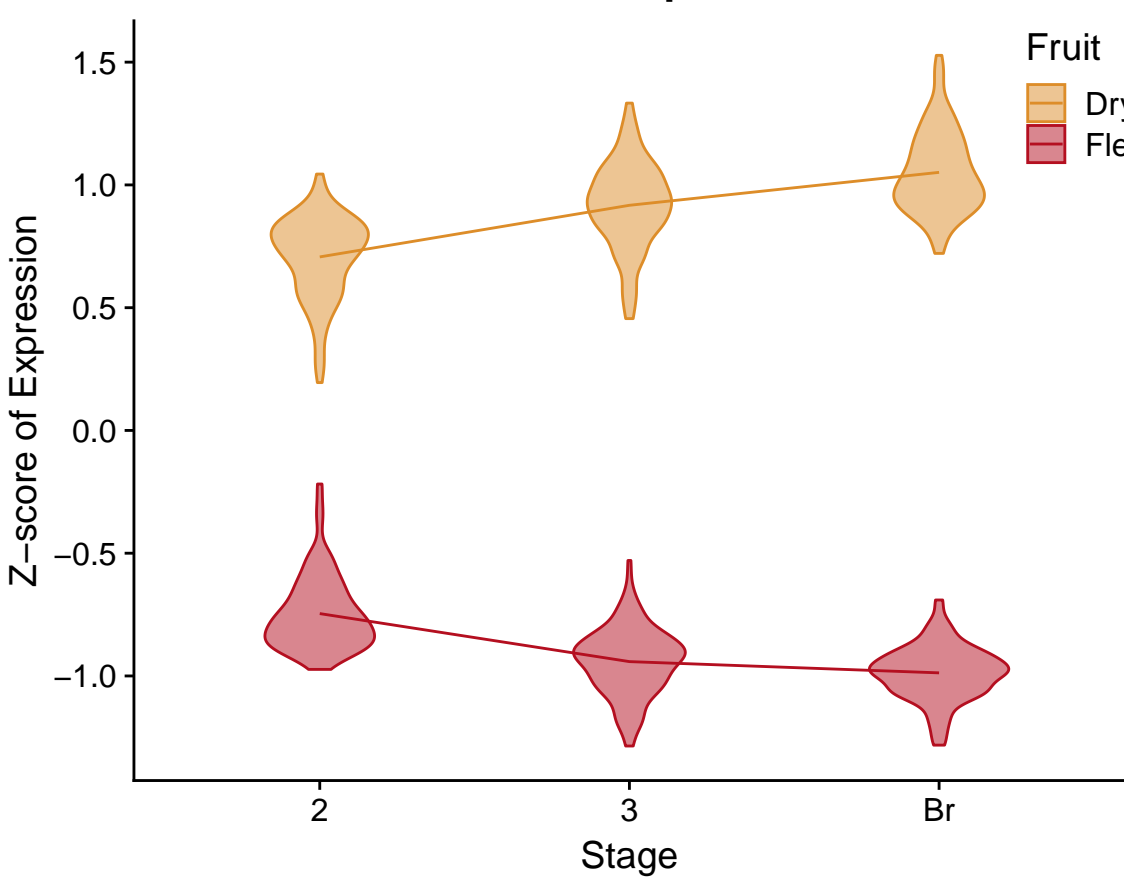


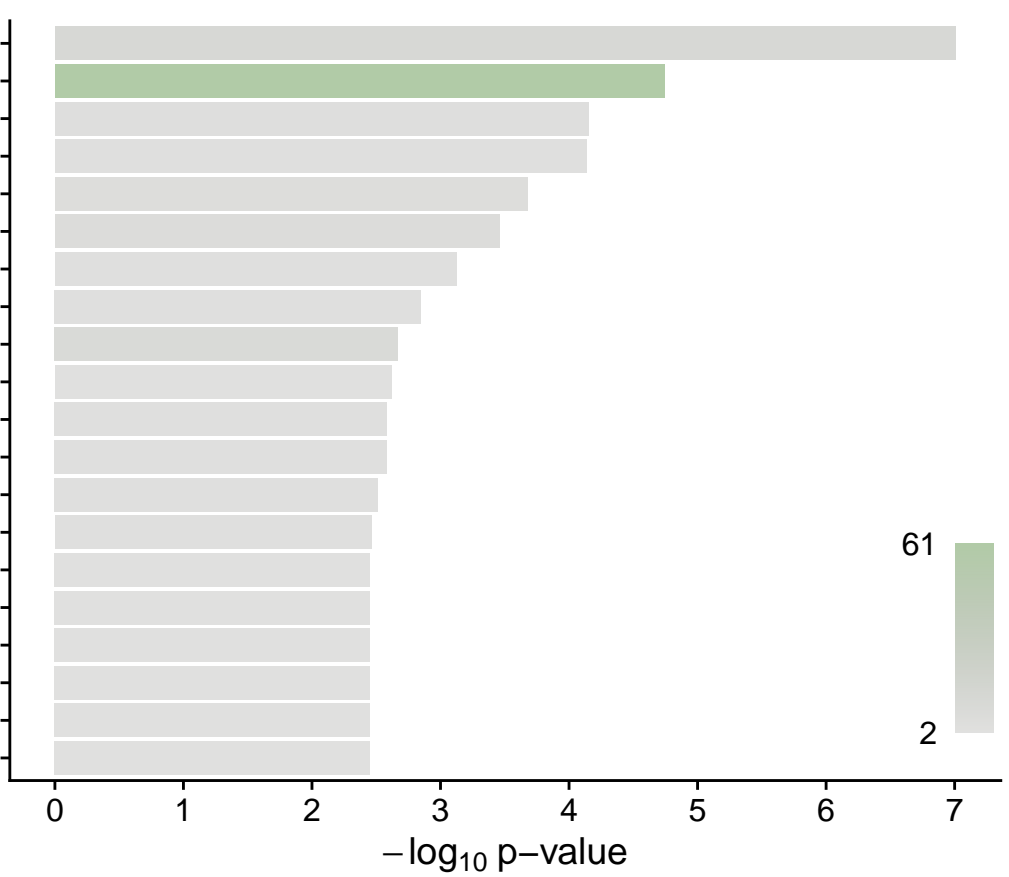
Cluster 1 Expression



B

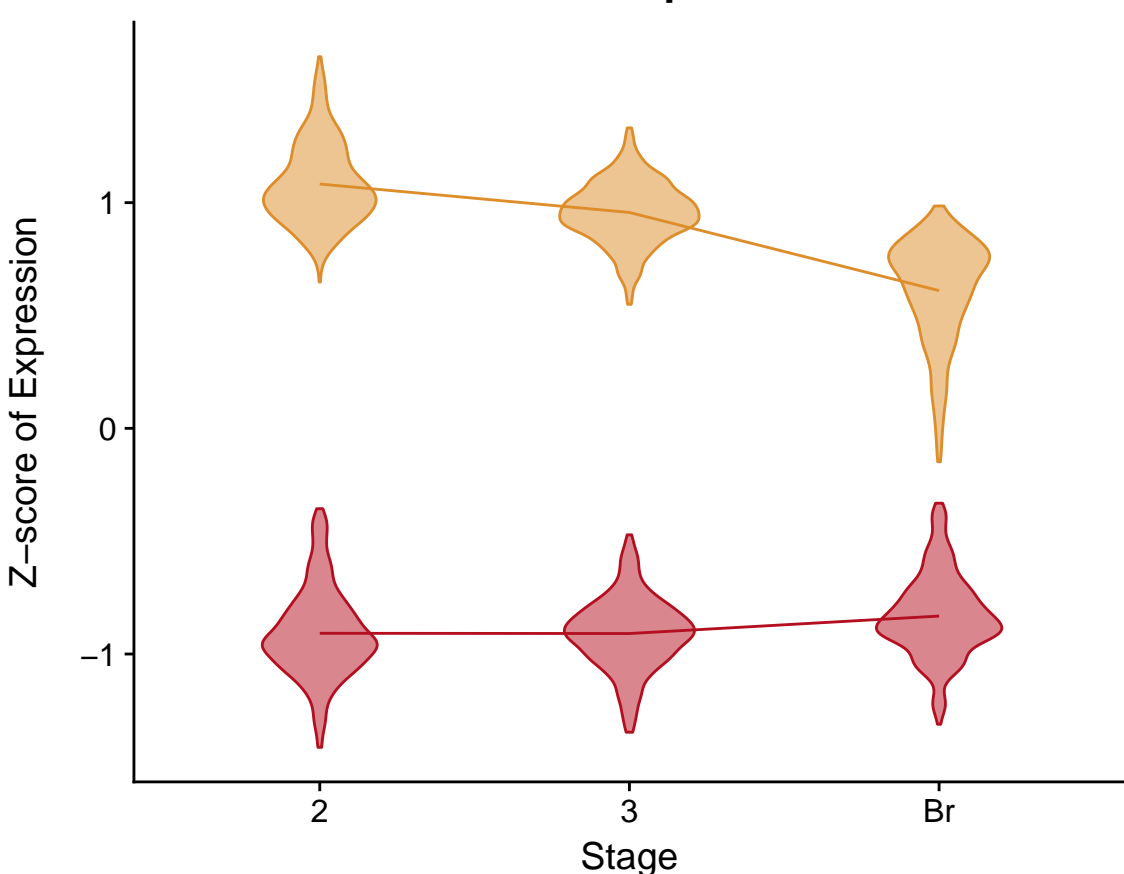
GO:0055114, oxidation–reduction proces
GO:0008152, metabolic process
GO:0015979, photosynthesis
GO:0007005, mitochondrion organization
GO:0055085, transmembrane transport
GO:0006412, translation
GO:0015995, chlorophyll biosynthetic p
GO:0051707, response to other organism
GO:0006950, response to stress
GO:0035304, regulation of protein dep
GO:0030154, cell differentiation
GO:0006605, protein targeting
GO:0072594, establishment of protein I
GO:0010629, negative regulation of gen
GO:0006096, glycolytic process
GO:0009247, glycolipid biosynthetic pr
GO:0080134, regulation of response to
GO:0070838, divalent metal ion transpo
GO:0043094, cellular metabolic compoun
GO:0051640, organelle localization

