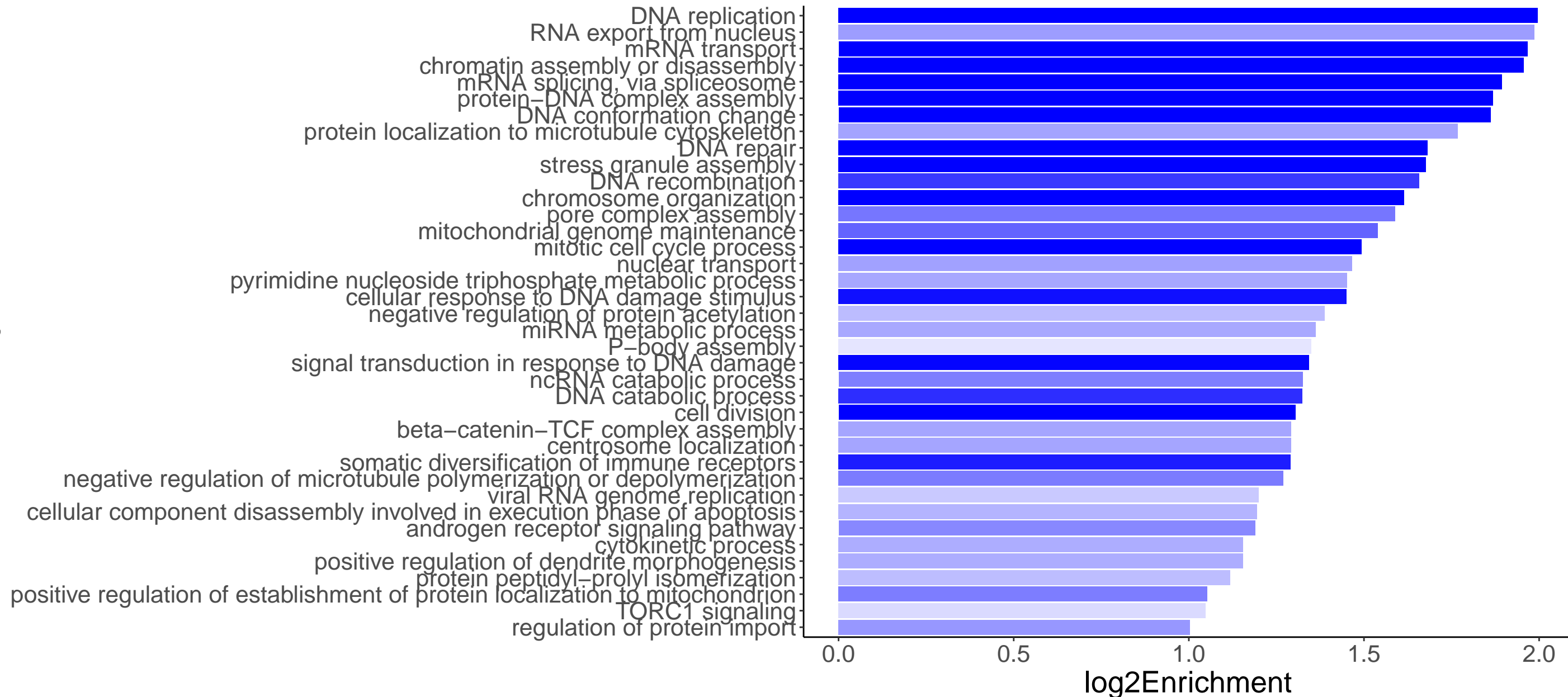


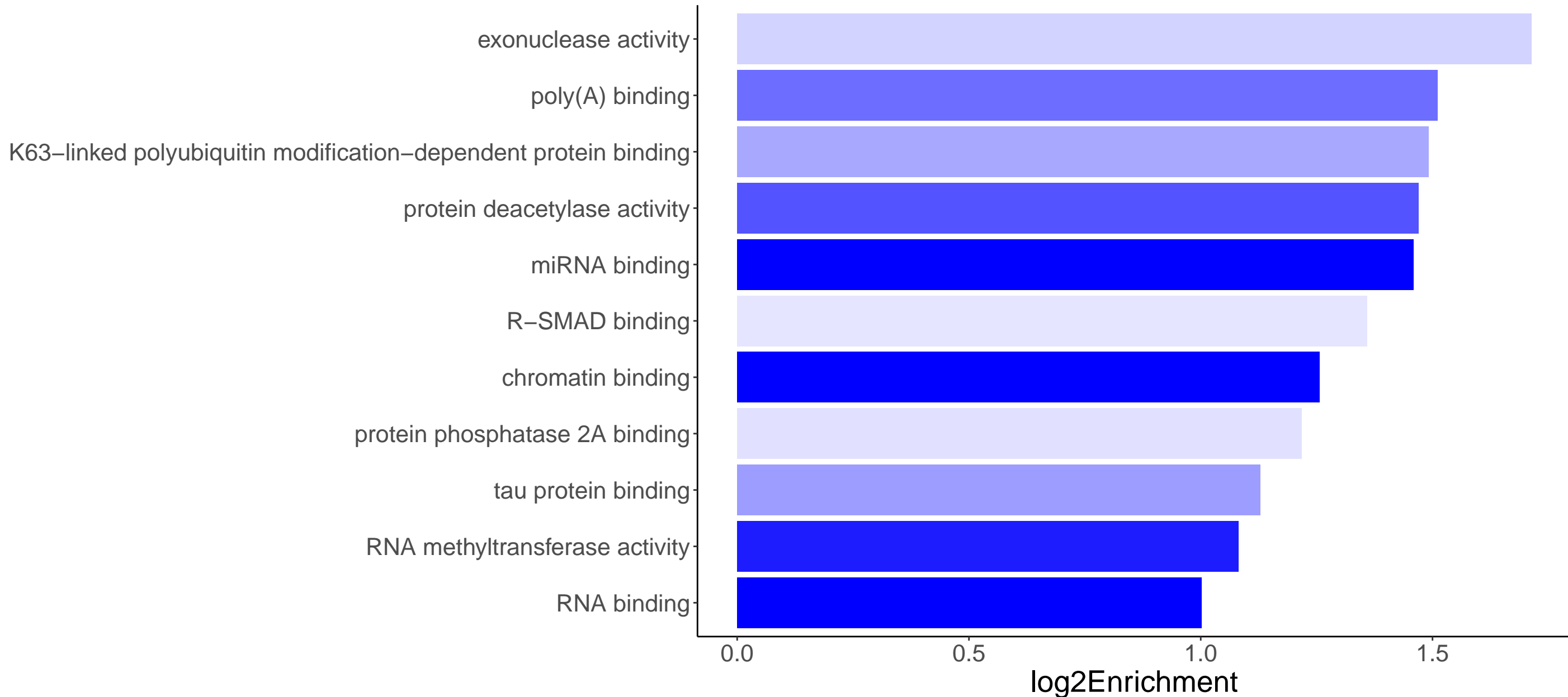
Original module 1 BP enrichment

Term



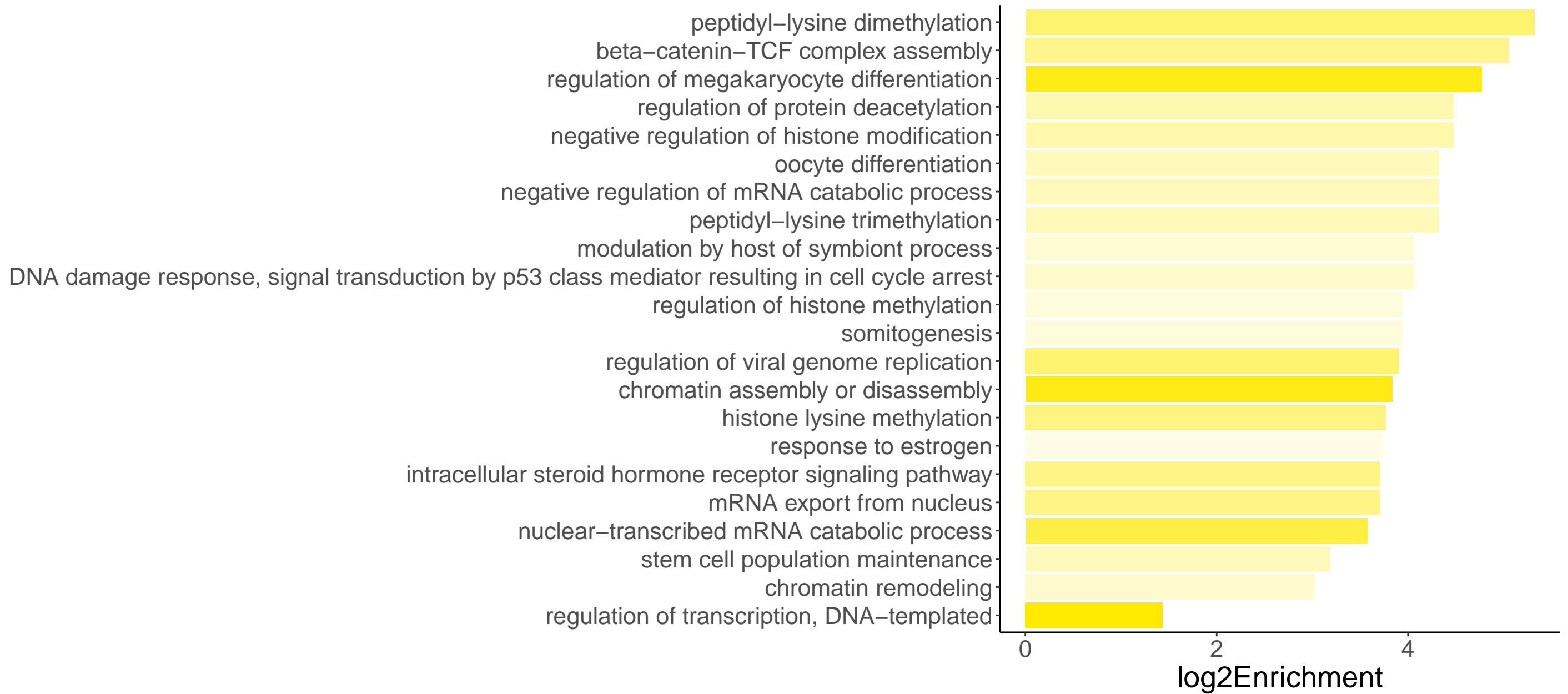
Original module 1 MF enrichment

Term



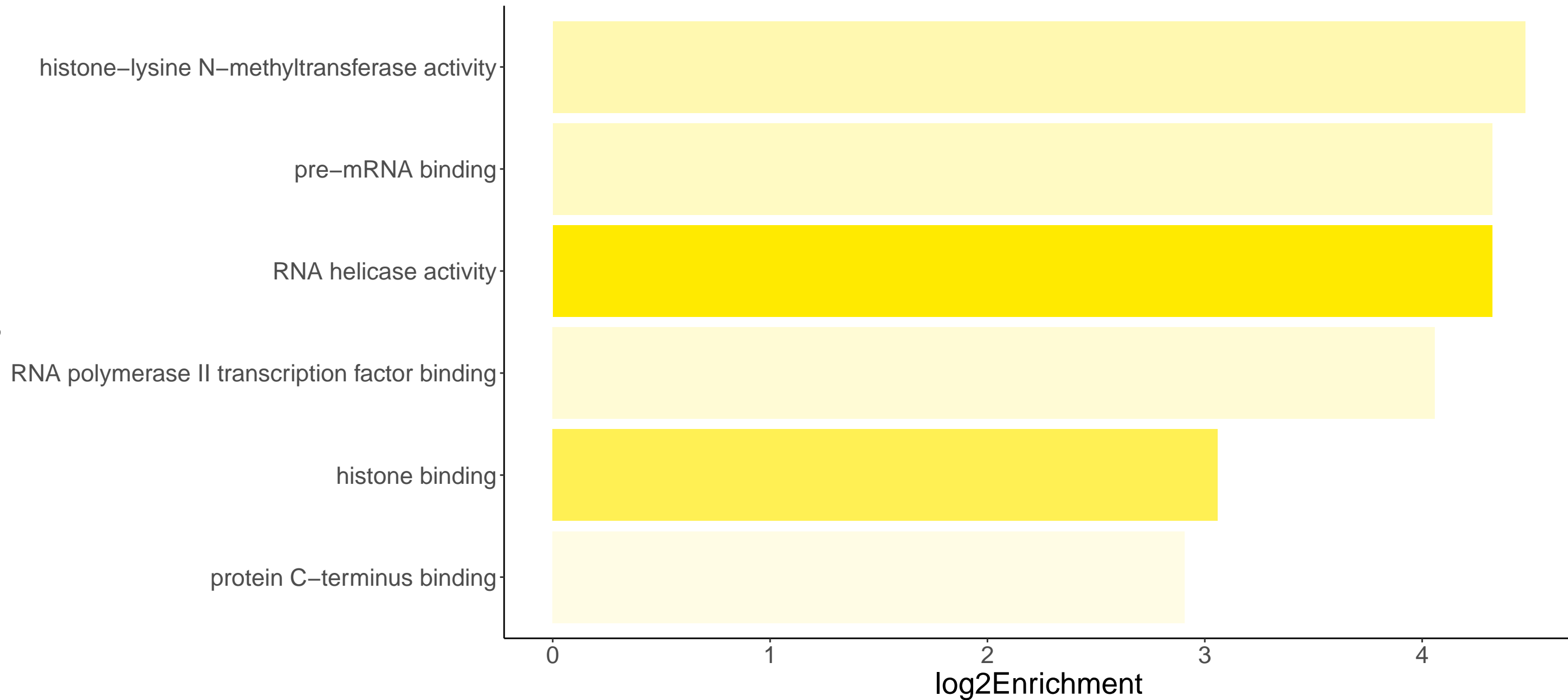
Re-clustered module 1.1.1 BP enrichment

Term



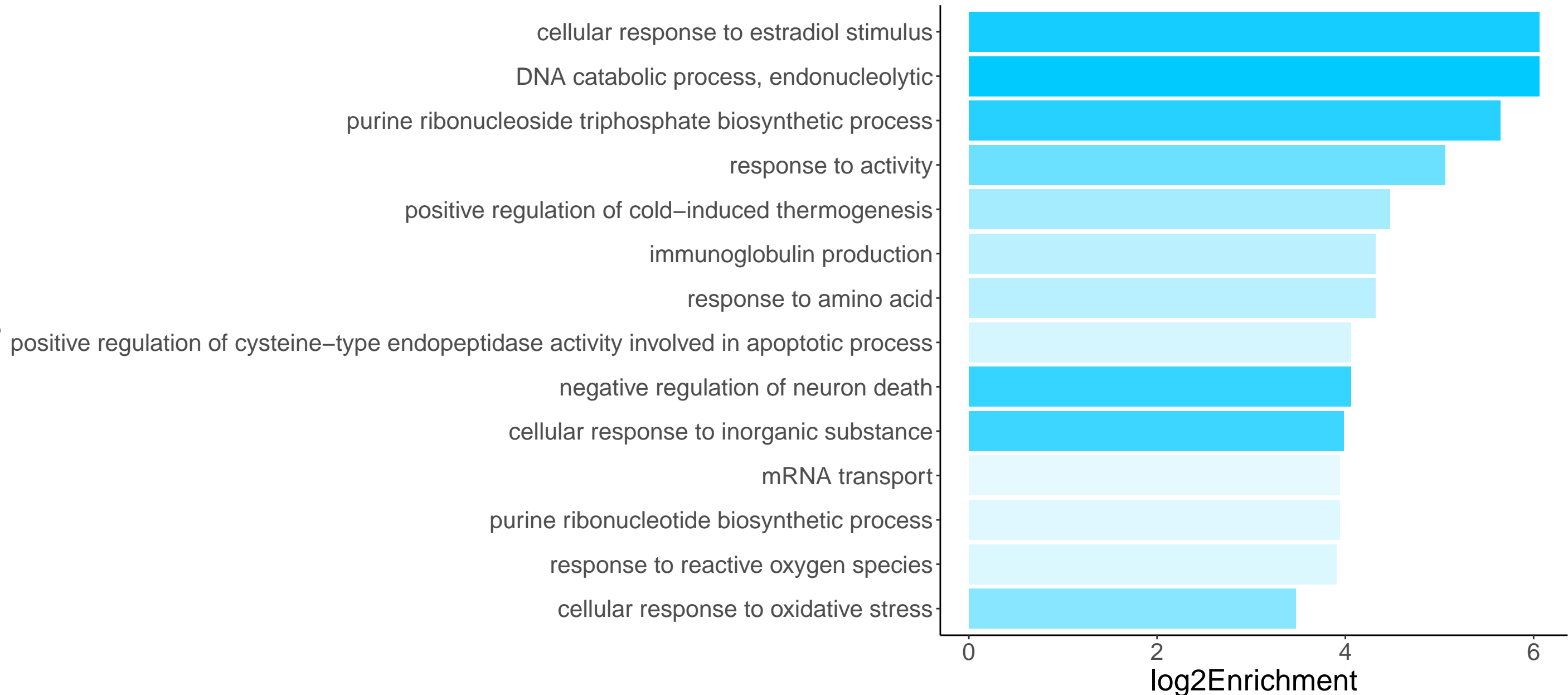
Re-clustered module 1.1.1 MF enrichment

Term



Re-clustered module 1.1.11 BP enrichment

Term



Re-clustered module 1.1.11 MF enrichment

Term

promoter-specific chromatin binding

chromatin DNA binding

single-stranded DNA binding

protein phosphatase binding

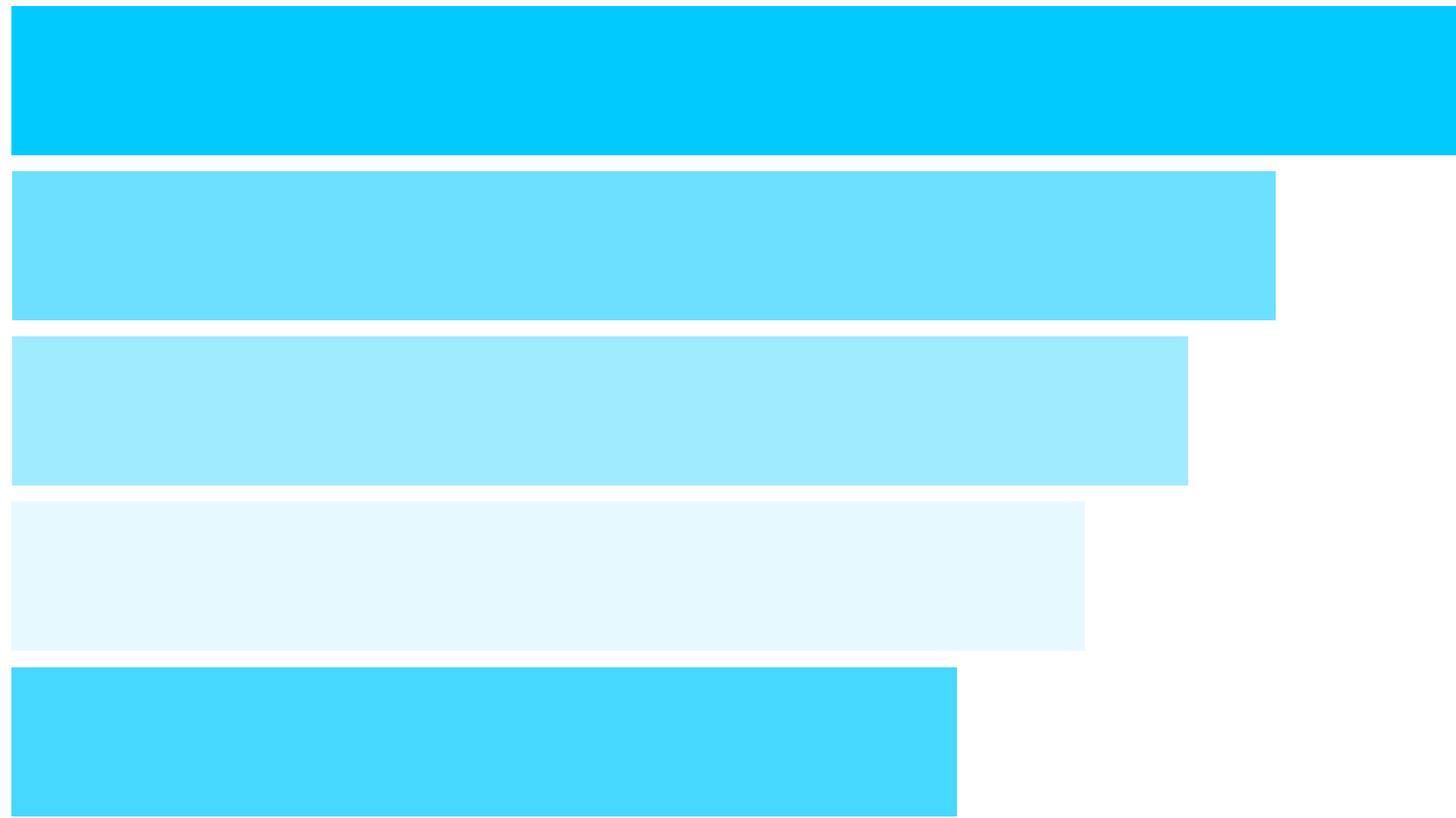
ubiquitin protein ligase binding

0

2

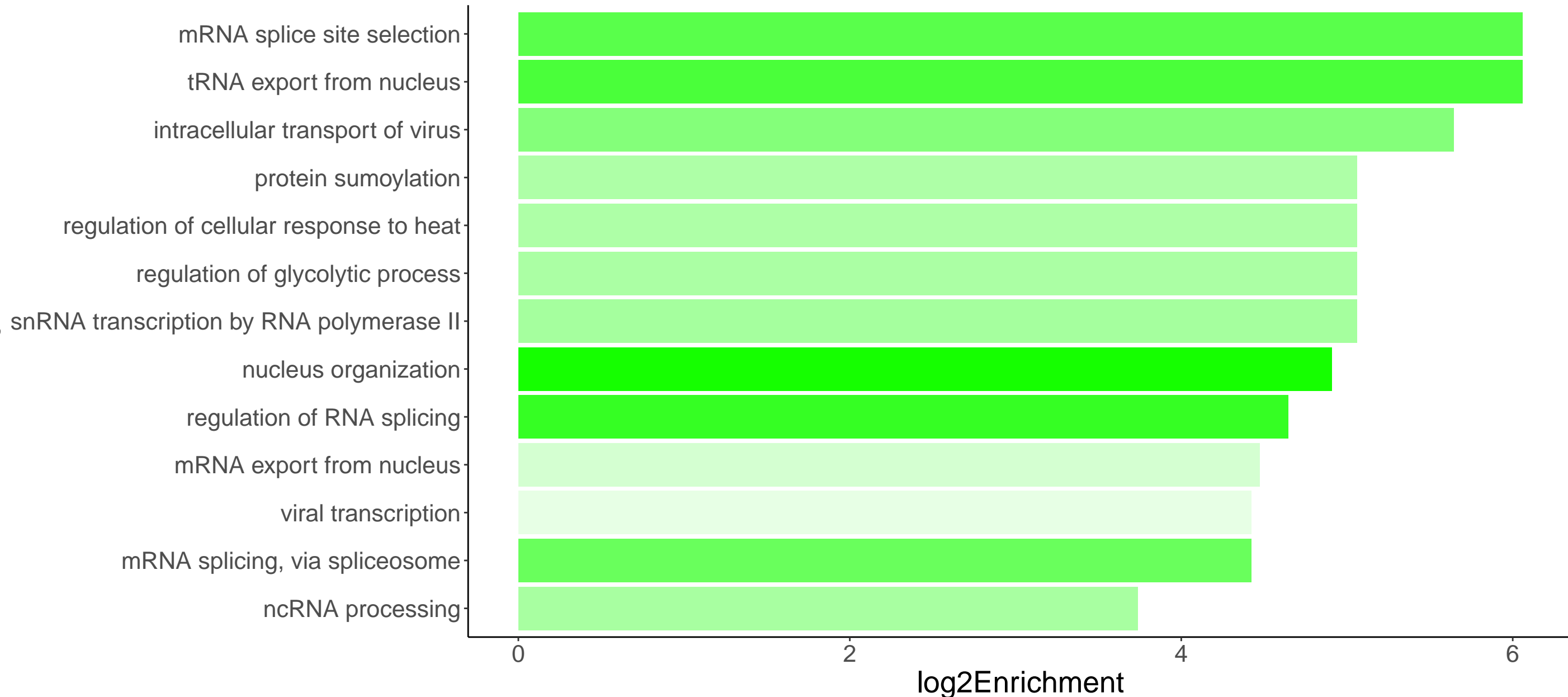
4

log2Enrichment



Re-clustered module 1.1.12 BP enrichment

Term



Re-clustered module 1.1.12 MF enrichment

Term

mRNA 3'-UTR binding

0

1

2

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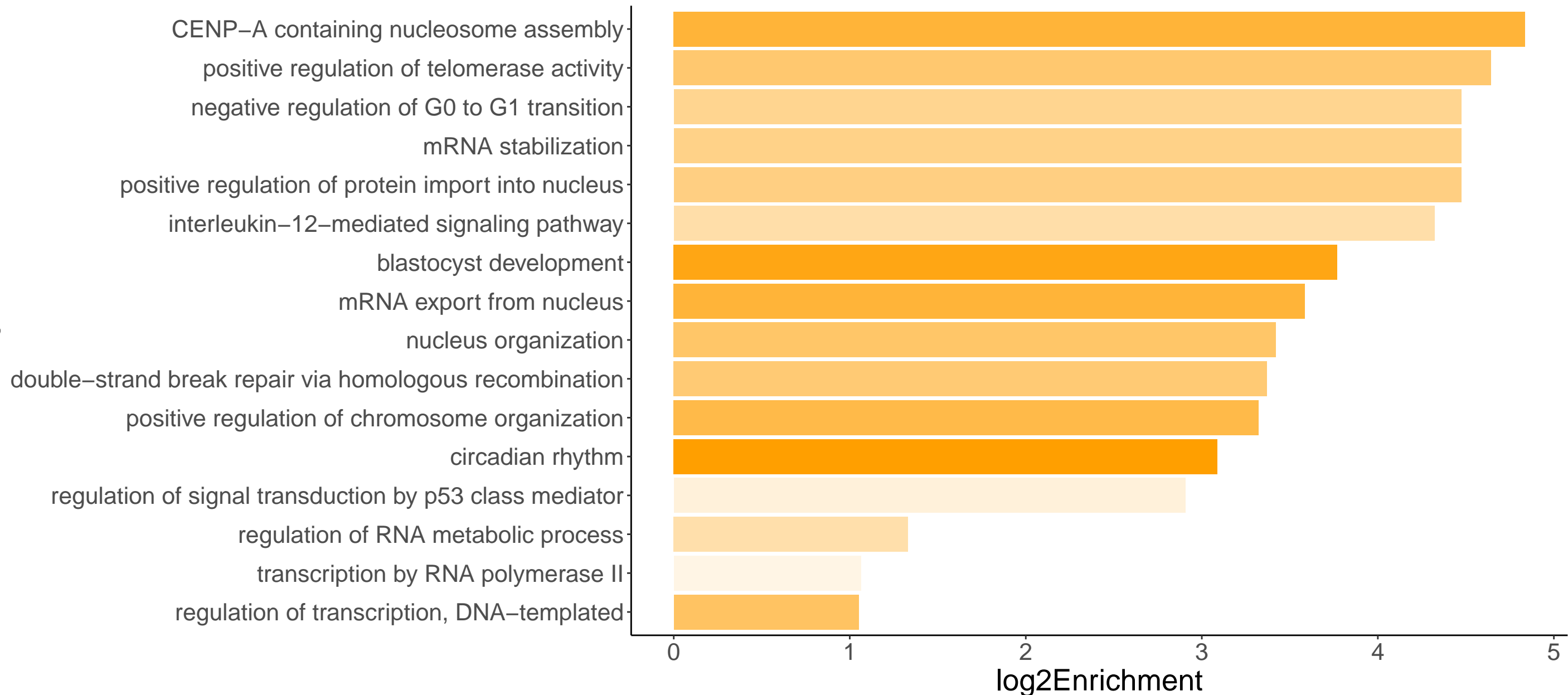
4

log2Enrichment



Re-clustered module 1.1.13 BP enrichment

Term



Re-clustered module 1.1.13 MF enrichment

Term

nuclear localization sequence binding

DNA secondary structure binding

miRNA binding

telomeric DNA binding

histone deacetylase binding

single-stranded DNA binding

double-stranded DNA binding

0

1

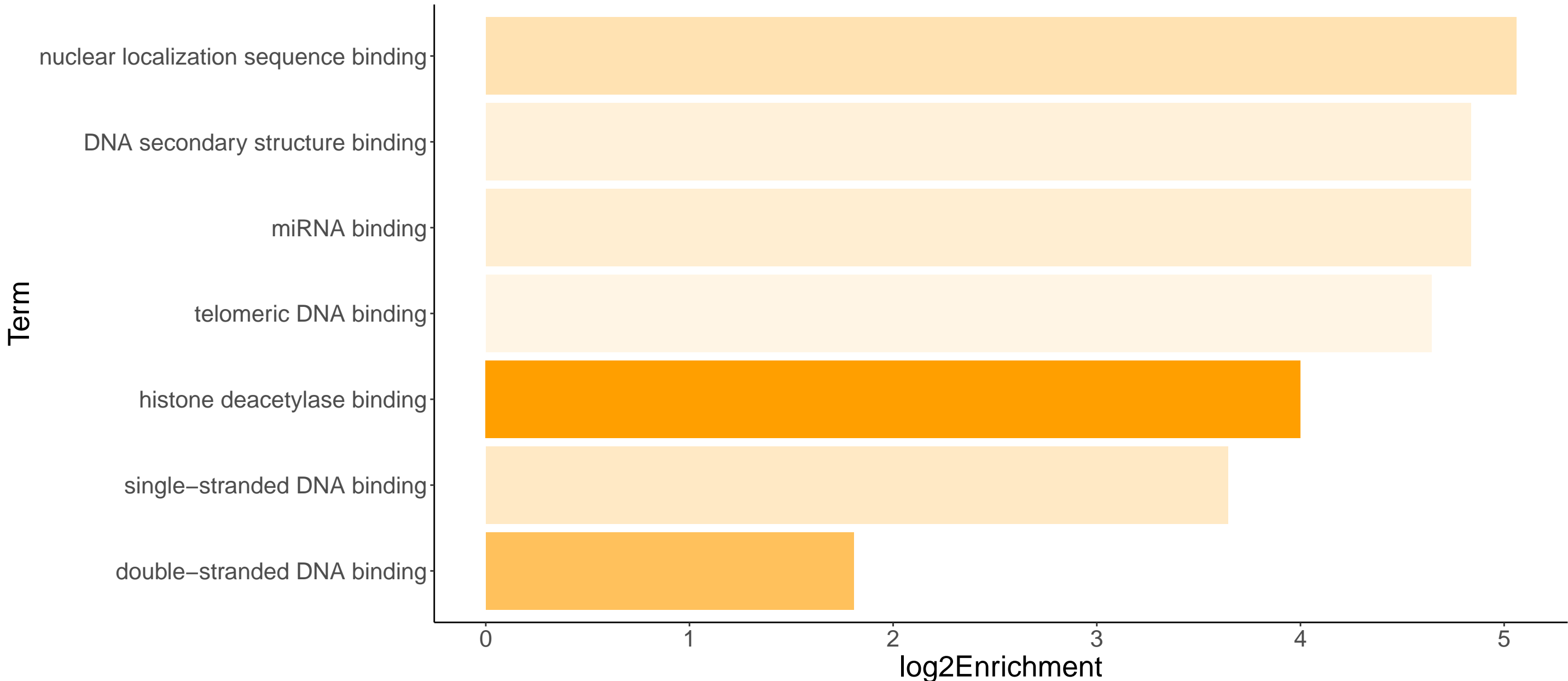
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log2Enrichment



Re-clustered module 1.1.14 BP enrichment

Term



Re-clustered module 1.1.14 MF enrichment

Term

core promoter sequence-specific DNA binding

nucleosome binding

activating transcription factor binding

single-stranded DNA binding

transcription coregulator activity

0

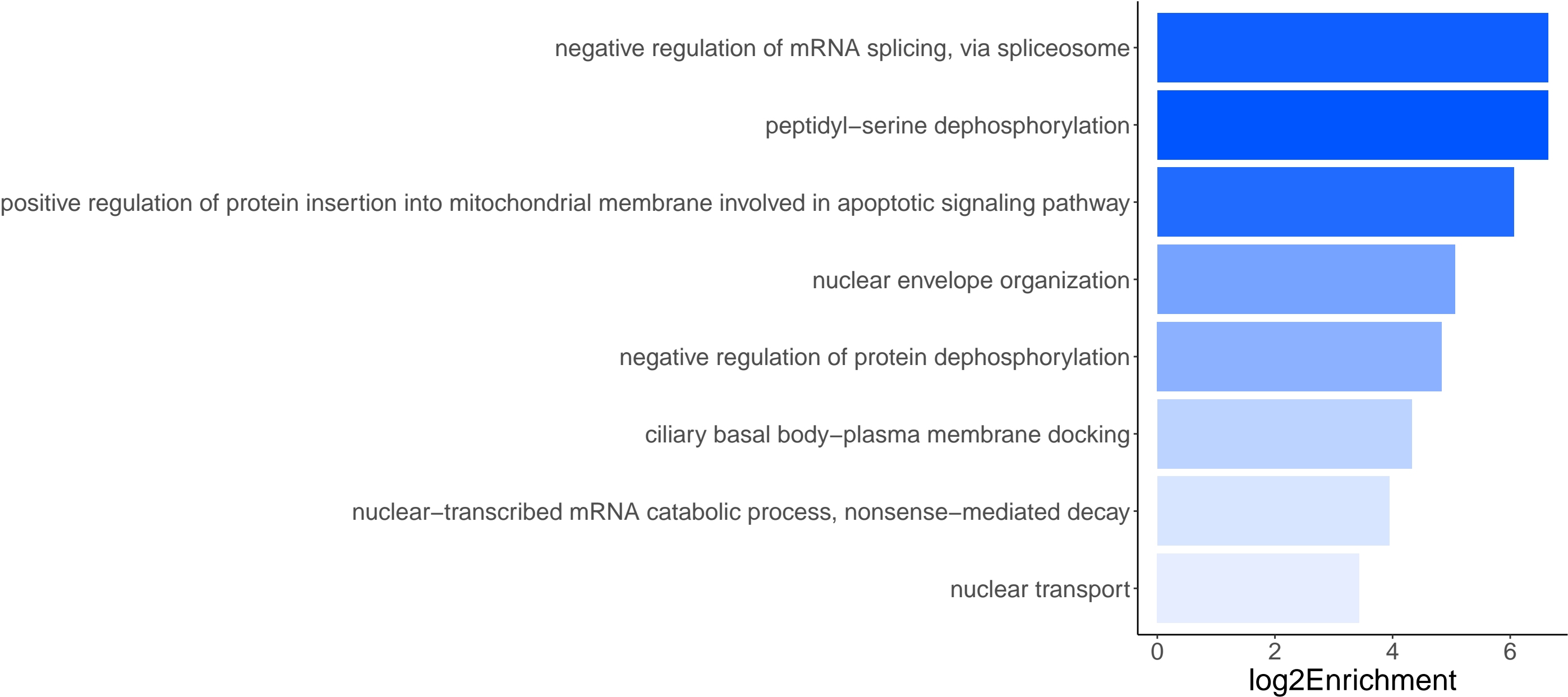
2

4

log2Enrichment



Term



Re-clustered module 1.1.15 MF enrichment

Term

protein serine/threonine phosphatase activity

protein N-terminus binding

protein heterodimerization activity

protein domain specific binding

0

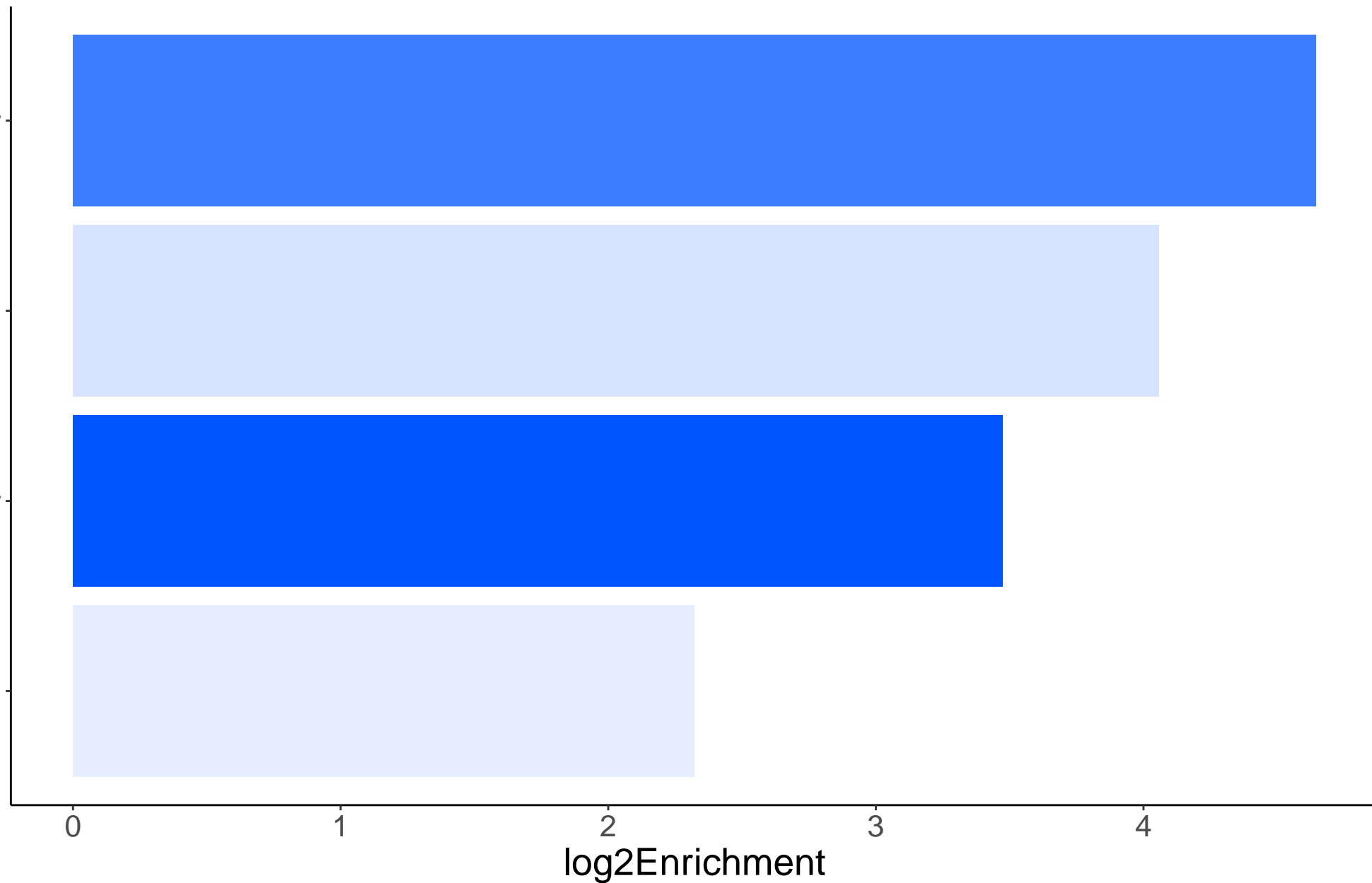
1

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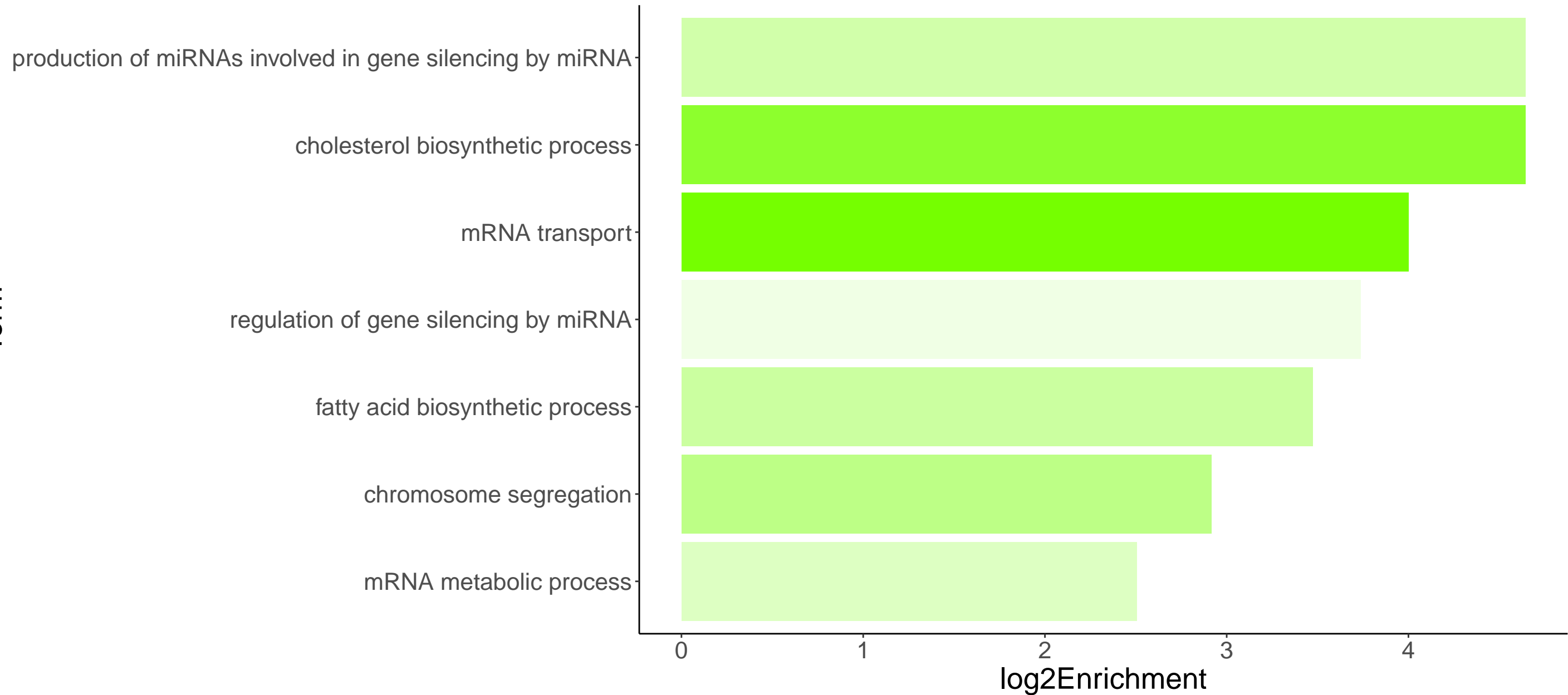
4

log2Enrichment



Re-clustered module 1.1.2 BP enrichment

Term



Re-clustered module 1.1.2 MF enrichment

Term

log2Enrichment



Re-clustered module 1.1.3 BP enrichment

Term

RNA phosphodiester bond hydrolysis, exonucleolytic

regulation of alternative mRNA splicing, via spliceosome

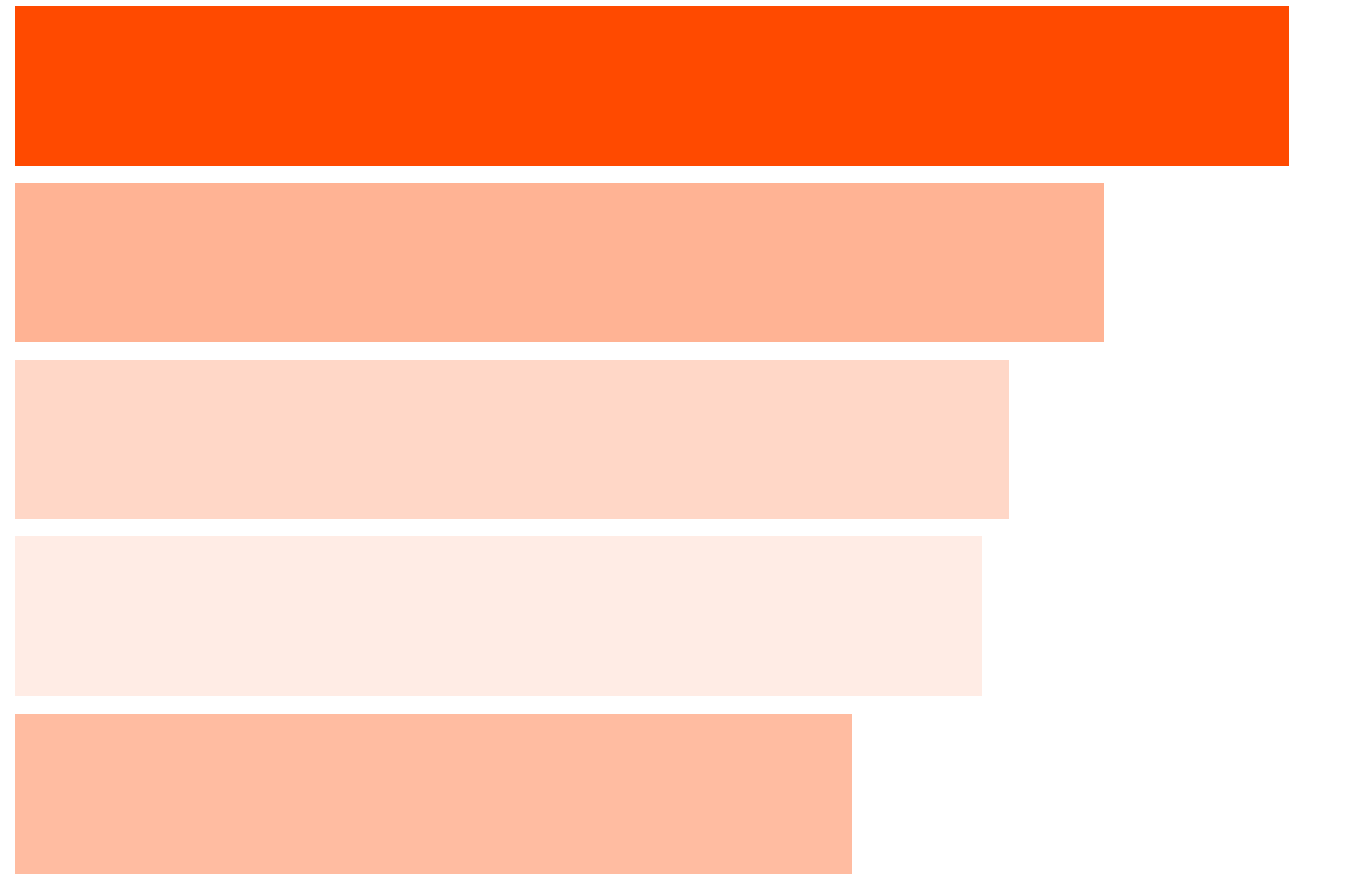
chromosome separation

excitatory postsynaptic potential

mRNA splicing, via spliceosome

0 1 2 3 4 5

log2Enrichment



Re-clustered module 1.1.3 MF enrichment

Term

poly(U) RNA binding

3'-5'-exoribonuclease activity

snRNA binding

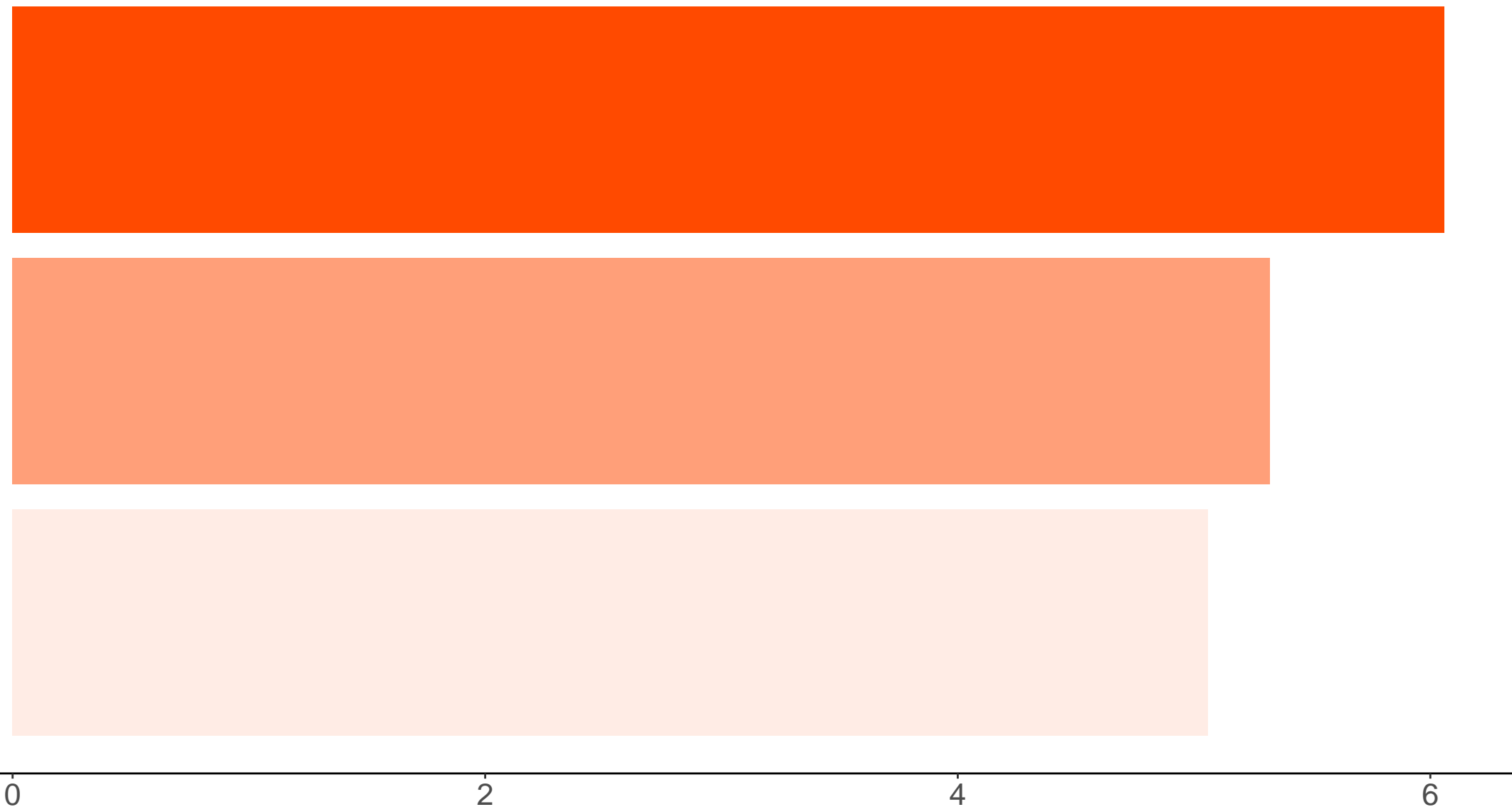
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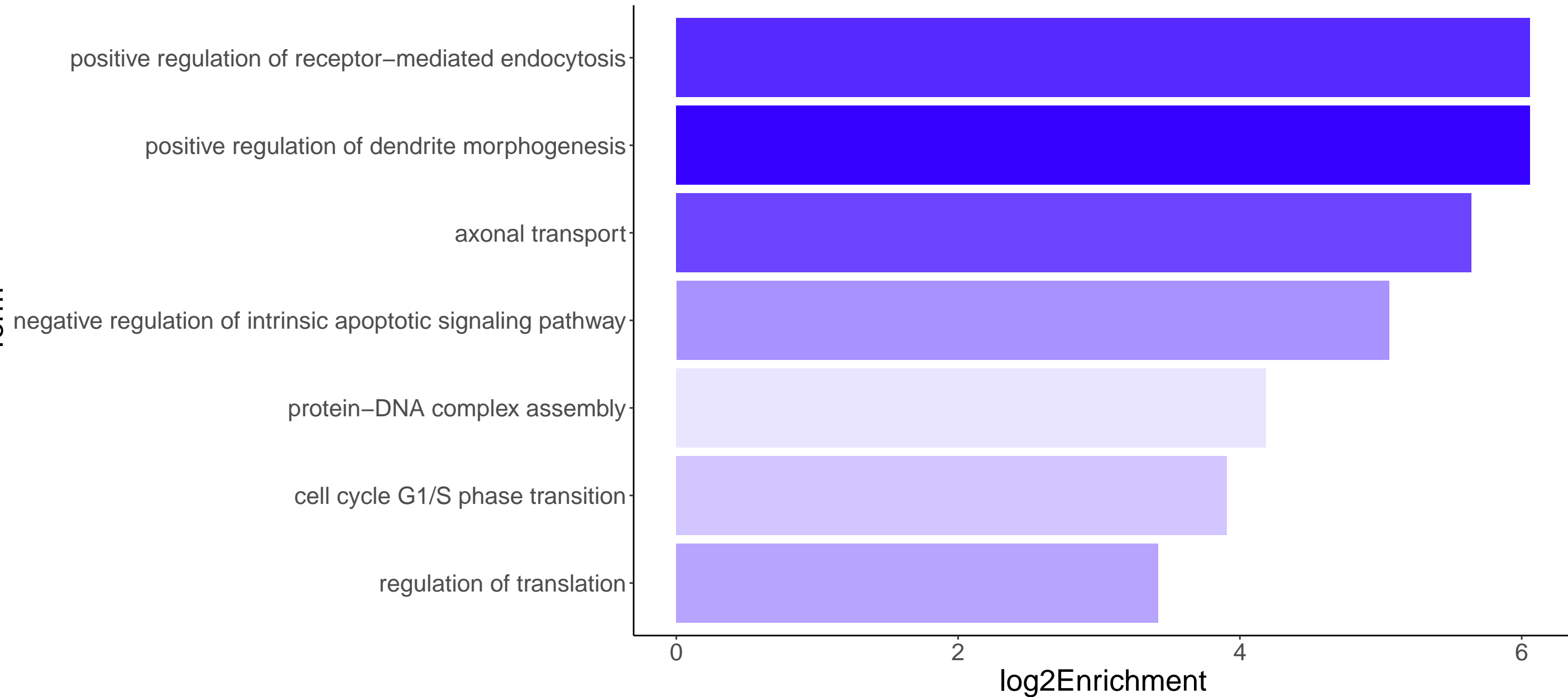
6

