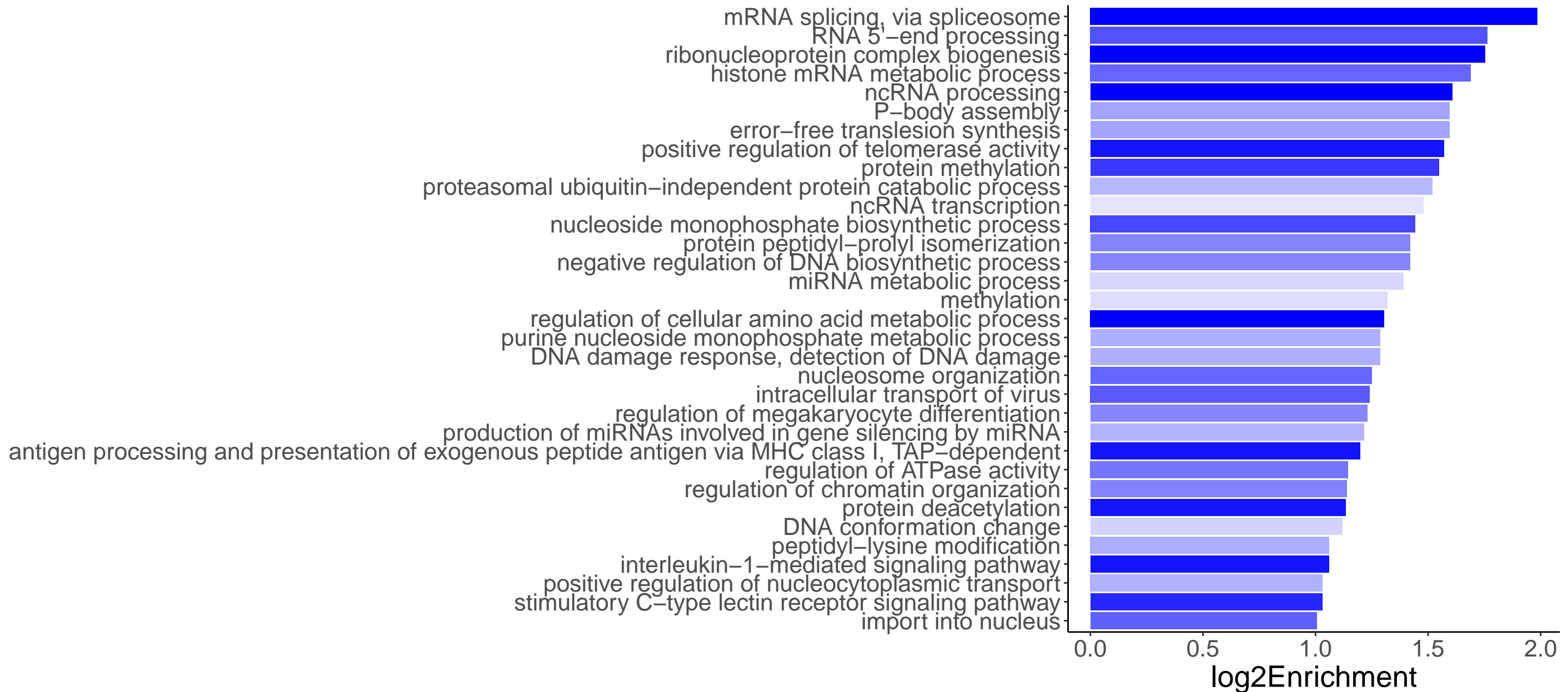
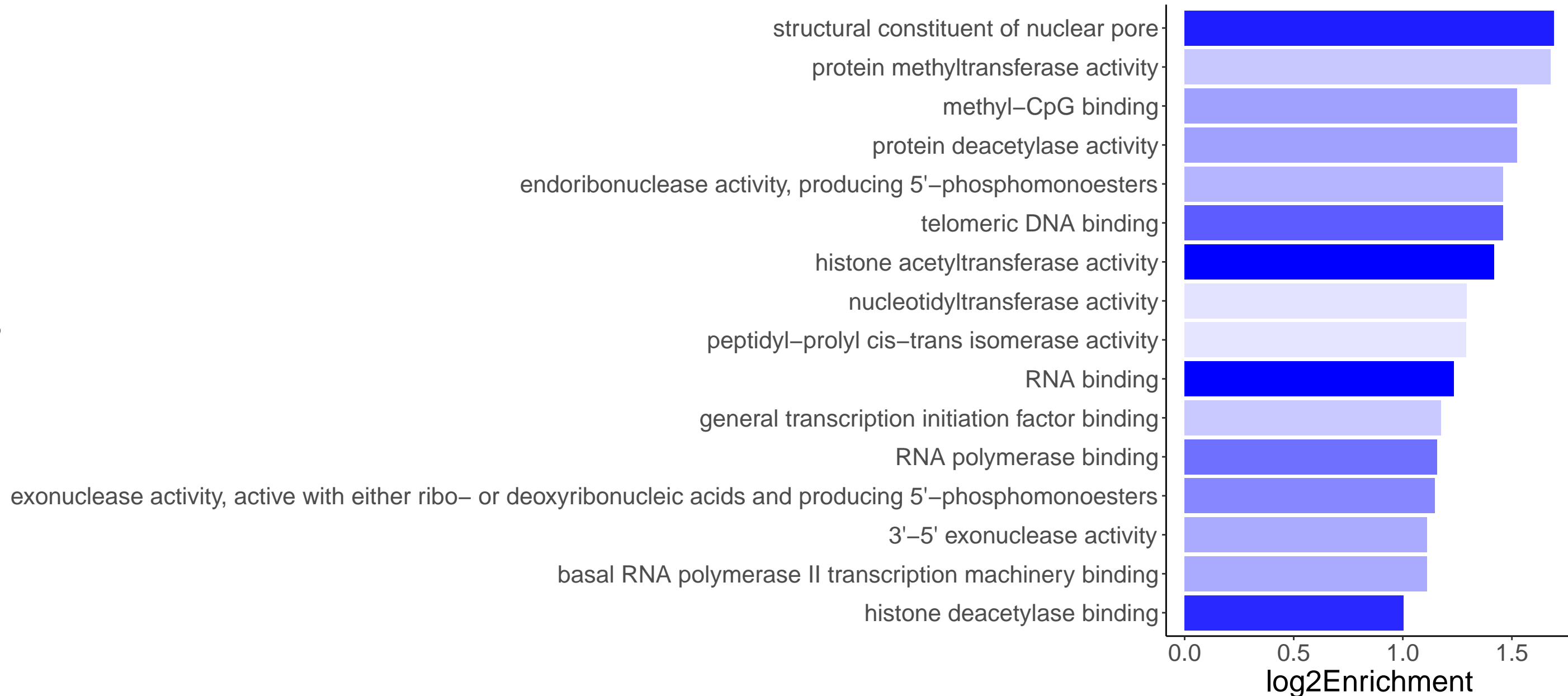


