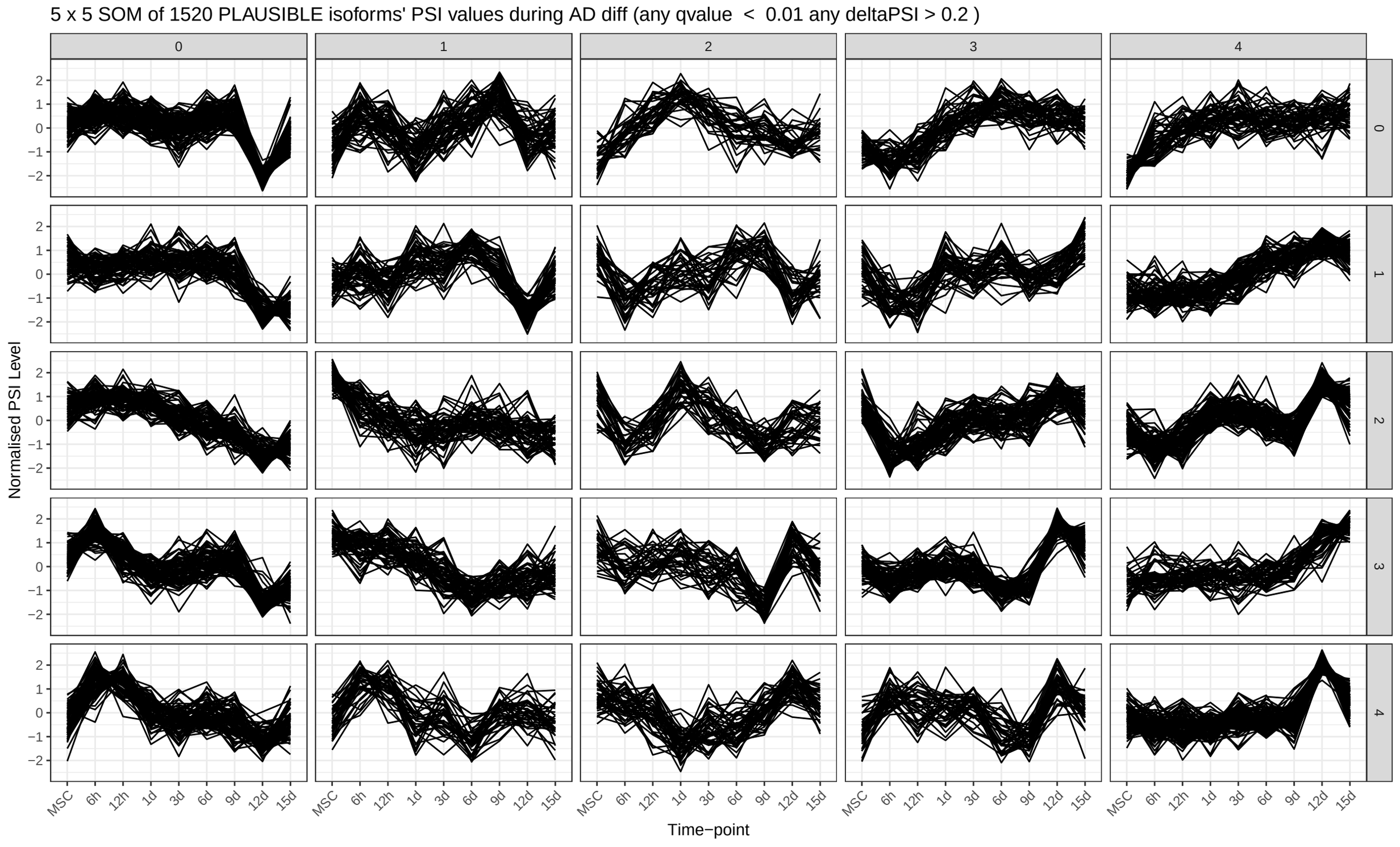
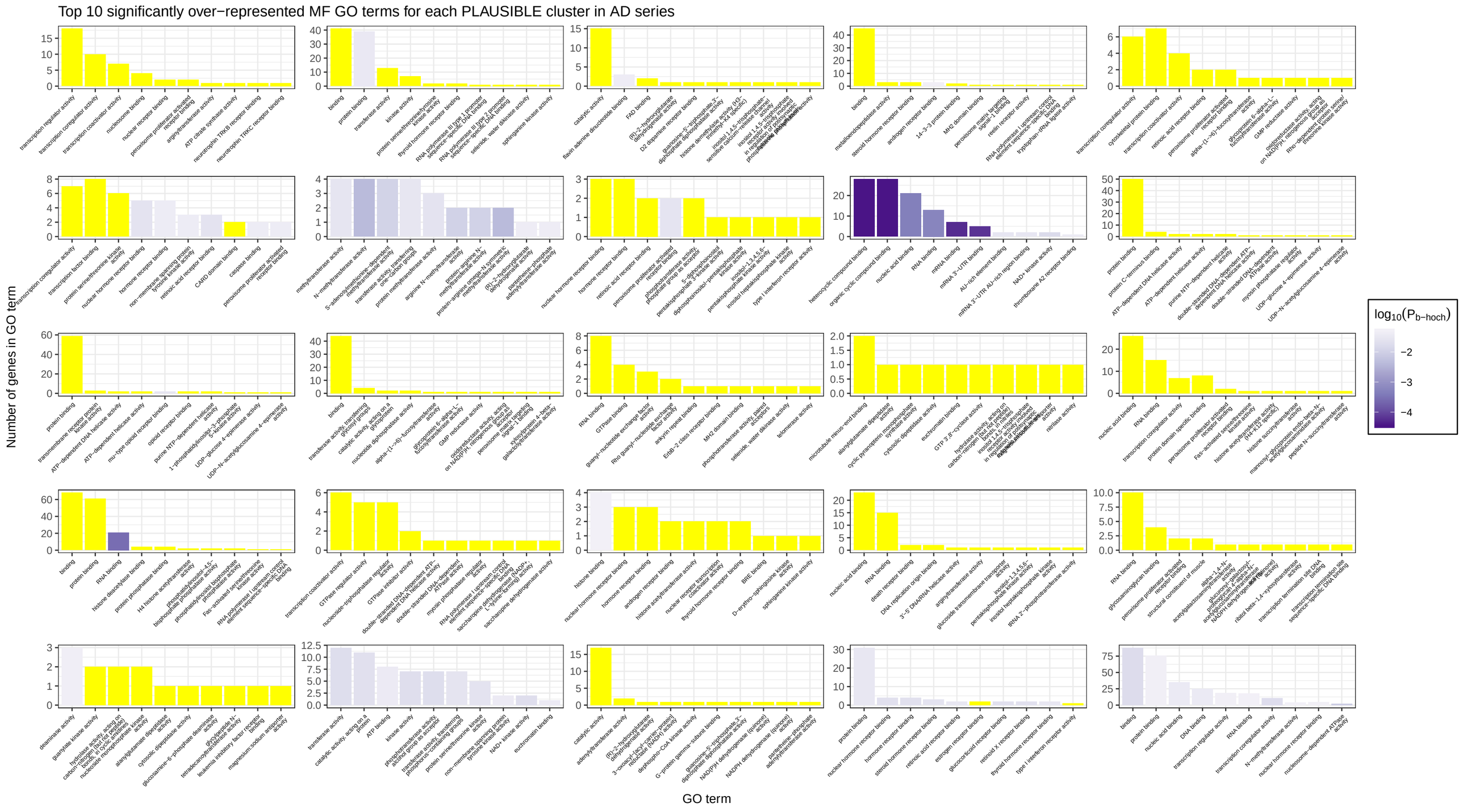
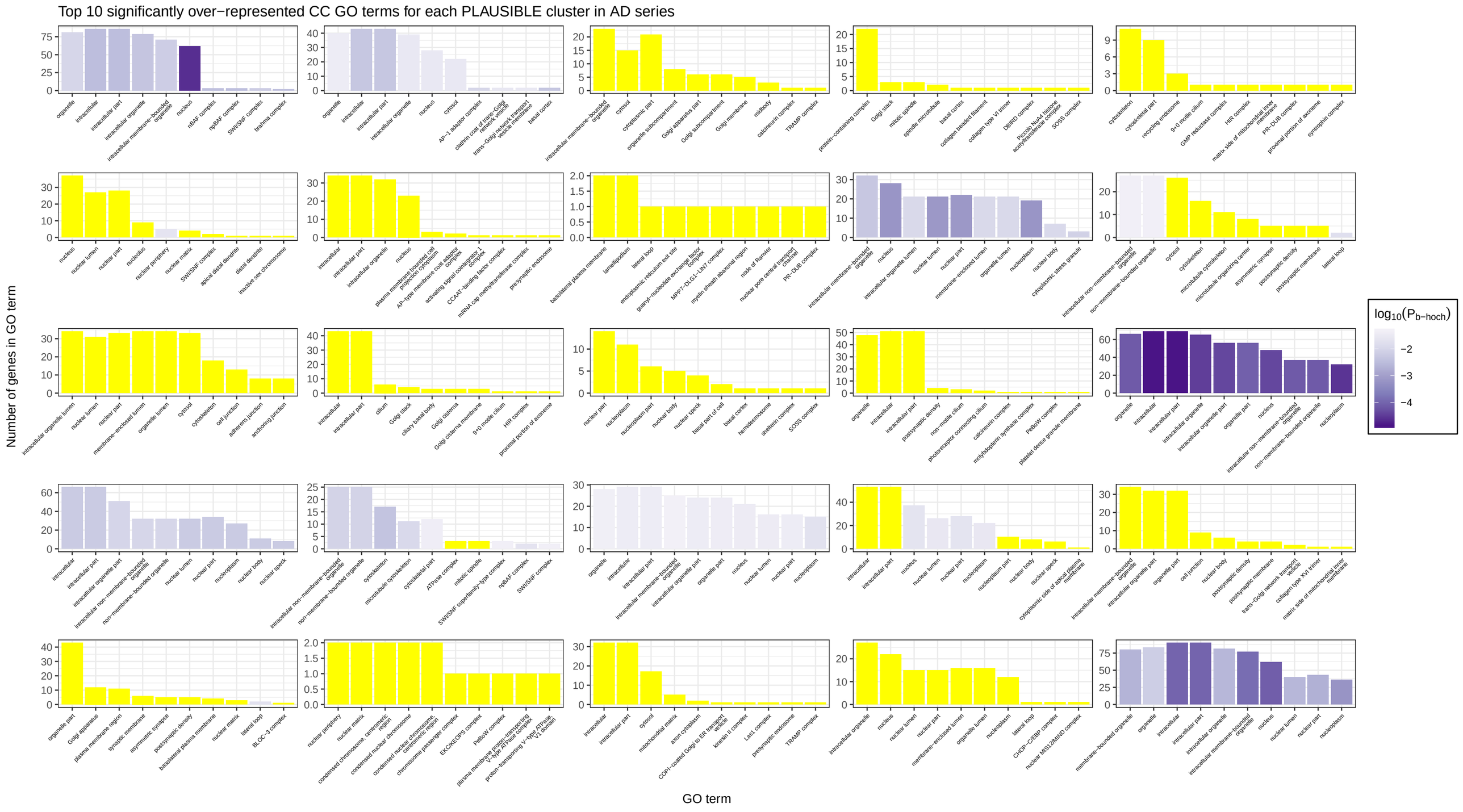
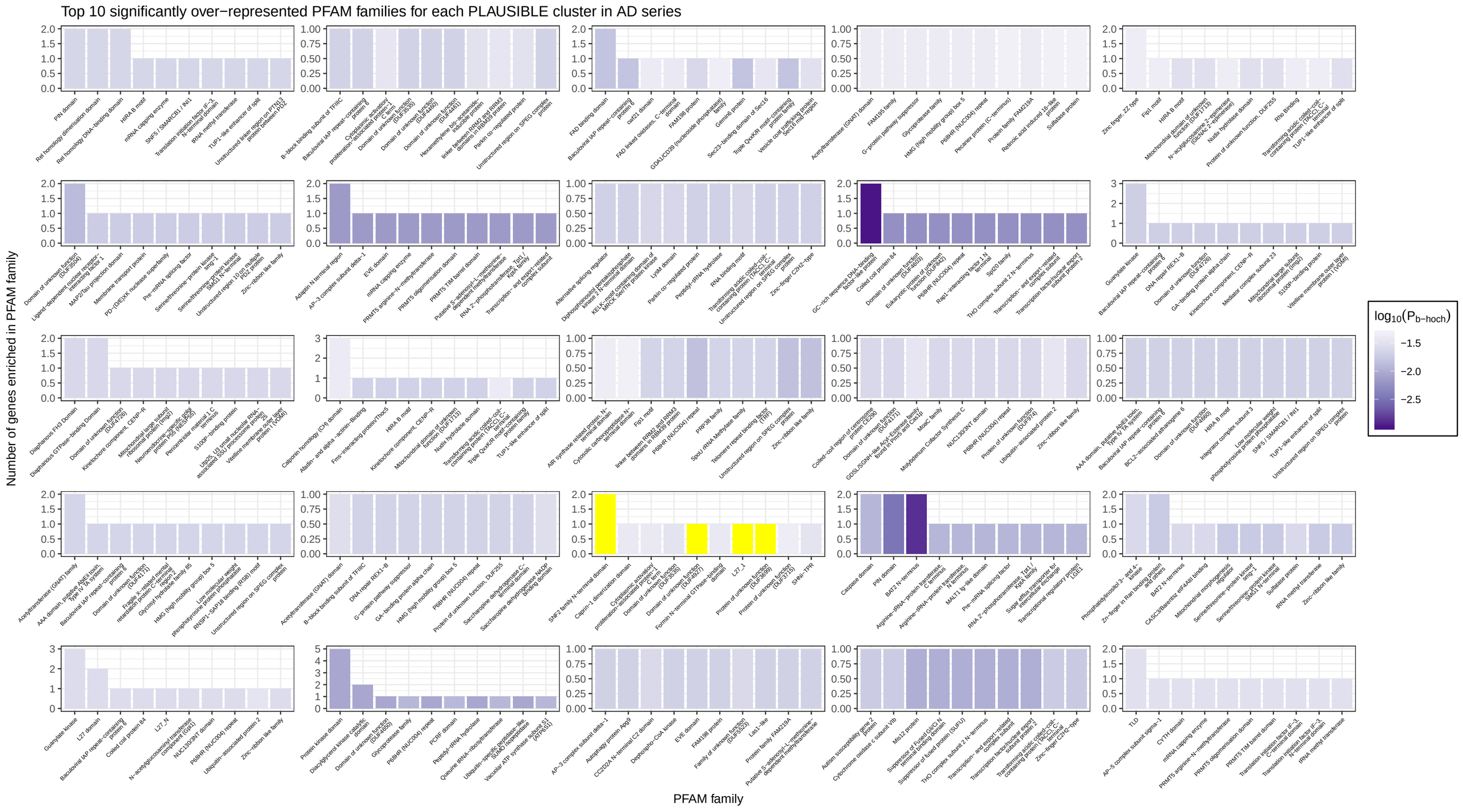
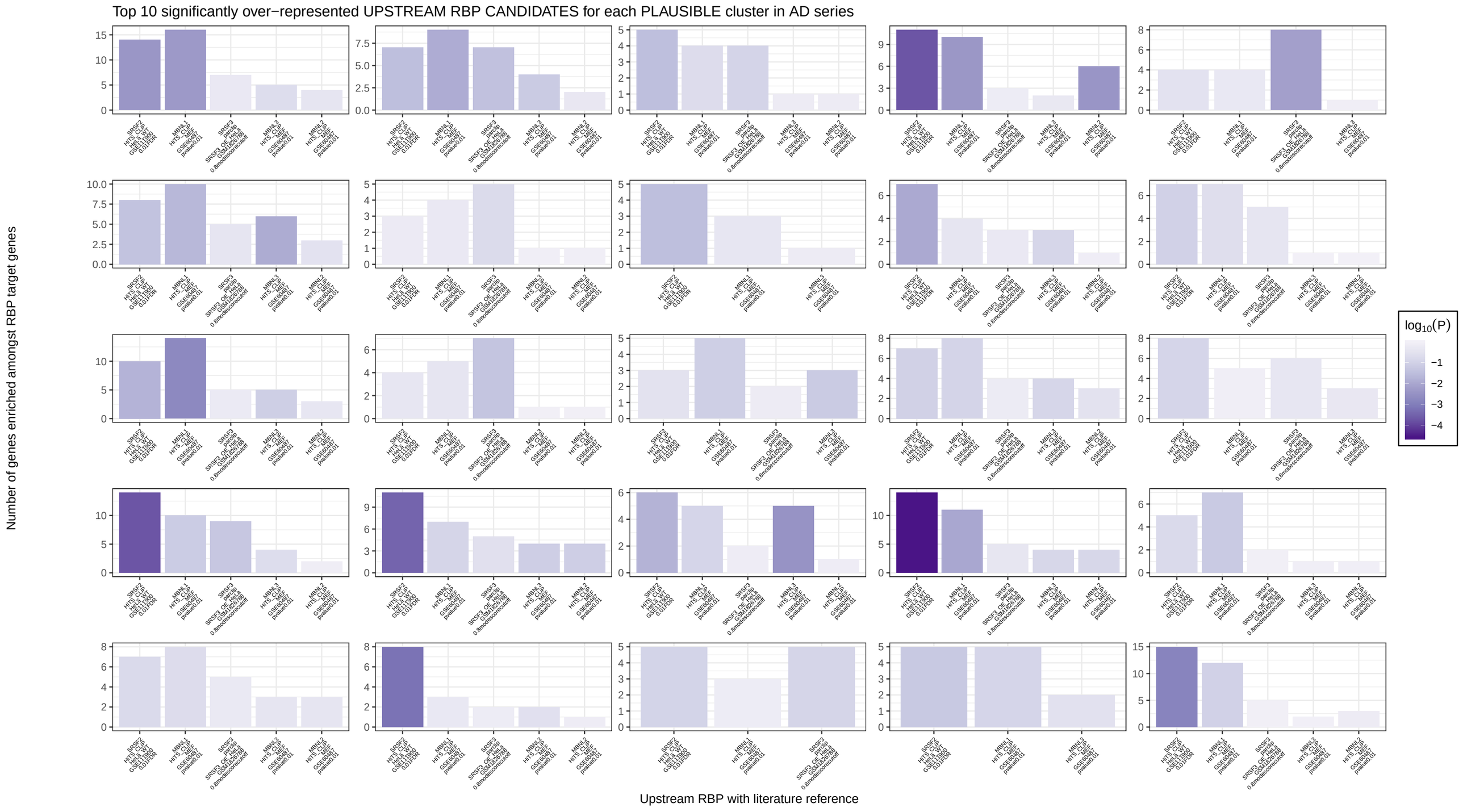

