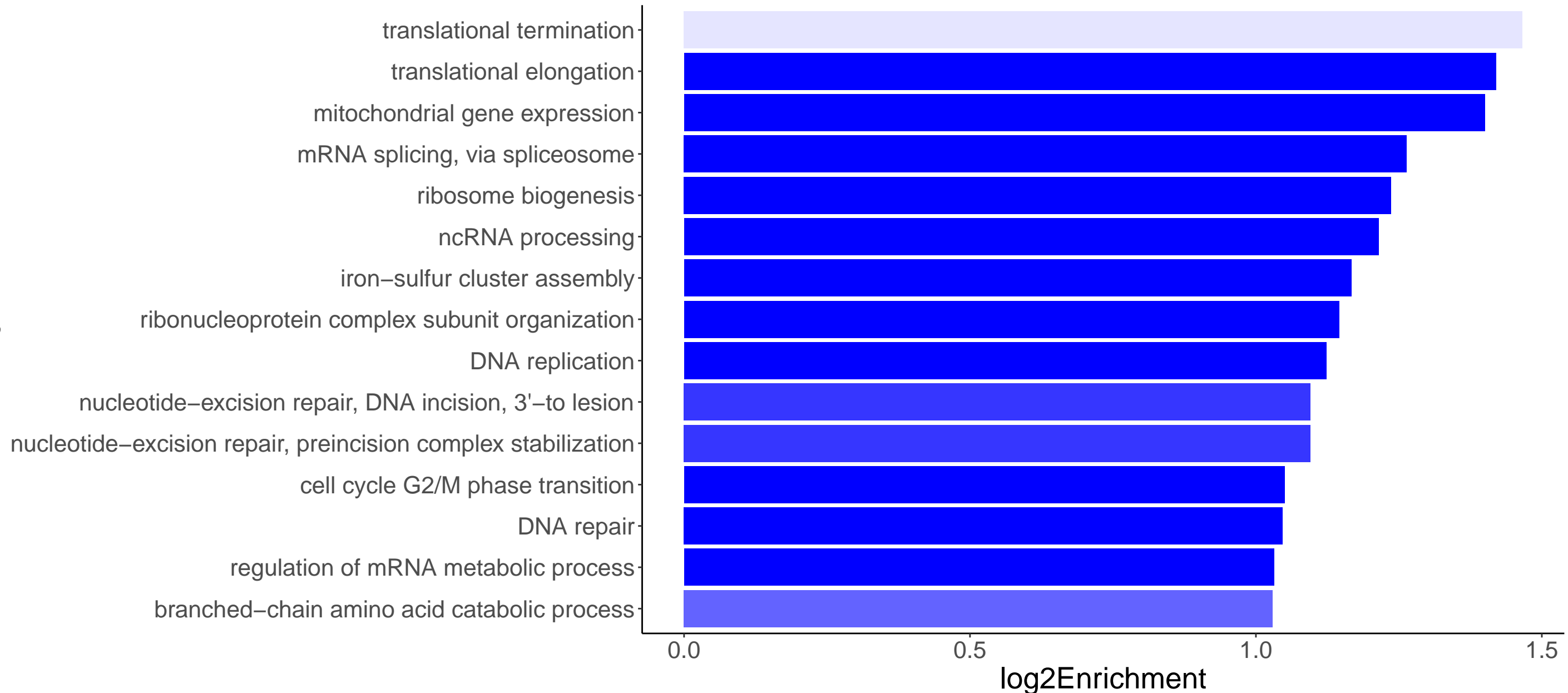


# Original module 3 BP enrichment

Term



Original module 3 MF enrichment

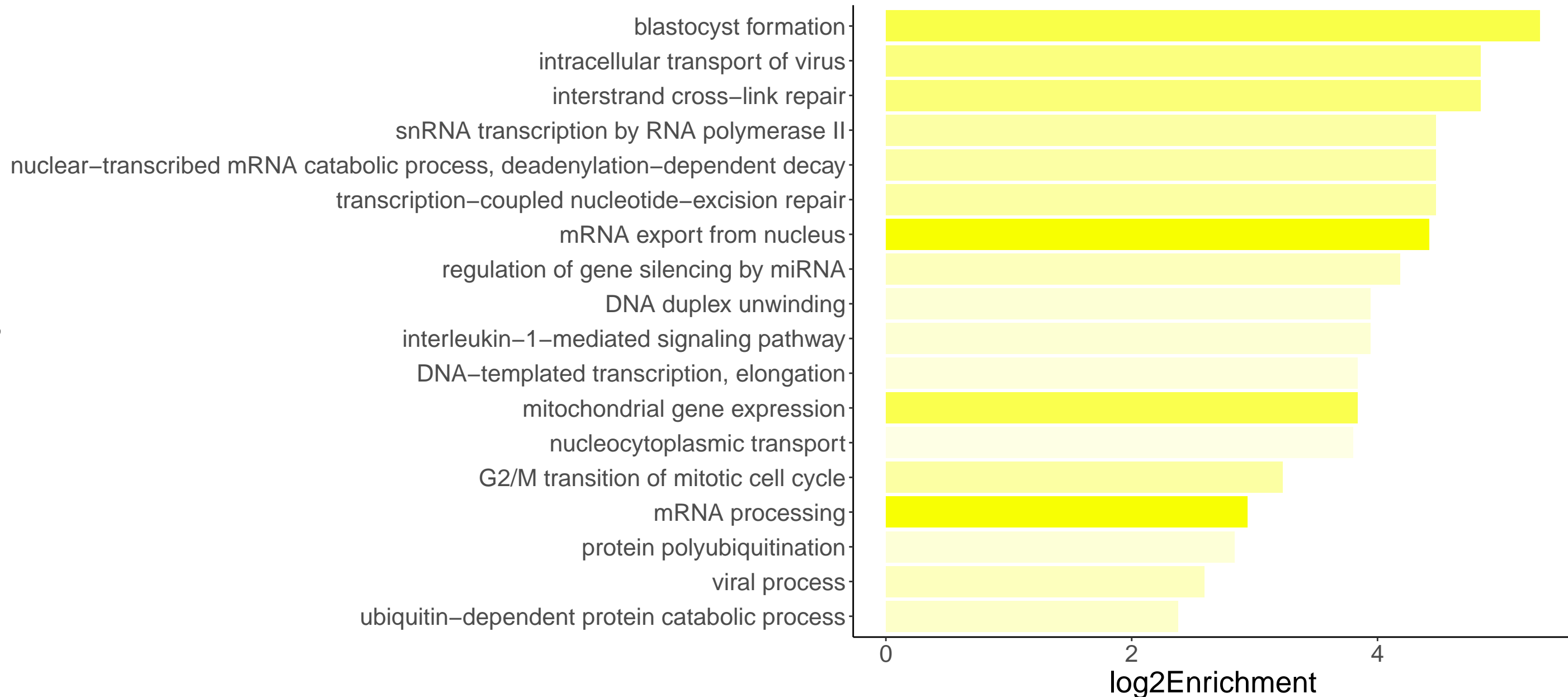
Term

log2Enrichment



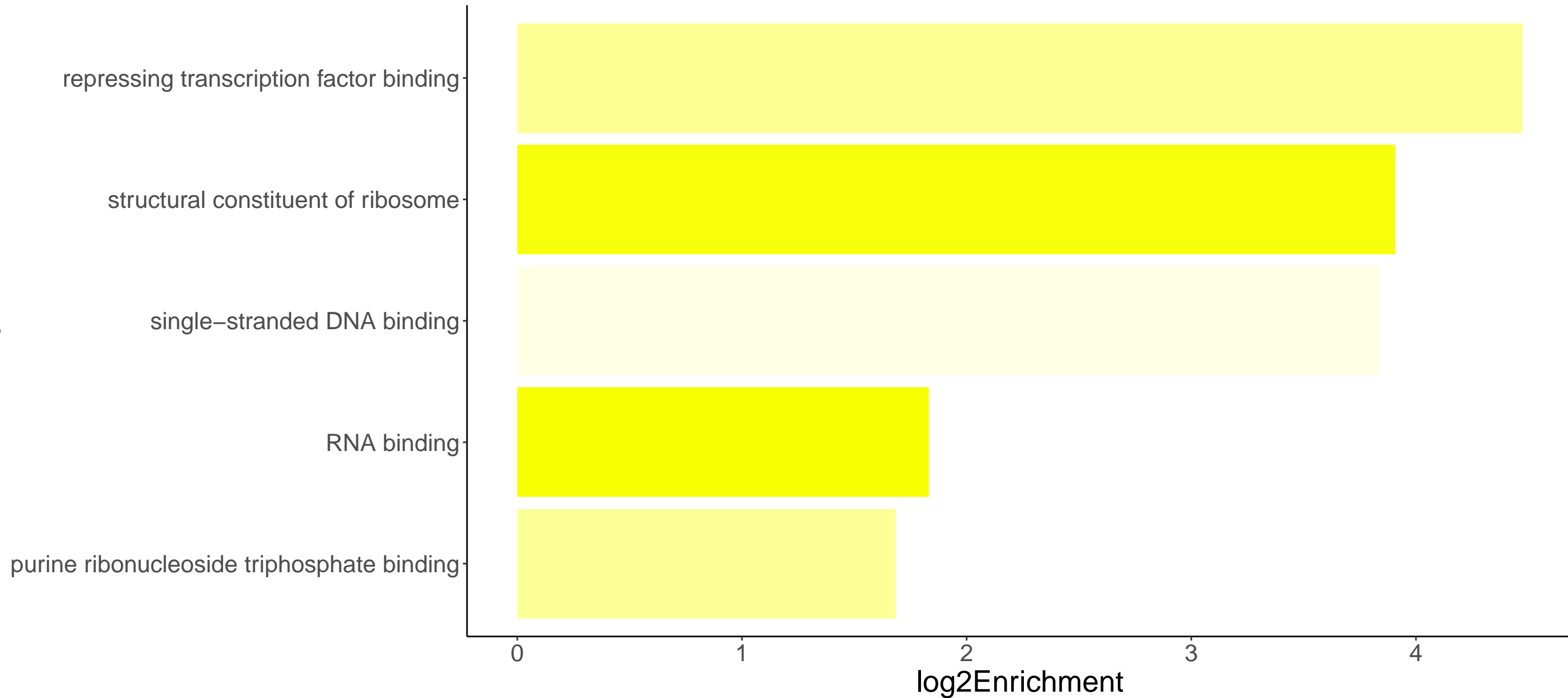
# Re-clustered module 3.11.12 BP enrichment

Term



# Re-clustered module 3.11.12 MF enrichment

Term



# Re-clustered module 3.11.14 BP enrichment

Term

regulation of cellular response to heat

mRNA export from nucleus

0

1

2

3

4

log2Enrichment



Re-clustered module 3.11.14 MF enrichment

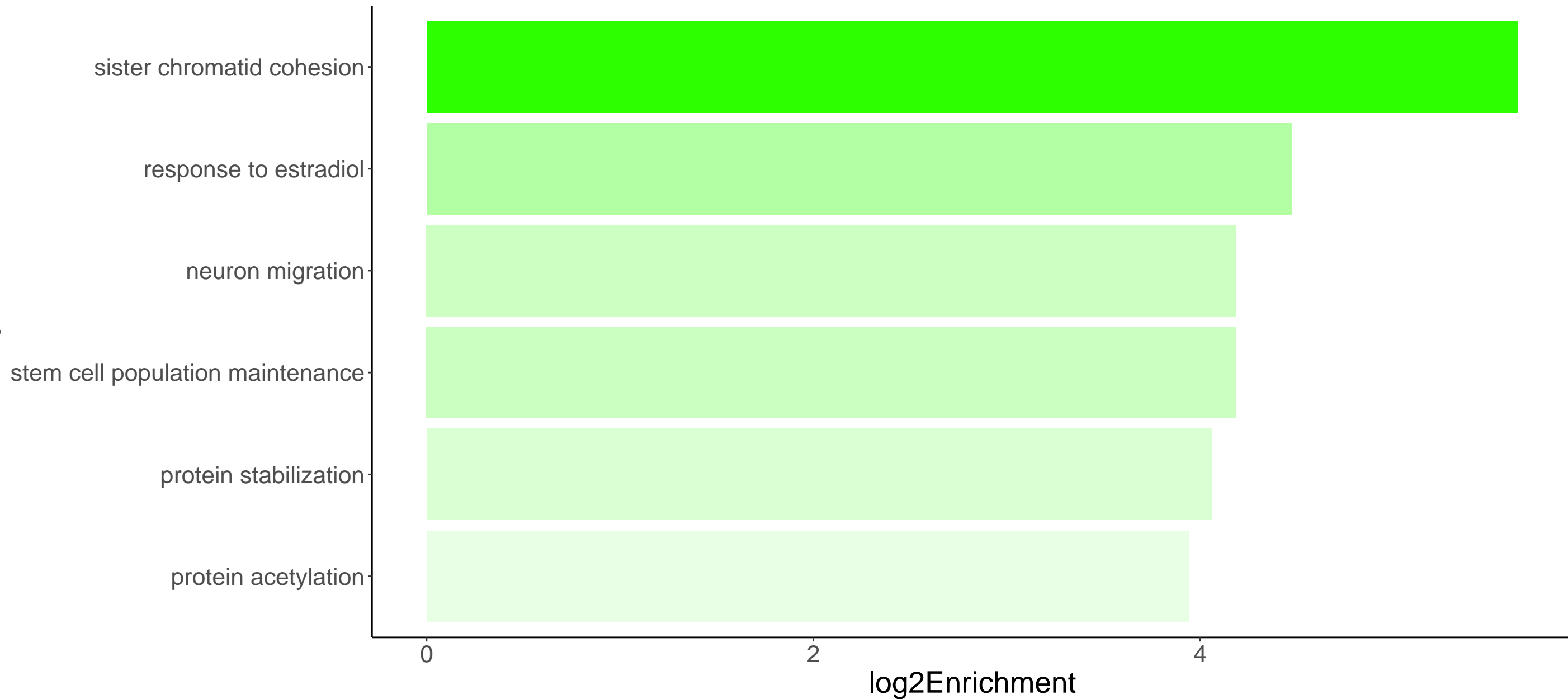
Term

log2Enrichment



# Re-clustered module 3.11.15 BP enrichment

Term



# Re-clustered module 3.11.15 MF enrichment

Term

N-acetyltransferase activity

repressing transcription factor binding

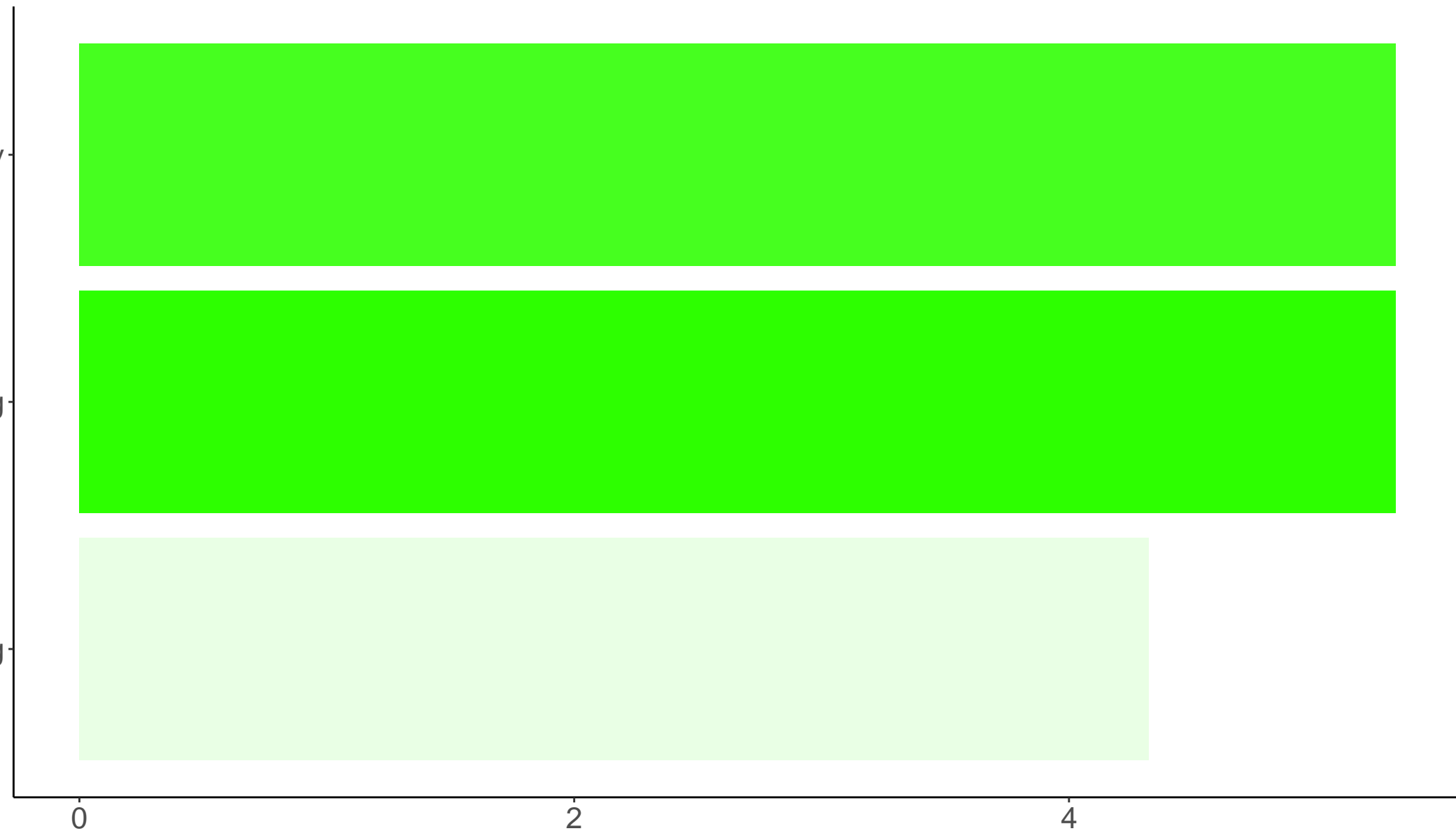
protein phosphatase binding

0

2

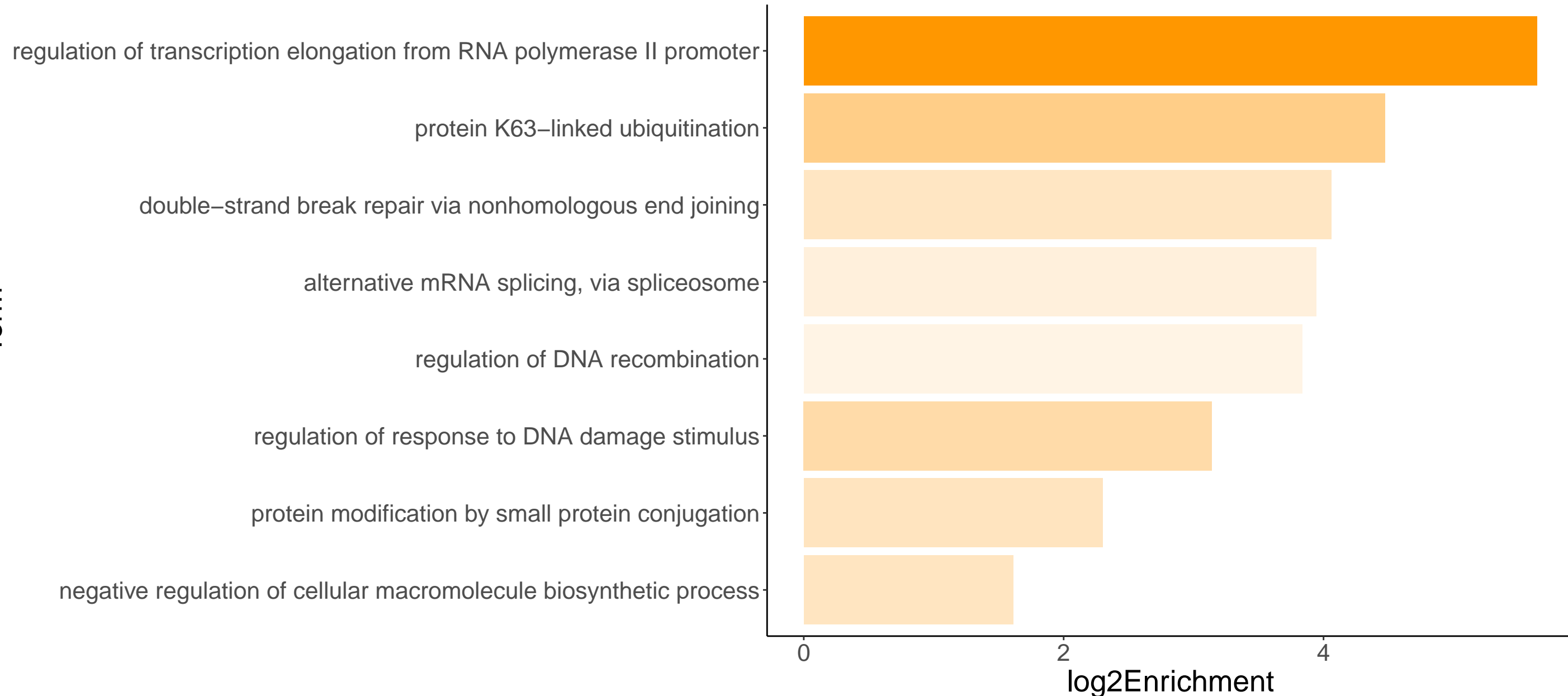
4

log2Enrichment





## Re-clustered module 3.11.16 BP enrichment



# Re-clustered module 3.11.16 MF enrichment

Term

nucleosome binding

ubiquitin-protein transferase activity

mRNA binding

0

1

2

3

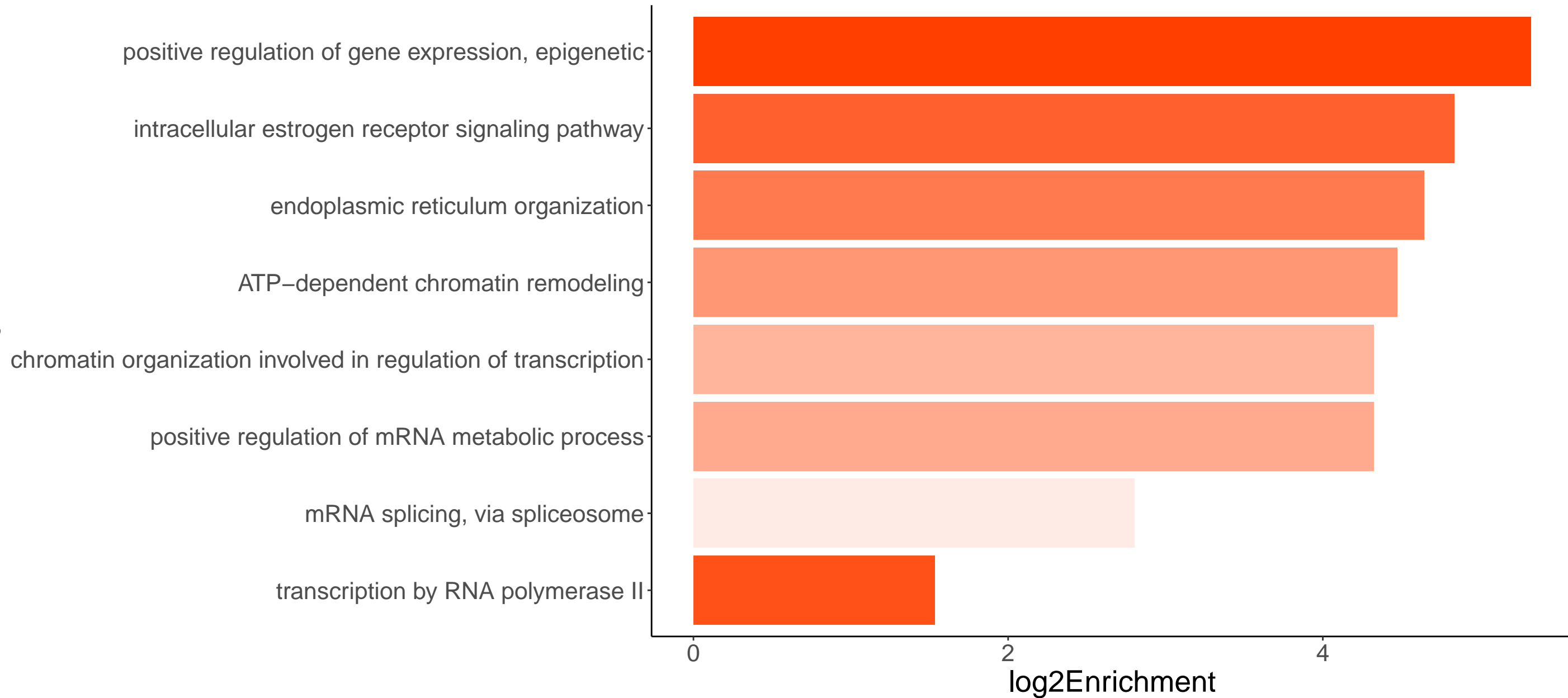
4

log2Enrichment



## Re-clustered module 3.11.17 BP enrichment

Term



# Re-clustered module 3.11.17 MF enrichment

Term

nucleosome binding

nuclear receptor binding

DNA binding

0

1

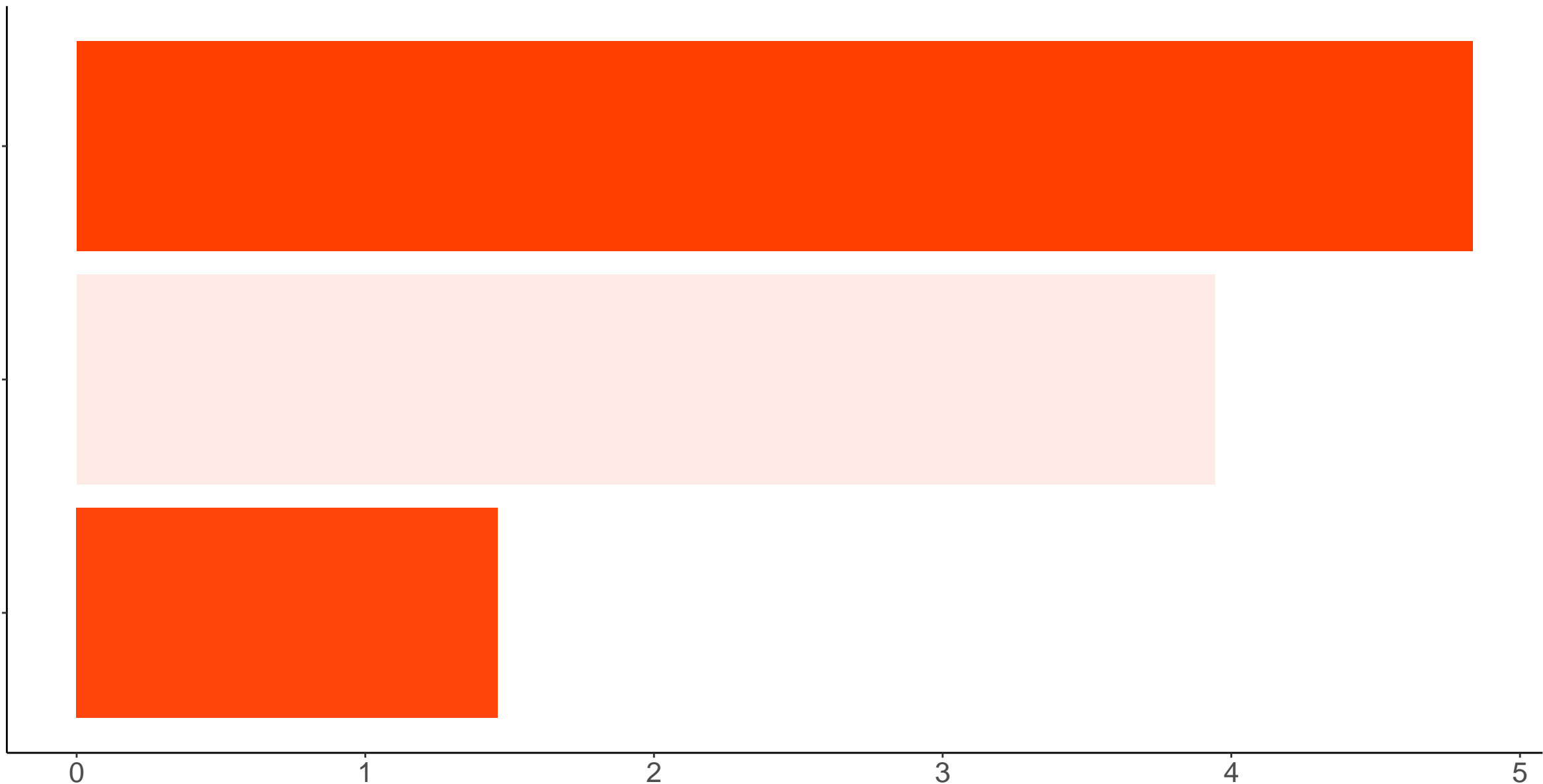
2

3

4

5

log2Enrichment



# Re-clustered module 3.11.18.1 BP enrichment

Term

endoplasmic reticulum organization

alpha-amino acid catabolic process

cell maturation

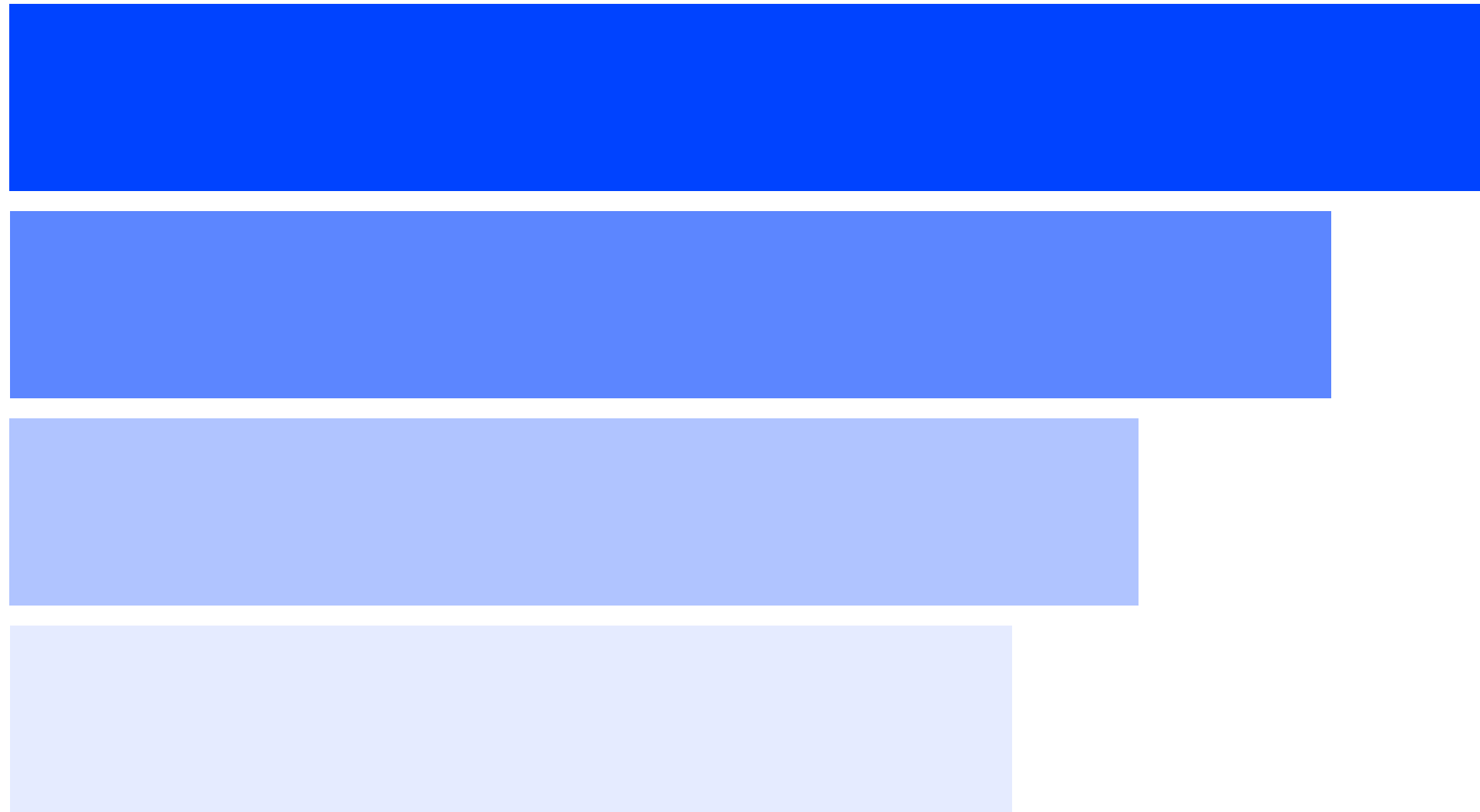
protein complex oligomerization

0

2

4

log2Enrichment



Re-clustered module 3.11.18.1 MF enrichment

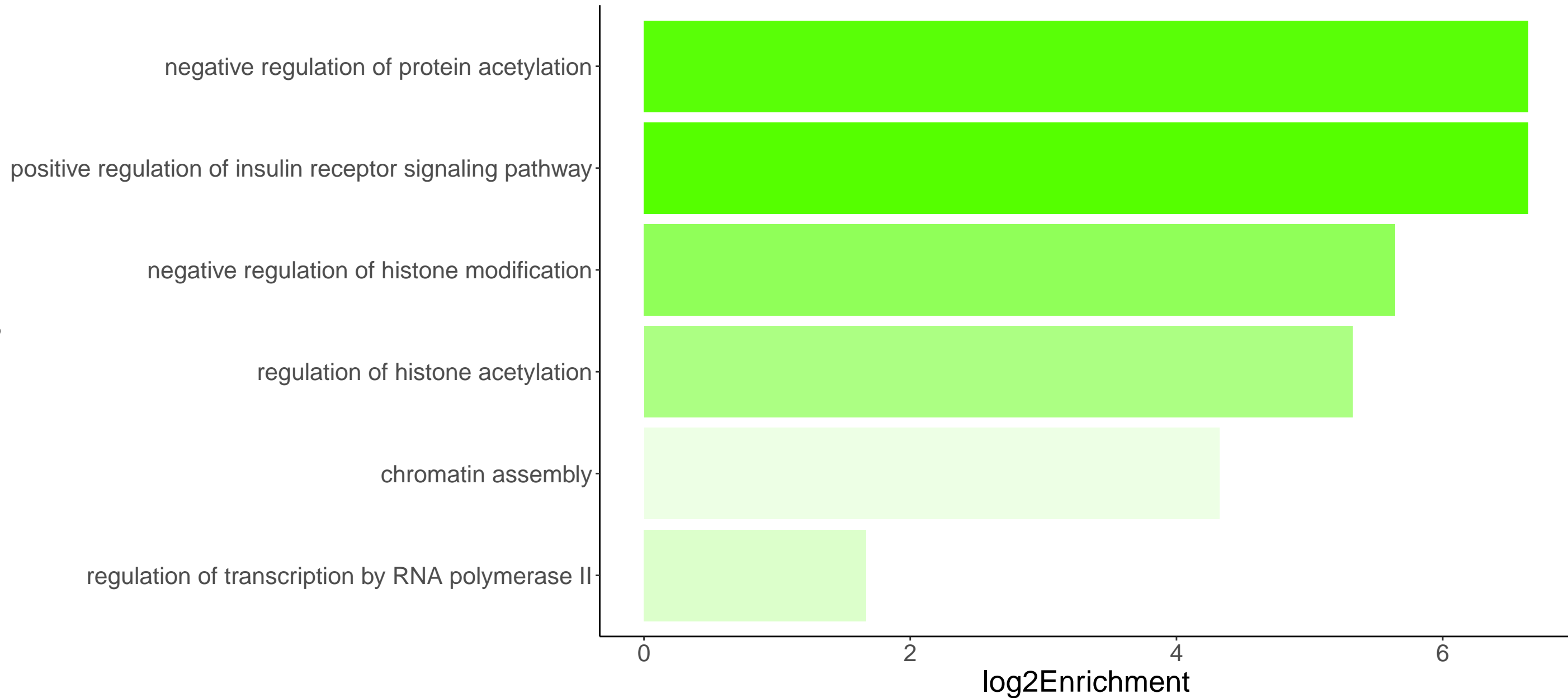
Term

log2Enrichment



# Re-clustered module 3.11.18.3 BP enrichment

Term



# Re-clustered module 3.11.18.3 MF enrichment

Term

DNA-binding transcription activator activity

DNA binding

0

1

2

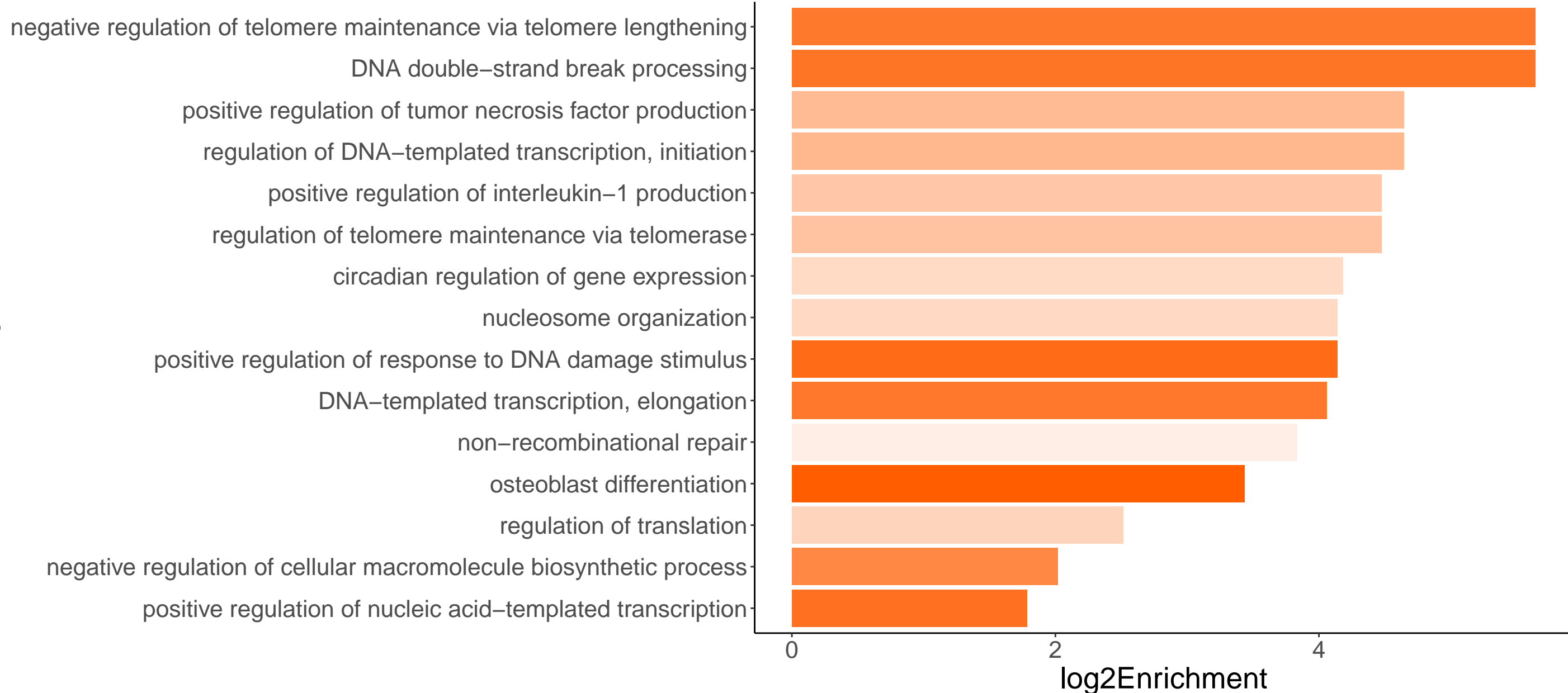
log2Enrichment





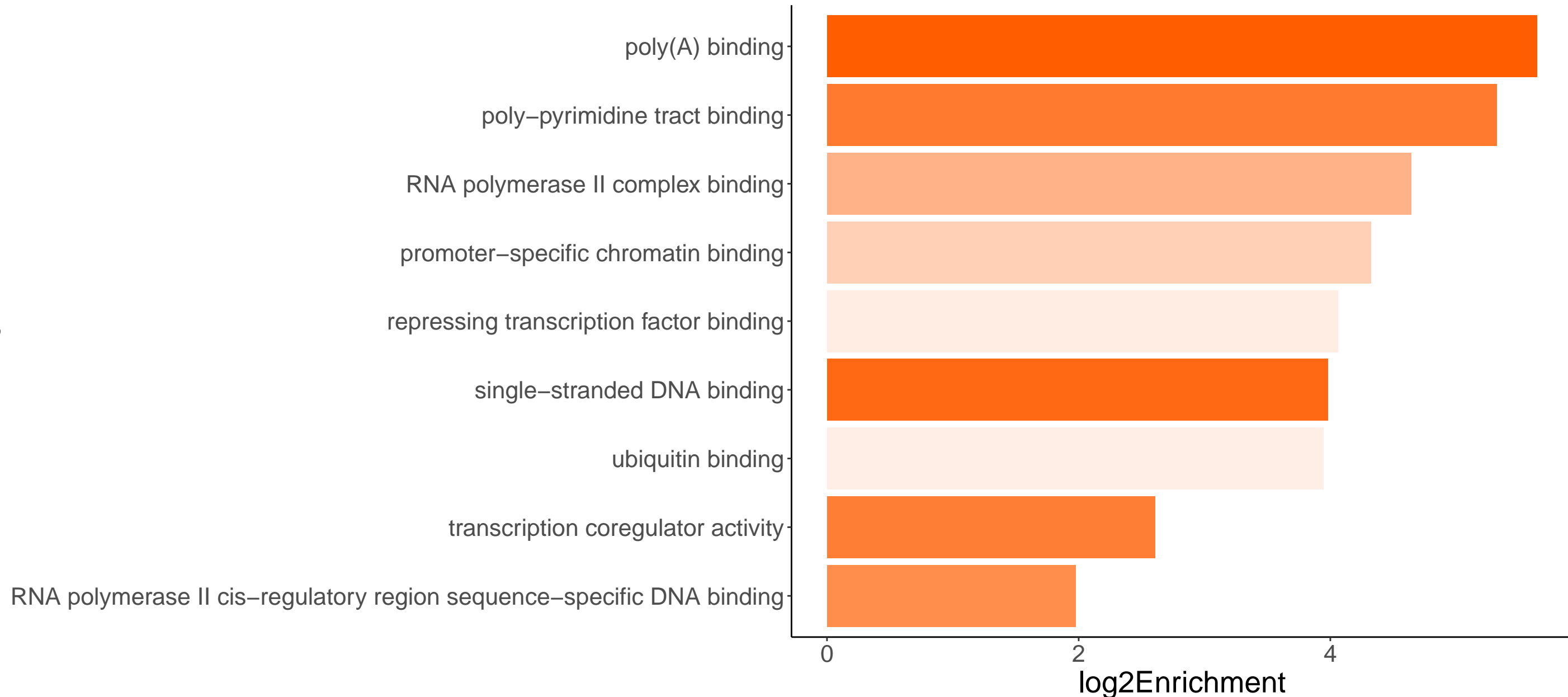
## Re-clustered module 3.11.18.6 BP enrichment

Term



# Re-clustered module 3.11.18.6 MF enrichment

Term



## Re-clustered module 3.11.2 BP enrichment

Term



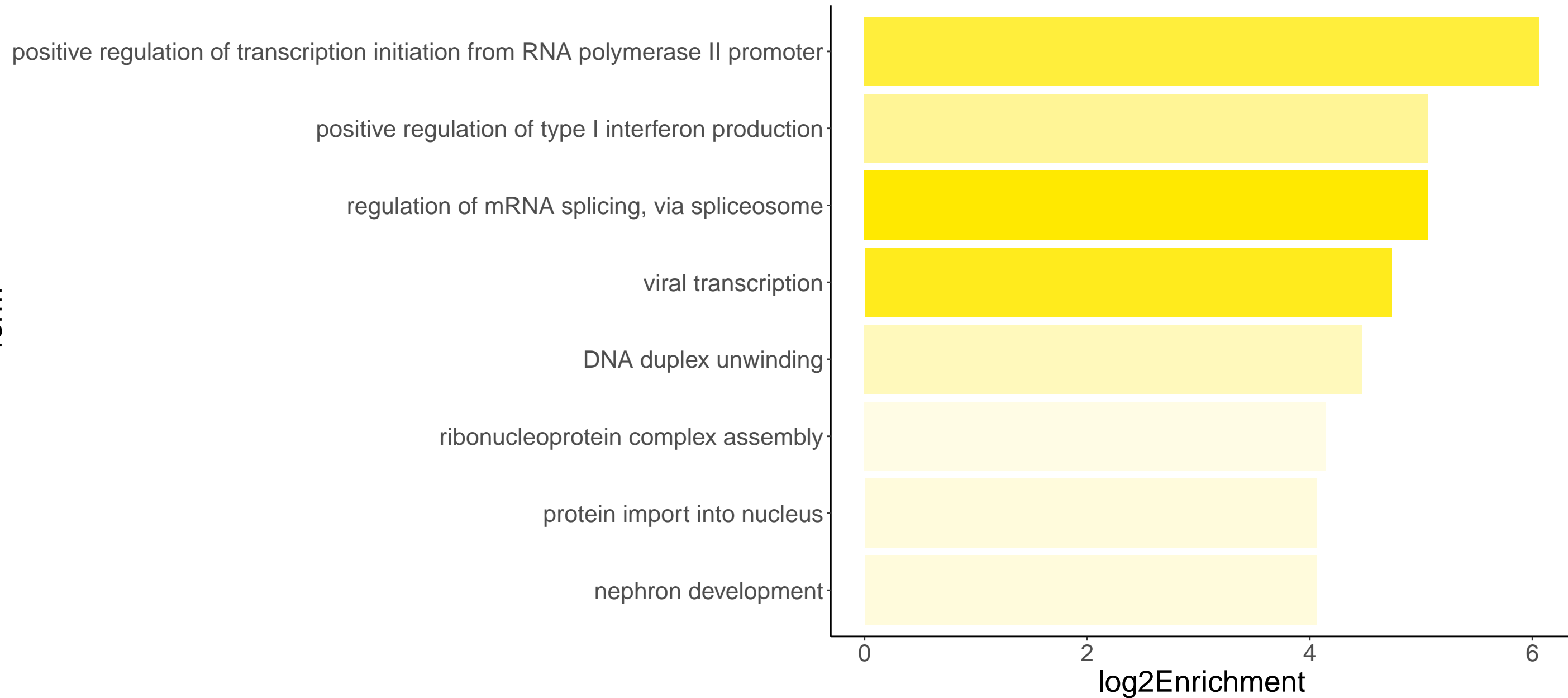
Re-clustered module 3.11.2 MF enrichment

Term

log2Enrichment



## Re-clustered module 3.11.22 BP enrichment



# Re-clustered module 3.11.22 MF enrichment

Term

structural constituent of nuclear pore

RNA polymerase II complex binding

helicase activity

transcription coregulator activity

RNA binding

0

2

4

6

log2Enrichment



## Re-clustered module 3.11.23.2 BP enrichment

Term

histone lysine demethylation

negative regulation of telomere maintenance via telomere lengthening

regulation of transcription initiation from RNA polymerase II promoter

RNA phosphodiester bond hydrolysis, exonucleolytic

DNA methylation

regulation of telomere maintenance via telomerase

regulation of multicellular organism growth

chromatin organization involved in negative regulation of transcription

regulation of TOR signaling

histone acetylation

DNA damage response, signal transduction by p53 class mediator

positive regulation of nucleic acid-templated transcription

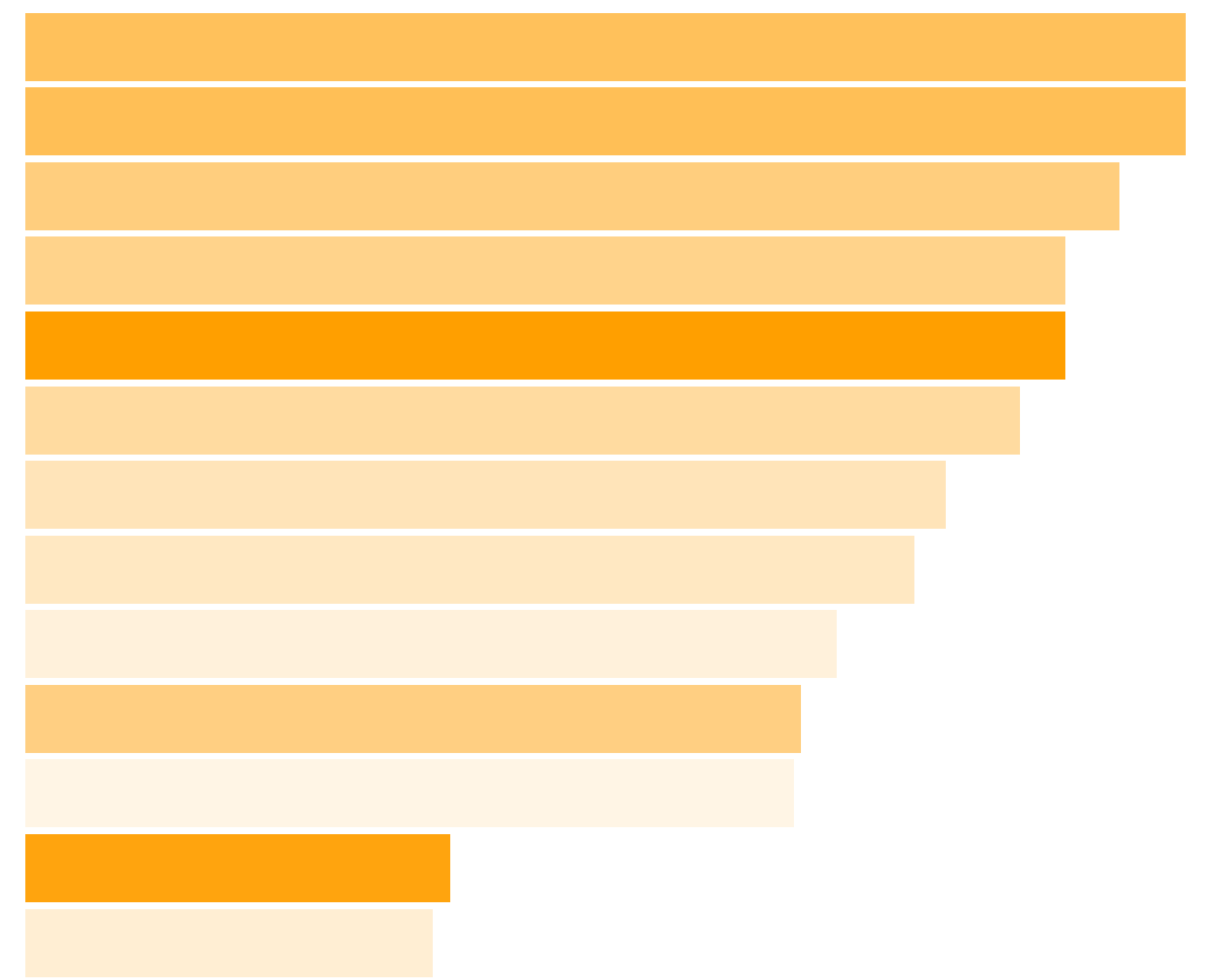
negative regulation of cellular macromolecule biosynthetic process