Cluster 1 GO Enrichment



C

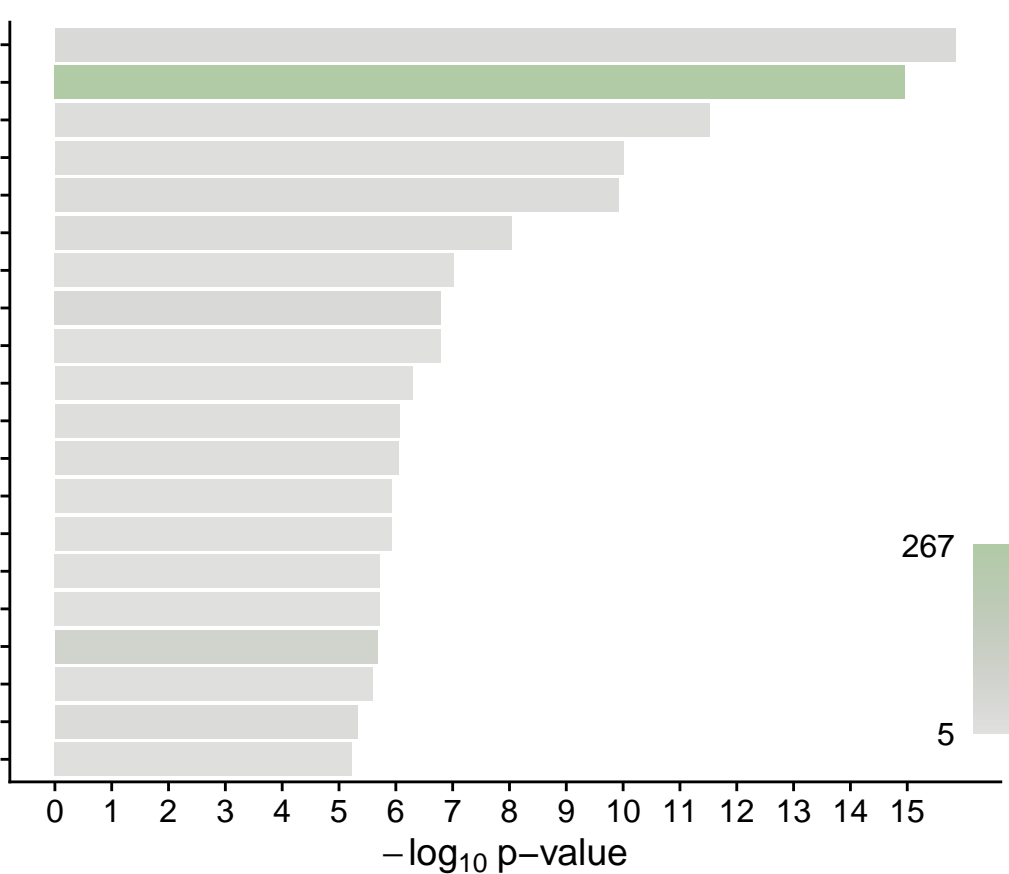
Cluster 2 Expression



D

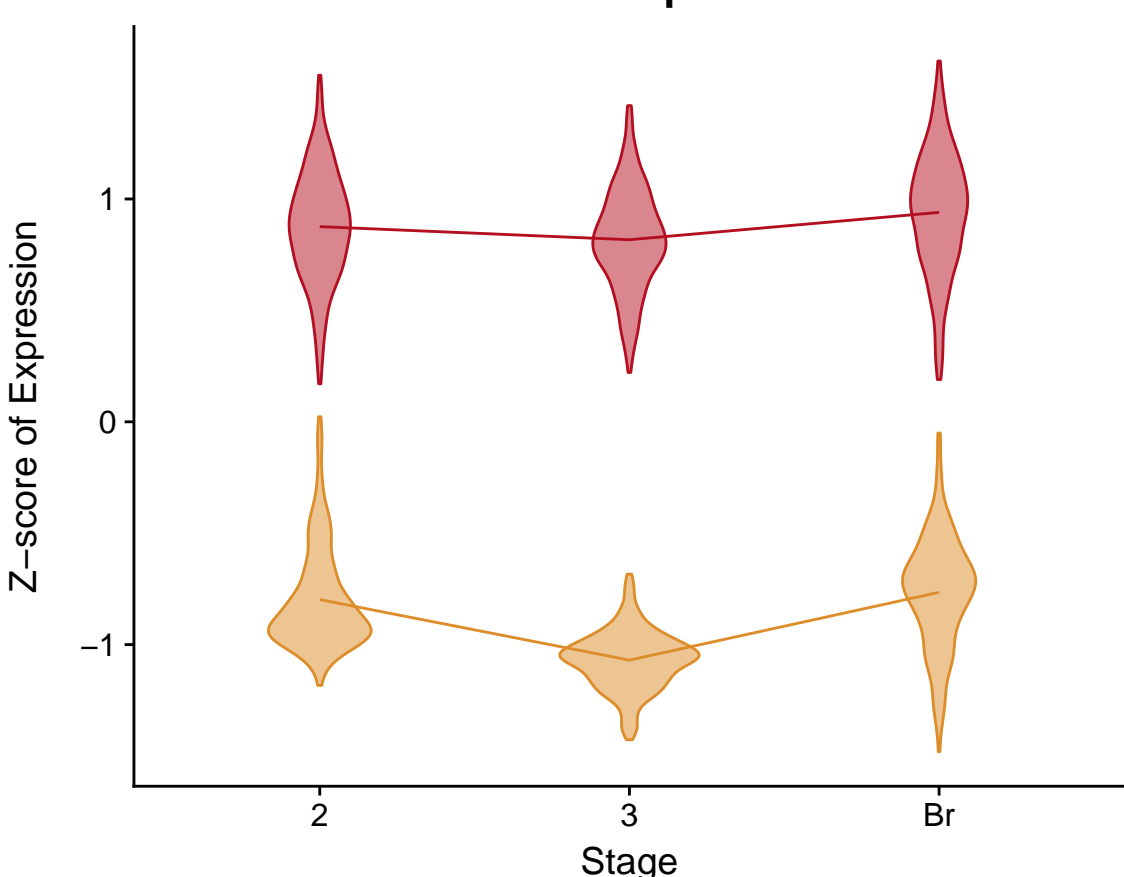
GO:0055114, oxidation–reduction proces
GO:0008152, metabolic process
GO:0006355, regulation of transcriptio
GO:0009069, serine family amino acid m
GO:0006468, protein phosphorylation
GO:0006508, proteolysis
GO:0006281, DNA repair
GO:0016310, phosphorylation
GO:0006511, ubiquitin–dependent protei
GO:0006635, fatty acid beta–oxidation
GO:0032259, methylation
GO:0006412, translation
GO:0006555, methionine metabolic proce
GO:0016558, protein import into peroxi
GO:0010035, response to inorganic subs
GO:0006094, gluconeogenesis
GO:0044267, cellular protein metabolic
GO:0006457, protein folding
GO:1901605, alpha–amino acid metabolic
GO:0030001, metal ion transport