5 x 5 SOM of 1520 PLAUSIBLE isoforms' PSI values during AD diff (any qvalue < 0.01 any deltaPSI > 0.2 )
0
1
2
3
4
Normalised PSI Level
2
1
0
−1
−2
MSC
6h
12h
1d
3d
6d
9d
12d
15d
Time−point

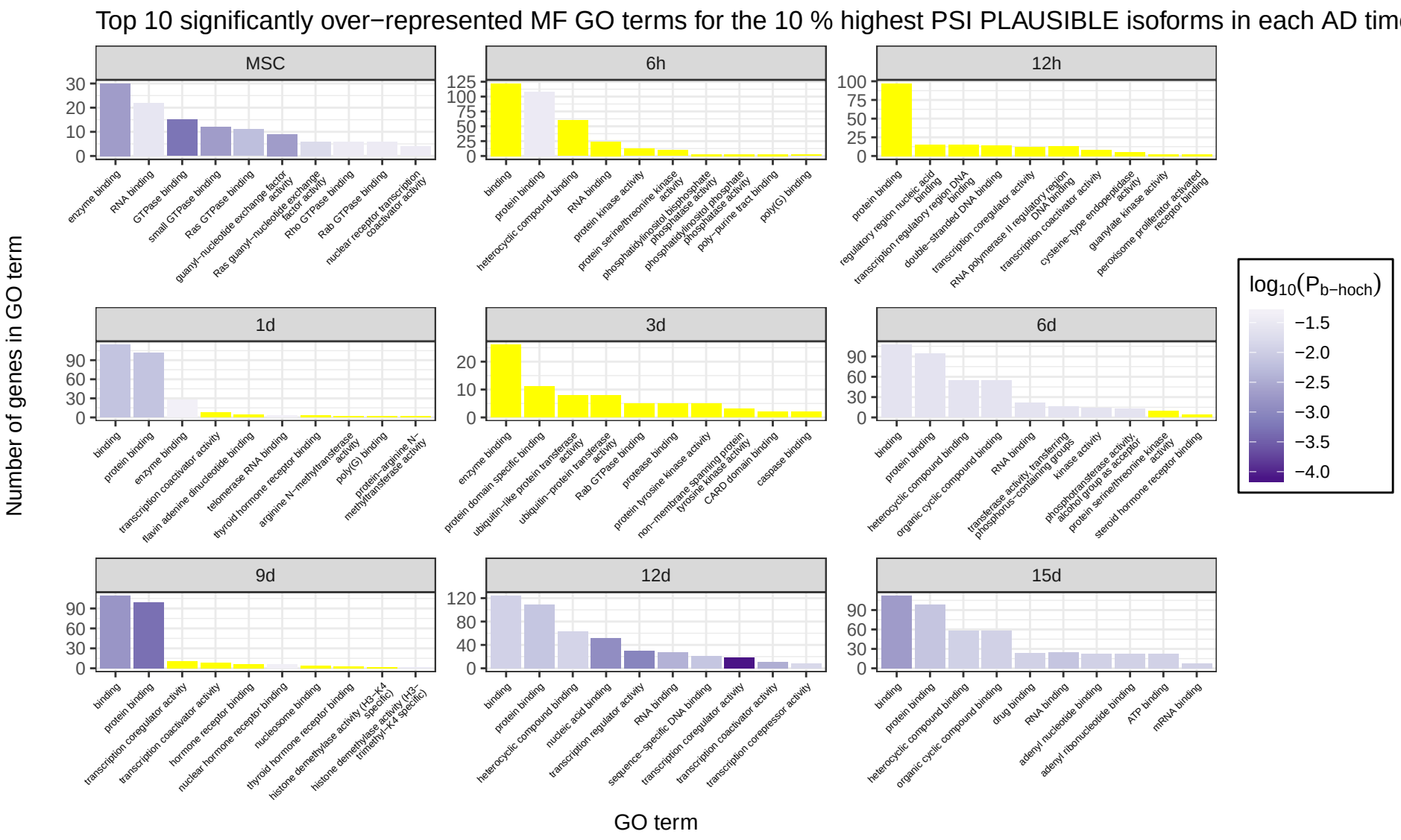

Top 10 significantly over−represented MF GO terms for each PLAUSIBLE cluster in AD series
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
transcription regulator activity
transcription coregulator activity
transcription coactivator activity
nuclease binding
nuclear receptor binding
peroxisome proliferator activated receptor binding
arginine transferase activity
ATP citrate synthase activity
neurotrophin TRKB receptor binding
neurotrophin TRKC receptor binding
binding
protein binding
transferase activity
kinase activity
protein serine/threonine/tyrosine kinase activity
thyroid hormone receptor binding
RNA polymerase II type 1 promoter sequence−specific DNA binding
RNA polymerase III type 1 promoter sequence−specific DNA binding
selenide, water dikinase activity
sphinganine kinase activity
catalytic activity
flavin adenine dinucleotide binding
FAD binding
(R)−2−hydroxyglutarate dehydrogenase activity
D2 dopamine receptor binding
guanosine−3',5'−bispyrophosphate 3'−diphosphate diphosphatase activity
histone demethylase activity (H3−K4 specific)
inositol 1,4,5−trisphosphate−sensitive calcium−release channel activity
inositol 1,4,5−trisphosphate receptor activity involved in regulation of postsynaptic cytosolic calcium ion concentration
phosphatidylinositol−3,4,5−trisphosphate 5−phosphatase activity
metallocarboxypeptidase activity
steroid hormone receptor binding
androgen receptor binding
14−3−3 protein binding
MH2 domain binding
peroxisome matrix targeting signal−1 binding
reelin receptor activity
RNA polymerase I upstream control element sequence−specific DNA binding
tryptophan−tRNA ligase activity
cytoskeletal protein binding
transcription coactivator activity
retinoic acid receptor binding
peroxisome proliferator activated receptor binding
alpha−(1−>6)−fucosyltransferase activity
glycoprotein 6−alpha−L−fucosyltransferase activity
GMP reductase activity
oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor
Rho−dependent protein serine/threonine kinase activity
transcription coregulator activity
transcription factor binding
protein serine/threonine kinase activity
nuclear hormone receptor binding
hormone receptor binding
non−membrane spanning protein tyrosine kinase activity
retinoic acid receptor binding
CARD domain binding
caspase binding
peroxisome proliferator activated receptor binding
methyltransferase activity
N−methyltransferase activity
S−adenosylmethionine−dependent methyltransferase activity
transferase activity, transferring one−carbon groups
protein methyltransferase activity
arginine N−methyltransferase activity
protein−arginine N−methyltransferase activity
protein−arginine omega−N symmetric methyltransferase activity
(R)−2−hydroxyglutarate dehydrogenase activity
pantetheine−phosphate adenylyltransferase activity
nuclear hormone receptor binding
hormone receptor binding
retinoic acid receptor binding
peroxisome proliferator activated receptor binding
phosphotransferase activity, phosphate group as acceptor
pentakisphosphate 3−kinase activity
5−diphosphoinositol−pentakisphosphate kinase activity
diphosphoinositol−pentakisphosphate kinase activity
inositol−1,3,4,5,6−pentakisphosphate kinase activity
inositol heptakisphosphate kinase activity
type I interferon receptor activity
heterocyclic compound binding
organic cyclic compound binding
nucleic acid binding
RNA binding
mRNA binding
mRNA 3'−UTR binding
AU−rich element binding
mRNA 3'−UTR AU−rich region binding
NAD+ kinase activity
thromboxane A2 receptor binding
protein binding
protein C−terminus binding
ATP−dependent DNA helicase activity
ATP−dependent helicase activity
purine NTP−dependent helicase activity
double−stranded DNA−dependent ATP−dependent DNA helicase activity
double−stranded DNA−dependent ATPase activity
myosin phosphatase regulator activity
UDP−glucose 4−epimerase activity
UDP−N−acetylglucosamine 4−epimerase activity
protein binding
transmembrane receptor protein kinase activity
ATP−dependent DNA helicase activity
ATP−dependent helicase activity
mu−type opioid receptor binding
opioid receptor binding
purine NTP−dependent helicase activity
1−phosphatidylinositol−3−phosphate 5−kinase activity
UDP−glucose 4−epimerase activity
UDP−N−acetylglucosamine 4−epimerase activity
binding
transferase activity, transferring glycosyl groups
catalytic activity, acting on a glycoprotein
nucleotide diphosphatase activity
alpha−(1−>6)−fucosyltransferase activity
glycoprotein 6−alpha−L−fucosyltransferase activity
GMP reductase activity
oxidoreductase activity, acting on NAD(P)H, nitrogenous group as acceptor
peroxisome matrix targeting signal−1 binding
galactosylxylosylprotein 4−beta−galactosyltransferase activity
RNA binding
GTPase binding
guanyl−nucleotide exchange factor activity
Rho guanyl−nucleotide exchange factor activity
ankyrin repeat binding
ErbB−2 class receptor binding
MH2 domain binding
phosphotransferase activity, paired acceptors
selenide, water dikinase activity
telomerase activity
microtubule minus−end binding
alanylglutamate dipeptidase activity
cyclic pyranopterin monophosphate synthase activity
cytosolic dipeptidase activity
euchromatin binding
GTP 3',8'−cyclase activity
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in linear amidines
inositol 1,4,5−trisphosphate receptor activity involved in regulation of postsynaptic cytosolic calcium ion concentration
nitrilase activity
nucleic acid binding
RNA binding
transcription coregulator activity
protein domain specific binding
peroxisome proliferator activated receptor binding
Fas−activated serine/threonine kinase activity
histone acetyltransferase activity (H4−K12 specific)
histone succinyltransferase activity
mannosyl−glycoprotein endo−beta−N−acetylglucosaminidase activity
peptide N−succinyltransferase activity
binding
protein binding
RNA binding
histone deacetylase binding
protein phosphatase binding
H4 histone acetyltransferase activity
phosphatidylinositol−4,5−bisphosphate phosphatase activity
phosphatidylinositol bisphosphate phosphatase activity
Fas−activated serine/threonine kinase activity
RNA polymerase I upstream control element sequence−specific DNA binding
transcription coactivator activity
GTPase regulator activity
nucleoside−triphosphatase regulator activity
GTPase inhibitor activity
double−stranded DNA−dependent ATP−dependent DNA helicase activity
double−stranded DNA−dependent ATPase activity
myosin phosphatase regulator activity
RNA polymerase I upstream control element sequence−specific DNA binding
saccharopine dehydrogenase (NADP+, L−lysine−forming) activity
saccharopine dehydrogenase activity
histone binding
nuclear hormone receptor binding
hormone receptor binding
androgen receptor binding
histone acetyltransferase activity
nuclear receptor transcription coactivator activity
thyroid hormone receptor binding
BRE binding
D−erythro−sphingosine kinase activity
sphinganine kinase activity
nucleic acid binding
RNA binding
death receptor binding
DNA replication origin binding
3'−5' DNA/RNA helicase activity
arginyltransferase activity
glucoside transmembrane transporter activity
inositol−1,3,4,5,6−pentakisphosphate kinase activity
inositol heptakisphosphate kinase activity
tRNA 2'−phosphotransferase activity
RNA binding
glycosaminoglycan binding
peroxisome proliferator activated receptor binding
structural constituent of muscle
acetylgalactosaminyltransferase activity
alpha−1,4−N−acetylglucosaminyltransferase activity
glucuronyl−galactosyl−proteoglycan 4−alpha−N−acetylglucosaminyltransferase activity
NADPH dehydrogenase (quinone) activity
ribitol beta−1,4−xylosyltransferase activity
transcription termination site DNA binding
transcription termination site sequence−specific DNA binding
deaminase activity
guanylate kinase activity
hydrolase activity, acting on carbon−nitrogen (but not peptide) bonds, in cyclic amidines
nucleoside monophosphate kinase activity
alanylglutamate dipeptidase activity
cytosolic dipeptidase activity
glucosamine−6−phosphate deaminase activity
glycopeptide N−tetradecanoyltransferase activity
leukemia inhibitory factor receptor binding
magnesium−sodium antiporter activity
transferase activity
catalytic activity, acting on a protein
ATP binding
kinase activity
phosphotransferase activity, alcohol group as acceptor
transferase activity, transferring phosphorus−containing groups
protein serine/threonine kinase activity
non−membrane spanning protein tyrosine kinase activity
NAD+ kinase activity
euchromatin binding
catalytic activity
adenylyltransferase activity
(R)−2−hydroxyglutarate dehydrogenase activity
3−oxoacyl−[acyl−carrier−protein] reductase (NADH) activity
dephospho−CoA kinase activity
G−protein gamma−subunit binding
guanosine−5'−trisphosphate 3'−diphosphate diphosphatase activity
NAD(P)H dehydrogenase (quinone) activity
NADPH dehydrogenase (quinone) activity
pantetheine−phosphate adenylyltransferase activity
protein binding
nuclear hormone receptor binding
hormone receptor binding
steroid hormone receptor binding
retinoic acid receptor binding
estrogen receptor binding
glucocorticoid receptor binding
retinoid X receptor binding
thyroid hormone receptor binding
type I interferon receptor activity
binding
protein binding
nucleic acid binding
DNA binding
transcription regulator activity
RNA binding
transcription coregulator activity
N−methyltransferase activity
nuclear hormone receptor binding
nucleosome−dependent ATPase activity

