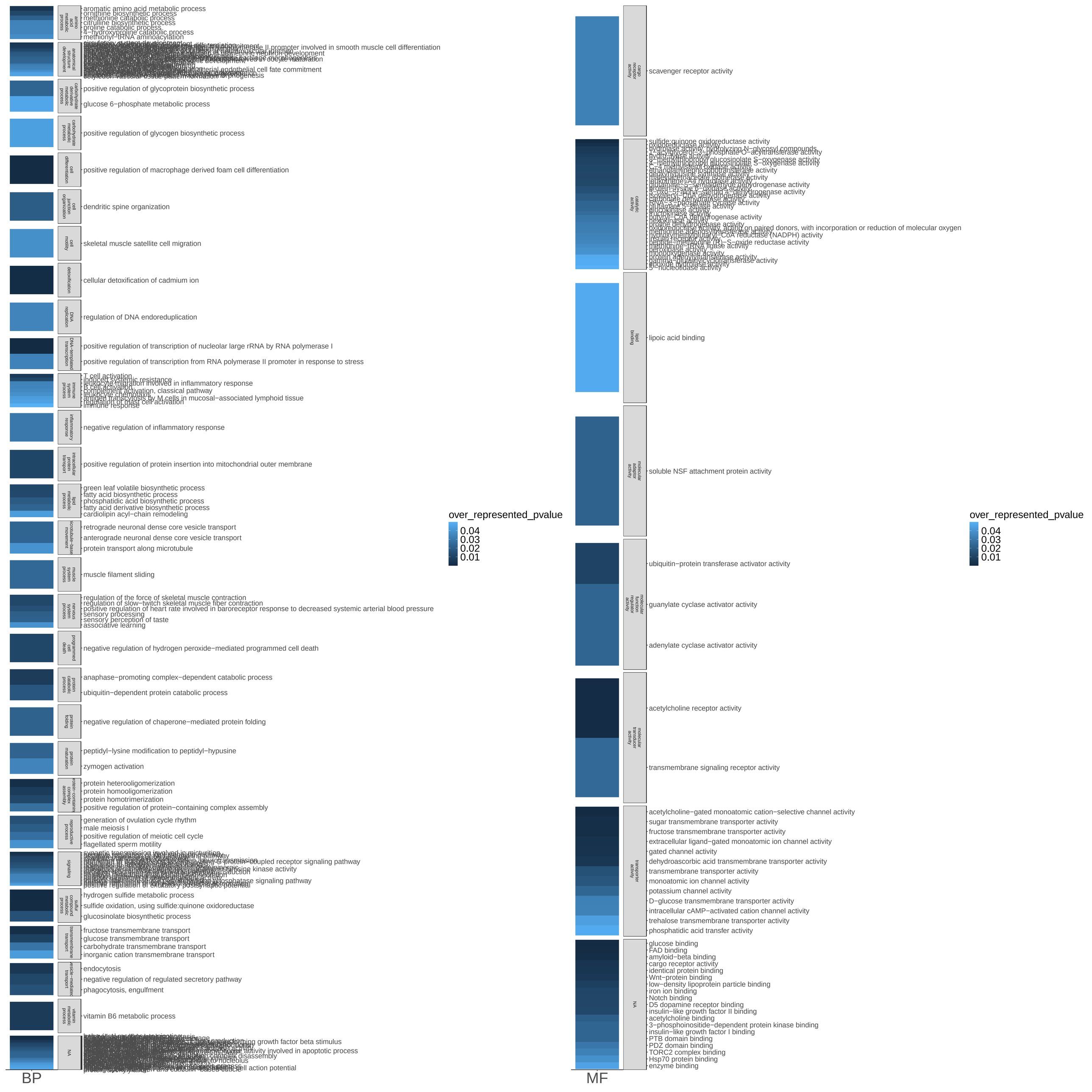
BP
aromatic amino acid metabolic process
ornithine biosynthetic process
methionine catabolic process
citrulline biosynthetic process
proline catabolic process
4−hydroxyproline catabolic process
methionyl−tRNA aminoacylation
anatomical structure development
positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation
metanephric nephron development
oocyte maturation involved in oocyte maturation
arterial endothelial cell fate commitment
carbohydrate derivative metabolic process
positive regulation of glycoprotein biosynthetic process
glucose 6−phosphate metabolic process
carbohydrate metabolic process
positive regulation of glycogen biosynthetic process
cell differentiation
positive regulation of macrophage derived foam cell differentiation
cell junction organization
dendritic spine organization
cell motility
skeletal muscle satellite cell migration
detoxification
cellular detoxification of cadmium ion
DNA replication
regulation of DNA endoreduplication
DNA−templated transcription
positive regulation of transcription of nucleolar large rRNA by RNA polymerase I
positive regulation of transcription from RNA polymerase II promoter in response to stress
immune system process
T cell activation
innate immune response
leukocyte migration involved in inflammatory response
B cell activation
complement activation, classical pathway
leukocyte chemotaxis
antigen transcytosis by M cells in mucosal−associated lymphoid tissue
regulation of mast cell activation
immune response
inflammatory response
negative regulation of inflammatory response
intracellular protein transport
positive regulation of protein insertion into mitochondrial outer membrane
lipid metabolic process
green leaf volatile biosynthetic process
fatty acid biosynthetic process
phosphatidic acid biosynthetic process
fatty acid derivative biosynthetic process
cardiolipin acyl−chain remodeling
microtubule−based movement
retrograde neuronal dense core vesicle transport
anterograde neuronal dense core vesicle transport
protein transport along microtubule
muscle system process
muscle filament sliding
nervous system process
regulation of the force of skeletal muscle contraction
regulation of slow−twitch skeletal muscle fiber contraction
positive regulation of heart rate involved in baroreceptor response to decreased systemic arterial blood pressure
sensory processing
sensory perception of taste
associative learning
programmed cell death
negative regulation of hydrogen peroxide−mediated programmed cell death
protein catabolic process
anaphase−promoting complex−dependent catabolic process
ubiquitin−dependent protein catabolic process
protein folding
negative regulation of chaperone−mediated protein folding
protein maturation
peptidyl−lysine modification to peptidyl−hypusine
zymogen activation
protein−containing complex assembly
protein heterooligomerization
protein homooligomerization
protein homotrimerization
positive regulation of protein−containing complex assembly
reproductive process
generation of ovulation cycle rhythm
male meiosis I
positive regulation of meiotic cell cycle
flagellated sperm motility
