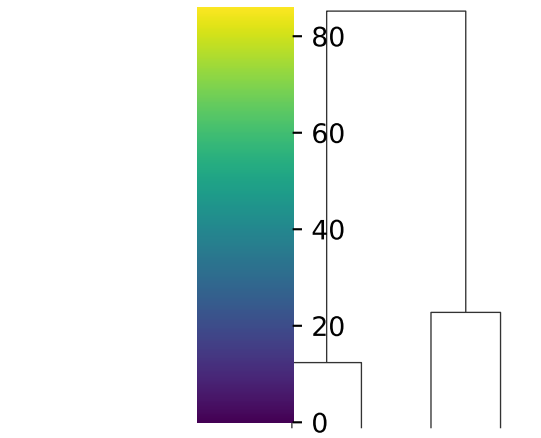
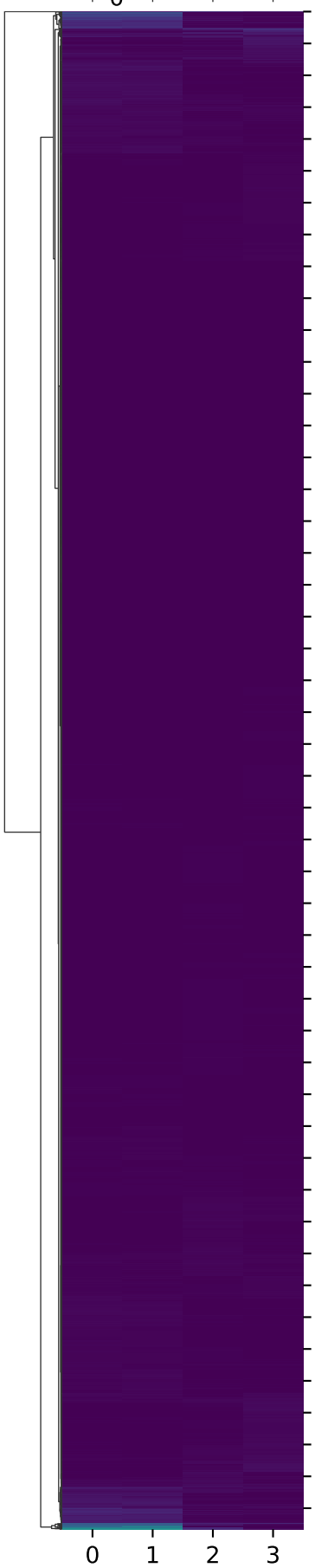
Pathway Enrichment Heatmap





RNA binding (GO:0003723)
regulation of anatomical structure morphogenesis (GO:0022603)
mitochondrial fragmentation involved in apoptotic process (GO:0043653)
positive regulation of cell-substrate adhesion (GO:0010811)
regulation of pinocytosis (GO:0048548)
axon development (GO:0061564)
nuclear body organization (GO:0030575)
skeletal system development (GO:0001501)
cellular response to steroid hormone stimulus (GO:0071383)
chemorepellent activity (GO:0045499)
regulation of striated muscle cell differentiation (GO:0051153)
positive regulation of T cell apoptotic process (GO:0070234)
glycine transmembrane transporter activity (GO:0015187)
regulation of glycogen metabolic process (GO:0070873)
neural crest cell development (GO:0014032)
5-phosphoribose 1-diphosphate metabolic process (GO:0046391)
neuroepithelial cell differentiation (GO:0060563)
neutrophil migration (GO:1990266)
IgG binding (GO:0019864)
entry of bacterium into host cell (GO:0035635)
endonuclease activity (GO:0004519)
peptidyl-lysine monomethylation (GO:0018026)
response to prostaglandin (GO:0034694)
regulation of double-strand break repair via homologous recombination (GO:0010569)
polynucleotide adenylyltransferase activity (GO:0004652)
integrin activation (GO:0033622)
negative regulation of excitatory postsynaptic potential (GO:0090394)
patched binding (GO:0005113)
positive regulation of vascular associated smooth muscle cell proliferation (GO:1904707)
receptor antagonist activity (GO:0048019)
histone H2A monoubiquitination (GO:0035518)
anterograde axonal protein transport (GO:0099641)
positive regulation of membrane invagination (GO:1905155)
vascular associated smooth muscle cell differentiation (GO:0035886)
mRNA 5'-splice site recognition (GO:0000395)
organonitrogen compound biosynthetic process (GO:1901566)
negative regulation of intracellular protein transport (GO:0090317)
positive regulation of autophagy of mitochondrion in response to mitochondrial depolarization (GO:1904925)
vasculature development (GO:0001944)
plasma membrane organization (GO:0007009)
negative regulation of epithelial cell migration (GO:0010633)
barbed-end actin filament capping (GO:0051016)
negative regulation of T cell receptor signaling pathway (GO:0050860)
nucleotide-excision repair, DNA incision, 3'-to lesion (GO:0006295)
positive regulation of chemokine (C-X-C motif) ligand 2 production (GO:2000343)
insulin receptor signaling pathway (GO:0008286)
Protein digestion and absorption
RNA transport (GO:0050658)

Term