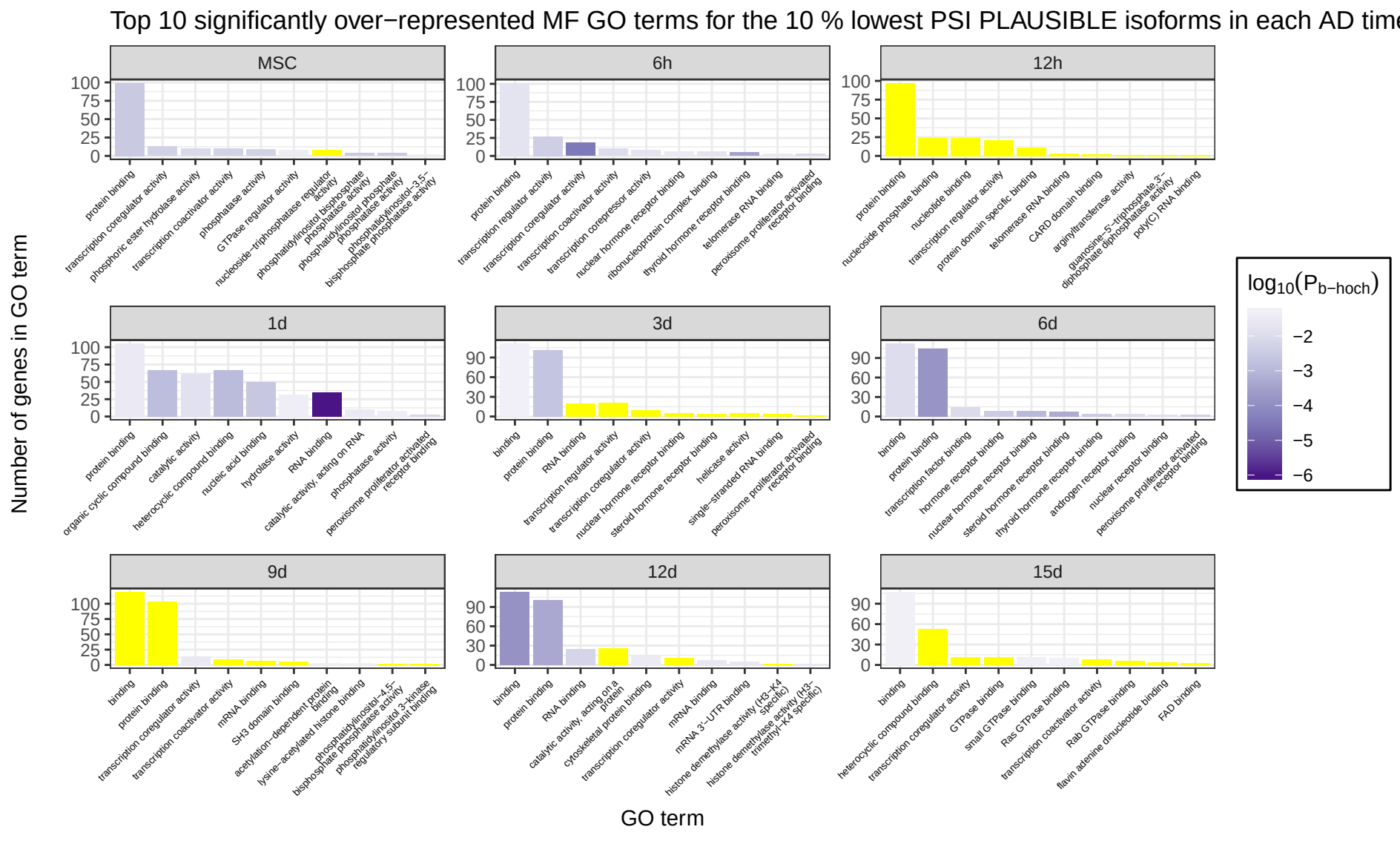
Top 10 significantly over−represented BP GO terms for each PLAUSIBLE cluster in AD series
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
regulation of primary metabolic process
nucleic acid metabolic process
positive regulation of DNA−binding transcription factor activity
body morphogenesis
chromatin disassembly
nucleosome disassembly
protein−DNA complex disassembly
embryonic body morphogenesis
regulation of hematopoietic stem cell proliferation
signal transduction downstream of smoothened
positive regulation of extracellular matrix organization
regulation of extracellular matrix organization
astral microtubule organization
basement membrane assembly involved in embryonic body morphogenesis
negative regulation of wound healing, spreading of epidermal cells
positive regulation of basement membrane assembly involved in embryonic body morphogenesis
positive regulation of basement membrane assembly involved in morphogenesis
regulation of basement membrane assembly involved in embryonic body morphogenesis
regulation of basement membrane organization
regulation of wound healing, spreading of epidermal cells
selenocysteine metabolic process
response to inorganic substance
vesicle budding from membrane
cellular response to estradiol stimulus
cellular response to nitric oxide
cellular response to reactive nitrogen species
response to nitric oxide
response to testosterone
cellular response to carbon monoxide
doxorubicin transport
ncRNA polyadenylation involved in polyadenylation−dependent nuclear mRNA catabolic process
regulation of anatomical structure morphogenesis
intracellular receptor signaling pathway
androgen receptor signaling pathway
body morphogenesis
regulation of cilium assembly
embryonic body morphogenesis
negative regulation of cilium assembly
negative regulation of fibroblast growth factor receptor signaling pathway
negative regulation of interleukin−2 production
regulation of protein exit from endoplasmic reticulum
central nervous system development
regulation of microtubule−based process
cellular response to ketone
mitotic spindle organization
N−glycan fucosylation
olfactory nerve morphogenesis
olfactory nerve structural organization
positive regulation of polarized epithelial cell differentiation
pronephric nephron morphogenesis
pronephric nephron tubule morphogenesis
regulation of gene expression
cellular response to organic substance
regulation of DNA−binding transcription factor activity
negative regulation of nervous system development
negative regulation of neurogenesis
positive regulation of DNA−binding transcription factor activity
negative regulation of cell projection organization
negative regulation of neuron projection development
regulation of androgen receptor signaling pathway
cellular response to UV−C
cellular pigmentation
cellular pigment accumulation
endosome to melanosome transport
endosome to pigment granule transport
Golgi to vacuole transport
peptidyl−arginine methylation to symmetrical−dimethyl arginine
peptidyl−arginine N−methylation
peptidyl−arginine omega−N−methylation
pigment accumulation
pigment granule maturation
cortical microtubule organization
monoubiquitinated histone deubiquitination
monoubiquitinated histone H2A deubiquitination
negative regulation of peroxisome proliferator activated receptor signaling pathway
positive regulation of peroxisome proliferator activated receptor signaling pathway
positive regulation of nuclear receptor transcription coactivator activity
positive regulation of retinoic acid receptor signaling pathway
protein localization to pericentriolar material
regulation of membrane repolarization during ventricular cardiac muscle cell action potential
regulation of cardiac muscle cell action potential involved in regulation of contraction
regulation of voltage−gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization
nucleic acid metabolic process
cellular nitrogen compound metabolic process
gene expression
cellular aromatic compound metabolic process
heterocycle metabolic process
nucleobase−containing compound metabolic process
organic cyclic compound metabolic process
RNA metabolic process
mRNA metabolic process
mRNA processing
chromosome organization
regulation of chromosome organization
chromosome segregation
regulation of chromosome segregation
regulation of sister chromatid segregation
bicellular tight junction assembly
regulation of metaphase/anaphase transition of cell cycle
regulation of mitotic metaphase/anaphase transition
tight junction assembly
regulation of mismatch repair
cellular component organization or biogenesis
cytoskeleton organization
microtubule−based process
microtubule cytoskeleton organization
positive regulation of ossification
positive regulation of osteoblast differentiation
epiboly
epiboly involved in wound healing
wound healing, spreading of cells
establishment of Sertoli cell barrier
cellular component organization or biogenesis
cellular component organization
organelle organization
cell cycle
nerve development
epithelial cell proliferation involved in liver morphogenesis
glomerular filtration
hepatocyte proliferation
regulation of hepatocyte proliferation
renal filtration
RNA processing
basal protein localization
negative regulation of establishment of protein−containing complex localization to telomere
negative regulation of establishment of protein localization to telomere
negative regulation of establishment of RNA localization to telomere
positive regulation of establishment of protein−containing complex localization to telomere
regulation of establishment of protein−containing complex localization to telomere
regulation of establishment of RNA localization to telomere
regulation of shelterin complex assembly
shelterin complex assembly
regulation of small GTPase mediated signal transduction
ciliary basal body−plasma membrane docking
endosome to lysosome transport
immature B cell differentiation
methylation−dependent chromatin silencing
regulation of production of miRNAs involved in gene silencing by miRNA
regulation of production of small RNA involved in gene silencing by miRNA
doxorubicin transport
macroautophagy by TORC1 signaling
negative regulation of cellular ketone metabolic process by regulation of transcription from RNA polymerase II promoter
organelle organization
cell cycle
cell cycle process
regulation of cell cycle
mitotic cell cycle
mitotic cell cycle process
cell projection assembly
plasma membrane bounded cell projection assembly
RNA splicing
regulation of chromosome organization
mRNA metabolic process
RNA processing
mRNA processing
RNA splicing
dephosphorylation
covalent chromatin modification
negative regulation of cellular amide metabolic process
inositol phosphate metabolic process
positive regulation of histone modification
negative regulation of centriole replication
cellular component organization or biogenesis
anatomical structure development
cellular component organization
cellular developmental process
