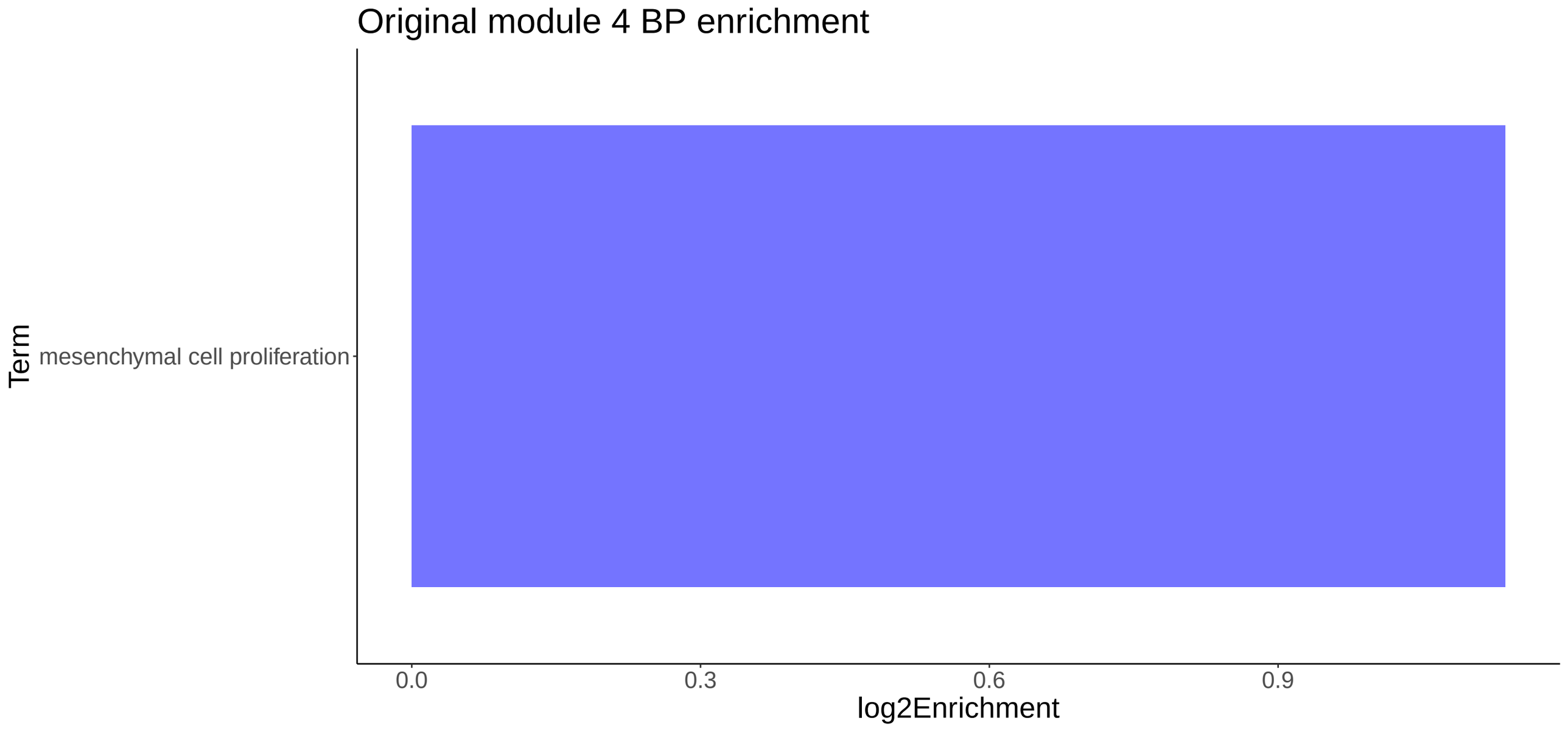
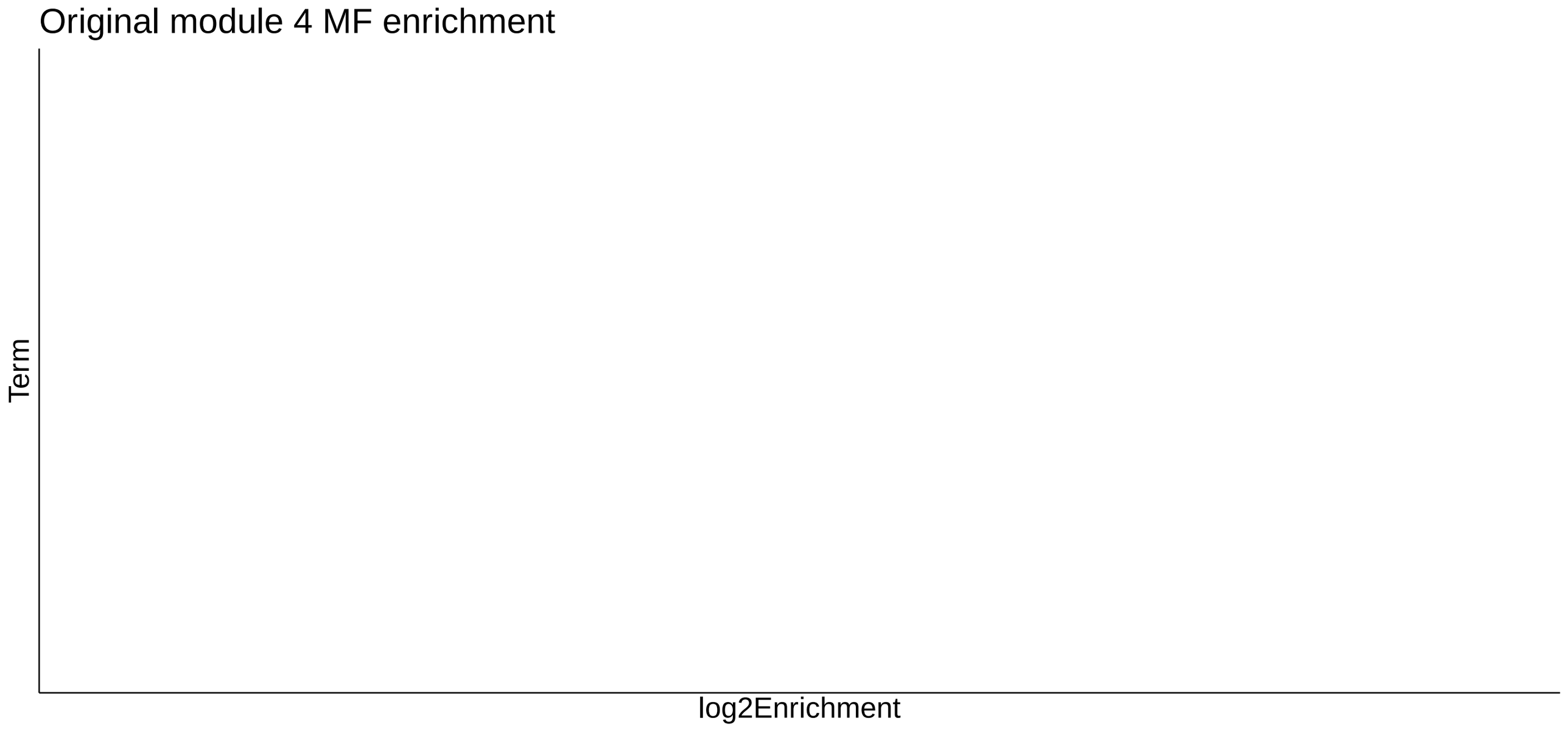
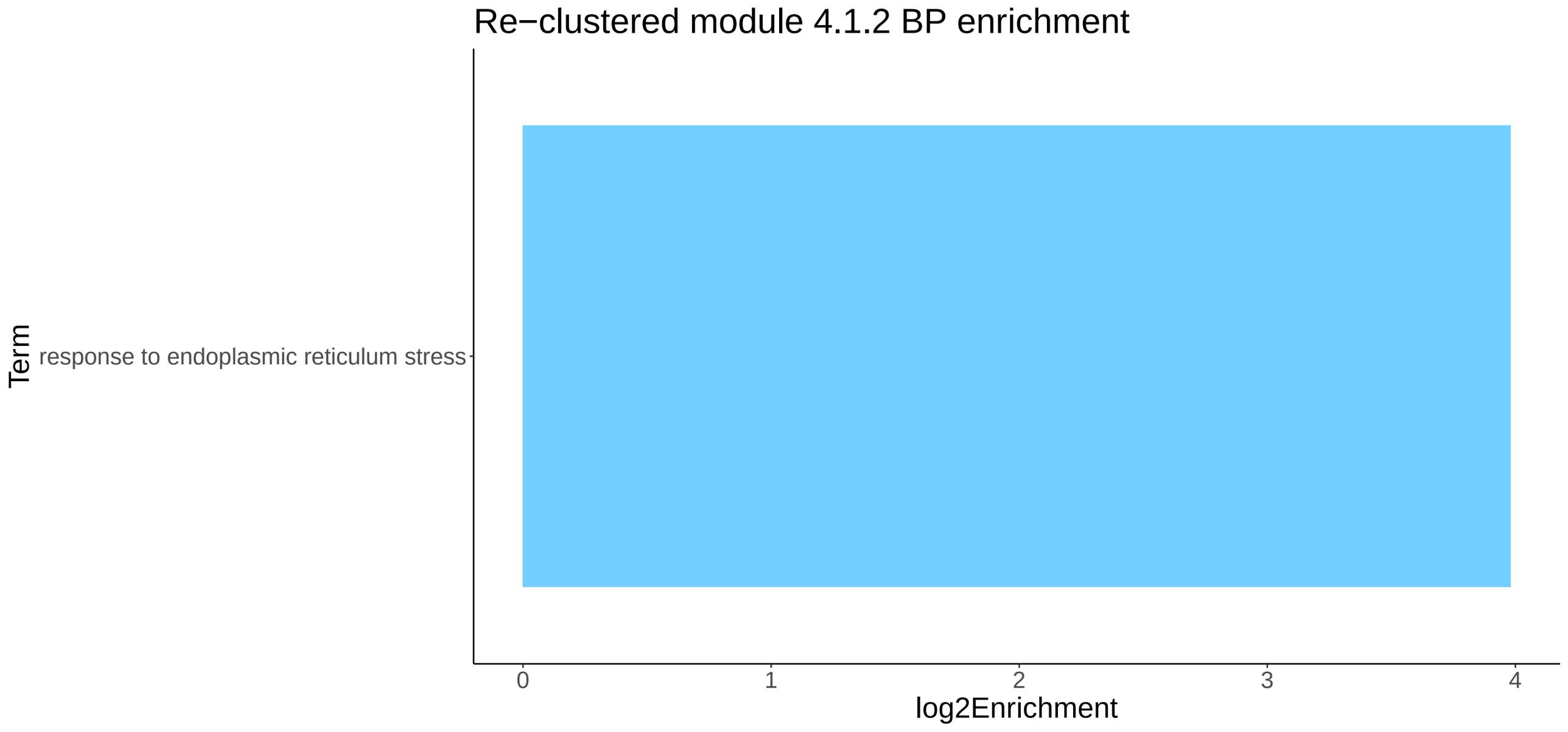
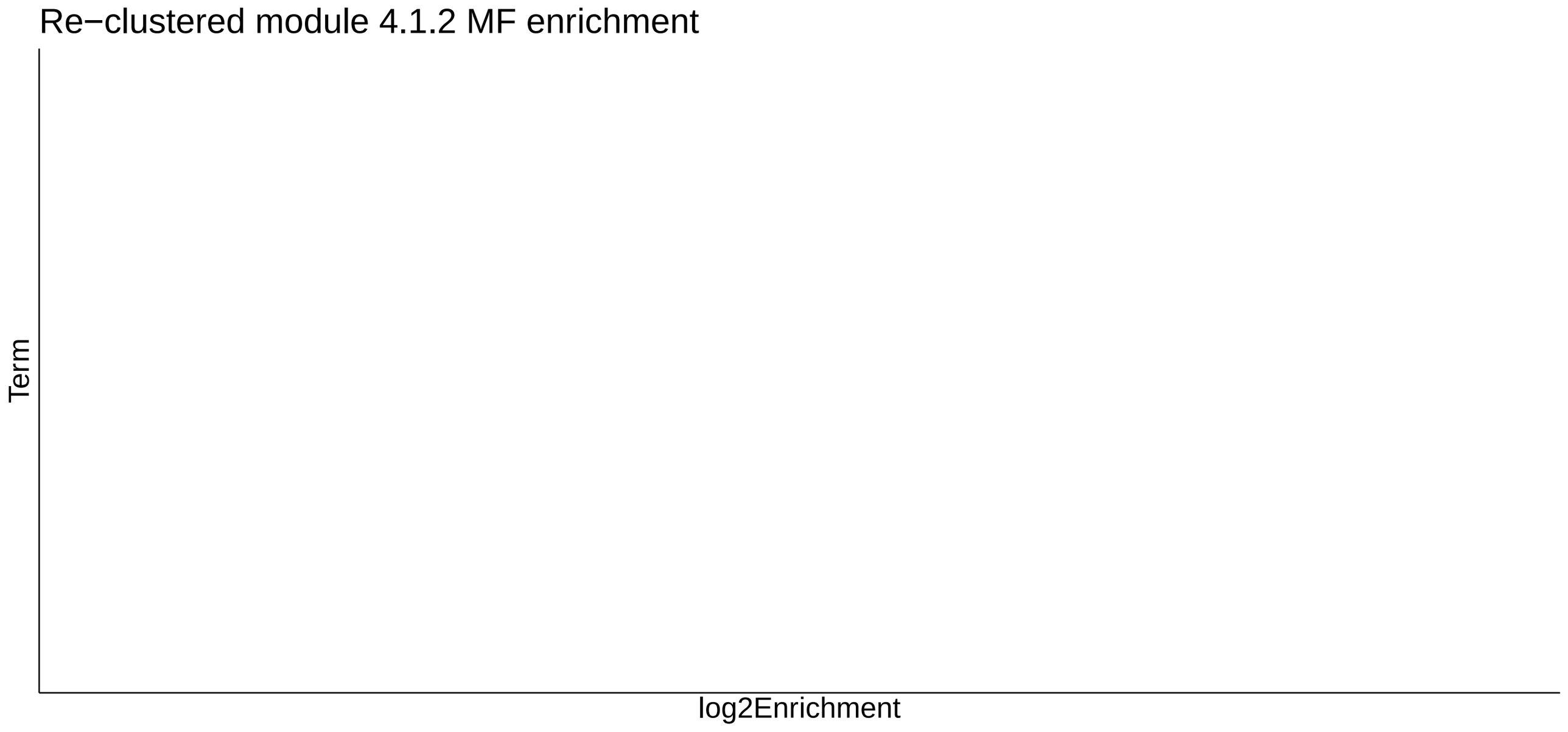
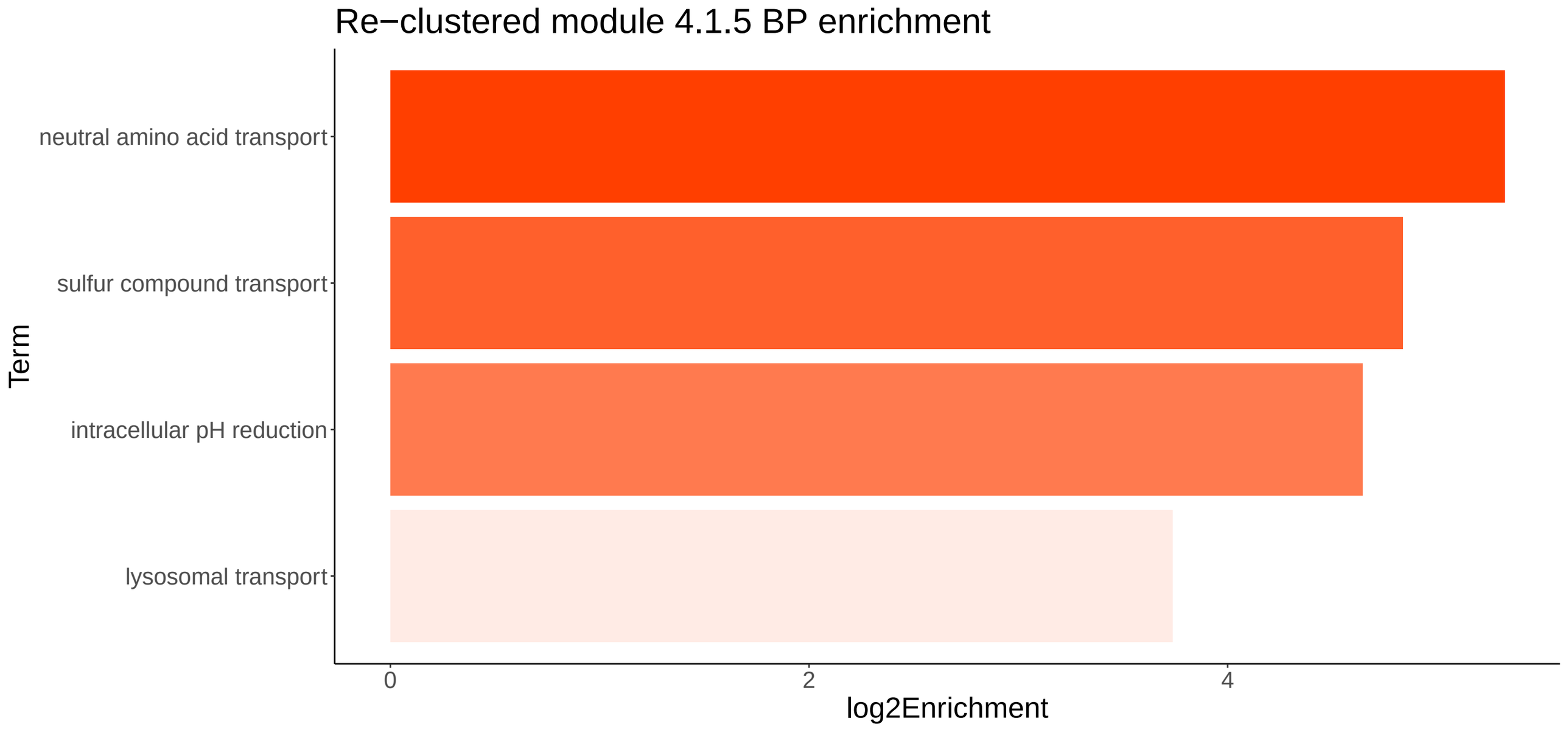
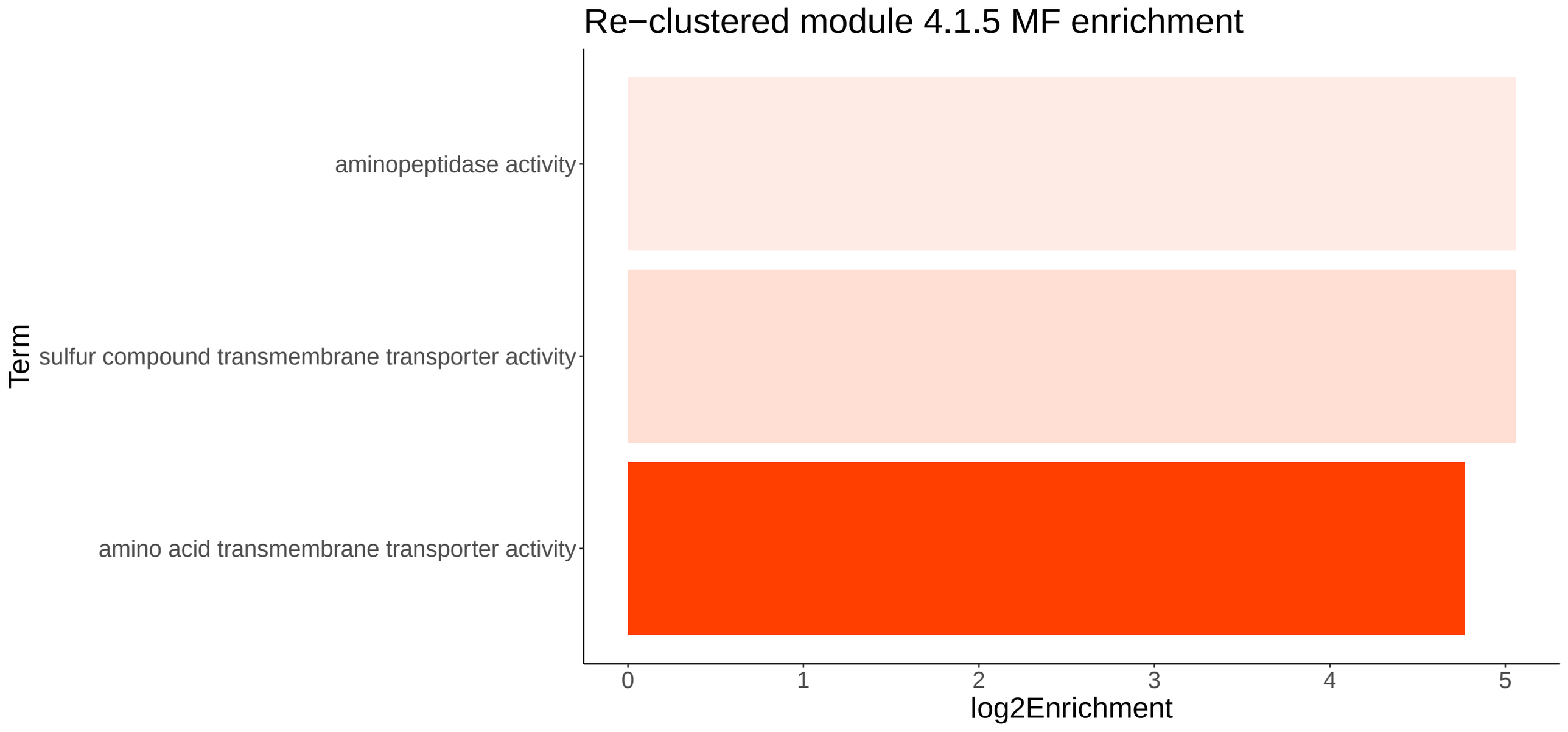

Original module 4 BP enrichment
Term
mesenchymal cell proliferation
0.0
0.3
0.6
0.9
log2Enrichment

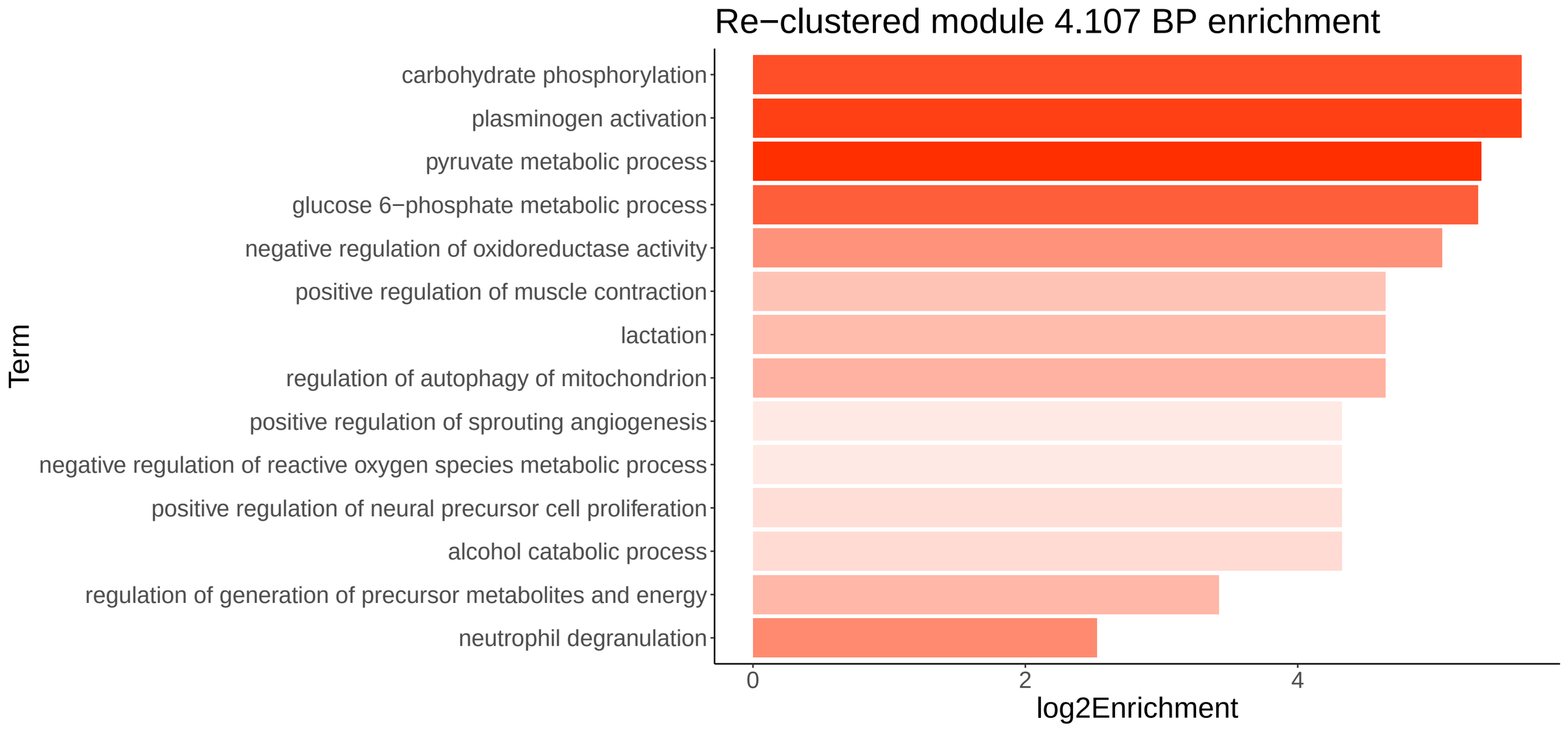

Original module 4 MF enrichment
Term
log2Enrichment

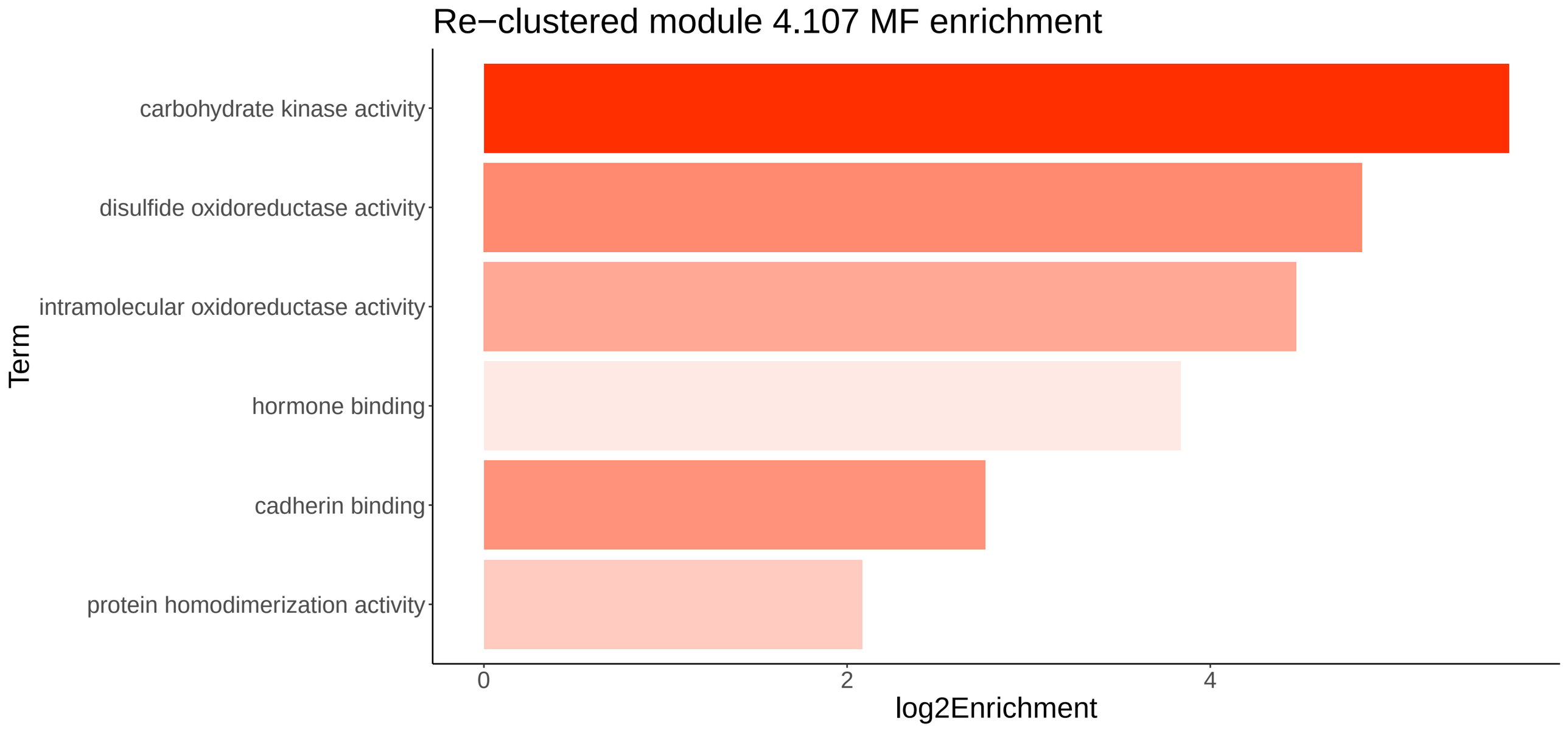

Re−clustered module 4.1.2 BP enrichment
Term
response to endoplasmic reticulum stress
0
1
2
3
4
log2Enrichment

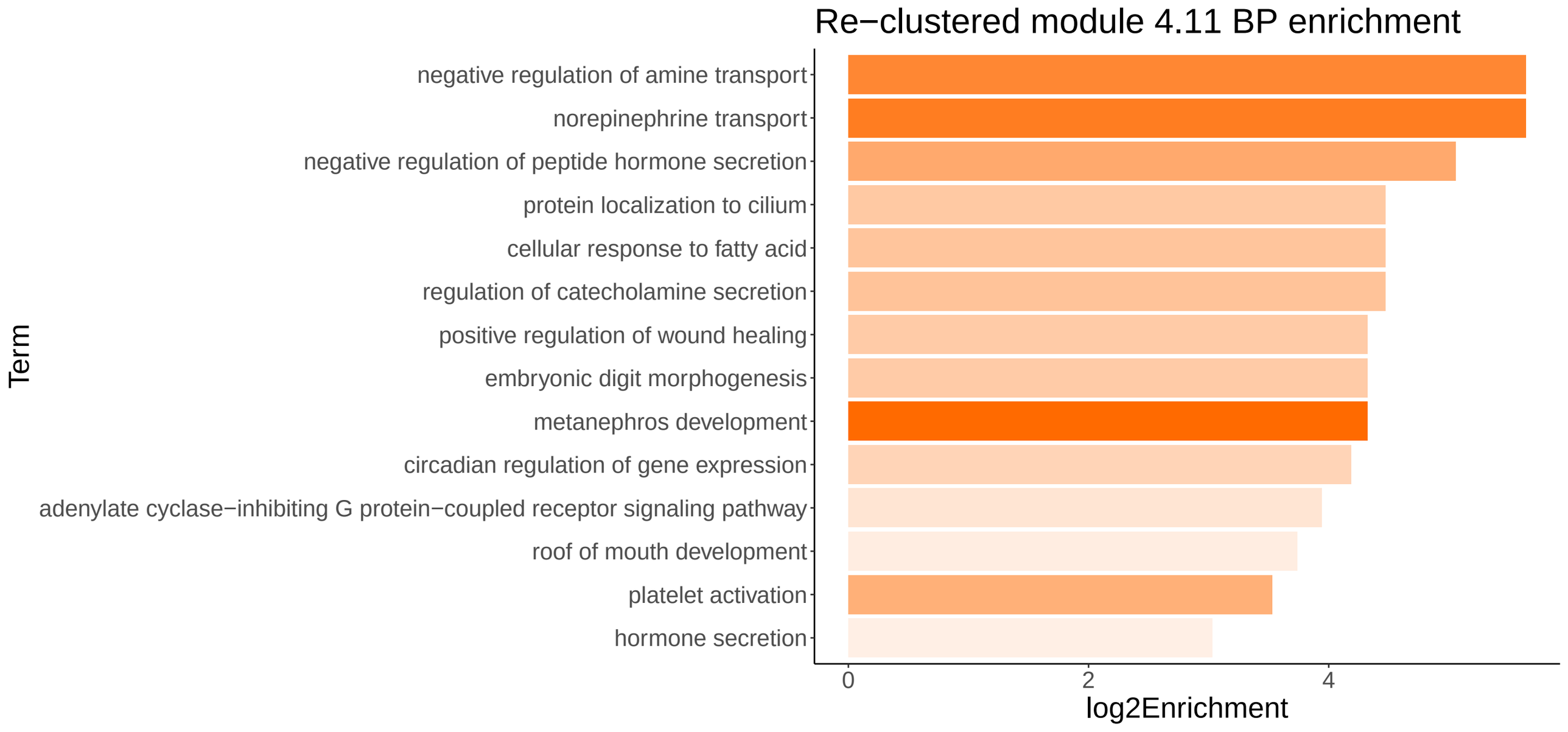

Re−clustered module 4.1.2 MF enrichment
Term
log2Enrichment

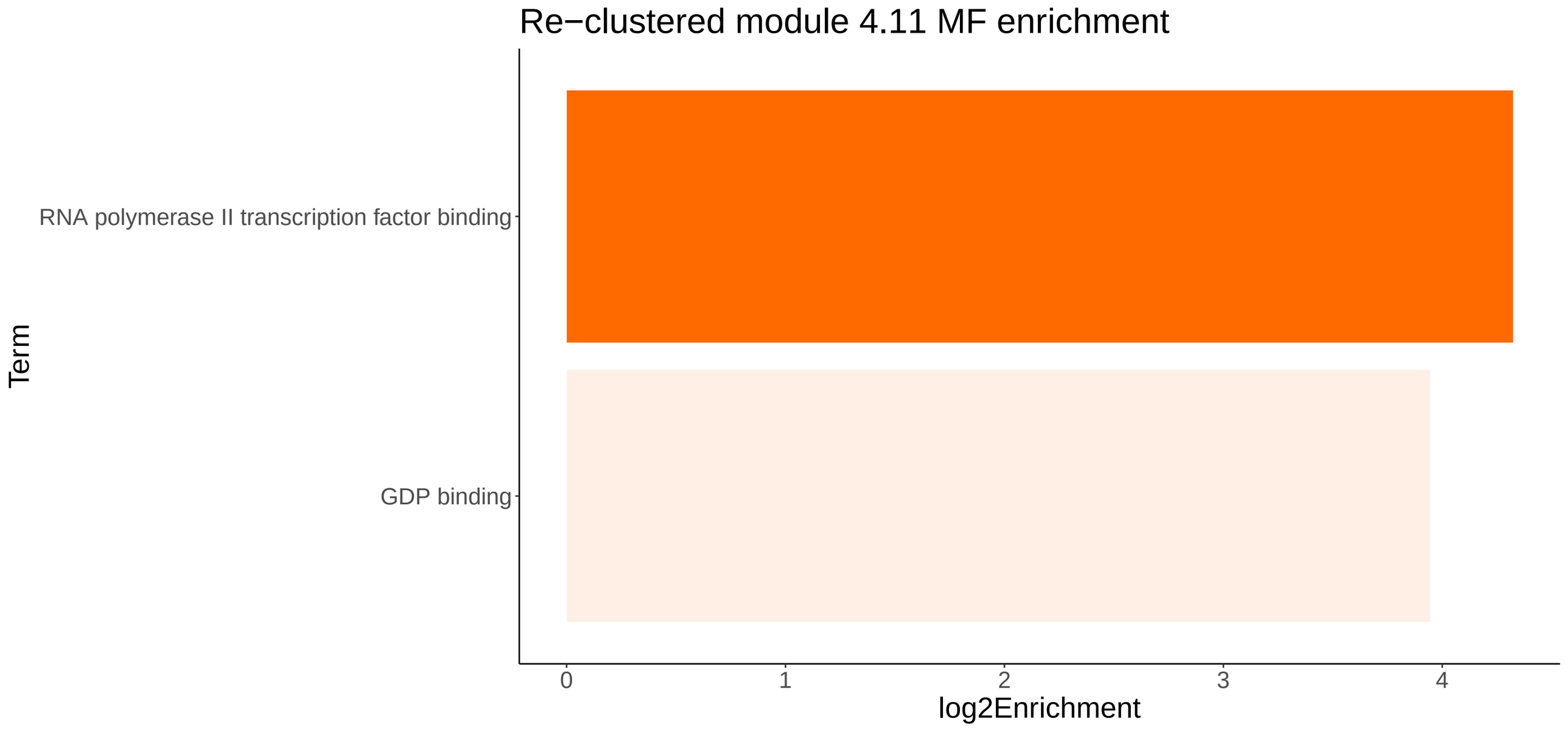

Re−clustered module 4.1.5 BP enrichment
neutral amino acid transport
sulfur compound transport
intracellular pH reduction
lysosomal transport
Term
0
2
4
log2Enrichment

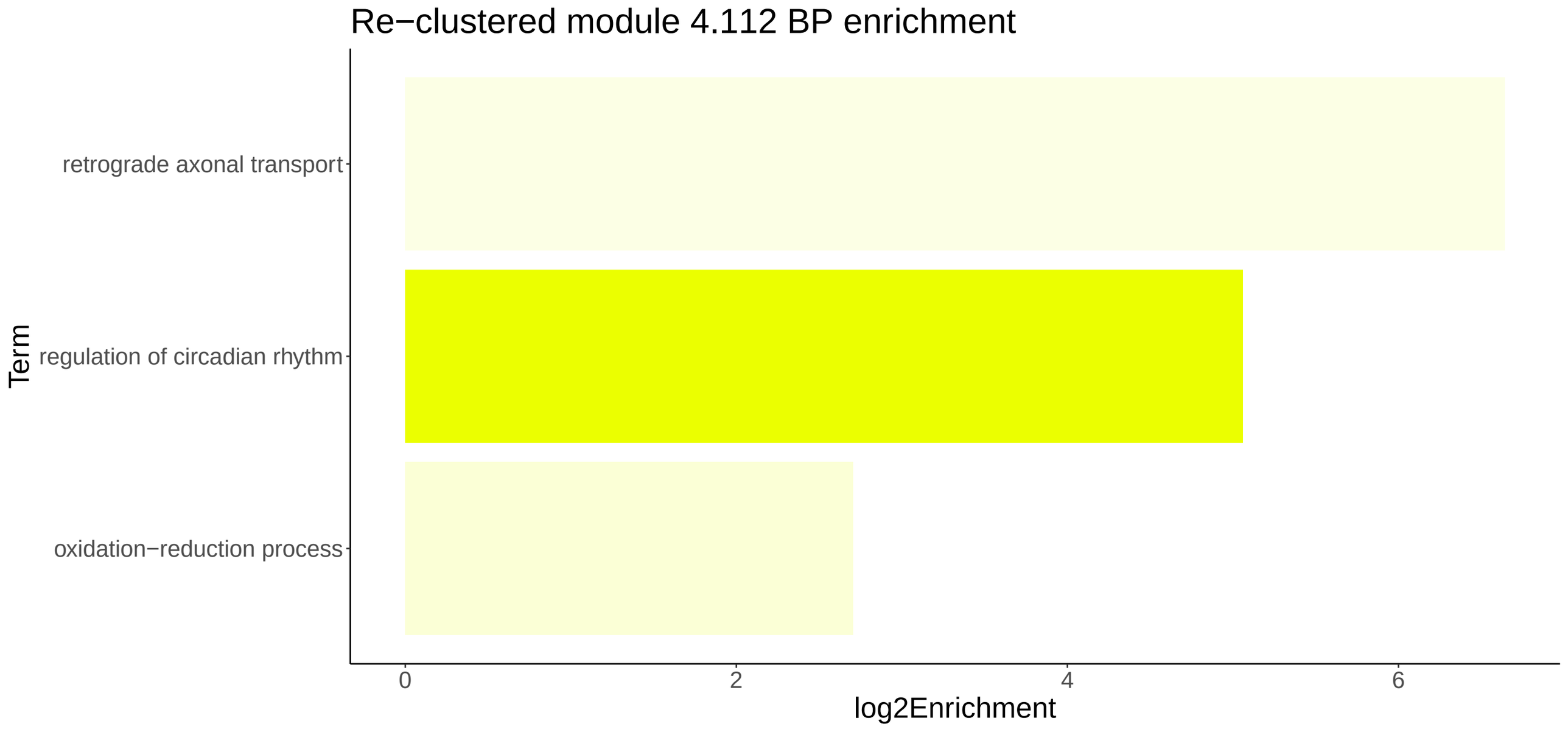

Re−clustered module 4.1.5 MF enrichment
Term
aminopeptidase activity
sulfur compound transmembrane transporter activity
amino acid transmembrane transporter activity
0
1
2
3
4
5
log2Enrichment

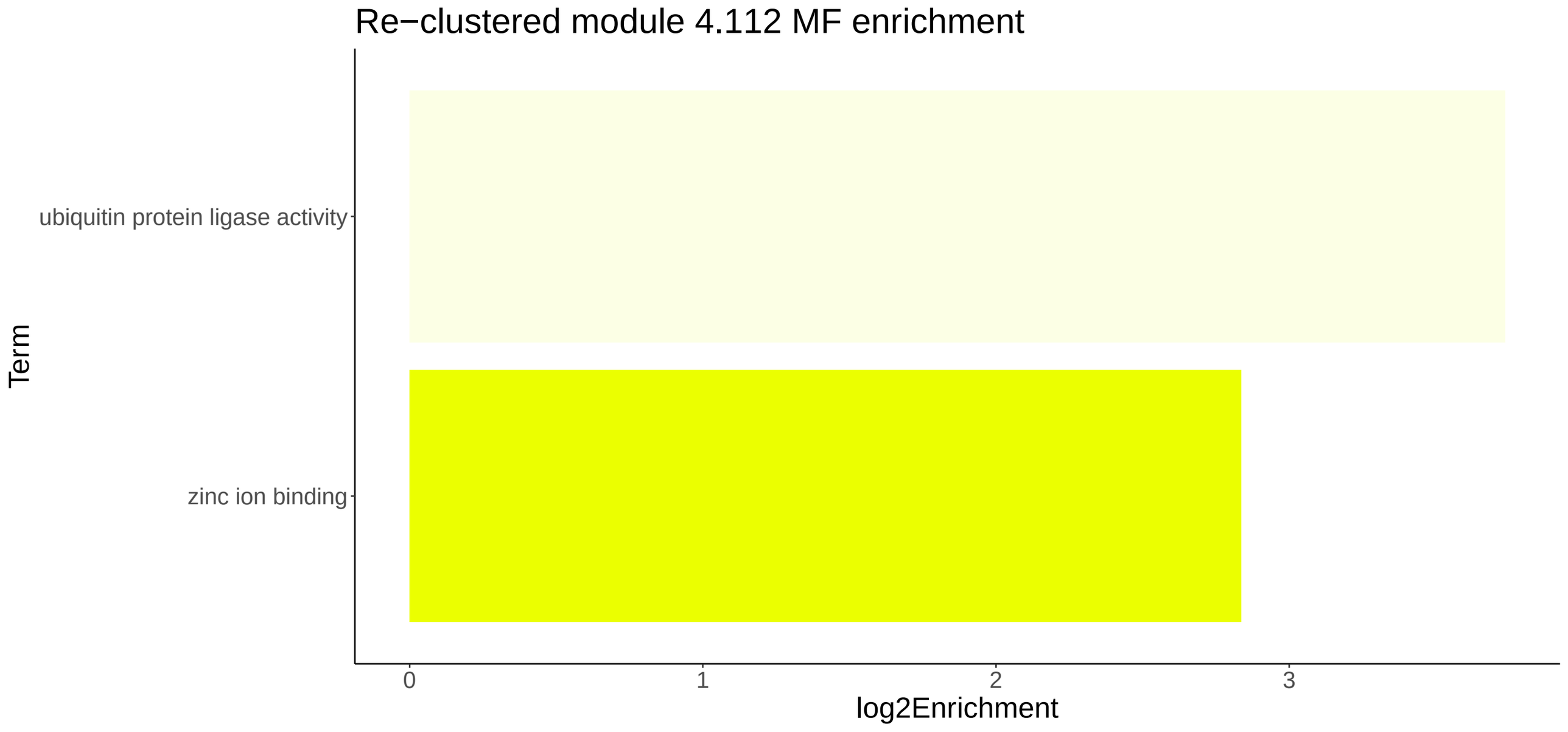

Re−clustered module 4.107 BP enrichment
carbohydrate phosphorylation
plasminogen activation
pyruvate metabolic process
glucose 6−phosphate metabolic process
negative regulation of oxidoreductase activity
positive regulation of muscle contraction
lactation
regulation of autophagy of mitochondrion
positive regulation of sprouting angiogenesis
negative regulation of reactive oxygen species metabolic process
positive regulation of neural precursor cell proliferation
alcohol catabolic process
regulation of generation of precursor metabolites and energy
neutrophil degranulation
Term
0
2
4
log2Enrichment

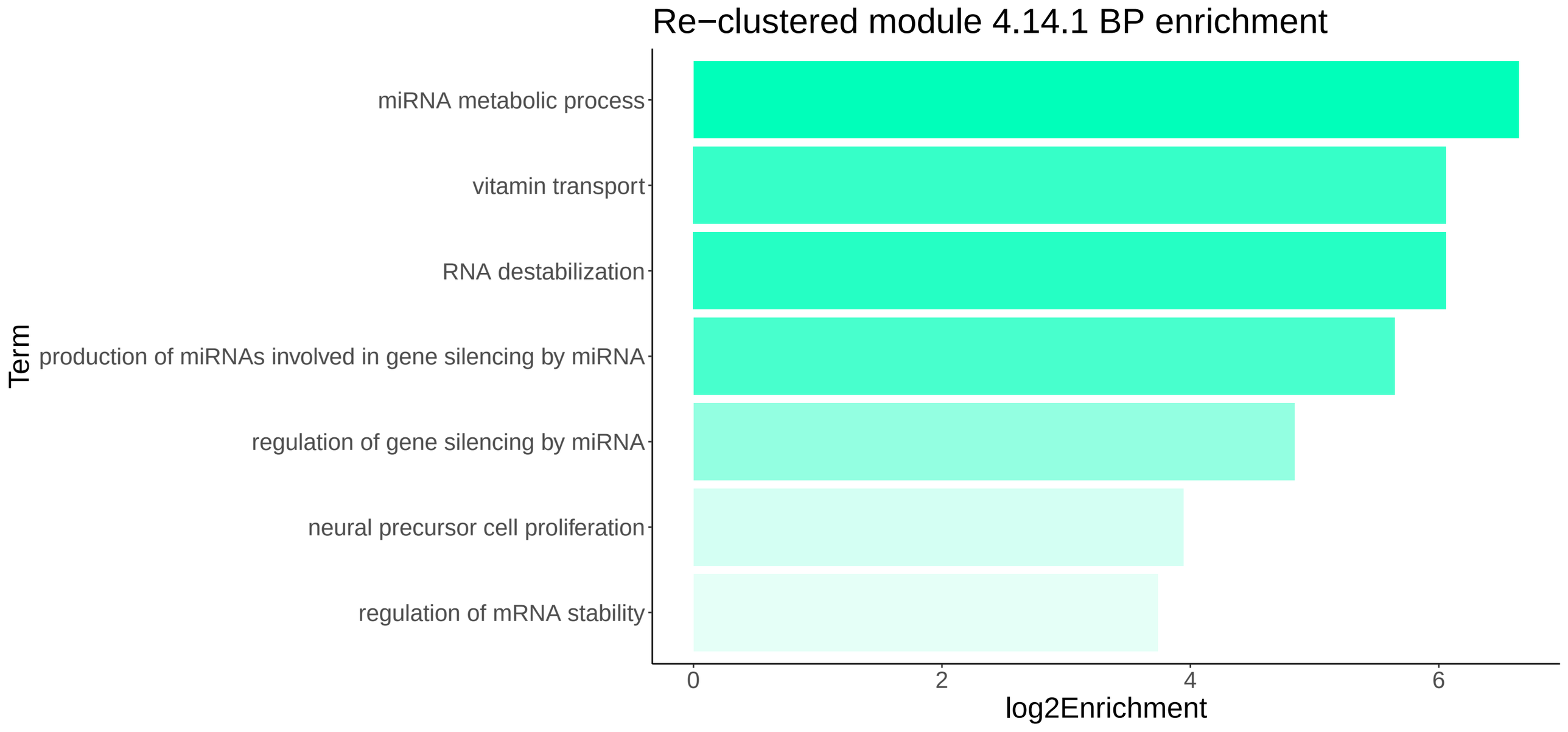

Re−clustered module 4.107 MF enrichment
carbohydrate kinase activity
disulfide oxidoreductase activity
intramolecular oxidoreductase activity
hormone binding
cadherin binding
protein homodimerization activity
Term
0
2
4
log2Enrichment

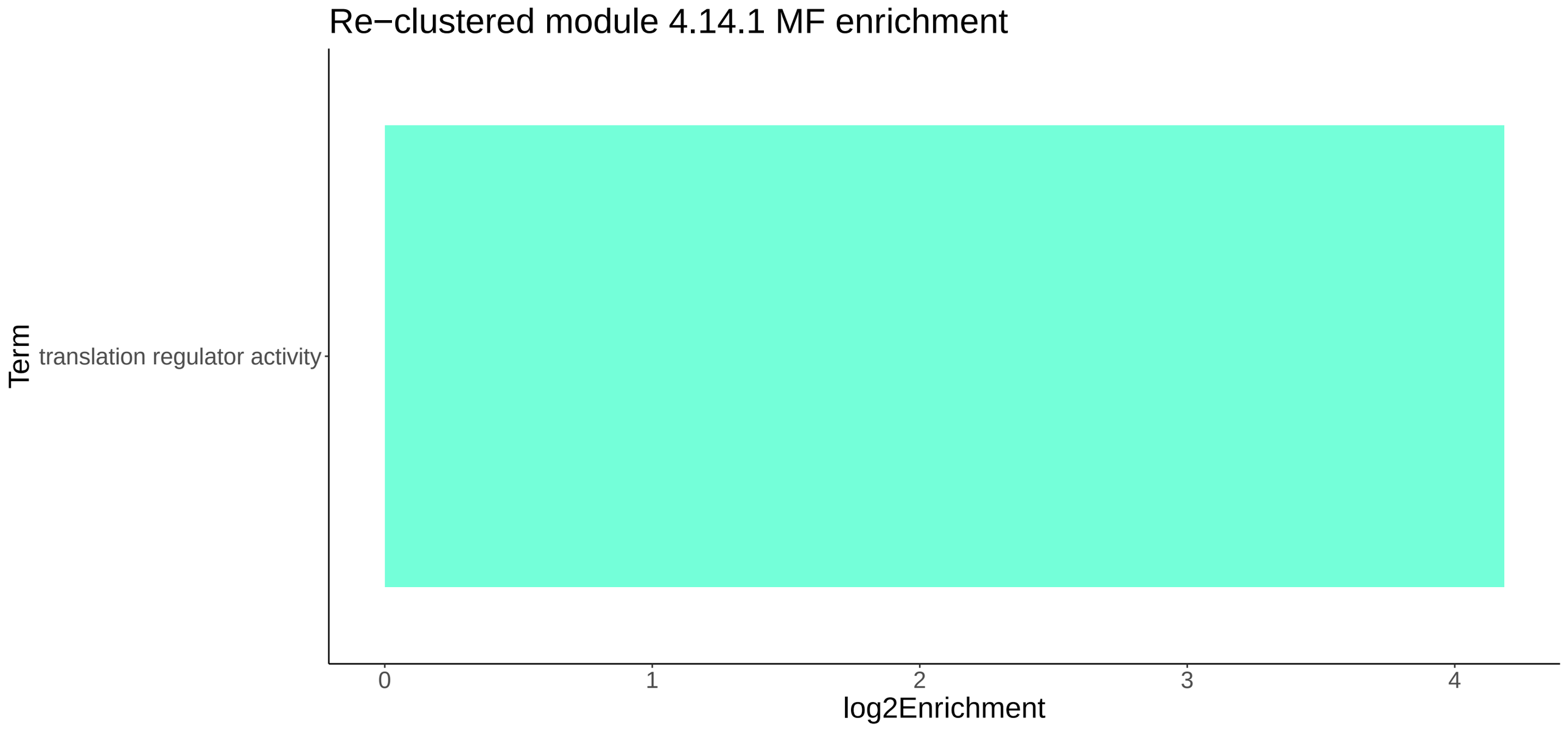

Re−clustered module 4.11 BP enrichment
negative regulation of amine transport
norepinephrine transport
negative regulation of peptide hormone secretion
protein localization to cilium
cellular response to fatty acid
regulation of catecholamine secretion
positive regulation of wound healing
embryonic digit morphogenesis
metanephros development
circadian regulation of gene expression
adenylate cyclase−inhibiting G protein−coupled receptor signaling pathway
roof of mouth development
platelet activation
hormone secretion
Term
0
2
4
log2Enrichment

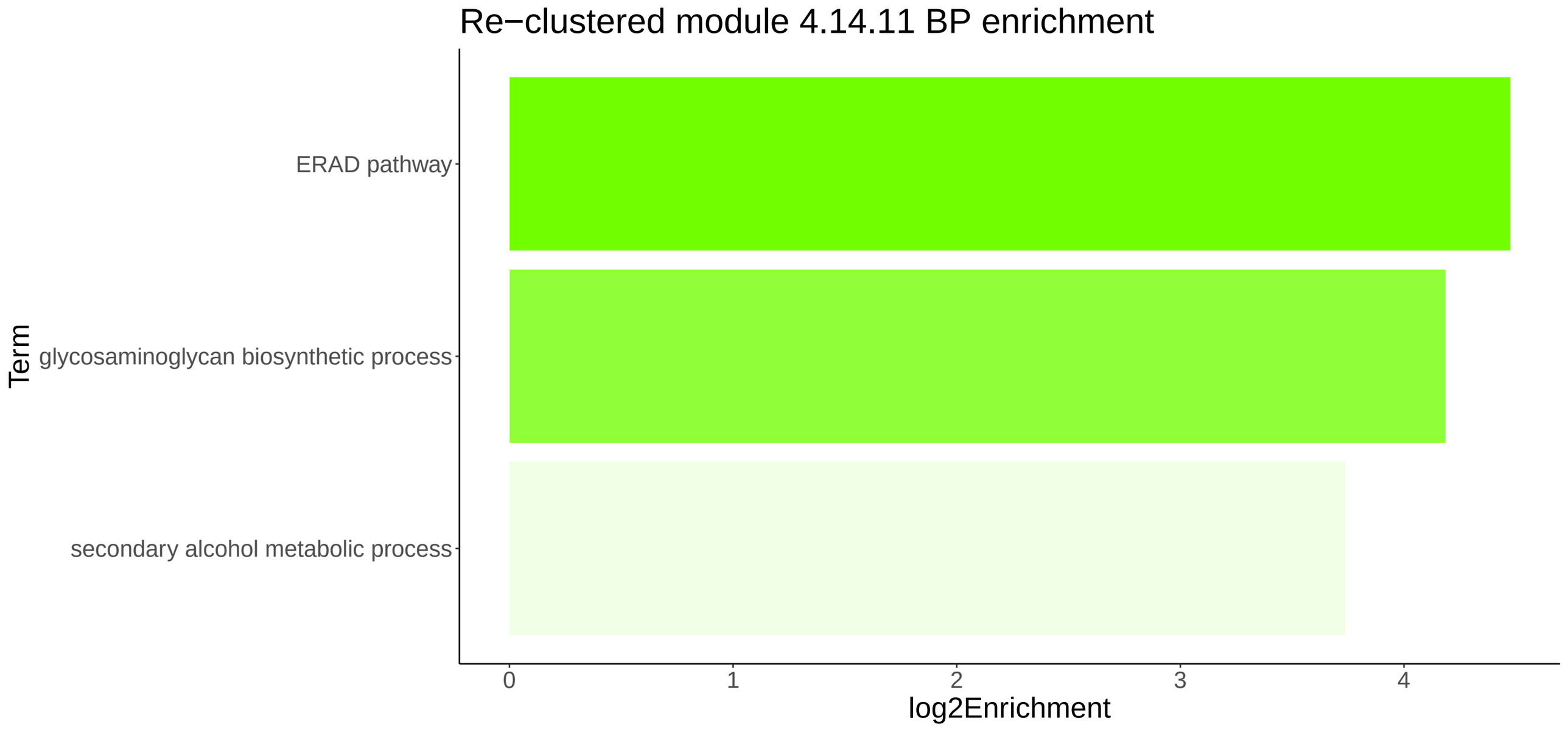

Re−clustered module 4.11 MF enrichment
RNA polymerase II transcription factor binding
GDP binding
Term
0
1
2
3
4
log2Enrichment

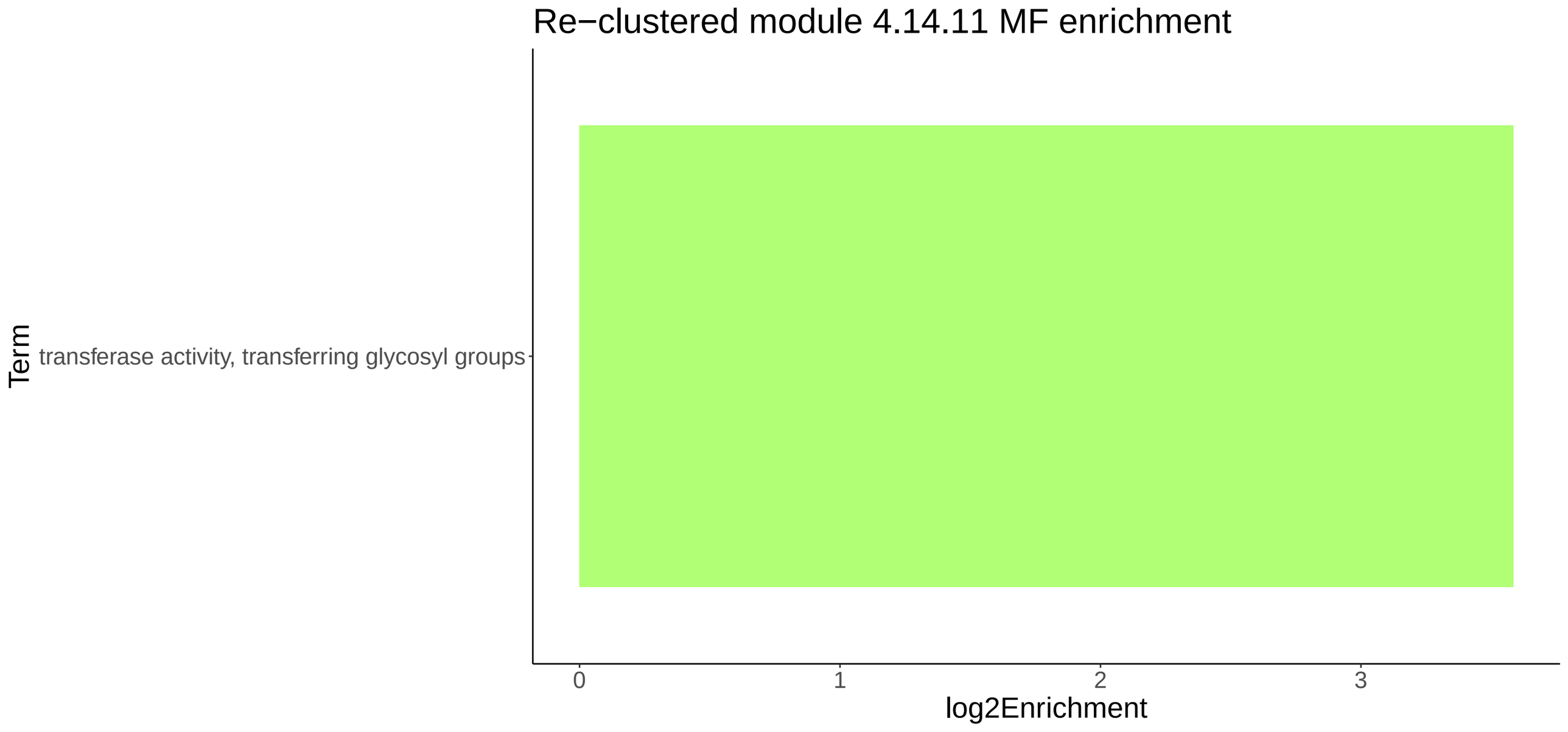

Re−clustered module 4.112 BP enrichment
Term
retrograde axonal transport
regulation of circadian rhythm
oxidation−reduction process
0
2
4
6
log2Enrichment

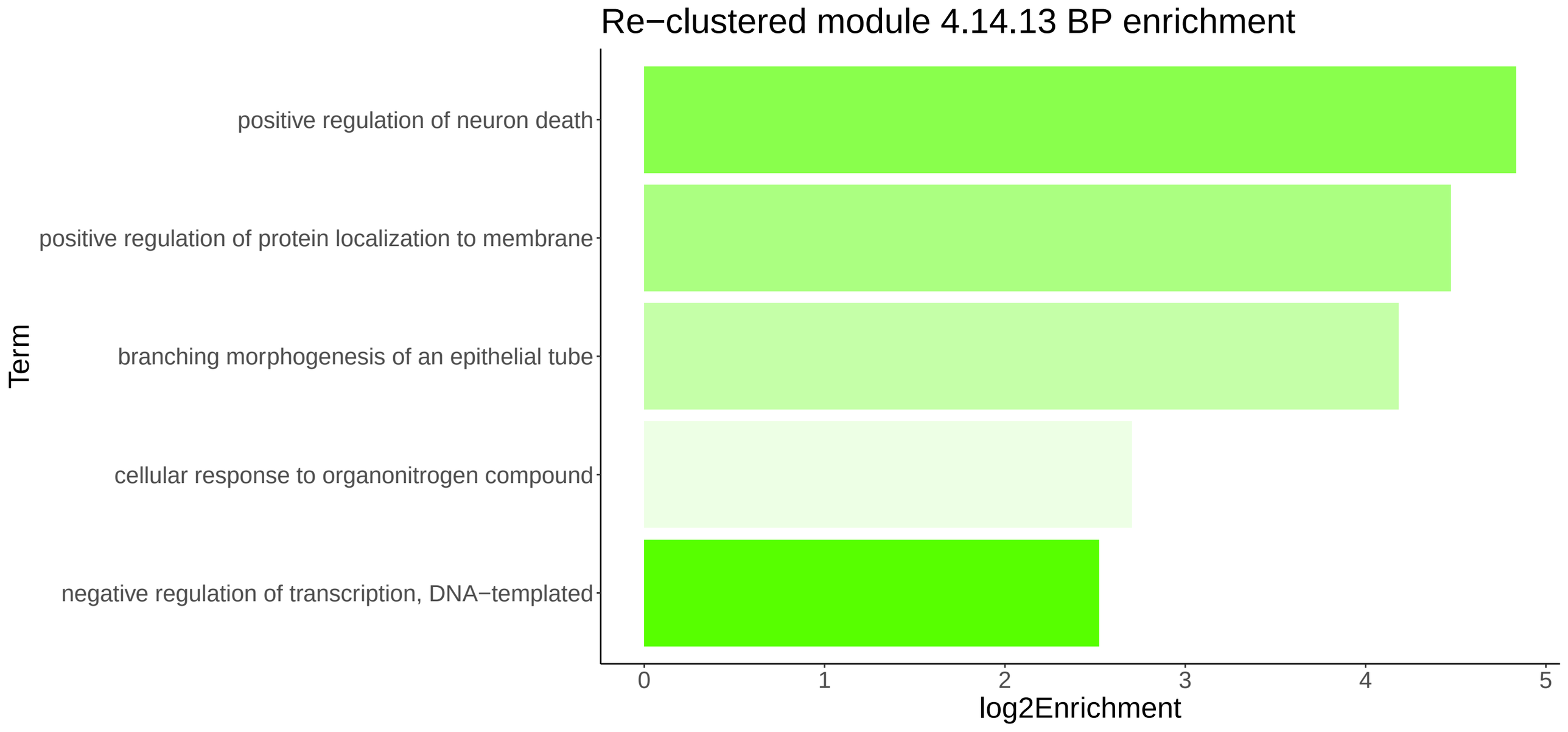

Re−clustered module 4.112 MF enrichment
Term
ubiquitin protein ligase activity
zinc ion binding
0
1
2
3
log2Enrichment

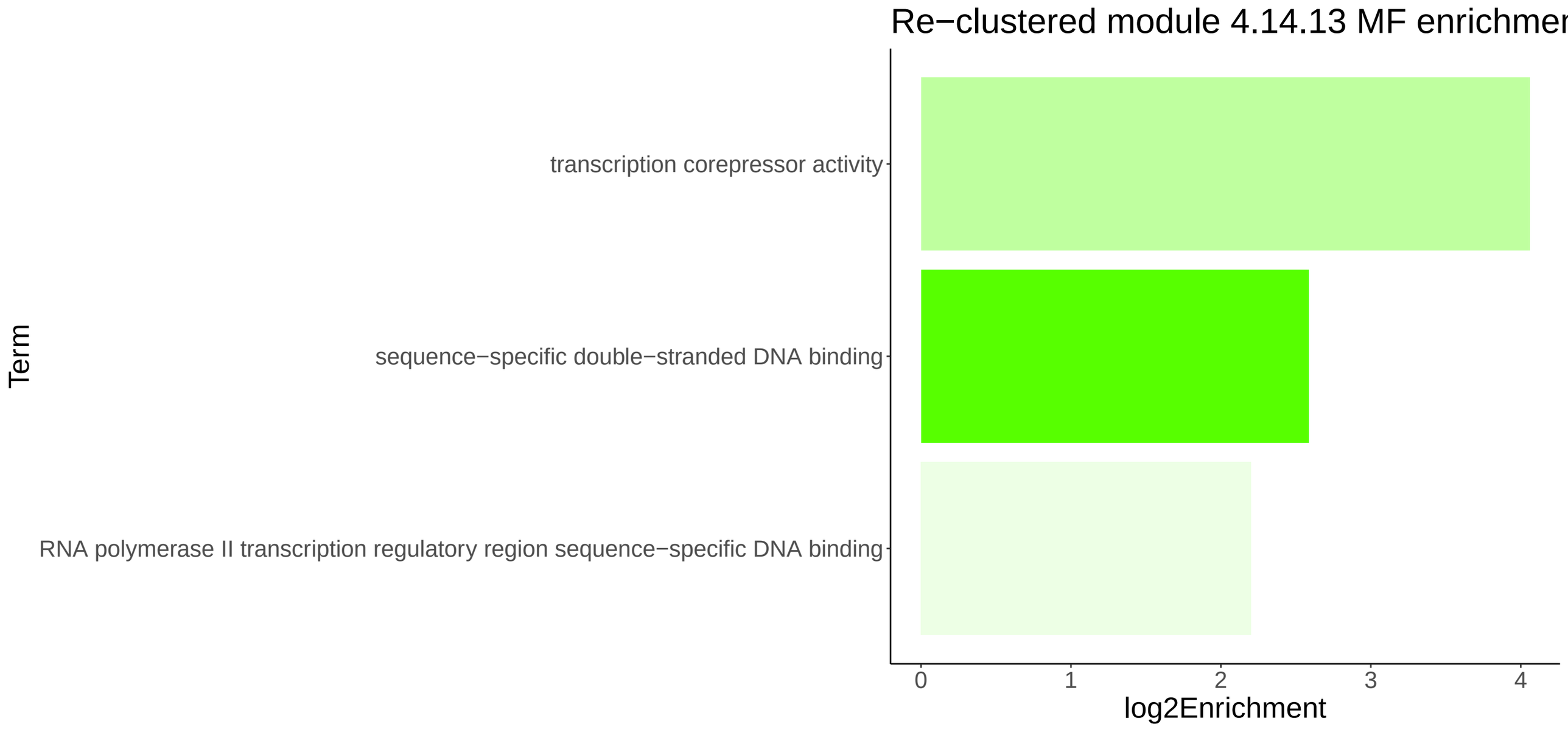

Re−clustered module 4.14.1 BP enrichment
Term
miRNA metabolic process
vitamin transport
RNA destabilization
production of miRNAs involved in gene silencing by miRNA
regulation of gene silencing by miRNA
neural precursor cell proliferation
regulation of mRNA stability
0
2
4
6
log2Enrichment

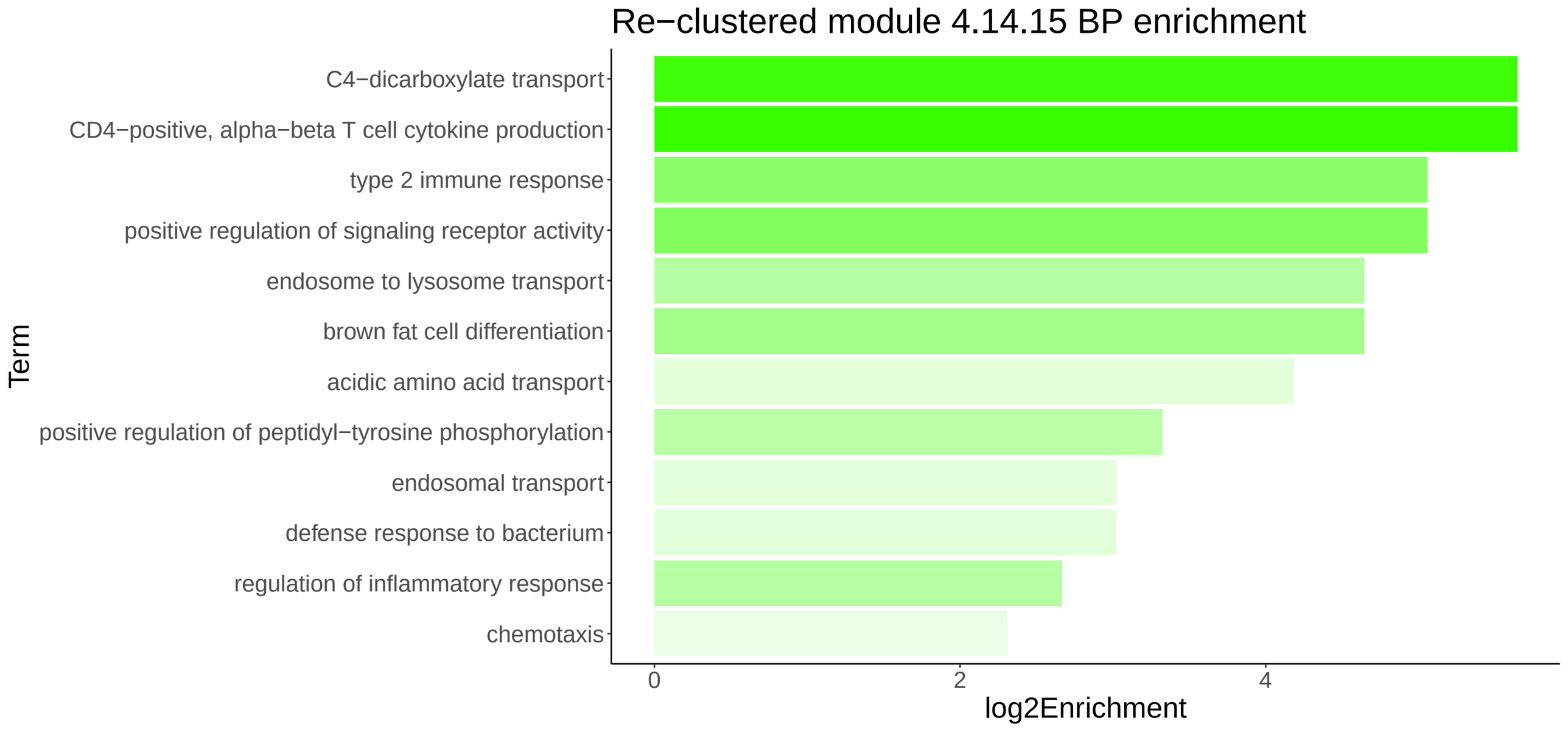

Re−clustered module 4.14.1 MF enrichment
Term
translation regulator activity
0
1
2
3
4
log2Enrichment

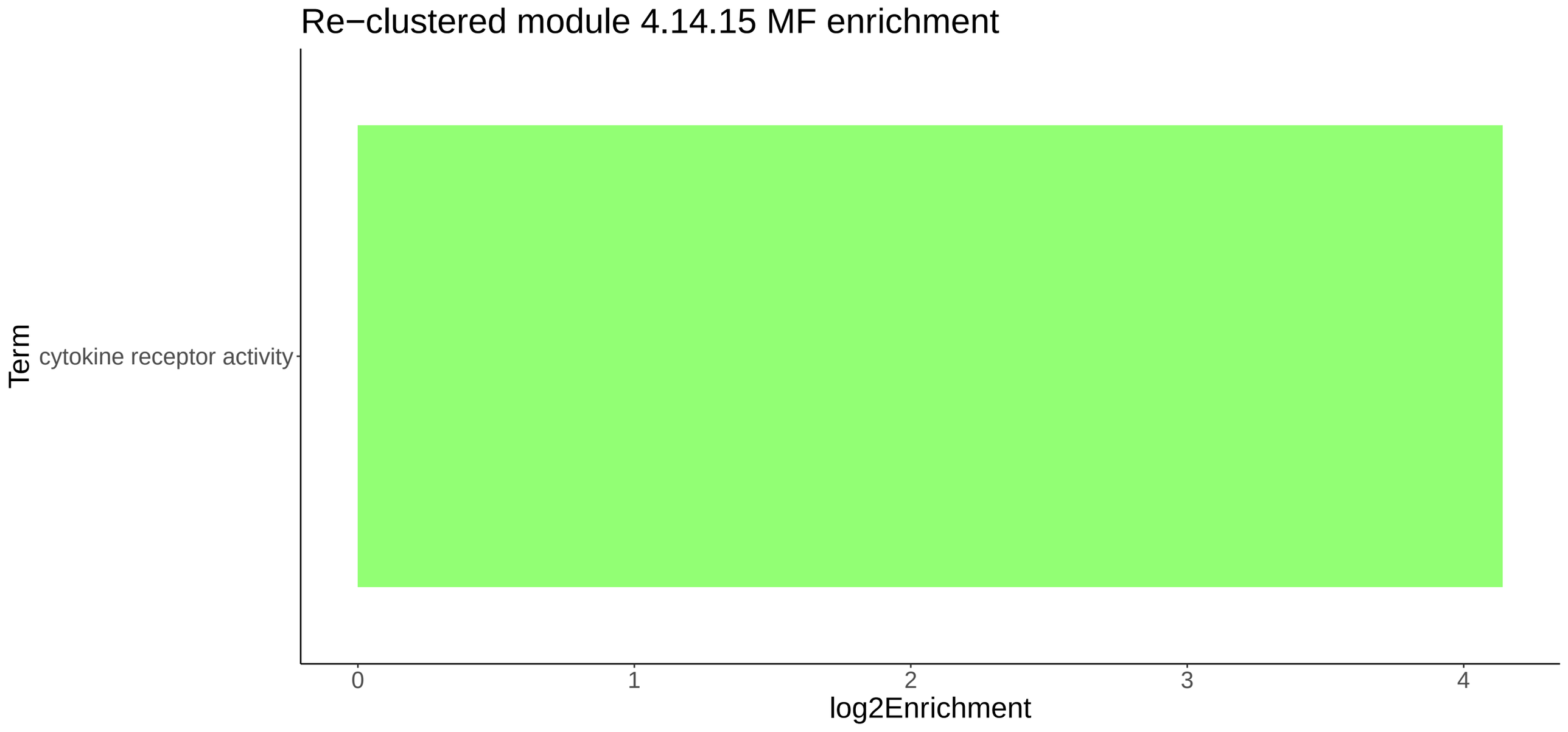

Re−clustered module 4.14.11 BP enrichment
Term
ERAD pathway
glycosaminoglycan biosynthetic process
secondary alcohol metabolic process
0
1
2
3
4
log2Enrichment

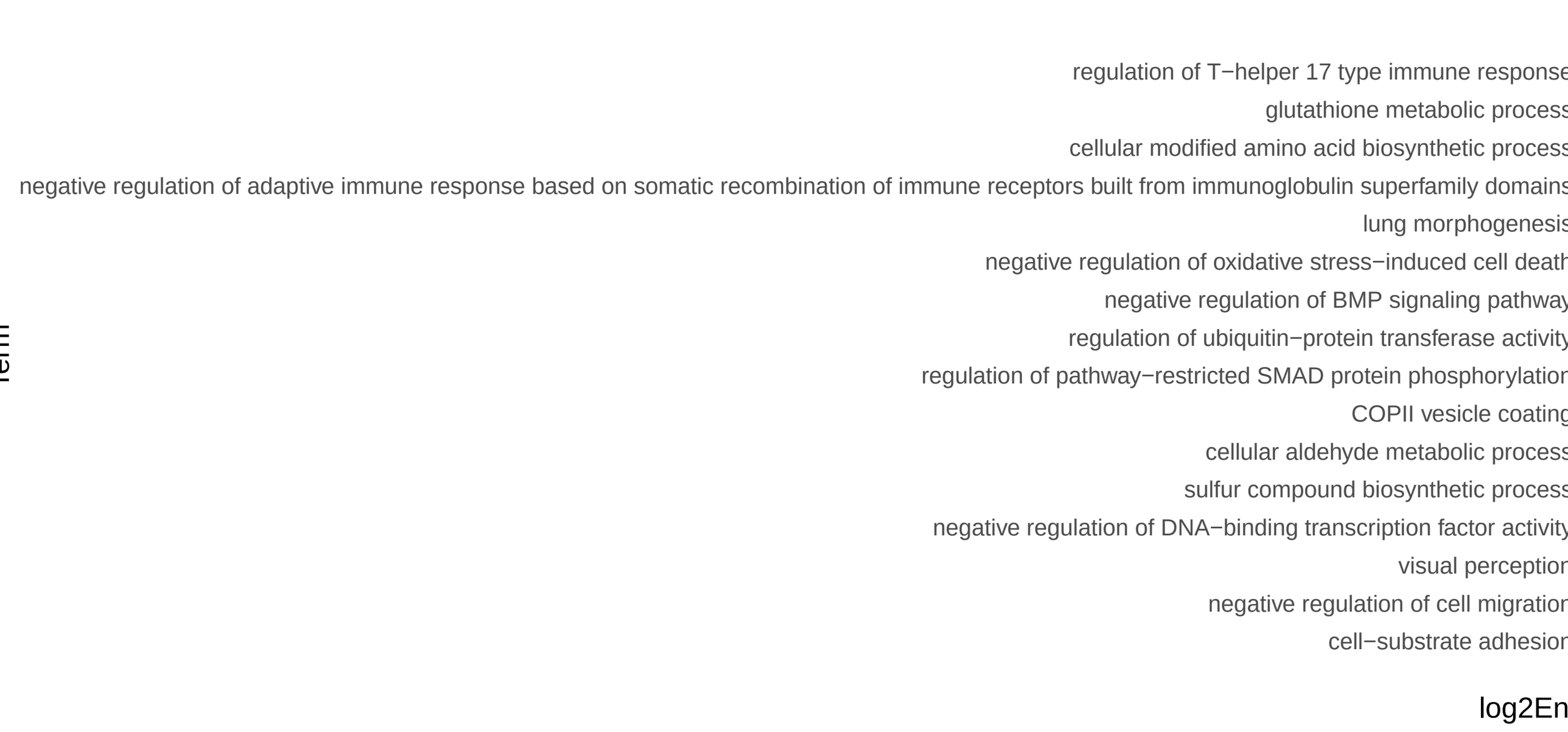

Re−clustered module 4.14.11 MF enrichment
Term
transferase activity, transferring glycosyl groups
0
1
2
3
log2Enrichment

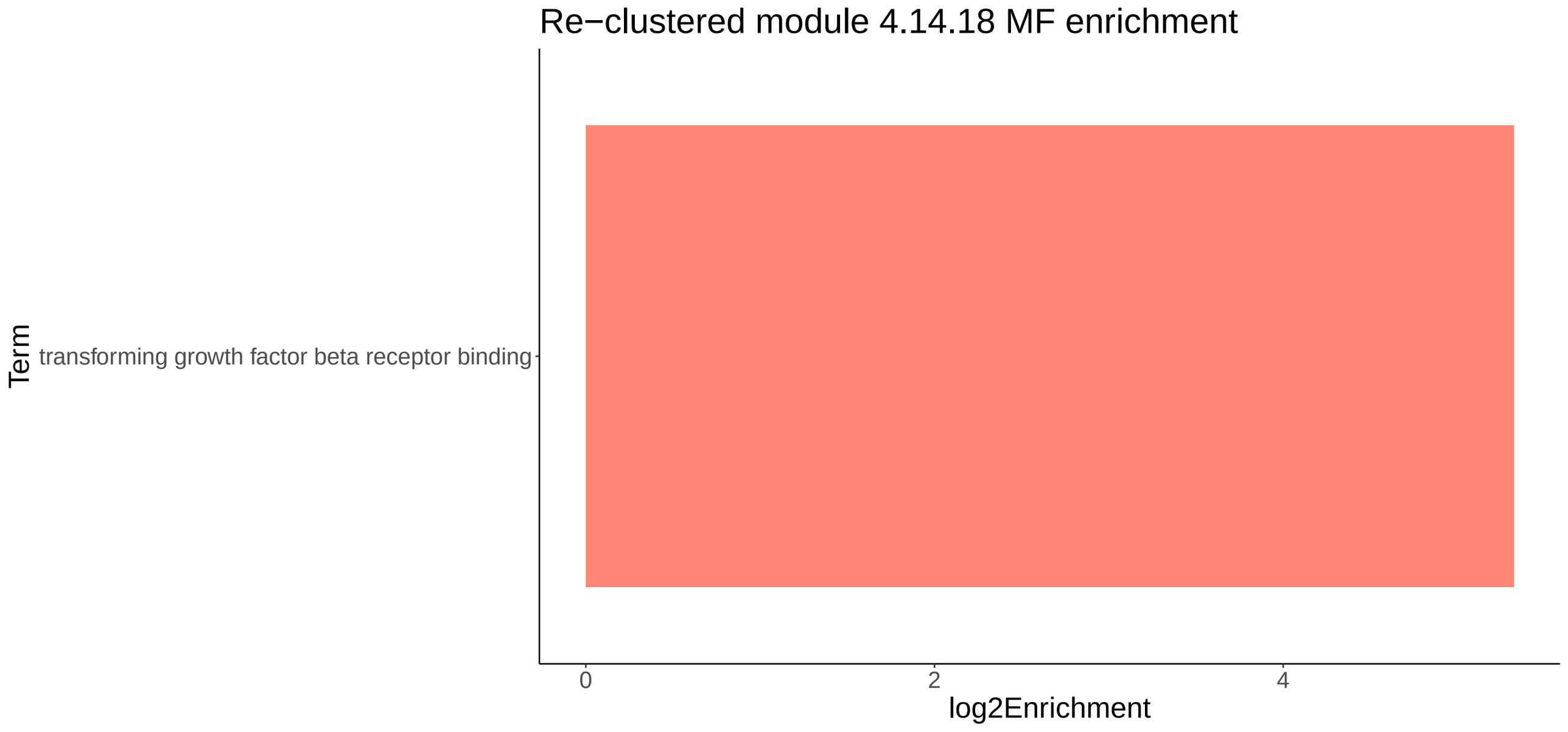

Re−clustered module 4.14.13 BP enrichment
positive regulation of neuron death
positive regulation of protein localization to membrane
branching morphogenesis of an epithelial tube
cellular response to organonitrogen compound
negative regulation of transcription, DNA−templated
Term
0
1
2
3
4
5
log2Enrichment

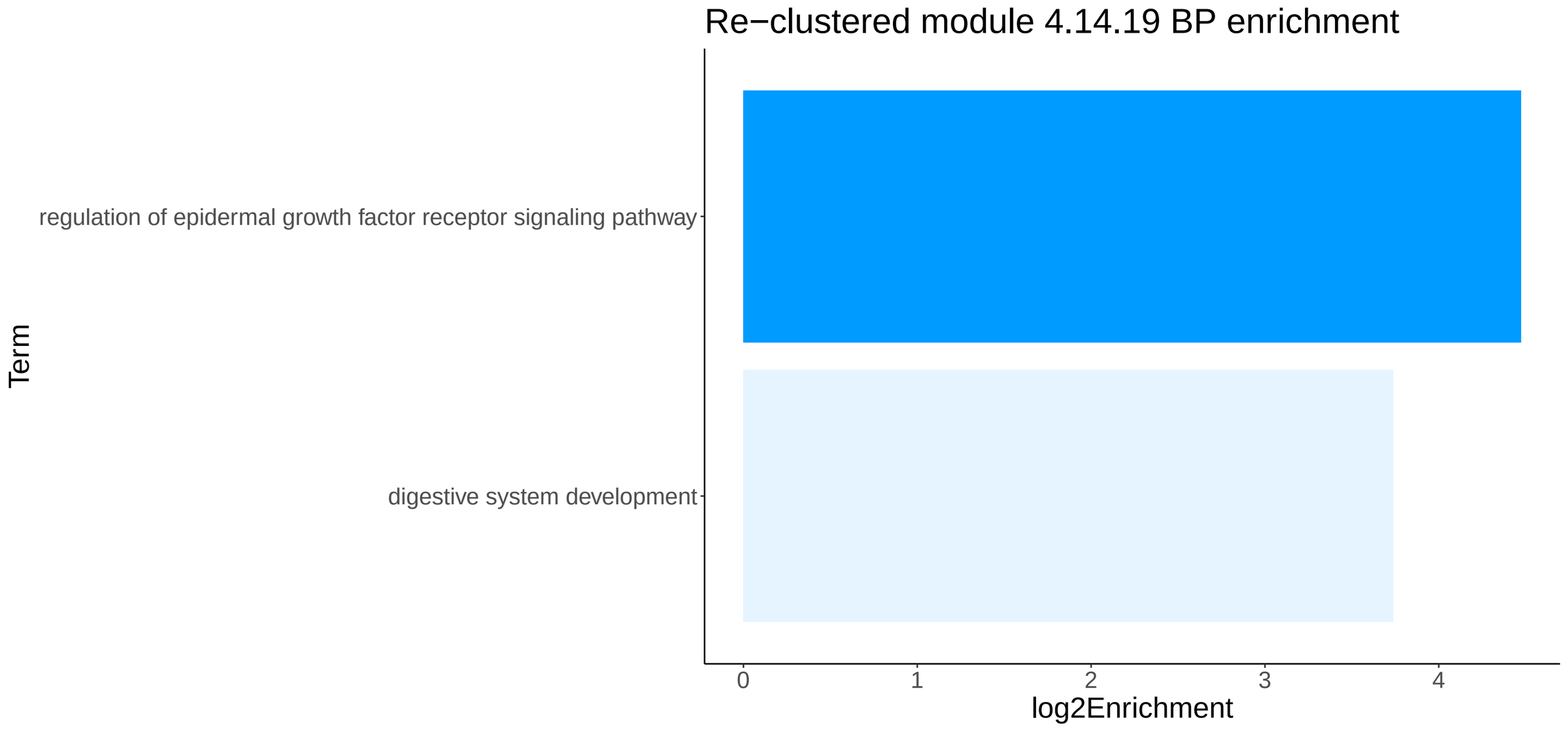

Re−clustered module 4.14.13 MF enrichmer
Term
transcription corepressor activity
sequence−specific double−stranded DNA binding
RNA polymerase II transcription regulatory region sequence−specific DNA binding
0
1
2
3
4
log2Enrichment

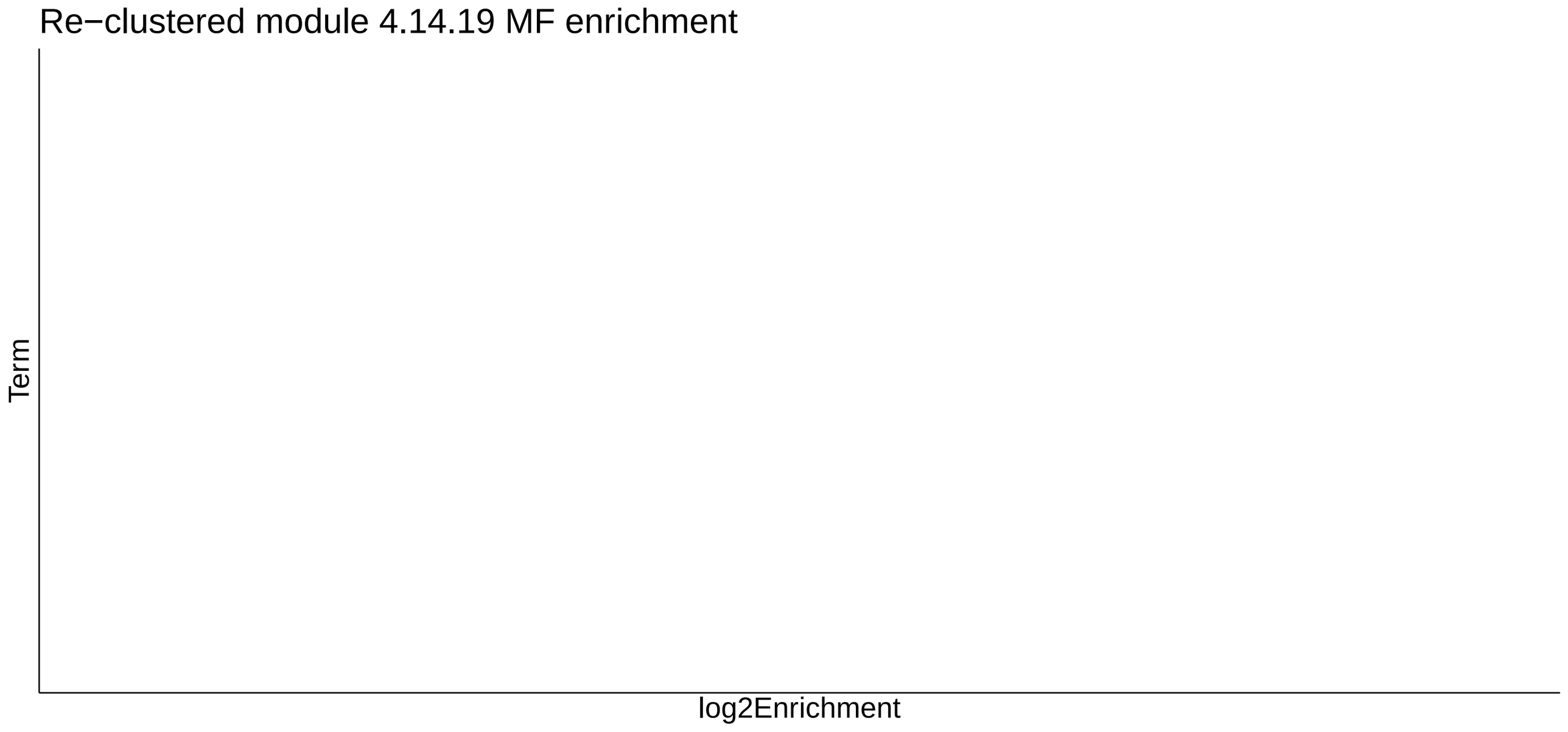

Re−clustered module 4.14.15 BP enrichment
C4−dicarboxylate transport
CD4−positive, alpha−beta T cell cytokine production
type 2 immune response
positive regulation of signaling receptor activity
endosome to lysosome transport
brown fat cell differentiation
acidic amino acid transport
positive regulation of peptidyl−tyrosine phosphorylation
endosomal transport
defense response to bacterium
regulation of inflammatory response
chemotaxis
Term
0
2
4
log2Enrichment

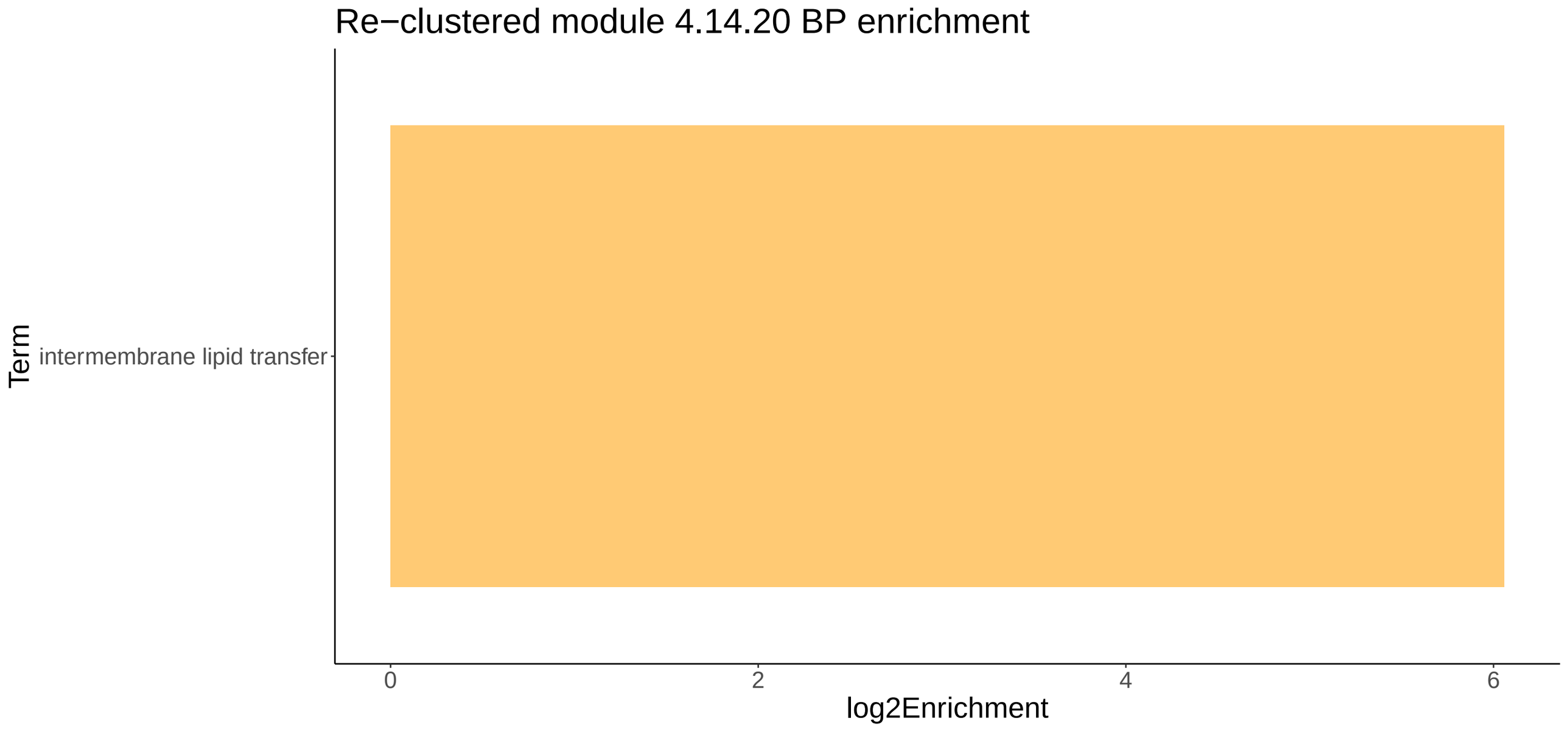

Re−clustered module 4.14.15 MF enrichment
Term
cytokine receptor activity
0
1
2
3
4
log2Enrichment


regulation of T−helper 17 type immune response
glutathione metabolic process
cellular modified amino acid biosynthetic process
negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
lung morphogenesis
negative regulation of oxidative stress−induced cell death
negative regulation of BMP signaling pathway
regulation of ubiquitin−protein transferase activity
regulation of pathway−restricted SMAD protein phosphorylation
COPII vesicle coating
cellular aldehyde metabolic process
sulfur compound biosynthetic process
negative regulation of DNA−binding transcription factor activity
visual perception
negative regulation of cell migration
cell−substrate adhesion
log2En

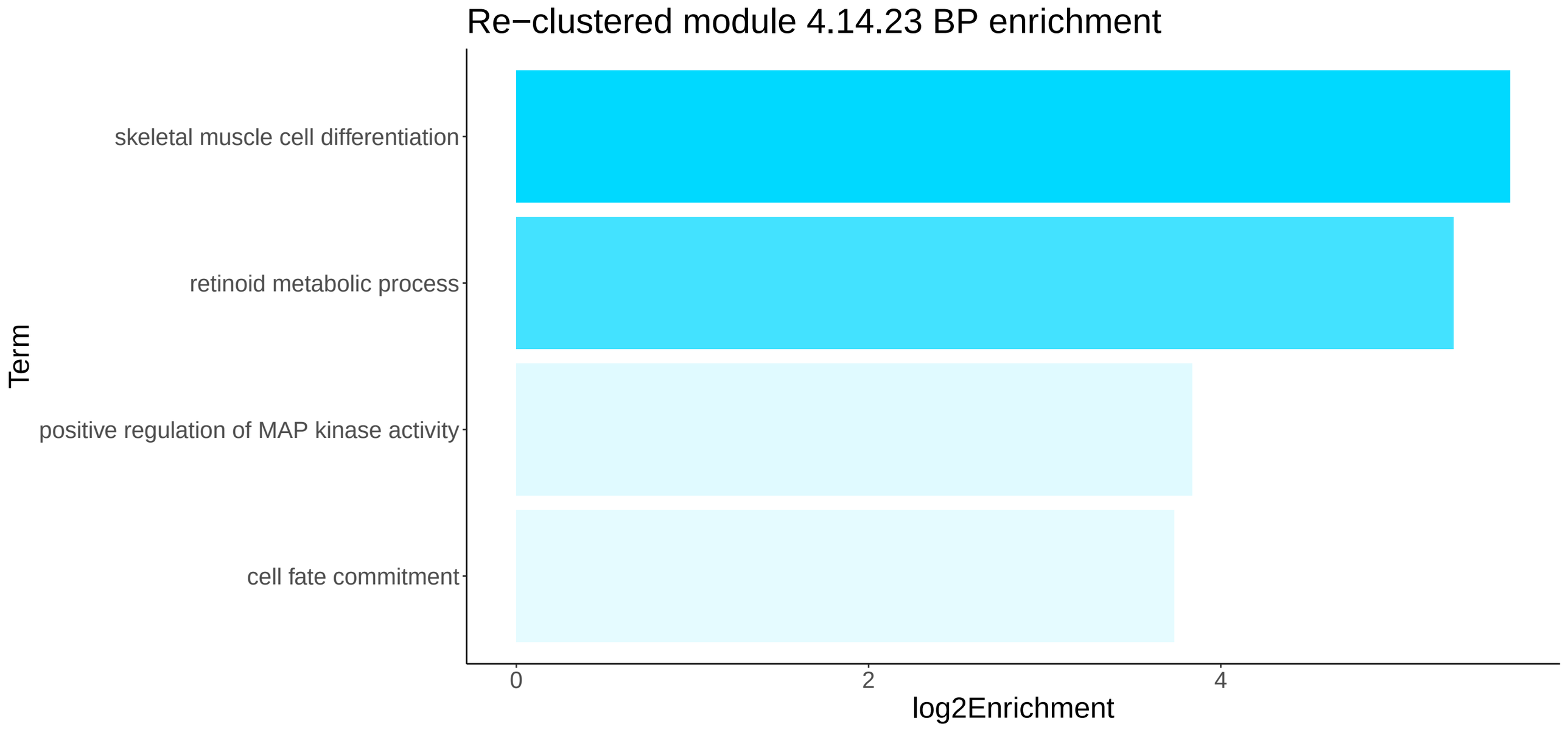

Re−clustered module 4.14.18 MF enrichment
Term
transforming growth factor beta receptor binding
0
2
4
log2Enrichment


Re−clustered module 4.14.19 BP enrichment
Term
regulation of epidermal growth factor receptor signaling pathway
digestive system development
0
1
2
3
4
log2Enrichment

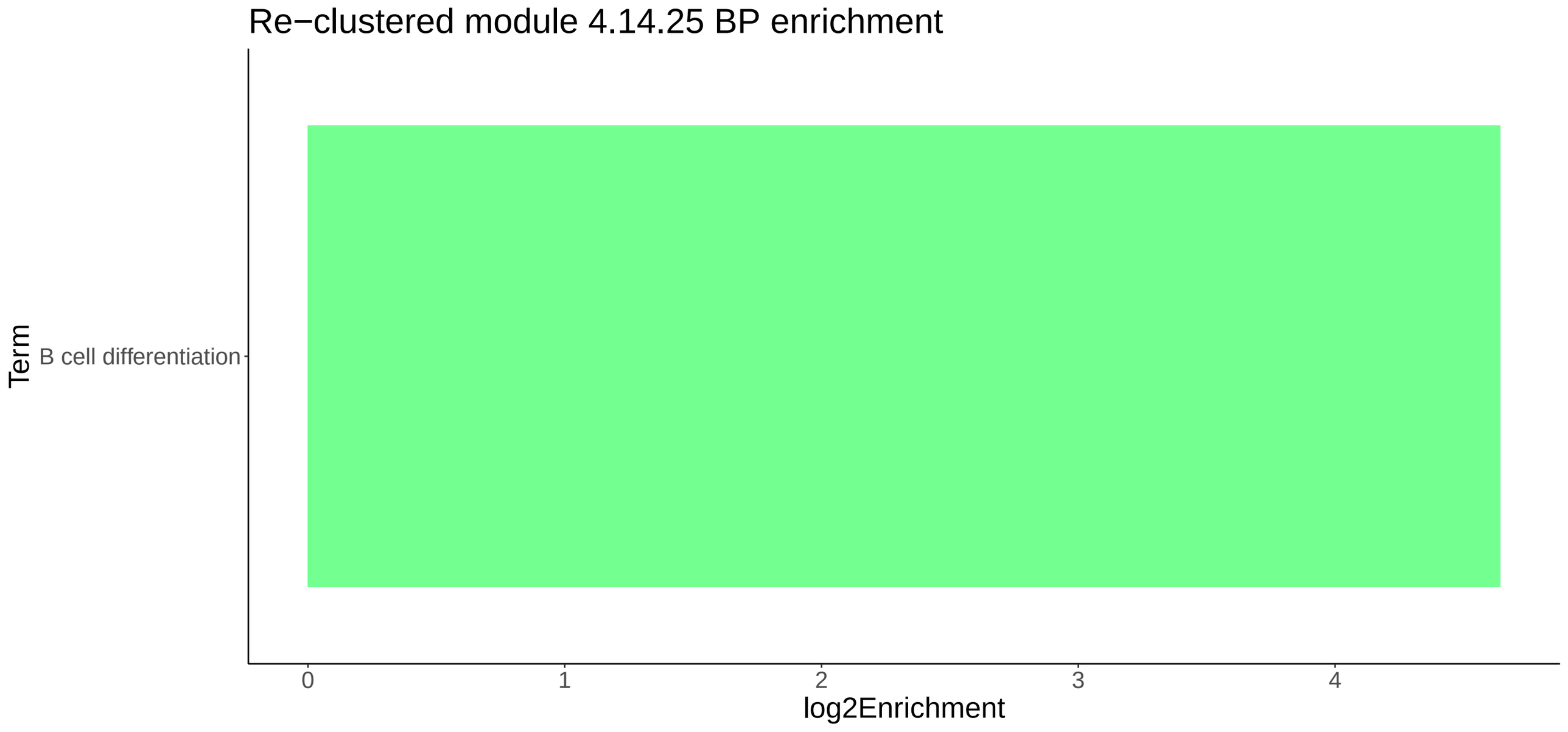

Re−clustered module 4.14.19 MF enrichment
Term
log2Enrichment

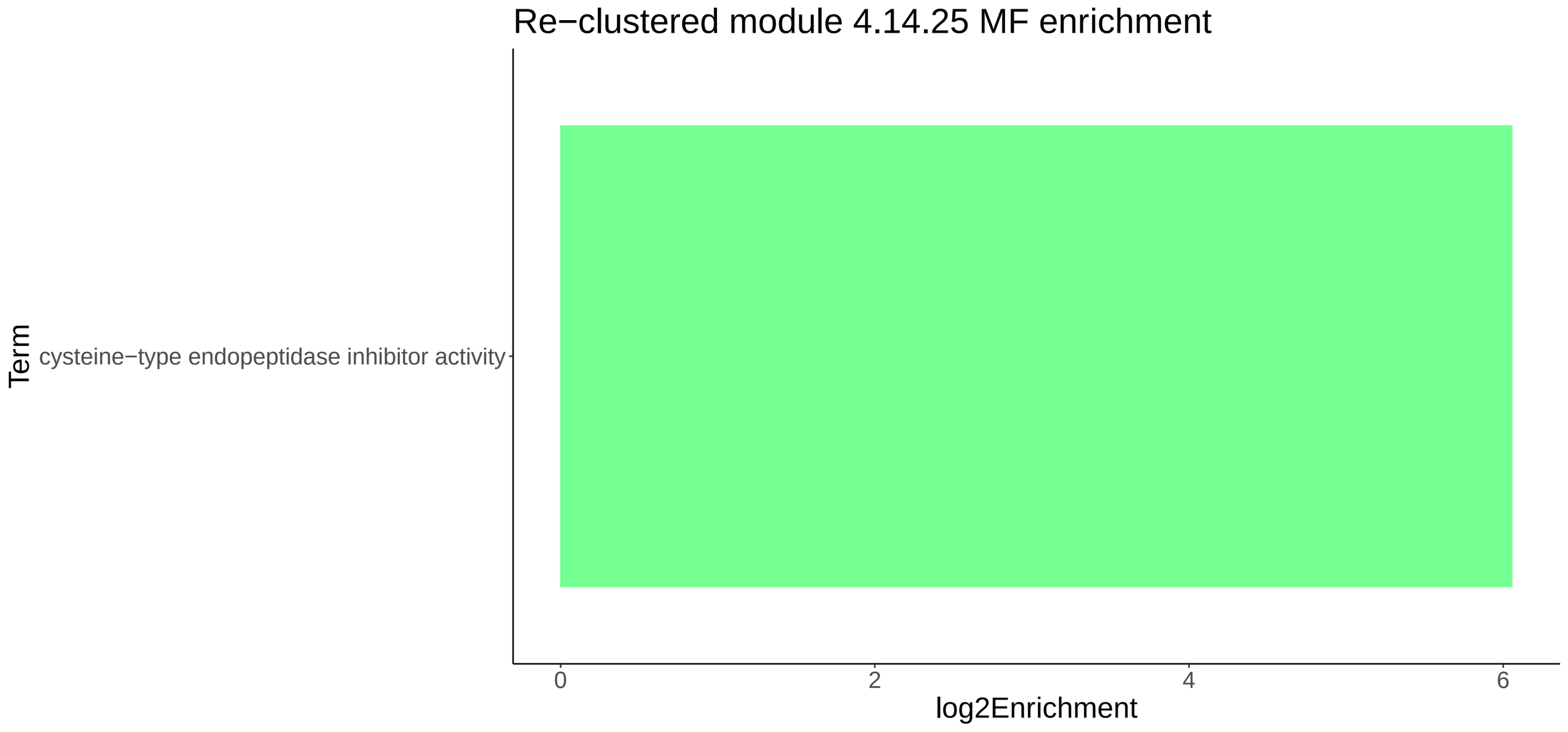

Re−clustered module 4.14.20 BP enrichment
Term
intermembrane lipid transfer
0
2
4
6
log2Enrichment

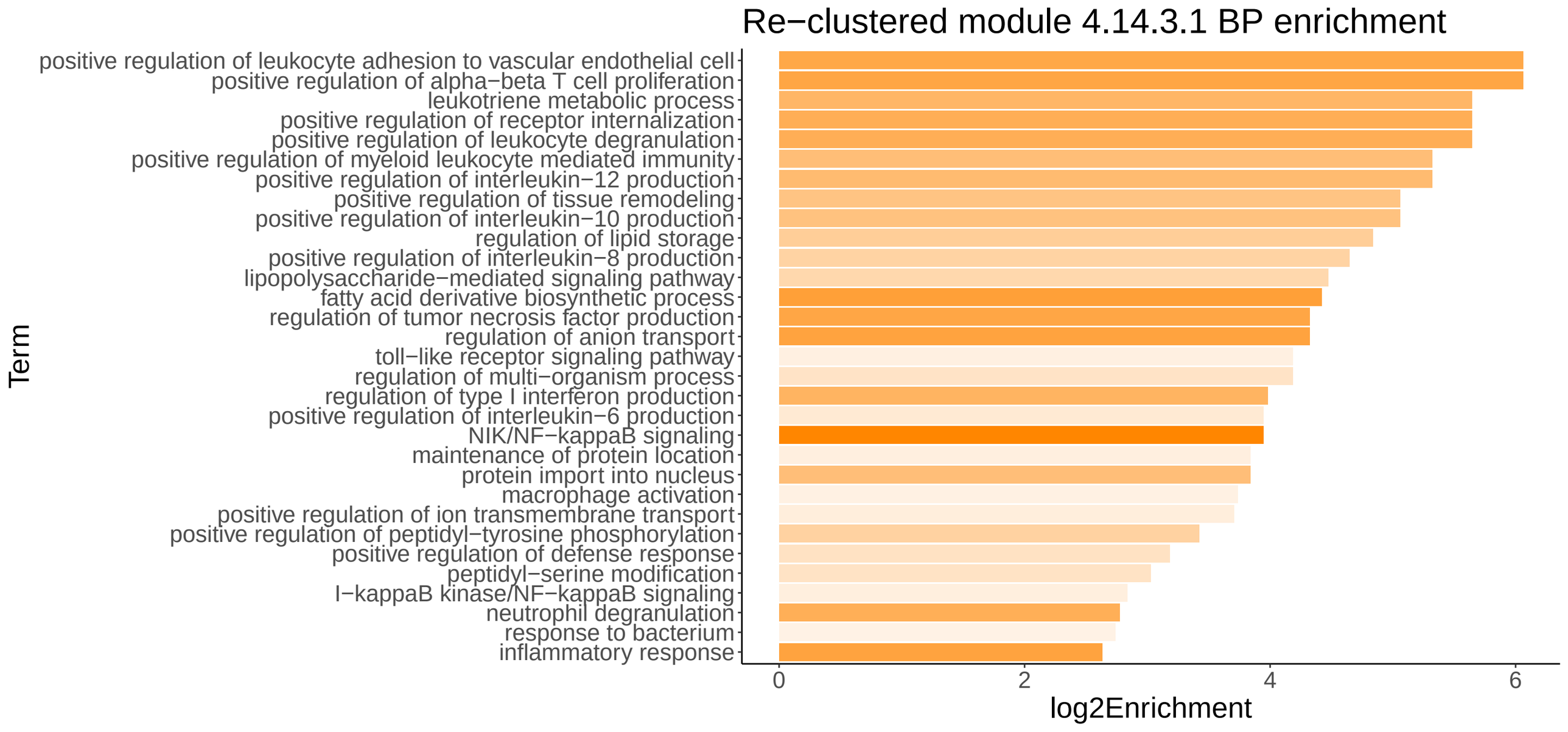

Re−clustered module 4.14.20 MF enrichment
Term
log2Enrichment

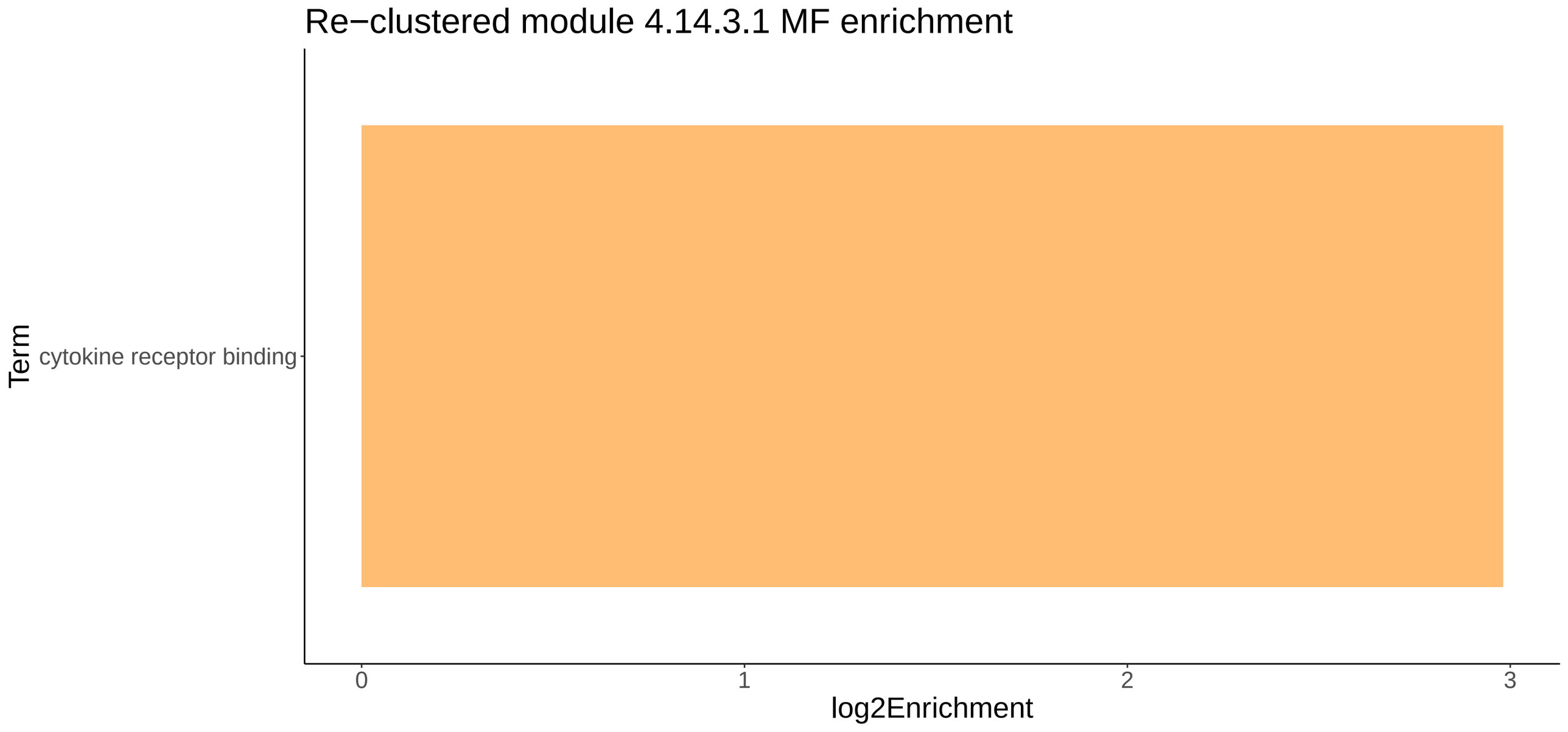

Re−clustered module 4.14.23 BP enrichment
skeletal muscle cell differentiation
retinoid metabolic process
positive regulation of MAP kinase activity
cell fate commitment
Term
0
2
4
log2Enrichment

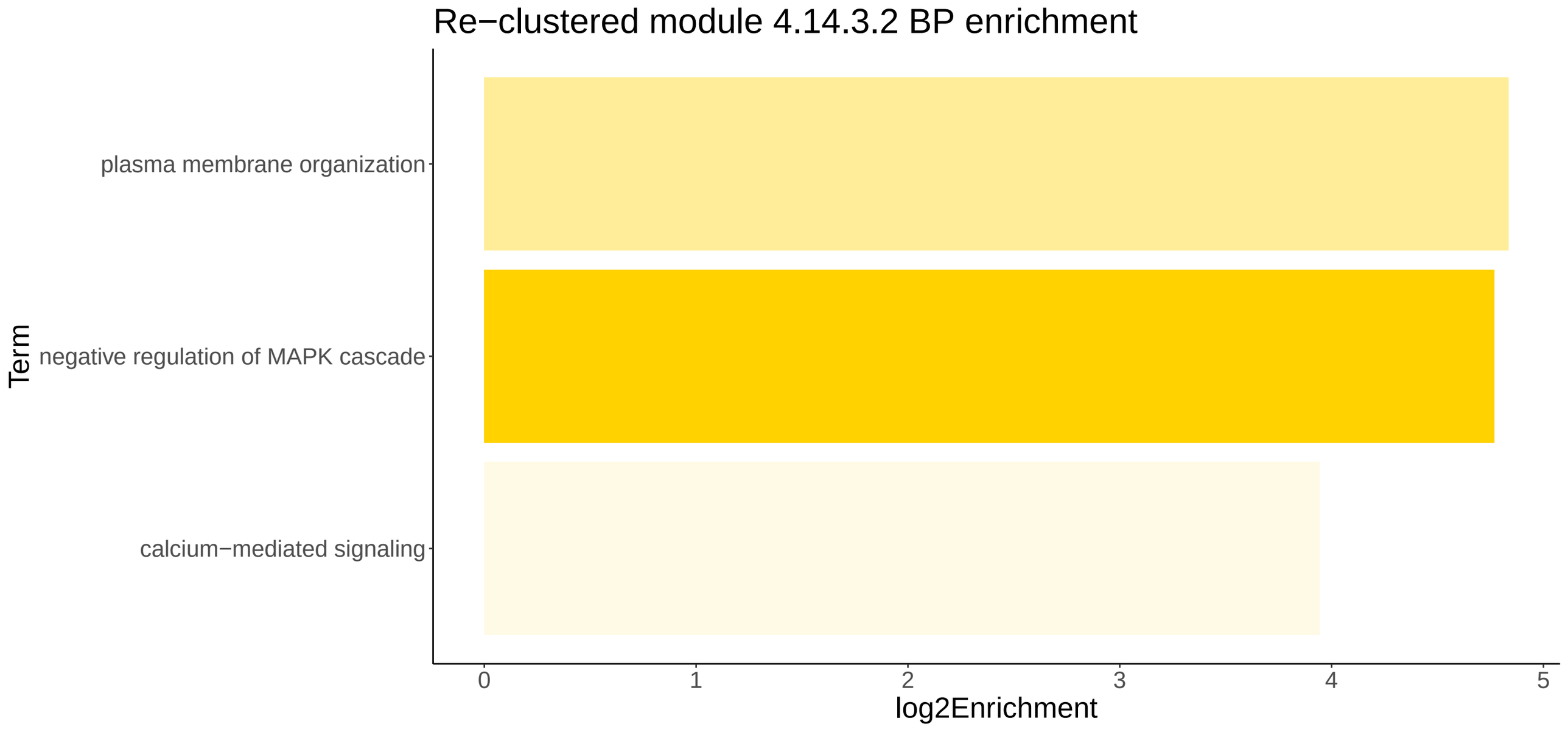

Re−clustered module 4.14.23 MF enrichment
Term
log2Enrichment

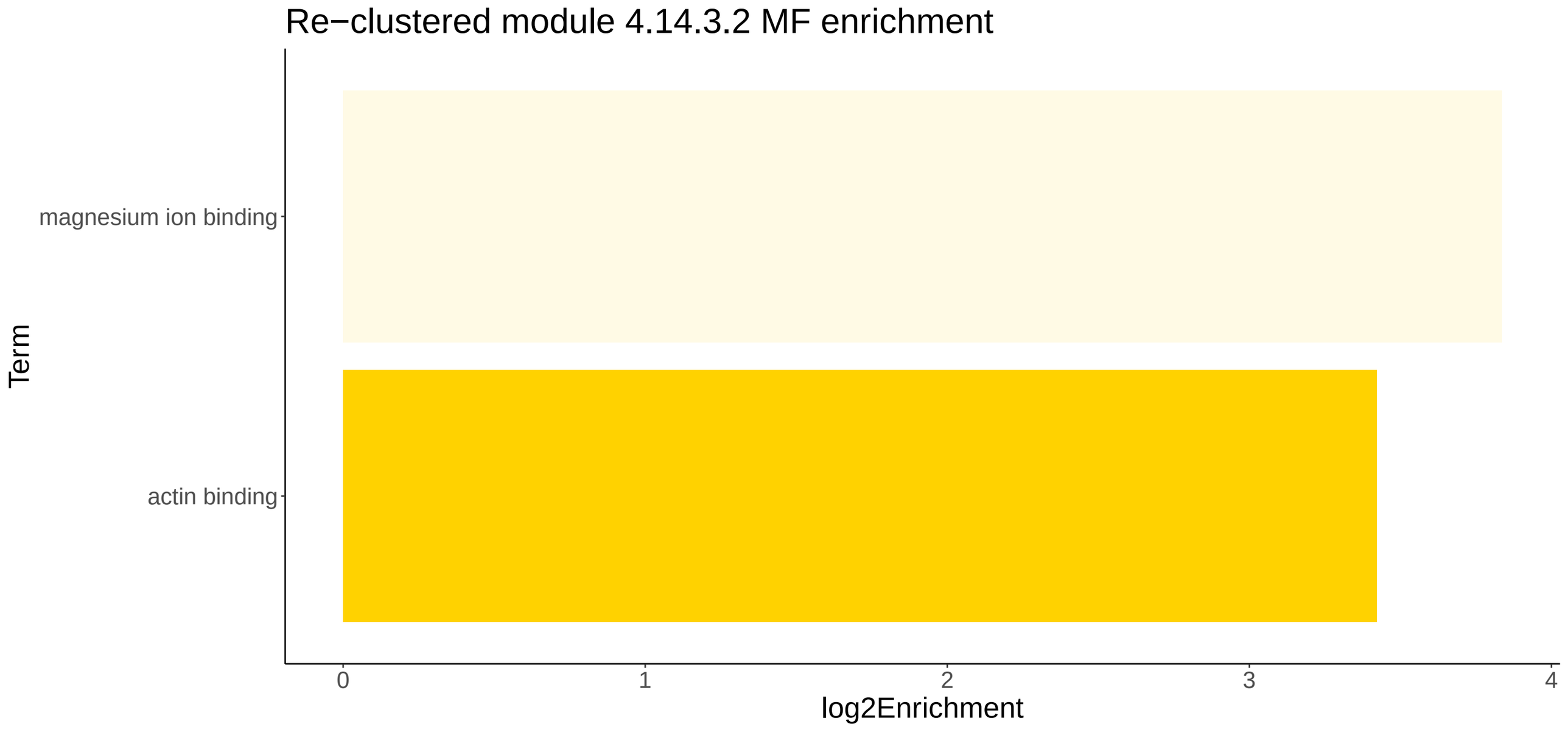

Re−clustered module 4.14.25 BP enrichment
Term
B cell differentiation
0
1
2
3
4
log2Enrichment

