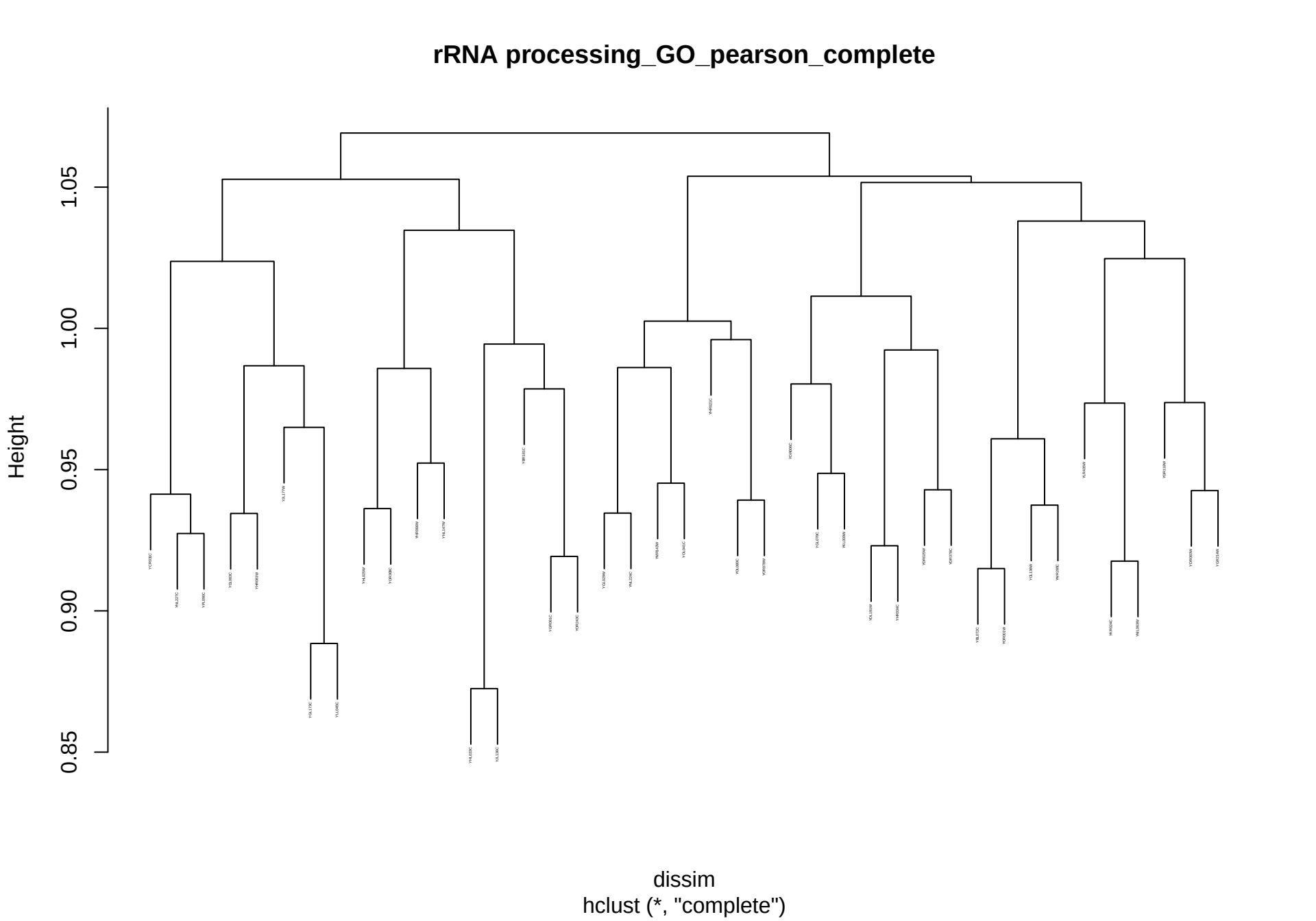
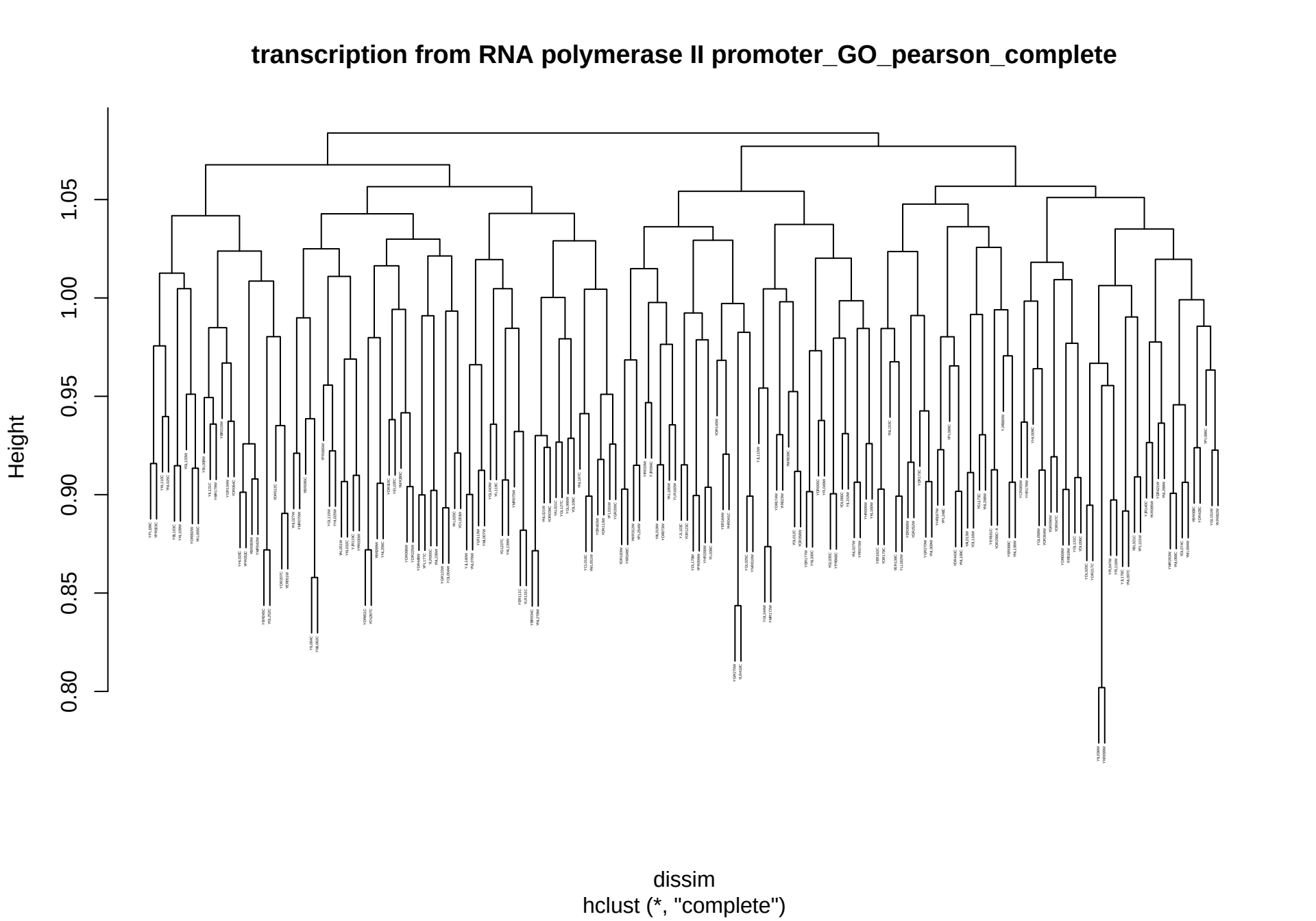
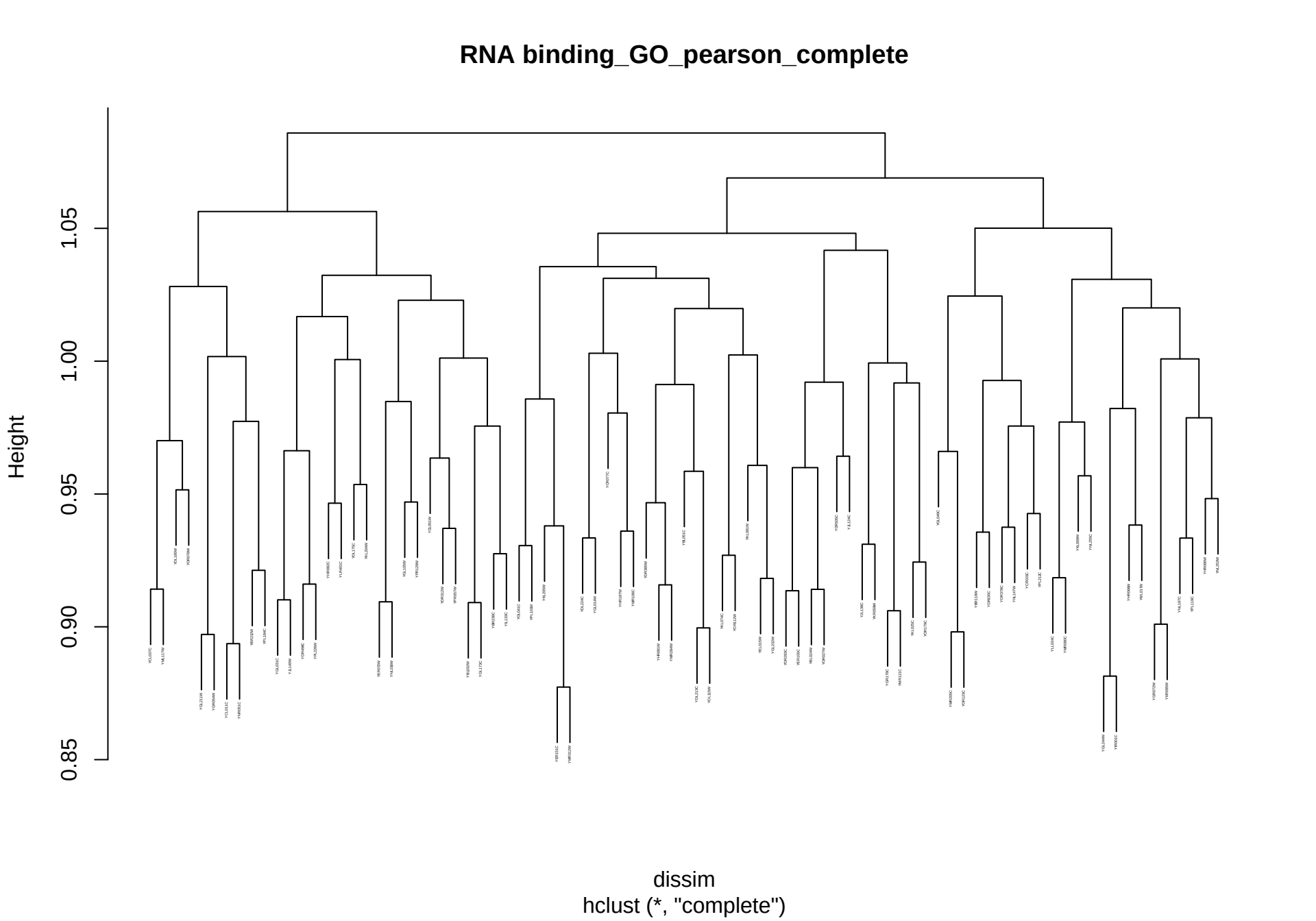
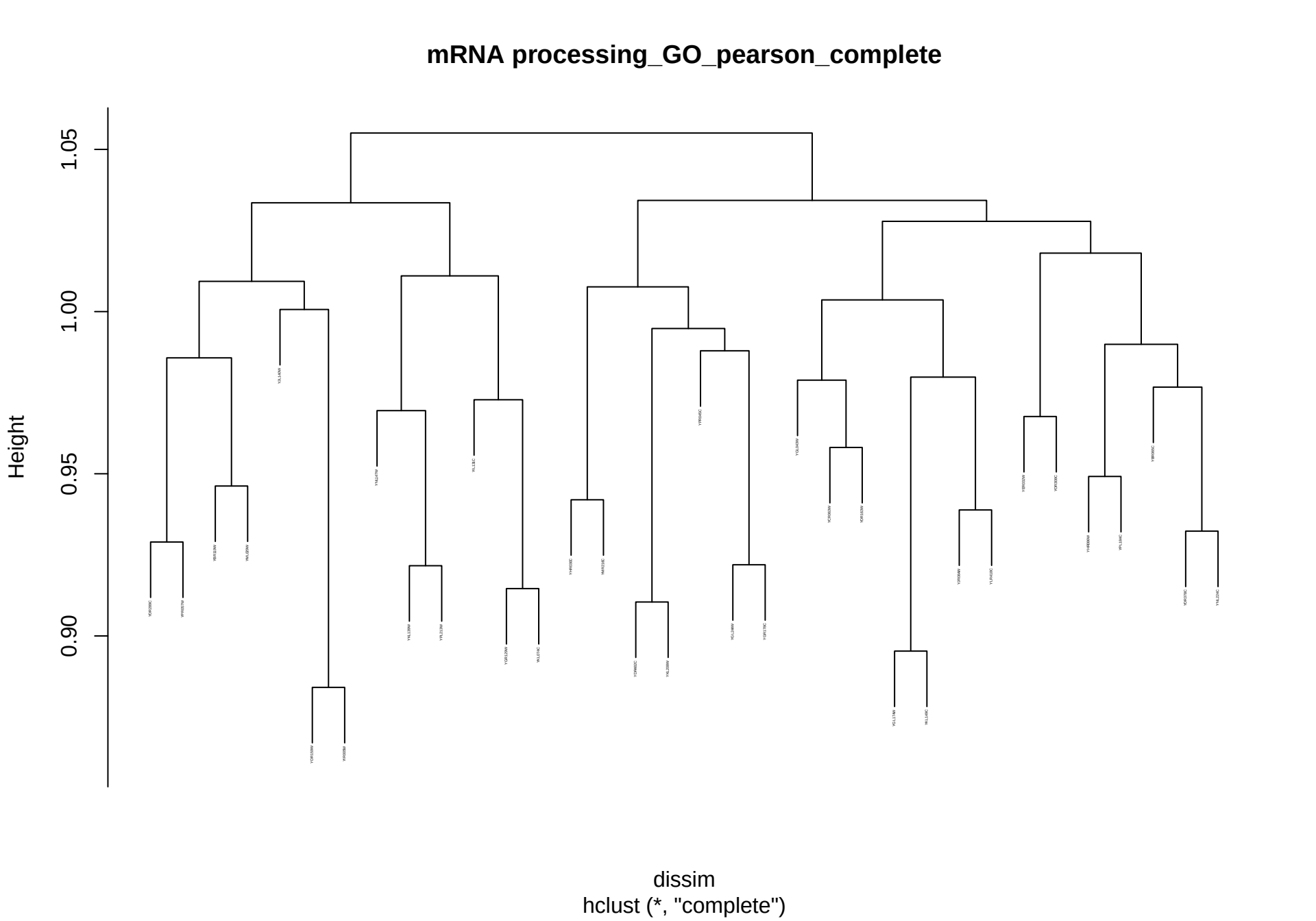
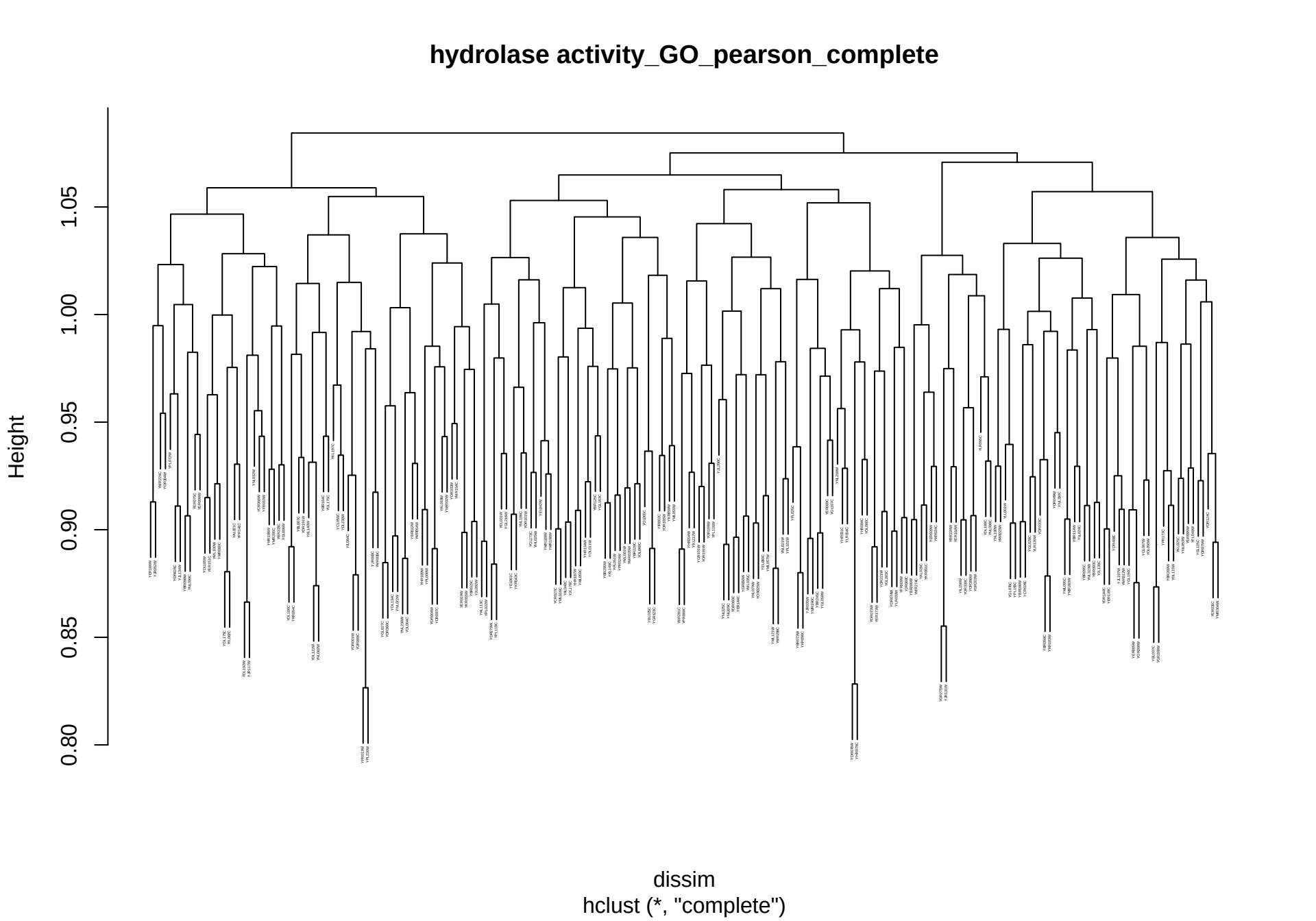
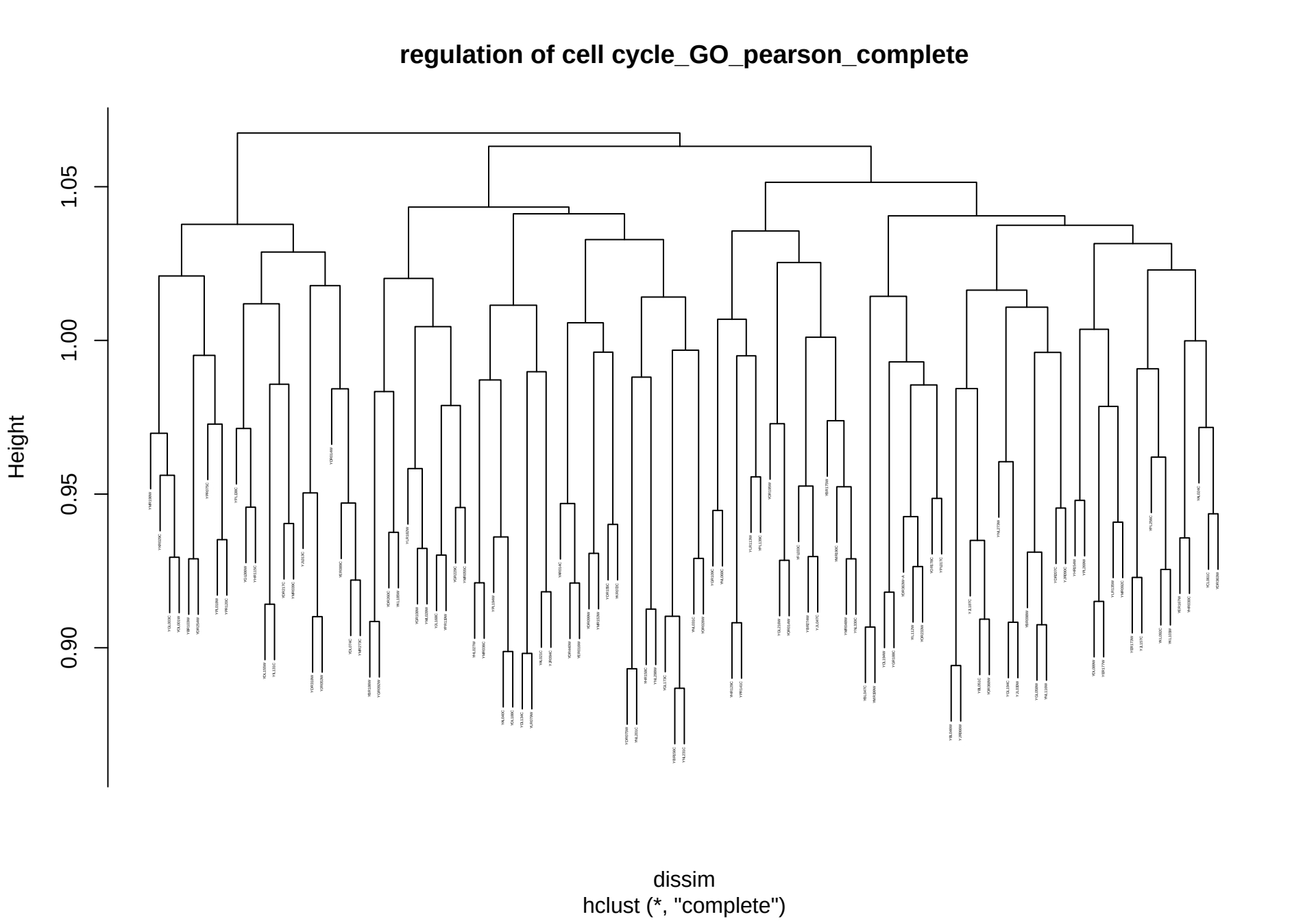

rRNA processing_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

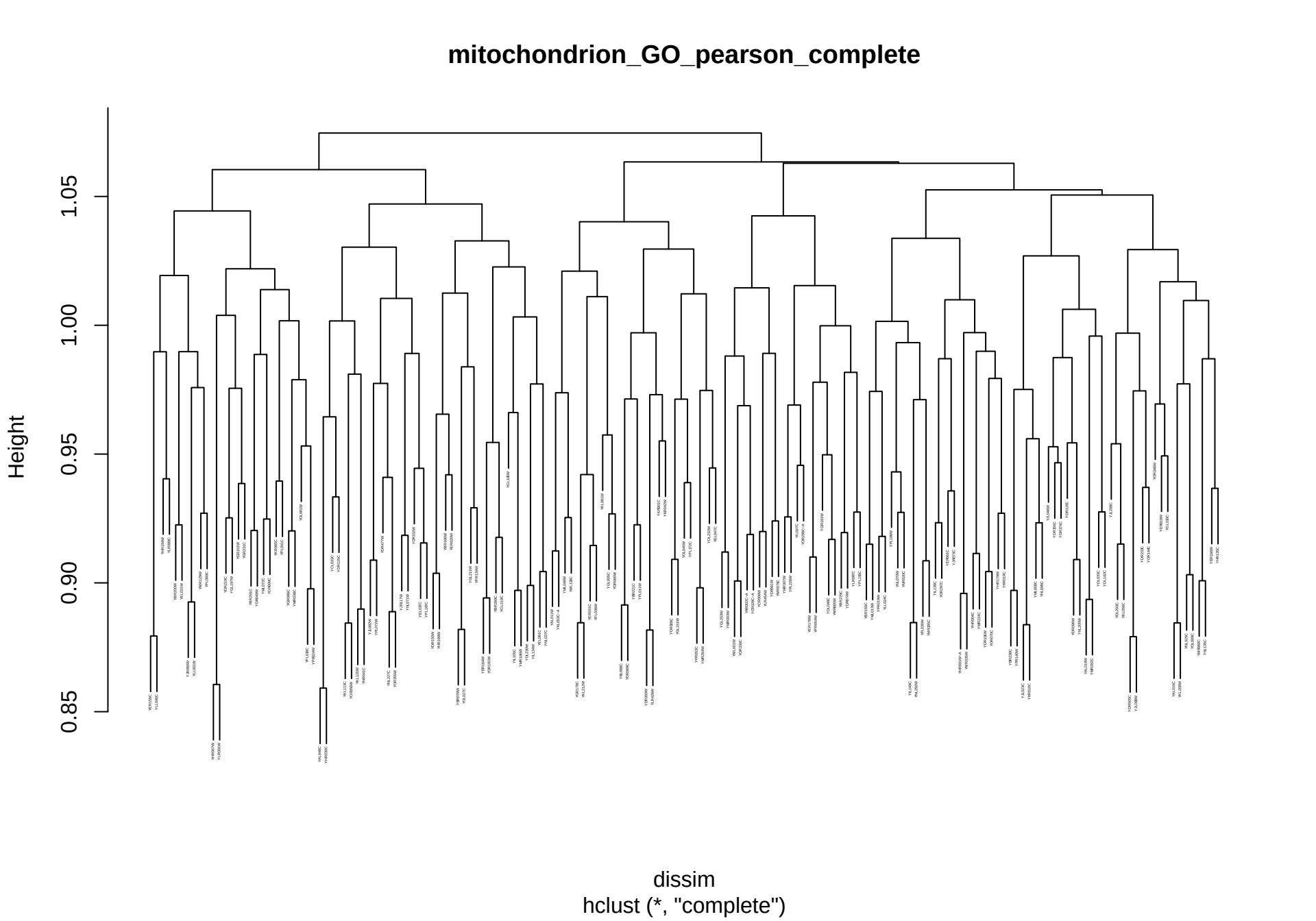

transcription from RNA polymerase II promoter_GO_pearson_complete
Height
0.80
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

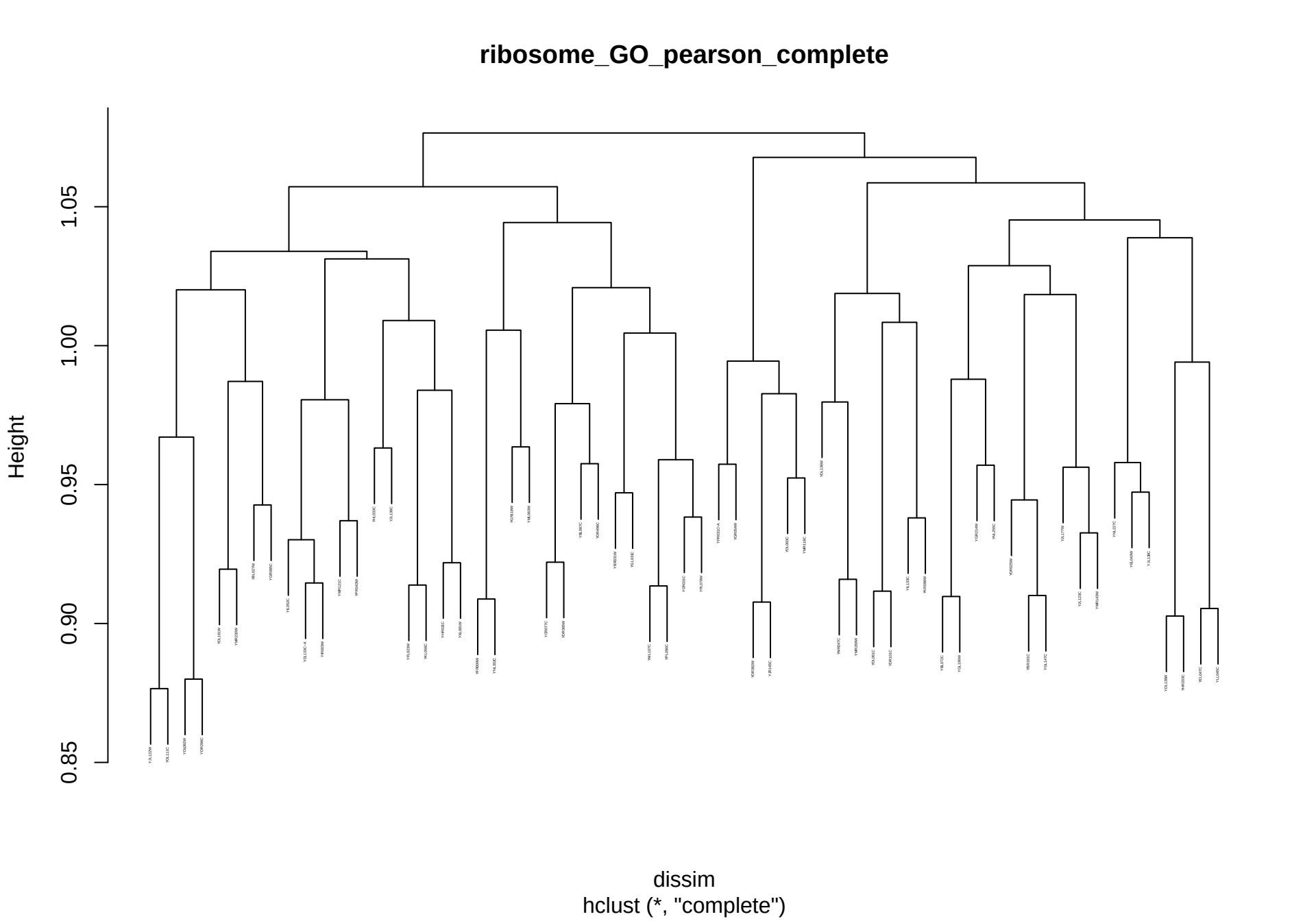

RNA binding_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

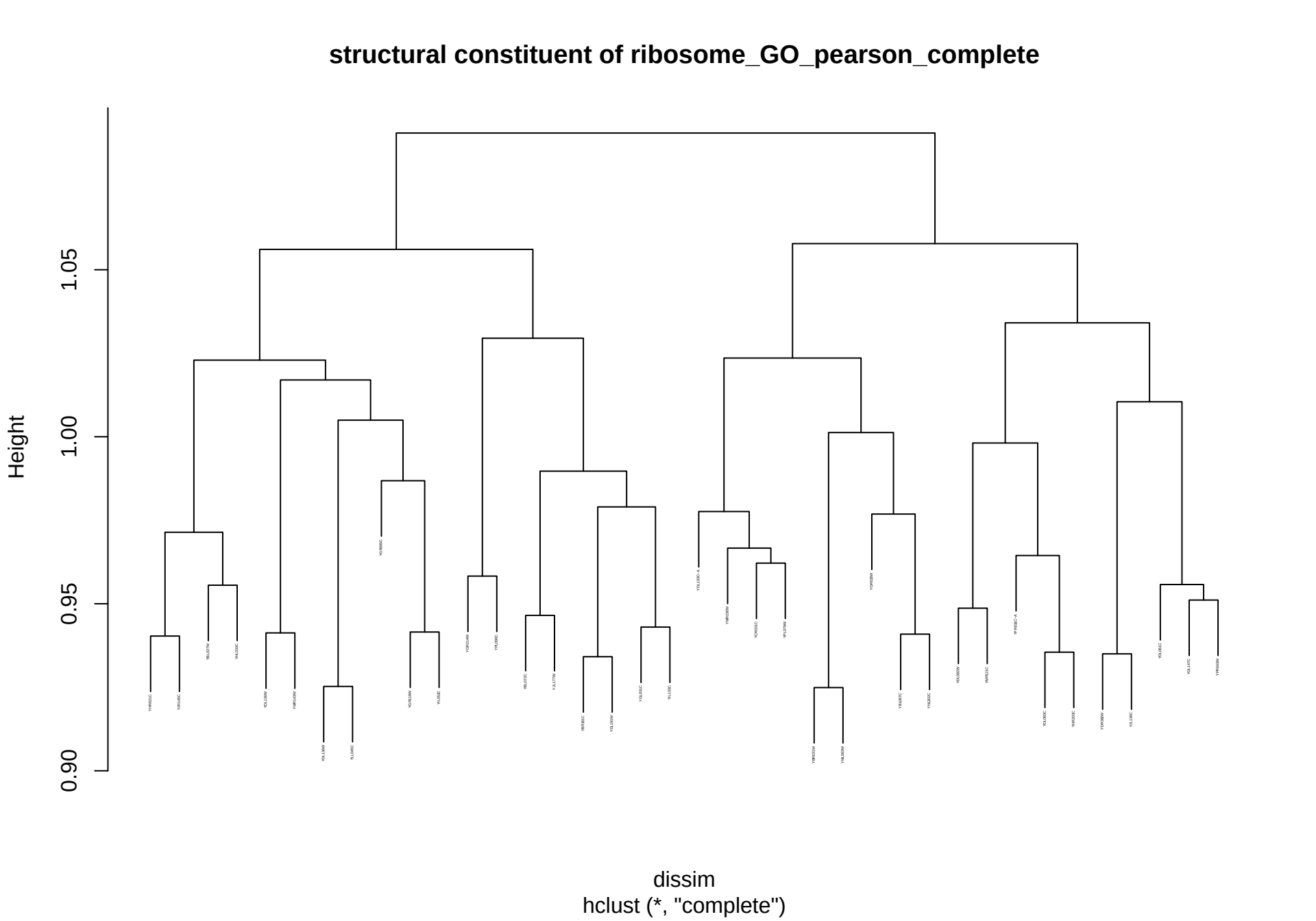

mRNA processing_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

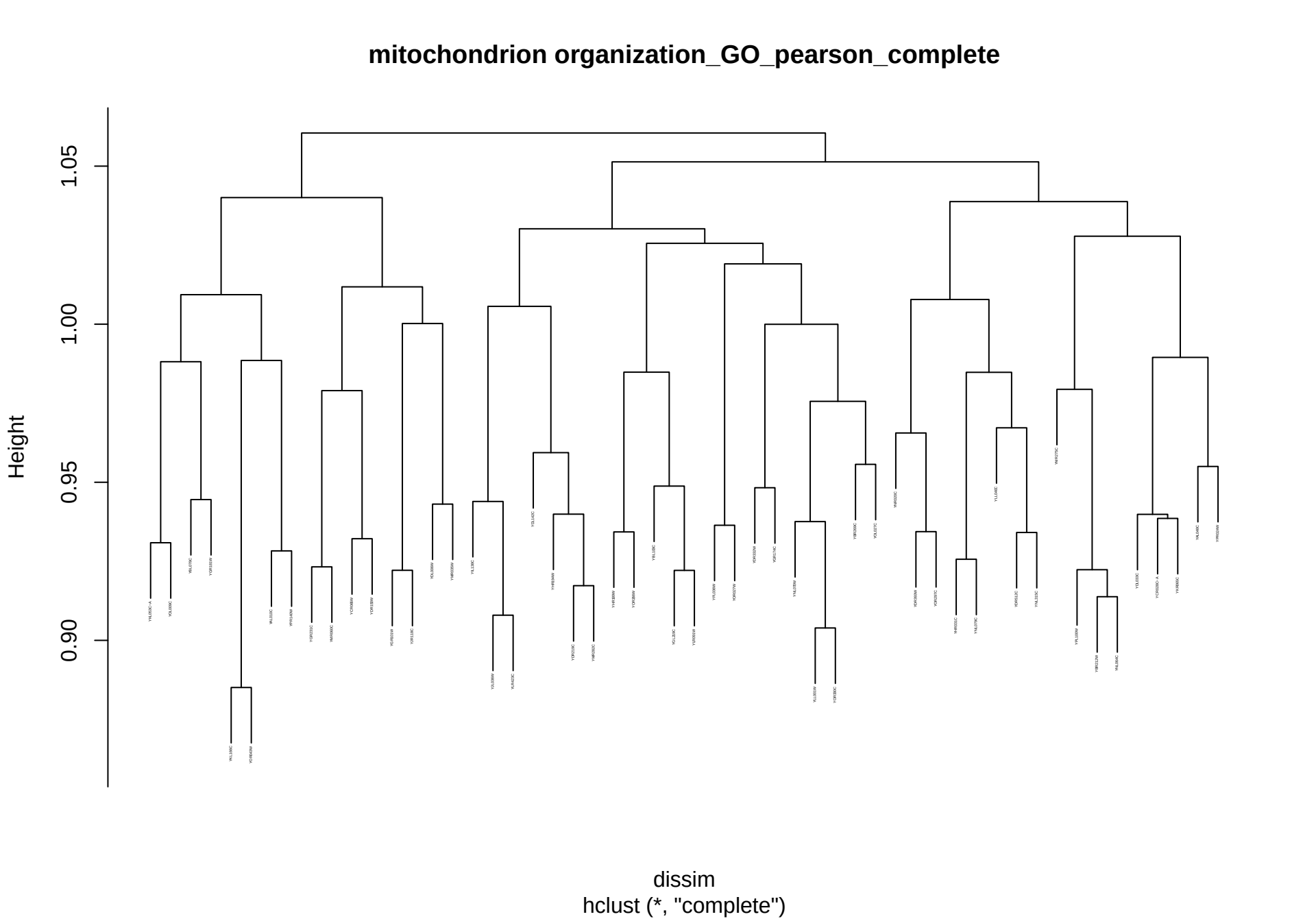

hydrolase activity_GO_pearson_complete
Height
0.80
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

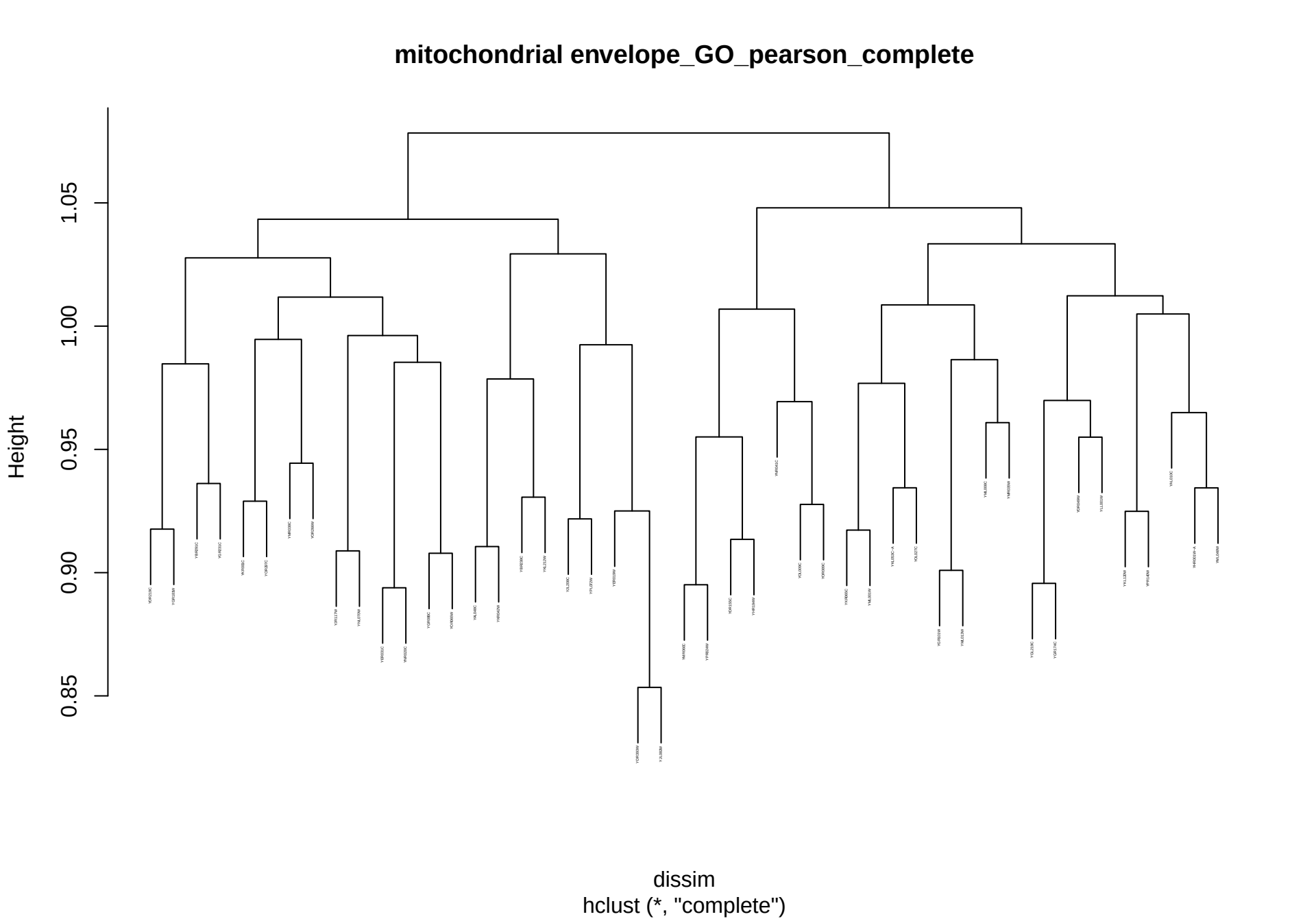

regulation of cell cycle_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

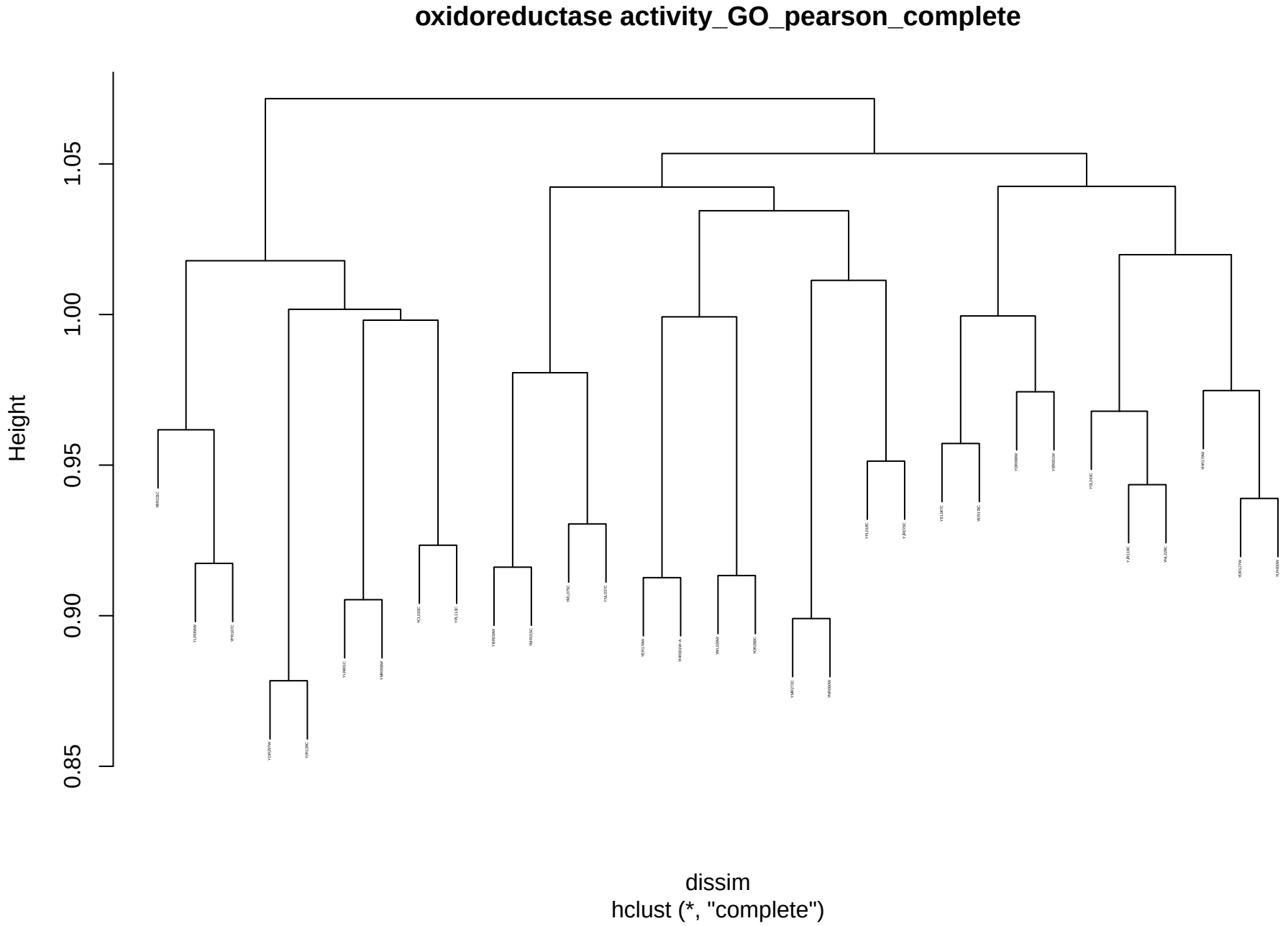

mitochondrion_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")


ribosome_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

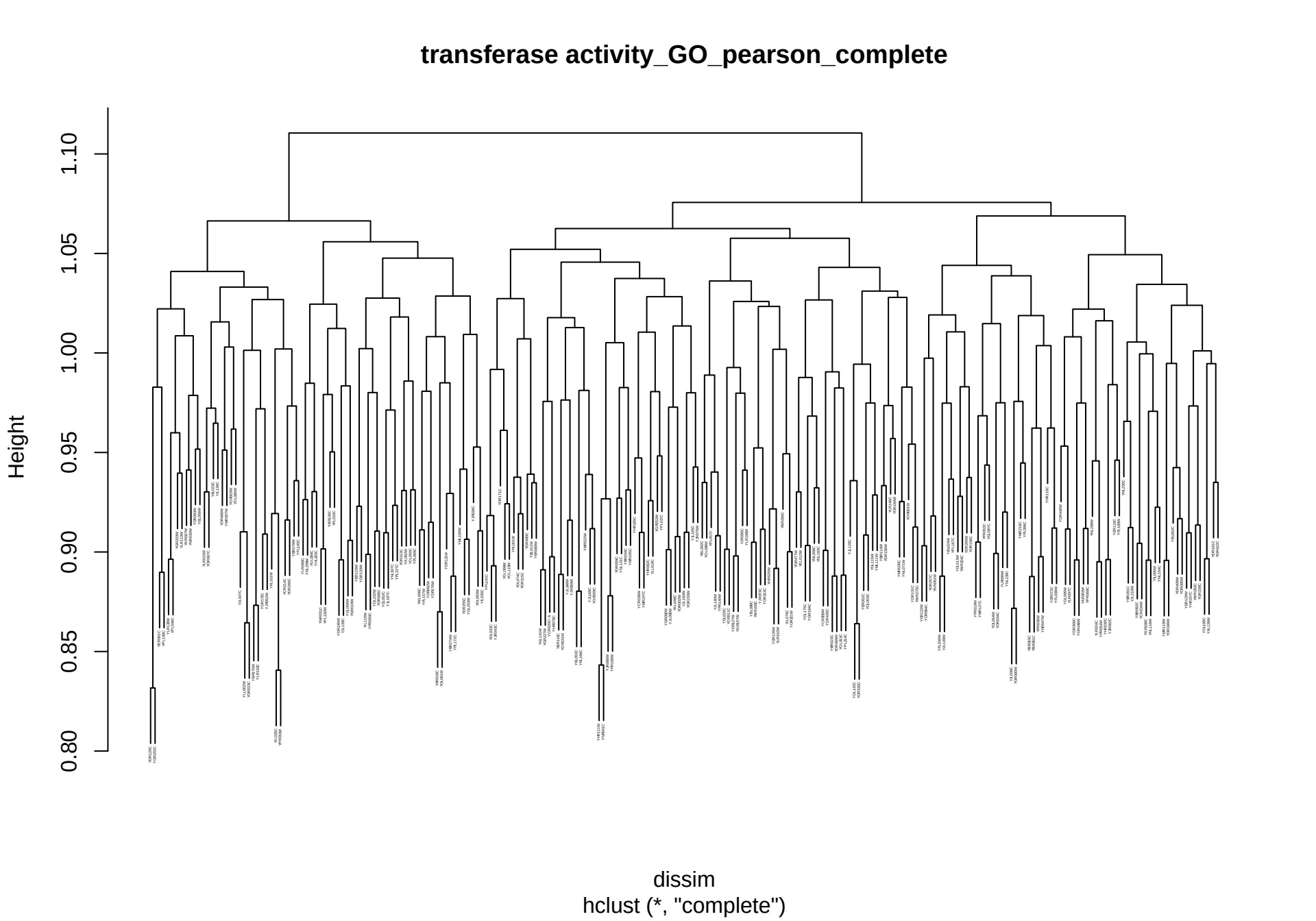

structural constituent of ribosome_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