organelle organization
cytoskeleton organization
microtubule cytoskeleton organization
centrosome cycle
microtubule organizing center organization
regulation of peroxisome proliferator activated receptor signaling pathway
cellular component organization or biogenesis
cellular component organization
organelle organization
regulation of nucleobase−containing compound metabolic process
chromosome organization
chromatin organization
covalent chromatin modification
histone modification
histone H2A−K5 acetylation
sphinganine−1−phosphate biosynthetic process
macromolecule metabolic process
nucleic acid metabolic process
mRNA metabolic process
RNA processing
mRNA processing
RNA splicing
RNA splicing, via spliceosome
transesterification reactions with bulged adenosine as nucleophile
alternative mRNA splicing, via spliceosome
axo−dendritic protein transport
regulation of RNA splicing
fibroblast growth factor receptor signaling pathway
positive regulation of cell−substrate adhesion
positive regulation of DNA−templated transcription, initiation
cellular response to vitamin B1
lamellipodium assembly involved in anatomical cell migration
olfactory nerve morphogenesis
olfactory nerve structural organization
positive regulation of DNA−templated transcription, termination
response to formaldehyde
regulation of cell communication
negative regulation of nucleic acid−templated transcription
negative regulation of transcription, DNA−templated
negative regulation of transcription by RNA polymerase II
GDP metabolic process
GMP metabolic process
myelin assembly
regulation of production of miRNAs involved in gene silencing by miRNA
regulation of production of small RNA involved in gene silencing by RNA
regulation of ventricular cardiac muscle cell action potential
macromolecule modification
peptidyl−amino acid modification
tRNA modification
rRNA processing
positive regulation of ceramide biosynthetic process
positive regulation of sphingolipid biosynthetic process
protein kinase C signaling
regulation of ceramide biosynthetic process
regulation of membrane lipid metabolic process
regulation of sphingolipid biosynthetic process
motile cilium assembly
regulation of stem cell population maintenance
epidermal stem cell homeostasis
ncRNA polyadenylation involved in polyadenylation−dependent nuclear mRNA catabolic process
negative regulation of hepatocyte apoptotic process
positive regulation of axo−dendritic protein transport
positive regulation of axo−dendritic protein transport
establishment of or maintenance of cell polarity regulating cell shape
regulation of axo−dendritic protein transport
regulation of establishment of or maintenance of cell polarity regulating cell shape
regulation of hepatocyte apoptotic process
nucleic acid metabolic process
cellular aromatic compound metabolic process
heterocycle metabolic process
nucleobase−containing compound metabolic process
organic cyclic compound metabolic process
RNA metabolic process
nuclear transport
nucleocytoplasmic transport
cytoplasmic microtubule organization
plasma membrane ATP synthesis coupled electron transport
avoidance of defenses of other organism involved in symbiotic interaction
avoidance of host defenses
evasion or tolerance by virus of host immune response
evasion or tolerance of defenses of other organism involved in symbiotic interaction
evasion or tolerance of host defenses
evasion or tolerance of host defenses by virus
evasion or tolerance of host immune response
evasion or tolerance of other organism involved in symbiotic interaction
signal transduction downstream of smoothened

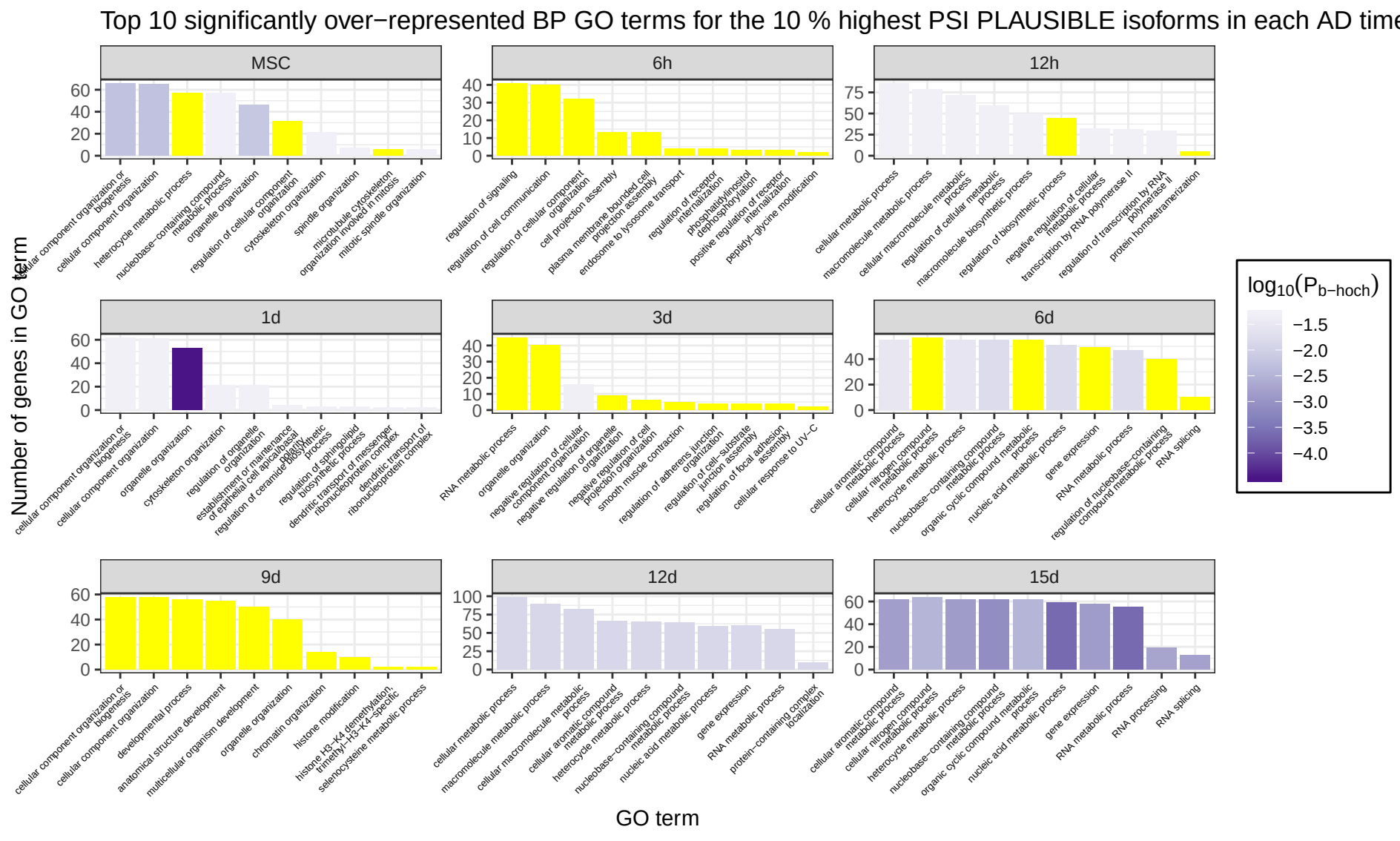

Top 10 significantly over−represented CC GO terms for each PLAUSIBLE cluster in AD series
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
organelle
intracellular
intracellular part
intracellular organelle
intracellular membrane−bounded organelle
nucleus
nBAF complex
npBAF complex
SWI/SNF complex
brahma complex
cytosol
AP−1 adaptor complex
clathrin coat of trans−Golgi network vesicle
trans−Golgi network transport vesicle membrane
basal cortex
cytoplasmic part
organelle subcompartment
Golgi apparatus part
Golgi subcompartment
Golgi membrane
midbody
calcineurin complex
TRAMP complex
protein−containing complex
Golgi stack
mitotic spindle
spindle microtubule
collagen beaded filament
collagen type VI trimer
DBIRD complex
Picrotin Nu44 histone acetyltransferase complex
SOSS complex
cytoskeleton
cytoskeletal part
recycling endosome
9+0 motile cilium
GMP reductase complex
HIR complex
matrix side of mitochondrial inner membrane
PR−DUB complex
proximal portion of axoneme
syntrophin complex
nuclear lumen
nuclear part
nucleolus
nuclear periphery
nuclear matrix
SWI/SNF complex
apical dendrite
distal dendrite
inactive sex chromosome
plasma membrane bounded cell projection cytoplasm
AP−type membrane coat adaptor complex
activating signal cointegrator 1 complex
CCAAT−binding factor complex
mRNA cap methyltransferase complex
presynaptic endosome
basolateral plasma membrane
lamellipodium
lateral loop
endoplasmic reticulum exit site
guanyl−nucleotide exchange factor complex
MPP7−DLG1−LIN7 complex
myelin sheath abaxonal region
node of Ranvier
nuclear pore central transport channel
PR−DUB complex
intracellular membrane−bounded organelle
intracellular organelle lumen
membrane−enclosed lumen
organelle lumen
nucleoplasm
nuclear body
cytoplasmic stress granule
intracellular non−membrane−bounded organelle
non−membrane−bounded organelle
microtubule cytoskeleton
microtubule organizing center
asymmetric synapse
postsynaptic density
postsynaptic membrane
intracellular organelle lumen
membrane−enclosed lumen
cytosol
cell junction
adherens junction
anchoring junction
cilium
Golgi stack
ciliary basal body
Golgi cisterna
Golgi cisterna membrane
9+0 motile cilium
HIR complex
proximal portion of axoneme
nucleoplasm part
nuclear speck
basal part of cell
basal cortex
hemidesmosome
shelterin complex
SOSS complex
postsynaptic density
non−motile cilium
photoreceptor connecting cilium
calcineurin complex
molybdopterin synthase complex
PeBoW complex
platelet dense granule membrane
intracellular non−membrane−bounded organelle
non−membrane−bounded organelle
nucleoplasm
intracellular organelle part
organelle part
nucleolus
nuclear speck
cytoplasmic side of apical plasma membrane
cell junction
postsynaptic membrane
trans−Golgi network transport vesicle
collagen type XVI trimer
matrix side of mitochondrial inner membrane
organelle part
Golgi apparatus
plasma membrane region
synaptic membrane
asymmetric synapse
basolateral plasma membrane
BLOC−3 complex
condensed chromosome, centromeric region
condensed nuclear chromosome
chromosome passenger complex
EKC/KEOPS complex
PeBoW complex
plasma membrane proton−transporting V−type ATPase complex
proton−transporting V−type ATPase, V1 domain
axon cytoplasm
COPI−coated Golgi to ER transport vesicle
kinesin II complex
Las1 complex
intracellular organelle
CHOP−C/EBP complex
nuclear MIS12/MIND complex