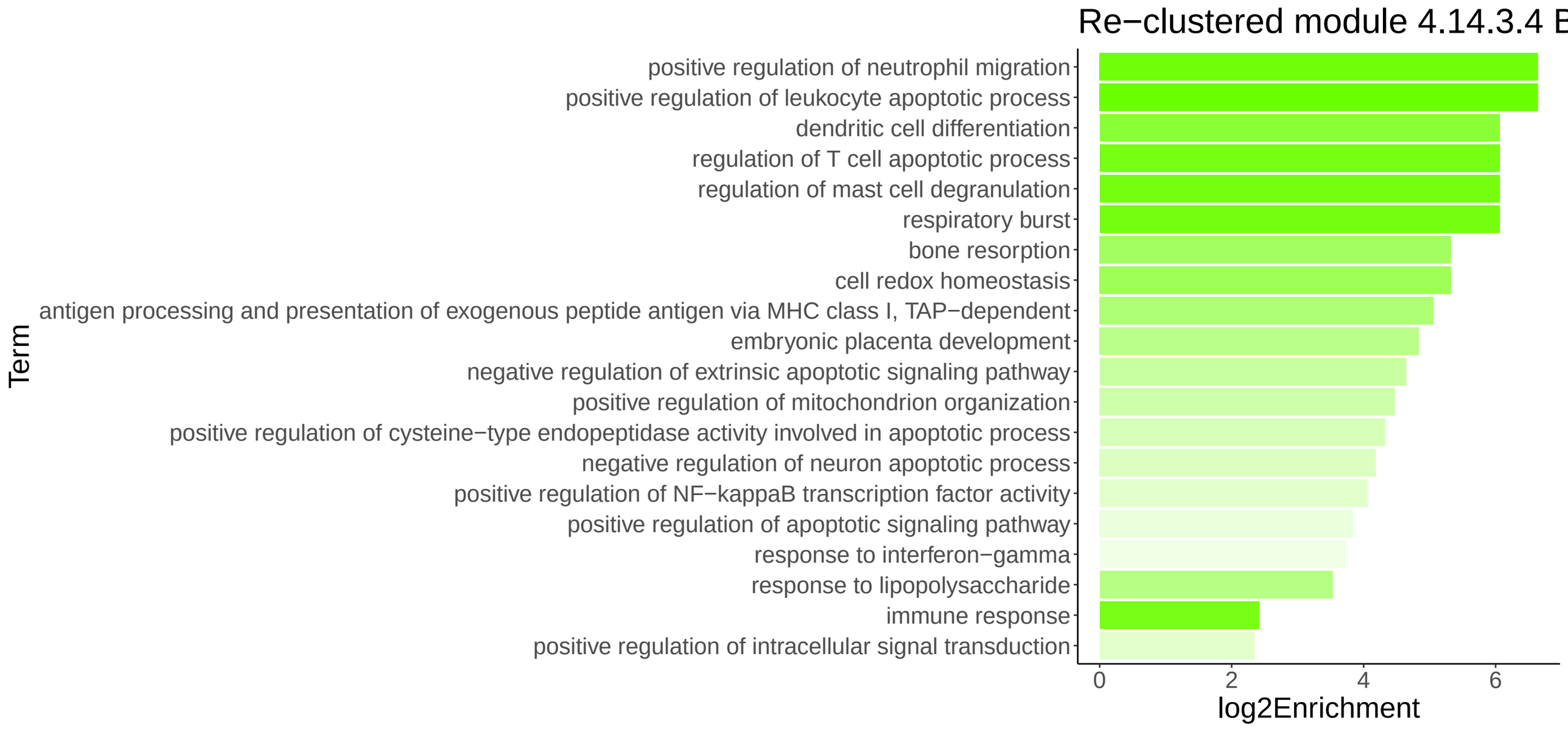

Re−clustered module 4.14.25 MF enrichment
Term
cysteine−type endopeptidase inhibitor activity
0
2
4
6
log2Enrichment

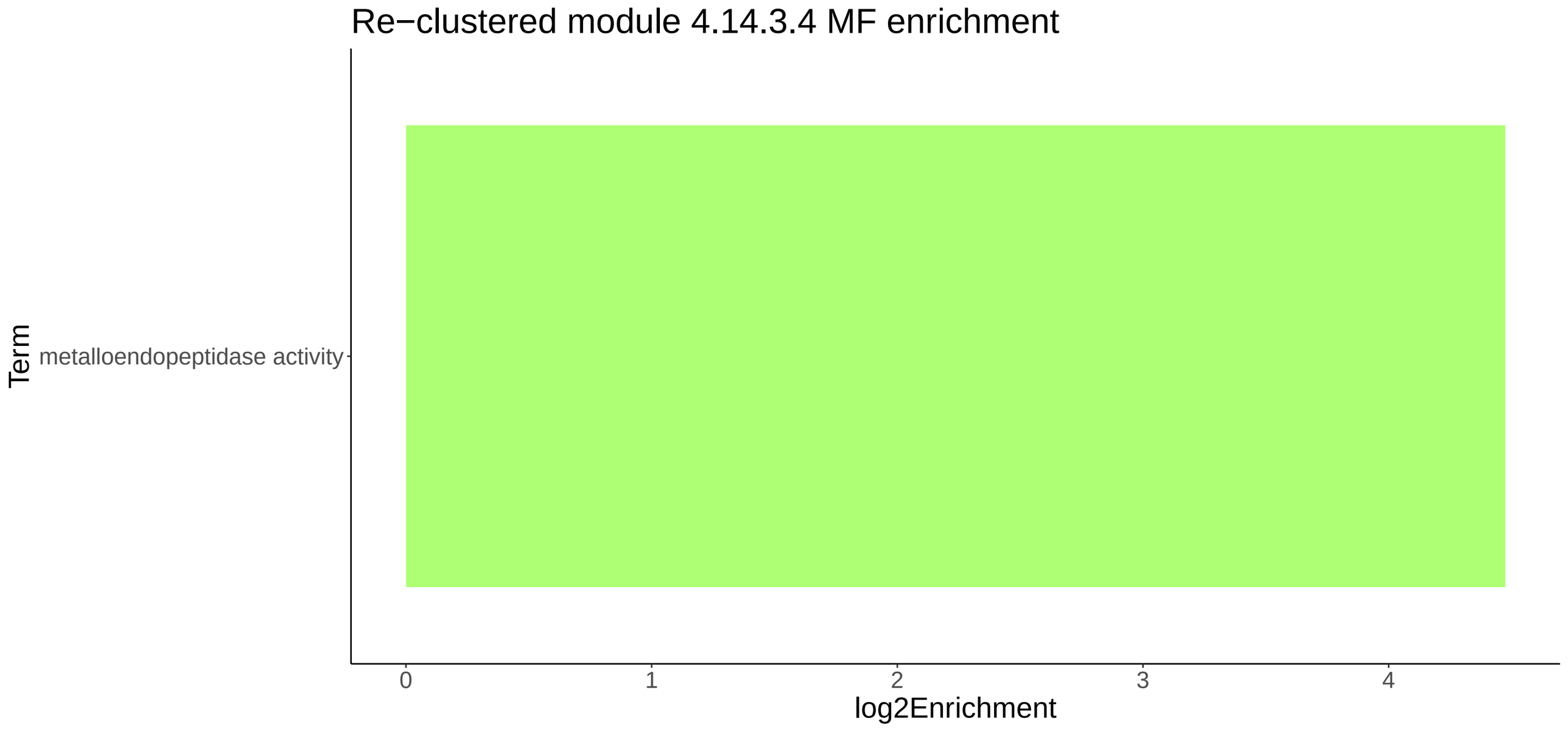

Re−clustered module 4.14.3.1 BP enrichment
positive regulation of leukocyte adhesion to vascular endothelial cell
positive regulation of alpha−beta T cell proliferation
leukotriene metabolic process
positive regulation of receptor internalization
positive regulation of leukocyte degranulation
positive regulation of myeloid leukocyte mediated immunity
positive regulation of interleukin−12 production
positive regulation of tissue remodeling
positive regulation of interleukin−10 production
regulation of lipid storage
positive regulation of interleukin−8 production
lipopolysaccharide−mediated signaling pathway
fatty acid derivative biosynthetic process
regulation of tumor necrosis factor production
regulation of anion transport
toll−like receptor signaling pathway
regulation of multi−organism process
regulation of type I interferon production
positive regulation of interleukin−6 production
NIK/NF−kappaB signaling
maintenance of protein location
protein import into nucleus
macrophage activation
positive regulation of ion transmembrane transport
positive regulation of peptidyl−tyrosine phosphorylation
positive regulation of defense response
peptidyl−serine modification
I−kappaB kinase/NF−kappaB signaling
neutrophil degranulation
response to bacterium
inflammatory response
Term
0
2
4
6
log2Enrichment

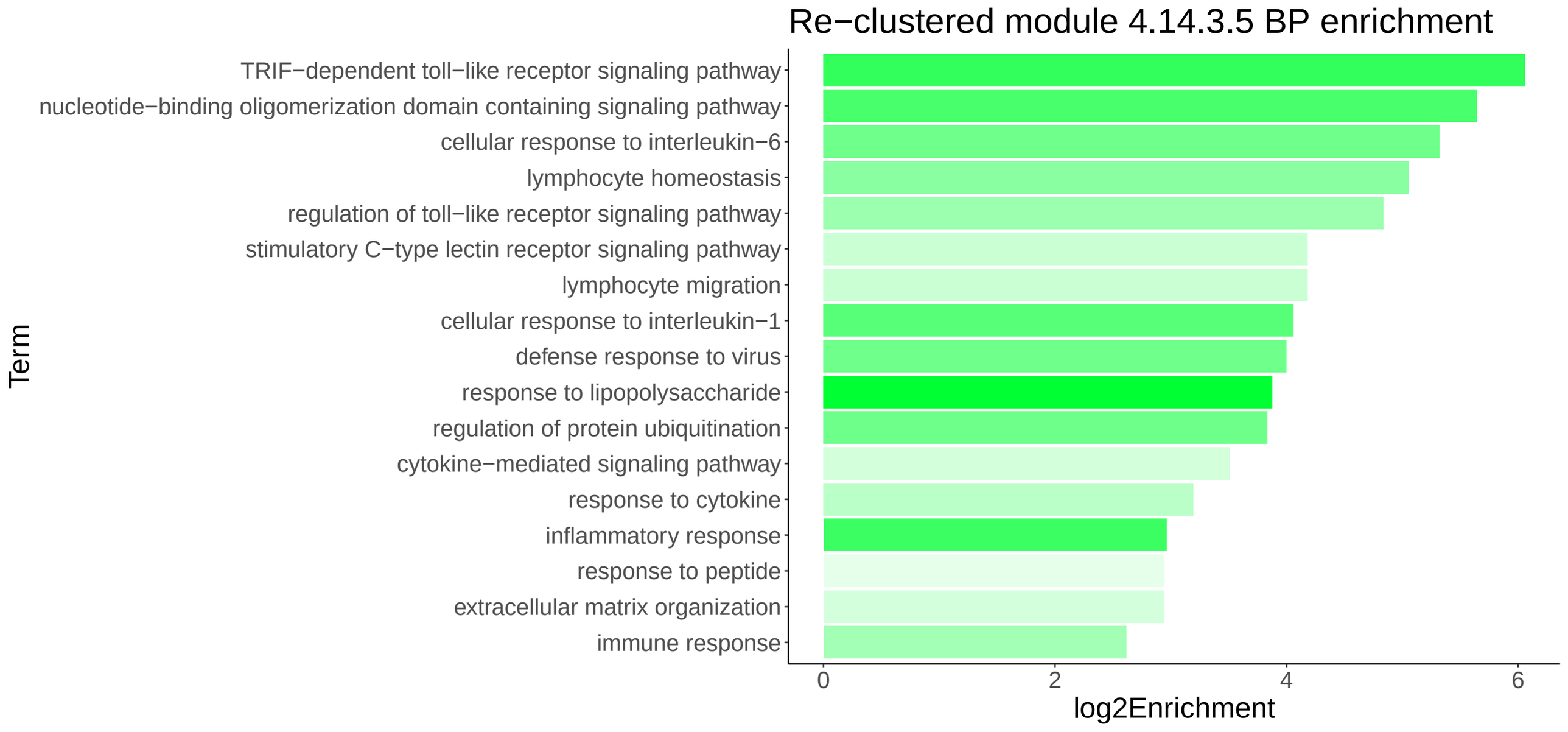

Re−clustered module 4.14.3.1 MF enrichment
Term
cytokine receptor binding
0
1
2
3
log2Enrichment

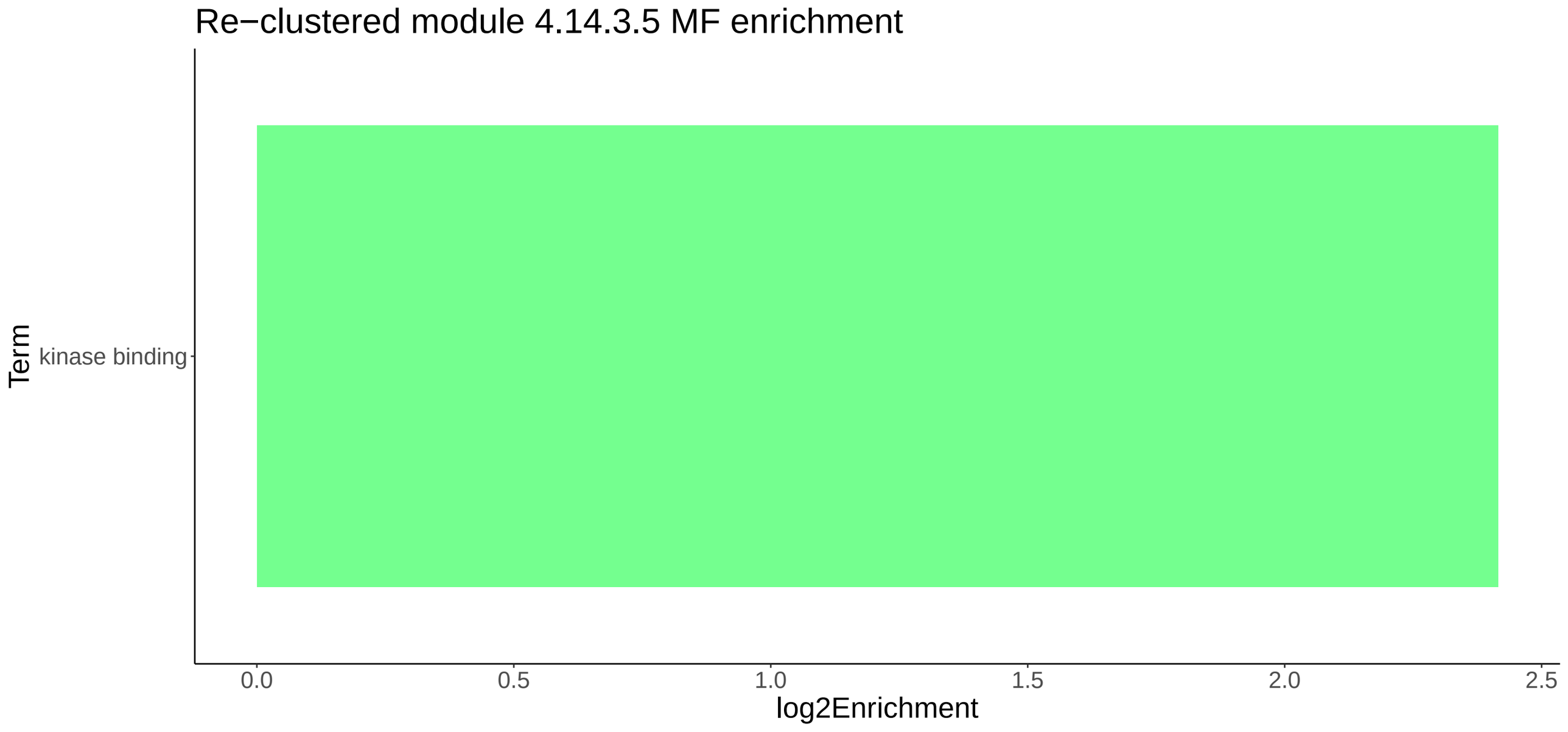

Re−clustered module 4.14.3.2 BP enrichment
Term
plasma membrane organization
negative regulation of MAPK cascade
calcium−mediated signaling
0
1
2
3
4
5
log2Enrichment

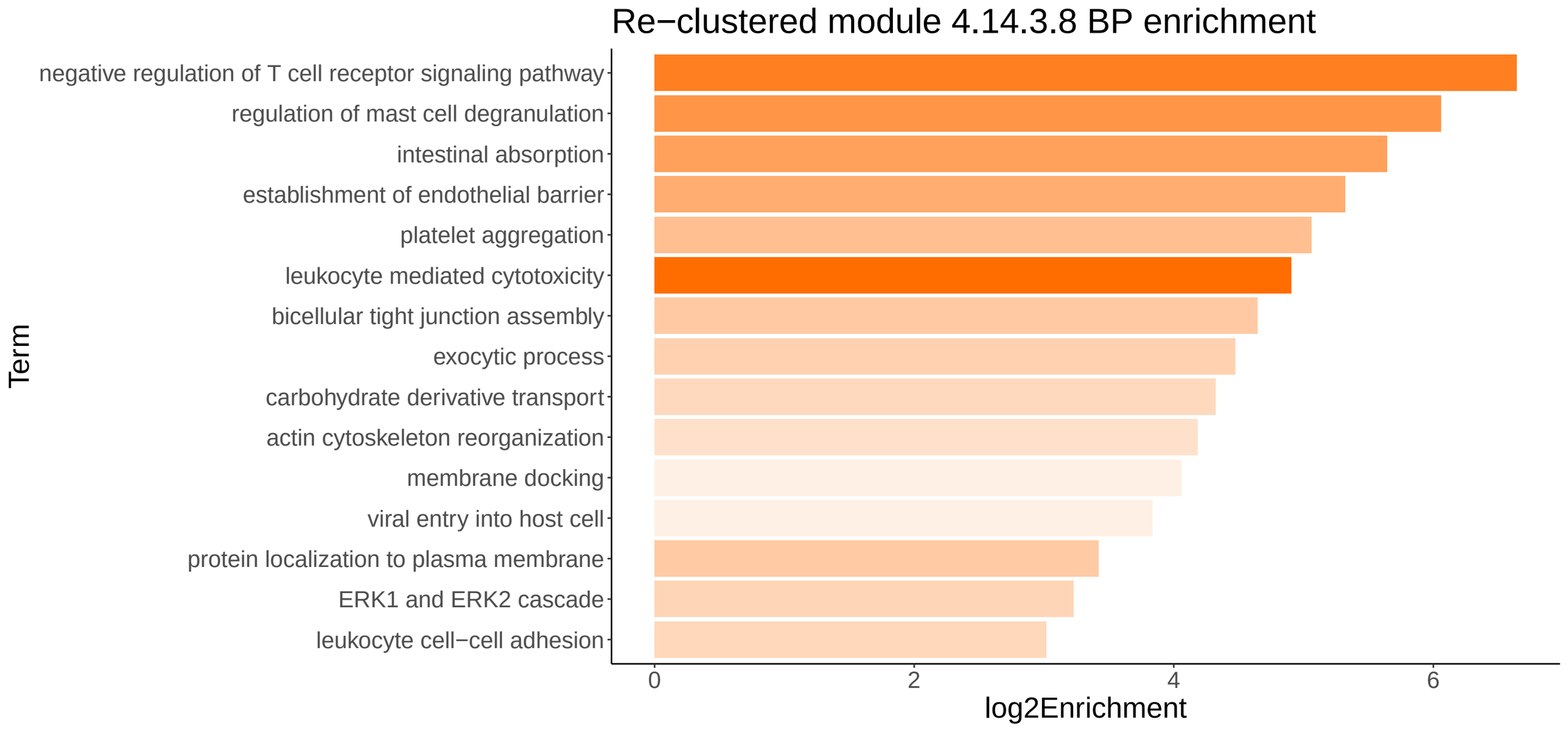

Re−clustered module 4.14.3.2 MF enrichment
Term
magnesium ion binding
actin binding
0
1
2
3
4
log2Enrichment

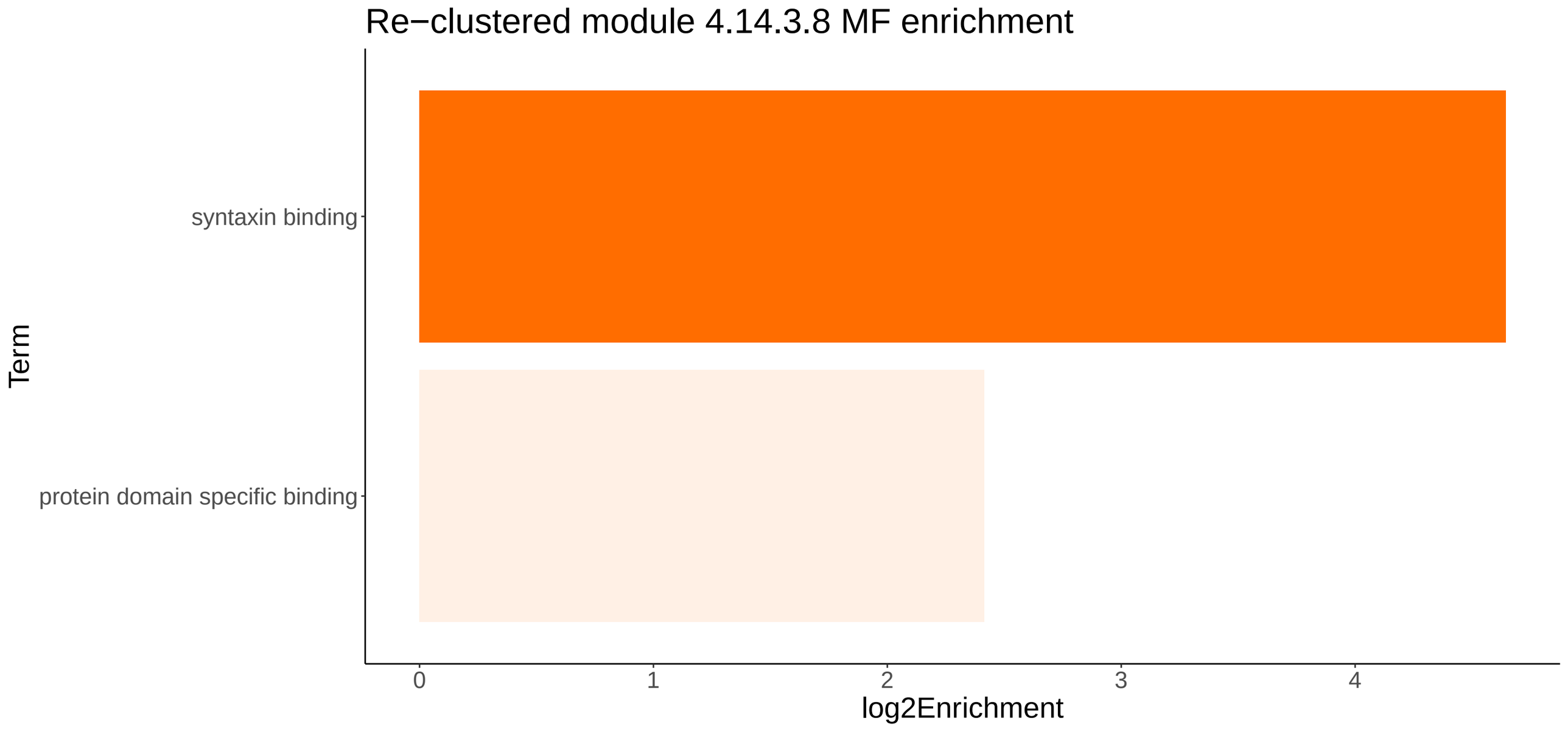

Re−clustered module 4.14.3.4 B
positive regulation of neutrophil migration
positive regulation of leukocyte apoptotic process
dendritic cell differentiation
regulation of T cell apoptotic process
regulation of mast cell degranulation
respiratory burst
bone resorption
cell redox homeostasis
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
embryonic placenta development
negative regulation of extrinsic apoptotic signaling pathway
positive regulation of mitochondrion organization
positive regulation of cysteine−type endopeptidase activity involved in apoptotic process
negative regulation of neuron apoptotic process
positive regulation of NF−kappaB transcription factor activity
positive regulation of apoptotic signaling pathway
response to interferon−gamma
response to lipopolysaccharide
immune response
positive regulation of intracellular signal transduction
Term
0
2
4
6
log2Enrichment

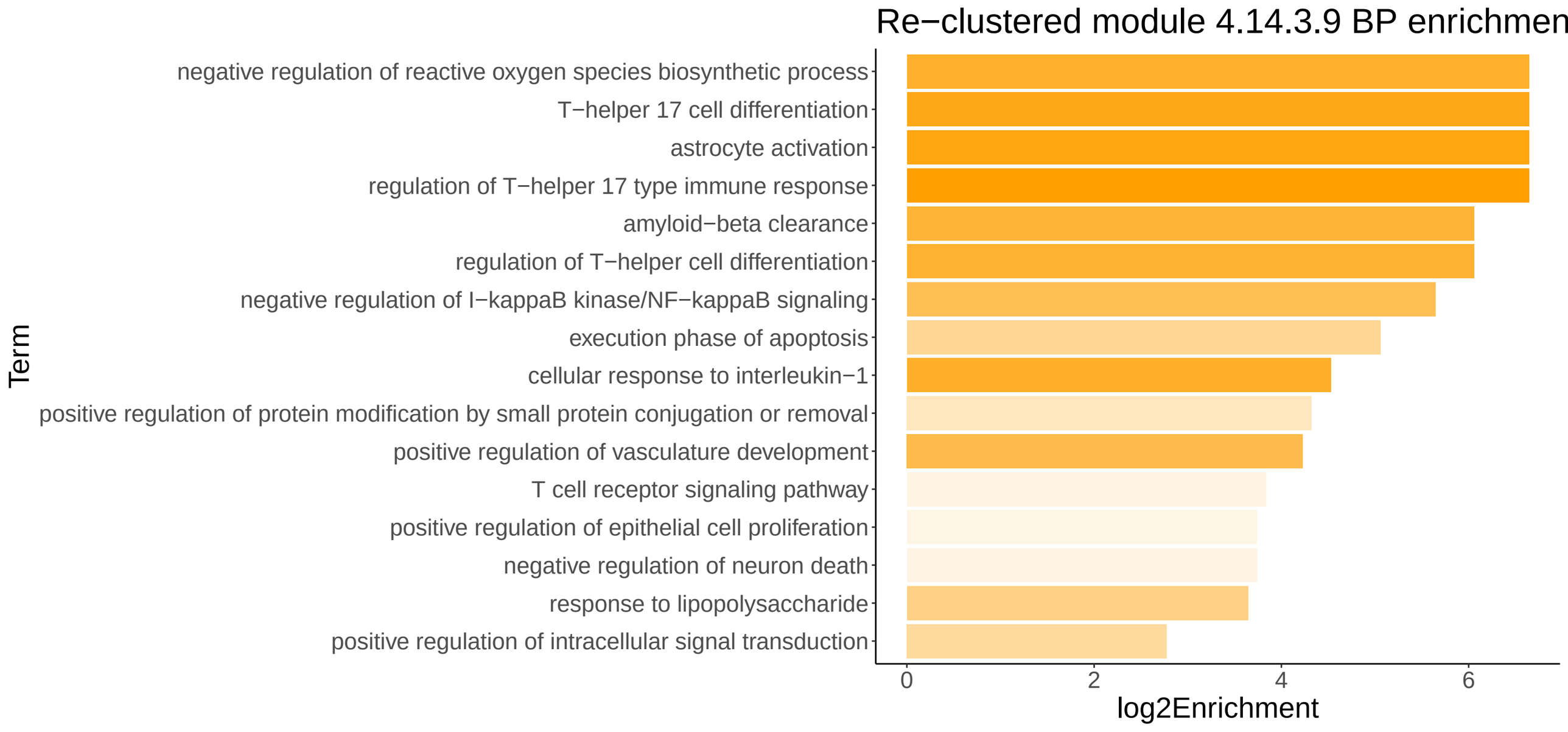

Re−clustered module 4.14.3.4 MF enrichment
Term
metalloendopeptidase activity
0
1
2
3
4
log2Enrichment

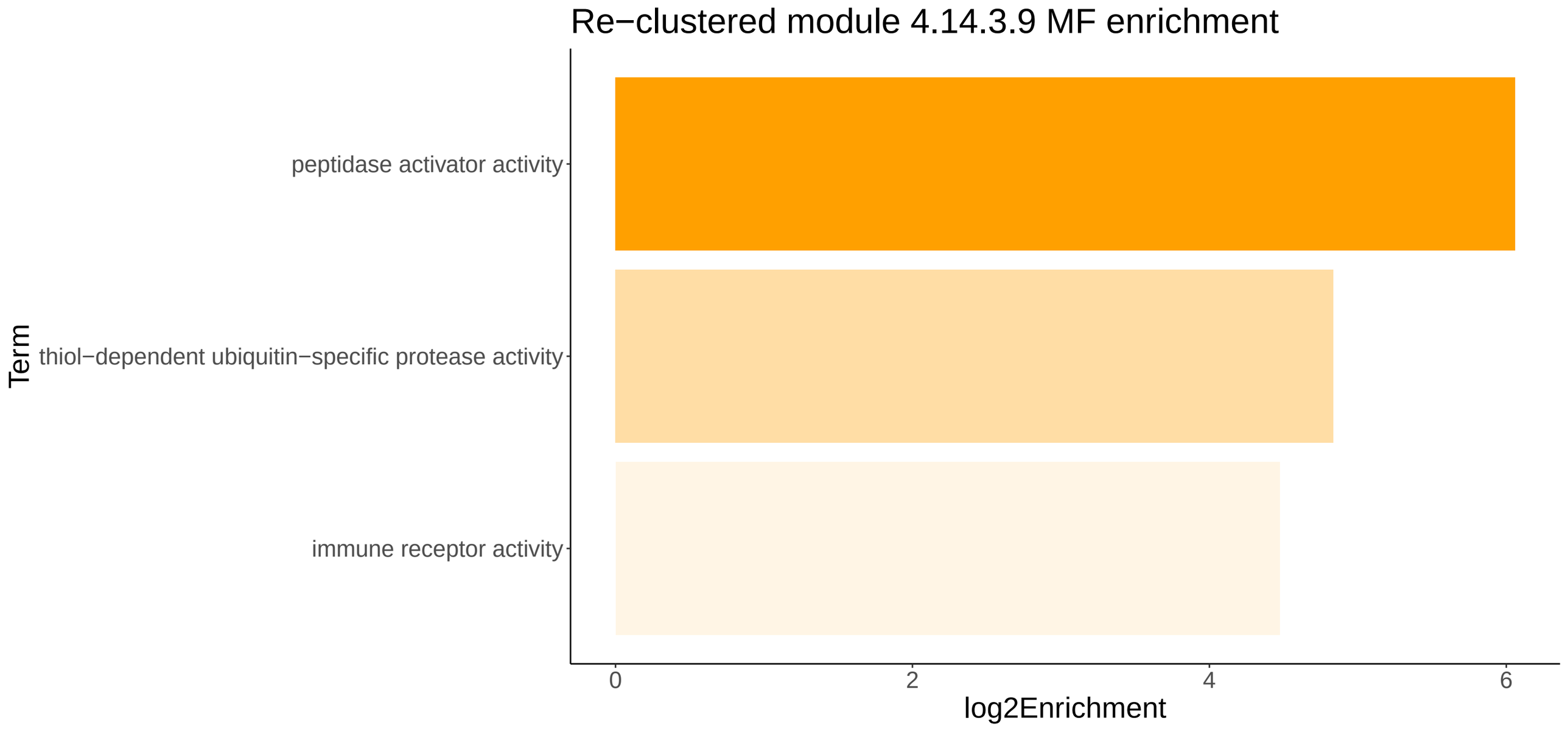

Re−clustered module 4.14.3.5 BP enrichment
TRIF−dependent toll−like receptor signaling pathway
nucleotide−binding oligomerization domain containing signaling pathway
cellular response to interleukin−6
lymphocyte homeostasis
regulation of toll−like receptor signaling pathway
stimulatory C−type lectin receptor signaling pathway
lymphocyte migration
cellular response to interleukin−1
defense response to virus
response to lipopolysaccharide
regulation of protein ubiquitination
cytokine−mediated signaling pathway
response to cytokine
inflammatory response
response to peptide
extracellular matrix organization
immune response
Term
0
2
4
6
log2Enrichment

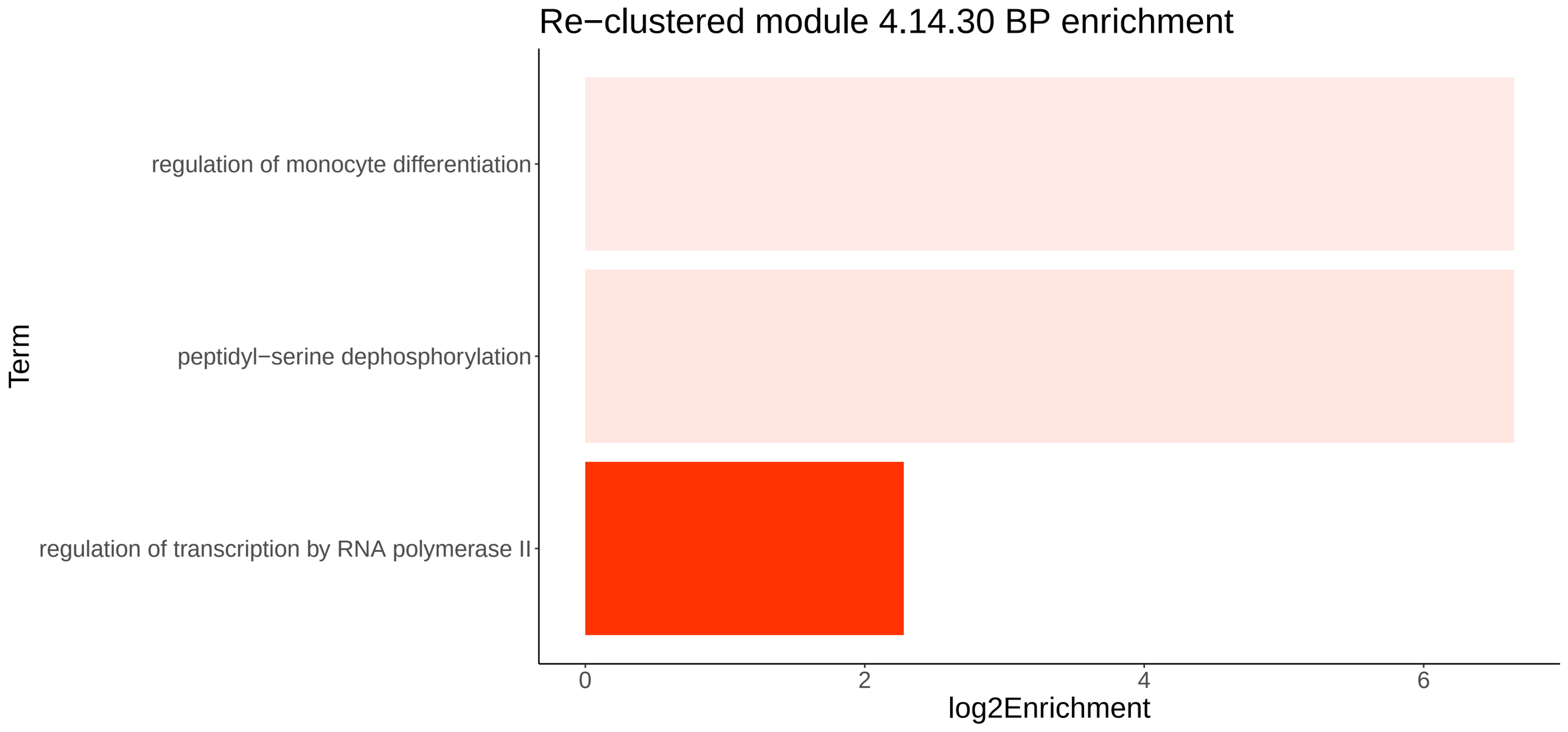

Re−clustered module 4.14.3.5 MF enrichment
Term
kinase binding
0.0
0.5
1.0
1.5
2.0
2.5
log2Enrichment

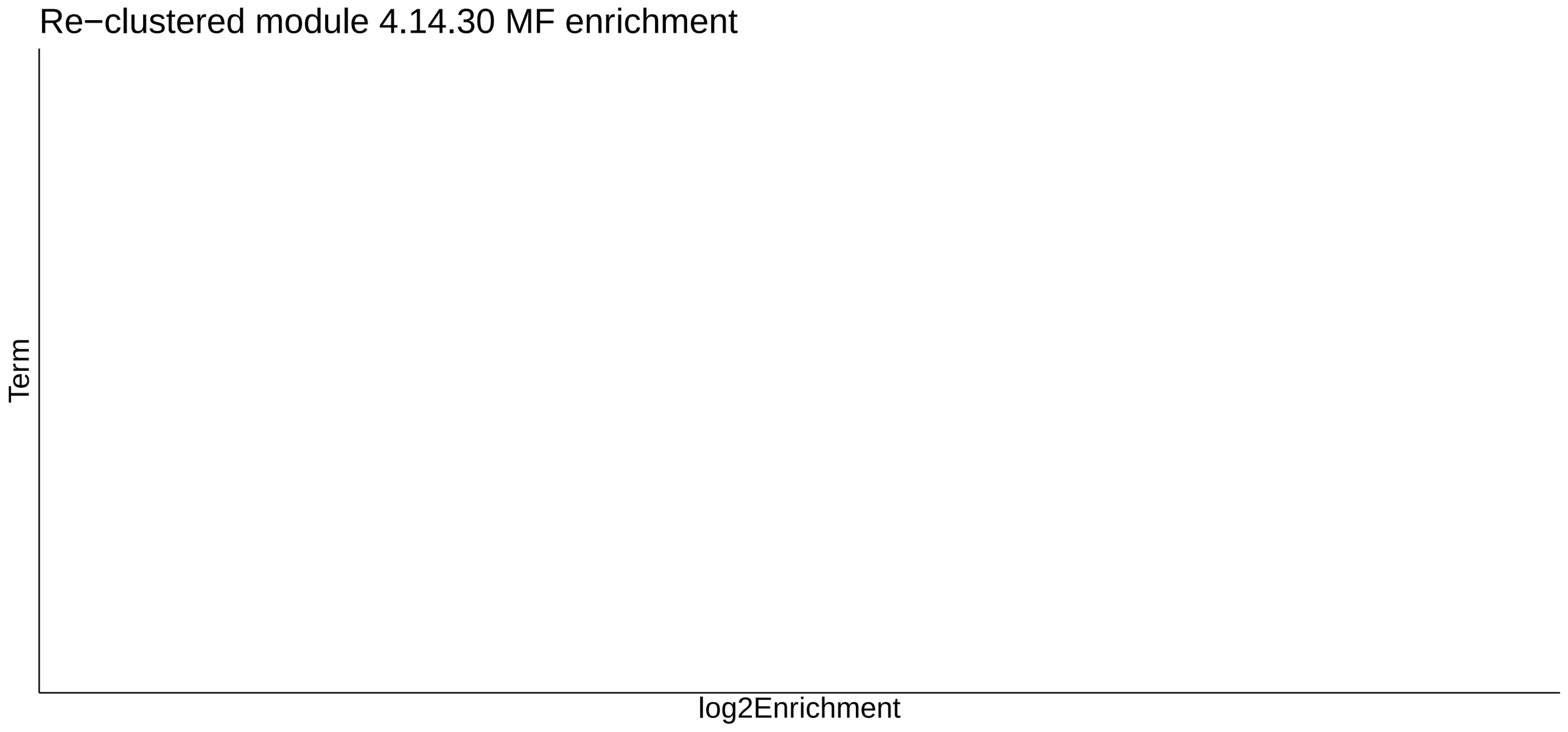

Re−clustered module 4.14.3.8 BP enrichment
negative regulation of T cell receptor signaling pathway
regulation of mast cell degranulation
intestinal absorption
establishment of endothelial barrier
platelet aggregation
leukocyte mediated cytotoxicity
bicellular tight junction assembly
exocytic process
carbohydrate derivative transport
actin cytoskeleton reorganization
membrane docking
viral entry into host cell
protein localization to plasma membrane
ERK1 and ERK2 cascade
leukocyte cell−cell adhesion
Term
0
2
4
6
log2Enrichment

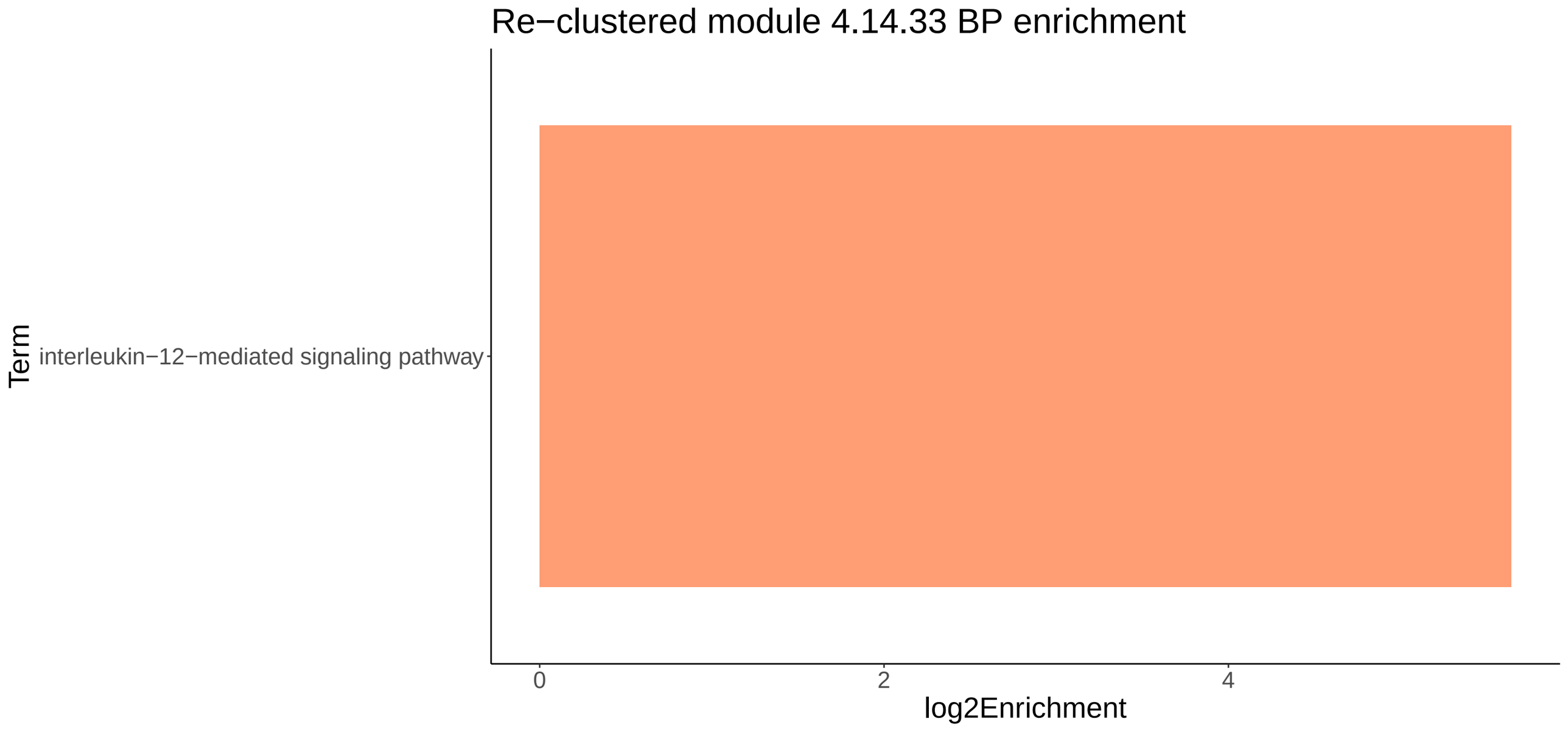

Re−clustered module 4.14.3.8 MF enrichment
Term
syntaxin binding
protein domain specific binding
0
1
2
3
4
log2Enrichment

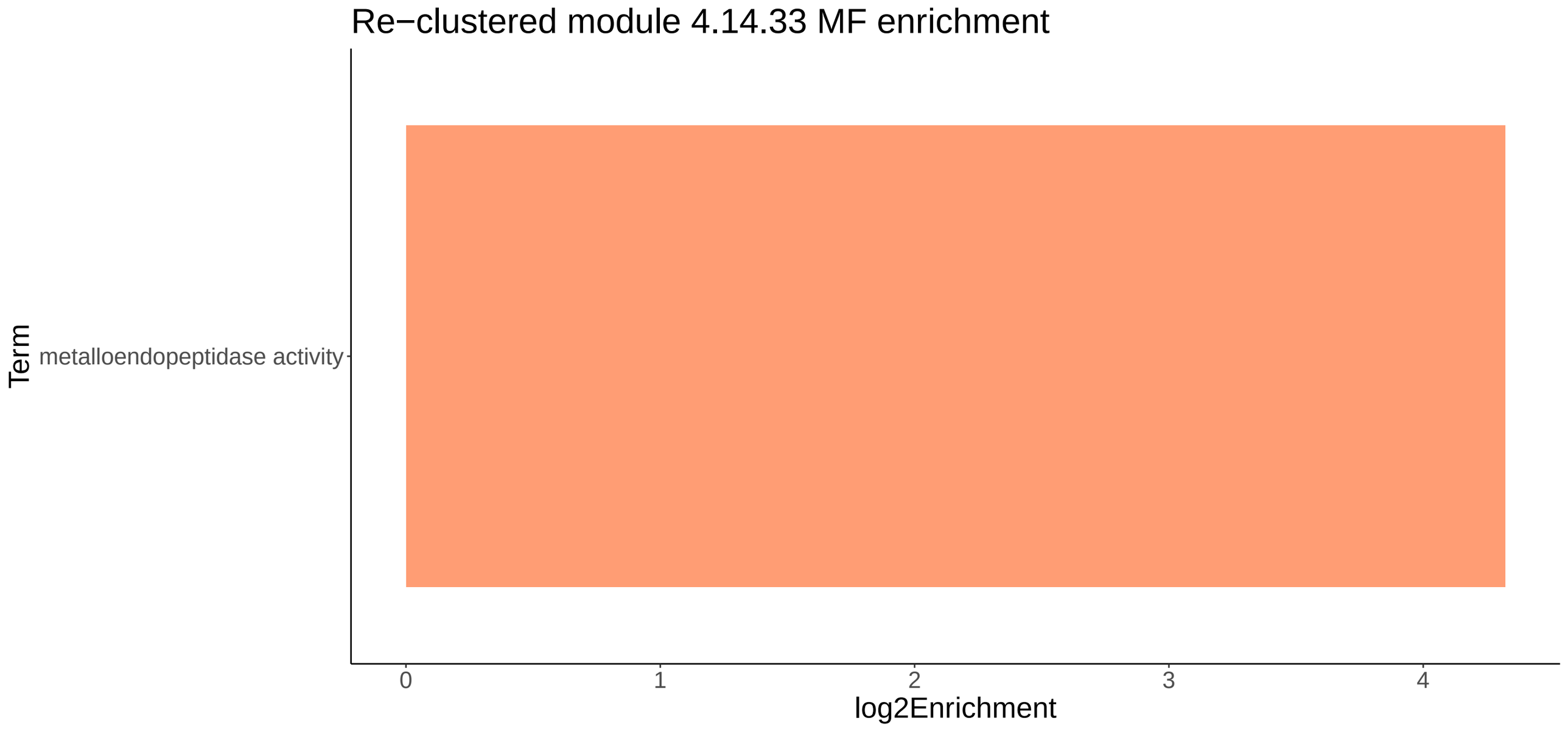

Re−clustered module 4.14.3.9 BP enrichmen
Term
negative regulation of reactive oxygen species biosynthetic process
T−helper 17 cell differentiation
astrocyte activation
regulation of T−helper 17 type immune response
amyloid−beta clearance
regulation of T−helper cell differentiation
negative regulation of I−kappaB kinase/NF−kappaB signaling
execution phase of apoptosis
cellular response to interleukin−1
positive regulation of protein modification by small protein conjugation or removal
positive regulation of vasculature development
T cell receptor signaling pathway
positive regulation of epithelial cell proliferation
negative regulation of neuron death
response to lipopolysaccharide
positive regulation of intracellular signal transduction
0
2
4
6
log2Enrichment

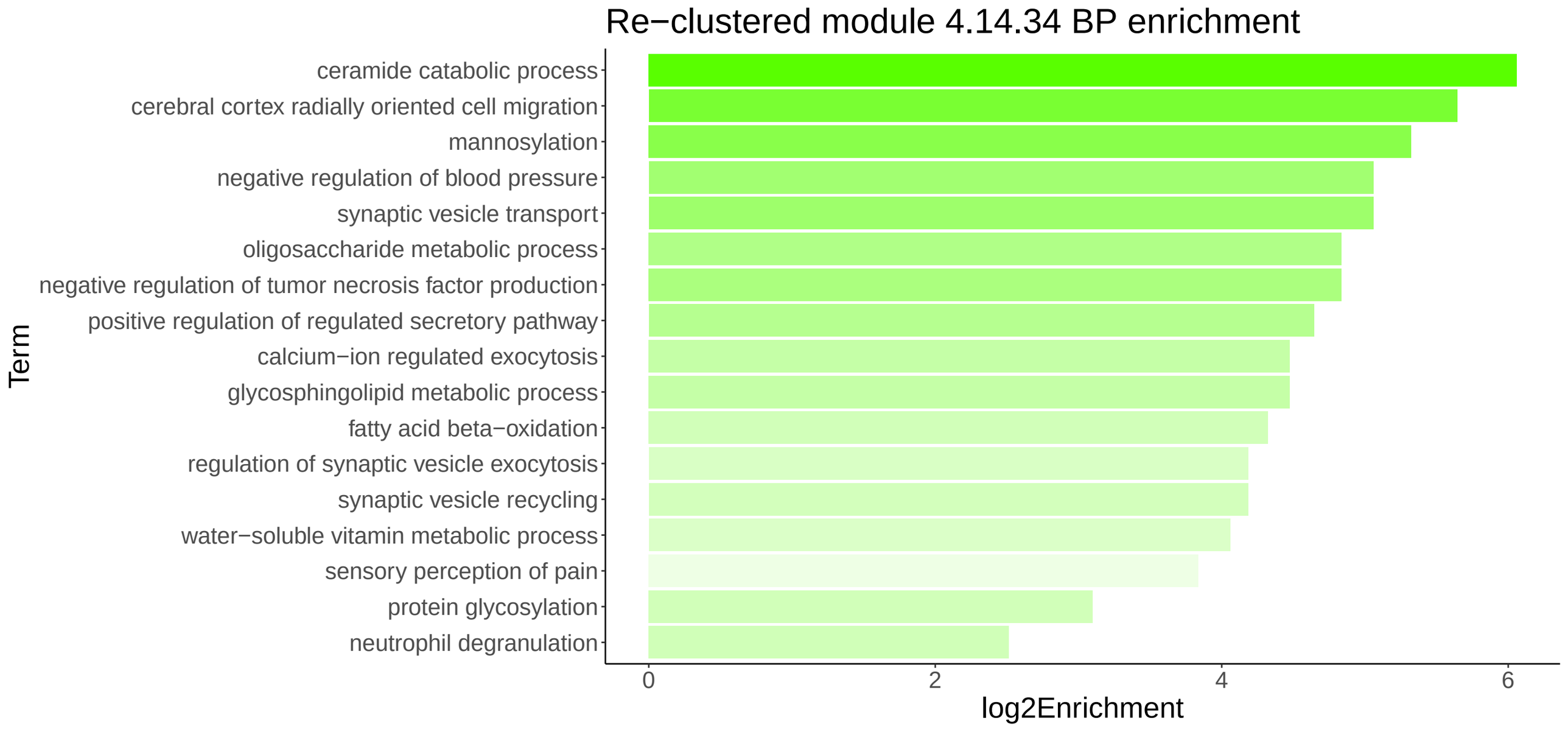

Re−clustered module 4.14.3.9 MF enrichment
Term
peptidase activator activity
thiol−dependent ubiquitin−specific protease activity
immune receptor activity
0
2
4
6
log2Enrichment

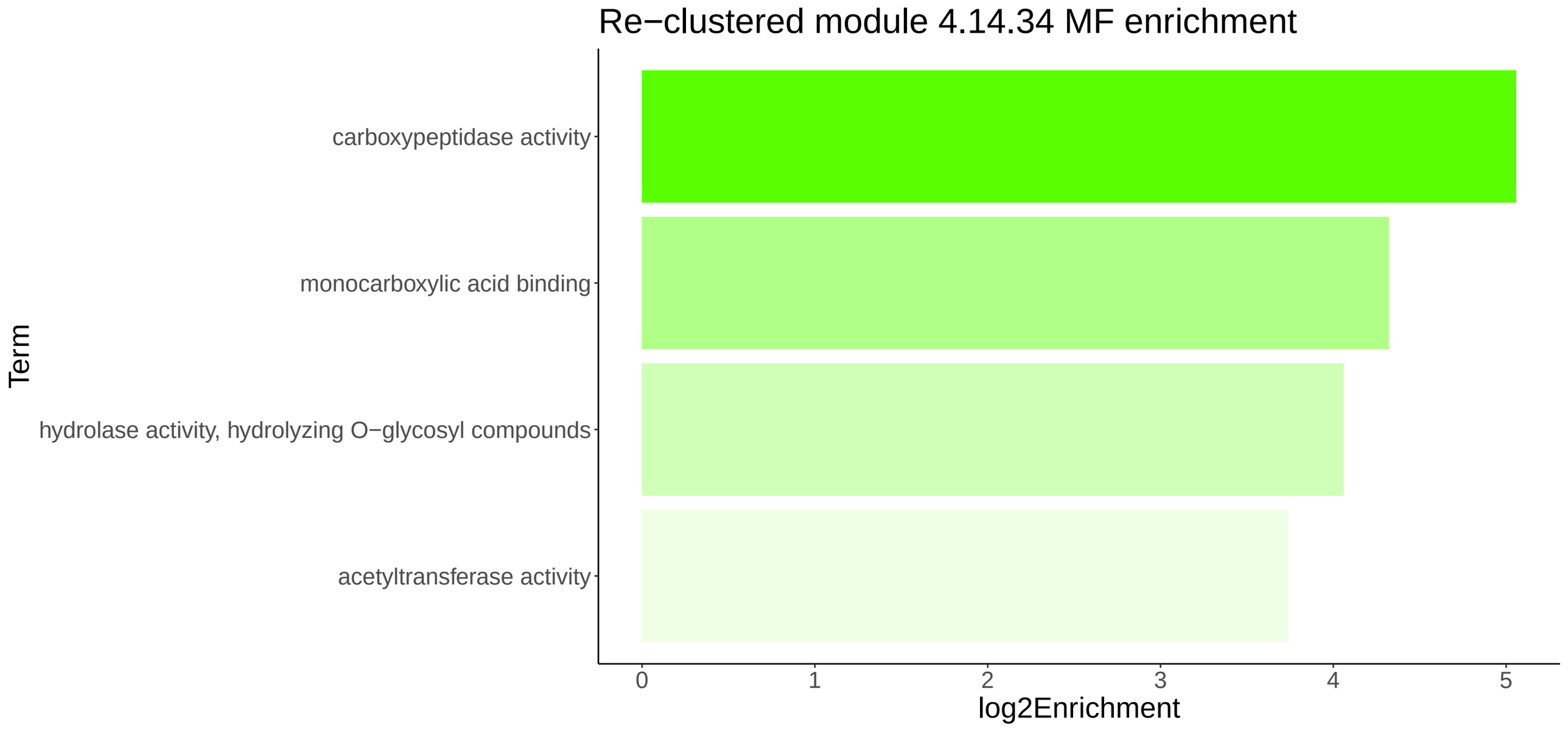

Re−clustered module 4.14.30 BP enrichment
Term
regulation of monocyte differentiation
peptidyl−serine dephosphorylation
regulation of transcription by RNA polymerase II
0
2
4
6
log2Enrichment

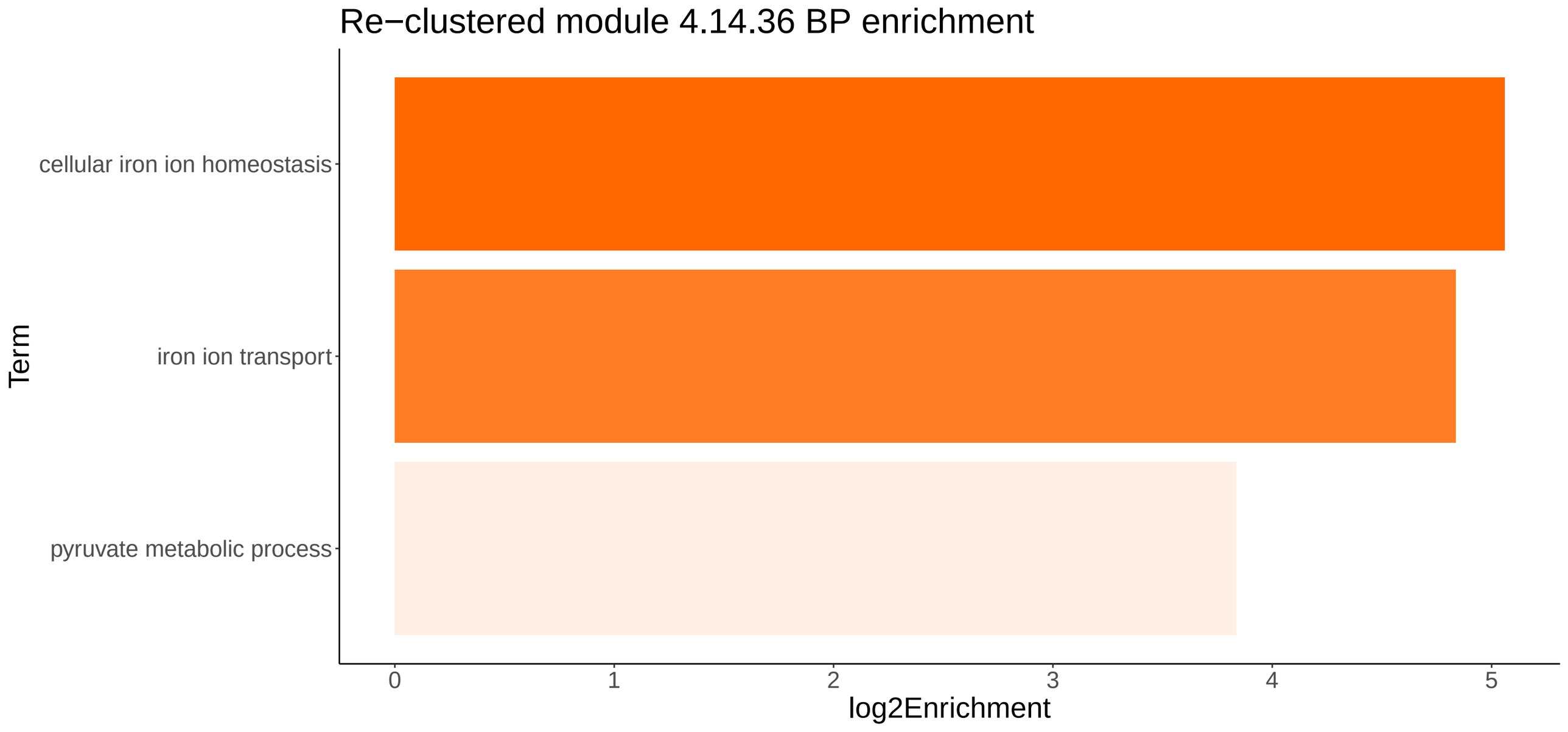

Re−clustered module 4.14.30 MF enrichment
Term
log2Enrichment

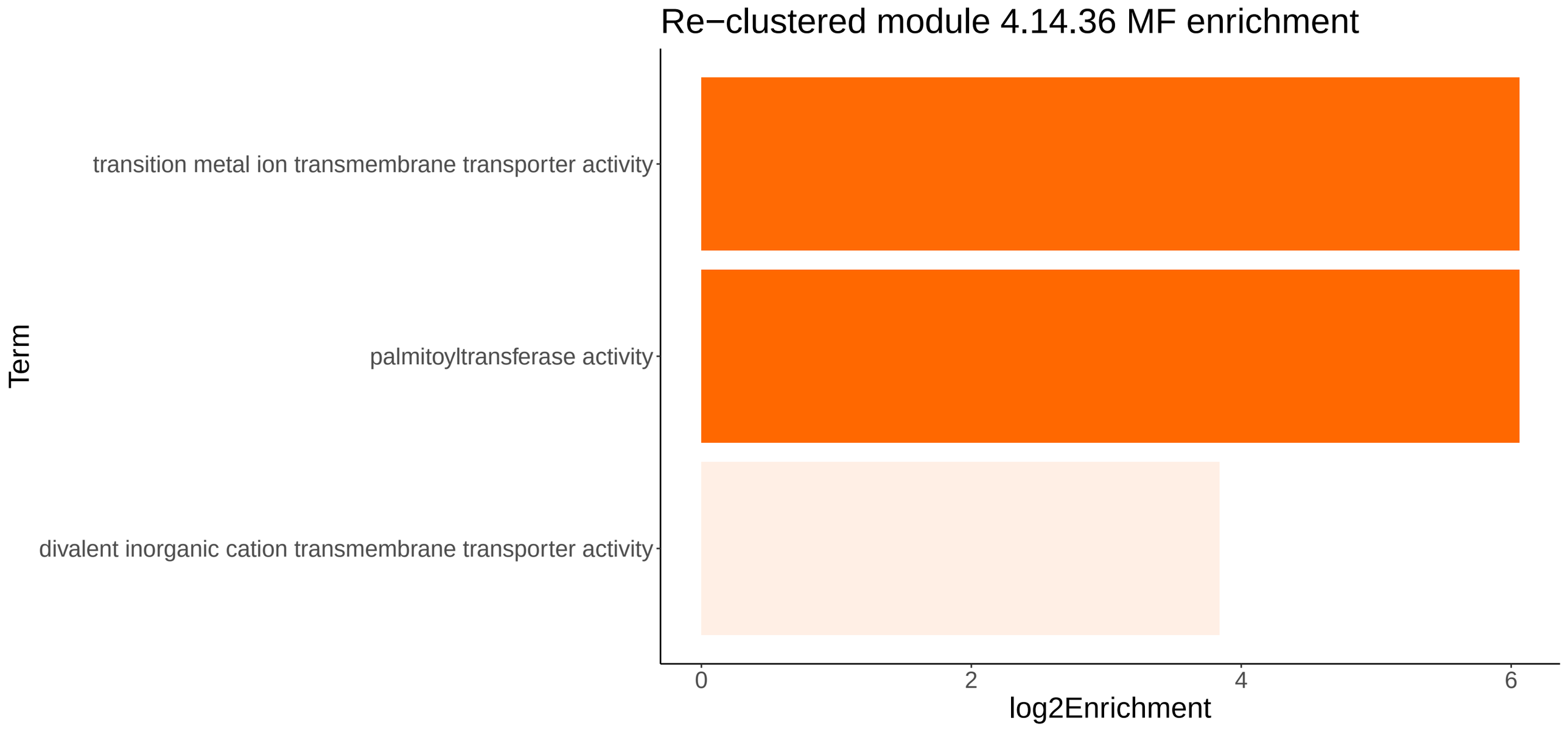

Re−clustered module 4.14.33 BP enrichment
Term
interleukin−12−mediated signaling pathway
0
2
4
log2Enrichment

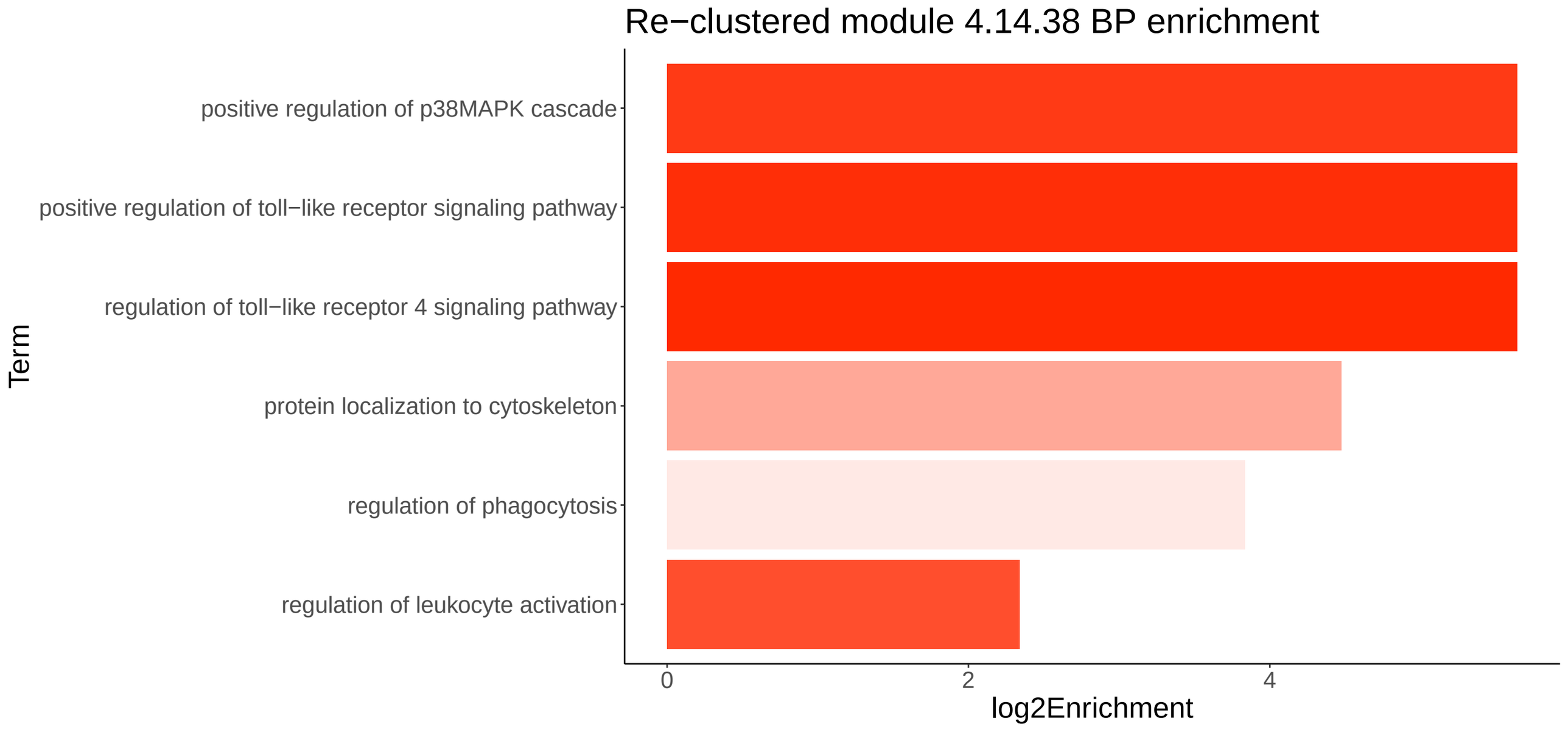

Re−clustered module 4.14.33 MF enrichment
Term
metalloendopeptidase activity
0
1
2
3
4
log2Enrichment

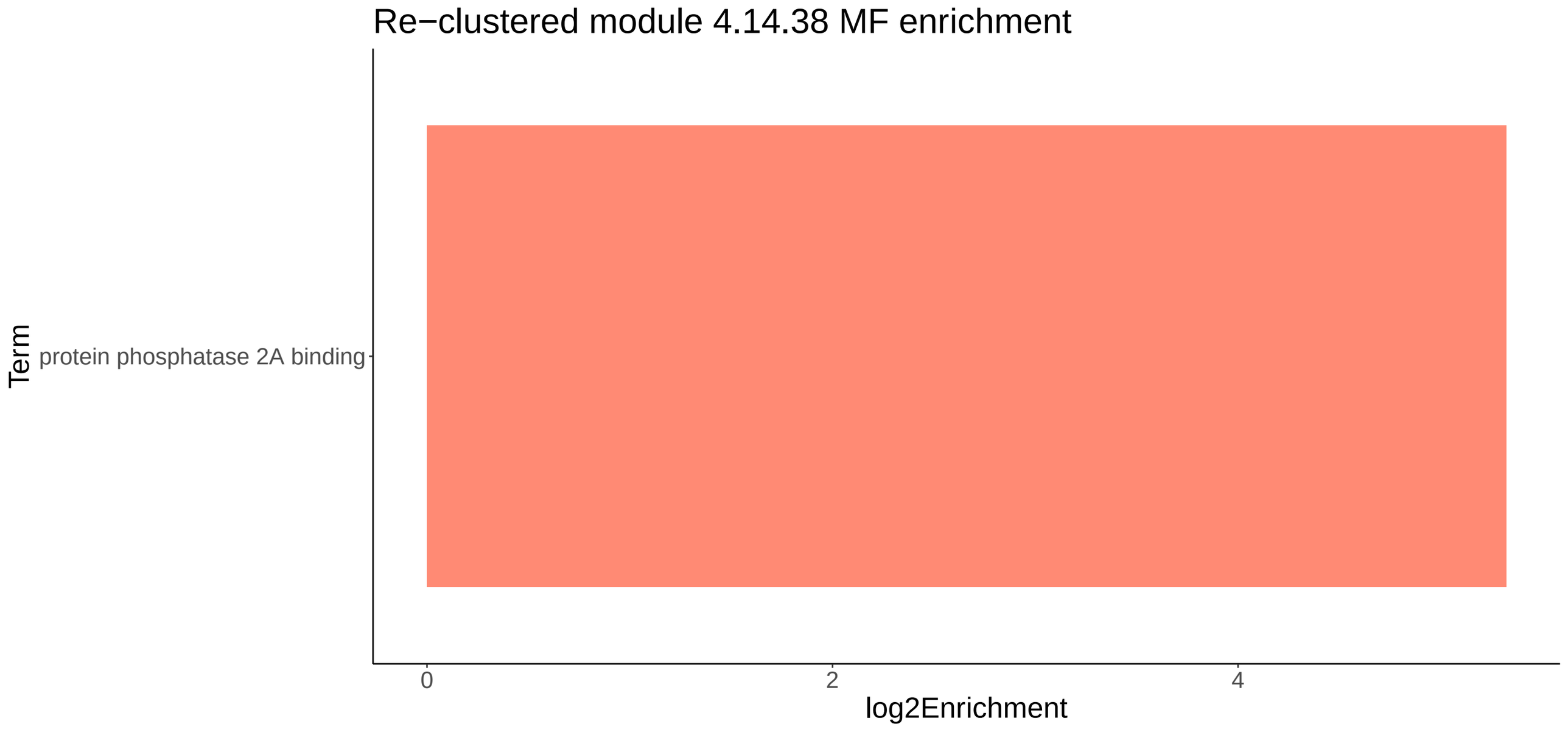

Re−clustered module 4.14.34 BP enrichment
ceramide catabolic process
cerebral cortex radially oriented cell migration
mannosylation
negative regulation of blood pressure
synaptic vesicle transport
oligosaccharide metabolic process
negative regulation of tumor necrosis factor production
positive regulation of regulated secretory pathway
calcium−ion regulated exocytosis
glycosphingolipid metabolic process
fatty acid beta−oxidation
regulation of synaptic vesicle exocytosis
synaptic vesicle recycling
water−soluble vitamin metabolic process
sensory perception of pain
protein glycosylation
neutrophil degranulation
Term
0
2
4
6
log2Enrichment

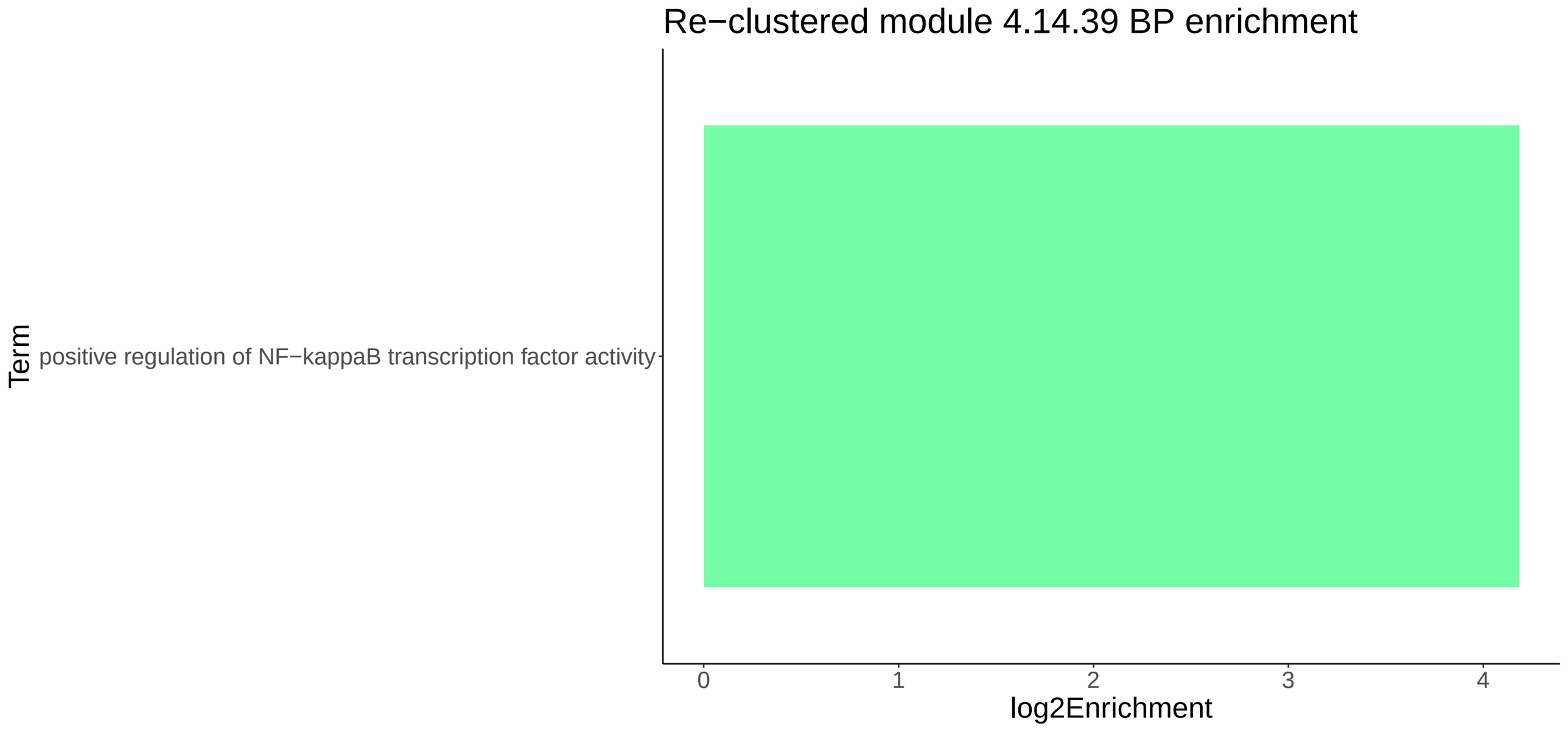

Re−clustered module 4.14.34 MF enrichment
Term
carboxypeptidase activity
monocarboxylic acid binding
hydrolase activity, hydrolyzing O−glycosyl compounds
acetyltransferase activity
0
1
2
3
4
5
log2Enrichment


Re−clustered module 4.14.36 BP enrichment
Term
cellular iron ion homeostasis
iron ion transport
pyruvate metabolic process
0
1
2
3
4
5
log2Enrichment

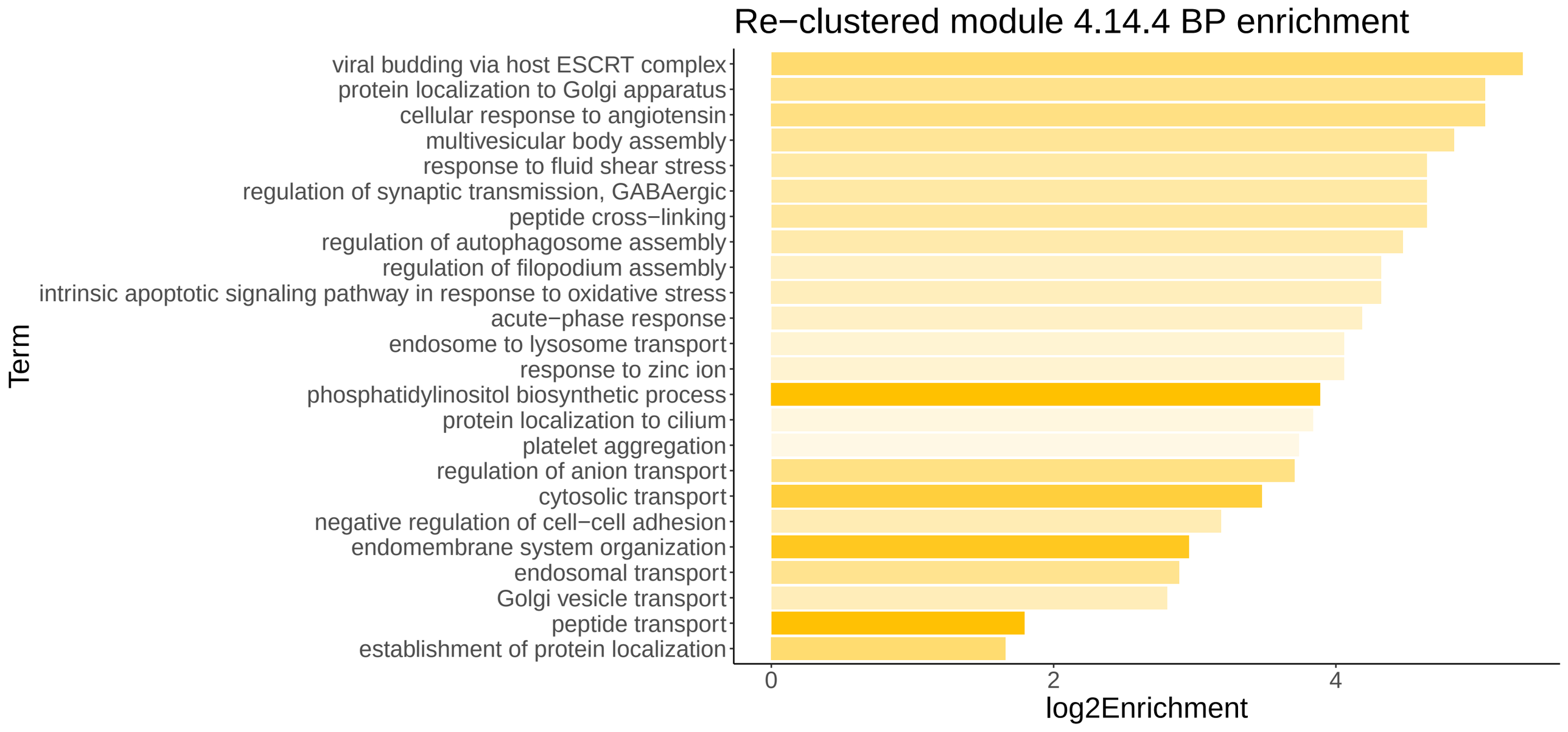

Re−clustered module 4.14.36 MF enrichment
transition metal ion transmembrane transporter activity
palmitoyltransferase activity
divalent inorganic cation transmembrane transporter activity
Term
0
2
4
6
log2Enrichment

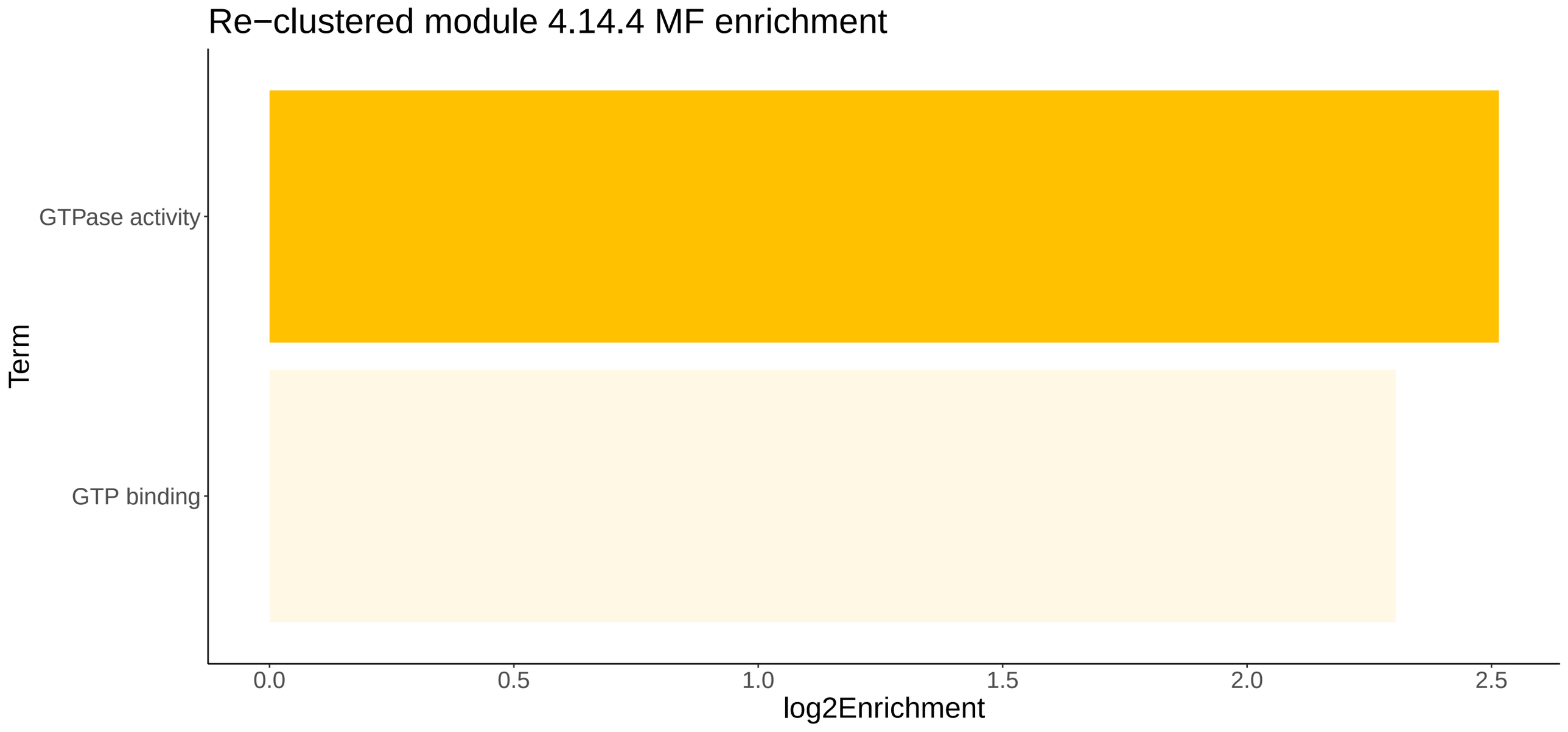

Re−clustered module 4.14.38 BP enrichment
positive regulation of p38MAPK cascade
positive regulation of toll−like receptor signaling pathway
regulation of toll−like receptor 4 signaling pathway
protein localization to cytoskeleton
regulation of phagocytosis
regulation of leukocyte activation
Term
0
2
4
log2Enrichment

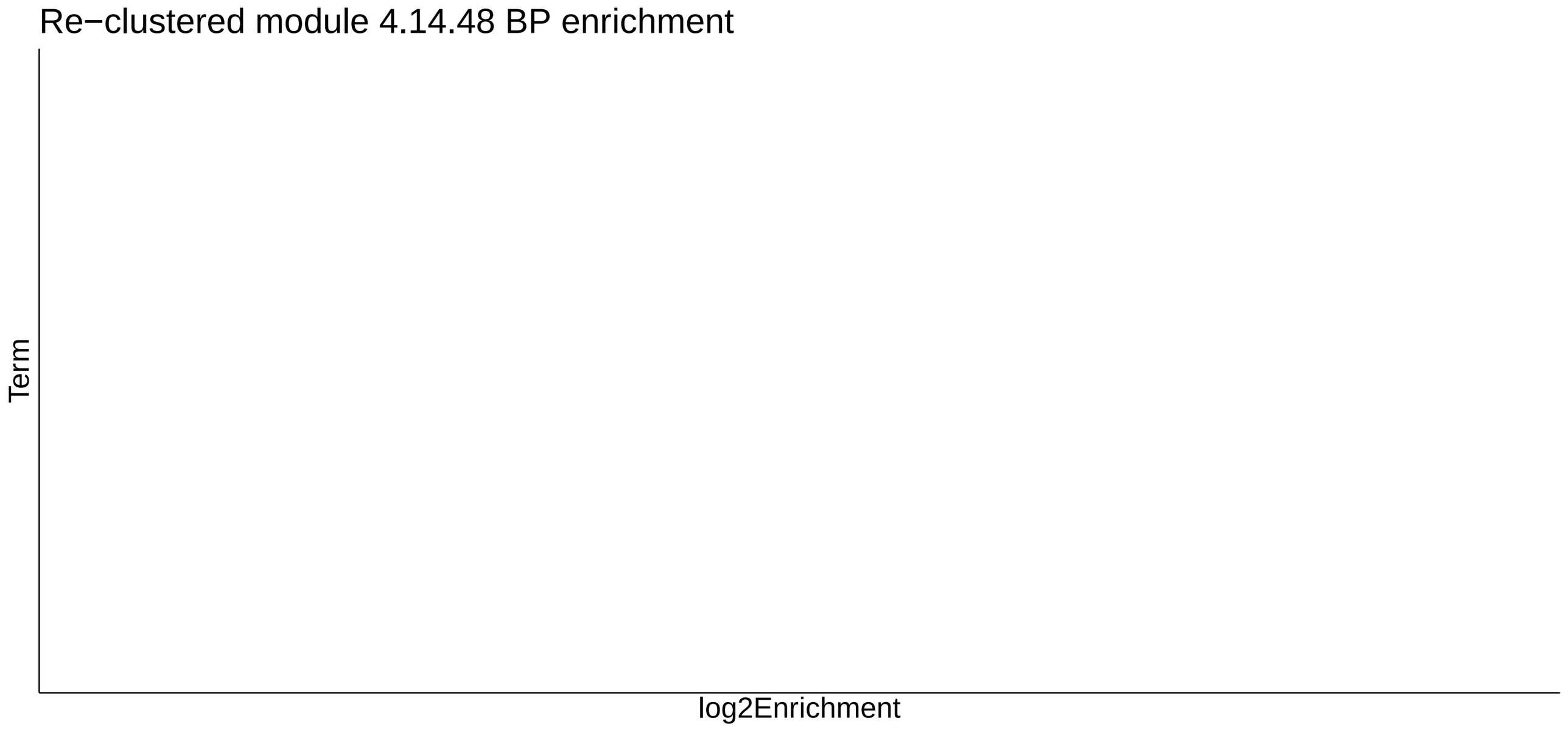

Re−clustered module 4.14.38 MF enrichment
Term
protein phosphatase 2A binding
0
2
4
log2Enrichment

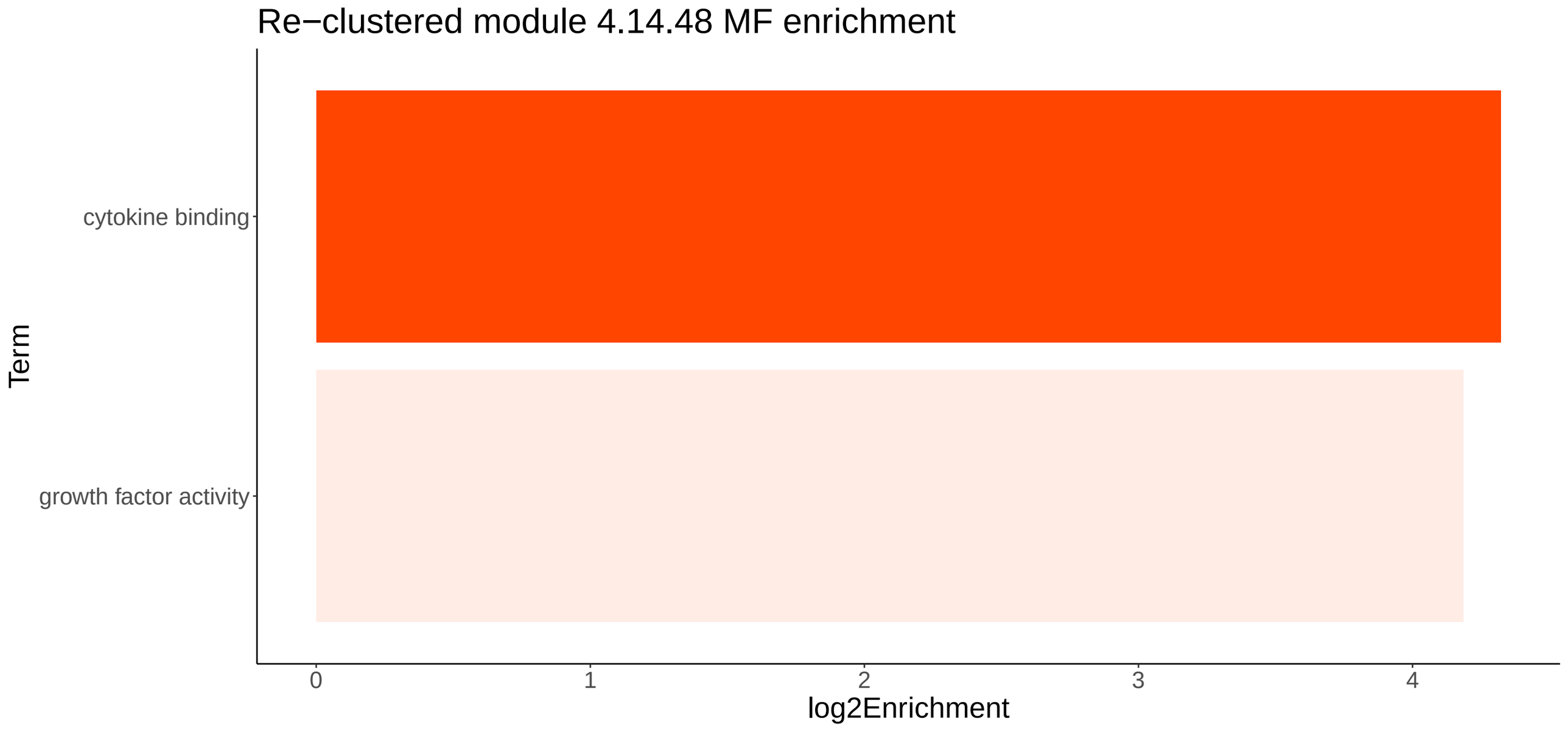

Re−clustered module 4.14.39 BP enrichment
Term
positive regulation of NF−kappaB transcription factor activity
0
1
2
3
4
log2Enrichment

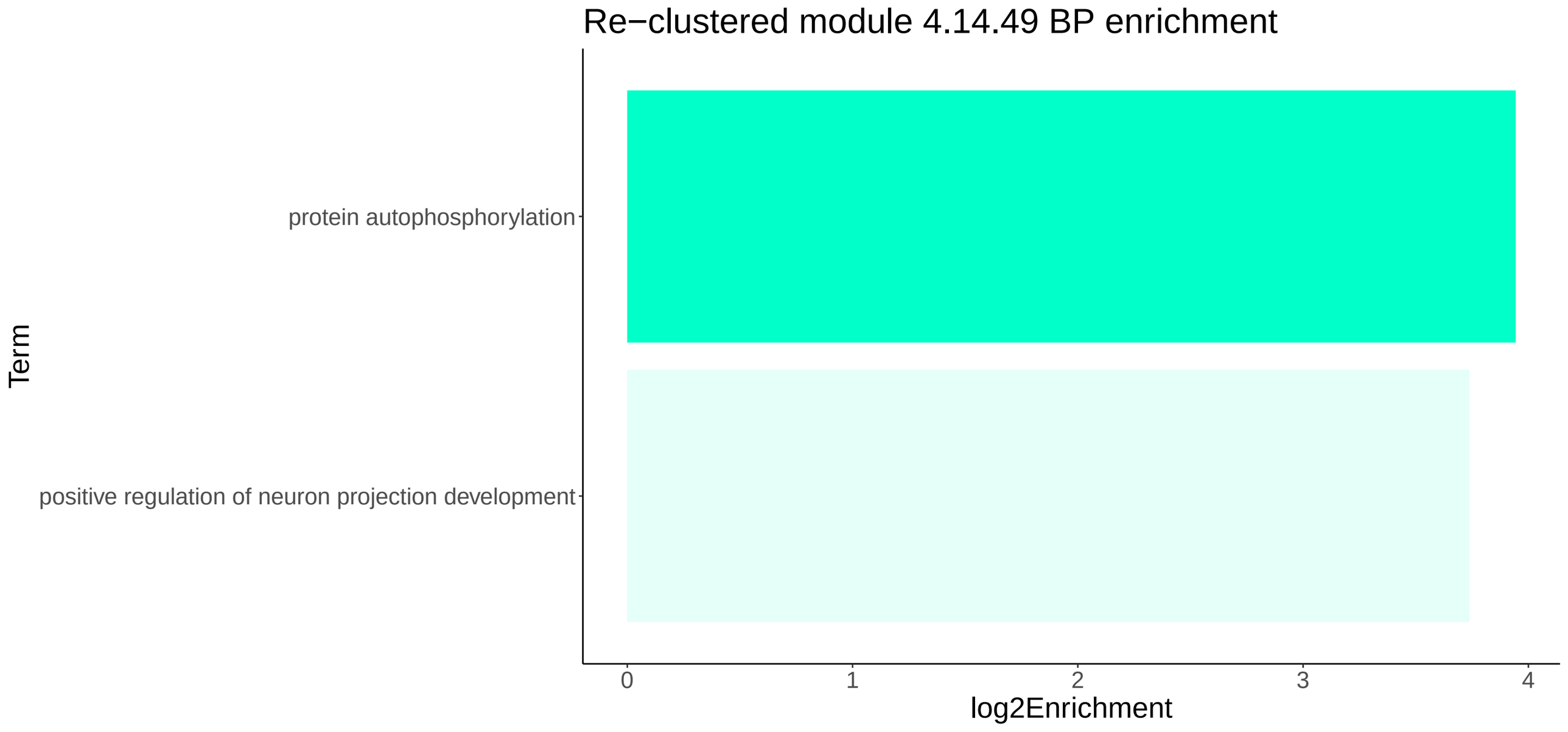

Re−clustered module 4.14.39 MF enrichment
Term
log2Enrichment

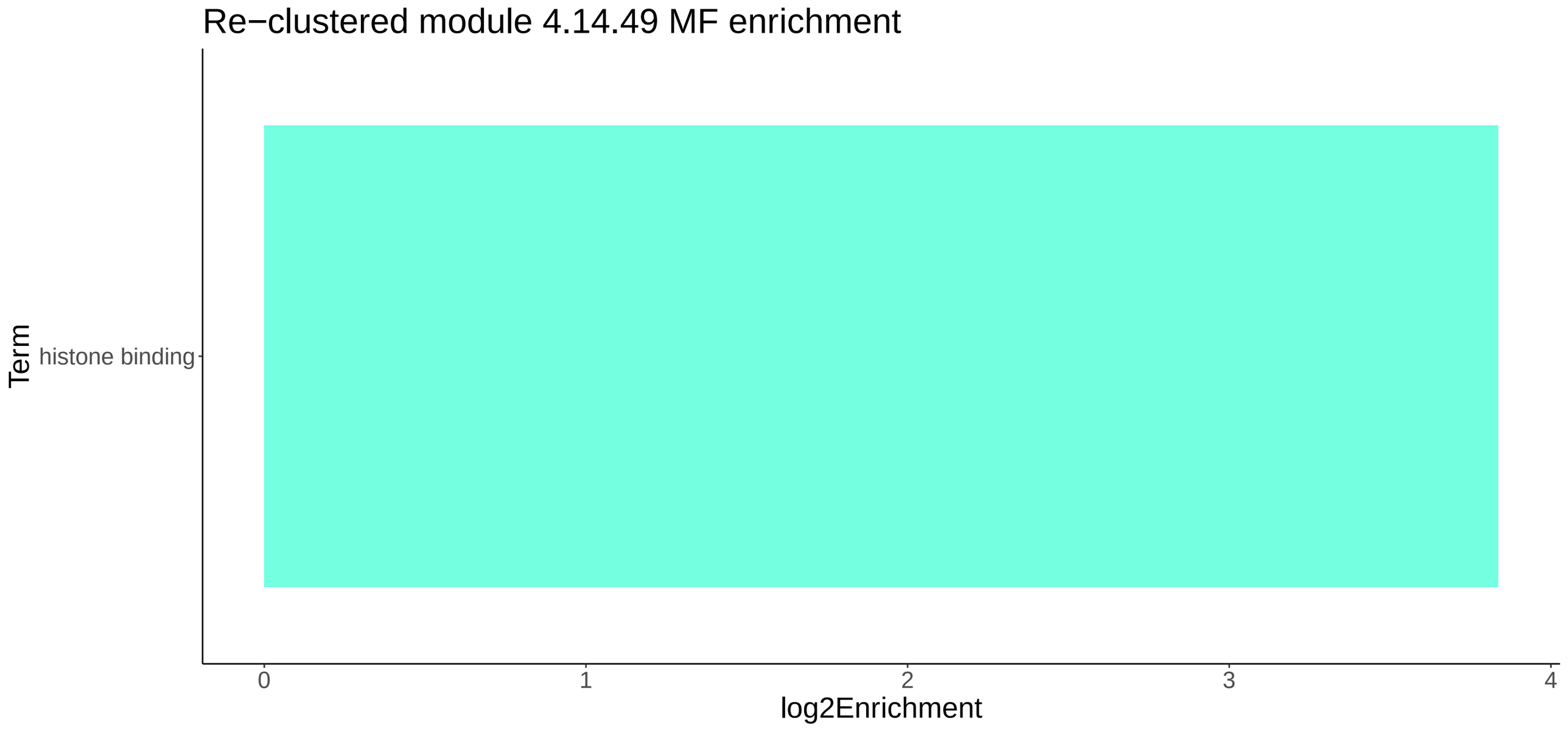

Re−clustered module 4.14.4 BP enrichment
viral budding via host ESCRT complex
protein localization to Golgi apparatus
cellular response to angiotensin
multivesicular body assembly
response to fluid shear stress
regulation of synaptic transmission, GABAergic
peptide cross−linking
regulation of autophagosome assembly
regulation of filopodium assembly
intrinsic apoptotic signaling pathway in response to oxidative stress
acute−phase response
endosome to lysosome transport
response to zinc ion
phosphatidylinositol biosynthetic process
protein localization to cilium
platelet aggregation
regulation of anion transport
cytosolic transport
negative regulation of cell−cell adhesion
endomembrane system organization
endosomal transport
Golgi vesicle transport
peptide transport
establishment of protein localization
Term
0
2
4
log2Enrichment

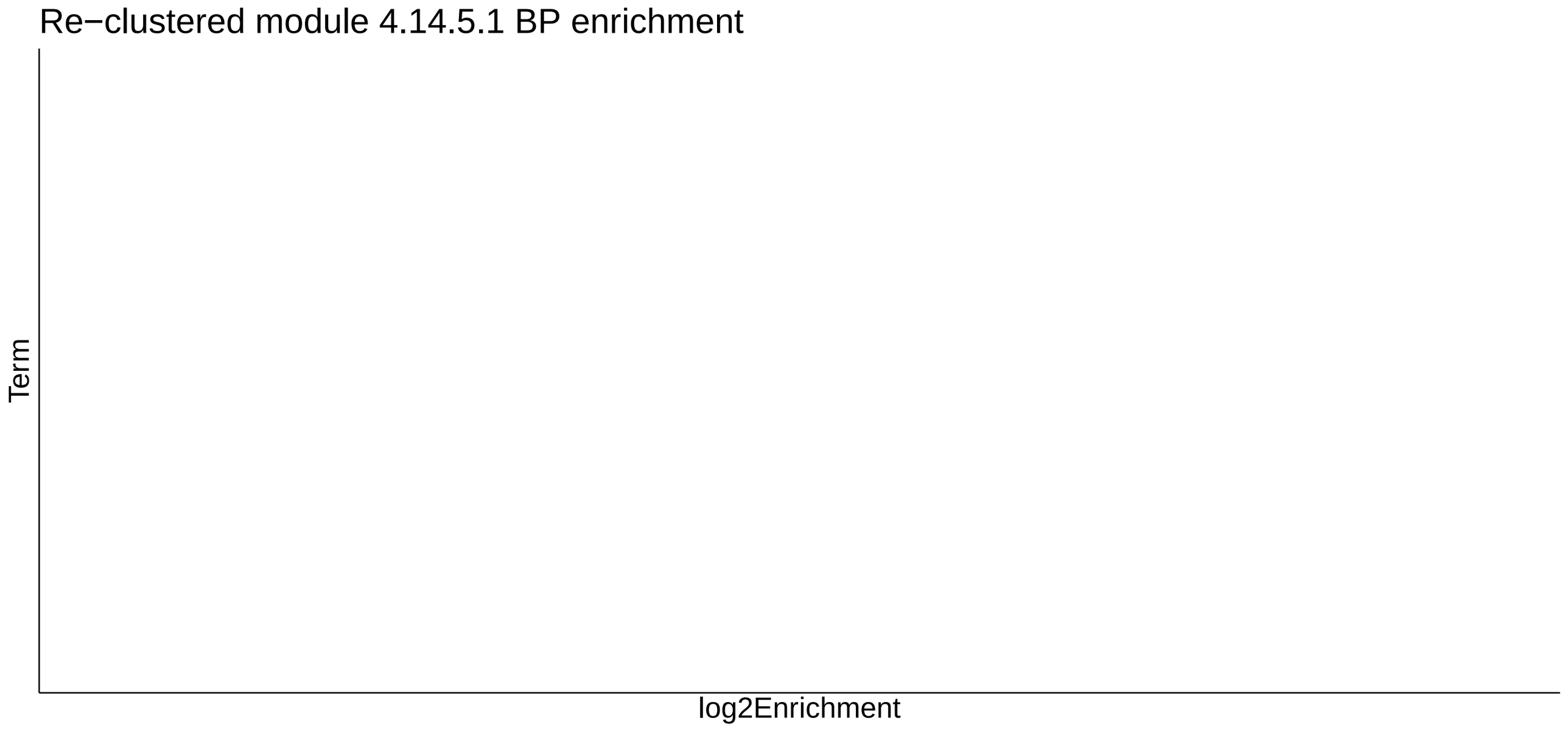

Re−clustered module 4.14.4 MF enrichment
Term
GTPase activity
GTP binding
0.0
0.5
1.0
1.5
2.0
2.5
log2Enrichment

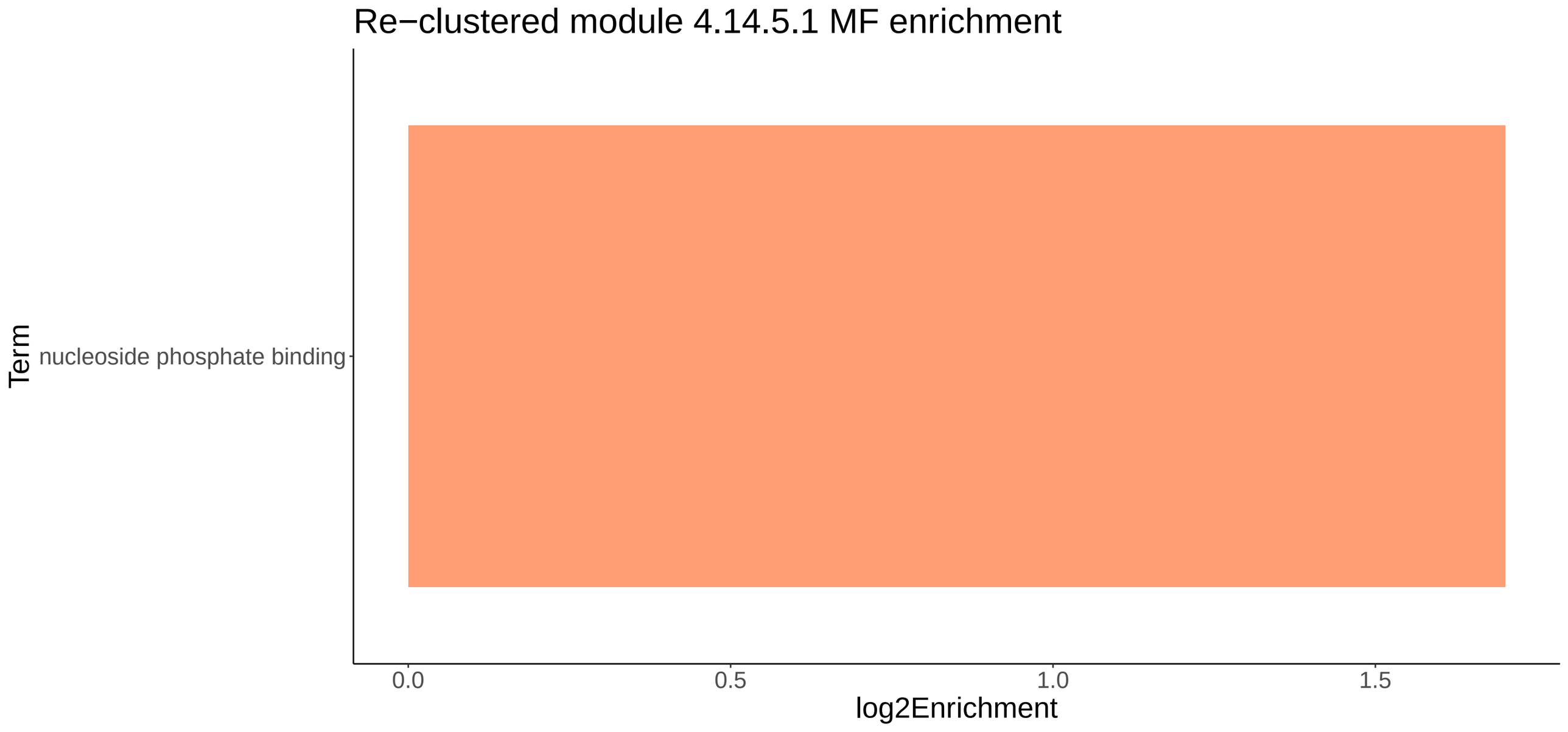

Re−clustered module 4.14.48 BP enrichment
Term
log2Enrichment

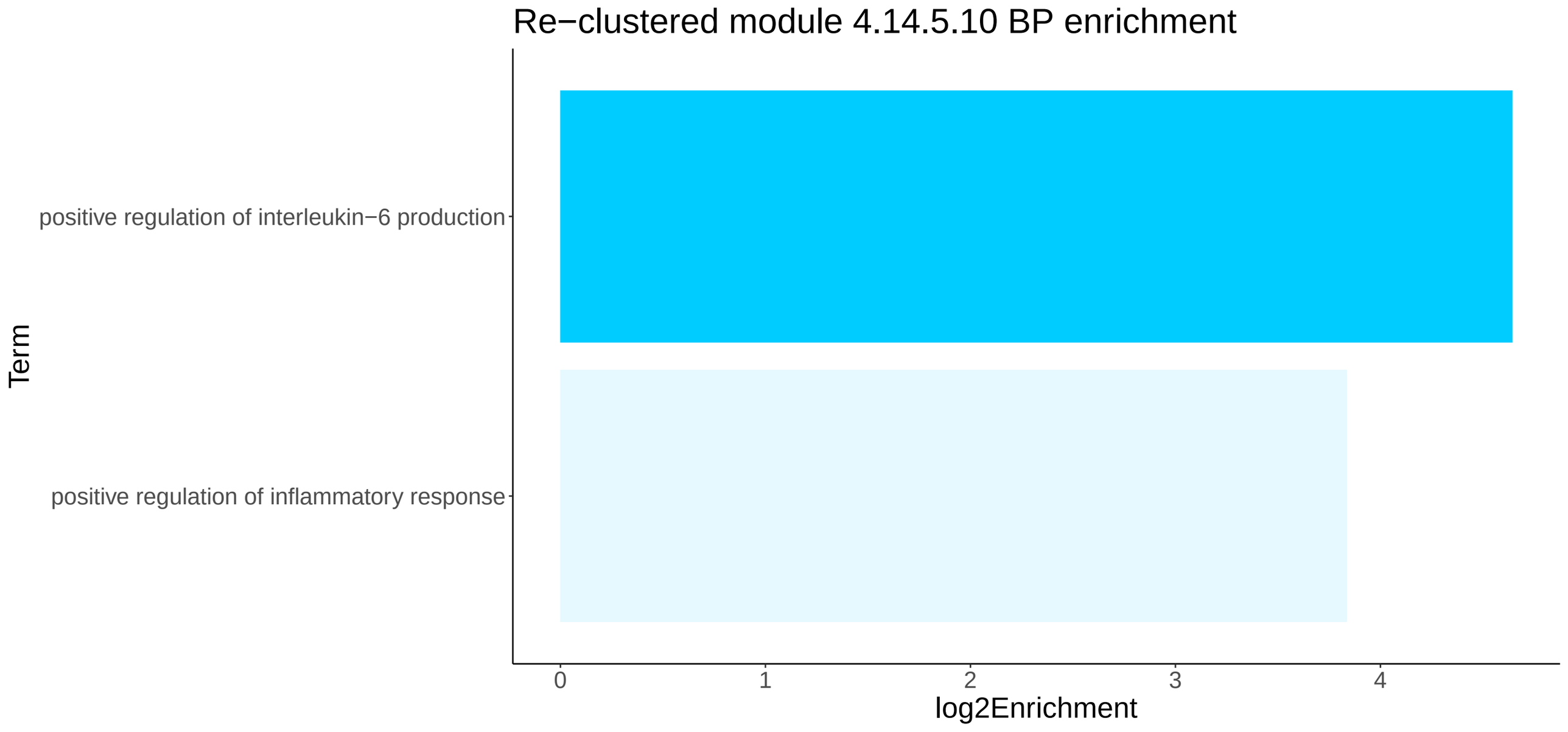

Re−clustered module 4.14.48 MF enrichment
Term
cytokine binding
growth factor activity
0
1
2
3
4
log2Enrichment

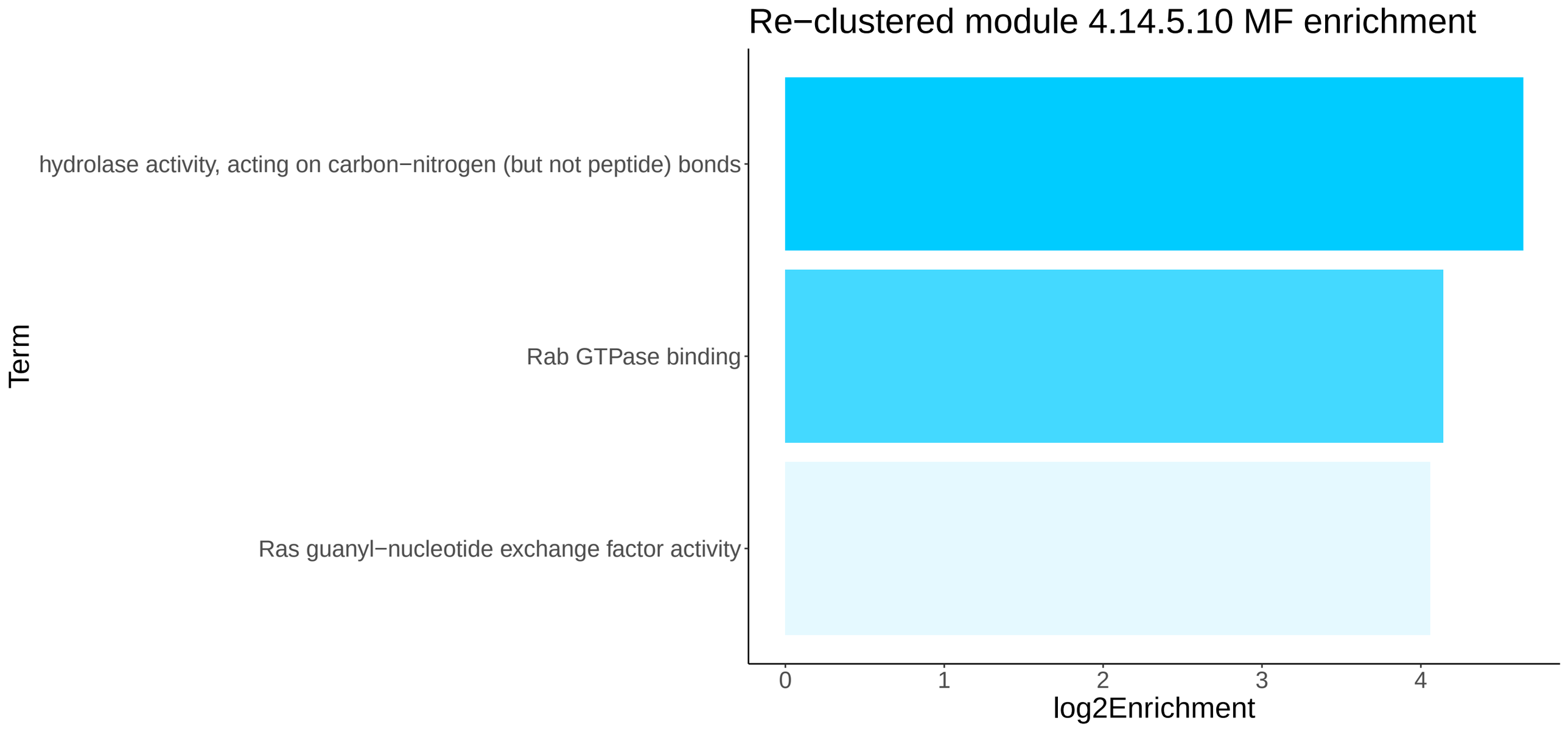

Re−clustered module 4.14.49 BP enrichment
Term
protein autophosphorylation
positive regulation of neuron projection development
0
1
2
3
4
log2Enrichment