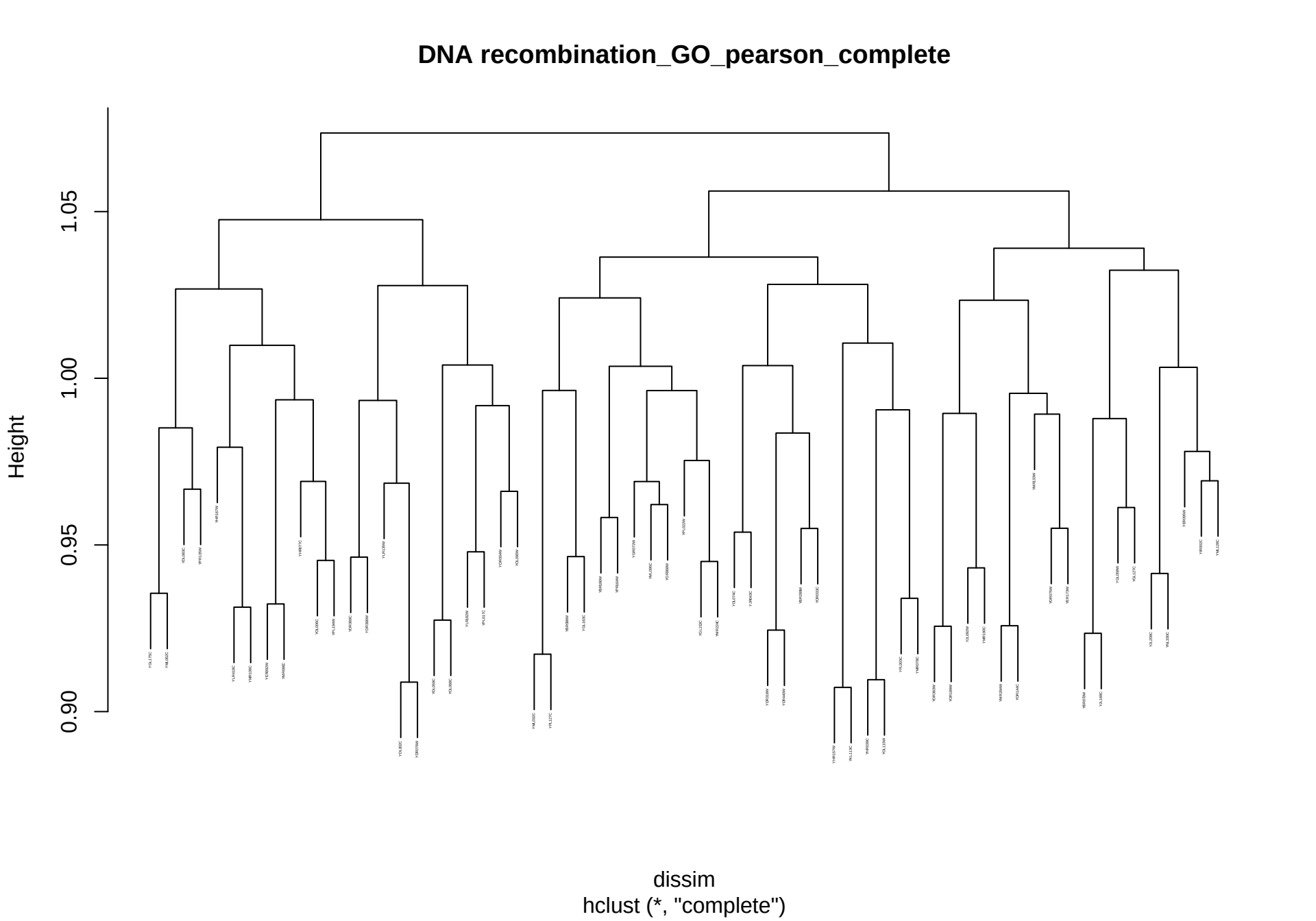

mitochondrion organization_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

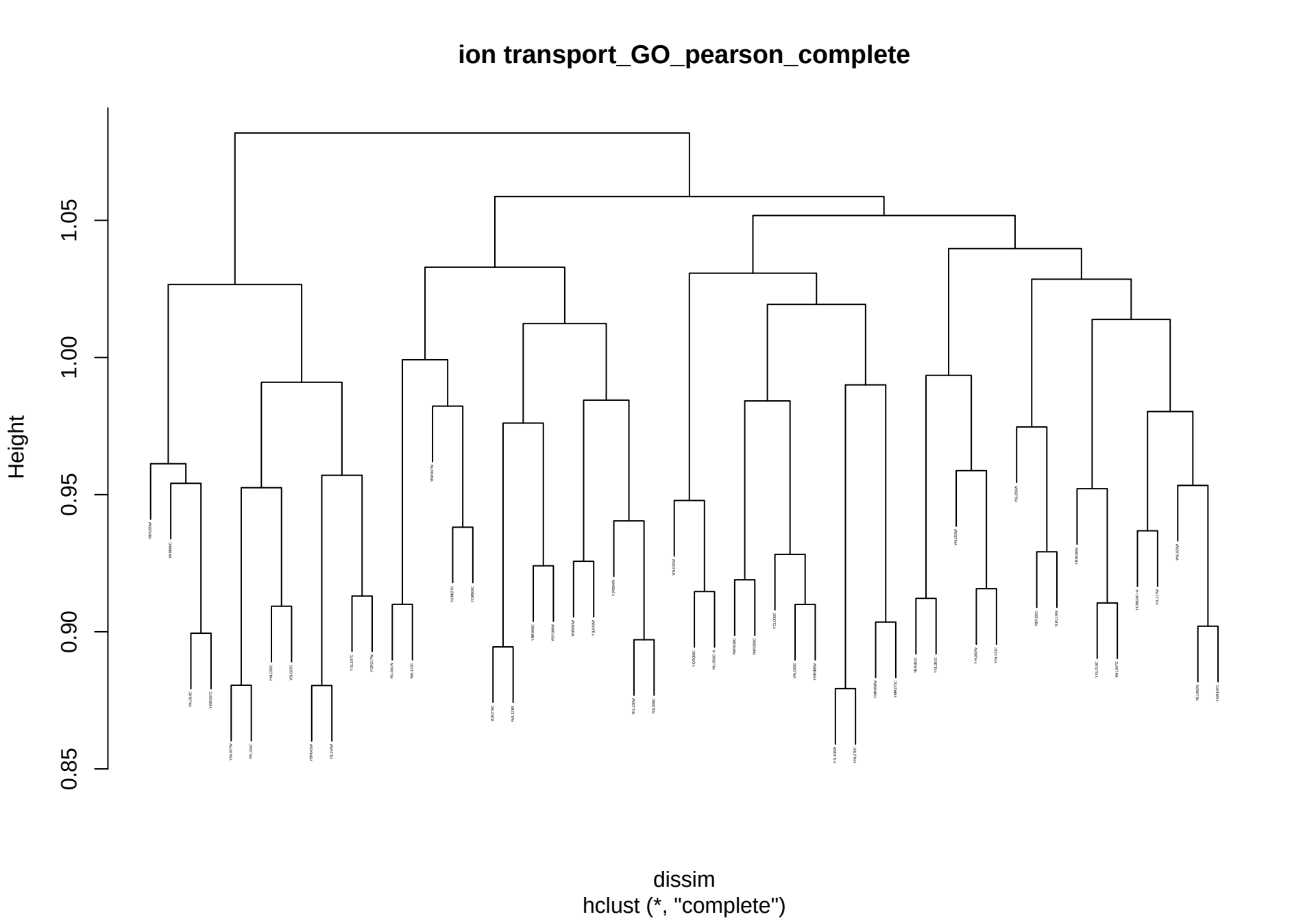

mitochondrial envelope_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

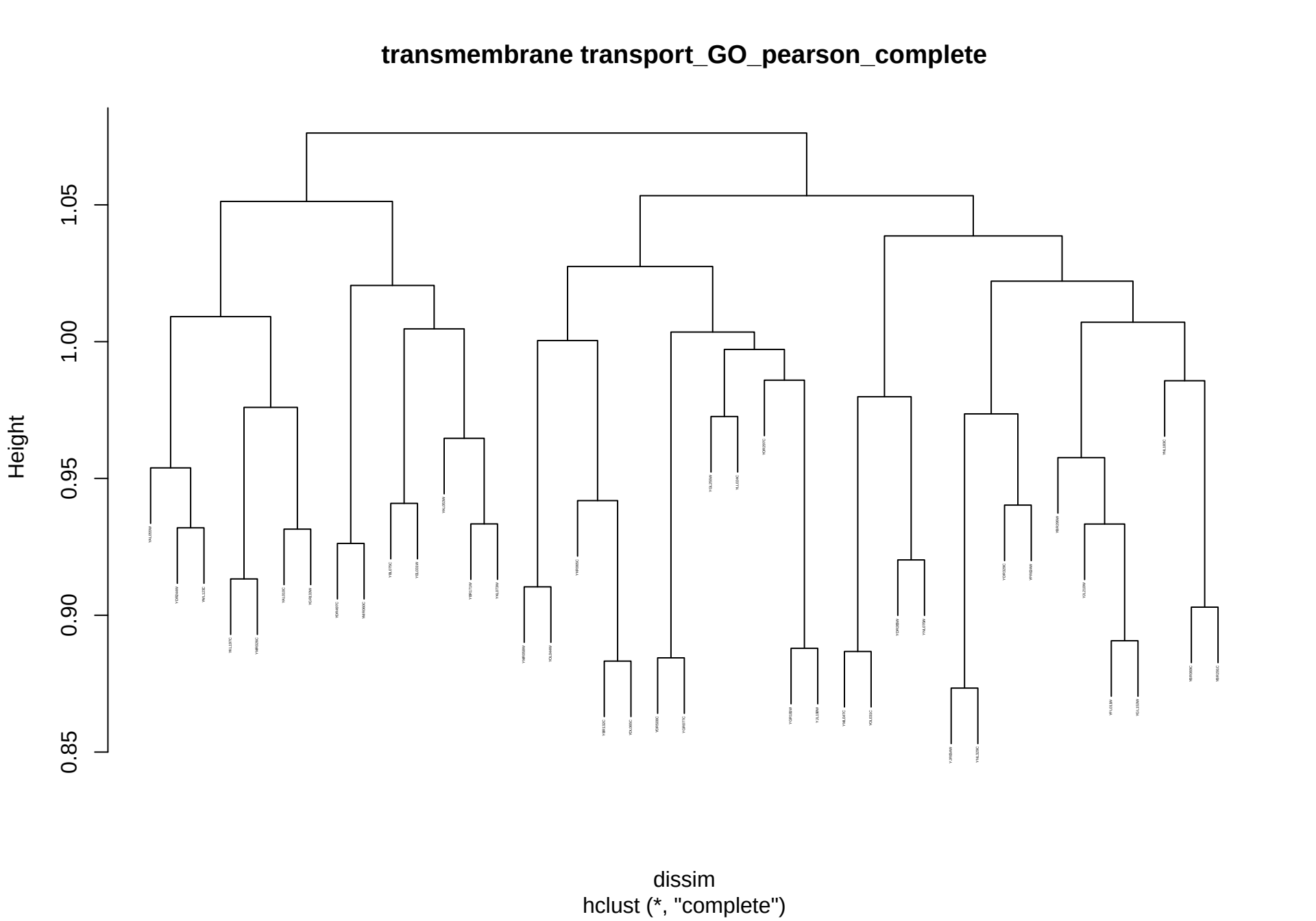

oxidoreductase activity_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

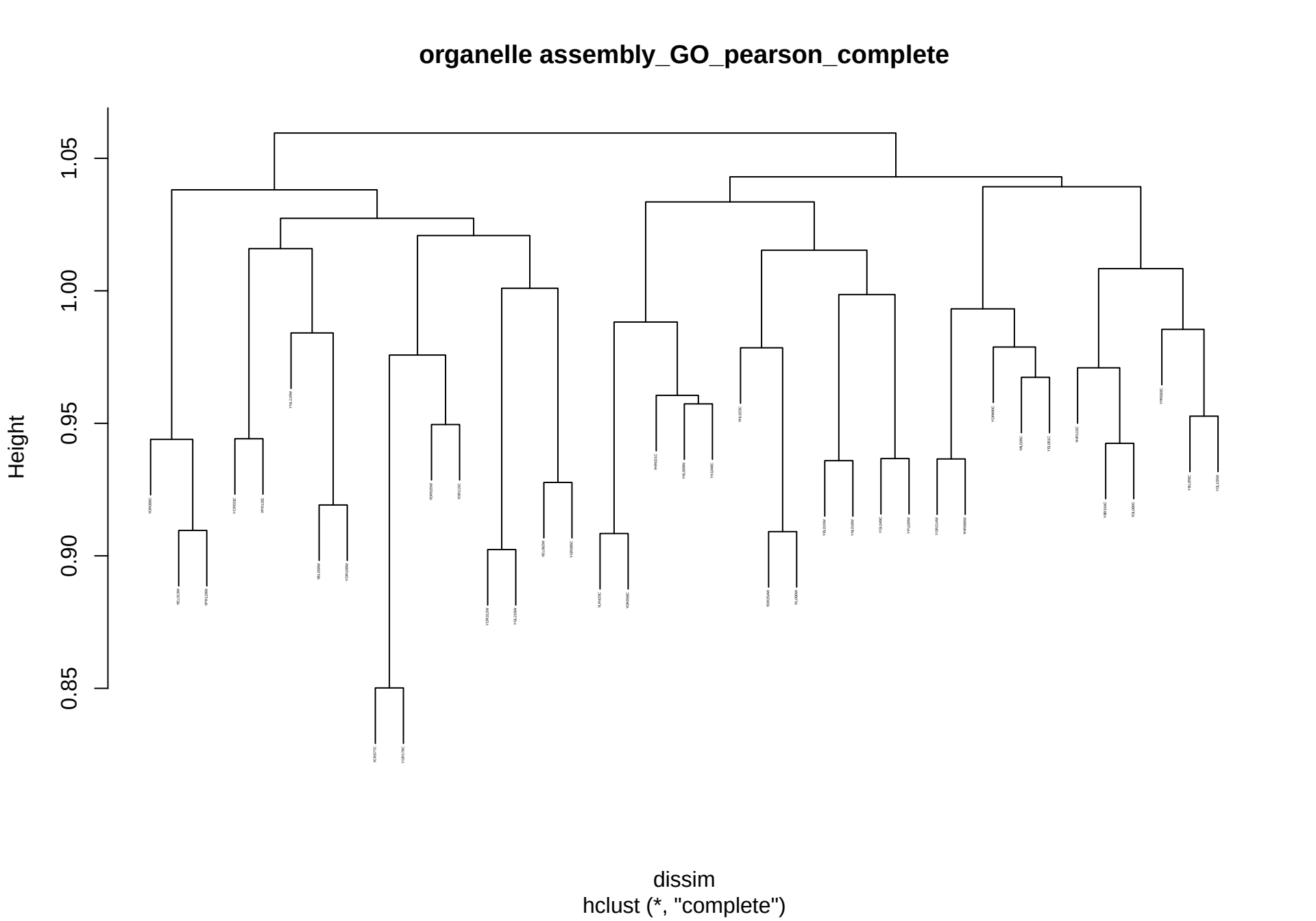

transmembrane transporter activity_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

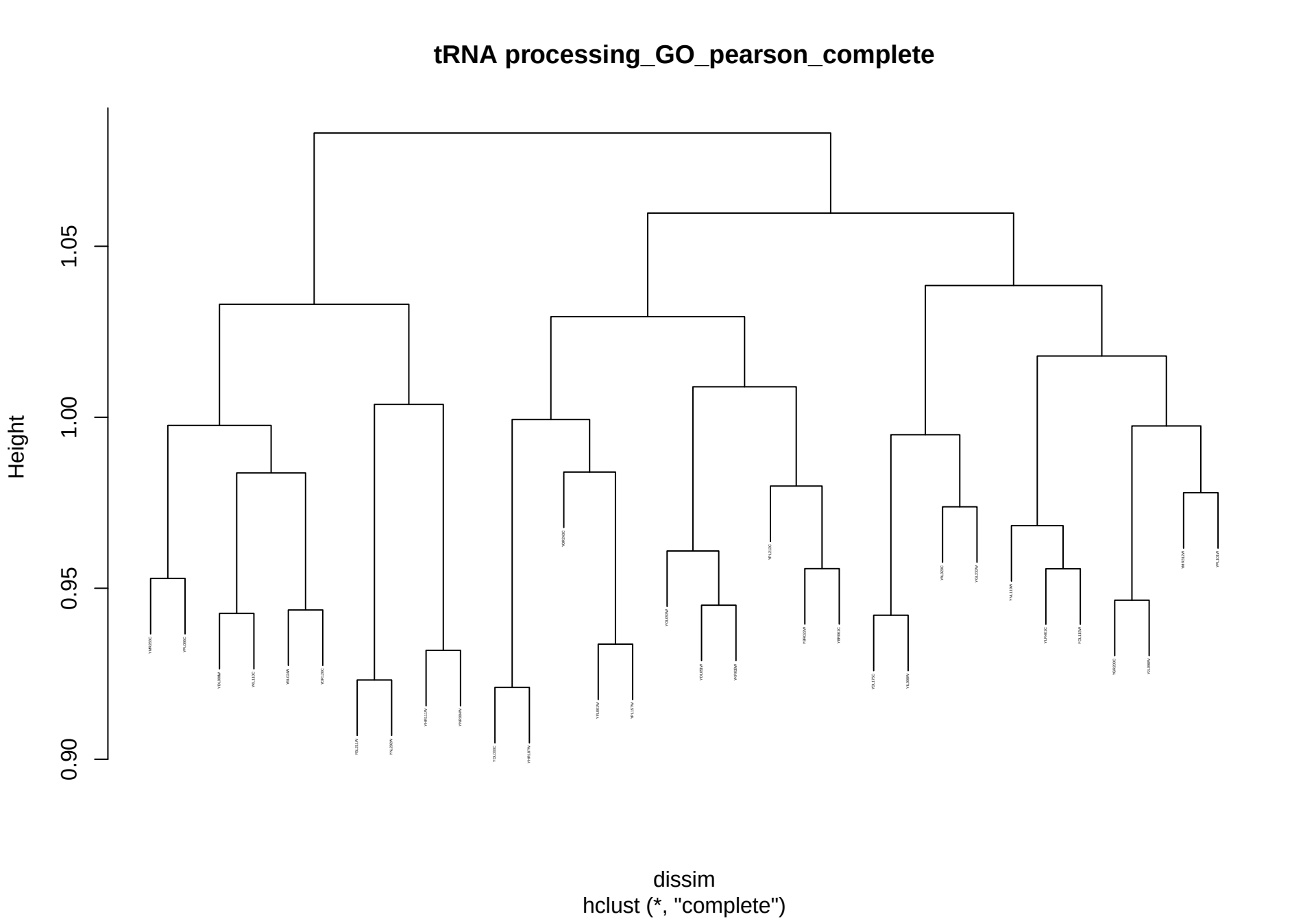

transferase activity_GO_pearson_complete
Height
0.80
0.85
0.90
0.95
1.00
1.05
1.10
dissim
hclust (*, "complete")