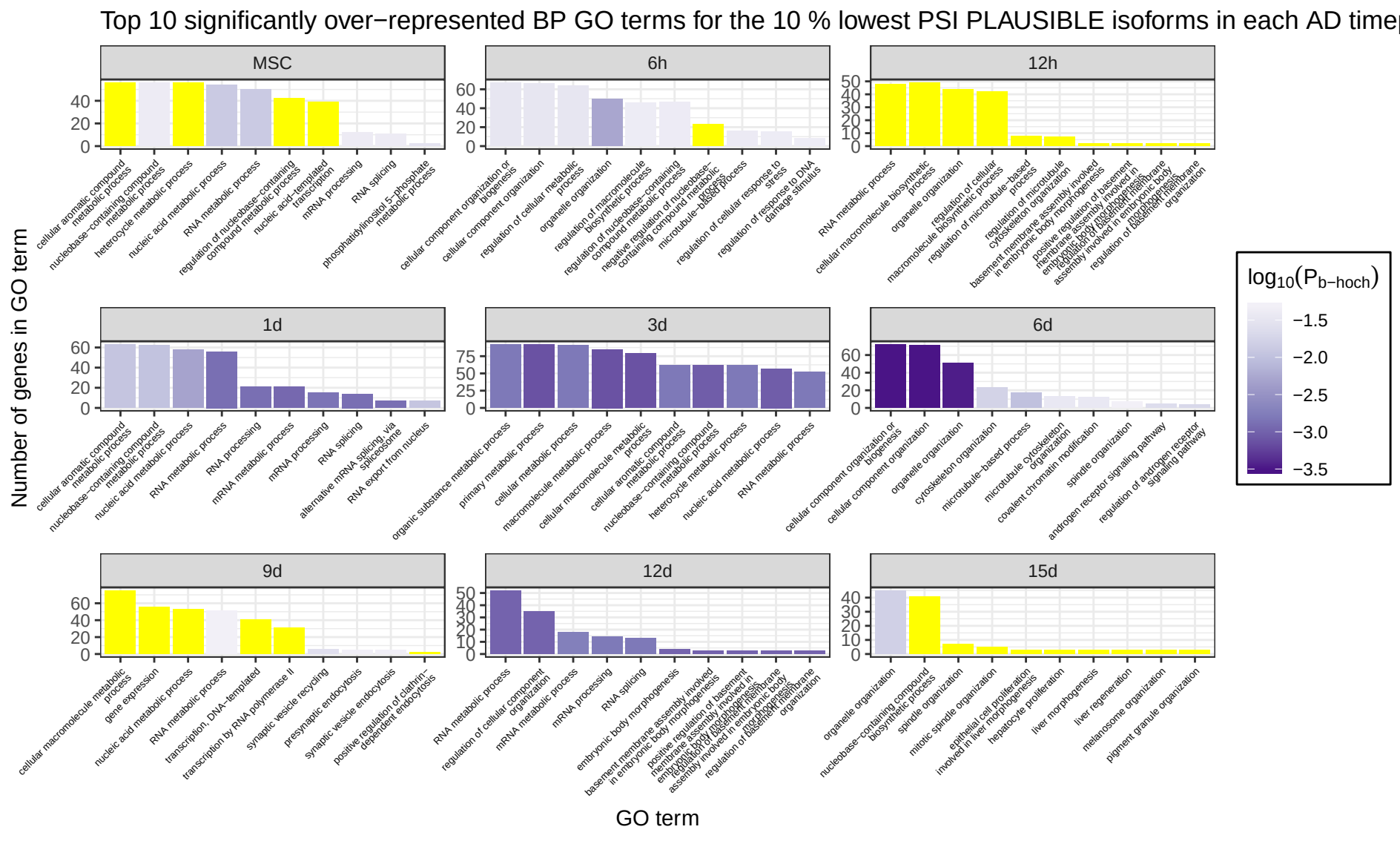

Top 10 significantly over−represented PFAM families for each PLAUSIBLE cluster in AD series
Number of genes enriched in PFAM family
PFAM family
log10(Pb−hoch)
−1.5
−2.0
−2.5

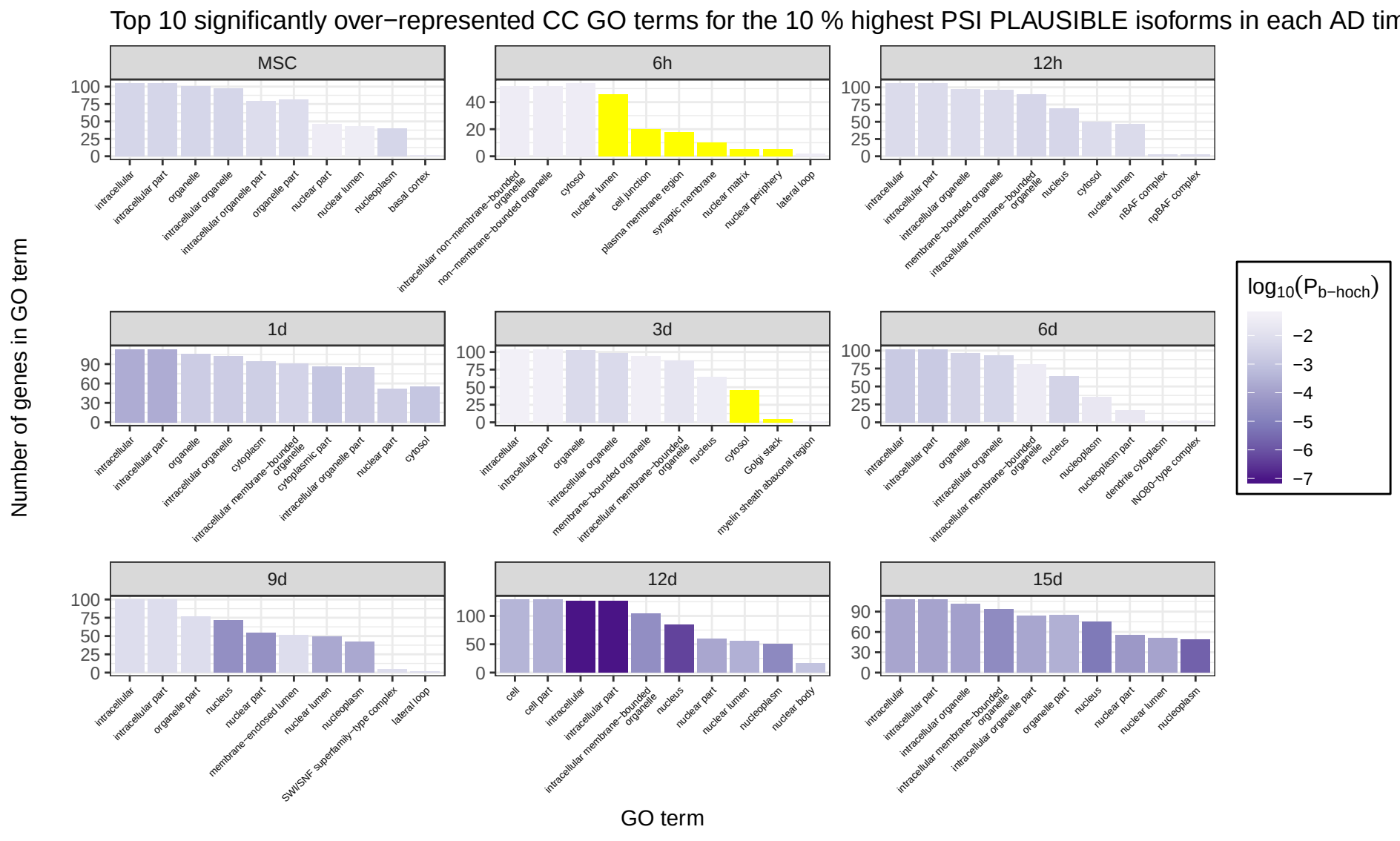

Top 10 significantly over−represented UPSTREAM RBP CANDIDATES for each PLAUSIBLE cluster in AD series
Number of genes enriched amongst RBP target genes
Upstream RBP with literature reference
log10(P)
−1
−2
−3
−4