0

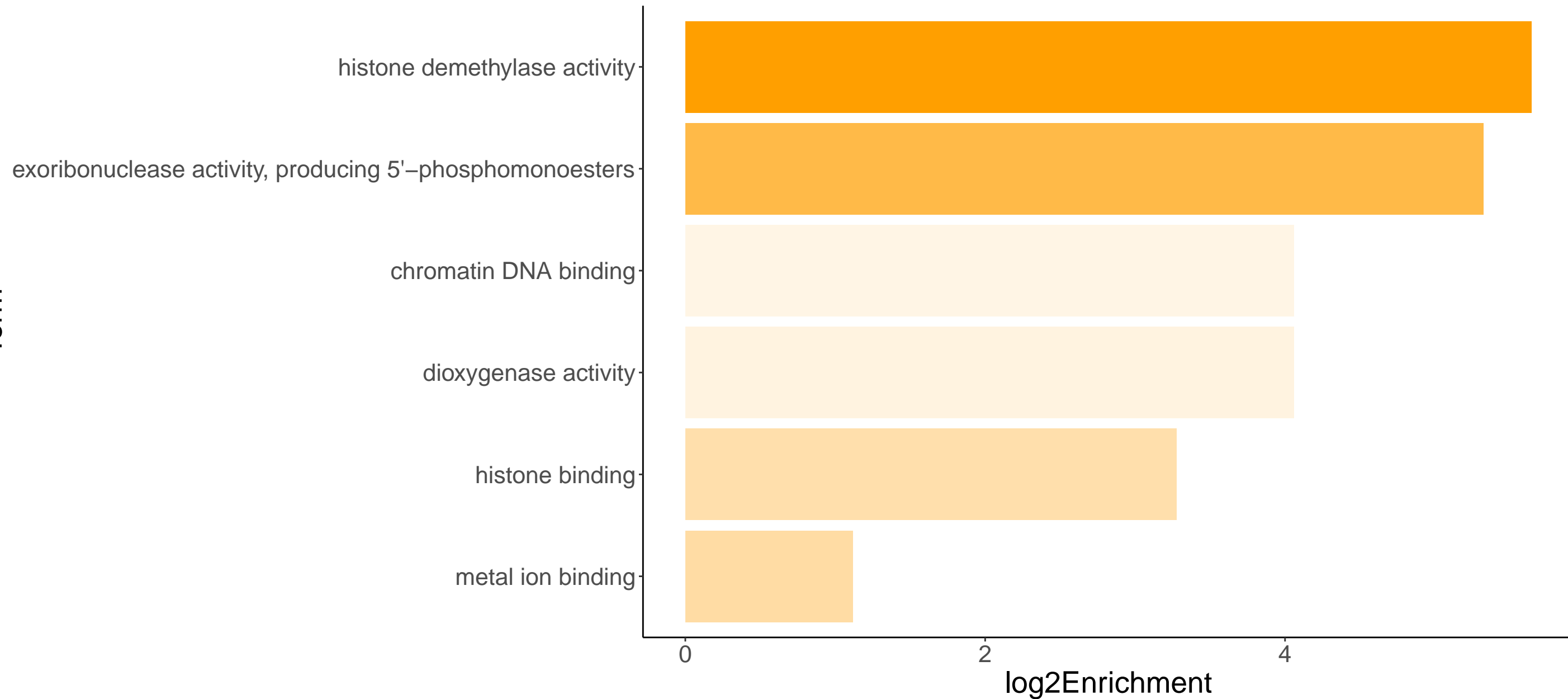
2

4

log2Enrichment



## Re-clustered module 3.11.23.2 MF enrichment





# Re-clustered module 3.11.23.3 BP enrichment

Term

blastocyst formation

regulation of postsynaptic membrane neurotransmitter receptor levels

regulation of peptide hormone secretion

0

2

4

6

log2Enrichment



# Re-clustered module 3.11.23.3 MF enrichment

Term

GDP binding

purine ribonucleoside triphosphate binding

0

1

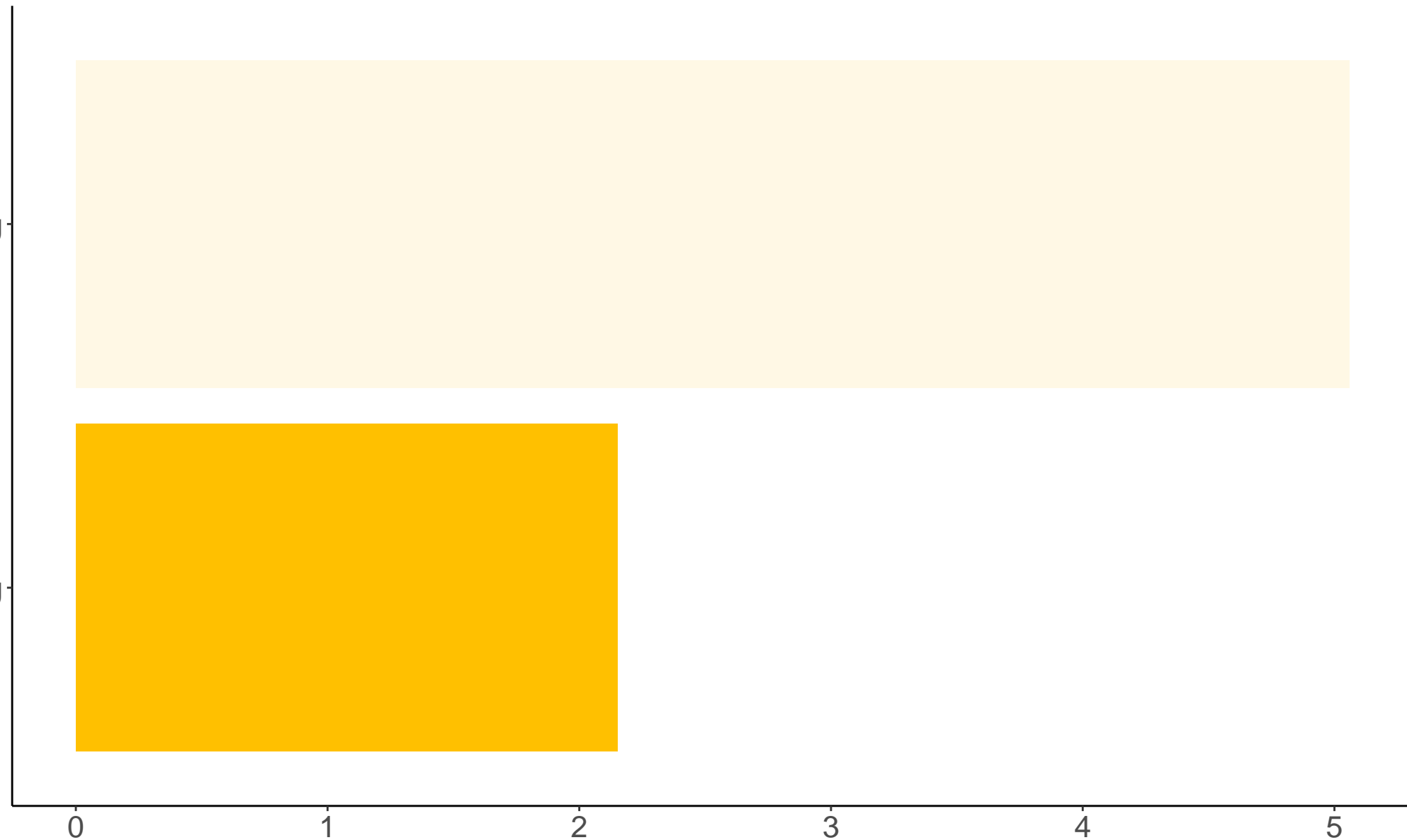
2

3

4

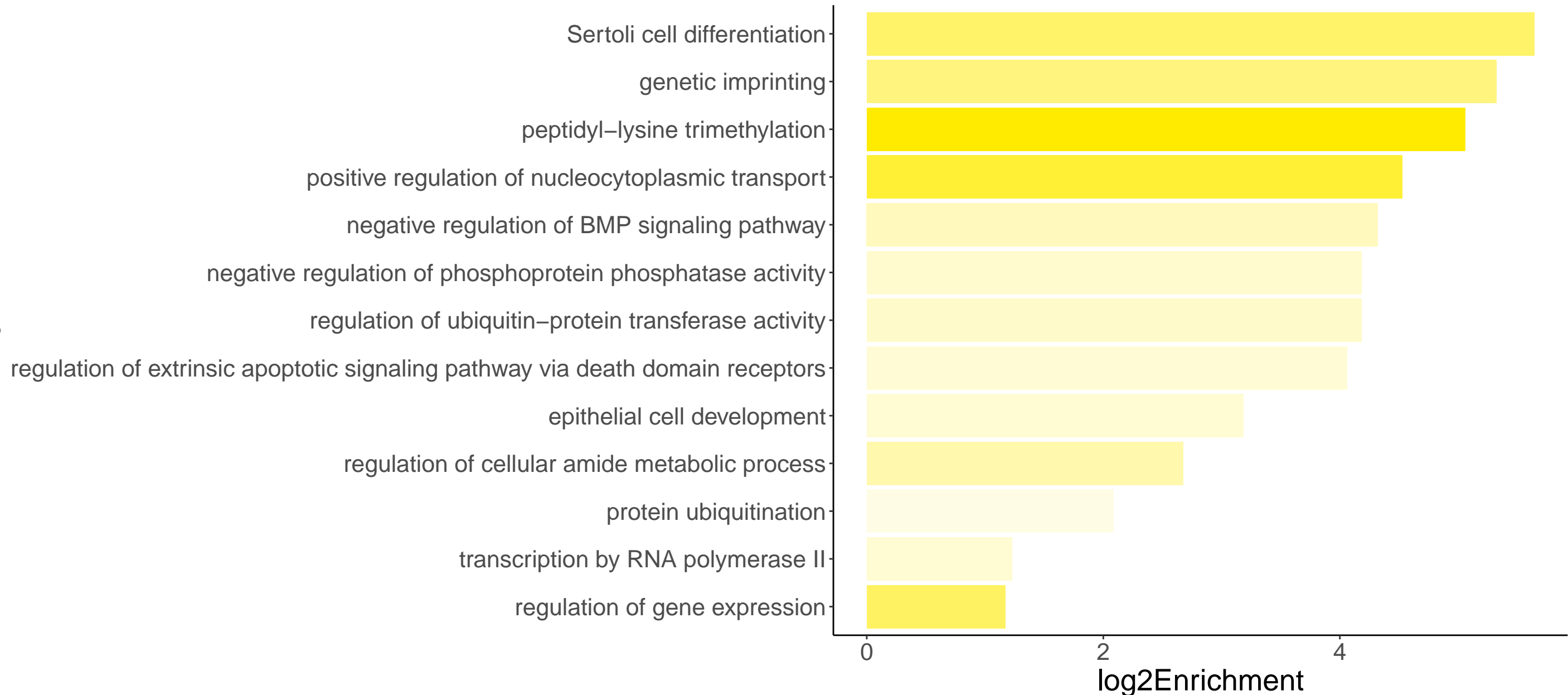
5

log2Enrichment



# Re-clustered module 3.11.23.5 BP enrichment

Term



# Re-clustered module 3.11.23.5 MF enrichment

Term

miRNA binding

RNA polymerase II repressing transcription factor binding

protein phosphorylated amino acid binding

protein serine/threonine phosphatase activity

histone deacetylase binding

ubiquitin-protein transferase activity

0

1

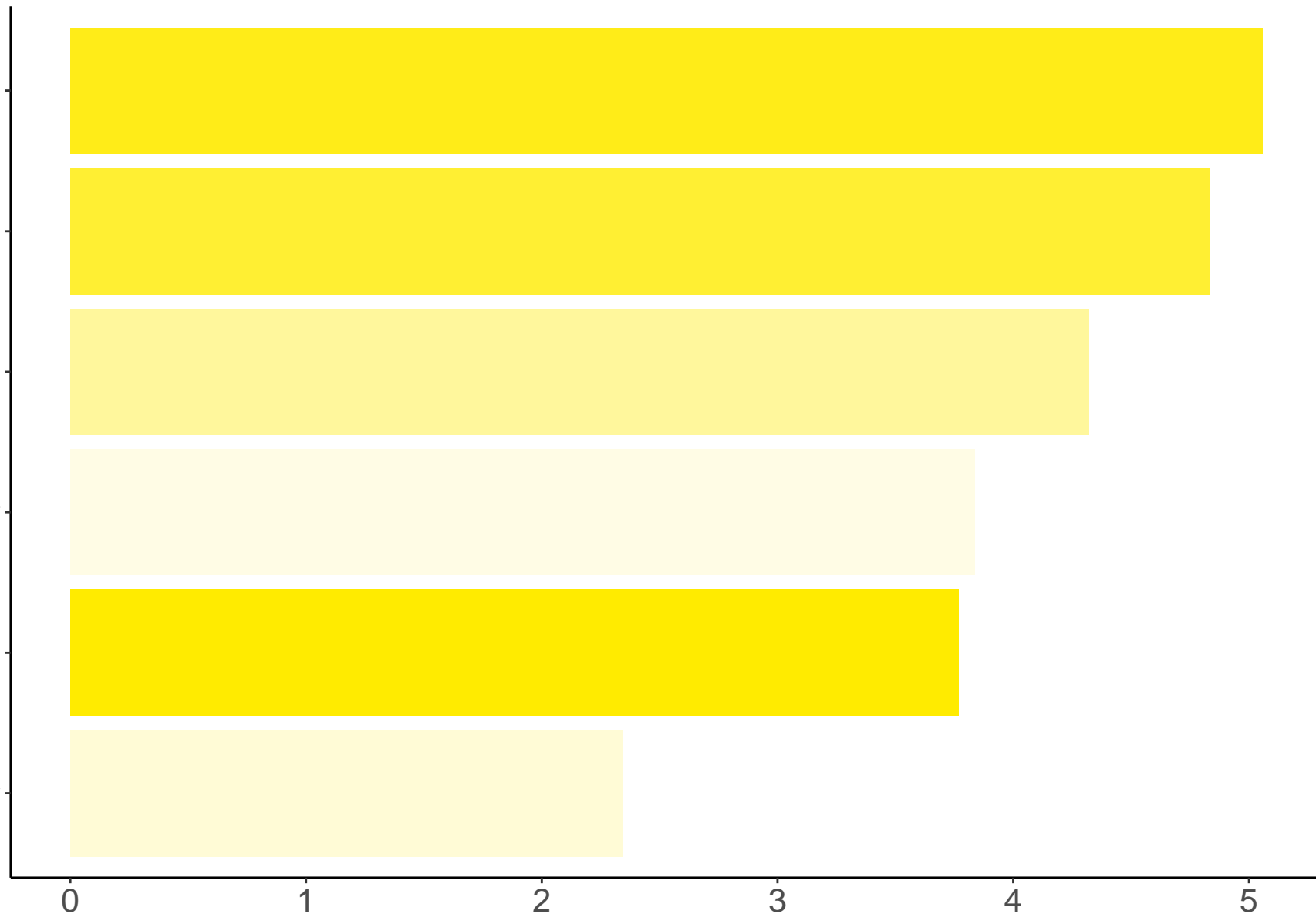
2

3

4

5

log2Enrichment



# Re-clustered module 3.11.23.7 BP enrichment

Term

histone H4 acetylation

positive regulation of canonical Wnt signaling pathway

chromatin organization

0

2

4

log2Enrichment



# Re-clustered module 3.11.23.7 MF enrichment

Term

histone acetyltransferase activity

protein serine/threonine phosphatase activity

0

2

4

log2Enrichment



# Re-clustered module 3.11.23.8 BP enrichment

Term

nuclear-transcribed mRNA poly(A) tail shortening

mRNA destabilization

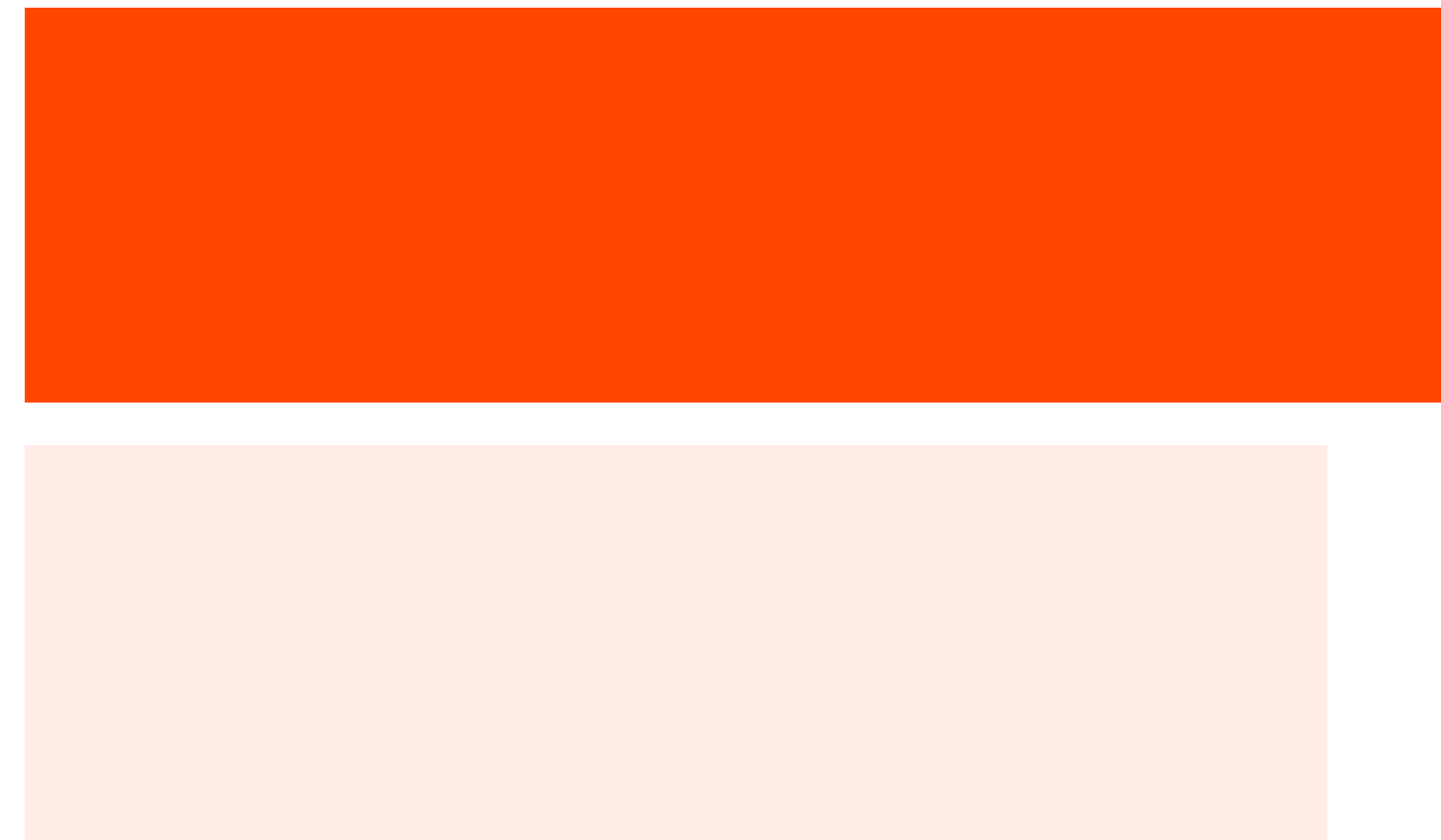
0

2

4

6

log2Enrichment



Re-clustered module 3.11.23.8 MF enrichment

Term

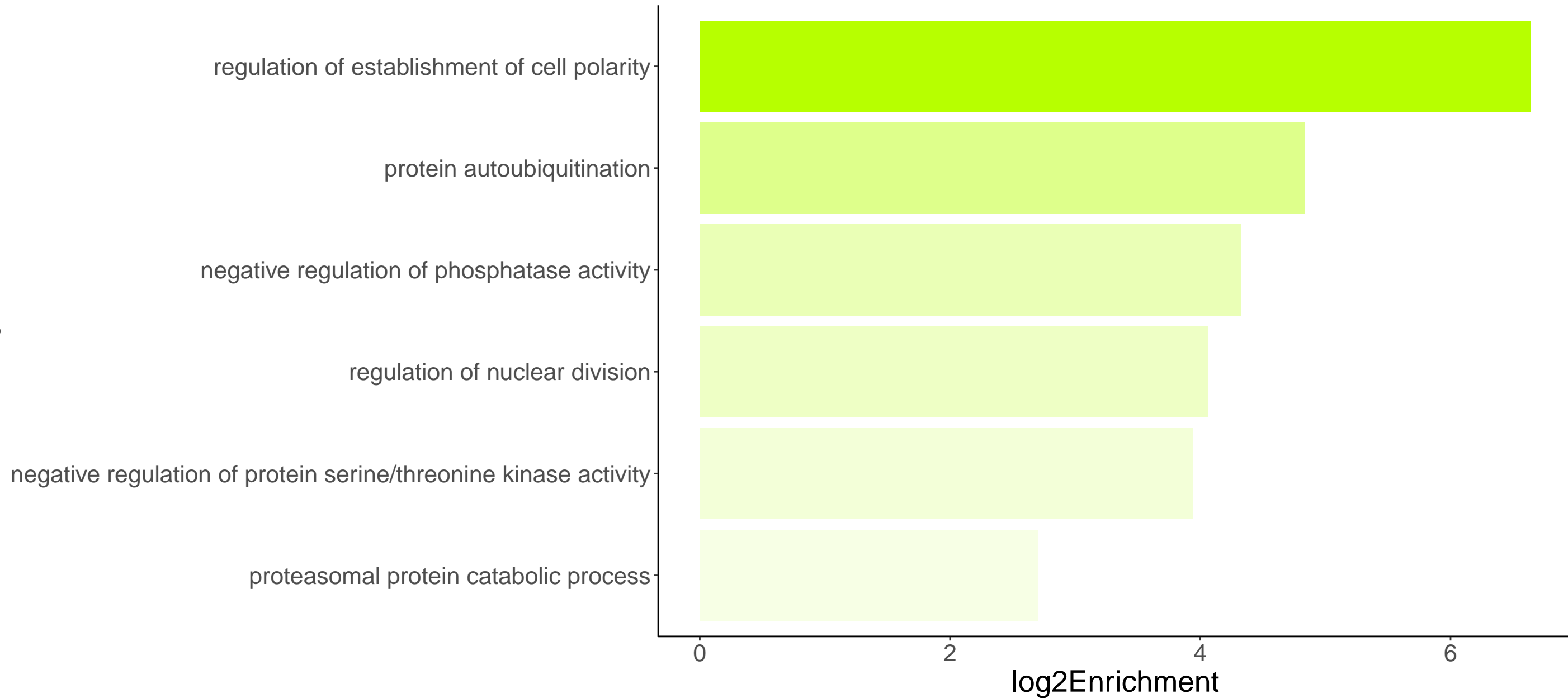
log2Enrichment





## Re-clustered module 3.11.24 BP enrichment

Term



# Re-clustered module 3.11.24 MF enrichment

Term

GTPase regulator activity

ubiquitin-protein transferase activity

protein domain specific binding

0

1

2

3

log2Enrichment



# Re-clustered module 3.11.27 BP enrichment

Term

phosphatidylinositol 3-kinase signaling

0

1

2

3

4

log2Enrichment



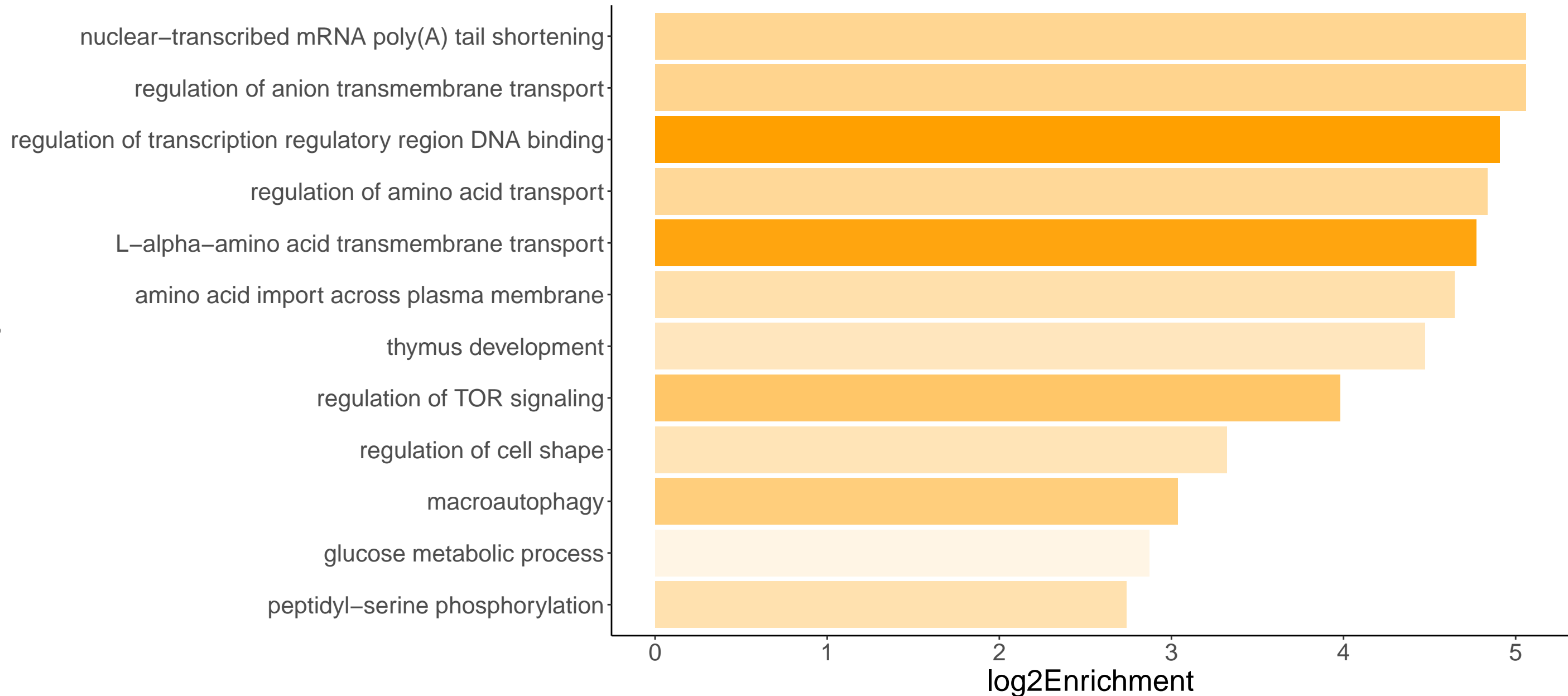
Re-clustered module 3.11.27 MF enrichment

Term

log2Enrichment



## Re-clustered module 3.11.28 BP enrichment



# Re-clustered module 3.11.28 MF enrichment

Term

palmitoyltransferase activity

0

1

2

3

4

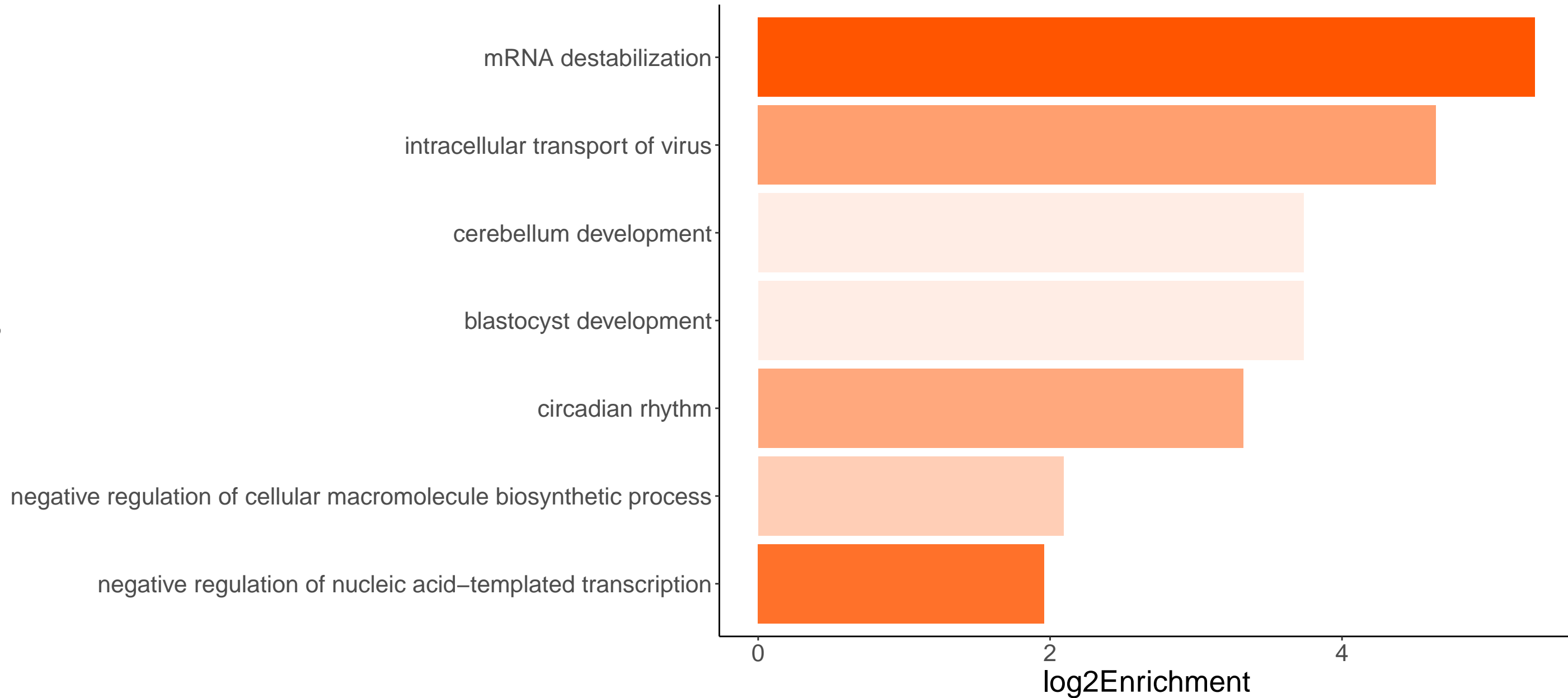
5

log2Enrichment



# Re-clustered module 3.11.29 BP enrichment

Term



# Re-clustered module 3.11.29 MF enrichment

Term

DNA secondary structure binding

histone binding

heterocyclic compound binding

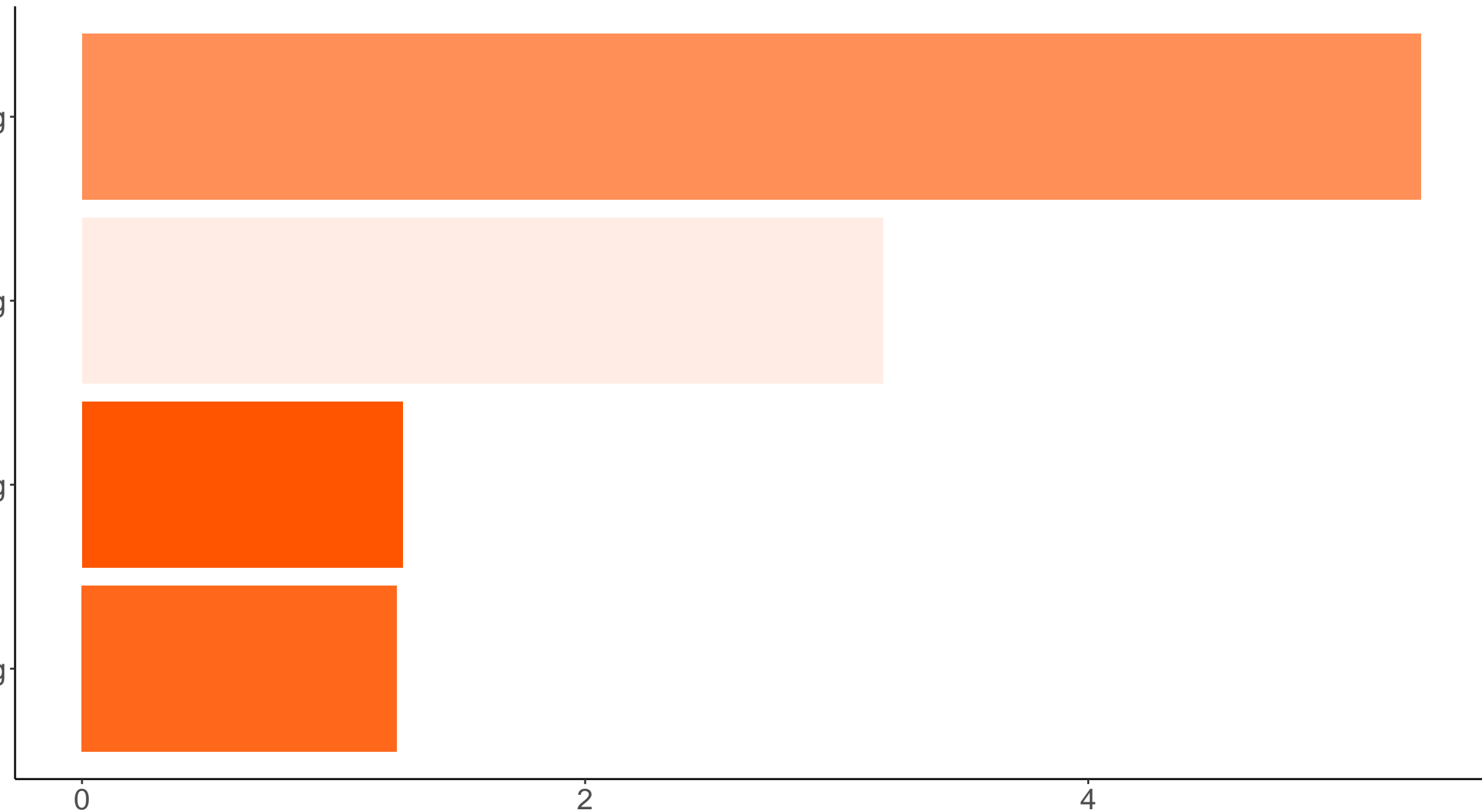
organic cyclic compound binding

0

2

4

log2Enrichment





# Re-clustered module 3.11.39 BP enrichment

Term

histone H3 acetylation

0

2

4

log2Enrichment



# Re-clustered module 3.11.39 MF enrichment

Term

histone acetyltransferase activity

histone binding

0

2

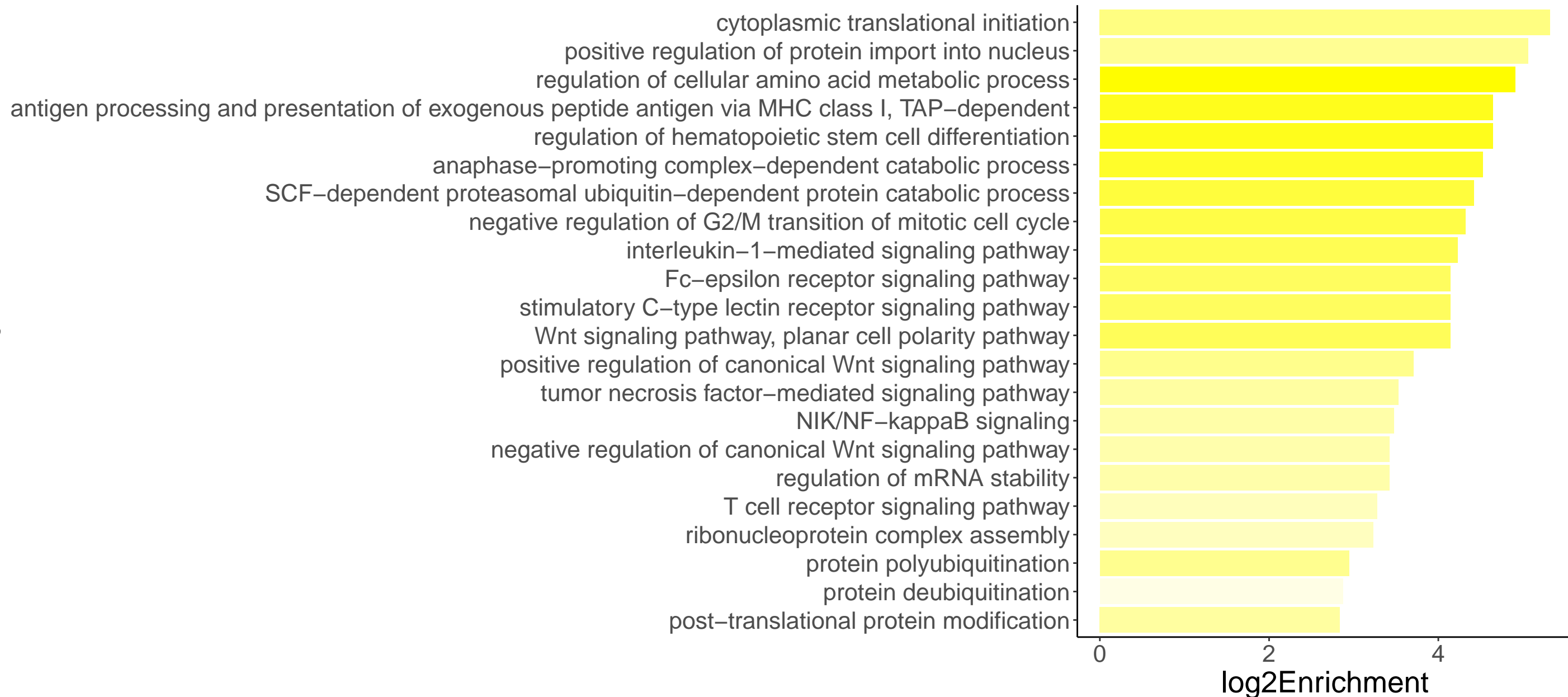
4

6

log2Enrichment

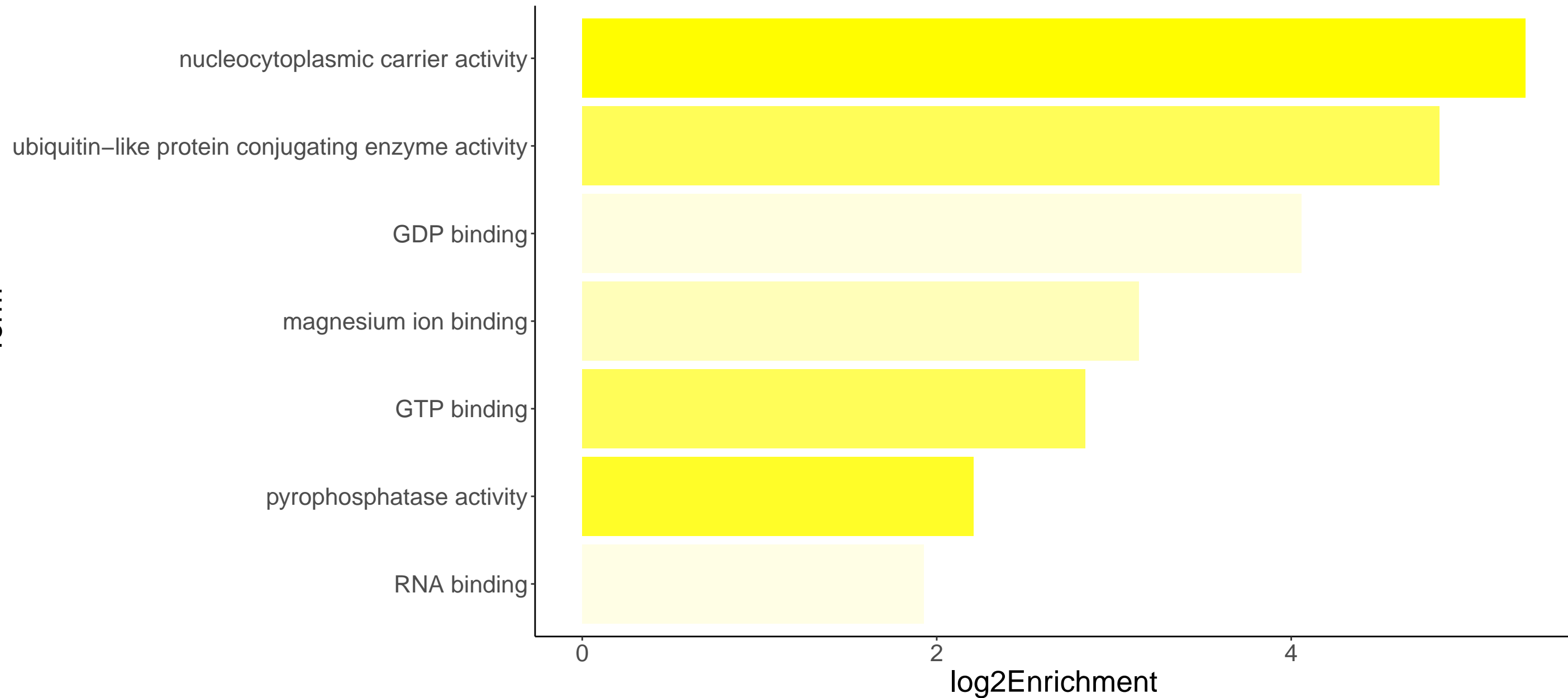


# Re-clustered module 3.11.4 BP



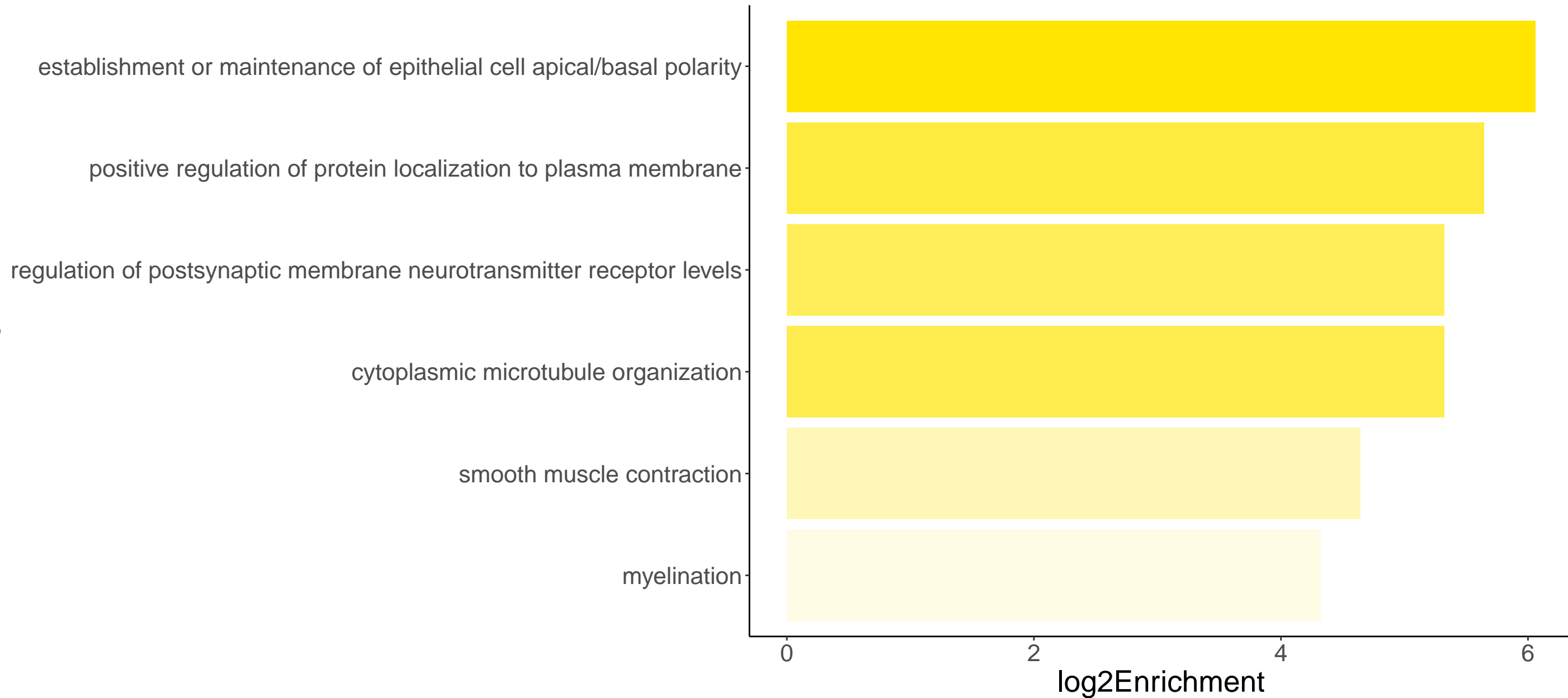
## Re-clustered module 3.11.4 MF enrichment

