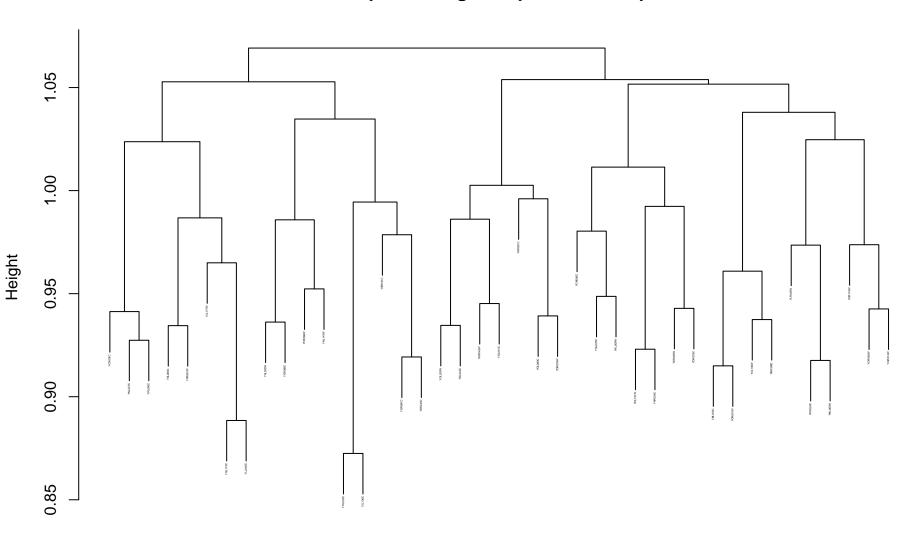
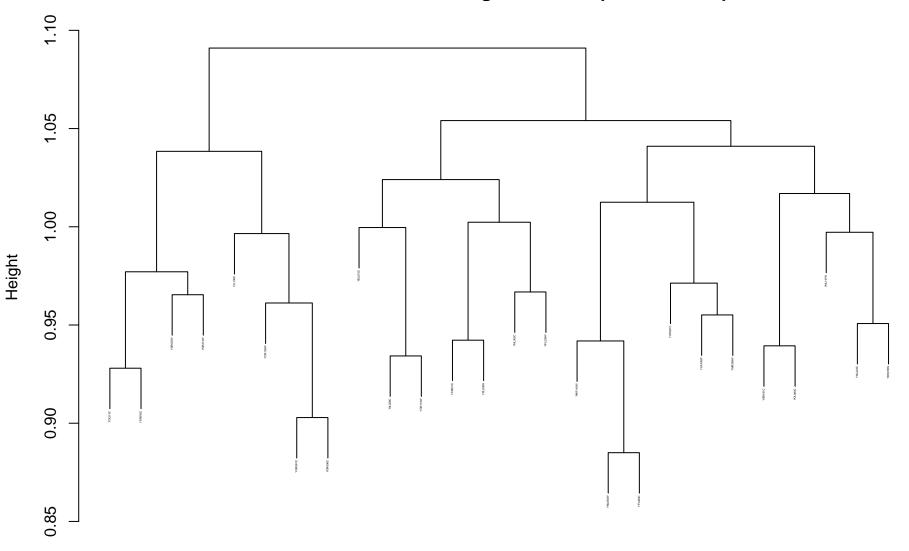
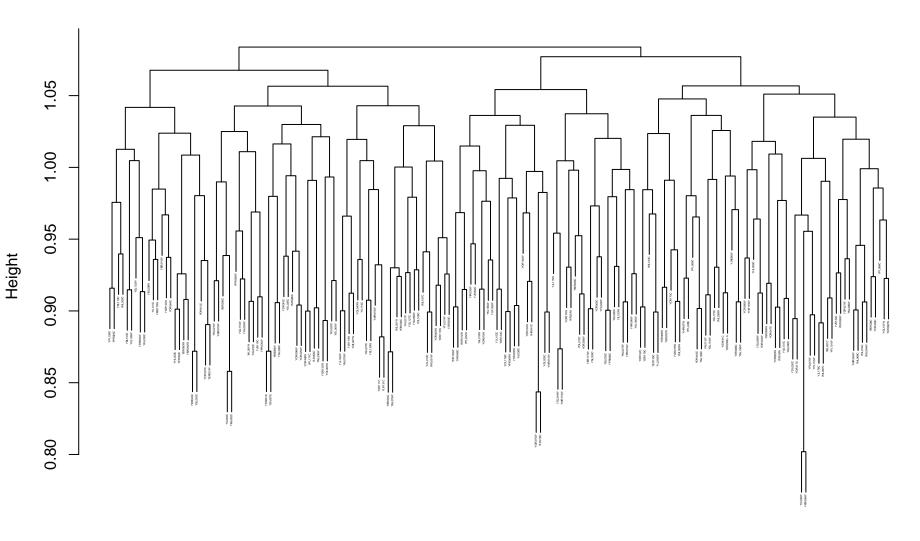
rRNA processing_GO_pearson_complete



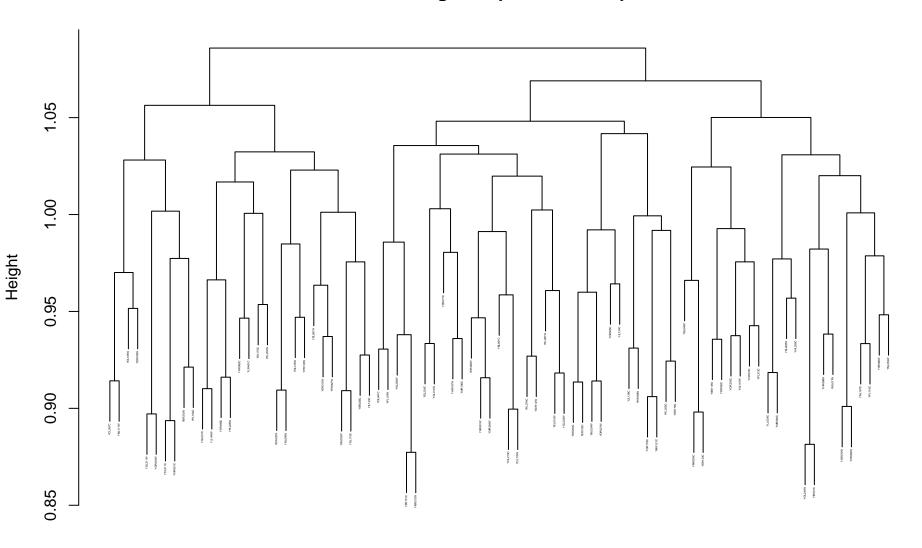
ribosomal small subunit biogenesis_GO_pearson_complete



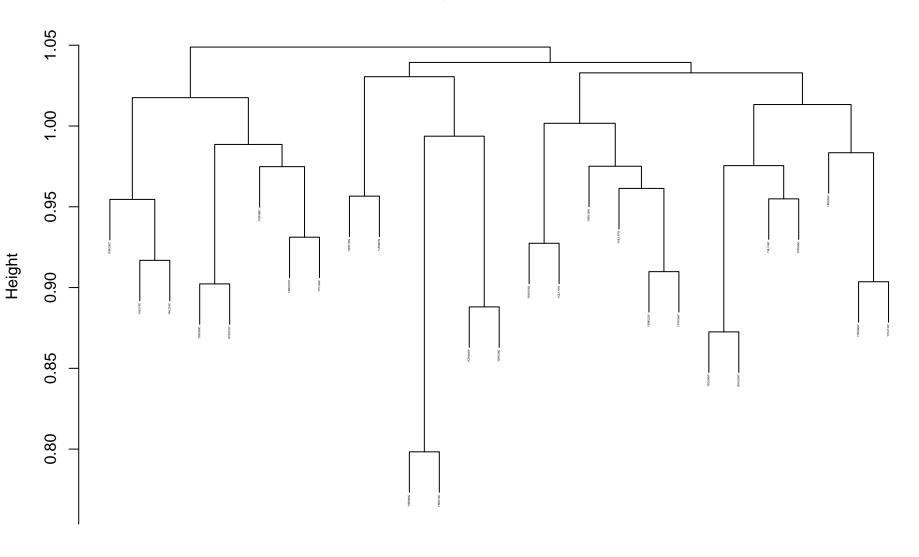
transcription from RNA polymerase II promoter_GO_pearson_complete



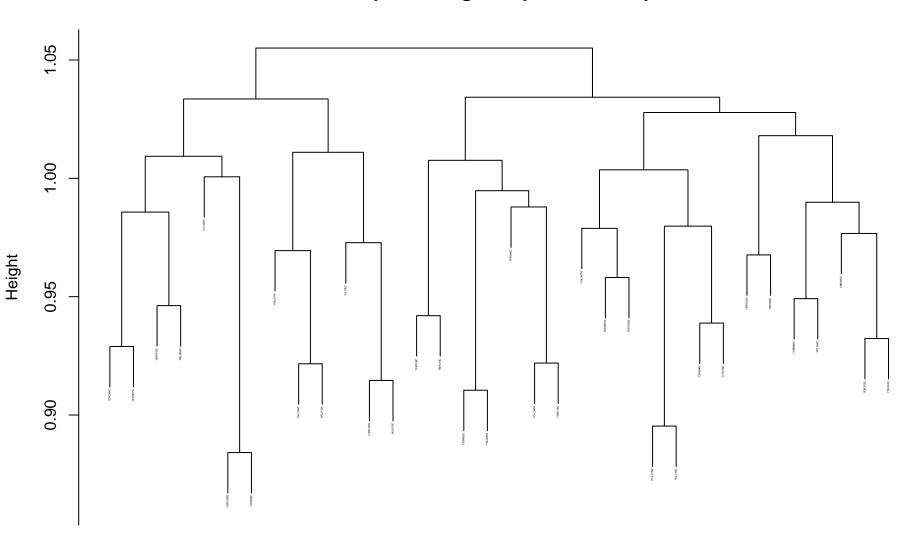
RNA binding_GO_pearson_complete



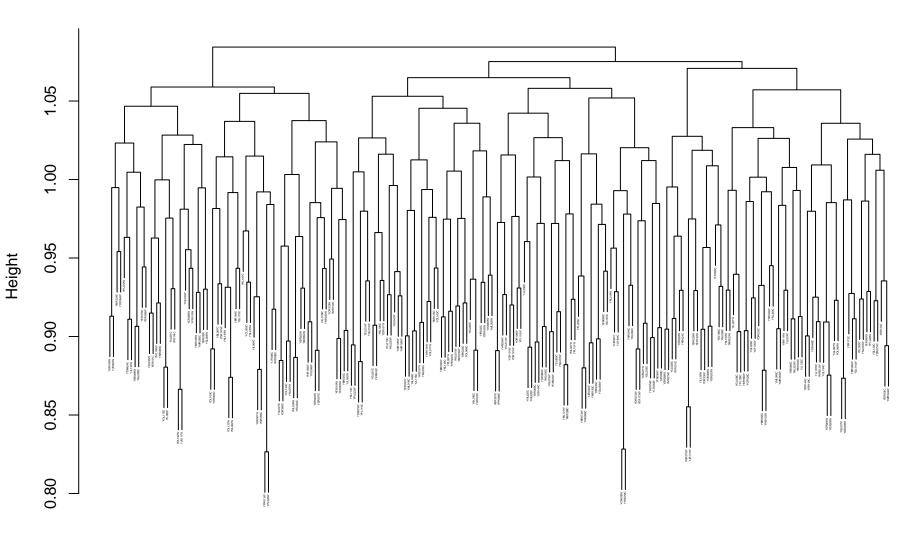
RNA splicing_GO_pearson_complete



mRNA processing_GO_pearson_complete

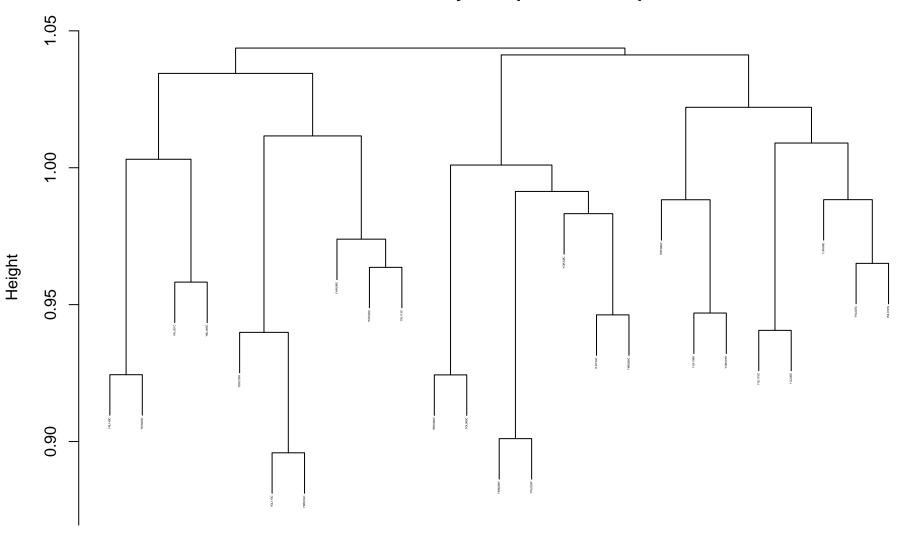


hydrolase activity_GO_pearson_complete



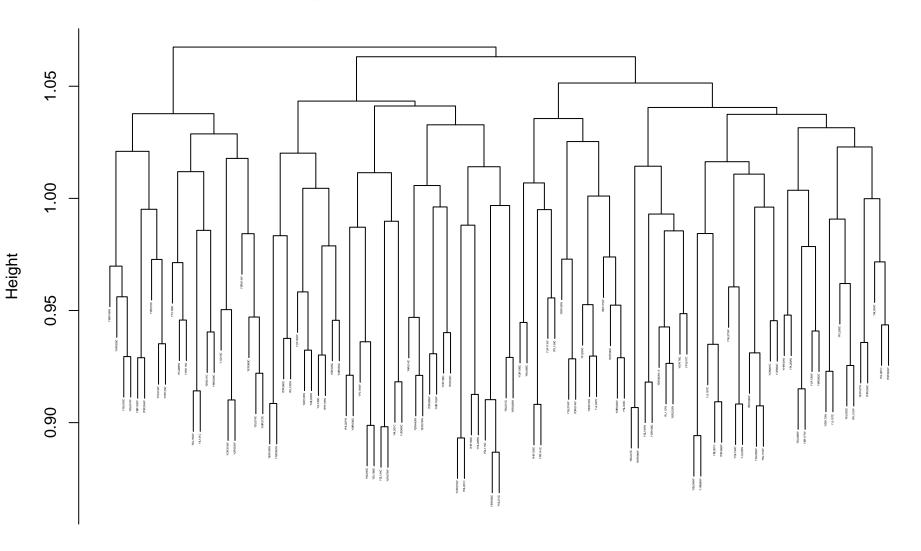
dissim hclust (*, "complete")

nuclease activity_GO_pearson_complete

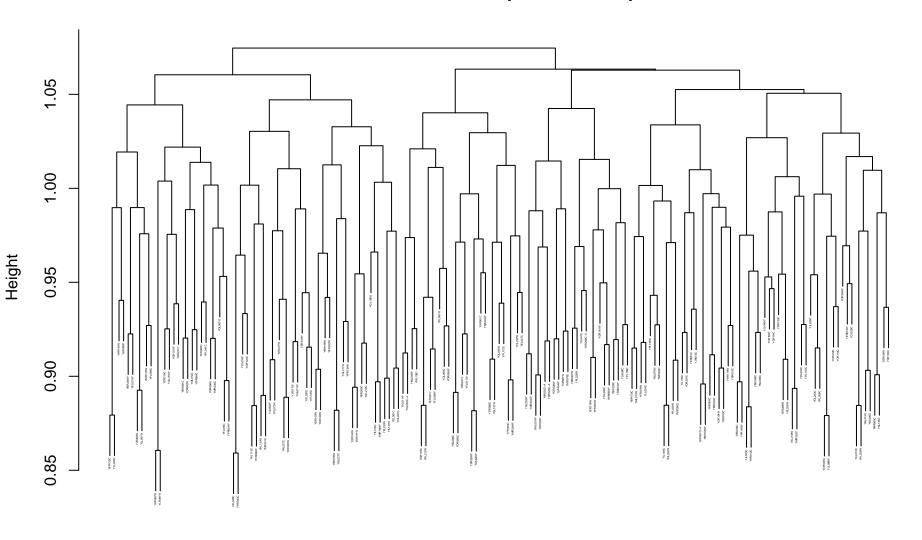


dissim hclust (*, "complete")

regulation of cell cycle_GO_pearson_complete

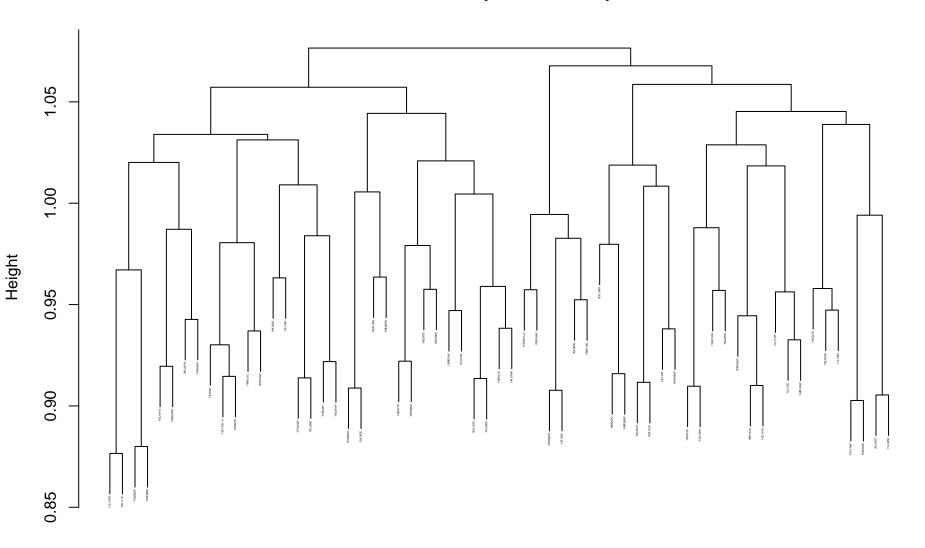


mitochondrion_GO_pearson_complete

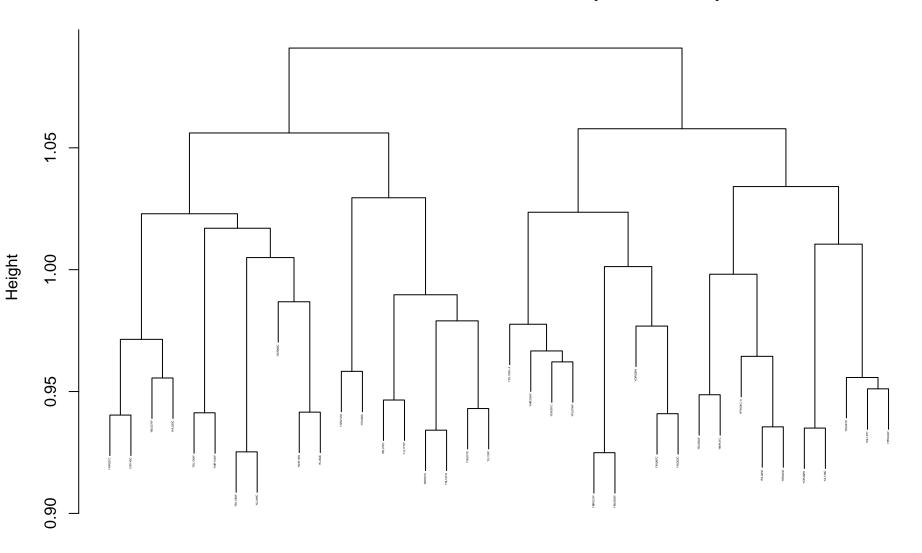


dissim hclust (*, "complete")

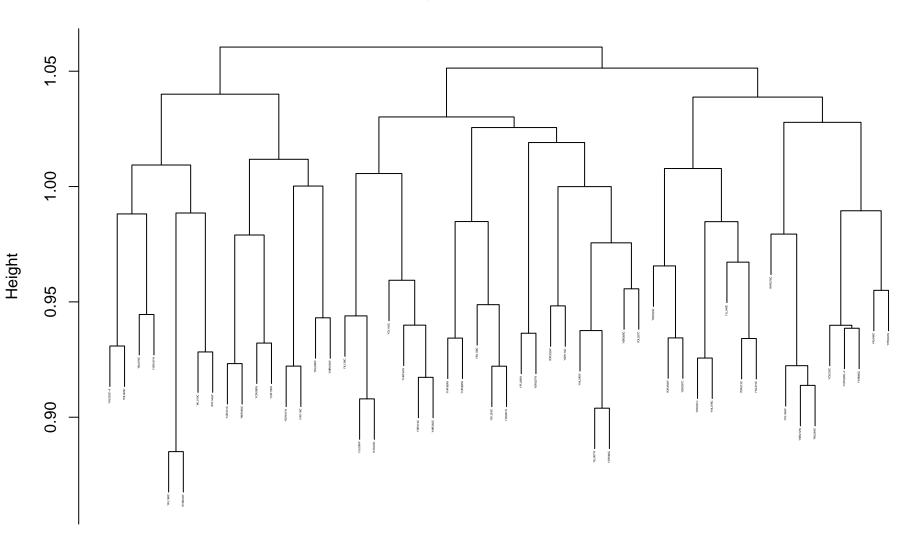
ribosome_GO_pearson_complete



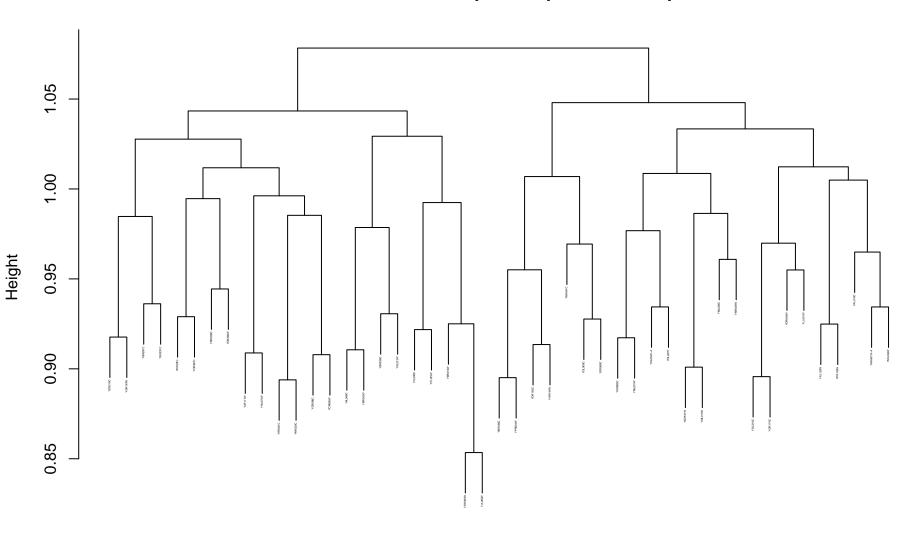
structural constituent of ribosome_GO_pearson_complete



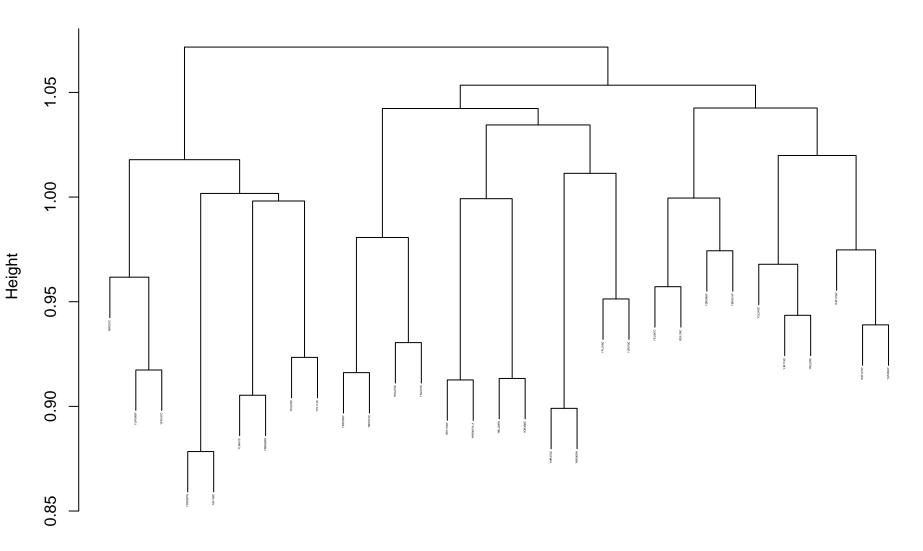
$mit ochondrion\ or ganization _GO_pearson_complete$



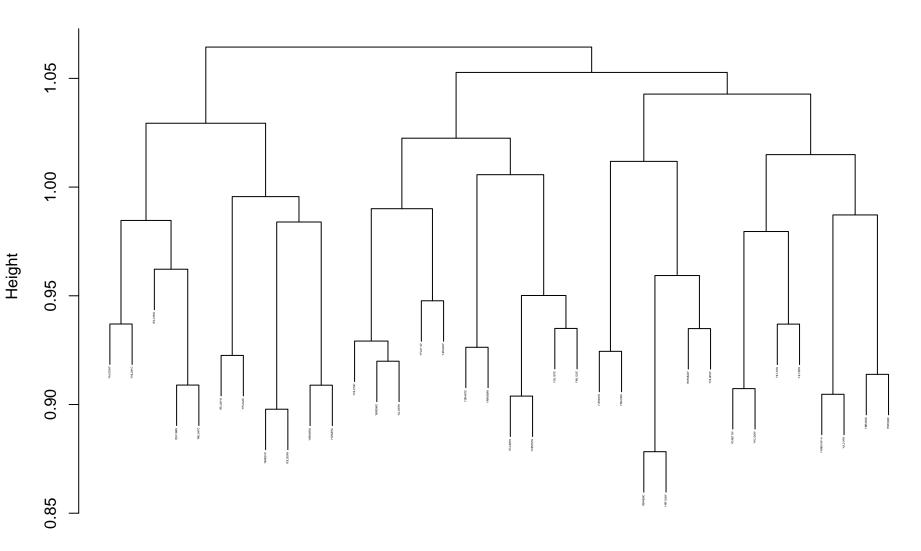
mitochondrial envelope_GO_pearson_complete