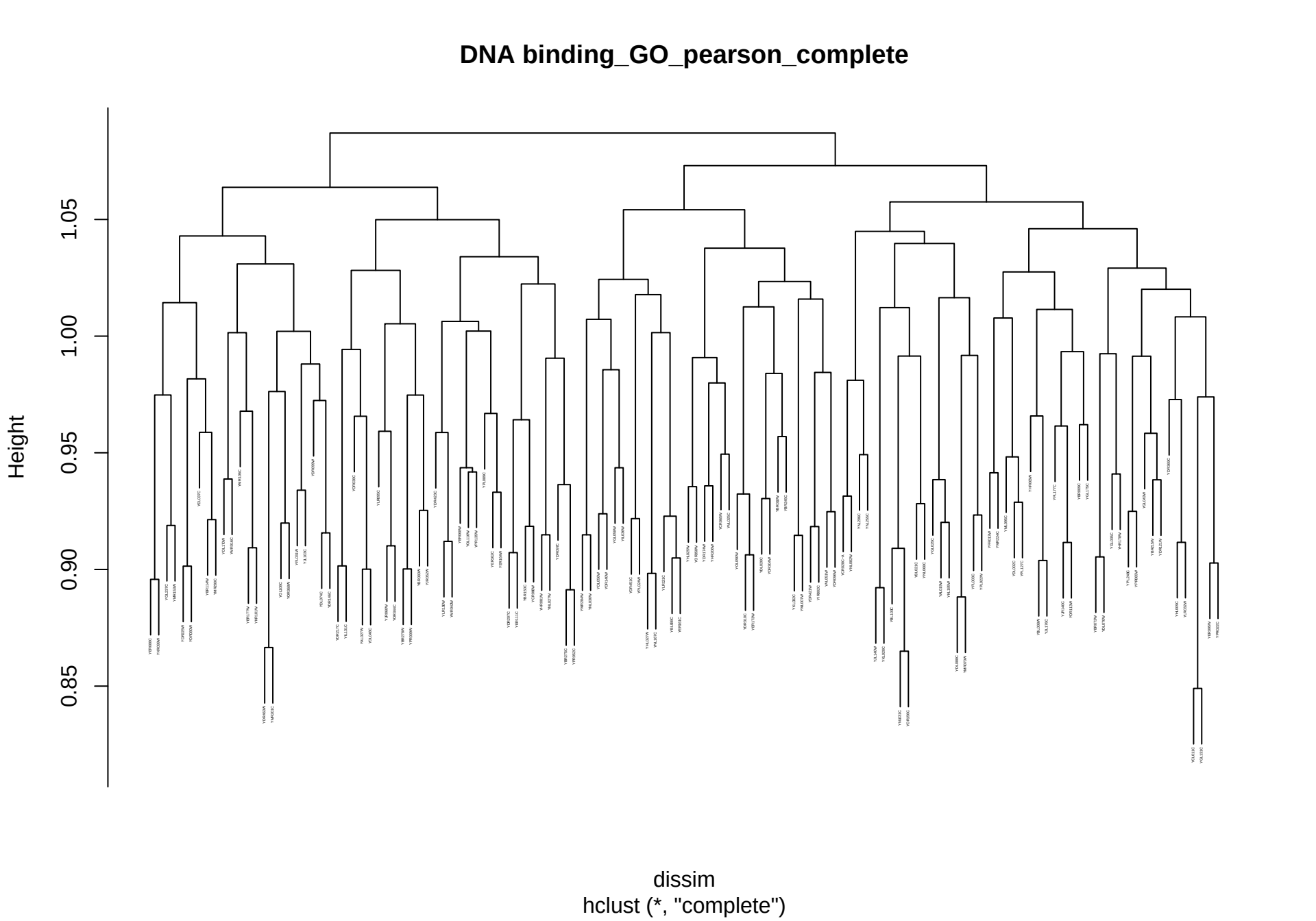

DNA recombination_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

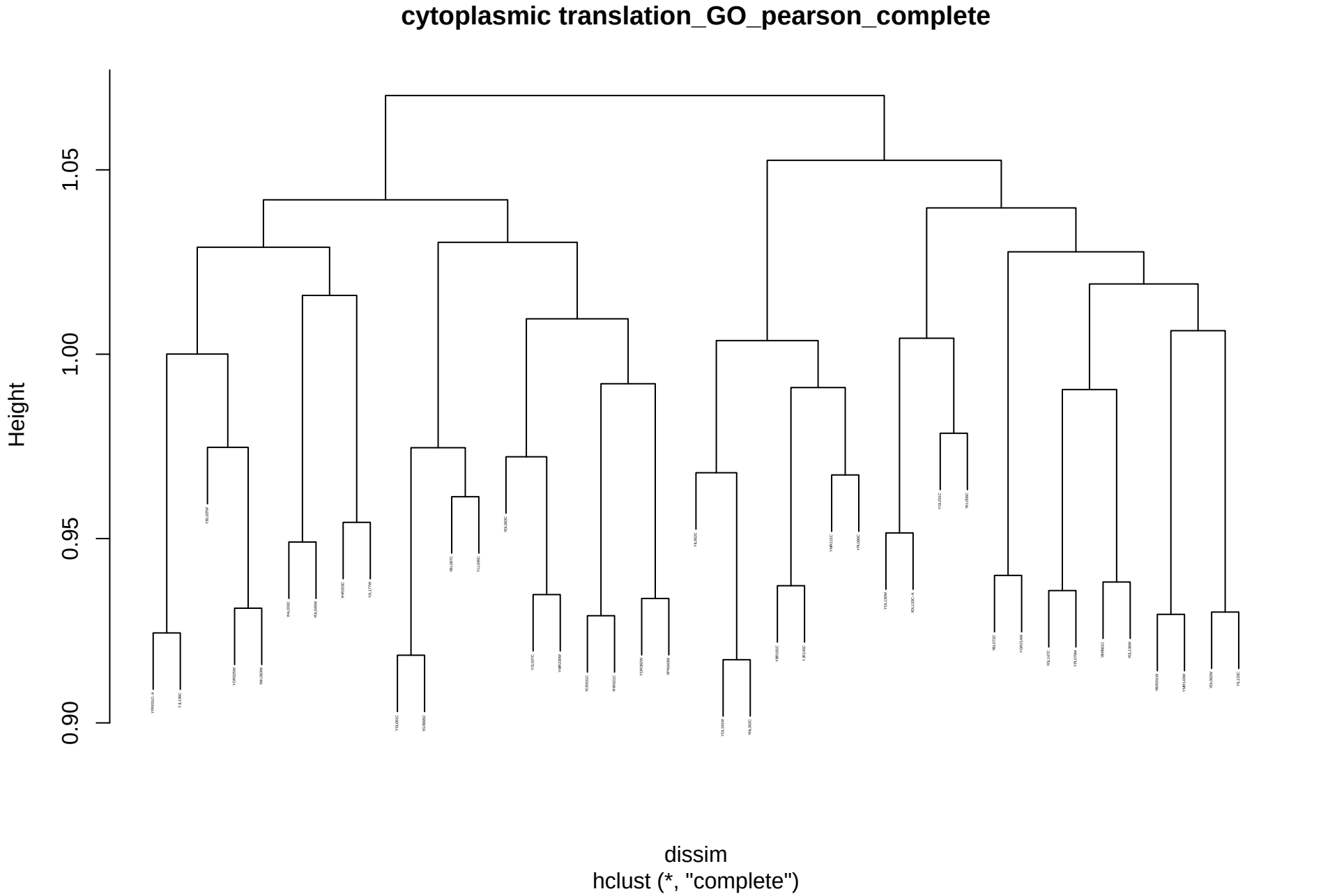

ion transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

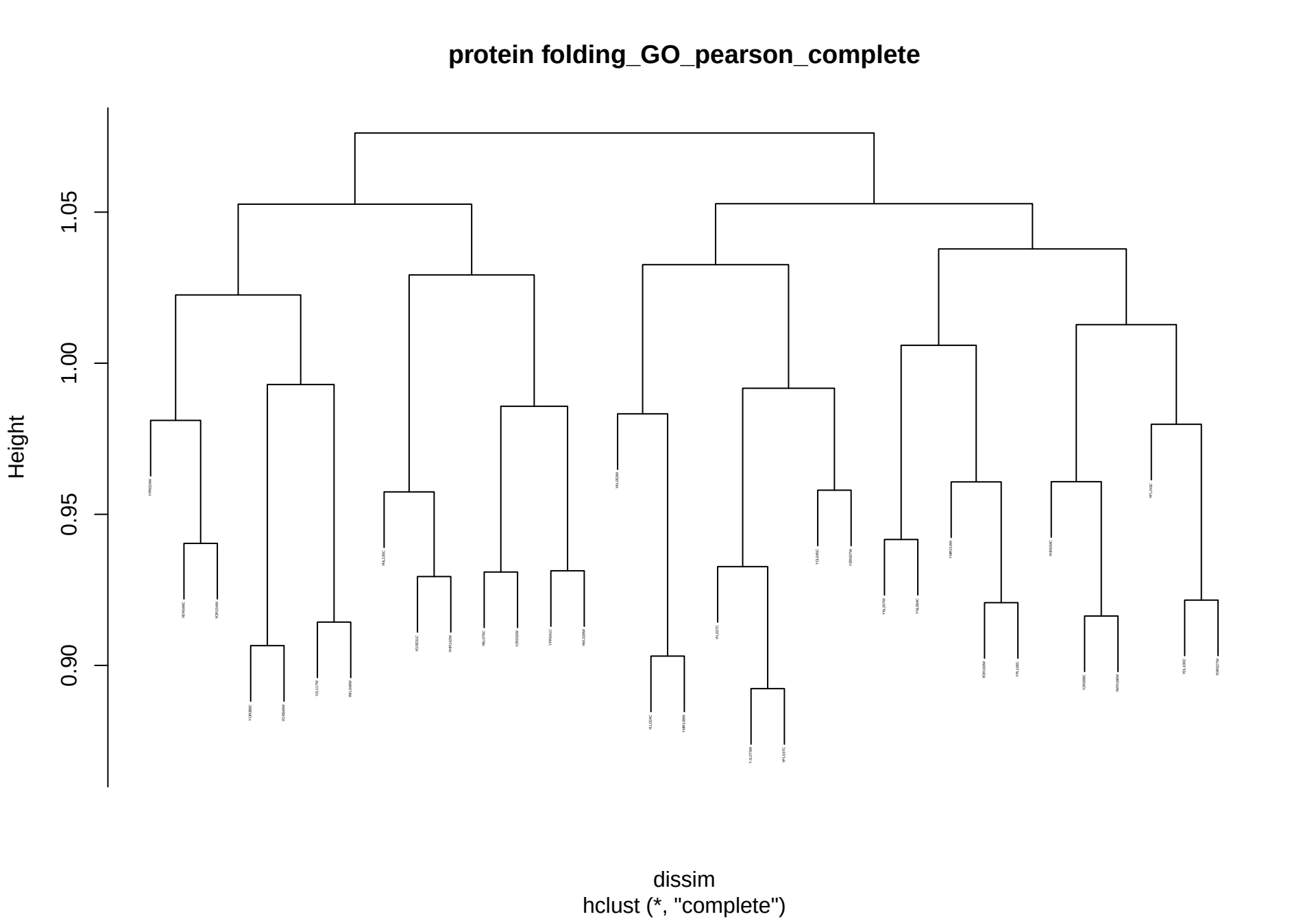

transmembrane transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

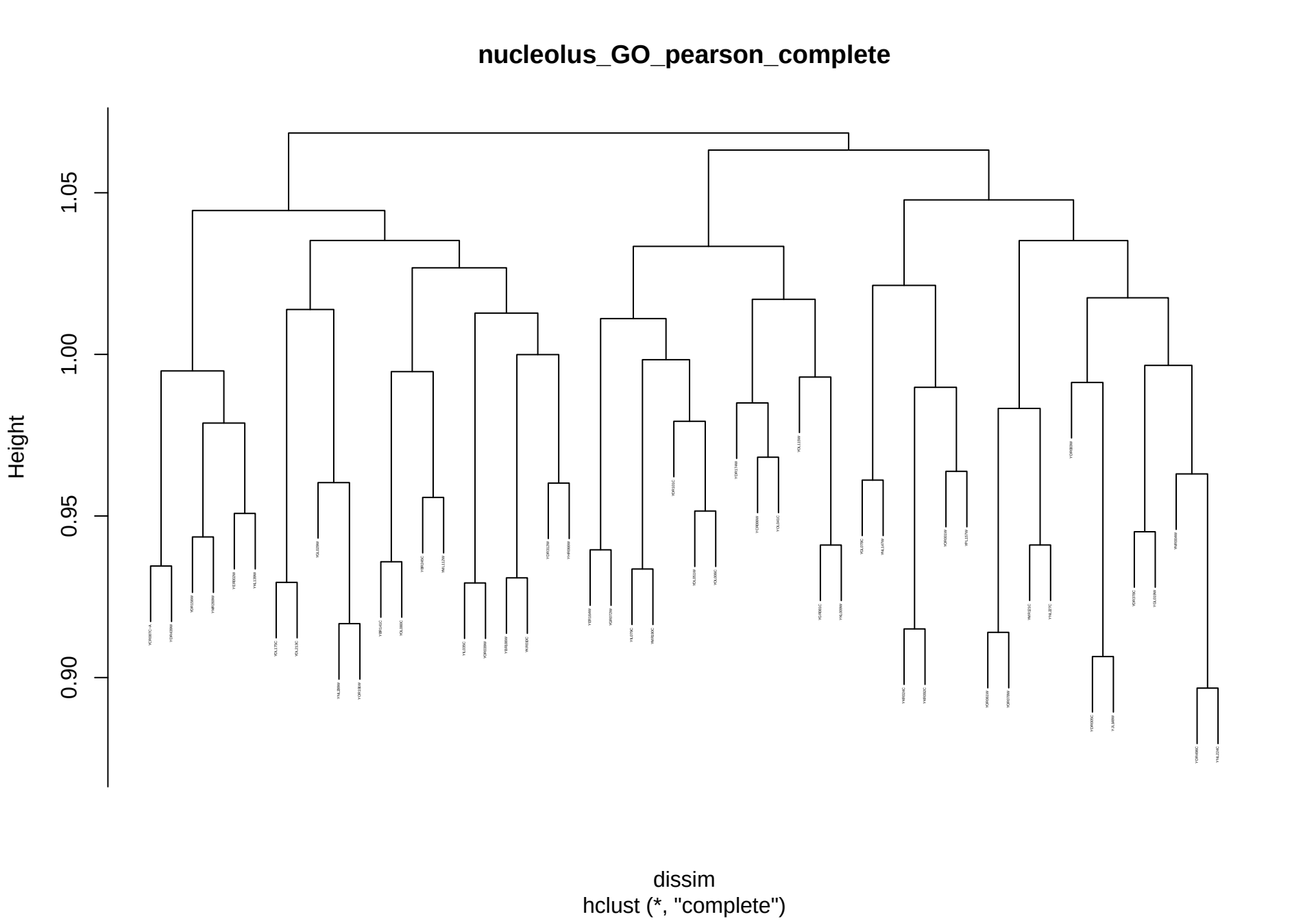

organelle assembly_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

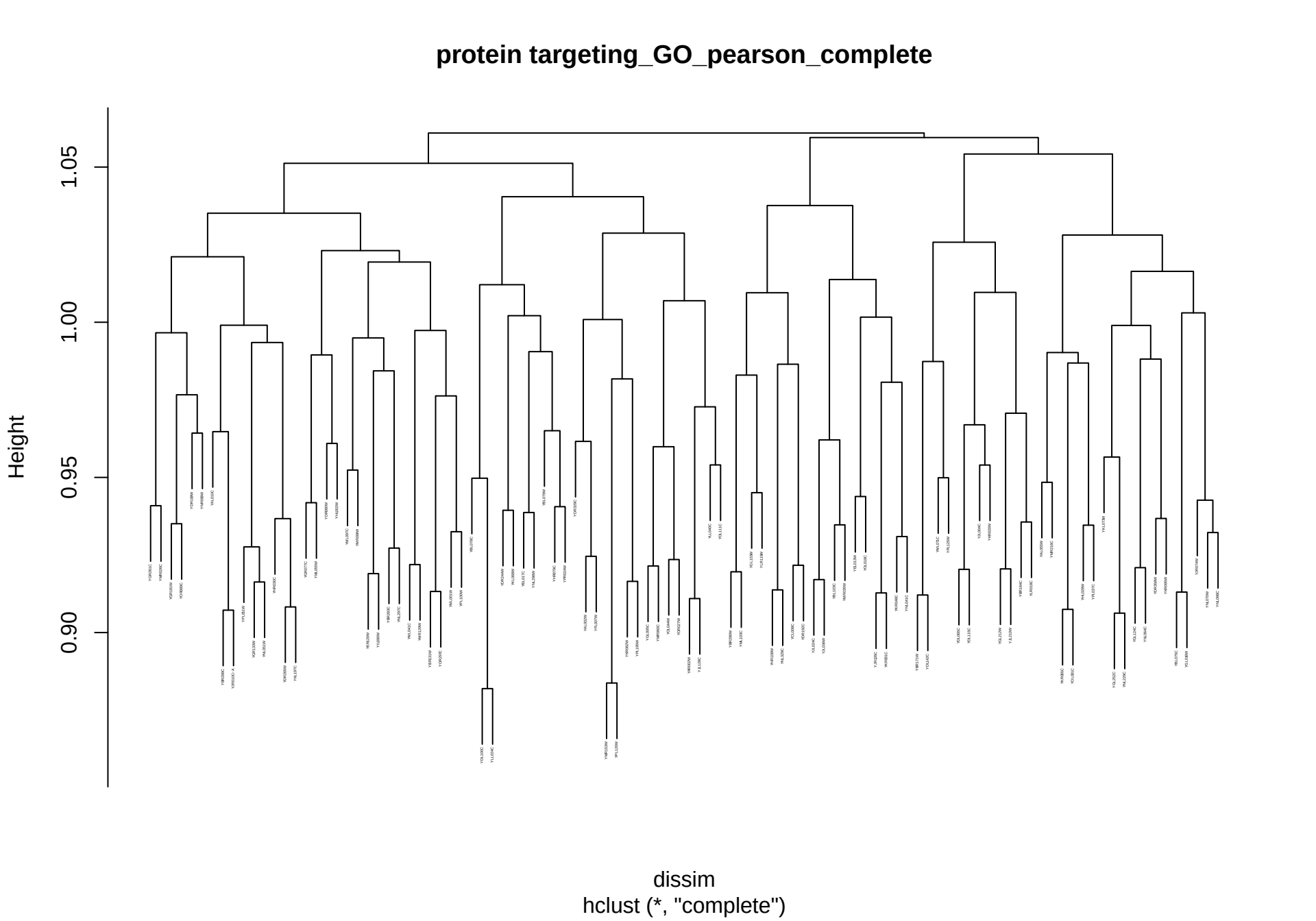

tRNA processing_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

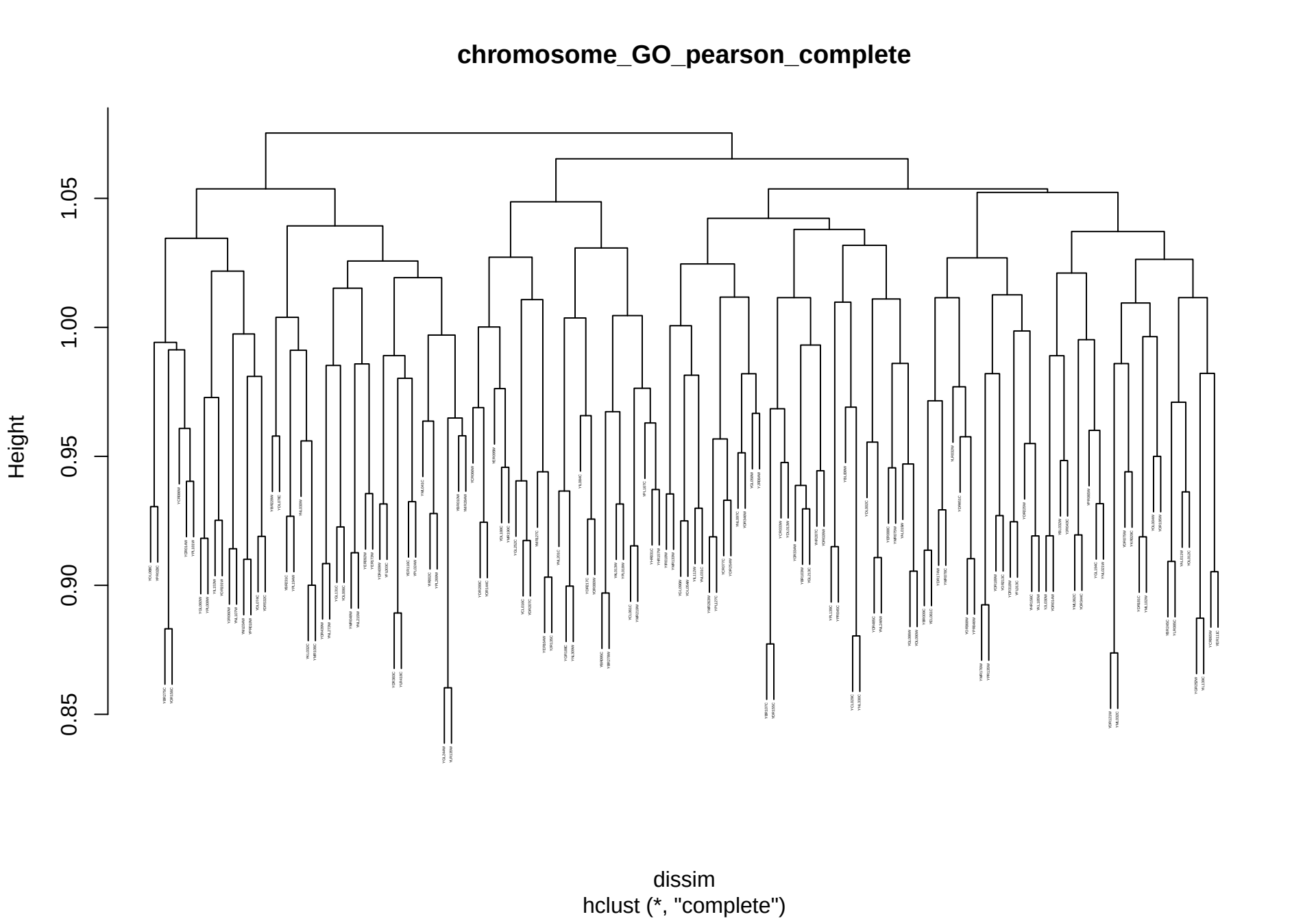

DNA binding_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

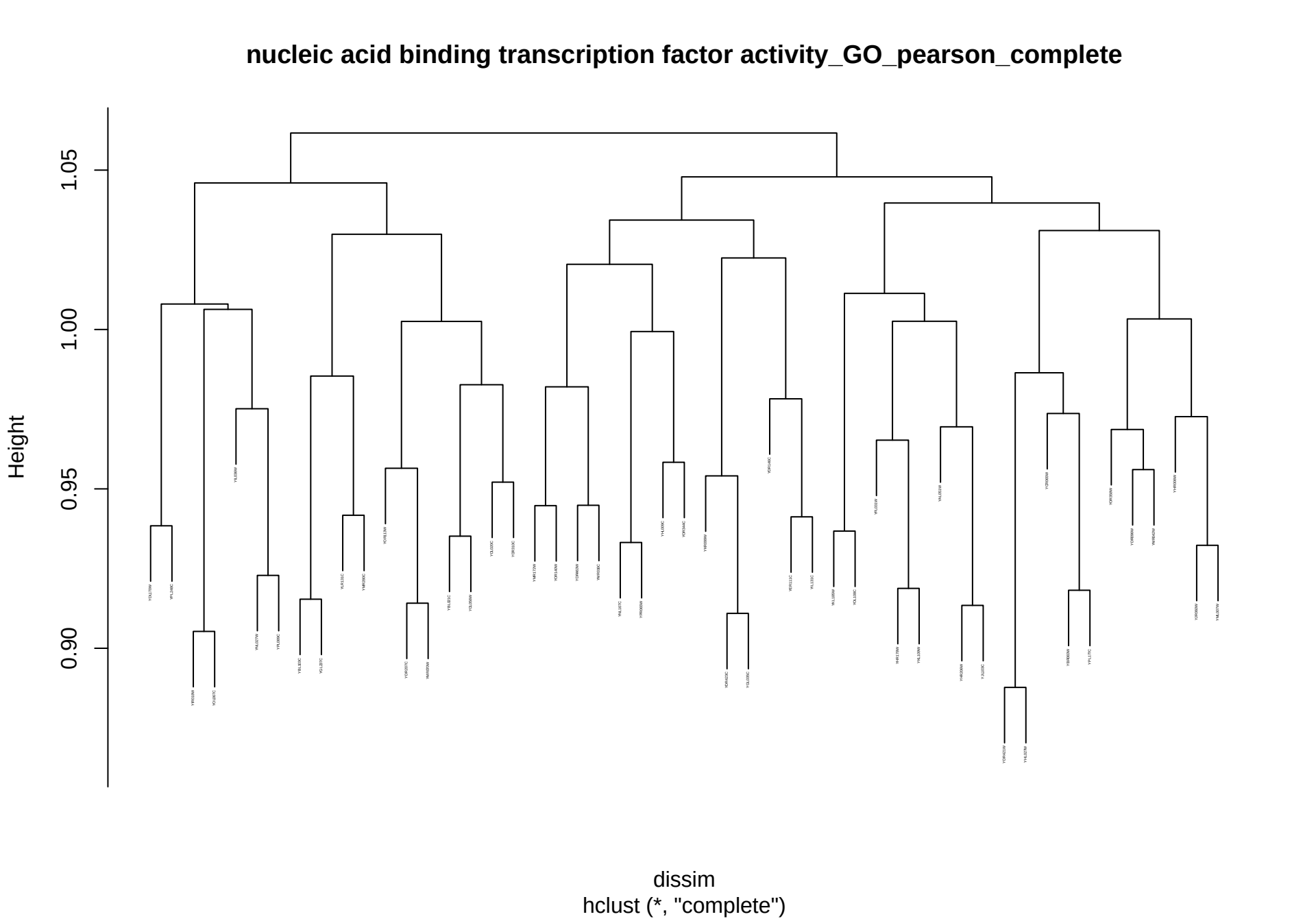

cytoplasmic translation_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")


protein folding_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

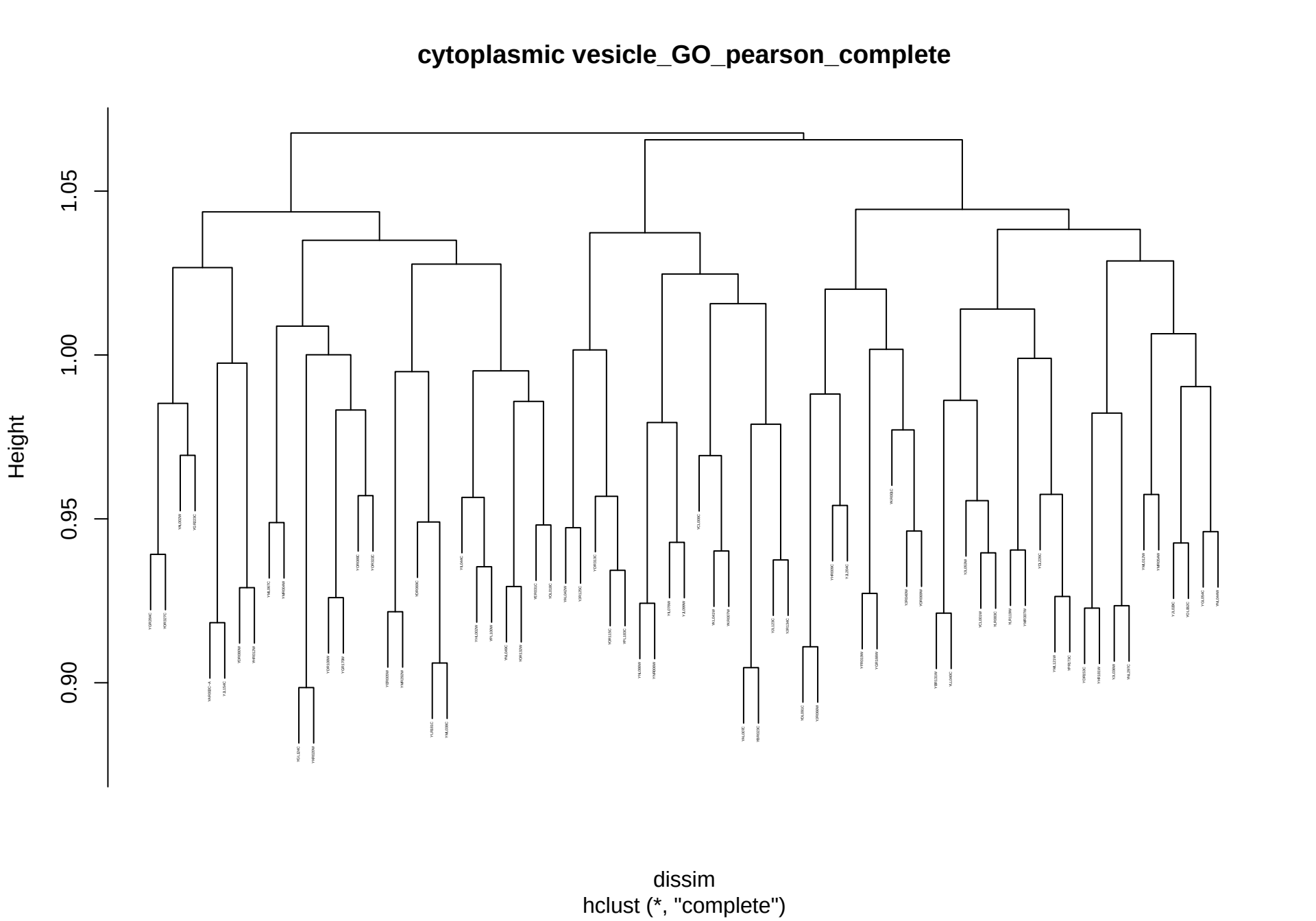

nucleolus_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

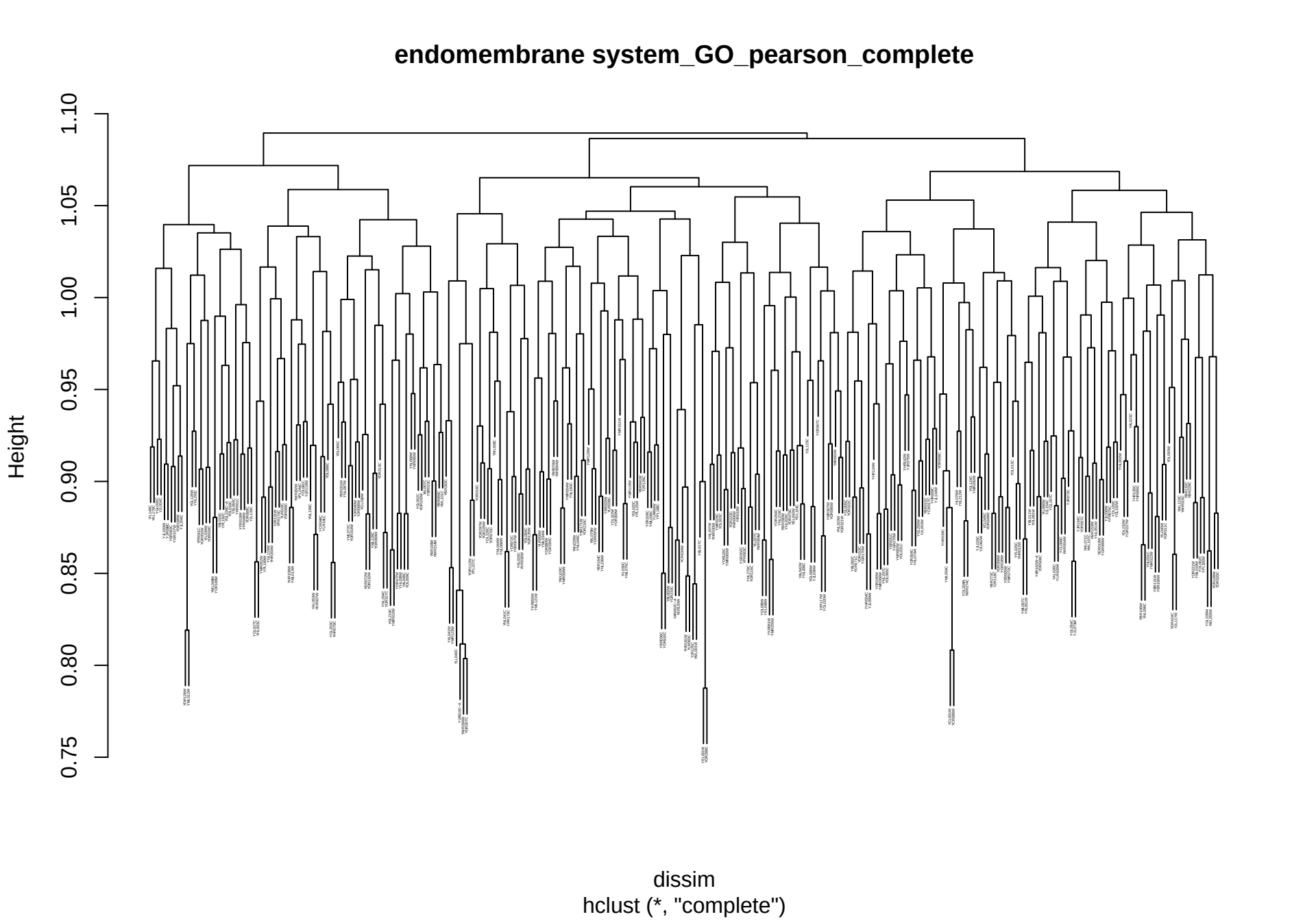

protein targeting_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

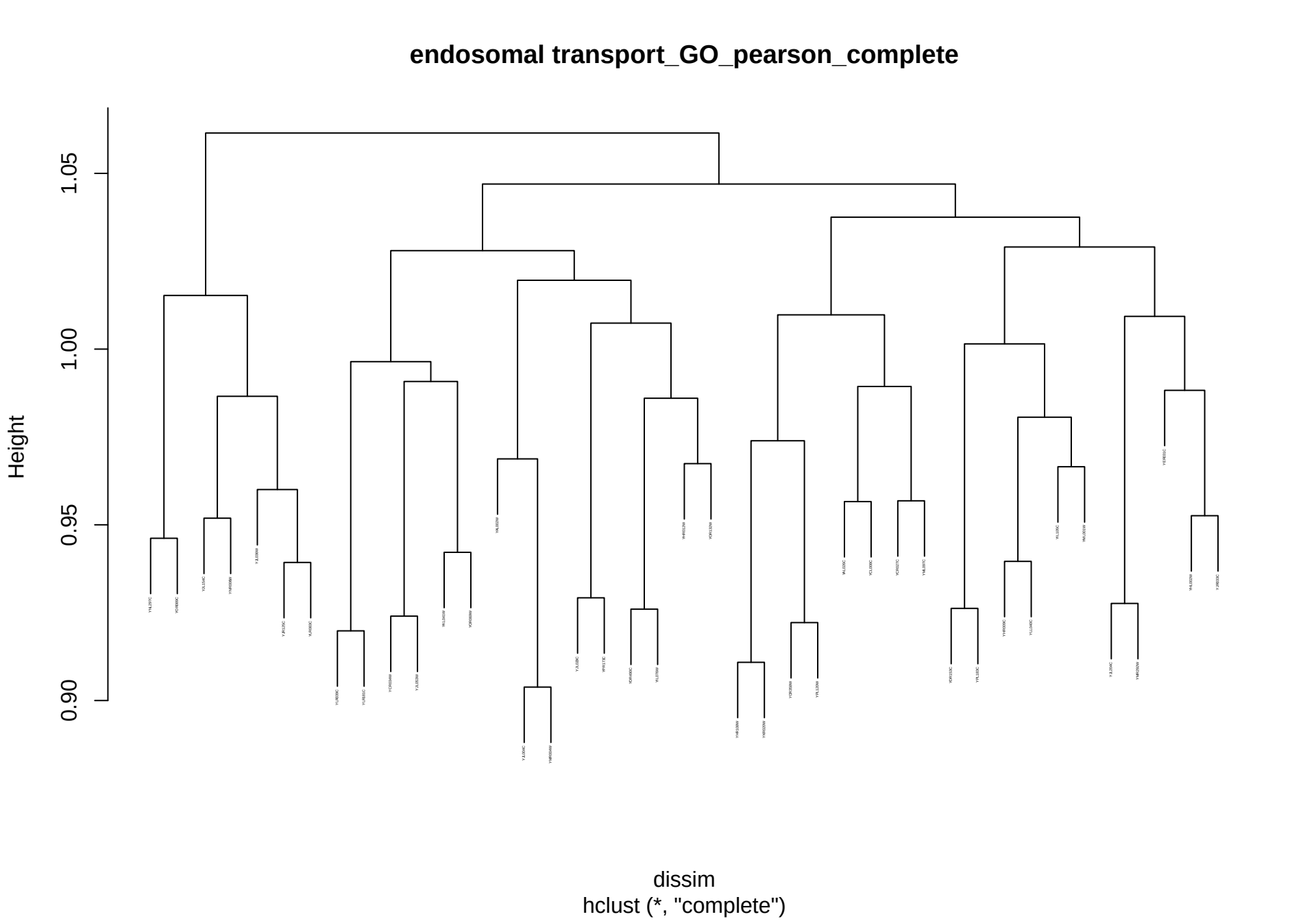

chromosome_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

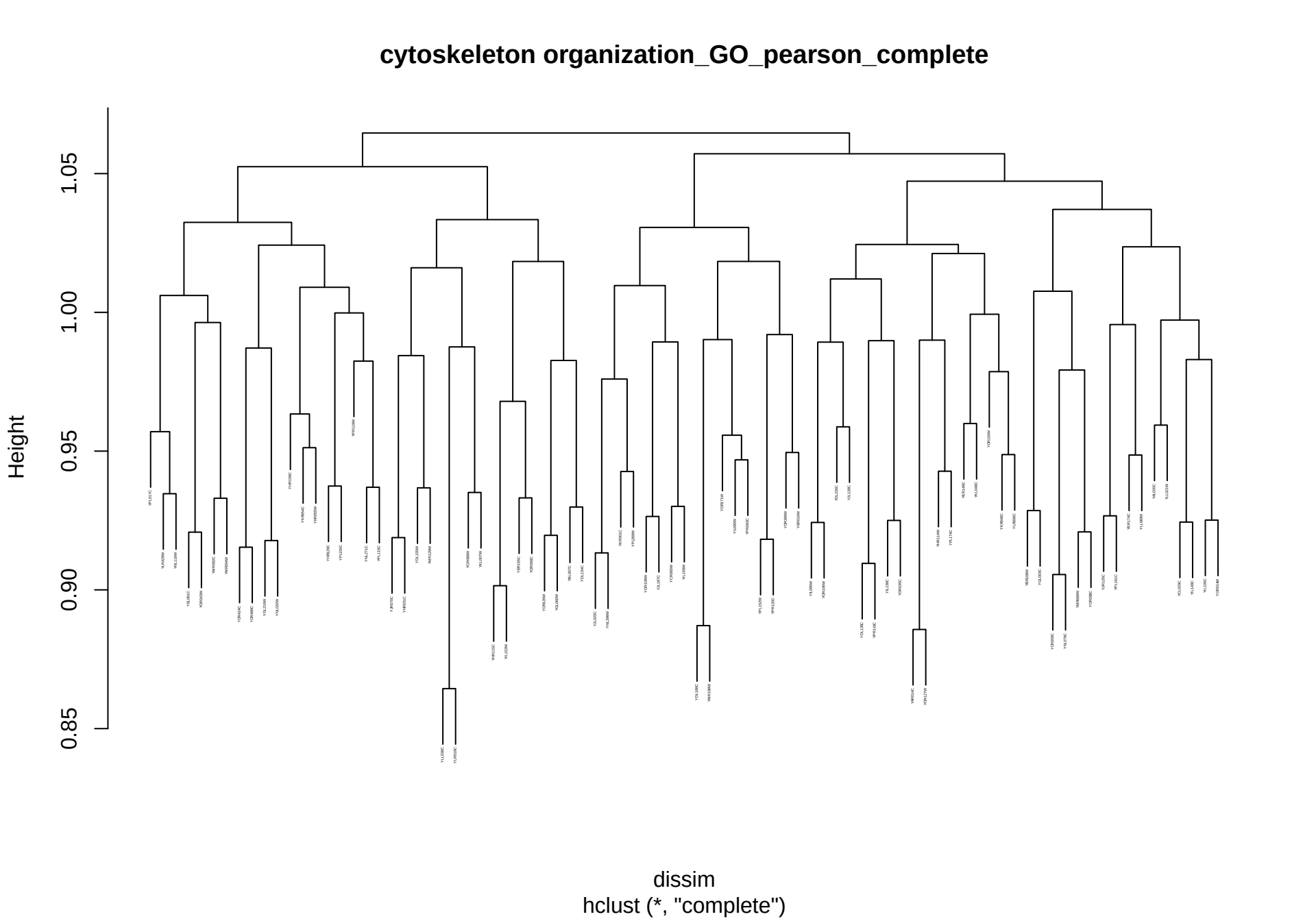

nucleic acid binding transcription factor activity_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

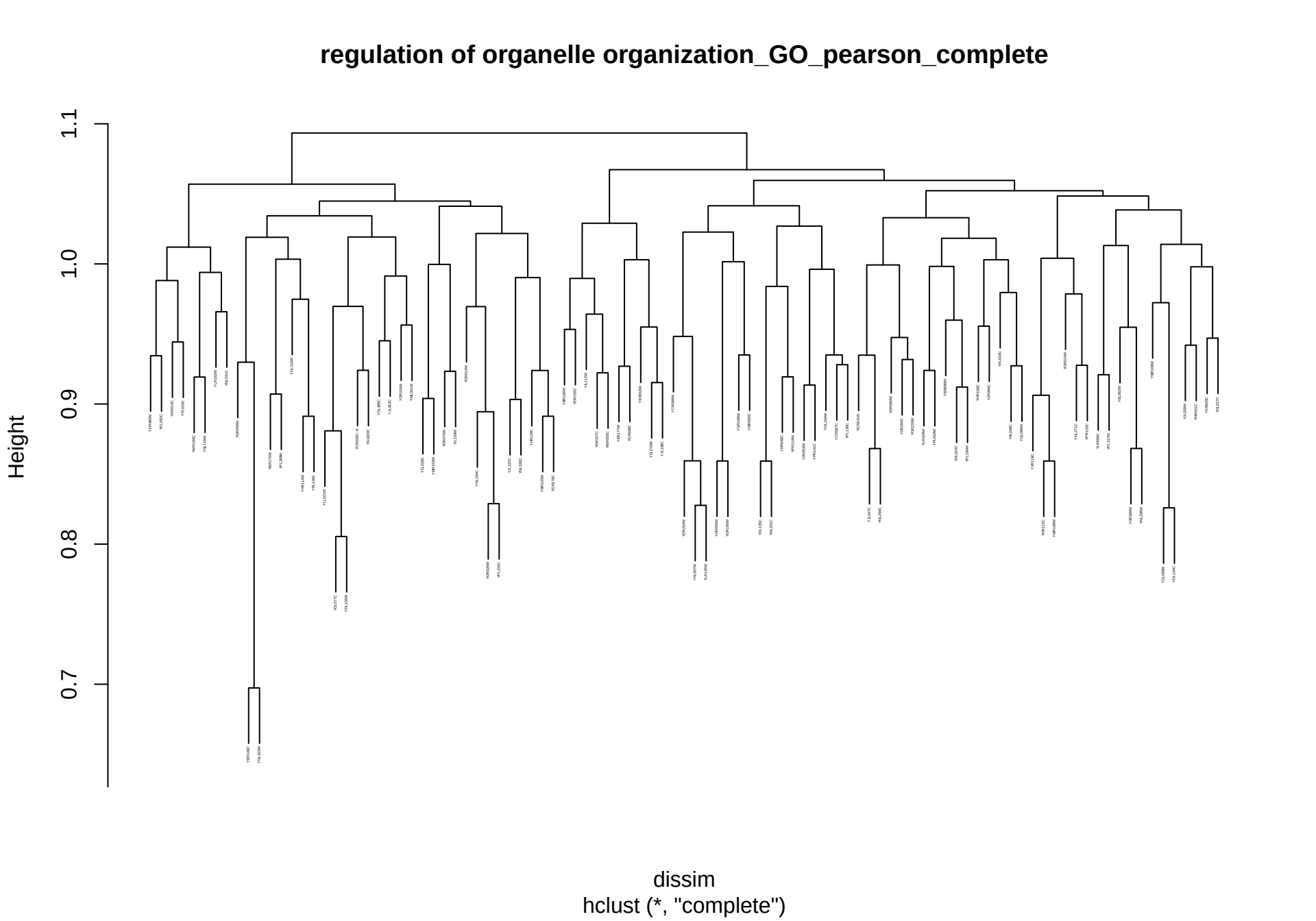

transcription factor activity, protein binding_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

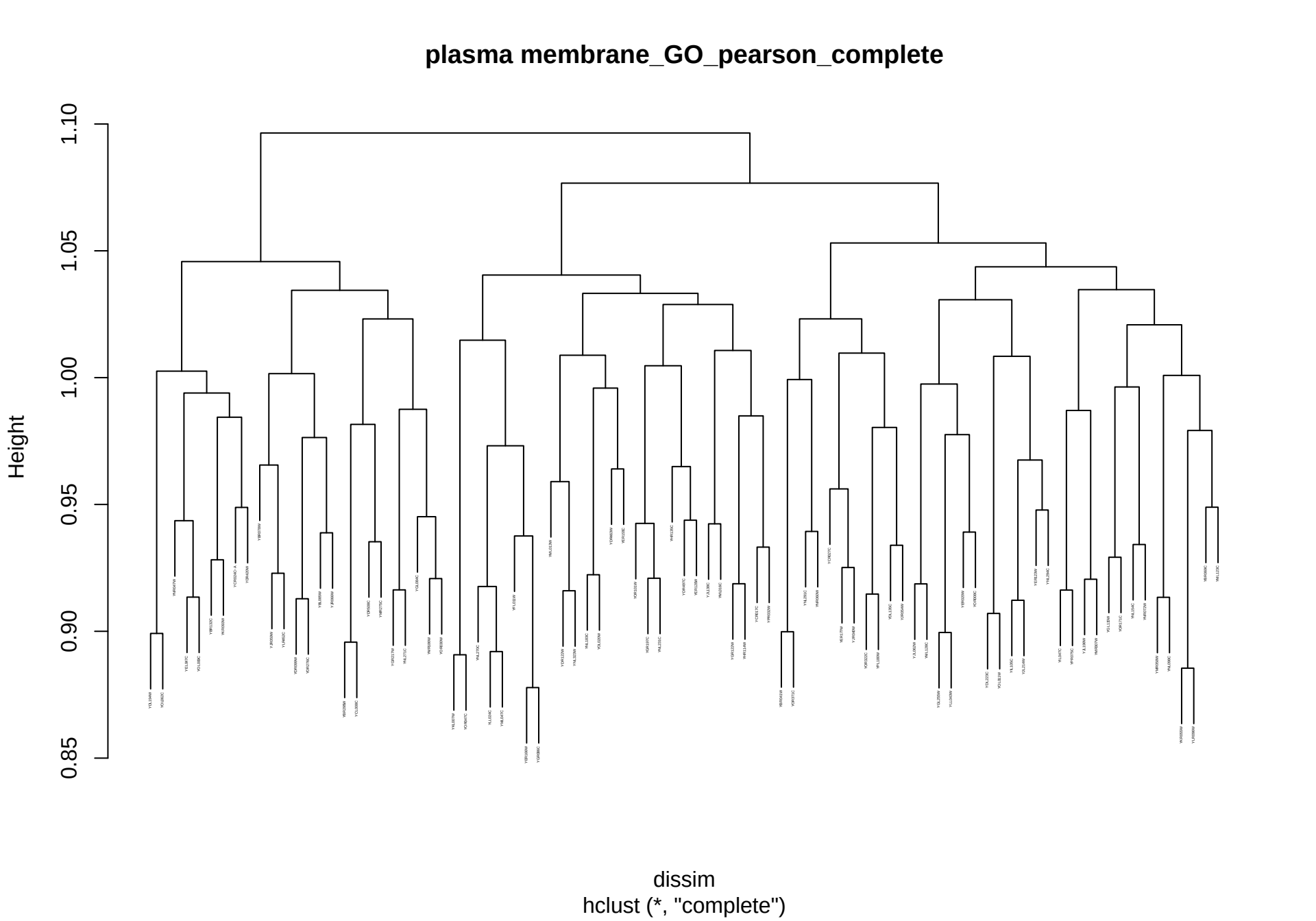

cytoplasmic vesicle_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

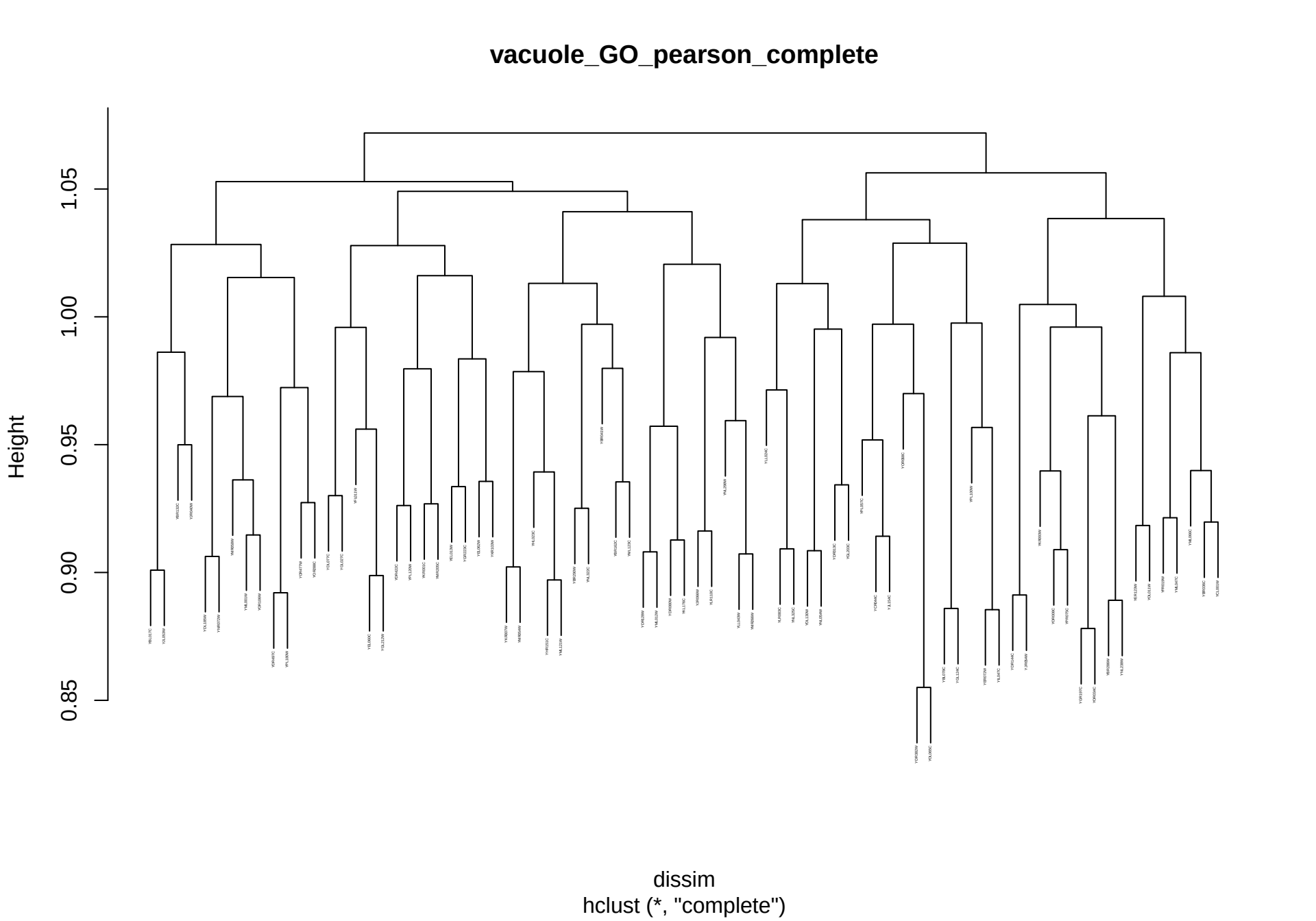

endomembrane system_GO_pearson_complete
Height
1.10
1.05
1.00
0.95
0.90
0.85
0.80
0.75
dissim
hclust (*, "complete")

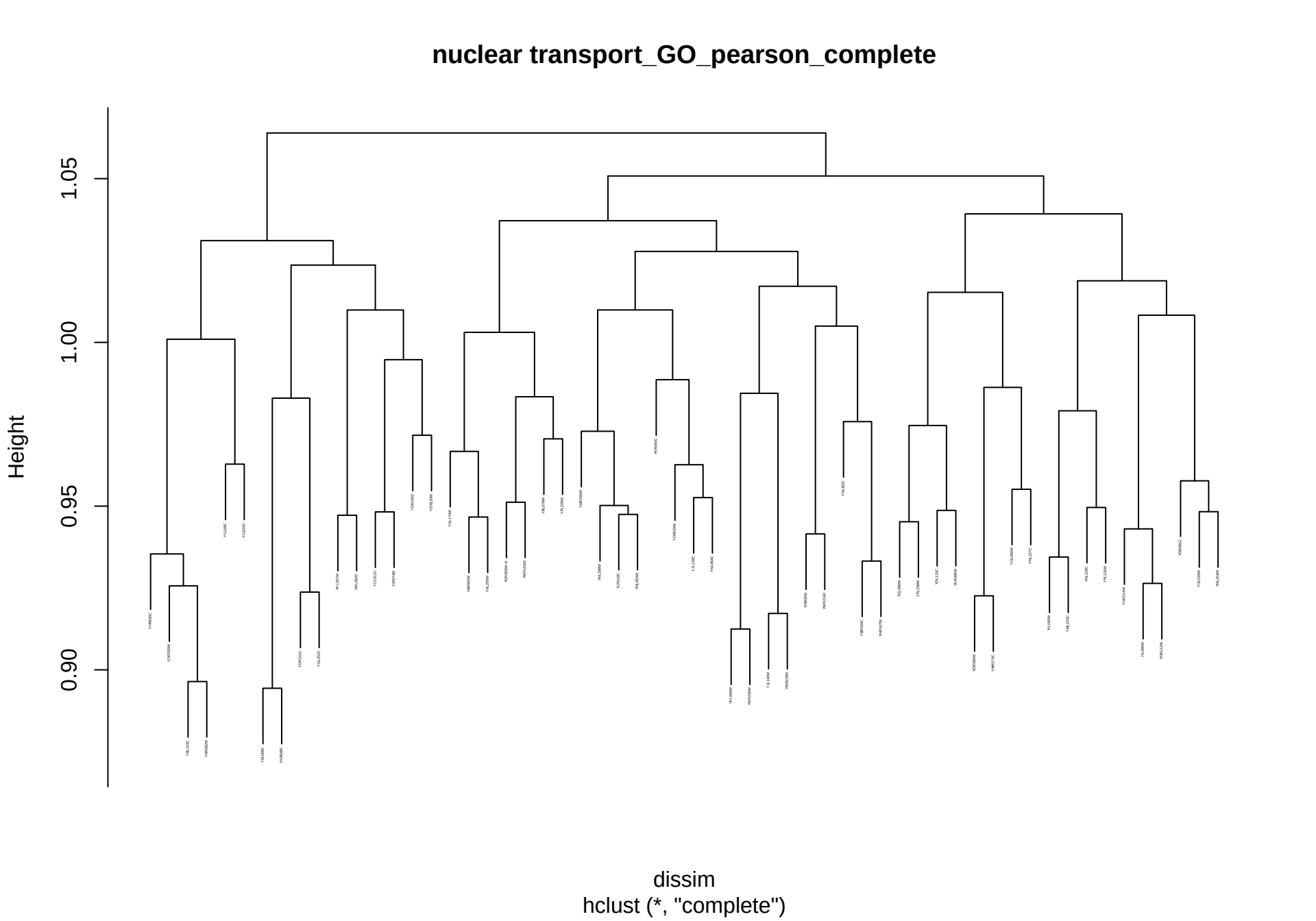

endosomal transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

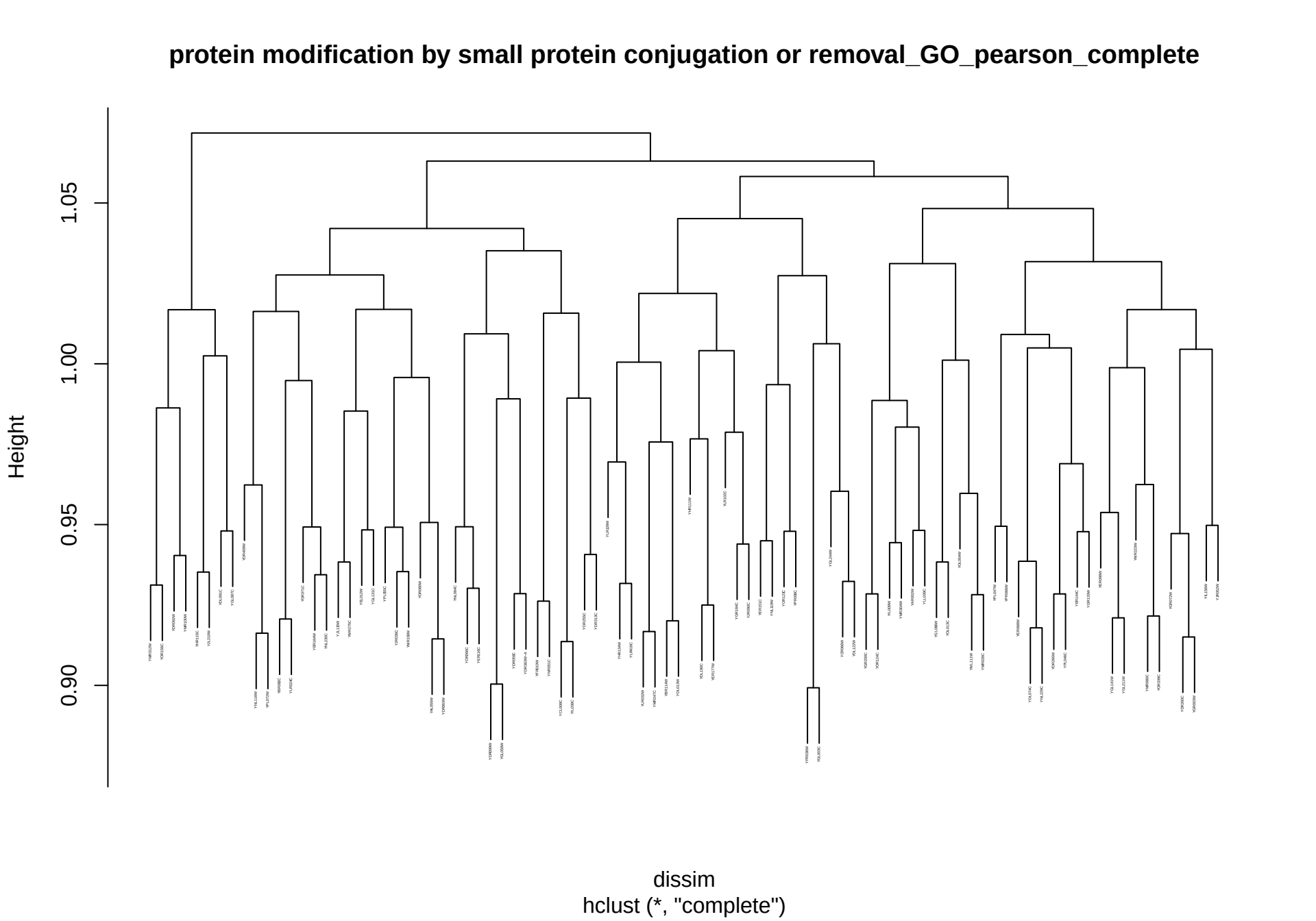

cytoskeleton organization_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

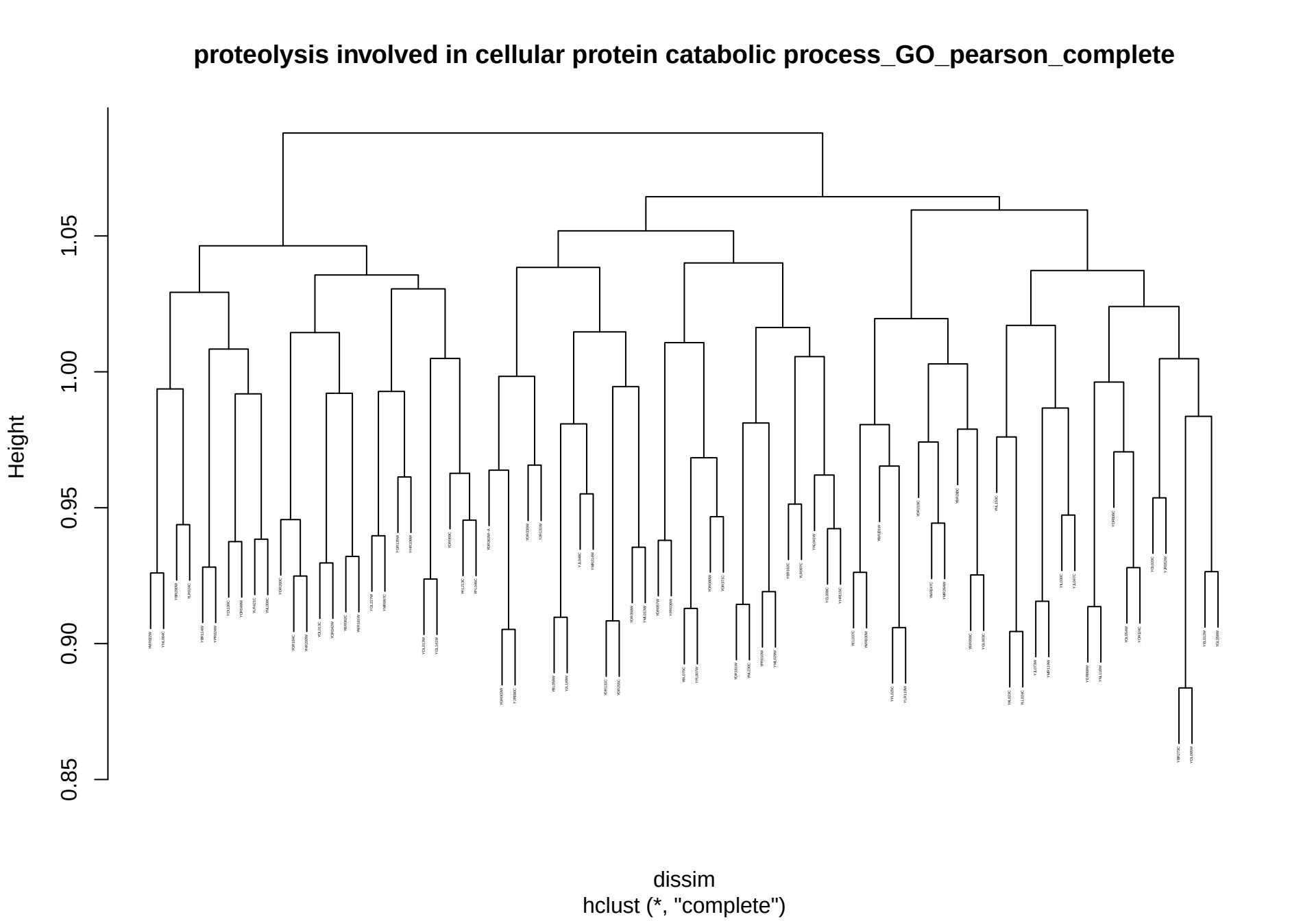

regulation of organelle organization_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
dissim
hclust (*, "complete")

