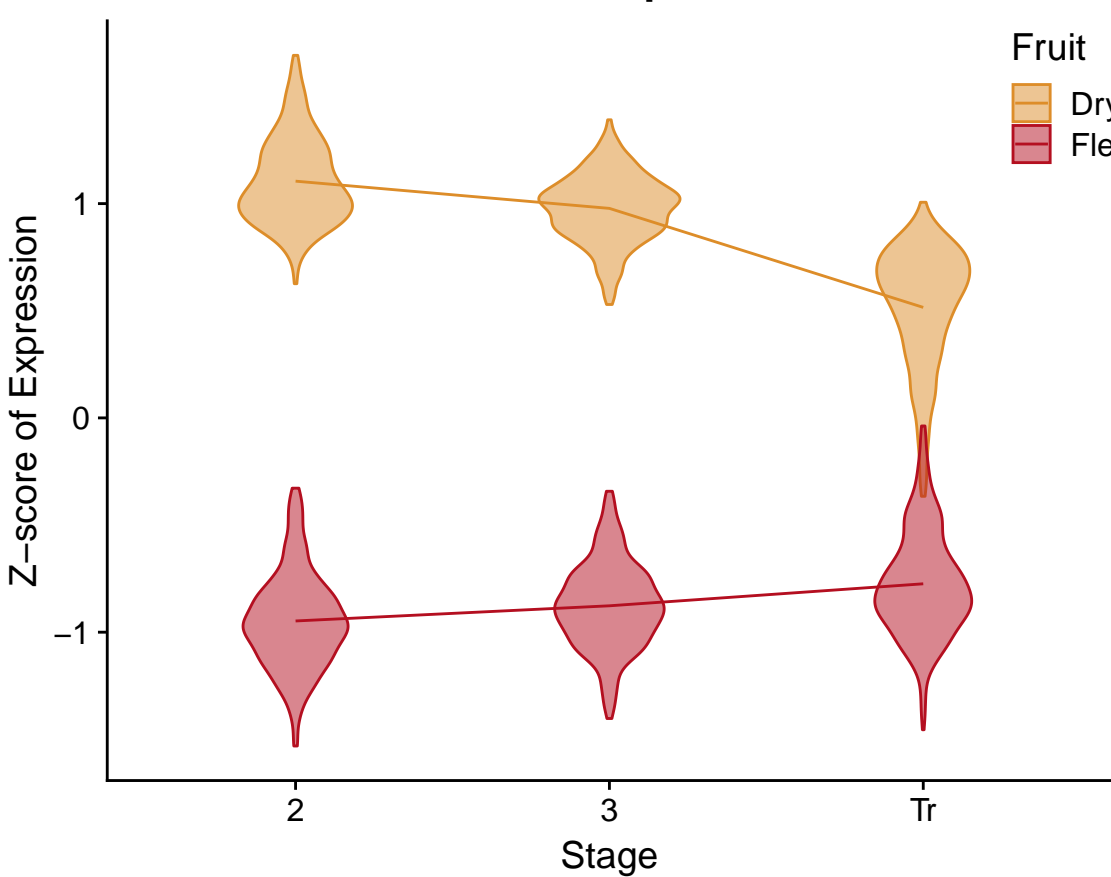


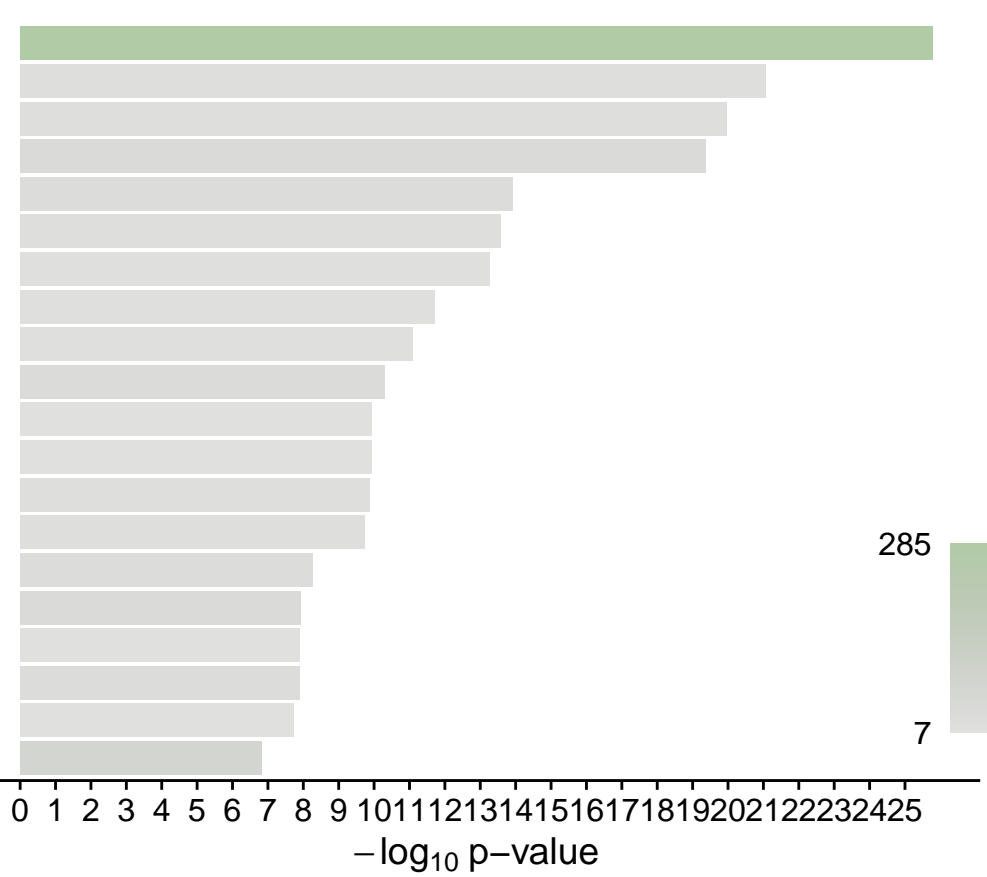
Cluster 1 Expression



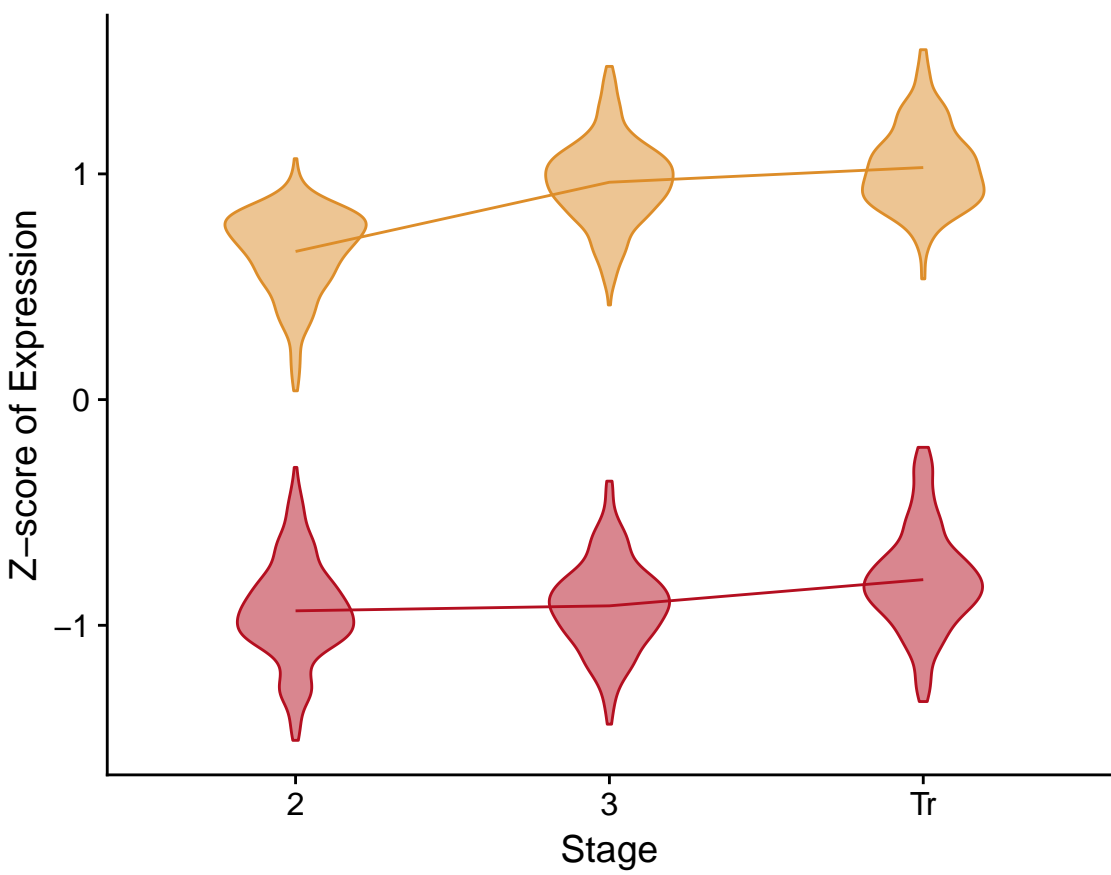
B

GO:0008152, metabolic process
GO:0019288, isopentenyl diphosphate bi
GO:0006098, pentose-phosphate shunt
GO:0055114, oxidation-reduction proces
GO:0006508, proteolysis
GO:0006364, rRNA processing
GO:0019252, starch biosynthetic proces
GO:0010027, thylakoid membrane organiz
GO:0010207, photosystem II assembly
GO:0015979, photosynthesis
GO:0015995, chlorophyll biosynthetic p
GO:0000023, maltose metabolic process
GO:0006355, regulation of transcriptio
GO:0006412, translation
GO:0055085, transmembrane transport
GO:0016310, phosphorylation
GO:0009639, response to red or far red
GO:0006351, transcription, DNA-templat
GO:0016117, carotenoid biosynthetic pr
GO:0044267, cellular protein metabolic

