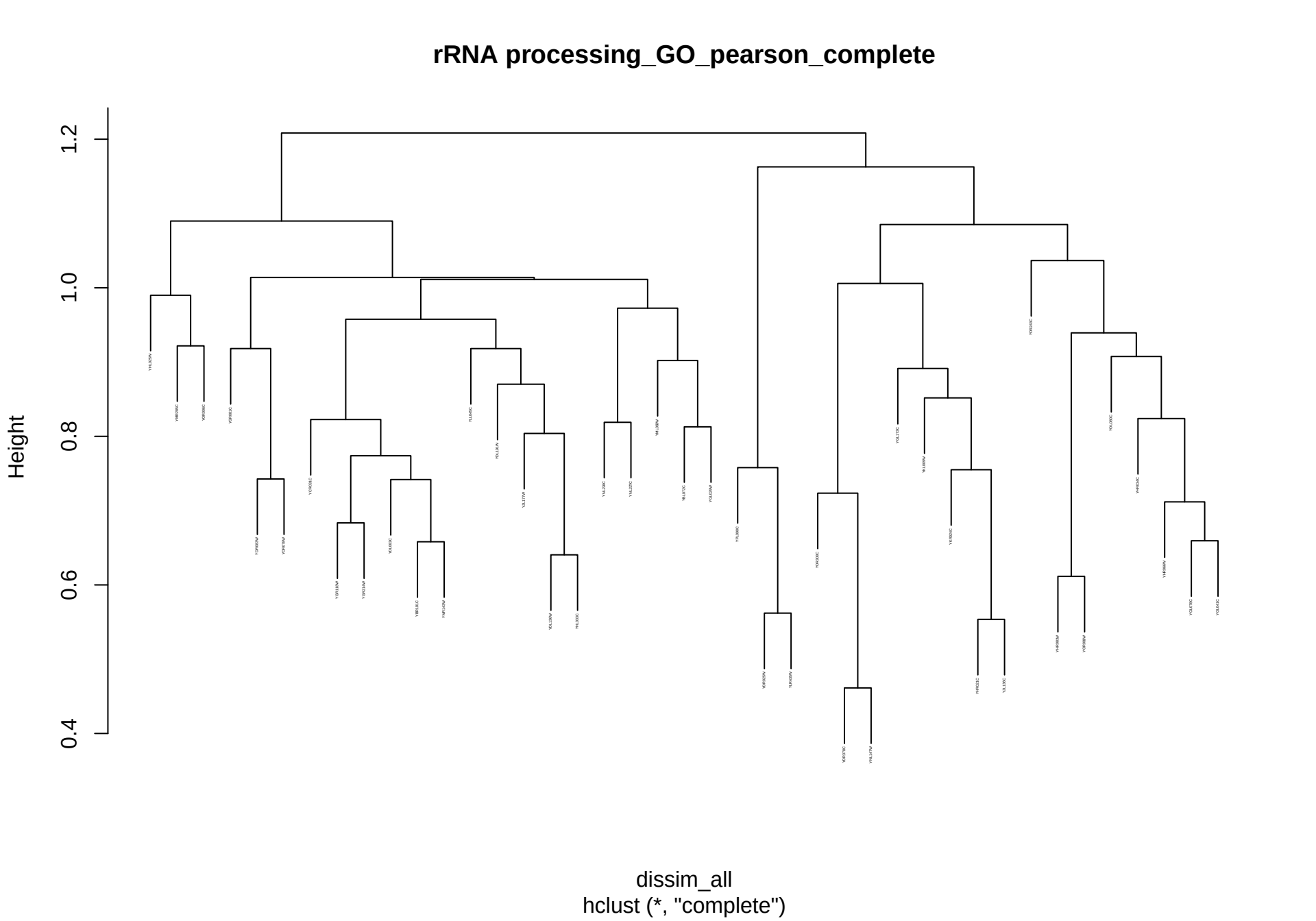
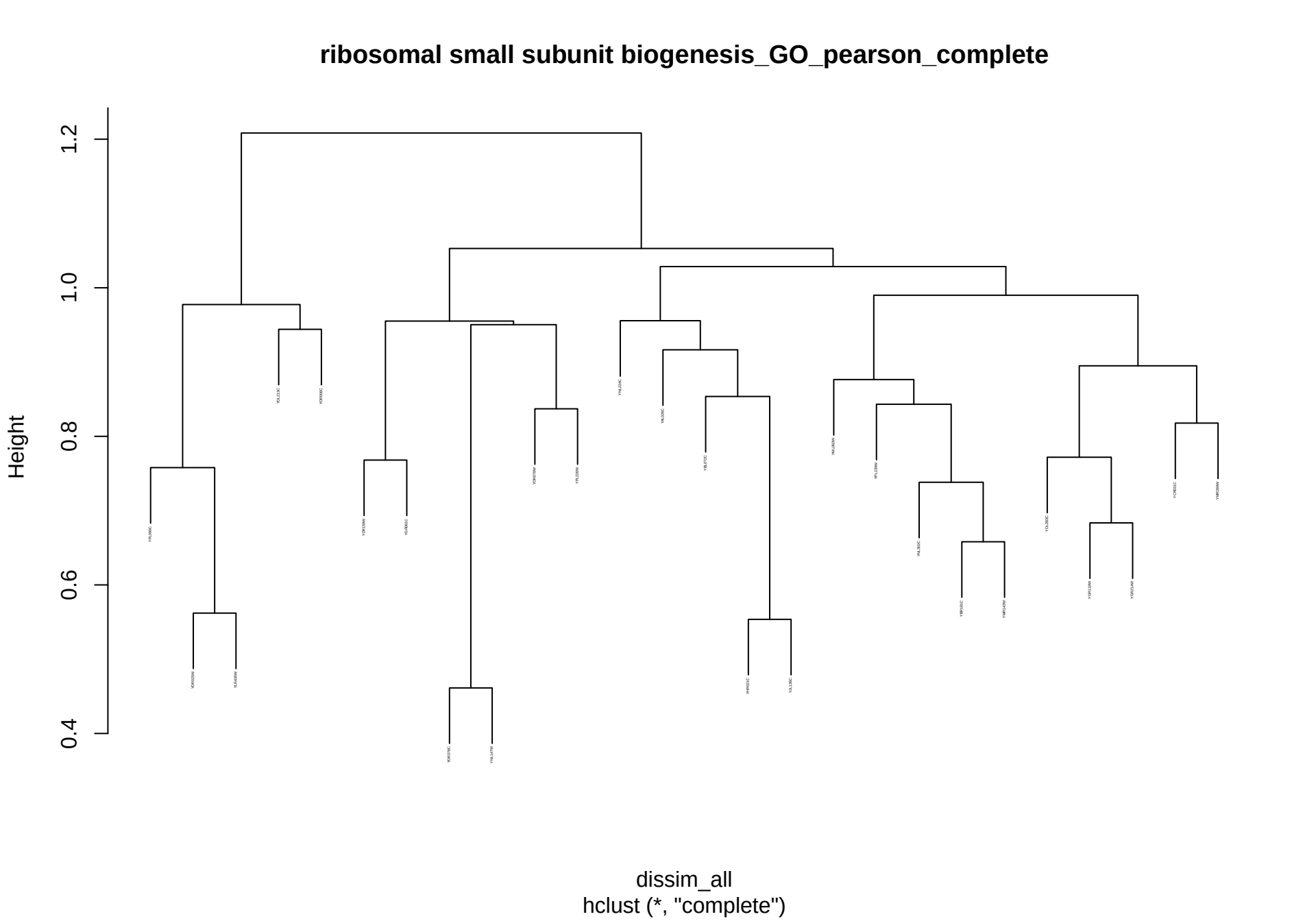
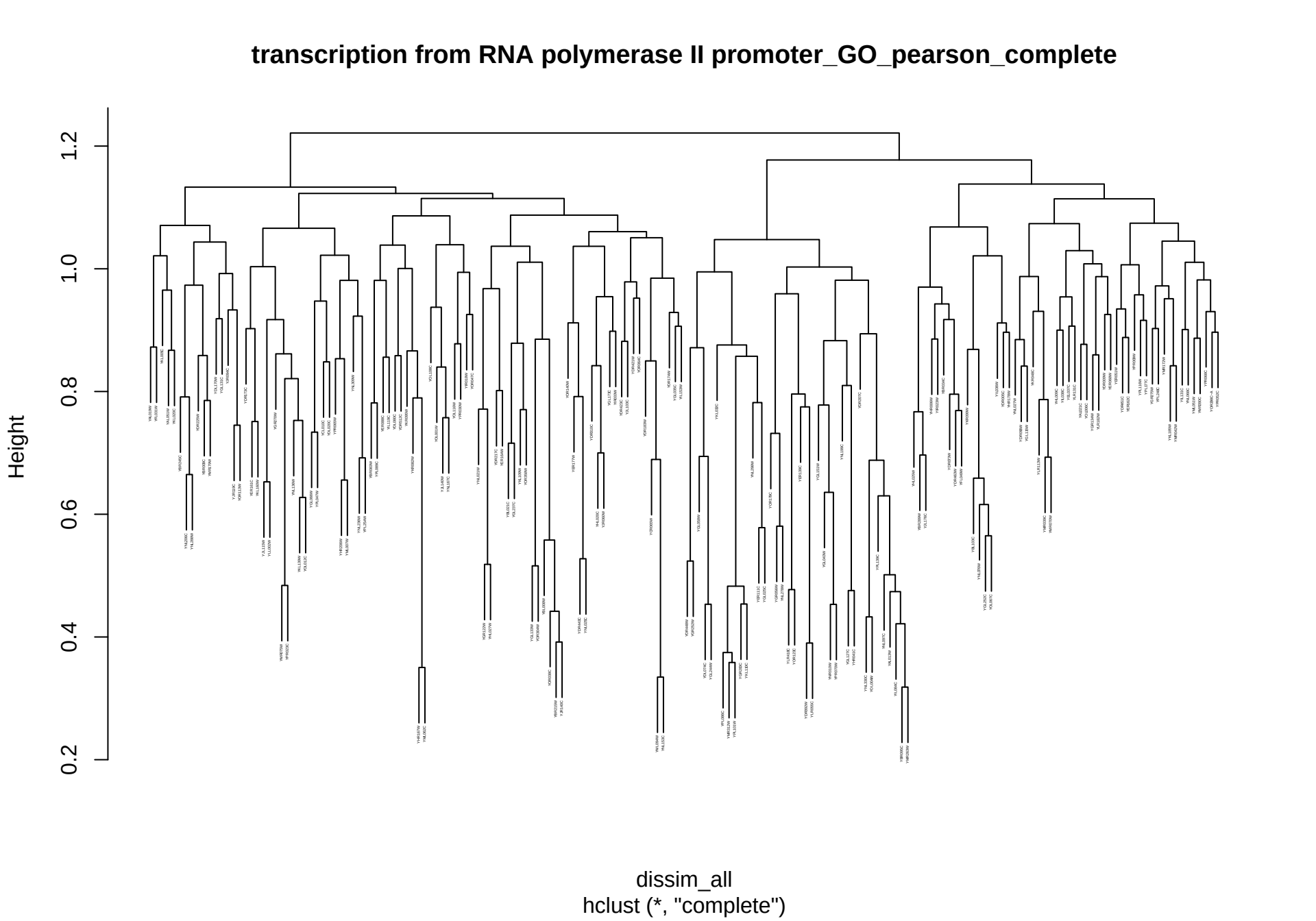
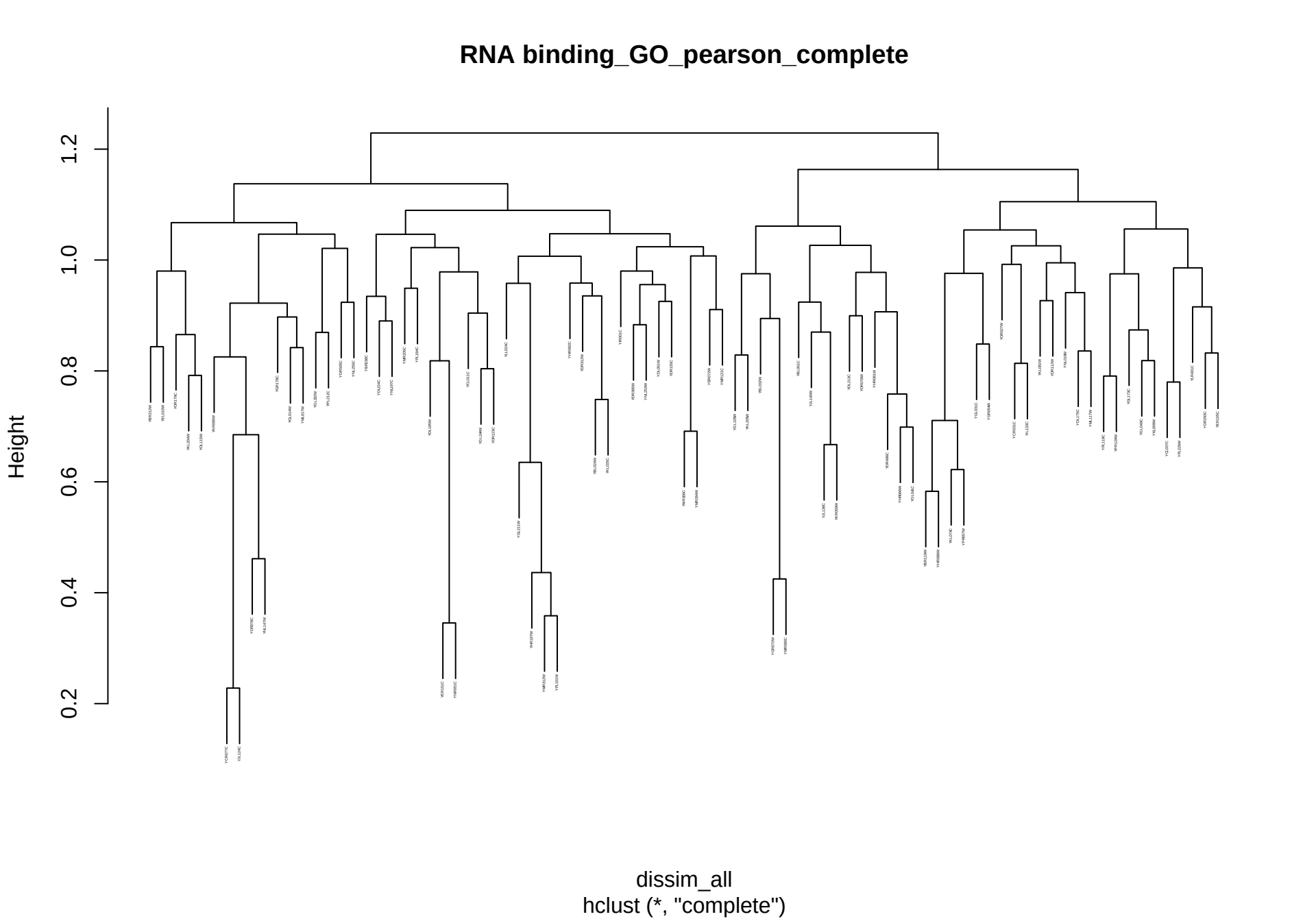
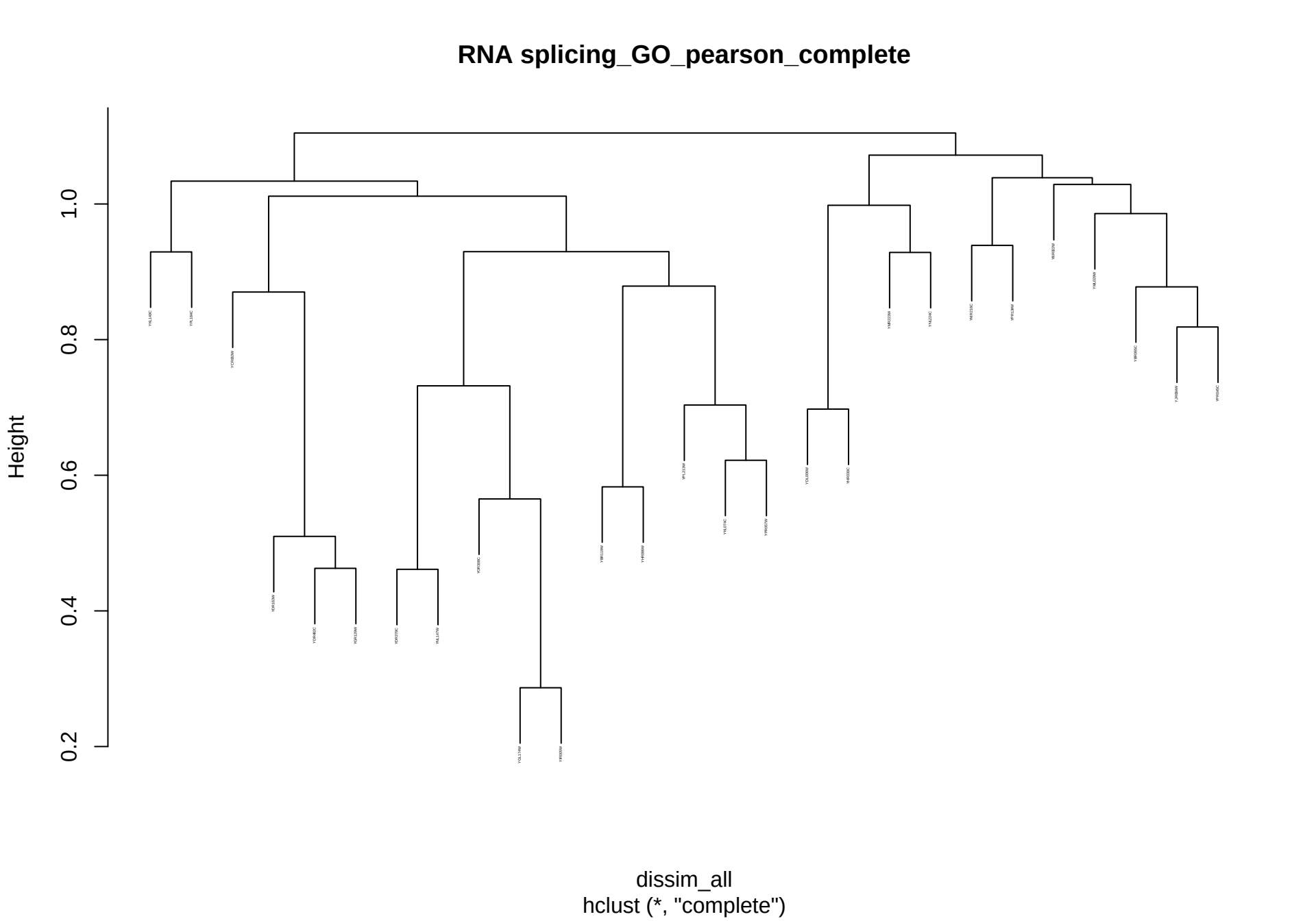
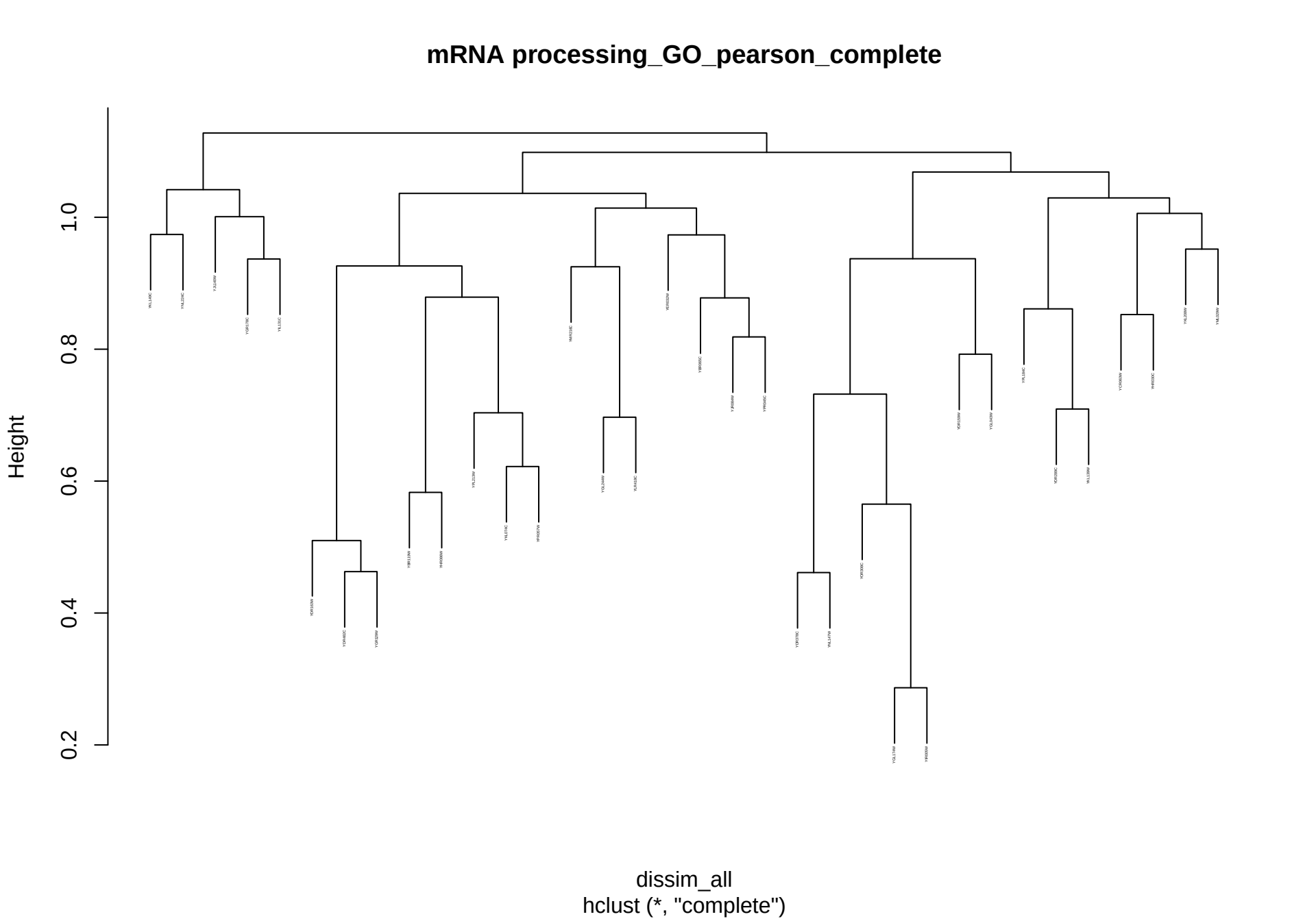

