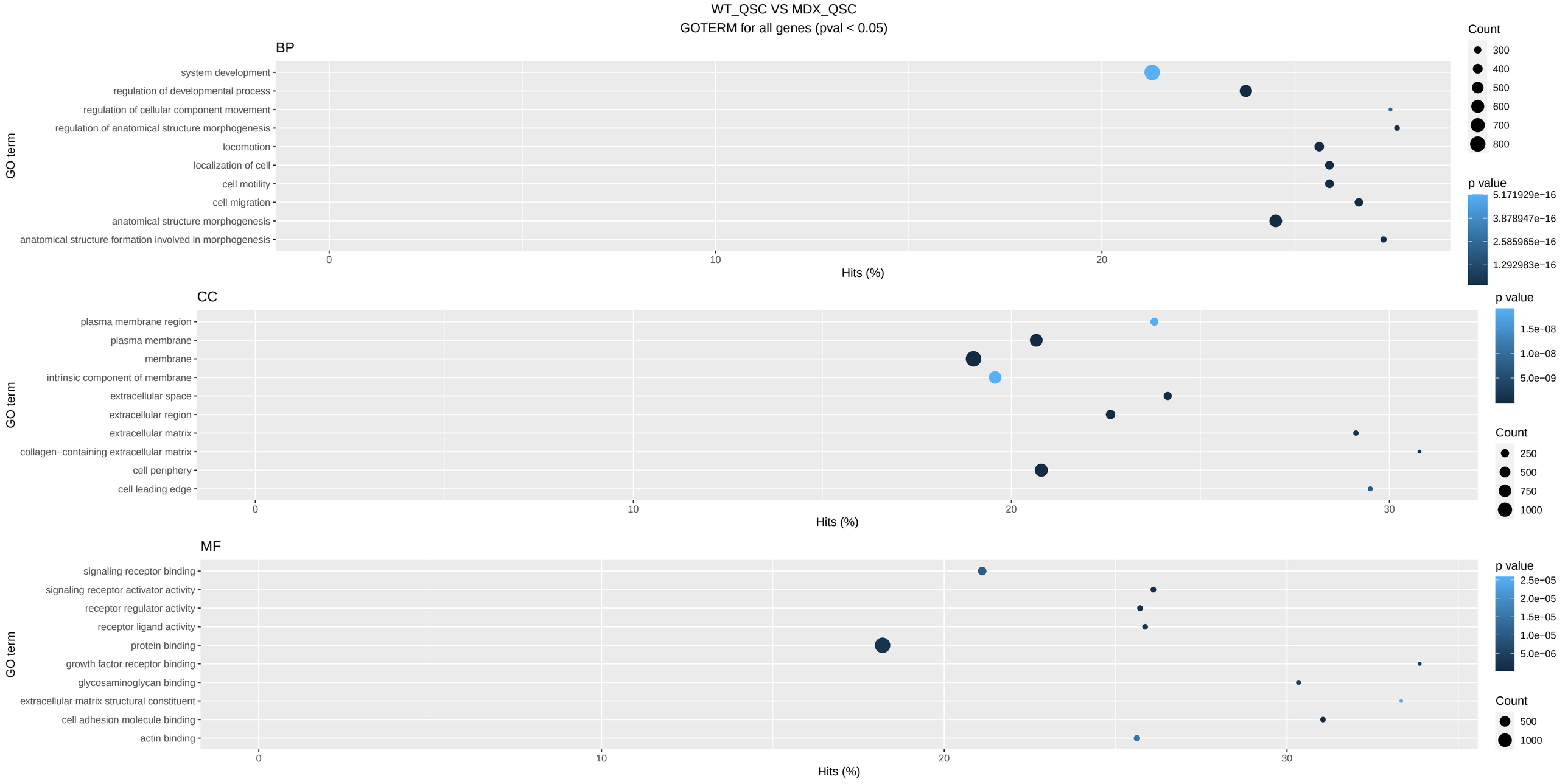
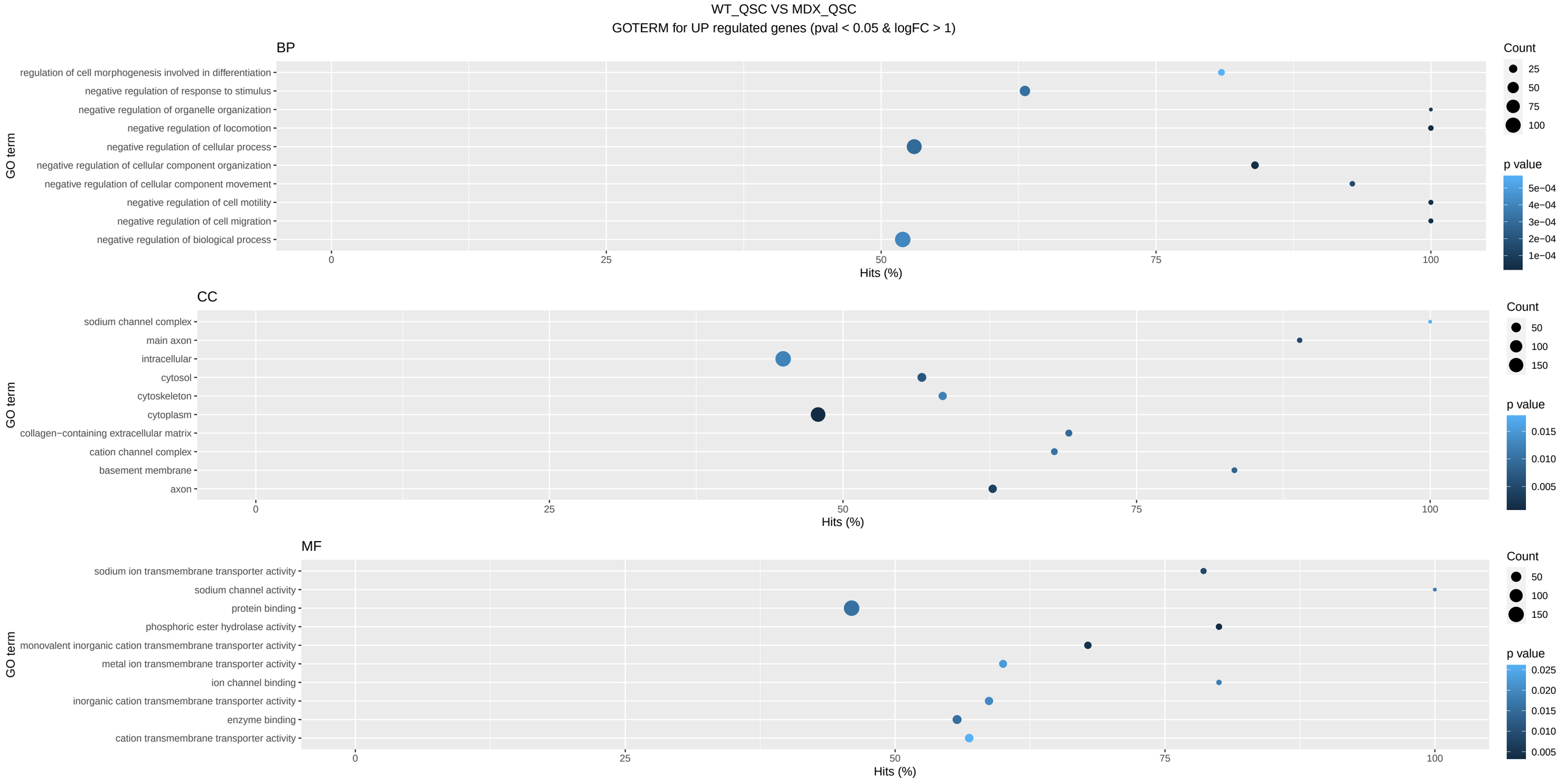
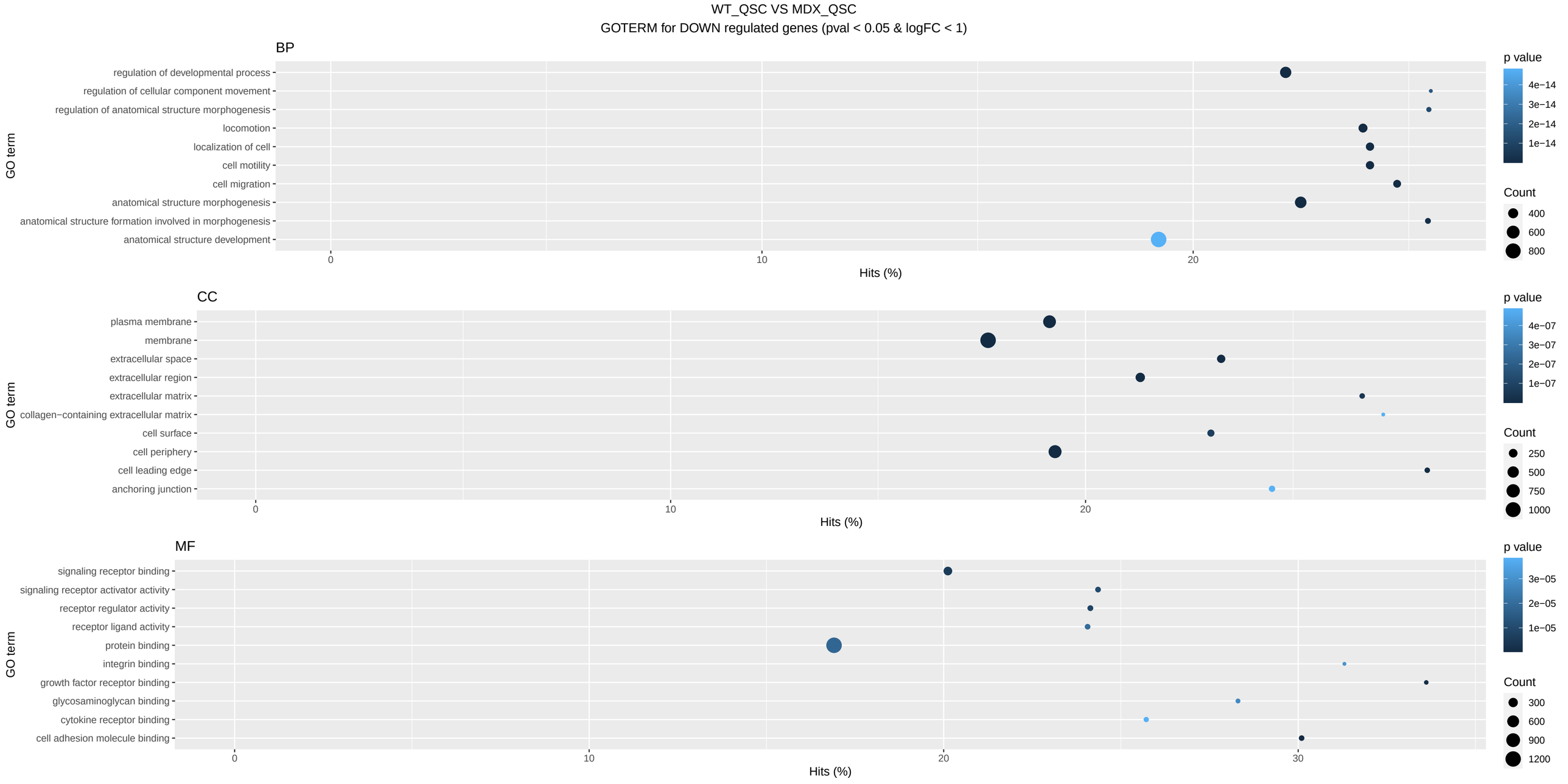
