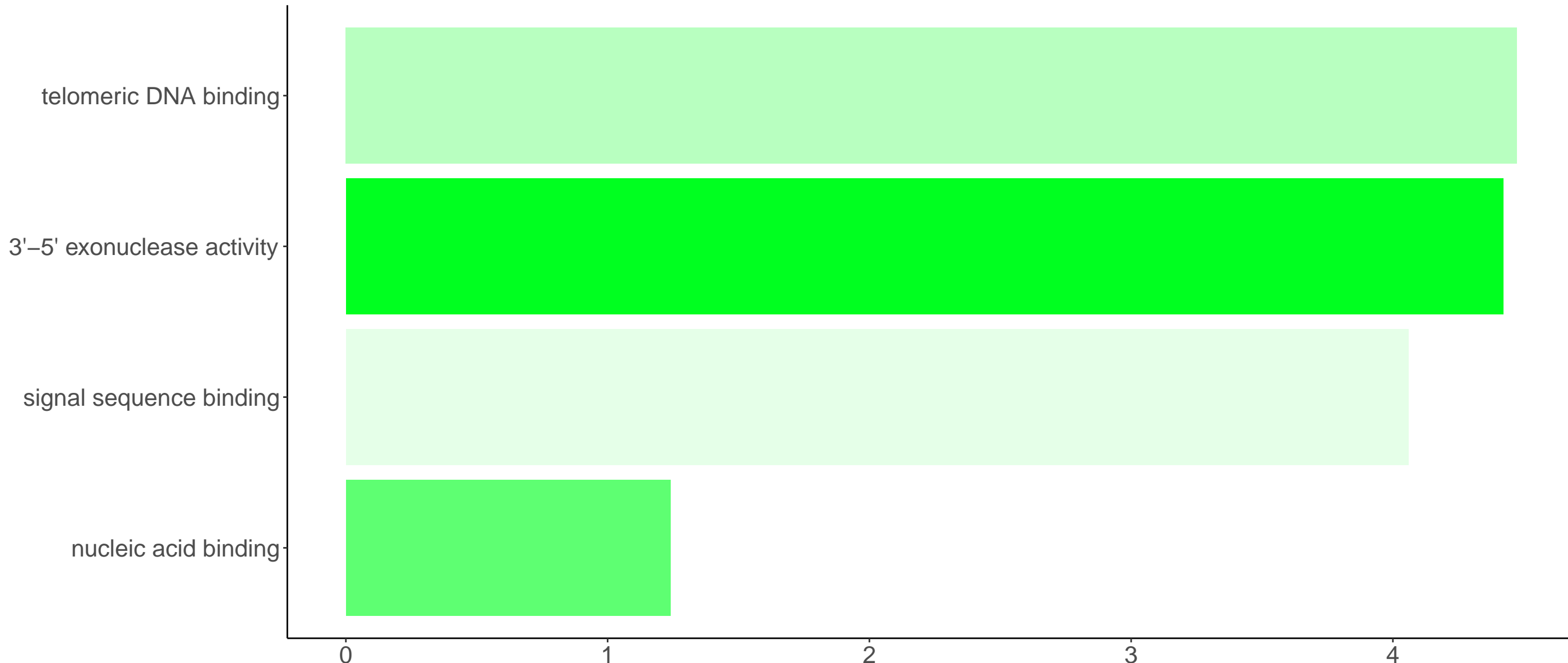
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