Term



## Re-clustered module 3.11.47 BP enrichment

Term



# Re-clustered module 3.11.47 MF enrichment

Term

calcium-dependent protein serine/threonine kinase activity

Rho GTPase binding

cadherin binding

purine ribonucleoside triphosphate binding

0

2

4

6

log2Enrichment



## Re-clustered module 3.11.5 BP enrichment

Term

negative regulation of histone modification

protein K48-linked ubiquitination

intracellular estrogen receptor signaling pathway

protein autoubiquitination

regulation of DNA recombination

DNA repair

0

1

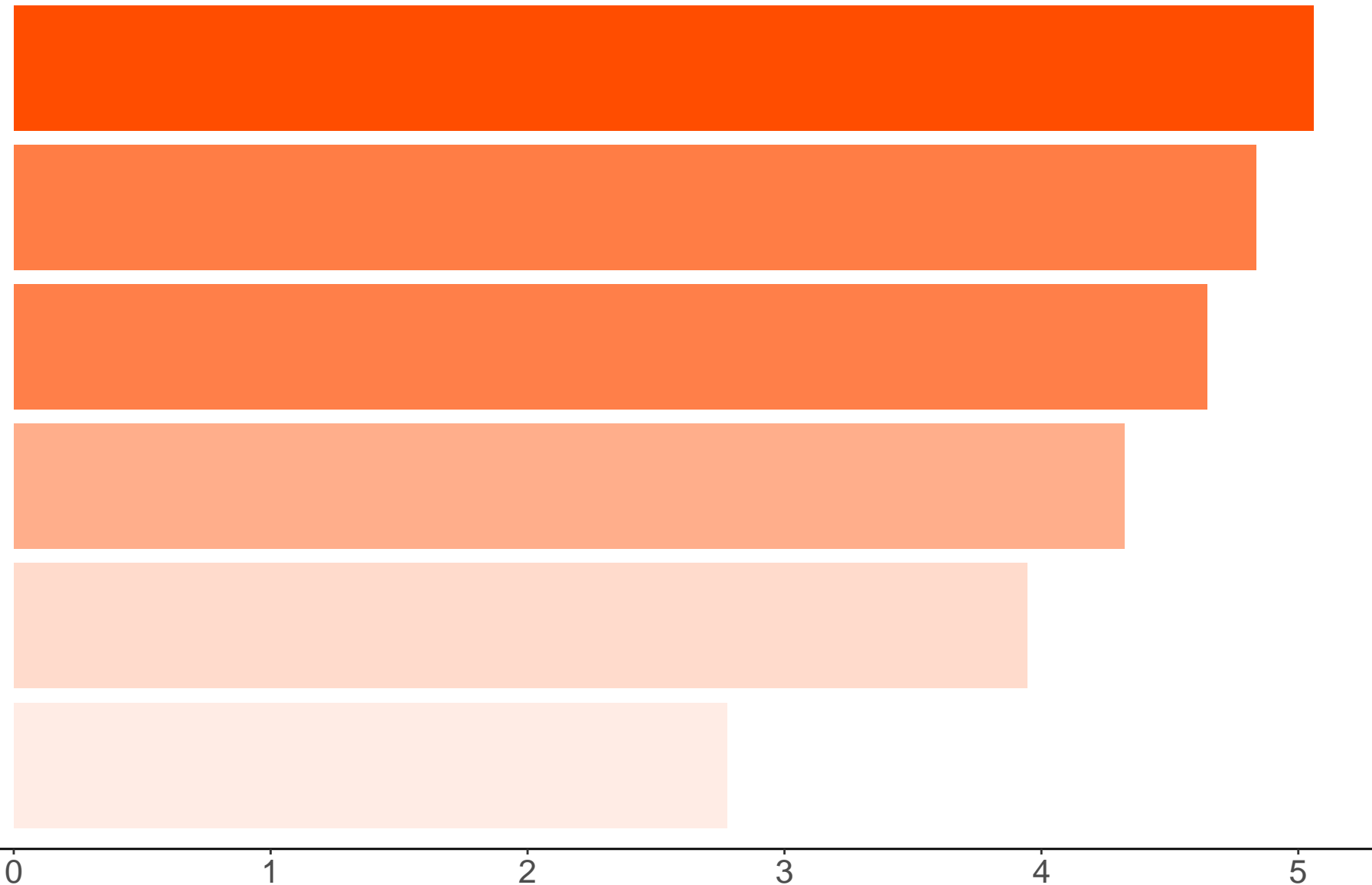
2

3

4

5

log2Enrichment



# Re-clustered module 3.11.5 MF enrichment

Term

ubiquitin conjugating enzyme activity

0

1

2

3

4

5

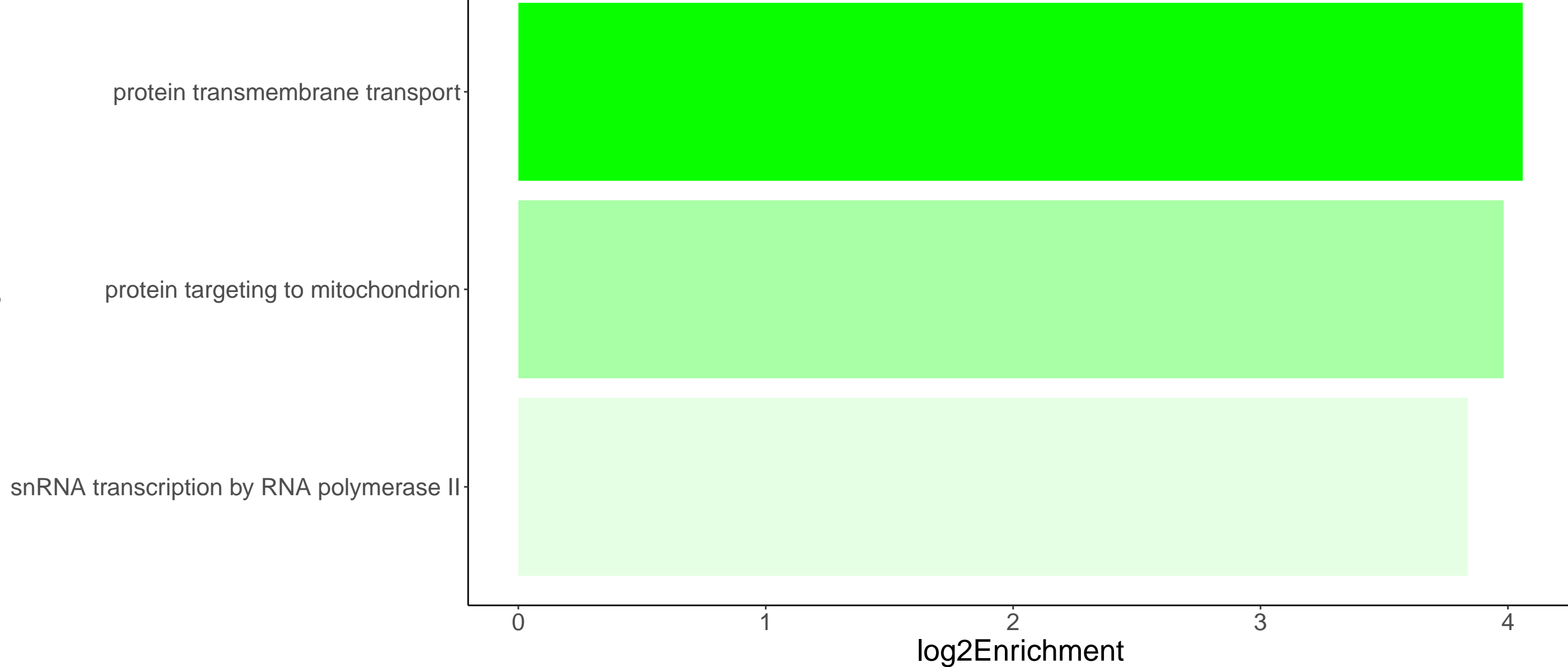
log2Enrichment





# Re-clustered module 3.11.6 BP enrichment

Term



Re-clustered module 3.11.6 MF enrichment

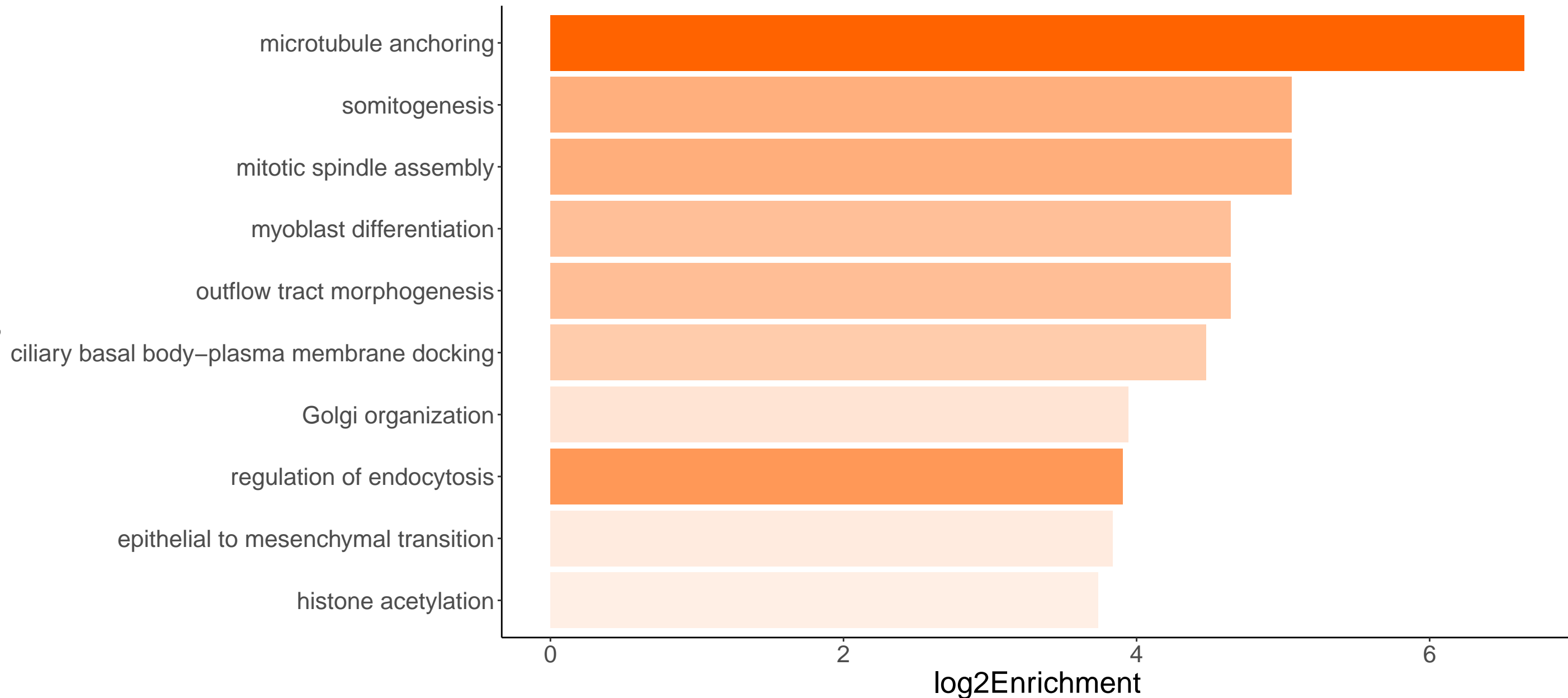
Term

log2Enrichment



## Re-clustered module 3.11.8.1 BP enrichment

Term



# Re-clustered module 3.11.8.1 MF enrichment

Term

histone acetyltransferase activity

0

1

2

3

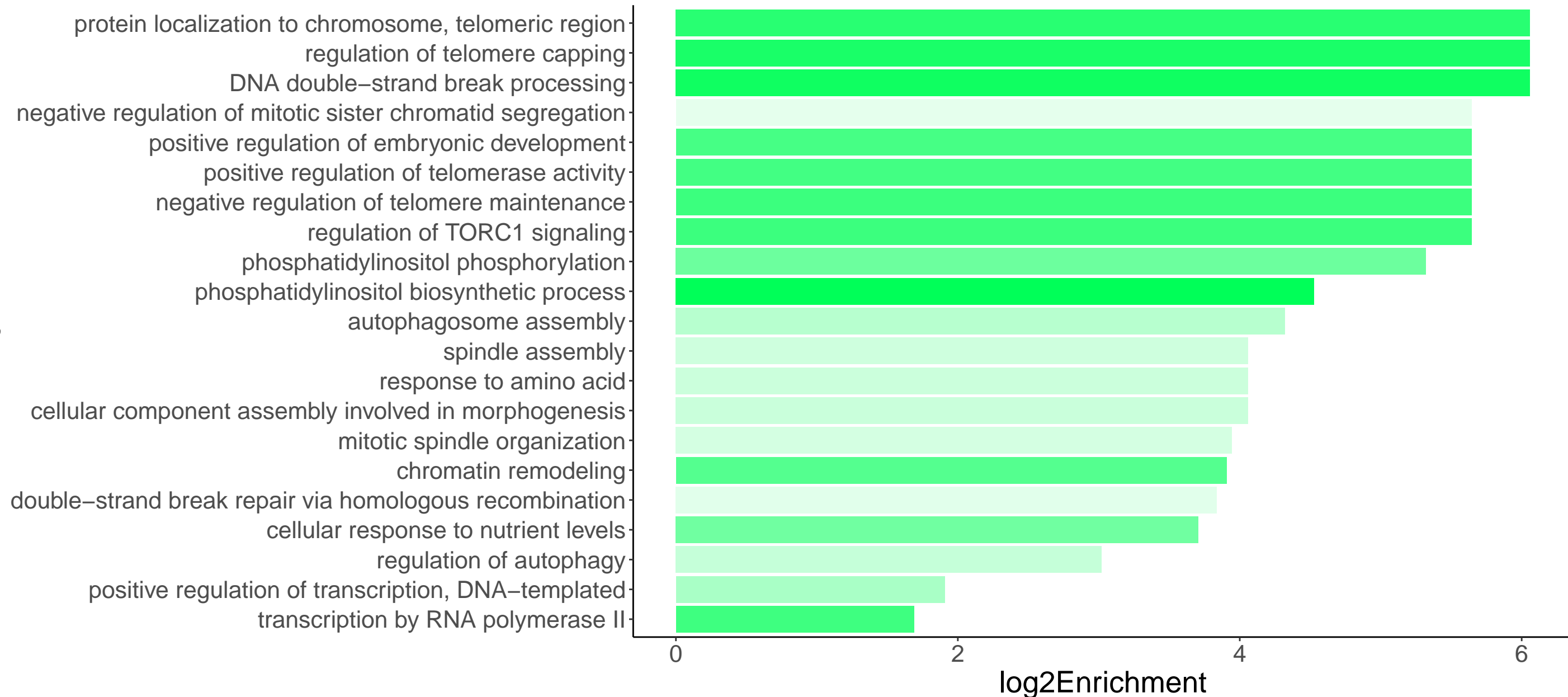
4

5

log2Enrichment



## Re-clustered module 3.11.8.2 BP enrichment



# Re-clustered module 3.11.8.2 MF enrichment

Term

DNA-dependent ATPase activity

histone binding

chromatin binding

DNA binding

0

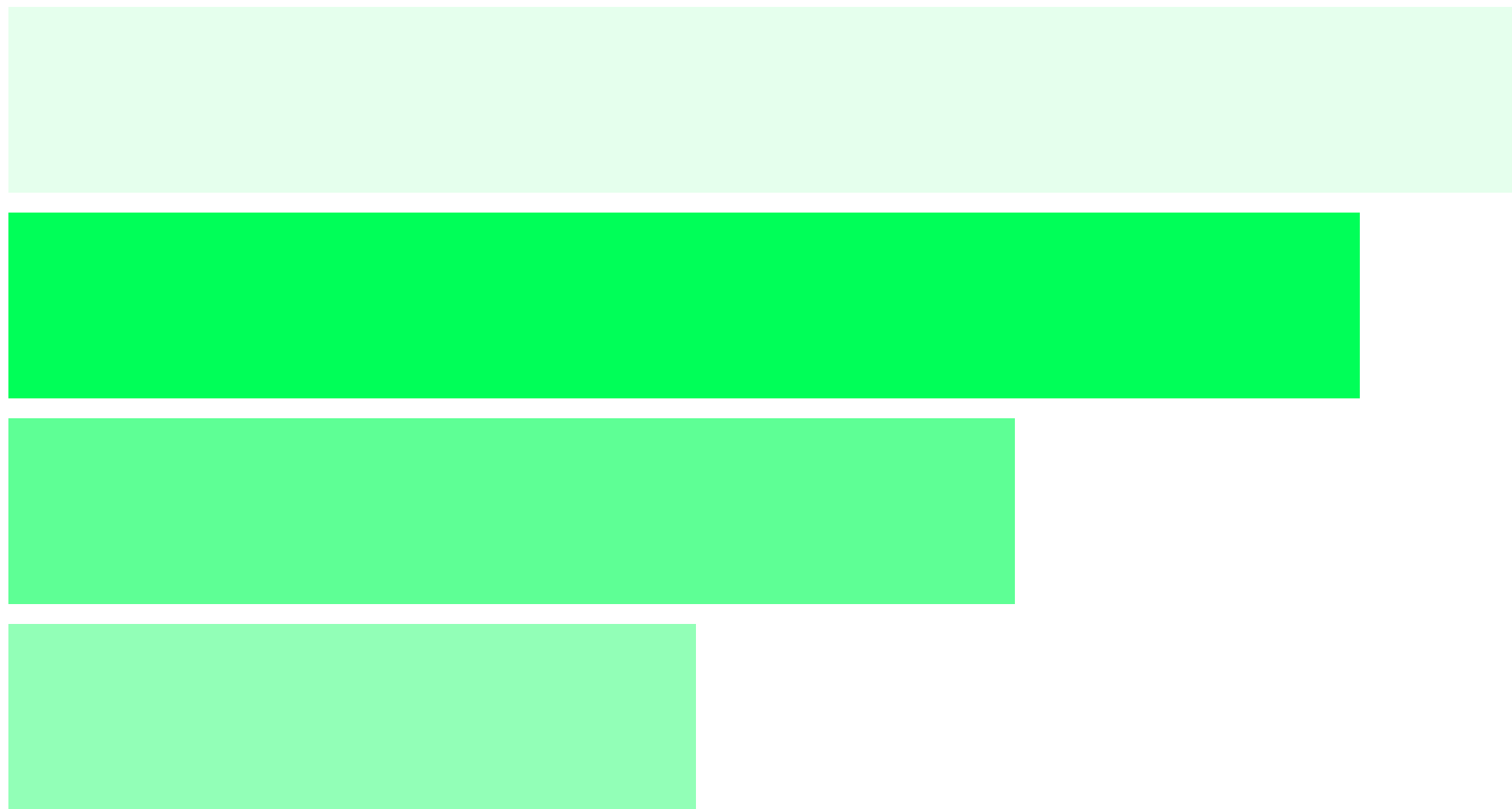
1

2

3

4

log2Enrichment



# Re-clustered module 3.11.8.4 BP enrichment

Term

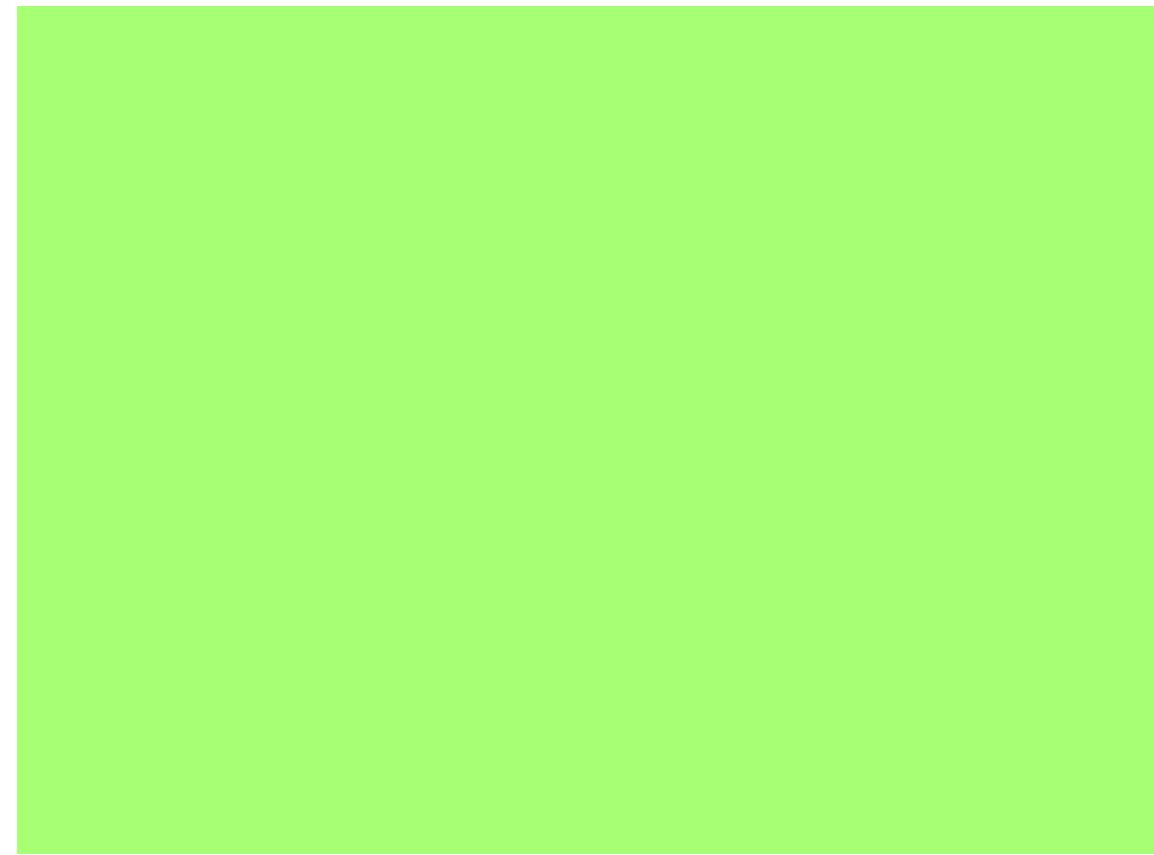
positive regulation of proteasomal ubiquitin-dependent protein catabolic process

0

2

4

log2Enrichment



Re-clustered module 3.11.8.4 MF enrichment

Term

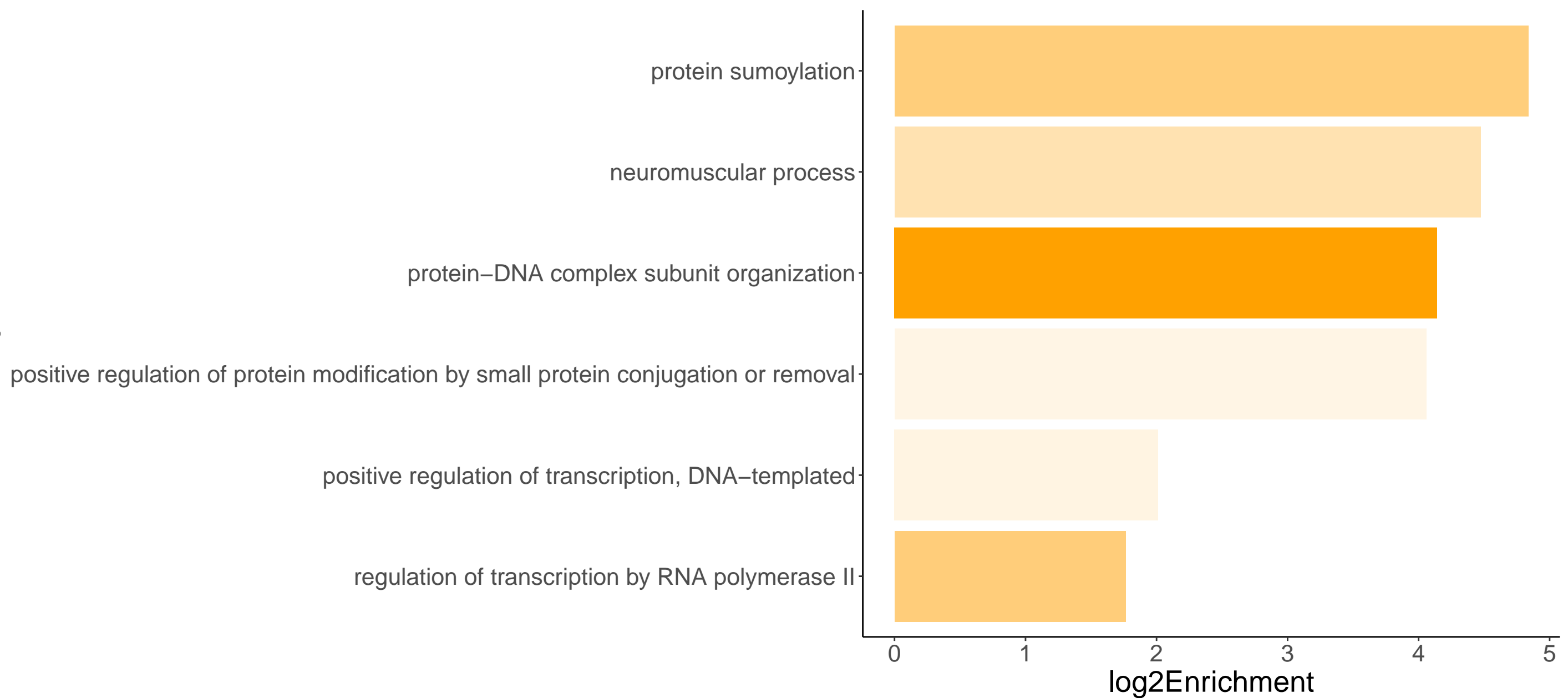
log2Enrichment





# Re-clustered module 3.11.8.5 BP enrichment

Term



# Re-clustered module 3.11.8.5 MF enrichment

Term

RNA polymerase II transcription factor binding

histone binding

transcription coregulator activity

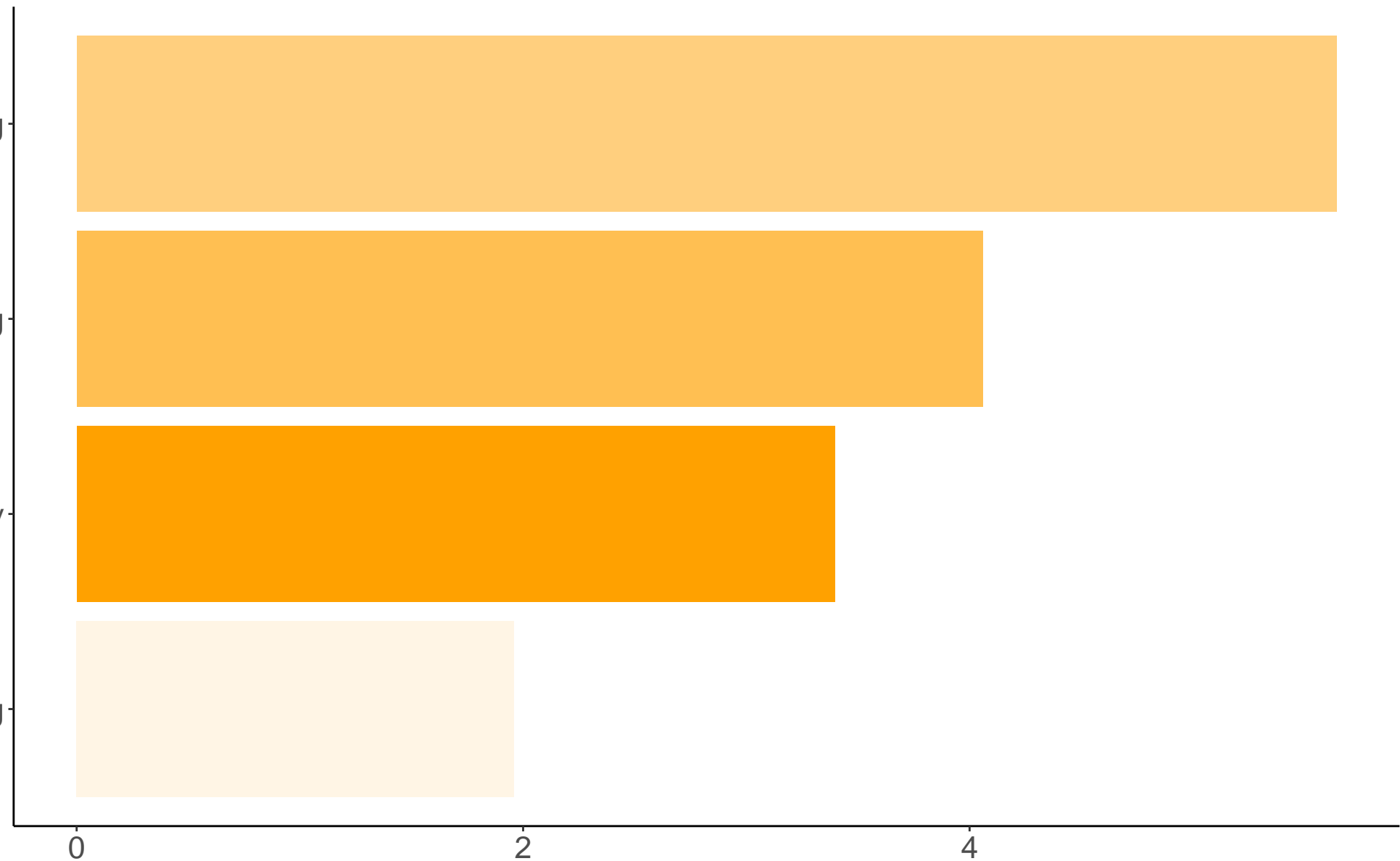
DNA binding

0

2

4

log2Enrichment



# Re-clustered module 3.12.15 BP enrichment

Term

centriole replication

RNA splicing

nuclear export

G2/M transition of mitotic cell cycle

0

1

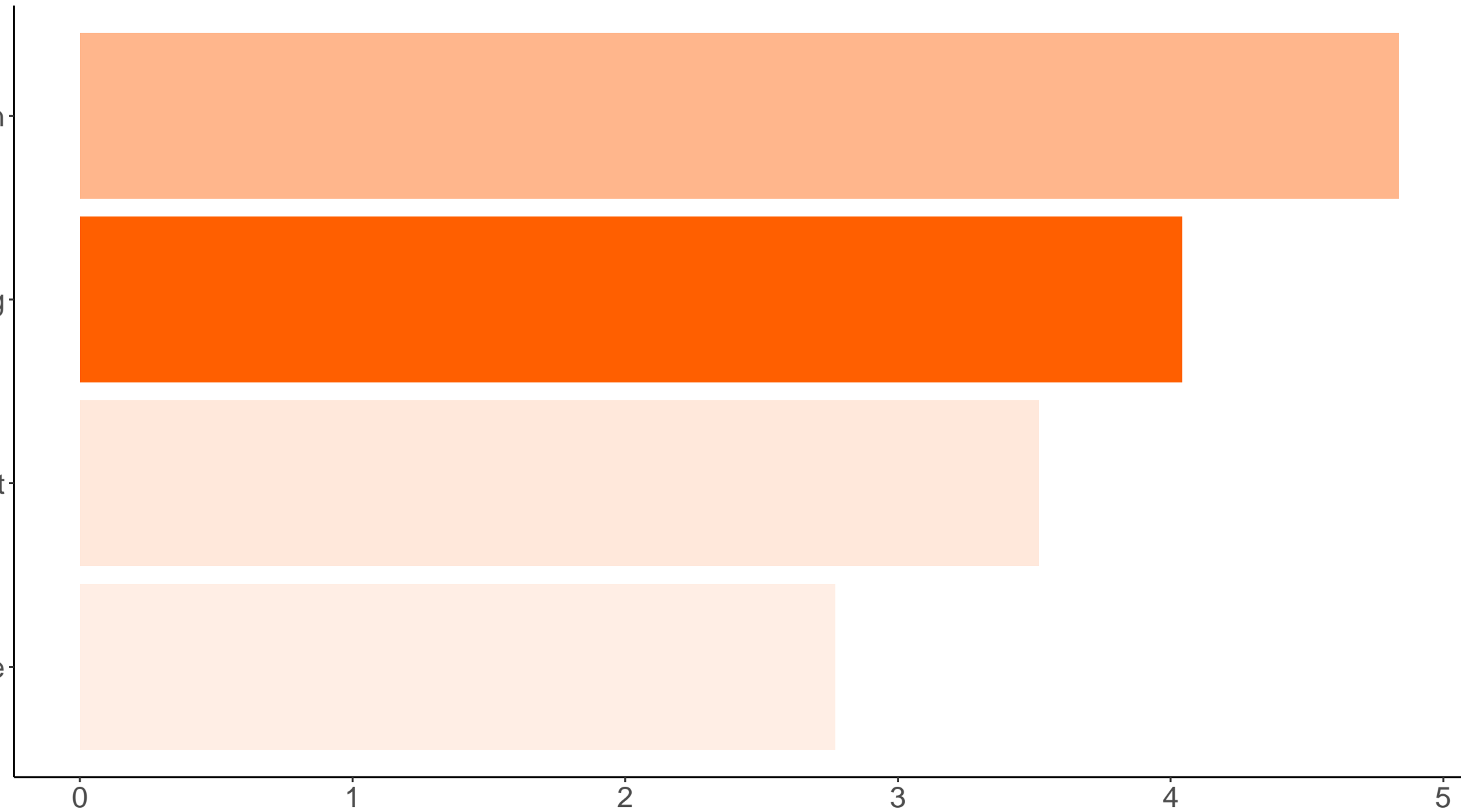
2

3

4

5

log2Enrichment



# Re-clustered module 3.12.15 MF enrichment

Term

thyroid hormone receptor binding

nuclear receptor transcription coactivator activity

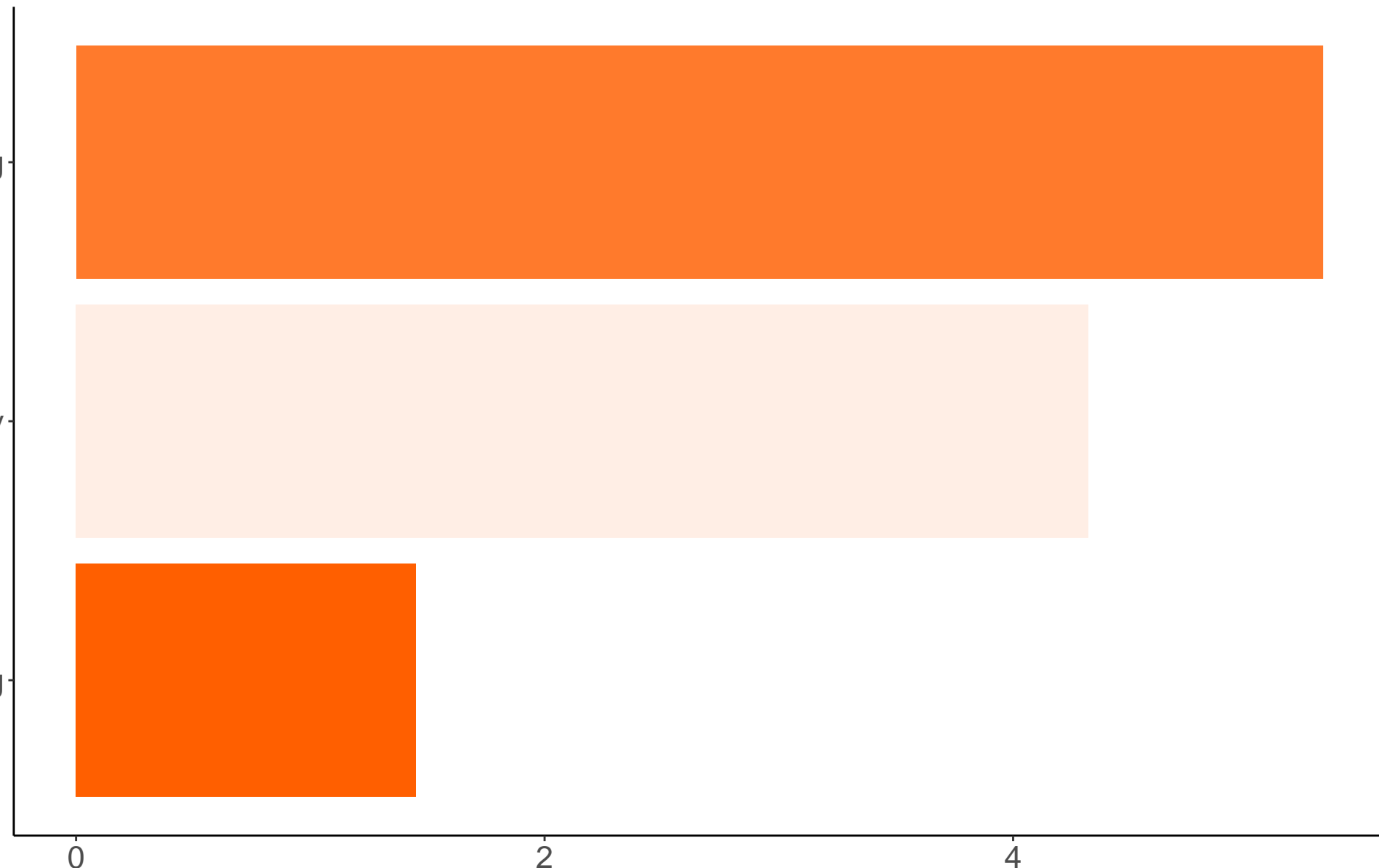
DNA binding

0

2

4

log2Enrichment



# Re-clustered module 3.12.16 BP enrichment

Term

histone acetylation

RNA phosphodiester bond hydrolysis

mRNA processing

0

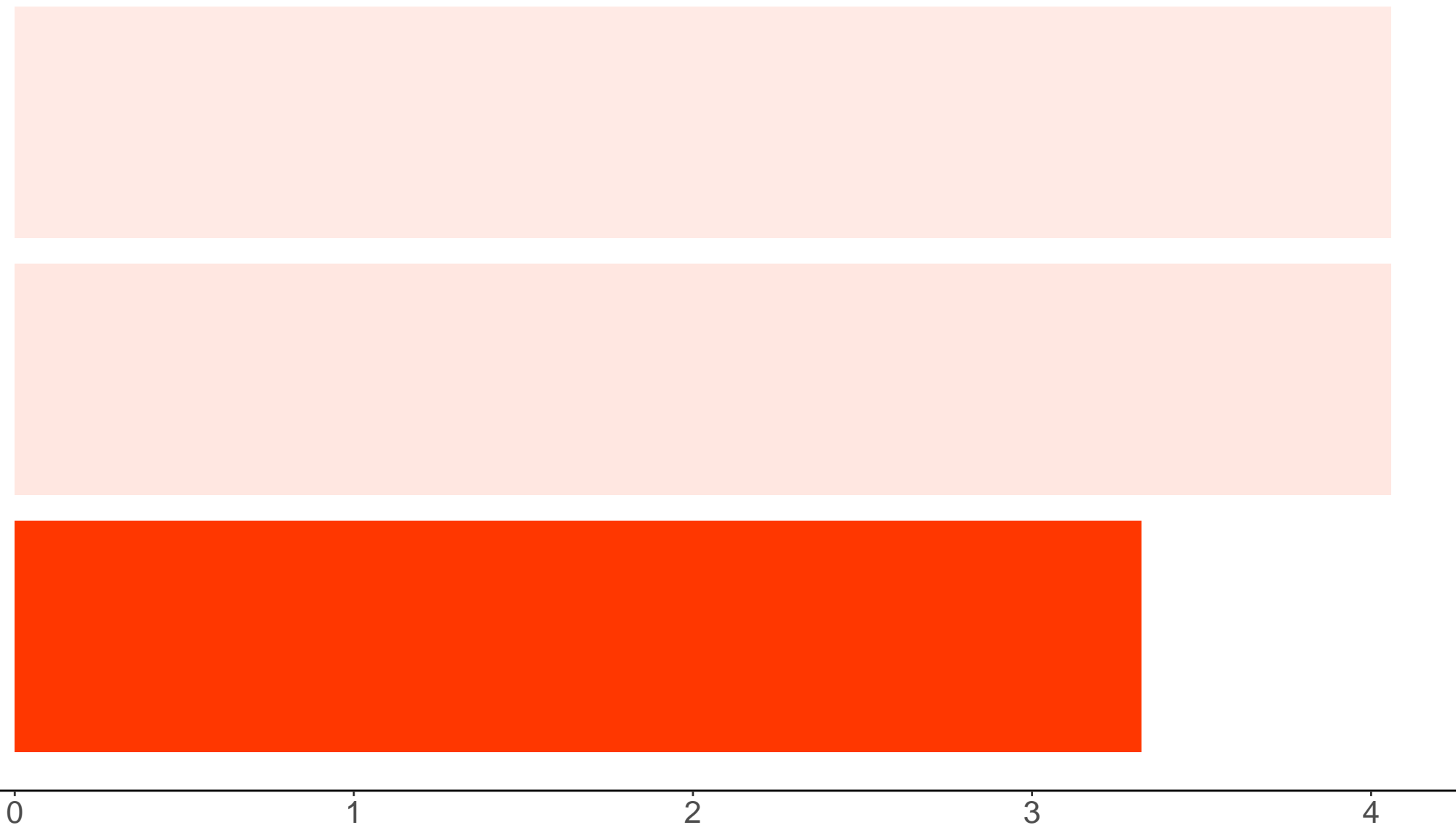
1

2

3

4

log2Enrichment



# Re-clustered module 3.12.16 MF enrichment

Term

transcription corepressor activity

RNA binding

0

1

2

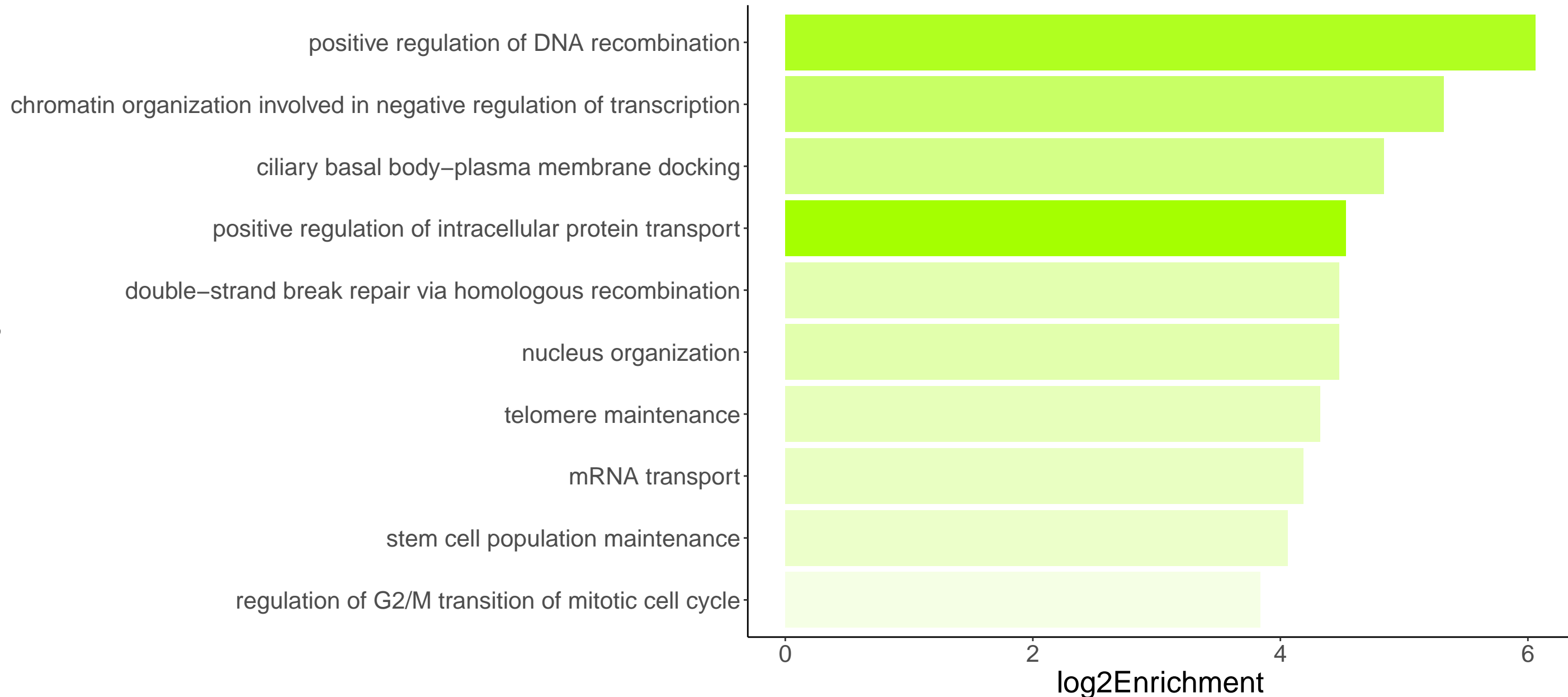
3

log2Enrichment



## Re-clustered module 3.12.24 BP enrichment

Term



# Re-clustered module 3.12.24 MF enrichment

Term

methyltransferase activity

0

1

2

3

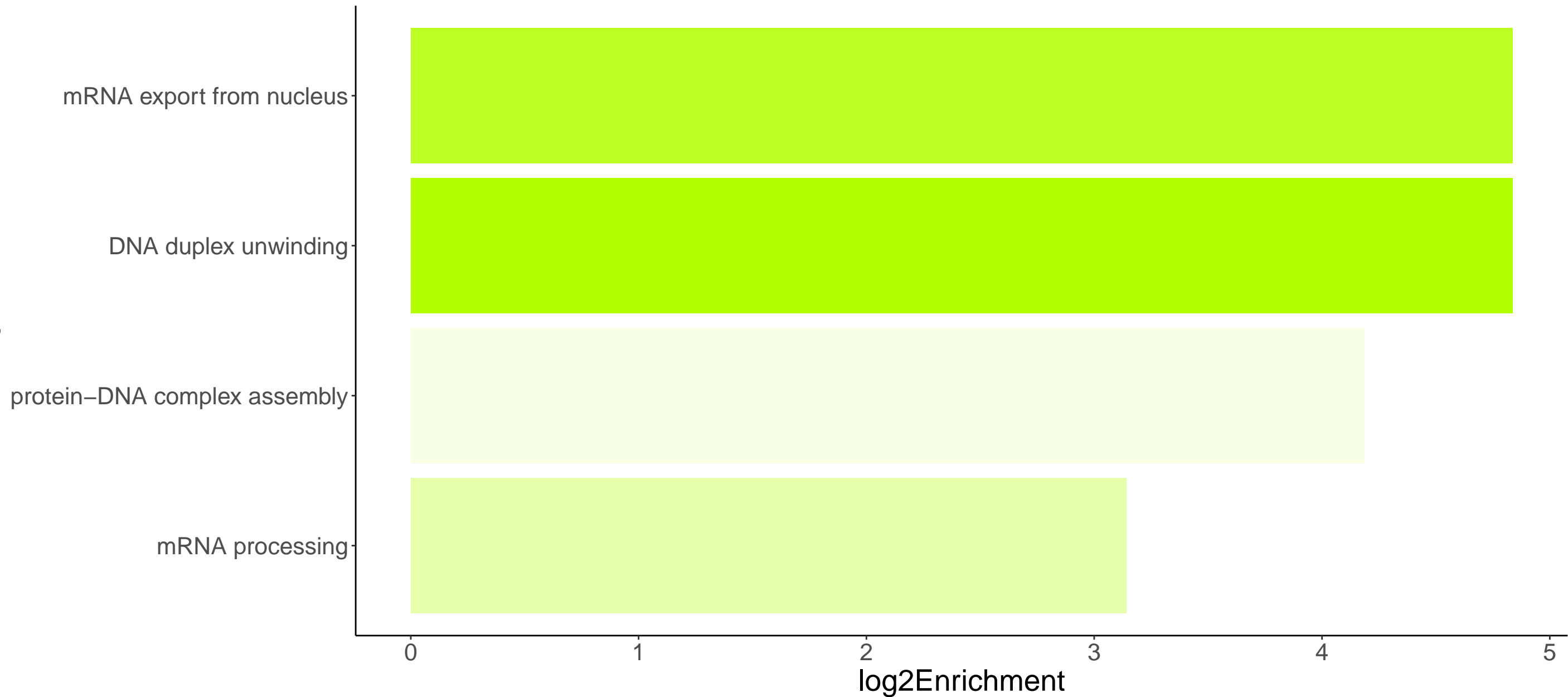
log2Enrichment





# Re-clustered module 3.12.7.1 BP enrichment

Term



# Re-clustered module 3.12.7.1 MF enrichment

Term

DNA helicase activity

protein N-terminus binding

protein C-terminus binding

histone binding

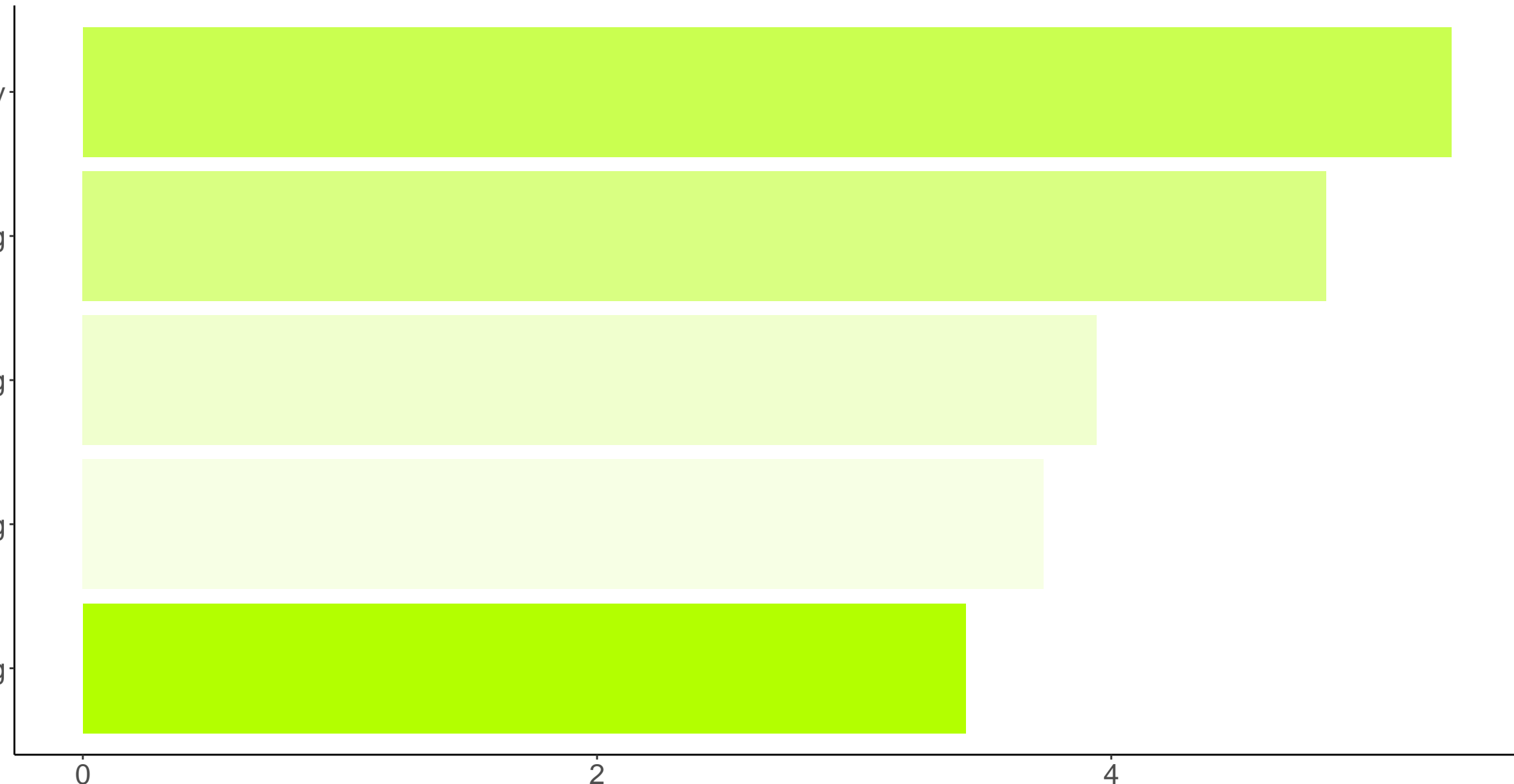
chromatin binding

0

2

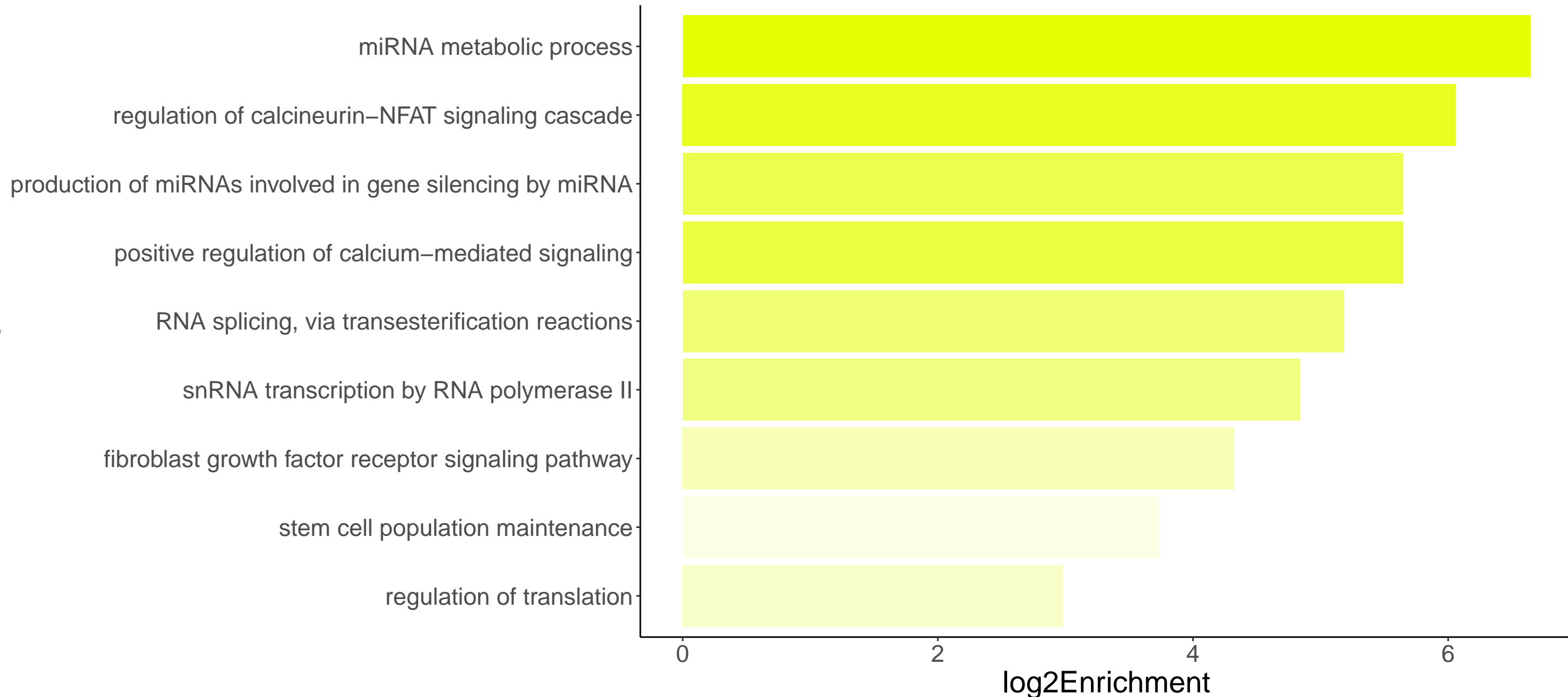
4

log2Enrichment



## Re-clustered module 3.12.7.2 BP enrichment

Term



# Re-clustered module 3.12.7.2 MF enrichment

Term

mRNA 3'-UTR AU-rich region binding

RNA helicase activity

0

2

4

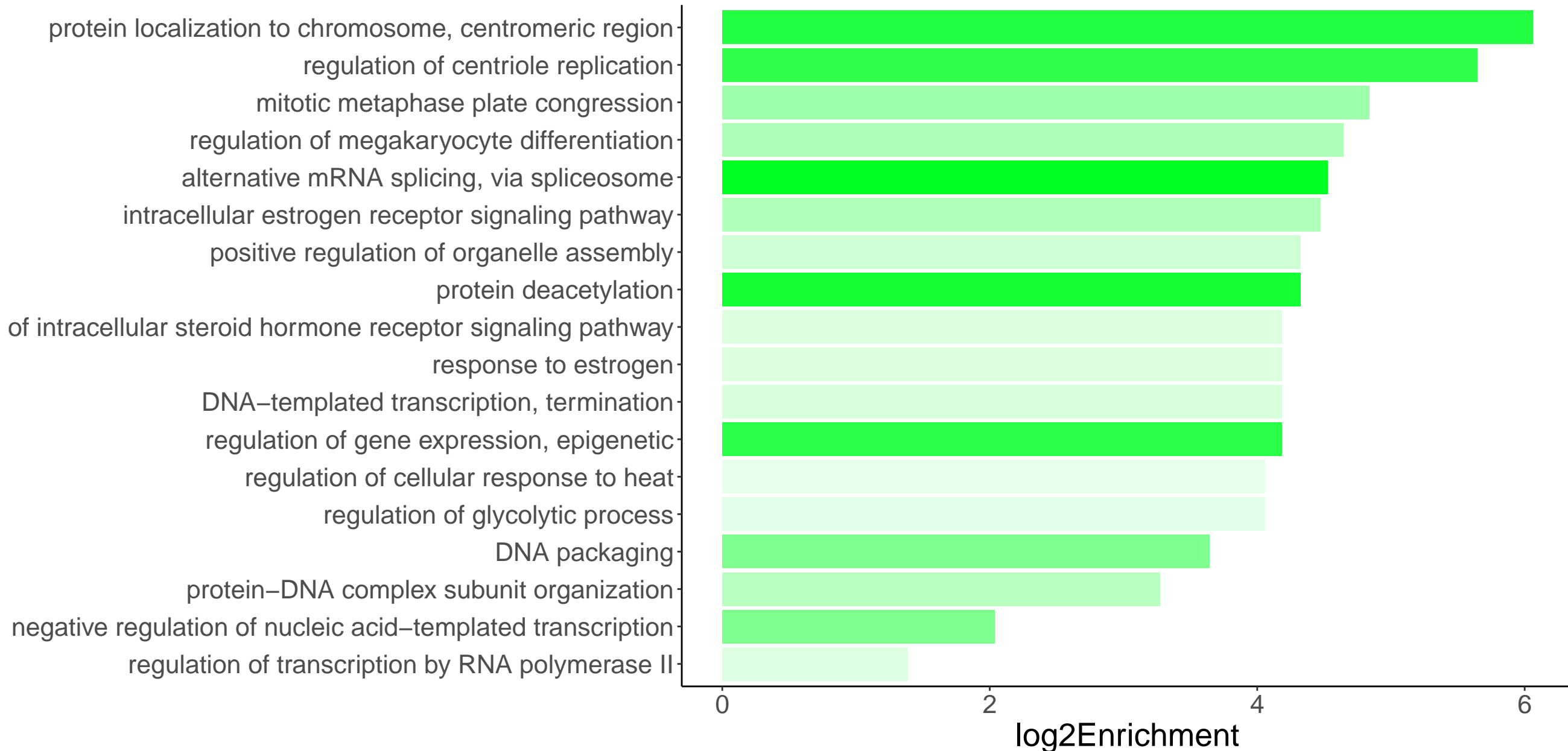
6

log2Enrichment



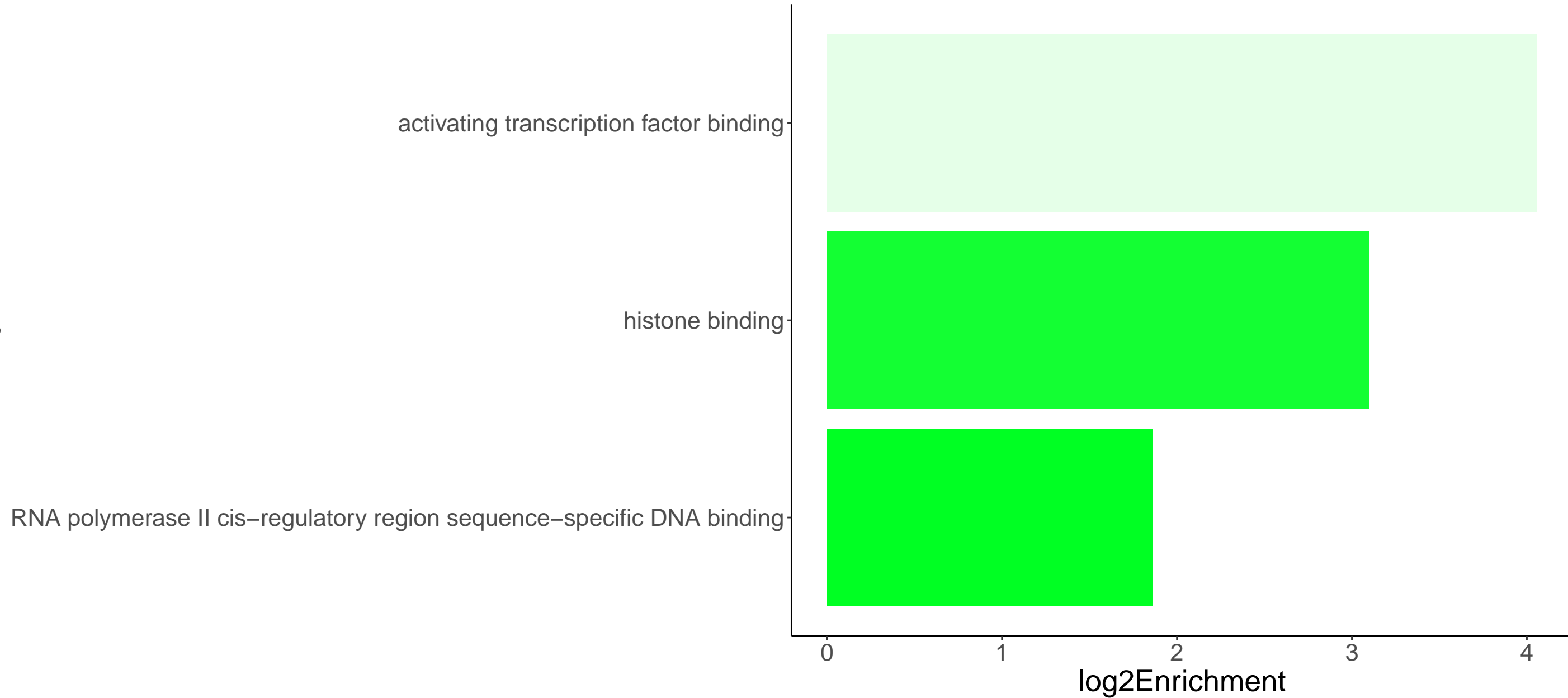
# Re-clustered module 3.12.7.3 BP enrichment