Original module 16 BP enrichment

Term



Term



Re-clustered module 16.10 BP enrichment

Term

TRIF-dependent toll-like receptor signaling pathway

DNA damage response, detection of DNA damage

protein targeting to peroxisome

cytoplasmic translation

viral transcription

ribonucleoprotein complex biogenesis

mRNA metabolic process

0

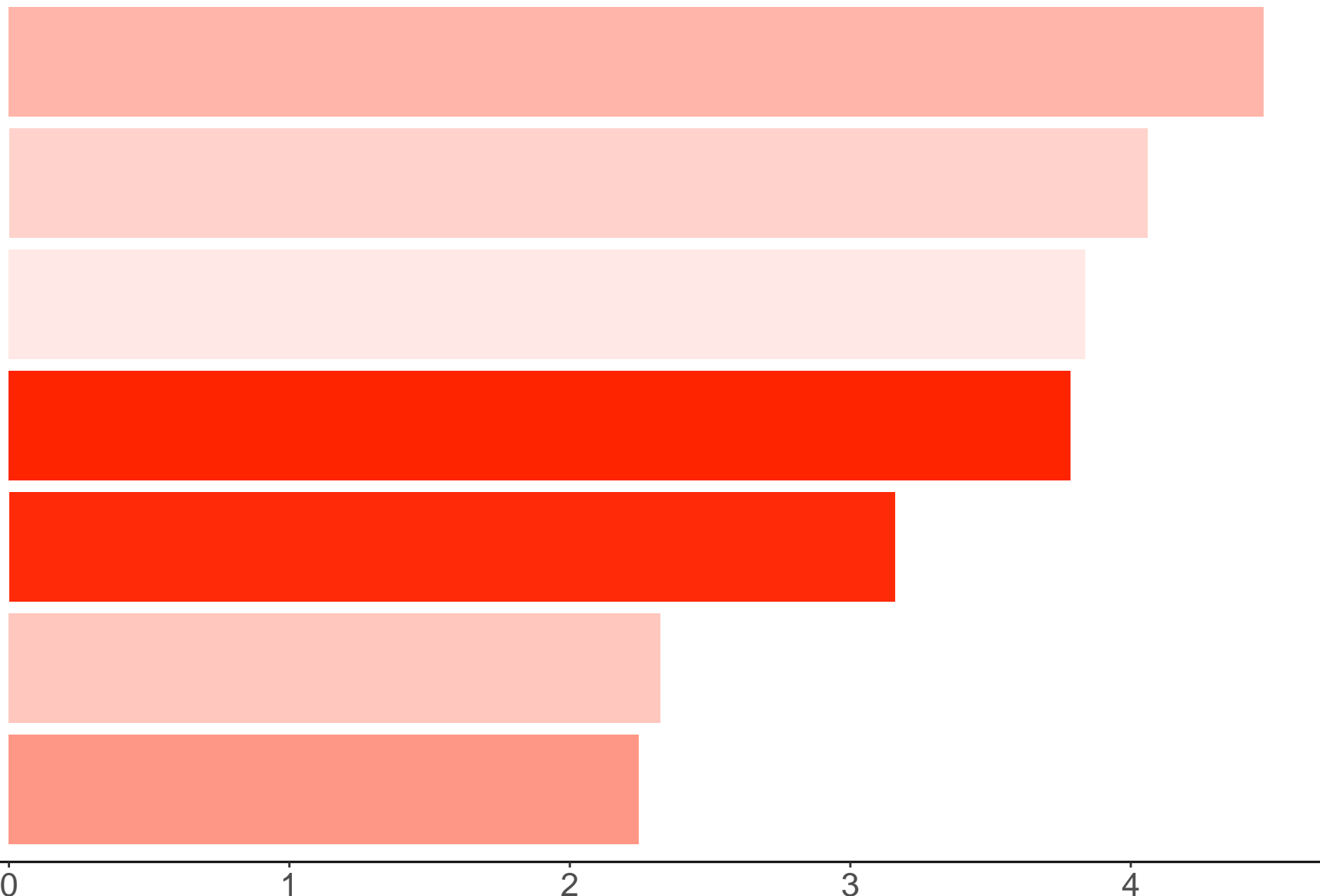
1

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log2Enrichment



Re-clustered module 16.10 MF enrichment

Term

ribosome binding

translation regulator activity, nucleic acid binding

0

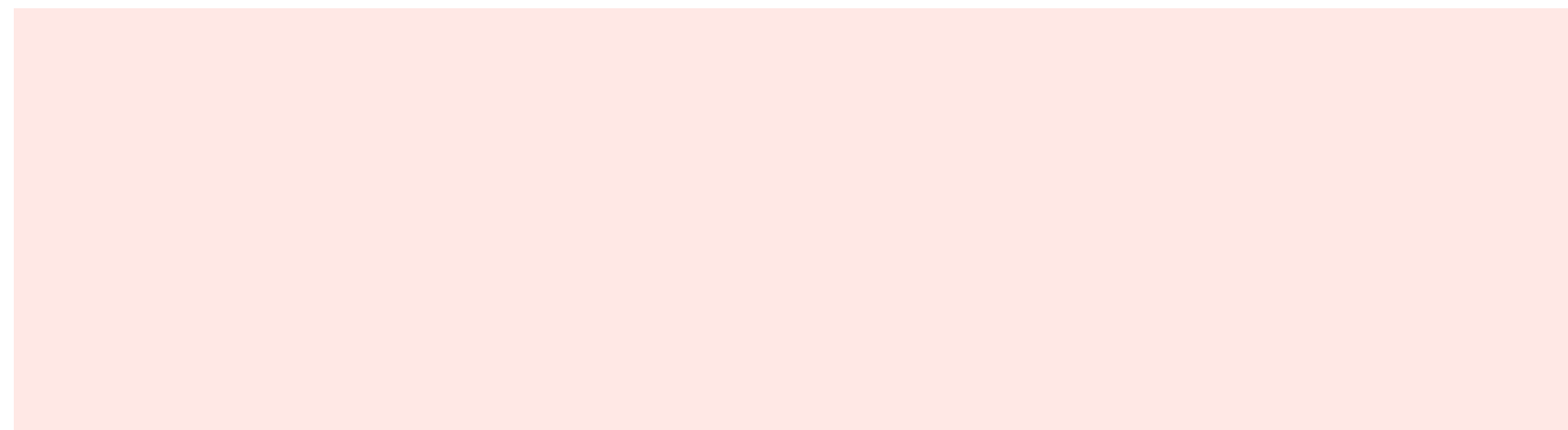
1

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log2Enrichment



Re-clustered module 16.15.17 BP enrichment

Term

response to ethanol

carboxylic acid metabolic process

viral process

0

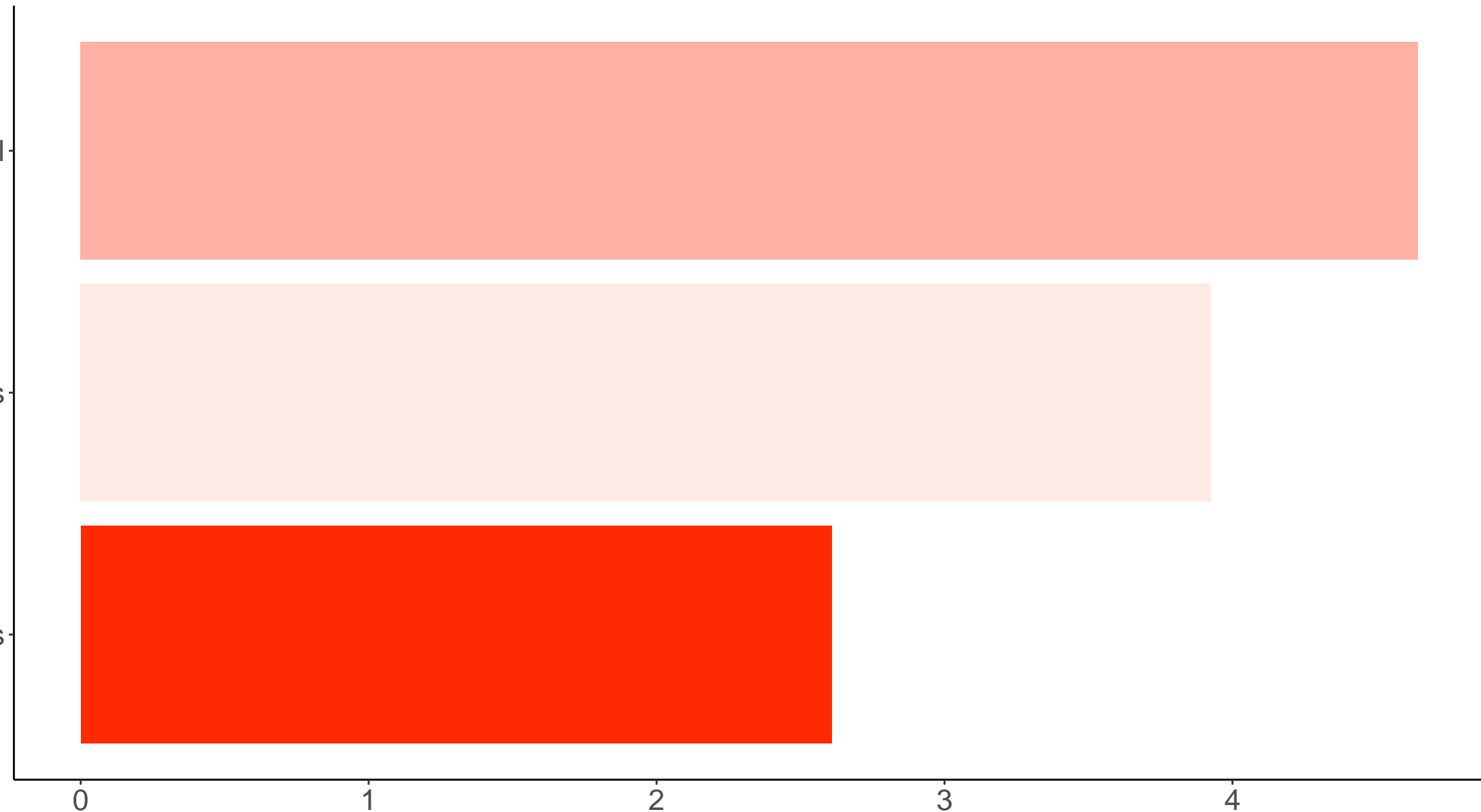
1

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log2Enrichment



Re-clustered module 16.15.17 MF enrichment

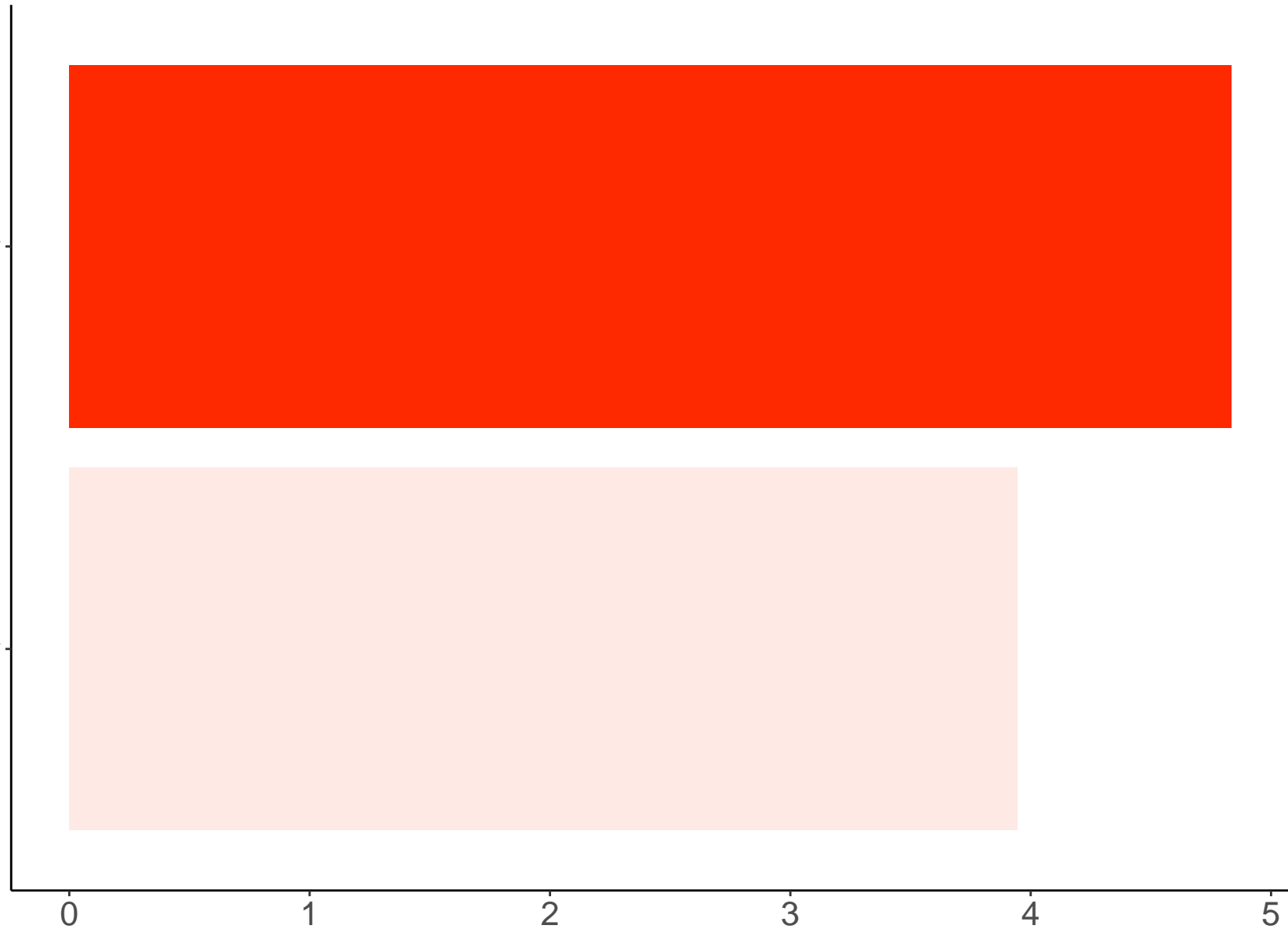
Term

N-methyltransferase activity

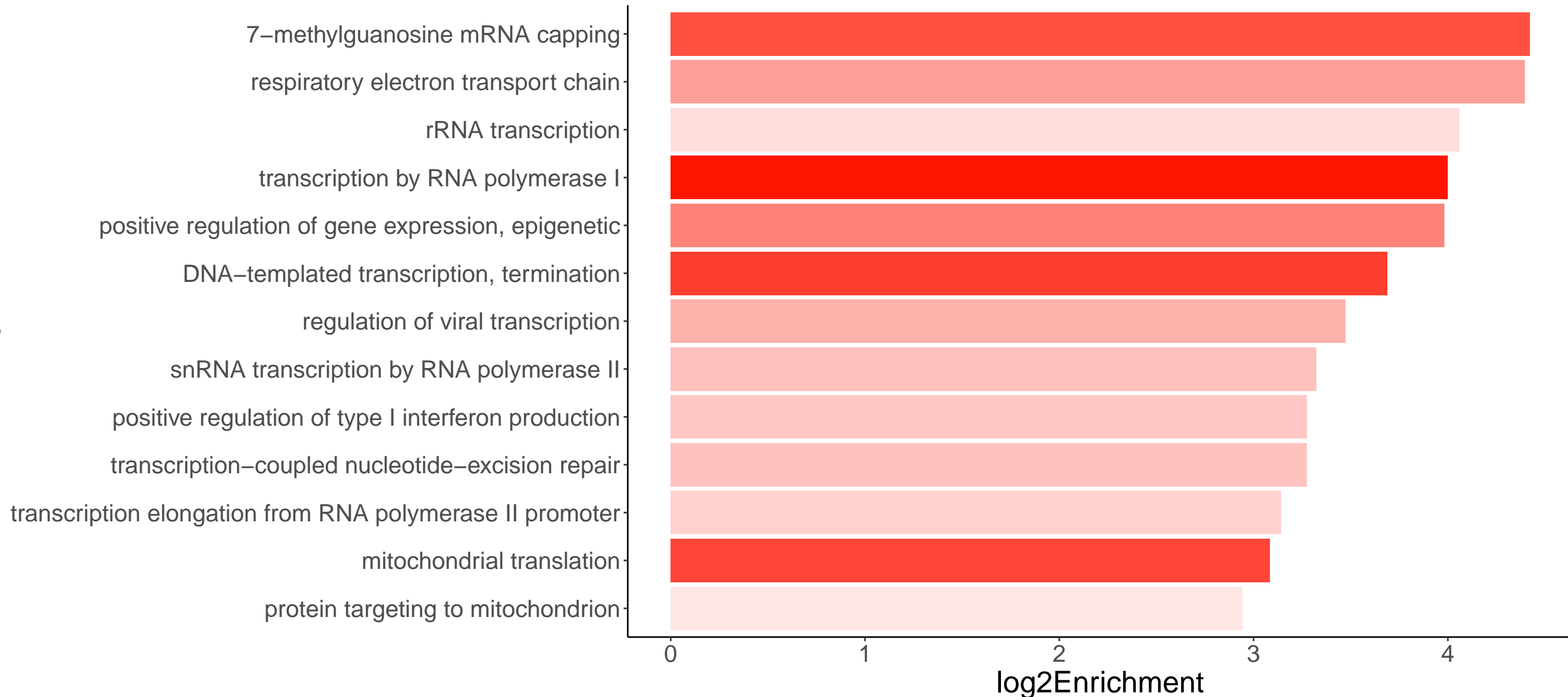
S-adenosylmethionine-dependent methyltransferase activity