rRNA processing_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

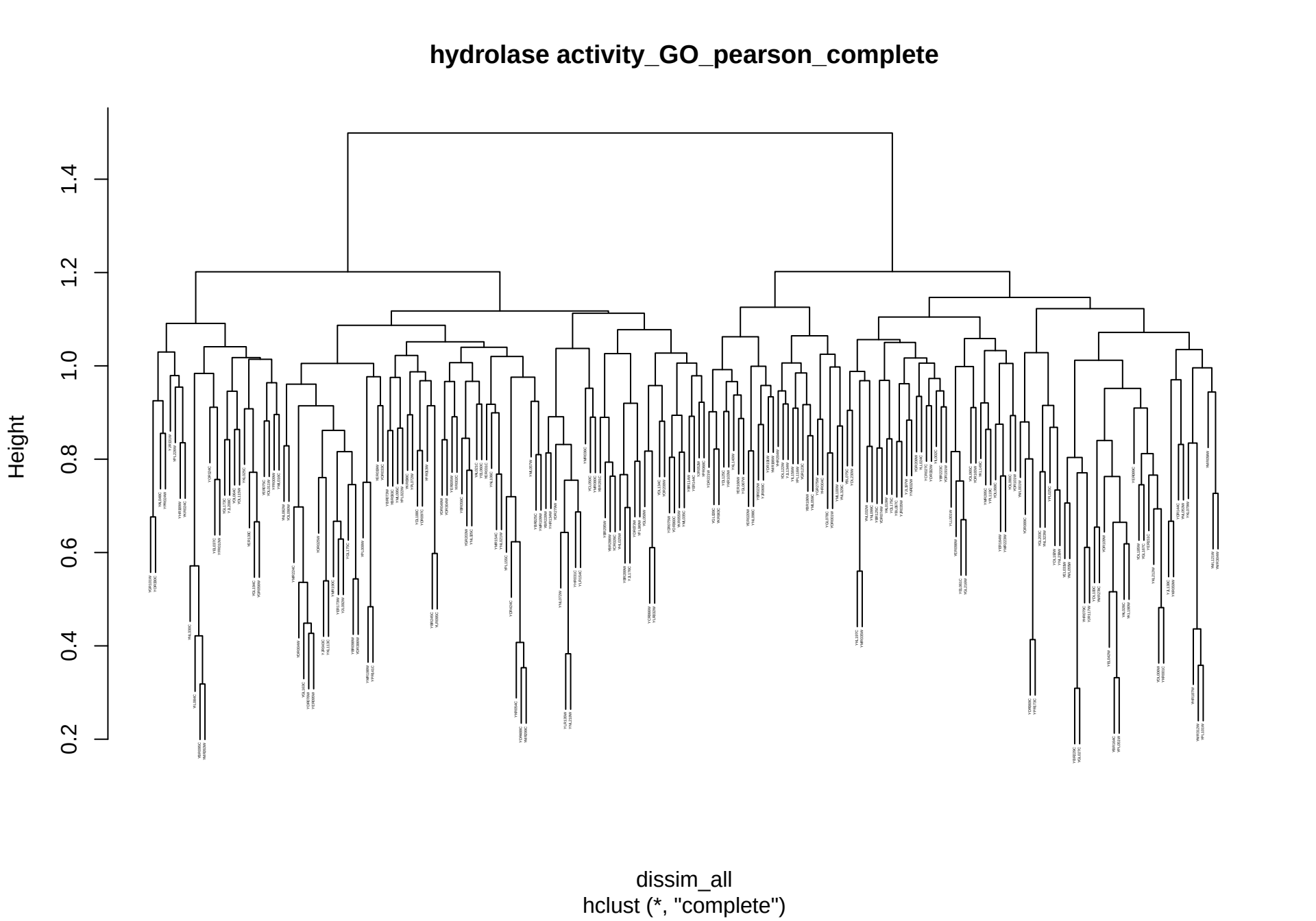

ribosomal small subunit biogenesis_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

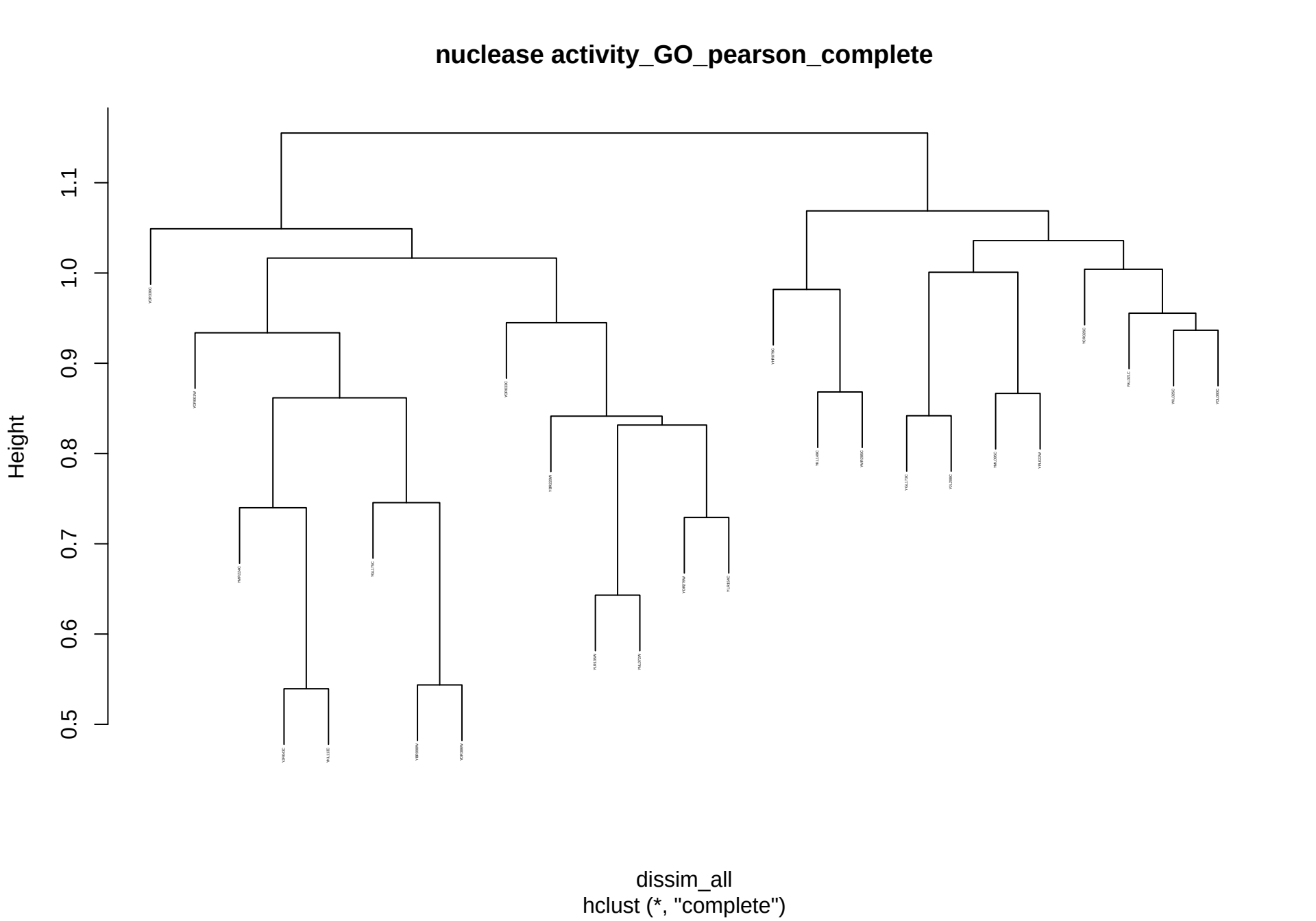

transcription from RNA polymerase II promoter_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