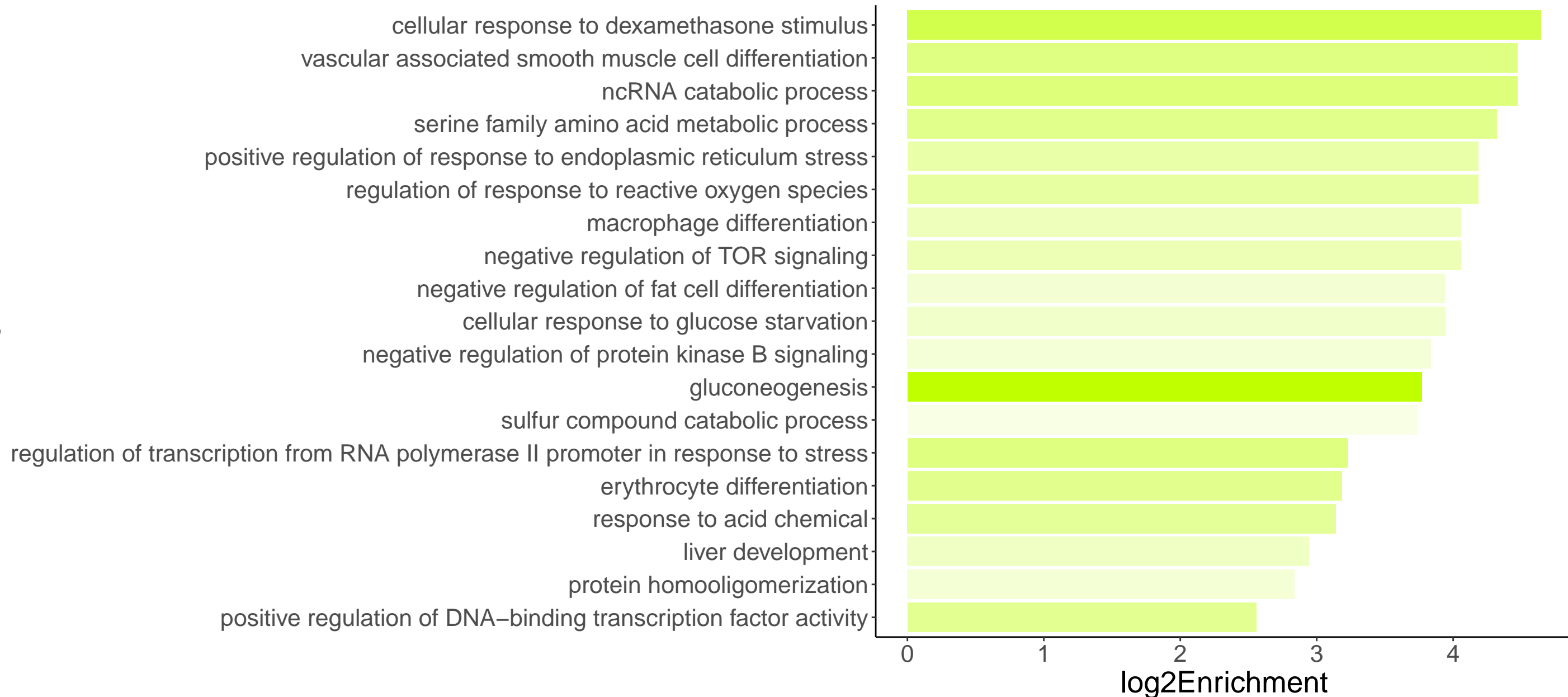
4

