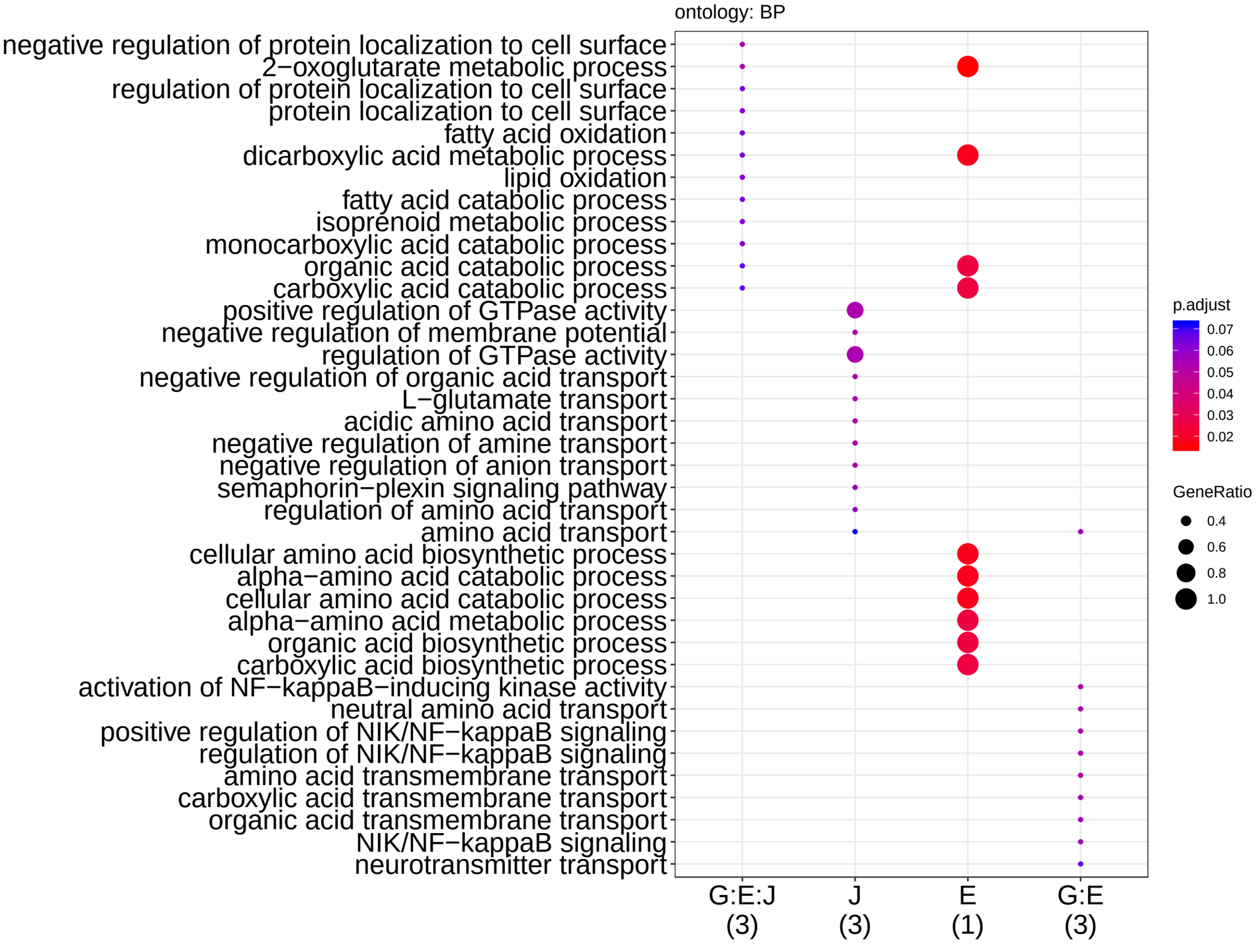
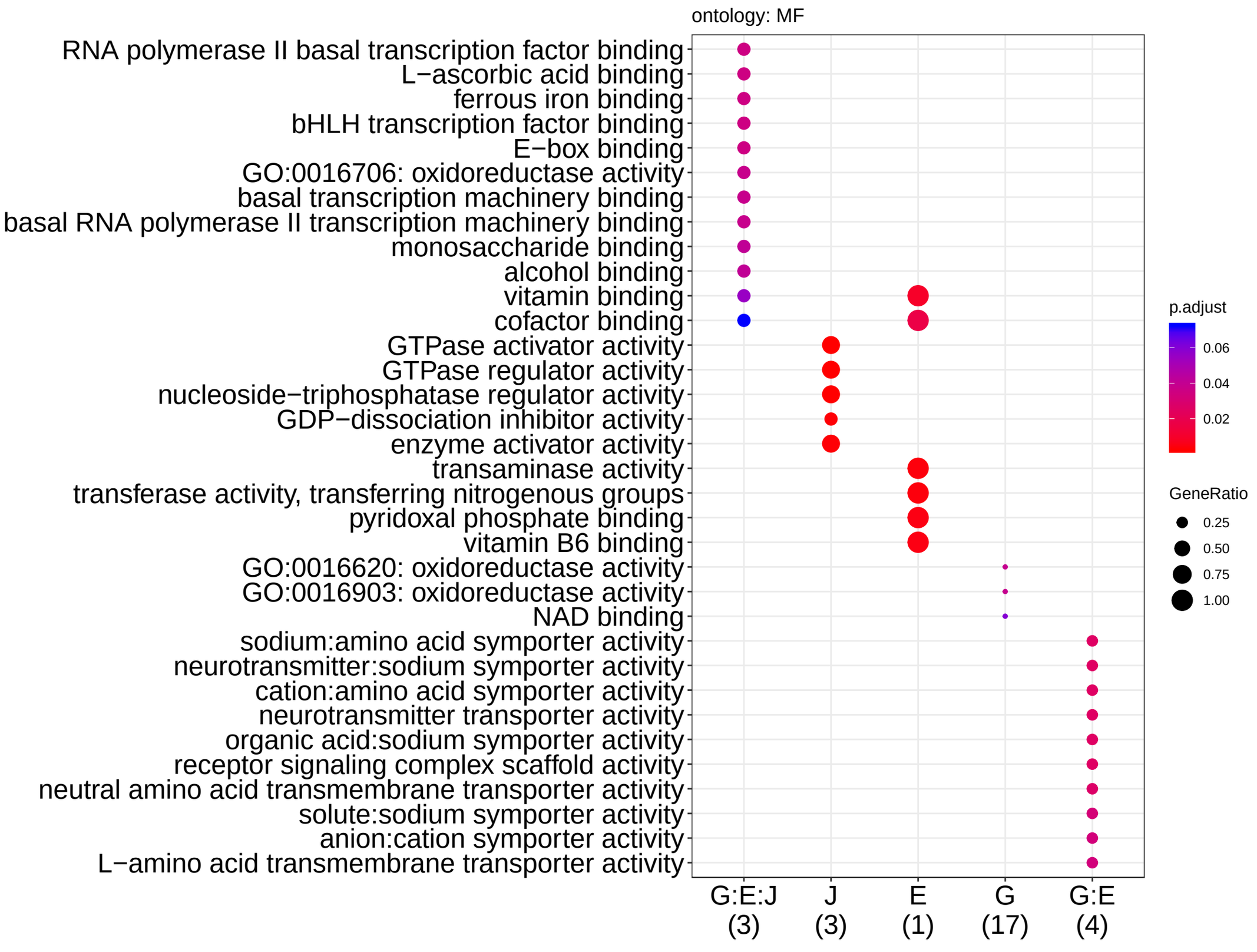
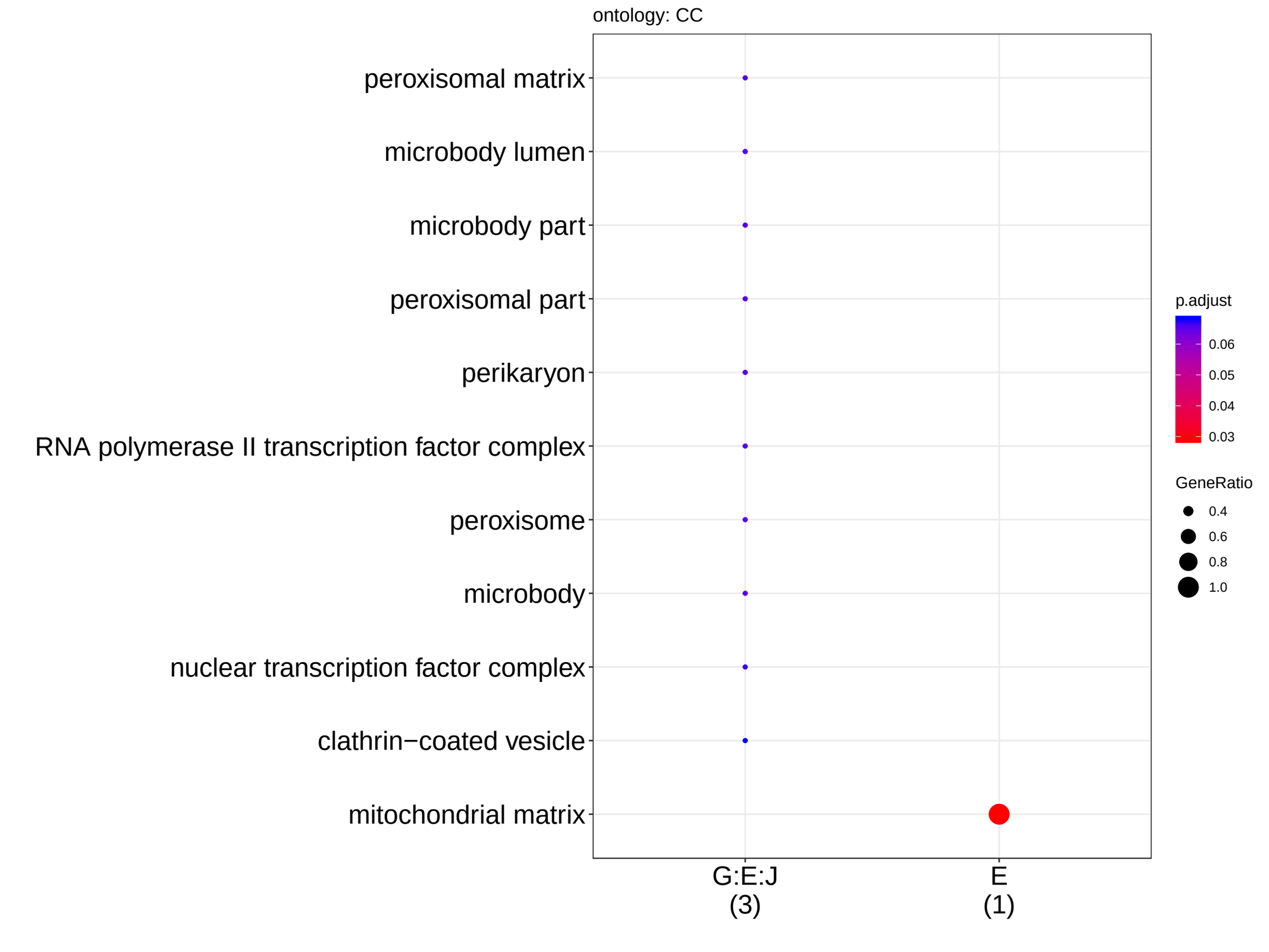
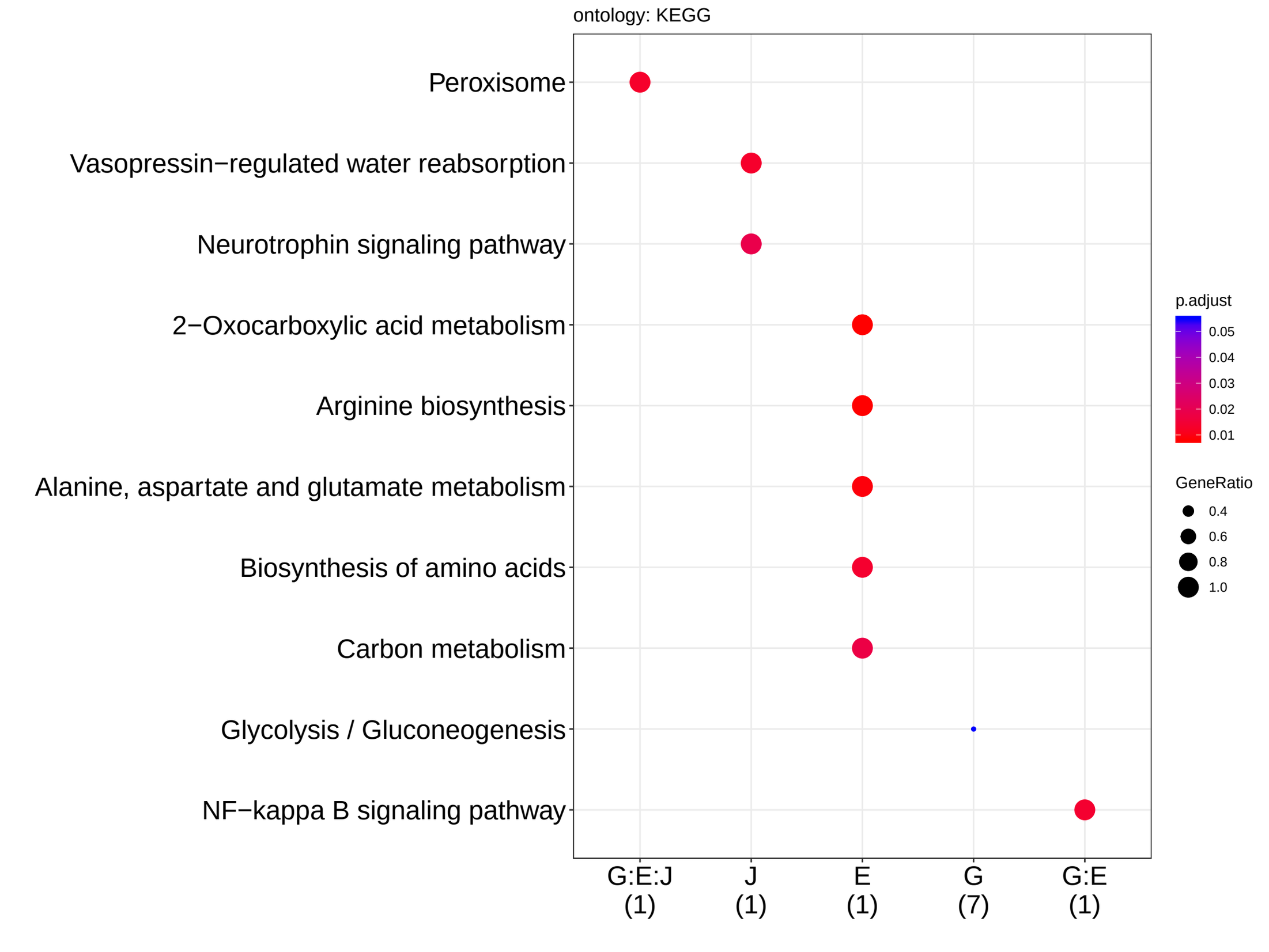

ontology: BP
negative regulation of protein localization to cell surface
2−oxoglutarate metabolic process
regulation of protein localization to cell surface
protein localization to cell surface
fatty acid oxidation
dicarboxylic acid metabolic process
lipid oxidation
fatty acid catabolic process
isoprenoid metabolic process
monocarboxylic acid catabolic process
organic acid catabolic process
carboxylic acid catabolic process
positive regulation of GTPase activity
negative regulation of membrane potential
regulation of GTPase activity
negative regulation of organic acid transport
L−glutamate transport
acidic amino acid transport
negative regulation of amine transport
negative regulation of anion transport
