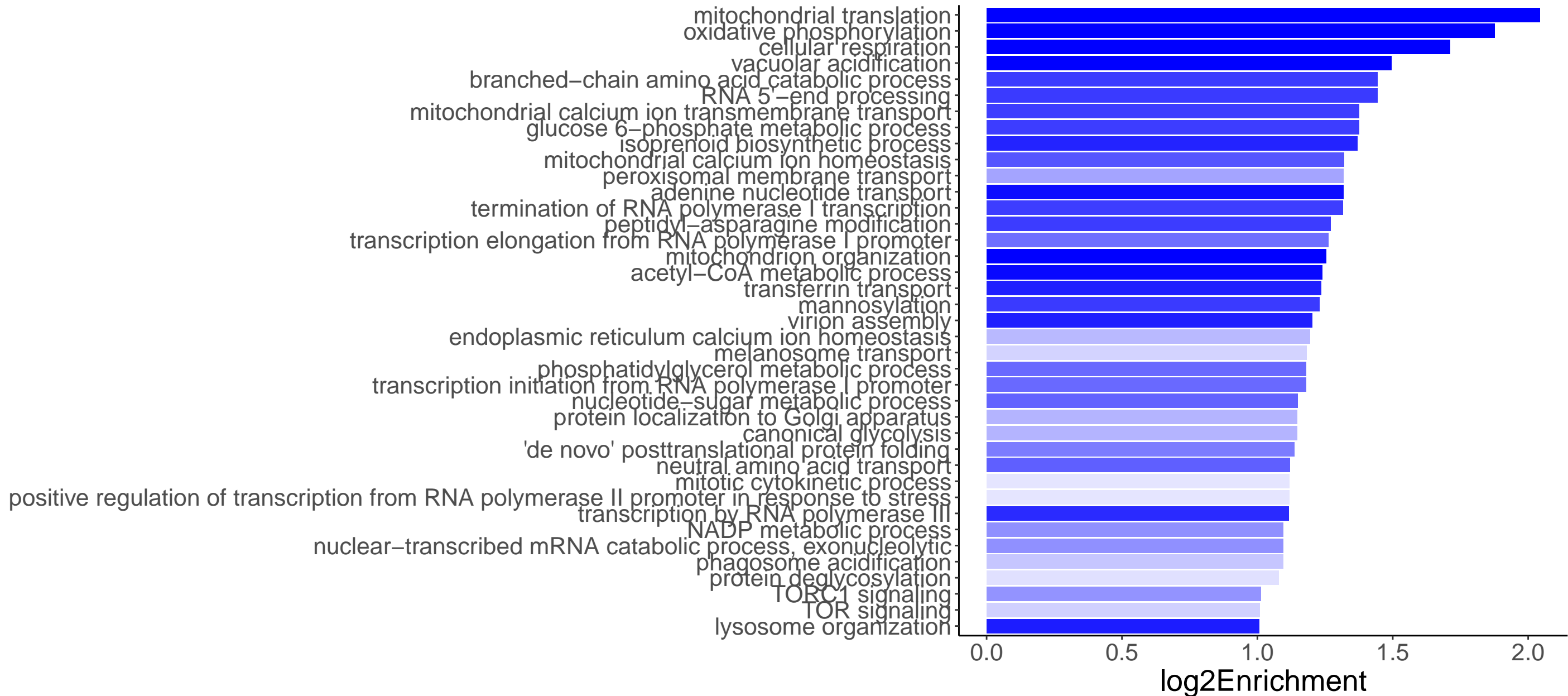


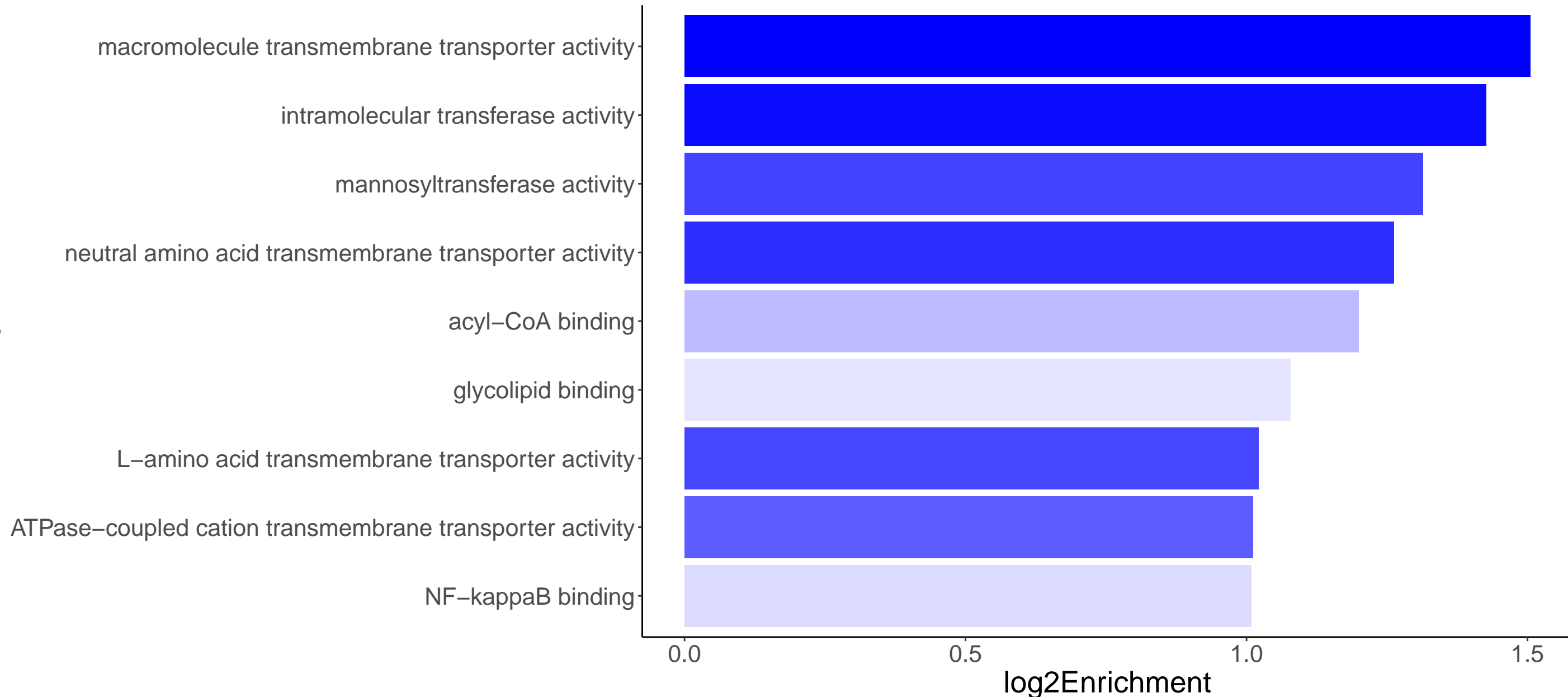
Original module 16 BP enrichment

Term



Original module 16 MF enrichment

Term



Re-clustered module 16.1 BP enrichment

Term

cellular metabolic compound salvage

mRNA export from nucleus

transcription initiation from RNA polymerase II promoter

mRNA processing

0

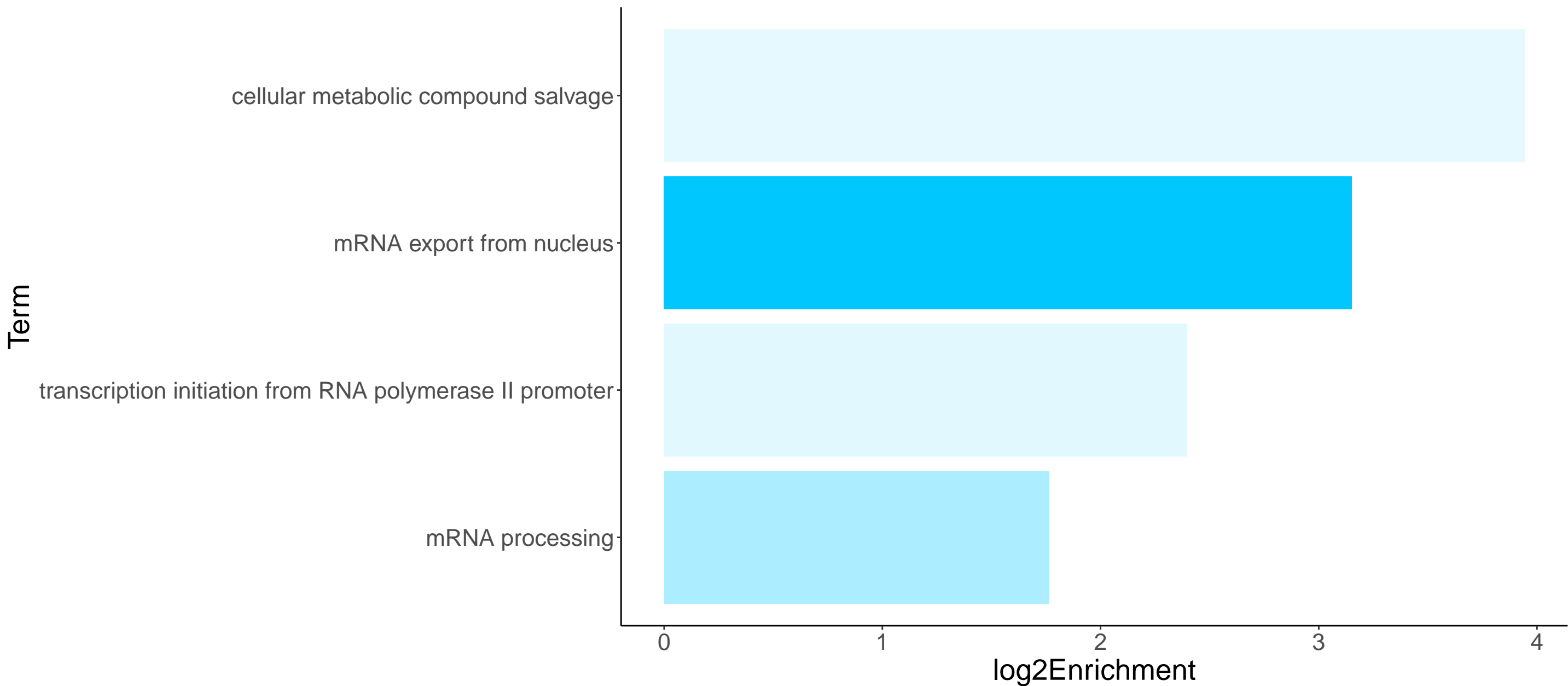
1

2

3

4

log2Enrichment



Re-clustered module 16.1 MF enrichment

Term

DNA-directed DNA polymerase activity

DNA-directed 5'–3' RNA polymerase activity

steroid dehydrogenase activity

thiolester hydrolase activity

0

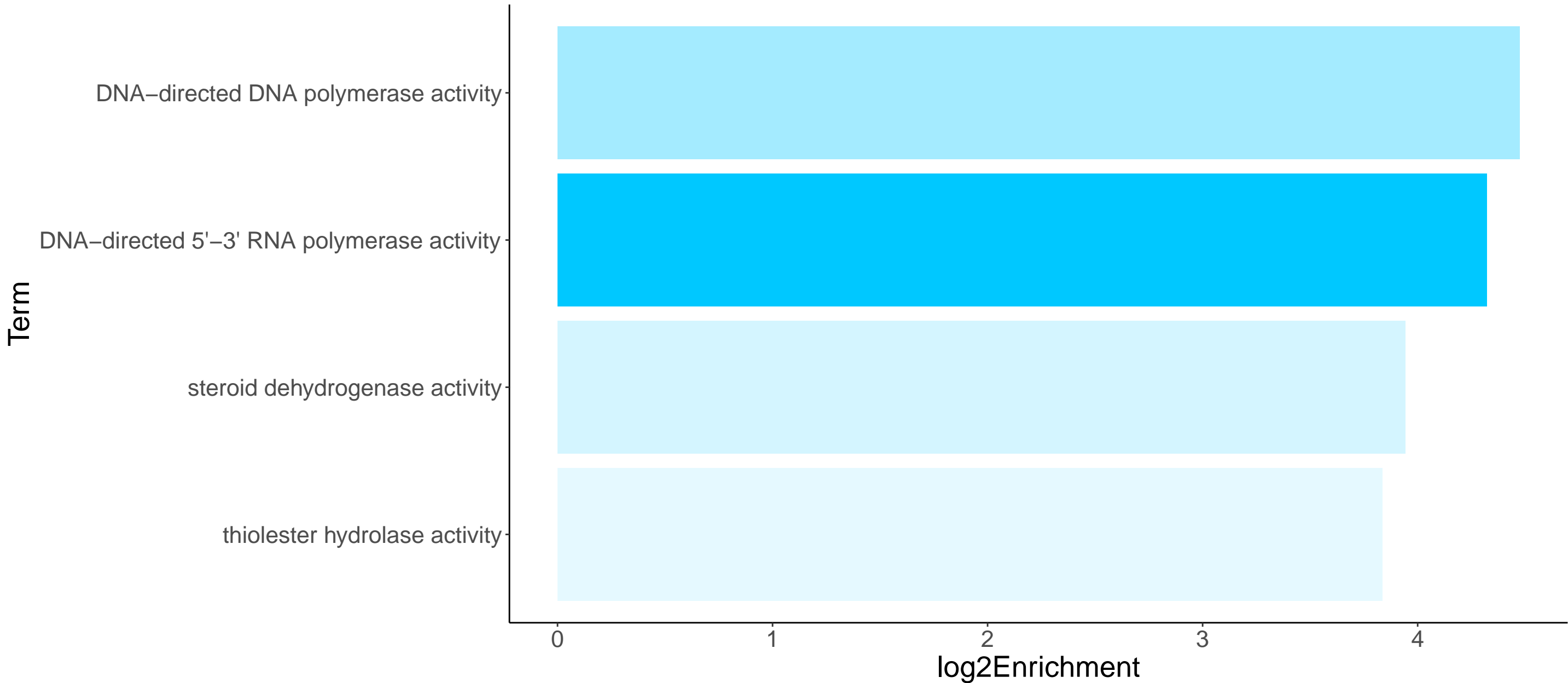
1

2

3

4

log2Enrichment



Re-clustered module 16.10.1 BP enrichment

Term

mitochondrial RNA metabolic process

tRNA methylation

fatty acid catabolic process

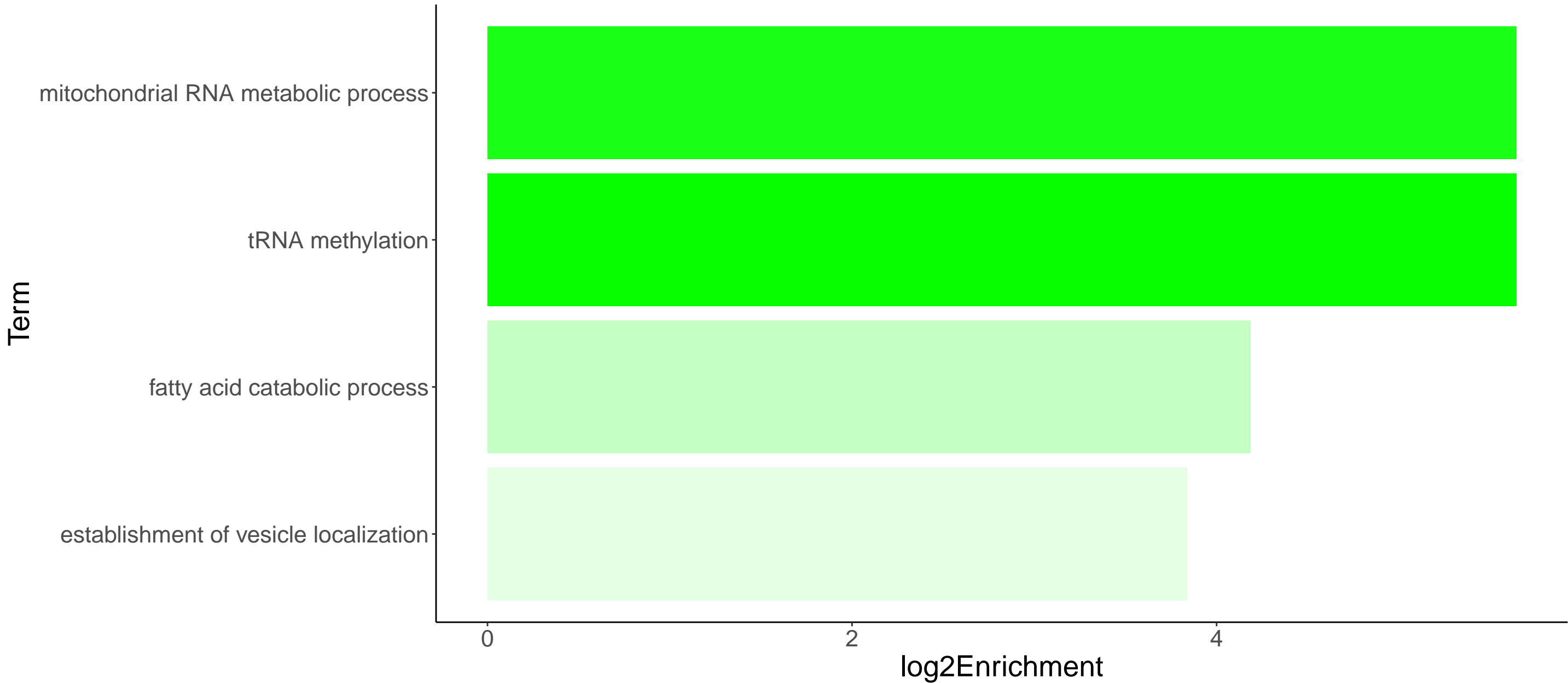
establishment of vesicle localization

0

2

4

log2Enrichment



Re-clustered module 16.10.1 MF enrichment

Term

tRNA methyltransferase activity

GTP binding

0

2

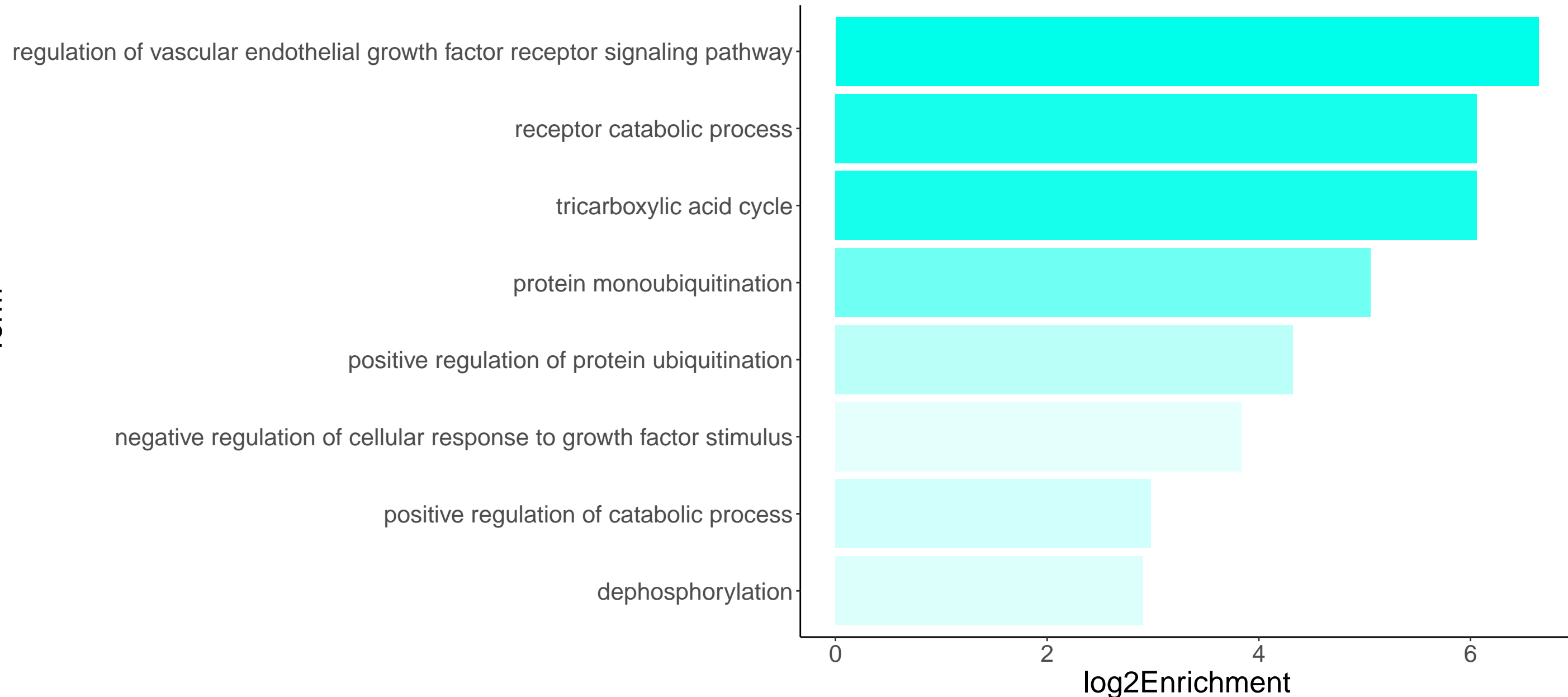
4

6

log2Enrichment



Re-clustered module 16.10.2 BP enrichment



Re-clustered module 16.10.2 MF enrichment

Term

protein-macromolecule adaptor activity

0

1

2

3

log2Enrichment



Re-clustered module 16.10.3 BP enrichment

Term

log2Enrichment



Re-clustered module 16.10.3 MF enrichment

Term

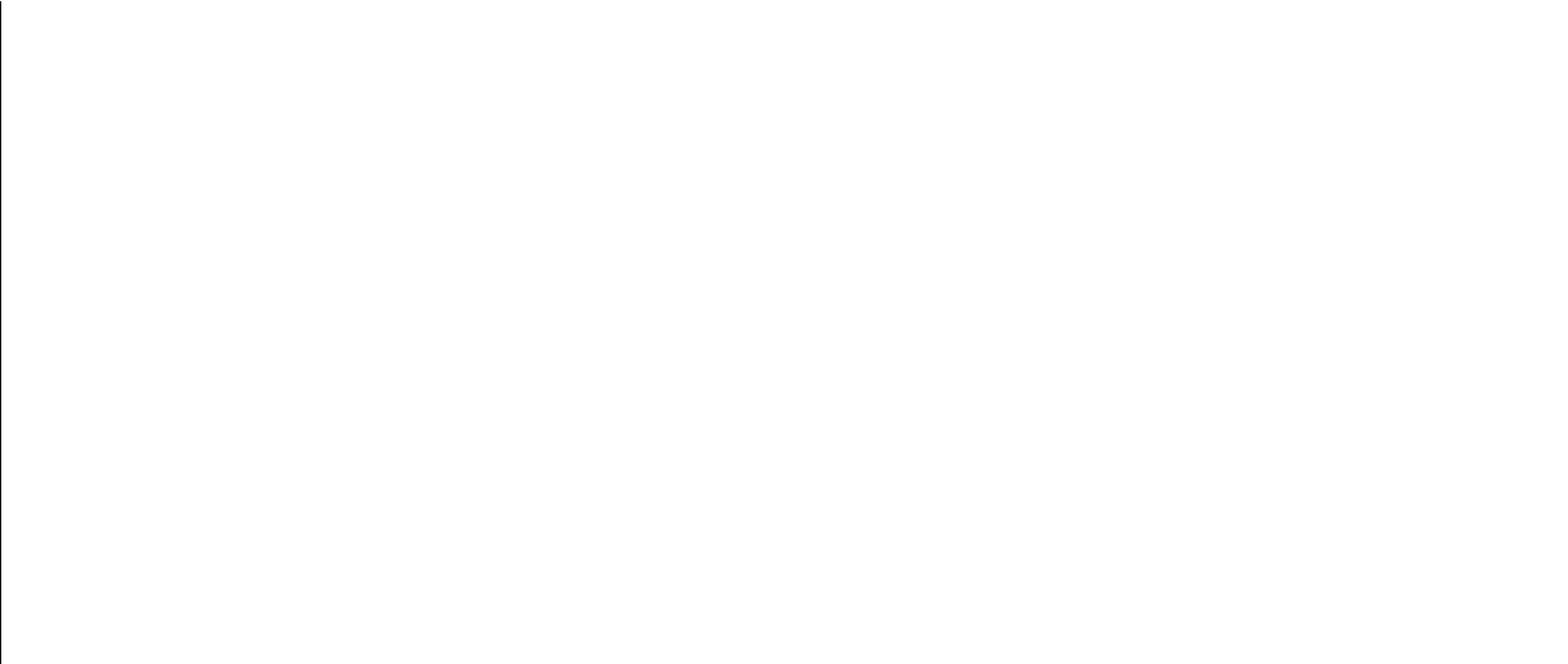
log2Enrichment



Re-clustered module 16.10.4 BP enrichment

Term

log2Enrichment



Re-clustered module 16.10.4 MF enrichment

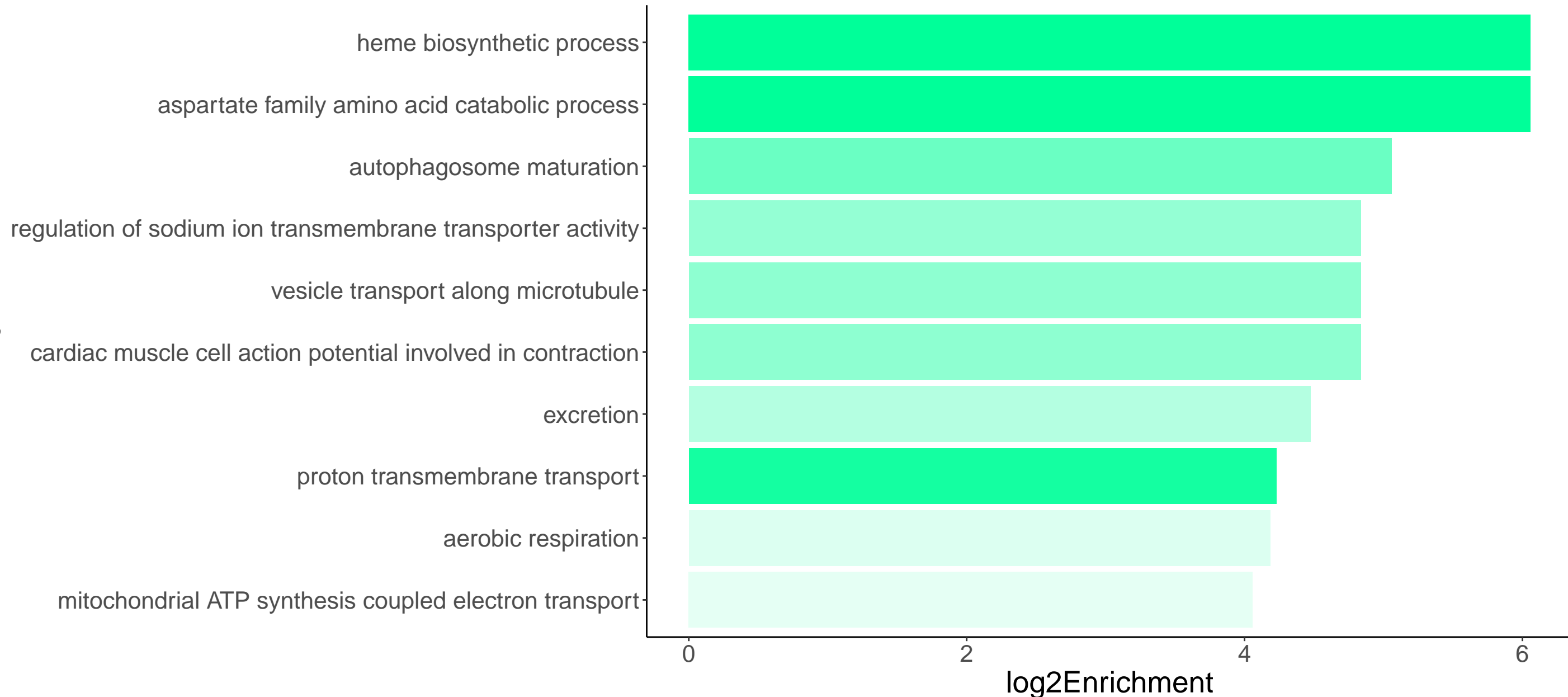
Term

log2Enrichment



Re-clustered module 16.10.5 BP enrichment

Term



Re-clustered module 16.10.5 MF enrichment

Term

ankyrin binding

pyridoxal phosphate binding

electron transfer activity

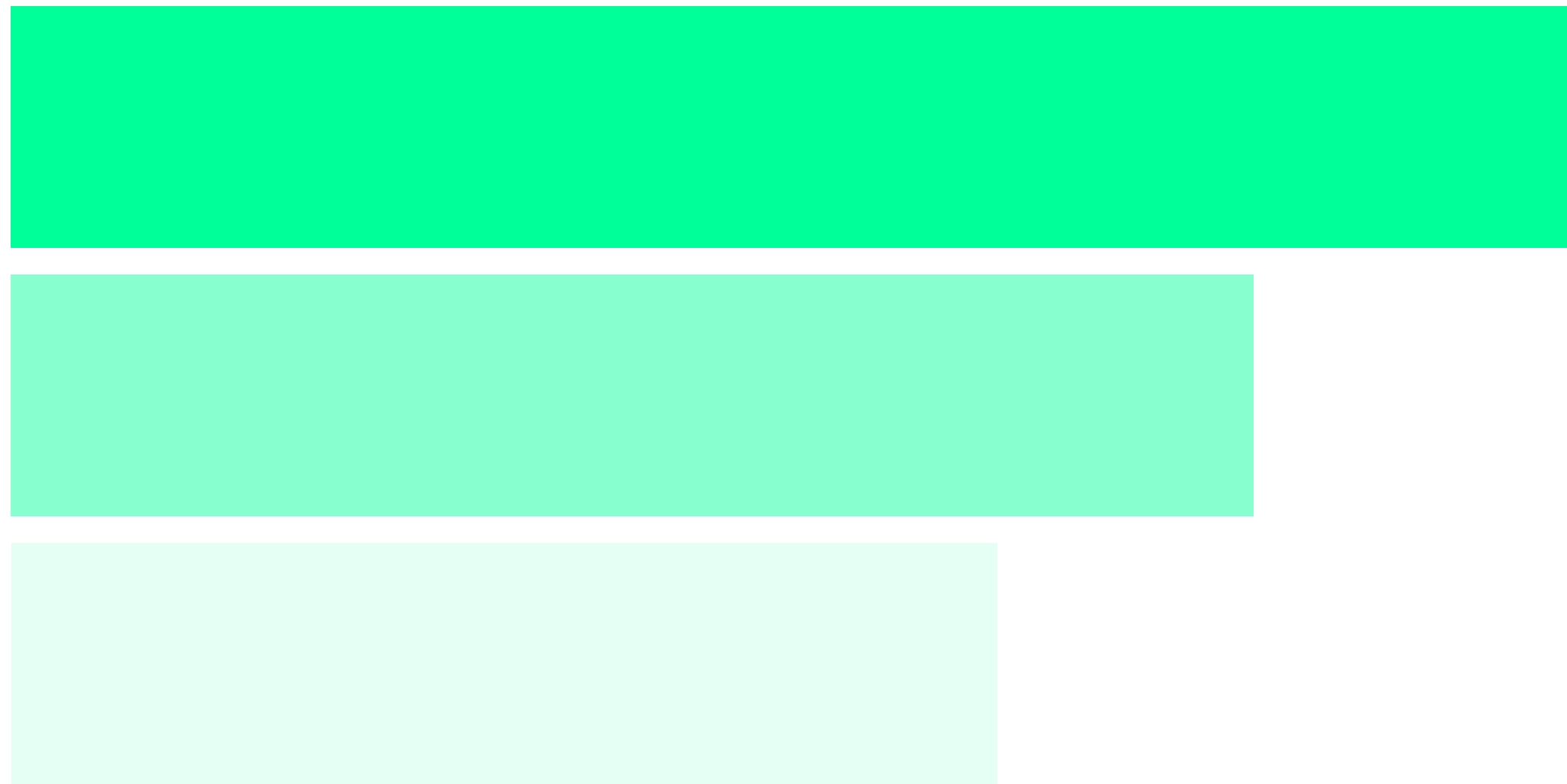
0

2

4

6

log2Enrichment



Re-clustered module 16.10.6 BP enrichment

Term

tricarboxylic acid cycle

alpha-amino acid catabolic process

0

2

4

6

log2Enrichment



Re-clustered module 16.10.6 MF enrichment

Term

catalytic activity, acting on a tRNA

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.10.7 BP enrichment

Term

mitochondrial translation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.10.7 MF enrichment

Term

log2Enrichment



Re-clustered module 16.10.8 BP enrichment

Term

alpha-amino acid catabolic process

translational elongation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.10.8 MF enrichment

Term

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

translation factor activity, RNA binding

0

2

4

6

log2Enrichment



Re-clustered module 16.10.9 BP enrichment

Term

log2Enrichment



Re-clustered module 16.10.9 MF enrichment

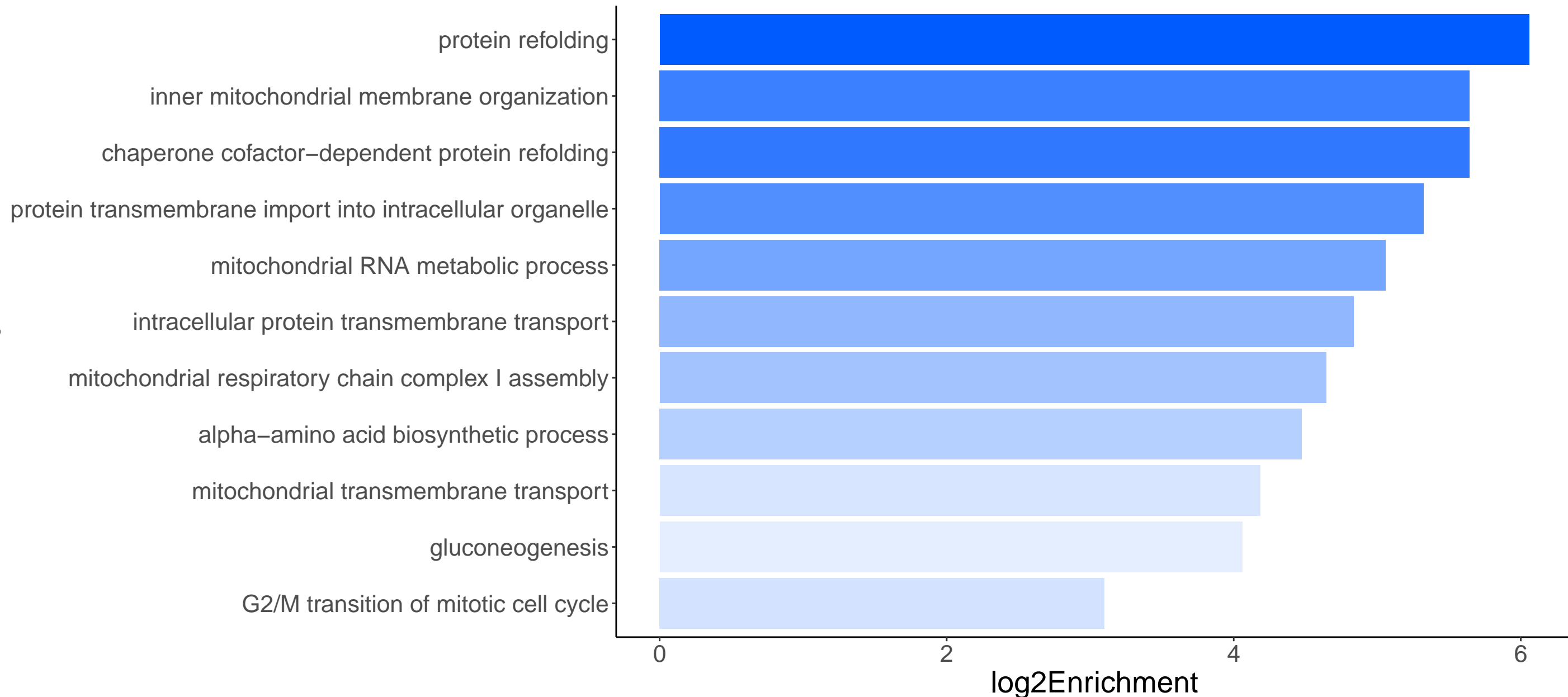
Term

log2Enrichment



Re-clustered module 16.11.1 BP enrichment

Term



Re-clustered module 16.11.1 MF enrichment

Term

misfolded protein binding

protein folding chaperone

chaperone binding

heat shock protein binding

ATPase activity

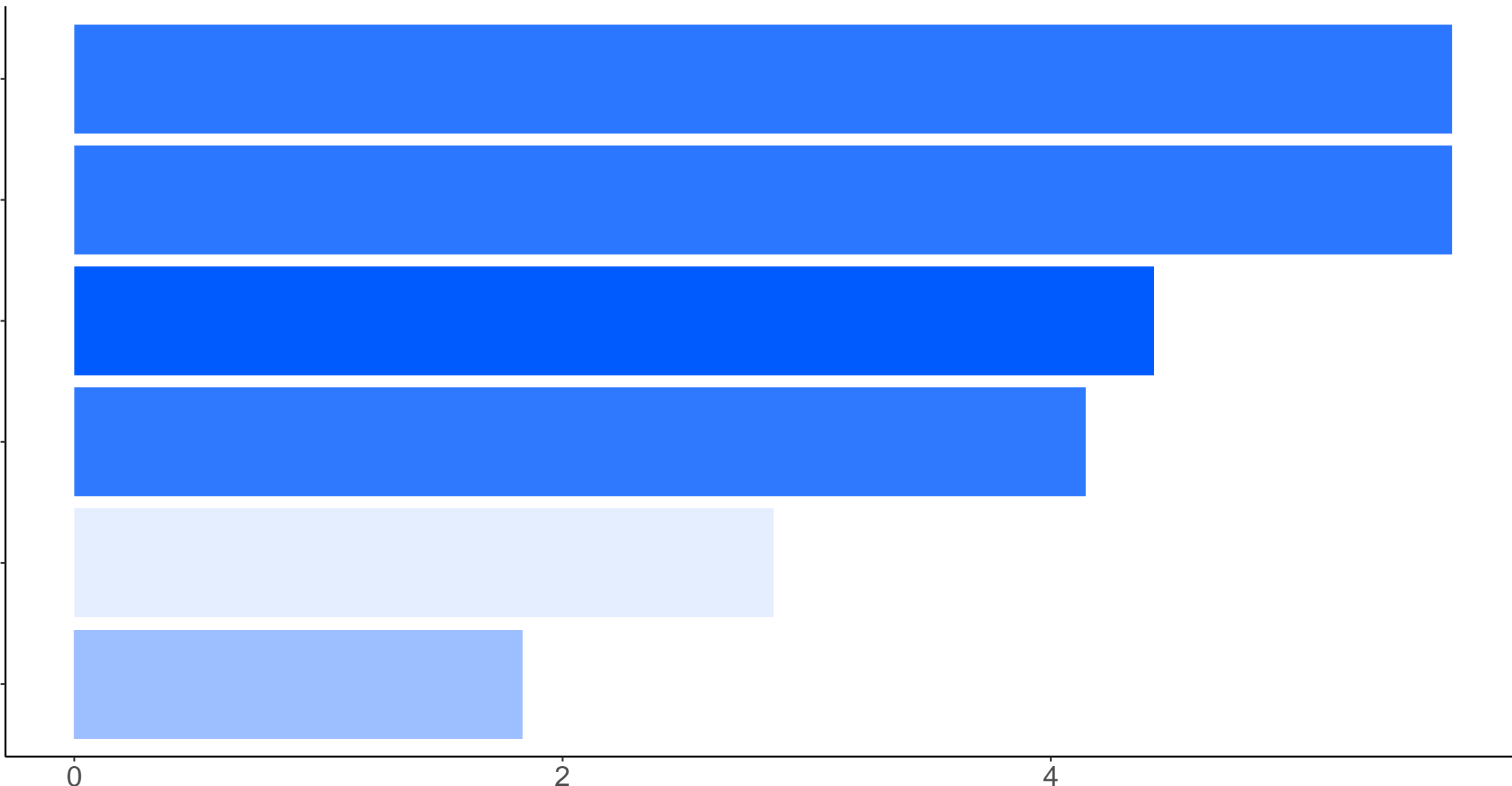
ATP binding

0

2

4

log2Enrichment



Re-clustered module 16.11.11 BP enrichment

Term

natural killer cell mediated cytotoxicity

regulation of mitochondrial membrane potential

glutamine family amino acid metabolic process

dicarboxylic acid metabolic process

liver development

0

2

4

log2Enrichment



Re-clustered module 16.11.11 MF enrichment

Term

oxidoreductase activity, acting on the CH-NH group of donors

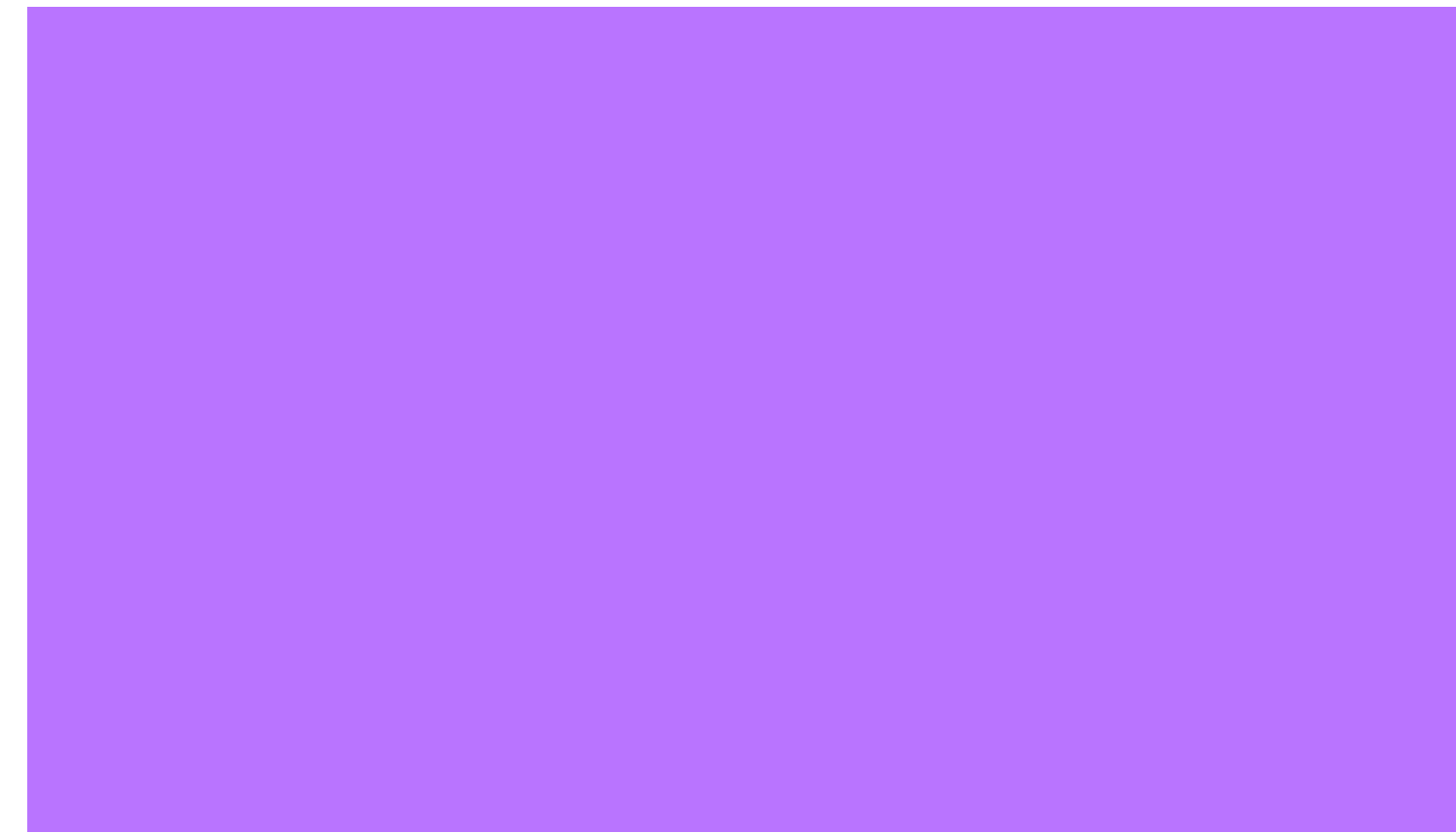
0

2

4

6

log2Enrichment



Re-clustered module 16.11.2 BP enrichment

Term

positive regulation of proteasomal ubiquitin-dependent protein catabolic process

protein sumoylation

cellular oxidant detoxification

activation of GTPase activity

0

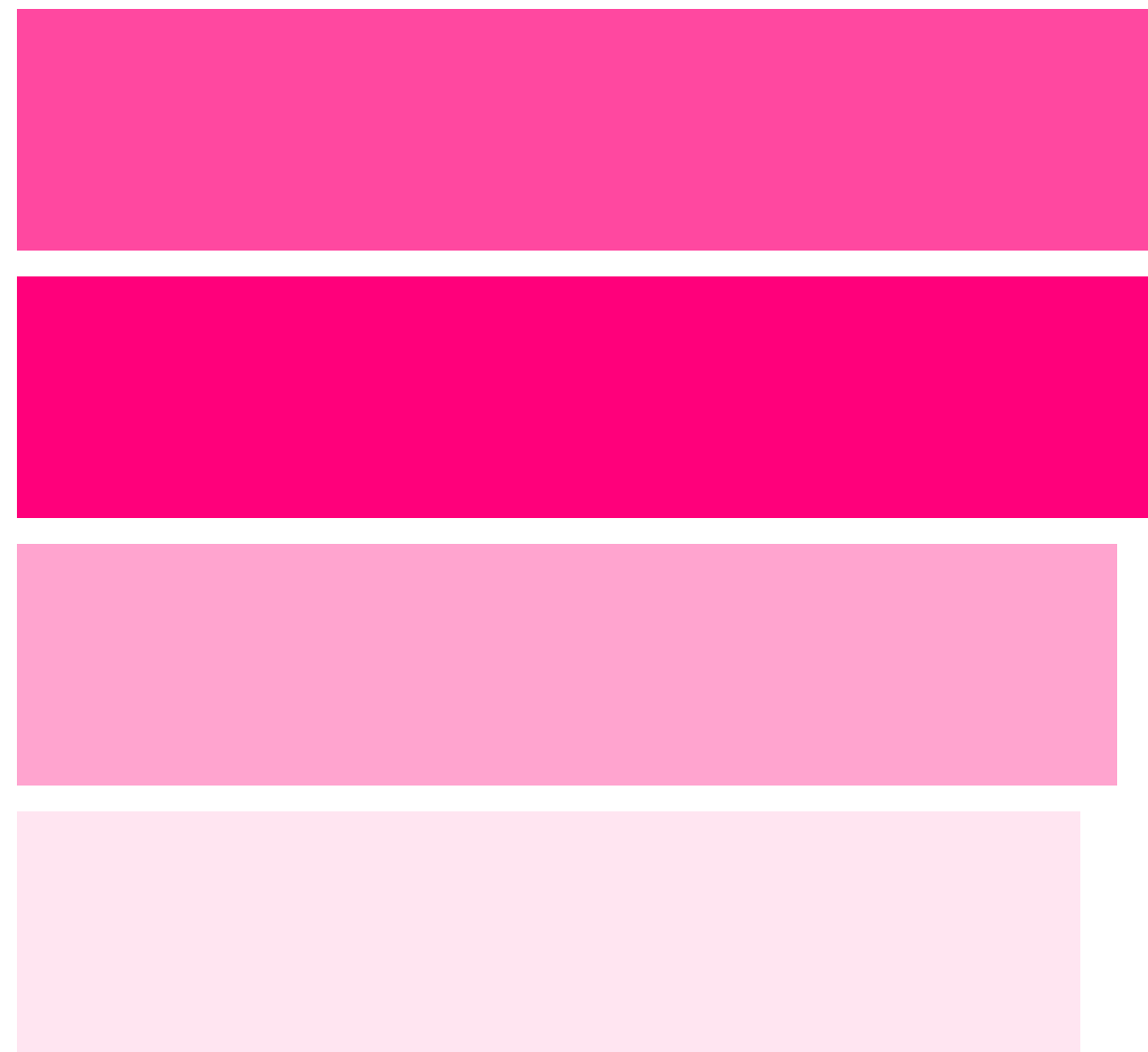
1

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3

4

log2Enrichment



Re-clustered module 16.11.2 MF enrichment

Term

ubiquitin-like protein binding

ubiquitin-like protein transferase activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.11.3 BP enrichment

Term

protein transmembrane import into intracellular organelle

intracellular protein transmembrane transport

protein targeting to mitochondrion

regulation of translational initiation

mitochondrial transmembrane transport

actin cytoskeleton reorganization

positive regulation of hormone secretion

positive regulation of leukocyte differentiation

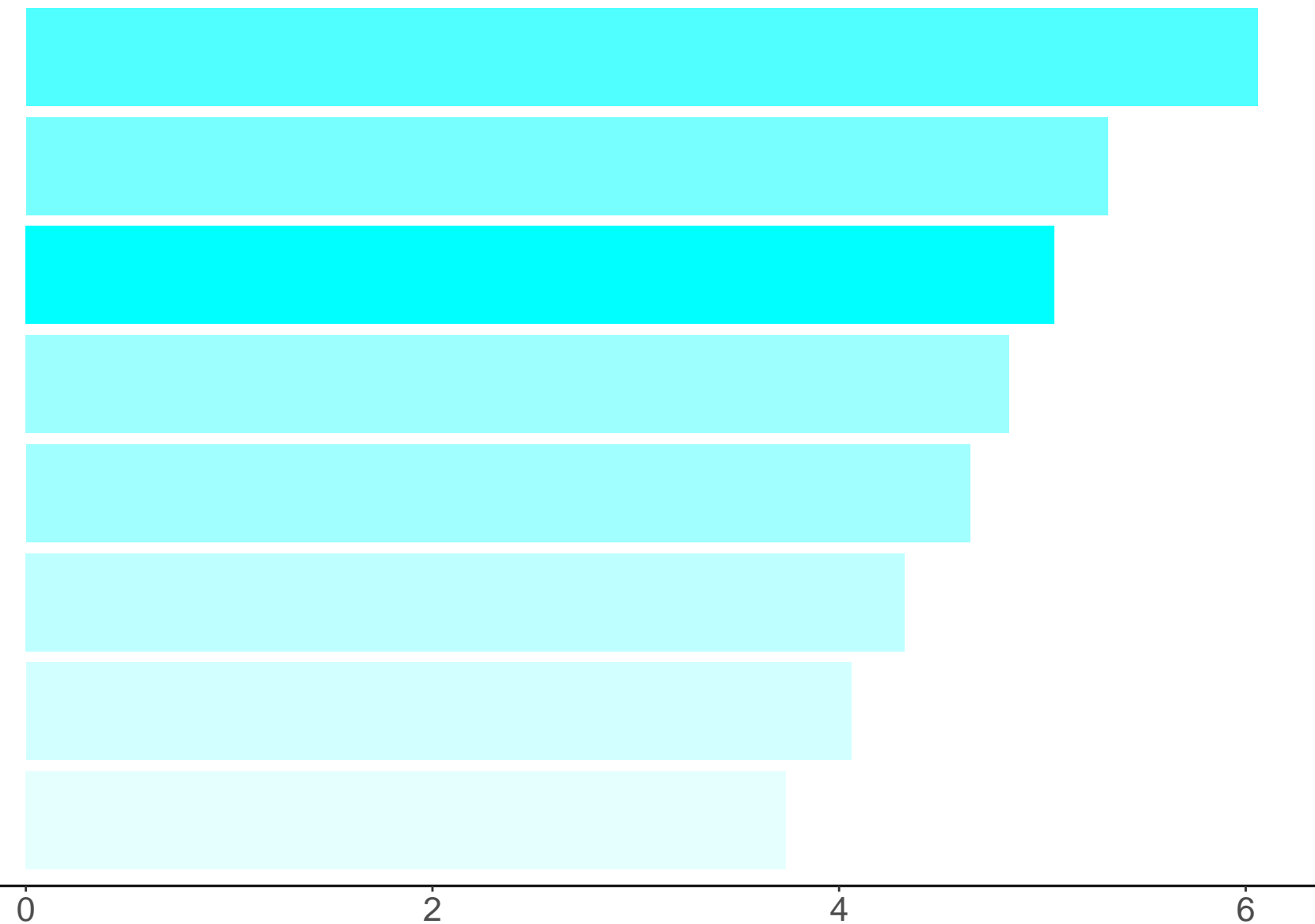
0

2

4

6

log2Enrichment



Re-clustered module 16.11.3 MF enrichment

Term

translation initiation factor activity

ribonucleoprotein complex binding

0

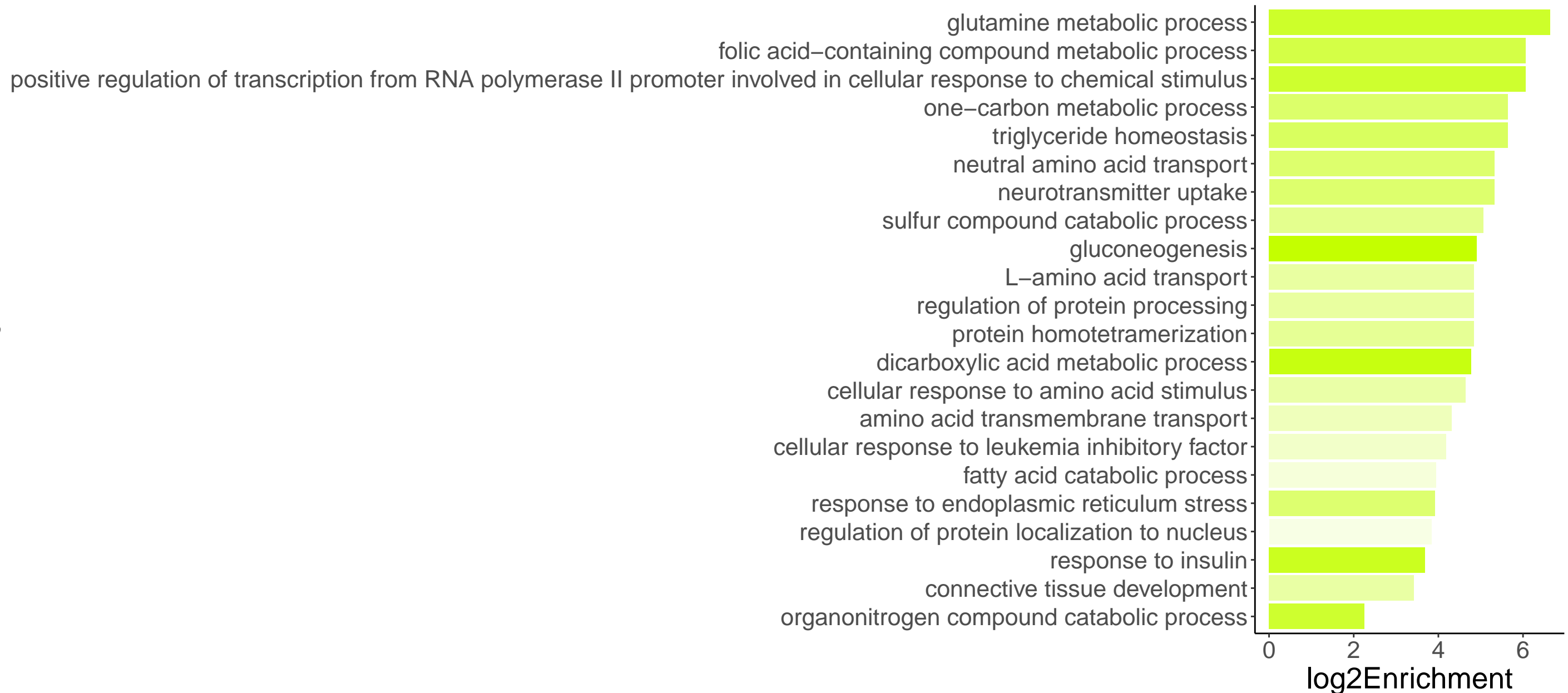
2

4

log2Enrichment



Term



Re-clustered module 16.11.4 MF enrichment

Term

neutral amino acid transmembrane transporter activity

organic acid:sodium symporter activity

L-amino acid transmembrane transporter activity

manganese ion binding

histone deacetylase binding

0

2

4

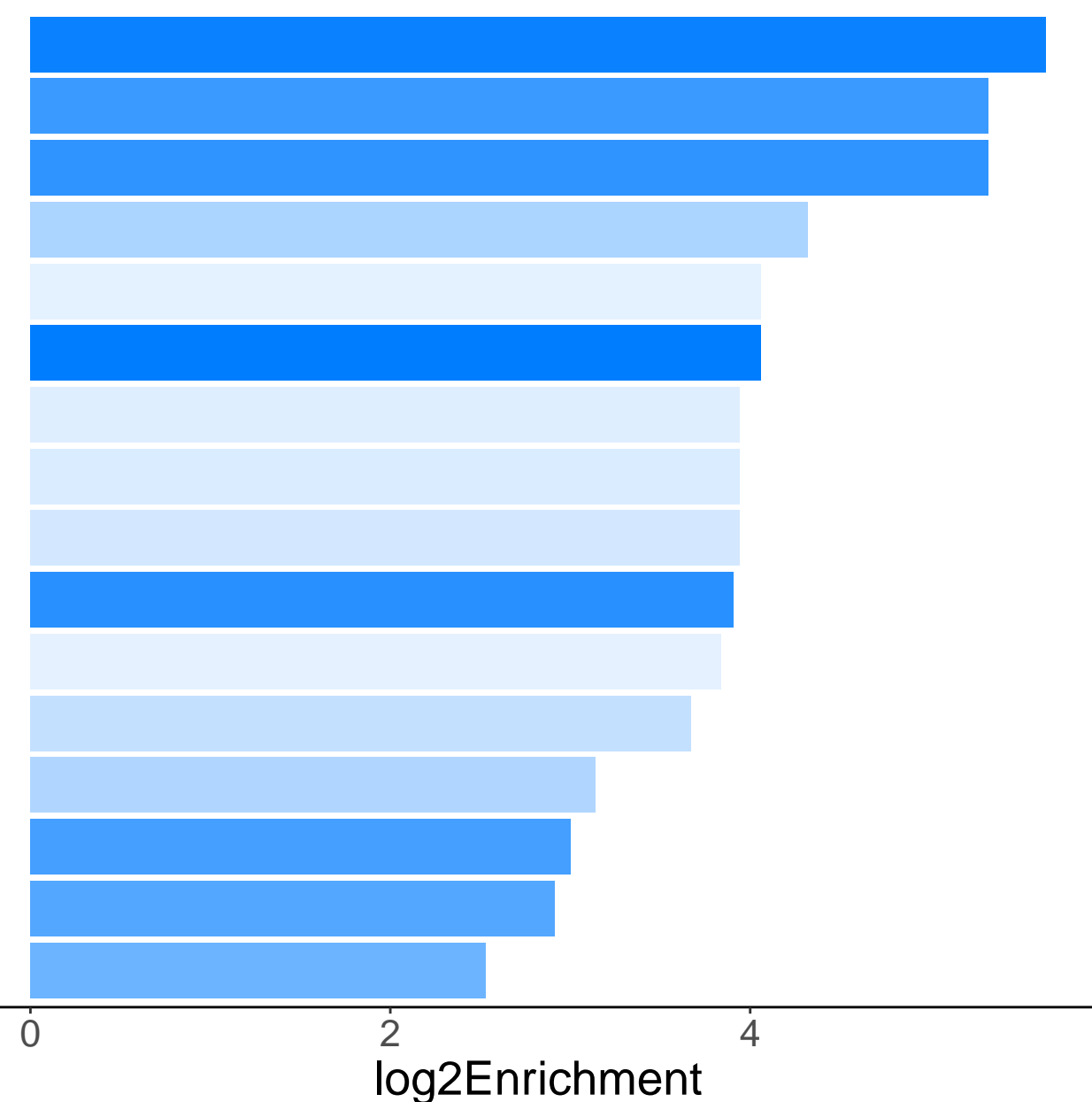
log2Enrichment



Re-clustered module 16.11.5 BP enrichment

Term

protein localization to Golgi apparatus
regulation of protein targeting to membrane
protein localization to microtubule organizing center
regulation of viral transcription
positive regulation of mitochondrion organization
phosphatidylinositol biosynthetic process
protein lipidation
positive regulation of proteasomal ubiquitin-dependent protein catabolic process
transcription elongation from RNA polymerase II promoter
Golgi organization
autophagosome assembly
Golgi vesicle transport
endosomal transport
positive regulation of cellular protein localization
positive regulation of protein transport
intracellular protein transport



