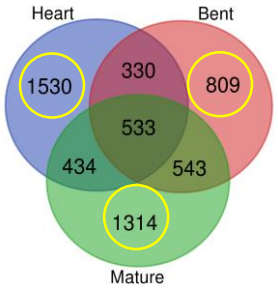
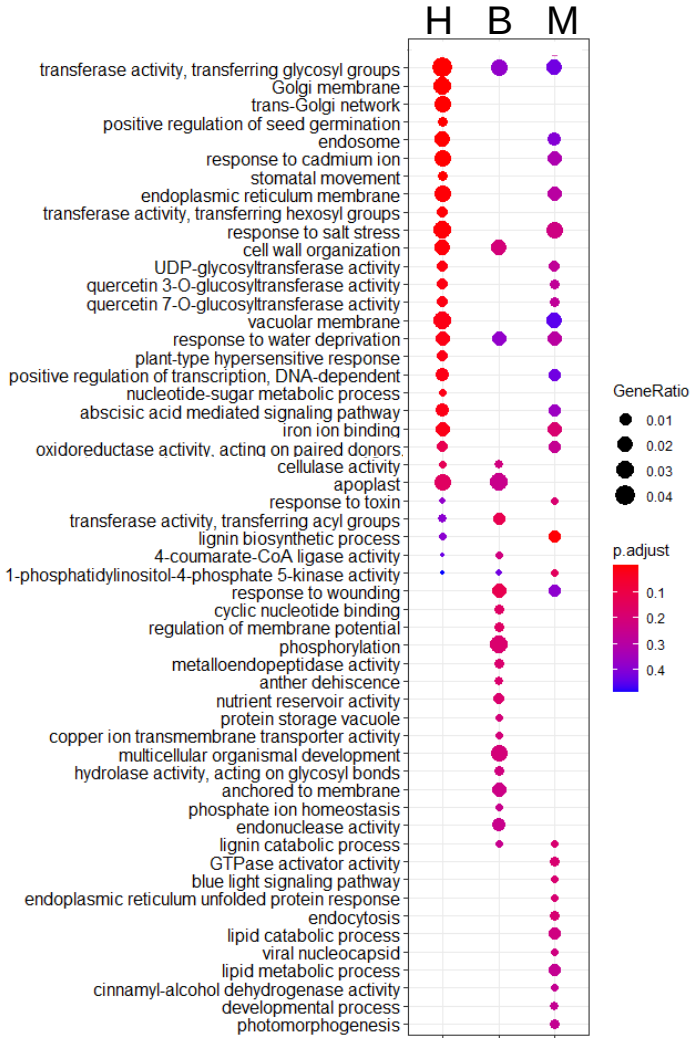
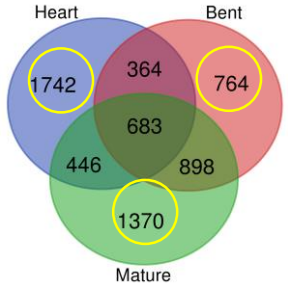
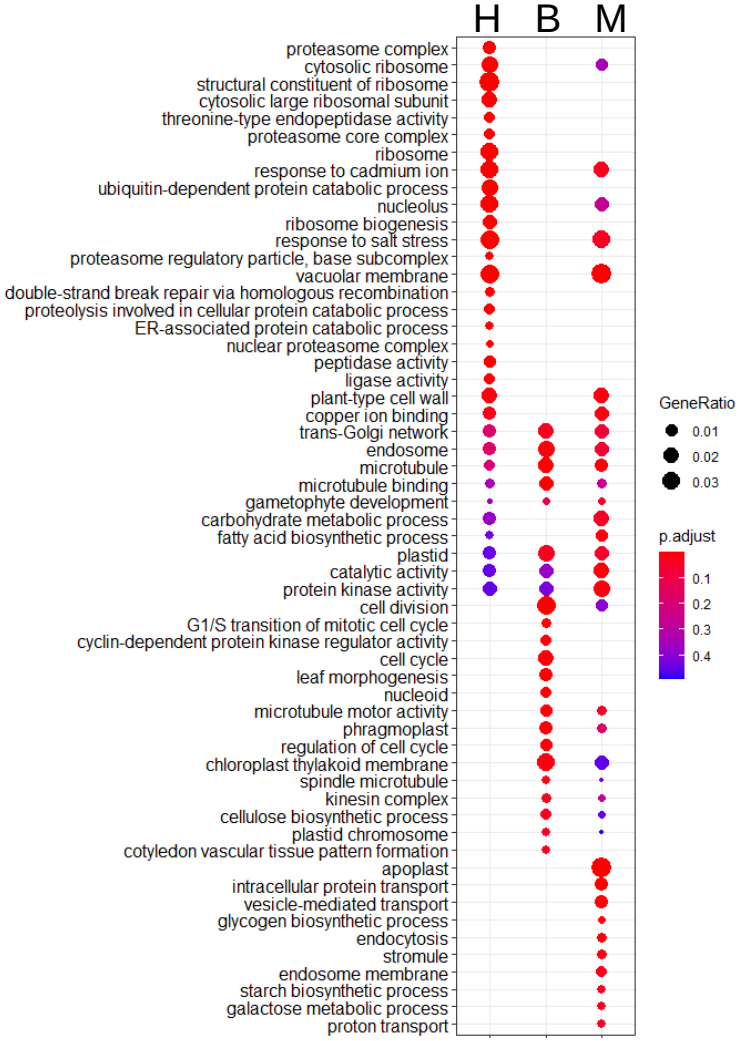
A


