

Cluster	GO term (p-value)
1	
2	C-22 sterol desaturase activity (1.40×10^{-2}) detection of fungus (2.34×10^{-2})
3	cytidine deaminase activity (3.51×10^{-3}) response to singlet oxygen (4.58×10^{-3}) nucleoside catabolic process (6.11×10^{-3}) cytidine deamination (6.11×10^{-3}) defense response signaling pathway, resistance gene-independent (6.11×10^{-3}) cytidine metabolic process (6.11×10^{-3}) pyrimidine ribonucleoside catabolic process (6.11×10^{-3}) pyrimidine nucleoside metabolic process (7.63×10^{-3}) defense response signaling pathway, resistance gene-dependent (8.4×10^{-3}) response to stress (1.10×10^{-2}) ribonucleoside metabolic process (1.22×10^{-2}) intrinsic to endoplasmic reticulum membrane (1.22×10^{-2}) magnesium ion binding (1.25×10^{-2}) activation of immune response (1.68×10^{-2}) positive regulation of immune system process (1.68×10^{-2}) positive regulation of innate immune response (1.68×10^{-2}) systemic acquired resistance (2.06×10^{-2}) regulation of immune response (2.06×10^{-2}) plant-type hypersensitive response (2.36×10^{-2}) positive regulation of response to stimulus (3.20×10^{-2}) monooxygenase activity (3.26×10^{-2}) hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds (3.37×10^{-2}) regulation of defense response (3.5×10^{-2}) microsome (3.67×10^{-2}) membrane fraction (4.54×10^{-2})
4	
5	protein serine/threonine phosphatase complex (9.9×10^{-6}) protein serine/threonine phosphatase activity (1.79×10^{-5}) protein amino acid dephosphorylation (6.12×10^{-4}) phosphatase activity (8.16×10^{-4}) guanosine tetraphosphate metabolic process (3.56×10^{-3}) hydrolase activity, acting on ester bonds (5.29×10^{-3}) purine ribonucleoside metabolic process (1.24×10^{-2}) negative regulation of abscisic acid mediated signaling (4.54×10^{-2})
6	response to insect (2.04×10^{-3}) jasmonic acid and ethylene-dependent systemic resistance (6.71×10^{-3}) response to starvation (8.33×10^{-3}) response to extracellular stimulus (1.16×10^{-2}) response to ethylene stimulus (2.64×10^{-2}) response to jasmonic acid stimulus (2.64×10^{-2}) response to external stimulus (2.69×10^{-2})

innate immune response (3.04×10^{-2})
 immune system process (3.28×10^{-2})
 calcium ion binding (3.98×10^{-2})

7

8 autophagy (3.2×10^{-2})

9 lactoylglutathione lyase activity (1.02×10^{-3})
 response to sucrose stimulus (5.19×10^{-3})
 aging (1.05×10^{-2})
 response to carbohydrate stimulus (1.08×10^{-2})
 endomembrane system (1.58×10^{-2})
 lyase activity (4.53×10^{-2})

10 hydrolase activity, hydrolyzing O-glycosyl compounds (4.98×10^{-2})
 cellular response to sucrose starvation (2.44×10^{-3})
 asparagine synthase (glutamine-hydrolyzing) activity (3.07×10^{-3})
 water homeostasis (9.77×10^{-3})
 acyl carrier activity (1.13×10^{-2})
 cellular potassium ion homeostasis (1.22×10^{-2})
 response to absence of light (2.68×10^{-2})
 monovalent inorganic cation homeostasis (2.68×10^{-2})
 sodium:hydrogen antiporter activity (3.26×10^{-2})
 solute:hydrogen antiporter activity (4.99×10^{-2})

11 immune system process (6.89×10^{-5})
 drug transporter activity (7.76×10^{-4})
 negative regulation of defense response (8.52×10^{-4})
 plasma membrane (1.81×10^{-2})
 auxin efflux (1.96×10^{-2})
 xenobiotic-transporting ATPase activity (2.54×10^{-2})
 multidrug efflux pump activity (2.54×10^{-2})
 ATPase activity (3.2×10^{-2})
 response to humidity (3.91×10^{-2})
 positive regulation of cellular defense response (3.91×10^{-2})
 positive regulation of cell size (3.91×10^{-2})

12 sphingolipid delta-4 desaturase activity (2.68×10^{-3})
 methionine adenosyltransferase activity (1.07×10^{-2})
 positive regulation of anthocyanin metabolic process (1.59×10^{-2})
 S-adenosylmethionine biosynthetic process (3.18×10^{-2})
 double-stranded DNA binding (3.48×10^{-2})
 positive regulation of flavonoid biosynthetic process (3.97×10^{-2})
 lipid transporter activity (4.28×10^{-2})

13 NAD+ ADP-ribosyltransferase activity (1.17×10^{-3})
 oxygen and reactive oxygen species metabolic process (7.52×10^{-3})
 response to salt stress (4.01×10^{-2})