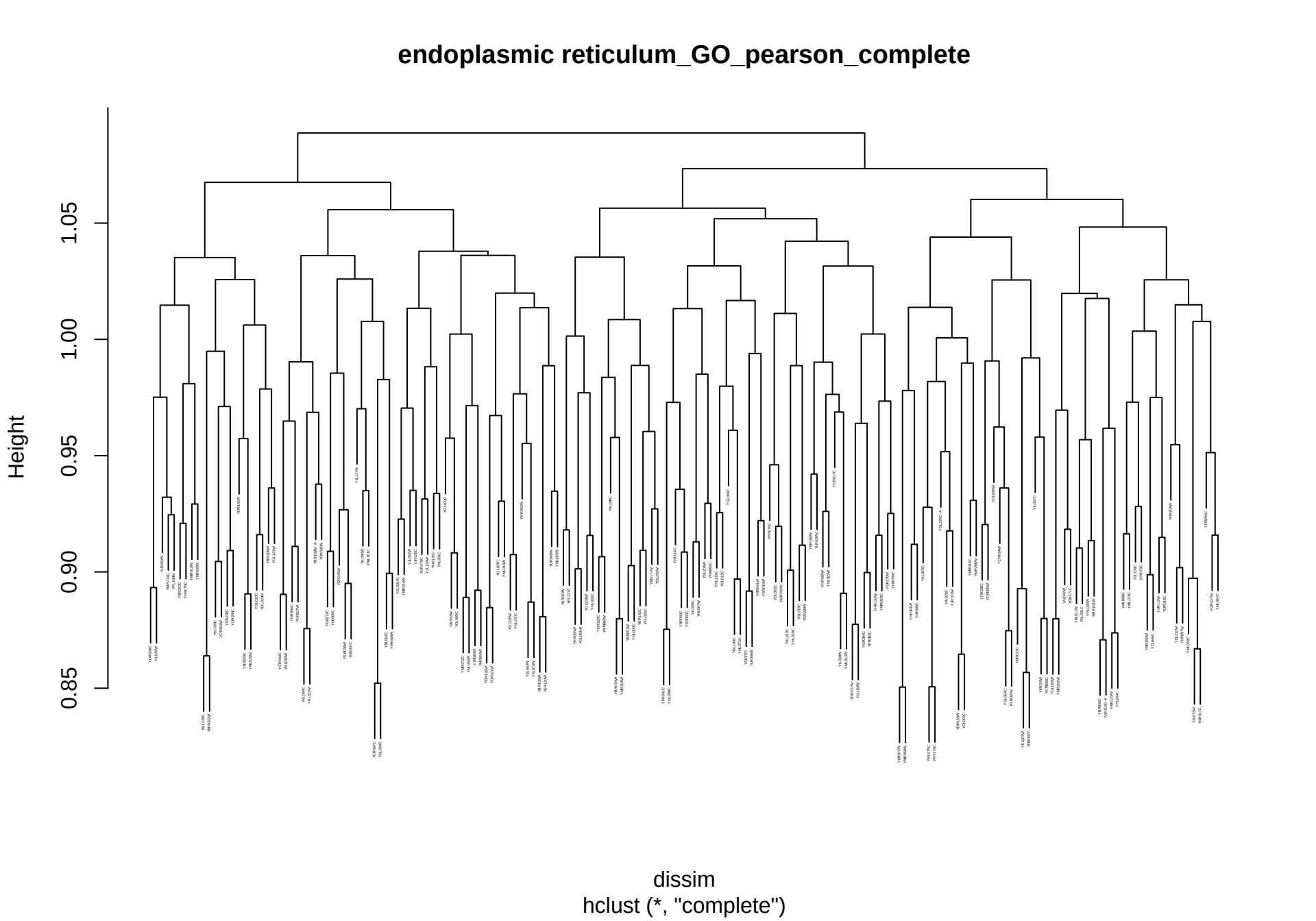

plasma membrane_GO_pearson_complete
Height
1.10
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

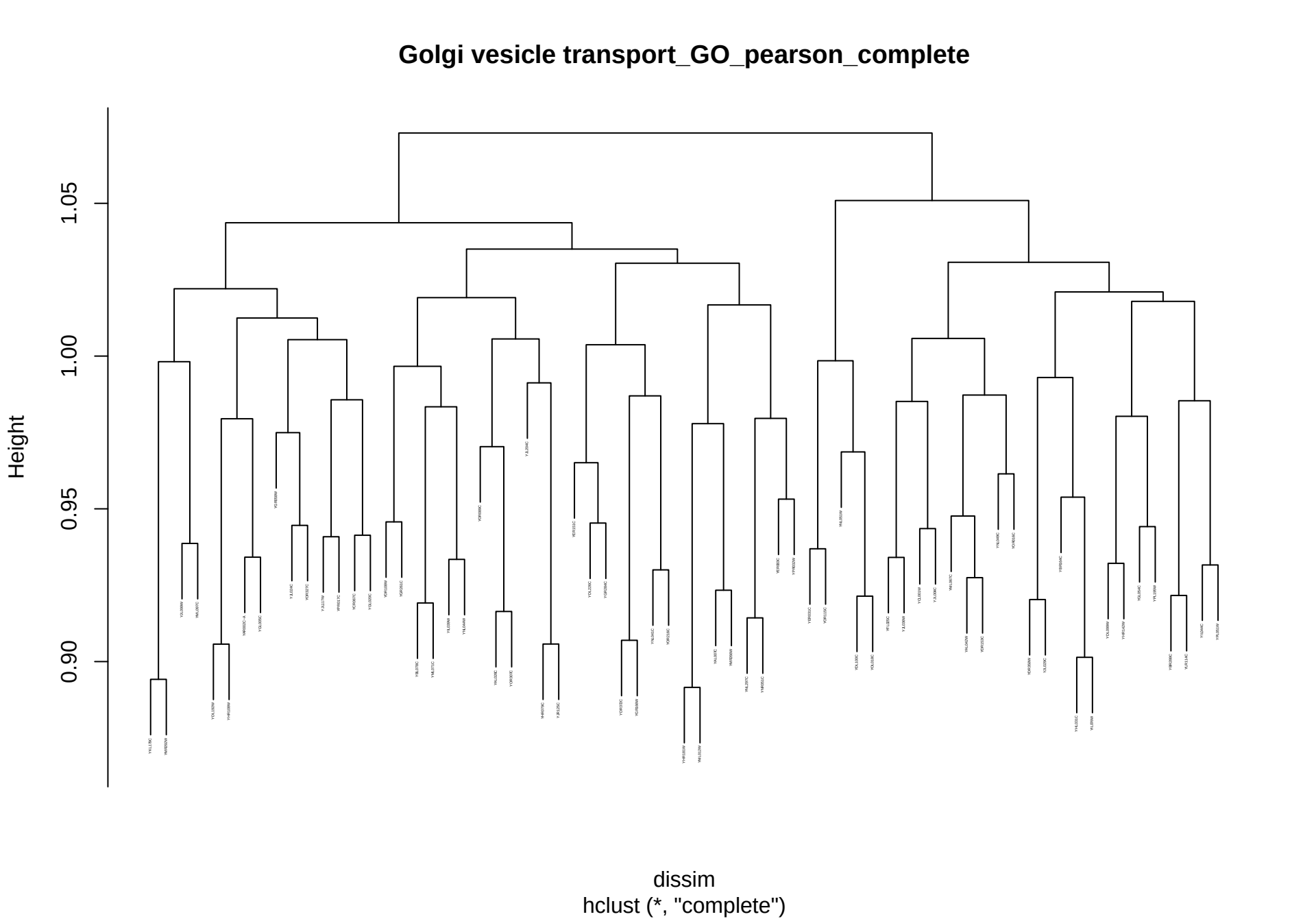

vacuole_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

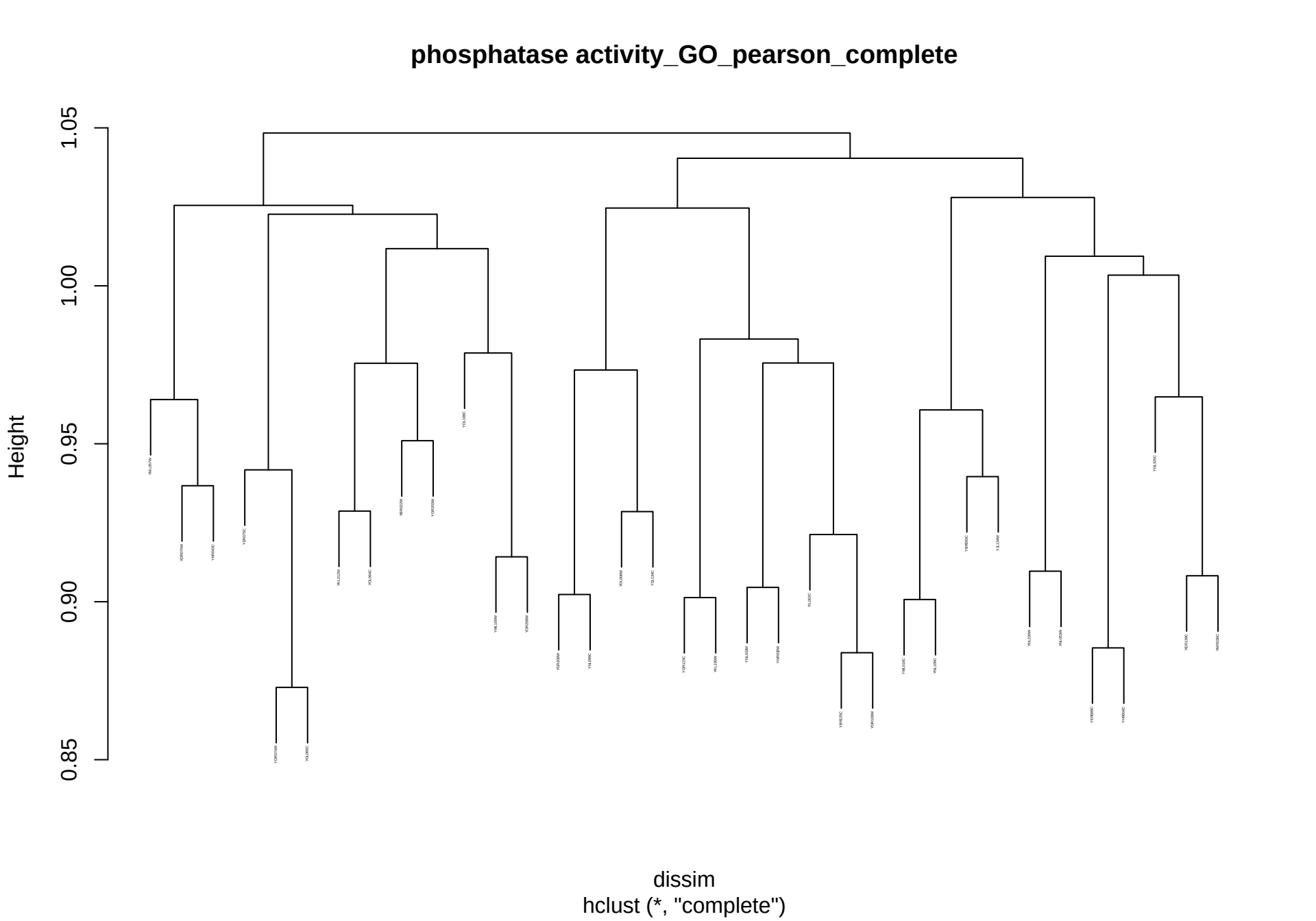

nuclear transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

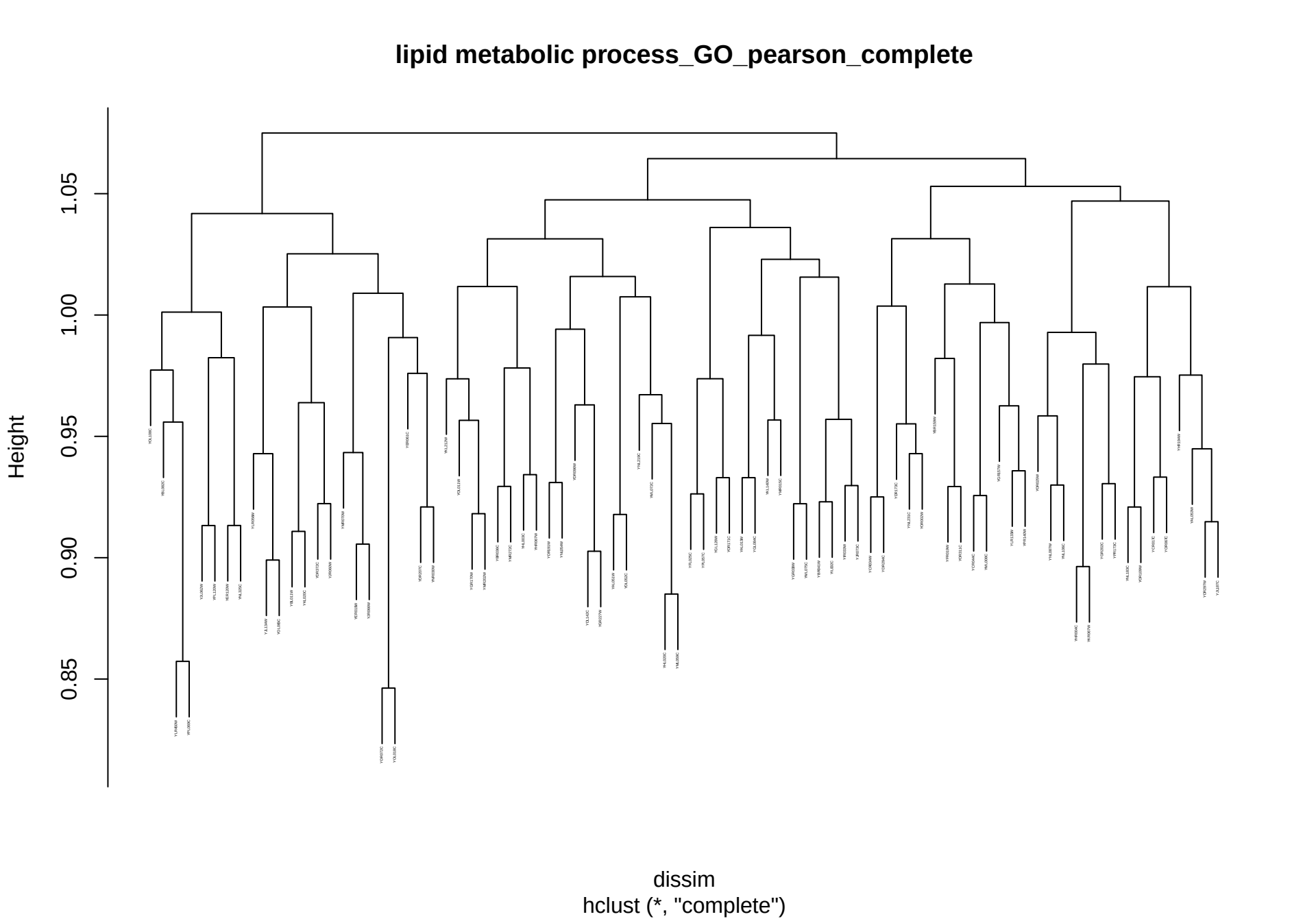

protein modification by small protein conjugation or removal_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

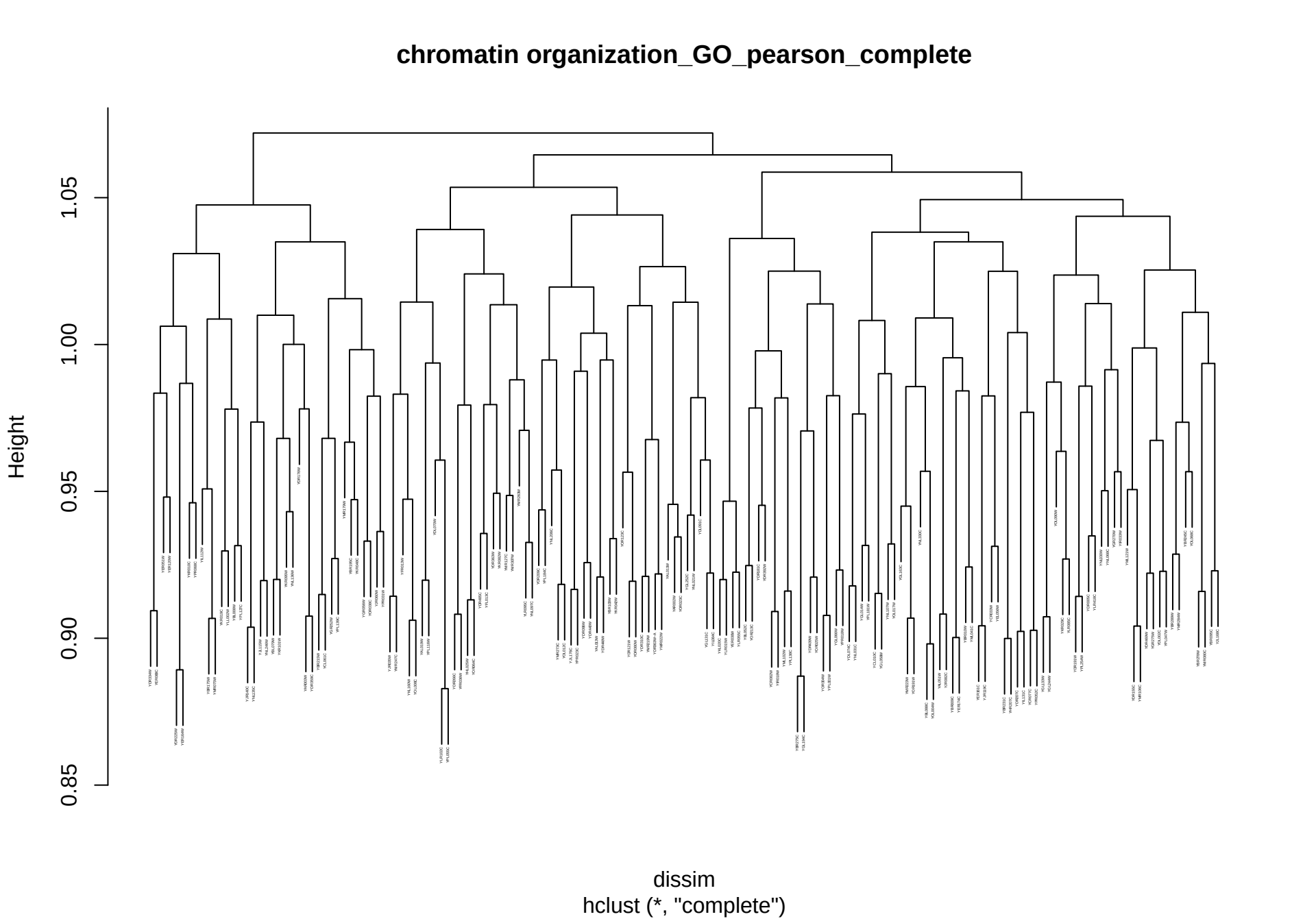

proteolysis involved in cellular protein catabolic process_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

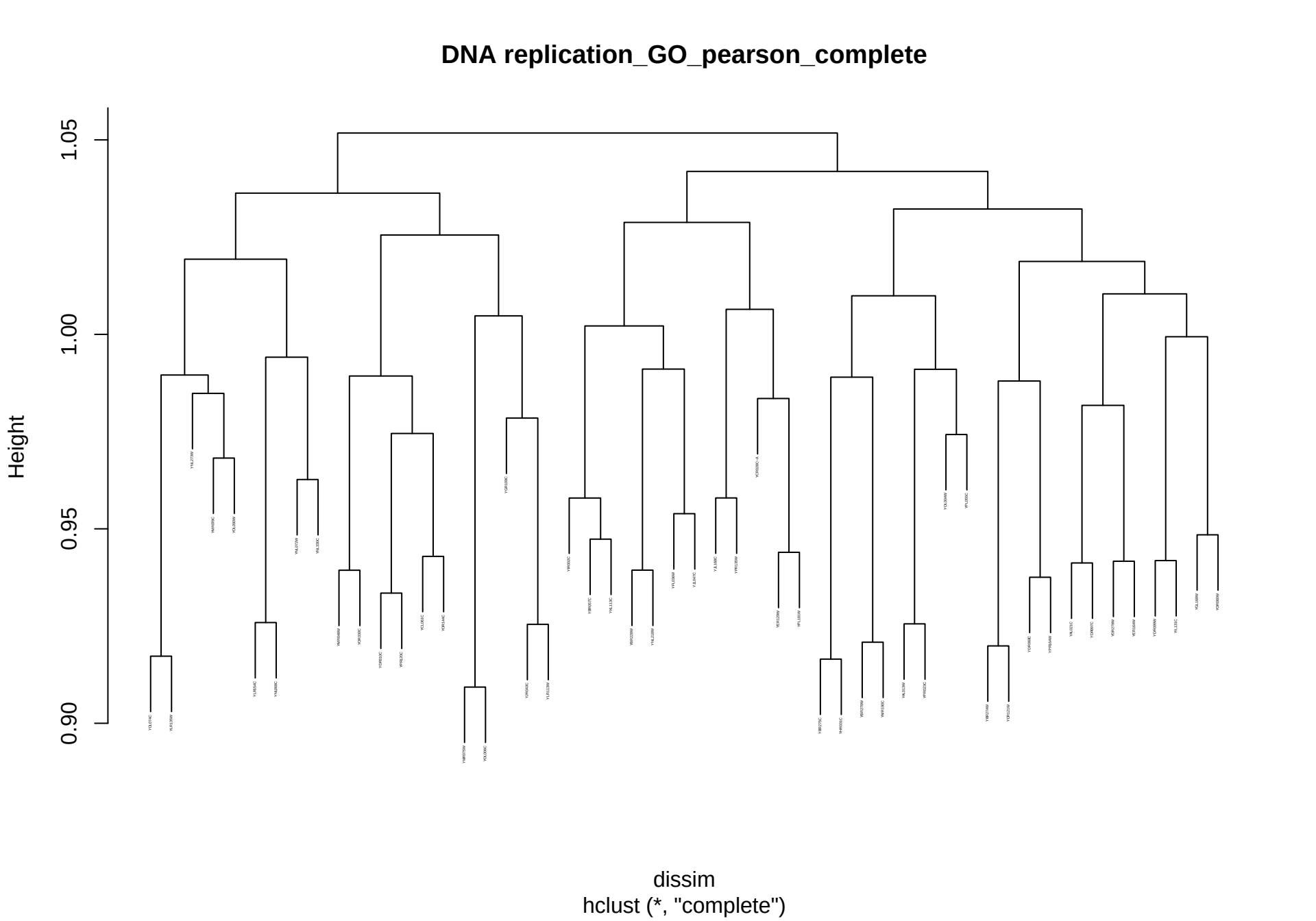

endoplasmic reticulum_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

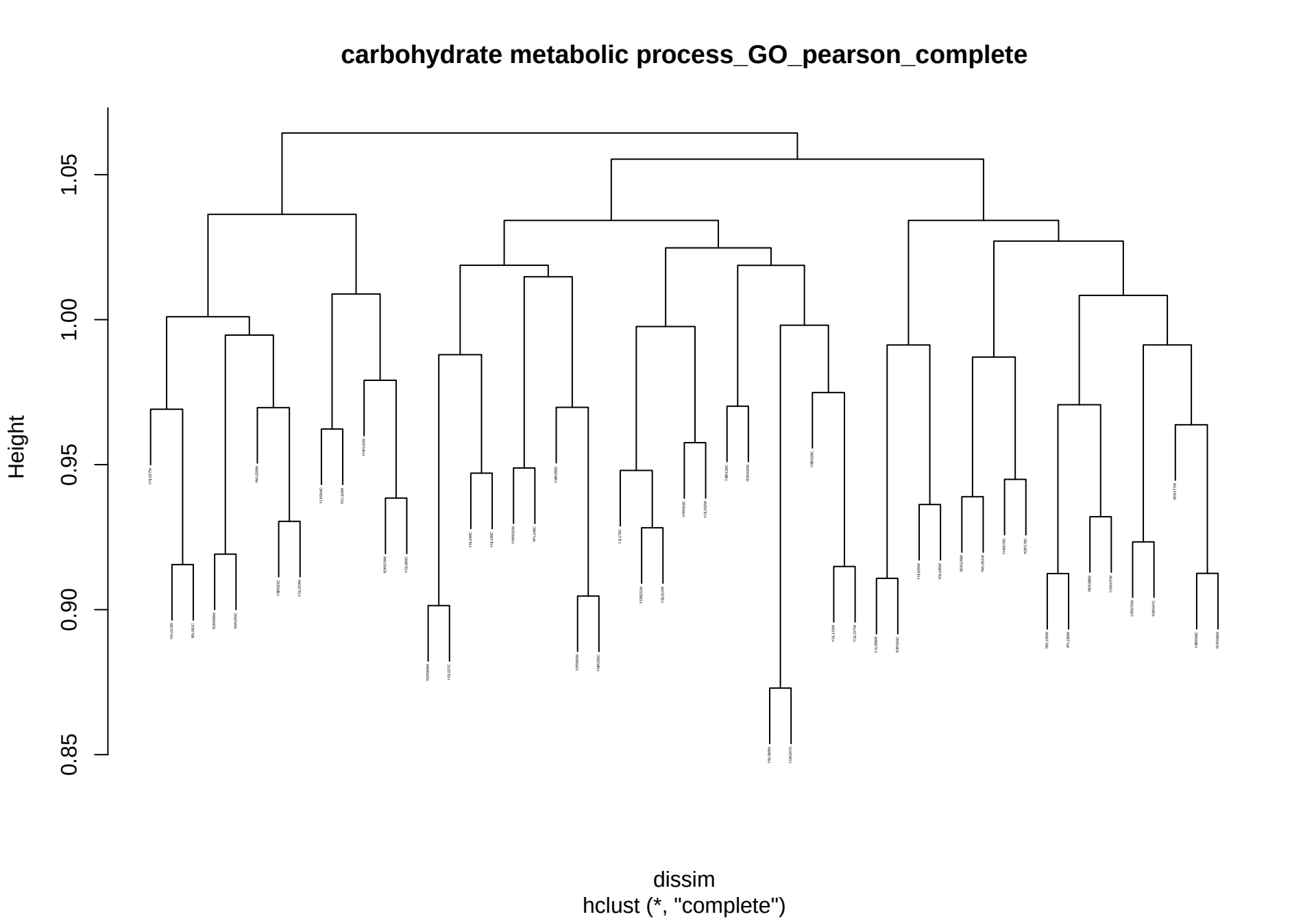

Golgi vesicle transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

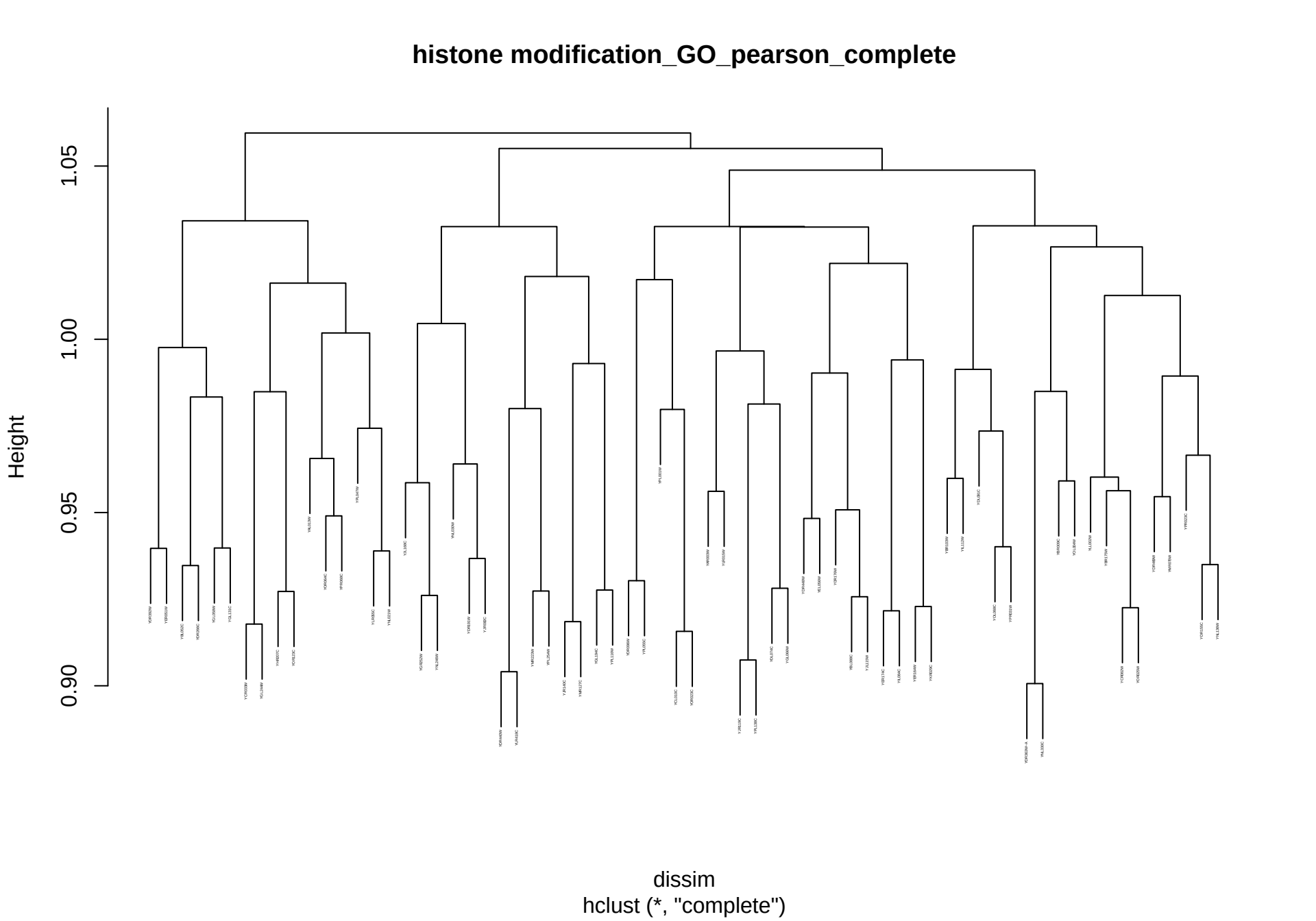

phosphatase activity_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

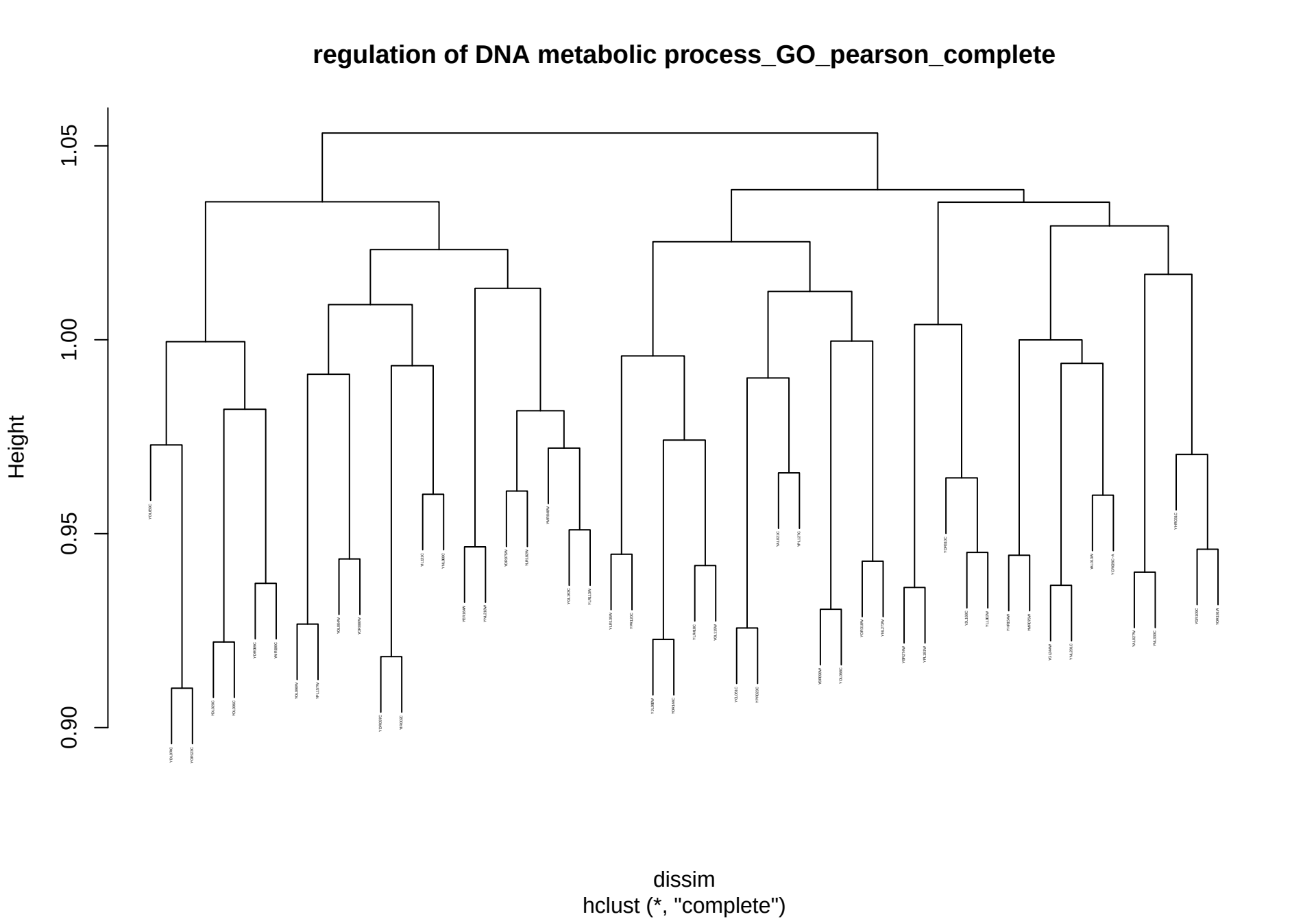

lipid metabolic process_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

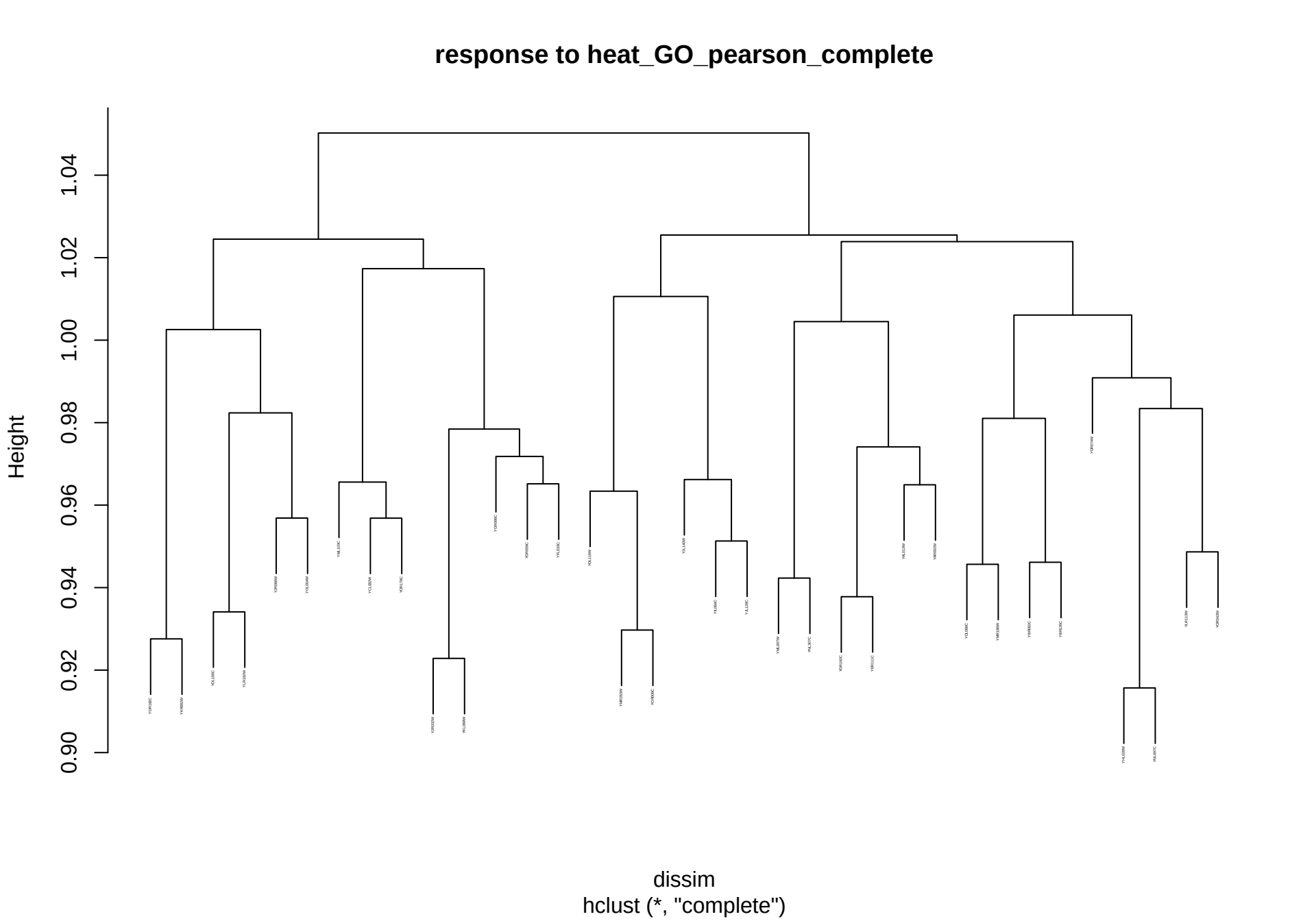

chromatin organization_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

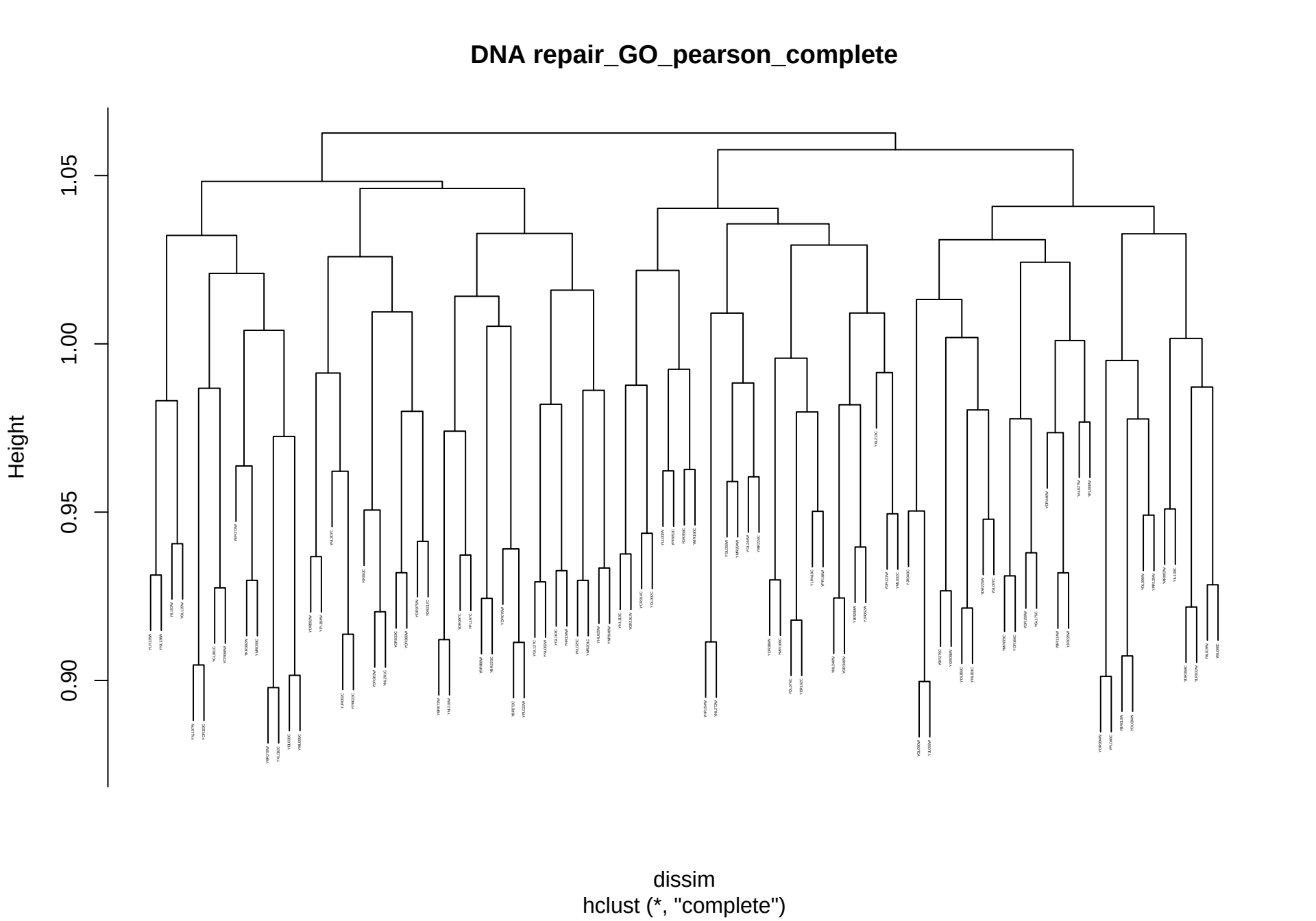

DNA replication_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

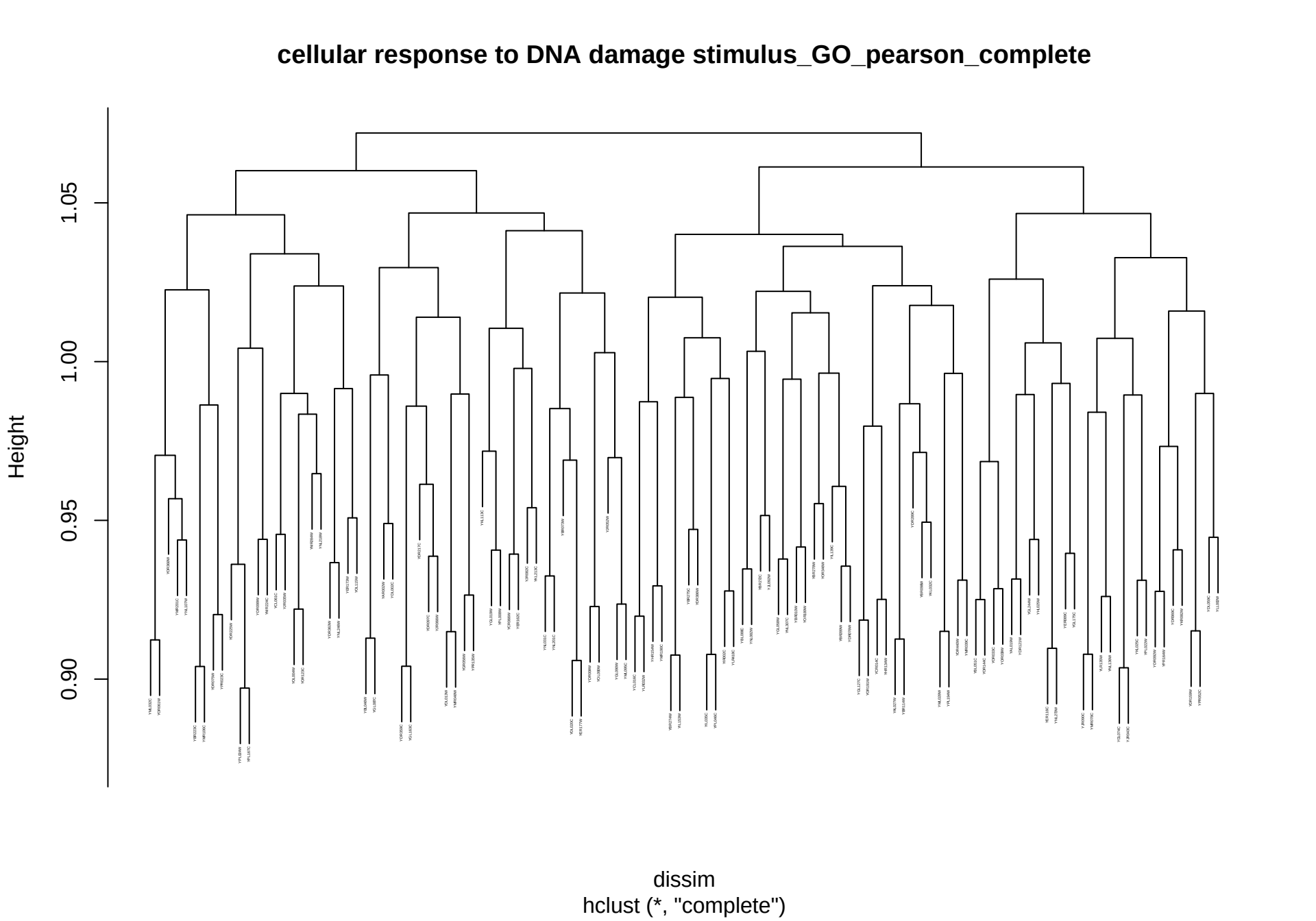

carbohydrate metabolic process_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