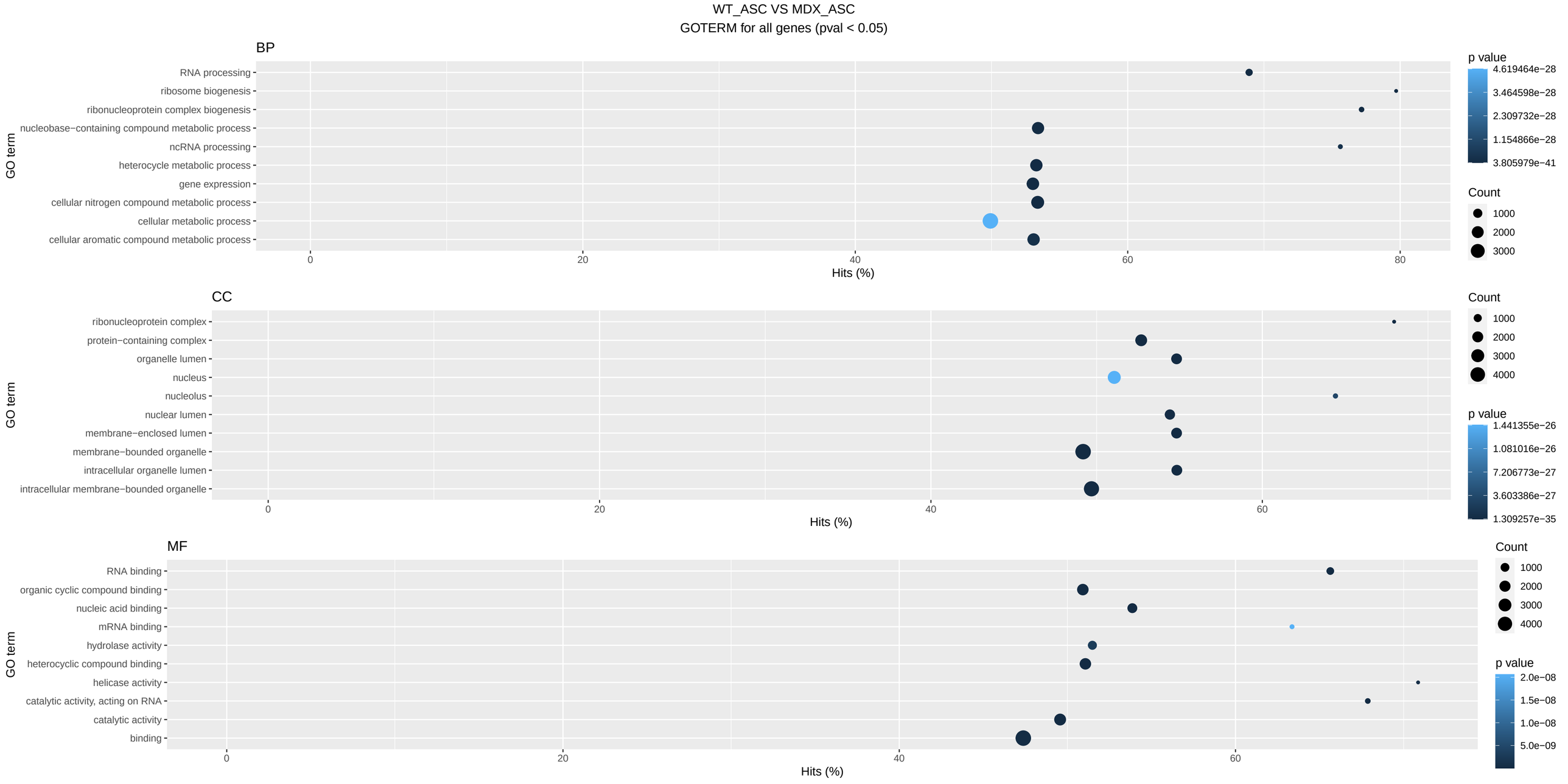
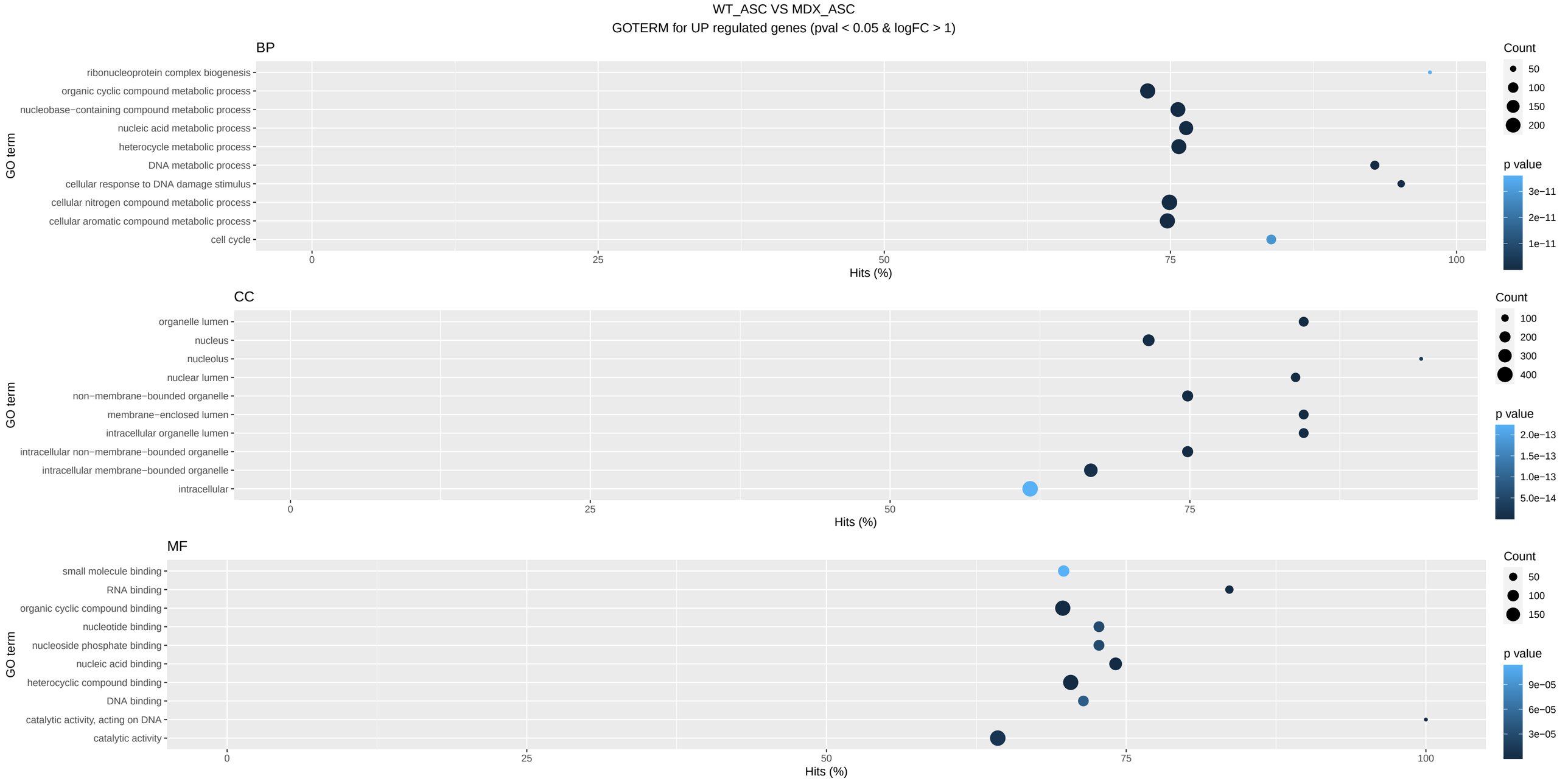
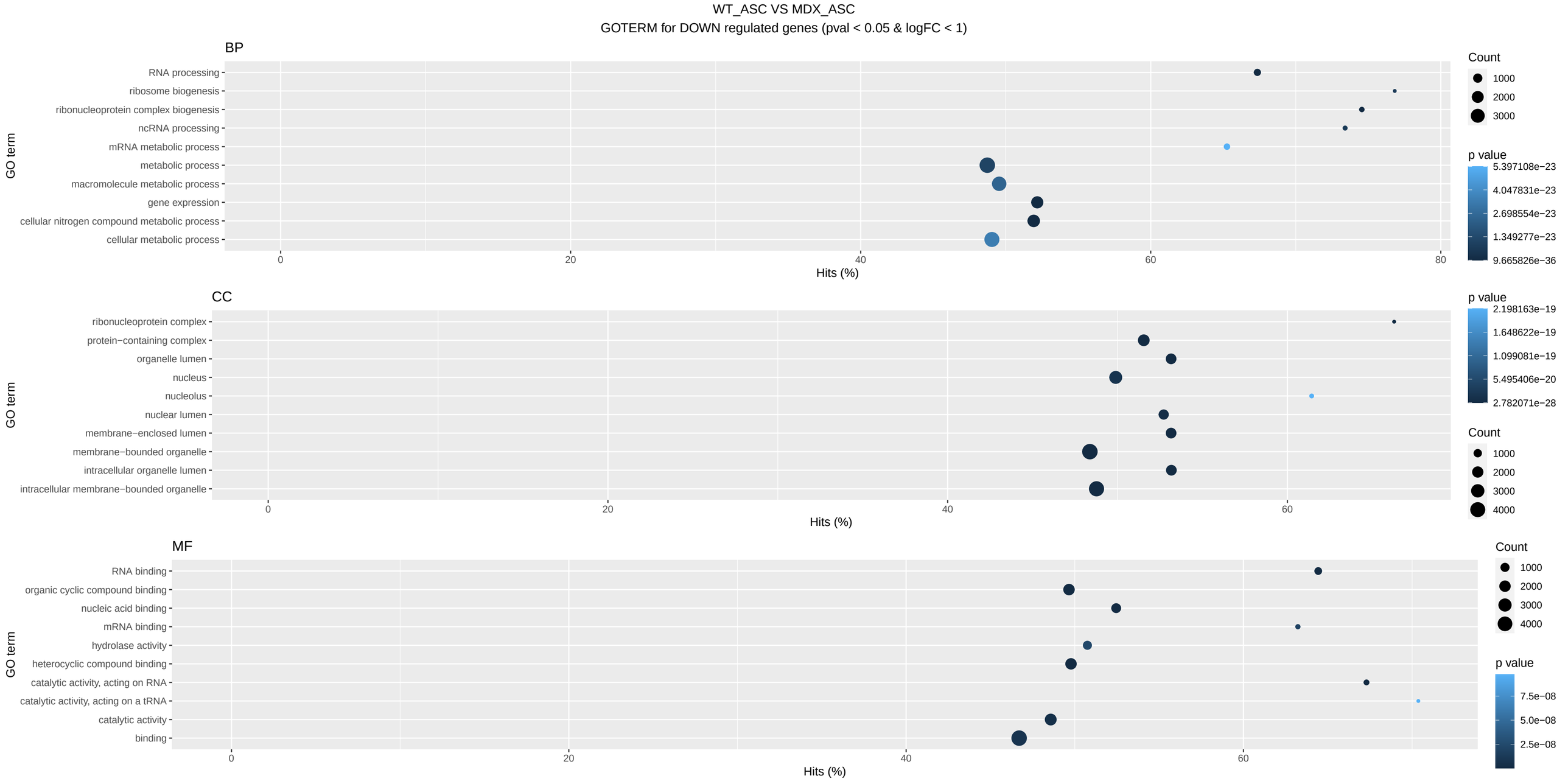