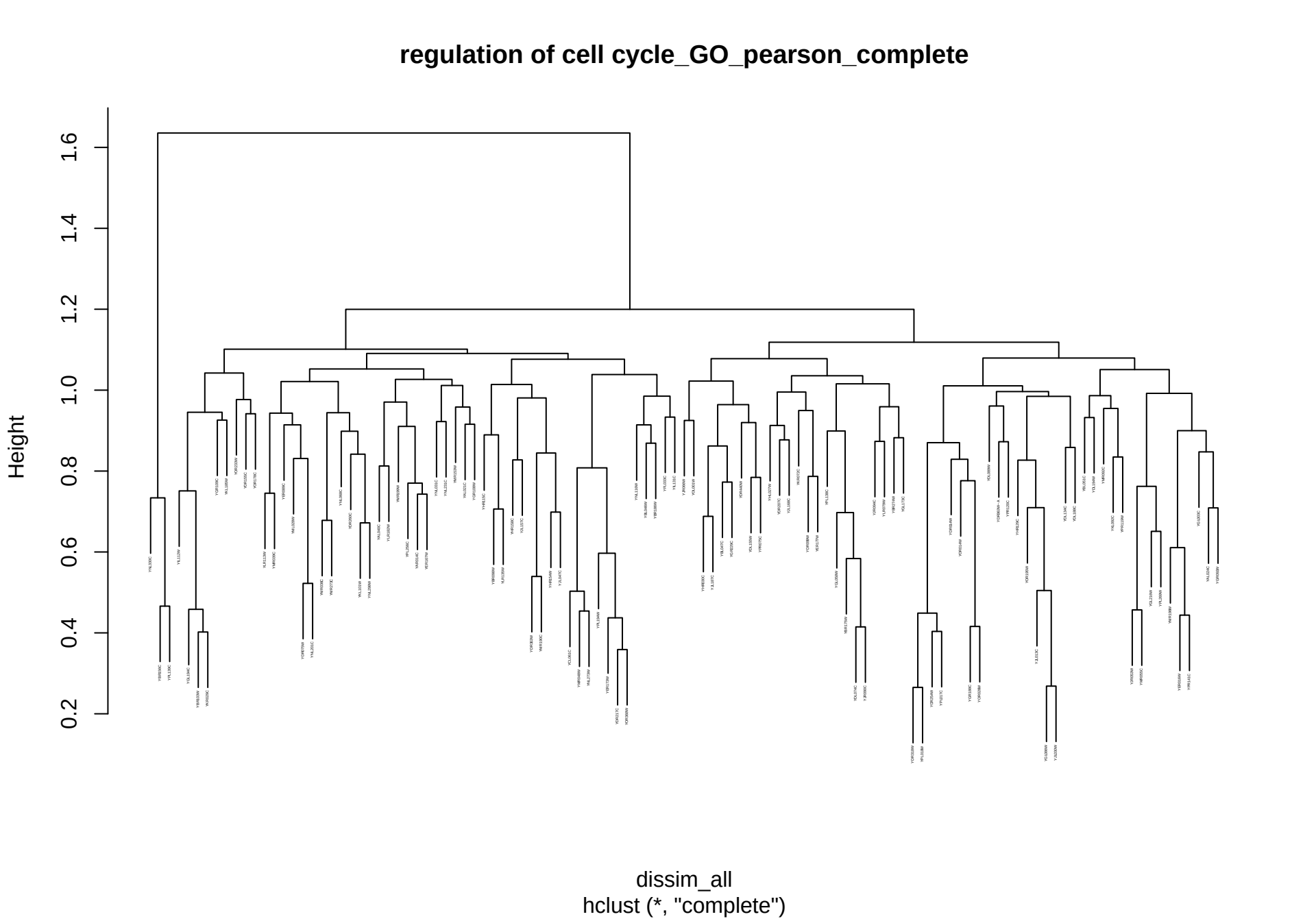

RNA binding_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

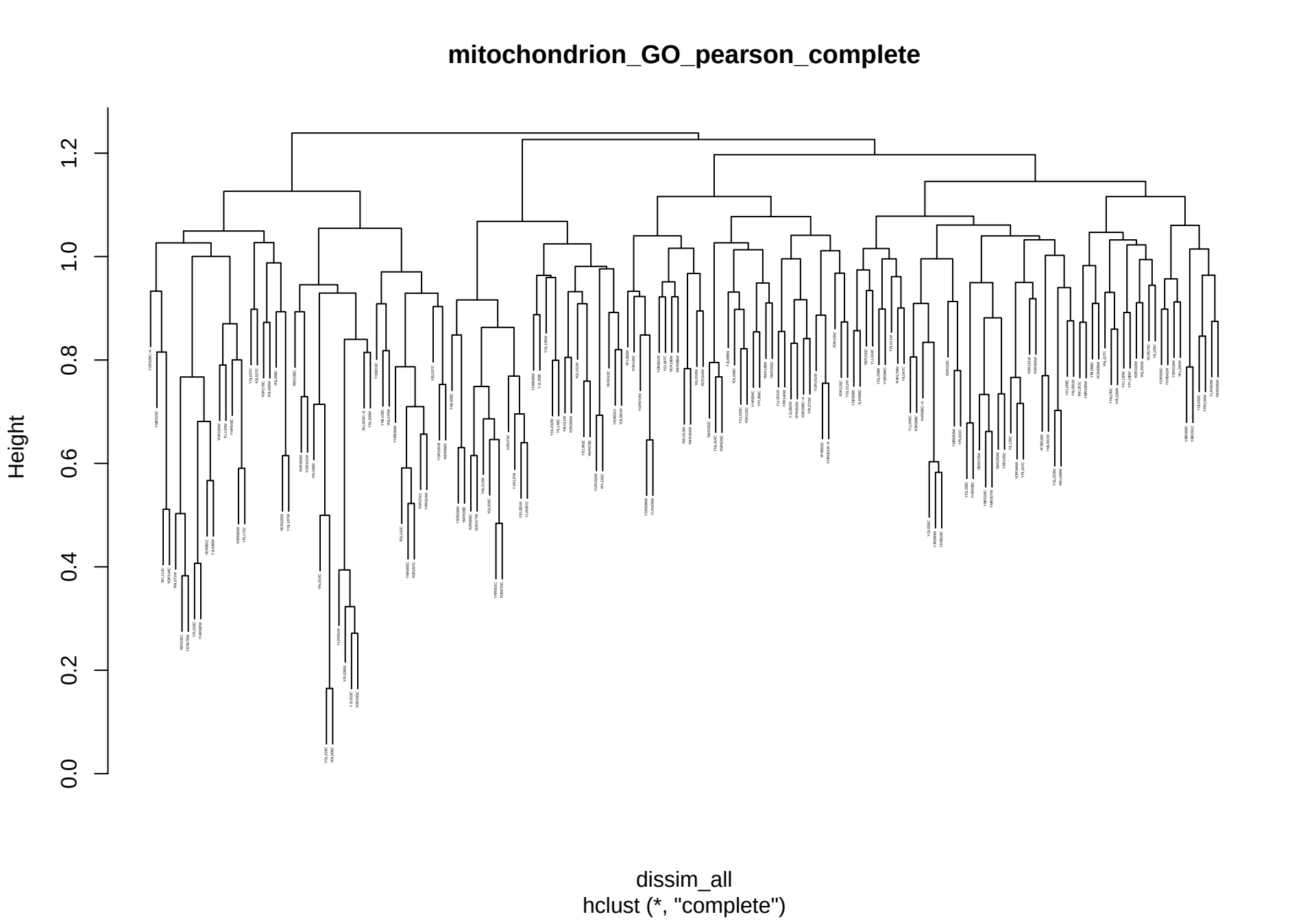

RNA splicing_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

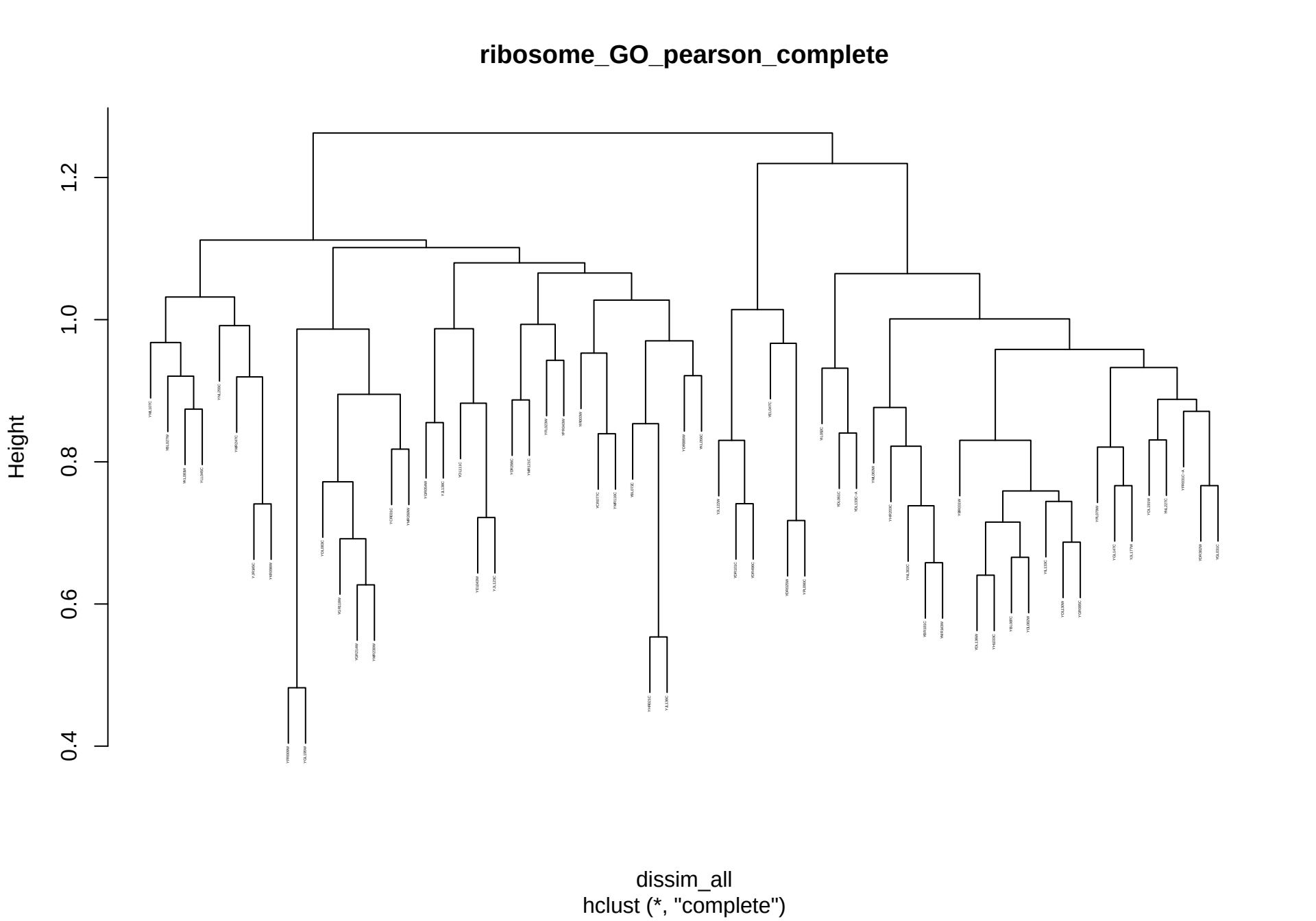

mRNA processing_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

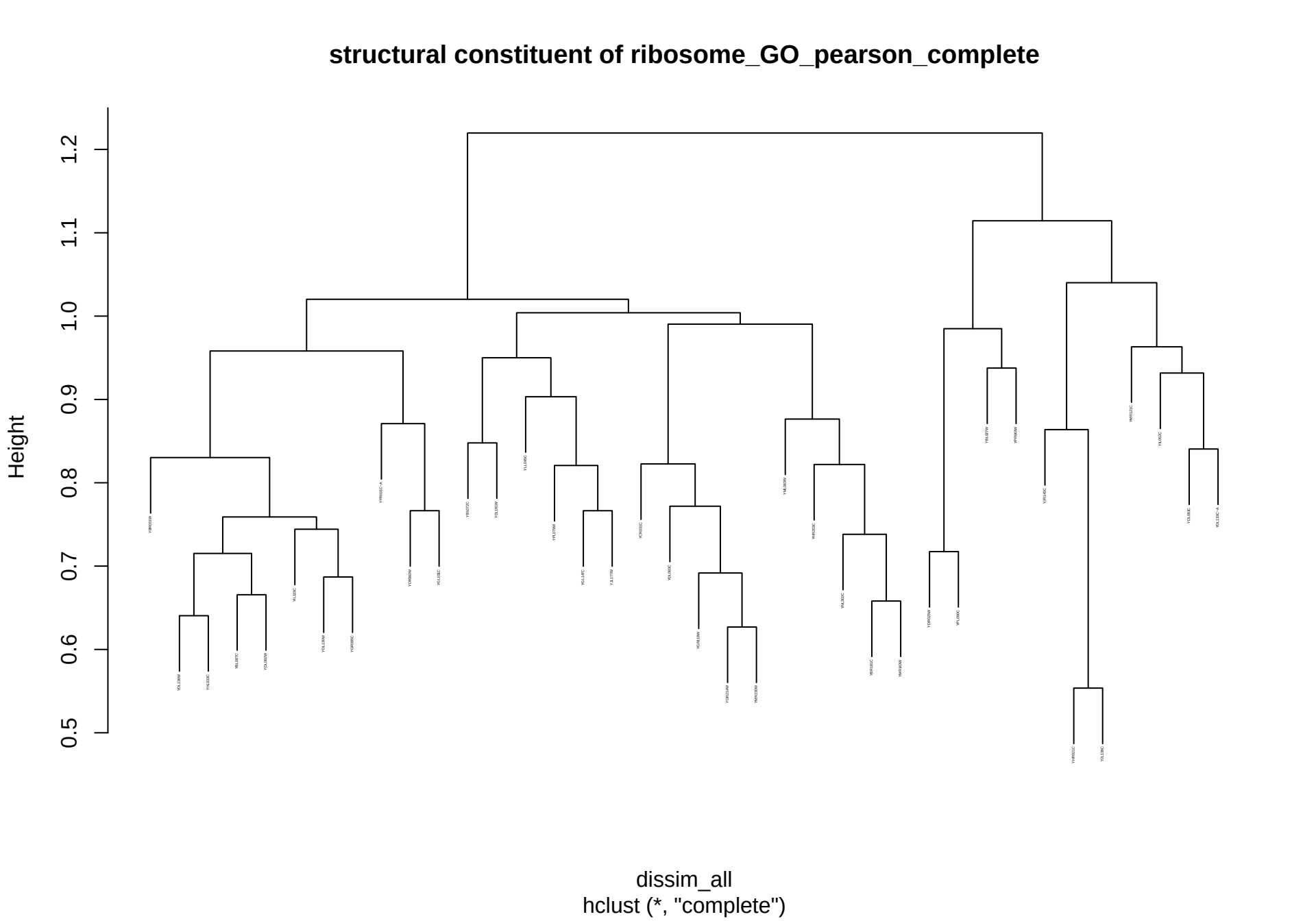

hydrolase activity_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")