log2Enrichment



Re-clustered module 1.1.4 BP enrichment

Term



Re-clustered module 1.1.4 MF enrichment

Term

translation factor activity, RNA binding

cysteine-type endopeptidase activity

GTPase activity

magnesium ion binding

GTP binding

0

1

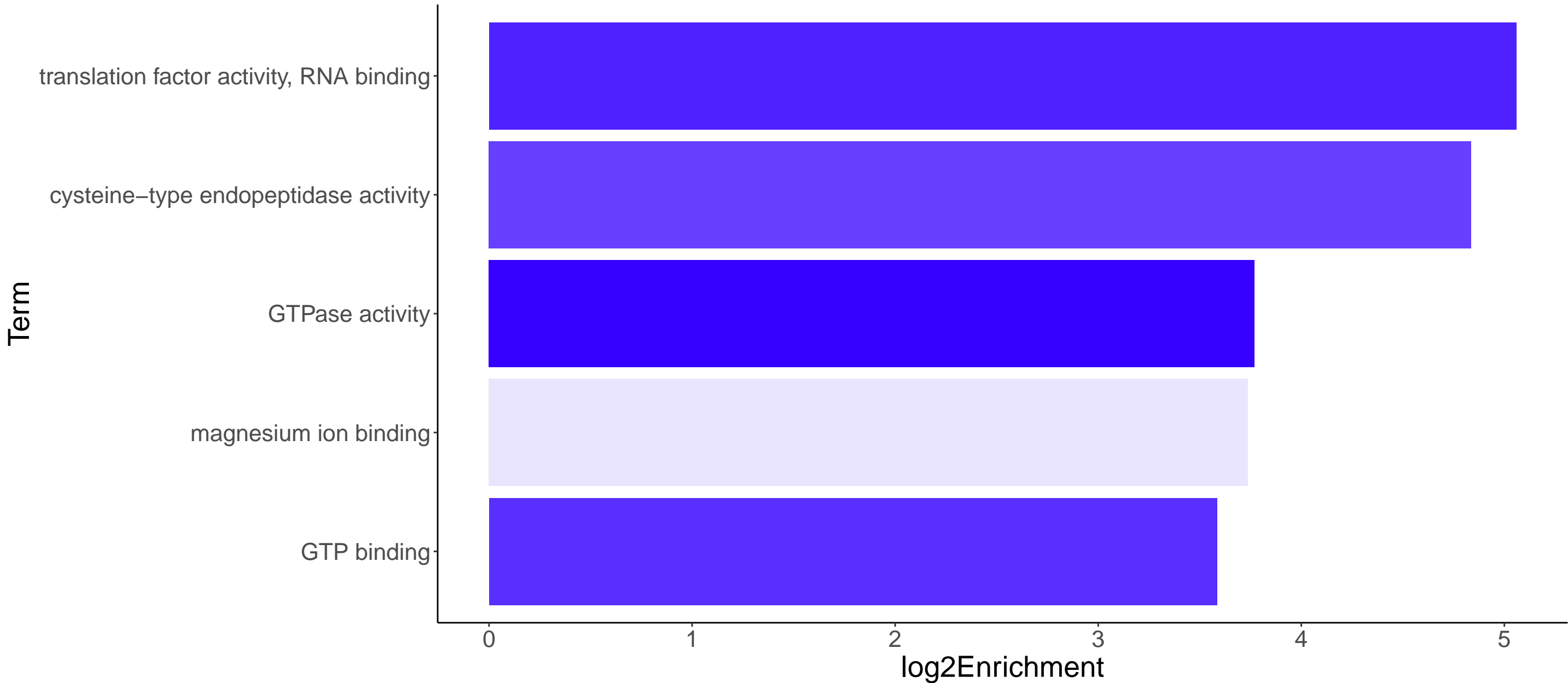
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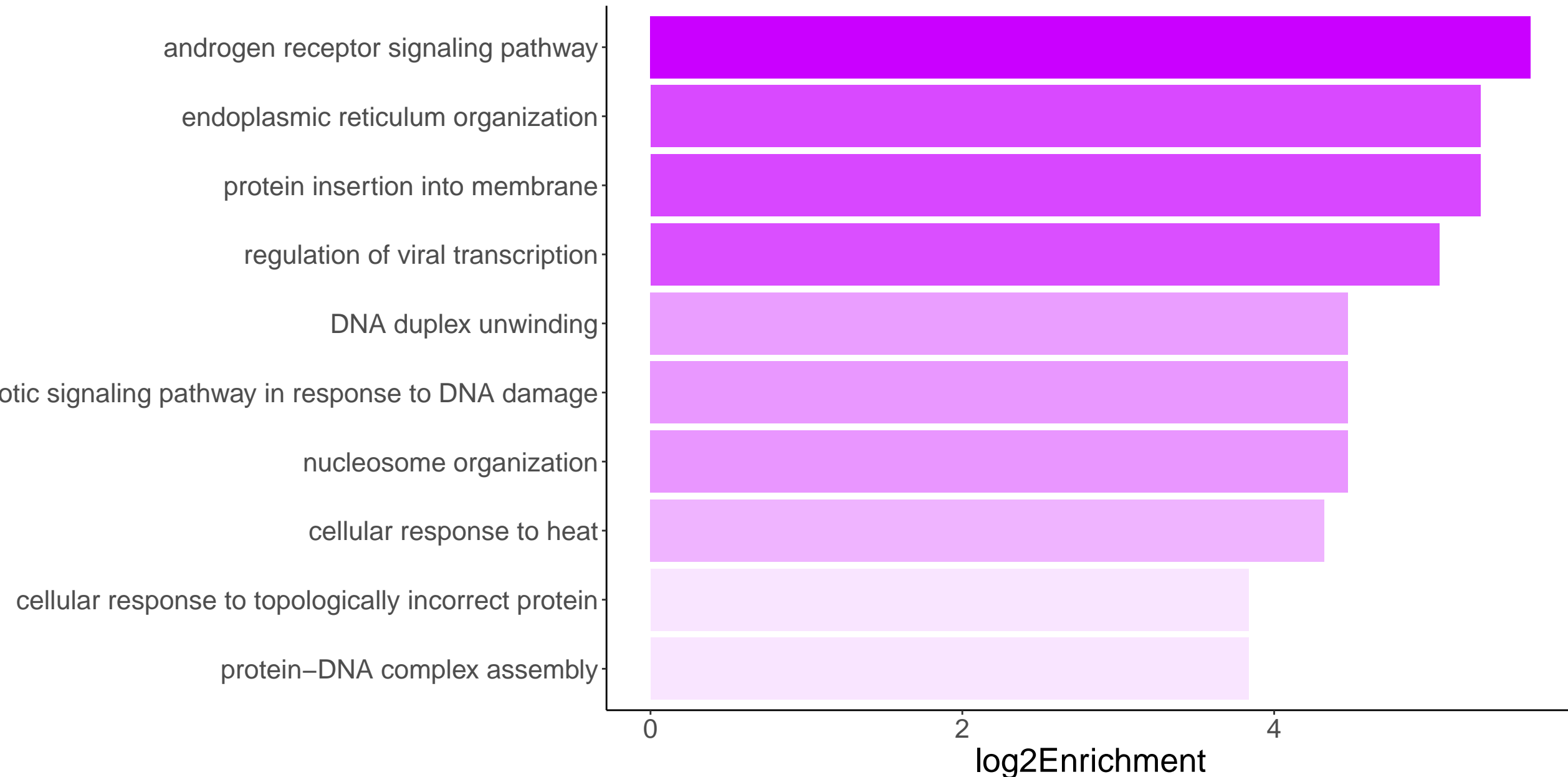
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log2Enrichment



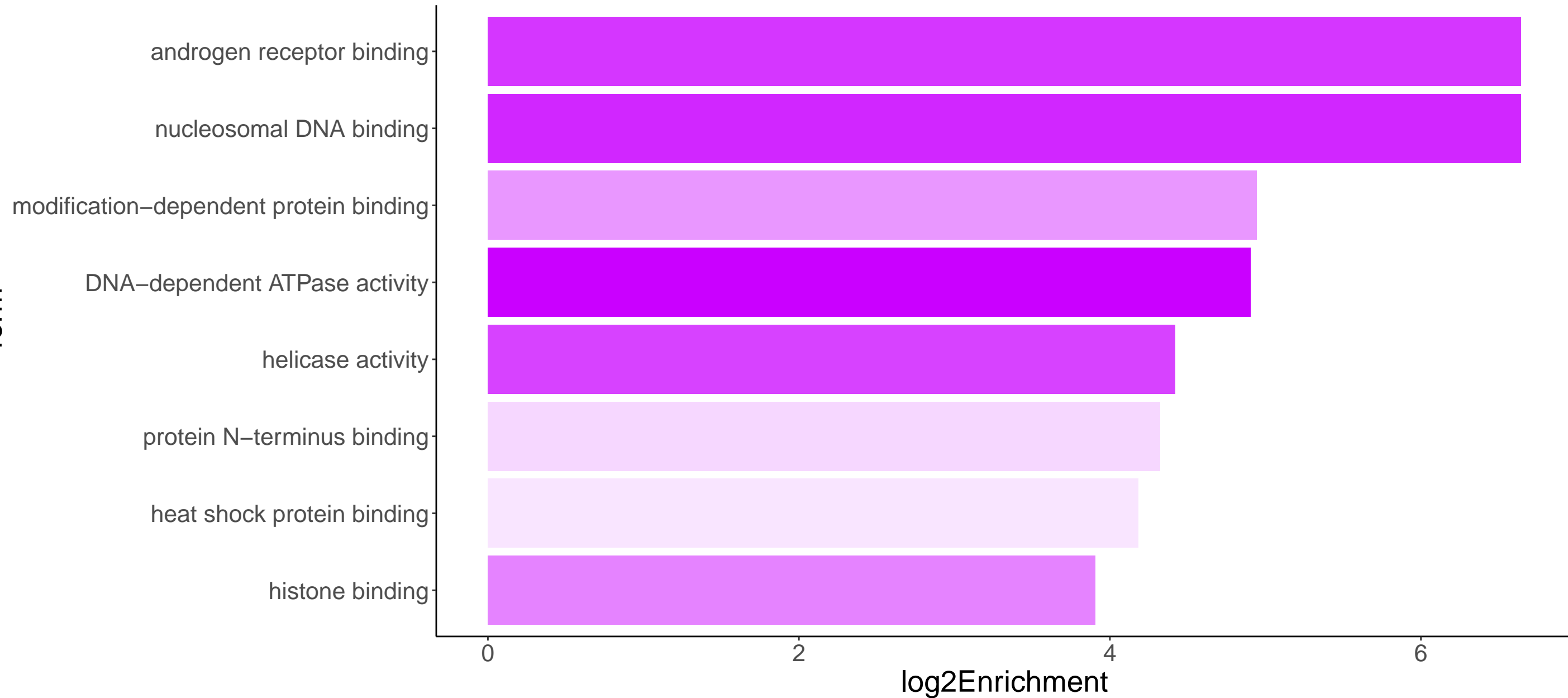
Re-clustered module 1.1.5 BP enrichment

Term



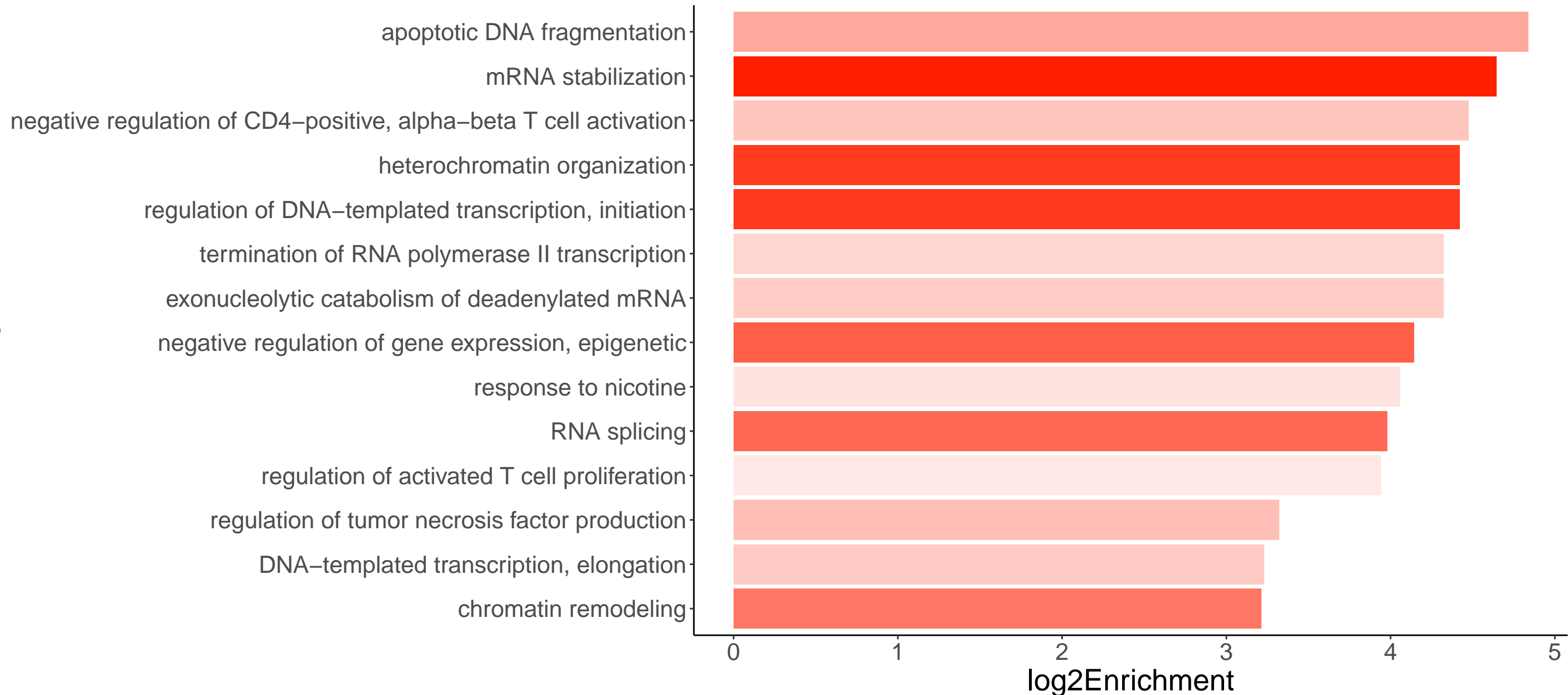
Re-clustered module 1.1.5 MF enrichment

Term



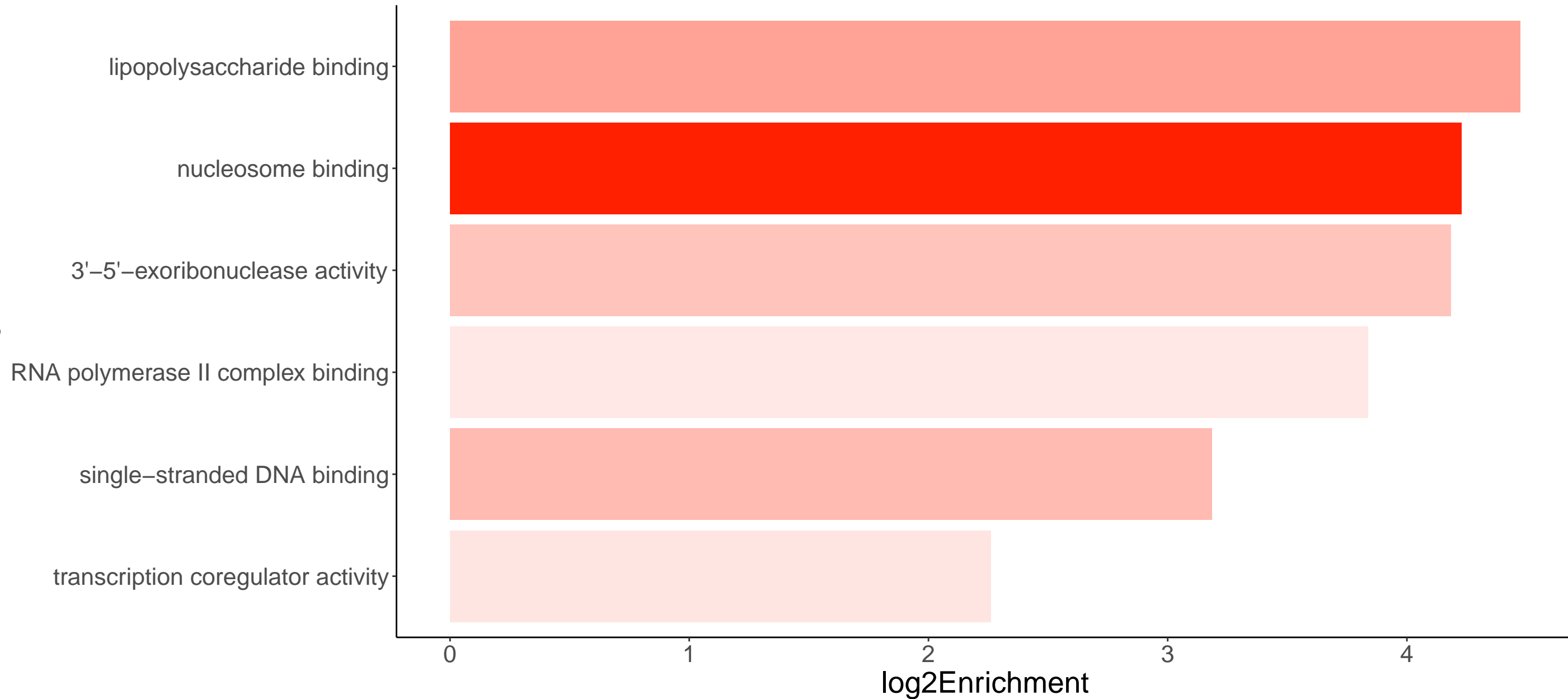
Re-clustered module 1.1.6 BP enrichment

Term



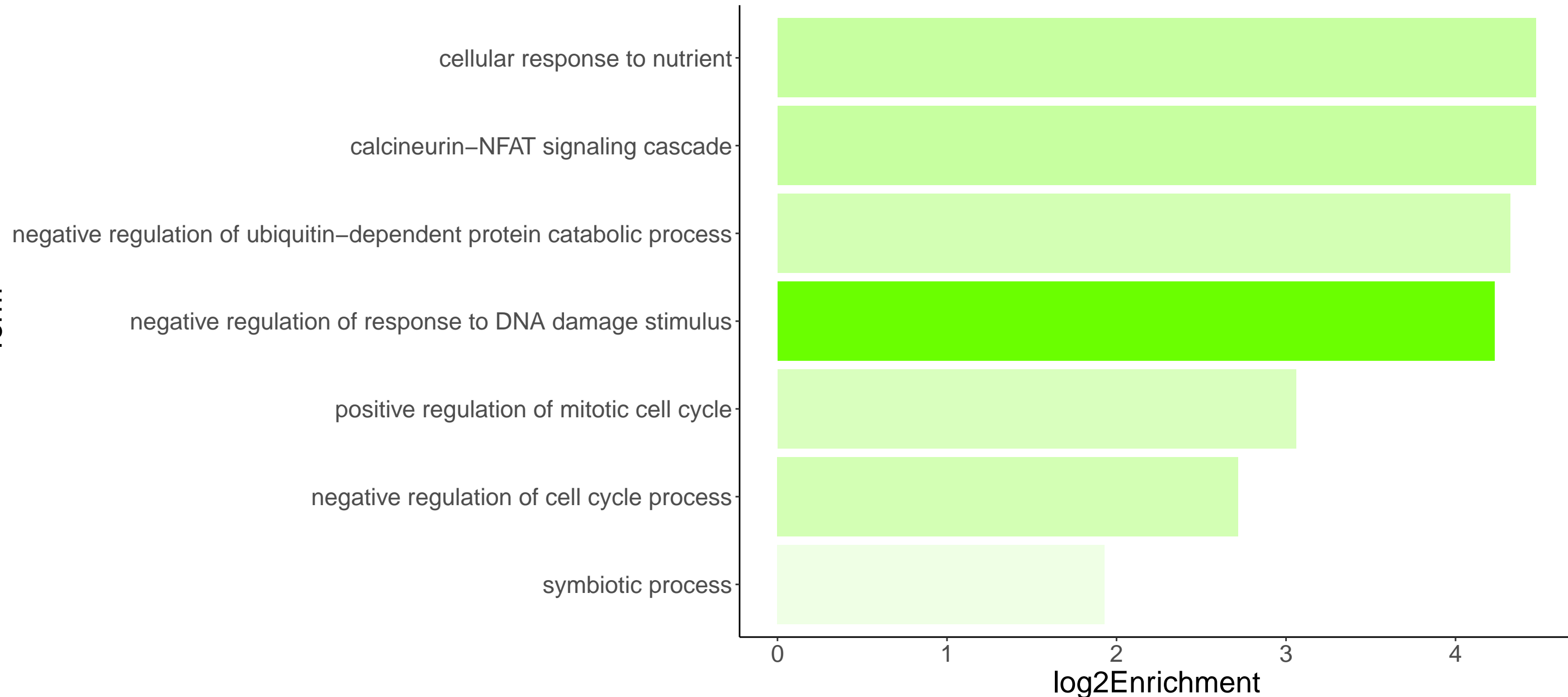
Re-clustered module 1.1.6 MF enrichment

Term



Re-clustered module 1.1.7 BP enrichment

Term



Re-clustered module 1.1.7 MF enrichment

Term

telomeric DNA binding

RNA polymerase II complex binding

0

1

2

3

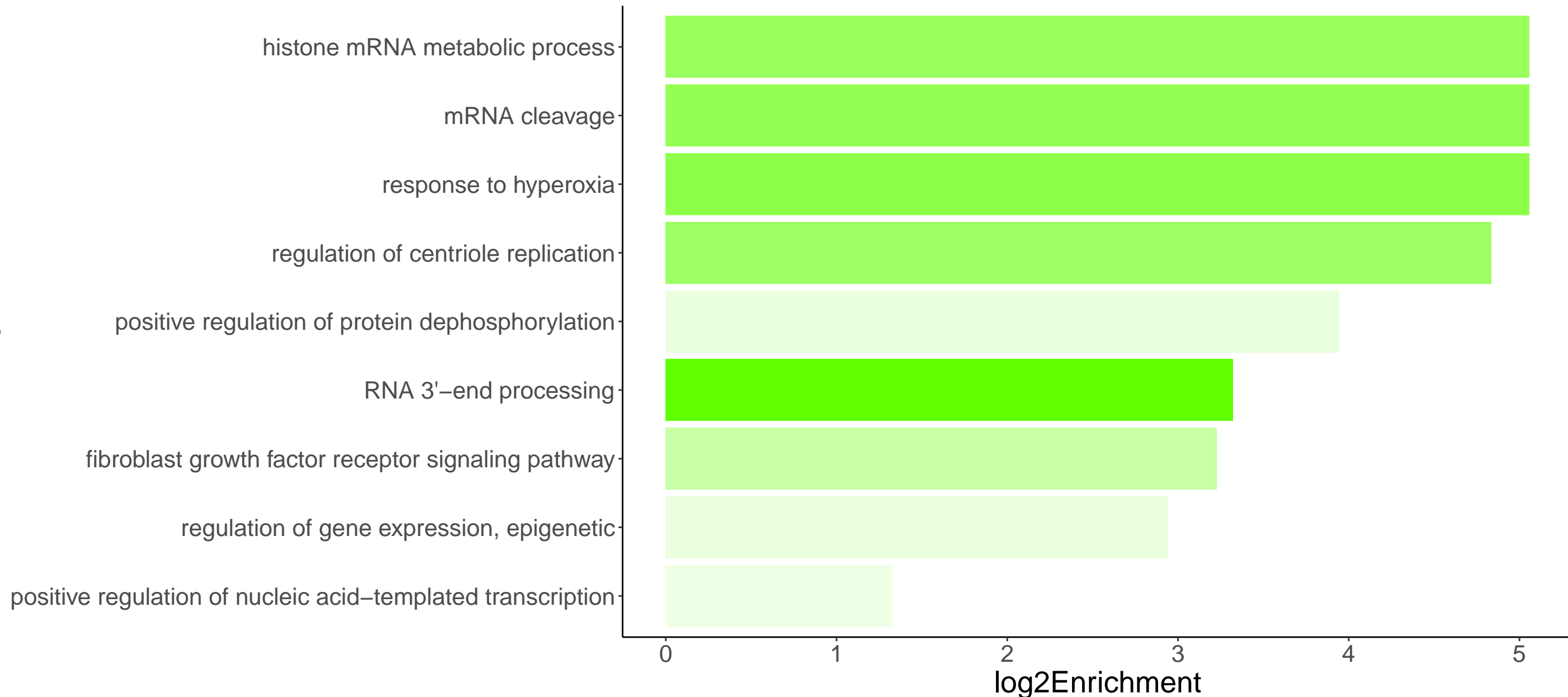
4

log2Enrichment



Re-clustered module 1.1.8 BP enrichment

Term



Re-clustered module 1.1.8 MF enrichment

Term

transcription coactivator activity

0

1

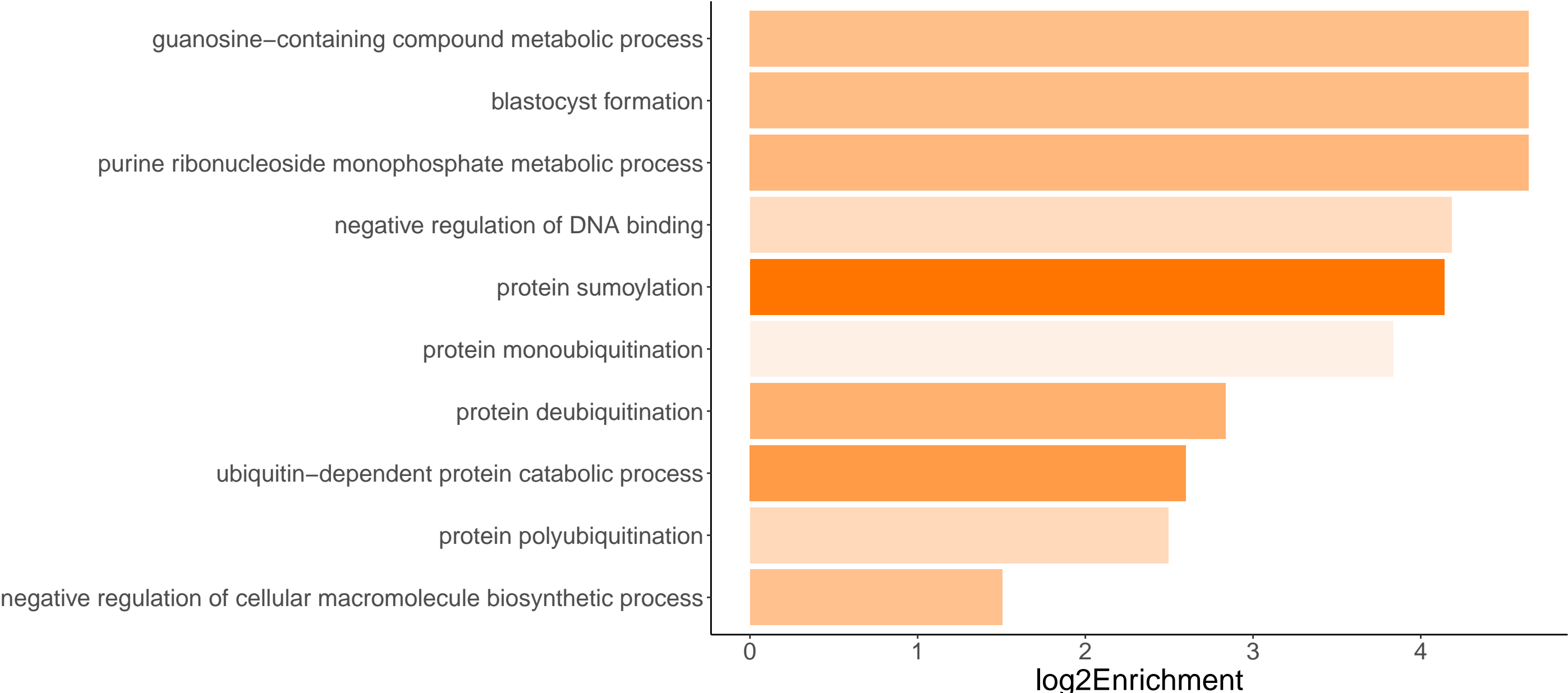
2

log2Enrichment



Re-clustered module 1.1.9 BP enrichment

Term



Re-clustered module 1.1.9 MF enrichment

Term

nucleosome binding

pre-mRNA binding

ribonucleoprotein complex binding

0

1

2

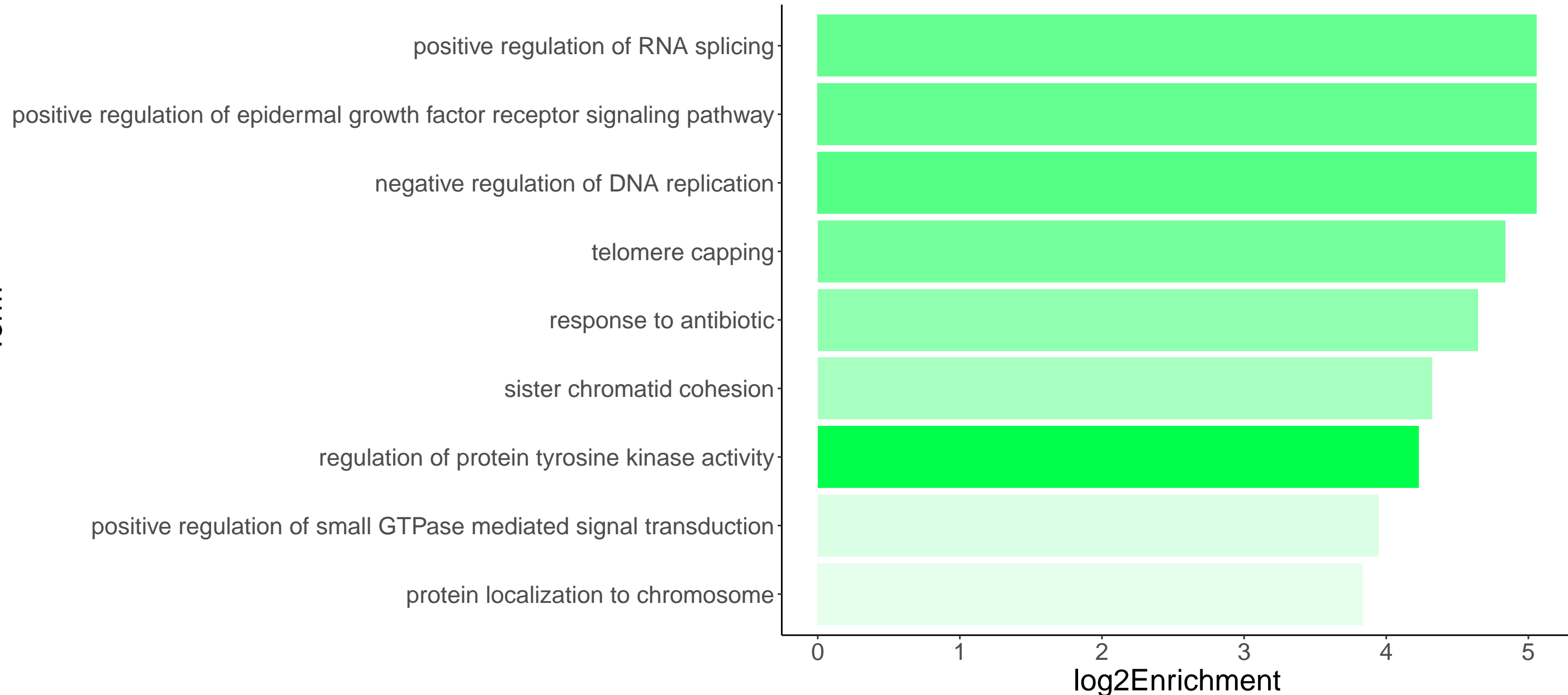
3

4

log2Enrichment



Re-clustered module 1.10.1 BP enrichment



Re-clustered module 1.10.1 MF enrichment

Term

tau-protein kinase activity

SH3 domain binding

0

2

4

log2Enrichment



Re-clustered module 1.10.10 BP enrichment

Term

centriole replication

positive regulation of mRNA catabolic process

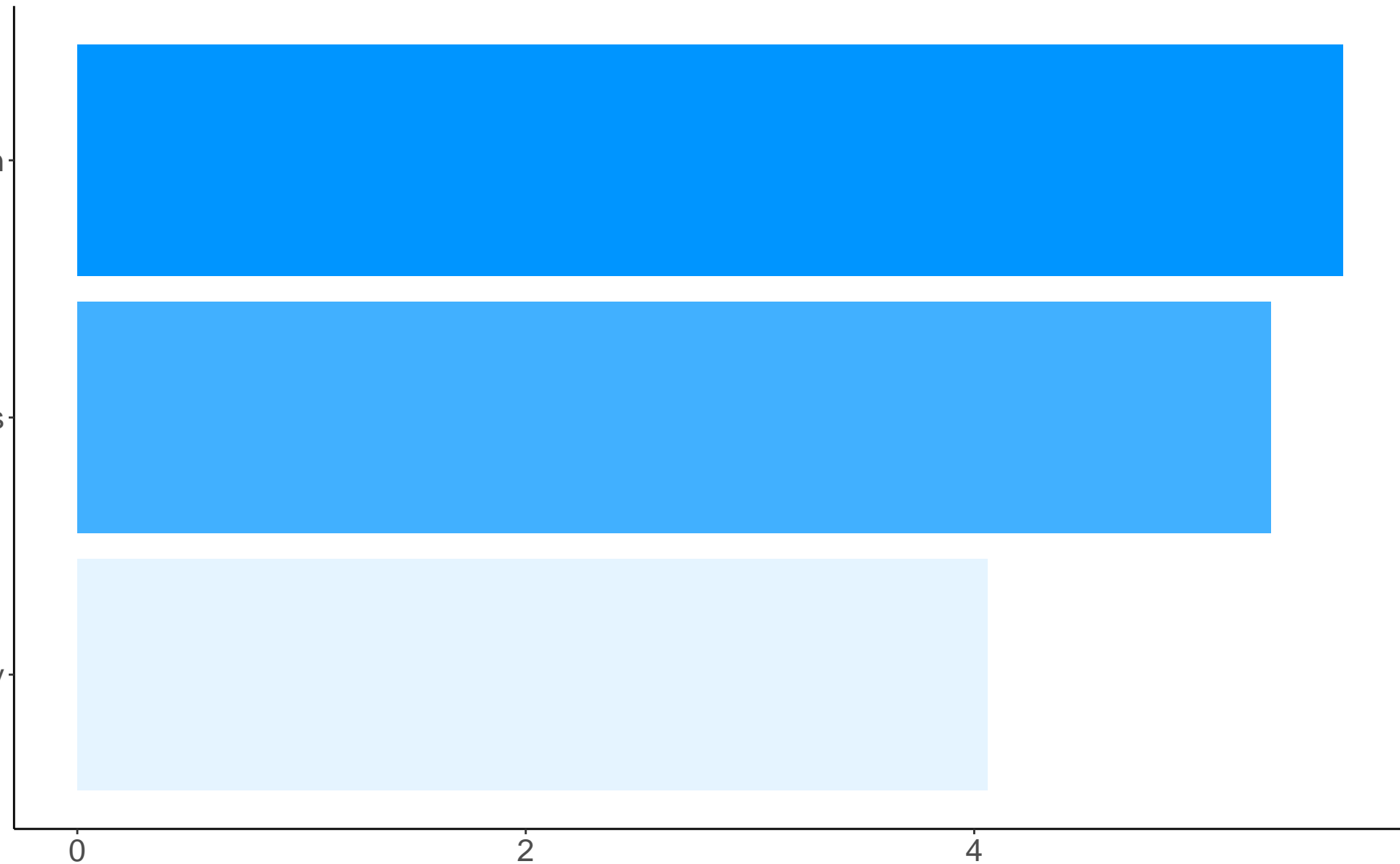
spindle assembly

0

2

4

log2Enrichment



Re-clustered module 1.10.10 MF enrichment

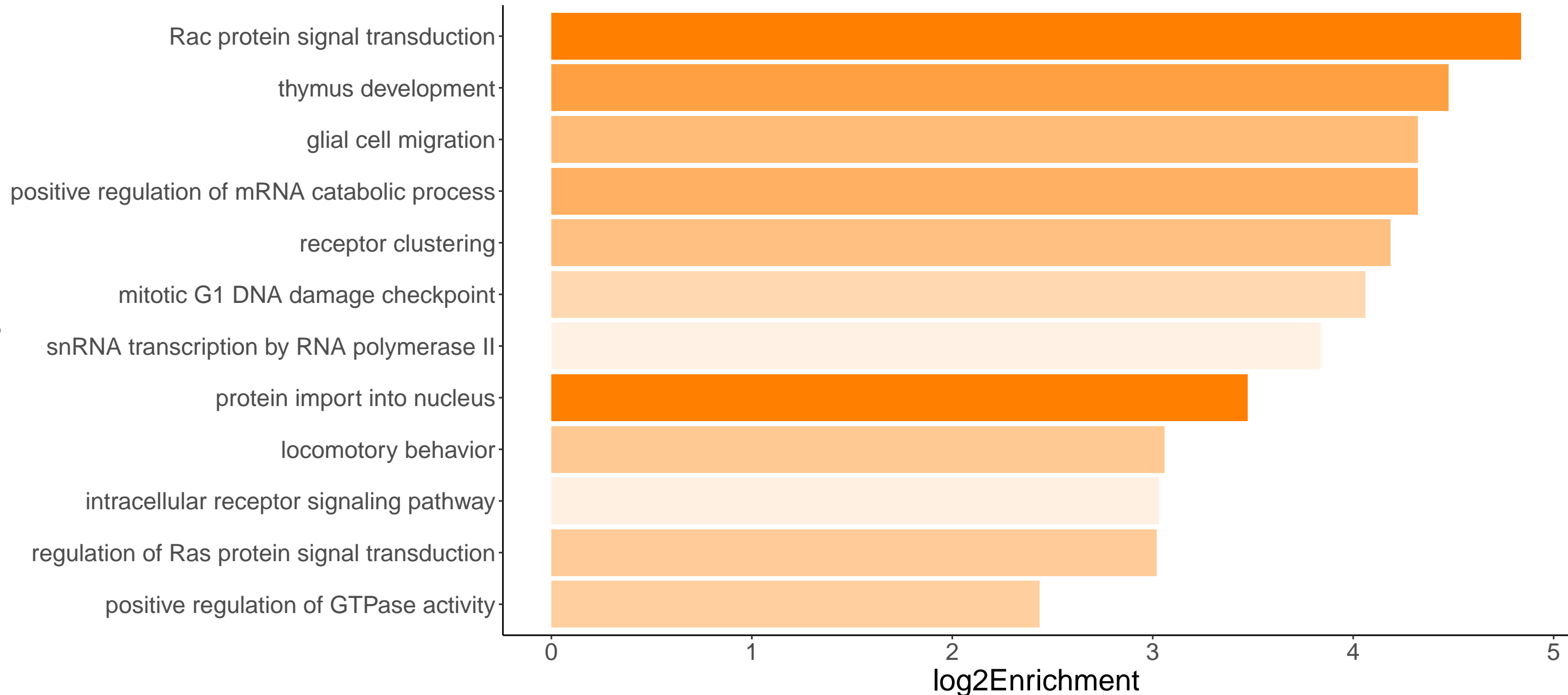
Term

log2Enrichment



Re-clustered module 1.10.11 BP enrichment

Term



Re-clustered module 1.10.11 MF enrichment

Term

RNA polymerase II complex binding

ubiquitin protein ligase activity

cadherin binding

protein domain specific binding

0

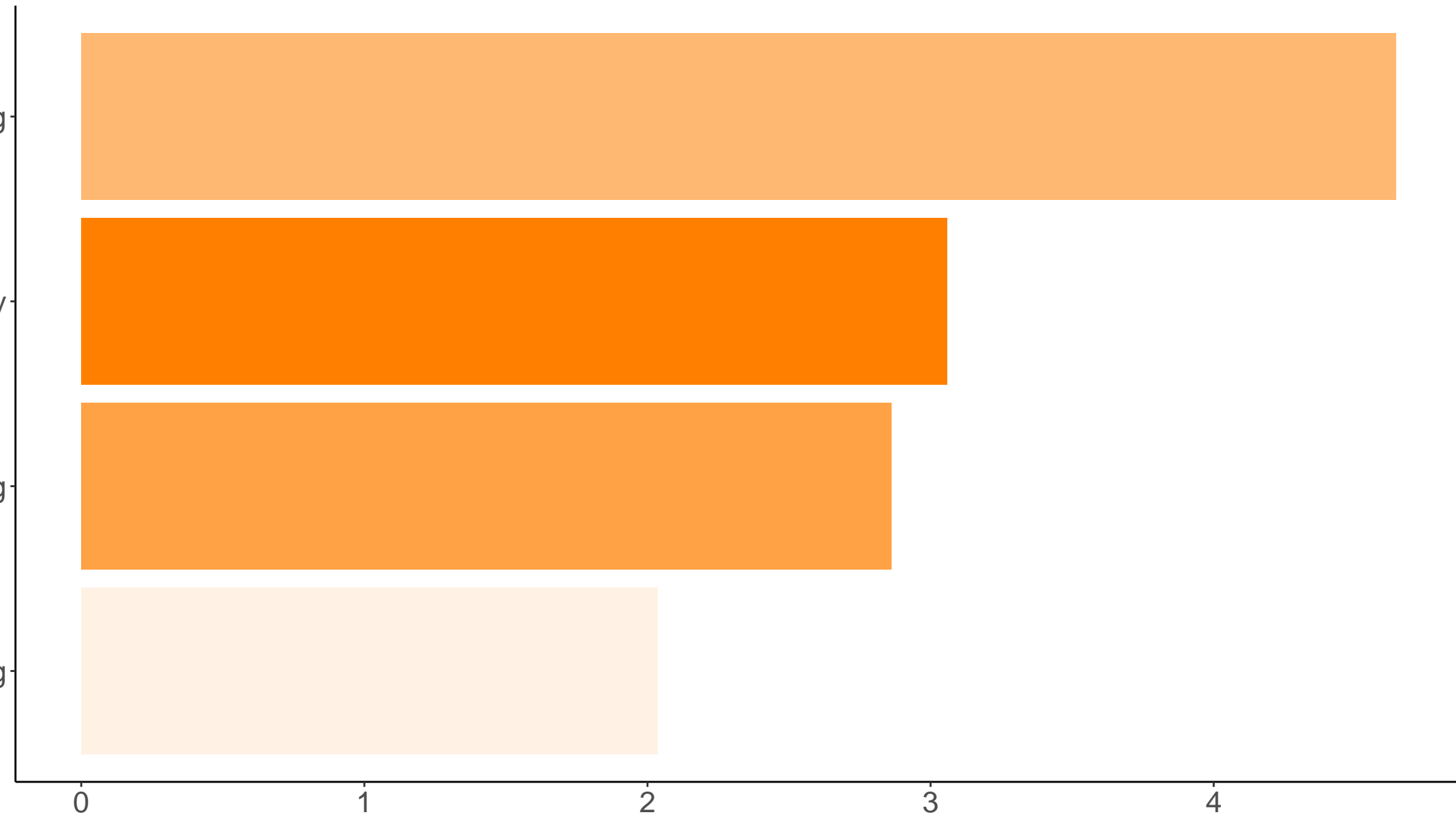
1

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log2Enrichment



Re-clustered module 1.10.12 BP enrichment

Term

insulin receptor signaling pathway

protein deubiquitination

0

1

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3

4

log2Enrichment



Re-clustered module 1.10.12 MF enrichment

Term

log2Enrichment



Re-clustered module 1.10.13 BP enrichment

Term

sterol transport

0

1

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3

4

log2Enrichment



Re-clustered module 1.10.13 MF enrichment

Term

log2Enrichment



Re-clustered module 1.10.14 BP enrichment

Term

log2Enrichment



Re-clustered module 1.10.14 MF enrichment

Term

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

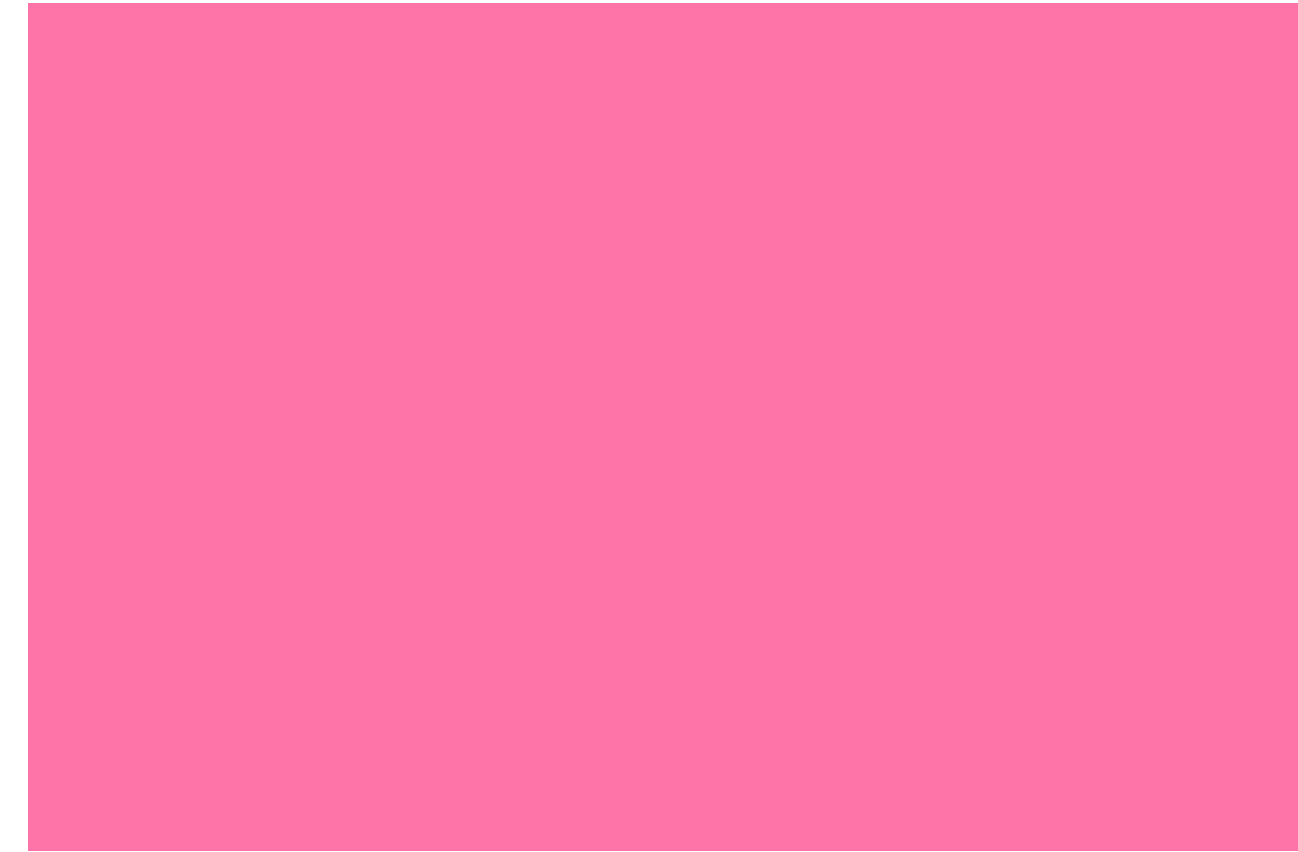
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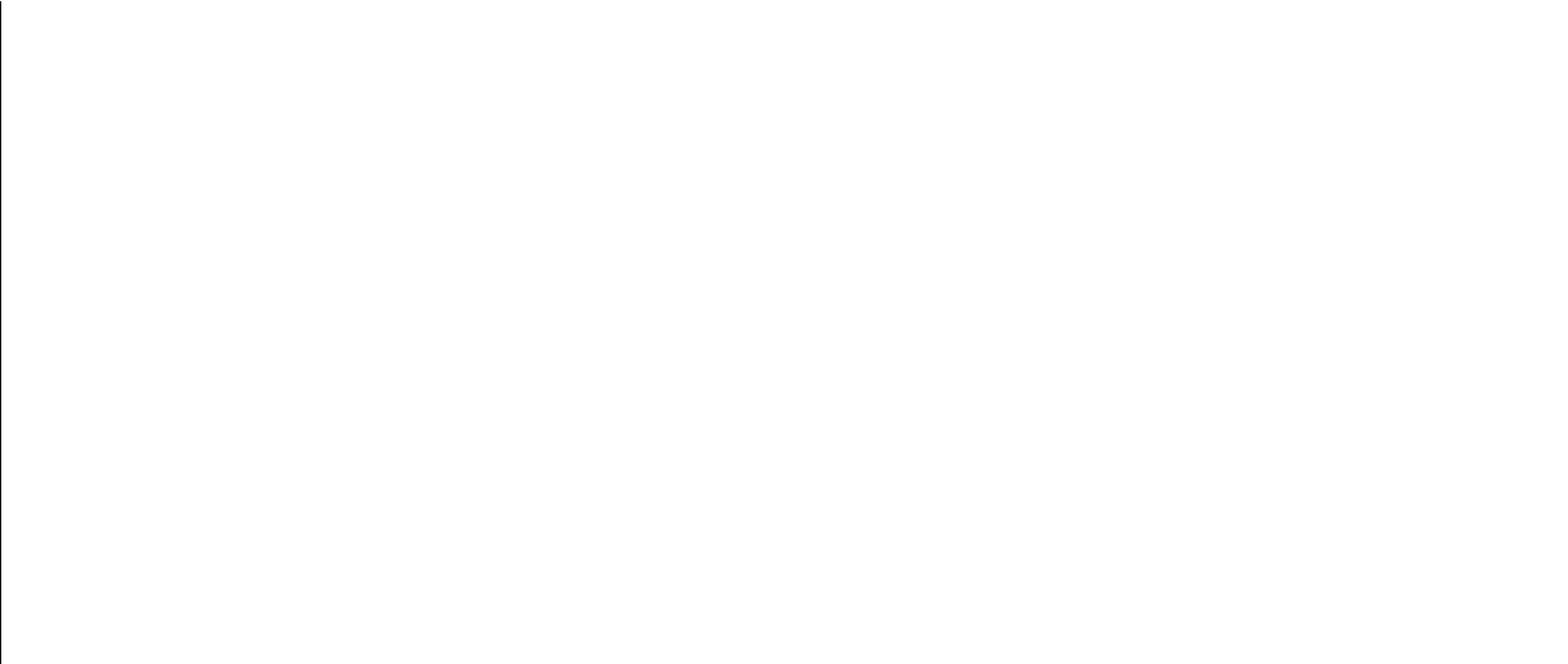
log2Enrichment



