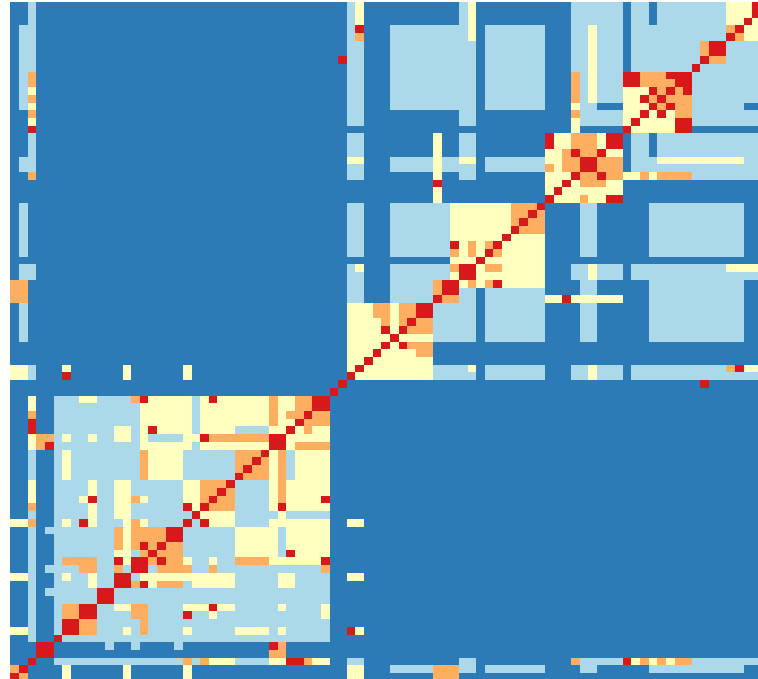
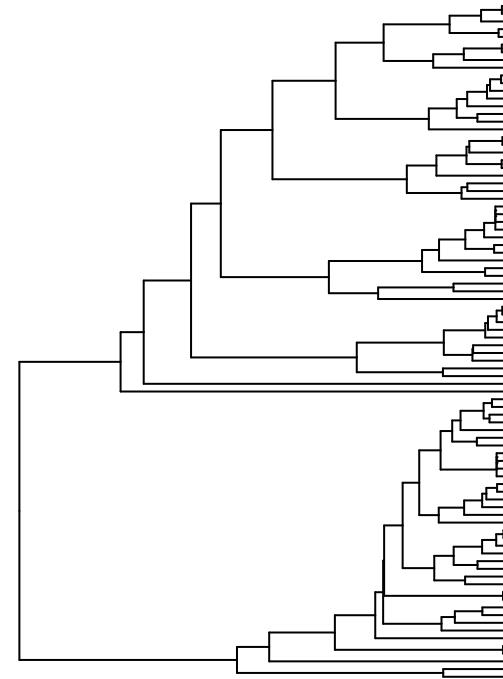
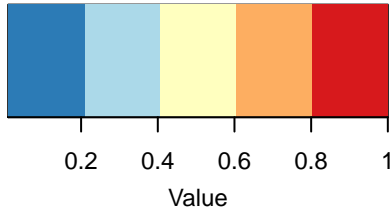


## Color Key



GO:1904159: axonemal central apparatus assembly  
GO:0009395: mRNA 5'-splice site recognition  
GO:0071555: cell wall organization  
GO:0031532: actin cytoskeleton reorganization  
GO:0034058: endosomal vesicle fusion  
GO:0057374: sensory neuron axon guidance  
GO:0072486: photoreceptor cell axon guidance  
GO:0030317: flagellated sperm motility  
GO:0040316: embryonic cleavage  
GO:0006659: phosphatidylserine biosynthetic process  
GO:0006247: glycolytic biosynthetic process  
GO:0009093: branched-chain amino acid catabolic process  
GO:0006482: protein demethylation  
GO:0006766: vitamin metabolic process  
GO:0015344: protein grand/germination  
GO:0006002: fructose 6-phosphate metabolic process  
GO:0006008: biosynthetic process  
GO:0071383: cellular response to basal hormone stimulus  
GO:0071380: cellular response to prostaglandin E stimulus  
GO:0001602: cellular response to virus  
GO:0031669: cellular response to nutrient levels  
GO:0031670: cellular response to nutrient  
GO:0007720: pyrimidine dimer repair by nucleotide-excision repair  
GO:0036944: response to muscle stretch  
GO:0014850: response to muscle activity  
GO:0026206: response to retinoic acid  
GO:0060068: vagina development  
GO:0007517: muscle organ development  
GO:0060216: definitive hemopoiesis  
GO:0060438: trachea development  
GO:0021553: olfactory nerve development  
GO:0003223: ventricular compact myocardium morphogenesis  
GO:0081156: pulmonary artery morphogenesis  
GO:0021591: ventricular septum development  
GO:0001886: endothelial cell morphogenesis  
GO:0020064: epithelial cell development  
GO:0007569: branching involved in blood vessel morphogenesis  
GO:0001139: secondary heart field specification  
GO:0007632: visual behavior  
GO:0017175: D-aspartate import across plasma membrane  
GO:0015813: L-glutamate transmembrane transport  
GO:1804407: fatty acid import across plasma membrane  
GO:0030267: intracellular cholesterol transport  
GO:0006636: neurotransmitter transport  
GO:0006622: protein targeting to lysosome  
GO:0088719: sodium ion import across plasma membrane  
GO:0006957: pinocytosis  