Re-clustered module 16.11.5 MF enrichment

Term

protein N-terminus binding

0

1

2

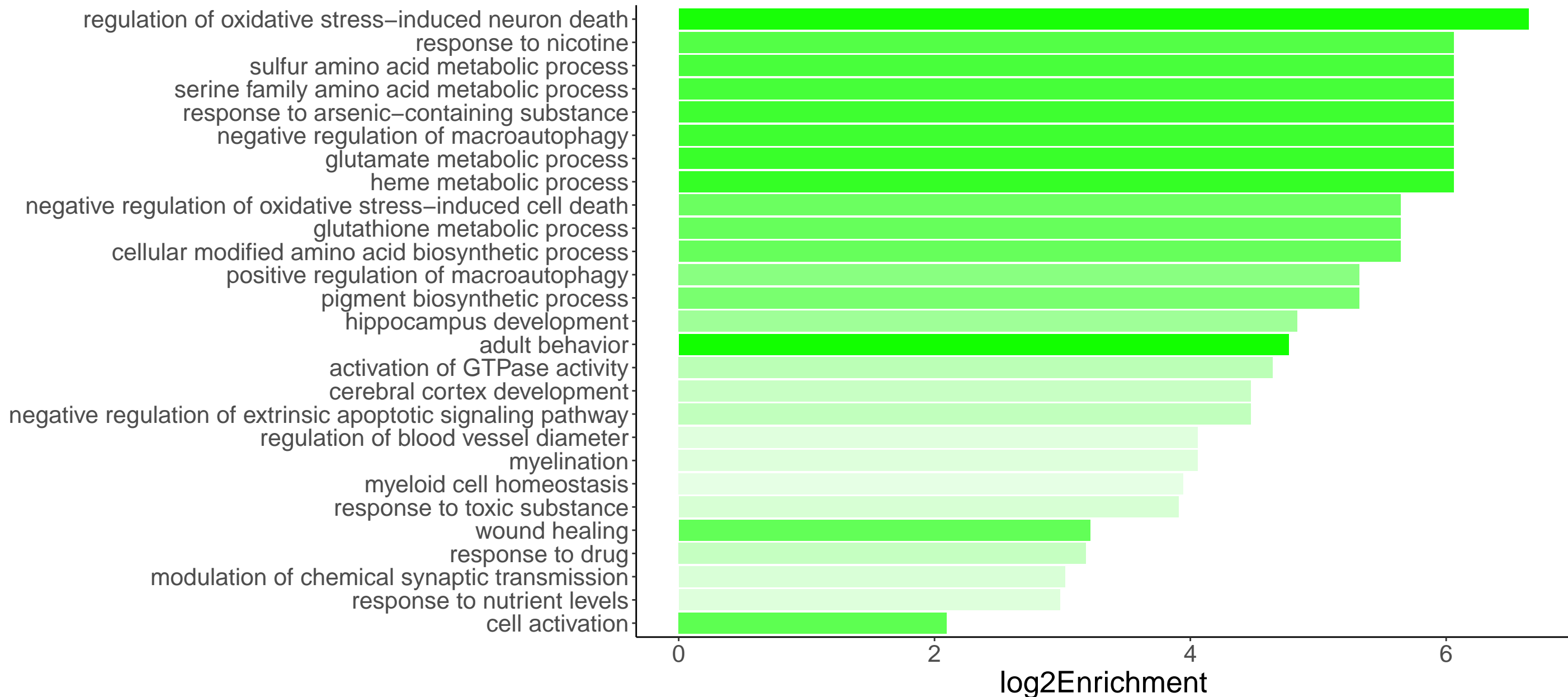
3

log2Enrichment



Re-clustered module 16.11.9 BP enrichment

Term



Re-clustered module 16.11.9 MF enrichment

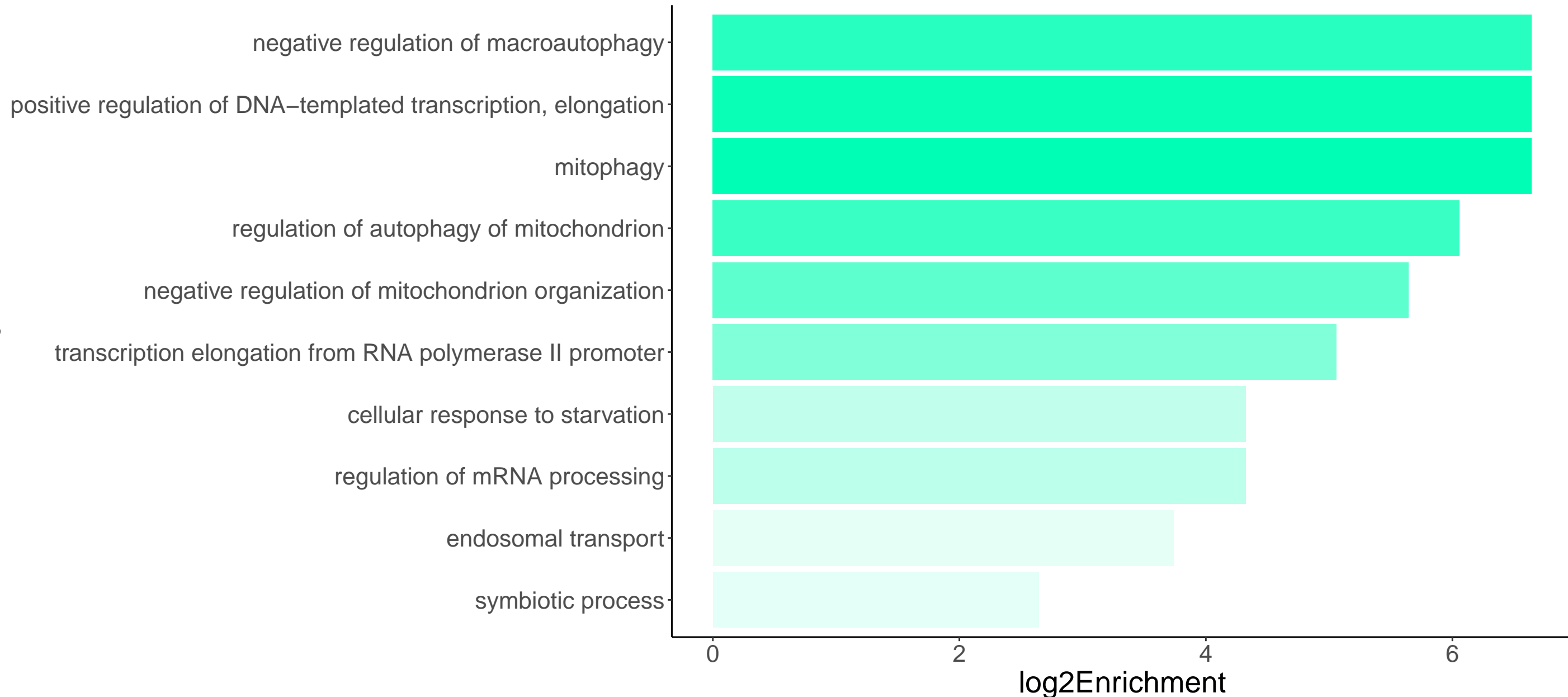
Term

log2Enrichment



Re-clustered module 16.12.1 BP enrichment

Term



Re-clustered module 16.12.1 MF enrichment

Term

Rab GTPase binding

enzyme activator activity

0

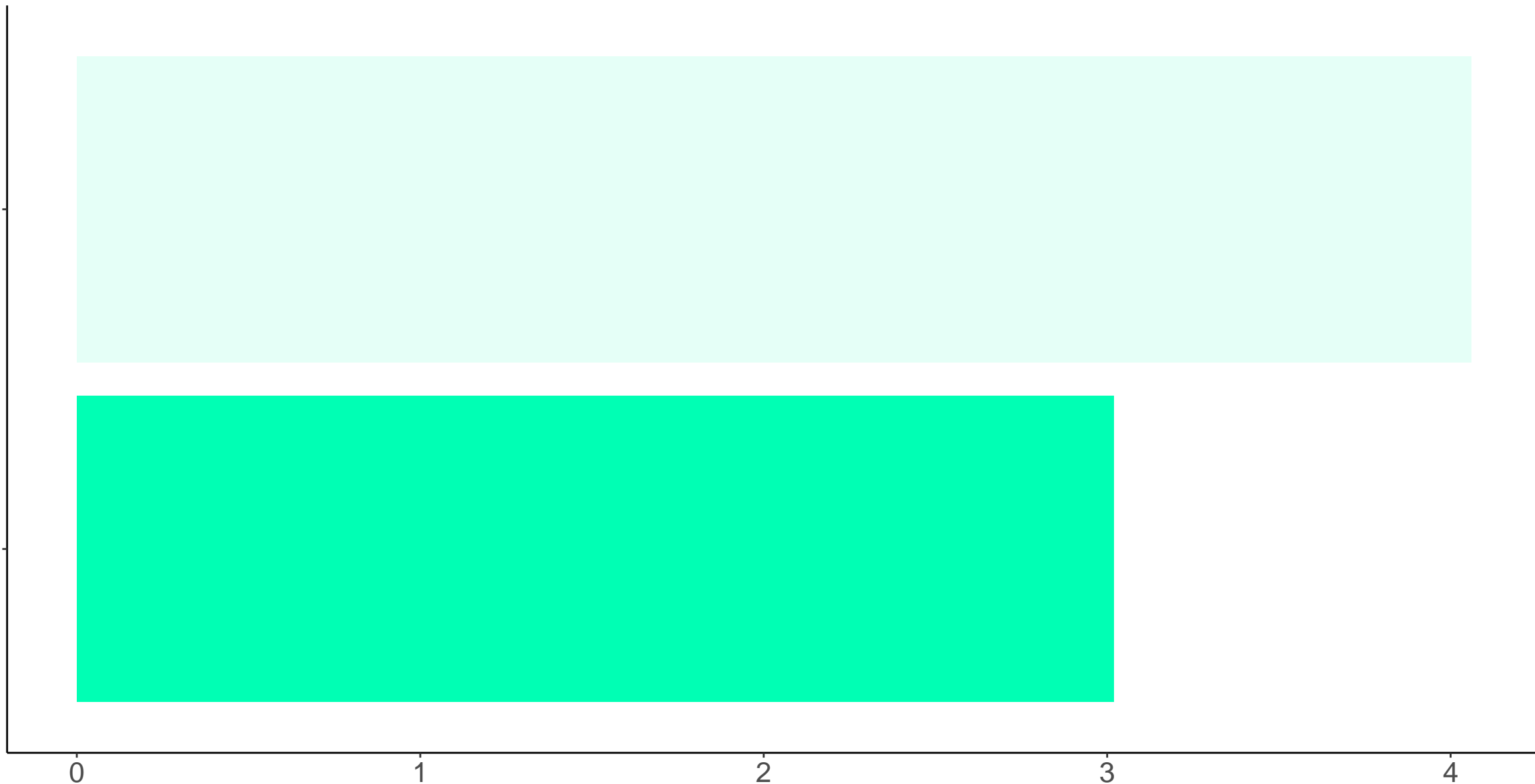
1

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3

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log2Enrichment



Re-clustered module 16.12.10 BP enrichment

Term

negative regulation of blood pressure

organelle localization by membrane tethering

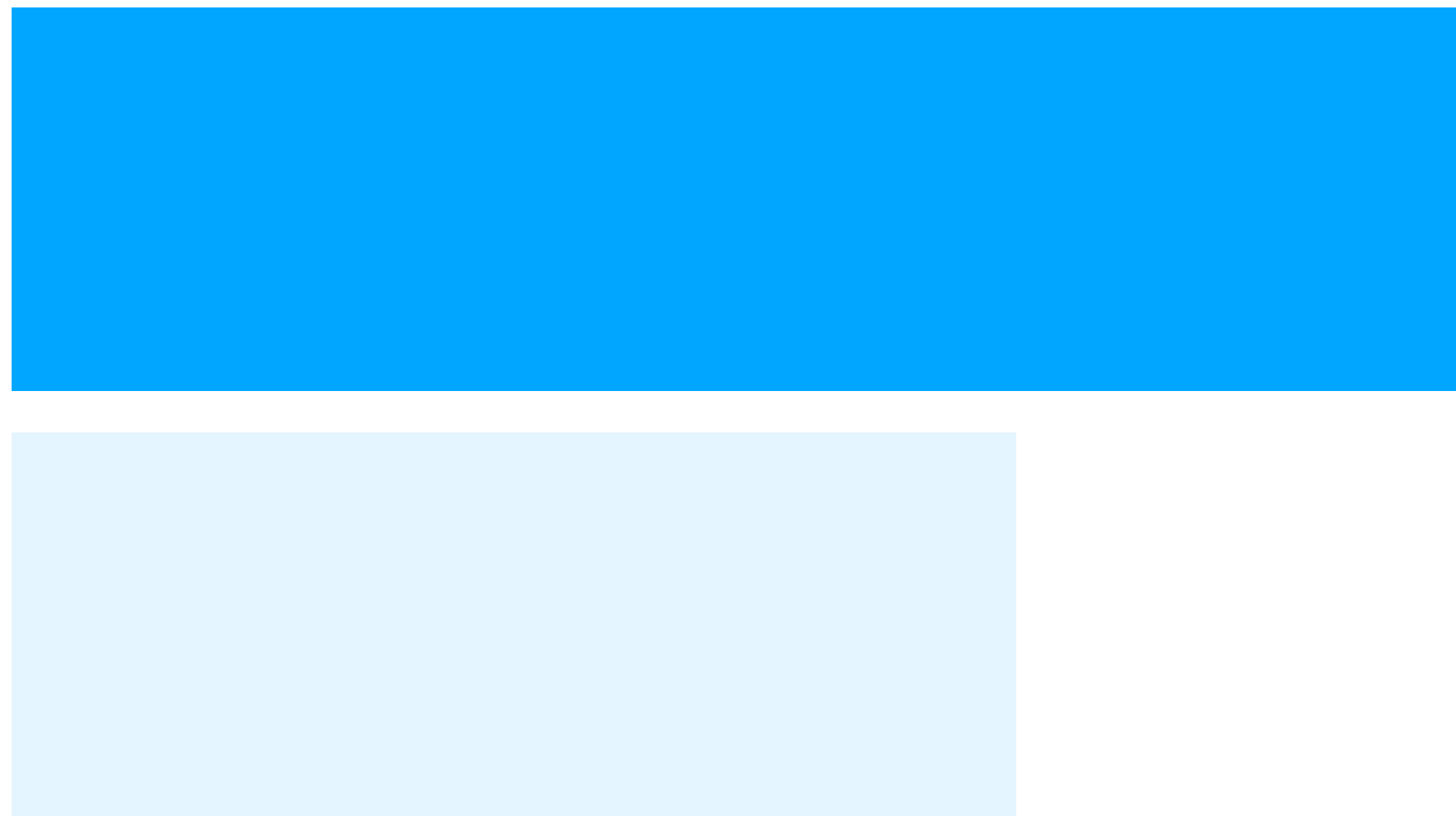
0

2

4

6

log2Enrichment



Re-clustered module 16.12.10 MF enrichment

Term

carboxypeptidase activity

serine-type peptidase activity

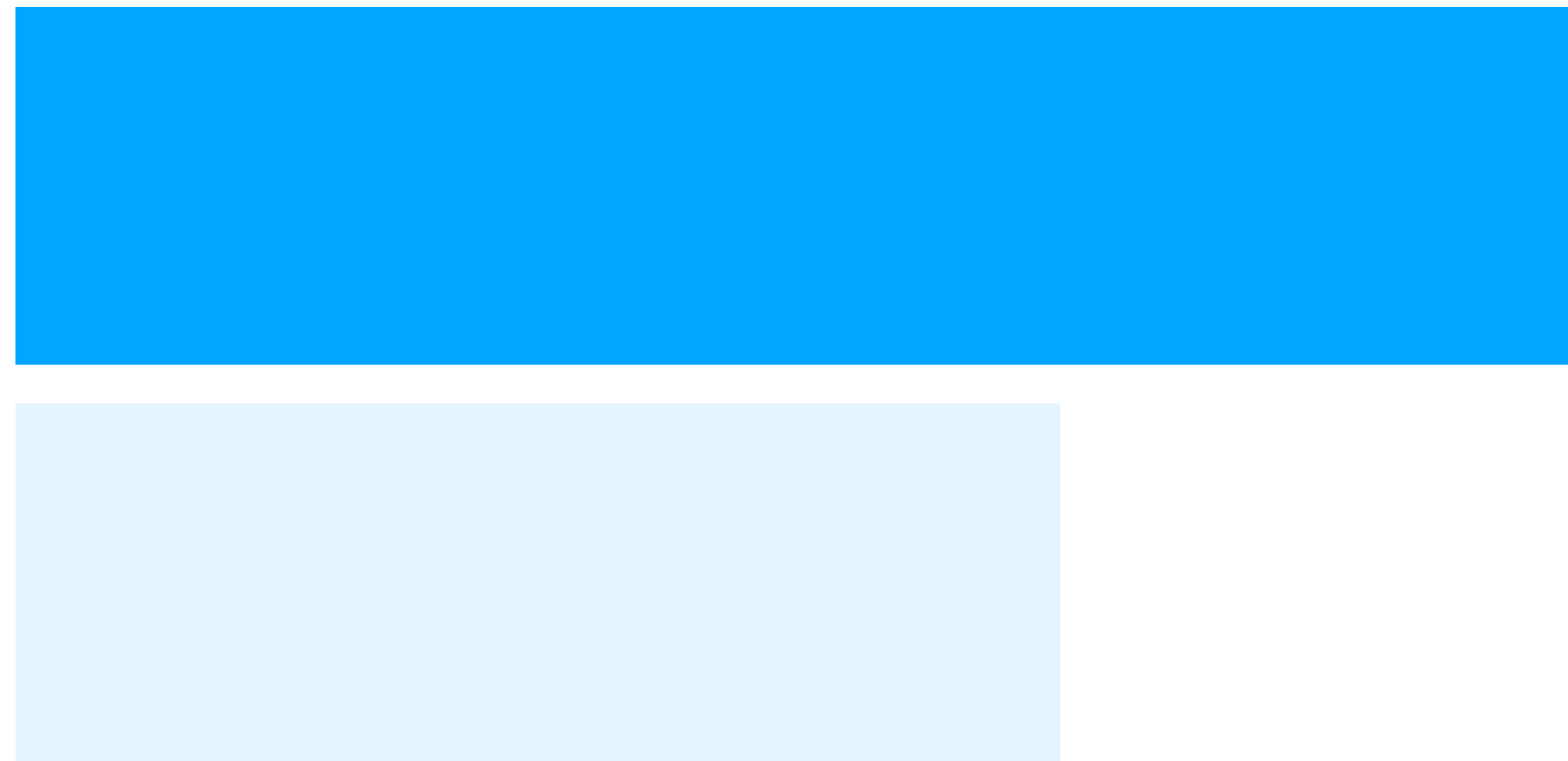
0

2

4

6

log2Enrichment



Re-clustered module 16.12.12 BP enrichment

Term

protein folding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.12.12 MF enrichment

Term

log2Enrichment



Re-clustered module 16.12.13 BP enrichment

Term

tRNA aminoacylation
sulfur compound transport
lysosome organization
sterol homeostasis
lysosomal transport

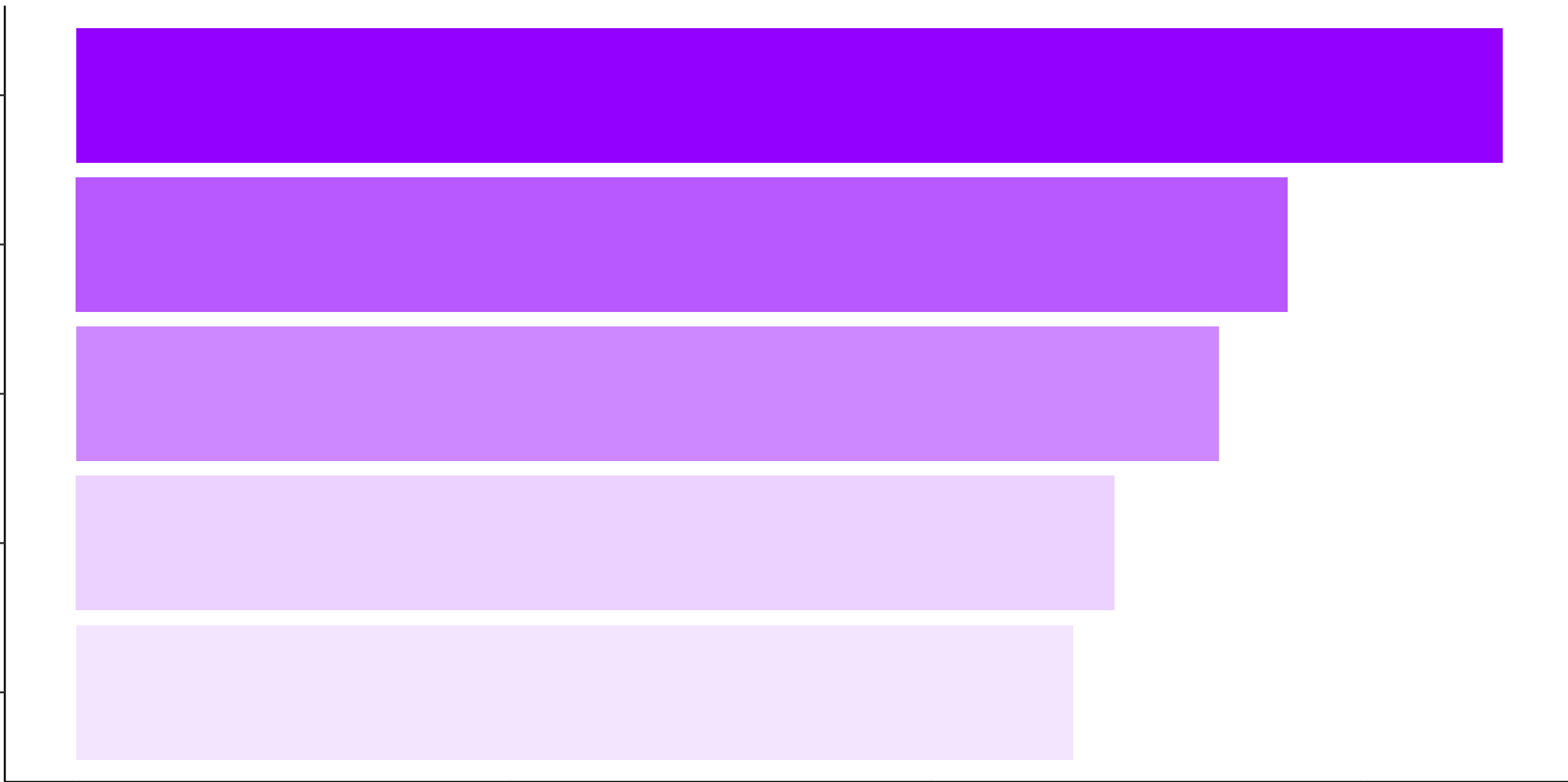
0

2

4

6

log2Enrichment



Re-clustered module 16.12.13 MF enrichment

Term

sulfur compound transmembrane transporter activity

amide transmembrane transporter activity

catalytic activity, acting on a tRNA

transmembrane transporter activity

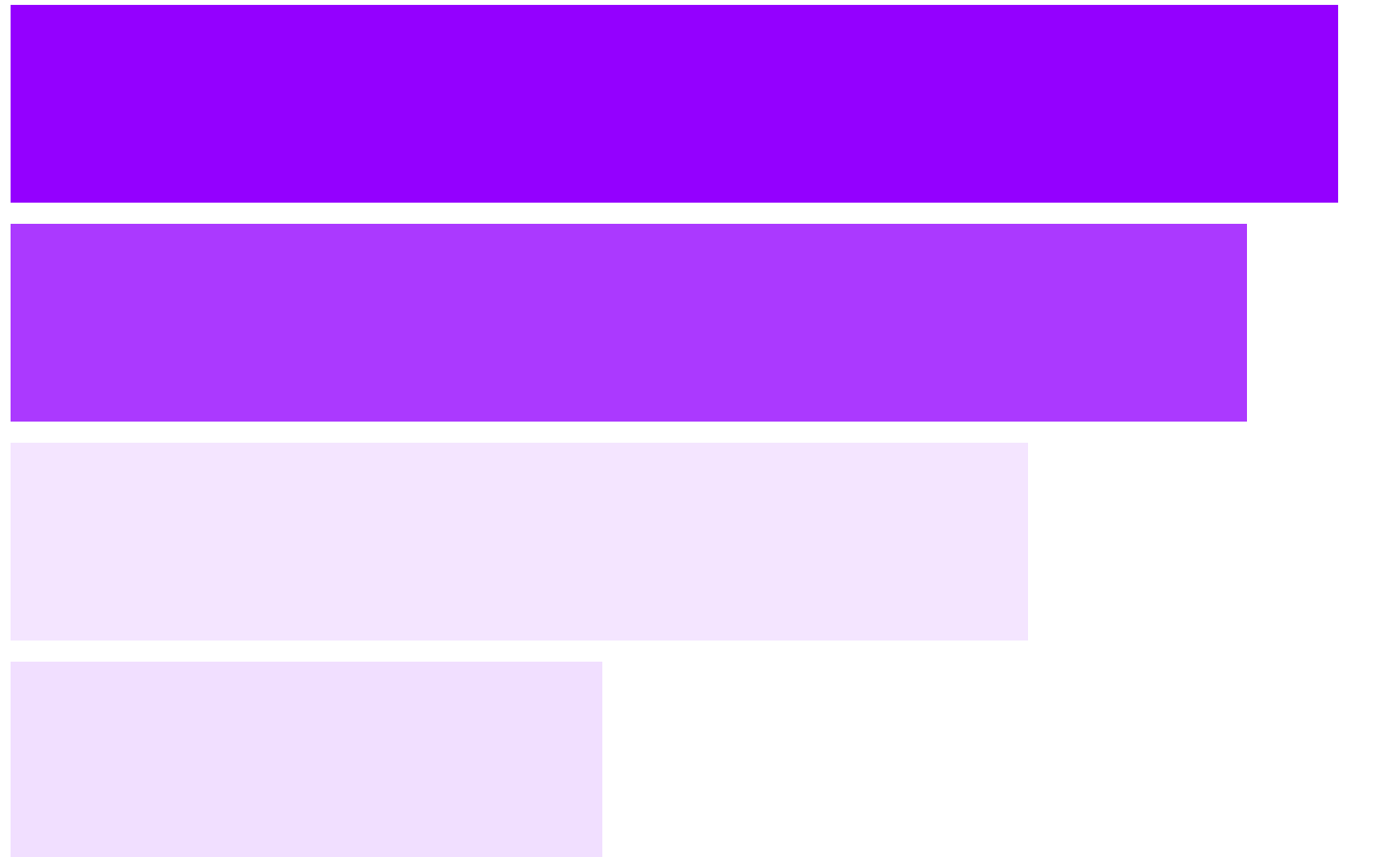
0

2

4

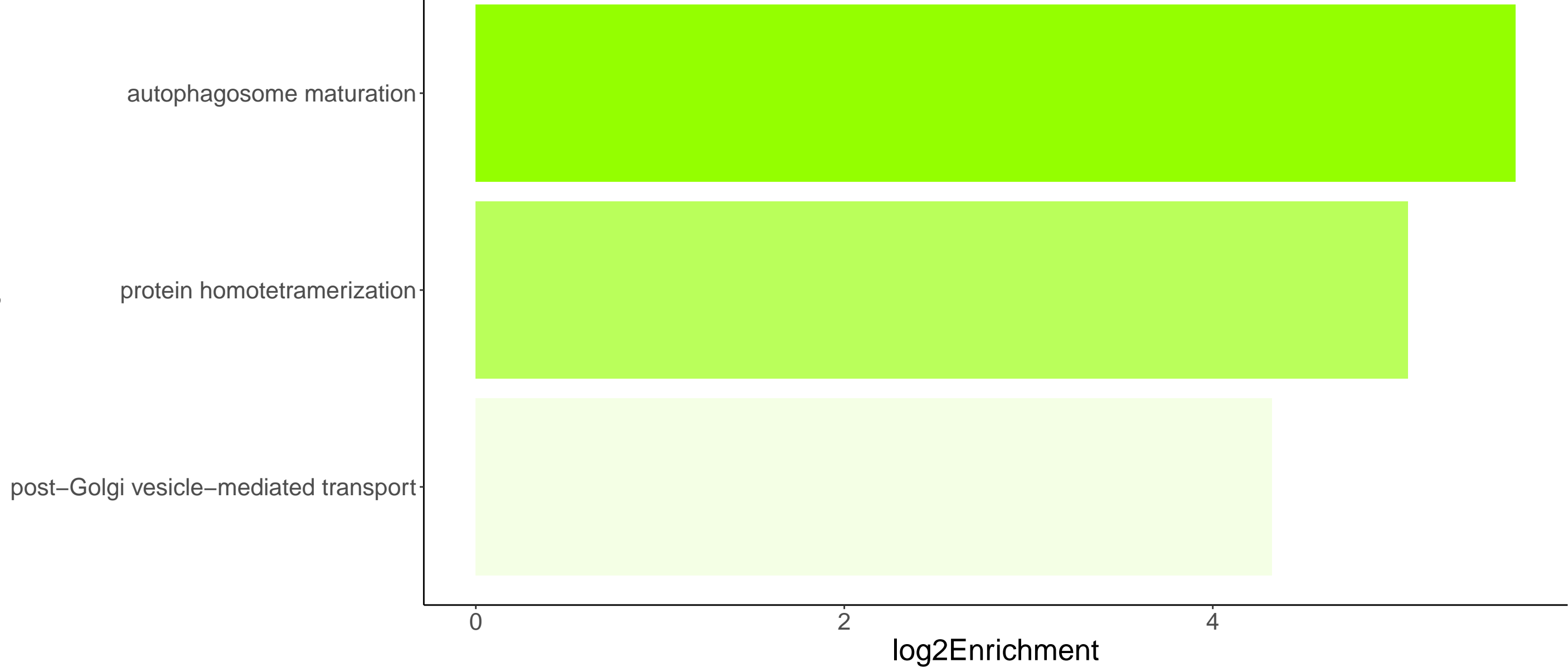
6

log2Enrichment



Re-clustered module 16.12.2 BP enrichment

Term



Re-clustered module 16.12.2 MF enrichment

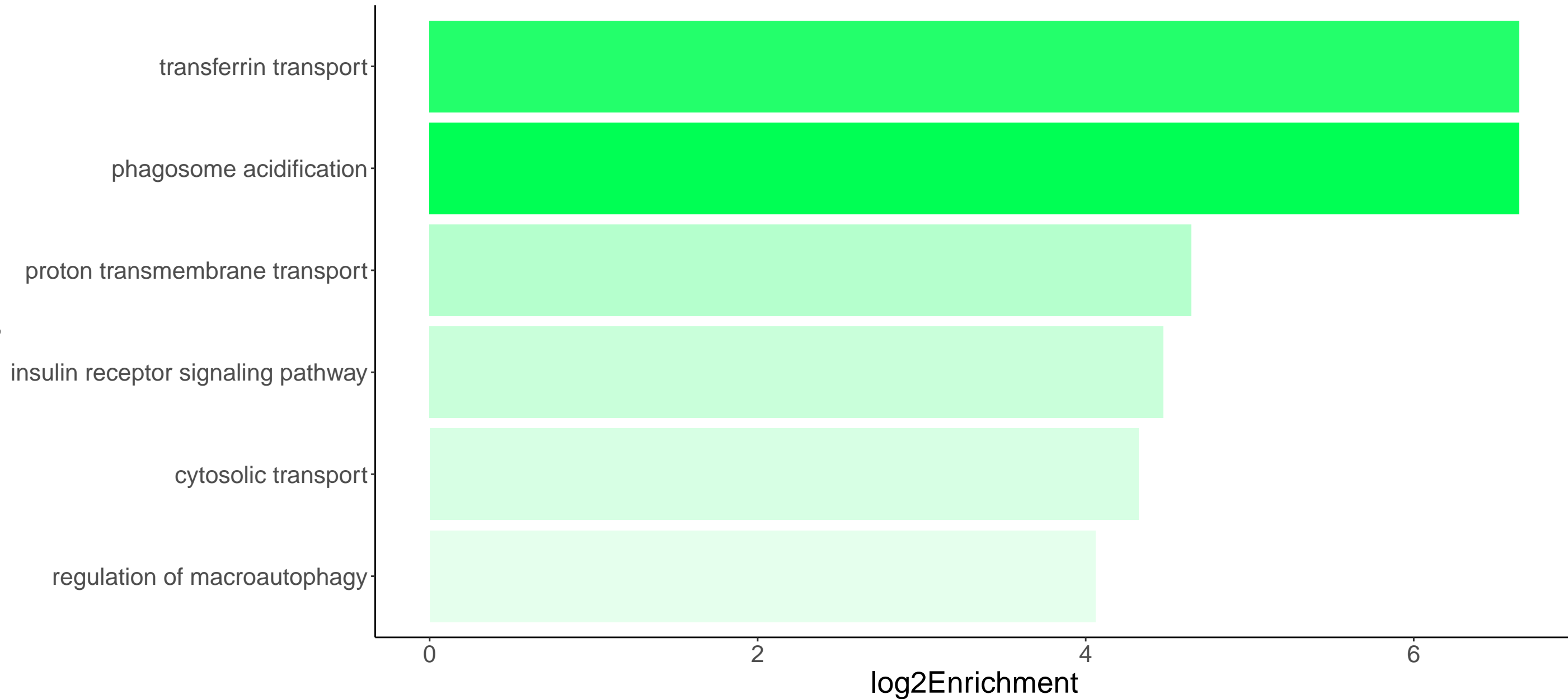
Term

log2Enrichment



Re-clustered module 16.12.3 BP enrichment

Term



Re-clustered module 16.12.3 MF enrichment

Term

ion transmembrane transporter activity, phosphorylative mechanism

pyrophosphate hydrolysis-driven proton transmembrane transporter activity

ATPase-coupled cation transmembrane transporter activity

pyrophosphatase activity

0

2

4

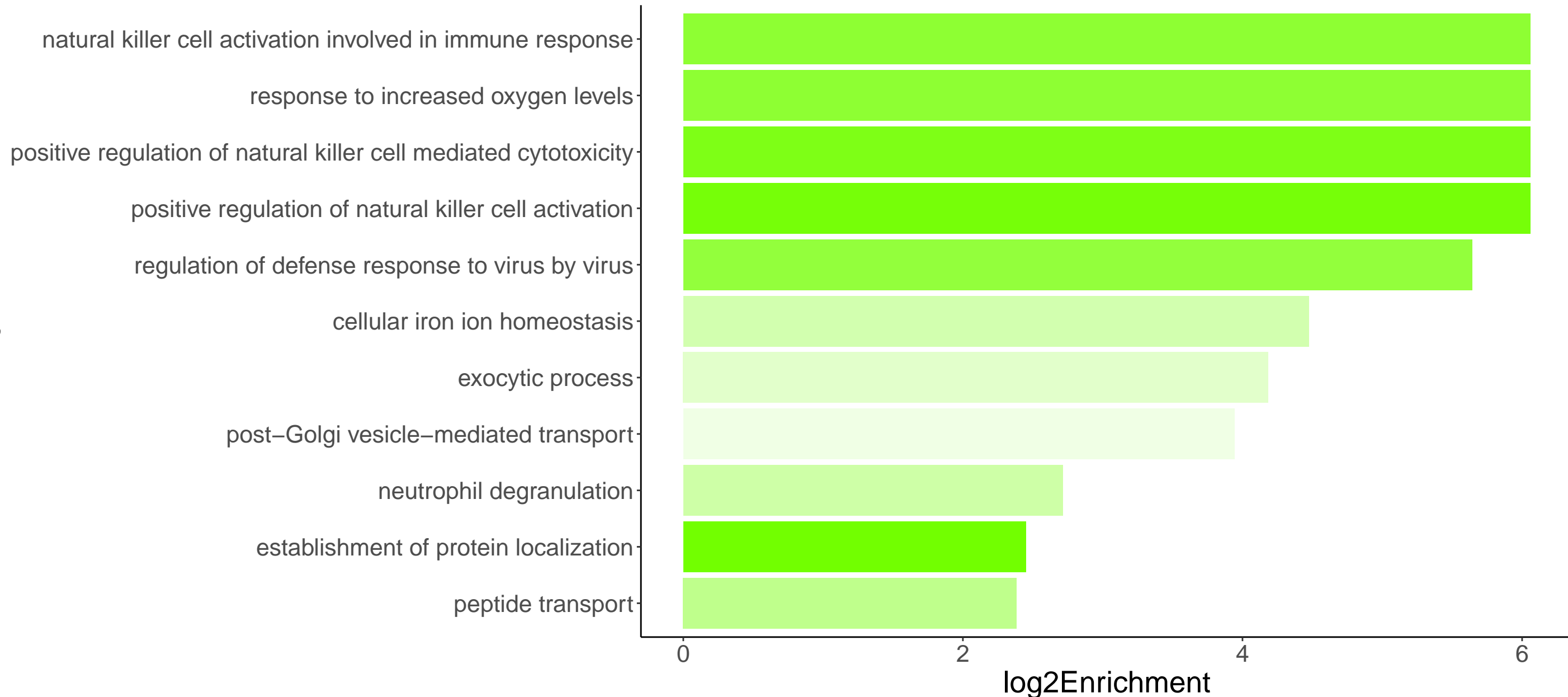
6

log2Enrichment



Re-clustered module 16.12.5 BP enrichment

Term



Re-clustered module 16.12.5 MF enrichment

Term

ion transmembrane transporter activity, phosphorylative mechanism

GDP binding

ATPase binding

chaperone binding

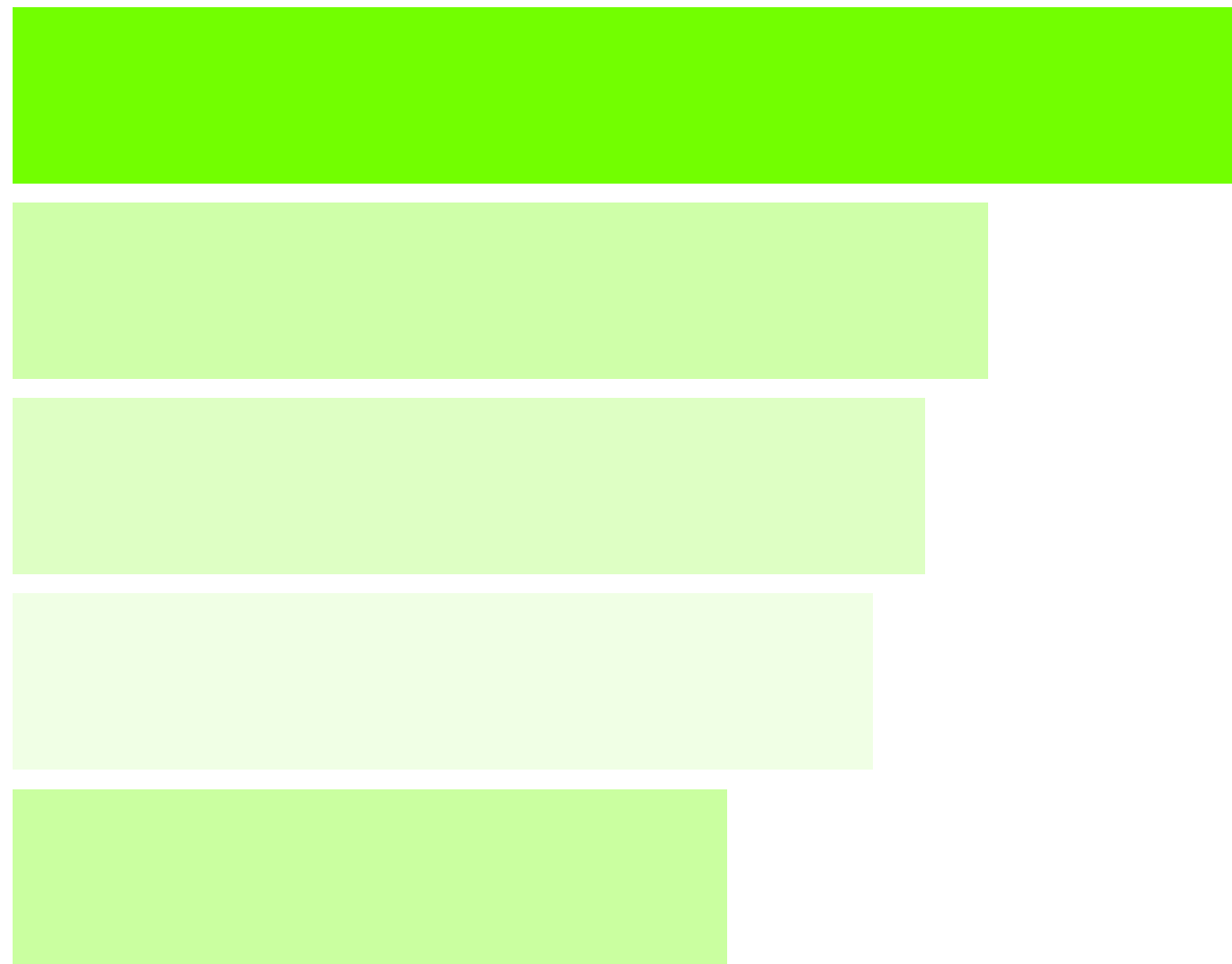
protein-macromolecule adaptor activity

0

2

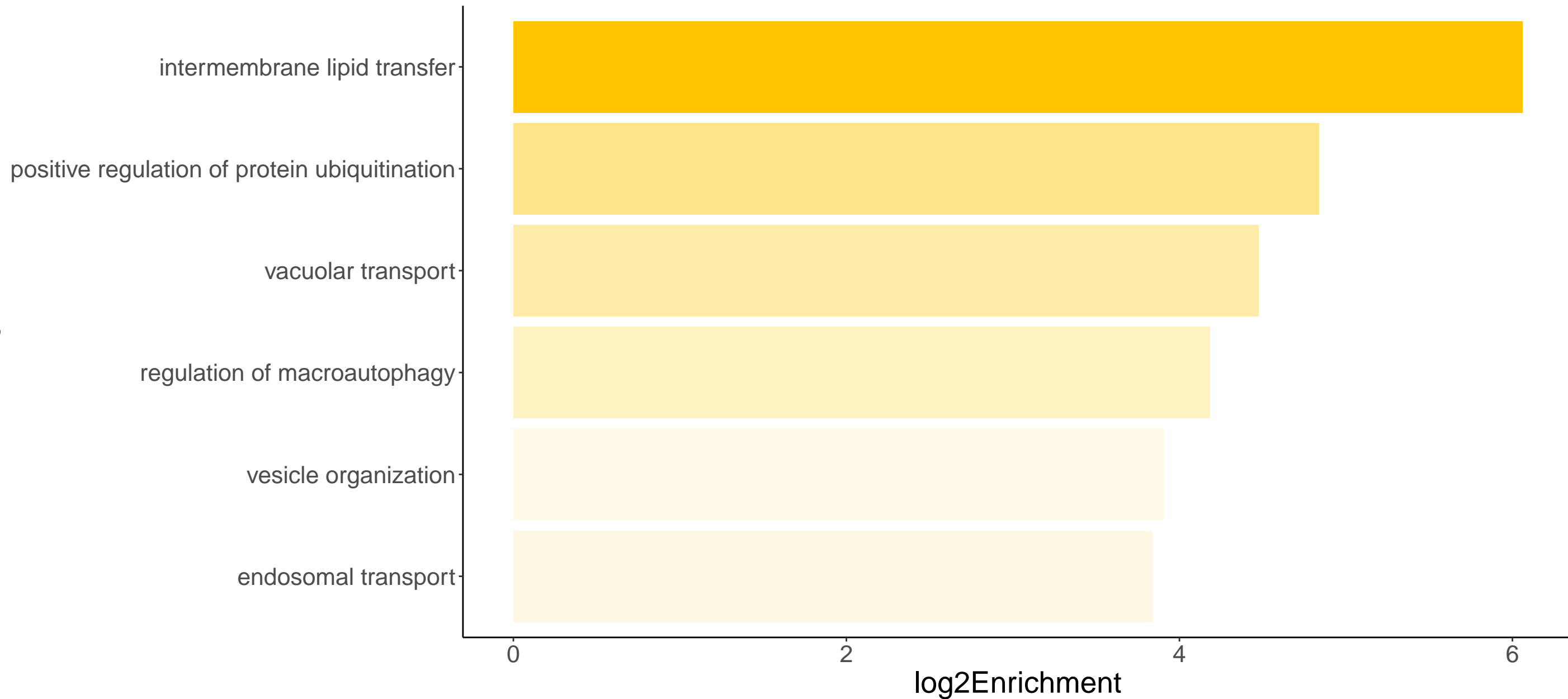
4

log2Enrichment



Re-clustered module 16.12.7 BP enrichment

Term



Re-clustered module 16.12.7 MF enrichment

Term

molecular adaptor activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.12.8 BP enrichment

Term

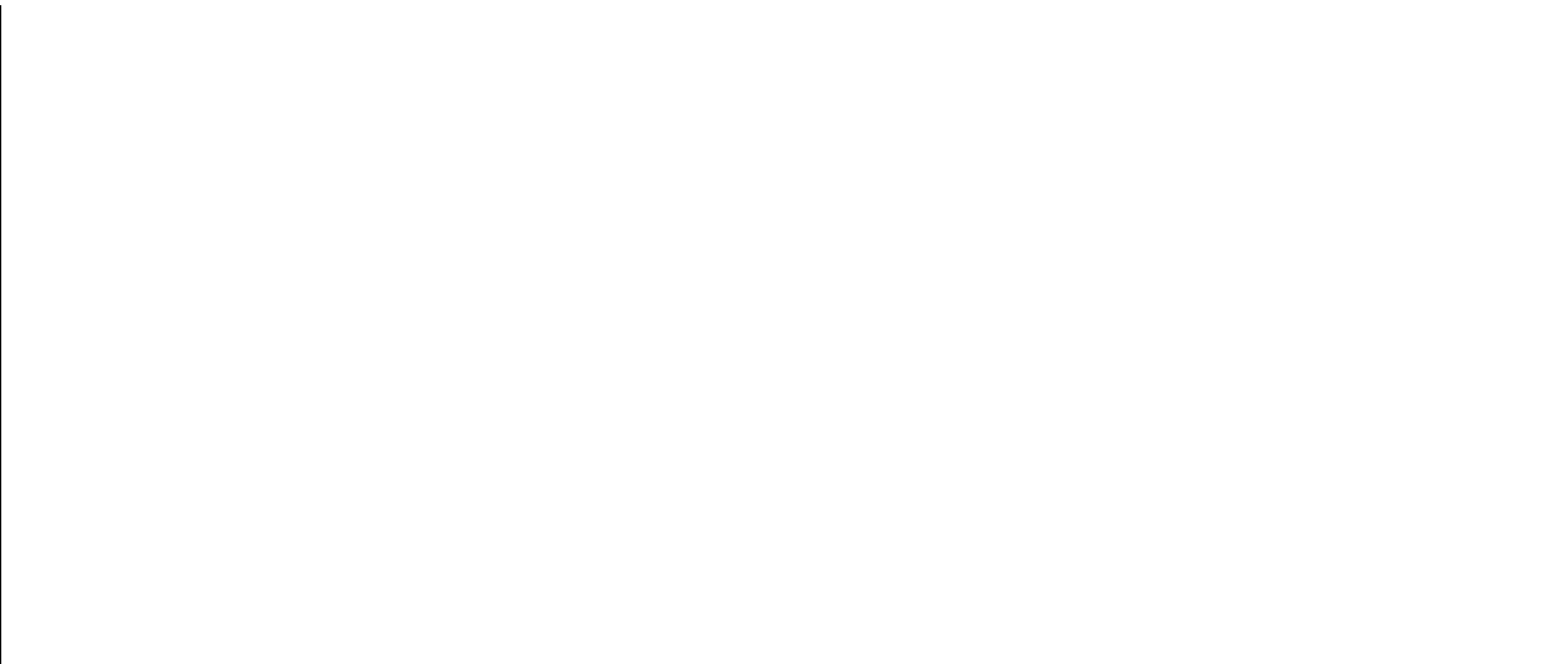
log2Enrichment



Re-clustered module 16.12.8 MF enrichment

Term

log2Enrichment



Re-clustered module 16.12.9 BP enrichment

Term

protein folding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.12.9 MF enrichment

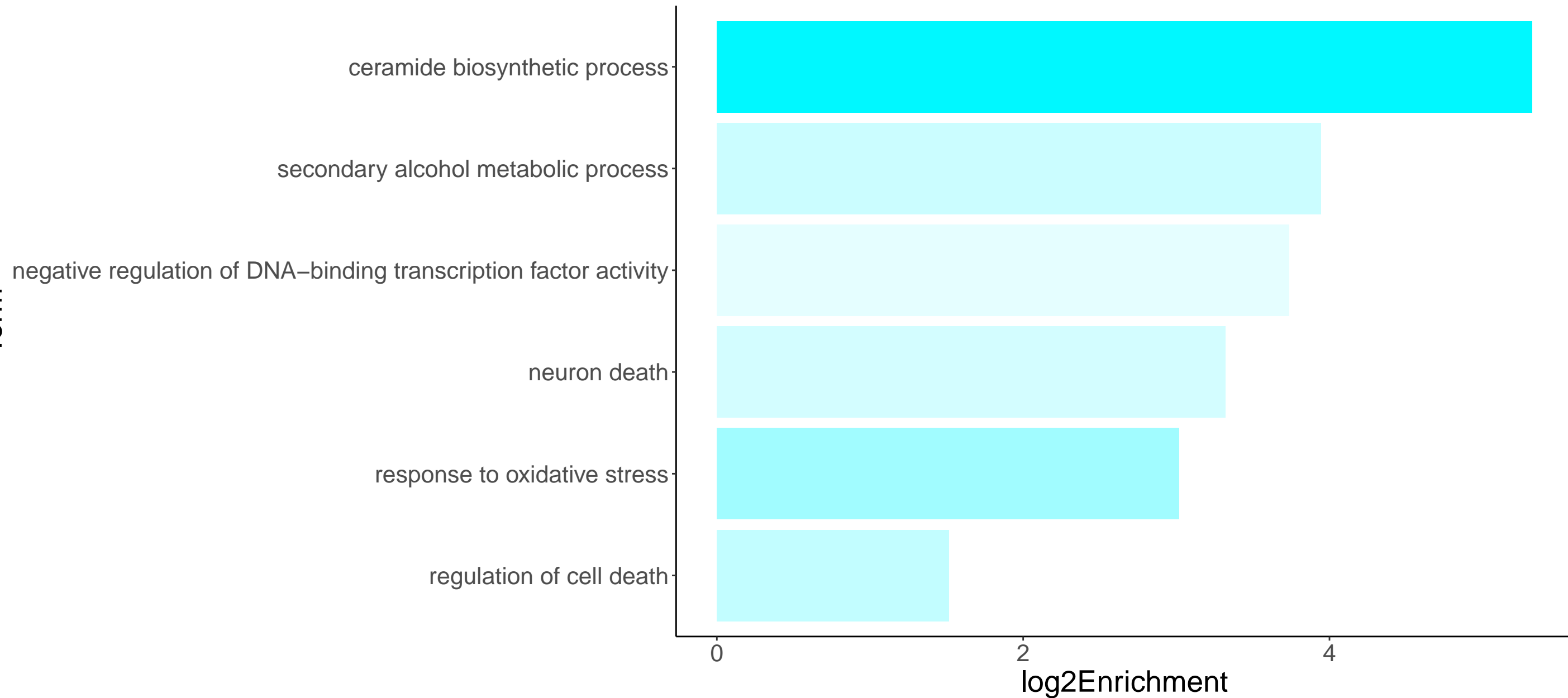
Term

log2Enrichment



Re-clustered module 16.13.1 BP enrichment

Term



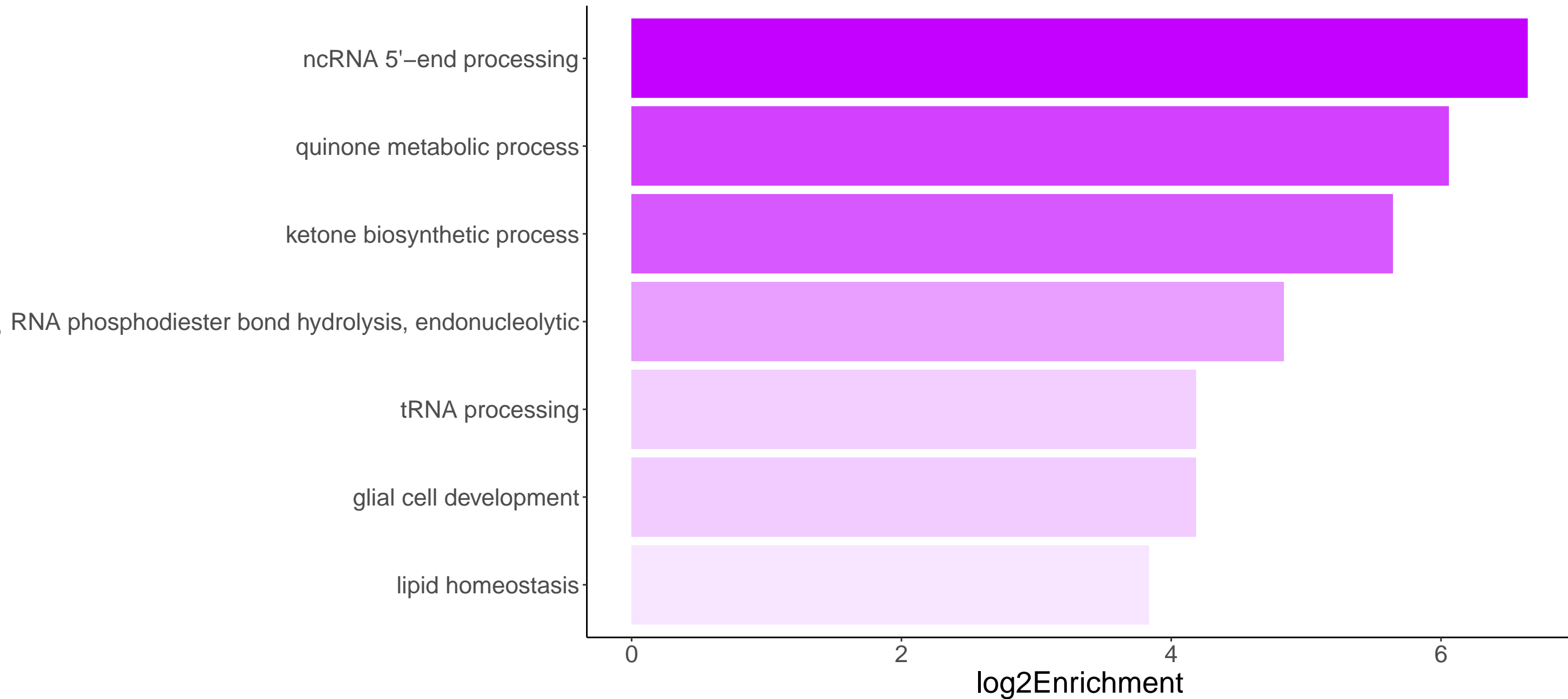
Re-clustered module 16.13.1 MF enrichment

Term



Re-clustered module 16.13.2 BP enrichment

Term



Re-clustered module 16.13.2 MF enrichment

Term

endoribonuclease activity, producing 5'-phosphomonoesters

catalytic activity, acting on a tRNA

motor activity

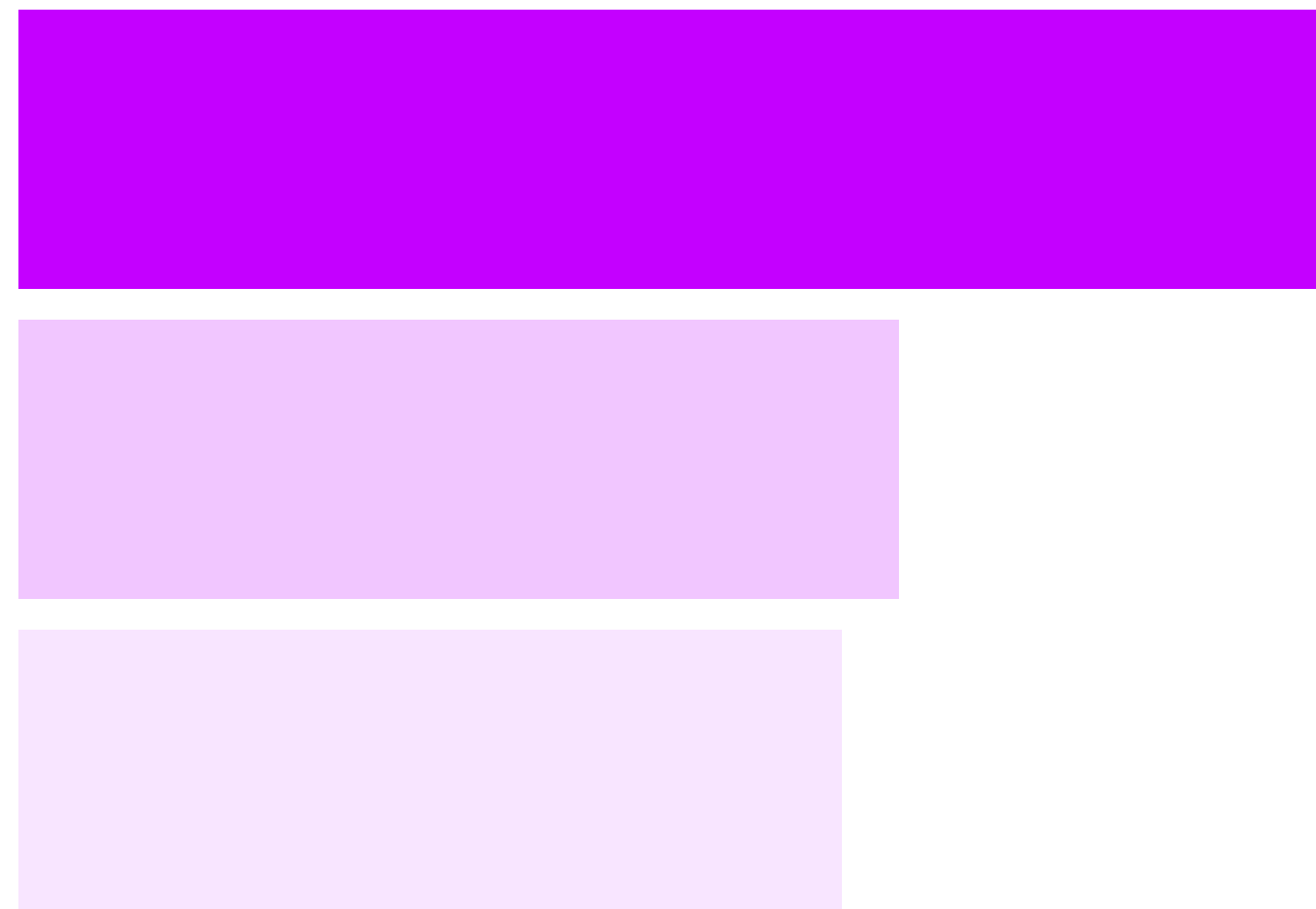
0

2

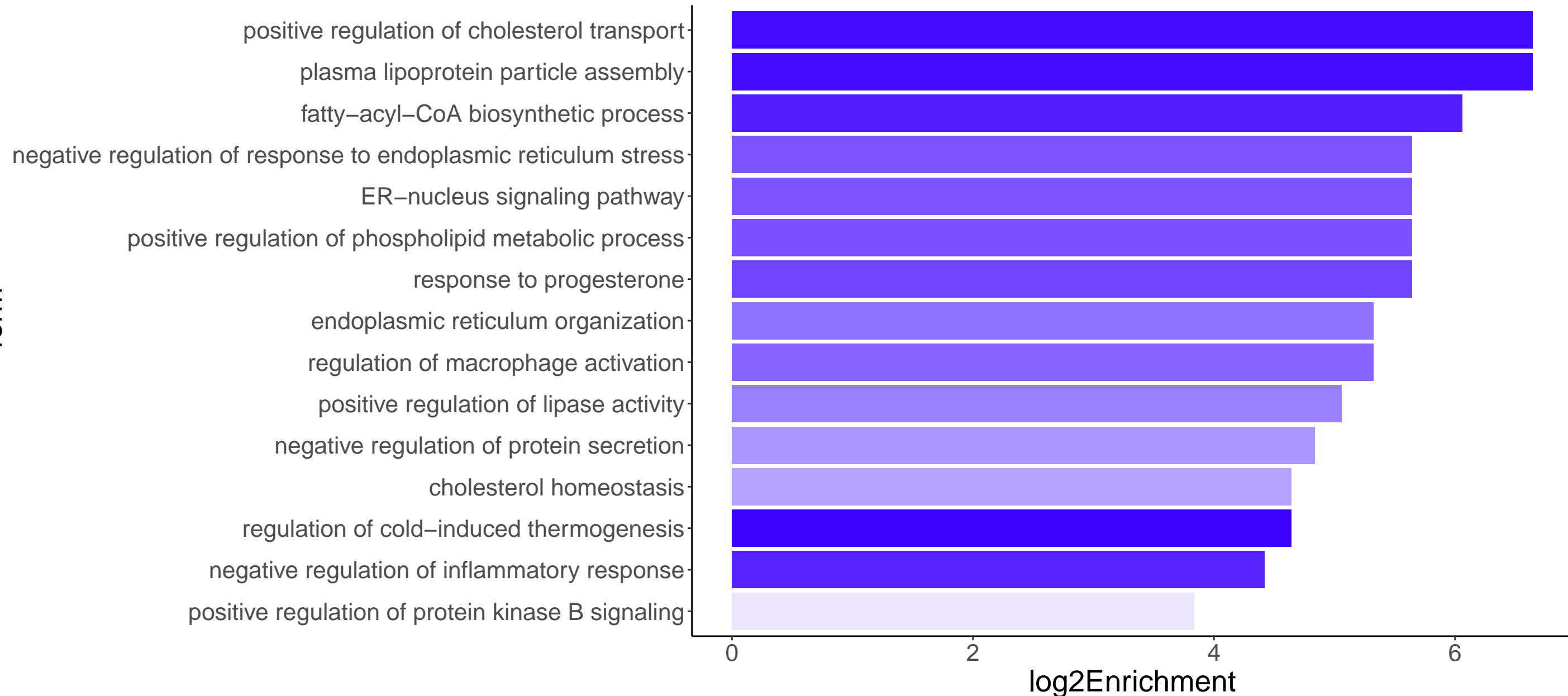
4

6

log2Enrichment



Re-clustered module 16.13.3 BP enrichment



Re-clustered module 16.13.3 MF enrichment

Term

nuclear receptor activity

0

2

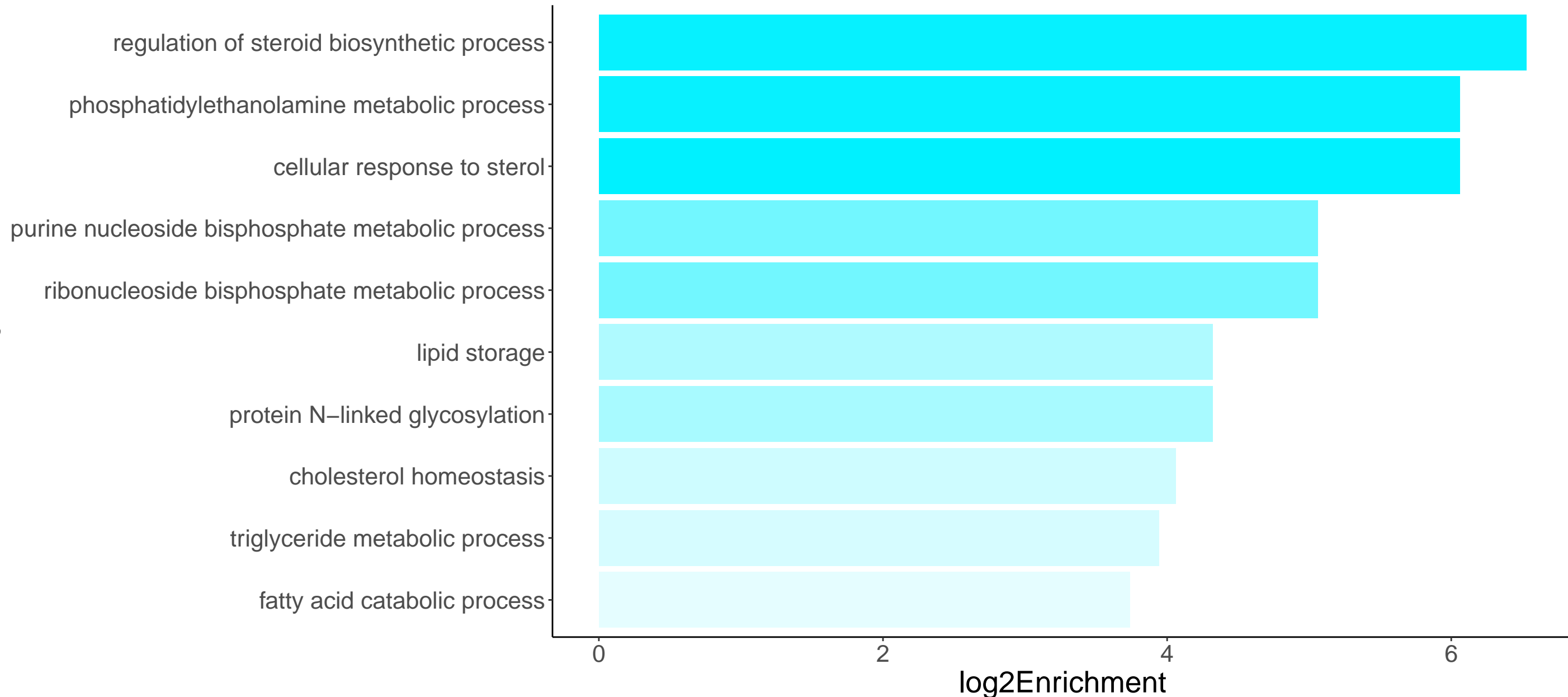
4

log2Enrichment



Re-clustered module 16.13.7 BP enrichment

Term



reductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of

NADP

sterol

identical protein

lc

Re-clustered module 16.14.1 BP enrichment

Term

GPI anchor biosynthetic process

acyl-CoA metabolic process

0

2

4

log2Enrichment



Re-clustered module 16.14.1 MF enrichment

Term

carbon-carbon lyase activity

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.14.10 BP enrichment

Term

lung epithelial cell differentiation

mRNA polyadenylation

RNA phosphodiester bond hydrolysis, exonucleolytic

phospholipid biosynthetic process

0

2

4

6

log2Enrichment



Re-clustered module 16.14.10 MF enrichment

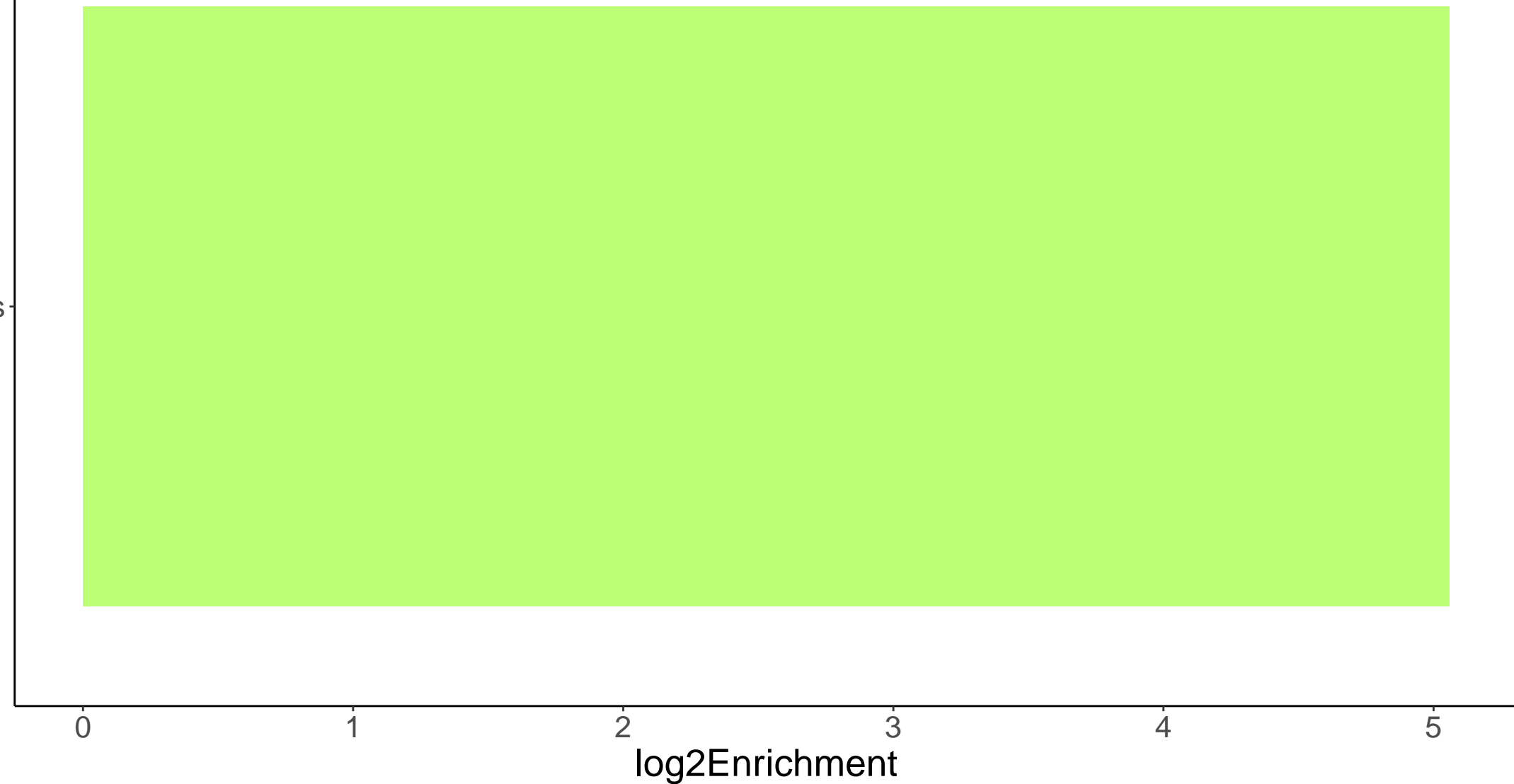
Term

log2Enrichment



Re-clustered module 16.14.11 BP enrichment

Term
ribosomal large subunit biogenesis



Re-clustered module 16.14.11 MF enrichment

Term

log2Enrichment



Re-clustered module 16.14.12 BP enrichment

Term

mitochondrial translational termination

mitochondrial translational elongation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.14.12 MF enrichment