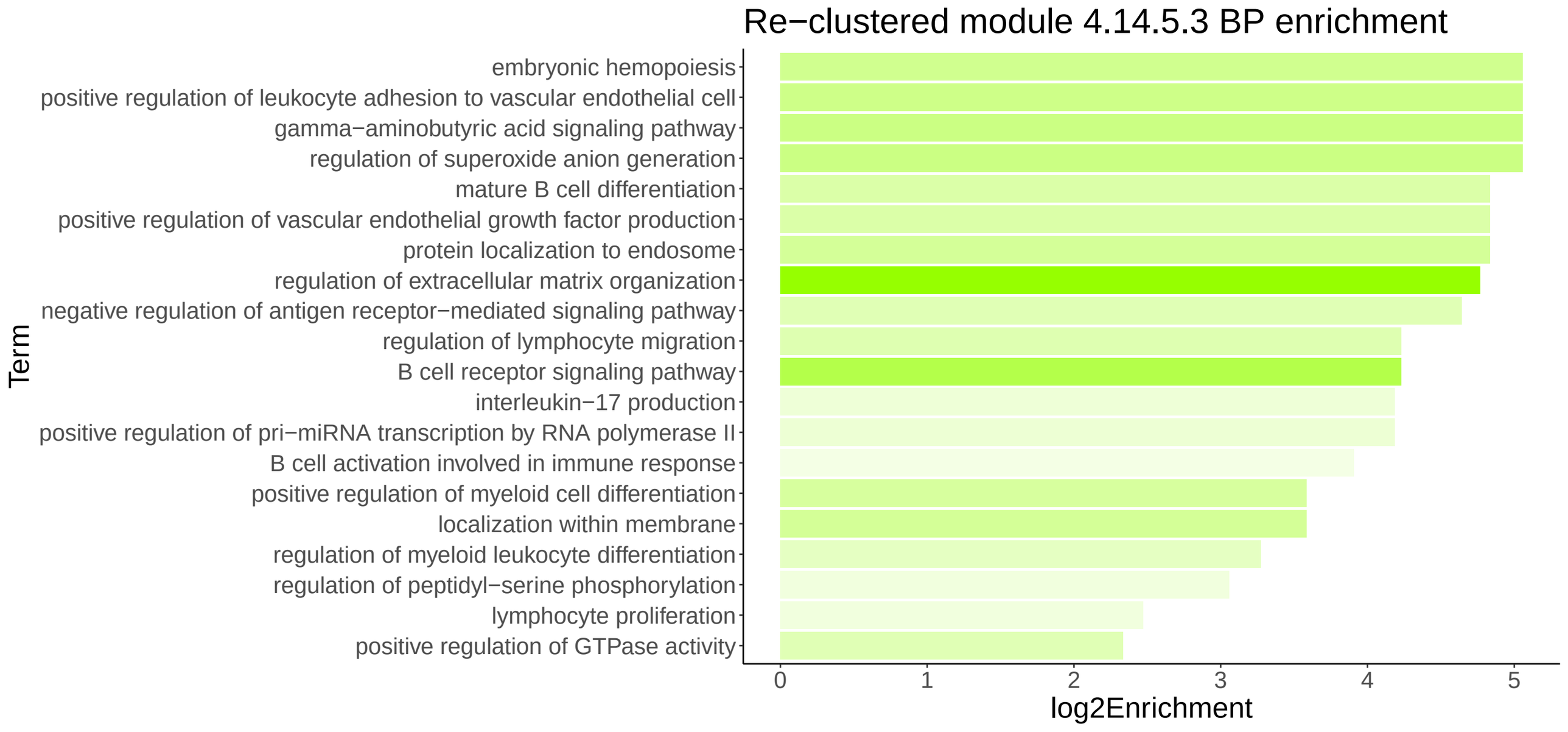

Re−clustered module 4.14.49 MF enrichment
Term
histone binding
0
1
2
3
4
log2Enrichment

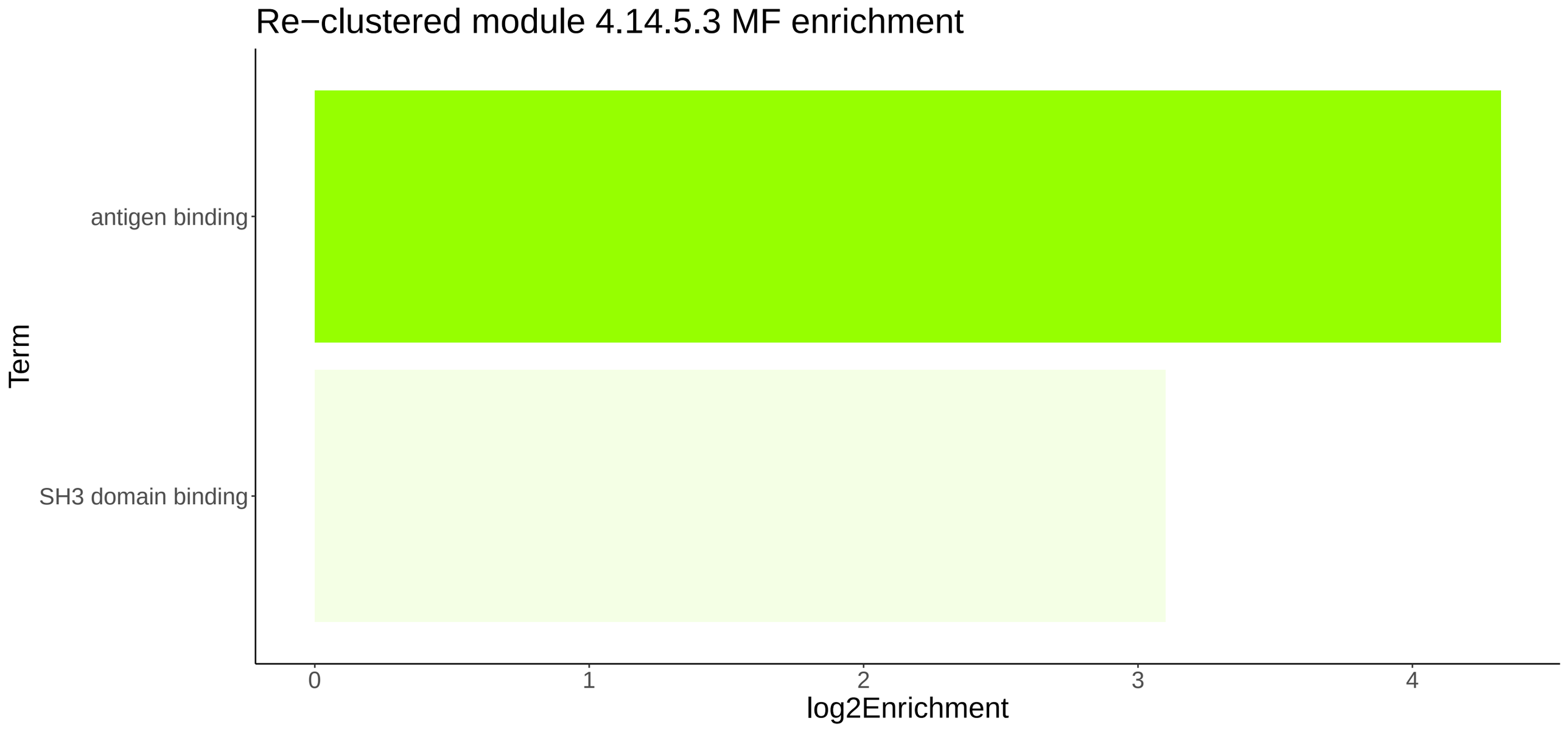

Re−clustered module 4.14.5.1 BP enrichment
Term
log2Enrichment

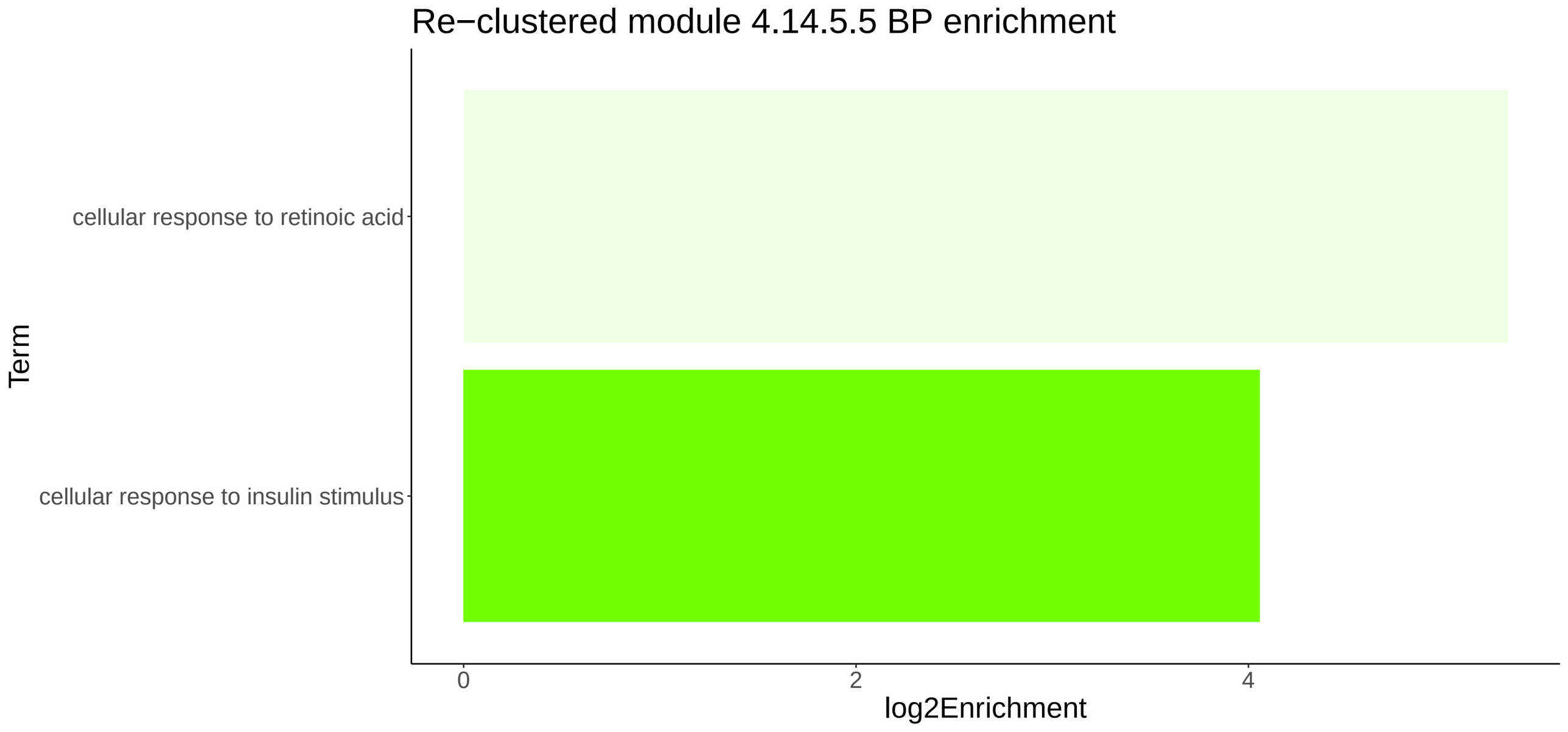

Re−clustered module 4.14.5.1 MF enrichment
Term
nucleoside phosphate binding
0.0
0.5
1.0
1.5
log2Enrichment

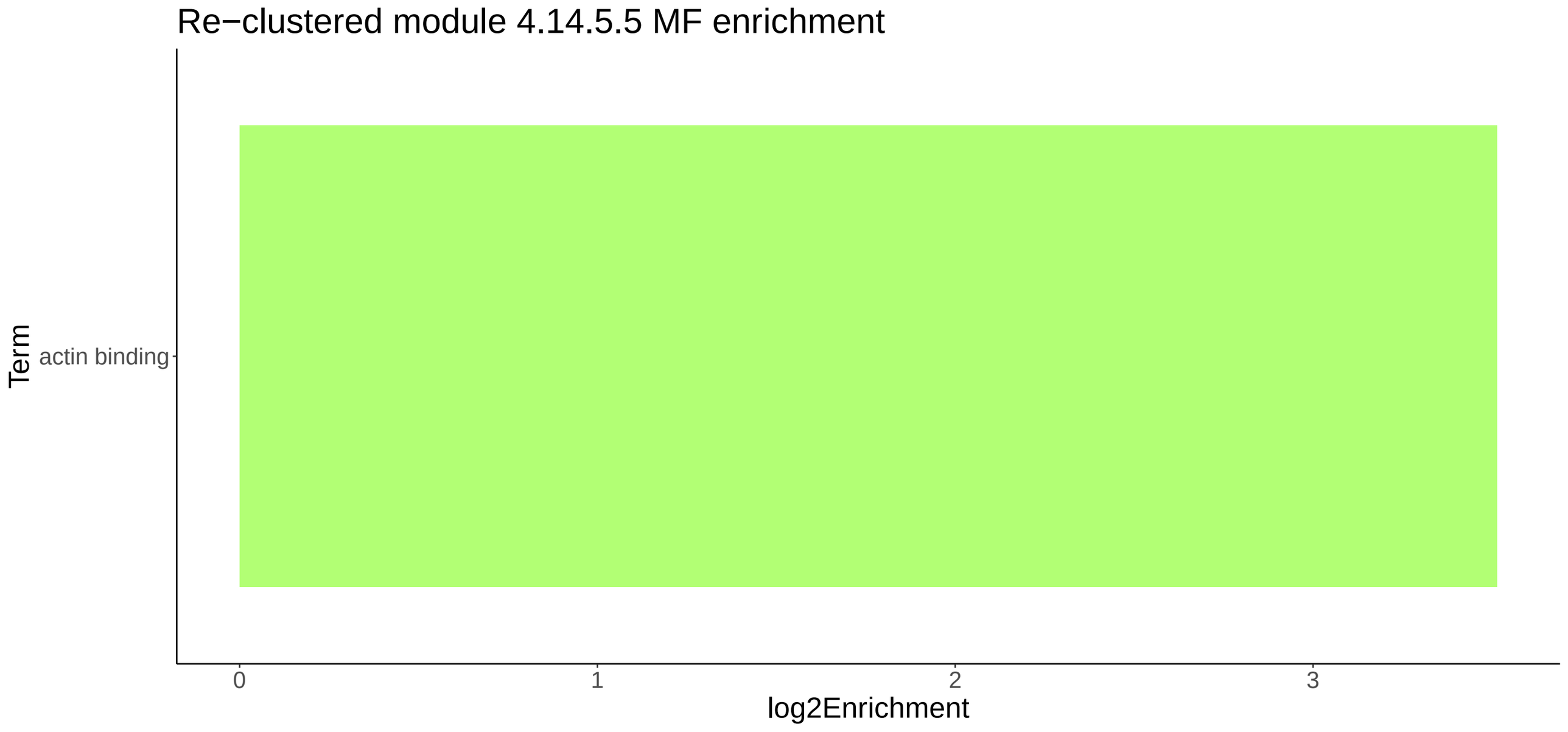

Re−clustered module 4.14.5.10 BP enrichment
positive regulation of interleukin−6 production
positive regulation of inflammatory response
Term
0
1
2
3
4
log2Enrichment

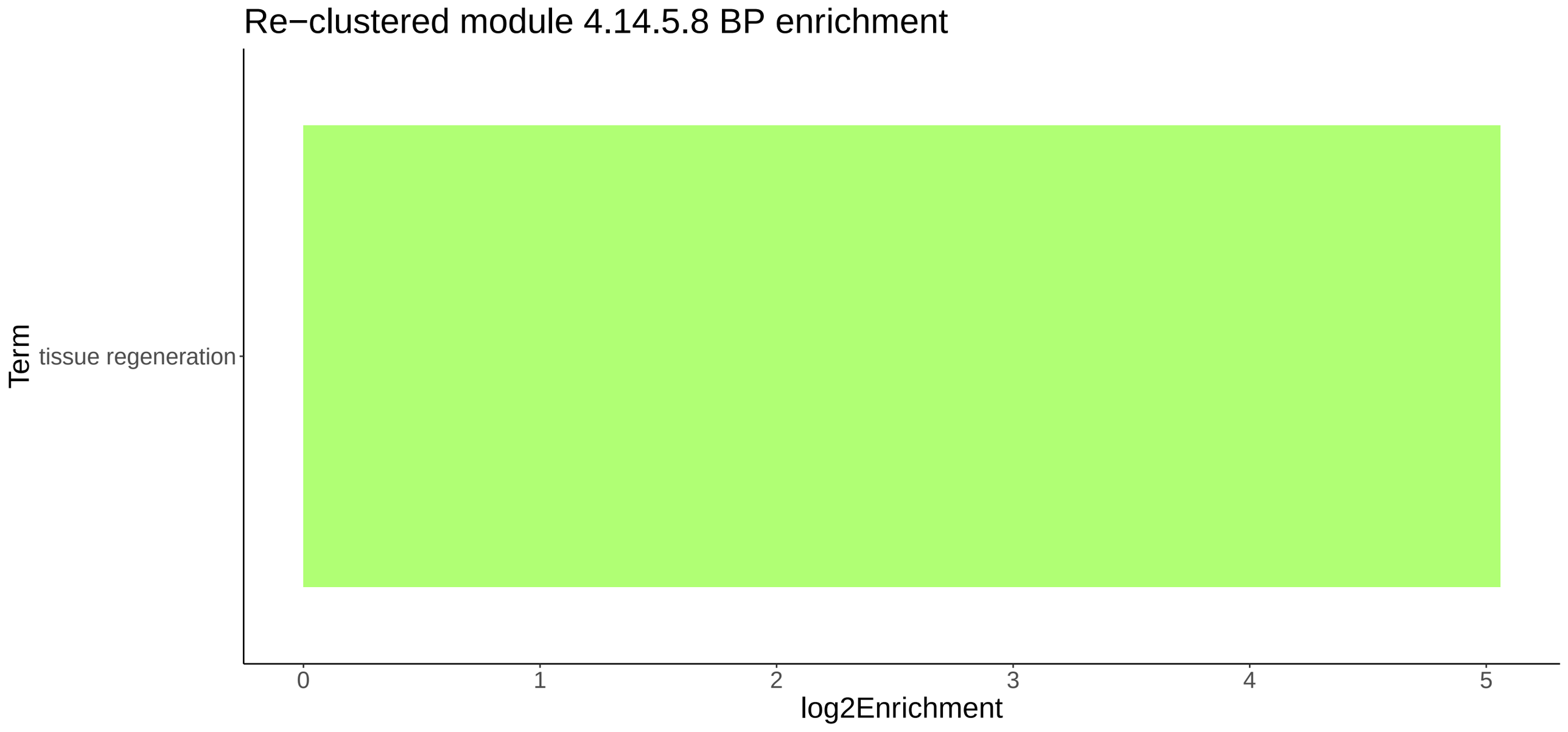

Re−clustered module 4.14.5.10 MF enrichment
Term
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
Rab GTPase binding
Ras guanyl−nucleotide exchange factor activity
0
1
2
3
4
log2Enrichment

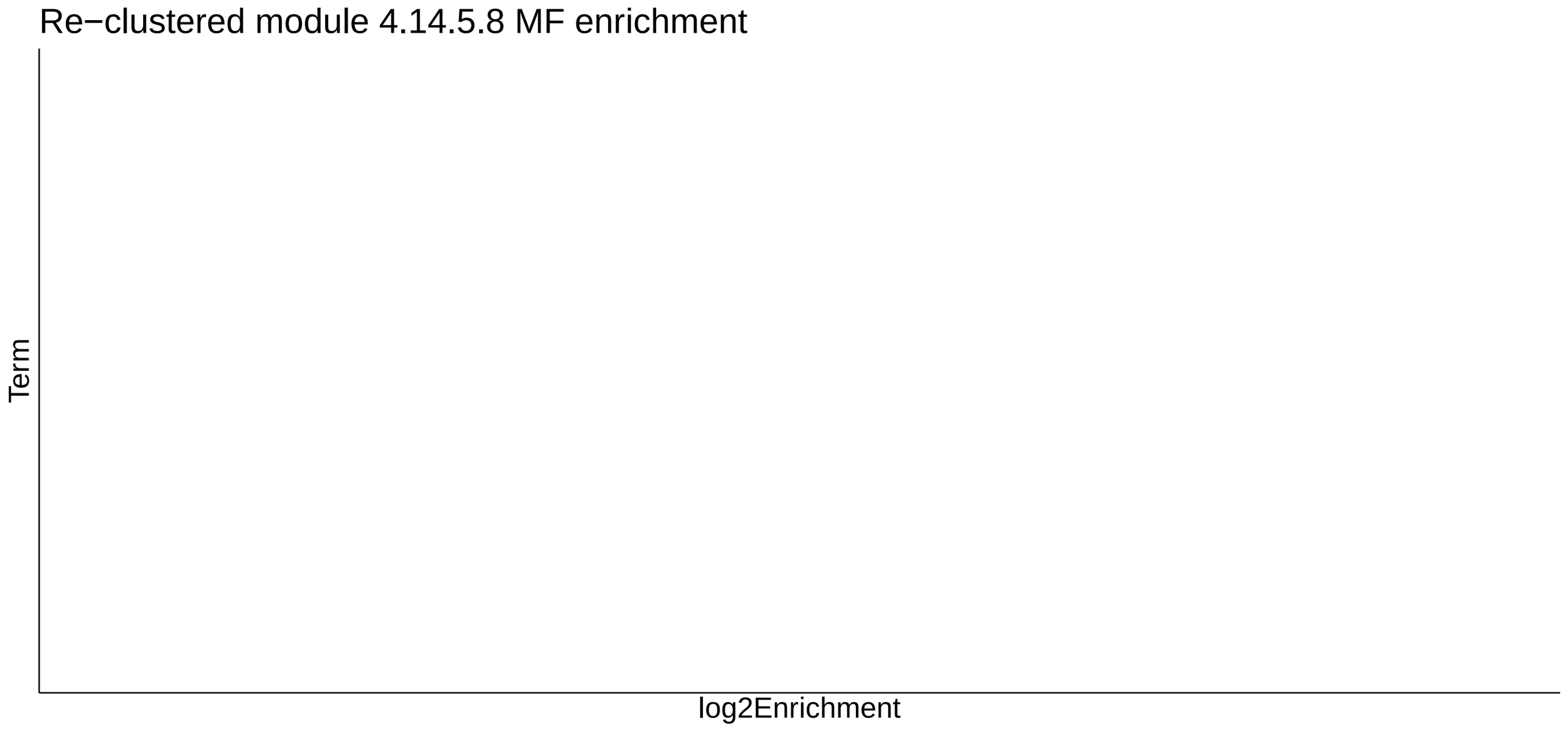

Re−clustered module 4.14.5.3 BP enrichment
Term
embryonic hemopoiesis
positive regulation of leukocyte adhesion to vascular endothelial cell
gamma−aminobutyric acid signaling pathway
regulation of superoxide anion generation
mature B cell differentiation
positive regulation of vascular endothelial growth factor production
protein localization to endosome
regulation of extracellular matrix organization
negative regulation of antigen receptor−mediated signaling pathway
regulation of lymphocyte migration
B cell receptor signaling pathway
interleukin−17 production
positive regulation of pri−miRNA transcription by RNA polymerase II
B cell activation involved in immune response
positive regulation of myeloid cell differentiation
localization within membrane
regulation of myeloid leukocyte differentiation
regulation of peptidyl−serine phosphorylation
lymphocyte proliferation
positive regulation of GTPase activity
0
1
2
3
4
5
log2Enrichment

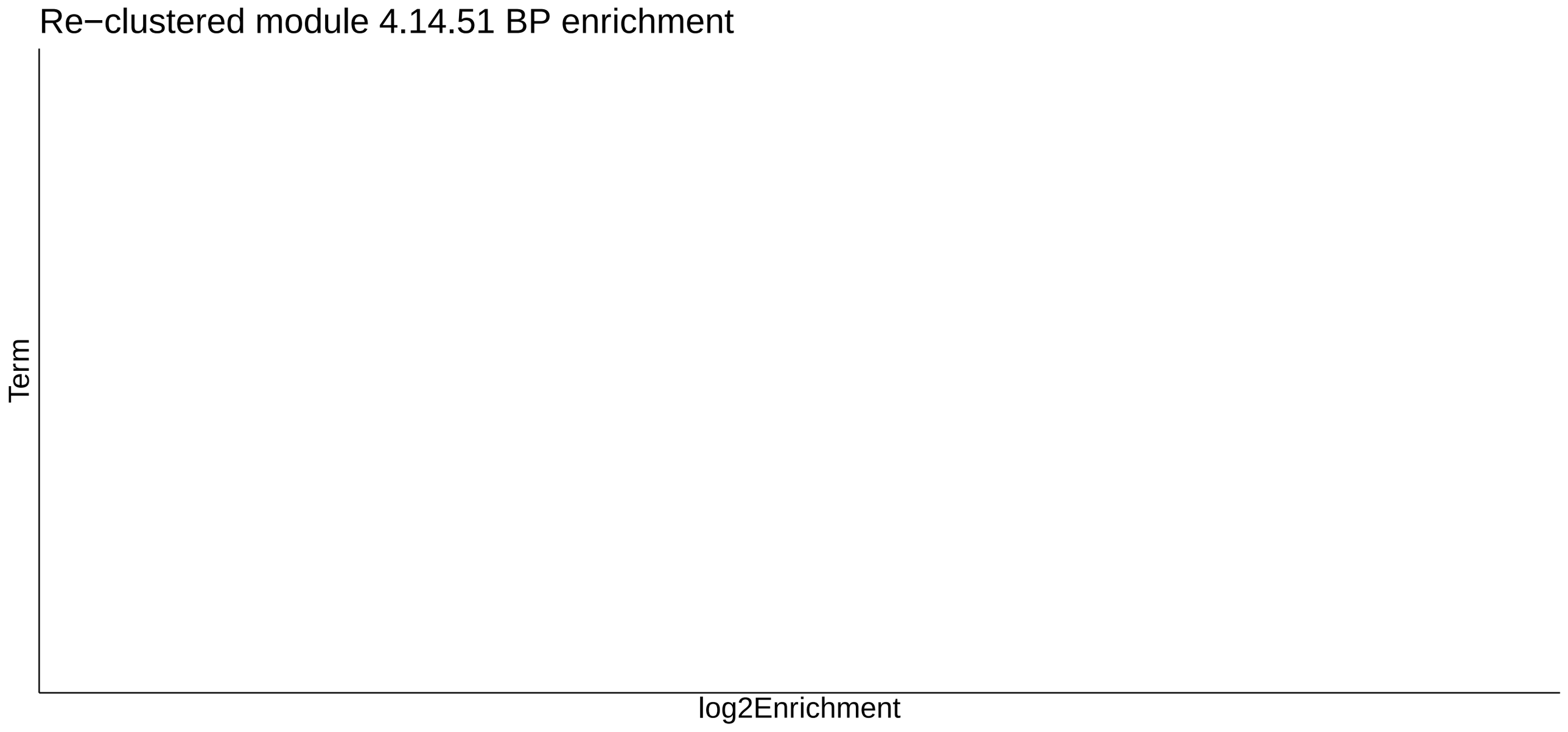

Re−clustered module 4.14.5.3 MF enrichment
Term
antigen binding
SH3 domain binding
0
1
2
3
4
log2Enrichment


Re−clustered module 4.14.5.5 BP enrichment
Term
cellular response to retinoic acid
cellular response to insulin stimulus
0
2
4
log2Enrichment

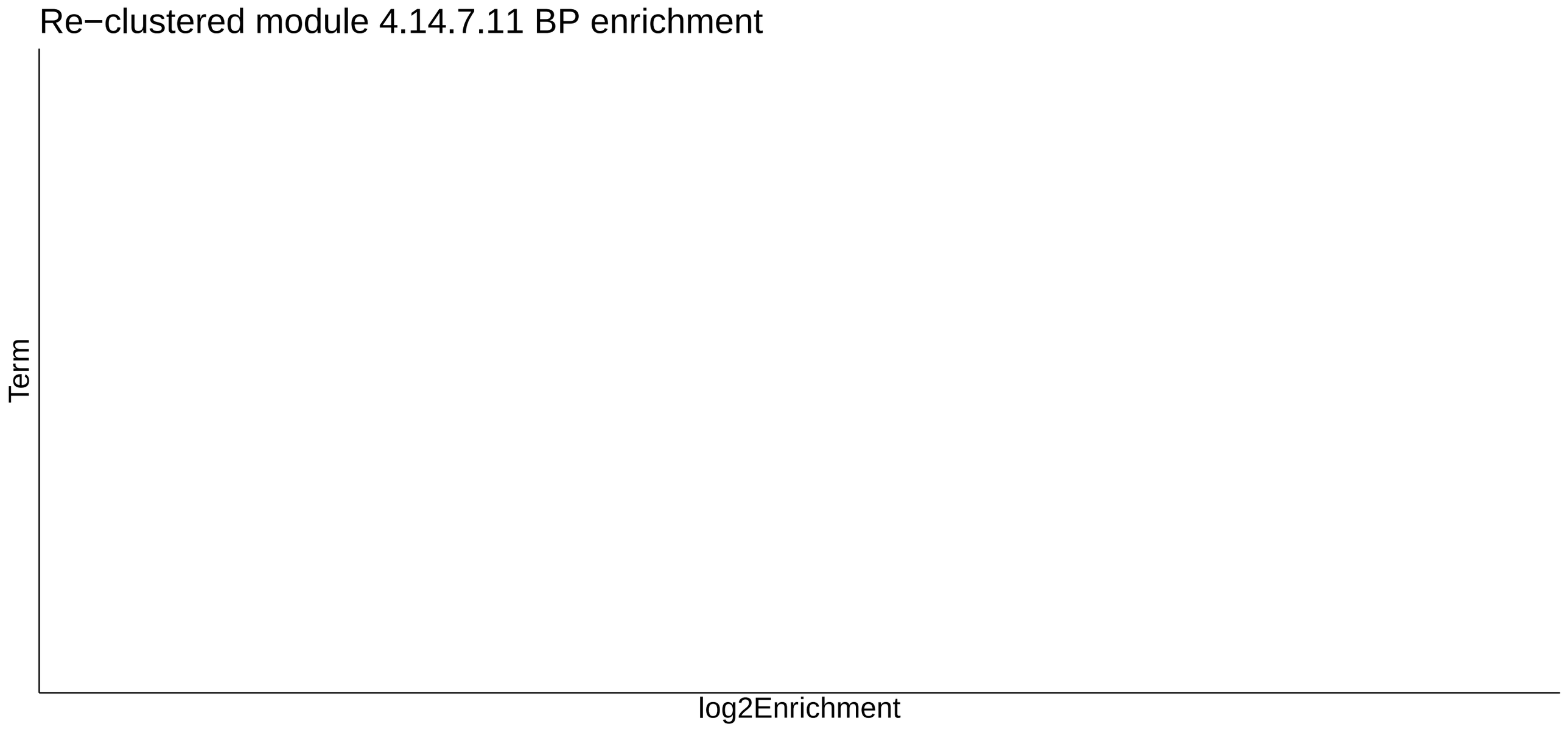

Re−clustered module 4.14.5.5 MF enrichment
Term
actin binding
0
1
2
3
log2Enrichment

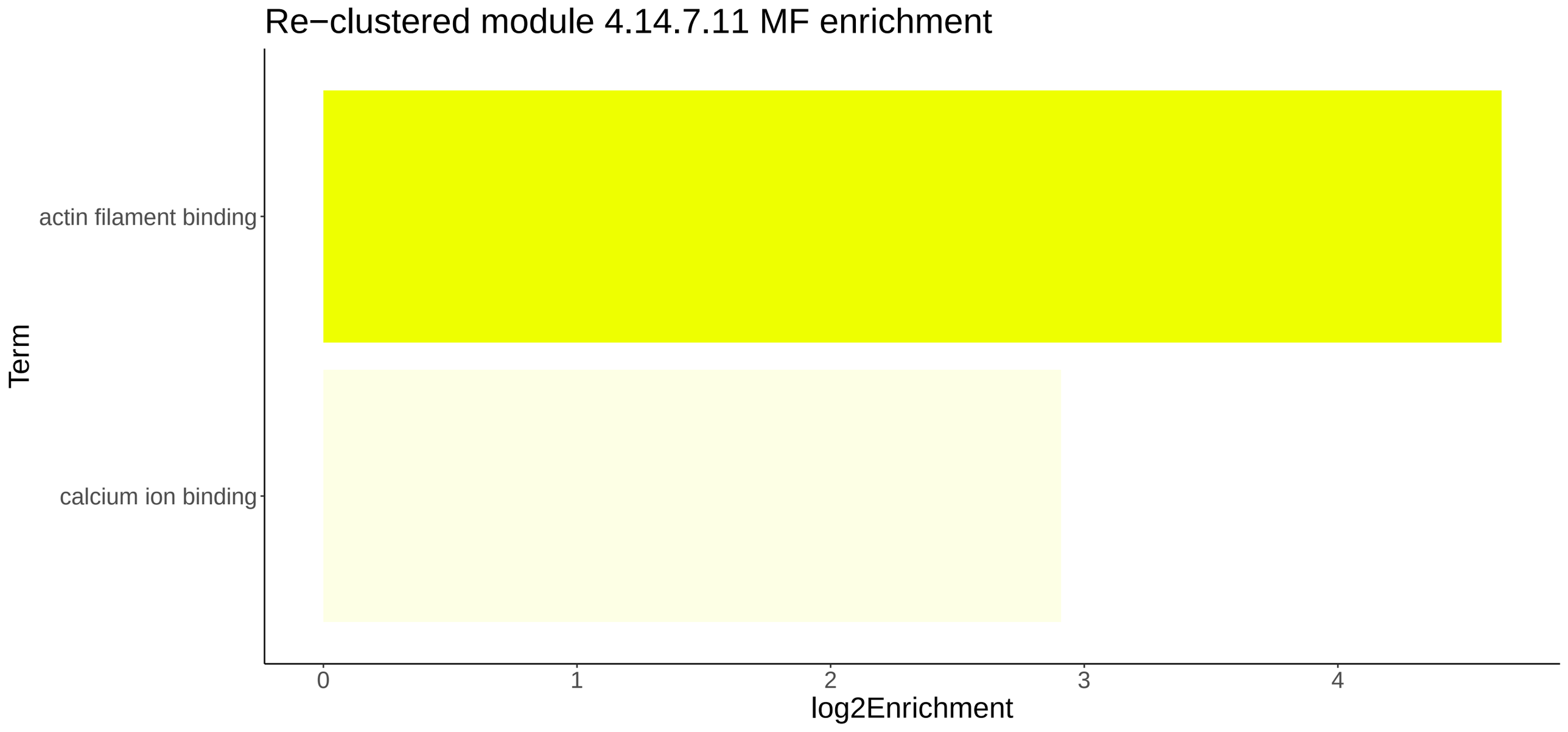

Re−clustered module 4.14.5.8 BP enrichment
Term
tissue regeneration
0
1
2
3
4
5
log2Enrichment

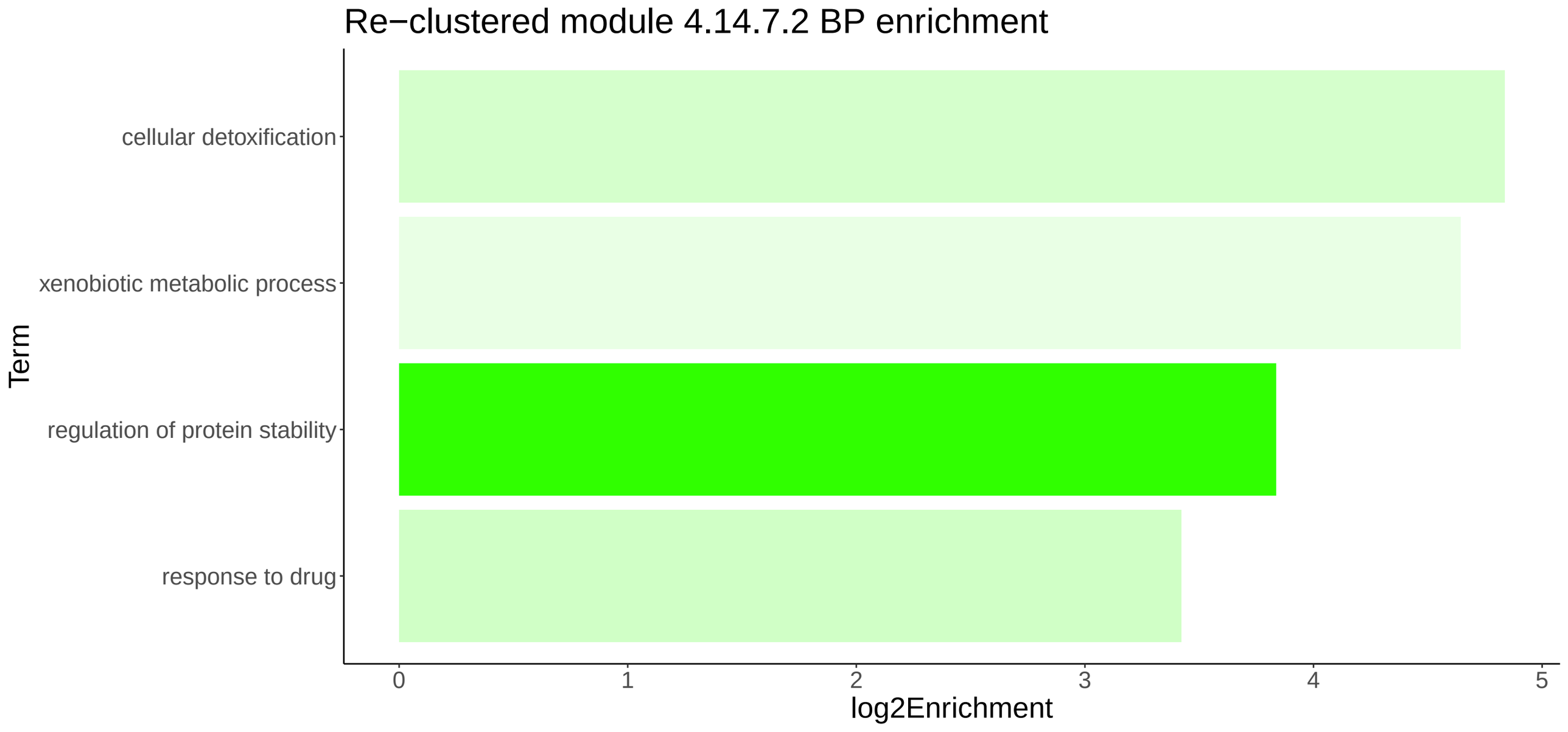

Re−clustered module 4.14.5.8 MF enrichment
Term
log2Enrichment

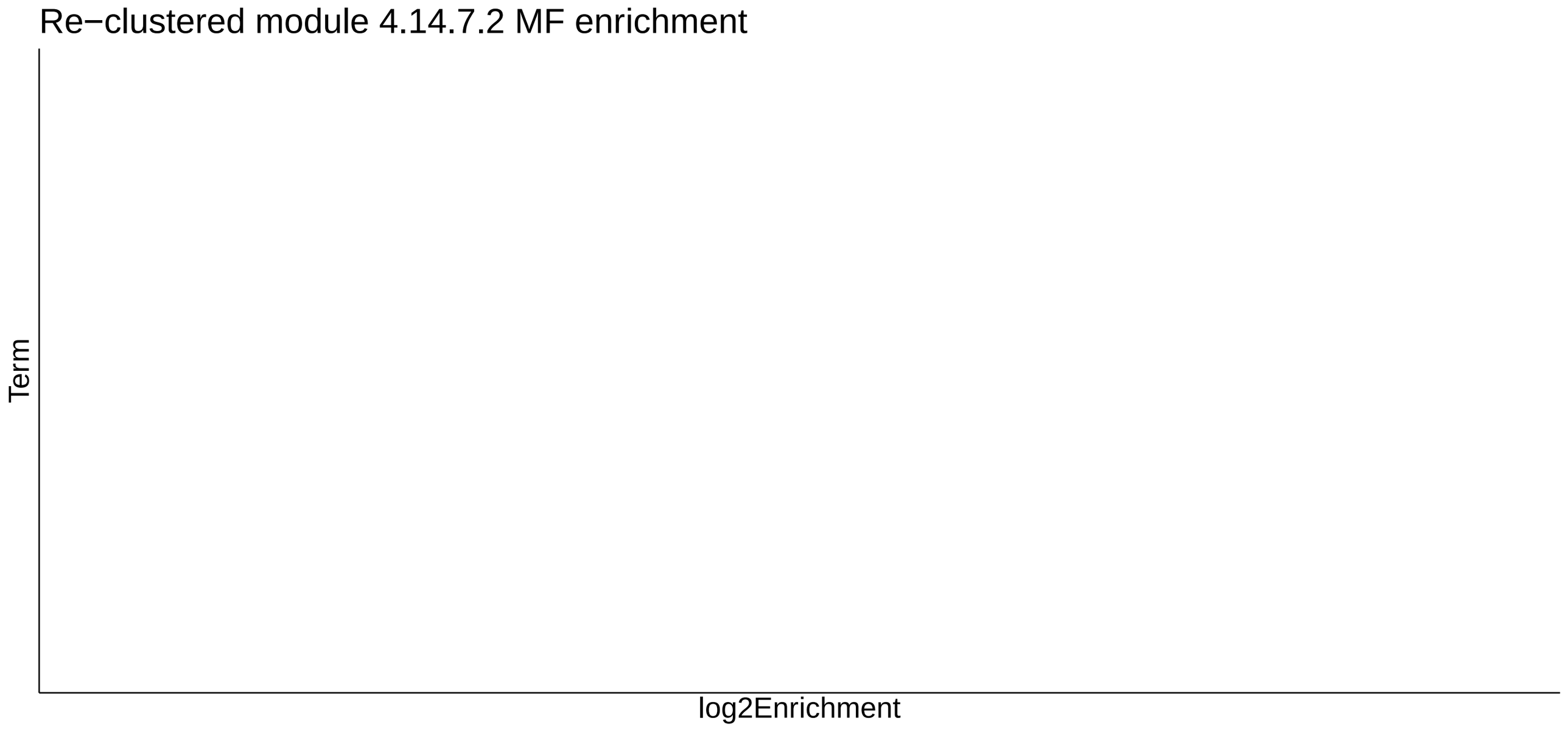

Re−clustered module 4.14.51 BP enrichment
Term
log2Enrichment

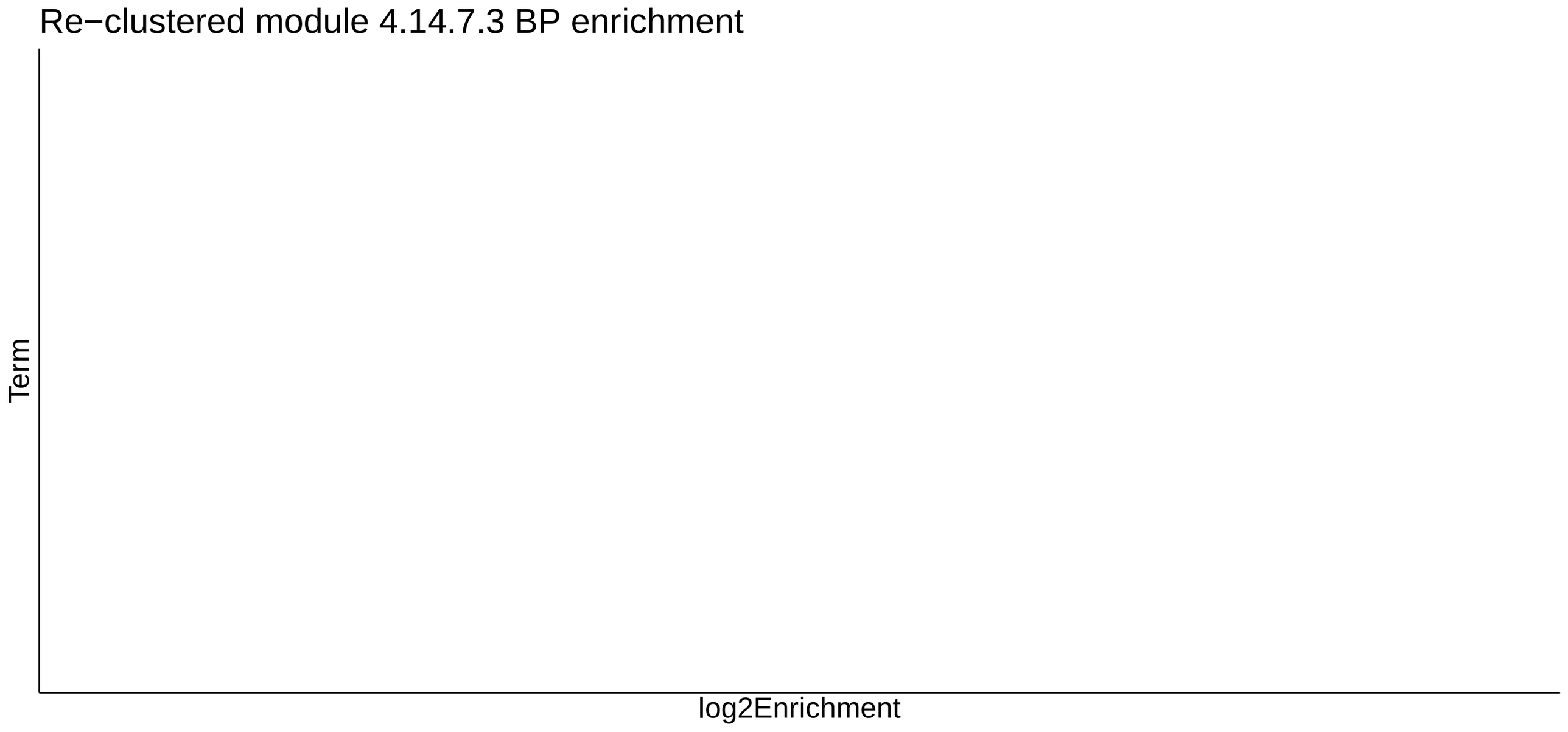

Re−clustered module 4.14.51 MF enrichment
Term
log2Enrichment

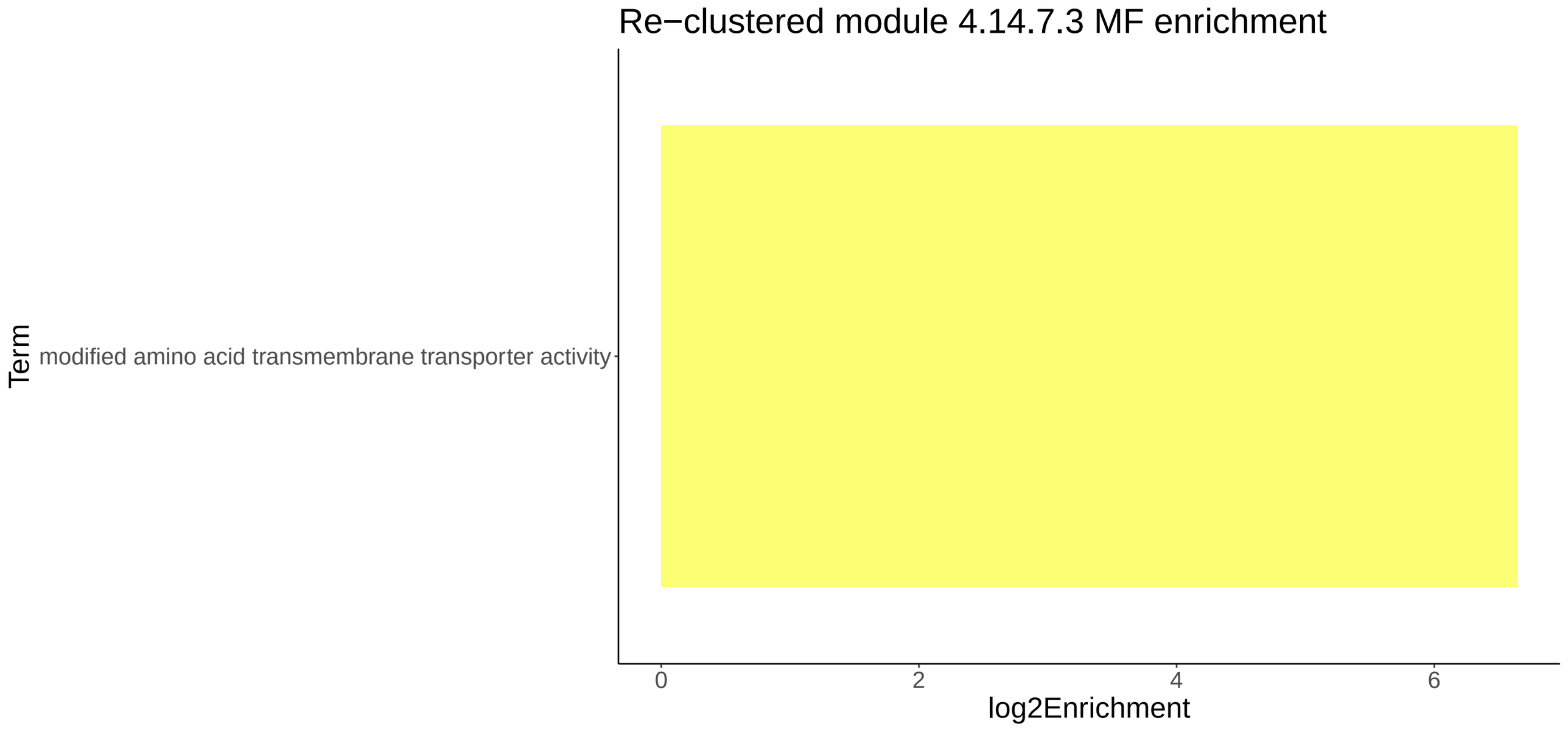

Re−clustered module 4.14.7.11 BP enrichment
Term
log2Enrichment

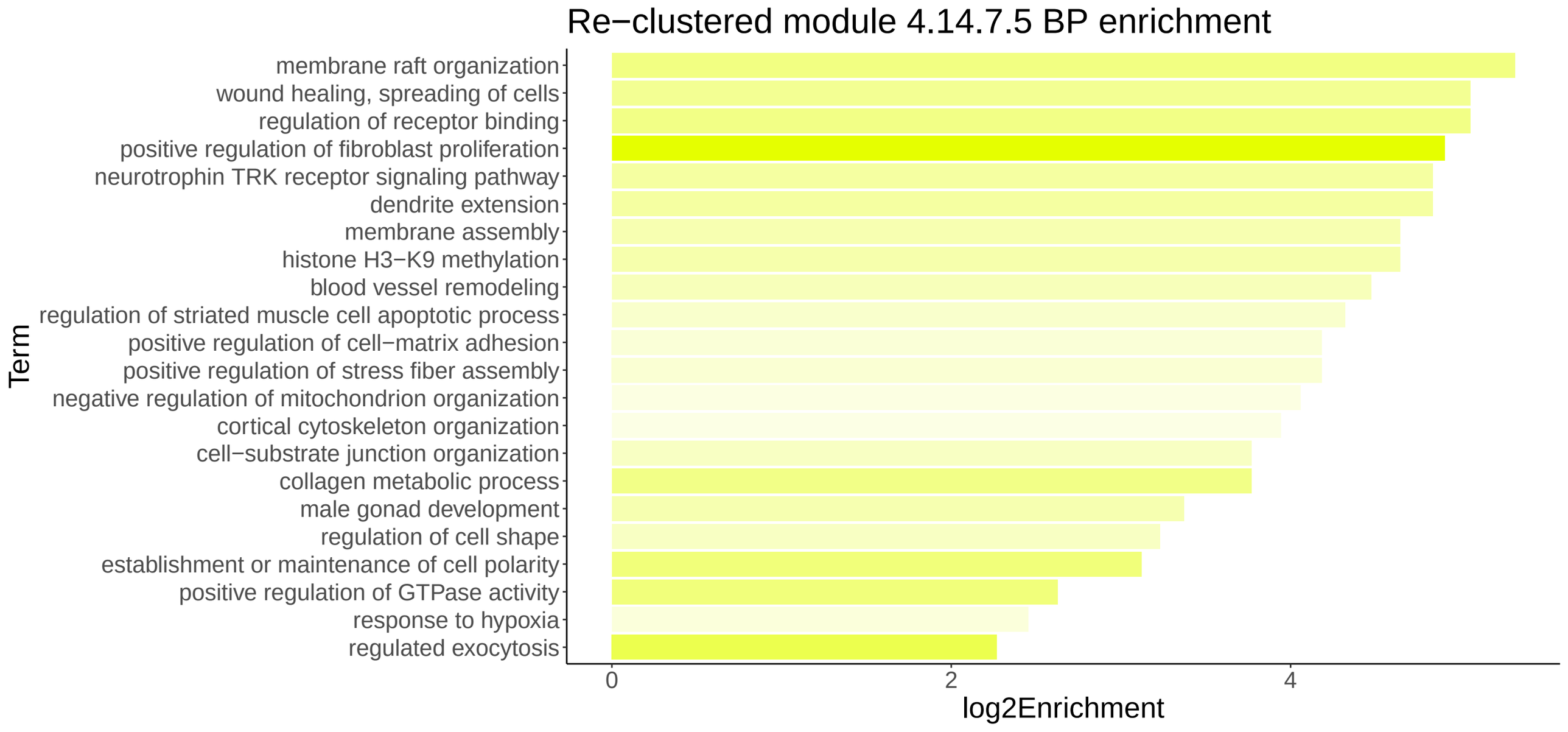

Re−clustered module 4.14.7.11 MF enrichment
actin filament binding
calcium ion binding
Term
0
1
2
3
4
log2Enrichment

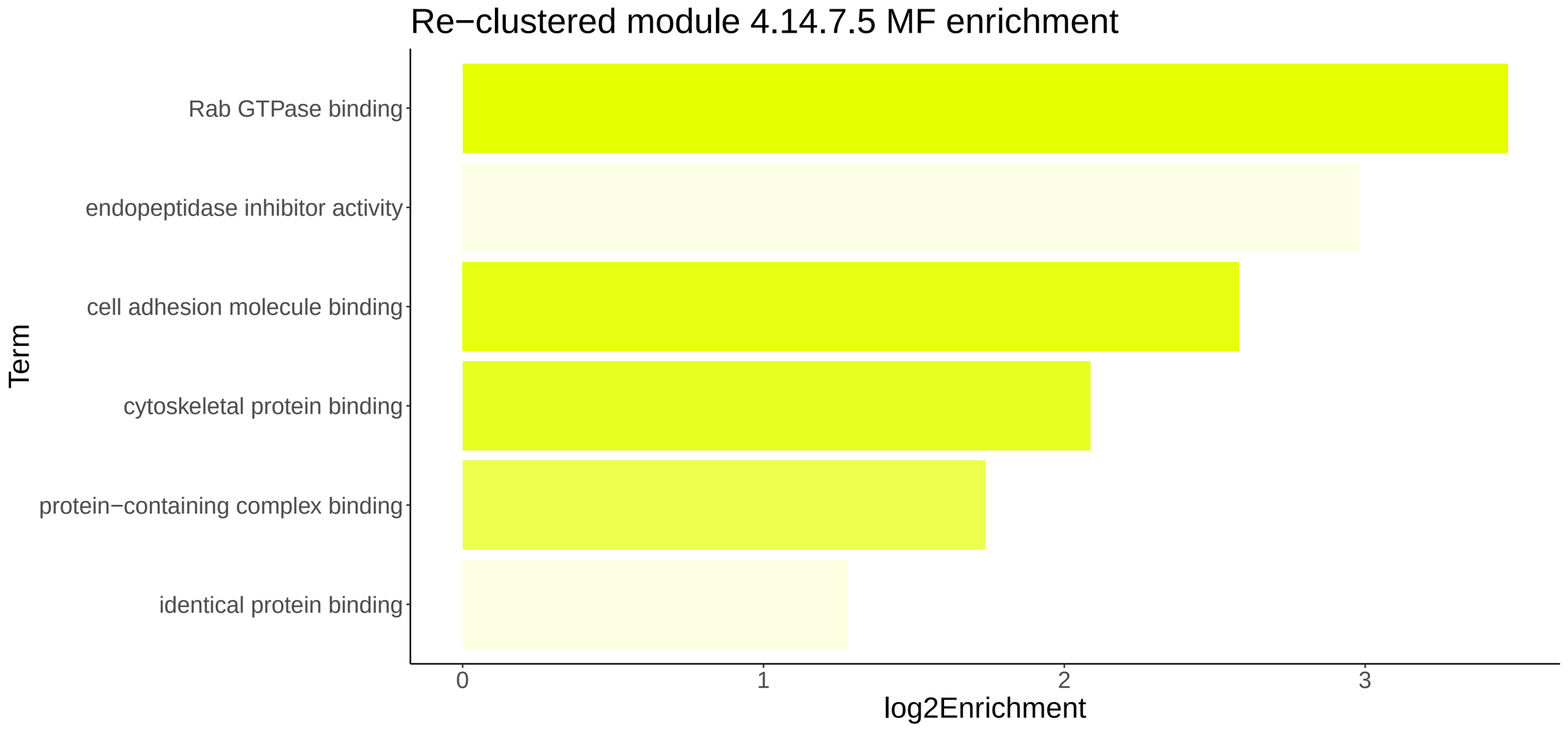

Re−clustered module 4.14.7.2 BP enrichment
cellular detoxification
xenobiotic metabolic process
regulation of protein stability
response to drug
Term
0
1
2
3
4
5
log2Enrichment

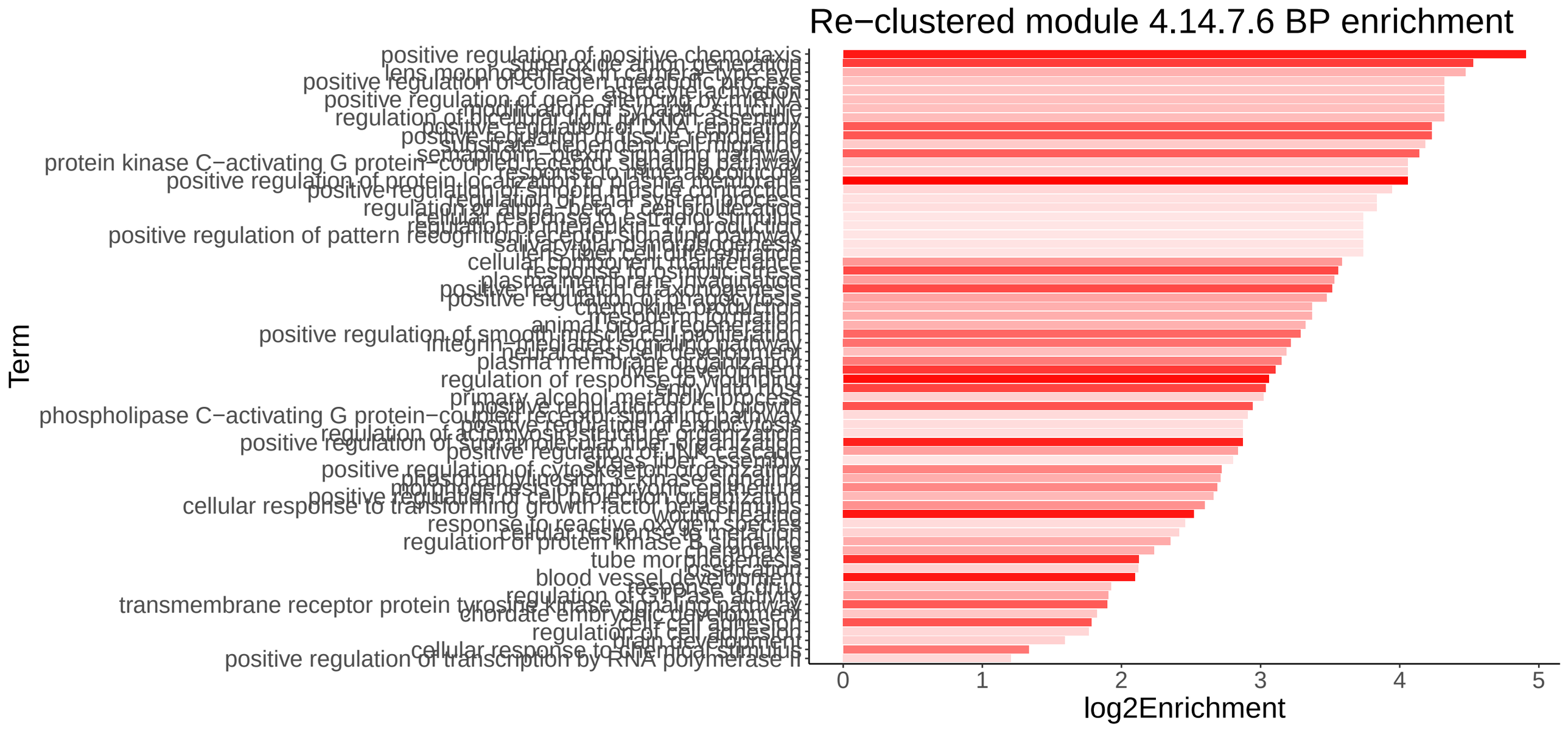

Re−clustered module 4.14.7.2 MF enrichment
Term
log2Enrichment

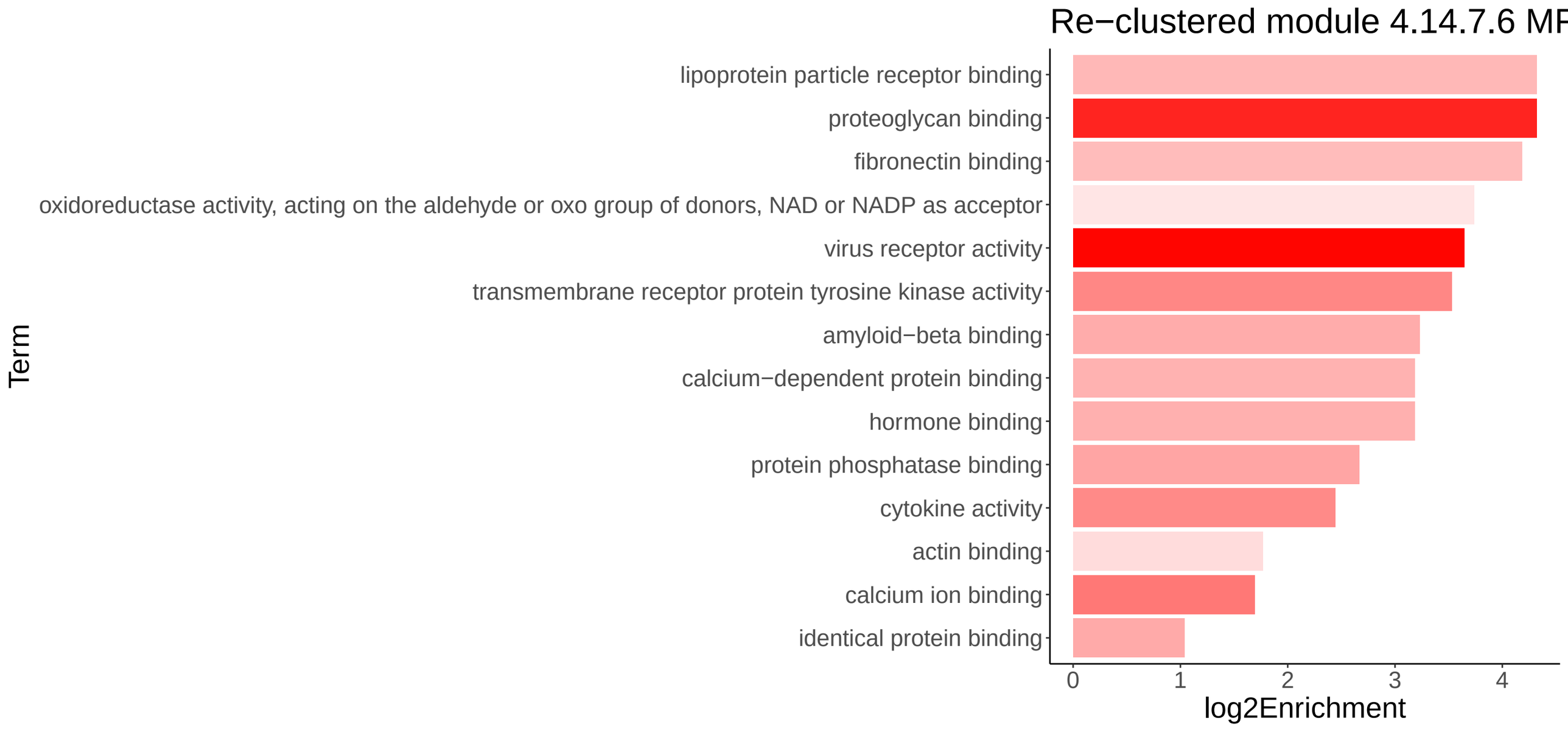

Re−clustered module 4.14.7.3 BP enrichment
Term
log2Enrichment

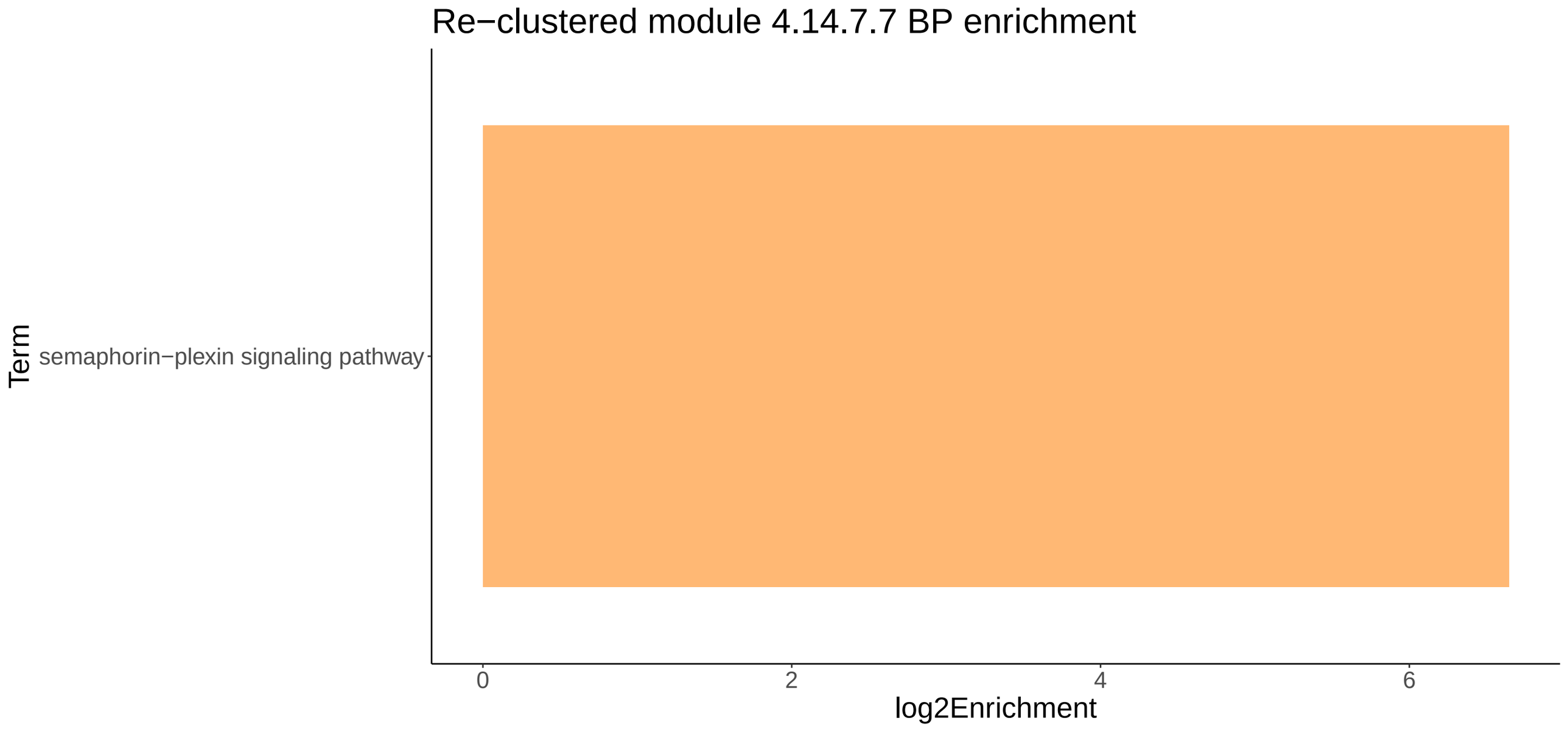

Re−clustered module 4.14.7.3 MF enrichment
Term
modified amino acid transmembrane transporter activity
0
2
4
6
log2Enrichment

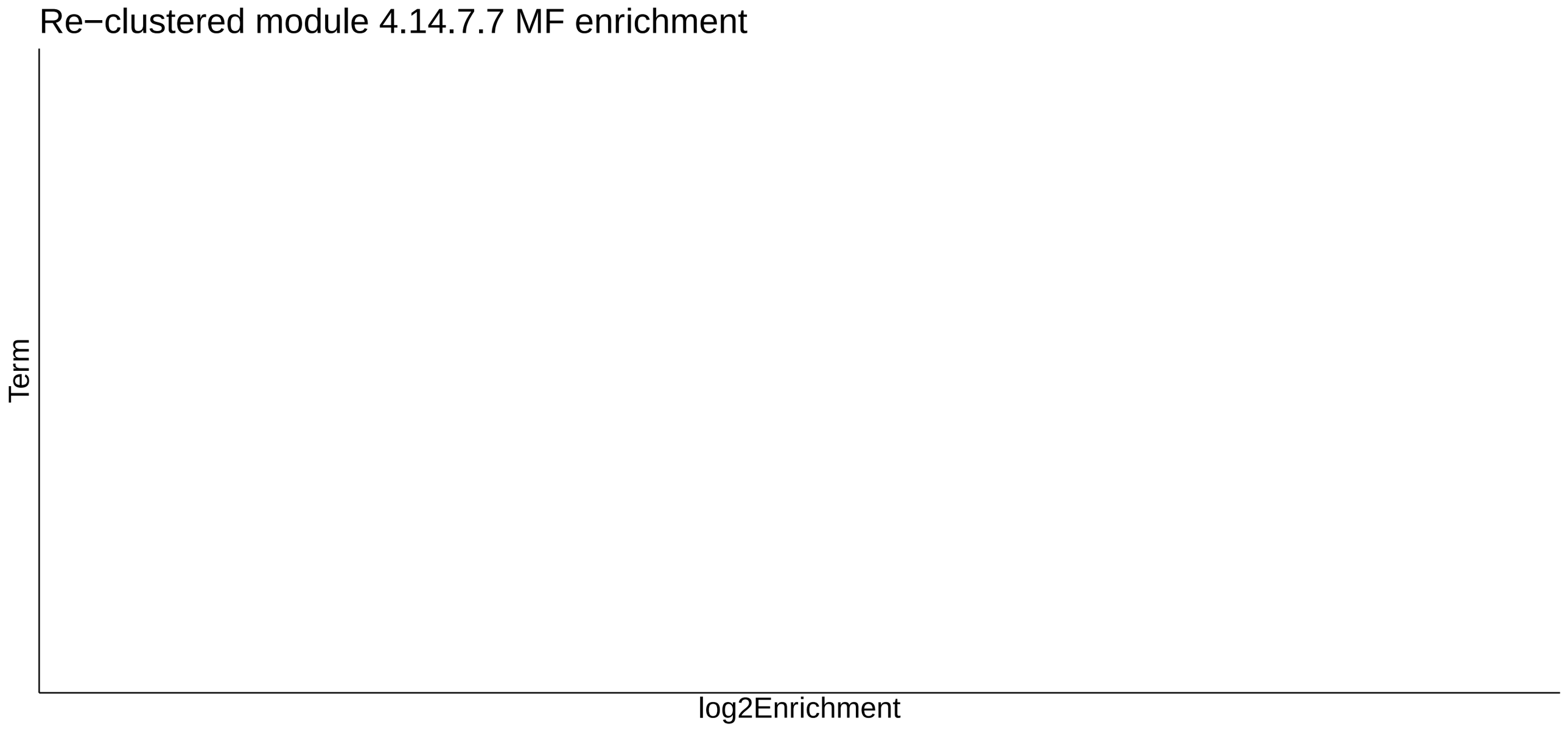

Re−clustered module 4.14.7.5 BP enrichment
membrane raft organization
wound healing, spreading of cells
regulation of receptor binding
positive regulation of fibroblast proliferation
neurotrophin TRK receptor signaling pathway
dendrite extension
membrane assembly
histone H3−K9 methylation
blood vessel remodeling
regulation of striated muscle cell apoptotic process
positive regulation of cell−matrix adhesion
positive regulation of stress fiber assembly
negative regulation of mitochondrion organization
cortical cytoskeleton organization
cell−substrate junction organization
collagen metabolic process
male gonad development
regulation of cell shape
establishment or maintenance of cell polarity
positive regulation of GTPase activity
response to hypoxia
regulated exocytosis
Term
0
2
4
log2Enrichment


Re−clustered module 4.14.7.5 MF enrichment
Rab GTPase binding
endopeptidase inhibitor activity
cell adhesion molecule binding
cytoskeletal protein binding
protein−containing complex binding
identical protein binding
Term
0
1
2
3
log2Enrichment


Re−clustered module 4.14.7.6 BP enrichment
Term
positive regulation of positive chemotaxis
superoxide anion generation
lens morphogenesis in camera−type eye
positive regulation of collagen metabolic process
astrocyte activation
positive regulation of gene silencing by miRNA
modification of synaptic structure
regulation of blood vessel diameter
positive regulation of DNA repair
positive regulation of tissue remodeling
substrate−dependent cell migration
semaphorin−plexin signaling pathway
protein kinase C−activating G protein−coupled receptor signaling pathway
response to mineralocorticoid
positive regulation of protein localization to plasma membrane
positive regulation of smooth muscle contraction
regulation of renal system process
regulation of alpha−beta T cell proliferation
cellular response to estradiol stimulus
regulation of interleukin−17 production
positive regulation of pattern recognition receptor signaling pathway
salivary gland morphogenesis
liver development
cellular component maintenance
response to osmotic stress
plasma membrane fusion
positive regulation of axonogenesis
positive regulation of phagocytosis
chemokine production
mesoderm formation
animal organ regeneration
positive regulation of smooth muscle cell proliferation
integrin−mediated signaling pathway
neural crest cell development
plasma membrane organization
liver development
regulation of response to wounding
embryo development
primary alcohol metabolic process
positive regulation of cell growth
phospholipase C−activating G protein−coupled receptor signaling pathway
positive regulation of endocytosis
regulation of actin cytoskeleton organization
positive regulation of supramolecular fiber organization
positive regulation of JUN kinase activity
sister chromatid segregation
positive regulation of cytoskeleton organization
phosphatidylinositol 3−kinase signaling
morphogenesis of embryonic epithelium
positive regulation of cell projection organization
cellular response to transforming growth factor beta stimulus
wound healing
response to reactive oxygen species
cellular response to metal ion
regulation of protein kinase B signaling
chemotaxis
tube morphogenesis
ossification
blood vessel development
response to drug
regulation of GTPase activity
transmembrane receptor protein tyrosine kinase signaling pathway
chordate embryonic development
cell adhesion
regulation of cell adhesion
brain development
cellular response to chemical stimulus
positive regulation of transcription by RNA polymerase II
0
1
2
3
4
5
log2Enrichment

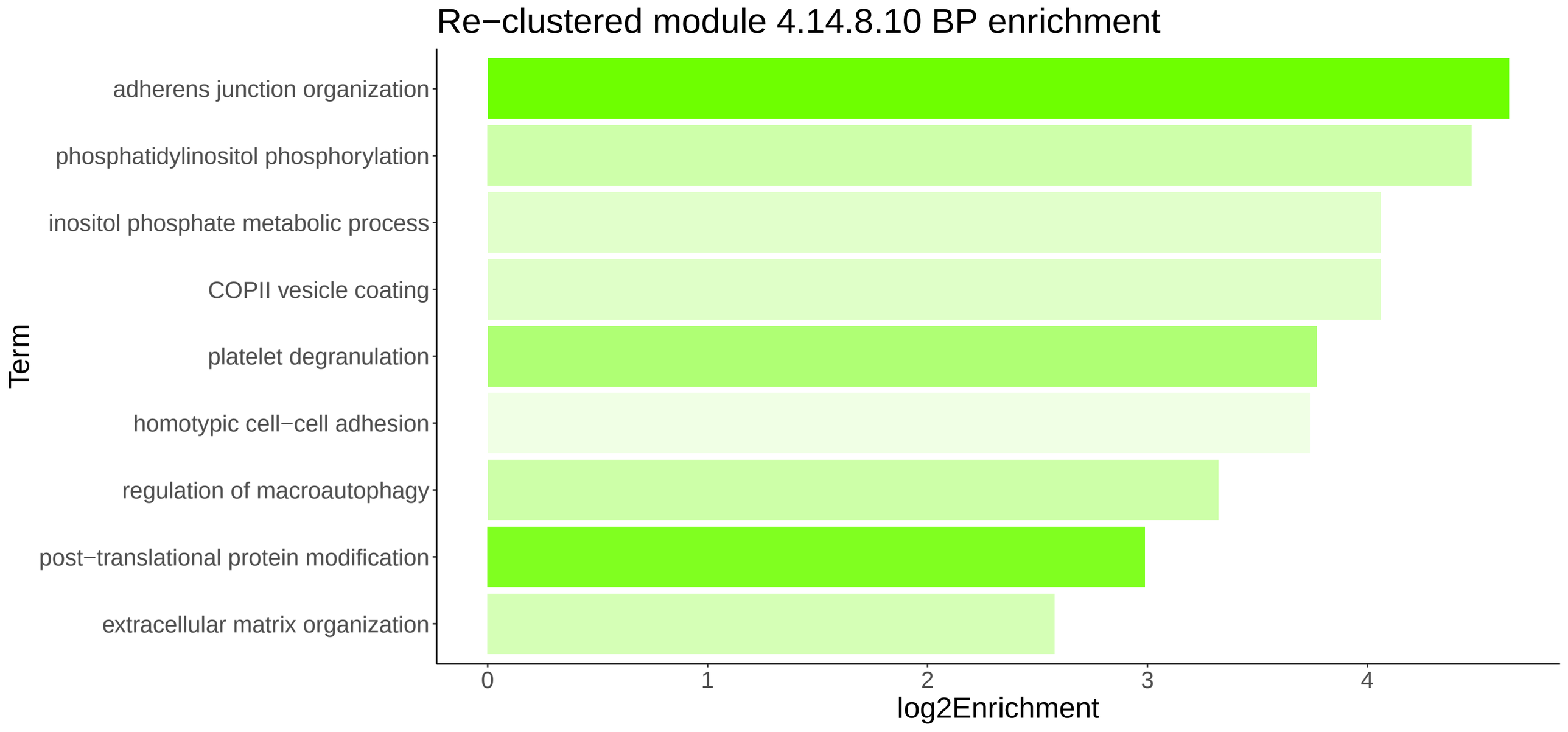

Re−clustered module 4.14.7.6 MF
lipoprotein particle receptor binding
proteoglycan binding
fibronectin binding
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
virus receptor activity
transmembrane receptor protein tyrosine kinase activity
amyloid−beta binding
calcium−dependent protein binding
hormone binding
protein phosphatase binding
cytokine activity
actin binding
calcium ion binding
identical protein binding
Term
0
1
2
3
4
log2Enrichment

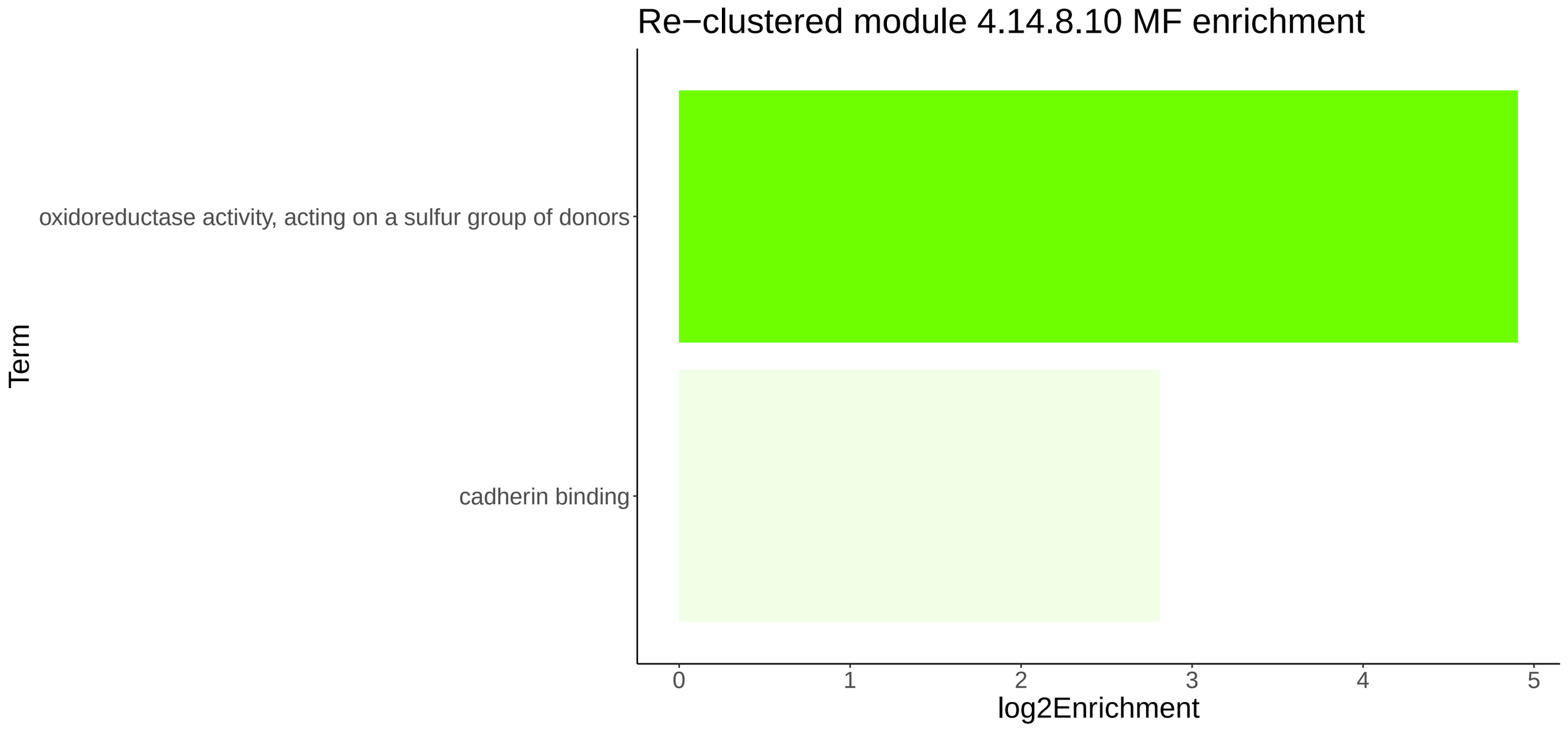

Re−clustered module 4.14.7.7 BP enrichment
Term
semaphorin−plexin signaling pathway
0
2
4
6
log2Enrichment

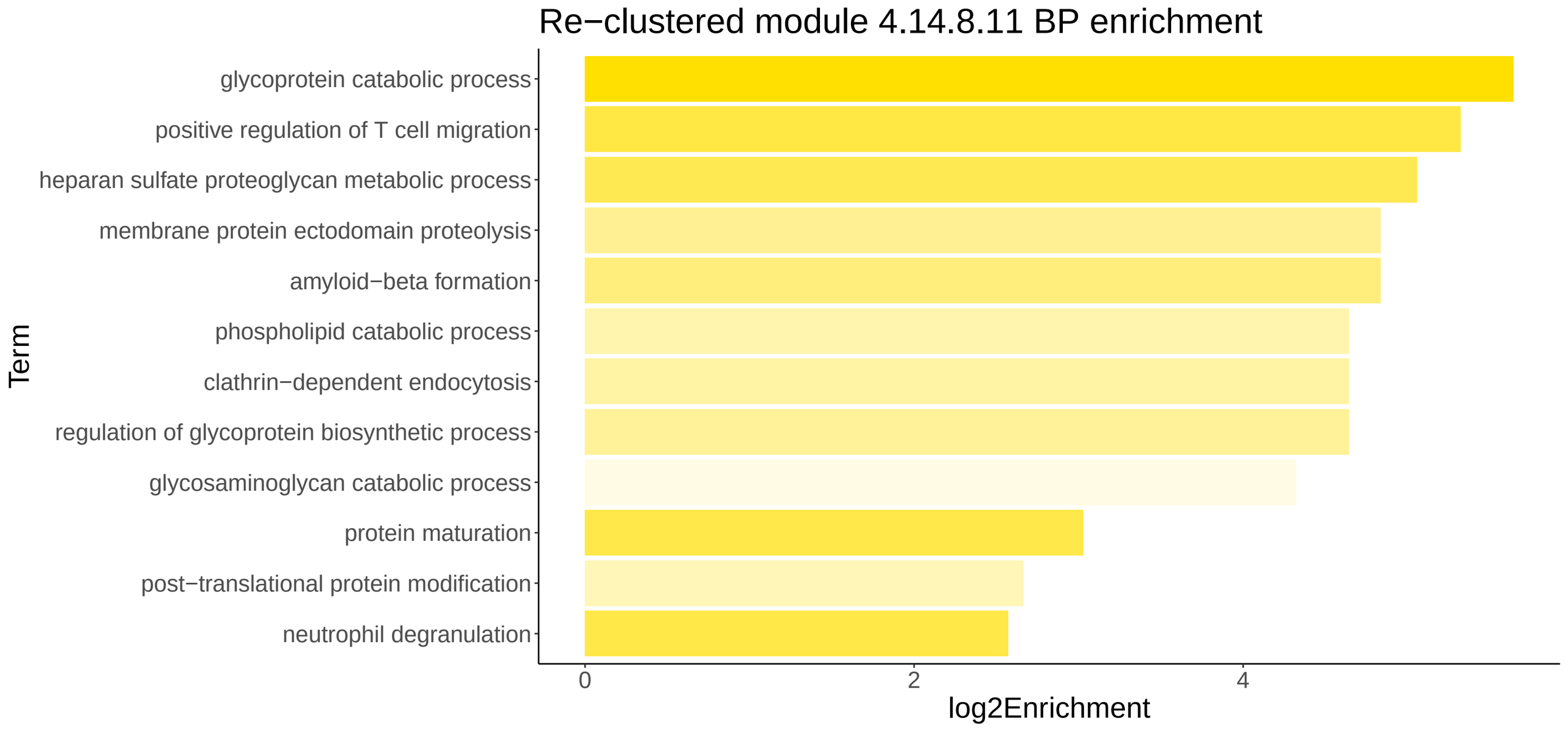

Re−clustered module 4.14.7.7 MF enrichment
Term
log2Enrichment

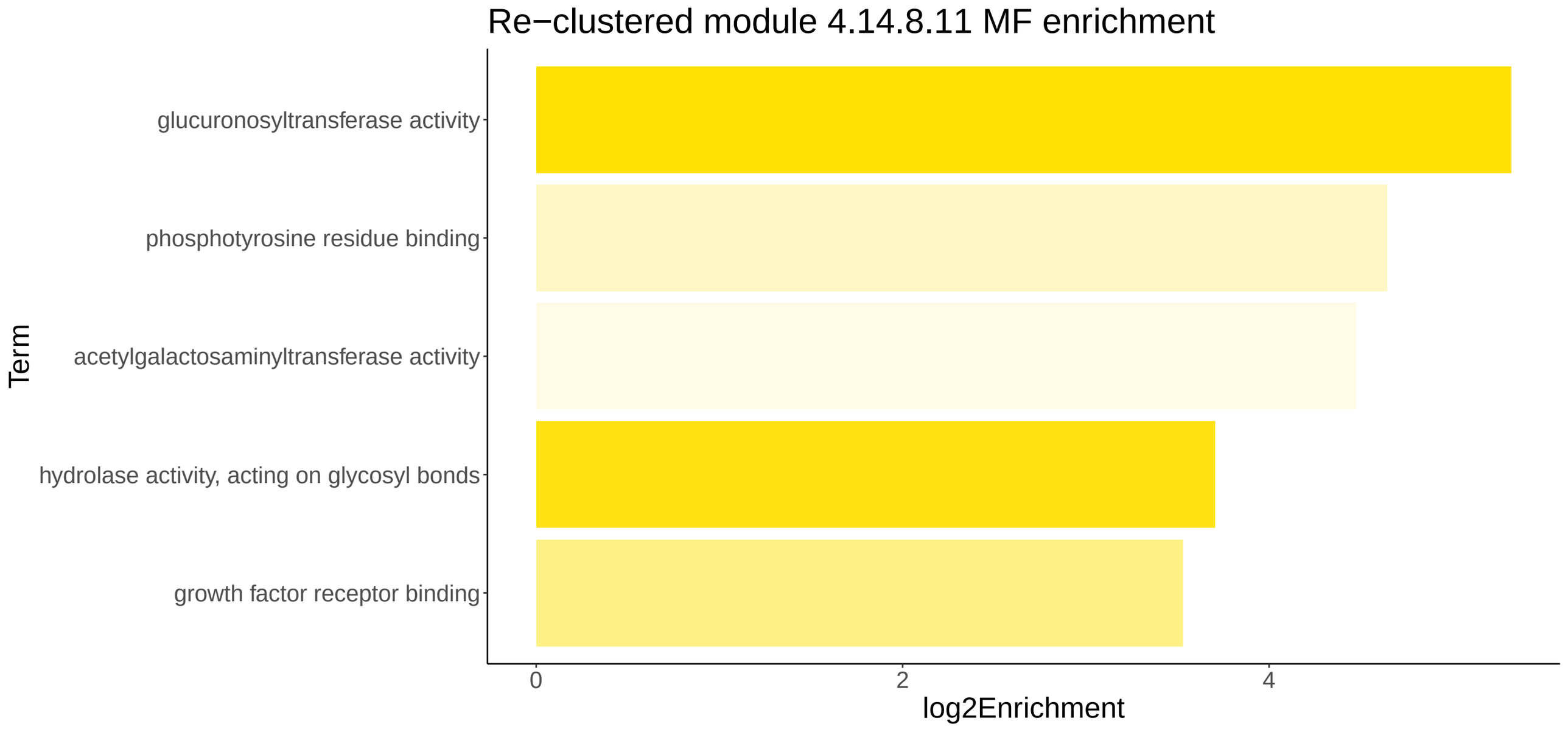

Re−clustered module 4.14.71 BP enrichment
Term
DNA damage response, signal transduction by p53 class mediator
0
1
2
3
4
5
log2Enrichment

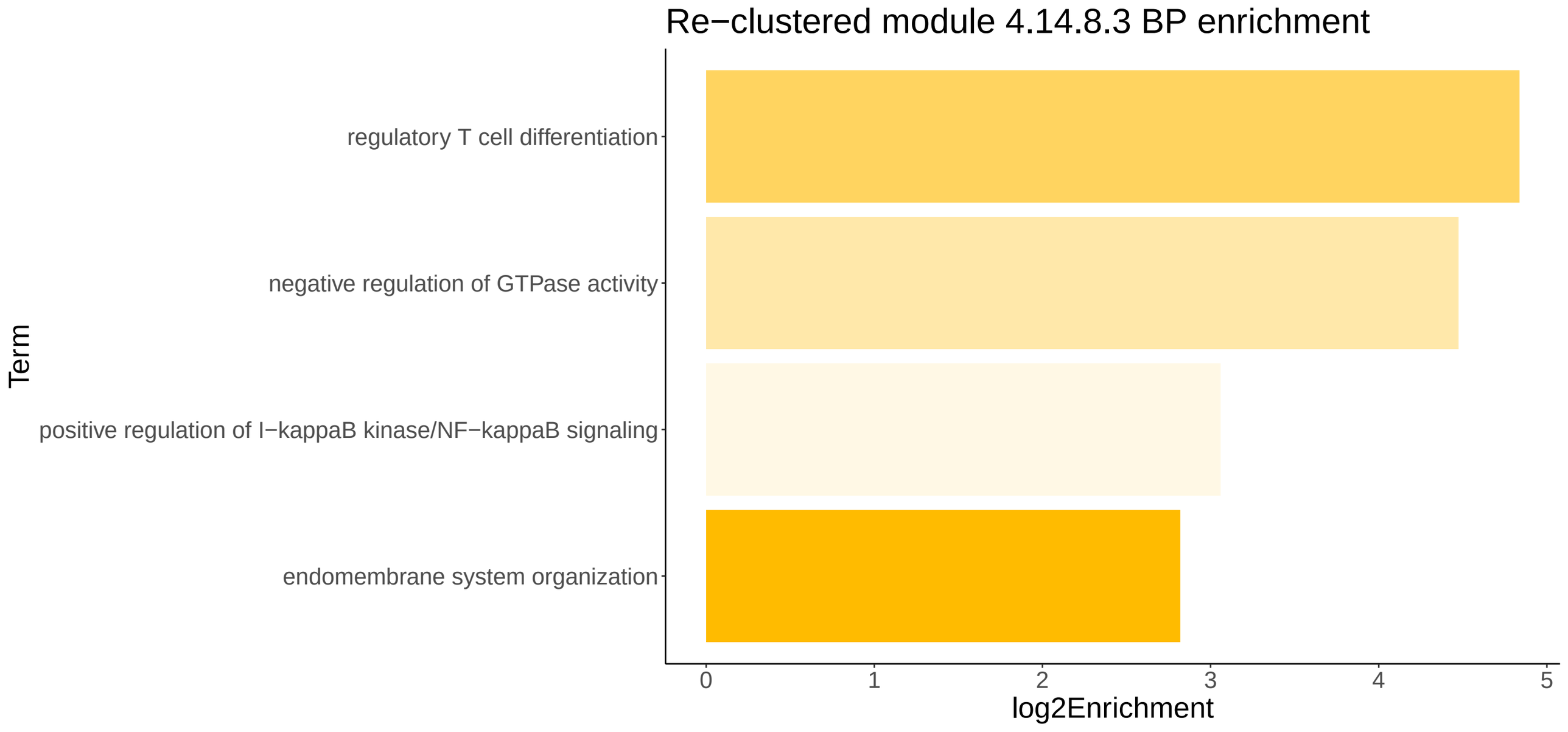

Re−clustered module 4.14.71 MF enrichment
Term
log2Enrichment

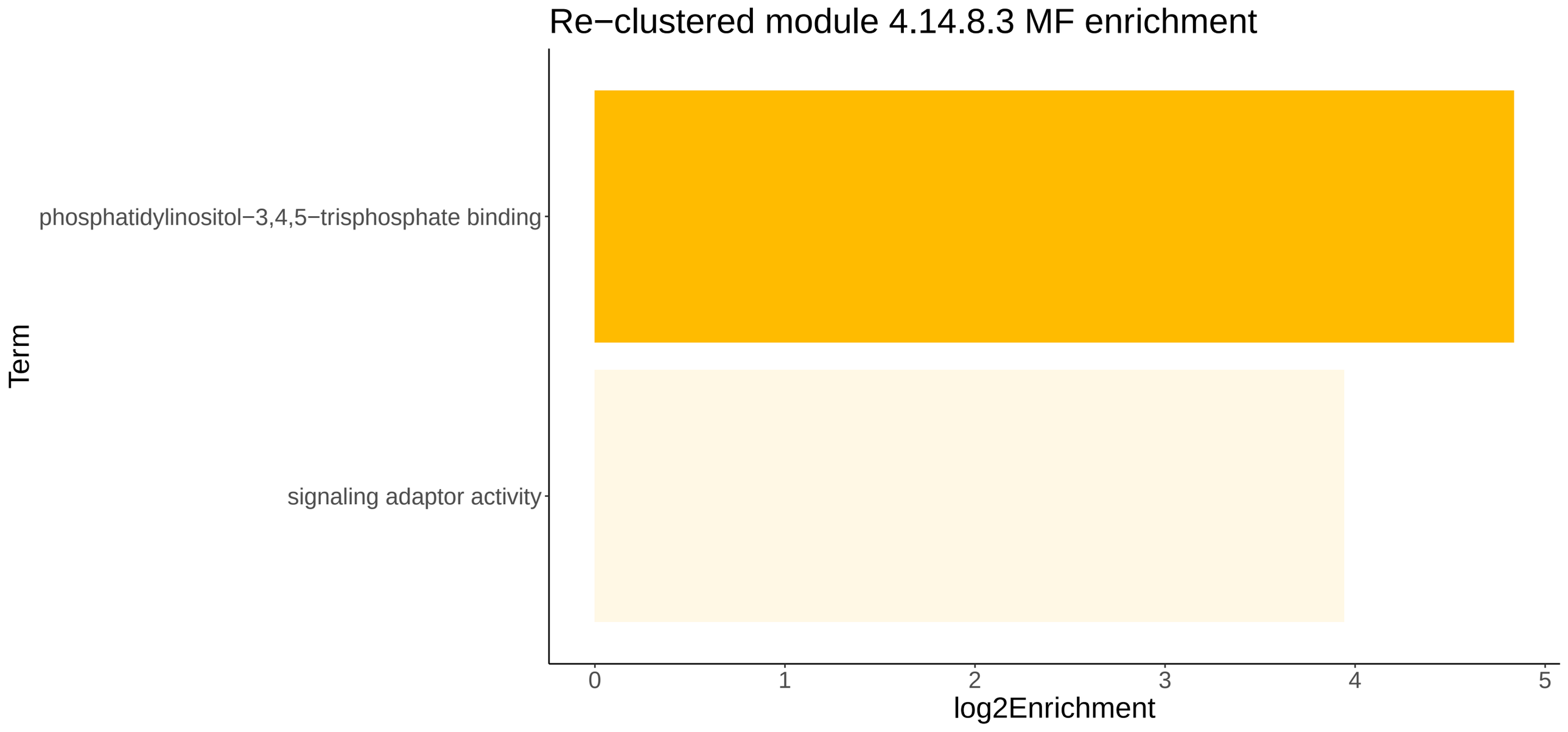

Re−clustered module 4.14.8.10 BP enrichment
adherens junction organization
phosphatidylinositol phosphorylation
inositol phosphate metabolic process
COPII vesicle coating
platelet degranulation
homotypic cell−cell adhesion
regulation of macroautophagy
post−translational protein modification
extracellular matrix organization
Term
0
1
2
3
4
log2Enrichment

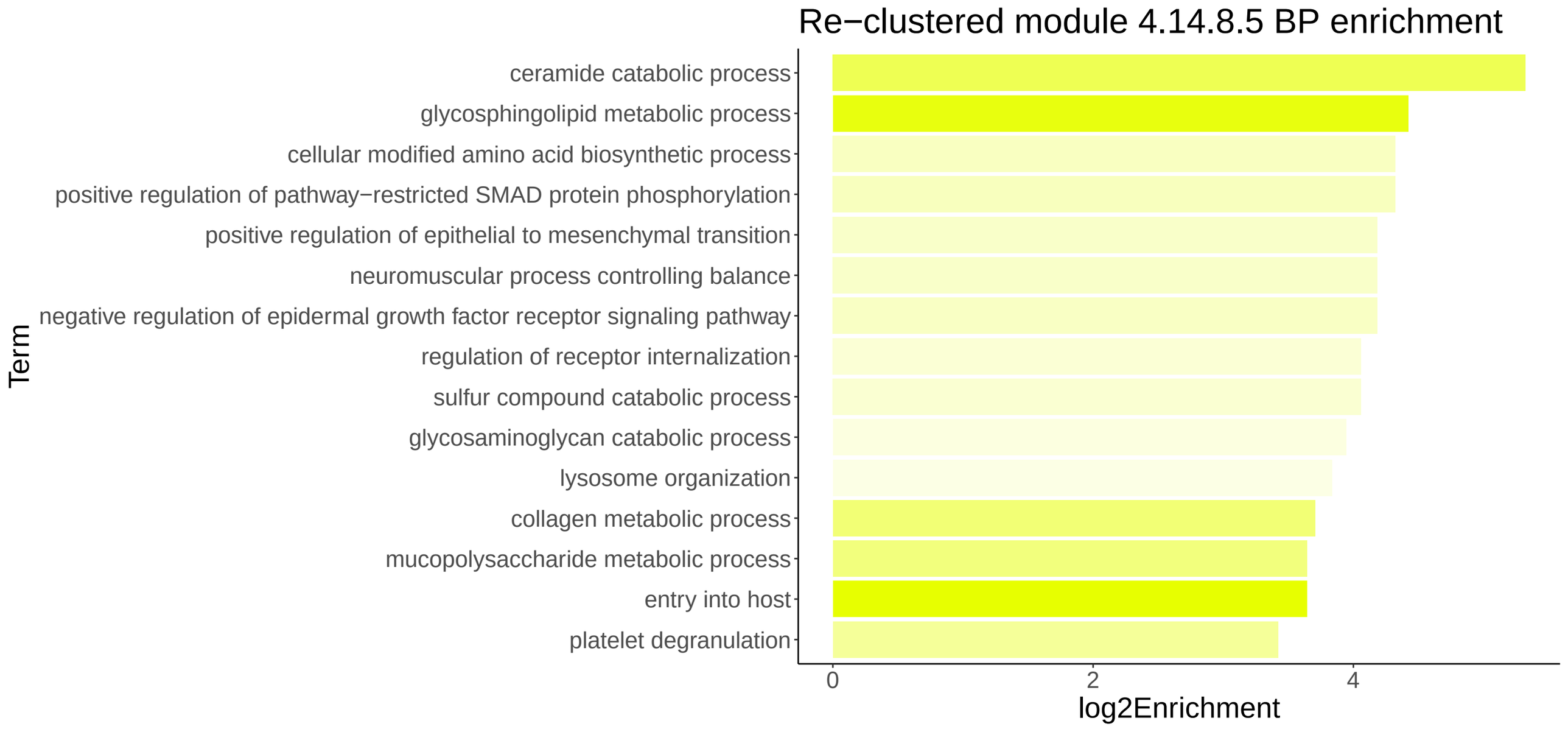

Re−clustered module 4.14.8.10 MF enrichment
Term
oxidoreductase activity, acting on a sulfur group of donors
cadherin binding
0
1
2
3
4
5
log2Enrichment

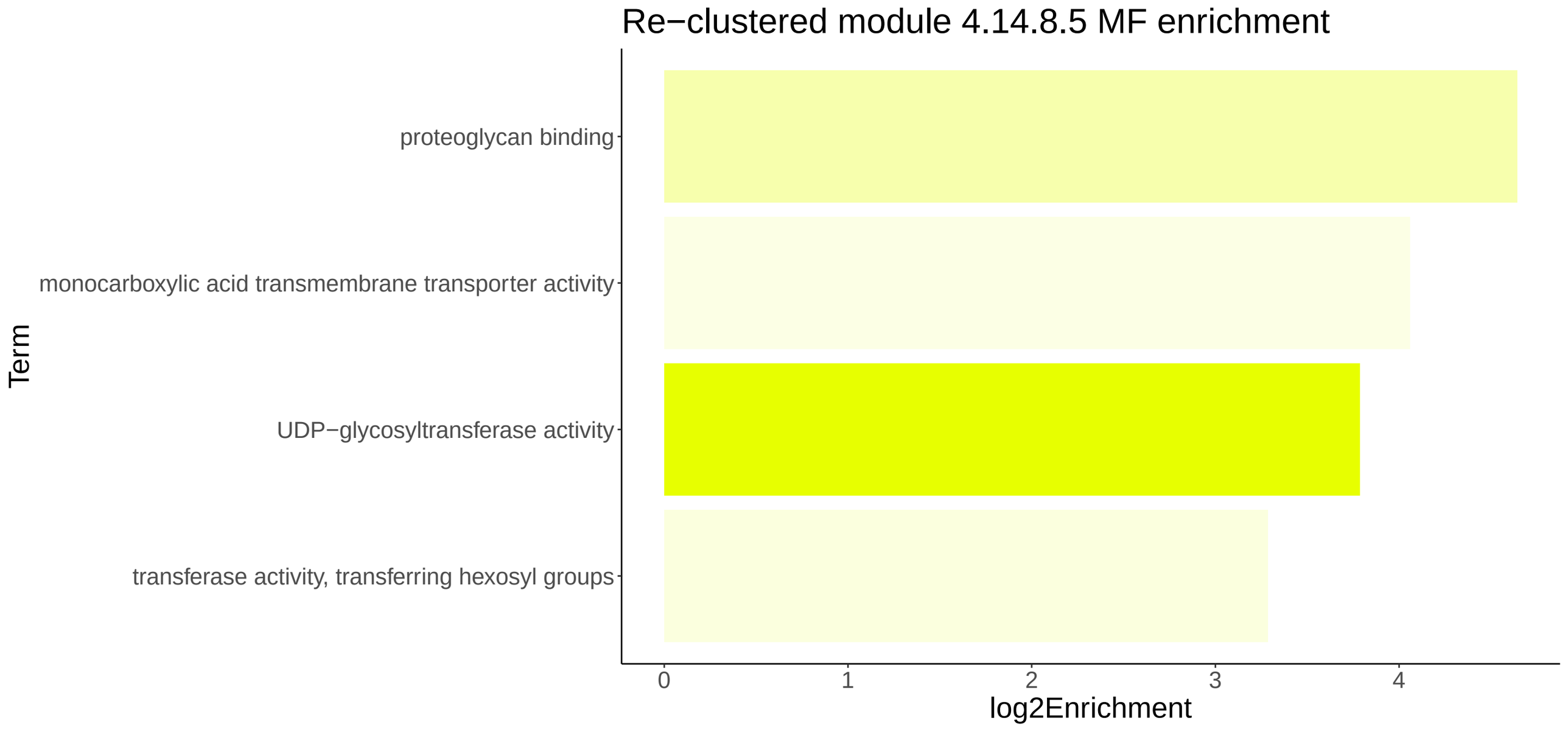

Re−clustered module 4.14.8.11 BP enrichment
glycoprotein catabolic process
positive regulation of T cell migration
heparan sulfate proteoglycan metabolic process
membrane protein ectodomain proteolysis
amyloid−beta formation
phospholipid catabolic process
clathrin−dependent endocytosis
regulation of glycoprotein biosynthetic process
glycosaminoglycan catabolic process
protein maturation
post−translational protein modification
neutrophil degranulation
Term
0
2
4
log2Enrichment

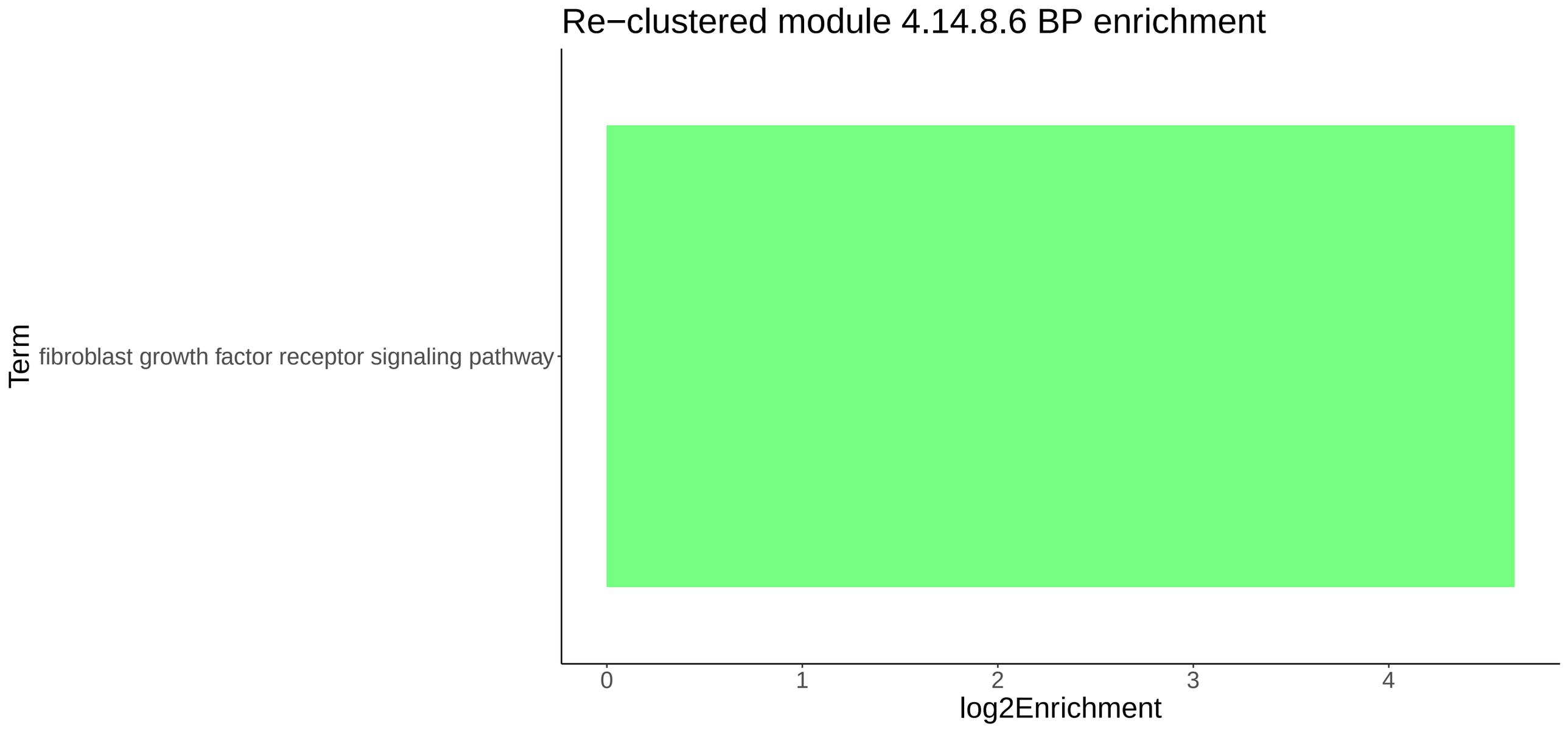

Re−clustered module 4.14.8.11 MF enrichment
Term
glucuronosyltransferase activity
phosphotyrosine residue binding
acetylgalactosaminyltransferase activity
hydrolase activity, acting on glycosyl bonds
growth factor receptor binding
0
2
4
log2Enrichment


Re−clustered module 4.14.8.3 BP enrichment
Term
regulatory T cell differentiation
negative regulation of GTPase activity
positive regulation of I−kappaB kinase/NF−kappaB signaling
endomembrane system organization
0
1
2
3
4
5
log2Enrichment

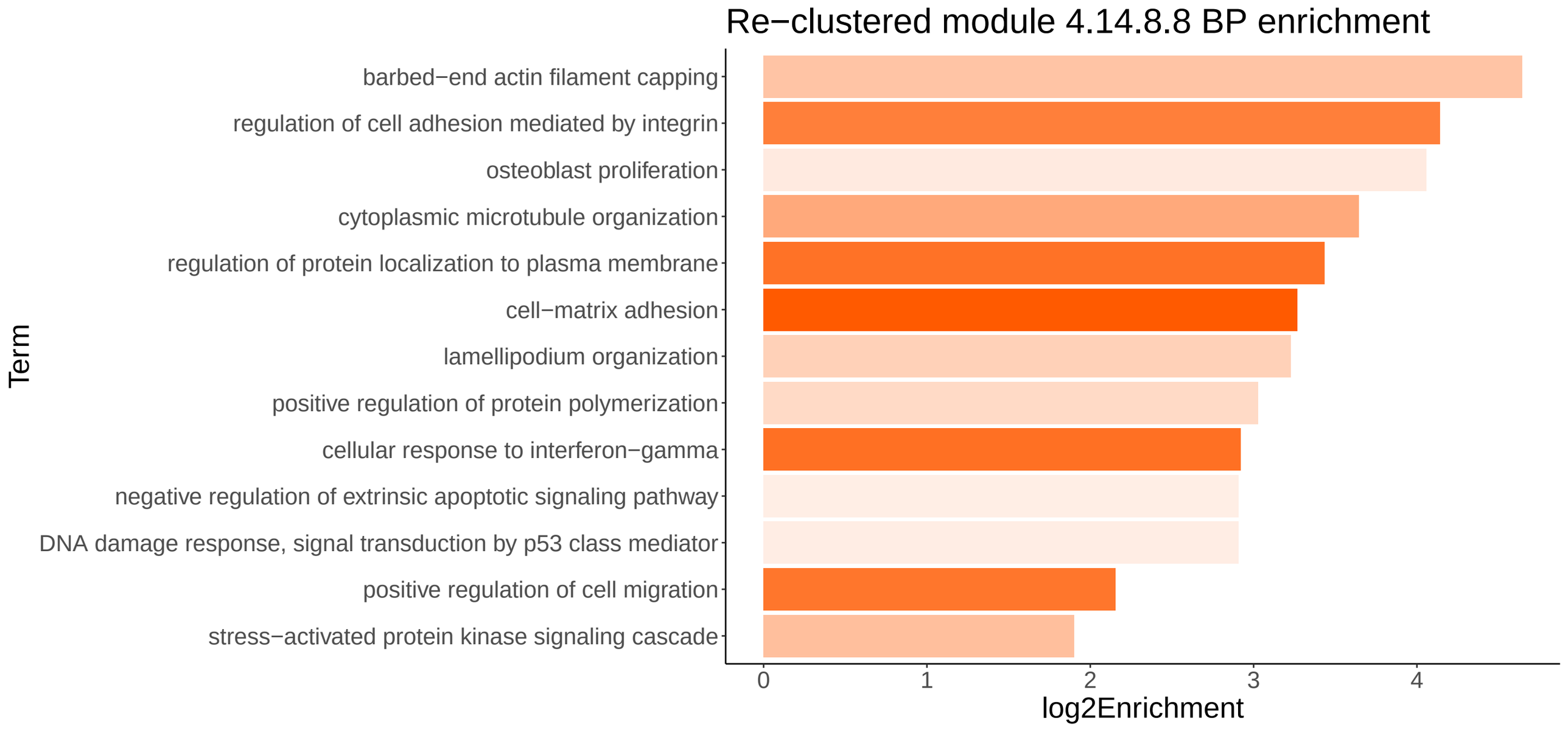

Re−clustered module 4.14.8.3 MF enrichment
Term
phosphatidylinositol−3,4,5−trisphosphate binding
signaling adaptor activity
0
1
2
3
4
5
log2Enrichment

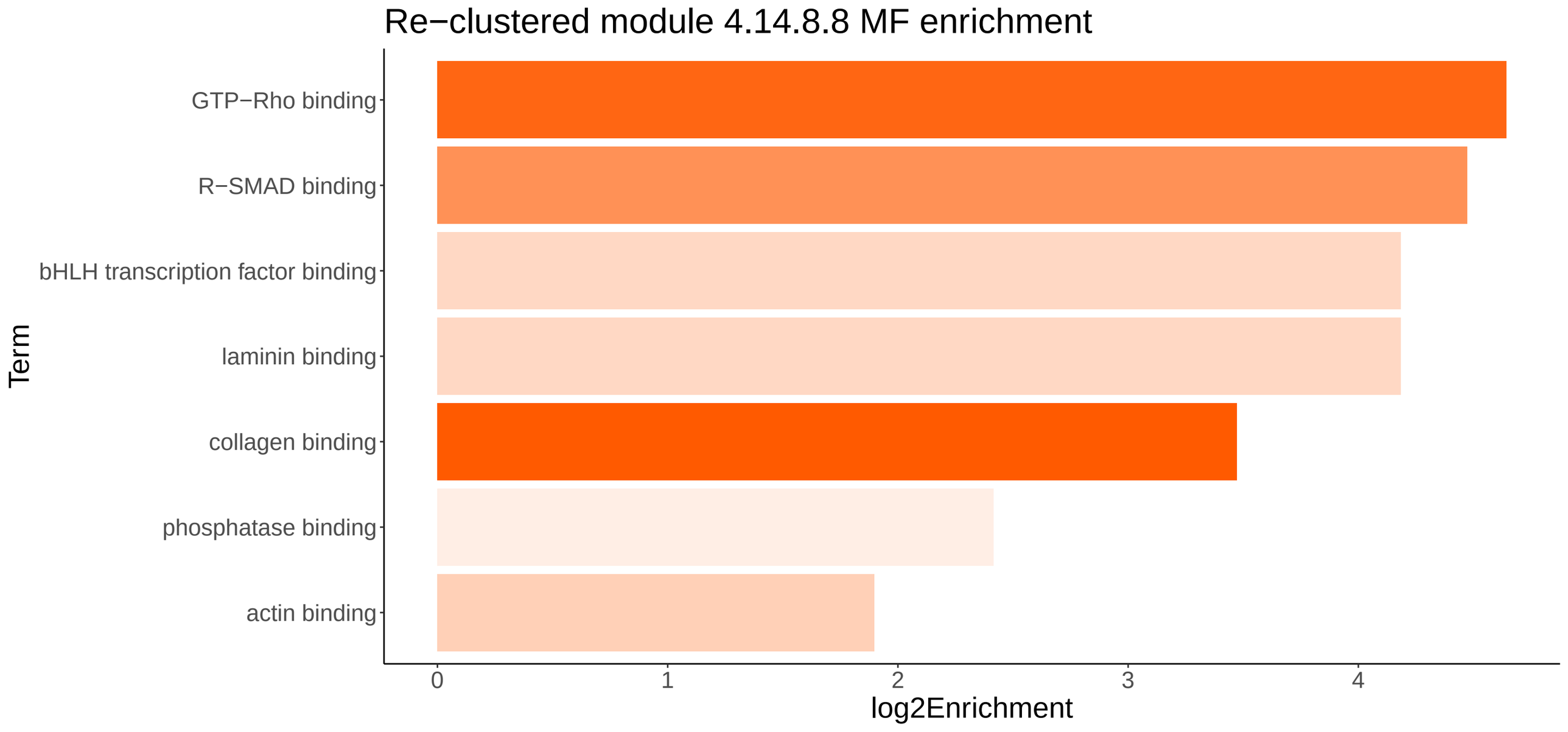

Re−clustered module 4.14.8.5 BP enrichment
Term
ceramide catabolic process
glycosphingolipid metabolic process
cellular modified amino acid biosynthetic process
positive regulation of pathway−restricted SMAD protein phosphorylation
positive regulation of epithelial to mesenchymal transition
neuromuscular process controlling balance
negative regulation of epidermal growth factor receptor signaling pathway
regulation of receptor internalization
sulfur compound catabolic process
glycosaminoglycan catabolic process
lysosome organization
collagen metabolic process
mucopolysaccharide metabolic process
entry into host
platelet degranulation
0
2
4
log2Enrichment

