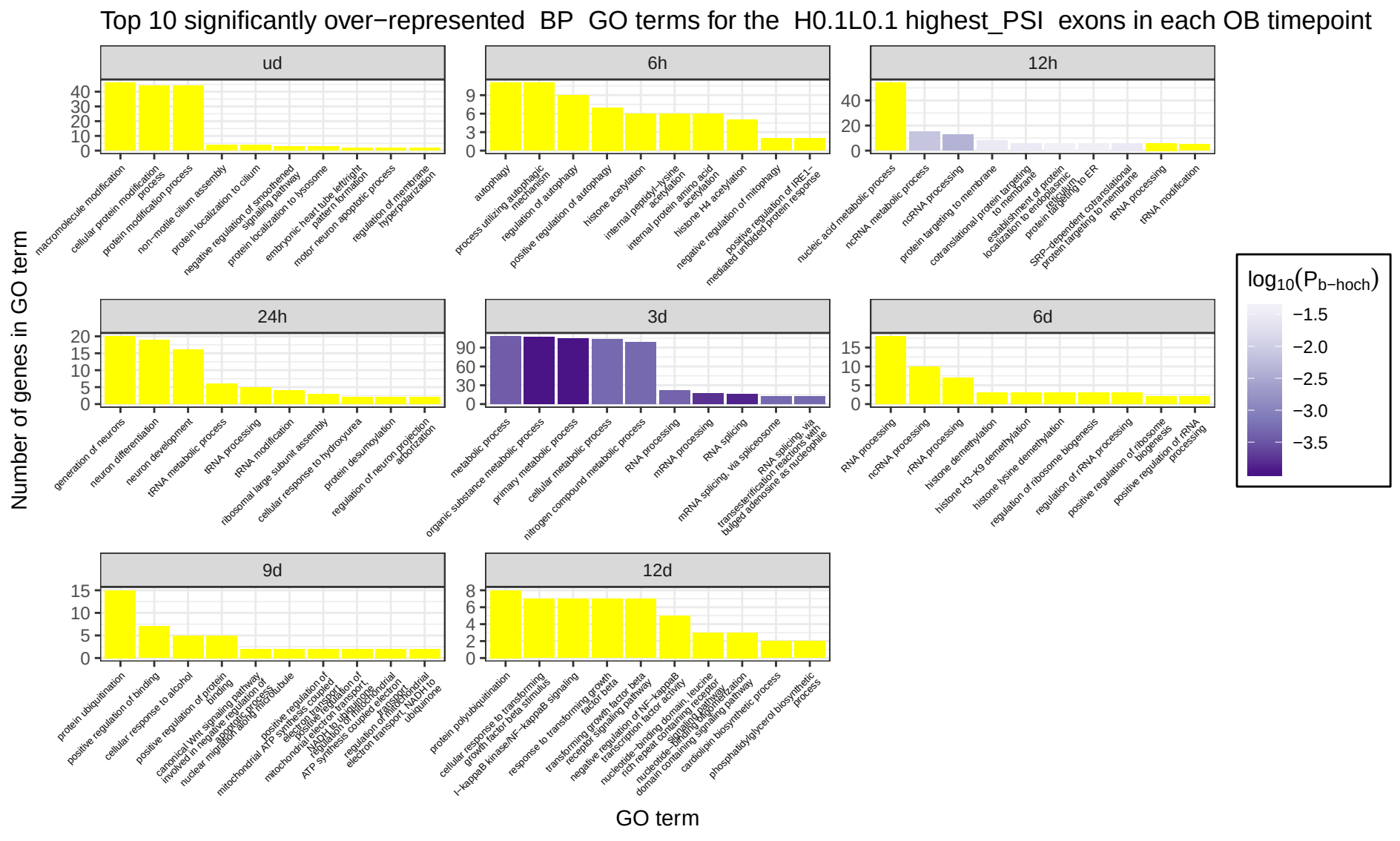
Top 10 significantly over−represented BP GO terms for the H0.1L0.1 highest_PSI exons in each OB timepoint
ud
6h
12h
24h
3d
6d
9d
12d
Number of genes in GO term
GO term
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0
−3.5
macromolecule modification
cellular protein modification process
protein modification process
non−motile cilium assembly
protein localization to cilium
negative regulation of smoothened signaling pathway
protein localization to lysosome
embryonic heart tube left/right pattern formation
motor neuron apoptotic process
regulation of membrane hyperpolarization
autophagy
process utilizing autophagic mechanism
regulation of autophagy
positive regulation of autophagy
histone acetylation
internal peptidyl−lysine acetylation
internal protein amino acid acetylation
histone H4 acetylation
negative regulation of mitophagy
positive regulation of IRE1−mediated unfolded protein response
nucleic acid metabolic process
ncRNA metabolic process
ncRNA processing
protein targeting to membrane
cotranslational protein targeting to membrane
establishment of protein localization to endoplasmic reticulum
protein targeting to ER
SRP−dependent cotranslational protein targeting to membrane
tRNA processing
tRNA modification
generation of neurons
neuron differentiation
neuron development
tRNA metabolic process
tRNA processing
tRNA modification
ribosomal large subunit assembly
cellular response to hydroxyurea
protein desumoylation
regulation of neuron projection arborization
metabolic process
organic substance metabolic process
primary metabolic process
cellular metabolic process
nitrogen compound metabolic process
RNA processing
mRNA processing
RNA splicing
mRNA splicing, via spliceosome
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
RNA processing
ncRNA processing
rRNA processing
histone demethylation
histone H3−K9 demethylation
histone lysine demethylation
regulation of ribosome biogenesis
regulation of rRNA processing
positive regulation of ribosome biogenesis
positive regulation of rRNA processing
protein ubiquitination
positive regulation of binding
cellular response to alcohol
positive regulation of protein binding
canonical Wnt signaling pathway involved in negative regulation of apoptotic process
nuclear migration along microtubule
positive regulation of electron transport, NADH to ubiquinone
mitochondrial ATP synthesis coupled electron transport
mitochondrial electron transport, NADH to ubiquinone
regulation of mitochondrial ATP synthesis coupled electron transport
regulation of mitochondrial electron transport, NADH to ubiquinone
protein polyubiquitination
cellular response to transforming growth factor beta stimulus
I−kappaB kinase/NF−kappaB signaling
response to transforming growth factor beta
transforming growth factor beta receptor signaling pathway
negative regulation of NF−kappaB transcription factor activity
nucleotide−binding domain, leucine rich repeat containing receptor signaling pathway
nucleotide−binding oligomerization domain containing signaling pathway
cardiolipin biosynthetic process
phosphatidylglycerol biosynthetic process