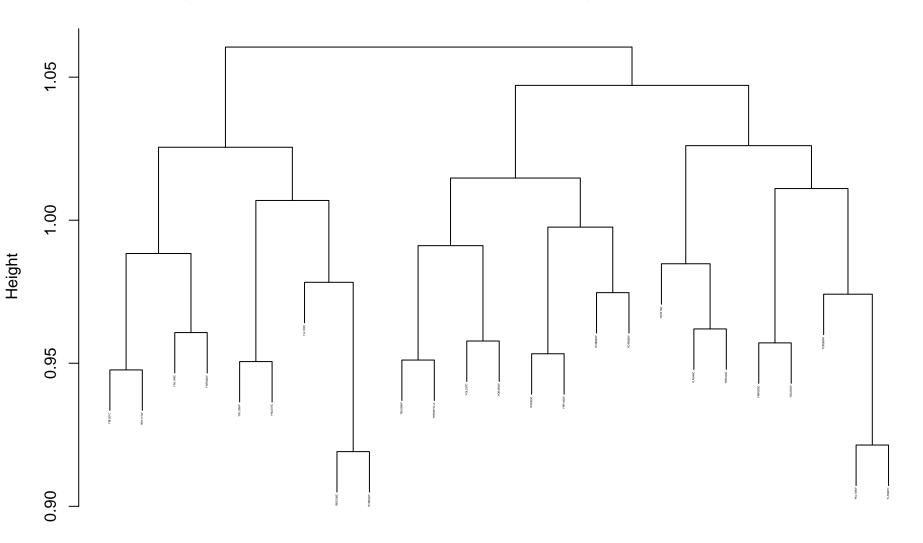
oxidoreductase activity_GO_pearson_complete



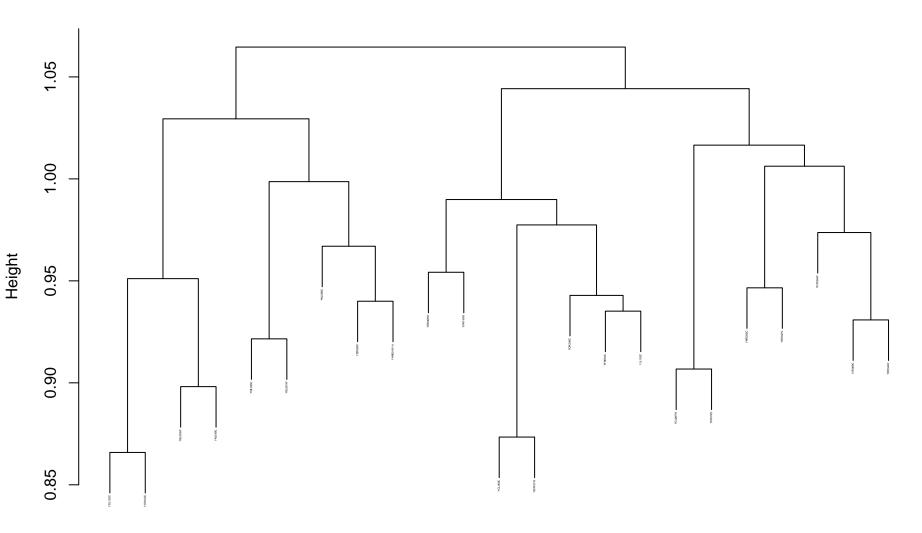
transmembrane transporter activity_GO_pearson_complete



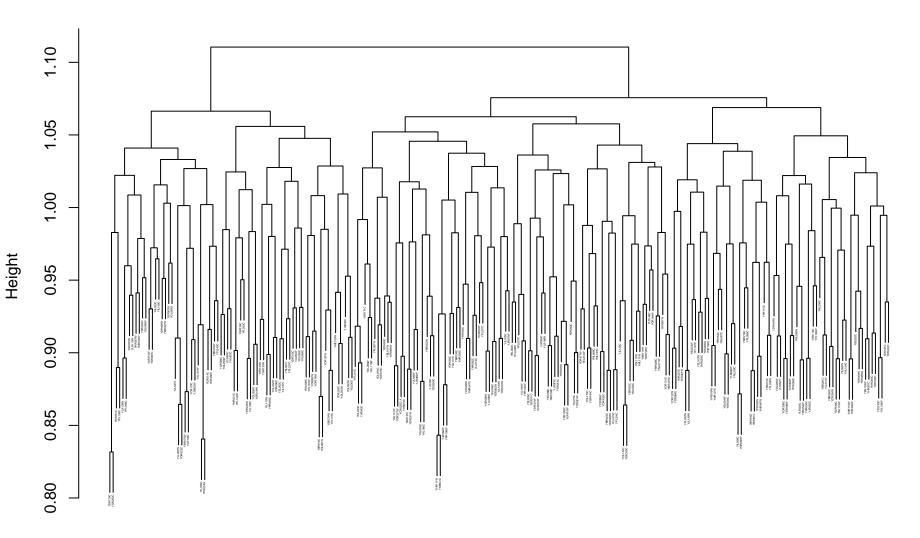
generation of precursor metabolites and energy_GO_pearson_complete



nucleobase-containing small molecule metabolic process_GO_pearson_complete

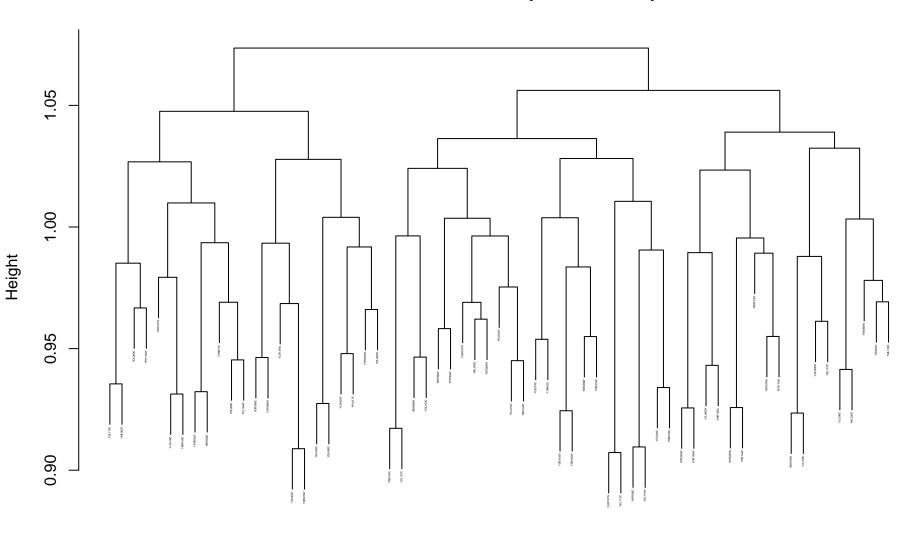


transferase activity_GO_pearson_complete

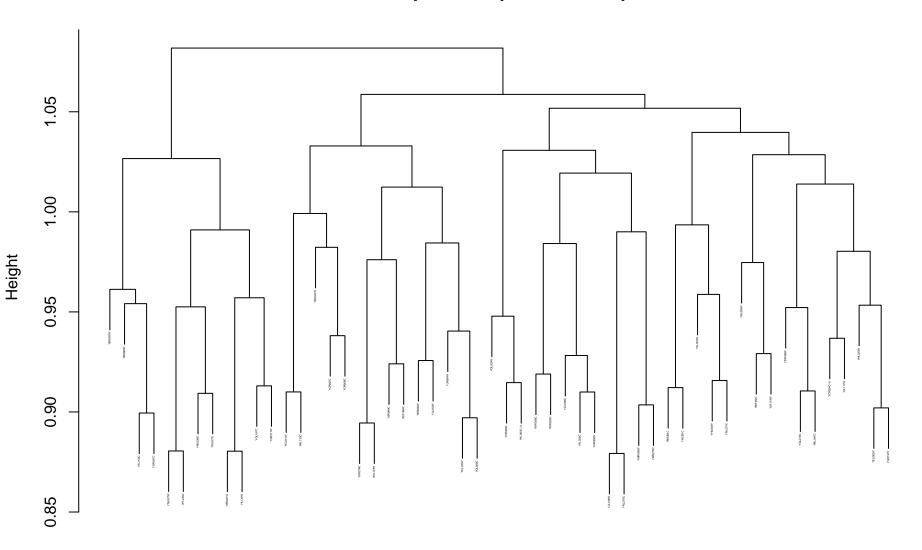


dissim hclust (*, "complete")

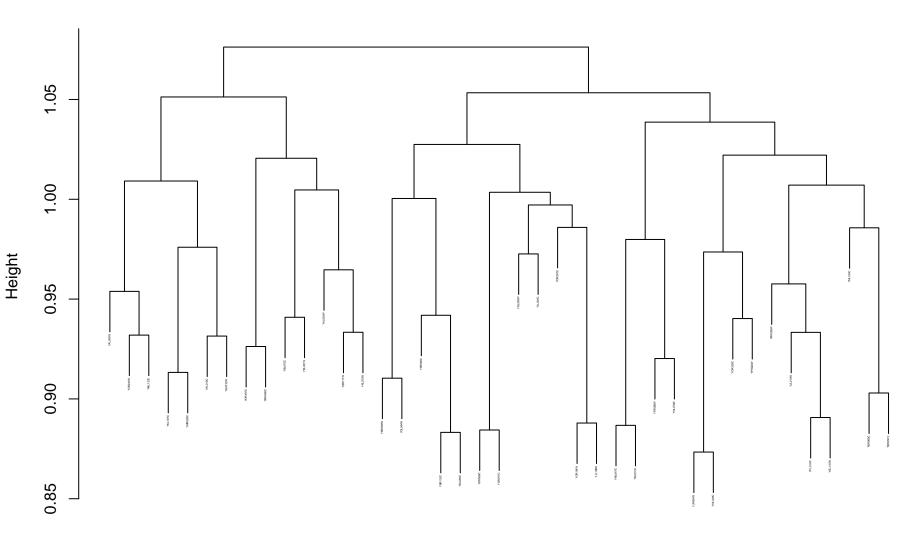
DNA recombination_GO_pearson_complete



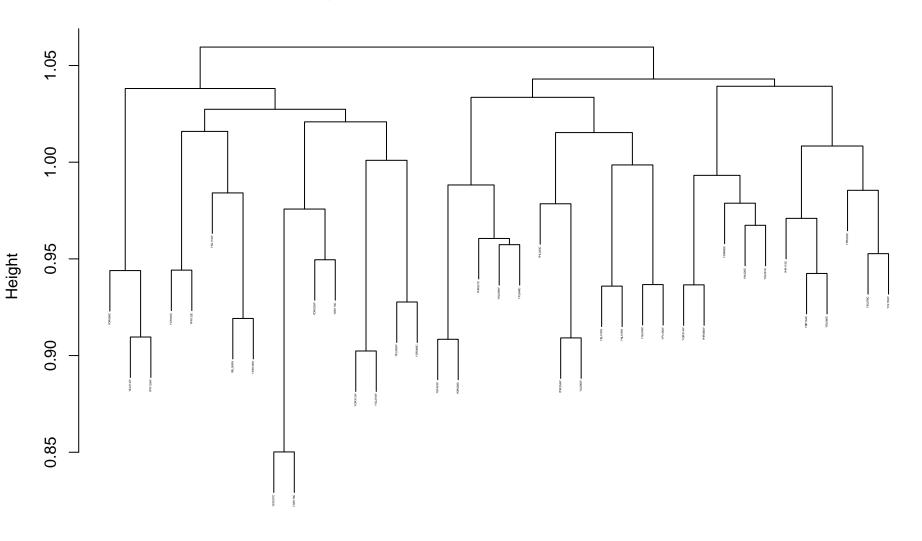
ion transport_GO_pearson_complete



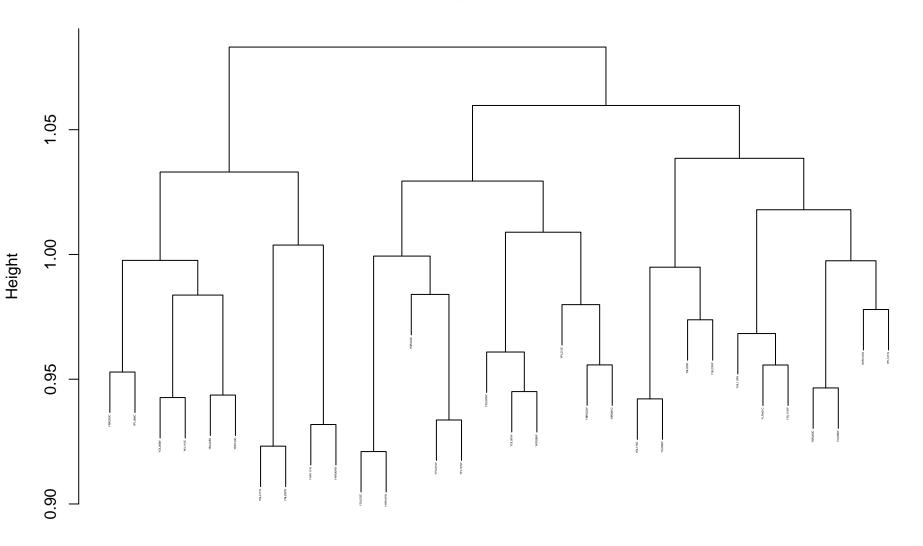
transmembrane transport_GO_pearson_complete



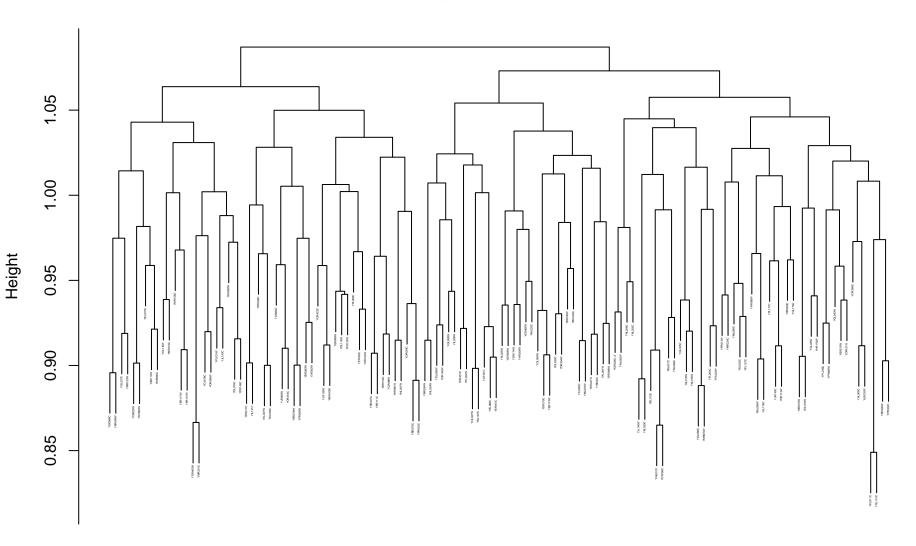
organelle assembly_GO_pearson_complete



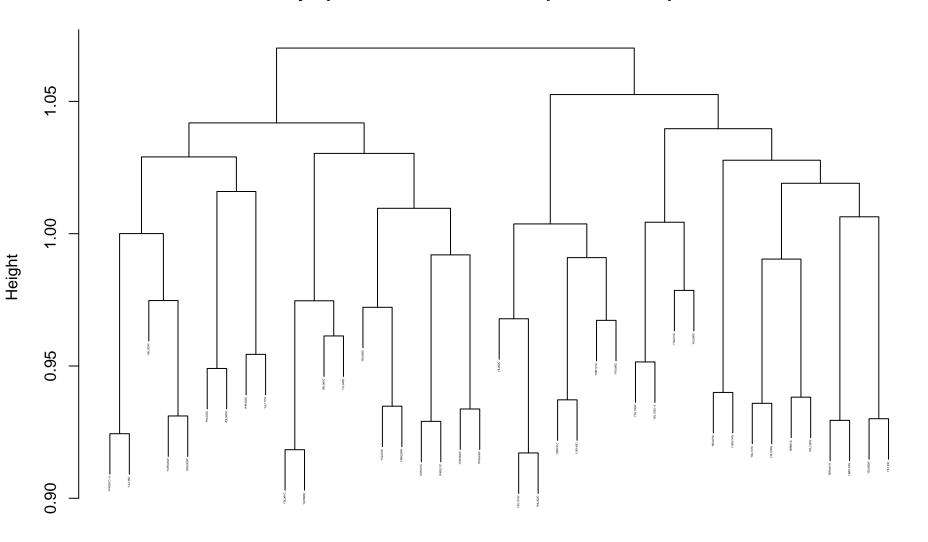
tRNA processing_GO_pearson_complete



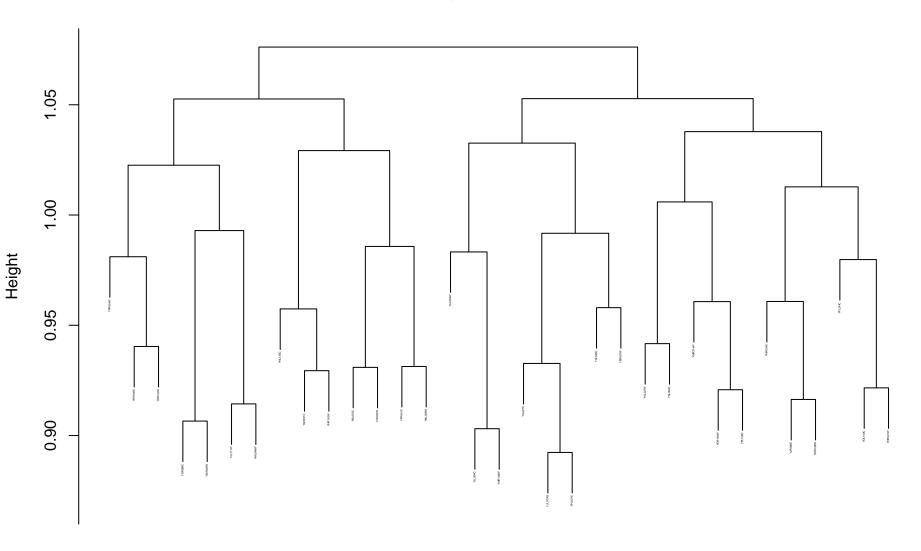
DNA binding_GO_pearson_complete



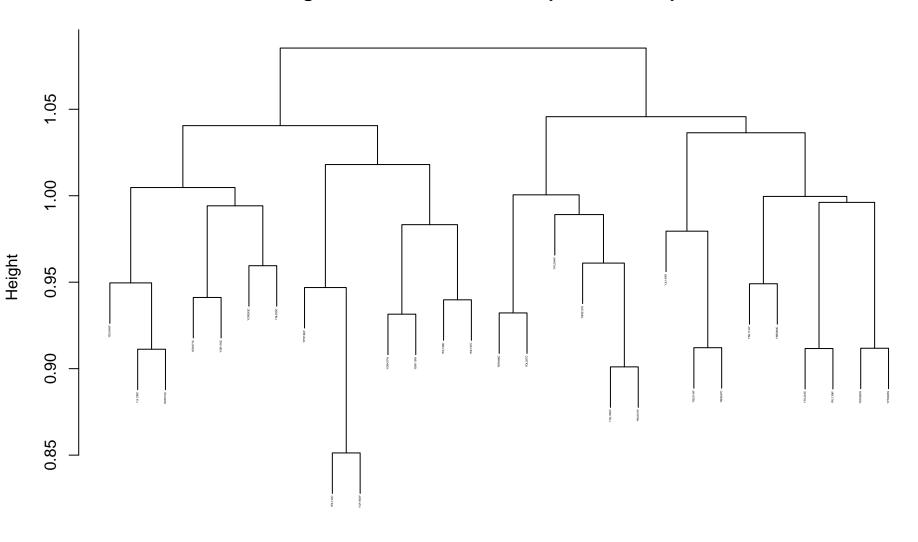
cytoplasmic translation_GO_pearson_complete



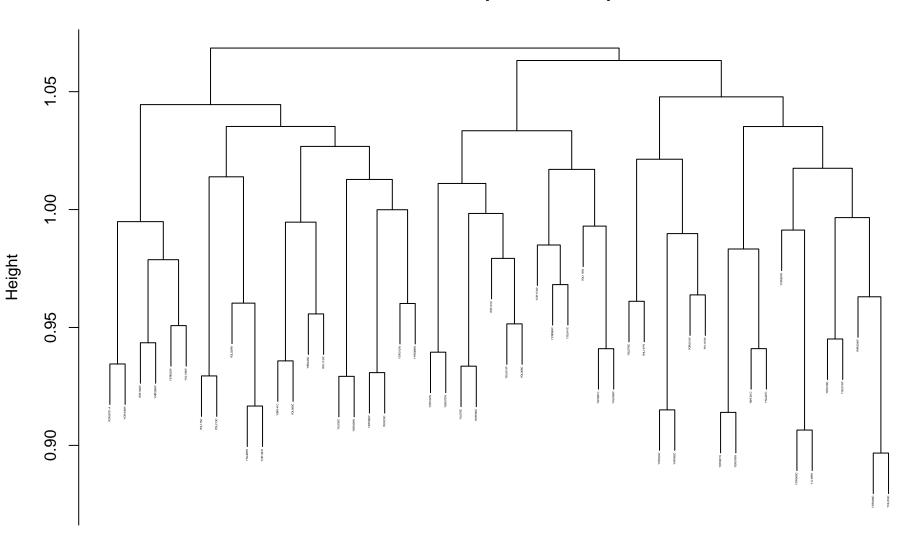
protein folding_GO_pearson_complete



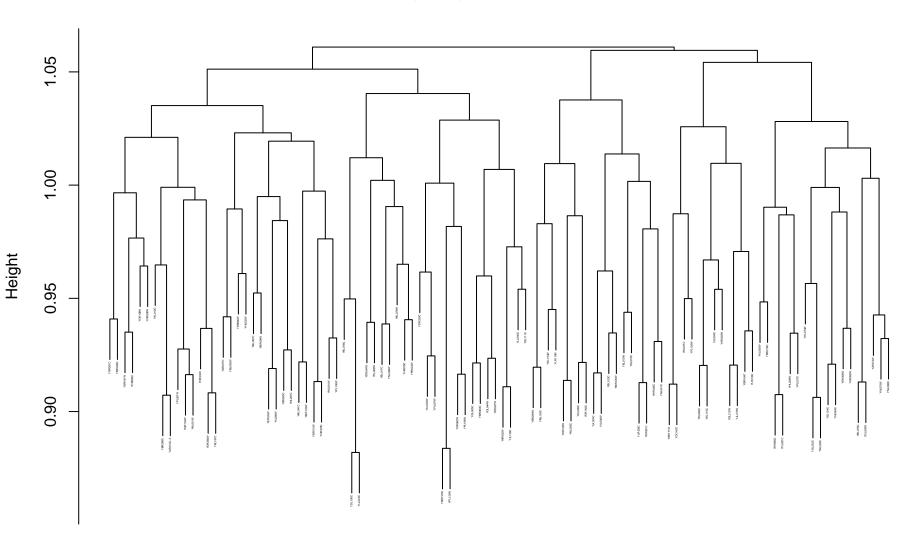
regulation of translation_GO_pearson_complete



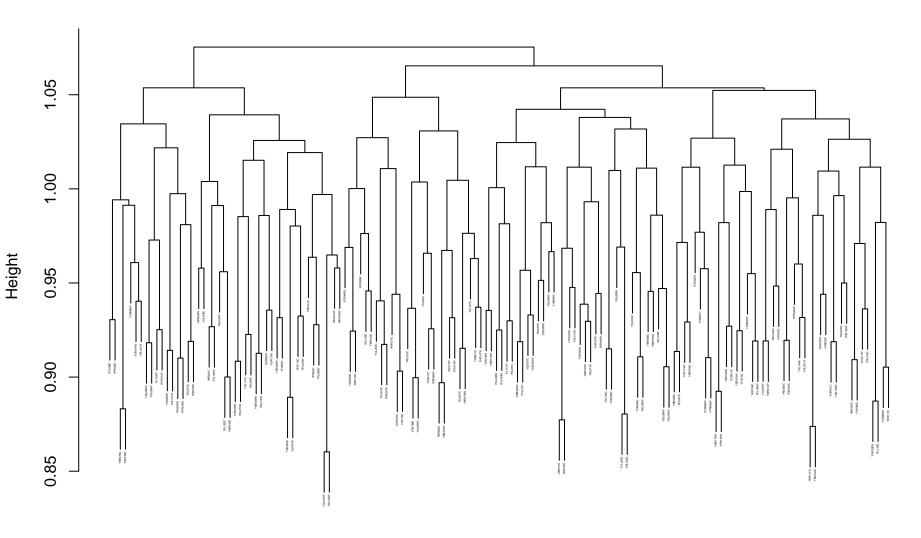
nucleolus_GO_pearson_complete



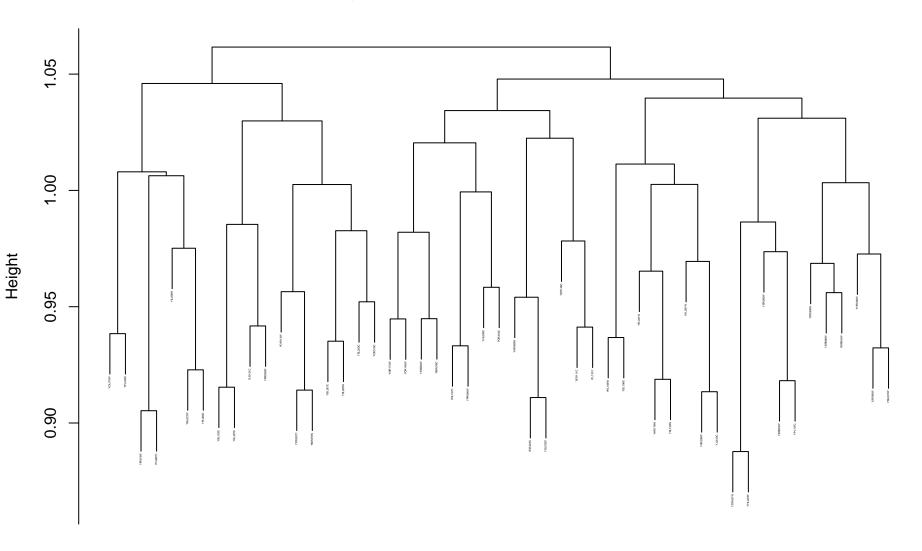
$protein\ targeting_GO_pearson_complete$