Term



# Re-clustered module 3.12.7.3 MF enrichment

Term



# Re-clustered module 3.12.8.1 BP enrichment

Term

diacylglycerol metabolic process

regulation of chromatin binding

histone H4-K16 acetylation

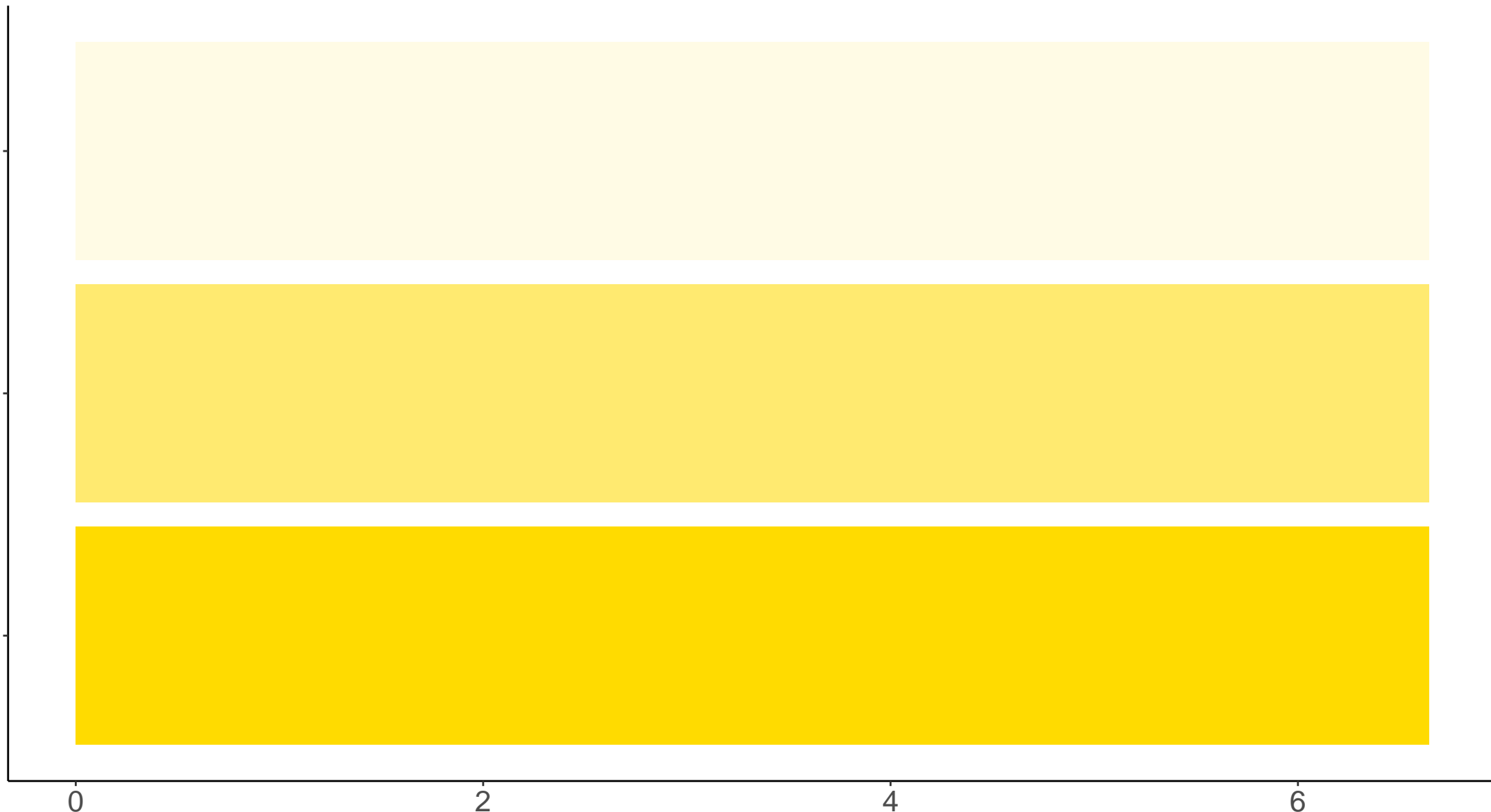
0

2

4

6

log2Enrichment



Re-clustered module 3.12.8.1 MF enrichment

Term

log2Enrichment





# Re-clustered module 3.12.8.4 BP enrichment

Term

serine family amino acid metabolic process

alpha-amino acid catabolic process

0

2

4

log2Enrichment



# Re-clustered module 3.12.8.4 MF enrichment

Term

gamma-tubulin binding

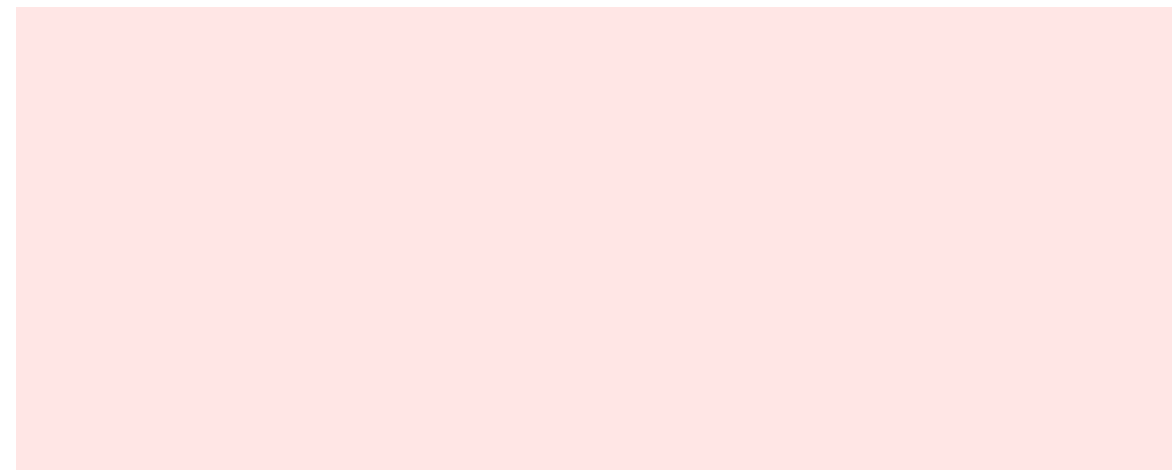
hydrolase activity, hydrolyzing O-glycosyl compounds

0

2

4

log2Enrichment



# Re-clustered module 3.12.8.5 BP enrichment

Term

myoblast proliferation

RNA splicing

mRNA processing

fibroblast growth factor receptor signaling pathway

mRNA transport

0

2

4

log2Enrichment



# Re-clustered module 3.12.8.5 MF enrichment

Term

cyclin-dependent protein serine/threonine kinase regulator activity

protein serine/threonine/tyrosine kinase activity

RNA polymerase binding

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.12.8.7 BP enrichment

Term

detection of chemical stimulus involved in sensory perception of bitter taste

regulation of mRNA splicing, via spliceosome

negative regulation of protein catabolic process

regulation of signal transduction by p53 class mediator

RNA splicing

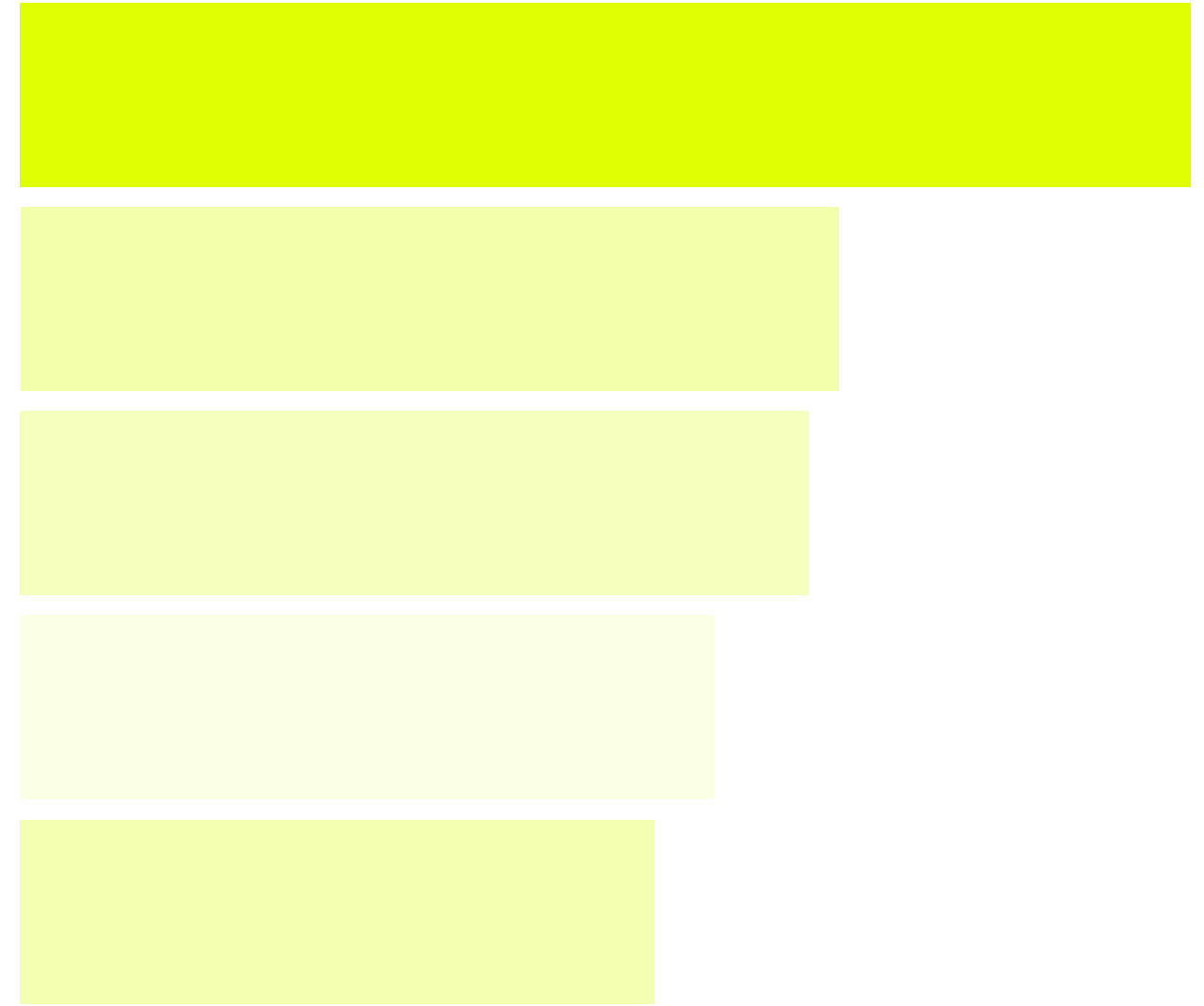
0

2

4

6

log2Enrichment



# Re-clustered module 3.12.8.7 MF enrichment

Term

taste receptor activity

0

2

4

6

log2Enrichment



# Re-clustered module 3.12.9 BP enrichment

Term

DNA replication-independent nucleosome assembly

negative regulation of phosphatase activity

0

2

4

log2Enrichment



Re-clustered module 3.12.9 MF enrichment

Term

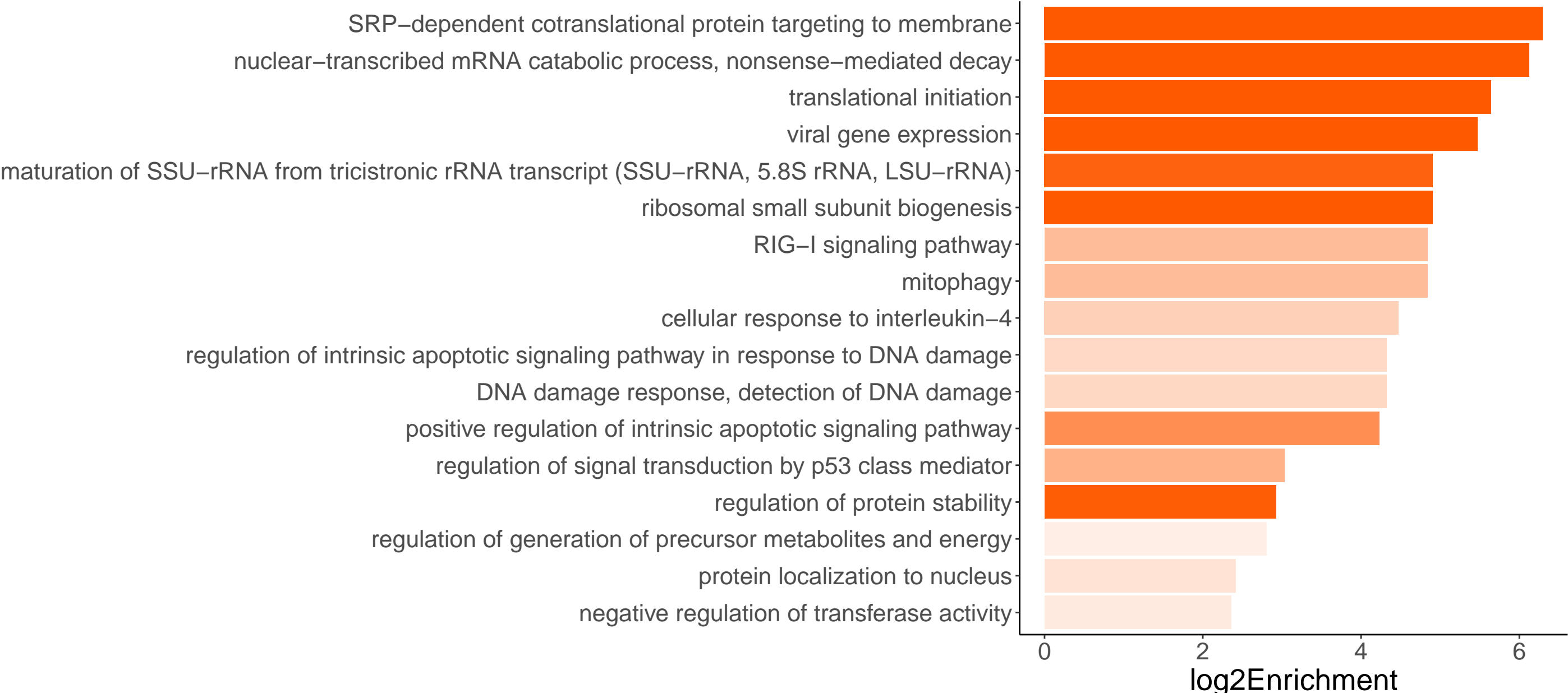
log2Enrichment





Re-clustered module 3.121 BP enr

Term



# Re-clustered module 3.121 MF enrichment

Term

structural constituent of ribosome

protein N-terminus binding

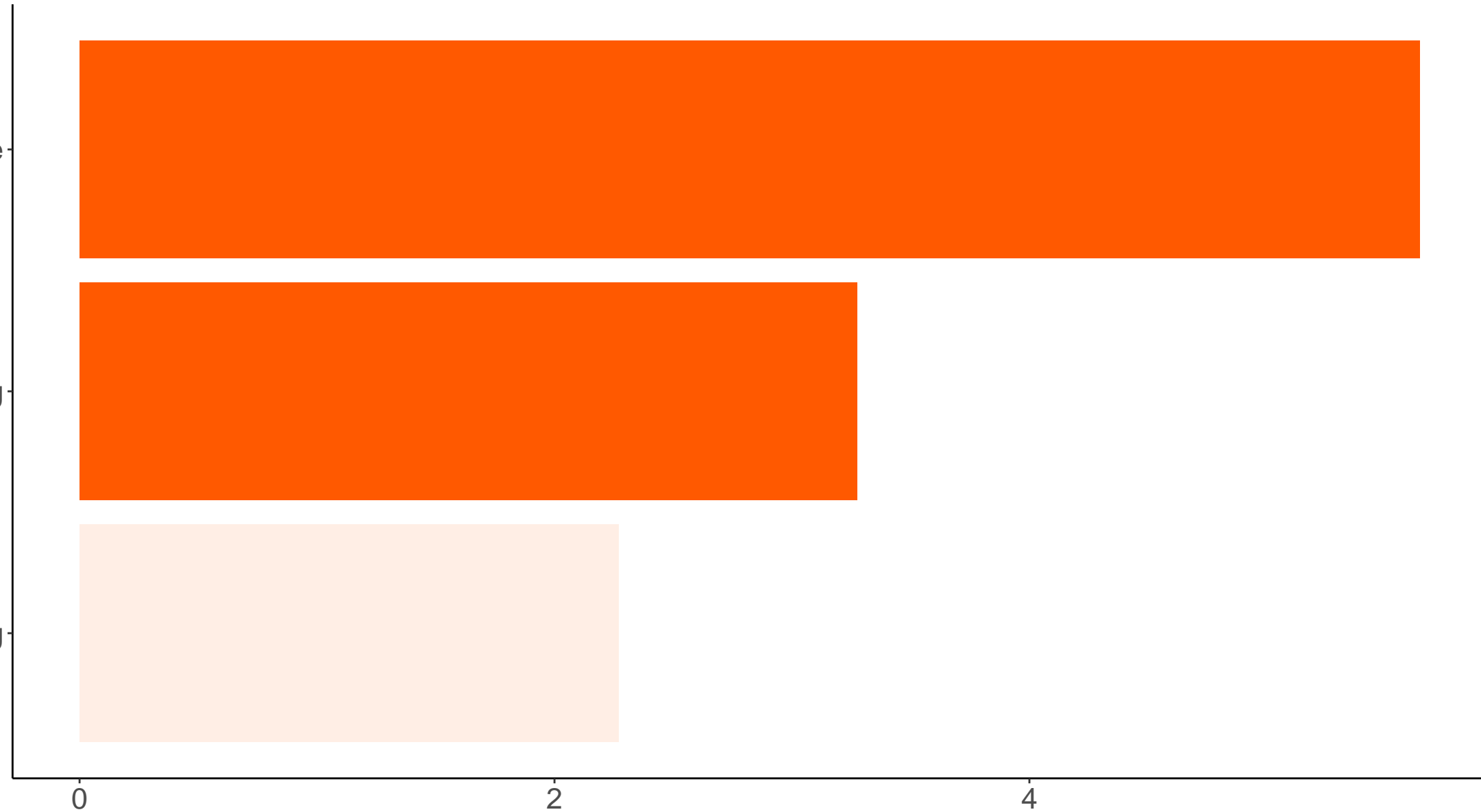
ubiquitin protein ligase binding

0

2

4

log2Enrichment



# Re-clustered module 3.139 BP enrichment

Term

regulation of mitochondrial fission

cilium organization

0

2

4

6

log2Enrichment



Re-clustered module 3.139 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.18.1 BP enrichment

Term

regulation of synaptic vesicle exocytosis

cell aging

positive regulation of protein secretion

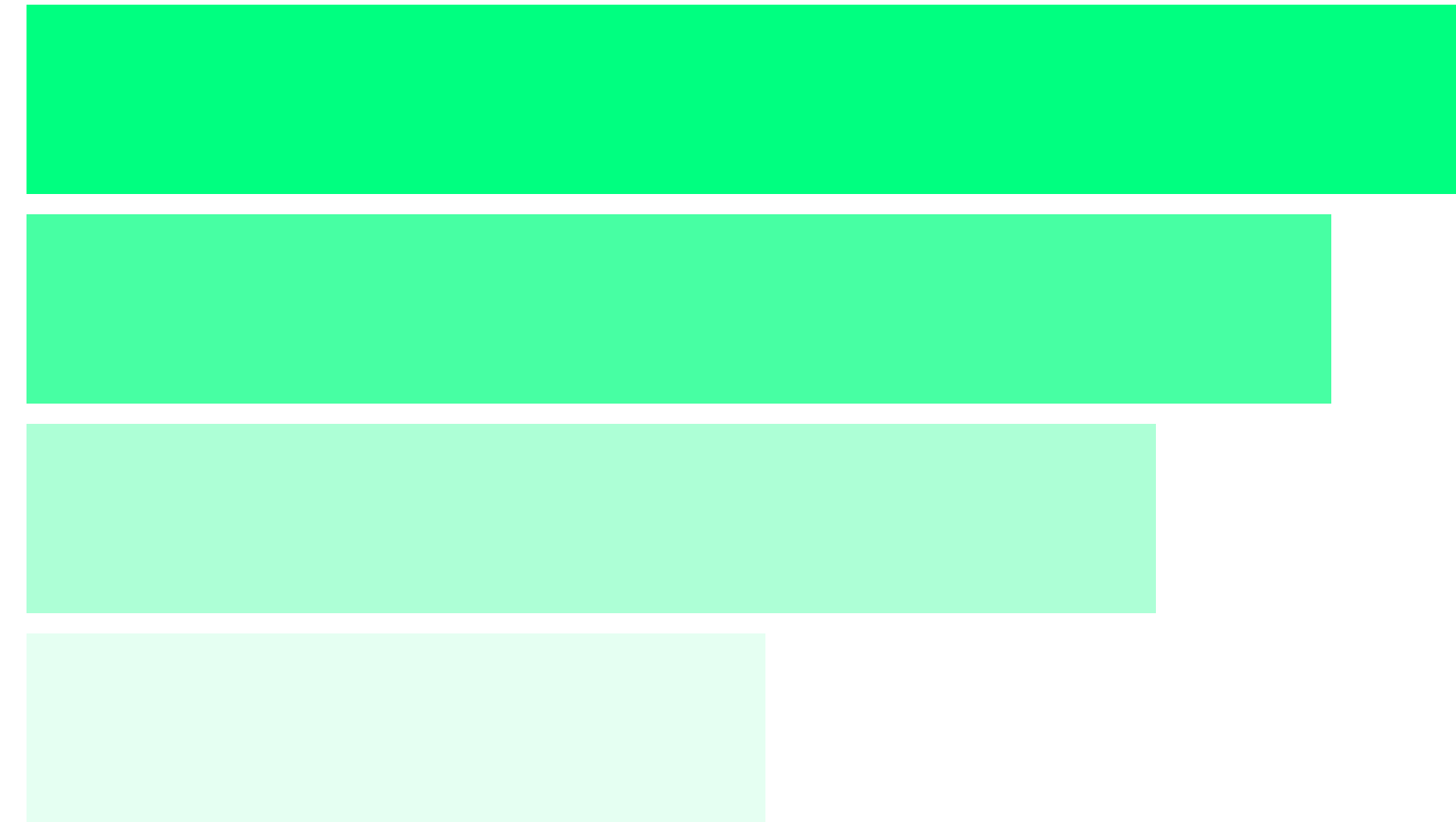
translation

0

2

4

log2Enrichment



Re-clustered module 3.18.1 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.18.10 BP enrichment