0 1 2 3 4 5

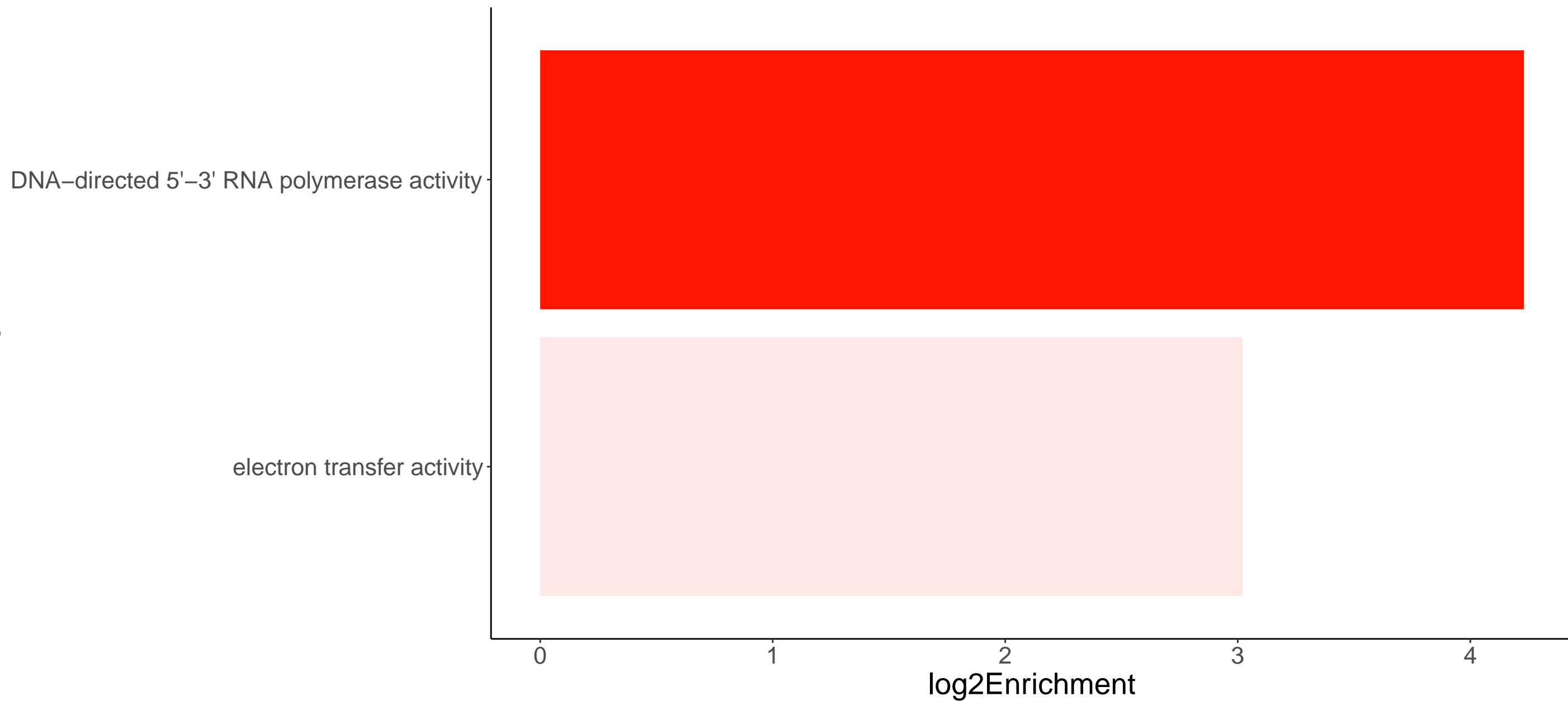
log2Enrichment



Re-clustered module 16.15.2 BP enrichment

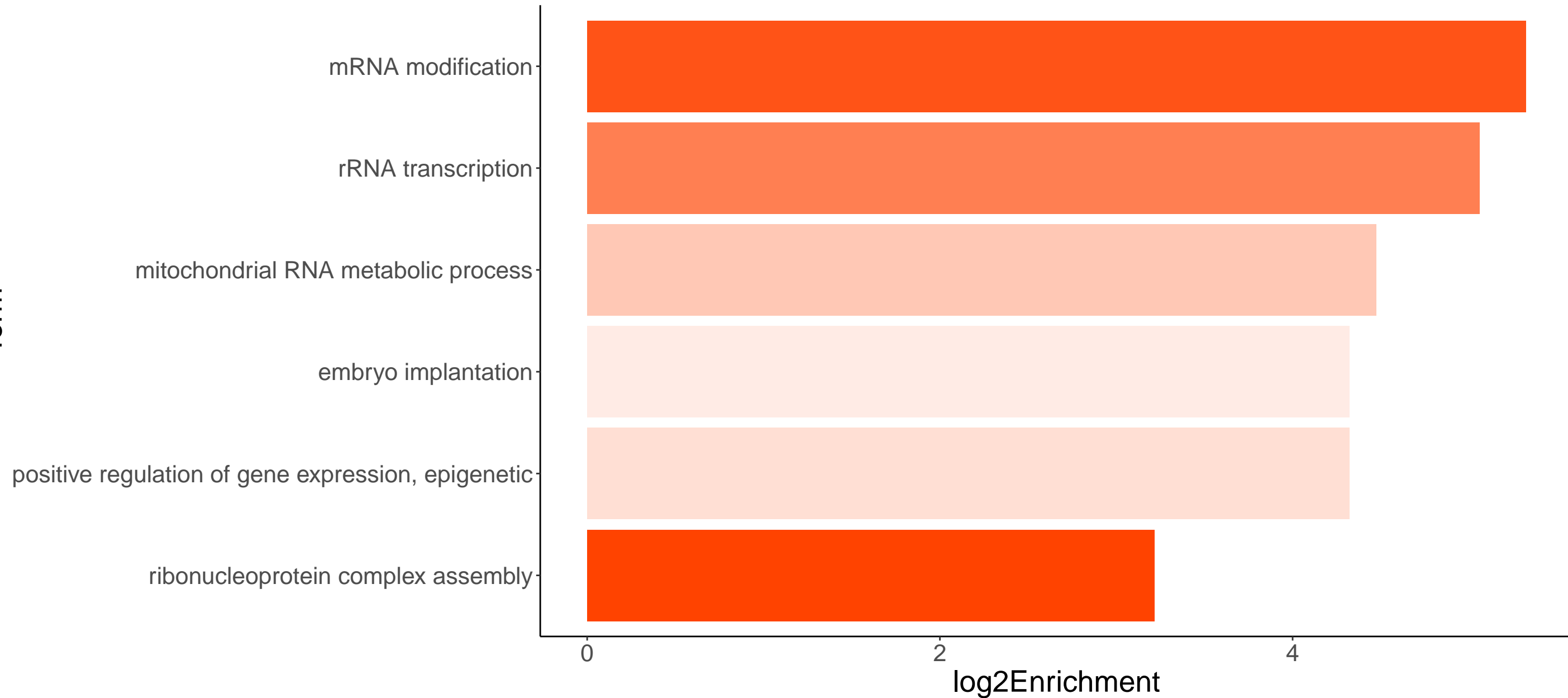


Re-clustered module 16.15.2 MF enrichment



Re-clustered module 16.15.3 BP enrichment

Term



Re-clustered module 16.15.3 MF enrichment

Term

intramolecular transferase activity

ribosome binding

basal RNA polymerase II transcription machinery binding

helicase activity

catalytic activity, acting on DNA

0

2

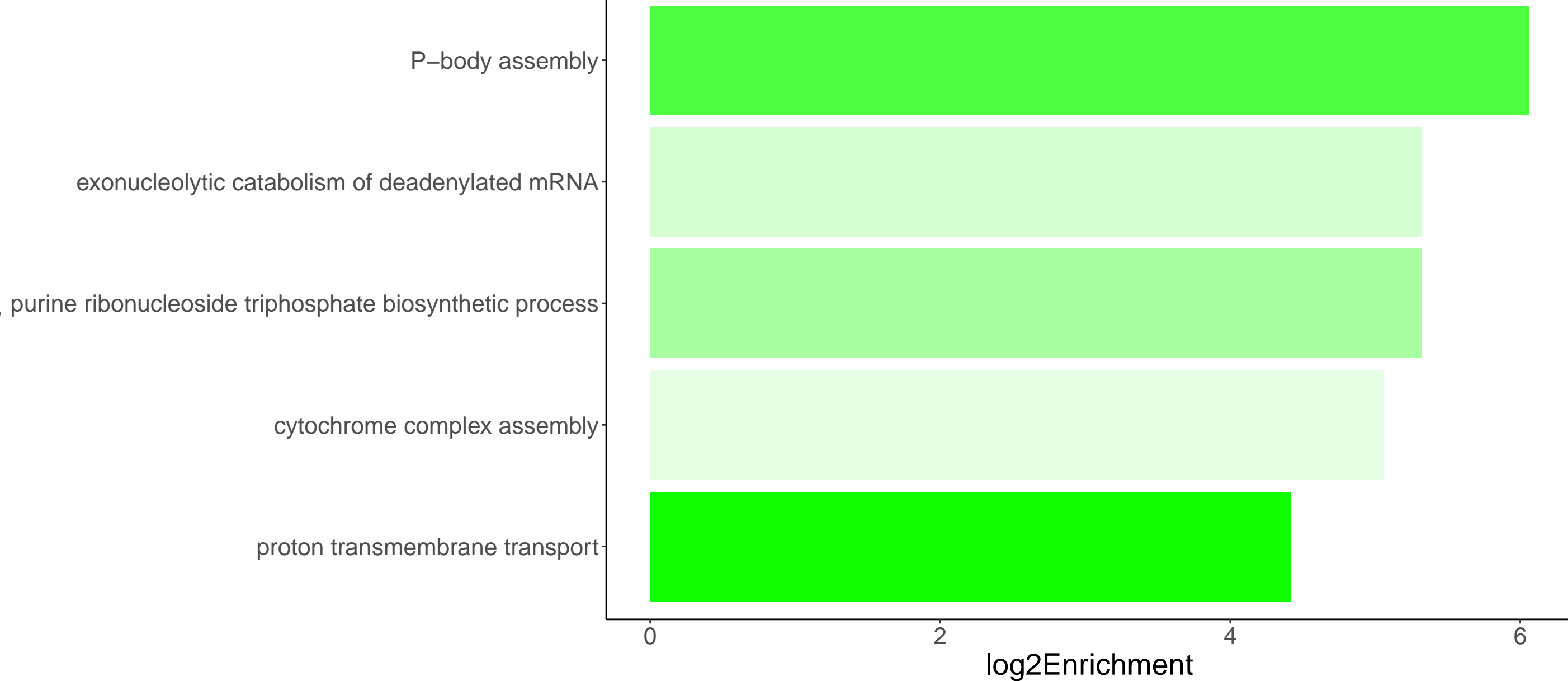
4

log2Enrichment



Re-clustered module 16.15.4 BP enrichment

Term



Re-clustered module 16.15.4 MF enrichment

Term

snRNA binding

proton transmembrane transporter activity

structural constituent of ribosome

0

1

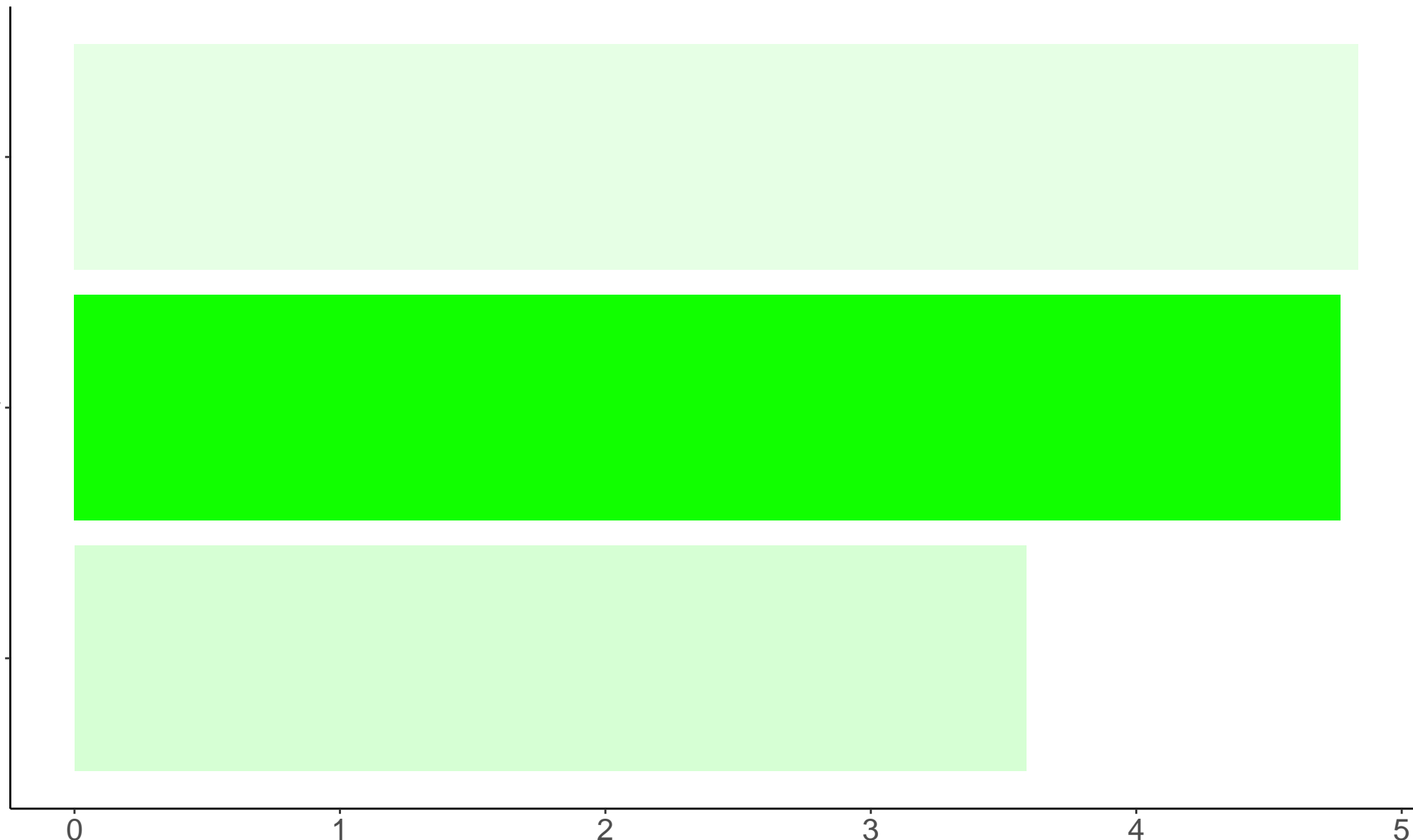
2

3

4

5

log2Enrichment



Term

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

blastocyst formation

rRNA processing

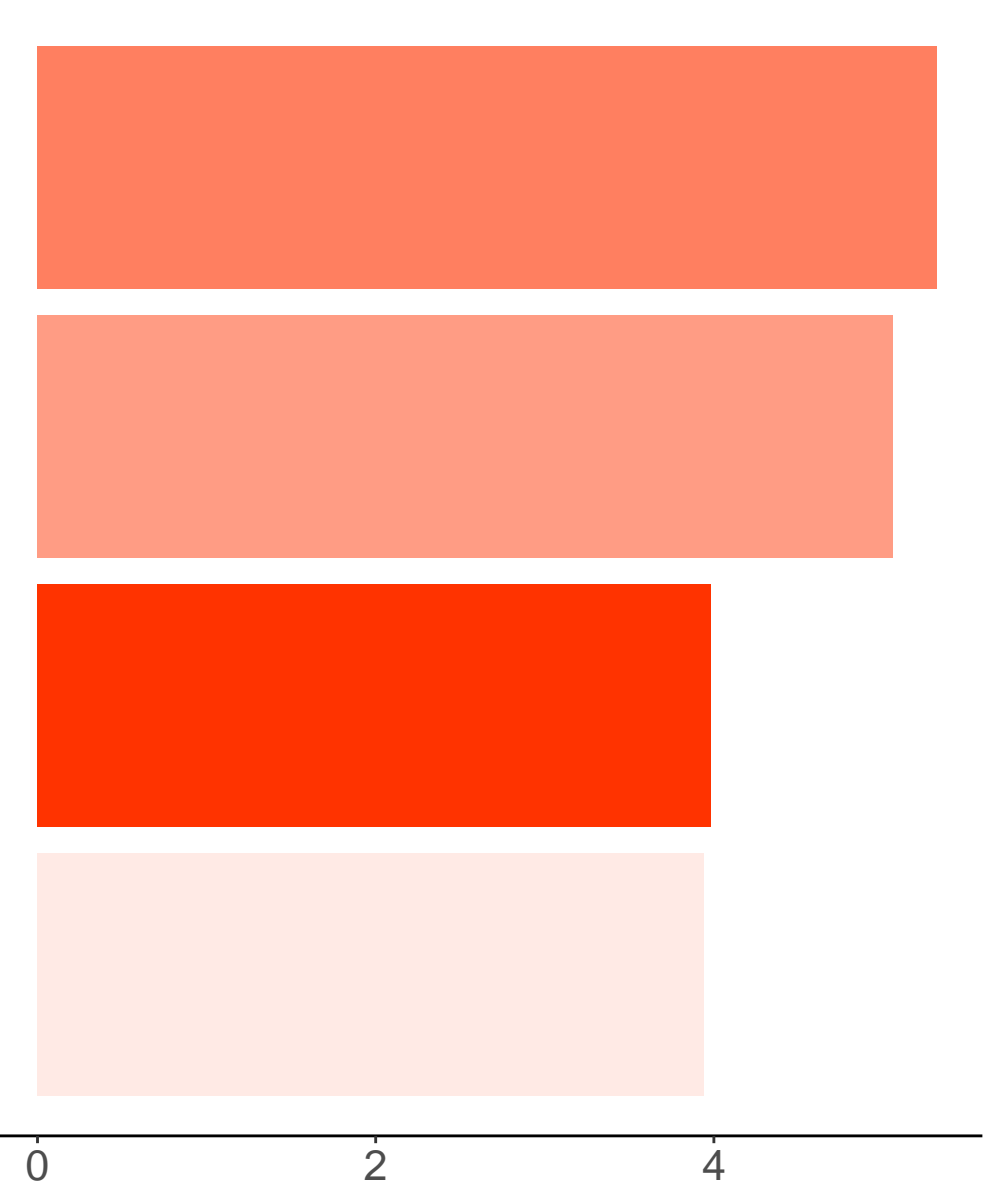
tRNA modification

0

2

4

log2Enrichment



Re-clustered module 16.15.5 MF enrichment

Term

snoRNA binding

0

2

4

log2Enrichment



Re-clustered module 16.15.8 BP enrichment

Term

aerobic respiration

mitochondrial ATP synthesis coupled electron transport