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

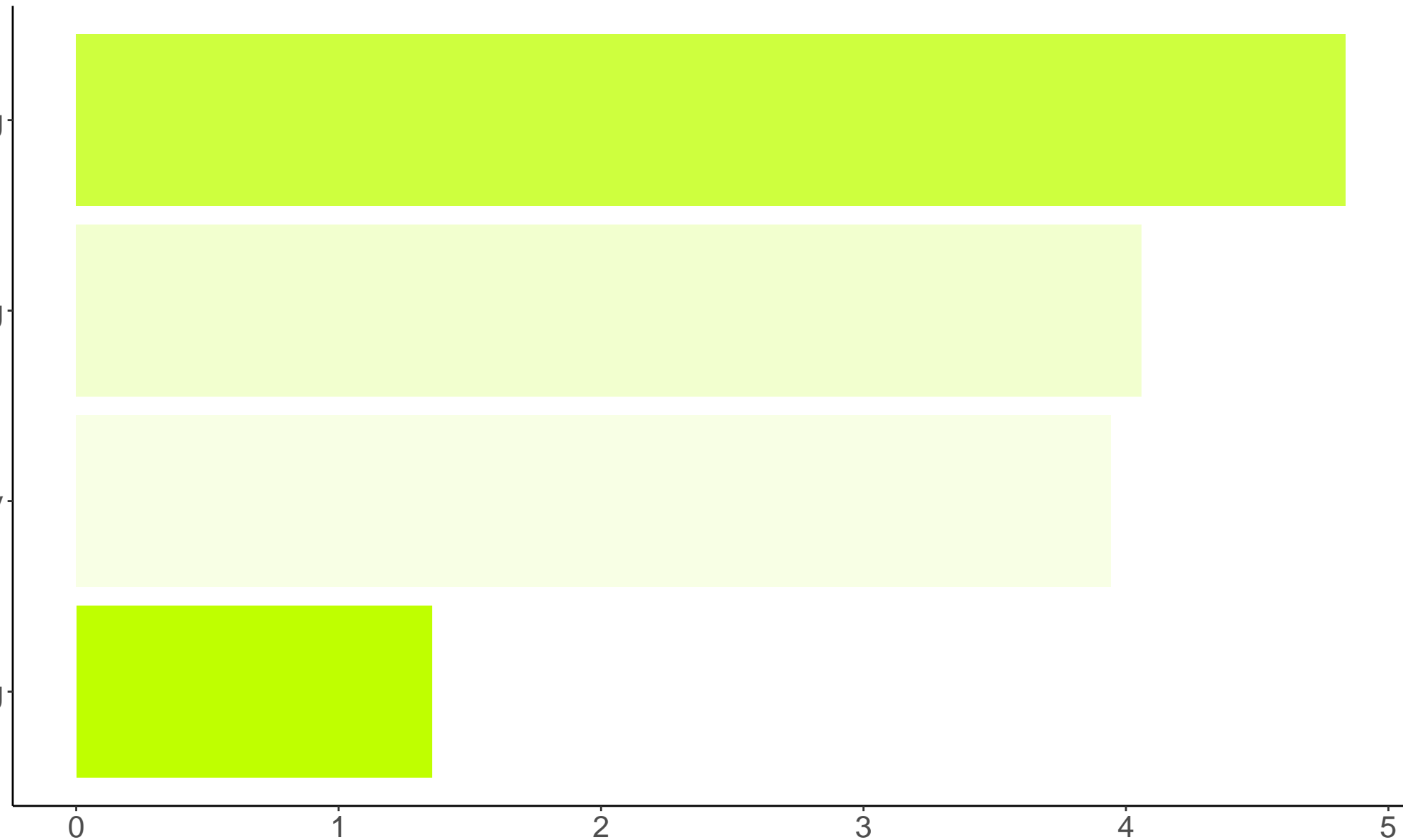
