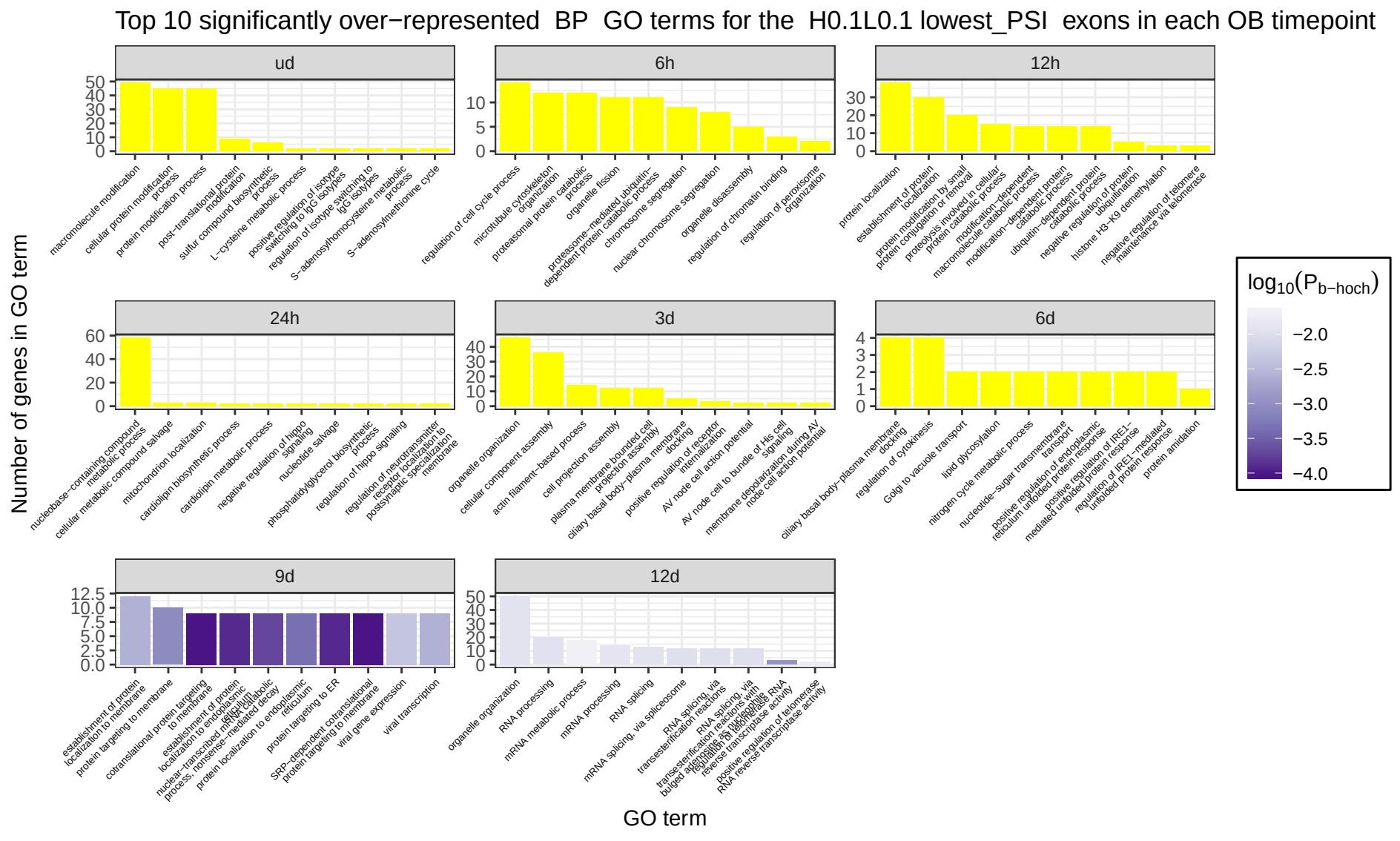
Top 10 significantly over−represented BP GO terms for the H0.1L0.1 lowest_PSI exons in each OB timepoint
ud
6h
12h
24h
3d
6d
9d
12d
Number of genes in GO term
GO term
log10(Pb−hoch)
−2.0
−2.5
−3.0
−3.5
−4.0
macromolecule modification
cellular protein modification process
protein modification process
post−translational protein modification
sulfur compound biosynthetic process
L−cysteine metabolic process
positive regulation of isotype switching to IgG isotypes
regulation of isotype switching to IgG isotypes
S−adenosylhomocysteine metabolic process
S−adenosylmethionine cycle
regulation of cell cycle process
microtubule cytoskeleton organization
proteasomal protein catabolic process
organelle fission
proteasome−mediated ubiquitin−dependent protein catabolic process
chromosome segregation
nuclear chromosome segregation
organelle disassembly
regulation of chromatin binding
regulation of peroxisome organization
protein localization
establishment of protein localization
protein modification by small protein conjugation or removal
proteolysis involved in cellular protein catabolic process
modification−dependent macromolecule catabolic process
modification−dependent protein catabolic process
ubiquitin−dependent protein catabolic process
negative regulation of protein ubiquitination
histone H3−K9 demethylation
negative regulation of telomere maintenance via telomerase
nucleobase−containing compound metabolic process
cellular metabolic compound salvage
mitochondrion localization
cardiolipin biosynthetic process
cardiolipin metabolic process
negative regulation of hippo signaling
nucleotide salvage
phosphatidylglycerol biosynthetic process
regulation of hippo signaling
regulation of neurotransmitter receptor localization to postsynaptic specialization membrane
organelle organization
cellular component assembly
actin filament−based process
cell projection assembly
plasma membrane bounded cell projection assembly
ciliary basal body−plasma membrane docking
positive regulation of receptor internalization
AV node cell action potential
AV node cell to bundle of His cell signaling
membrane depolarization during AV node cell action potential
ciliary basal body−plasma membrane docking
regulation of cytokinesis
Golgi to vacuole transport
lipid glycosylation
nitrogen cycle metabolic process
nucleotide−sugar transmembrane transport
positive regulation of endoplasmic reticulum unfolded protein response
positive regulation of IRE1−mediated unfolded protein response
regulation of IRE1−mediated unfolded protein response
protein amidation
establishment of protein localization to membrane
protein targeting to membrane
cotranslational protein targeting to membrane
establishment of protein localization to endoplasmic reticulum
nuclear−transcribed mRNA catabolic process, nonsense−mediated decay
protein localization to endoplasmic reticulum
protein targeting to ER
SRP−dependent cotranslational protein targeting to membrane
viral gene expression
viral transcription
organelle organization
RNA processing
mRNA metabolic process
mRNA processing
RNA splicing
mRNA splicing, via spliceosome
RNA splicing, via transesterification reactions
RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
RNA splicing
regulation of telomerase activity
positive regulation of telomerase activity
RNA reverse transcriptase activity