WT_QSC VS MDX_QSC
GOTERM for all genes (pval < 0.05)
BP
GO term
system development
regulation of developmental process
regulation of cellular component movement
regulation of anatomical structure morphogenesis
locomotion
localization of cell
cell motility
cell migration
anatomical structure morphogenesis
anatomical structure formation involved in morphogenesis
0
10
20
Hits (%)
Count
300
400
500
600
700
800
p value
5.171929e−16
3.878947e−16
2.585965e−16
1.292983e−16
CC
GO term
plasma membrane region
plasma membrane
membrane
intrinsic component of membrane
extracellular space
extracellular region
extracellular matrix
collagen−containing extracellular matrix
cell periphery
cell leading edge
0
10
20
30
Hits (%)
p value
1.5e−08
1.0e−08
5.0e−09
Count
250
500
750
1000
MF
GO term
signaling receptor binding
signaling receptor activator activity
receptor regulator activity
receptor ligand activity
protein binding
growth factor receptor binding
glycosaminoglycan binding
extracellular matrix structural constituent
cell adhesion molecule binding
actin binding
0
10
20
30
Hits (%)
p value
2.5e−05
2.0e−05
1.5e−05
1.0e−05
5.0e−06
Count
500
1000

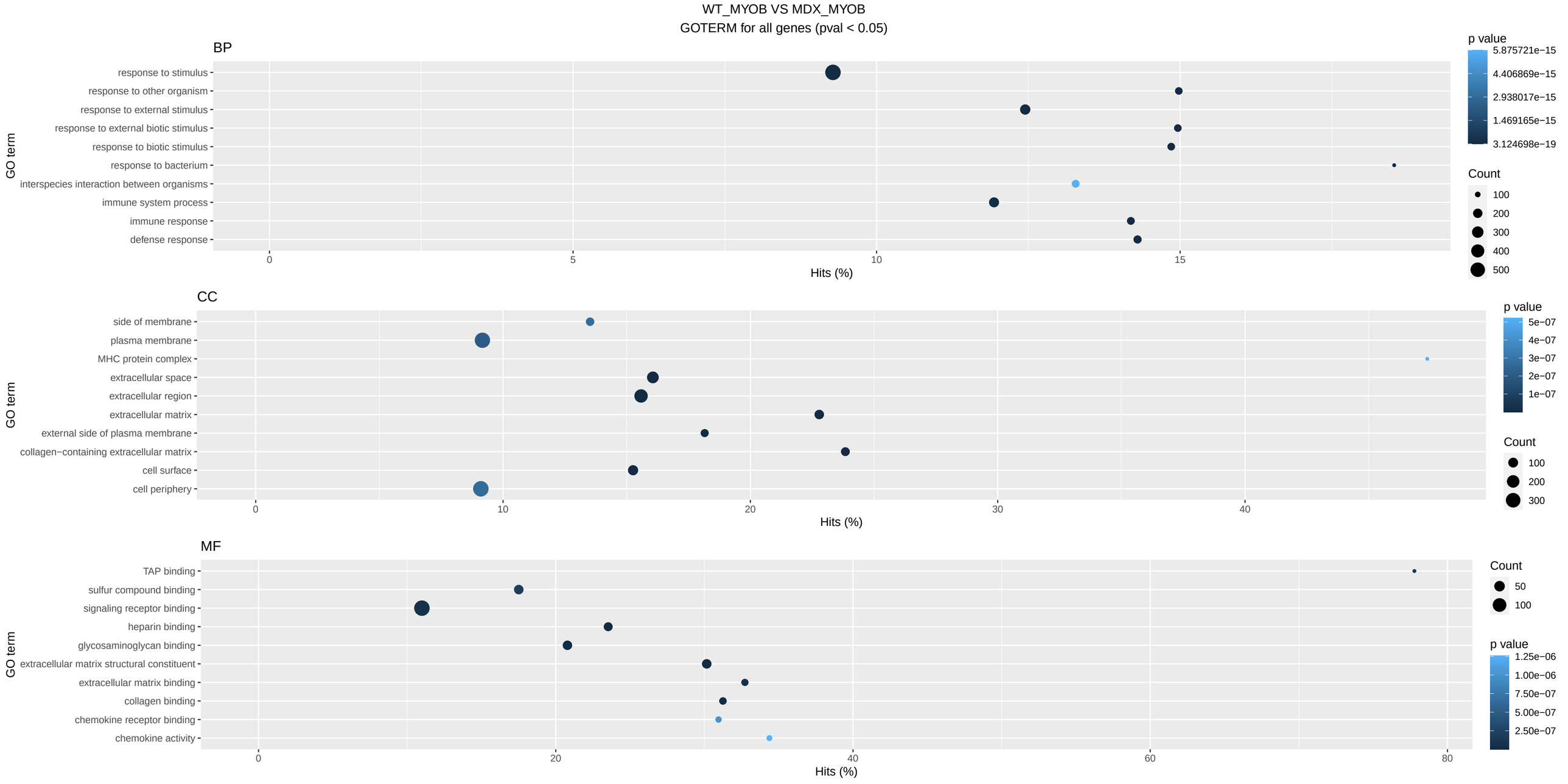

WT_QSC VS MDX_QSC
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
regulation of cell morphogenesis involved in differentiation
negative regulation of response to stimulus
negative regulation of organelle organization
negative regulation of locomotion
negative regulation of cellular process
negative regulation of cellular component organization
negative regulation of cellular component movement
negative regulation of cell motility
negative regulation of cell migration
negative regulation of biological process
GO term
0
25
50
75
100
Hits (%)
Count
25
50
75
100
p value
5e−04
4e−04
3e−04
2e−04
1e−04
CC
sodium channel complex
main axon
intracellular
cytosol
cytoskeleton
cytoplasm
collagen−containing extracellular matrix
cation channel complex
basement membrane
axon
GO term
0
25
50
75
100
Hits (%)
Count
50
100
150
p value
0.015
0.010
0.005
MF
sodium ion transmembrane transporter activity
sodium channel activity
protein binding
phosphoric ester hydrolase activity
monovalent inorganic cation transmembrane transporter activity
metal ion transmembrane transporter activity
ion channel binding
inorganic cation transmembrane transporter activity
enzyme binding
cation transmembrane transporter activity
GO term
0
25
50
75
100
Hits (%)
Count
50
100
150
p value
0.025
0.020
0.015
0.010
0.005

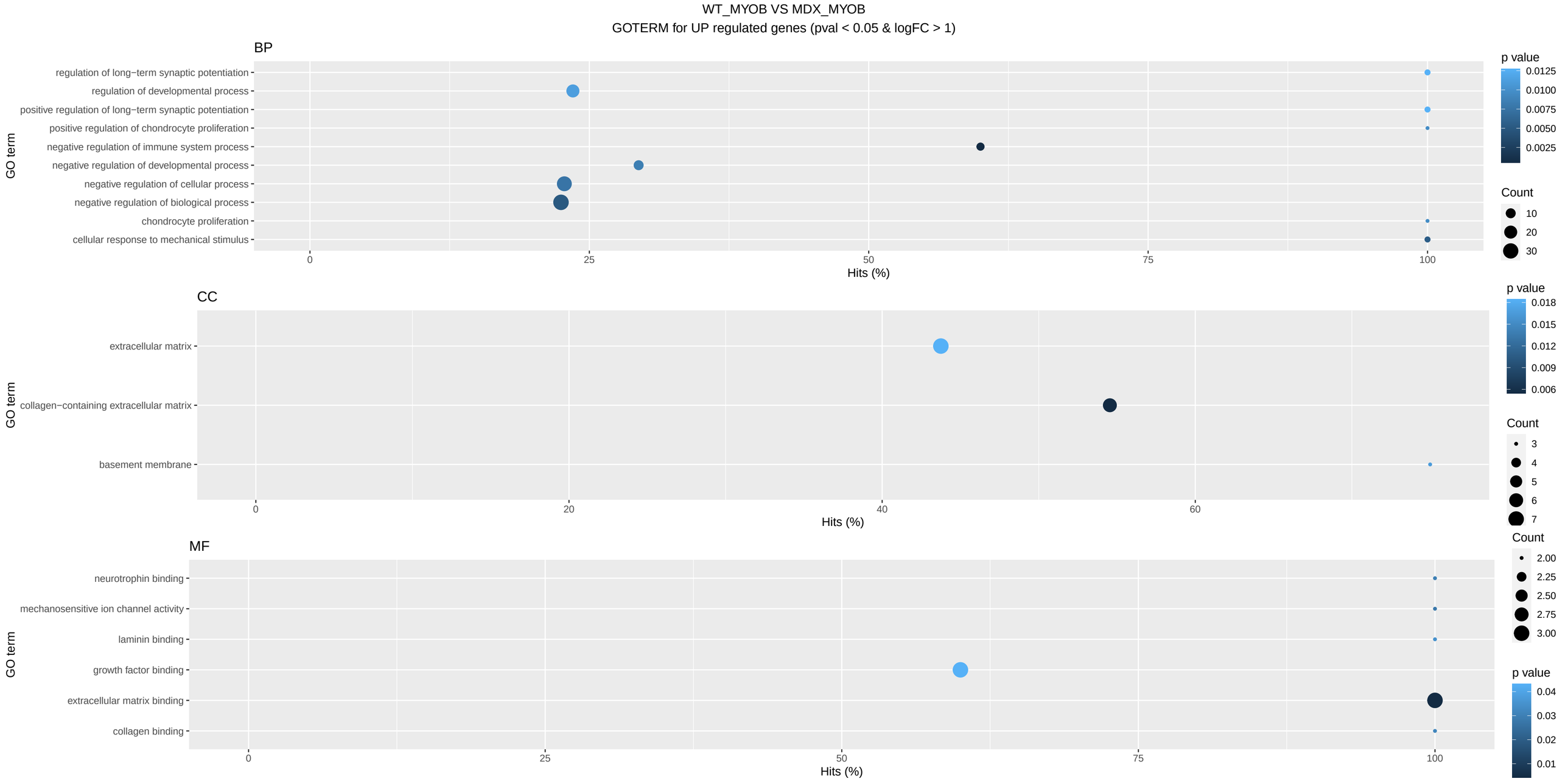

WT_QSC VS MDX_QSC
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
regulation of developmental process
regulation of cellular component movement
regulation of anatomical structure morphogenesis
locomotion
localization of cell
cell motility
cell migration
anatomical structure morphogenesis
anatomical structure formation involved in morphogenesis
anatomical structure development
GO term
0
10
20
Hits (%)
p value
4e−14
3e−14
2e−14
1e−14
Count
400
600
800
CC
plasma membrane
membrane
extracellular space
extracellular region
extracellular matrix
collagen−containing extracellular matrix
cell surface
cell periphery
cell leading edge
anchoring junction
GO term
0
10
20
Hits (%)
p value
4e−07
3e−07
2e−07
1e−07
Count
250
500
750
1000
MF
signaling receptor binding
signaling receptor activator activity
receptor regulator activity
receptor ligand activity
protein binding
integrin binding
growth factor receptor binding
glycosaminoglycan binding
cytokine receptor binding
cell adhesion molecule binding
GO term
0
10
20
30
Hits (%)
p value
3e−05
2e−05
1e−05
Count
300
600
900
1200