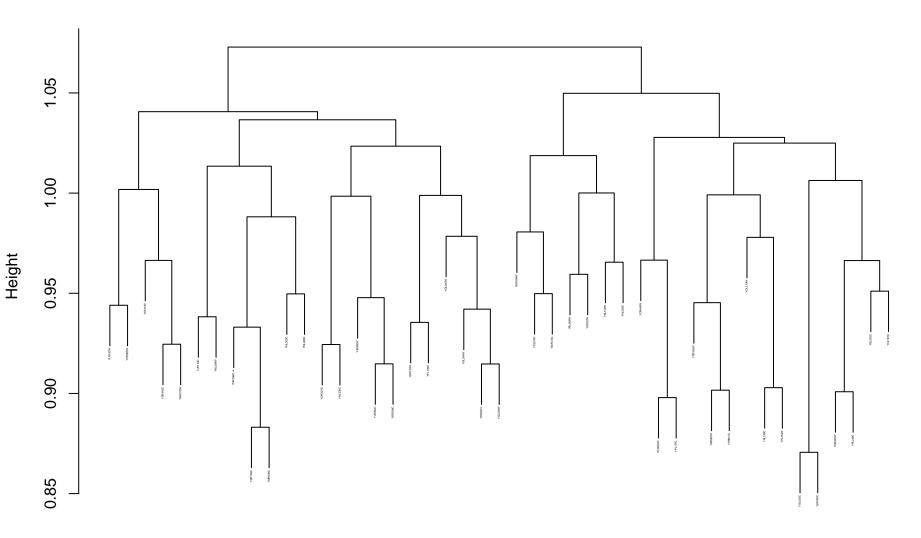
chromosome_GO_pearson_complete



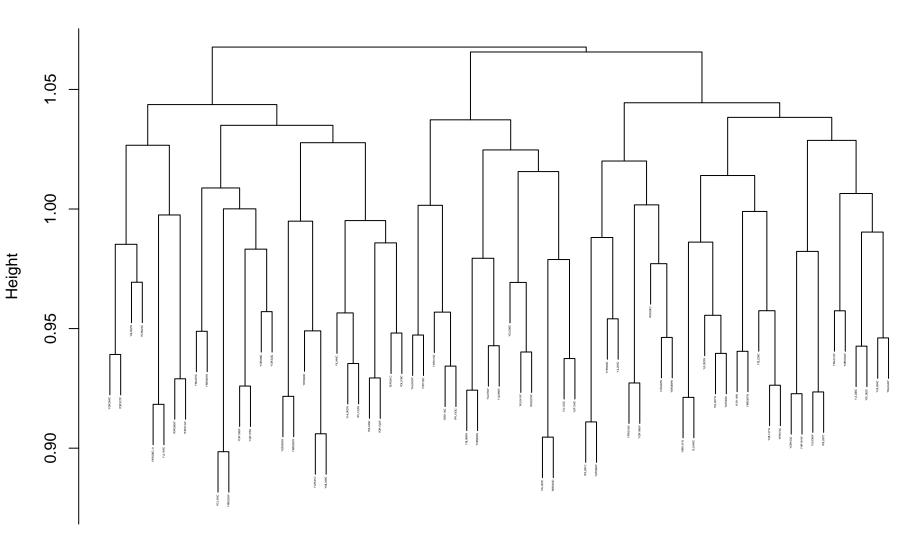
nucleic acid binding transcription factor activity_GO_pearson_complete



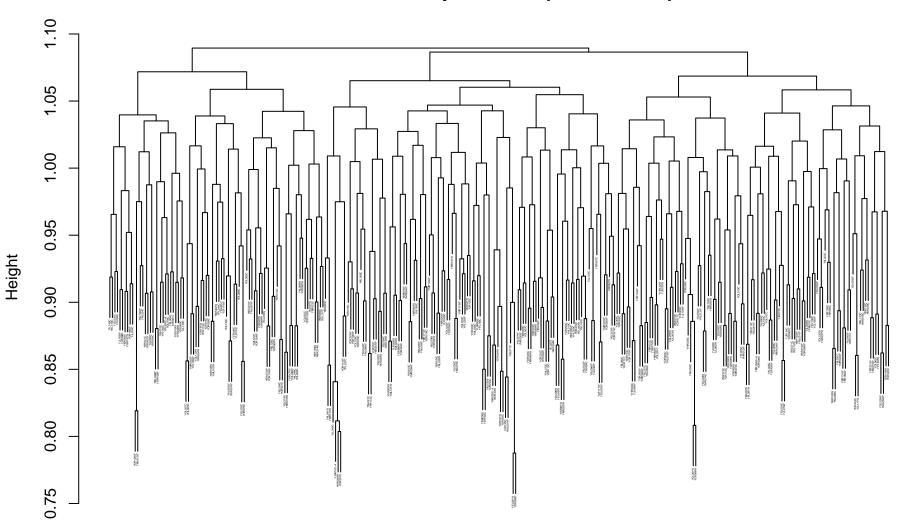
transcription factor activity, protein binding_GO_pearson_complete



cytoplasmic vesicle_GO_pearson_complete

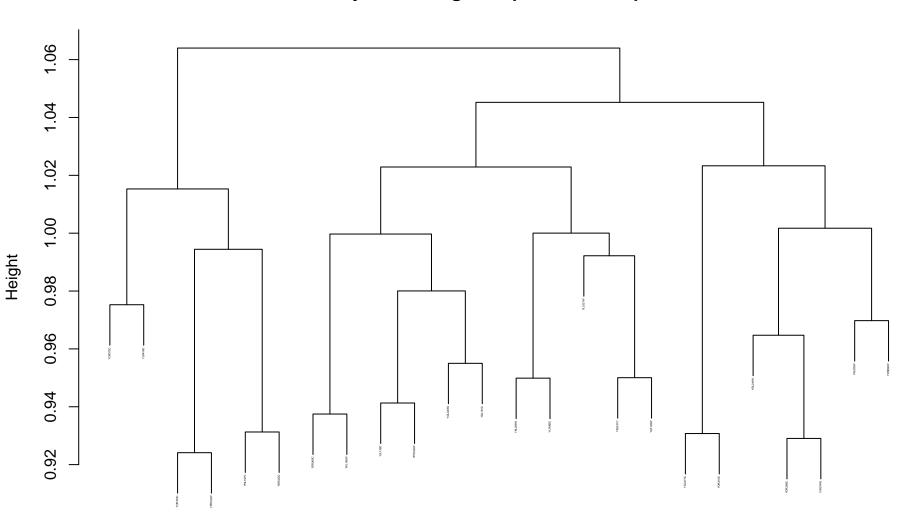


endomembrane system_GO_pearson_complete



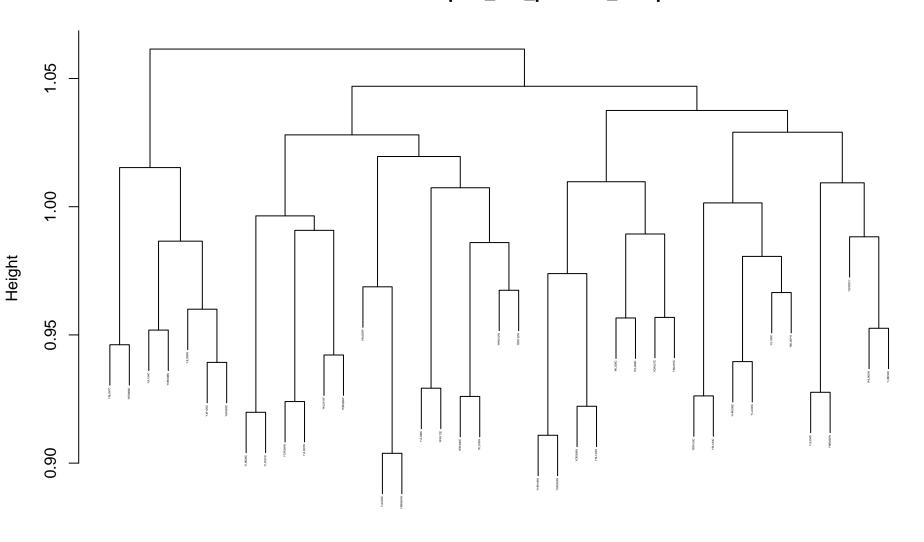
dissim hclust (*, "complete")

enzyme binding_GO_pearson_complete

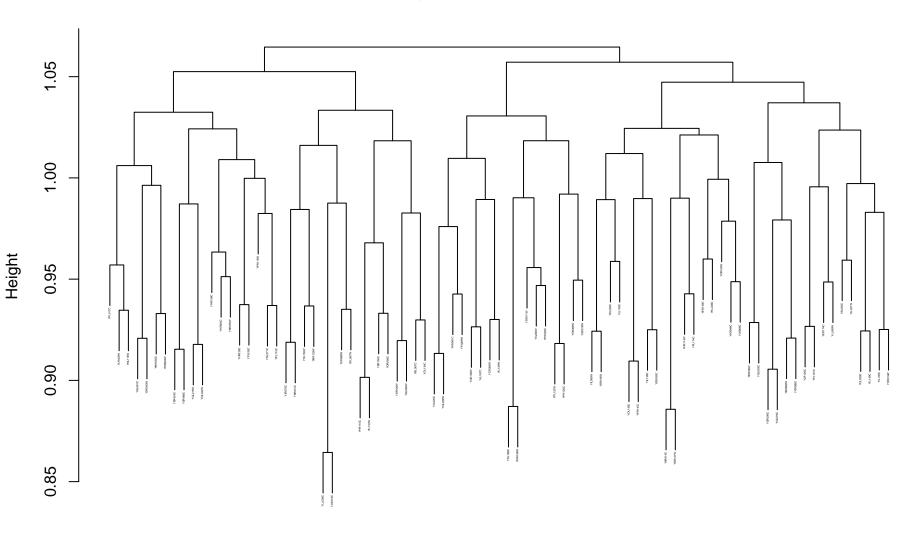


dissim hclust (*, "complete")

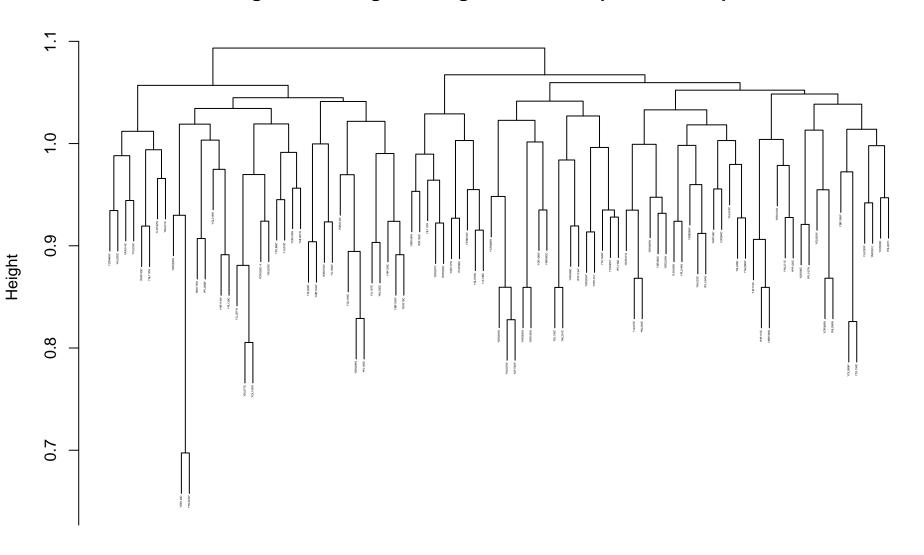
endosomal transport_GO_pearson_complete



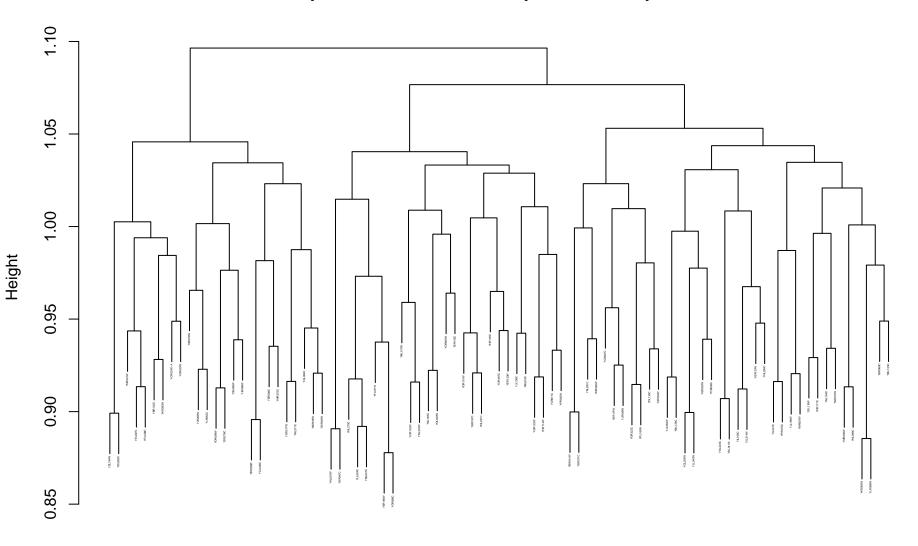
cytoskeleton organization_GO_pearson_complete



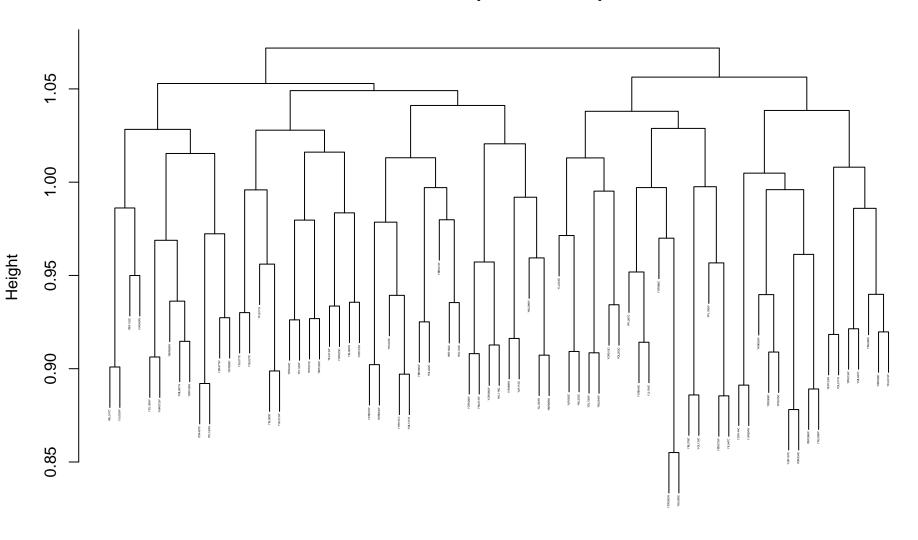
regulation of organelle organization_GO_pearson_complete



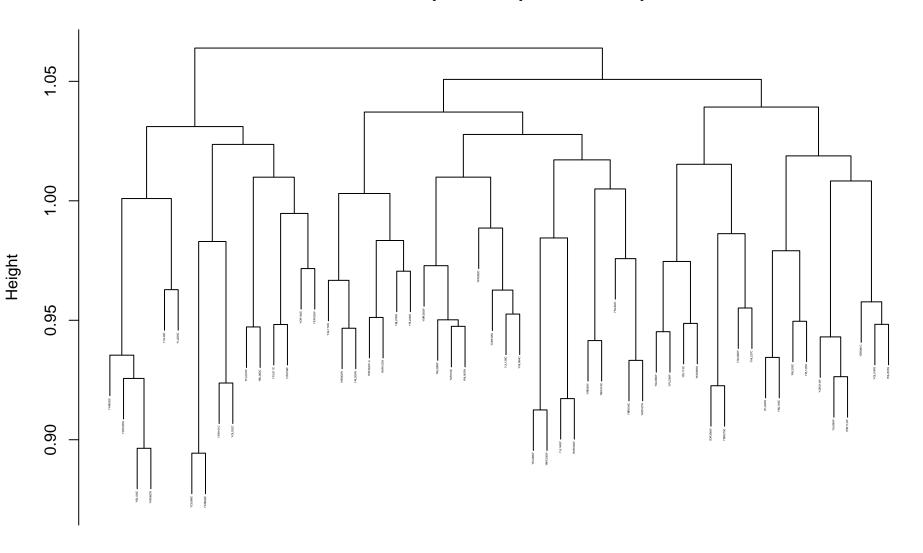
plasma membrane_GO_pearson_complete



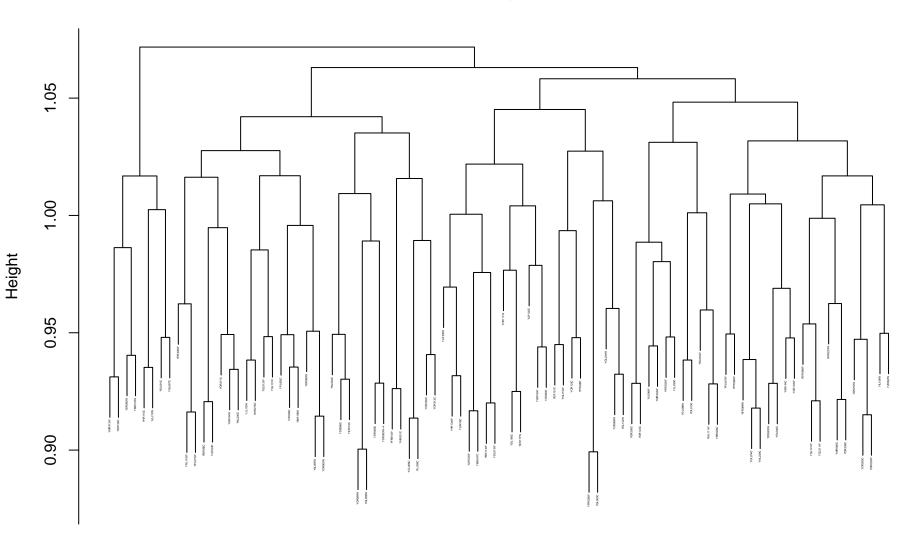
vacuole_GO_pearson_complete



nuclear transport_GO_pearson_complete

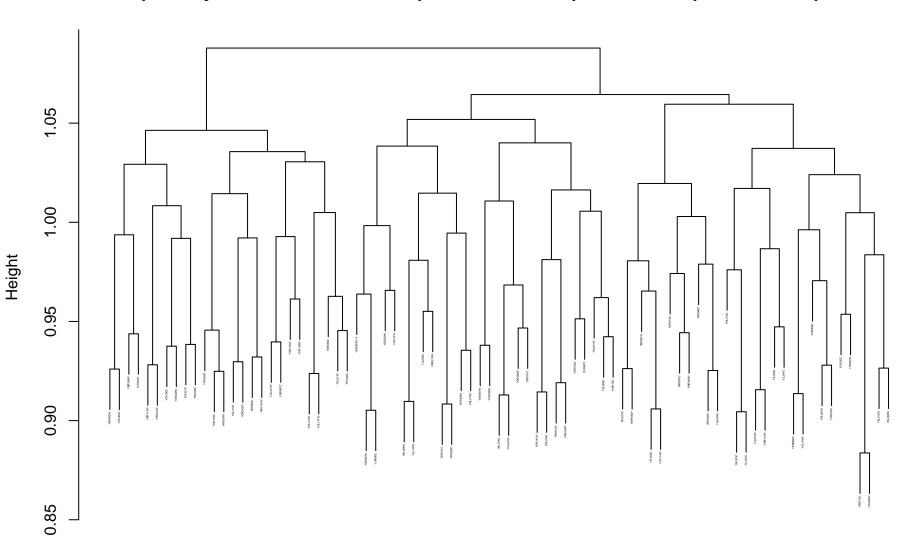


protein modification by small protein conjugation or removal_GO_pearson_complete

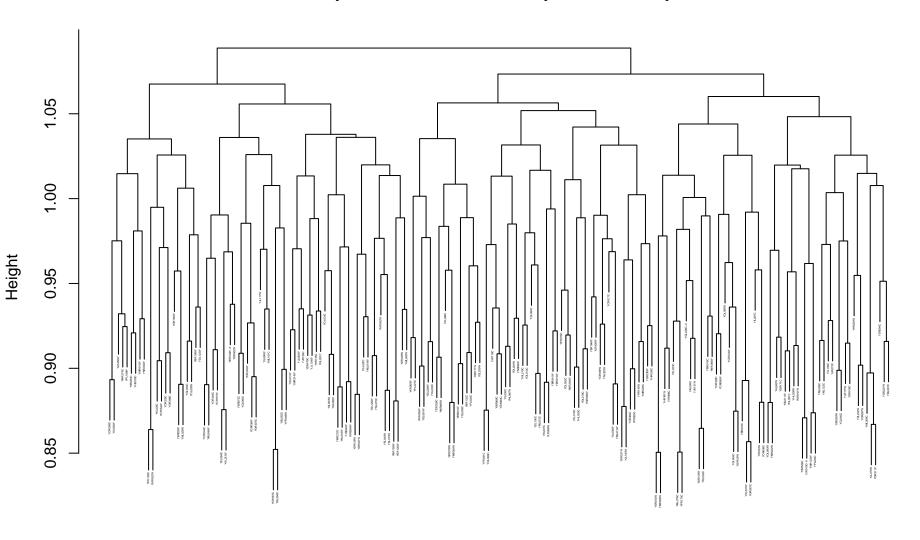


dissim hclust (*, "complete")

proteolysis involved in cellular protein catabolic process_GO_pearson_complete

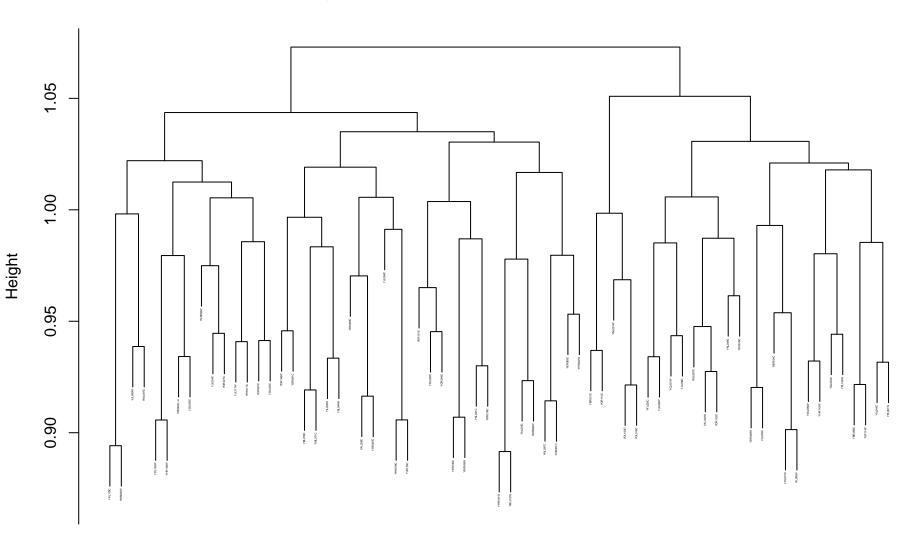


endoplasmic reticulum_GO_pearson_complete

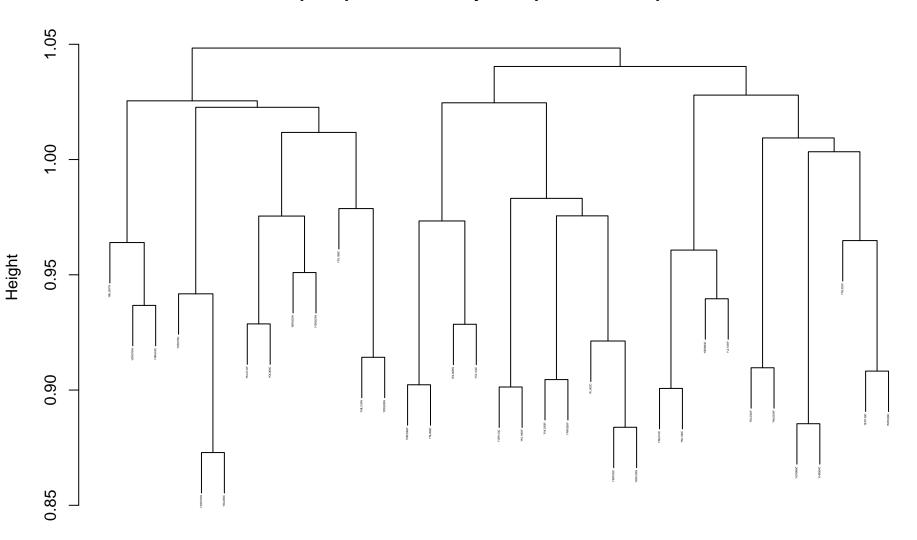


dissim hclust (*, "complete")

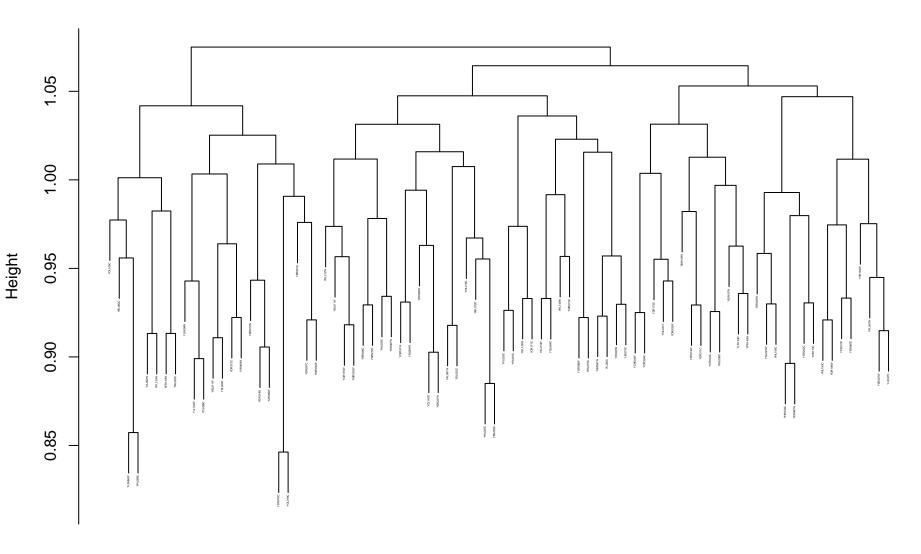
Golgi vesicle transport_GO_pearson_complete



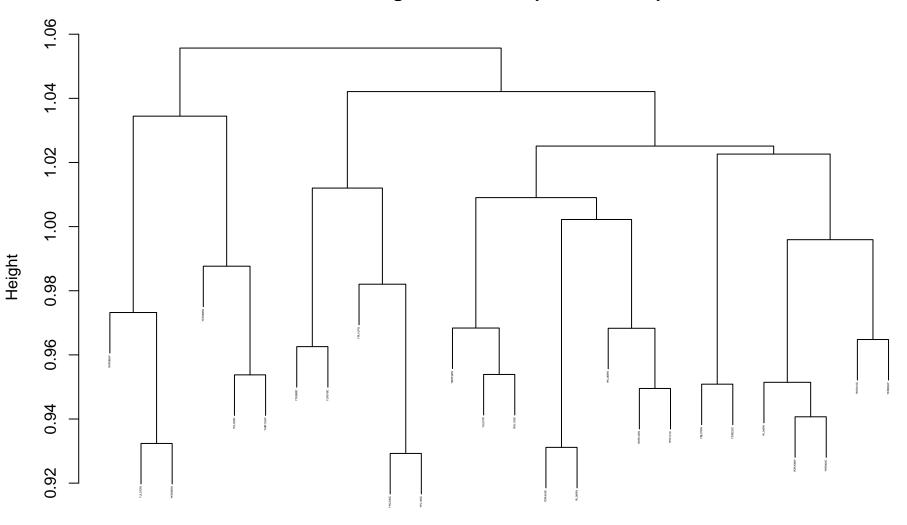
phosphatase activity_GO_pearson_complete