Term

mitochondrial translation

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.18.10 MF enrichment

Term

RNA binding

0.0

0.5

1.0

1.5

2.0

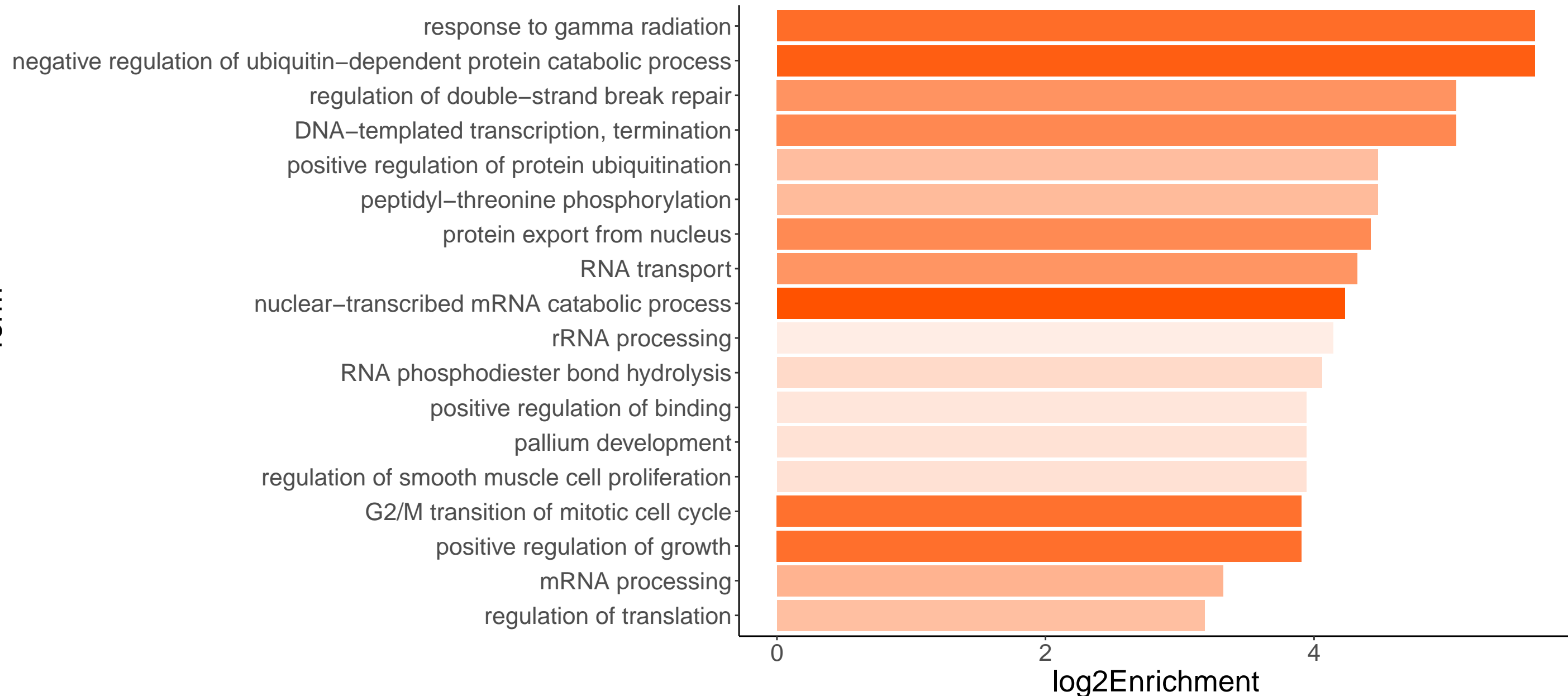
log2Enrichment





# Re-clustered module 3.18.12 BP enrichment

Term



# Re-clustered module 3.18.12 MF enrichment

Term

nucleocytoplasmic carrier activity

Ran GTPase binding

protein N-terminus binding

ribonucleoprotein complex binding

RNA binding

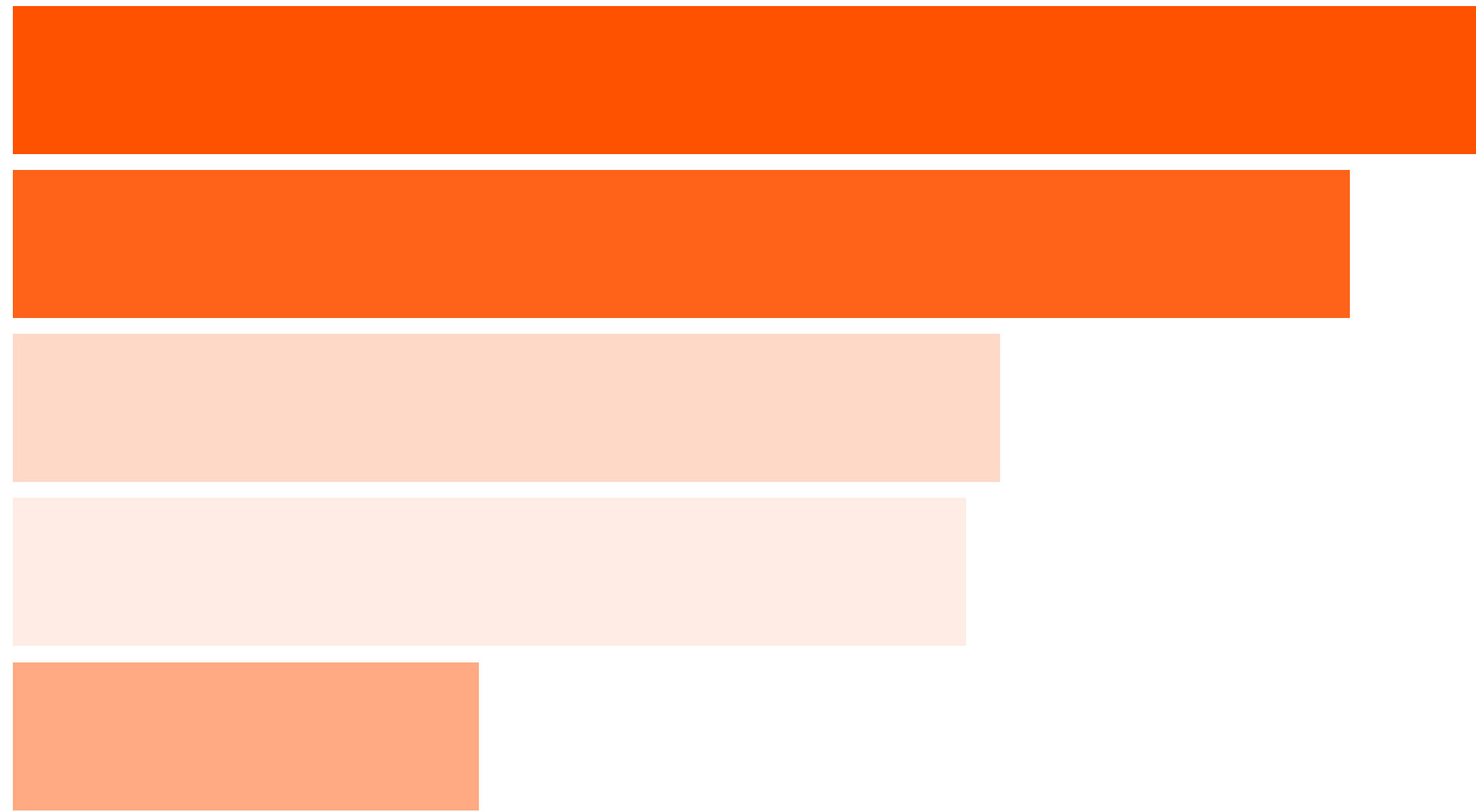
0

2

4

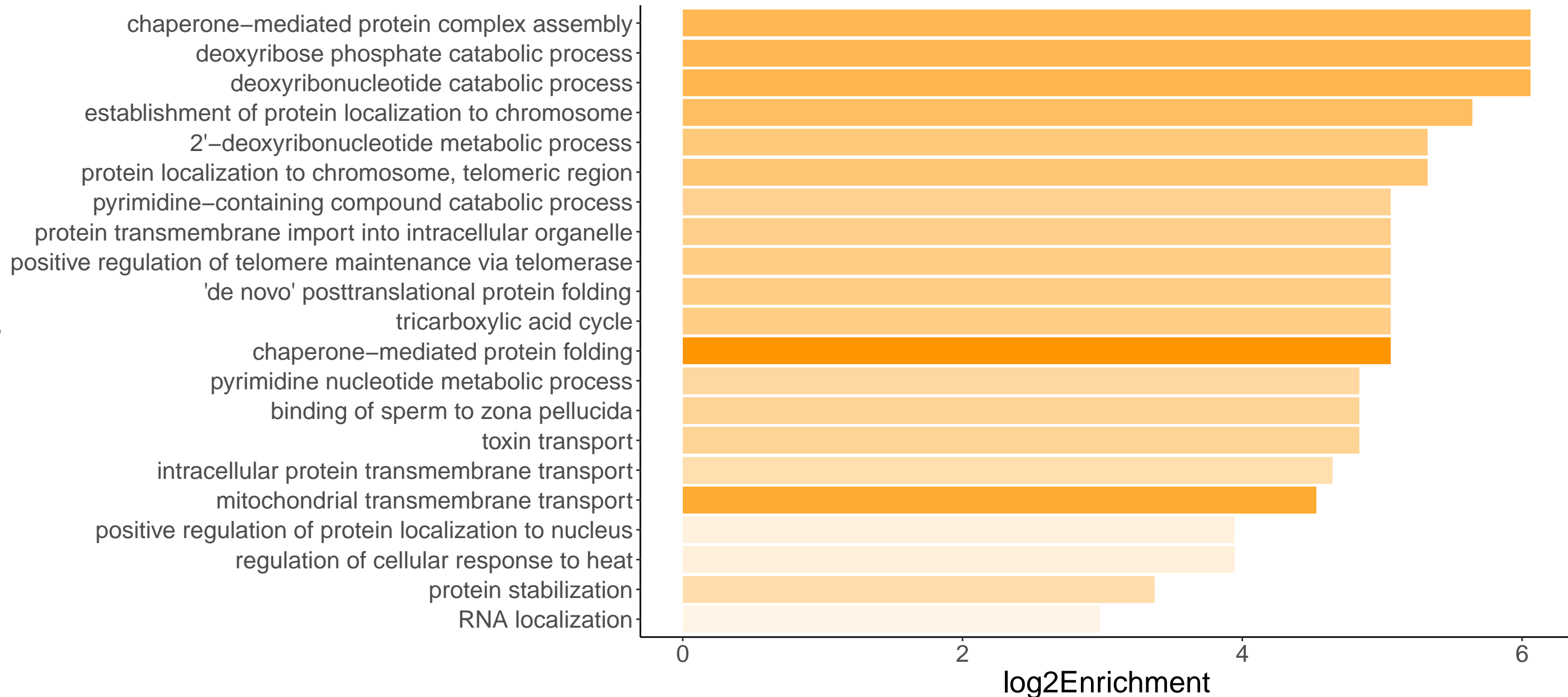
6

log2Enrichment



# Re-clustered module 3.18.15 BP enrichment

Term



# Re-clustered module 3.18.15 MF enrichment

Term

RNA helicase activity

unfolded protein binding

ribonucleoprotein complex binding

0

1

2

3

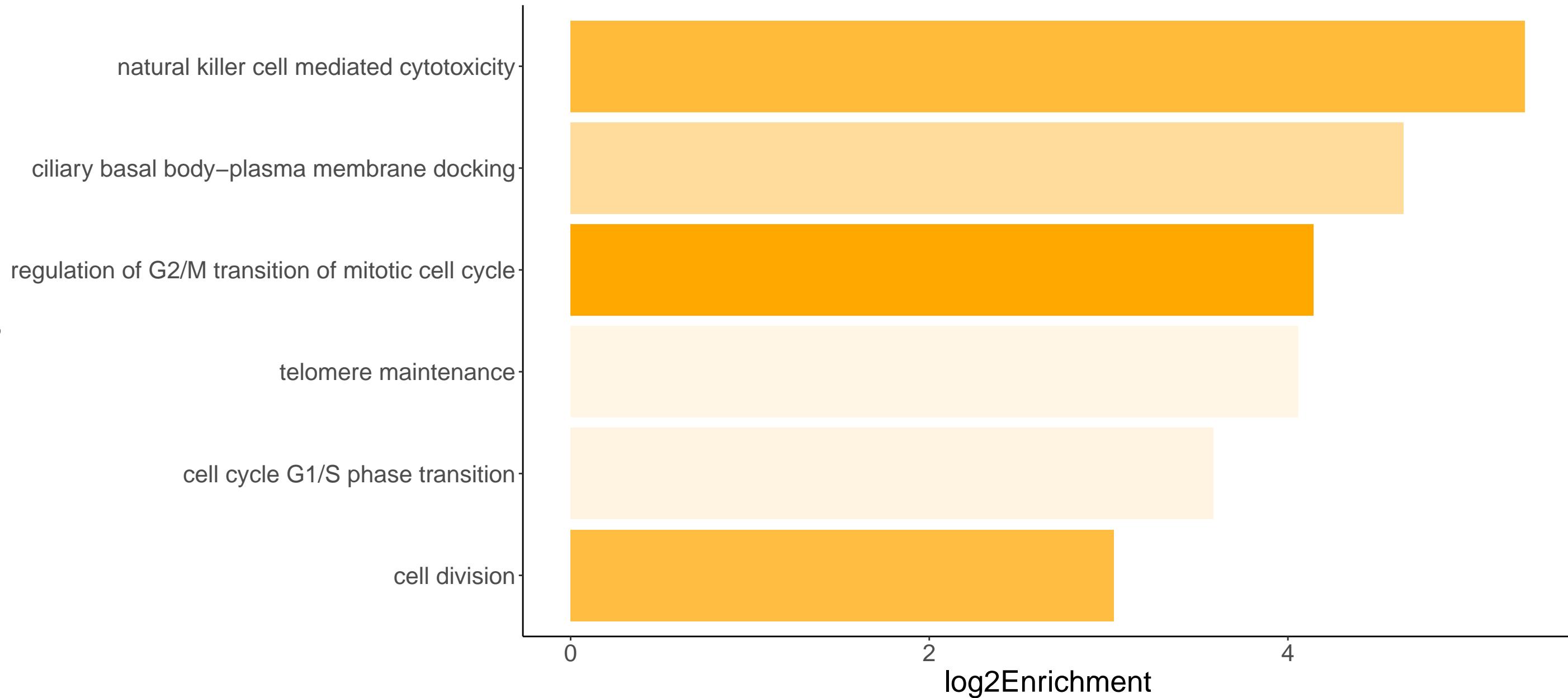
4

log2Enrichment



## Re-clustered module 3.18.23 BP enrichment

Term



# Re-clustered module 3.18.23 MF enrichment

Term

MHC protein binding

double-stranded RNA binding

GTP binding

0

2

4

6

log2Enrichment



Re-clustered module 3.18.28.14 BP enrichment

Term

log2Enrichment



# Re-clustered module 3.18.28.14 MF enrichment

Term

RNA helicase activity

S-adenosylmethionine-dependent methyltransferase activity

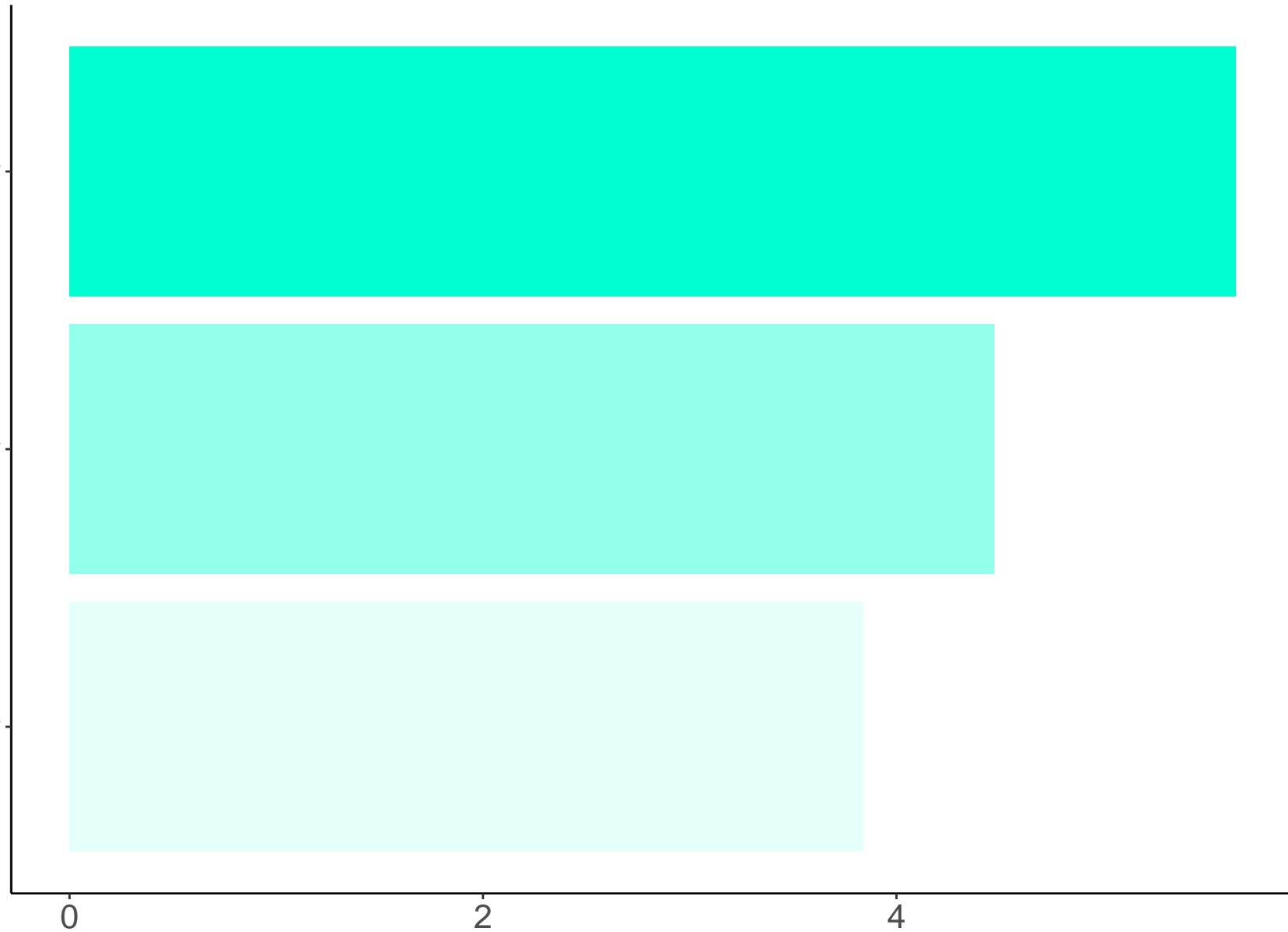
protein heterodimerization activity

0

2

4

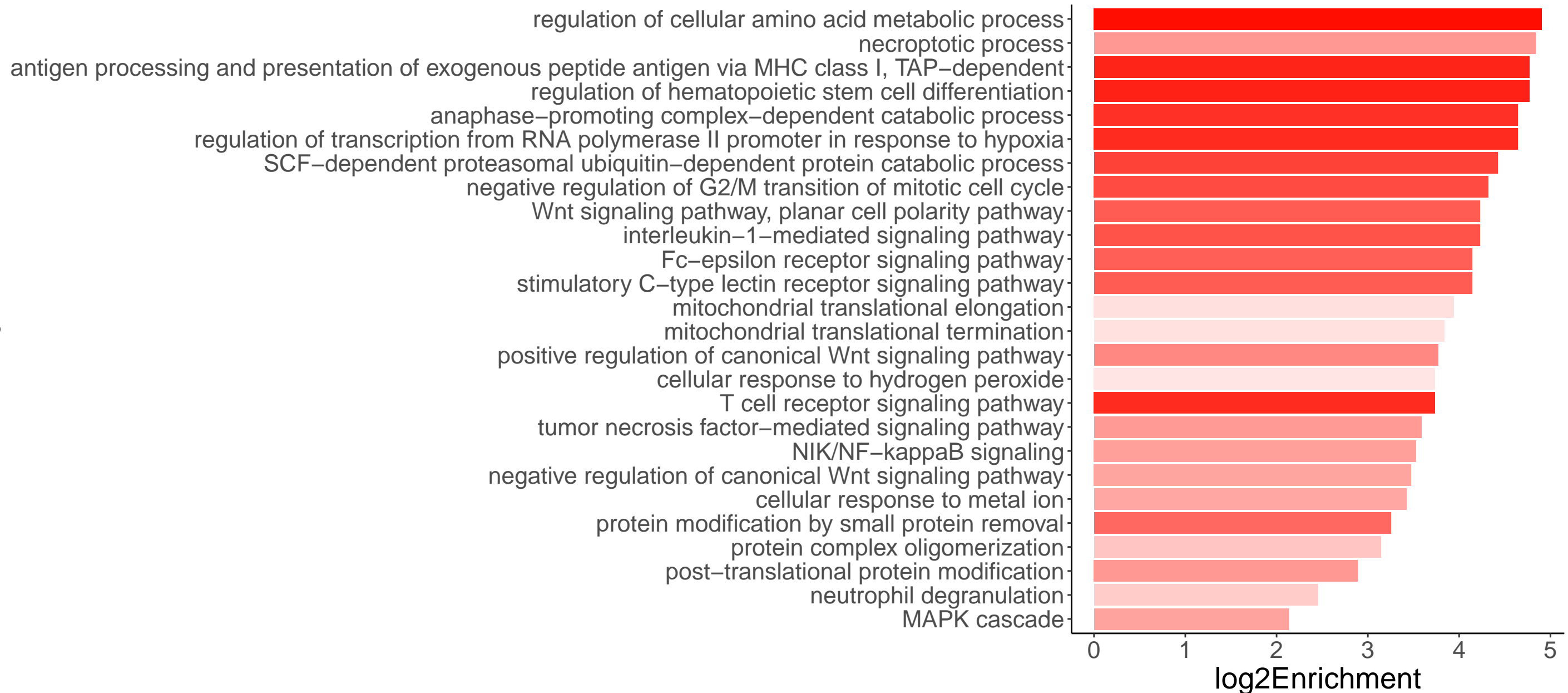
log2Enrichment





# Re-clustered module 3.18.28.2

Term



# Re-clustered module 3.18.28.2 MF enrichment

Term

mRNA 3'-UTR binding

protein serine/threonine phosphatase activity

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.18.28.4 BP

Term

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

blastocyst formation

RNA phosphodiester bond hydrolysis, endonucleolytic

chromatin assembly

negative regulation of apoptotic signaling pathway

0

2

4

log2Enrichment



# Re-clustered module 3.18.28.4 MF enrichment

Term

nuclear receptor transcription coactivator activity

scaffold protein binding

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.18.28.7 BP enrichment

Term

mitochondrial RNA metabolic process

RNA methylation

0

2

4

log2Enrichment



# Re-clustered module 3.18.28.7 MF enrichment

Term

RNA methyltransferase activity

unfolded protein binding

structural constituent of ribosome

0

1

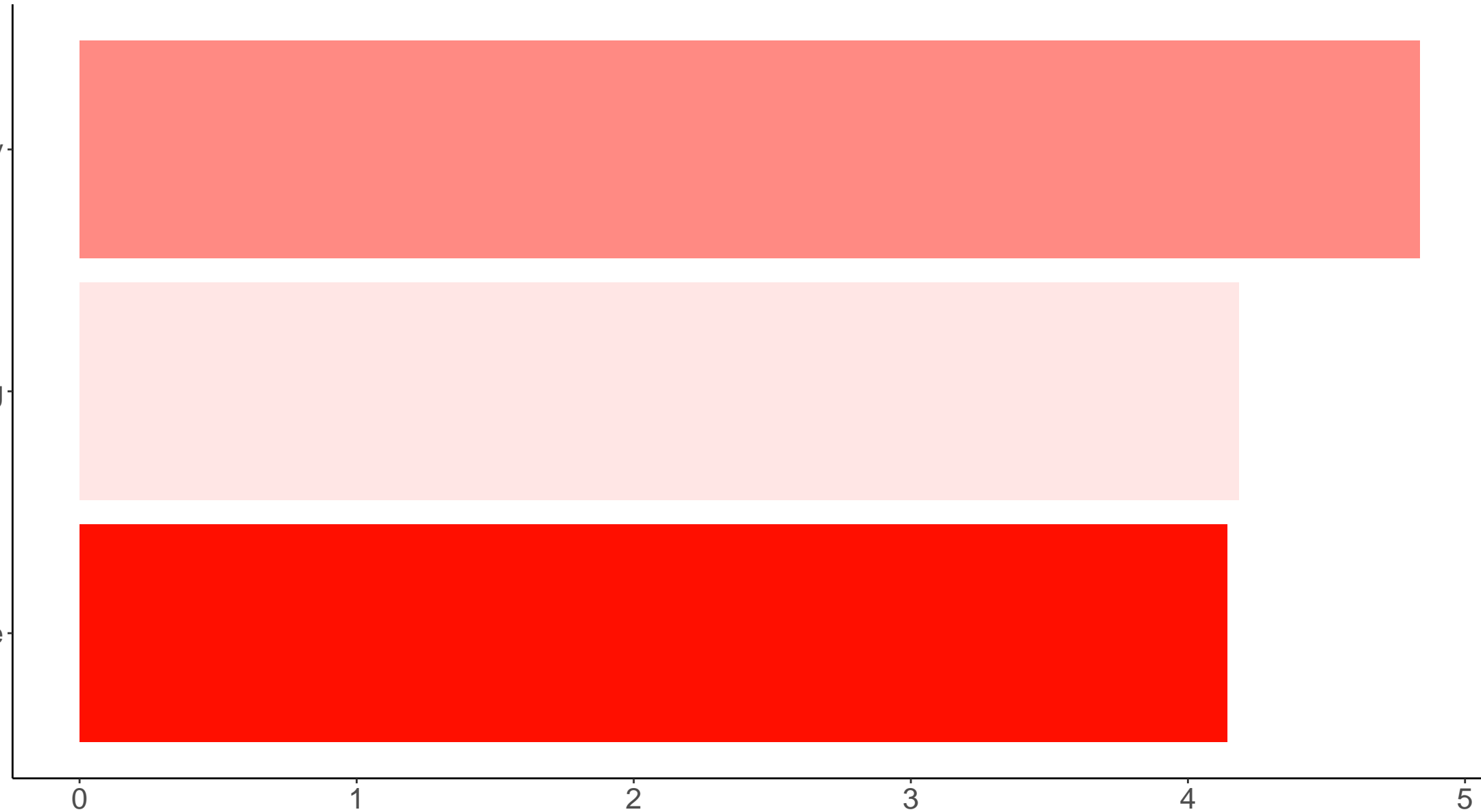
2

3

4

5

log2Enrichment



# Re-clustered module 3.18.3 BP enrichment

Term

histone deubiquitination

translational elongation

regulation of synaptic plasticity

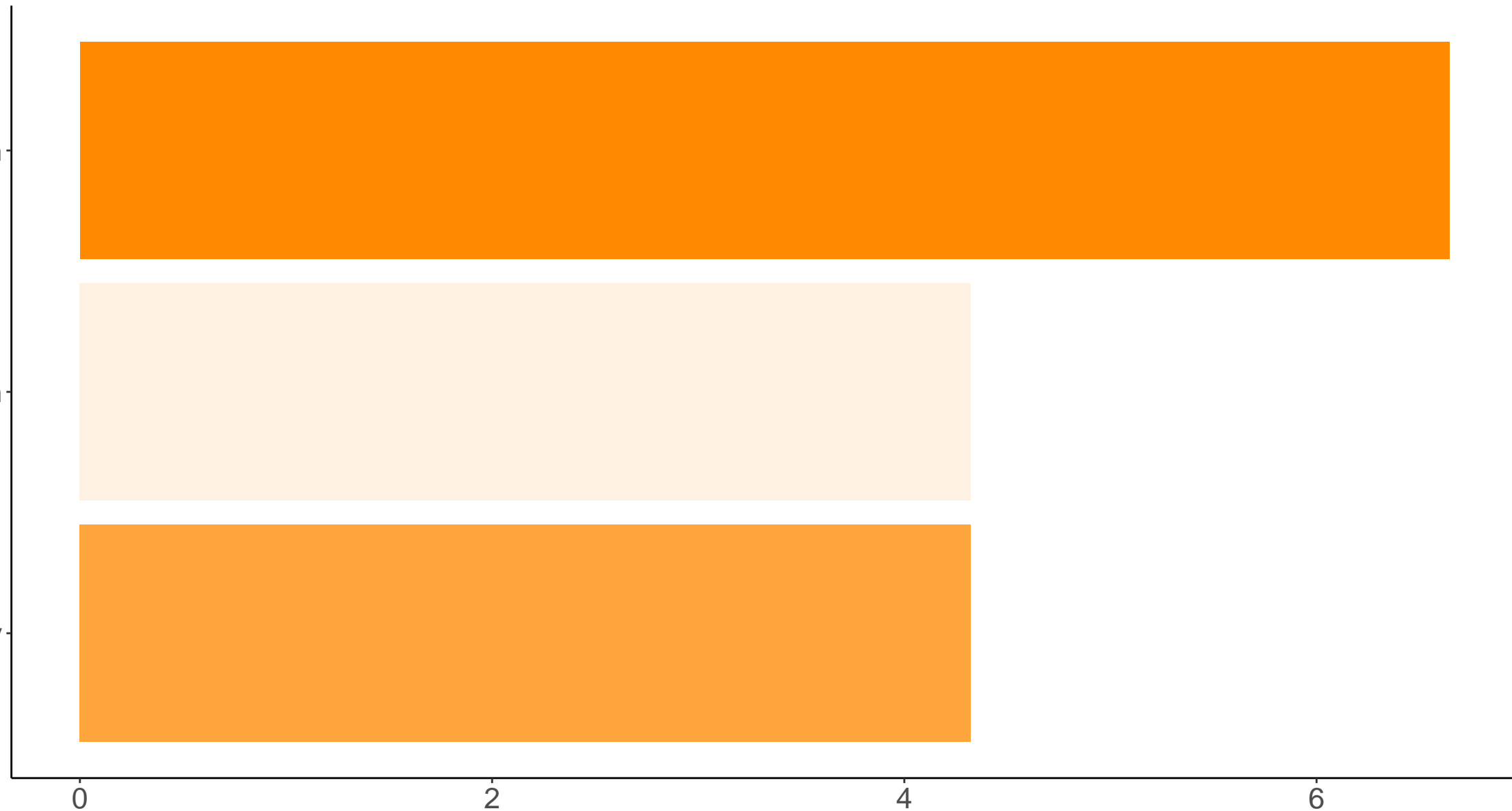
0

2

4

6

log2Enrichment



# Re-clustered module 3.18.3 MF enrichment

Term

rRNA binding

0

2

4

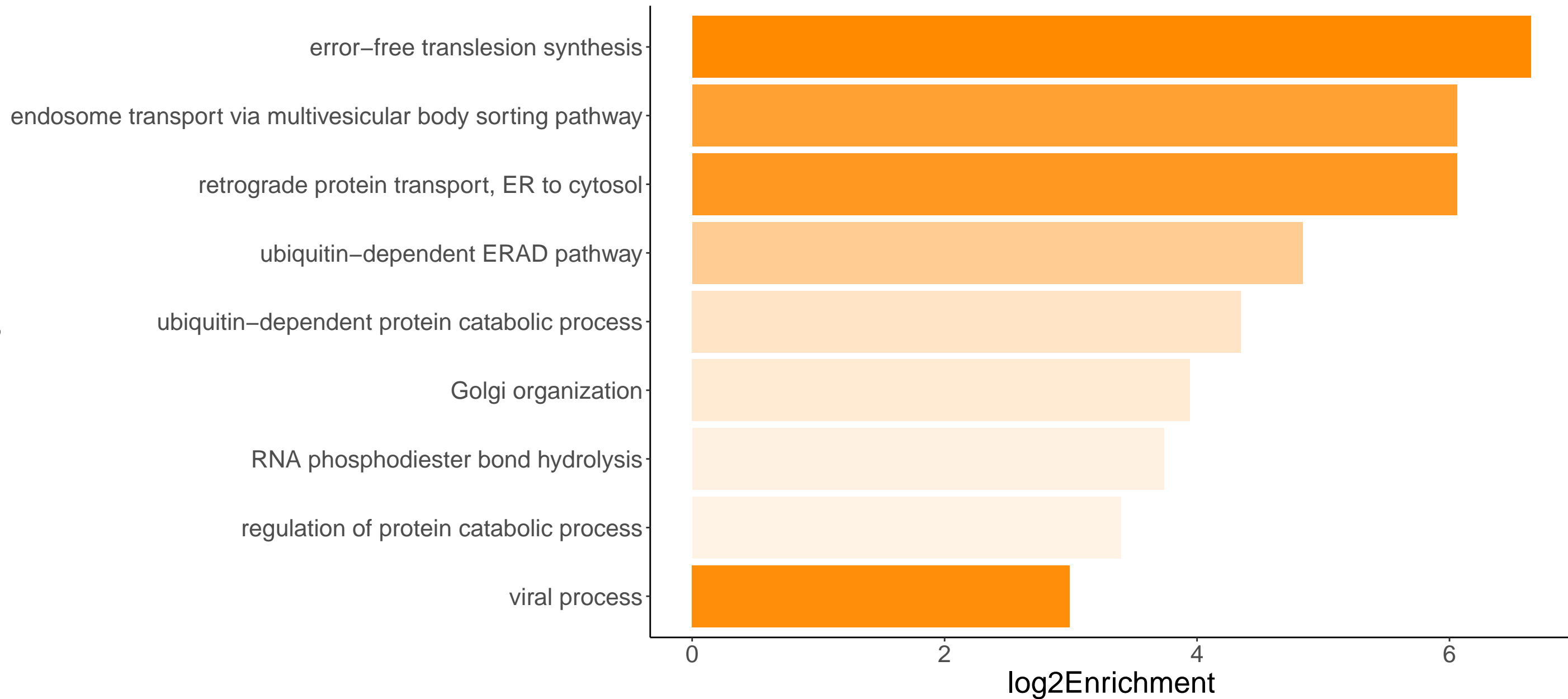
log2Enrichment





## Re-clustered module 3.18.36 BP enrichment

Term



# Re-clustered module 3.18.36 MF enrichment

Term

peptidase activator activity

ubiquitin binding

ubiquitin protein ligase binding

0

2

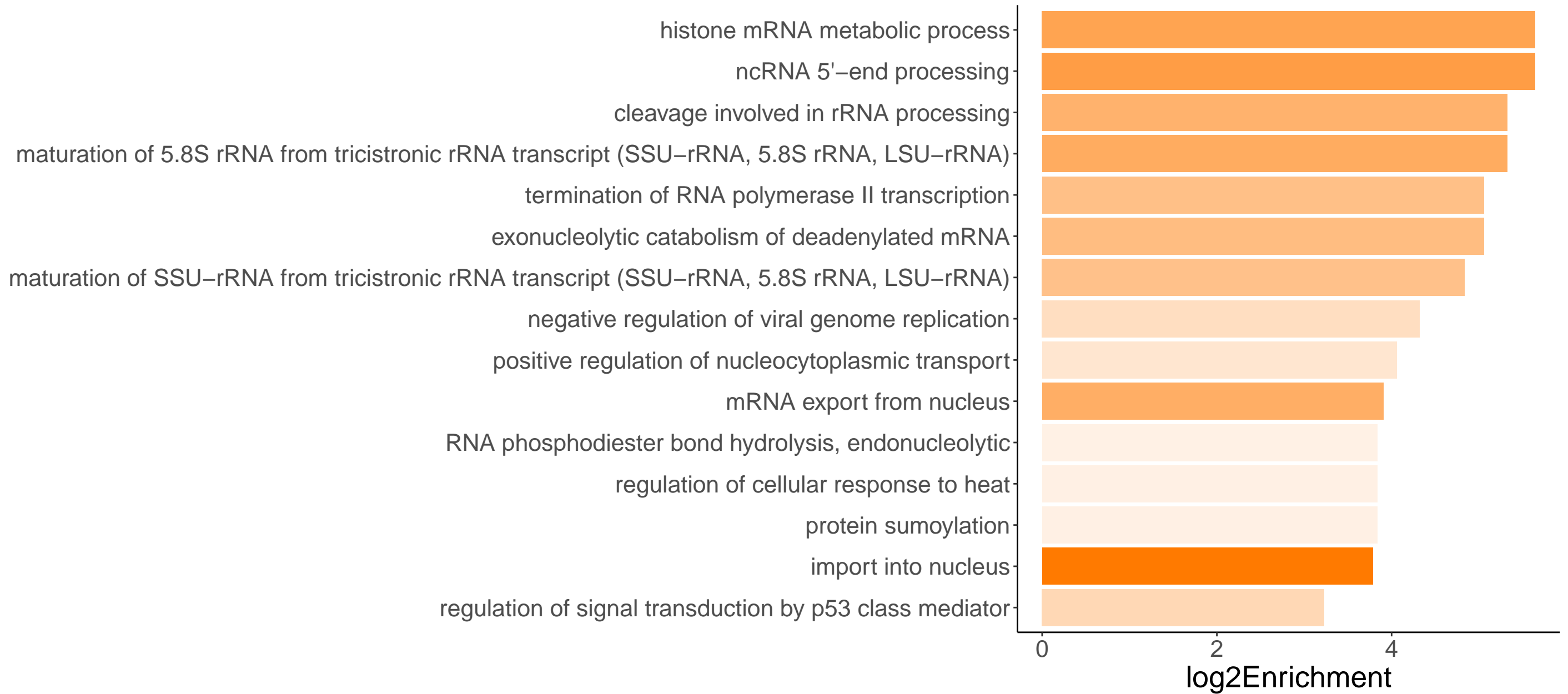
4

log2Enrichment



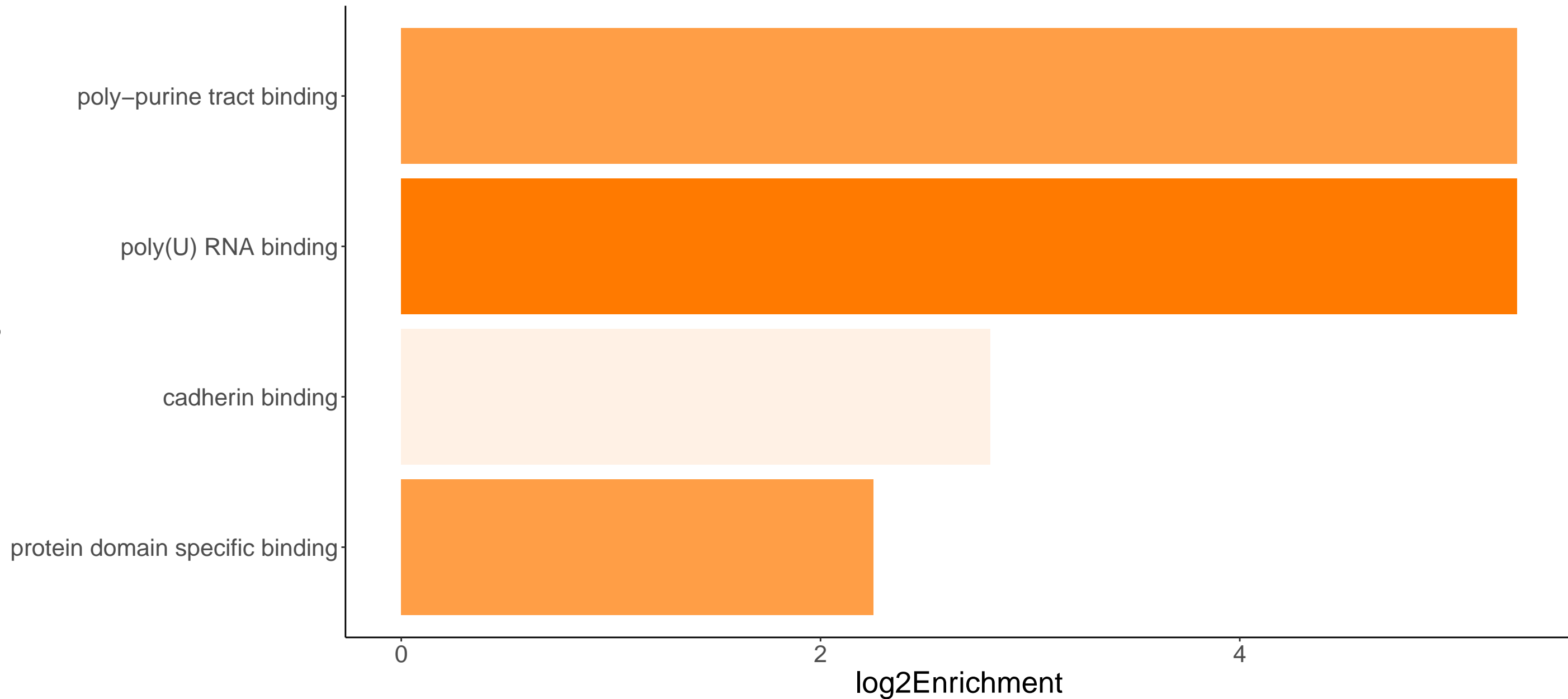
Re-clustered module 3.18.4 BP enrichment

Term



# Re-clustered module 3.18.4 MF enrichment

Term



Re-clustered module 3.18.42 BP enrichment

Term

log2Enrichment



Re-clustered module 3.18.42 MF enrichment

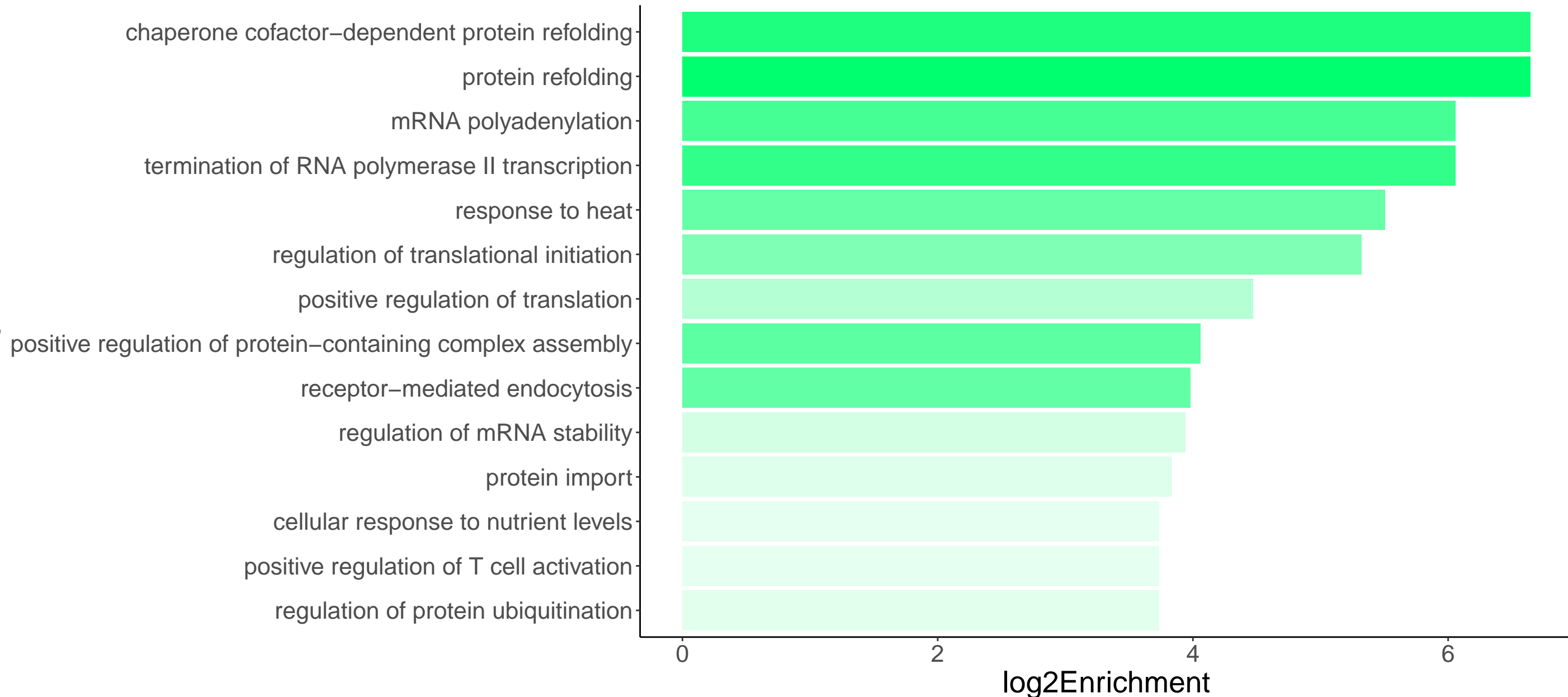
Term

log2Enrichment



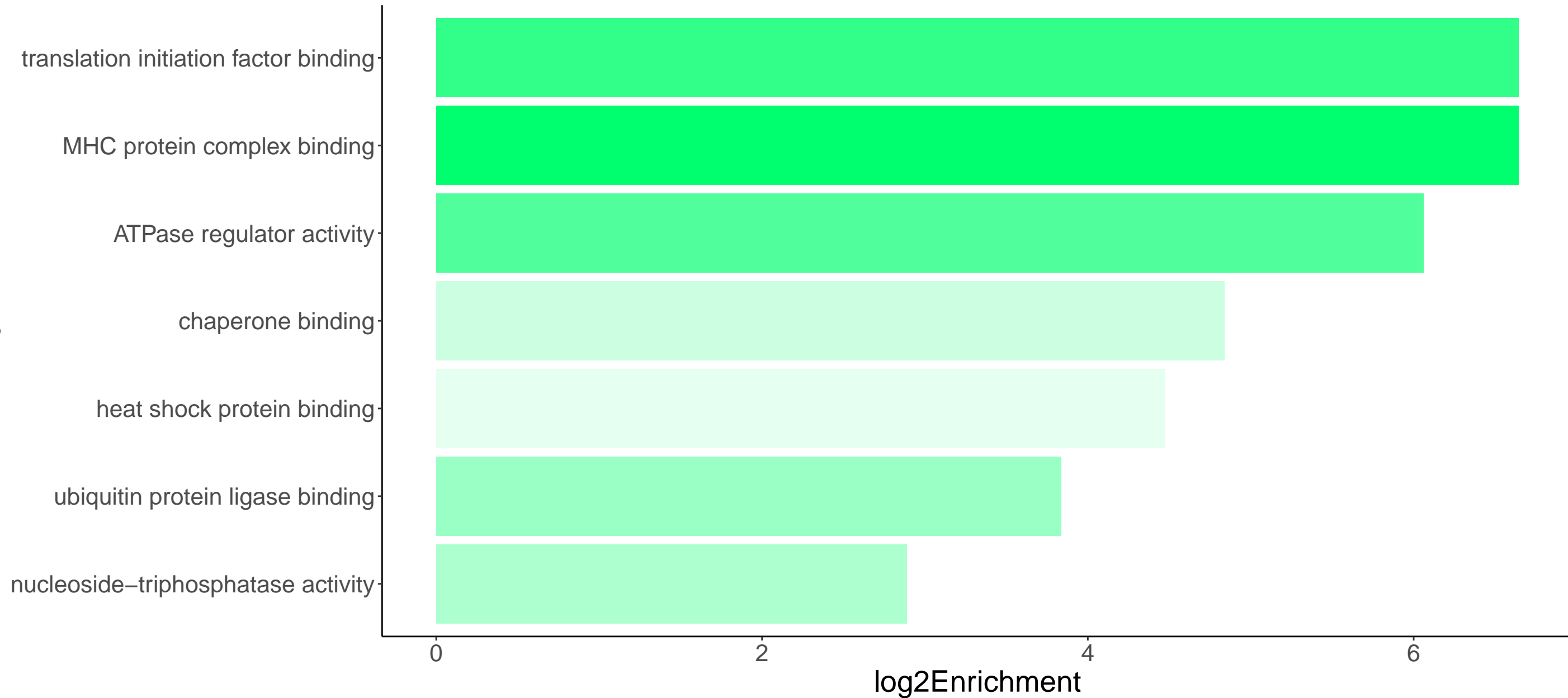
## Re-clustered module 3.18.5 BP enrichment

Term



# Re-clustered module 3.18.5 MF enrichment

Term





# Re-clustered module 3.18.6 BP enrichment

Term

cellular ketone metabolic process

MAPK cascade

0

1

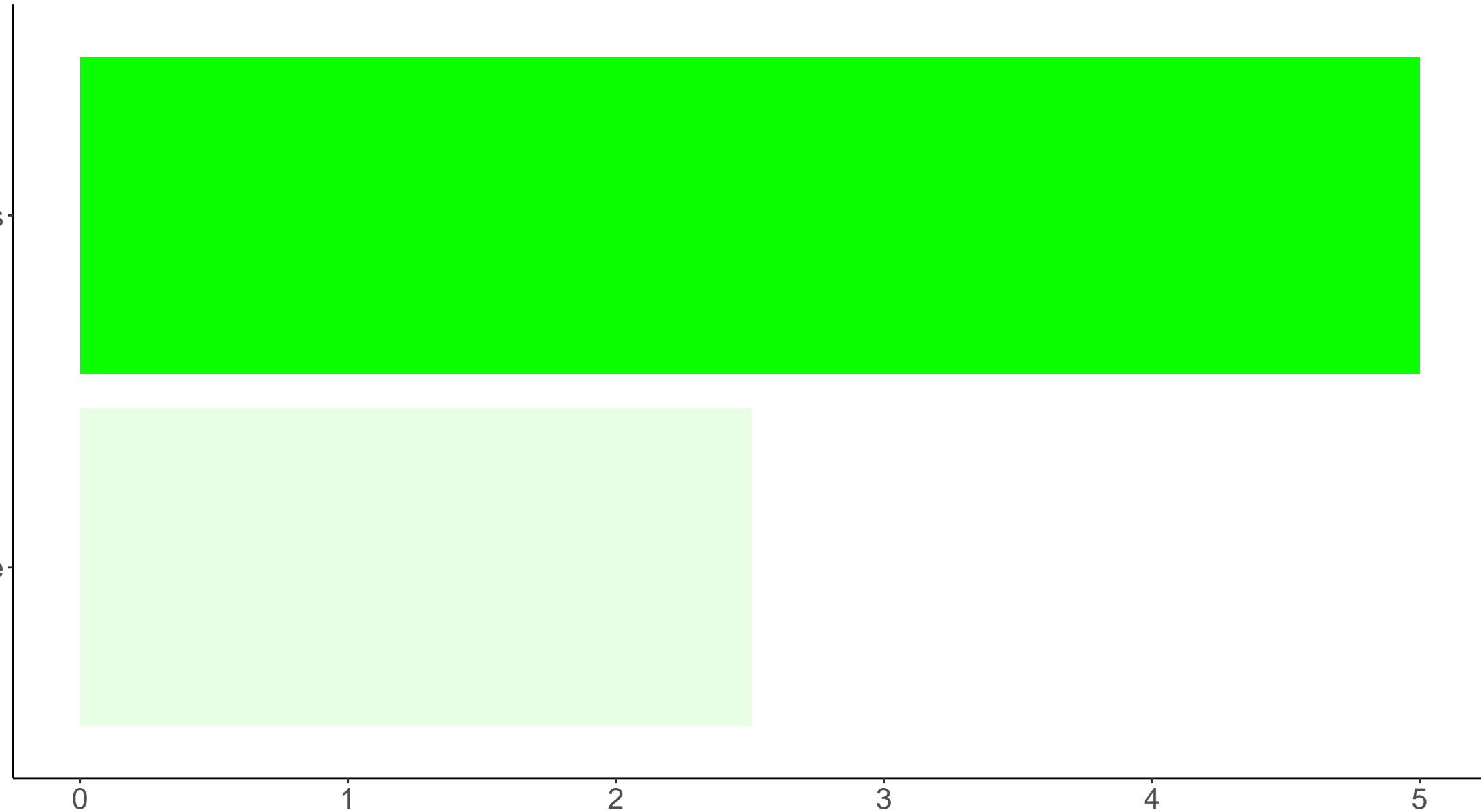
2

3

4

5

log2Enrichment



# Re-clustered module 3.18.6 MF enrichment

Term

S-adenosylmethionine-dependent methyltransferase activity

0

1

2

3

log2Enrichment



# Re-clustered module 3.18.7 BP enrichment

Term

mRNA export from nucleus

0

1

2

3

4

5

log2Enrichment



# Re-clustered module 3.18.7 MF enrichment

Term

carboxy-lyase activity

phosphoprotein phosphatase activity

0

2

4

6

log2Enrichment



# Re-clustered module 3.18.9.10 BP enrichment

Term

ribosomal large subunit biogenesis

mitochondrial translational elongation

mitochondrial translational termination

regulation of protein localization to nucleus

regulation of RNA stability

0

2

4

log2Enrichment



# Re-clustered module 3.18.9.10 MF enrichment

Term structural constituent of ribosome

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.18.9.4 BP enrichment

Term

ribosome biogenesis

RNA phosphodiester bond hydrolysis, endonucleolytic

negative regulation of proteasomal protein catabolic process

regulation of multi-organism process

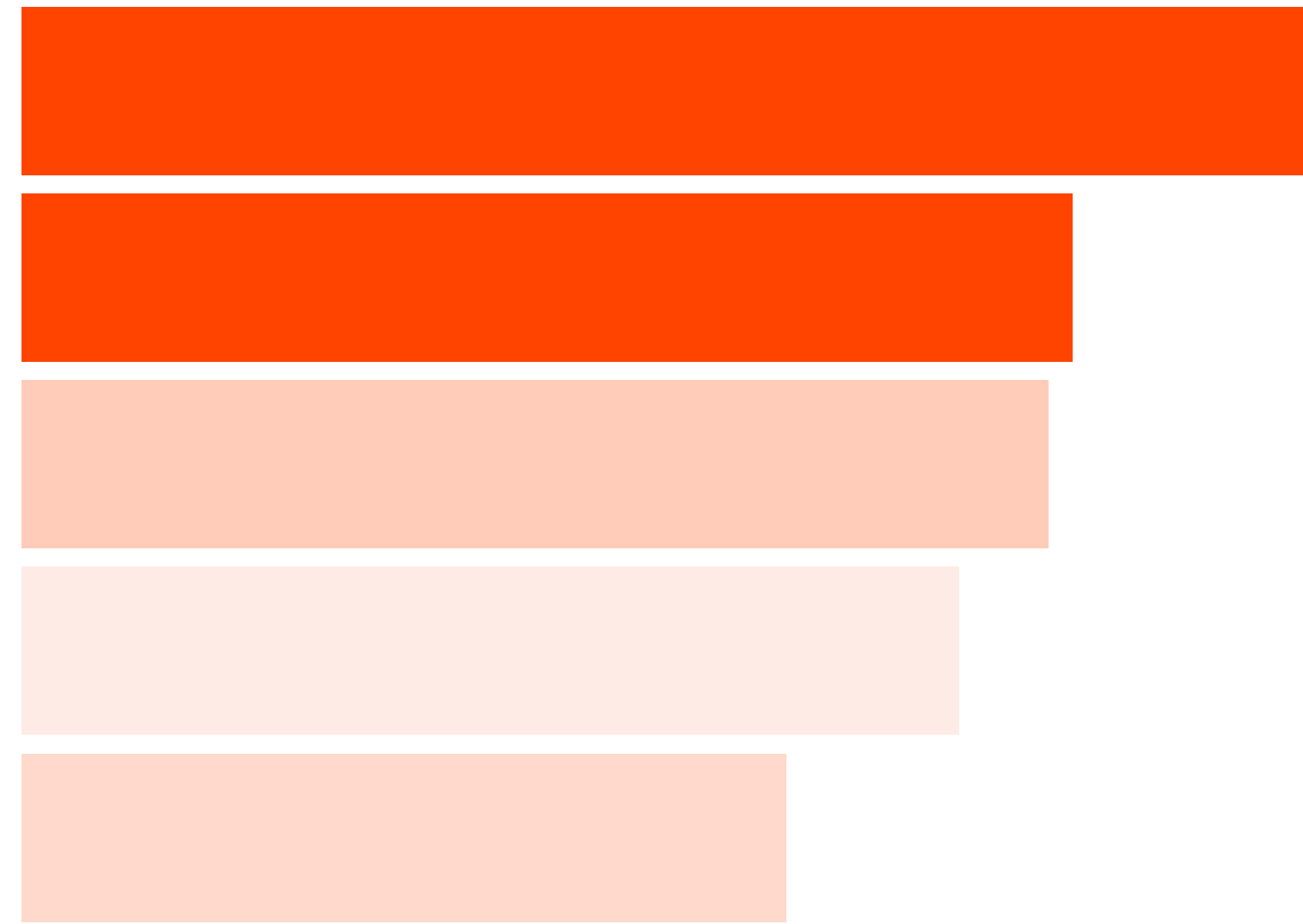
defense response to virus

0

2

4

log2Enrichment



# Re-clustered module 3.18.9.4 MF enrichment

Term

RNA helicase activity

0

1

2

3

4

log2Enrichment





# Re-clustered module 3.18.9.5 BP enrichment

Term

mitochondrial gene expression

ribosomal large subunit biogenesis

0

2

4

6

log2Enrichment



Re-clustered module 3.18.9.5 MF enrichment

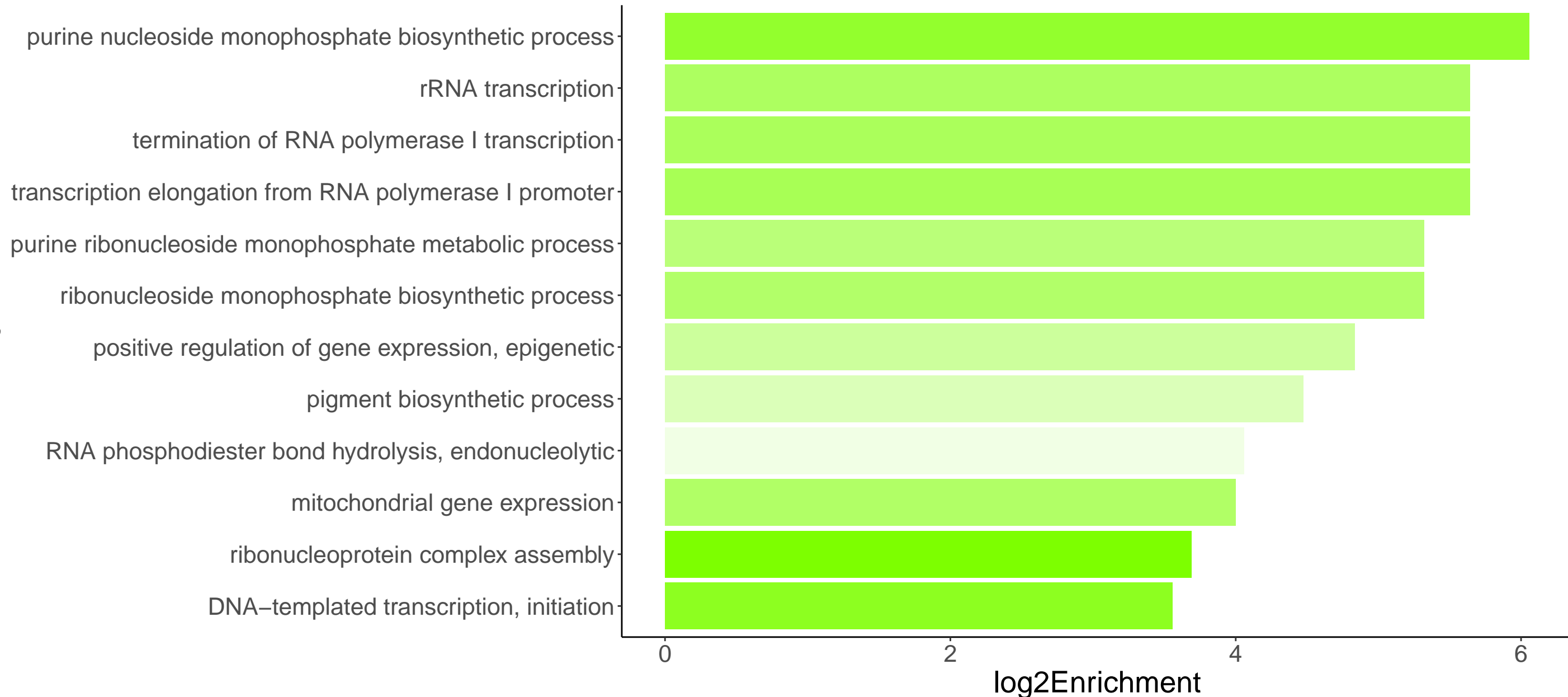
Term

log2Enrichment



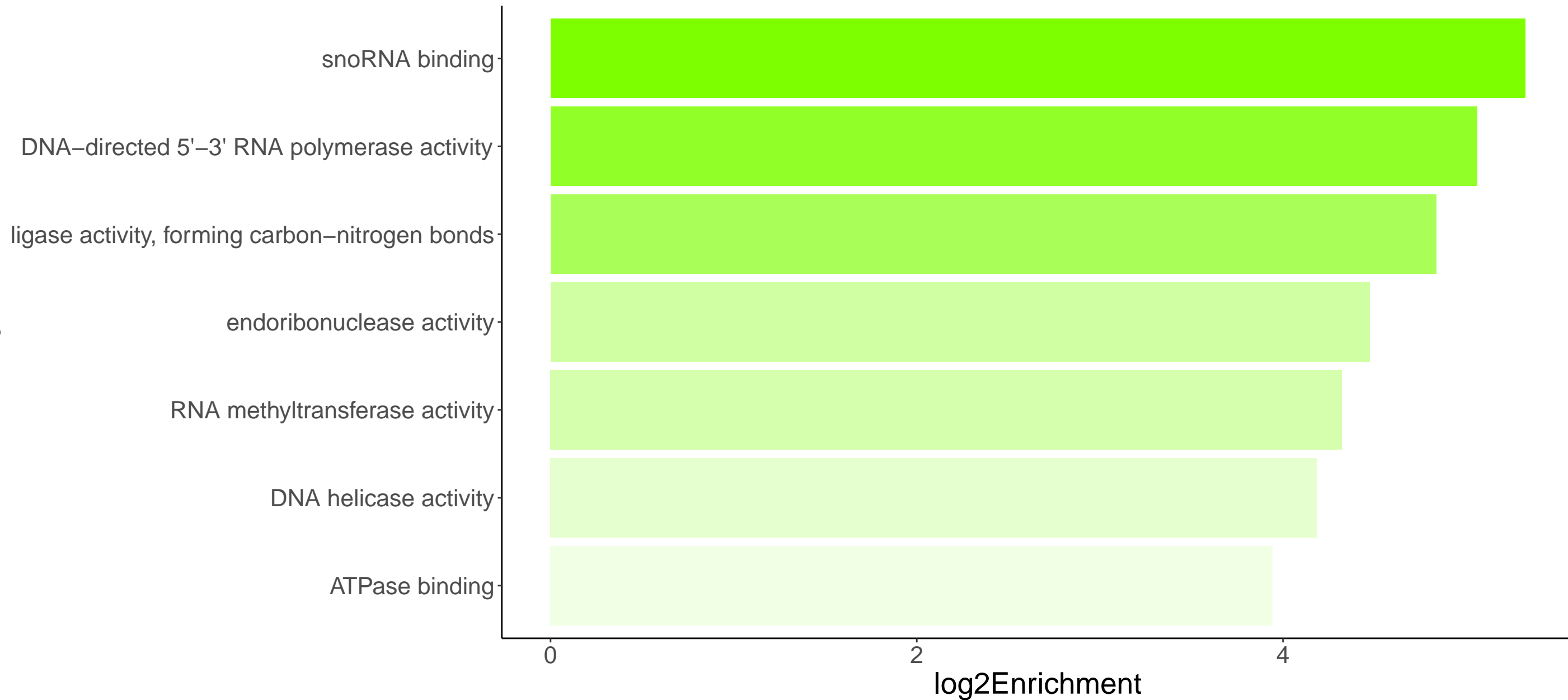
## Re-clustered module 3.18.9.6 BP enrichment