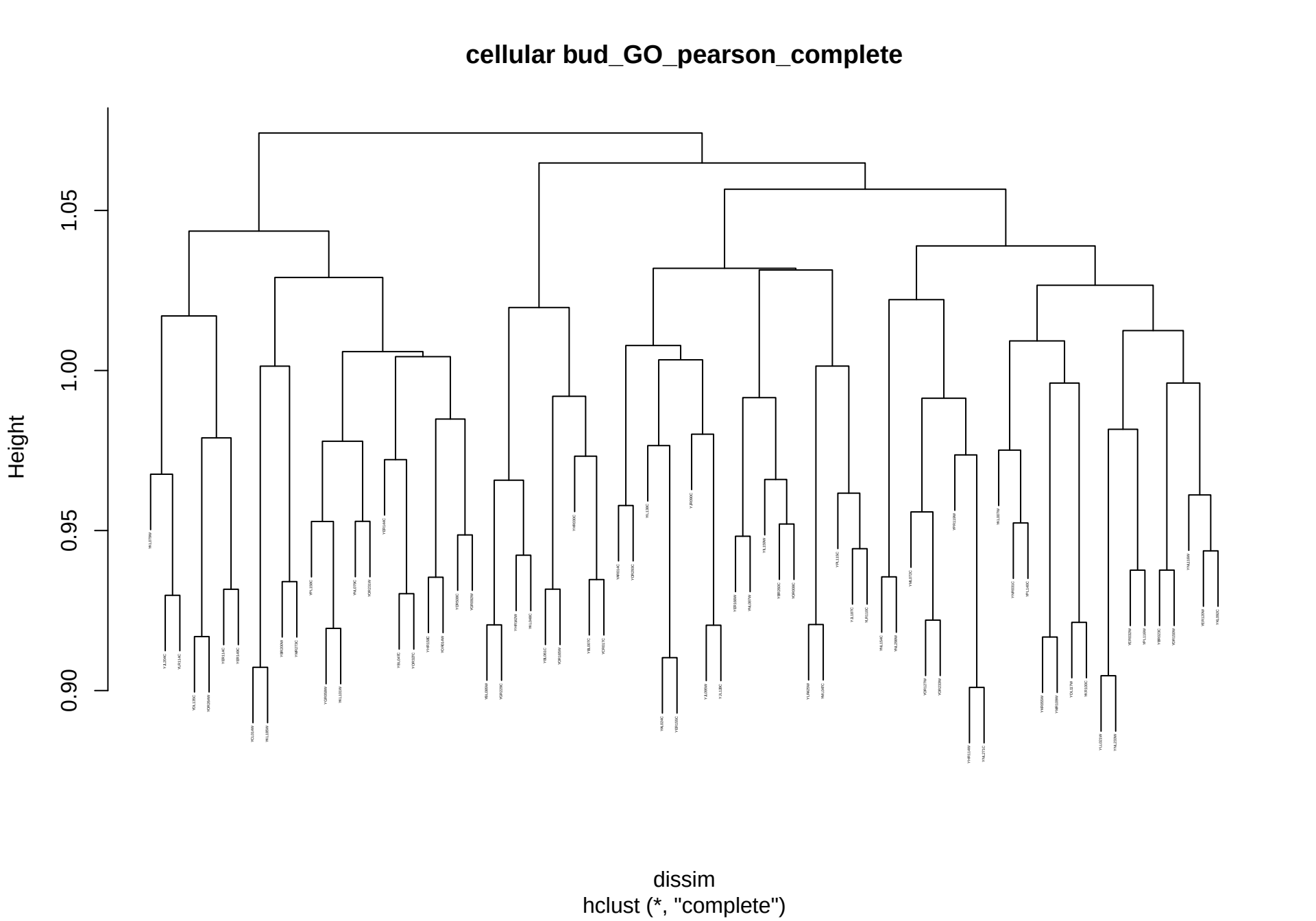

histone modification_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

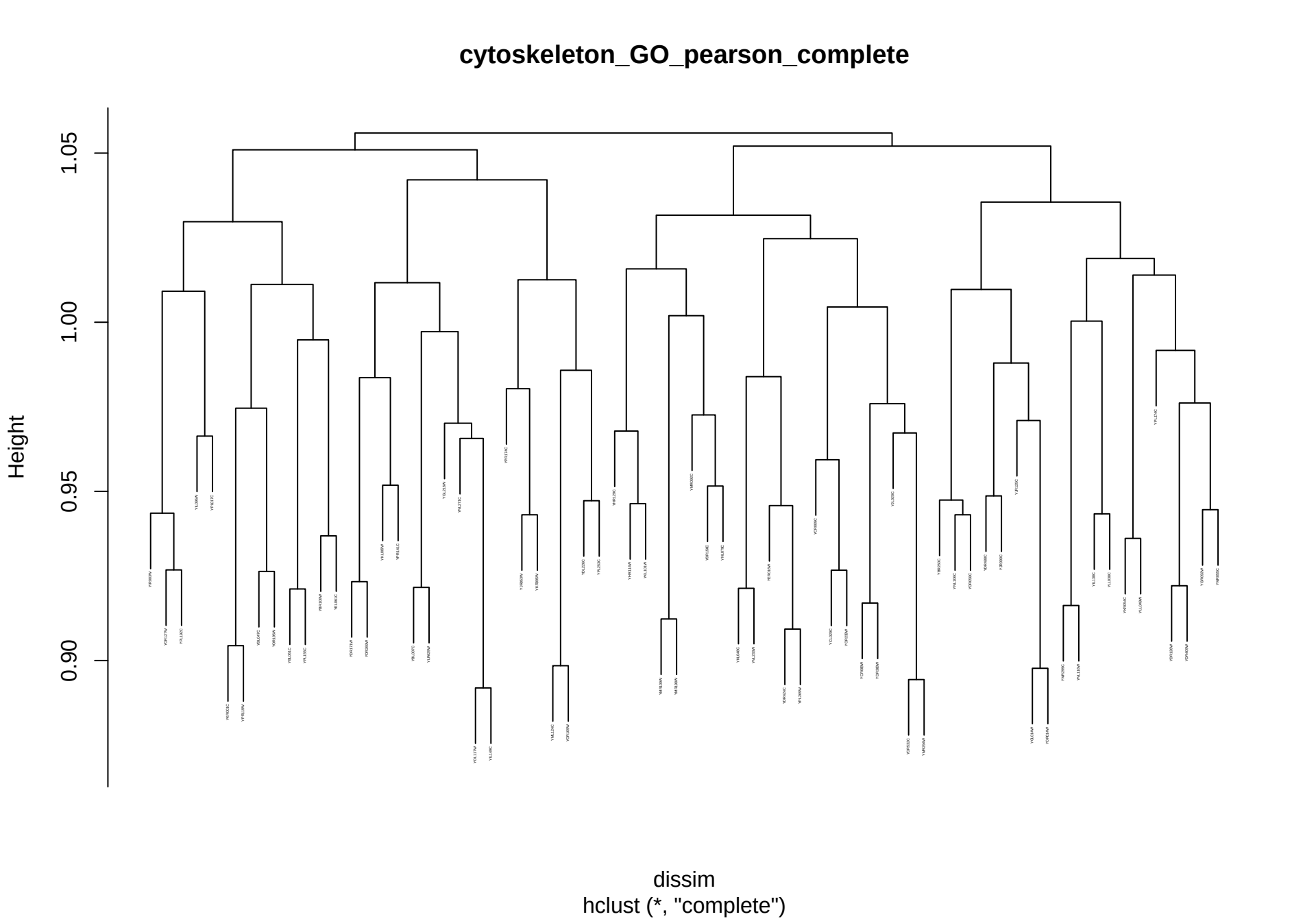

regulation of DNA metabolic process_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

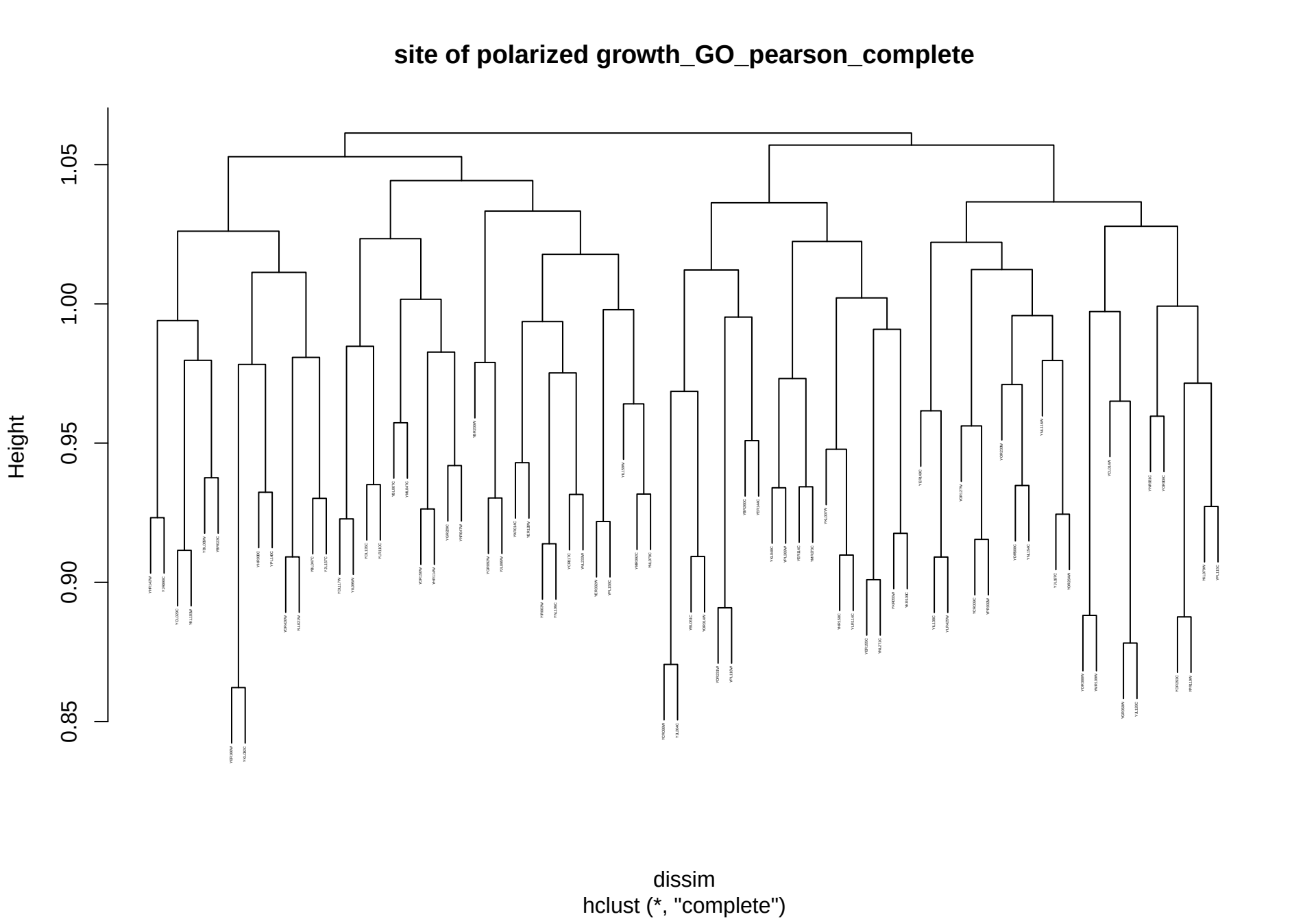

response to heat_GO_pearson_complete
Height
0.90
0.92
0.94
0.96
0.98
1.00
1.02
1.04
dissim
hclust (*, "complete")

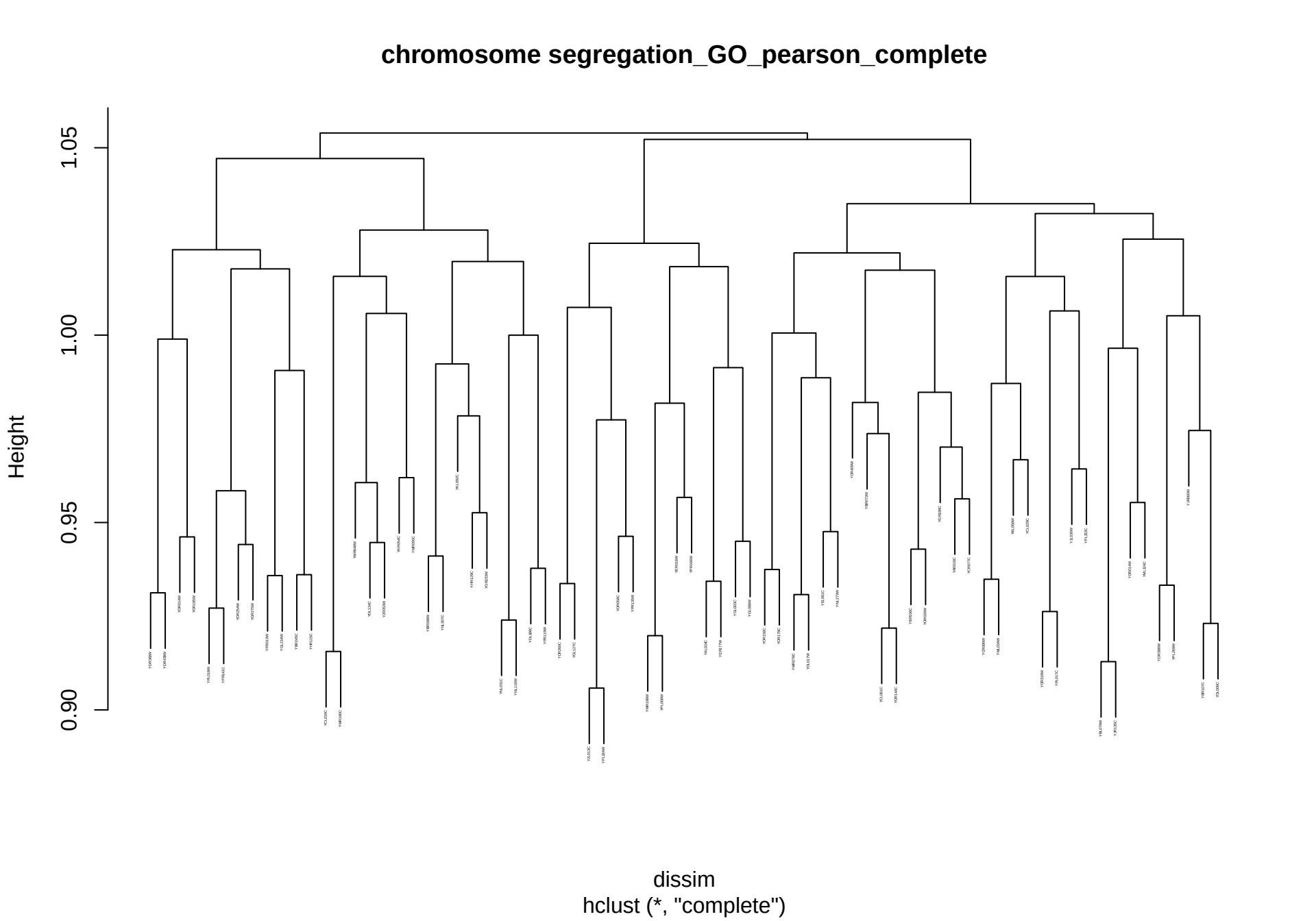

DNA repair_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

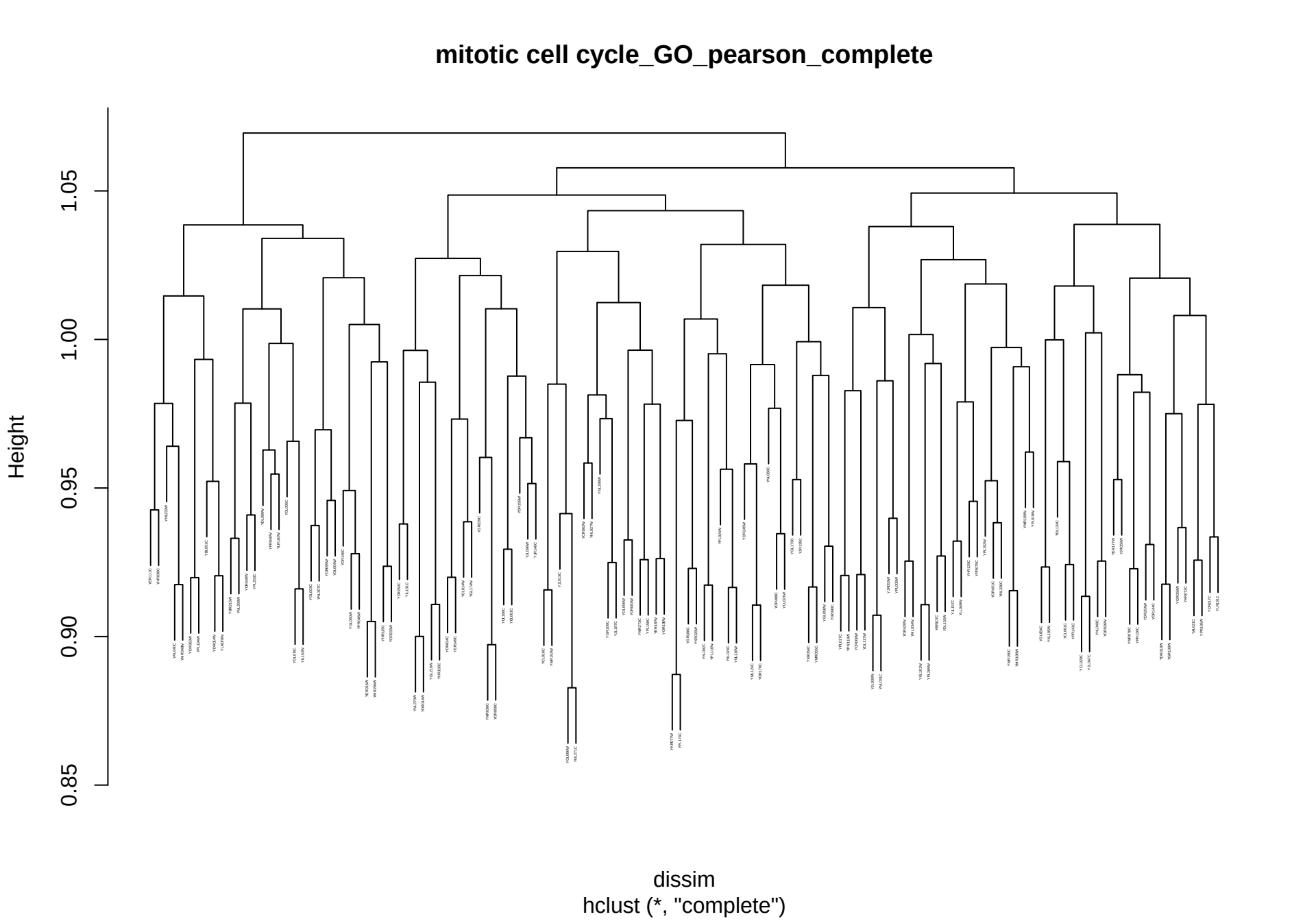

cellular response to DNA damage stimulus_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