Cluster 2 GO Enrichment



E

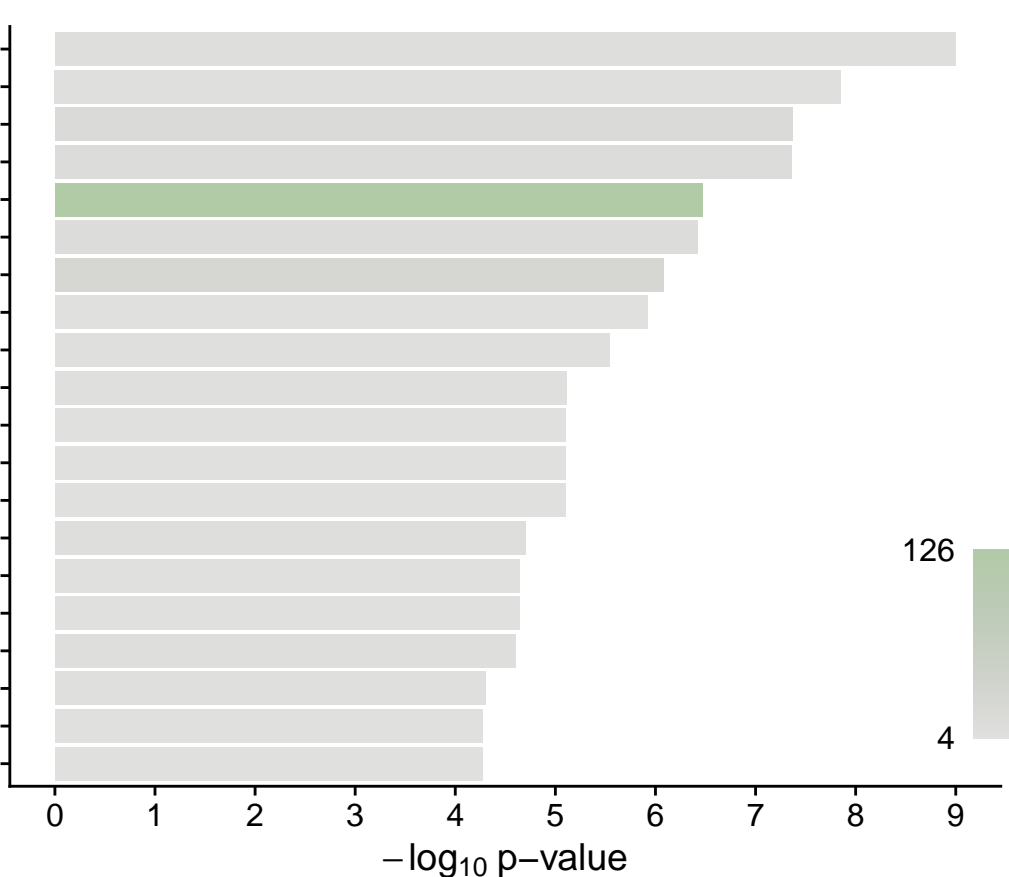
Cluster 3 Expression



F

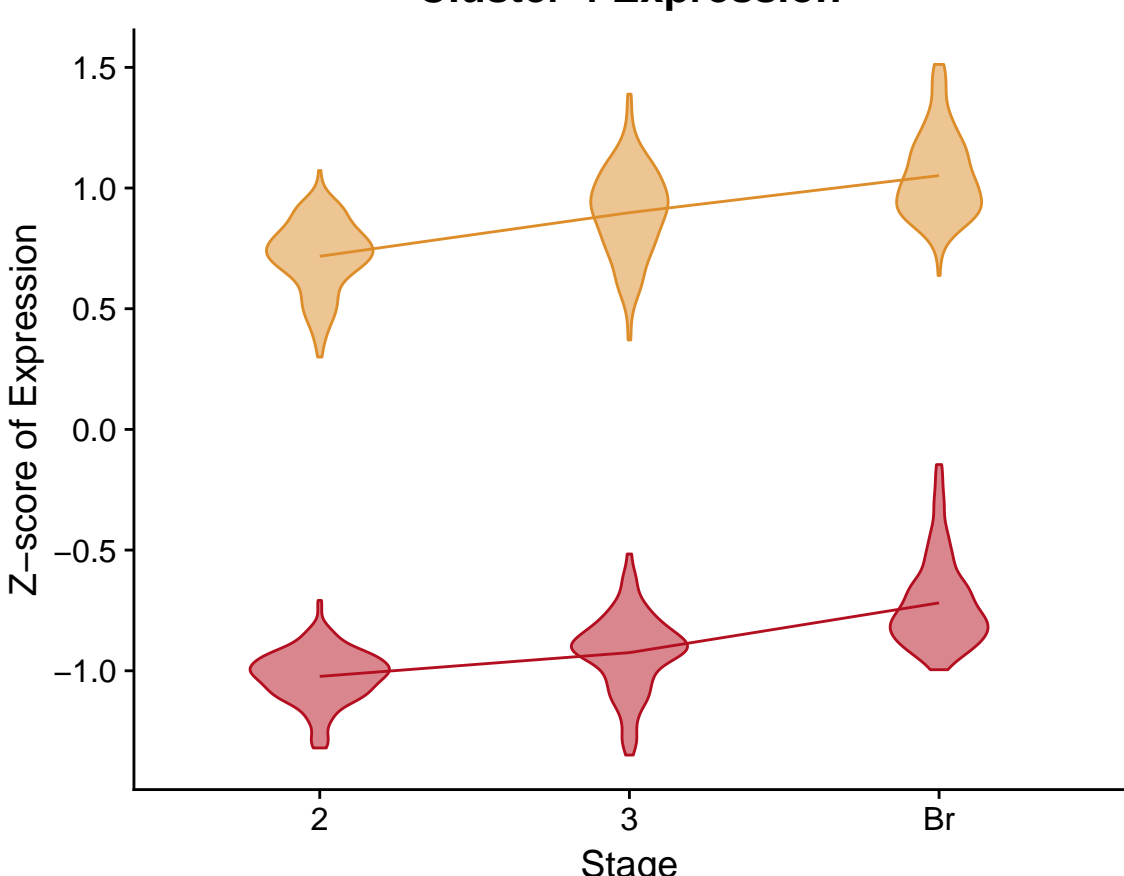
GO:0016192, vesicle–mediated transport
GO:0009813, flavonoid biosynthetic pro
GO:0055114, oxidation–reduction proces
GO:0006355, regulation of transcriptio
GO:0008152, metabolic process
GO:0055085, transmembrane transport
GO:0019438, aromatic compound biosynth
GO:0008643, carbohydrate transport
GO:0071555, cell wall organization
GO:0090558, plant epidermis developmen
GO:0071695, anatomical structure matur
GO:0010015, root morphogenesis
GO:1901264, carbohydrate derivative tr
GO:0051276, chromosome organization
GO:0009640, photomorphogenesis
GO:0048646, anatomical structure forma
GO:0006468, protein phosphorylation
GO:0015931, nucleobase–containing comp
GO:0031324, negative regulation of cel
GO:0051172, negative regulation of nit