Re-clustered module 1.10.15 BP enrichment

Term

log2Enrichment



Re-clustered module 1.10.15 MF enrichment

Term

log2Enrichment



Re-clustered module 1.10.16 BP enrichment

Term

regulation of androgen receptor signaling pathway

negative regulation of intracellular steroid hormone receptor signaling pathway

transcription by RNA polymerase II

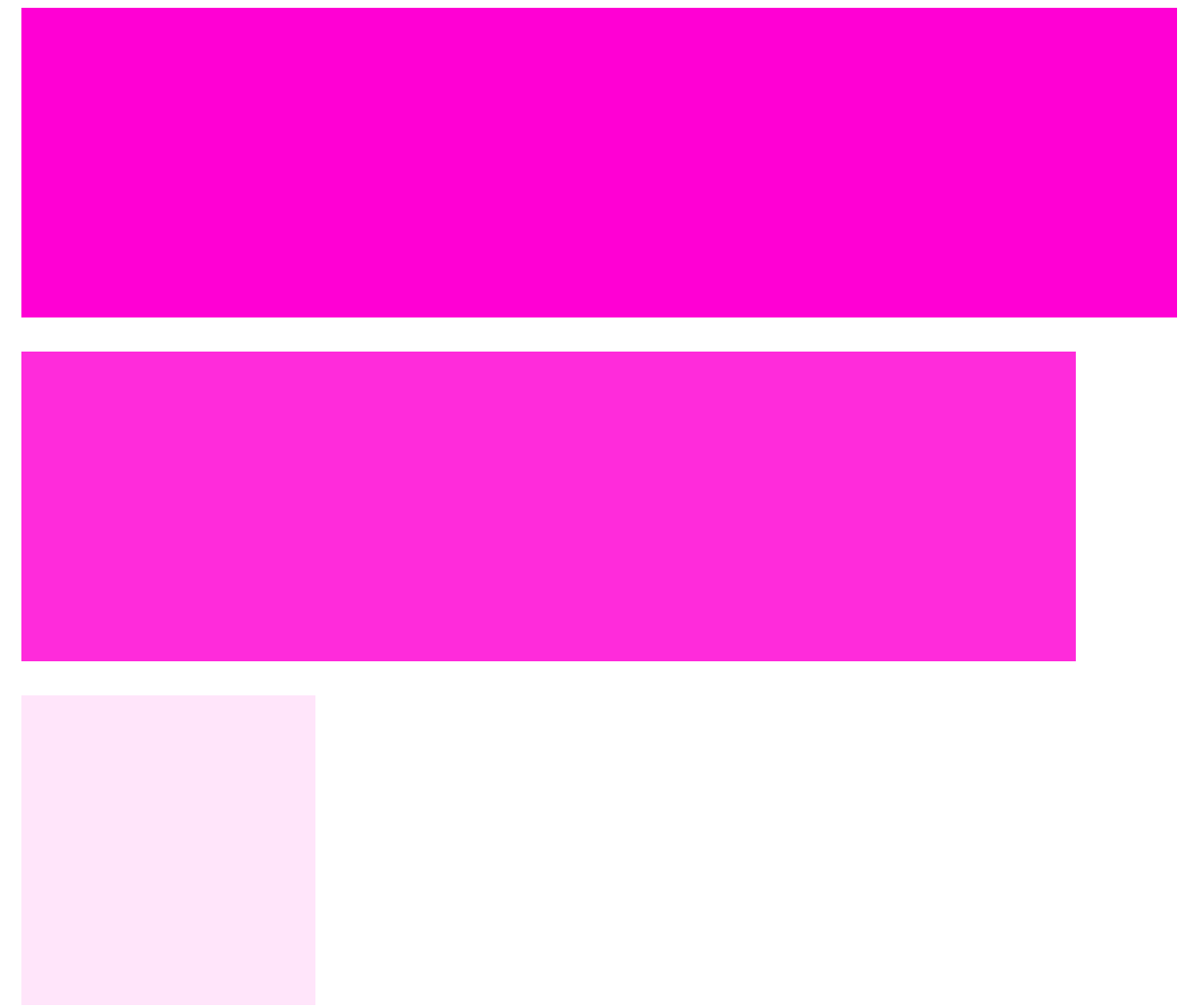
0

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log2Enrichment



Re-clustered module 1.10.16 MF enrichment

Term

histone deacetylase binding

transcription coregulator activity

0

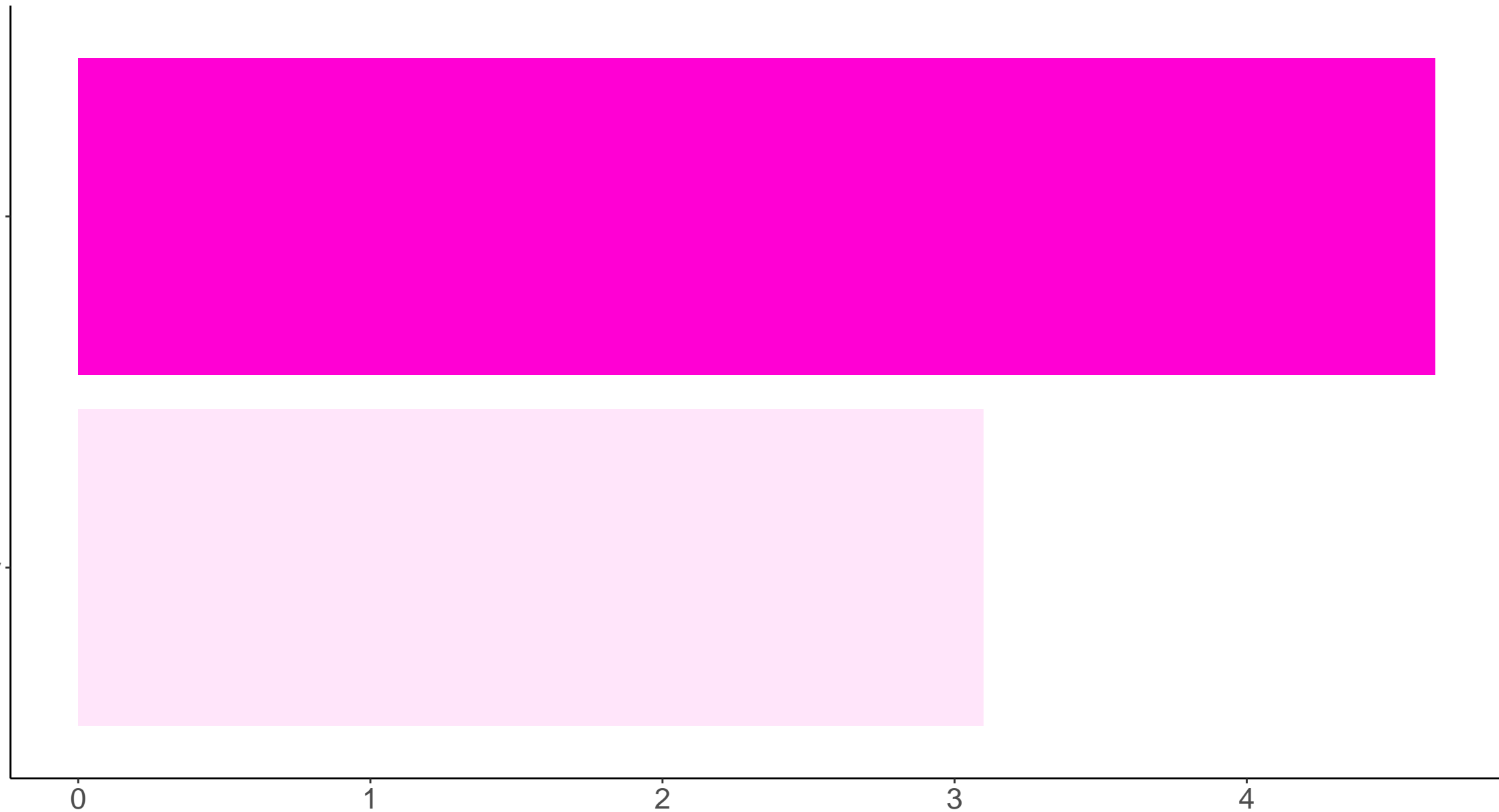
1

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log2Enrichment



Re-clustered module 1.10.17 BP enrichment

Term

negative regulation of transcription, DNA-templated

regulation of transcription by RNA polymerase II

histone ubiquitination

regulation of gastrulation

0

2

4

log2Enrichment



Re-clustered module 1.10.17 MF enrichment

Term

nuclear receptor transcription coactivator activity

RNA polymerase II transcription regulatory region sequence-specific DNA binding

0

2

4

log2Enrichment



Re-clustered module 1.10.18 BP enrichment

Term

endocytic recycling

regulation of phosphoprotein phosphatase activity

0

1

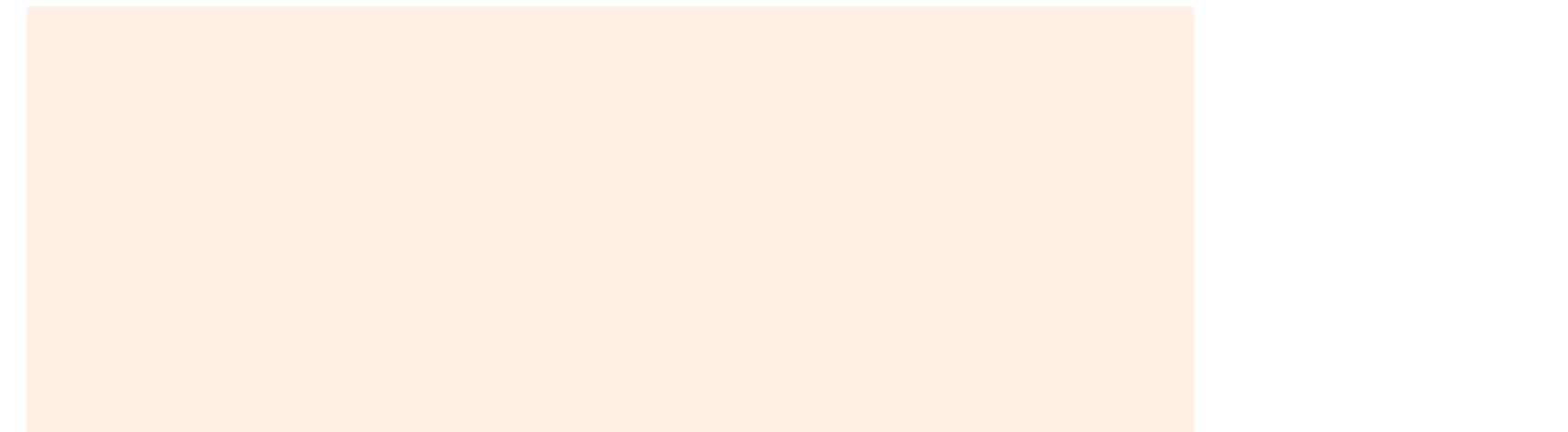
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log2Enrichment



Re-clustered module 1.10.18 MF enrichment

Term

protein phosphatase 2A binding

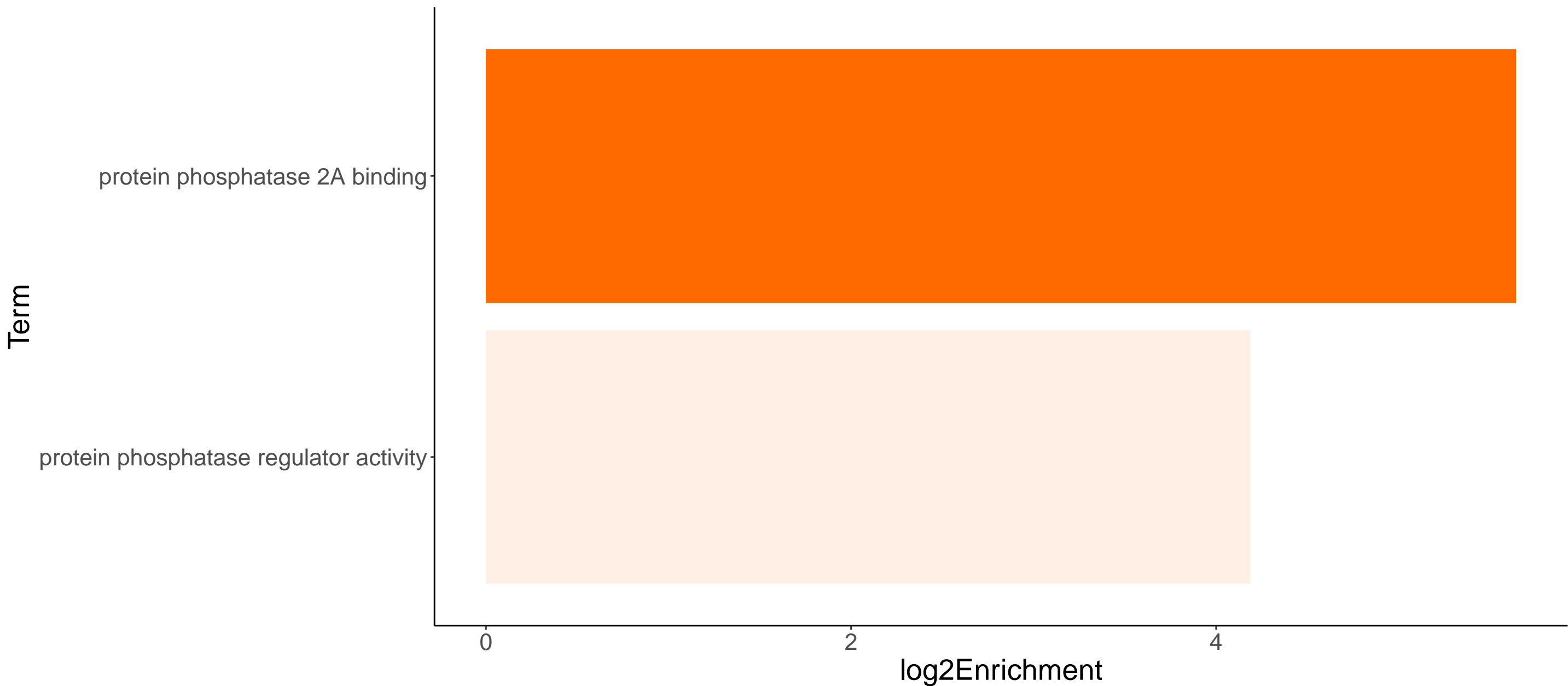
protein phosphatase regulator activity

0

2

4

log2Enrichment



Re-clustered module 1.10.19 BP enrichment

Term

peptidyl-lysine trimethylation

regulation of transforming growth factor beta receptor signaling pathway

response to UV

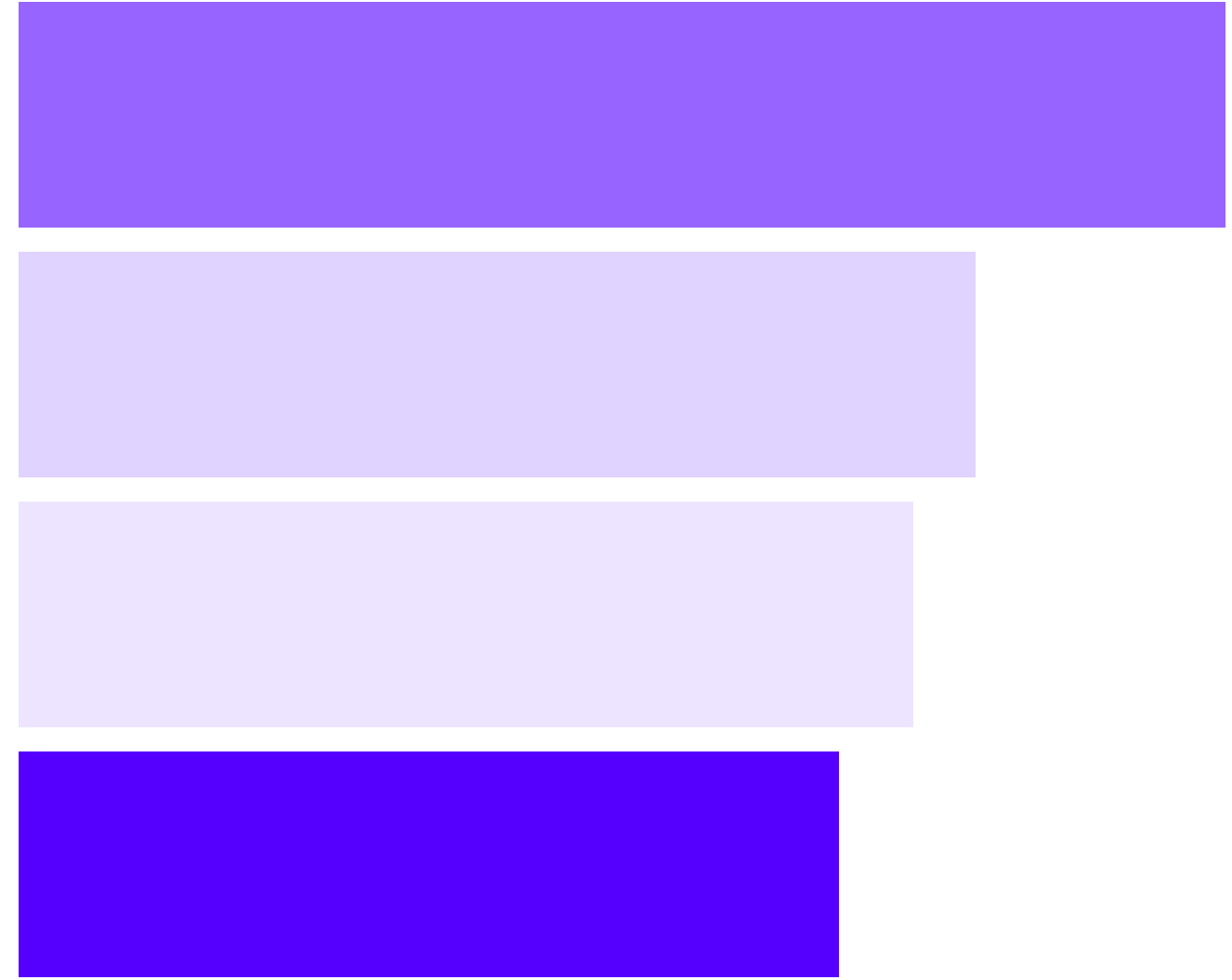
histone modification

0

2

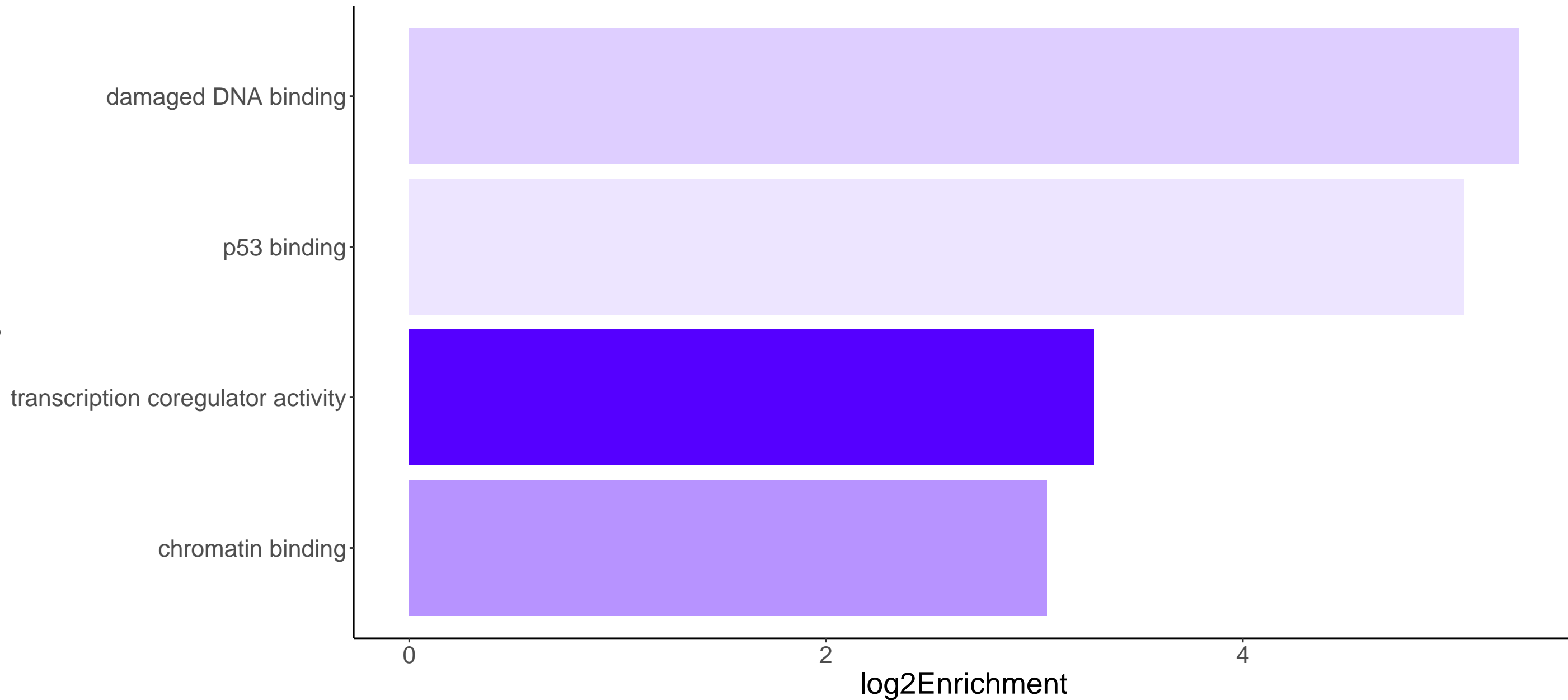
4

log2Enrichment



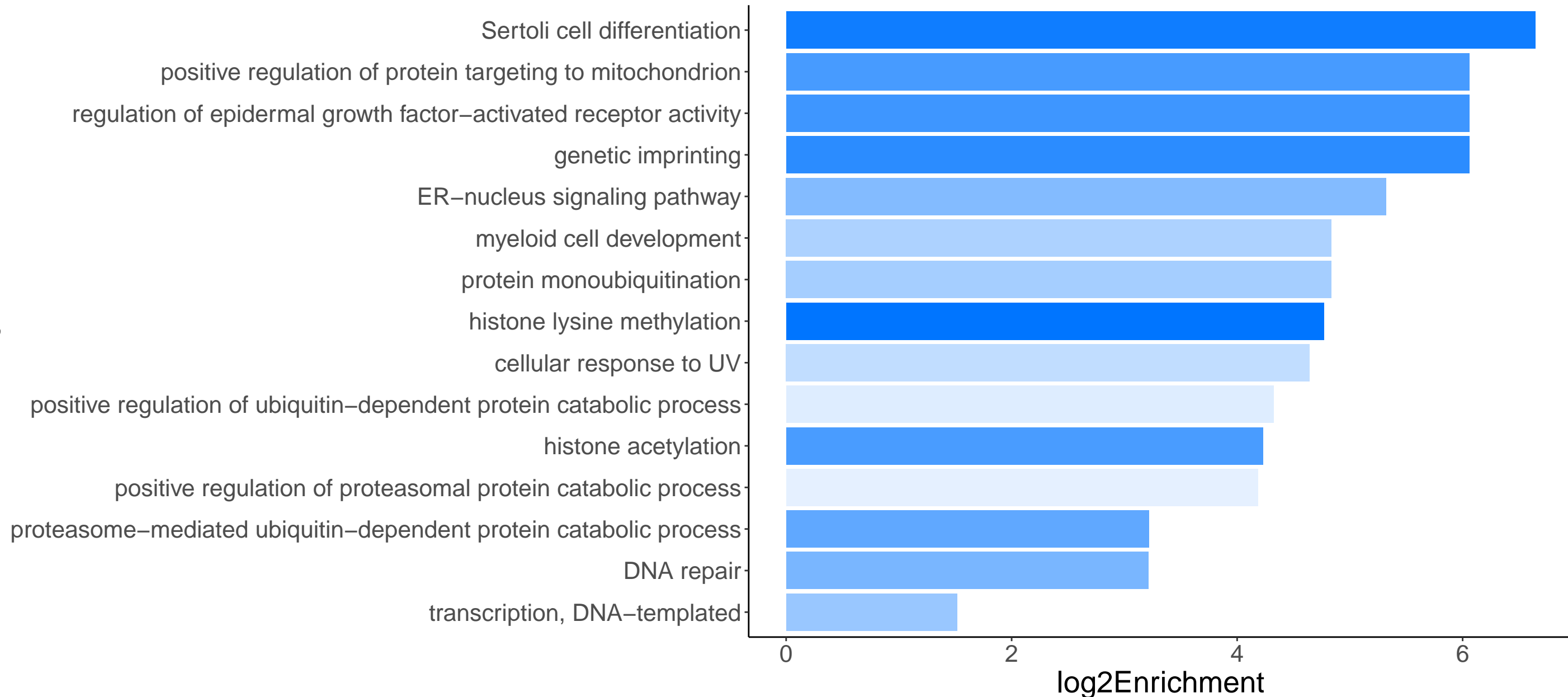
Re-clustered module 1.10.19 MF enrichment

Term



Re-clustered module 1.10.2 BP enrichment

Term



Re-clustered module 1.10.2 MF enrichment

Term

RNA polymerase II complex binding

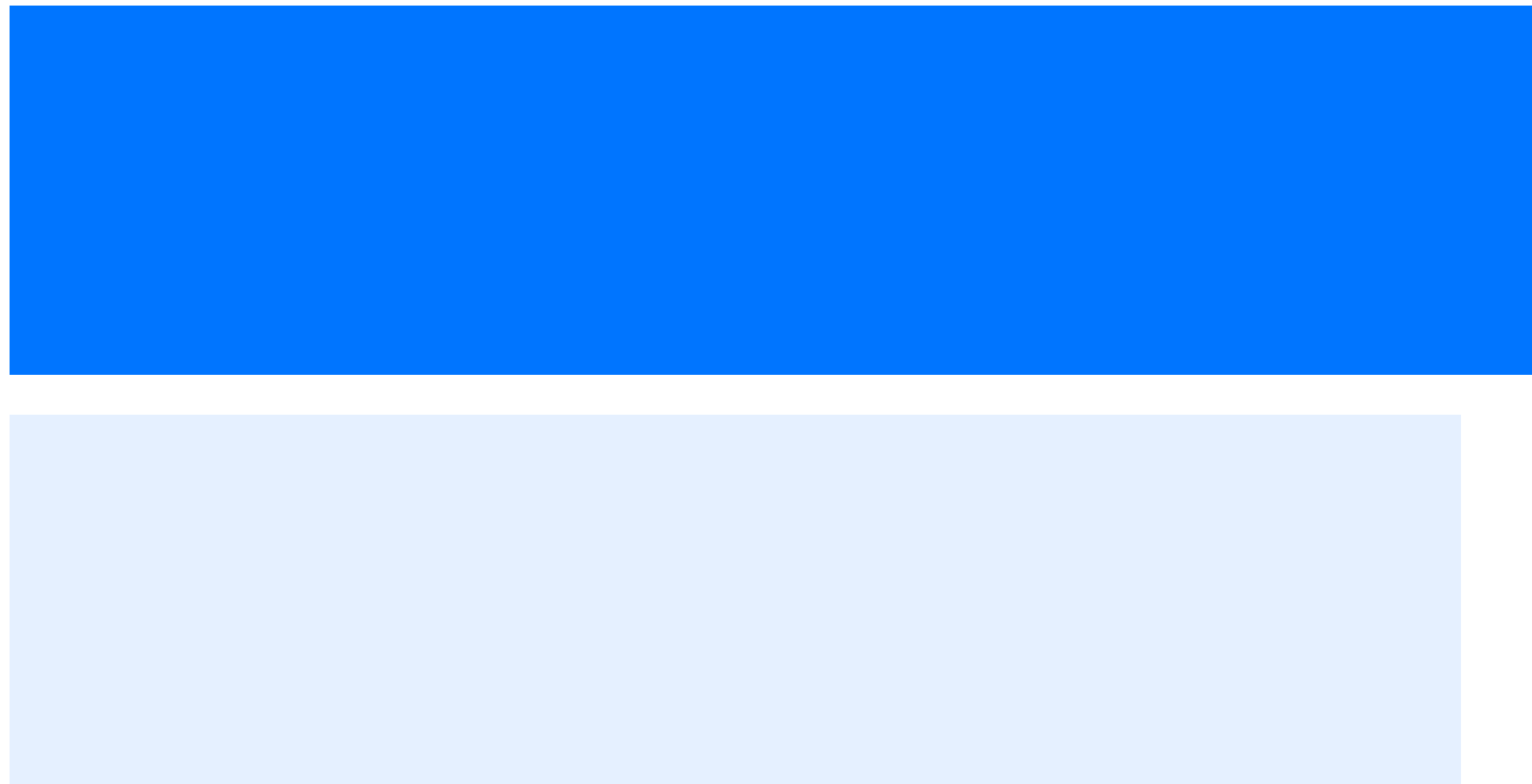
histone acetyltransferase activity

0

2

4

log2Enrichment

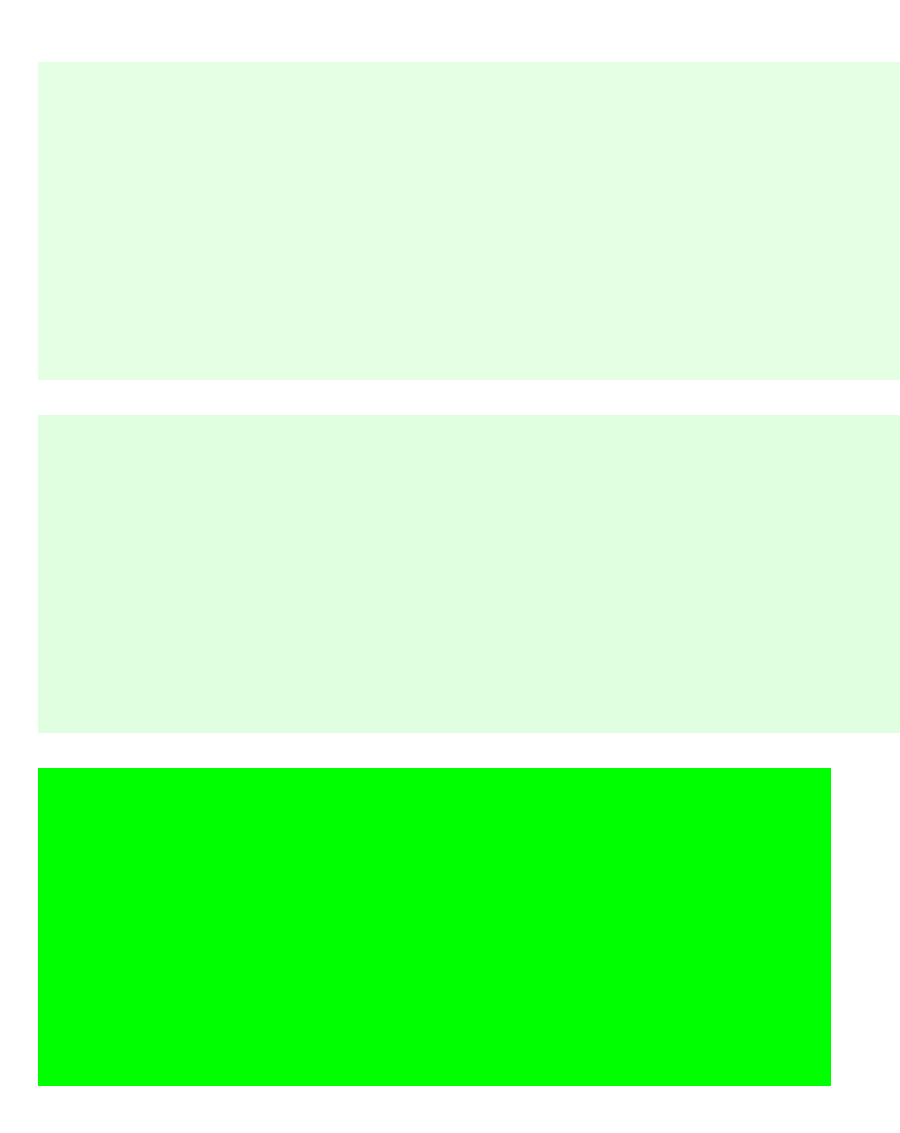


Term

negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway

regulation of transforming growth factor beta receptor signaling pathway

endosomal transport



log2Enrichment

Term	log2Enrichment
negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	~4.2
regulation of transforming growth factor beta receptor signaling pathway	~4.2
endosomal transport	~3.8

Re-clustered module 1.10.3 MF enrichment

Term

ubiquitin-like protein transferase activity

zinc ion binding

0

1

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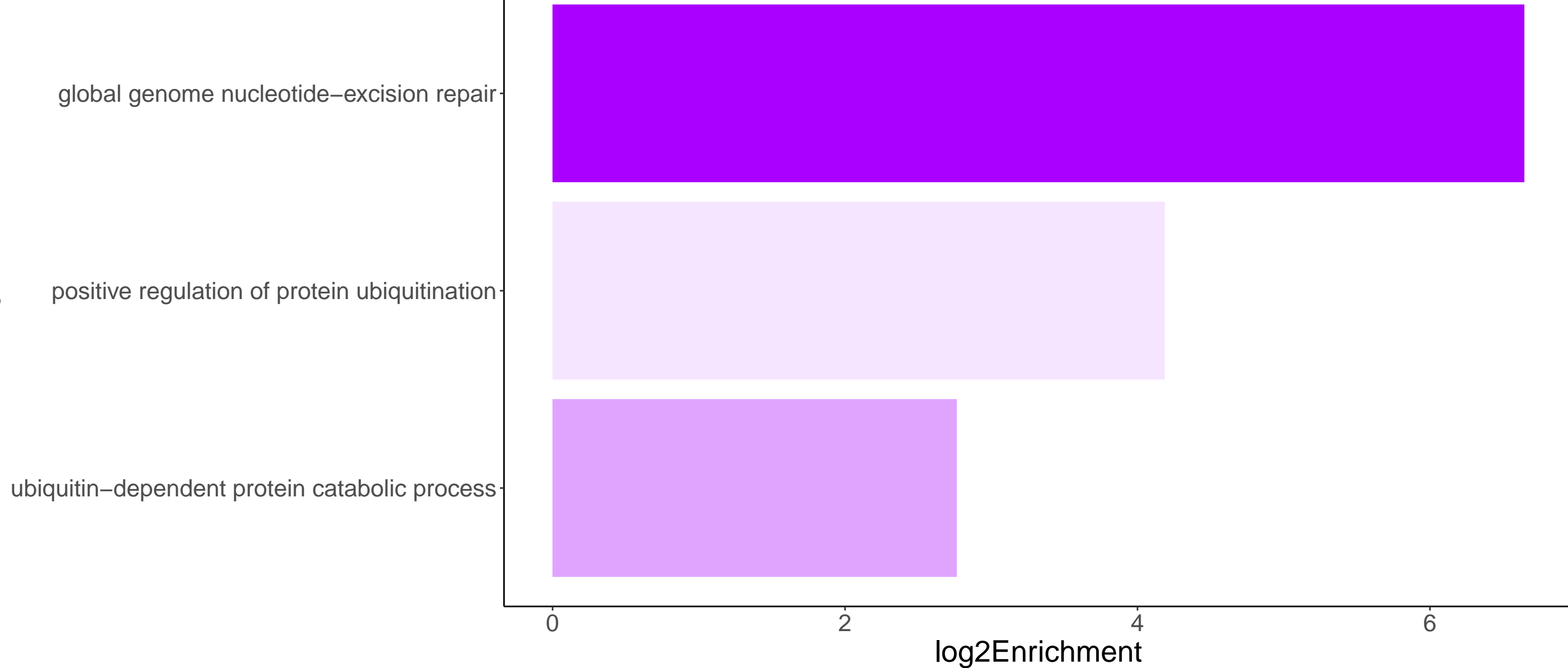
3

log2Enrichment



Re-clustered module 1.10.4 BP enrichment

Term



Re-clustered module 1.10.4 MF enrichment

Term

thiol-dependent ubiquitin-specific protease activity

cysteine-type peptidase activity

ubiquitin-protein transferase activity

0

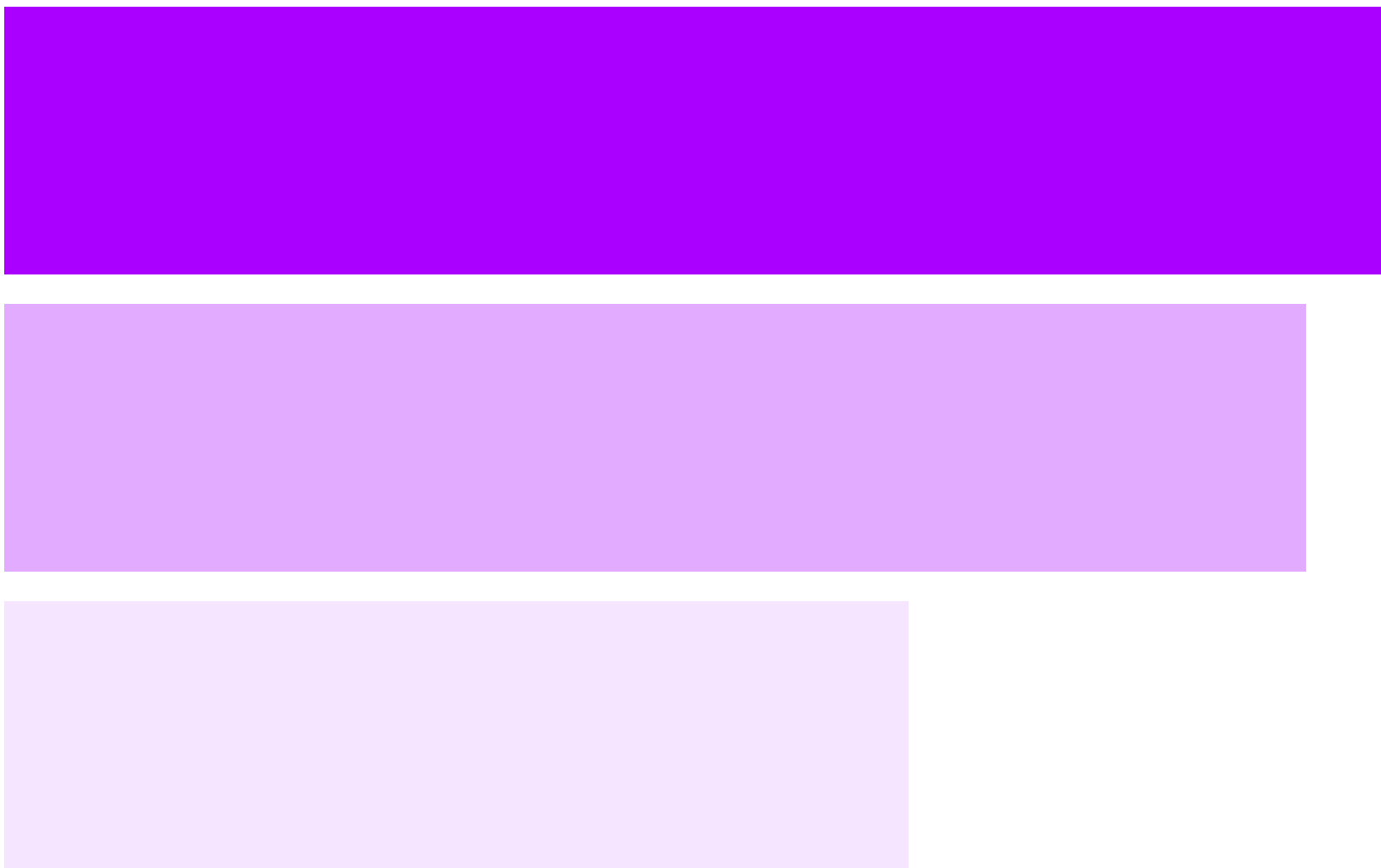
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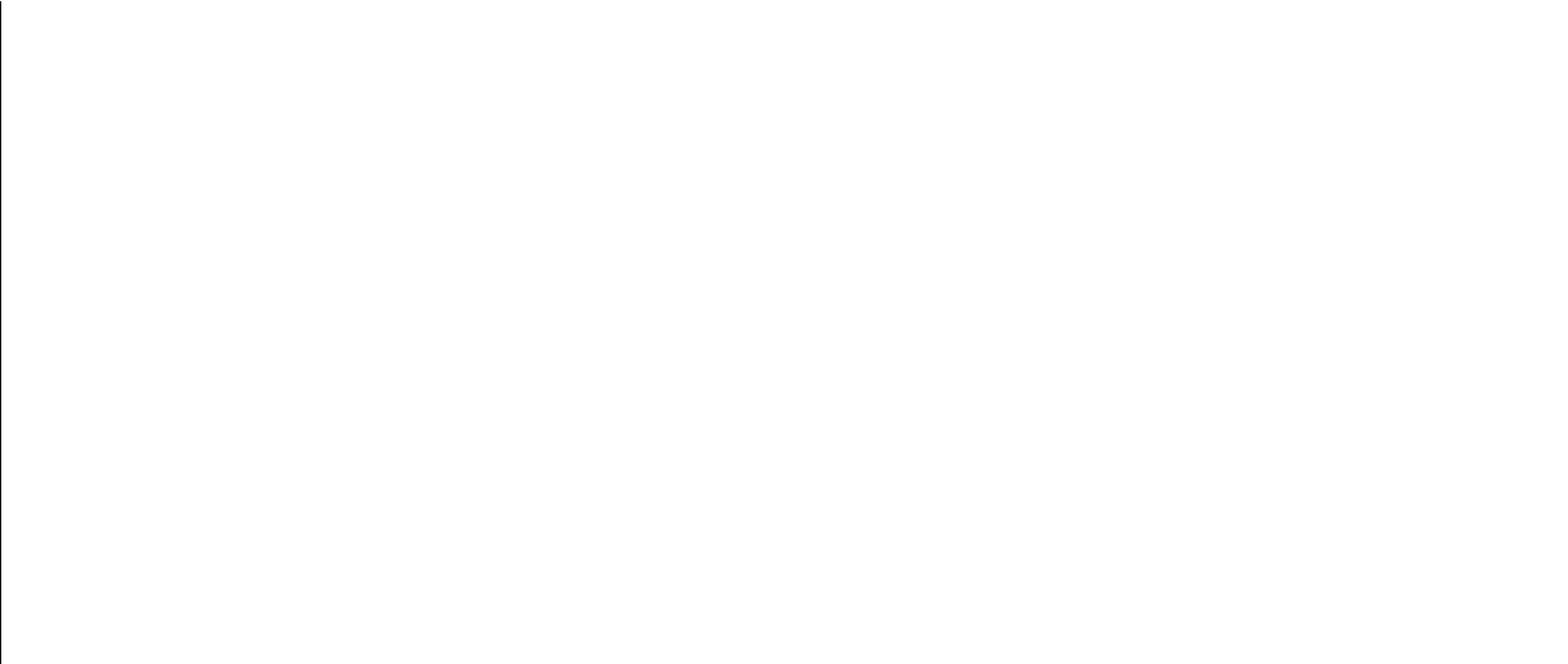
log2Enrichment