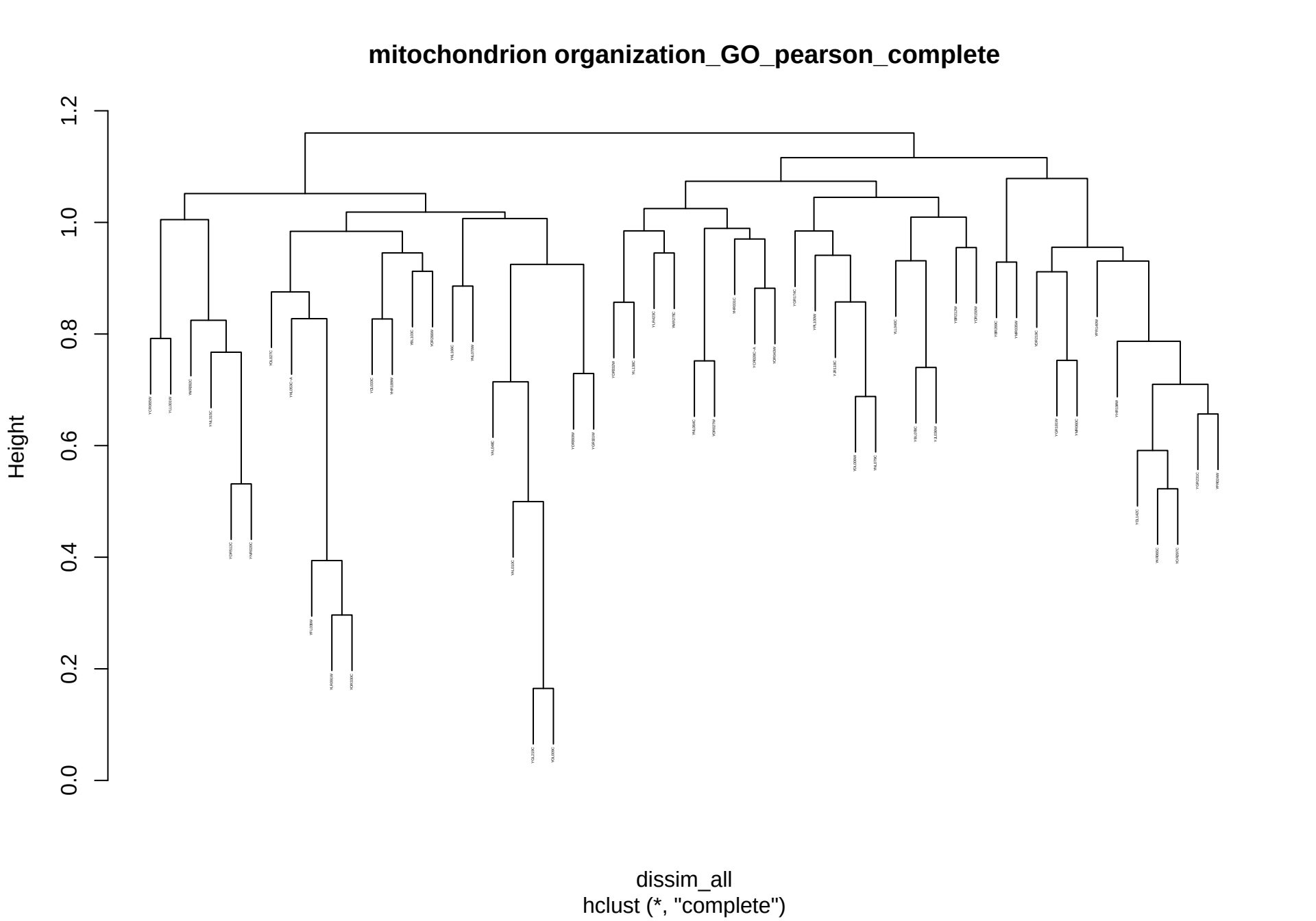

nuclease activity_GO_pearson_complete
Height
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

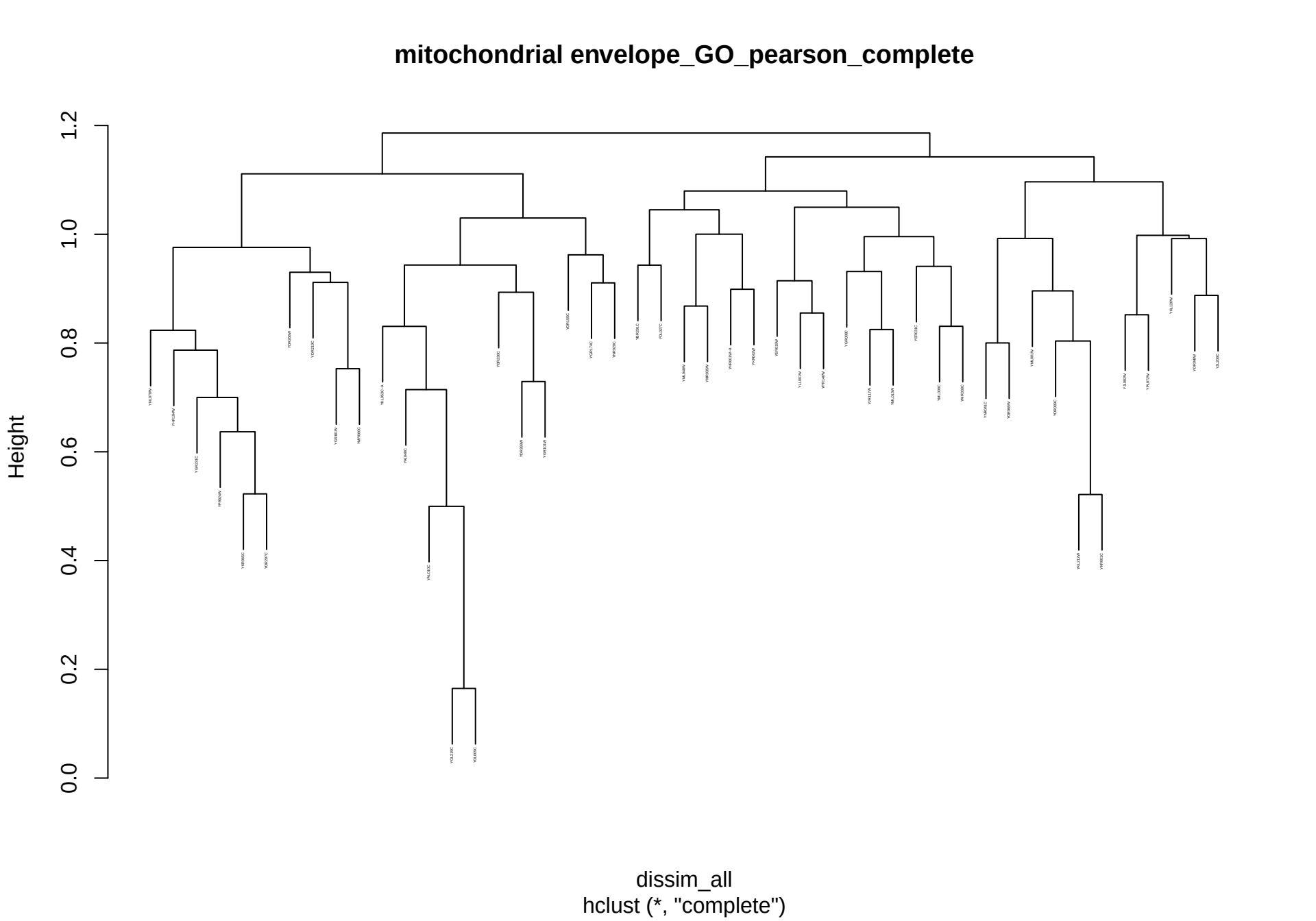

regulation of cell cycle_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
dissim_all
hclust (*, "complete")

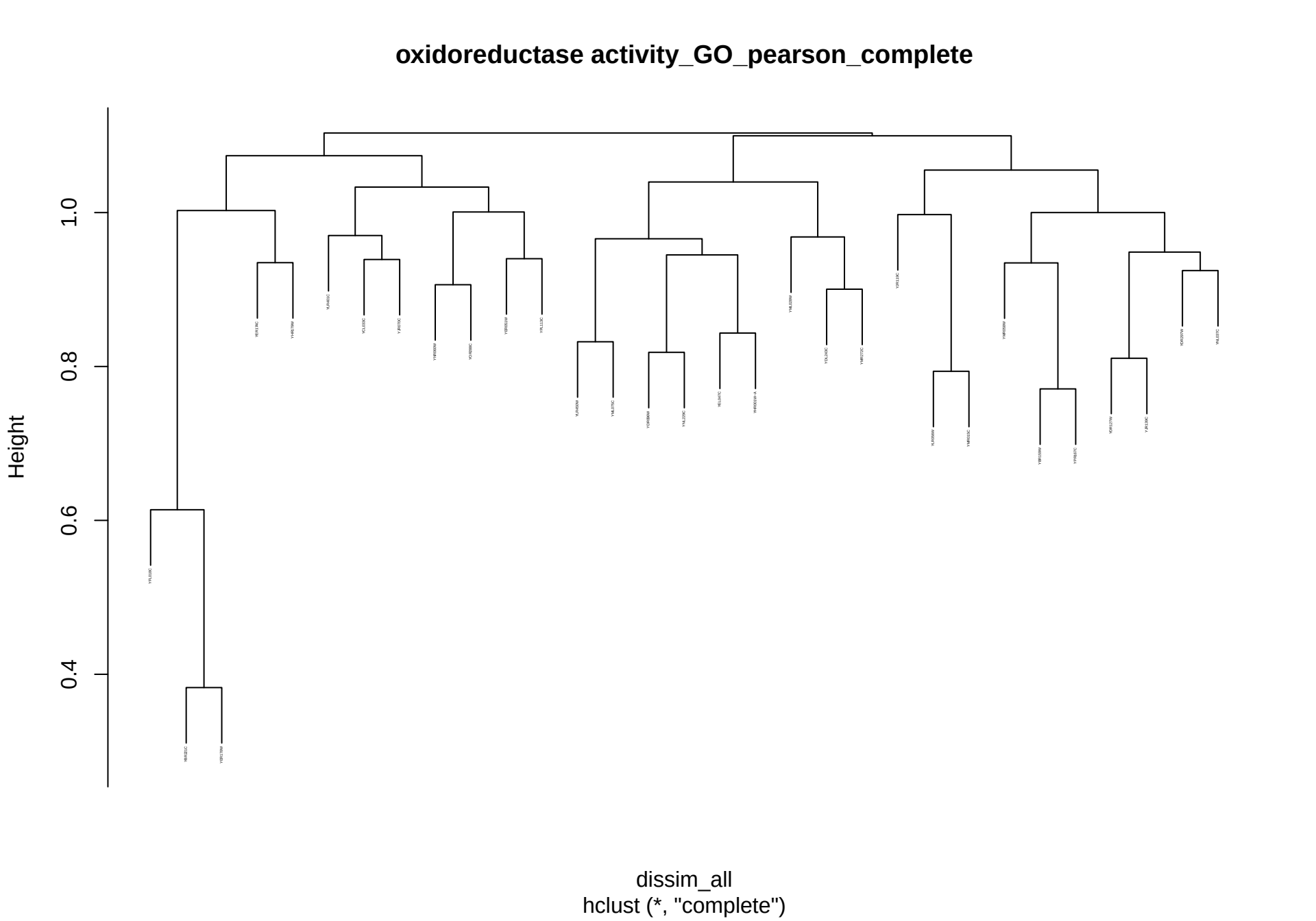

mitochondrion_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

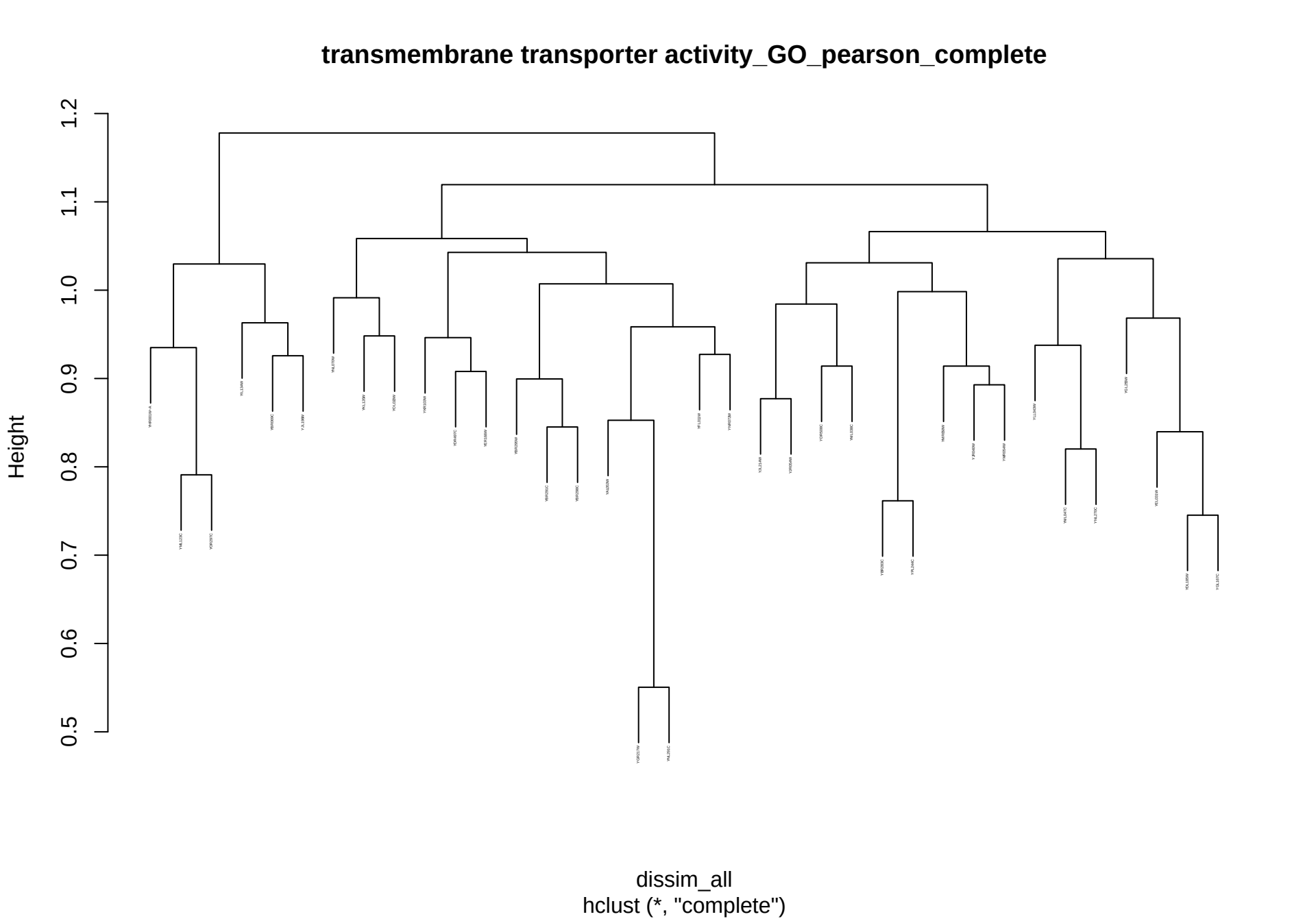

ribosome_GO_pearson_complete
Height
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