Heart
Bent
Mature
1530
330
809
533
434
543
1314


H B M
transferase activity, transferring glycosyl groups
Golgi membrane
trans-Golgi network
positive regulation of seed germination
endosome
response to cadmium ion
stomatal movement
endoplasmic reticulum membrane
transferase activity, transferring hexosyl groups
response to salt stress
cell wall organization
UDP-glycosyltransferase activity
quercetin 3-O-glucosyltransferase activity
quercetin 7-O-glucosyltransferase activity
vacuolar membrane
response to water deprivation
plant-type hypersensitive response
positive regulation of transcription, DNA-dependent
nucleotide-sugar metabolic process
abscisic acid mediated signaling pathway
iron ion binding
oxidoreductase activity, acting on paired donors,
cellulase activity
apoplast
response to toxin
transferase activity, transferring acyl groups
lignin biosynthetic process
4-coumarate-CoA ligase activity
1-phosphatidylinositol-4-phosphate 5-kinase activity
response to wounding
cyclic nucleotide binding
regulation of membrane potential
phosphorylation
metalloendopeptidase activity
anther dehiscence
nutrient reservoir activity
protein storage vacuole
copper ion transmembrane transporter activity
multicellular organismal development
hydrolase activity, acting on glycosyl bonds
anchored to membrane
phosphate ion homeostasis
endonuclease activity
lignin catabolic process
GTPase activator activity
blue light signaling pathway
endoplasmic reticulum unfolded protein response
endocytosis
lipid catabolic process
viral nucleocapsid
lipid metabolic process
cinnamyl-alcohol dehydrogenase activity
developmental process
photomorphogenesis
GeneRatio
0.01
0.02
0.03
0.04
p.adjust
0.1
0.2
0.3
0.4

B


Heart
Bent
Mature
1742
364
764
683
446
898
1370


H B M
proteasome complex
cytosolic ribosome
structural constituent of ribosome
cytosolic large ribosomal subunit
threonine-type endopeptidase activity
proteasome core complex
ribosome
response to cadmium ion
ubiquitin-dependent protein catabolic process
nucleolus
ribosome biogenesis
response to salt stress
proteasome regulatory particle, base subcomplex
vacuolar membrane
double-strand break repair via homologous recombination
proteolysis involved in cellular protein catabolic process
ER-associated protein catabolic process
nuclear proteasome complex
peptidase activity
ligase activity
plant-type cell wall
copper ion binding
trans-Golgi network
endosome
microtubule
microtubule binding
gametophyte development
carbohydrate metabolic process
fatty acid biosynthetic process
plastid
catalytic activity
protein kinase activity
cell division
G1/S transition of mitotic cell cycle
cyclin-dependent protein kinase regulator activity
cell cycle
leaf morphogenesis
nucleoid
microtubule motor activity
phragmoplast
regulation of cell cycle
chloroplast thylakoid membrane
spindle microtubule
kinesin complex
cellulose biosynthetic process
plastid chromosome
cotyledon vascular tissue pattern formation
apoplast
intracellular protein transport
vesicle-mediated transport
glycogen biosynthetic process
endocytosis
stromule
endosome membrane
starch biosynthetic process
galactose metabolic process
proton transport
GeneRatio
0.01
0.02
0.03
p.adjust
0.1
0.2
0.3
0.4