Re-clustered module 1.10.5 BP enrichment

Term

log2Enrichment



Re-clustered module 1.10.5 MF enrichment

Term

log2Enrichment



Re-clustered module 1.10.7 BP enrichment

Term

innervation

protein ubiquitination

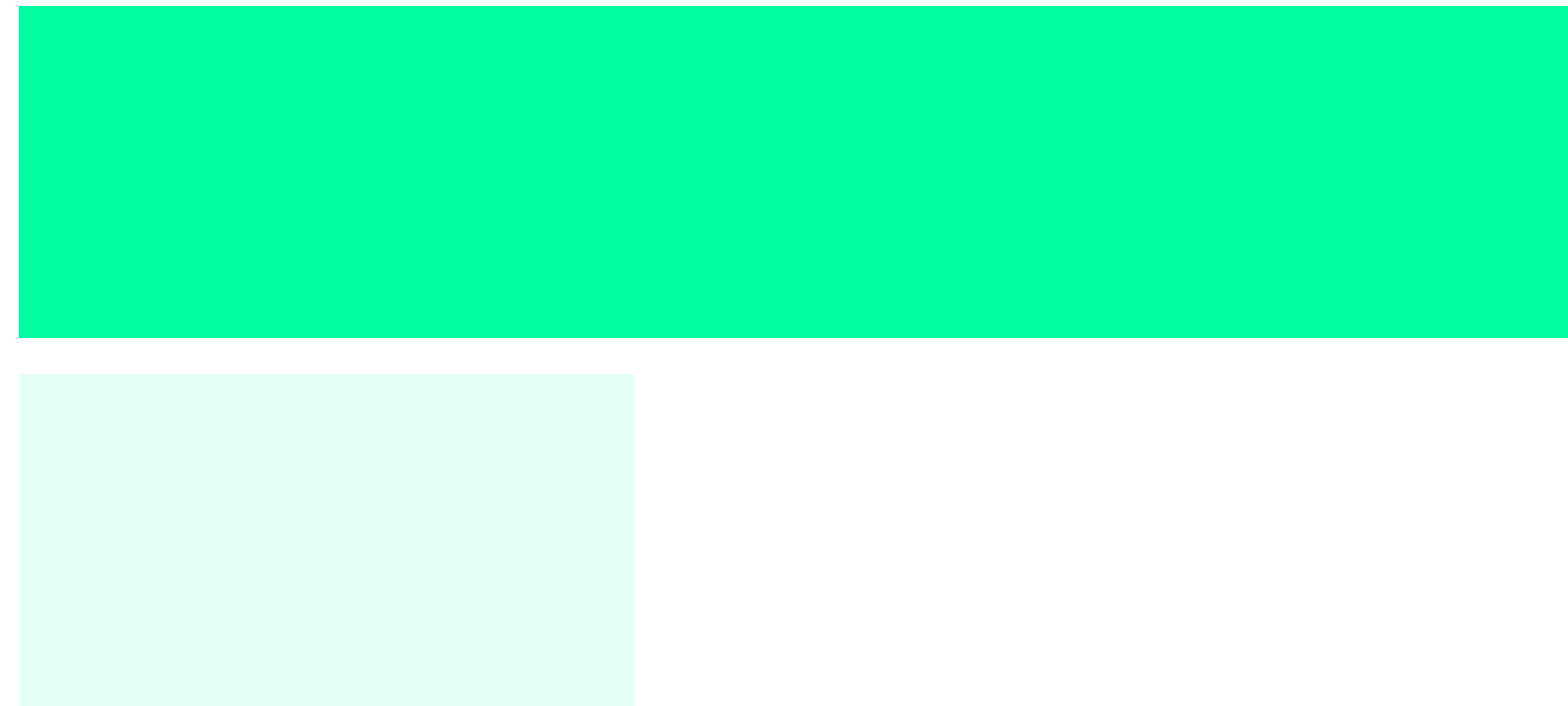
0

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6

log2Enrichment



Re-clustered module 1.10.7 MF enrichment

Term

repressing transcription factor binding

transcription corepressor activity

ubiquitin protein ligase activity

0

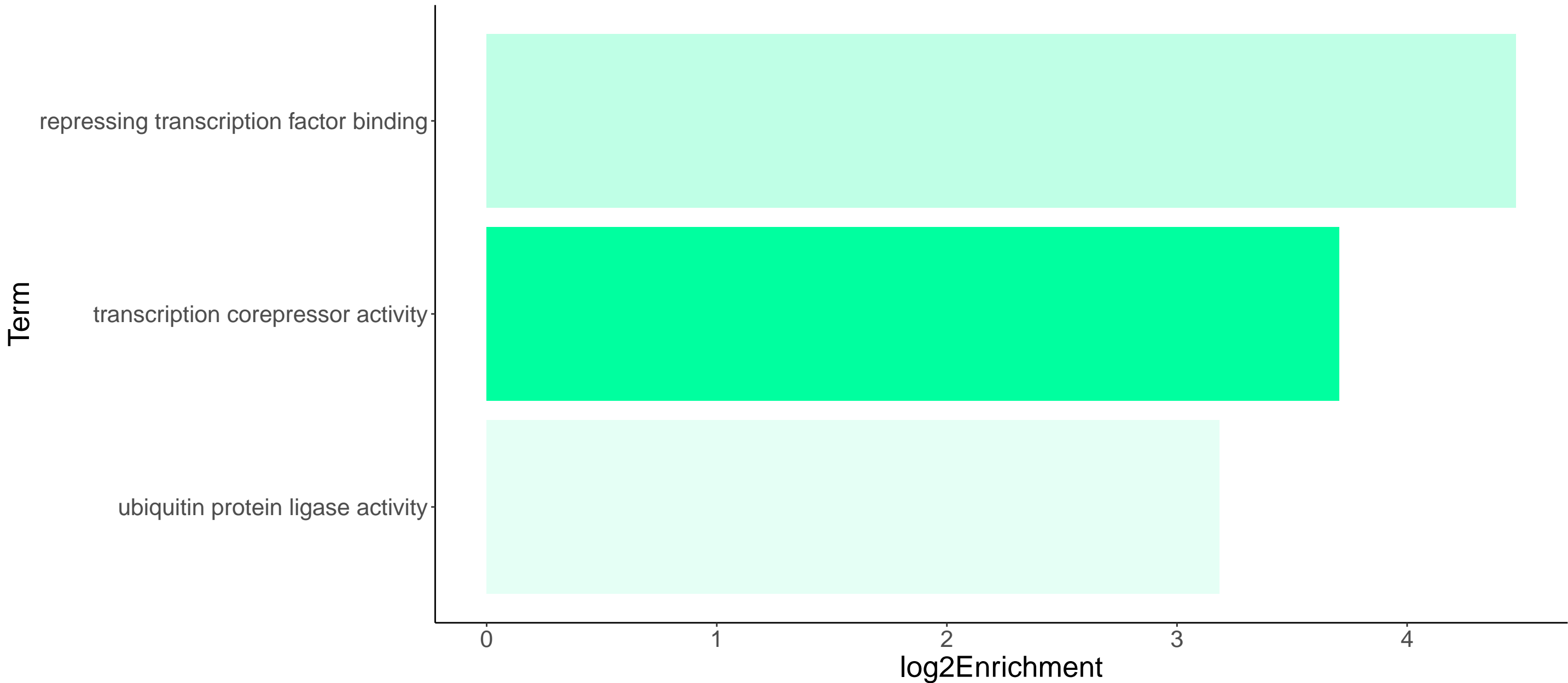
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log2Enrichment



Re-clustered module 1.10.8 BP enrichment

Term

hippocampus development

regulation of axon extension

negative regulation of neuron differentiation

entry into host

positive regulation of protein transport

0

1

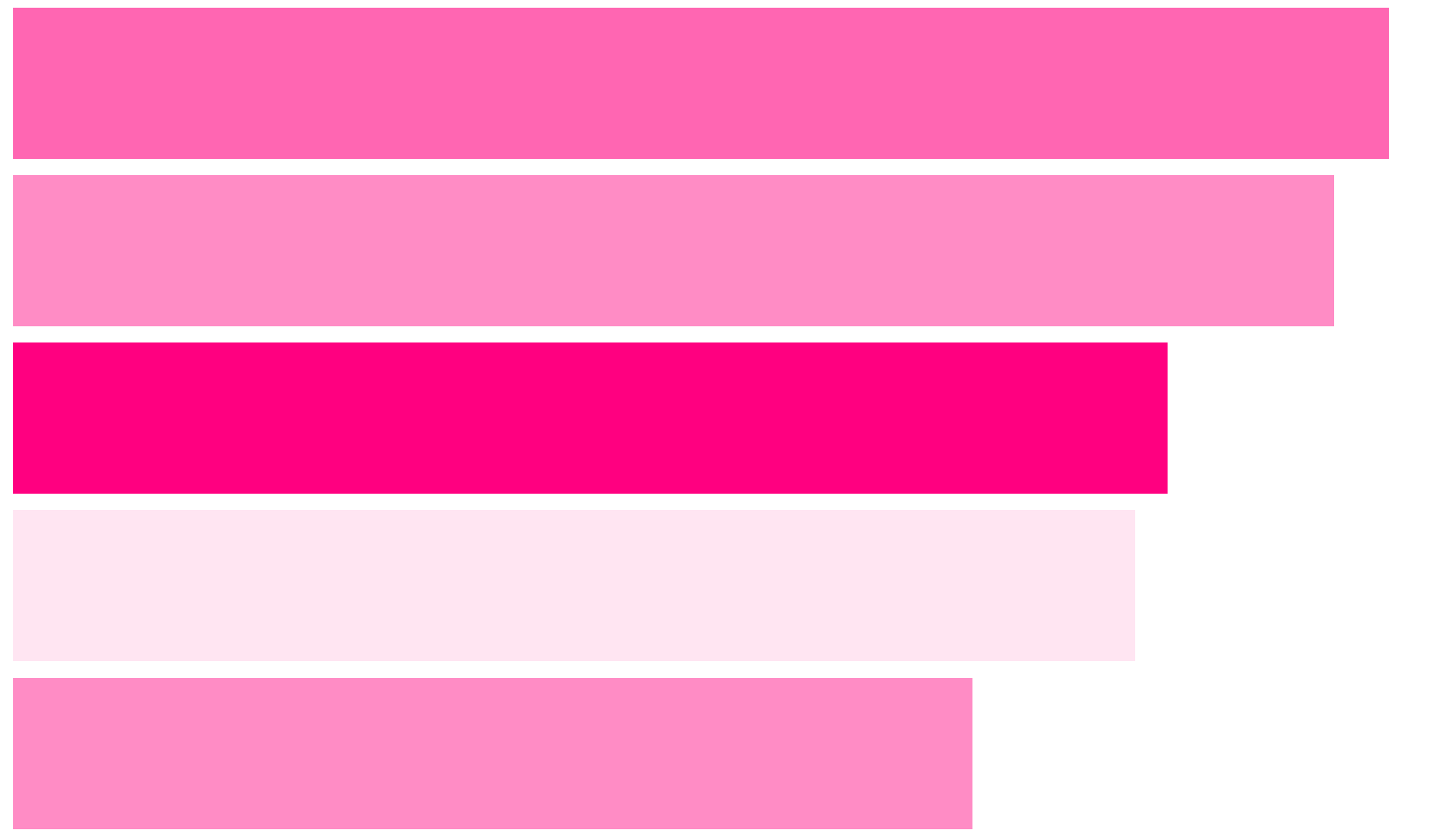
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log2Enrichment



Re-clustered module 1.10.8 MF enrichment

Term

log2Enrichment



Re-clustered module 1.10.9 BP enrichment

Term

negative regulation of microtubule depolymerization

protein K63-linked ubiquitination

positive regulation of NIK/NF-kappaB signaling

Fc-epsilon receptor signaling pathway

activation of protein kinase activity

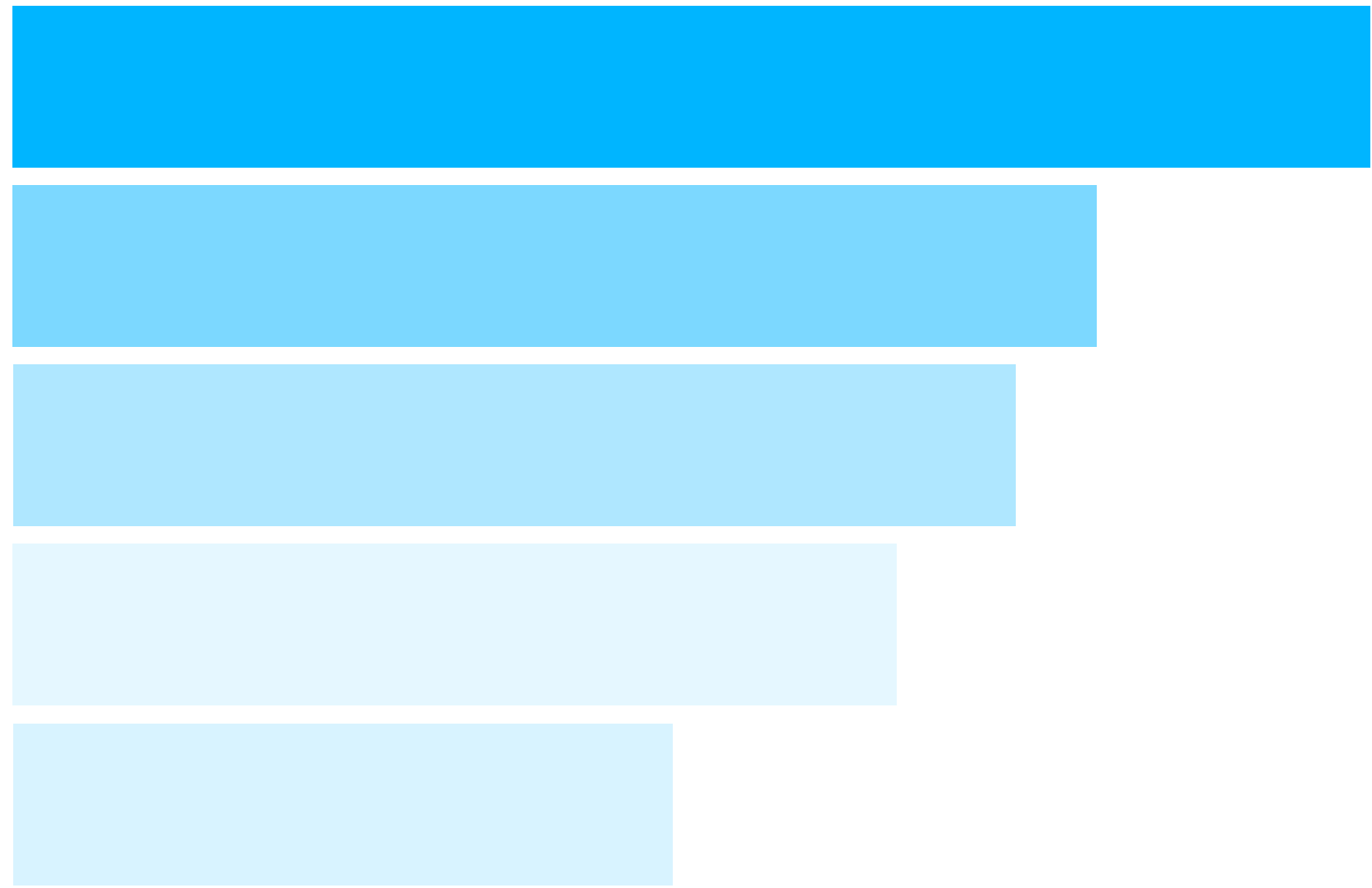
0

2

4

6

log2Enrichment



Re-clustered module 1.10.9 MF enrichment

Term

RNA binding

0.0

0.5

1.0

1.5

log2Enrichment



Re-clustered module 1.11 BP enrichment

Term

termination of RNA polymerase II transcription

hormone biosynthetic process

glycosphingolipid metabolic process

protein sumoylation

regulation of glycolytic process

0

1

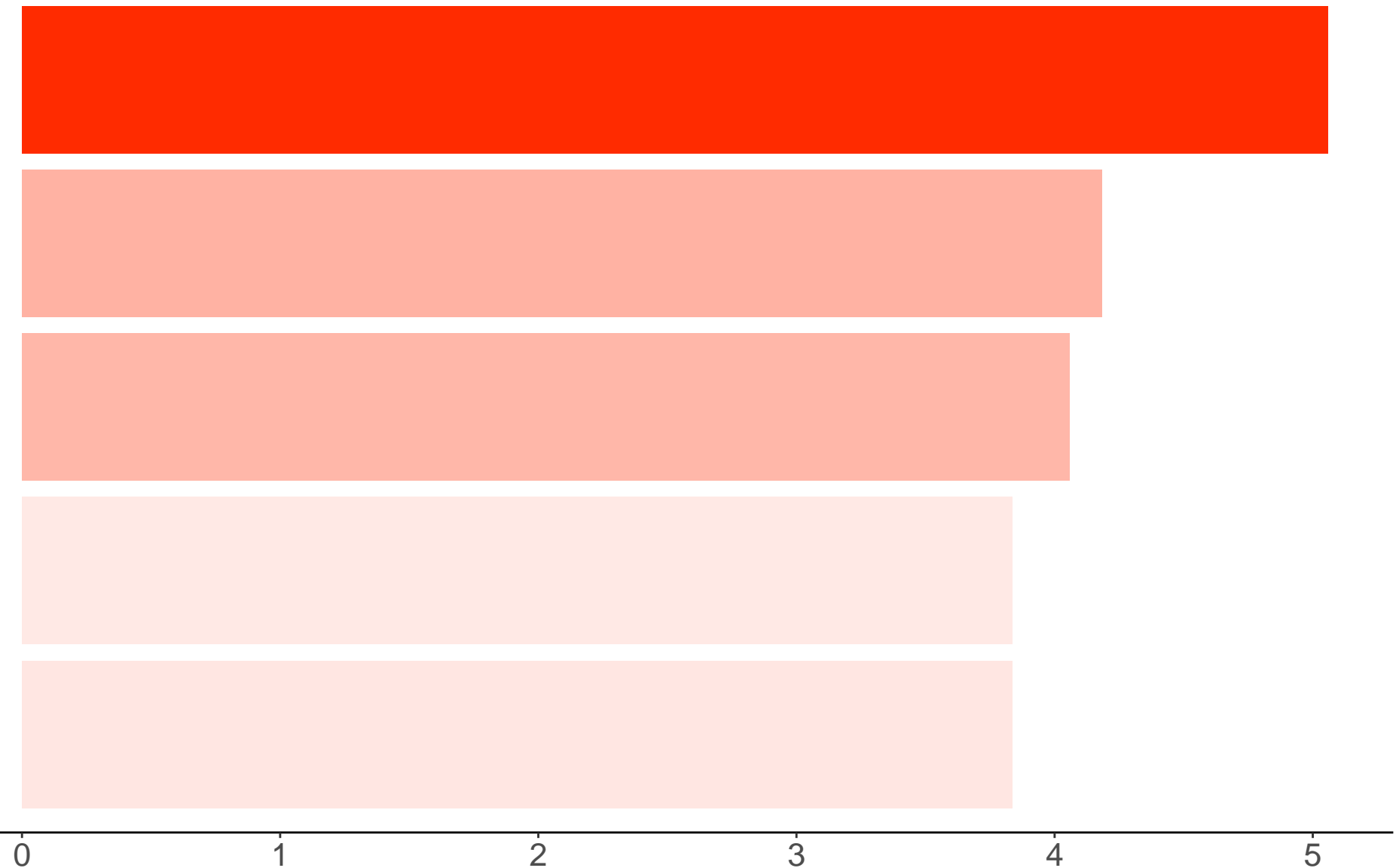
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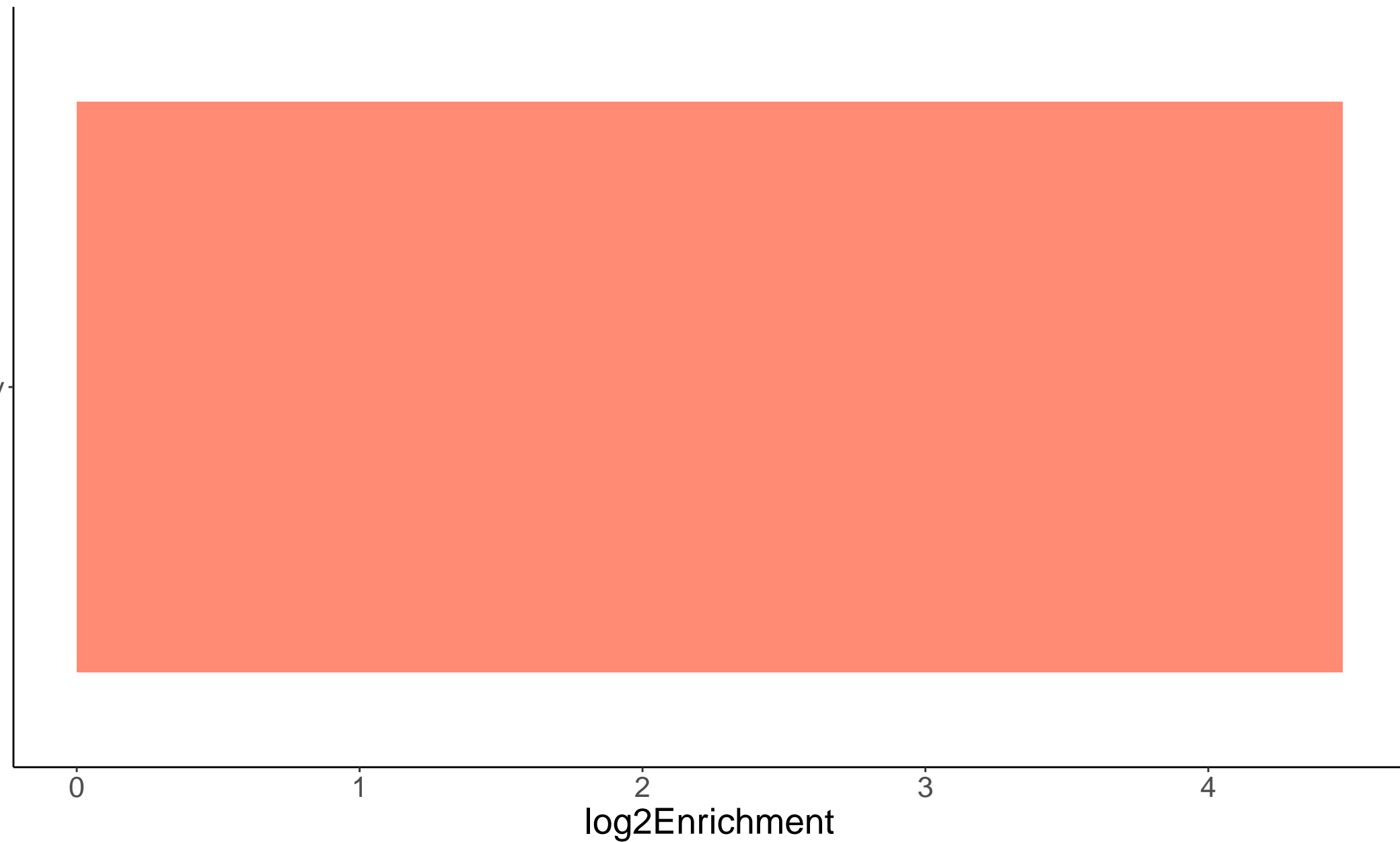
5

log2Enrichment



Re-clustered module 1.11 MF enrichment

Term
acetylglucosaminyltransferase activity



Re-clustered module 1.12.1 BP enrichment

Term

somite development

regulation of transcription by RNA polymerase II

0

1

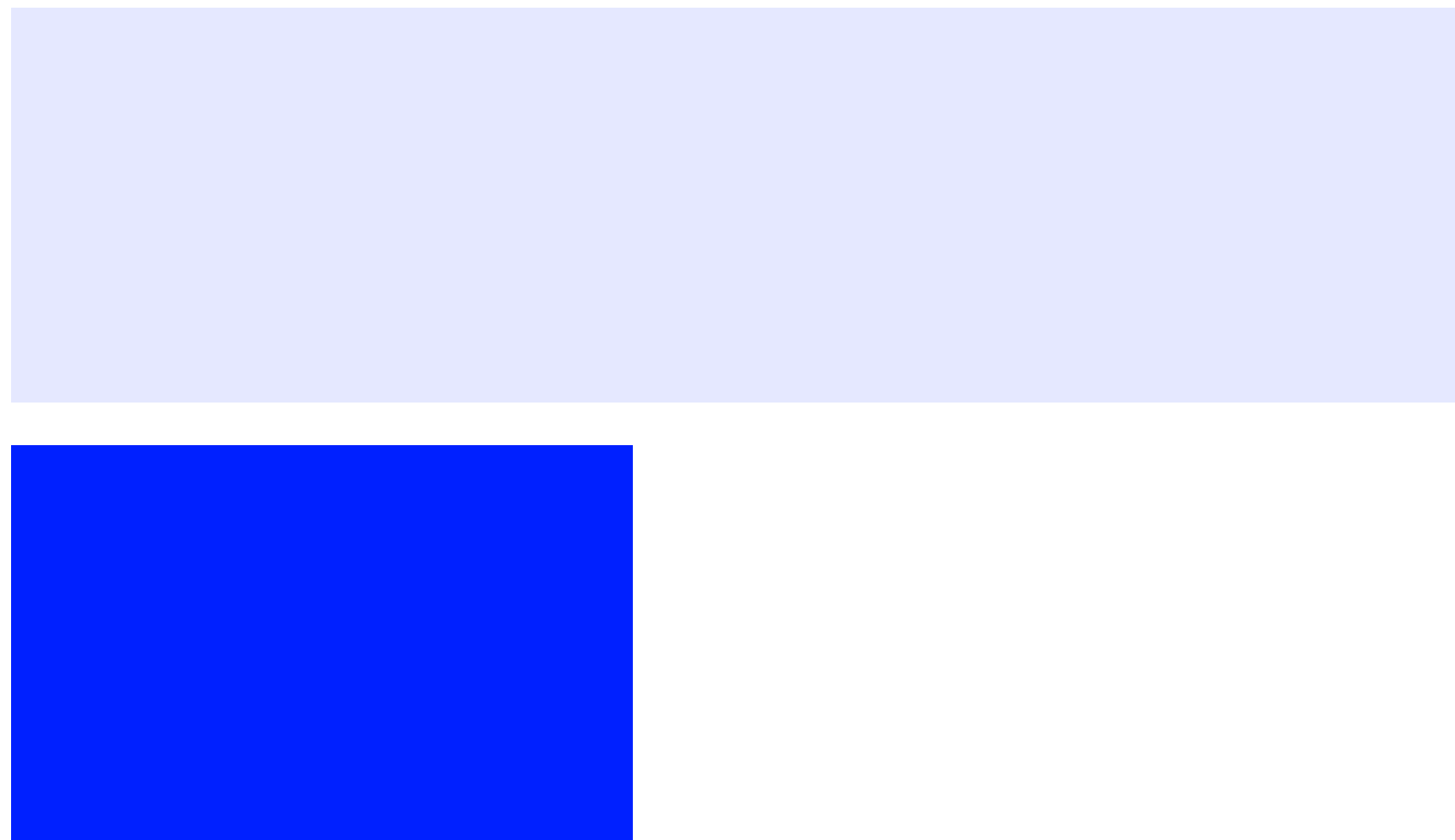
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log2Enrichment



Re-clustered module 1.12.1 MF enrichment

Term

RNA polymerase II transcription regulatory region sequence-specific DNA binding

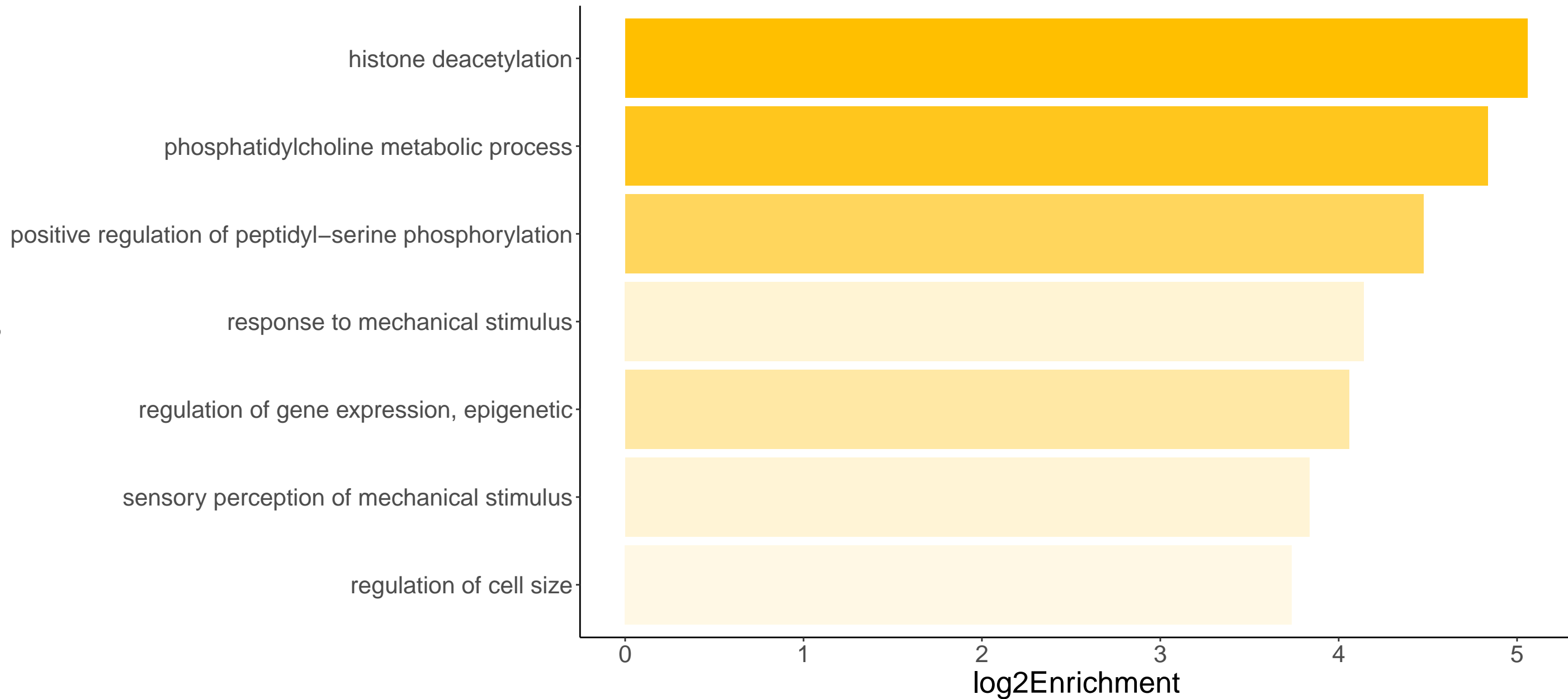
DNA-binding transcription factor activity, RNA polymerase II-specific

0.0 0.5 1.0 1.5 2.0 2.5
log2Enrichment



Re-clustered module 1.12.10 BP enrichment

Term



Re-clustered module 1.12.10 MF enrichment

Term

hormone activity

0

1

2

3

4

log2Enrichment



Re-clustered module 1.12.11 BP enrichment

Term

histone H3–K4 methylation

histone H4 acetylation

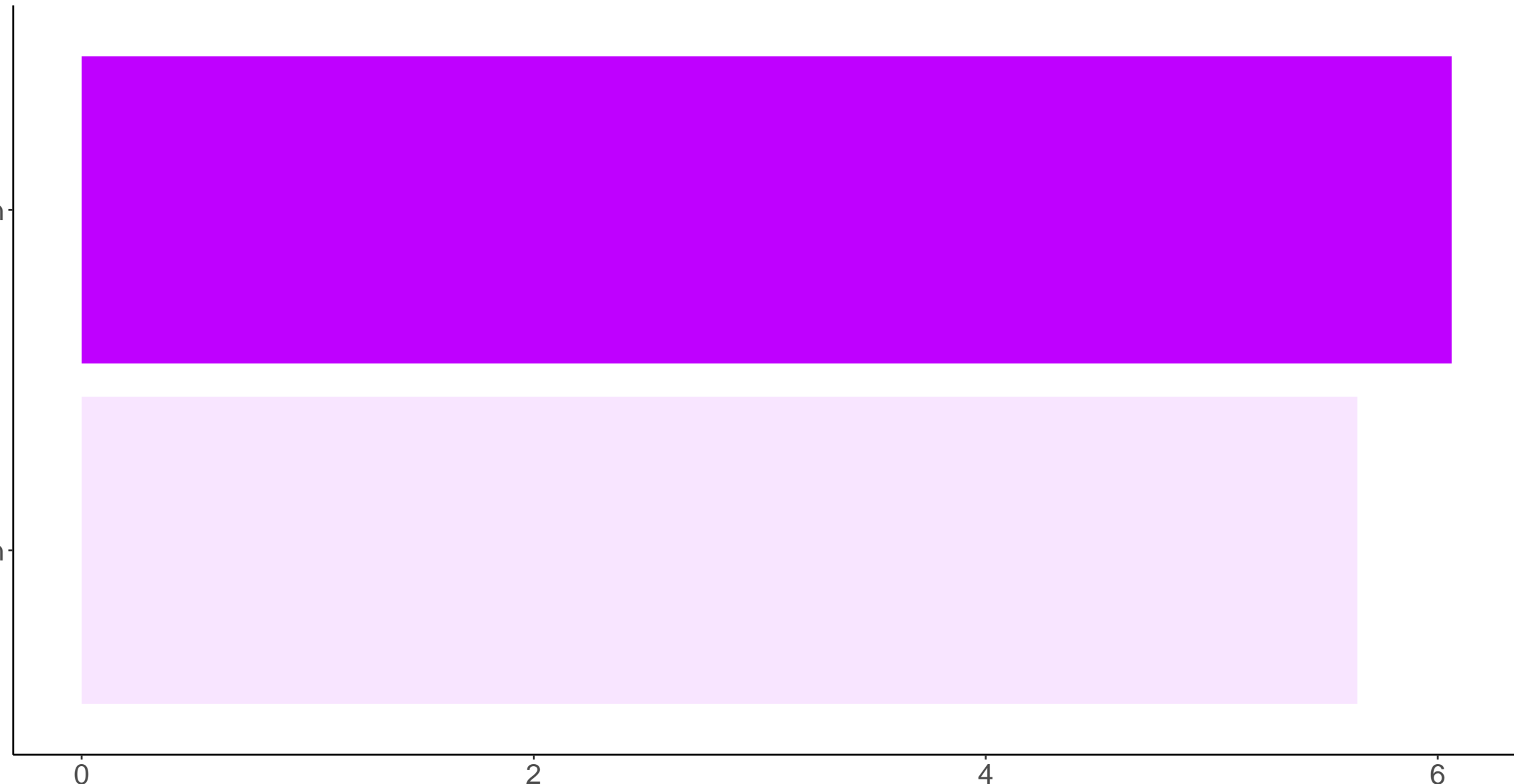
0

2

4

6

log2Enrichment



Re-clustered module 1.12.11 MF enrichment

Term

histone-lysine N-methyltransferase activity

0

2

4

6

log2Enrichment



Re-clustered module 1.12.12 BP enrichment

Term

regulation of alternative mRNA splicing, via spliceosome

regulation of striated muscle tissue development

gene expression

0

1

2

3

4

log2Enrichment



Re-clustered module 1.12.12 MF enrichment

Term

DNA binding

0.0

0.5

1.0

log2Enrichment



Re-clustered module 1.12.13 BP enrichment

Term

insulin-like growth factor receptor signaling pathway

0

2

4

6

log2Enrichment



Re-clustered module 1.12.13 MF enrichment

Term

log2Enrichment



Re-clustered module 1.12.14 BP enrichment

Term

log2Enrichment



Re-clustered module 1.12.14 MF enrichment

Term

log2Enrichment



Re-clustered module 1.12.15 BP enrichment

Term

log2Enrichment



Re-clustered module 1.12.15 MF enrichment

Term

log2Enrichment



Re-clustered module 1.12.2 BP enrichment

Term

oligosaccharide metabolic process

RNA methylation

0

1

2

3

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log2Enrichment



Re-clustered module 1.12.2 MF enrichment

Term

gamma-tubulin binding

hydrolase activity, hydrolyzing O-glycosyl compounds

amyloid-beta binding

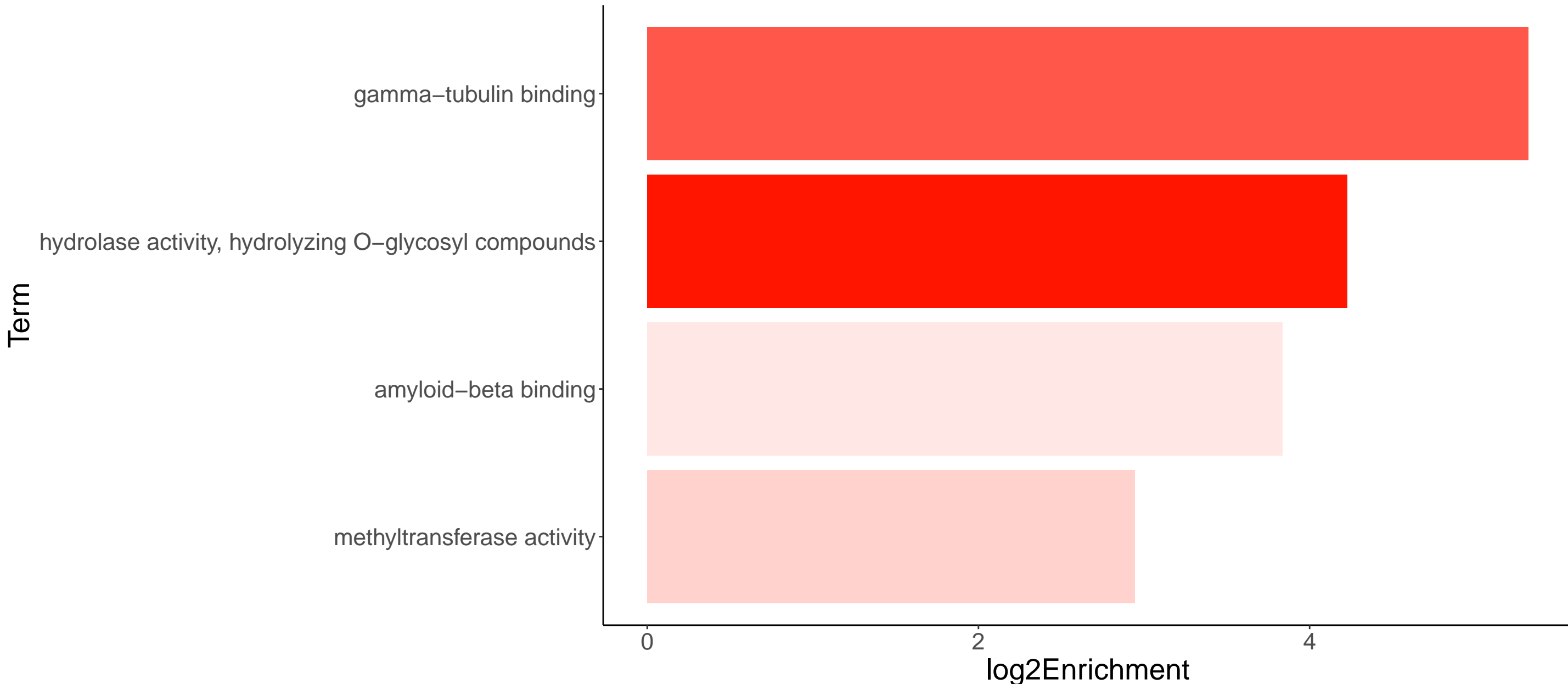
methyltransferase activity

0

2

4

log2Enrichment



Re-clustered module 1.12.3 BP enrichment

Term

regulation of mRNA splicing, via spliceosome

0

1

2

3

4

log2Enrichment



Re-clustered module 1.12.3 MF enrichment

Term

nucleic acid binding

0.0

0.5

1.0

log2Enrichment



Re-clustered module 1.12.4 BP enrichment

Term

protein autophosphorylation

RNA splicing

0

1

2

3

log2Enrichment



Re-clustered module 1.12.4 MF enrichment

Term

protein serine/threonine/tyrosine kinase activity

0

1

2

3

4

5

log2Enrichment



Re-clustered module 1.12.5 BP enrichment

Term

positive regulation of DNA-templated transcription, elongation

positive regulation of response to DNA damage stimulus

DNA damage checkpoint

RNA splicing

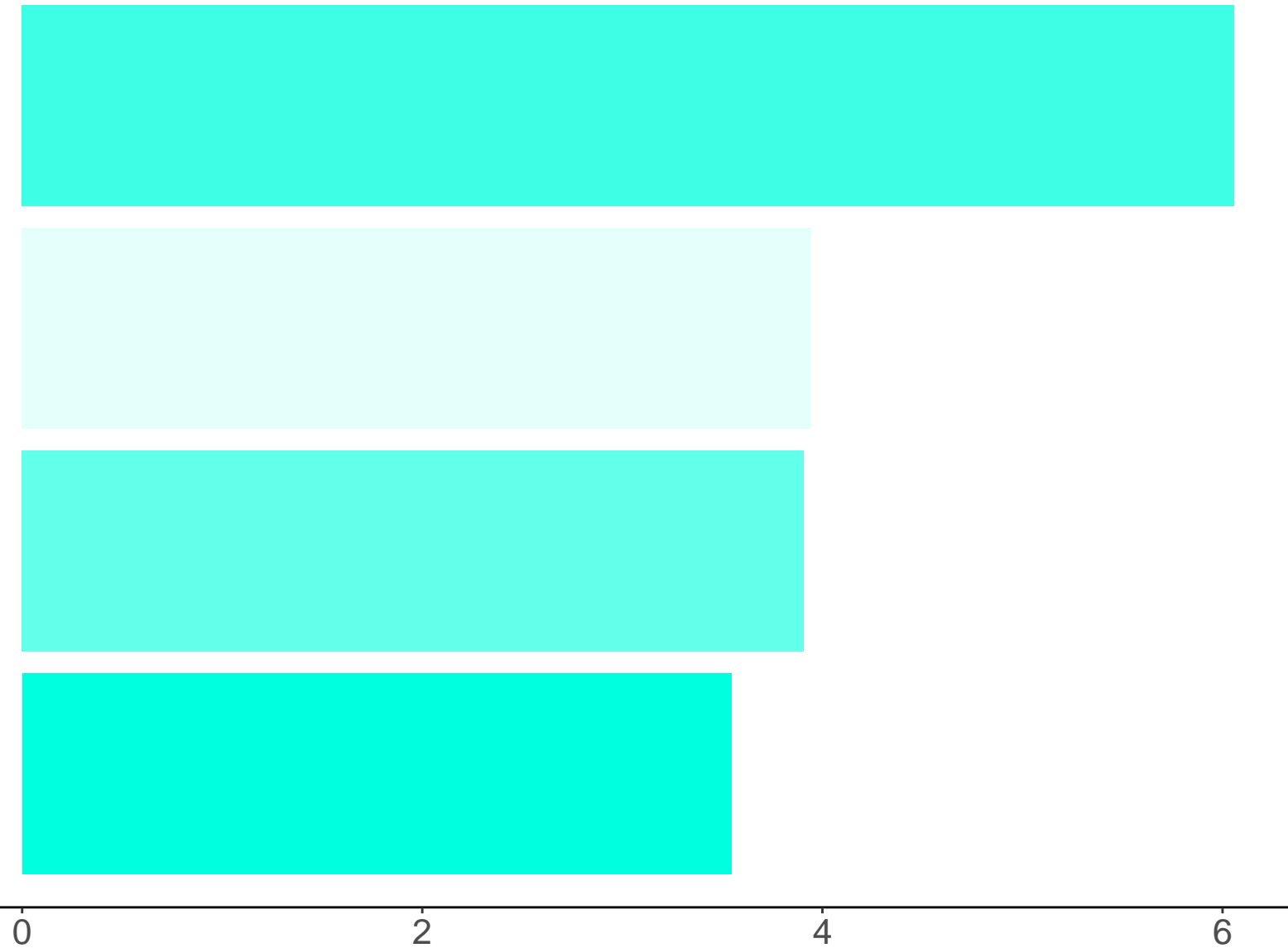
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6

log2Enrichment



Re-clustered module 1.12.5 MF enrichment

Term

RNA binding

0.0

0.5

1.0

1.5

log2Enrichment



Re-clustered module 1.12.6 BP enrichment

Term

regulation of signal transduction by p53 class mediator

histone lysine methylation

histone deubiquitination

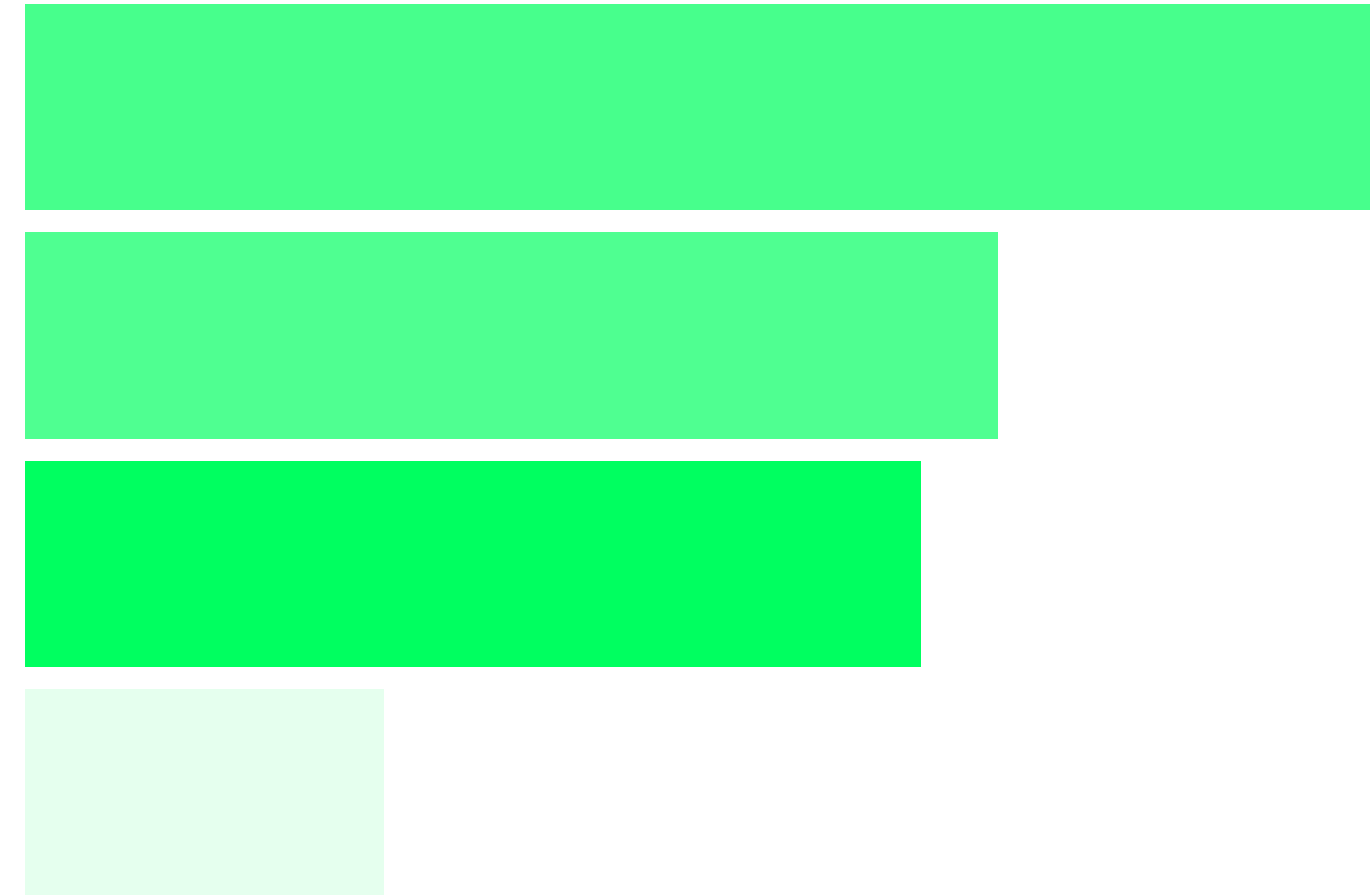
positive regulation of transcription, DNA-templated