Term

electron transfer activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.14.13 BP enrichment

Term

inner mitochondrial membrane organization

protein insertion into mitochondrial membrane

protein targeting to mitochondrion

sensory perception of sound

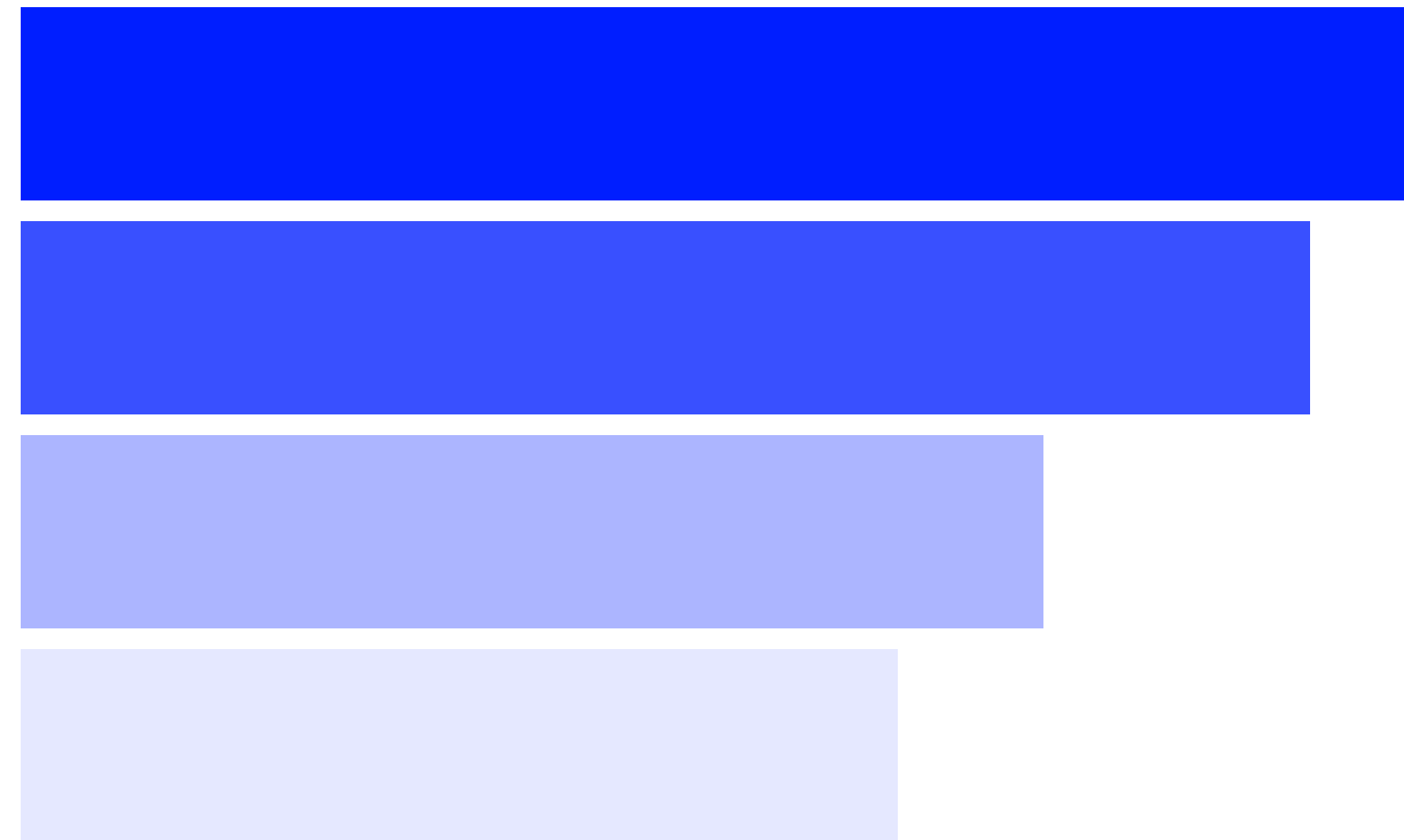
0

2

4

6

log2Enrichment



Re-clustered module 16.14.13 MF enrichment

Term

RNA binding

0.0

0.5

1.0

1.5

log2Enrichment



Re-clustered module 16.14.14 BP enrichment

Term

rRNA modification

inner mitochondrial membrane organization

mitochondrial ATP synthesis coupled electron transport

ribonucleoprotein complex biogenesis

0 1 2 3 4 5

log2Enrichment



Re-clustered module 16.14.14 MF enrichment

Term

rRNA methyltransferase activity

intramolecular transferase activity

NADH dehydrogenase (ubiquinone) activity

catalytic activity, acting on a tRNA

0

1

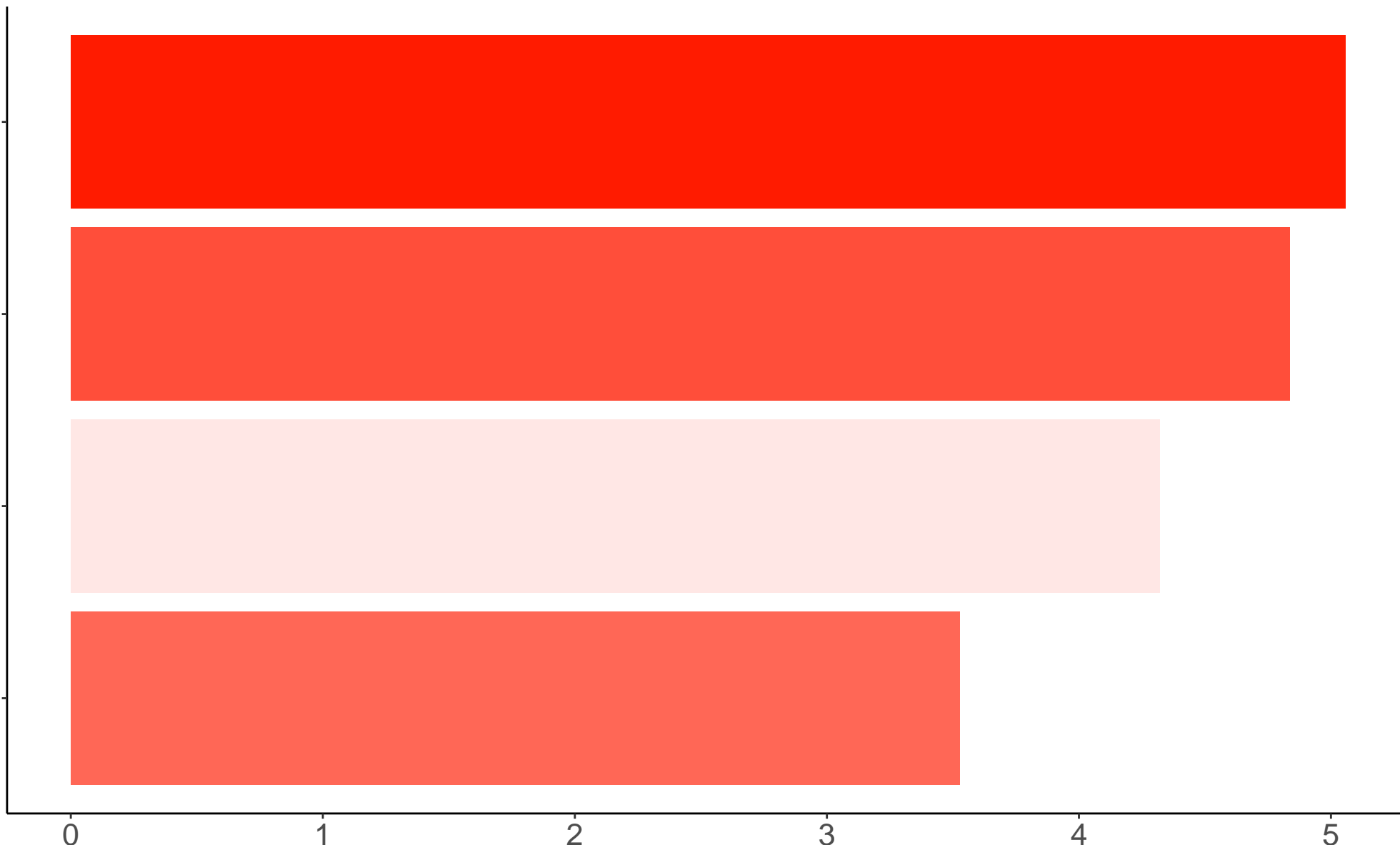
2

3

4

5

log2Enrichment



Re-clustered module 16.14.15 BP enrichment

Term

nucleobase metabolic process

cellular metabolic compound salvage

purine ribonucleoside monophosphate metabolic process

pigment biosynthetic process

purine ribonucleoside metabolic process

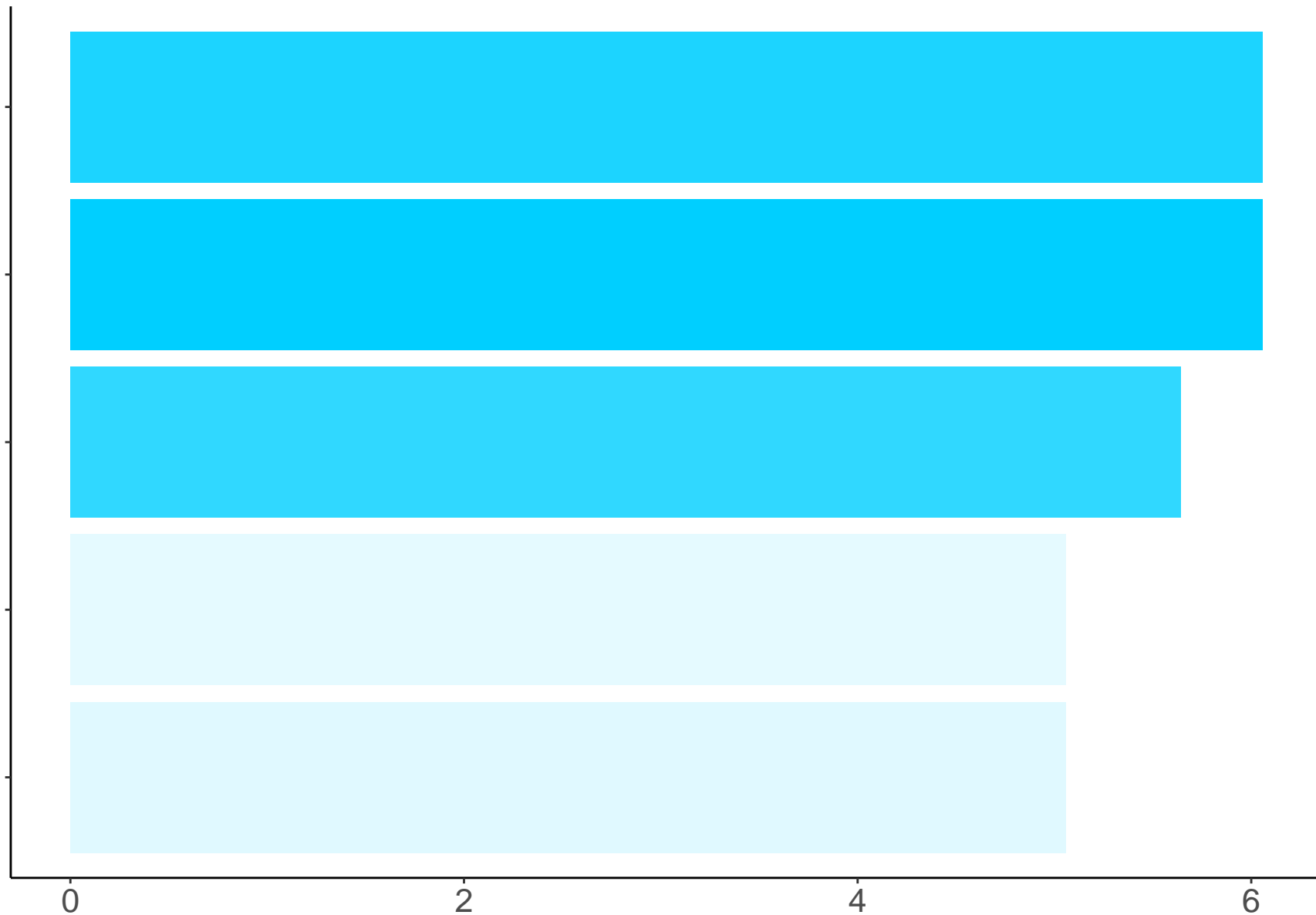
0

2

4

6

log2Enrichment



Re-clustered module 16.14.15 MF enrichment

Term structural constituent of ribosome

0

1

2

3

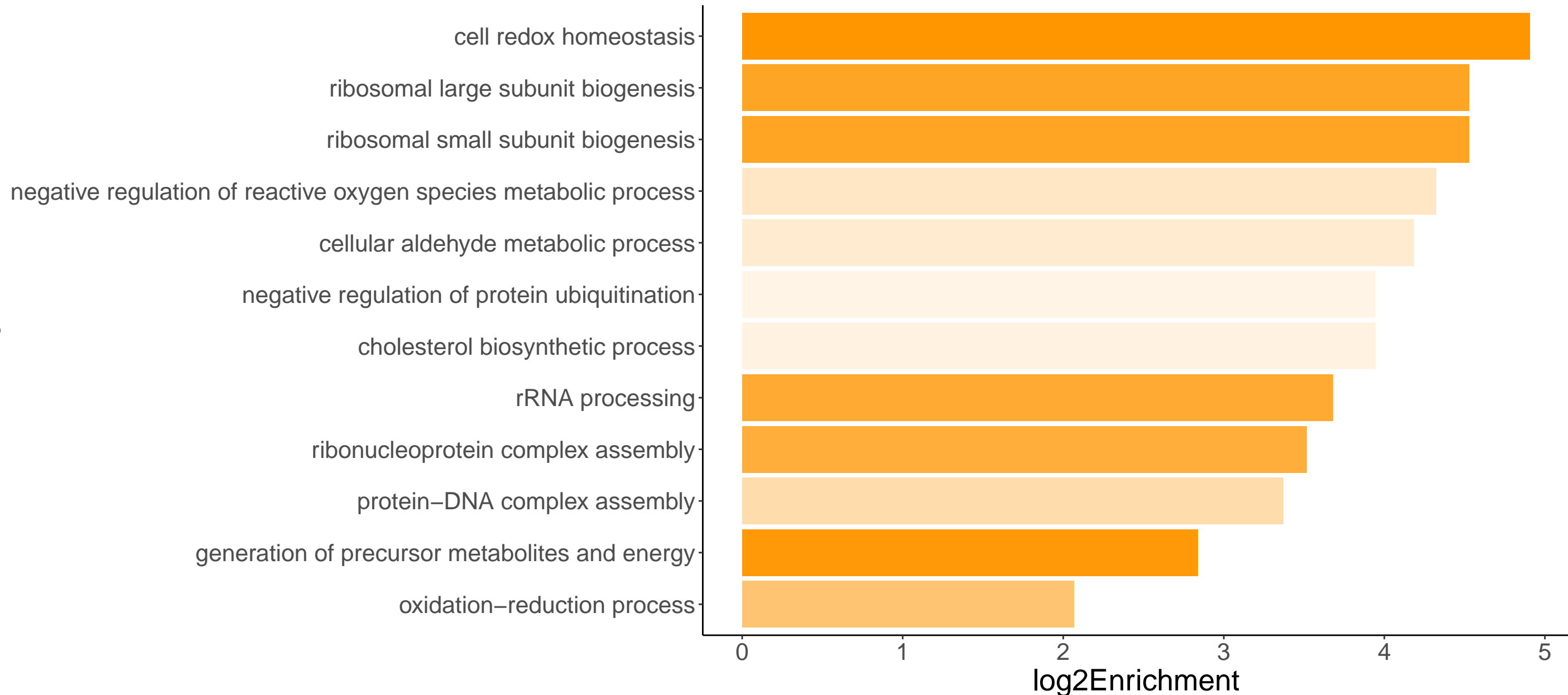
4

log2Enrichment



Re-clustered module 16.14.2 BP enrichment

Term



Re-clustered module 16.14.2 MF enrichment

Term

NADP binding

monosaccharide binding

magnesium ion binding

0

1

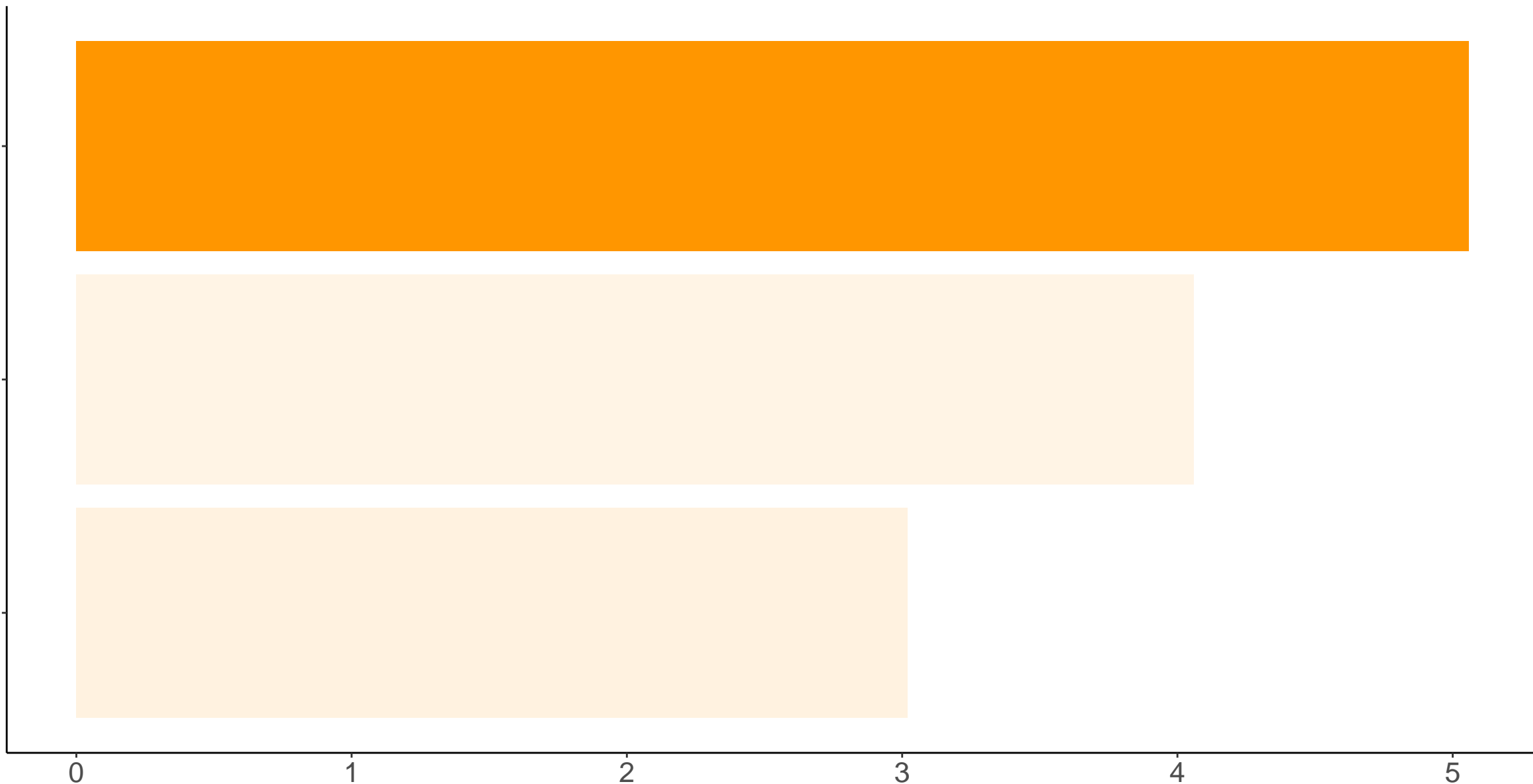
2

3

4

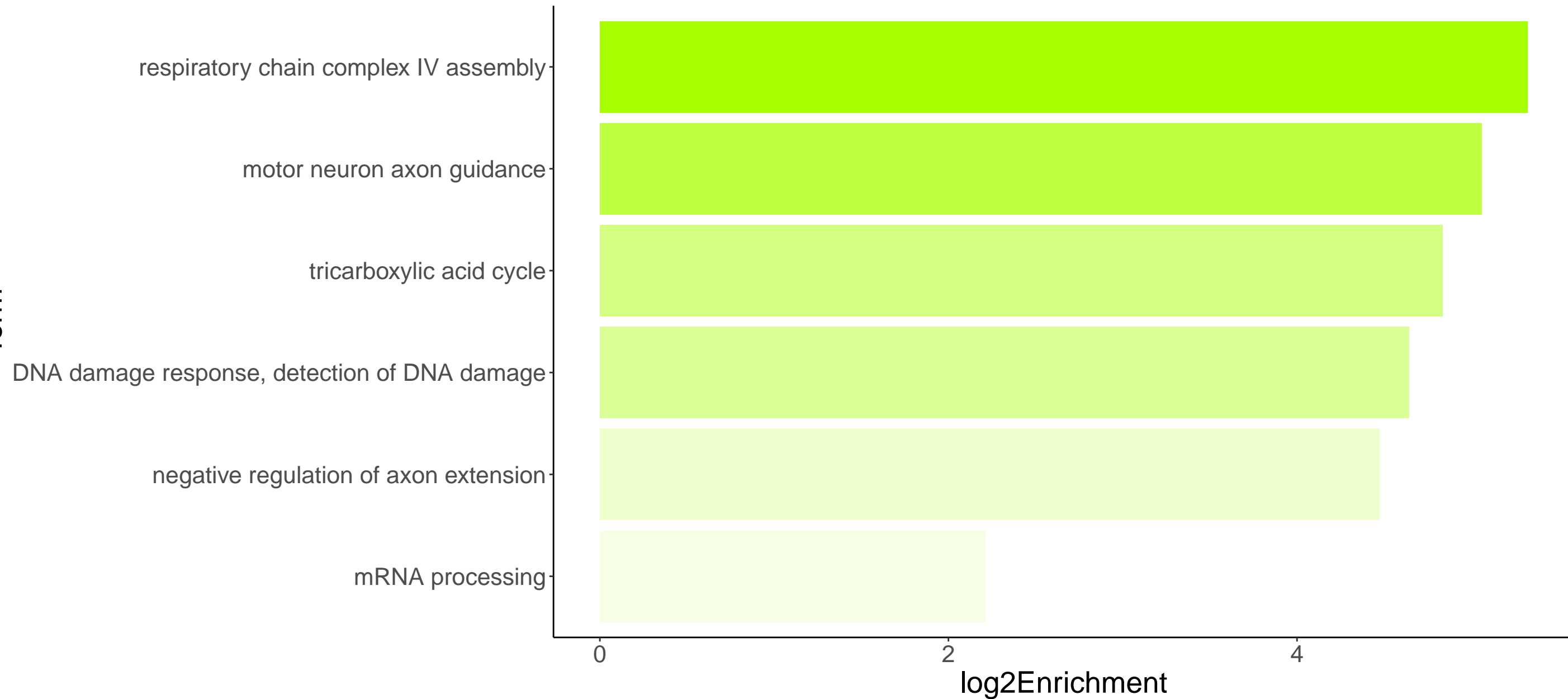
5

log2Enrichment



Re-clustered module 16.14.3 BP enrichment

Term



Re-clustered module 16.14.3 MF enrichment

Term

electron transfer activity

structural constituent of ribosome

0

1

2

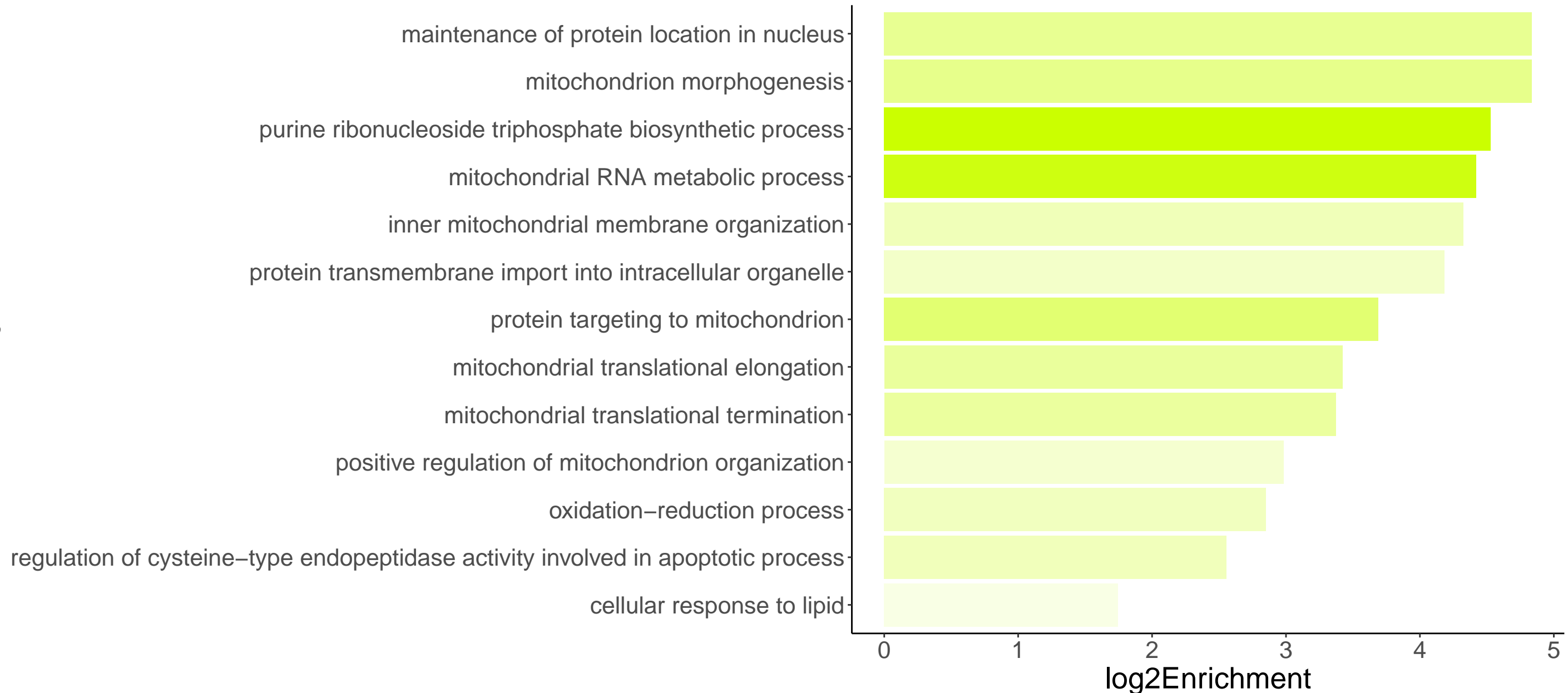
3

log2Enrichment



Re-clustered module 16.14.4 BP enrichment

Term



Re-clustered module 16.14.4 MF enrichment

Term

steroid hormone receptor activity

phosphotransferase activity, phosphate group as acceptor

nucleobase-containing compound kinase activity

0

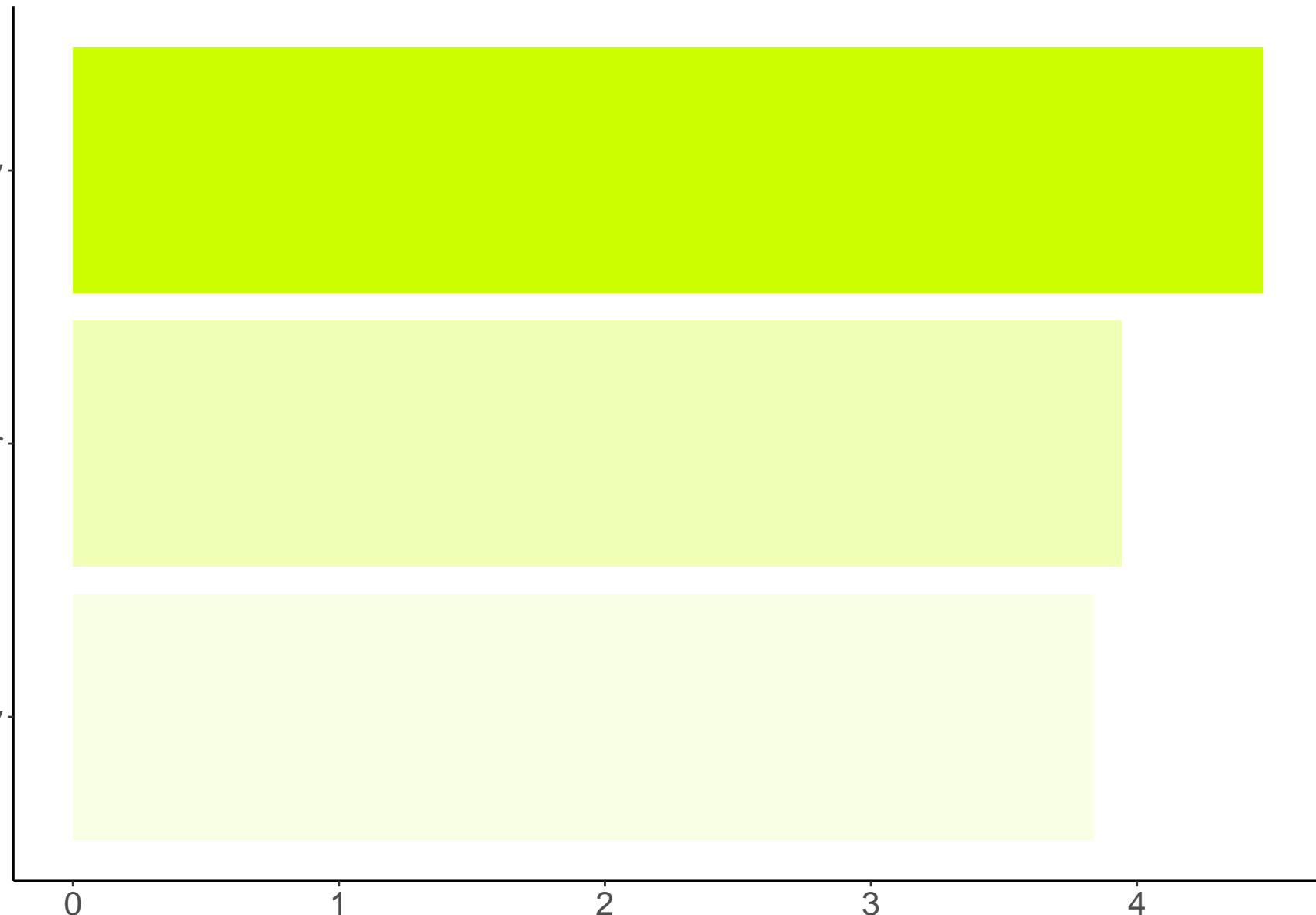
1

2

3

4

log2Enrichment



Re-clustered module 16.14.5 BP enrichment

Term

mitochondrial translational elongation

mitochondrial ATP synthesis coupled electron transport

mitochondrial translational termination

protein targeting to mitochondrion

cellular respiration

0

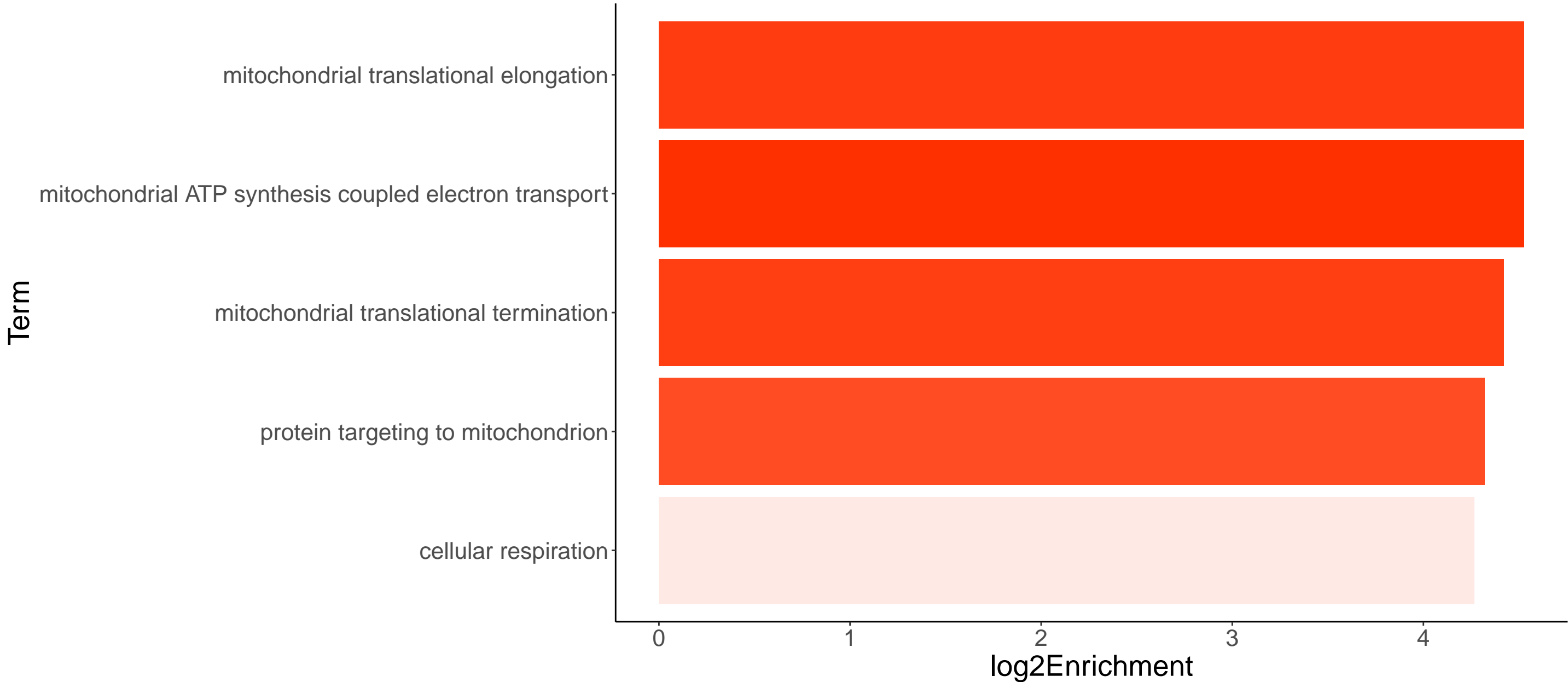
1

2

3

4

log2Enrichment



Re-clustered module 16.14.5 MF enrichment

Term structural constituent of ribosome

0

1

2

3

log2Enrichment



Re-clustered module 16.14.6 BP enrichment

Term

mitochondrial translation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.14.6 MF enrichment

Term

electron transfer activity

0

1

2

3

4

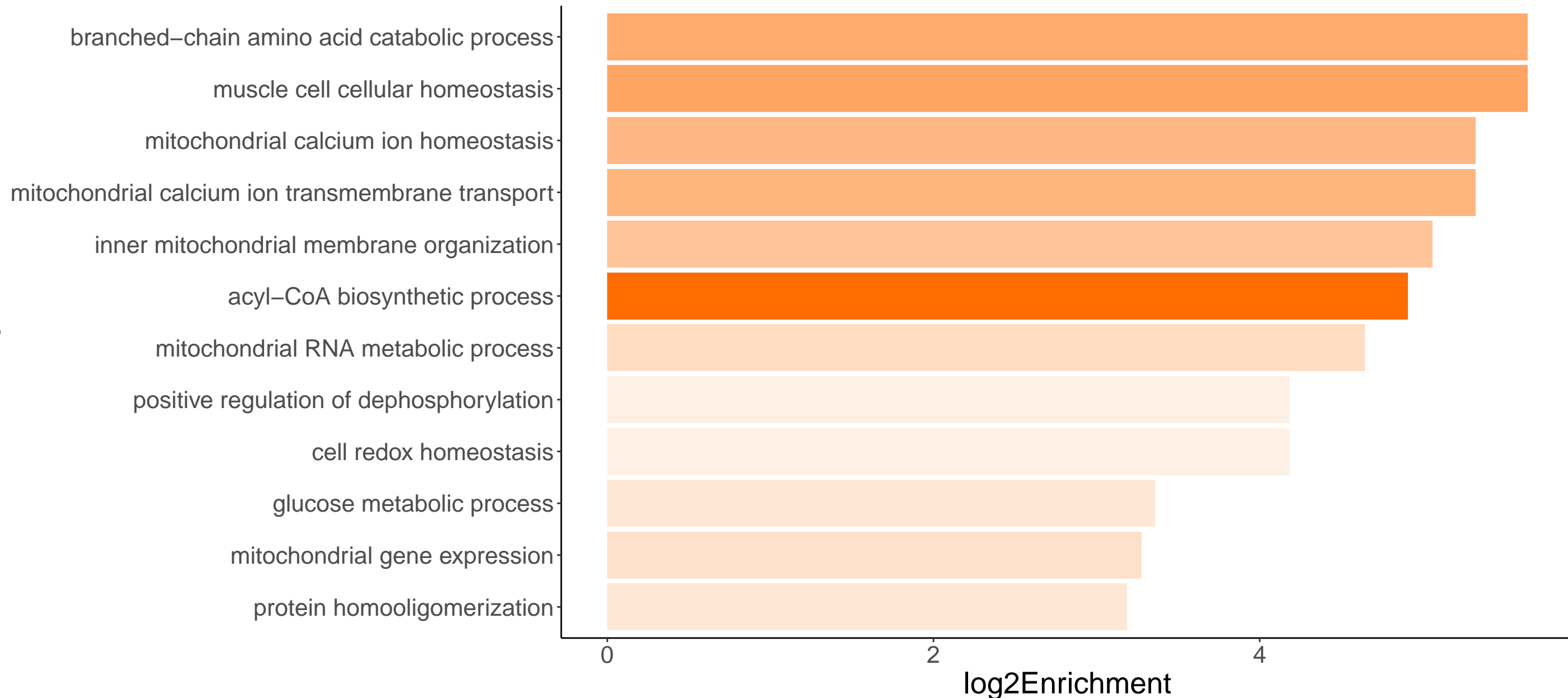
5

log2Enrichment



Re-clustered module 16.14.7 BP enrichment

Term



Re-clustered module 16.14.7 MF

Term

oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor

NAD binding

protein self-association

ribosome binding

oxidoreductase activity, acting on a sulfur group of donors

electron transfer activity

0 1 2 3 4 5
log2Enrichment



Re-clustered module 16.14.8 BP enrichment

Term

iron-sulfur cluster assembly

mitochondrial respiratory chain complex assembly

mitochondrial translation

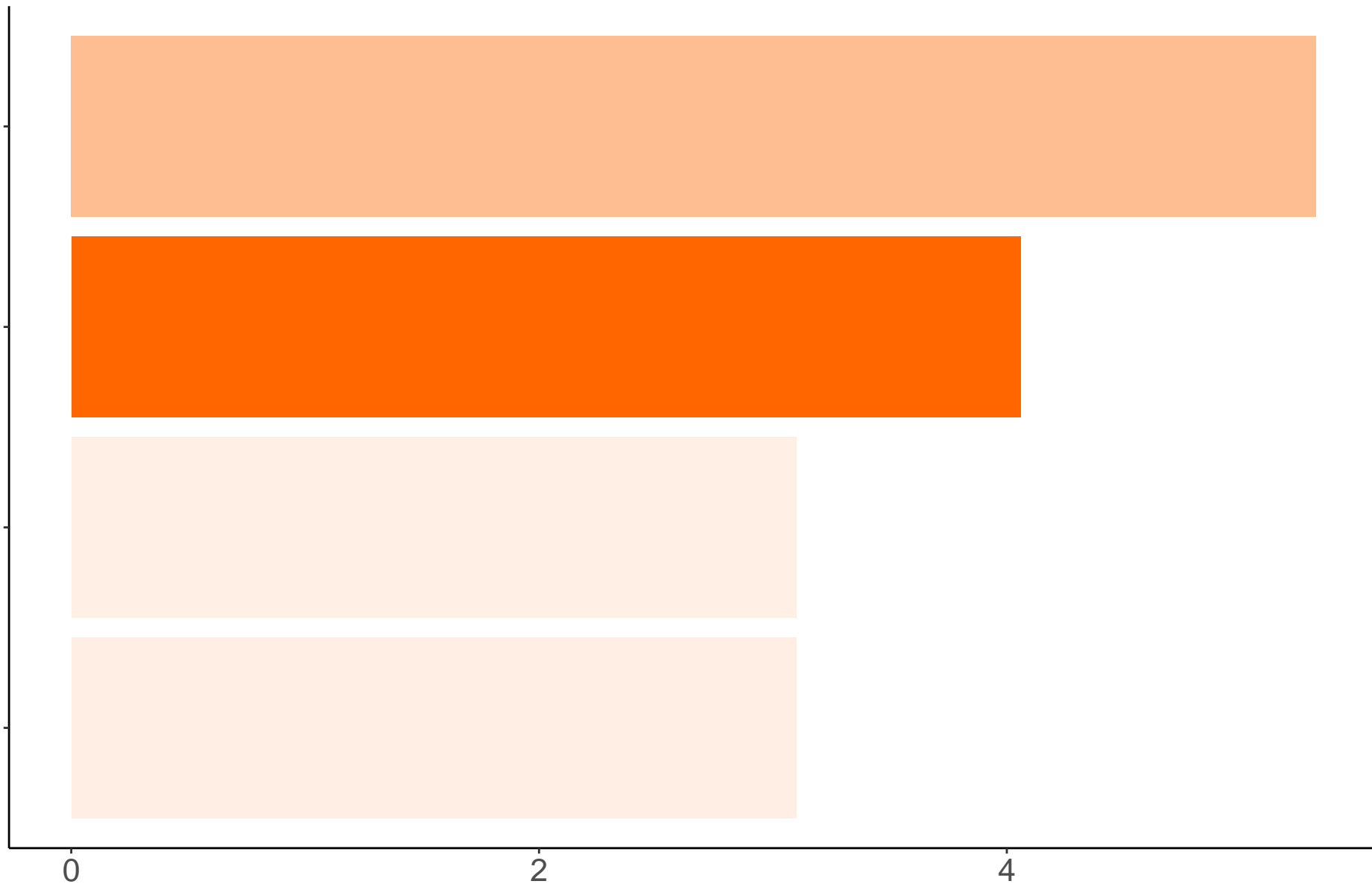
translational elongation

0

2

4

log2Enrichment



Re-clustered module 16.14.8 MF enrichment

Term

NADH dehydrogenase (ubiquinone) activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.14.9 BP enrichment

Term

tRNA modification

0

1

2

3

4

log2Enrichment



Re-clustered module 16.14.9 MF enrichment

Term

4 iron, 4 sulfur cluster binding

carbon-carbon lyase activity

structural constituent of ribosome

RNA binding

0

1

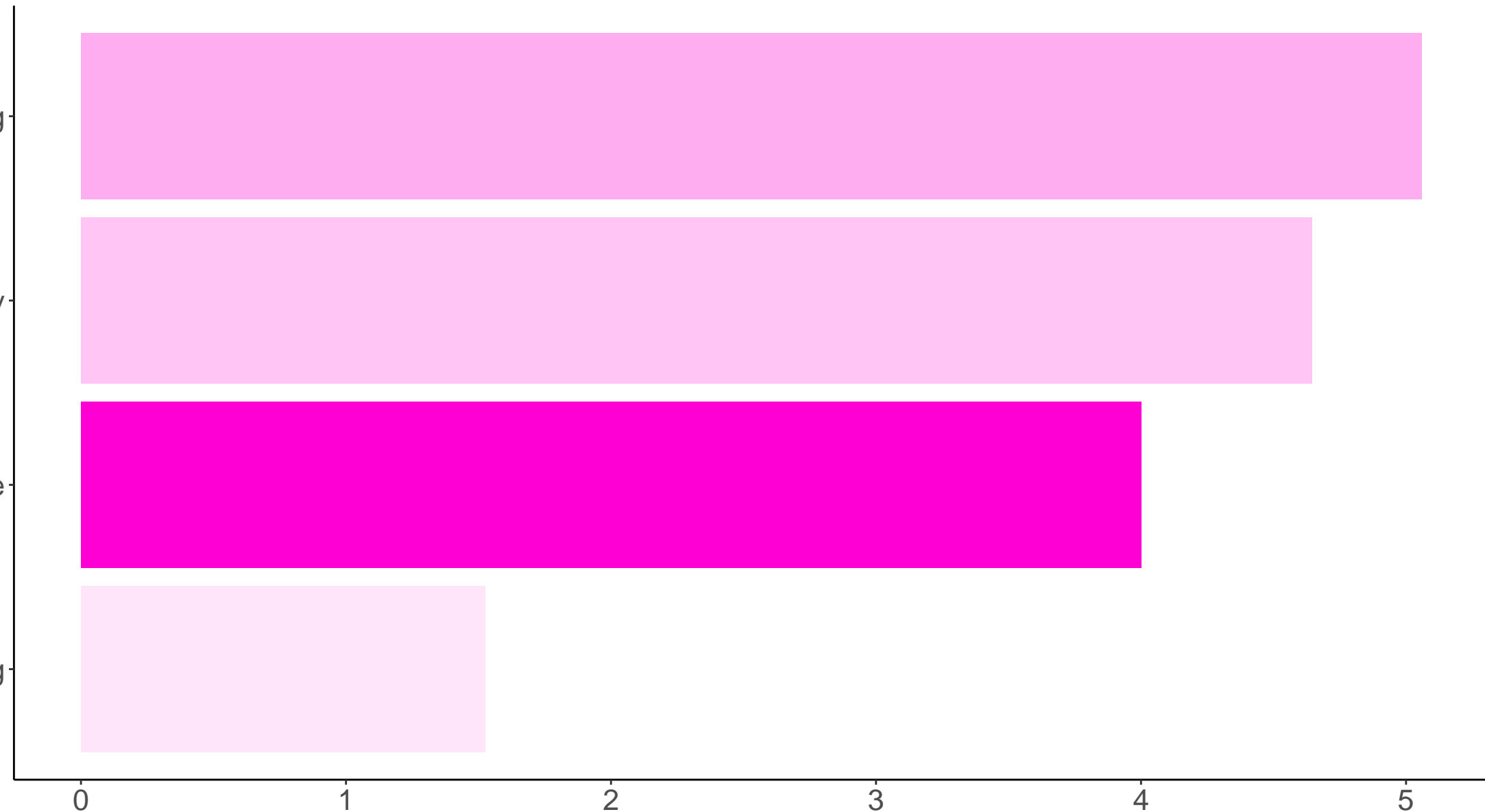
2

3

4

5

log2Enrichment



Re-clustered module 16.15.1 BP enrichment

Term

endosome transport via multivesicular body sorting pathway

proteasome-mediated ubiquitin-dependent protein catabolic process

aerobic respiration

regulation of protein catabolic process

mitotic cell cycle

double-strand break repair

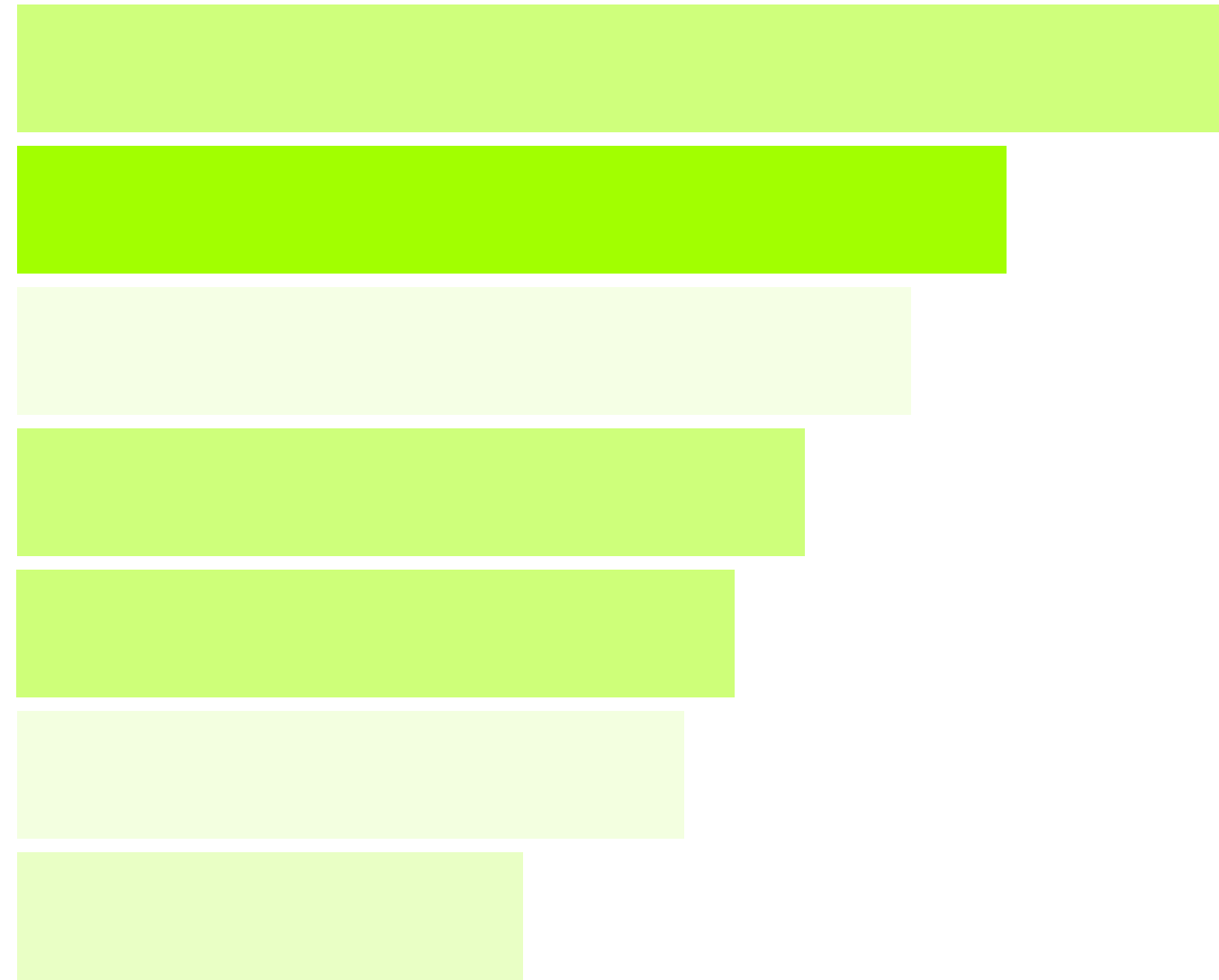
viral process

0

2

4

log2Enrichment



Re-clustered module 16.15.1 MF enrichment

Term

peptidase activator activity

thiol-dependent ubiquitin-specific protease activity

ubiquitin binding

cysteine-type endopeptidase activity

0

1

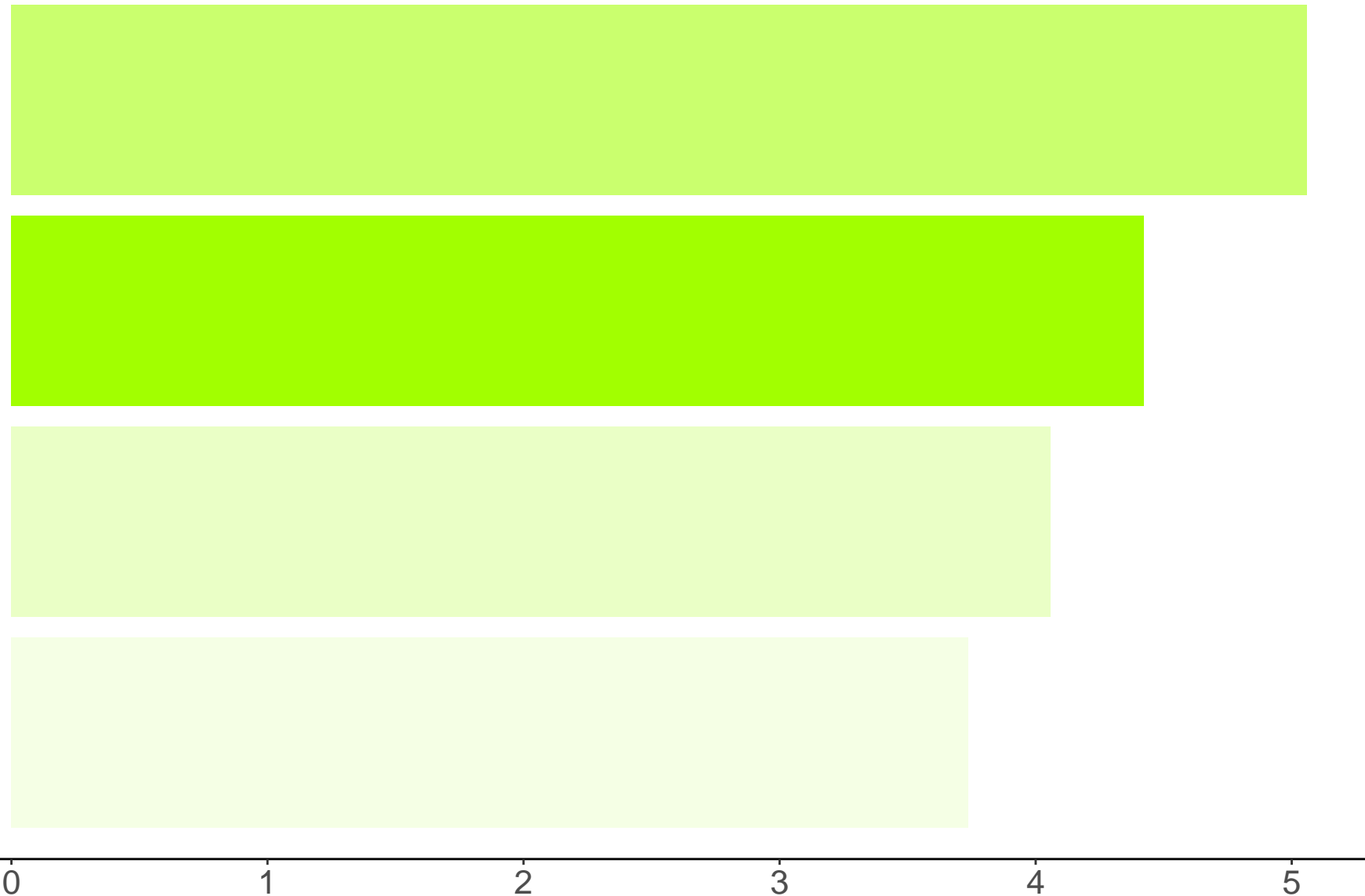
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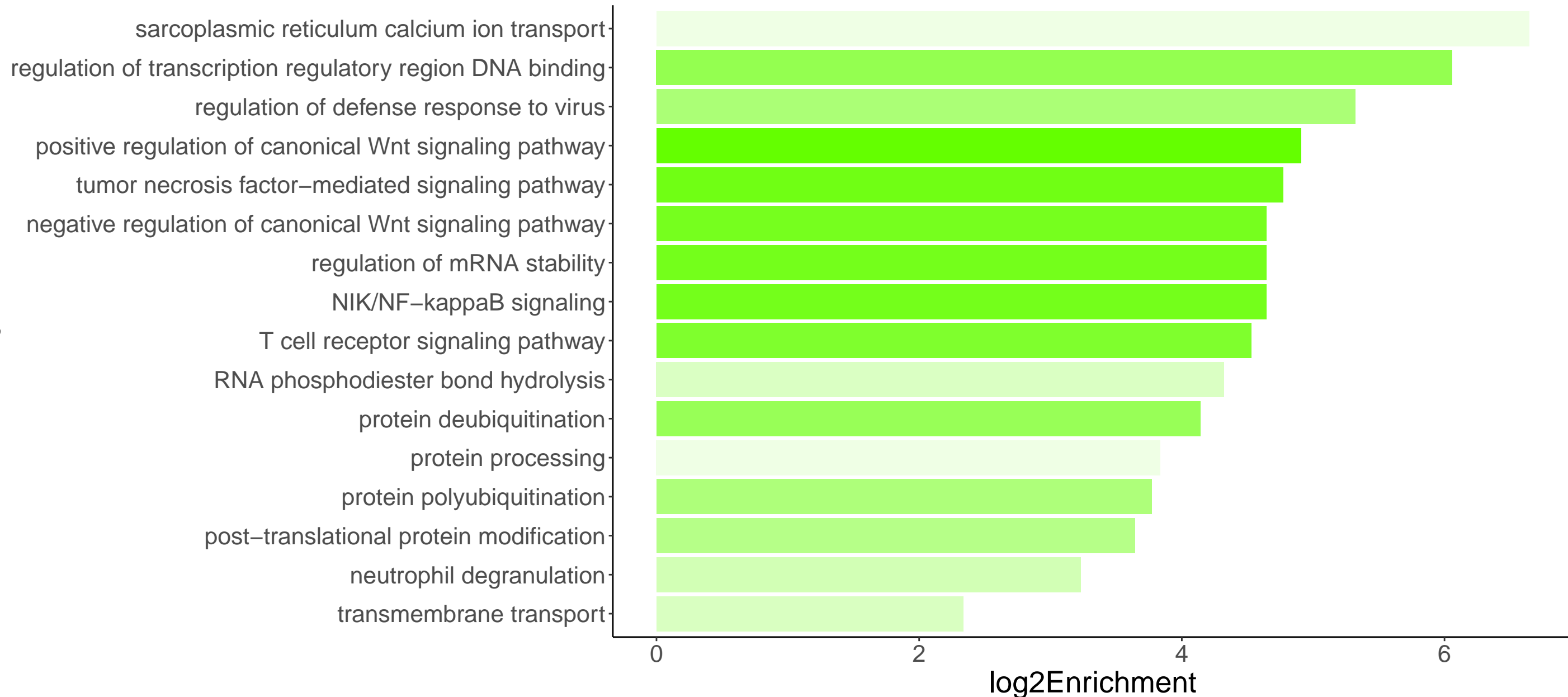
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log2Enrichment