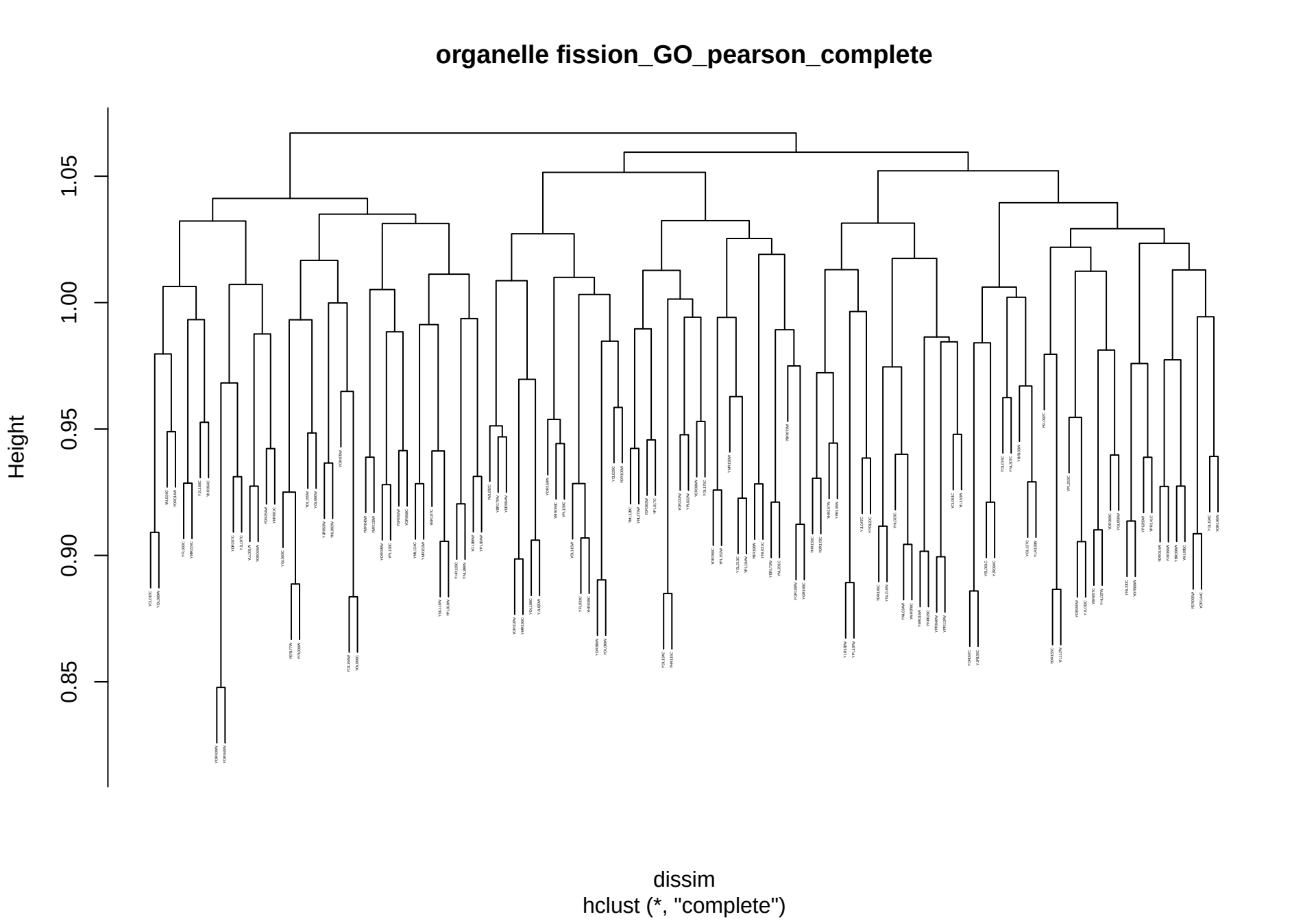

cellular bud_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

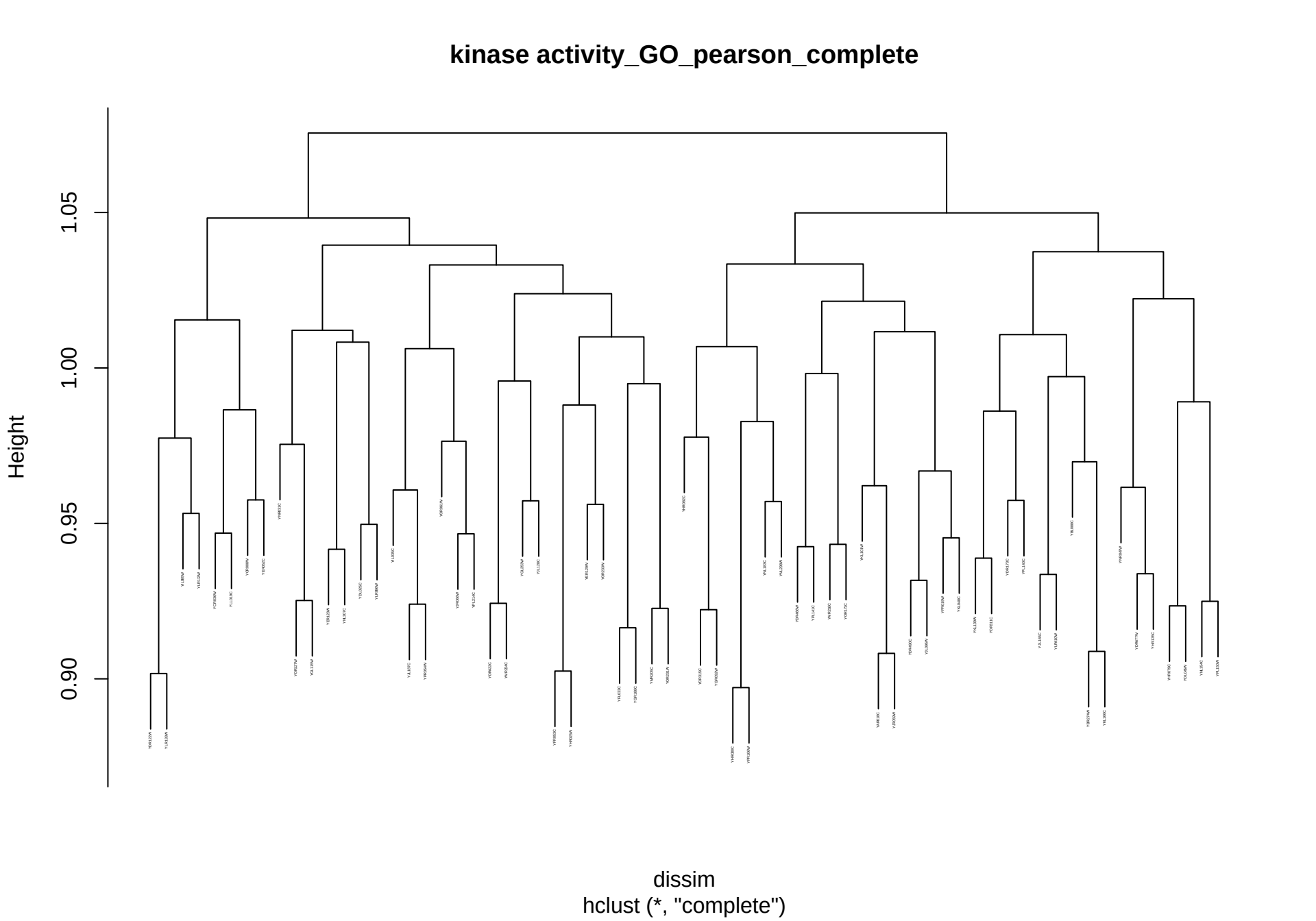

cytoskeleton_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

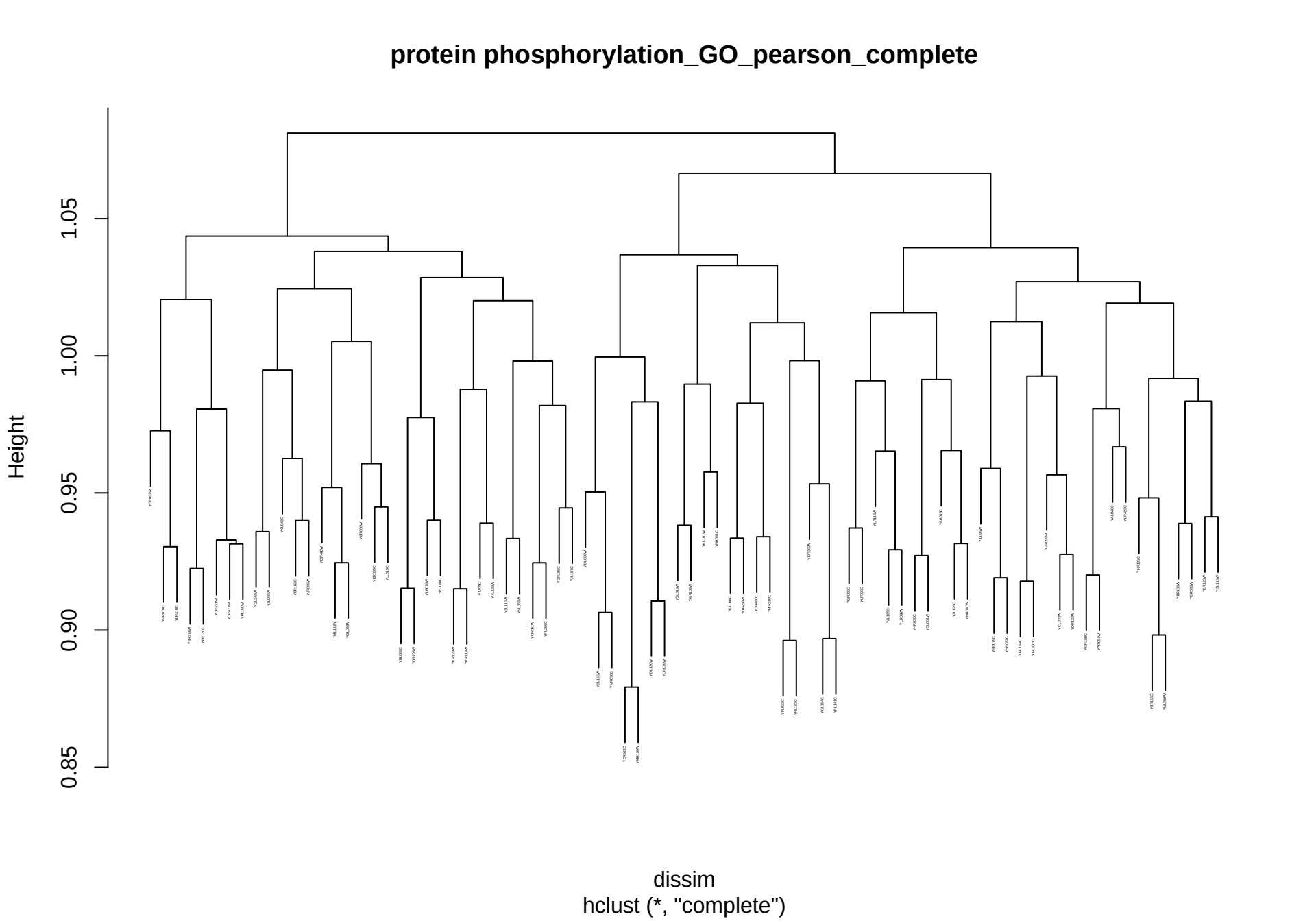

site of polarized growth_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

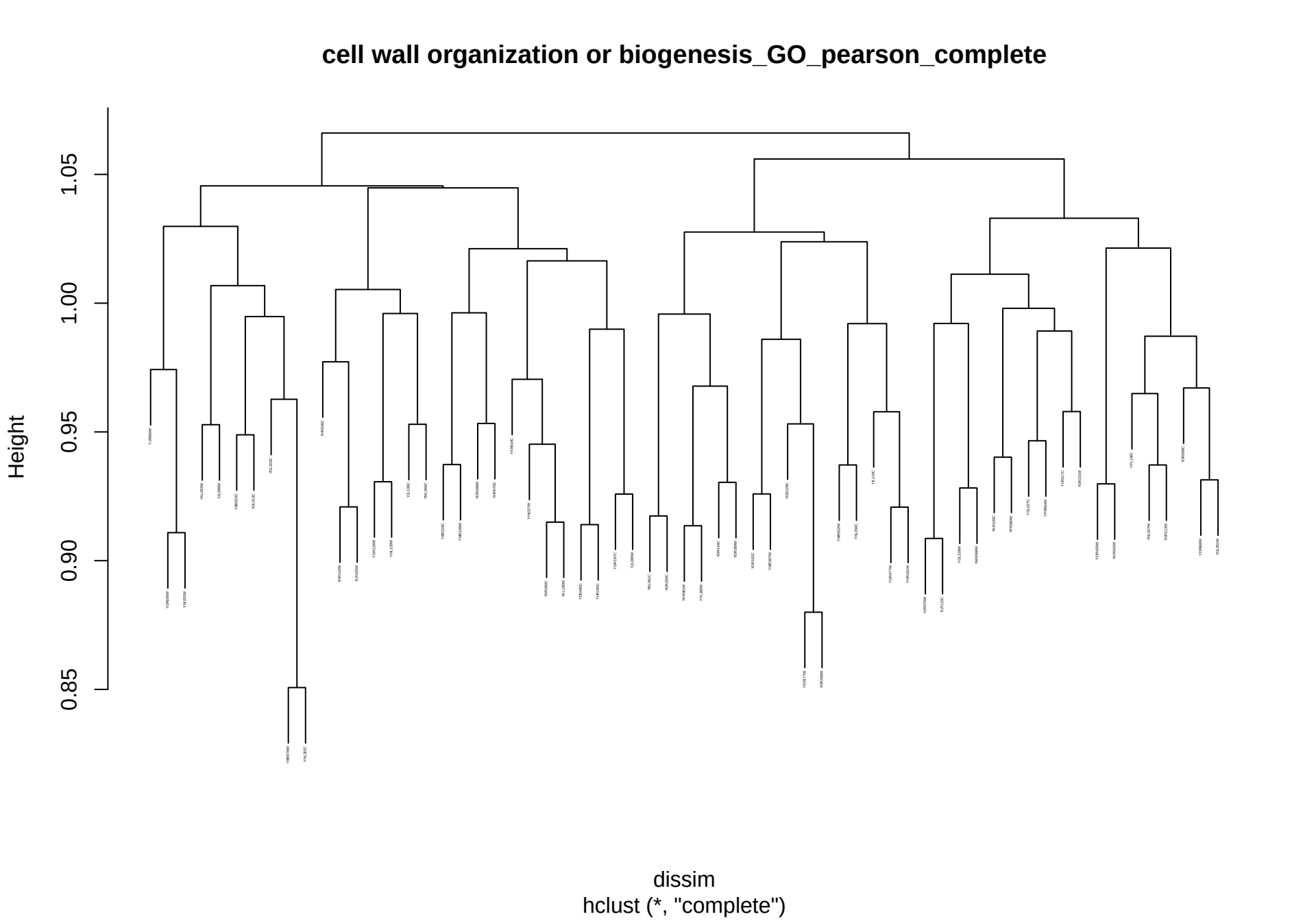

chromosome segregation_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

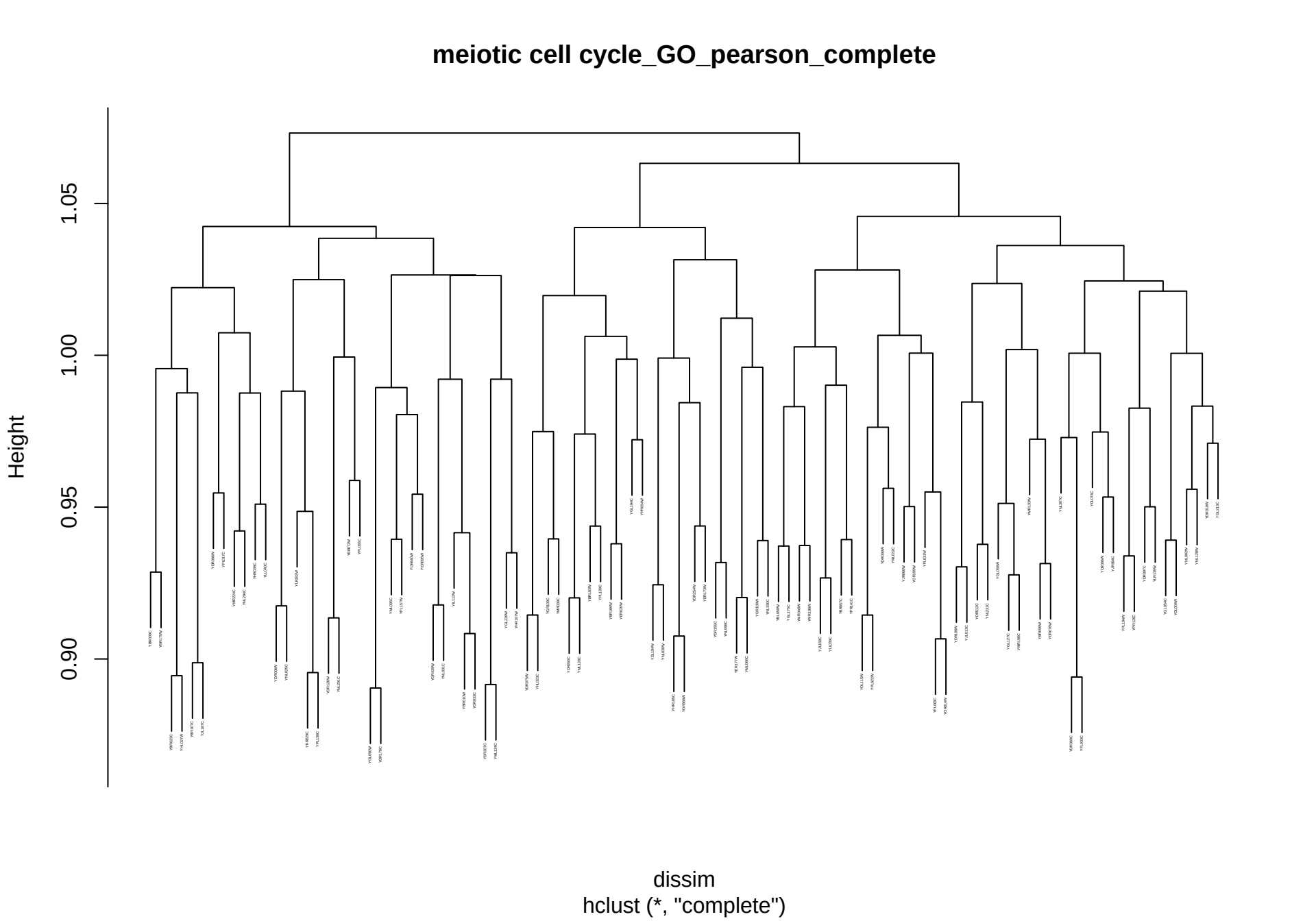

mitotic cell cycle_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

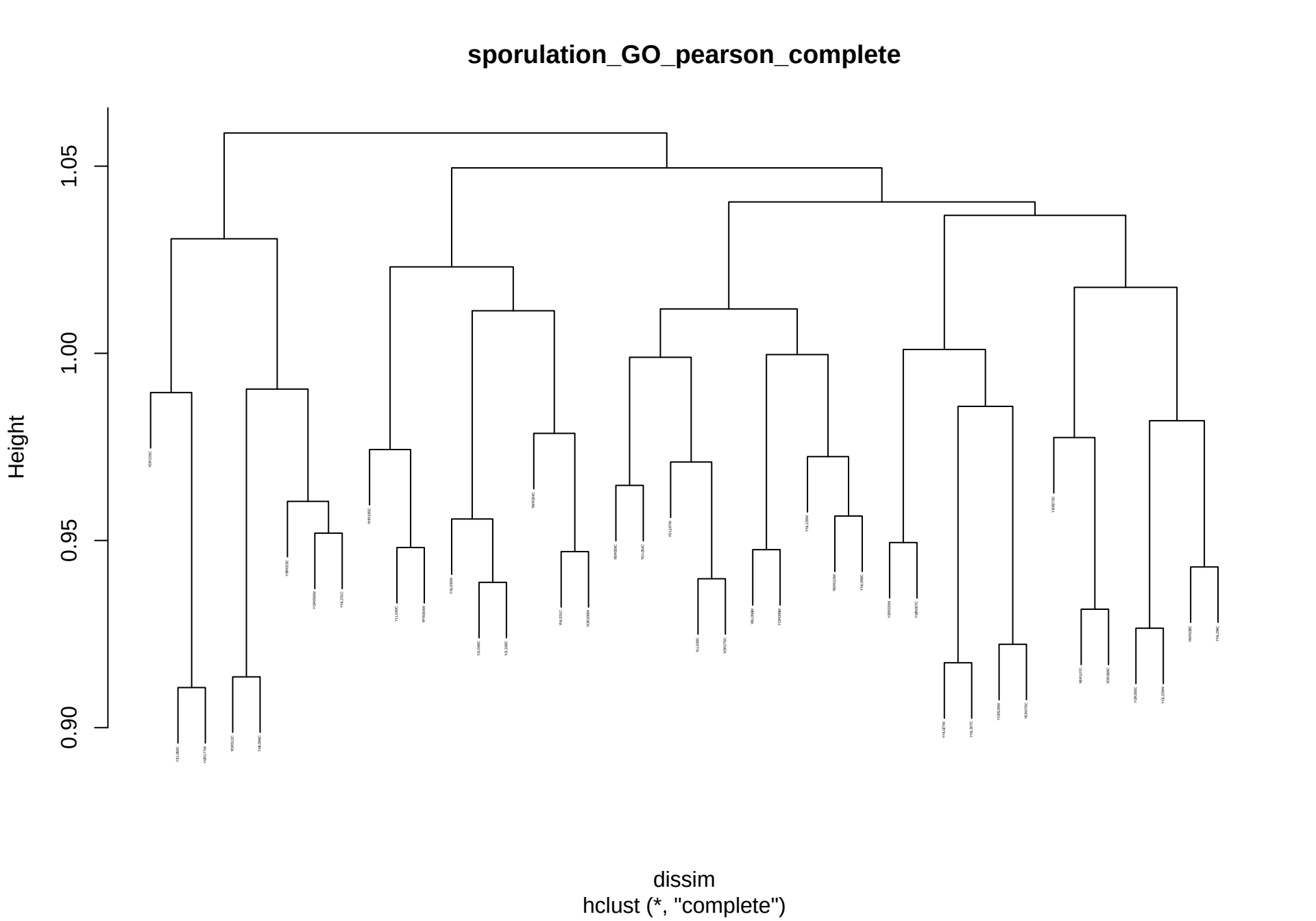

organelle fission_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

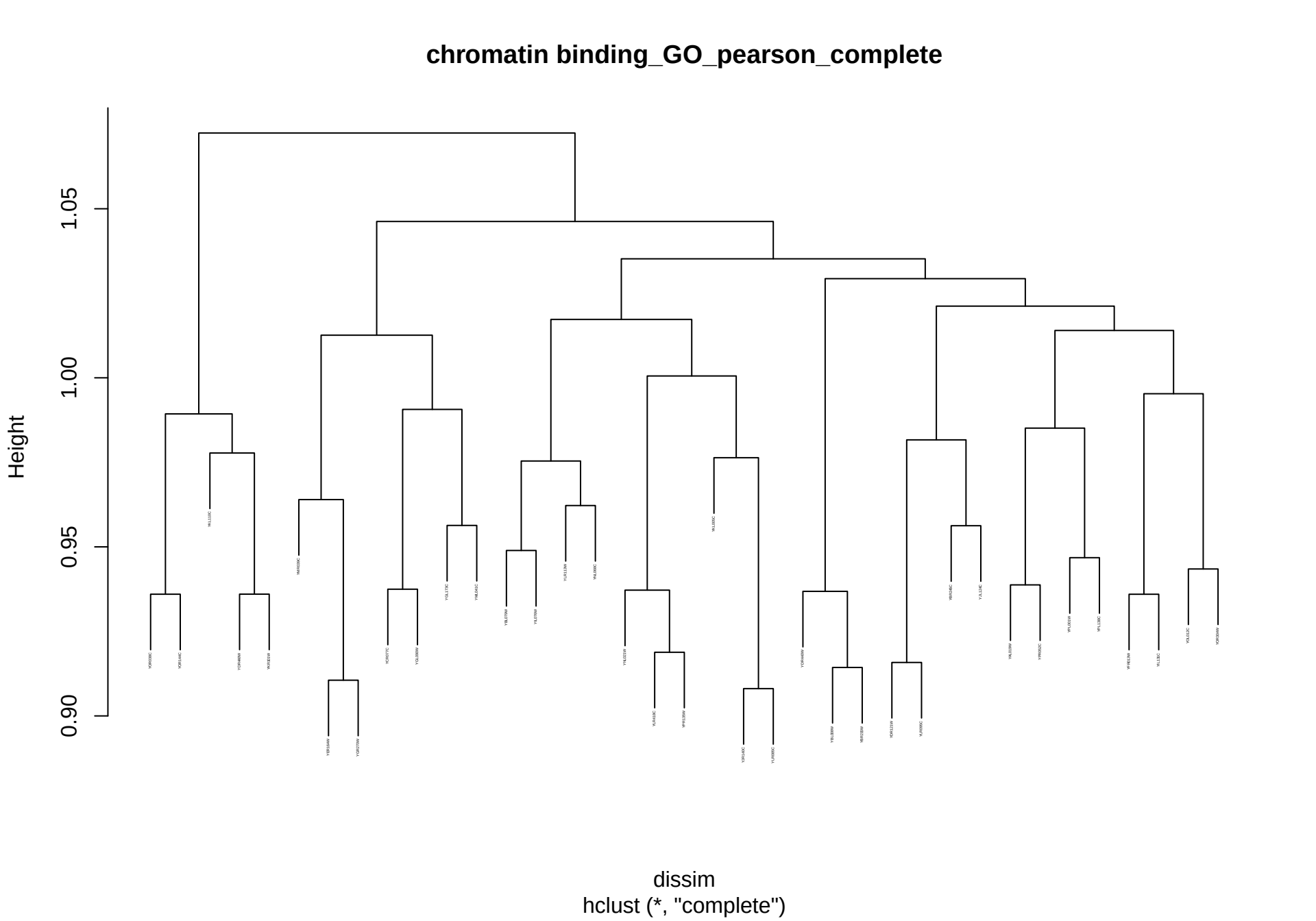

kinase activity_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

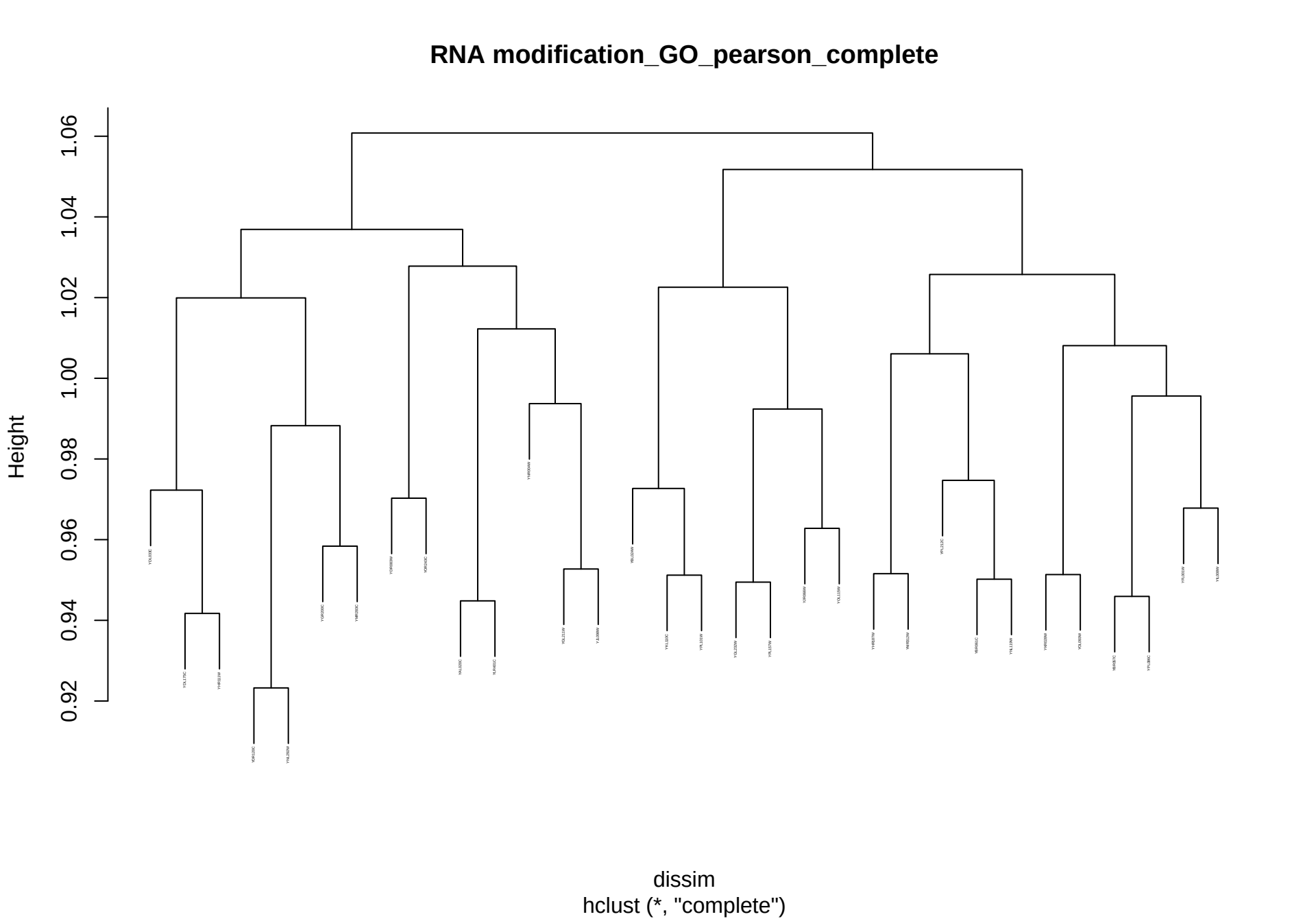

protein phosphorylation_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

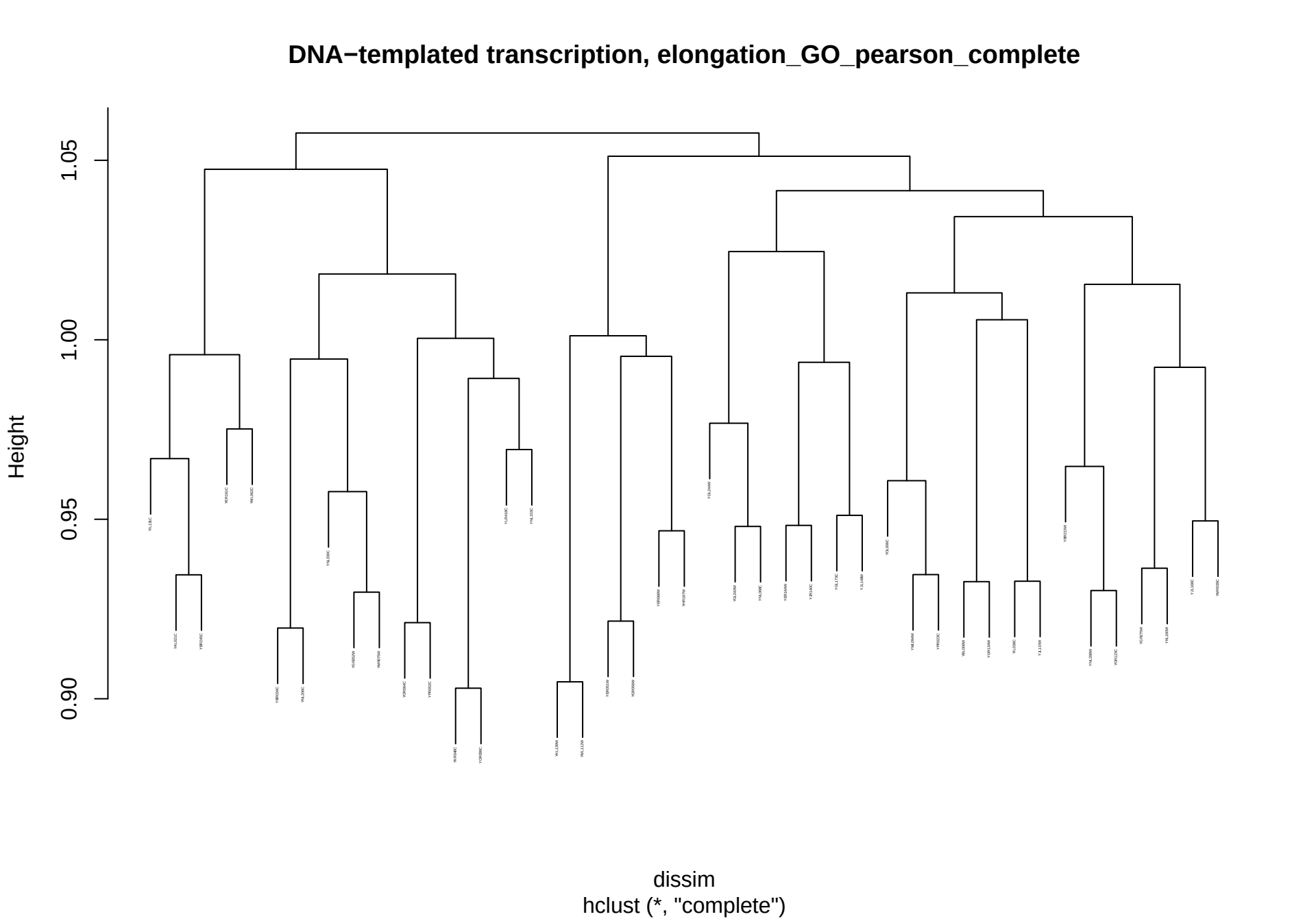

cell wall organization or biogenesis_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

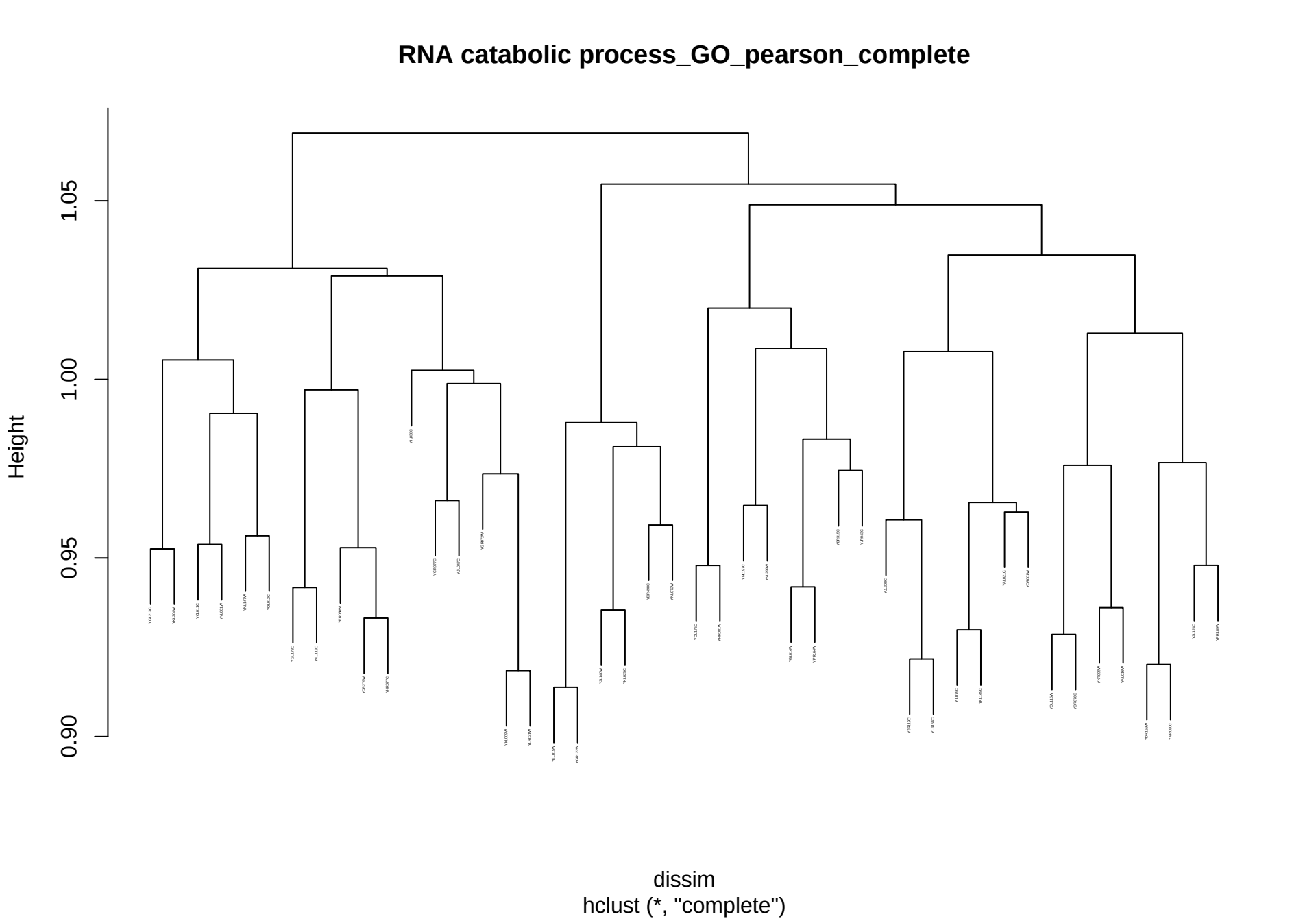

meiotic cell cycle_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

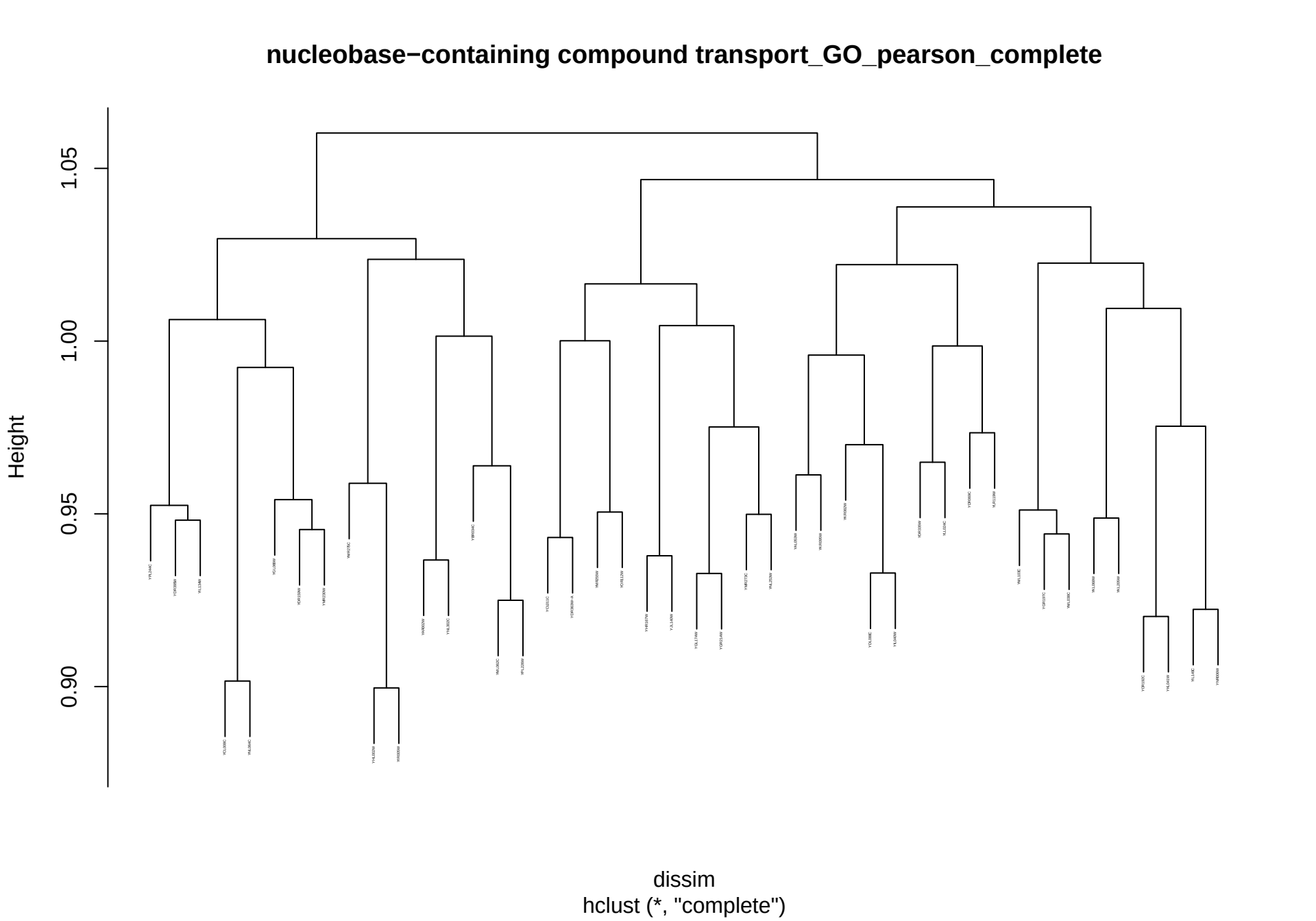

sporulation_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

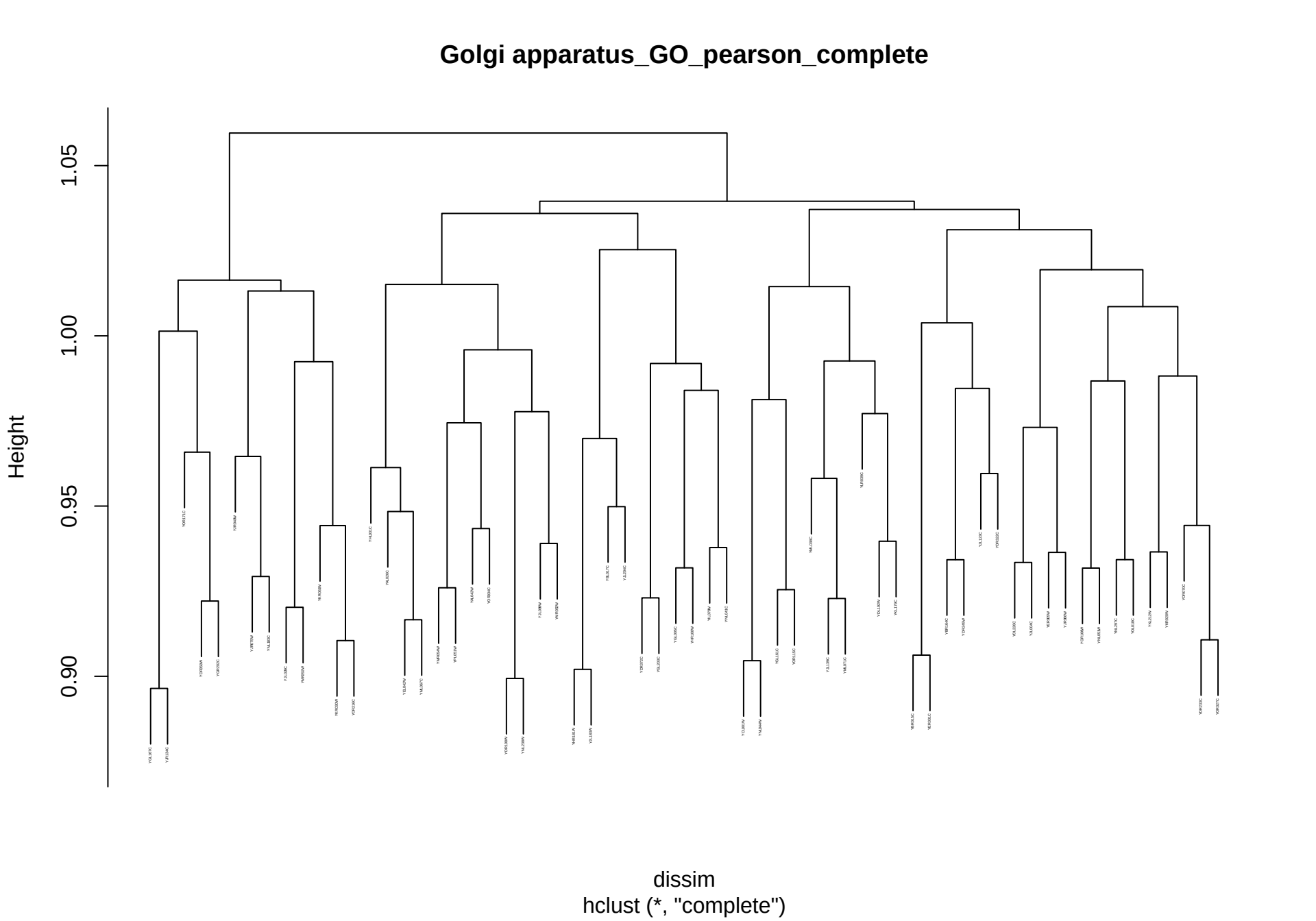

chromatin binding_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

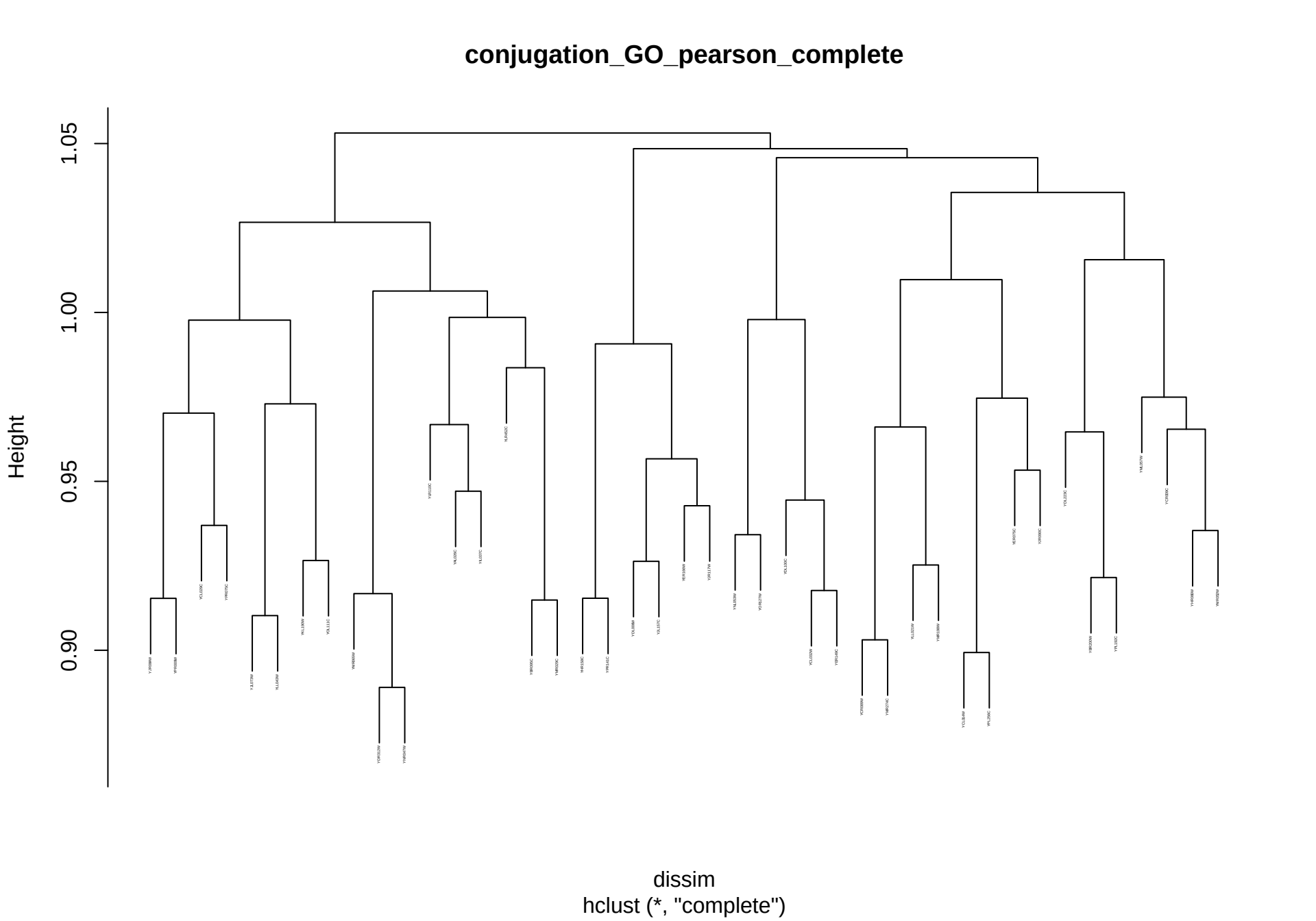

RNA modification_GO_pearson_complete
Height
0.92
0.94
0.96
0.98
1.00
1.02
1.04
1.06
dissim
hclust (*, "complete")

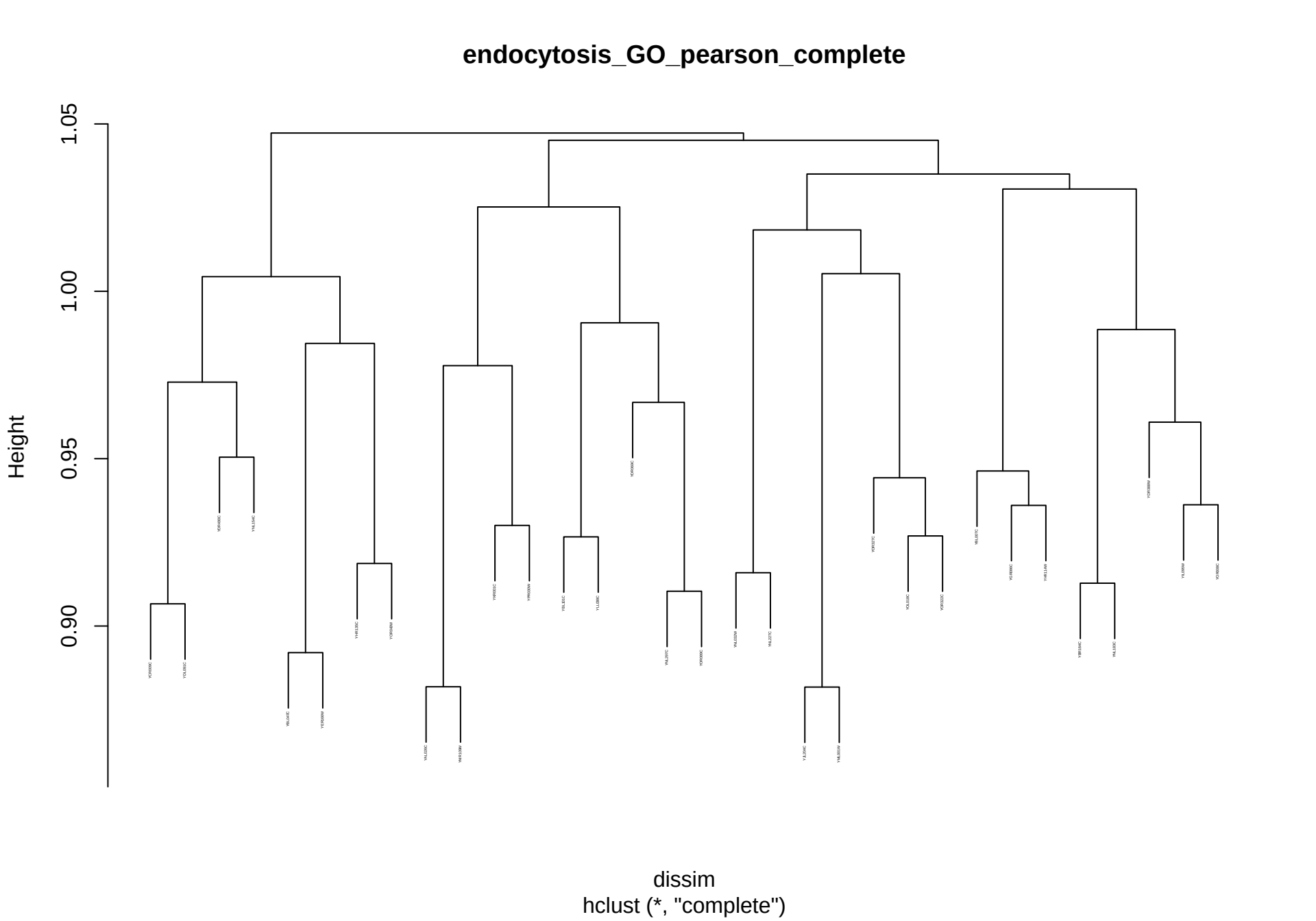

DNA−templated transcription, elongation_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

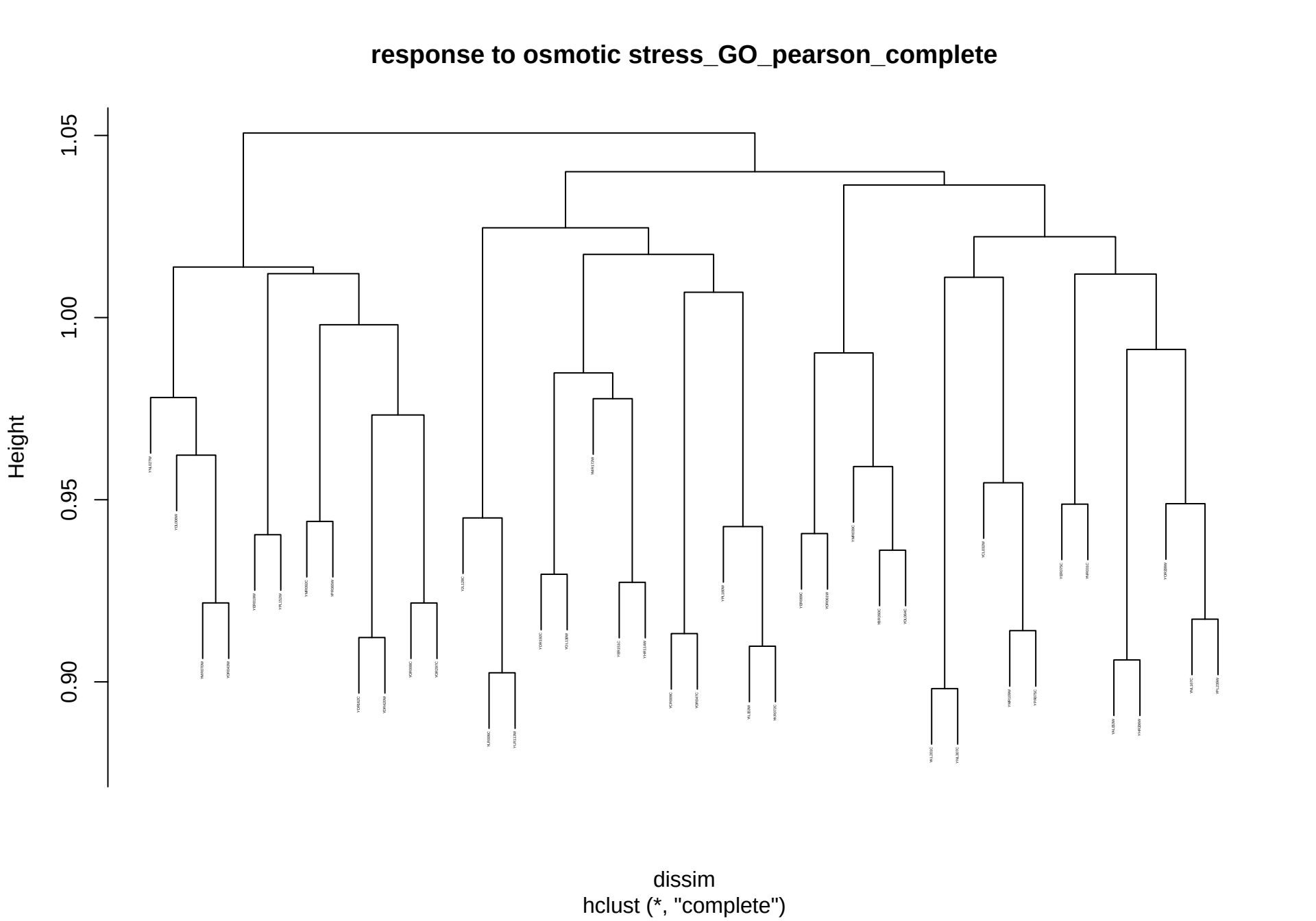

RNA catabolic process_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

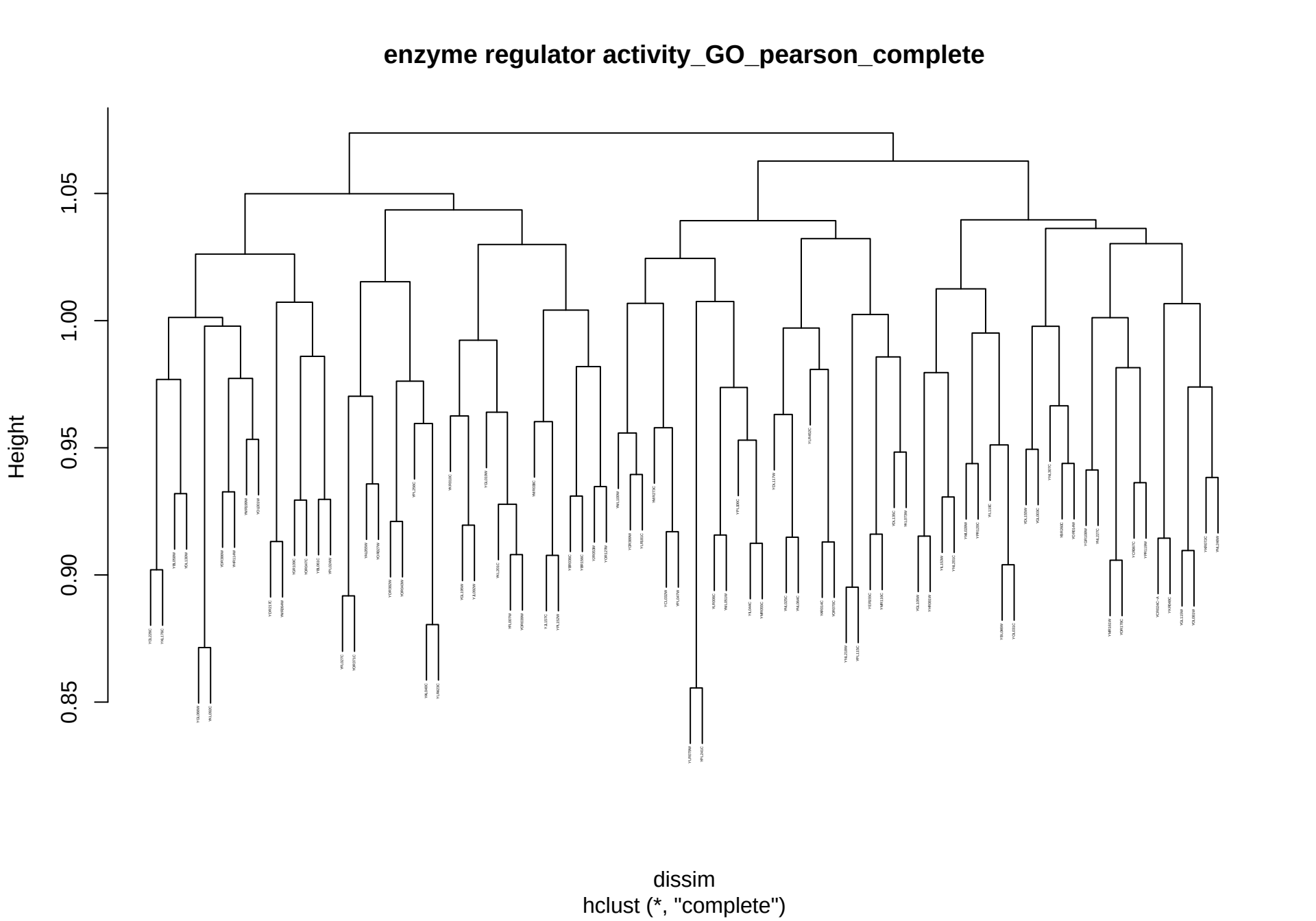

nucleobase−containing compound transport_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