0

2

4

log2Enrichment



Re-clustered module 1.12.6 MF enrichment

Term

protein serine/threonine/tyrosine kinase activity

0

1

2

3

4

log2Enrichment



Re-clustered module 1.12.7 BP enrichment

Term

log2Enrichment



Re-clustered module 1.12.7 MF enrichment

Term

log2Enrichment



Re-clustered module 1.12.9 BP enrichment

Term

DNA replication-independent nucleosome assembly

positive regulation of G1/S transition of mitotic cell cycle

negative regulation of phosphatase activity

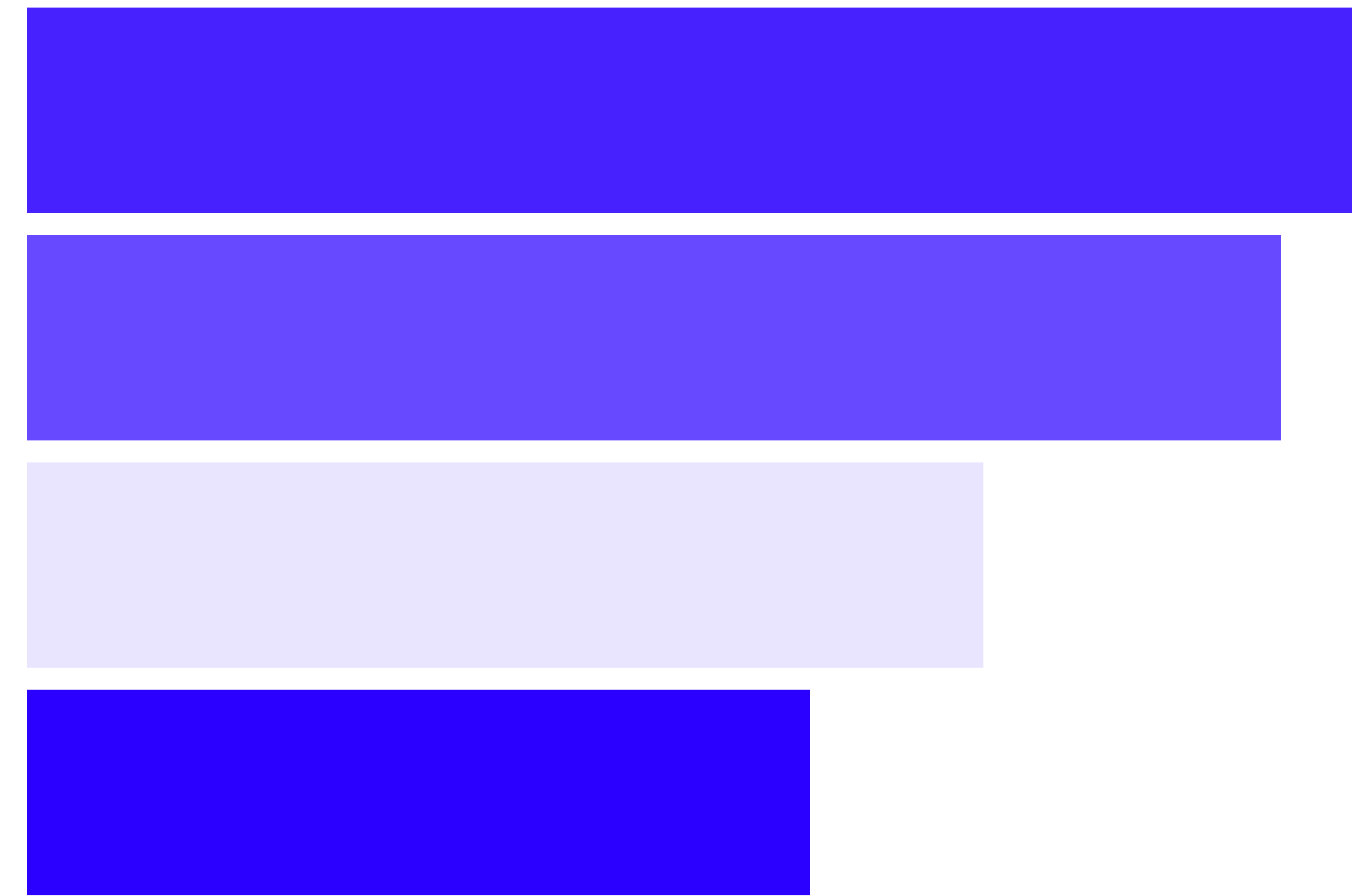
cilium assembly

0

2

4

log2Enrichment



Re-clustered module 1.12.9 MF enrichment

Term

endopeptidase activity

0

1

2

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log2Enrichment



Re-clustered module 1.13 BP enrichment

Term

female gamete generation

0

1

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log2Enrichment



Re-clustered module 1.13 MF enrichment

Term

catalytic activity, acting on a tRNA

helicase activity

0

1

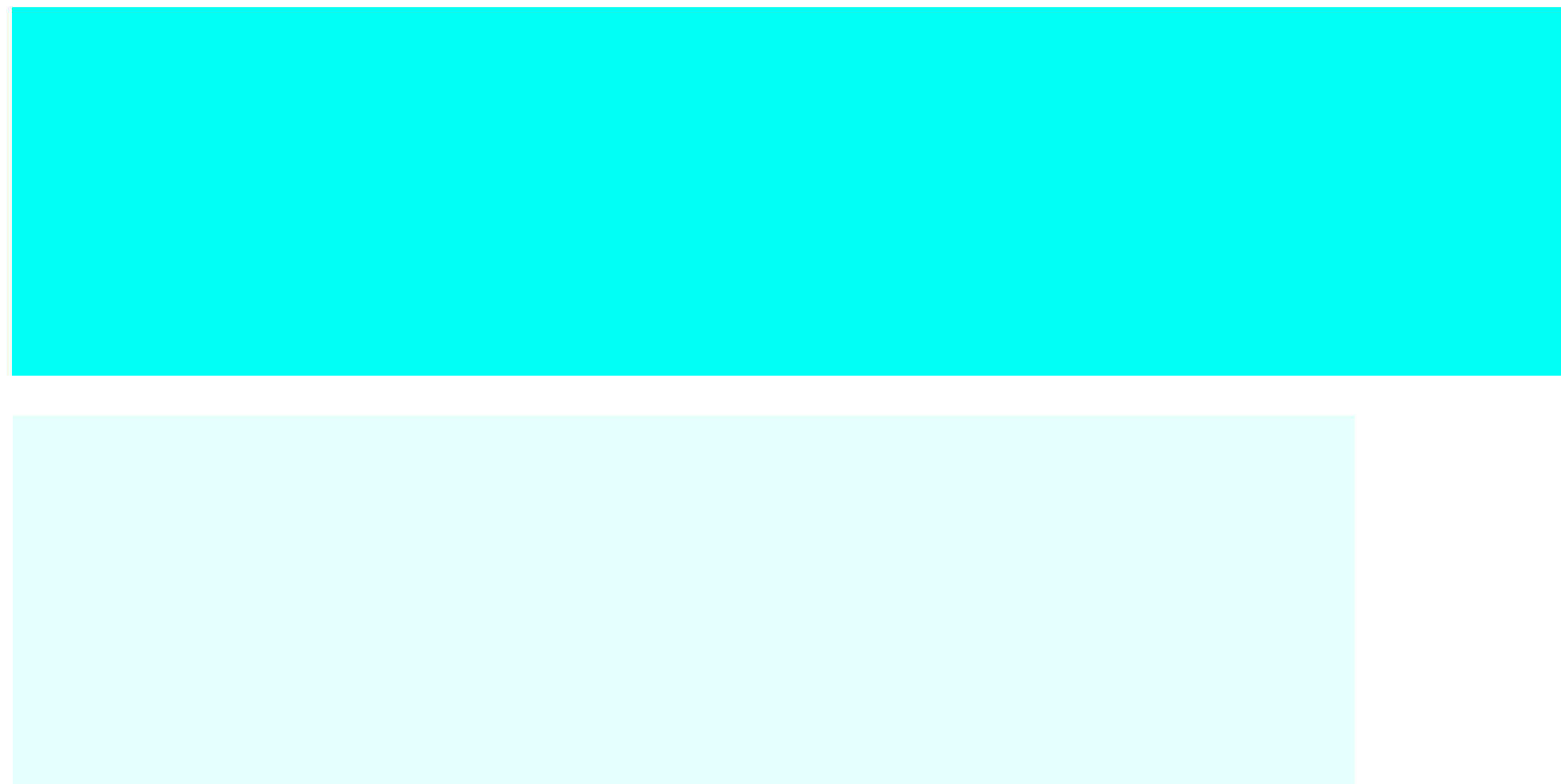
2

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log2Enrichment



Re-clustered module 1.14 BP enrichment

Term

regulation of telomere maintenance via telomerase

telomere capping

tRNA modification

transcription elongation from RNA polymerase II promoter

0

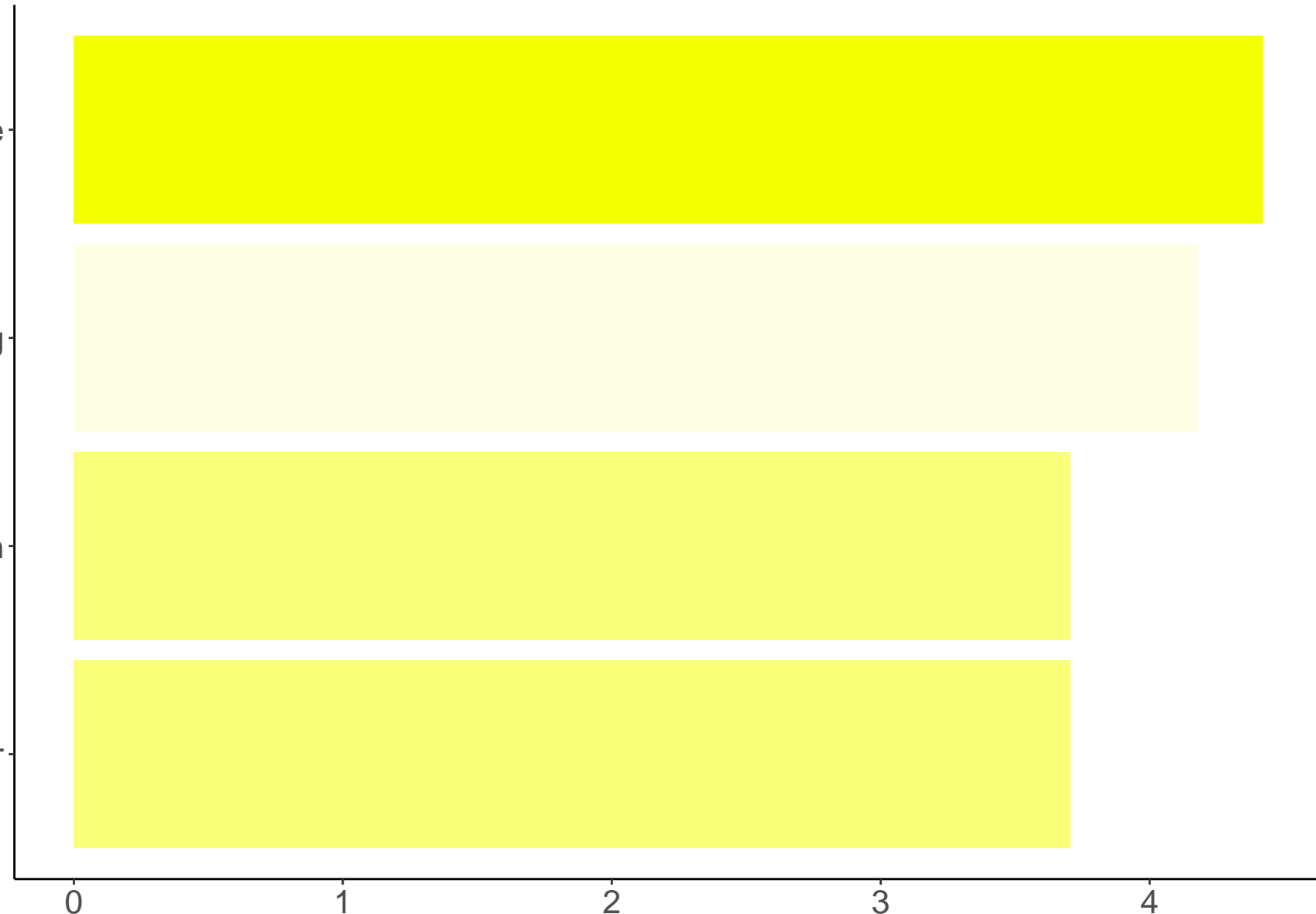
1

2

3

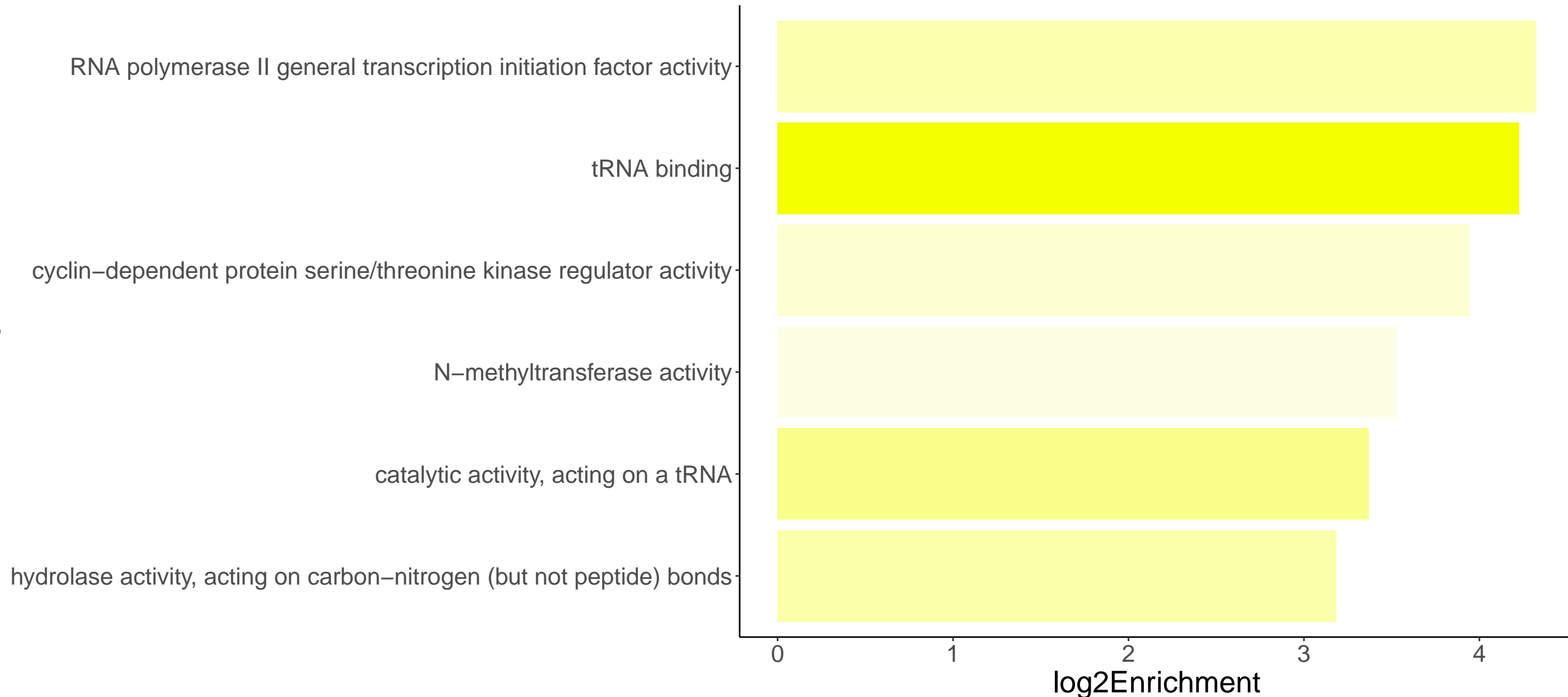
4

log2Enrichment



Re-clustered module 1.14 MF enrichment

Term



Re-clustered module 1.15.1 BP enrichment

Term

nucleoside metabolic process

mRNA 3'-end processing

0

1

2

3

4

log2Enrichment



Re-clustered module 1.15.1 MF enrichment

Term

RNA polymerase II complex binding

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

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

DNA binding

0

1

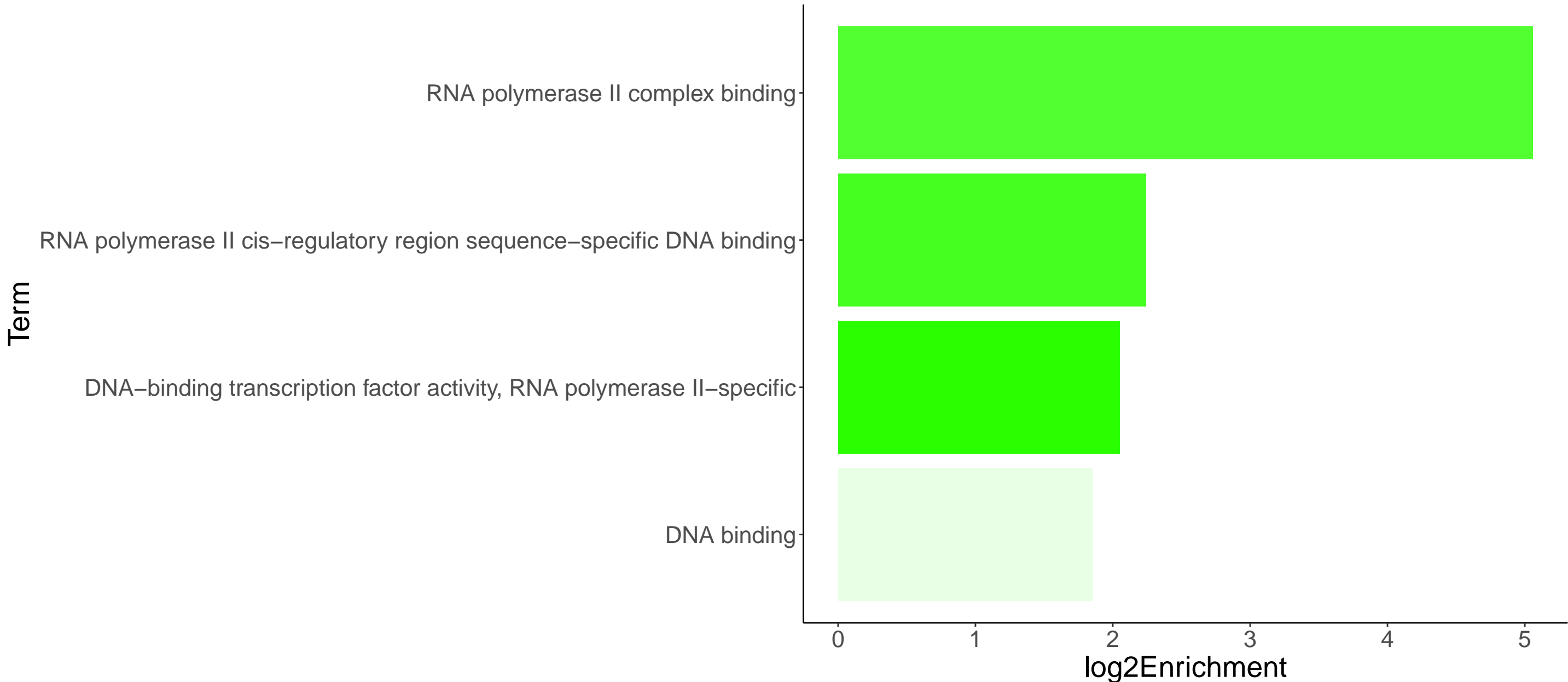
2

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log2Enrichment



Re-clustered module 1.15.11 BP enrichment

Term

log2Enrichment



Re-clustered module 1.15.11 MF enrichment

Term

log2Enrichment



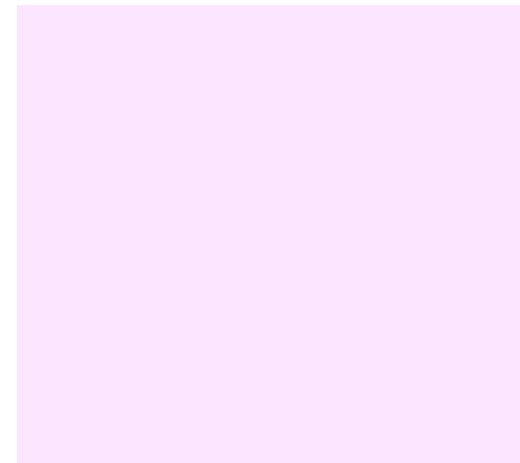
Term

diacylglycerol metabolic process

positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus

0 2 4 6

log2Enrichment



Re-clustered module 1.15.2 MF enrichment

Term

log2Enrichment



Re-clustered module 1.15.3 BP enrichment

Term

protein ADP-ribosylation

viral RNA genome replication

positive regulation of axon extension

regulation of megakaryocyte differentiation

histone H4 acetylation

chromatin assembly or disassembly

DNA packaging

0

1

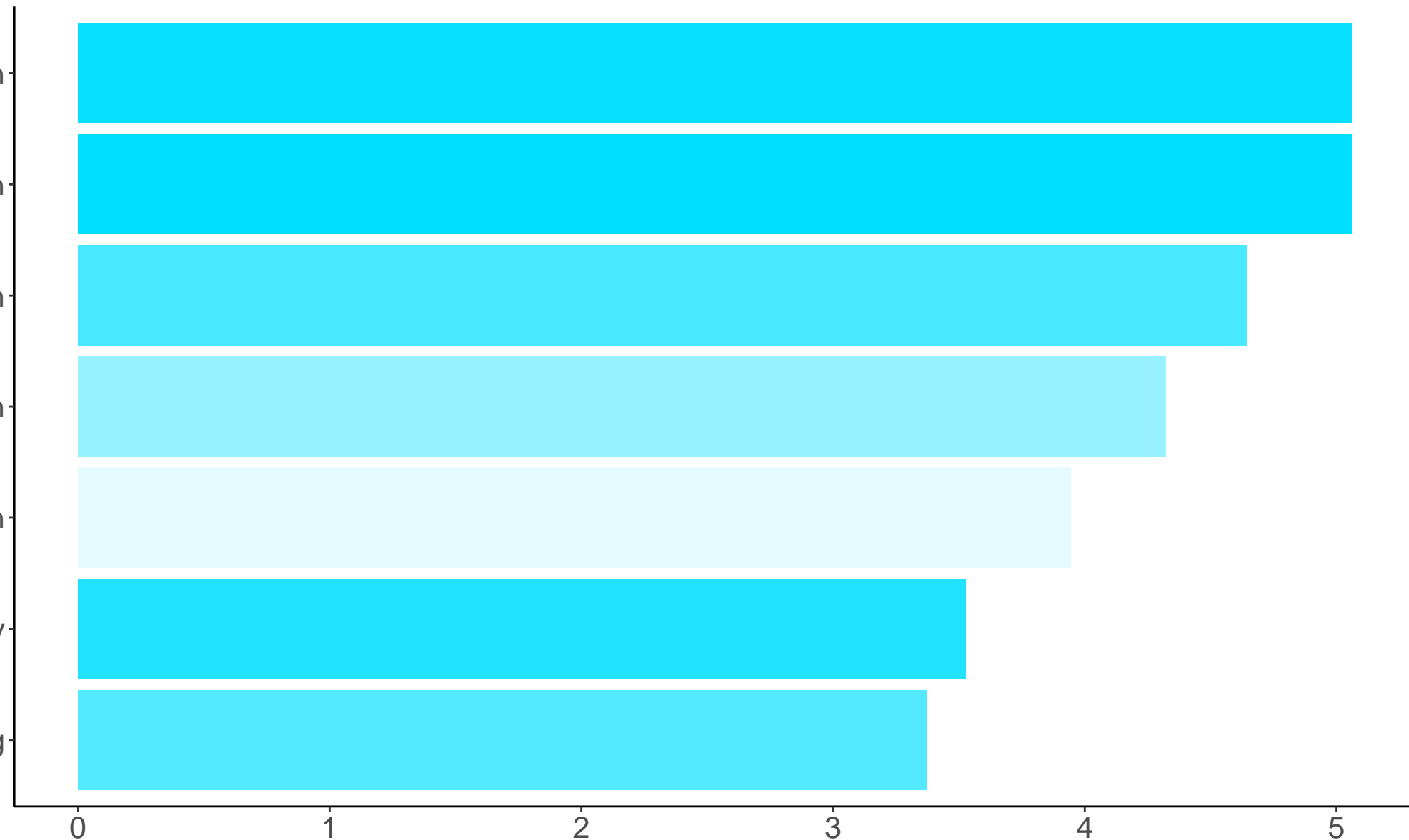
2

3

4

5

log2Enrichment



Re-clustered module 1.15.3 MF enrichment

Term

histone acetyltransferase activity

ubiquitin-like protein transferase activity

metal ion binding

0

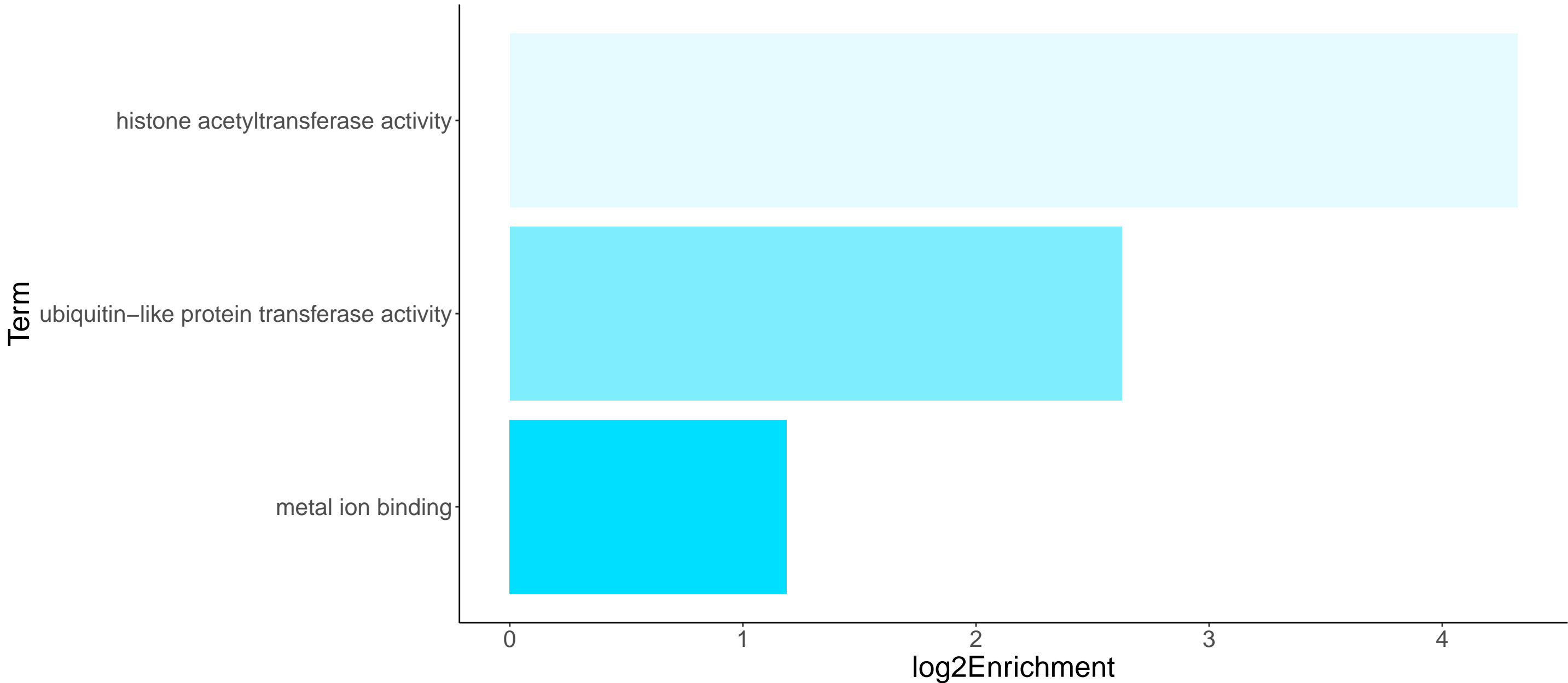
1

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3

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log2Enrichment



Re-clustered module 1.15.4 BP enrichment

Term

log2Enrichment



Re-clustered module 1.15.4 MF enrichment

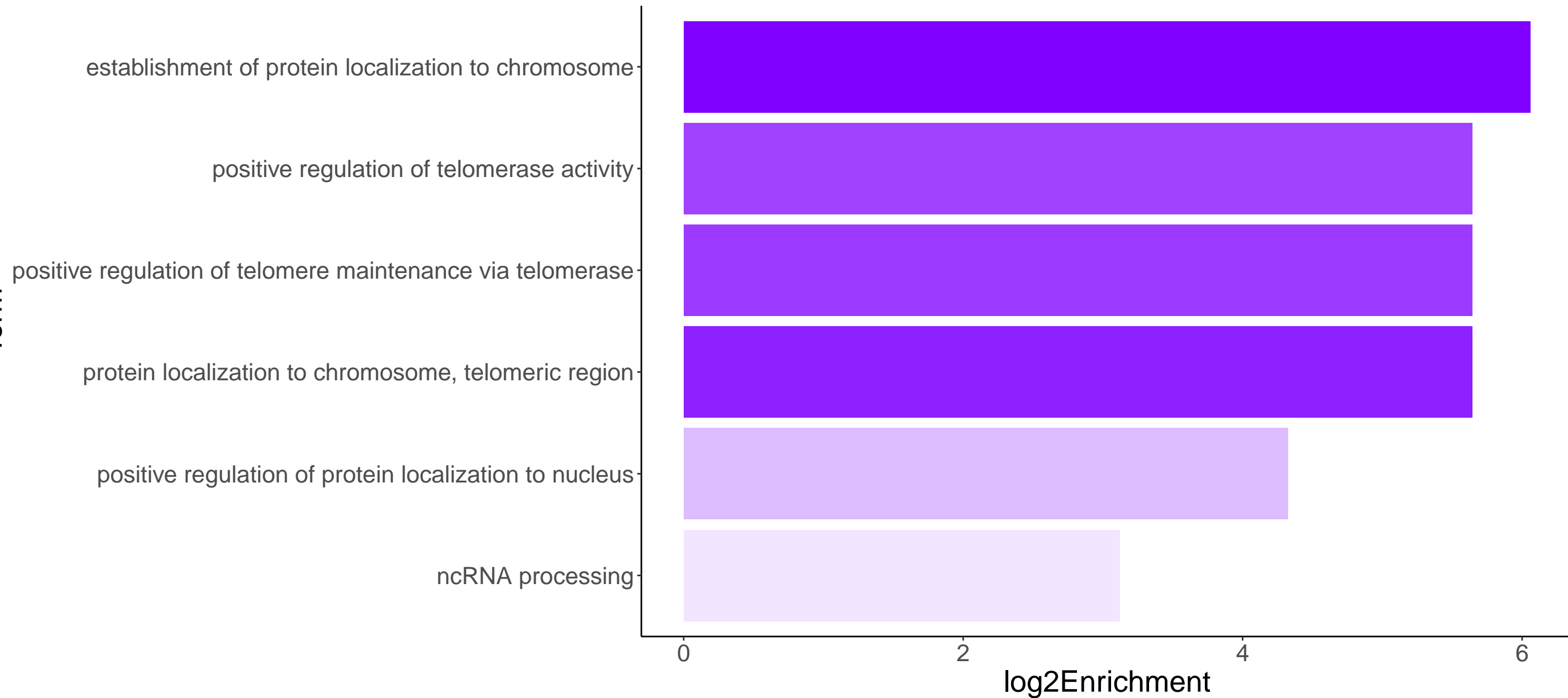
Term

log2Enrichment



Re-clustered module 1.15.5 BP enrichment

Term



Re-clustered module 1.15.5 MF enrichment

Term

snoRNA binding

0

2

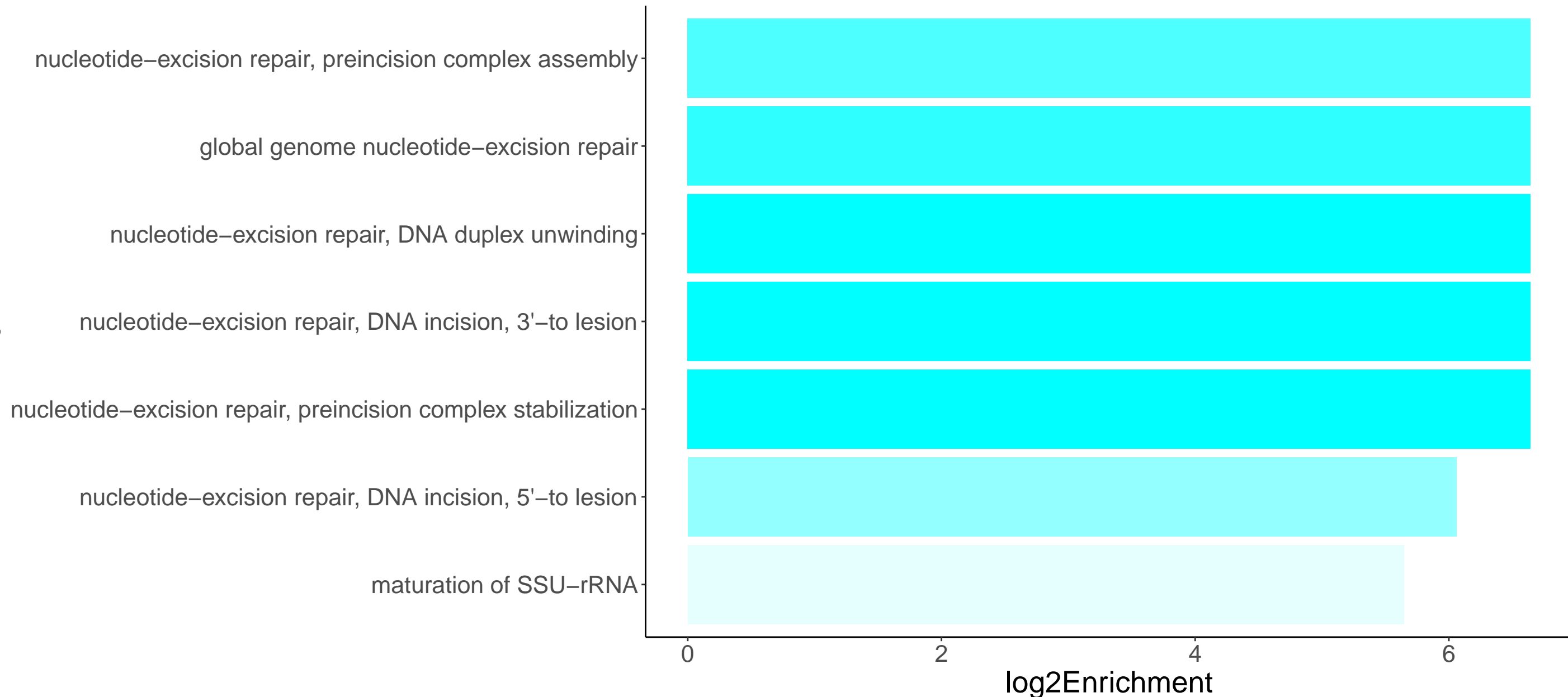
4

log2Enrichment



Re-clustered module 1.15.6 BP enrichment

Term



Re-clustered module 1.15.6 MF enrichment

Term

RNA polymerase II general transcription initiation factor activity

0

2

4

6

log2Enrichment



Re-clustered module 1.15.7 BP enrichment

Term

tRNA methylation

0

2

4

log2Enrichment



Re-clustered module 1.15.7 MF enrichment

Term

tRNA methyltransferase activity

0

2

4

6

log2Enrichment



Re-clustered module 1.15.8 BP enrichment

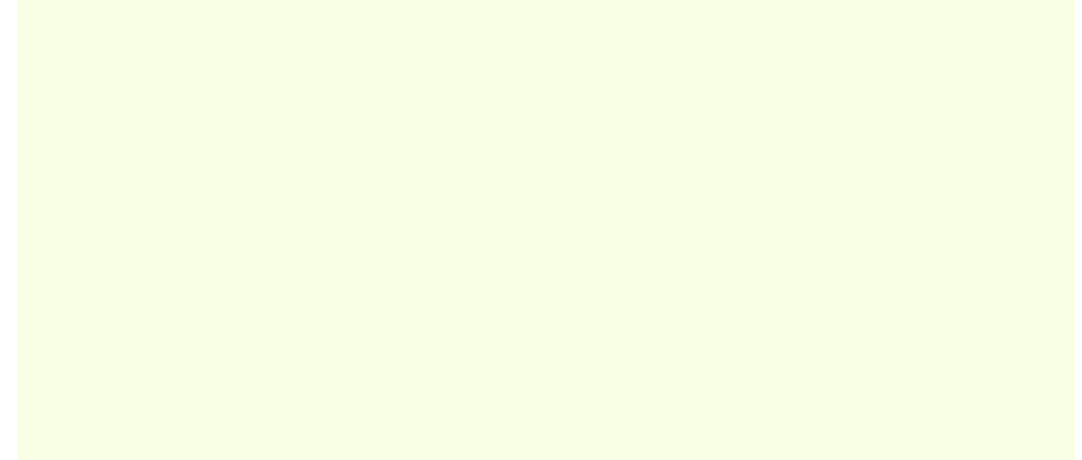
Term

negative regulation of defense response to virus

regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway

0 2 4 6

log2Enrichment



Re-clustered module 1.15.8 MF enrichment

Term

deacetylase activity

0

1

2

3

4

5

log2Enrichment



Re-clustered module 1.15.9 BP enrichment

Term

DNA damage response, signal transduction by p53 class mediator

RNA phosphodiester bond hydrolysis

0

1

2

3

4

log2Enrichment



Re-clustered module 1.15.9 MF enrichment

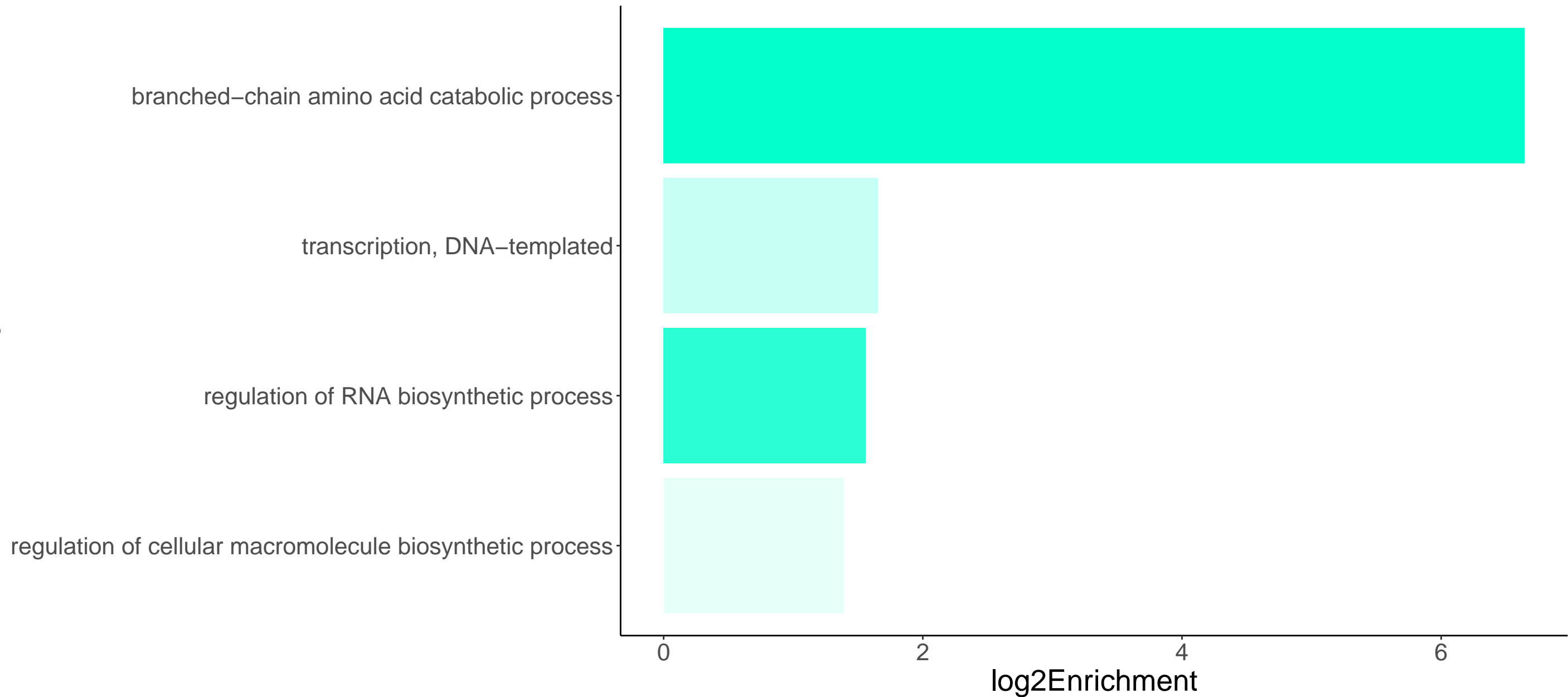
Term

log2Enrichment



Re-clustered module 1.16 BP enrichment

Term



Re-clustered module 1.16 MF enrichment

Term

metal ion binding

0.0

0.5

1.0

log2Enrichment



Re-clustered module 1.17.2 BP enrichment

Term

epithelial cell differentiation involved in kidney development

ATP-dependent chromatin remodeling

kidney morphogenesis

skeletal system development

0

2

4

log2Enrichment



Re-clustered module 1.17.2 MF enrichment

Term

histone acetyltransferase activity

DNA-dependent ATPase activity

histone binding

chromatin binding

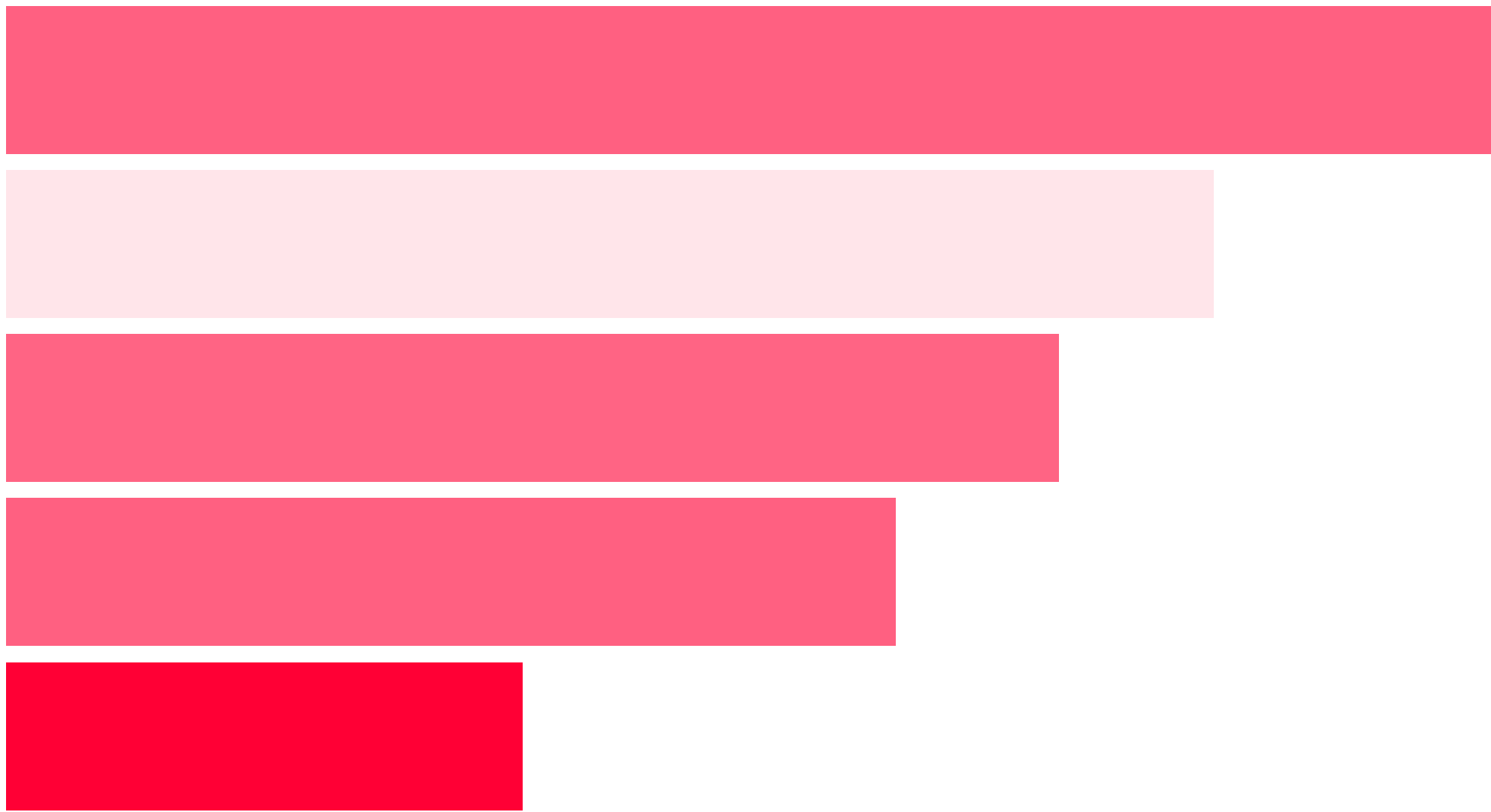
DNA binding

0

2

4

log2Enrichment



Re-clustered module 1.17.3 BP enrichment

Term

regulation of microtubule polymerization

cellular response to hypoxia

0

2

4

log2Enrichment



Re-clustered module 1.17.3 MF enrichment

Term

log2Enrichment



Re-clustered module 1.17.5 BP enrichment

Term

response to ethanol

sphingolipid metabolic process

cellular modified amino acid metabolic process

0

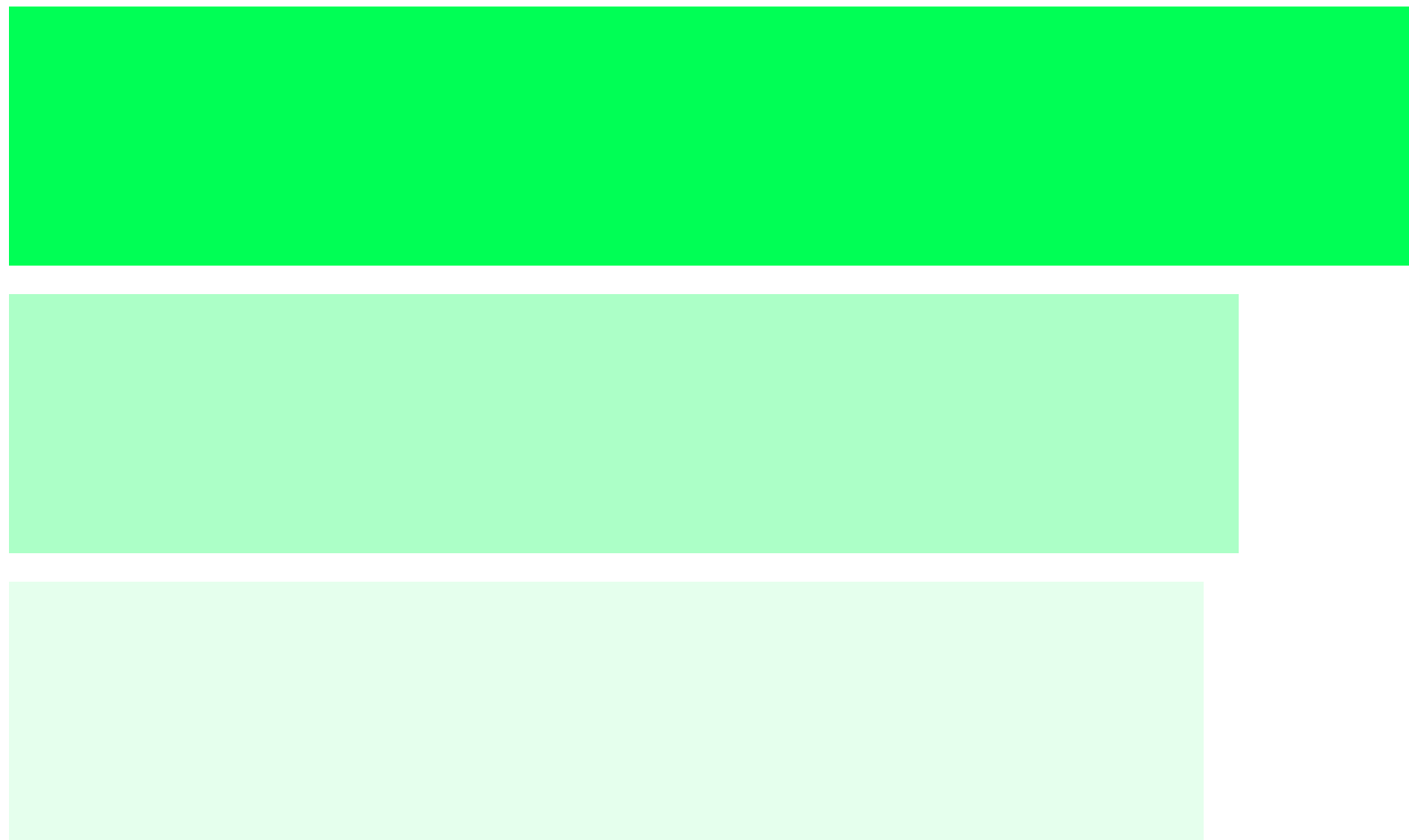
1

2

3

4

log2Enrichment



Re-clustered module 1.17.5 MF enrichment

Term

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

0.0

0.5

1.0

1.5

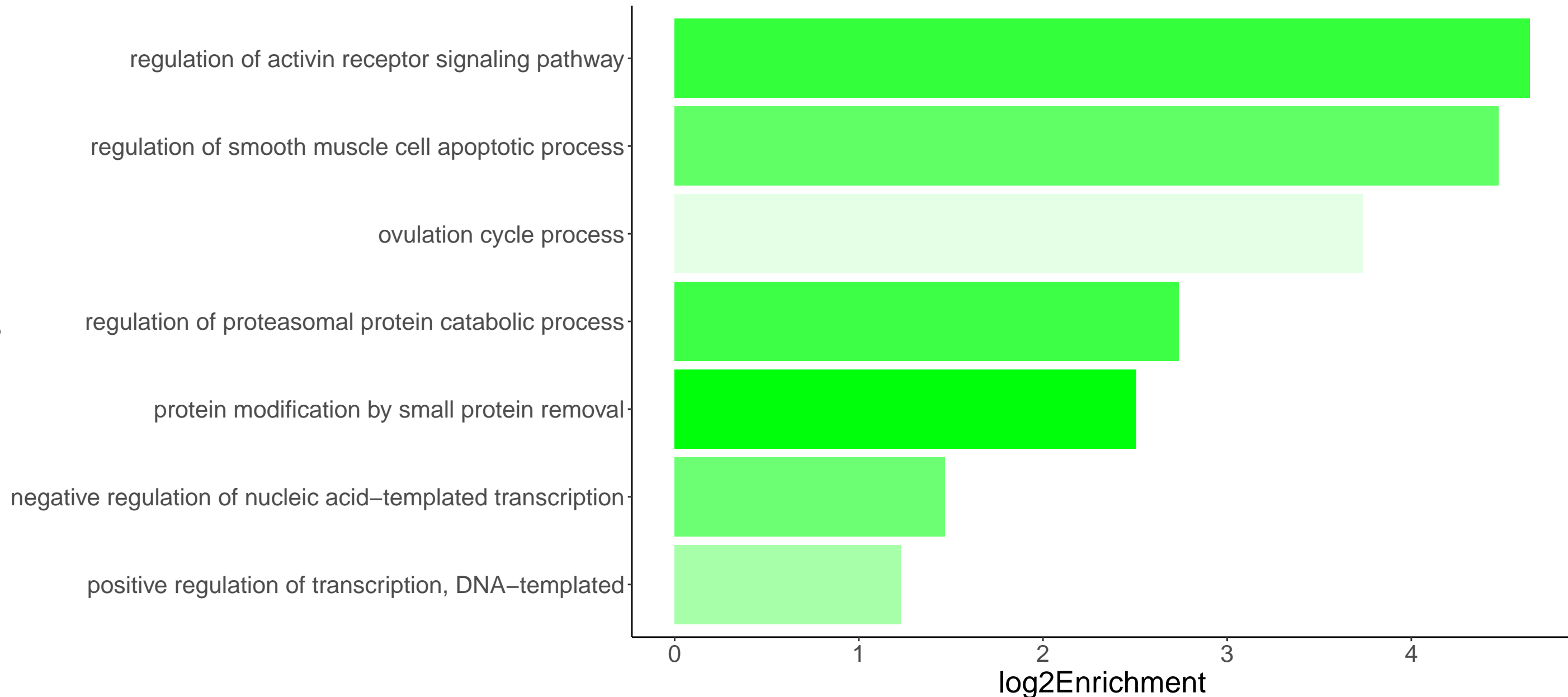
2.0

log2Enrichment



Re-clustered module 1.18 BP enrichment

Term



Re-clustered module 1.18 MF enrichment

Term

R-SMAD binding

disordered domain specific binding

cysteine-type peptidase activity

0

1

2

3

4

5