Re-clustered module 16.15.10 BP enrichment

Term



Re-clustered module 16.15.10 MF enrichment

Term

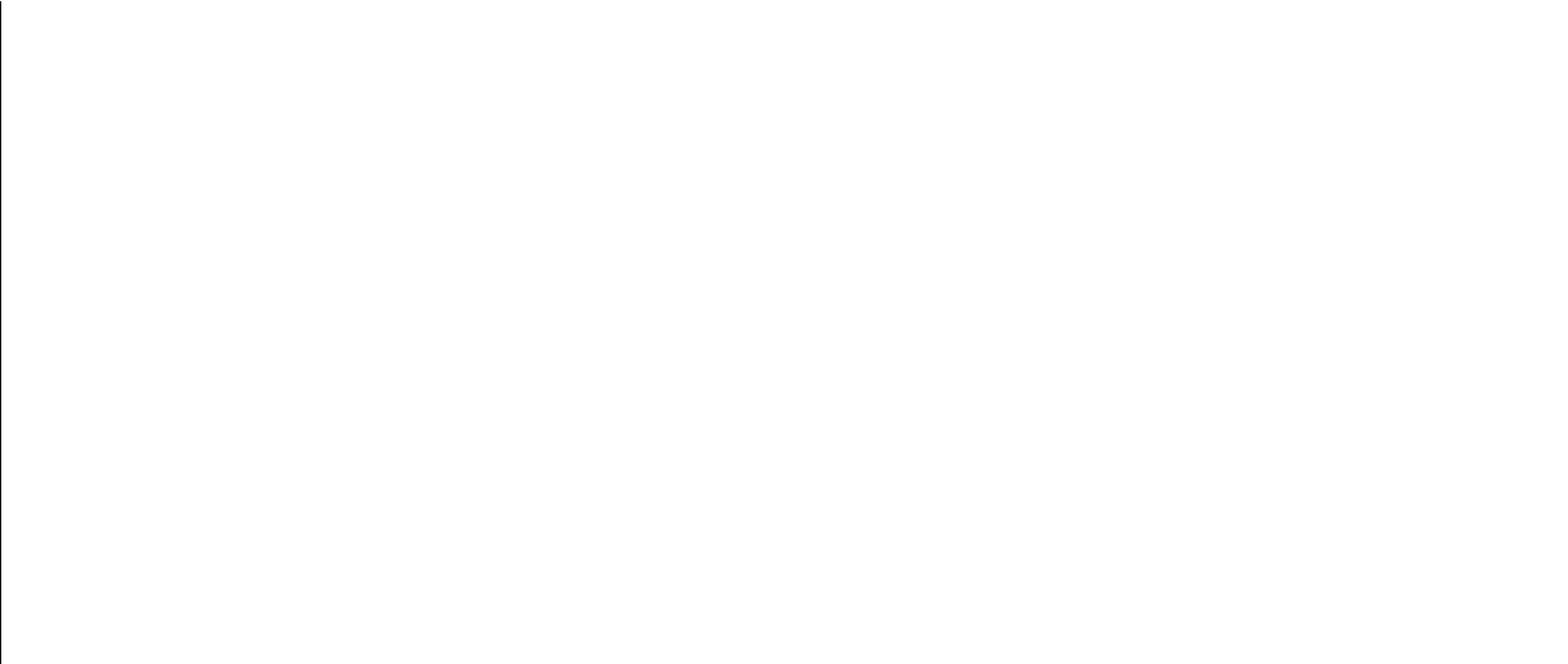
log2Enrichment



Re-clustered module 16.15.12 BP enrichment

Term

log2Enrichment



Re-clustered module 16.15.12 MF enrichment

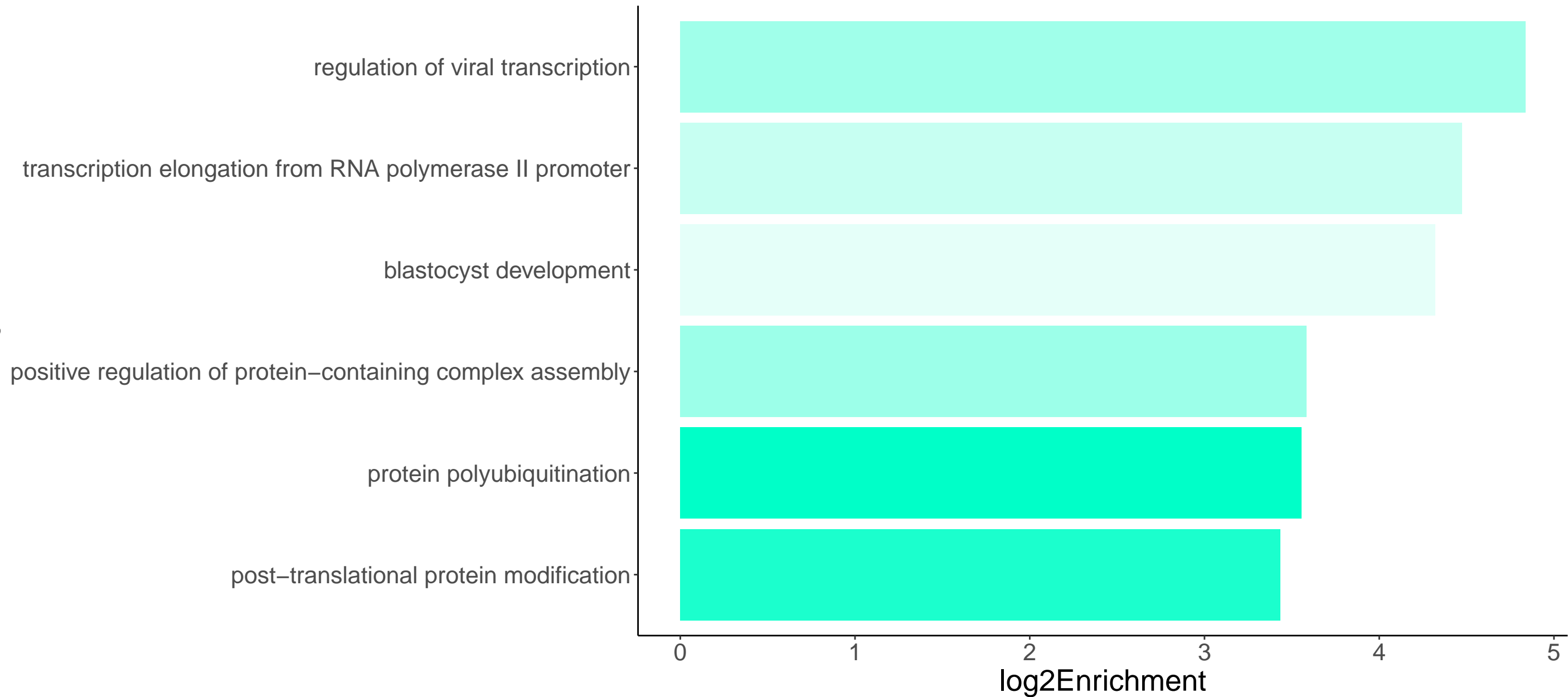
Term

log2Enrichment



Re-clustered module 16.15.2 BP enrichment

Term



Re-clustered module 16.15.2 MF enrichment

Term

ATPase activity

0

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log2Enrichment



Re-clustered module 16.15.3 BP enrichment

Term

nucleosome organization

positive regulation of Wnt signaling pathway

protein deubiquitination

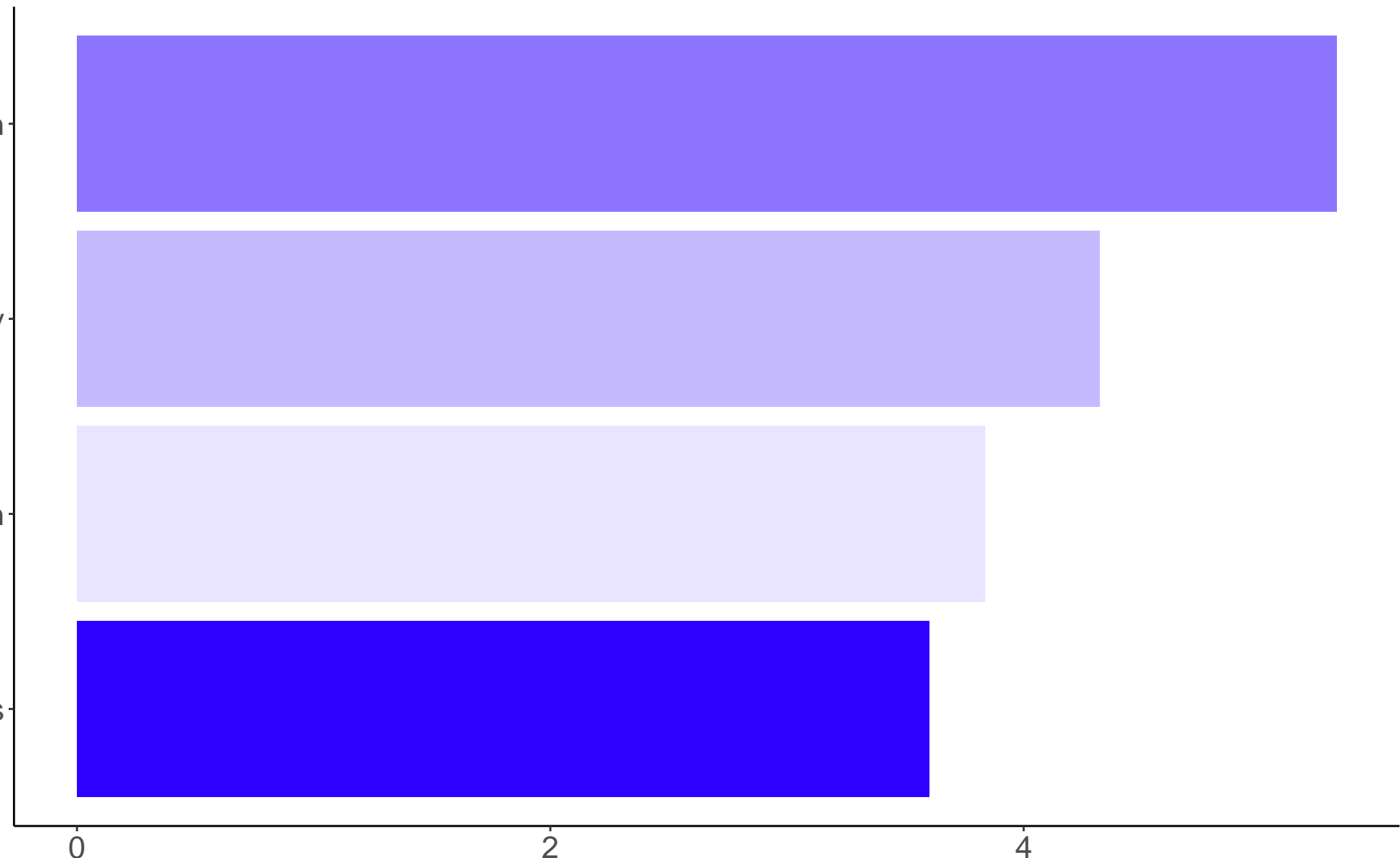
ubiquitin-dependent protein catabolic process

0

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log2Enrichment



Re-clustered module 16.15.3 MF enrichment

Term

histone binding

0

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log2Enrichment



Re-clustered module 16.15.4 BP enrichment

Term

mRNA destabilization

regulation of cytoplasmic translation

regulation of hematopoietic progenitor cell differentiation

positive regulation of translation

regulation of stem cell differentiation

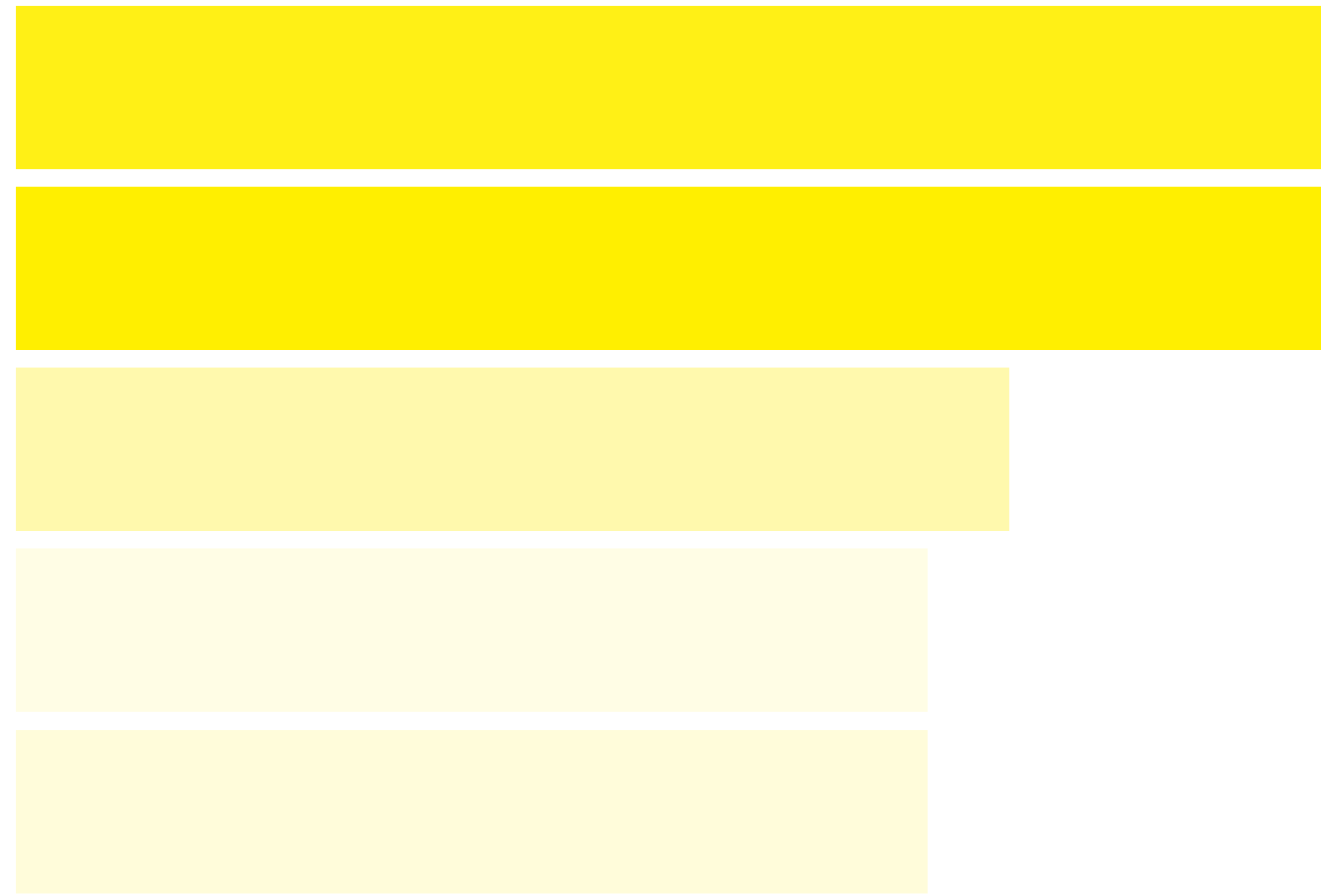
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log2Enrichment



Re-clustered module 16.15.4 MF enrichment

Term

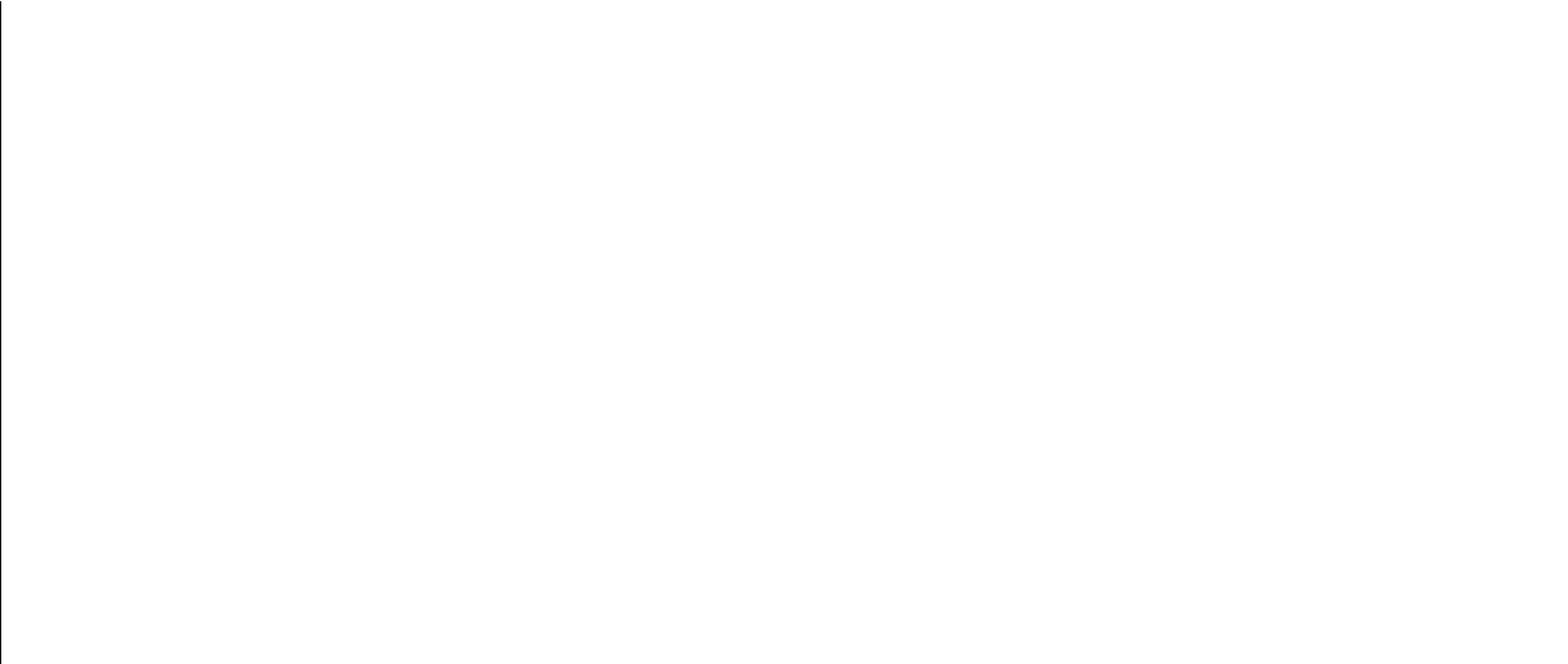
log2Enrichment



Re-clustered module 16.15.5 BP enrichment

Term

log2Enrichment



Re-clustered module 16.15.5 MF enrichment

Term

log2Enrichment



Re-clustered module 16.15.6 BP enrichment

Term

tRNA modification

purine ribonucleotide biosynthetic process

0

1

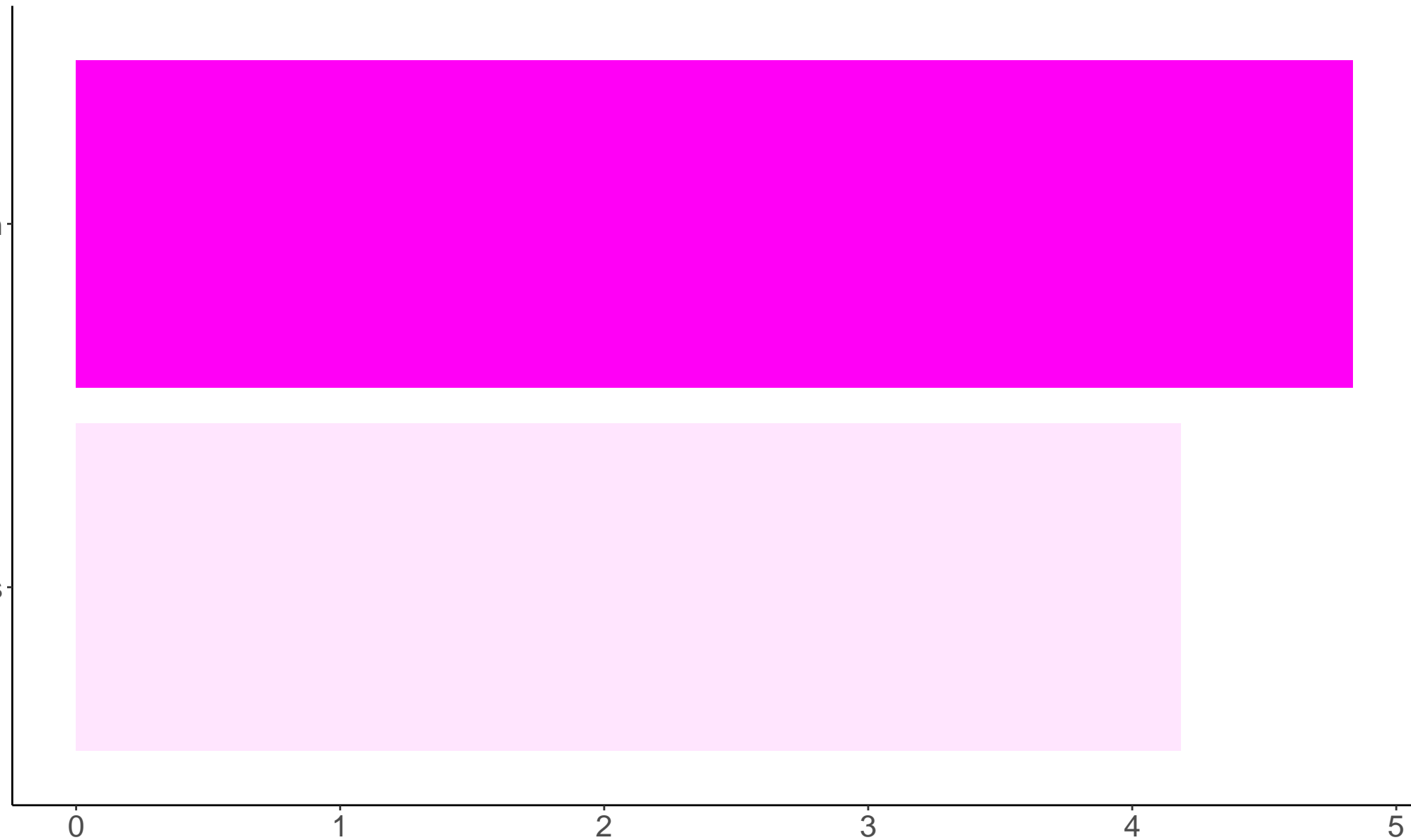
2

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log2Enrichment



Re-clustered module 16.15.6 MF enrichment

Term

catalytic activity, acting on a tRNA

0

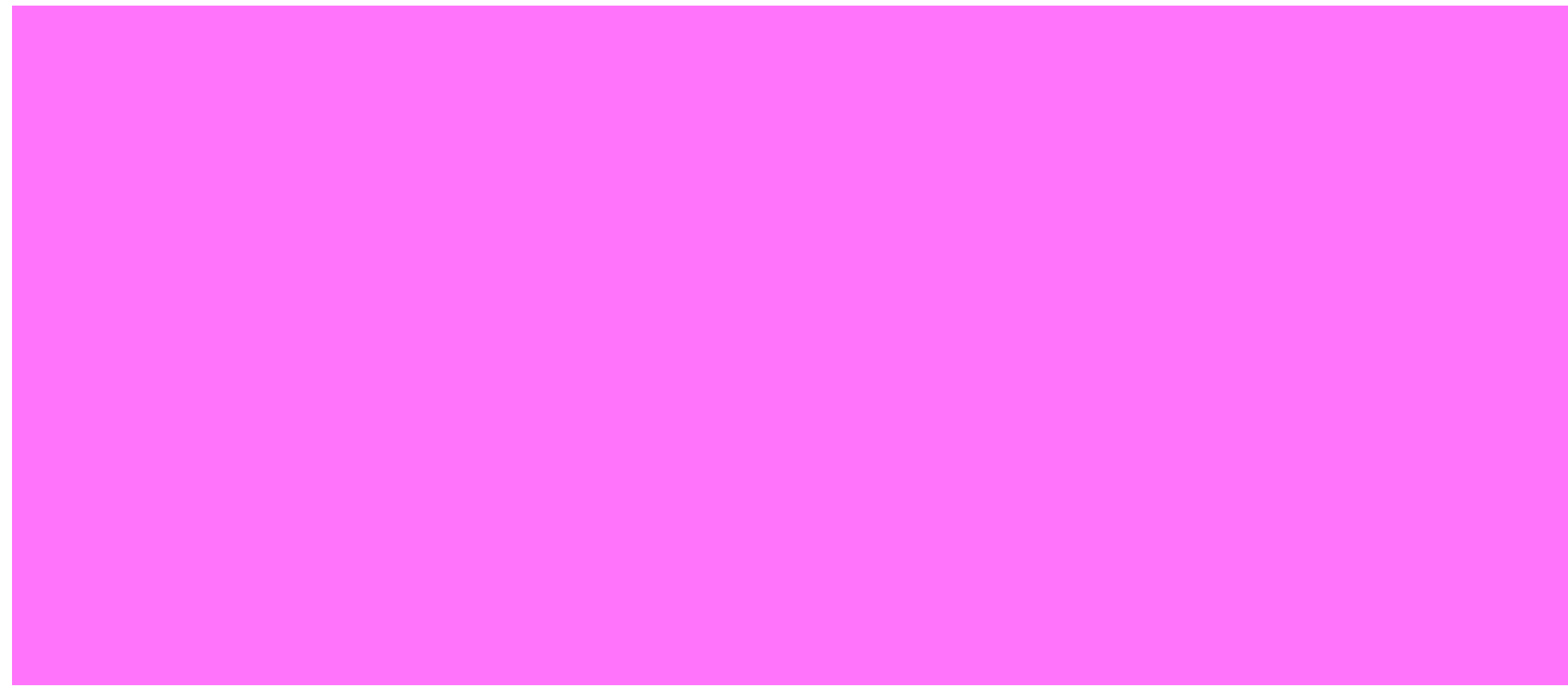
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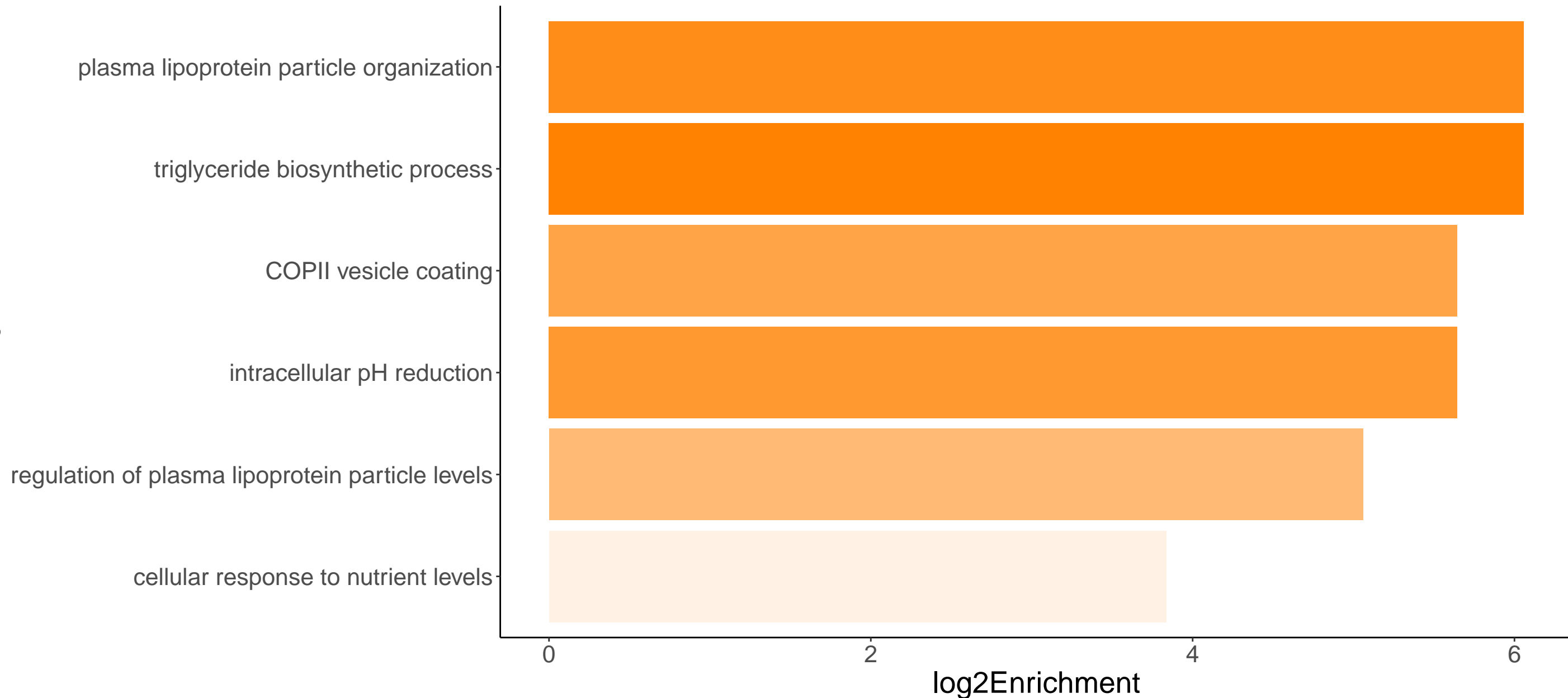
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log2Enrichment



Re-clustered module 16.15.7 BP enrichment

Term



Re-clustered module 16.15.7 MF enrichment

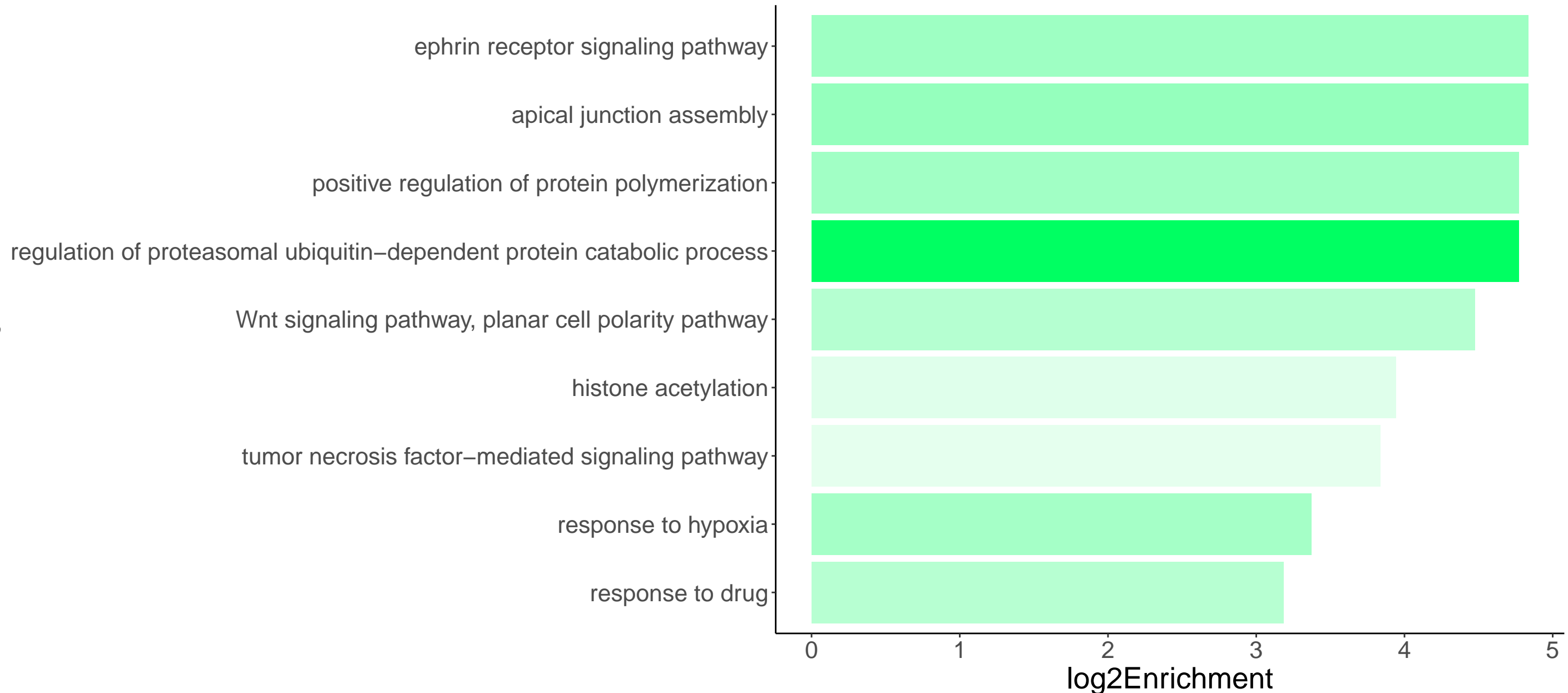
Term

log2Enrichment



Re-clustered module 16.15.9 BP enrichment

Term



Re-clustered module 16.15.9 MF enrichment

Term

polyubiquitin modification-dependent protein binding

GDP binding

0

2

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log2Enrichment



Re-clustered module 16.16.1 BP enrichment

Term

nucleotide–sugar metabolic process

endosome to lysosome transport

mitochondrial translational termination

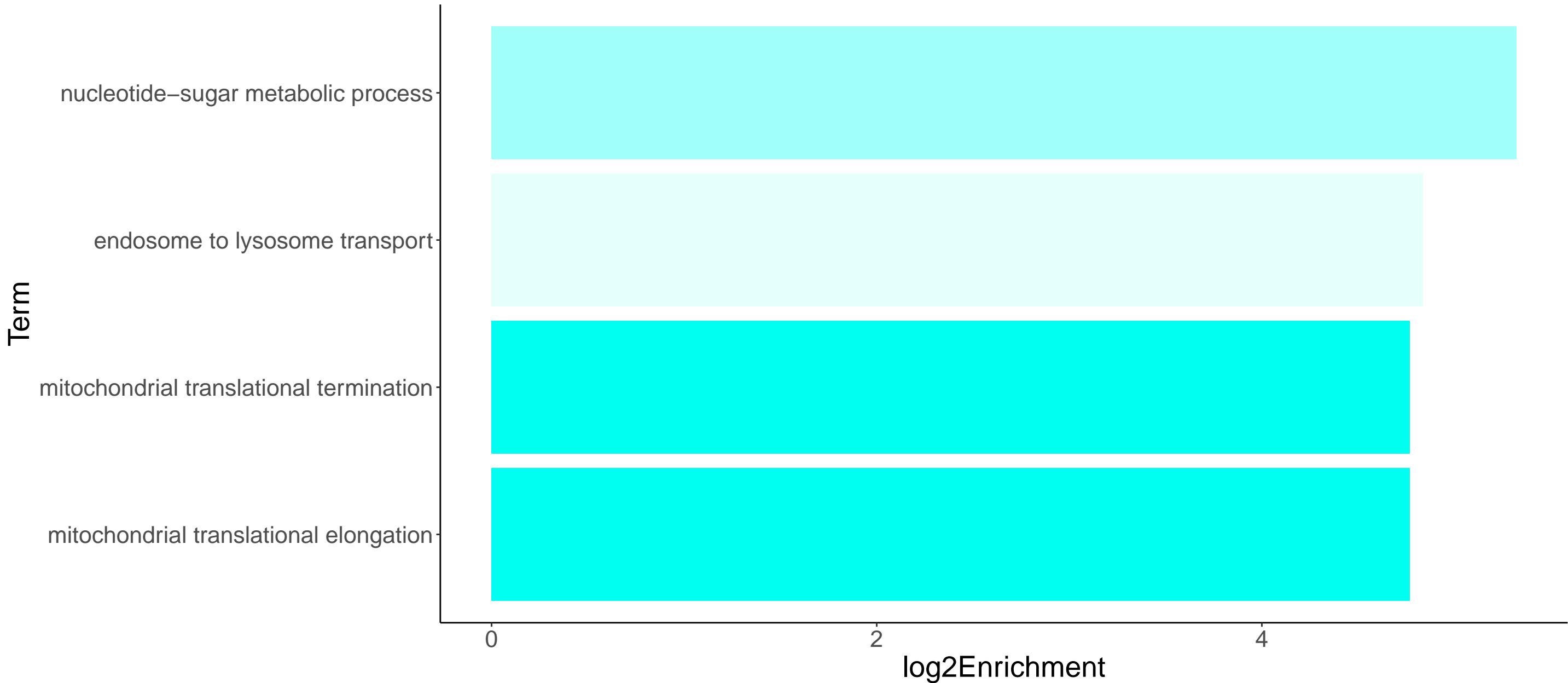
mitochondrial translational elongation

0

2

4

log2Enrichment



Re-clustered module 16.16.1 MF enrichment

Term

log2Enrichment



Re-clustered module 16.16.10 BP enrichment

Term

cellular response to hypoxia

0

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log2Enrichment



Re-clustered module 16.16.10 MF enrichment

Term

catalytic activity, acting on a tRNA

0

1

2

3

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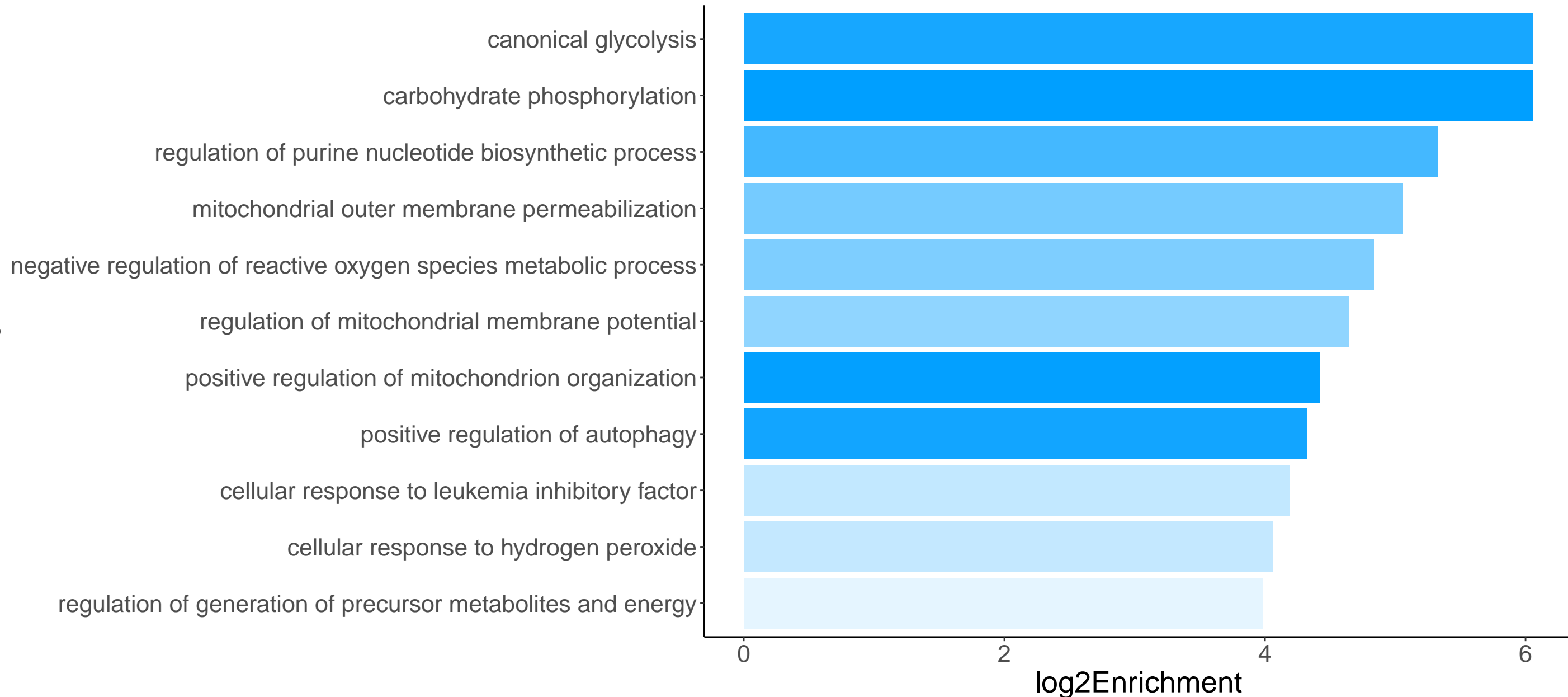
5

log2Enrichment



Re-clustered module 16.16.2 BP enrichment

Term



Re-clustered module 16.16.2 MF enrichment

Term

carbohydrate kinase activity

monosaccharide binding

dioxygenase activity

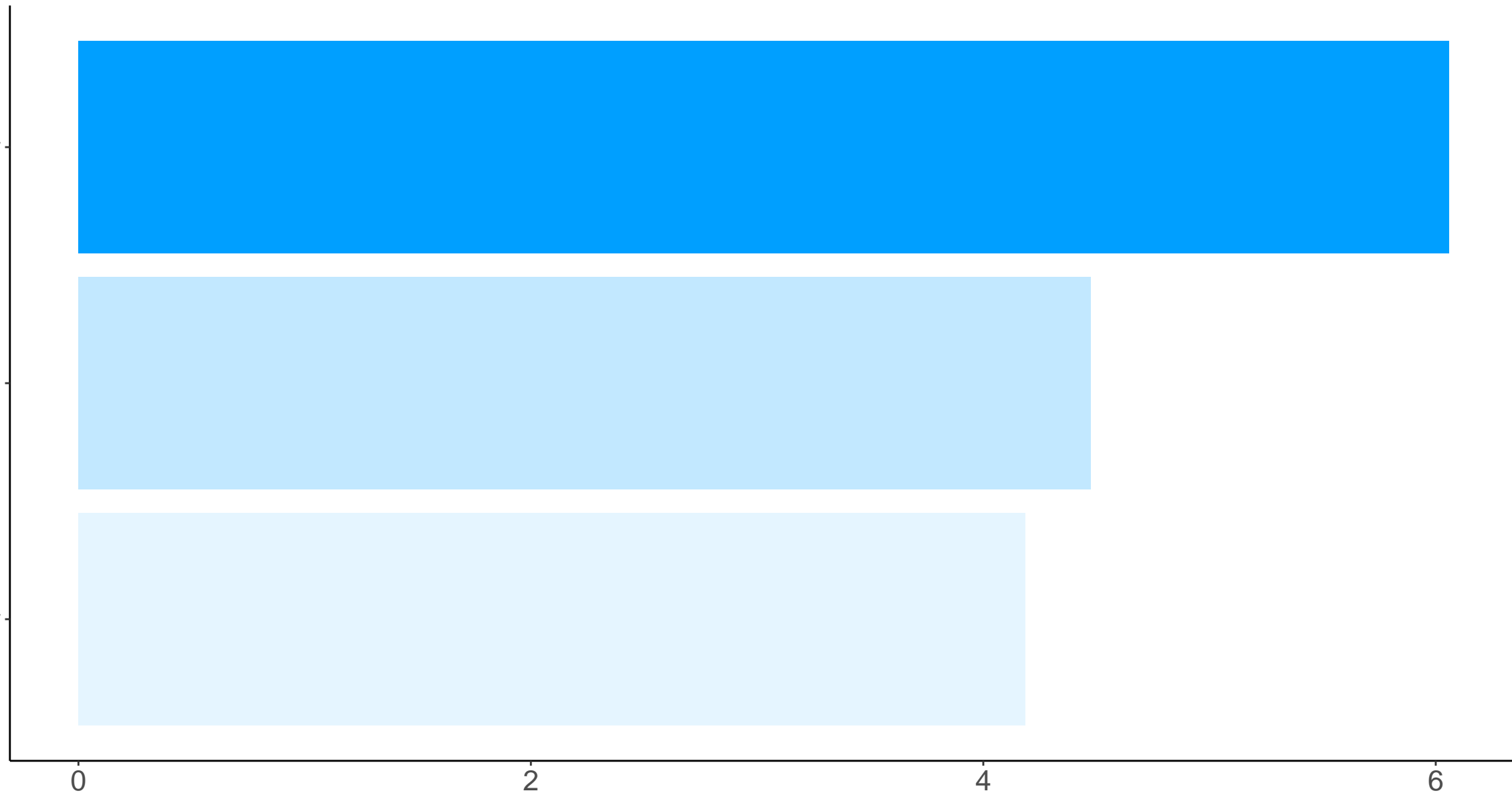
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log2Enrichment



Re-clustered module 16.16.3 BP enrichment

Term

negative regulation of oxidoreductase activity

protein homotetramerization

purine ribonucleotide biosynthetic process

response to hypoxia

neutrophil degranulation

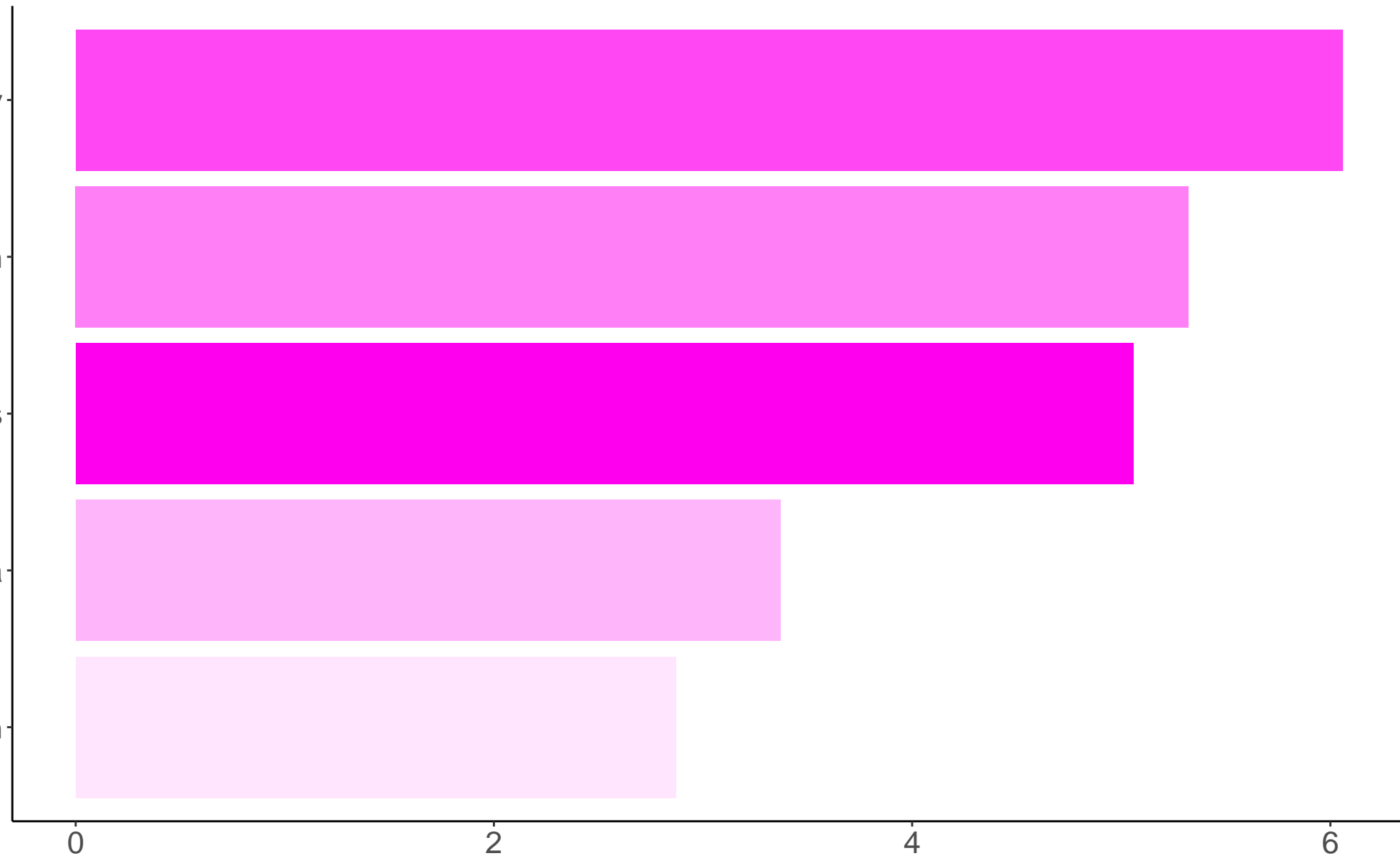
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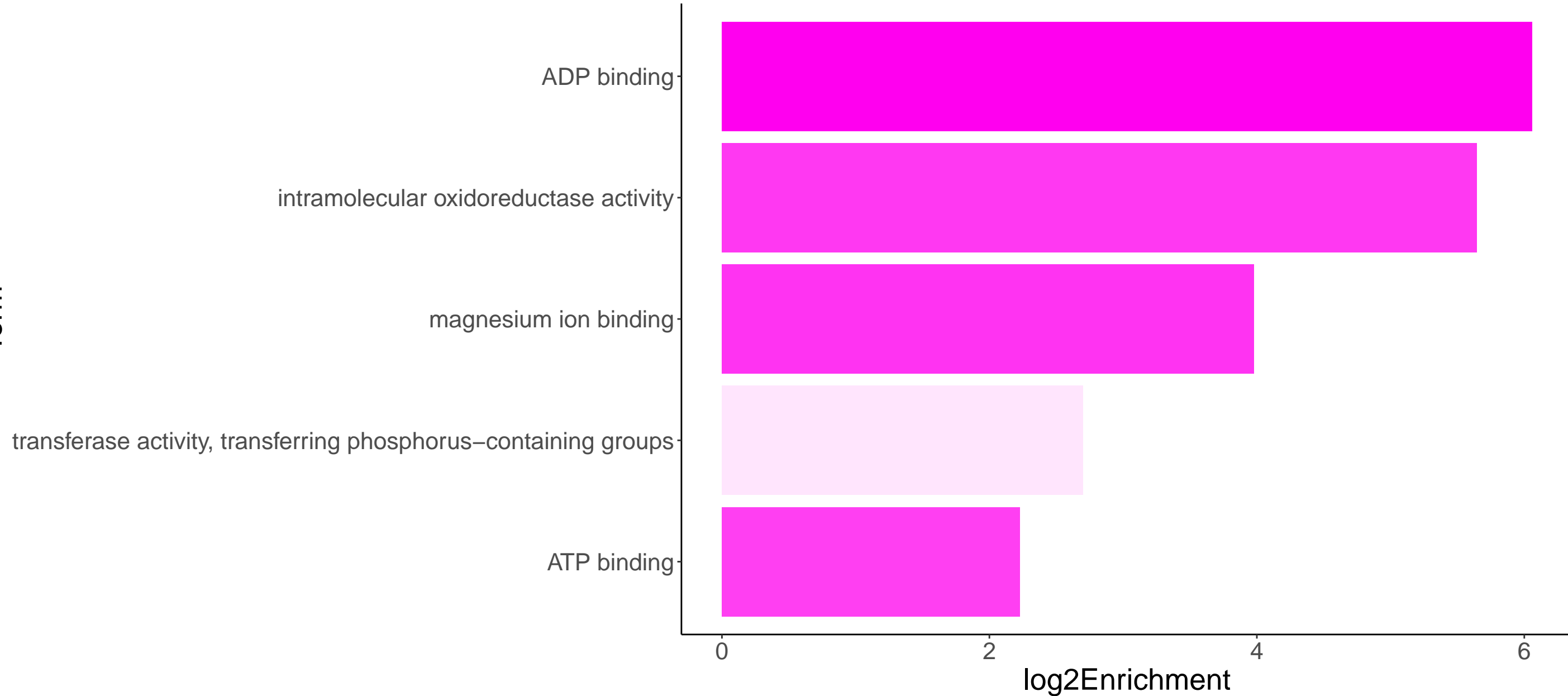
6

log2Enrichment



Re-clustered module 16.16.3 MF enrichment

Term



Re-clustered module 16.16.4 BP enrichment

Term

phosphatidylinositol biosynthetic process

plasma membrane organization

0

1

2

3

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5

log2Enrichment



Re-clustered module 16.16.4 MF enrichment

Term

alcohol binding

0

2

4

log2Enrichment



Re-clustered module 16.16.5 BP enrichment

Term

log2Enrichment



Re-clustered module 16.16.5 MF enrichment

Term

cysteine-type peptidase activity

0

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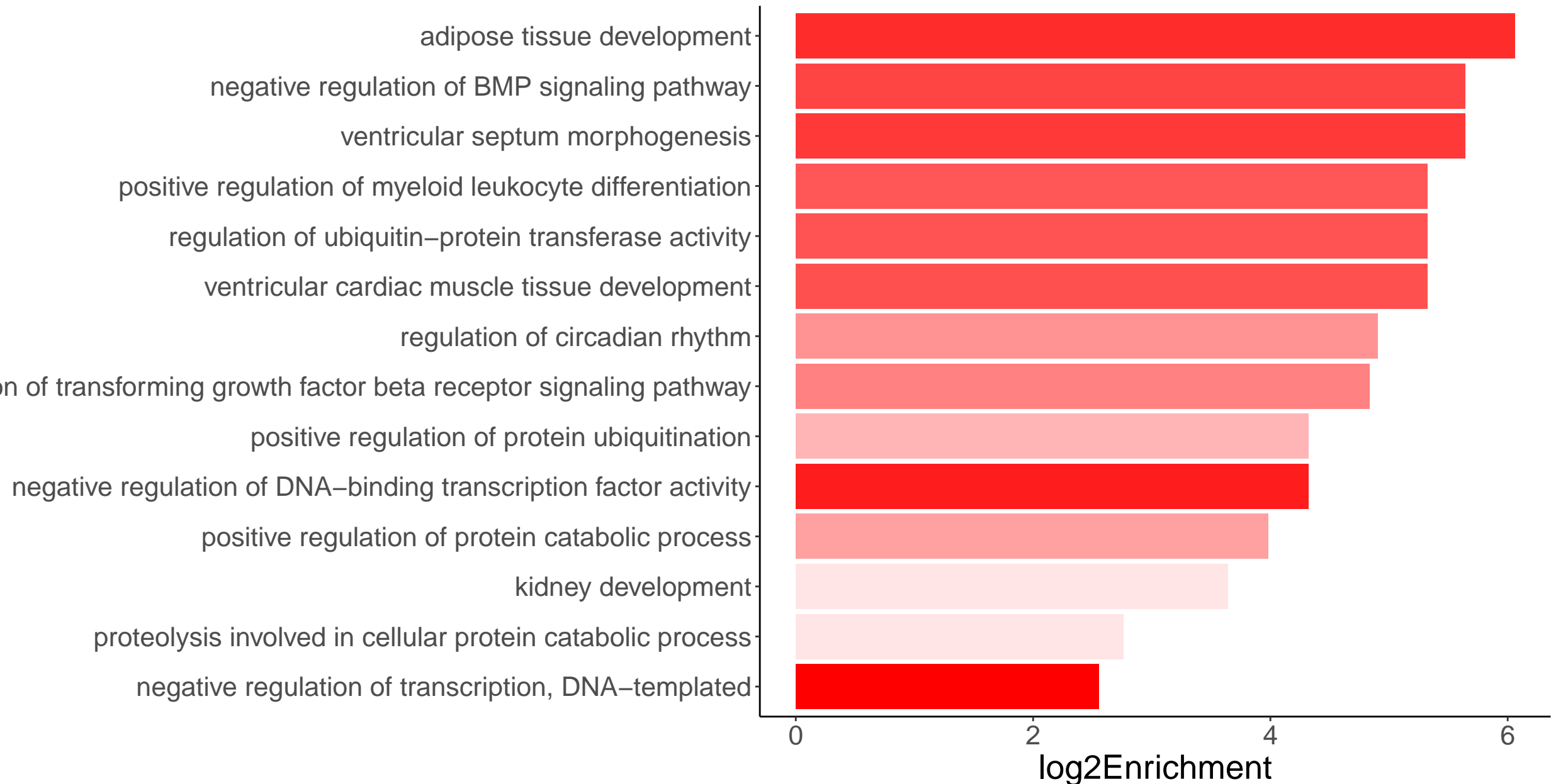
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log2Enrichment



Re-clustered module 16.16.9 BP enrichment

Term



Re-clustered module 16.16.9 MF enrichment

Term

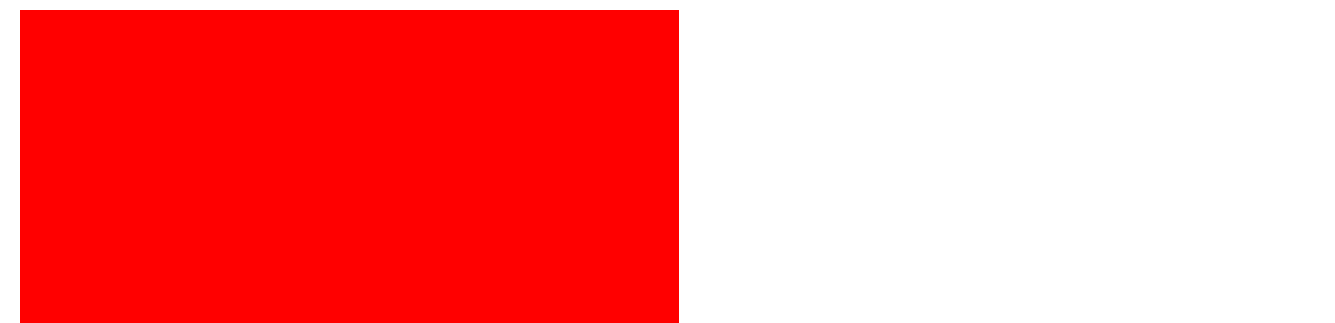
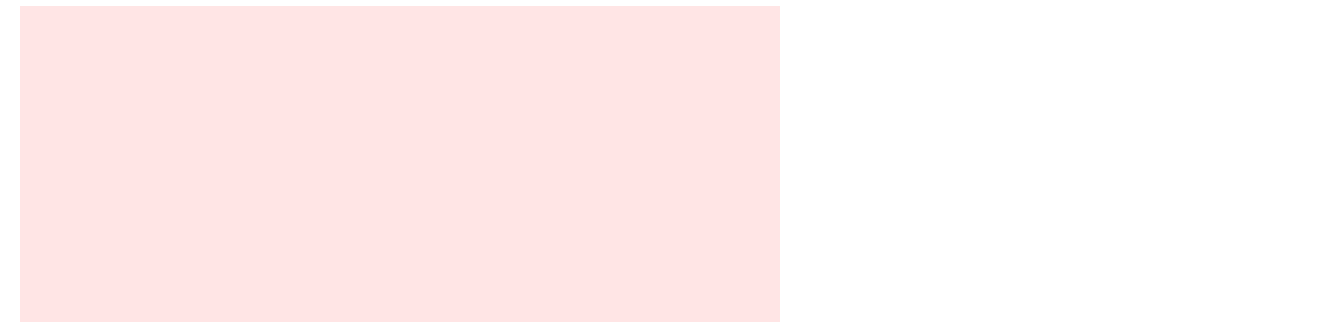
SMAD binding

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

cis-regulatory region sequence-specific DNA binding

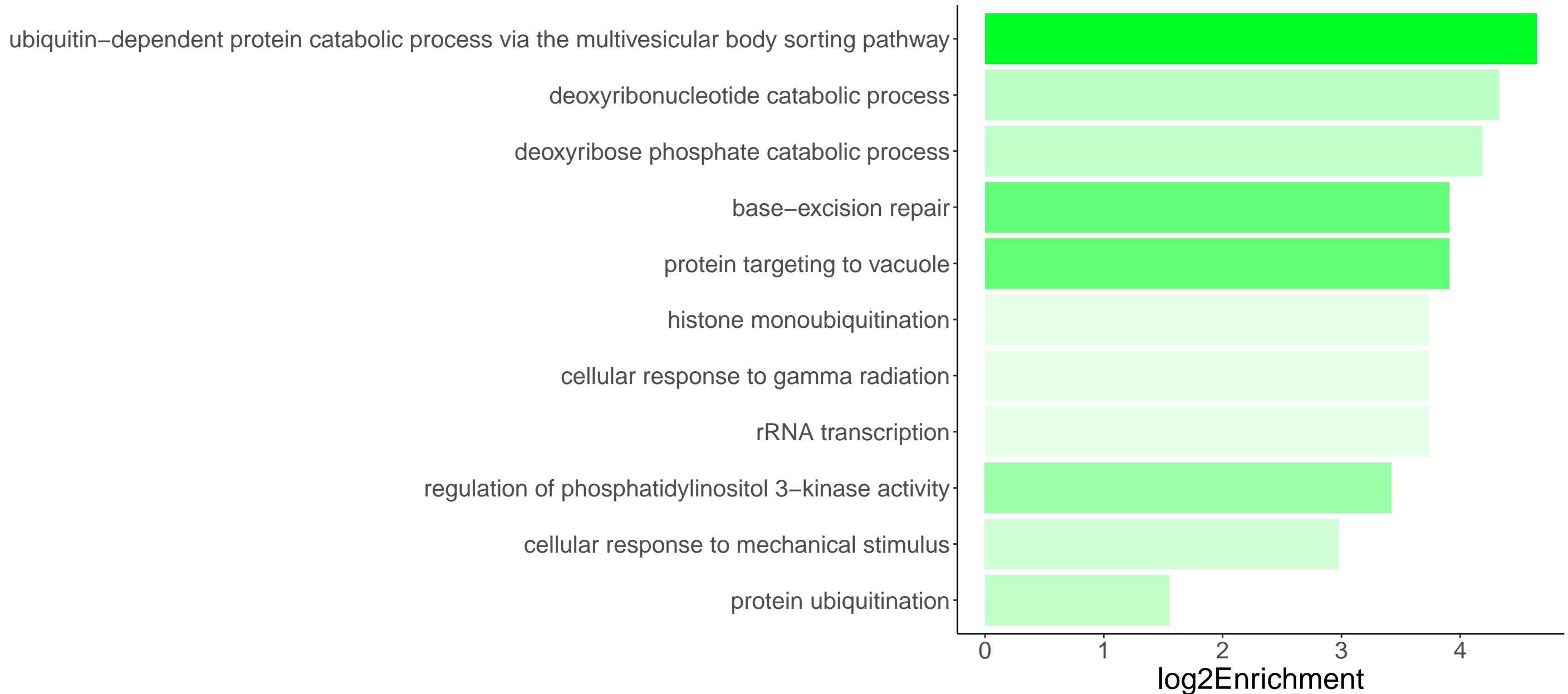
0 1 2 3 4 5

log2Enrichment



Re-clustered module 16.17 BP enrichment

Term



Re-clustered module 16.17 MF enrichment

Term

sphingolipid binding

phosphatidylinositol-4-phosphate binding

ubiquitin-protein transferase activity

0

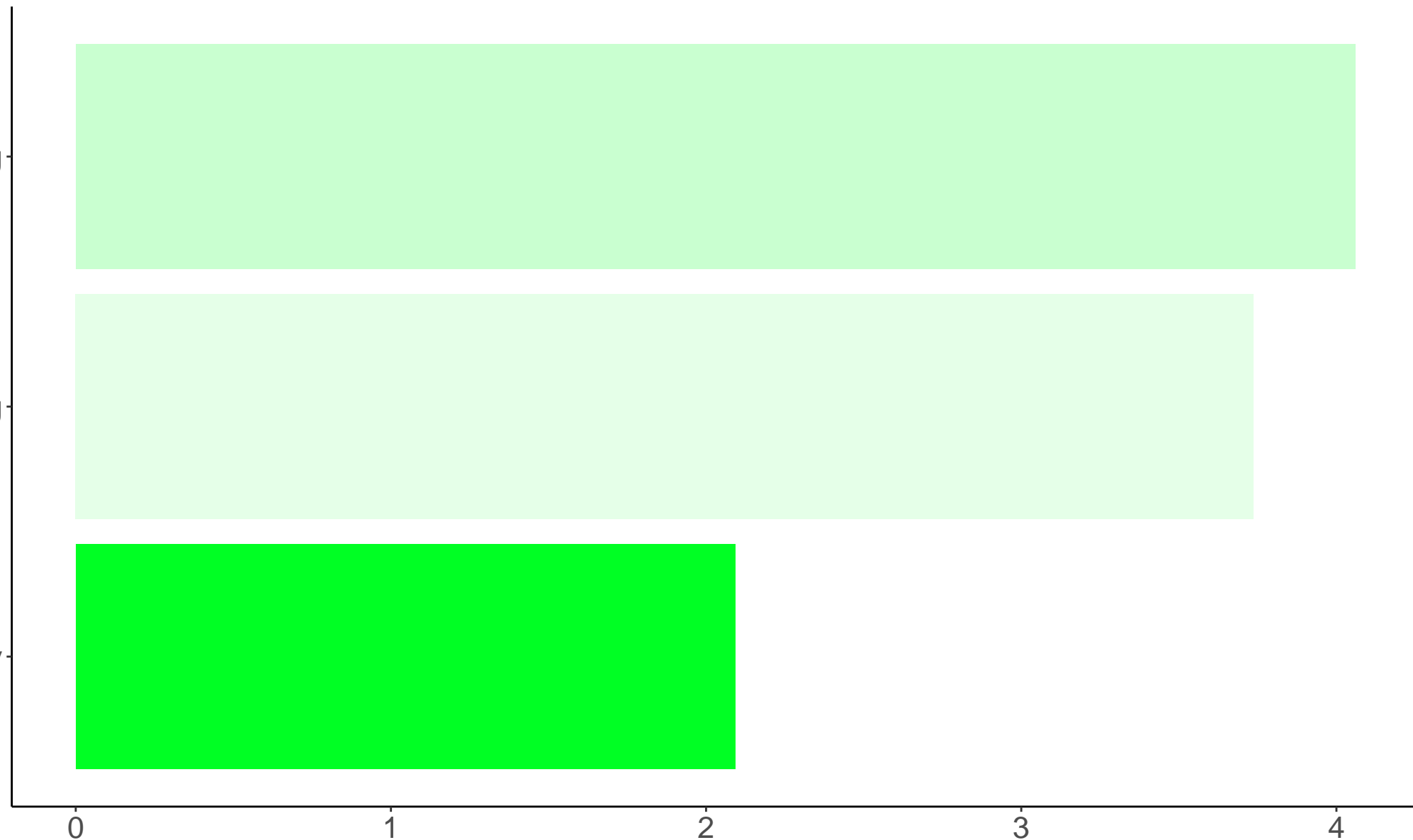
1

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log2Enrichment



Re-clustered module 16.18 BP enrichment

Term

cartilage development involved in endochondral bone morphogenesis

positive regulation of excitatory postsynaptic potential

neuromuscular process controlling balance

learning

0

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4

log2Enrichment



Re-clustered module 16.18 MF enrichment

Term

ionotropic glutamate receptor binding

SNAP receptor activity

0

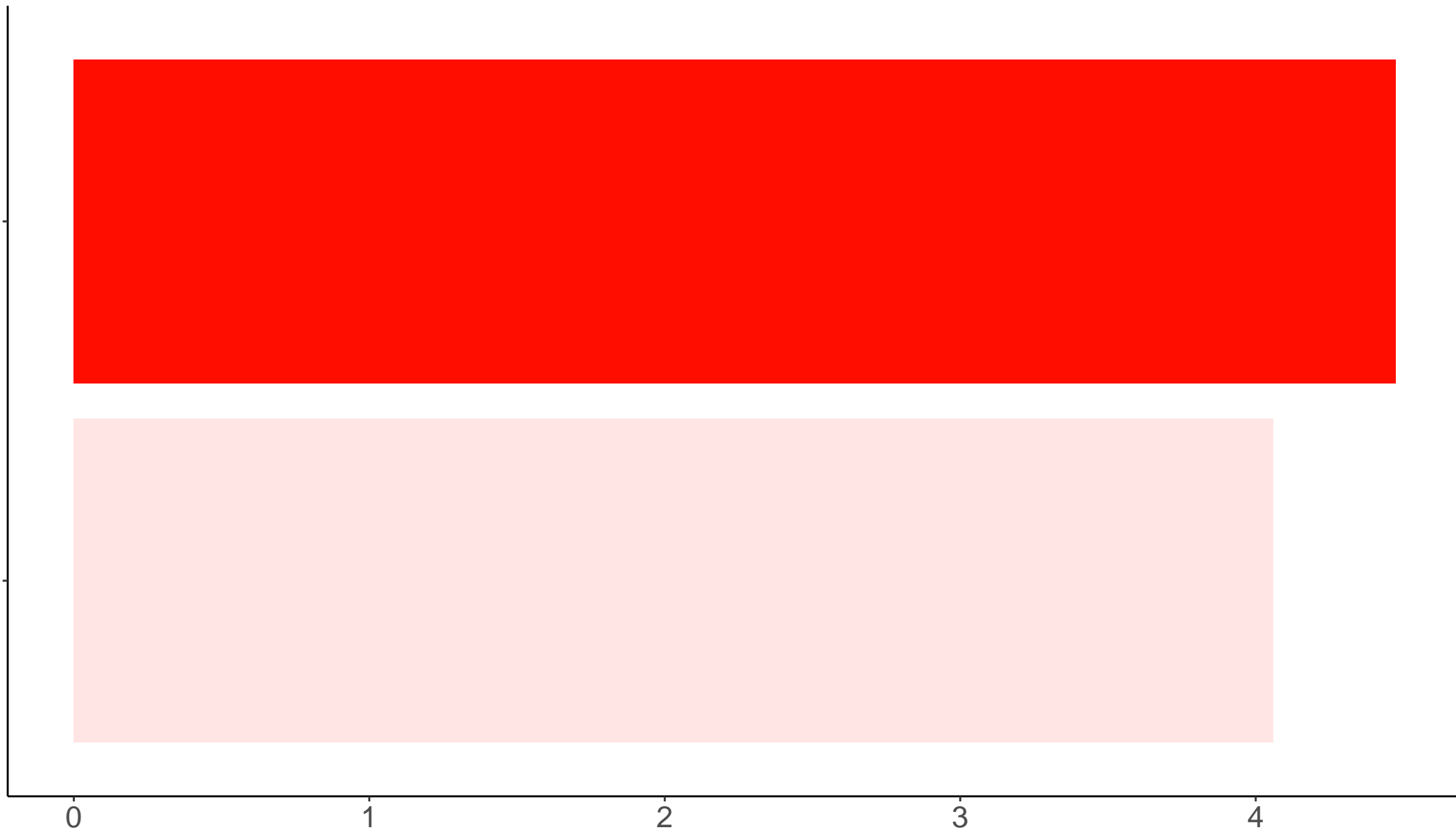
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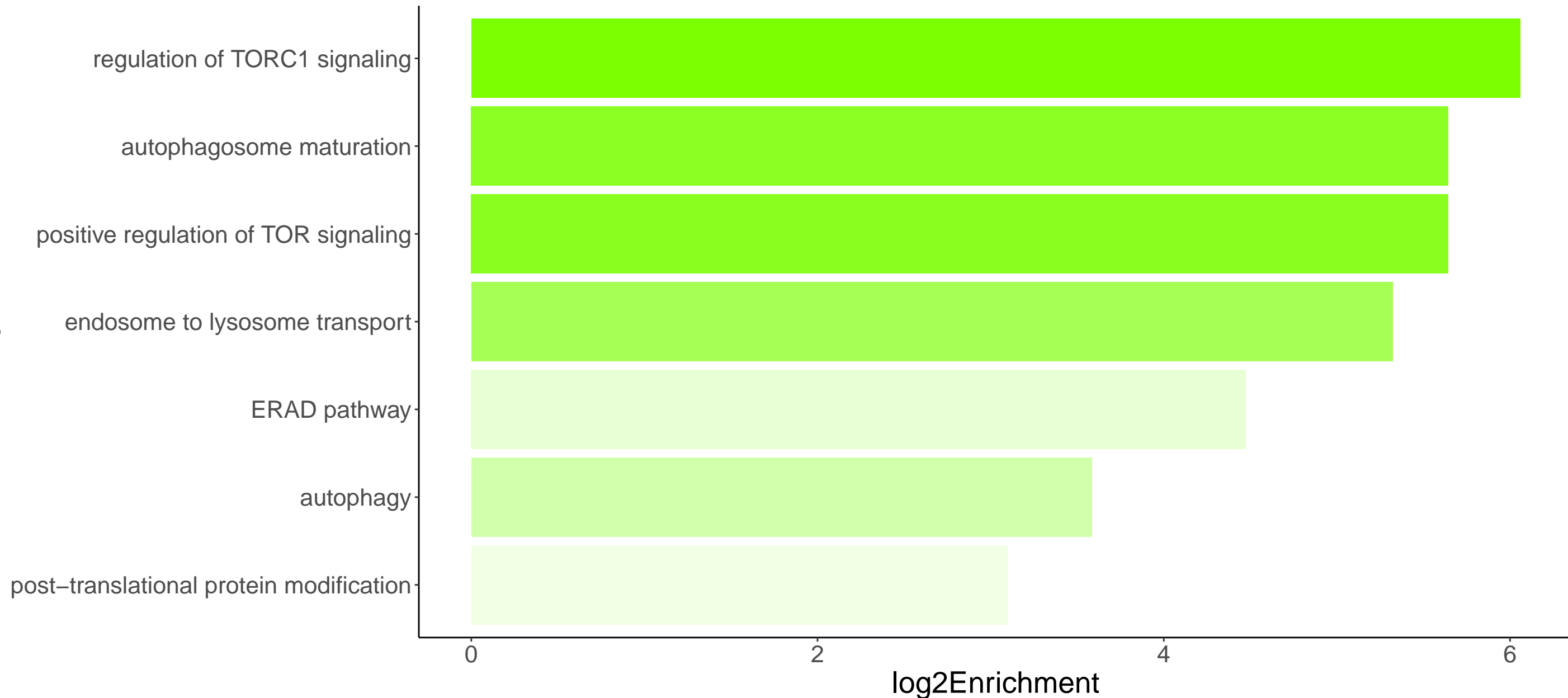
4