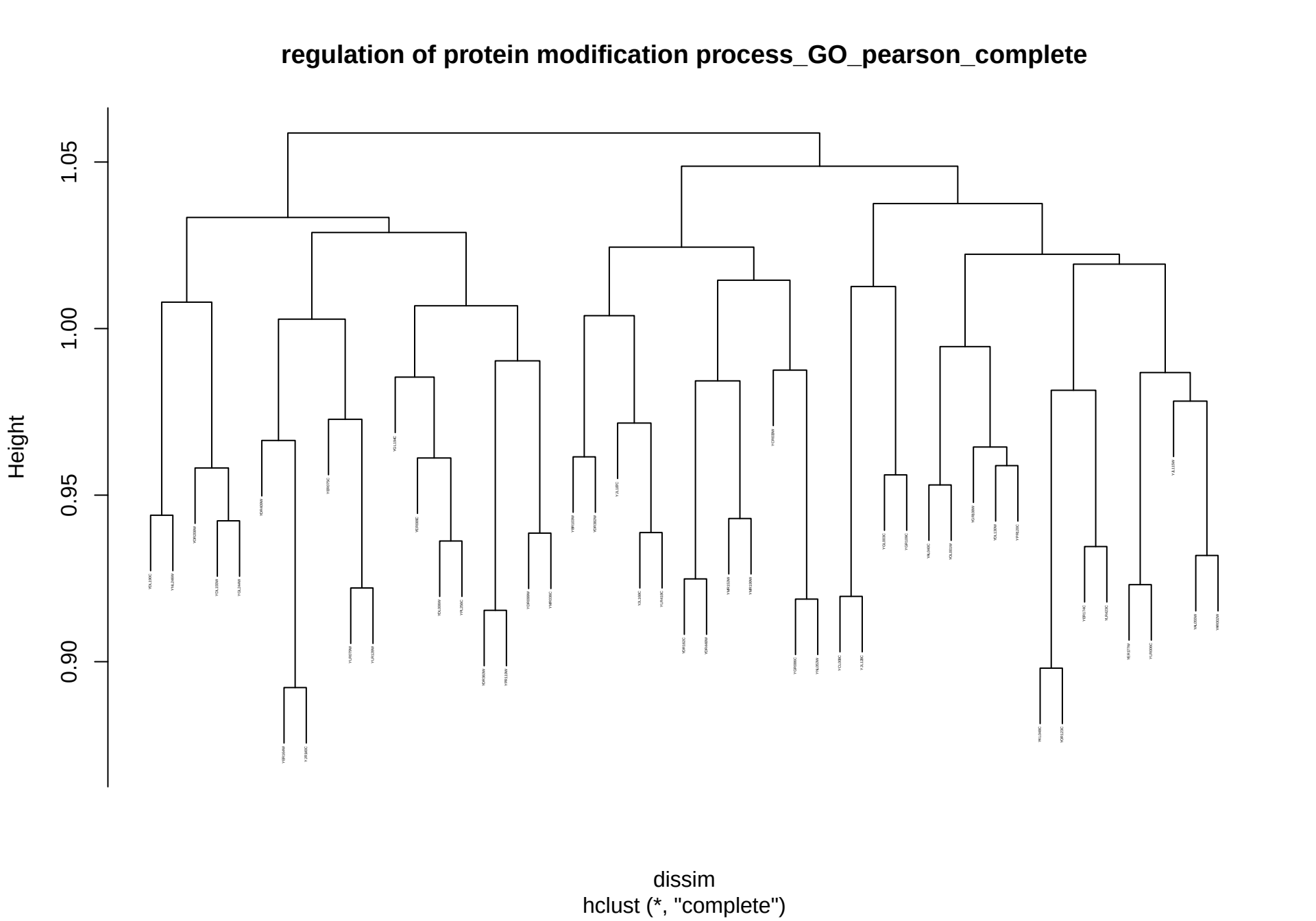

Golgi apparatus_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

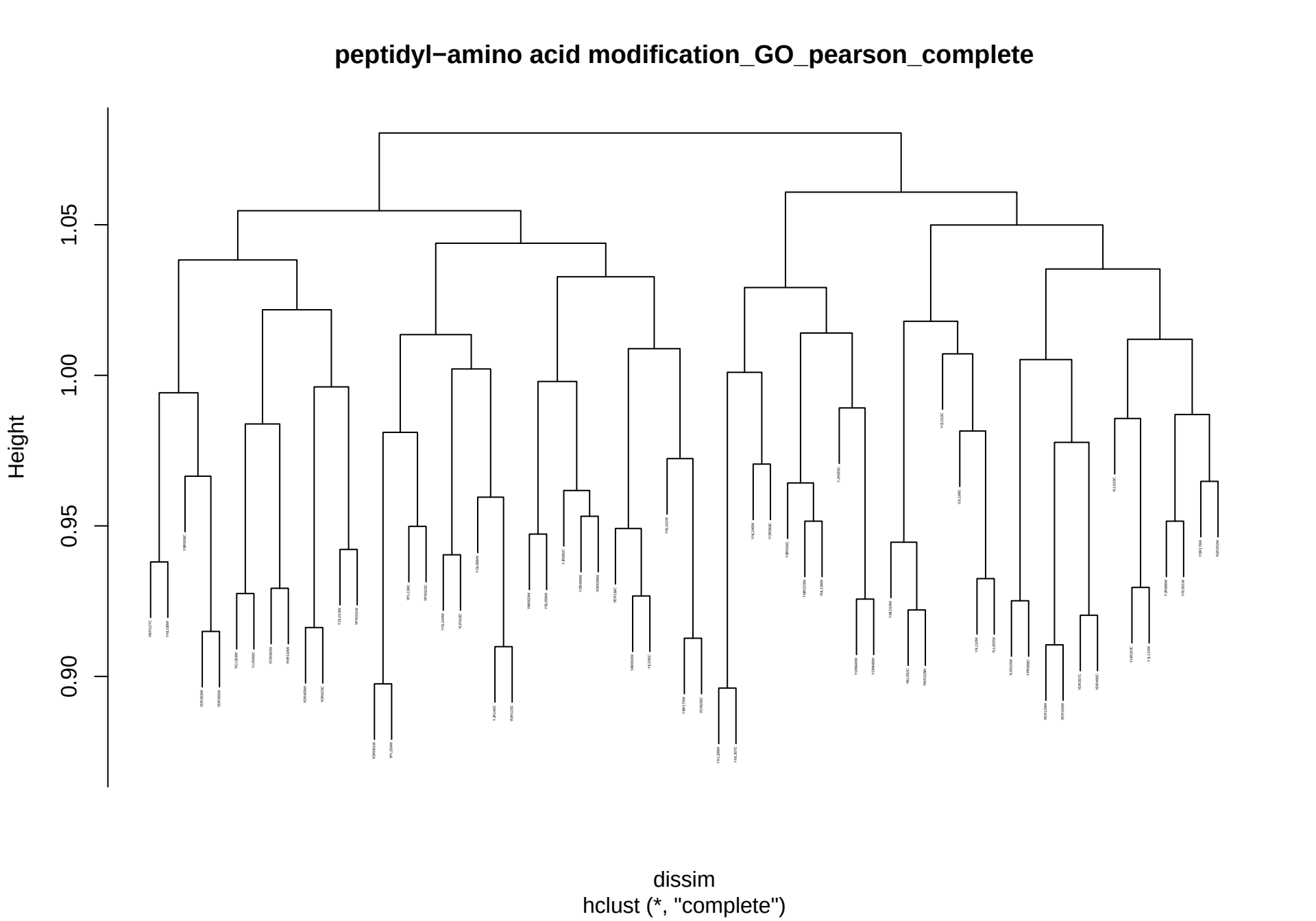

conjugation_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

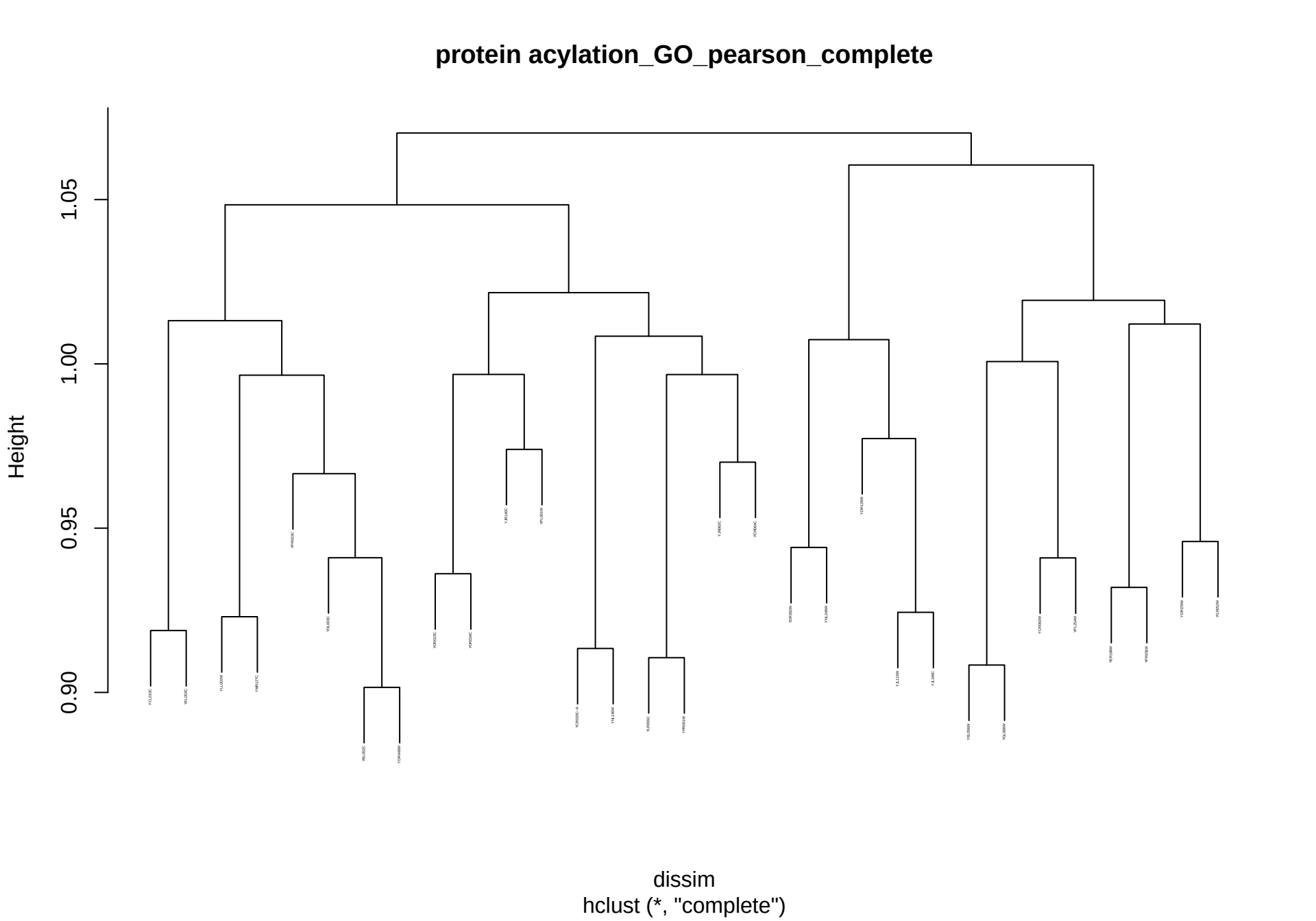

endocytosis_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

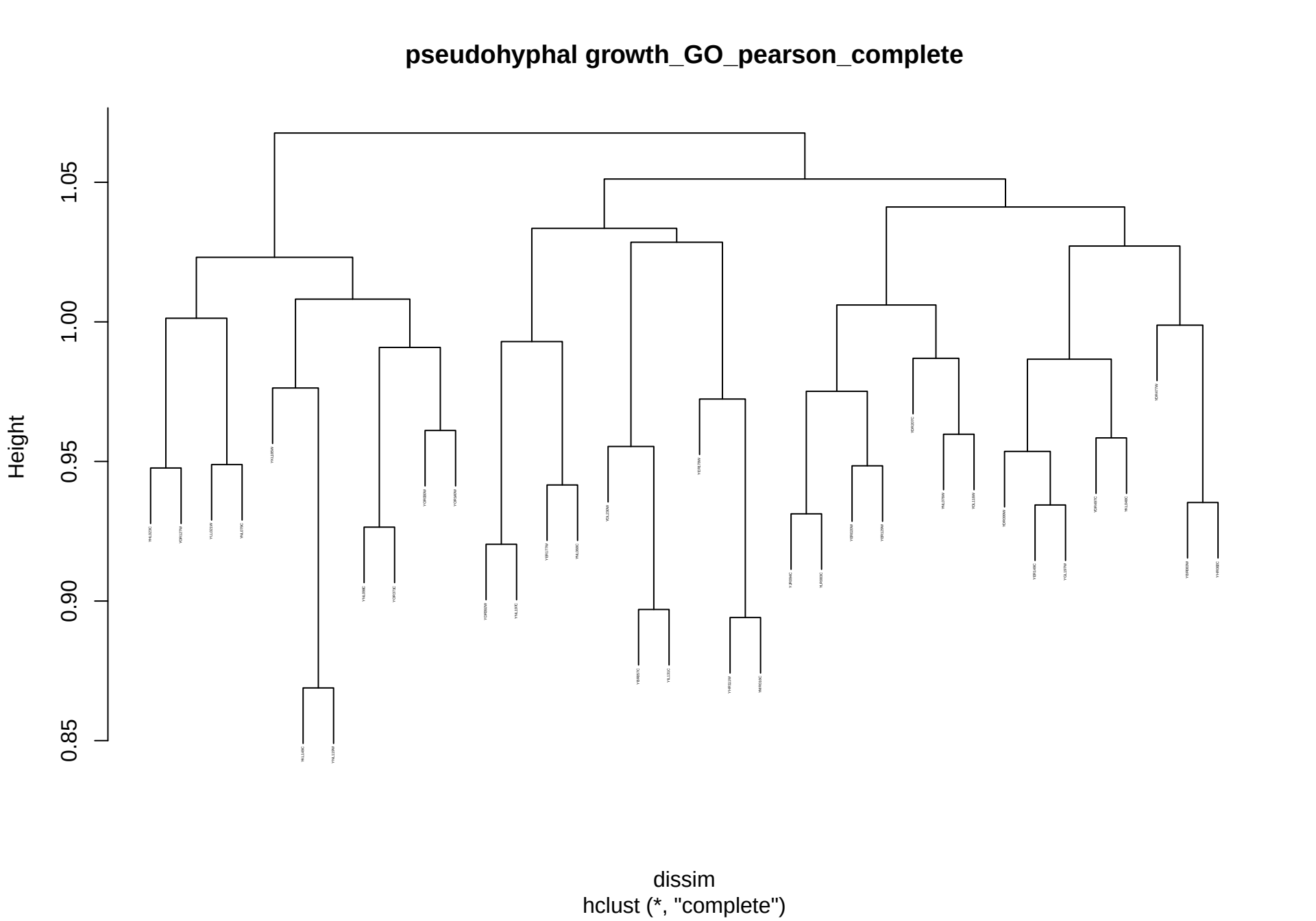

response to osmotic stress_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

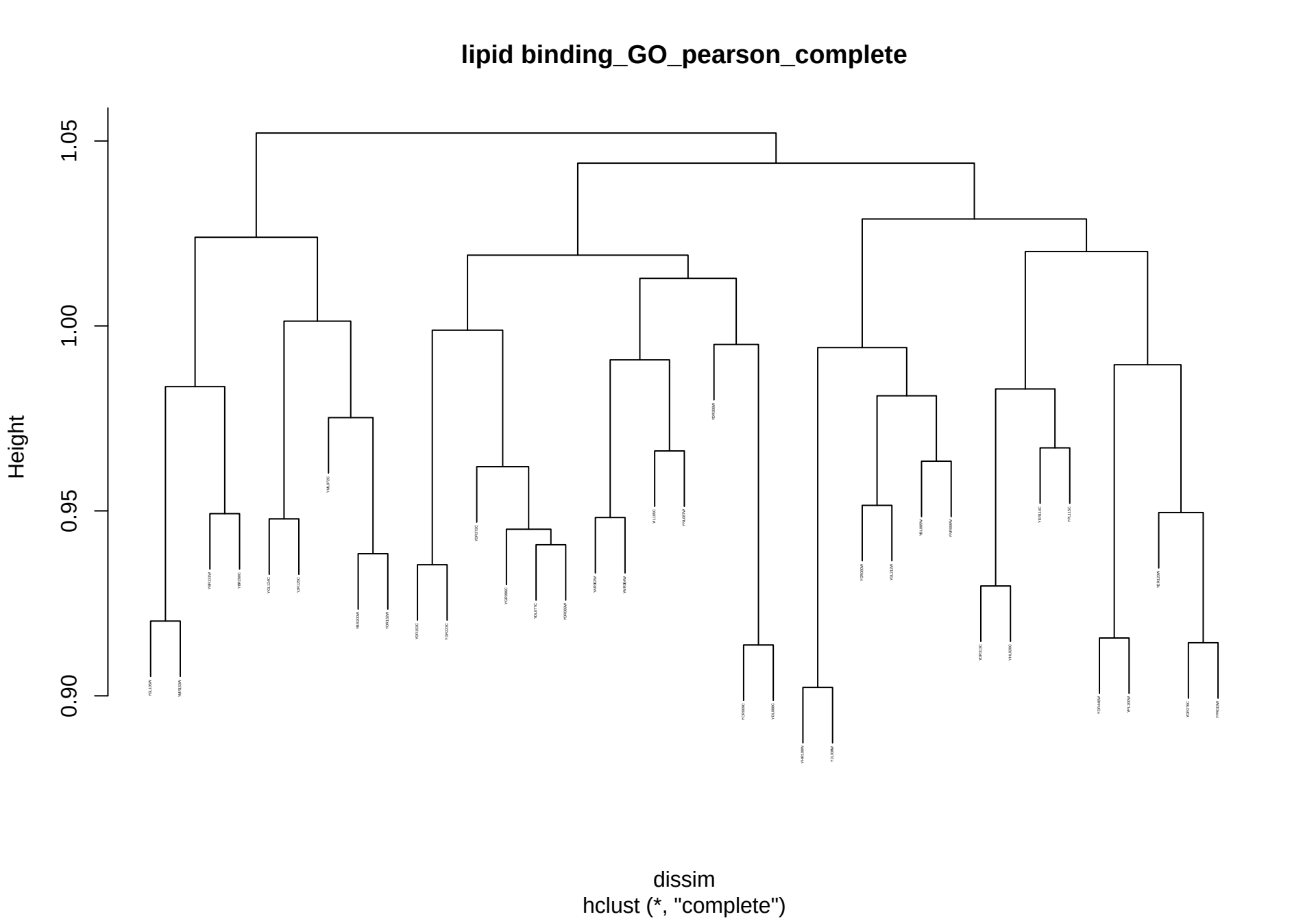

enzyme regulator activity_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

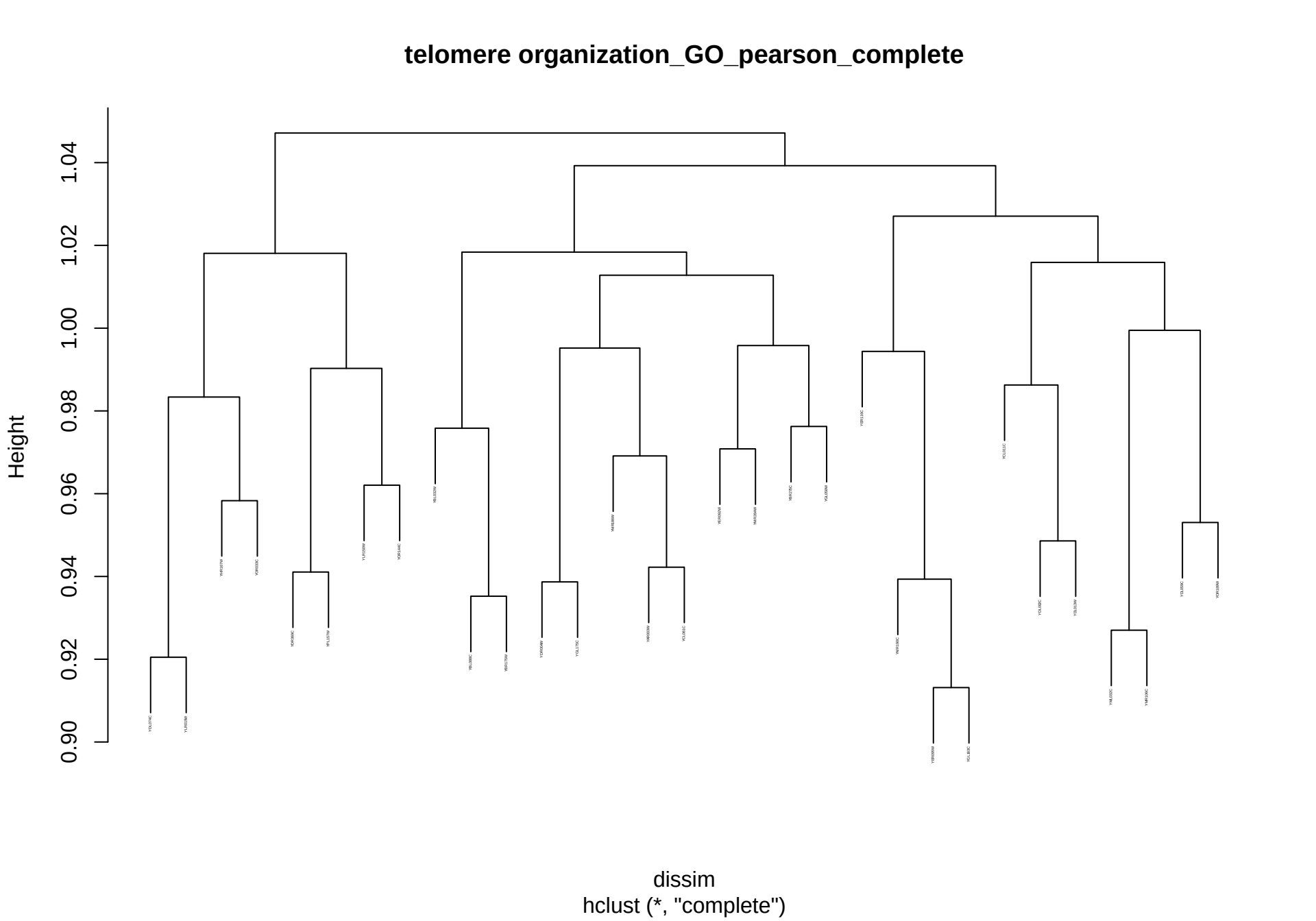

regulation of protein modification process_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

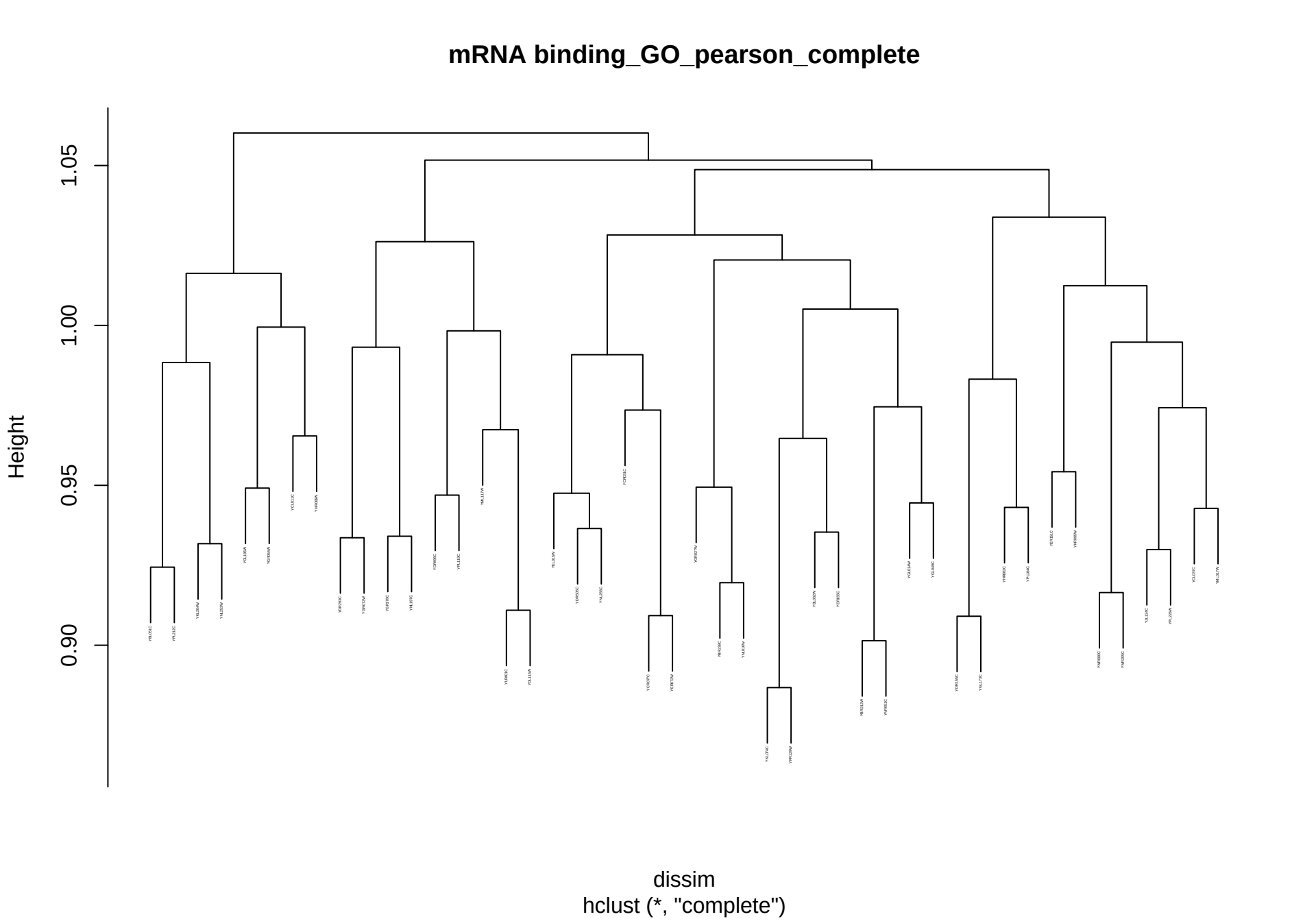

peptidyl−amino acid modification_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

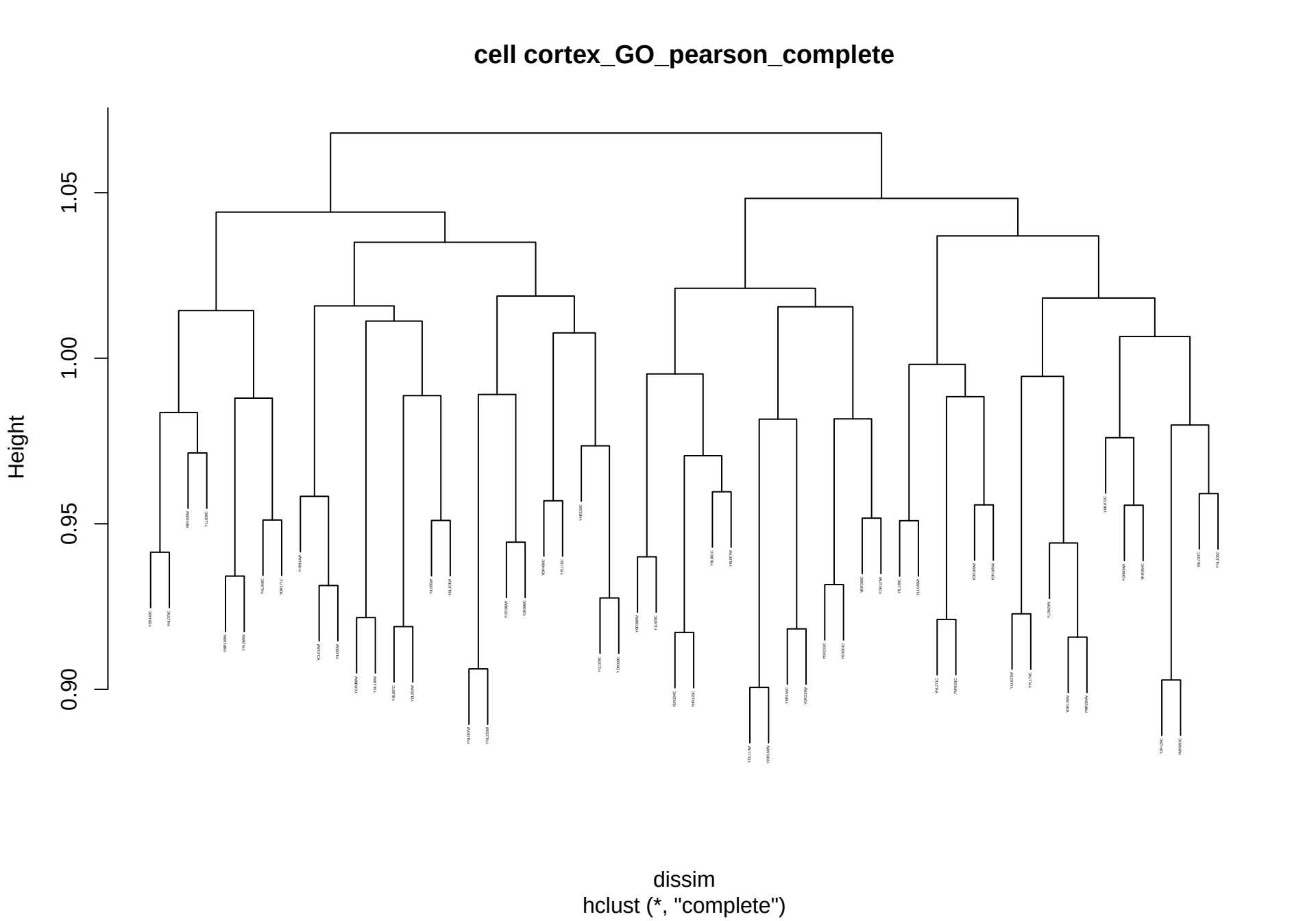

protein acylation_GO_pearson_complete
Height
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

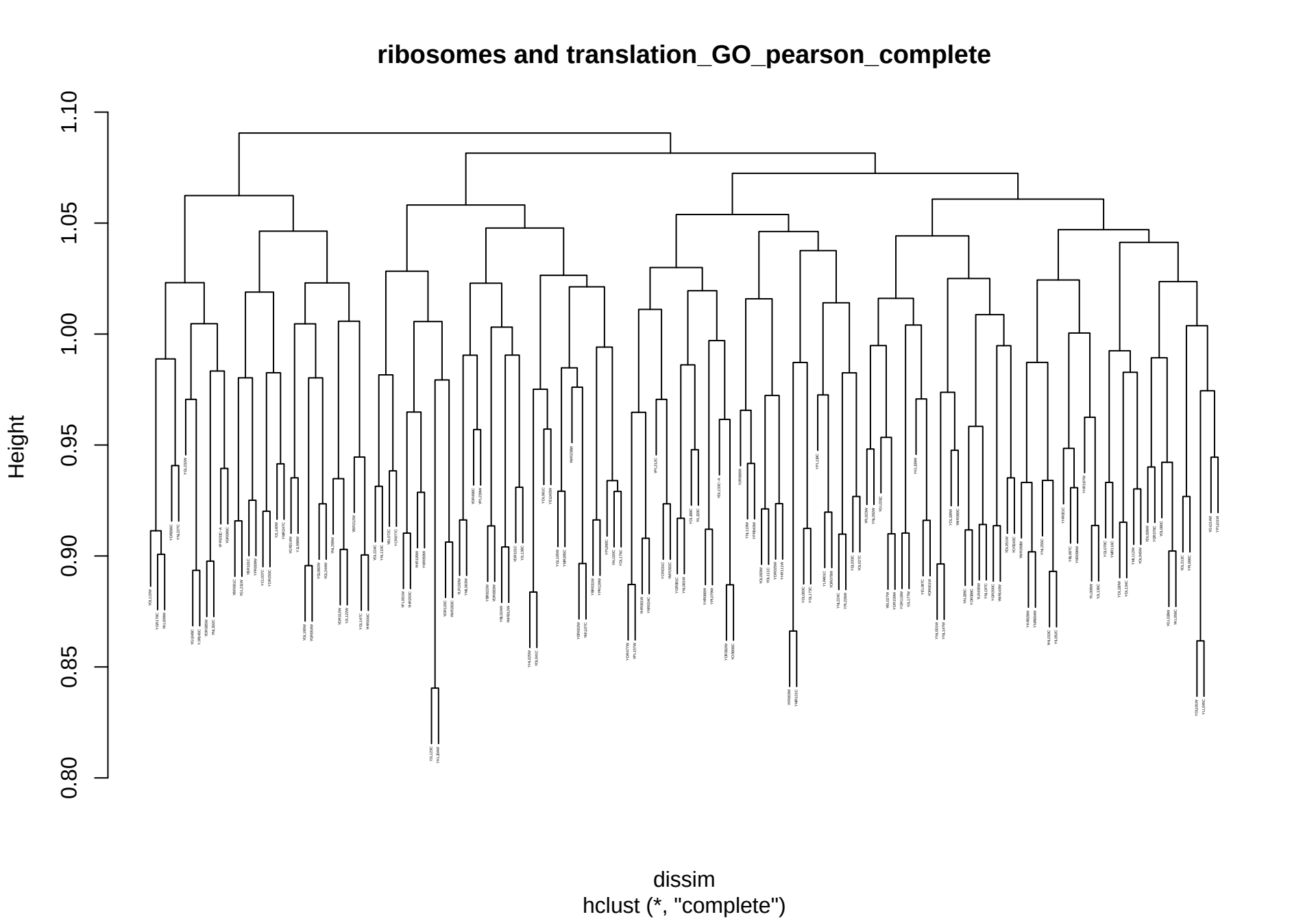

pseudohyphal growth_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

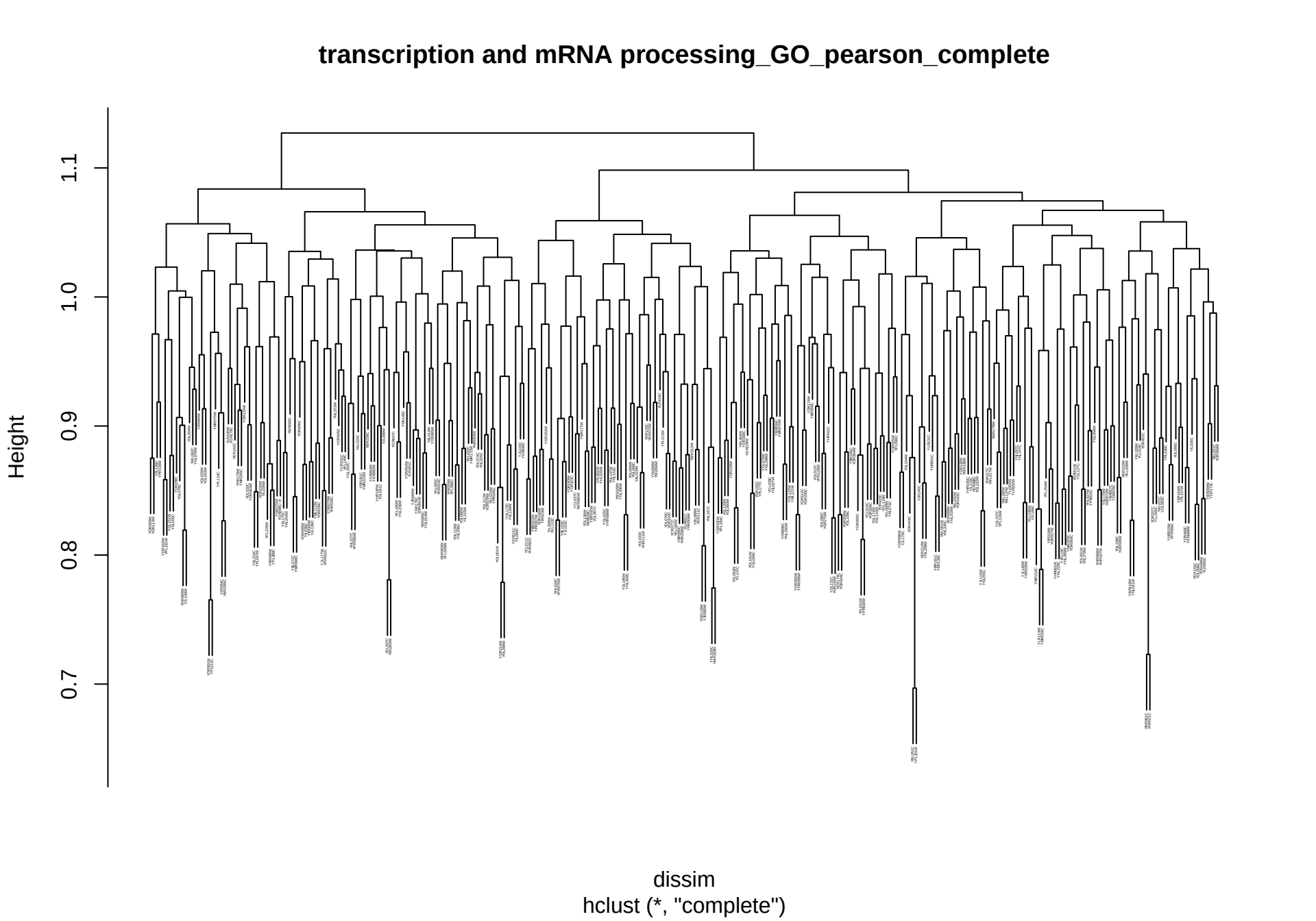

lipid binding_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

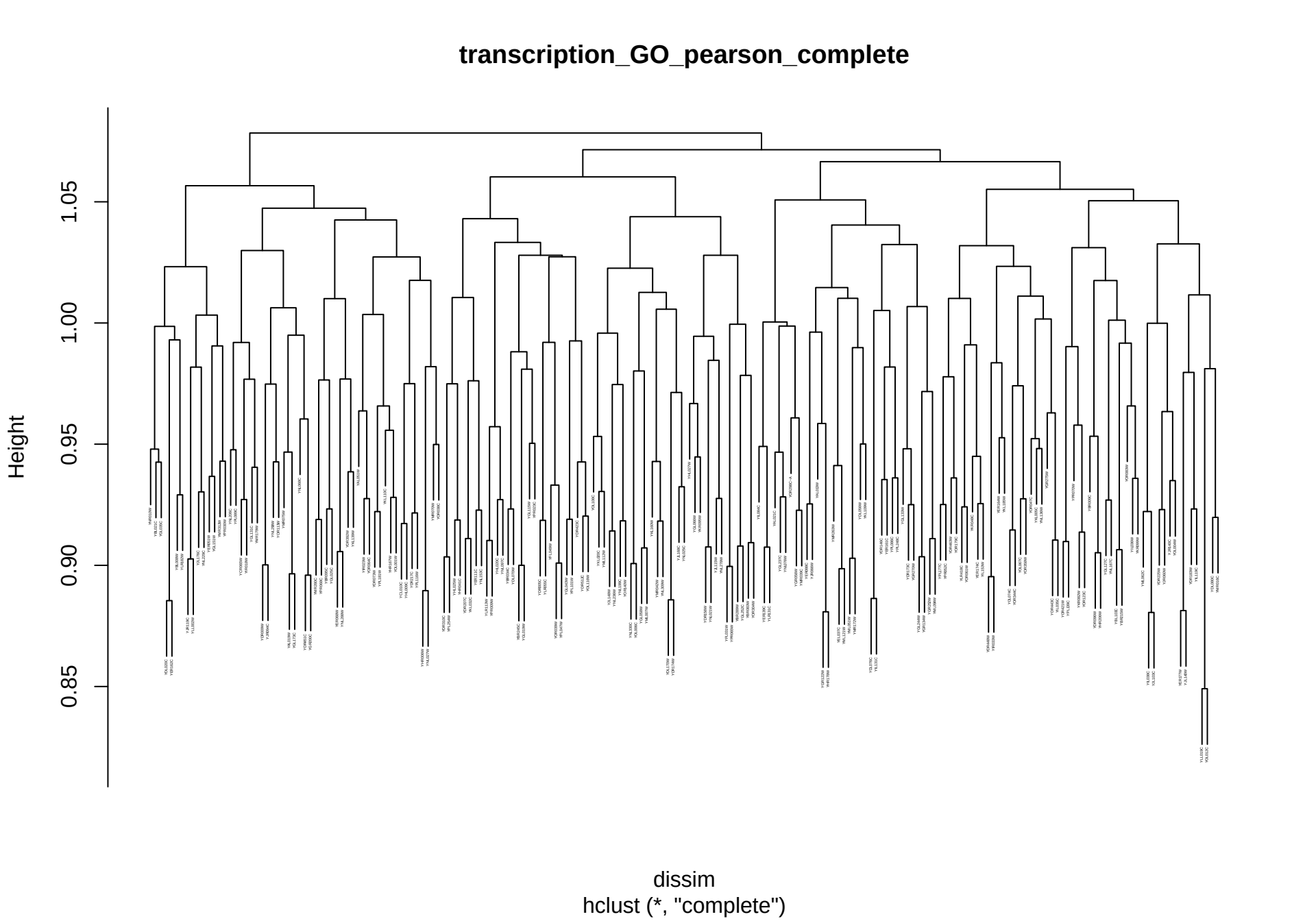

telomere organization_GO_pearson_complete
Height
0.90
0.92
0.94
0.96
0.98
1.00
1.02
1.04
dissim
hclust (*, "complete")

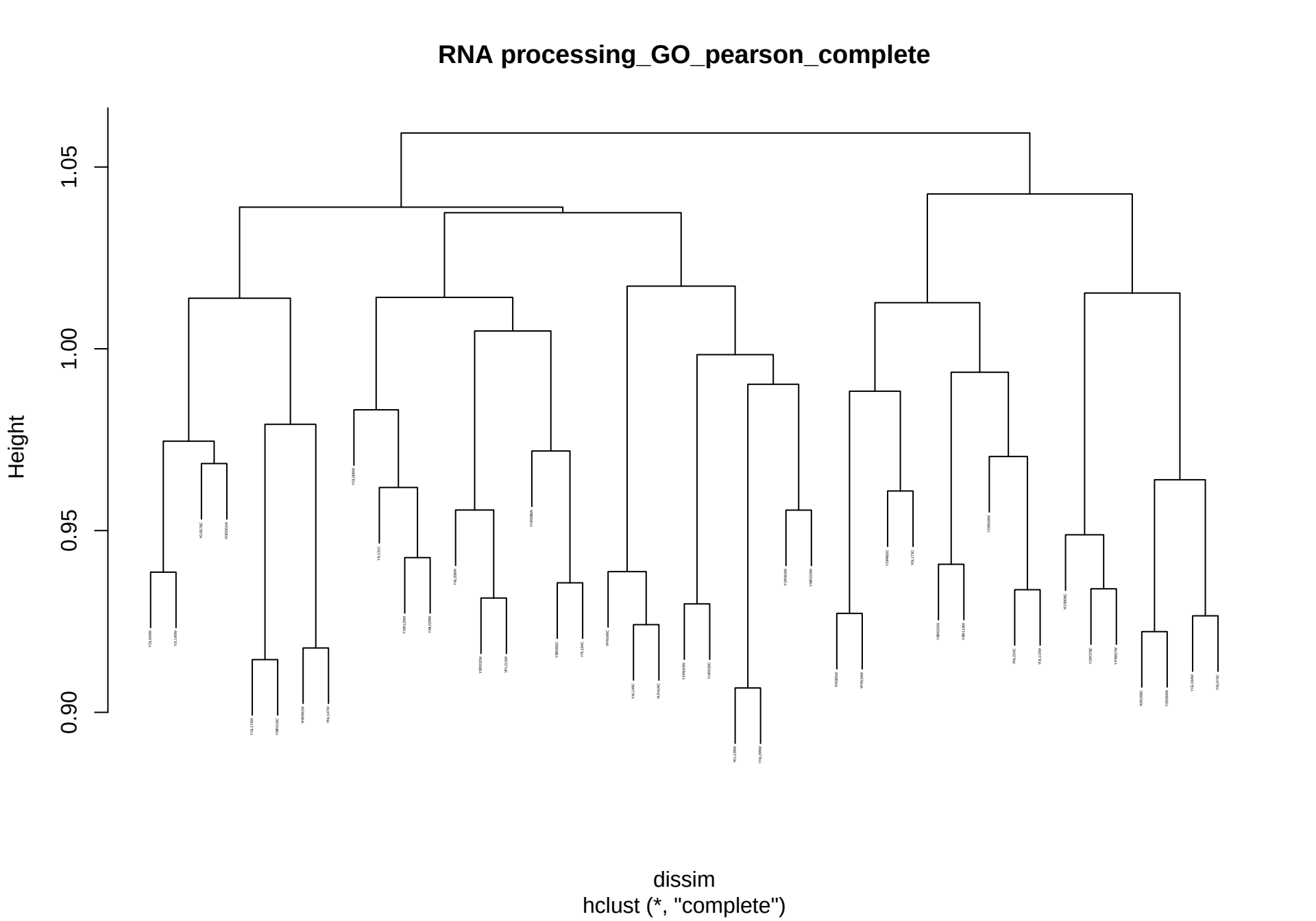

mRNA binding_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

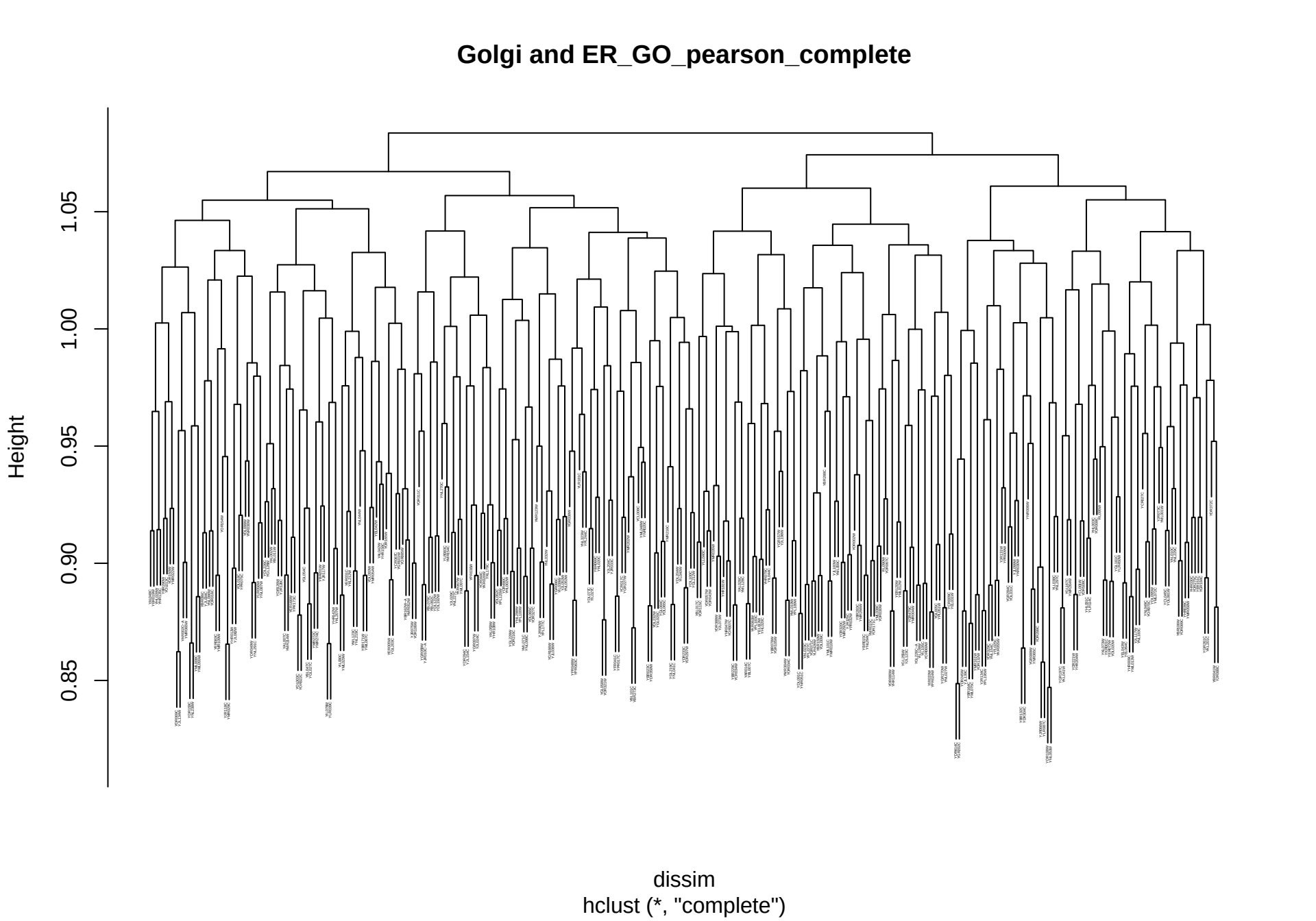

cell cortex_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

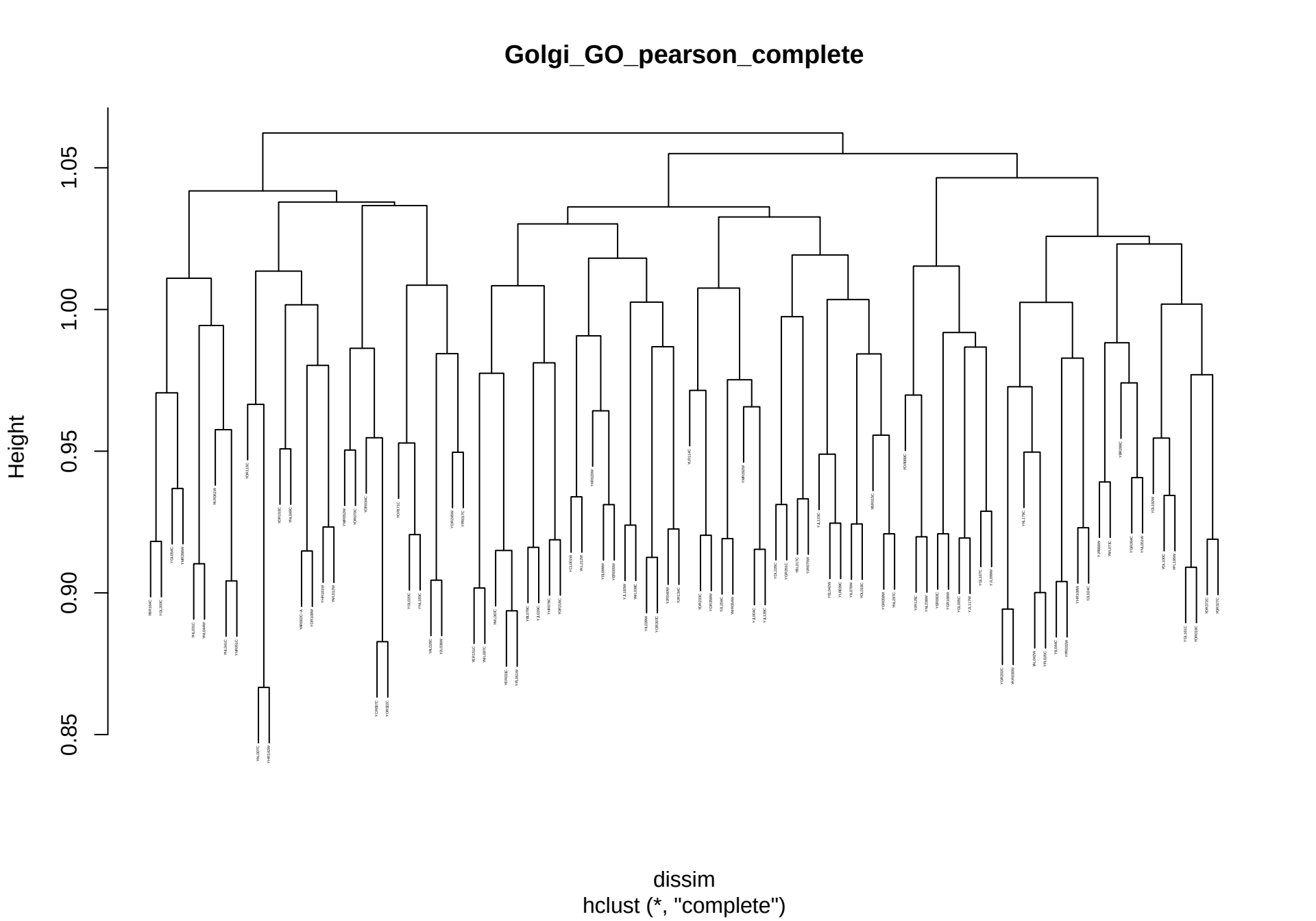

ribosomes and translation_GO_pearson_complete
Height
1.10
1.05
1.00
0.95
0.90
0.85
0.80
dissim
hclust (*, "complete")