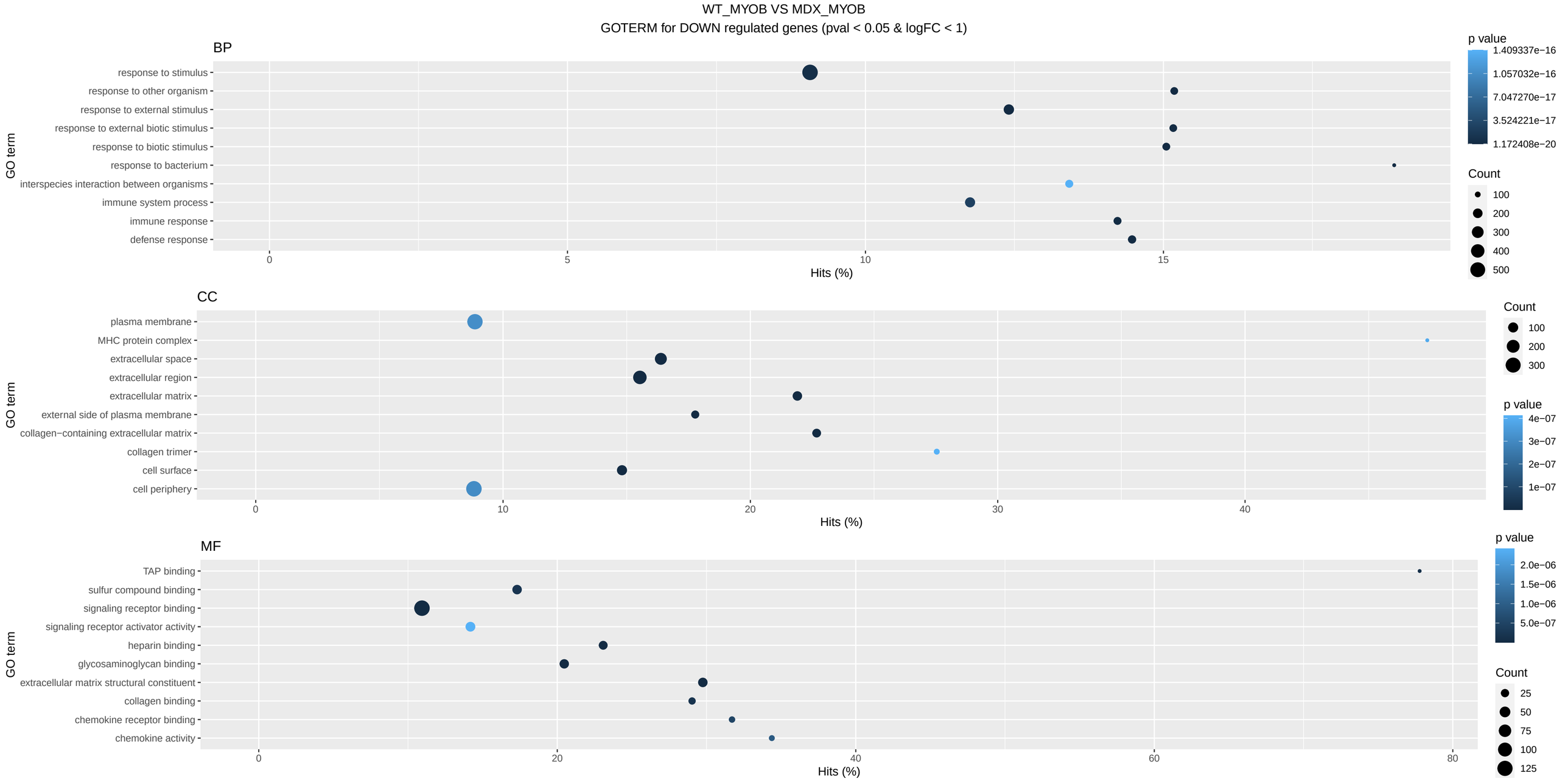

WT_ASC VS MDX_ASC
GOTERM for all genes (pval < 0.05)
BP
RNA processing
ribosome biogenesis
ribonucleoprotein complex biogenesis
nucleobase−containing compound metabolic process
ncRNA processing
heterocycle metabolic process
gene expression
cellular nitrogen compound metabolic process
cellular metabolic process
cellular aromatic compound metabolic process
GO term
0
20
40
60
80
Hits (%)
p value
4.619464e−28
3.464598e−28
2.309732e−28
1.154866e−28
3.805979e−41
Count
1000
2000
3000
CC
ribonucleoprotein complex
protein−containing complex
organelle lumen
nucleus
nucleolus
nuclear lumen
membrane−enclosed lumen
membrane−bounded organelle
intracellular organelle lumen
intracellular membrane−bounded organelle
GO term
0
20
40
60
Hits (%)
Count
1000
2000
3000
4000
p value
1.441355e−26
1.081016e−26
7.206773e−27
3.603386e−27
1.309257e−35
MF
RNA binding
organic cyclic compound binding
nucleic acid binding
mRNA binding
hydrolase activity
heterocyclic compound binding
helicase activity
catalytic activity, acting on RNA
catalytic activity
binding
GO term
0
20
40
60
Hits (%)
Count
1000
2000
3000
4000
p value
2.0e−08
1.5e−08
1.0e−08
5.0e−09

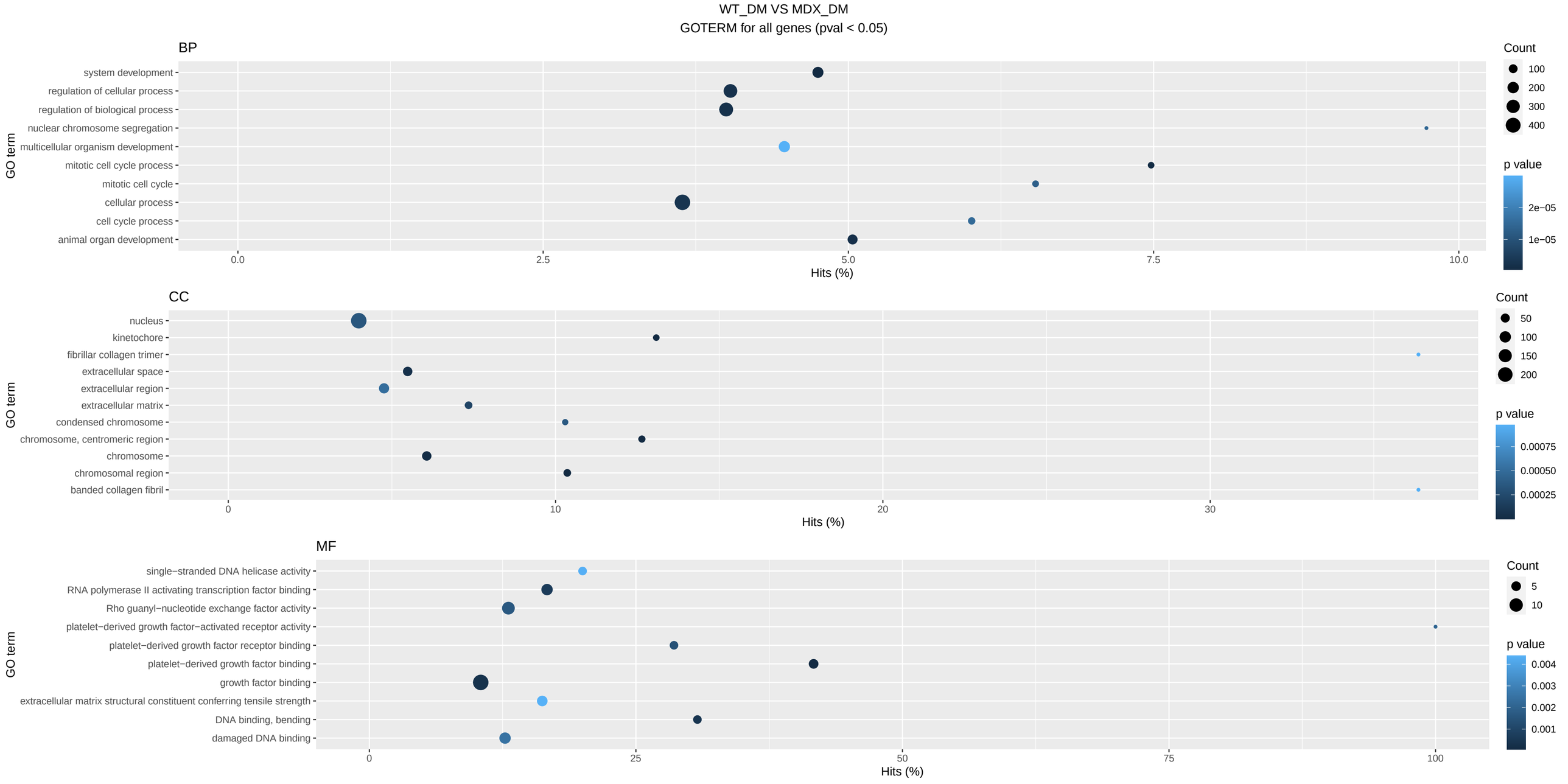

WT_ASC VS MDX_ASC
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
ribonucleoprotein complex biogenesis
organic cyclic compound metabolic process
nucleobase−containing compound metabolic process
nucleic acid metabolic process
heterocycle metabolic process
DNA metabolic process
cellular response to DNA damage stimulus
cellular nitrogen compound metabolic process
cellular aromatic compound metabolic process
cell cycle
GO term
0
25
50
75
100
Hits (%)
Count
50
100
150
200
p value
3e−11
2e−11
1e−11
CC
organelle lumen
nucleus
nucleolus
nuclear lumen
non−membrane−bounded organelle
membrane−enclosed lumen
intracellular organelle lumen
intracellular non−membrane−bounded organelle
intracellular membrane−bounded organelle
intracellular
GO term
0
25
50
75
Hits (%)
Count
100
200
300
400
p value
2.0e−13
1.5e−13
1.0e−13
5.0e−14
MF
small molecule binding
RNA binding
organic cyclic compound binding
nucleotide binding
nucleoside phosphate binding
nucleic acid binding
heterocyclic compound binding
DNA binding
catalytic activity, acting on DNA
catalytic activity
GO term
0
25
50
75
100
Hits (%)
Count
50
100
150
p value
9e−05
6e−05
3e−05

