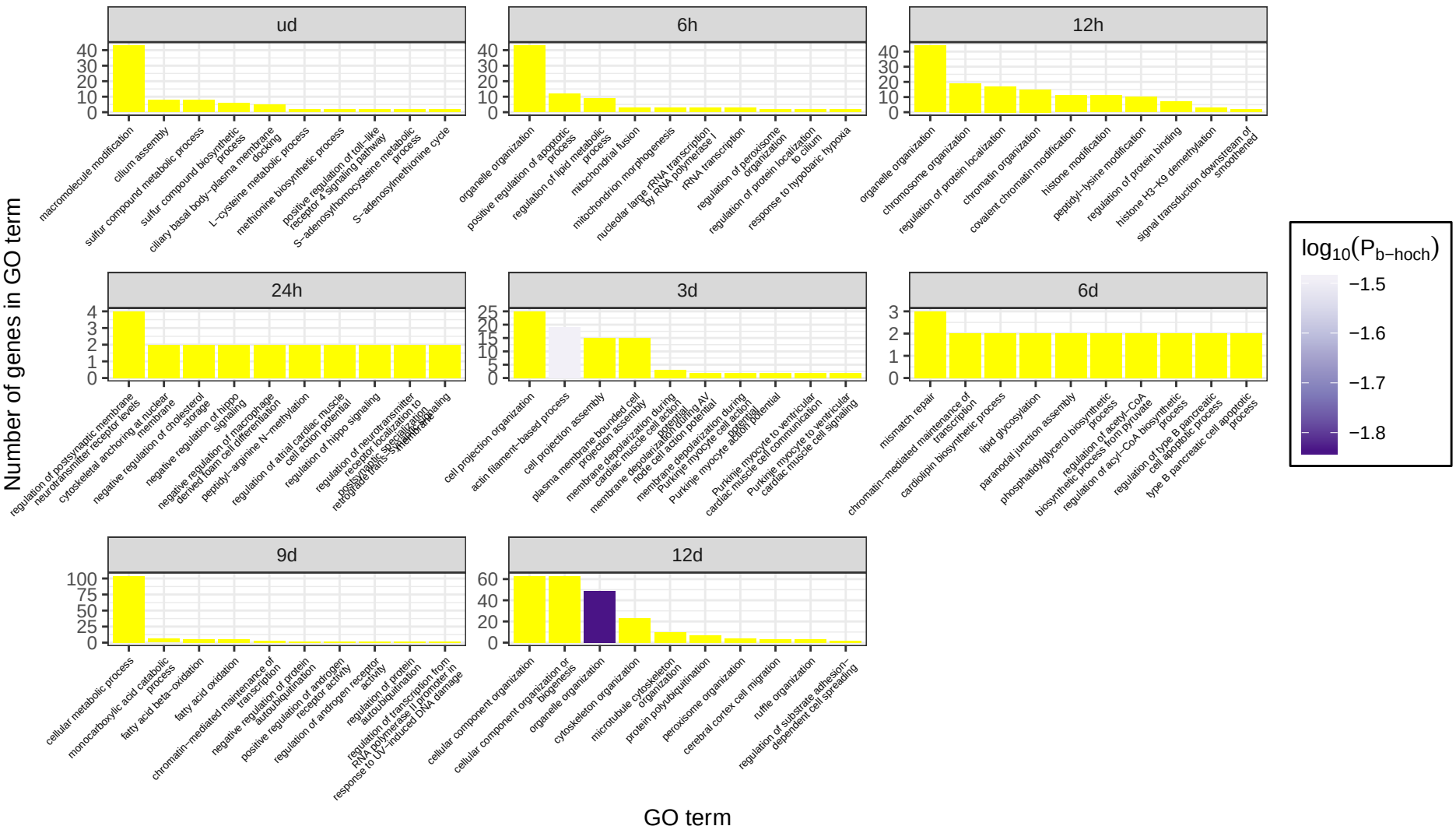
Top 10 significantly over−represented BP GO terms for the H0.1L0.1 lowest_PSI exons in each OB timepoint
ud
6h
12h
24h
3d
6d
9d
12d
Number of genes in GO term
GO term
log10(Pb−hoch)
−1.5
−1.6
−1.7
−1.8
macromolecule modification
cilium assembly
sulfur compound metabolic process
sulfur compound biosynthetic process
ciliary basal body−plasma membrane docking
L−cysteine metabolic process
methionine biosynthetic process
positive regulation of toll−like receptor 4 signaling pathway
S−adenosylhomocysteine metabolic process
S−adenosylmethionine cycle
organelle organization
positive regulation of apoptotic process
regulation of lipid metabolic process
mitochondrial fusion
mitochondrion morphogenesis
nucleolar large rRNA transcription by RNA polymerase I
rRNA transcription
regulation of peroxisome organization
regulation of protein localization to cilium
response to hypobaric hypoxia
organelle organization
chromosome organization
regulation of protein localization
chromatin organization
covalent chromatin modification
histone modification
peptidyl−lysine modification
regulation of protein binding
histone H3−K9 demethylation
signal transduction downstream of smoothened
regulation of postsynaptic membrane neurotransmitter receptor levels
cytoskeletal anchoring at nuclear membrane
negative regulation of cholesterol storage
negative regulation of hippo signaling
negative regulation of macrophage derived foam cell differentiation
peptidyl−arginine N−methylation
regulation of atrial cardiac muscle cell action potential
regulation of hippo signaling
regulation of neurotransmitter receptor localization to postsynaptic specialization
retrograde trans−synaptic signaling
cell projection organization
actin filament−based process
cell projection assembly
plasma membrane bounded cell projection assembly
membrane depolarization during cardiac muscle cell action potential
membrane depolarization during AV node cell action potential
membrane depolarization during Purkinje myocyte cell action potential
Purkinje myocyte to ventricular cardiac muscle cell communication
Purkinje myocyte to ventricular cardiac muscle cell signalling
mismatch repair
chromatin−mediated maintenance of transcription
cardiolipin biosynthetic process
lipid glycosylation
paranodal junction assembly
phosphatidylglycerol biosynthetic process
regulation of acetyl−CoA biosynthetic process from pyruvate
regulation of acyl−CoA biosynthetic process
regulation of type B pancreatic cell apoptotic process
type B pancreatic cell apoptotic process
cellular metabolic process
monocarboxylic acid catabolic process
fatty acid beta−oxidation
fatty acid oxidation
chromatin−mediated maintenance of transcription
negative regulation of protein autoubiquitination
positive regulation of androgen receptor activity
regulation of androgen receptor activity
regulation of protein autoubiquitination
regulation of transcription from RNA polymerase II promoter in response to UV−induced DNA damage
cellular component organization
cellular component organization or biogenesis
organelle organization
cytoskeleton organization
microtubule cytoskeleton organization
protein polyubiquitination
peroxisome organization
cerebral cortex cell migration
ruffle organization
regulation of substrate adhesion−dependent cell spreading