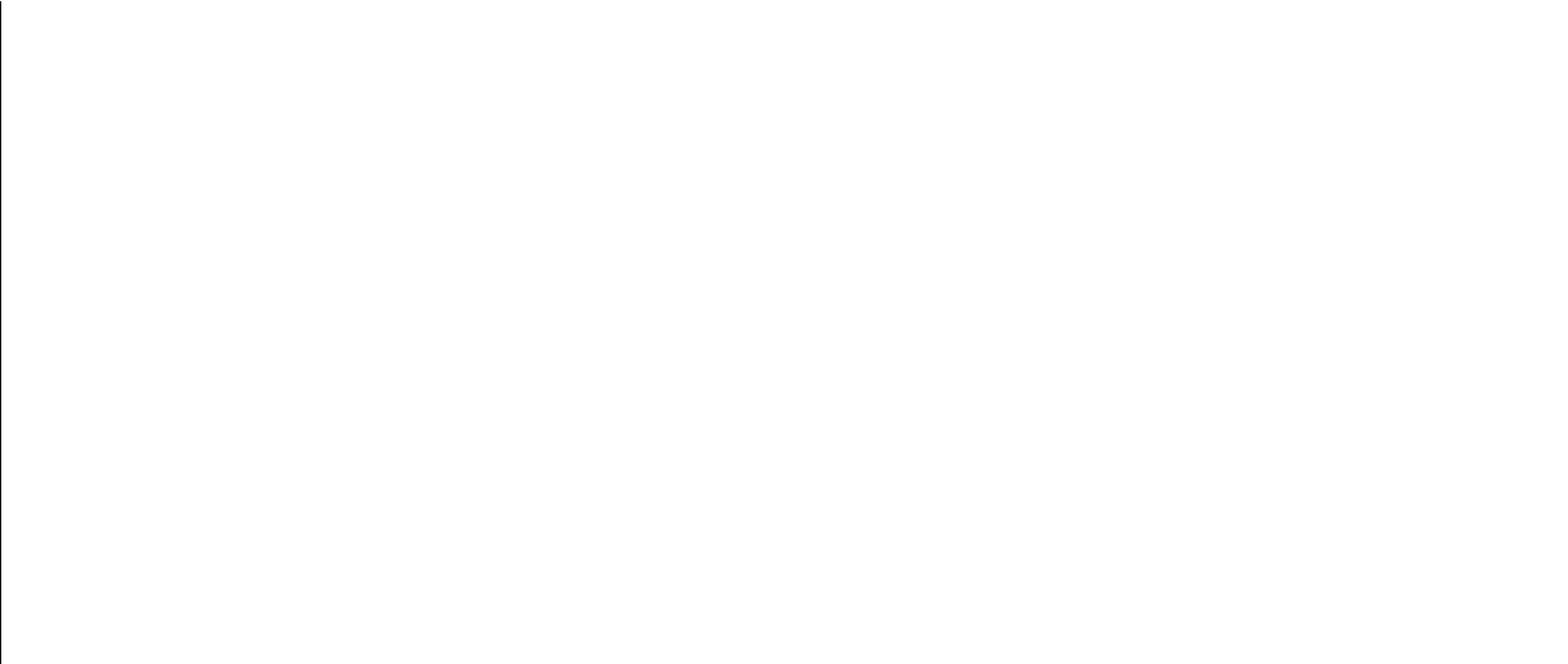
log2Enrichment



Re-clustered module 1.2.1 BP enrichment

Term

log2Enrichment



Re-clustered module 1.2.1 MF enrichment

Term

log2Enrichment



Re-clustered module 1.2.2 BP enrichment

Term

cytoplasmic translational initiation

interleukin-6-mediated signaling pathway

negative regulation of ERK1 and ERK2 cascade

negative regulation of hemopoiesis

ribonucleoprotein complex assembly

viral gene expression

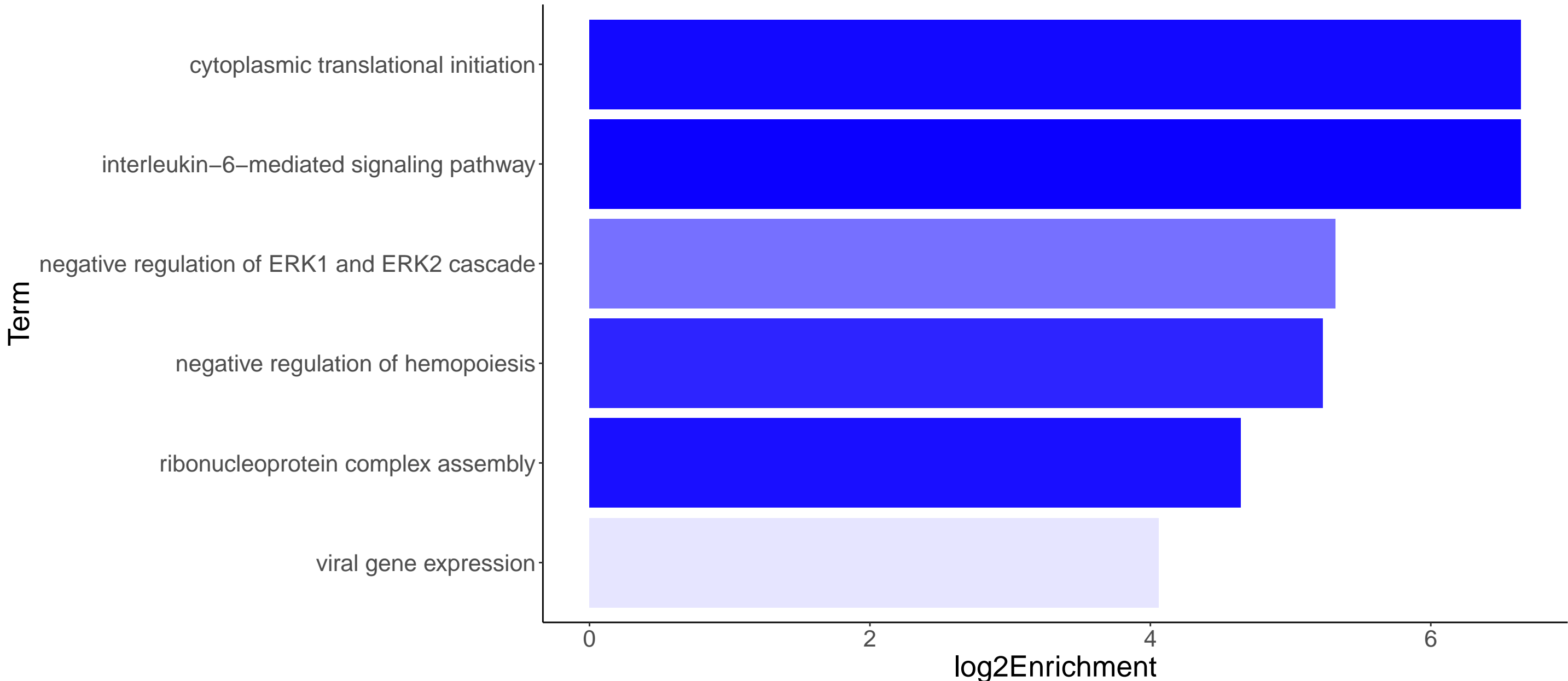
0

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6

log2Enrichment



Re-clustered module 1.2.2 MF enrichment

Term

translation initiation factor activity

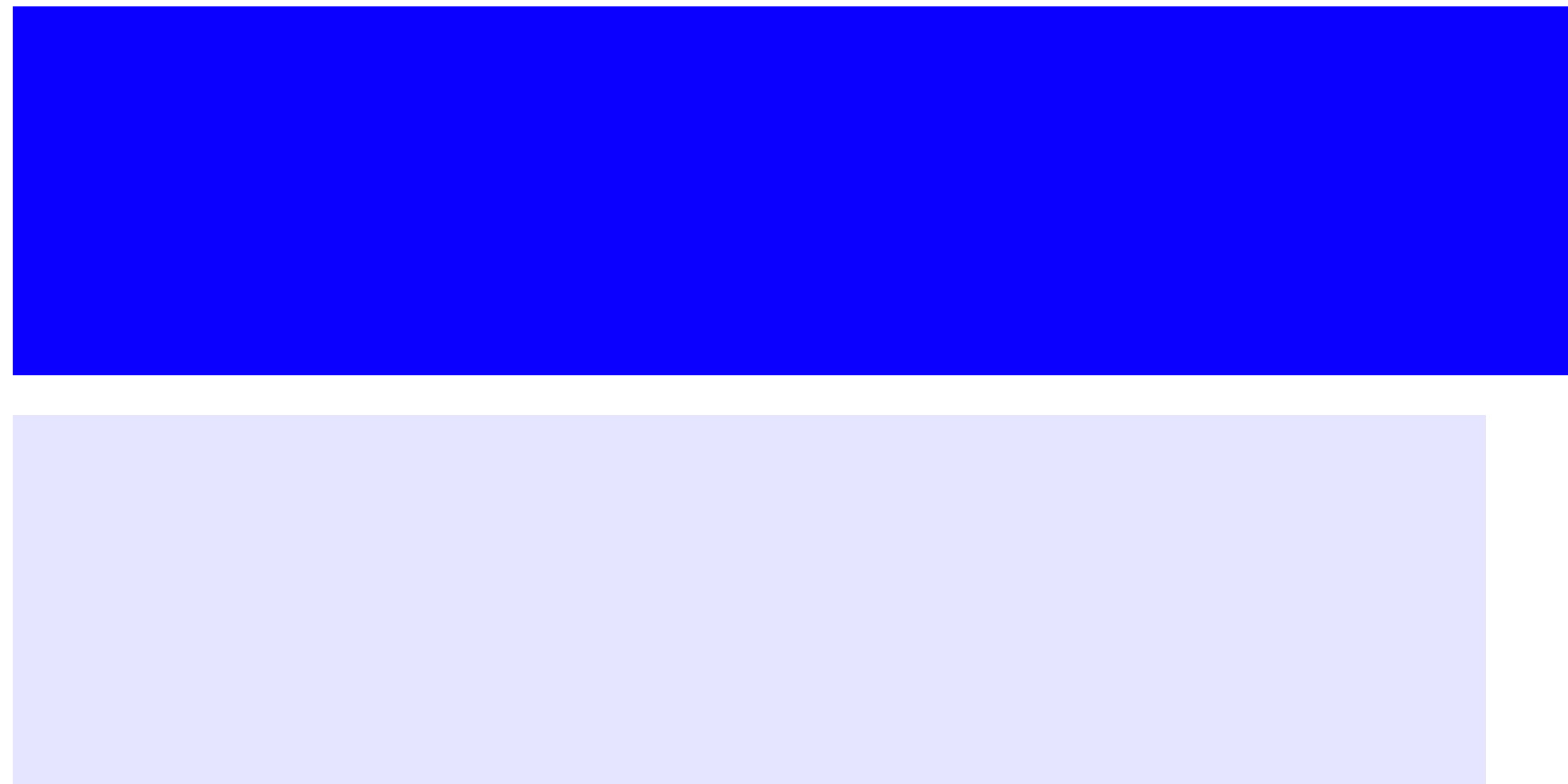
receptor tyrosine kinase binding

0

2

4

log2Enrichment



Re-clustered module 1.2.3 BP enrichment

Term

regulation of phosphoprotein phosphatase activity

0

1

2

3

4

log2Enrichment



Re-clustered module 1.2.3 MF enrichment

Term

protein phosphatase regulator activity

transcription coregulator activity

0

1

2

3

4

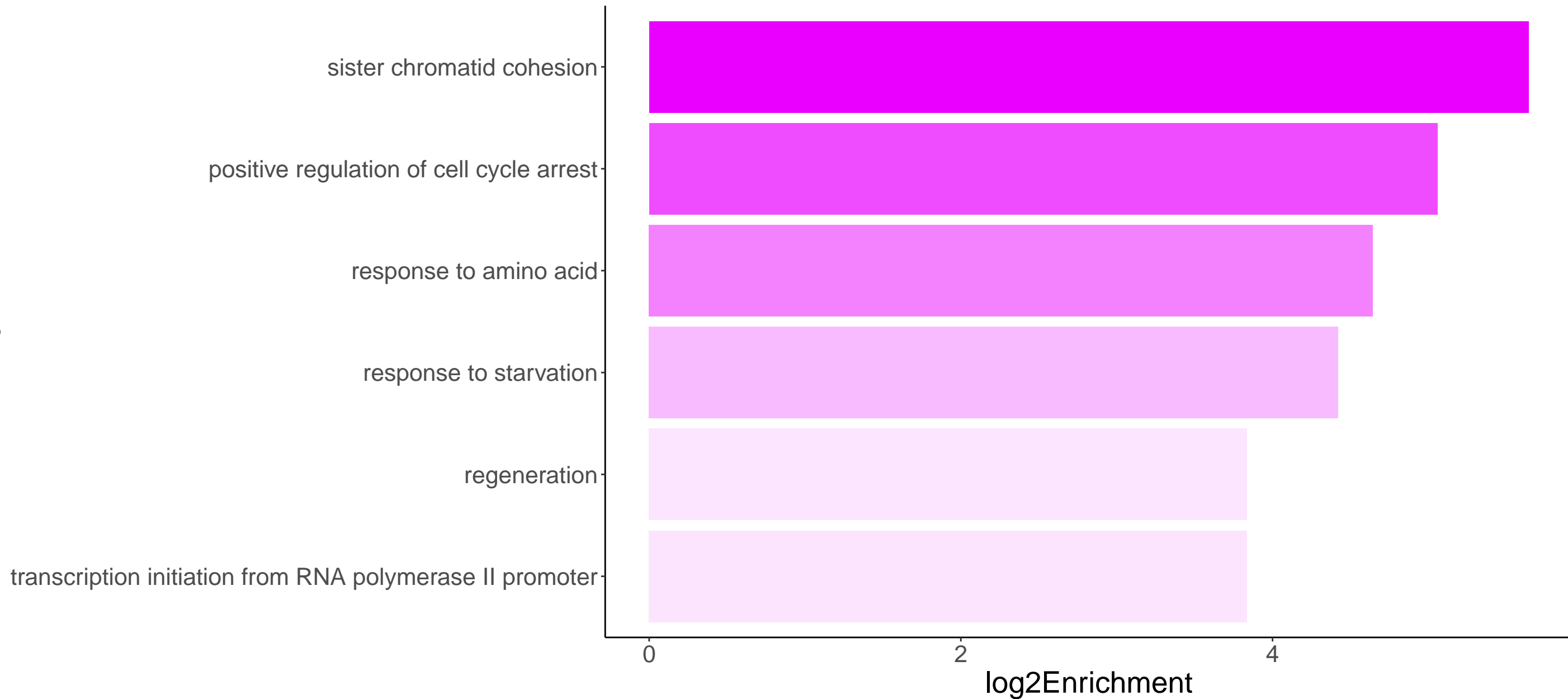
5

log2Enrichment



Re-clustered module 1.2.4 BP enrichment

Term



Re-clustered module 1.2.4 MF enrichment

Term

transcription corepressor activity

0

1

2

3

4

log2Enrichment



Re-clustered module 1.2.5 BP enrichment

Term

negative regulation of cardiac muscle tissue growth

histone deacetylation

regulation of oxidative stress-induced cell death

response to heat

protein deubiquitination

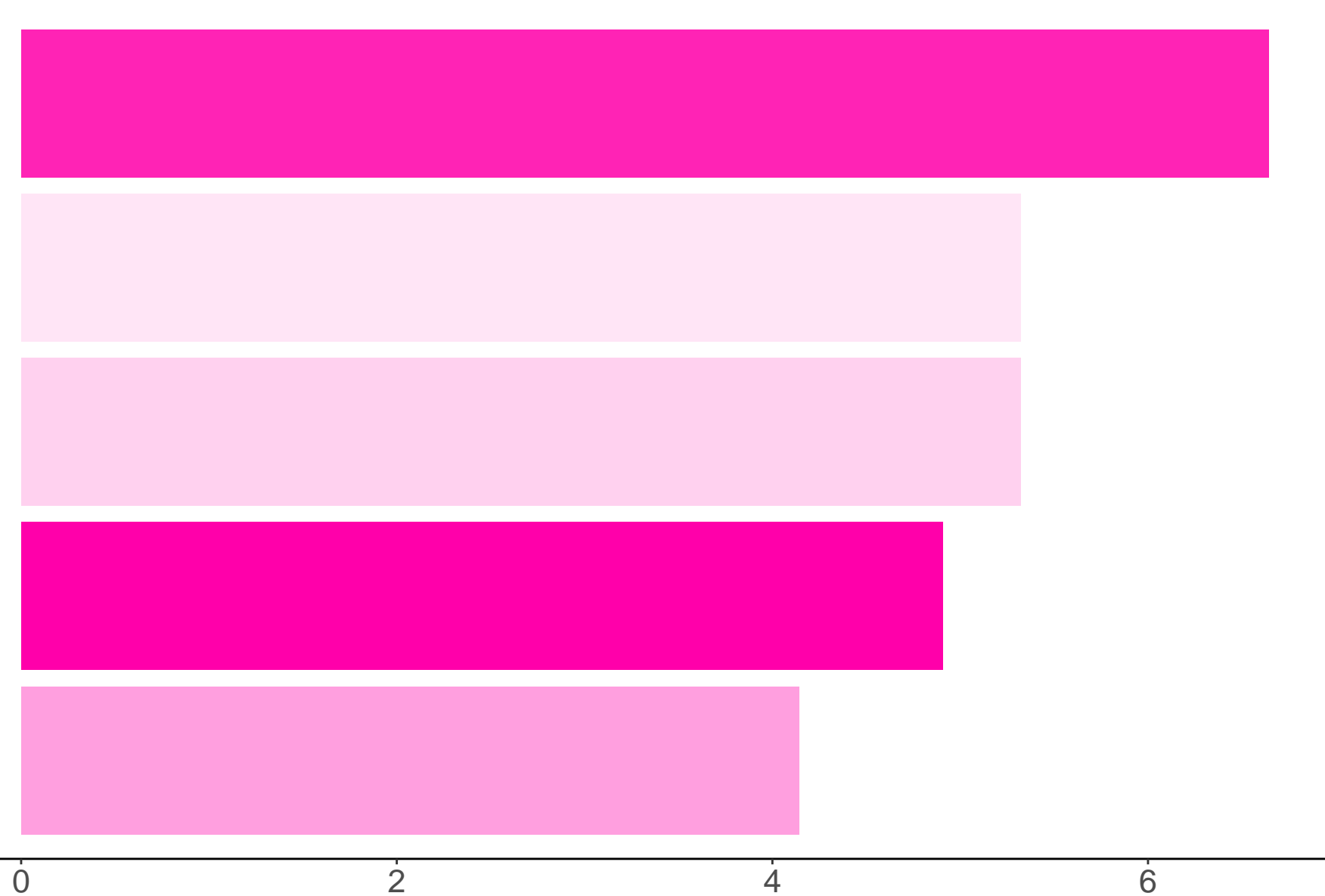
0

2

4

6

log2Enrichment



Re-clustered module 1.2.5 MF enrichment

Term

ubiquitin protein ligase binding

0

1

2

3

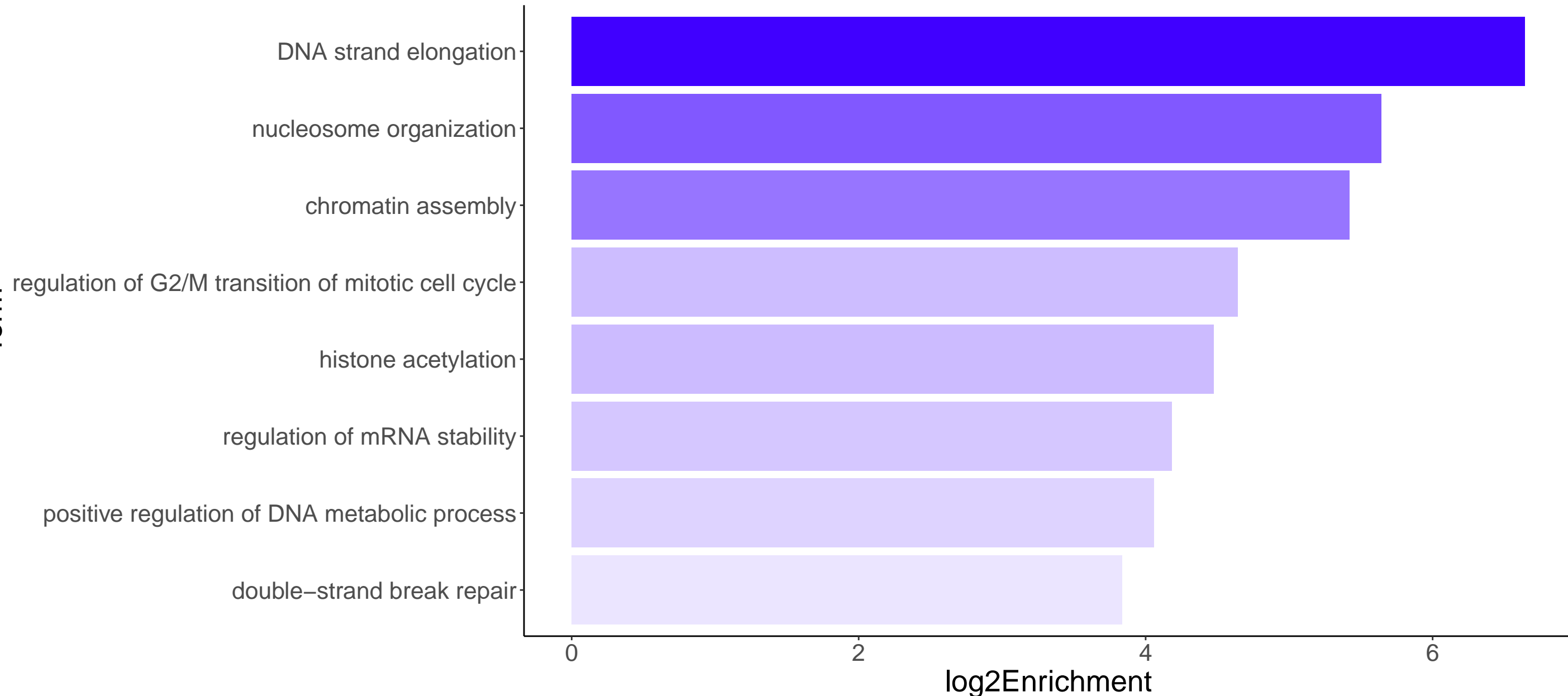
4

log2Enrichment



Re-clustered module 1.2.6 BP enrichment

Term



Re-clustered module 1.2.6 MF enrichment

Term

histone binding

0

1

2

3

log2Enrichment



Re-clustered module 1.24 BP enrichment

Term

log2Enrichment



Re-clustered module 1.24 MF enrichment

Term

poly(U) RNA binding

0

2

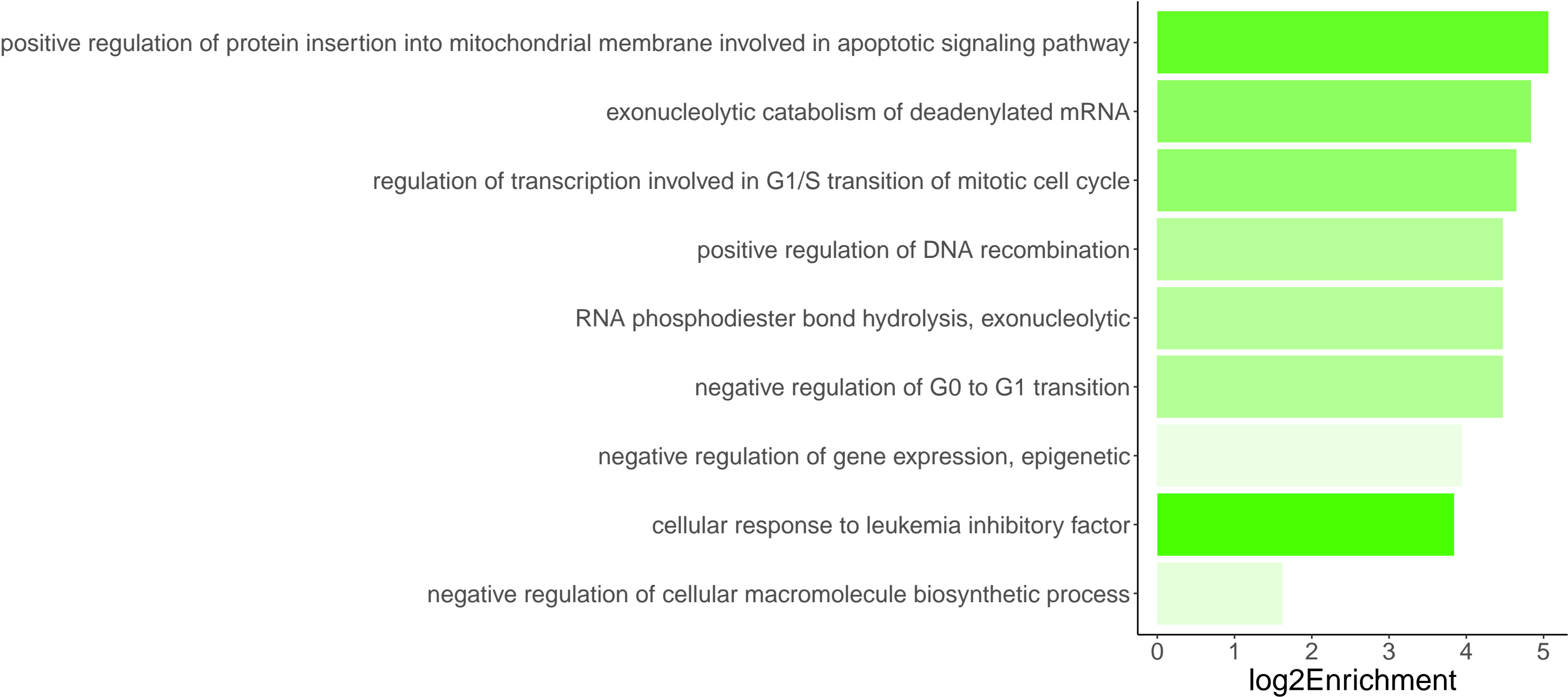
4

6

log2Enrichment

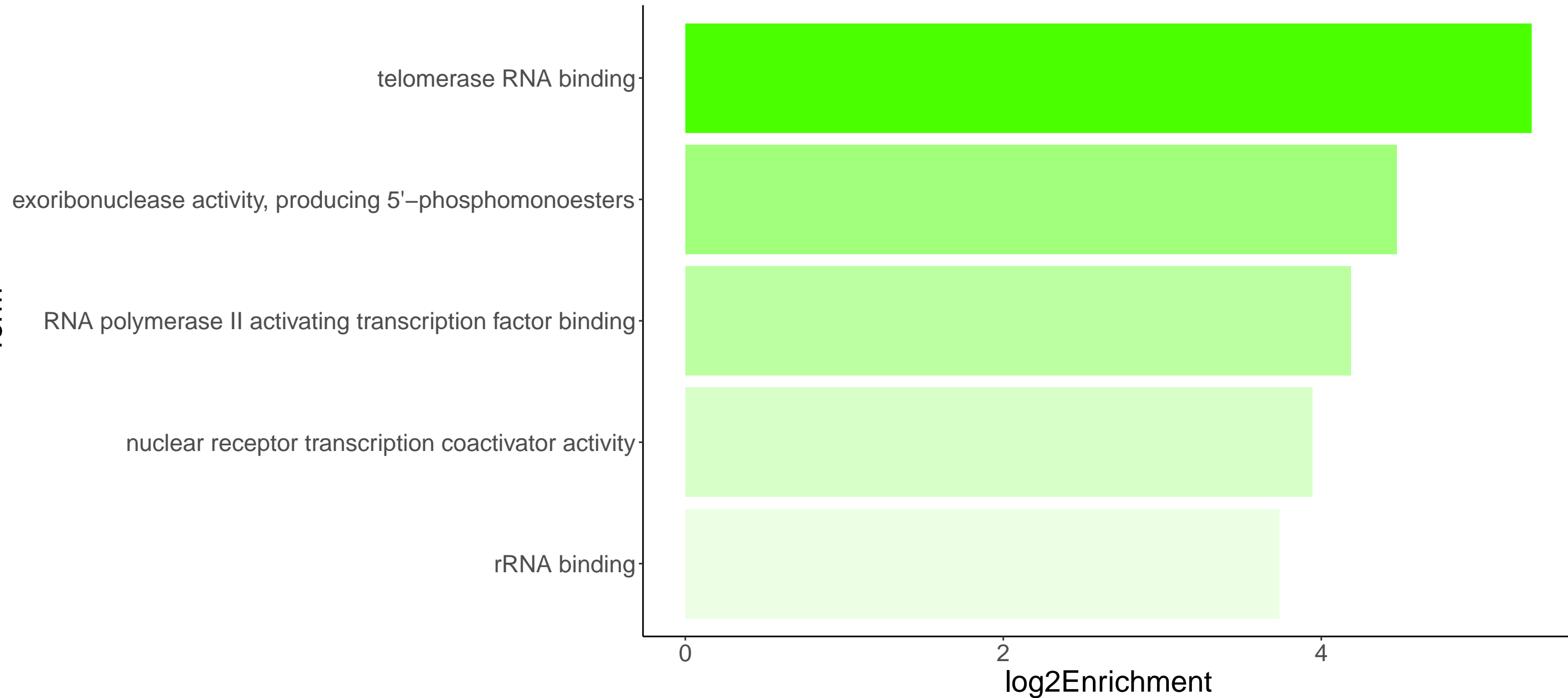


Term



Re-clustered module 1.3 MF enrichment

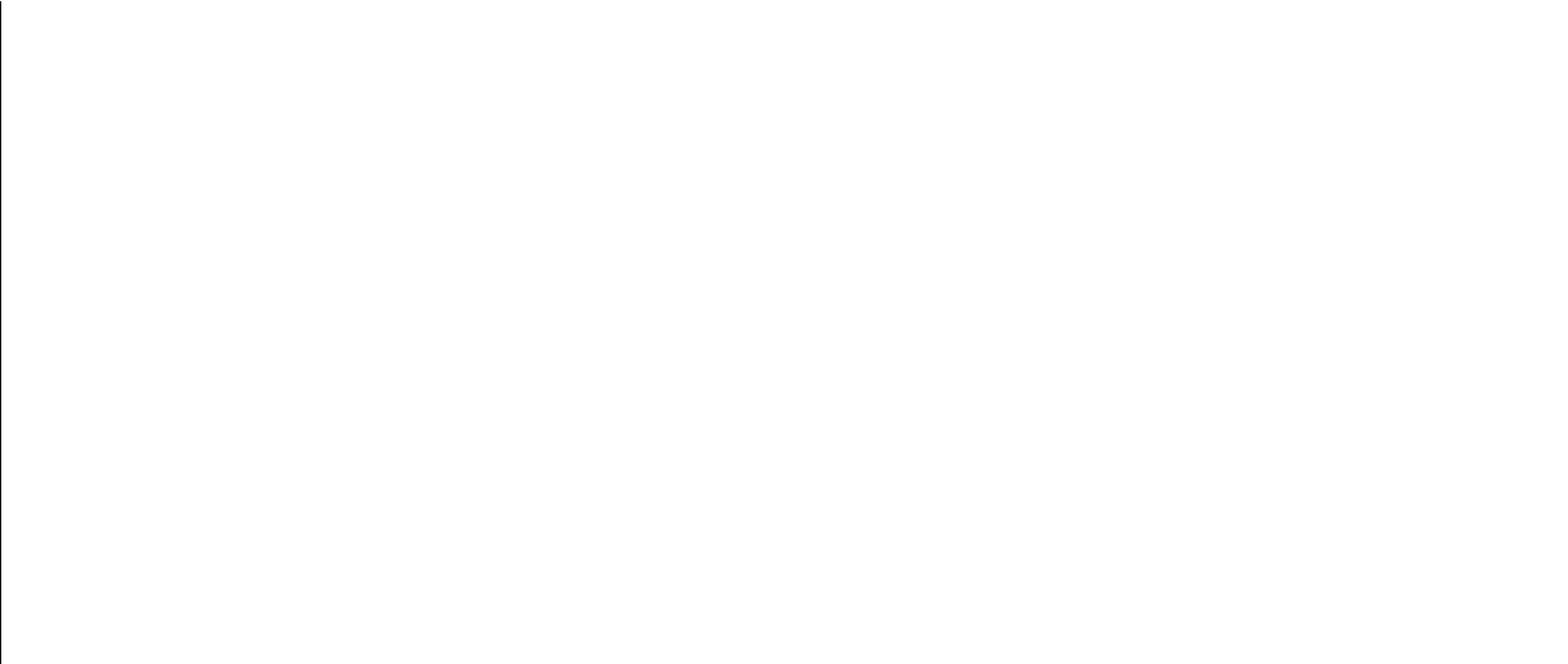
Term



Re-clustered module 1.4.1 BP enrichment

Term

log2Enrichment



Re-clustered module 1.4.1 MF enrichment

Term

log2Enrichment



Re-clustered module 1.4.10 BP enrichment

Term

regulation of glycogen biosynthetic process

positive regulation of glucose metabolic process

0

2

4

6

log2Enrichment



Re-clustered module 1.4.10 MF enrichment

Term

log2Enrichment



Re-clustered module 1.4.11 BP enrichment

Term

left/right pattern formation

0

2

4

6

log2Enrichment



Re-clustered module 1.4.11 MF enrichment

Term

WW domain binding

0

2

4

6

log2Enrichment



Re-clustered module 1.4.2 BP enrichment

Term

SRP-dependent cotranslational protein targeting to membrane

0

2

4

log2Enrichment



Re-clustered module 1.4.2 MF enrichment

Term

nucleoside monophosphate kinase activity

0

2

4

6

log2Enrichment



Re-clustered module 1.4.3 BP enrichment

Term

mRNA cis splicing, via spliceosome

-0.050

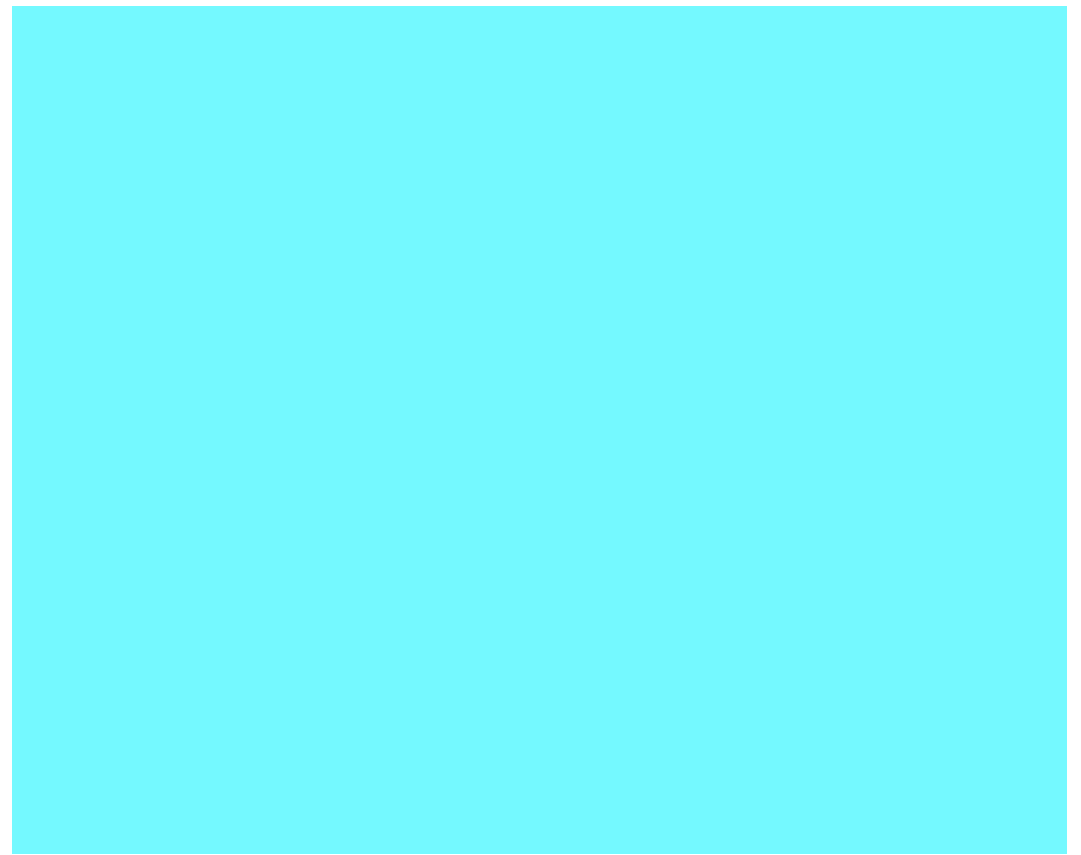
-0.025

0.000

0.025

0.050

log2Enrichment



Re-clustered module 1.4.3 MF enrichment

Term

log2Enrichment



Re-clustered module 1.4.4 BP enrichment

Term

positive regulation of cysteine-type endopeptidase activity involved in apoptotic process

0 1 2 3 4

log2Enrichment



Re-clustered module 1.4.4 MF enrichment

Term

log2Enrichment



Re-clustered module 1.4.5 BP enrichment

Term

lens fiber cell differentiation

lens morphogenesis in camera-type eye

-0.050

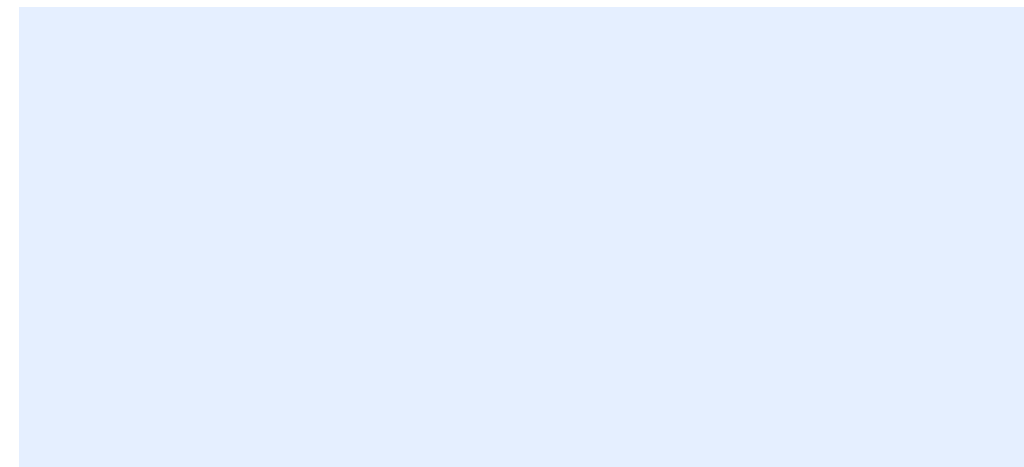
-0.025

0.000

0.025

0.050

log2Enrichment



Re-clustered module 1.4.5 MF enrichment

Term

structural constituent of eye lens

-0.050

-0.025

0.000

0.025

0.050

log2Enrichment



Re-clustered module 1.4.6 BP enrichment

Term

regulation of transcription by RNA polymerase II

0.0

0.5

1.0

1.5

log2Enrichment



Re-clustered module 1.4.6 MF enrichment

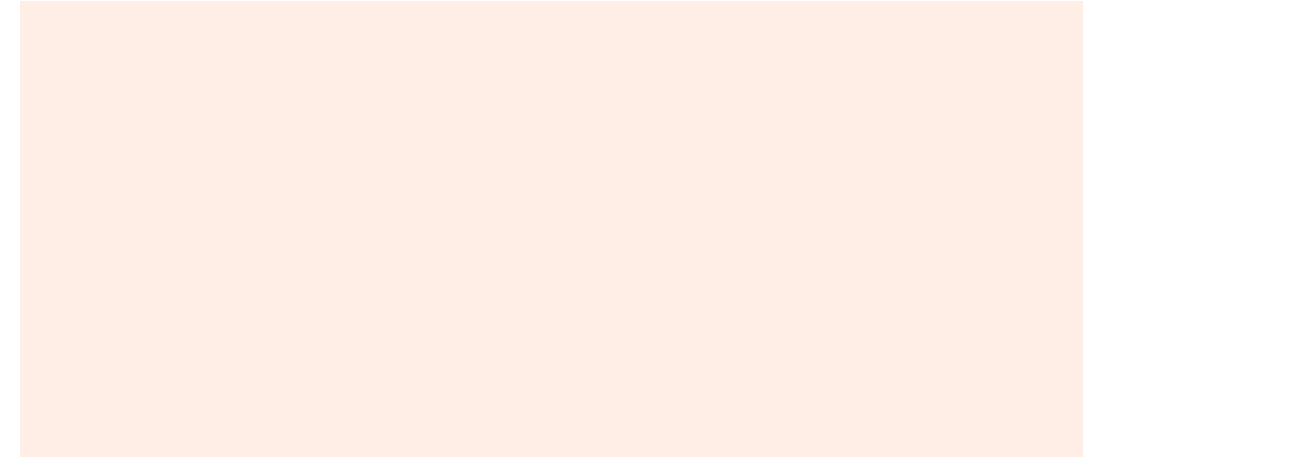
Term

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

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

0.0 0.5 1.0 1.5 2.0 2.5

log2Enrichment



Re-clustered module 1.4.7 BP enrichment

Term

cytokine biosynthetic process

regulation of fibroblast growth factor receptor signaling pathway

0

2

4

6

log2Enrichment



Re-clustered module 1.4.7 MF enrichment

Term

endoribonuclease activity, producing 5'-phosphomonoesters

fibroblast growth factor binding

0

2

4

6

log2Enrichment



Re-clustered module 1.4.8 BP enrichment

Term

maintenance of protein location in cell

negative regulation of actin filament polymerization

0

2

4

6

log2Enrichment



Re-clustered module 1.4.8 MF enrichment

Term

actin monomer binding

-0.050

-0.025

0.000

0.025

0.050

log2Enrichment



Re-clustered module 1.4.9 BP enrichment

Term

entrainment of circadian clock by photoperiod

blastocyst hatching

regulation of double-strand break repair via nonhomologous end joining

mitotic G2 DNA damage checkpoint

protein localization to chromatin

regulation of translation in response to stress

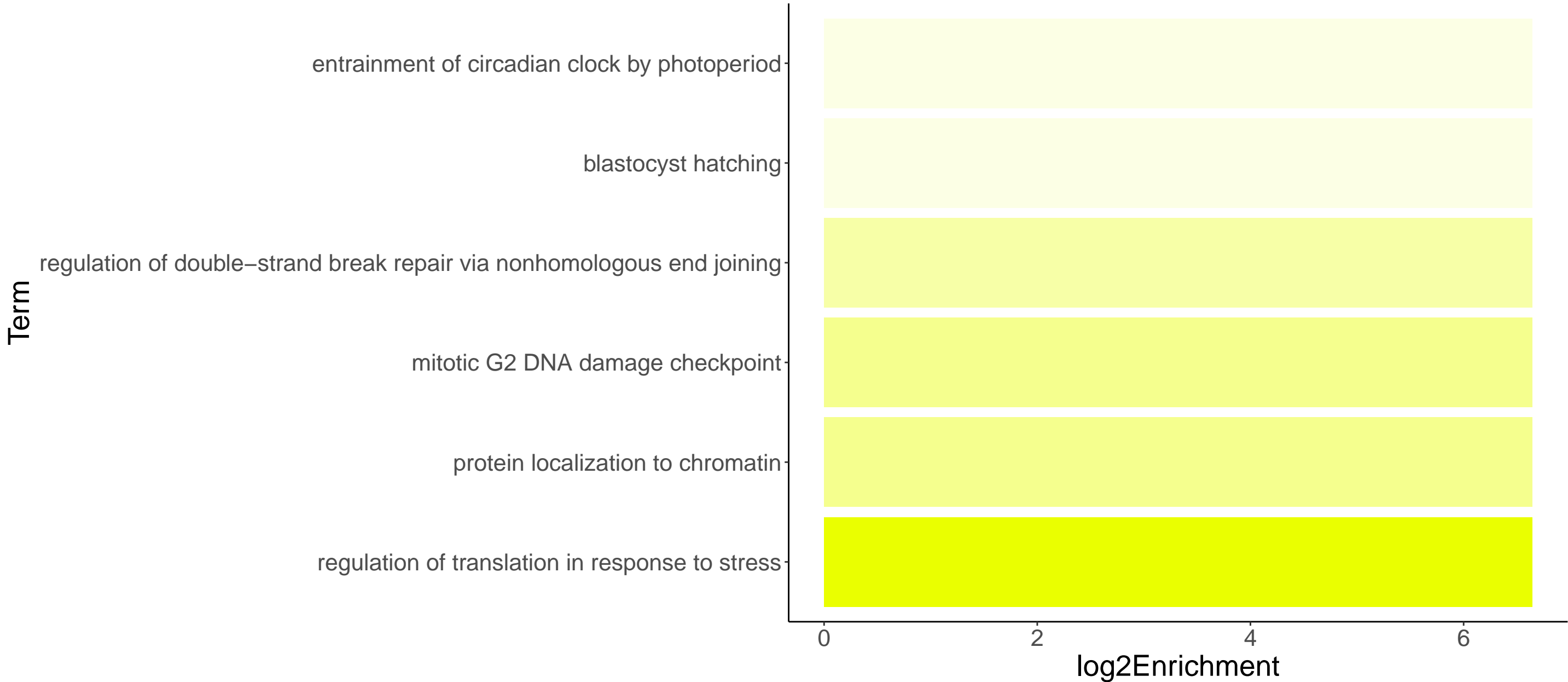
0

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log2Enrichment



Re-clustered module 1.4.9 MF enrichment

Term

taste receptor activity

0

2

4

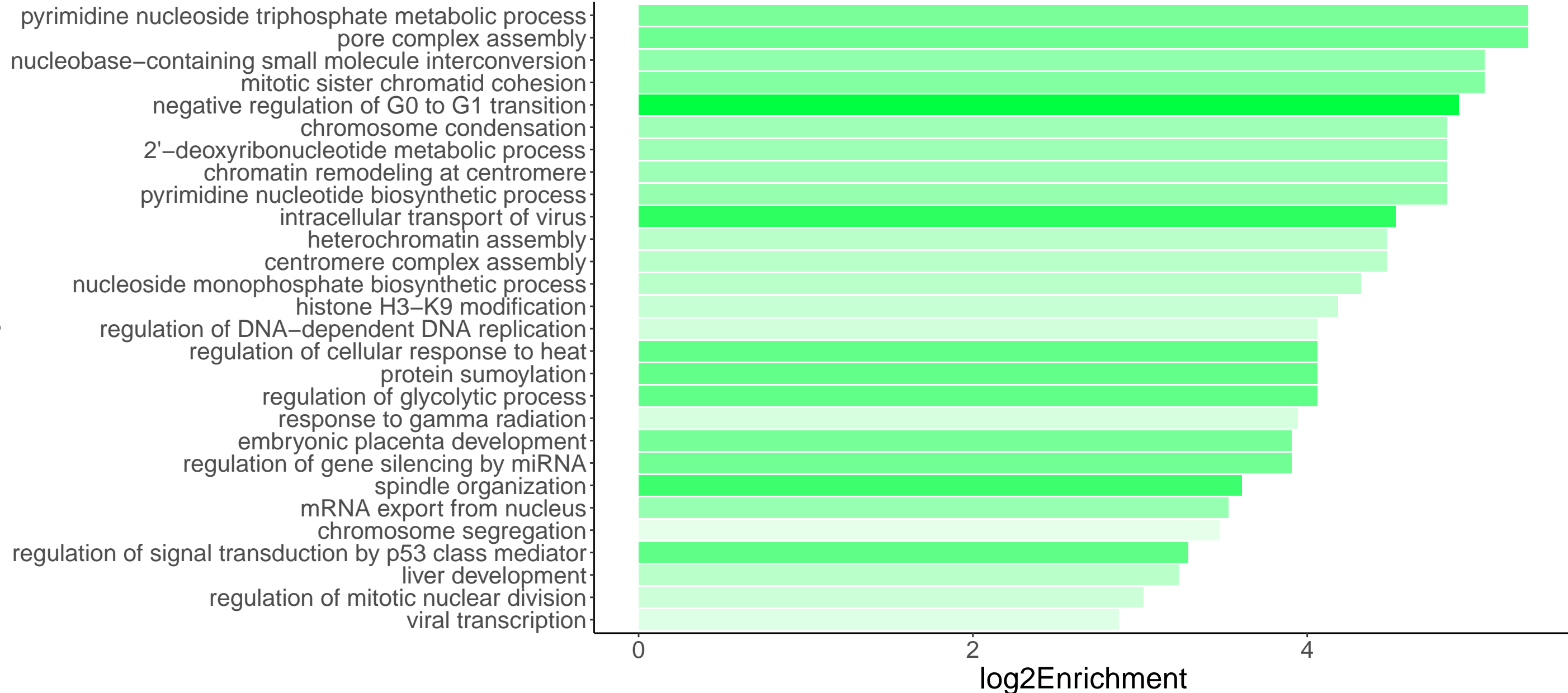
6

log2Enrichment



Re-clustered module 1.5.1 BP enrichment

Term



Re-clustered module 1.5.1 MF enrichment

Term

structural constituent of nuclear pore

DNA-dependent ATPase activity

helicase activity

DNA binding

0

1

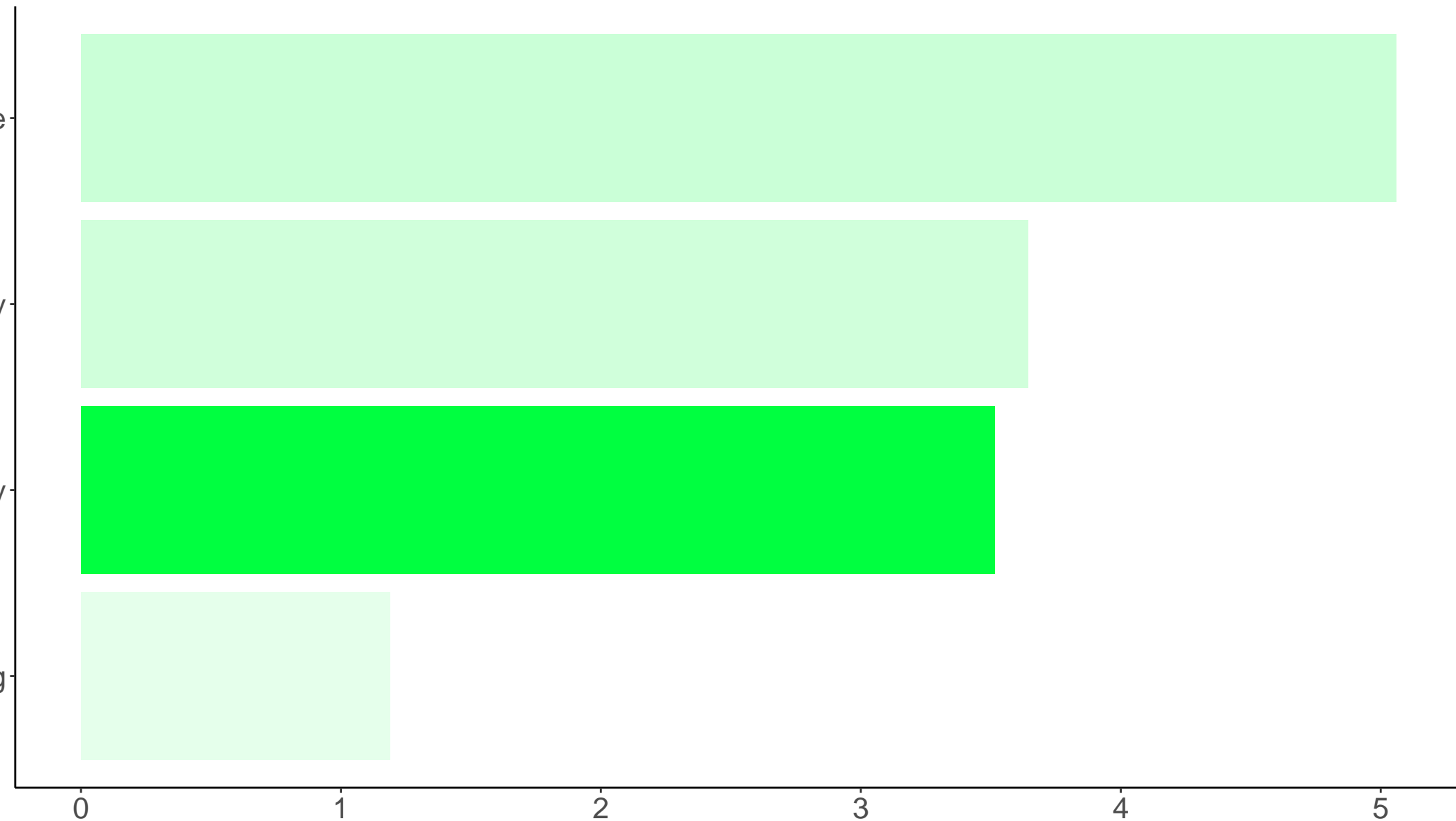
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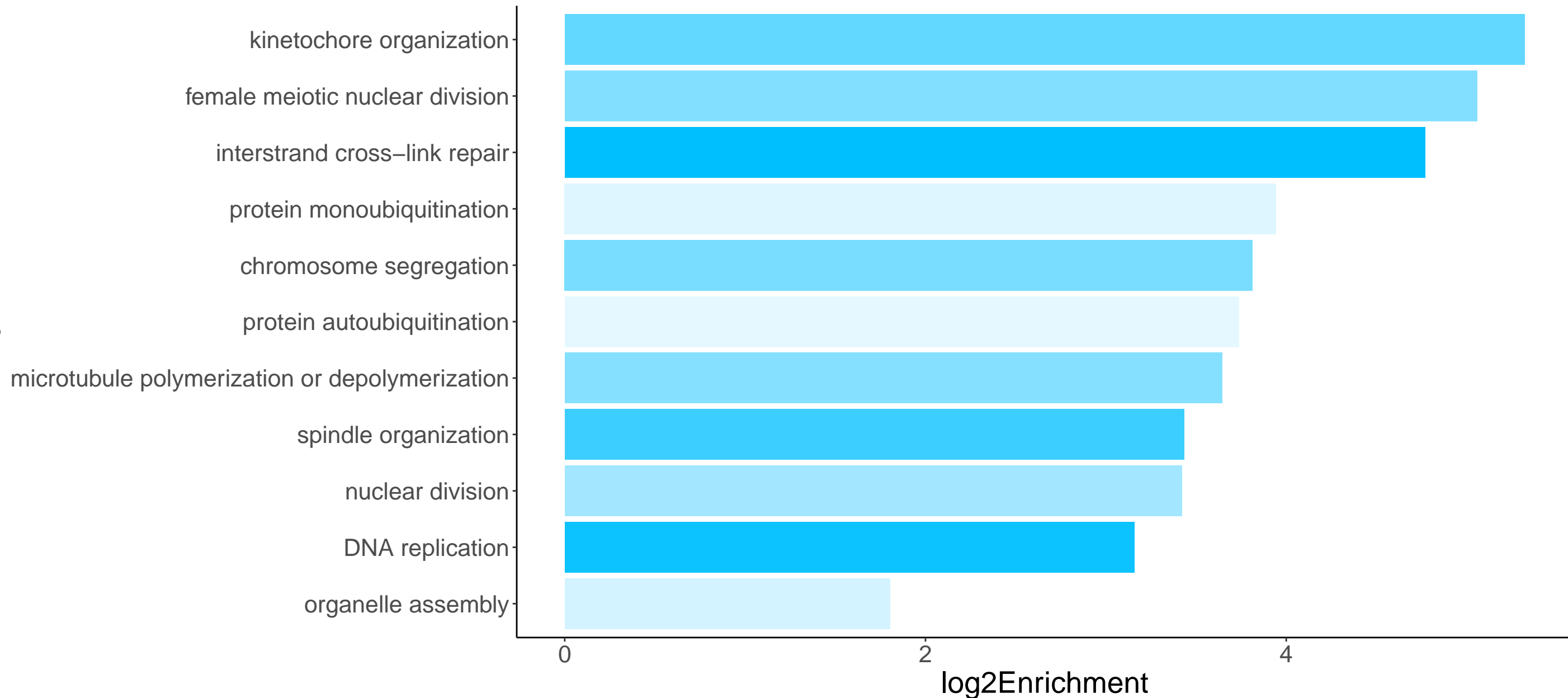
4