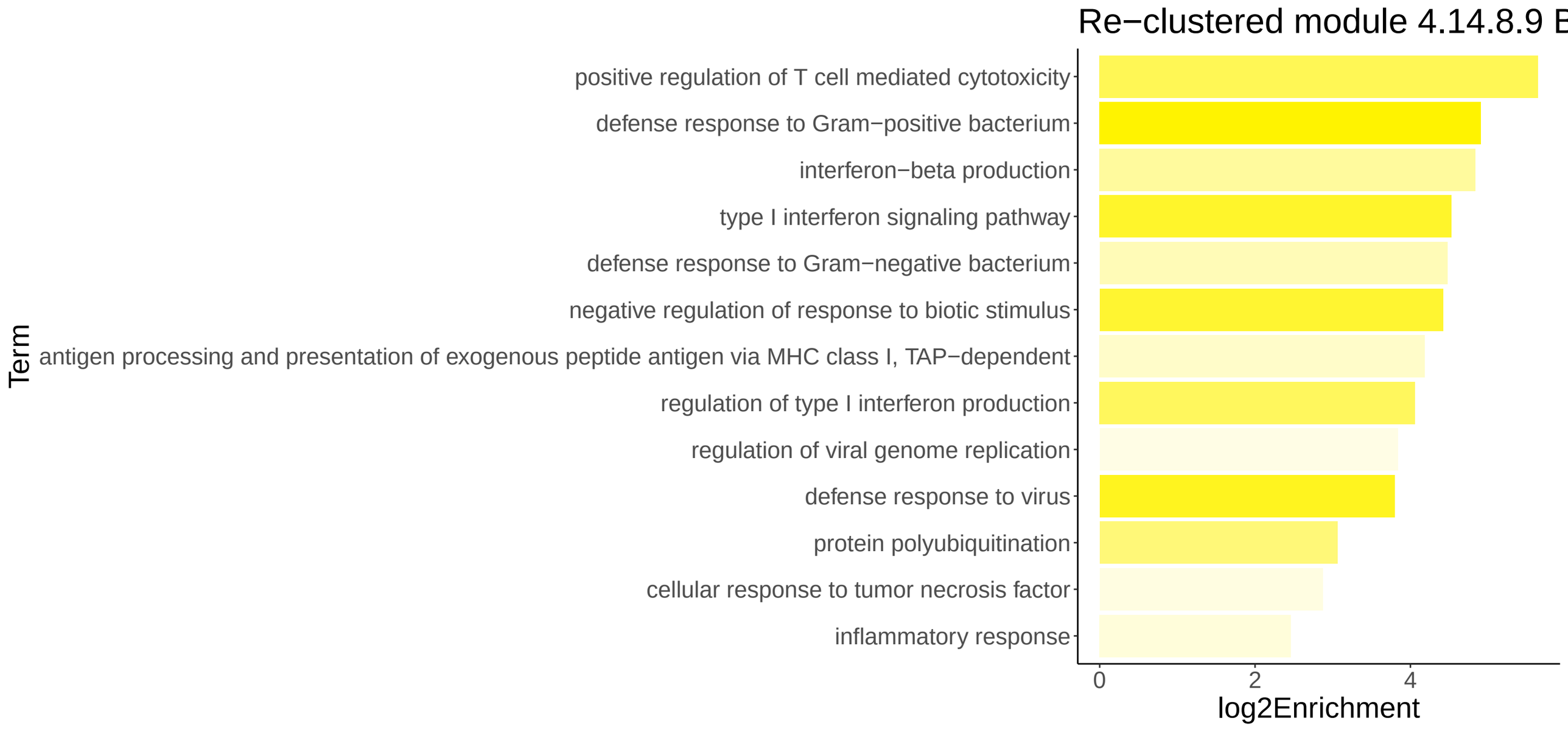

Re−clustered module 4.14.8.5 MF enrichment
proteoglycan binding
monocarboxylic acid transmembrane transporter activity
UDP−glycosyltransferase activity
transferase activity, transferring hexosyl groups
Term
0
1
2
3
4
log2Enrichment

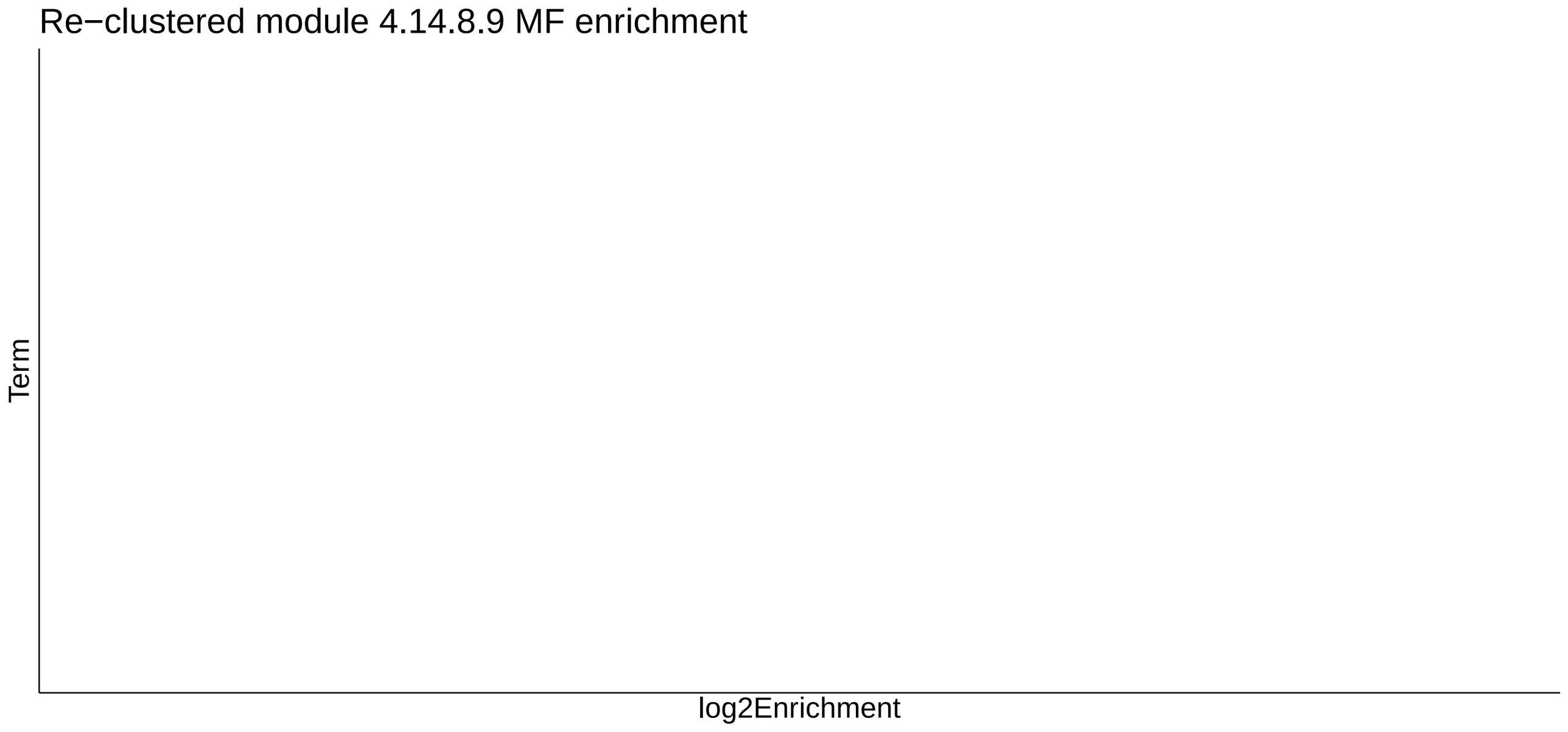

Re−clustered module 4.14.8.6 BP enrichment
Term
fibroblast growth factor receptor signaling pathway
0
1
2
3
4
log2Enrichment

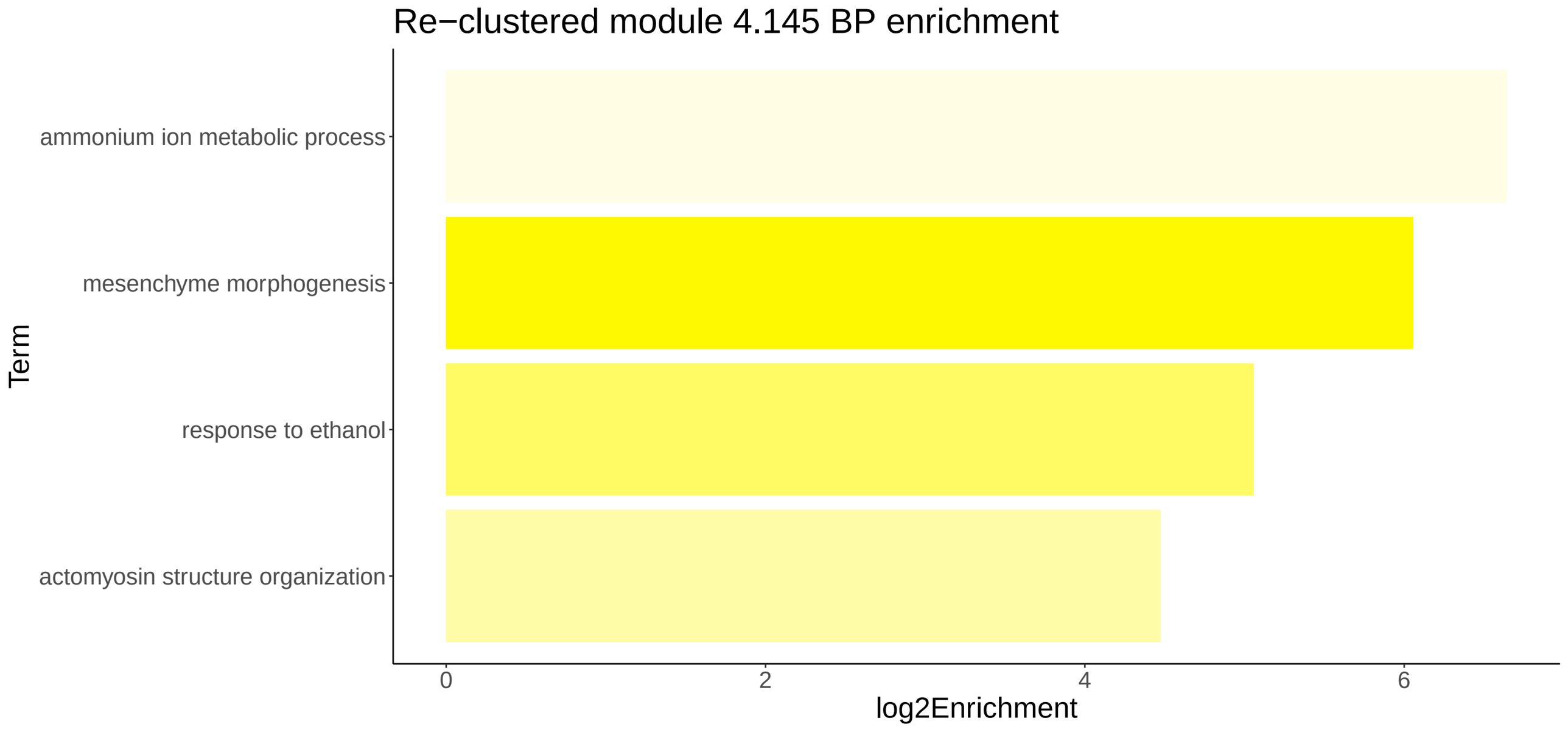

Re−clustered module 4.14.8.6 MF enrichment
Term
log2Enrichment

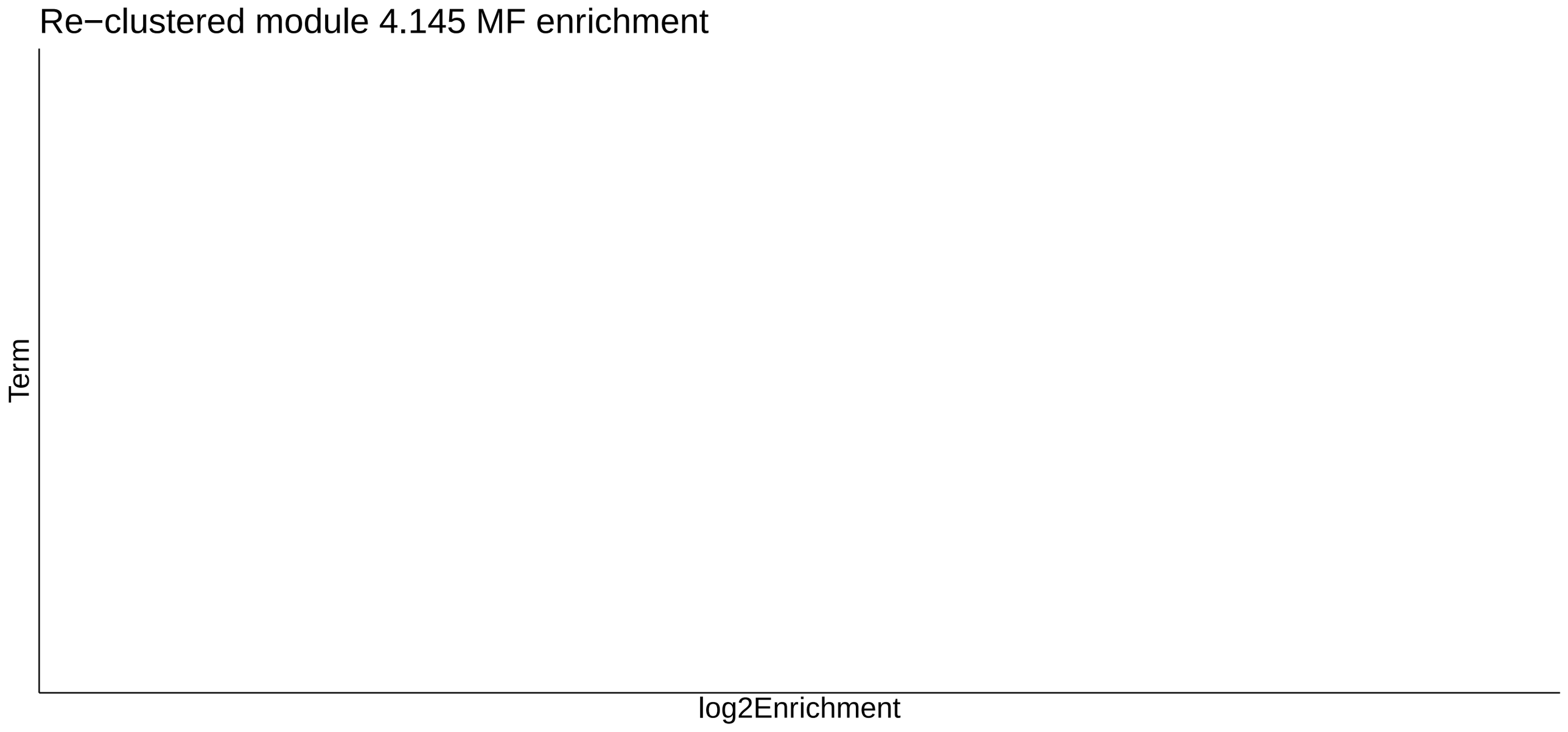

Re−clustered module 4.14.8.8 BP enrichment
barbed−end actin filament capping
regulation of cell adhesion mediated by integrin
osteoblast proliferation
cytoplasmic microtubule organization
regulation of protein localization to plasma membrane
cell−matrix adhesion
lamellipodium organization
positive regulation of protein polymerization
cellular response to interferon−gamma
negative regulation of extrinsic apoptotic signaling pathway
DNA damage response, signal transduction by p53 class mediator
positive regulation of cell migration
stress−activated protein kinase signaling cascade
Term
0
1
2
3
4
log2Enrichment

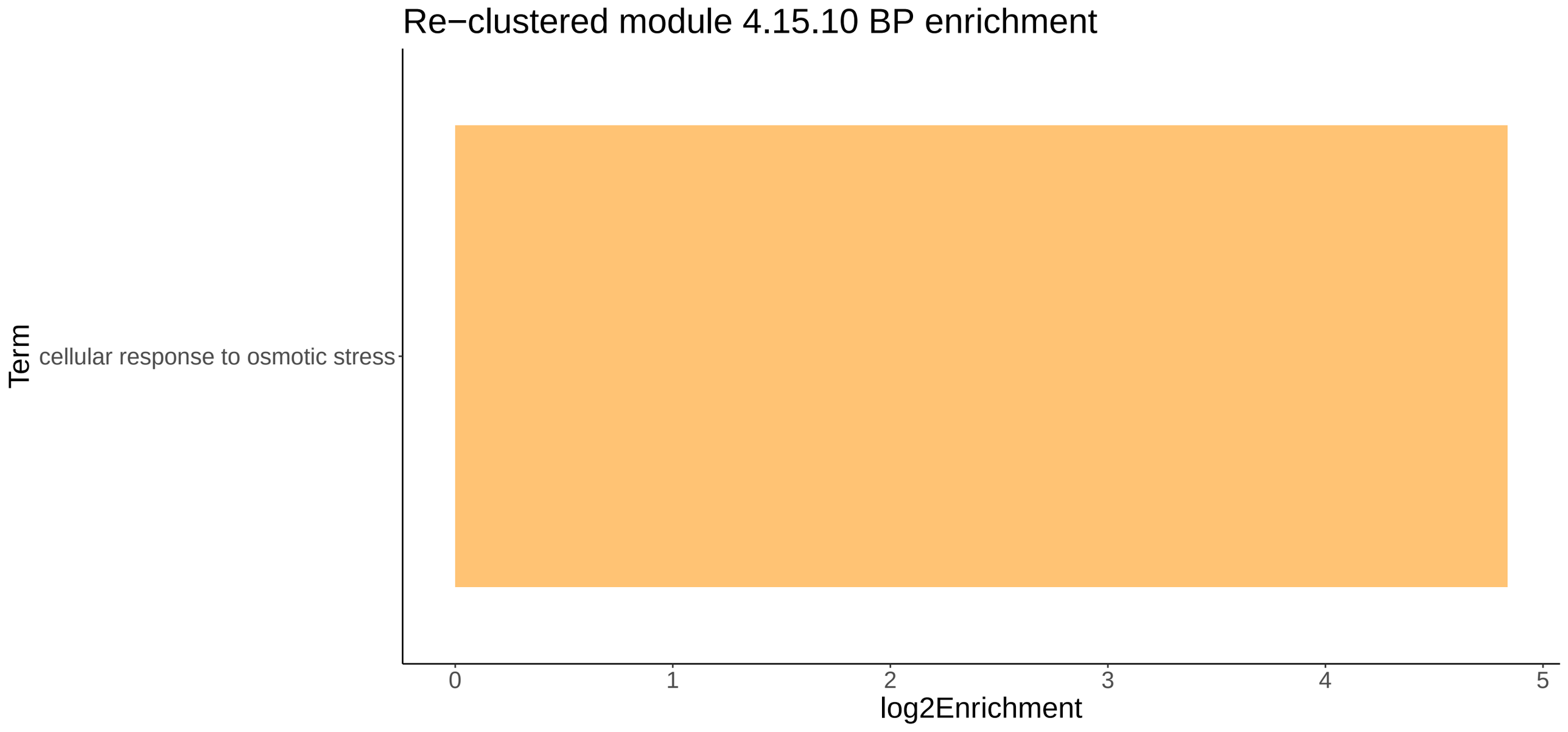

Re−clustered module 4.14.8.8 MF enrichment
GTP−Rho binding
R−SMAD binding
bHLH transcription factor binding
laminin binding
collagen binding
phosphatase binding
actin binding
Term
0
1
2
3
4
log2Enrichment

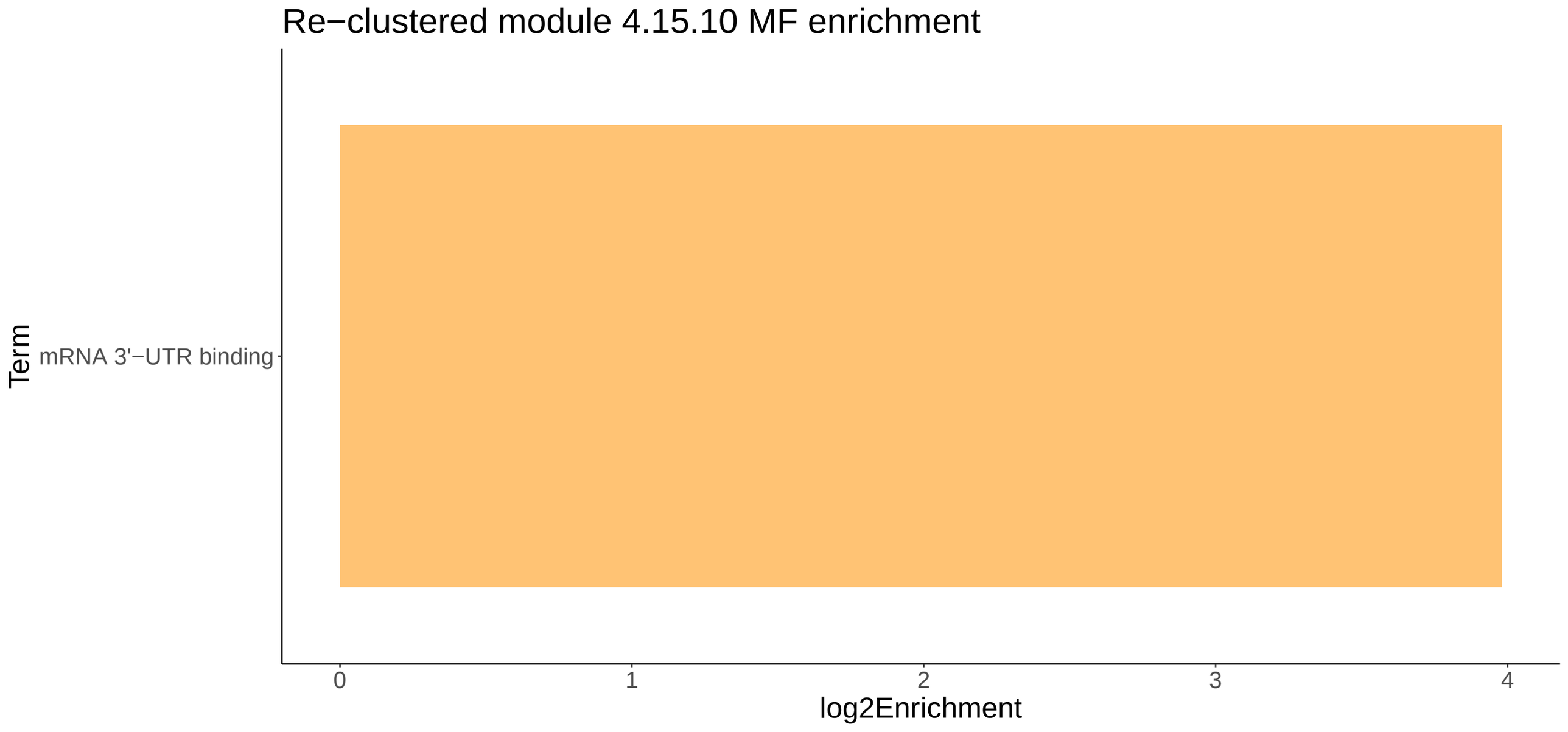

Re−clustered module 4.14.8.9 B
positive regulation of T cell mediated cytotoxicity
defense response to Gram−positive bacterium
interferon−beta production
type I interferon signaling pathway
defense response to Gram−negative bacterium
negative regulation of response to biotic stimulus
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
regulation of type I interferon production
regulation of viral genome replication
defense response to virus
protein polyubiquitination
cellular response to tumor necrosis factor
inflammatory response
Term
0
2
4
log2Enrichment

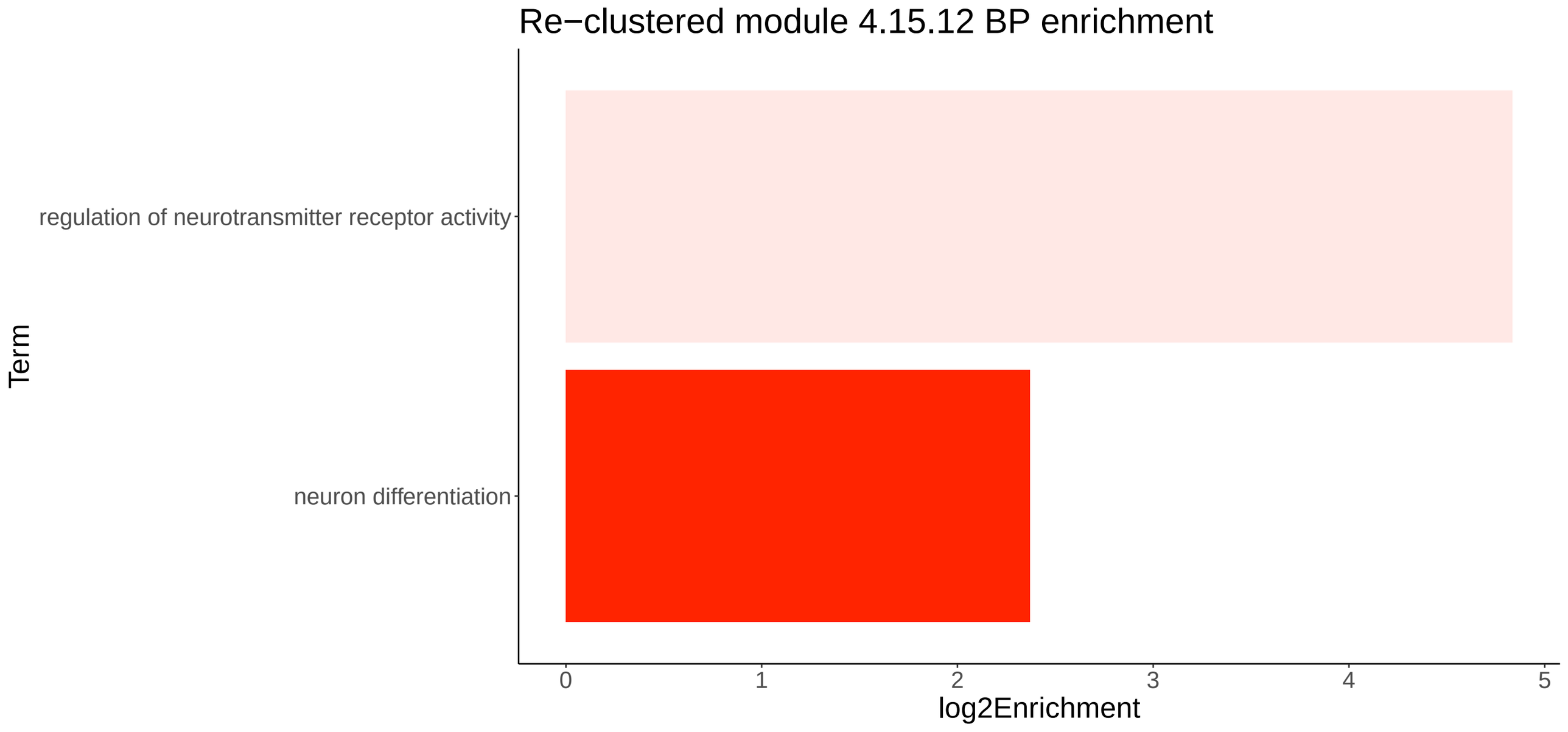

Re−clustered module 4.14.8.9 MF enrichment
Term
log2Enrichment

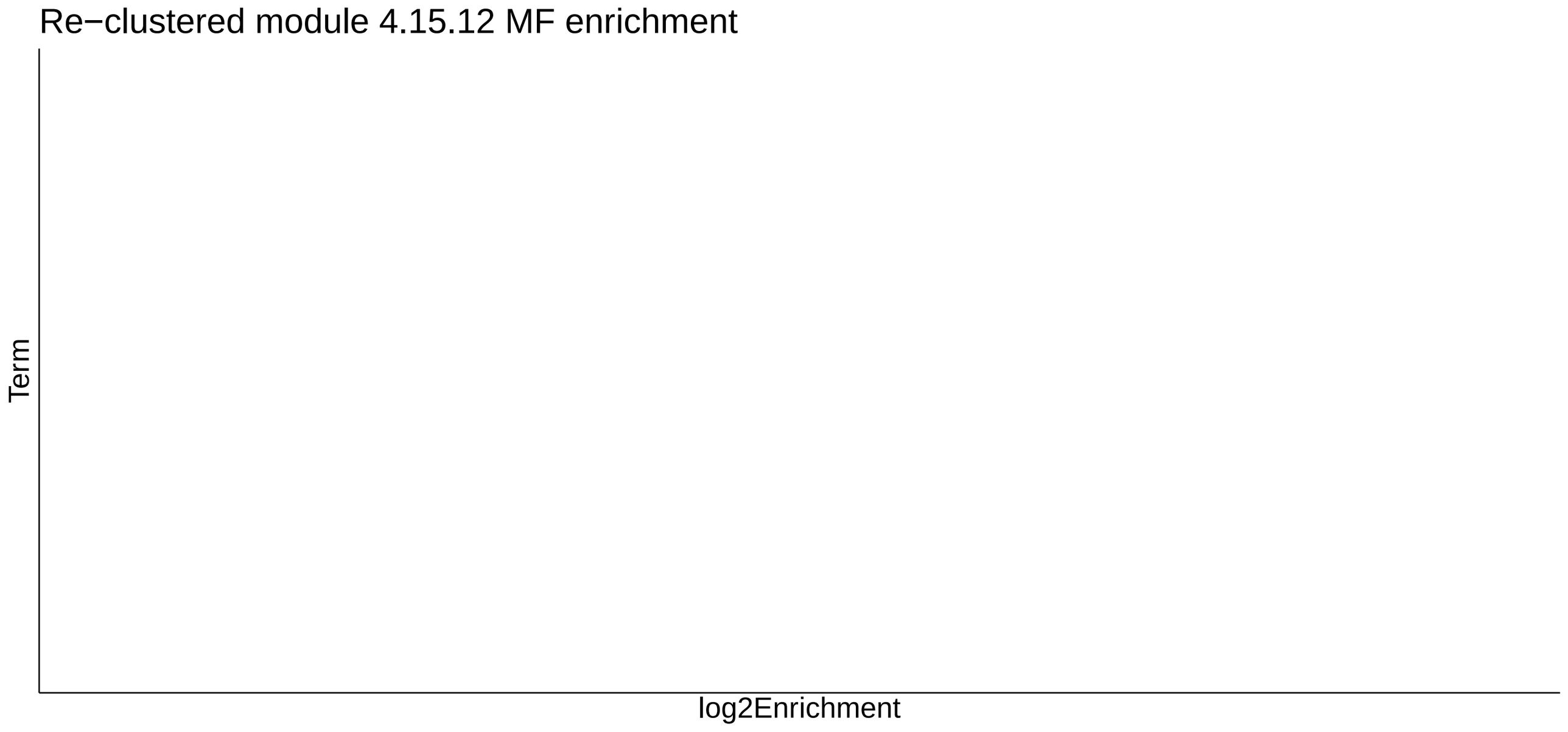

Re−clustered module 4.145 BP enrichment
ammonium ion metabolic process
mesenchyme morphogenesis
response to ethanol
actomyosin structure organization
Term
0
2
4
6
log2Enrichment

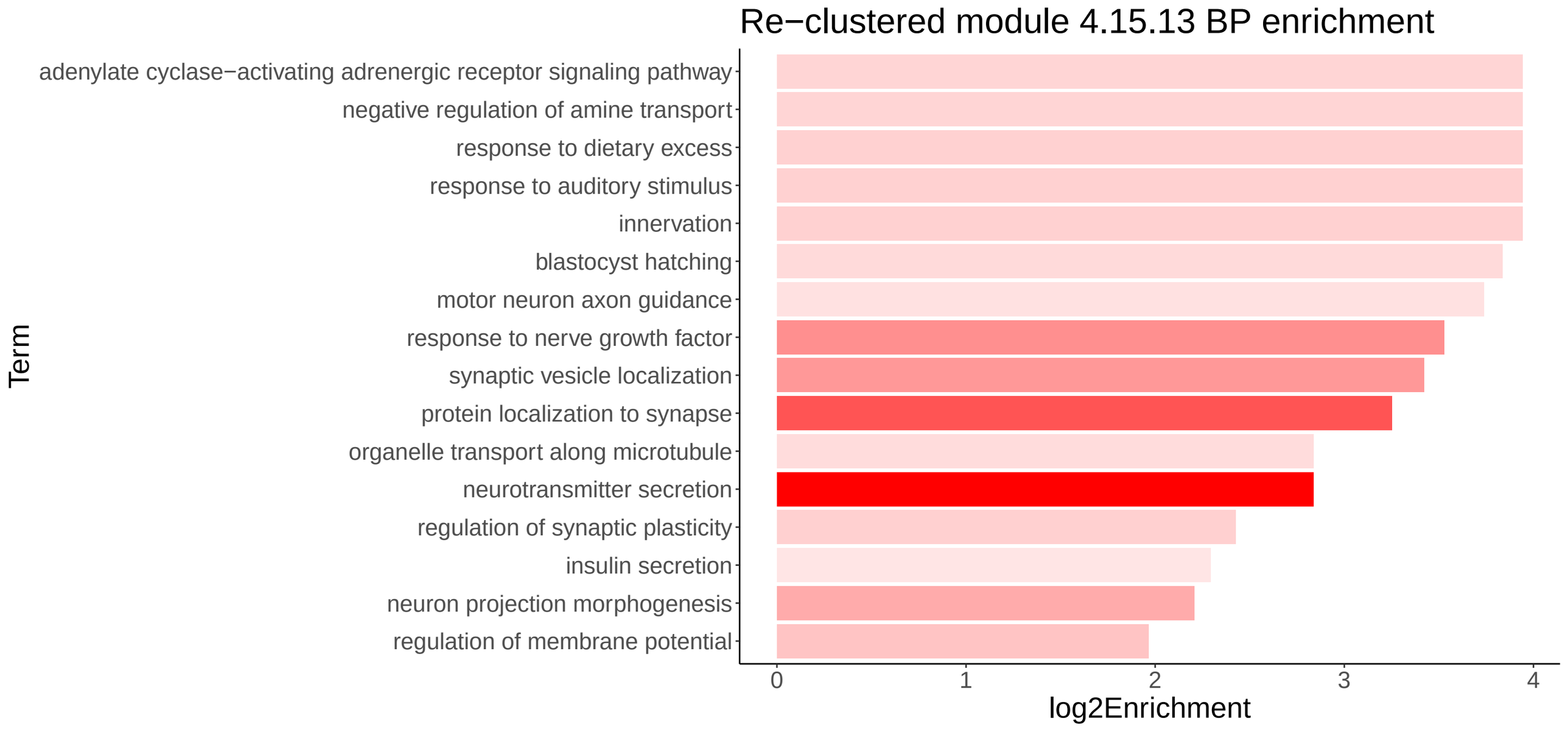

Re−clustered module 4.145 MF enrichment
Term
log2Enrichment

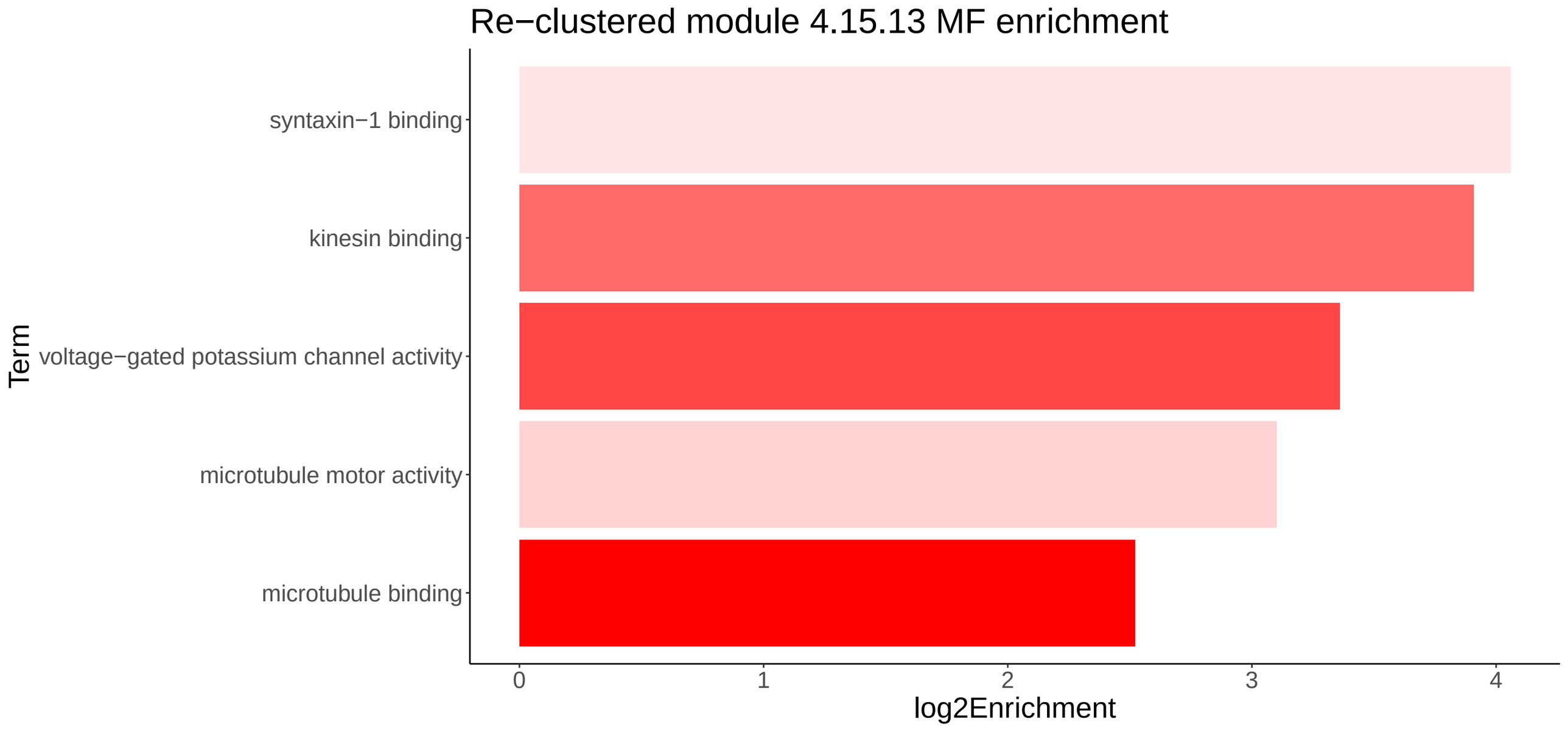

Re−clustered module 4.15.10 BP enrichment
Term
cellular response to osmotic stress
0
1
2
3
4
5
log2Enrichment

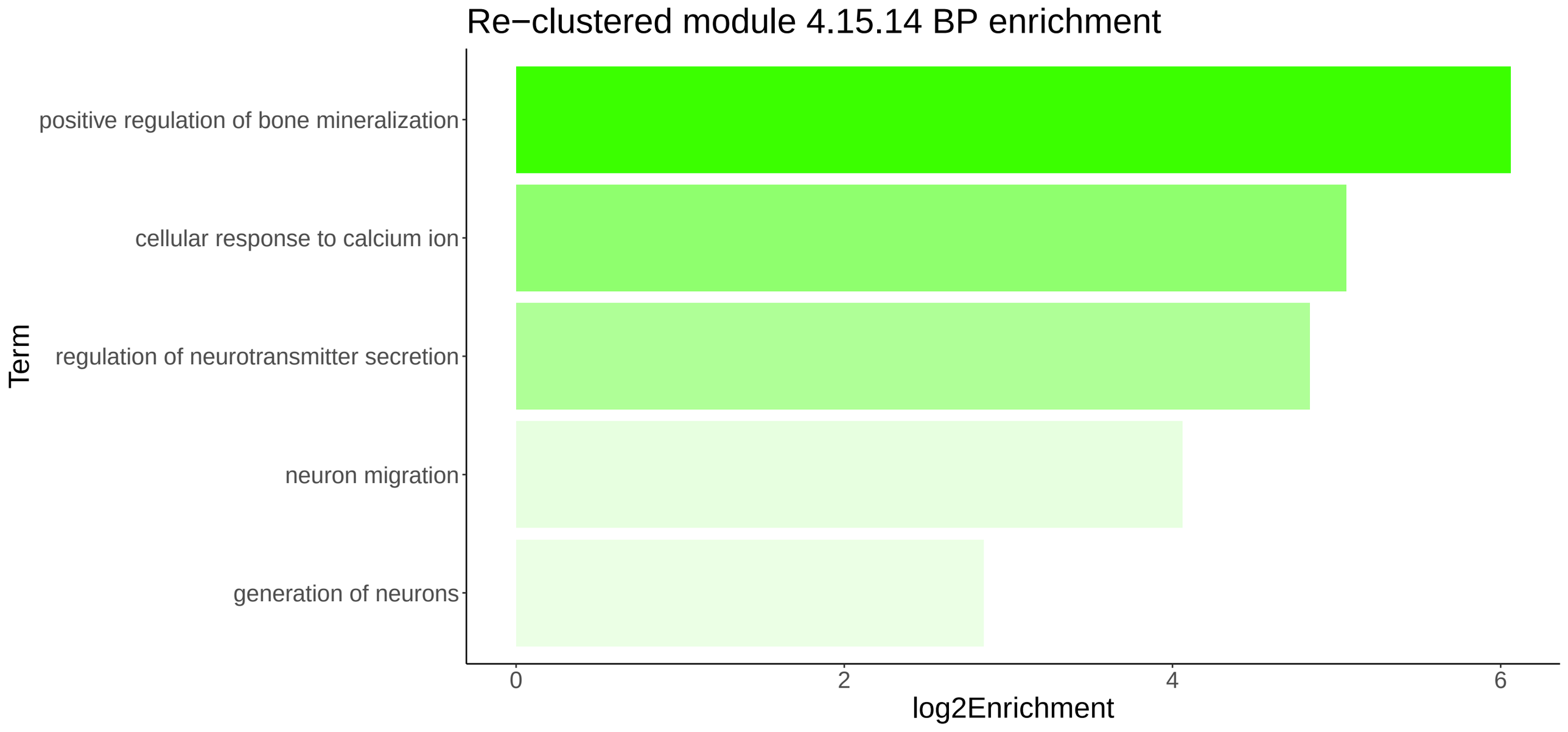

Re−clustered module 4.15.10 MF enrichment
Term
mRNA 3'−UTR binding
0
1
2
3
4
log2Enrichment

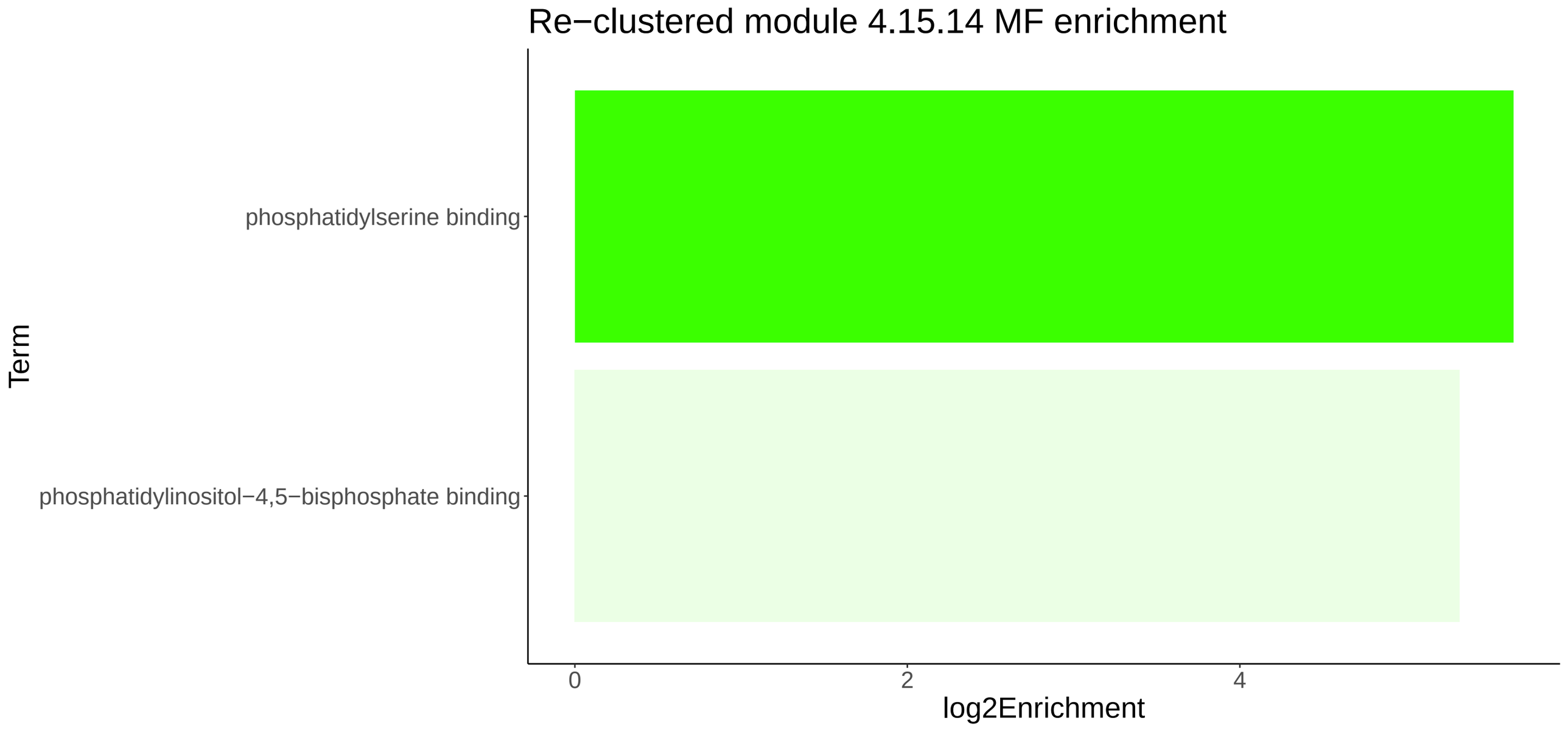

Re−clustered module 4.15.12 BP enrichment
Term
regulation of neurotransmitter receptor activity
neuron differentiation
0
1
2
3
4
5
log2Enrichment

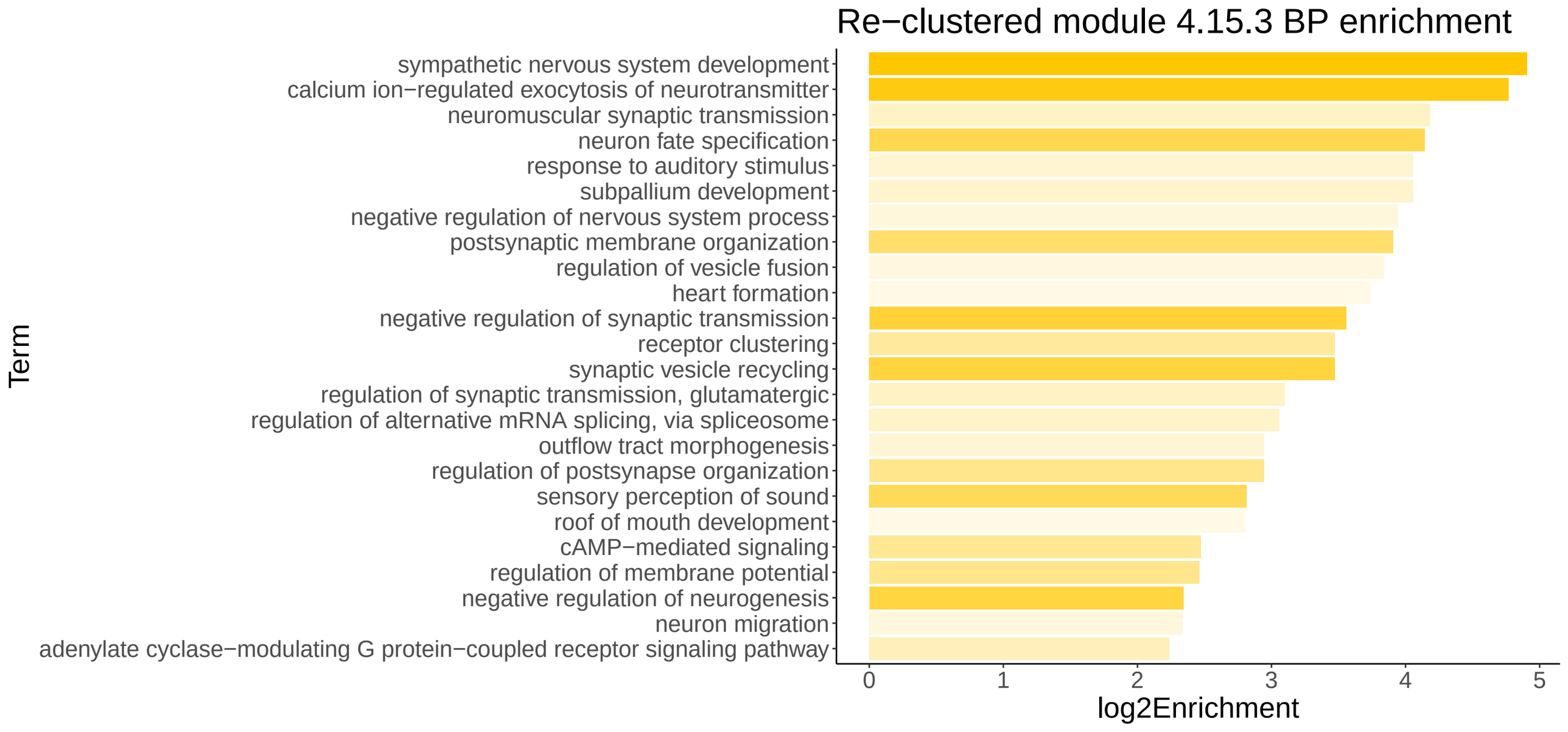

Re−clustered module 4.15.12 MF enrichment
Term
log2Enrichment

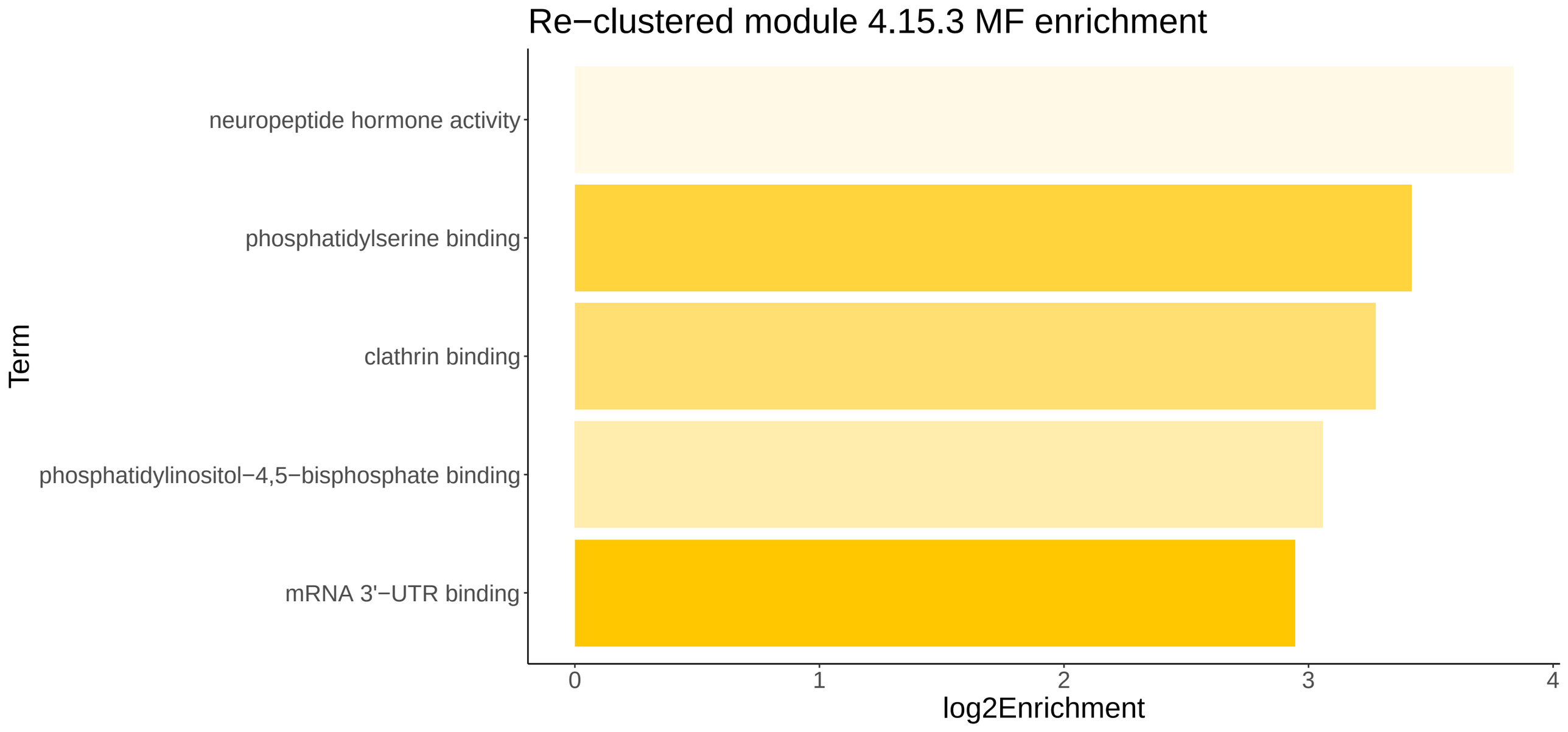

Re−clustered module 4.15.13 BP enrichment
adenylate cyclase−activating adrenergic receptor signaling pathway
negative regulation of amine transport
response to dietary excess
response to auditory stimulus
innervation
blastocyst hatching
motor neuron axon guidance
response to nerve growth factor
synaptic vesicle localization
protein localization to synapse
organelle transport along microtubule
neurotransmitter secretion
regulation of synaptic plasticity
insulin secretion
neuron projection morphogenesis
regulation of membrane potential
Term
0
1
2
3
4
log2Enrichment

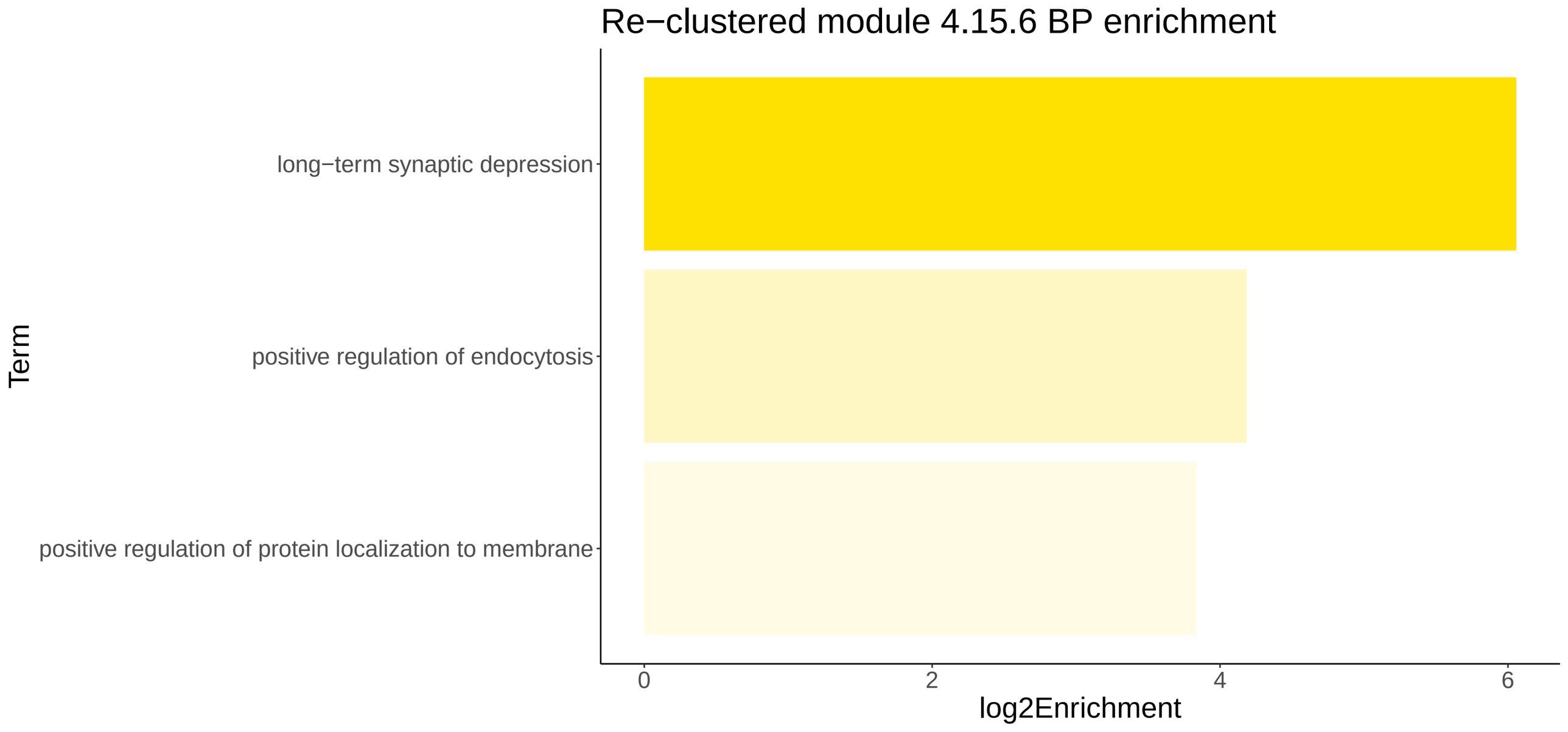

Re−clustered module 4.15.13 MF enrichment
Term
syntaxin−1 binding
kinesin binding
voltage−gated potassium channel activity
microtubule motor activity
microtubule binding
0
1
2
3
4
log2Enrichment

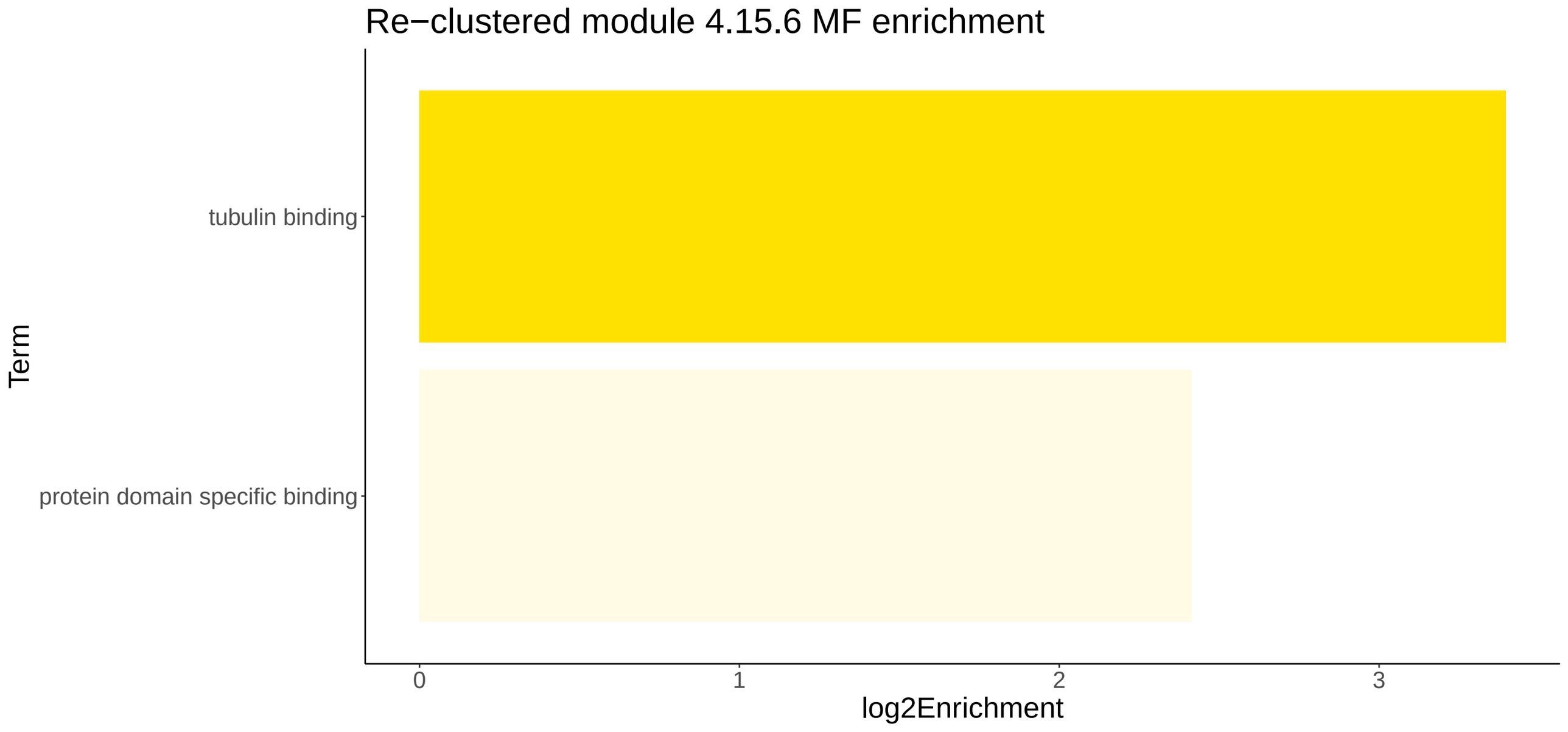

Re−clustered module 4.15.14 BP enrichment
positive regulation of bone mineralization
cellular response to calcium ion
regulation of neurotransmitter secretion
neuron migration
generation of neurons
Term
0
2
4
6
log2Enrichment

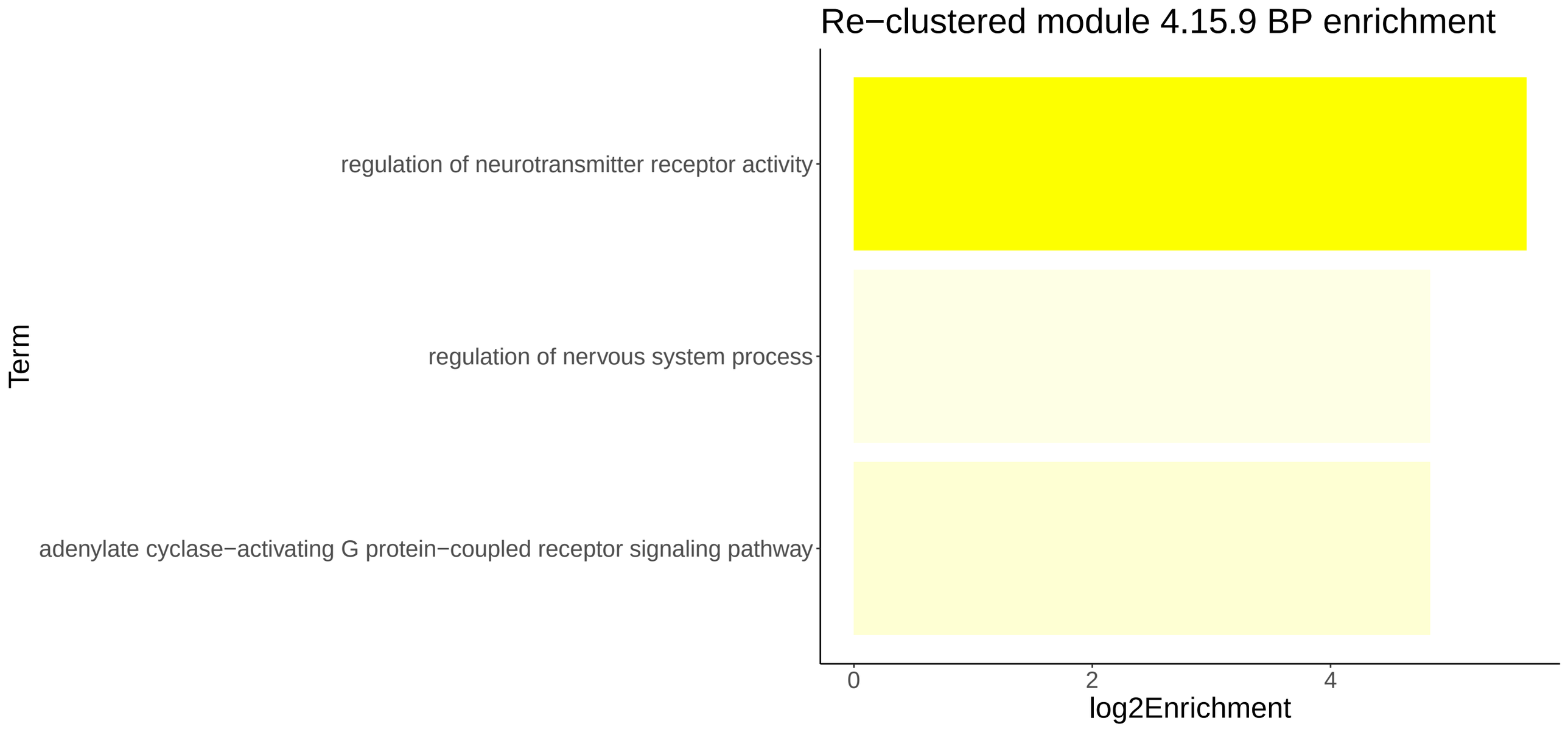

Re−clustered module 4.15.14 MF enrichment
Term
phosphatidylserine binding
phosphatidylinositol−4,5−bisphosphate binding
0
2
4
log2Enrichment

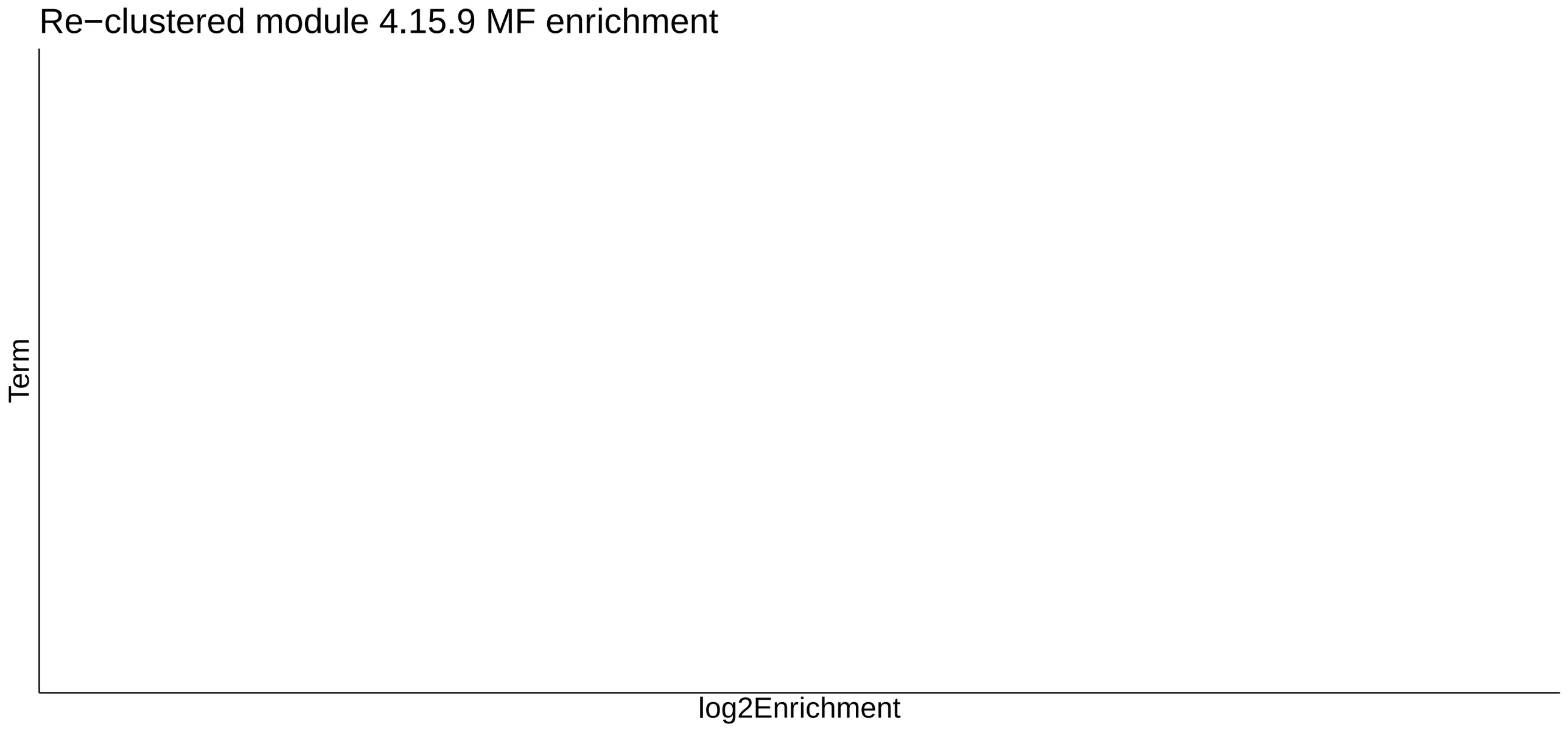

Re−clustered module 4.15.3 BP enrichment
Term
sympathetic nervous system development
calcium ion−regulated exocytosis of neurotransmitter
neuromuscular synaptic transmission
neuron fate specification
response to auditory stimulus
subpallium development
negative regulation of nervous system process
postsynaptic membrane organization
regulation of vesicle fusion
heart formation
negative regulation of synaptic transmission
receptor clustering
synaptic vesicle recycling
regulation of synaptic transmission, glutamatergic
regulation of alternative mRNA splicing, via spliceosome
outflow tract morphogenesis
regulation of postsynapse organization
sensory perception of sound
roof of mouth development
cAMP−mediated signaling
regulation of membrane potential
negative regulation of neurogenesis
neuron migration
adenylate cyclase−modulating G protein−coupled receptor signaling pathway
0
1
2
3
4
5
log2Enrichment

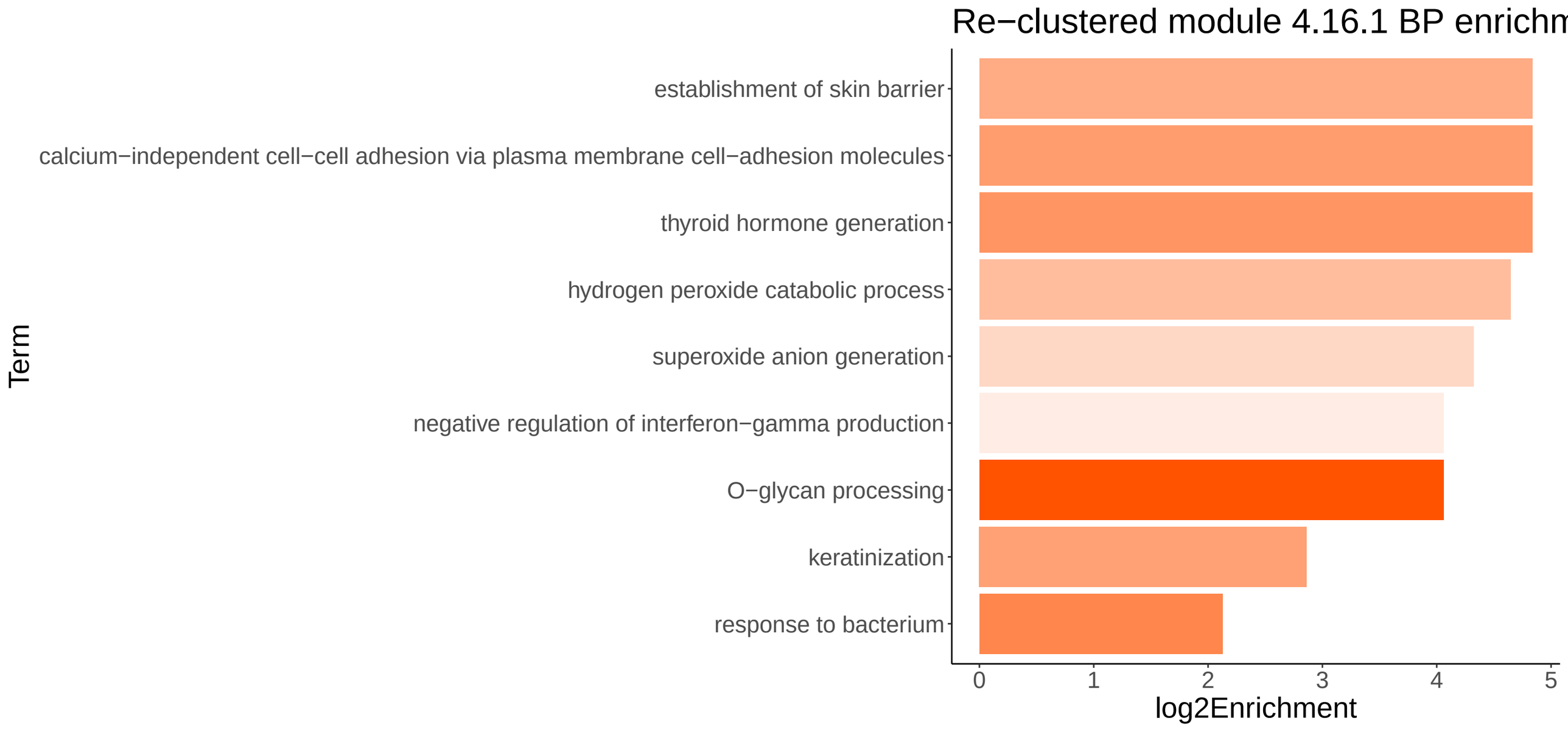

Re−clustered module 4.15.3 MF enrichment
Term
neuropeptide hormone activity
phosphatidylserine binding
clathrin binding
phosphatidylinositol−4,5−bisphosphate binding
mRNA 3'−UTR binding
0
1
2
3
4
log2Enrichment

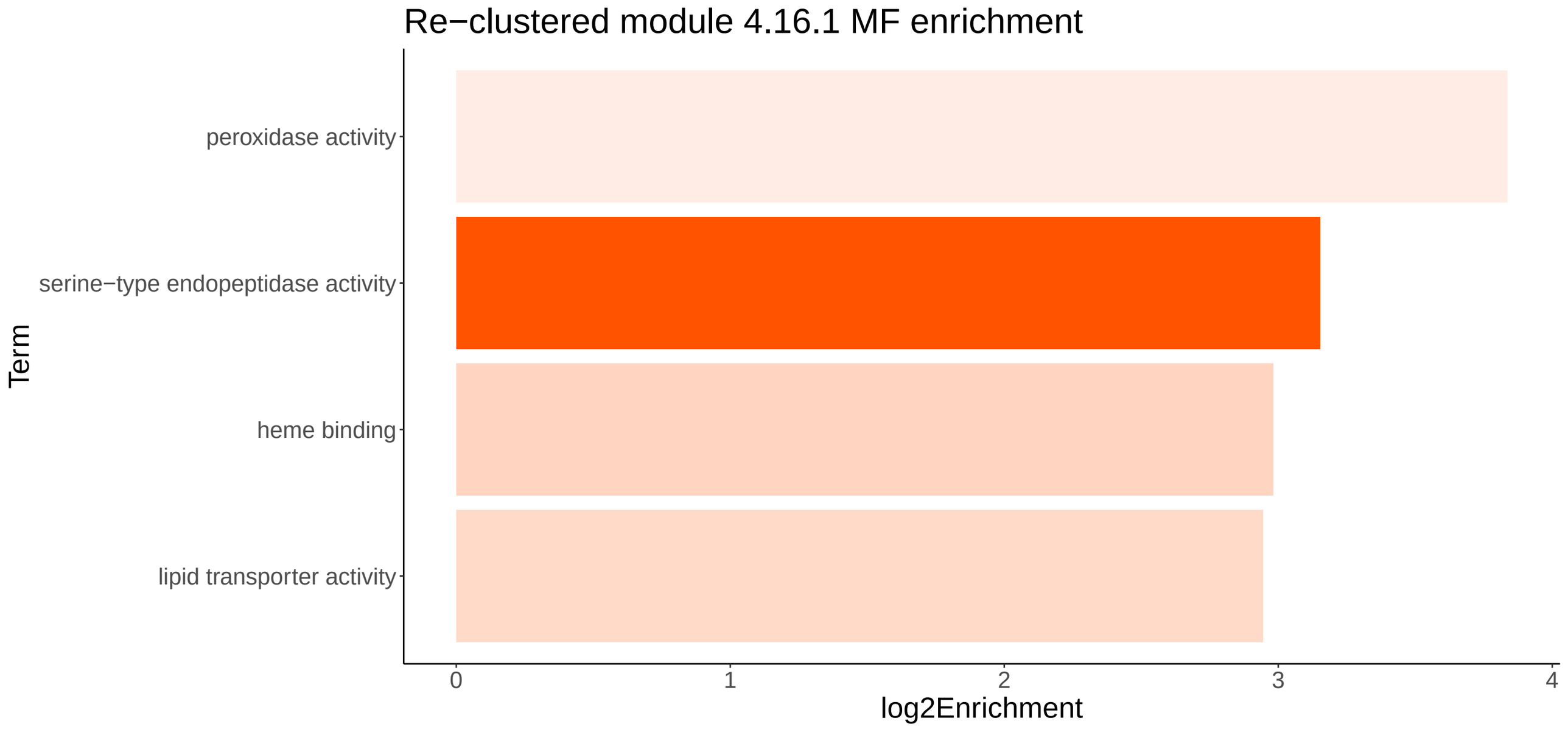

Re−clustered module 4.15.6 BP enrichment
Term
long−term synaptic depression
positive regulation of endocytosis
positive regulation of protein localization to membrane
0
2
4
6
log2Enrichment

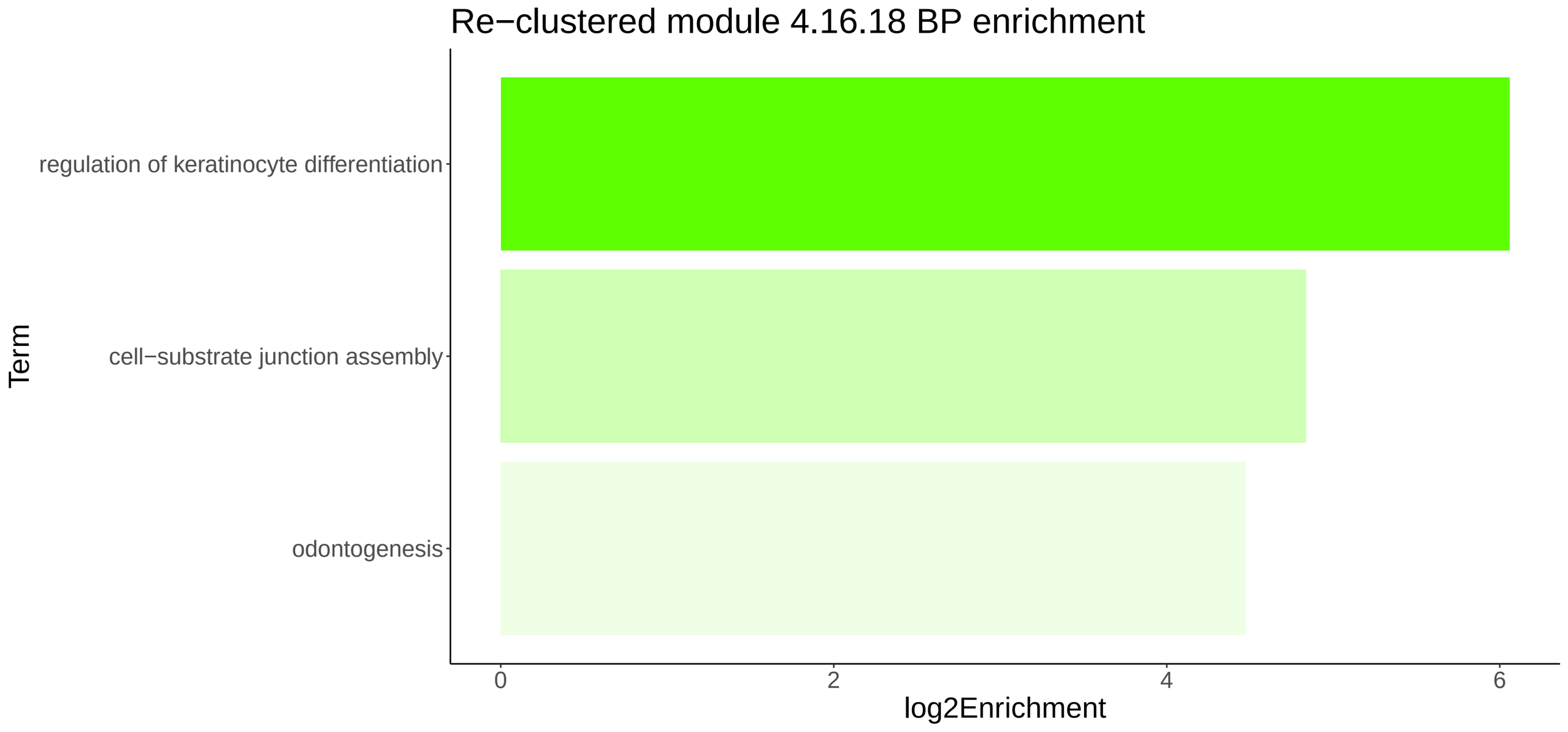

Re−clustered module 4.15.6 MF enrichment
Term
tubulin binding
protein domain specific binding
0
1
2
3
log2Enrichment

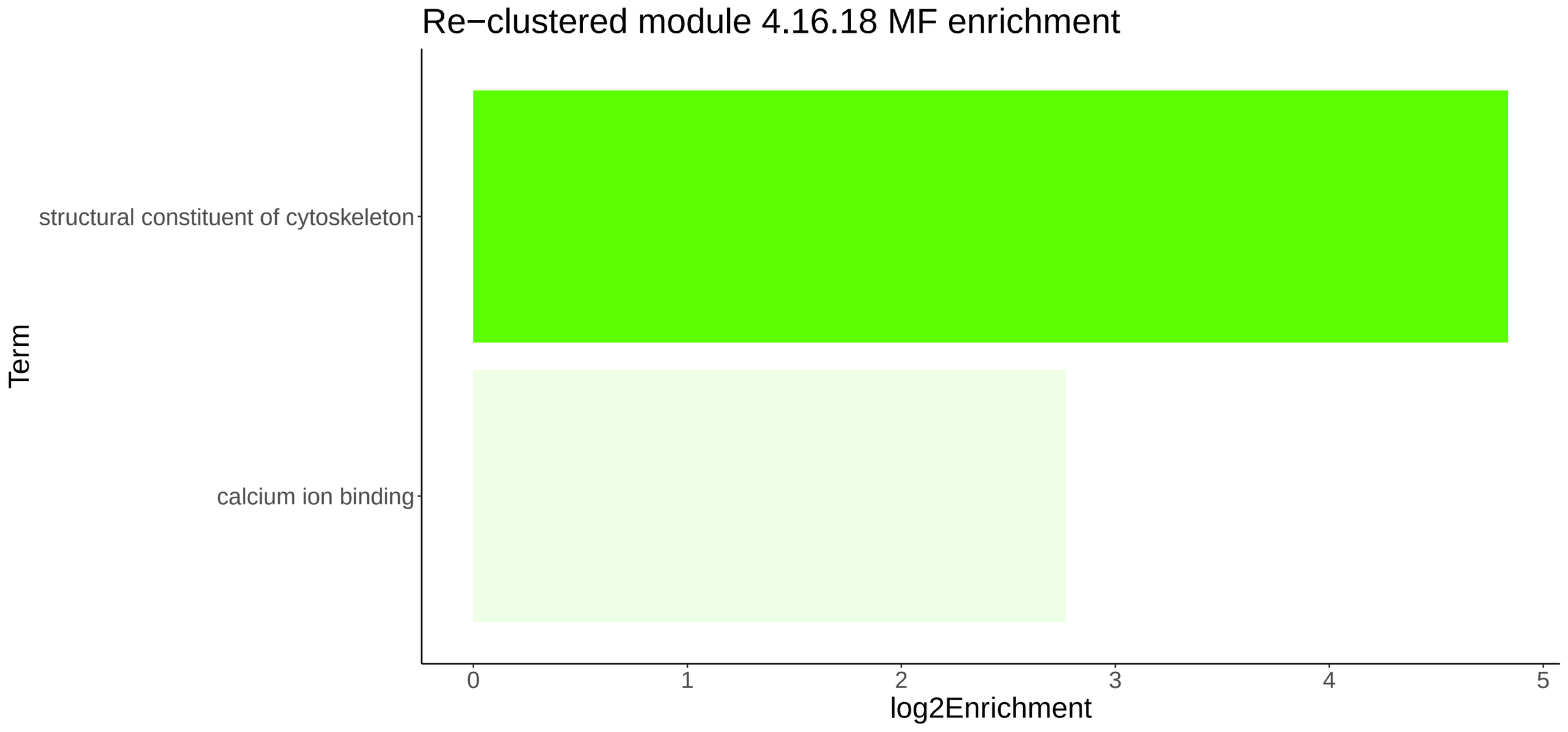

Re−clustered module 4.15.9 BP enrichment
Term
regulation of neurotransmitter receptor activity
regulation of nervous system process
adenylate cyclase−activating G protein−coupled receptor signaling pathway
0
2
4
log2Enrichment

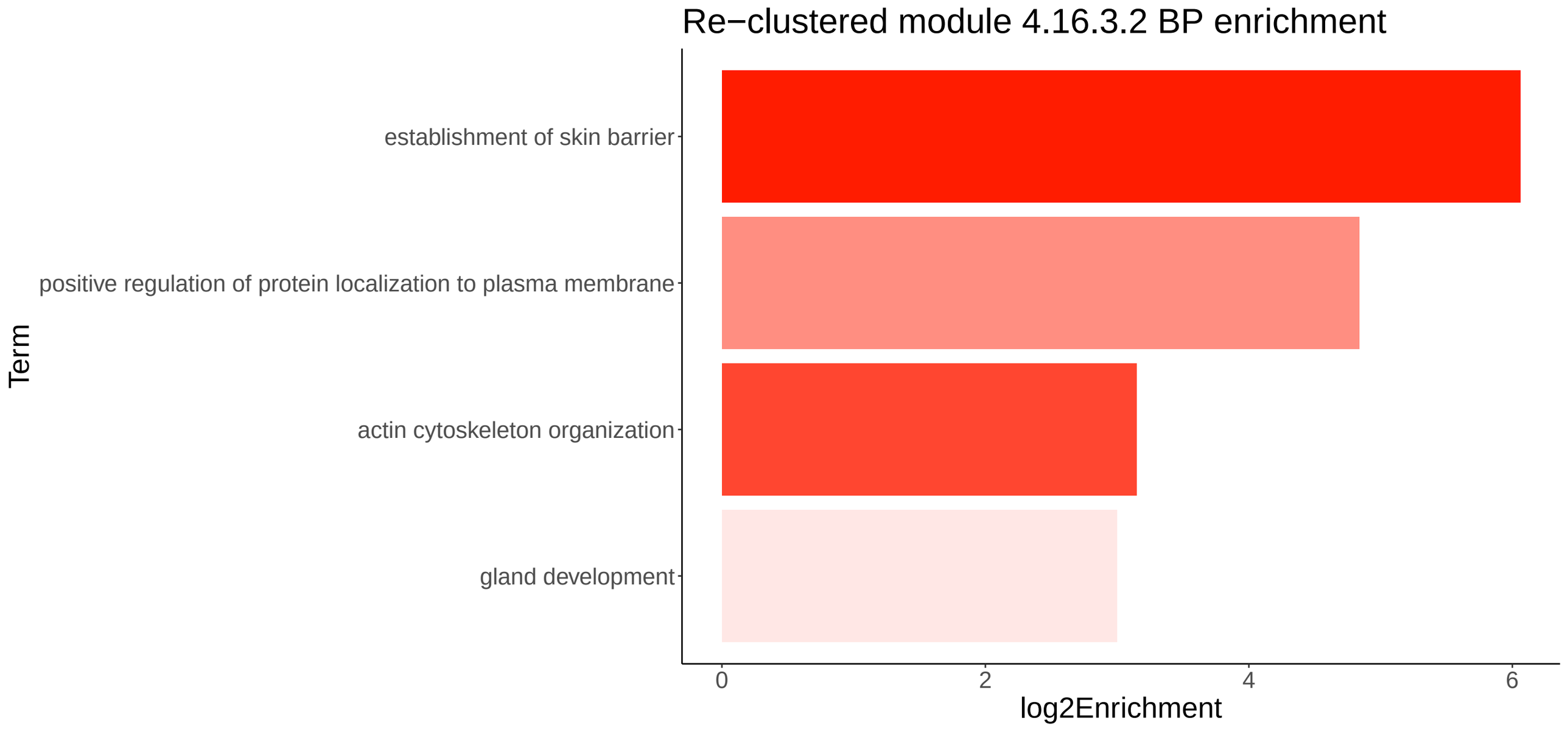

Re−clustered module 4.15.9 MF enrichment
Term
log2Enrichment

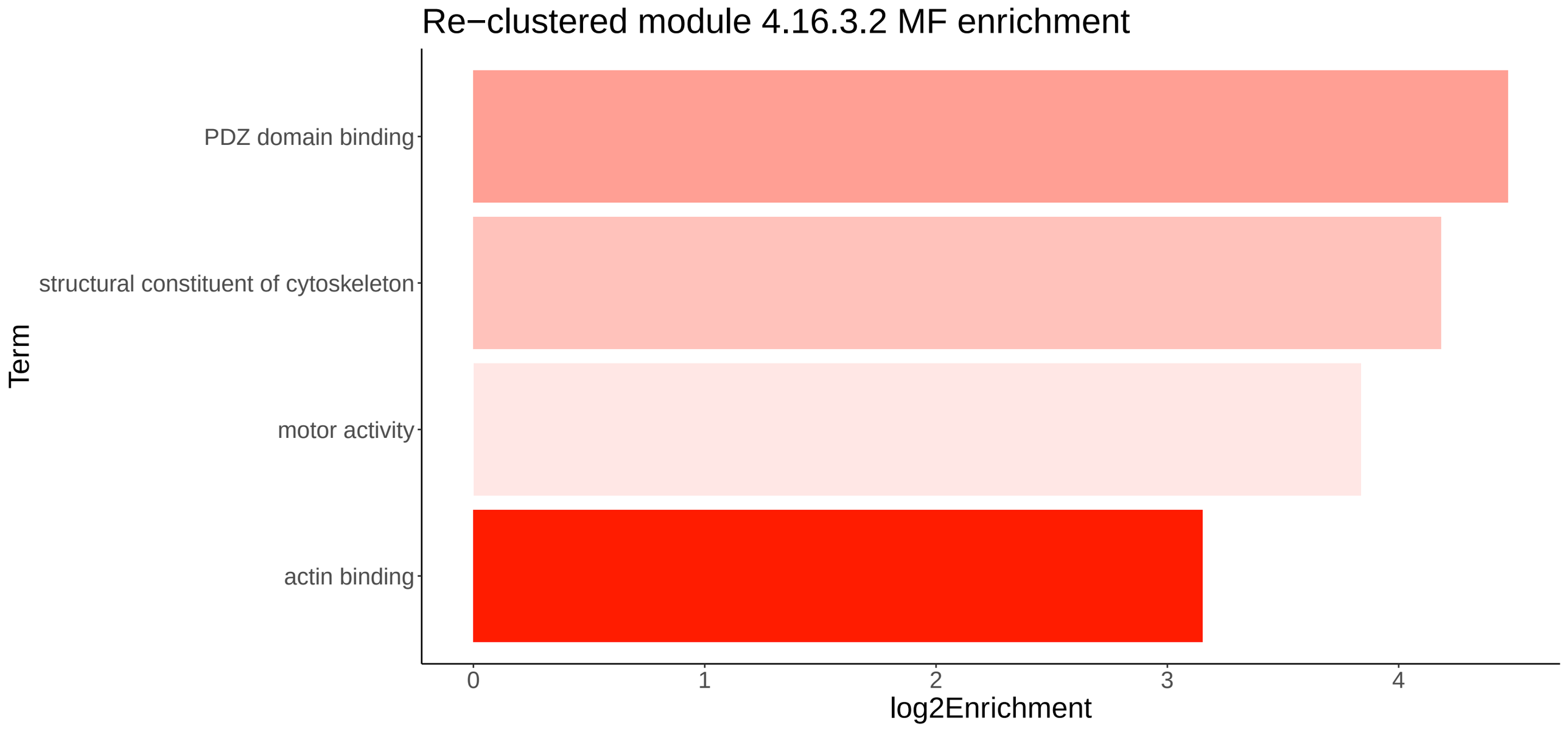

Re−clustered module 4.16.1 BP enrichm
establishment of skin barrier
calcium−independent cell−cell adhesion via plasma membrane cell−adhesion molecules
thyroid hormone generation
hydrogen peroxide catabolic process
superoxide anion generation
negative regulation of interferon−gamma production
O−glycan processing
keratinization
response to bacterium
Term
0
1
2
3
4
5
log2Enrichment

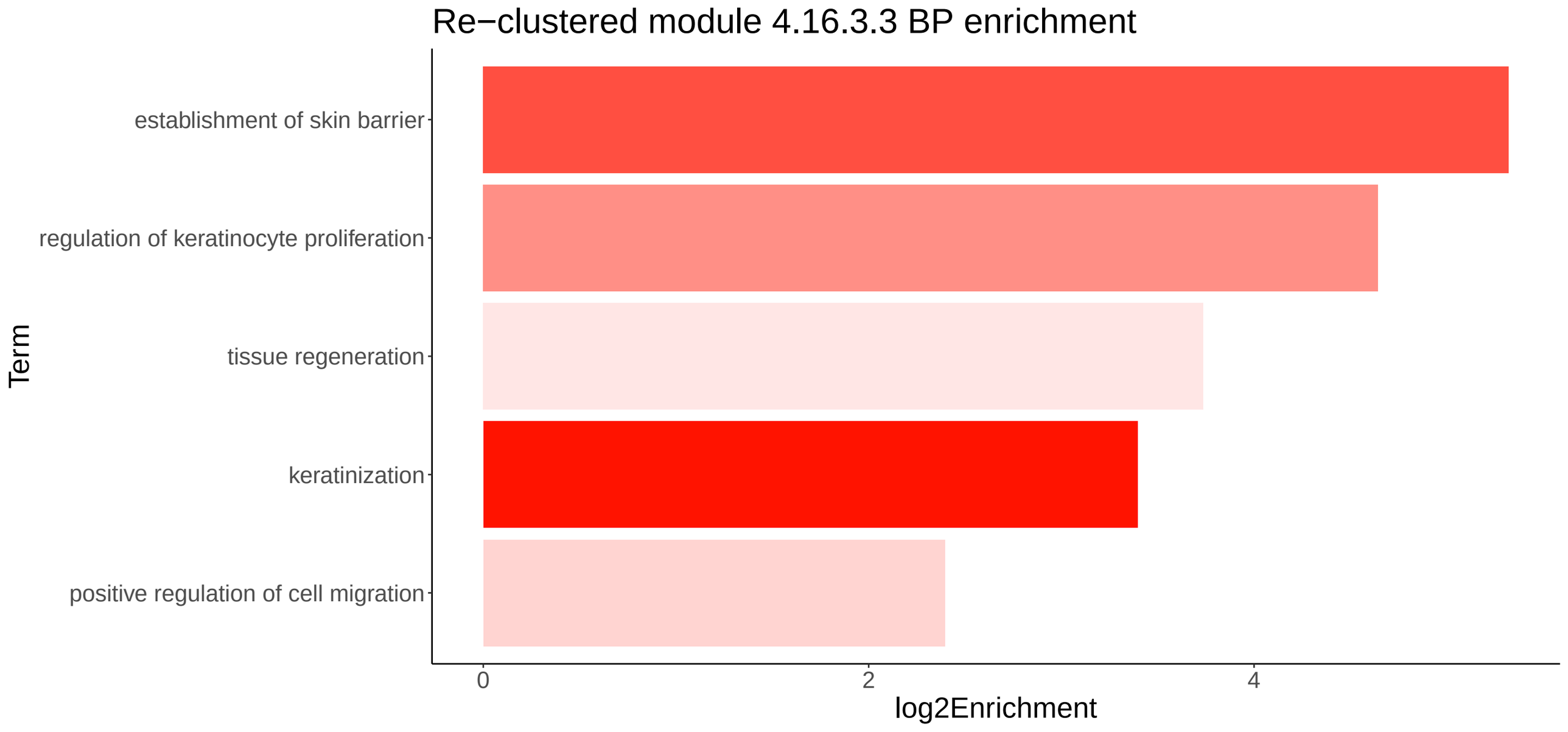

Re−clustered module 4.16.1 MF enrichment
peroxidase activity
serine−type endopeptidase activity
heme binding
lipid transporter activity
Term
0
1
2
3
4
log2Enrichment

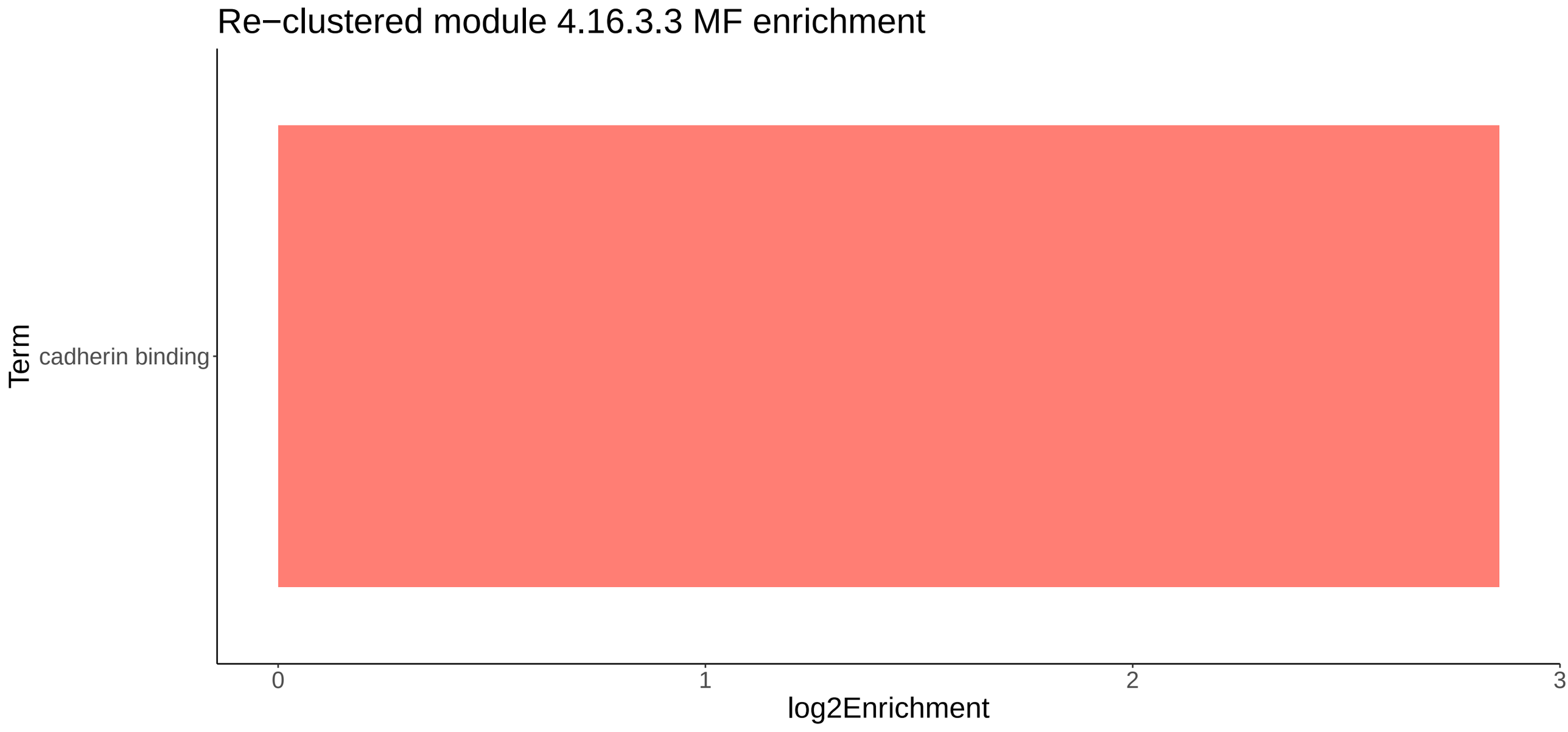

Re−clustered module 4.16.18 BP enrichment
Term
regulation of keratinocyte differentiation
cell−substrate junction assembly
odontogenesis
0
2
4
6
log2Enrichment

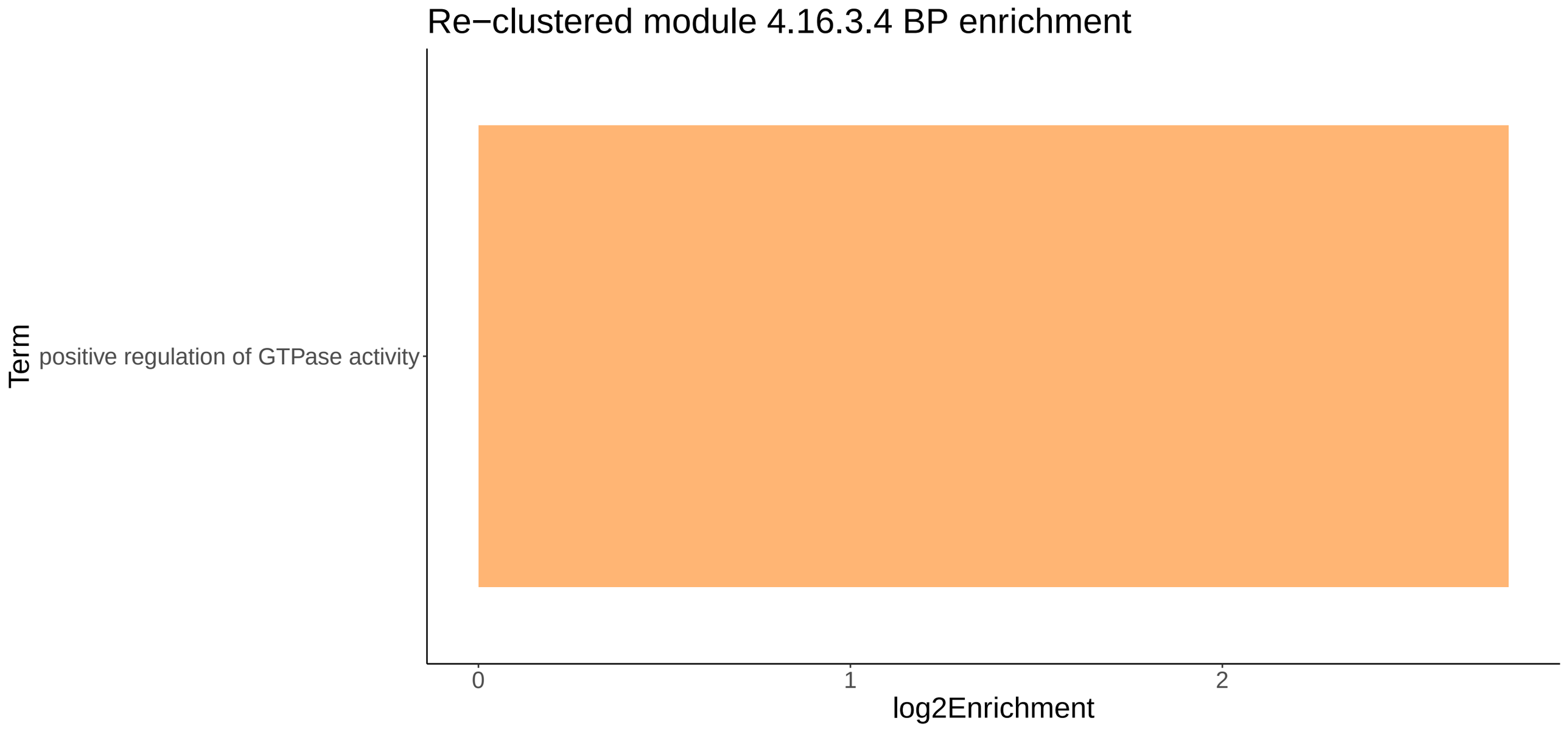

Re−clustered module 4.16.18 MF enrichment
Term
structural constituent of cytoskeleton
calcium ion binding
0
1
2
3
4
5
log2Enrichment

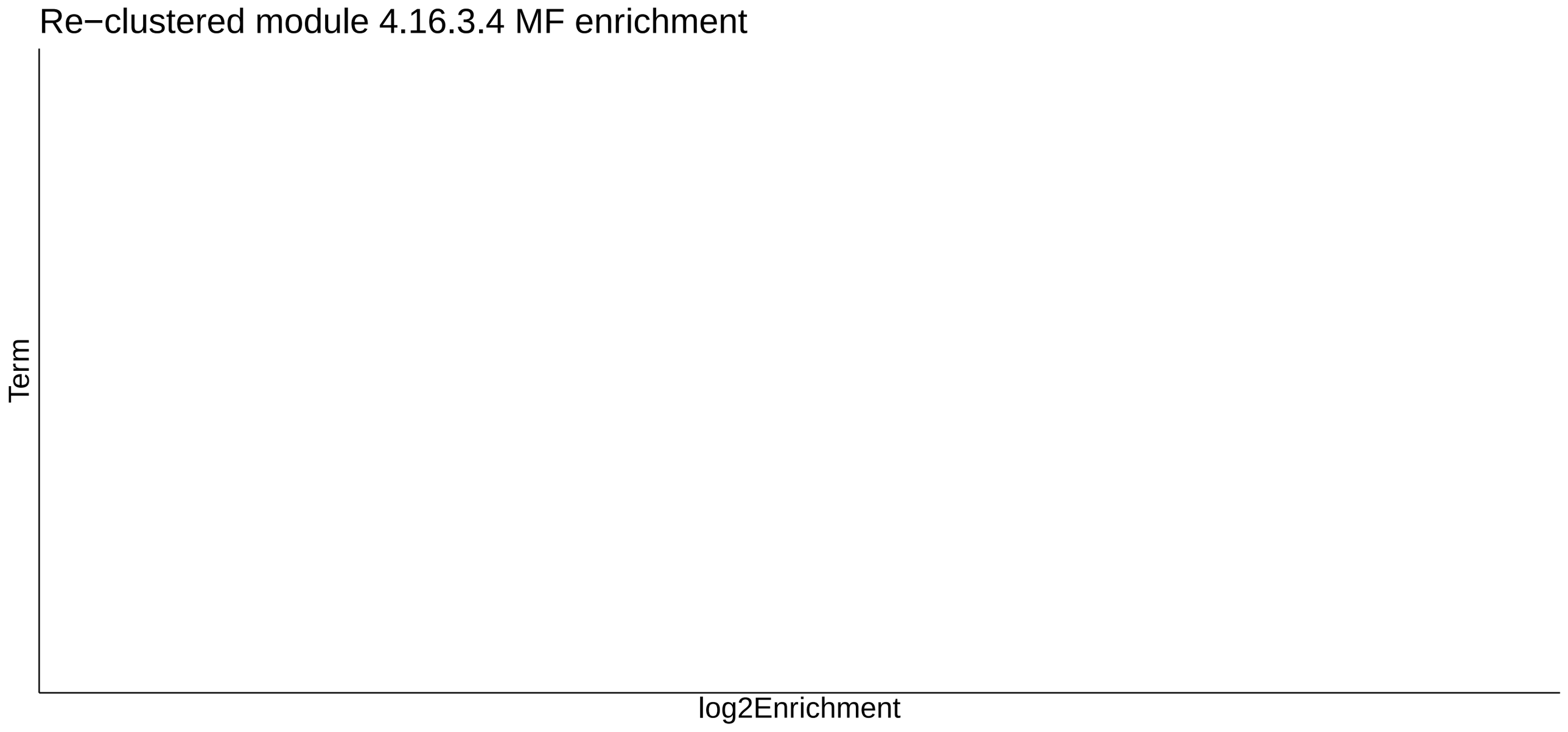

Re−clustered module 4.16.3.2 BP enrichment
establishment of skin barrier
positive regulation of protein localization to plasma membrane
actin cytoskeleton organization
gland development
Term
0
2
4
6
log2Enrichment

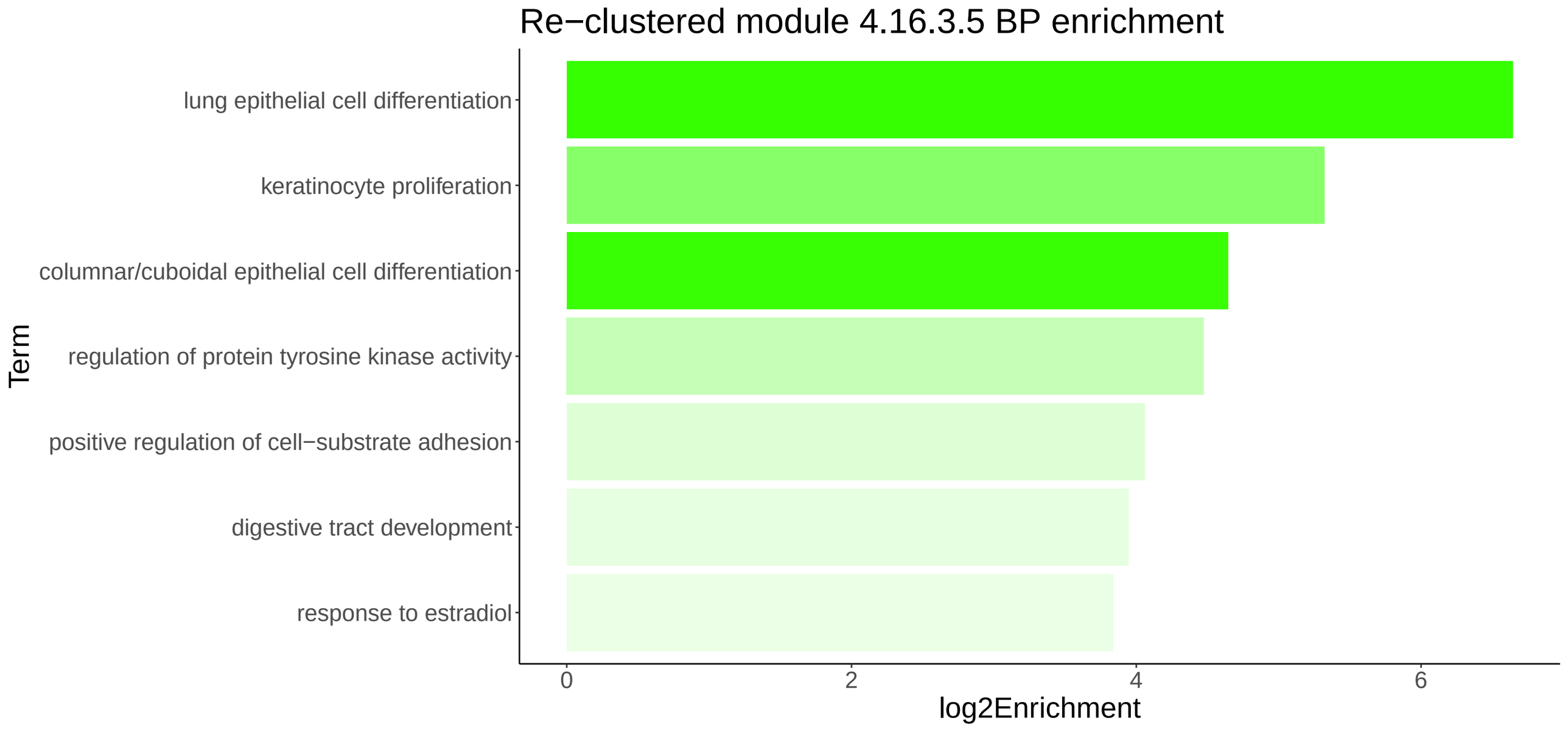

Re−clustered module 4.16.3.2 MF enrichment
PDZ domain binding
structural constituent of cytoskeleton
motor activity
actin binding
Term
0
1
2
3
4
log2Enrichment

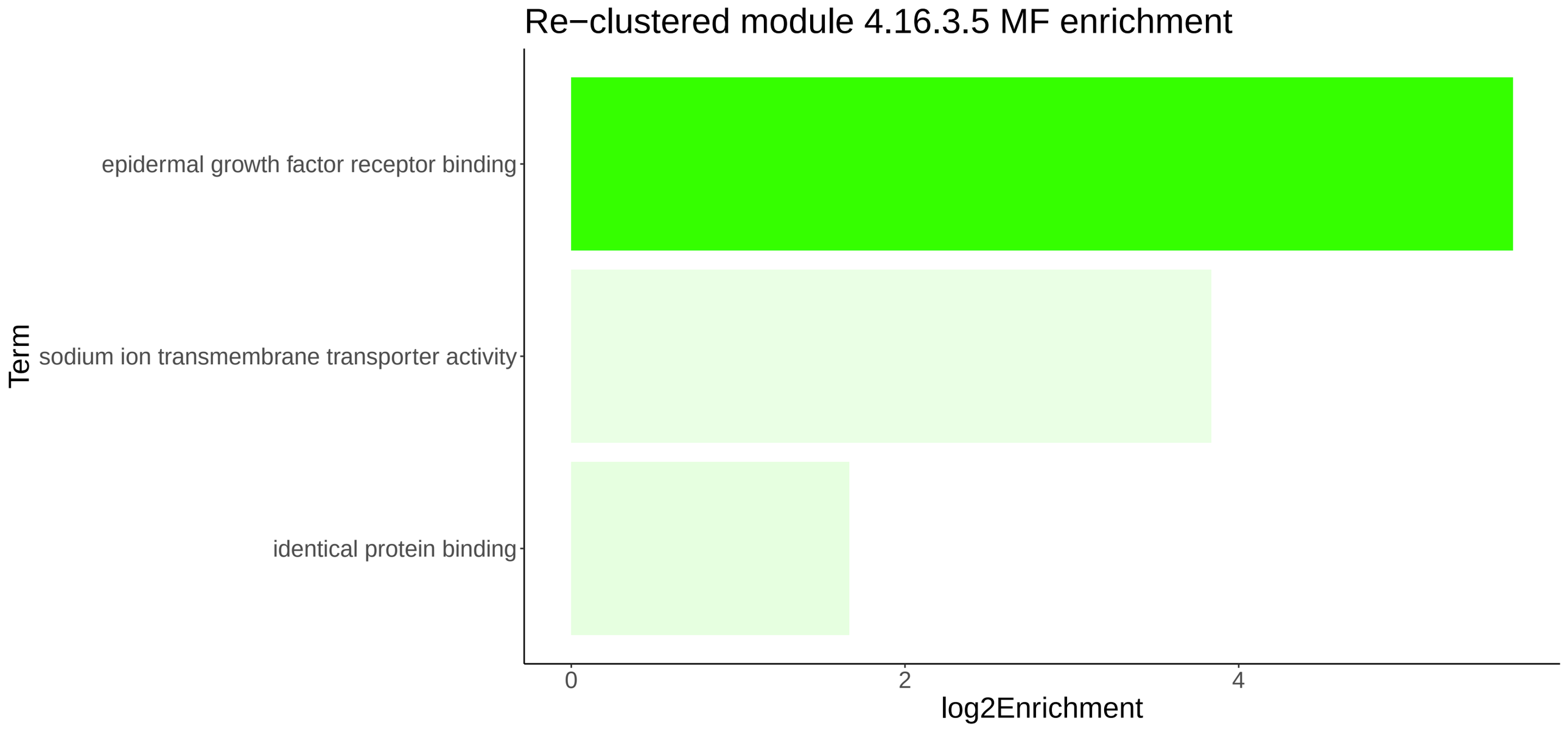

Re−clustered module 4.16.3.3 BP enrichment
establishment of skin barrier
regulation of keratinocyte proliferation
tissue regeneration
keratinization
positive regulation of cell migration
Term
0
2
4
log2Enrichment

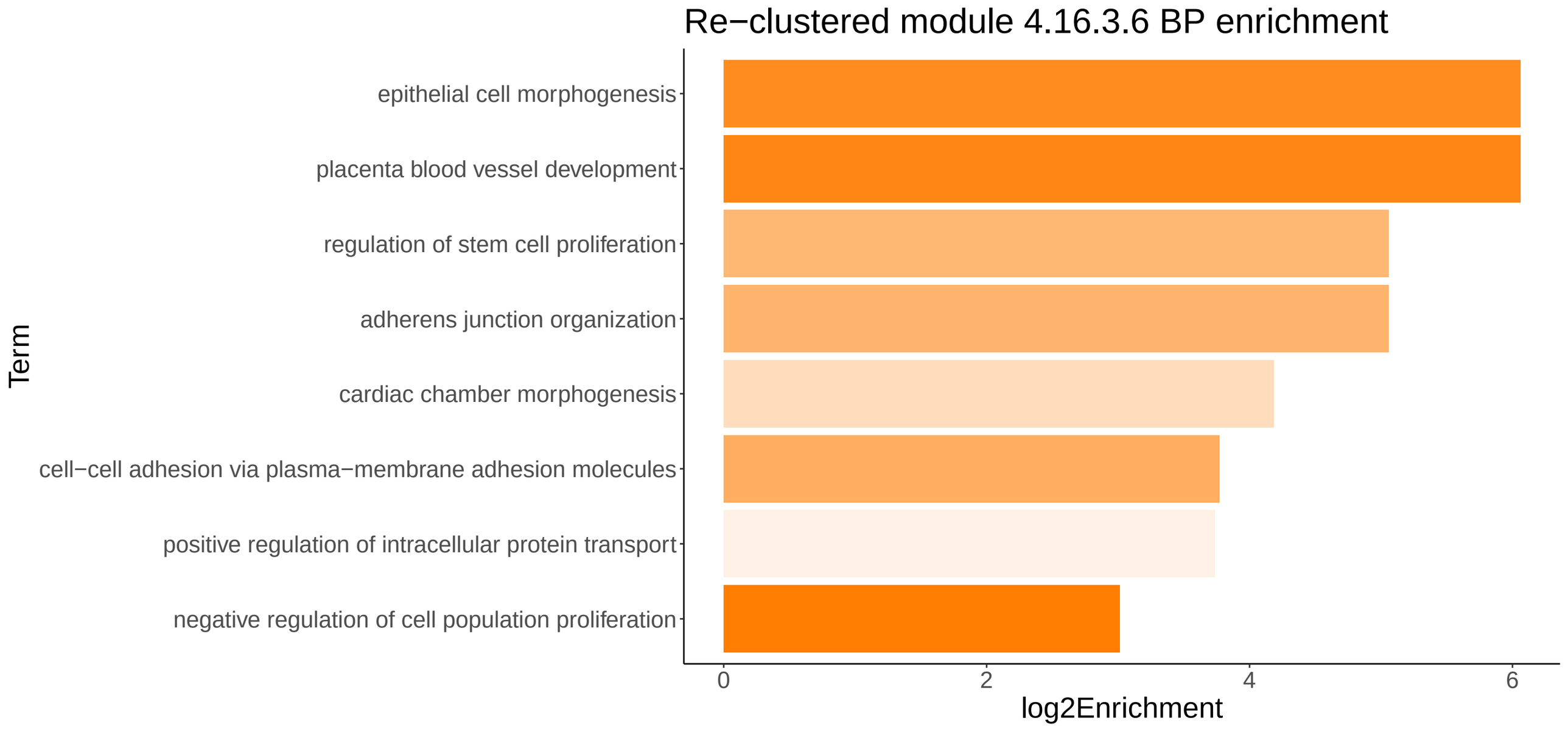

Re−clustered module 4.16.3.3 MF enrichment
Term
cadherin binding
0
1
2
3
log2Enrichment