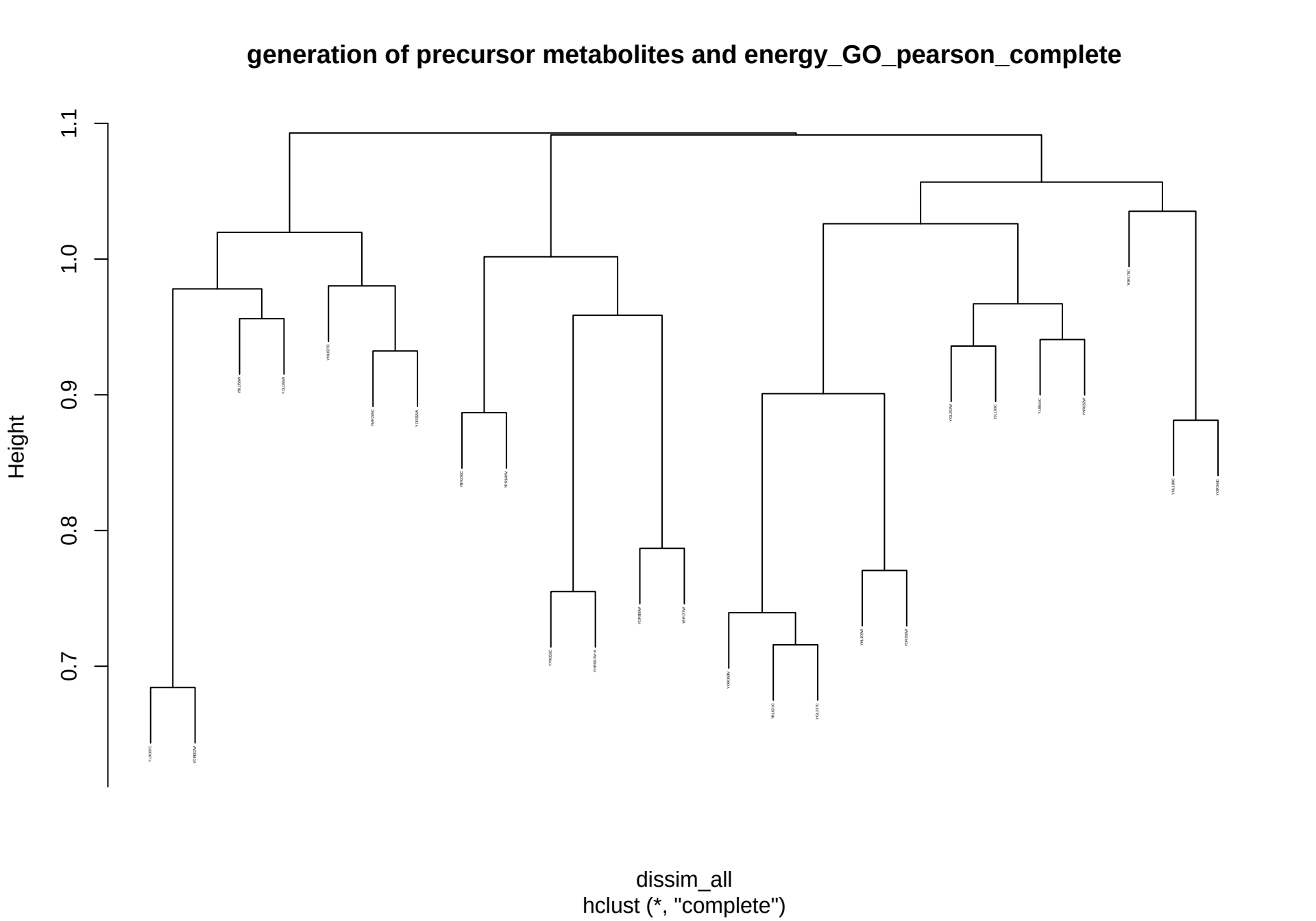

structural constituent of ribosome_GO_pearson_complete
Height
0.5
0.6
0.7
0.8
0.9
1.0
1.1
1.2
dissim_all
hclust (*, "complete")