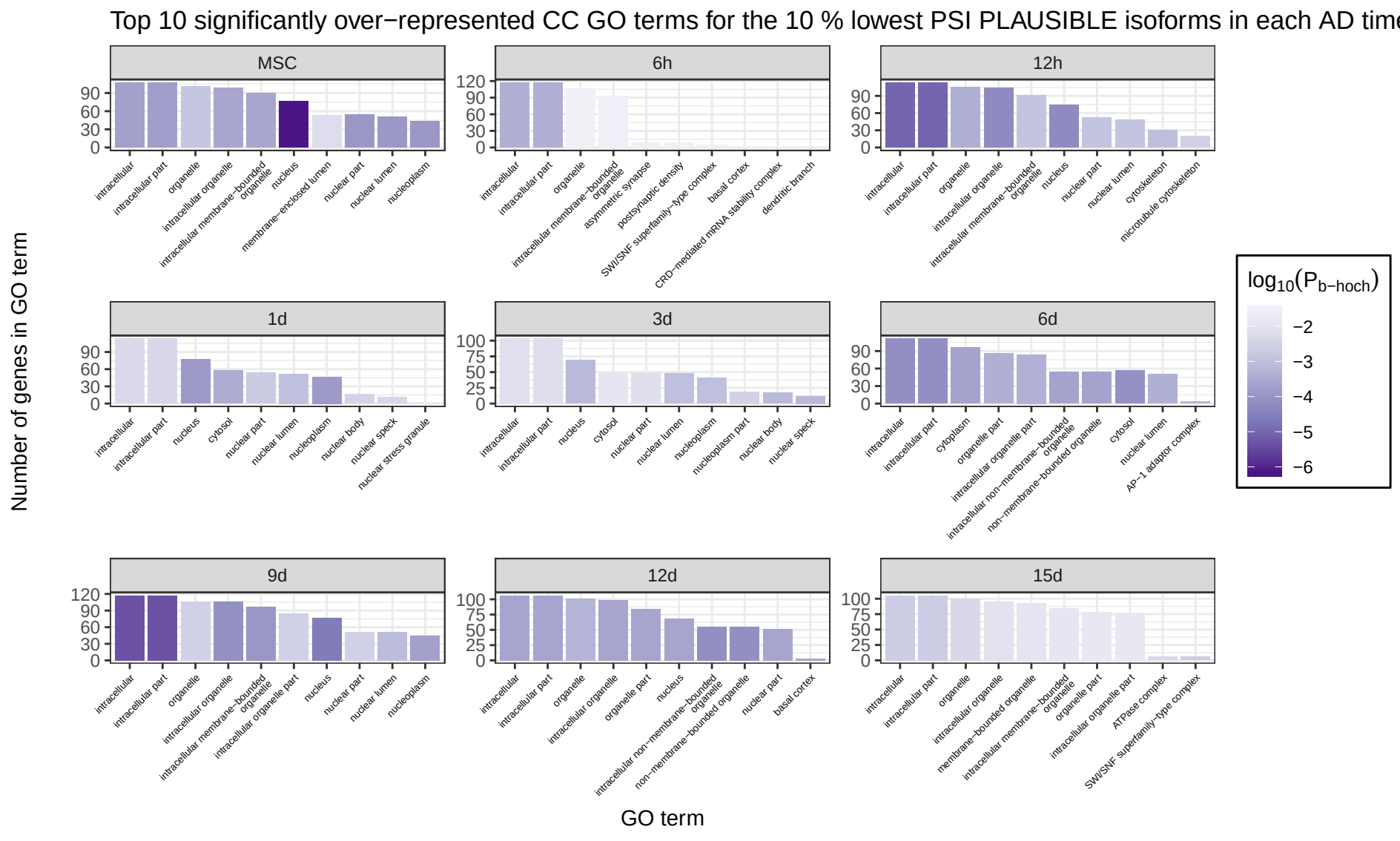

Top 10 significantly over−represented MF GO terms for the 10 % highest PSI PLAUSIBLE isoforms in each AD tim
MSC
6h
12h
1d
3d
6d
9d
12d
15d
enzyme binding
RNA binding
GTPase binding
small GTPase binding
Ras GTPase binding
guanyl−nucleotide exchange factor activity
Ras guanyl−nucleotide exchange factor activity
Rho GTPase binding
Rab GTPase binding
nuclear receptor transcription coactivator activity
binding
protein binding
heterocyclic compound binding
RNA binding
protein kinase activity
protein serine/threonine kinase activity
phosphatidylinositol bisphosphate phosphatase activity
phosphatidylinositol phosphate phosphatase activity
poly−purine tract binding
poly(G) binding
protein binding
regulatory region nucleic acid binding
transcription regulatory region DNA binding
double−stranded DNA binding
transcription coregulator activity
RNA polymerase II regulatory region DNA binding
transcription coactivator activity
cysteine−type endopeptidase activity
guanylate kinase activity
peroxisome proliferator activated receptor binding
binding
protein binding
enzyme binding
transcription coactivator activity
flavin adenine dinucleotide binding
telomerase RNA binding
thyroid hormone receptor binding
arginine N−methyltransferase activity
poly(G) binding
protein−arginine N−methyltransferase activity
enzyme binding
protein domain specific binding
ubiquitin−like protein transferase activity
ubiquitin−protein transferase activity
Rab GTPase binding
protease binding
protein tyrosine kinase activity
non−membrane spanning protein tyrosine kinase activity
CARD domain binding
caspase binding
binding
protein binding
heterocyclic compound binding
organic cyclic compound binding
RNA binding
transferase activity,transferring phosphorus−containing groups
kinase activity
phosphotransferase activity, alcohol group as acceptor
protein serine/threonine kinase activity
steroid hormone receptor binding
binding
protein binding
transcription coregulator activity
transcription coactivator activity
hormone receptor binding
nuclear hormone receptor binding
nucleosome binding
thyroid hormone receptor binding
histone demethylase activity (H3−K4 specific)
histone demethylase activity (H3−trimethyl−K4 specific)
binding
protein binding
heterocyclic compound binding
nucleic acid binding
transcription regulator activity
RNA binding
sequence−specific DNA binding
transcription coregulator activity
transcription coactivator activity
transcription corepressor activity
binding
protein binding
heterocyclic compound binding
organic cyclic compound binding
drug binding
RNA binding
adenyl nucleotide binding
adenyl ribonucleotide binding
ATP binding
mRNA binding
Number of genes in GO term
GO term
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0
−3.5
−4.0

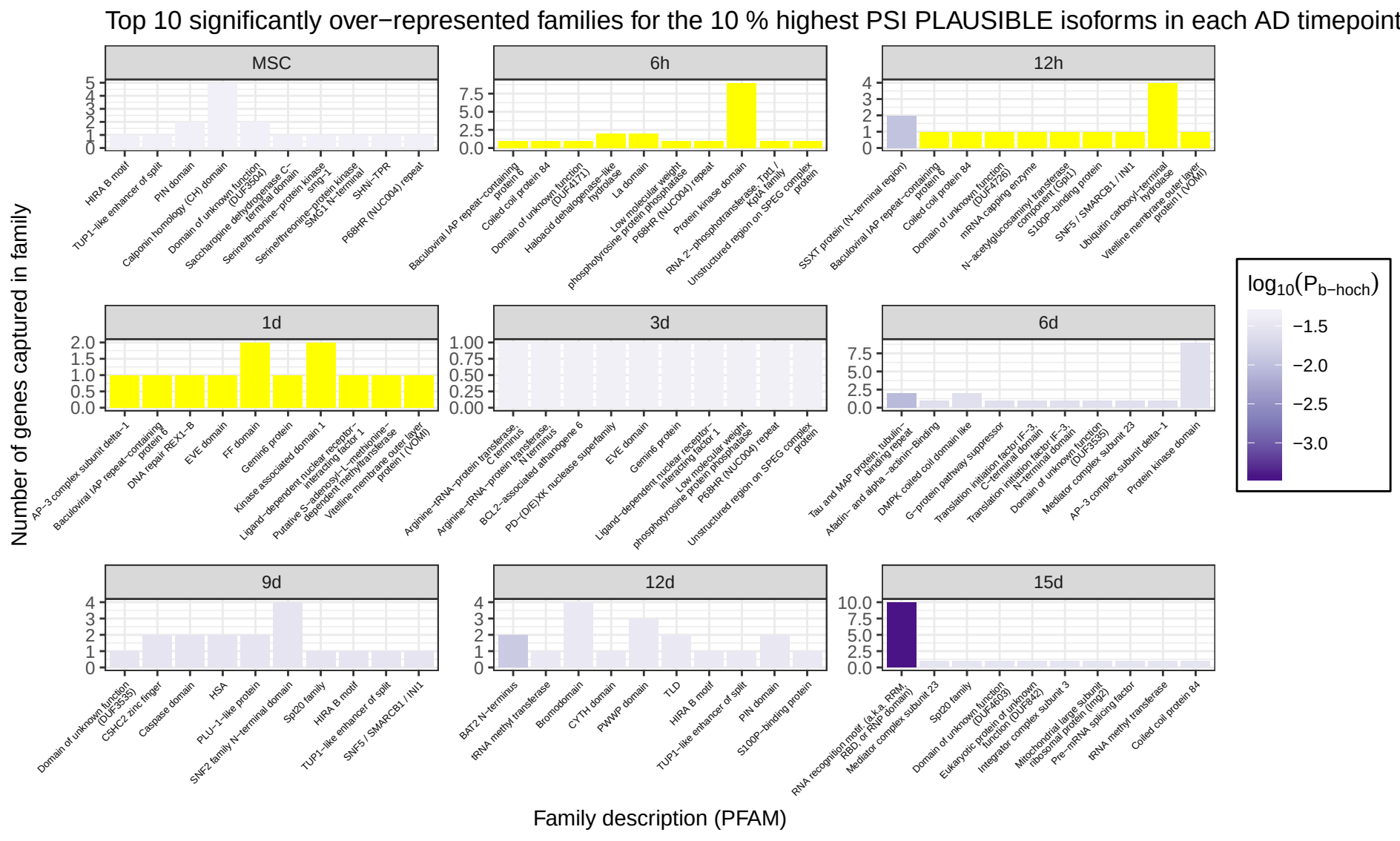

Top 10 significantly over−represented MF GO terms for the 10 % lowest PSI PLAUSIBLE isoforms in each AD time
MSC
6h
12h
1d
3d
6d
9d
12d
15d
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
−5
−6
protein binding
transcription coregulator activity
phosphoric ester hydrolase activity
transcription coactivator activity
phosphatase activity
GTPase regulator activity
nucleoside−triphosphatase regulator activity
phosphatidylinositol bisphosphate phosphatase activity
phosphatidylinositol phosphate phosphatase activity
phosphatidylinositol−3,5−bisphosphate phosphatase activity
transcription regulator activity
transcription corepressor activity
nuclear hormone receptor binding
ribonucleoprotein complex binding
thyroid hormone receptor binding
telomerase RNA binding
peroxisome proliferator activated receptor binding
nucleoside phosphate binding
nucleotide binding
protein domain specific binding
CARD domain binding
arginyltransferase activity
guanosine−5'−triphosphate 3'−diphosphate diphosphatase activity
poly(C) RNA binding
organic cyclic compound binding
catalytic activity
heterocyclic compound binding
nucleic acid binding
hydrolase activity
RNA binding
catalytic activity, acting on RNA
phosphatase activity
binding
helicase activity
single−stranded RNA binding
transcription factor binding
hormone receptor binding
androgen receptor binding
nuclear receptor binding
mRNA binding
SH3 domain binding
acetylation−dependent protein binding
lysine−acetylated histone binding
phosphatidylinositol−4,5−bisphosphate phosphatase activity
phosphatidylinositol 3−kinase regulatory subunit binding
RNA binding
catalytic activity, acting on a protein
cytoskeletal protein binding
mRNA 3'−UTR binding
histone demethylase activity (H3−K4 specific)
histone demethylase activity (H3−trimethyl−K4 specific)
heterocyclic compound binding
GTPase binding
small GTPase binding
Ras GTPase binding
Rab GTPase binding
flavin adenine dinucleotide binding
FAD binding