Cluster 3 GO Enrichment



G

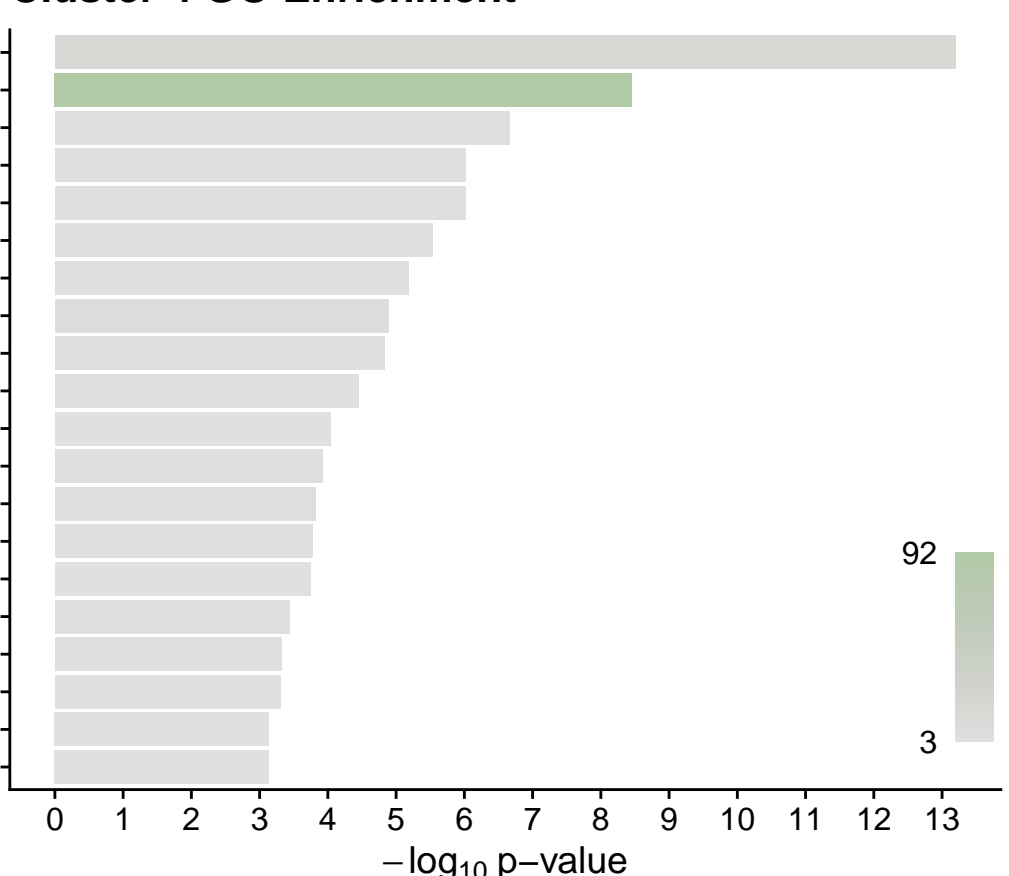
Cluster 4 Expression



H

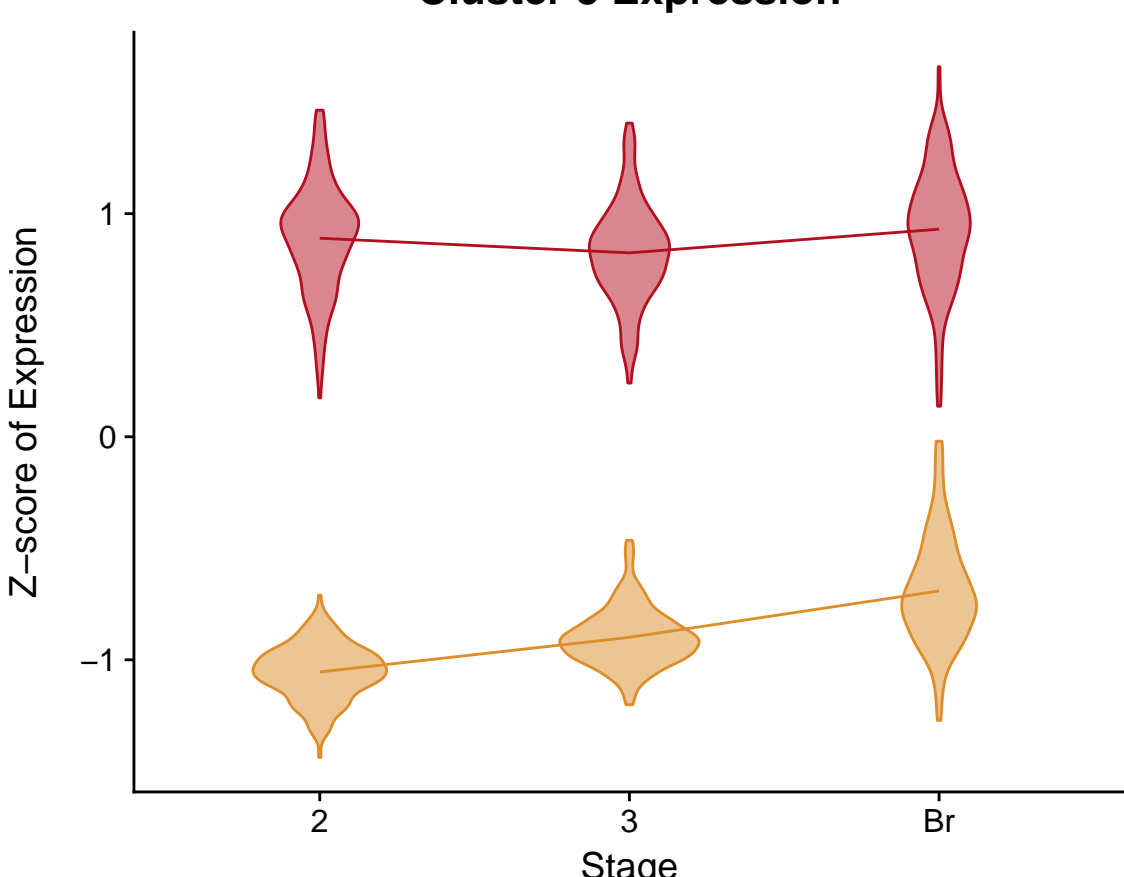
GO:0055114, oxidation–reduction proces
GO:0008152, metabolic process
GO:0006098, pentose–phosphate shunt
GO:0045492, xylan biosynthetic process
GO:0010413, glucuronoxylan metabolic p
GO:0009637, response to blue light
GO:0030003, cellular cation homeostasi
GO:0005982, starch metabolic process
GO:0005985, sucrose metabolic process
GO:0009657, plastid organization
GO:0009832, plant–type cell wall bioge
GO:0043085, positive regulation of cat
GO:0006508, proteolysis
GO:0019288, isopentenyl diphosphate bi
GO:0043648, dicarboxylic acid metaboli
GO:0006468, protein phosphorylation
GO:0006364, rRNA processing
GO:0016999, antibiotic metabolic proce
GO:0009639, response to red or far red
GO:0010207, photosystem II assembly