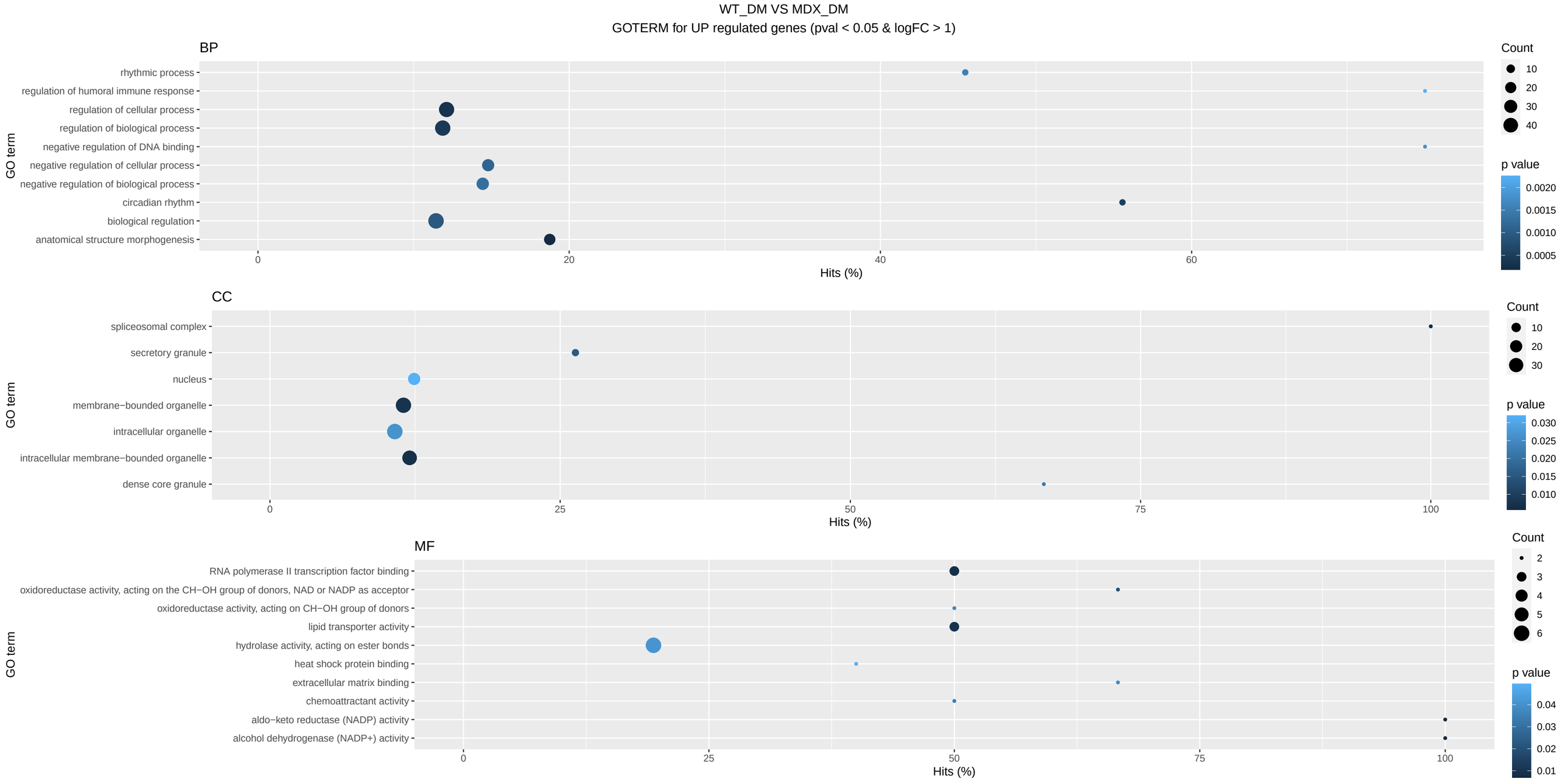

WT_ASC VS MDX_ASC
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
RNA processing
ribosome biogenesis
ribonucleoprotein complex biogenesis
ncRNA processing
mRNA metabolic process
metabolic process
macromolecule metabolic process
gene expression
cellular nitrogen compound metabolic process
cellular metabolic process
GO term
0
20
40
60
80
Hits (%)
Count
1000
2000
3000
p value
5.397108e−23
4.047831e−23
2.698554e−23
1.349277e−23
9.665826e−36
CC
ribonucleoprotein complex
protein−containing complex
organelle lumen
nucleus
nucleolus
nuclear lumen
membrane−enclosed lumen
membrane−bounded organelle
intracellular organelle lumen
intracellular membrane−bounded organelle
GO term
0
20
40
60
Hits (%)
p value
2.198163e−19
1.648622e−19
1.099081e−19
5.495406e−20
2.782071e−28
Count
1000
2000
3000
4000
MF
RNA binding
organic cyclic compound binding
nucleic acid binding
mRNA binding
hydrolase activity
heterocyclic compound binding
catalytic activity, acting on RNA
catalytic activity, acting on a tRNA
catalytic activity
binding
GO term
0
20
40
60
Hits (%)
Count
1000
2000
3000
4000
p value
7.5e−08
5.0e−08
2.5e−08

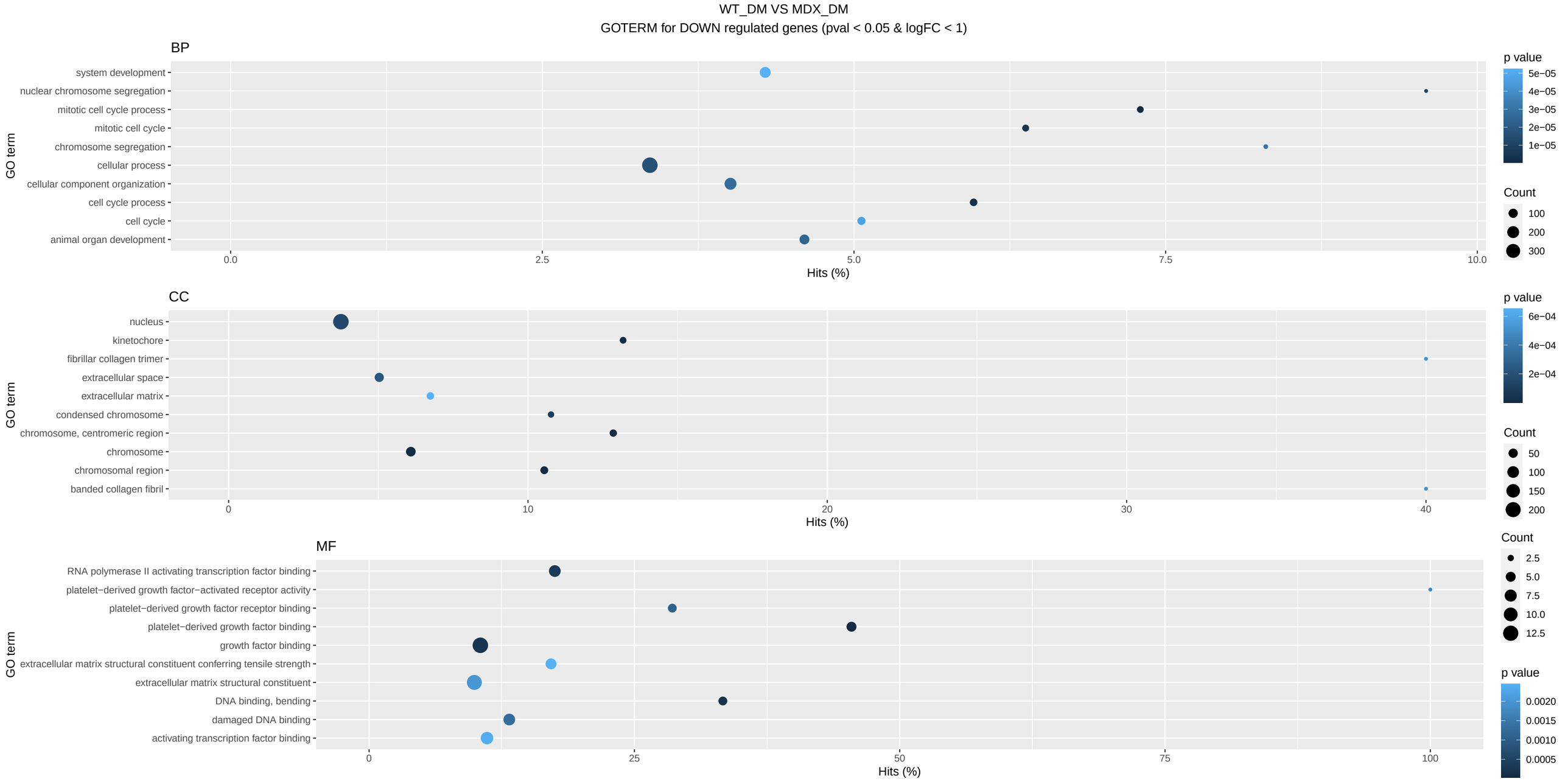

WT_MYOB VS MDX_MYOB
GOTERM for all genes (pval < 0.05)
BP
response to stimulus
response to other organism
response to external stimulus
response to external biotic stimulus
response to biotic stimulus
response to bacterium
interspecies interaction between organisms
immune system process
immune response
defense response
GO term
0
5
10
15
Hits (%)
p value
5.875721e−15
4.406869e−15
2.938017e−15
1.469165e−15
3.124698e−19
Count
100
200
300
400
500
CC
side of membrane
plasma membrane
MHC protein complex
extracellular space
extracellular region
extracellular matrix
external side of plasma membrane
collagen−containing extracellular matrix
cell surface
cell periphery
GO term
0
10
20
30
40
Hits (%)
p value
5e−07
4e−07
3e−07
2e−07
1e−07
Count
100
200
300
MF
TAP binding
sulfur compound binding
signaling receptor binding
heparin binding
glycosaminoglycan binding
extracellular matrix structural constituent
extracellular matrix binding
collagen binding
chemokine receptor binding
chemokine activity
GO term
0
20
40
60
80
Hits (%)
Count
50
100
p value
1.25e−06
1.00e−06
7.50e−07
5.00e−07
2.50e−07