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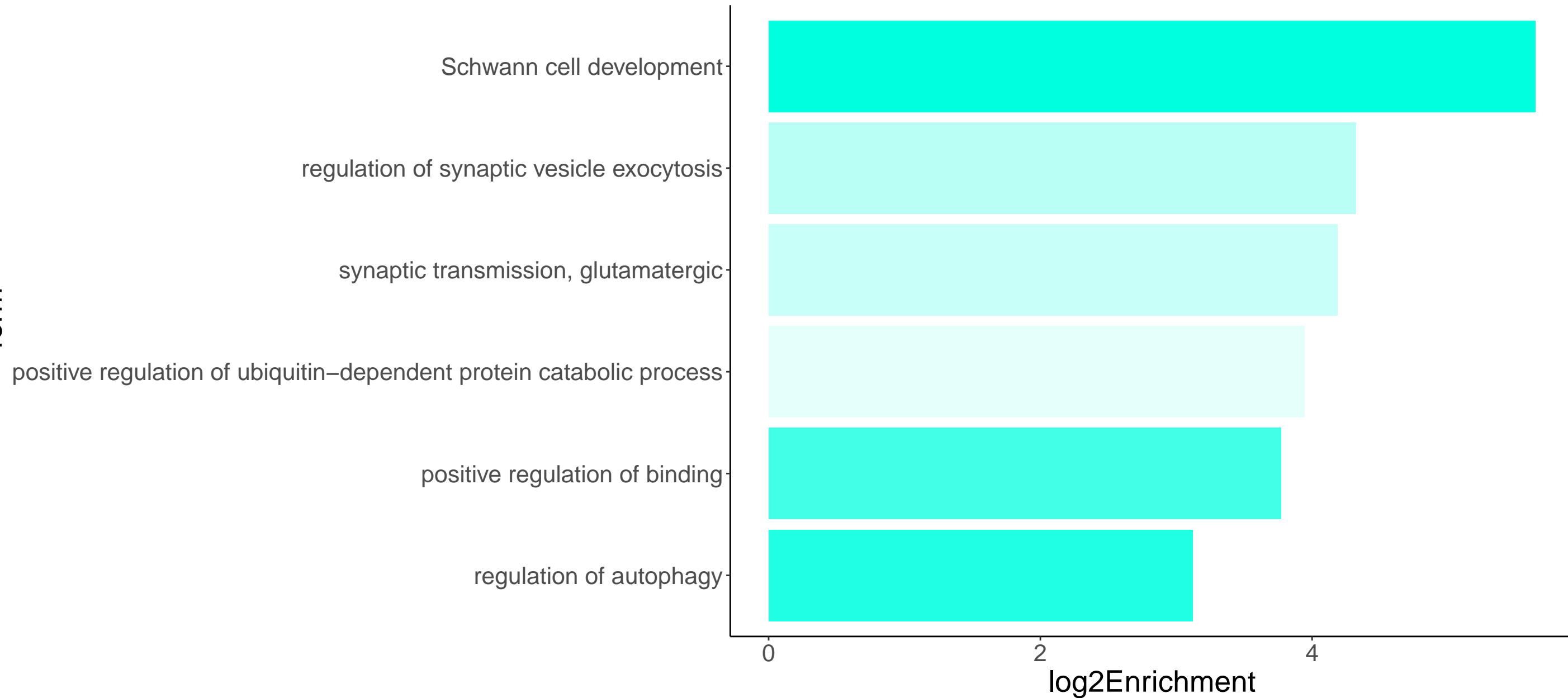
5