Cluster 4 GO Enrichment



I

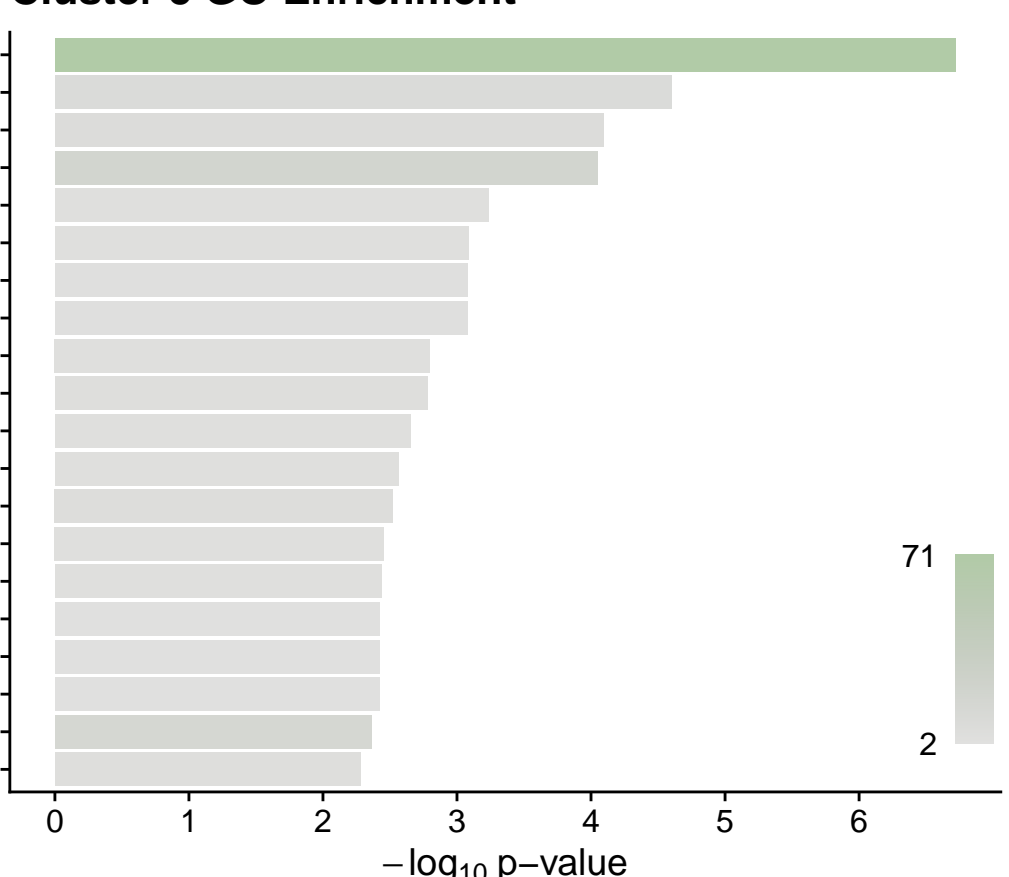
Cluster 5 Expression



J

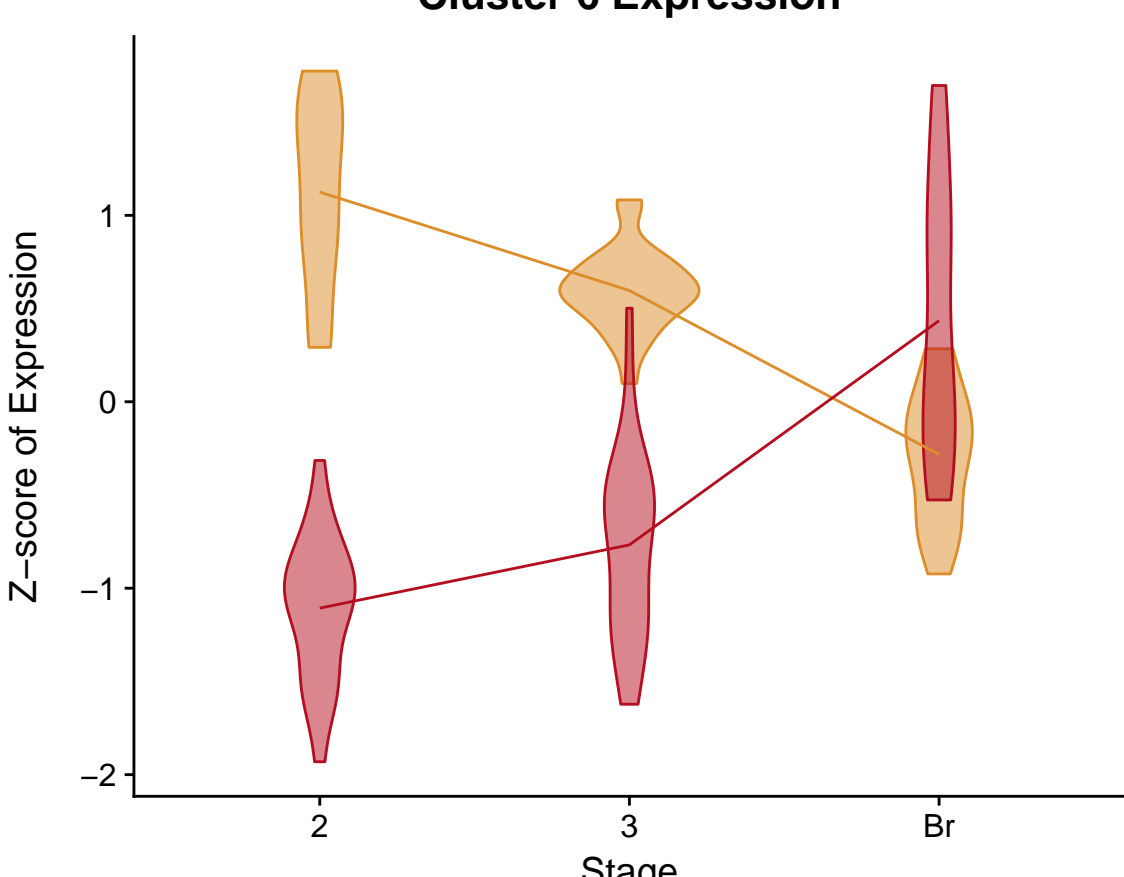
GO:0008152, metabolic process
GO:0006468, protein phosphorylation
GO:0015031, protein transport
GO:0006810, transport
GO:0006397, mRNA processing
GO:0006081, cellular aldehyde metaboli
GO:0090305, nucleic acid phosphodiester
GO:0006633, fatty acid biosynthetic pr
GO:0009069, serine family amino acid m
GO:0006355, regulation of transcriptio
GO:1901615, organic hydroxy compound m
GO:0051276, chromosome organization
GO:0055114, oxidation–reduction proces
GO:0006886, intracellular protein tran
GO:0019684, photosynthesis, light reac
GO:0030488, tRNA methylation
GO:0042364, water–soluble vitamin bios
GO:0009743, response to carbohydrate
GO:0006796, phosphate–containing compo
GO:0055085, transmembrane transport

