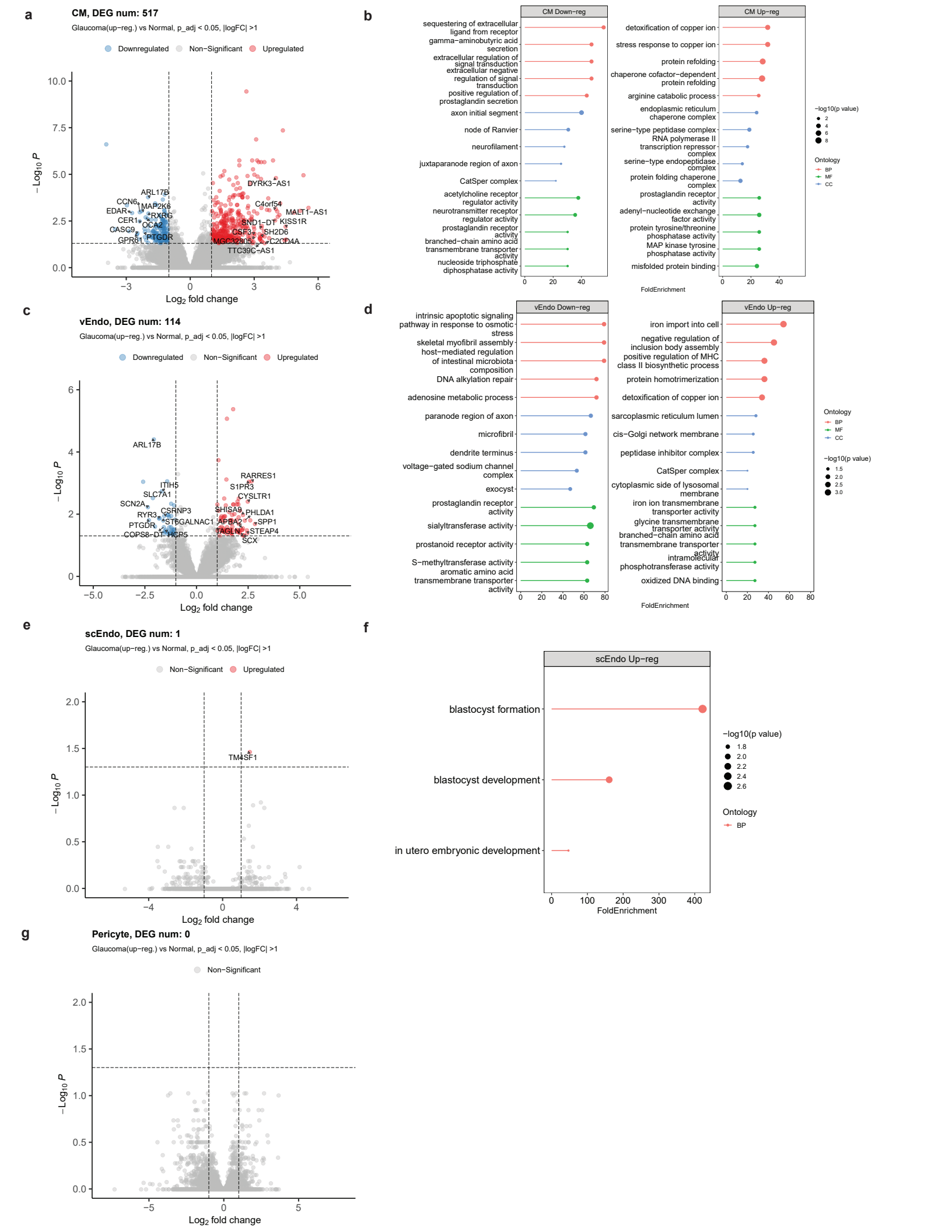
a
CM, DEG num: 517
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
Downregulated
Non−Significant
Upregulated
−Log10 P
Log2 fold change
ARL17B
CCN6
MAP2K6
EDAR
RXRG
CER1
OCA2
CASC9
PTGDR
GPR61
DYRK3−AS1
C4orf54
MALT1−AS1
SND1−DT
KISS1R
CSF3
SH2D6
MGC32805
C2CD4A
TTC39C−AS1
b
CM Down−reg
sequestering of extracellular ligand from receptor
gamma−aminobutyric acid secretion
extracellular regulation of signal transduction
extracellular negative regulation of signal transduction
positive regulation of prostaglandin secretion
axon initial segment
node of Ranvier
neurofilament
juxtaparanode region of axon
CatSper complex
acetylcholine receptor regulator activity
neurotransmitter receptor regulator activity
prostaglandin receptor activity
branched−chain amino acid transmembrane transporter activity
nucleoside triphosphate diphosphatase activity
CM Up−reg
detoxification of copper ion
stress response to copper ion
protein refolding
chaperone cofactor−dependent protein refolding
arginine catabolic process
endoplasmic reticulum chaperone complex
serine−type peptidase complex
RNA polymerase II transcription repressor complex
serine−type endopeptidase complex
protein folding chaperone complex
prostaglandin receptor activity
adenyl−nucleotide exchange factor activity
protein tyrosine/threonine phosphatase activity
MAP kinase tyrosine phosphatase activity
misfolded protein binding
FoldEnrichment
−log10(p value)
Ontology
BP
MF
CC
c
vEndo, DEG num: 114
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
Downregulated
Non−Significant
Upregulated
−Log10 P
Log2 fold change
ARL17B
ITIH5
SLC7A1
SCN2A
RYR3
CSRNP3
PTGDR
ST6GALNAC1
COPS8−DT
HCP5
RARRES1
S1PR3
CYSLTR1
SHISA9
PHLDA1
APBA2
SPP1
TAGLN
STEAP4
SCX
d
vEndo Down−reg
intrinsic apoptotic signaling pathway in response to osmotic stress
skeletal myofibril assembly
host−mediated regulation of intestinal microbiota composition
DNA alkylation repair
adenosine metabolic process
paranode region of axon
microfibril
dendrite terminus
voltage−gated sodium channel complex
exocyst
prostaglandin receptor activity
sialyltransferase activity
prostanoid receptor activity
S−methyltransferase activity
aromatic amino acid transmembrane transporter activity
vEndo Up−reg
iron import into cell
negative regulation of inclusion body assembly
positive regulation of MHC class II biosynthetic process
protein homotrimerization
detoxification of copper ion
sarcoplasmic reticulum lumen
cis−Golgi network membrane
peptidase inhibitor complex
CatSper complex
cytoplasmic side of lysosomal membrane
iron ion transmembrane transporter activity
glycine transmembrane transporter activity
branched−chain amino acid transmembrane transporter activity
intramolecular phosphotransferase activity
oxidized DNA binding
FoldEnrichment
Ontology
BP
MF
CC
−log10(p value)
e
scEndo, DEG num: 1
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
Non−Significant
Upregulated
−Log10 P
Log2 fold change
TM4SF1
f
scEndo Up−reg
blastocyst formation
blastocyst development
in utero embryonic development
FoldEnrichment
−log10(p value)
Ontology
BP
g
Pericyte, DEG num: 0
Glaucoma(up−reg.) vs Normal, p_adj < 0.05, |logFC| >1
Non−Significant
−Log10 P
Log2 fold change