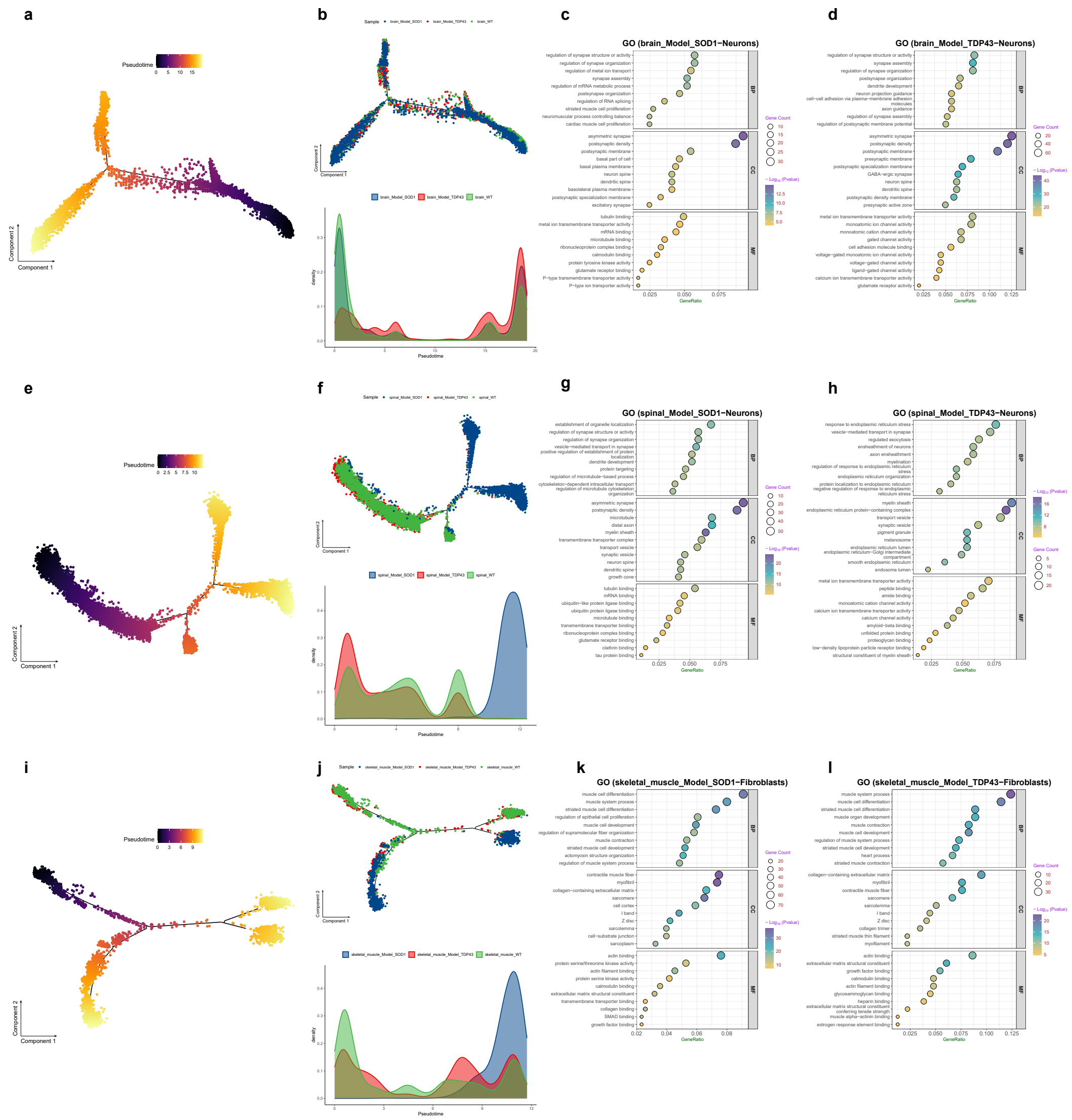
a
Pseudotime
0 5 10 15
Component 1
Component 2
b
Sample brain_Model_SOD1 brain_Model_TDP43 brain_WT
Component 1
Component 2
brain_Model_SOD1 brain_Model_TDP43 brain_WT
density
Pseudotime
c
GO (brain_Model_SOD1−Neurons)
regulation of synapse structure or activity
regulation of synapse organization
regulation of metal ion transport
synapse assembly
regulation of mRNA metabolic process
postsynapse organization
regulation of RNA splicing
striated muscle cell proliferation
neuromuscular process controlling balance
cardiac muscle cell proliferation
asymmetric synapse
postsynaptic density
postsynaptic membrane
basal part of cell
basal plasma membrane
neuron spine
dendritic spine
basolateral plasma membrane
postsynaptic specialization membrane
excitatory synapse
tubulin binding
metal ion transmembrane transporter activity
mRNA binding
microtubule binding
ribonucleoprotein complex binding
calmodulin binding
protein tyrosine kinase activity
glutamate receptor binding
P−type transmembrane transporter activity
P−type ion transporter activity
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)
d
GO (brain_Model_TDP43−Neurons)
regulation of synapse structure or activity
synapse assembly
regulation of synapse organization
postsynapse organization
dendrite development
neuron projection guidance
cell−cell adhesion via plasma−membrane adhesion molecules
axon guidance
regulation of synapse assembly
regulation of postsynaptic membrane potential
asymmetric synapse
postsynaptic density
postsynaptic membrane
presynaptic membrane
postsynaptic specialization membrane
GABA−ergic synapse
neuron spine
dendritic spine
postsynaptic density membrane
presynaptic active zone
metal ion transmembrane transporter activity
monoatomic ion channel activity
monoatomic cation channel activity
gated channel activity
cell adhesion molecule binding
voltage−gated monoatomic ion channel activity
voltage−gated channel activity
ligand−gated channel activity
calcium ion transmembrane transporter activity
glutamate receptor activity
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)
e
Pseudotime
0 2.5 5 7.5 10
Component 1
Component 2
f
Sample spinal_Model_SOD1 spinal_Model_TDP43 spinal_WT
Component 1
Component 2
spinal_Model_SOD1 spinal_Model_TDP43 spinal_WT
density
Pseudotime
g
GO (spinal_Model_SOD1−Neurons)
establishment of organelle localization
regulation of synapse structure or activity
regulation of synapse organization
vesicle−mediated transport in synapse
positive regulation of establishment of protein localization
dendrite development
protein targeting
regulation of microtubule−based process
cytoskeleton−dependent intracellular transport
regulation of microtubule cytoskeleton organization
asymmetric synapse
postsynaptic density
microtubule
distal axon
myelin sheath
transmembrane transporter complex
transport vesicle
synaptic vesicle
neuron spine
dendritic spine
growth cone
tubulin binding
mRNA binding
ubiquitin−like protein ligase binding
ubiquitin protein ligase binding
microtubule binding
transmembrane transporter binding