RNA phosphodiester bond hydrolysis

0

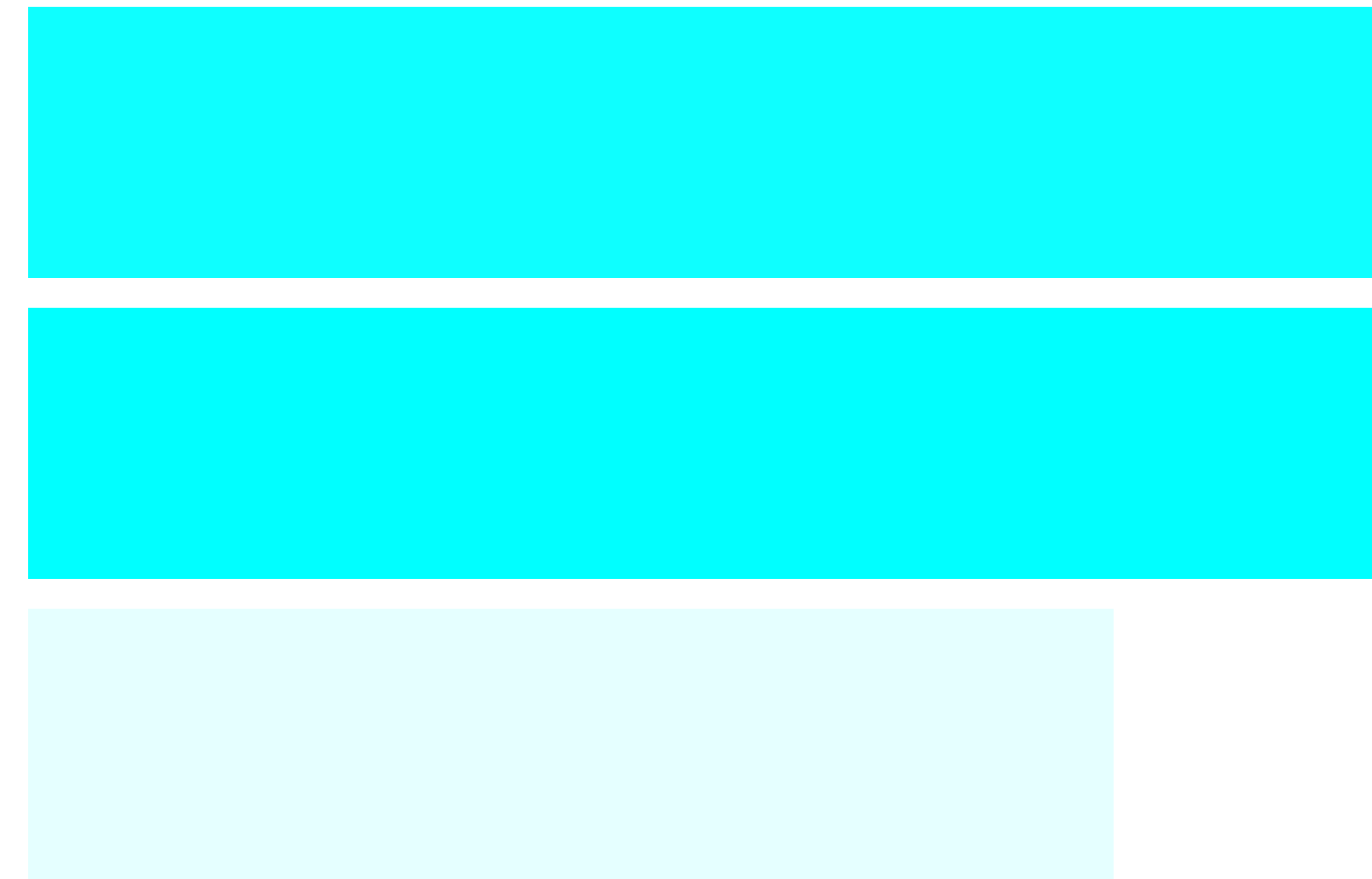
1

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3

4

log2Enrichment



Re-clustered module 16.15.8 MF enrichment

Term

heat shock protein binding

unfolded protein binding

RNA binding

0

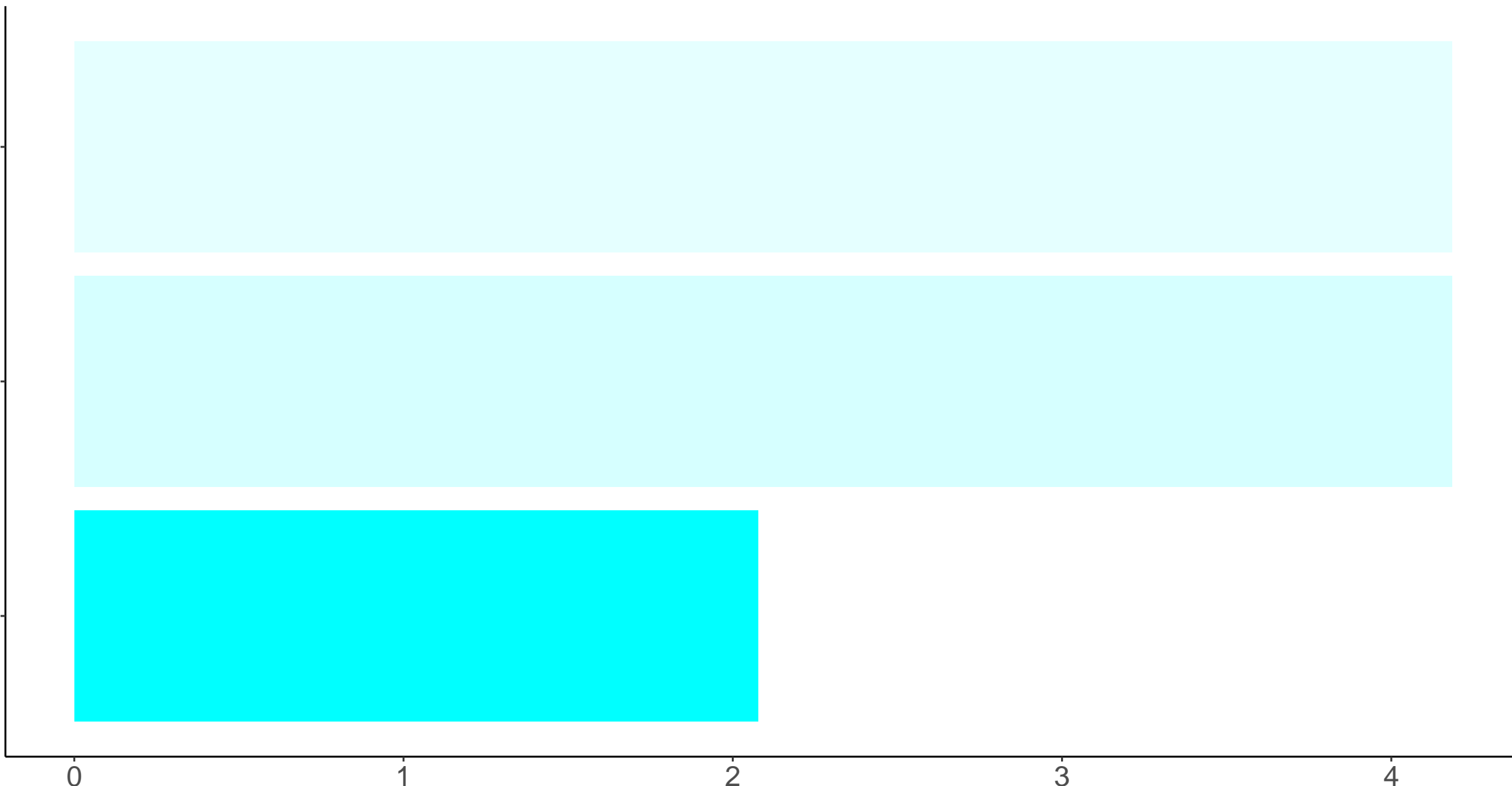
1

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3

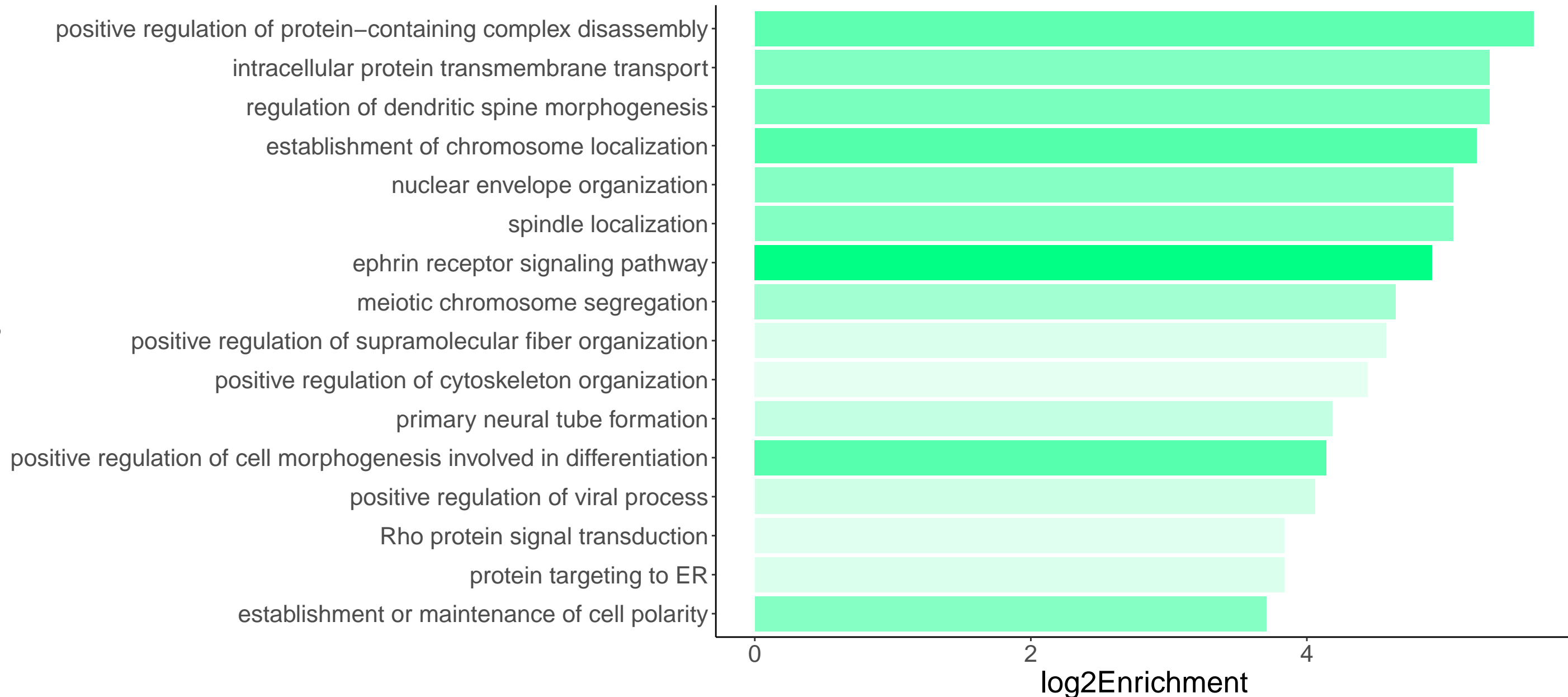
4

log2Enrichment



Re-clustered module 16.21 BP enrichment

Term



Re-clustered module 16.21 MF enrichment

Term

structural constituent of cytoskeleton

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.22 BP enrichment

Term

mRNA polyadenylation

positive regulation of mRNA metabolic process

protein homooligomerization

positive regulation of Wnt signaling pathway

0

2

4

6

log2Enrichment



Re-clustered module 16.22 MF enrichment

Term

log2Enrichment



Re-clustered module 16.3 BP enrichment

Term

ncRNA 3'-end processing

fatty acid catabolic process

mitochondrial gene expression

mRNA processing

0

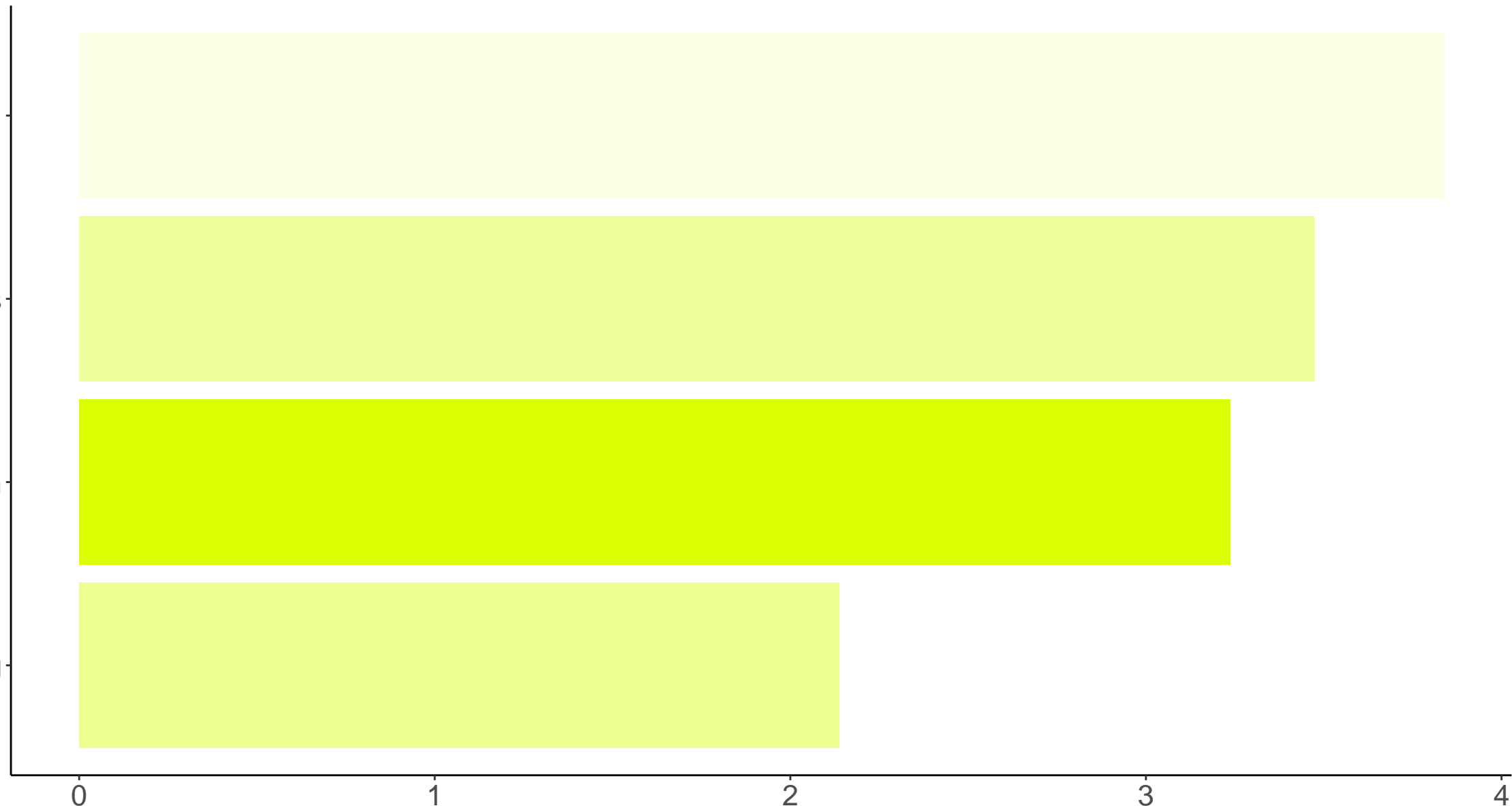
1

2

3

4

log2Enrichment



Re-clustered module 16.3 MF enrichment

Term

5'–3' RNA polymerase activity