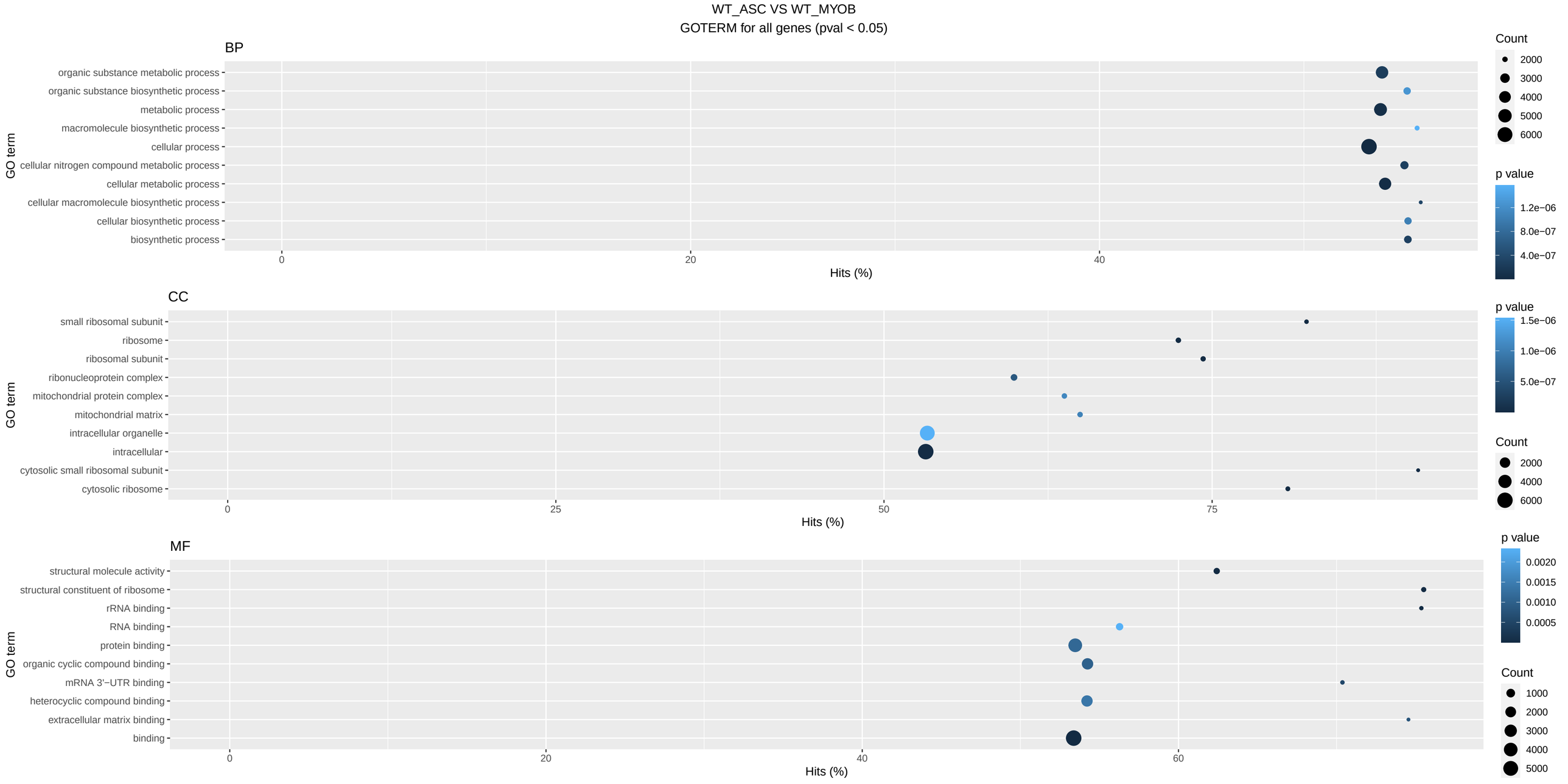

WT_MYOB VS MDX_MYOB
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
regulation of long−term synaptic potentiation
regulation of developmental process
positive regulation of long−term synaptic potentiation
positive regulation of chondrocyte proliferation
negative regulation of immune system process
negative regulation of developmental process
negative regulation of cellular process
negative regulation of biological process
chondrocyte proliferation
cellular response to mechanical stimulus
GO term
0
25
50
75
100
Hits (%)
p value
0.0125
0.0100
0.0075
0.0050
0.0025
Count
10
20
30
CC
extracellular matrix
collagen−containing extracellular matrix
basement membrane
GO term
0
20
40
60
Hits (%)
p value
0.018
0.015
0.012
0.009
0.006
Count
3
4
5
6
7
MF
neurotrophin binding
mechanosensitive ion channel activity
laminin binding
growth factor binding
extracellular matrix binding
collagen binding
GO term
0
25
50
75
100
Hits (%)
Count
2.00
2.25
2.50
2.75
3.00
p value
0.04
0.03
0.02
0.01

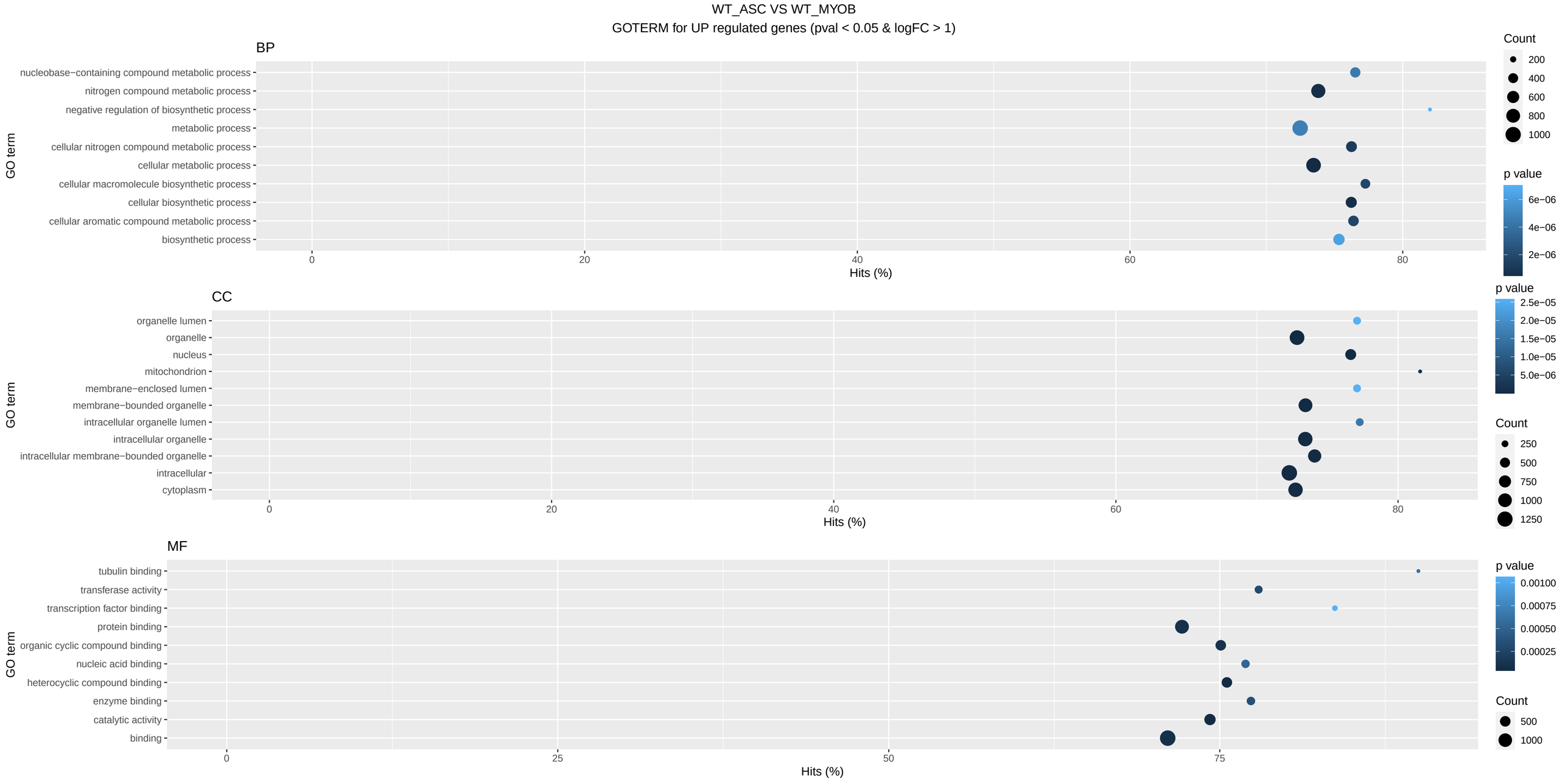

WT_MYOB VS MDX_MYOB
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
response to stimulus
response to other organism
response to external stimulus
response to external biotic stimulus
response to biotic stimulus
response to bacterium
interspecies interaction between organisms
immune system process
immune response
defense response
GO term
0
5
10
15
Hits (%)
p value
1.409337e−16
1.057032e−16
7.047270e−17
3.524221e−17
1.172408e−20
Count
100
200
300
400
500
CC
plasma membrane
MHC protein complex
extracellular space
extracellular region
extracellular matrix
external side of plasma membrane
collagen−containing extracellular matrix
collagen trimer
cell surface
cell periphery
GO term
0
10
20
30
40
Hits (%)
Count
100
200
300
p value
4e−07
3e−07
2e−07
1e−07
MF
TAP binding
sulfur compound binding
signaling receptor binding
signaling receptor activator activity
heparin binding
glycosaminoglycan binding
extracellular matrix structural constituent
collagen binding
chemokine receptor binding
chemokine activity
GO term
0
20
40
60
80
Hits (%)
p value
2.0e−06
1.5e−06
1.0e−06
5.0e−07
Count
25
50
75
100
125