5

log2Enrichment



Re-clustered module 1.5.10 BP enrichment



Re-clustered module 1.5.10 MF enrichment

Term

single-stranded DNA binding

0

1

2

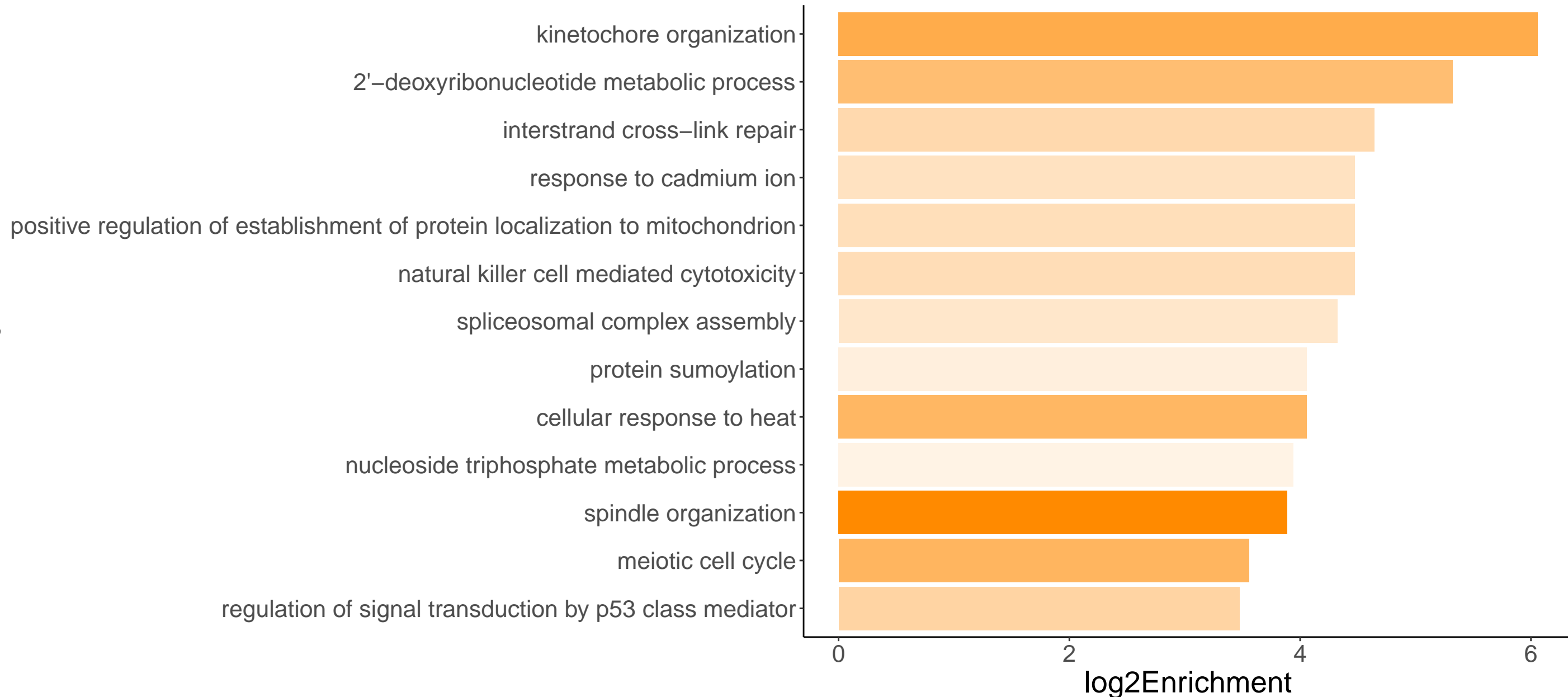
3

log2Enrichment



Re-clustered module 1.5.11 BP enrichment

Term



Re-clustered module 1.5.11 MF enrichment

Term

MHC protein binding

double-stranded RNA binding

magnesium ion binding

protein heterodimerization activity

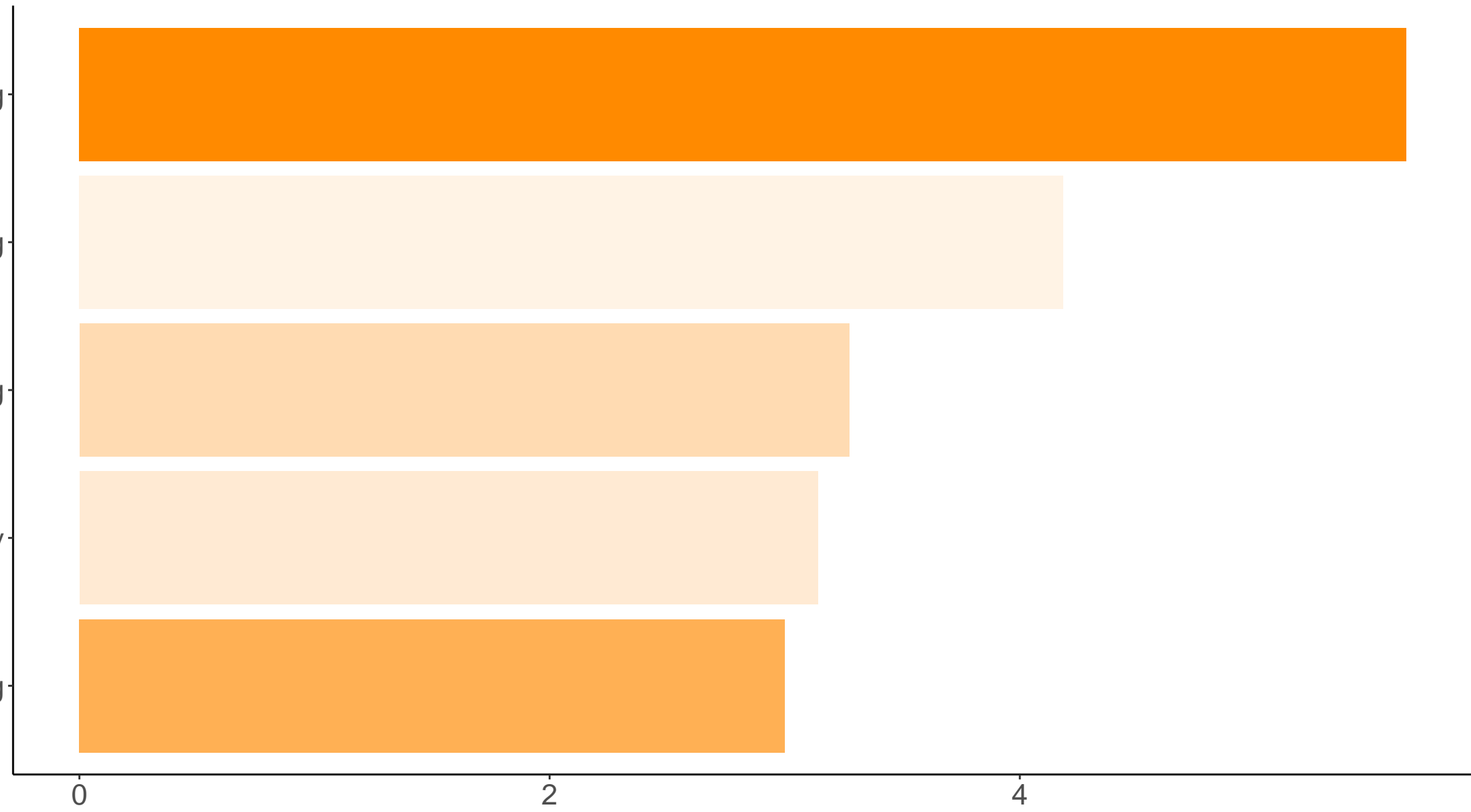
GTP binding

0

2

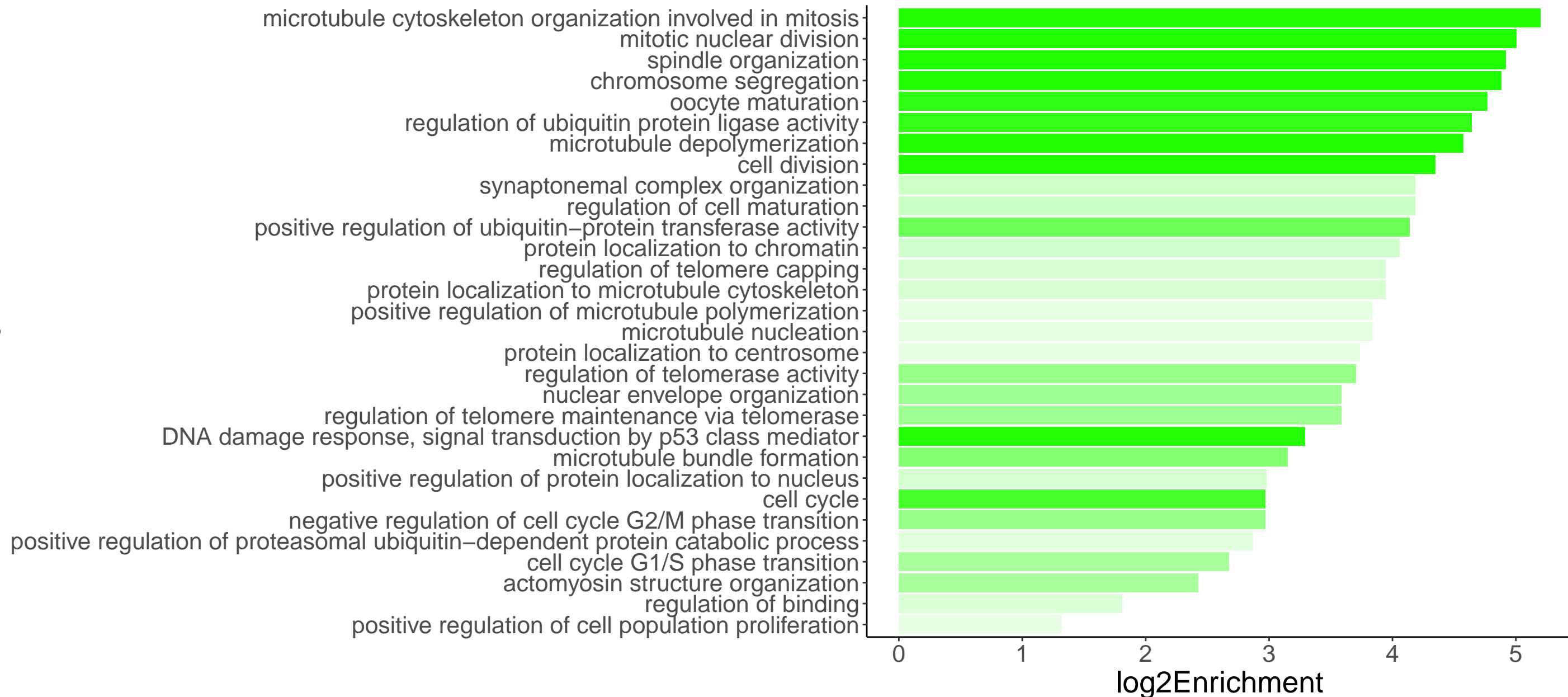
4

log2Enrichment



Re-clustered module 1.5.2 BP enrichment

Term



Re-clustered module 1.5.2 MF enrichment

Term

dynein complex binding

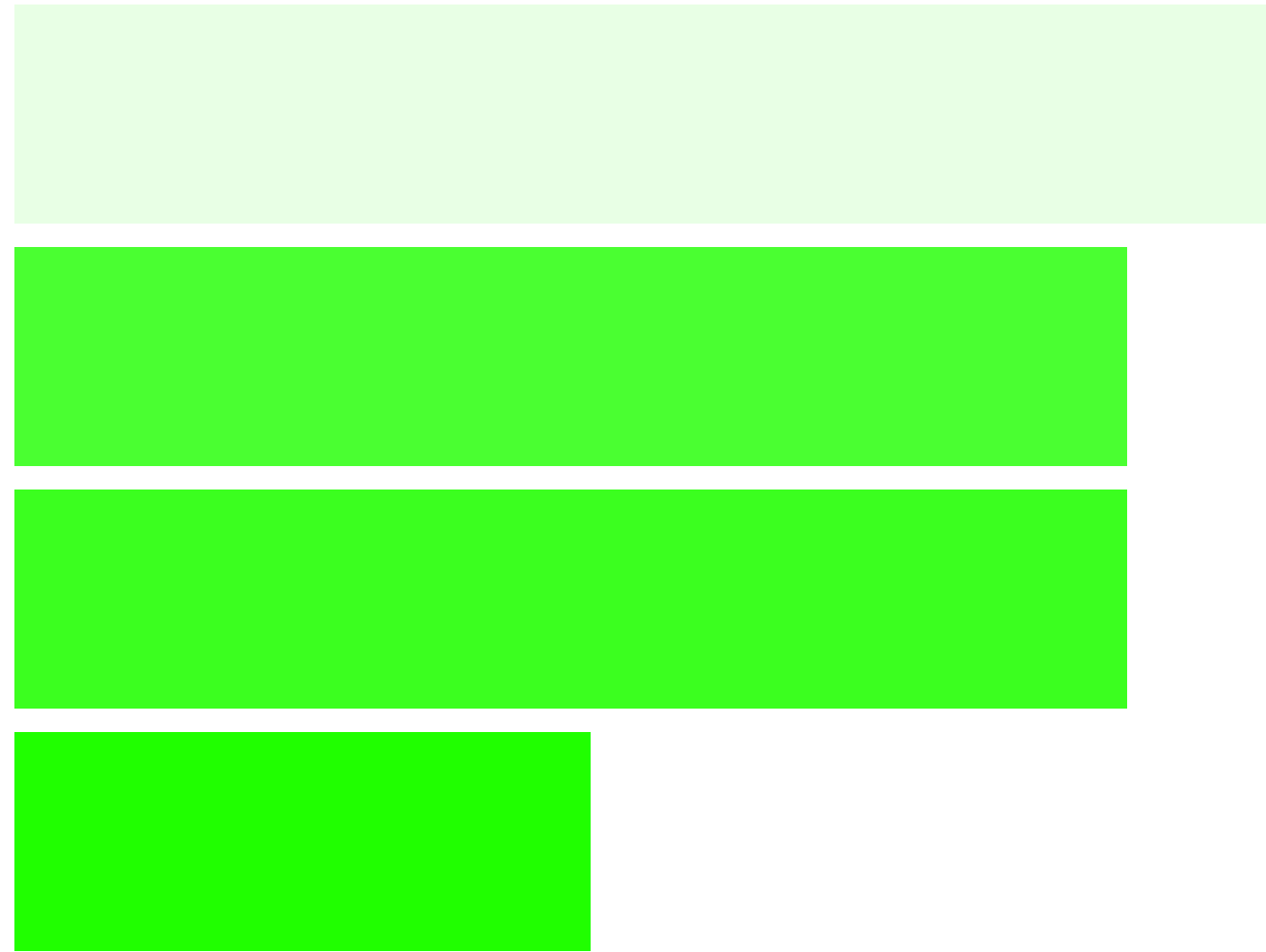
cyclin-dependent protein serine/threonine kinase regulator activity

protein serine/threonine/tyrosine kinase activity

protein serine/threonine kinase activity

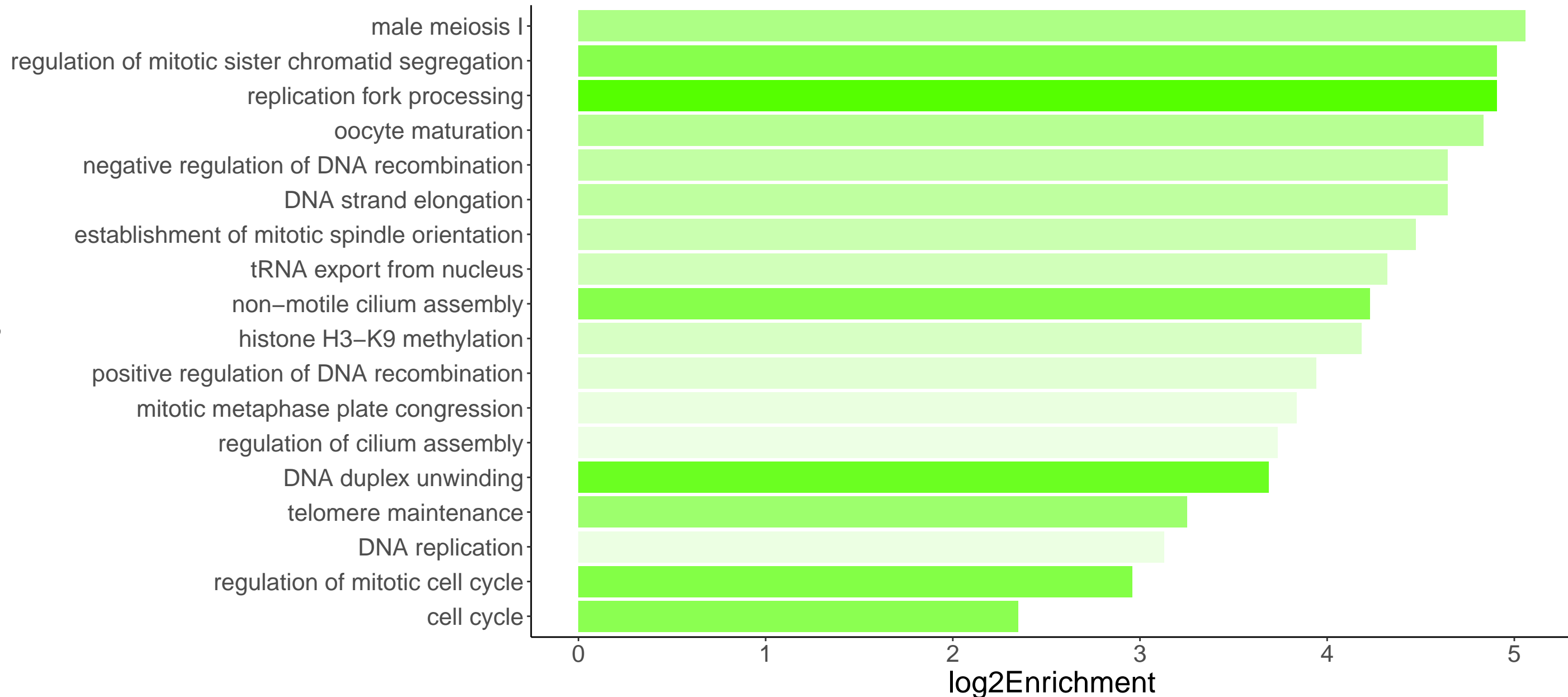
0 1 2 3 4

log2Enrichment



Re-clustered module 1.5.3 BP enrichment

Term



Re-clustered module 1.5.3 MF enrichment

Term

gamma-tubulin binding

structural constituent of nuclear pore

histone-lysine N-methyltransferase activity

single-stranded DNA binding

chromatin binding

0

1

2

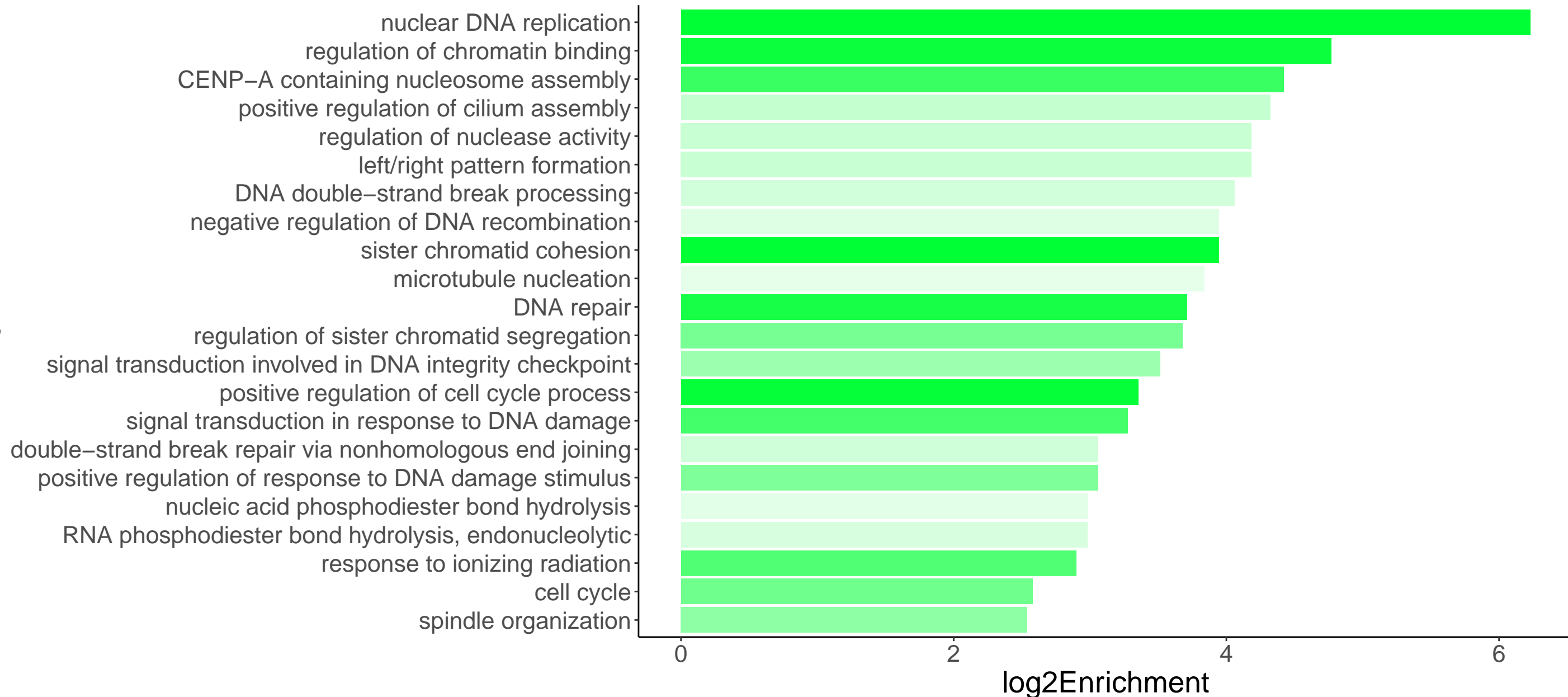
3

4

log2Enrichment



Re-clustered module 1.5.4 BP enrichment



Re-clustered module 1.5.4 MF enrichment

Term

DNA secondary structure binding

4 iron, 4 sulfur cluster binding

0

1

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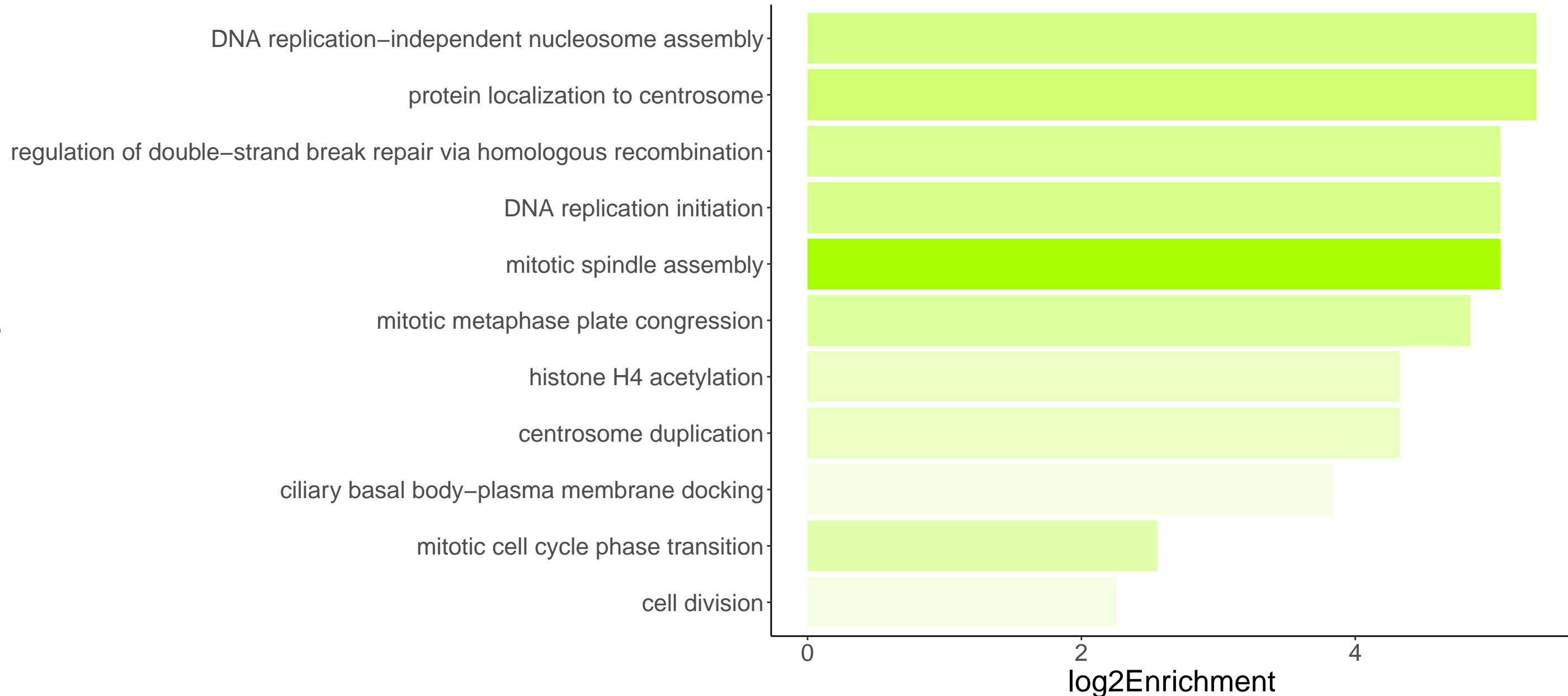
4

log2Enrichment



Re-clustered module 1.5.5 BP enrichment

Term



Re-clustered module 1.5.5 MF enrichment

Term

histone acetyltransferase activity

microtubule motor activity

histone binding

0

1

2

3

4

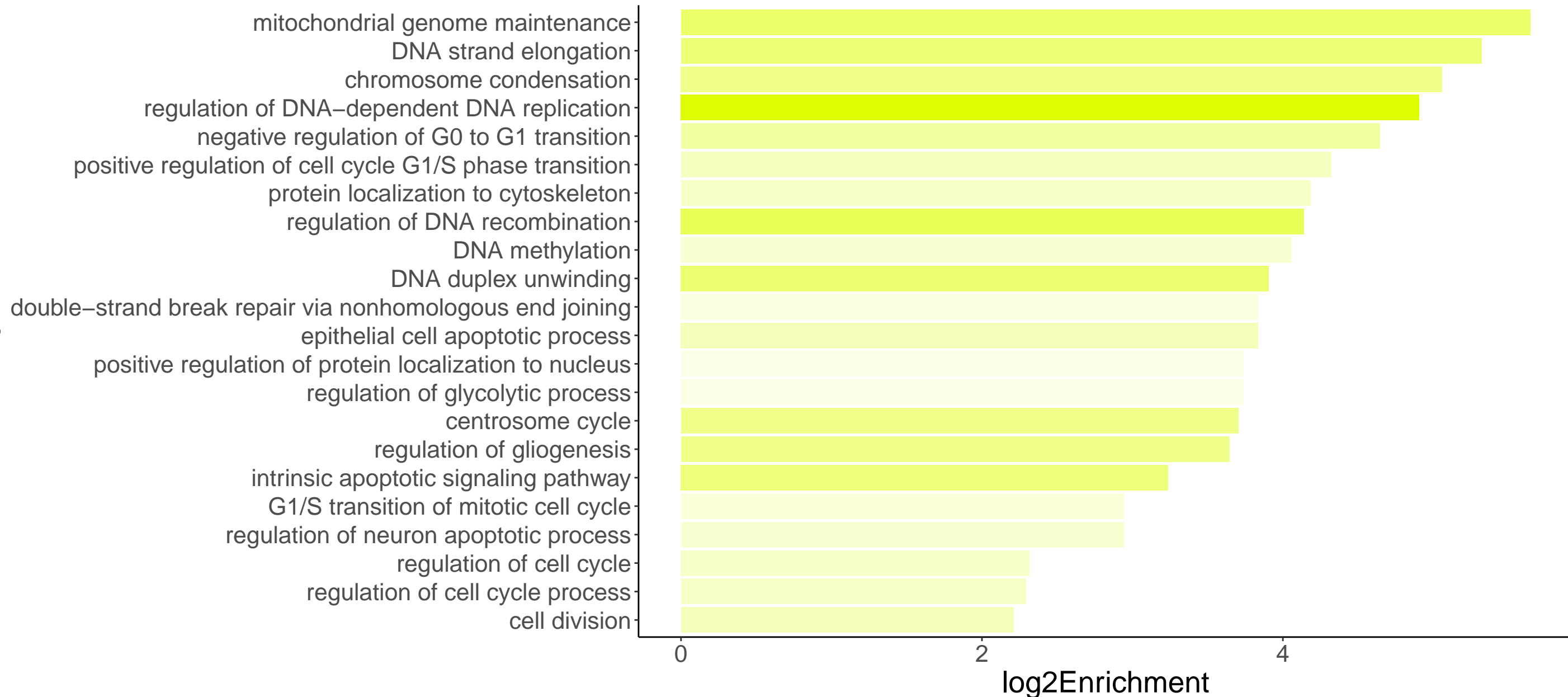
5

log2Enrichment



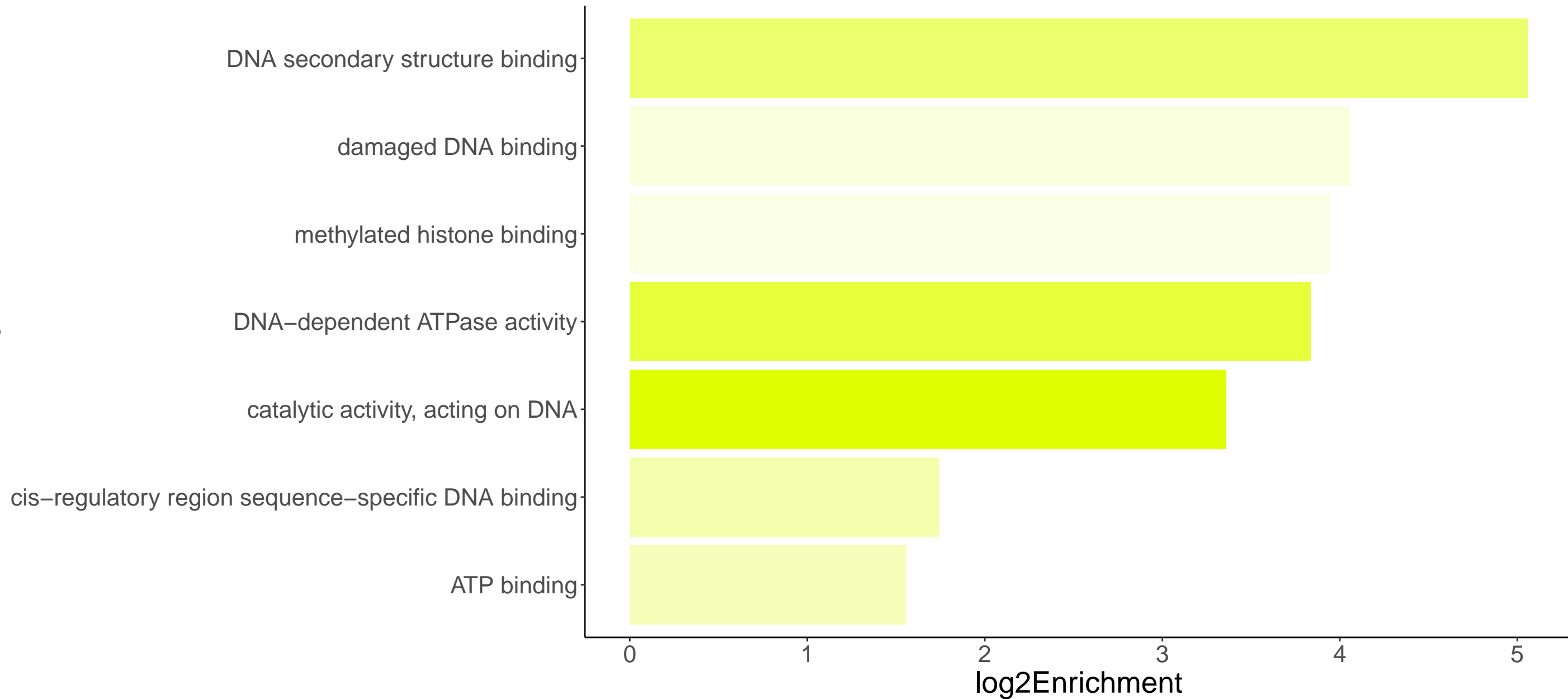
Re-clustered module 1.5.6 BP enrichment

Term



Re-clustered module 1.5.6 MF enrichment

Term



Re-clustered module 1.5.7 BP enrichment

Term

tumor necrosis factor-mediated signaling pathway

negative regulation of canonical Wnt signaling pathway

regulation of mRNA stability

NIK/NF-kappaB signaling

T cell receptor signaling pathway

protein deubiquitination

protein polyubiquitination

post-translational protein modification

0

1

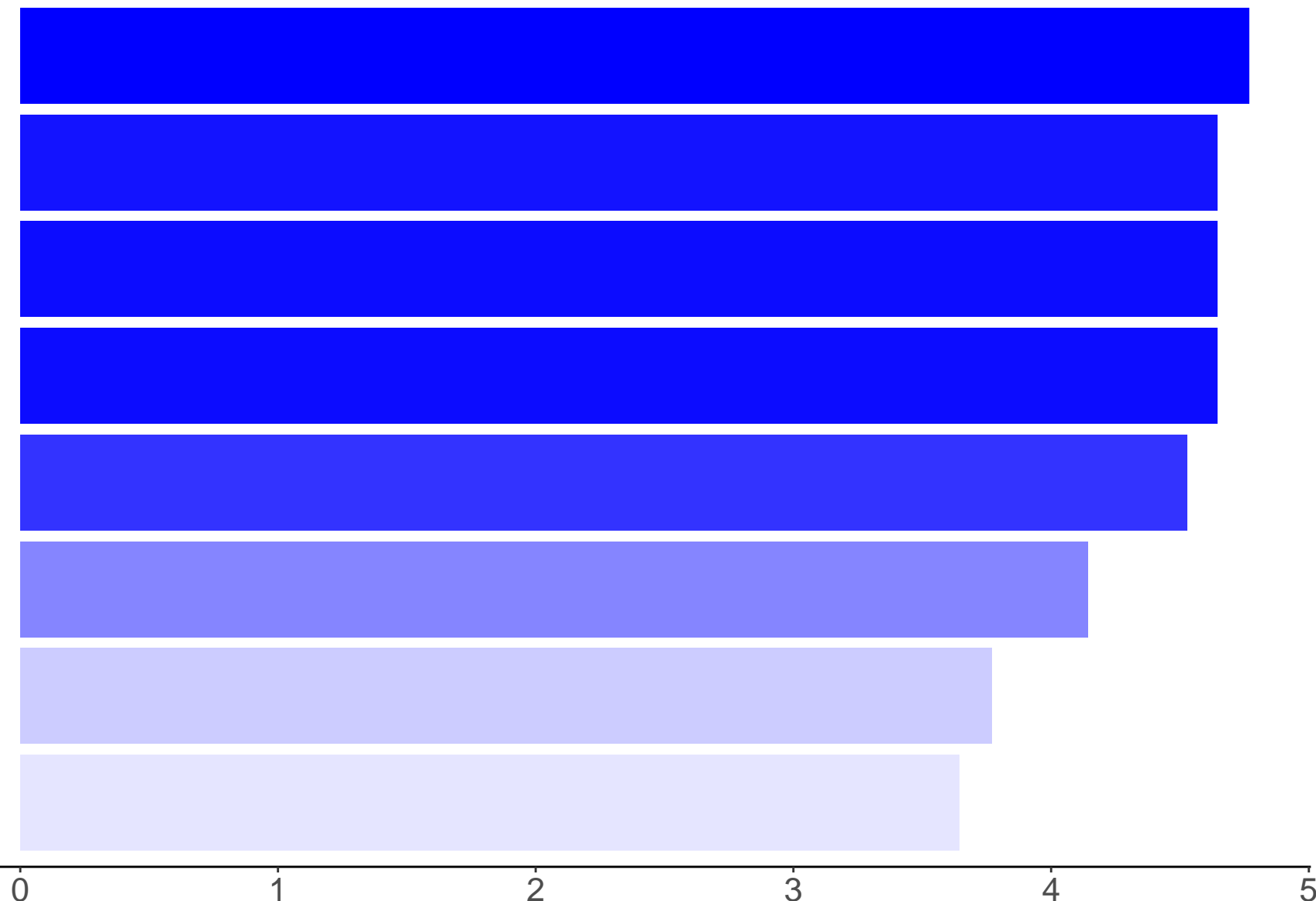
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log2Enrichment