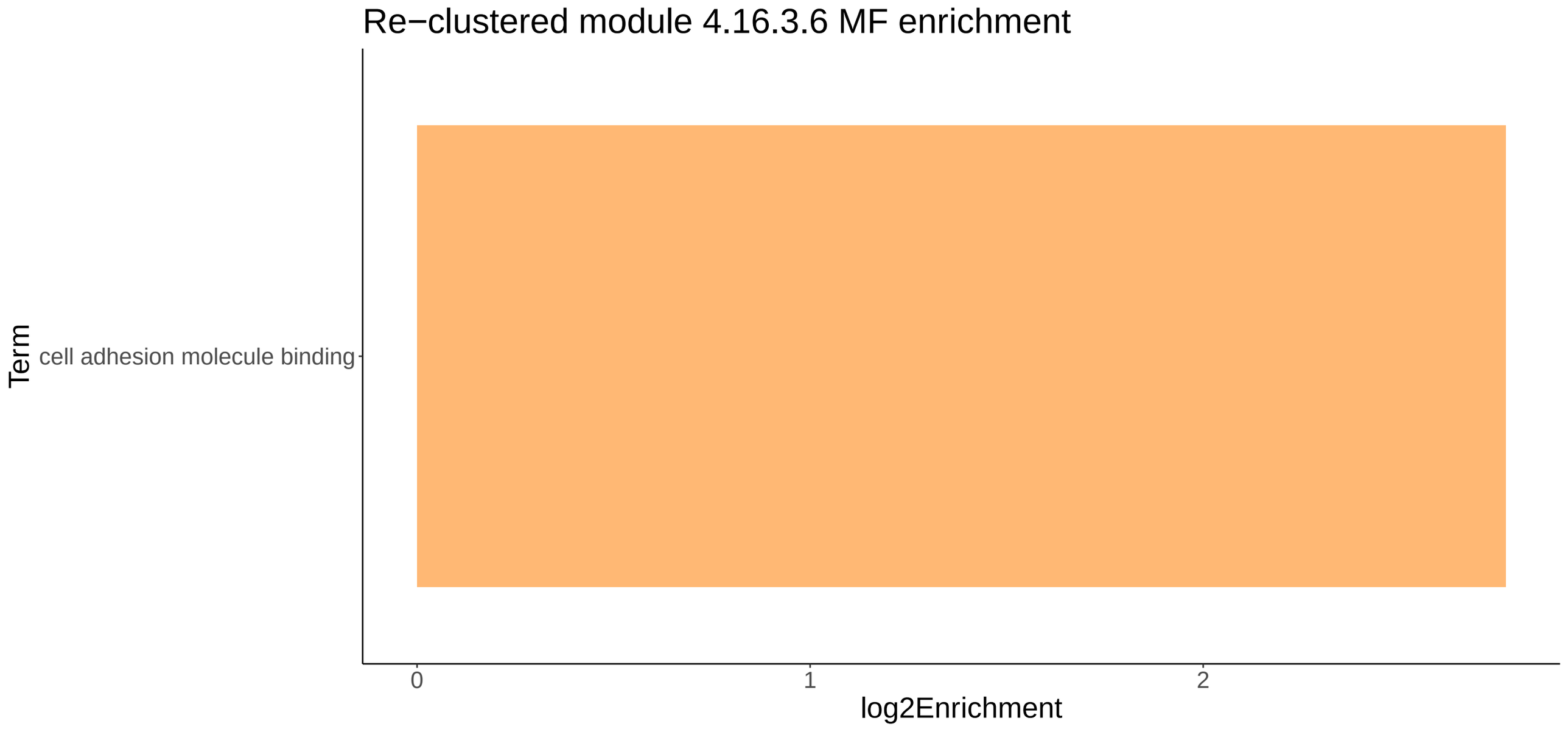

Re−clustered module 4.16.3.4 BP enrichment
Term
positive regulation of GTPase activity
0
1
2
log2Enrichment

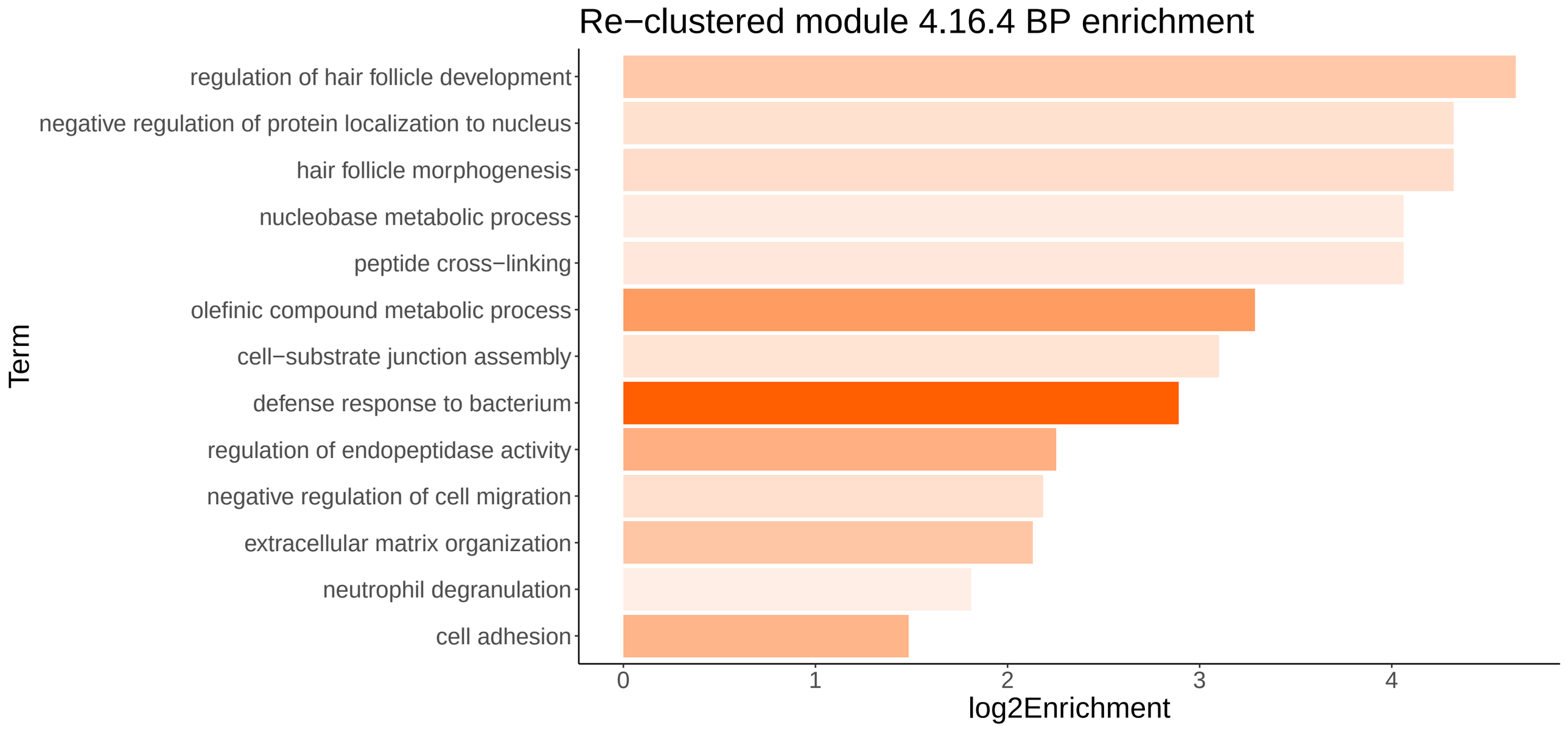

Re−clustered module 4.16.3.4 MF enrichment
Term
log2Enrichment


Re−clustered module 4.16.3.5 BP enrichment
lung epithelial cell differentiation
keratinocyte proliferation
columnar/cuboidal epithelial cell differentiation
regulation of protein tyrosine kinase activity
positive regulation of cell−substrate adhesion
digestive tract development
response to estradiol
Term
0
2
4
6
log2Enrichment


Re−clustered module 4.16.3.5 MF enrichment
Term
epidermal growth factor receptor binding
sodium ion transmembrane transporter activity
identical protein binding
0
2
4
log2Enrichment


Re−clustered module 4.16.3.6 BP enrichment
Term
epithelial cell morphogenesis
placenta blood vessel development
regulation of stem cell proliferation
adherens junction organization
cardiac chamber morphogenesis
cell−cell adhesion via plasma−membrane adhesion molecules
positive regulation of intracellular protein transport
negative regulation of cell population proliferation
0
2
4
6
log2Enrichment


Re−clustered module 4.16.3.6 MF enrichment
Term
cell adhesion molecule binding
0
1
2
log2Enrichment

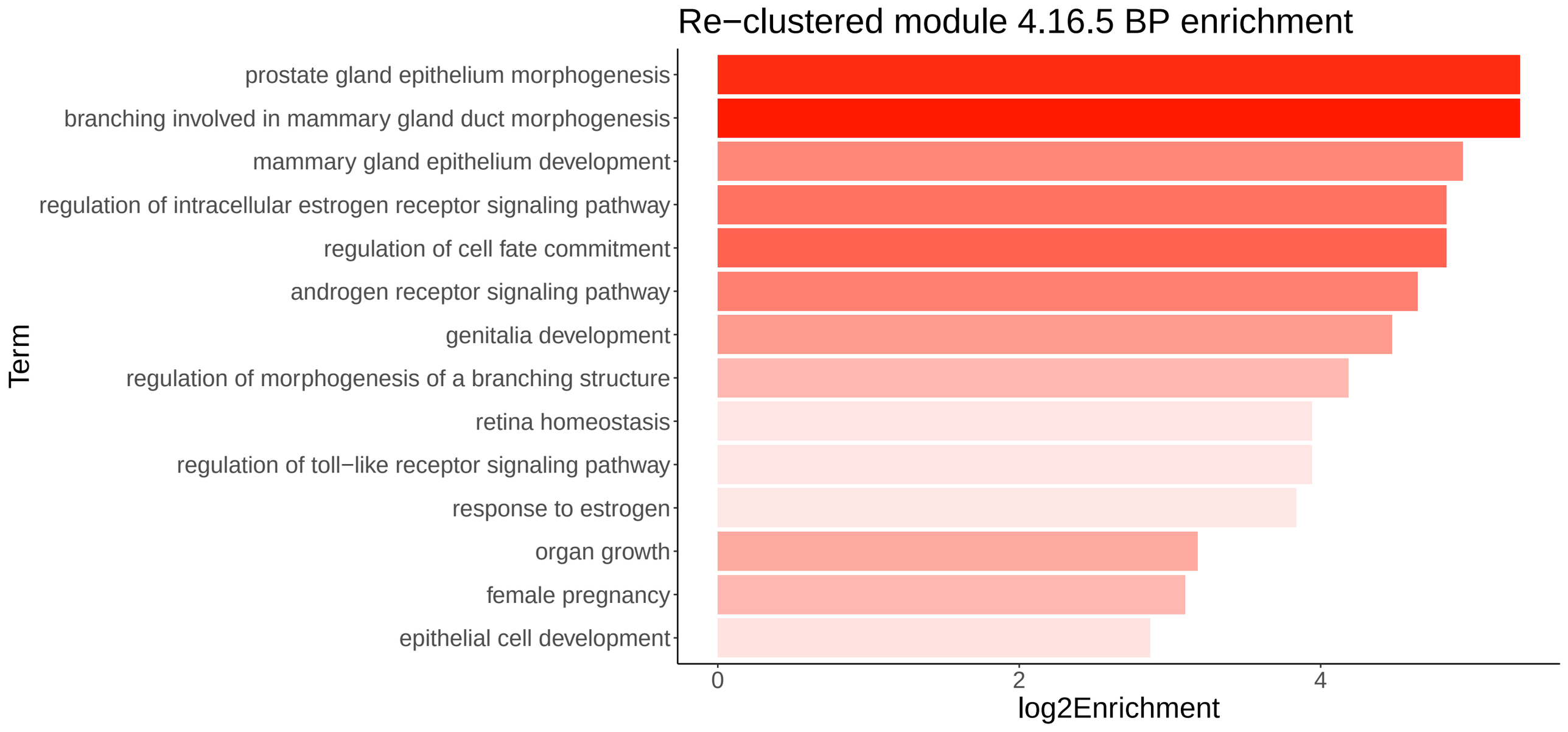

Re−clustered module 4.16.4 BP enrichment
regulation of hair follicle development
negative regulation of protein localization to nucleus
hair follicle morphogenesis
nucleobase metabolic process
peptide cross−linking
olefinic compound metabolic process
cell−substrate junction assembly
defense response to bacterium
regulation of endopeptidase activity
negative regulation of cell migration
extracellular matrix organization
neutrophil degranulation
cell adhesion
Term
0
1
2
3
4
log2Enrichment

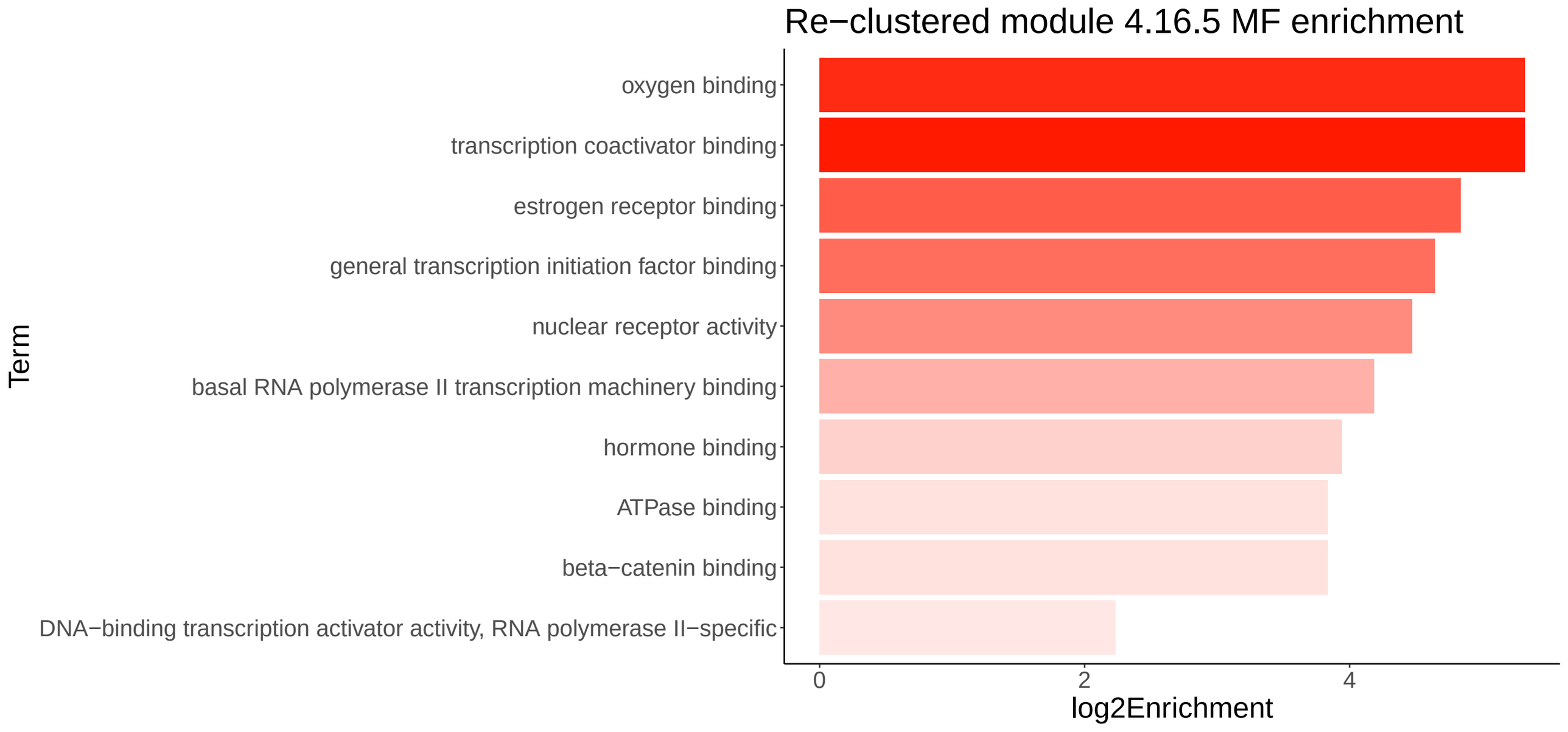
gap junctio

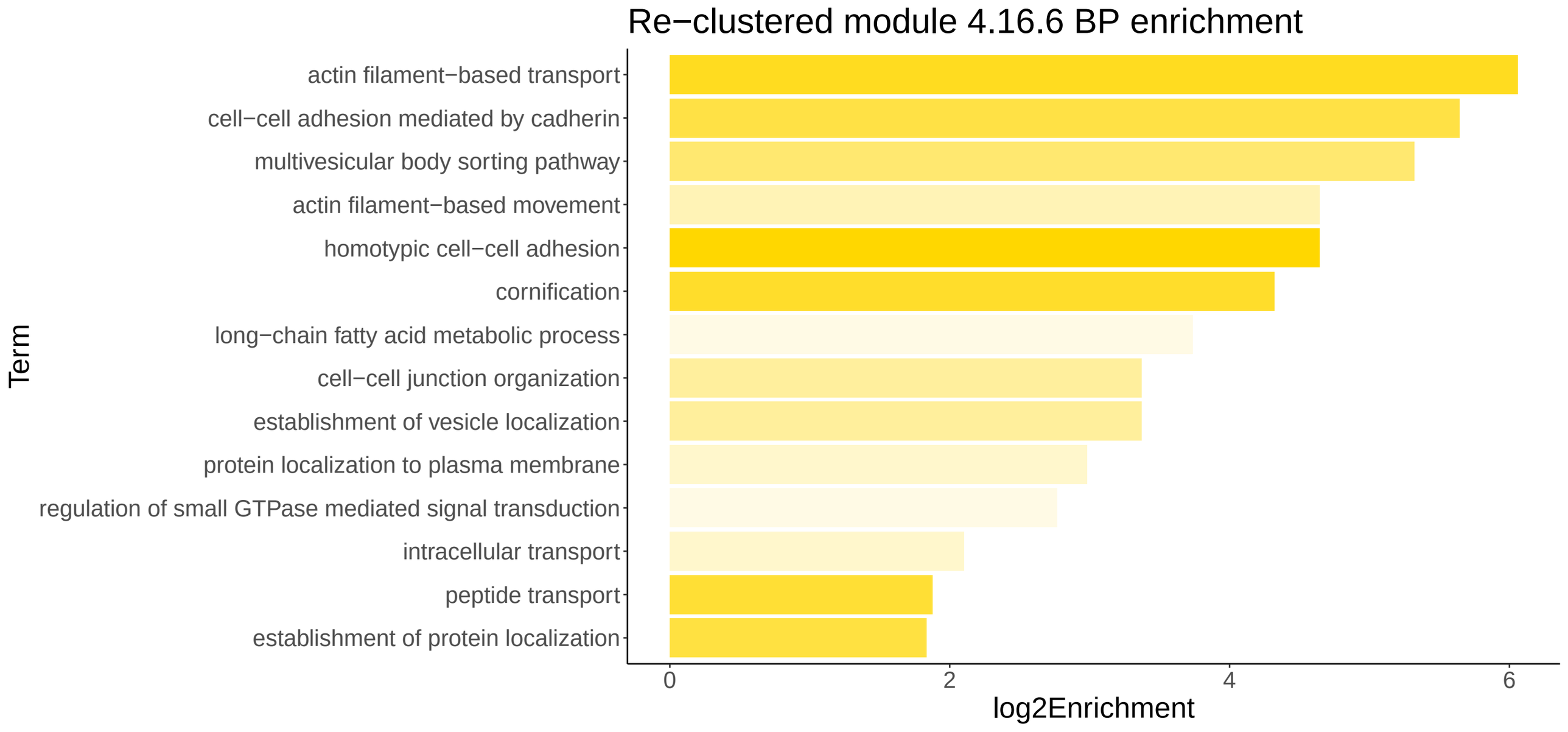
fatty acid

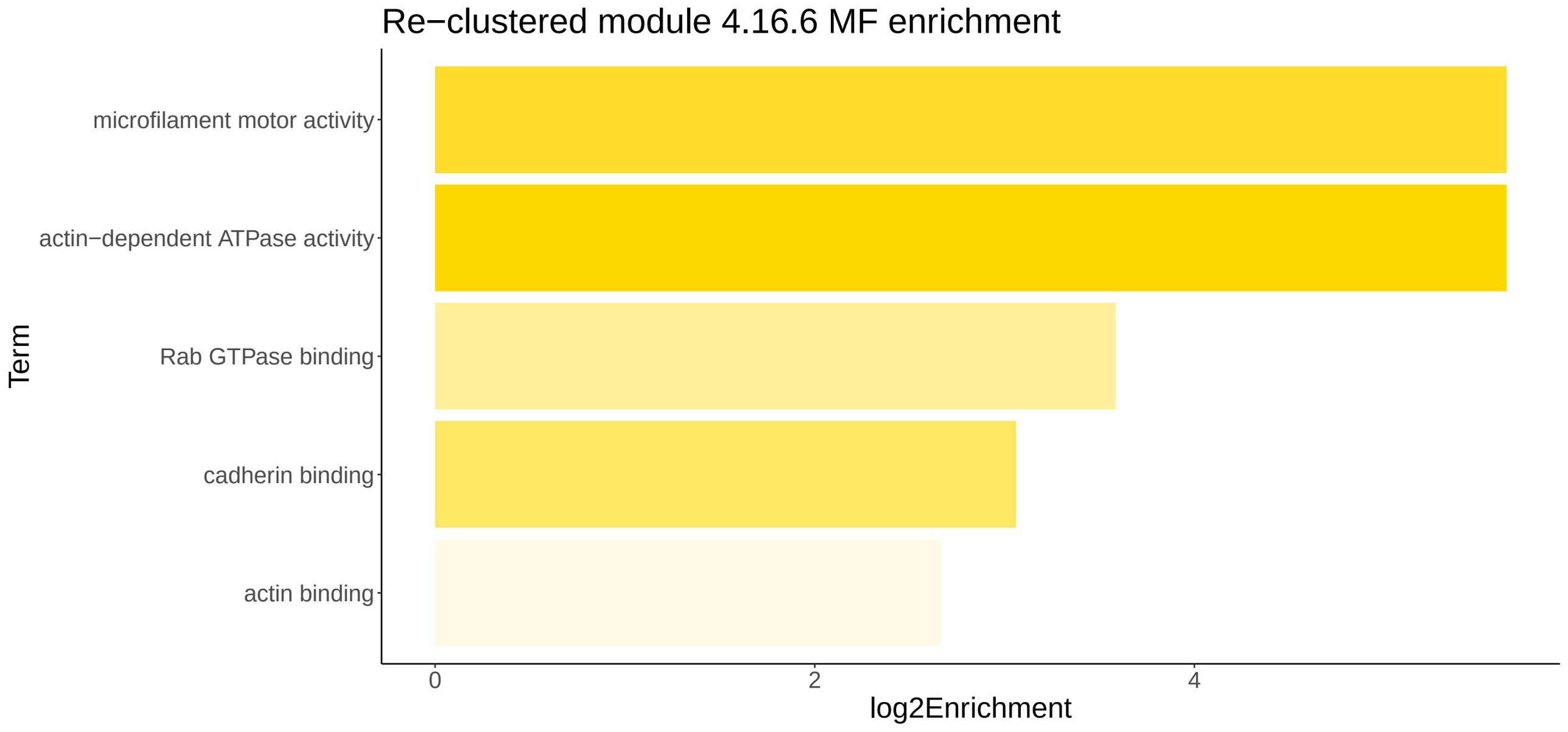
activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of on

endopeptidas

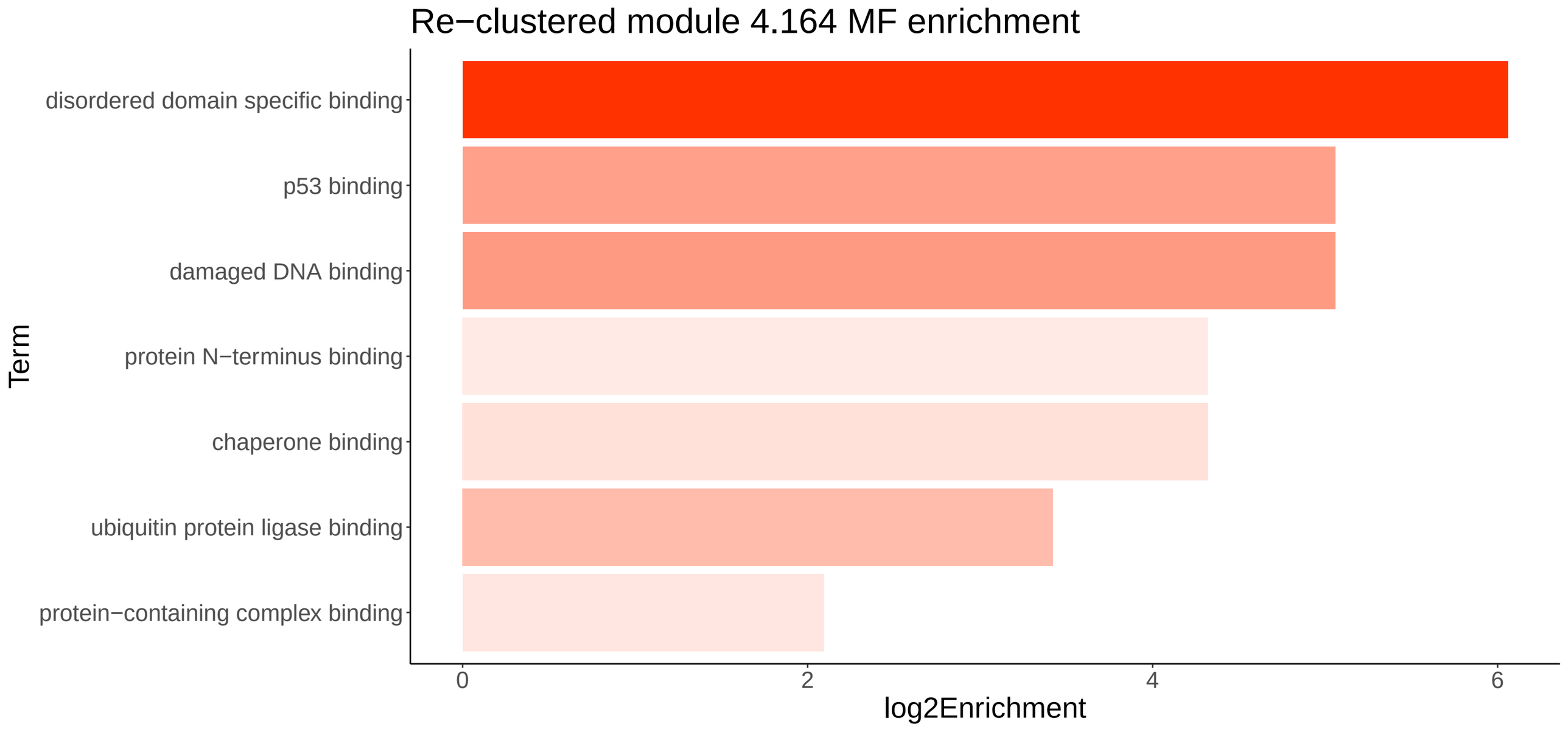

Re−clustered module 4.16.5 BP enrichment
prostate gland epithelium morphogenesis
branching involved in mammary gland duct morphogenesis
mammary gland epithelium development
regulation of intracellular estrogen receptor signaling pathway
regulation of cell fate commitment
androgen receptor signaling pathway
genitalia development
regulation of morphogenesis of a branching structure
retina homeostasis
regulation of toll−like receptor signaling pathway
response to estrogen
organ growth
female pregnancy
epithelial cell development
Term
0
2
4
log2Enrichment

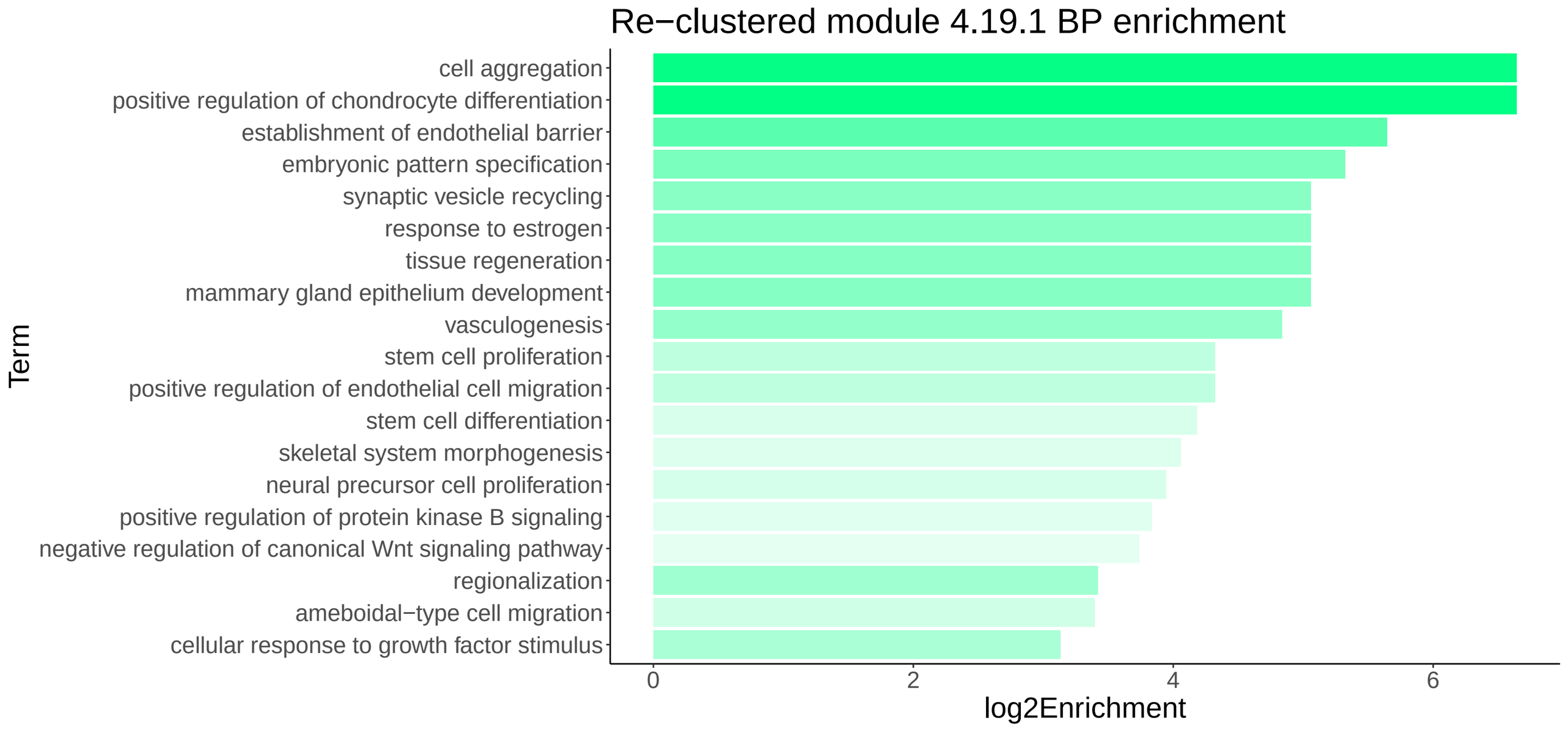

Re−clustered module 4.16.5 MF enrichment
Term
oxygen binding
transcription coactivator binding
estrogen receptor binding
general transcription initiation factor binding
nuclear receptor activity
basal RNA polymerase II transcription machinery binding
hormone binding
ATPase binding
beta−catenin binding
DNA−binding transcription activator activity, RNA polymerase II−specific
0
2
4
log2Enrichment

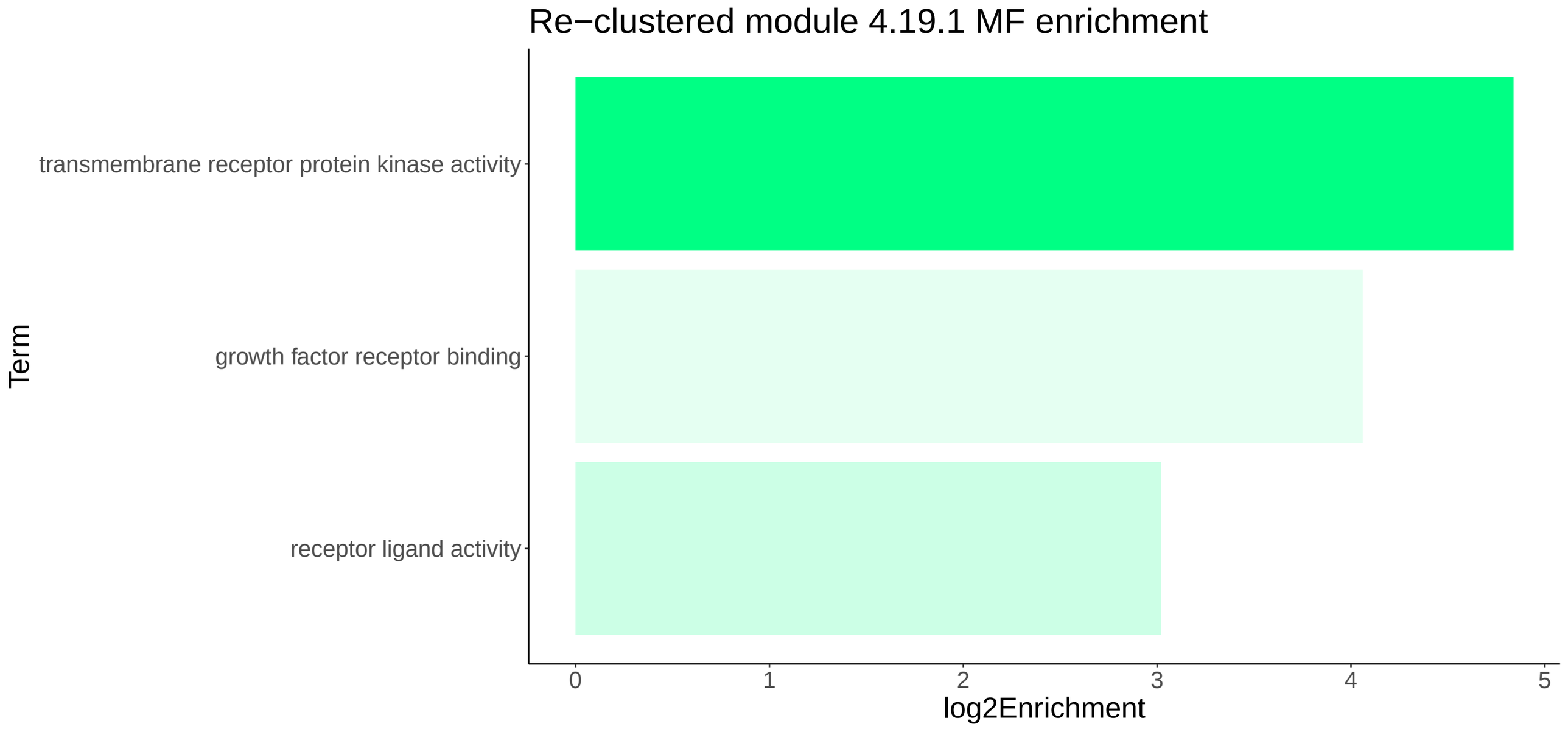

Re−clustered module 4.16.6 BP enrichment
actin filament−based transport
cell−cell adhesion mediated by cadherin
multivesicular body sorting pathway
actin filament−based movement
homotypic cell−cell adhesion
cornification
long−chain fatty acid metabolic process
cell−cell junction organization
establishment of vesicle localization
protein localization to plasma membrane
regulation of small GTPase mediated signal transduction
intracellular transport
peptide transport
establishment of protein localization
Term
0
2
4
6
log2Enrichment

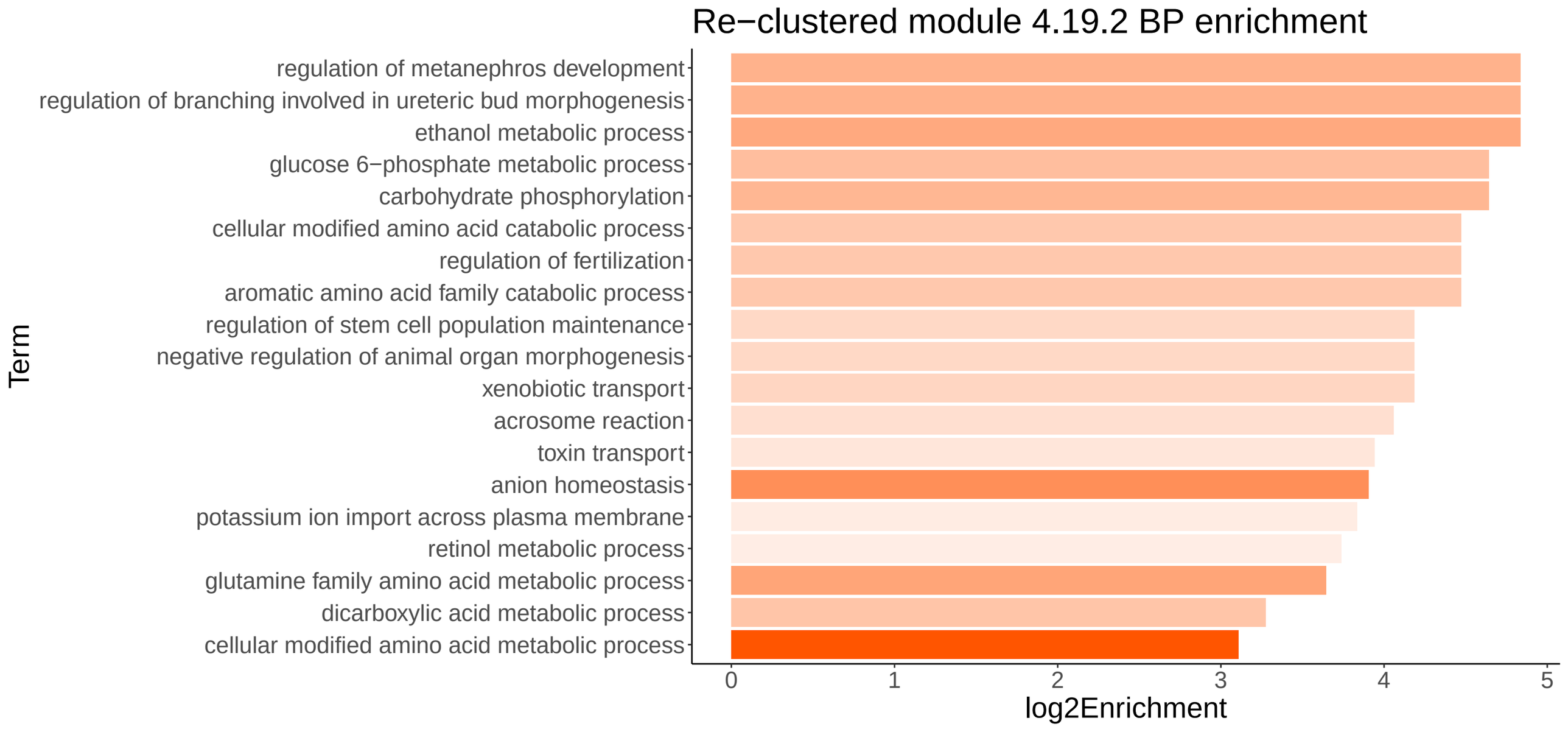

Re−clustered module 4.16.6 MF enrichment
microfilament motor activity
actin−dependent ATPase activity
Rab GTPase binding
cadherin binding
actin binding
Term
0
2
4
log2Enrichment

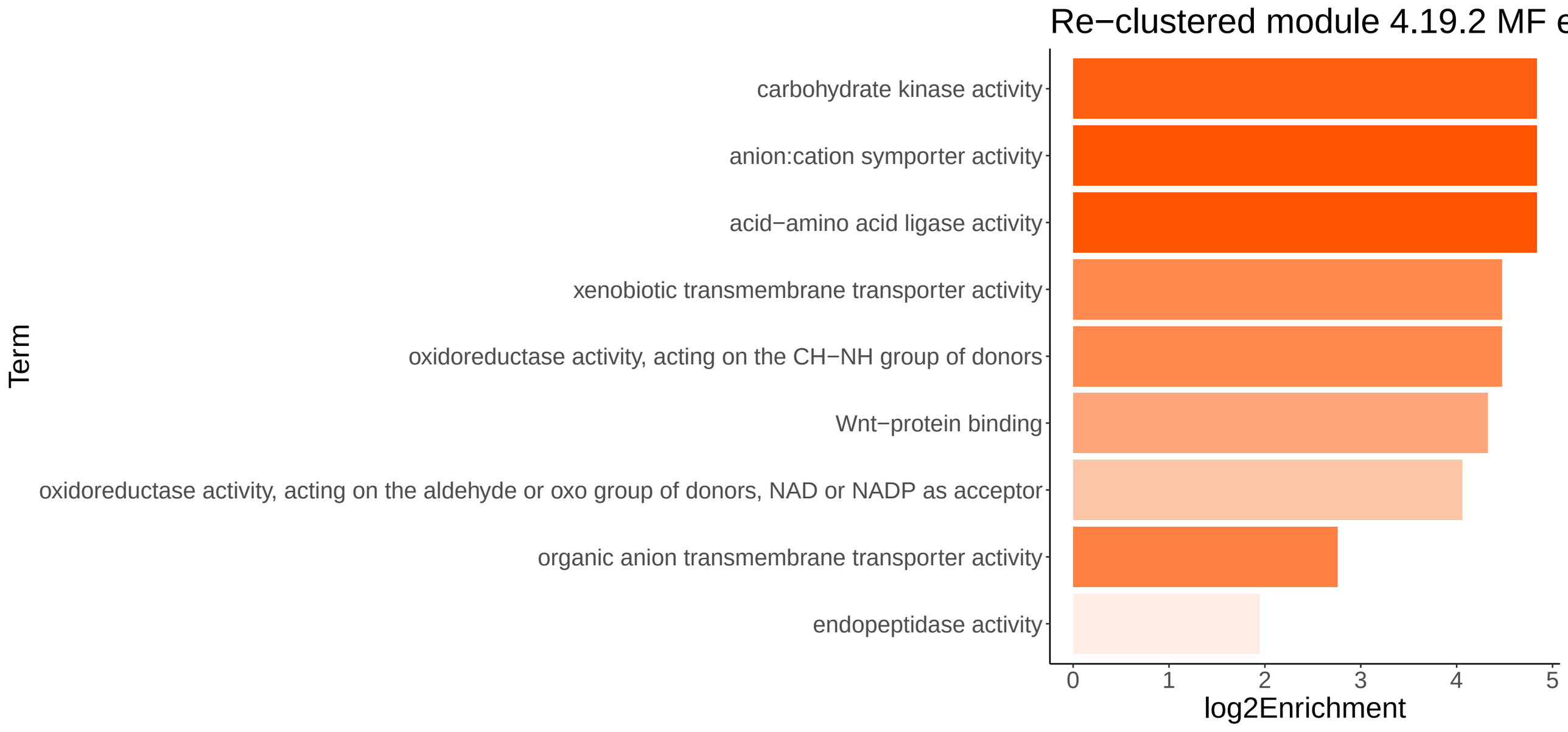

Re−clustered module 4.16
Term
nucleotide−excision repair, DNA damage recognition
nucleotide−excision repair, DNA duplex unwinding
positive regulation of protein export from nucleus
G1 DNA damage checkpoint
protein insertion into mitochondrial membrane involved in apoptotic signaling pathway
response to X−ray
nucleotide−excision repair, preincision complex assembly
positive regulation of leukocyte apoptotic process
positive regulation of release of cytochrome c from mitochondria
response to salt stress
global genome nucleotide−excision repair
mitotic DNA damage checkpoint
negative regulation of DNA biosynthetic process
regulation of execution phase of apoptosis
positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
programmed necrotic cell death
T cell apoptotic process
response to antibiotic
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
positive regulation of neuron apoptotic process
positive regulation of intrinsic apoptotic signaling pathway
regulation of lymphocyte apoptotic process
protein autoubiquitination
cellular senescence
regulation of vascular associated smooth muscle cell proliferation
autophagy of mitochondrion
cardiac septum morphogenesis
activation of cysteine−type endopeptidase activity involved in apoptotic process
negative regulation of protein binding
positive regulation of reactive oxygen species metabolic process
cellular response to starvation
tissue remodeling
response to toxic substance
B cell differentiation
cellular response to DNA damage stimulus
positive regulation of protein−containing complex assembly
protein deubiquitination
protein localization to nucleus
regulation of protein stability
response to drug
leukocyte proliferation
positive regulation of programmed cell death
0
2
4
6
log2Enrichment

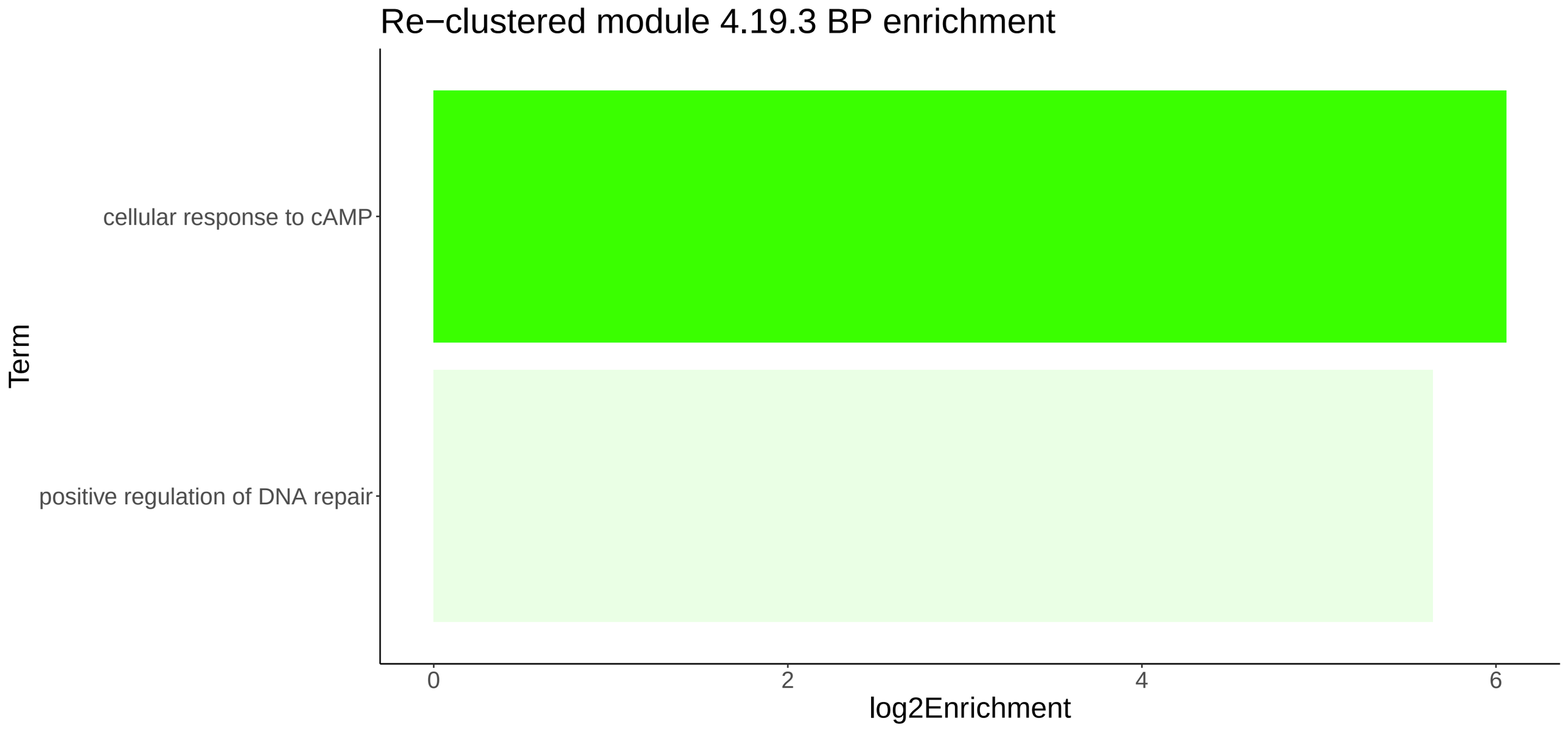

Re−clustered module 4.164 MF enrichment
disordered domain specific binding
p53 binding
damaged DNA binding
protein N−terminus binding
chaperone binding
ubiquitin protein ligase binding
protein−containing complex binding
Term
0
2
4
6
log2Enrichment

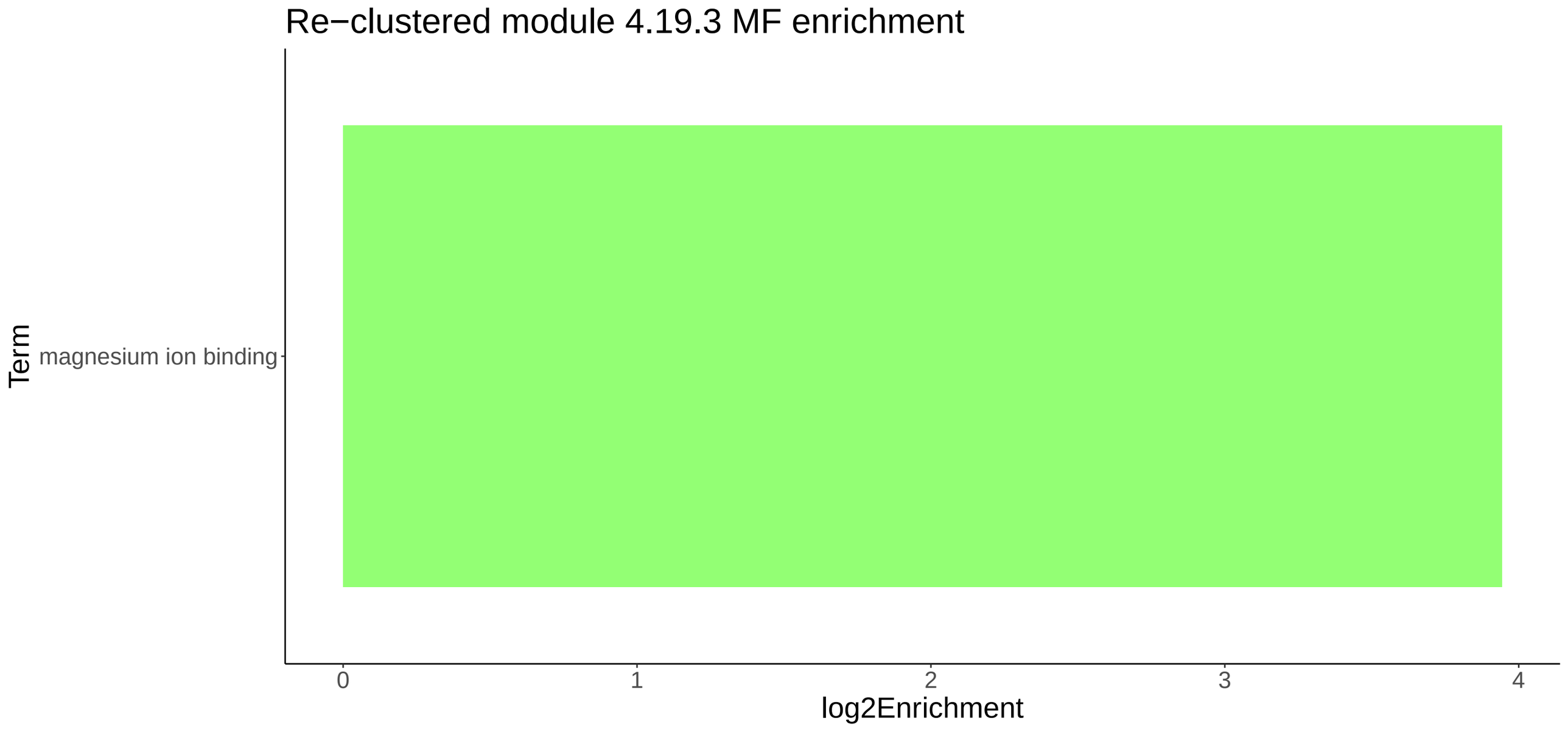

Re−clustered module 4.19.1 BP enrichment
cell aggregation
positive regulation of chondrocyte differentiation
establishment of endothelial barrier
embryonic pattern specification
synaptic vesicle recycling
response to estrogen
tissue regeneration
mammary gland epithelium development
vasculogenesis
stem cell proliferation
positive regulation of endothelial cell migration
stem cell differentiation
skeletal system morphogenesis
neural precursor cell proliferation
positive regulation of protein kinase B signaling
negative regulation of canonical Wnt signaling pathway
regionalization
ameboidal−type cell migration
cellular response to growth factor stimulus
Term
0
2
4
6
log2Enrichment

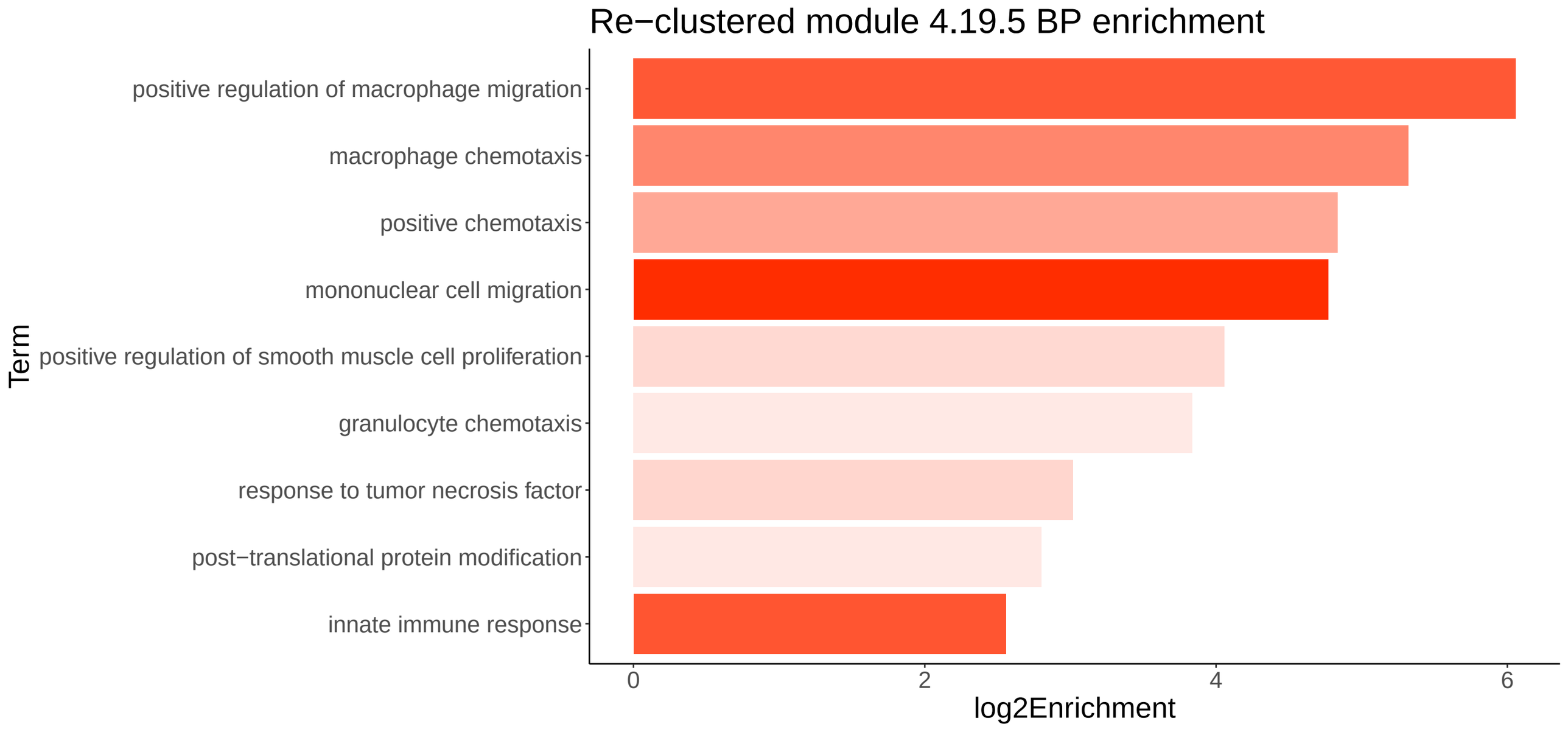

Re−clustered module 4.19.1 MF enrichment
transmembrane receptor protein kinase activity
growth factor receptor binding
receptor ligand activity
Term
0
1
2
3
4
5
log2Enrichment

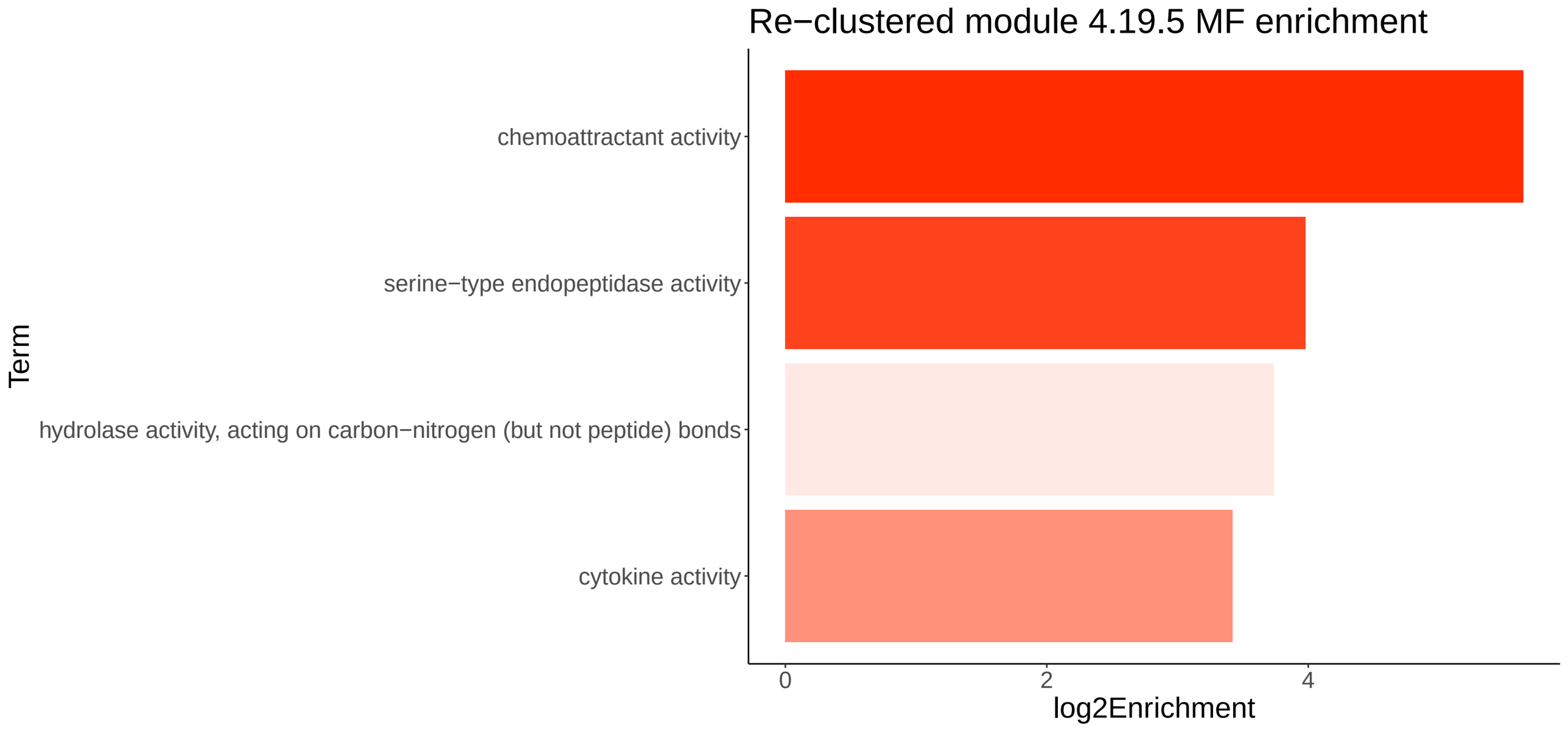

Re−clustered module 4.19.2 BP enrichment
regulation of metanephros development
regulation of branching involved in ureteric bud morphogenesis
ethanol metabolic process
glucose 6−phosphate metabolic process
carbohydrate phosphorylation
cellular modified amino acid catabolic process
regulation of fertilization
aromatic amino acid family catabolic process
regulation of stem cell population maintenance
negative regulation of animal organ morphogenesis
xenobiotic transport
acrosome reaction
toxin transport
anion homeostasis
potassium ion import across plasma membrane
retinol metabolic process
glutamine family amino acid metabolic process
dicarboxylic acid metabolic process
cellular modified amino acid metabolic process
Term
0
1
2
3
4
5
log2Enrichment

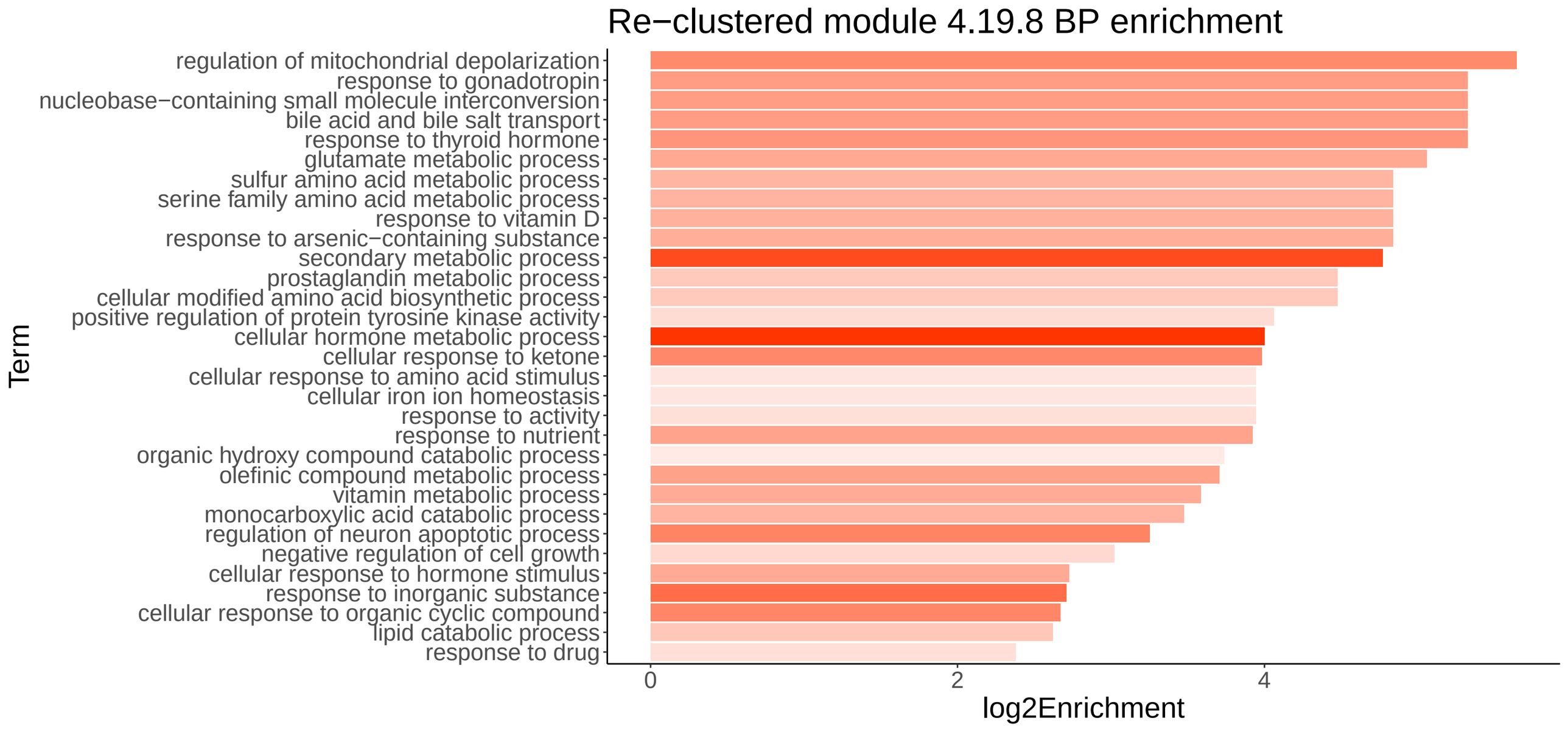

Re−clustered module 4.19.2 MF e
Term
carbohydrate kinase activity
anion:cation symporter activity
acid−amino acid ligase activity
xenobiotic transmembrane transporter activity
oxidoreductase activity, acting on the CH−NH group of donors
Wnt−protein binding
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor
organic anion transmembrane transporter activity
endopeptidase activity
0
1
2
3
4
5
log2Enrichment


Re−clustered module 4.19.3 BP enrichment
Term
cellular response to cAMP
positive regulation of DNA repair
0
2
4
6
log2Enrichment


Re−clustered module 4.19.3 MF enrichment
Term
magnesium ion binding
0
1
2
3
4
log2Enrichment


Re−clustered module 4.19.5 BP enrichment
positive regulation of macrophage migration
macrophage chemotaxis
positive chemotaxis
mononuclear cell migration
positive regulation of smooth muscle cell proliferation
granulocyte chemotaxis
response to tumor necrosis factor
post−translational protein modification
innate immune response
Term
0
2
4
6
log2Enrichment


Re−clustered module 4.19.5 MF enrichment
Term
chemoattractant activity
serine−type endopeptidase activity
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds
cytokine activity
0
2
4
log2Enrichment


Re−clustered module 4.19.8 BP enrichment
regulation of mitochondrial depolarization
response to gonadotropin
nucleobase−containing small molecule interconversion
bile acid and bile salt transport
response to thyroid hormone
glutamate metabolic process
sulfur amino acid metabolic process
serine family amino acid metabolic process
response to vitamin D
response to arsenic−containing substance
secondary metabolic process
prostaglandin metabolic process
cellular modified amino acid biosynthetic process
positive regulation of protein tyrosine kinase activity
cellular hormone metabolic process
cellular response to ketone
cellular response to amino acid stimulus
cellular iron ion homeostasis
response to activity
response to nutrient
organic hydroxy compound catabolic process
olefinic compound metabolic process
vitamin metabolic process
monocarboxylic acid catabolic process
regulation of neuron apoptotic process
negative regulation of cell growth
cellular response to hormone stimulus
response to inorganic substance
cellular response to organic cyclic compound
lipid catabolic process
response to drug
Term
0
2
4
log2Enrichment

acid−amino acid ligase

steroid dehydrogenase activity, acting on the CH−OH group of donors, NAD or NADP as a

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

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

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

NADP

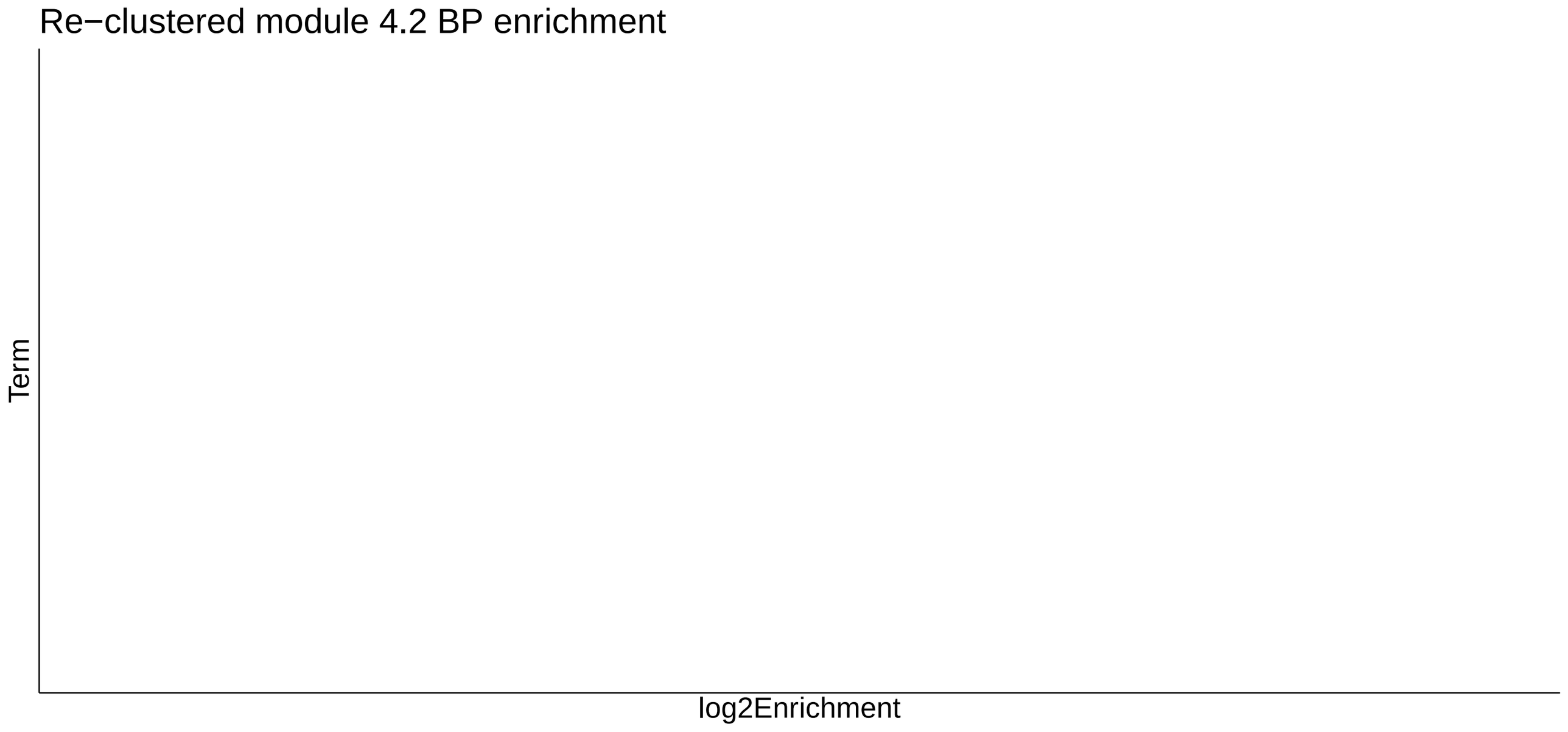
oxidoreductase activity, acting on a sulfur group of

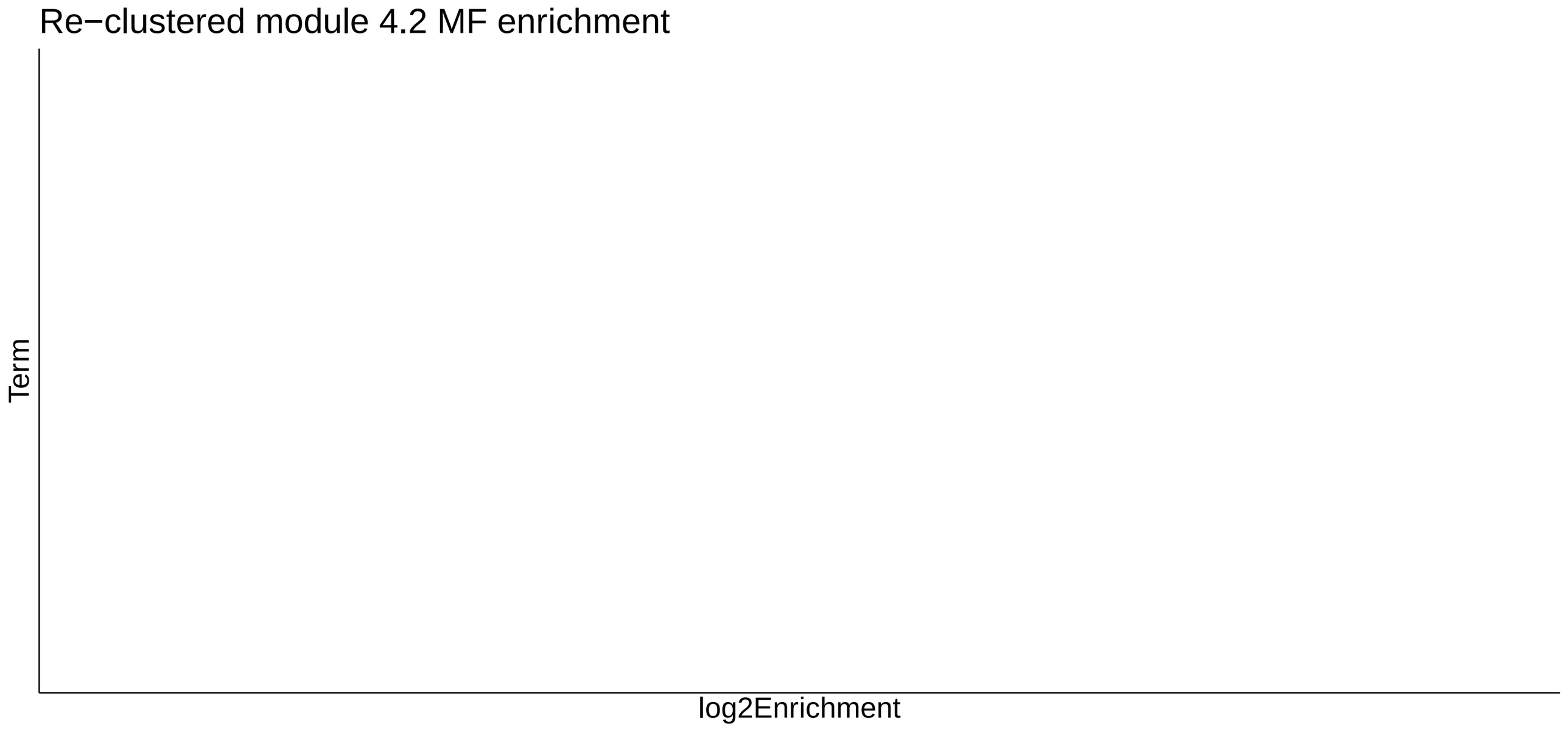
oxidoreductase activity, acting on CH−OH group of

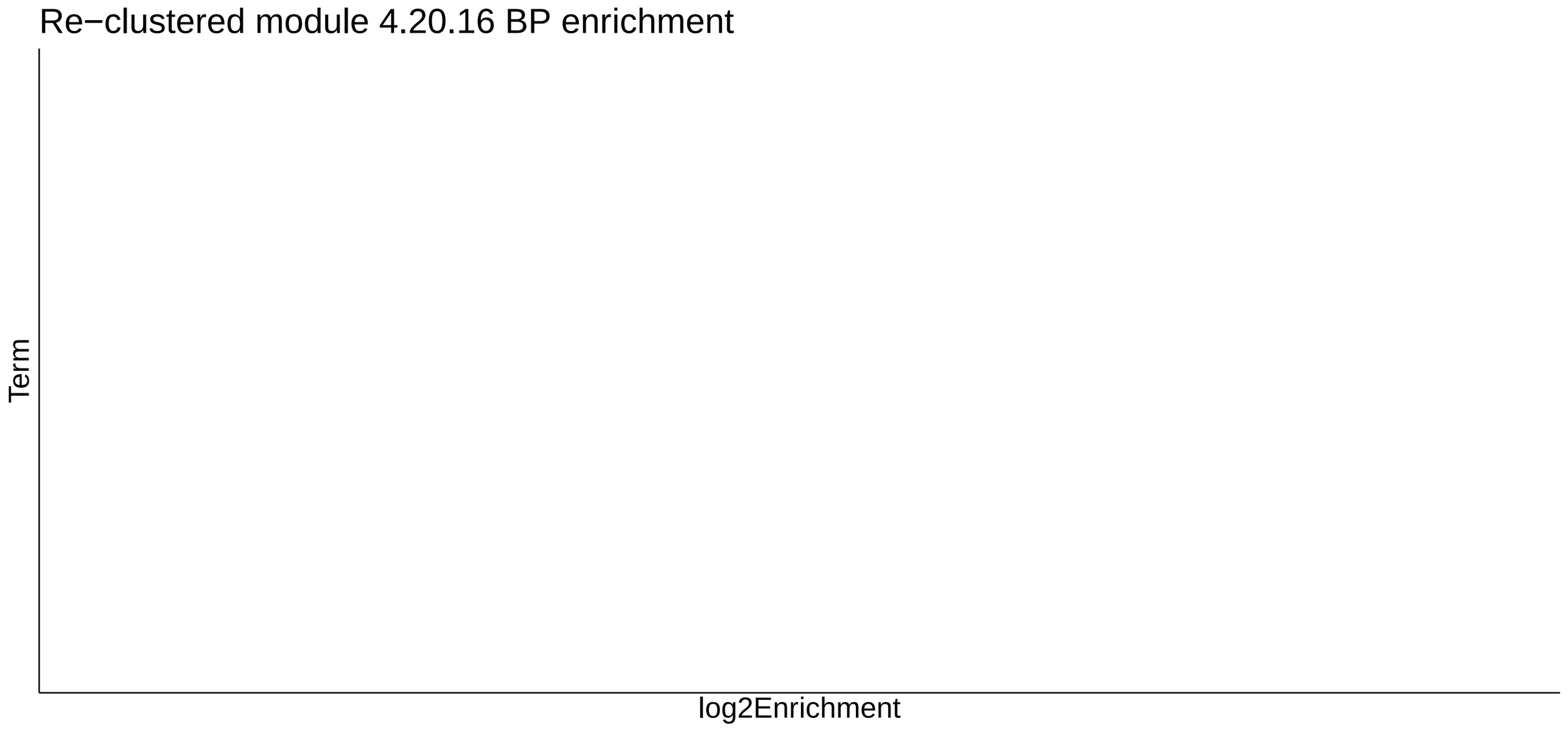
monosaccharide

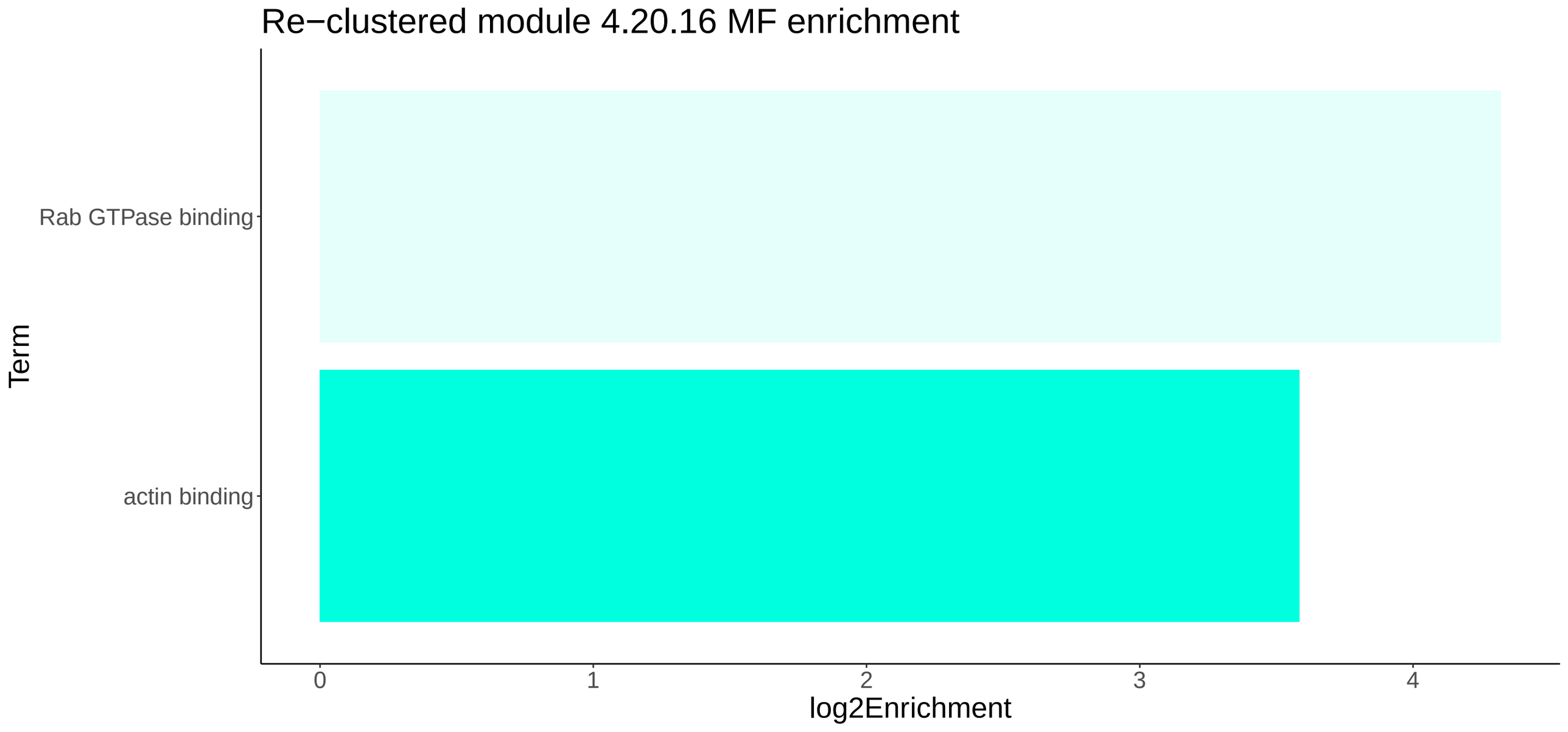
identical protein

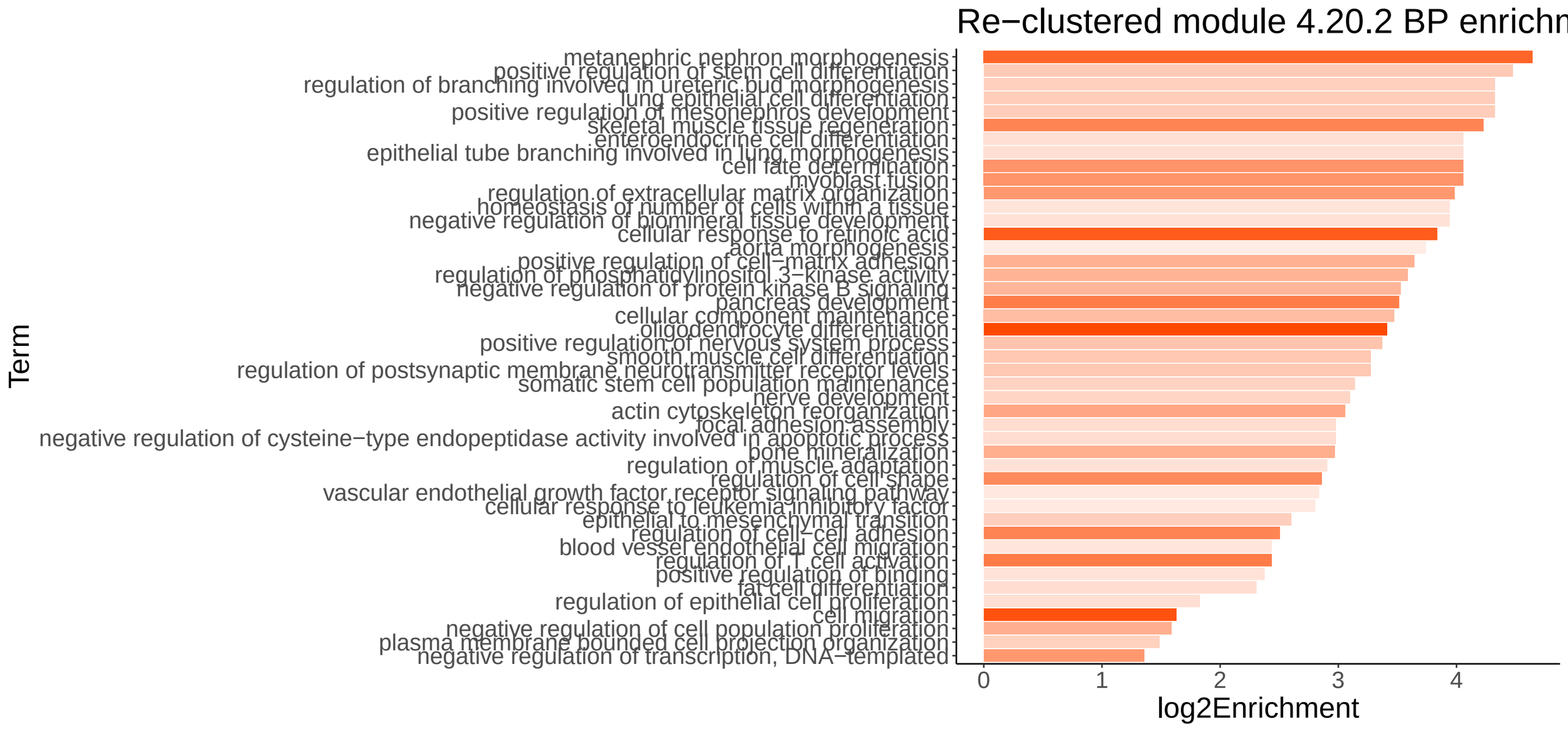
lo

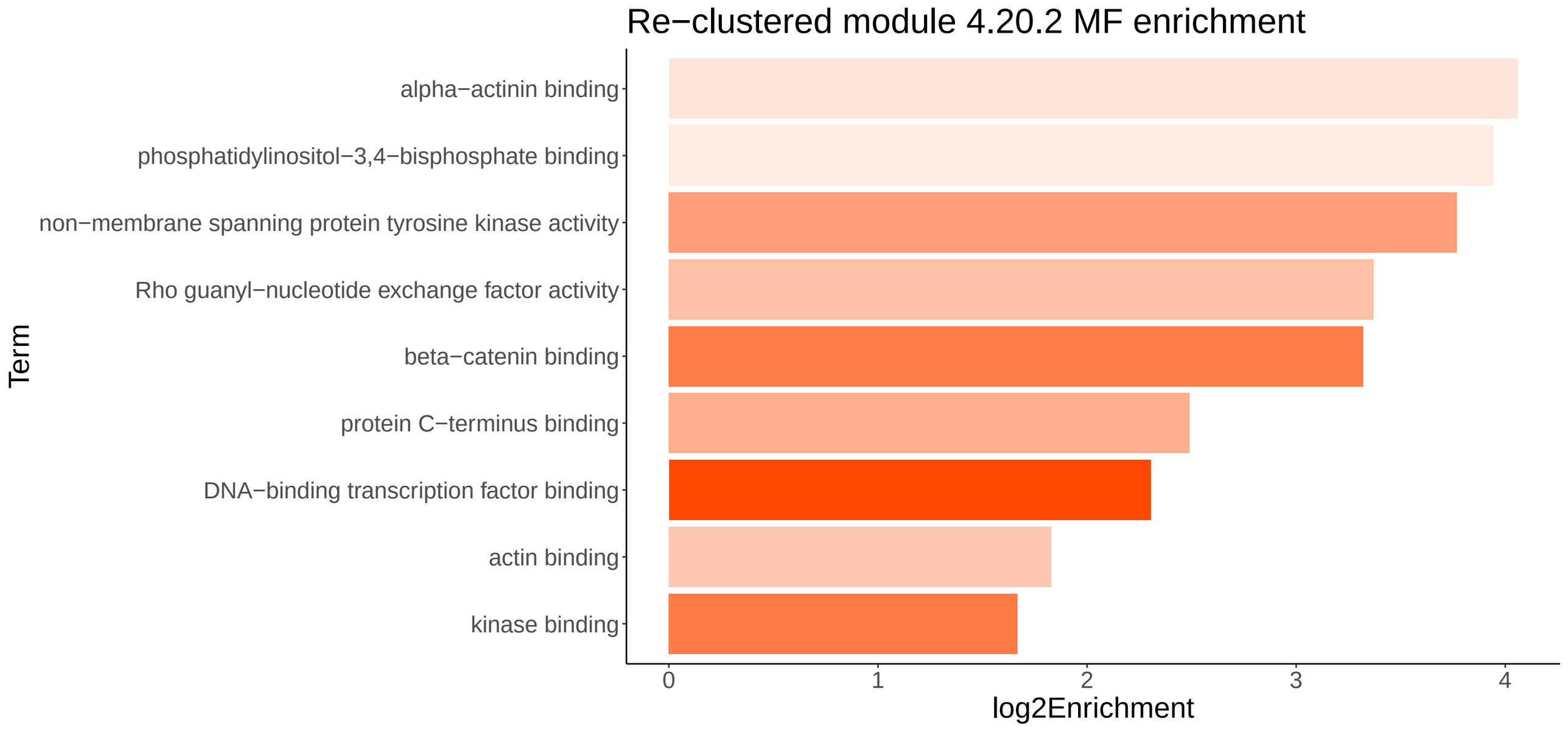

Re−clustered module 4.2 BP enrichment
Term
log2Enrichment


Re−clustered module 4.2 MF enrichment
Term
log2Enrichment


Re−clustered module 4.20.16 BP enrichment
Term
log2Enrichment

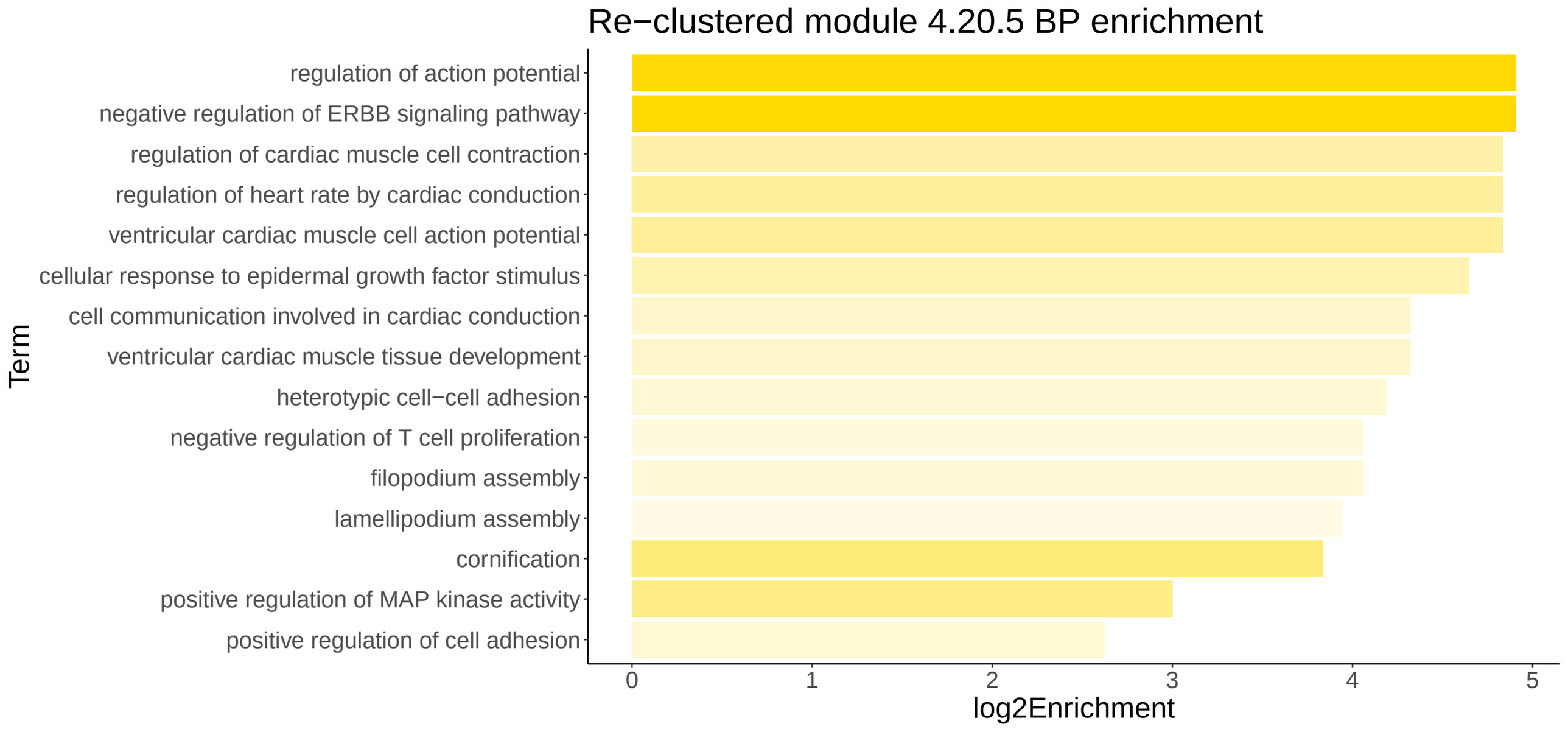

Re−clustered module 4.20.16 MF enrichment
Term
Rab GTPase binding
actin binding
0
1
2
3
4
log2Enrichment

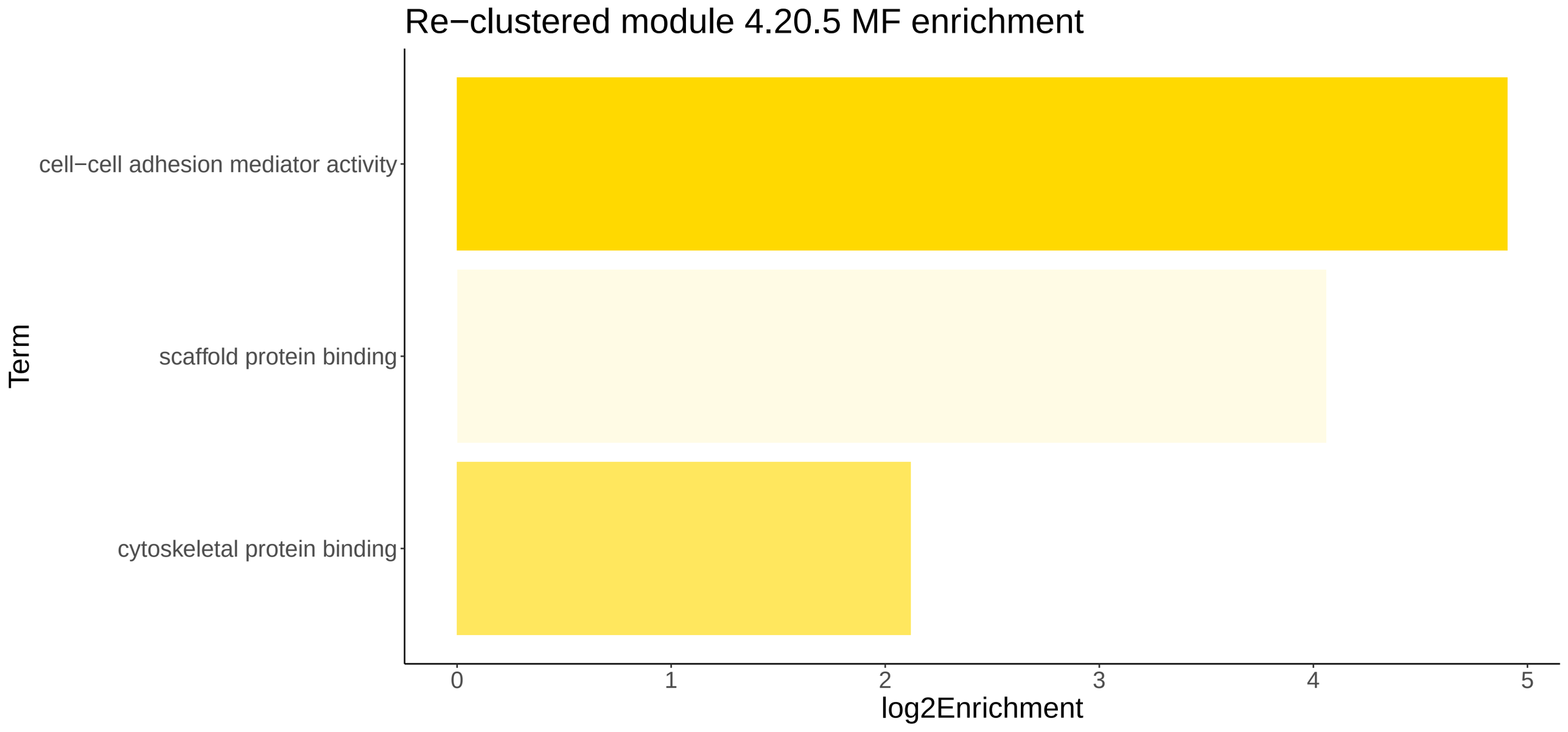

Re−clustered module 4.20.2 BP enrichm
Term
metanephric nephron morphogenesis
positive regulation of stem cell differentiation
regulation of branching involved in ureteric bud morphogenesis
lung epithelial cell differentiation
positive regulation of mesonephros development
skeletal muscle tissue regeneration
enteroendocrine cell differentiation
epithelial tube branching involved in lung morphogenesis
cell fate determination
myoblast fusion
regulation of extracellular matrix organization
homeostasis of number of cells within a tissue
negative regulation of biomineral tissue development
cellular response to retinoic acid
aorta morphogenesis
positive regulation of cell−matrix adhesion
regulation of phosphatidylinositol 3−kinase activity
negative regulation of protein kinase B signaling
pancreas development
cellular component maintenance
oligodendrocyte differentiation
positive regulation of nervous system process
smooth muscle cell differentiation
regulation of postsynaptic membrane neurotransmitter receptor levels
somatic stem cell population maintenance
nerve development
actin cytoskeleton reorganization
focal adhesion assembly
negative regulation of cysteine−type endopeptidase activity involved in apoptotic process
bone mineralization
regulation of muscle adaptation
regulation of cell shape
vascular endothelial growth factor receptor signaling pathway
cellular response to leukemia inhibitory factor
epithelial to mesenchymal transition
regulation of cell−cell adhesion
blood vessel endothelial cell migration
regulation of T cell activation
positive regulation of binding
fat cell differentiation
regulation of epithelial cell proliferation
cell migration
negative regulation of cell population proliferation
plasma membrane bounded cell projection organization
negative regulation of transcription, DNA−templated
0
1
2
3
4
log2Enrichment

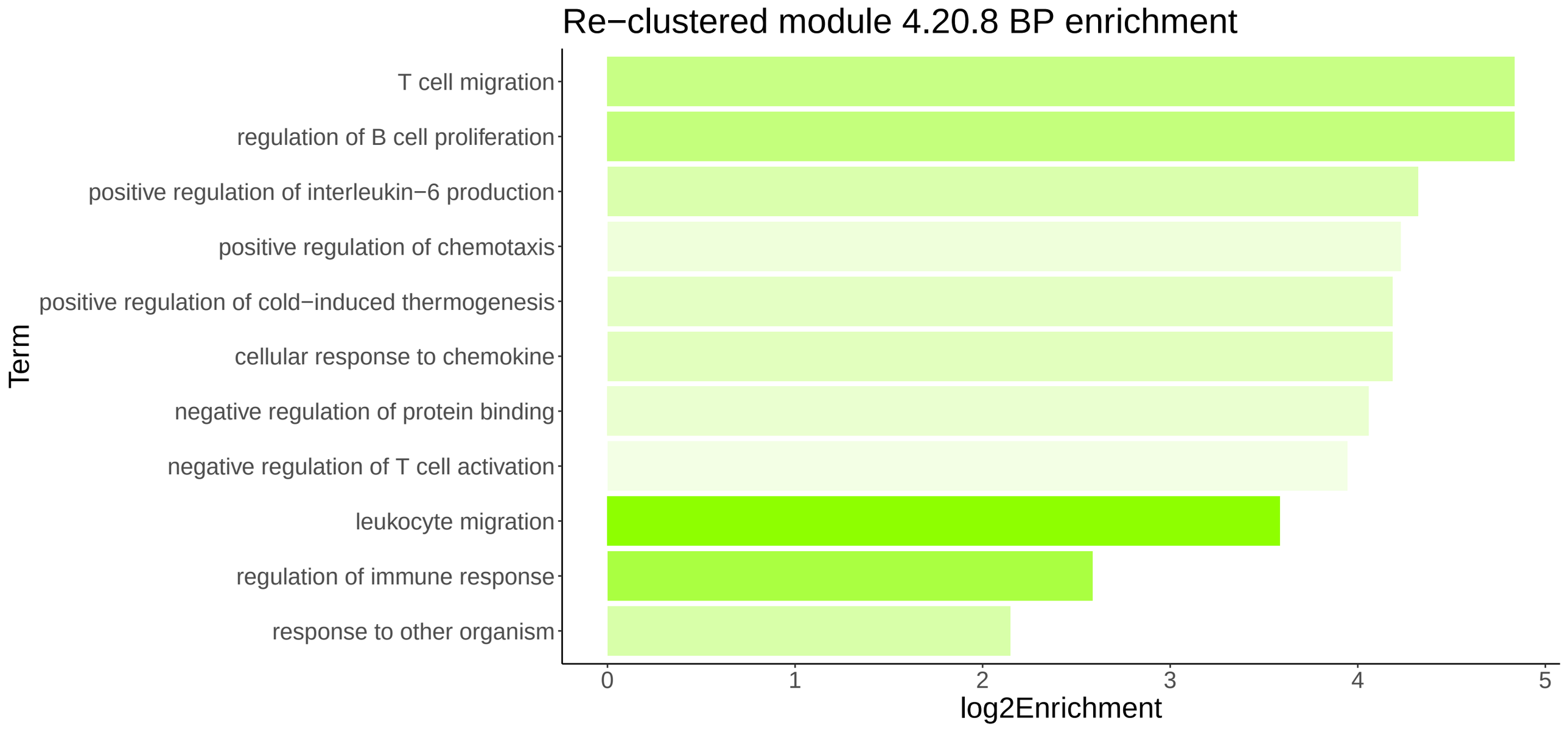

Re−clustered module 4.20.2 MF enrichment
alpha−actinin binding
phosphatidylinositol−3,4−bisphosphate binding
non−membrane spanning protein tyrosine kinase activity
Rho guanyl−nucleotide exchange factor activity
beta−catenin binding
protein C−terminus binding
DNA−binding transcription factor binding
actin binding
kinase binding
Term
0
1
2
3
4
log2Enrichment

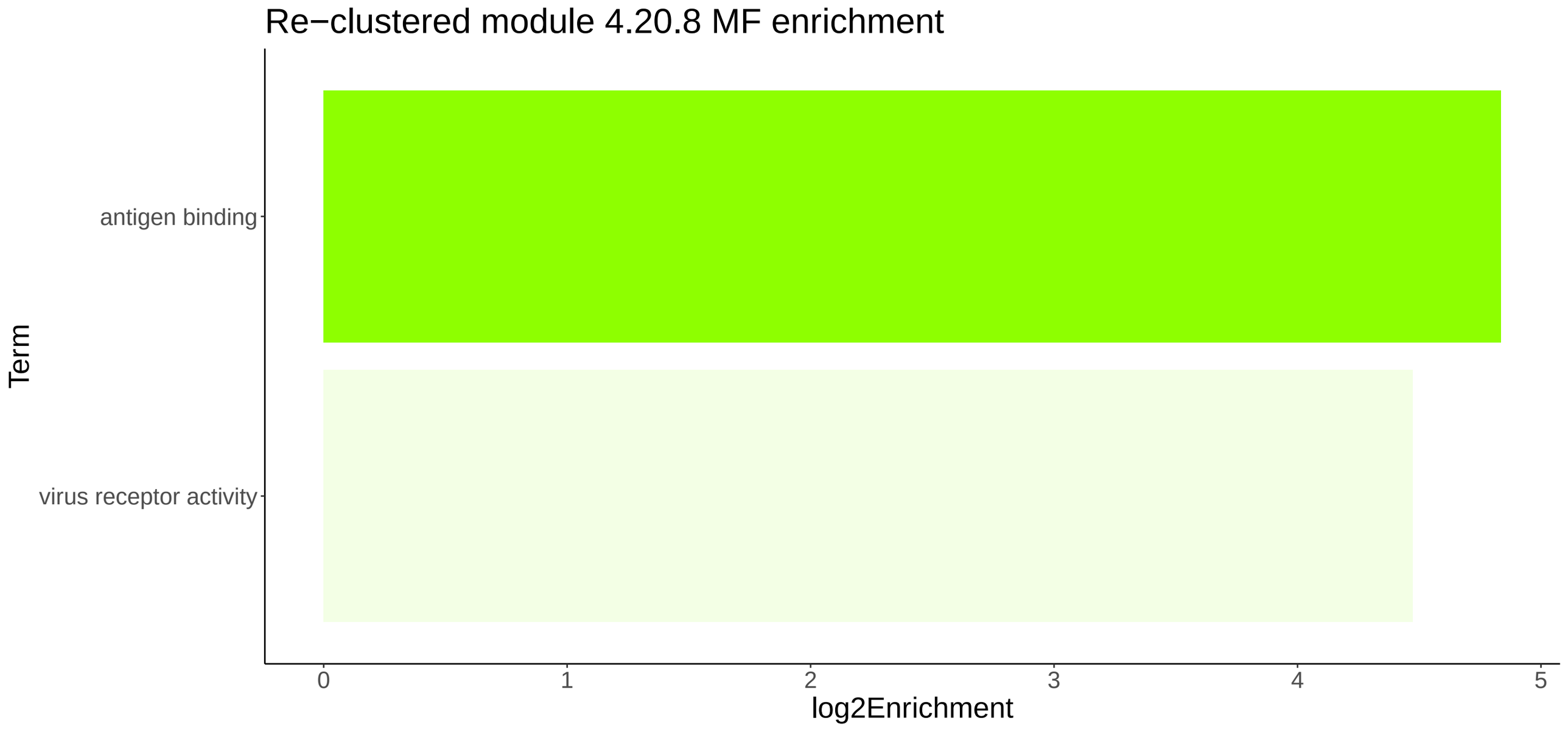

Re−clustered module 4.20.3 BP enrichment
Term
branching involved in salivary gland morphogenesis
outflow tract septum morphogenesis
retinal ganglion cell axon guidance
metanephric nephron tubule development
regulation of metanephros development
regulation of SMAD protein signal transduction
cell differentiation involved in metanephros development
positive regulation of heart rate
negative regulation of defense response to virus
regulation of gastrulation
epithelial tube branching involved in lung morphogenesis
negative regulation of axon extension involved in axon guidance
regulation of receptor binding
regulation of extracellular matrix organization
positive regulation of sprouting angiogenesis
negative regulation of NIK/NF−kappaB signaling
cranial nerve development
negative regulation of cell−substrate adhesion
integrin−mediated signaling pathway
tissue regeneration
regulation of systemic arterial blood pressure
negative regulation of transforming growth factor beta receptor signaling pathway
regulation of dendritic spine development
regulation of cell shape
positive regulation of epithelial cell proliferation
Rho protein signal transduction
establishment or maintenance of cell polarity
mesenchyme development
regulation of GTPase activity
positive regulation of cell motility
cell morphogenesis
anatomical structure formation involved in morphogenesis
muscle tissue development
cell−cell adhesion
0
1
2
3
4
5
log2Enrichment

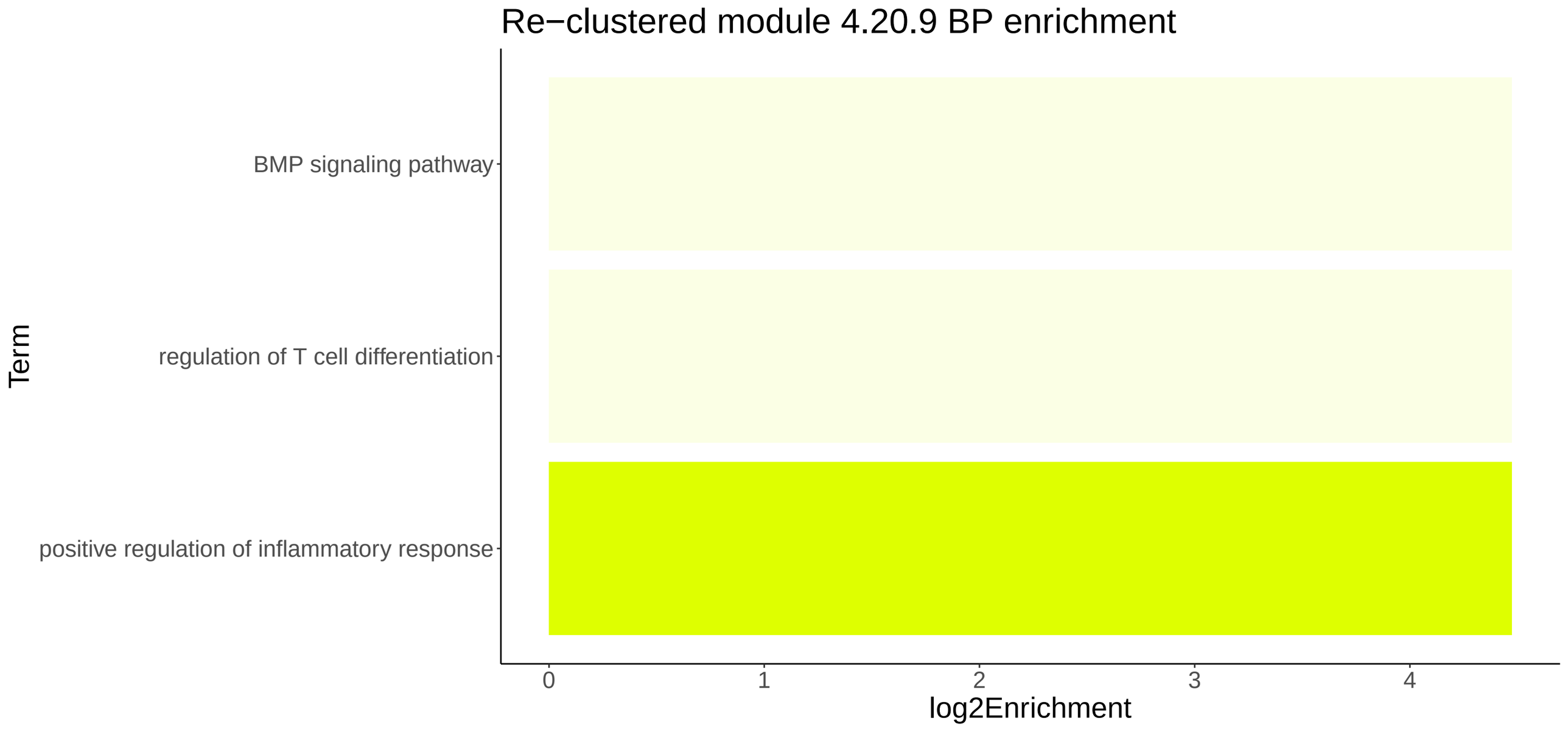

Re−clustered module 4.20.3 MF enrichment
insulin−like growth factor binding
G−protein alpha−subunit binding
chemorepellent activity
Wnt−protein binding
phosphatidylinositol−4,5−bisphosphate binding
GTPase regulator activity
Term
0
1
2
3
4
log2Enrichment

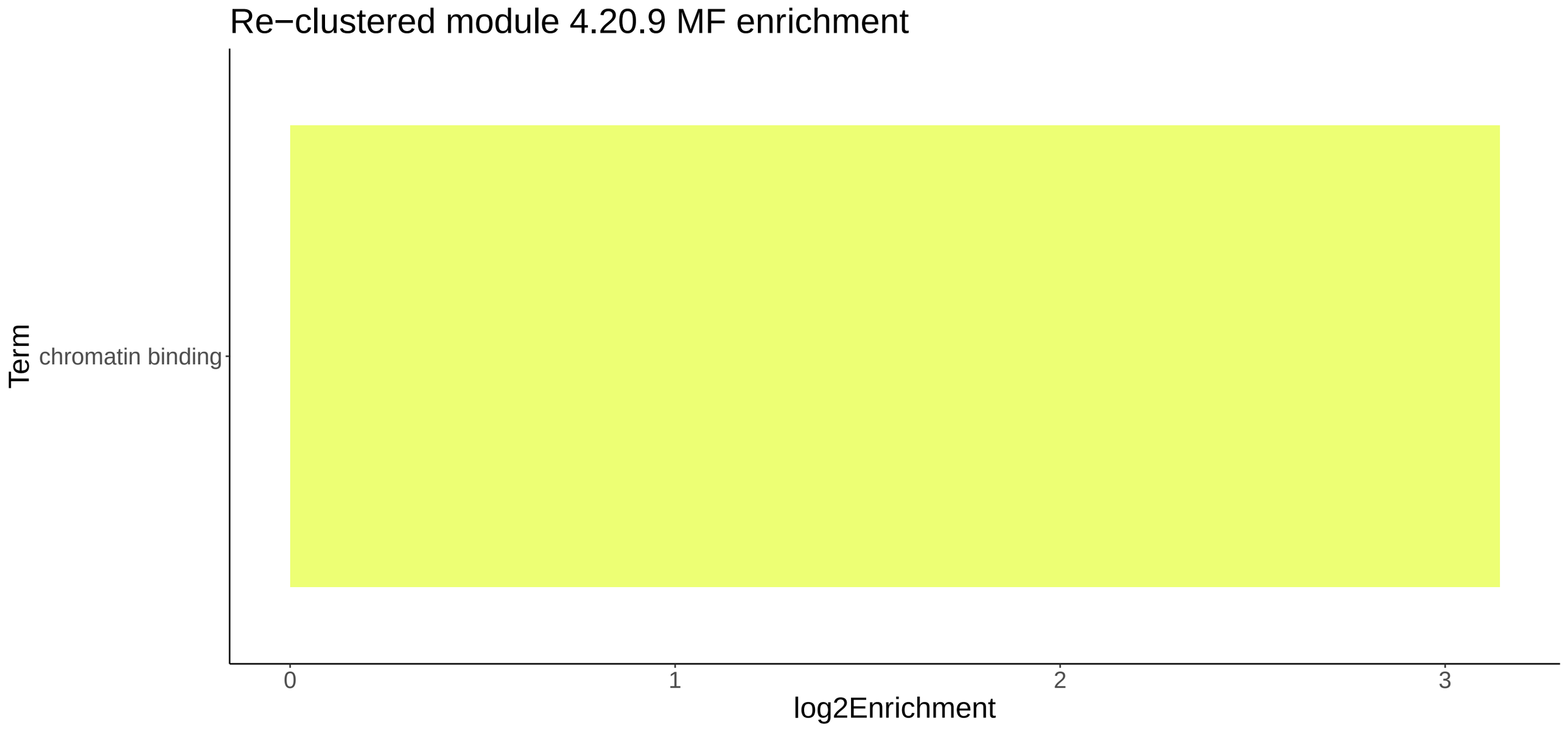

Re−clustered module 4.20.5 BP enrichment
regulation of action potential
negative regulation of ERBB signaling pathway
regulation of cardiac muscle cell contraction
regulation of heart rate by cardiac conduction
ventricular cardiac muscle cell action potential
cellular response to epidermal growth factor stimulus
cell communication involved in cardiac conduction
ventricular cardiac muscle tissue development
heterotypic cell−cell adhesion
negative regulation of T cell proliferation
filopodium assembly
lamellipodium assembly
cornification
positive regulation of MAP kinase activity
positive regulation of cell adhesion
Term
0
1
2
3
4
5
log2Enrichment

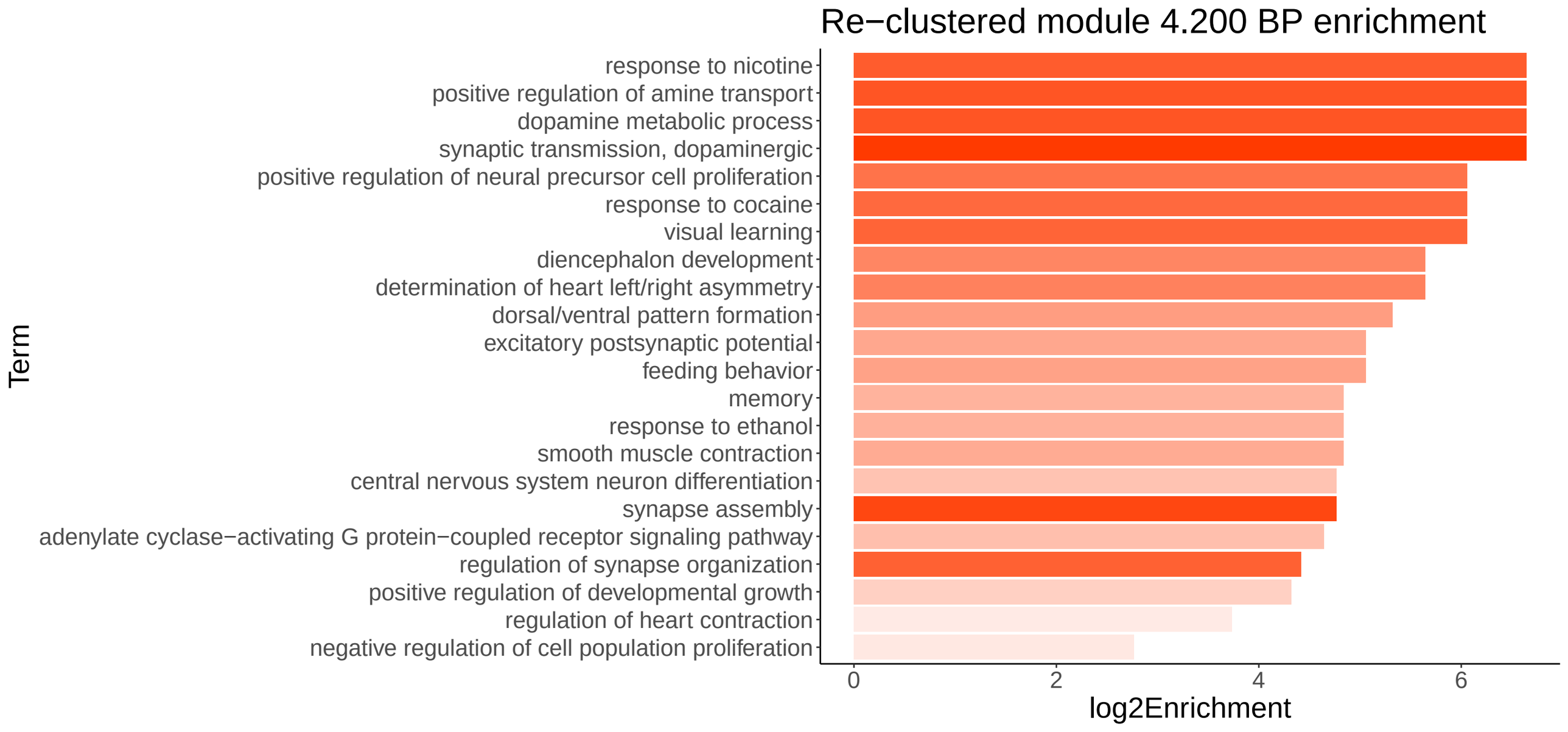

Re−clustered module 4.20.5 MF enrichment
Term
cell−cell adhesion mediator activity
scaffold protein binding
cytoskeletal protein binding
0
1
2
3
4
5
log2Enrichment