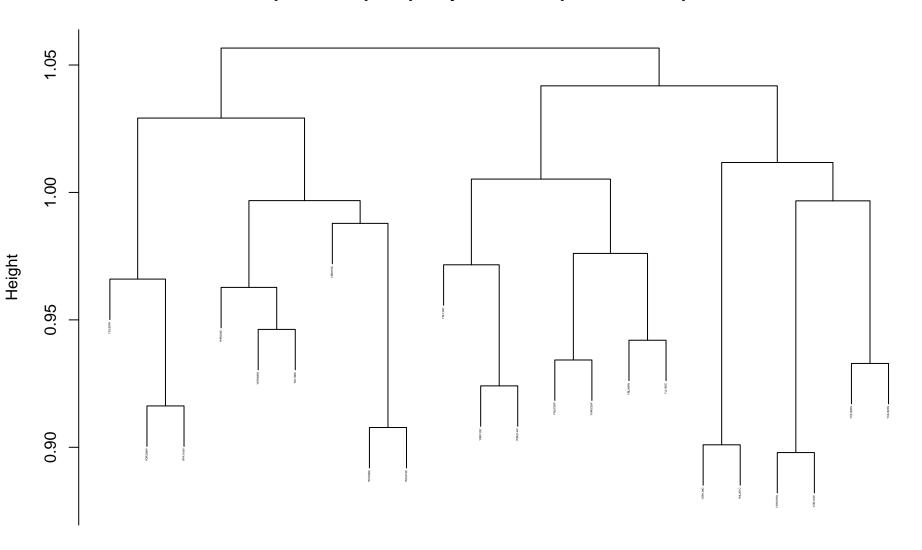
lipid metabolic process_GO_pearson_complete



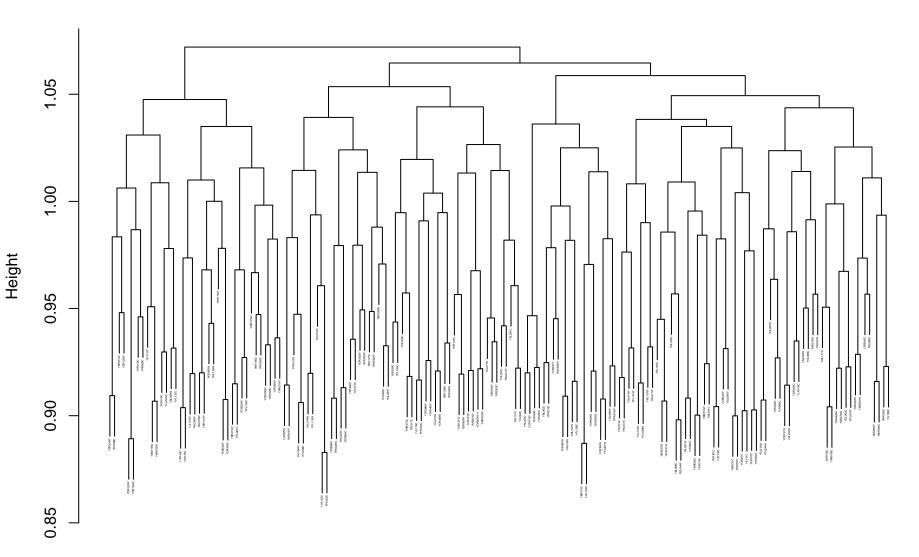
nucleus organization_GO_pearson_complete



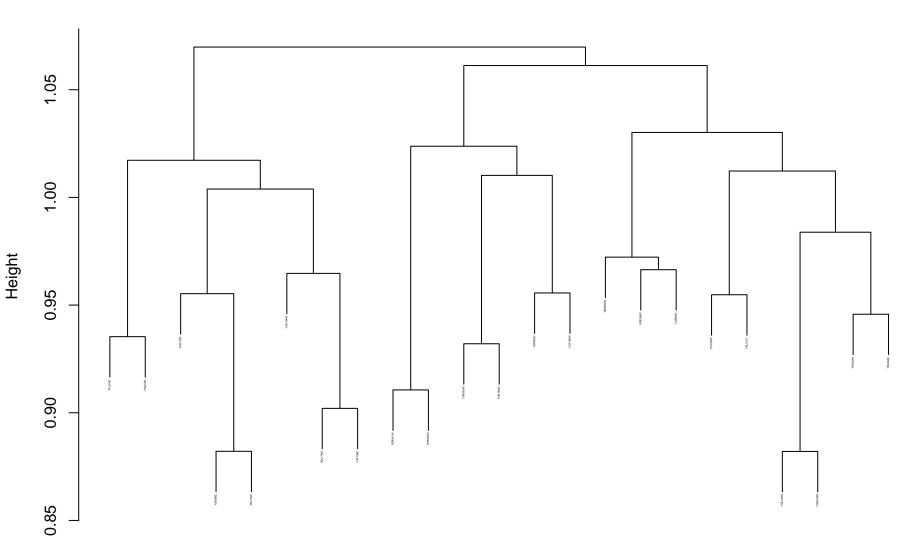
protein dephosphorylation_GO_pearson_complete



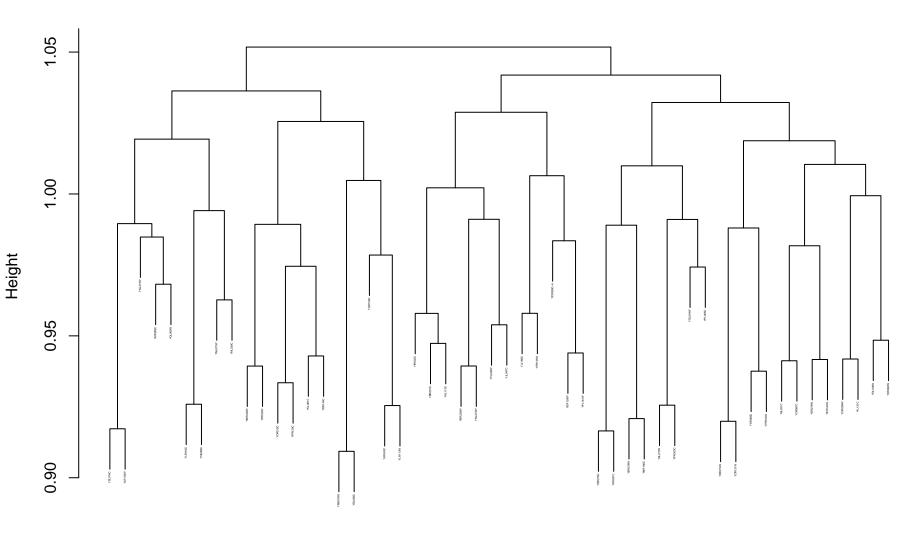
$chromatin\ organization_GO_pearson_complete$



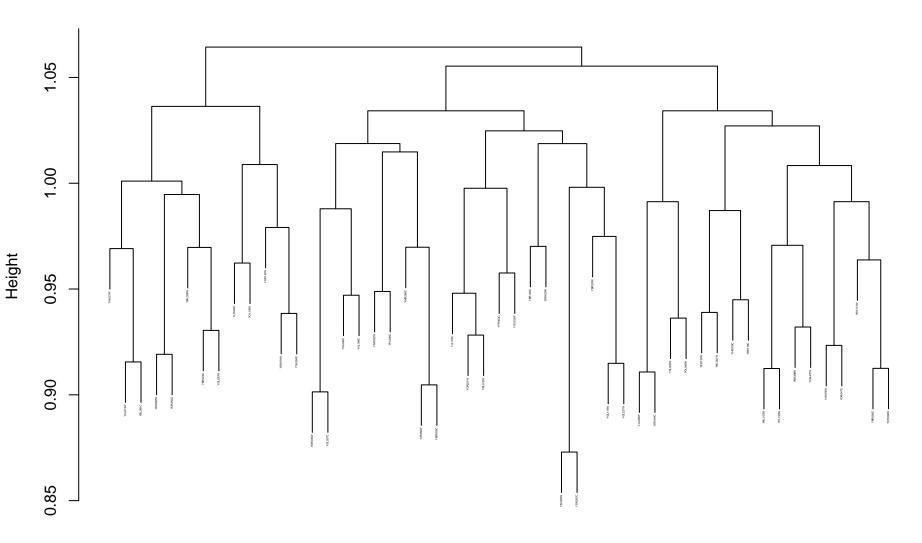
cellular amino acid metabolic process_GO_pearson_complete



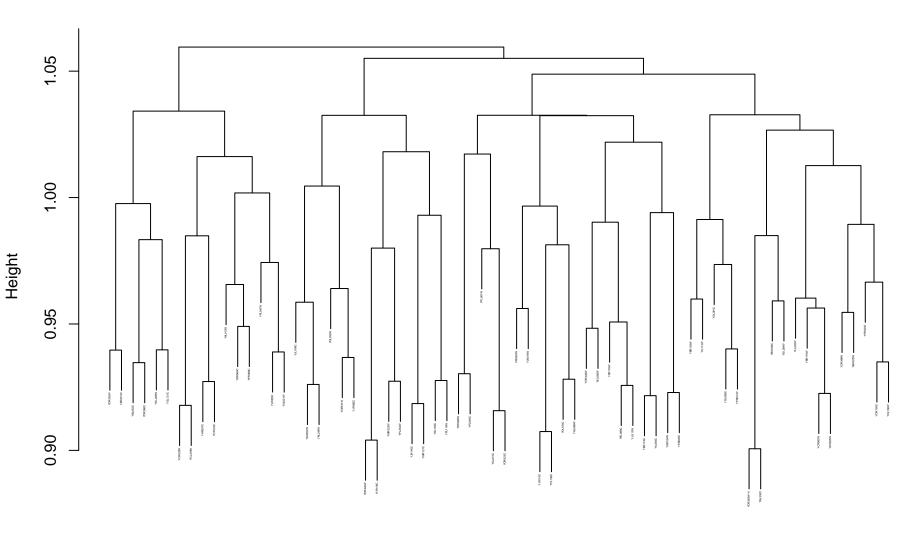
DNA replication_GO_pearson_complete



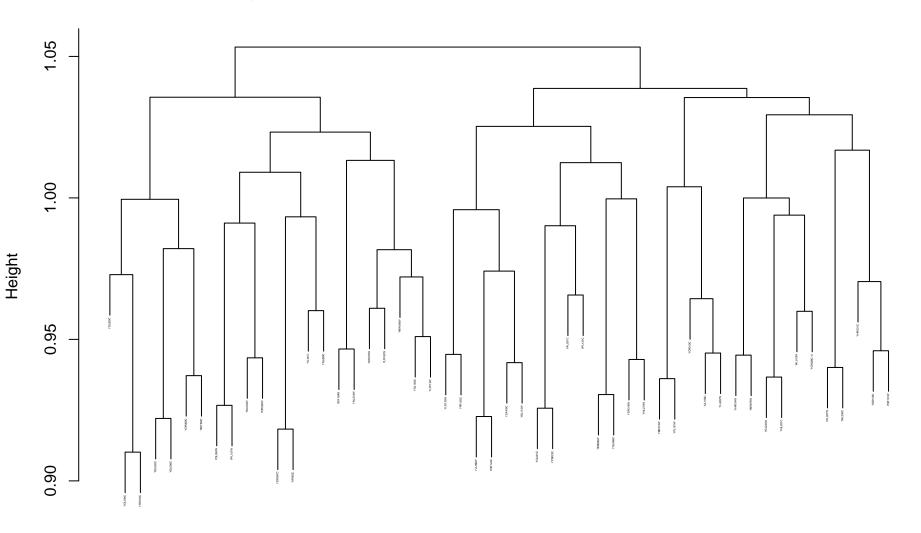
carbohydrate metabolic process_GO_pearson_complete



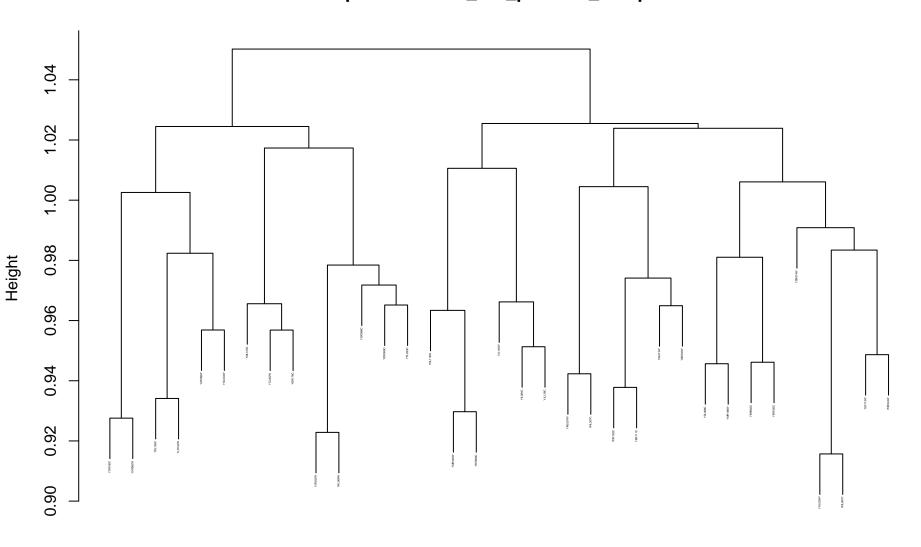
histone modification_GO_pearson_complete



regulation of DNA metabolic process_GO_pearson_complete

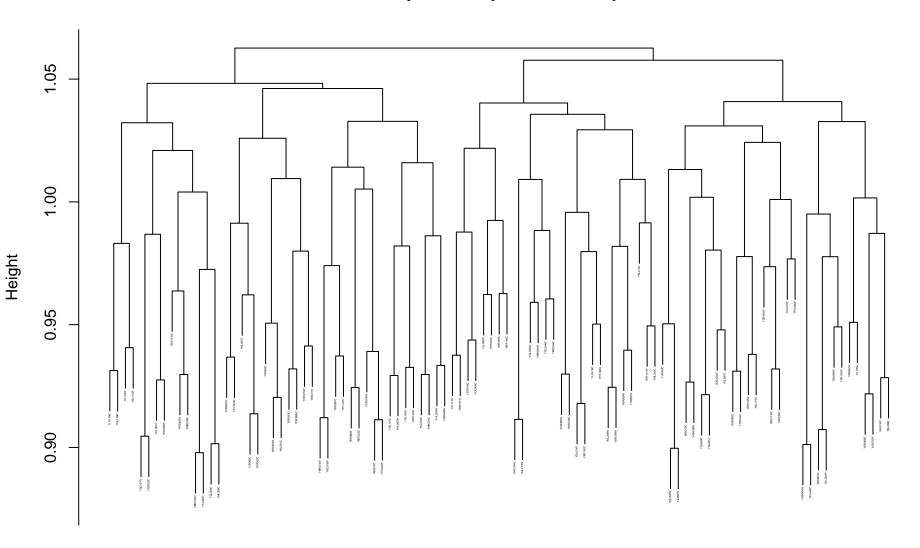


response to heat_GO_pearson_complete

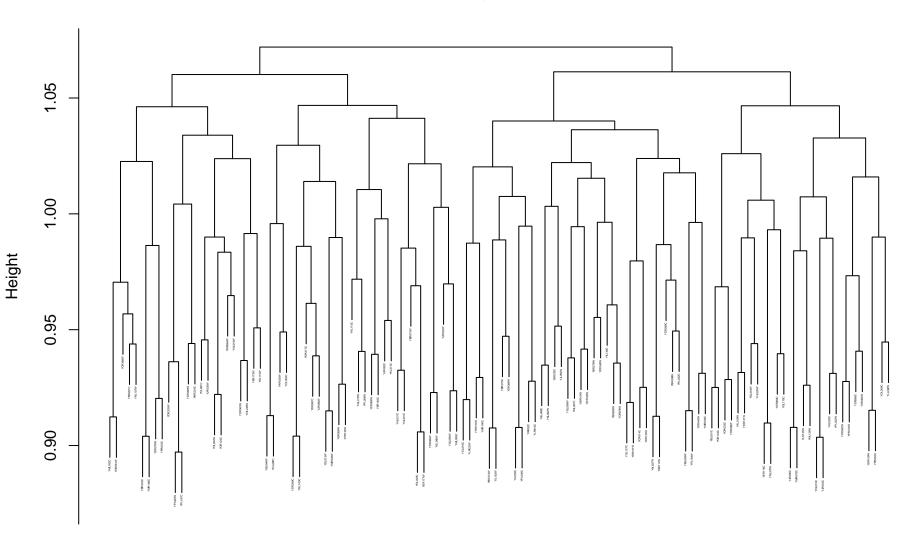


dissim hclust (*, "complete")

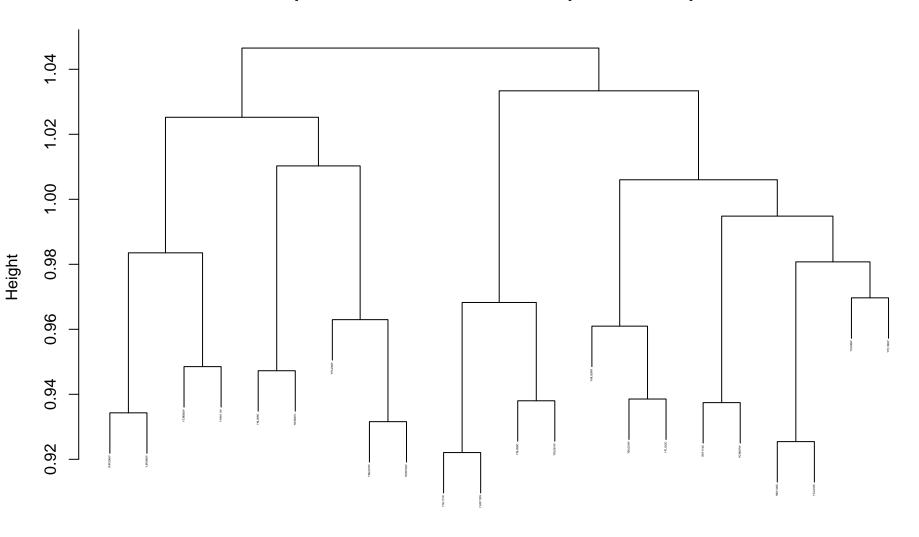
DNA repair_GO_pearson_complete



cellular response to DNA damage stimulus_GO_pearson_complete

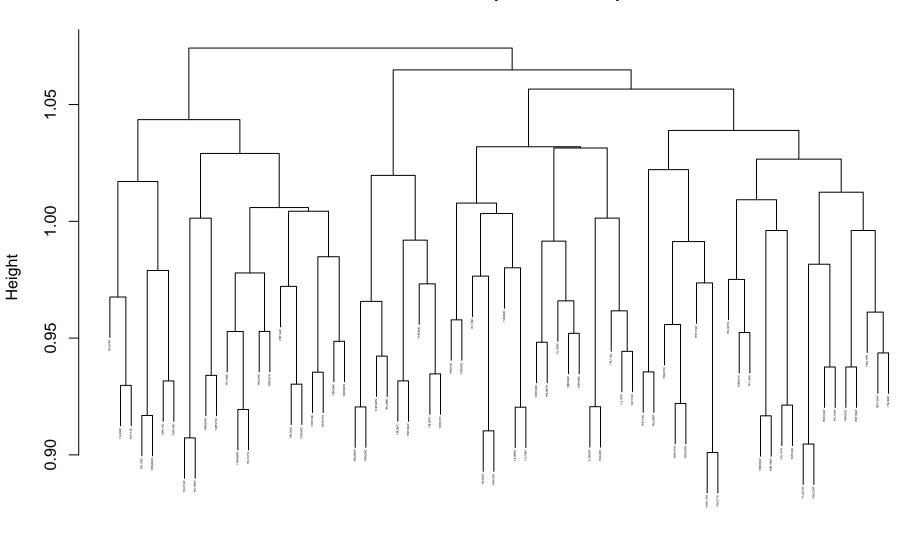


response to oxidative stress_GO_pearson_complete



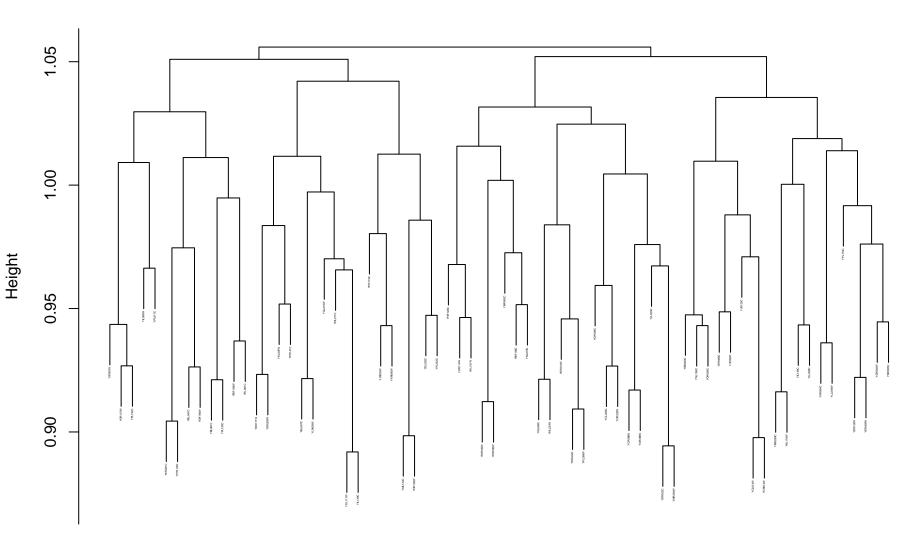
dissim hclust (*, "complete")

cellular bud_GO_pearson_complete

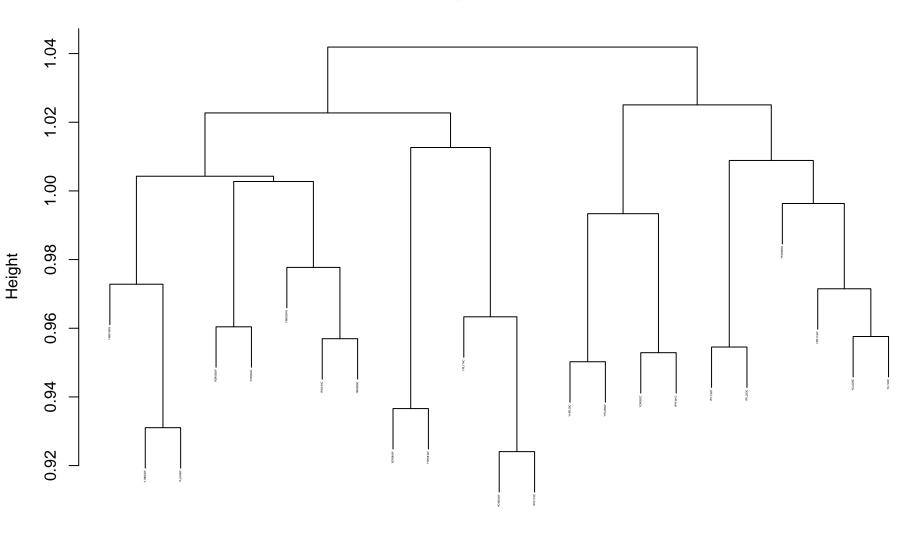


dissim hclust (*, "complete")

cytoskeleton_GO_pearson_complete

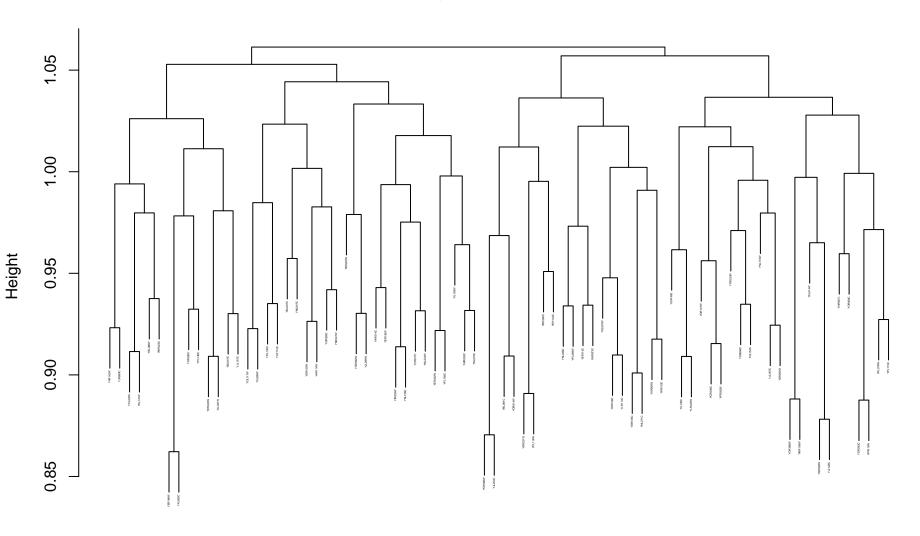


microtubule organizing center_GO_pearson_complete

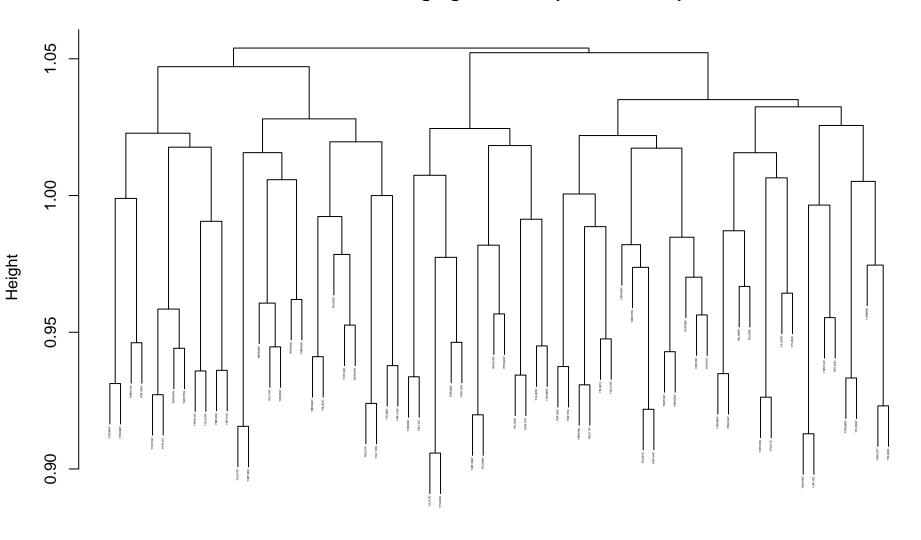


dissim hclust (*, "complete")