Term



# Re-clustered module 3.18.9.6 MF enrichment

Term



# Re-clustered module 3.18.9.7 BP enrichment

Term

rRNA processing

RNA phosphodiester bond hydrolysis

regulation of protein ubiquitination

0

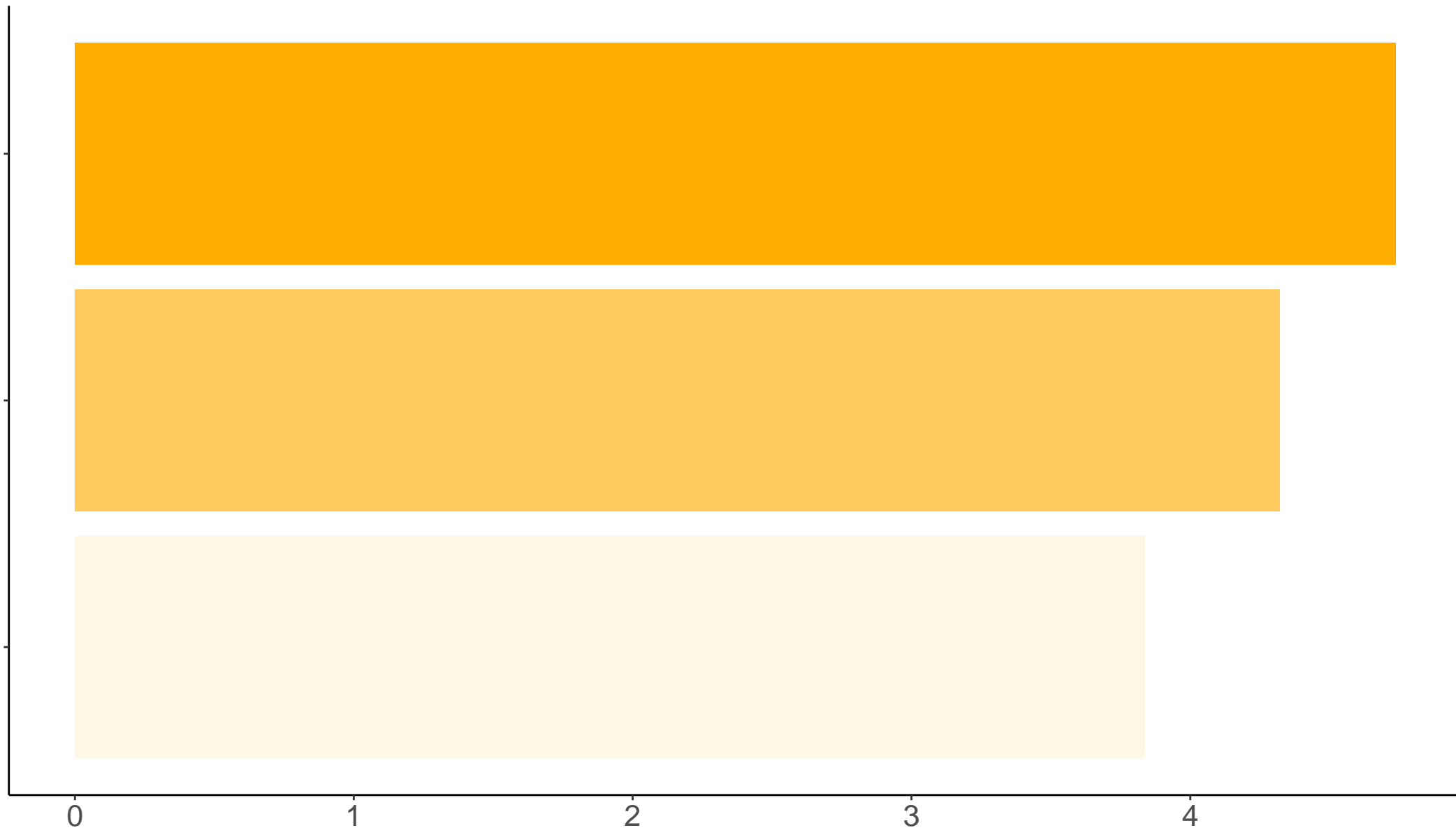
1

2

3

4

log2Enrichment



# Re-clustered module 3.18.9.7 MF enrichment

Term

S-adenosylmethionine-dependent methyltransferase activity

N-methyltransferase activity

ribosome binding

RNA binding

0

2

4

log2Enrichment



Re-clustered module 3.18.9.8 BP enrichment

Term

log2Enrichment



Re-clustered module 3.18.9.8 MF enrichment

Term

log2Enrichment





# Re-clustered module 3.19 BP enrichment

Term

neural crest cell migration

activation of GTPase activity

cell division

0

1

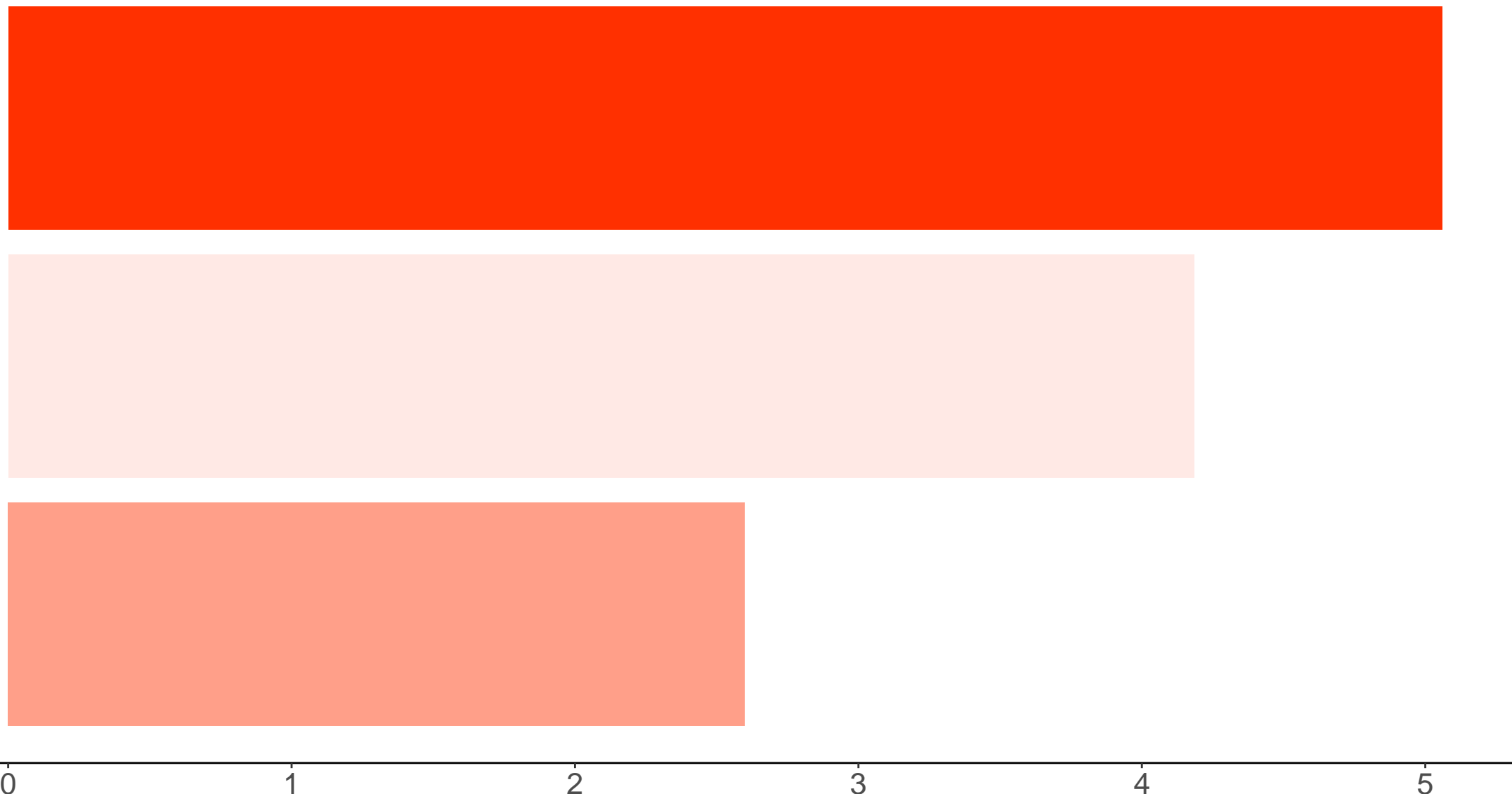
2

3

4

5

log2Enrichment



# Re-clustered module 3.19 MF enrichment

Term

Rac GTPase binding

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.22 BP enrichment

Term

regulation of double-strand break repair

nucleic acid phosphodiester bond hydrolysis

transcription by RNA polymerase II

0

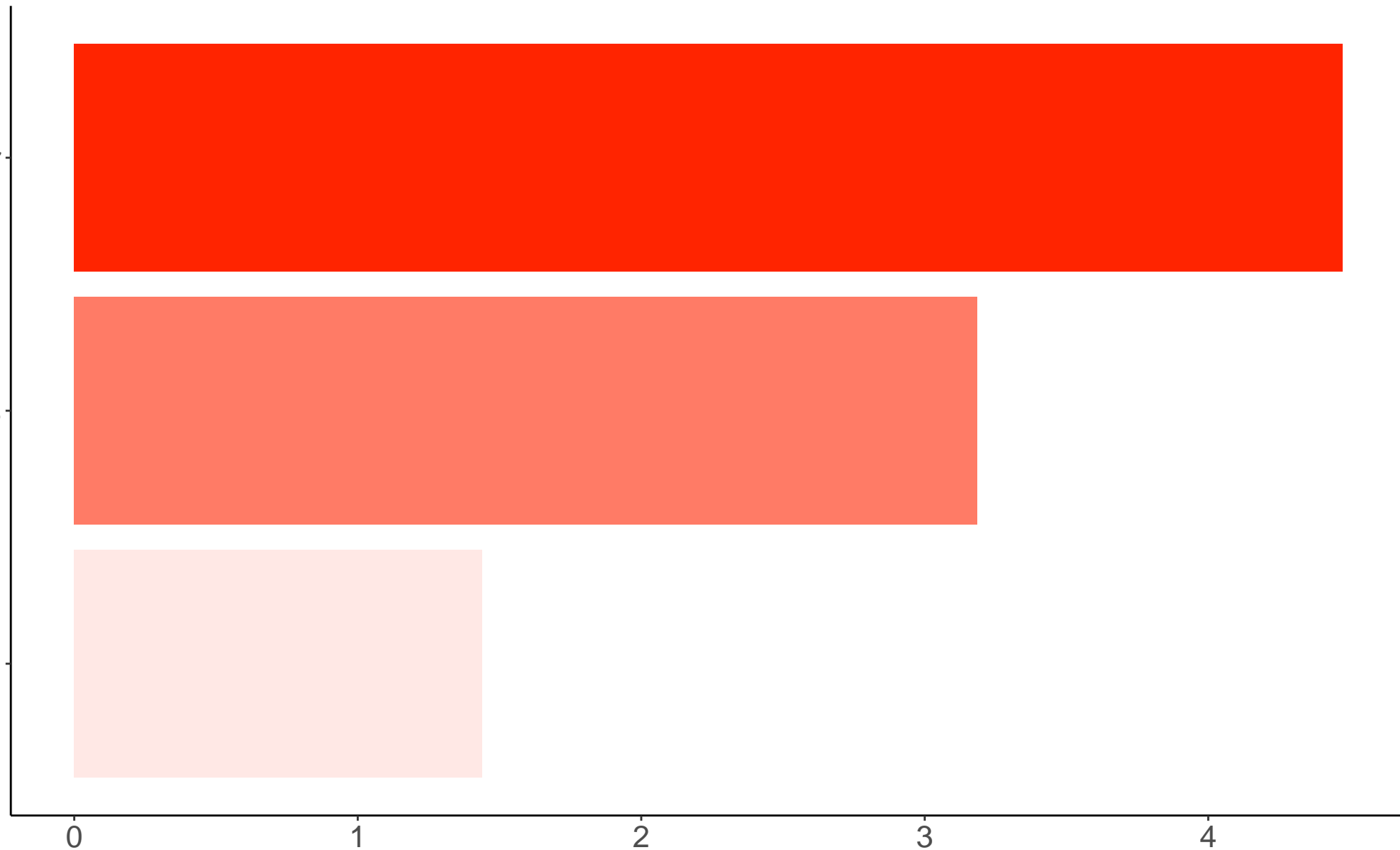
1

2

3

4

log2Enrichment



Re-clustered module 3.22 MF enrichment

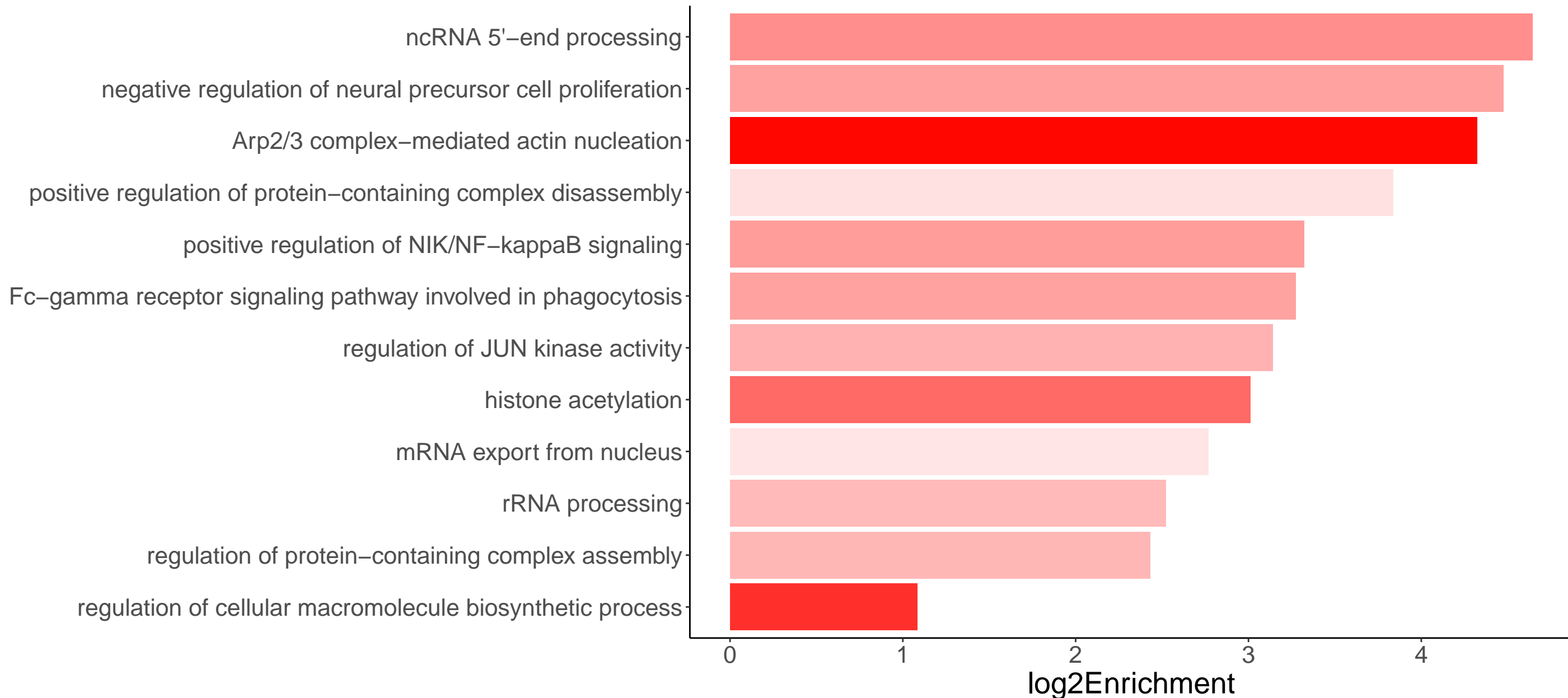
Term

log2Enrichment



# Re-clustered module 3.23 BP enrichment

Term



# Re-clustered module 3.23 MF enrichment

Term

RNA polymerase II general transcription initiation factor activity

actin binding

transcription coregulator activity

protein-containing complex binding

0

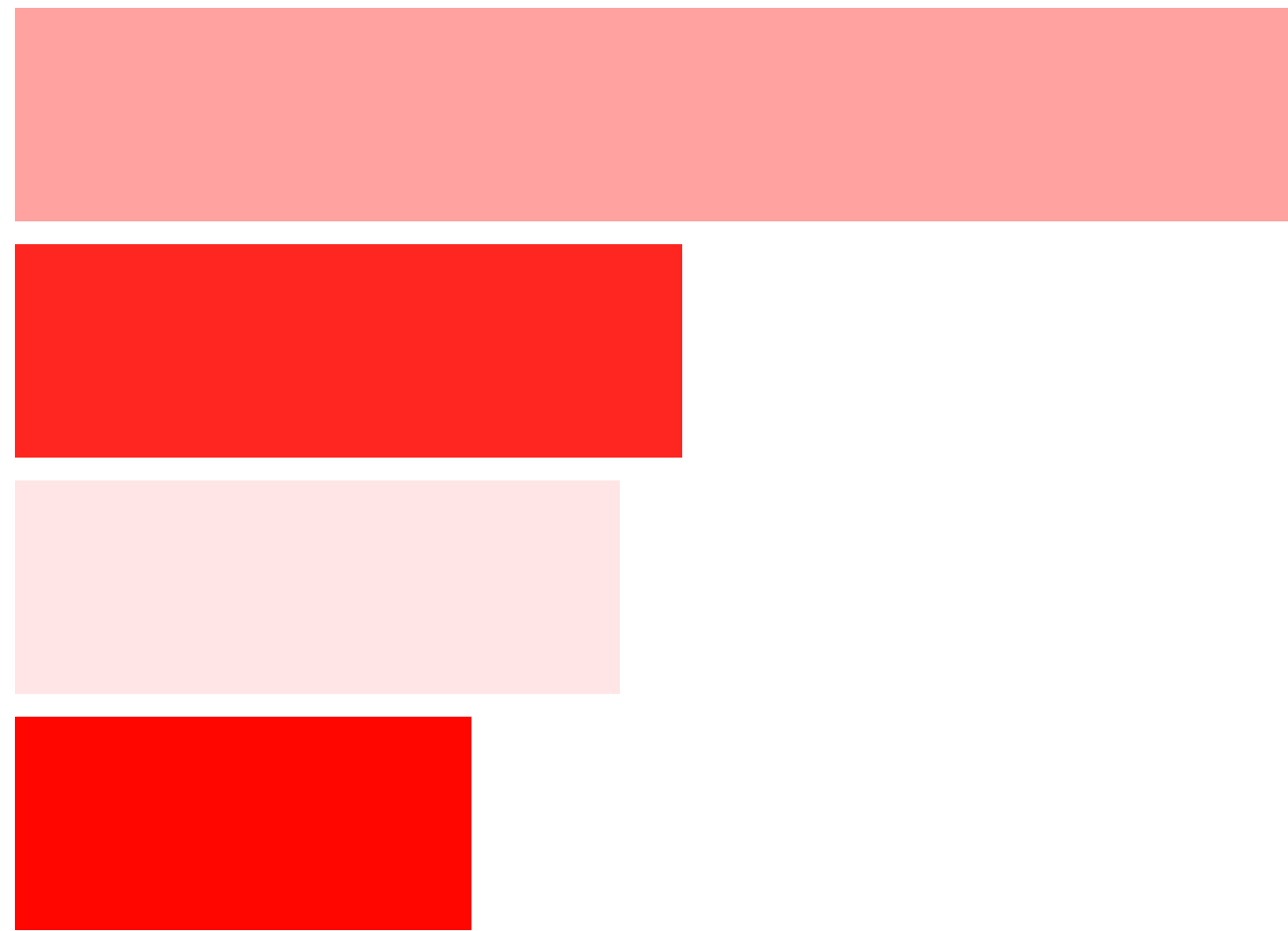
1

2

3

4

log2Enrichment



# Re-clustered module 3.26 BP enrichment

Term

cellular metabolic compound salvage

purine ribonucleoside metabolic process

response to starvation

protein import

0

2

4

6

log2Enrichment



# Re-clustered module 3.26 MF enrichment

Term

heme binding

0

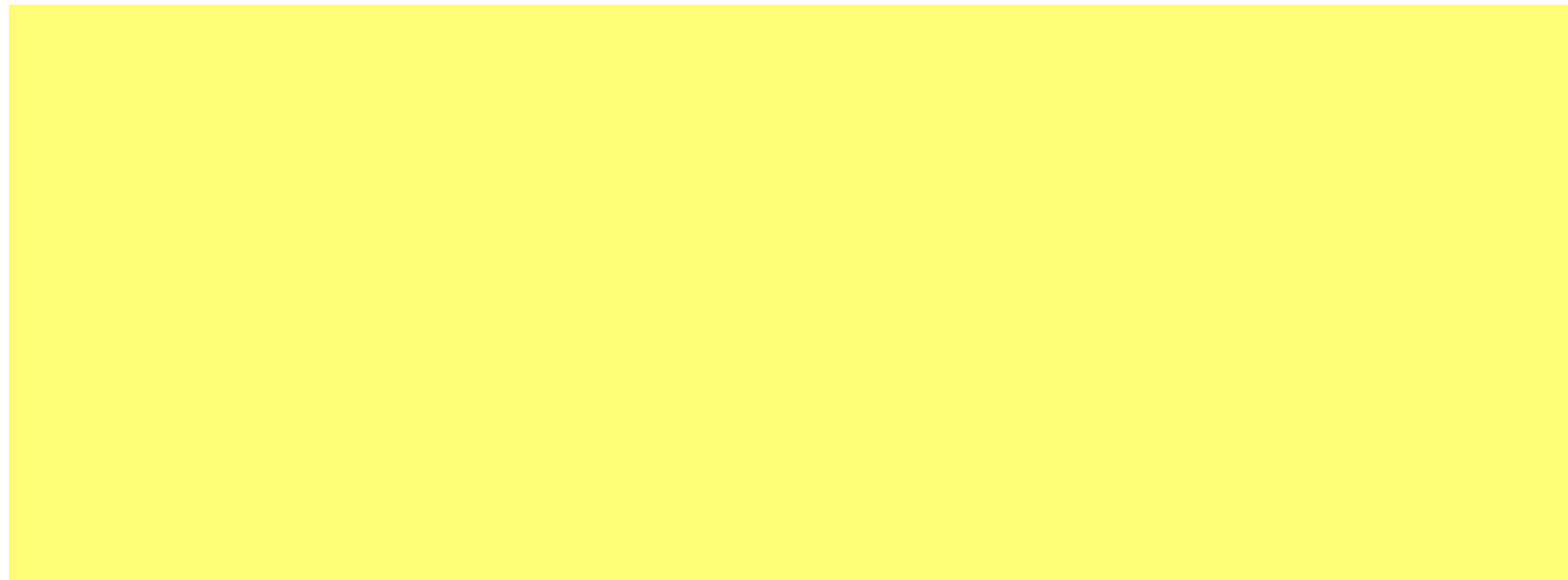
1

2

3

4

log2Enrichment





# Re-clustered module 3.28.15 BP enrichment

Term

tRNA aminoacylation for protein translation

mitochondrial RNA metabolic process

respiratory electron transport chain

mitochondrial gene expression

fatty acid metabolic process

0

2

4

6

log2Enrichment



# Re-clustered module 3.28.15 MF enrichment

Term

NADH dehydrogenase (ubiquinone) activity

catalytic activity, acting on a tRNA

protein homodimerization activity

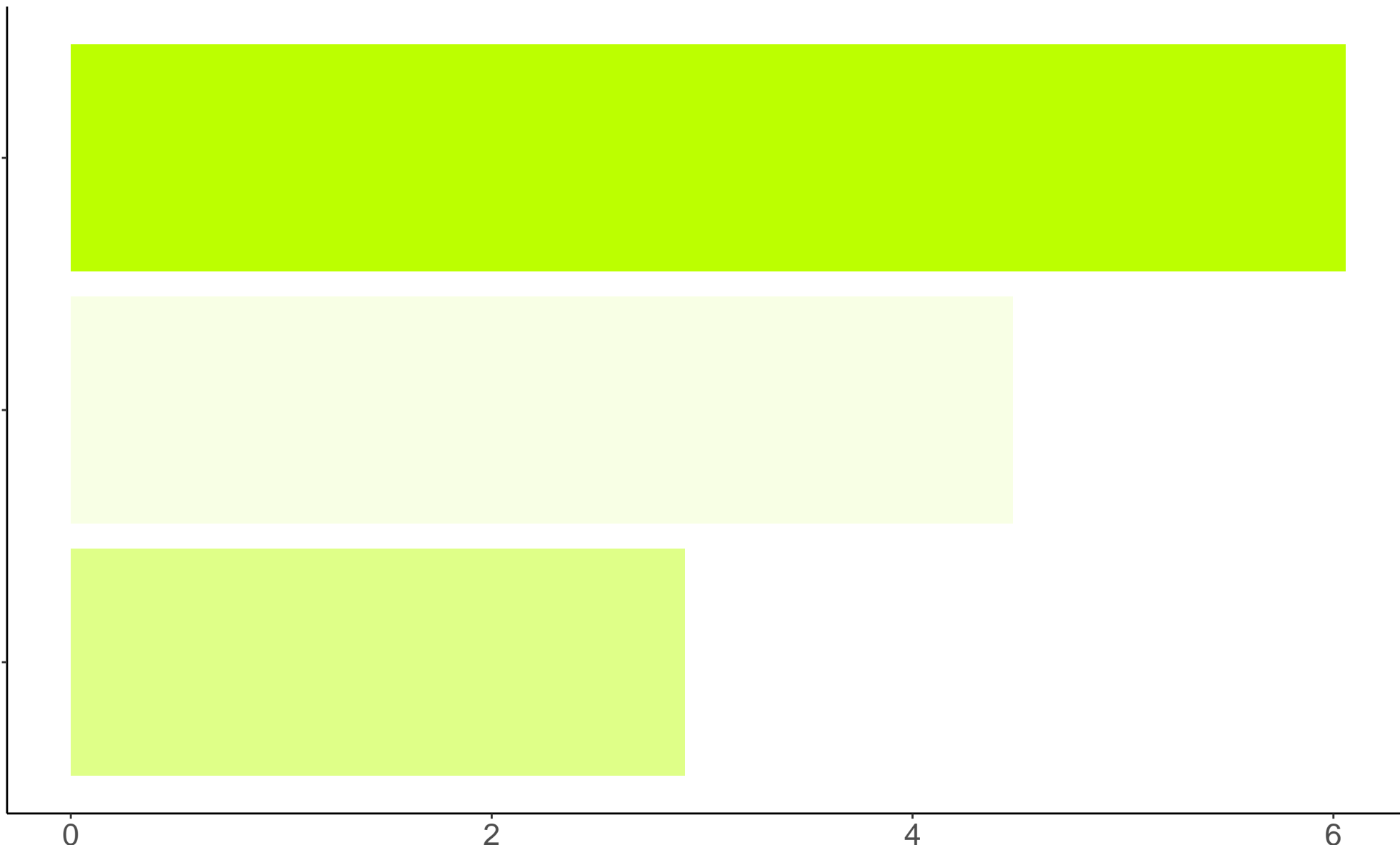
0

2

4

6

log2Enrichment



# Re-clustered module 3.28.19 BP enrichment

Term

cytoplasmic translation

SRP-dependent cotranslational protein targeting to membrane

nuclear-transcribed mRNA catabolic process, nonsense-mediated decay

translational initiation

0 1 2 3 4

log2Enrichment



# Re-clustered module 3.28.19 MF enrichment

Term

ribosome binding

0

1

2

3

4

5

log2Enrichment



# Re-clustered module 3.28.5 BP enrichment

Term

tRNA methylation

mitochondrial RNA metabolic process

protein O-linked glycosylation

0

1

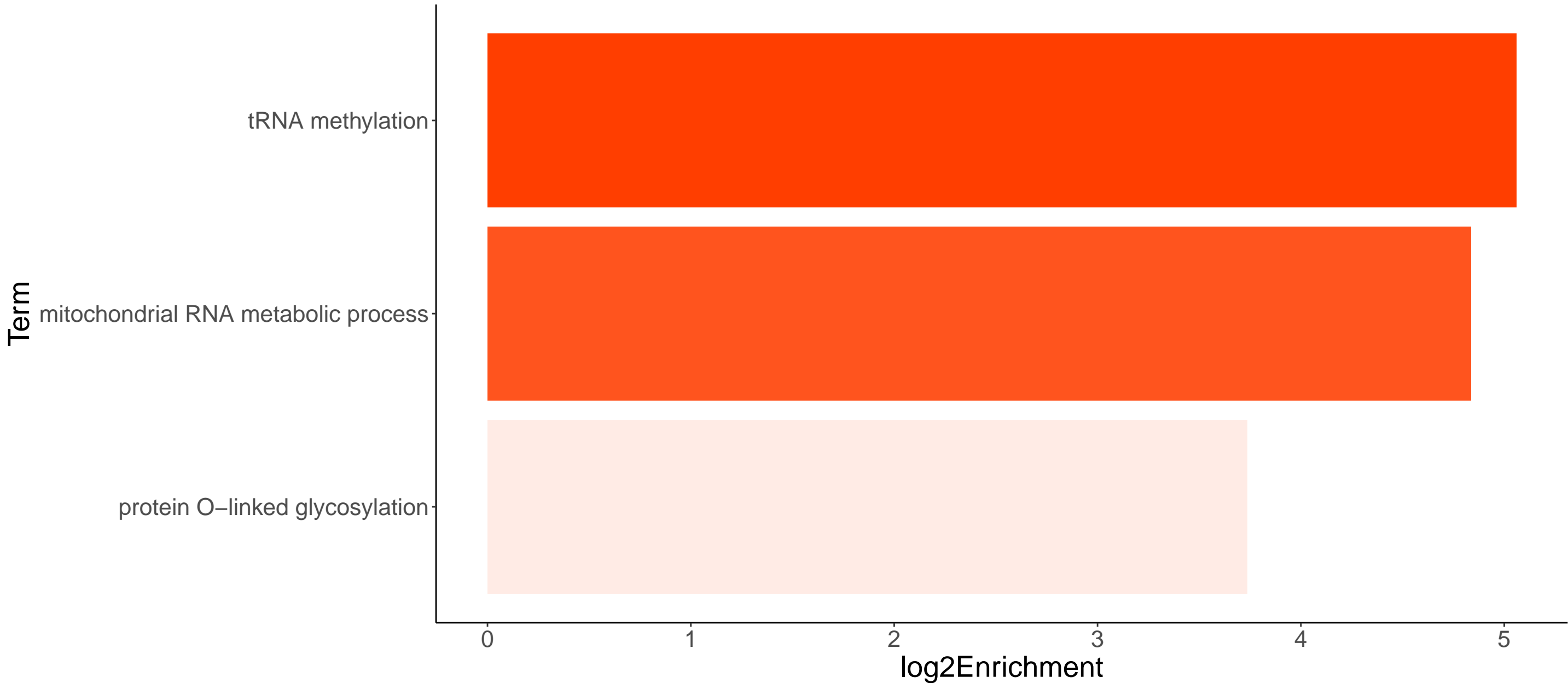
2

3

4

5

log2Enrichment



# Re-clustered module 3.28.5 MF enrichment

Term

tRNA methyltransferase activity

0

2

4

log2Enrichment



# Re-clustered module 3.28.6 BP enrichment

Term

mitochondrial translational termination

mitochondrial translational elongation

0

2

4

log2Enrichment



# Re-clustered module 3.28.6 MF enrichment

Term

ubiquitin-like protein conjugating enzyme activity

structural constituent of ribosome

0

2

4

6

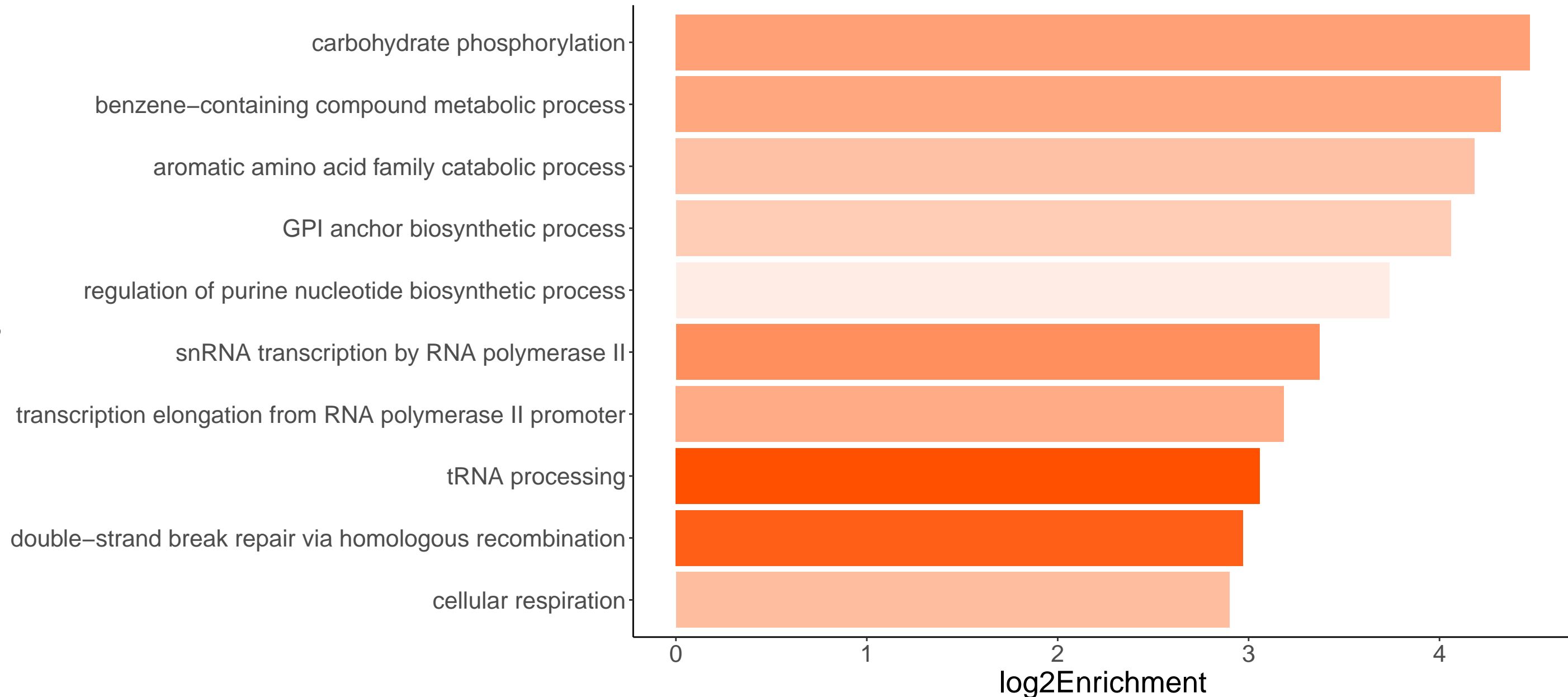
log2Enrichment





## Re-clustered module 3.28.7 BP enrichment

Term



# Re-clustered module 3.28.7 MF enrichment

Term

RNA polymerase II general transcription initiation factor activity

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

catalytic activity, acting on a tRNA

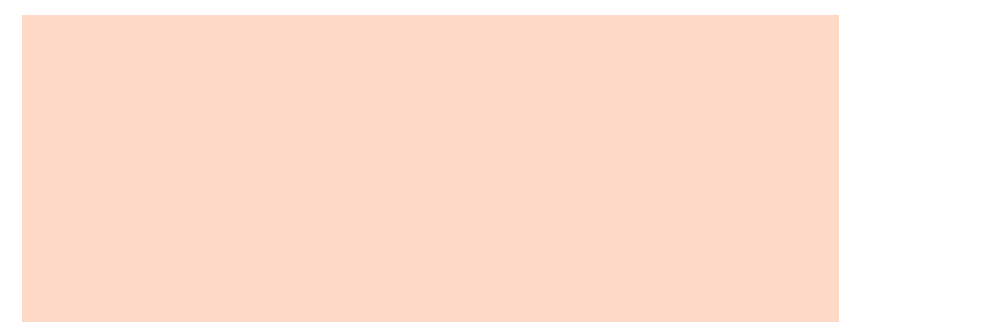
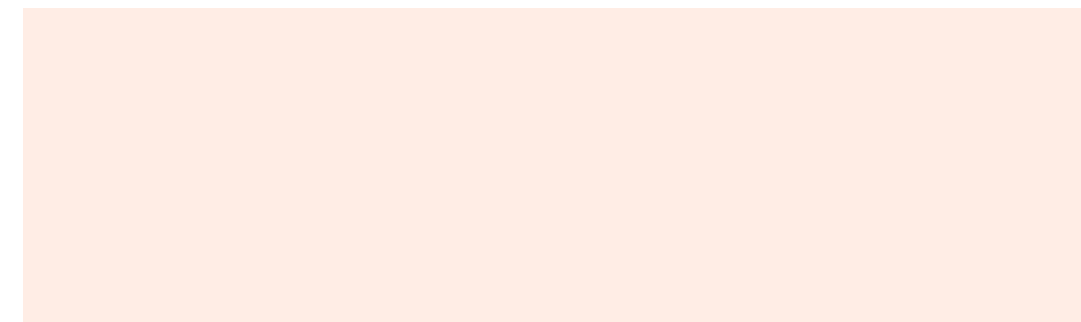
0

1

2

3

log2Enrichment



# Re-clustered module 3.28.9 BP enrichment

Term negative regulation of kinase activity

0

1

2

3

4

log2Enrichment



Re-clustered module 3.28.9 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.29.11 BP enrichment

Term

cytochrome complex assembly

inner mitochondrial membrane organization

rRNA modification

cellular respiration

0

2

4

6

log2Enrichment



# Re-clustered module 3.29.11 MF enrichment

Term

NADH dehydrogenase (ubiquinone) activity

rRNA binding

catalytic activity, acting on a tRNA

0

1

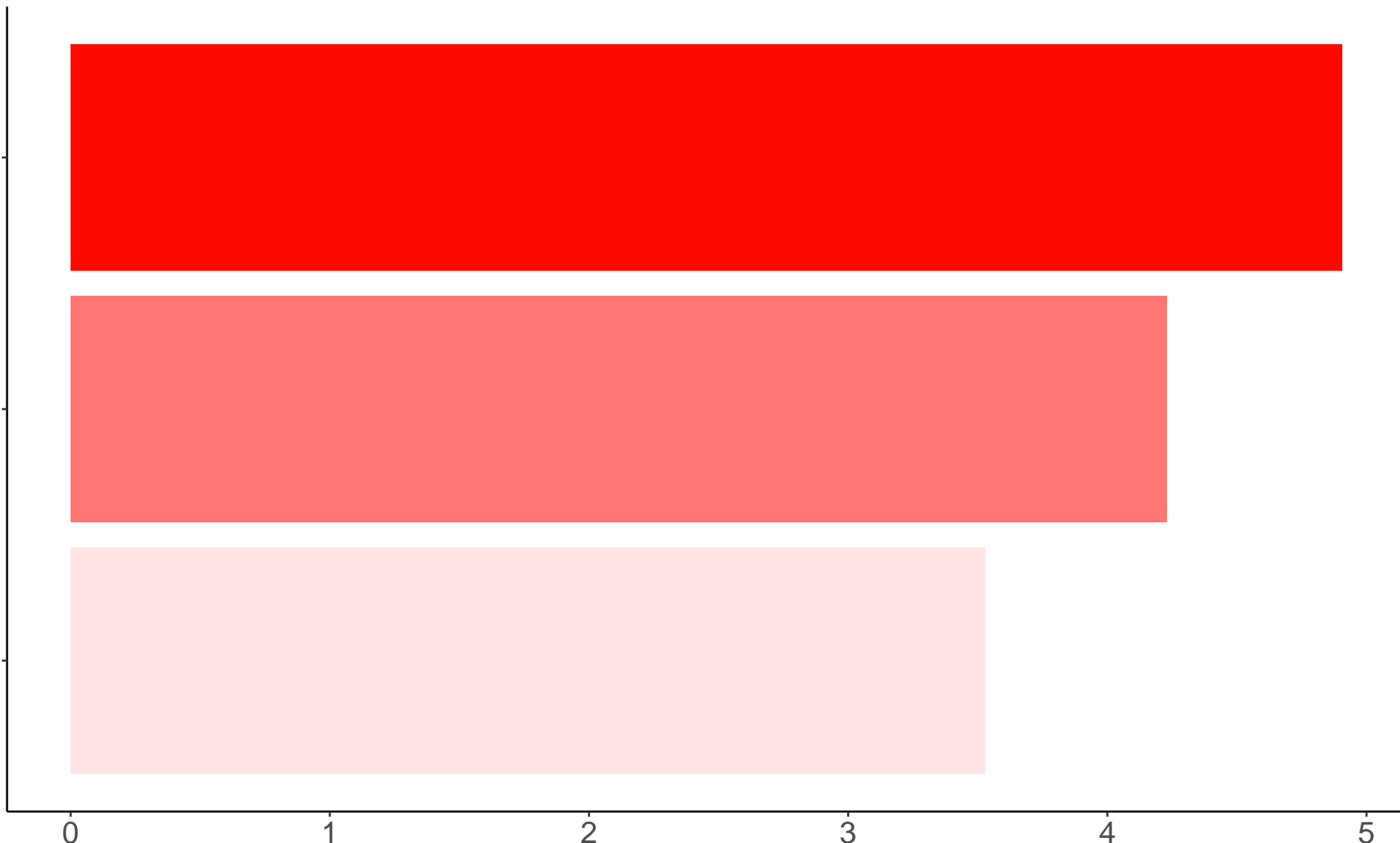
2

3

4

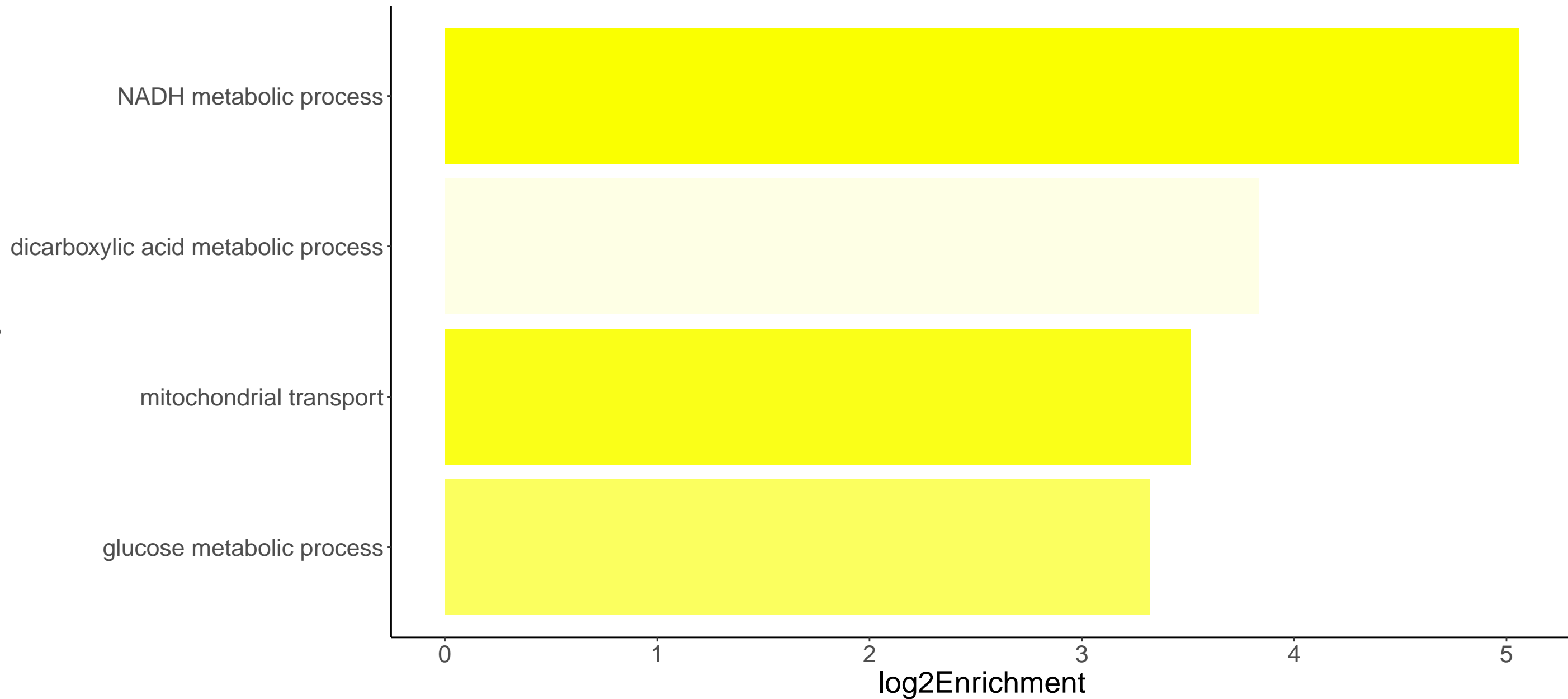
5

log2Enrichment



# Re-clustered module 3.29.2 BP enrichment

Term



# Re-clustered module 3.29.2 MF enrichment

Term

4 iron, 4 sulfur cluster binding

NAD binding

electron transfer activity

metalloendopeptidase activity

0

1

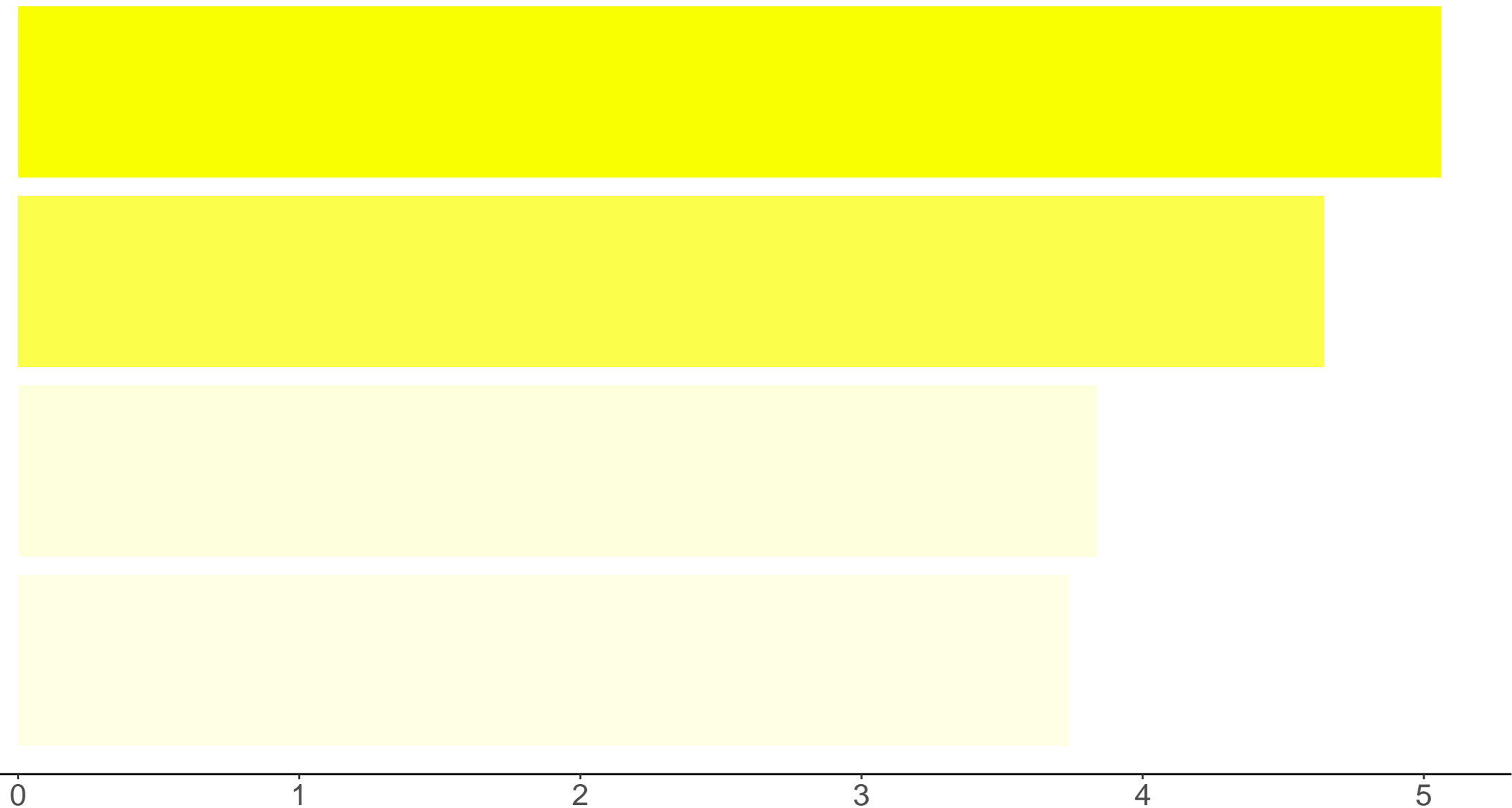
2

3

4

5

log2Enrichment





Re-clustered module 3.29.3 BP enrichment

Term

log2Enrichment



Re-clustered module 3.29.3 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.29.4 BP enrichment