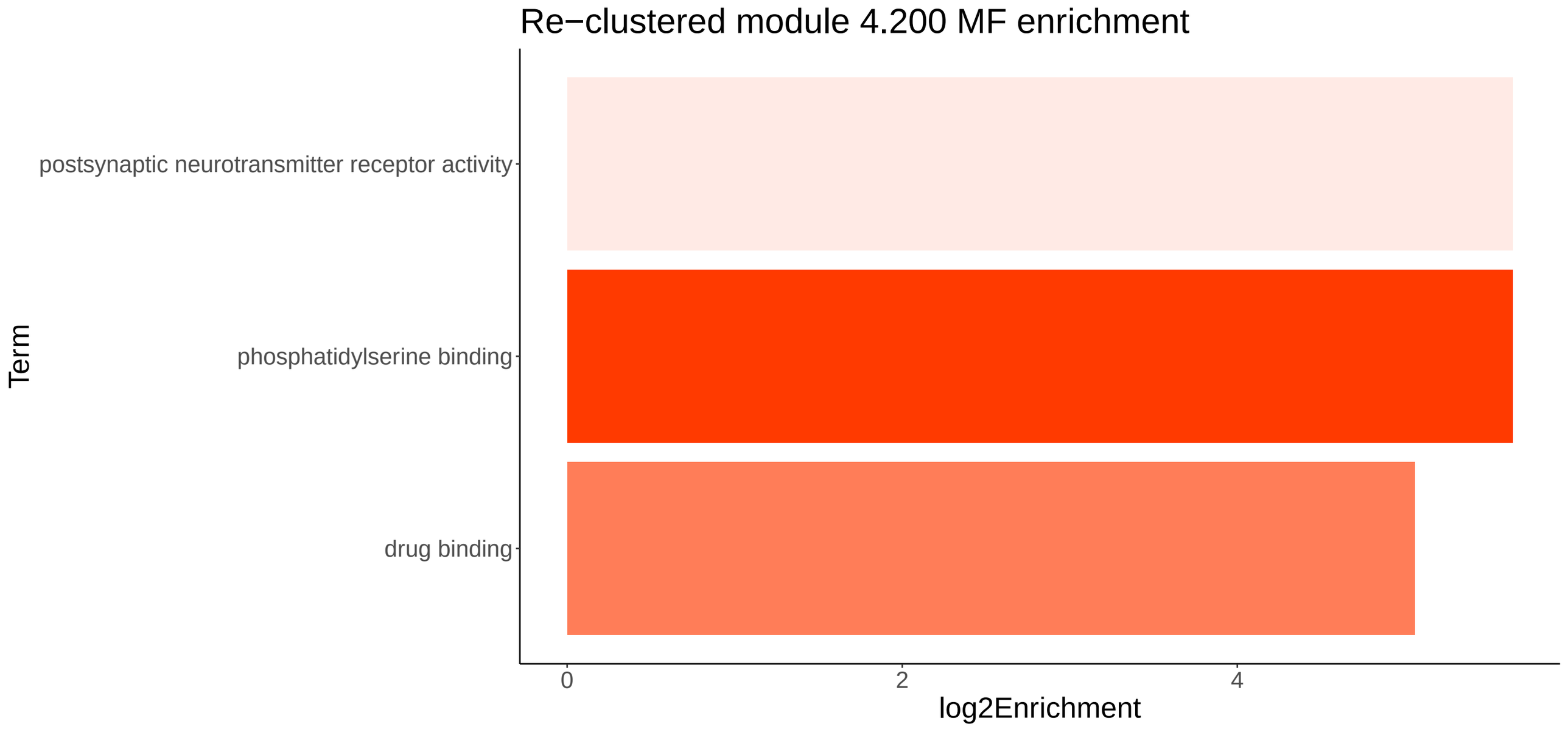

Re−clustered module 4.20.8 BP enrichment
T cell migration
regulation of B cell proliferation
positive regulation of interleukin−6 production
positive regulation of chemotaxis
positive regulation of cold−induced thermogenesis
cellular response to chemokine
negative regulation of protein binding
negative regulation of T cell activation
leukocyte migration
regulation of immune response
response to other organism
Term
0
1
2
3
4
5
log2Enrichment

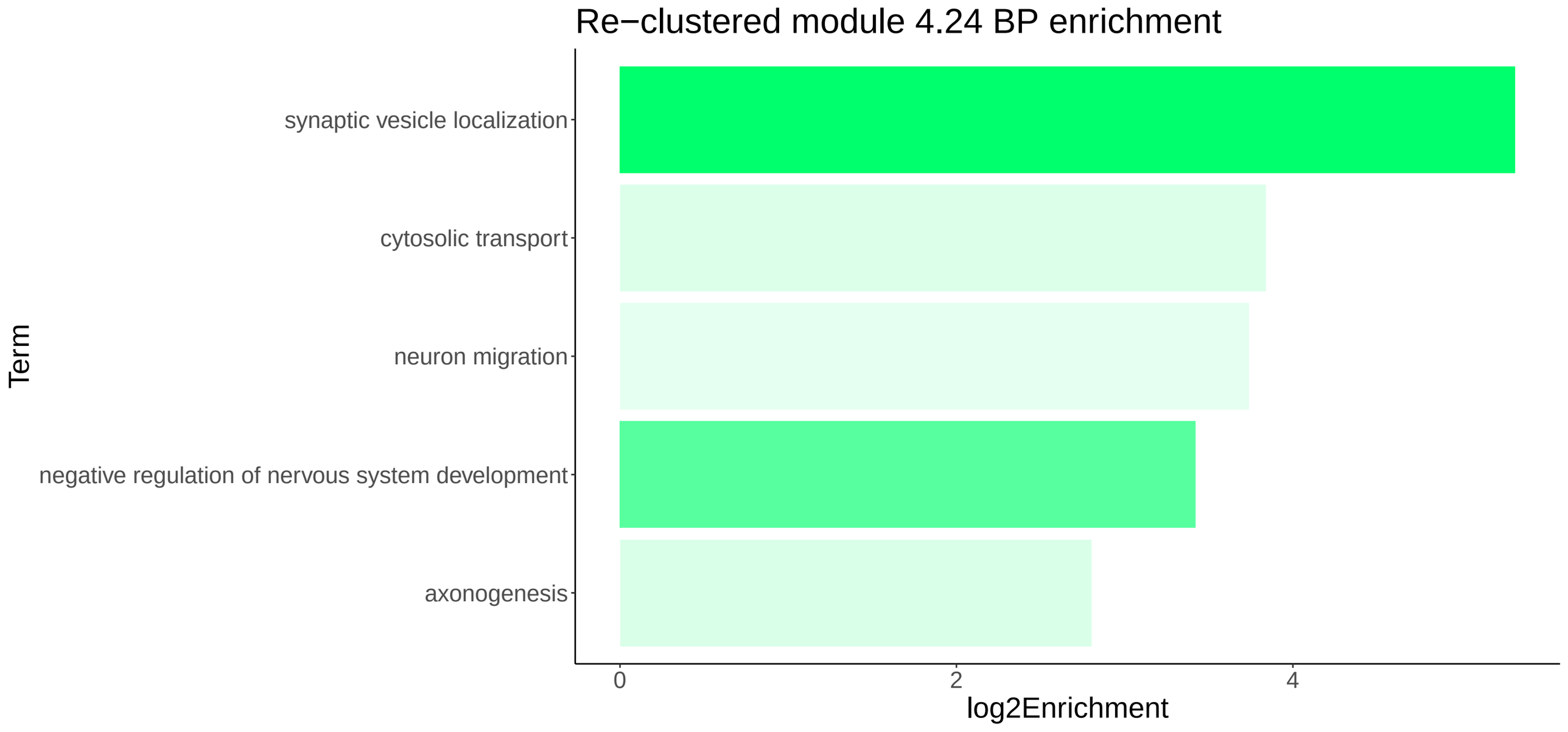

Re−clustered module 4.20.8 MF enrichment
Term
antigen binding
virus receptor activity
0
1
2
3
4
5
log2Enrichment

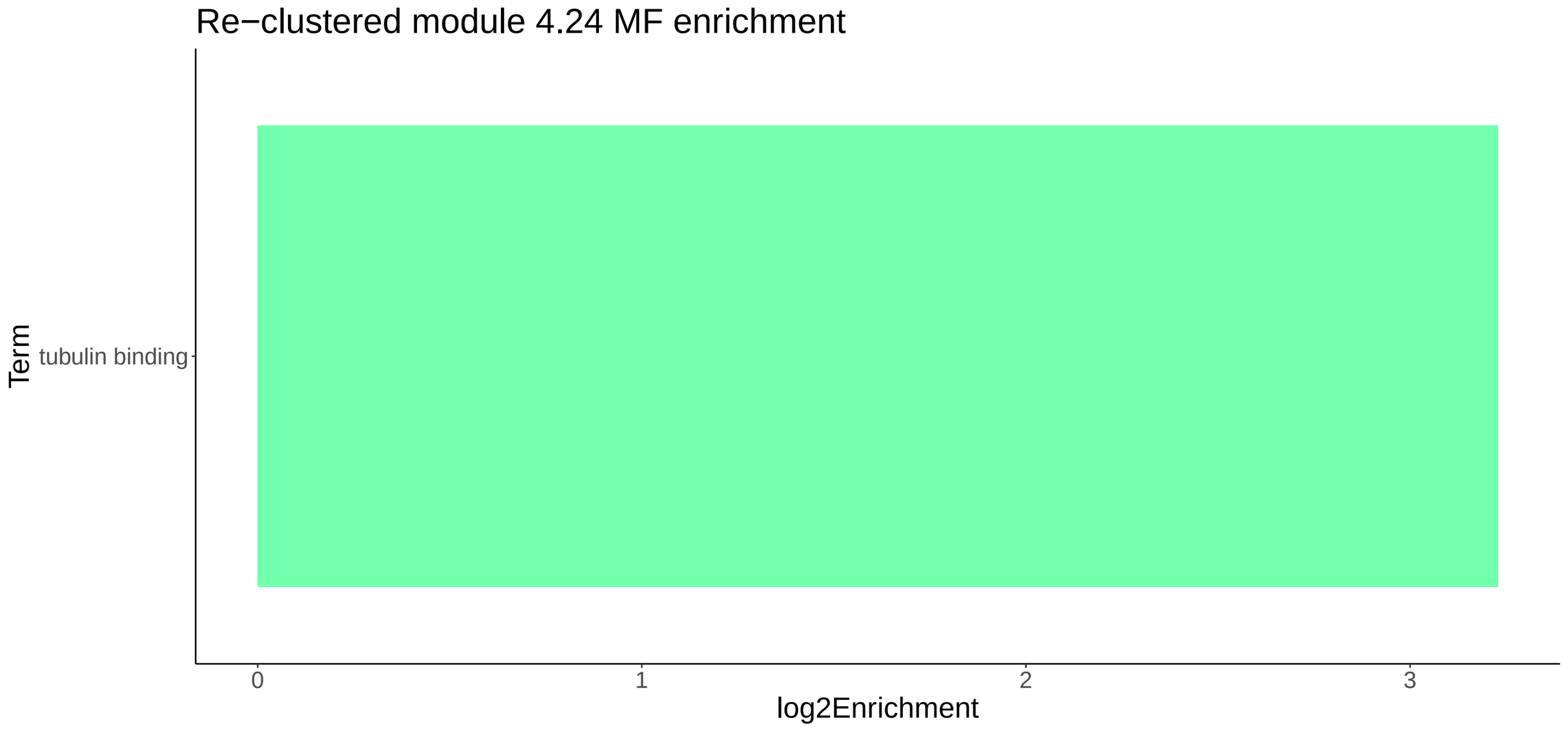

Re−clustered module 4.20.9 BP enrichment
Term
BMP signaling pathway
regulation of T cell differentiation
positive regulation of inflammatory response
0
1
2
3
4
log2Enrichment

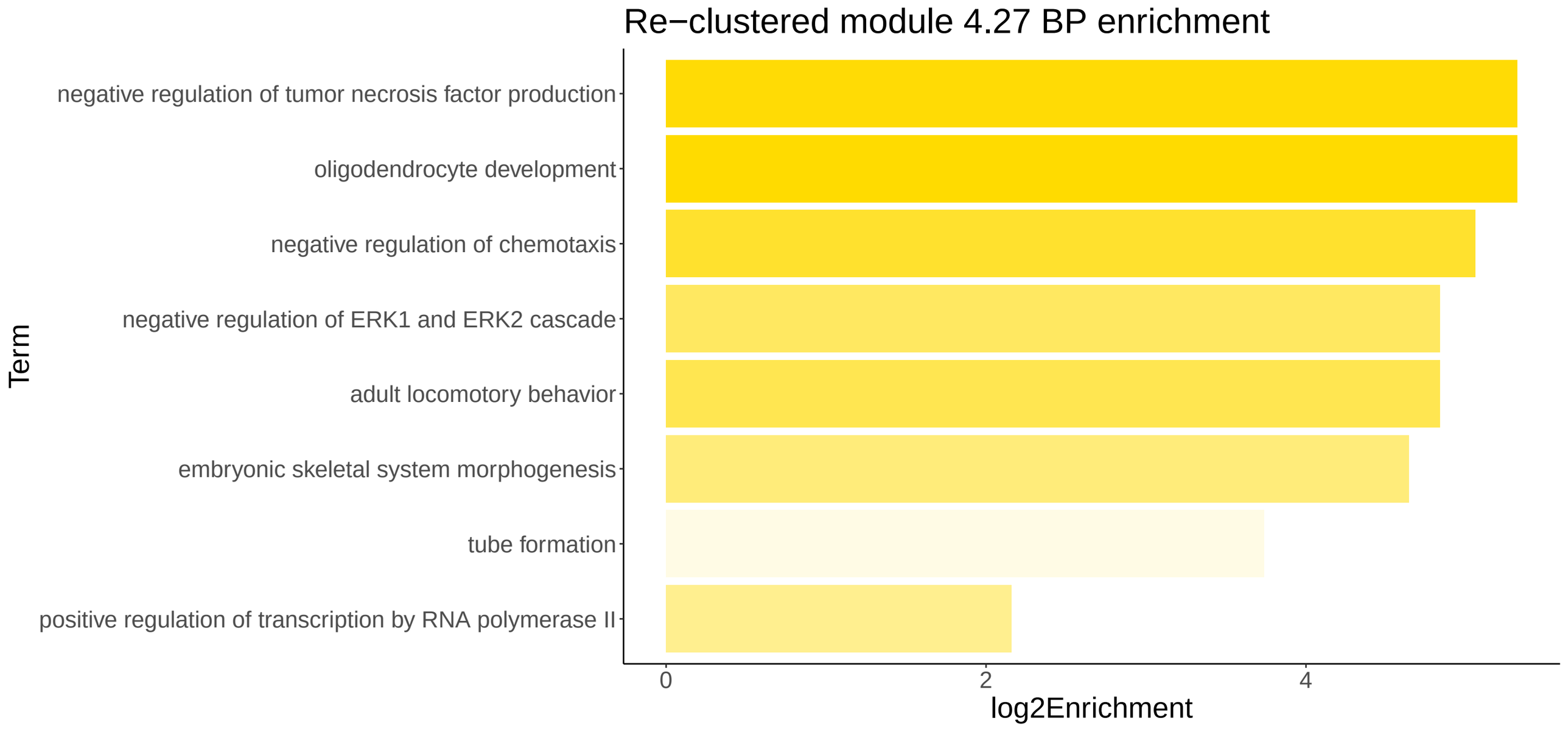

Re−clustered module 4.20.9 MF enrichment
Term
chromatin binding
0
1
2
3
log2Enrichment

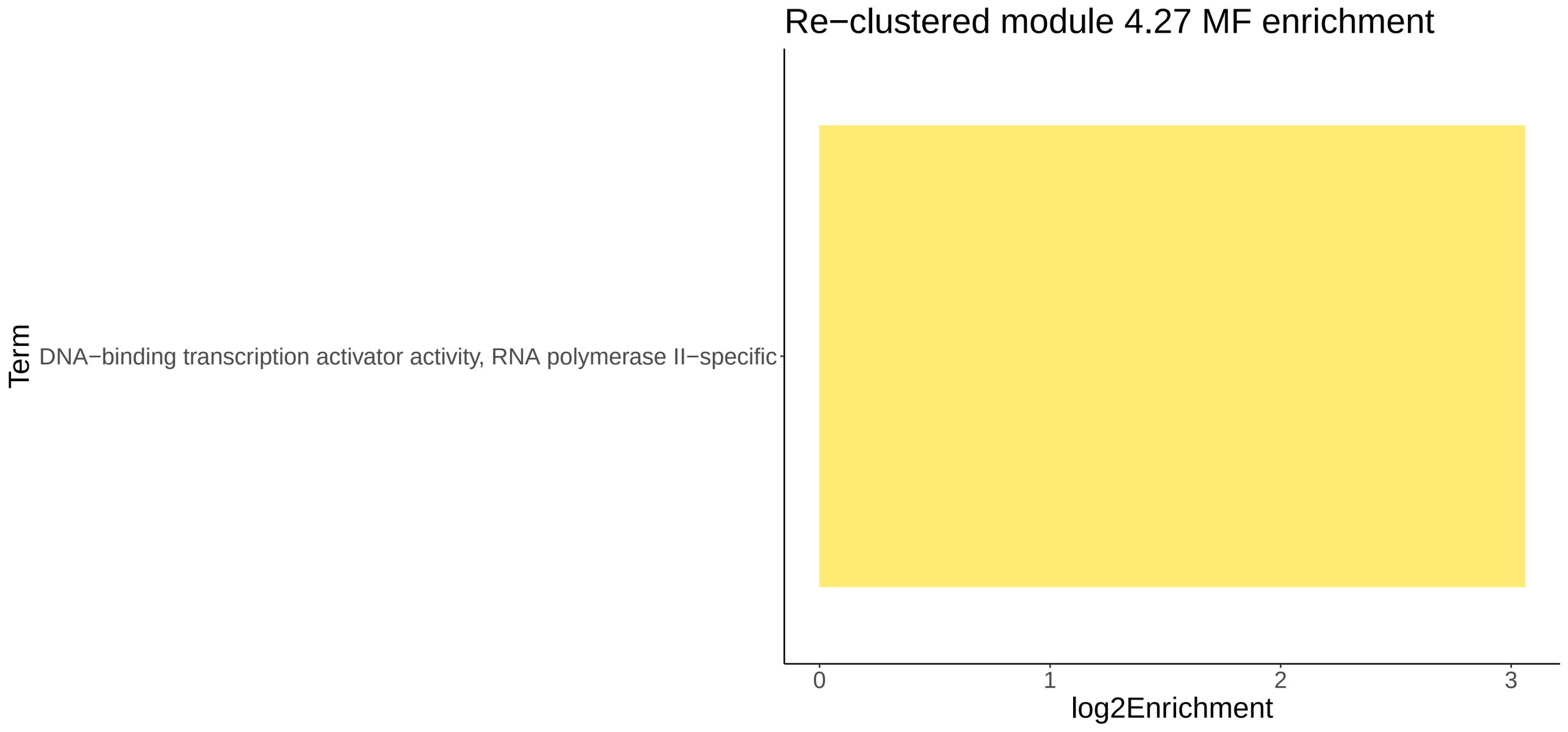

Re−clustered module 4.200 BP enrichment
response to nicotine
positive regulation of amine transport
dopamine metabolic process
synaptic transmission, dopaminergic
positive regulation of neural precursor cell proliferation
response to cocaine
visual learning
diencephalon development
determination of heart left/right asymmetry
dorsal/ventral pattern formation
excitatory postsynaptic potential
feeding behavior
memory
response to ethanol
smooth muscle contraction
central nervous system neuron differentiation
synapse assembly
adenylate cyclase−activating G protein−coupled receptor signaling pathway
regulation of synapse organization
positive regulation of developmental growth
regulation of heart contraction
negative regulation of cell population proliferation
Term
0
2
4
6
log2Enrichment

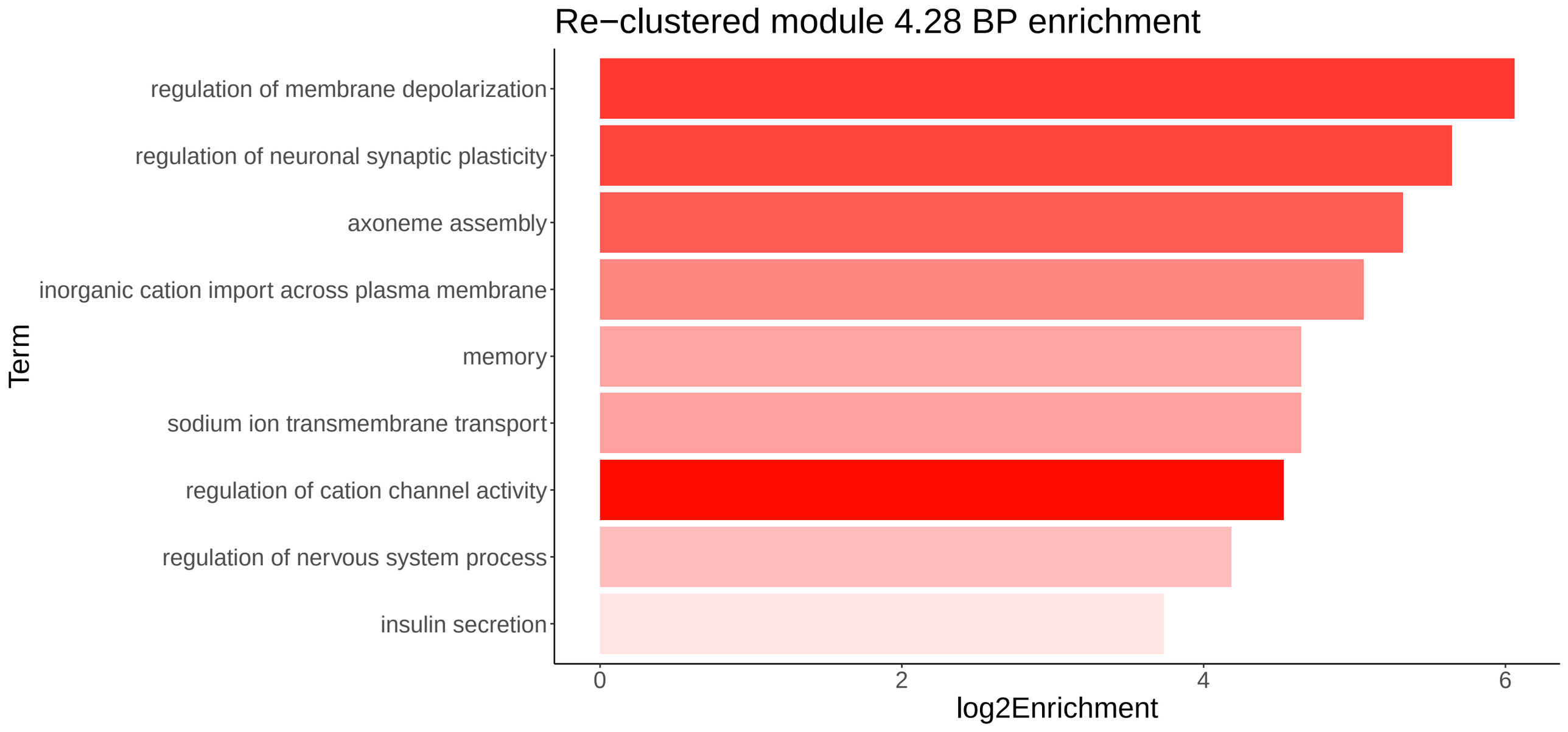

Re−clustered module 4.200 MF enrichment
Term
postsynaptic neurotransmitter receptor activity
phosphatidylserine binding
drug binding
0
2
4
log2Enrichment

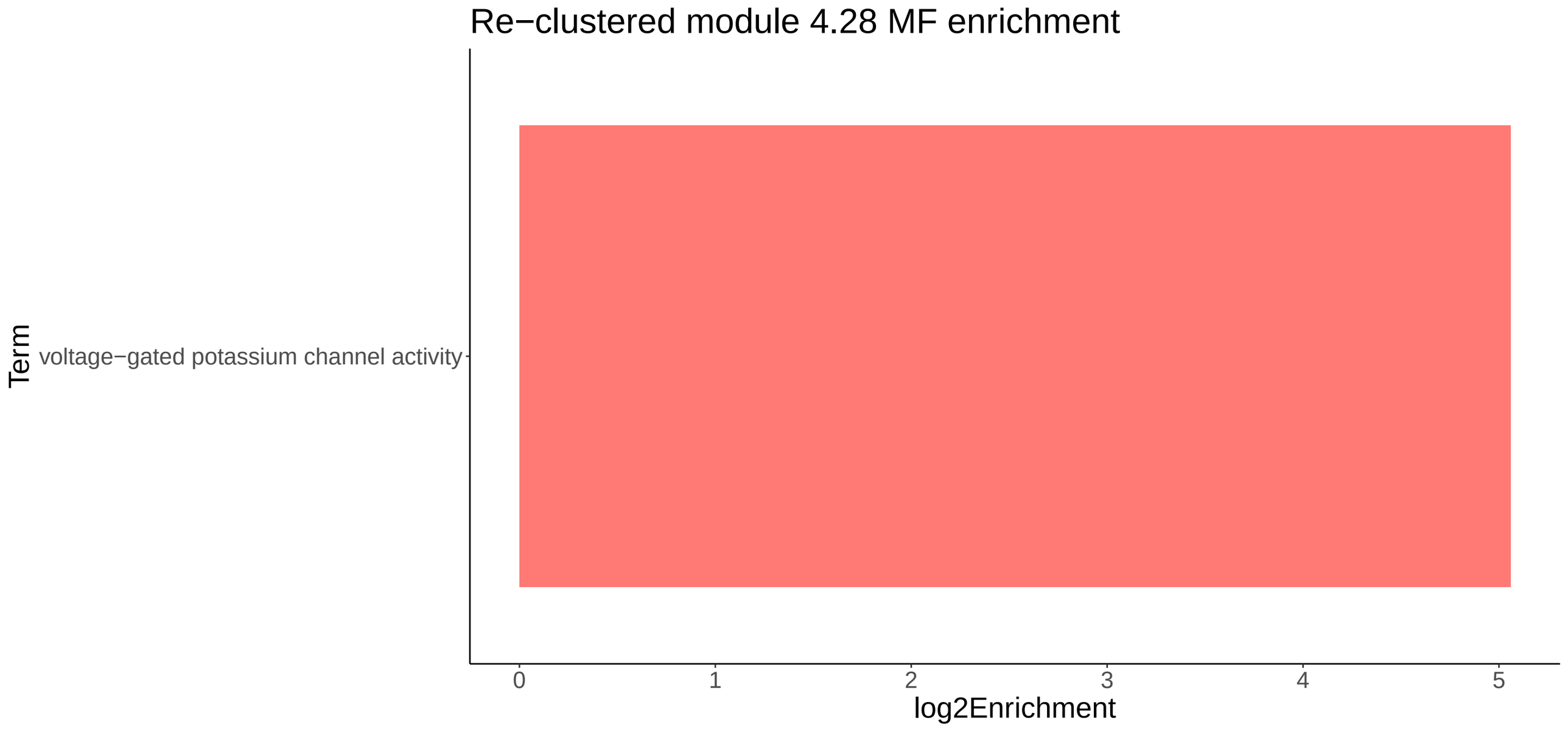

Re−clustered module 4.24 BP enrichment
Term
synaptic vesicle localization
cytosolic transport
neuron migration
negative regulation of nervous system development
axonogenesis
0
2
4
log2Enrichment

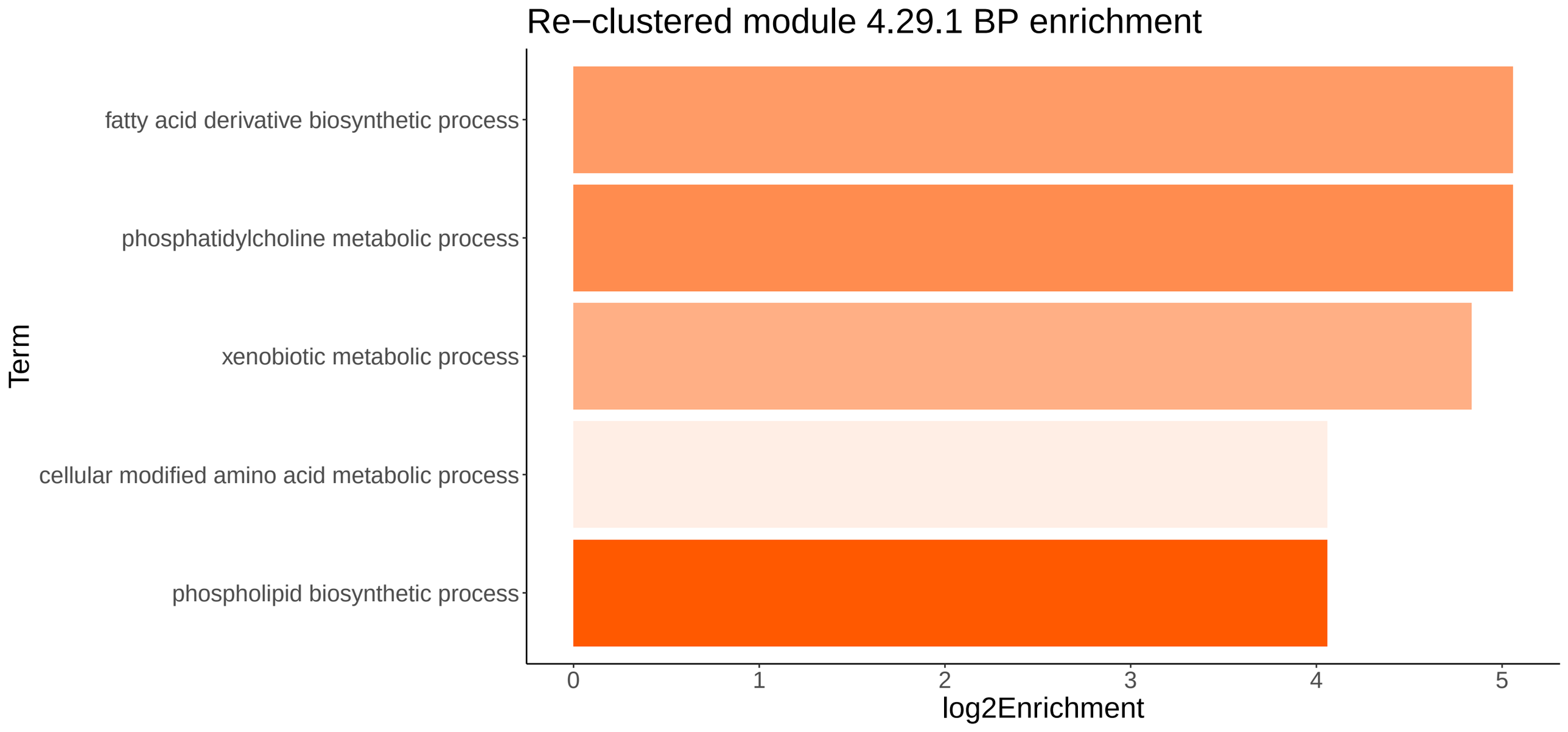

Re−clustered module 4.24 MF enrichment
Term
tubulin binding
0
1
2
3
log2Enrichment

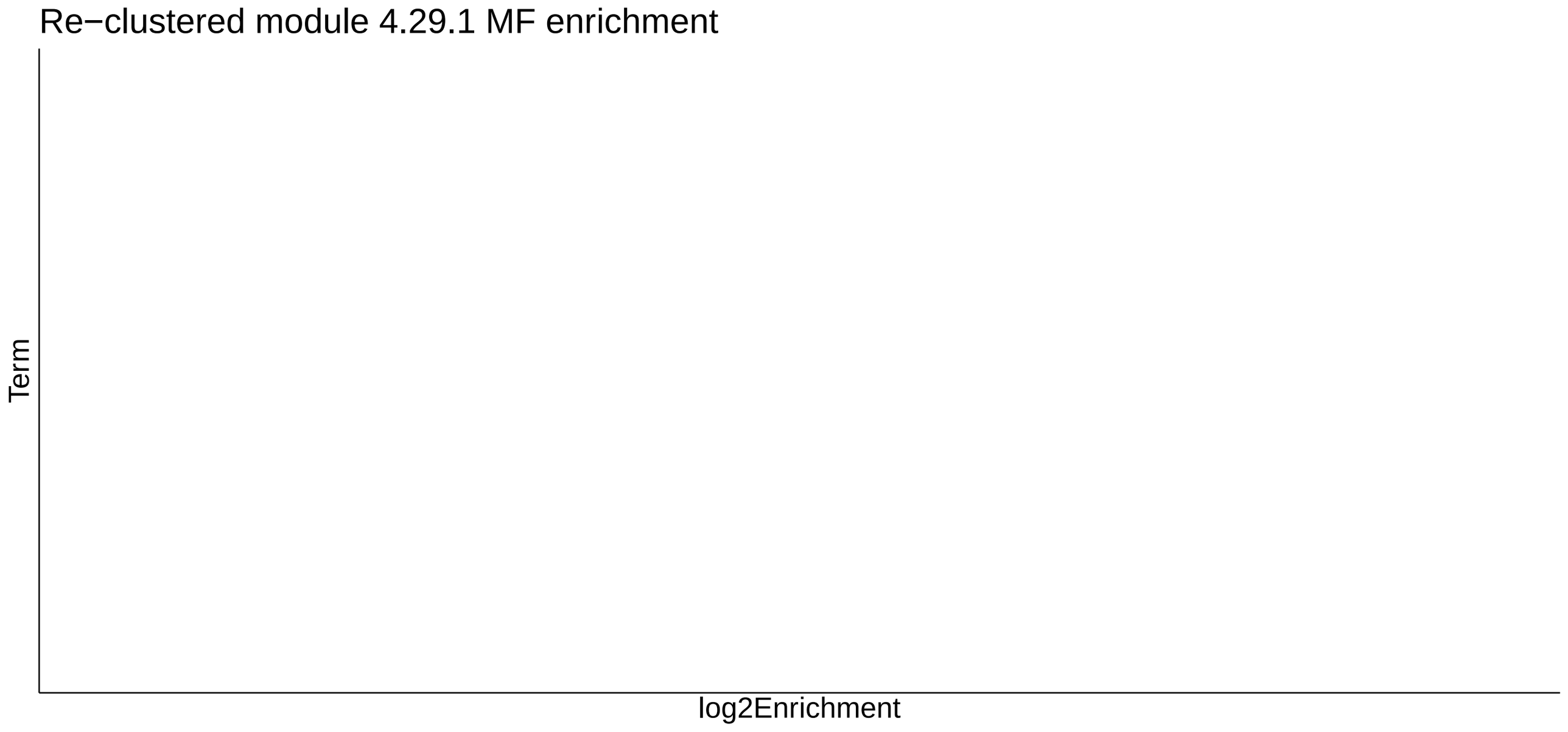

Re−clustered module 4.27 BP enrichment
negative regulation of tumor necrosis factor production
oligodendrocyte development
negative regulation of chemotaxis
negative regulation of ERK1 and ERK2 cascade
adult locomotory behavior
embryonic skeletal system morphogenesis
tube formation
positive regulation of transcription by RNA polymerase II
Term
0
2
4
log2Enrichment

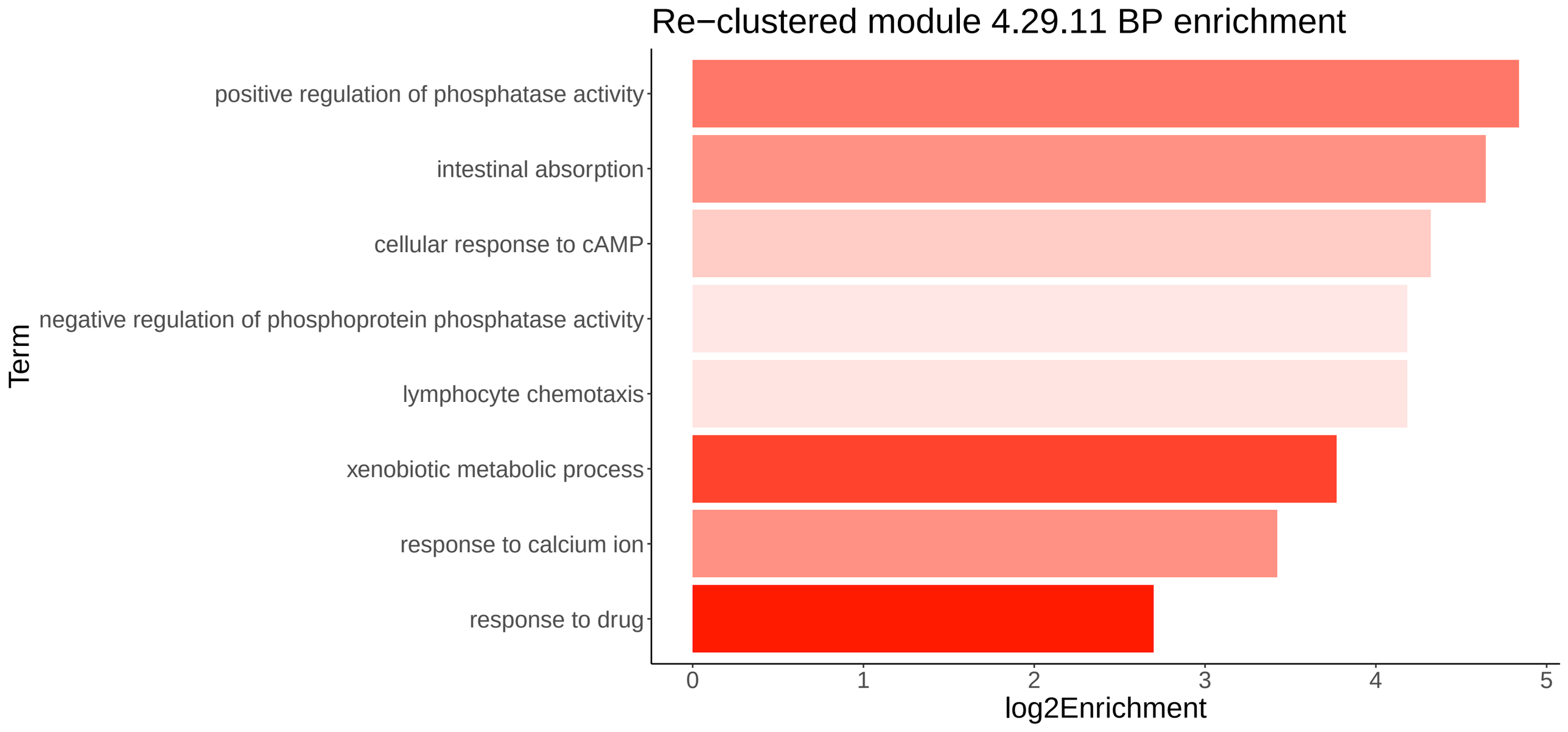

Re−clustered module 4.27 MF enrichment
Term
DNA−binding transcription activator activity, RNA polymerase II−specific
0
1
2
3
log2Enrichment

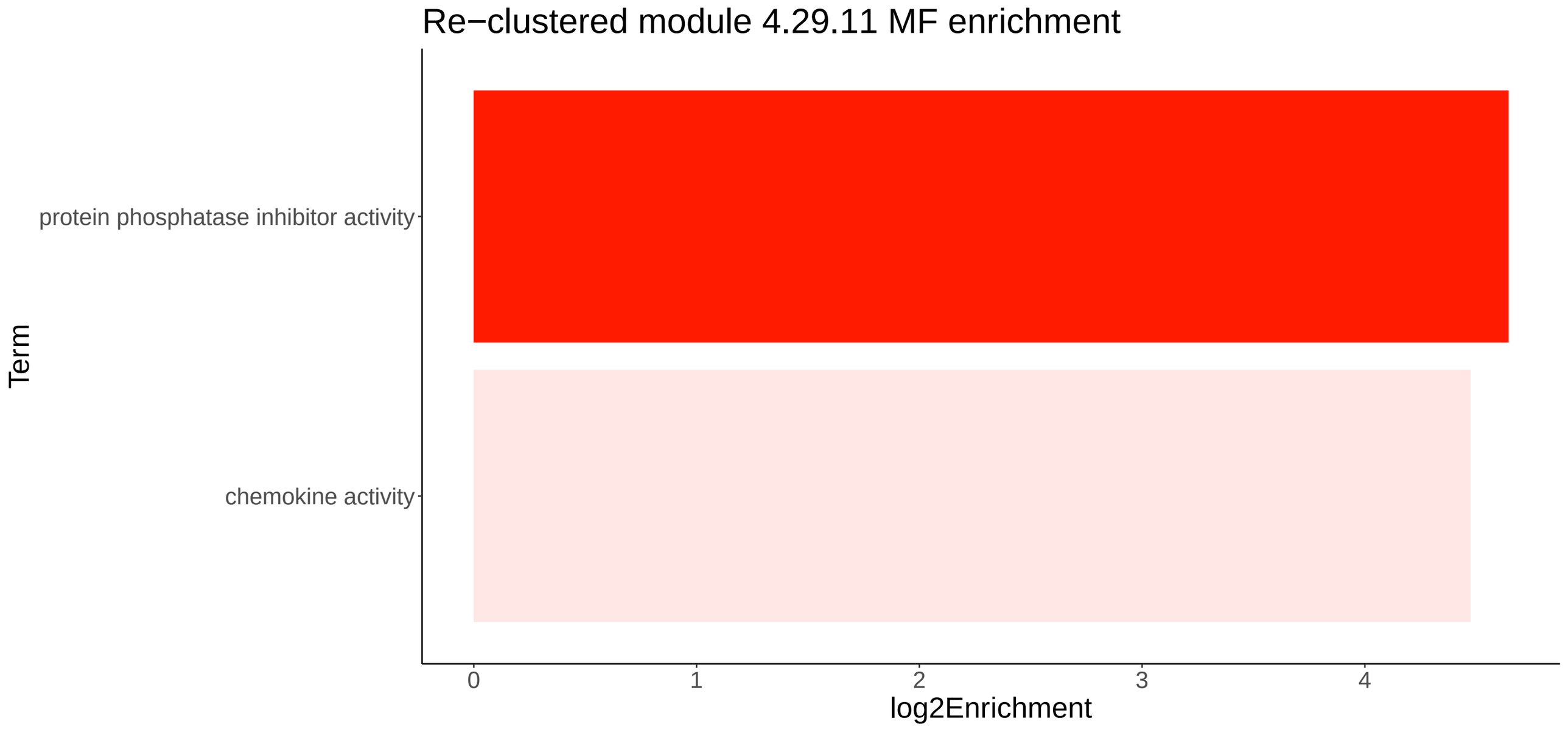

Re−clustered module 4.28 BP enrichment
regulation of membrane depolarization
regulation of neuronal synaptic plasticity
axoneme assembly
inorganic cation import across plasma membrane
memory
sodium ion transmembrane transport
regulation of cation channel activity
regulation of nervous system process
insulin secretion
Term
0
2
4
6
log2Enrichment

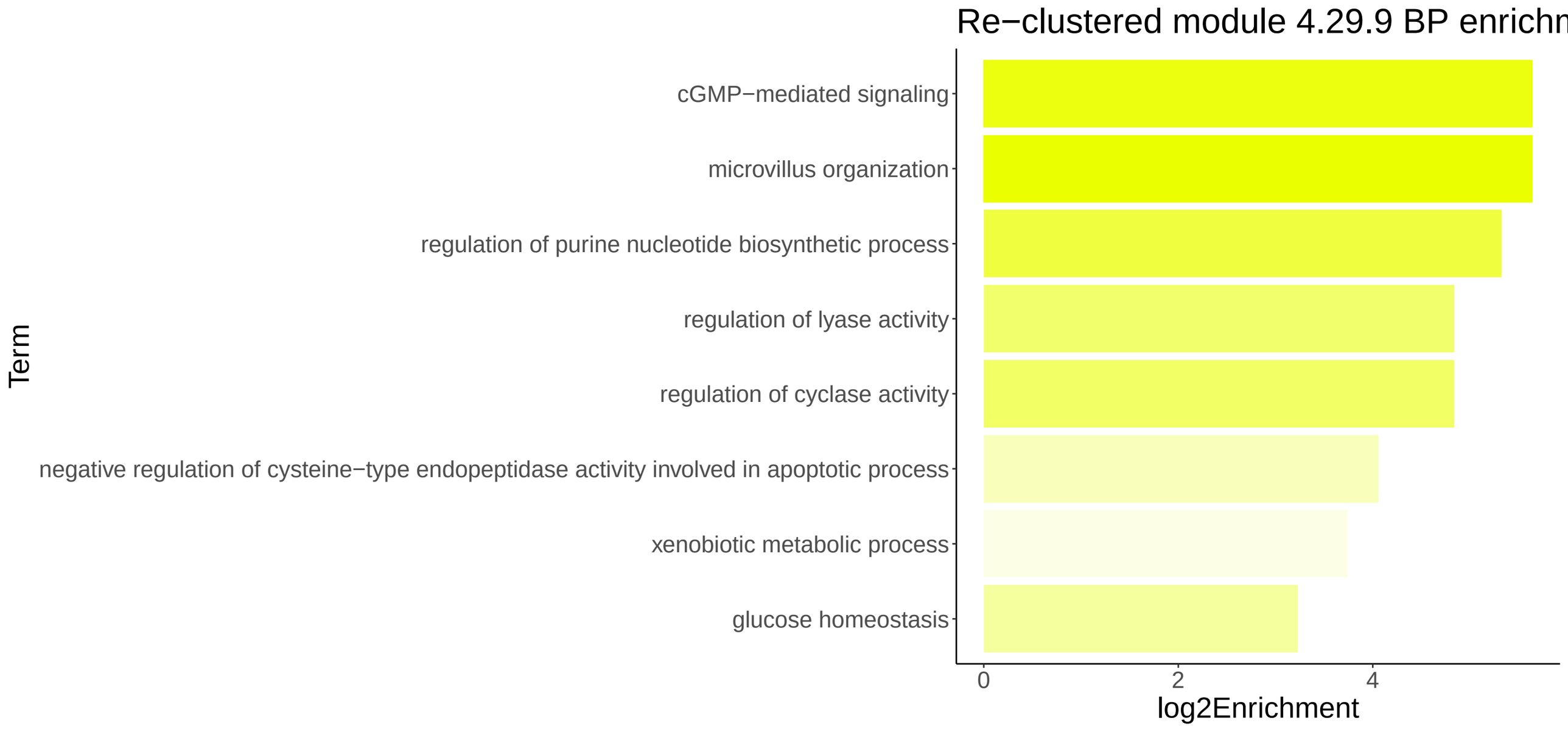

Re−clustered module 4.28 MF enrichment
Term
voltage−gated potassium channel activity
0
1
2
3
4
5
log2Enrichment

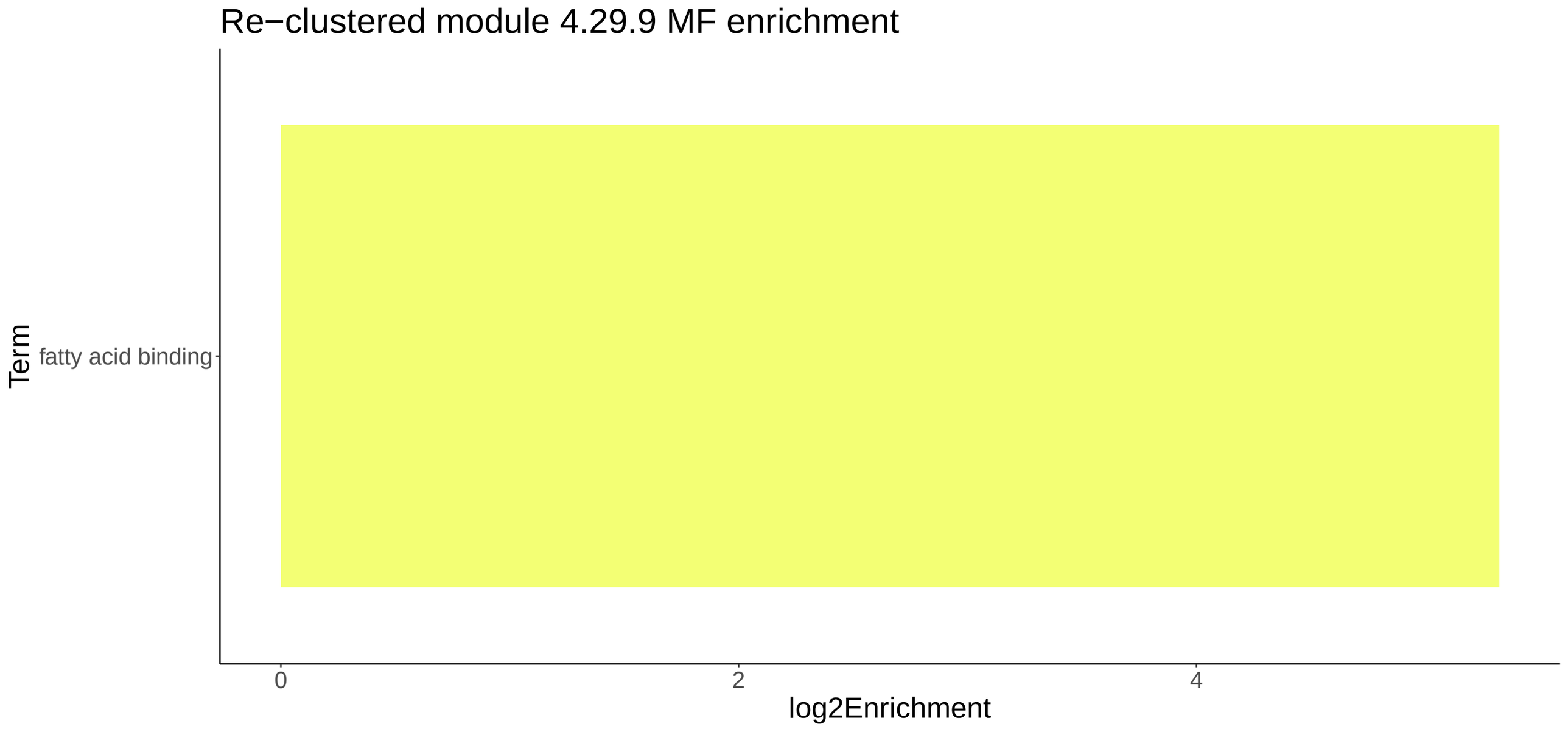

Re−clustered module 4.29.1 BP enrichment
Term
fatty acid derivative biosynthetic process
phosphatidylcholine metabolic process
xenobiotic metabolic process
cellular modified amino acid metabolic process
phospholipid biosynthetic process
0
1
2
3
4
5
log2Enrichment

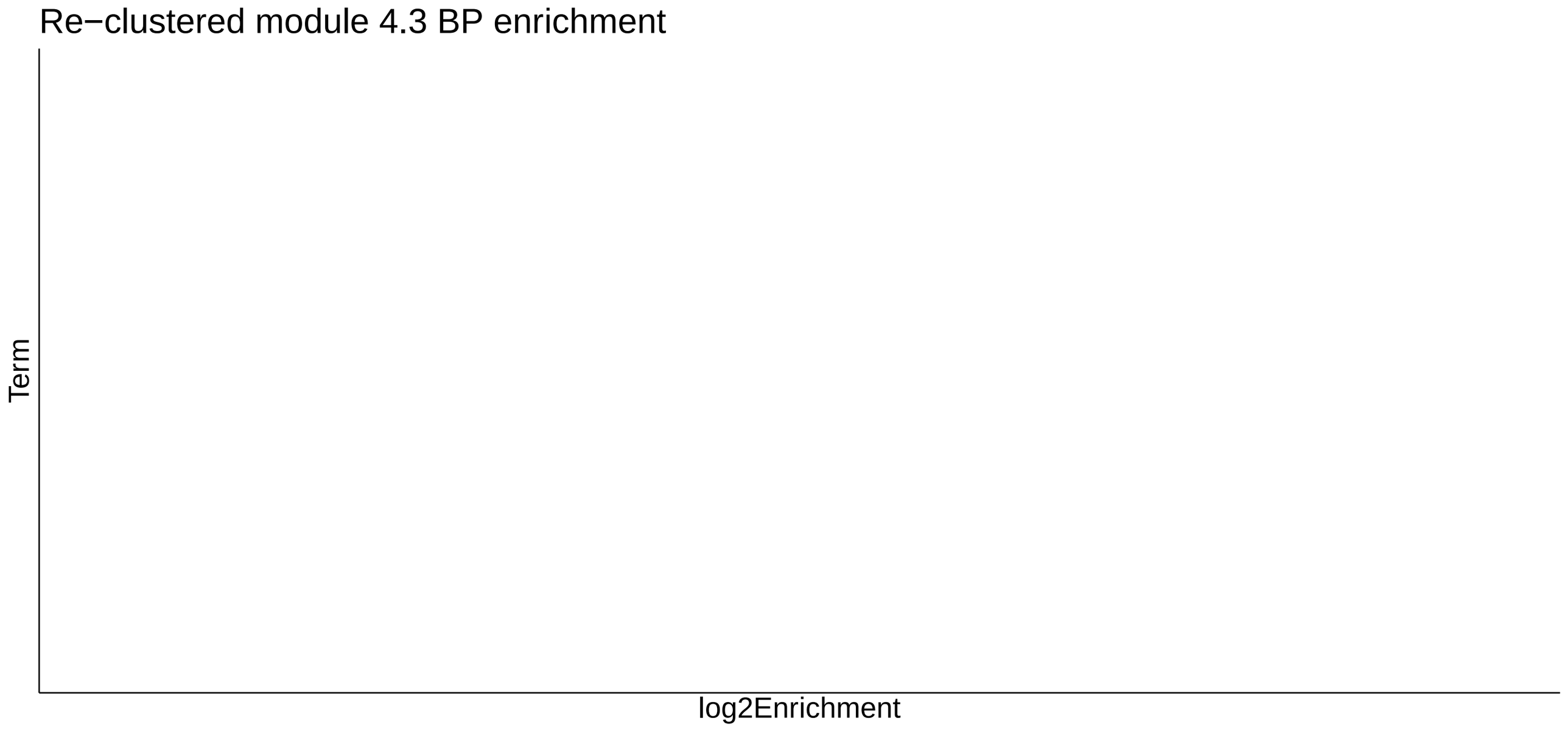

Re−clustered module 4.29.1 MF enrichment
Term
log2Enrichment

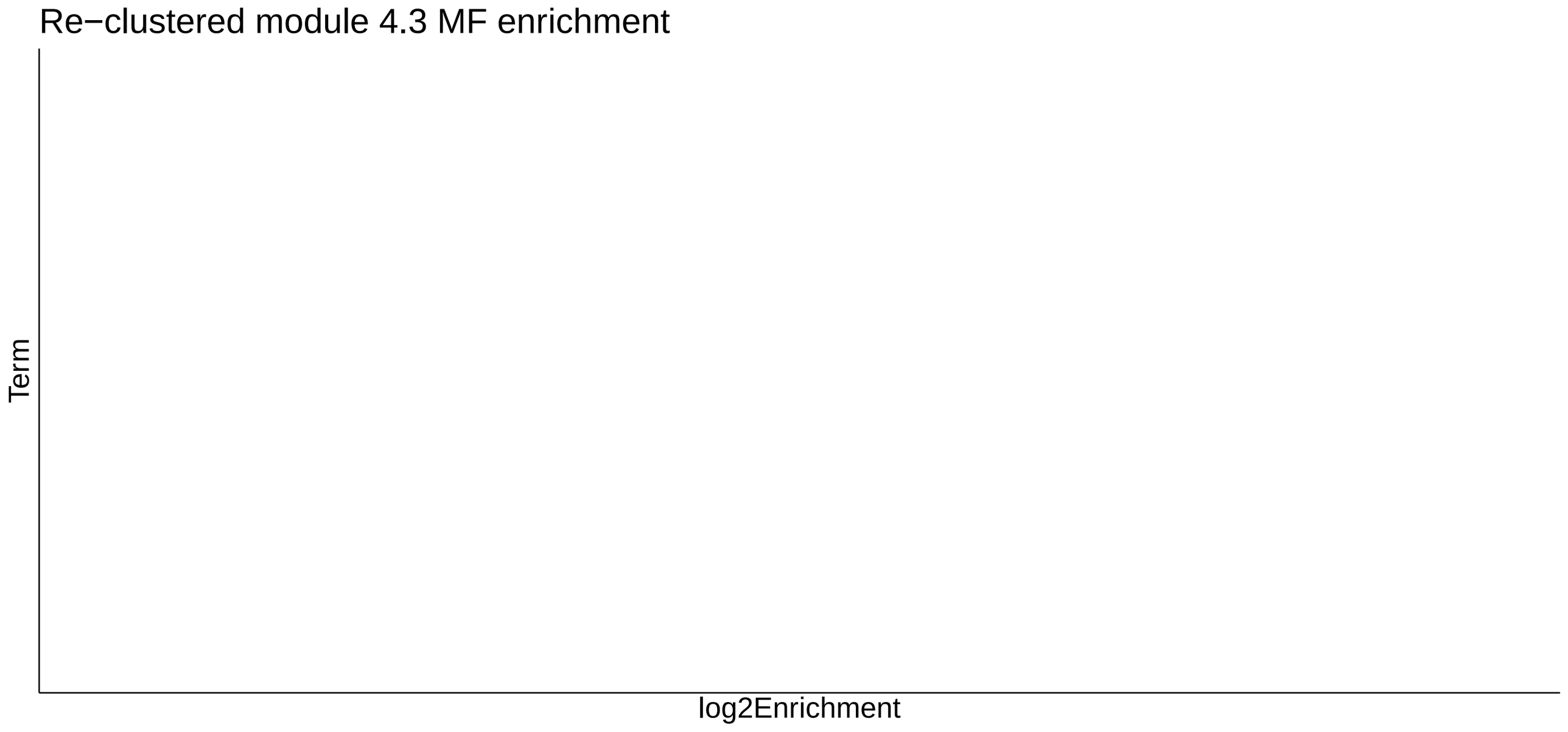

Re−clustered module 4.29.11 BP enrichment
positive regulation of phosphatase activity
intestinal absorption
cellular response to cAMP
negative regulation of phosphoprotein phosphatase activity
lymphocyte chemotaxis
xenobiotic metabolic process
response to calcium ion
response to drug
Term
0
1
2
3
4
5
log2Enrichment

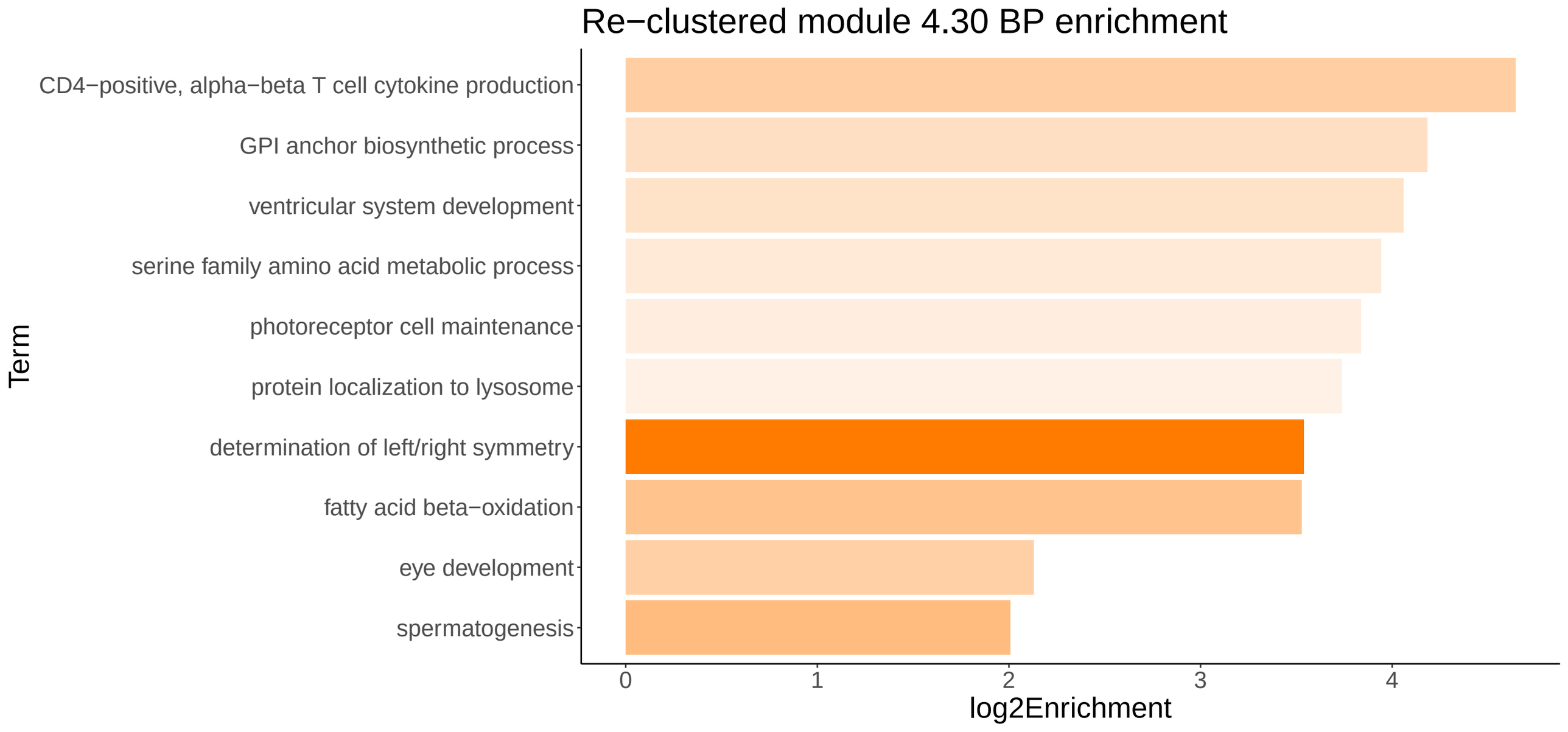

Re−clustered module 4.29.11 MF enrichment
protein phosphatase inhibitor activity
chemokine activity
Term
0
1
2
3
4
log2Enrichment

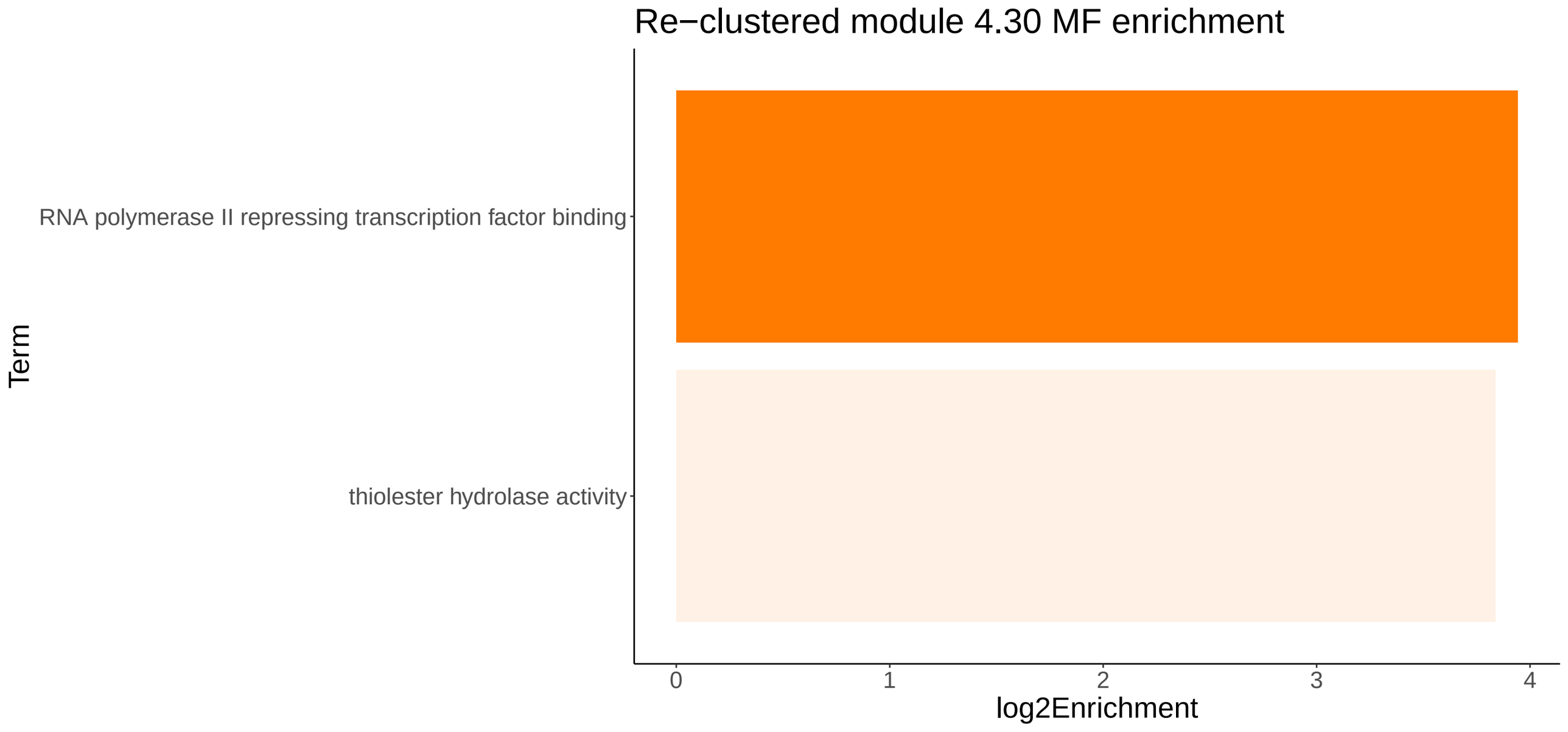

Re−clustered module 4.29.9 BP enrichm
Term
cGMP−mediated signaling
microvillus organization
regulation of purine nucleotide biosynthetic process
regulation of lyase activity
regulation of cyclase activity
negative regulation of cysteine−type endopeptidase activity involved in apoptotic process
xenobiotic metabolic process
glucose homeostasis
0
2
4
log2Enrichment

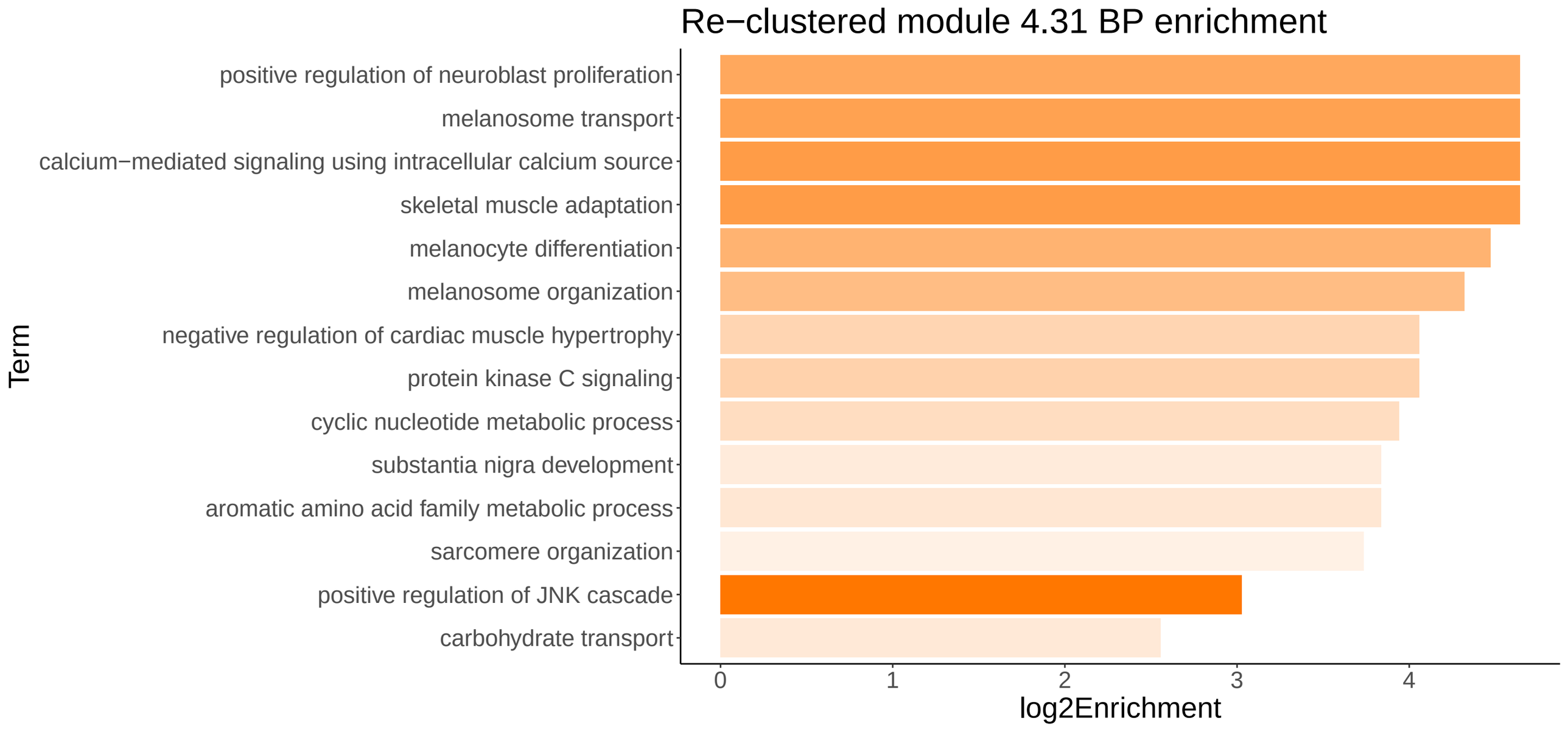

Re−clustered module 4.29.9 MF enrichment
Term
fatty acid binding
0
2
4
log2Enrichment

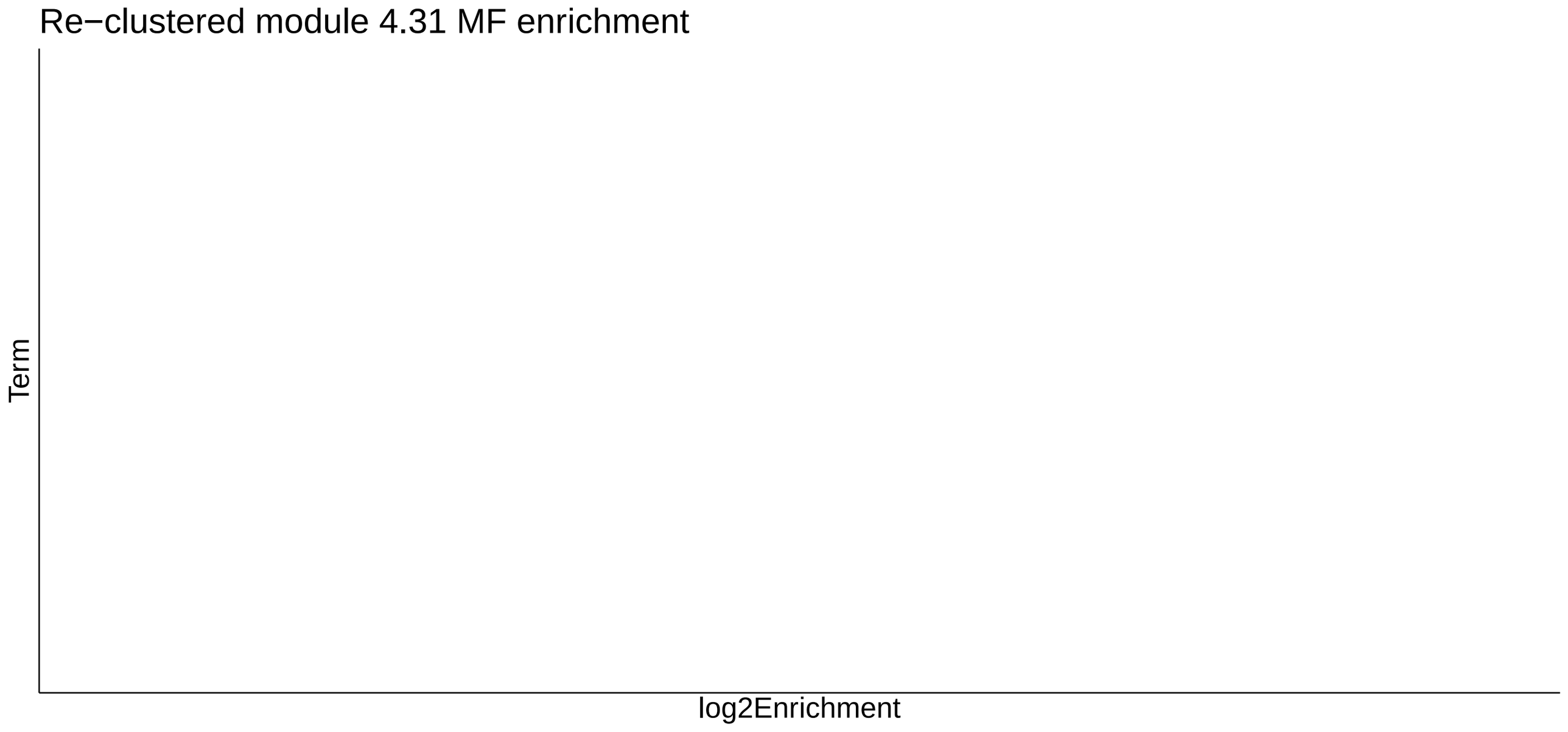

Re−clustered module 4.3 BP enrichment
Term
log2Enrichment

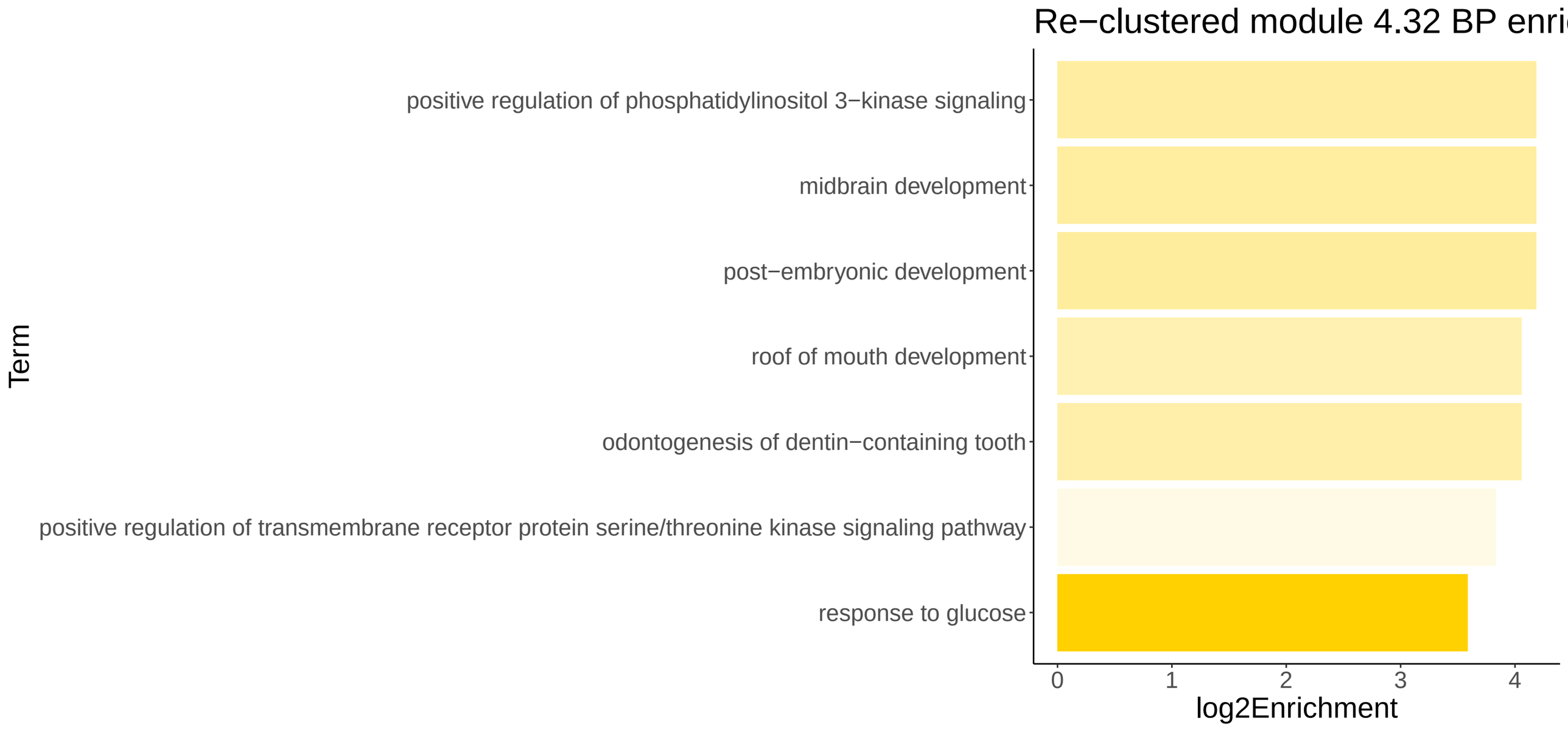

Re−clustered module 4.3 MF enrichment
Term
log2Enrichment

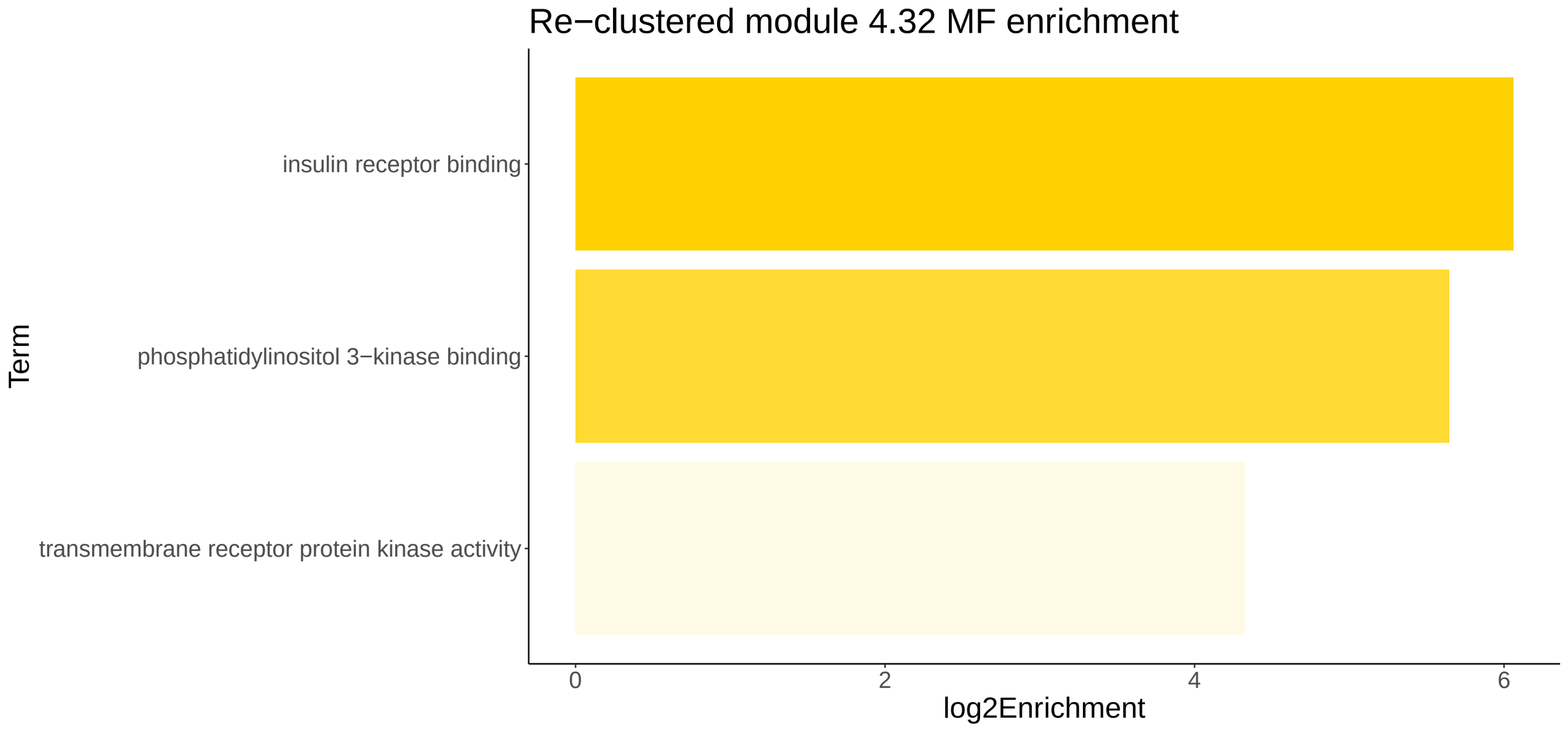

Re−clustered module 4.30 BP enrichment
CD4−positive, alpha−beta T cell cytokine production
GPI anchor biosynthetic process
ventricular system development
serine family amino acid metabolic process
photoreceptor cell maintenance
protein localization to lysosome
determination of left/right symmetry
fatty acid beta−oxidation
eye development
spermatogenesis
Term
0
1
2
3
4
log2Enrichment

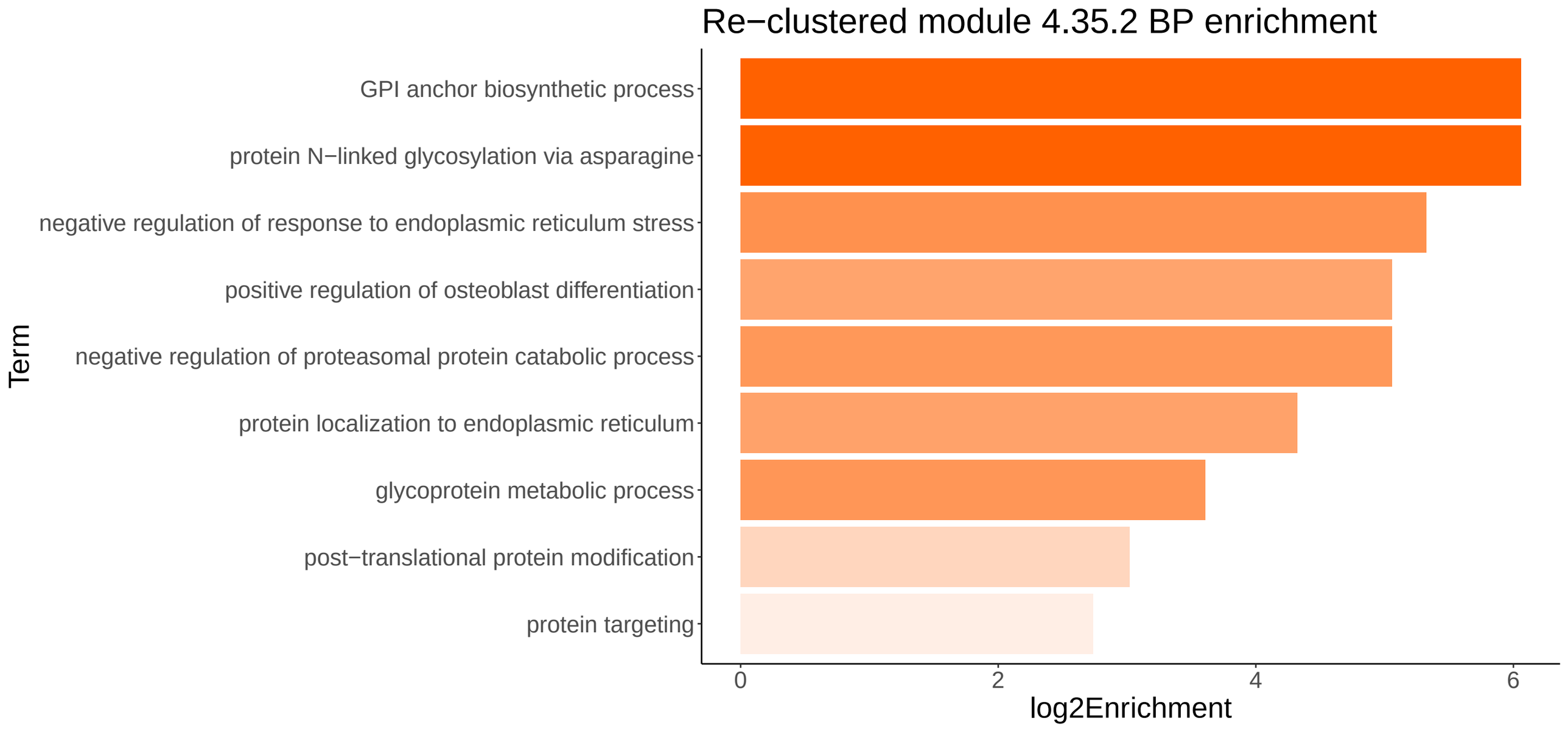

Re−clustered module 4.30 MF enrichment
RNA polymerase II repressing transcription factor binding
thiolester hydrolase activity
Term
0
1
2
3
4
log2Enrichment

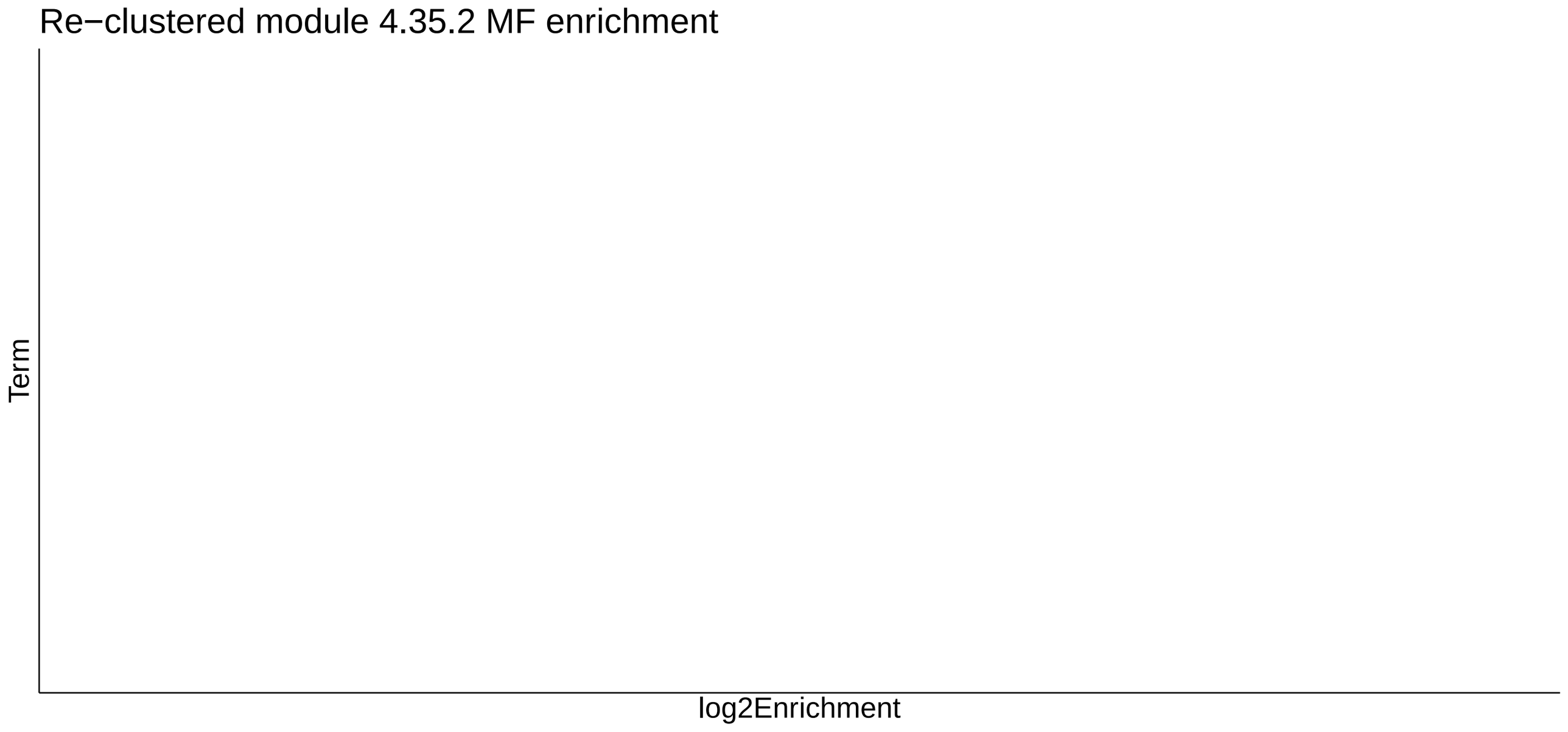

Re−clustered module 4.31 BP enrichment
positive regulation of neuroblast proliferation
melanosome transport
calcium−mediated signaling using intracellular calcium source
skeletal muscle adaptation
melanocyte differentiation
melanosome organization
negative regulation of cardiac muscle hypertrophy
protein kinase C signaling
cyclic nucleotide metabolic process
substantia nigra development
aromatic amino acid family metabolic process
sarcomere organization
positive regulation of JNK cascade
carbohydrate transport
Term
0
1
2
3
4
log2Enrichment

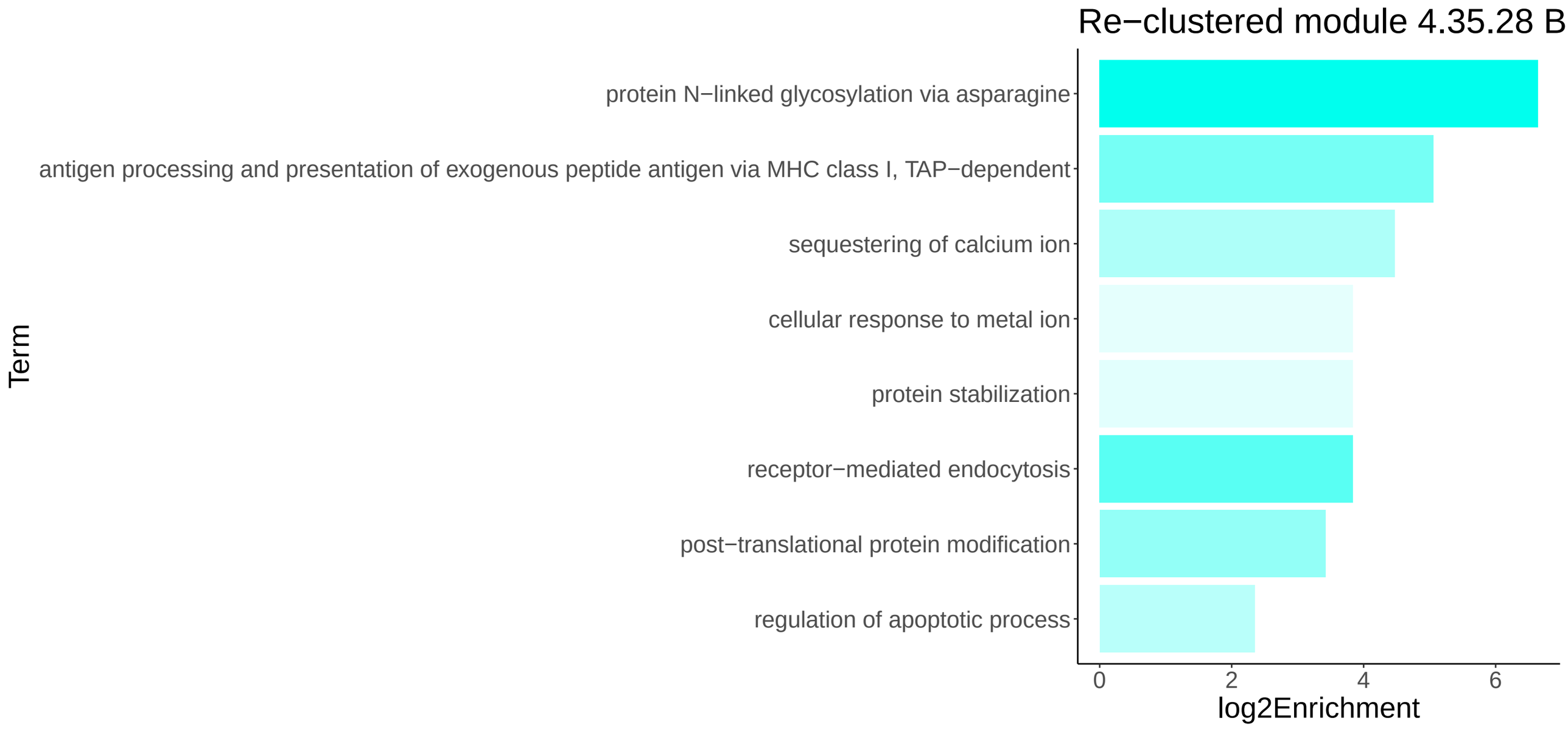

Re−clustered module 4.31 MF enrichment
Term
log2Enrichment

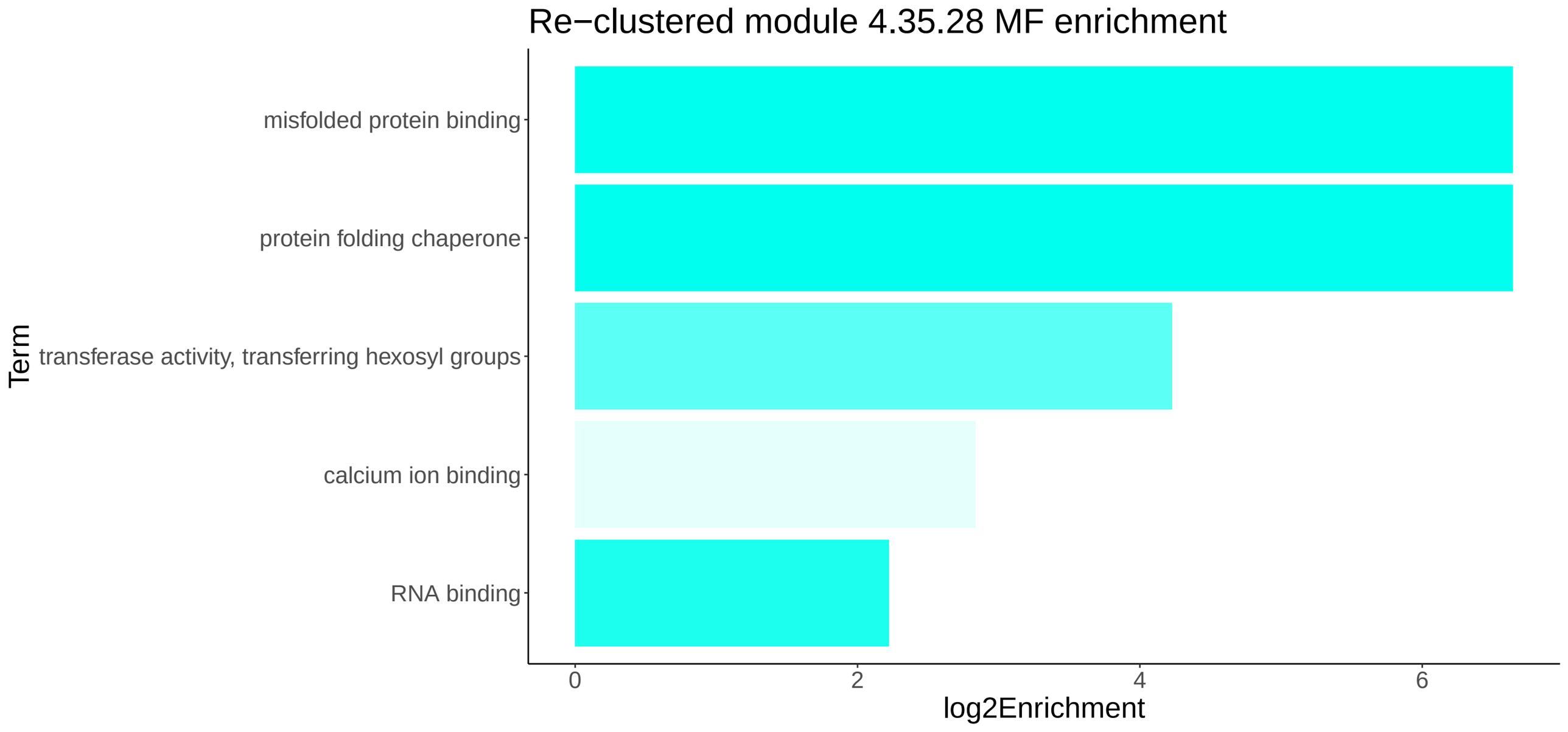

Re−clustered module 4.32 BP enri
positive regulation of phosphatidylinositol 3−kinase signaling
midbrain development
post−embryonic development
roof of mouth development
odontogenesis of dentin−containing tooth
positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway
response to glucose
Term
0
1
2
3
4
log2Enrichment

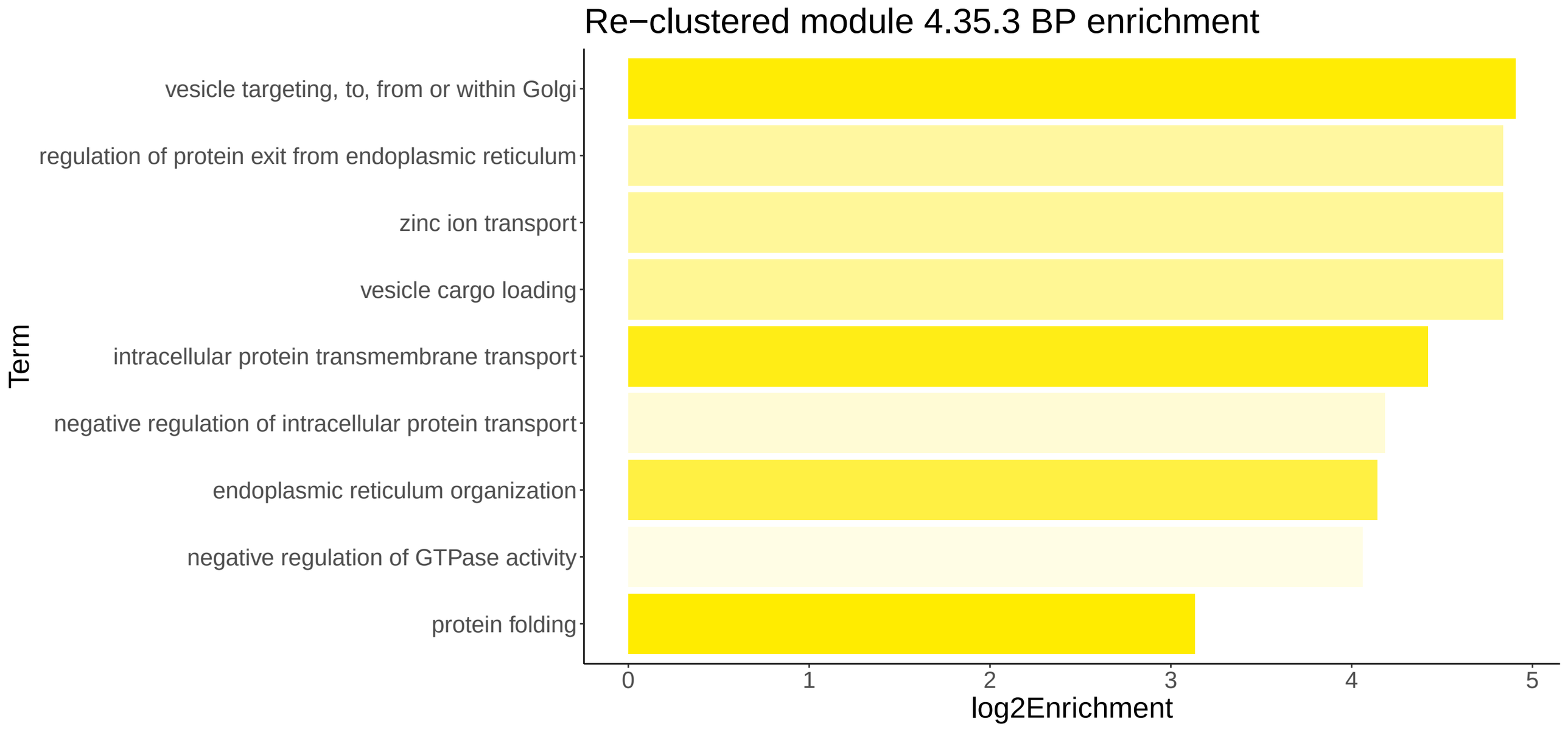

Re−clustered module 4.32 MF enrichment
Term
insulin receptor binding
phosphatidylinositol 3−kinase binding
transmembrane receptor protein kinase activity
0
2
4
6
log2Enrichment

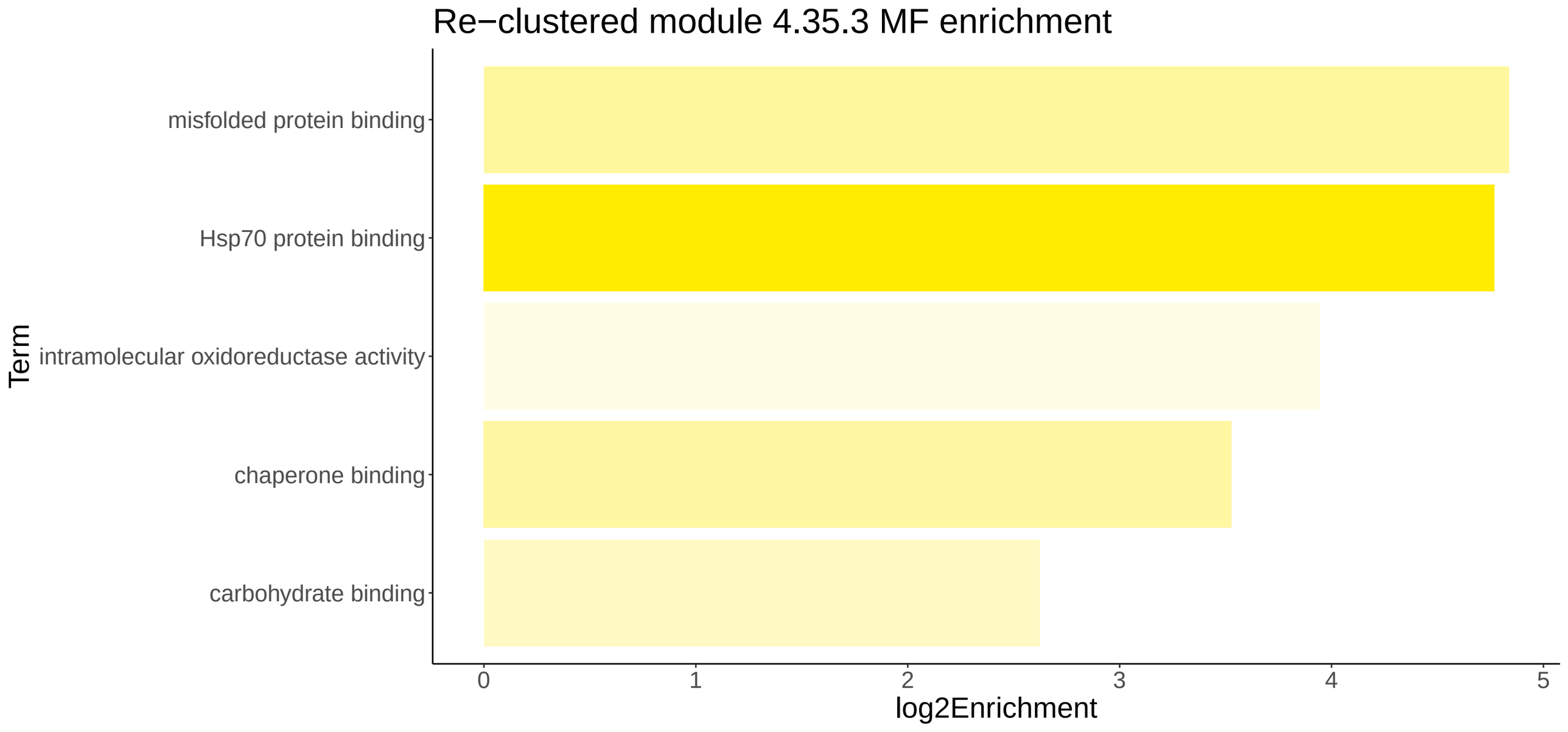

Re−clustered module 4.35.2 BP enrichment
GPI anchor biosynthetic process
protein N−linked glycosylation via asparagine
negative regulation of response to endoplasmic reticulum stress
positive regulation of osteoblast differentiation
negative regulation of proteasomal protein catabolic process
protein localization to endoplasmic reticulum
glycoprotein metabolic process
post−translational protein modification
protein targeting
Term
0
2
4
6
log2Enrichment

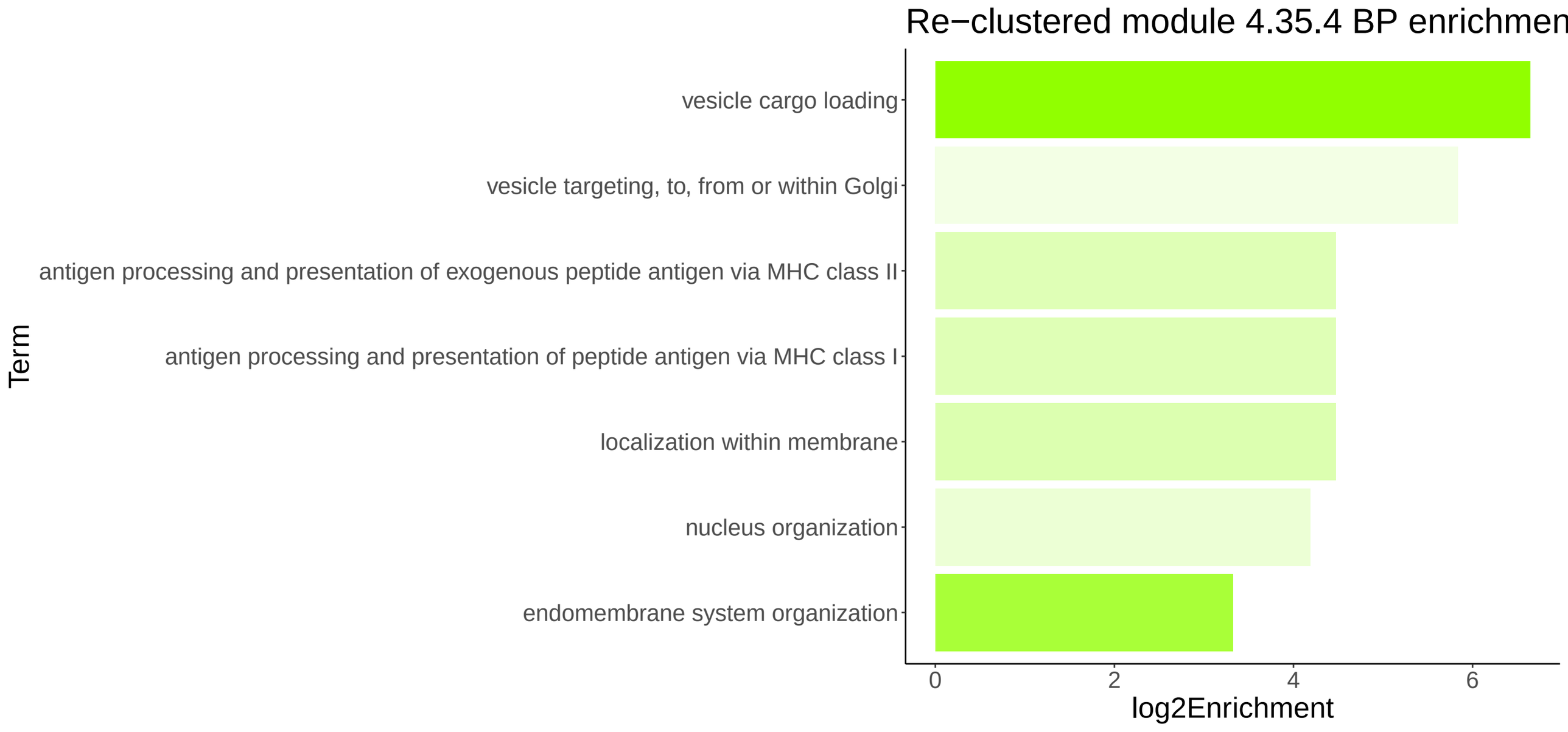

Re−clustered module 4.35.2 MF enrichment
Term
log2Enrichment

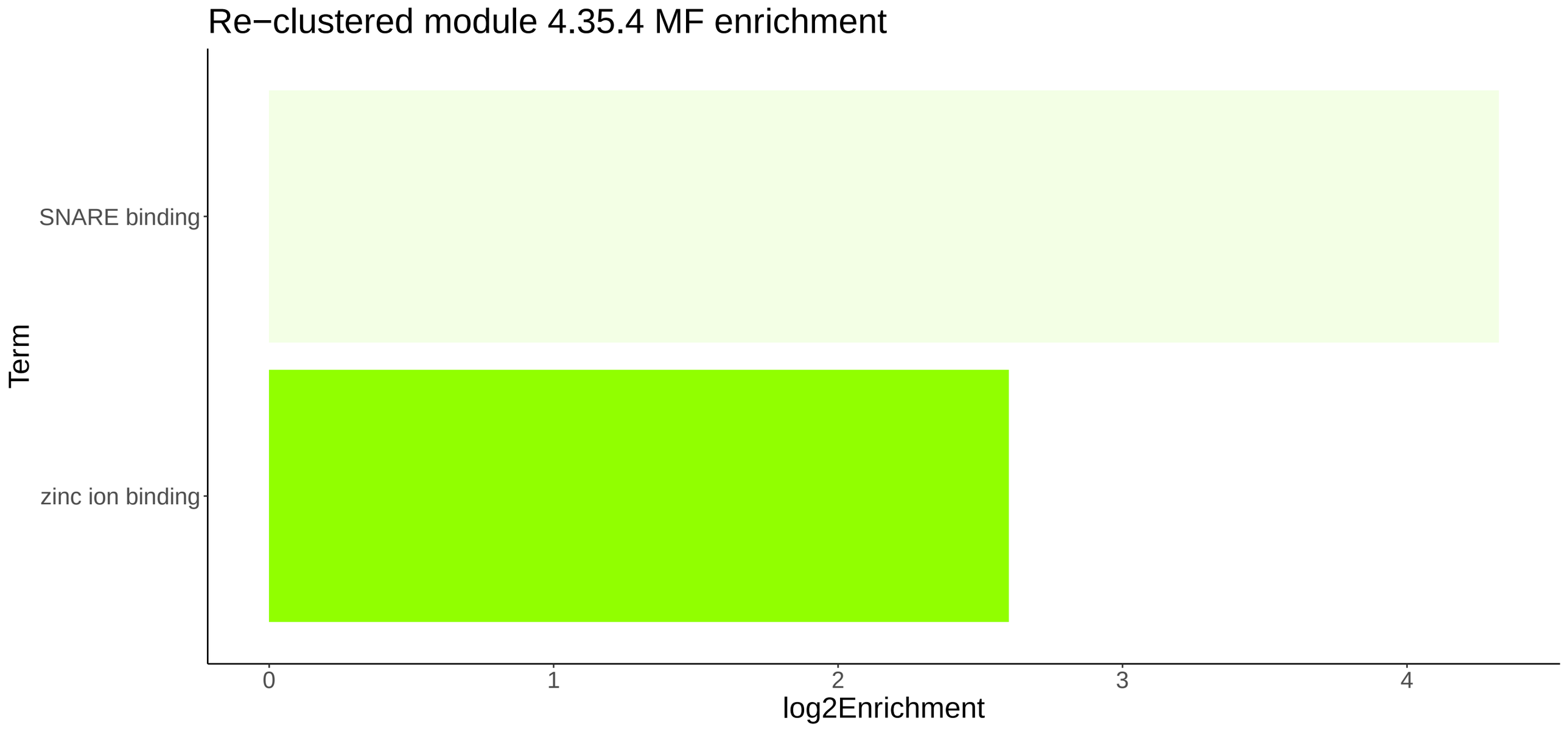

Re−clustered module 4.35.28 B
protein N−linked glycosylation via asparagine
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
sequestering of calcium ion
cellular response to metal ion
protein stabilization
receptor−mediated endocytosis
post−translational protein modification
regulation of apoptotic process
Term
0
2
4
6
log2Enrichment

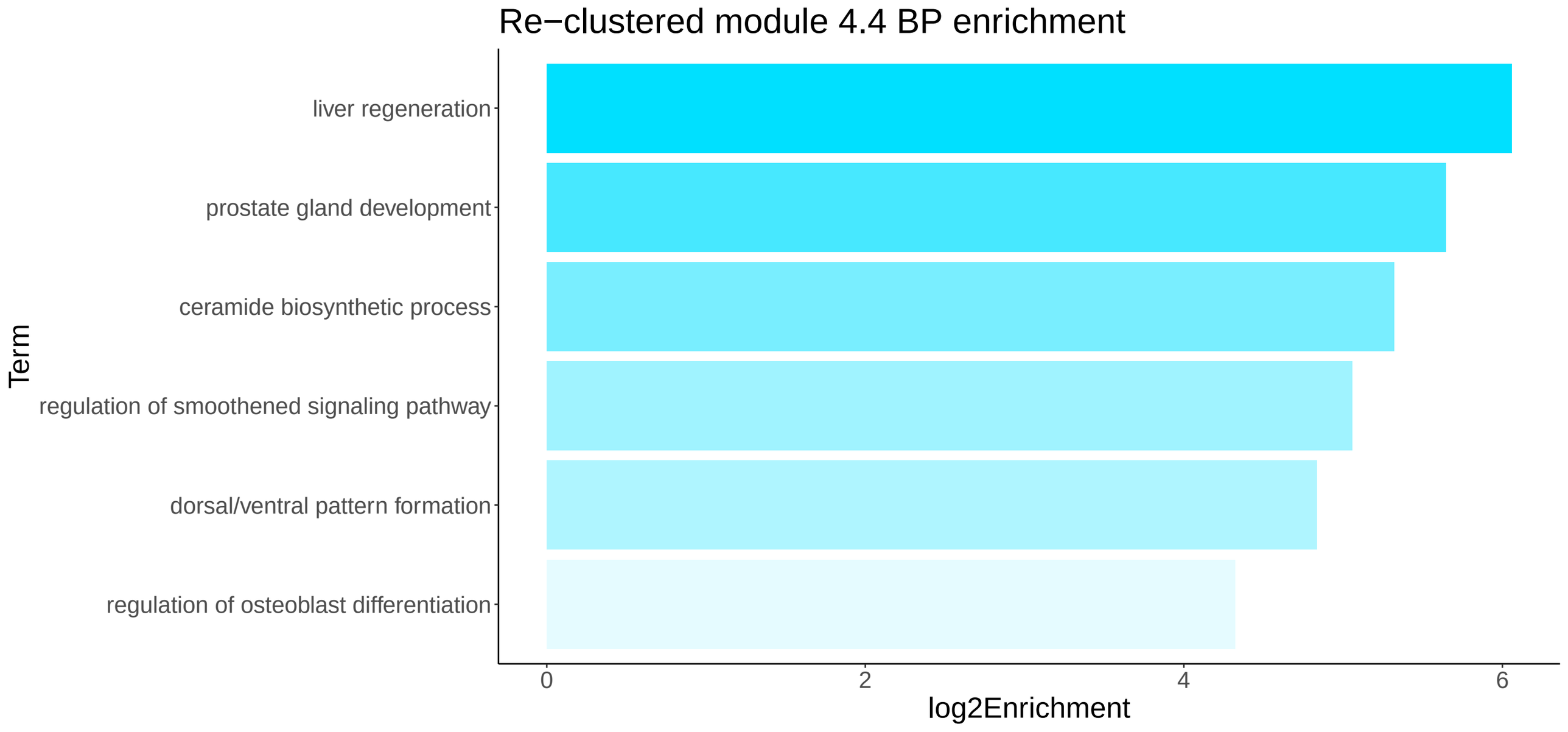

Re−clustered module 4.35.28 MF enrichment
misfolded protein binding
protein folding chaperone
transferase activity, transferring hexosyl groups
calcium ion binding
RNA binding
Term
0
2
4
6
log2Enrichment