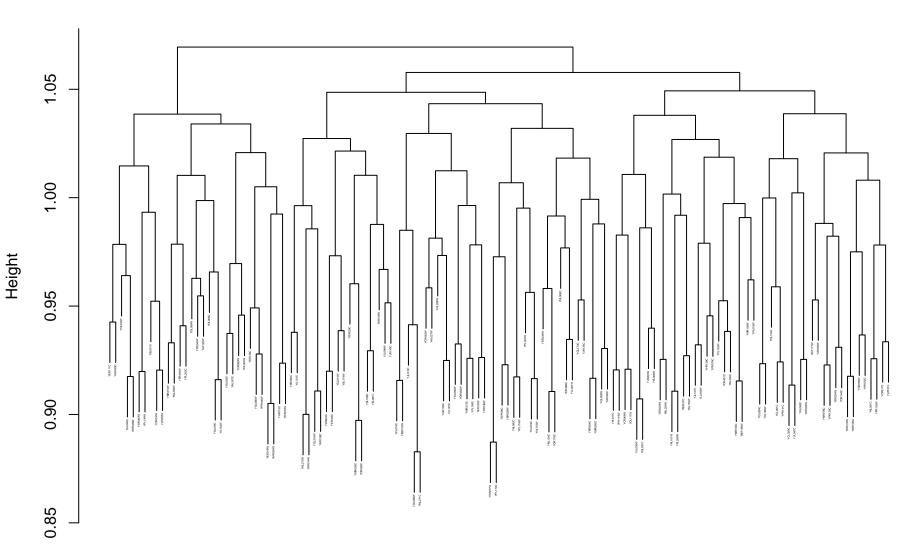
site of polarized growth_GO_pearson_complete



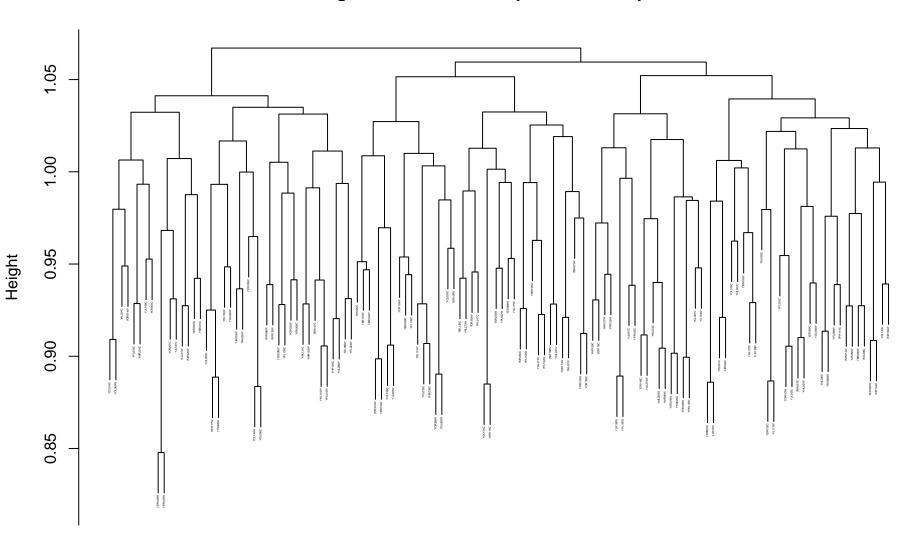
chromosome segregation_GO_pearson_complete



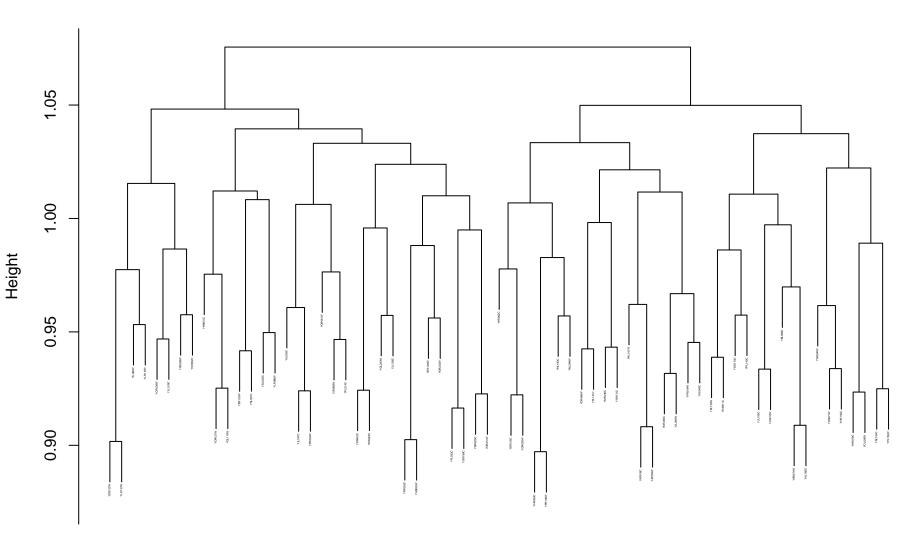
mitotic cell cycle_GO_pearson_complete



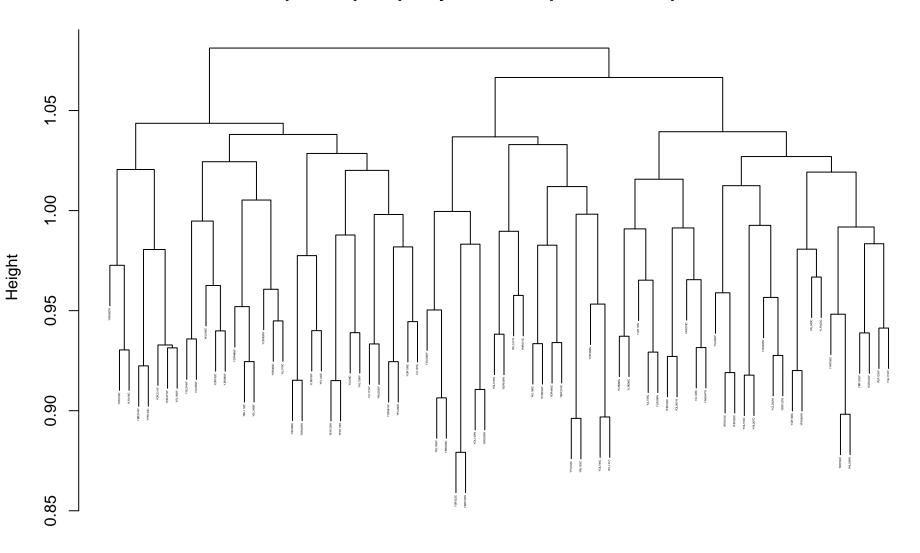
organelle fission_GO_pearson_complete



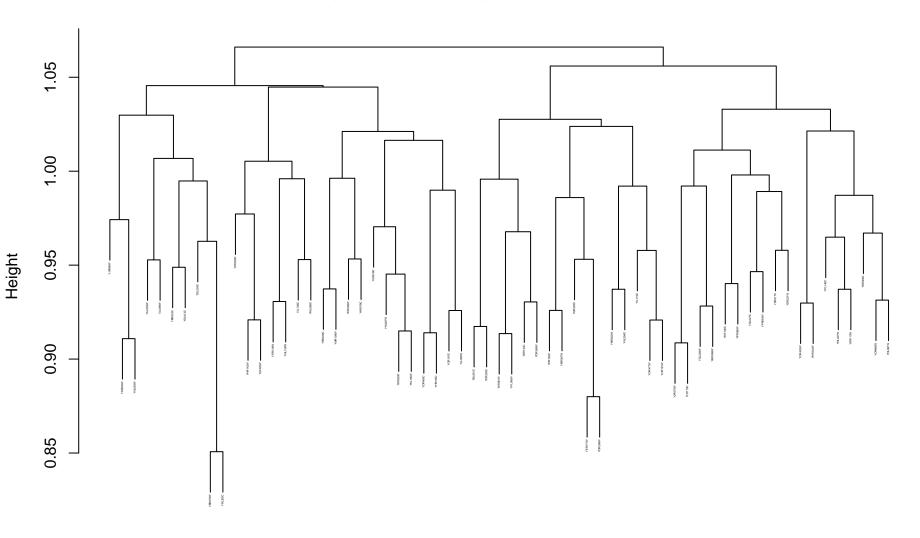
kinase activity_GO_pearson_complete



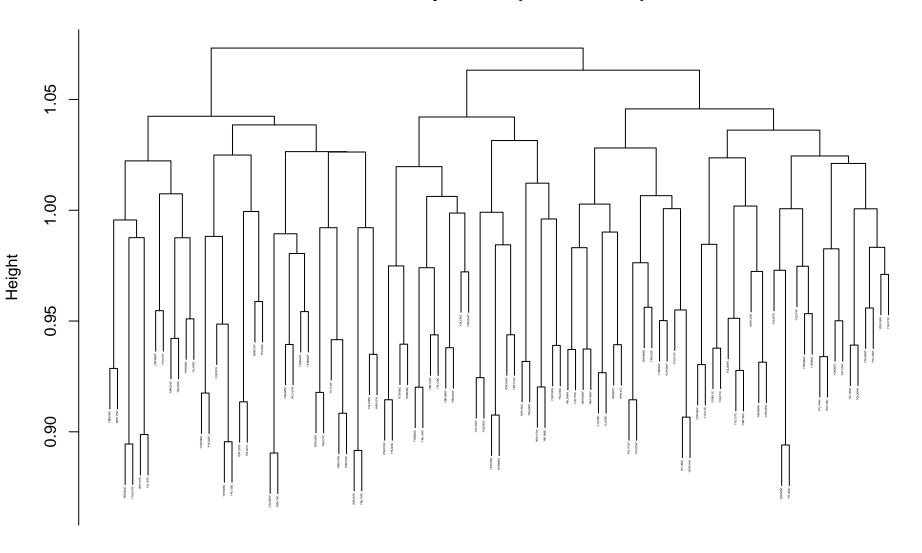
protein phosphorylation_GO_pearson_complete



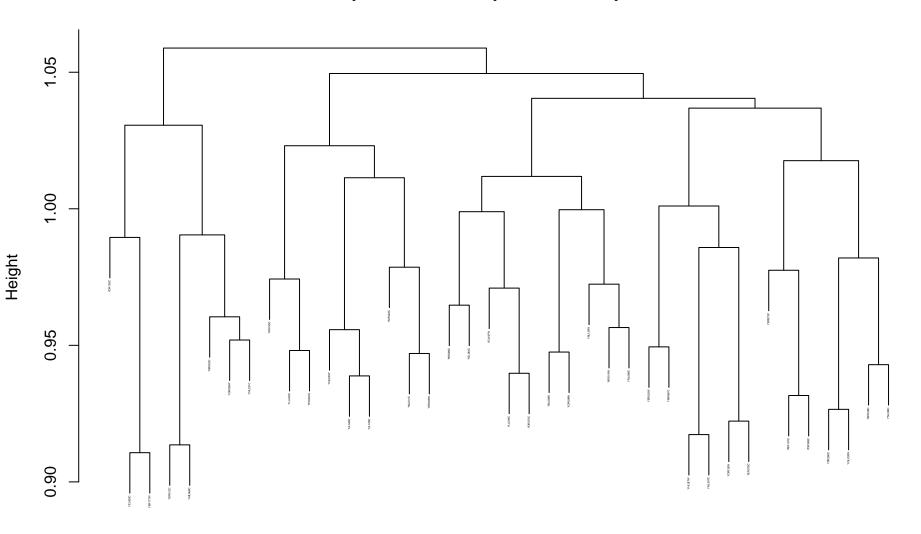
cell wall organization or biogenesis_GO_pearson_complete



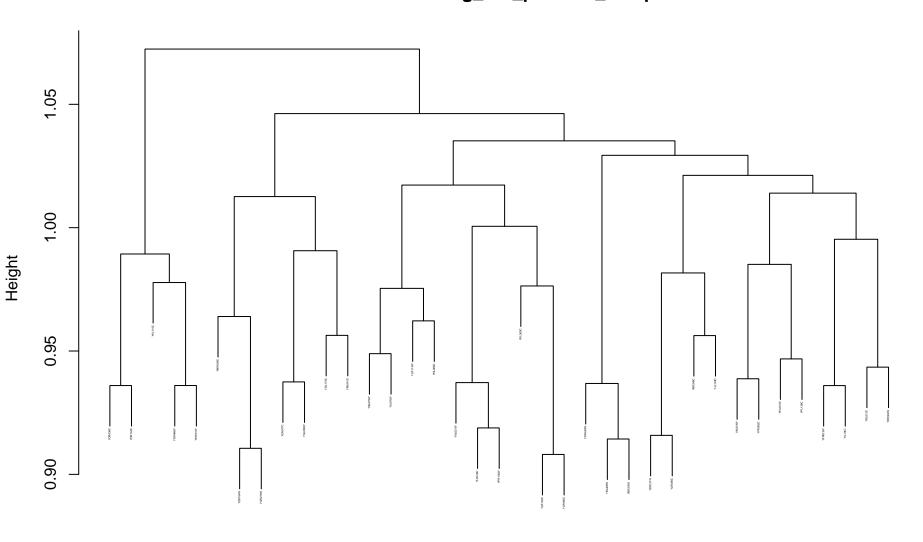
meiotic cell cycle_GO_pearson_complete



sporulation_GO_pearson_complete

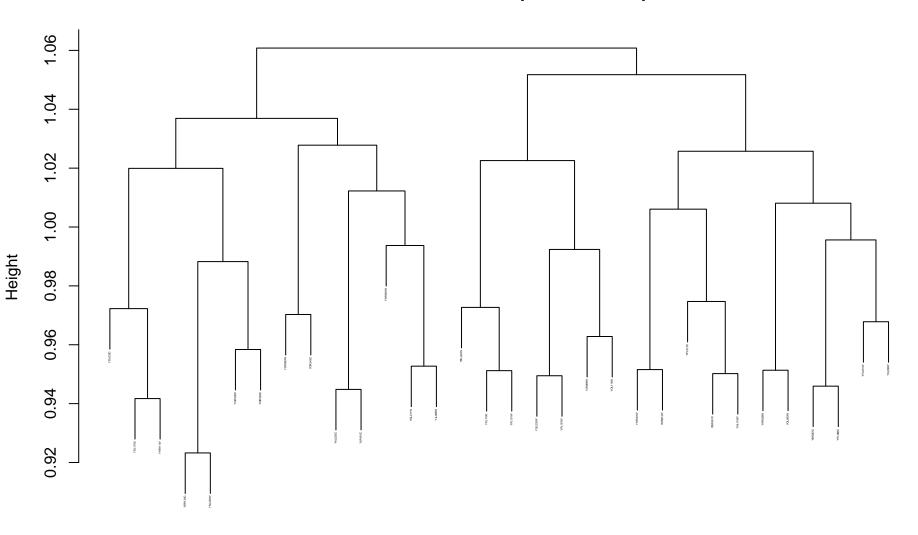


chromatin binding_GO_pearson_complete



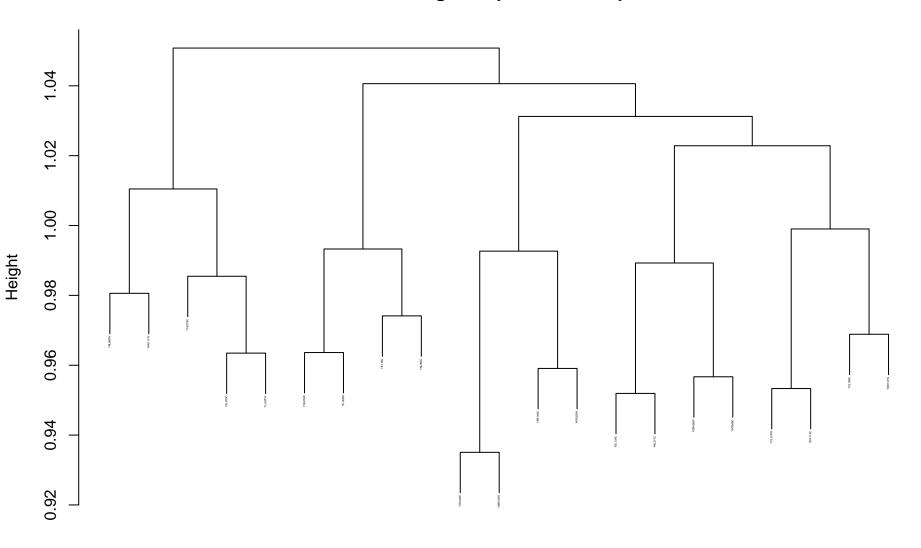
dissim hclust (*, "complete")

RNA modification_GO_pearson_complete



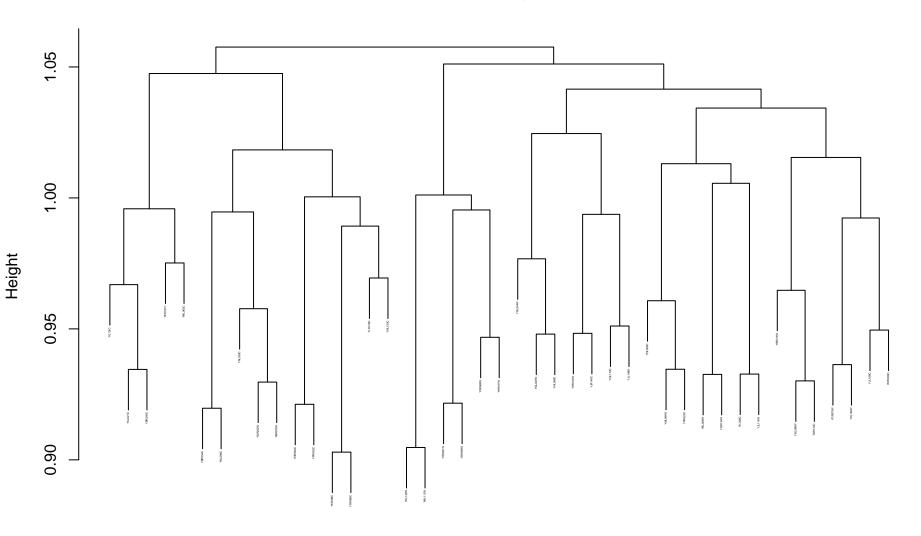
dissim hclust (*, "complete")

cell budding_GO_pearson_complete

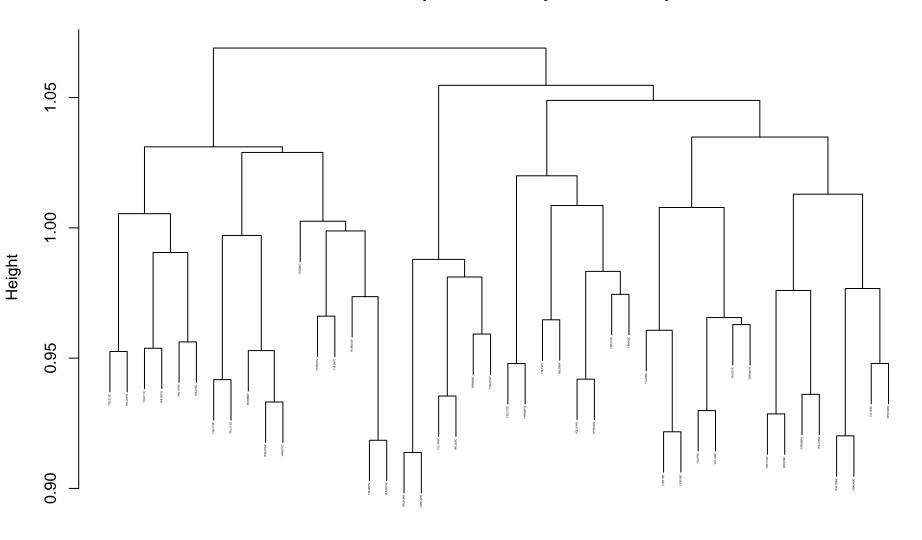


dissim hclust (*, "complete")

DNA-templated transcription, elongation_GO_pearson_complete

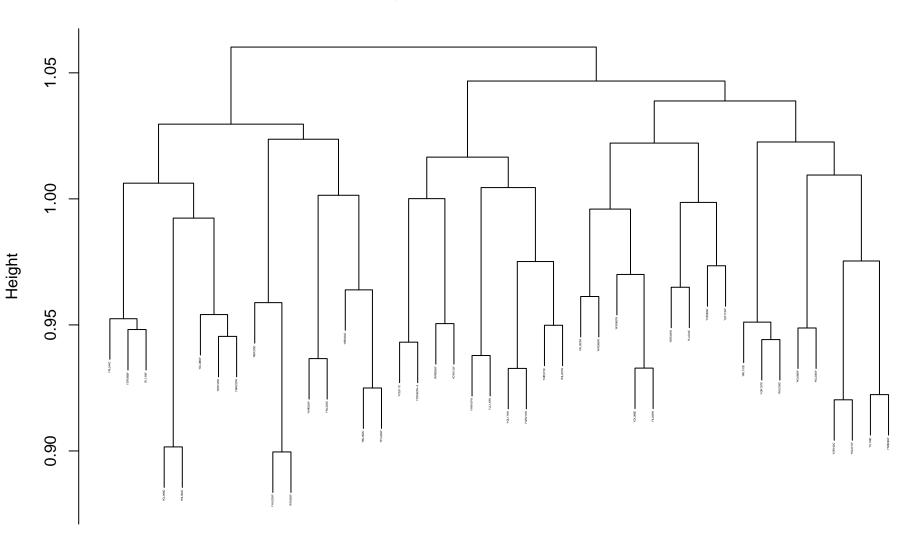


RNA catabolic process_GO_pearson_complete

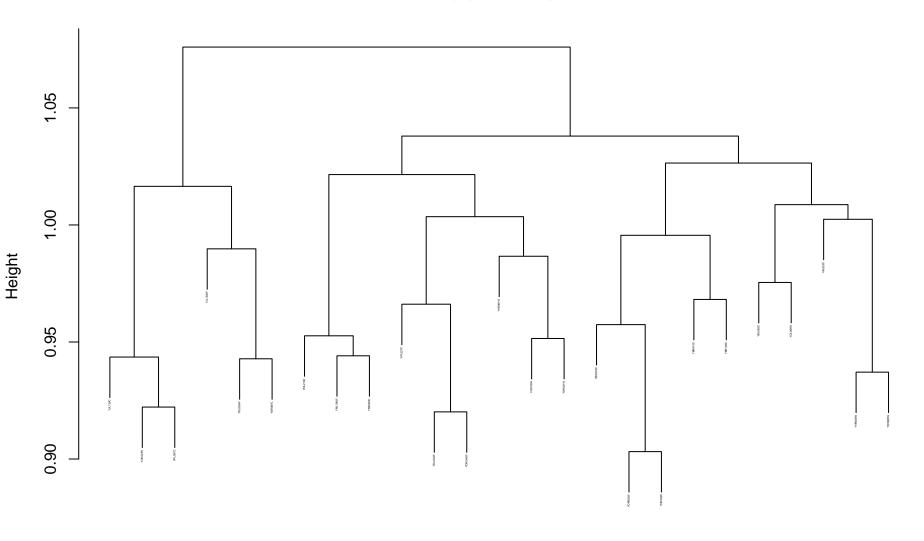


dissim hclust (*, "complete")

nucleobase-containing compound transport_GO_pearson_complete

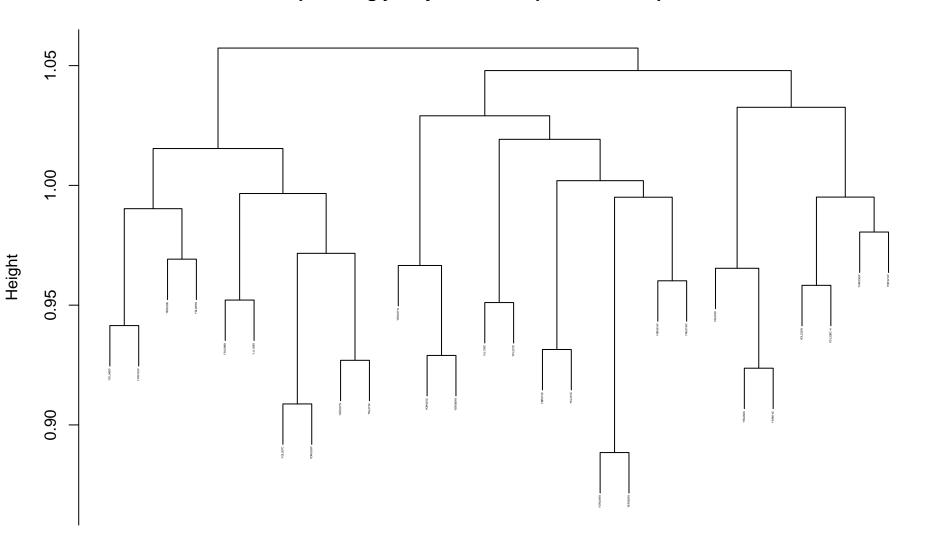


transferase activity, transferring glycosyl groups_GO_pearson_complete

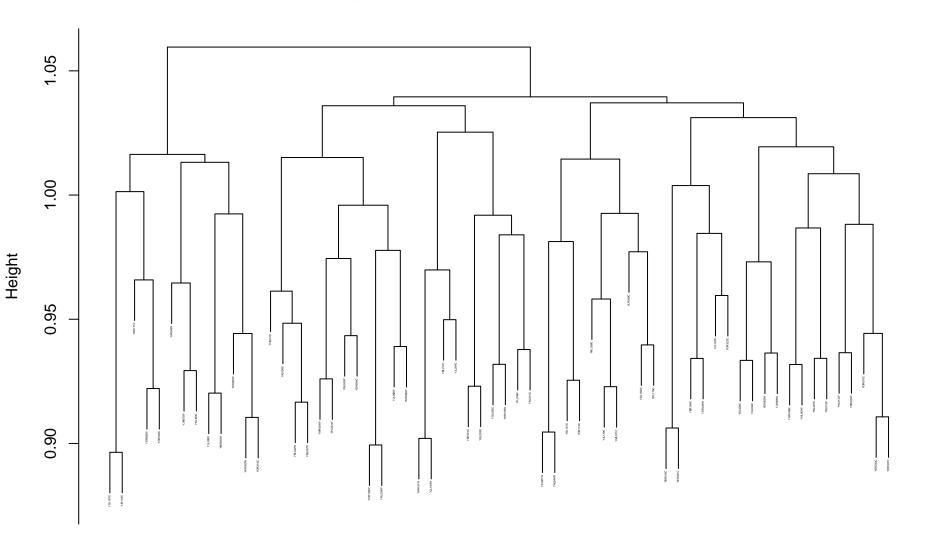


dissim hclust (*, "complete")