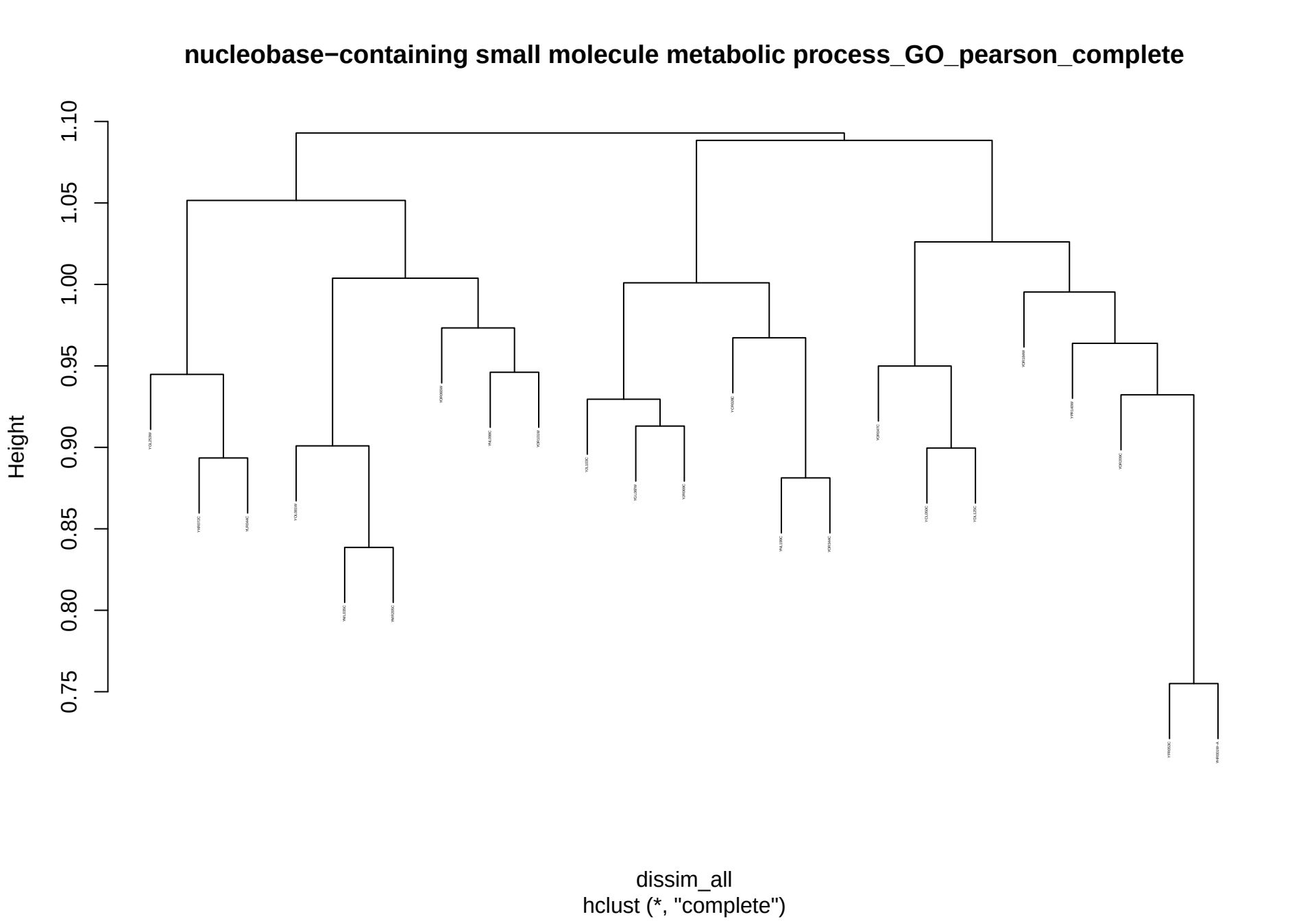

mitochondrion organization_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

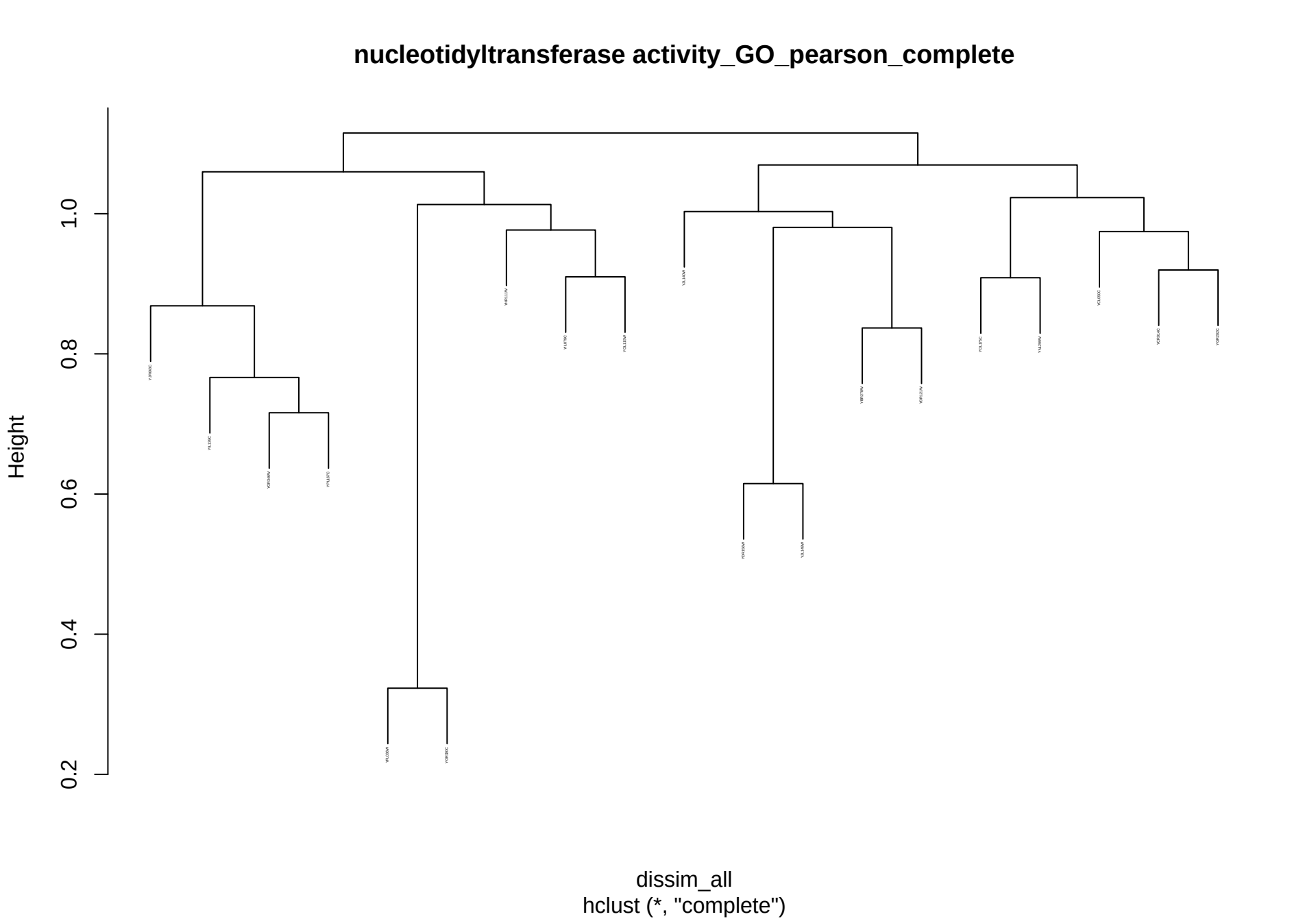

mitochondrial envelope_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

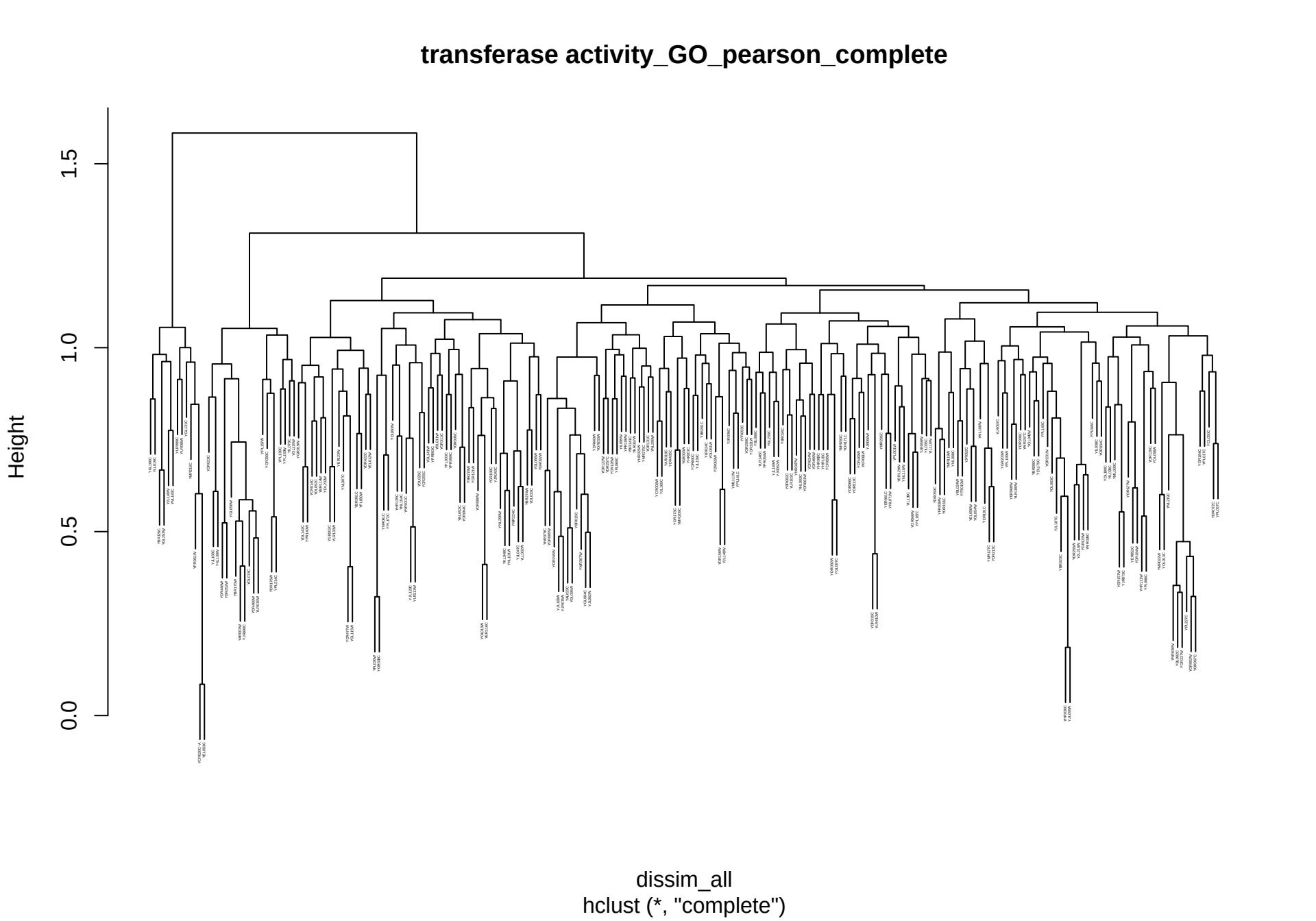

oxidoreductase activity_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

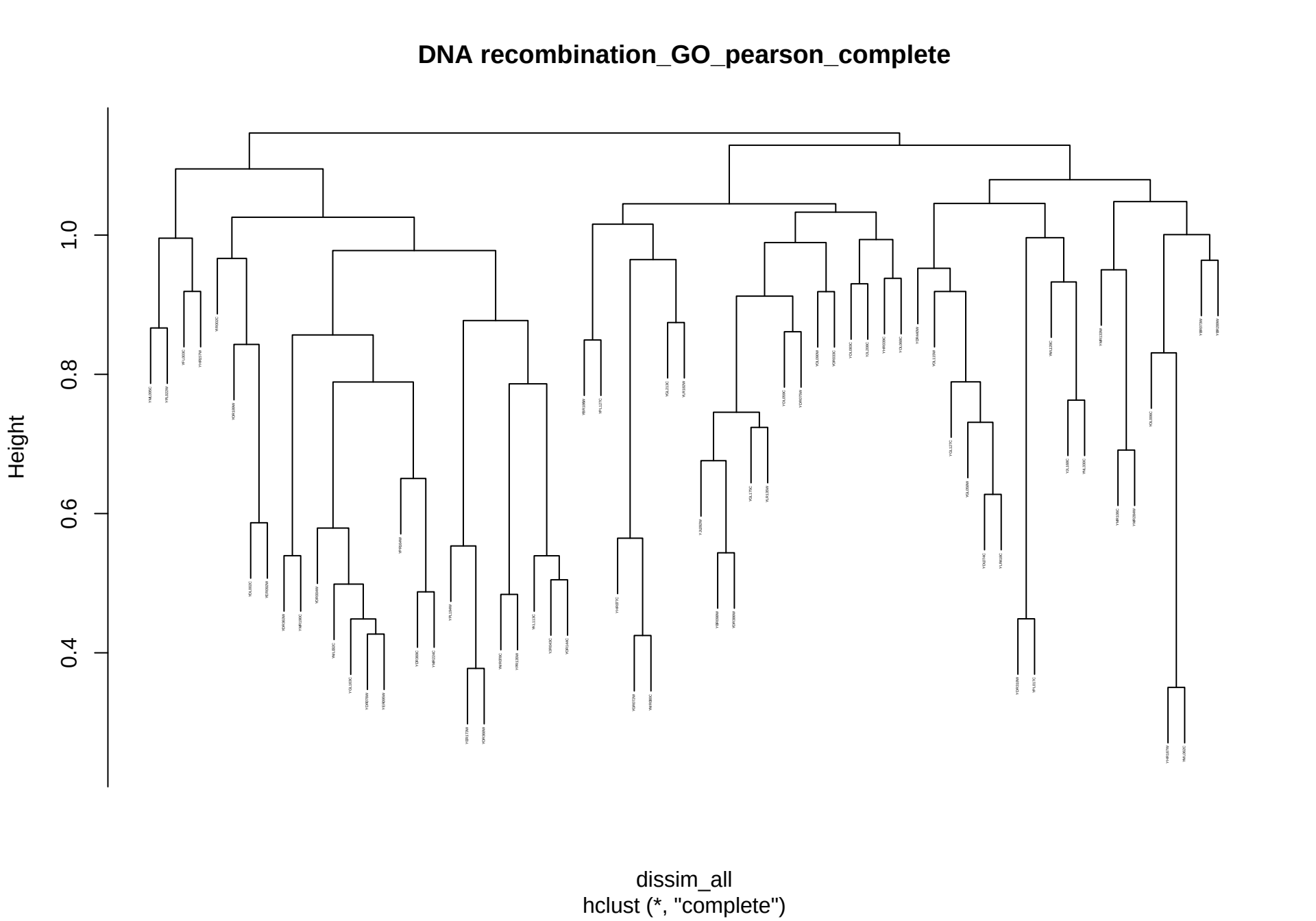

transmembrane transporter activity_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
dissim_all
hclust (*, "complete")

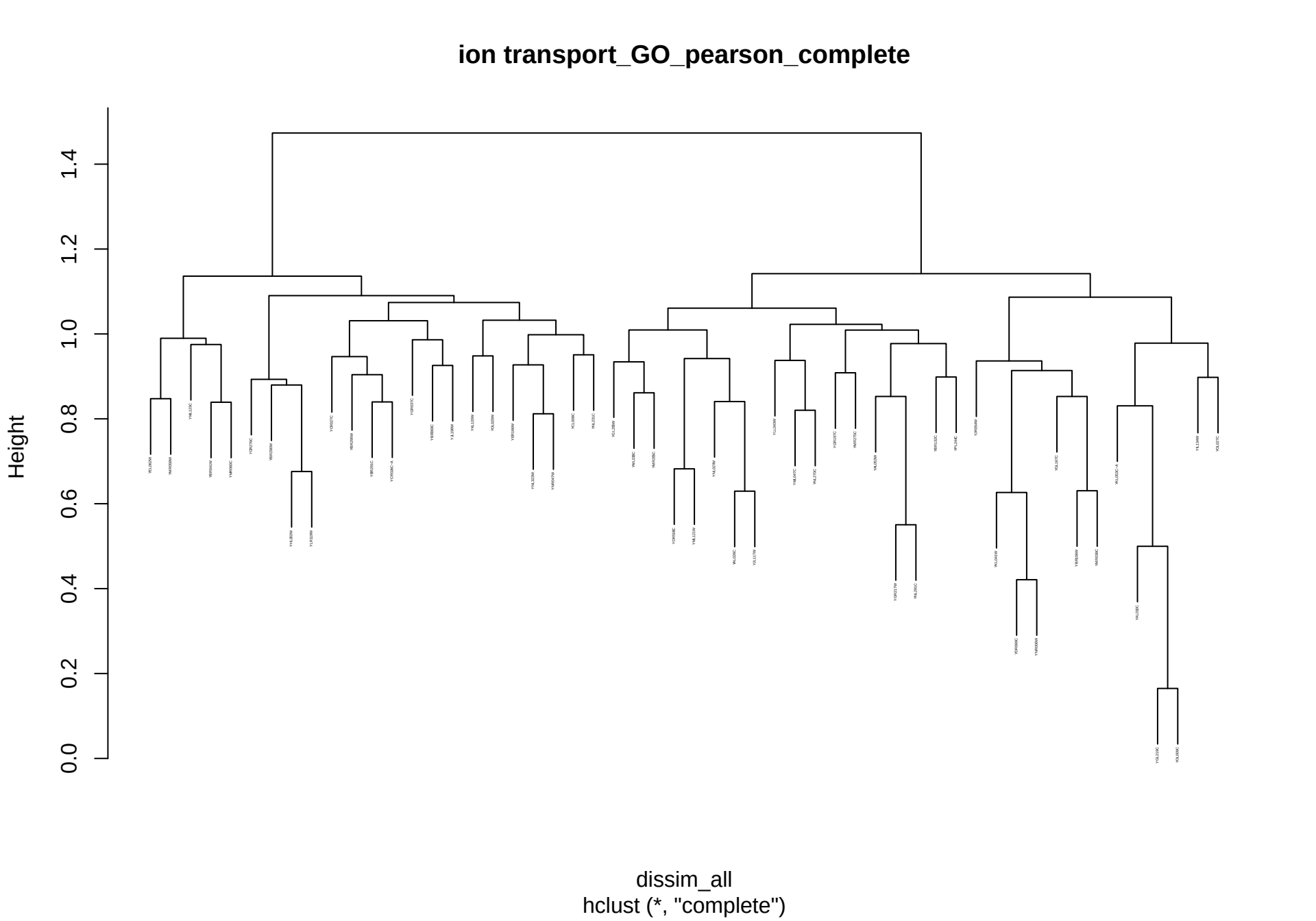

generation of precursor metabolites and energy_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
dissim_all
hclust (*, "complete")

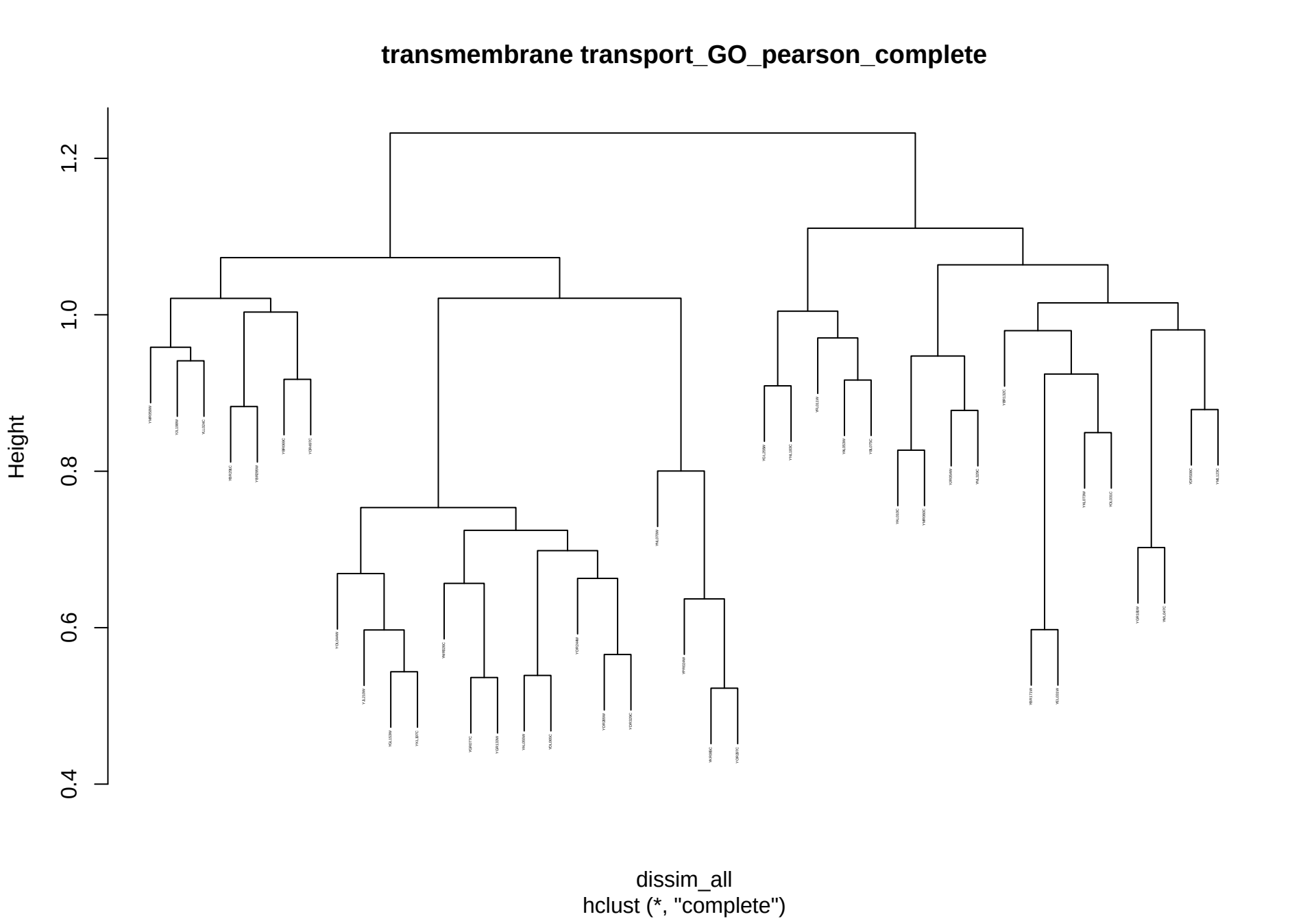

nucleobase−containing small molecule metabolic process_GO_pearson_complete
Height
1.10
1.05
1.00
0.95
0.90
0.85
0.80
0.75
dissim_all
hclust (*, "complete")

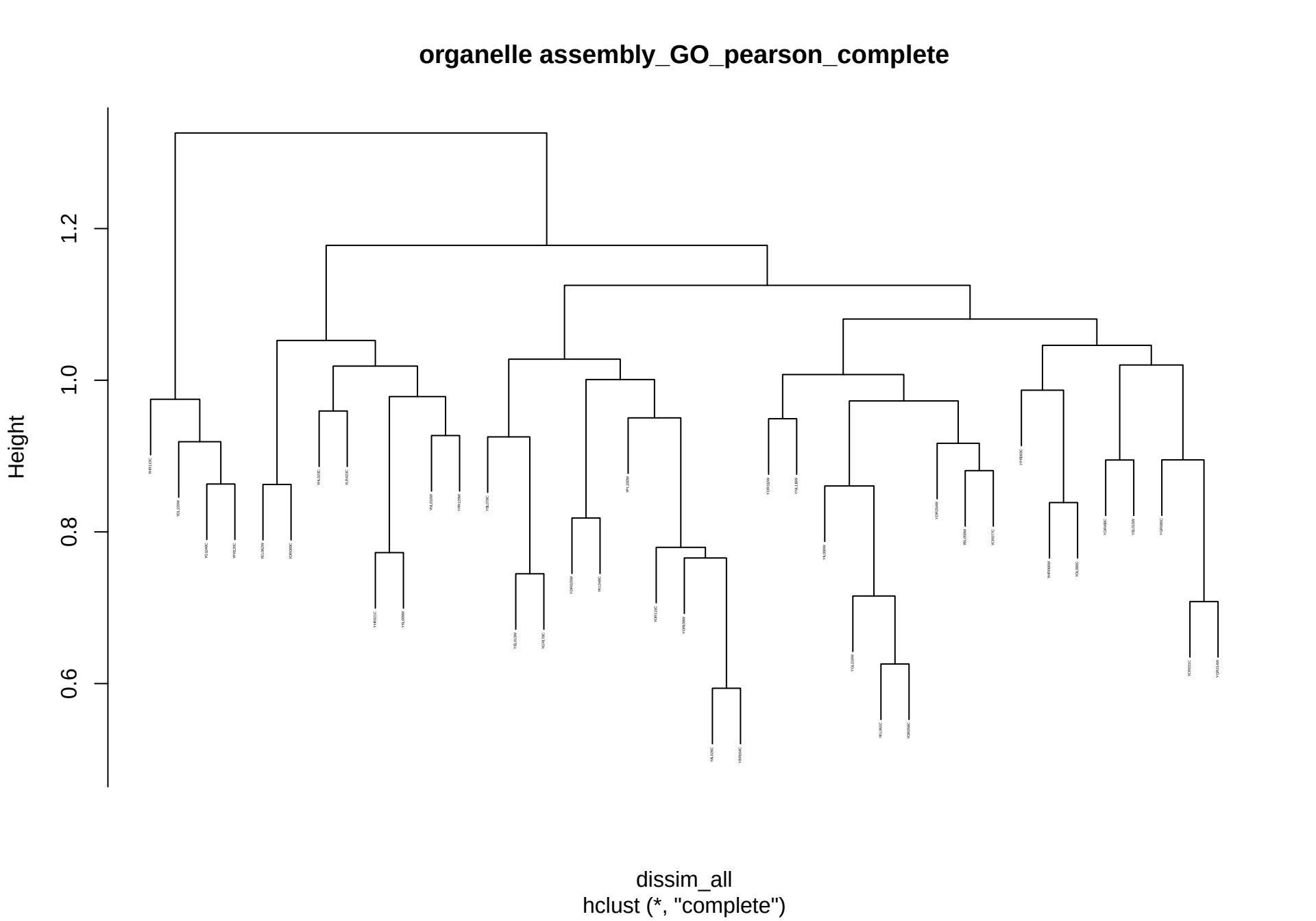

nucleotidyltransferase activity_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")


transferase activity_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")