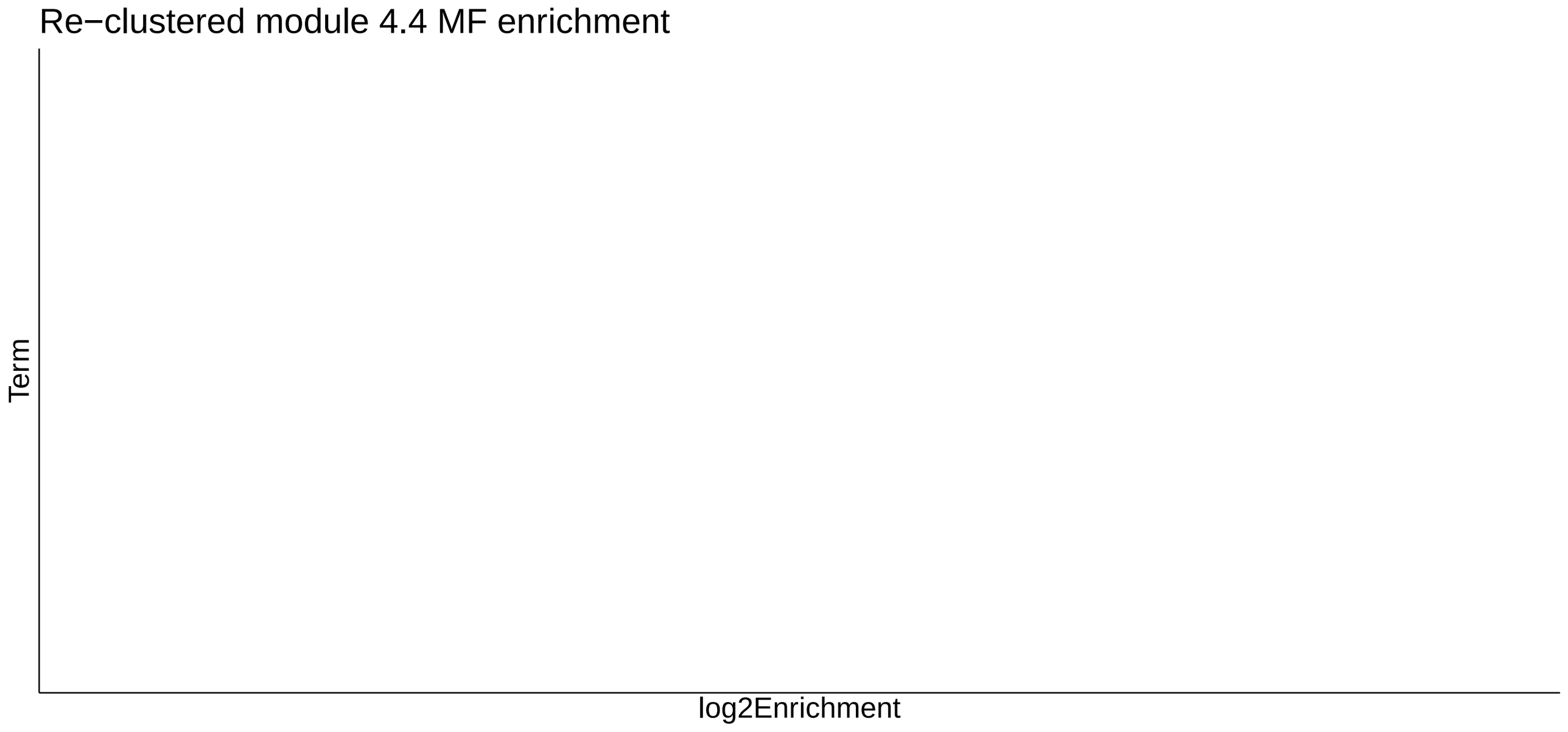

Re−clustered module 4.35.3 BP enrichment
vesicle targeting, to, from or within Golgi
regulation of protein exit from endoplasmic reticulum
zinc ion transport
vesicle cargo loading
intracellular protein transmembrane transport
negative regulation of intracellular protein transport
endoplasmic reticulum organization
negative regulation of GTPase activity
protein folding
Term
0
1
2
3
4
5
log2Enrichment

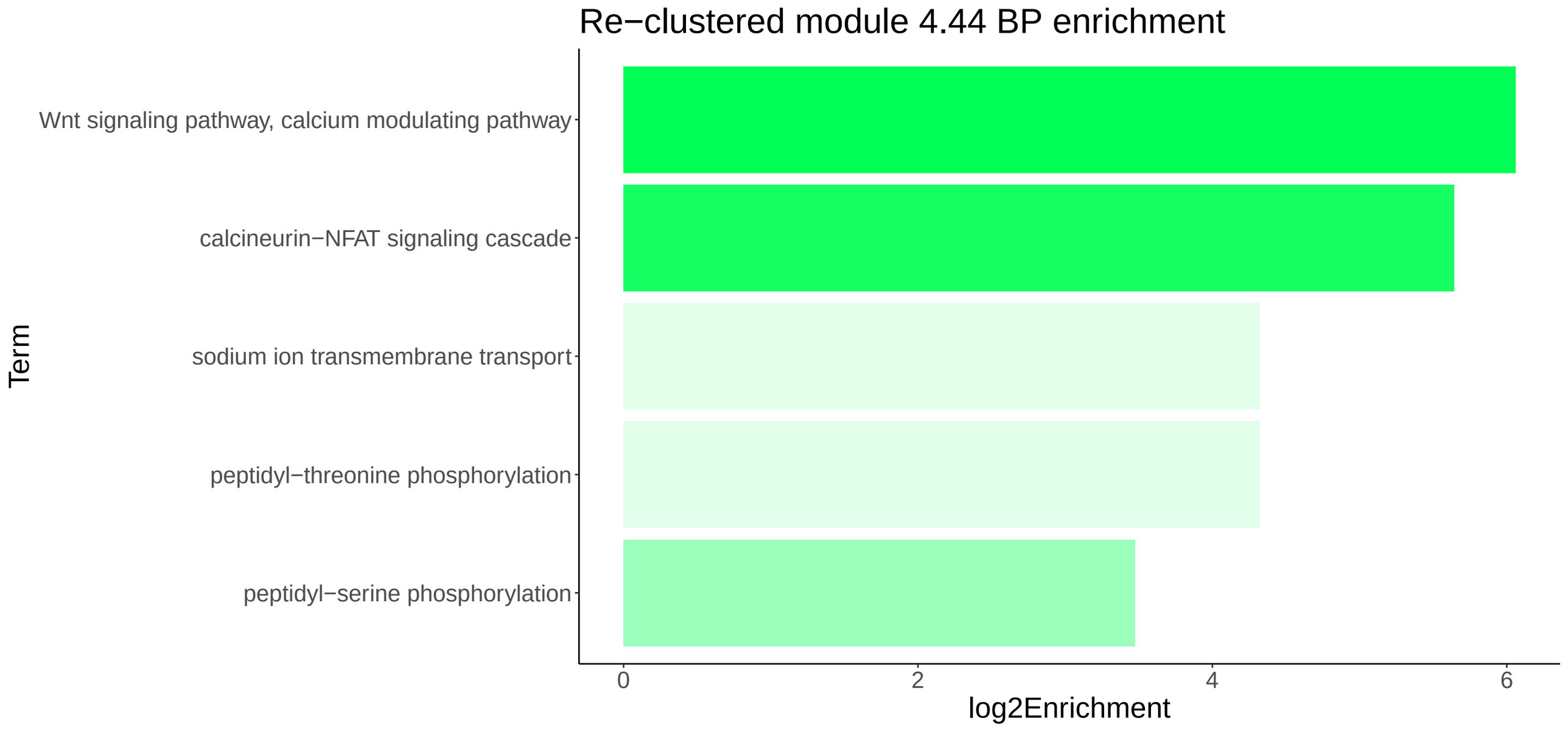

Re−clustered module 4.35.3 MF enrichment
misfolded protein binding
Hsp70 protein binding
intramolecular oxidoreductase activity
chaperone binding
carbohydrate binding
Term
0
1
2
3
4
5
log2Enrichment

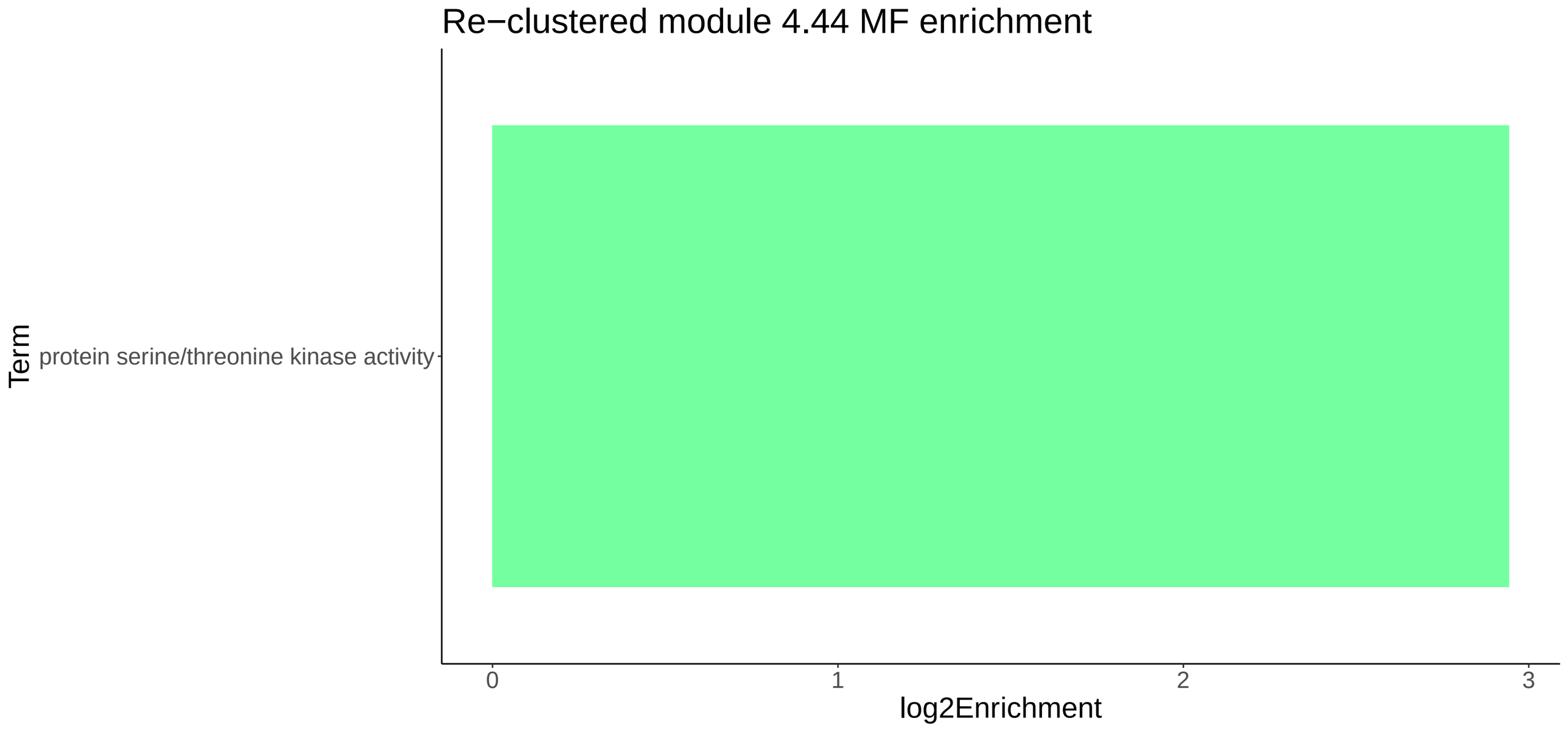

Re−clustered module 4.35.4 BP enrichmen
vesicle cargo loading
vesicle targeting, to, from or within Golgi
antigen processing and presentation of exogenous peptide antigen via MHC class II
antigen processing and presentation of peptide antigen via MHC class I
localization within membrane
nucleus organization
endomembrane system organization
Term
0
2
4
6
log2Enrichment

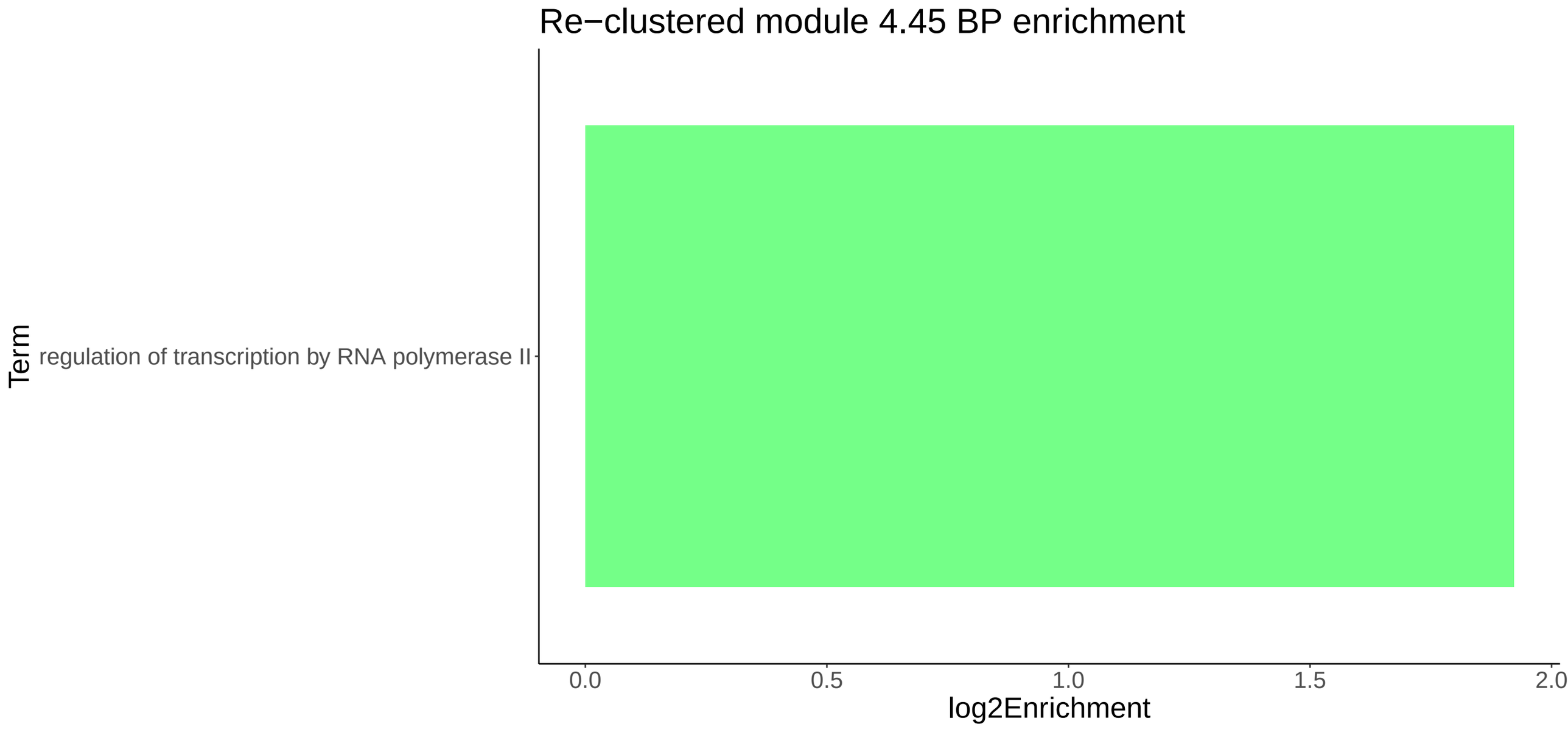

Re−clustered module 4.35.4 MF enrichment
Term
SNARE binding
zinc ion binding
0
1
2
3
4
log2Enrichment

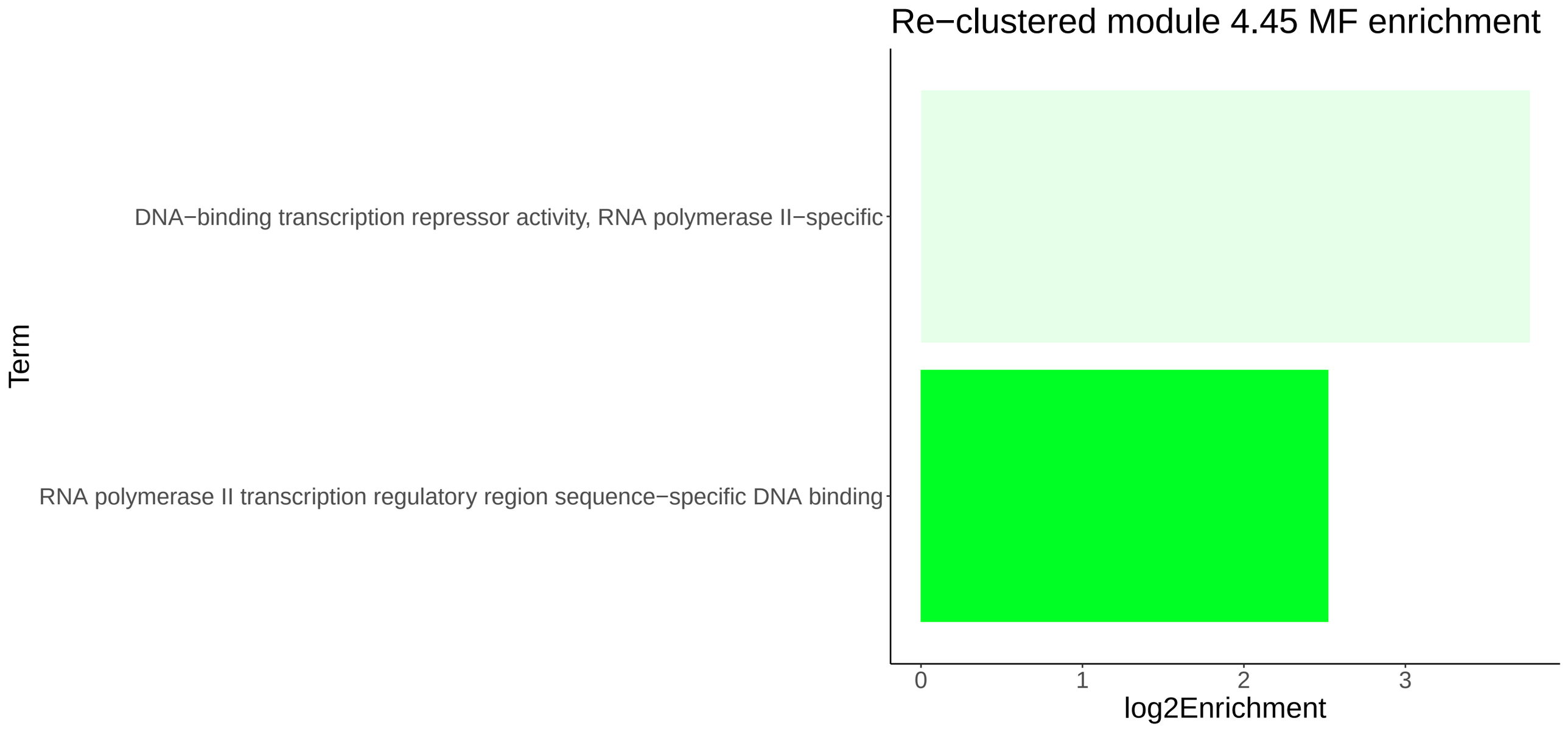

Re−clustered module 4.4 BP enrichment
liver regeneration
prostate gland development
ceramide biosynthetic process
regulation of smoothened signaling pathway
dorsal/ventral pattern formation
regulation of osteoblast differentiation
Term
0
2
4
6
log2Enrichment

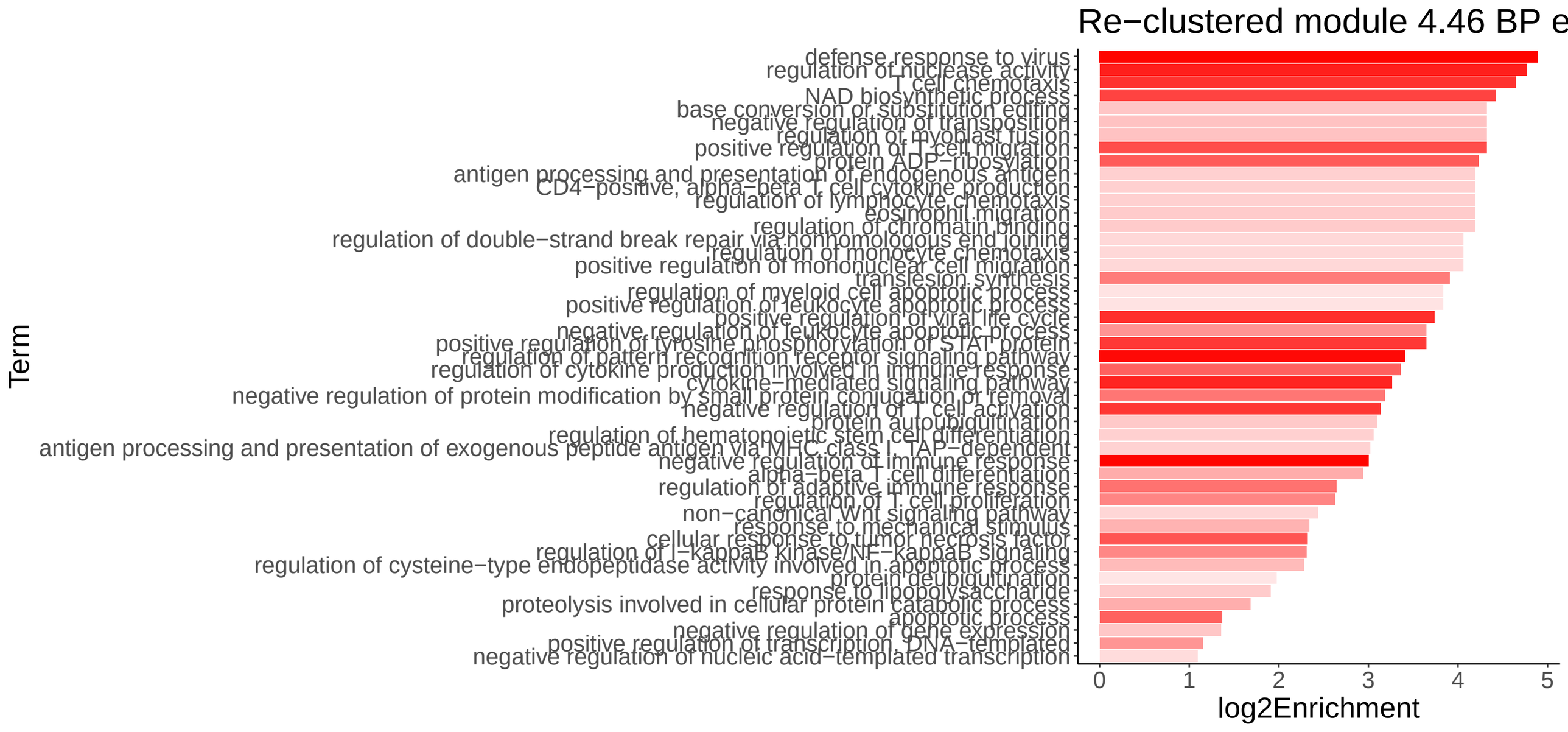

Re−clustered module 4.4 MF enrichment
Term
log2Enrichment

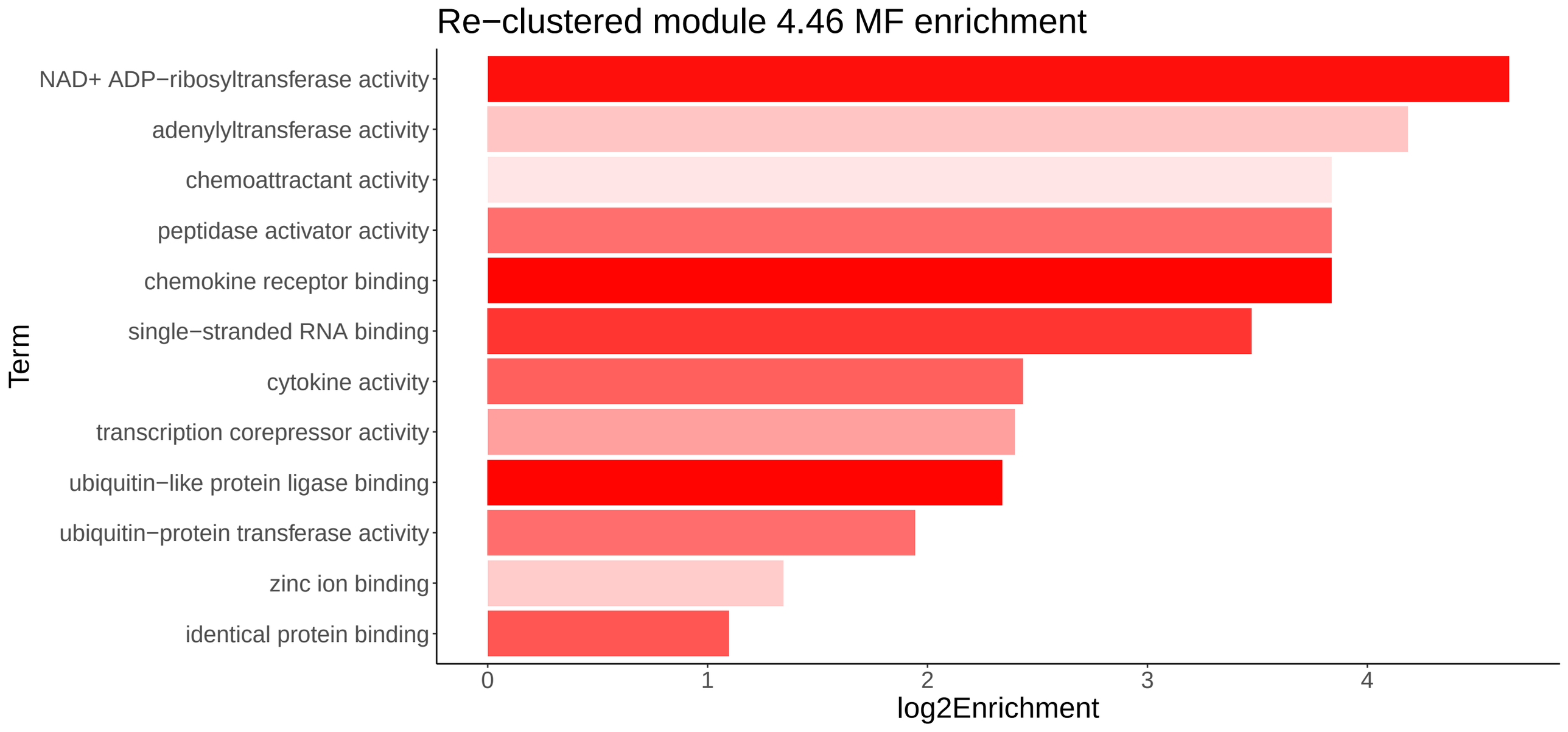

Re−clustered module 4.44 BP enrichment
Wnt signaling pathway, calcium modulating pathway
calcineurin−NFAT signaling cascade
sodium ion transmembrane transport
peptidyl−threonine phosphorylation
peptidyl−serine phosphorylation
Term
0
2
4
6
log2Enrichment

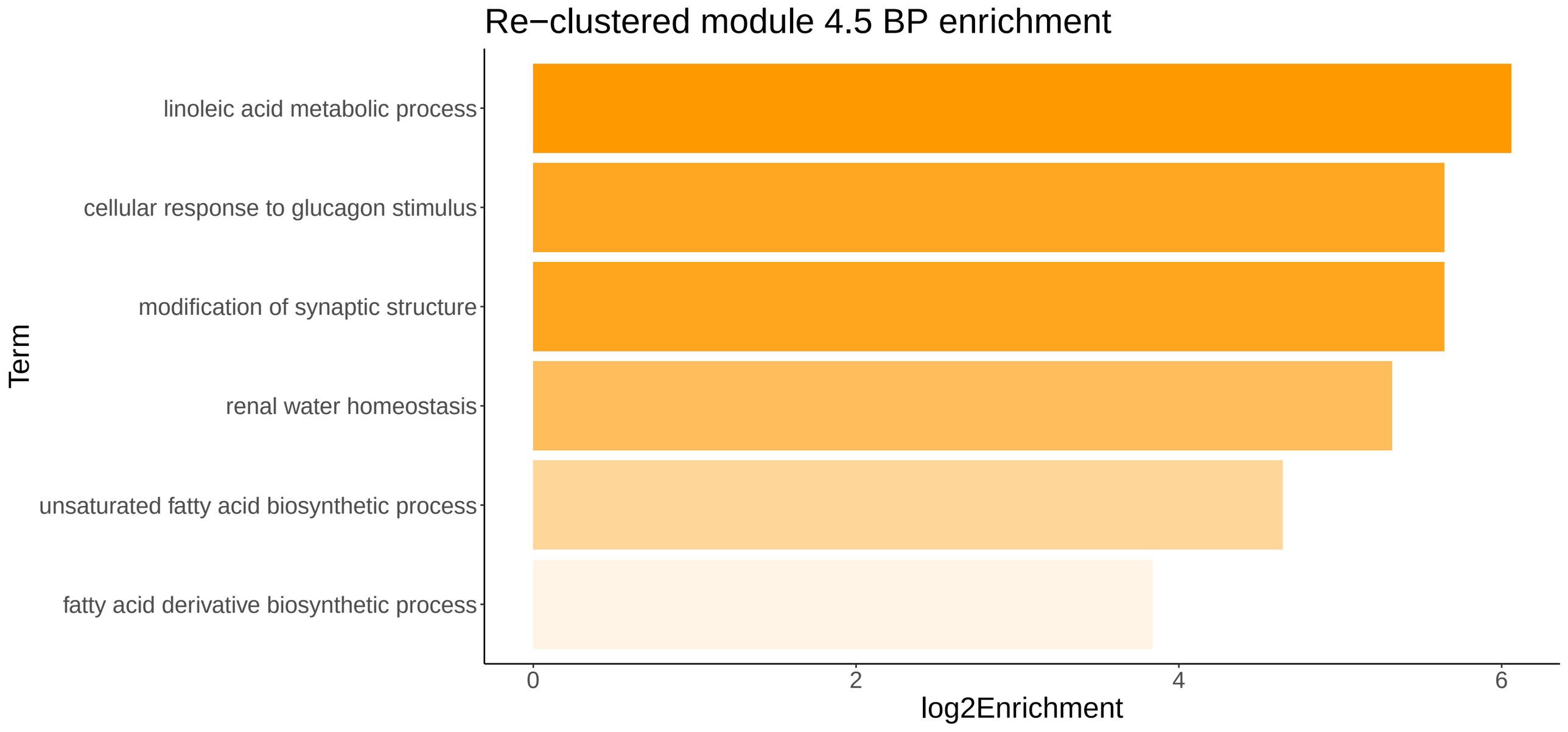

Re−clustered module 4.44 MF enrichment
Term
protein serine/threonine kinase activity
0
1
2
3
log2Enrichment

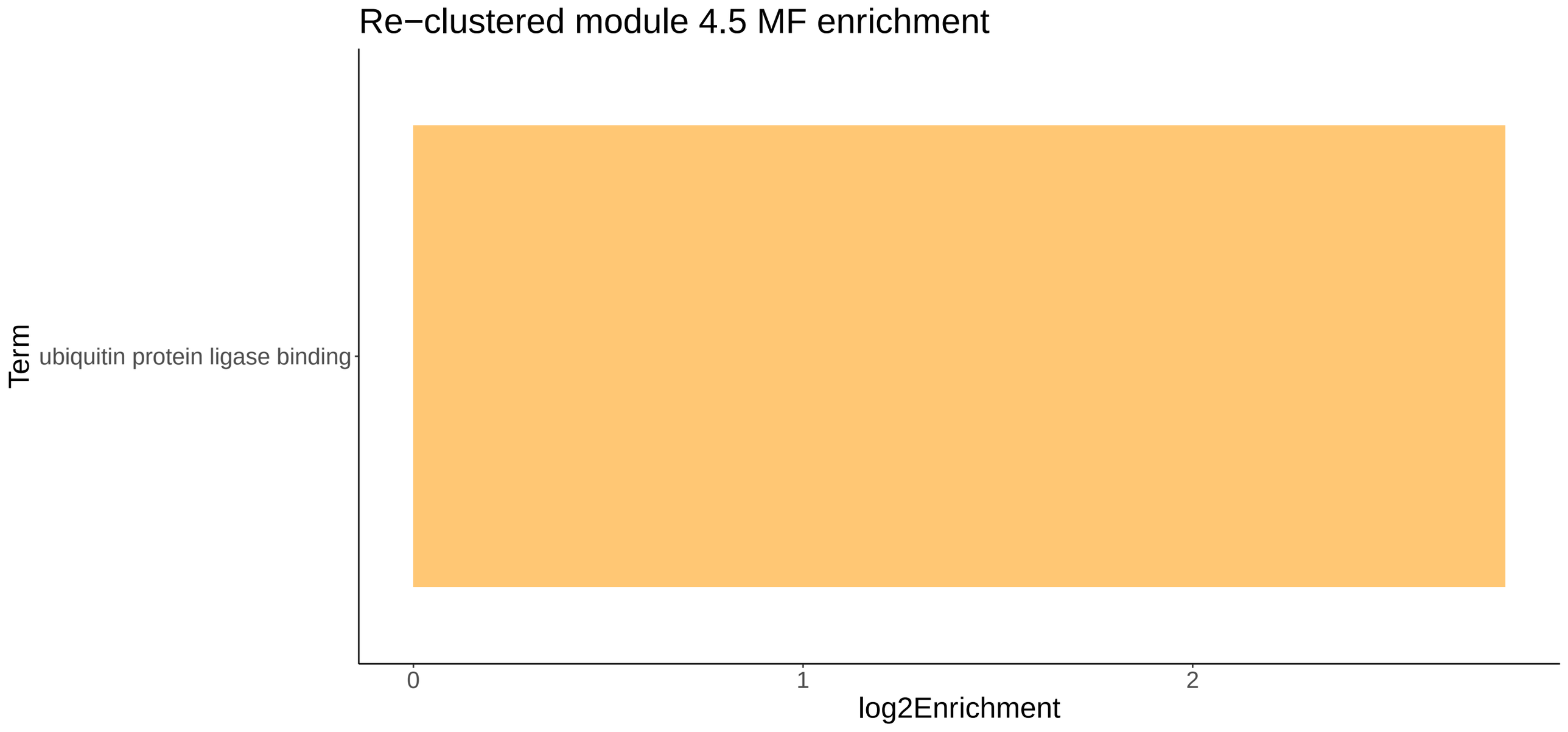

Re−clustered module 4.45 BP enrichment
Term
regulation of transcription by RNA polymerase II
0.0
0.5
1.0
1.5
2.0
log2Enrichment

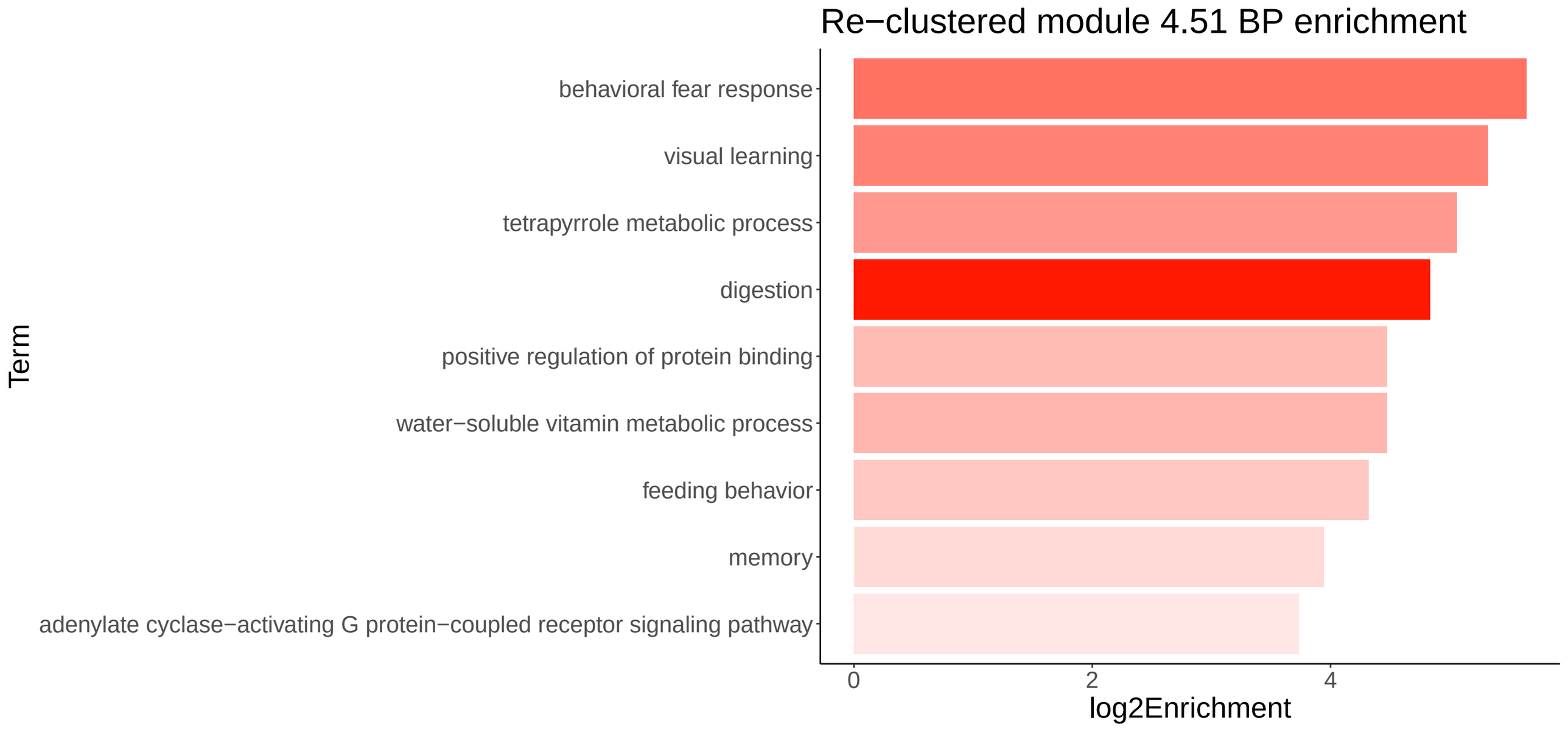

Re−clustered module 4.45 MF enrichment
Term
DNA−binding transcription repressor activity, RNA polymerase II−specific
RNA polymerase II transcription regulatory region sequence−specific DNA binding
0
1
2
3
log2Enrichment

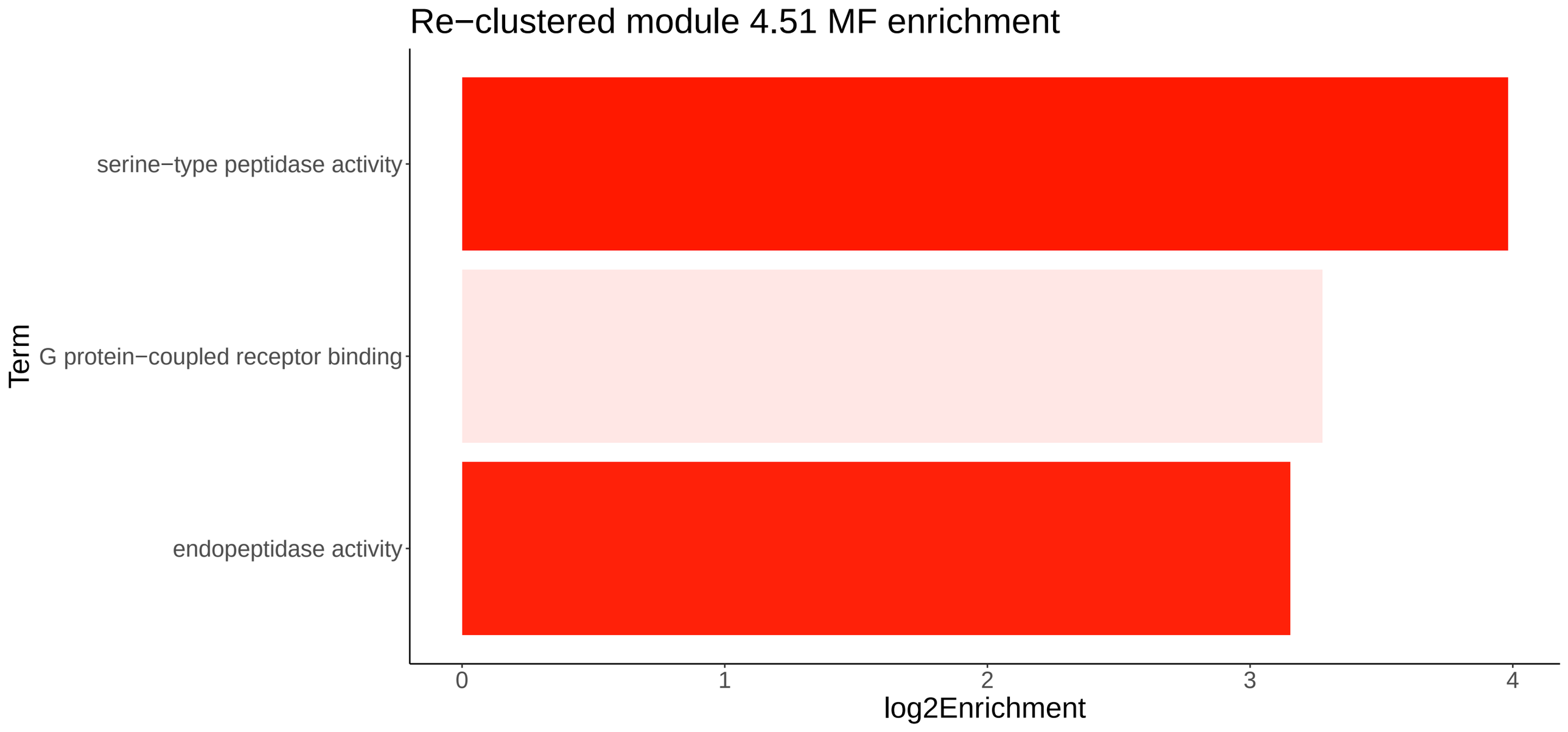

Re−clustered module 4.46 BP e
Term
defense response to virus
regulation of nuclease activity
T cell chemotaxis
NAD biosynthetic process
base conversion or substitution editing
negative regulation of transposition
regulation of myoblast fusion
positive regulation of T cell migration
protein ADP−ribosylation
antigen processing and presentation of endogenous antigen
CD4−positive, alpha−beta T cell cytokine production
regulation of lymphocyte chemotaxis
eosinophil migration
regulation of chromatin binding
regulation of double−strand break repair via nonhomologous end joining
regulation of monocyte chemotaxis
positive regulation of mononuclear cell migration
translesion synthesis
regulation of myeloid cell apoptotic process
positive regulation of leukocyte apoptotic process
positive regulation of viral life cycle
negative regulation of leukocyte apoptotic process
positive regulation of tyrosine phosphorylation of STAT protein
regulation of pattern recognition receptor signaling pathway
regulation of cytokine production involved in immune response
cytokine−mediated signaling pathway
negative regulation of protein modification by small protein conjugation or removal
negative regulation of T cell activation
protein autoubiquitination
regulation of hematopoietic stem cell differentiation
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP−dependent
negative regulation of immune response
alpha−beta T cell differentiation
regulation of adaptive immune response
regulation of T cell proliferation
non−canonical Wnt signaling pathway
response to mechanical stimulus
cellular response to tumor necrosis factor
regulation of I−kappaB kinase/NF−kappaB signaling
regulation of cysteine−type endopeptidase activity involved in apoptotic process
protein deubiquitination
response to lipopolysaccharide
proteolysis involved in cellular protein catabolic process
apoptotic process
negative regulation of gene expression
positive regulation of transcription, DNA−templated
negative regulation of nucleic acid−templated transcription
0
1
2
3
4
5
log2Enrichment

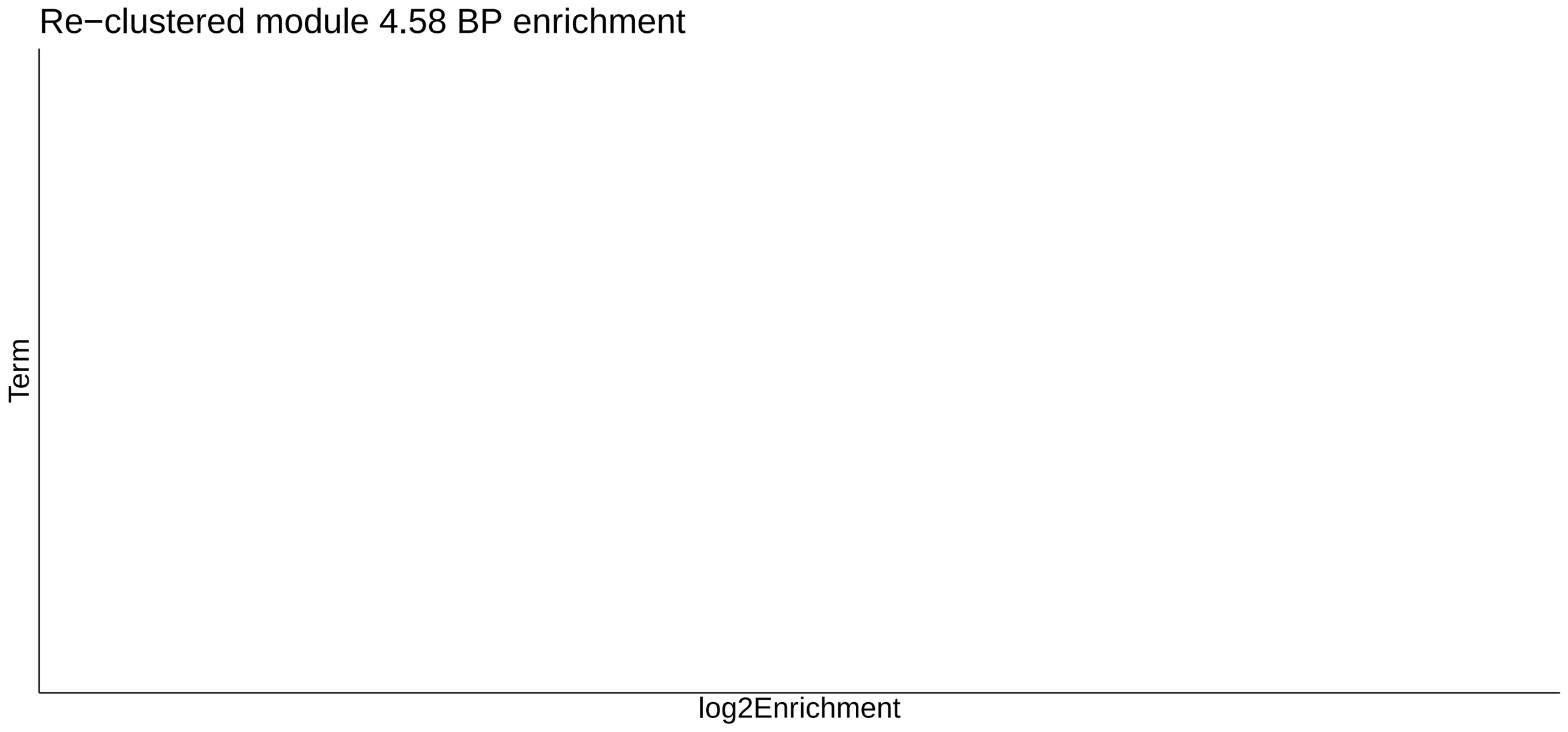

Re−clustered module 4.46 MF enrichment
NAD+ ADP−ribosyltransferase activity
adenylyltransferase activity
chemoattractant activity
peptidase activator activity
chemokine receptor binding
single−stranded RNA binding
cytokine activity
transcription corepressor activity
ubiquitin−like protein ligase binding
ubiquitin−protein transferase activity
zinc ion binding
identical protein binding
Term
0
1
2
3
4
log2Enrichment

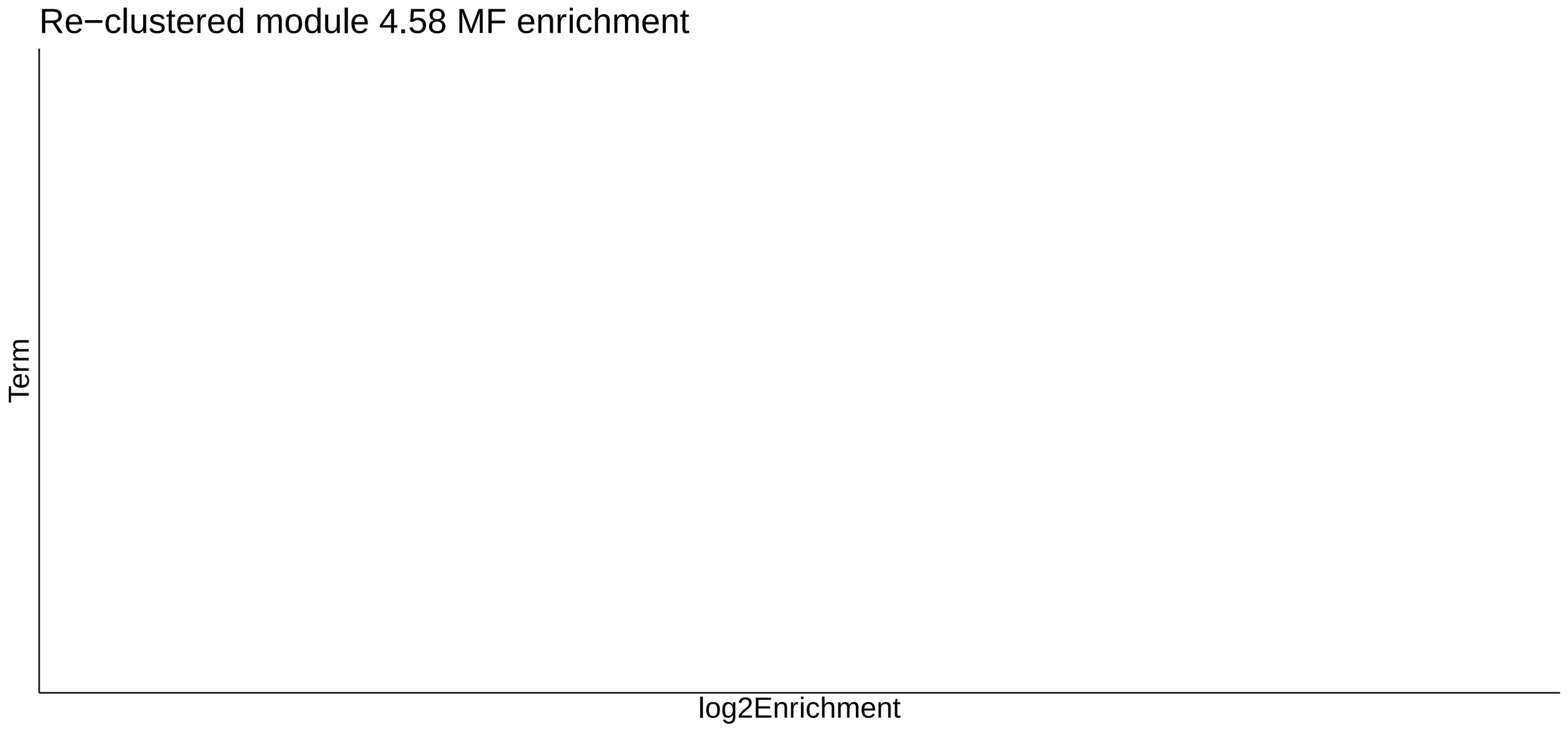

Re−clustered module 4.5 BP enrichment
linoleic acid metabolic process
cellular response to glucagon stimulus
modification of synaptic structure
renal water homeostasis
unsaturated fatty acid biosynthetic process
fatty acid derivative biosynthetic process
Term
0
2
4
6
log2Enrichment

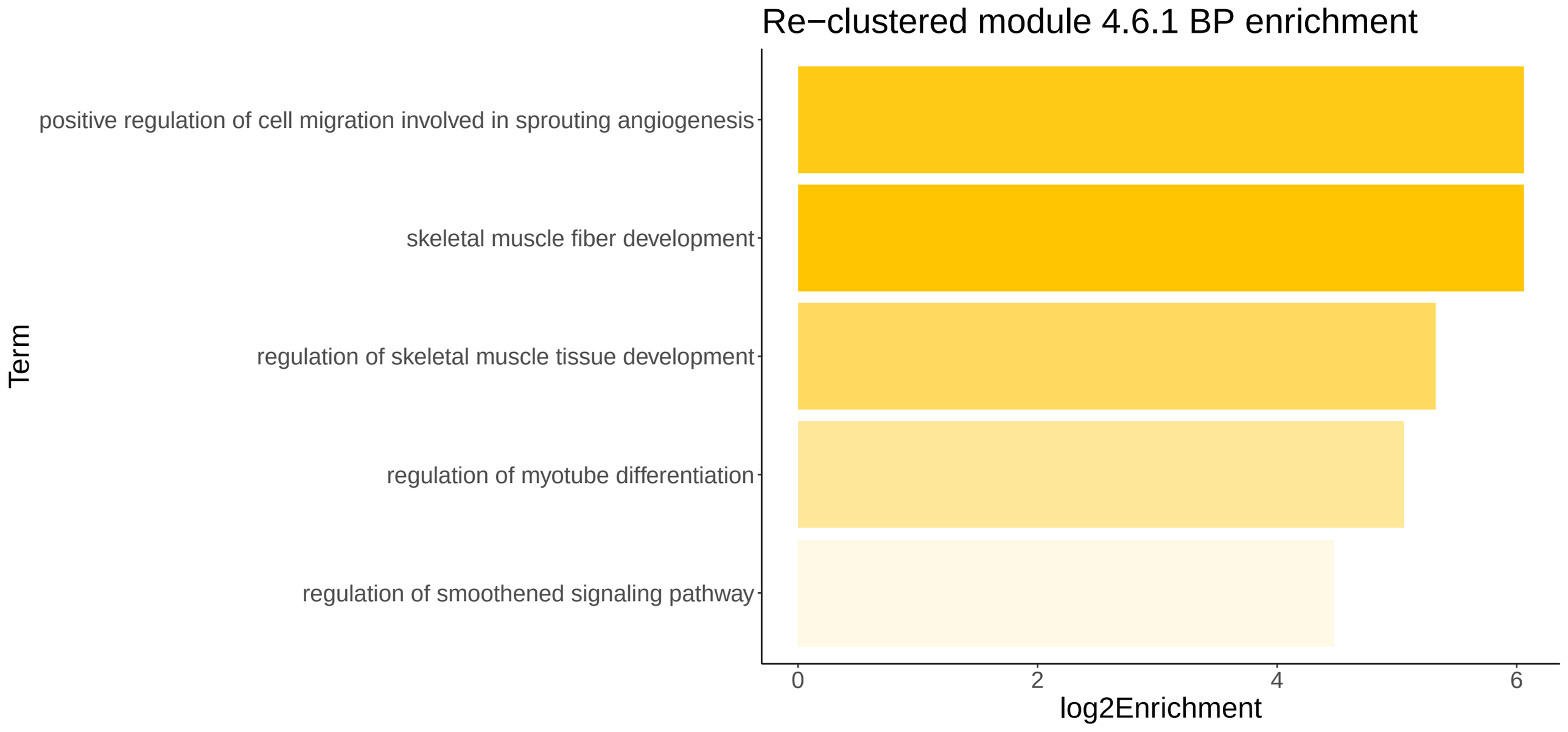

Re−clustered module 4.5 MF enrichment
Term
ubiquitin protein ligase binding
0
1
2
log2Enrichment

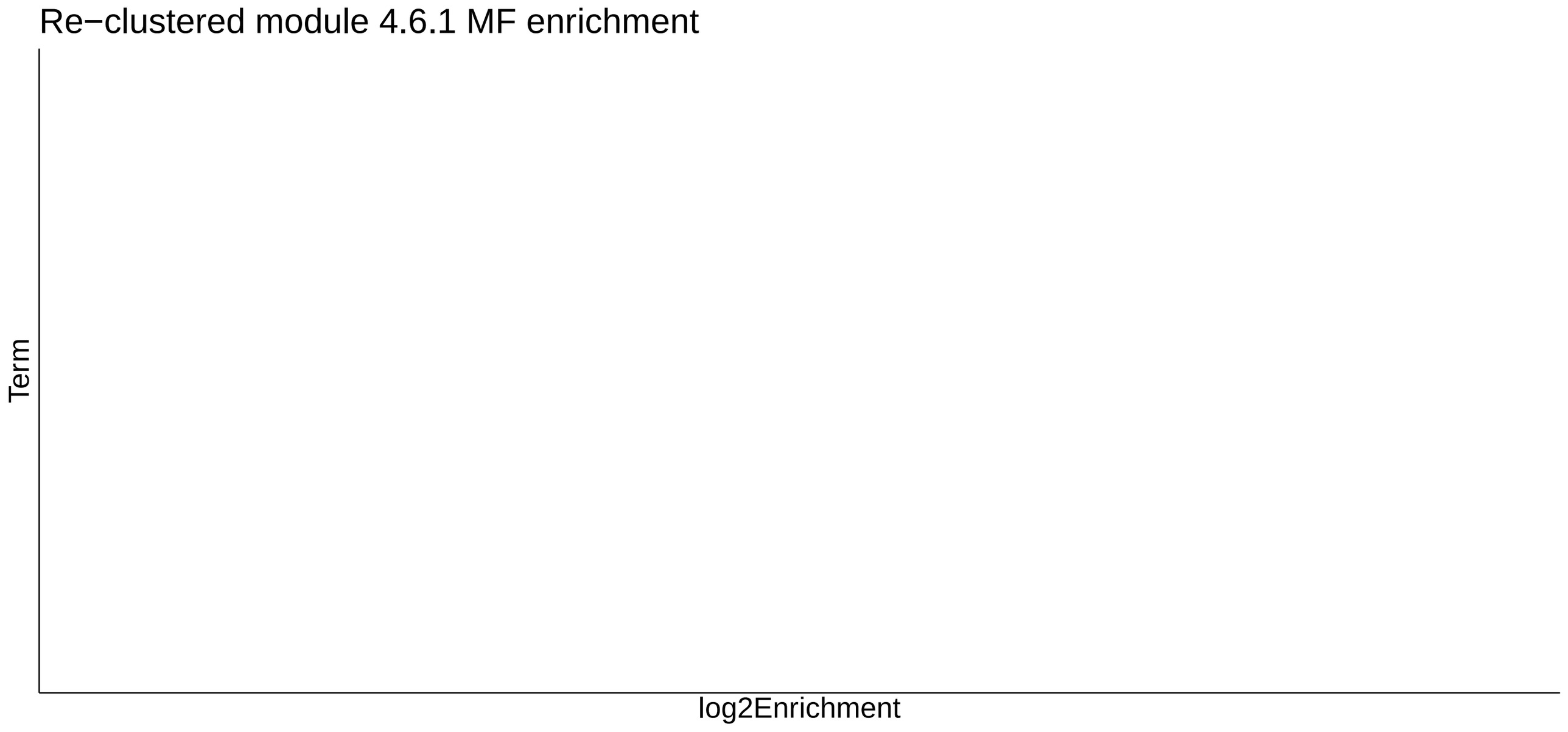

Re−clustered module 4.51 BP enrichment
Term
behavioral fear response
visual learning
tetrapyrrole metabolic process
digestion
positive regulation of protein binding
water−soluble vitamin metabolic process
feeding behavior
memory
adenylate cyclase−activating G protein−coupled receptor signaling pathway
0
2
4
log2Enrichment

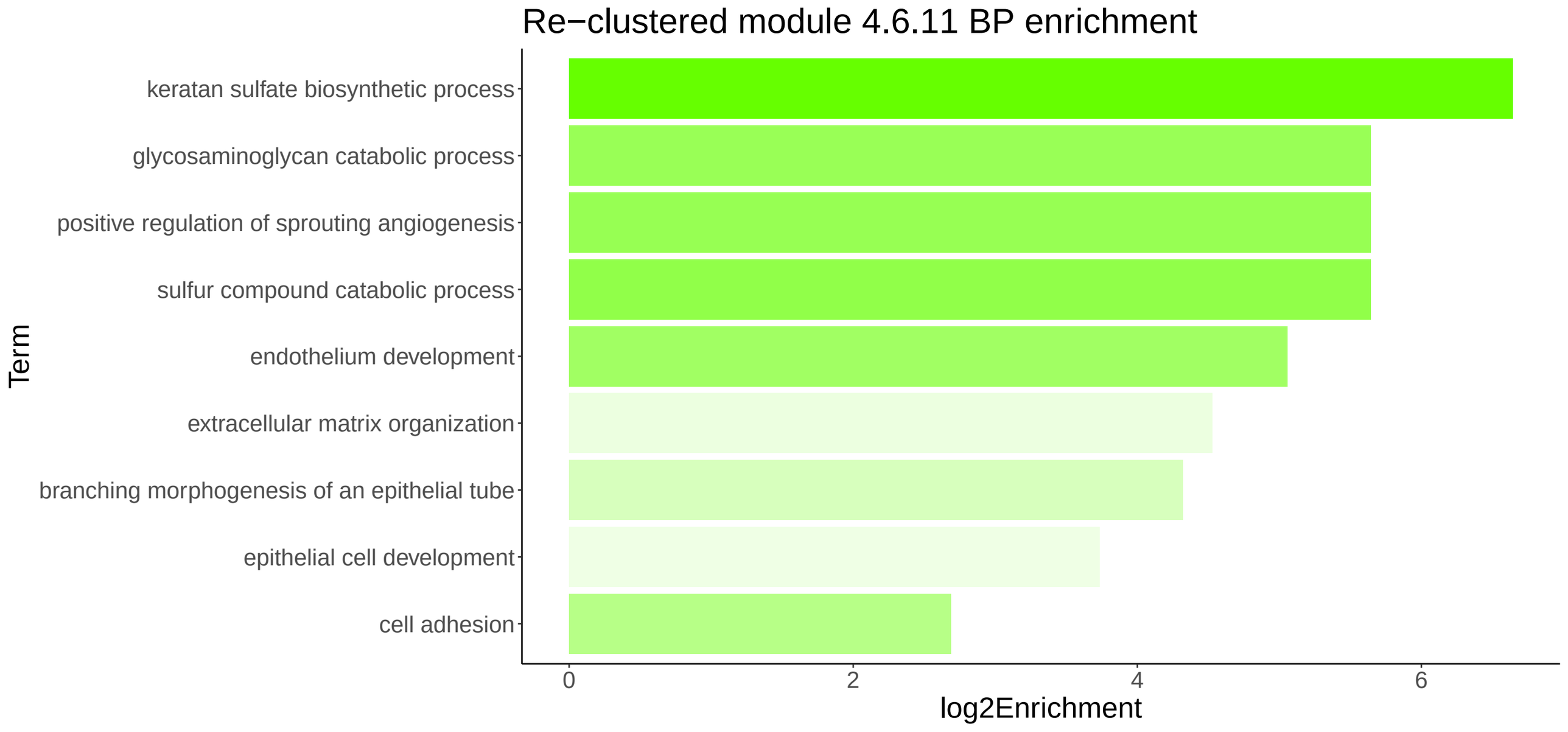

Re−clustered module 4.51 MF enrichment
Term
serine−type peptidase activity
G protein−coupled receptor binding
endopeptidase activity
0
1
2
3
4
log2Enrichment

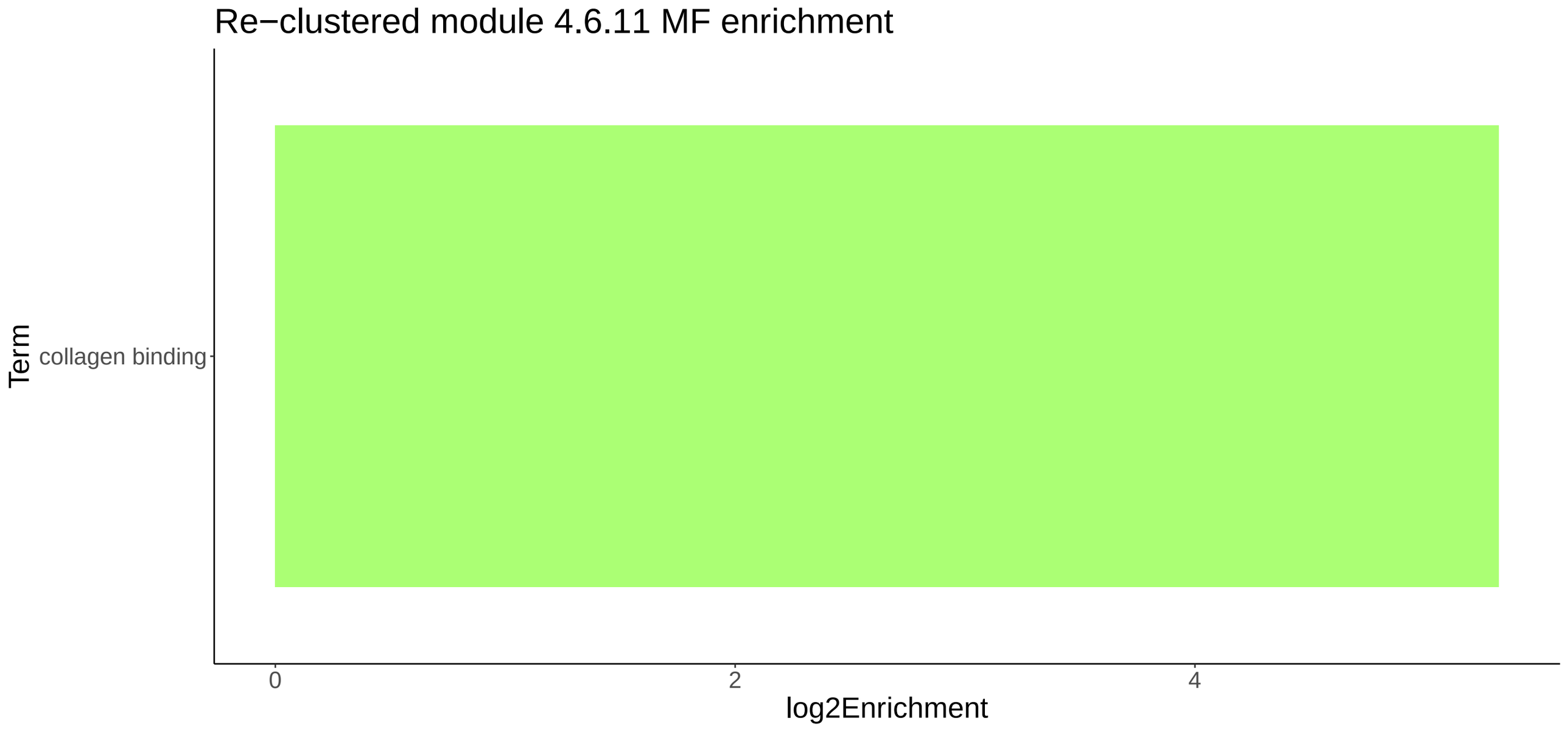

Re−clustered module 4.58 BP enrichment
Term
log2Enrichment

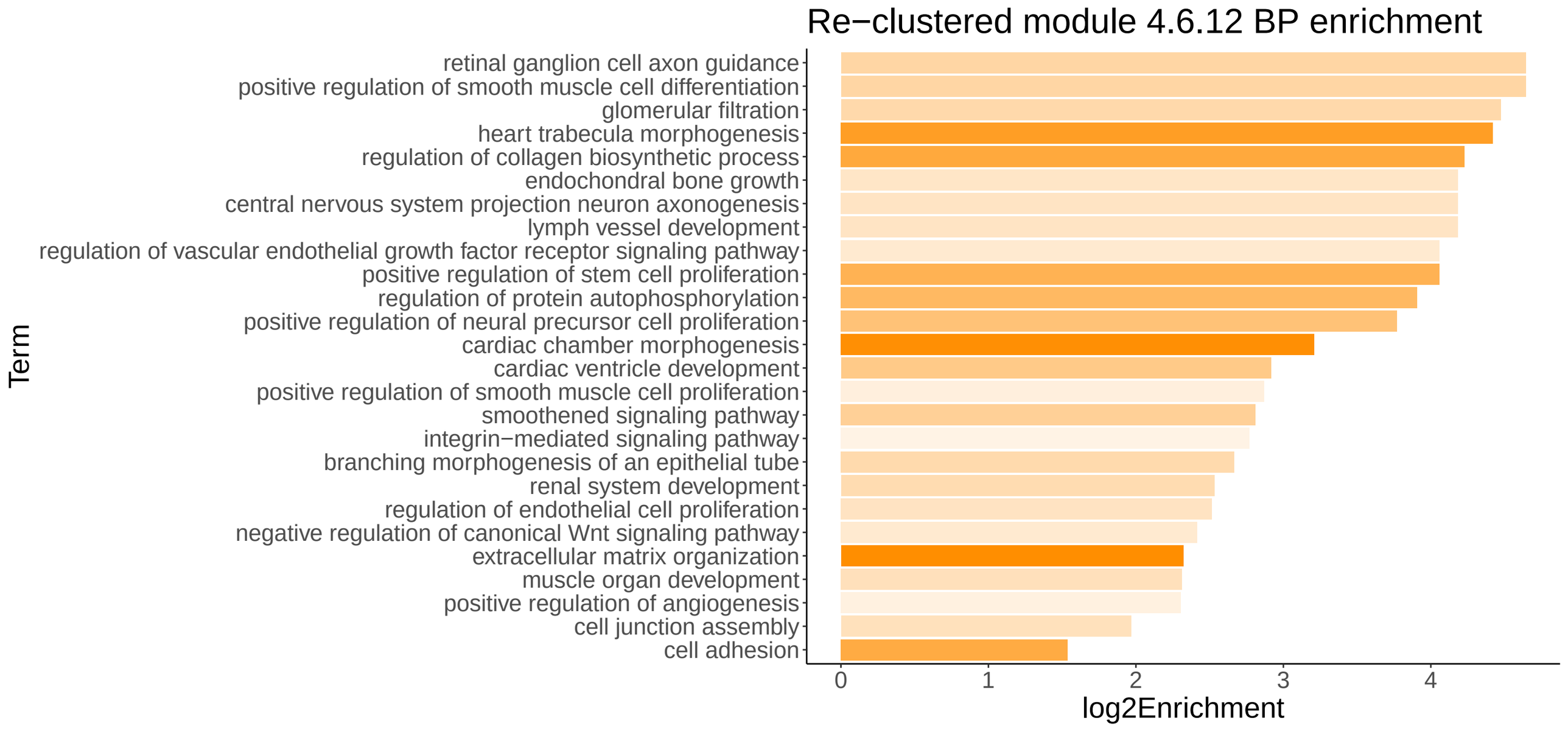

Re−clustered module 4.58 MF enrichment
Term
log2Enrichment

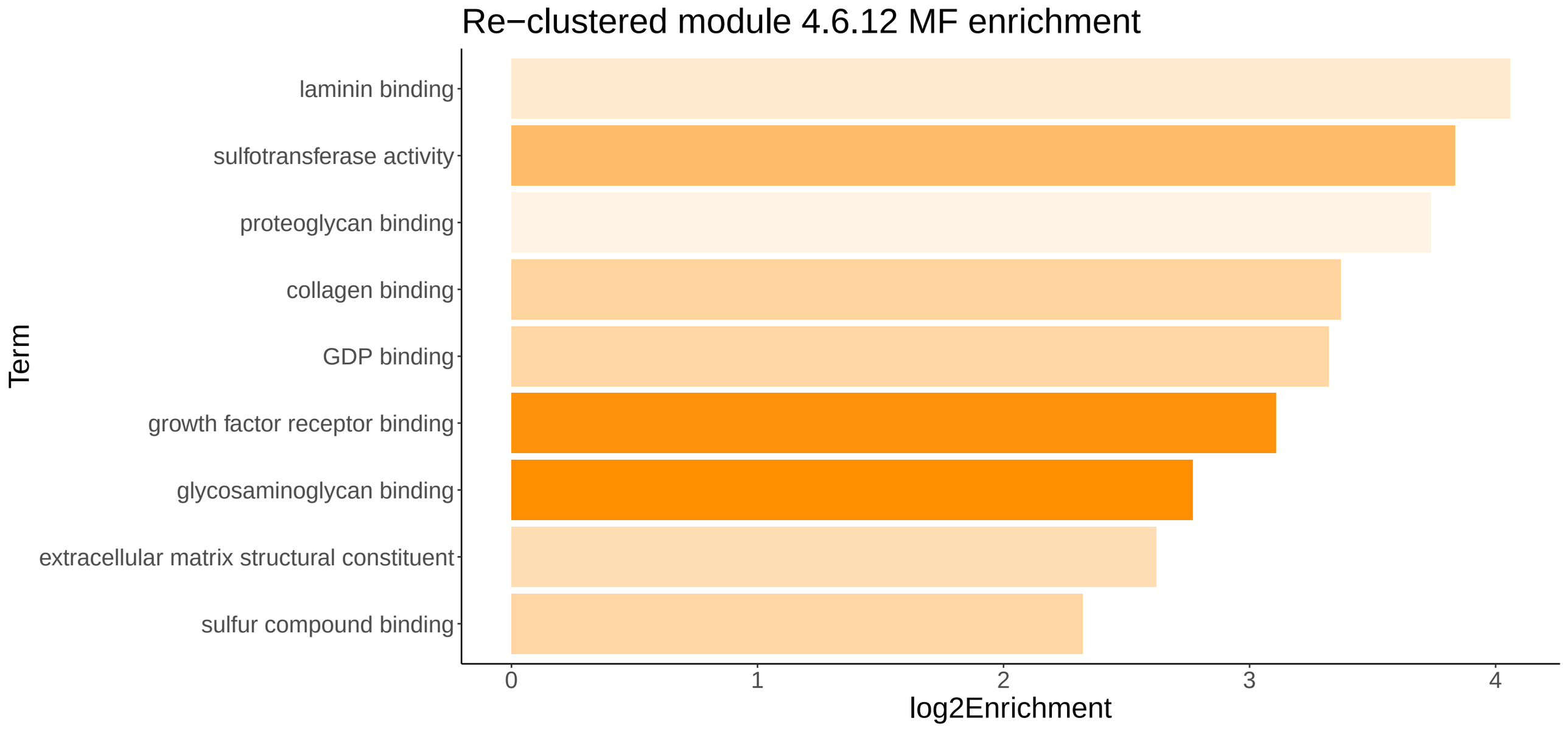

Re−clustered module 4.6.1 BP enrichment
positive regulation of cell migration involved in sprouting angiogenesis
skeletal muscle fiber development
regulation of skeletal muscle tissue development
regulation of myotube differentiation
regulation of smoothened signaling pathway
Term
0
2
4
6
log2Enrichment

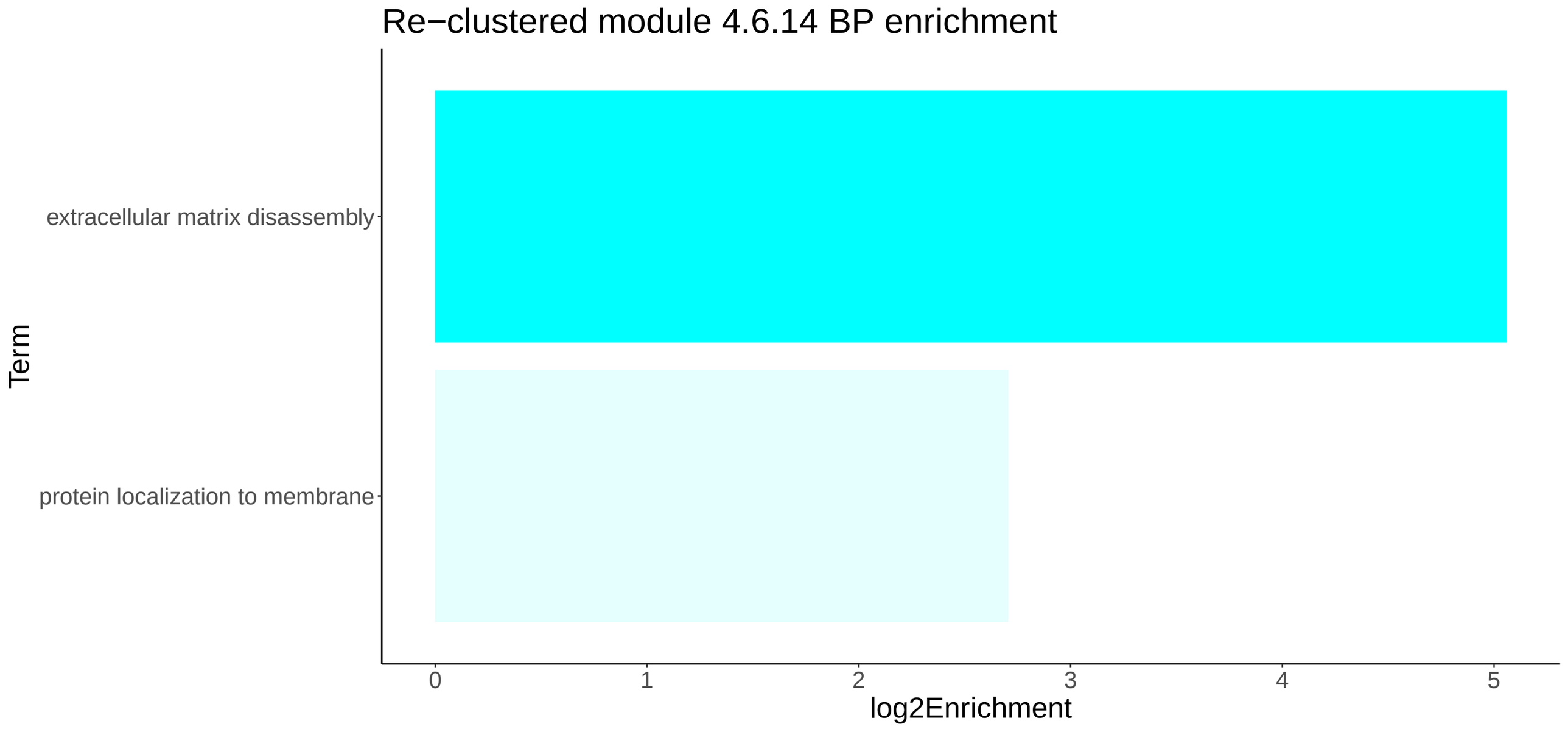

Re−clustered module 4.6.1 MF enrichment
Term
log2Enrichment

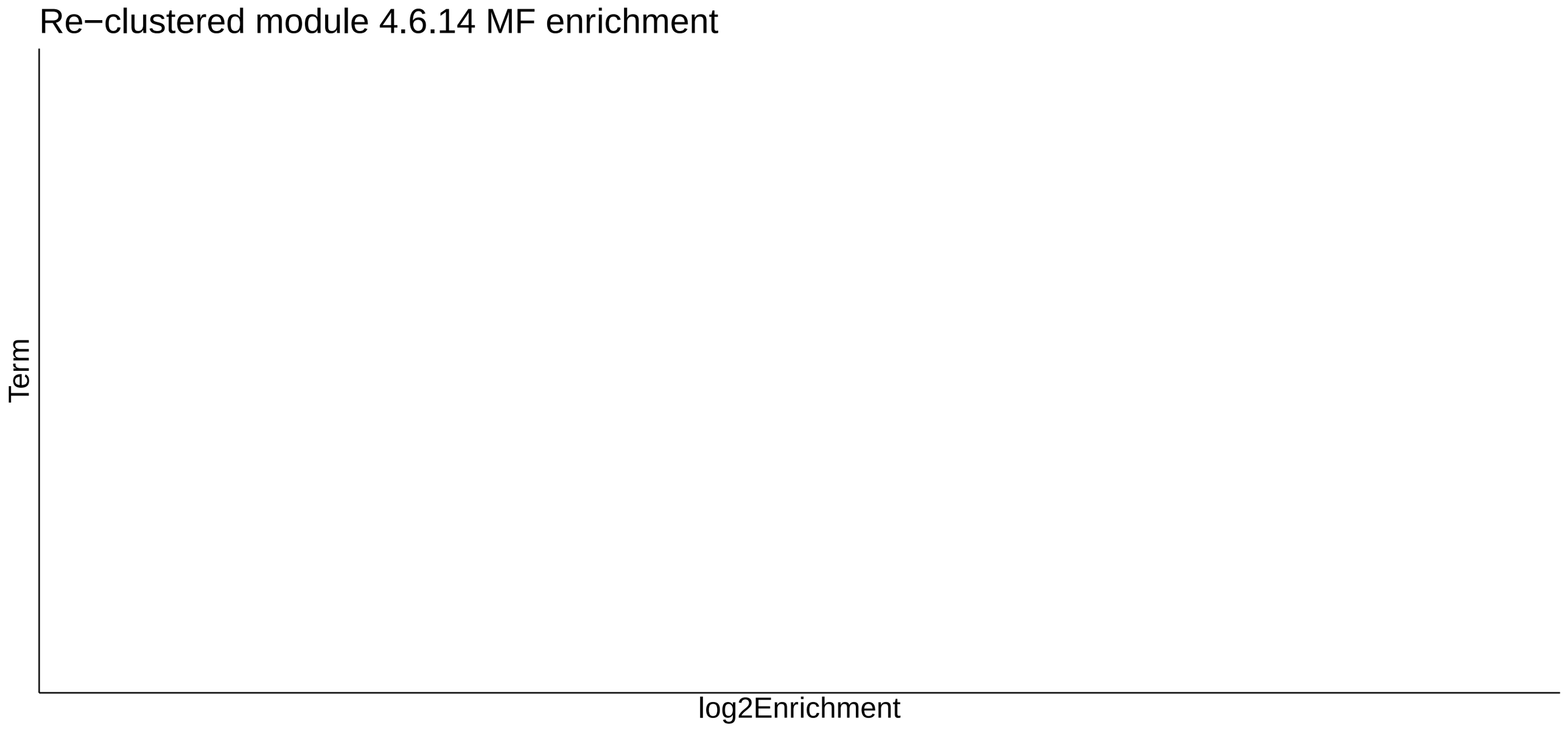

Re−clustered module 4.6.11 BP enrichment
keratan sulfate biosynthetic process
glycosaminoglycan catabolic process
positive regulation of sprouting angiogenesis
sulfur compound catabolic process
endothelium development
extracellular matrix organization
branching morphogenesis of an epithelial tube
epithelial cell development
cell adhesion
Term
0
2
4
6
log2Enrichment

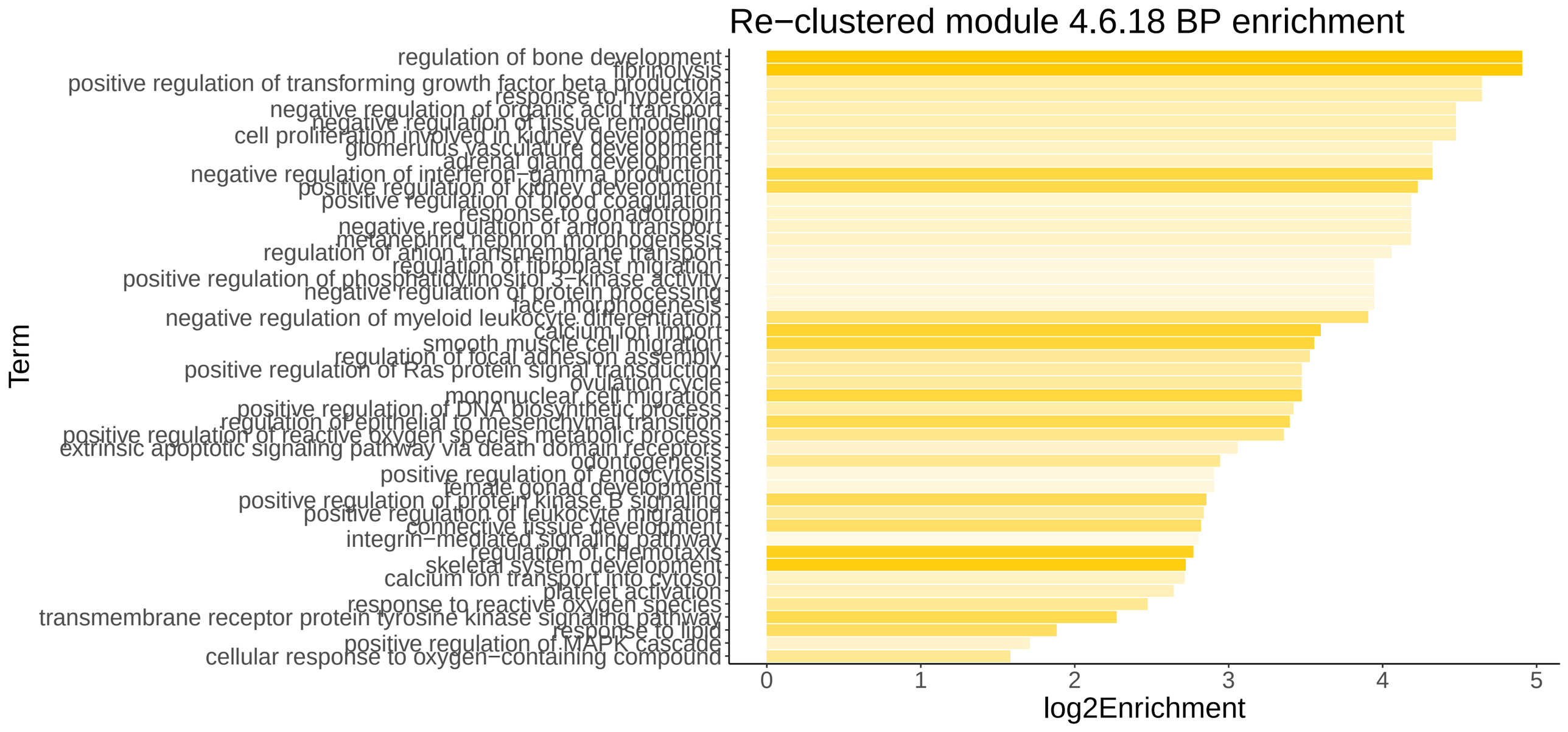

Re−clustered module 4.6.11 MF enrichment
Term
collagen binding
0
2
4
log2Enrichment

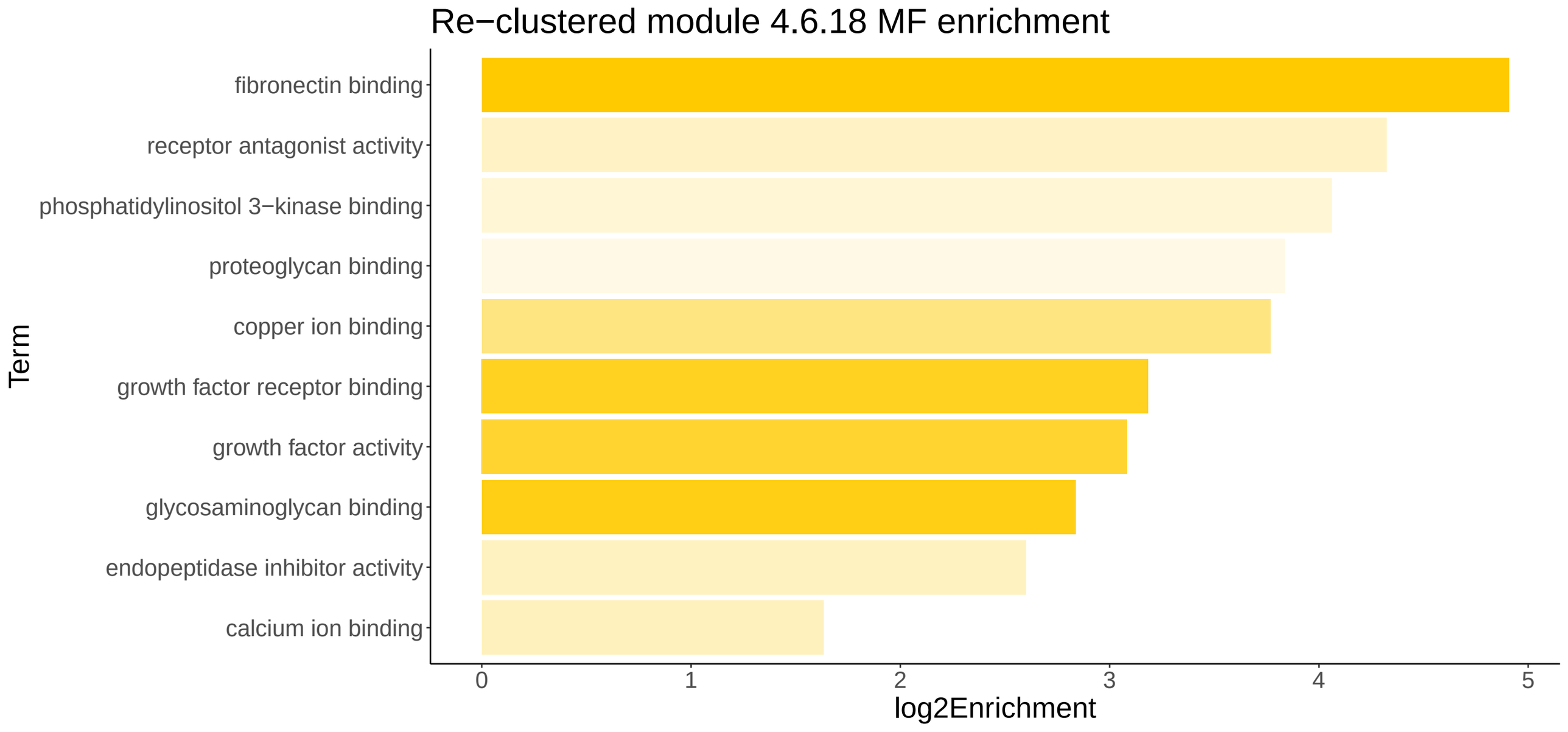

Re−clustered module 4.6.12 BP enrichment
Term
retinal ganglion cell axon guidance
positive regulation of smooth muscle cell differentiation
glomerular filtration
heart trabecula morphogenesis
regulation of collagen biosynthetic process
endochondral bone growth
central nervous system projection neuron axonogenesis
lymph vessel development
regulation of vascular endothelial growth factor receptor signaling pathway
positive regulation of stem cell proliferation
regulation of protein autophosphorylation
positive regulation of neural precursor cell proliferation
cardiac chamber morphogenesis
cardiac ventricle development
positive regulation of smooth muscle cell proliferation
smoothened signaling pathway
integrin−mediated signaling pathway
branching morphogenesis of an epithelial tube
renal system development
regulation of endothelial cell proliferation
negative regulation of canonical Wnt signaling pathway
extracellular matrix organization
muscle organ development
positive regulation of angiogenesis
cell junction assembly
cell adhesion
0
1
2
3
4
log2Enrichment

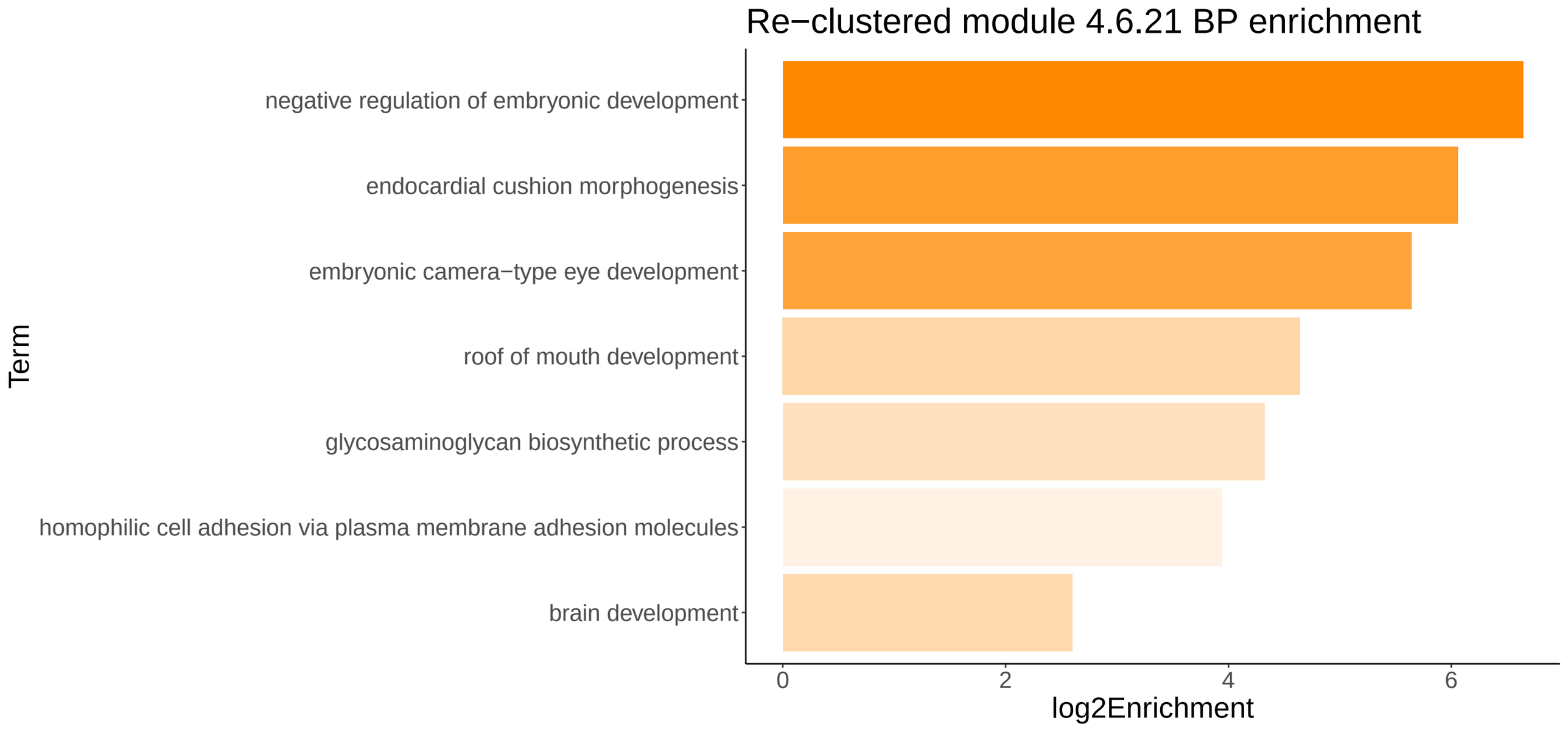

Re−clustered module 4.6.12 MF enrichment
Term
laminin binding
sulfotransferase activity
proteoglycan binding
collagen binding
GDP binding
growth factor receptor binding
glycosaminoglycan binding
extracellular matrix structural constituent
sulfur compound binding
0
1
2
3
4
log2Enrichment

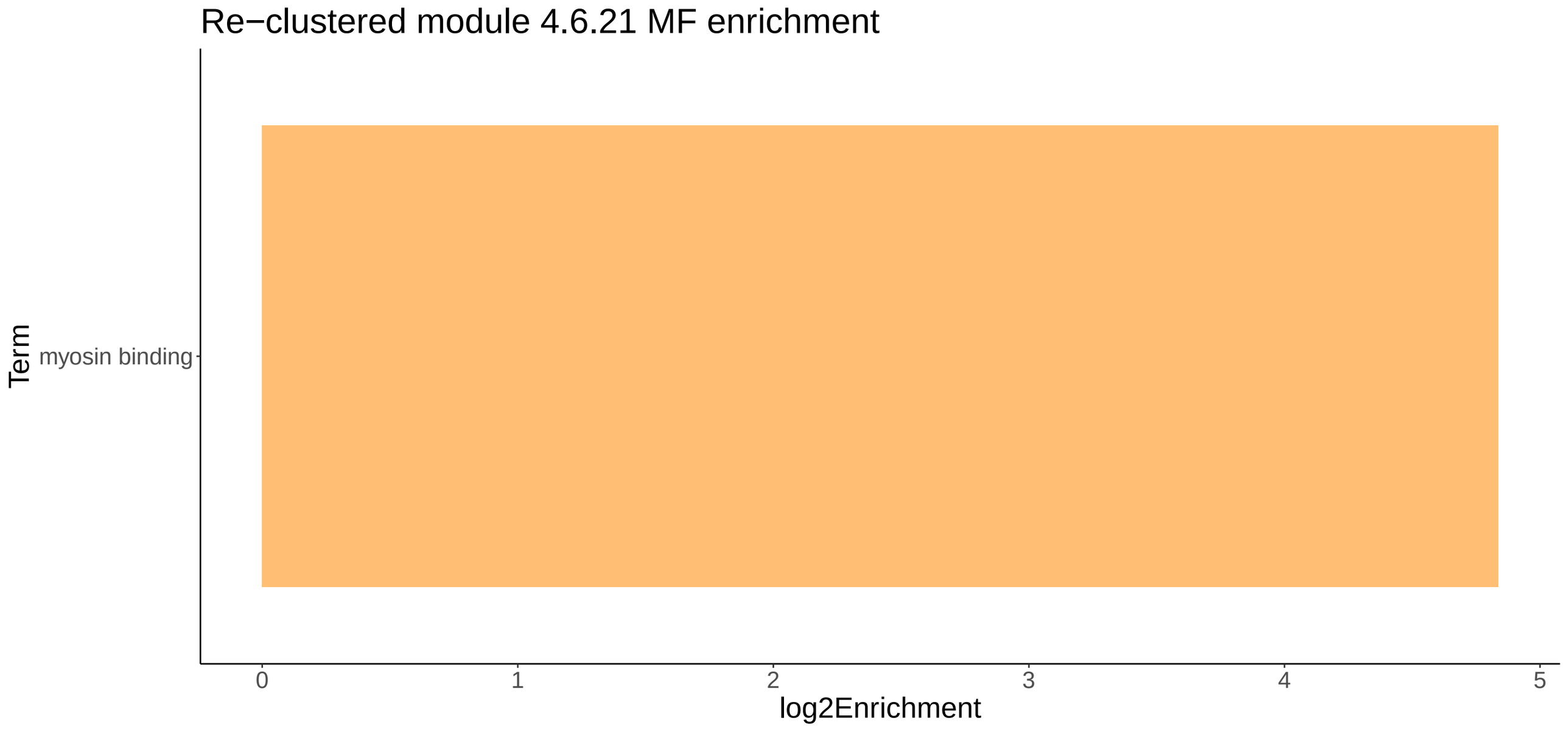

Re−clustered module 4.6.14 BP enrichment
Term
extracellular matrix disassembly
protein localization to membrane
0
1
2
3
4
5
log2Enrichment

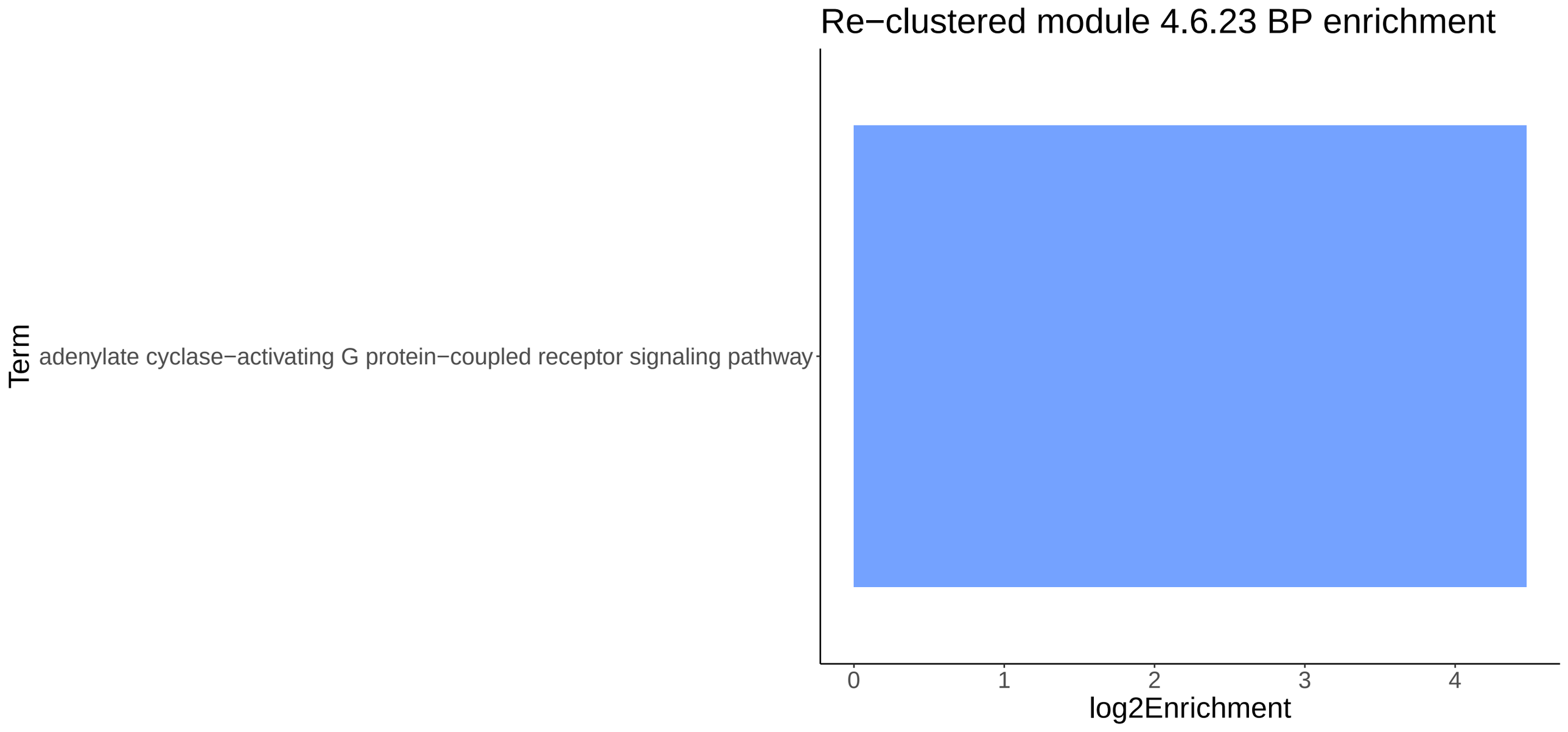

Re−clustered module 4.6.14 MF enrichment
Term
log2Enrichment


Re−clustered module 4.6.18 BP enrichment
Term
regulation of bone development
fibrinolysis
positive regulation of transforming growth factor beta production
response to hyperoxia
negative regulation of organic acid transport
negative regulation of tissue remodeling
cell proliferation involved in kidney development
glomerulus vasculature development
adrenal gland development
negative regulation of interferon−gamma production
positive regulation of kidney development
positive regulation of blood coagulation
response to gonadotropin
negative regulation of anion transport
metanephric nephron morphogenesis
regulation of anion transmembrane transport
regulation of fibroblast migration
positive regulation of phosphatidylinositol 3−kinase activity
negative regulation of protein processing
face morphogenesis
negative regulation of myeloid leukocyte differentiation
calcium ion import
smooth muscle cell migration
regulation of focal adhesion assembly
positive regulation of Ras protein signal transduction
ovulation cycle
mononuclear cell migration
positive regulation of DNA biosynthetic process
regulation of epithelial to mesenchymal transition
positive regulation of reactive oxygen species metabolic process
extrinsic apoptotic signaling pathway via death domain receptors
odontogenesis
positive regulation of endocytosis
female gonad development
positive regulation of protein kinase B signaling
positive regulation of leukocyte migration
connective tissue development
integrin−mediated signaling pathway
regulation of chemotaxis
skeletal system development
calcium ion transport into cytosol
platelet activation
response to reactive oxygen species
transmembrane receptor protein tyrosine kinase signaling pathway
response to lipid
positive regulation of MAPK cascade
cellular response to oxygen−containing compound
0
1
2
3
4
5
log2Enrichment

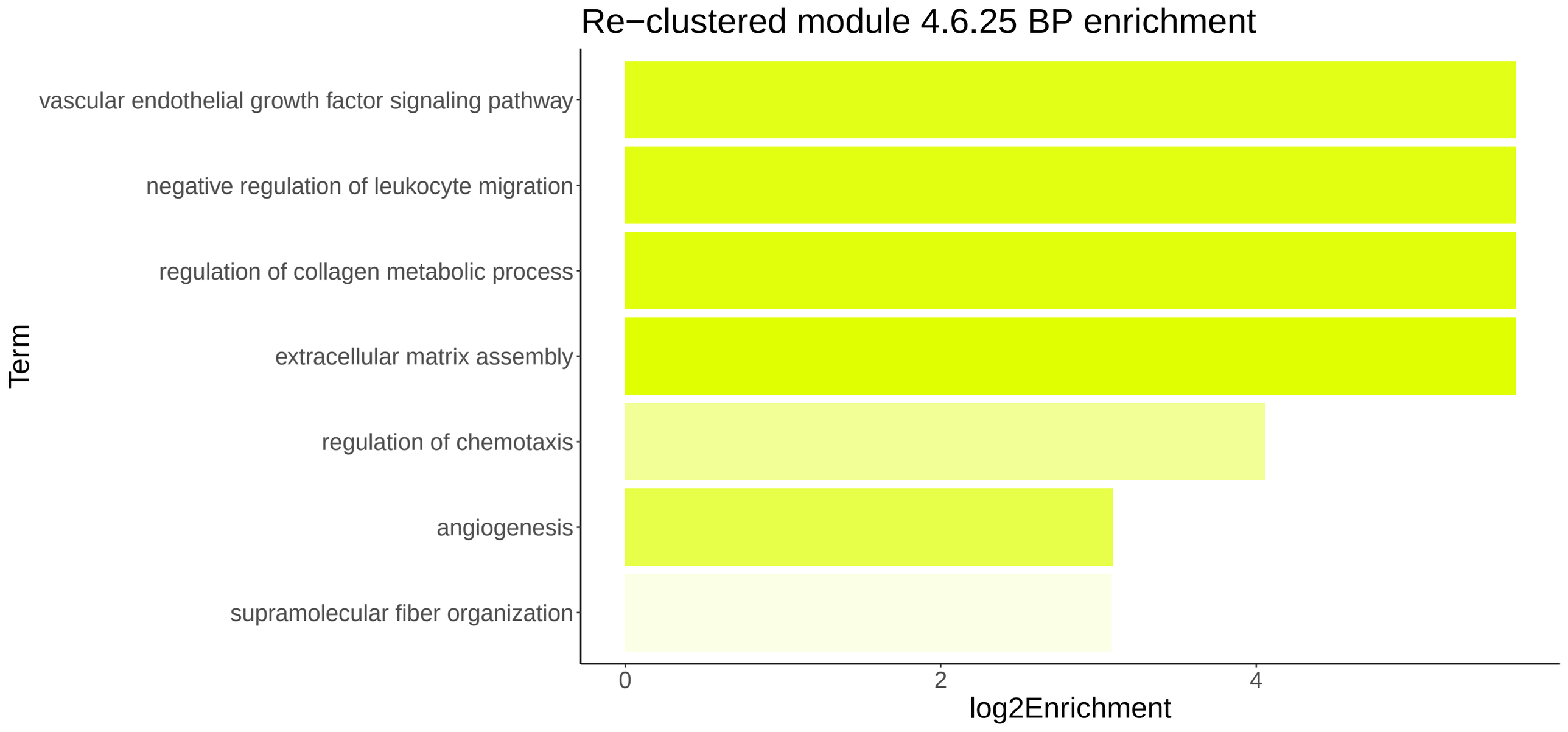

Re−clustered module 4.6.18 MF enrichment
fibronectin binding
receptor antagonist activity
phosphatidylinositol 3−kinase binding
proteoglycan binding
copper ion binding
growth factor receptor binding
growth factor activity
glycosaminoglycan binding
endopeptidase inhibitor activity
calcium ion binding
Term
0
1
2
3
4
5
log2Enrichment


Re−clustered module 4.6.21 BP enrichment
negative regulation of embryonic development
endocardial cushion morphogenesis
embryonic camera−type eye development
roof of mouth development
glycosaminoglycan biosynthetic process
homophilic cell adhesion via plasma membrane adhesion molecules
brain development
Term
0
2
4
6
log2Enrichment

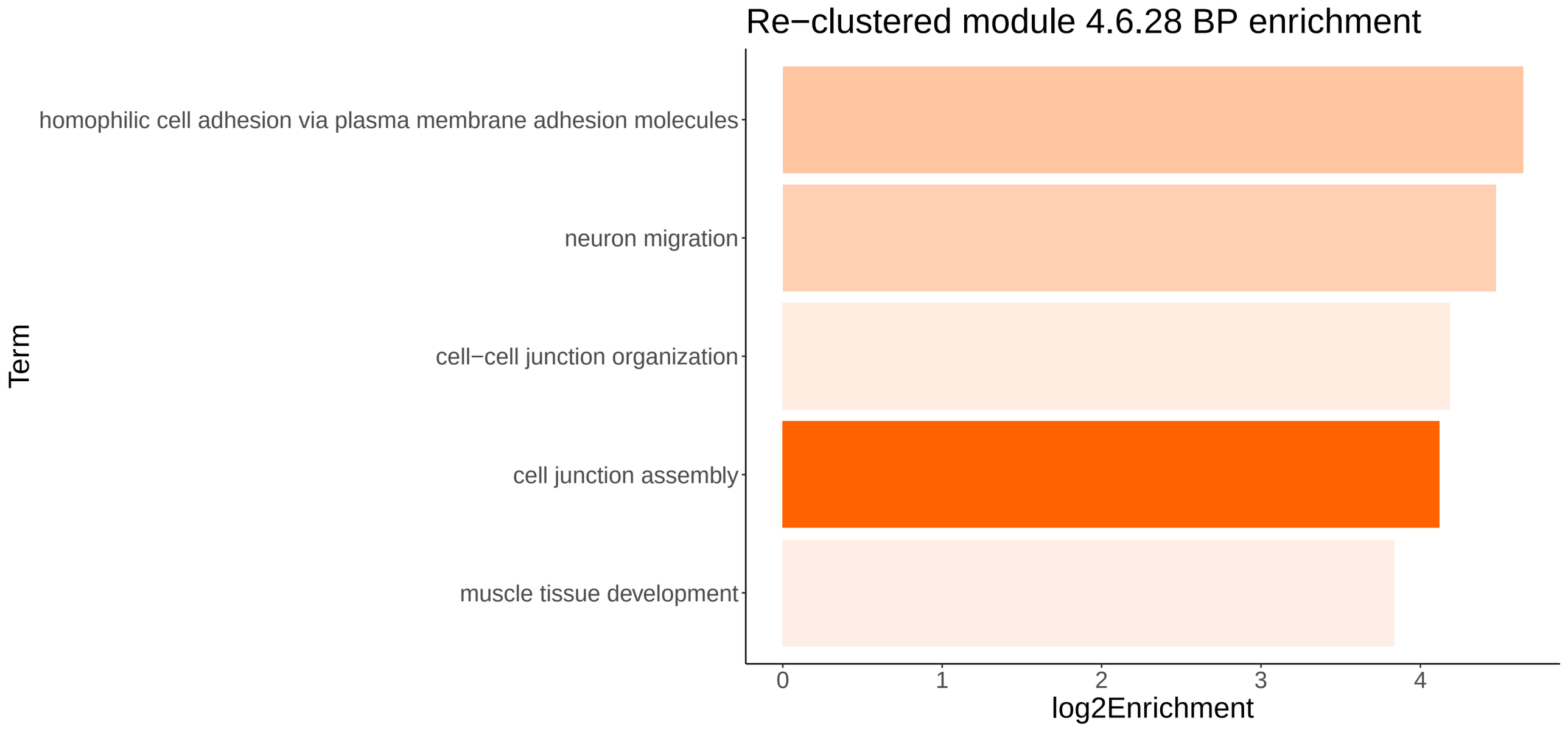

Re−clustered module 4.6.21 MF enrichment
Term
myosin binding
0
1
2
3
4
5
log2Enrichment

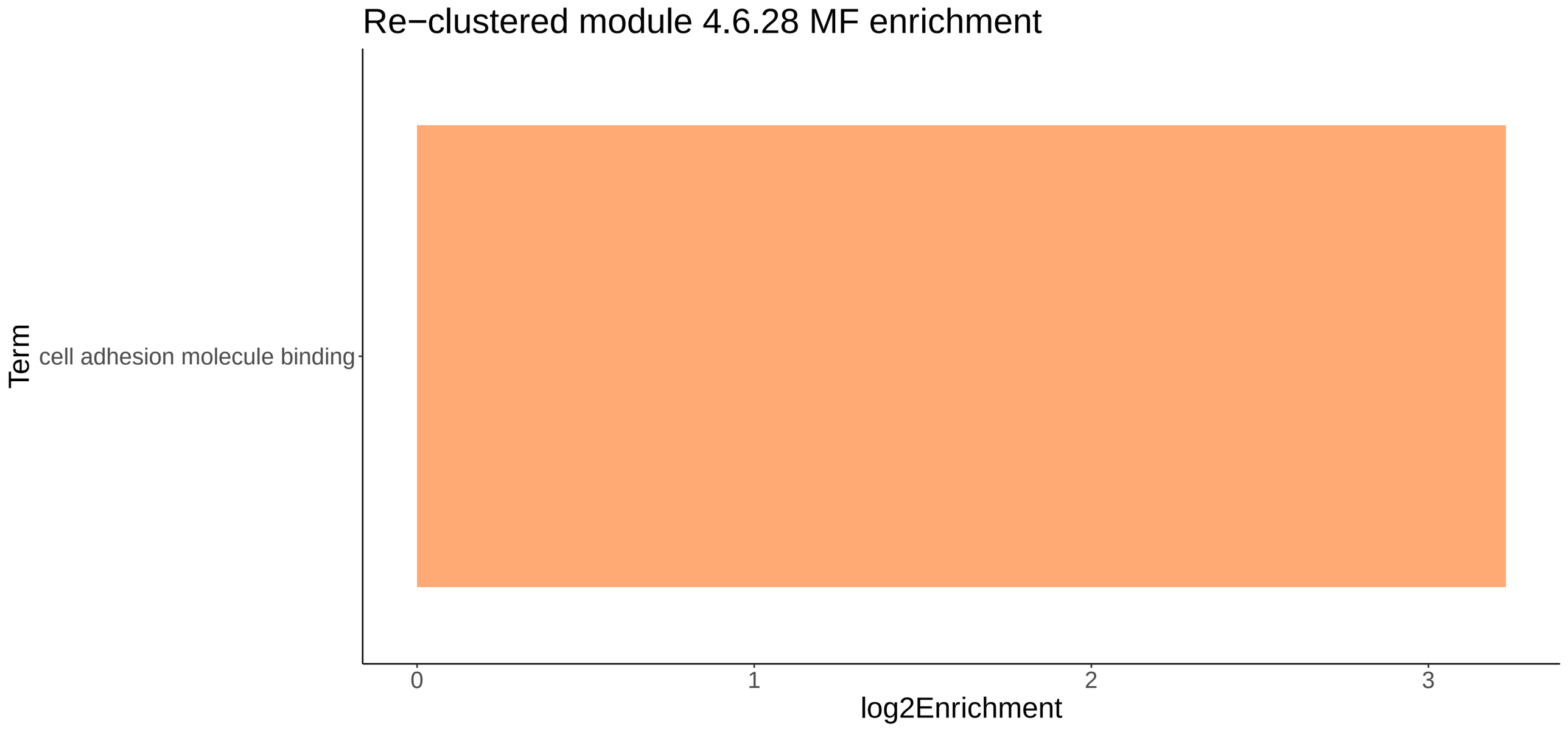

Re−clustered module 4.6.23 BP enrichment
Term
adenylate cyclase−activating G protein−coupled receptor signaling pathway
0
1
2
3
4
log2Enrichment

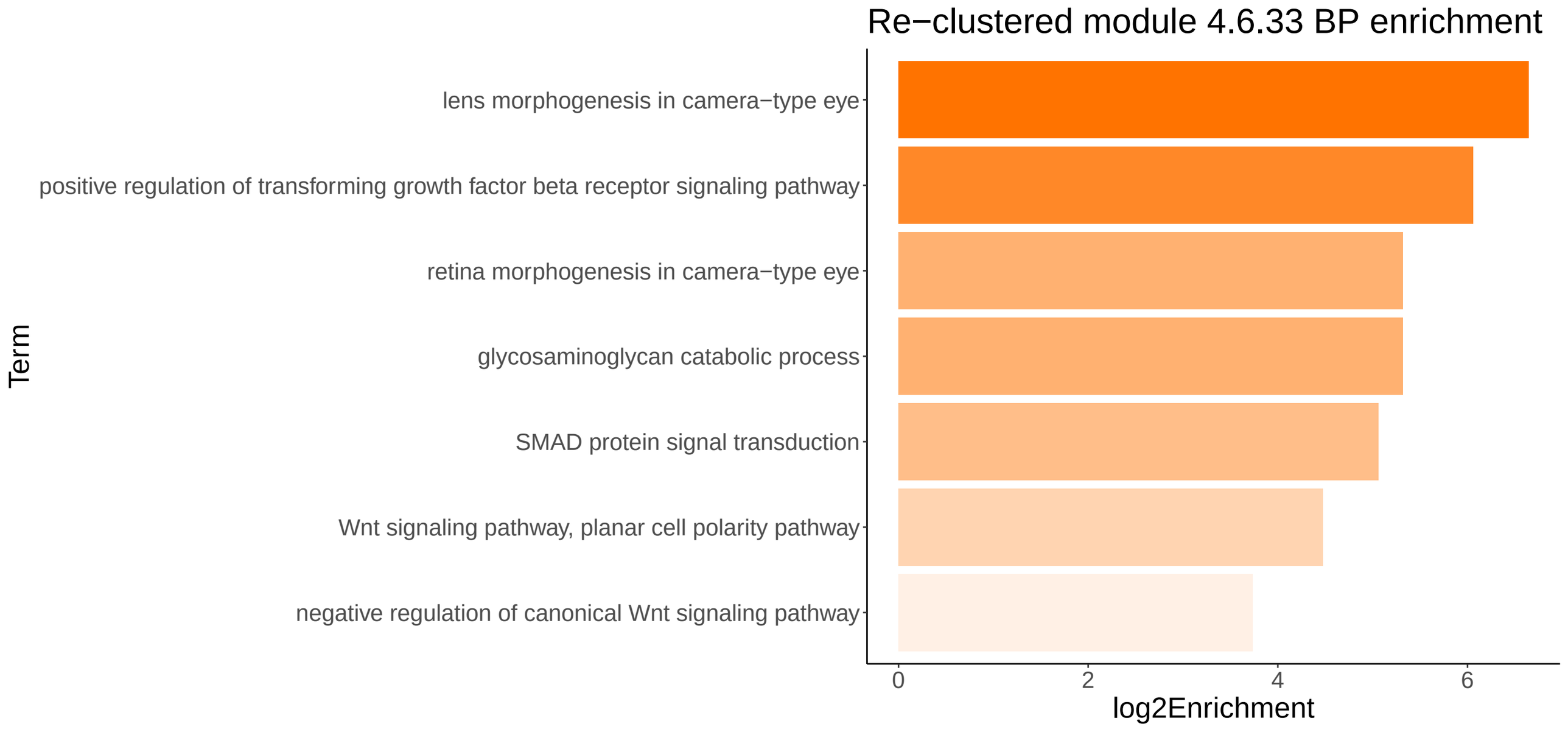

Re−clustered module 4.6.23 MF enrichment
Term
log2Enrichment

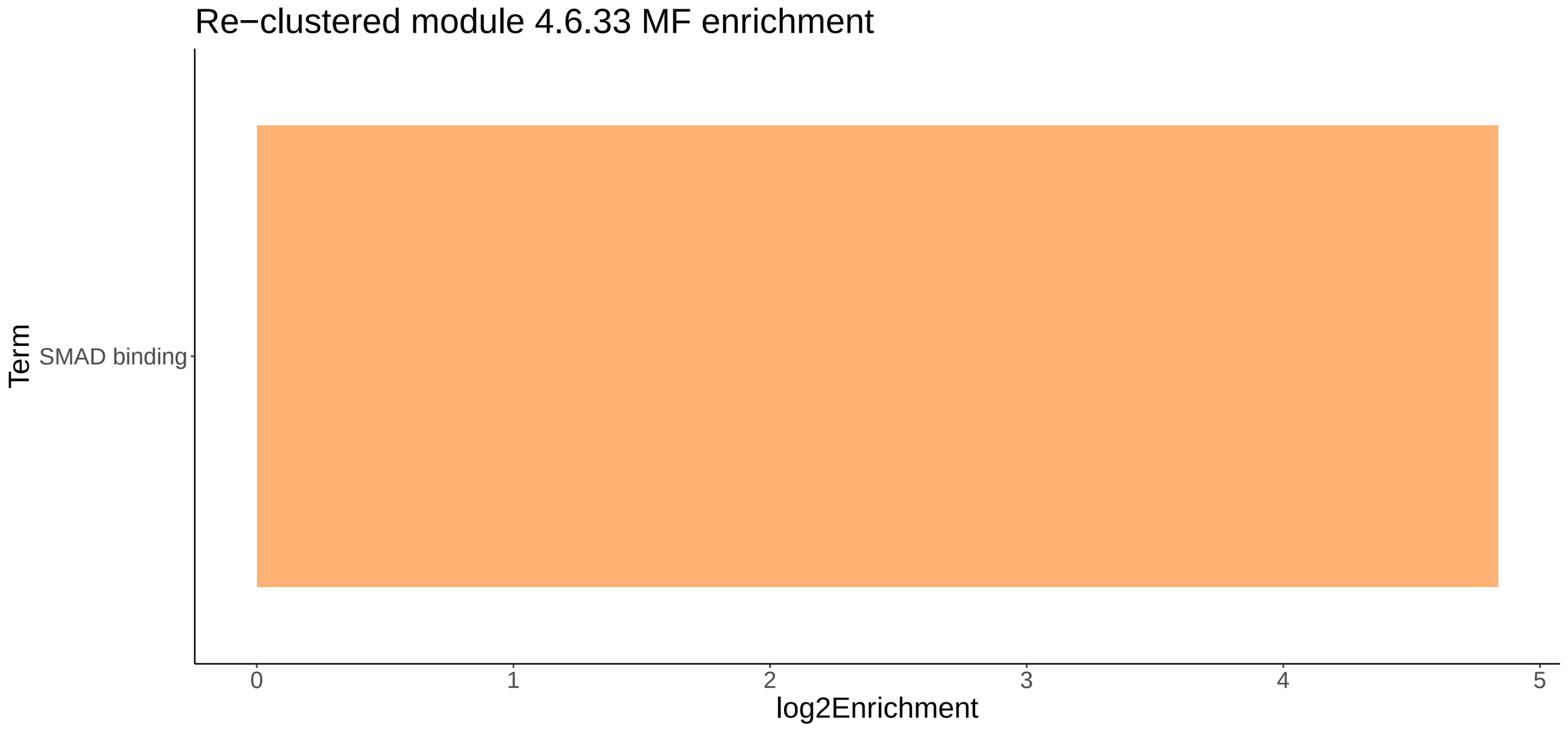

Re−clustered module 4.6.25 BP enrichment
vascular endothelial growth factor signaling pathway
negative regulation of leukocyte migration
regulation of collagen metabolic process
extracellular matrix assembly
regulation of chemotaxis
angiogenesis
supramolecular fiber organization
Term
0
2
4
log2Enrichment