Cluster 1 GO Enrichment



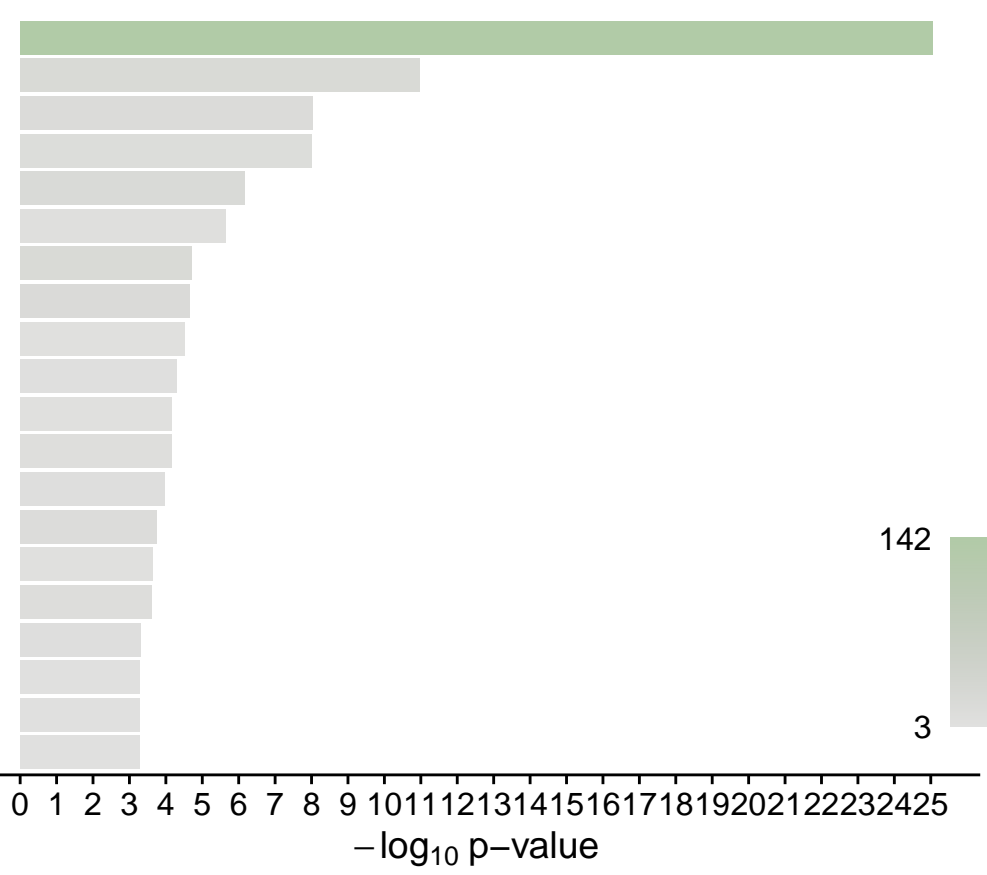
Cluster 2 Expression



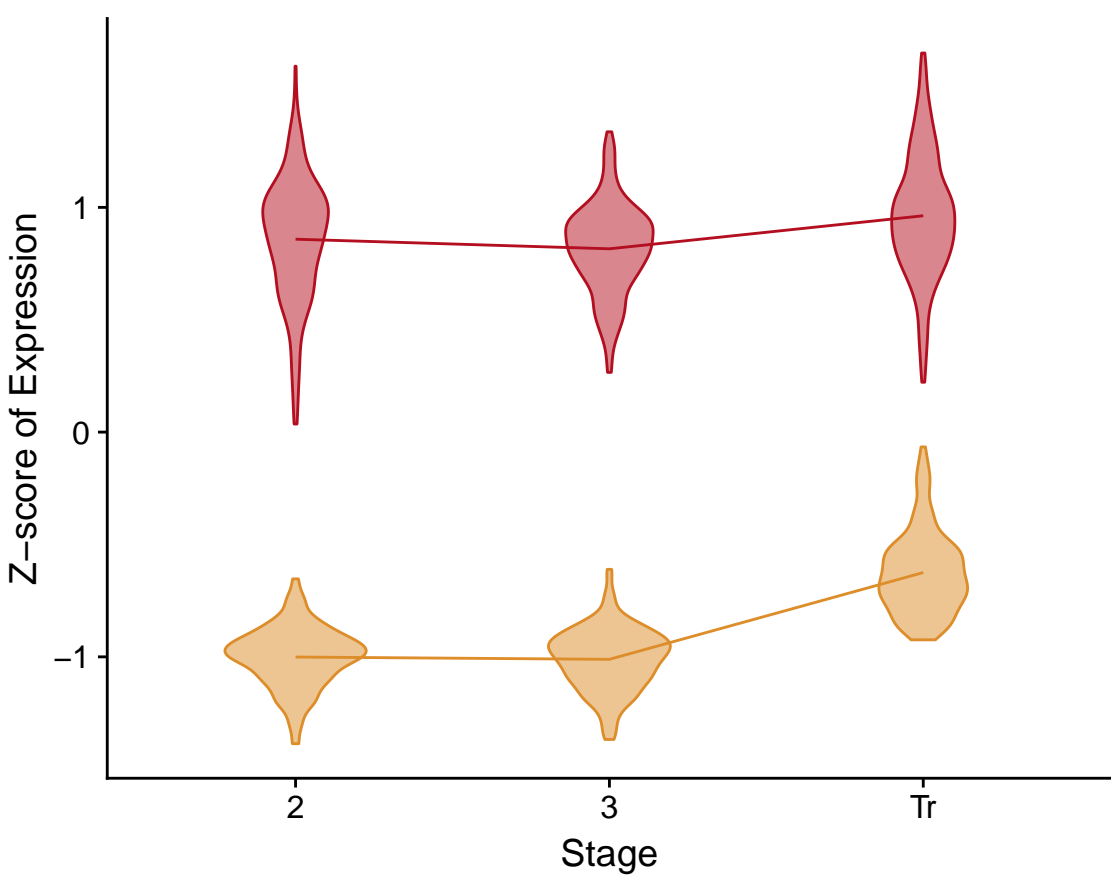
D

GO:0008152, metabolic process
GO:0055114, oxidation-reduction proces
GO:0006468, protein phosphorylation
GO:0006355, regulation of transcriptio
GO:0044248, cellular catabolic process
GO:0009755, hormone-mediated signaling
GO:0019438, aromatic compound biosynth
GO:1901566, organonitrogen compound bi
GO:0006635, fatty acid beta-oxidation
GO:0009793, embryo development ending
GO:0015996, chlorophyll catabolic proc
GO:0006508, proteolysis
GO:0017144, drug metabolic process
GO:0048731, system development
GO:1901617, organic hydroxy compound b
GO:0055085, transmembrane transport
GO:0090407, organophosphate biosynthes
GO:0006497, protein lipidation
GO:0009267, cellular response to starv
GO:0009247, glycolipid biosynthetic pr