semaphorin−plexin signaling pathway
regulation of amino acid transport
amino acid transport
cellular amino acid biosynthetic process
alpha−amino acid catabolic process
cellular amino acid catabolic process
alpha−amino acid metabolic process
organic acid biosynthetic process
carboxylic acid biosynthetic process
activation of NF−kappaB−inducing kinase activity
neutral amino acid transport
positive regulation of NIK/NF−kappaB signaling
regulation of NIK/NF−kappaB signaling
amino acid transmembrane transport
carboxylic acid transmembrane transport
organic acid transmembrane transport
NIK/NF−kappaB signaling
neurotransmitter transport
G:E:J (3)
J (3)
E (1)
G:E (3)
p.adjust
0.07
0.06
0.05
0.04
0.03
0.02
GeneRatio
0.4
0.6
0.8
1.0


ontology: MF
RNA polymerase II basal transcription factor binding
L−ascorbic acid binding
ferrous iron binding
bHLH transcription factor binding
E−box binding
GO:0016706: oxidoreductase activity
basal transcription machinery binding
basal RNA polymerase II transcription machinery binding
monosaccharide binding
alcohol binding
vitamin binding
cofactor binding
GTPase activator activity
GTPase regulator activity
nucleoside−triphosphatase regulator activity
GDP−dissociation inhibitor activity
enzyme activator activity
transaminase activity
transferase activity, transferring nitrogenous groups
pyridoxal phosphate binding
vitamin B6 binding
GO:0016620: oxidoreductase activity
GO:0016903: oxidoreductase activity
NAD binding
sodium:amino acid symporter activity
neurotransmitter:sodium symporter activity
cation:amino acid symporter activity
neurotransmitter transporter activity
organic acid:sodium symporter activity
receptor signaling complex scaffold activity
neutral amino acid transmembrane transporter activity
solute:sodium symporter activity
anion:cation symporter activity
L−amino acid transmembrane transporter activity
G:E:J (3)
J (3)
E (1)
G (17)
G:E (4)
p.adjust
0.06
0.04
0.02
GeneRatio
0.25
0.50
0.75
1.00


ontology: CC
peroxisomal matrix
microbody lumen
microbody part
peroxisomal part
perikaryon
RNA polymerase II transcription factor complex
peroxisome
microbody
nuclear transcription factor complex
clathrin−coated vesicle
mitochondrial matrix
G:E:J
(3)
E
(1)
p.adjust
0.06
0.05
0.04
0.03
GeneRatio
0.4
0.6
0.8
1.0


ontology: KEGG
Peroxisome
Vasopressin−regulated water reabsorption
Neurotrophin signaling pathway
2−Oxocarboxylic acid metabolism
Arginine biosynthesis
Alanine, aspartate and glutamate metabolism
Biosynthesis of amino acids
Carbon metabolism
Glycolysis / Gluconeogenesis
NF−kappa B signaling pathway
G:E:J (1)
J (1)
E (1)
G (7)
G:E (1)
p.adjust
0.05
0.04
0.03
0.02
0.01
GeneRatio
0.4
0.6
0.8
1.0