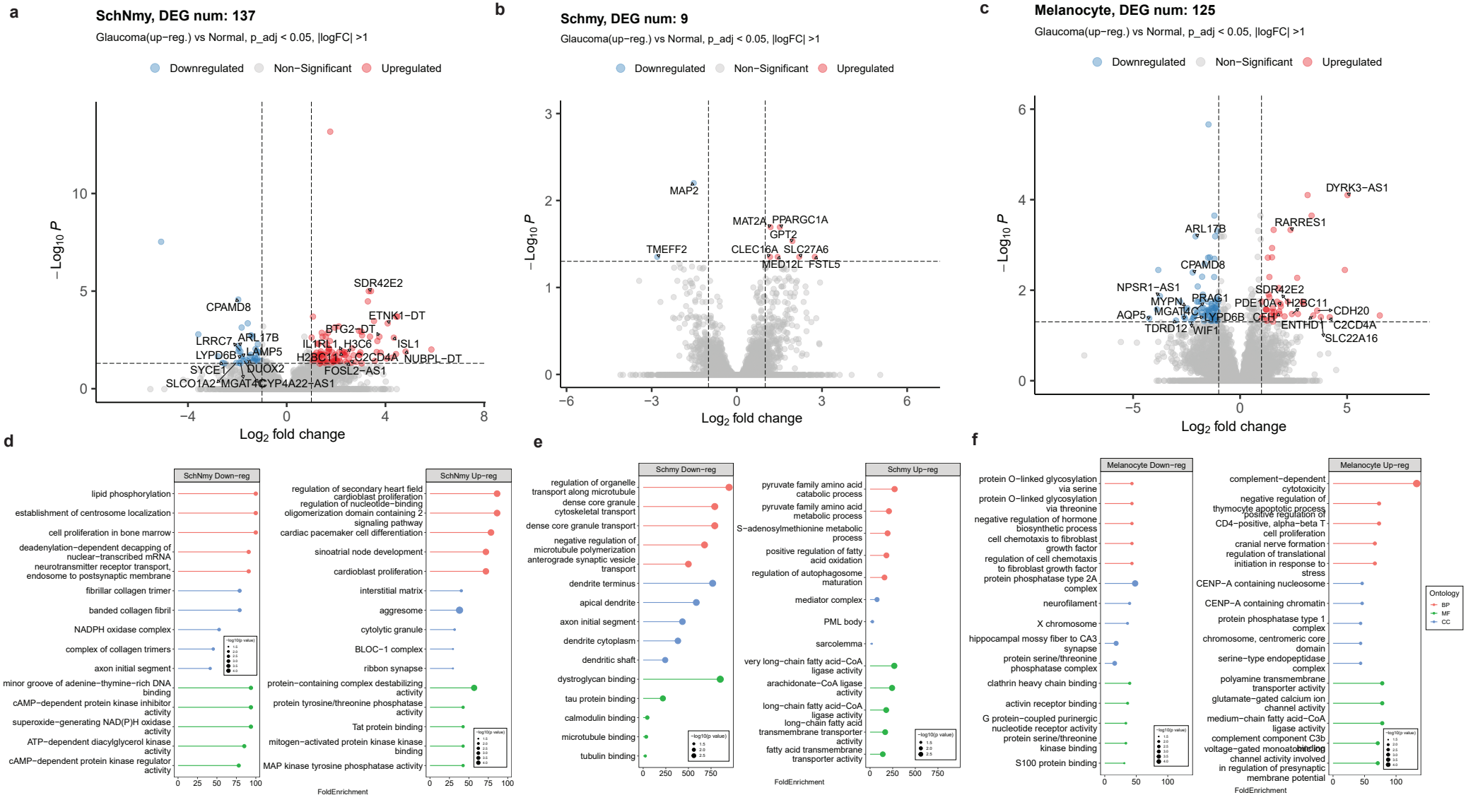
a
SchNmy, DEG num: 137
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
Downregulated
Non−Significant
Upregulated
−Log10 P
Log2 fold change
SDR42E2
CPAMD8
ETNK1−DT
BTG2−DT
LRRC7
ARL17B
IL1RL1
H3C6
ISL1
LYPD6B
LAMP5
H2BC11
C2CD4A
NUBPL−DT
SYCE1
DUOX2
FOSL2−AS1
SLCO1A2
MGAT4C
CYP4A22−AS1
b
Schmy, DEG num: 9
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
MAP2
MAT2A
PPARGC1A
GPT2
TMEFF2
CLEC16A
SLC27A6
MED12L
FSTL5
c
Melanocyte, DEG num: 125
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
DYRK3−AS1
RARRES1
ARL17B
CPAMD8
NPSR1−AS1
SDR42E2
MYPN
PRAG1
PDE10A
H2BC11
CDH20
AQP5
MGAT4C
LYPD6B
CFH
ENTHD1
C2CD4A
TDRD12
WIF1
SLC22A16
d
SchNmy Down−reg
lipid phosphorylation
establishment of centrosome localization
cell proliferation in bone marrow
deadenylation−dependent decapping of nuclear−transcribed mRNA
neurotransmitter receptor transport, endosome to postsynaptic membrane
fibrillar collagen trimer
banded collagen fibril
NADPH oxidase complex
complex of collagen trimers
axon initial segment
minor groove of adenine−thymine−rich DNA binding
cAMP−dependent protein kinase inhibitor activity
superoxide−generating NAD(P)H oxidase activity
ATP−dependent diacylglycerol kinase activity
cAMP−dependent protein kinase regulator activity
SchNmy Up−reg
regulation of secondary heart field cardioblast proliferation
regulation of nucleotide−binding oligomerization domain containing 2 signaling pathway
cardiac pacemaker cell differentiation
sinoatrial node development
cardioblast proliferation
interstitial matrix
aggresome
cytolytic granule
BLOC−1 complex
ribbon synapse
protein−containing complex destabilizing activity
protein tyrosine/threonine phosphatase activity
Tat protein binding
mitogen−activated protein kinase kinase binding
MAP kinase tyrosine phosphatase activity
−log10(p value)
FoldEnrichment
e
Schmy Down−reg
regulation of organelle transport along microtubule
dense core granule cytoskeletal transport
dense core granule transport