signaling
sulfur compound metabolic process
hydrogen sulfide metabolic process
sulfide oxidation, using sulfide:quinone oxidoreductase
glucosinolate biosynthetic process
transmembrane transport
fructose transmembrane transport
glucose transmembrane transport
carbohydrate transmembrane transport
inorganic cation transmembrane transport
vesicle−mediated transport
endocytosis
negative regulation of regulated secretory pathway
phagocytosis, engulfment
vitamin metabolic process
vitamin B6 metabolic process
NA
MF
cargo receptor activity
scavenger receptor activity
catalytic activity
sulfide:quinone oxidoreductase activity
oxidoreductase activity
1−acylglycerol−3−phosphate O−acyltransferase activity
hydro−lyase activity
2−hydroxyethanesulfonate sulfotransferase activity
deoxyhypusine synthase activity
malate dehydrogenase (decarboxylating) (NADP+) activity
glutamate−5−semialdehyde dehydrogenase activity
protein−lysine 6−oxidase activity
3−oxo−5−alpha−steroid 4−dehydrogenase activity
acyl−CoA dehydrogenase activity
carbonate dehydratase activity
cAMP−dependent protein kinase activity
glutamate 5−kinase activity
glucokinase activity
fructokinase activity
butyryl−CoA dehydrogenase activity
hexokinase activity
proline dehydrogenase activity
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
methionine adenosyltransferase activity
cytochrome−b5 reductase activity, acting on NAD(P)H
insulin receptor activity
peptide−methionine (R)−S−oxide reductase activity
methionine−tRNA ligase activity
deoxidase activity
monooxygenase activity
protein adenylyltransferase activity
gamma−glutamyltransferase activity
peroxide hydrolase activity
5'−nucleotidase activity
lipid binding
lipoic acid binding
molecular adaptor activity
soluble NSF attachment protein activity
molecular function regulator activity
ubiquitin−protein transferase activator activity
guanylate cyclase activator activity
adenylate cyclase activator activity
molecular transducer activity
acetylcholine receptor activity
transmembrane signaling receptor activity
transporter activity
acetylcholine−gated monoatomic cation−selective channel activity
sugar transmembrane transporter activity
fructose transmembrane transporter activity
extracellular ligand−gated monoatomic ion channel activity
gated channel activity
dehydroascorbic acid transmembrane transporter activity
transmembrane transporter activity
monoatomic ion channel activity
potassium channel activity
D−glucose transmembrane transporter activity
intracellular cAMP−activated cation channel activity
trehalose transmembrane transporter activity
phosphatidic acid transfer activity
NA
glucose binding
FAD binding
amyloid−beta binding
cargo receptor activity
identical protein binding
Wnt−protein binding
low−density lipoprotein particle binding
iron ion binding
Notch binding
D5 dopamine receptor binding
insulin−like growth factor II binding
acetylcholine binding
3−phosphoinositide−dependent protein kinase binding
insulin−like growth factor I binding
PTB domain binding
PDZ domain binding
TORC2 complex binding
Hsp70 protein binding
enzyme binding
over_represented_pvalue
0.04
0.03
0.02
0.01