Cluster 5 GO Enrichment



K

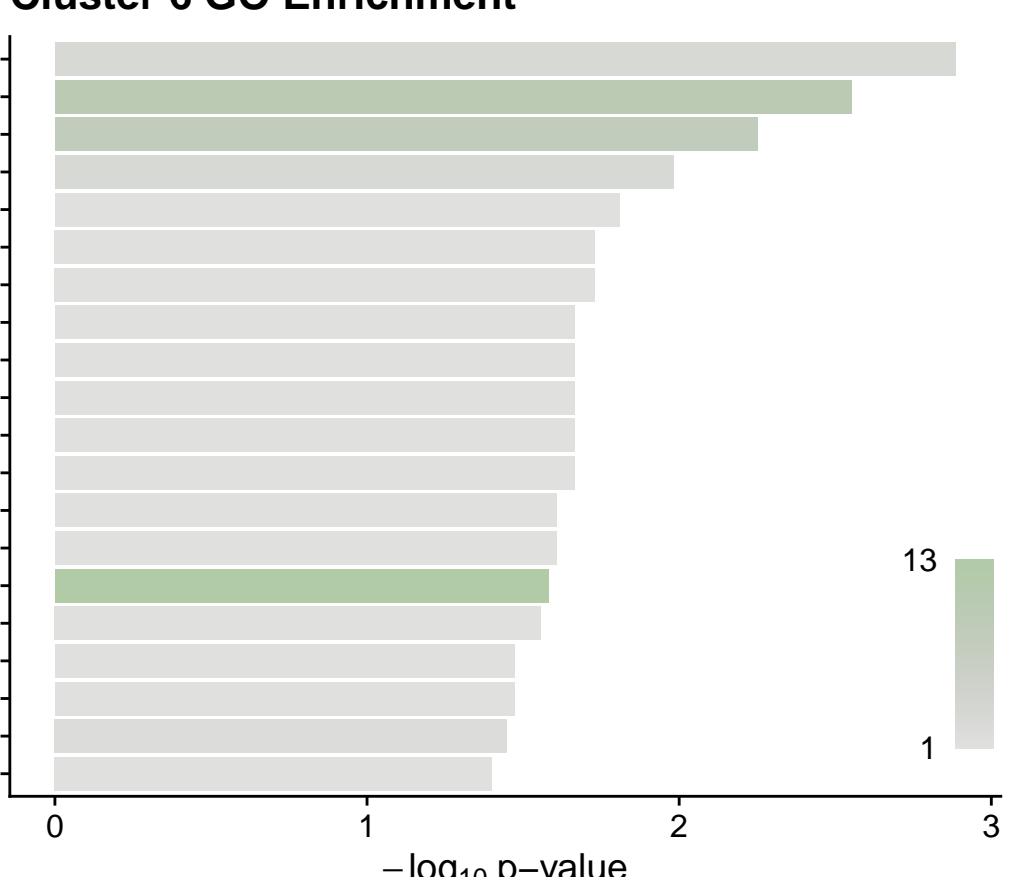
Cluster 6 Expression



L

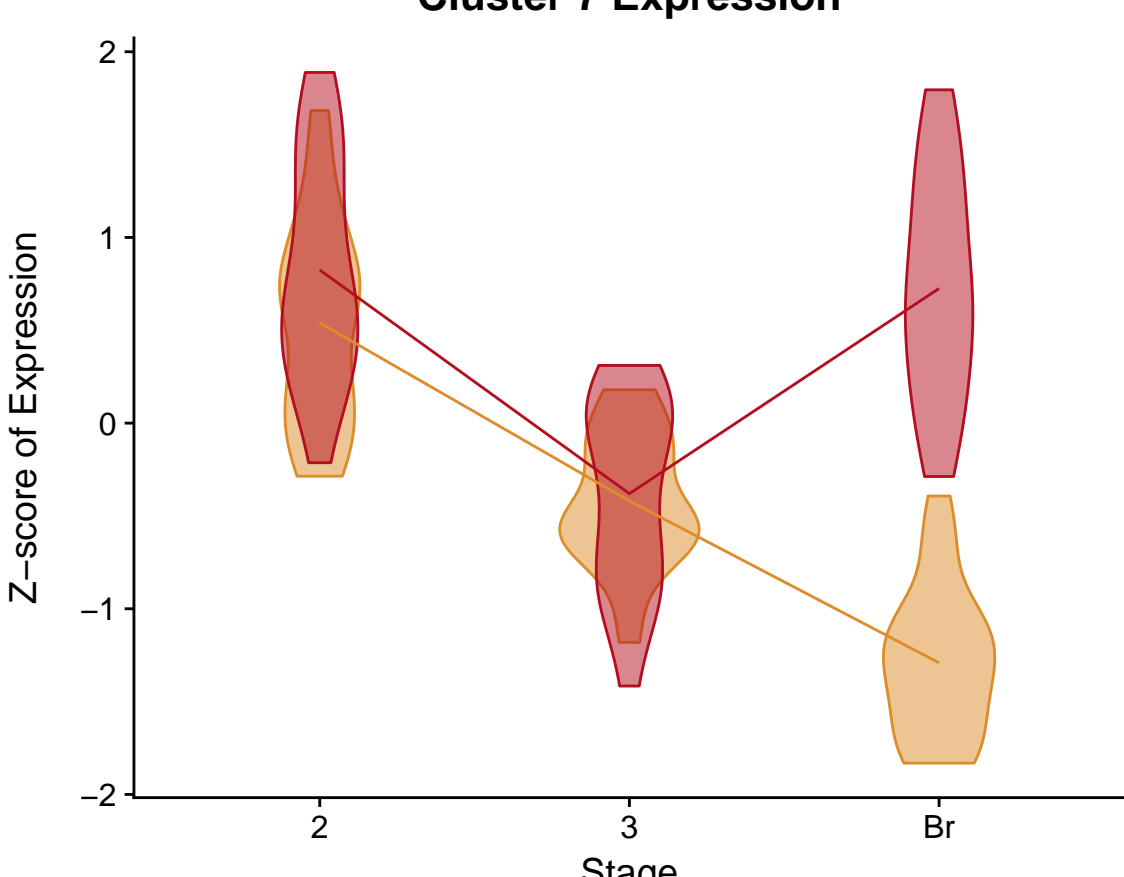
GO:0032259, methylation
GO:0071704, organic substance metaboli
GO:0044238, primary metabolic process
GO:0044281, small molecule metabolic p
GO:0006413, translational initiation
GO:0006417, regulation of translation
GO:0051130, positive regulation of cel
GO:0001522, pseudouridine synthesis
GO:0000398, mRNA splicing, via spliceo
GO:0046942, carboxylic acid transport
GO:0098656, anion transmembrane transp
GO:0010628, positive regulation of gen
GO:0031328, positive regulation of cel
GO:0010557, positive regulation of mac
GO:0008152, metabolic process
GO:0045454, cell redox homeostasis
GO:0051173, positive regulation of nit
GO:0046434, organophosphate catabolic
GO:0055114, oxidation–reduction proces
GO:0001510, RNA methylation