log2Enrichment



Re-clustered module 16.19.1 BP enrichment

Term



Re-clustered module 16.19.1 MF enrichment

Term

log2Enrichment



Re-clustered module 16.19.11 BP enrichment

Term

phosphatidylinositol 3-kinase signaling

response to mechanical stimulus

positive regulation of DNA-binding transcription factor activity

inflammatory response

0

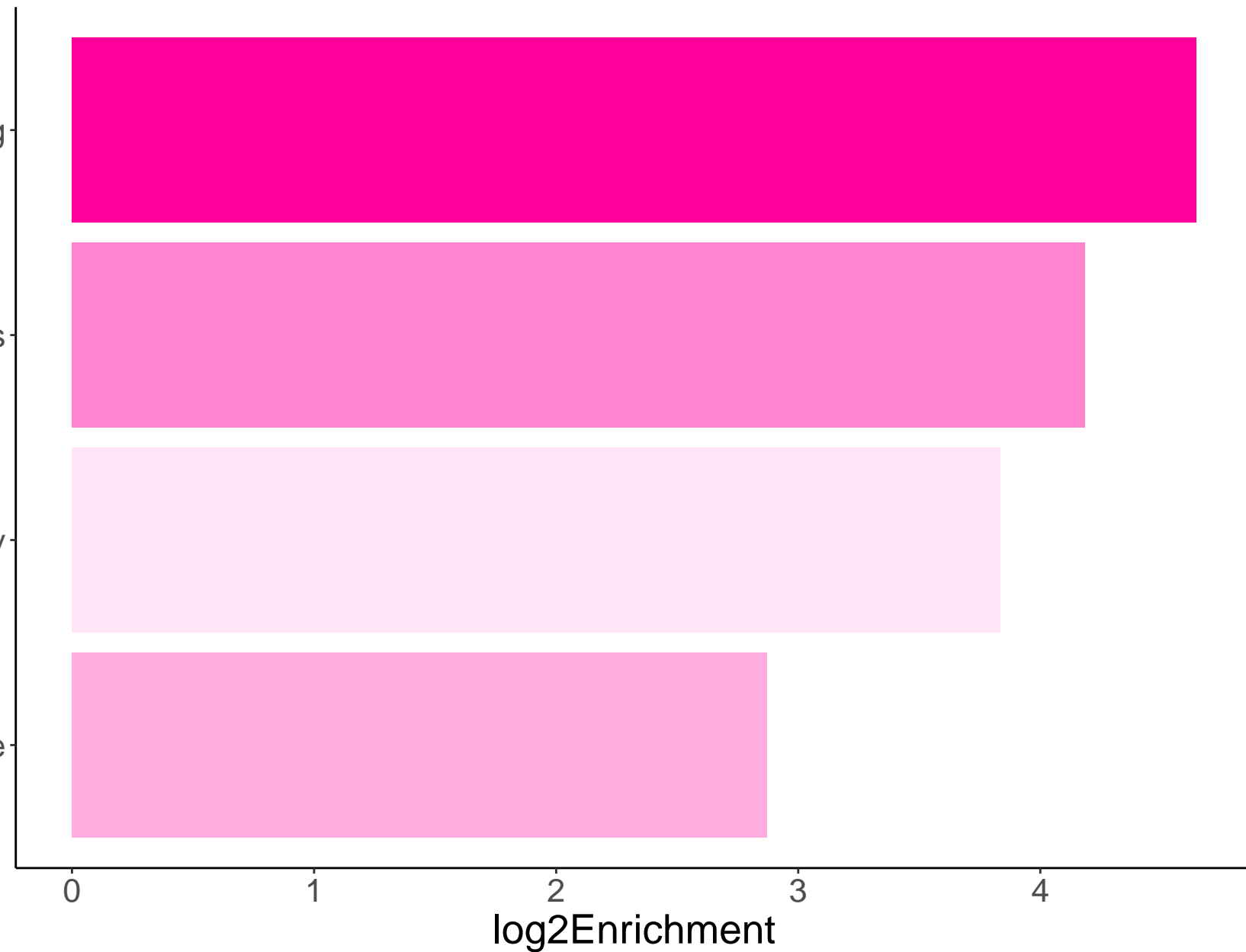
1

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log2Enrichment



Re-clustered module 16.19.11 MF enrichment

Term

log2Enrichment



Re-clustered module 16.19.12 BP enrichment

Term

log2Enrichment



Re-clustered module 16.19.12 MF enrichment

Term

PDZ domain binding

transcription corepressor activity

0

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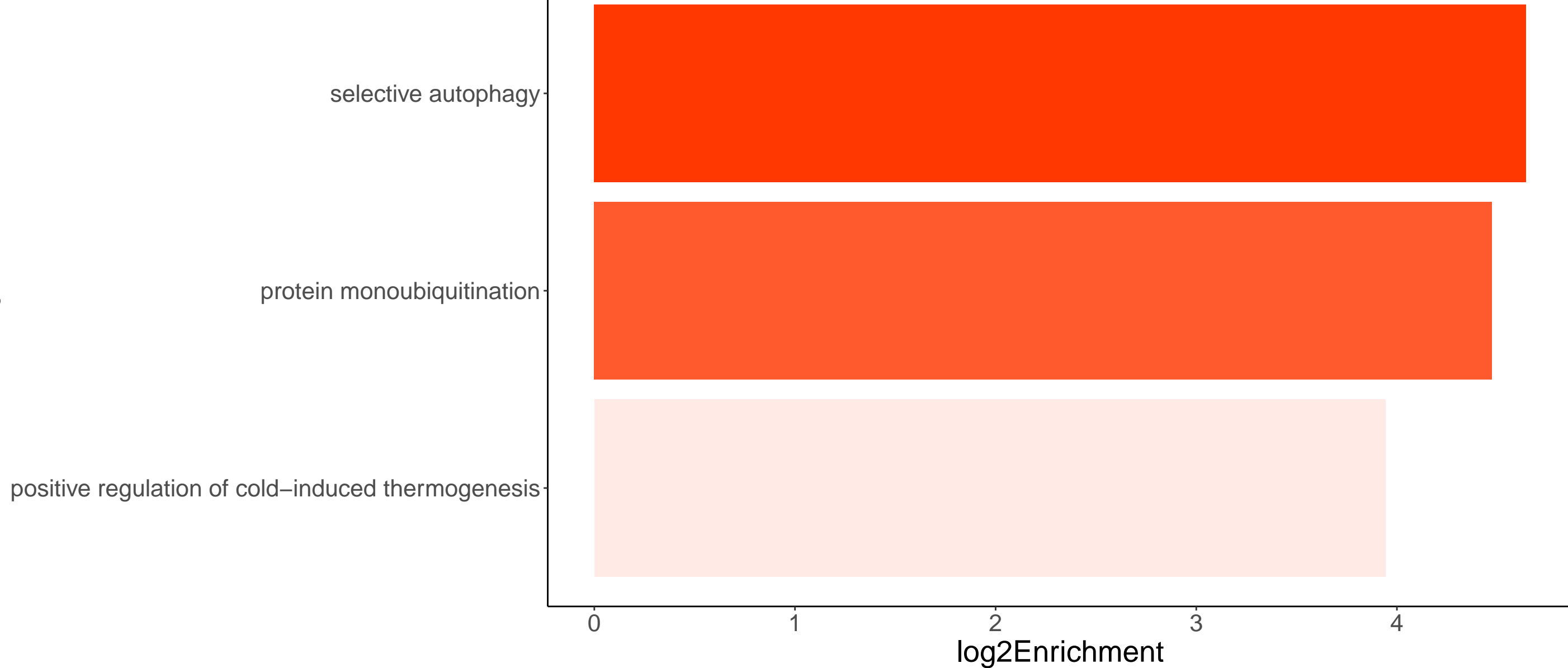
5

log2Enrichment



Re-clustered module 16.19.2 BP enrichment

Term



Re-clustered module 16.19.2 MF enrichment

Term

GTPase activity

0

1

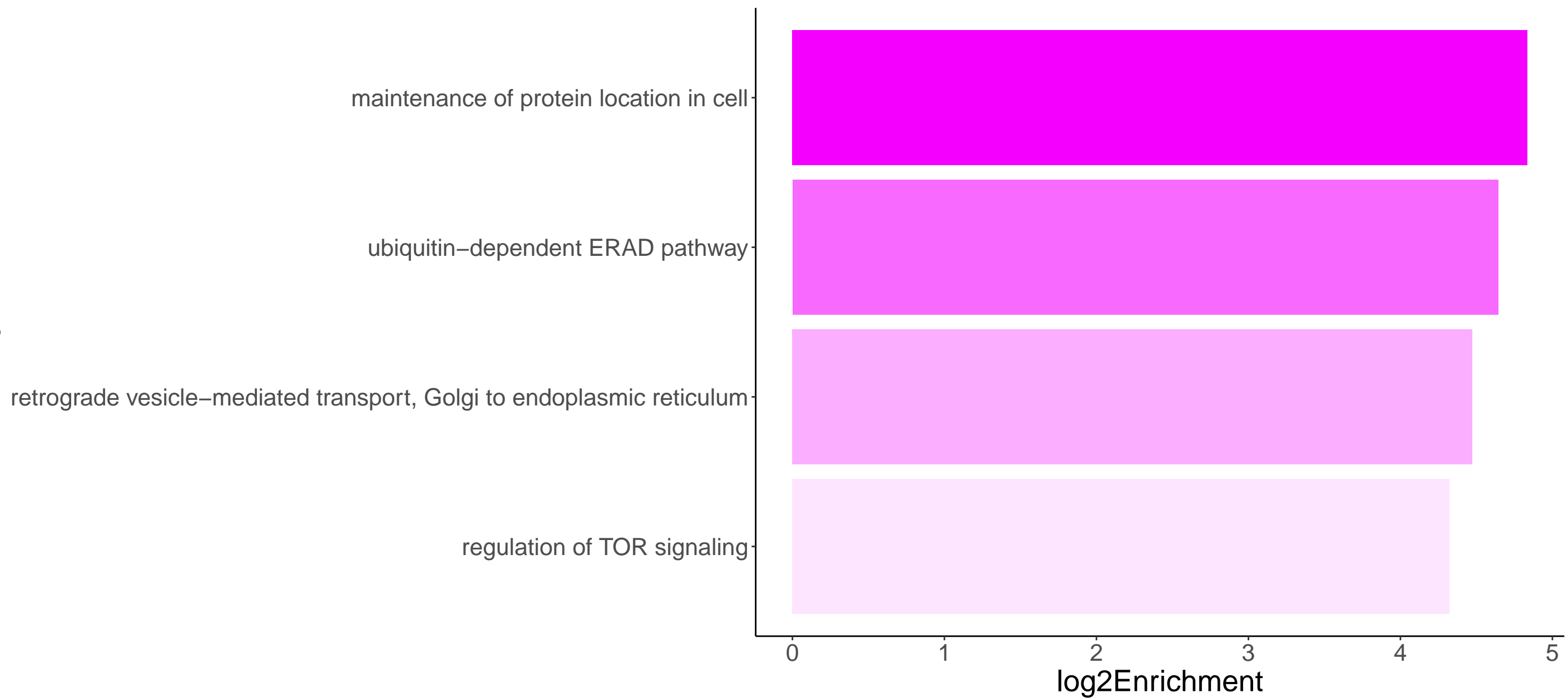
2

log2Enrichment



Re-clustered module 16.19.3 BP enrichment

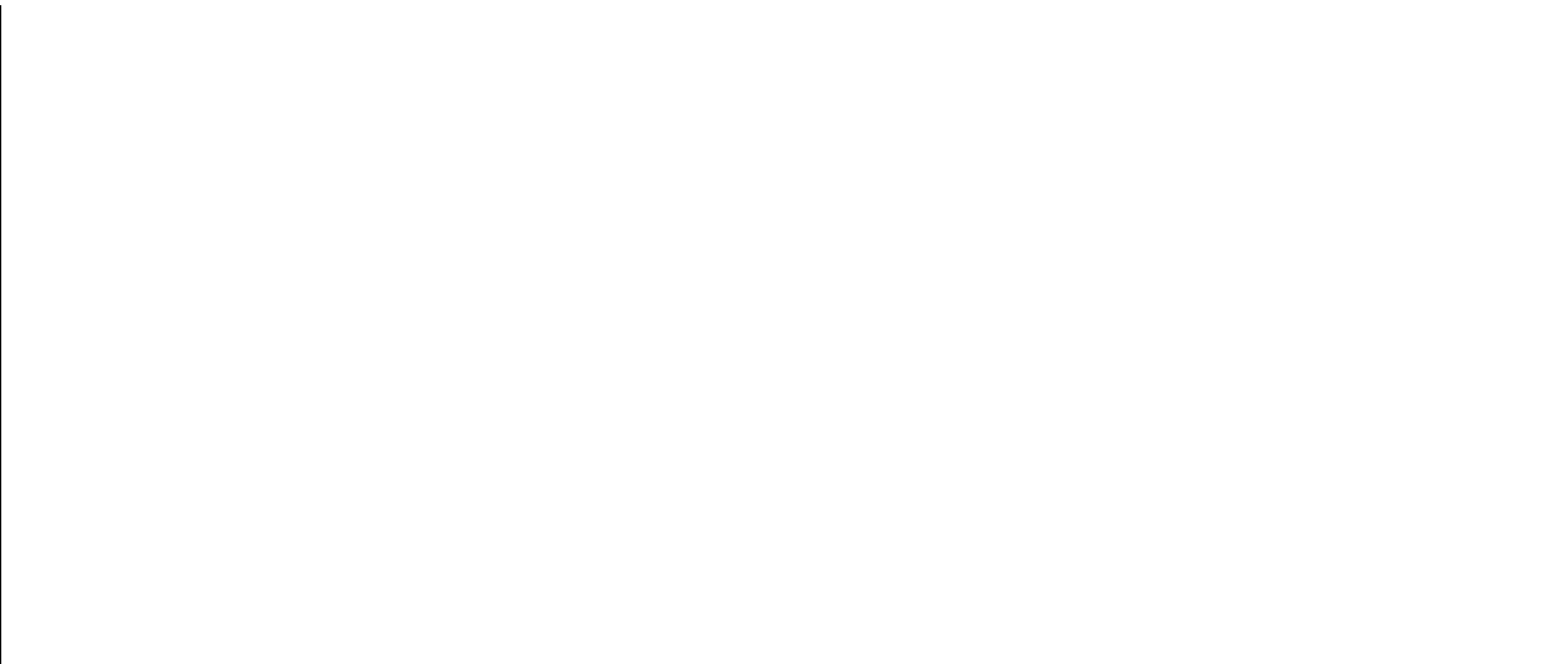
Term



Re-clustered module 16.19.3 MF enrichment

Term

log2Enrichment



Re-clustered module 16.19.4 BP enrichment

Term

regulation of phospholipid metabolic process

negative regulation of transcription, DNA-templated

0

1

2

3

4

log2Enrichment



Re-clustered module 16.19.4 MF enrichment

Term

log2Enrichment



Re-clustered module 16.19.5 BP enrichment

Term

histone demethylation

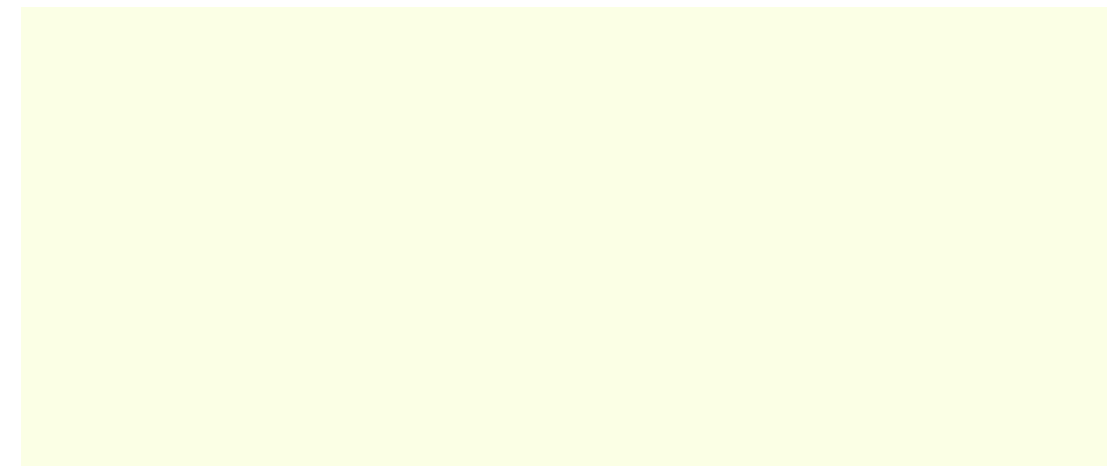
negative regulation of epidermal growth factor receptor signaling pathway

0

2

4

log2Enrichment



Re-clustered module 16.19.5 MF enrichment

Term

histone demethylase activity

Ran GTPase binding

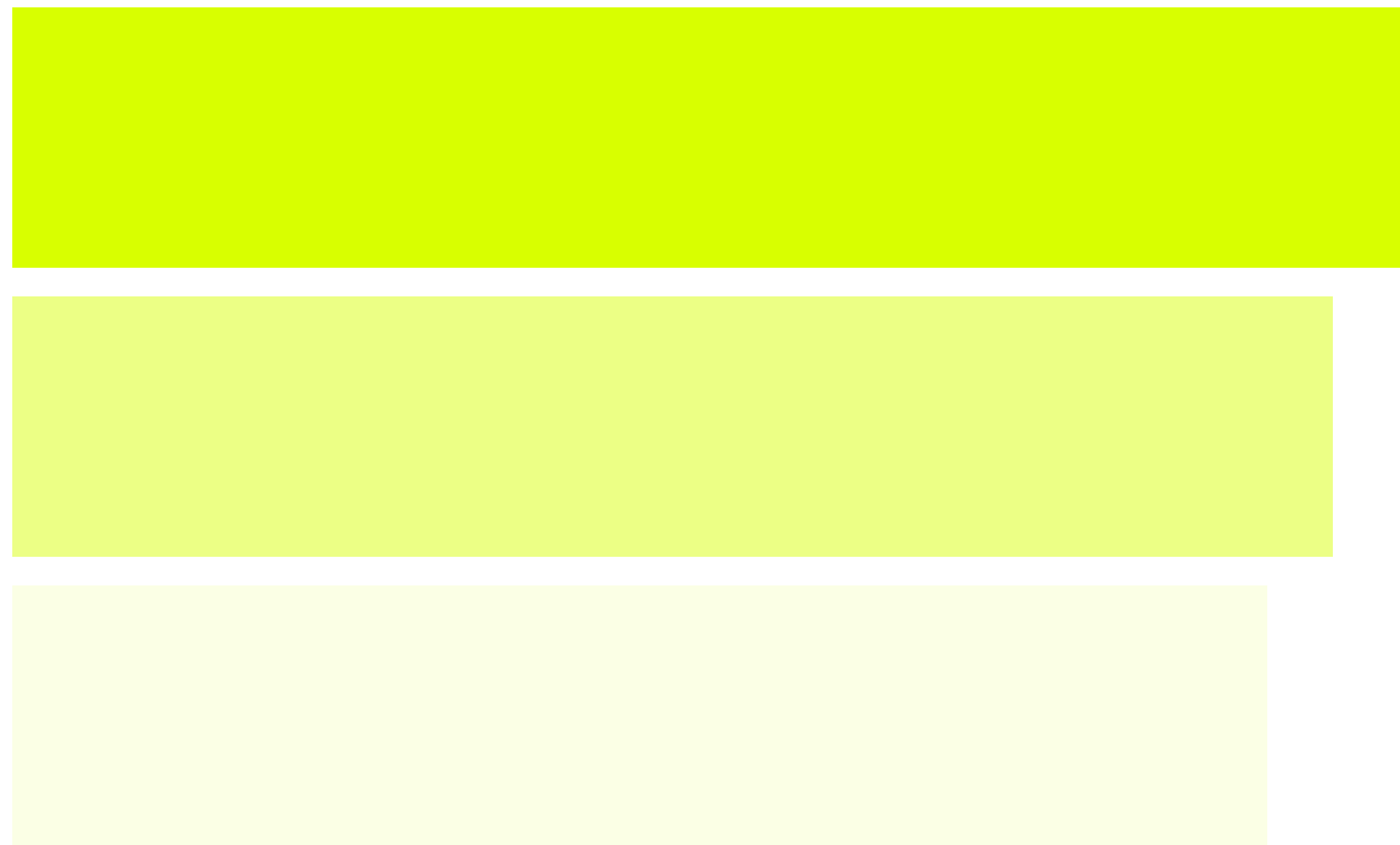
2-oxoglutarate-dependent dioxygenase activity

0

2

4

log2Enrichment



Re-clustered module 16.19.6 BP enrichment

Term

mRNA processing

regulation of transcription by RNA polymerase II

0

1

2

3

log2Enrichment



Re-clustered module 16.19.6 MF enrichment

Term transcription coregulator activity

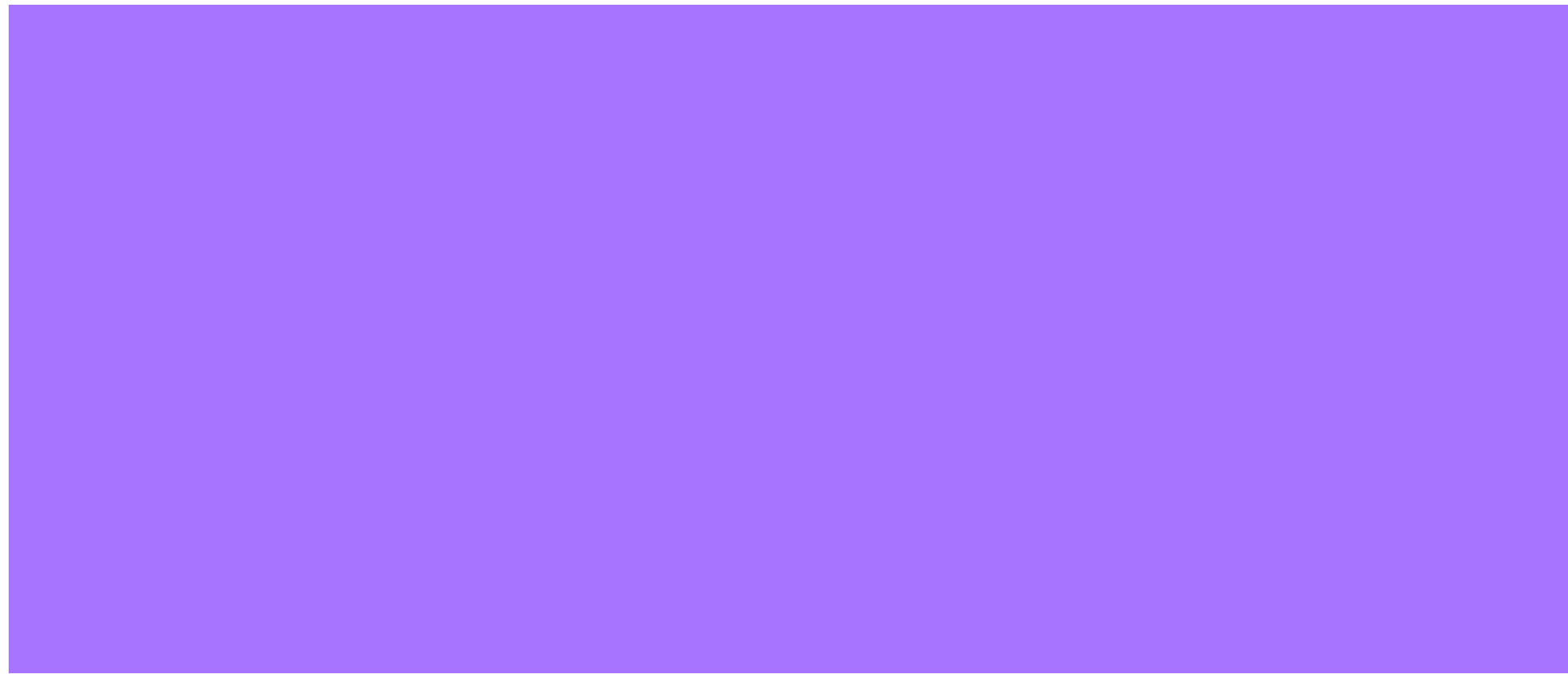
0

1

2

3

log2Enrichment



Re-clustered module 16.19.7 BP enrichment

Term

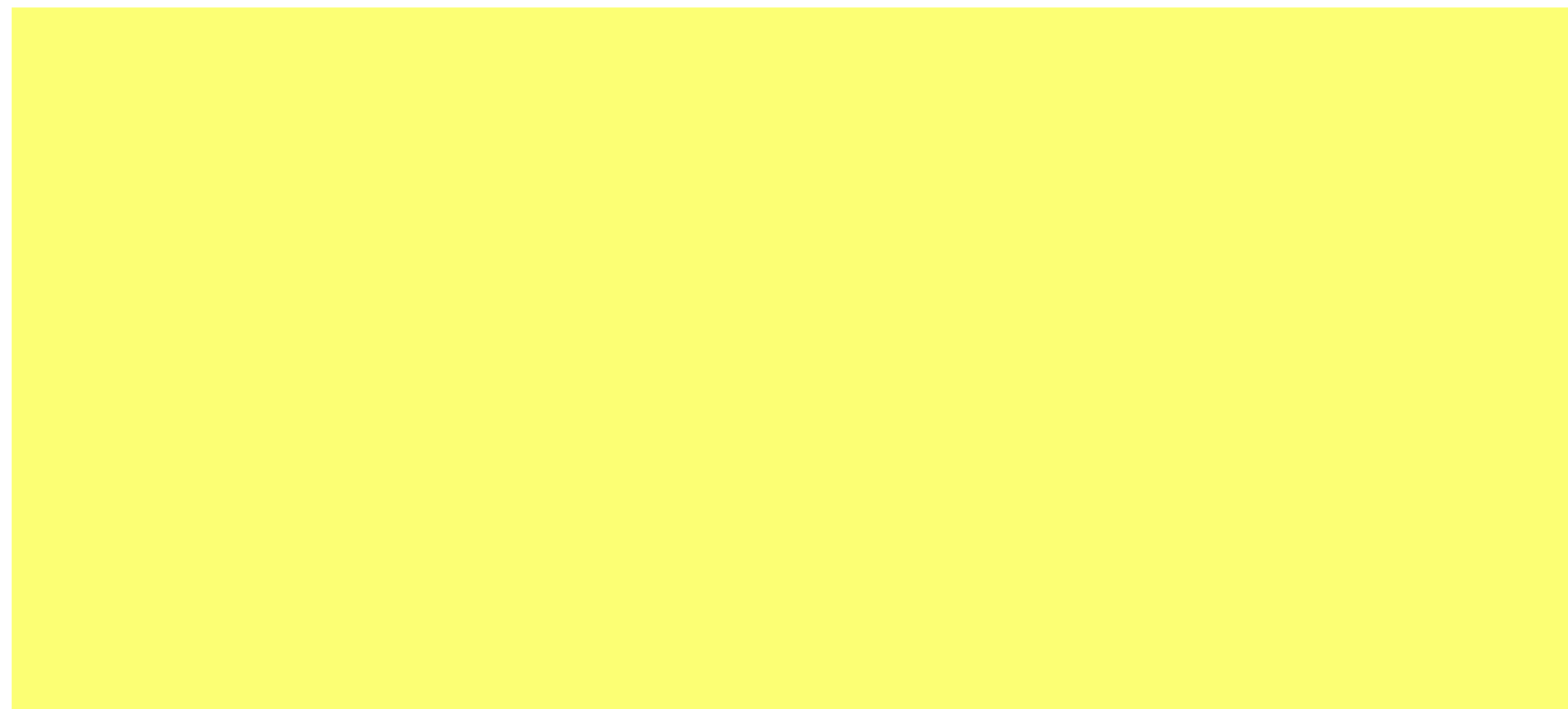
phosphatidylserine metabolic process

0

2

4

log2Enrichment



Re-clustered module 16.19.7 MF enrichment

Term

log2Enrichment



Re-clustered module 16.19.8 BP enrichment

Term

retrograde transport, endosome to Golgi

macroautophagy

cellular response to starvation

regulation of autophagy

0

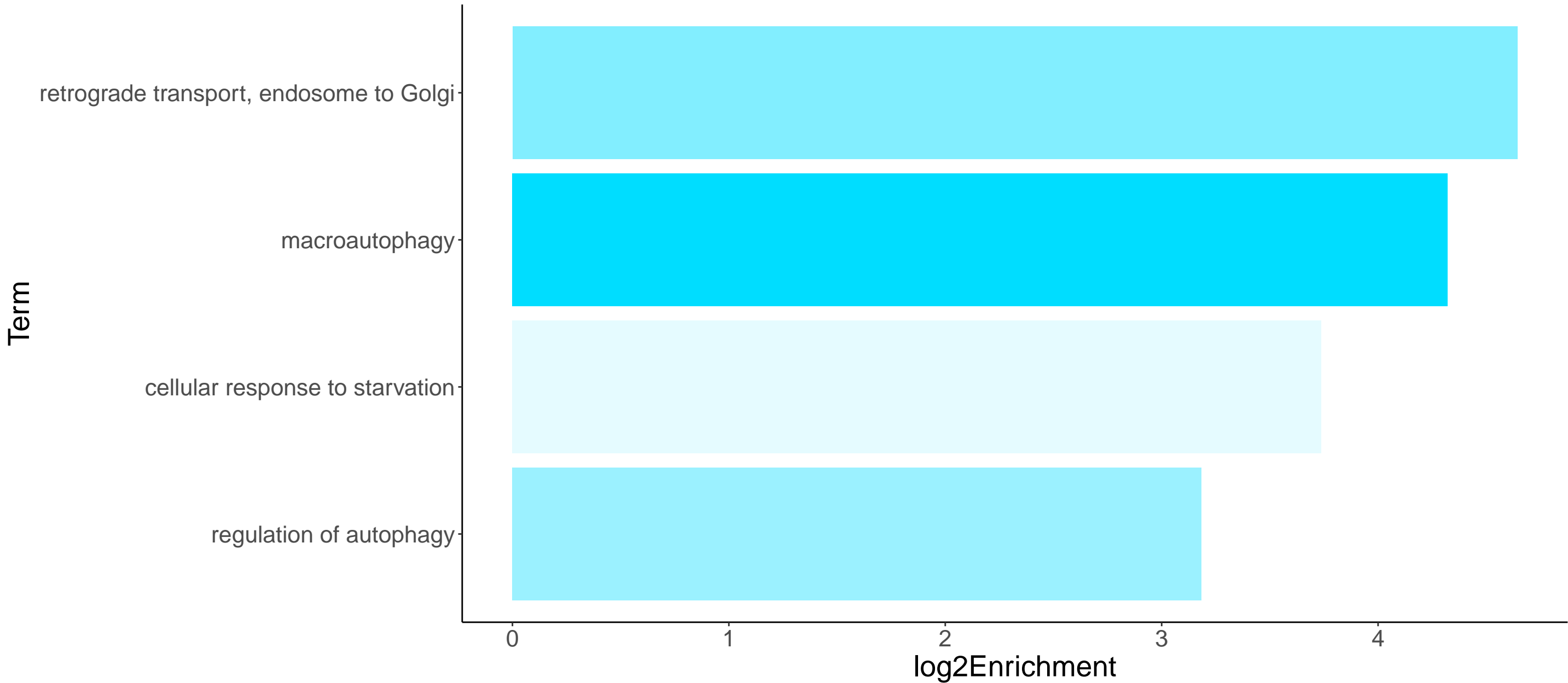
1

2

3

4

log2Enrichment



Re-clustered module 16.19.8 MF enrichment

Term

beta-tubulin binding

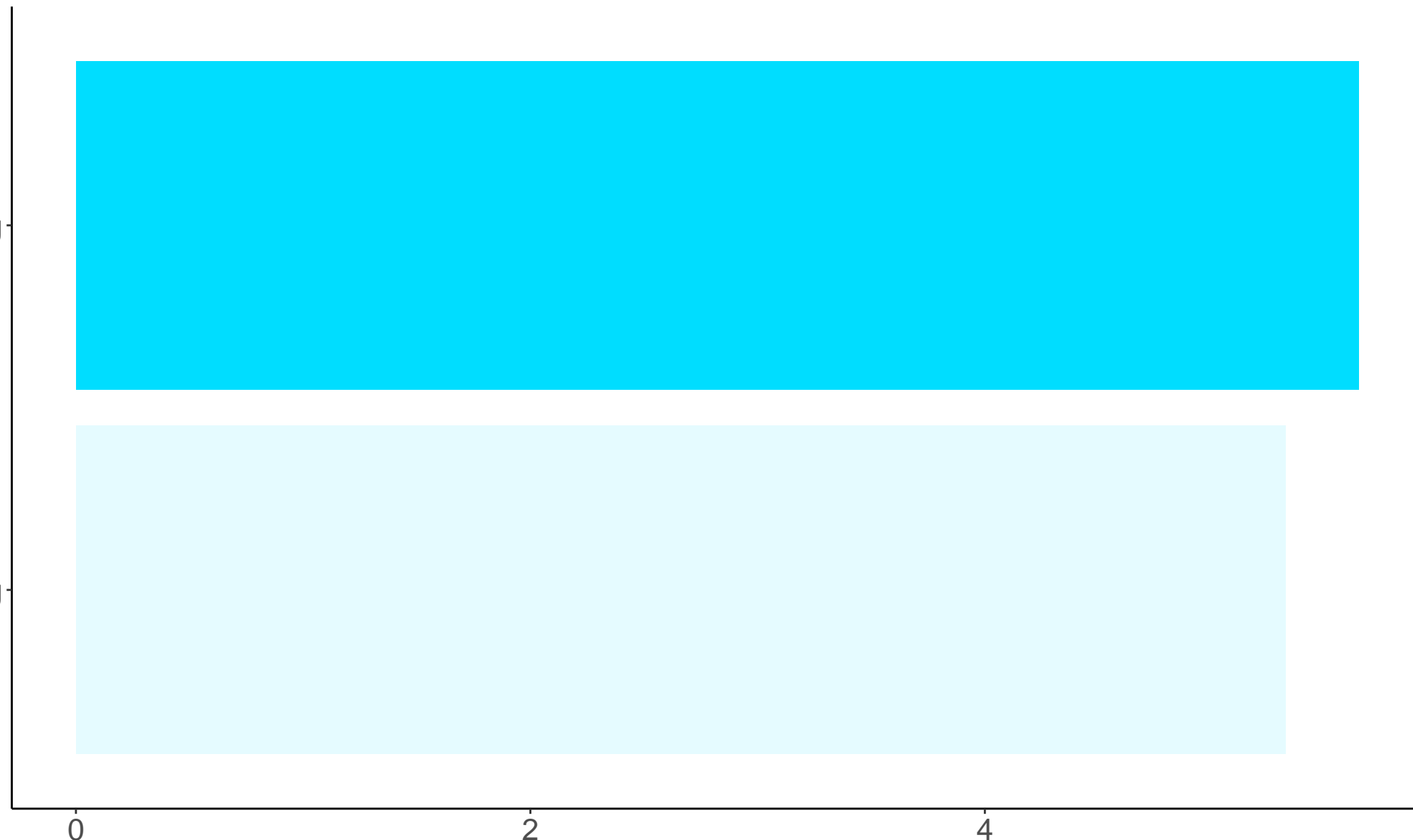
phosphatidylinositol-3-phosphate binding