ribonucleoprotein complex binding
glutamate receptor binding
clathrin binding
tau protein binding
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)
h
GO (spinal_Model_TDP43−Neurons)
response to endoplasmic reticulum stress
vesicle−mediated transport in synapse
regulated exocytosis
ensheathment of neurons
axon ensheathment
myelination
regulation of response to endoplasmic reticulum stress
endoplasmic reticulum organization
protein localization to endoplasmic reticulum
negative regulation of response to endoplasmic reticulum stress
myelin sheath
endoplasmic reticulum protein−containing complex
transport vesicle
synaptic vesicle
pigment granule
melanosome
endoplasmic reticulum lumen
endoplasmic reticulum−Golgi intermediate compartment
smooth endoplasmic reticulum
endosome lumen
metal ion transmembrane transporter activity
peptide binding
amide binding
monoatomic cation channel activity
calcium ion transmembrane transporter activity
calcium channel activity
amyloid−beta binding
unfolded protein binding
proteoglycan binding
low−density lipoprotein particle receptor binding
structural constituent of myelin sheath
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)
i
Pseudotime
0 3 6 9
Component 1
Component 2
j
Sample skeletal_muscle_Model_SOD1 skeletal_muscle_Model_TDP43 skeletal_muscle_WT
Component 1
Component 2
skeletal_muscle_Model_SOD1 skeletal_muscle_Model_TDP43 skeletal_muscle_WT
density
Pseudotime
k
GO (skeletal_muscle_Model_SOD1−Fibroblasts)
muscle cell differentiation
muscle system process
striated muscle cell differentiation
regulation of epithelial cell proliferation
muscle cell development
regulation of supramolecular fiber organization
muscle contraction
striated muscle cell development
actomyosin structure organization
regulation of muscle system process
contractile muscle fiber
myofibril
collagen−containing extracellular matrix
sarcomere
cell cortex
I band
Z disc
sarcolemma
cell−substrate junction
sarcoplasm
actin binding
protein serine/threonine kinase activity
actin filament binding
protein serine kinase activity
calmodulin binding
extracellular matrix structural constituent
transmembrane transporter binding
collagen binding
SMAD binding
growth factor binding
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)
l
GO (skeletal_muscle_Model_TDP43−Fibroblasts)
muscle system process
muscle cell differentiation
striated muscle cell differentiation
muscle organ development
muscle contraction
muscle cell development
regulation of muscle system process
striated muscle cell development
heart process
striated muscle contraction
collagen−containing extracellular matrix
myofibril
contractile muscle fiber
sarcomere
sarcolemma
I band
Z disc
collagen trimer
striated muscle thin filament
myofilament
actin binding
extracellular matrix structural constituent
growth factor binding
calmodulin binding
actin filament binding
glycosaminoglycan binding
heparin binding
extracellular matrix structural constituent conferring tensile strength
muscle alpha−actinin binding
estrogen response element binding
BP
CC
MF
GeneRatio
Gene Count
− Log10 (Pvalue)