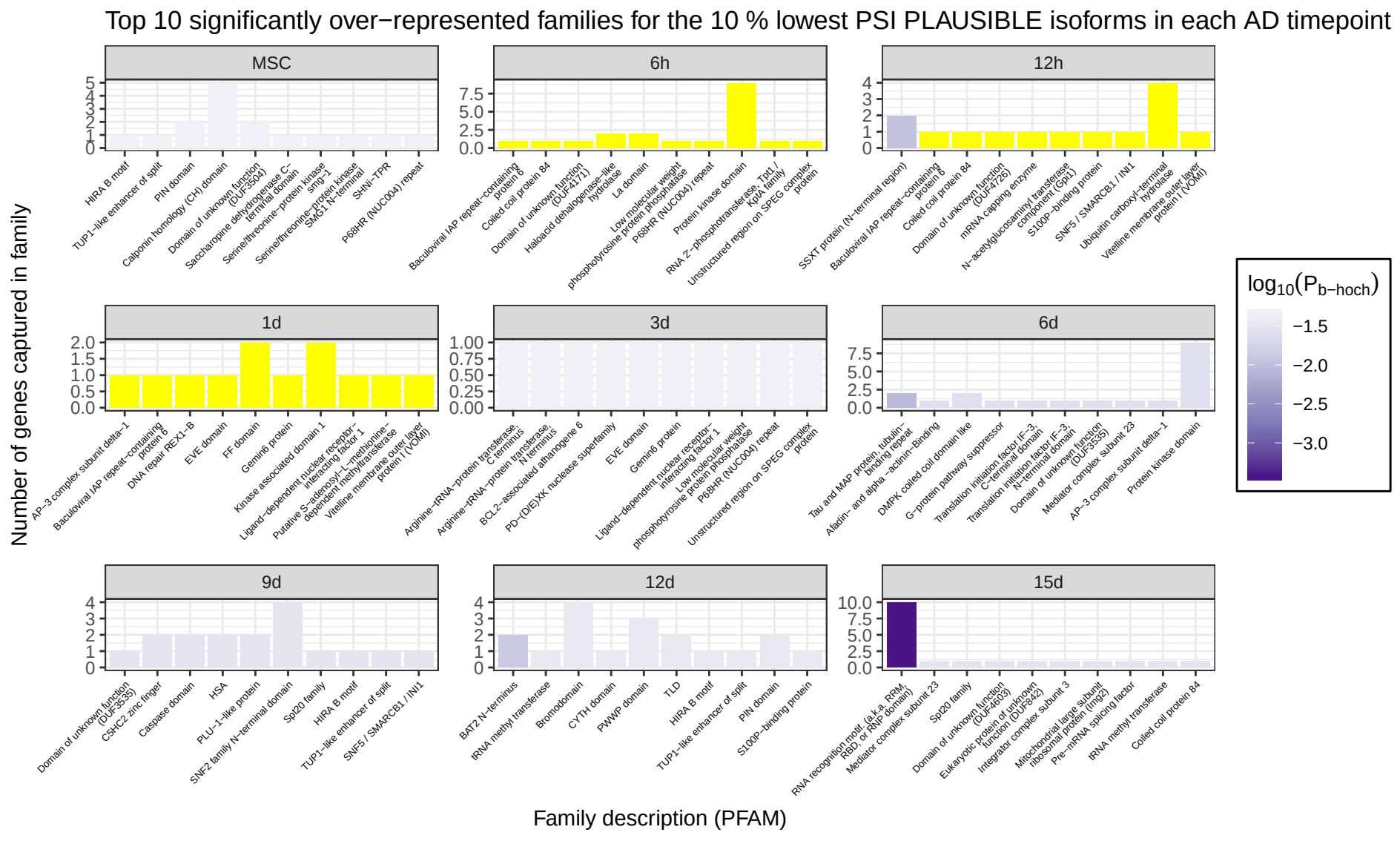

Top 10 significantly over−represented BP GO terms for the 10 % highest PSI PLAUSIBLE isoforms in each AD time
MSC
6h
12h
1d
3d
6d
9d
12d
15d
Number of genes in GO term
GO term
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0
−3.5
−4.0
cellular component organization or biogenesis
cellular component organization
heterocycle metabolic process
nucleobase−containing compound metabolic process
organelle organization
regulation of cellular component organization
cytoskeleton organization
spindle organization
microtubule cytoskeleton organization involved in mitosis
mitotic spindle organization
regulation of signaling
regulation of cell communication
regulation of cellular component organization
cell projection assembly
plasma membrane bounded cell projection assembly
endosome to lysosome transport
regulation of receptor internalization
phosphatidylinositol dephosphorylation
positive regulation of receptor internalization
peptidyl−glycine modification
cellular metabolic process
macromolecule metabolic process
cellular macromolecule metabolic process
regulation of cellular metabolic process
macromolecule biosynthetic process
regulation of biosynthetic process
negative regulation of cellular metabolic process
transcription by RNA polymerase II
regulation of transcription by RNA polymerase II
protein homotetramerization
cytoskeleton organization
regulation of organelle organization
establishment or maintenance of epithelial cell apicobasal polarity
regulation of ceramide biosynthetic process
regulation of sphingolipid biosynthetic process
dendritic transport of messenger ribonucleoprotein complex
dendritic transport of ribonucleoprotein complex
RNA metabolic process
negative regulation of cellular component organization
negative regulation of organelle organization
negative regulation of cell projection organization
smooth muscle contraction
regulation of adherens junction organization
regulation of cell−substrate junction assembly
regulation of focal adhesion assembly
cellular response to UV−C
cellular aromatic compound metabolic process
cellular nitrogen compound metabolic process
heterocycle metabolic process
nucleobase−containing compound metabolic process
organic cyclic compound metabolic process
nucleic acid metabolic process
gene expression
RNA processing
regulation of nucleobase−containing compound metabolic process
RNA splicing
developmental process
anatomical structure development
multicellular organism development
chromatin organization
histone modification
histone H3−K4 demethylation
trimethyl−H3−K4−specific selenocysteine metabolic process
protein−containing complex localization


Top 10 significantly over−represented BP GO terms for the 10 % lowest PSI PLAUSIBLE isoforms in each AD timep
MSC
6h
12h
1d
3d
6d
9d
12d
15d
Number of genes in GO term
GO term
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0
−3.5
cellular aromatic compound metabolic process
nucleobase−containing compound metabolic process
heterocycle metabolic process
nucleic acid metabolic process
RNA metabolic process
regulation of nucleobase−containing compound metabolic process
nucleic acid−templated transcription
mRNA processing
RNA splicing
phosphatidylinositol 5−phosphate metabolic process
cellular component organization or biogenesis
cellular component organization
regulation of cellular metabolic process
organelle organization
regulation of macromolecule biosynthetic process
regulation of nucleobase−containing compound metabolic process
negative regulation of nucleobase−containing compound metabolic process
microtubule−based process
regulation of cellular response to stress
regulation of response to DNA damage stimulus
RNA metabolic process
cellular macromolecule biosynthetic process
organelle organization
regulation of cellular macromolecule biosynthetic process
macromolecule biosynthetic process
regulation of microtubule−based process
regulation of microtubule cytoskeleton organization
positive regulation of basement membrane assembly involved in embryonic body morphogenesis
membrane assembly involved in embryonic body morphogenesis
regulation of basement membrane assembly involved in embryonic body morphogenesis
regulation of basement membrane organization
cellular aromatic compound metabolic process
nucleobase−containing compound metabolic process
nucleic acid metabolic process
RNA metabolic process
RNA processing
mRNA metabolic process
mRNA processing
RNA splicing
alternative mRNA splicing, via spliceosome
RNA export from nucleus
organic substance metabolic process
primary metabolic process
cellular metabolic process
macromolecule metabolic process
cellular macromolecule metabolic process
cellular aromatic compound metabolic process
nucleobase−containing compound metabolic process
heterocycle metabolic process
nucleic acid metabolic process
RNA metabolic process
cellular component organization or biogenesis
cellular component organization
organelle organization
cytoskeleton organization
microtubule−based process
microtubule cytoskeleton organization
covalent chromatin modification
spindle organization
androgen receptor signaling pathway
regulation of androgen receptor signaling pathway
cellular macromolecule metabolic process
gene expression
nucleic acid metabolic process
RNA metabolic process
transcription, DNA−templated
transcription by RNA polymerase II
synaptic vesicle recycling
presynaptic endocytosis
synaptic vesicle endocytosis
positive regulation of clathrin−dependent endocytosis
RNA metabolic process
regulation of cellular component organization
mRNA metabolic process
mRNA processing
RNA splicing
embryonic body morphogenesis
basement membrane assembly involved in embryonic body morphogenesis
membrane assembly involved in embryonic body morphogenesis
positive regulation of basement membrane assembly involved in embryonic body morphogenesis
regulation of basement membrane assembly involved in embryonic body morphogenesis
regulation of basement membrane organization
organelle organization
nucleobase−containing compound biosynthetic process
spindle organization
mitotic spindle organization
epithelial cell proliferation involved in liver morphogenesis
hepatocyte proliferation
liver morphogenesis
liver regeneration
melanosome organization
pigment granule organization

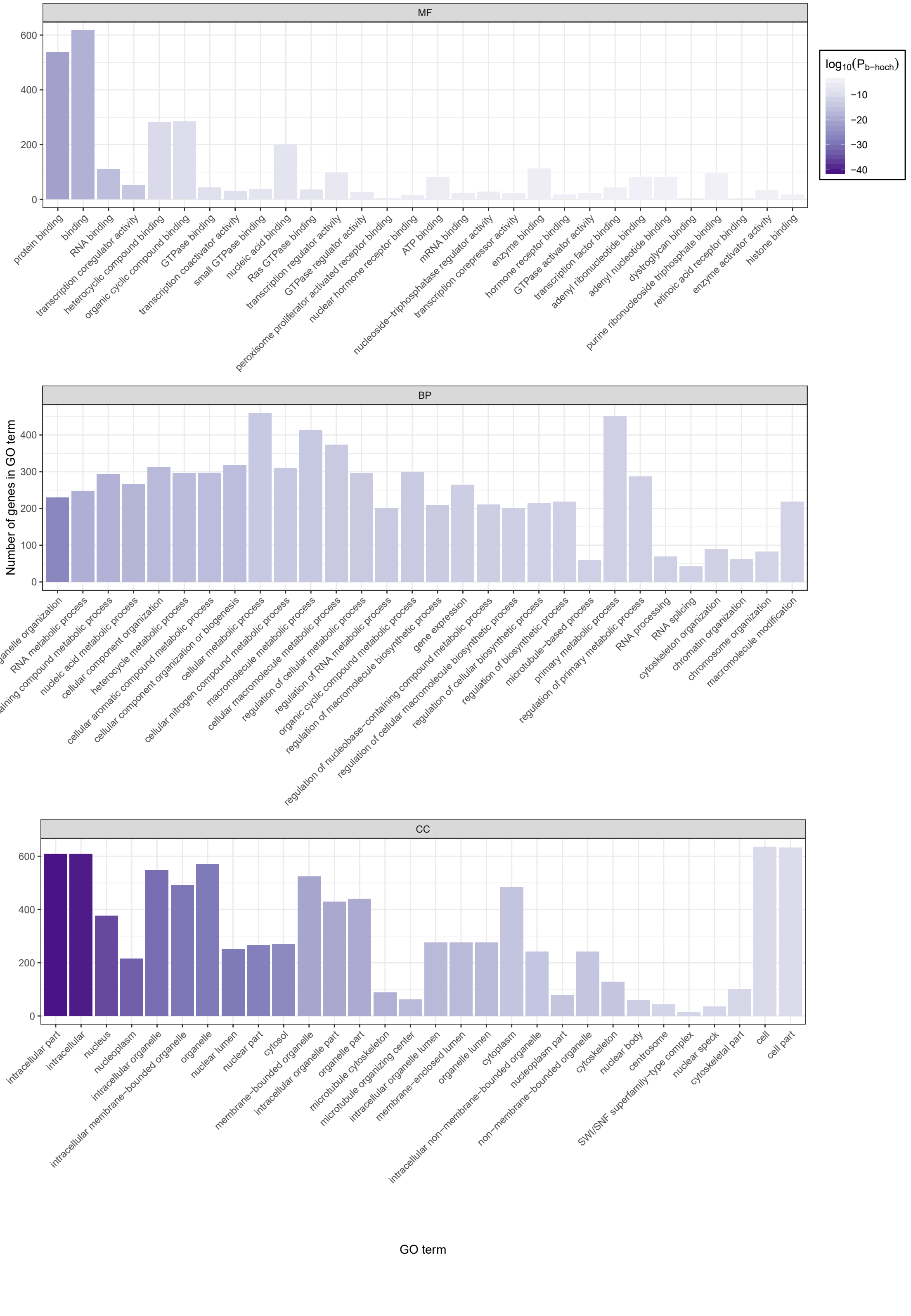

Top 10 significantly over−represented CC GO terms for the 10 % highest PSI PLAUSIBLE isoforms in each AD tim
MSC
intracellular
intracellular part
organelle
intracellular organelle
intracellular organelle part
organelle part
nuclear part
nuclear lumen
nucleoplasm
basal cortex
6h
intracellular non−membrane−bounded organelle
non−membrane−bounded organelle
cytosol
nuclear lumen
cell junction
plasma membrane region
synaptic membrane
nuclear matrix
nuclear periphery
lateral loop
12h
intracellular
intracellular part
intracellular organelle
membrane−bounded organelle
intracellular membrane−bounded organelle
nucleus
cytosol
nuclear lumen
nBAF complex
npBAF complex
1d
intracellular
intracellular part
organelle
intracellular organelle
cytoplasm
intracellular membrane−bounded organelle
cytoplasmic part
intracellular organelle part
nuclear part
cytosol
3d
intracellular
intracellular part
organelle
intracellular organelle
membrane−bounded organelle
intracellular membrane−bounded organelle
nucleus
cytosol
Golgi stack
myelin sheath abaxonal region
6d
intracellular
intracellular part
organelle
intracellular organelle
intracellular membrane−bounded organelle
nucleus
nucleoplasm
nucleoplasm part
dendrite cytoplasm
INO80−type complex
9d
intracellular
intracellular part
organelle part
nucleus
nuclear part
membrane−enclosed lumen
nuclear lumen
nucleoplasm
SWI/SNF superfamily−type complex
lateral loop
12d
cell
cell part
intracellular
intracellular part
intracellular membrane−bounded organelle
nucleus
nuclear part
nuclear lumen
nucleoplasm
nuclear body
15d
intracellular
intracellular part
intracellular organelle
intracellular membrane−bounded organelle
intracellular organelle part
organelle part
nucleus
nuclear part
nuclear lumen
nucleoplasm
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
−5
−6
−7