0

1

2

3

4

log2Enrichment



Re-clustered module 16.30 BP enrichment

Term

interstrand cross-link repair

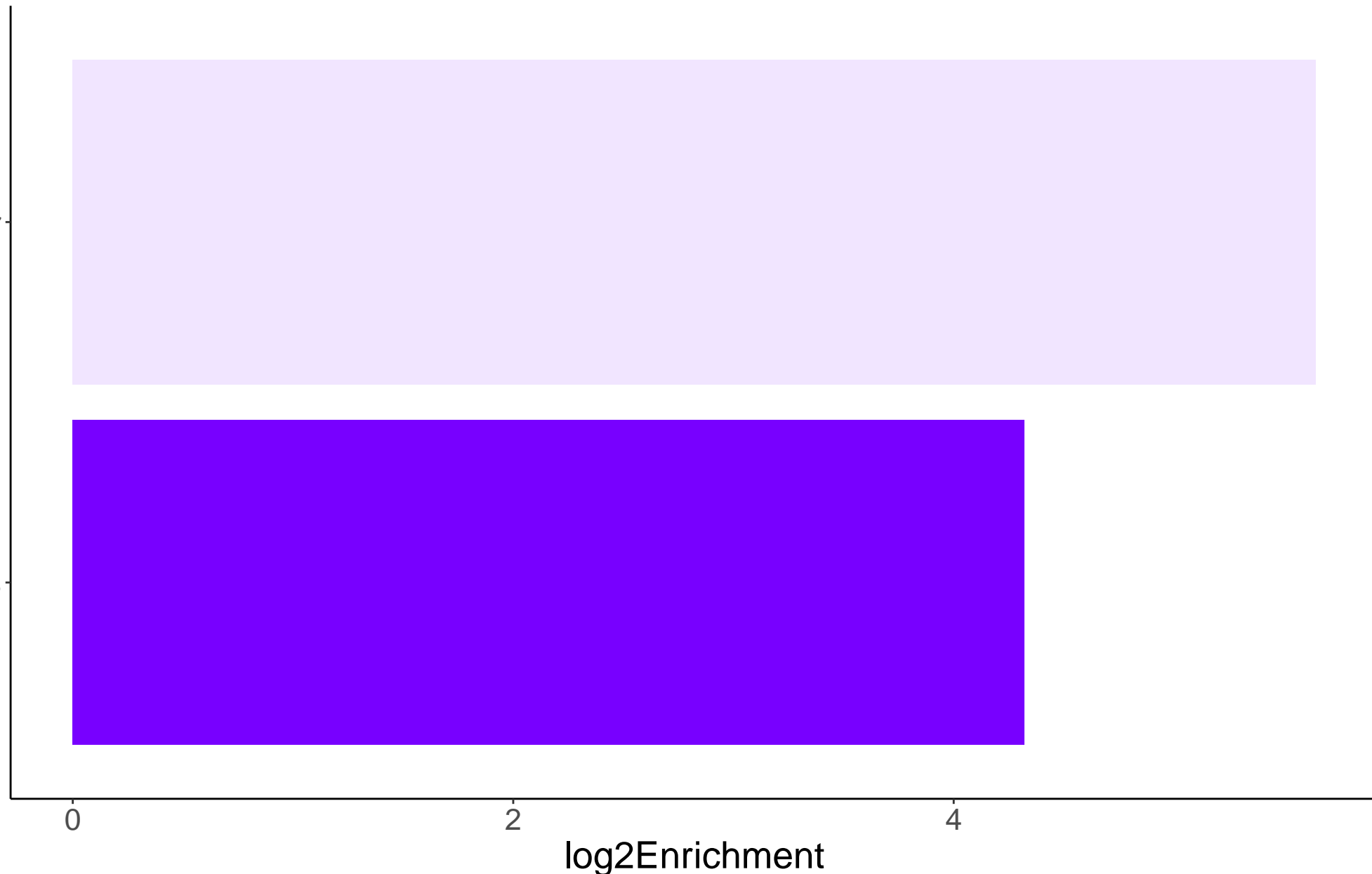
nucleic acid phosphodiester bond hydrolysis

0

2

4

log2Enrichment



Re-clustered module 16.30 MF enrichment

Term

endonuclease activity

nucleic acid binding

0

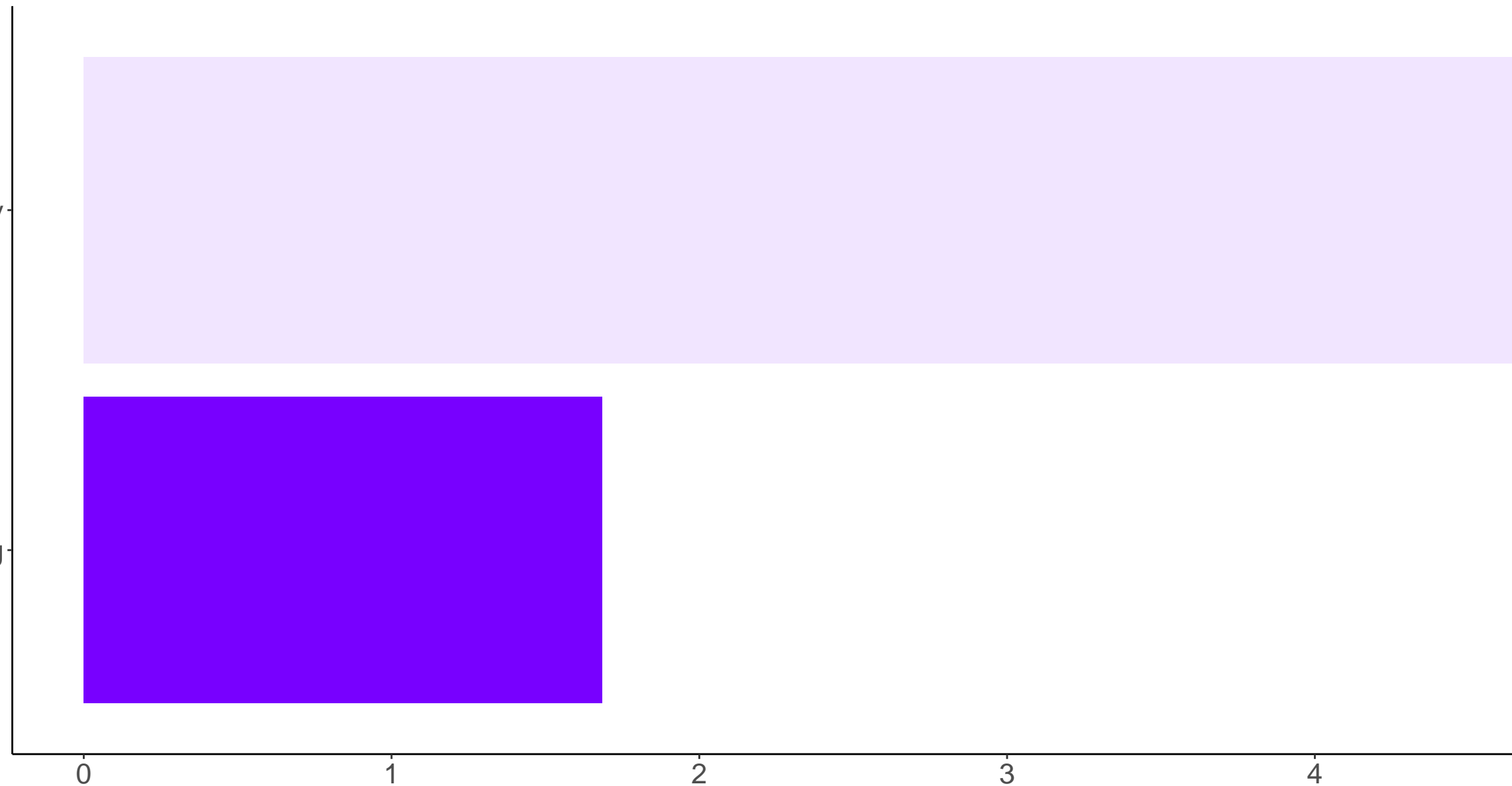
1

2

3

4

log2Enrichment



Re-clustered module 16.31 BP enrichment

Term

transcription elongation from RNA polymerase II promoter

0

1

2

3

4

log2Enrichment



Re-clustered module 16.31 MF enrichment

Term

RNA binding

0.0

0.5

1.0

1.5

2.0

log2Enrichment



Re-clustered module 16.32 BP enrichment

Term

regulation of signal transduction by p53 class mediator

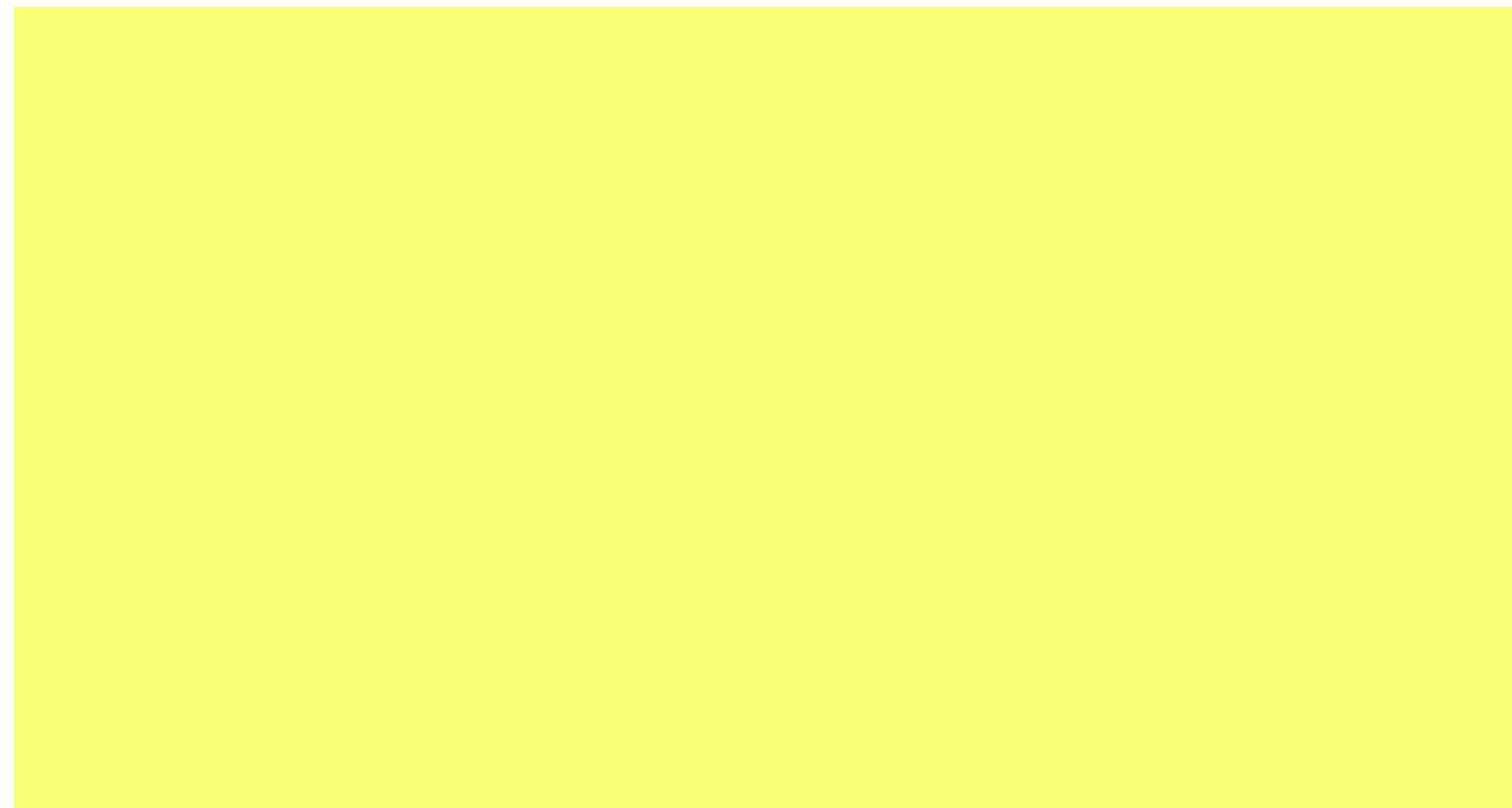
0

1

2

3

log2Enrichment



Re-clustered module 16.32 MF enrichment

Term

log2Enrichment



Re-clustered module 16.34 BP enrichment

Term

regulation of histone deacetylation

0

2

4

6

log2Enrichment



Re-clustered module 16.34 MF enrichment

Term

log2Enrichment



Re-clustered module 16.35 BP enrichment

Term

protein folding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.35 MF enrichment