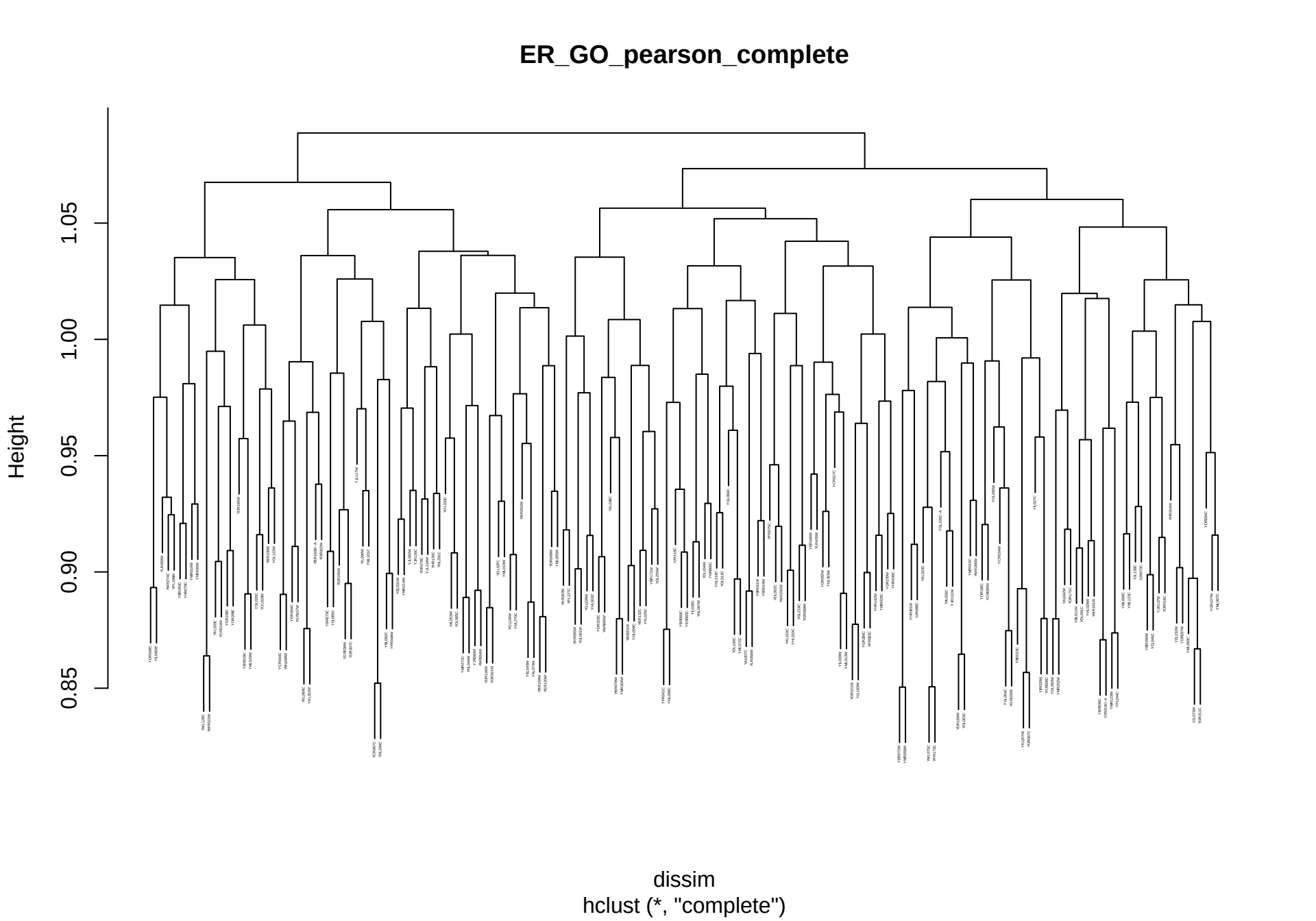

transcription and mRNA processing_GO_pearson_complete
Height
0.7
0.8
0.9
1.0
1.1
dissim
hclust (*, "complete")

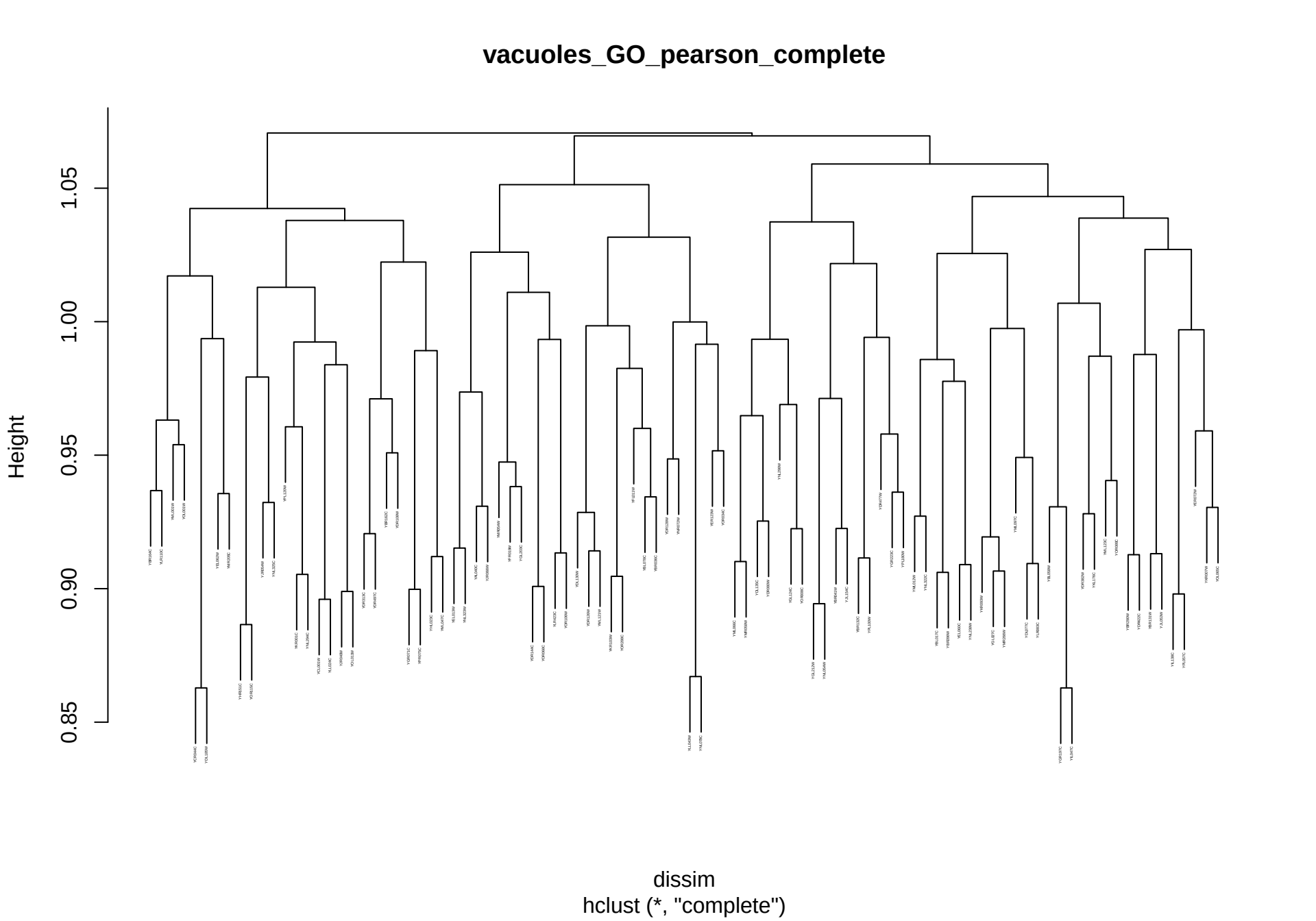

transcription_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

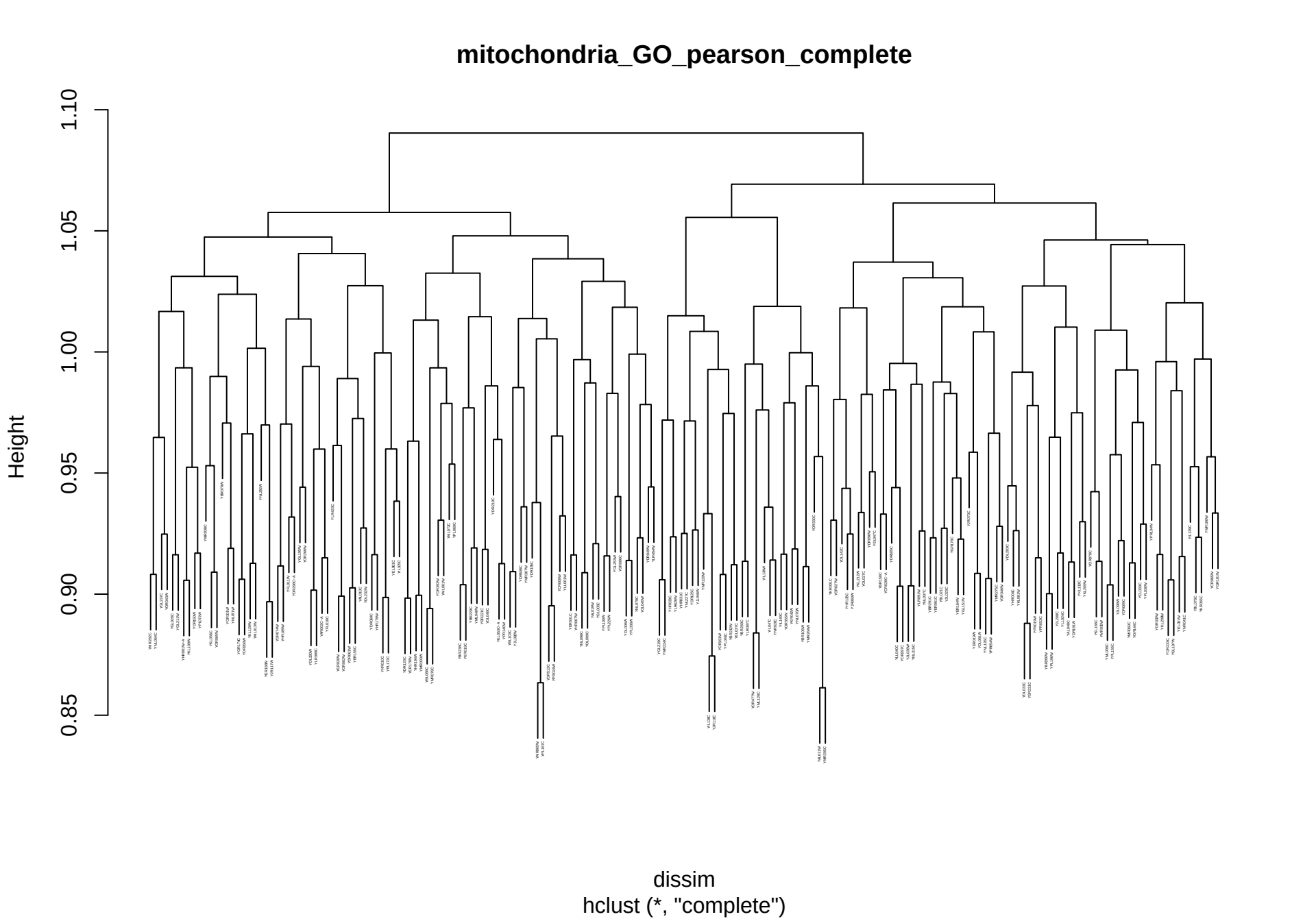

RNA processing_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")

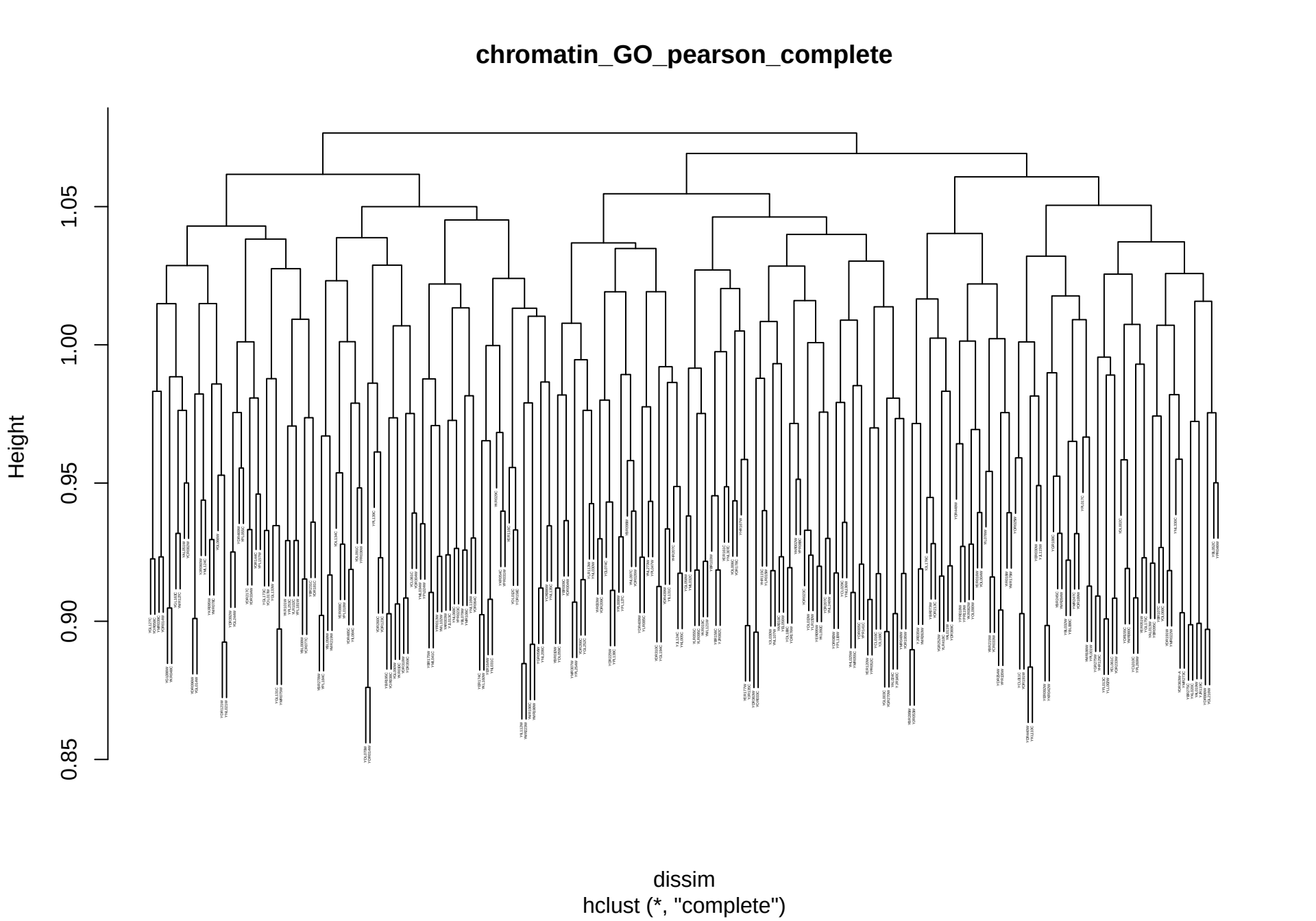

Golgi and ER_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

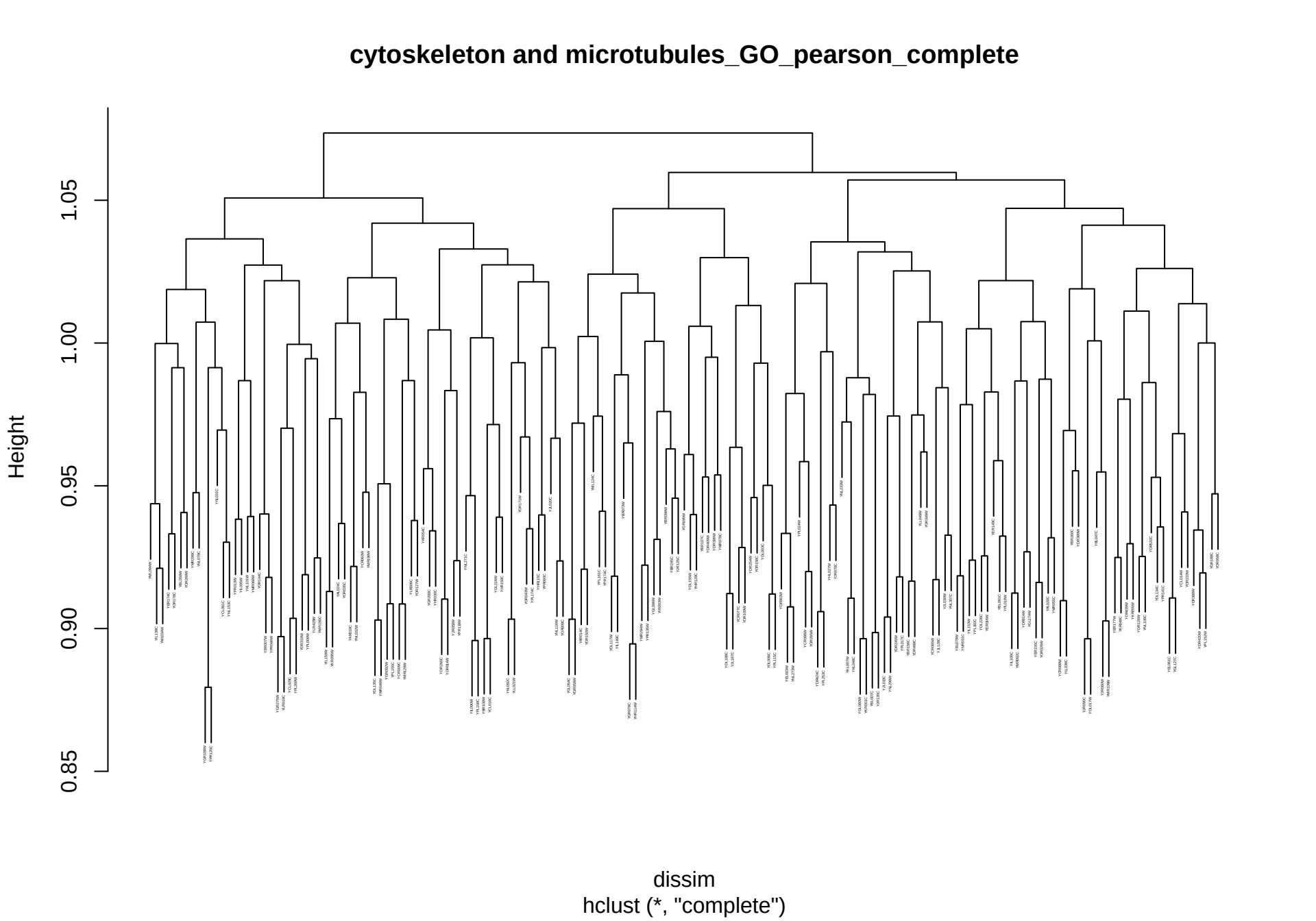

Golgi_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

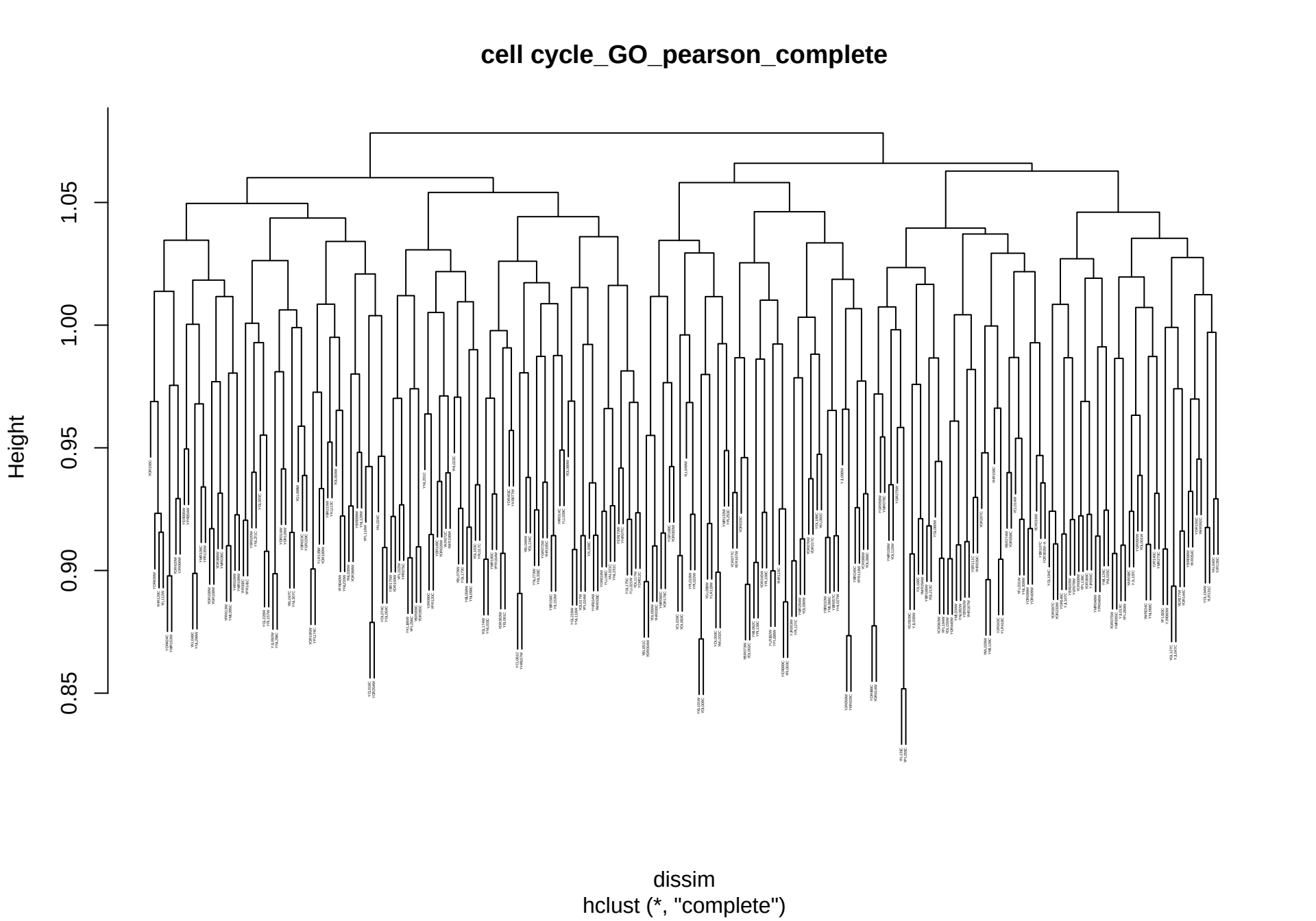

ER_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

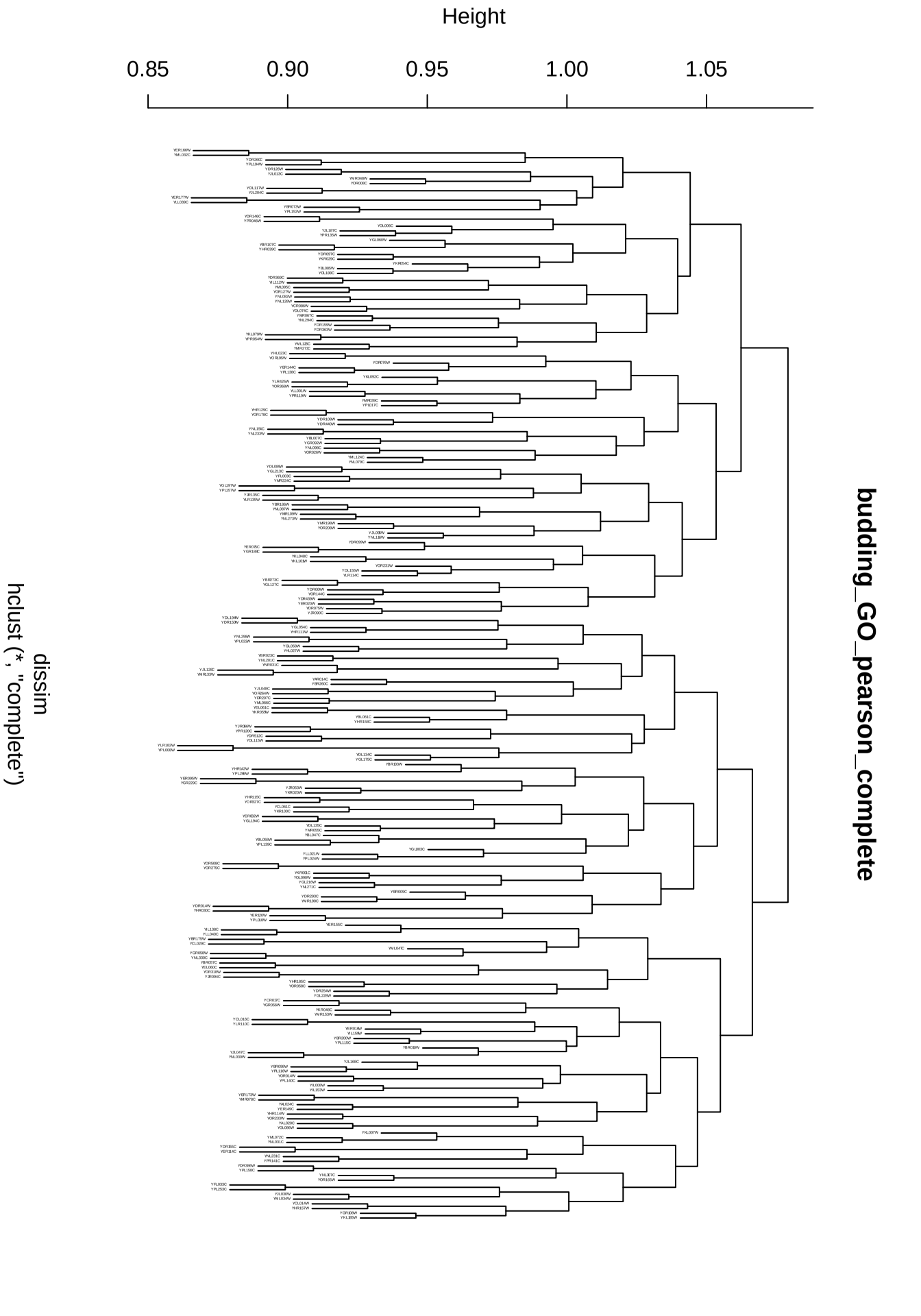

vacuoles_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
0.85
dissim
hclust (*, "complete")

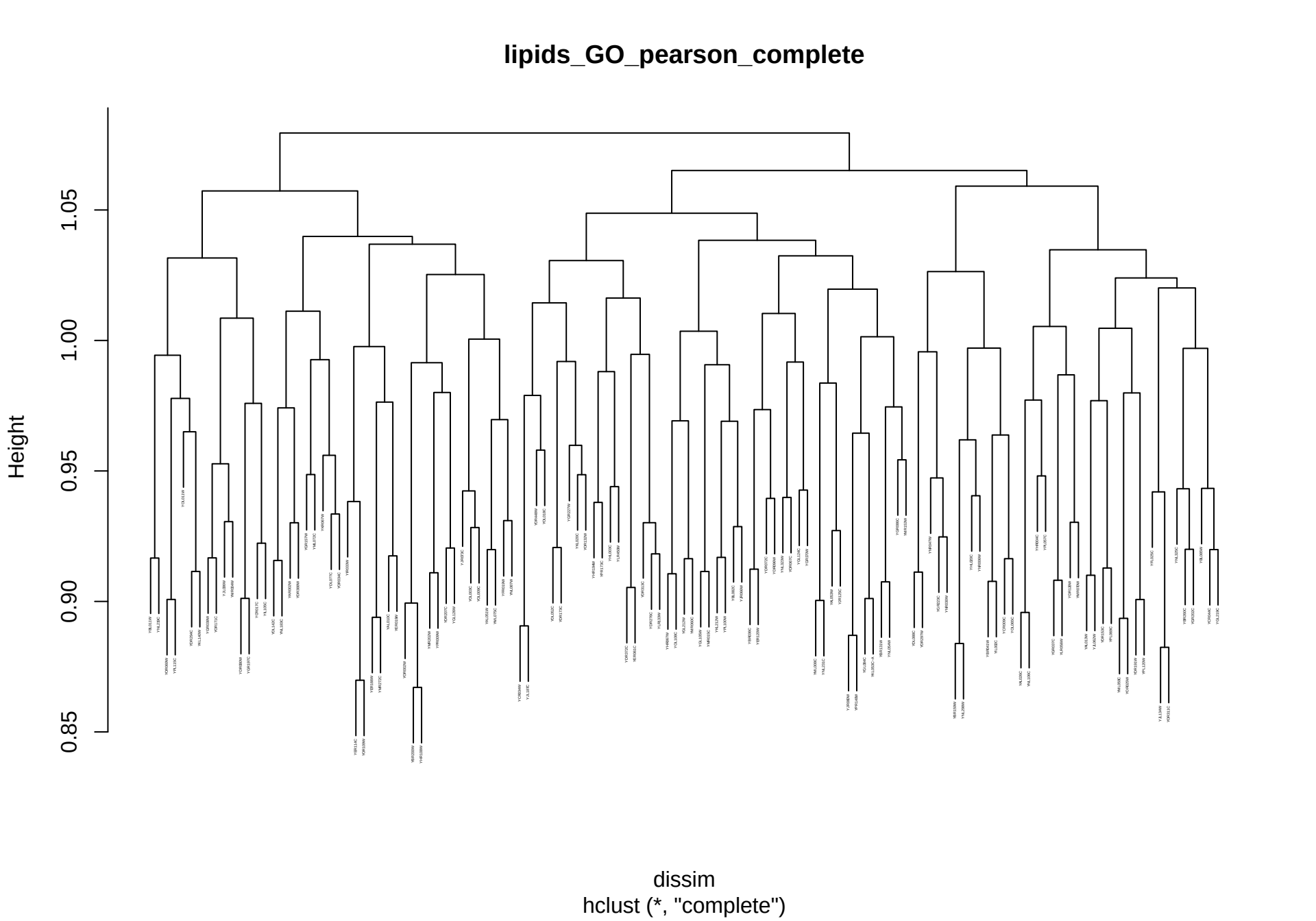

mitochondria_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
1.10
dissim
hclust (*, "complete")

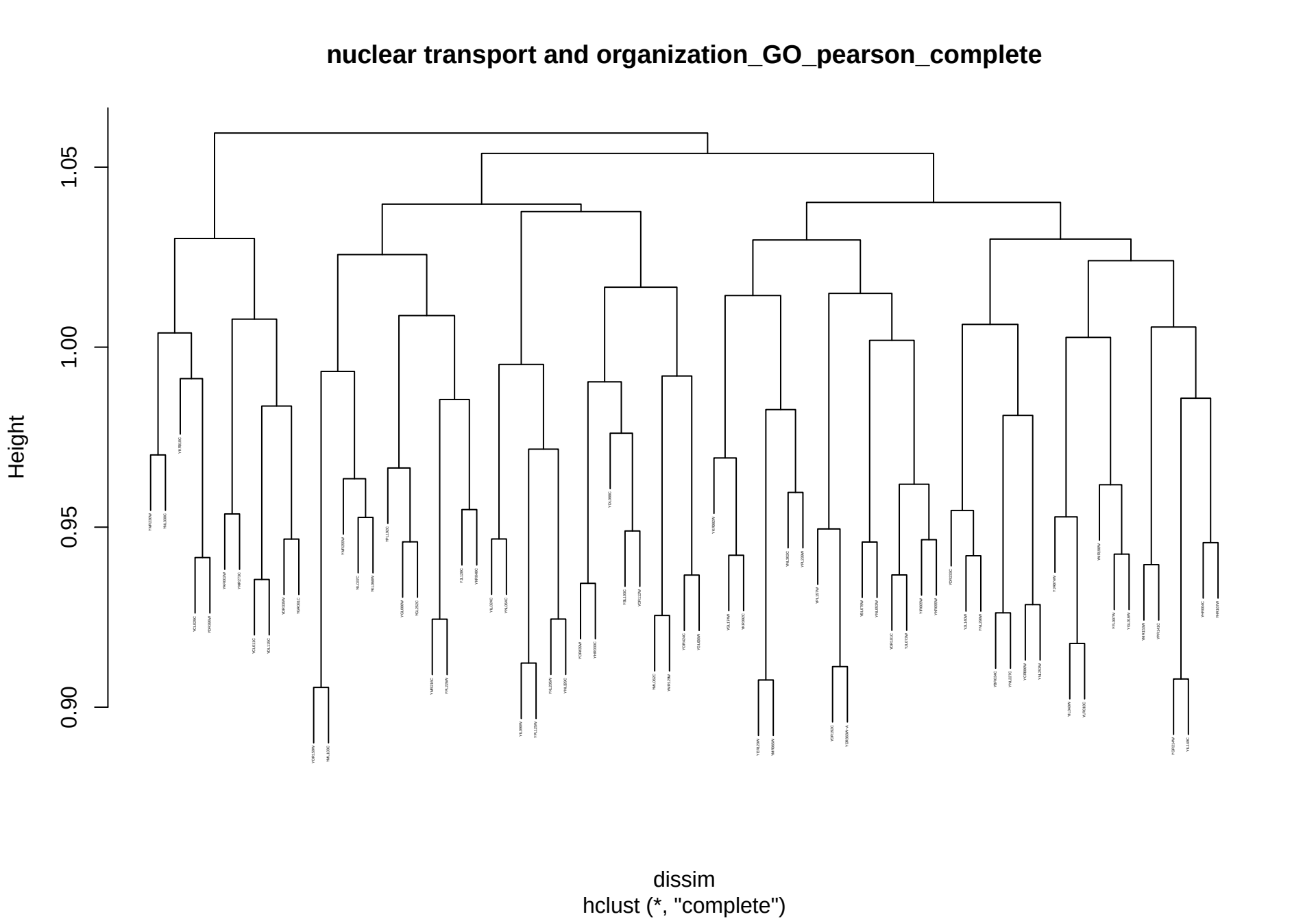

chromatin_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

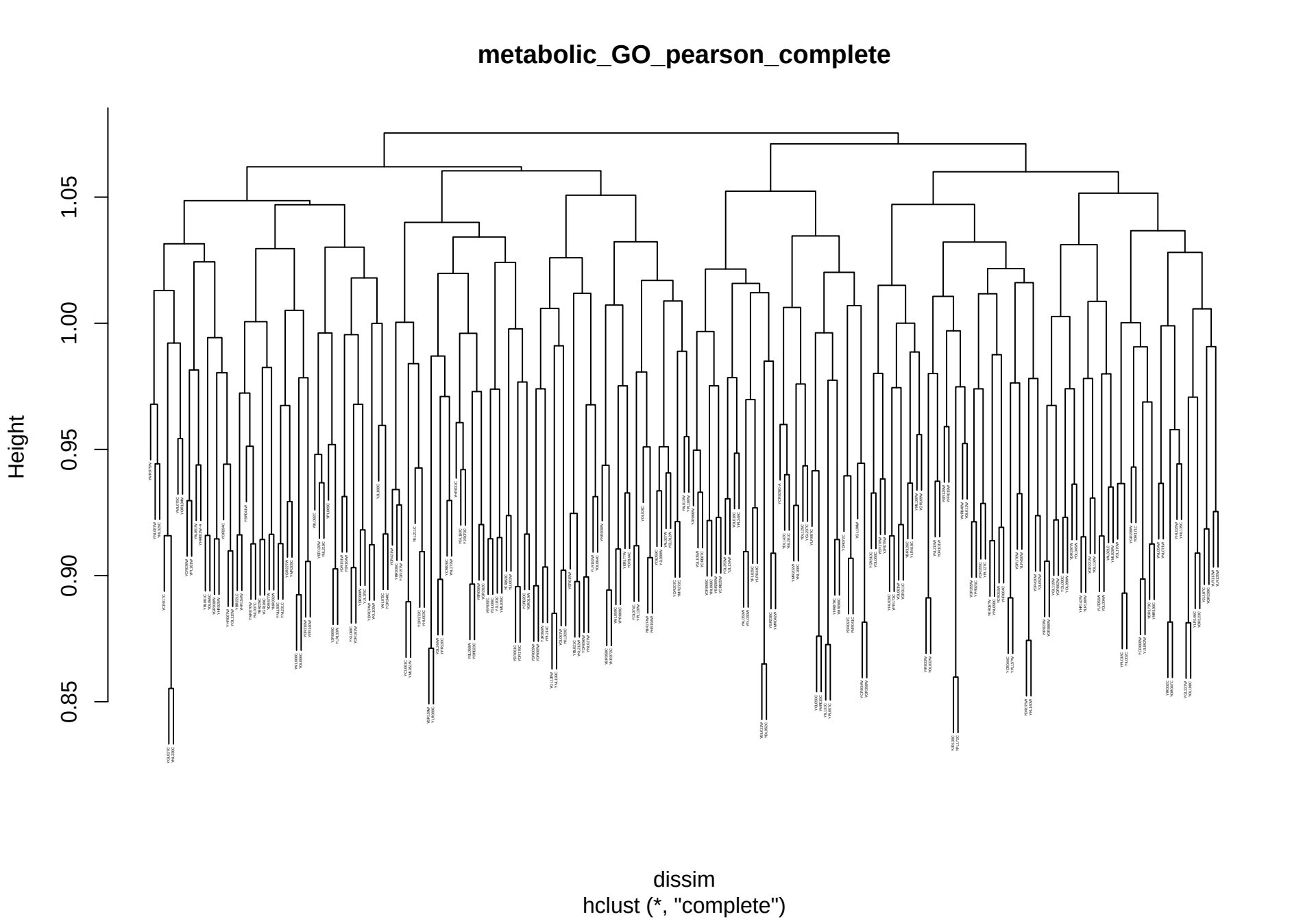

cytoskeleton and microtubules_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")


cell cycle_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")


Height
0.85
0.90
0.95
1.00
1.05
budding_GO_pearson_complete
dissim
hclust (*, "complete")


lipids_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")


nuclear transport and organization_GO_pearson_complete
Height
1.05
1.00
0.95
0.90
dissim
hclust (*, "complete")


metabolic_GO_pearson_complete
Height
0.85
0.90
0.95
1.00
1.05
dissim
hclust (*, "complete")

whole_library_pearson_complete
Height
0.75
0.80
0.85
0.90
0.95
1.00
1.05
1.10
dissim
hclust (*, "complete")