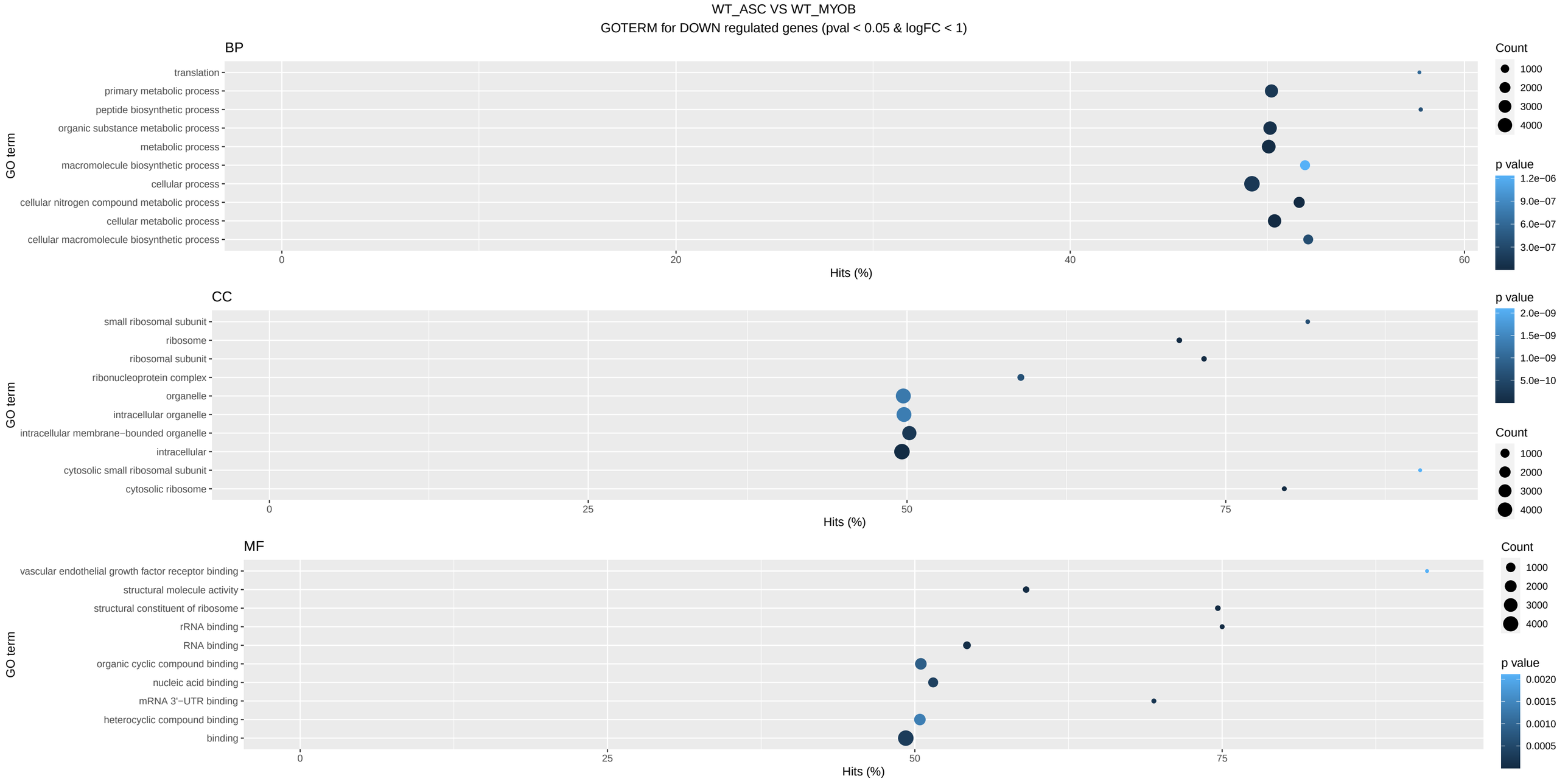

WT_DM VS MDX_DM
GOTERM for all genes (pval < 0.05)
BP
system development
regulation of cellular process
regulation of biological process
nuclear chromosome segregation
multicellular organism development
mitotic cell cycle process
mitotic cell cycle
cellular process
cell cycle process
animal organ development
GO term
0.0
2.5
5.0
7.5
10.0
Hits (%)
Count
100
200
300
400
p value
2e−05
1e−05
CC
nucleus
kinetochore
fibrillar collagen trimer
extracellular space
extracellular region
extracellular matrix
condensed chromosome
chromosome, centromeric region
chromosome
chromosomal region
banded collagen fibril
GO term
0
10
20
30
Hits (%)
Count
50
100
150
200
p value
0.00075
0.00050
0.00025
MF
single−stranded DNA helicase activity
RNA polymerase II activating transcription factor binding
Rho guanyl−nucleotide exchange factor activity
platelet−derived growth factor−activated receptor activity
platelet−derived growth factor receptor binding
platelet−derived growth factor binding
growth factor binding
extracellular matrix structural constituent conferring tensile strength
DNA binding, bending
damaged DNA binding
GO term
0
25
50
75
100
Hits (%)
Count
5
10
p value
0.004
0.003
0.002
0.001

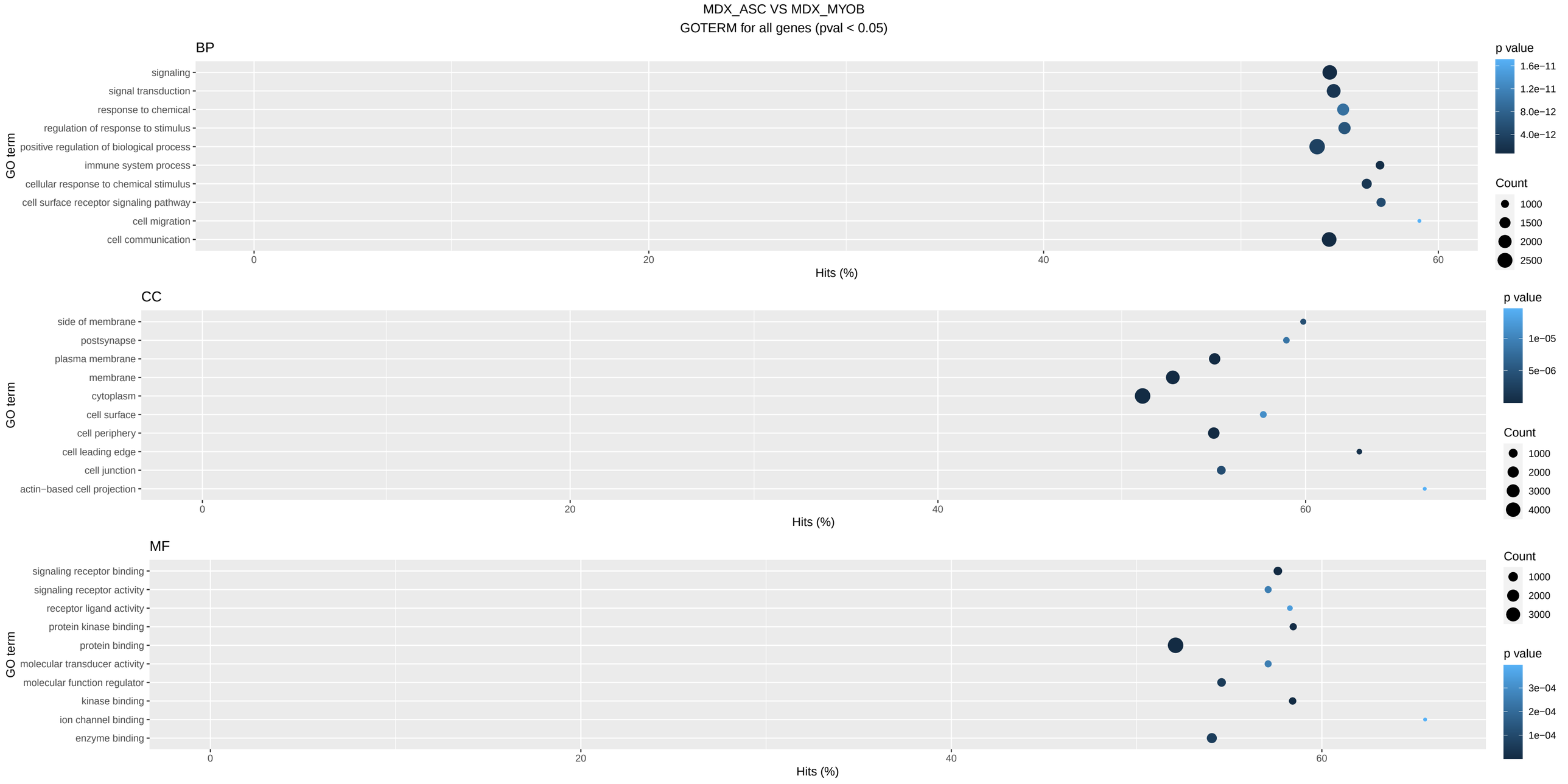

WT_DM VS MDX_DM
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
rhythmic process
regulation of humoral immune response
regulation of cellular process
regulation of biological process
negative regulation of DNA binding
negative regulation of cellular process
negative regulation of biological process
circadian rhythm
biological regulation
anatomical structure morphogenesis
GO term
0
20
40
60
Hits (%)
Count
10
20
30
40
p value
0.0020
0.0015
0.0010
0.0005
CC
spliceosomal complex
secretory granule
nucleus
membrane−bounded organelle
intracellular organelle
intracellular membrane−bounded organelle
dense core granule
GO term
0
25
50
75
100
Hits (%)
Count
10
20
30
p value
0.030
0.025
0.020
0.015
0.010
MF
RNA polymerase II transcription factor binding
oxidoreductase activity, acting on the CH−OH group of donors, NAD or NADP as acceptor
oxidoreductase activity, acting on CH−OH group of donors
lipid transporter activity
hydrolase activity, acting on ester bonds
heat shock protein binding
extracellular matrix binding
chemoattractant activity
aldo−keto reductase (NADP) activity
alcohol dehydrogenase (NADP+) activity
GO term
0
25
50
75
100
Hits (%)
Count
2
3
4
5
6
p value
0.04
0.03
0.02
0.01

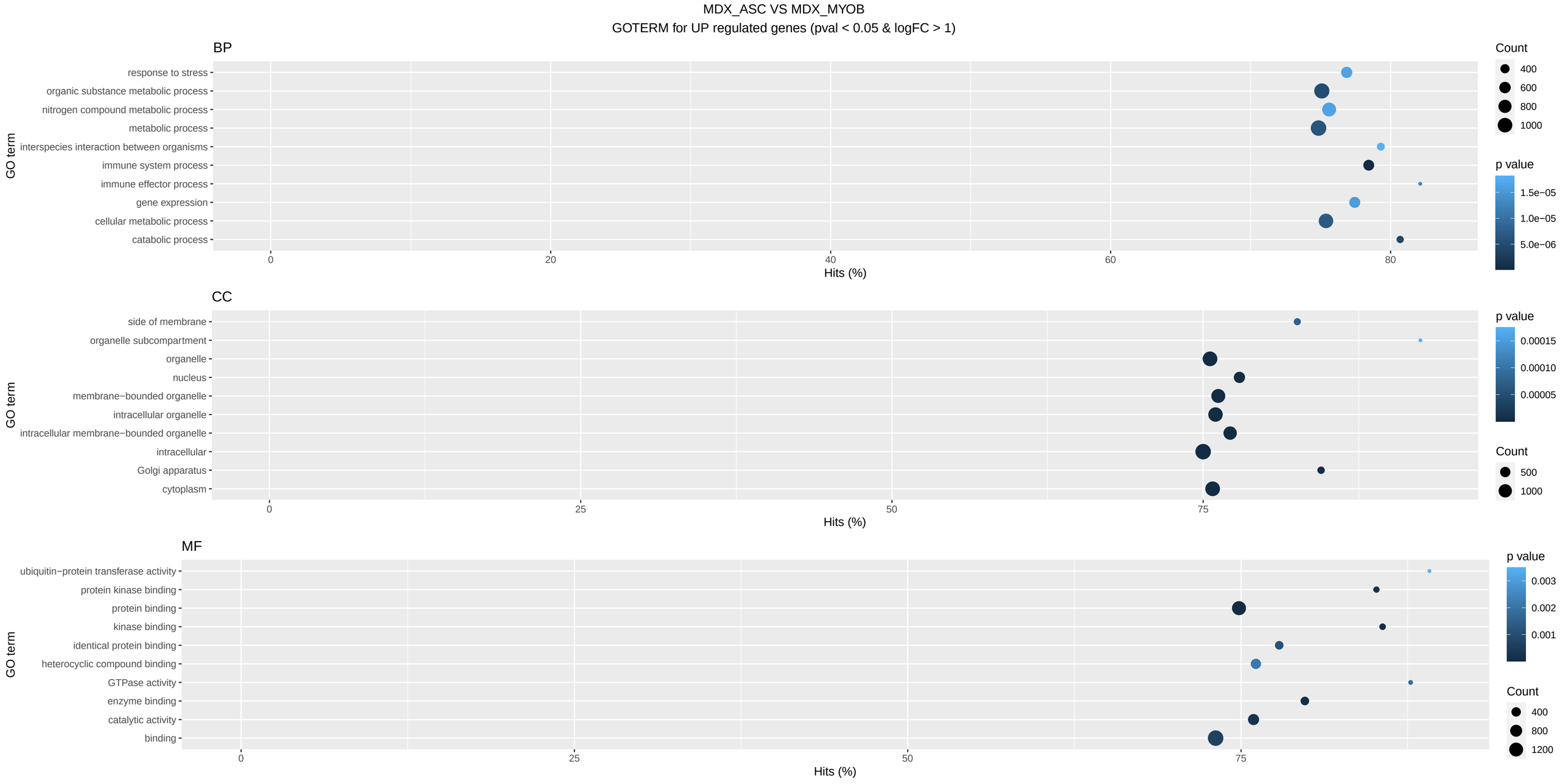

WT_DM VS MDX_DM
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
system development
nuclear chromosome segregation
mitotic cell cycle process
mitotic cell cycle
chromosome segregation
cellular process
cellular component organization
cell cycle process
cell cycle
animal organ development
GO term
0.0
2.5
5.0
7.5
10.0
Hits (%)
p value
5e−05
4e−05
3e−05
2e−05
1e−05
Count
100
200
300
CC
nucleus
kinetochore
fibrillar collagen trimer
extracellular space
extracellular matrix
condensed chromosome
chromosome, centromeric region
chromosome
chromosomal region
banded collagen fibril
GO term
0
10
20
30
40
Hits (%)
p value
6e−04
4e−04
2e−04
Count
50
100
150
200
MF
RNA polymerase II activating transcription factor binding
platelet−derived growth factor−activated receptor activity
platelet−derived growth factor receptor binding
platelet−derived growth factor binding
growth factor binding
extracellular matrix structural constituent conferring tensile strength
extracellular matrix structural constituent
DNA binding, bending
damaged DNA binding
activating transcription factor binding
GO term
0
25
50
75
100
Hits (%)
Count
2.5
5.0
7.5
10.0
12.5
p value
0.0020
0.0015
0.0010
0.0005