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

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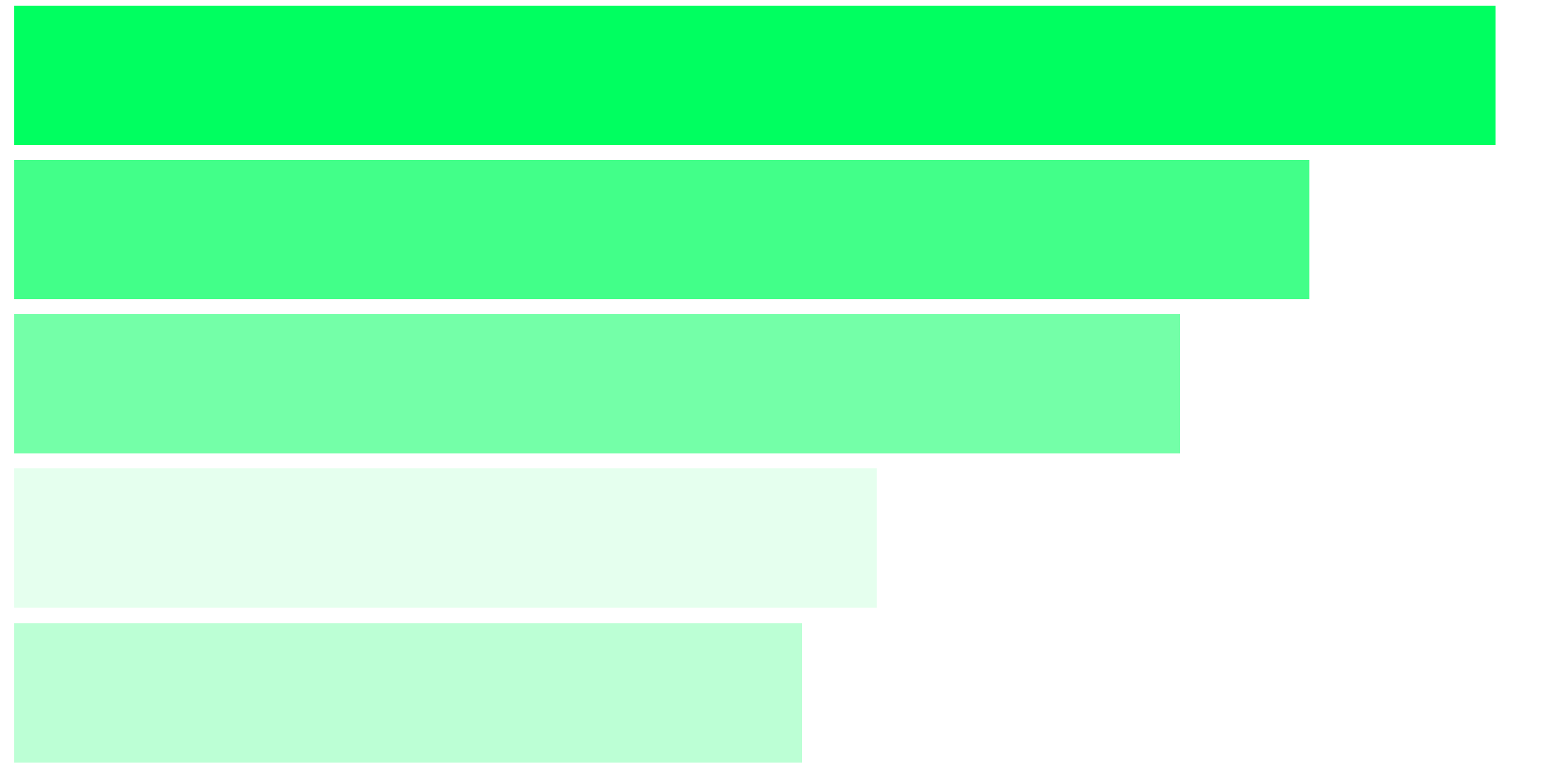
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log2Enrichment