Term

RNA helicase activity

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.36 BP enrichment

Term

cellular response to leukemia inhibitory factor

0

1

2

3

4

log2Enrichment



Re-clustered module 16.36 MF enrichment

Term

log2Enrichment



Re-clustered module 16.37 BP enrichment

Term

positive regulation of epidermal growth factor receptor signaling pathway

DNA-templated transcription, termination

positive regulation of organelle assembly

mRNA export from nucleus

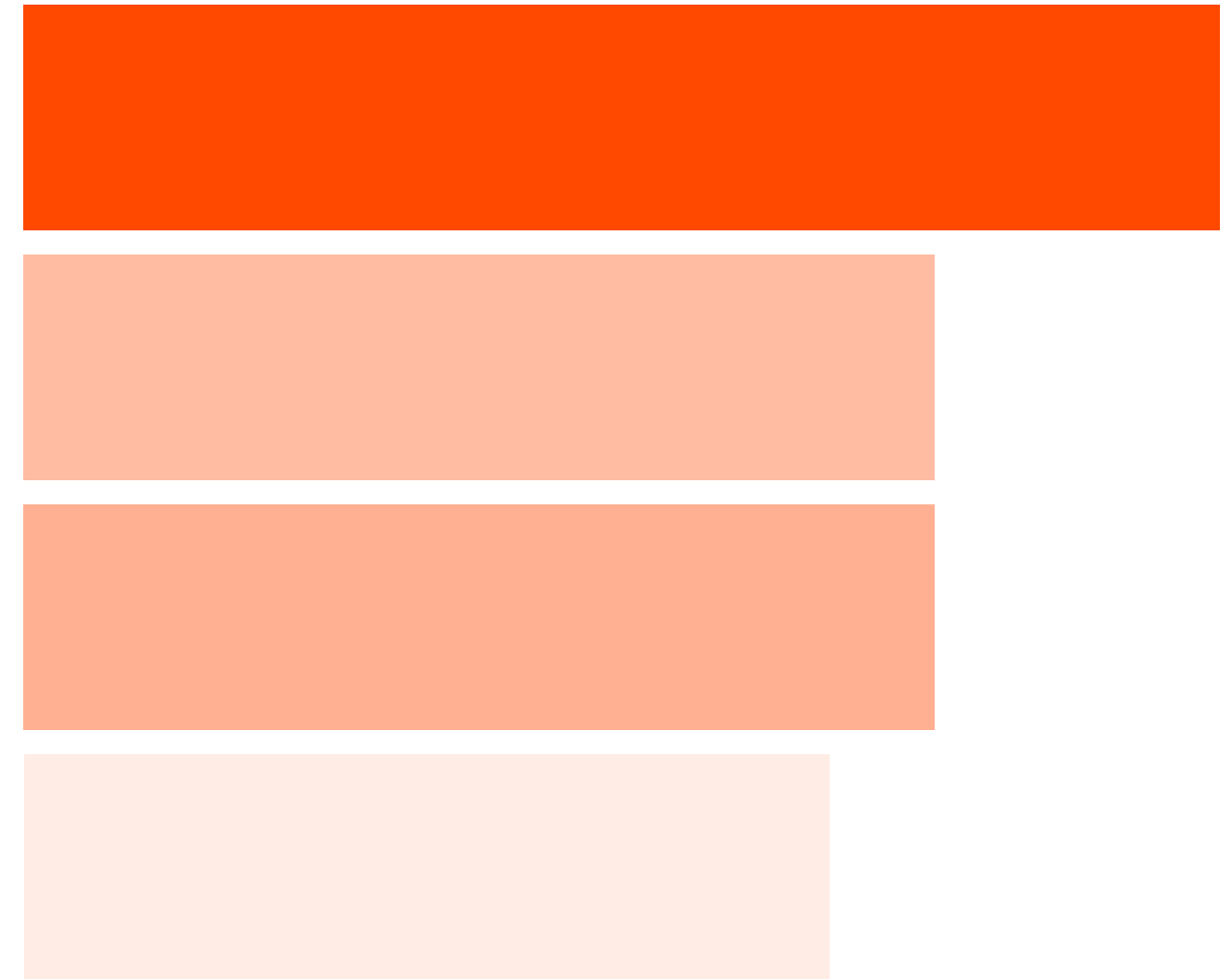
0

2

4

6

log2Enrichment



Re-clustered module 16.37 MF enrichment

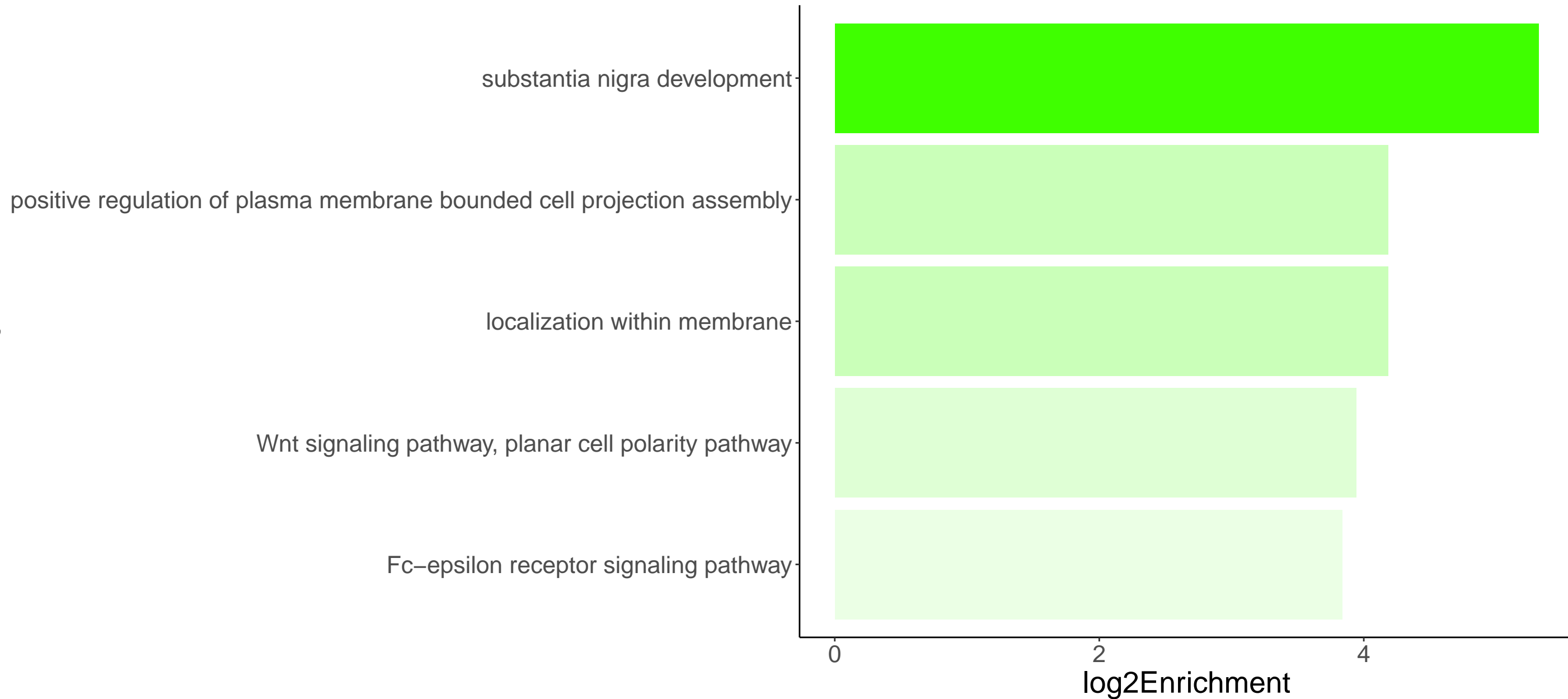
Term

log2Enrichment



Re-clustered module 16.40 BP enrichment

Term



Re-clustered module 16.40 MF enrichment

Term

ATPase binding

GDP binding

nucleotidyltransferase activity

GTP binding

pyrophosphatase activity

0

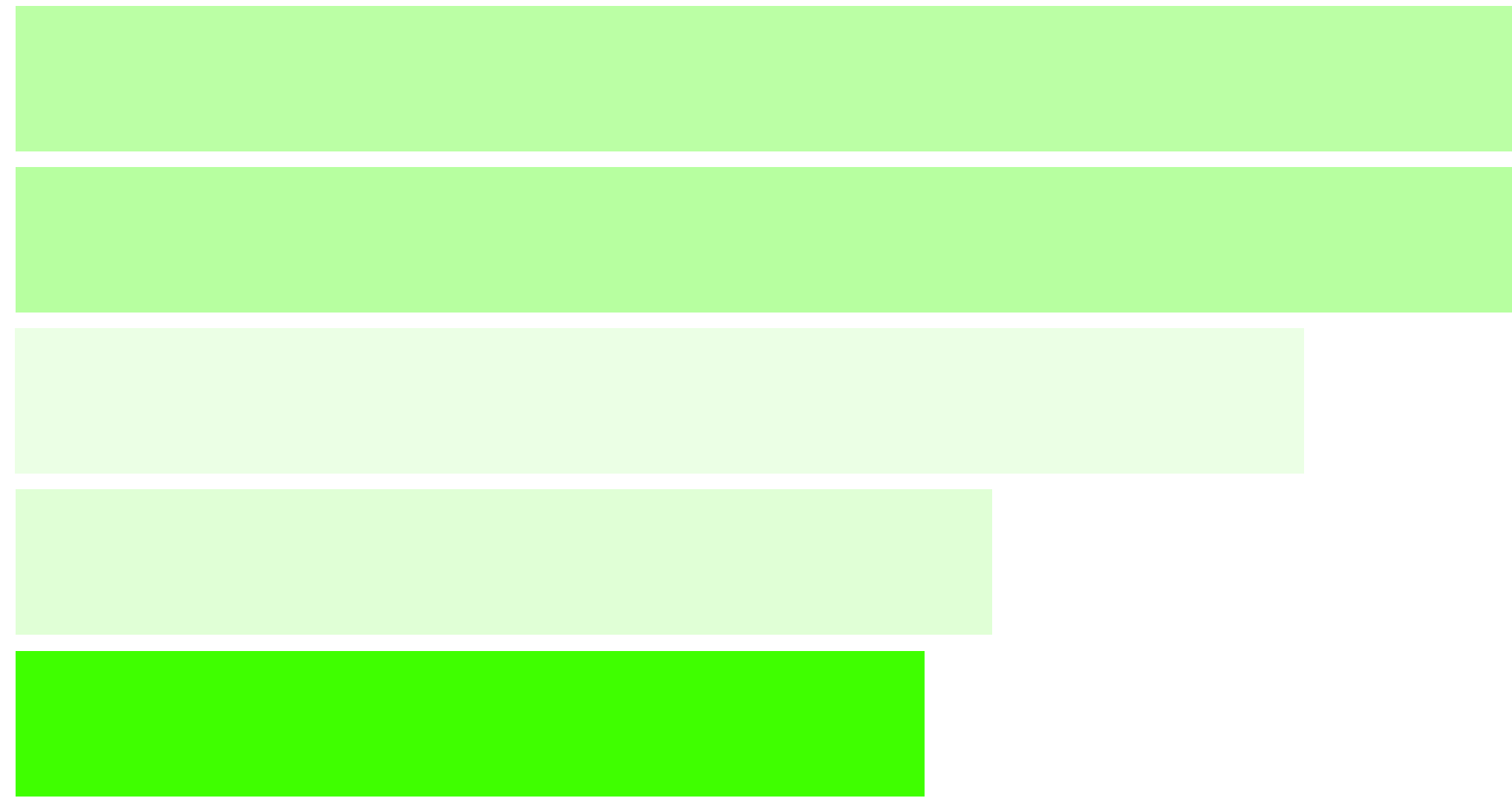
1

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3

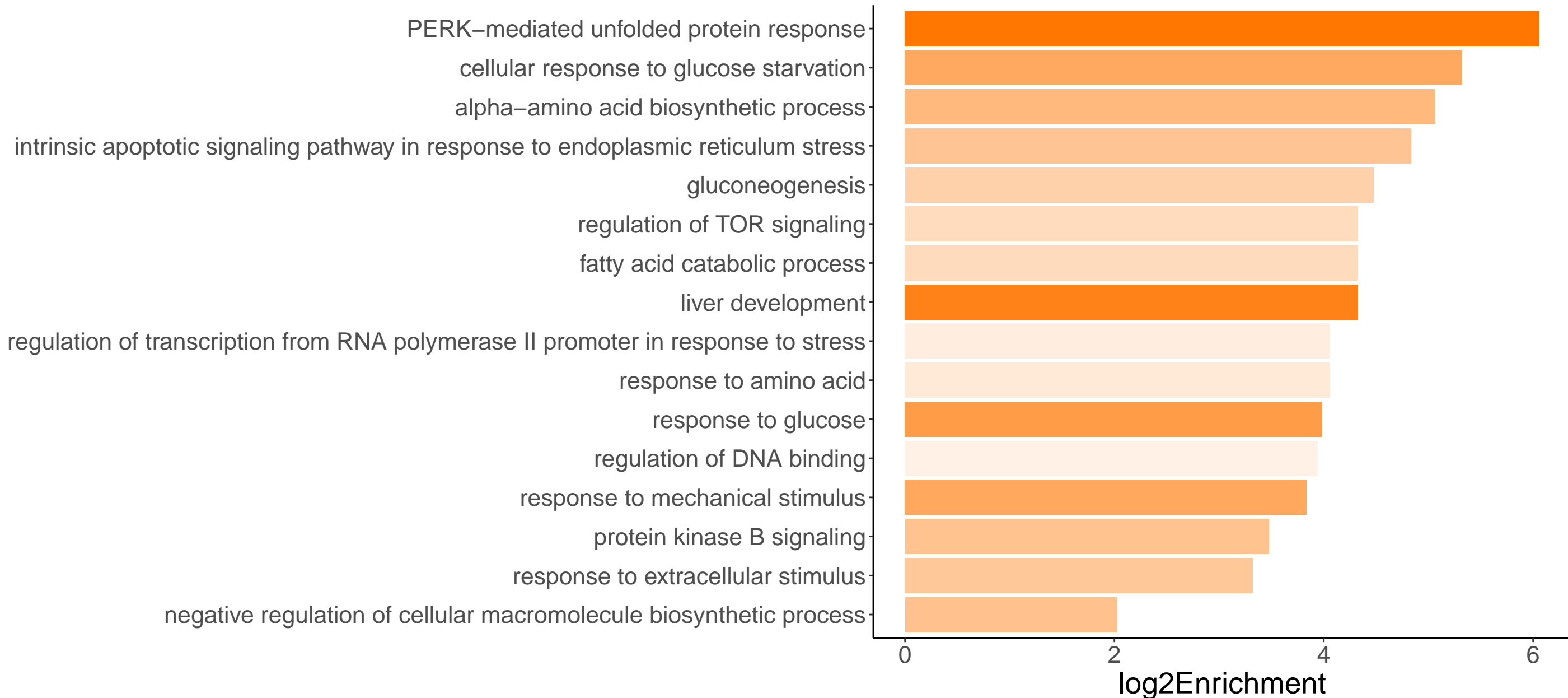
4

log2Enrichment



Re-clustered module 16.41 BP enrichment

Term



Re-clustered module 16.41 MF enrichment

Term

DNA binding

0.0

0.5

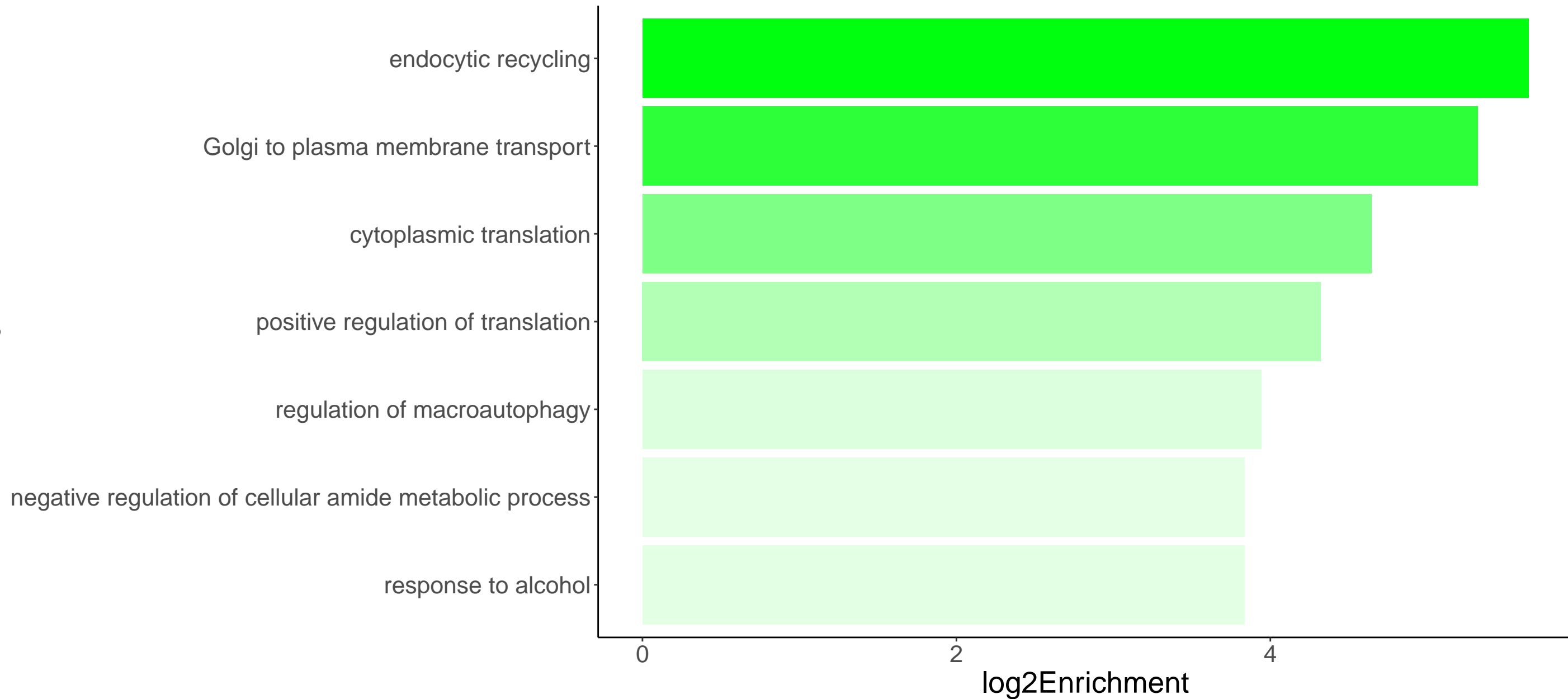
1.0

log2Enrichment



Re-clustered module 16.44 BP enrichment

Term



Re-clustered module 16.44 MF enrichment

Term

ribonucleoprotein complex binding

cadherin binding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.5 BP enrichment