Cluster 2 GO Enrichment



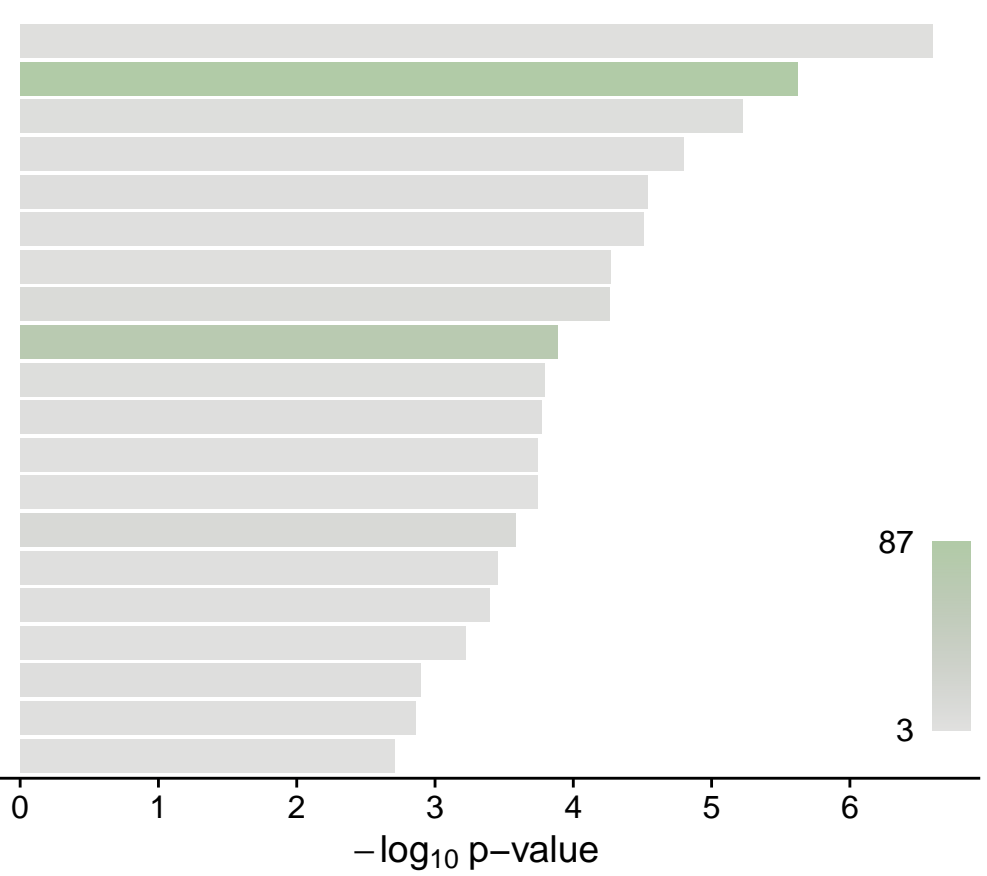
Cluster 3 Expression



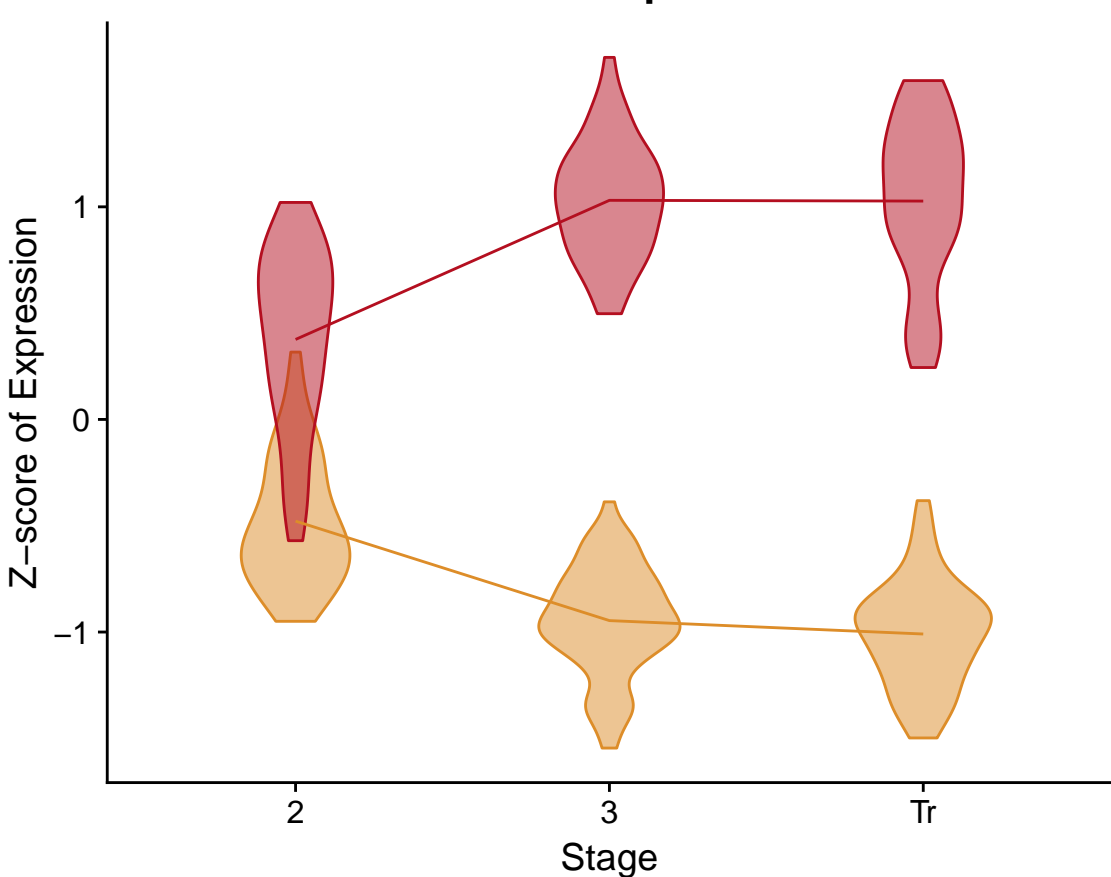
F

GO:0009553, embryo sac development
GO:0008152, metabolic process
GO:0006281, DNA repair
GO:0048609, multicellular organismal r
GO:0009072, aromatic amino acid family
GO:1901606, alpha-amino acid catabolic
GO:0032259, methylation
GO:0055114, oxidation-reduction proces
GO:0071704, organic substance metaboli
GO:0003006, developmental process invo
GO:0034655, nucleobase-containing comp
GO:0042278, purine nucleoside metaboli
GO:0019953, sexual reproduction
GO:0006996, organelle organization
GO:0006325, chromatin organization
GO:0030154, cell differentiation
GO:0048573, photoperiodism, flowering
GO:0006355, regulation of transcriptio
GO:0016192, vesicle-mediated transport
GO:0006310, DNA recombination