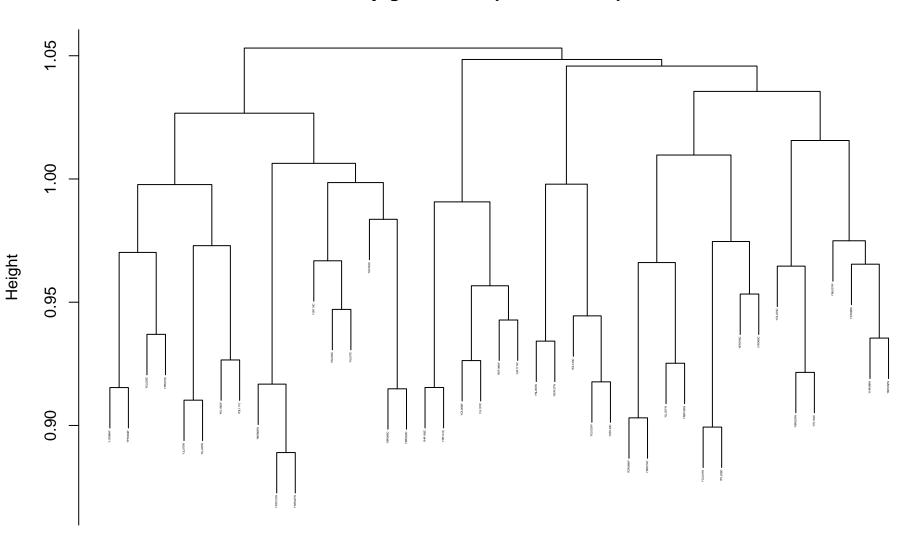
protein glycosylation_GO_pearson_complete



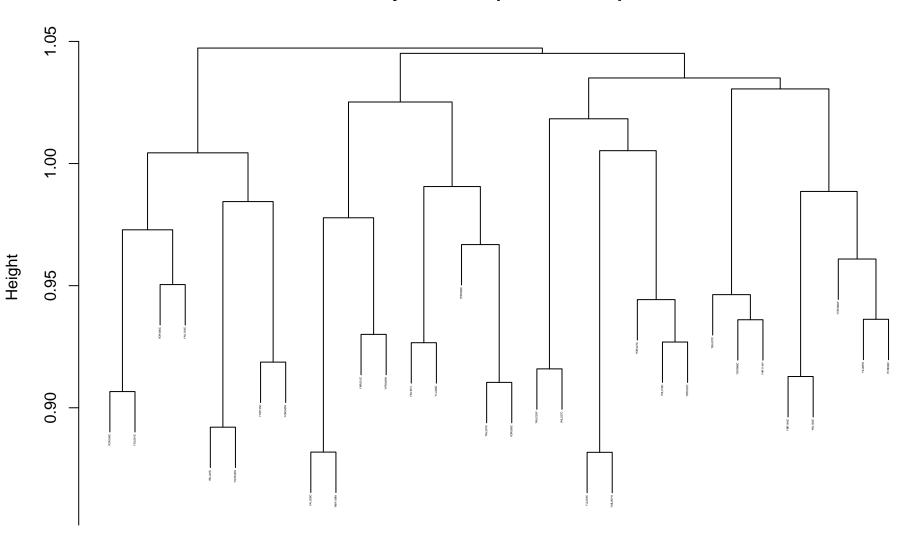
Golgi apparatus_GO_pearson_complete



conjugation_GO_pearson_complete

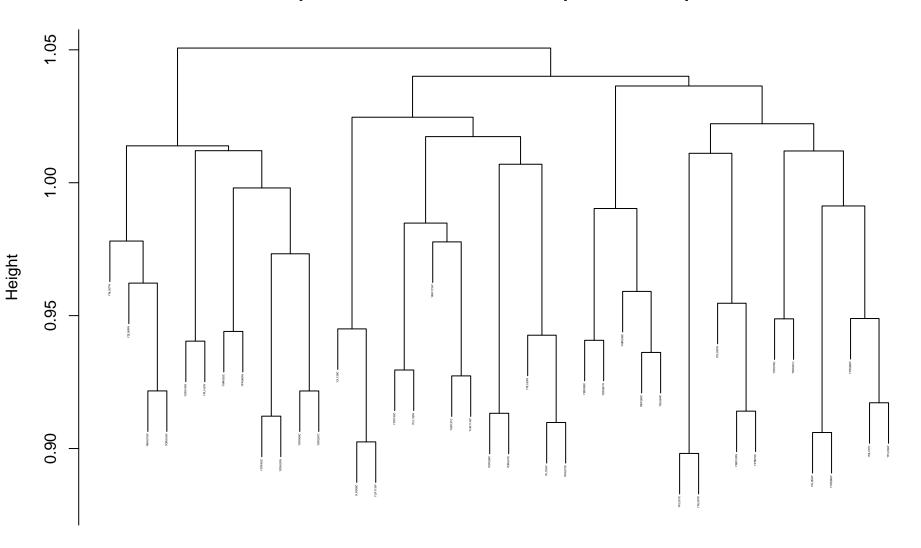


$endocytosis_GO_pearson_complete\\$

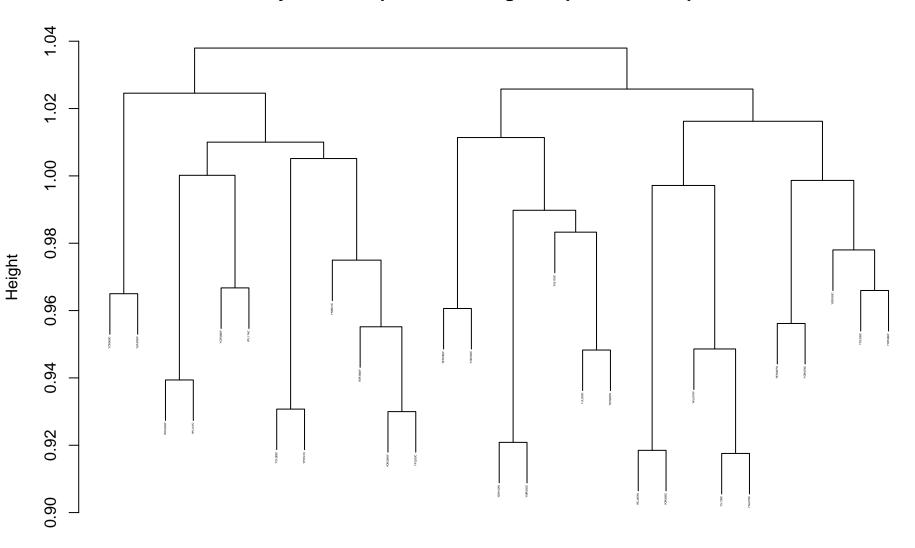


dissim hclust (*, "complete")

response to osmotic stress_GO_pearson_complete

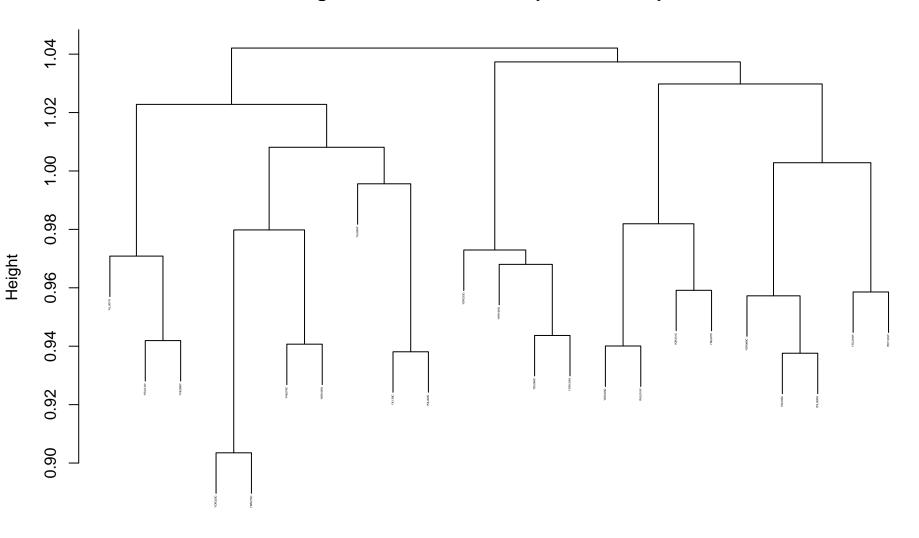


cytoskeletal protein binding_GO_pearson_complete

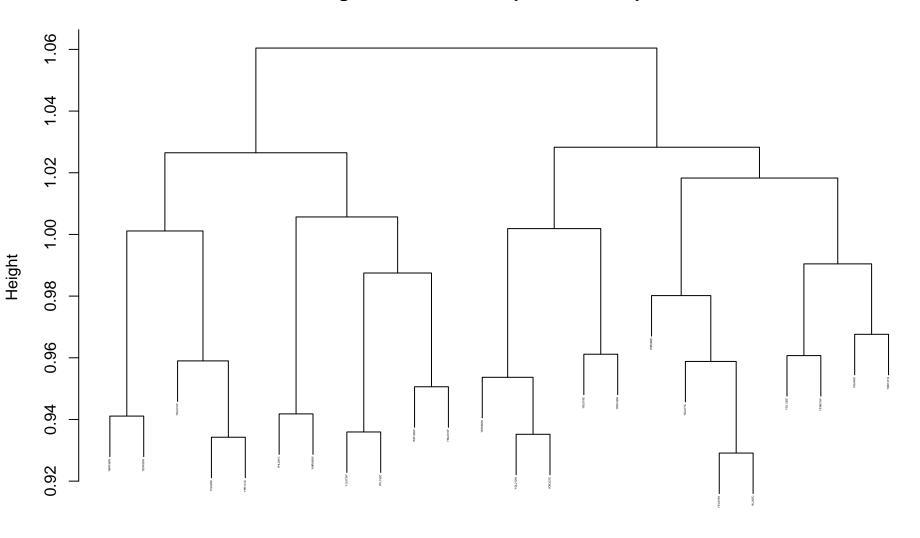


dissim hclust (*, "complete")

organelle inheritance_GO_pearson_complete

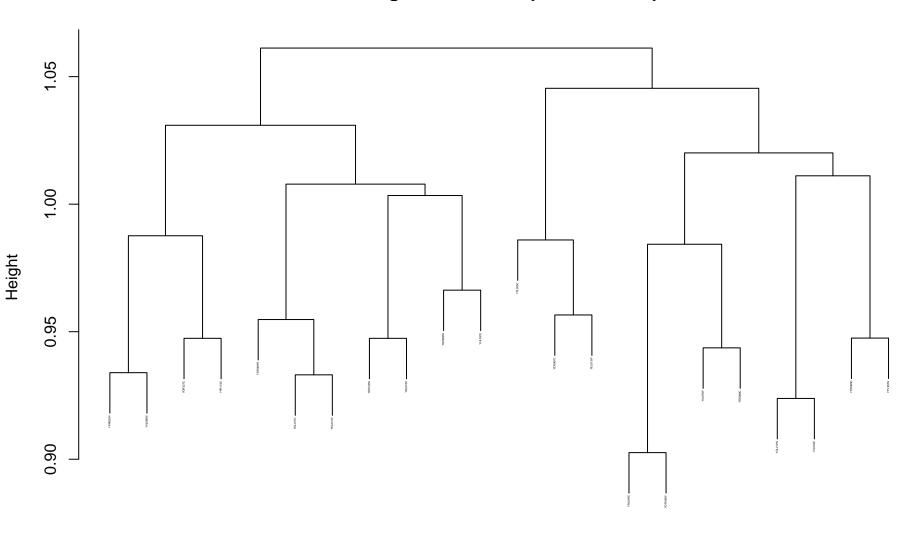


organelle fusion_GO_pearson_complete



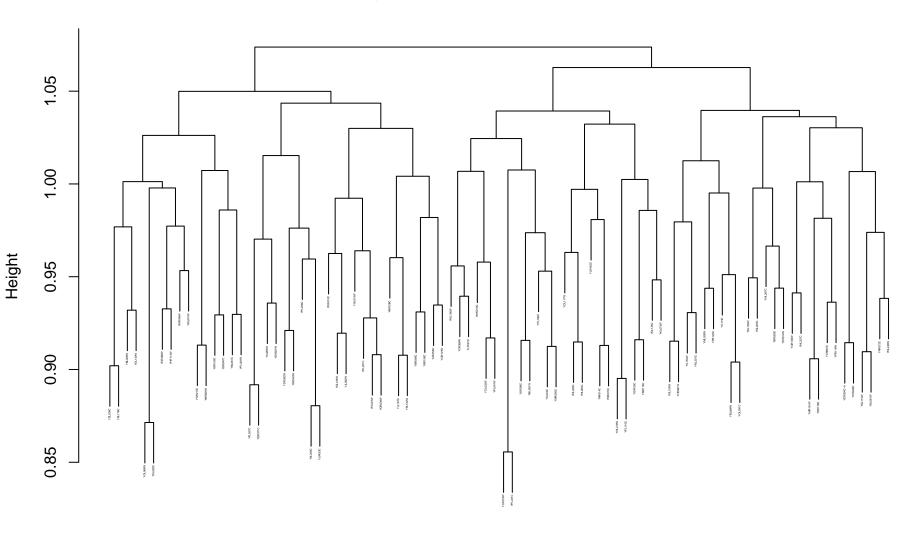
dissim hclust (*, "complete")

vesicle organization_GO_pearson_complete

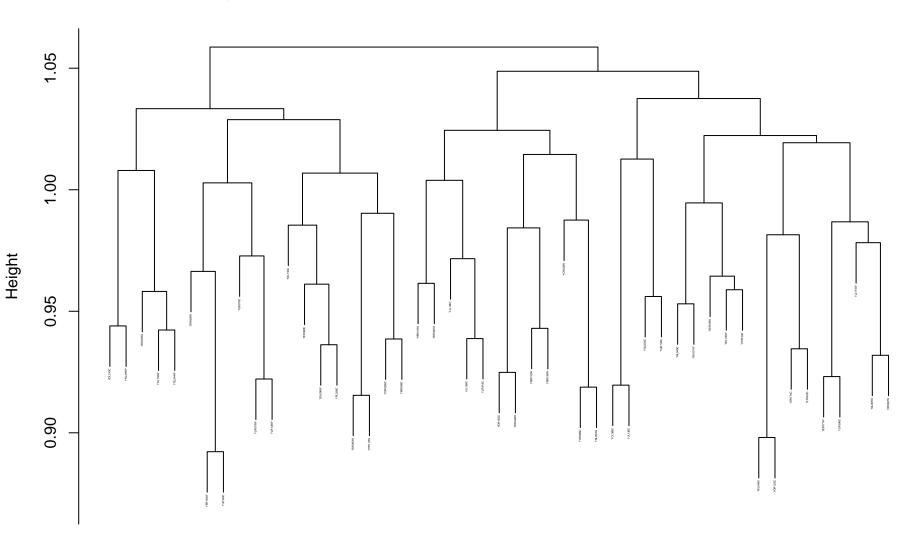


dissim hclust (*, "complete")

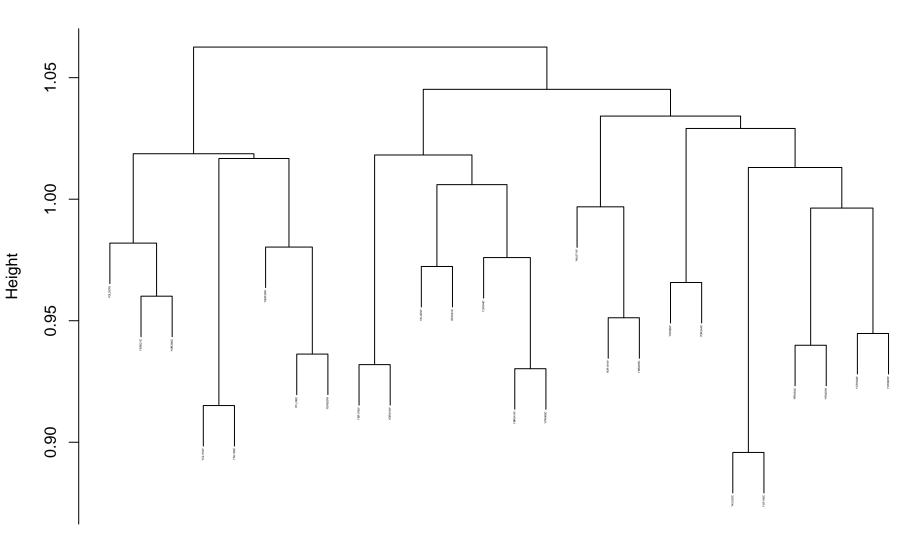
enzyme regulator activity_GO_pearson_complete



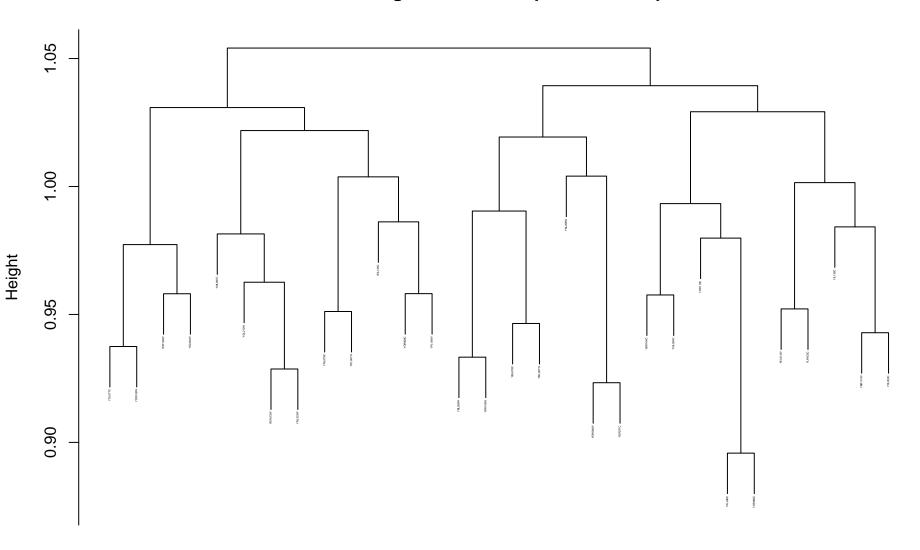
regulation of protein modification process_GO_pearson_complete



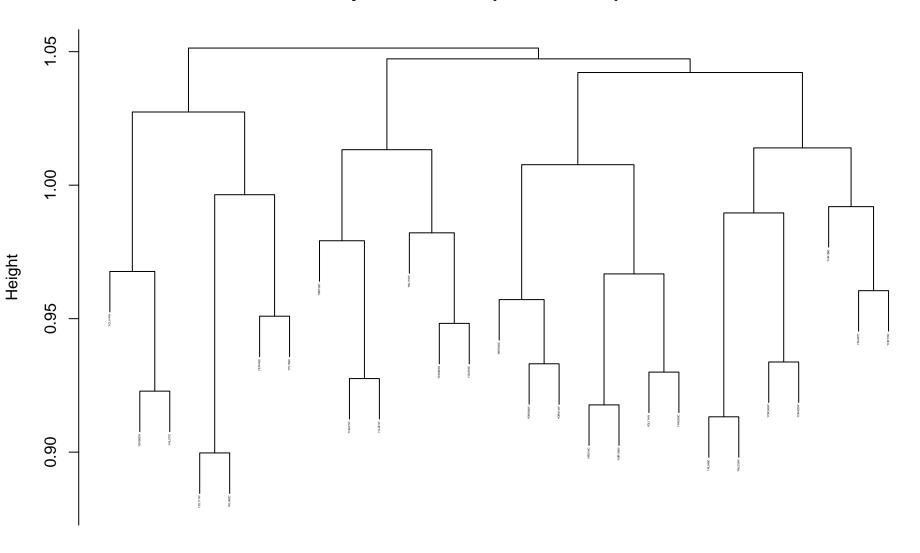
monocarboxylic acid metabolic process_GO_pearson_complete



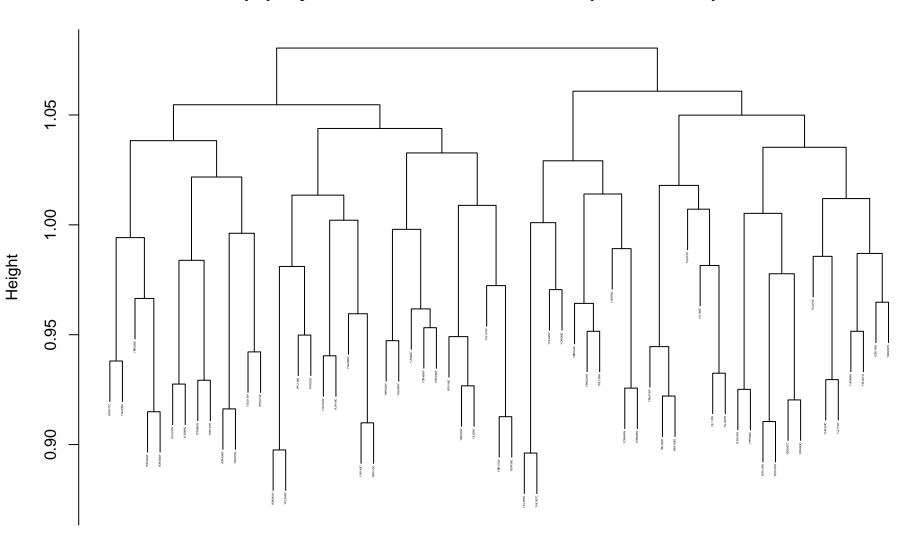
vacuole organization_GO_pearson_complete



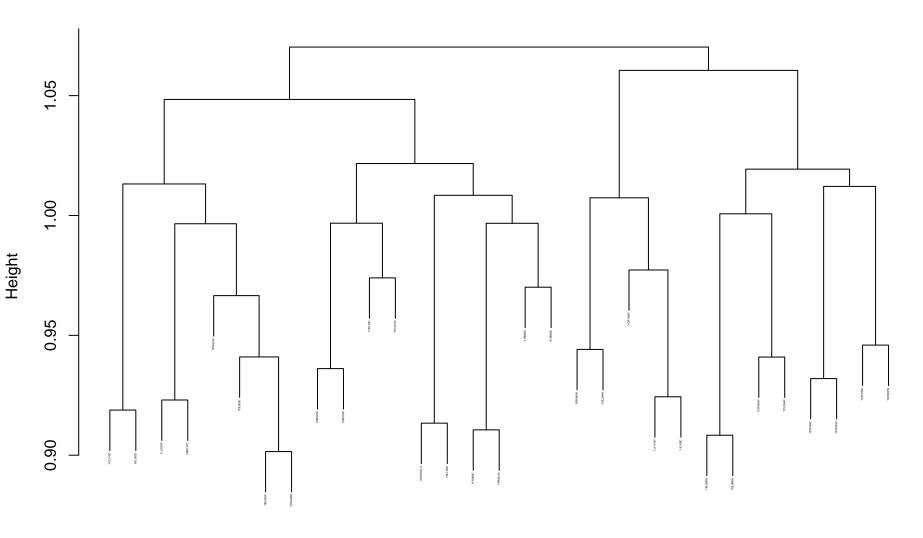
cytokinesis_GO_pearson_complete



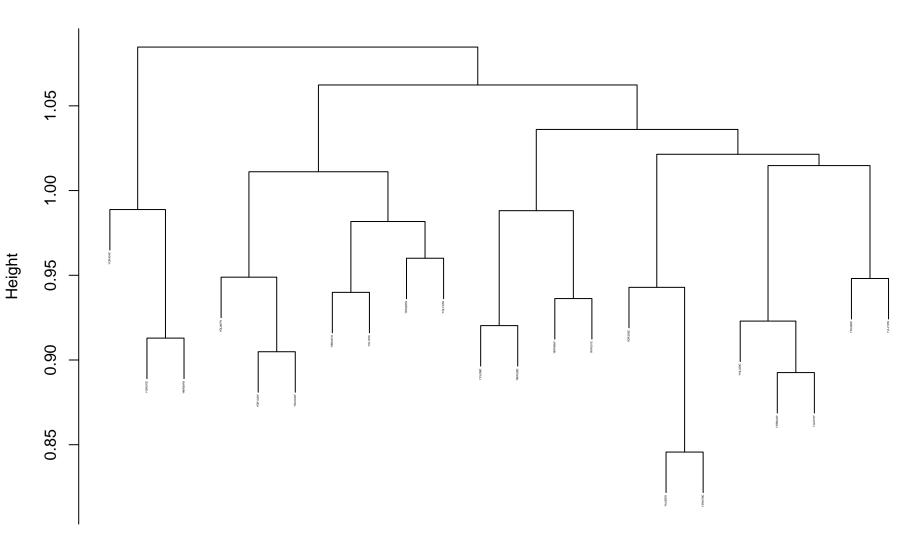
peptidyl-amino acid modification_GO_pearson_complete



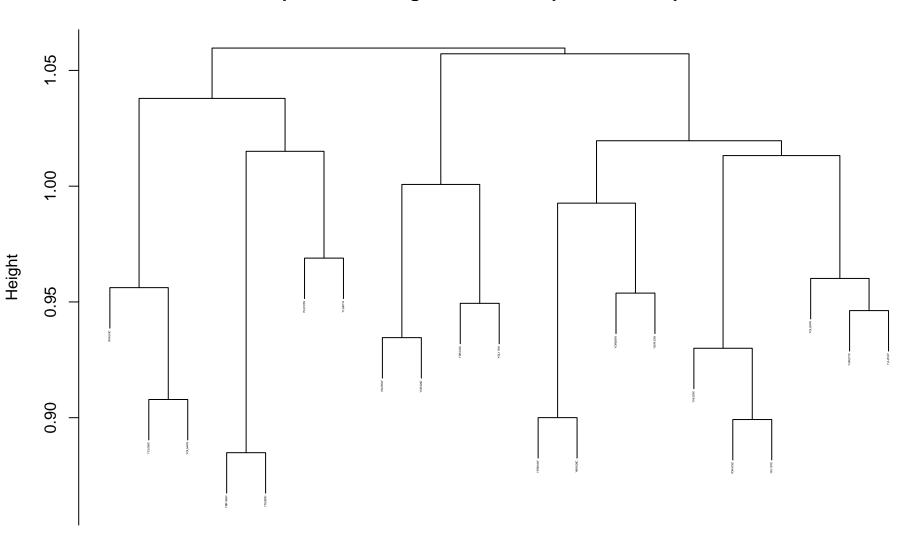
protein acylation_GO_pearson_complete



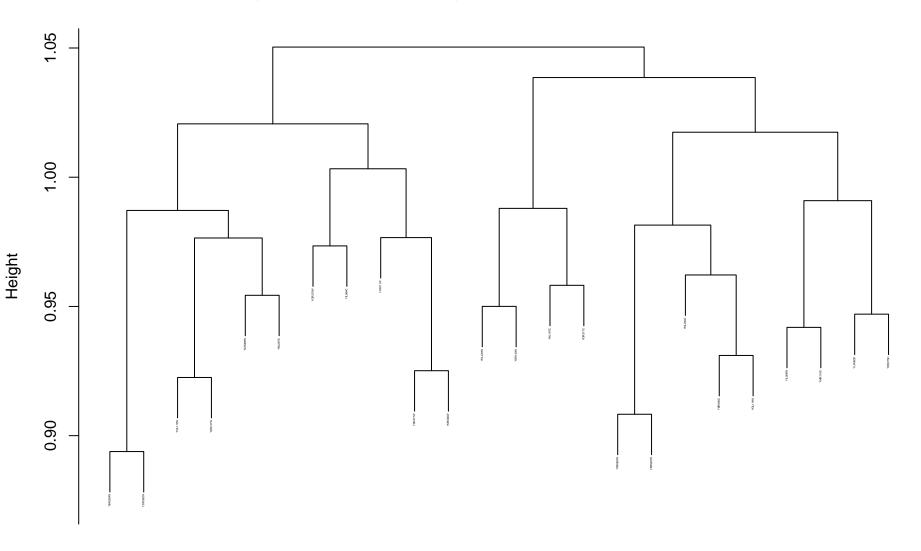
peroxisome_GO_pearson_complete



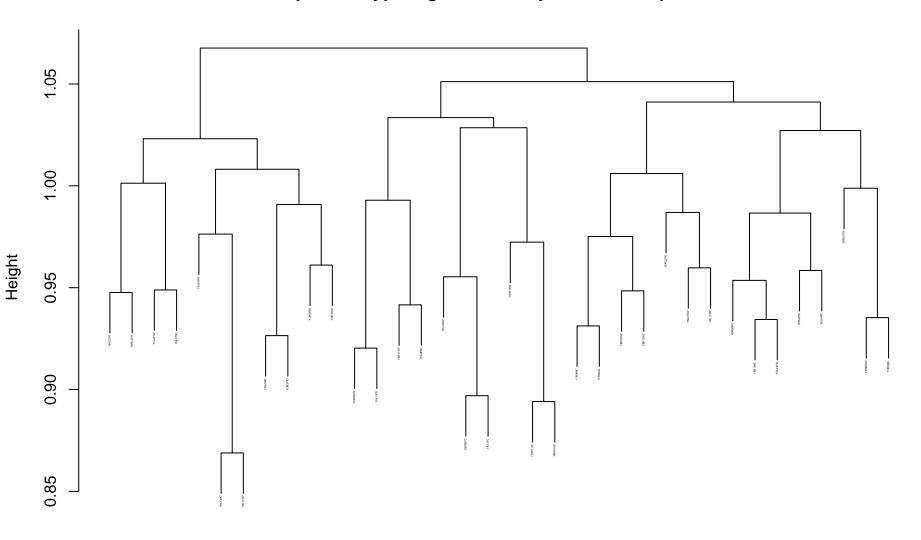
peroxisome organization_GO_pearson_complete