Re-clustered module 1.5.7 MF enrichment

Term

log2Enrichment



Re-clustered module 1.5.8 BP enrichment

Term

homologous chromosome segregation

0

2

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6

log2Enrichment



Re-clustered module 1.5.8 MF enrichment

Term

SH3 domain binding

0

2

4

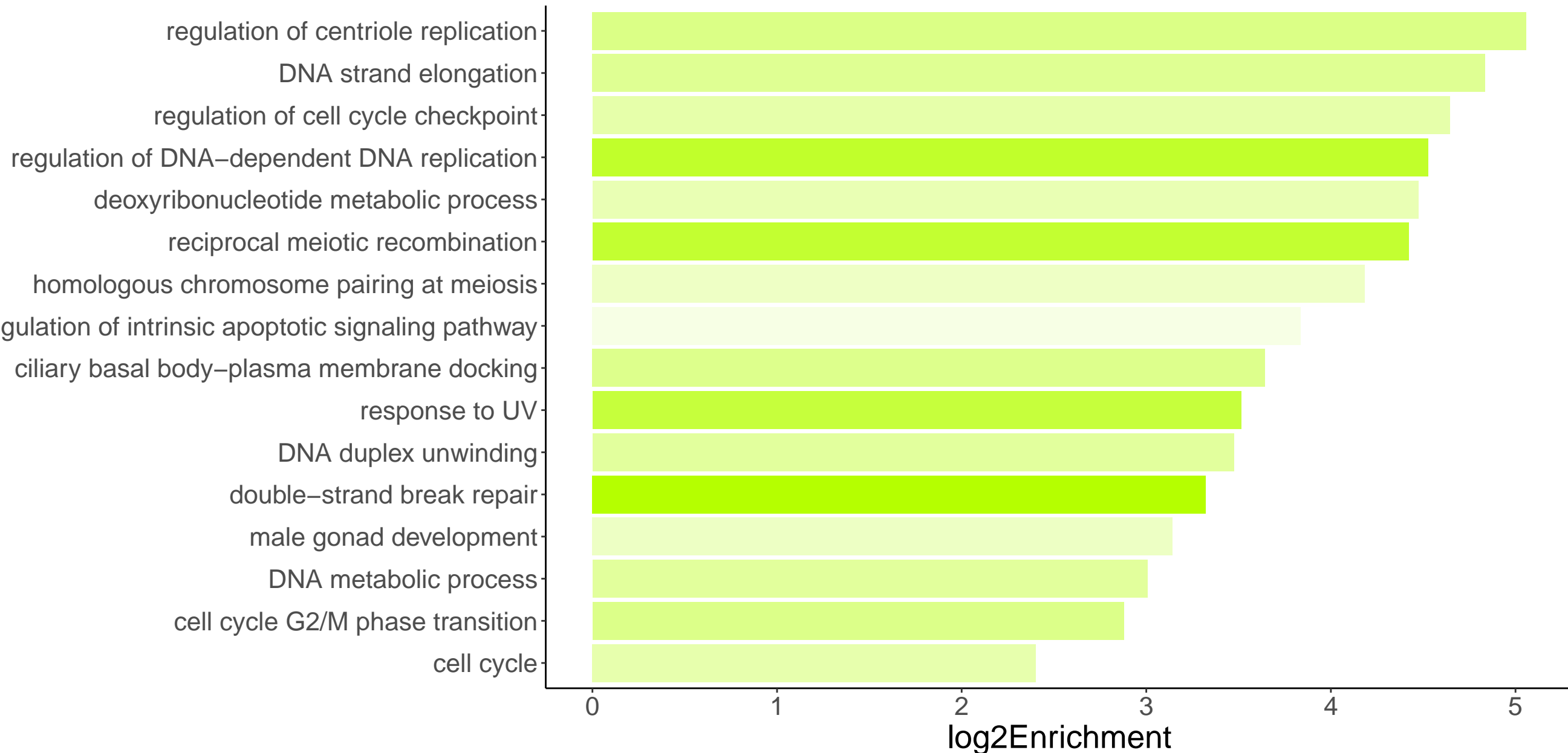
6

log2Enrichment



Re-clustered module 1.5.9 BP enrichment

Term



Re-clustered module 1.5.9 MF enrichment

Term

4 iron, 4 sulfur cluster binding

DNA-dependent ATPase activity

catalytic activity, acting on DNA

DNA binding

0

1

2

3

4

log2Enrichment



Re-clustered module 1.6 BP enrichment

Term

log2Enrichment



Re-clustered module 1.6 MF enrichment

Term

electron transfer activity

0

1

2

3

4

log2Enrichment



Re-clustered module 1.7.1 BP enrichment

Term

regulation of protein export from nucleus

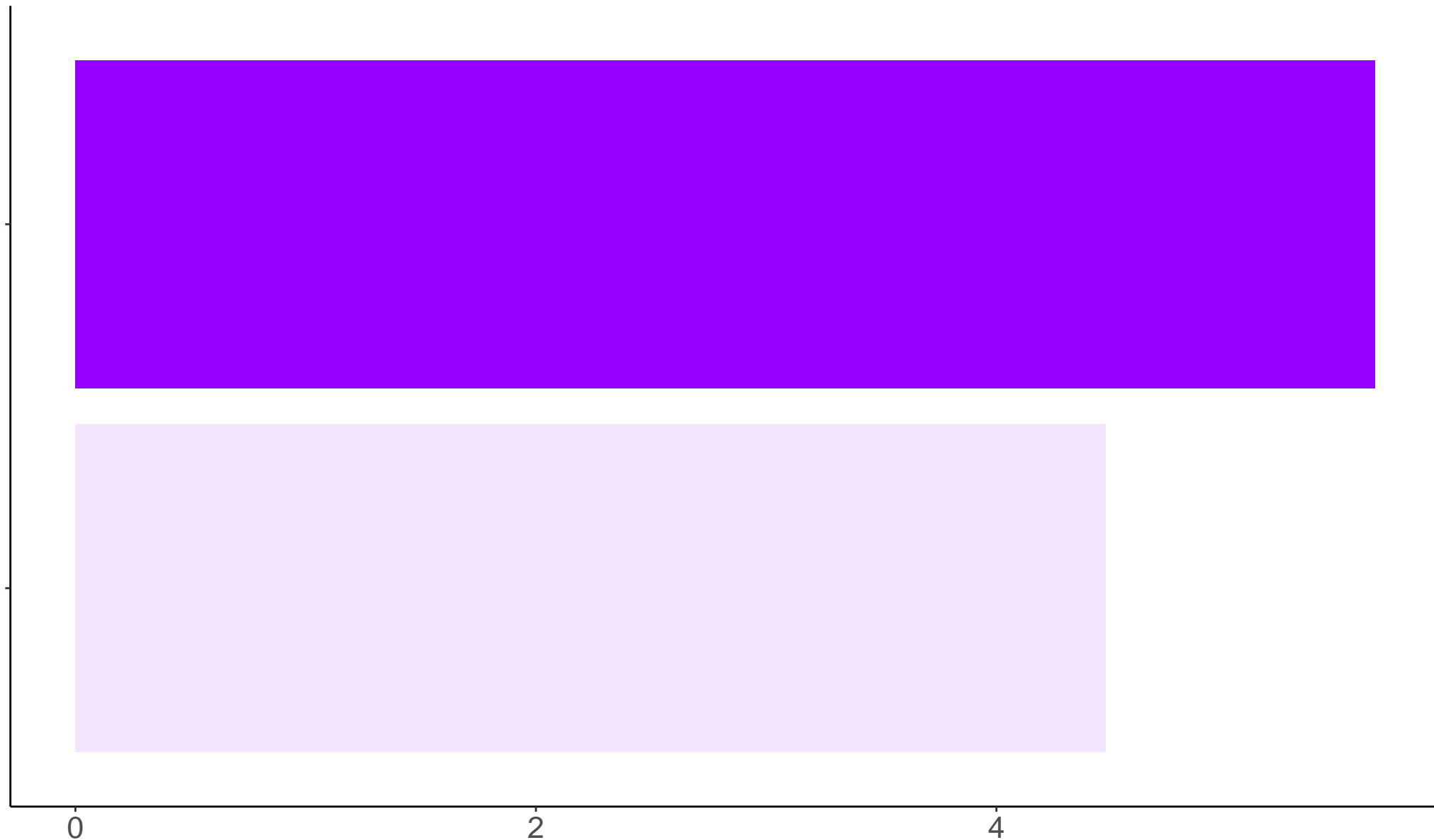
mRNA export from nucleus

0

2

4

log2Enrichment



Re-clustered module 1.7.1 MF enrichment

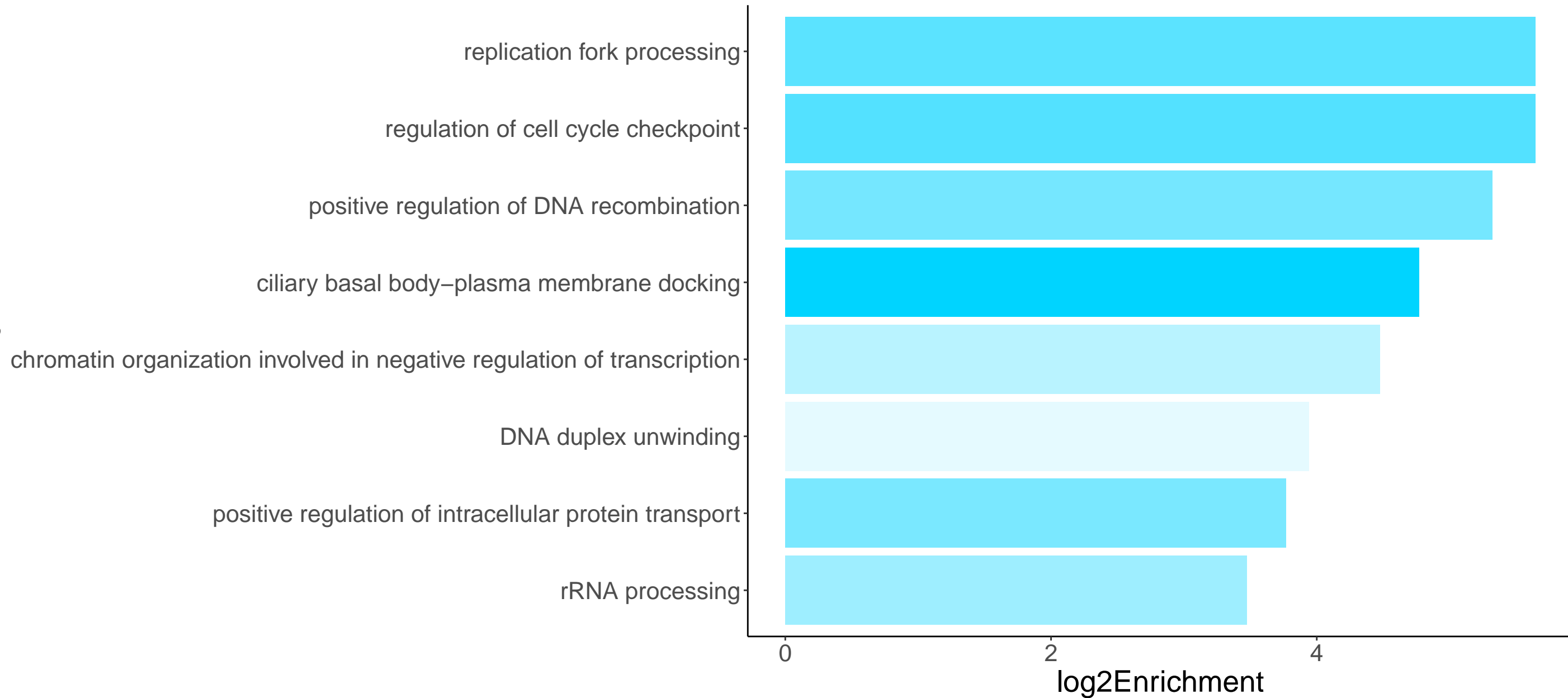
Term

log2Enrichment



Re-clustered module 1.7.10 BP enrichment

Term



Re-clustered module 1.7.10 MF enrichment

Term

helicase activity

0

1

2

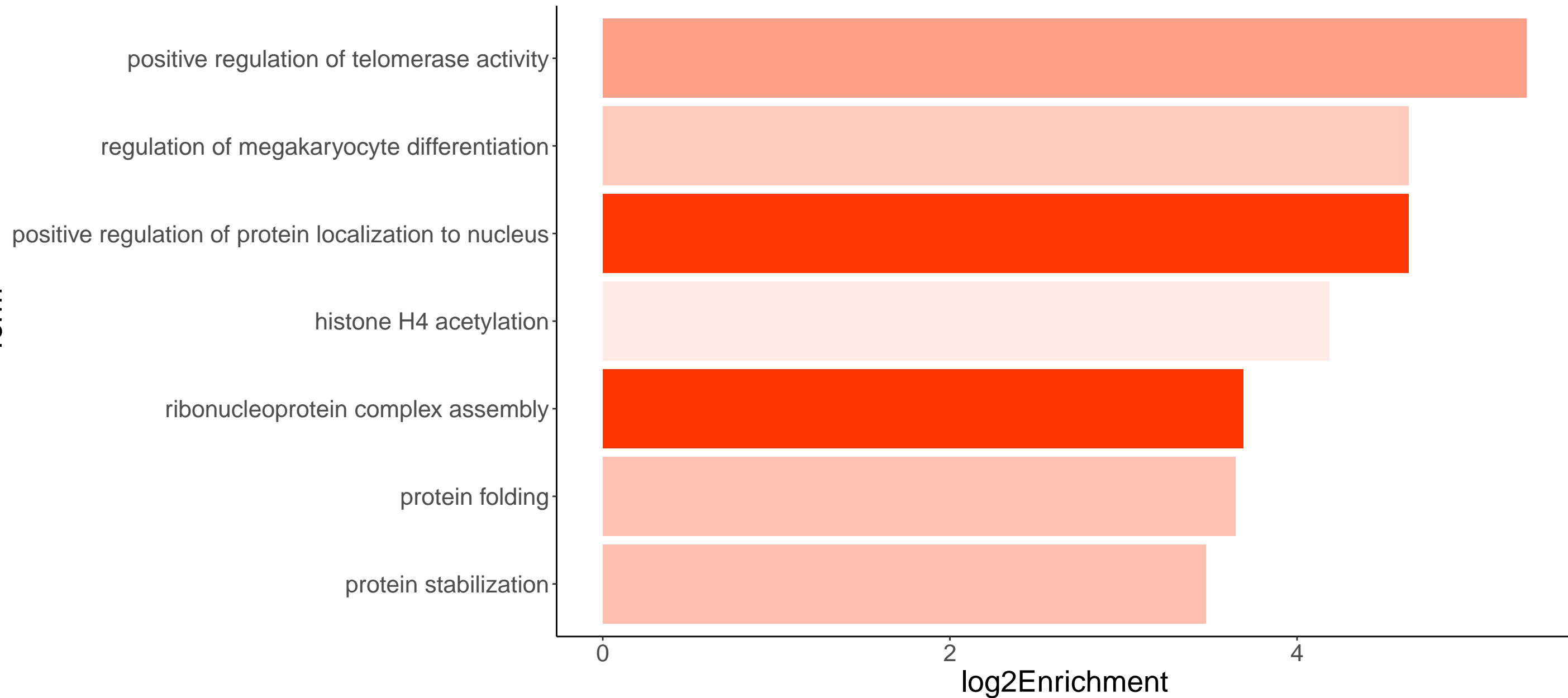
3

4

log2Enrichment



Re-clustered module 1.7.11 BP enrichment



Re-clustered module 1.7.11 MF enrichment

Term

histone methyltransferase activity

adenyl ribonucleotide binding

RNA binding

0

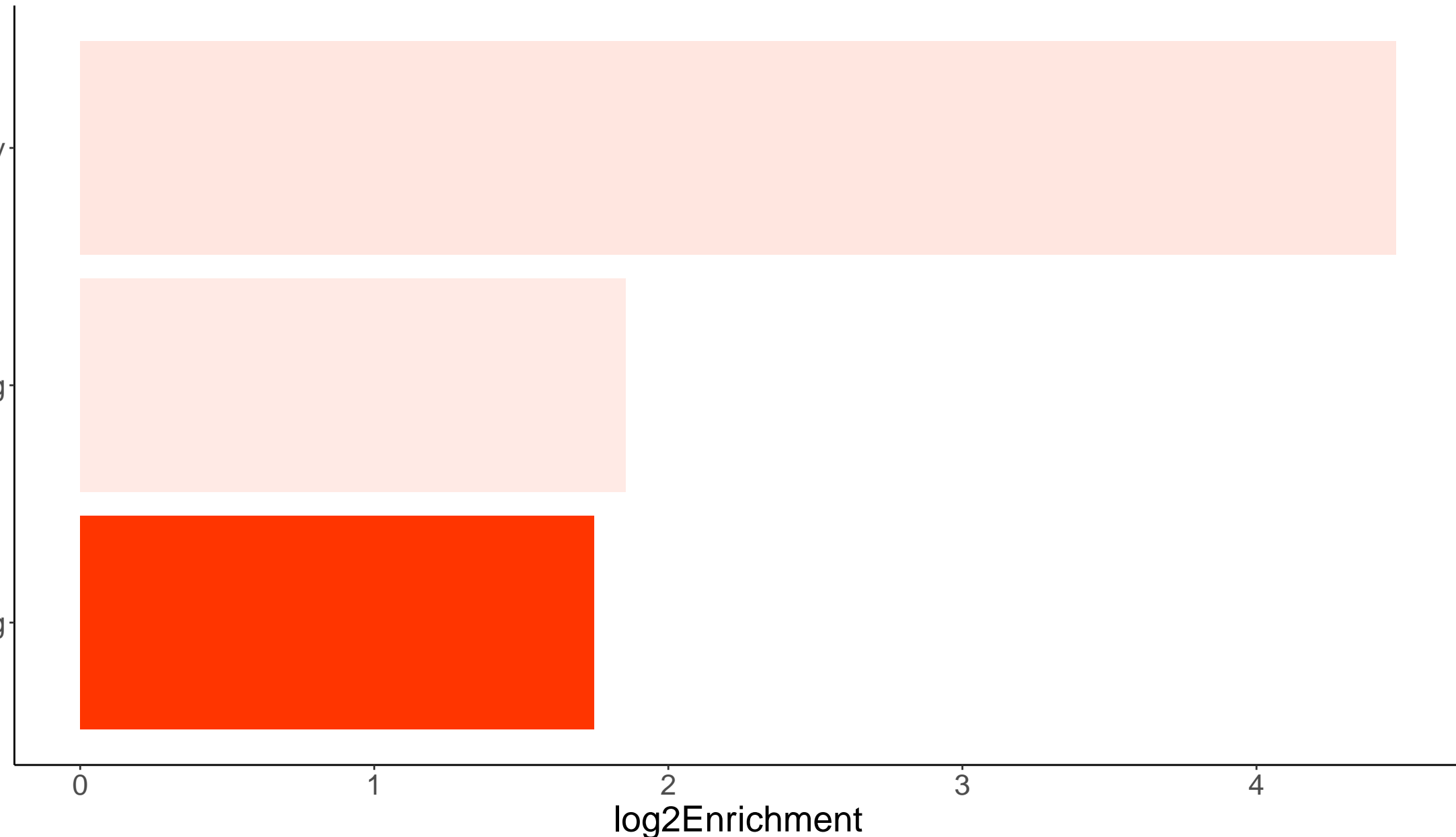
1

2

3

4

log2Enrichment



Re-clustered module 1.7.12 BP enrichment

Term

regulation of translational initiation

0

1

2

3

4

log2Enrichment



Re-clustered module 1.7.12 MF enrichment

Term

general transcription initiation factor binding

heat shock protein binding

0

2

4

log2Enrichment



Re-clustered module 1.7.13 BP enrichment

Term

ncRNA 3'-end processing

0

1

2

3

4

5

log2Enrichment



Re-clustered module 1.7.13 MF enrichment

Term

log2Enrichment



Re-clustered module 1.7.14 BP enrichment

Term

transition metal ion transport

0

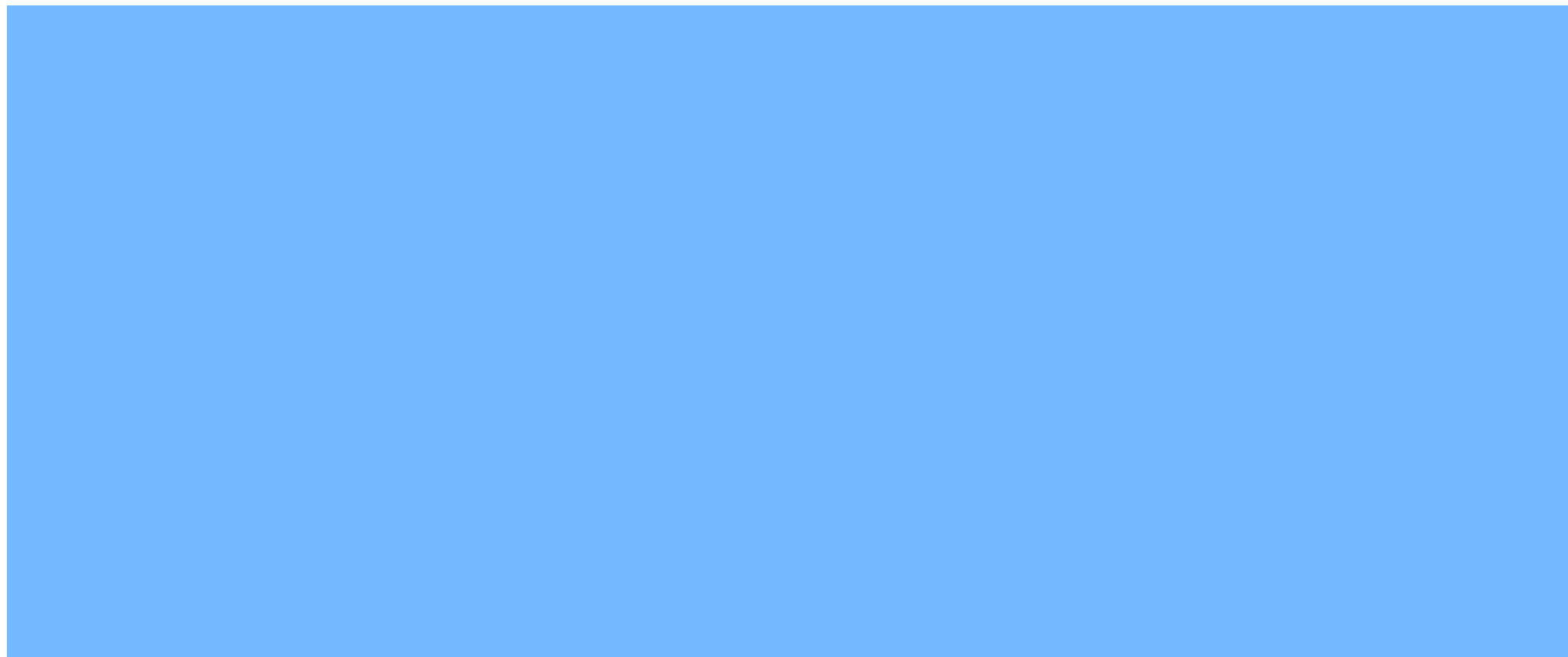
1

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log2Enrichment



Re-clustered module 1.7.14 MF enrichment

Term

nucleic acid binding

0.0

0.5

1.0

1.5

log2Enrichment



Re-clustered module 1.7.15 BP enrichment

Term

log2Enrichment



Re-clustered module 1.7.15 MF enrichment

Term

log2Enrichment



Re-clustered module 1.7.17 BP enrichment

Term
protein peptidyl-prolyl isomerization

0

1

2

3

4

5

log2Enrichment



Re-clustered module 1.7.17 MF enrichment

Term

zinc ion binding

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

RNA polymerase II transcription regulatory region sequence-specific DNA binding

0.0 0.5 1.0 1.5 2.0

log2Enrichment



Re-clustered module 1.7.2 BP enrichment

Term

7-methylguanosine mRNA capping

vesicle transport along microtubule

axonal transport

blastocyst development

synaptic vesicle recycling

cellular response to dopamine

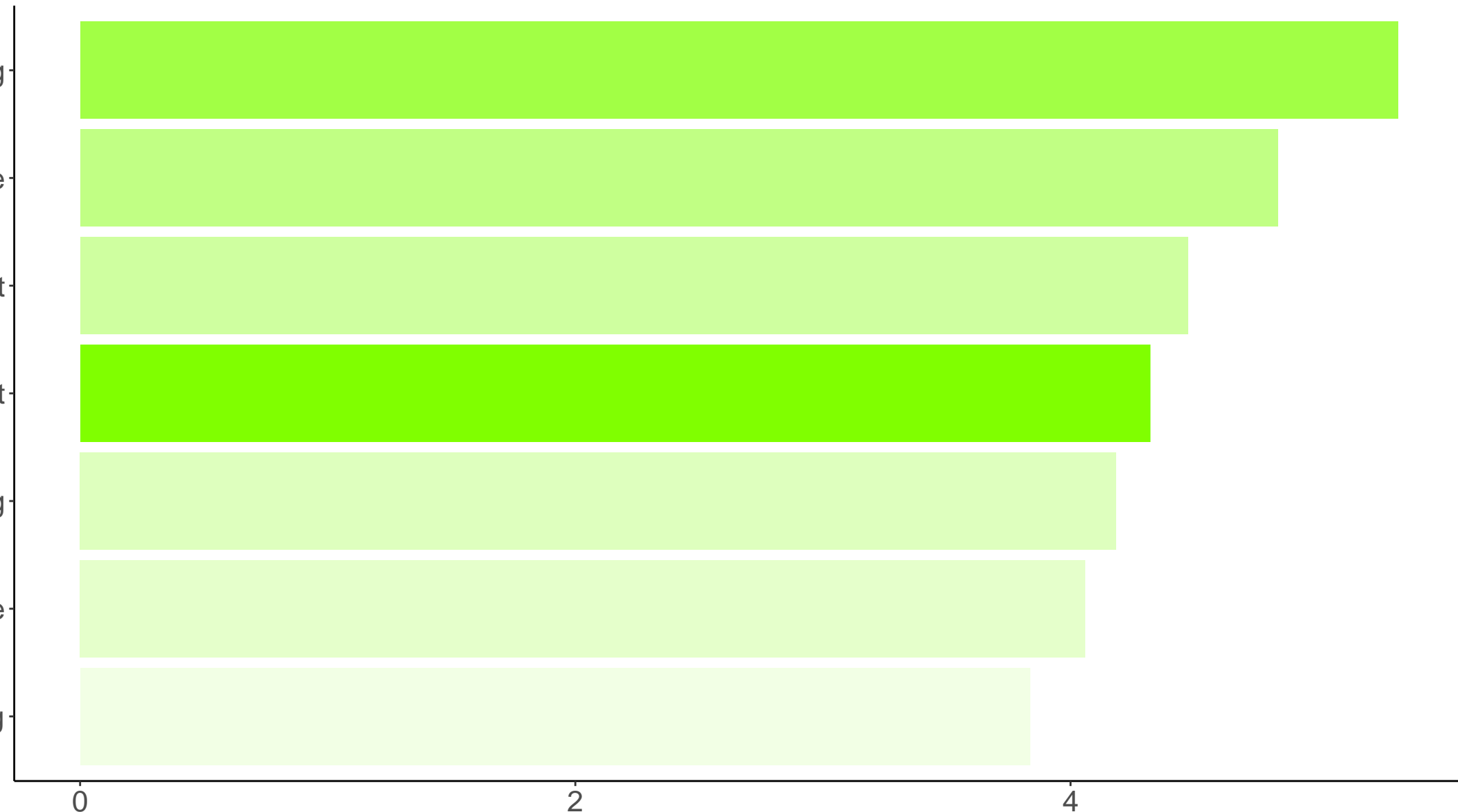
mRNA 3'-end processing

0

2

4

log2Enrichment



Re-clustered module 1.7.2 MF enrichment

Term

GDP binding

GTP binding

0

1

2

3

4

log2Enrichment



Re-clustered module 1.7.3 BP enrichment

Term

positive regulation of transcription by RNA polymerase I

regulation of DNA-templated transcription, elongation

tRNA modification

mitochondrial translational elongation

rRNA processing

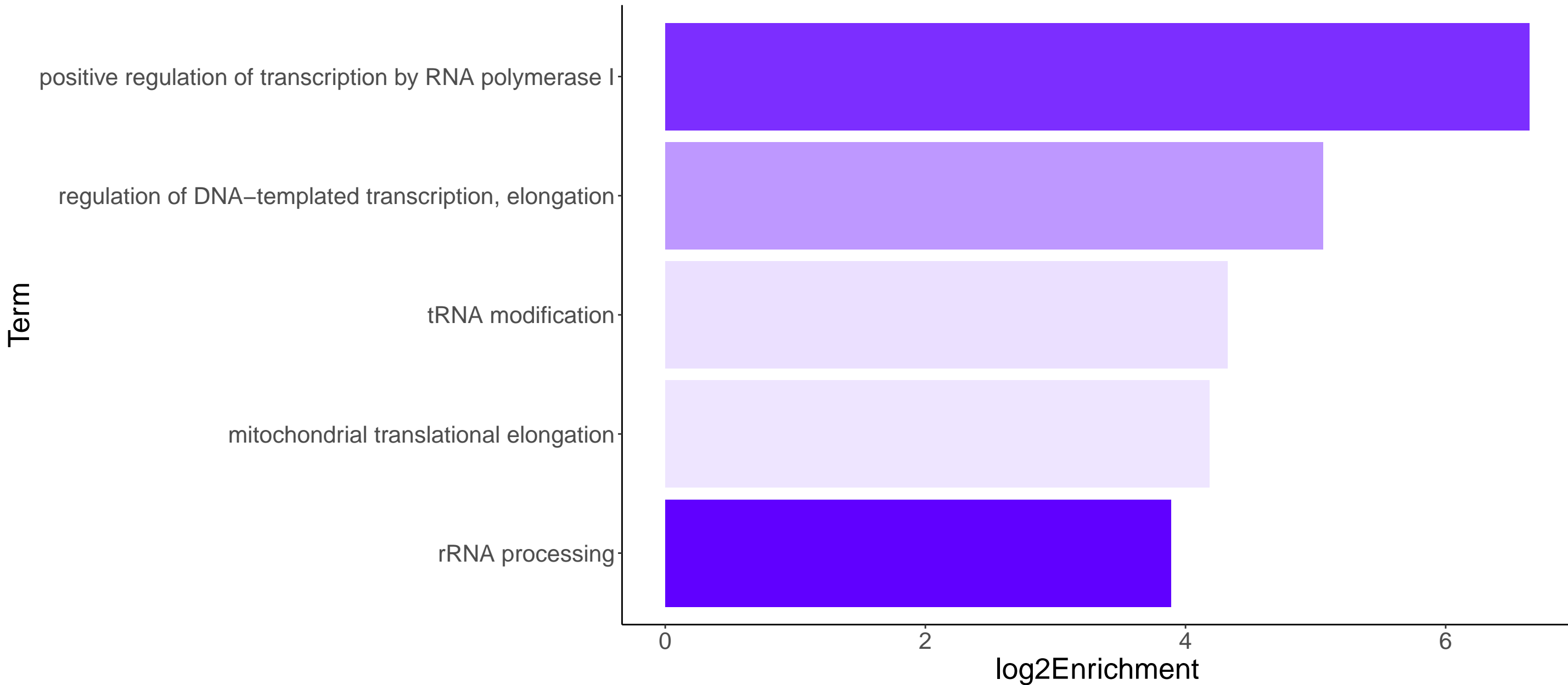
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log2Enrichment



Re-clustered module 1.7.3 MF enrichment

Term

log2Enrichment



Re-clustered module 1.7.4 BP enrichment

Term

blastocyst development

positive regulation of protein secretion

mRNA processing

0

1

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3

4

log2Enrichment



Re-clustered module 1.7.4 MF enrichment

Term

log2Enrichment



Re-clustered module 1.7.5 BP enrichment

Term

log2Enrichment



Re-clustered module 1.7.5 MF enrichment

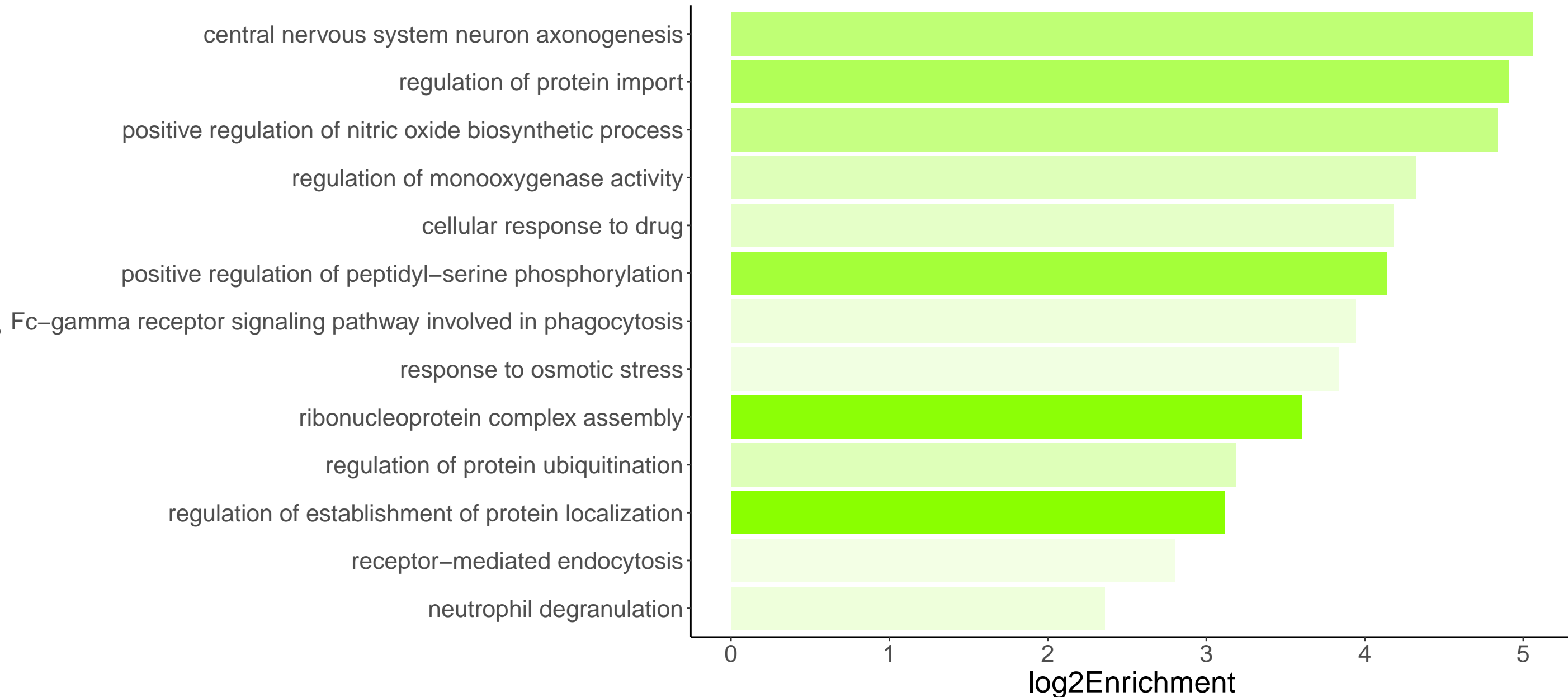
Term

log2Enrichment



Re-clustered module 1.7.6 BP enrichment

Term



Re-clustered module 1.7.6 MF enrichment

Term

tau protein binding

0

1

2

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4

5

log2Enrichment



Re-clustered module 1.7.7 BP enrichment

Term

nucleus organization

regulation of mRNA stability

0

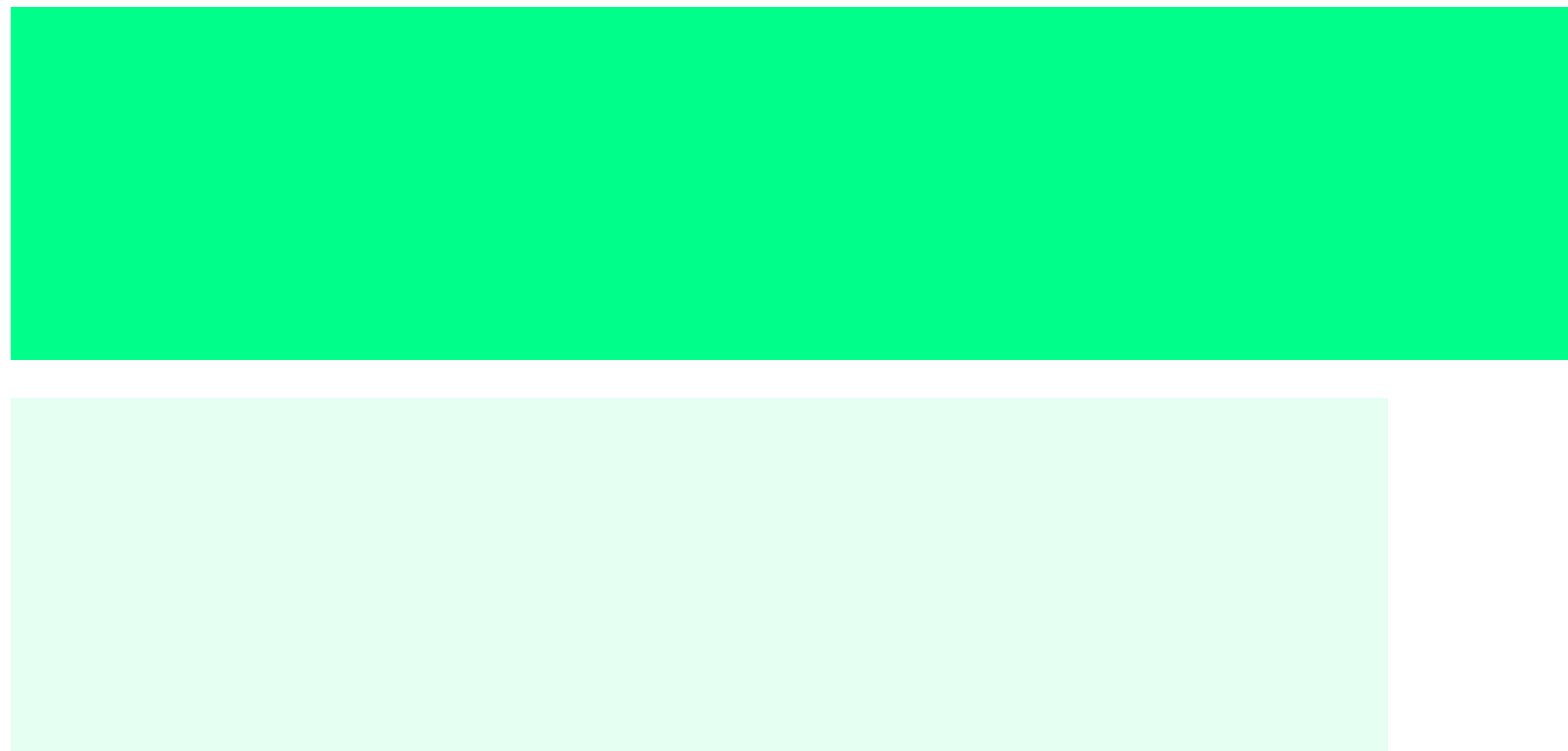
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log2Enrichment



Re-clustered module 1.7.7 MF enrichment

Term

Ran GTPase binding

N-methyltransferase activity

S-adenosylmethionine-dependent methyltransferase activity

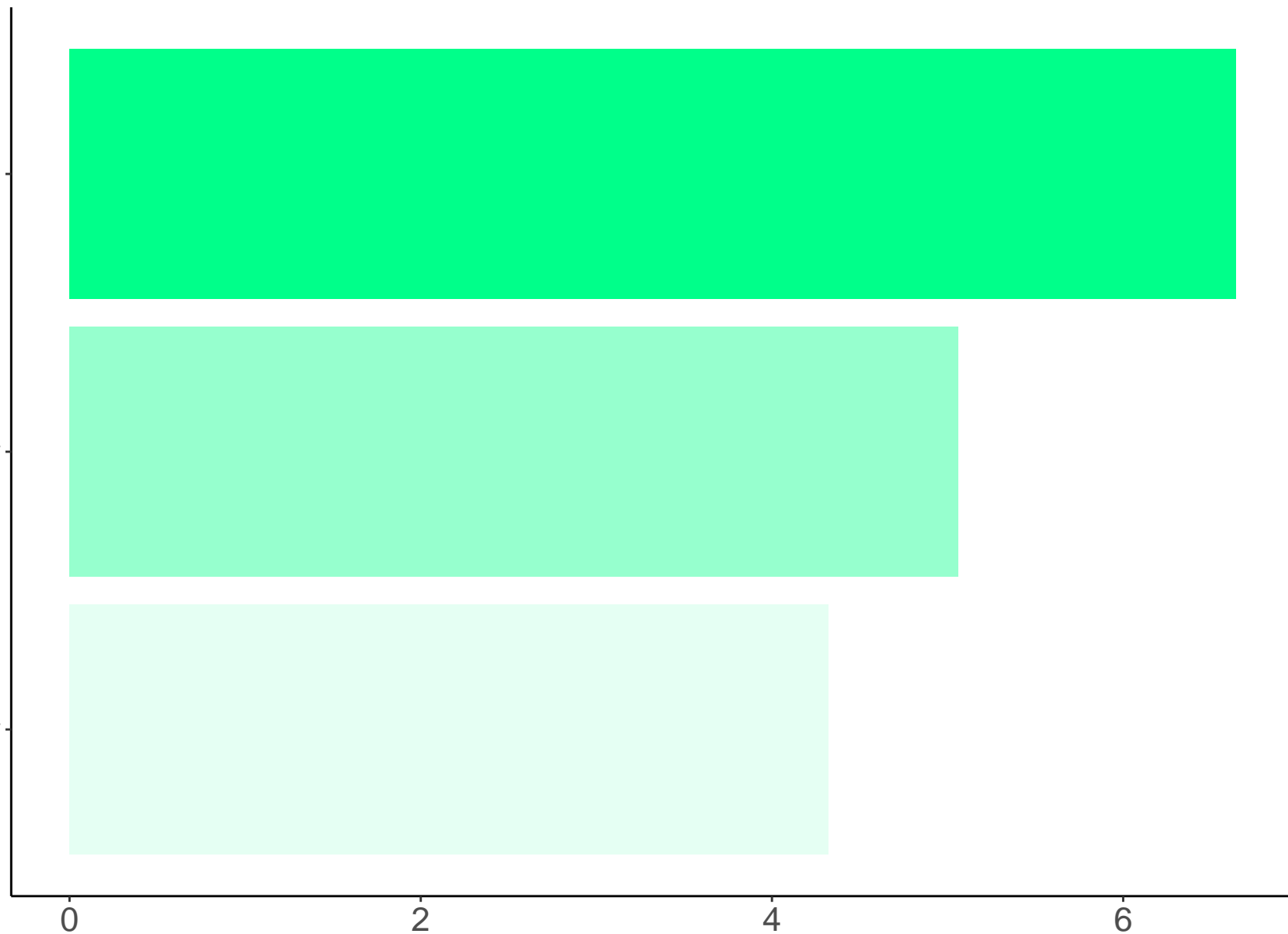
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log2Enrichment



Re-clustered module 1.7.8 BP enrichment

Term

negative regulation of fat cell differentiation

circadian regulation of gene expression

tRNA modification

regulation of circadian rhythm

neural precursor cell proliferation

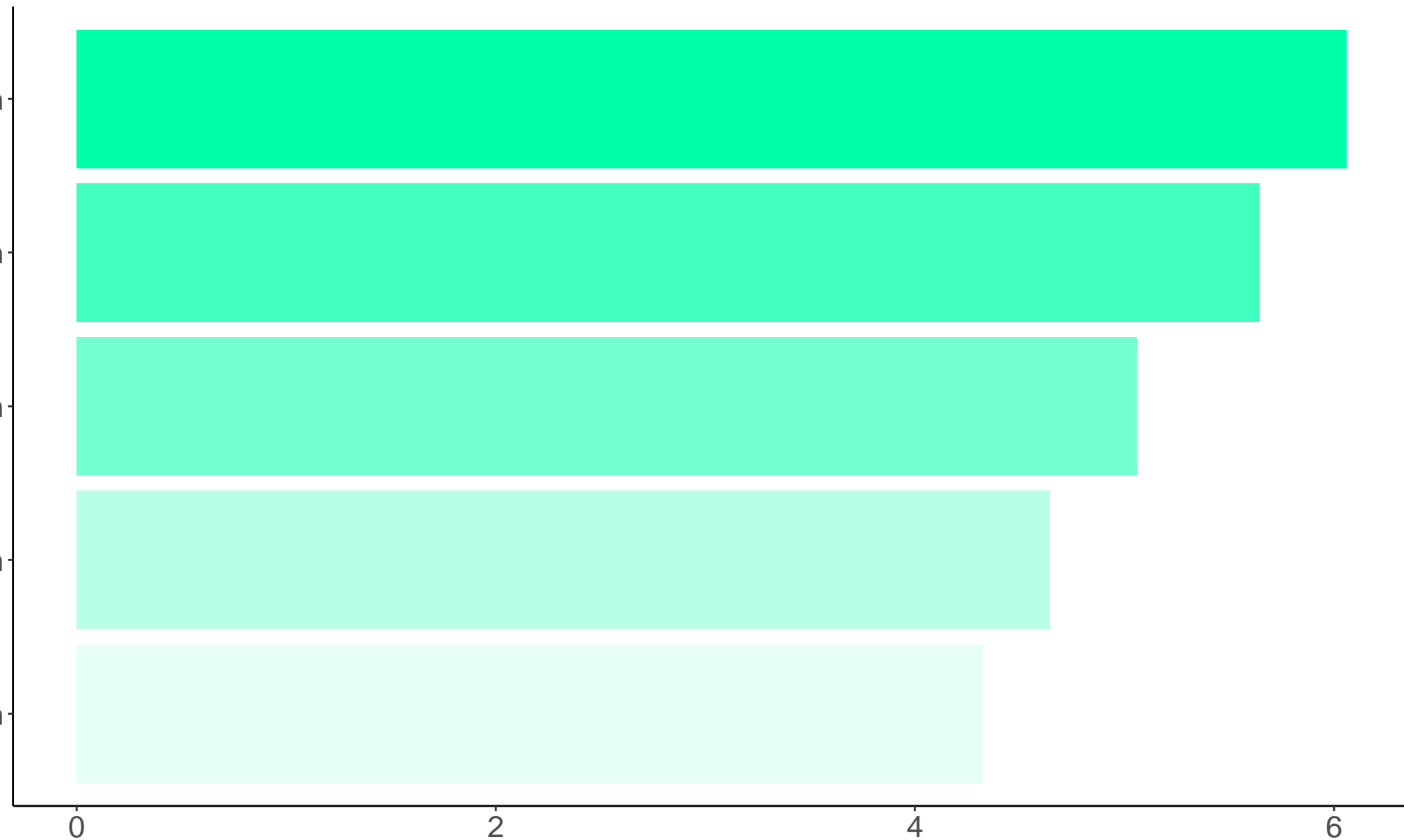
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log2Enrichment



Re-clustered module 1.7.8 MF enrichment

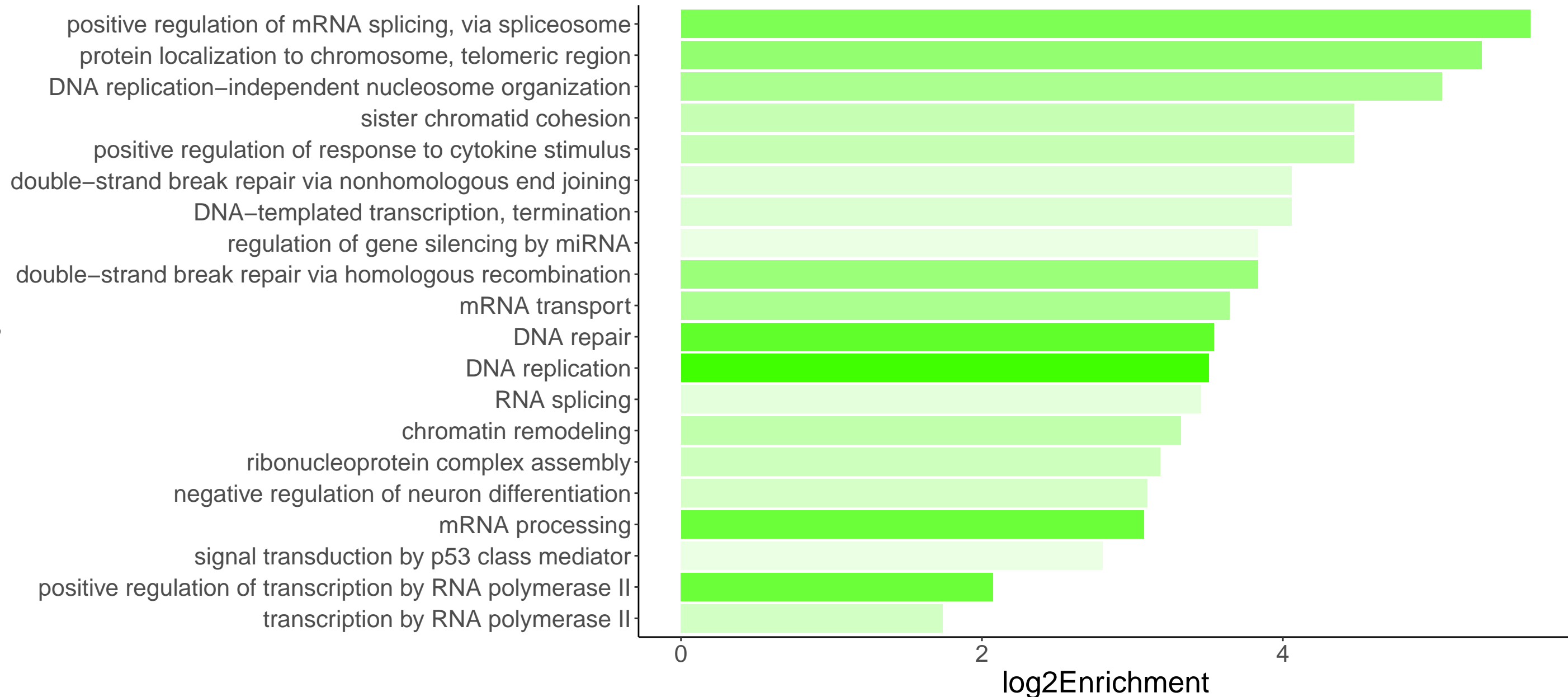
Term

log2Enrichment



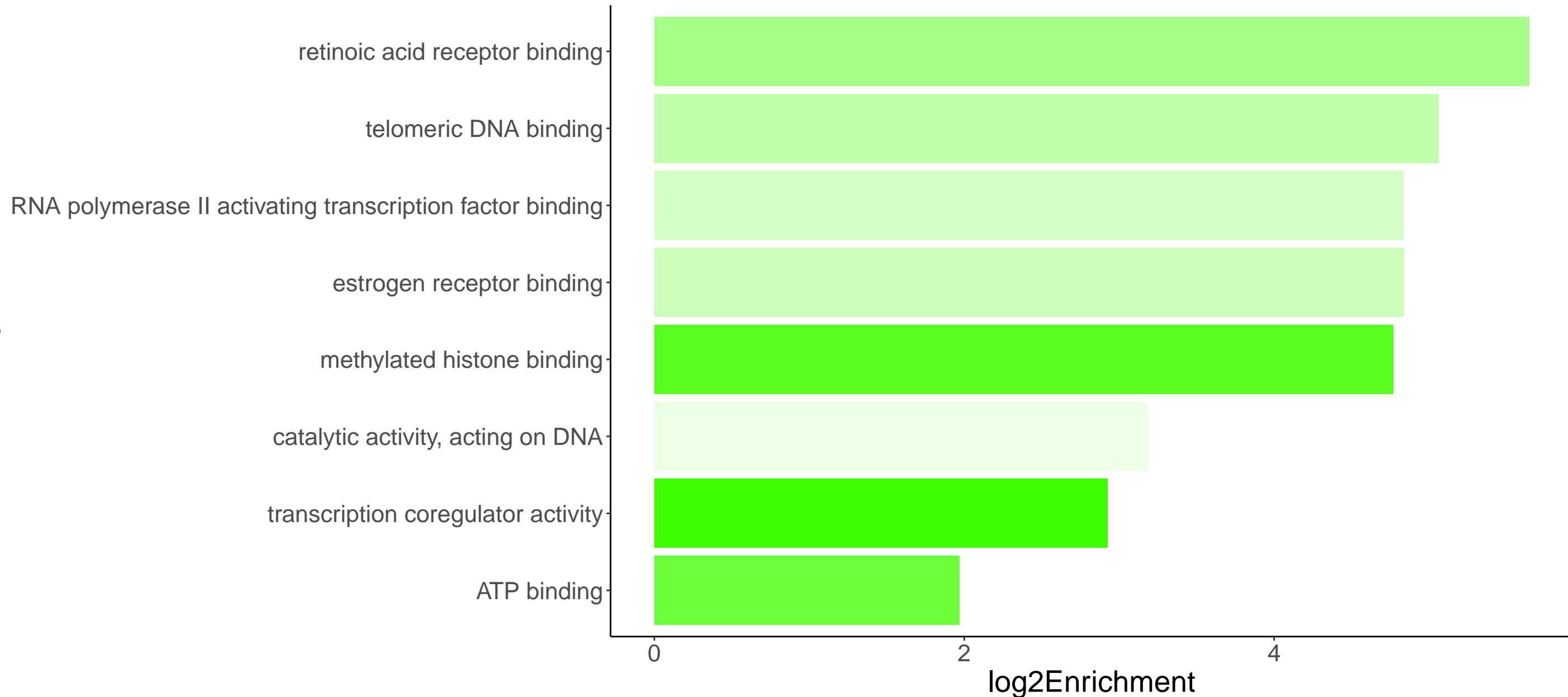
Re-clustered module 1.7.9 BP enrichment

Term



Re-clustered module 1.7.9 MF enrichment

Term



Re-clustered module 1.8 BP enrichment

Term

centrosome duplication

apical junction assembly

regulation of synapse assembly

regulation of G2/M transition of mitotic cell cycle

0

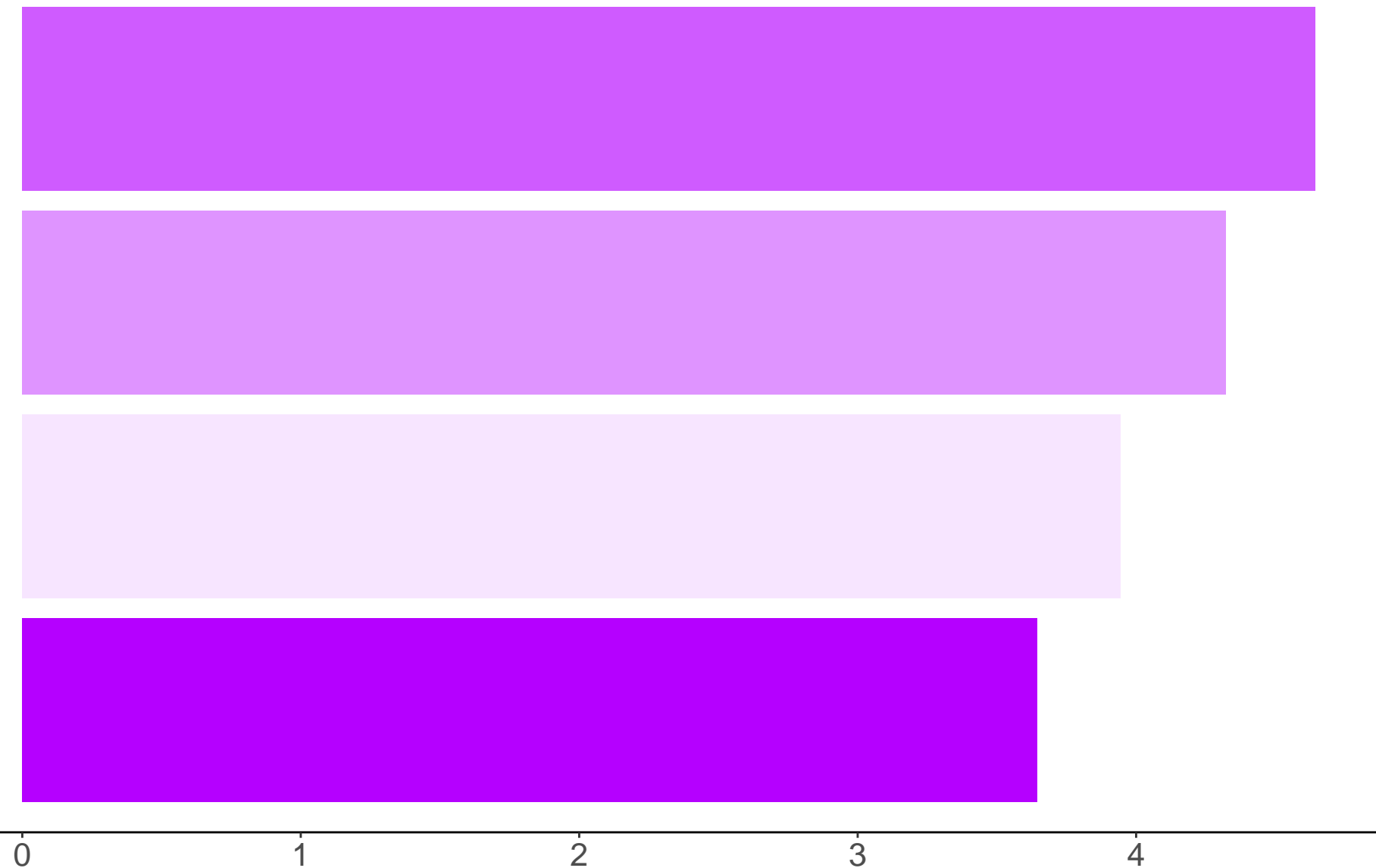
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log2Enrichment



Re-clustered module 1.8 MF enrichment

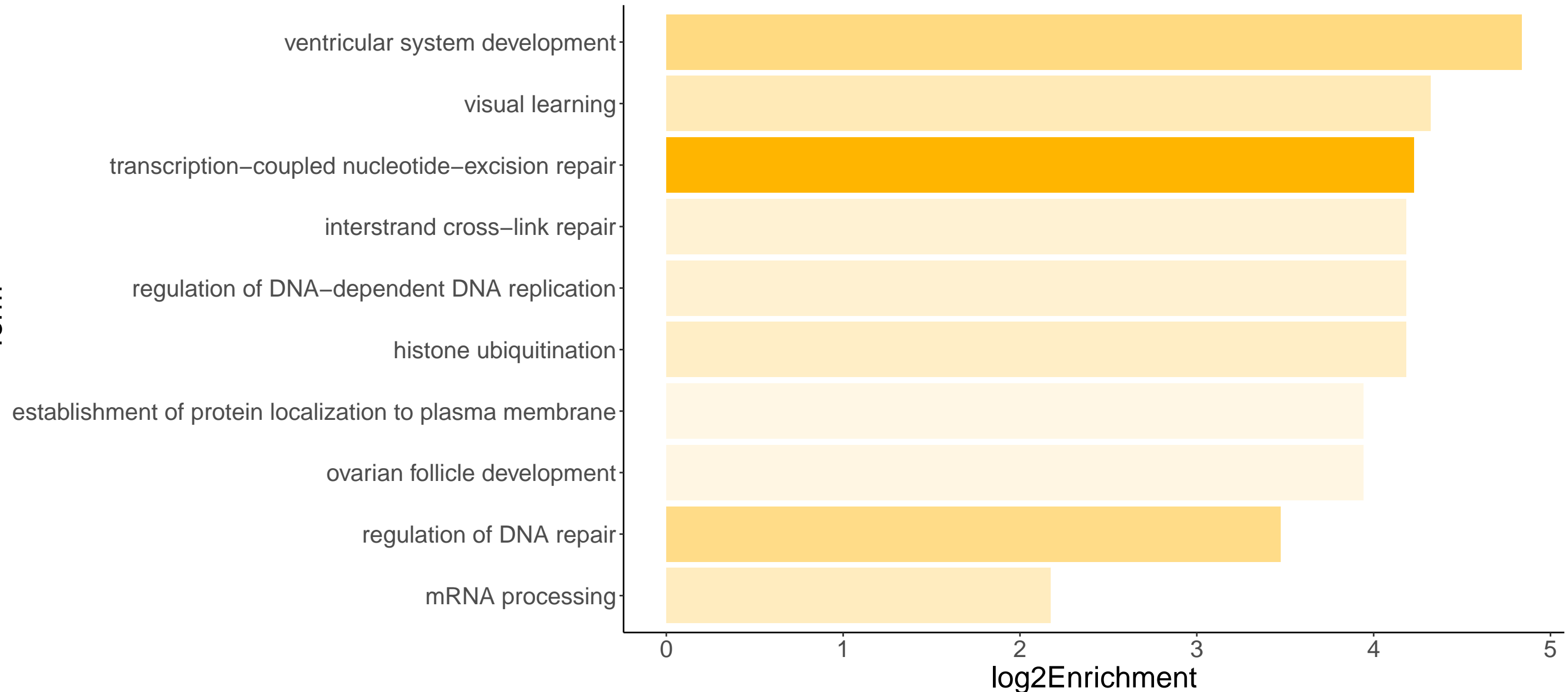
Term

log2Enrichment



Re-clustered module 1.9 BP enrichment

Term



Re-clustered module 1.9 MF enrichment

Term

ion channel inhibitor activity

nucleic acid binding

metal ion binding

0

1

2

3

4

log2Enrichment