Cluster 3 GO Enrichment



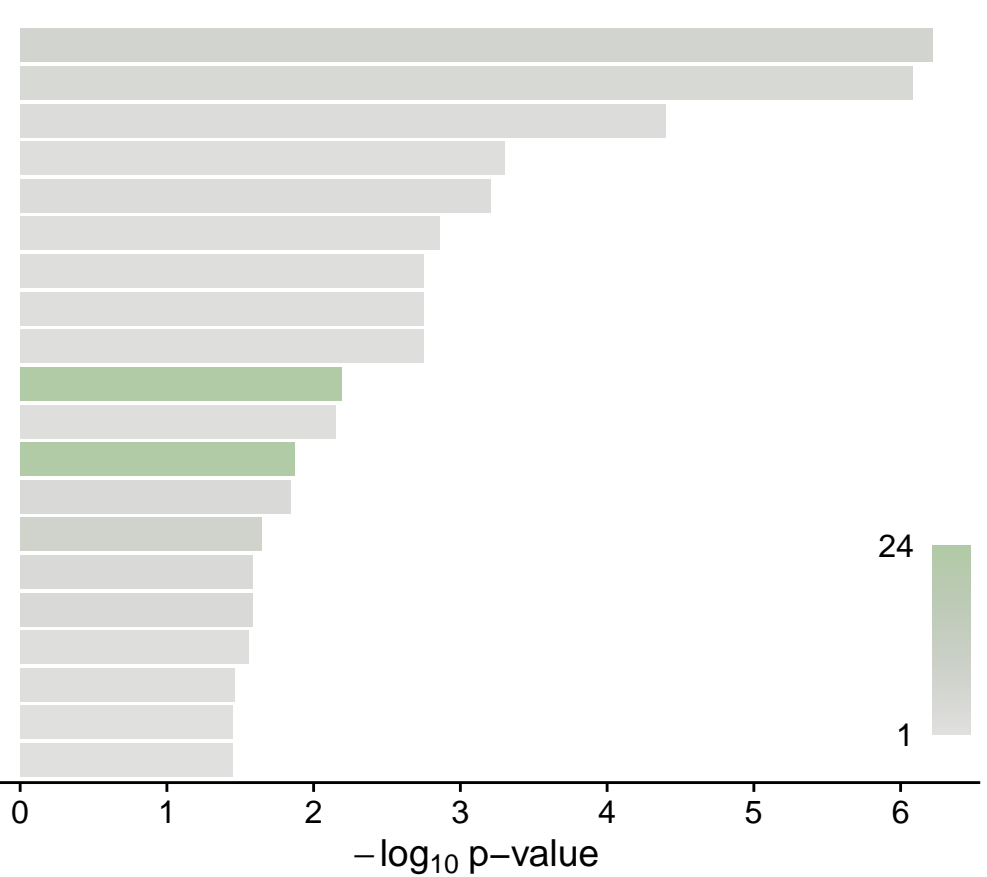
Cluster 4 Expression



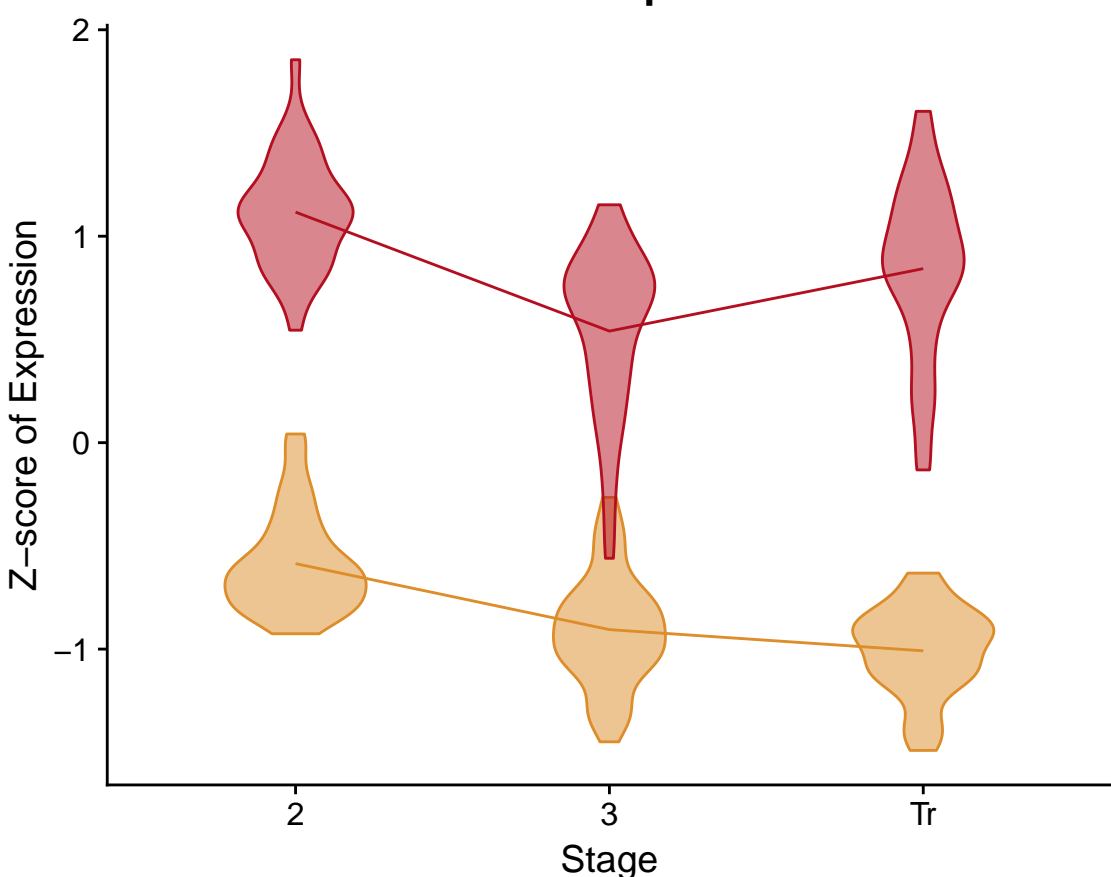
H

GO:0006468, protein phosphorylation
GO:0009069, serine family amino acid m
GO:0006261, DNA-dependent DNA replicat
GO:0000070, mitotic sister chromatid s
GO:0006281, DNA repair
GO:0055082, cellular chemical homeosta
GO:0006094, gluconeogenesis
GO:0006096, glycolytic process
GO:0016999, antibiotic metabolic proce
GO:0008152, metabolic process
GO:0005976, polysaccharide metabolic p
GO:0009987, cellular process
GO:0055114, oxidation-reduction proces
GO:0050896, response to stimulus
GO:0006260, DNA replication
GO:0042592, homeostatic process
GO:1901615, organic hydroxy compound m
GO:0071103, DNA conformation change
GO:0044036, cell wall macromolecule me
GO:0006413, translational initiation