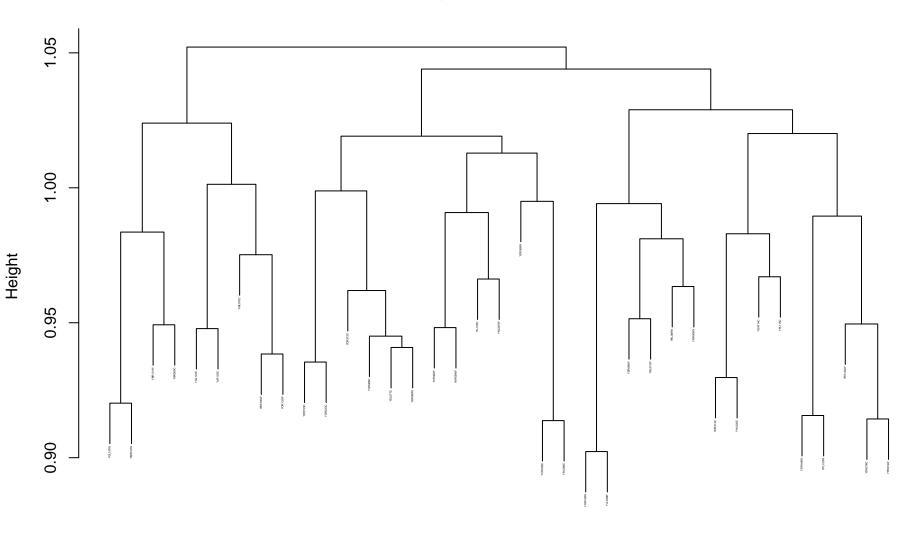
invasive growth in response to glucose limitation_GO_pearson_complete



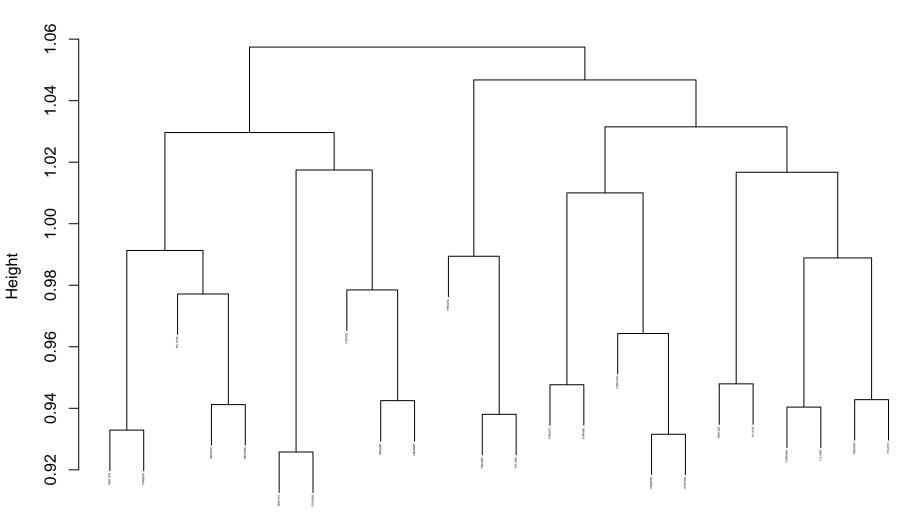
pseudohyphal growth_GO_pearson_complete



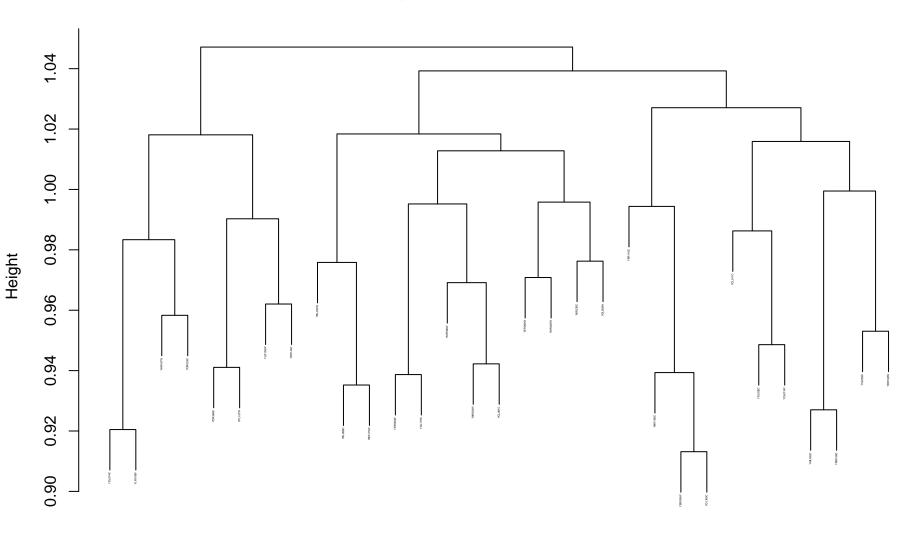
lipid binding_GO_pearson_complete



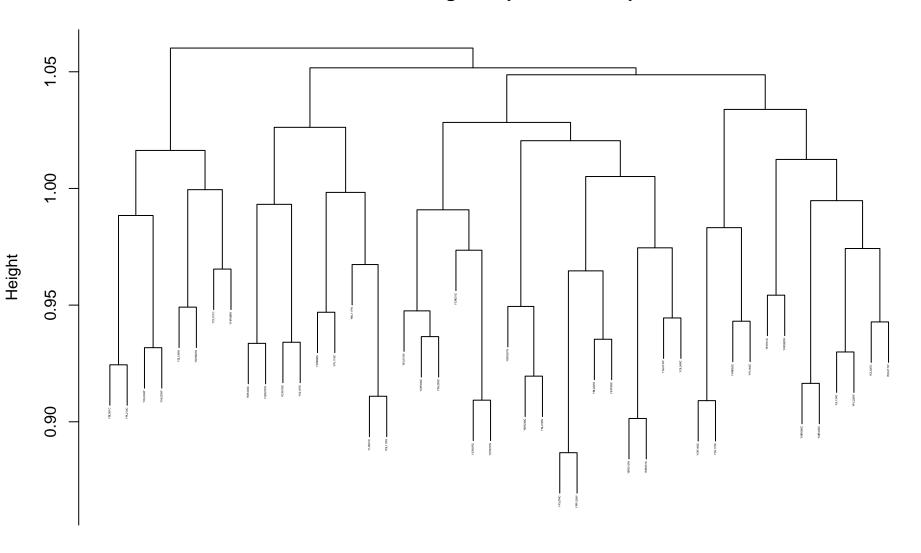
methyltransferase activity_GO_pearson_complete



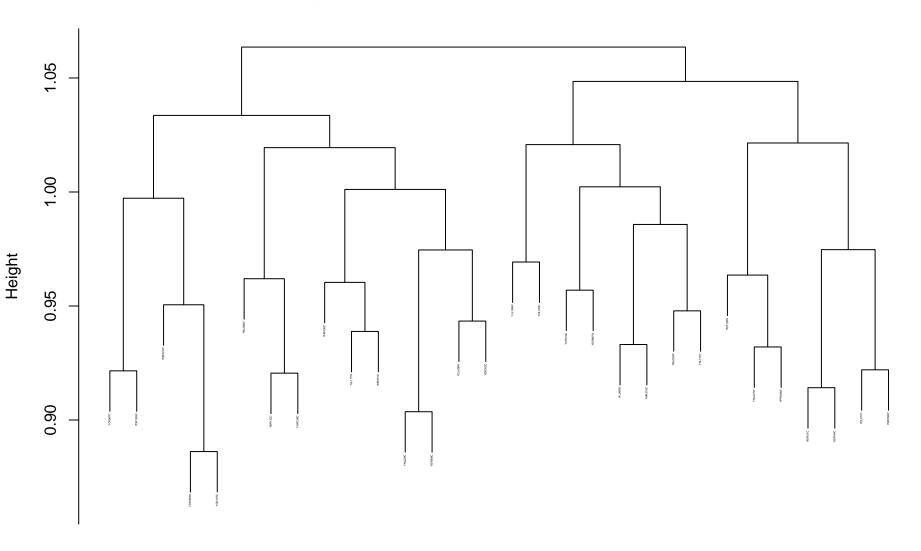
telomere organization_GO_pearson_complete



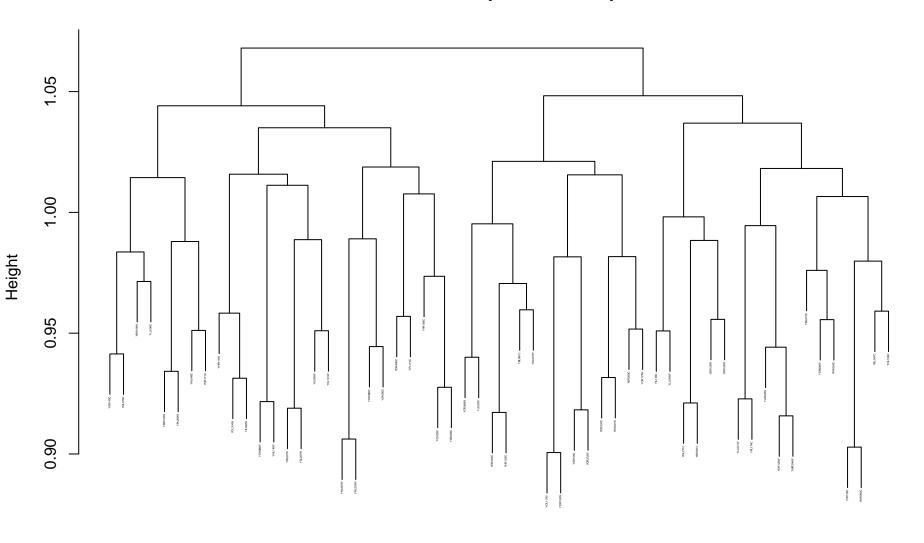
mRNA binding_GO_pearson_complete



regulation of transport_GO_pearson_complete

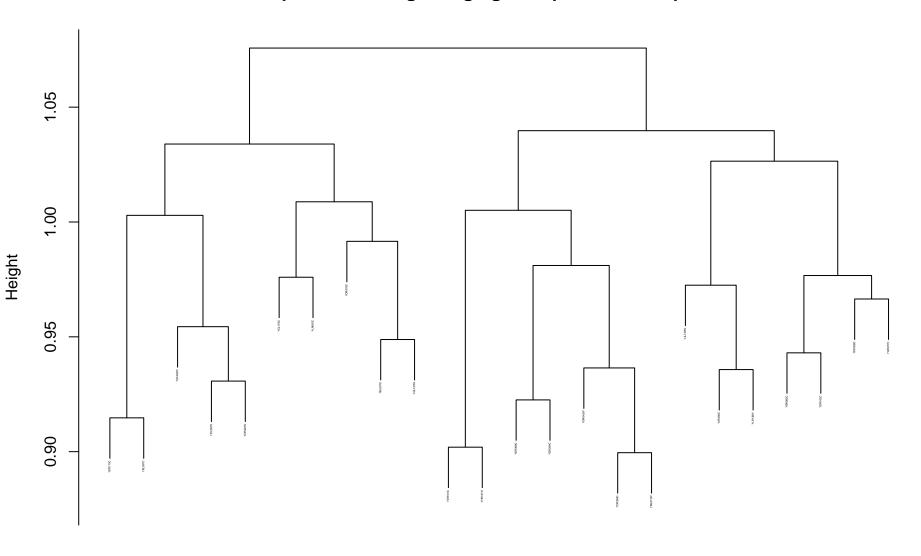


cell cortex_GO_pearson_complete

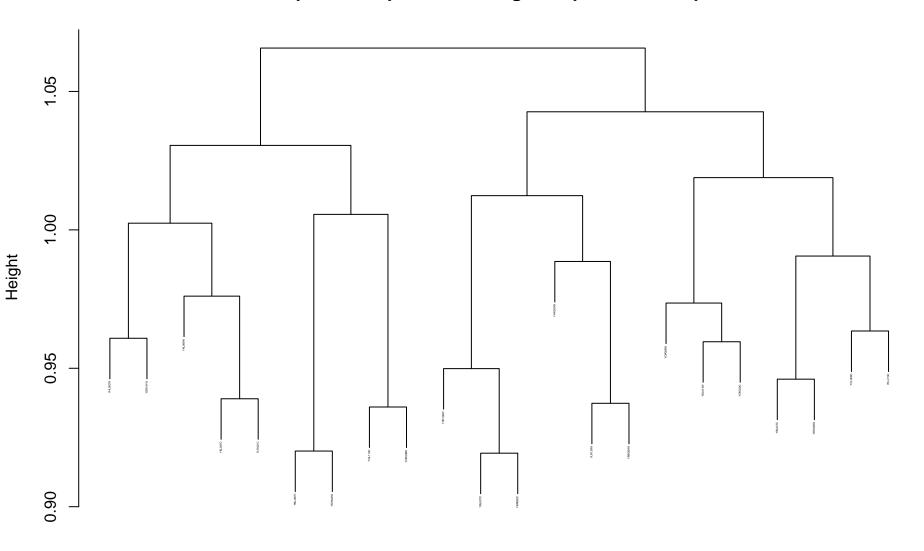


dissim hclust (*, "complete")

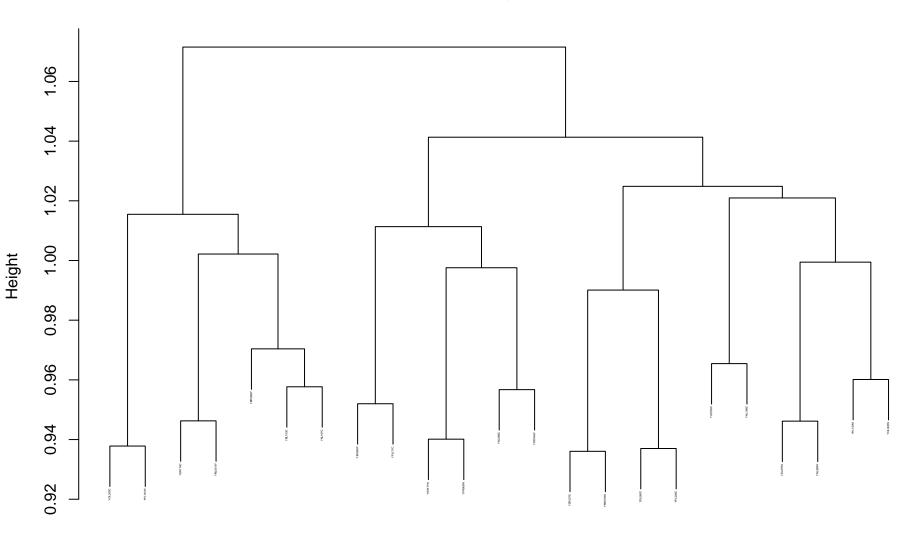
$protein\ binding,\ bridging_GO_pearson_complete$



ubiquitin-like protein binding_GO_pearson_complete

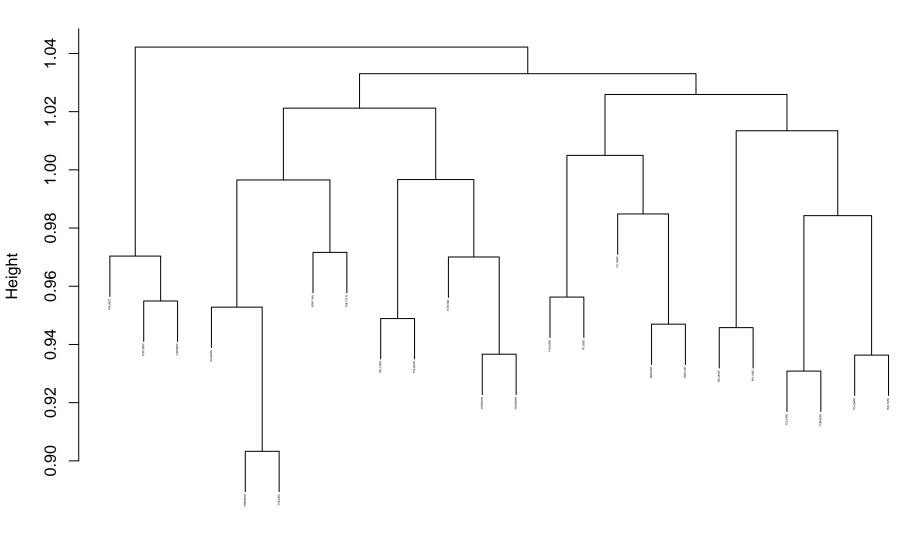


transcription factor binding_GO_pearson_complete

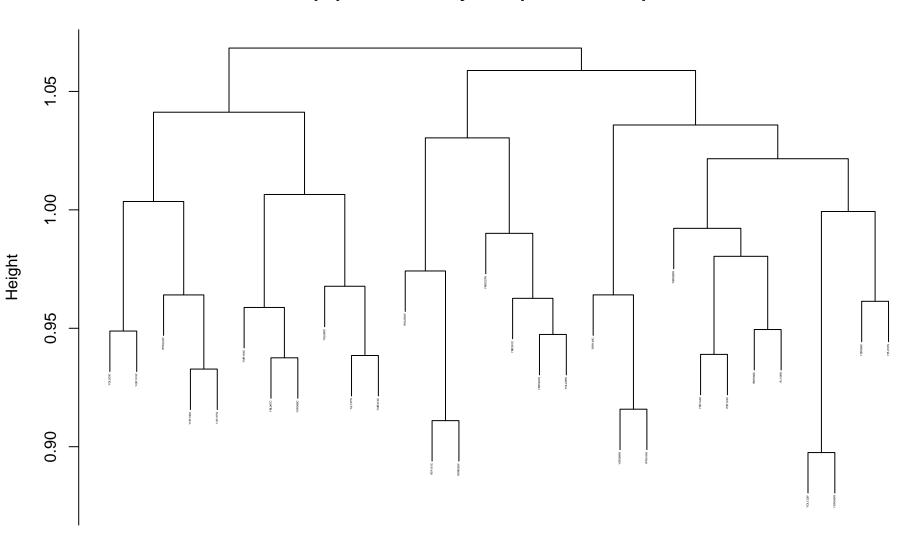


dissim hclust (*, "complete")

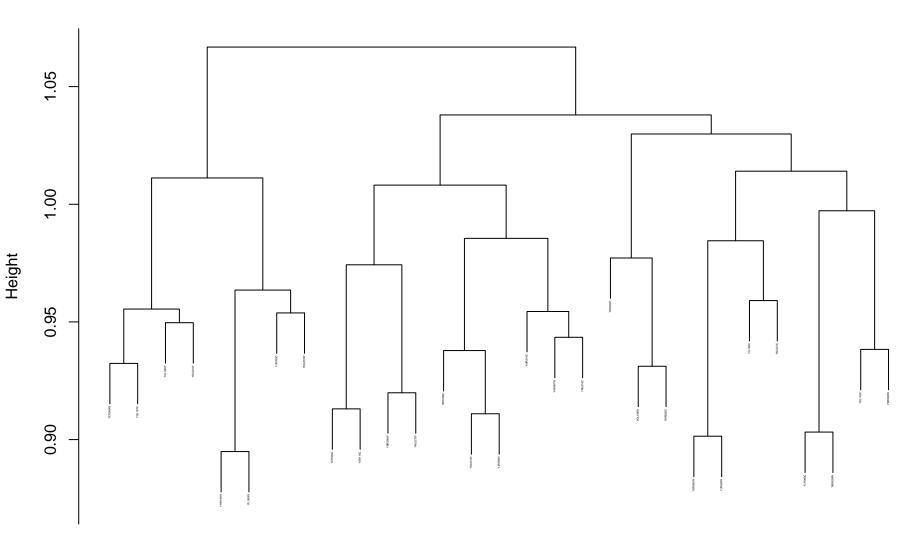
transcription from RNA polymerase I promoter_GO_pearson_complete



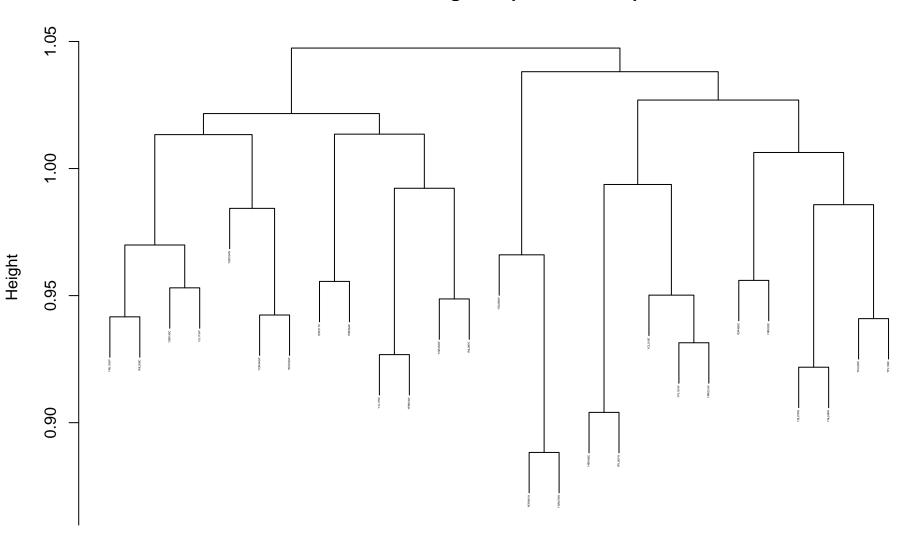
peptidase activity_GO_pearson_complete



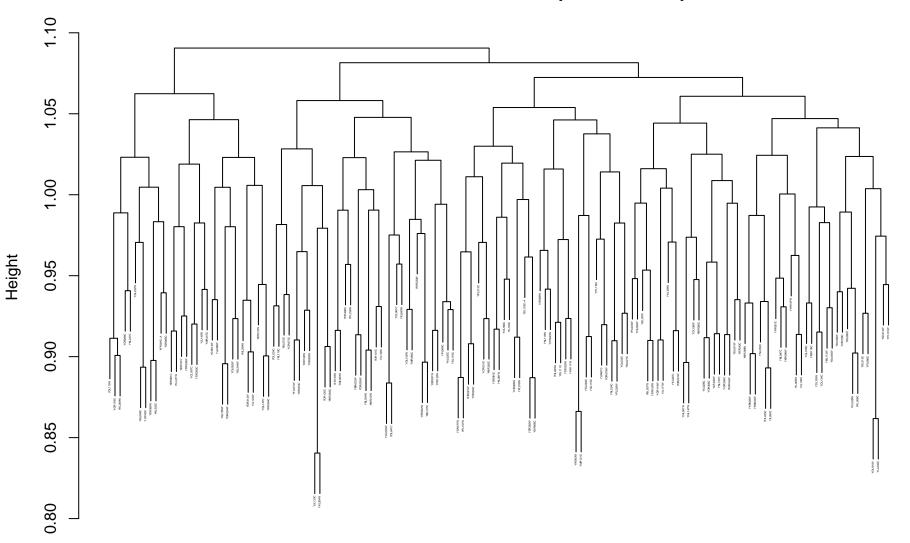
cellular ion homeostasis_GO_pearson_complete