Re-clustered module 4.7 MF enrichment

Term

pyridoxal phosphate binding

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

0

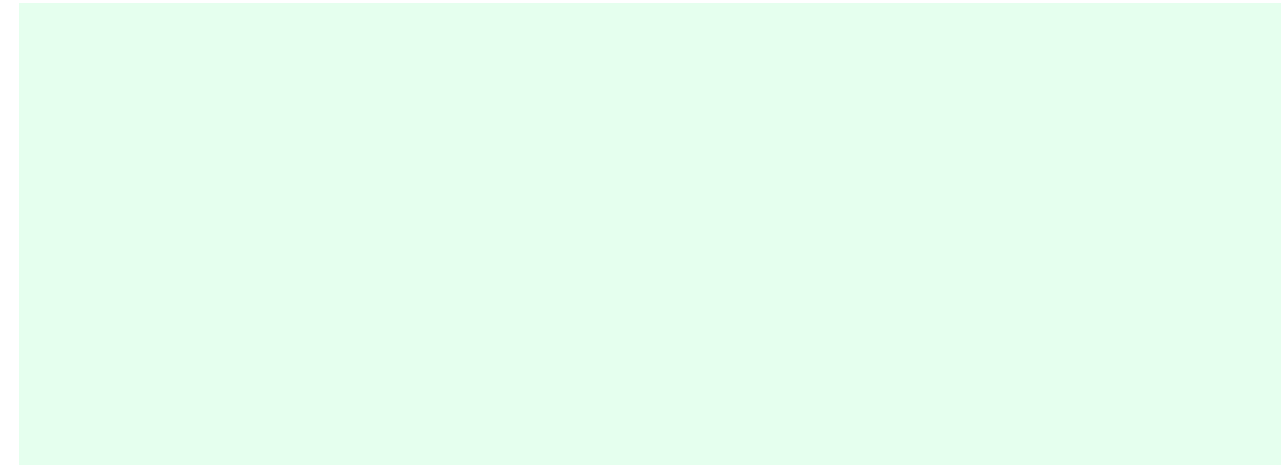
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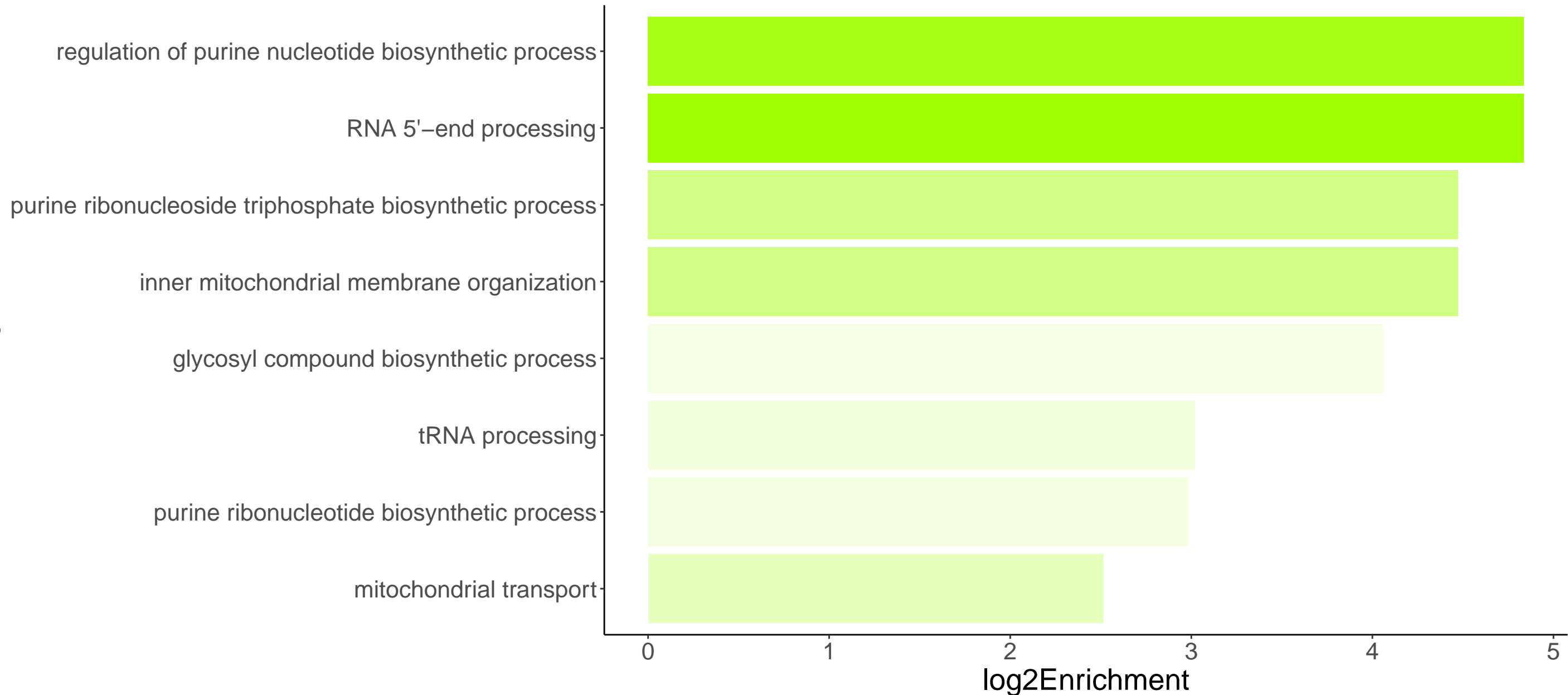
4