Cluster 4 GO Enrichment



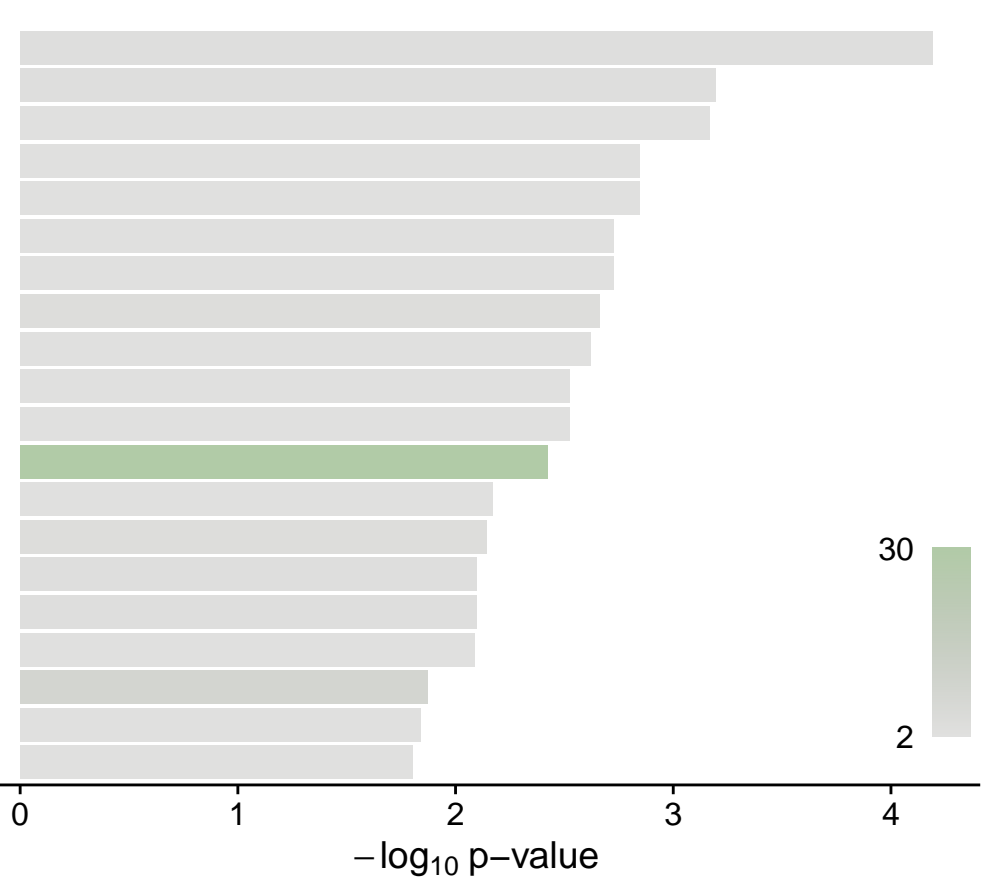
Cluster 5 Expression



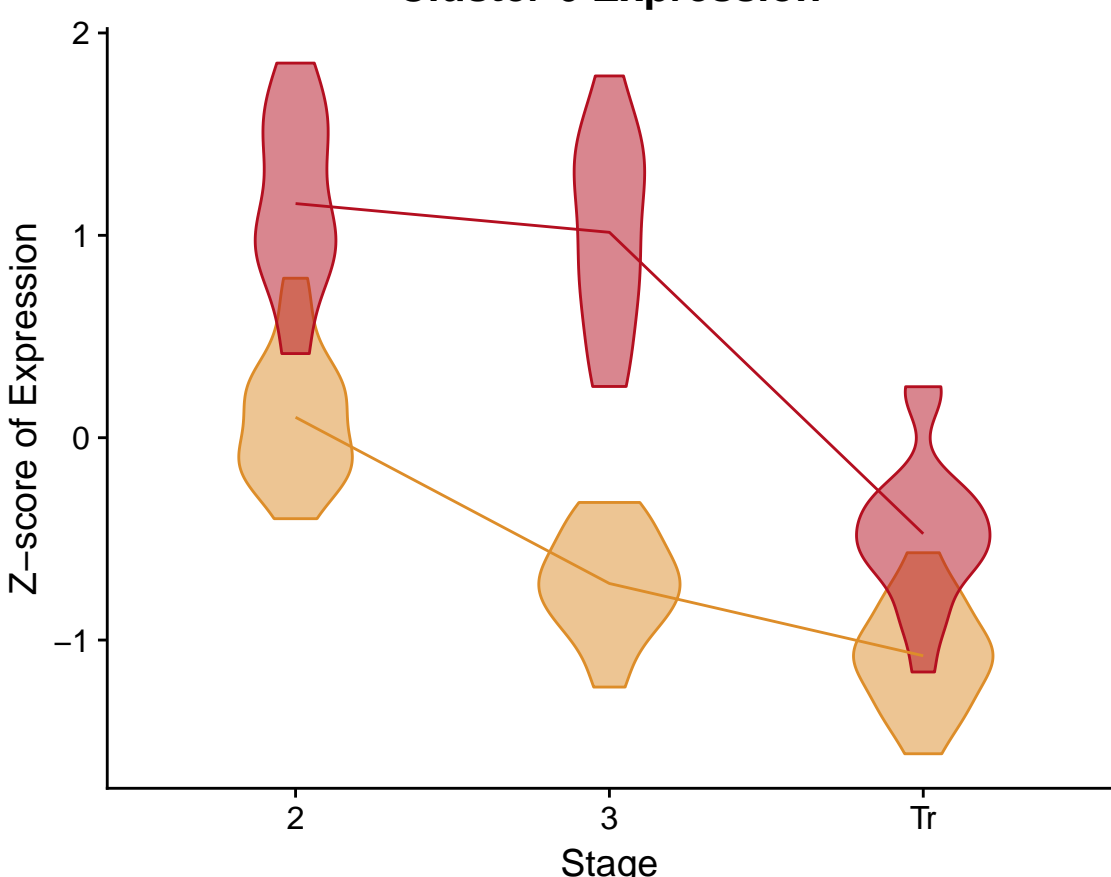
J

GO:0006310, DNA recombination
GO:0051052, regulation of DNA metaboli
GO:0045088, regulation of innate immun
GO:0034968, histone lysine methylation
GO:0033044, regulation of chromosome o
GO:0006612, protein targeting to membr
GO:0071555, cell wall organization
GO:0006396, RNA processing
GO:1902600, proton transmembrane trans
GO:0000280, nuclear division
GO:0005985, sucrose metabolic process
GO:0008152, metabolic process
GO:0006457, protein folding
GO:0006468, protein phosphorylation
GO:0016571, histone methylation
GO:0006974, cellular response to DNA d
GO:0032504, multicellular organism rep
GO:0050789, regulation of biological p
GO:0005982, starch metabolic process
GO:0072594, establishment of protein l