Term

endosome to lysosome transport

mitochondrial translational elongation

0

1

2

3

4

5

log2Enrichment



Re-clustered module 3.29.4 MF enrichment

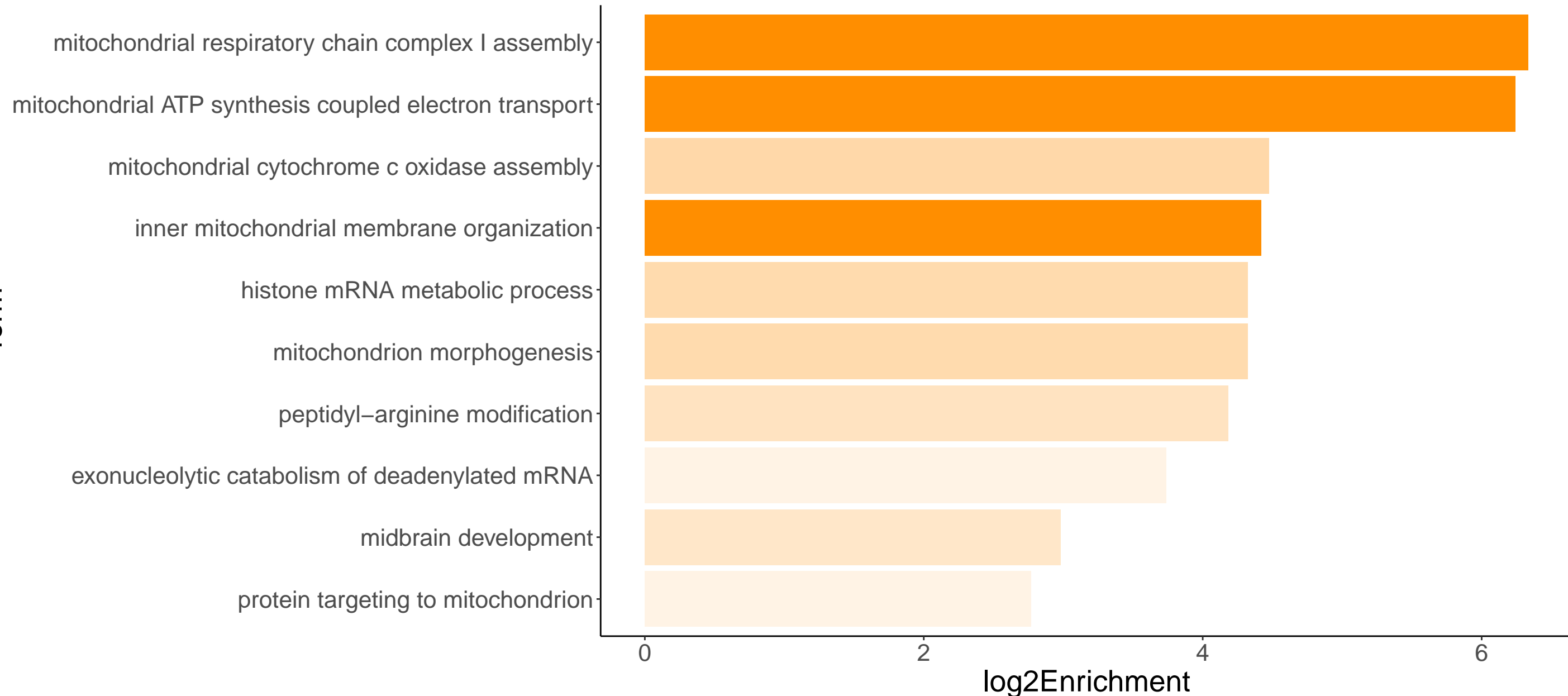
Term

log2Enrichment



# Re-clustered module 3.29.7 BP enrichment

Term



# Re-clustered module 3.29.7 MF enrichment

Term

NADH dehydrogenase (ubiquinone) activity

iron-sulfur cluster binding

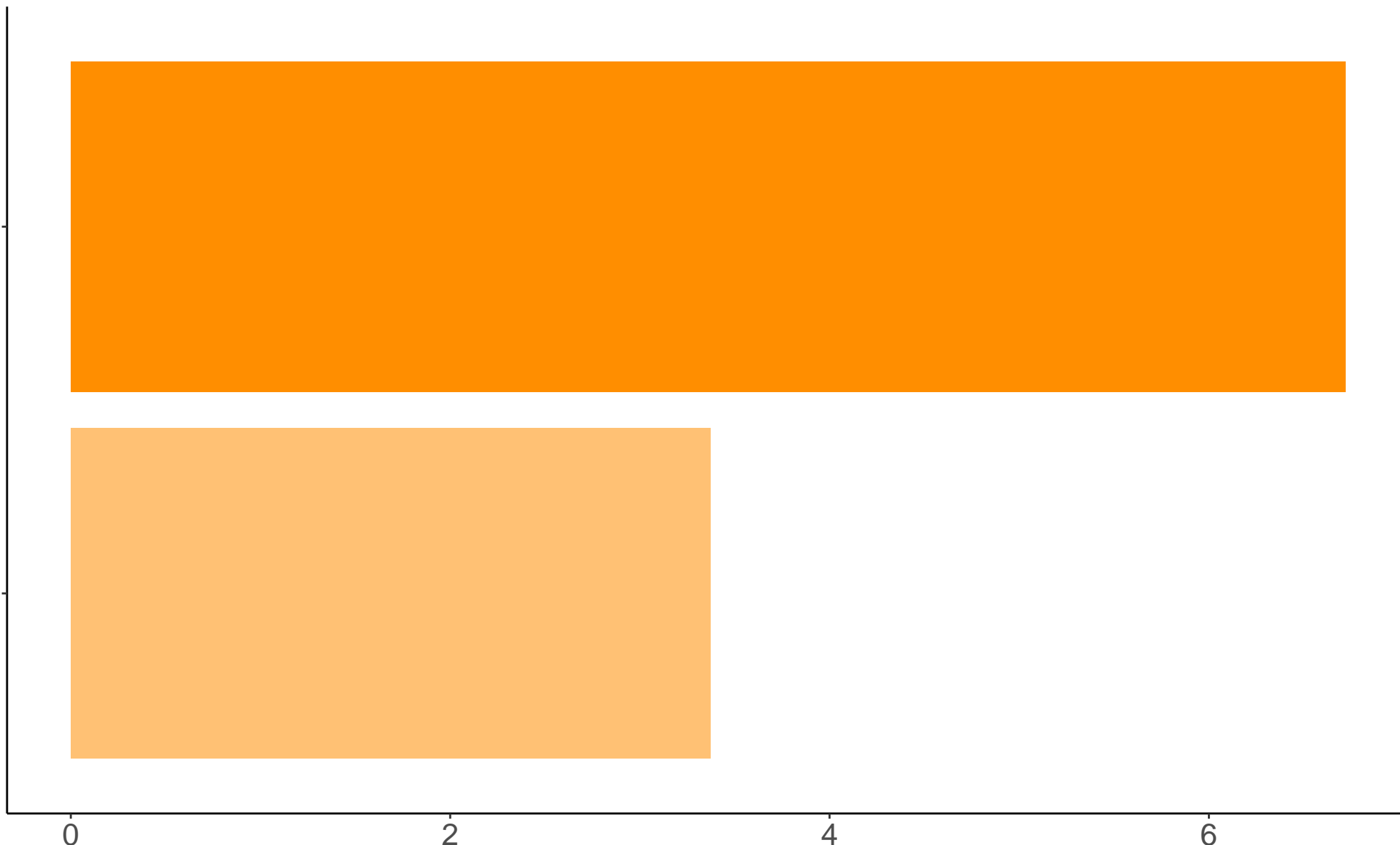
0

2

4

6

log2Enrichment



Re-clustered module 3.3 BP enrichment

Term

log2Enrichment



Re-clustered module 3.3 MF enrichment

Term

log2Enrichment





# Re-clustered module 3.317 BP enrichment

Term

cholesterol biosynthetic process

regulation of steroid biosynthetic process

cellular response to sterol

lipid storage

cholesterol homeostasis

cellular lipid metabolic process

oxidation-reduction process

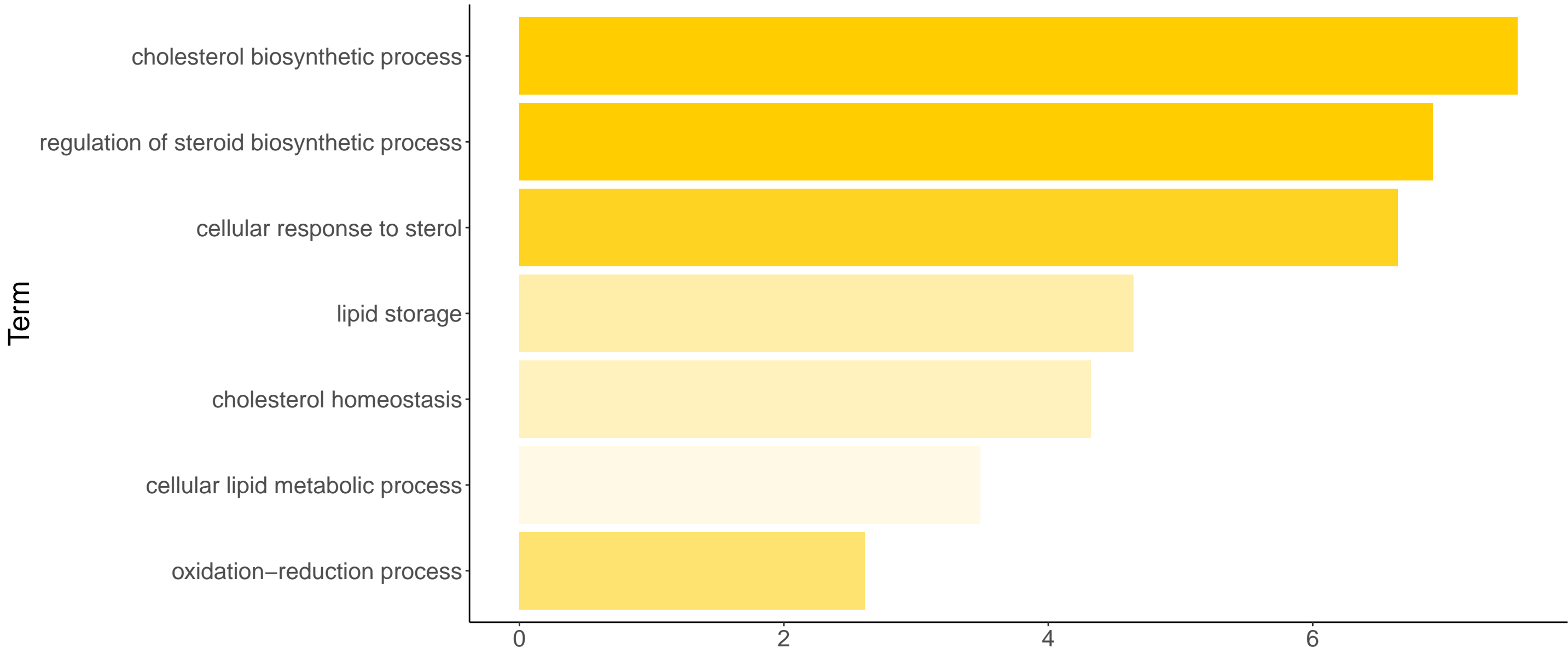
0

2

4

6

log2Enrichment



FAD

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

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

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

sterol

NADP

**Id**

# Re-clustered module 3.33.1 BP enrichment

Term

mammary gland development

0

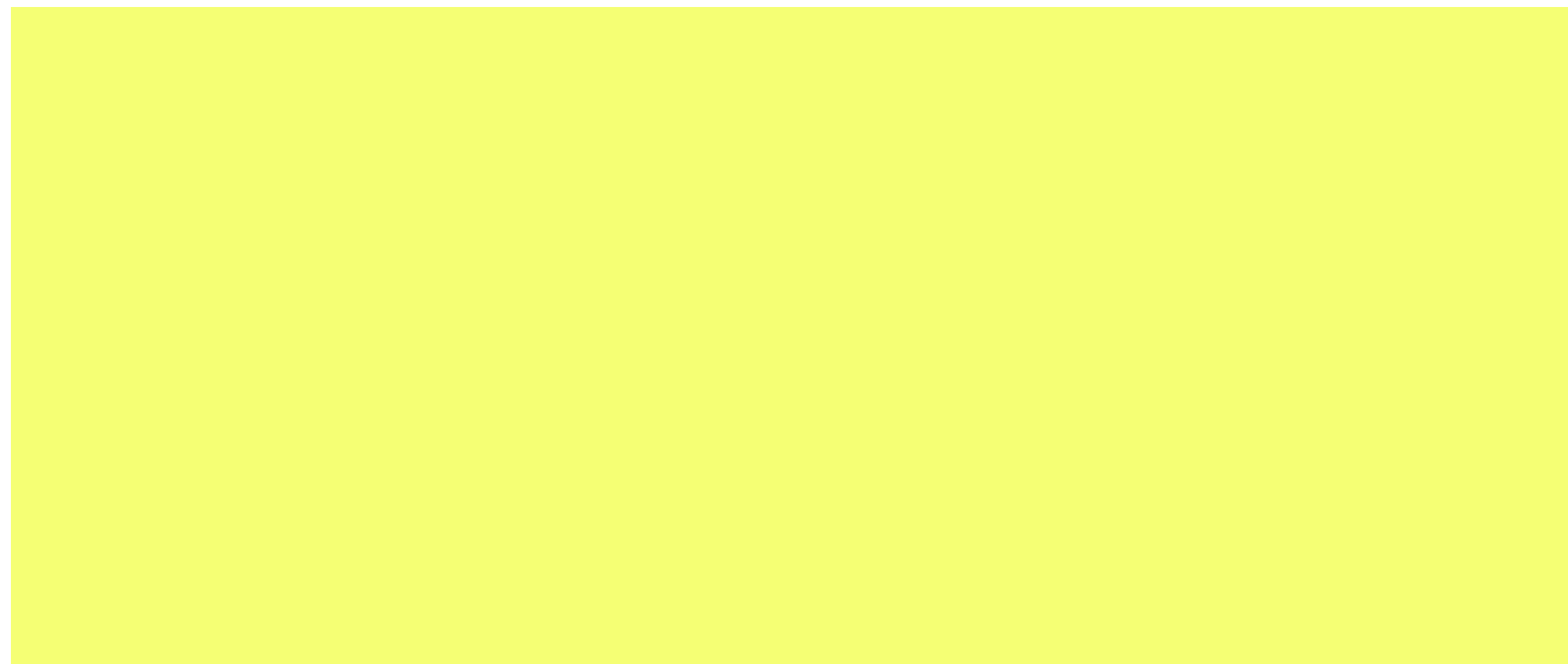
1

2

3

4

log2Enrichment



Re-clustered module 3.33.1 MF enrichment

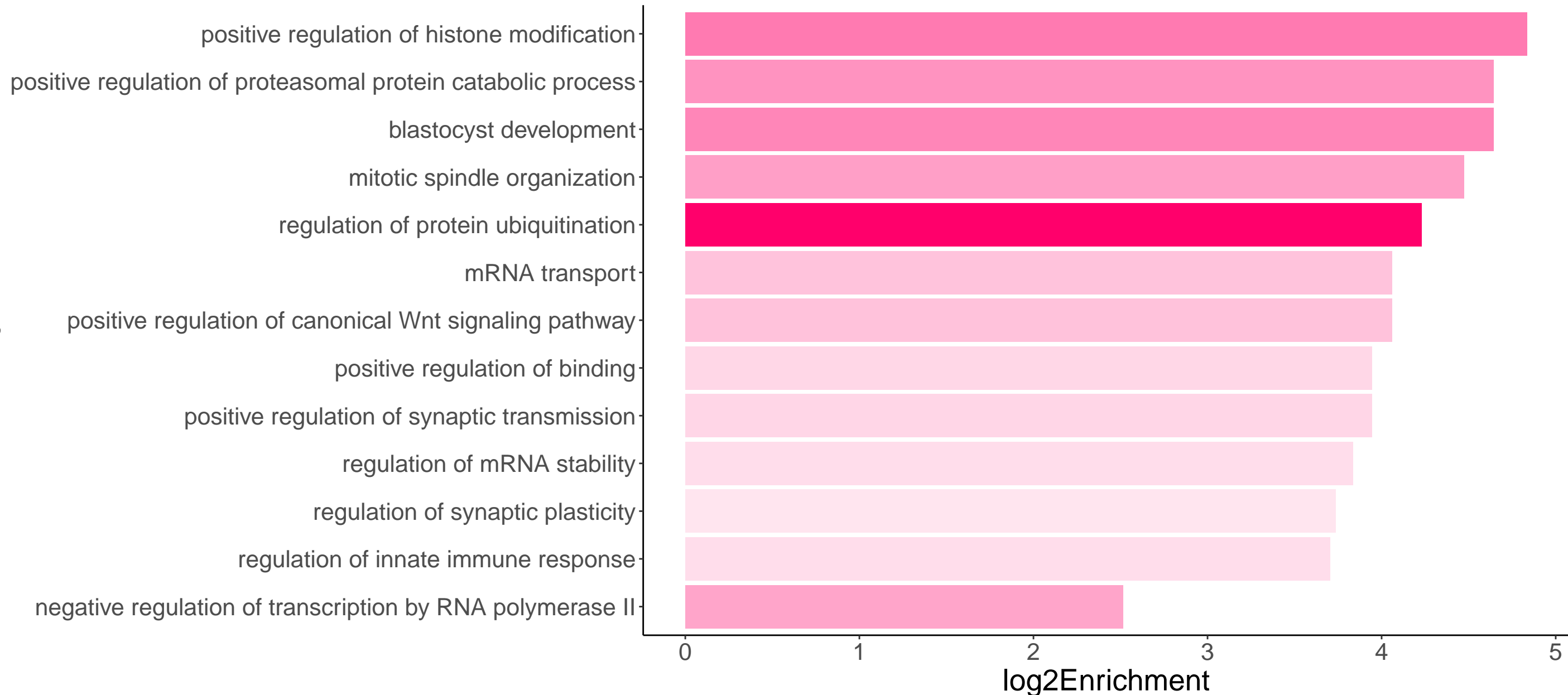
Term

log2Enrichment



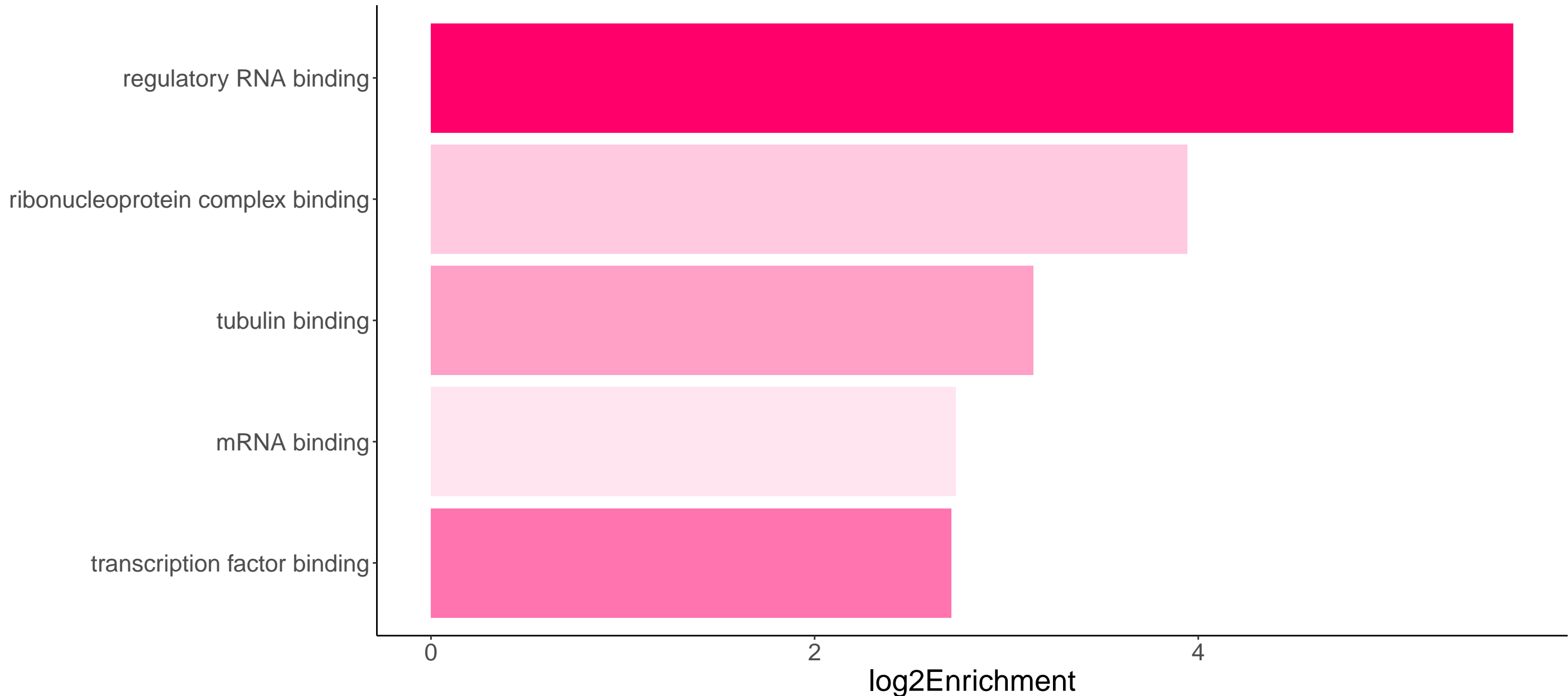
## Re-clustered module 3.33.13 BP enrichment

Term



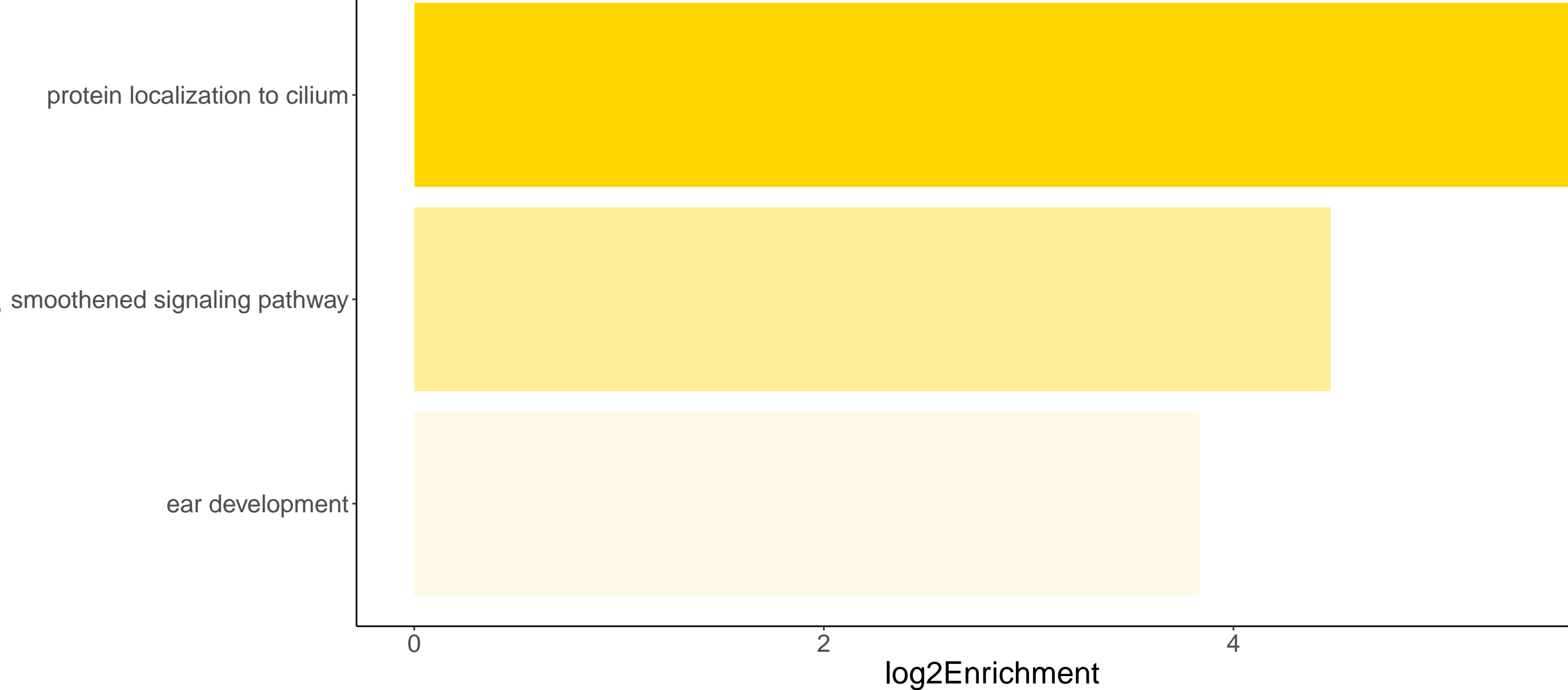
Re-clustered module 3.33.13 MF enrichment

Term



# Re-clustered module 3.33.2 BP enrichment

Term



Re-clustered module 3.33.2 MF enrichment

Term

log2Enrichment





Re-clustered module 3.33.20 BP enrichment

Term

log2Enrichment



Re-clustered module 3.33.20 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.33.4 BP enrichment

Term

negative regulation of translation

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.33.4 MF enrichment

Term

ATPase binding

0

1

2

3

4

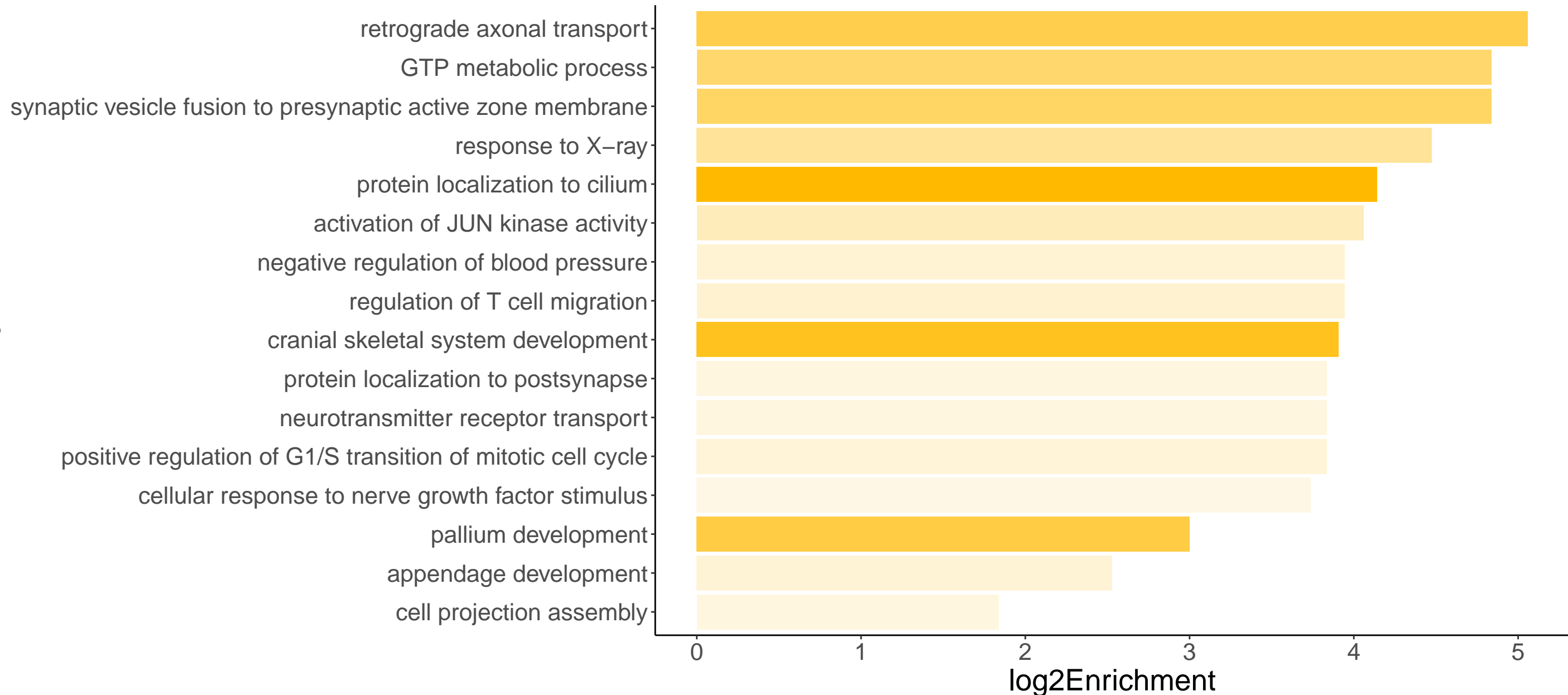
5

log2Enrichment



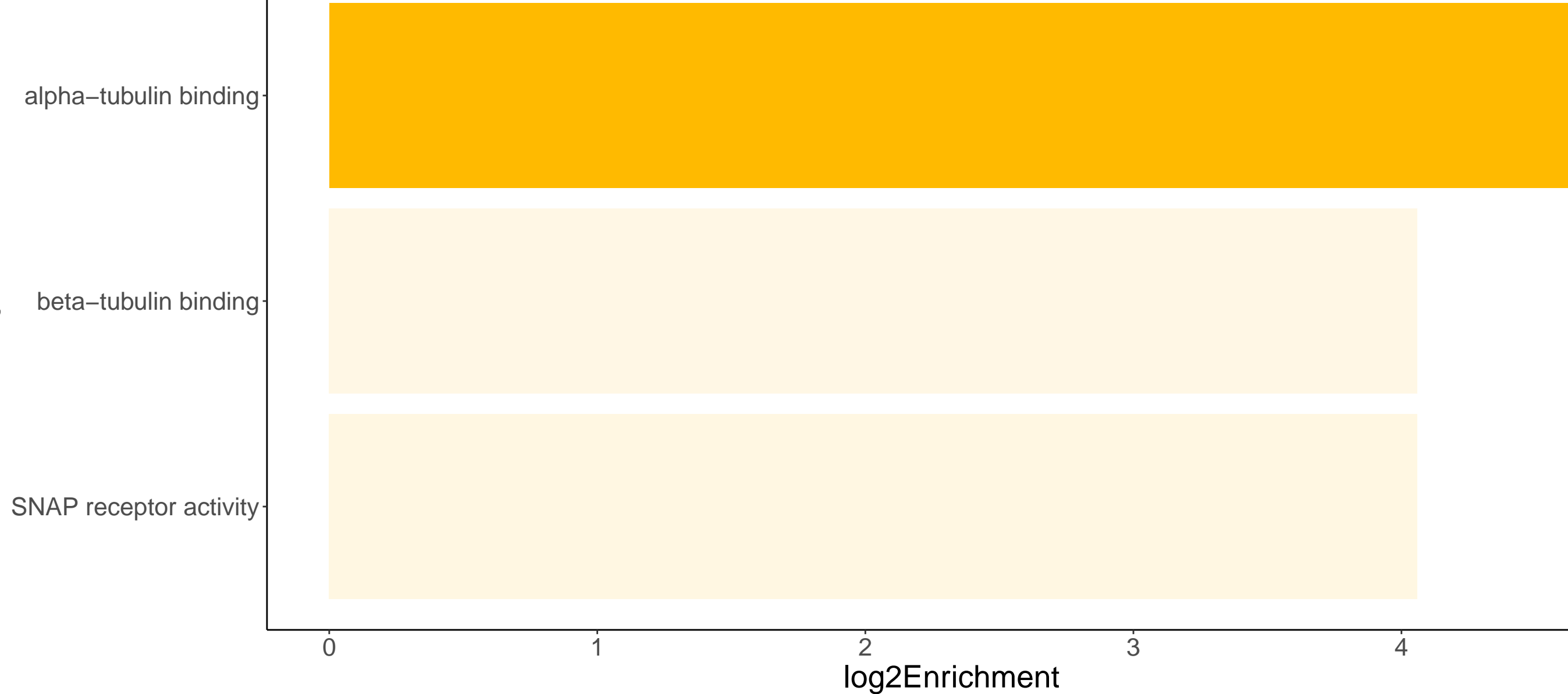
## Re-clustered module 3.33.6 BP enrichment

Term



# Re-clustered module 3.33.6 MF enrichment

Term



# Re-clustered module 3.33.8 BP enrichment

Term

regulation of multicellular organism growth

spindle organization

0

1

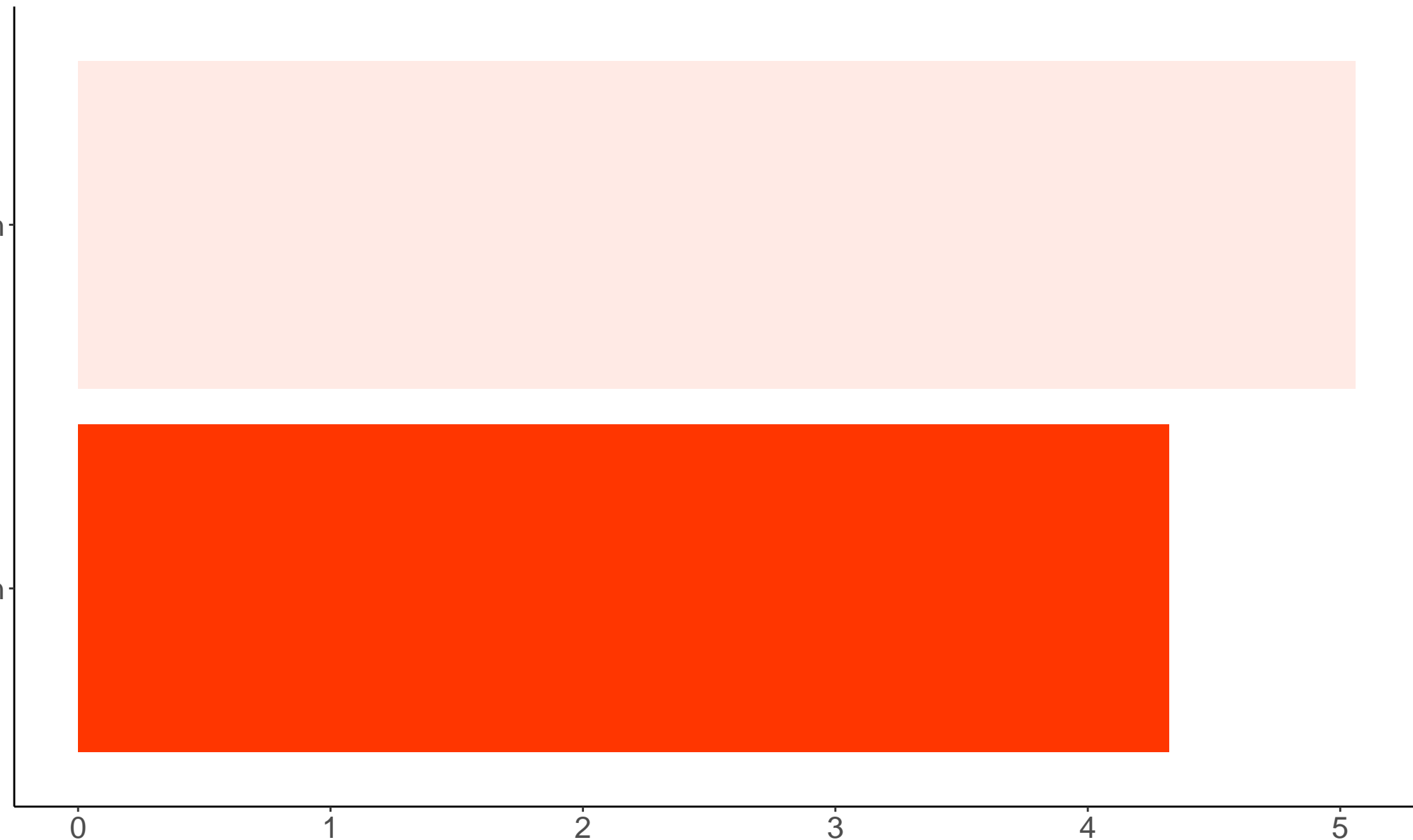
2

3

4

5

log2Enrichment



# Re-clustered module 3.33.8 MF enrichment

Term

motor activity

0

1

2

3

4

5

log2Enrichment

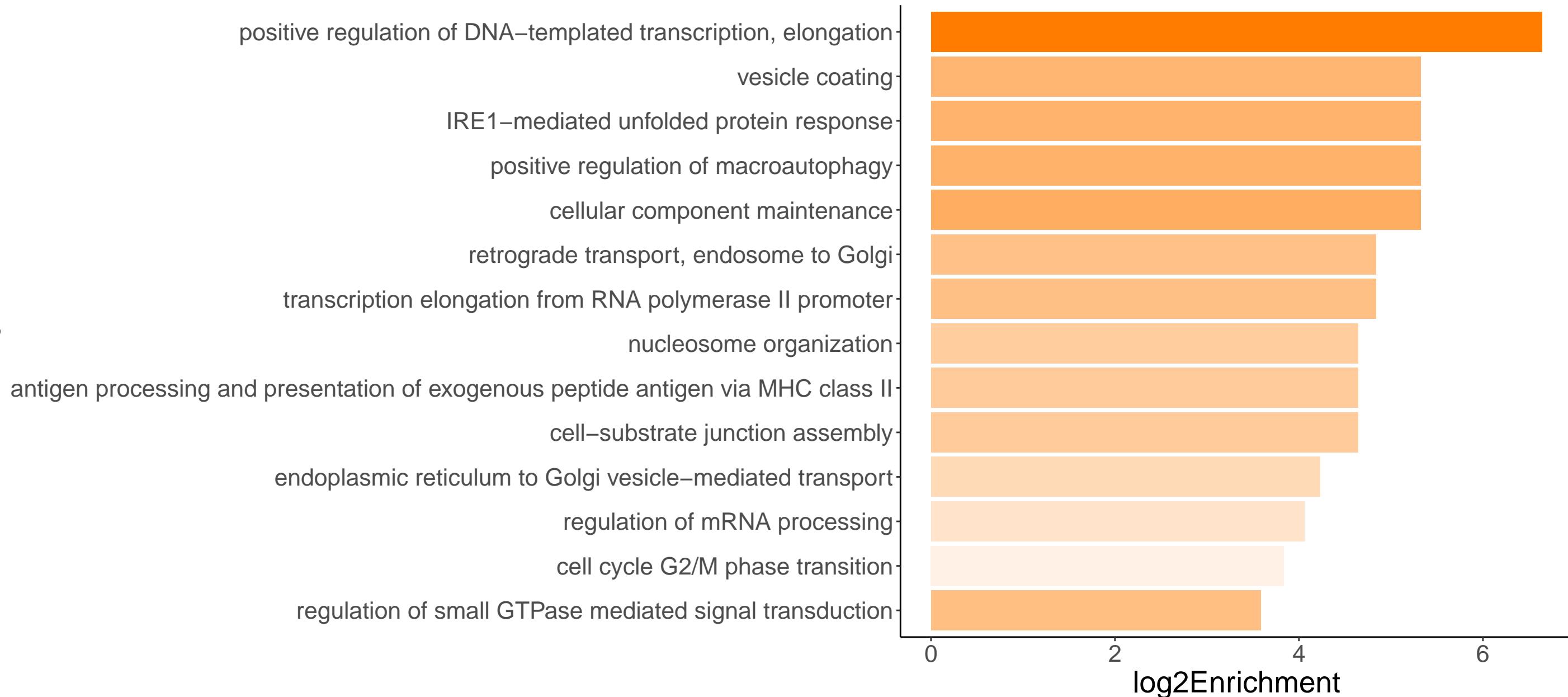
tubulin binding





# Re-clustered module 3.34.12 BP enrichment

Term



# Re-clustered module 3.34.12 MF enrichment

Term

tau protein binding

SNARE binding

motor activity

histone binding

chromatin binding

0

2

4

log2Enrichment



# Re-clustered module 3.34.3 BP enrichment

Term

regulation of meiotic nuclear division

heterochromatin assembly

positive regulation of proteasomal ubiquitin-dependent protein catabolic process

positive regulation of GTPase activity

intracellular protein transport

0

2

4

log2Enrichment



# Re-clustered module 3.34.3 MF enrichment

Term

peptidyl-prolyl cis-trans isomerase activity

Ran GTPase binding

nuclear receptor transcription coactivator activity

ubiquitin binding

enzyme activator activity

0

1

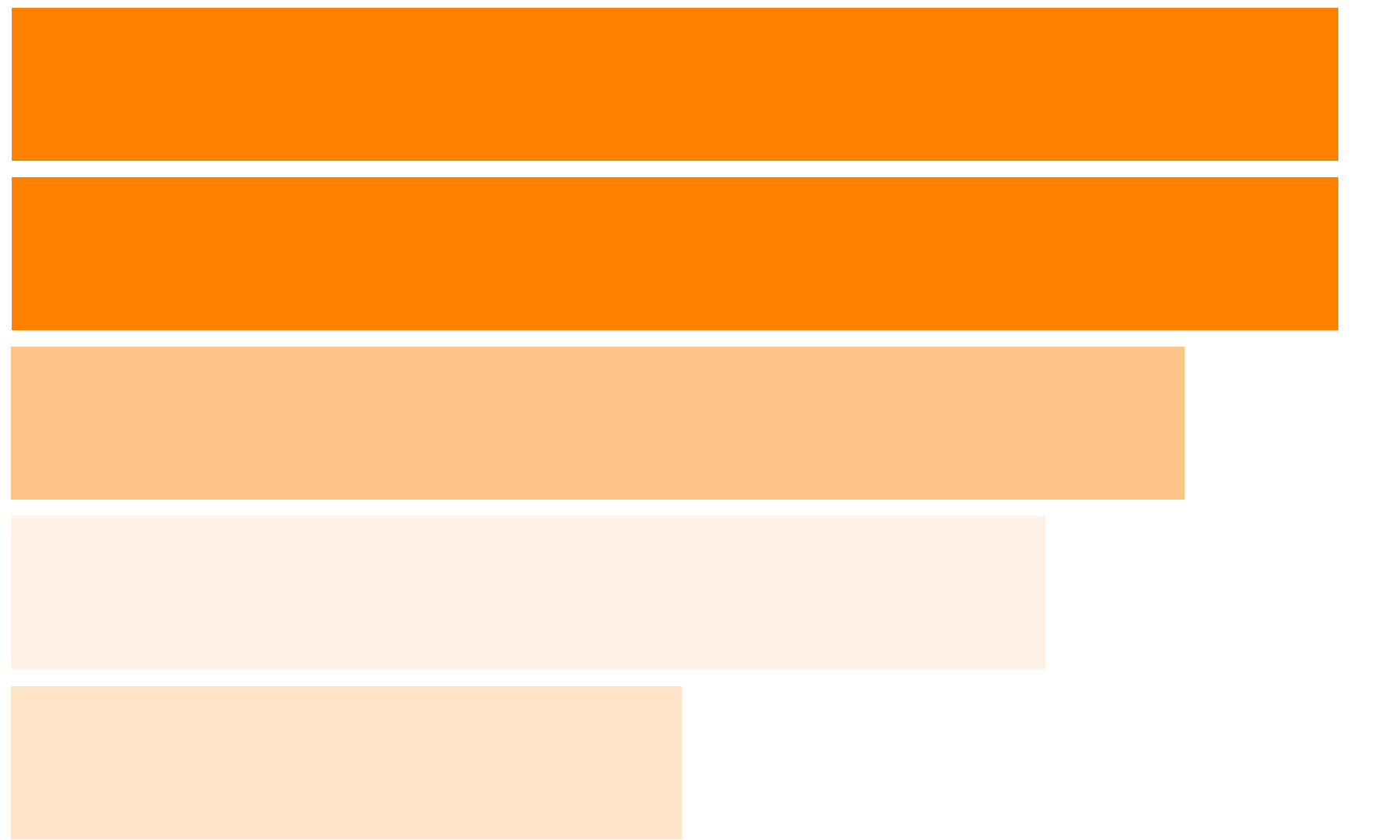
2

3

4

5

log2Enrichment



Re-clustered module 3.34.8 BP enrichment

Term

log2Enrichment



# Re-clustered module 3.34.8 MF enrichment

Term

protein C-terminus binding

0

1

2

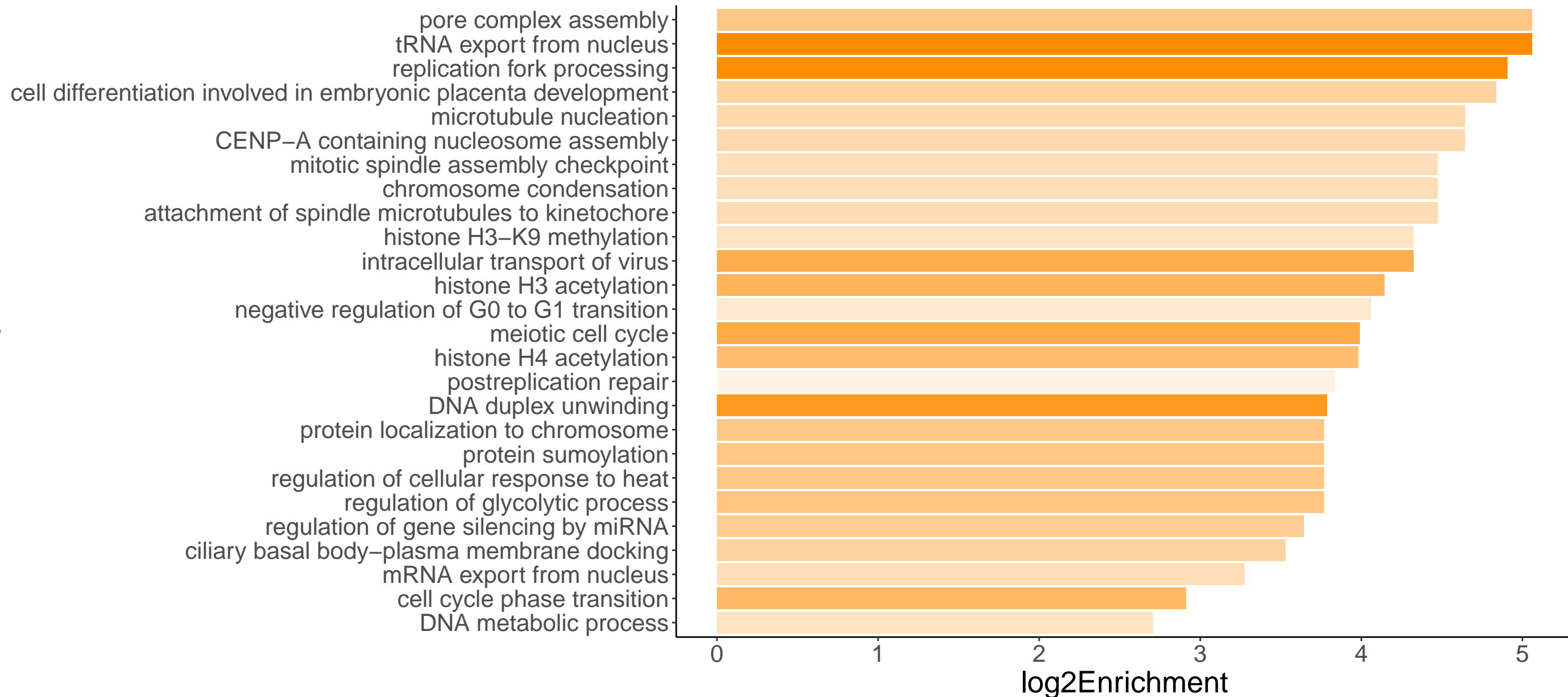
3

4

log2Enrichment

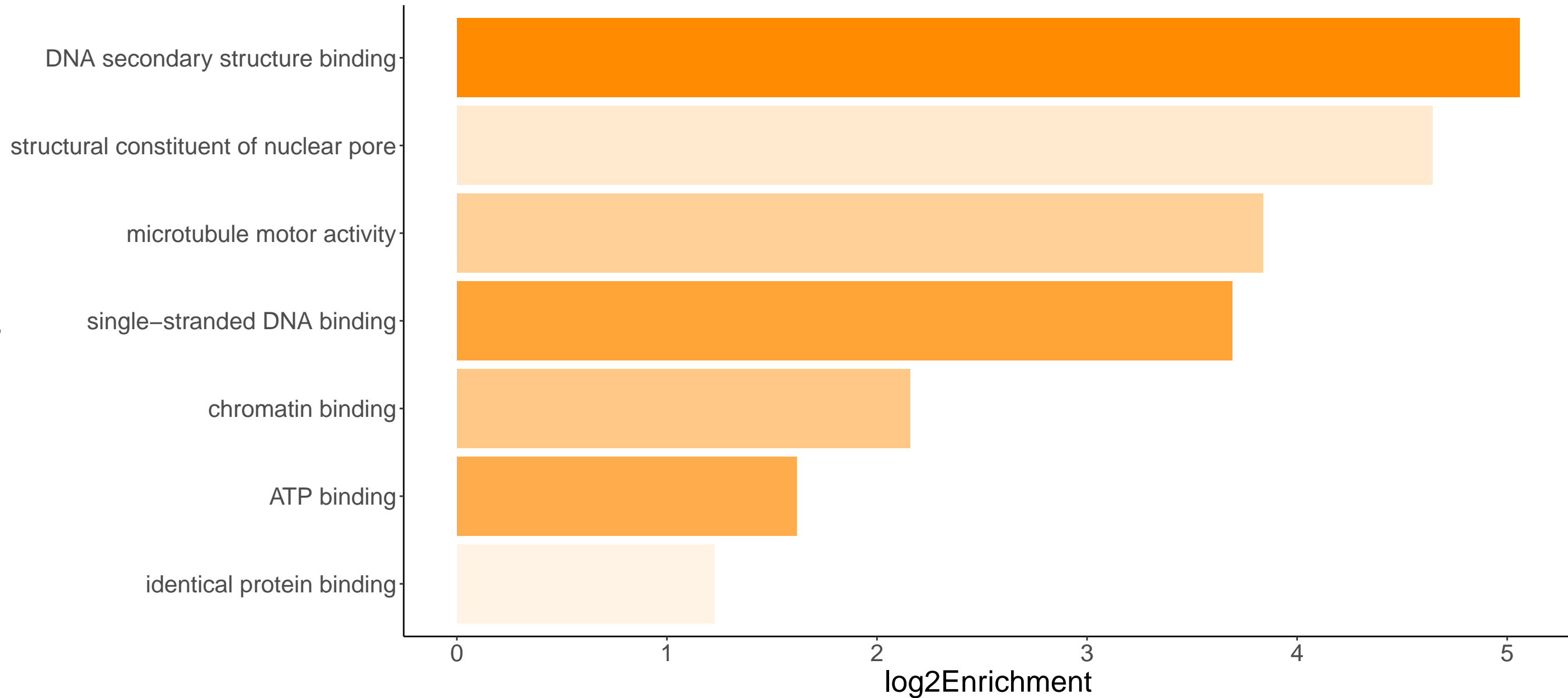


# Re-clustered module 3.37.1 BP enrichment



## Re-clustered module 3.37.1 MF enrichment

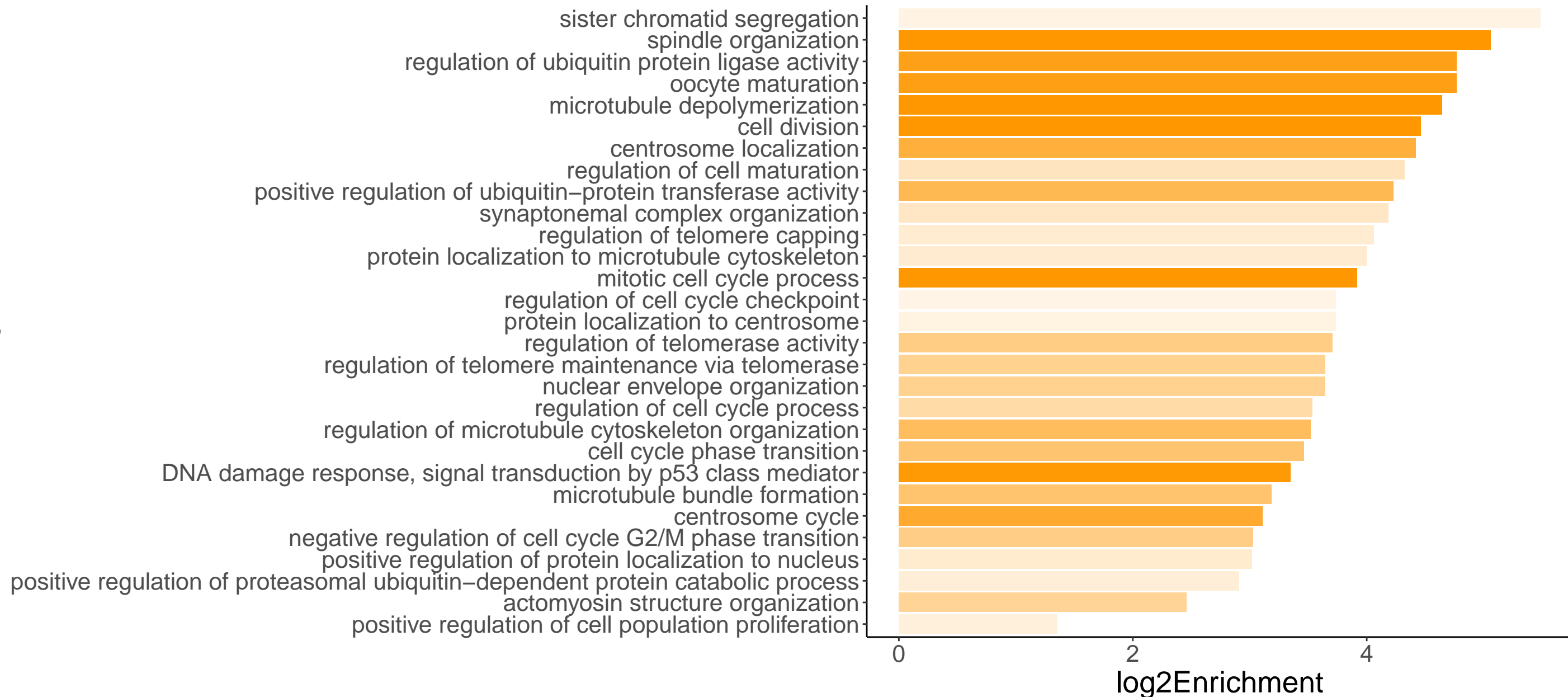
Term





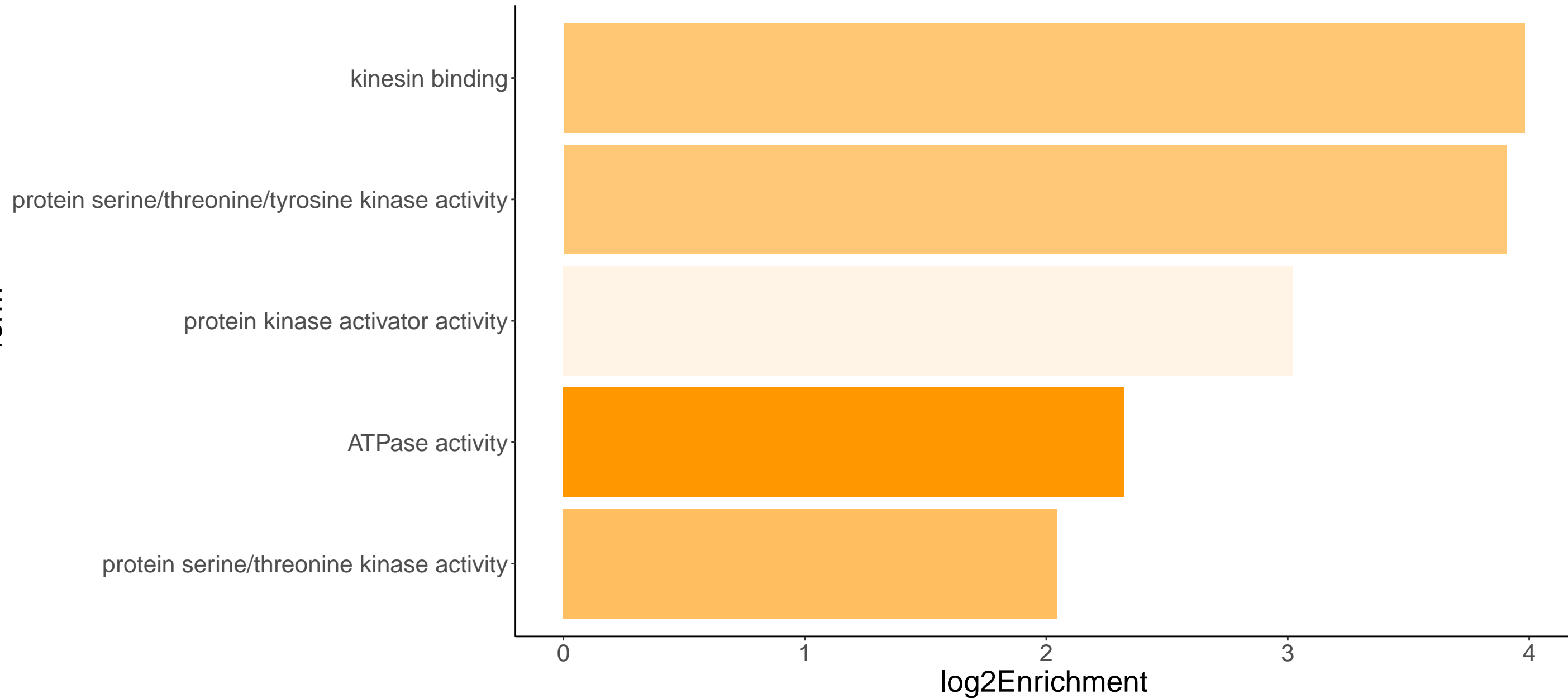
# Re-clustered module 3.37.3 BP enrichment