Term

snRNA transcription by RNA polymerase II

macromolecule methylation

0

1

2

3

4

log2Enrichment



Re-clustered module 16.5 MF enrichment

Term
ubiquitin-protein transferase activity

0

1

2

log2Enrichment



Re-clustered module 16.59 BP enrichment

Term

dolichol-linked oligosaccharide biosynthetic process

0

2

4

6

log2Enrichment



Re-clustered module 16.59 MF enrichment

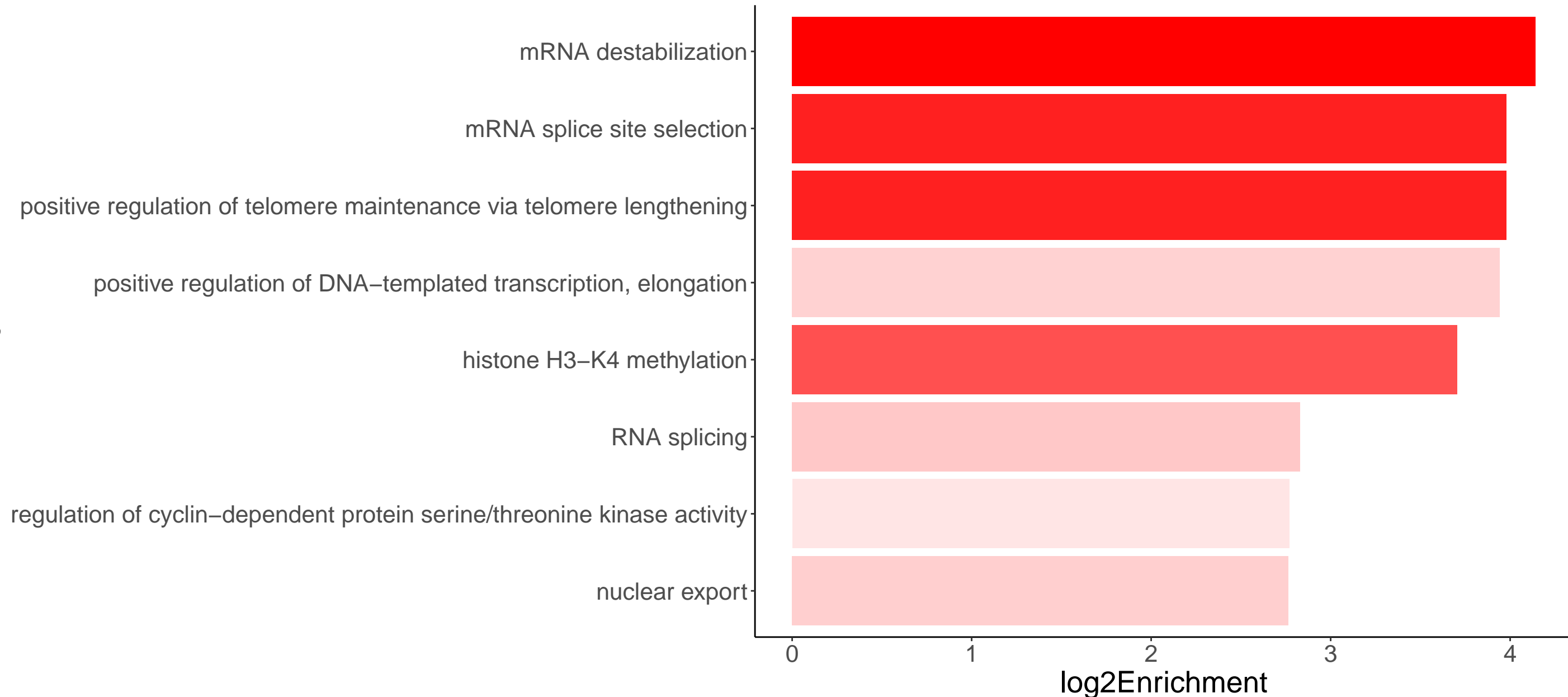
Term

log2Enrichment



Re-clustered module 16.6 BP enrichment

Term



Re-clustered module 16.6 MF enrichment

Term

telomeric DNA binding

cyclin-dependent protein serine/threonine kinase regulator activity

poly(U) RNA binding

transcription coactivator activity

DNA binding

0

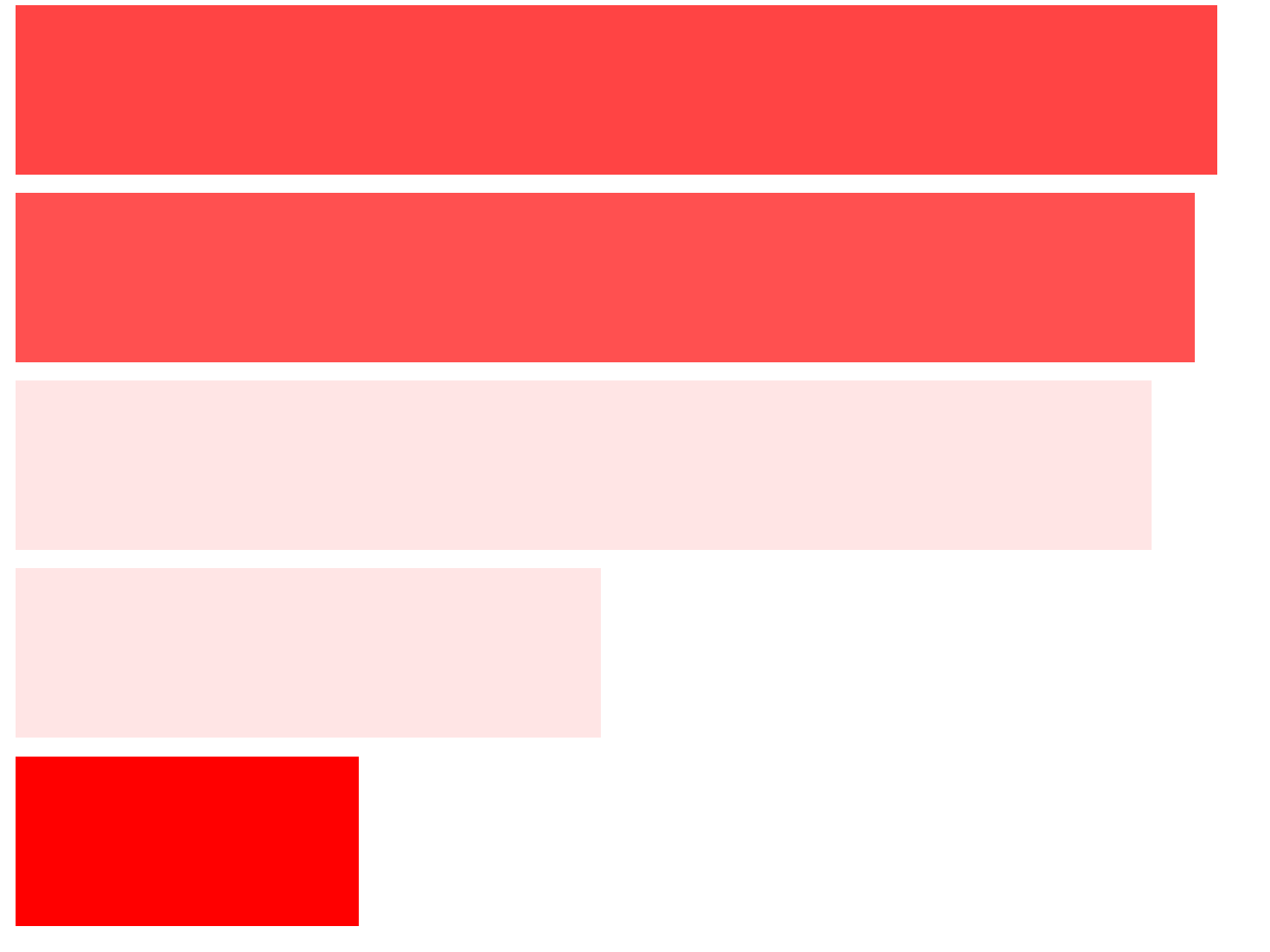
1

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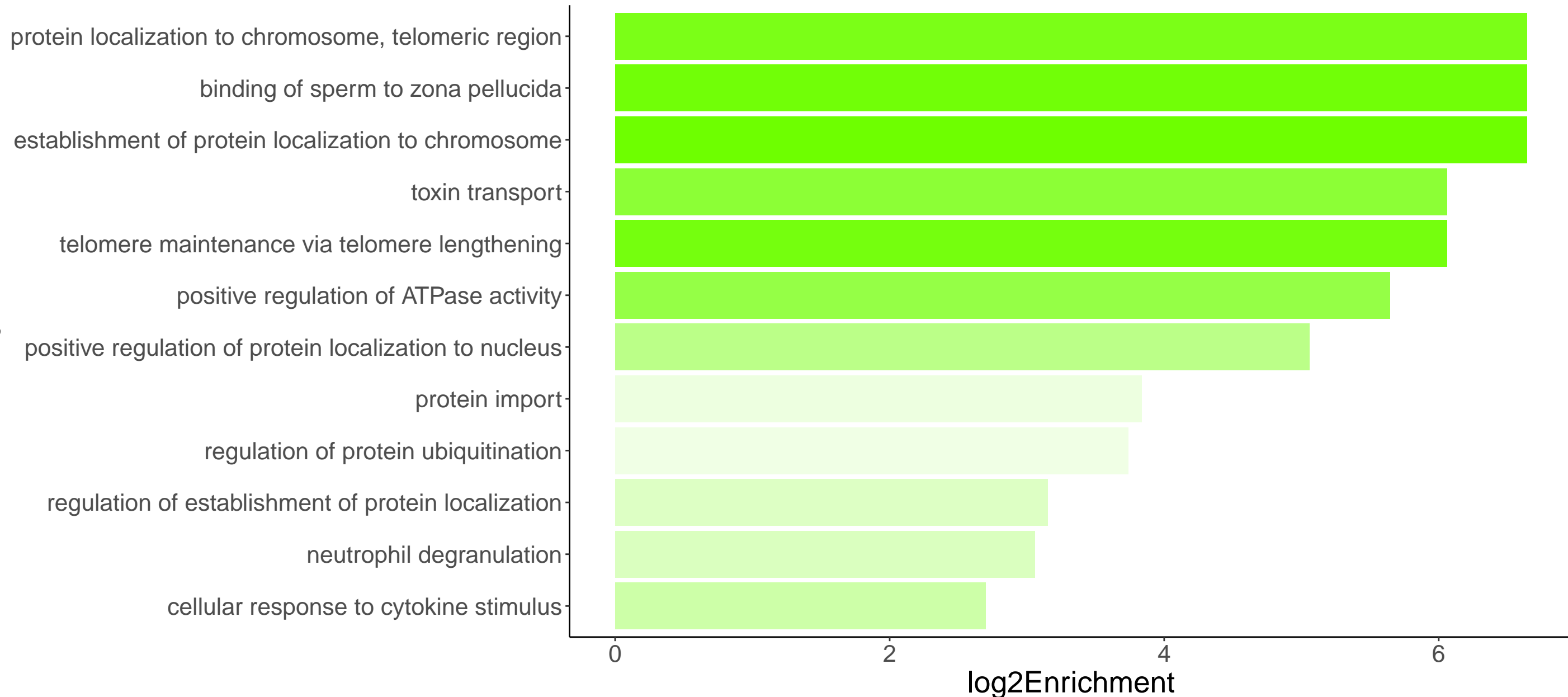
4

