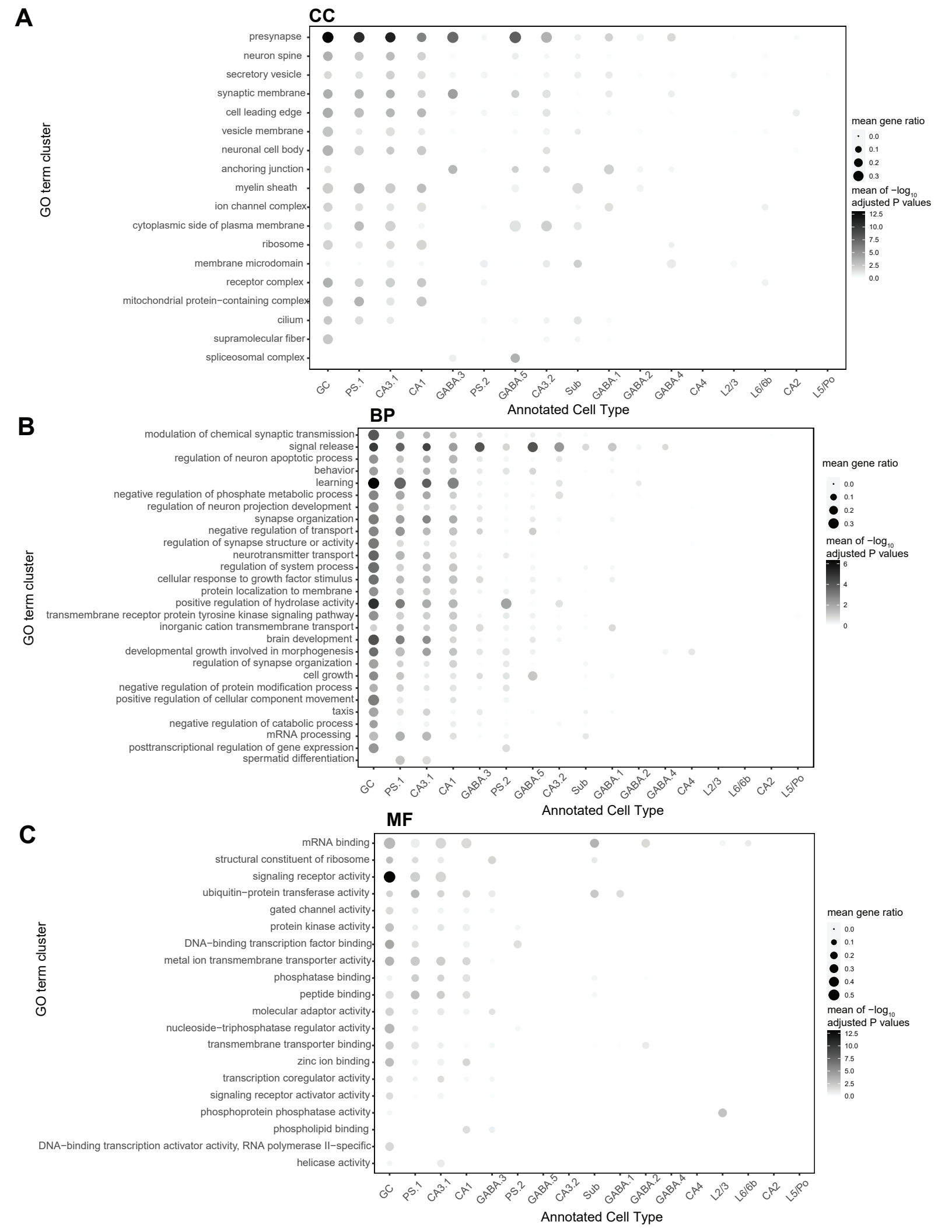
A
CC
GO term cluster
presynapse
neuron spine
secretory vesicle
synaptic membrane
cell leading edge
vesicle membrane
neuronal cell body
anchoring junction
myelin sheath
ion channel complex
cytoplasmic side of plasma membrane
ribosome
membrane microdomain
receptor complex
mitochondrial protein−containing complex
cilium
supramolecular fiber
spliceosomal complex
GC
PS.1
CA3.1
CA1
GABA.3
PS.2
GABA.5
CA3.2
Sub
GABA.1
GABA.2
GABA.4
CA4
L2/3
L6/6b
CA2
L5/Po
Annotated Cell Type
mean gene ratio
0.0
0.1
0.2
0.3
mean of −log10 adjusted P values
12.5
10.0
7.5
5.0
2.5
0.0
B
BP
GO term cluster
modulation of chemical synaptic transmission
signal release
regulation of neuron apoptotic process
behavior
learning
negative regulation of phosphate metabolic process
regulation of neuron projection development
synapse organization
negative regulation of transport
regulation of synapse structure or activity
neurotransmitter transport
regulation of system process
cellular response to growth factor stimulus
protein localization to membrane
positive regulation of hydrolase activity
transmembrane receptor protein tyrosine kinase signaling pathway
inorganic cation transmembrane transport
brain development
developmental growth involved in morphogenesis
regulation of synapse organization
cell growth
negative regulation of protein modification process
positive regulation of cellular component movement
taxis
negative regulation of catabolic process
mRNA processing
posttranscriptional regulation of gene expression
spermatid differentiation
GC
PS.1
CA3.1
CA1
GABA.3
PS.2
GABA.5
CA3.2
Sub
GABA.1
GABA.2
GABA.4
CA4
L2/3
L6/6b
CA2
L5/Po
Annotated Cell Type
mean gene ratio
0.0
0.1
0.2
0.3
mean of −log10 adjusted P values
6
4
2
0
C
MF
GO term cluster
mRNA binding
structural constituent of ribosome
signaling receptor activity
ubiquitin−protein transferase activity
gated channel activity
protein kinase activity
DNA−binding transcription factor binding
metal ion transmembrane transporter activity
phosphatase binding
peptide binding
molecular adaptor activity
nucleoside−triphosphatase regulator activity
transmembrane transporter binding
zinc ion binding
transcription coregulator activity
signaling receptor activator activity
phosphoprotein phosphatase activity
phospholipid binding
DNA−binding transcription activator activity, RNA polymerase II−specific
helicase activity
GC
PS.1
CA3.1
CA1
GABA.3
PS.2
GABA.5
CA3.2
Sub
GABA.1
GABA.2
GABA.4
CA4
L2/3
L6/6b
CA2
L5/Po
Annotated Cell Type
mean gene ratio
0.0
0.1
0.2
0.3
0.4
0.5
mean of −log10 adjusted P values
12.5
10.0
7.5
5.0
2.5
0.0