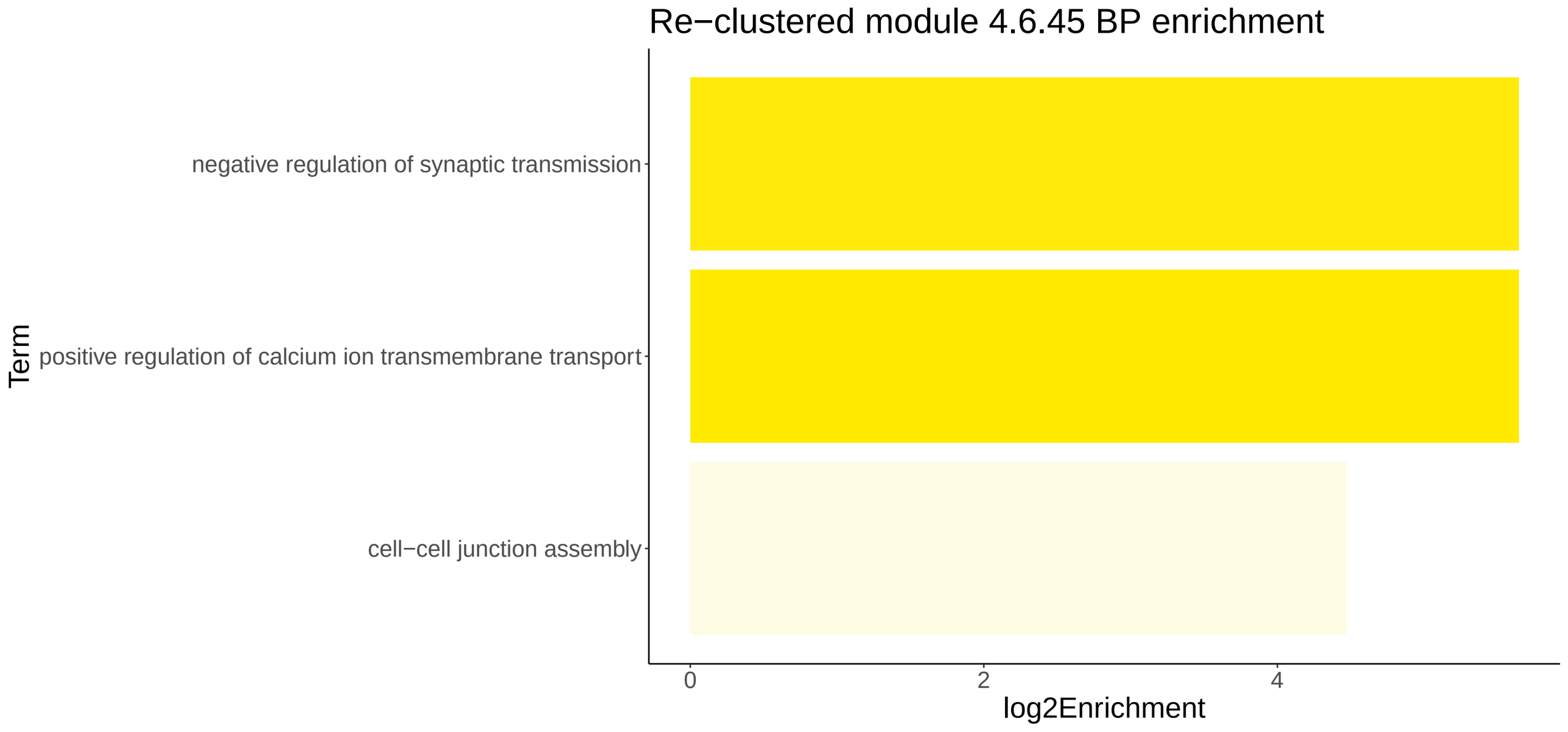

Re−clustered module 4.6.25 MF enrichment
Term
extracellular matrix structural constituent
integrin binding
0
1
2
3
4
log2Enrichment

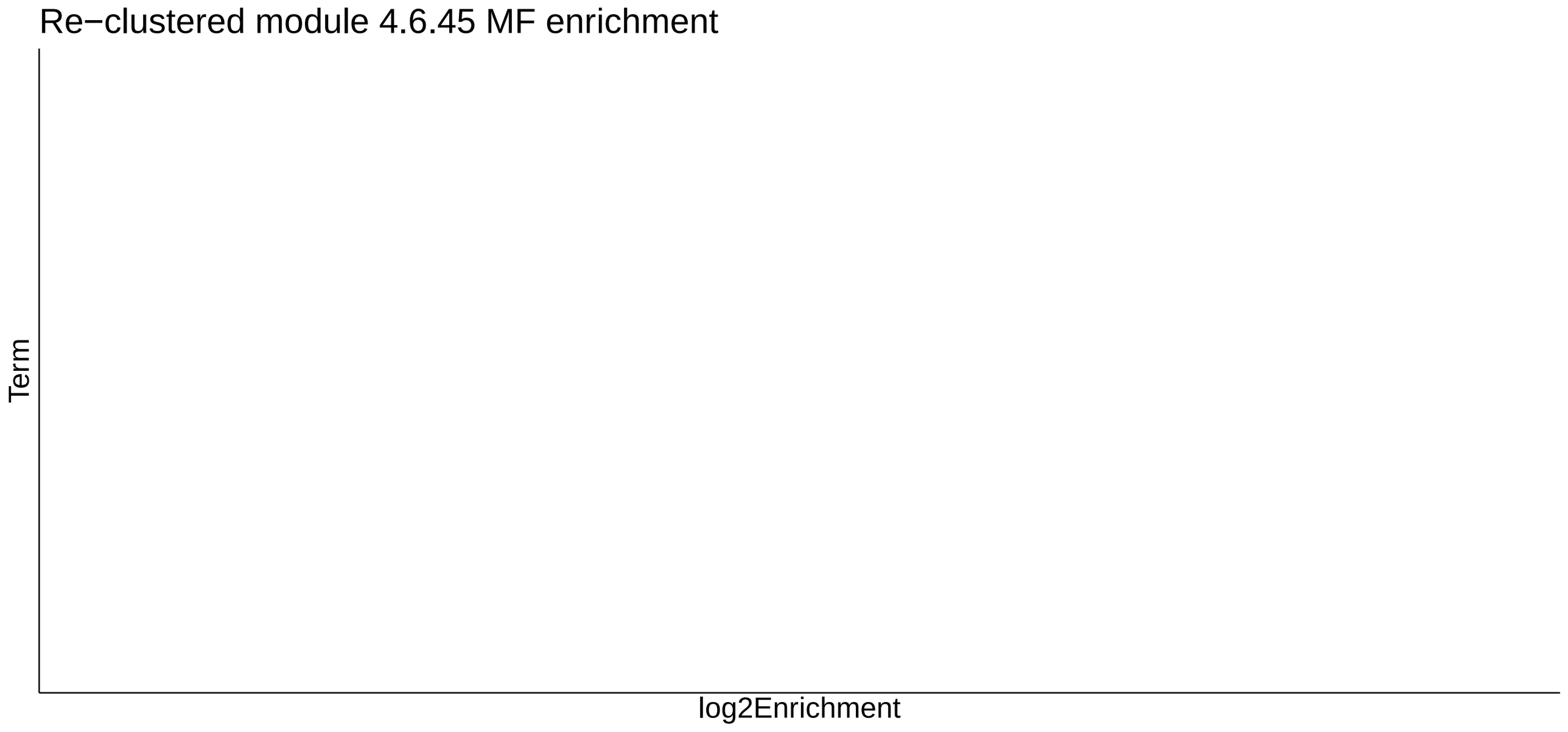

Re−clustered module 4.6.28 BP enrichment
homophilic cell adhesion via plasma membrane adhesion molecules
neuron migration
cell−cell junction organization
cell junction assembly
muscle tissue development
Term
0
1
2
3
4
log2Enrichment

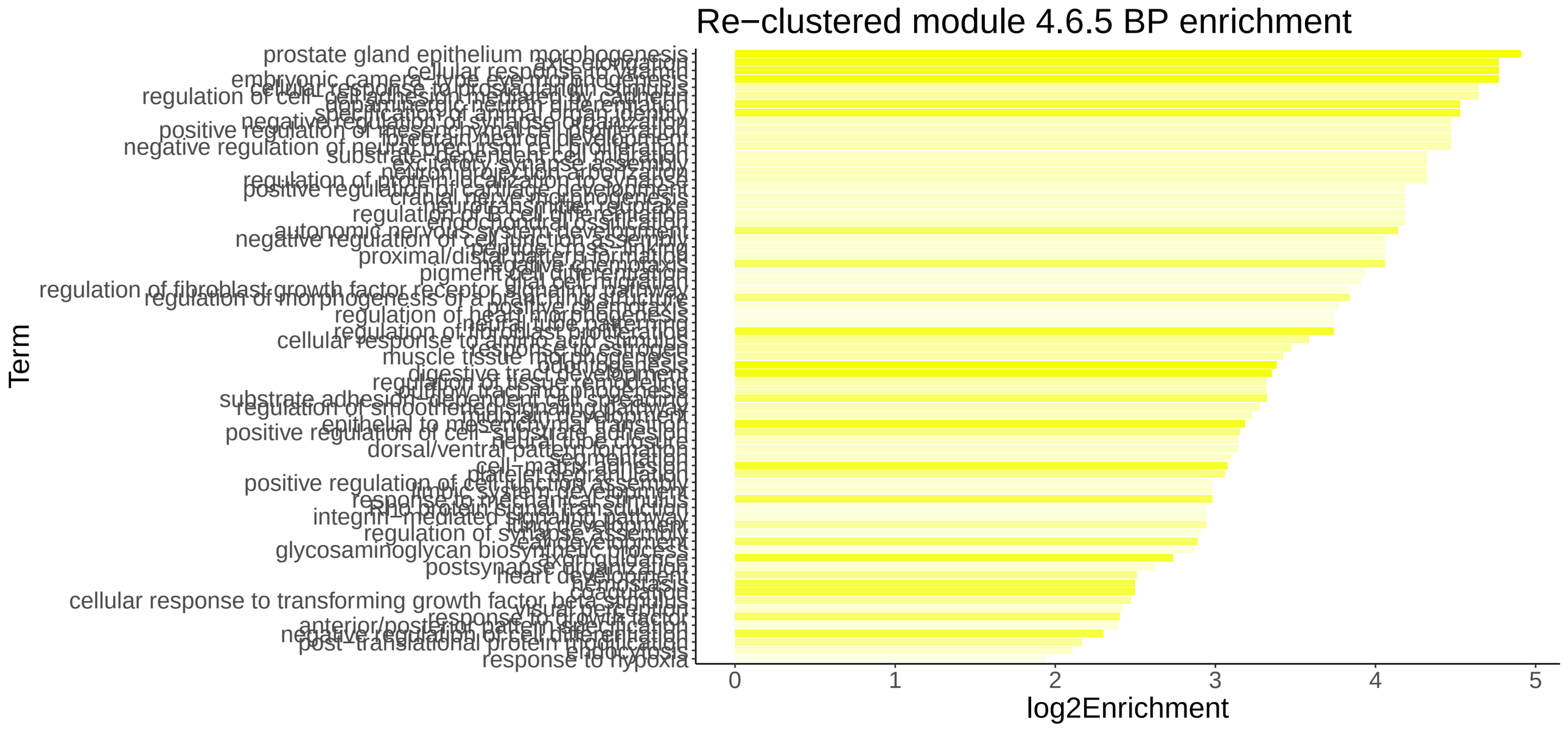

Re−clustered module 4.6.28 MF enrichment
Term
cell adhesion molecule binding
0
1
2
3
log2Enrichment

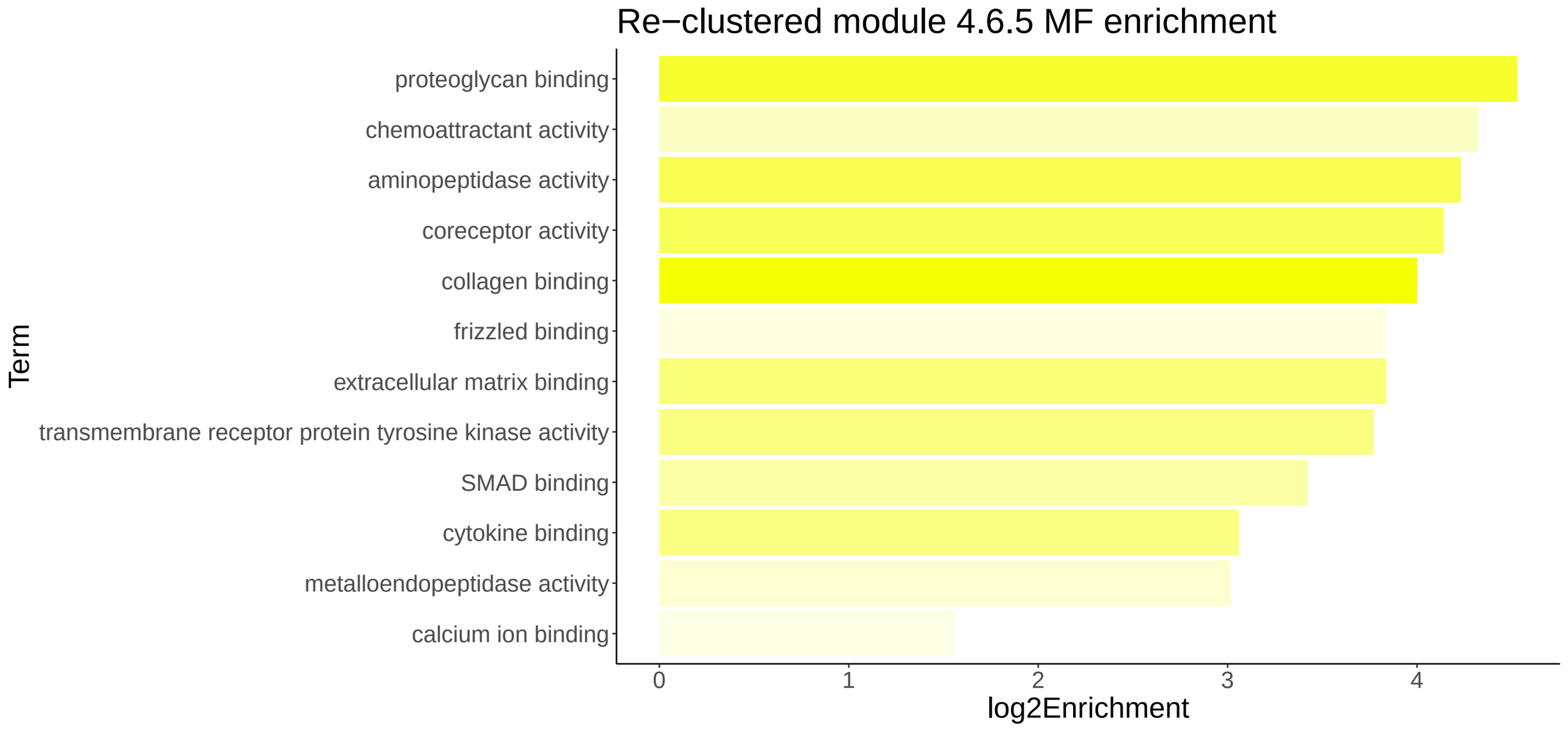

Re−clustered module 4.6.33 BP enrichment
Term
lens morphogenesis in camera−type eye
positive regulation of transforming growth factor beta receptor signaling pathway
retina morphogenesis in camera−type eye
glycosaminoglycan catabolic process
SMAD protein signal transduction
Wnt signaling pathway, planar cell polarity pathway
negative regulation of canonical Wnt signaling pathway
0
2
4
6
log2Enrichment

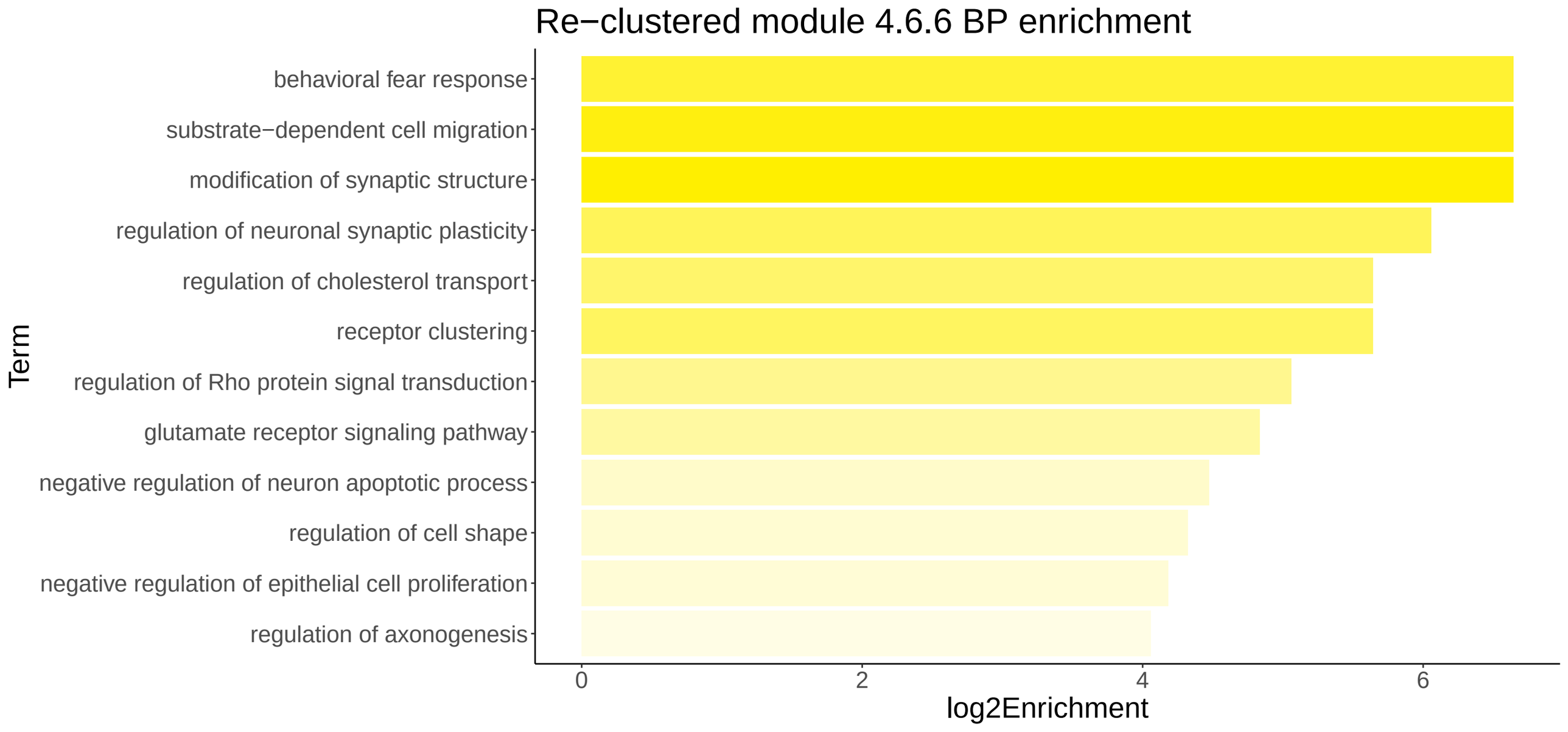

Re−clustered module 4.6.33 MF enrichment
Term
SMAD binding
0
1
2
3
4
5
log2Enrichment

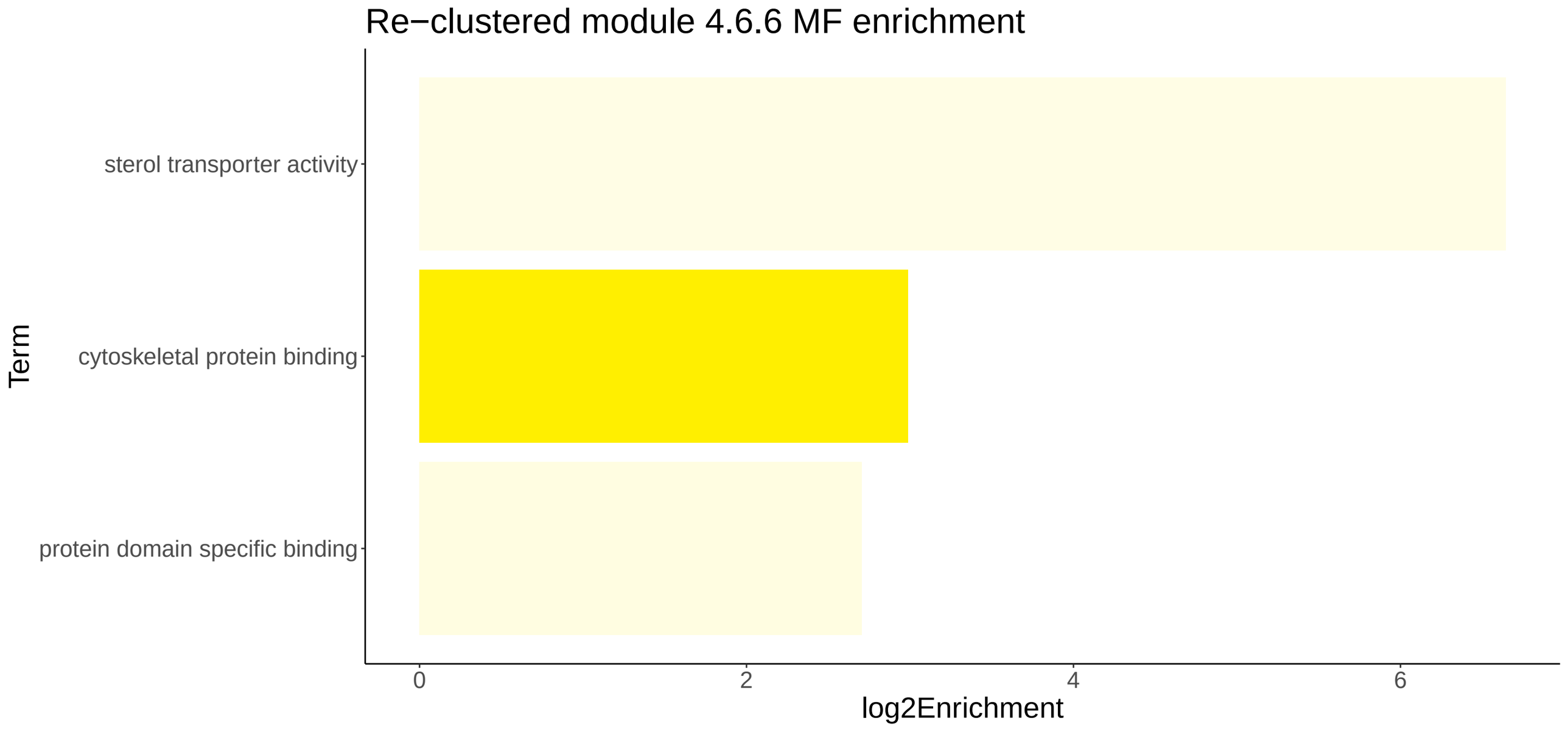

Re−clustered module 4.6.45 BP enrichment
Term
negative regulation of synaptic transmission
positive regulation of calcium ion transmembrane transport
cell−cell junction assembly
0
2
4
log2Enrichment

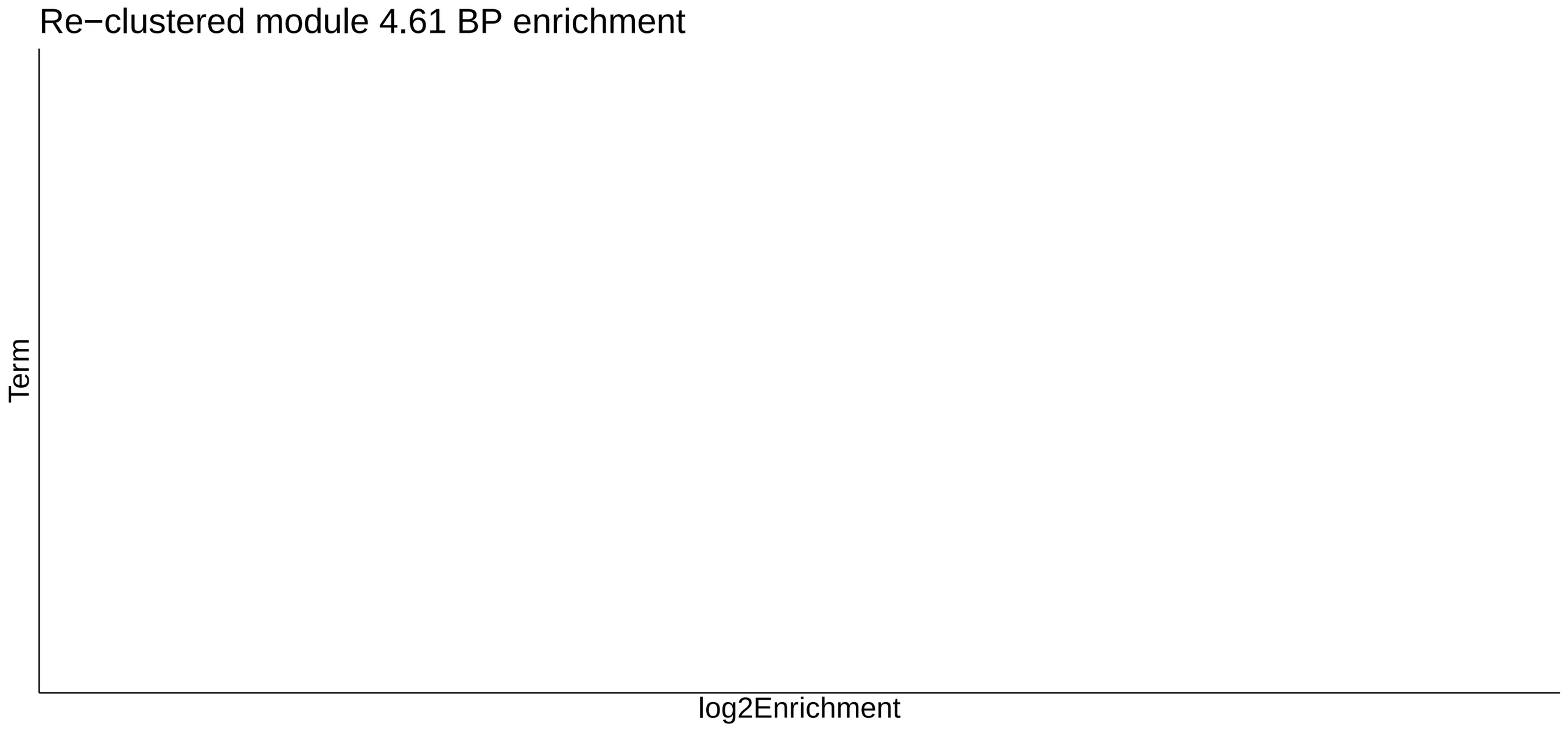

Re−clustered module 4.6.45 MF enrichment
Term
log2Enrichment

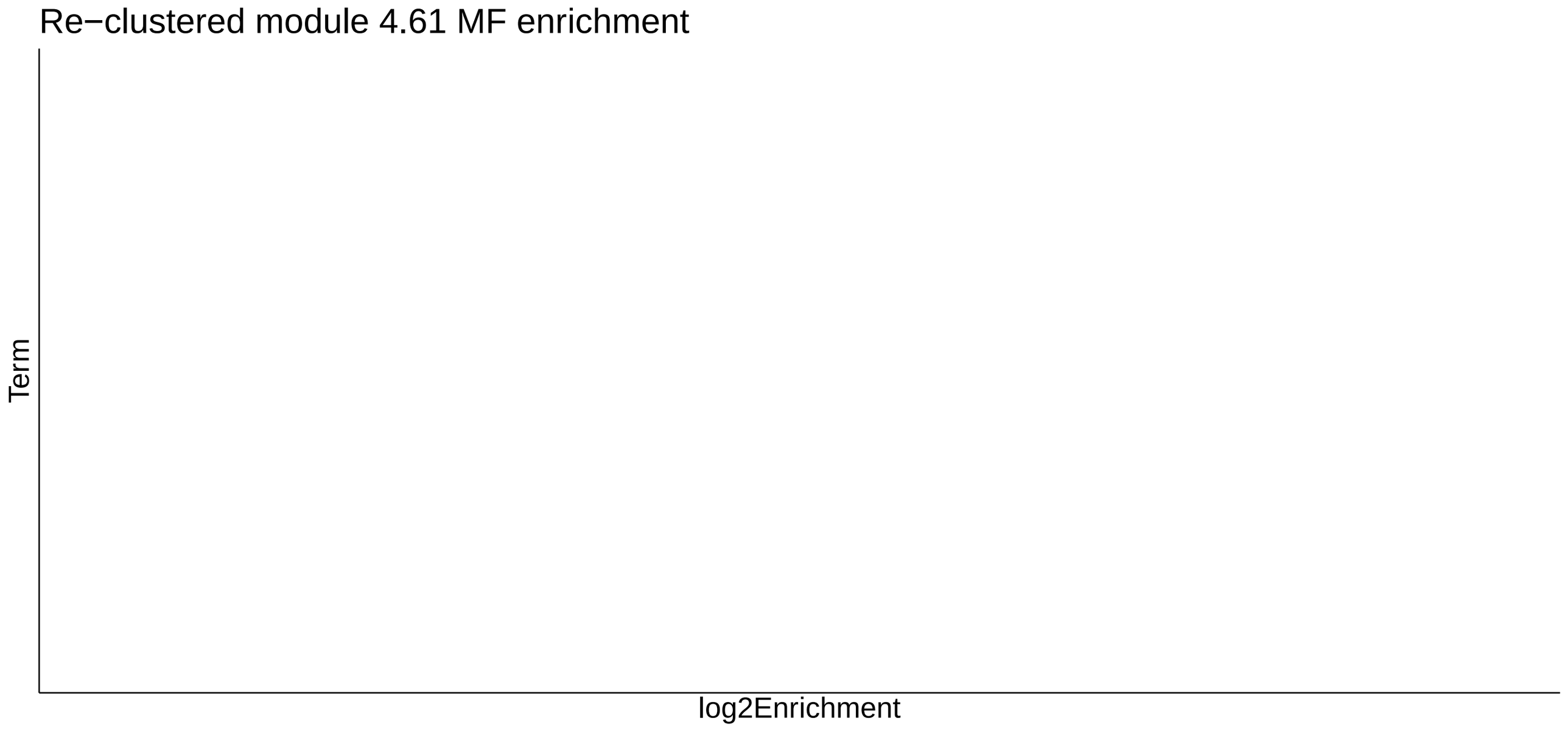

Re−clustered module 4.6.5 BP enrichment
Term
prostate gland epithelium morphogenesis
axis elongation
cellular response to vitamin
embryonic camera−type eye morphogenesis
cellular response to prostaglandin stimulus
regulation of cell−cell adhesion mediated by cadherin
dopaminergic neuron differentiation
specification of animal organ identity
negative regulation of synapse organization
positive regulation of mesenchymal cell proliferation
forebrain neuron development
negative regulation of neural precursor cell proliferation
substrate−dependent cell migration
excitatory synapse assembly
neuron projection arborization
regulation of protein localization to synapse
positive regulation of cartilage development
cranial nerve morphogenesis
neurotransmitter reuptake
regulation of cell differentiation
endochondral ossification
autonomic nervous system development
negative regulation of cell junction assembly
proximal/distal pattern formation
negative chemotaxis
pigment cell differentiation
regulation of fibroblast growth factor receptor signaling pathway
regulation of morphogenesis of a branching structure
positive chemotaxis
regulation of heart morphogenesis
regulation of neural tube patterning
cellular response to fibroblast proliferation
amino acid stimulus
muscle tissue morphogenesis
digestive tract development
regulation of tissue remodeling
substrate adhesion−dependent cell spreading
regulation of smoothened signaling pathway
neural crest development
epithelial to mesenchymal transition
positive regulation of cell−substrate adhesion
dorsal/ventral pattern formation
cell−matrix adhesion
platelet degranulation
positive regulation of cell junction assembly
immune system development
response to mechanical stimulus
PID protein signaling pathway
integrin−mediated signaling pathway
lung development
regulation of synapse assembly
gland development
glycosaminoglycan biosynthetic process
axon guidance
postsynapse organization
heart development
hemostasis
coagulation
cellular response to transforming growth factor beta stimulus
visual perception
response to growth factor
anterior/posterior pattern specification
negative regulation of cell differentiation
post−translational protein modification
endocytosis
response to hypoxia
0
1
2
3
4
5
log2Enrichment

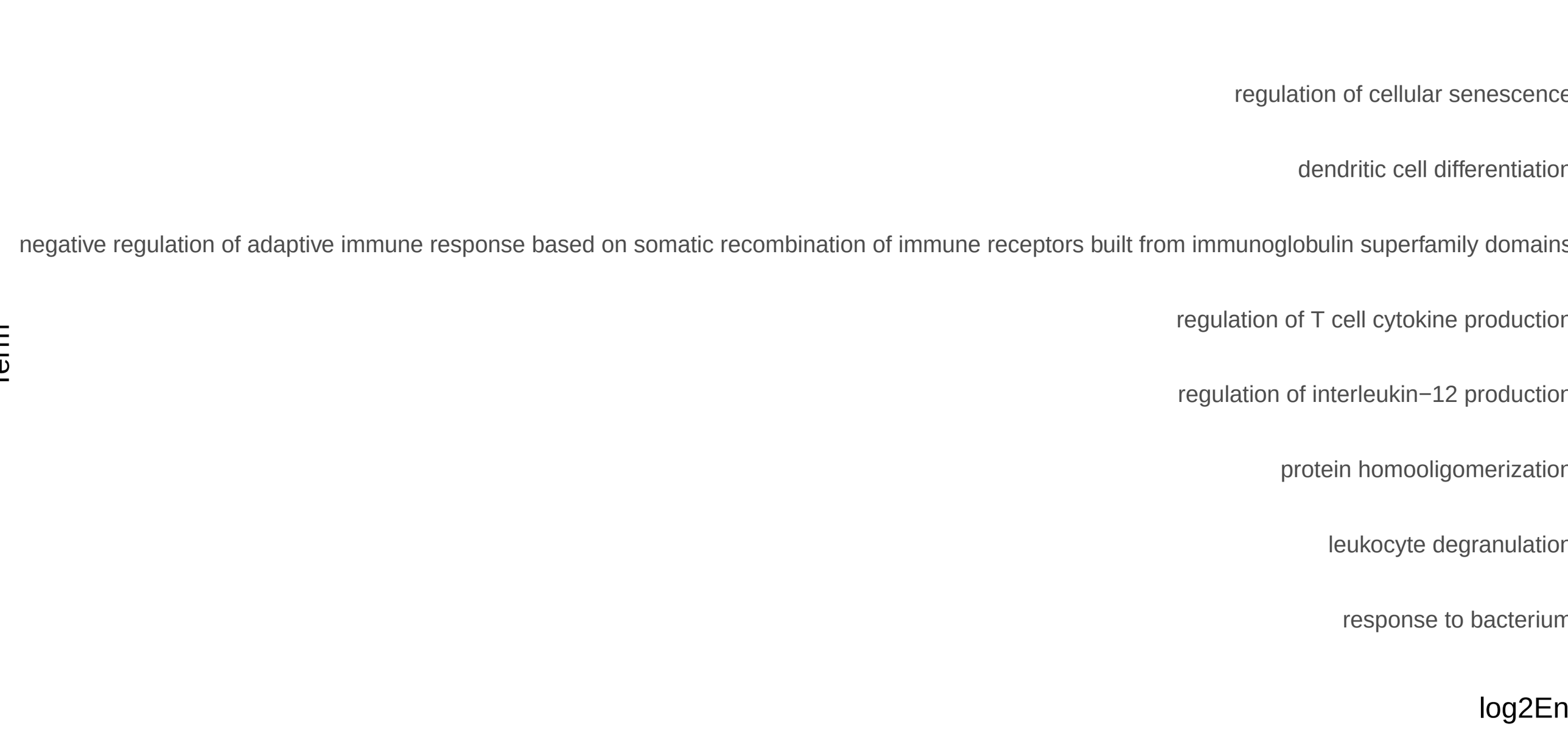

Re−clustered module 4.6.5 MF enrichment
proteoglycan binding
chemoattractant activity
aminopeptidase activity
coreceptor activity
collagen binding
frizzled binding
extracellular matrix binding
transmembrane receptor protein tyrosine kinase activity
SMAD binding
cytokine binding
metalloendopeptidase activity
calcium ion binding
Term
0
1
2
3
4
log2Enrichment

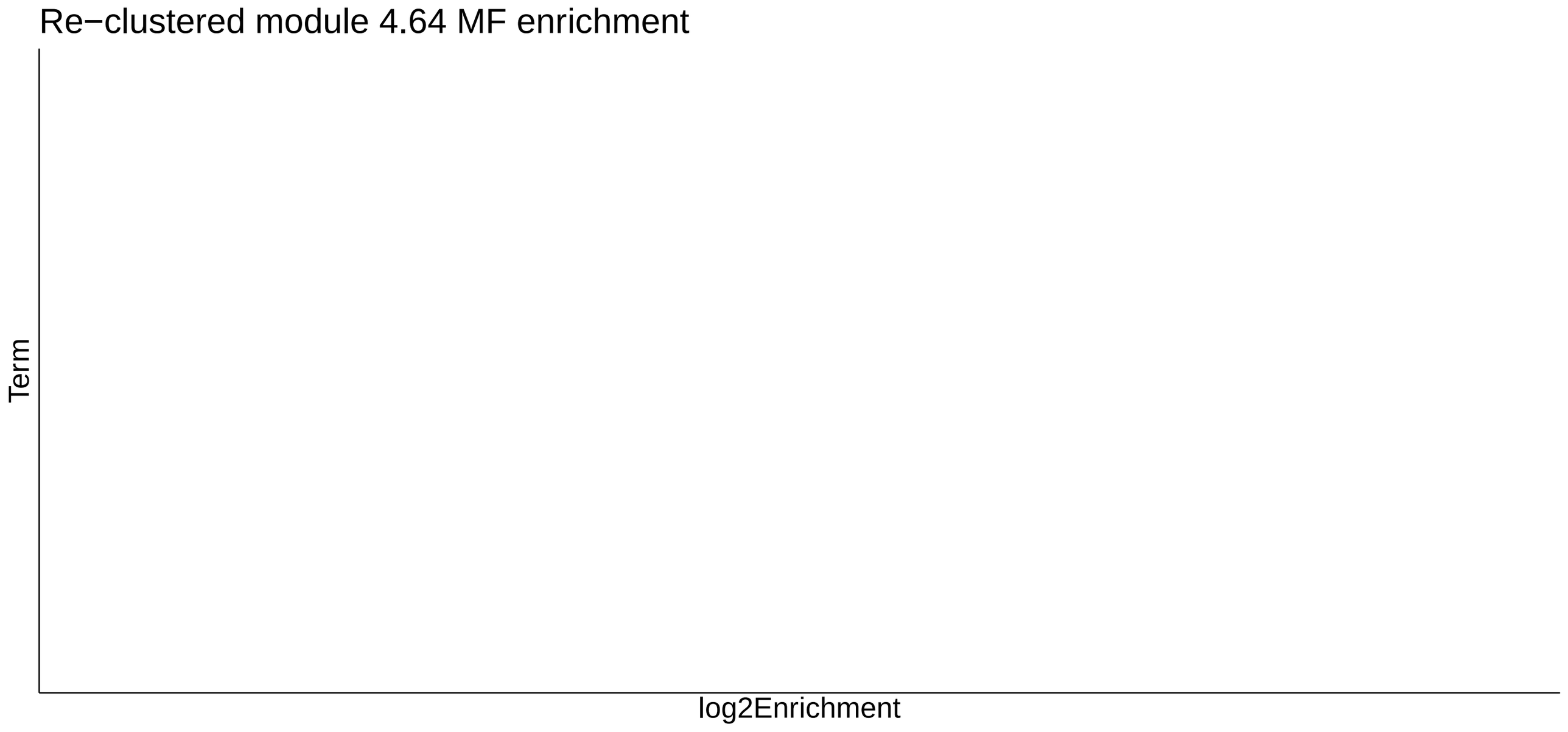

Re−clustered module 4.6.6 BP enrichment
behavioral fear response
substrate−dependent cell migration
modification of synaptic structure
regulation of neuronal synaptic plasticity
regulation of cholesterol transport
receptor clustering
regulation of Rho protein signal transduction
glutamate receptor signaling pathway
negative regulation of neuron apoptotic process
regulation of cell shape
negative regulation of epithelial cell proliferation
regulation of axonogenesis
Term
0
2
4
6
log2Enrichment

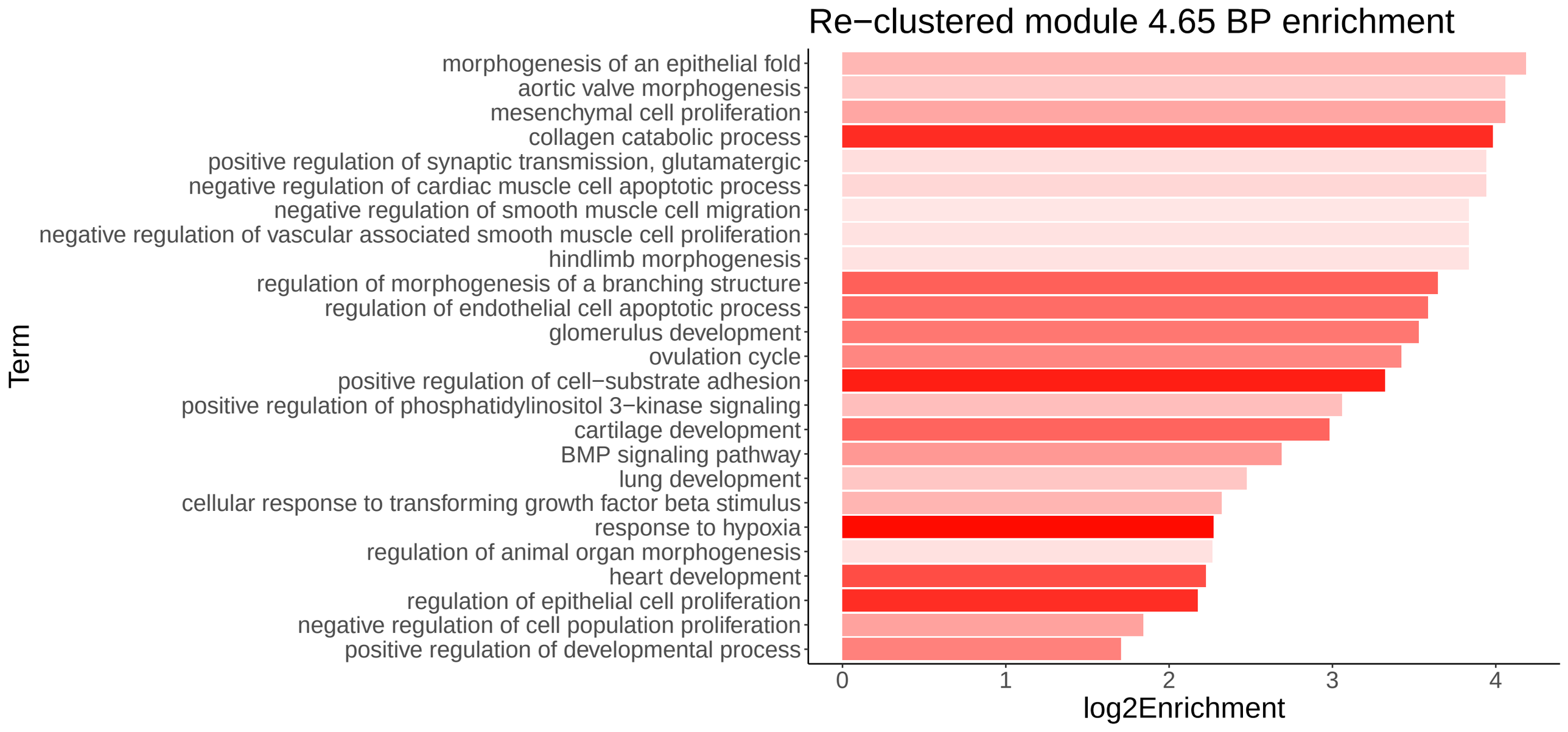

Re−clustered module 4.6.6 MF enrichment
Term
sterol transporter activity
cytoskeletal protein binding
protein domain specific binding
0
2
4
6
log2Enrichment

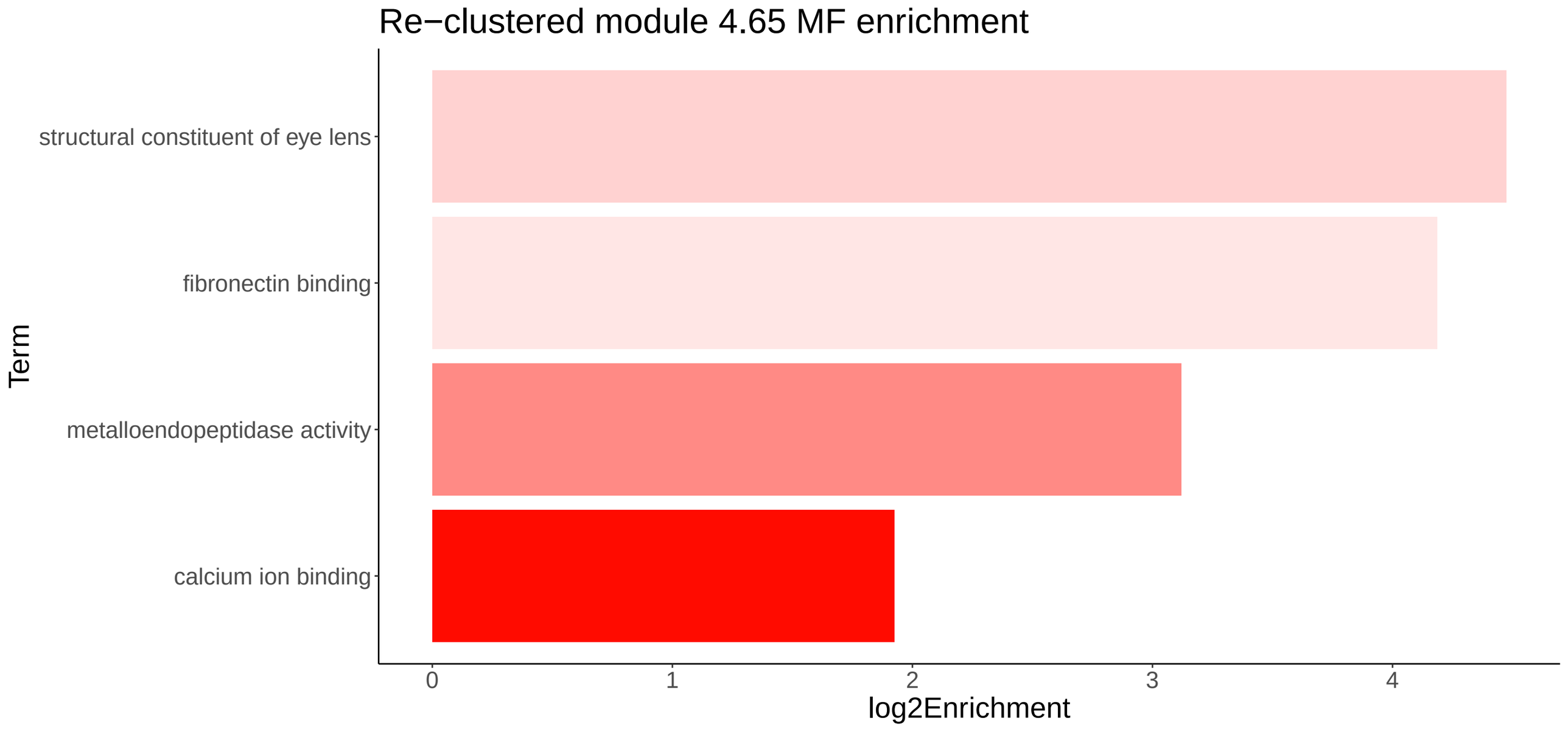

Re−clustered module 4.61 BP enrichment
Term
log2Enrichment

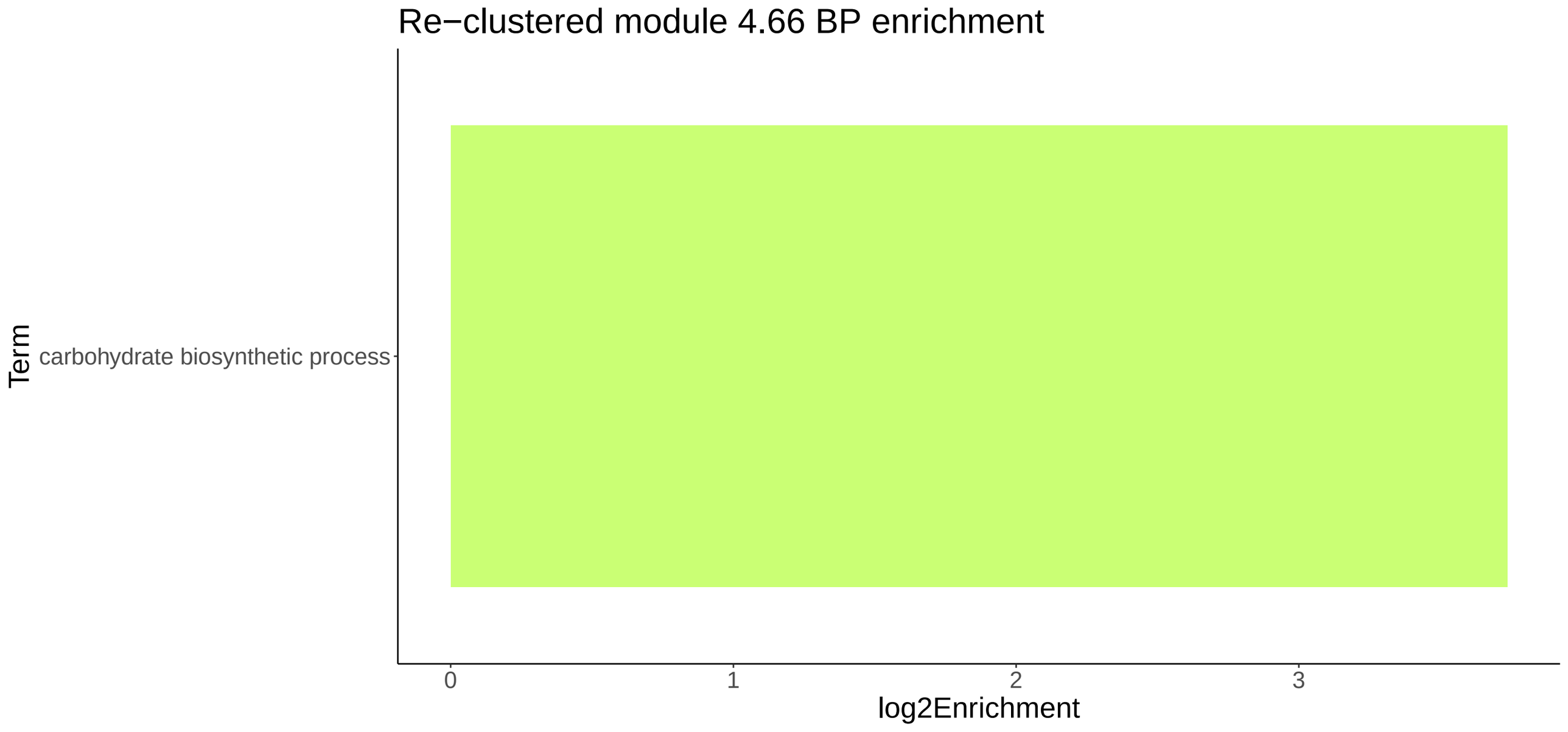

Re−clustered module 4.61 MF enrichment
Term
log2Enrichment

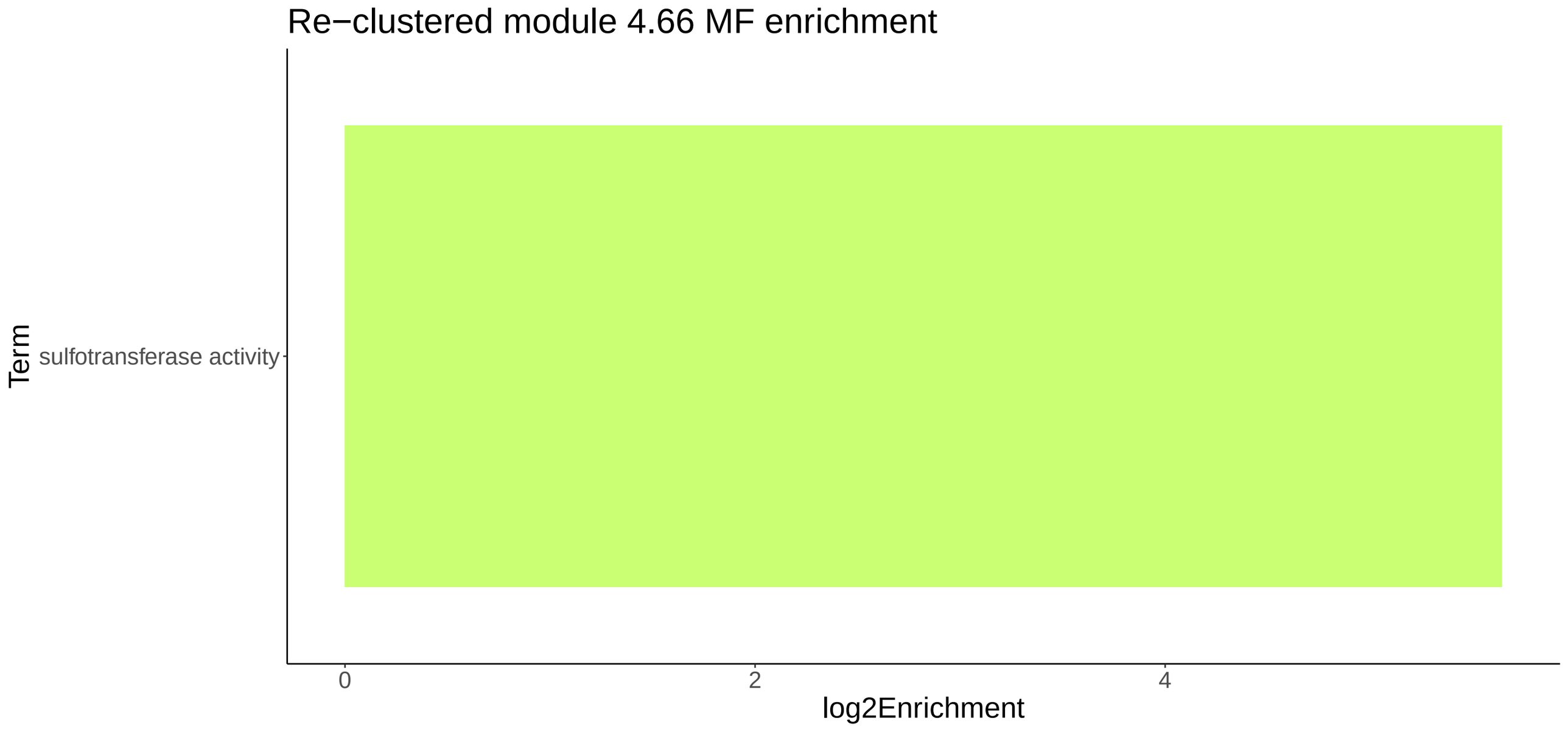

regulation of cellular senescence
dendritic cell differentiation
negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
regulation of T cell cytokine production
regulation of interleukin−12 production
protein homooligomerization
leukocyte degranulation
response to bacterium
log2En

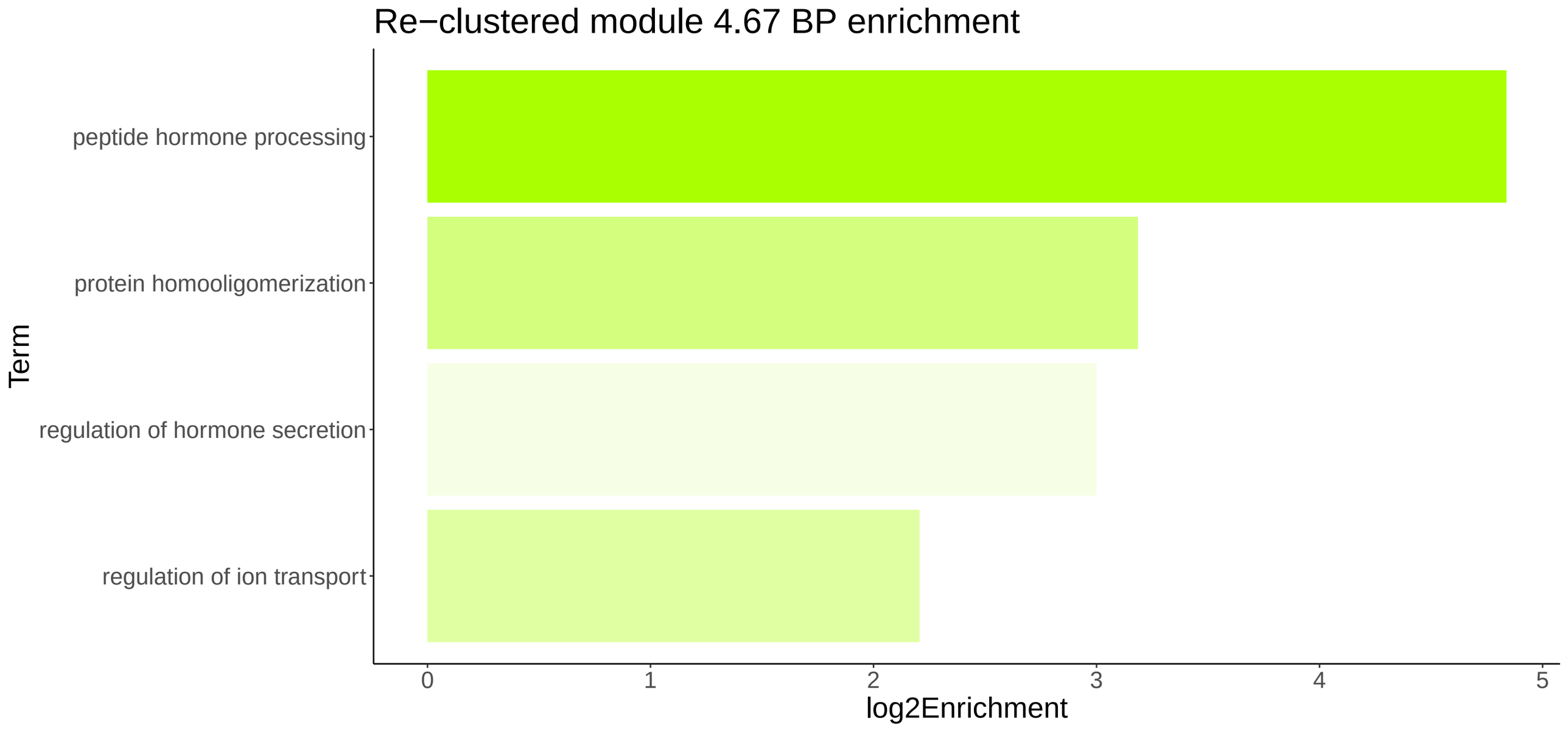

Re−clustered module 4.64 MF enrichment
Term
log2Enrichment

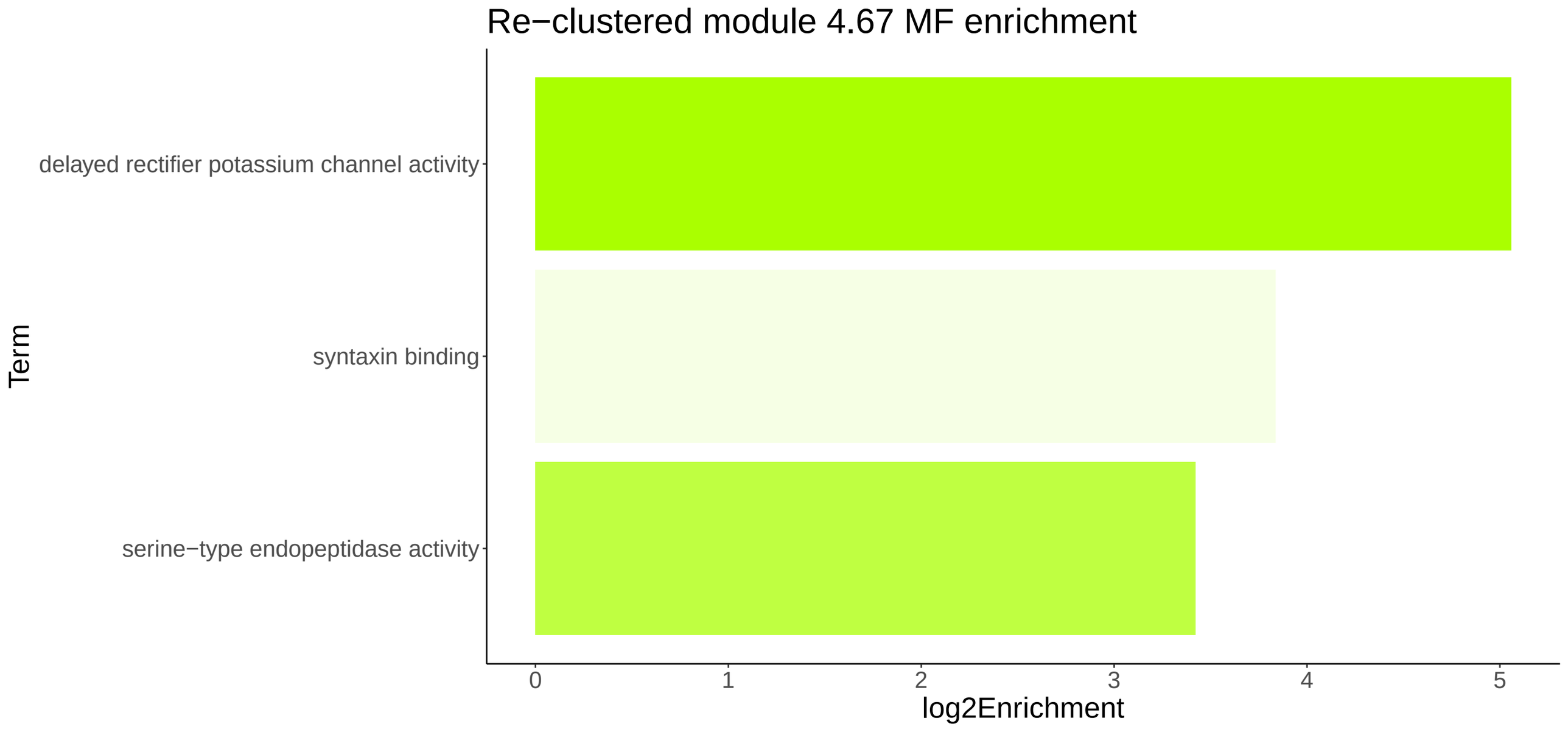

Re−clustered module 4.65 BP enrichment
Term
morphogenesis of an epithelial fold
aortic valve morphogenesis
mesenchymal cell proliferation
collagen catabolic process
positive regulation of synaptic transmission, glutamatergic
negative regulation of cardiac muscle cell apoptotic process
negative regulation of smooth muscle cell migration
negative regulation of vascular associated smooth muscle cell proliferation
hindlimb morphogenesis
regulation of morphogenesis of a branching structure
regulation of endothelial cell apoptotic process
glomerulus development
ovulation cycle
positive regulation of cell−substrate adhesion
positive regulation of phosphatidylinositol 3−kinase signaling
cartilage development
BMP signaling pathway
lung development
cellular response to transforming growth factor beta stimulus
response to hypoxia
regulation of animal organ morphogenesis
heart development
regulation of epithelial cell proliferation
negative regulation of cell population proliferation
positive regulation of developmental process
0
1
2
3
4
log2Enrichment

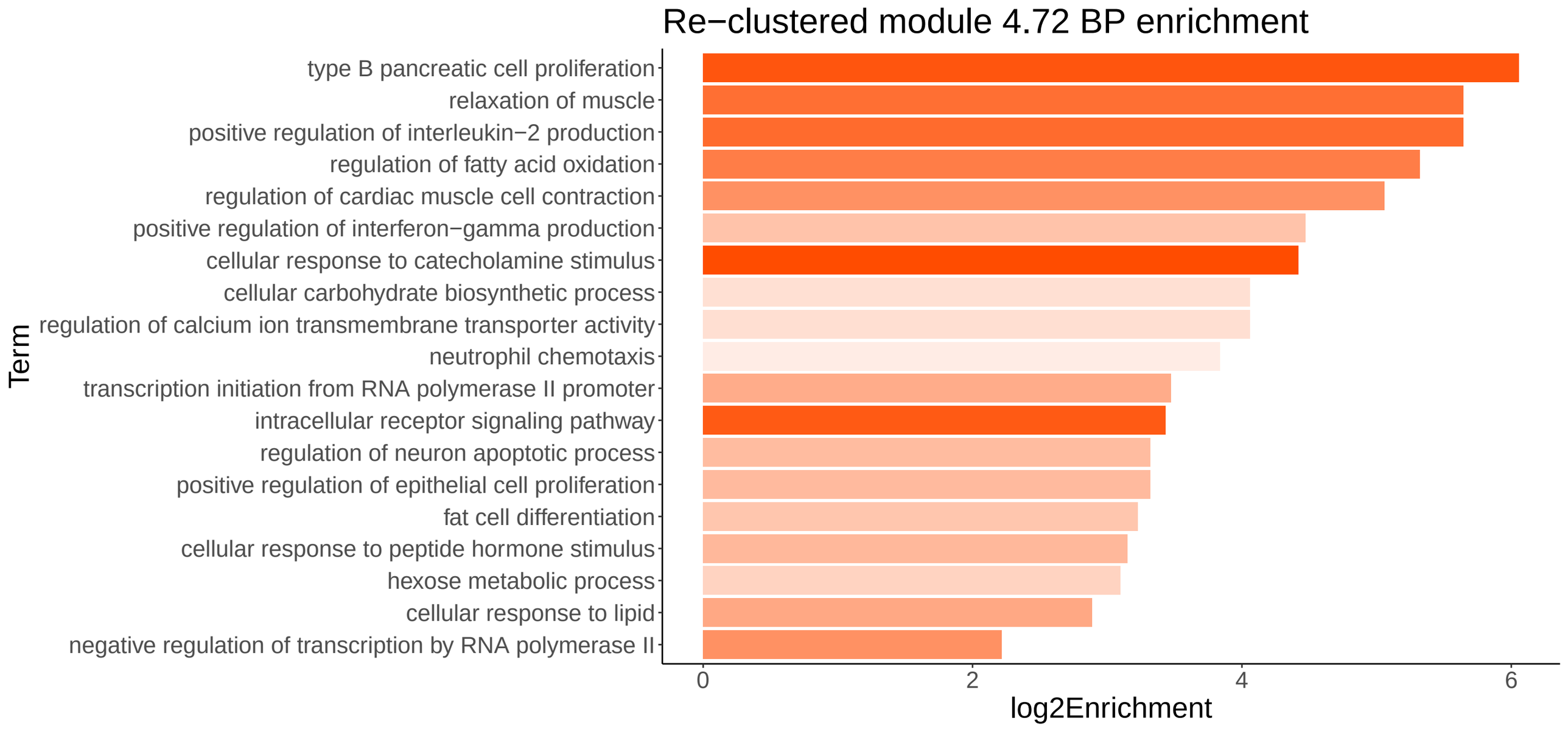

Re−clustered module 4.65 MF enrichment
structural constituent of eye lens
fibronectin binding
metalloendopeptidase activity
calcium ion binding
Term
0
1
2
3
4
log2Enrichment

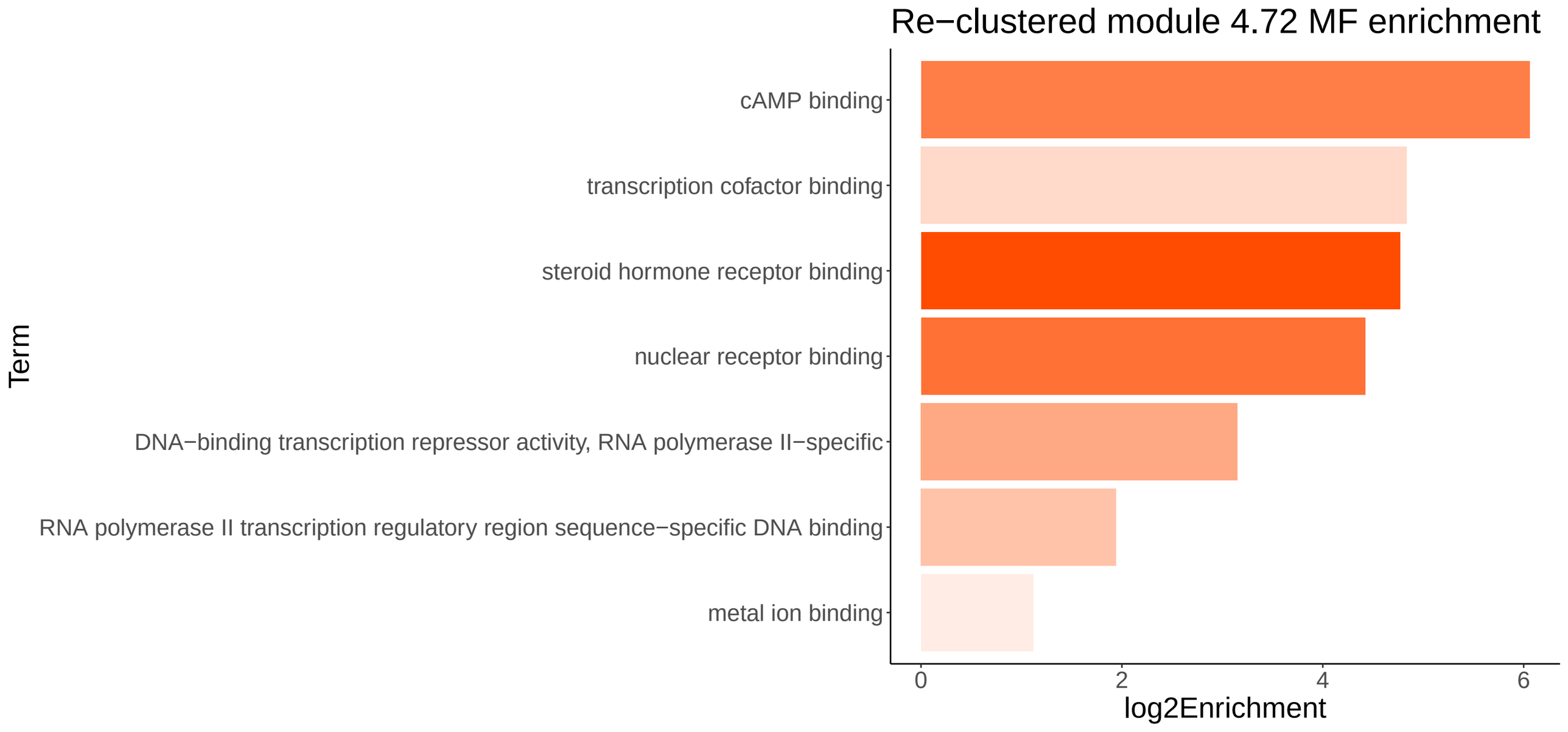

Re−clustered module 4.66 BP enrichment
Term
carbohydrate biosynthetic process
0
1
2
3
log2Enrichment

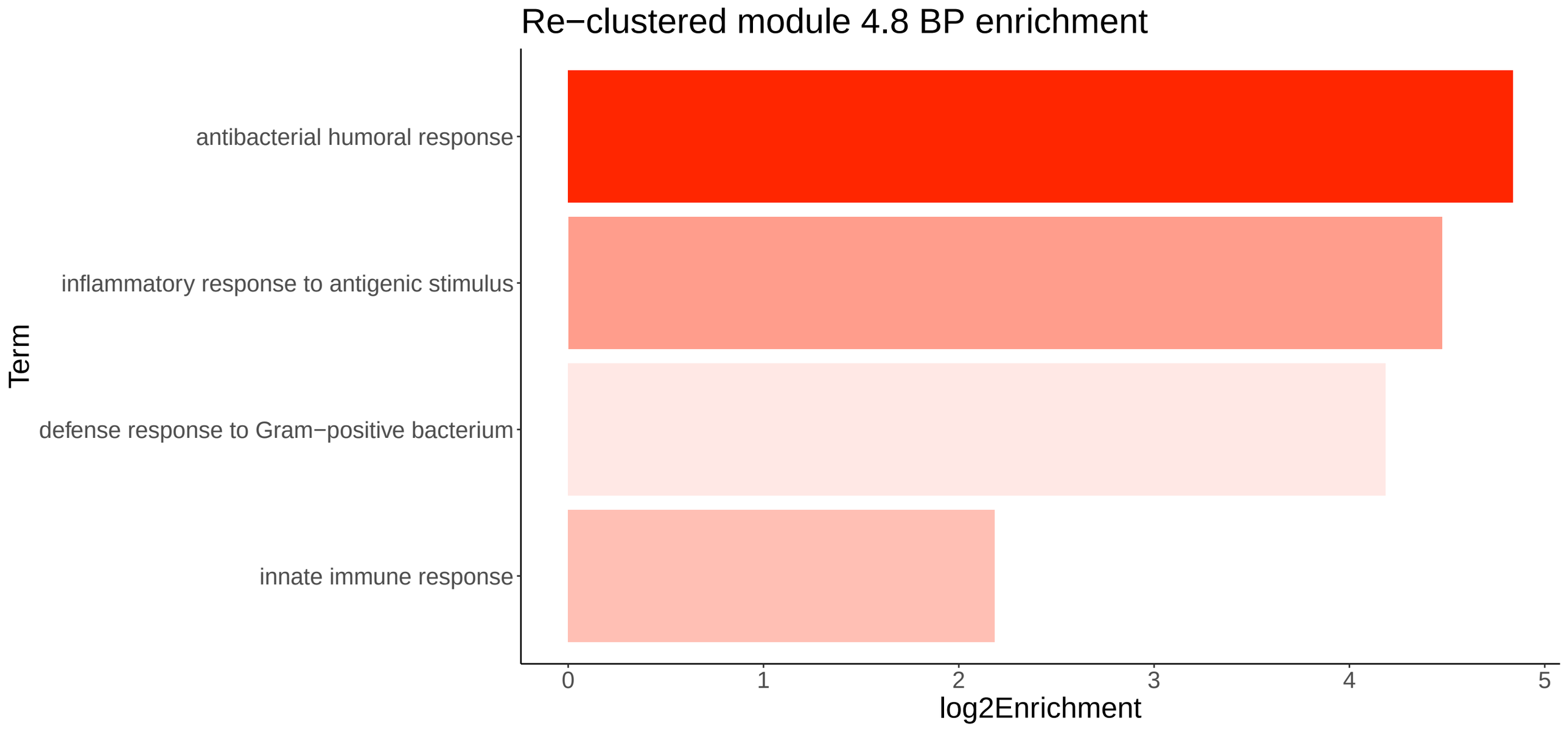

Re−clustered module 4.66 MF enrichment
Term
sulfotransferase activity
0
2
4
log2Enrichment

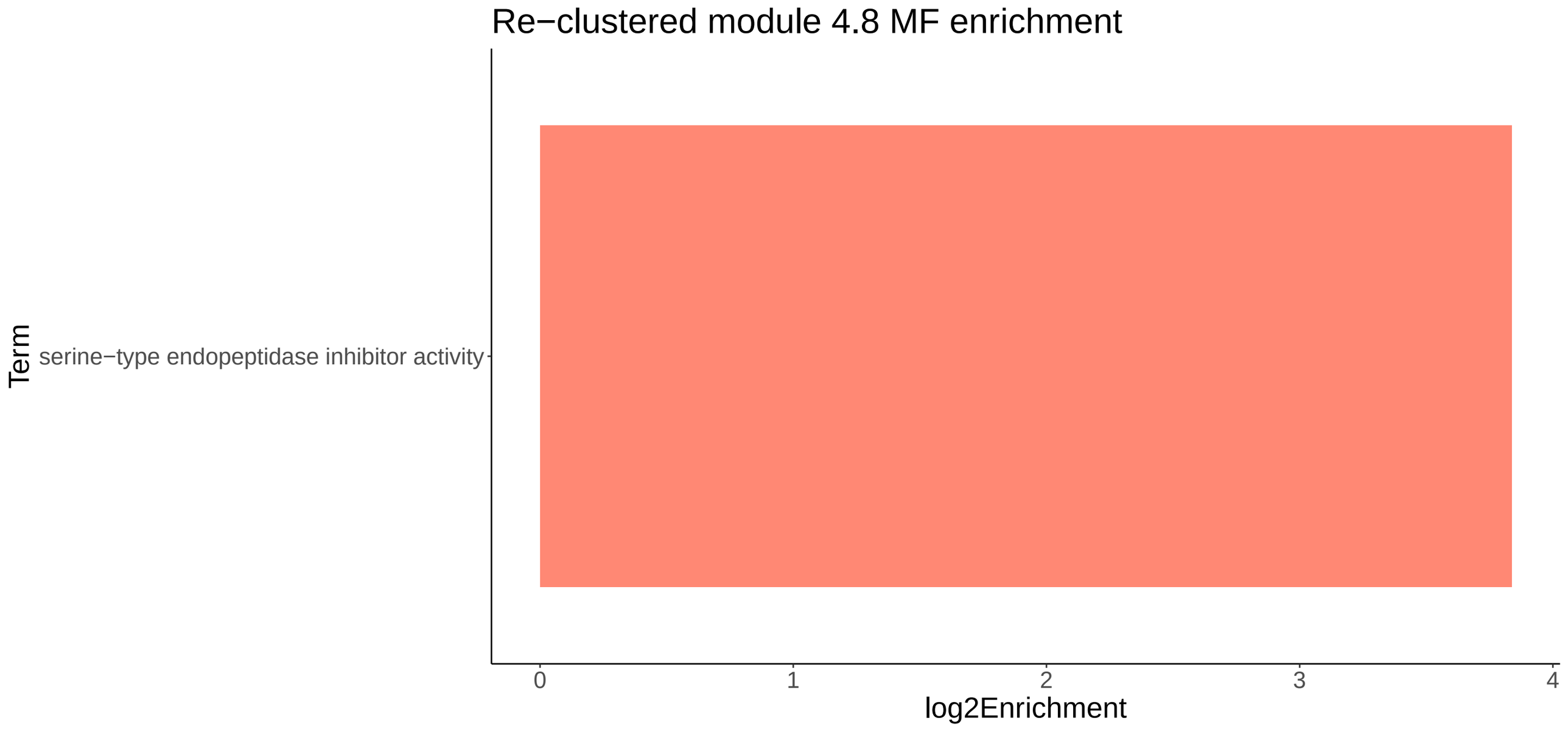

Re−clustered module 4.67 BP enrichment
peptide hormone processing
protein homooligomerization
regulation of hormone secretion
regulation of ion transport
Term
0
1
2
3
4
5
log2Enrichment

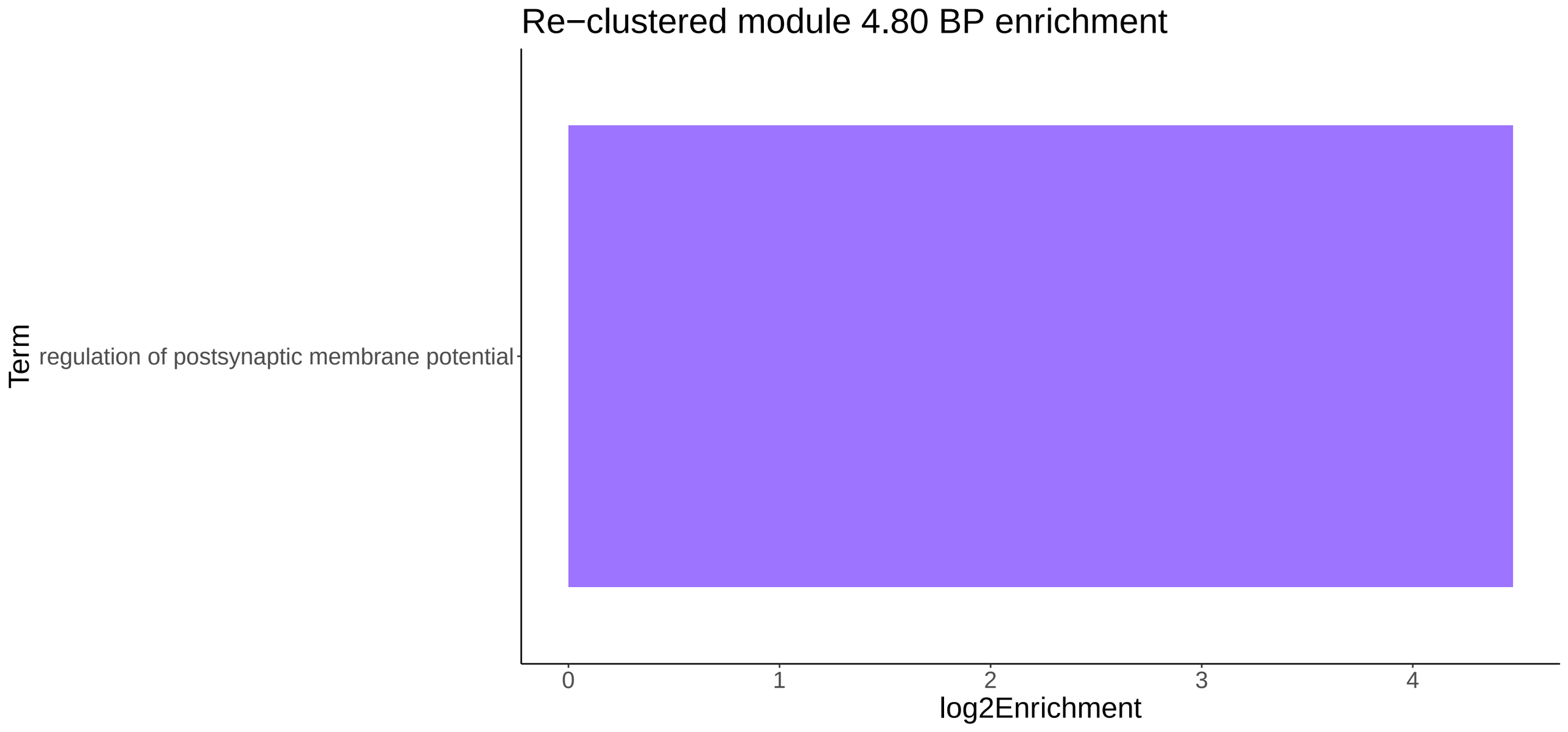

Re−clustered module 4.67 MF enrichment
Term
delayed rectifier potassium channel activity
syntaxin binding
serine−type endopeptidase activity
0
1
2
3
4
5
log2Enrichment

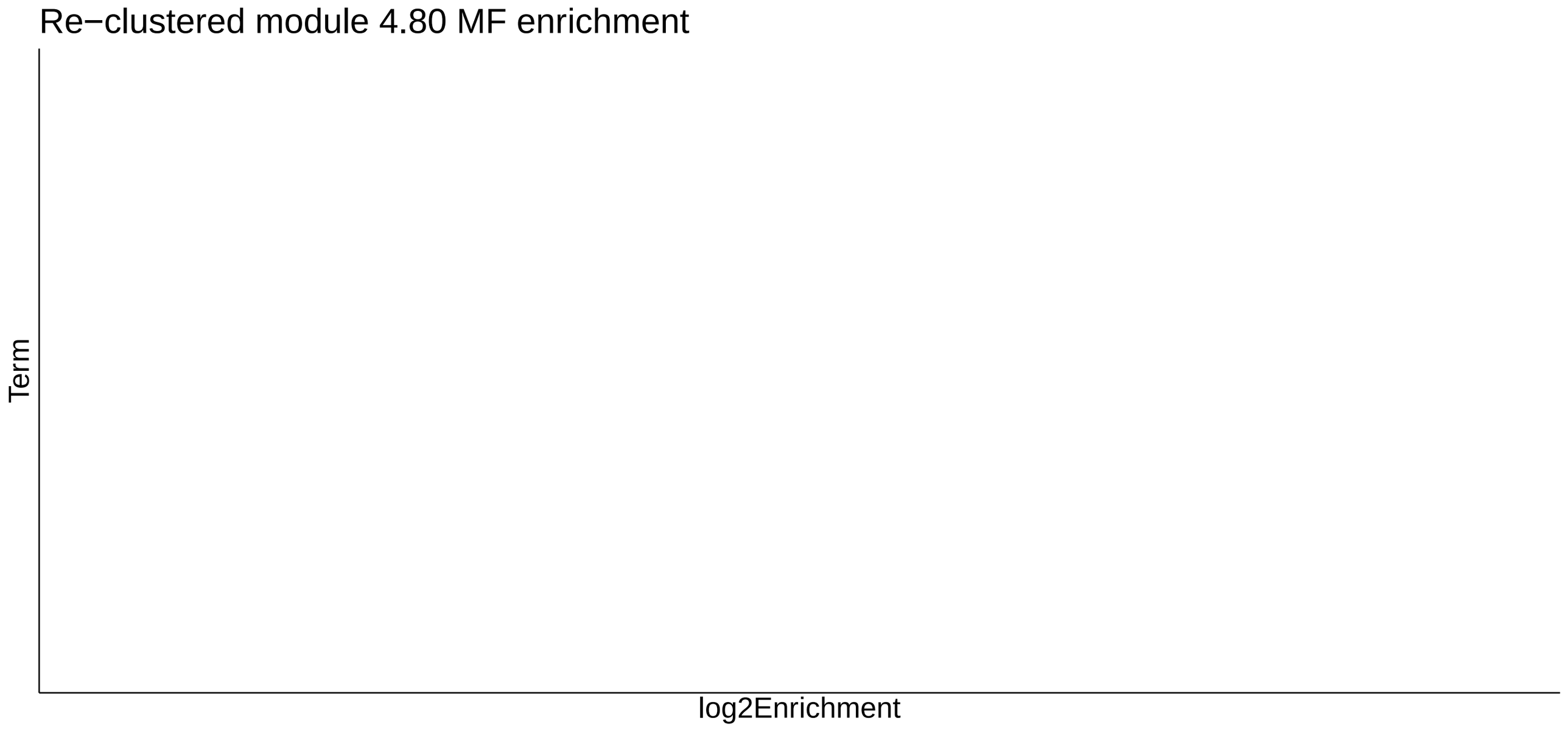

Re−clustered module 4.72 BP enrichment
type B pancreatic cell proliferation
relaxation of muscle
positive regulation of interleukin−2 production
regulation of fatty acid oxidation
regulation of cardiac muscle cell contraction
positive regulation of interferon−gamma production
cellular response to catecholamine stimulus
cellular carbohydrate biosynthetic process
regulation of calcium ion transmembrane transporter activity
neutrophil chemotaxis
transcription initiation from RNA polymerase II promoter
intracellular receptor signaling pathway
regulation of neuron apoptotic process
positive regulation of epithelial cell proliferation
fat cell differentiation
cellular response to peptide hormone stimulus
hexose metabolic process
cellular response to lipid
negative regulation of transcription by RNA polymerase II
Term
0
2
4
6
log2Enrichment

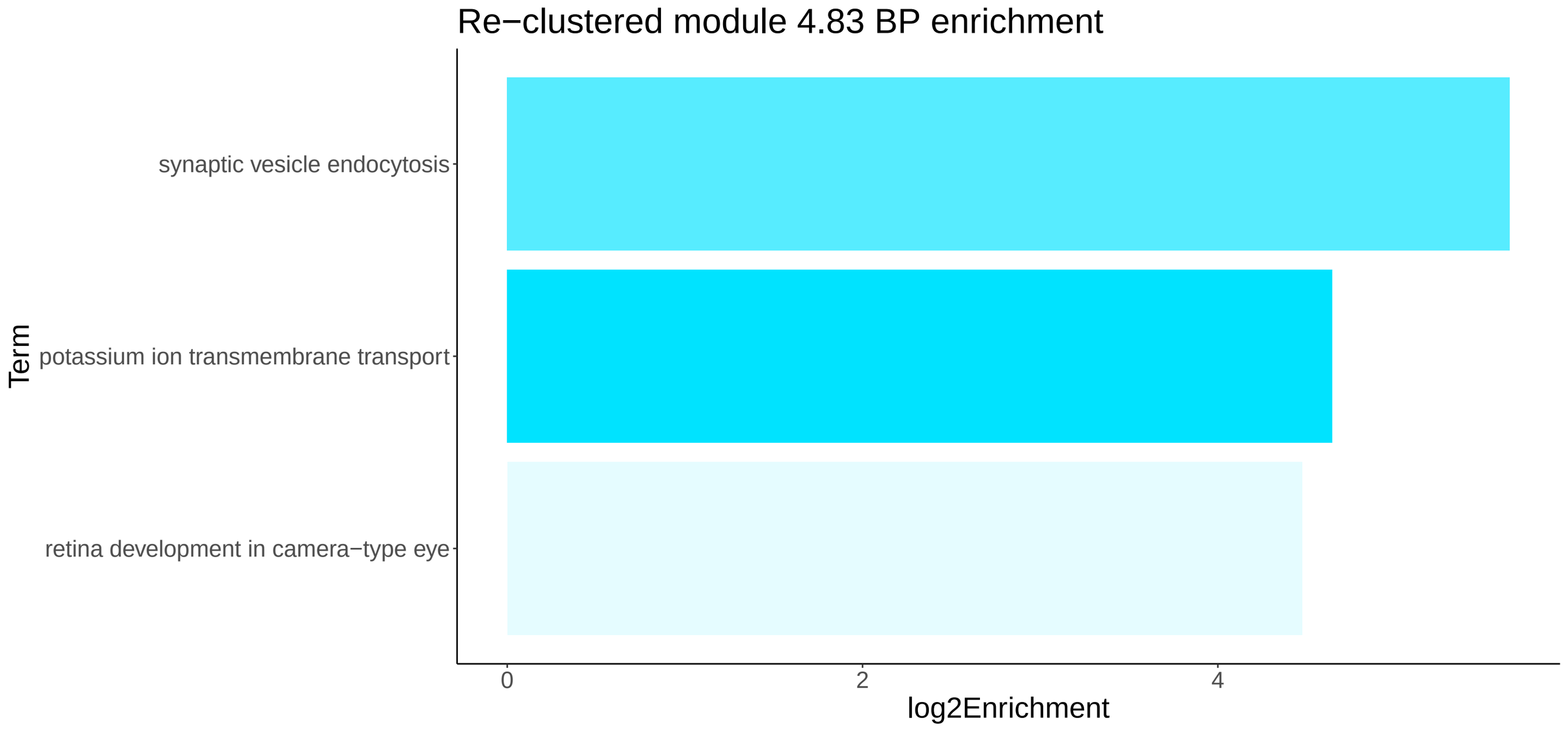

Re−clustered module 4.72 MF enrichment
Term
cAMP binding
transcription cofactor binding
steroid hormone receptor binding
nuclear receptor binding
DNA−binding transcription repressor activity, RNA polymerase II−specific
RNA polymerase II transcription regulatory region sequence−specific DNA binding
metal ion binding
0
2
4
6
log2Enrichment

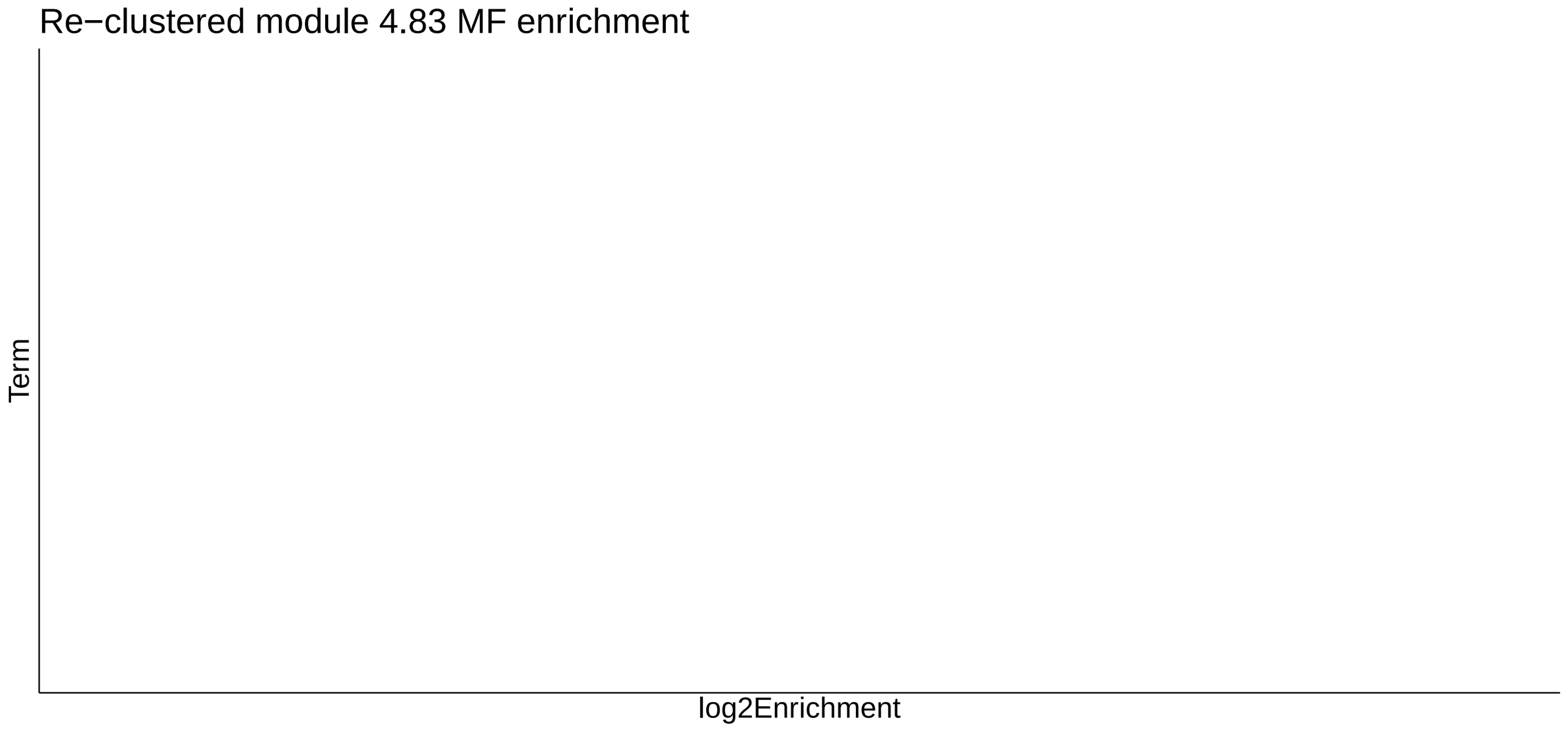

Re−clustered module 4.8 BP enrichment
Term
antibacterial humoral response
inflammatory response to antigenic stimulus
defense response to Gram−positive bacterium
innate immune response
0
1
2
3
4
5
log2Enrichment

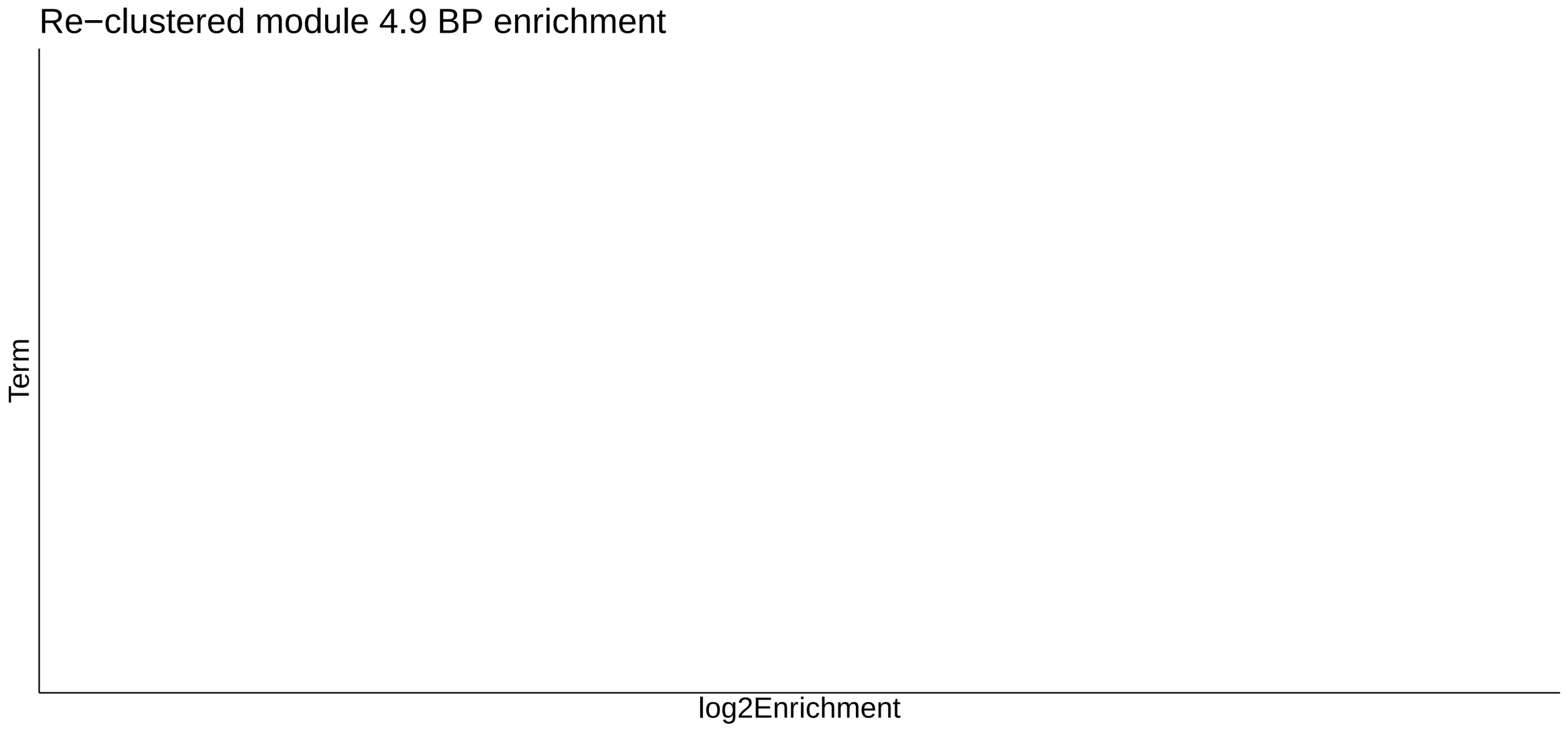

Re−clustered module 4.8 MF enrichment
Term
serine−type endopeptidase inhibitor activity
0
1
2
3
4
log2Enrichment

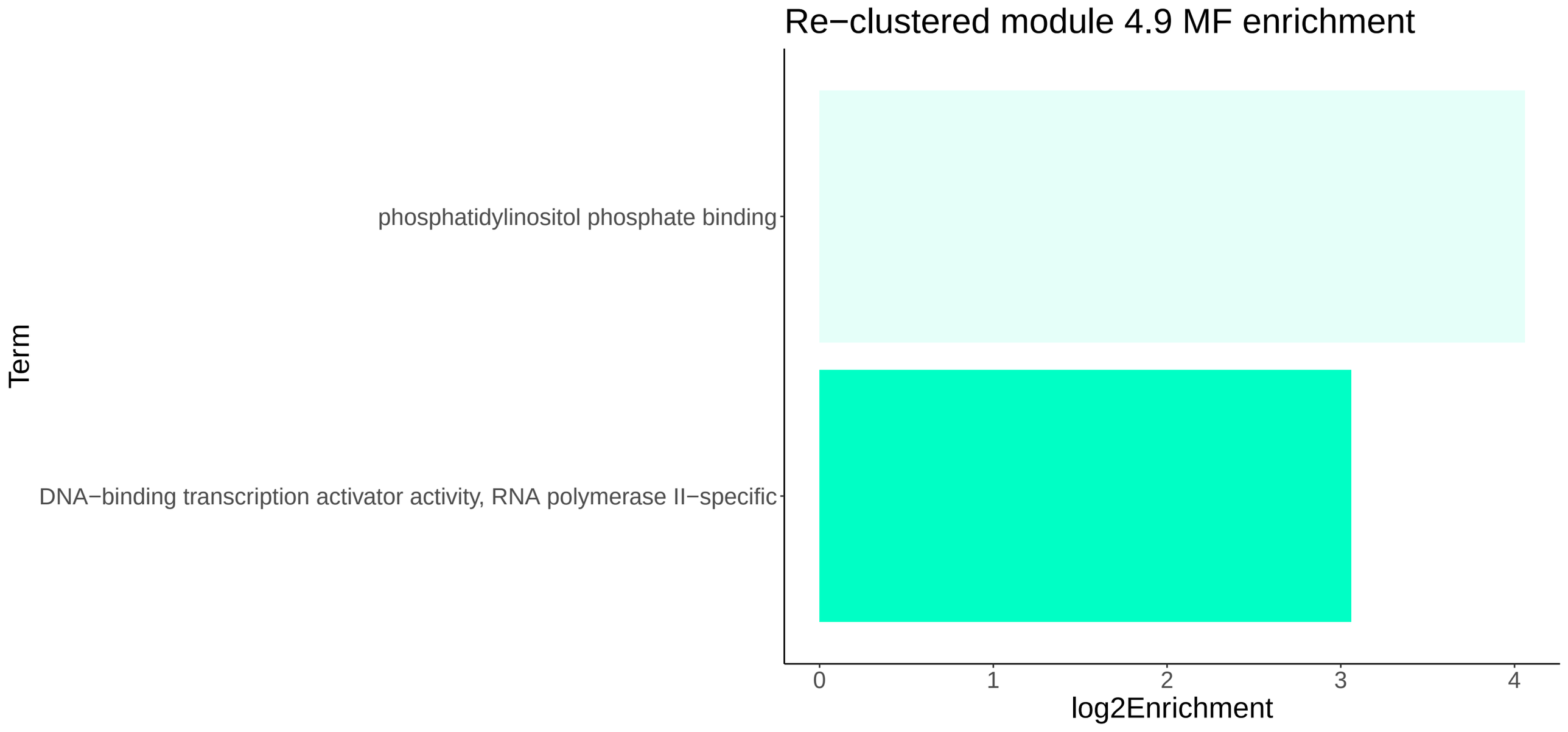

Re−clustered module 4.80 BP enrichment
Term
regulation of postsynaptic membrane potential
0
1
2
3
4
log2Enrichment


Re−clustered module 4.80 MF enrichment
Term
log2Enrichment

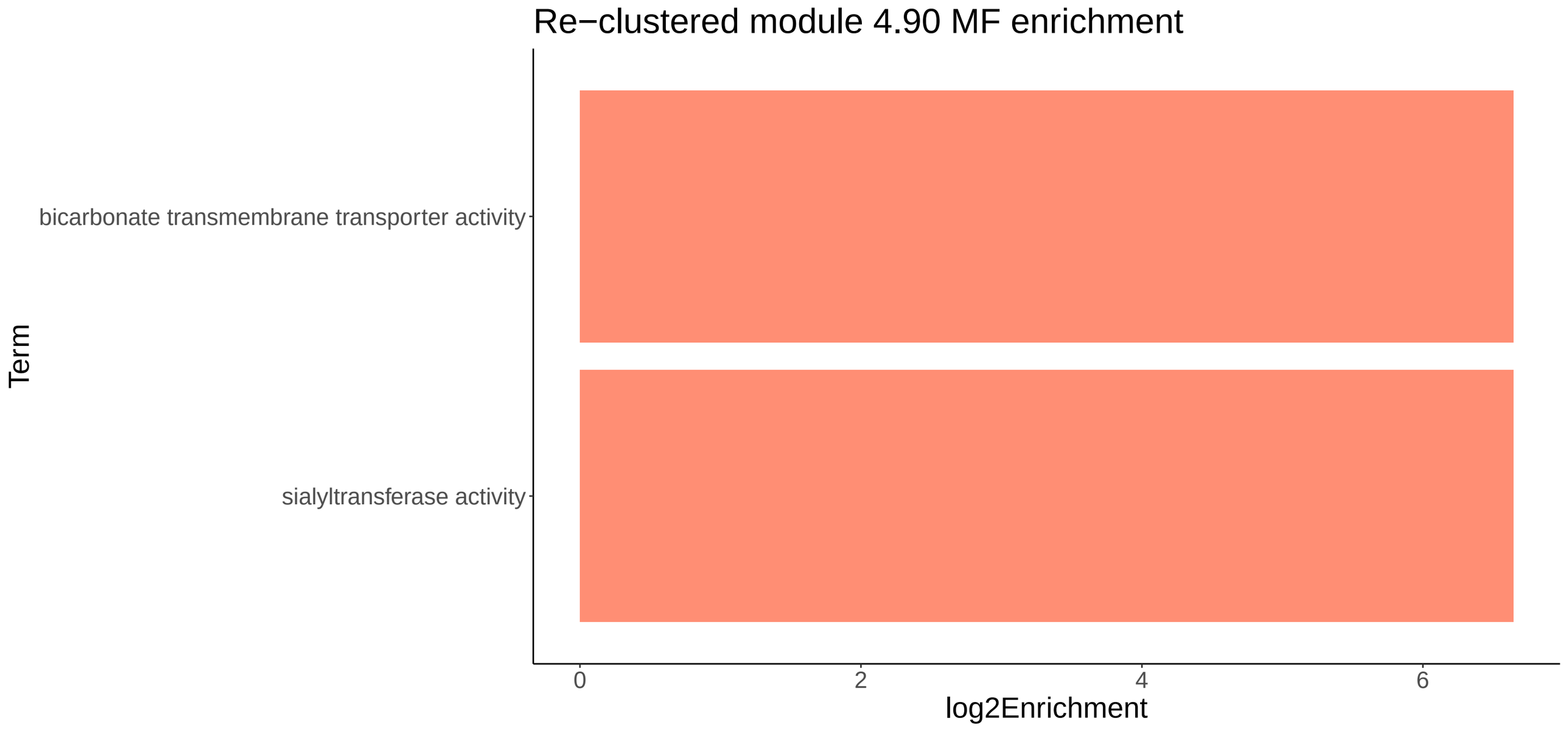

Re−clustered module 4.83 BP enrichment
Term
synaptic vesicle endocytosis
potassium ion transmembrane transport
retina development in camera−type eye
0
2
4
log2Enrichment

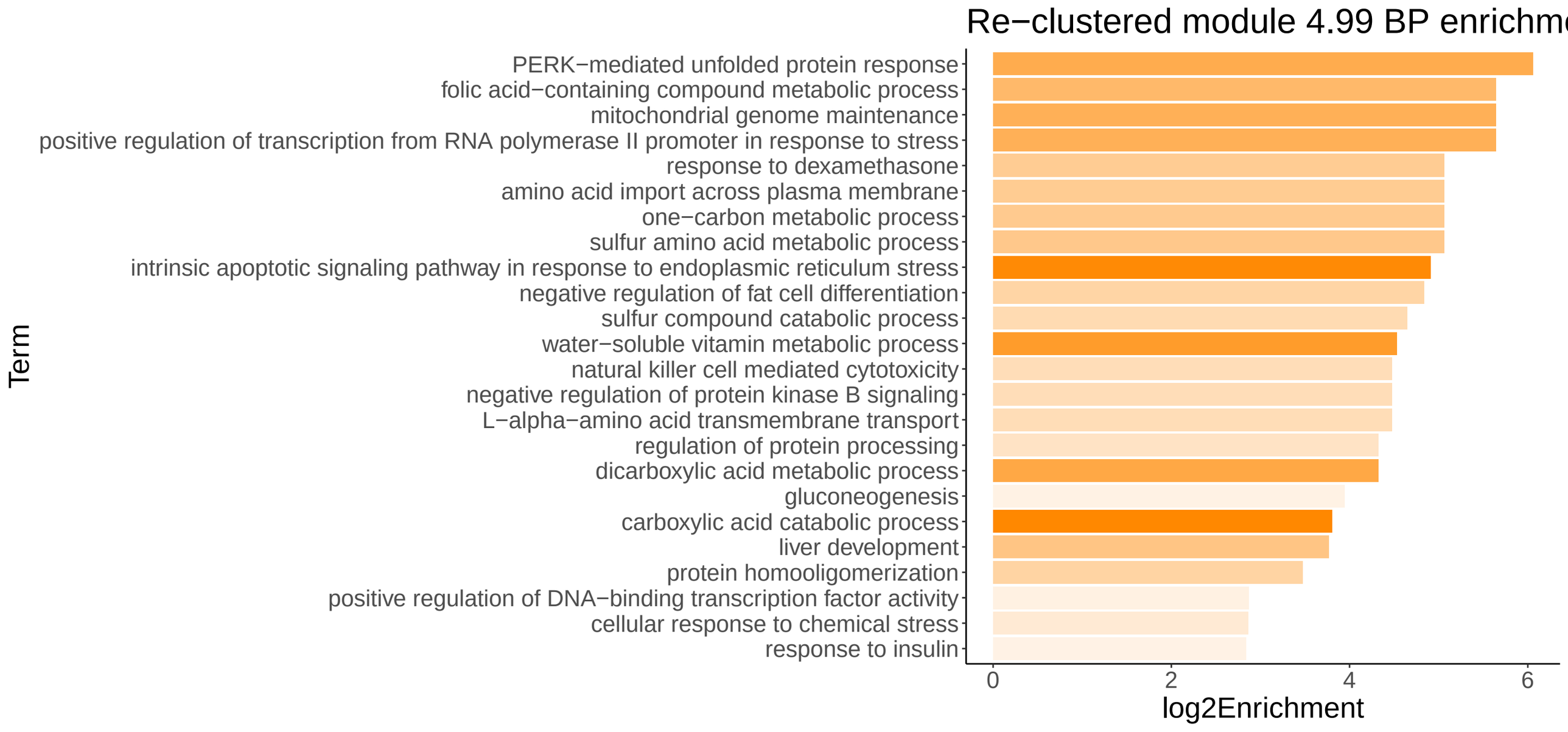

Re−clustered module 4.83 MF enrichment
Term
log2Enrichment

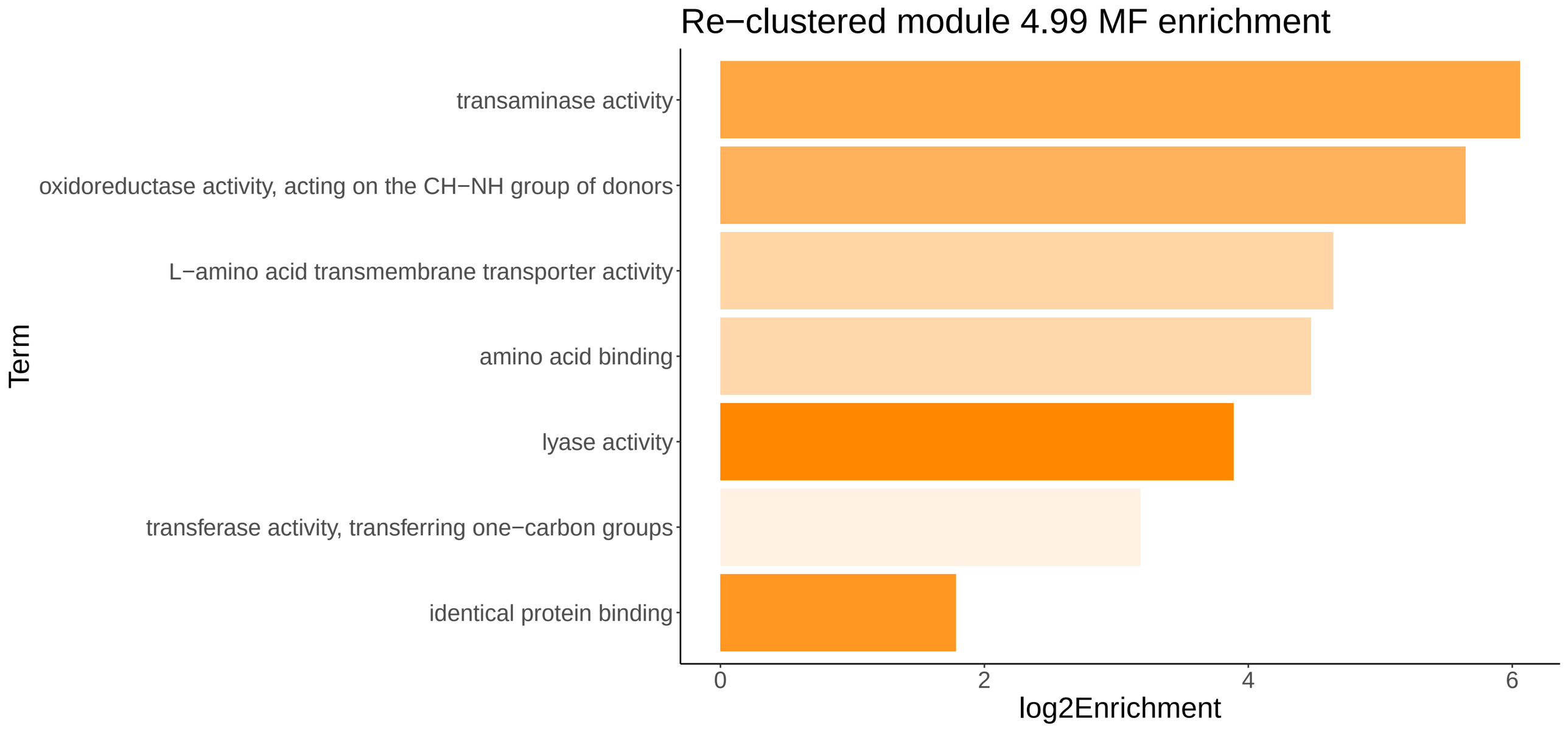

Re−clustered module 4.9 BP enrichment
Term
log2Enrichment


Re−clustered module 4.9 MF enrichment
Term
phosphatidylinositol phosphate binding
DNA−binding transcription activator activity, RNA polymerase II−specific
0
1
2
3
4
log2Enrichment


Re−clustered module 4.90 BP enrichment
outflow tract septum morphogenesis
cerebellar Purkinje cell layer development
cardiac atrium morphogenesis
innervation
pharyngeal system development
positive regulation of neurotransmitter secretion
cerebellar cortex formation
cell differentiation in hindbrain
atrial septum development
cardiac right ventricle morphogenesis
retinal ganglion cell axon guidance
negative regulation of neuron apoptotic process
central nervous system neuron differentiation
Term
0
2
4
6
log2Enrichment


Re−clustered module 4.90 MF enrichment
bicarbonate transmembrane transporter activity
sialyltransferase activity
Term
0
2
4
6
log2Enrichment


Re−clustered module 4.99 BP enrichme
PERK−mediated unfolded protein response
folic acid−containing compound metabolic process
mitochondrial genome maintenance
positive regulation of transcription from RNA polymerase II promoter in response to stress
response to dexamethasone
amino acid import across plasma membrane
one−carbon metabolic process
sulfur amino acid metabolic process
intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress
negative regulation of fat cell differentiation
sulfur compound catabolic process
water−soluble vitamin metabolic process
natural killer cell mediated cytotoxicity
negative regulation of protein kinase B signaling
L−alpha−amino acid transmembrane transport
regulation of protein processing
dicarboxylic acid metabolic process
gluconeogenesis
carboxylic acid catabolic process
liver development
protein homooligomerization
positive regulation of DNA−binding transcription factor activity
cellular response to chemical stress
response to insulin
Term
0
2
4
6
log2Enrichment


Re−clustered module 4.99 MF enrichment
transaminase activity
oxidoreductase activity, acting on the CH−NH group of donors
L−amino acid transmembrane transporter activity
amino acid binding
lyase activity
transferase activity, transferring one−carbon groups
identical protein binding
Term
0
2
4
6
log2Enrichment