DNA recombination_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

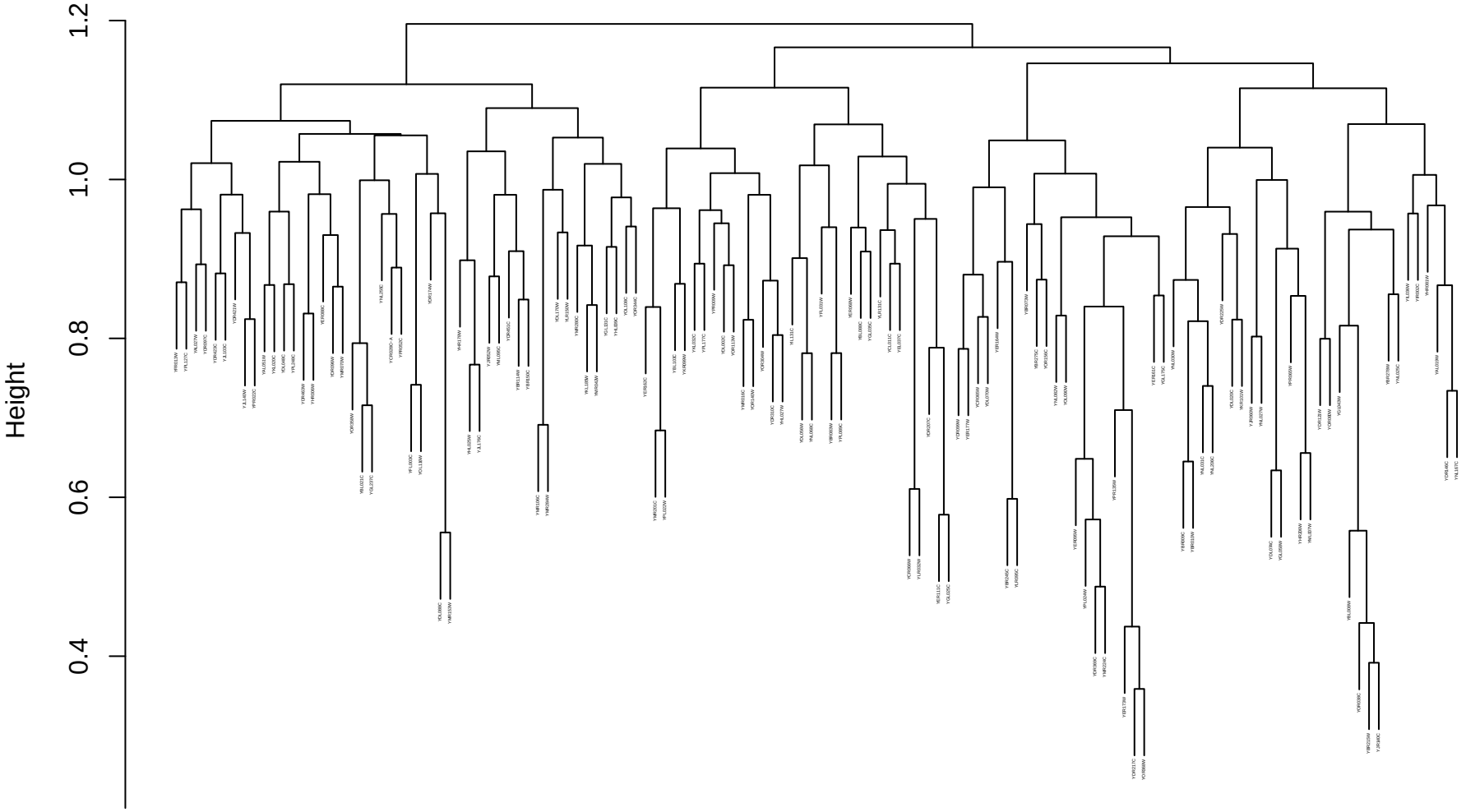

ion transport_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")


transmembrane transport_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

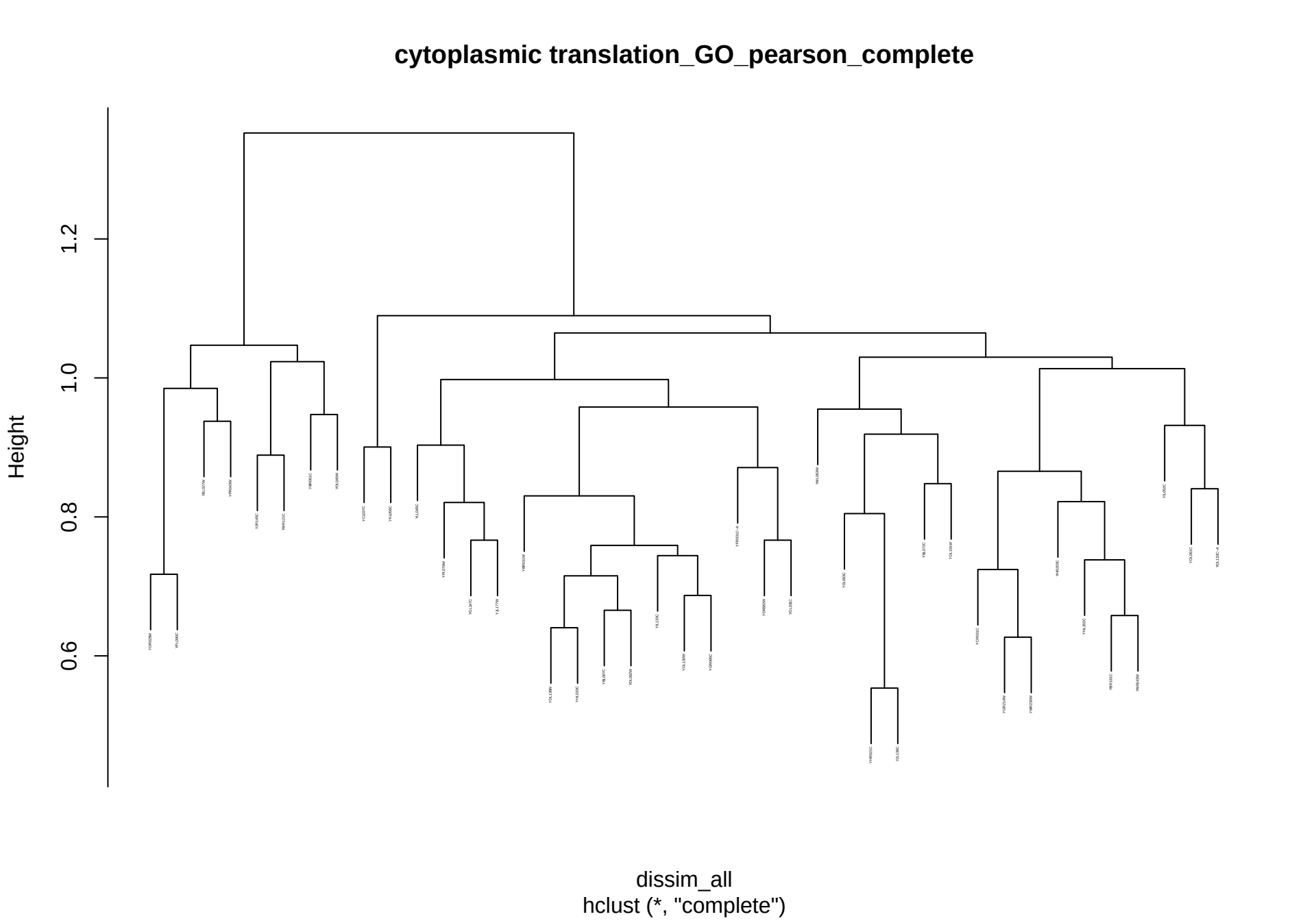

organelle assembly_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
dissim_all
hclust (*, "complete")

