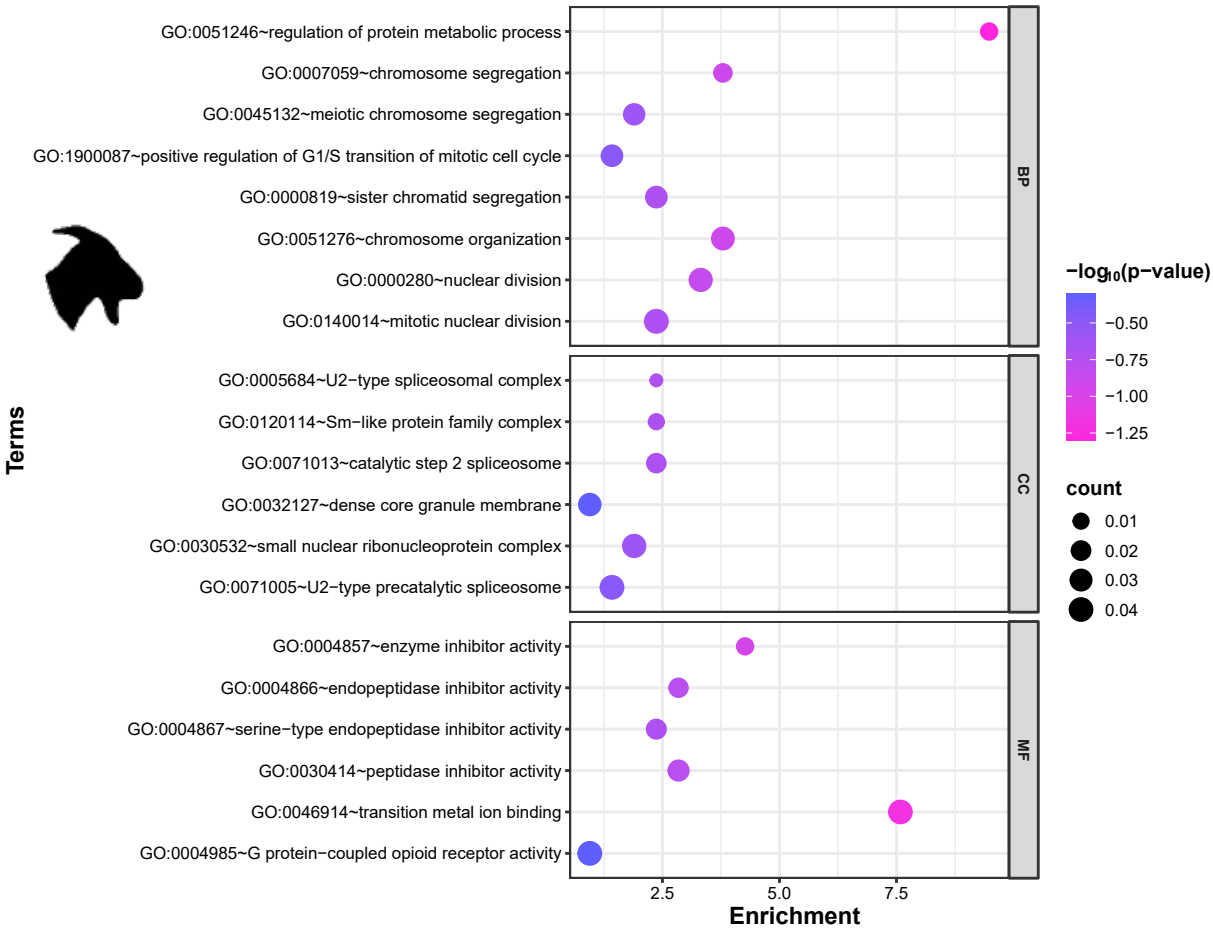
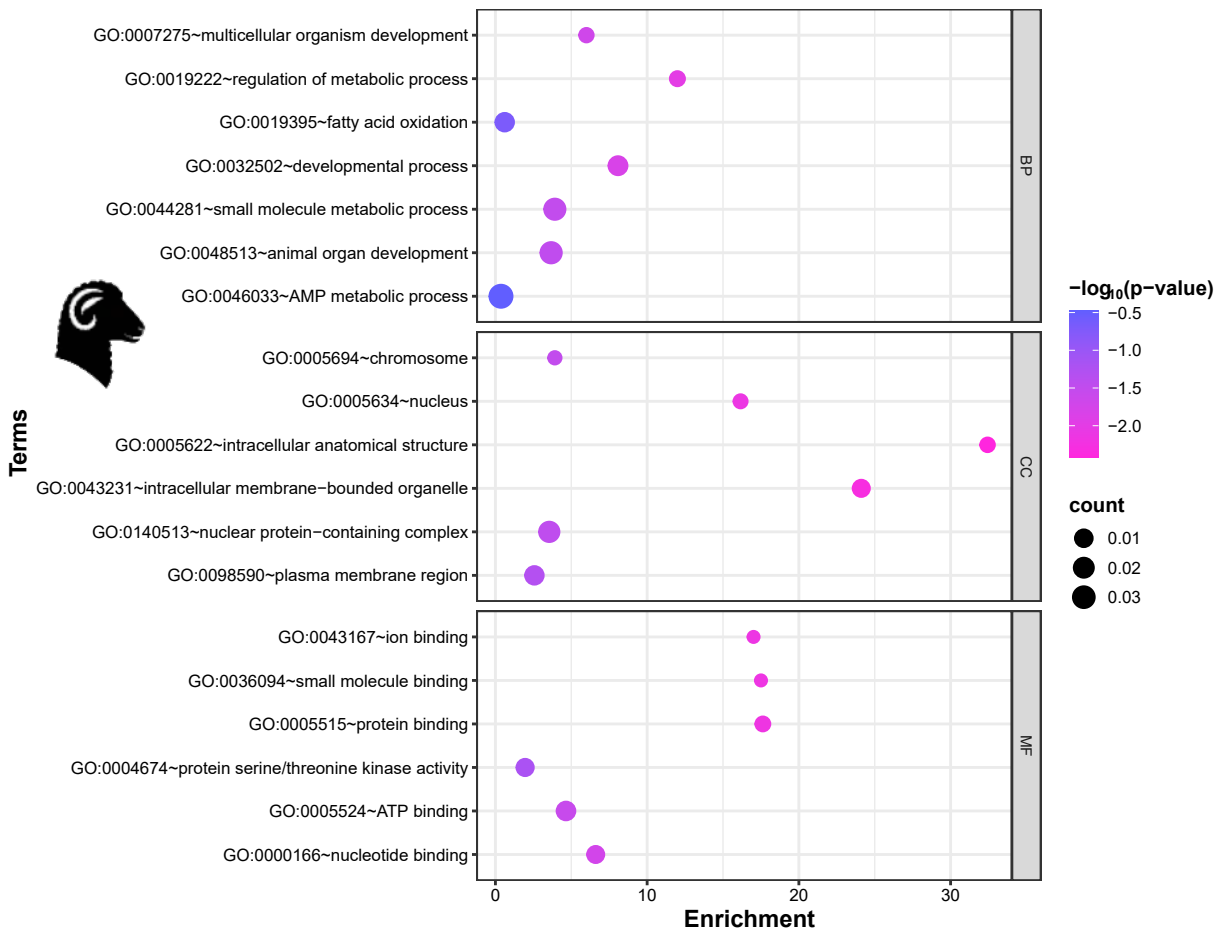

GO:0051246~regulation of protein metabolic process
GO:0007059~chromosome segregation
GO:0045132~meiotic chromosome segregation
GO:1900087~positive regulation of G1/S transition of mitotic cell cycle
GO:0000819~sister chromatid segregation
GO:0051276~chromosome organization
GO:0000280~nuclear division
GO:0140014~mitotic nuclear division
GO:0005684~U2−type spliceosomal complex
GO:0120114~Sm−like protein family complex
GO:0071013~catalytic step 2 spliceosome
GO:0032127~dense core granule membrane
GO:0030532~small nuclear ribonucleoprotein complex
GO:0071005~U2−type precatalytic spliceosome
GO:0004857~enzyme inhibitor activity
GO:0004866~endopeptidase inhibitor activity
GO:0004867~serine−type endopeptidase inhibitor activity
GO:0030414~peptidase inhibitor activity
GO:0046914~transition metal ion binding
GO:0004985~G protein−coupled opioid receptor activity
BP
CC
MF
Terms
2.5
5.0
7.5
Enrichment
−log10(p−value)
−0.50
−0.75
−1.00
−1.25
count
0.01
0.02
0.03
0.04


GO:0007275~multicellular organism development
GO:0019222~regulation of metabolic process
GO:0019395~fatty acid oxidation
GO:0032502~developmental process
GO:0044281~small molecule metabolic process
GO:0048513~animal organ development
GO:0046033~AMP metabolic process
GO:0005694~chromosome
GO:0005634~nucleus
GO:0005622~intracellular anatomical structure
GO:0043231~intracellular membrane−bounded organelle
GO:0140513~nuclear protein−containing complex
GO:0098590~plasma membrane region
GO:0043167~ion binding
GO:0036094~small molecule binding
GO:0005515~protein binding
GO:0004674~protein serine/threonine kinase activity
GO:0005524~ATP binding
GO:0000166~nucleotide binding
BP
CC
MF
Terms
0
10
20
30
Enrichment
−log10(p−value)
−0.5
−1.0
−1.5
−2.0
count
0.01
0.02
0.03