0

2

4

log2Enrichment



Re-clustered module 16.2.1 BP enrichment

Term

regulation of defense response to virus by virus

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

cytosolic transport

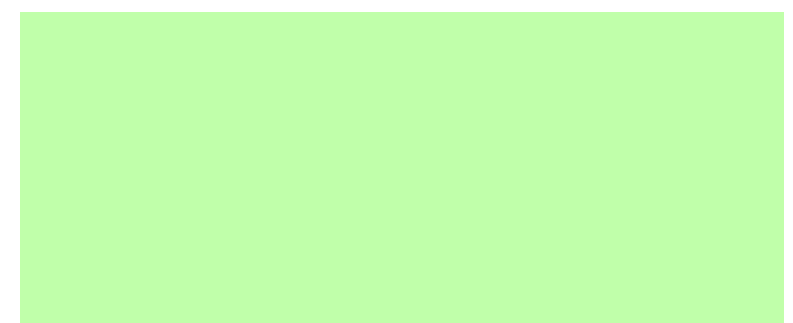
0

2

4

6

log2Enrichment



Re-clustered module 16.2.1 MF enrichment

Term

protein C-terminus binding

protein kinase binding

signaling receptor binding

0

1

2

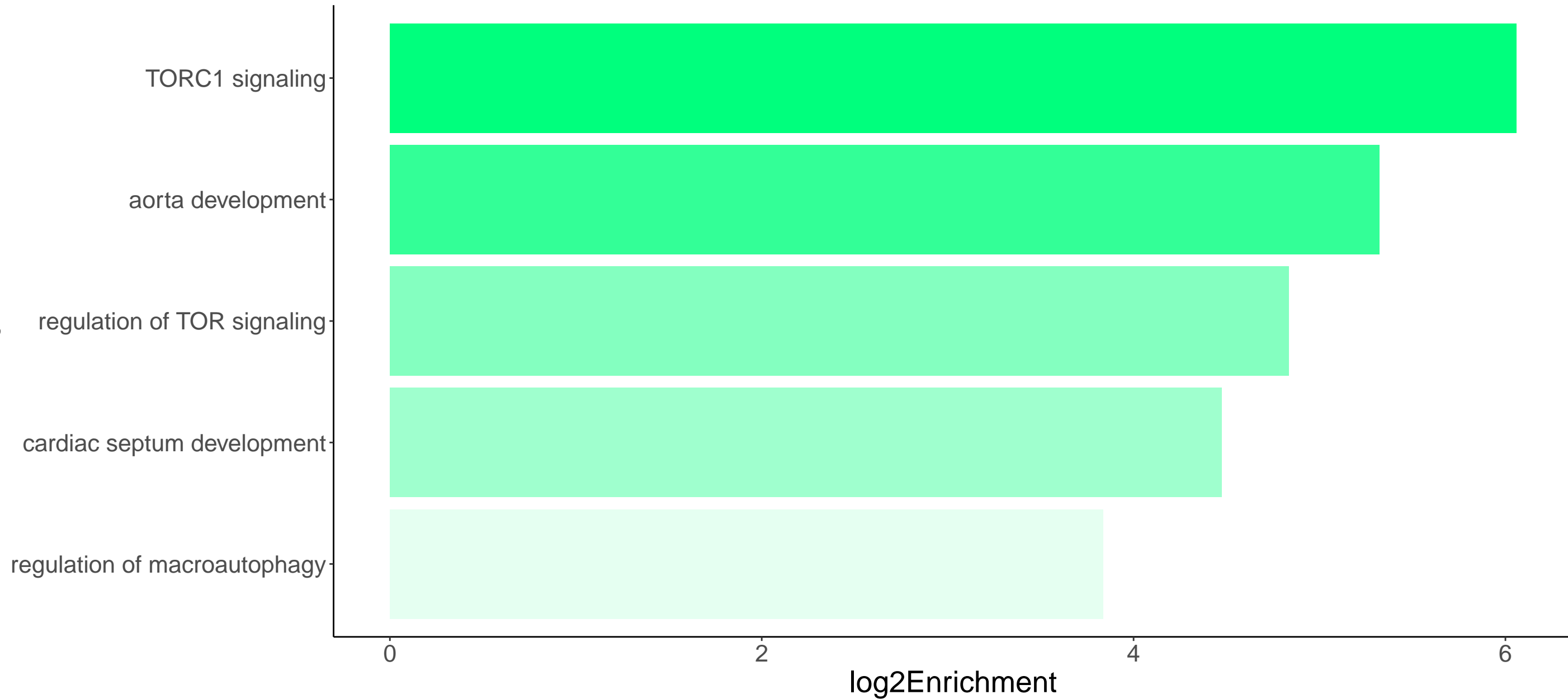
3

log2Enrichment



Re-clustered module 16.2.2 BP enrichment

Term



Re-clustered module 16.2.2 MF enrichment

Term

protein serine/threonine kinase activator activity

0

2

4

6

log2Enrichment



Re-clustered module 16.2.3 BP enrichment

Term regulation of chromatin organization

0

1

2

3

4

log2Enrichment



Re-clustered module 16.2.3 MF enrichment

Term

DNA binding

0.0

0.5

1.0

log2Enrichment



Re-clustered module 16.2.4 BP enrichment

Term

retrograde transport, endosome to Golgi

sterol metabolic process

regulation of macroautophagy

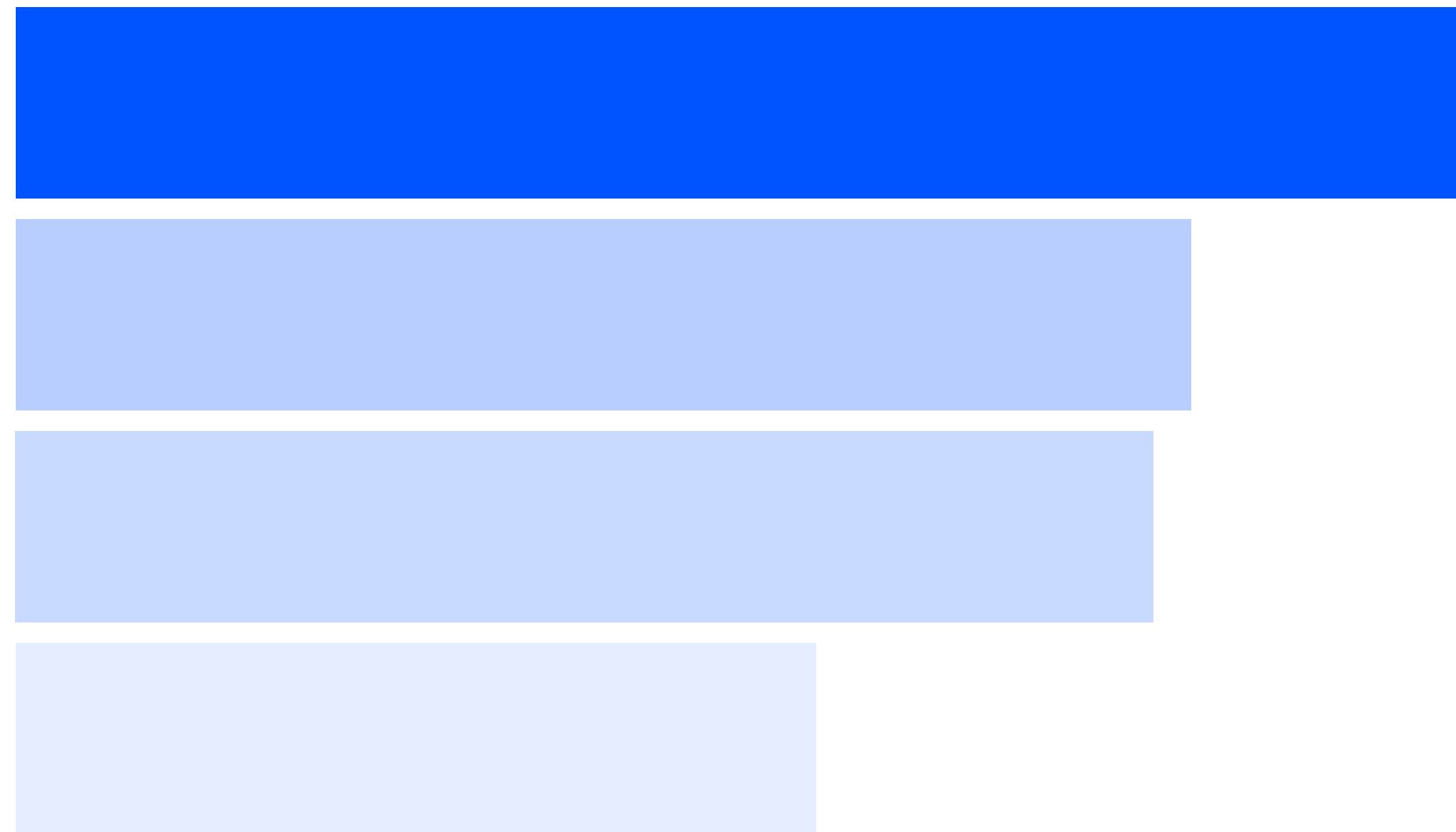
monocarboxylic acid metabolic process

0

2

4

log2Enrichment



Re-clustered module 16.2.4 MF enrichment

Term

log2Enrichment



Re-clustered module 16.2.6 BP enrichment

Term

log2Enrichment



Re-clustered module 16.2.6 MF enrichment

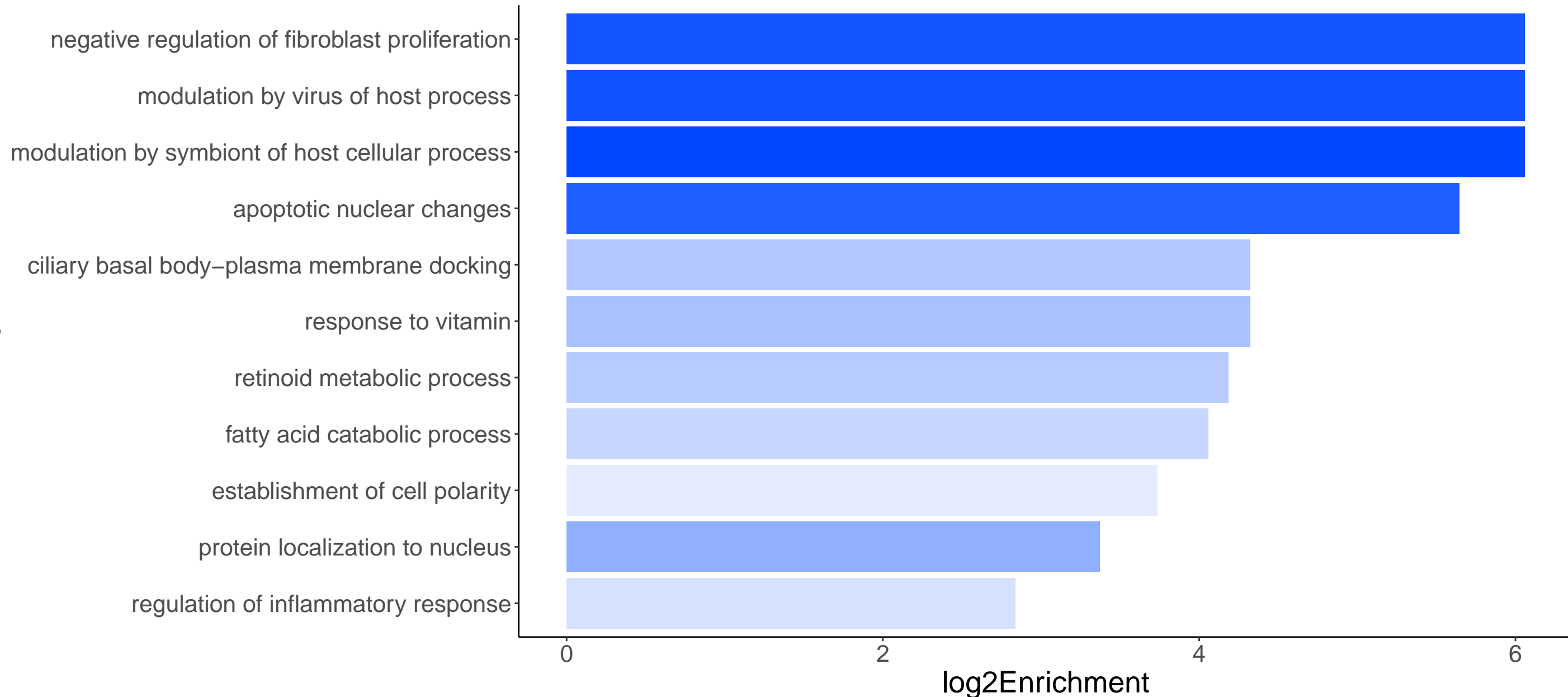
Term

log2Enrichment



Re-clustered module 16.20.1 BP enrichment

Term



Re-clustered module 16.20.1 MF enrichment

Term

nuclear import signal receptor activity

transcription coactivator binding

nuclear localization sequence binding

0

2

4

6

log2Enrichment



Re-clustered module 16.20.12 BP enrichment

Term

log2Enrichment



Re-clustered module 16.20.12 MF enrichment

Term

log2Enrichment



Re-clustered module 16.20.14 BP enrichment

Term

peptidyl-serine dephosphorylation

protein K48-linked deubiquitination

positive regulation of I-kappaB kinase/NF-kappaB signaling

chromosome segregation

ubiquitin-dependent protein catabolic process

cell cycle

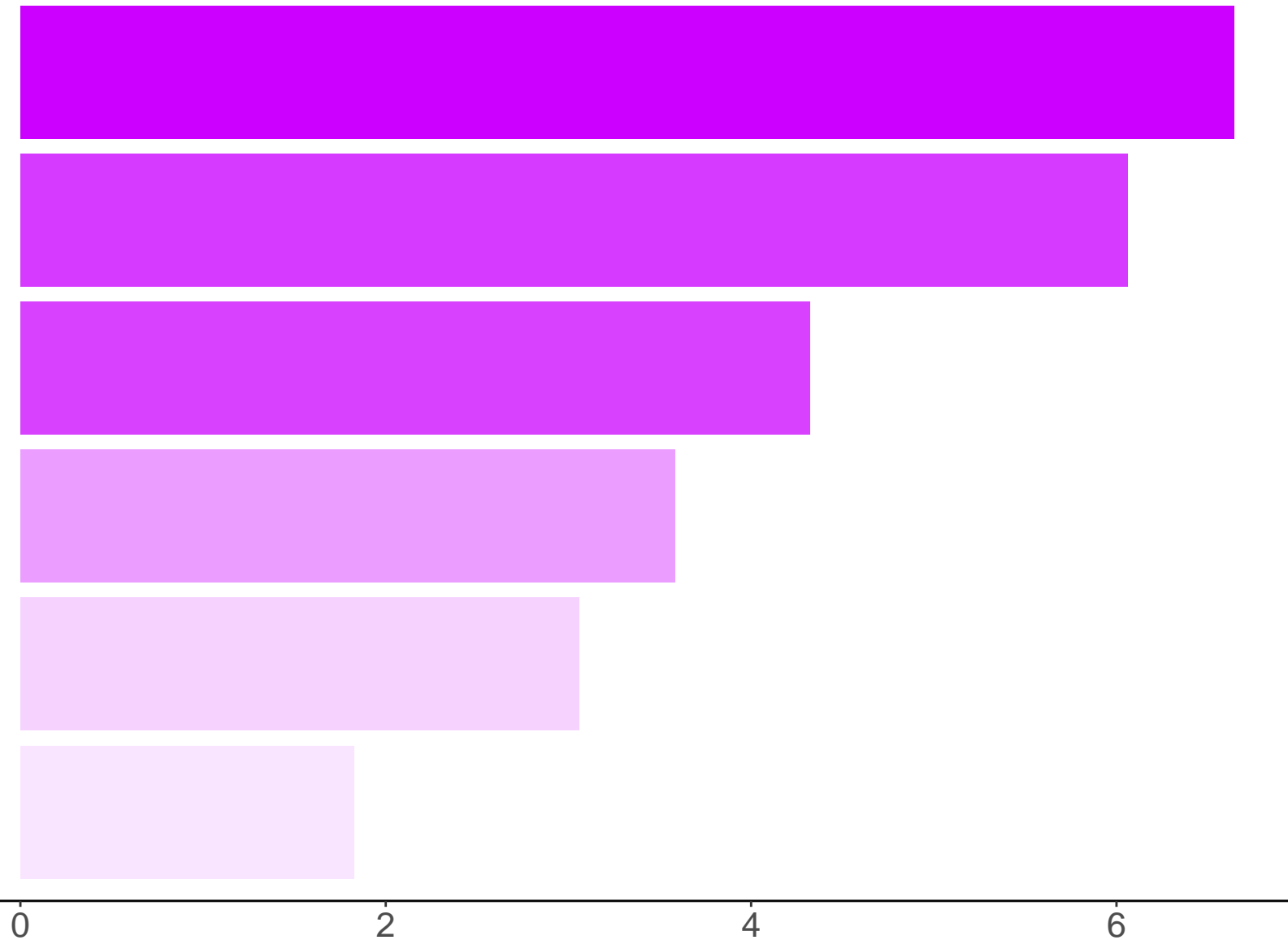
0

2

4

6

log2Enrichment



Re-clustered module 16.20.14 MF enrichment

Term

protein serine/threonine phosphatase activity

thiol-dependent ubiquitin-specific protease activity

cysteine-type peptidase activity

0

2

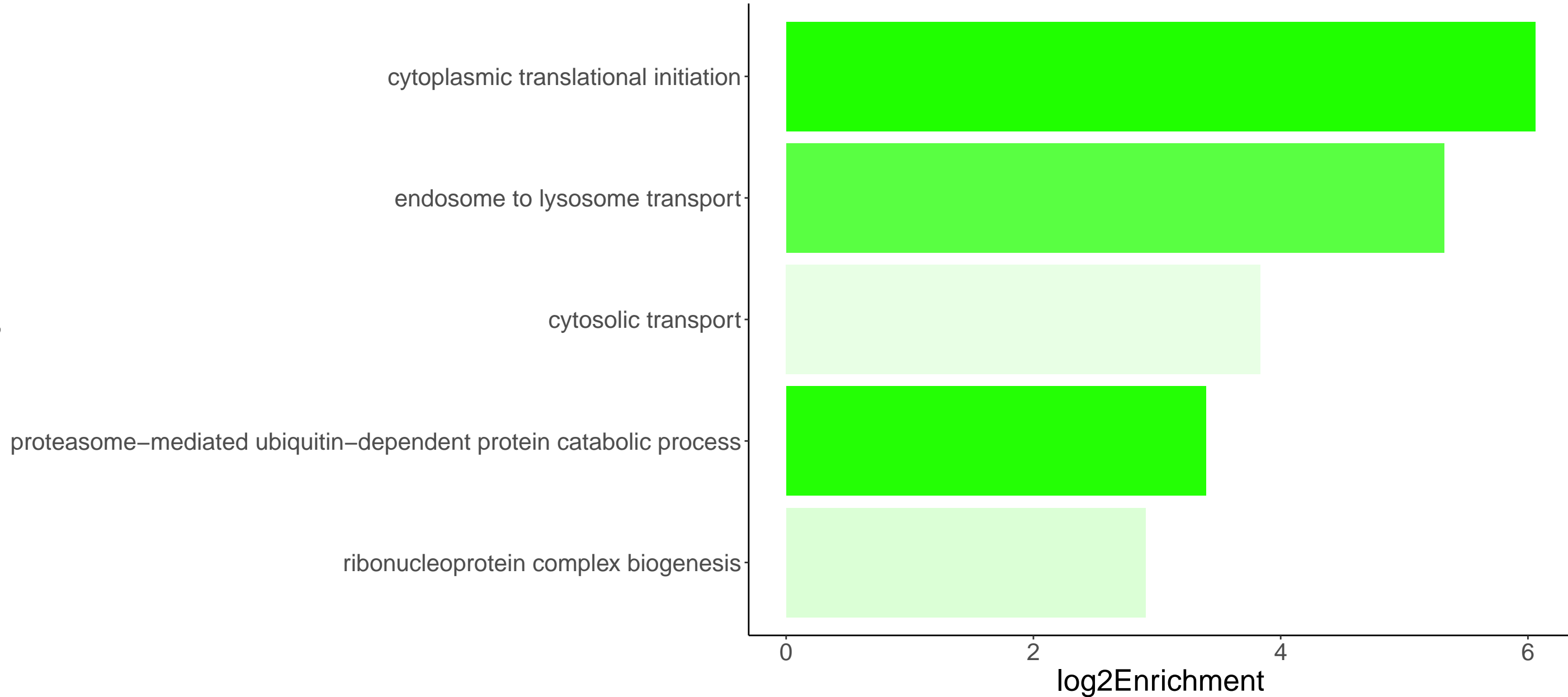
4

log2Enrichment



Re-clustered module 16.20.2 BP enrichment

Term



Re-clustered module 16.20.2 MF enrichment

Term

translation initiation factor activity

ribonucleoprotein complex binding

0

2

4

log2Enrichment



Re-clustered module 16.20.3 BP enrichment

Term

chromatin organization

0.0

0.5

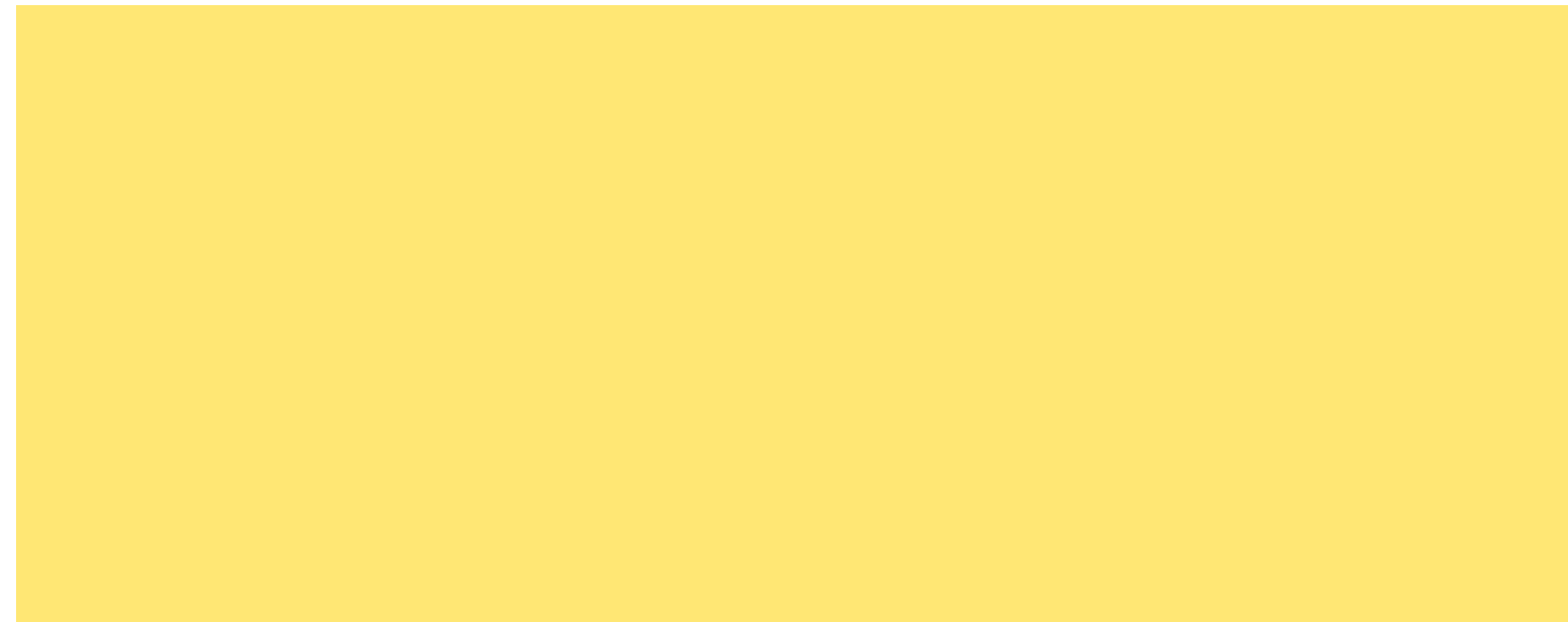
1.0

1.5

2.0

2.5

log2Enrichment



Re-clustered module 16.20.3 MF enrichment

Term

chromatin binding

zinc ion binding

0

1

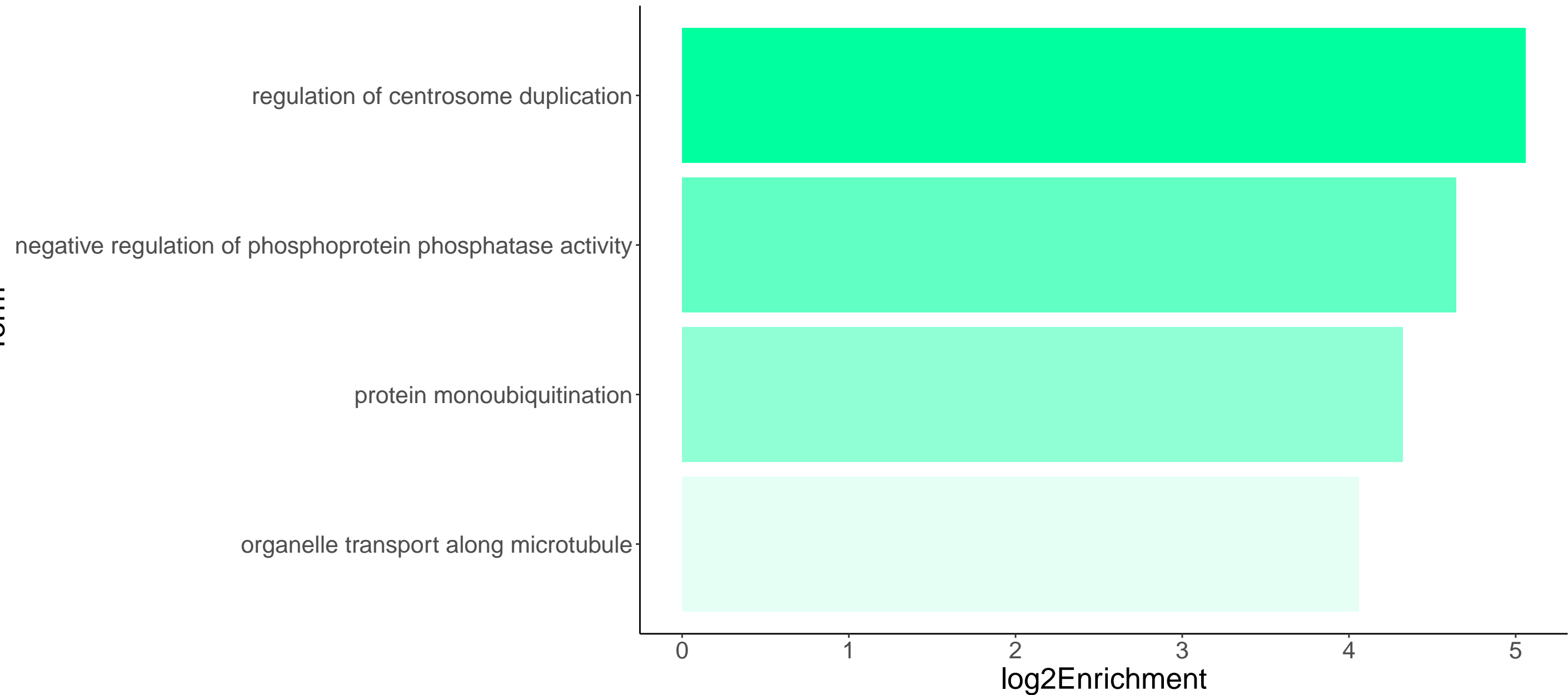
2

log2Enrichment



Re-clustered module 16.20.4 BP enrichment

Term



Re-clustered module 16.20.4 MF enrichment

Term

protein phosphatase 2A binding

protein phosphatase inhibitor activity

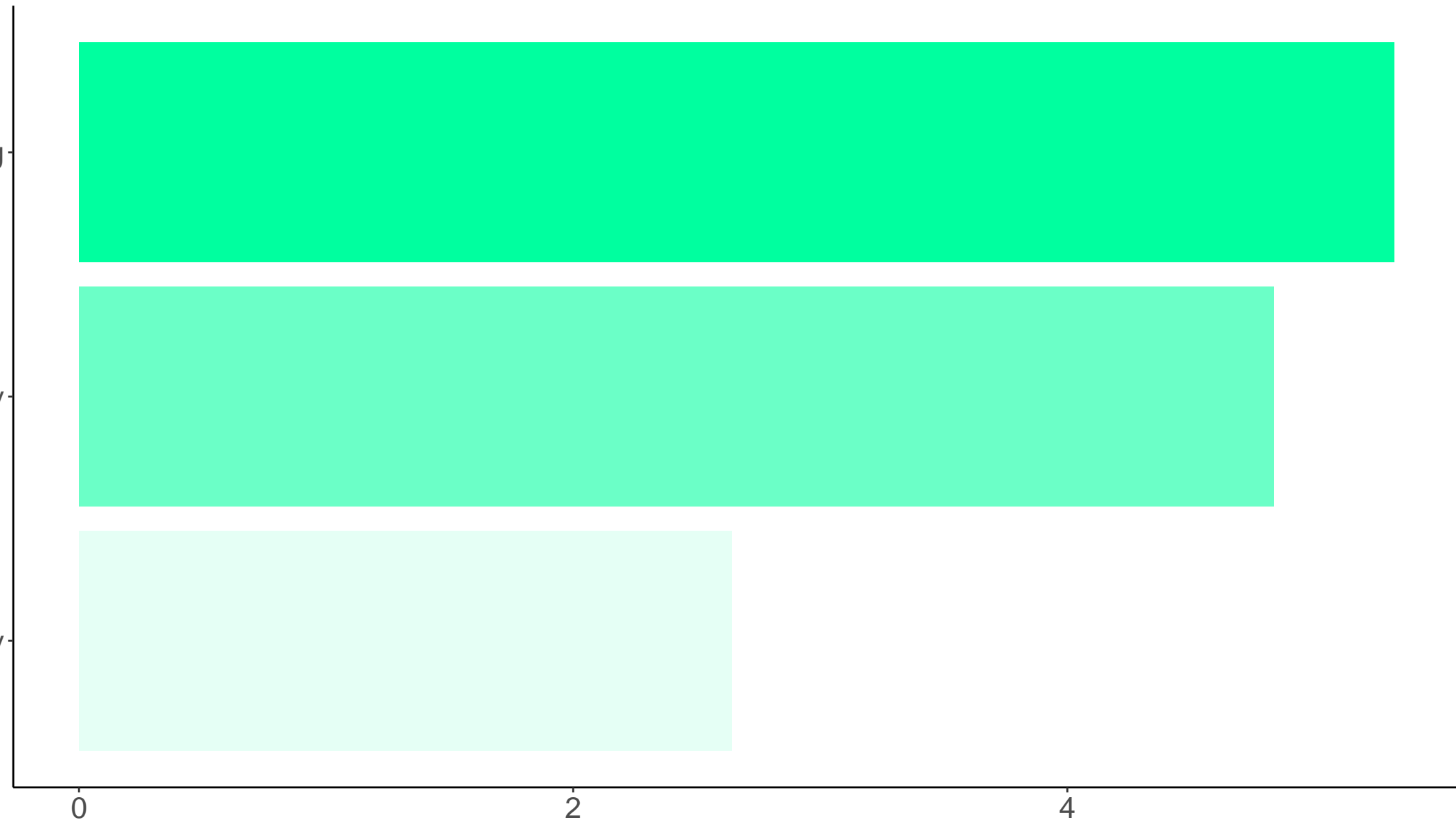
ubiquitin-protein transferase activity

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2

4

log2Enrichment



Re-clustered module 16.20.5 BP enrichment

Term

positive regulation of apoptotic signaling pathway

0

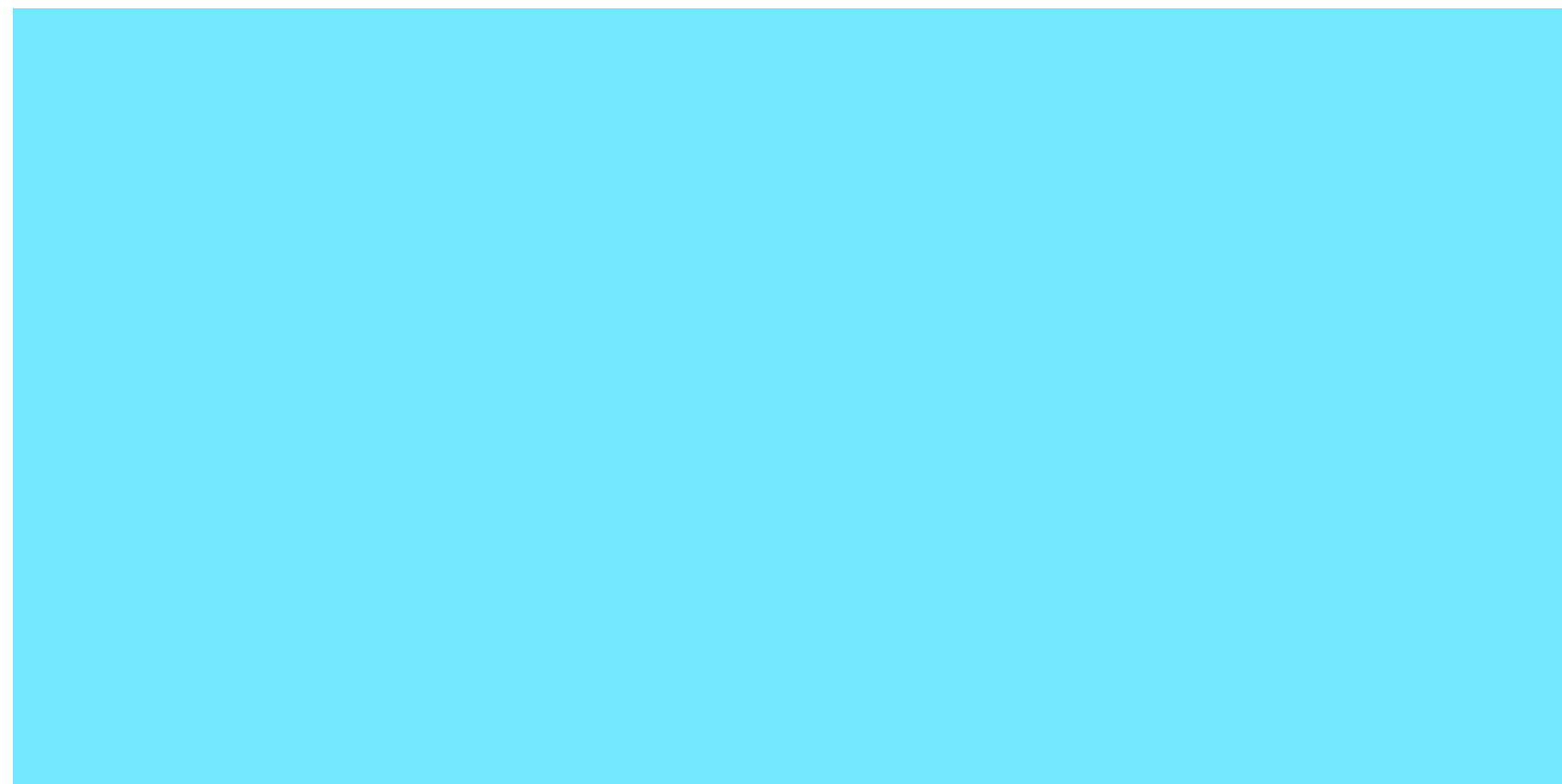
1

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log2Enrichment



Re-clustered module 16.20.5 MF enrichment

Term

cadherin binding

0

1

2

3

log2Enrichment



Re-clustered module 16.20.7 BP enrichment

Term

negative regulation of intrinsic apoptotic signaling pathway

0

1

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log2Enrichment



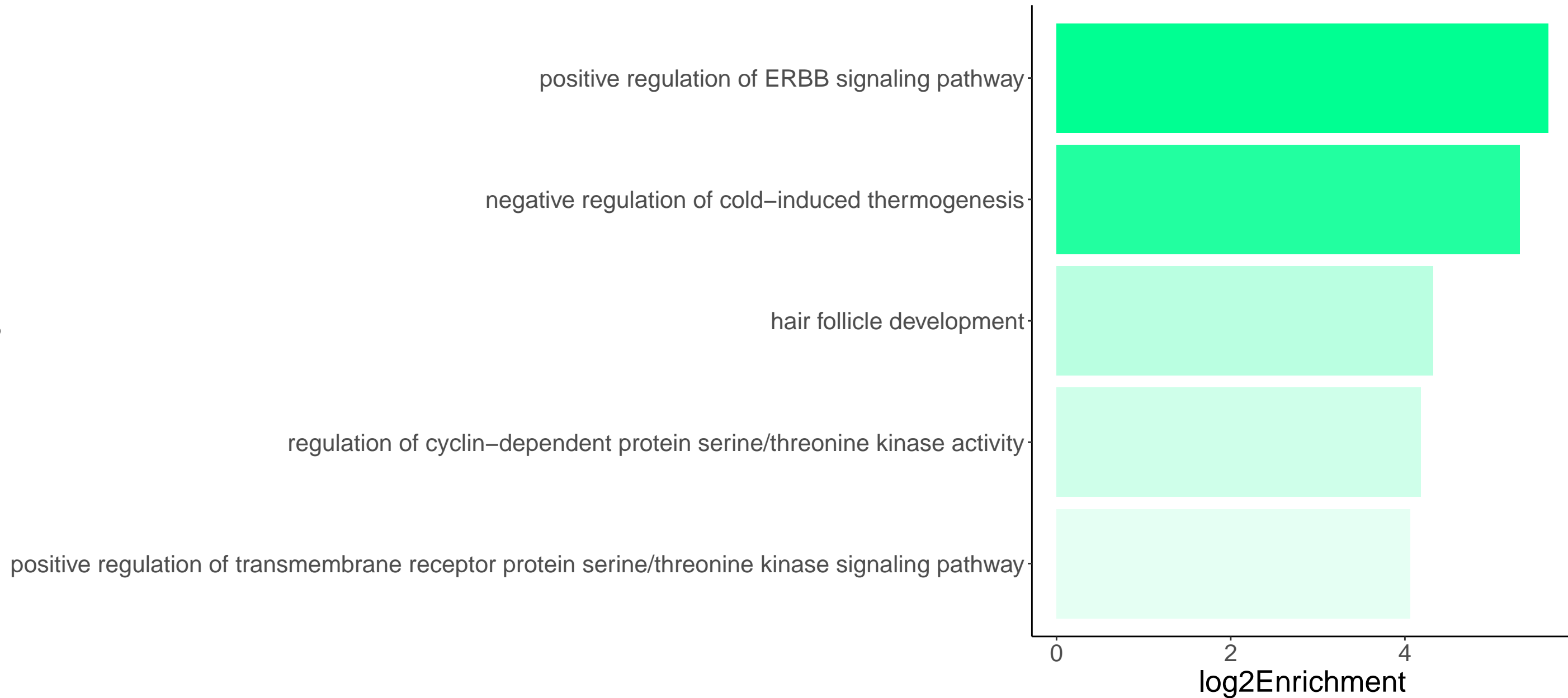
Re-clustered module 16.20.7 MF enrichment

Term

log2Enrichment



Term



Re-clustered module 16.20.8 MF enrichment

Term

log2Enrichment



Re-clustered module 16.20.9 BP enrichment

Term

positive regulation of glycoprotein biosynthetic process

activation of GTPase activity

regulation of phospholipid metabolic process

Golgi organization

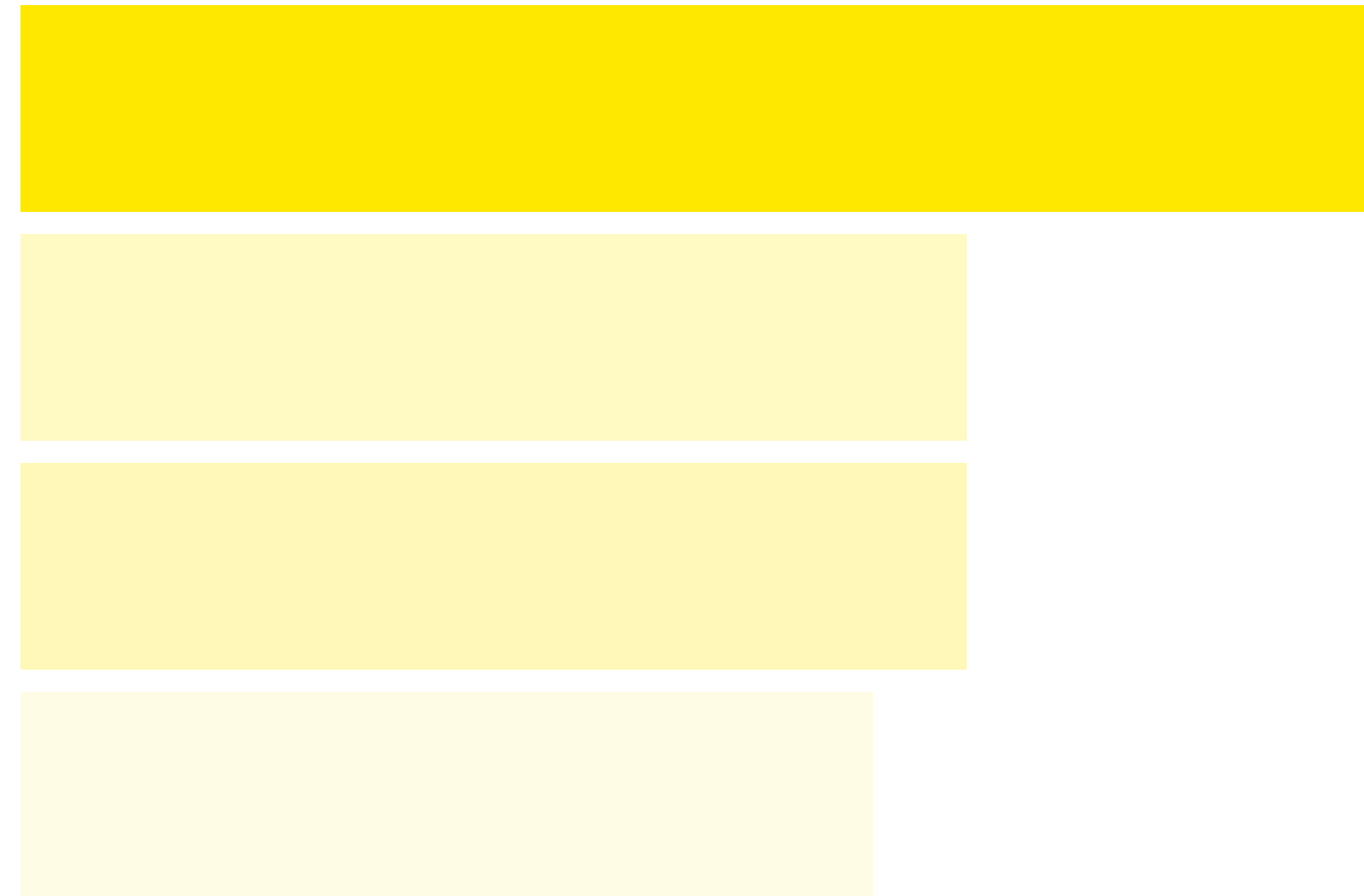
0

2

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log2Enrichment



Re-clustered module 16.20.9 MF enrichment

Term

protein phosphatase binding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.3.1 BP enrichment

Term

positive regulation of bone mineralization

calcium ion homeostasis

0

2

4

6

log2Enrichment



Re-clustered module 16.3.1 MF enrichment

Term

vitamin binding

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.3.10 BP enrichment

Term

regulation of sister chromatid cohesion

peptidyl-glutamic acid modification

tRNA methylation

cytoplasmic translation

rRNA processing

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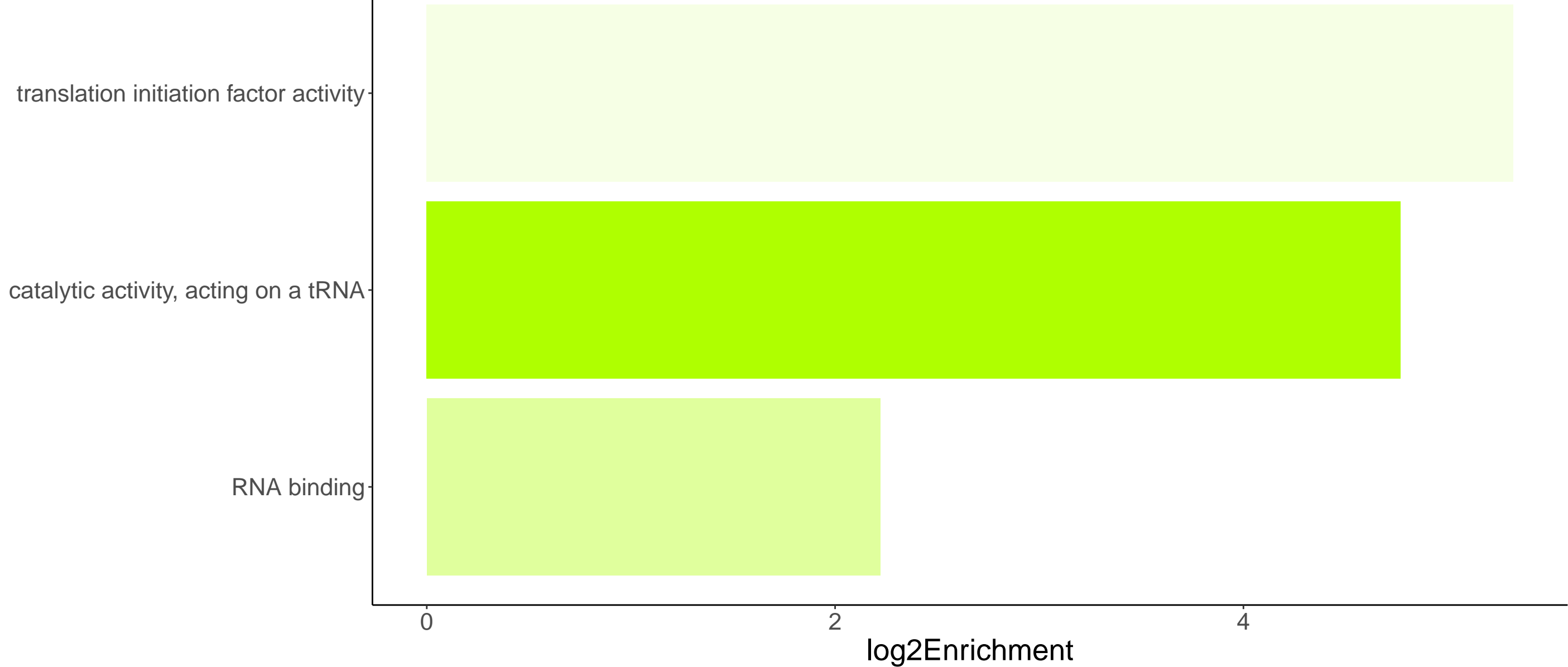
6

log2Enrichment



Re-clustered module 16.3.10 MF enrichment

Term



Re-clustered module 16.3.11 BP enrichment

Term

anaphase-promoting complex-dependent catabolic process

translational termination

0

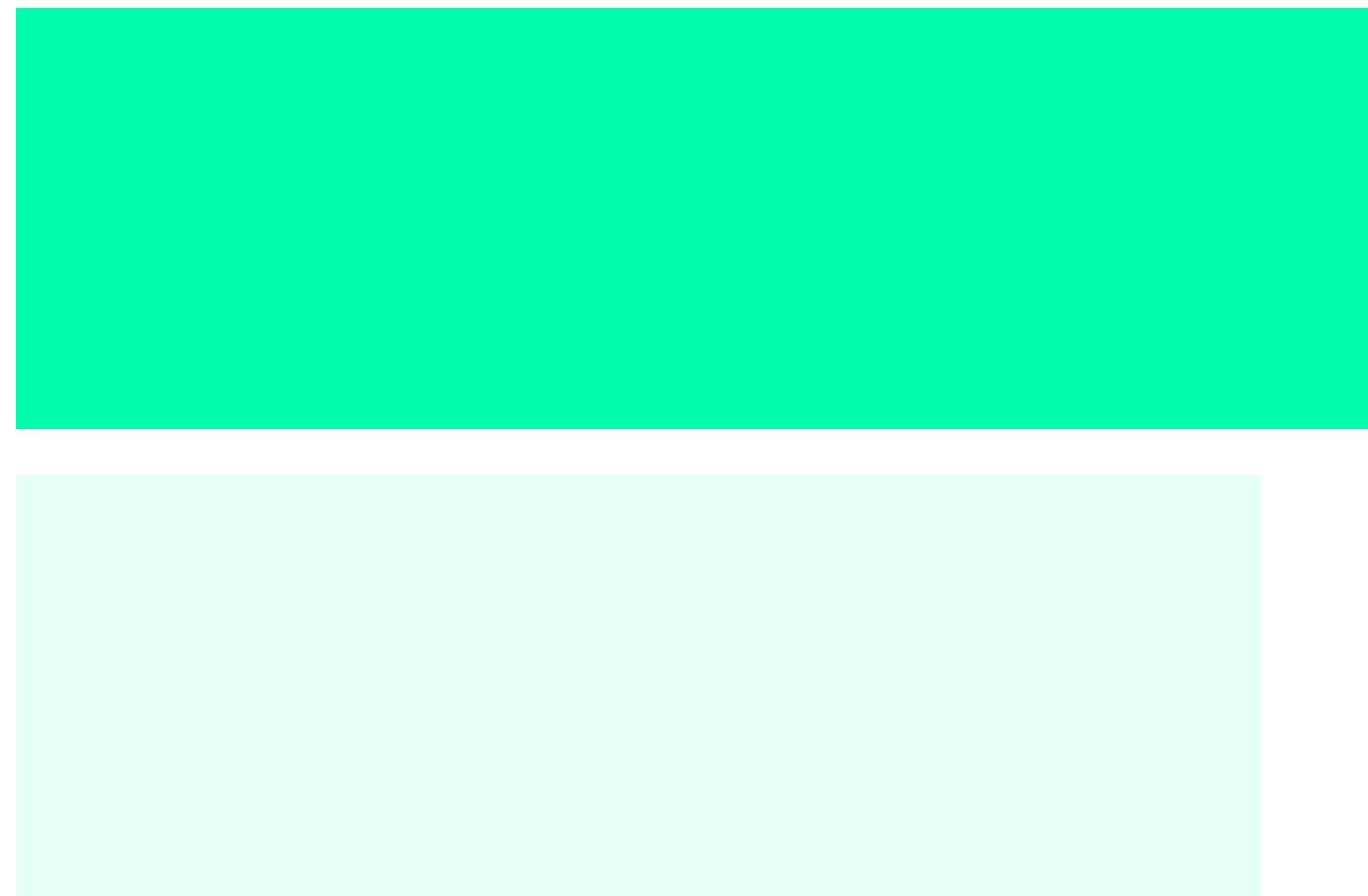
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log2Enrichment



Re-clustered module 16.3.11 MF enrichment

Term

5'–3' RNA polymerase activity

purine ribonucleoside triphosphate binding

0

1

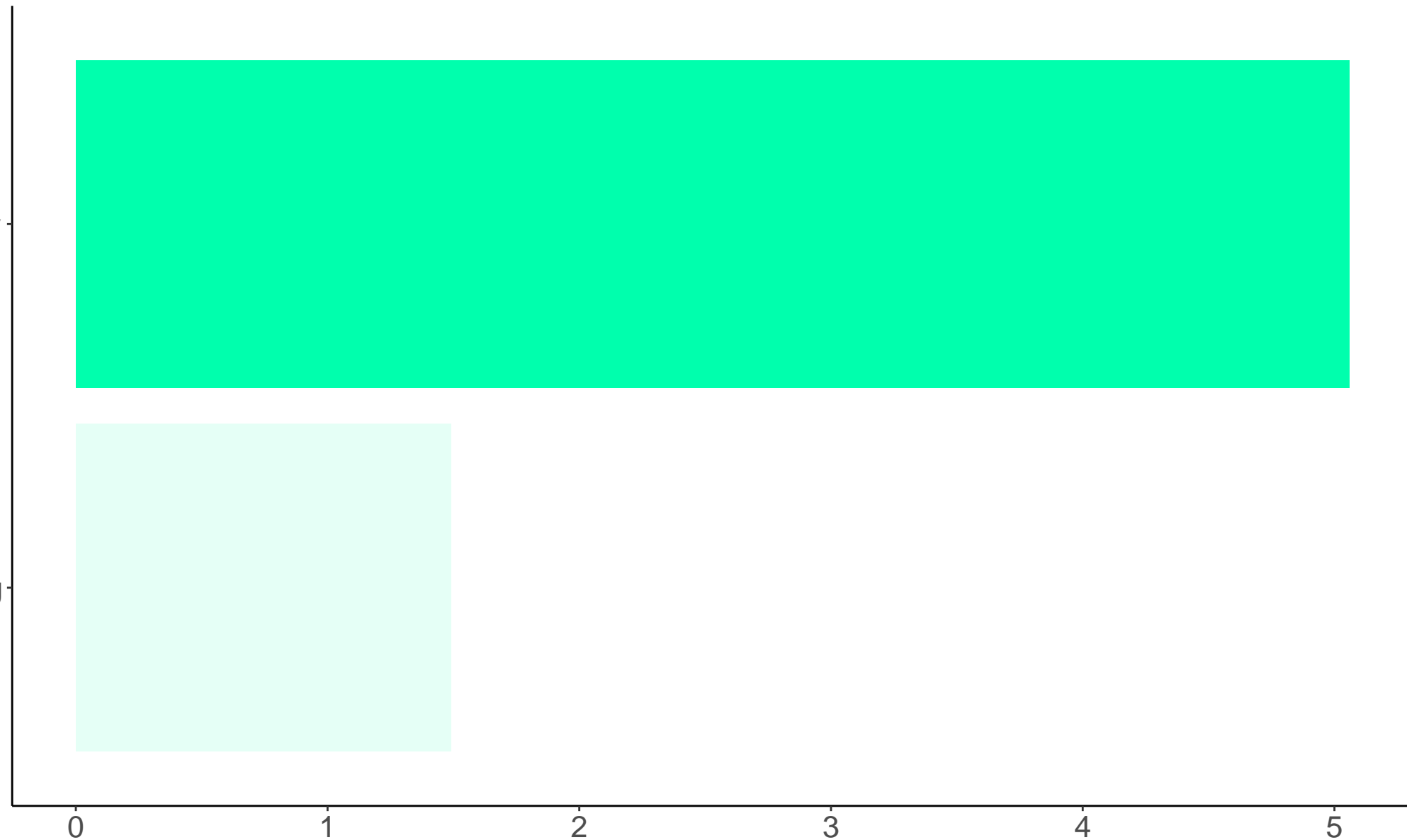
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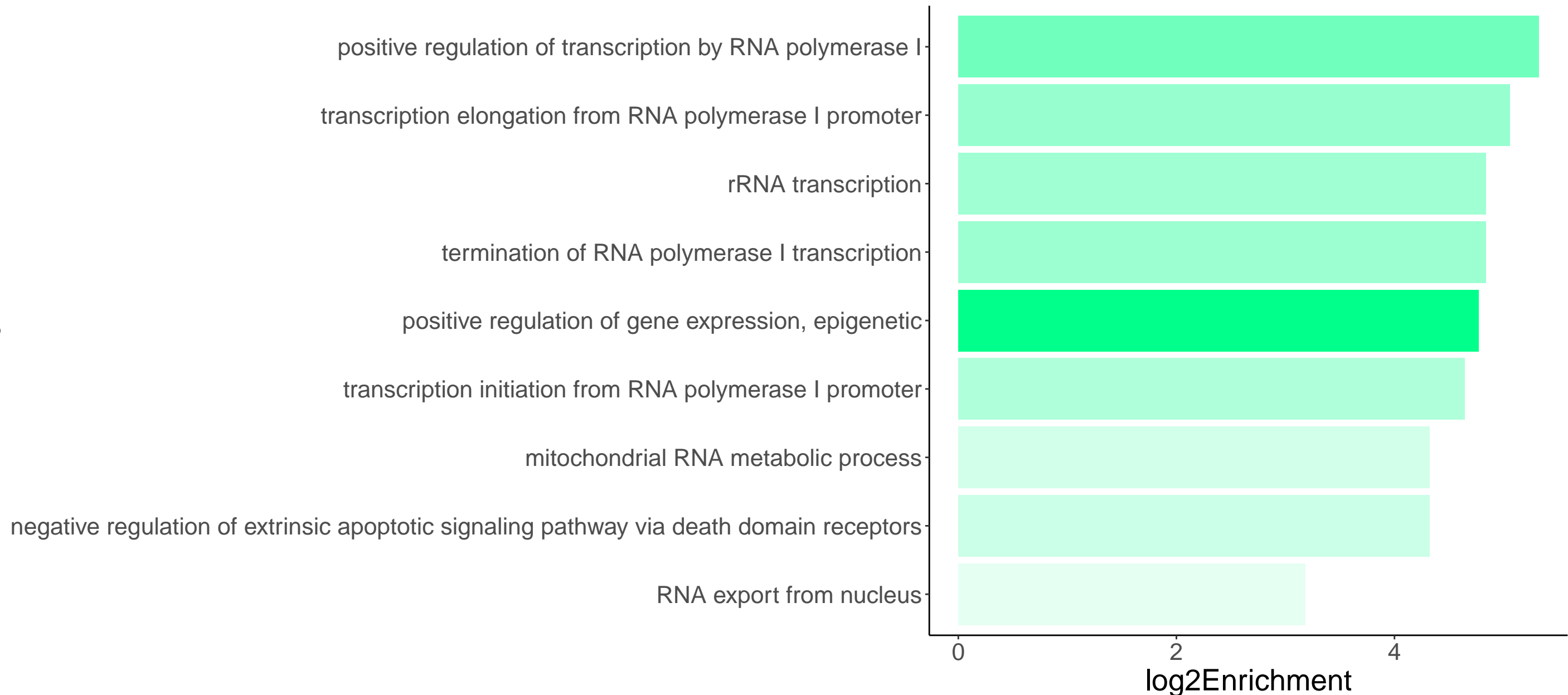
5

log2Enrichment



Re-clustered module 16.3.12 BP enrichment

Term



Re-clustered module 16.3.12 MF enrichment

Term

helicase activity

0

1

2

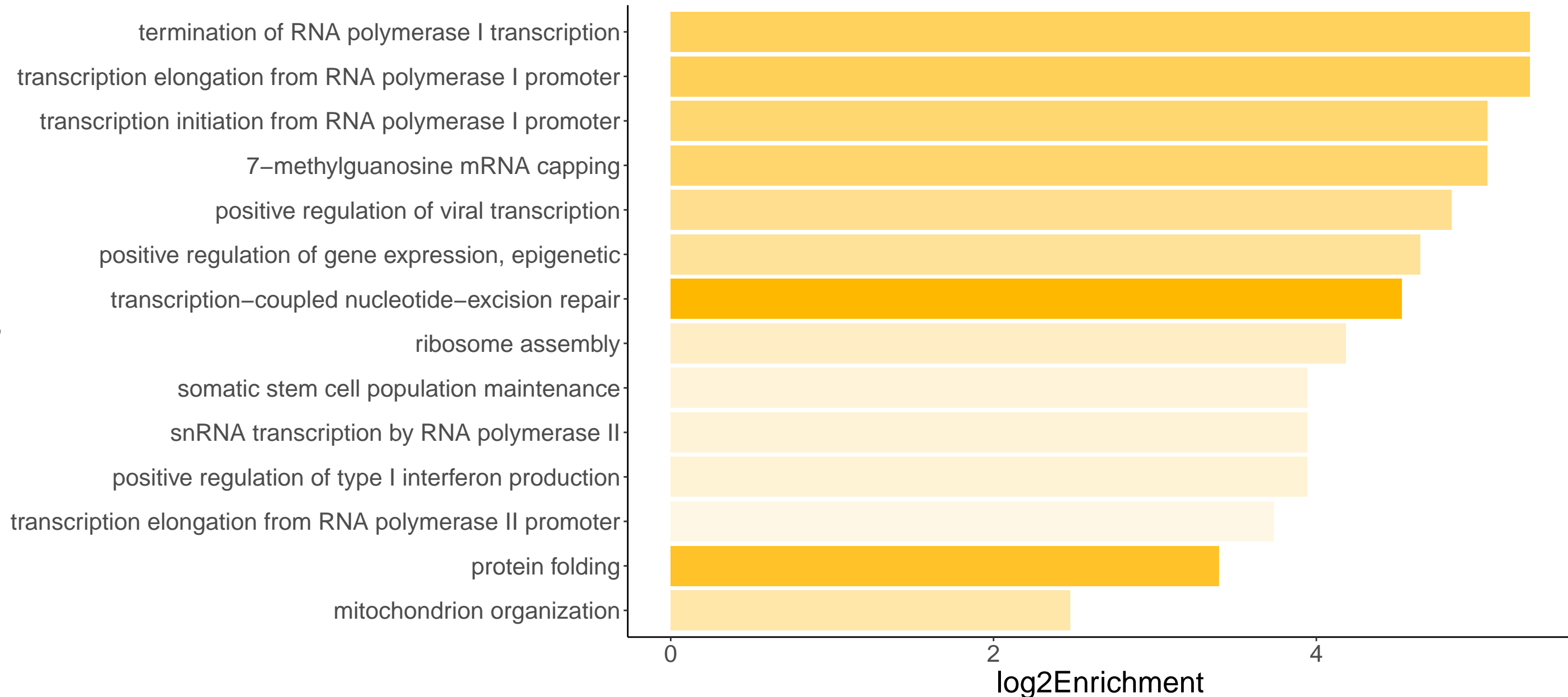
3

log2Enrichment



Re-clustered module 16.3.13 BP enrichment

Term



Re-clustered module 16.3.13 MF enrichment

Term

DNA-directed 5'–3' RNA polymerase activity

structural constituent of ribosome

nucleic acid binding

0

1

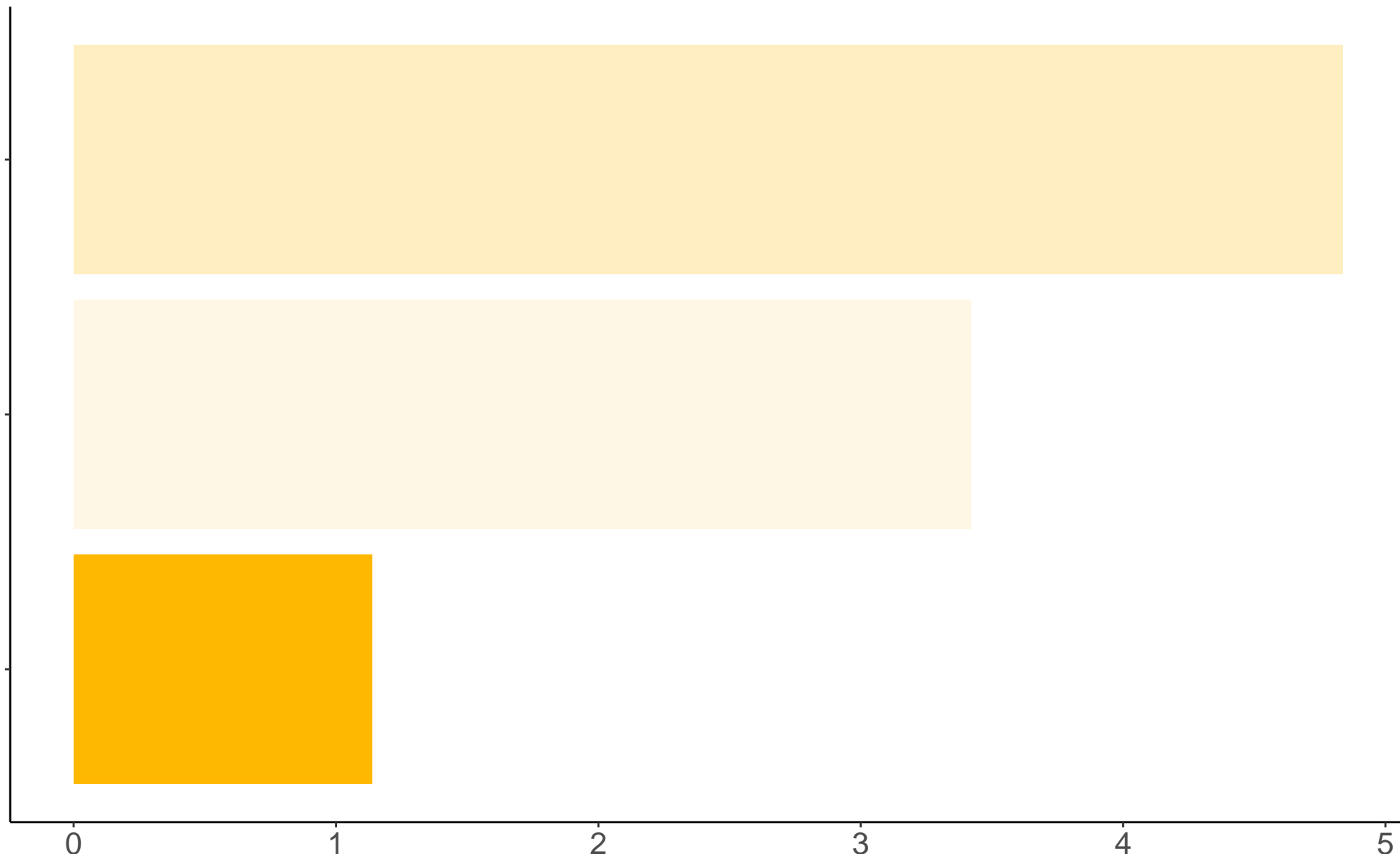
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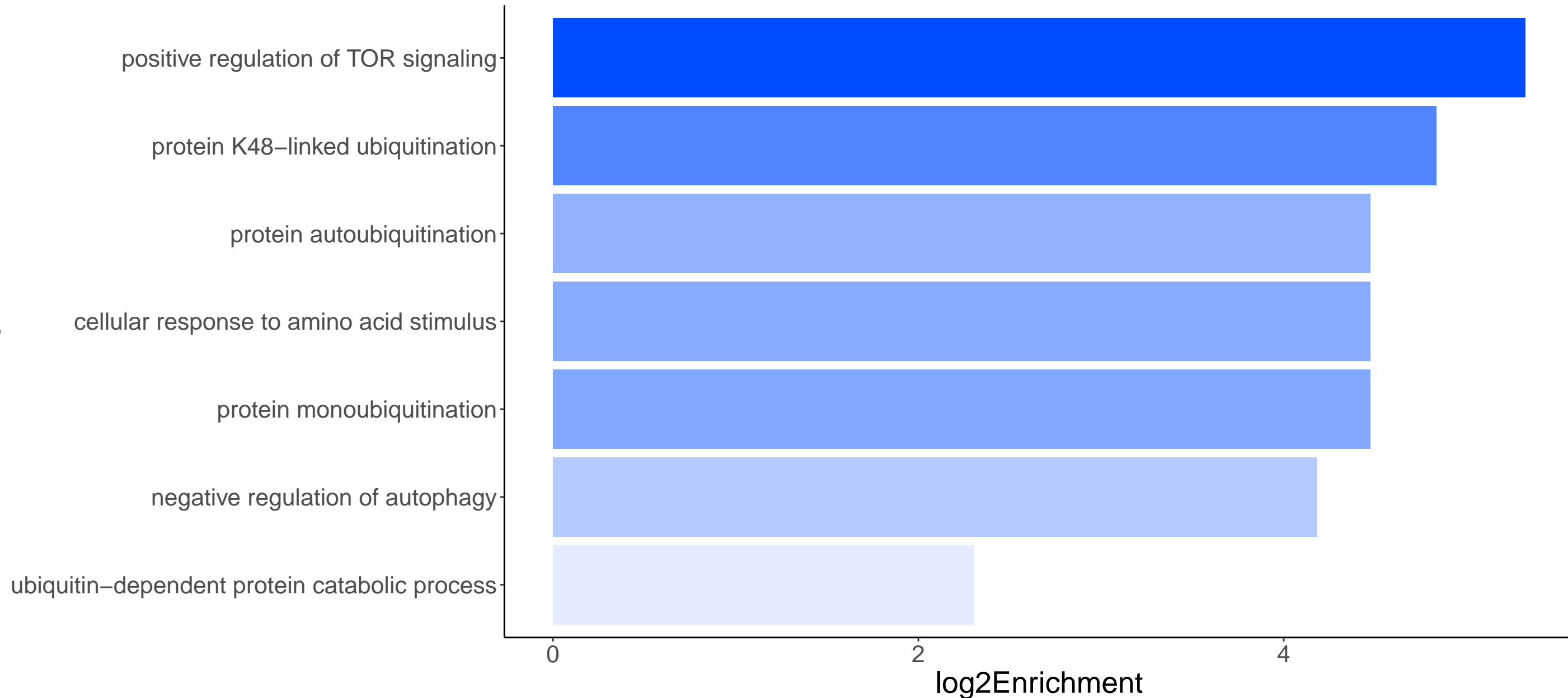
5

log2Enrichment



Re-clustered module 16.3.2 BP enrichment

Term



Re-clustered module 16.3.2 MF enrichment

Term

ubiquitin conjugating enzyme activity

RNA binding

0

1

2

3

4

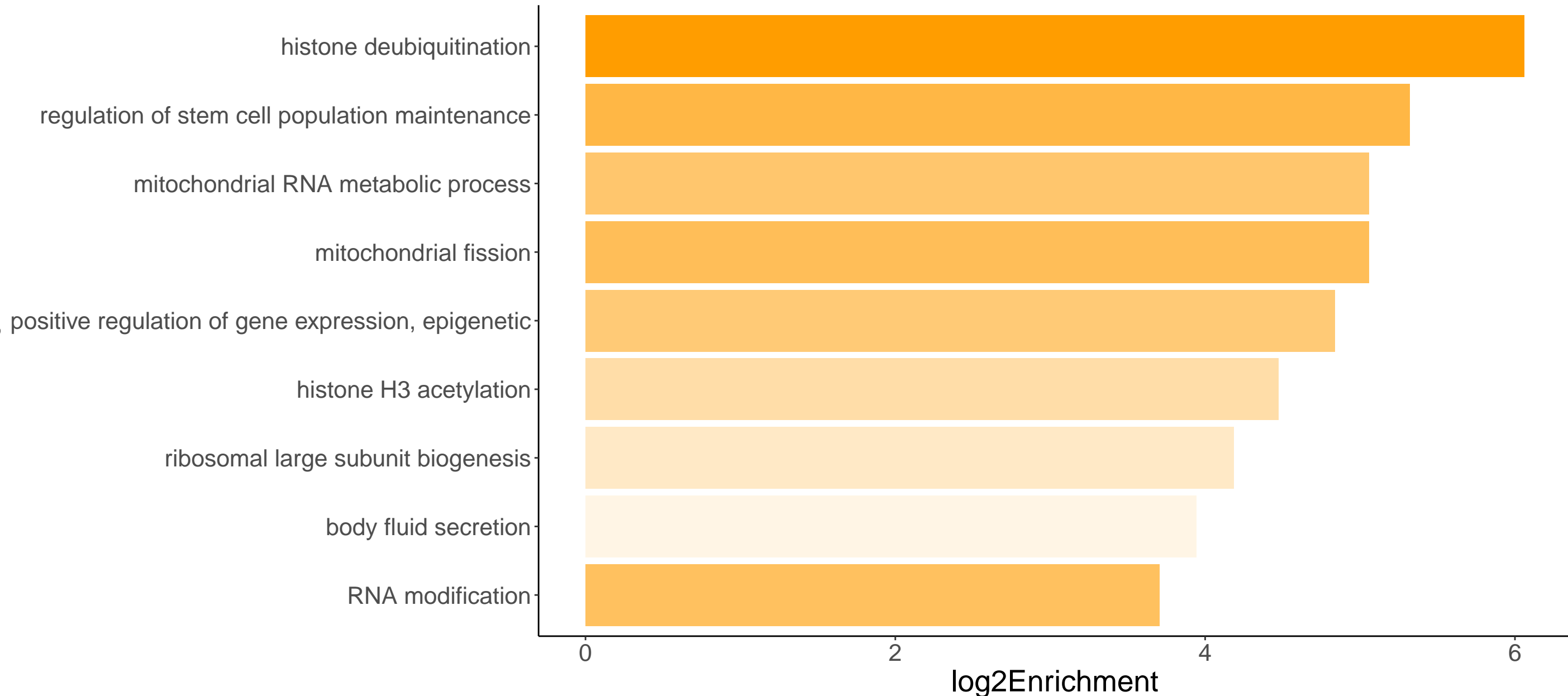
5

log2Enrichment



Re-clustered module 16.3.3 BP enrichment

Term



Re-clustered module 16.3.3 MF enrichment

Term

intramolecular transferase activity

histone acetyltransferase activity

rRNA binding

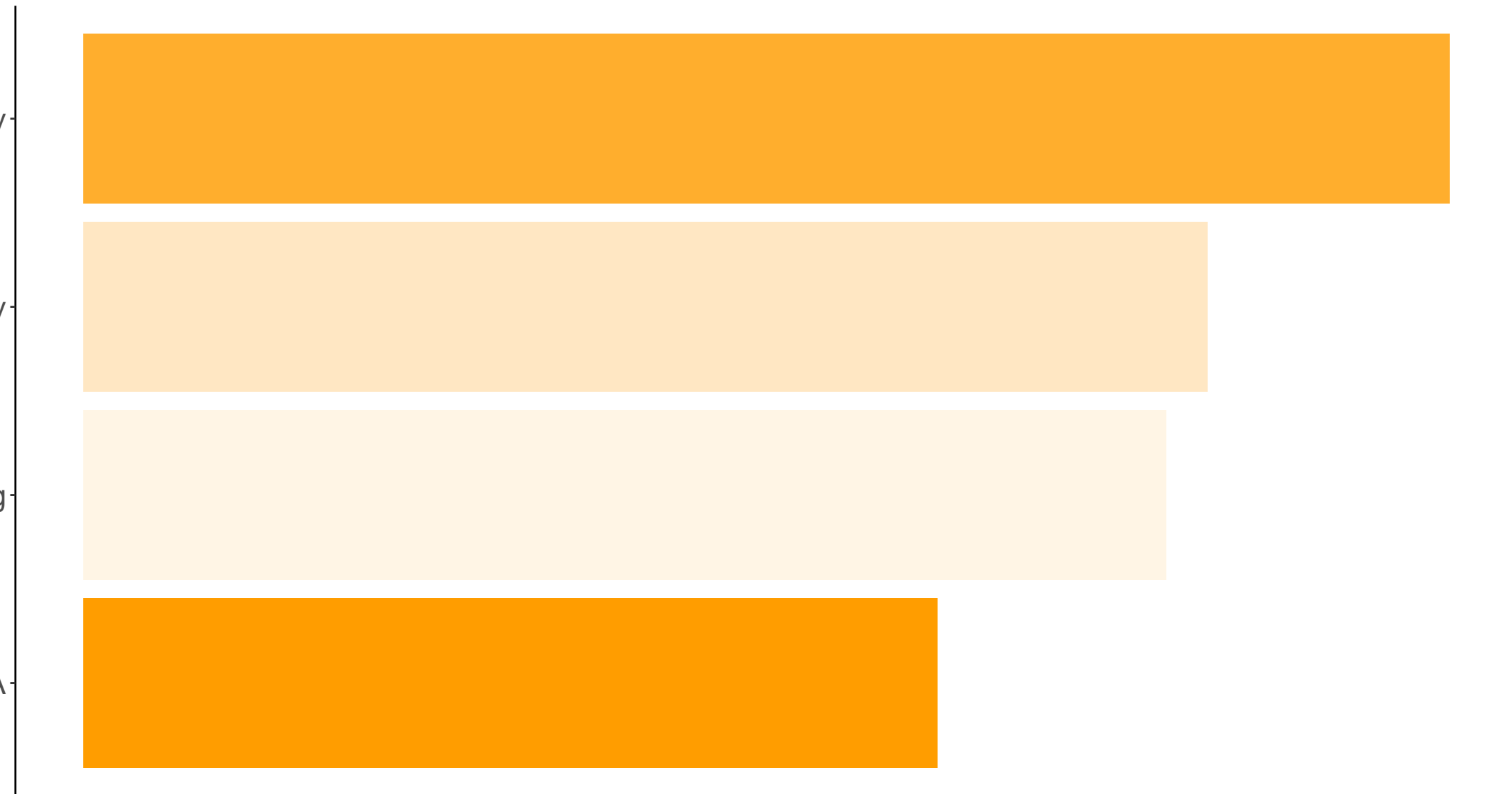
catalytic activity, acting on RNA

0

2

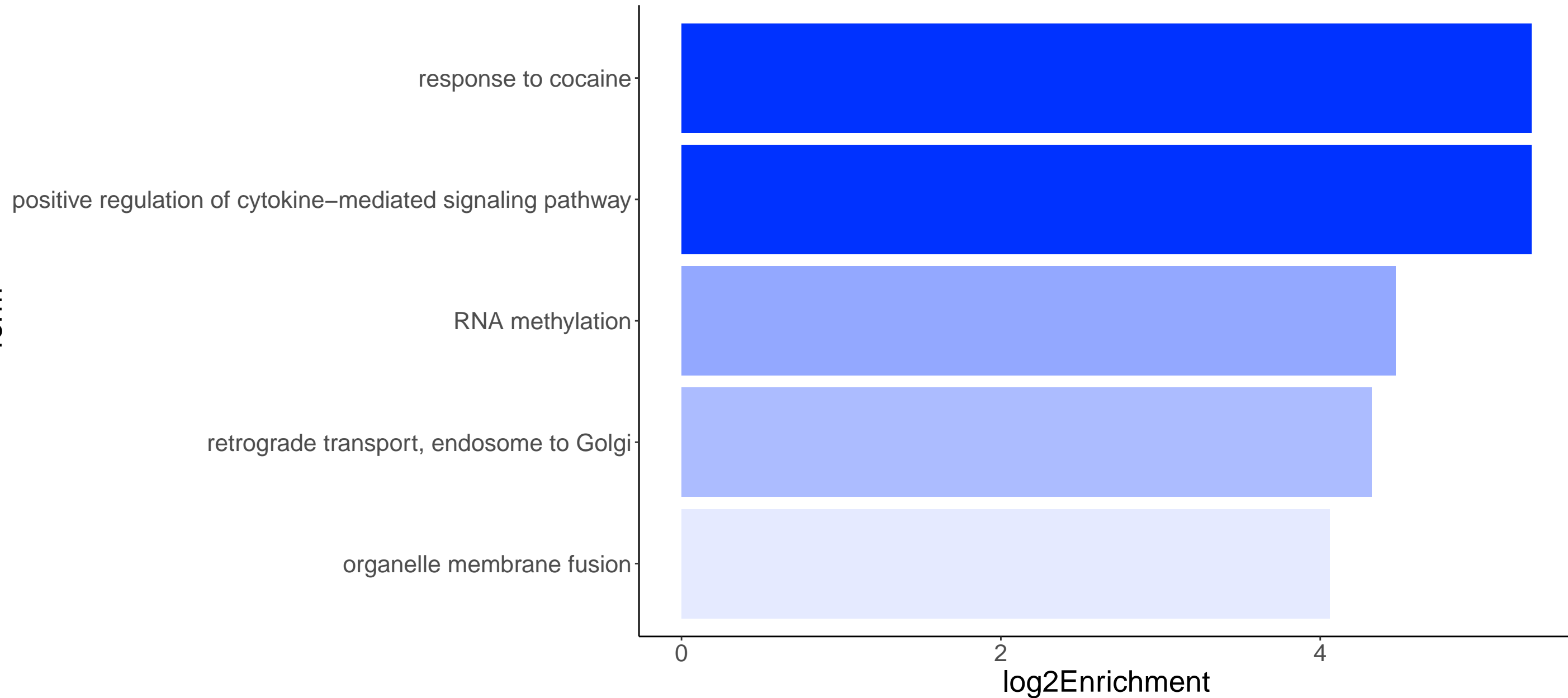
4

log2Enrichment



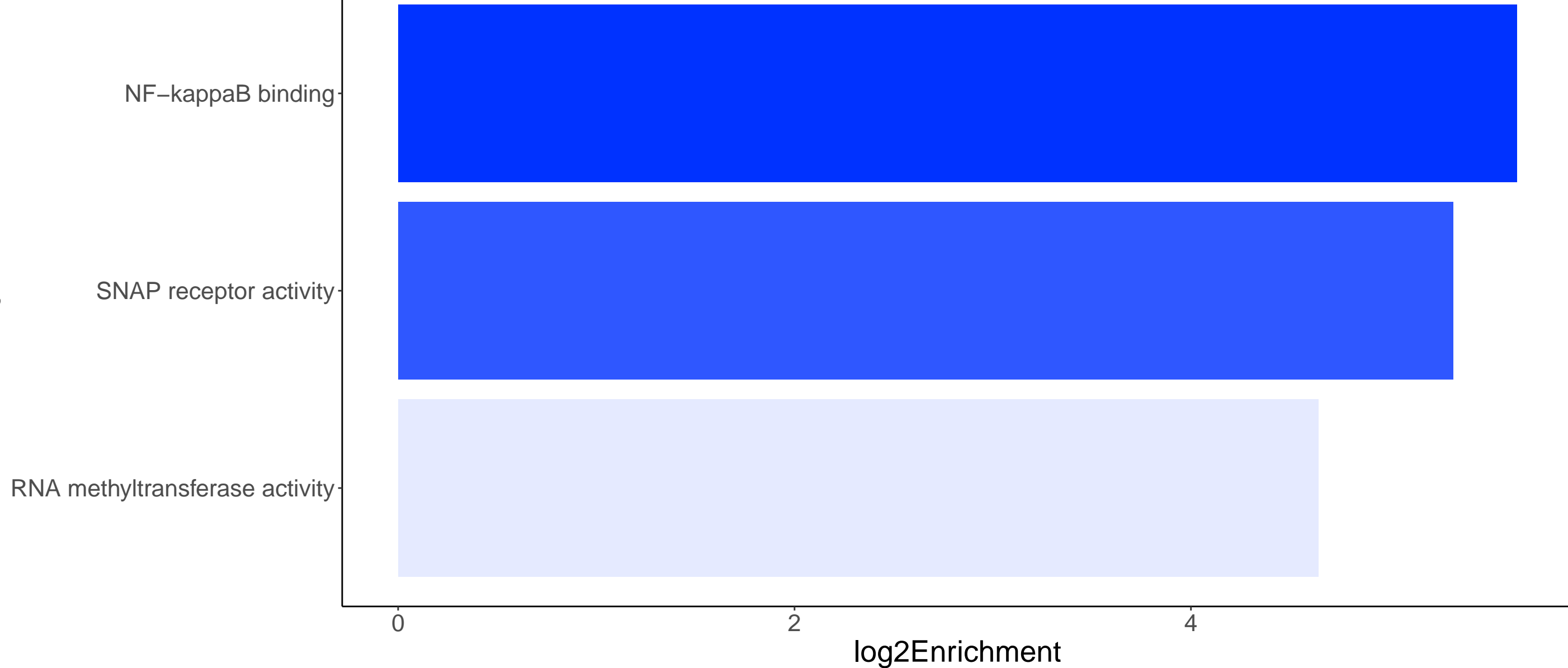
Re-clustered module 16.3.4 BP enrichment

Term



Re-clustered module 16.3.4 MF enrichment

Term



Re-clustered module 16.3.5 BP enr

Term

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

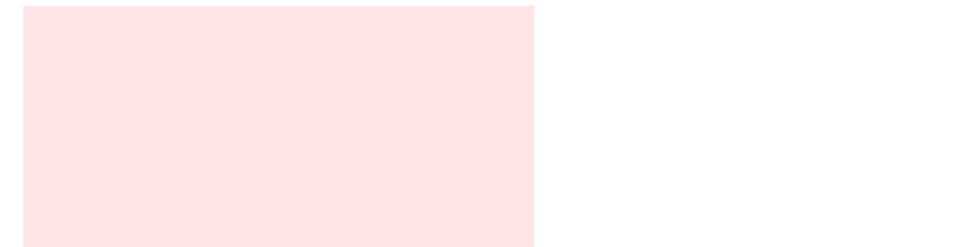
mitochondrial translational termination

translational elongation

regulation of signal transduction by p53 class mediator

log2Enrichment

0 1 2 3 4 5



Re-clustered module 16.3.5 MF enrichment

Term

dicarboxylic acid transmembrane transporter activity

S-adenosylmethionine-dependent methyltransferase activity

0

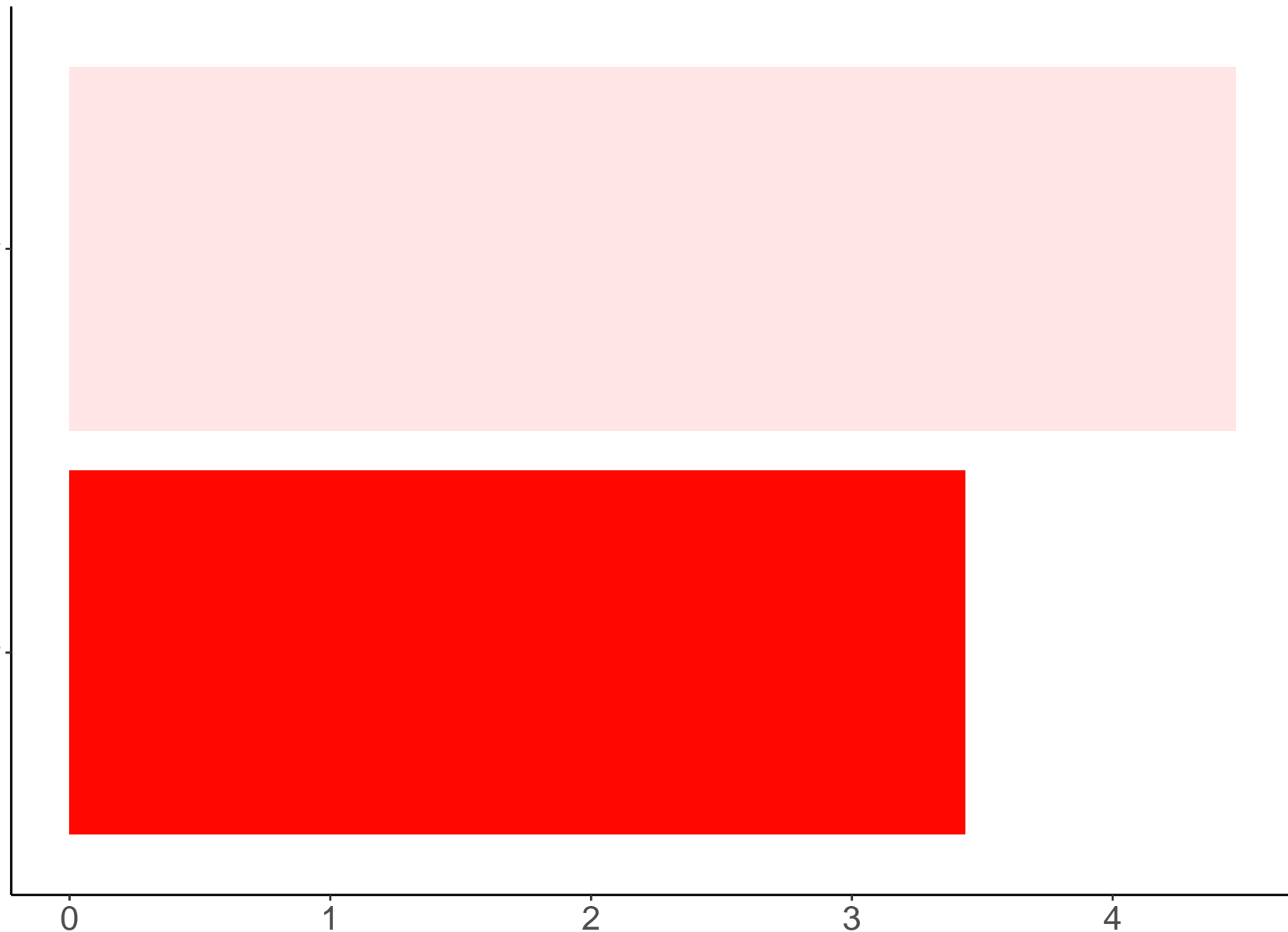
1

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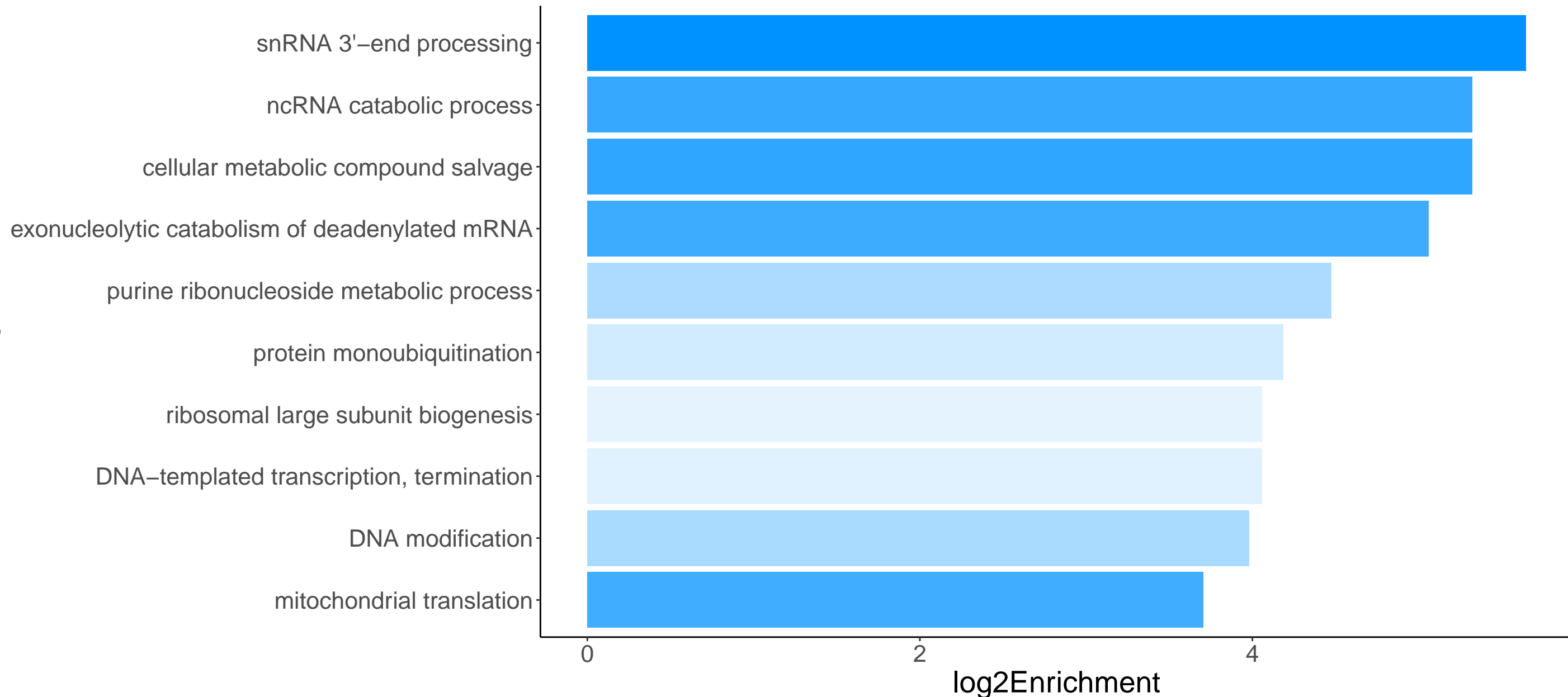
4

log2Enrichment



Re-clustered module 16.3.6 BP enrichment

Term



Re-clustered module 16.3.6 MF enrichment

Term

3'-5'-exoribonuclease activity

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.3.7 BP enrichment

Term

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

ATP biosynthetic process

blastocyst formation

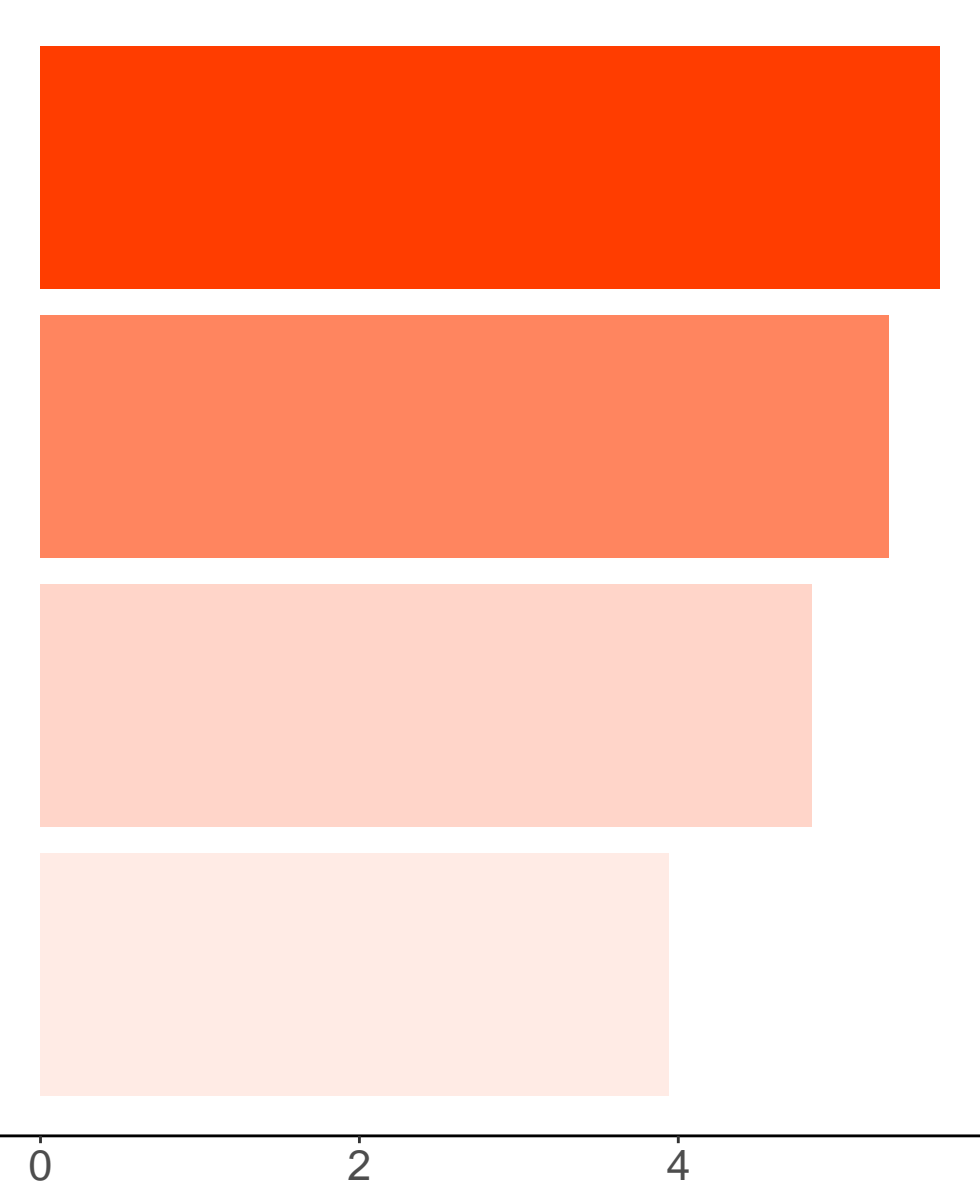
ribosome biogenesis

0

2

4

log2Enrichment



Re-clustered module 16.3.7 MF enrichment

Term

ribonucleoprotein complex binding

RNA binding

0

1

2

3

log2Enrichment



Re-clustered module 16.3.8 BP enrichment

Term

associative learning

RNA methylation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.3.8 MF enrichment