Cluster 6 GO Enrichment



M

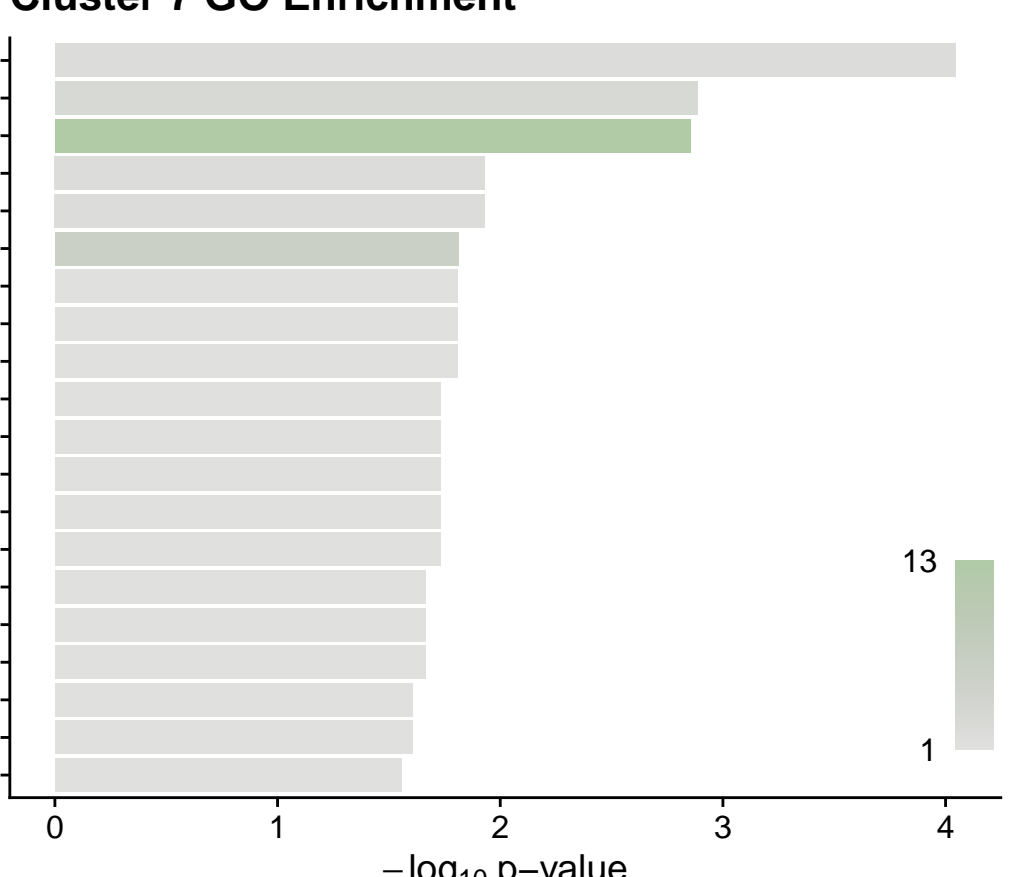
Cluster 7 Expression



N

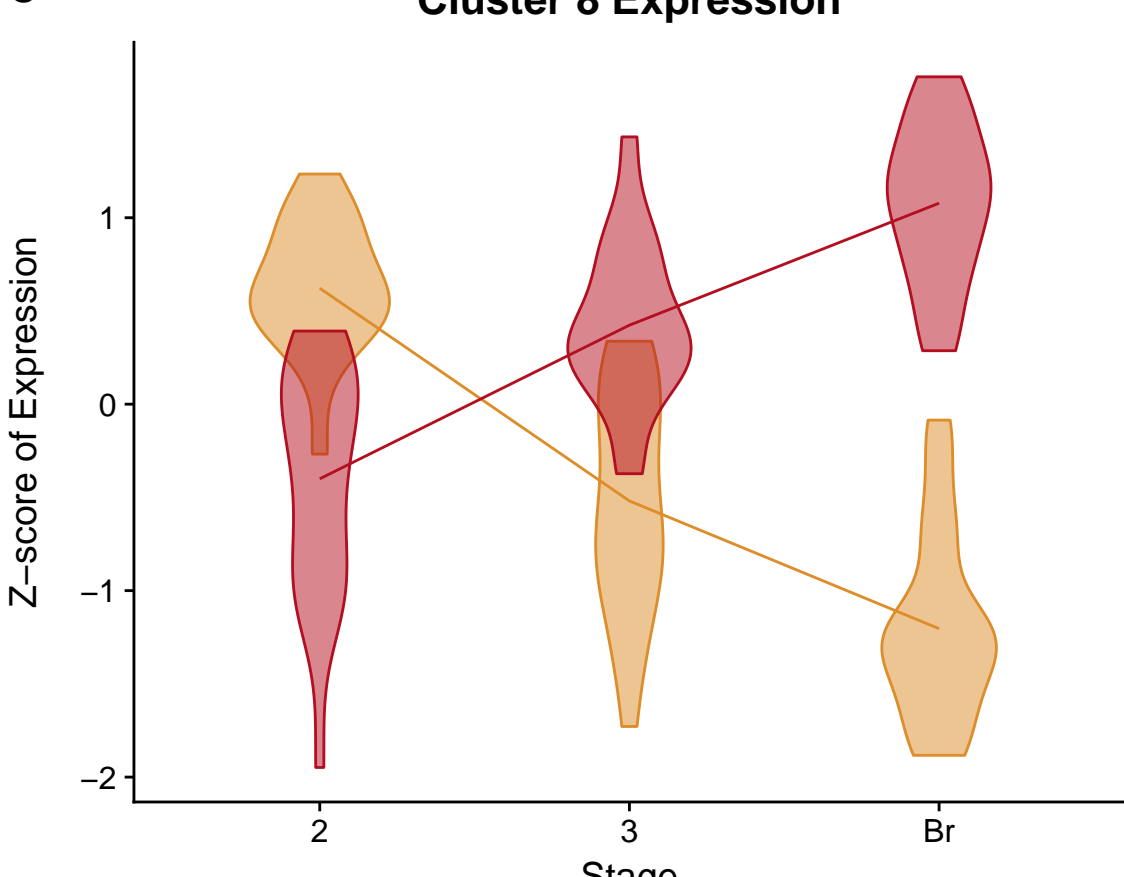
GO:0034968, histone lysine methylation
GO:0006790, sulfur compound metabolic
GO:0071704, organic substance metaboli
GO:0043603, cellular amide metabolic p
GO:0022414, reproductive process
GO:0034641, cellular nitrogen compound
GO:0008283, cell proliferation
GO:0006694, steroid biosynthetic proce
GO:0009414, response to water deprivat
GO:0071396, cellular response to lipid
GO:0042446, hormone biosynthetic proce
GO:0046677, response to antibiotic
GO:0006575, cellular modified amino ac
GO:0009636, response to toxic substanc
GO:0019760, glucosinolate metabolic pr
GO:0002226, microtubule cytoskeleton o
GO:0000413, protein peptidyl–prolyl is
GO:0009737, response to abscisic acid
GO:0006261, DNA–dependent DNA replicat
GO:0009965, leaf morphogenesis

Cluster 7 GO Enrichment



O

Cluster 8 Expression



P

GO:0019752, carboxylic acid metabolic
GO:0006779, porphyrin–containing compo
GO:0006793, phosphorus metabolic proce
GO:0046148, pigment biosynthetic proce
GO:0016226, iron–sulfur cluster assemb
GO:0009063, cellular amino acid catabo
GO:0009225, nucleotide–sugar metabolic
GO:0006413, translational initiation
GO:0000097, sulfur amino acid biosynth
GO:0042446, hormone biosynthetic proce
GO:0045893, positive regulation of tra
GO:0016579, protein deubiquitination
GO:0009965, leaf morphogenesis
GO:0006766, vitamin metabolic process
GO:0010207, photosystem II assembly
GO:0009555, pollen development
GO:0090305, nucleic acid phosphodiester
GO:0006633, fatty acid biosynthetic pr
GO:0019748, secondary metabolic proces
GO:0009072, aromatic amino acid family

Cluster 8 GO Enrichment