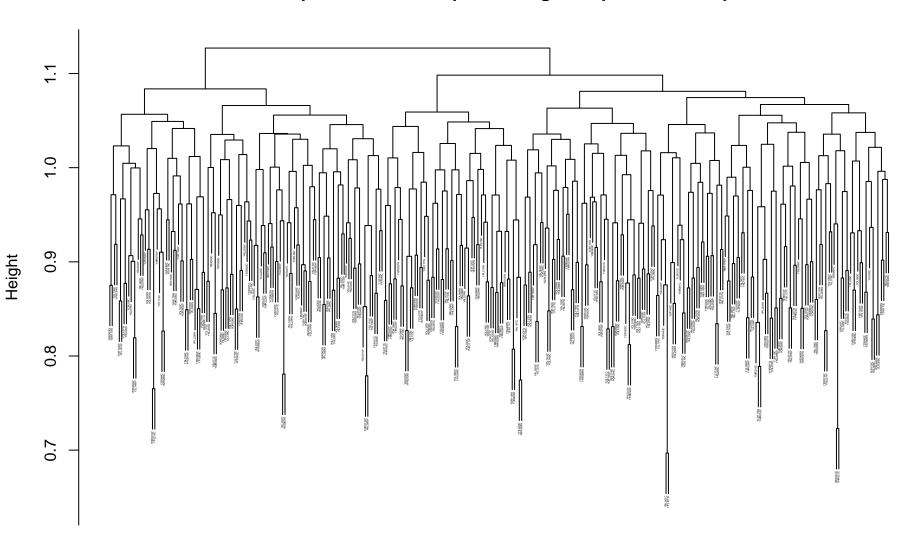
histone binding_GO_pearson_complete



ribosomes and translation_GO_pearson_complete

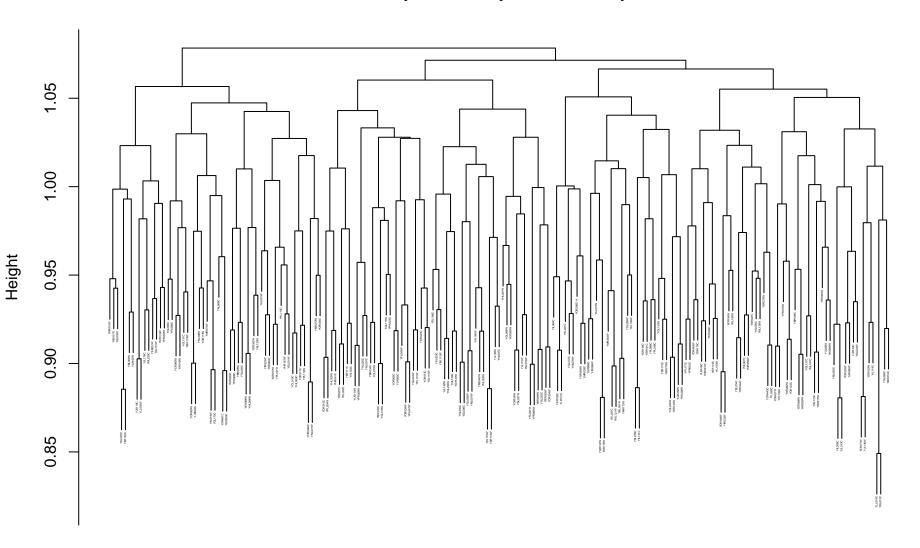


transcription and mRNA processing_GO_pearson_complete

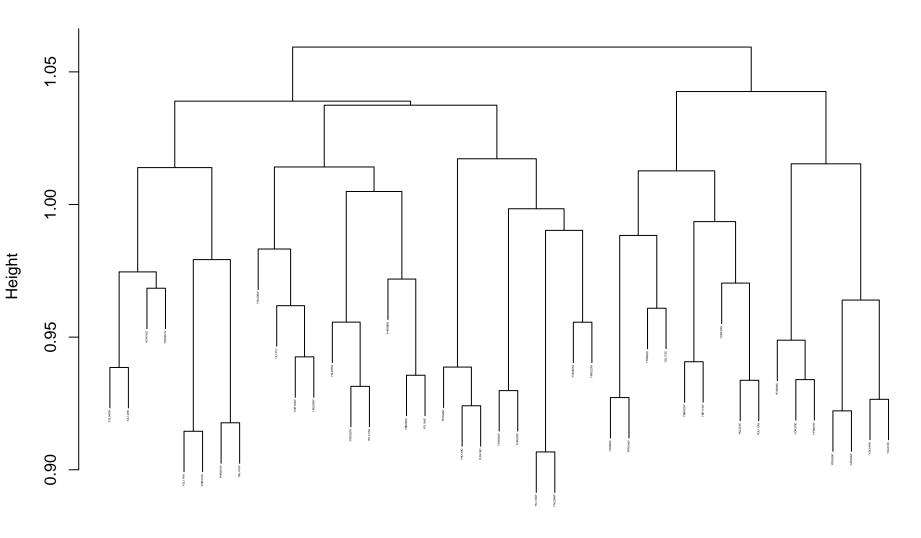


dissim hclust (*, "complete")

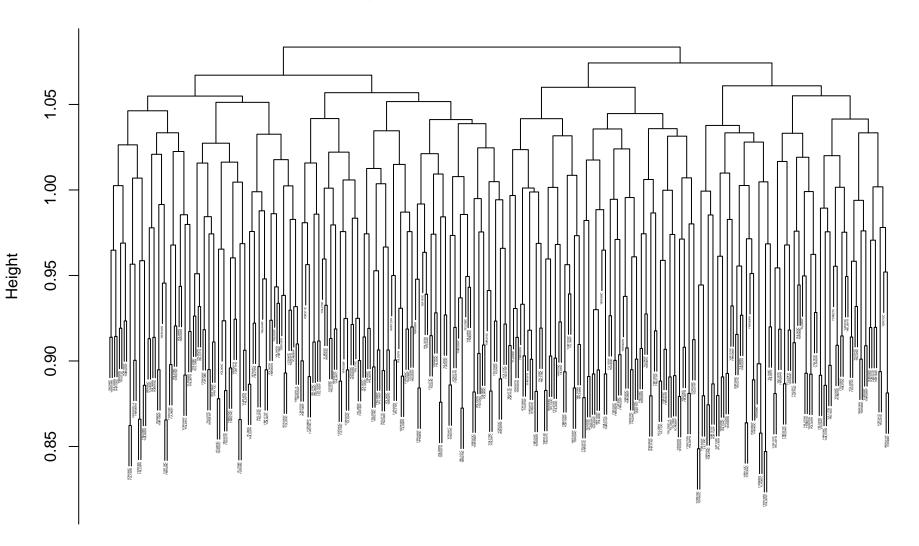
transcription_GO_pearson_complete



RNA processing_GO_pearson_complete

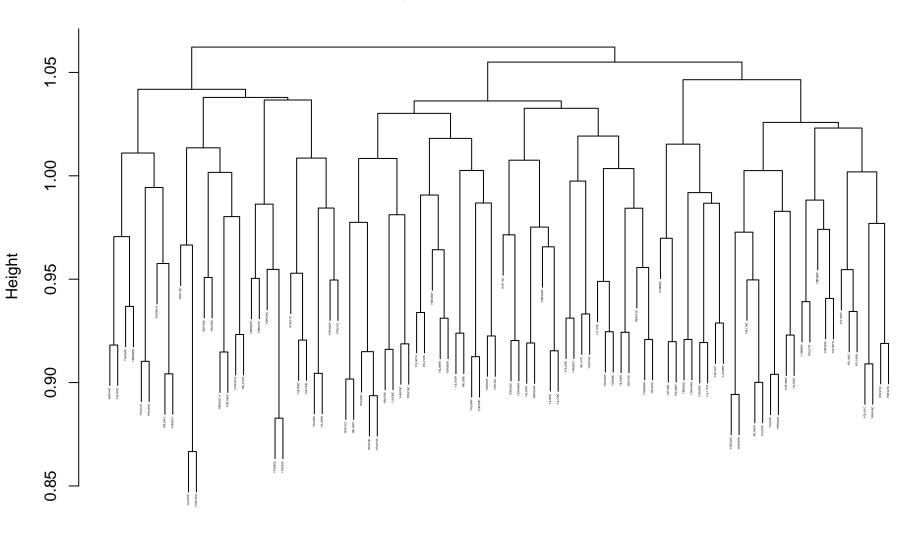


Golgi and ER_GO_pearson_complete

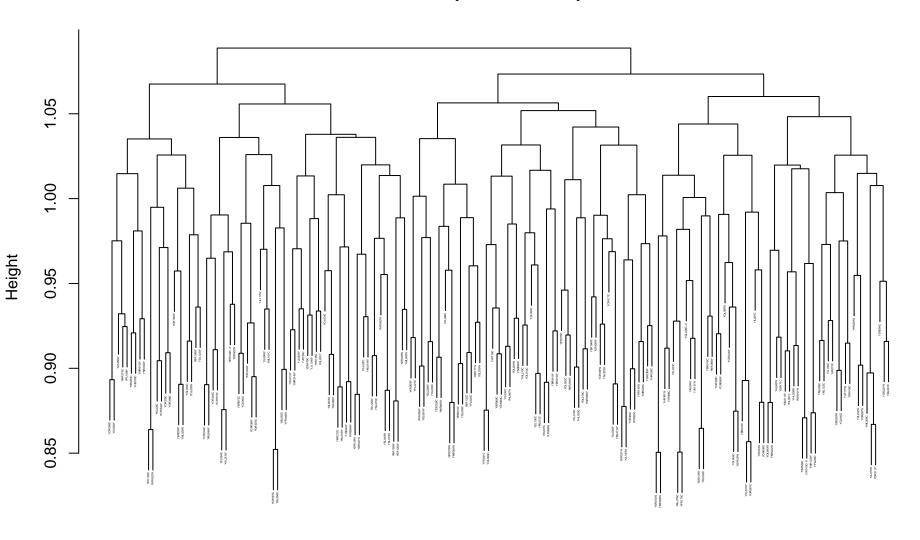


dissim hclust (*, "complete")

Golgi_GO_pearson_complete

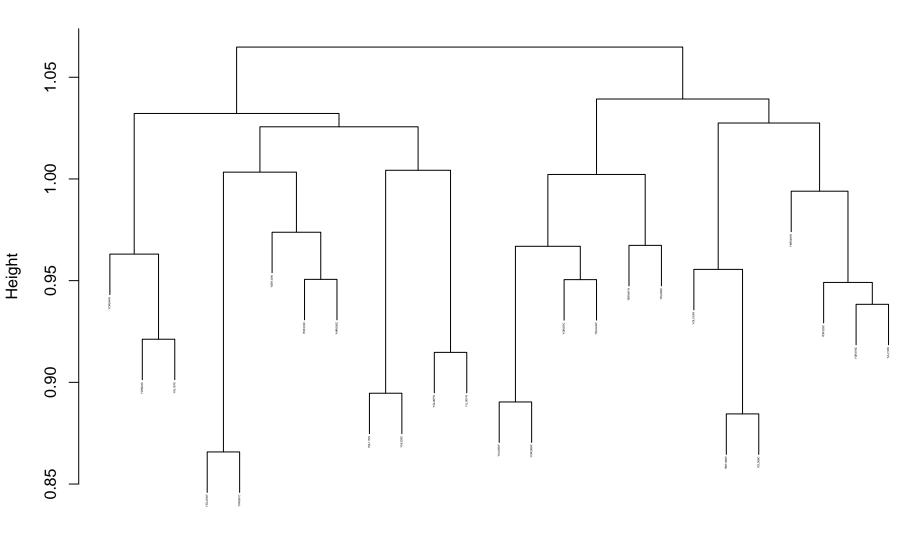


ER_GO_pearson_complete

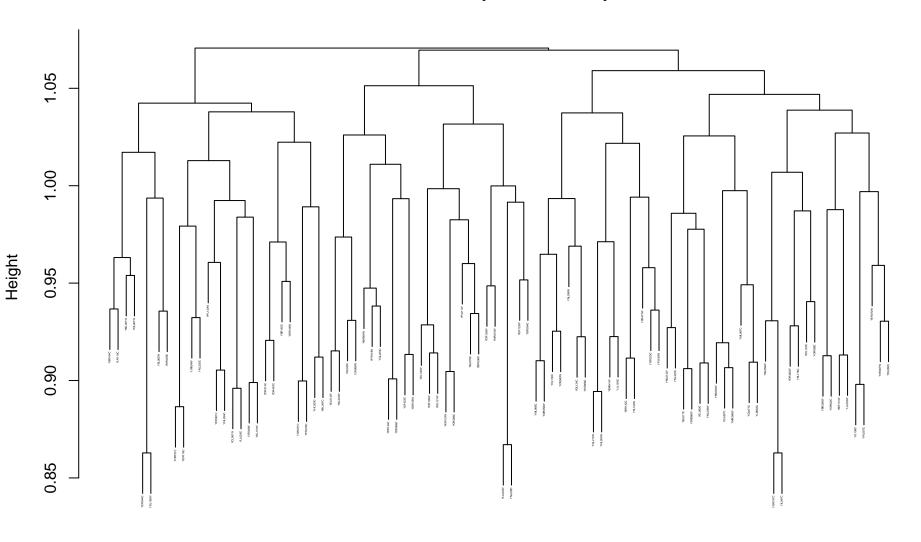


dissim hclust (*, "complete")

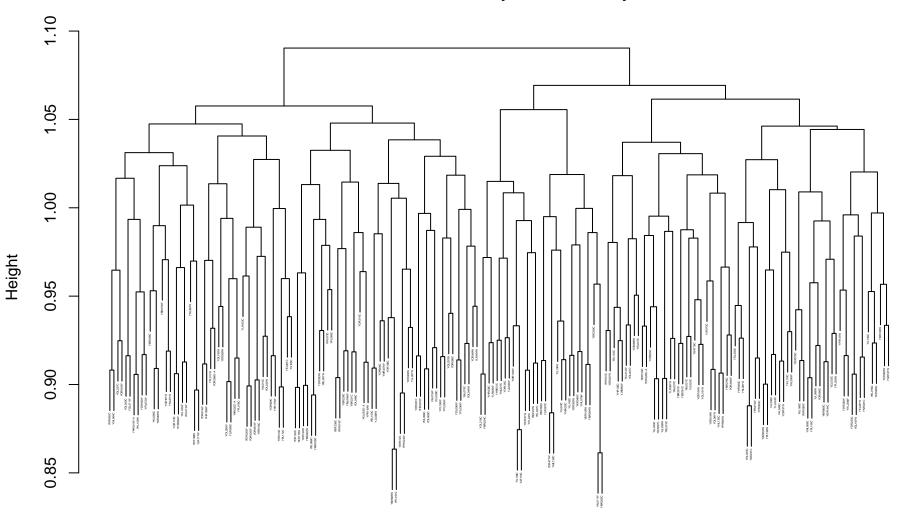
peroxisomes_GO_pearson_complete



vacuoles_GO_pearson_complete

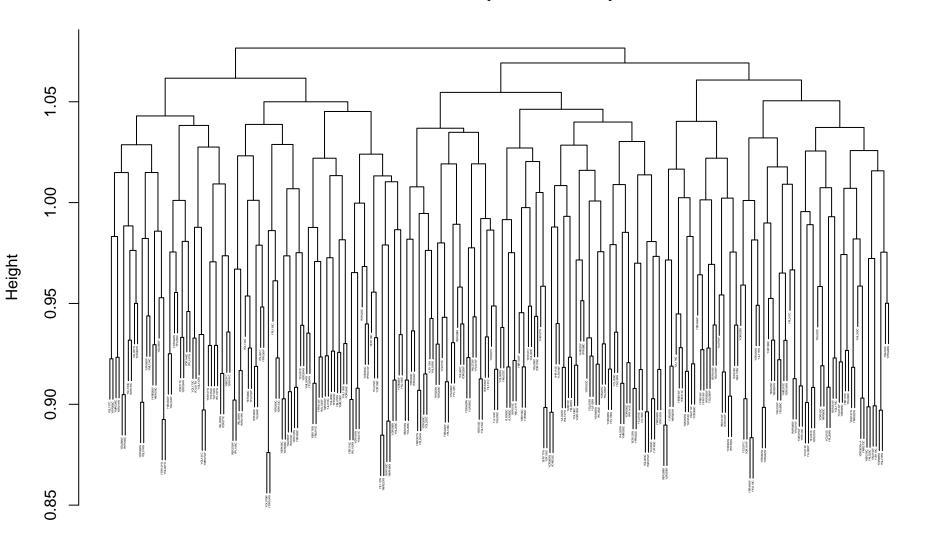


mitochondria_GO_pearson_complete



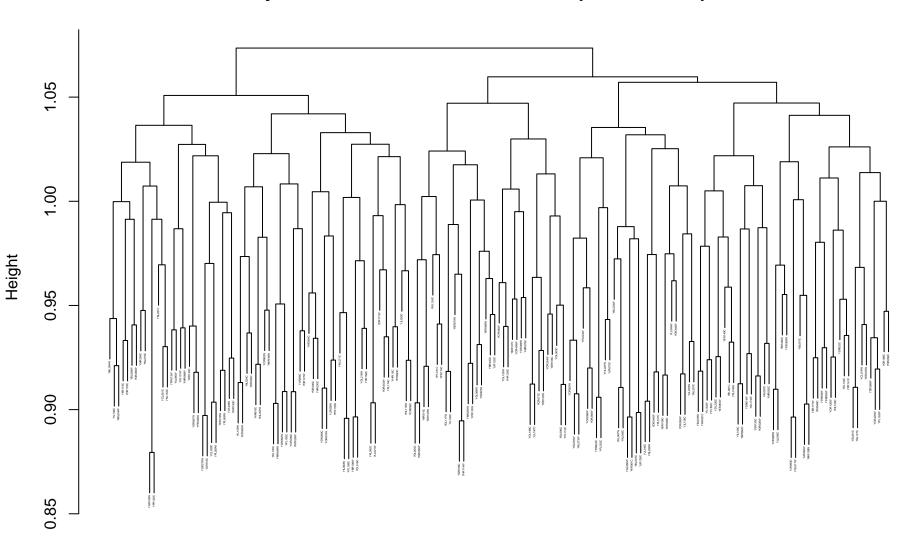
dissim hclust (*, "complete")

chromatin_GO_pearson_complete

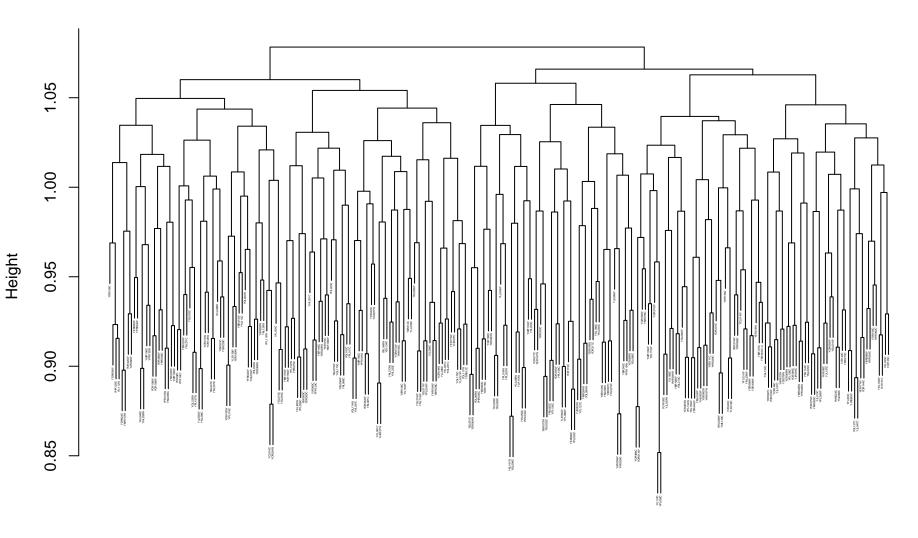


dissim hclust (*, "complete")

cytoskeleton and microtubules_GO_pearson_complete

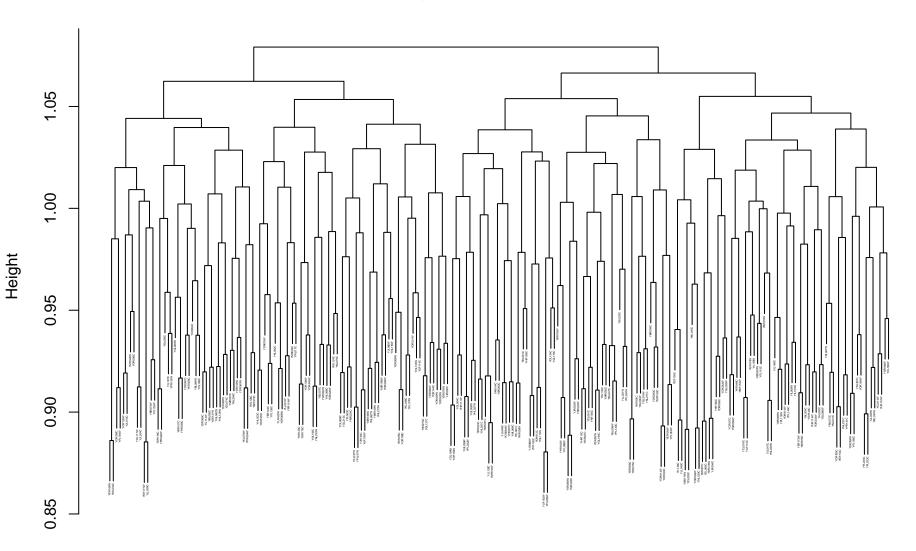


cell cycle_GO_pearson_complete



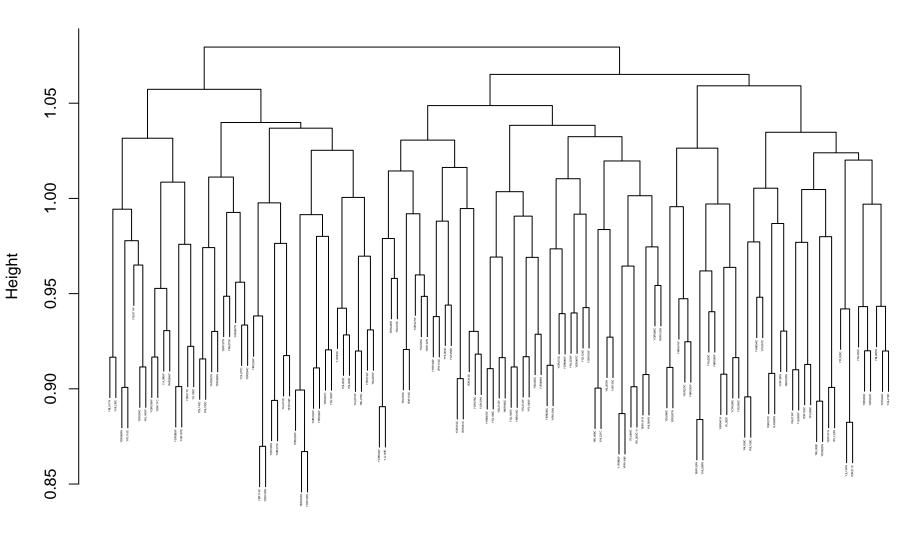
dissim hclust (*, "complete")

$budding_GO_pearson_complete$



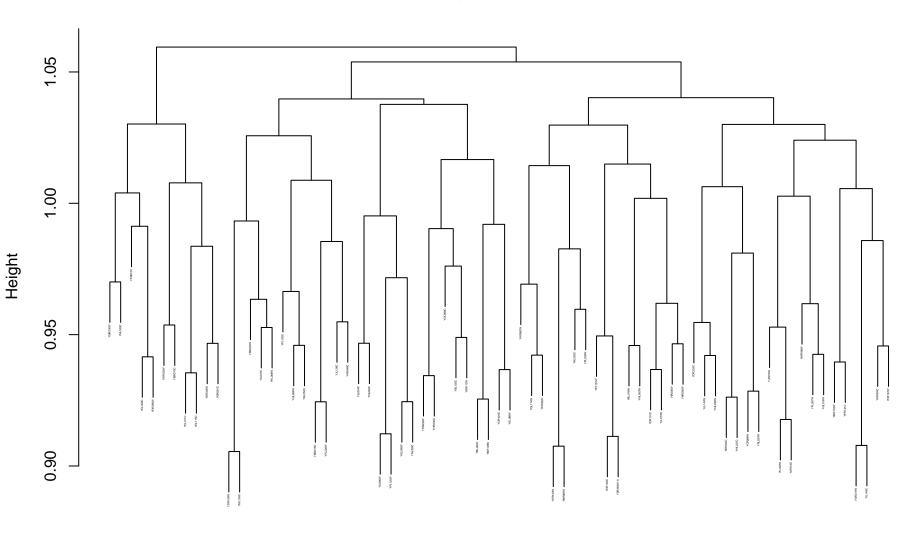
dissim hclust (*, "complete")

$lipids_GO_pearson_complete$

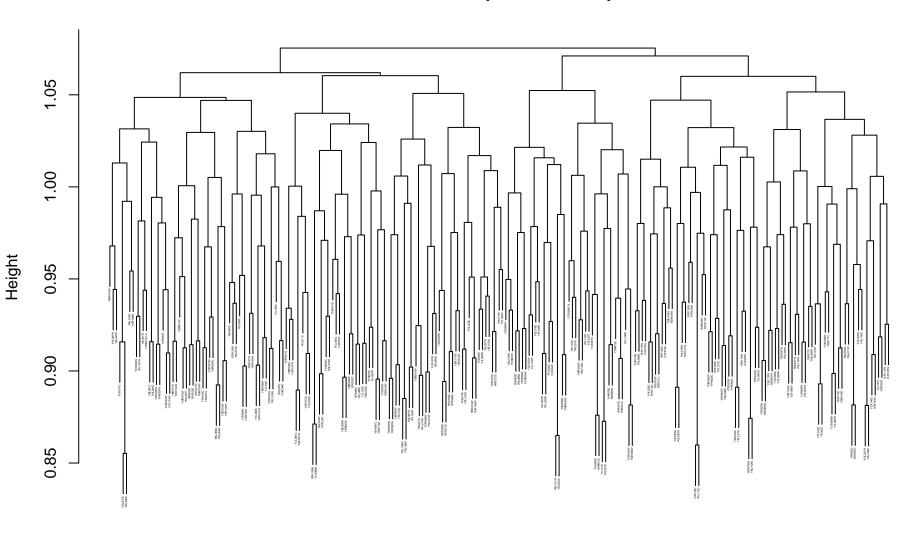


dissim hclust (*, "complete")

nuclear transport and organization_GO_pearson_complete

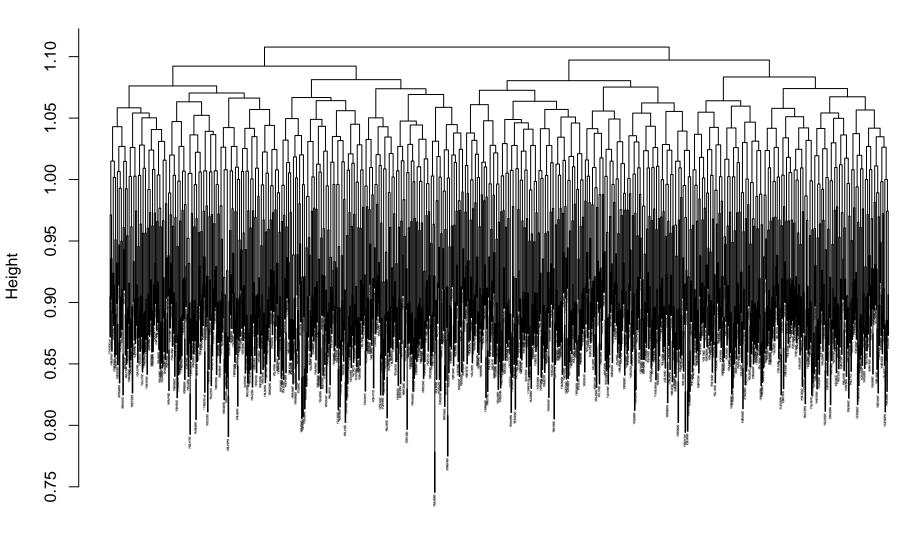


metabolic_GO_pearson_complete



dissim hclust (*, "complete")

whole_library_pearson_complete



dissim hclust (*, "complete")