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

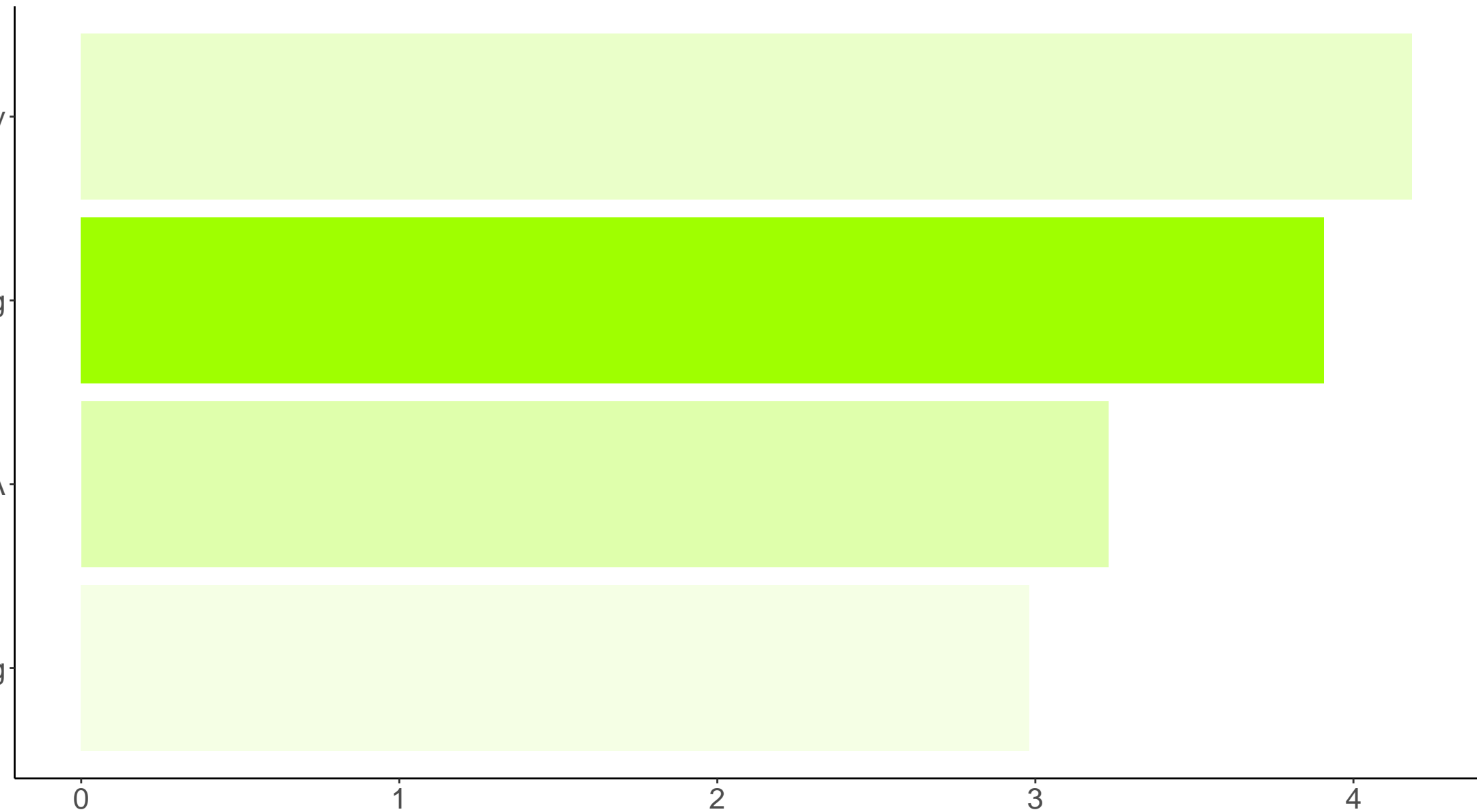
1

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4

log2Enrichment



Re-clustered module 4.9 BP enrichment

Term



Re-clustered module 4.9 MF enrichment

Term