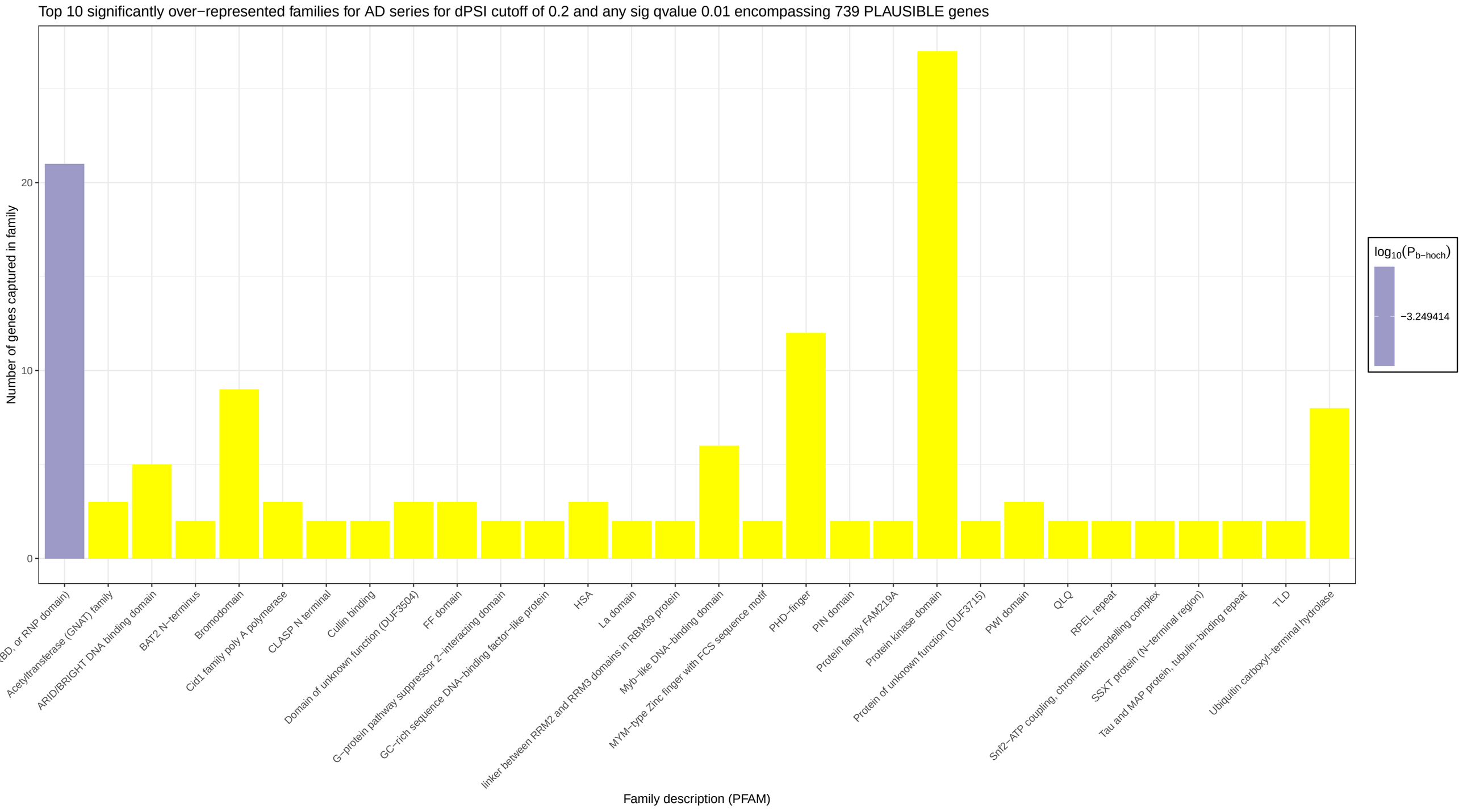

Top 10 significantly over−represented CC GO terms for the 10 % lowest PSI PLAUSIBLE isoforms in each AD time
MSC
intracellular
intracellular part
organelle
intracellular organelle
intracellular membrane−bounded organelle
nucleus
membrane−enclosed lumen
nuclear part
nuclear lumen
nucleoplasm
6h
intracellular
intracellular part
organelle
intracellular membrane−bounded organelle
asymmetric synapse
postsynaptic density
SWI/SNF superfamily−type complex
basal cortex
CRD−mediated mRNA stability complex
dendritic branch
12h
intracellular
intracellular part
organelle
intracellular organelle
intracellular membrane−bounded organelle
nucleus
nuclear part
nuclear lumen
cytoskeleton
microtubule cytoskeleton
1d
intracellular
intracellular part
nucleus
cytosol
nuclear part
nuclear lumen
nucleoplasm
nuclear body
nuclear speck
nuclear stress granule
3d
intracellular
intracellular part
nucleus
cytosol
nuclear part
nuclear lumen
nucleoplasm
nucleoplasm part
nuclear body
nuclear speck
6d
intracellular
intracellular part
cytoplasm
organelle part
intracellular organelle part
intracellular non−membrane−bounded organelle
non−membrane−bounded organelle
cytosol
nuclear lumen
AP−1 adaptor complex
9d
intracellular
intracellular part
organelle
intracellular organelle
intracellular membrane−bounded organelle
intracellular organelle part
nucleus
nuclear part
nuclear lumen
nucleoplasm
12d
intracellular
intracellular part
organelle
intracellular organelle
organelle part
nucleus
intracellular non−membrane−bounded organelle
non−membrane−bounded organelle
nuclear part
basal cortex
15d
intracellular
intracellular part
organelle
intracellular organelle
membrane−bounded organelle
intracellular membrane−bounded organelle
organelle part
intracellular organelle part
ATPase complex
SWI/SNF superfamily−type complex
Number of genes in GO term
GO term
log10(Pb−hoch)
−2
−3
−4
−5
−6


Top 10 significantly over−represented families for the 10 % highest PSI PLAUSIBLE isoforms in each AD timepoint
MSC
HIRA B motif
TUP1−like enhancer of split
PIN domain
Calponin homology (CH) domain
Domain of unknown function (DUF3504)
Saccharopine dehydrogenase C−terminal domain
Serine/threonine−protein kinase smg−1
Serine/threonine−protein kinase SMG1 N−terminal
SHNi−TPR
P68HR (NUC004) repeat
6h
Baculoviral IAP repeat−containing protein 6
Coiled coil protein 84
Domain of unknown function (DUF4171)
Haloacid dehalogenase−like hydrolase
La domain
Low molecular weight phosphotyrosine protein phosphatase
P68HR (NUC004) repeat
Protein kinase domain
RNA 2'−phosphotransferase, Tpt1 / KptA family
Unstructured region on SPEG complex protein
12h
SSXT protein (N−terminal region)
Baculoviral IAP repeat−containing protein 6
Coiled coil protein 84
Domain of unknown function (DUF4726)
mRNA capping enzyme
N−acetylglucosaminyl transferase component (Gpi1)
S100P−binding protein
SNF5 / SMARCB1 / INI1
Ubiquitin carboxyl−terminal hydrolase
Vitelline membrane outer layer protein I (VOMI)
1d
AP−3 complex subunit delta−1
Baculoviral IAP repeat−containing protein 6
DNA repair REX1−B
EVE domain
FF domain
Gemin6 protein
Kinase associated domain 1
Ligand−dependent nuclear receptor−interacting factor 1
Putative S−adenosyl−L−methionine−dependent methyltransferase
Vitelline membrane outer layer protein I (VOMI)
3d
Arginine−tRNA−protein transferase, C terminus
Arginine−tRNA−protein transferase, N terminus
BCL2−associated athanogene 6
PD−(D/E)XK nuclease superfamily
EVE domain
Gemin6 protein
Ligand−dependent nuclear receptor−interacting factor 1
Low molecular weight phosphotyrosine protein phosphatase
P68HR (NUC004) repeat
Unstructured region on SPEG complex protein
6d
Tau and MAP protein, tubulin−binding repeat
Afadin− and alpha −actinin−Binding
DMPK coiled coil domain like
G−protein pathway suppressor
Translation initiation factor IF−3, C−terminal domain
Translation initiation factor IF−3, N−terminal domain
Domain of unknown function (DUF3535)
Mediator complex subunit 23
AP−3 complex subunit delta−1
Protein kinase domain
9d
Domain of unknown function (DUF3535)
CSHC2 zinc finger
Caspase domain
HSA
PLU−1−like protein
SNF2 family N−terminal domain
Spt20 family
HIRA B motif
TUP1−like enhancer of split
SNF5 / SMARCB1 / INI1
12d
BAT2 N−terminus
tRNA methyl transferase
Bromodomain
CYTH domain
PWWP domain
TLD
HIRA B motif
TUP1−like enhancer of split
PIN domain
S100P−binding protein
15d
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
Mediator complex subunit 23
Spt20 family
Domain of unknown function (DUF4603)
Eukaryotic protein of unknown function (DUF842)
Integrator complex subunit 3
Mitochondrial large subunit ribosomal protein (mrp2)
Pre−mRNA splicing factor
tRNA methyl transferase
Coiled coil protein 84
Number of genes captured in family
Family description (PFAM)
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0


Top 10 significantly over−represented families for the 10 % lowest PSI PLAUSIBLE isoforms in each AD timepoint
MSC
HIRA B motif
TUP1−like enhancer of split
PIN domain
Calponin homology (CH) domain
Domain of unknown function (DUF3504)
Saccharopine dehydrogenase C−terminal domain
Serine/threonine−protein kinase smg−1
Serine/threonine−protein kinase SMG1 N−terminal
SHNi−TPR
P68HR (NUC004) repeat
6h
Baculoviral IAP repeat−containing protein 6
Coiled coil protein 84
Domain of unknown function (DUF4171)
Haloacid dehalogenase−like hydrolase
La domain
Low molecular weight phosphotyrosine protein phosphatase
P68HR (NUC004) repeat
Protein kinase domain
RNA 2'−phosphotransferase, Tpt1 / KptA family
Unstructured region on SPEG complex protein
12h
SSXT protein (N−terminal region)
Baculoviral IAP repeat−containing protein 6
Coiled coil protein 84
Domain of unknown function (DUF4726)
mRNA capping enzyme
N−acetylglucosaminyl transferase component (Gpi1)
S100P−binding protein
SNF5 / SMARCB1 / INI1
Ubiquitin carboxyl−terminal hydrolase
Vitelline membrane outer layer protein I (VOMI)
1d
AP−3 complex subunit delta−1
Baculoviral IAP repeat−containing protein 6
DNA repair REX1−B
EVE domain
FF domain
Gemin6 protein
Kinase associated domain 1
Ligand−dependent nuclear receptor−interacting factor 1
Putative S−adenosyl−L−methionine−dependent methyltransferase
Vitelline membrane outer layer protein I (VOMI)
3d
Arginine−tRNA−protein transferase, C terminus
Arginine−tRNA−protein transferase, N terminus
BCL2−associated athanogene 6
PD−(D/E)XK nuclease superfamily
EVE domain
Gemin6 protein
Ligand−dependent nuclear receptor−interacting factor 1
Low molecular weight phosphotyrosine protein phosphatase
P68HR (NUC004) repeat
Unstructured region on SPEG complex protein
6d
Tau and MAP protein, tubulin−binding repeat
Afadin− and alpha −actinin−Binding
DMPK coiled coil domain like
G−protein pathway suppressor
Translation initiation factor IF−3, C−terminal domain
Translation initiation factor IF−3, N−terminal domain
Domain of unknown function (DUF3535)
Mediator complex subunit 23
AP−3 complex subunit delta−1
Protein kinase domain
9d
Domain of unknown function (DUF3535)
CSHC2 zinc finger
Caspase domain
HSA
PLU−1−like protein
SNF2 family N−terminal domain
Spt20 family
HIRA B motif
TUP1−like enhancer of split
SNF5 / SMARCB1 / INI1
12d
BAT2 N−terminus
tRNA methyl transferase
Bromodomain
CYTH domain
PWWP domain
TLD
HIRA B motif
TUP1−like enhancer of split
PIN domain
S100P−binding protein
15d
RNA recognition motif. (a.k.a. RRM, RBD or RNP domain)
Mediator complex subunit 23
Spt20 family
Domain of unknown function (DUF4603)
Eukaryotic protein of unknown function (DUF842)
Integrator complex subunit 3
Mitochondrial large subunit ribosomal protein (mrp2)
Pre−mRNA splicing factor
tRNA methyl transferase
Coiled coil protein 84
Number of genes captured in family
Family description (PFAM)
log10(Pb−hoch)
−1.5
−2.0
−2.5
−3.0

Top 10 significantly over−represented GO terms for AD series for dPSI cutoff of 0.2 and any sig qvalue 0.01 encompassing 739  PLAUSIBLE genes




Top 10 significantly over−represented families for AD series for dPSI cutoff of 0.2 and any sig qvalue 0.01 encompassing 739 PLAUSIBLE genes
Number of genes captured in family
0
10
20
Family description (PFAM)
(BD, or RNP domain)
Acetyltransferase (GNAT) family
ARID/BRIGHT DNA binding domain
BAT2 N−terminus
Bromodomain
Cid1 family poly A polymerase
CLASP N terminal
Cullin binding
Domain of unknown function (DUF3504)
FF domain
G−protein pathway suppressor 2−interacting domain
GC−rich sequence DNA−binding factor−like protein
HSA
La domain
linker between RRM2 and RRM3 domains in RBM39 protein
Myb−like DNA−binding domain
MYM−type Zinc finger with FCS sequence motif
PHD−finger
PIN domain
Protein family FAM219A
Protein kinase domain
Protein of unknown function (DUF3715)
PWI domain
QLQ
RPEL repeat
Snf2−ATP coupling, chromatin remodelling complex
SSXT protein (N−terminal region)
Tau and MAP protein, tubulin−binding repeat
TLD
Ubiquitin carboxyl−terminal hydrolase
log10(Pb−hoch)
−3.249414