14

15 endoplasmic reticulum (4.99×10^{-8})
 protein folding (3.96×10^{-5})
 ATP binding (1.49×10^{-3})

adenyly nucleotide binding (1.80×10^{-3})
 purine ribonucleotide binding (3.19×10^{-3})
 nucleotide binding (7.03×10^{-3})
 regulation of meristem growth (1.57×10^{-2})
 protein secretion (1.71×10^{-2})
 regulation of meristem organization (1.99×10^{-2})
 endoplasmic reticulum lumen (2.07×10^{-2})
 regulation of growth (3.56×10^{-2})
 cytoplasm (4.26×10^{-2})
 16 chloroplast thylakoid membrane (2.13×10^{-5})
 thylakoid membrane (2.74×10^{-5})
 plastid thylakoid (8.4×10^{-5})
 photosynthetic membrane (1.79×10^{-4})
 chloroplast (2.94×10^{-4})
 intracellular organelle part (2.81×10^{-2})
 cytoplasmic part (2.99×10^{-2})
 17 autophagic vacuole (1.32×10^{-2})
 outward rectifier potassium channel activity (3.82×10^{-2})
 phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity (4.36×10^{-2})
 autophagy (4.74×10^{-2})
 18 nitrate reductase activity (7.8×10^{-4})
 prephenate dehydratase activity (2.34×10^{-3})
 arginate dehydratase activity (2.34×10^{-3})
 nitric oxide biosynthetic process (4.28×10^{-3})
 L-phenylalanine biosynthetic process (8.55×10^{-3})
 nitrate assimilation (9.98×10^{-3})
 nitrogen compound metabolic process (2.00×10^{-2})
 defense response to fungus, incompatible interaction (2.14×10^{-2})
 defense response to bacterium, incompatible interaction (3.42×10^{-2})
 carbon-oxygen lyase activity (4.3×10^{-2})
 19 jasmonate O-methyltransferase activity (1.27×10^{-2})
 6-phosphogluconolactonase activity (2.54×10^{-2})
 beta-carotene hydroxylase activity (2.54×10^{-2})
 1,2-diacylglycerol 3-beta-galactosyltransferase activity (3.8×10^{-2})
 20 protein serine/threonine phosphatase activity (4.73×10^{-3})
 21 extracellular matrix structural constituent (1.09×10^{-2})
 ubiquitin ligase complex (2.54×10^{-2})
 protein ubiquitination (3.24×10^{-2})
 extracellular matrix organization and biogenesis (3.28×10^{-2})
 peptide receptor activity (4.37×10^{-2})
 22 flavonol biosynthetic process (7.68×10^{-5})
 caffeate O-methyltransferase activity (4.78×10^{-3})
 flavonoid metabolic process (1.24×10^{-2})
 pigment metabolic process (3.32×10^{-2})
 beta-amylase activity (4.29×10^{-2})
 23 substrate-specific transmembrane transporter activity (1.25×10^{-3})

cation transmembrane transporter activity (1.76×10^{-3})
 anion transport (6.96×10^{-3})
 transporter activity (1.71×10^{-2})
 electron carrier activity (2.47×10^{-2})
 localization (2.58×10^{-2})
 rhamnogalacturonan II biosynthetic process (3.66×10^{-2})
 UDP-xylosyltransferase activity (4.29×10^{-2})
 metal ion transmembrane transporter activity (4.61×10^{-2})
 24 endomembrane system (1.57×10^{-2})
 protein ubiquitination (2.39×10^{-2})
 defense response to bacterium (2.48×10^{-2})
 25 endomembrane system (1.62×10^{-4})
 electron carrier activity (2.58×10^{-3})
 kinase activity (5.23×10^{-3})
 defense response to bacterium, incompatible interaction (1.26×10^{-2})
 immune system process (2.57×10^{-2})
 positive regulation of biosynthetic process (4.46×10^{-2})
 26 kinase activity (2.21×10^{-4})
 protein amino acid phosphorylation (3.04×10^{-4})
 oligopeptide transport (5.59×10^{-4})
 phosphate metabolic process (7.26×10^{-4})
 oligopeptide transporter activity (1.48×10^{-3})
 endomembrane system (4.22×10^{-3})
 protein modification process (8.92×10^{-3})
 transferase activity (2.23×10^{-2})
 27 hydrogen peroxide-mediated programmed cell death (3.06×10^{-3})
 ADP-ribose diphosphatase activity (3.51×10^{-3})
 NAD binding (1.05×10^{-2})
 28 urea transmembrane transporter activity (1.17×10^{-3})
 cyclic-nucleotide phosphodiesterase activity (2.34×10^{-3})
 isochorismate synthase activity (2.34×10^{-3})
 protein disulfide isomerase activity (4.68×10^{-3})
 salicylic acid biosynthetic process (8.55×10^{-3})
 solute:sodium symporter activity (1.05×10^{-2})
 phyloquinone biosynthetic process (1.43×10^{-2})
 tRNA splicing (1.71×10^{-2})
 cellular response to nitrogen starvation (1.71×10^{-2})
 vitamin K metabolic process (1.71×10^{-2})
 transporter activity (2.52×10^{-2})
 phosphate transport (3.42×10^{-2})
 intramolecular oxidoreductase activity (3.50×10^{-2})
 negative regulation of defense response (3.7×10^{-2})
 fat-soluble vitamin biosynthetic process (3.7×10^{-2})
 intramolecular transferase activity (4.07×10^{-2})
 quinone cofactor biosynthetic process (4.27×10^{-2})
 29 glycerol kinase activity (1.95×10^{-3})

tryptophan catabolic process (1.14×10^{-2})
biogenic amine catabolic process (1.14×10^{-2})
indole derivative catabolic process (1.14×10^{-2})
catabolic process (1.73×10^{-2})
chitinase activity (2.73×10^{-2})
camalexin biosynthetic process (2.85×10^{-2})
response to microbial phytotoxin (3.42×10^{-2})
indole phytoalexin metabolic process (3.42×10^{-2})
phytoalexin biosynthetic process (3.42×10^{-2})
glycerol catabolic process (3.99×10^{-2})
response to molecule of bacterial origin (4.56×10^{-2})
indoleacetic acid biosynthetic process (4.56×10^{-2})