Term



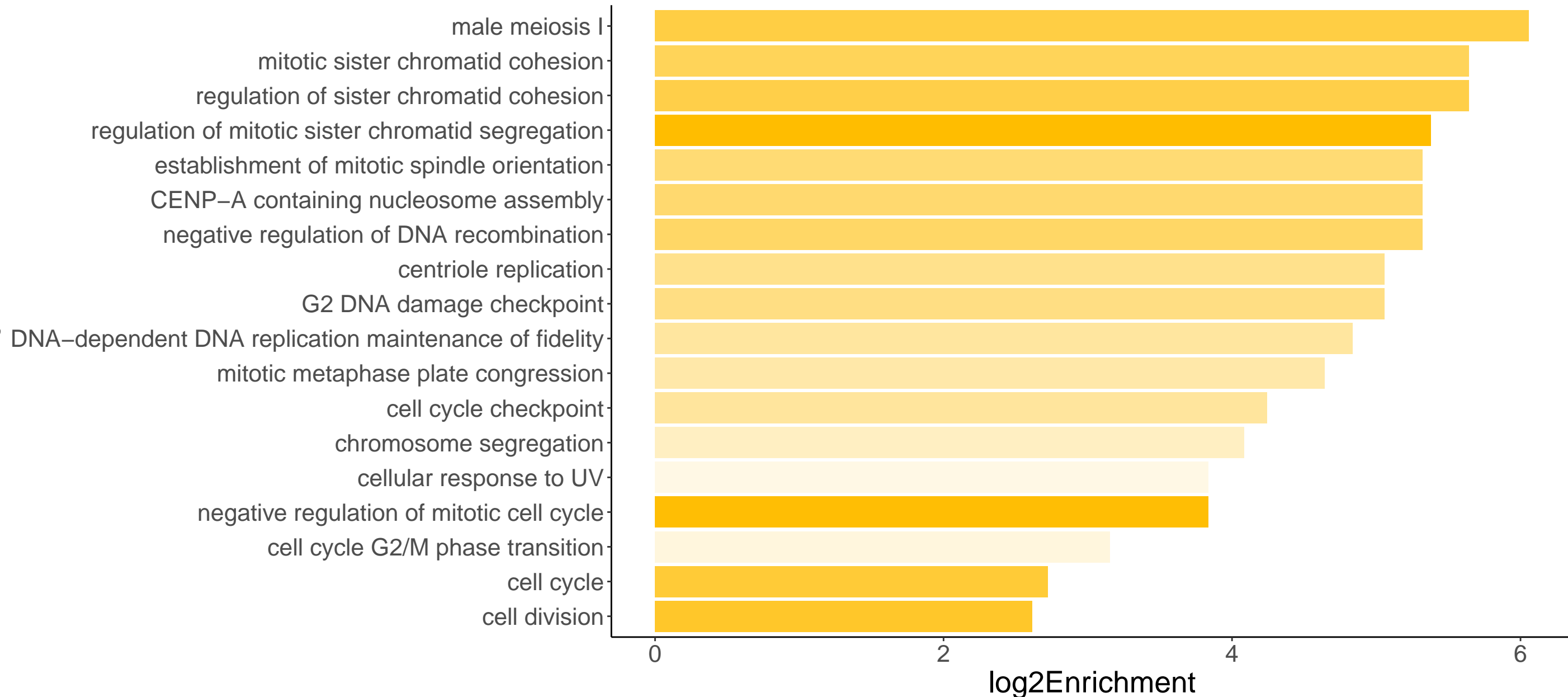
# Re-clustered module 3.37.3 MF enrichment

Term



## Re-clustered module 3.37.4 BP enrichment

Term



# Re-clustered module 3.37.4 MF enrichment

Term

RNA helicase activity

ATP binding

0

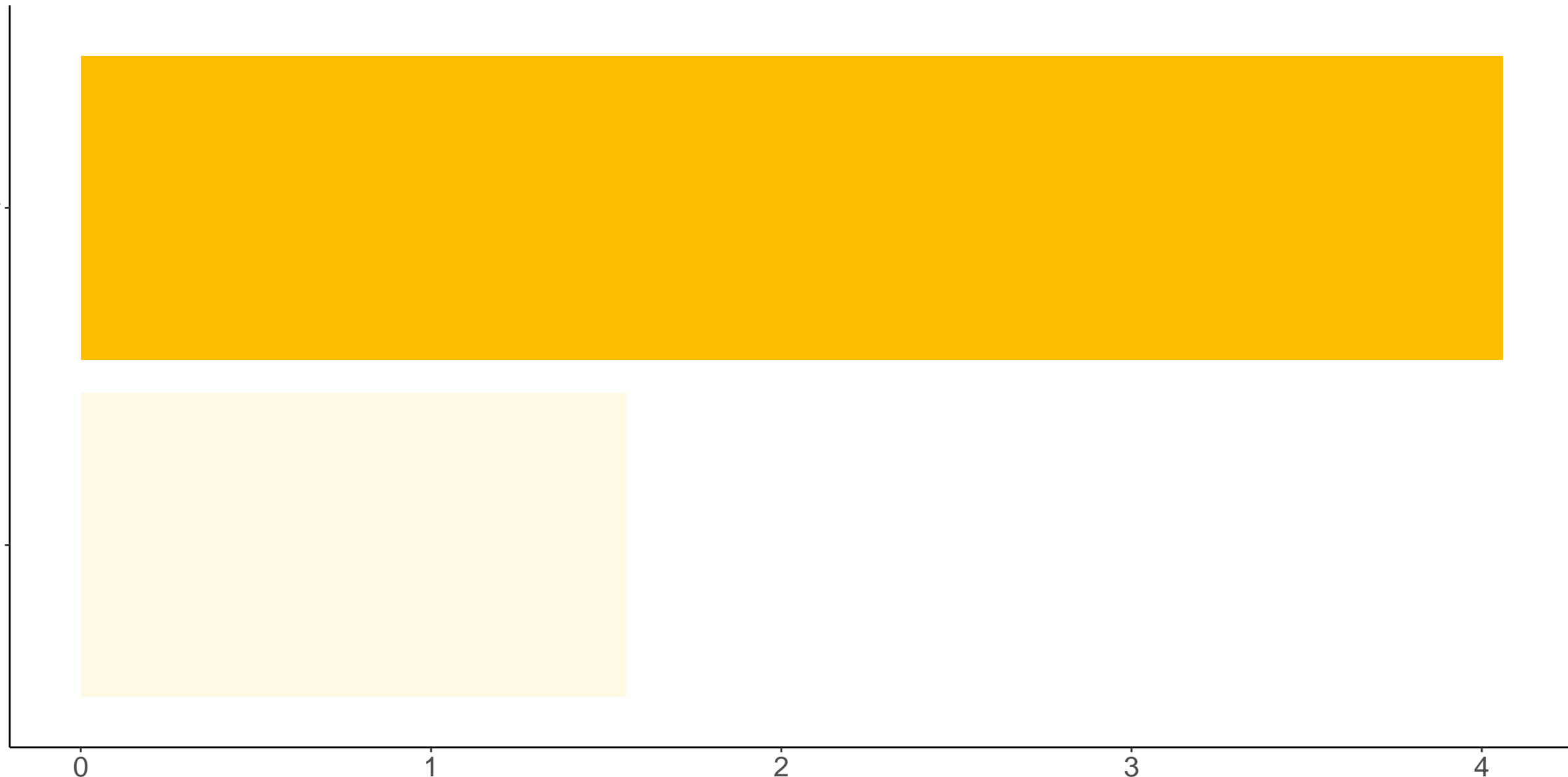
1

2

3

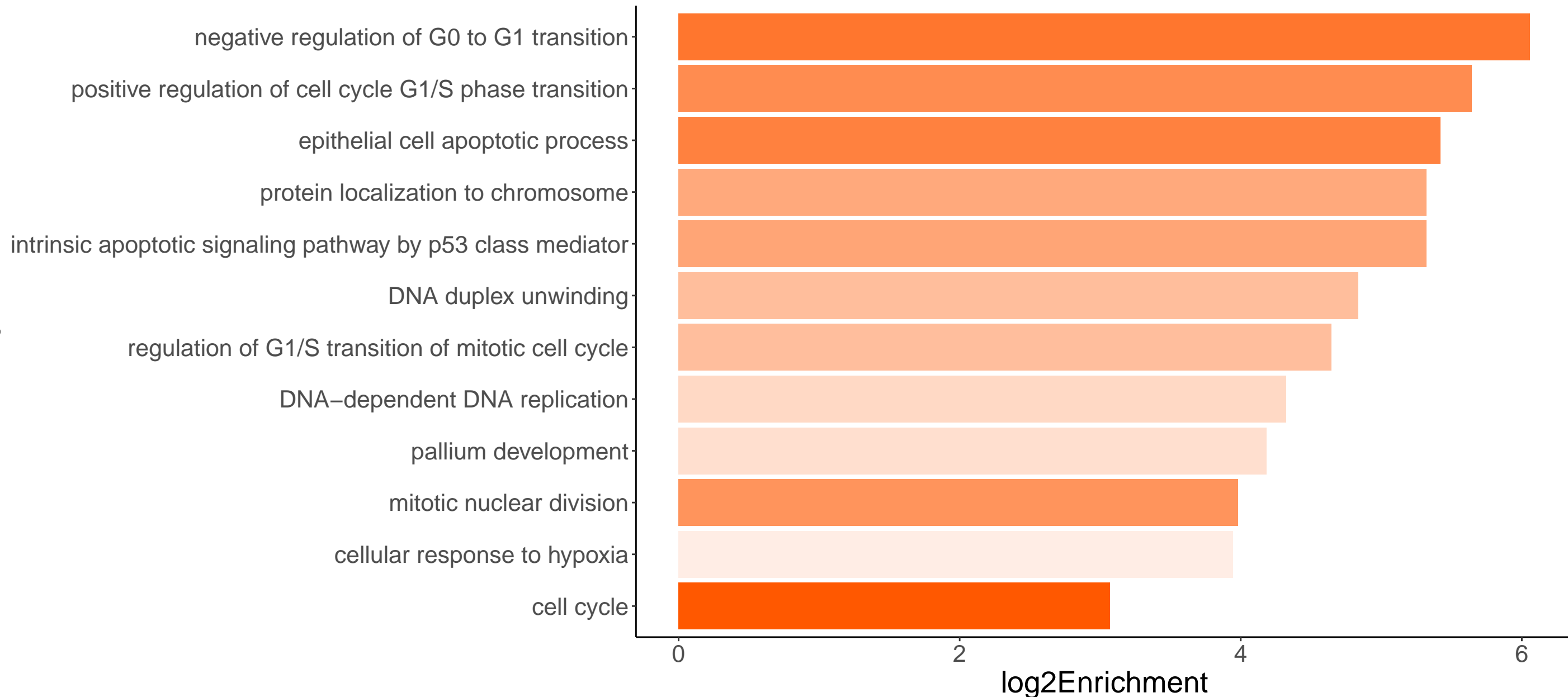
4

log2Enrichment



## Re-clustered module 3.37.5 BP enrichment

Term



# Re-clustered module 3.37.5 MF enrichment

Term

catalytic activity, acting on DNA

0

1

2

3

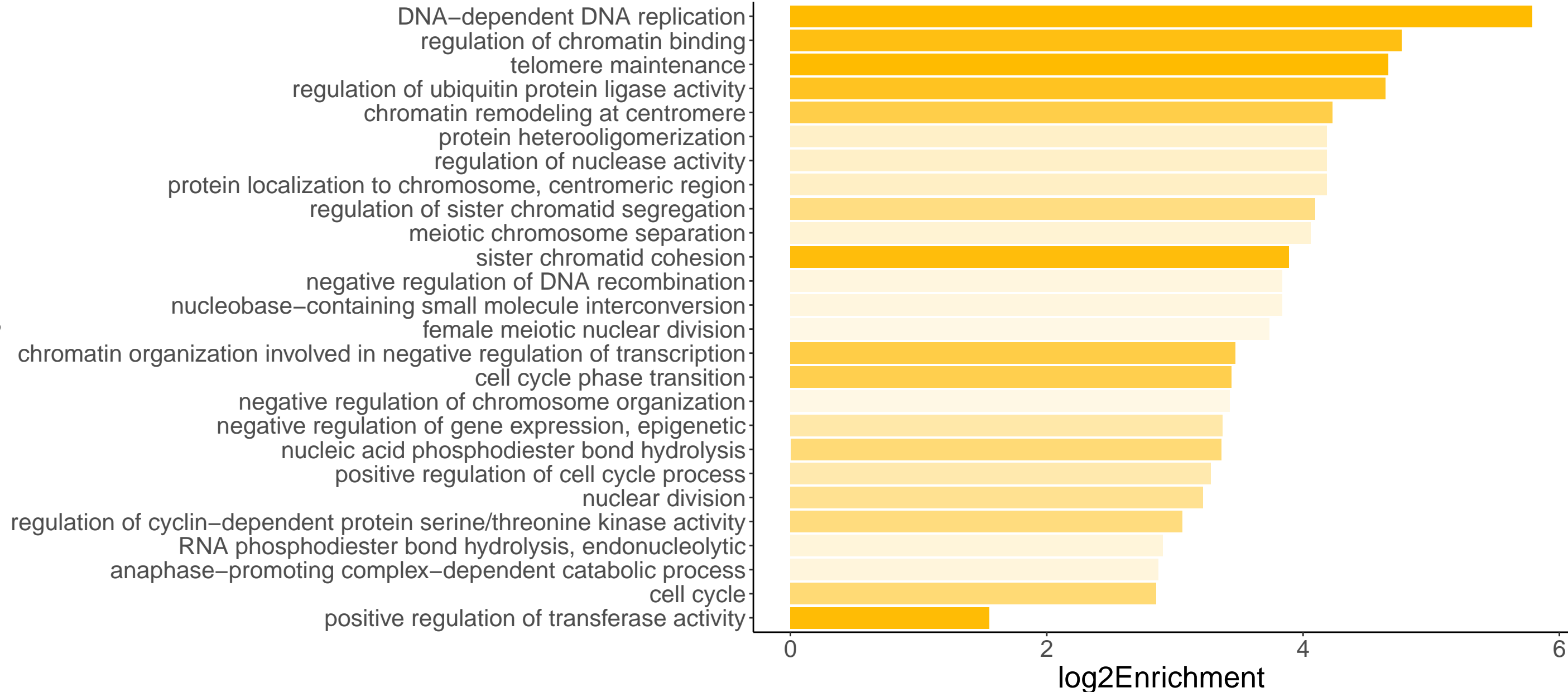
4

log2Enrichment



# Re-clustered module 3.37.8 BP enrichment

Term



# Re-clustered module 3.37.8 MF enrichment

Term

histone binding

0.0

0.5

1.0

1.5

2.0

2.5

log2Enrichment





# Re-clustered module 3.40 BP enrichment

Term

cellular response to ionizing radiation

0

2

4

log2Enrichment



# Re-clustered module 3.40 MF enrichment

Term

lyase activity

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.41 BP enrichment

Term

regulation of nitric-oxide synthase activity

inositol phosphate metabolic process

cellular response to alcohol

negative regulation of neuron death

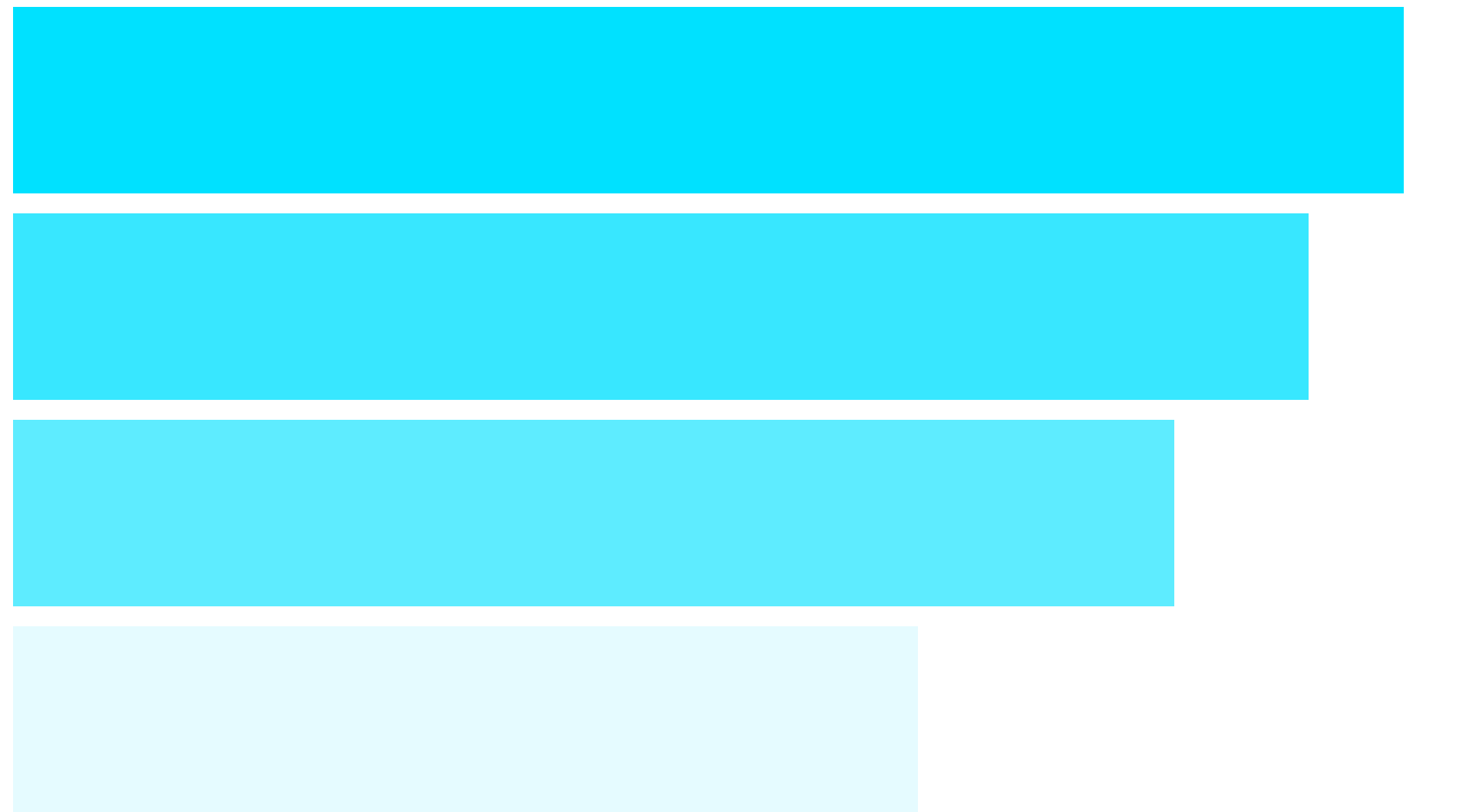
0

2

4

6

log2Enrichment



Re-clustered module 3.41 MF enrichment

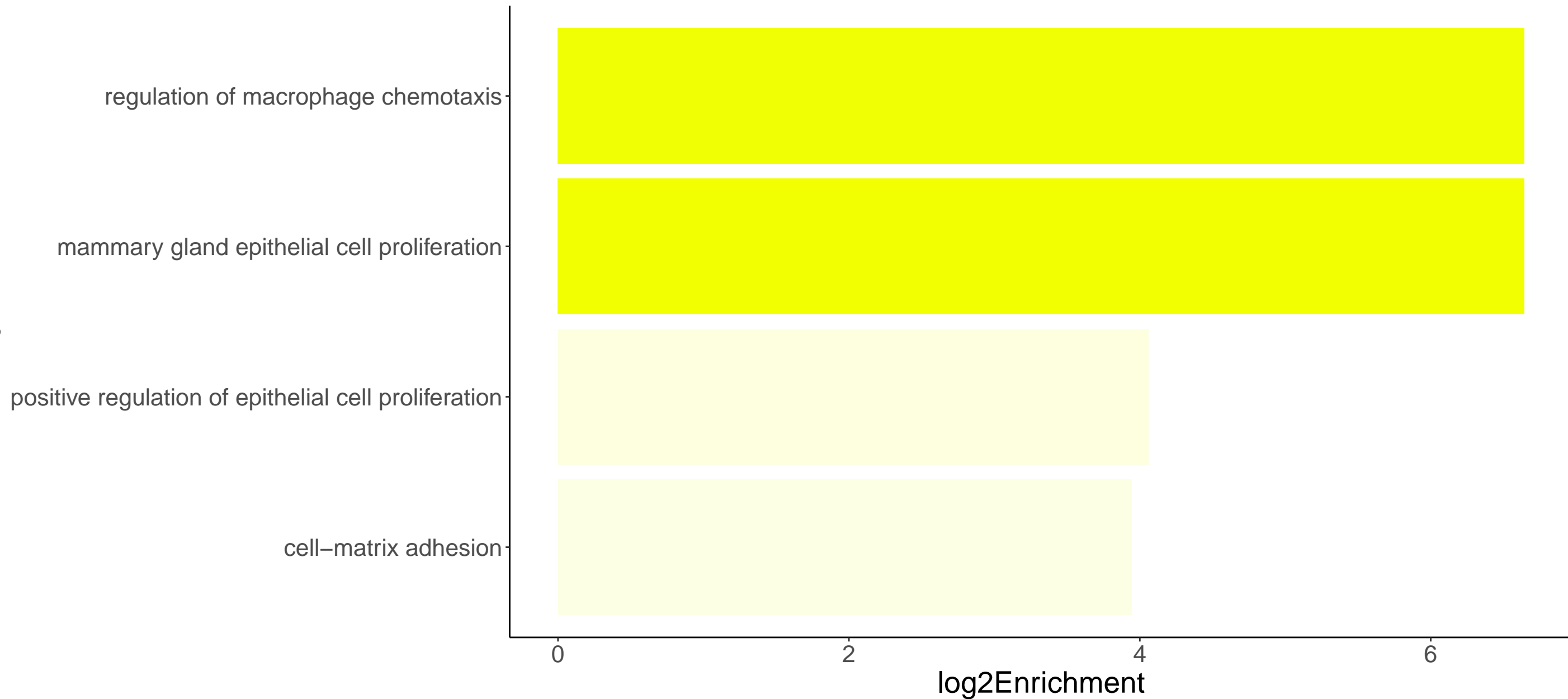
Term

log2Enrichment



# Re-clustered module 3.43 BP enrichment

Term



# Re-clustered module 3.43 MF enrichment

Term

extracellular matrix structural constituent

endopeptidase activity

calcium ion binding

0

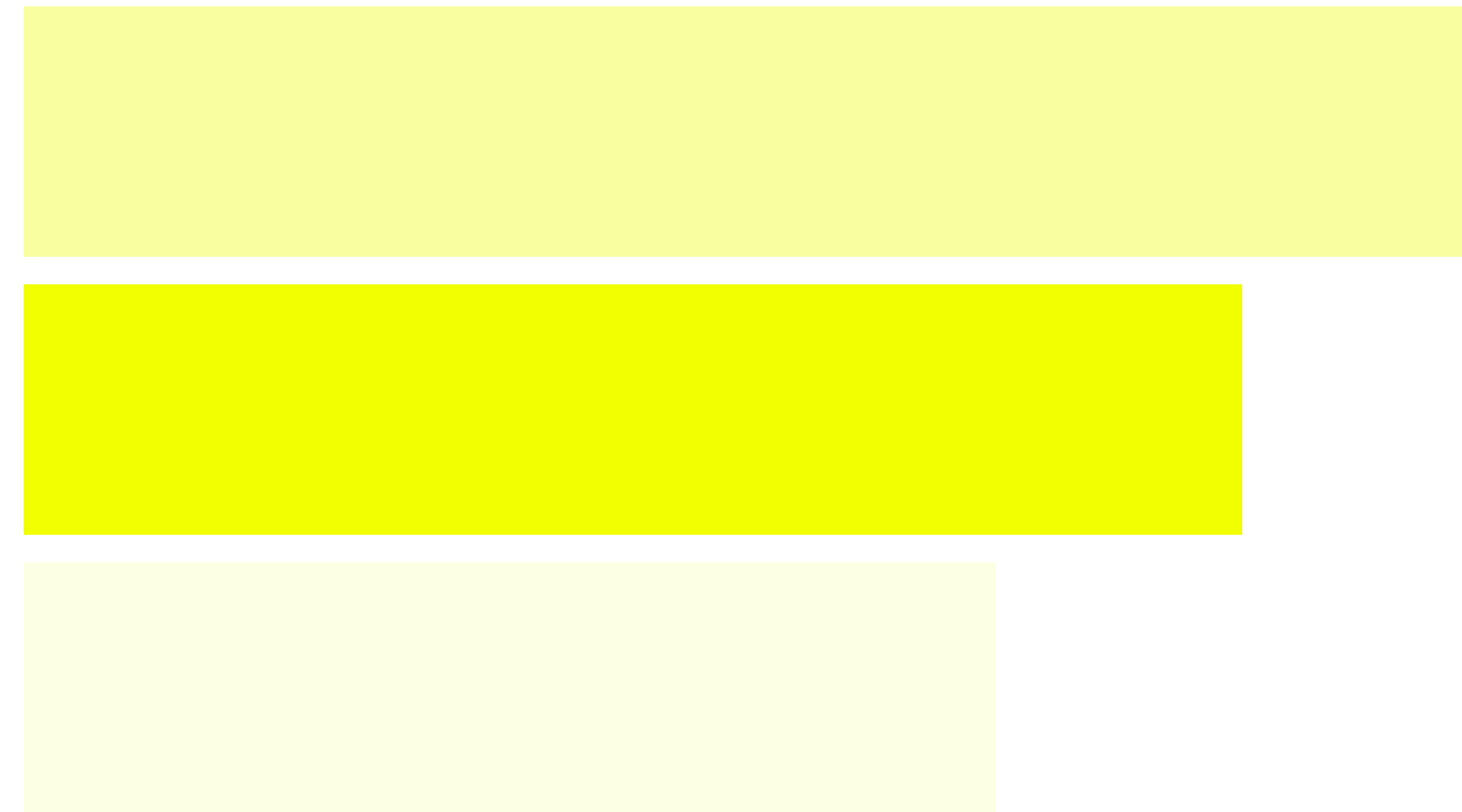
1

2

3

4

log2Enrichment



# Re-clustered module 3.44 BP enrichment

Term

regulation of microtubule cytoskeleton organization

0

1

2

3

4

log2Enrichment



Re-clustered module 3.44 MF enrichment

Term

log2Enrichment





Re-clustered module 3.49 BP enrichment

Term

log2Enrichment



# Re-clustered module 3.49 MF enrichment

Term

tRNA binding

ubiquitin binding

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.5 BP enrichment

Term

musculoskeletal movement

cellular oxidant detoxification

nucleic acid phosphodiester bond hydrolysis

cell division

0

1

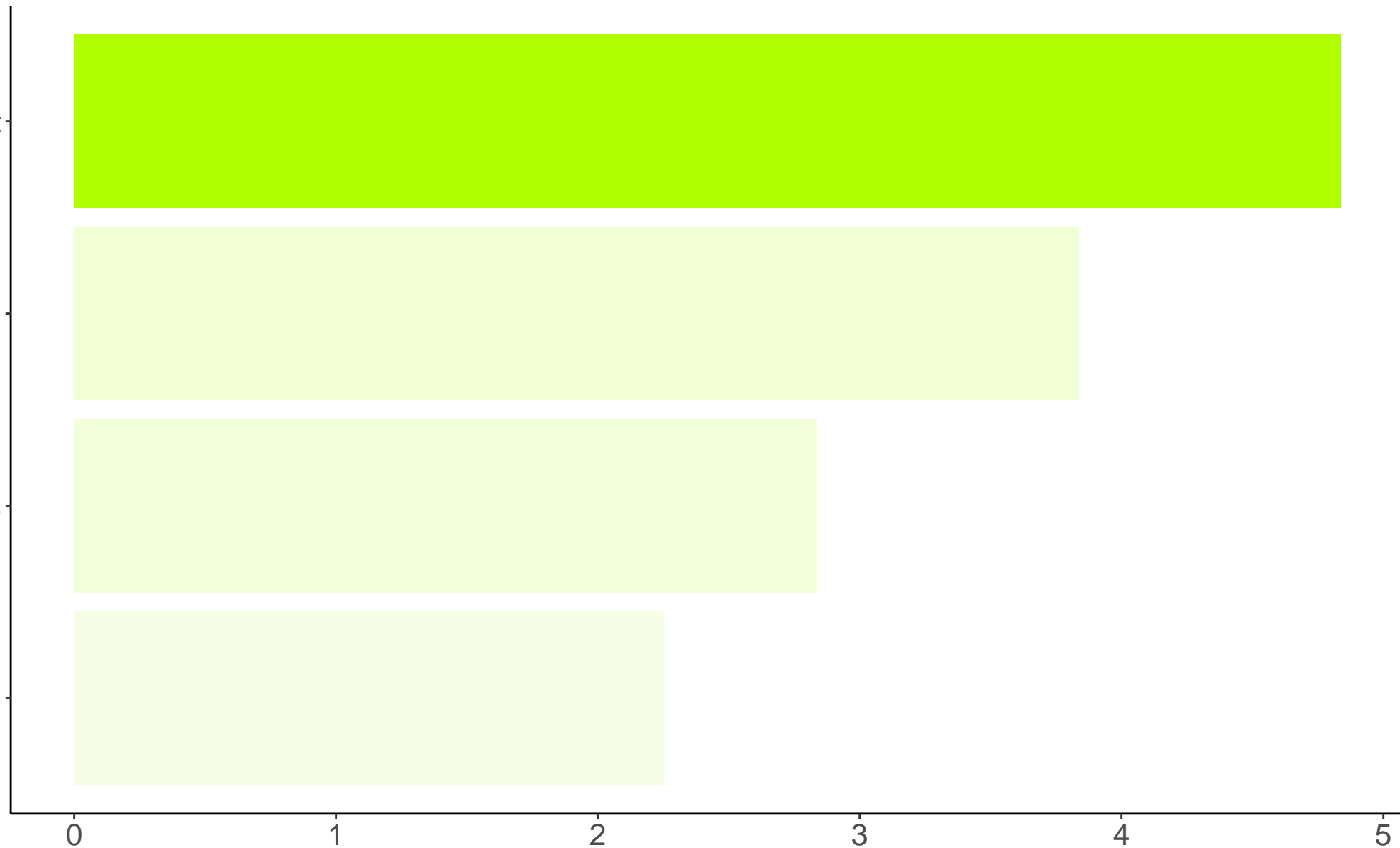
2

3

4

5

log2Enrichment



# Re-clustered module 3.5 MF enrichment

Term

disulfide oxidoreductase activity

0

1

2

3

4

5

log2Enrichment



# Re-clustered module 3.53 BP enrichment

Term

response to osmotic stress

response to calcium ion

negative regulation of transcription, DNA-templated

0

1

2

3

4

5

log2Enrichment



# Re-clustered module 3.53 MF enrichment

Term

protease binding

0

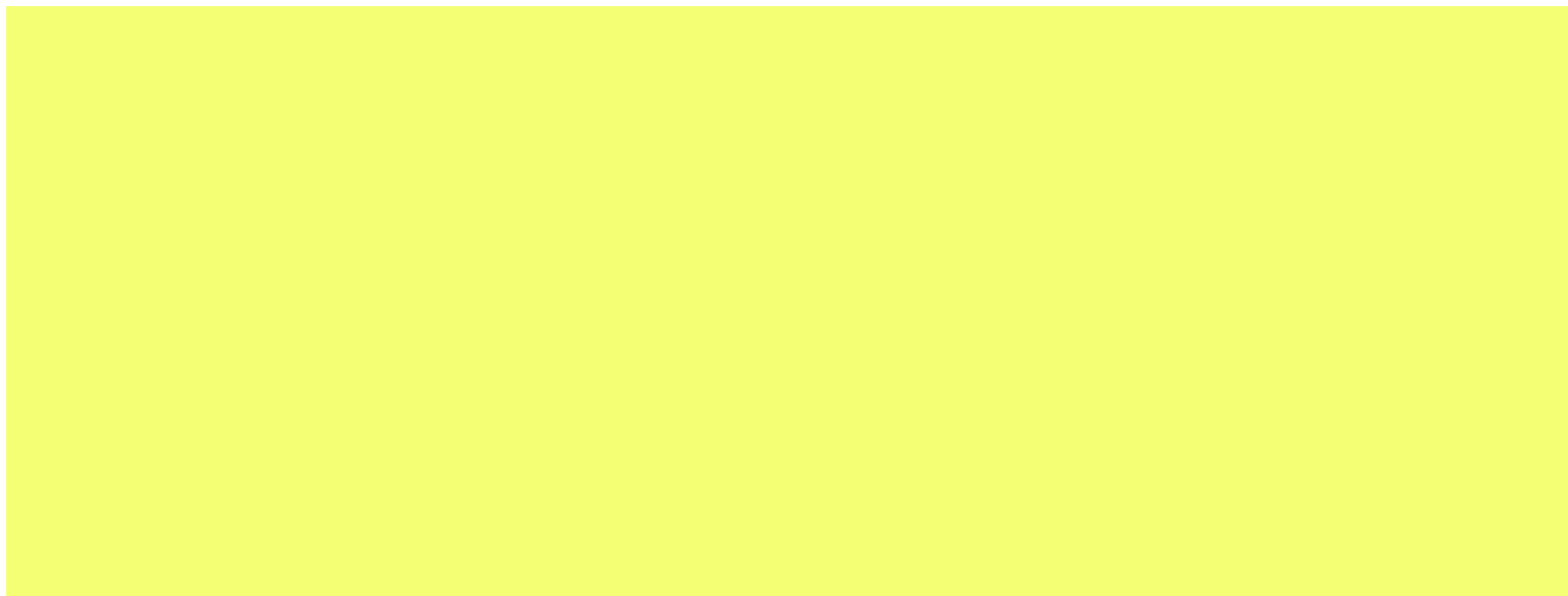
1

2

3

4

log2Enrichment



Re-clustered module 3.55 BP enrichment

Term

termination of RNA polymerase I transcription

transcription elongation from RNA polymerase I promoter

transcription initiation from RNA polymerase I promoter

cellular response to UV

peptidyl-tyrosine dephosphorylation

0

2

4

log2Enrichment



# Re-clustered module 3.55 MF enrichment

Term

ubiquitin binding

protein tyrosine phosphatase activity

0

1

2

3

4

5

log2Enrichment





Re-clustered module 3.57 BP enrichment

Term

log2Enrichment



# Re-clustered module 3.57 MF enrichment

Term

phospholipid transfer activity

0

2

4

6

log2Enrichment



# Re-clustered module 3.6 BP enrichment

Term

branched-chain amino acid catabolic process

positive regulation of DNA replication

peptidyl-lysine trimethylation

0

1

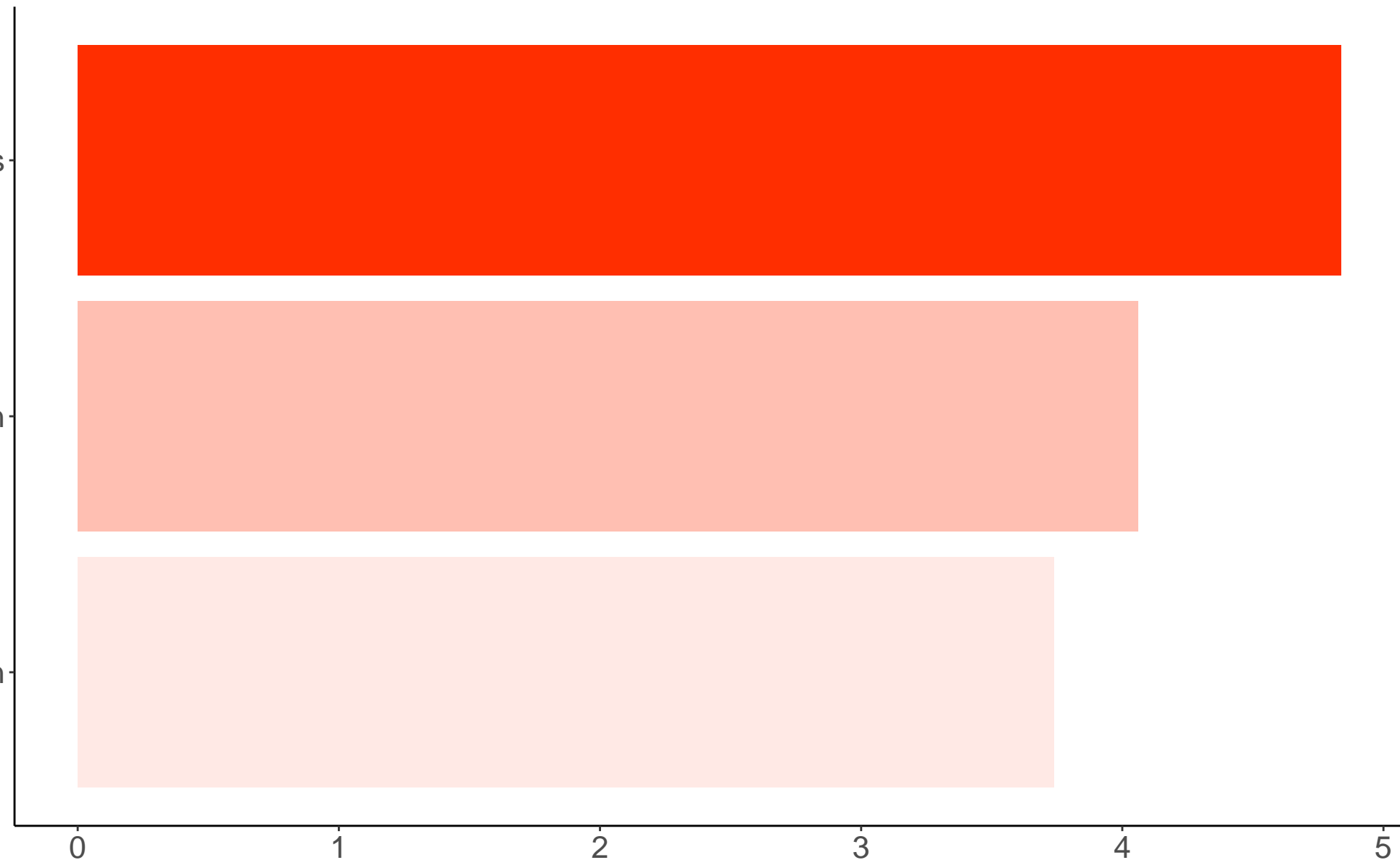
2

3

4

5

log2Enrichment



Re-clustered module 3.6 MF enrichment

Term

log2Enrichment



# Re-clustered module 3.61 BP enrichment

Term

modulation by virus of host process

modulation by symbiont of host cellular process

myeloid cell development

regulation of DNA recombination

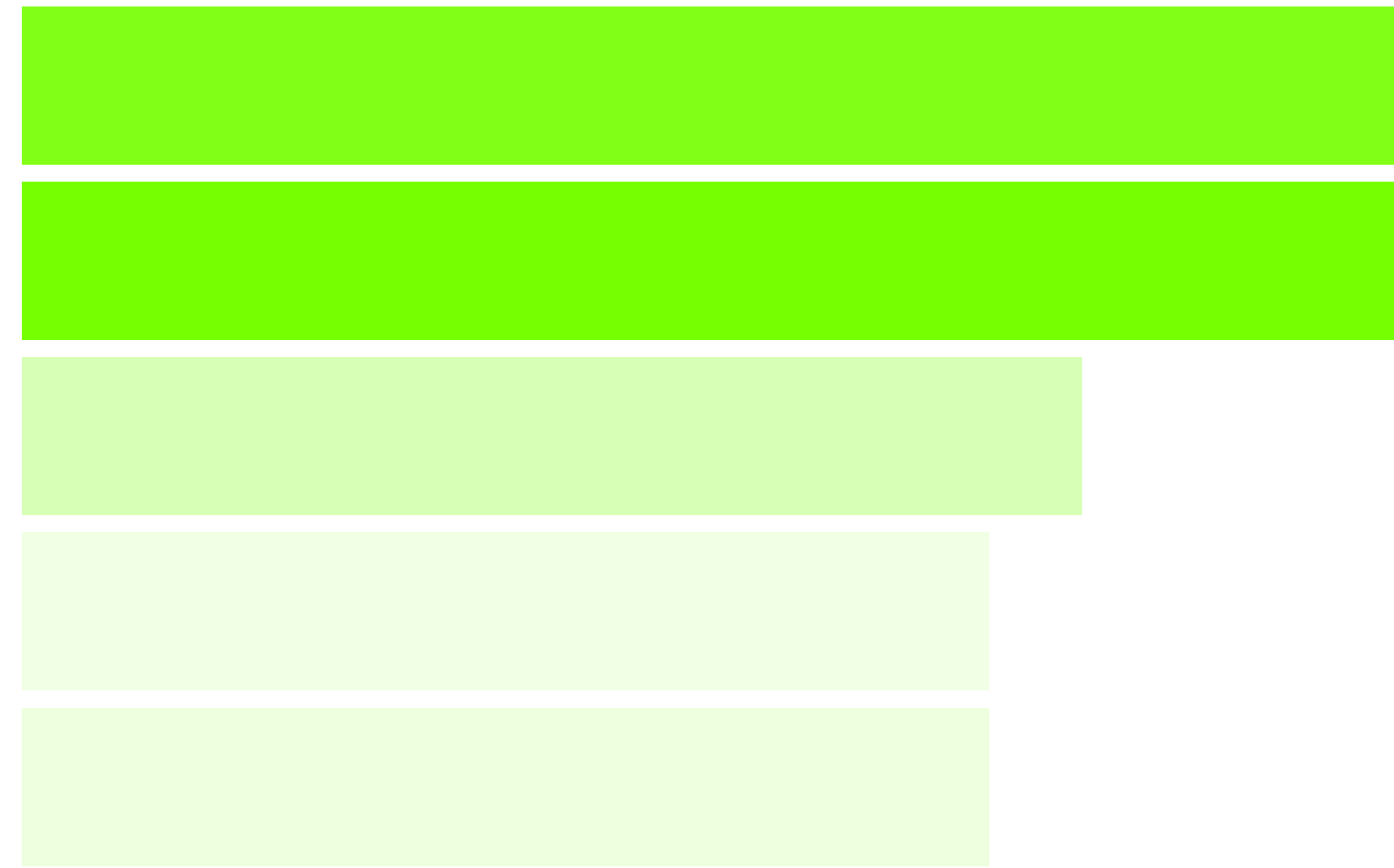
phospholipid transport

0

2

4

log2Enrichment



# Re-clustered module 3.61 MF enrichment

Term

nuclear import signal receptor activity

nuclear localization sequence binding

0

2

4

6

log2Enrichment



# Re-clustered module 3.63 BP enrichment

Term

protein localization to plasma membrane

regulation of canonical Wnt signaling pathway

0

1

2

3

4

log2Enrichment



# Re-clustered module 3.63 MF enrichment

Term

GTP-Rho binding

0

2

4

6

log2Enrichment





Re-clustered module 3.8 BP enrichment

Term

log2Enrichment



Re-clustered module 3.8 MF enrichment

Term

log2Enrichment



## Re-clustered module 3.80 BP enrichment

Term

Arp2/3 complex-mediated actin nucleation

ephrin receptor signaling pathway

Fc-gamma receptor signaling pathway involved in phagocytosis

membrane organization

0

2

4

6

log2Enrichment



# Re-clustered module 3.80 MF enrichment

Term

actin binding

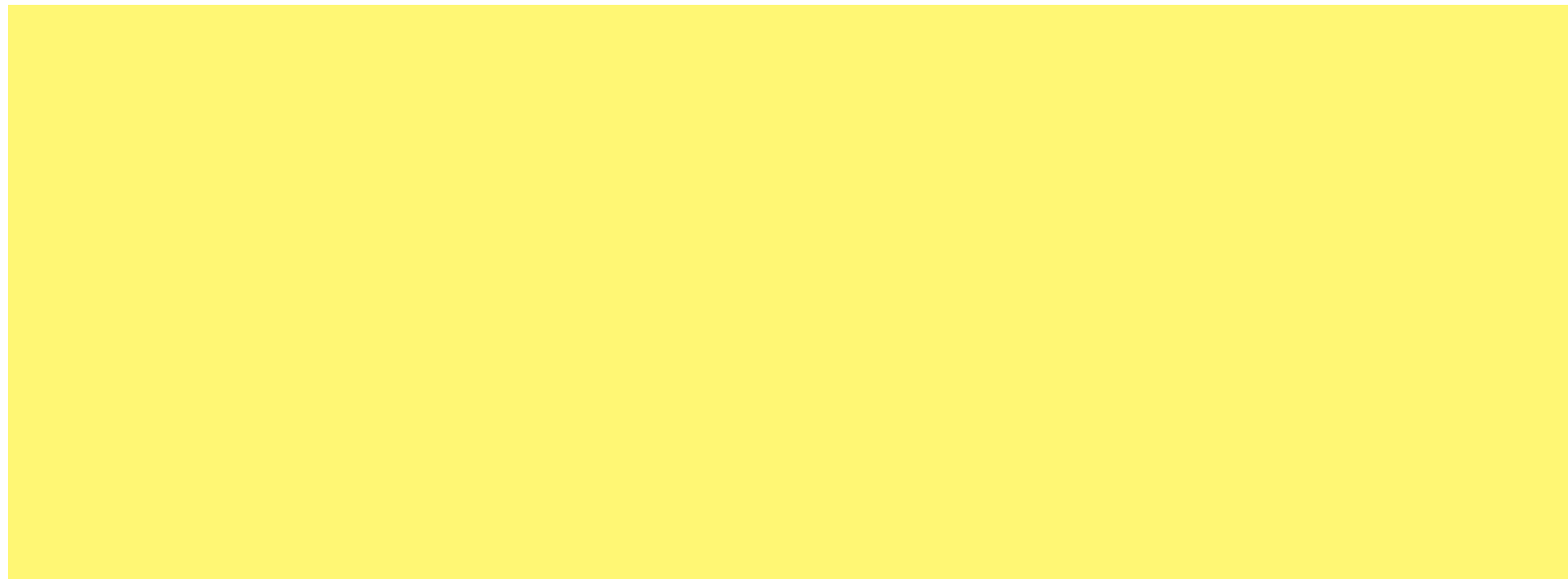
0

1

2

3

log2Enrichment



# Re-clustered module 3.89 BP enrichment

Term

negative regulation of JNK cascade

mannosylation

0

2

4

6

log2Enrichment



# Re-clustered module 3.89 MF enrichment

Term

exopeptidase activity

cysteine-type peptidase activity

0

1

2

3

4

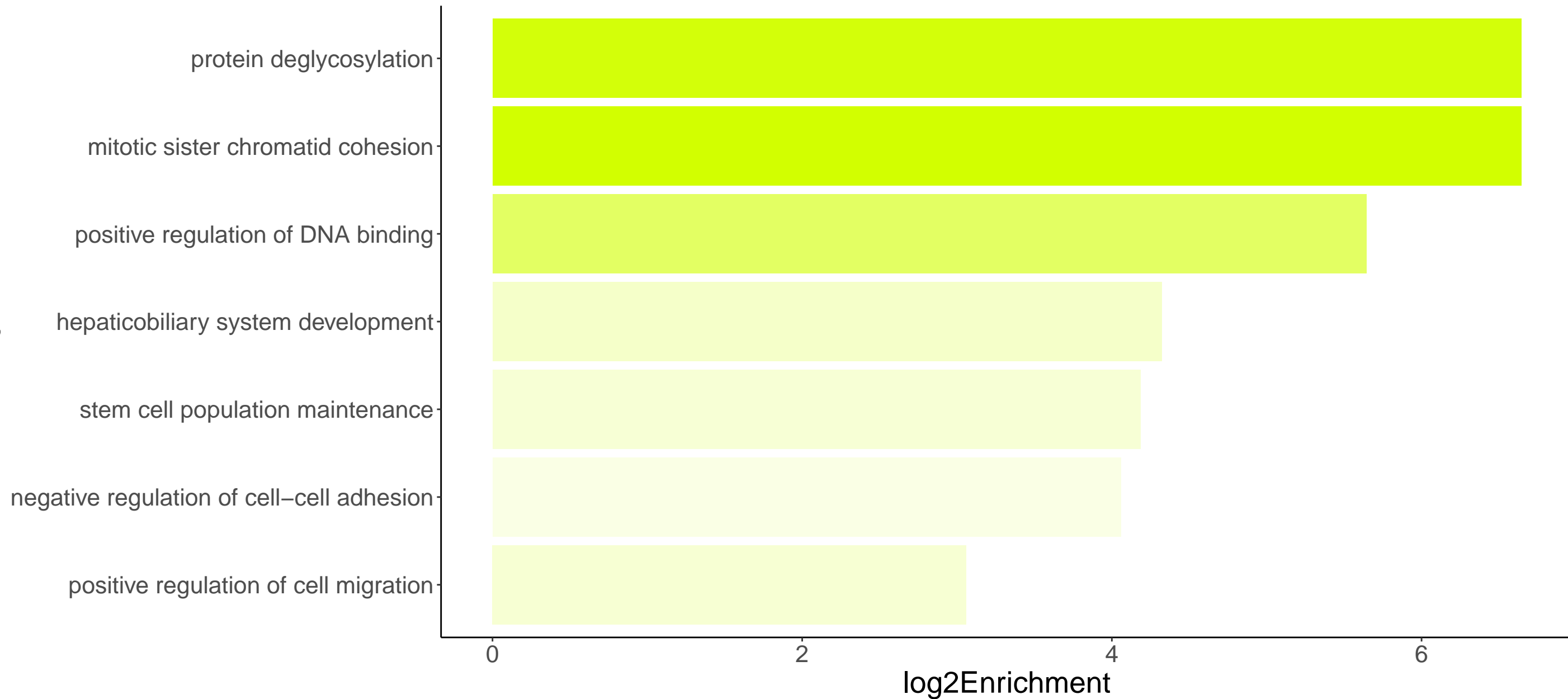
5

log2Enrichment



# Re-clustered module 3.9 BP enrichment

Term



# Re-clustered module 3.9 MF enrichment

Term

hydrolase activity, hydrolyzing O-glycosyl compounds

protein C-terminus binding

0

2

4

log2Enrichment





# Re-clustered module 3.92 BP enrichment

Term

SCF-dependent proteasomal ubiquitin-dependent protein catabolic process

inorganic anion transport

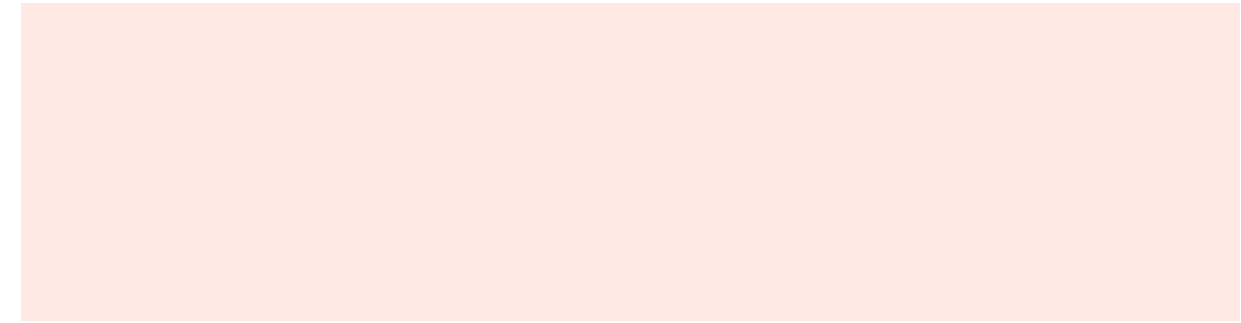
post-translational protein modification

0

2

4

log2Enrichment



# Re-clustered module 3.92 MF enrichment

Term

inorganic anion transmembrane transporter activity

ubiquitin-protein transferase activity

0

1

2

3

4

5

log2Enrichment