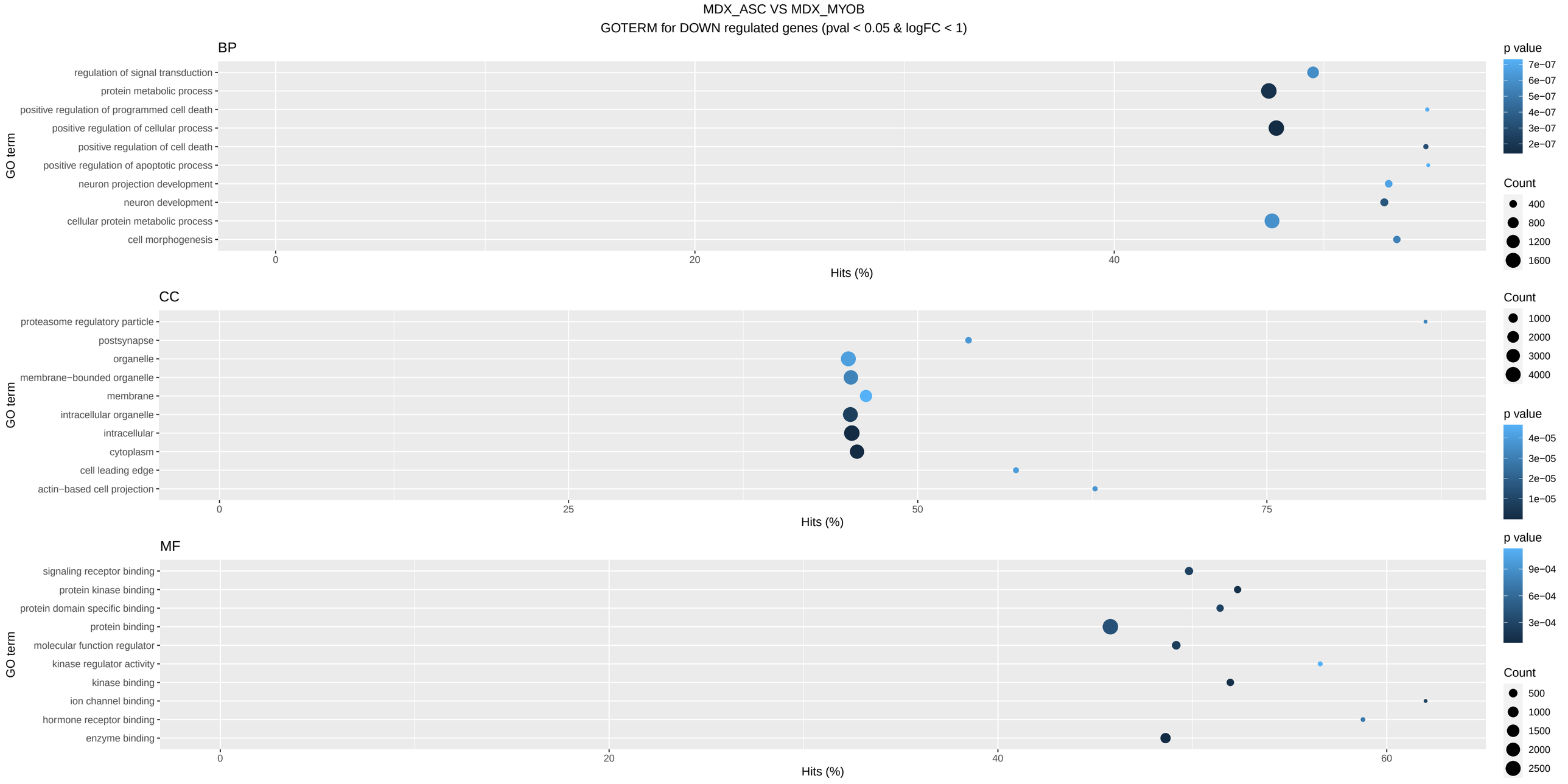

WT_ASC VS WT_MYOB
GOTERM for all genes (pval < 0.05)
BP
organic substance metabolic process
organic substance biosynthetic process
metabolic process
macromolecule biosynthetic process
cellular process
cellular nitrogen compound metabolic process
cellular metabolic process
cellular macromolecule biosynthetic process
cellular biosynthetic process
biosynthetic process
GO term
0
20
40
Hits (%)
Count
2000
3000
4000
5000
6000
p value
1.2e−06
8.0e−07
4.0e−07
CC
small ribosomal subunit
ribosome
ribosomal subunit
ribonucleoprotein complex
mitochondrial protein complex
mitochondrial matrix
intracellular organelle
intracellular
cytosolic small ribosomal subunit
cytosolic ribosome
GO term
0
25
50
75
Hits (%)
p value
1.5e−06
1.0e−06
5.0e−07
Count
2000
4000
6000
MF
structural molecule activity
structural constituent of ribosome
rRNA binding
RNA binding
protein binding
organic cyclic compound binding
mRNA 3'−UTR binding
heterocyclic compound binding
extracellular matrix binding
binding
GO term
0
20
40
60
Hits (%)
p value
0.0020
0.0015
0.0010
0.0005
Count
1000
2000
3000
4000
5000


WT_ASC VS WT_MYOB
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
nucleobase−containing compound metabolic process
nitrogen compound metabolic process
negative regulation of biosynthetic process
metabolic process
cellular nitrogen compound metabolic process
cellular metabolic process
cellular macromolecule biosynthetic process
cellular biosynthetic process
cellular aromatic compound metabolic process
biosynthetic process
GO term
0
20
40
60
80
Hits (%)
Count
200
400
600
800
1000
p value
6e−06
4e−06
2e−06
CC
organelle lumen
organelle
nucleus
mitochondrion
membrane−enclosed lumen
membrane−bounded organelle
intracellular organelle lumen
intracellular organelle
intracellular membrane−bounded organelle
intracellular
cytoplasm
GO term
0
20
40
60
80
Hits (%)
p value
2.5e−05
2.0e−05
1.5e−05
1.0e−05
5.0e−06
Count
250
500
750
1000
1250
MF
tubulin binding
transferase activity
transcription factor binding
protein binding
organic cyclic compound binding
nucleic acid binding
heterocyclic compound binding
enzyme binding
catalytic activity
binding
GO term
0
25
50
75
Hits (%)
p value
0.00100
0.00075
0.00050
0.00025
Count
500
1000


WT_ASC VS WT_MYOB
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
translation
primary metabolic process
peptide biosynthetic process
organic substance metabolic process
metabolic process
macromolecule biosynthetic process
cellular process
cellular nitrogen compound metabolic process
cellular metabolic process
cellular macromolecule biosynthetic process
GO term
0
20
40
60
Hits (%)
Count
1000
2000
3000
4000
p value
1.2e−06
9.0e−07
6.0e−07
3.0e−07
CC
small ribosomal subunit
ribosome
ribosomal subunit
ribonucleoprotein complex
organelle
intracellular organelle
intracellular membrane−bounded organelle
intracellular
cytosolic small ribosomal subunit
cytosolic ribosome
GO term
0
25
50
75
Hits (%)
p value
2.0e−09
1.5e−09
1.0e−09
5.0e−10
Count
1000
2000
3000
4000
MF
vascular endothelial growth factor receptor binding
structural molecule activity
structural constituent of ribosome
rRNA binding
RNA binding
organic cyclic compound binding
nucleic acid binding
mRNA 3'−UTR binding
heterocyclic compound binding
binding
GO term
0
25
50
75
Hits (%)
Count
1000
2000
3000
4000
p value
0.0020
0.0015
0.0010
0.0005


MDX_ASC VS MDX_MYOB
GOTERM for all genes (pval < 0.05)
BP
signaling
signal transduction
response to chemical
regulation of response to stimulus
positive regulation of biological process
immune system process
cellular response to chemical stimulus
cell surface receptor signaling pathway
cell migration
cell communication
GO term
0
20
40
60
Hits (%)
p value
1.6e−11
1.2e−11
8.0e−12
4.0e−12
Count
1000
1500
2000
2500
CC
side of membrane
postsynapse
plasma membrane
membrane
cytoplasm
cell surface
cell periphery
cell leading edge
cell junction
actin−based cell projection
GO term
0
20
40
60
Hits (%)
p value
1e−05
5e−06
Count
1000
2000
3000
4000
MF
signaling receptor binding
signaling receptor activity
receptor ligand activity
protein kinase binding
protein binding
molecular transducer activity
molecular function regulator
kinase binding
ion channel binding
enzyme binding
GO term
0
20
40
60
Hits (%)
Count
1000
2000
3000
p value
3e−04
2e−04
1e−04


MDX_ASC VS MDX_MYOB
GOTERM for UP regulated genes (pval < 0.05 & logFC > 1)
BP
response to stress
organic substance metabolic process
nitrogen compound metabolic process
metabolic process
interspecies interaction between organisms
immune system process
immune effector process
gene expression
cellular metabolic process
catabolic process
GO term
0
20
40
60
80
Hits (%)
Count
400
600
800
1000
p value
1.5e−05
1.0e−05
5.0e−06
CC
side of membrane
organelle subcompartment
organelle
nucleus
membrane−bounded organelle
intracellular organelle
intracellular membrane−bounded organelle
intracellular
Golgi apparatus
cytoplasm
GO term
0
25
50
75
Hits (%)
p value
0.00015
0.00010
0.00005
Count
500
1000
MF
ubiquitin−protein transferase activity
protein kinase binding
protein binding
kinase binding
identical protein binding
heterocyclic compound binding
GTPase activity
enzyme binding
catalytic activity
binding
GO term
0
25
50
75
Hits (%)
p value
0.003
0.002
0.001
Count
400
800
1200


MDX_ASC VS MDX_MYOB
GOTERM for DOWN regulated genes (pval < 0.05 & logFC < 1)
BP
regulation of signal transduction
protein metabolic process
positive regulation of programmed cell death
positive regulation of cellular process
positive regulation of cell death
positive regulation of apoptotic process
neuron projection development
neuron development
cellular protein metabolic process
cell morphogenesis
GO term
0
20
40
Hits (%)
p value
7e−07
6e−07
5e−07
4e−07
3e−07
2e−07
Count
400
800
1200
1600
CC
proteasome regulatory particle
postsynapse
organelle
membrane−bounded organelle
membrane
intracellular organelle
intracellular
cytoplasm
cell leading edge
actin−based cell projection
GO term
0
25
50
75
Hits (%)
Count
1000
2000
3000
4000
p value
4e−05
3e−05
2e−05
1e−05
MF
signaling receptor binding
protein kinase binding
protein domain specific binding
protein binding
molecular function regulator
kinase regulator activity
kinase binding
ion channel binding
hormone receptor binding
enzyme binding
GO term
0
20
40
60
Hits (%)
p value
9e−04
6e−04
3e−04
Count
500
1000
1500
2000
2500