Term

endodeoxyribonuclease activity

RNA methyltransferase activity

0

1

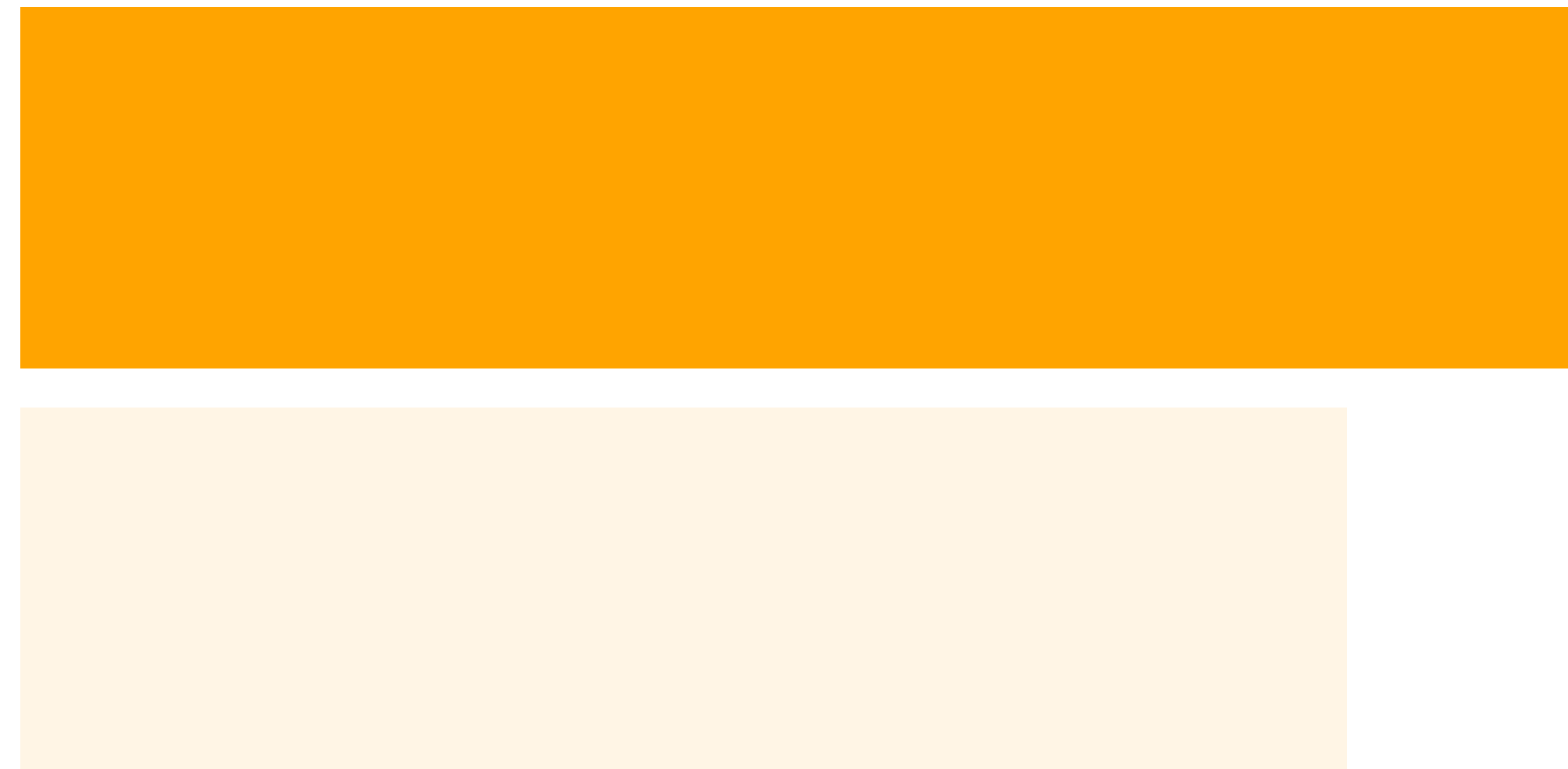
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4

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log2Enrichment



Re-clustered module 16.4.1 BP enrichment

Term

protein heterooligomerization

protein homooligomerization

0

2

4

6

log2Enrichment



Re-clustered module 16.4.1 MF enrichment

Term

log2Enrichment



Re-clustered module 16.4.10 BP enrichment

Term

response to ionizing radiation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.4.10 MF enrichment

Term

iron ion binding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.4.12 BP enrichment

Term

positive regulation of response to DNA damage stimulus

mitochondrial respiratory chain complex assembly

double-strand break repair

0

2

4

log2Enrichment



Re-clustered module 16.4.12 MF enrichment

Term

log2Enrichment



Re-clustered module 16.4.2 BP enrichment

Term

tRNA aminoacylation for protein translation

cerebral cortex cell migration

mitochondrial RNA metabolic process

mitochondrial translation

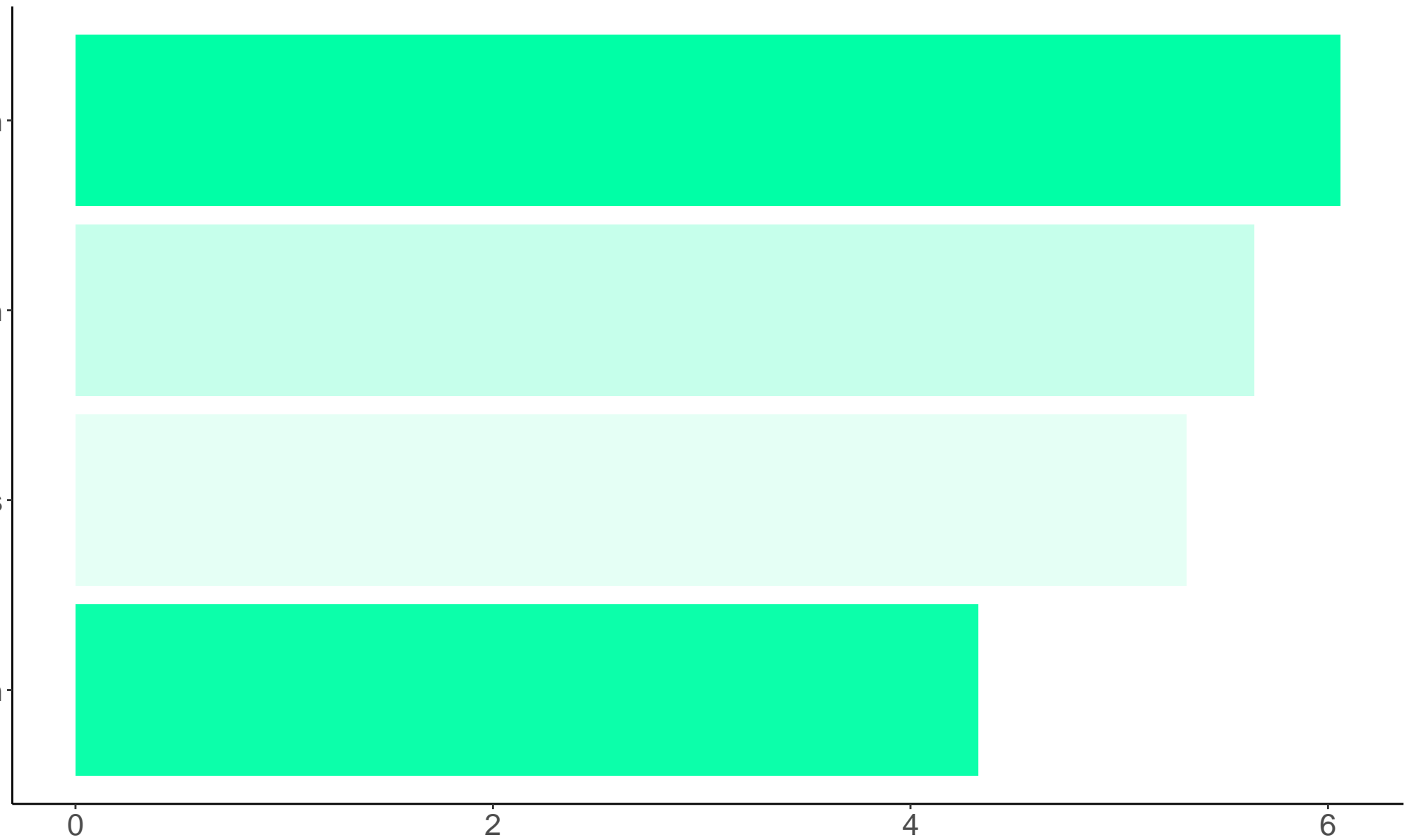
0

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log2Enrichment



Re-clustered module 16.4.2 MF enrichment

Term

aminoacyl-tRNA ligase activity

0

2

4

6

log2Enrichment



Re-clustered module 16.4.3 BP enrichment

Term

mitochondrial ATP synthesis coupled electron transport

aerobic respiration

proton transmembrane transport

RNA phosphodiester bond hydrolysis

regulation of translation

0

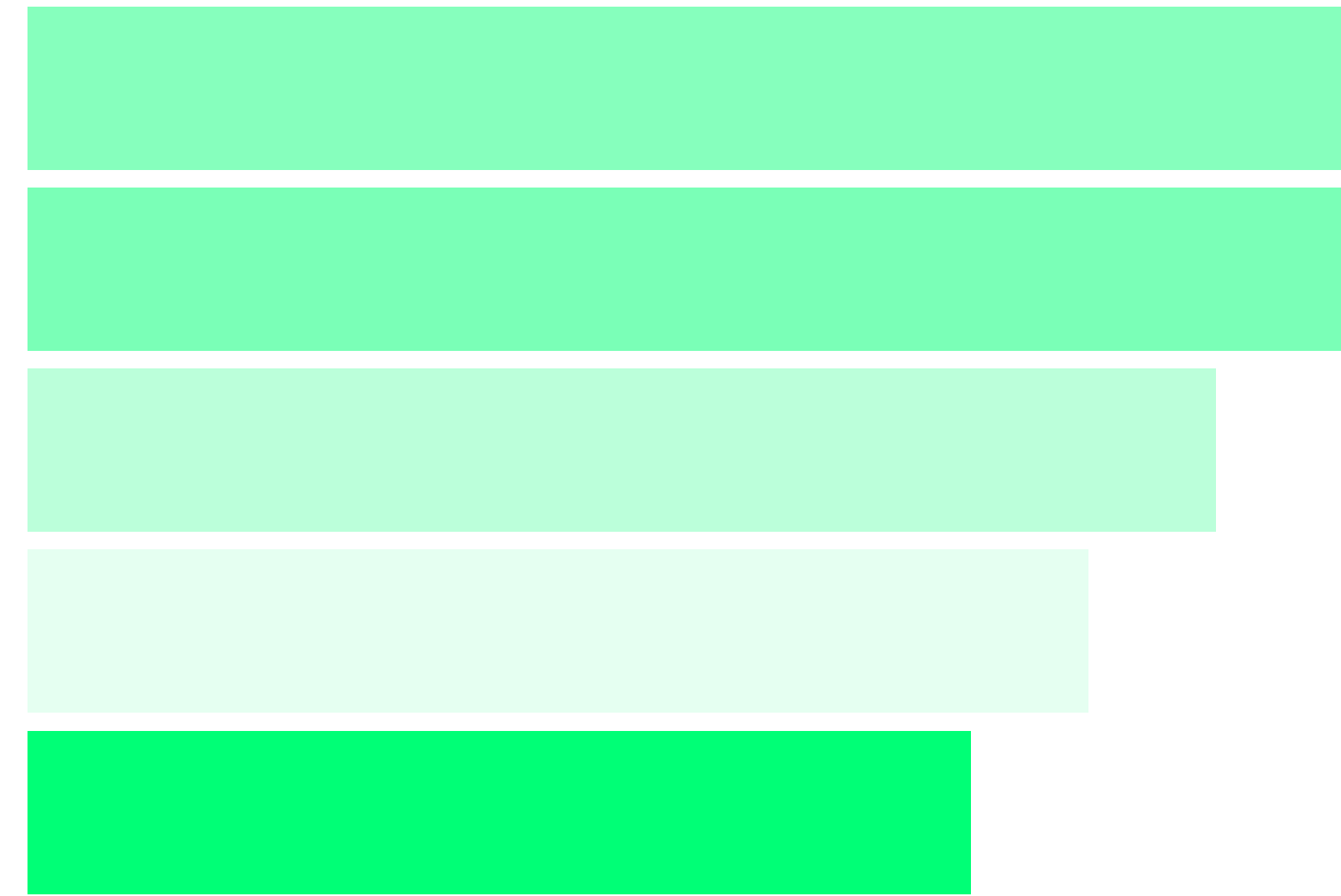
1

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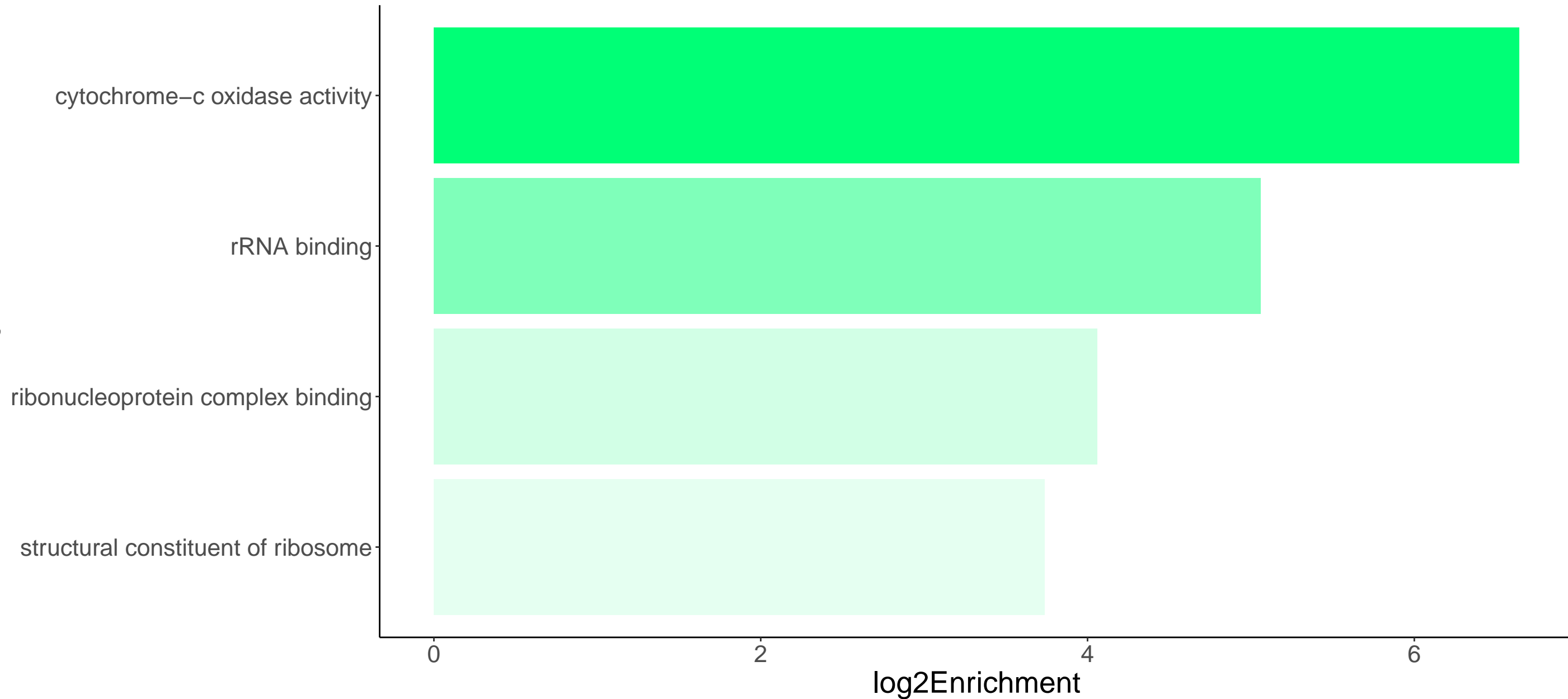
4

log2Enrichment



Re-clustered module 16.4.3 MF enrichment

Term



Re-clustered module 16.4.5 BP enrichment

Term

synaptic vesicle endocytosis

positive regulation of cell morphogenesis involved in differentiation

0

2

4

log2Enrichment



Re-clustered module 16.4.5 MF enrichment

Term

WW domain binding

SH3 domain binding

lyase activity

0

2

4

6

log2Enrichment



Re-clustered module 16.5.1 BP enrichment

Term

regulation of gene silencing by miRNA

viral transcription

fertilization

ribonucleoprotein complex subunit organization

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.5.1 MF enrichment

Term

log2Enrichment



Re-clustered module 16.5.2 BP enrichment

Term

protein targeting to membrane

0

1

2

3

4

log2Enrichment



Re-clustered module 16.5.2 MF enrichment

Term

log2Enrichment



Re-clustered module 16.5.3 BP enrichment

Term

negative regulation of GTPase activity

gonad development

0

2

4

6

log2Enrichment



Re-clustered module 16.5.3 MF enrichment

Term

log2Enrichment



Re-clustered module 16.5.4 BP enrichment

Term

regulation of protein binding

0

1

2

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log2Enrichment



Re-clustered module 16.5.4 MF enrichment

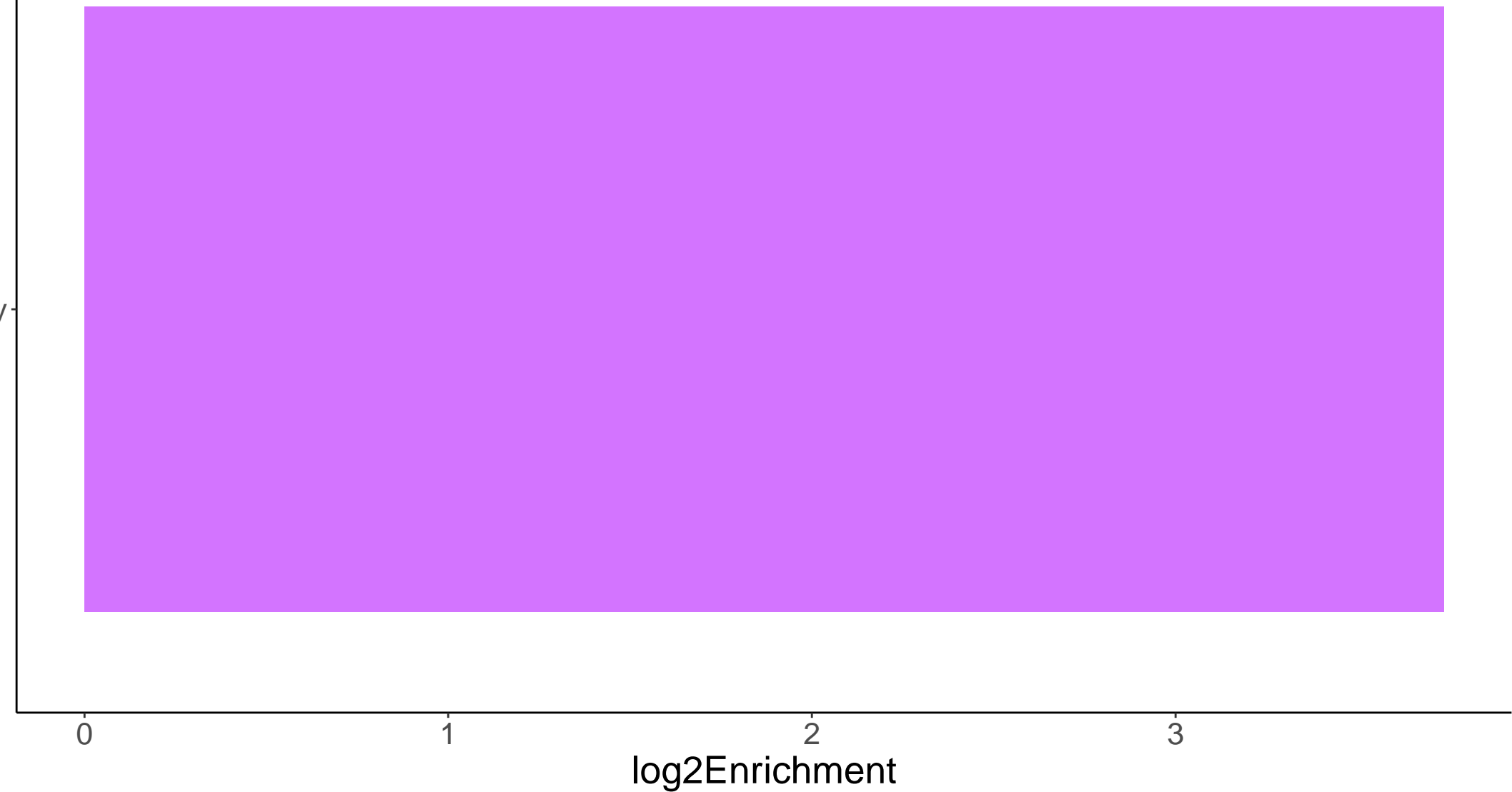
Term

log2Enrichment



Re-clustered module 16.5.5 BP enrichment

Term
ribonucleoprotein complex assembly



Re-clustered module 16.5.5 MF enrichment

Term

log2Enrichment



Re-clustered module 16.5.7 BP enrichment

Term

iron-sulfur cluster assembly

0

2

4

6

log2Enrichment



Re-clustered module 16.5.7 MF enrichment

Term

catalytic activity, acting on a tRNA

0

1

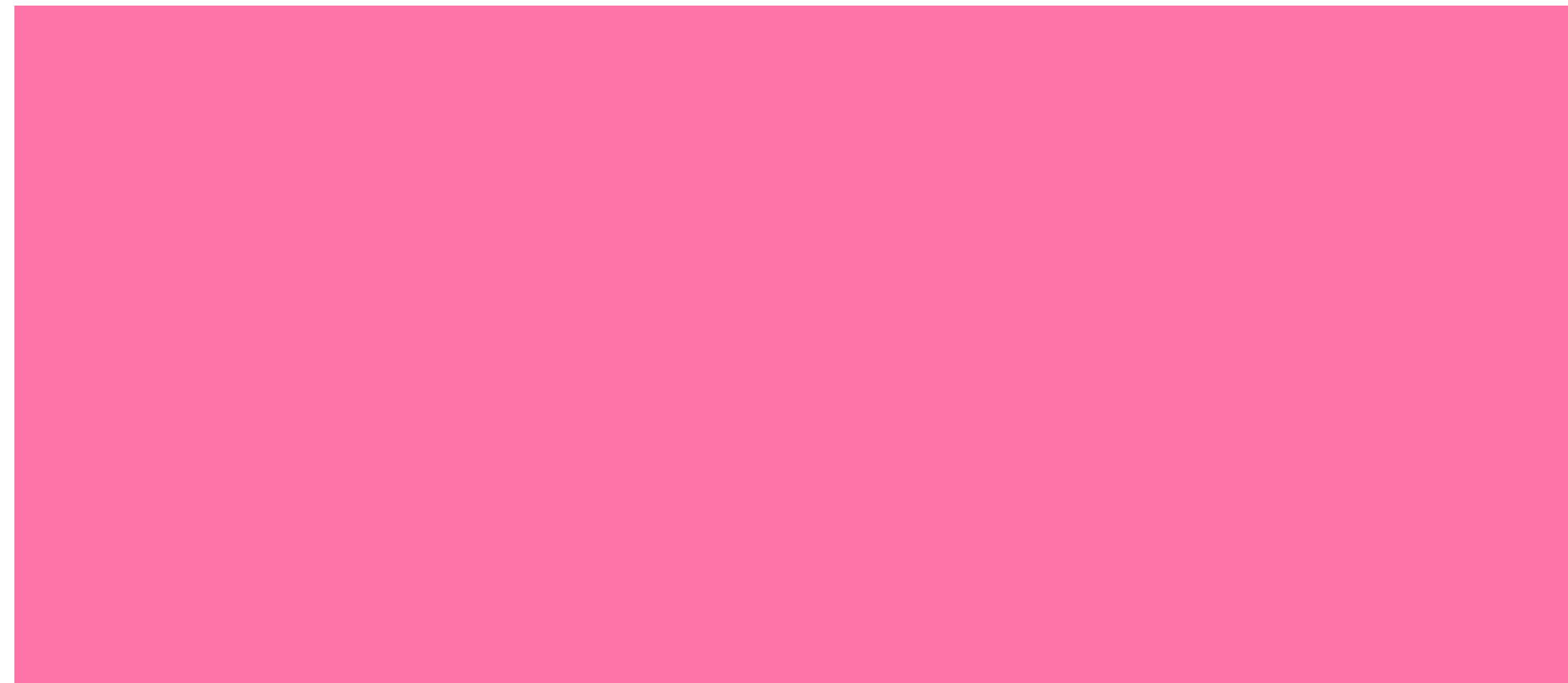
2

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log2Enrichment



Re-clustered module 16.6.2 BP enrichment

Term

log2Enrichment



Re-clustered module 16.6.2 MF enrichment

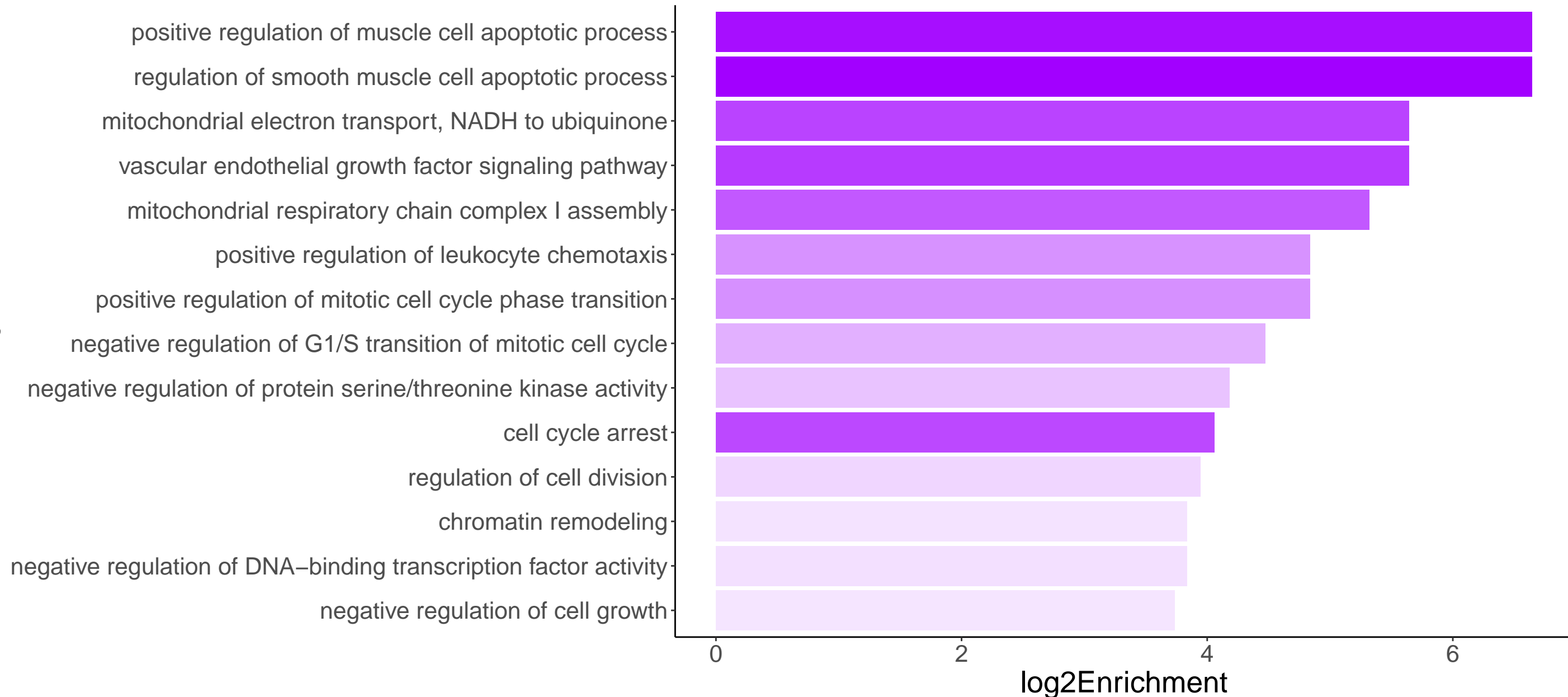
Term

log2Enrichment



Re-clustered module 16.6.4 BP enrichment

Term



Re-clustered module 16.6.4 MF enrichment

Term

growth factor receptor binding

growth factor activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.6.5 BP enrichment

Term

intracellular protein transport

0

1

2

log2Enrichment



Re-clustered module 16.6.5 MF enrichment

Term

log2Enrichment



Re-clustered module 16.6.6 BP enrichment

Term

negative regulation of lipid biosynthetic process

0

2

4

6

log2Enrichment



Re-clustered module 16.6.6 MF enrichment

Term

log2Enrichment



Re-clustered module 16.6.8 BP enrichment

Term

regulation of intracellular steroid hormone receptor signaling pathway

0

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log2Enrichment



Re-clustered module 16.6.8 MF enrichment

Term

nuclear receptor binding

0

1

2

3

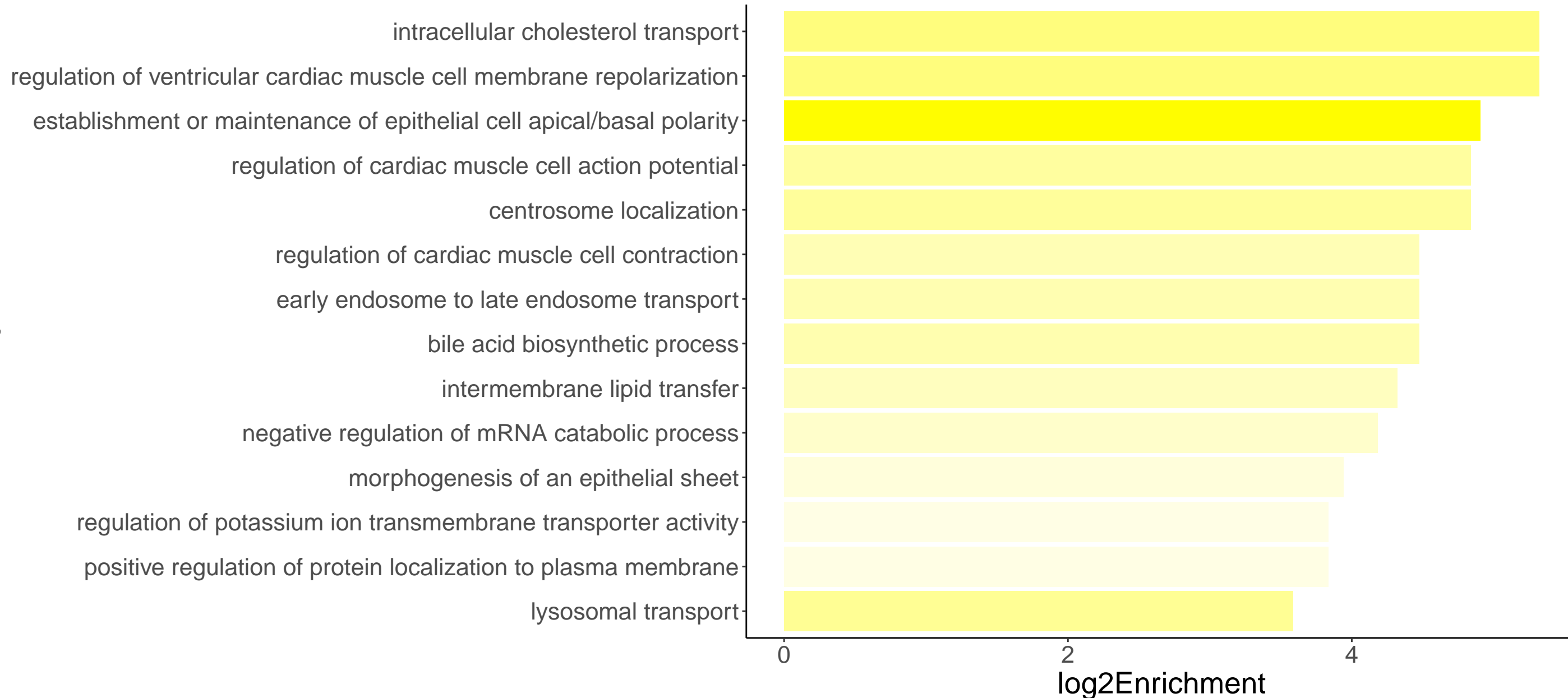
4

log2Enrichment



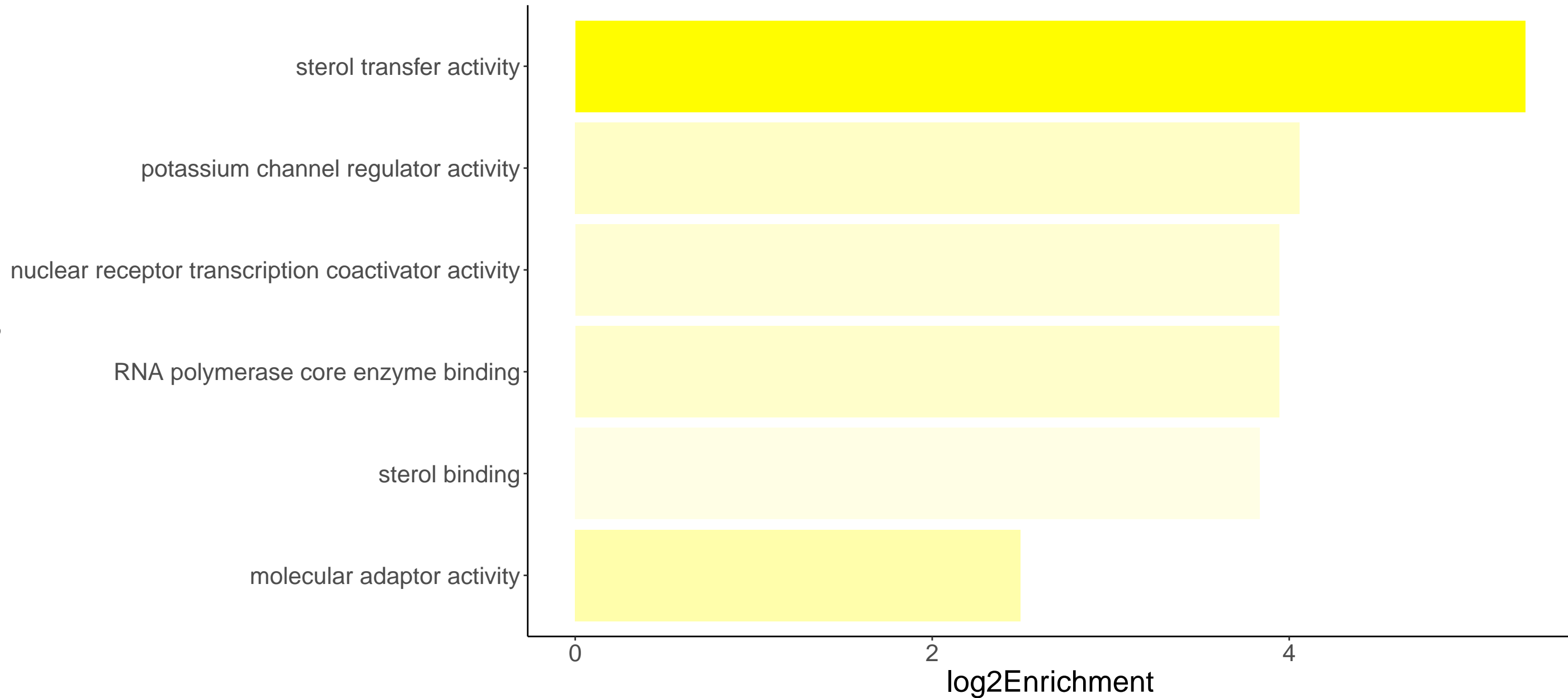
Re-clustered module 16.7.1 BP enrichment

Term



Re-clustered module 16.7.1 MF enrichment

Term



Re-clustered module 16.7.10 BP enrichment

Term

regulation of ERAD pathway

positive regulation of response to endoplasmic reticulum stress

ER–nucleus signaling pathway

positive regulation of proteasomal protein catabolic process

regulation of stem cell differentiation

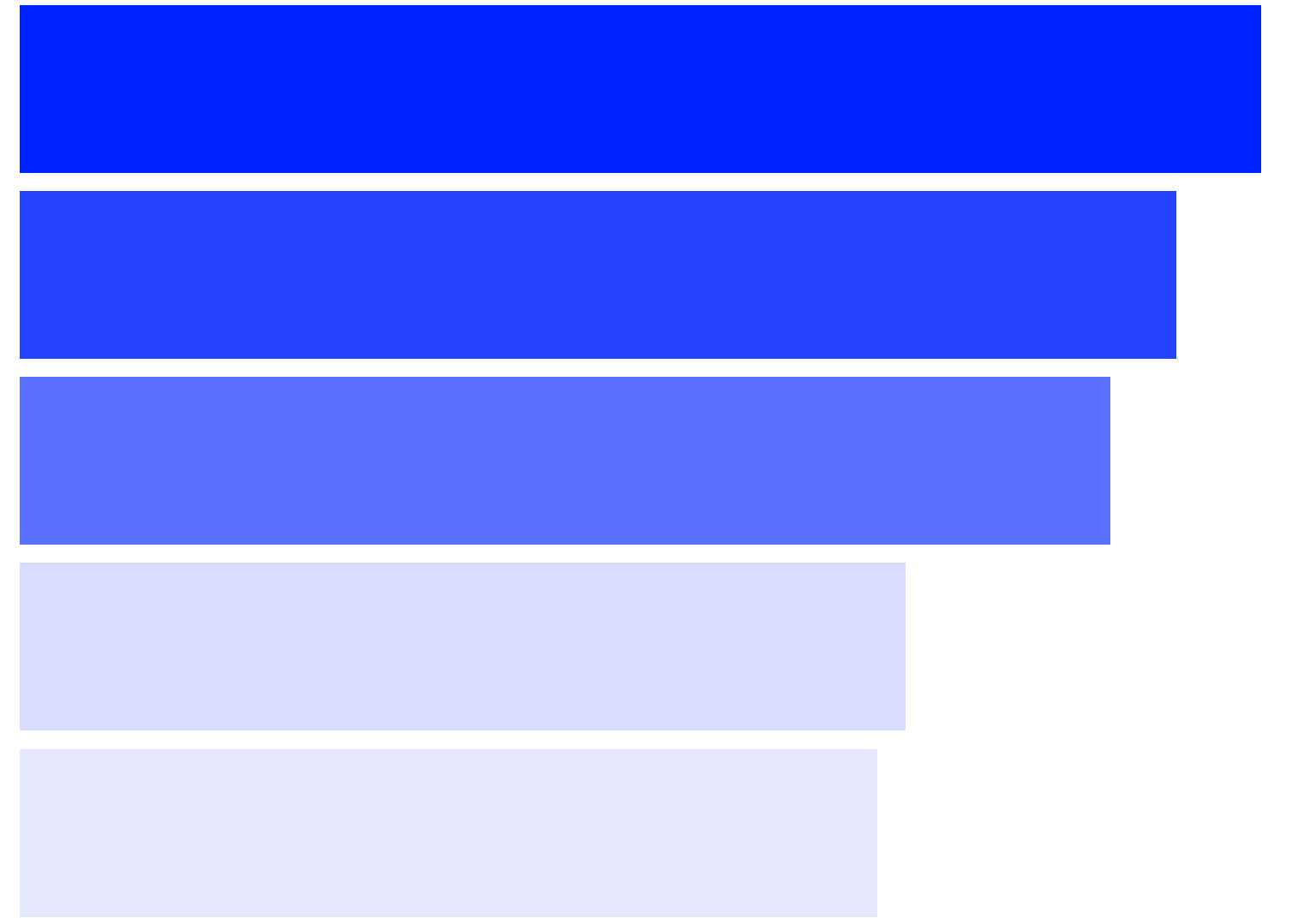
0

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6

log2Enrichment



Re-clustered module 16.7.10 MF enrichment

Term

hydrolase activity, acting on glycosyl bonds

0

1

2

3

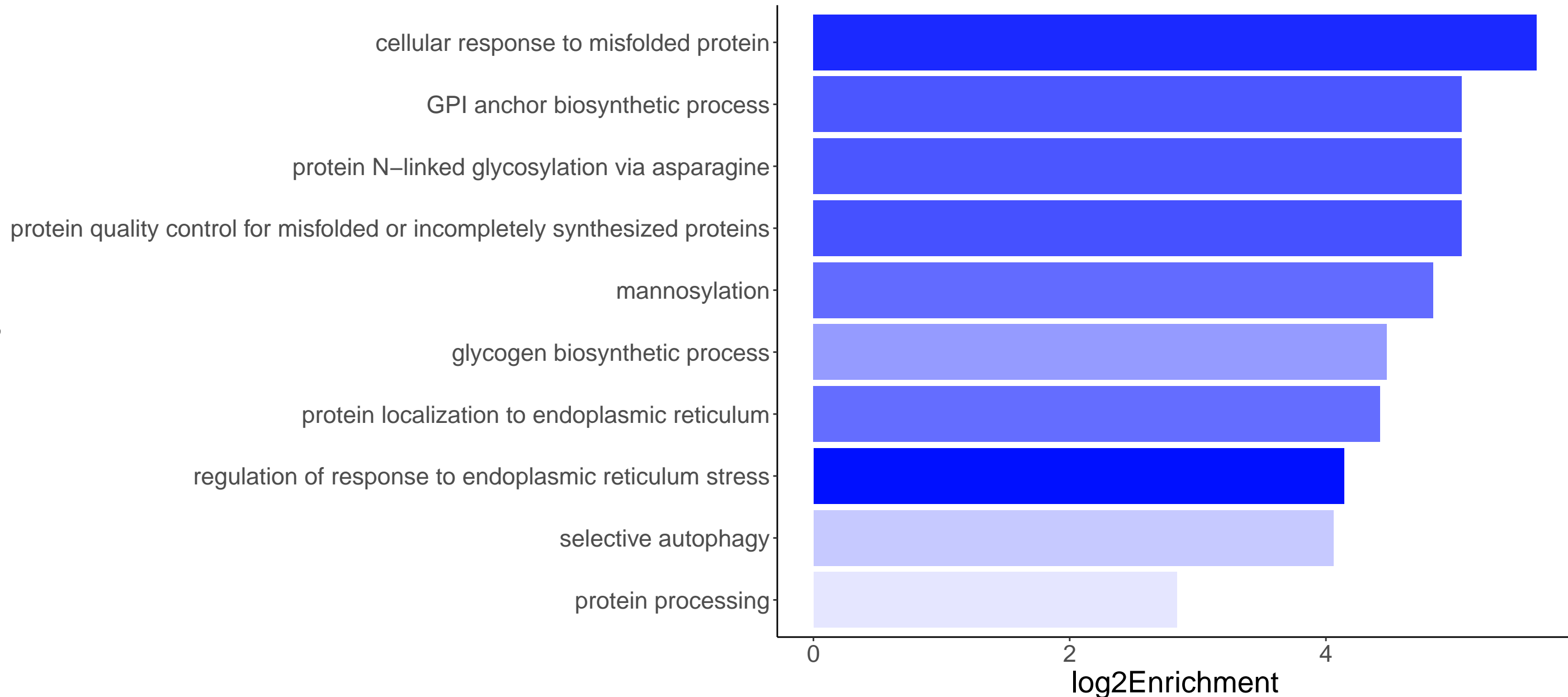
4

log2Enrichment



Re-clustered module 16.7.12 BP enrichment

Term



Re-clustered module 16.7.12 MF enrichment

Term

MHC protein binding

0

2

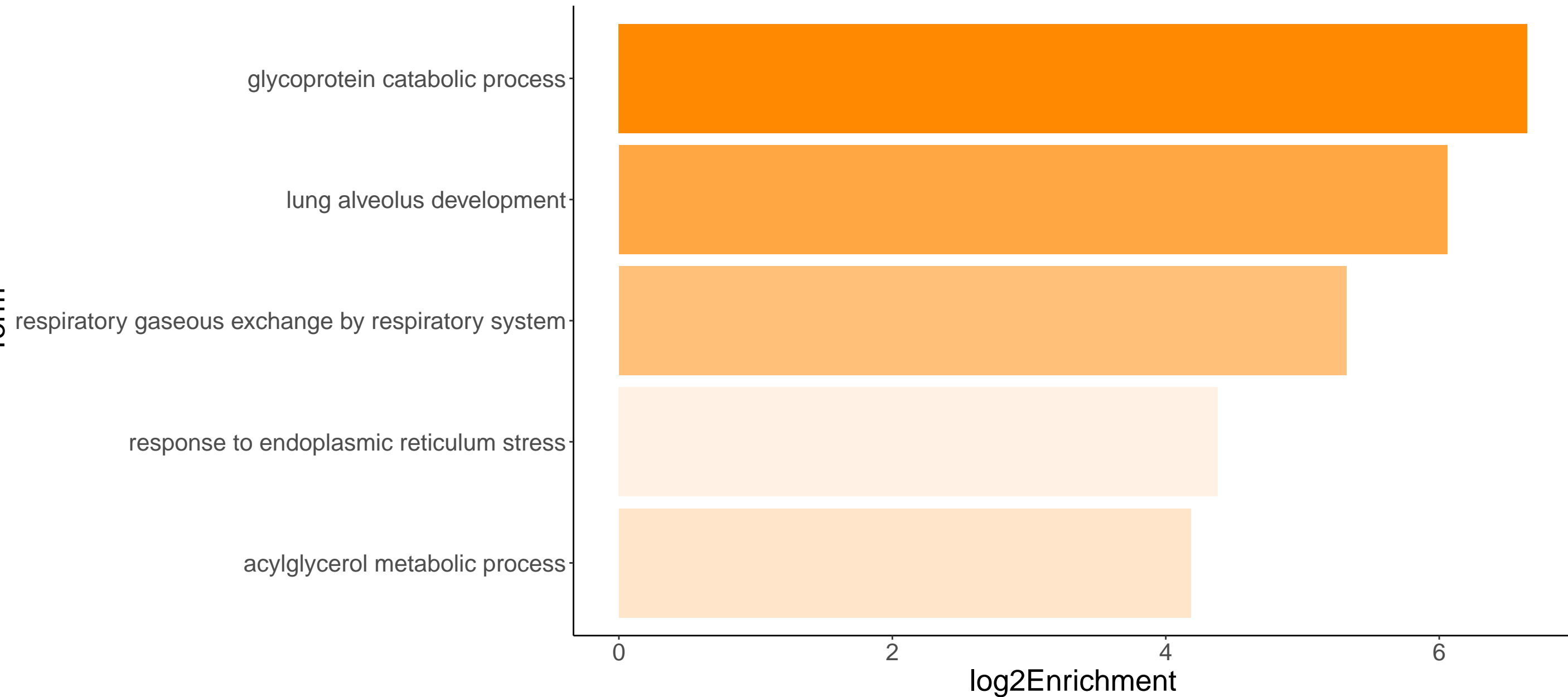
4

log2Enrichment



Re-clustered module 16.7.13 BP enrichment

Term



Re-clustered module 16.7.13 MF enrichment

Term

carboxylic ester hydrolase activity

calcium ion binding

0

1

2

3

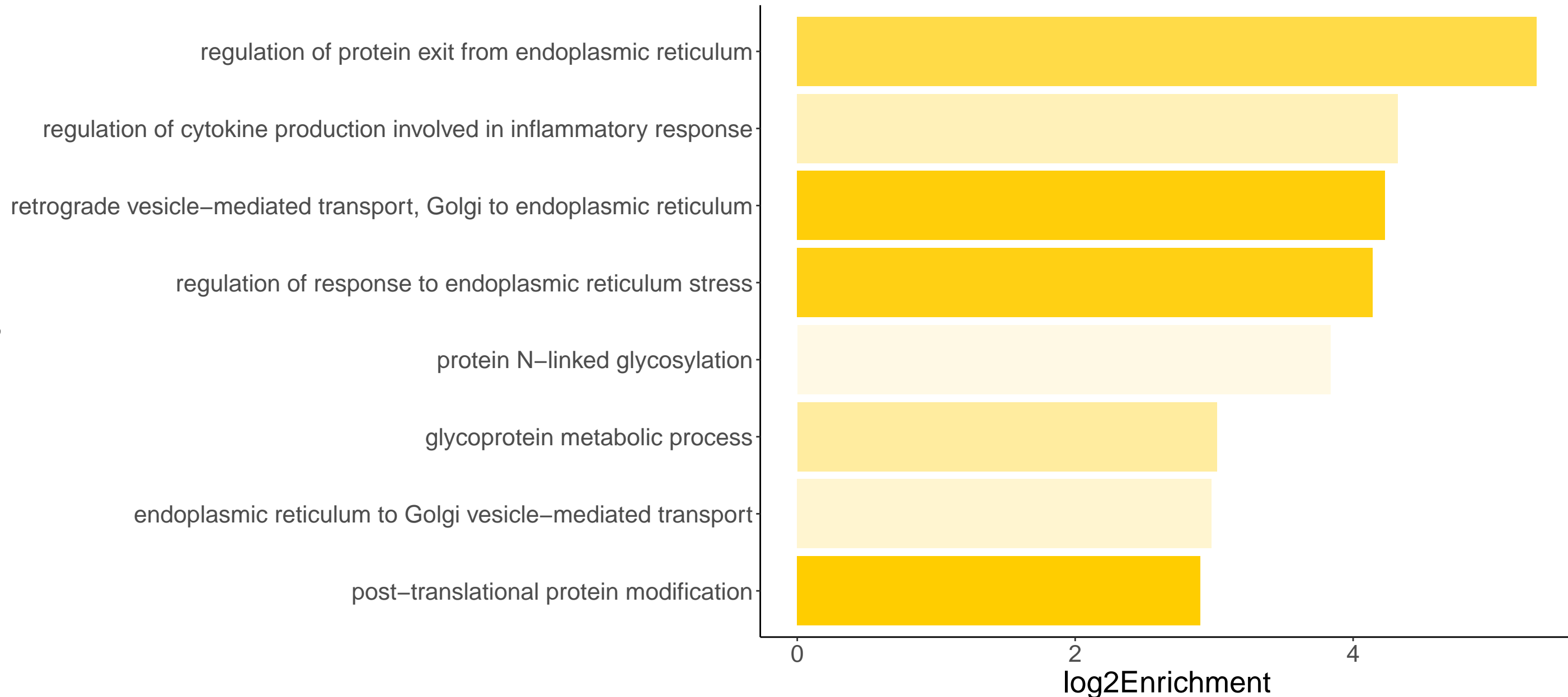
4

log2Enrichment



Re-clustered module 16.7.2 BP enrichment

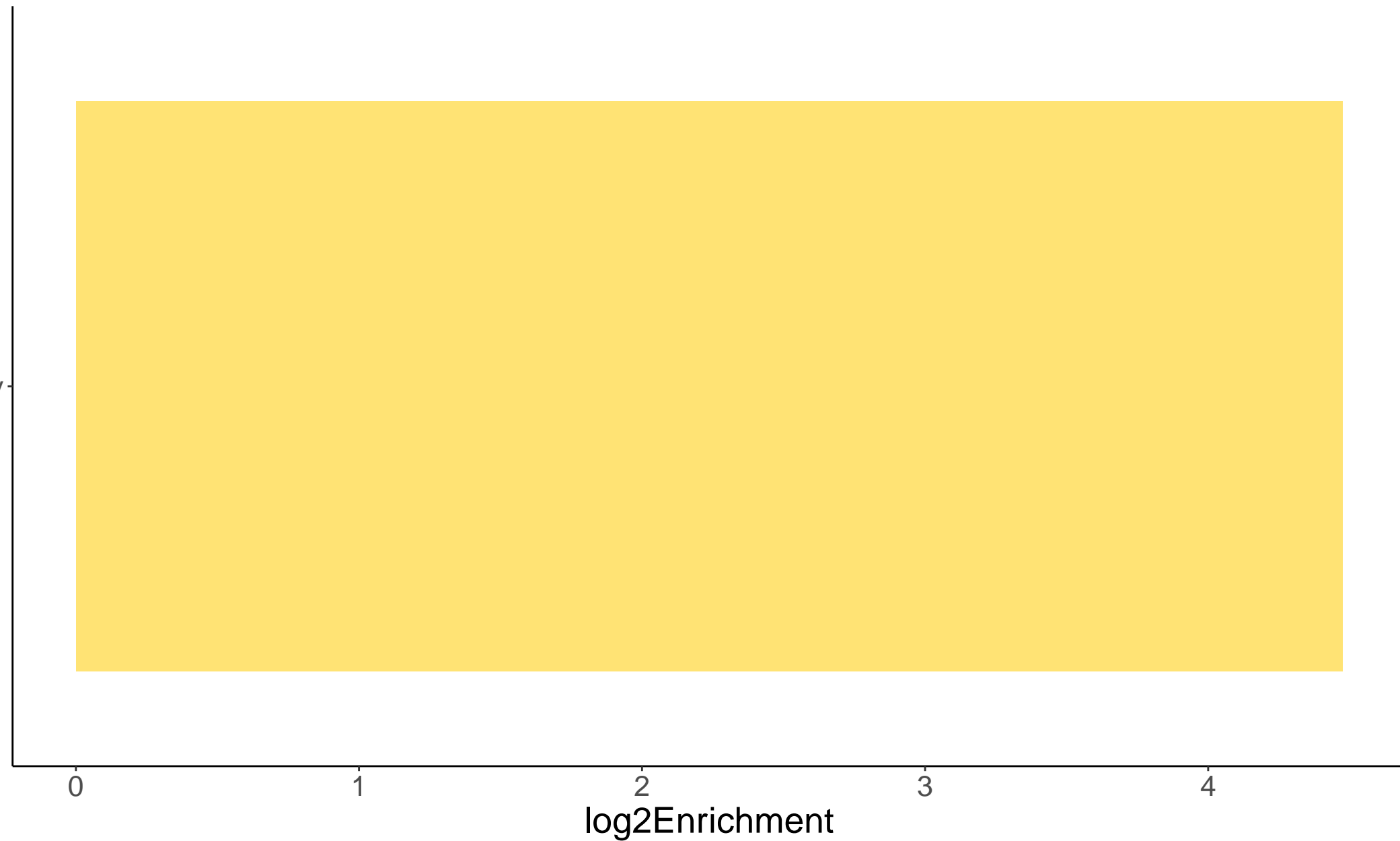
Term



Re-clustered module 16.7.2 MF enrichment

Term

intramolecular oxidoreductase activity



Re-clustered module 16.7.3 BP enrichment

Term

cellular response to misfolded protein

'de novo' posttranslational protein folding

ERAD pathway

retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum

0

2

4

log2Enrichment



Re-clustered module 16.7.3 MF enrichment

Term

Hsp70 protein binding

myosin binding

0

1

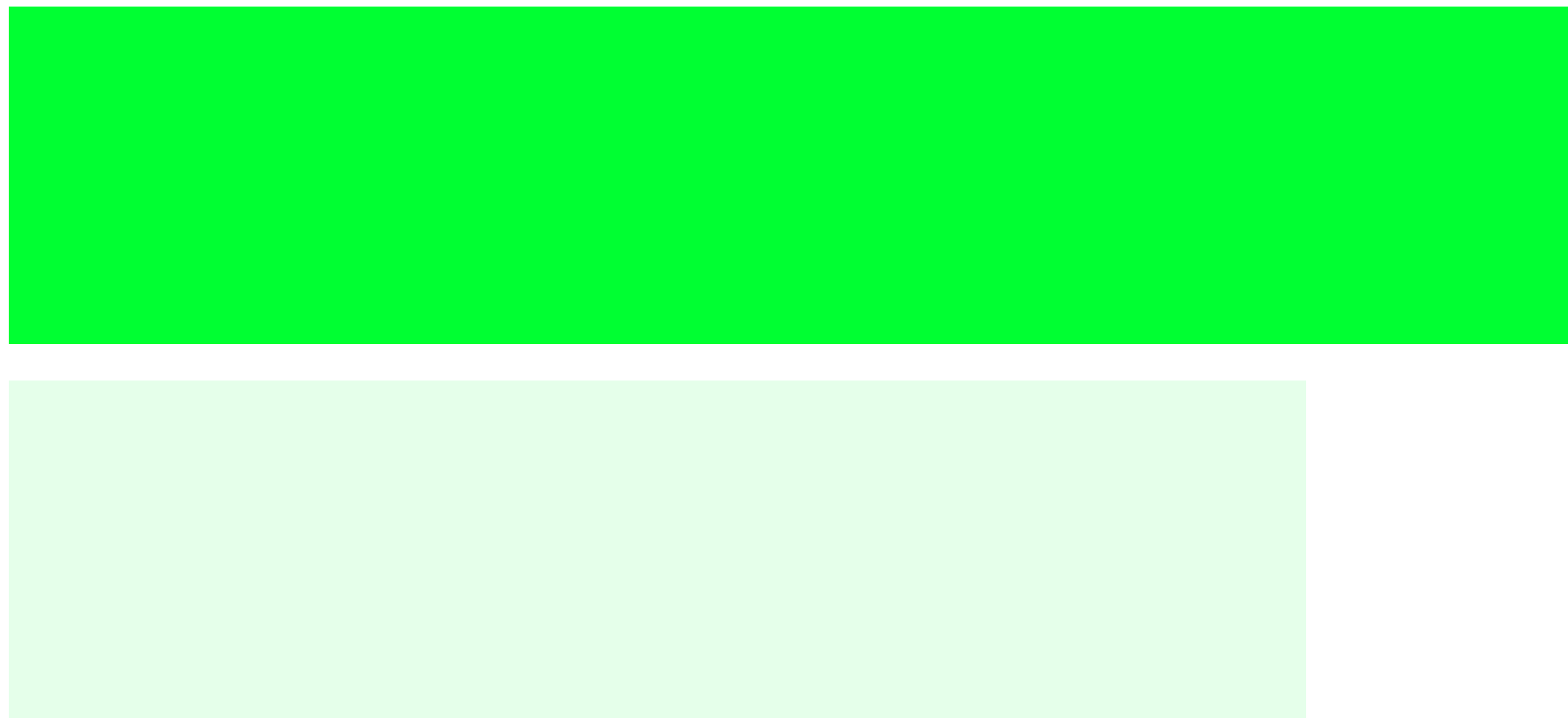
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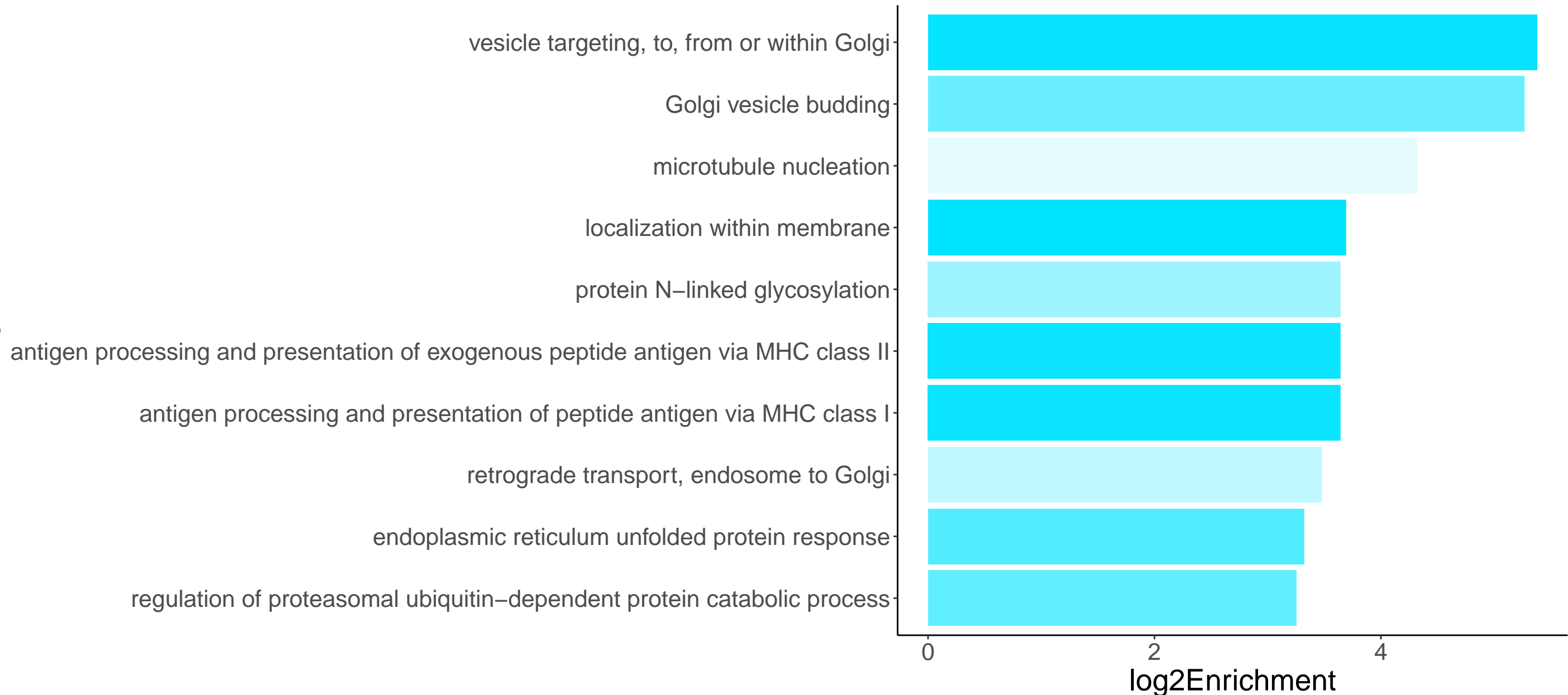
5