Cluster 5 GO Enrichment



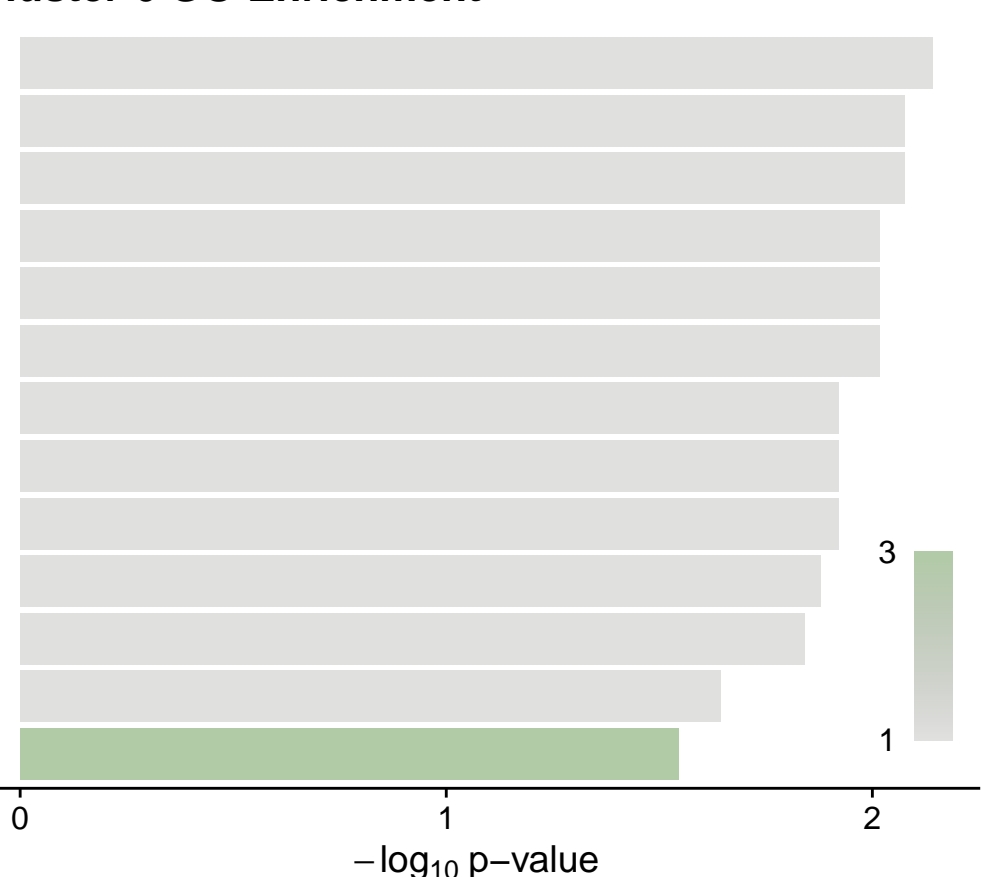
Cluster 6 Expression



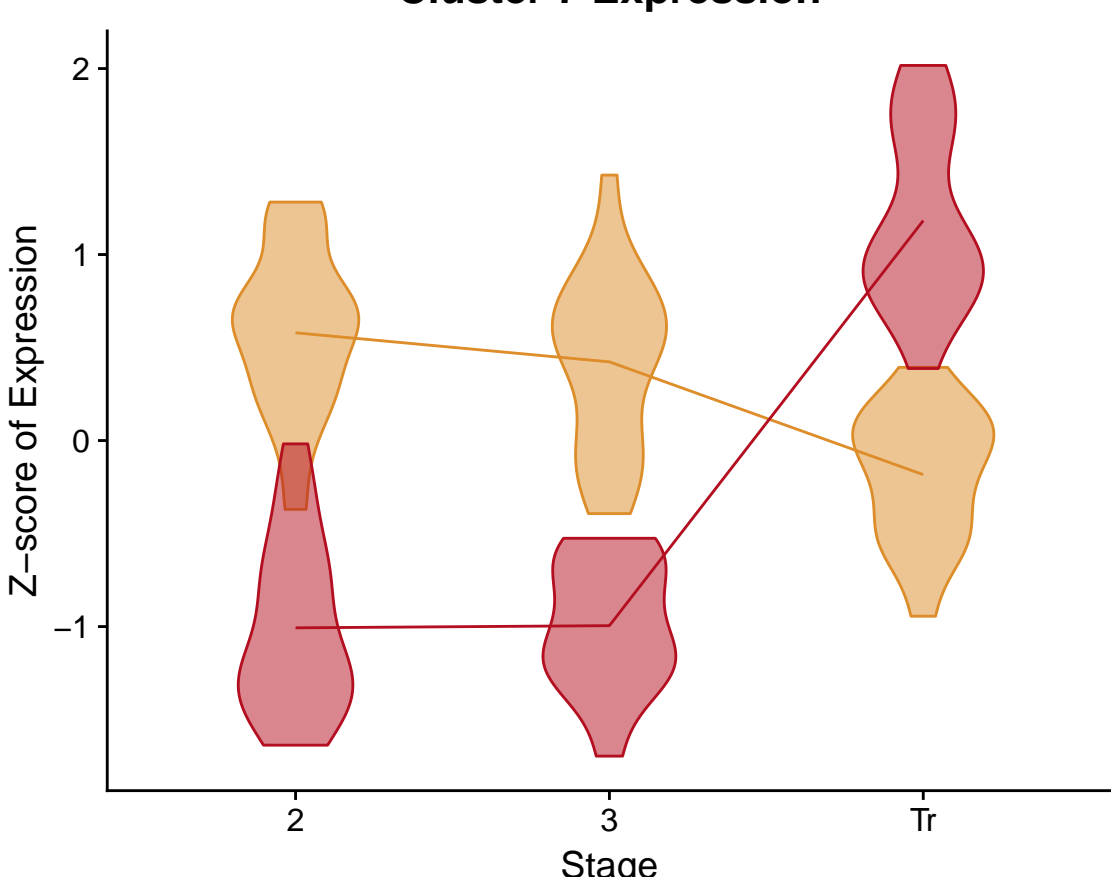
L

GO:0006275, regulation of DNA replicat
GO:0045892, negative regulation of tra
GO:0034968, histone lysine methylation
GO:0016458, gene silencing
GO:0000911, cytokinesis by cell plate
GO:0009909, regulation of flower devel
GO:0006261, DNA-dependent DNA replicat
GO:0000280, nuclear division
GO:0040029, regulation of gene express
GO:0071103, DNA conformation change
GO:0051726, regulation of cell cycle
GO:0009165, nucleotide biosynthetic pr
GO:0006464, cellular protein modificat