GO:0007016: cytoskeletal anchoring at plasma membrane  
GO:0048878: hormone secretion  
GO:0081642: chemotaxis of axon  
GO:0048111: rhythmic process  
GO:0051572: negative regulation of histone H3-K9 methylation  
GO:1804428: negative regulation of tubulin deacetylation  
GO:0048022: negative regulation of melanin biosynthetic process  
GO:0010426: negative regulation of gene expression  
GO:0042534: regulation of tumor necrosis factor biosynthetic process  
GO:0000185: activation of MAPK8 activity  
GO:0010861: negative regulation of endopeptidase activity  
GO:0070885: negative regulation of calcineurin-NFAT signaling cascade  
GO:0030204: negative regulation of Rho protein signal transduction  
GO:0053331: negative regulation of hippocampal signaling  
GO:0043518: negative regulation of DNA damage response, signal transduction by p53 class mediator  
GO:2000768: positive regulation of peptidyl-lysine acetylation  
GO:0032326: positive regulation of protein sumoylation  
GO:0051574: positive regulation of histone H3-K9 methylation  
GO:0043261: positive regulation of glycolytic process  
GO:0016236: positive regulation of macroautophagy  
GO:0032204: regulation of telomere maintenance  
GO:0048343: negative regulation of striated muscle tissue development  
GO:0048642: negative regulation of skeletal muscle tissue development  
GO:0045071: negative regulation of myoblast cell growth  
GO:0030486: negative regulation of type I interferon production  
GO:0048843: negative regulation of axon extension involved in axon guidance  
GO:0020294: regulation of cell morphogenesis  
GO:0010460: positive regulation of heart rate  
GO:0070447: positive regulation of oligodendrocyte progenitor proliferation  
GO:0016055: Wnt signaling pathway  
GO:0072723: Wnt signaling pathway, calcium modulating pathway  
GO:0045807: positive regulation of endocytosis  
GO:0036542: regulation of SNARE complex assembly  
GO:1903827: regulation of cellular protein localization  
GO:0050796: regulation of insulin secretion  
GO:0042752: regulation of circadian rhythm  
GO:0043362: negative regulation of DNA binding  
GO:1804743: negative regulation of telomeric DNA binding  
GO:0072344: reduce of stalled ribosome  
GO:0097008: energy homeostasis  
GO:0043114: regulation of vascular permeability