negative regulation of microtubule polymerization
anterograde synaptic vesicle transport
dendrite terminus
apical dendrite
axon initial segment
dendrite cytoplasm
dendritic shaft
dystroglycan binding
tau protein binding
calmodulin binding
microtubule binding
tubulin binding
Schmy Up−reg
pyruvate family amino acid catabolic process
pyruvate family amino acid metabolic process
S−adenosylmethionine metabolic process
positive regulation of fatty acid oxidation
regulation of autophagosome maturation
mediator complex
PML body
sarcolemma
very long−chain fatty acid−CoA ligase activity
arachidonate−CoA ligase activity
long−chain fatty acid−CoA ligase activity
long−chain fatty acid transmembrane transporter activity
fatty acid transmembrane transporter activity
f
Melanocyte Down−reg
protein O−linked glycosylation via serine
protein O−linked glycosylation via threonine
negative regulation of hormone biosynthetic process
cell chemotaxis to fibroblast growth factor
regulation of cell chemotaxis to fibroblast growth factor
protein phosphatase type 2A complex
neurofilament
X chromosome
hippocampal mossy fiber to CA3 synapse
protein serine/threonine phosphatase complex
clathrin heavy chain binding
activin receptor binding
G protein−coupled purinergic nucleotide receptor activity
protein serine/threonine kinase binding
S100 protein binding
Melanocyte Up−reg
complement−dependent cytotoxicity
negative regulation of thymocyte apoptotic process
positive regulation of CD4−positive, alpha−beta T cell proliferation
cranial nerve formation
regulation of translational initiation in response to stress
CENP−A containing nucleosome
CENP−A containing chromatin
protein phosphatase type 1 complex
chromosome, centromeric core domain
serine−type endopeptidase complex
polyamine transmembrane transporter activity
glutamate−gated calcium ion channel activity
medium−chain fatty acid−CoA ligase activity
complement component C3b binding
voltage−gated monoatomic ion channel activity involved in regulation of presynaptic membrane potential
Ontology
BP
MF
CC