Cluster 6 GO Enrichment



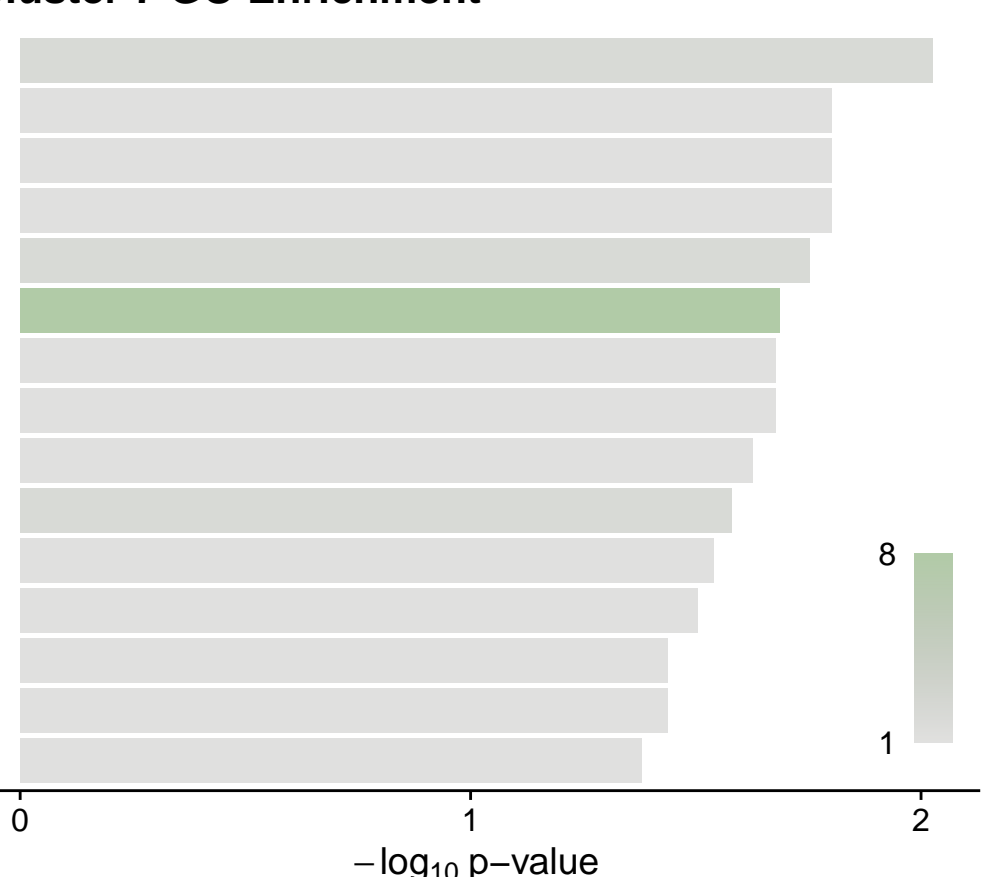
Cluster 7 Expression



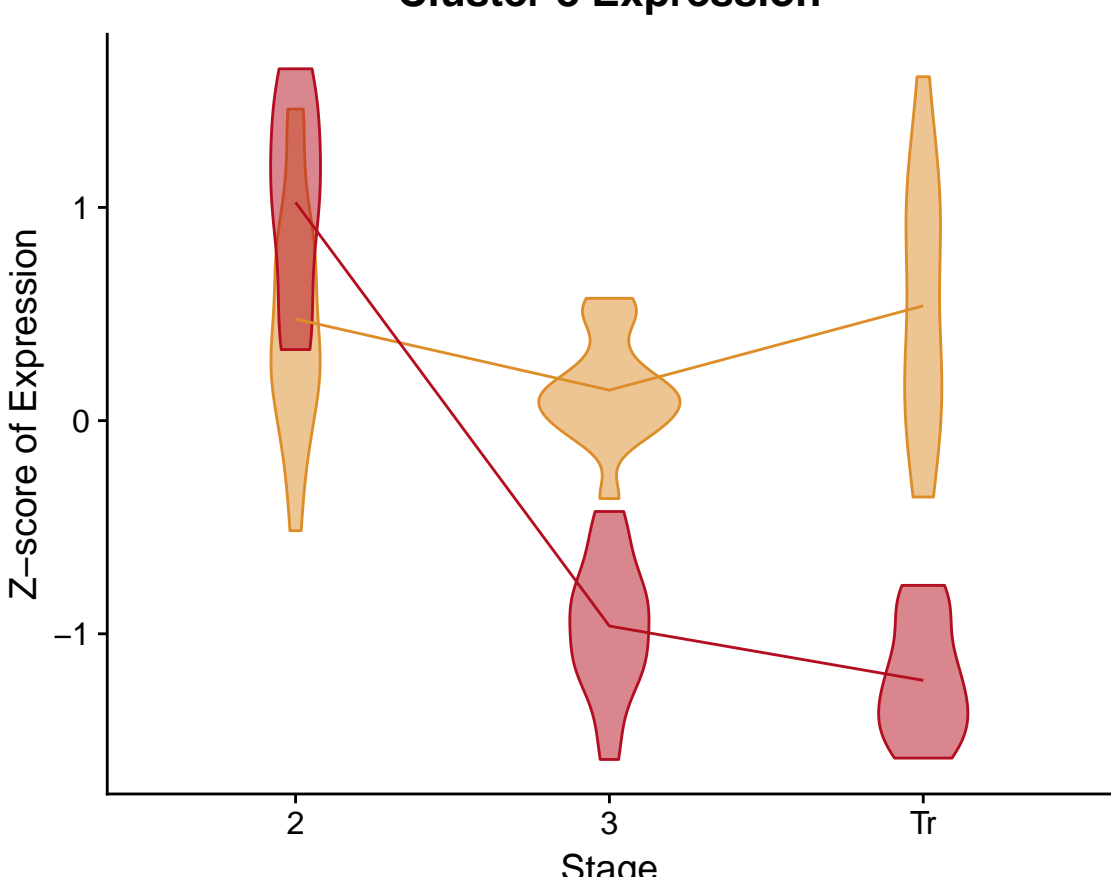
N

GO:0006468, protein phosphorylation
GO:0072593, reactive oxygen species me
GO:0000413, protein peptidyl-prolyl is
GO:0051640, organelle localization
GO:0009058, biosynthetic process
GO:0009987, cellular process
GO:0016556, mRNA modification
GO:0048193, Golgi vesicle transport
GO:0016999, antibiotic metabolic proce
GO:0016192, vesicle-mediated transport
GO:0009651, response to salt stress
GO:0009793, embryo development ending
GO:0016052, carbohydrate catabolic pro
GO:0009658, chloroplast organization
GO:0010027, thylakoid membrane organiz

Cluster 7 GO Enrichment



Cluster 8 Expression



P

GO:0006793, phosphorus metabolic proce
GO:0032501, multicellular organismal p
GO:0044036, cell wall macromolecule me
GO:0042546, cell wall biogenesis
GO:0070085, glycosylation
GO:0030258, lipid modification
GO:0007017, microtubule-based process
GO:0016192, vesicle-mediated transport
GO:0051704, multi-organism process

Cluster 8 GO Enrichment