log2Enrichment



Re-clustered module 16.7.4 BP enrichment

Term



Re-clustered module 16.7.4 MF enrichment

Term

SNAP receptor activity

protein kinase binding

0

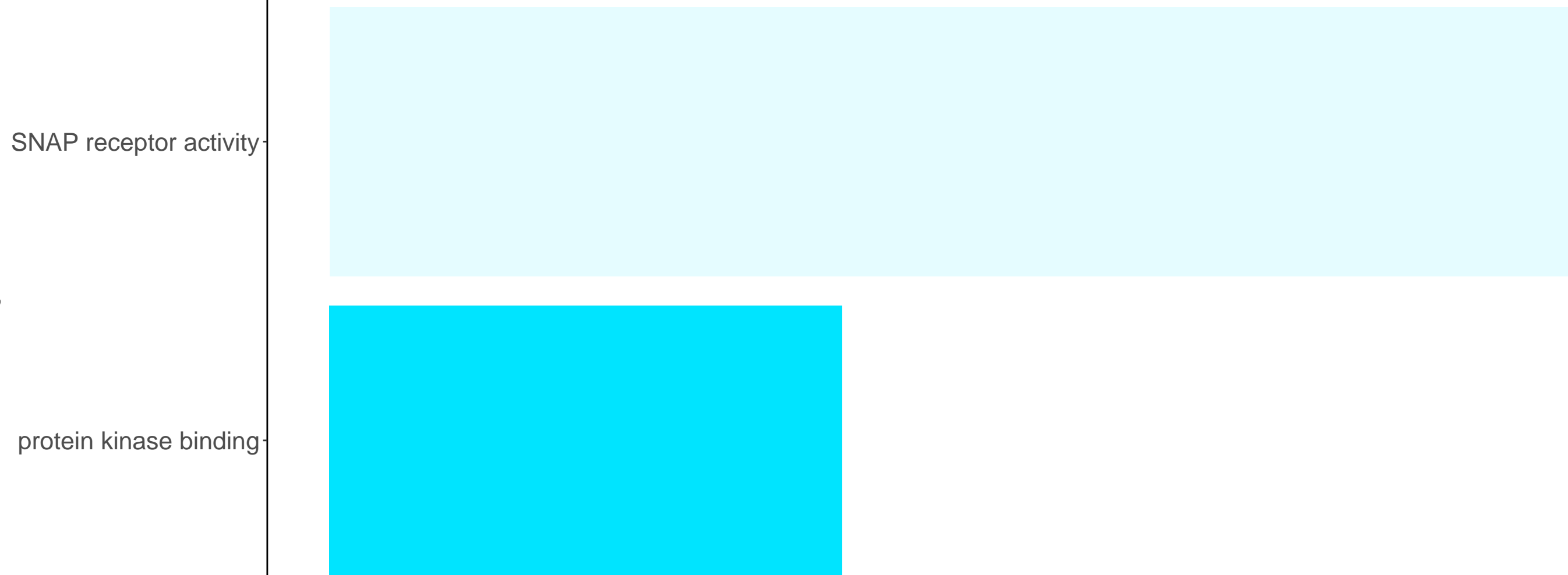
1

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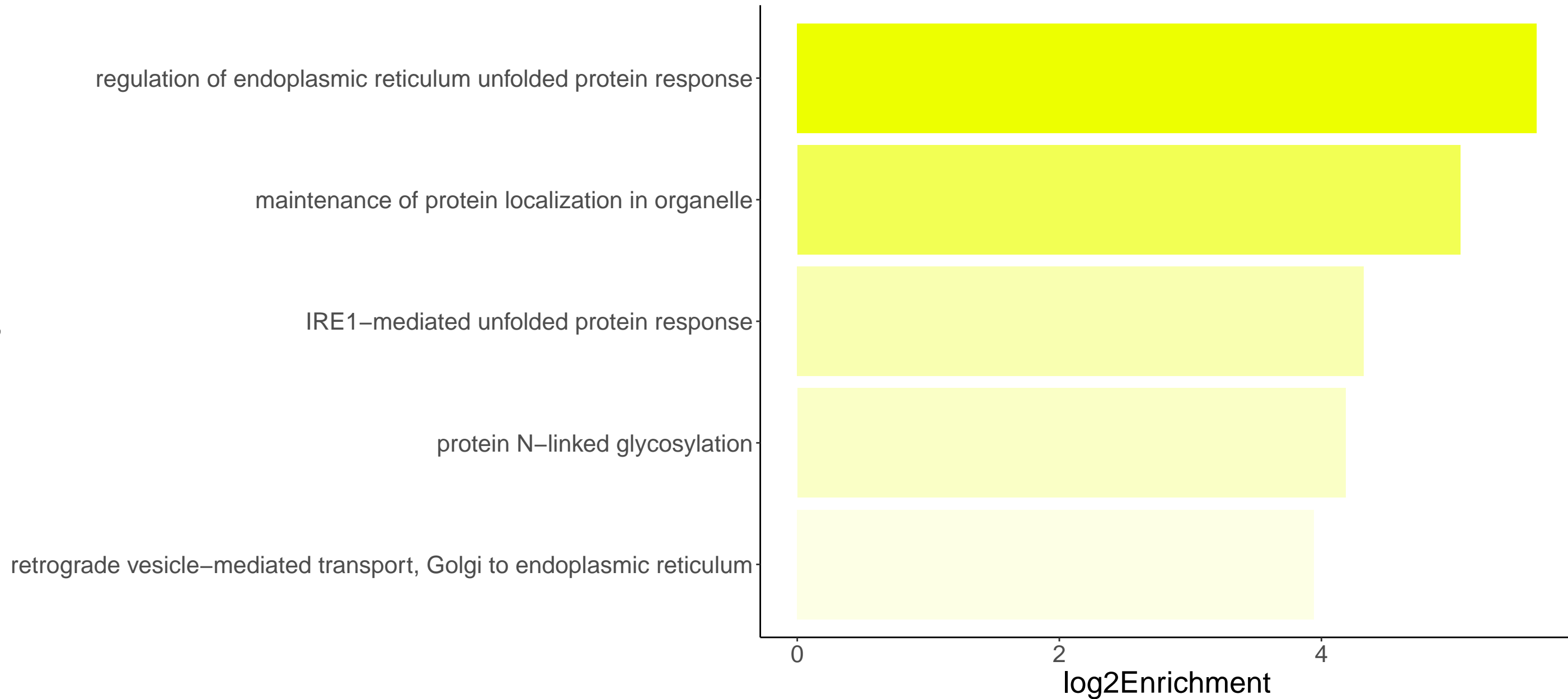
4

log2Enrichment



Re-clustered module 16.7.5 BP enrichment

Term



Re-clustered module 16.7.5 MF enrichment

Term

misfolded protein binding

transition metal ion transmembrane transporter activity

transferase activity, transferring alkyl or aryl (other than methyl) groups

heat shock protein binding

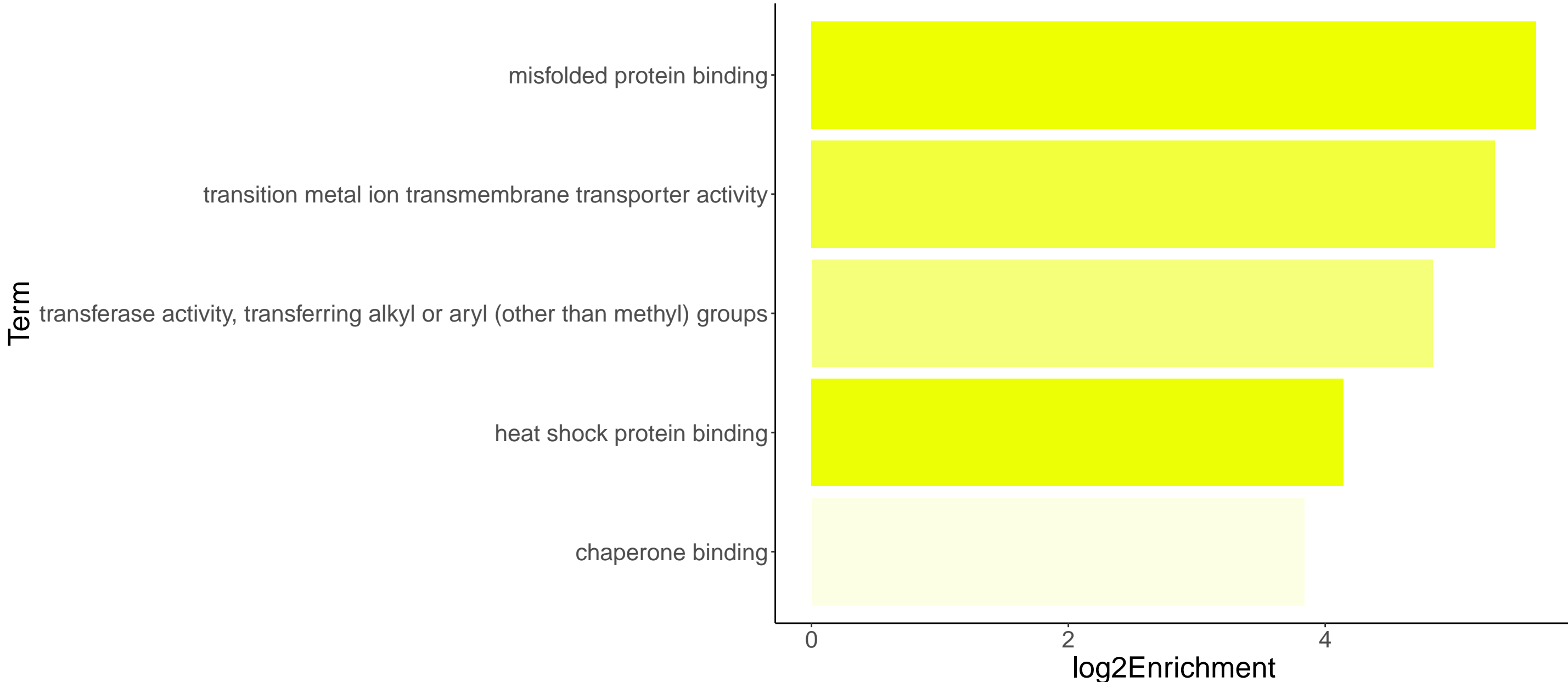
chaperone binding

0

2

4

log2Enrichment



Re-clustered module 16.7.6 BP enrichment

Term

gastrulation with mouth forming second

embryonic camera-type eye development

Golgi organization

vitamin metabolic process

post-translational protein modification

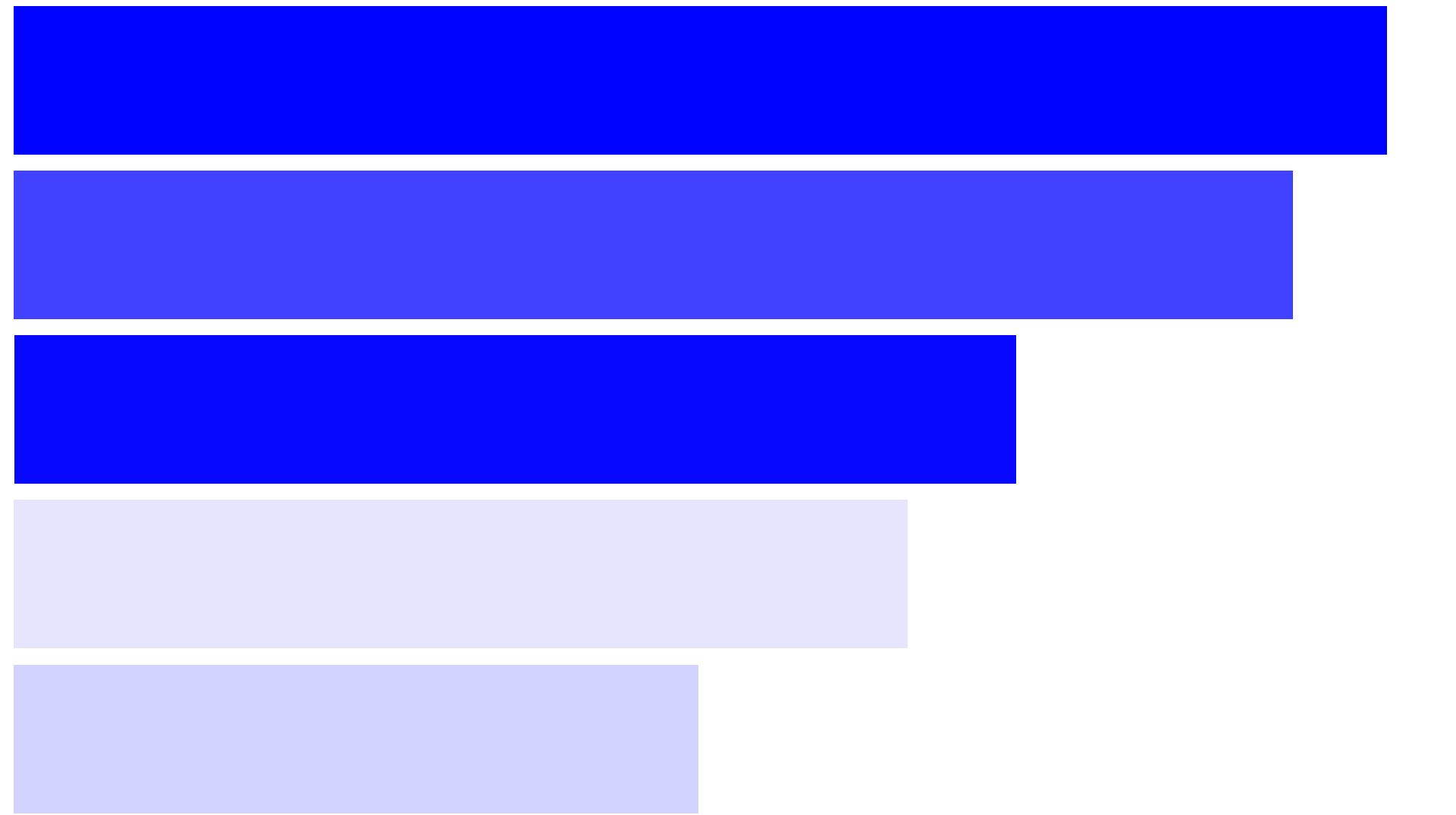
0

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4

6

log2Enrichment



Re-clustered module 16.7.6 MF enrichment

Term

GDP binding

GTPase activity

GTP binding

0

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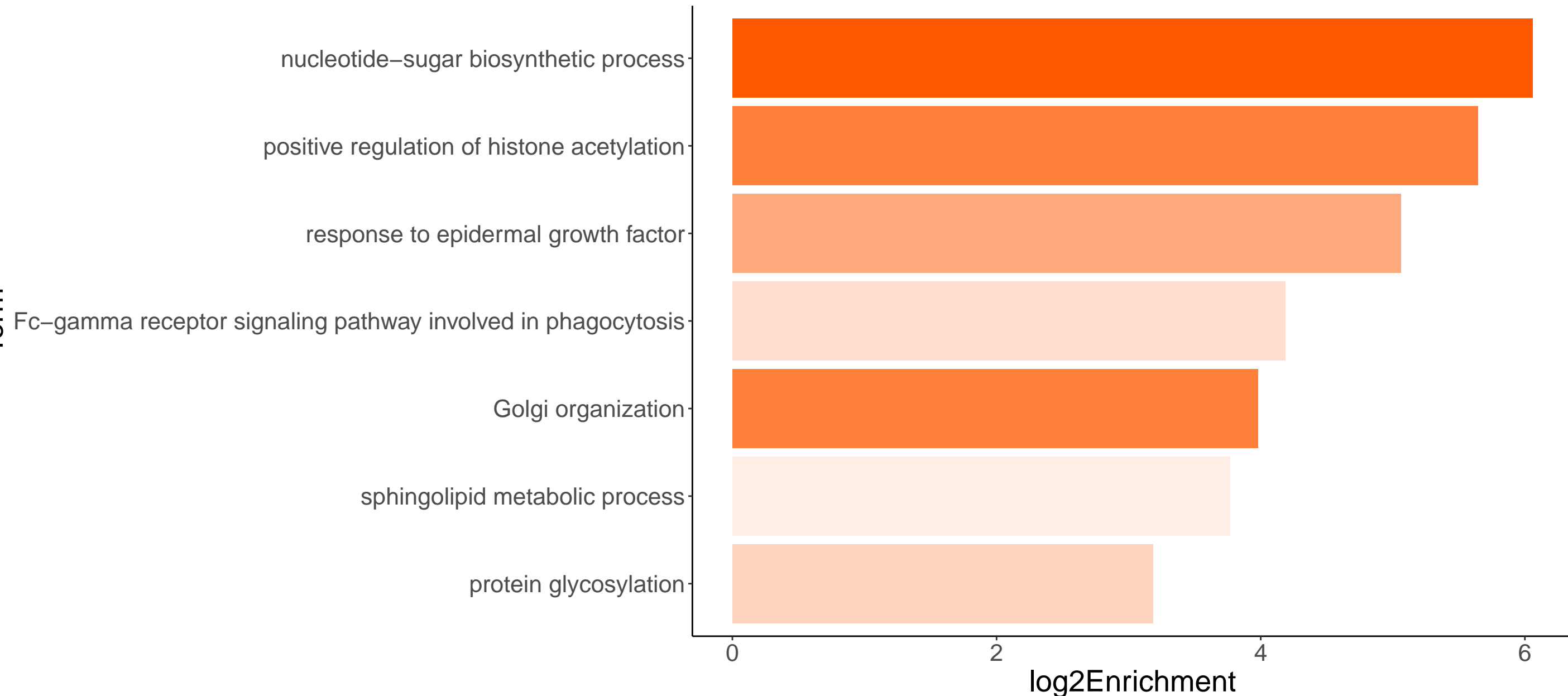
4

log2Enrichment



Re-clustered module 16.7.7 BP enrichment

Term



Re-clustered module 16.7.7 MF enrichment

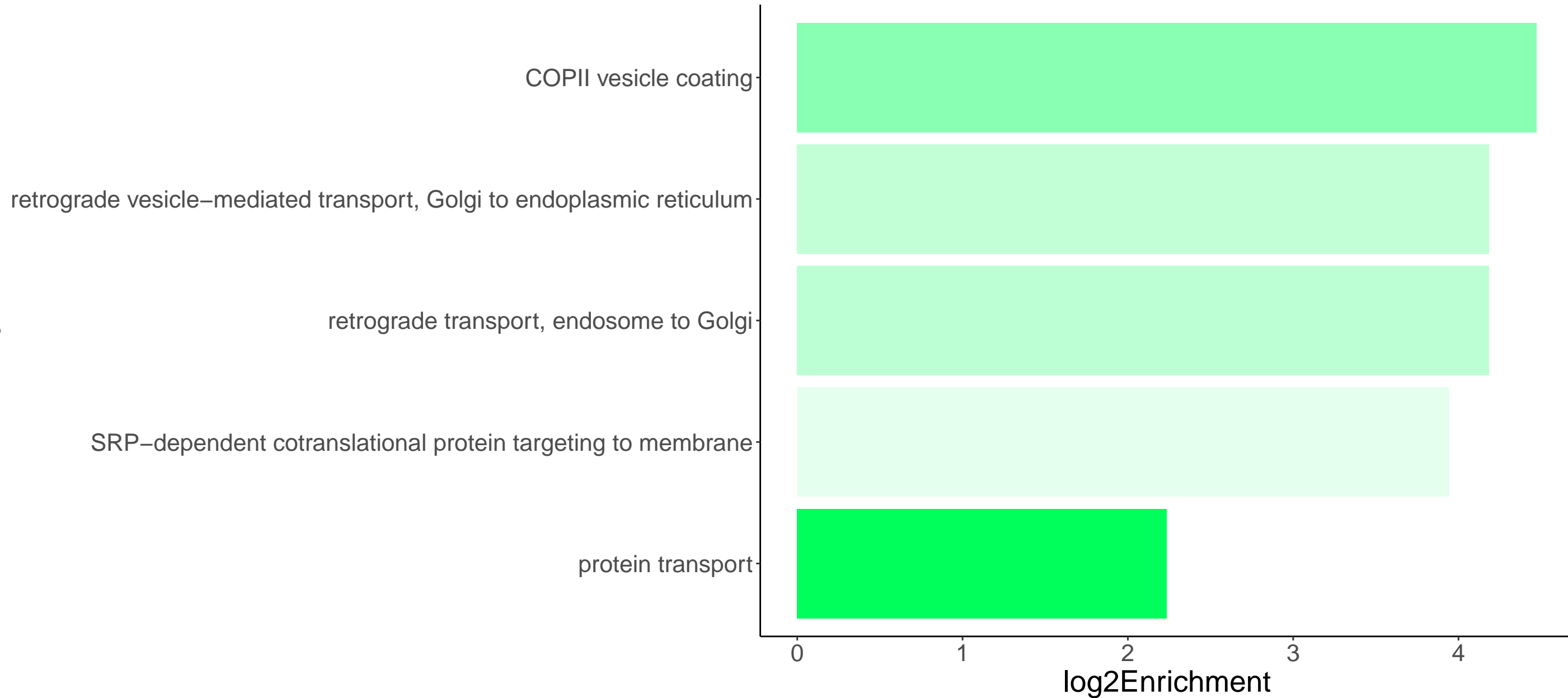
Term

log2Enrichment



Re-clustered module 16.7.8 BP enrichment

Term



Re-clustered module 16.7.8 MF enrichment

Term

unfolded protein binding

0

1

2

3

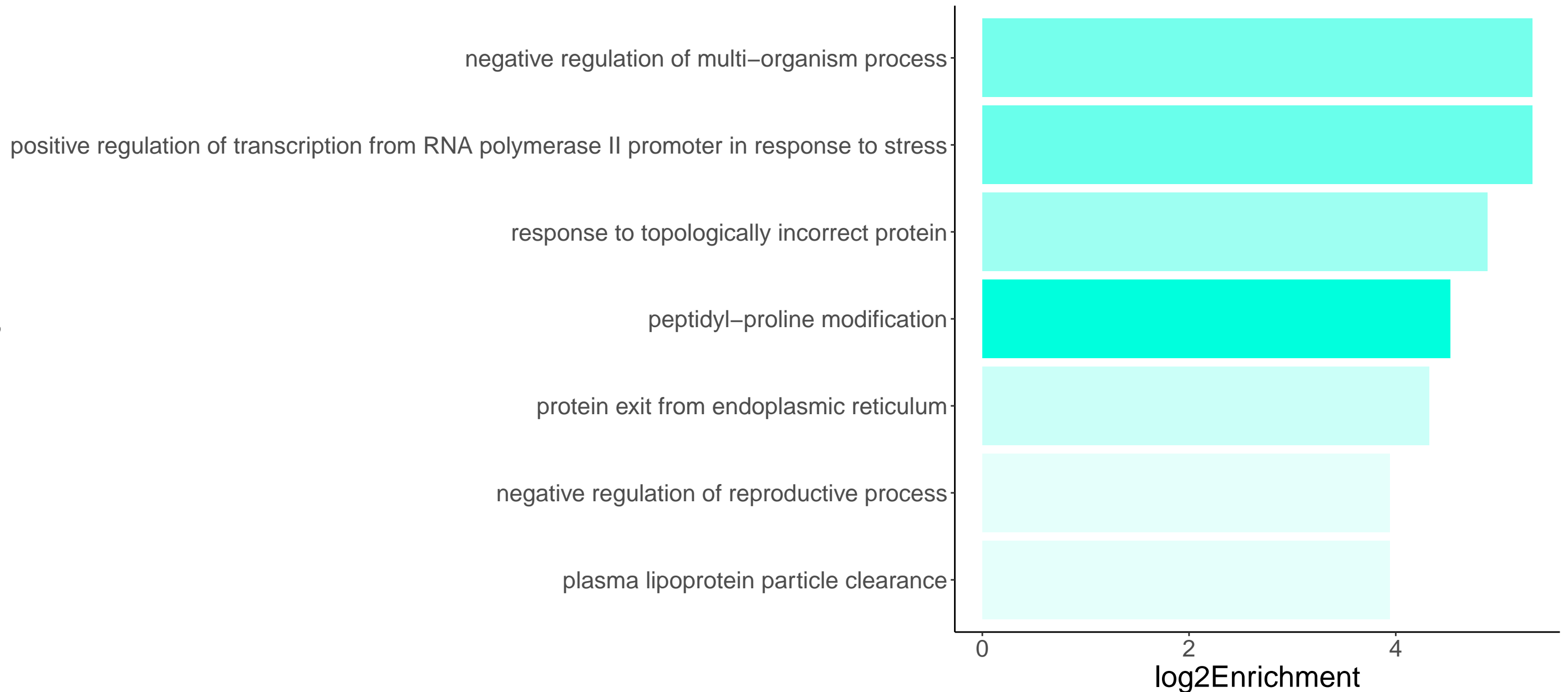
4

log2Enrichment



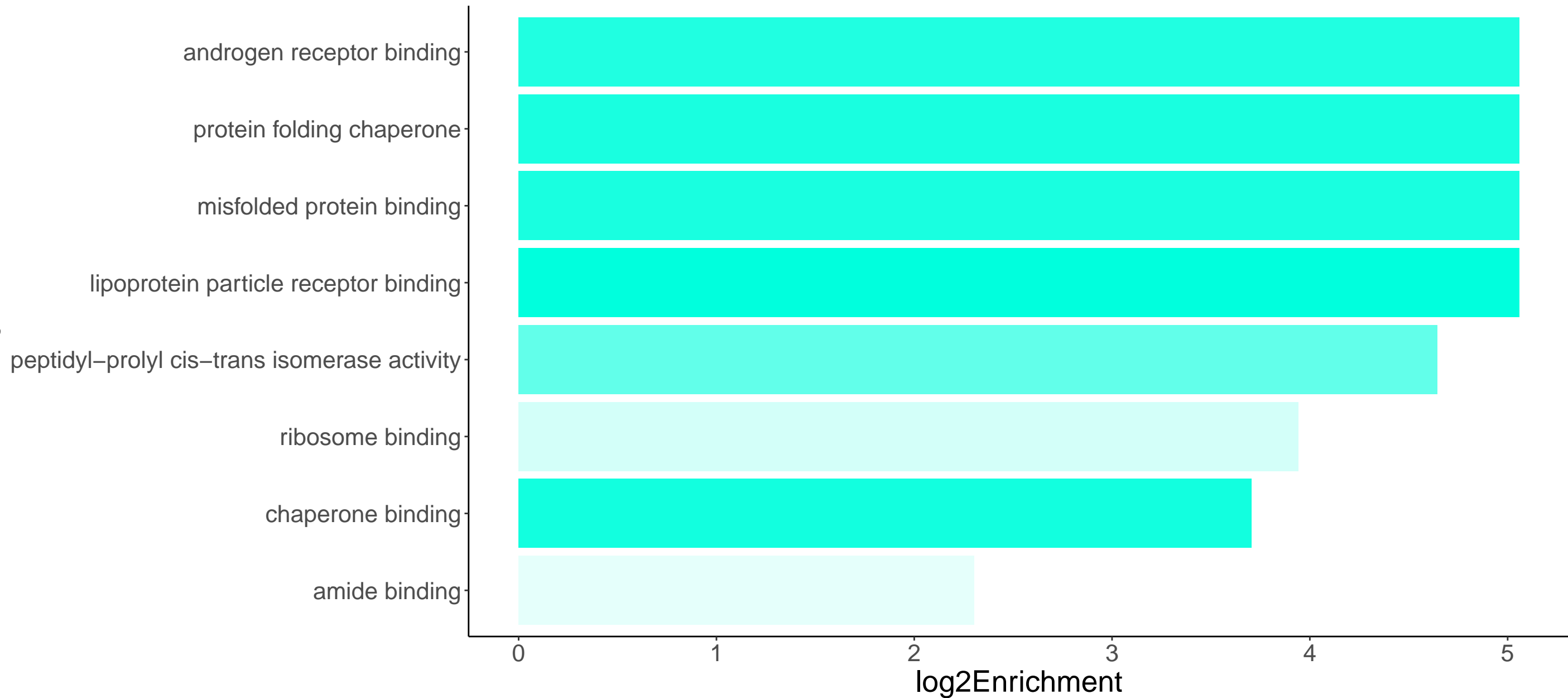
Re-clustered module 16.7.9 BP enrichment

Term



Re-clustered module 16.7.9 MF enrichment

Term



Re-clustered module 16.8.1 BP enrichment

Term

negative regulation of JNK cascade

mannosylation

0

2

4

6

log2Enrichment



Re-clustered module 16.8.1 MF enrichment

Term

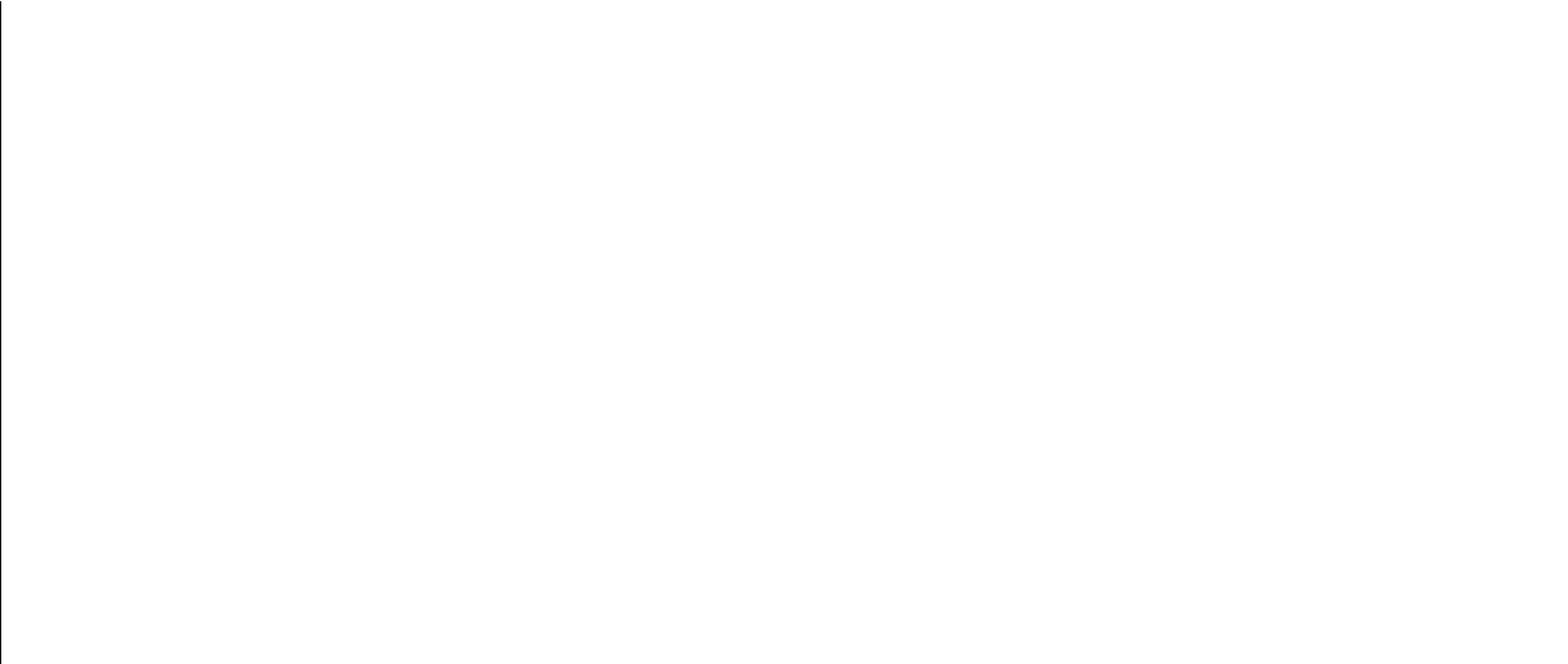
log2Enrichment



Re-clustered module 16.8.10 BP enrichment

Term

log2Enrichment



Re-clustered module 16.8.10 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.11 BP enrichment

Term

determination of left/right symmetry

pancreas development

digestive tract development

spermatid development

0

1

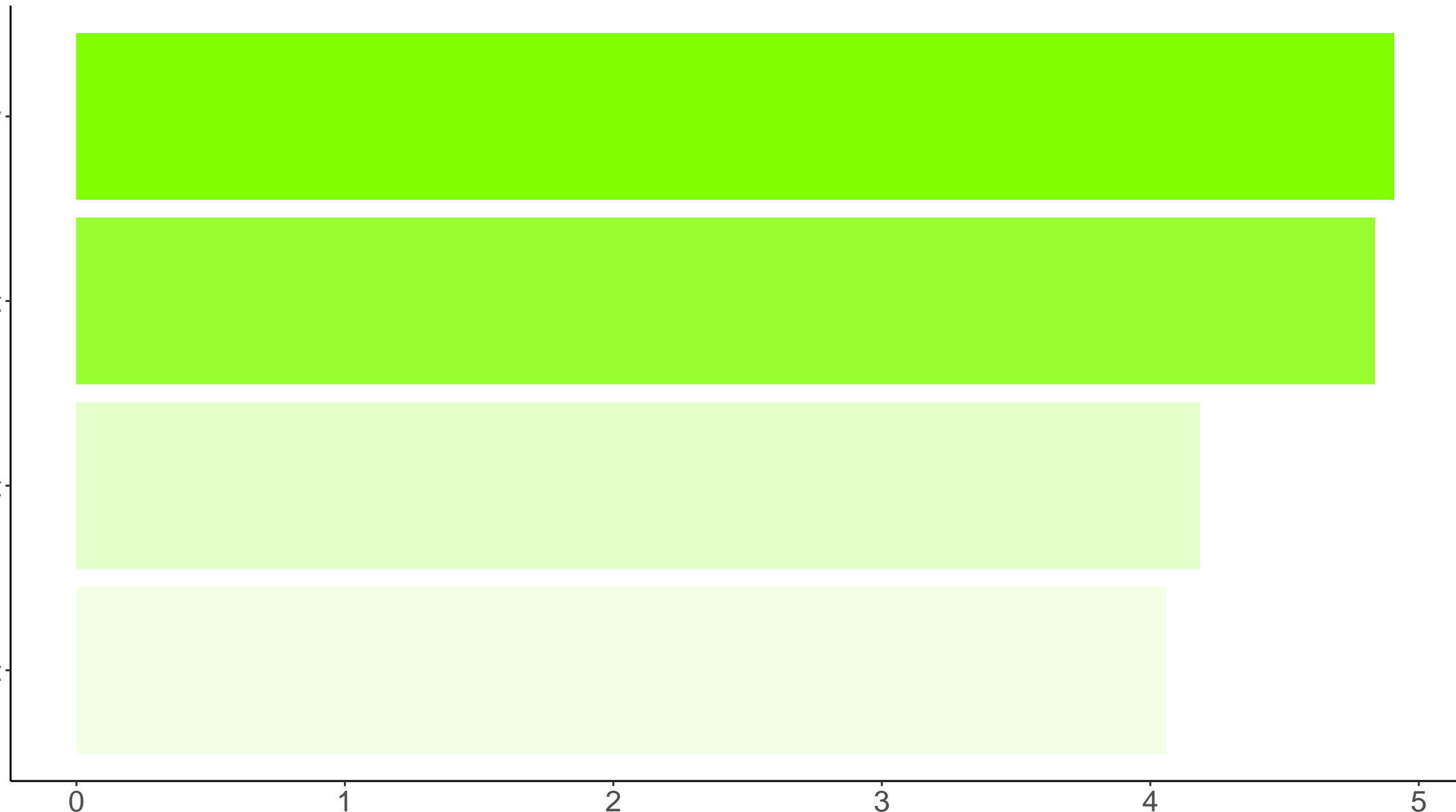
2

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4

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log2Enrichment



Re-clustered module 16.8.11 MF enrichment

Term

beta-tubulin binding

0

2

4

6

log2Enrichment



Re-clustered module 16.8.12 BP enrichment

Term

detection of stimulus involved in sensory perception of pain

detection of temperature stimulus

sensory perception of temperature stimulus

response to acidic pH

cellular response to pH

negative regulation of nervous system development

cilium assembly

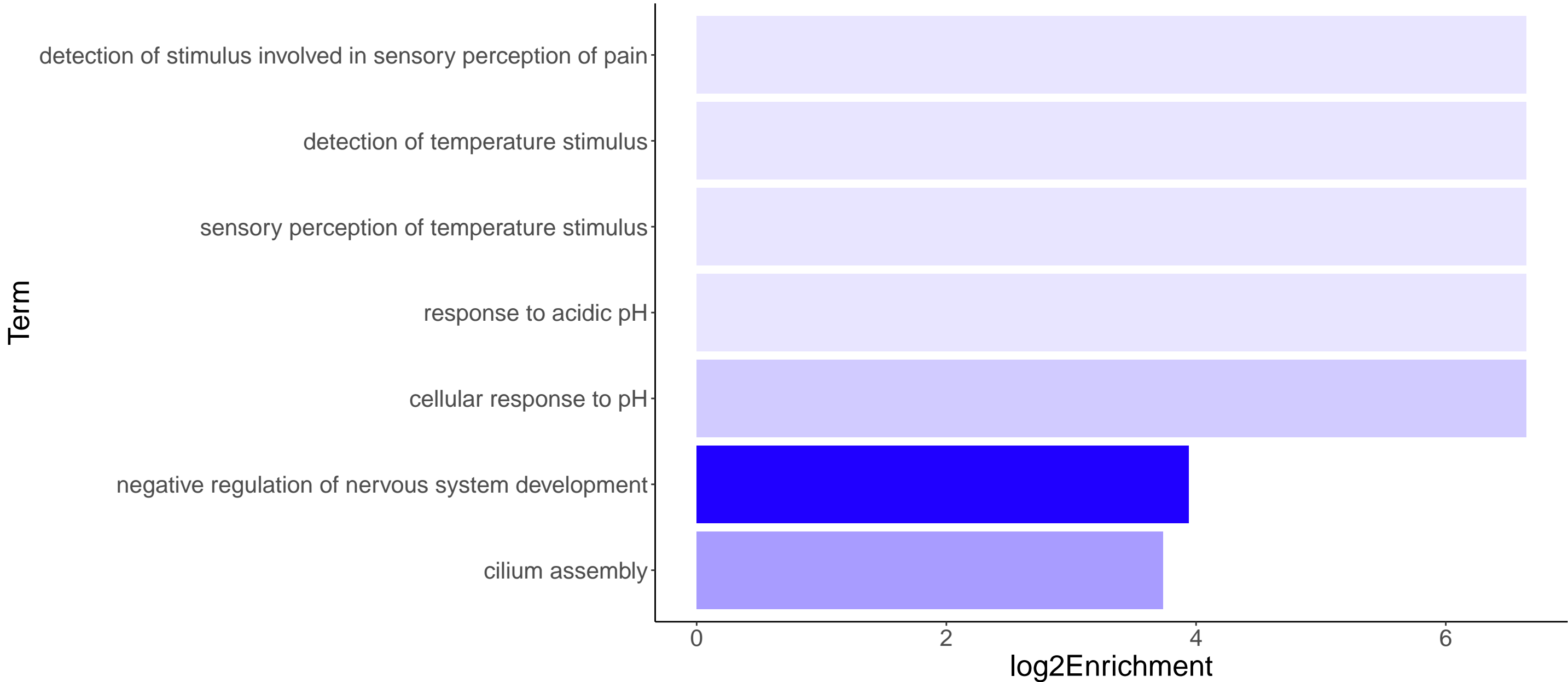
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6

log2Enrichment



Re-clustered module 16.8.12 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.13 BP enrichment

Term

intraciliary transport involved in cilium assembly

gluconeogenesis

smoothened signaling pathway

0

2

4

log2Enrichment



Re-clustered module 16.8.13 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.16 BP enrichment

Term

positive regulation of cell morphogenesis involved in differentiation

0

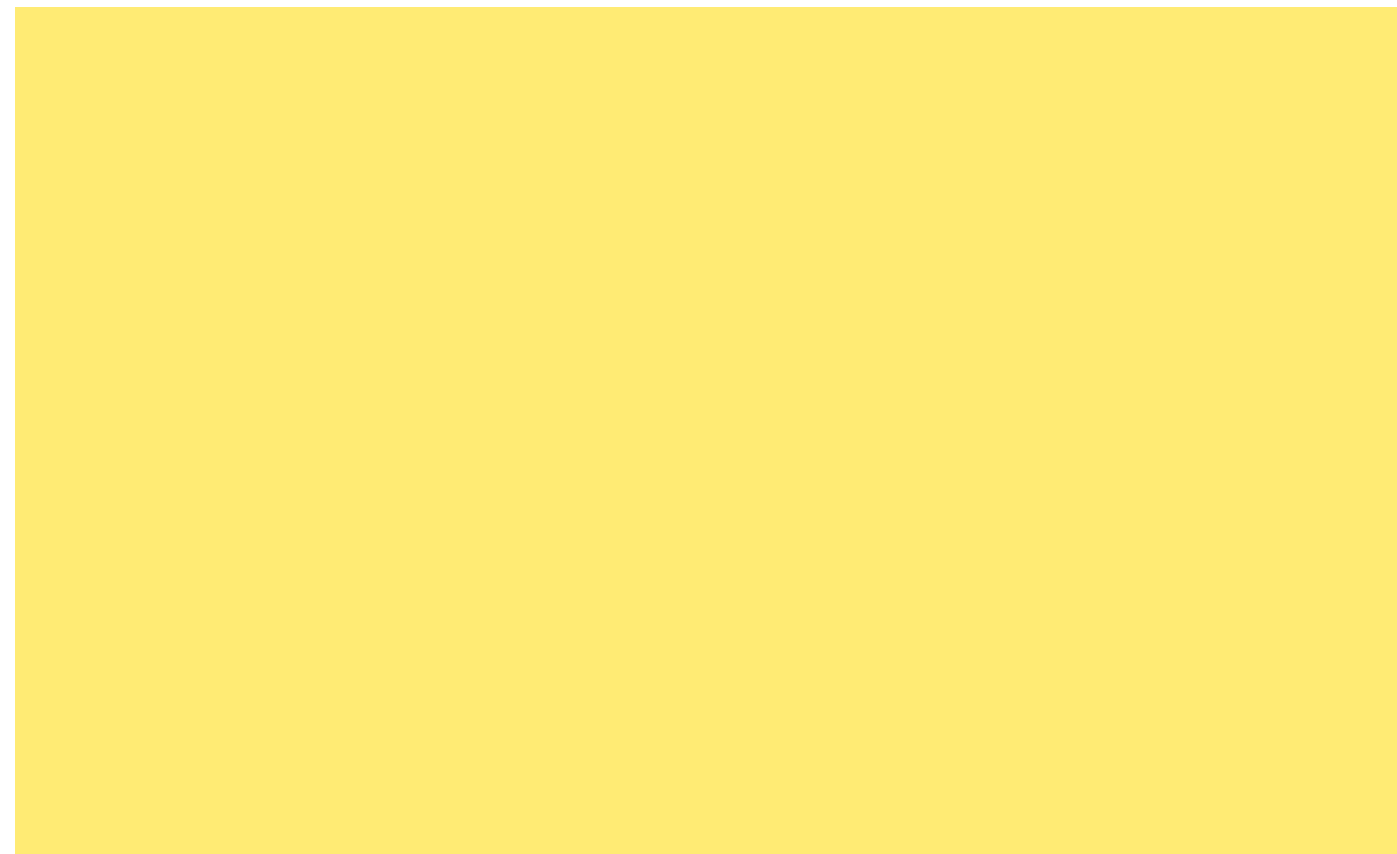
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log2Enrichment



Re-clustered module 16.8.16 MF enrichment

Term

single-stranded RNA binding

purine ribonucleoside triphosphate binding

0

2

4

log2Enrichment



Re-clustered module 16.8.2 BP enrichment

Term

regulation of macrophage chemotaxis

mammary gland epithelial cell proliferation

cilium-dependent cell motility

cilium movement

response to glucose

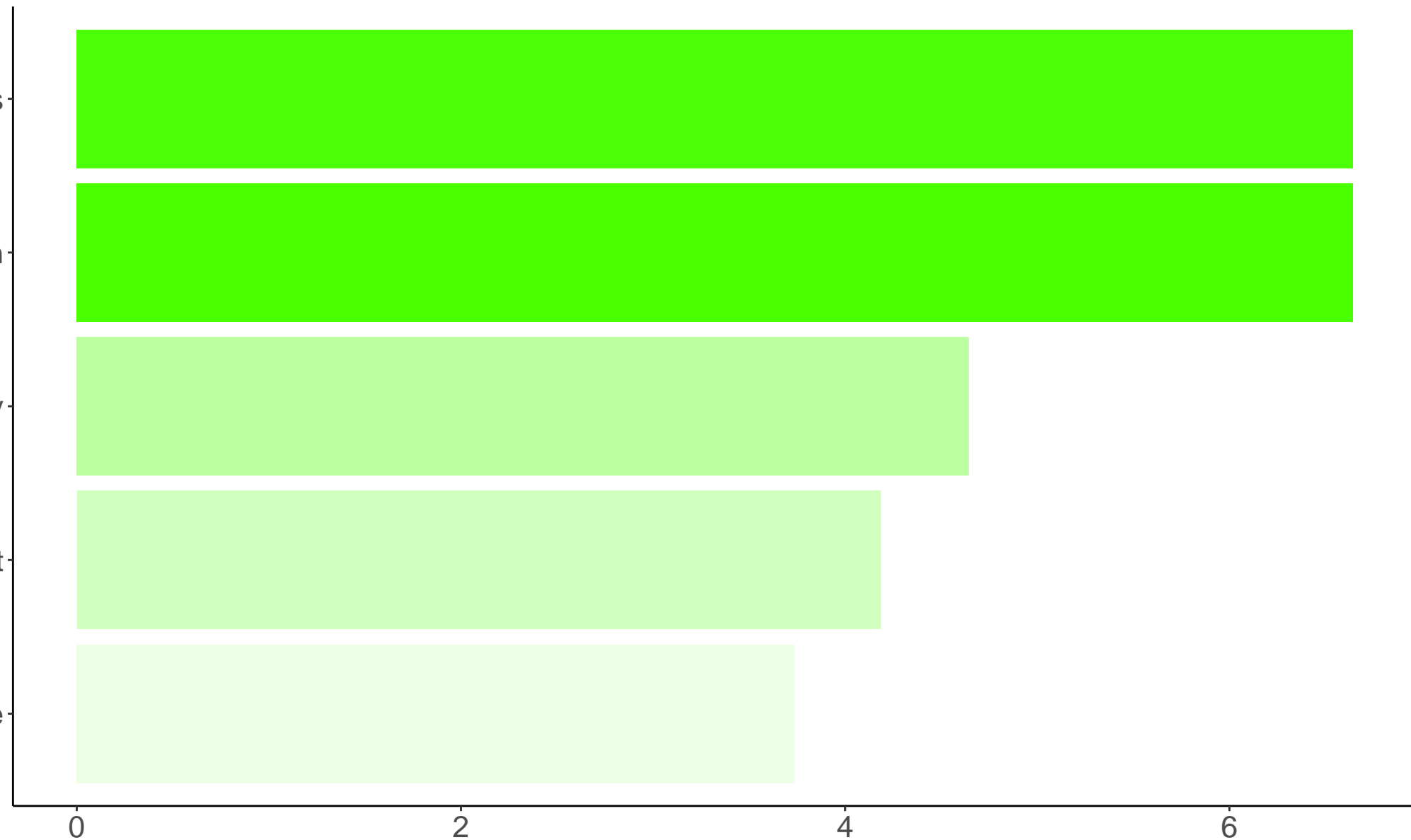
0

2

4

6

log2Enrichment



Re-clustered module 16.8.2 MF enrichment

Term

endopeptidase activity

calcium ion binding

0

1

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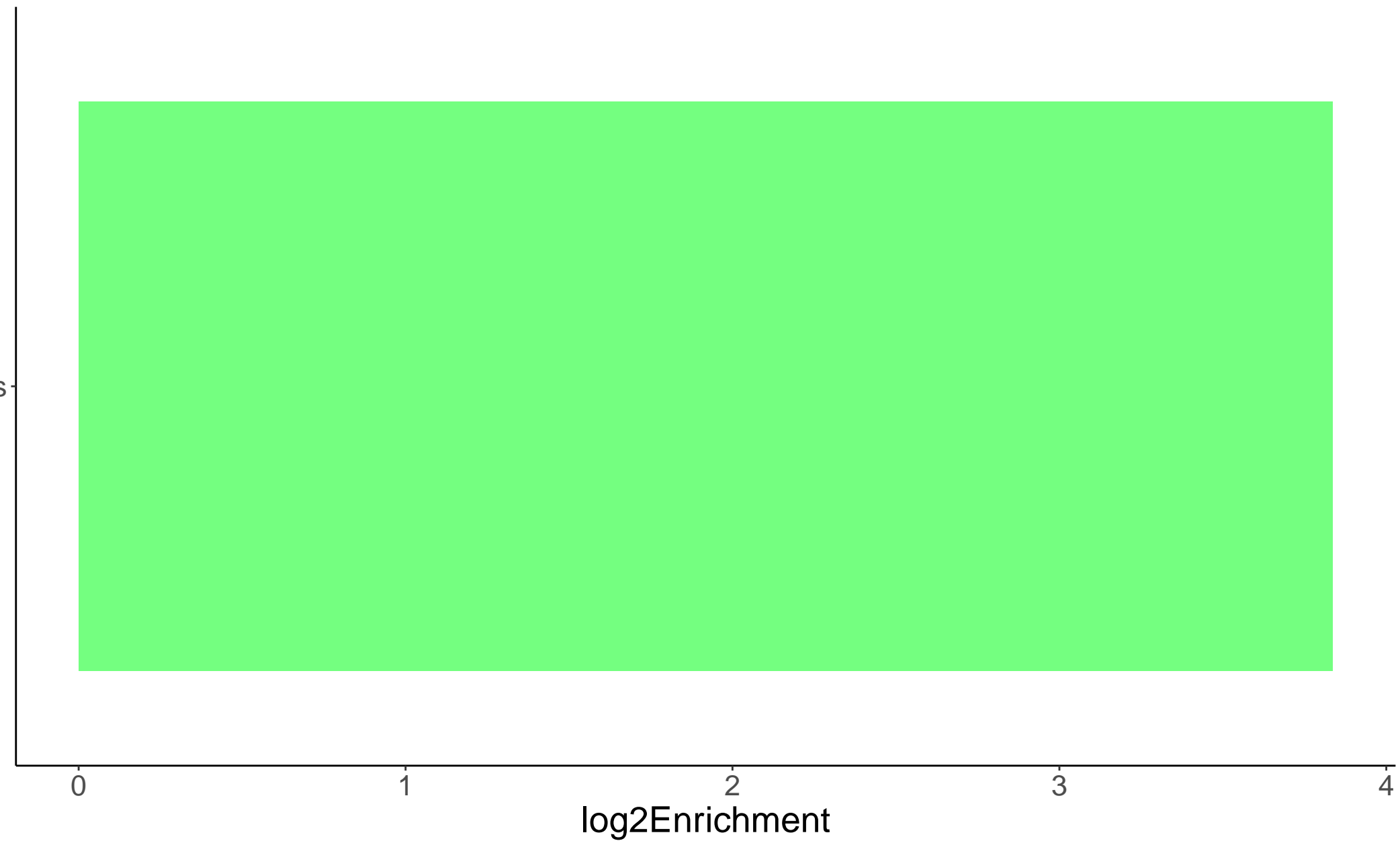
3

log2Enrichment



Re-clustered module 16.8.3 BP enrichment

Term
monocarboxylic acid catabolic process



Re-clustered module 16.8.3 MF enrichment

Term

manganese ion binding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.8.4 BP enrichment

Term

protein autoubiquitination

regulation of transcription by RNA polymerase II

0

1

2

3

4

log2Enrichment



Re-clustered module 16.8.4 MF enrichment

Term
ubiquitin-protein transferase activity

0

1

2

log2Enrichment



Re-clustered module 16.8.5 BP enrichment

Term

embryonic camera-type eye development

neural tube patterning

photoreceptor cell maintenance

Golgi to plasma membrane transport

embryonic digit morphogenesis

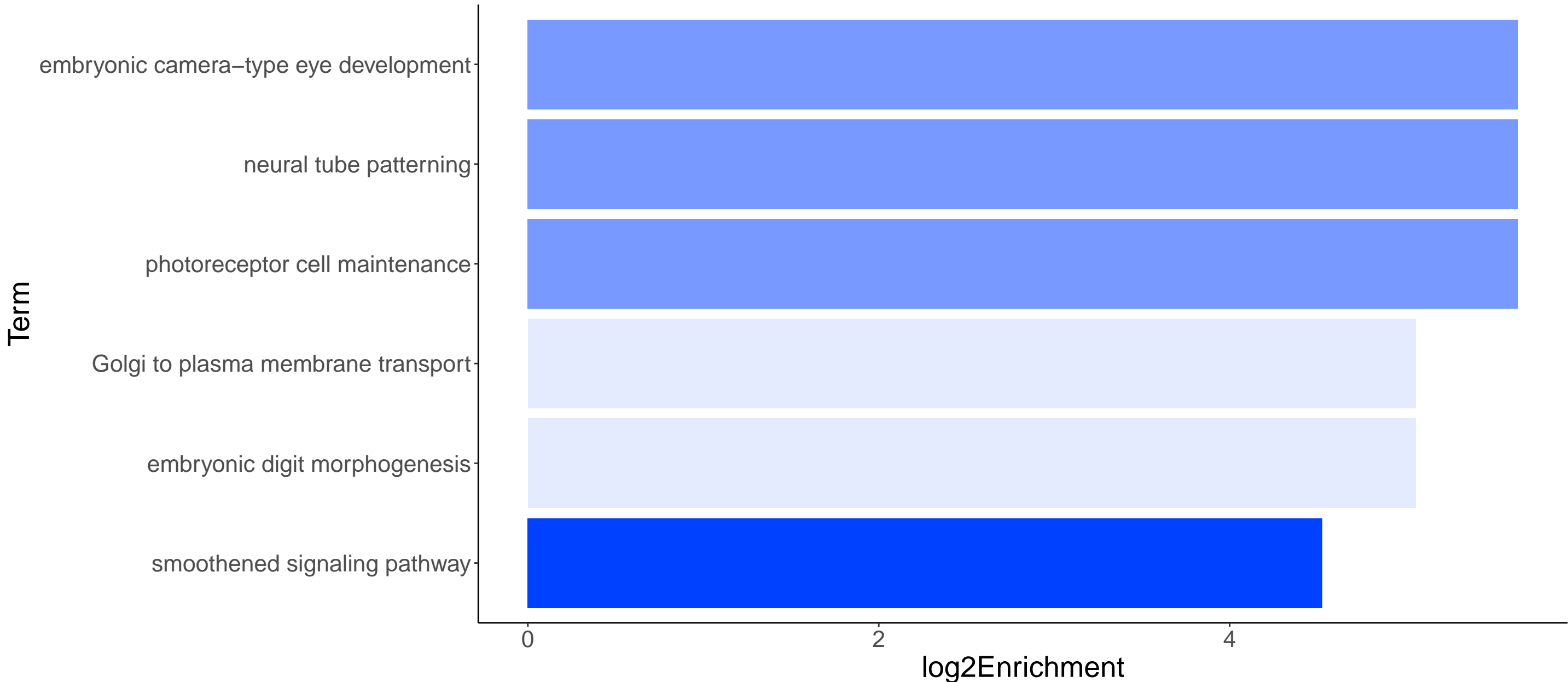
smoothened signaling pathway

0

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log2Enrichment



Re-clustered module 16.8.5 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.6 BP enrichment

Term

intraciliary transport

photoreceptor cell development

protein localization to cilium

transcription-coupled nucleotide-excision repair

cilium movement involved in cell motility

0

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log2Enrichment



Re-clustered module 16.8.6 MF enrichment

Term

modified amino acid binding

0

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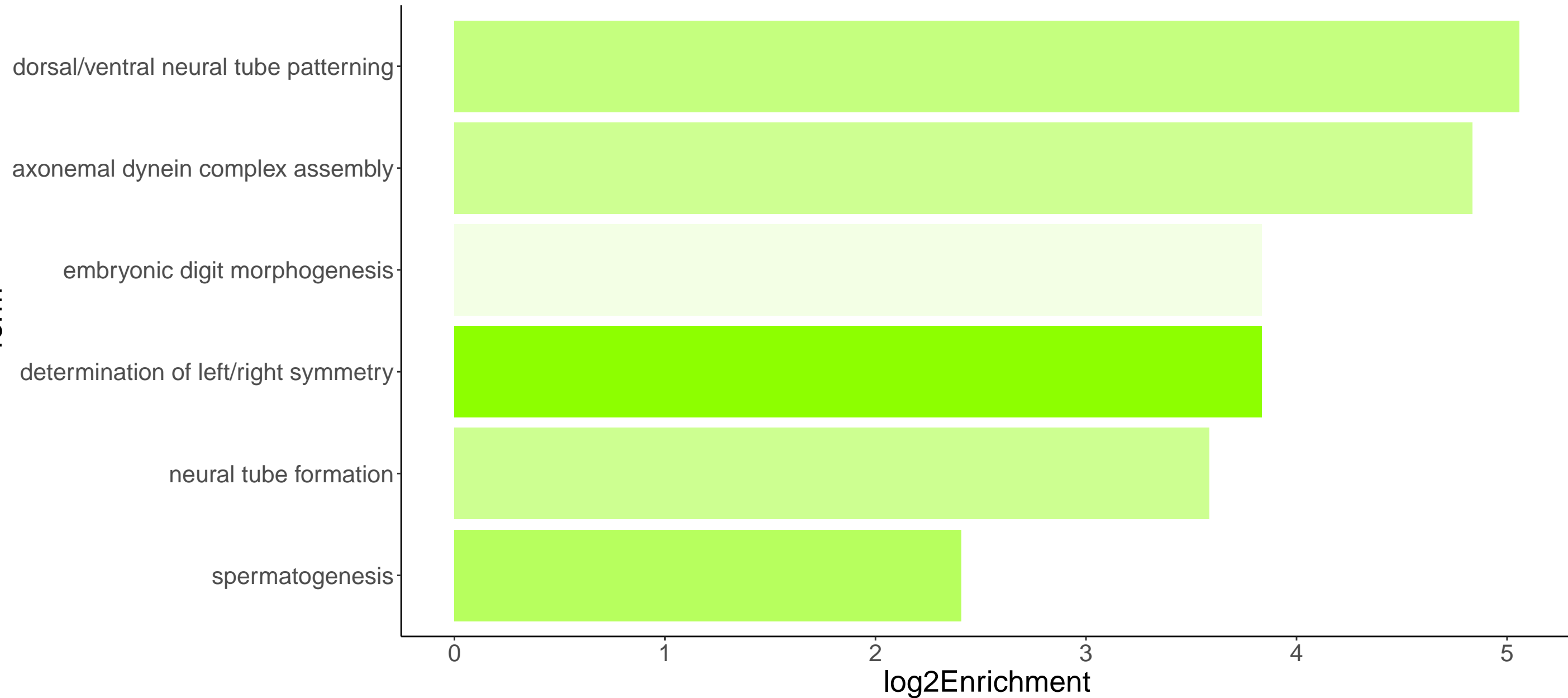
4

log2Enrichment



Re-clustered module 16.8.7 BP enrichment

Term



Re-clustered module 16.8.7 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.8 BP enrichment

Term

log2Enrichment



Re-clustered module 16.8.8 MF enrichment

Term

log2Enrichment



Re-clustered module 16.8.9 BP enrichment

Term

determination of left/right symmetry

protein localization to cilium

0

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log2Enrichment



Re-clustered module 16.8.9 MF enrichment

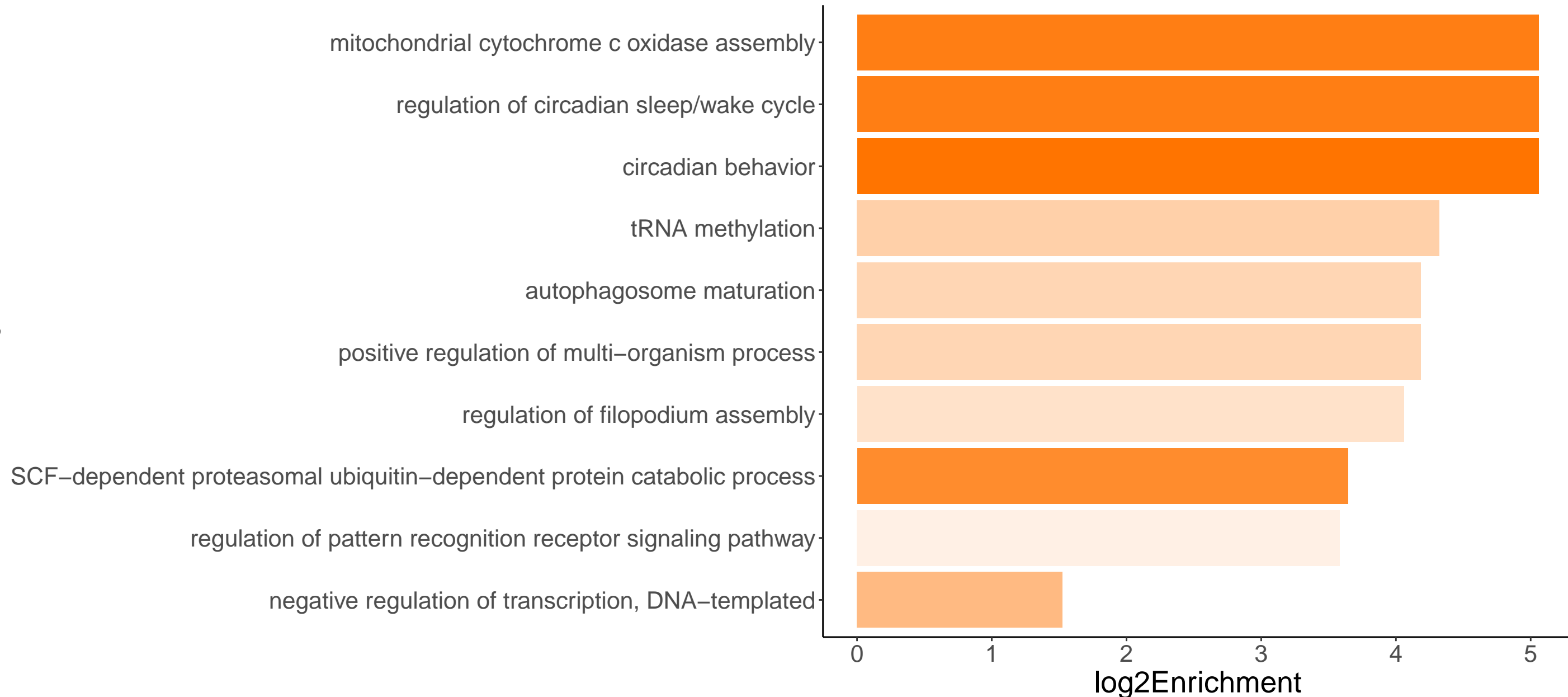
Term

log2Enrichment



Re-clustered module 16.9 BP enrichment

Term



Re-clustered module 16.9 MF enrichment

Term

tRNA methyltransferase activity

translation initiation factor binding

nuclear receptor activity

transcription factor binding

0

1

2

3

4

log2Enrichment