log2Enrichment



Re-clustered module 16.63 BP enrichment

Term



Re-clustered module 16.63 MF enrichment

Term

MHC protein complex binding

cadherin binding

protein domain specific binding

0

2

4

6

log2Enrichment



Re-clustered module 16.66 BP enrichment

Term

DNA replication-independent nucleosome assembly

protein localization to cilium

endocrine process

negative regulation of phosphatase activity

regulation of G1/S transition of mitotic cell cycle

cilium assembly

positive regulation of GTPase activity

0

1

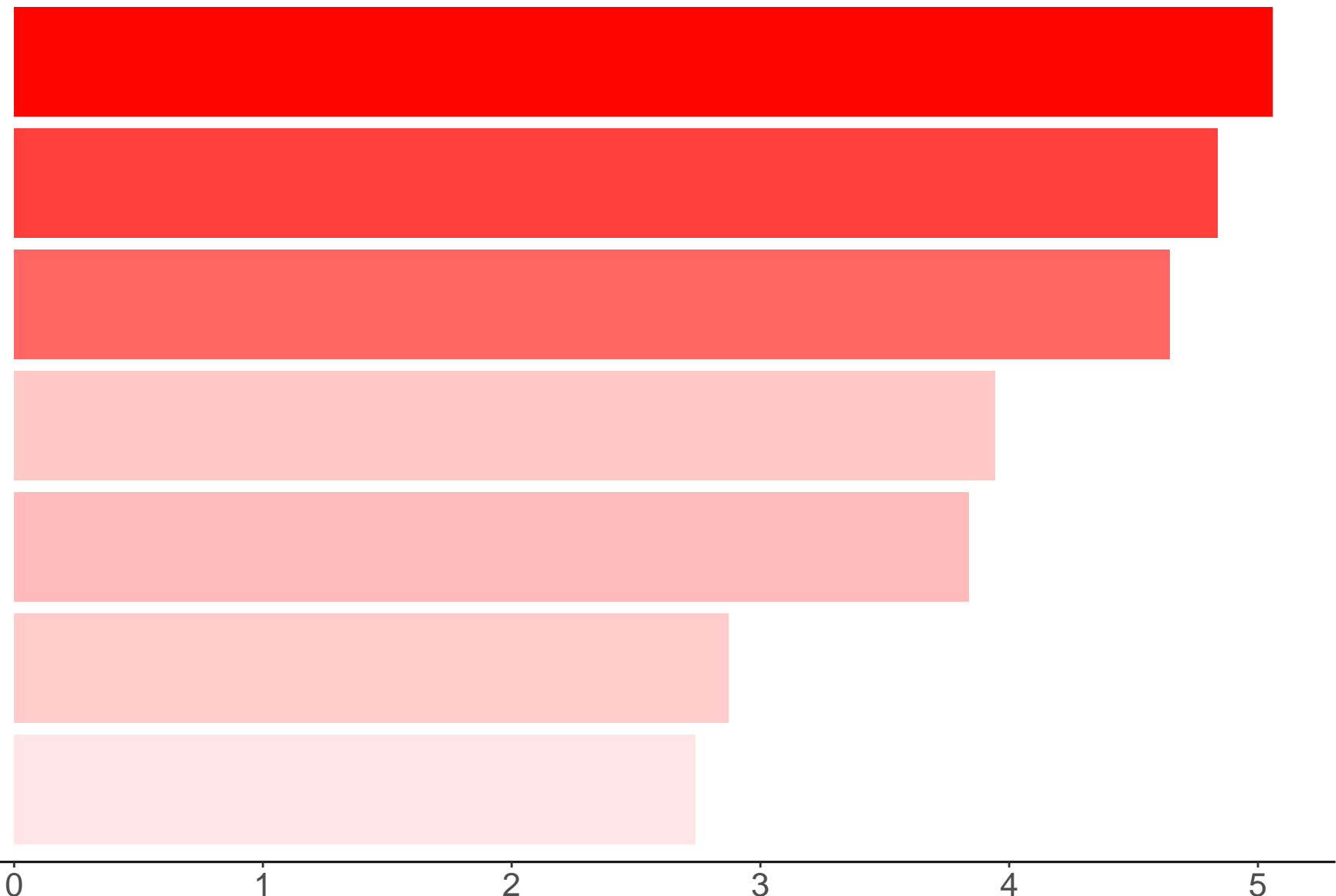
2

3

4

5

log2Enrichment



Re-clustered module 16.66 MF enrichment

Term

GTPase activator activity

0

1

2

3

log2Enrichment



Re-clustered module 16.8 BP enrichment

Term

negative regulation of microtubule depolymerization

ATP-dependent chromatin remodeling

DNA duplex unwinding

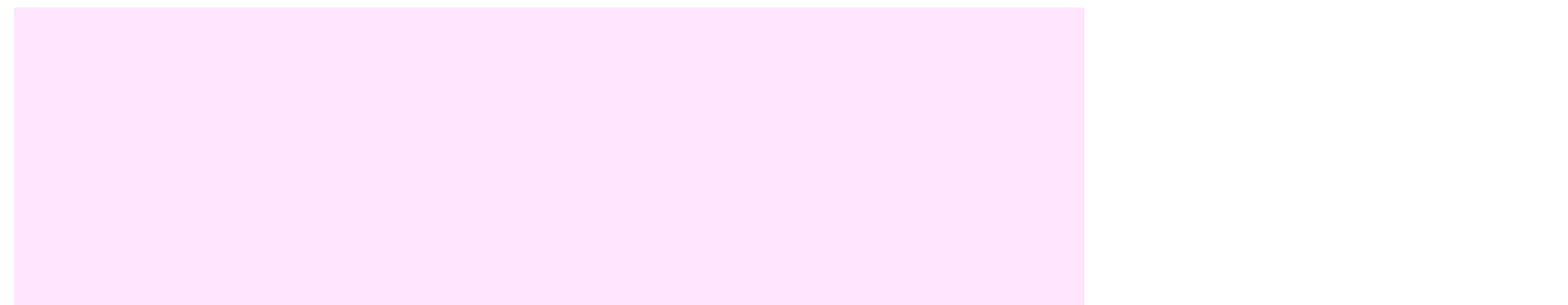
0

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6

log2Enrichment



Re-clustered module 16.8 MF enrichment

Term

DNA-dependent ATPase activity

catalytic activity, acting on DNA

chromatin binding

DNA binding

0

1

2

3

4

log2Enrichment



Re-clustered module 16.9.5 BP enrichment

Term

cellular response to ketone

0

1

2

3

4

5

log2Enrichment



Re-clustered module 16.9.5 MF enrichment

Term

heterocyclic compound binding

organic cyclic compound binding

0.00

0.25

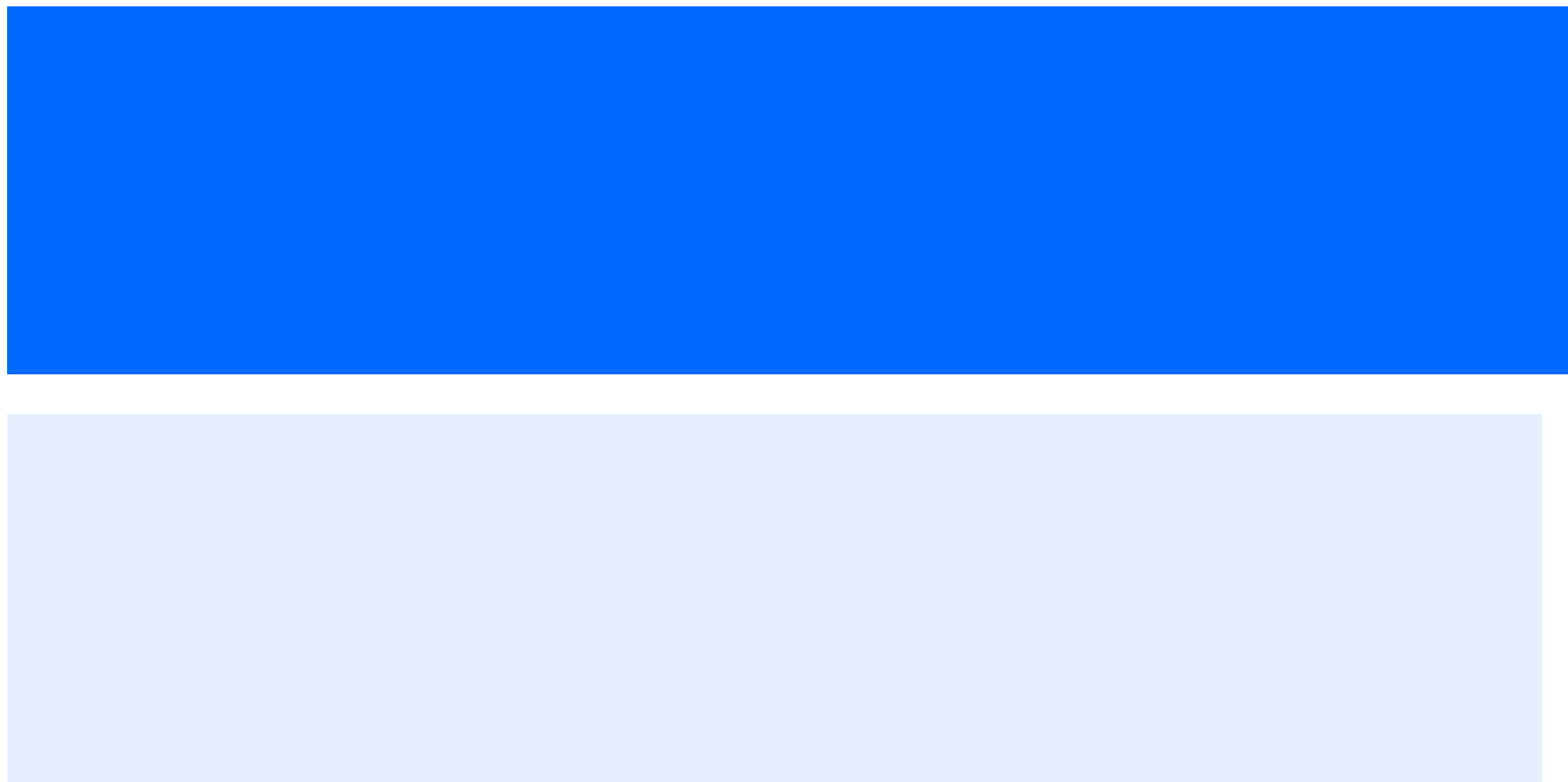
0.50

0.75

1.00

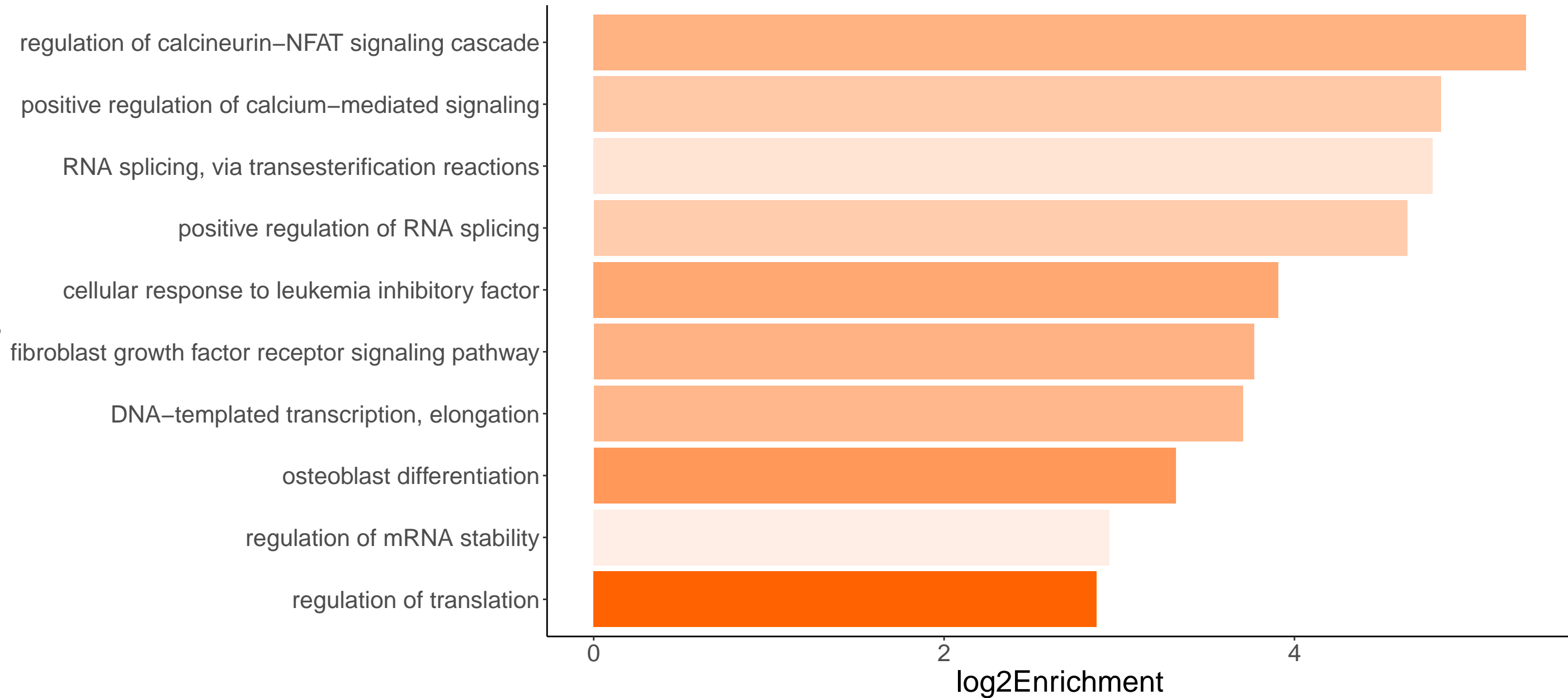
1.2

log2Enrichment



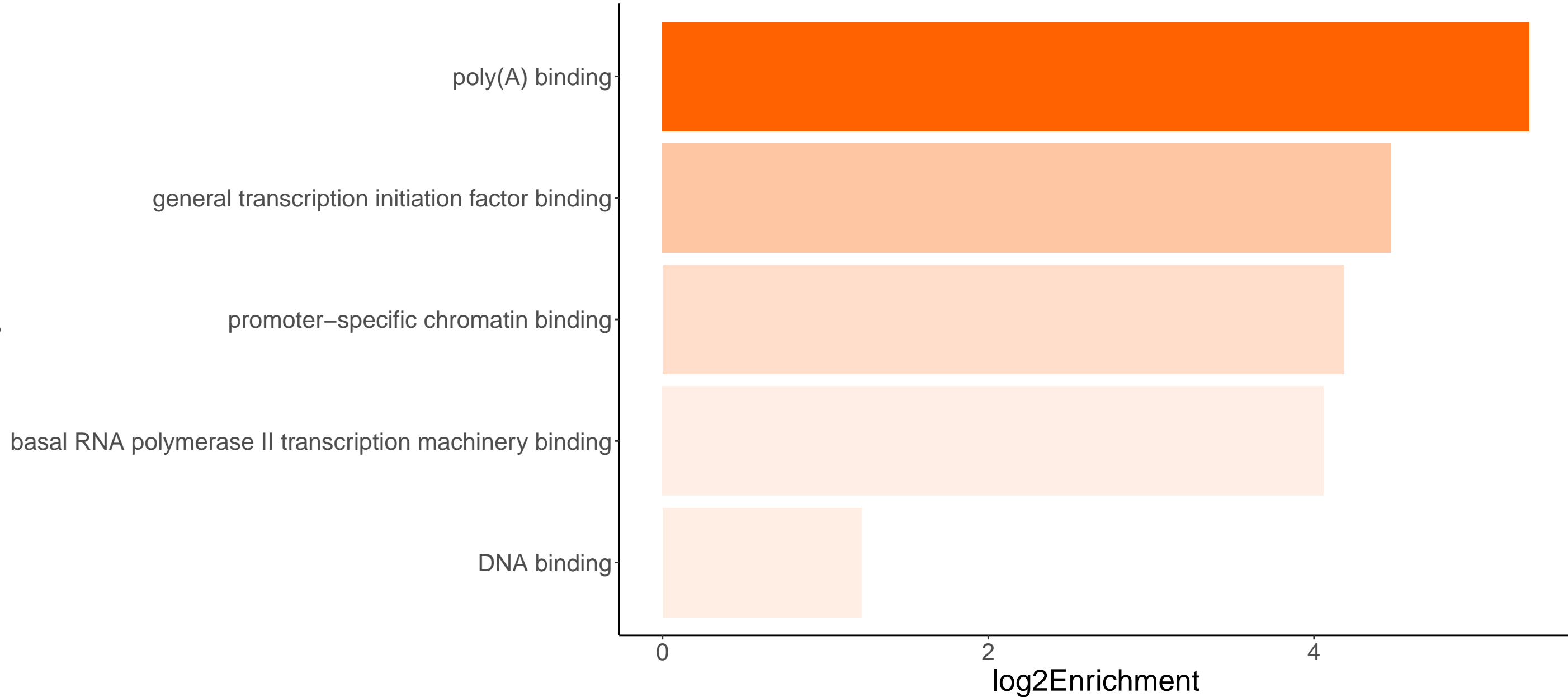
Re-clustered module 16.9.6 BP enrichment

Term



Re-clustered module 16.9.6 MF enrichment

Term



Re-clustered module 16.9.7 BP enrichment

Term

negative regulation of autophagy

blastocyst development

0

1

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3

4

log2Enrichment



Re-clustered module 16.9.7 MF enrichment

Term

transcription coregulator activity

sequence-specific DNA binding

0

1

2

3

log2Enrichment