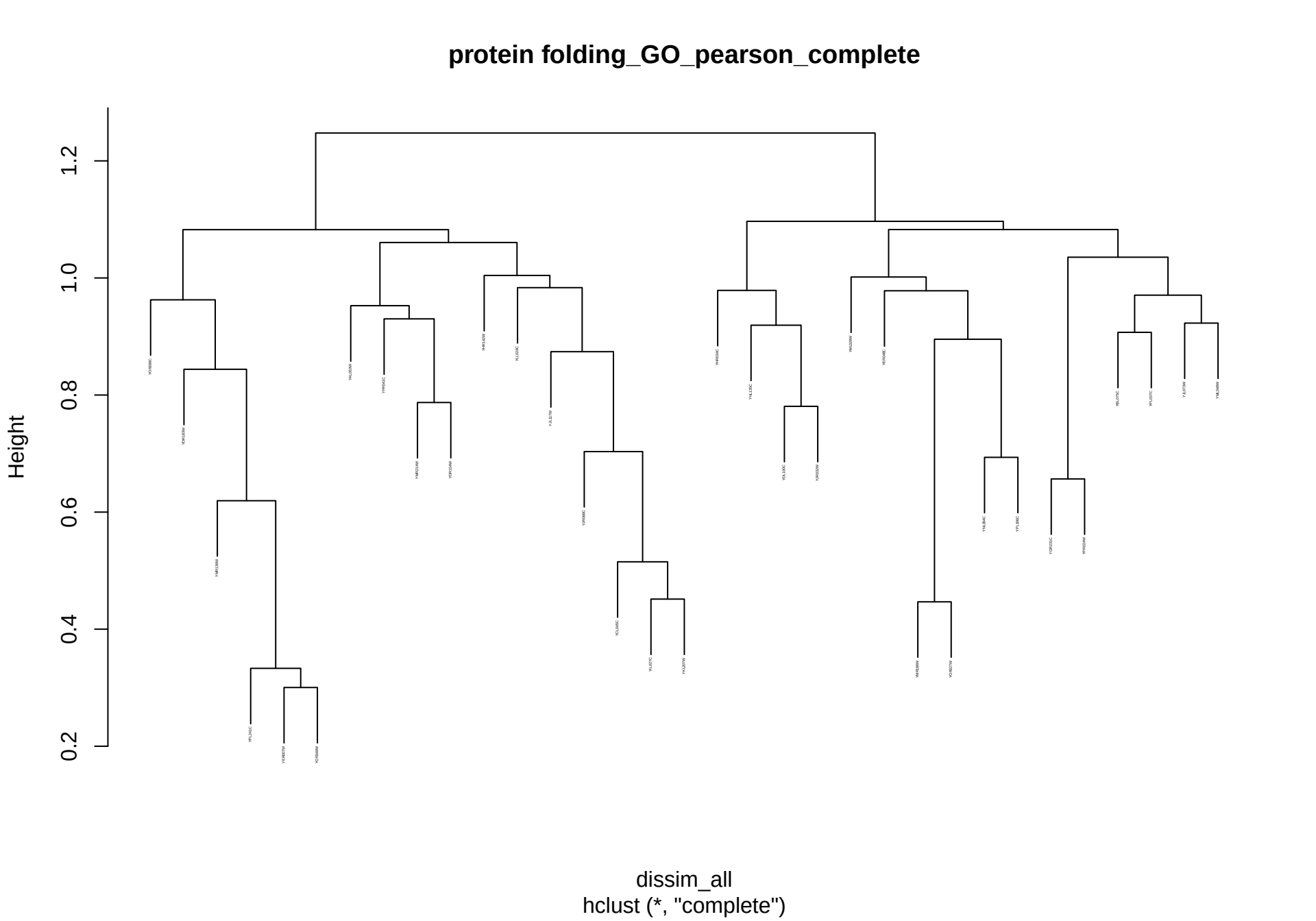

tRNA processing_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

DNA binding_GO_pearson_complete

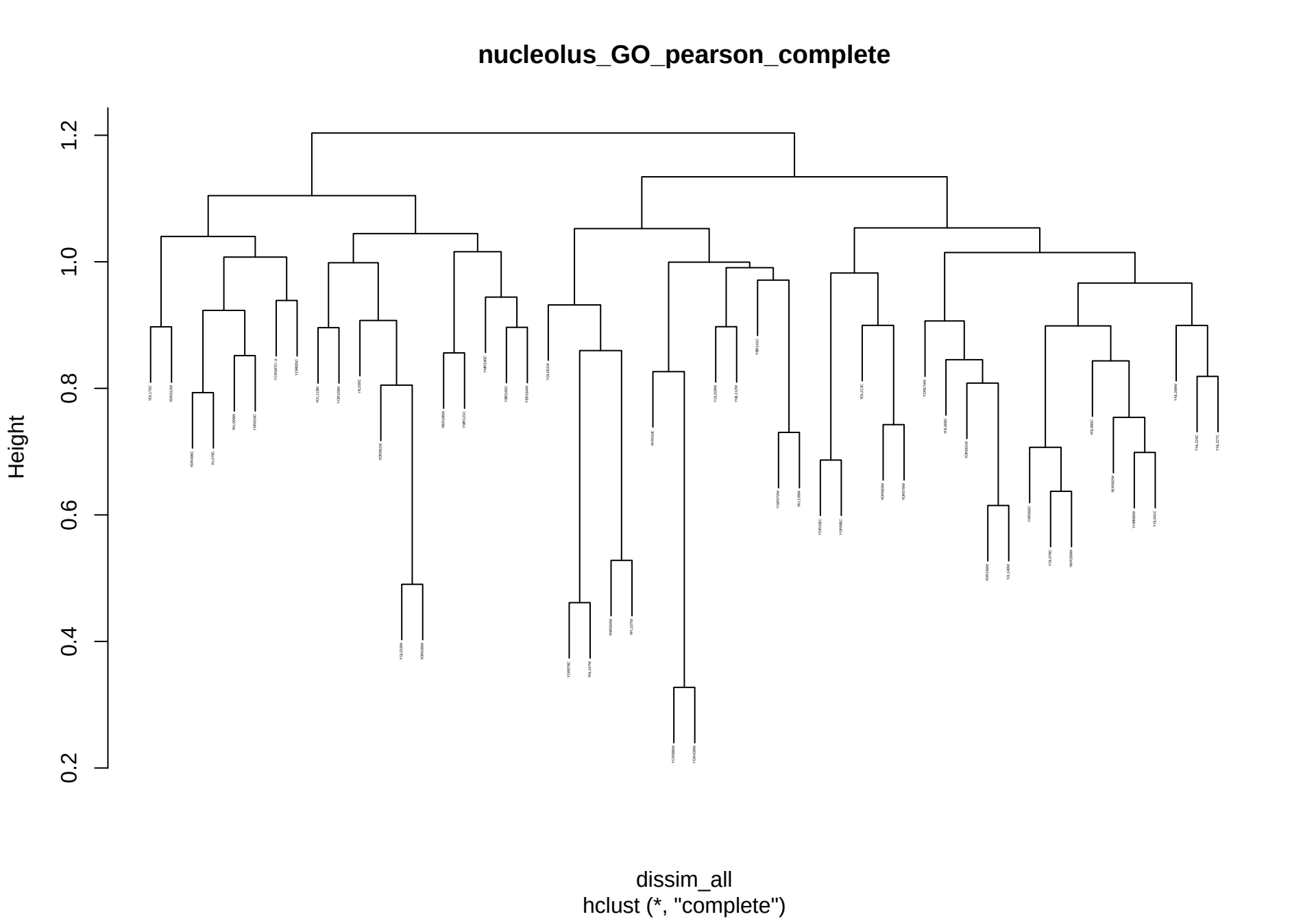


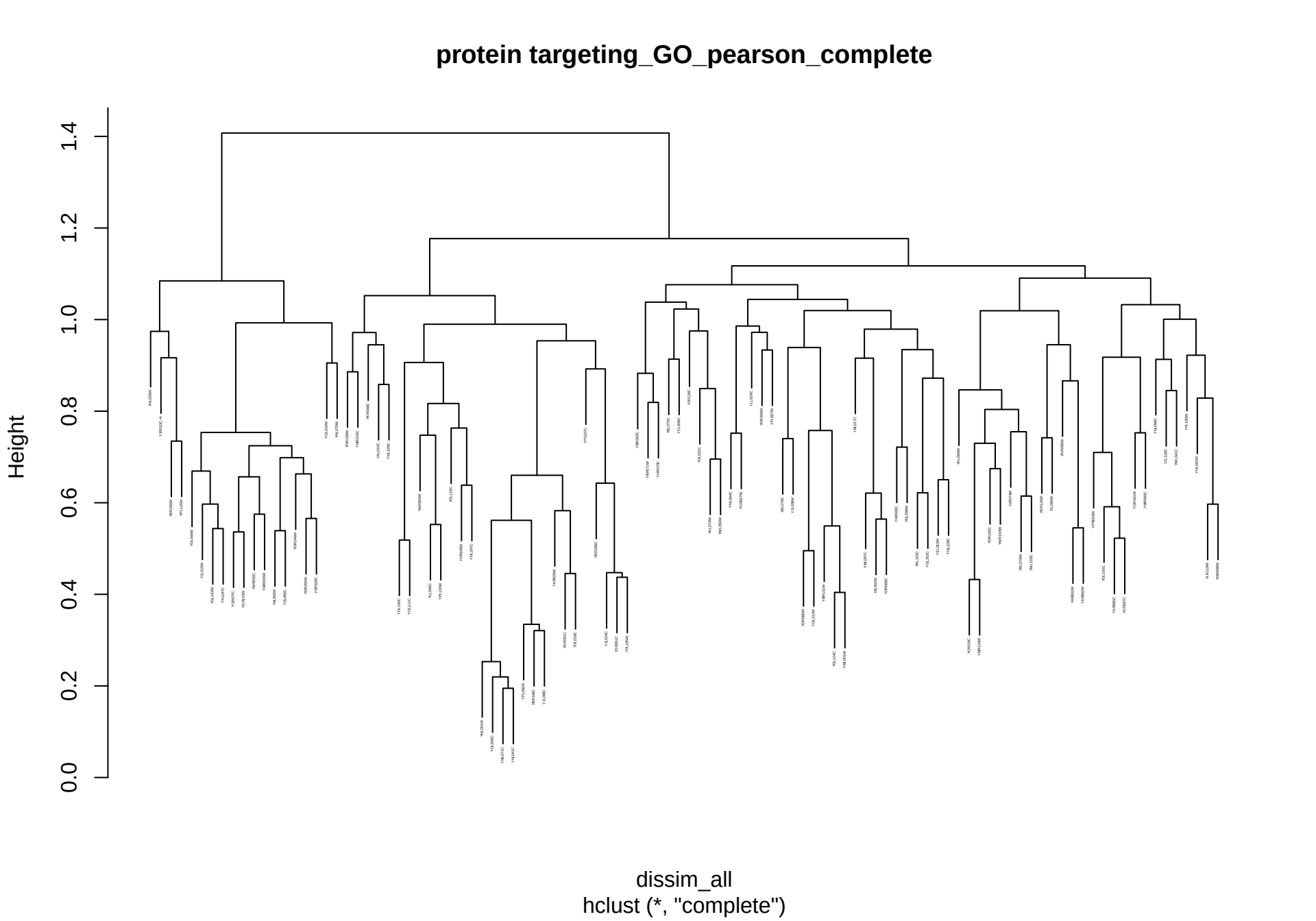
dissim_all
hclust (*, "complete")

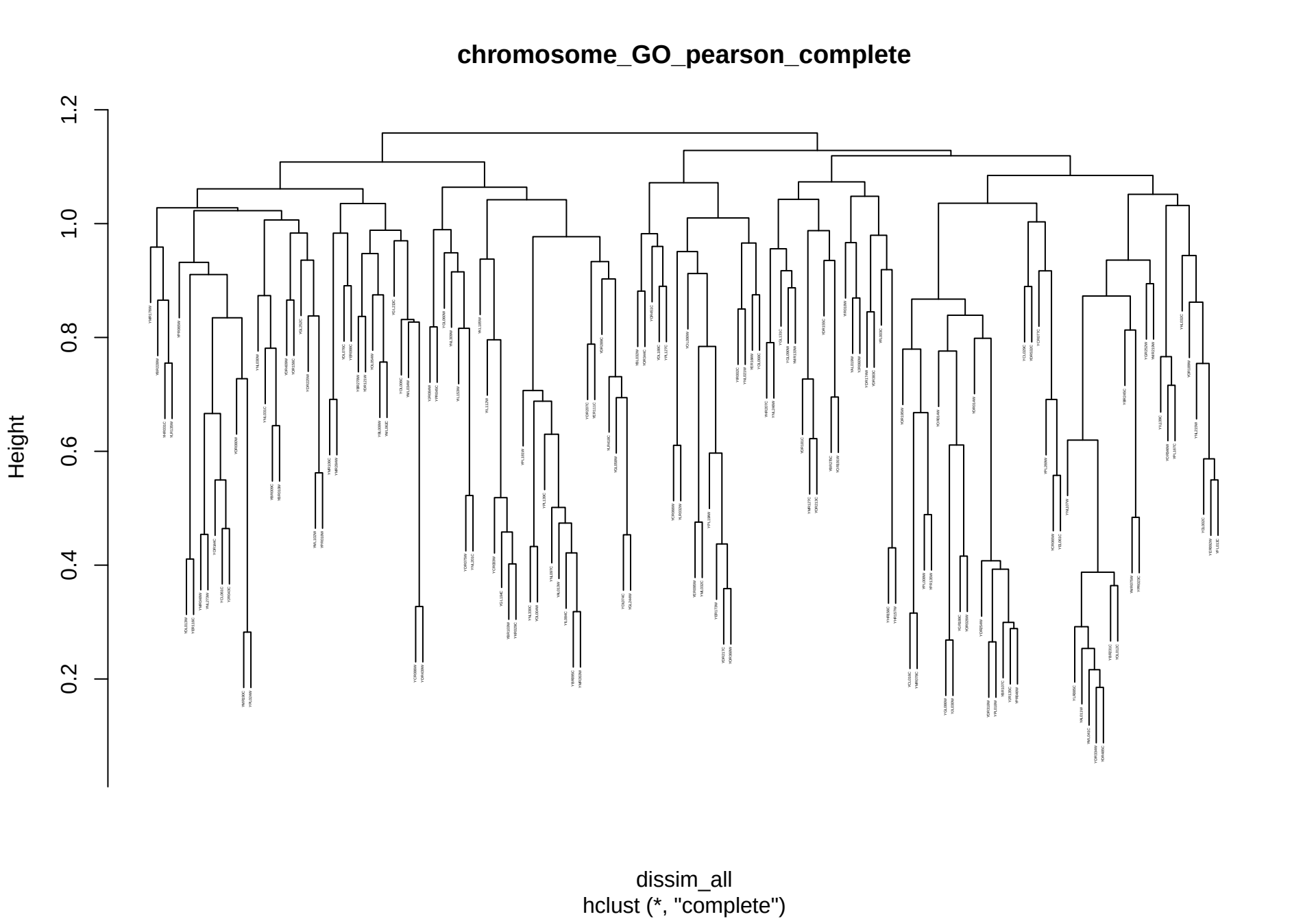

cytoplasmic translation_GO_pearson_complete
Height
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

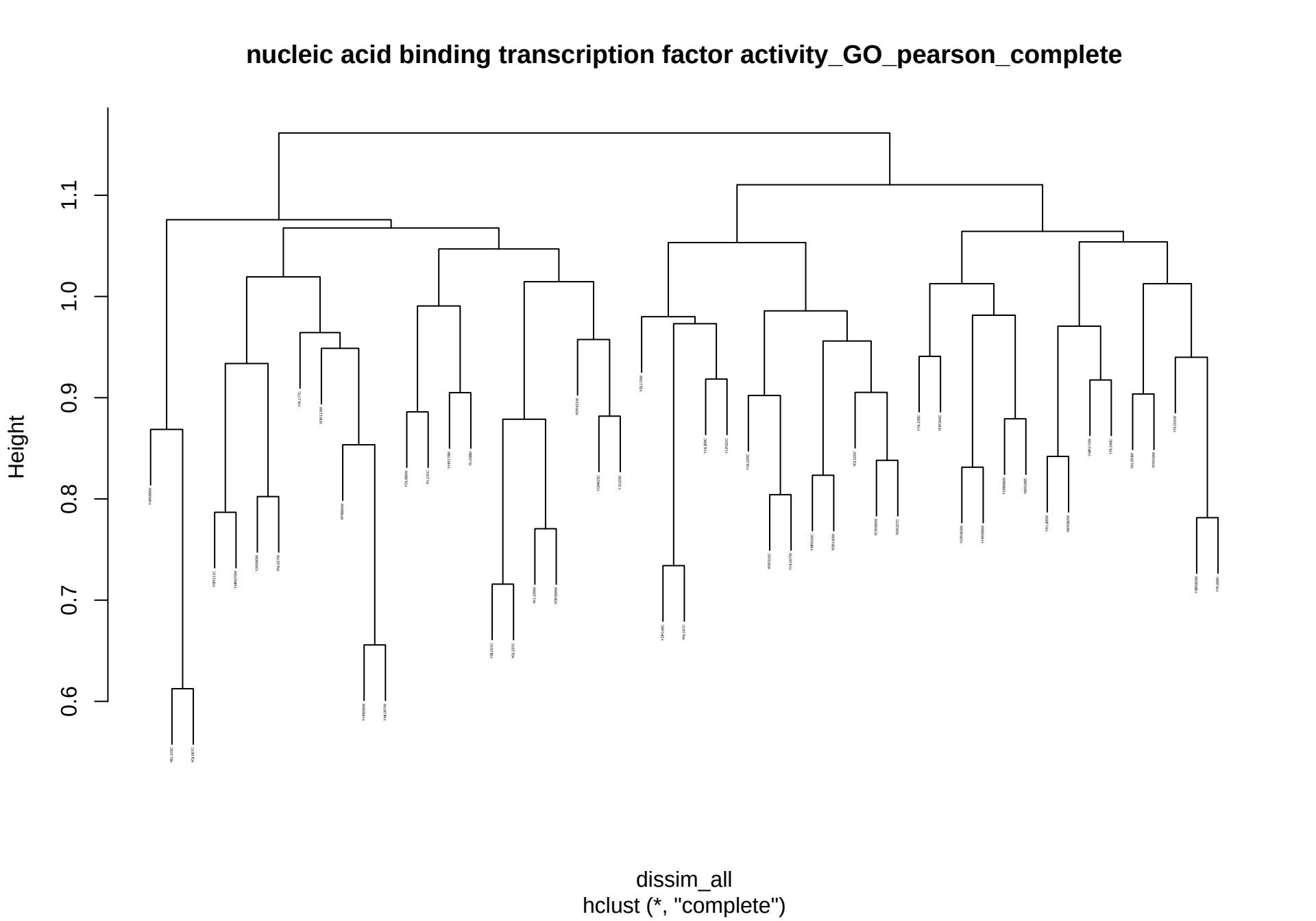

protein folding_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

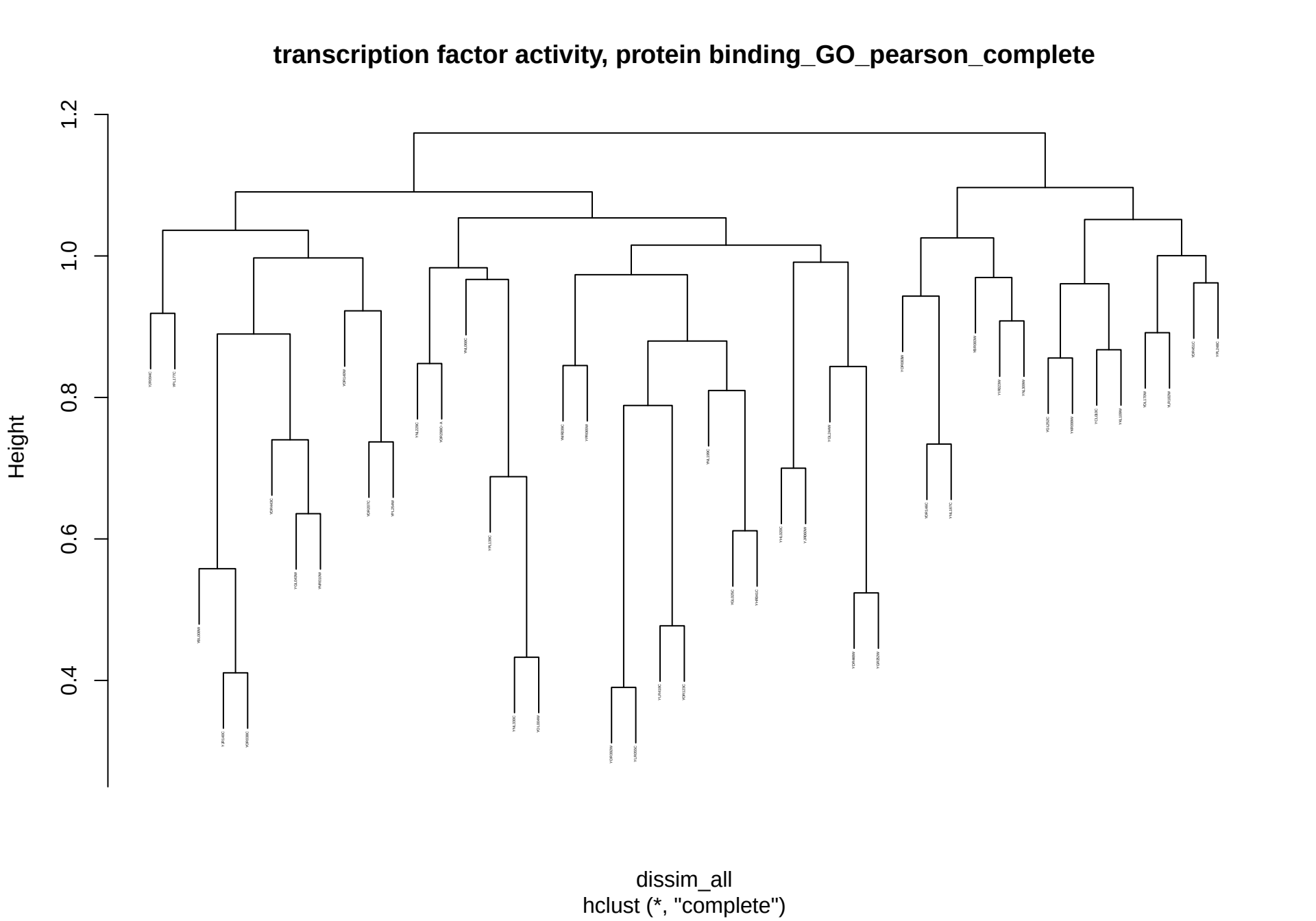

regulation of translation_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
dissim_all
hclust (*, "complete")

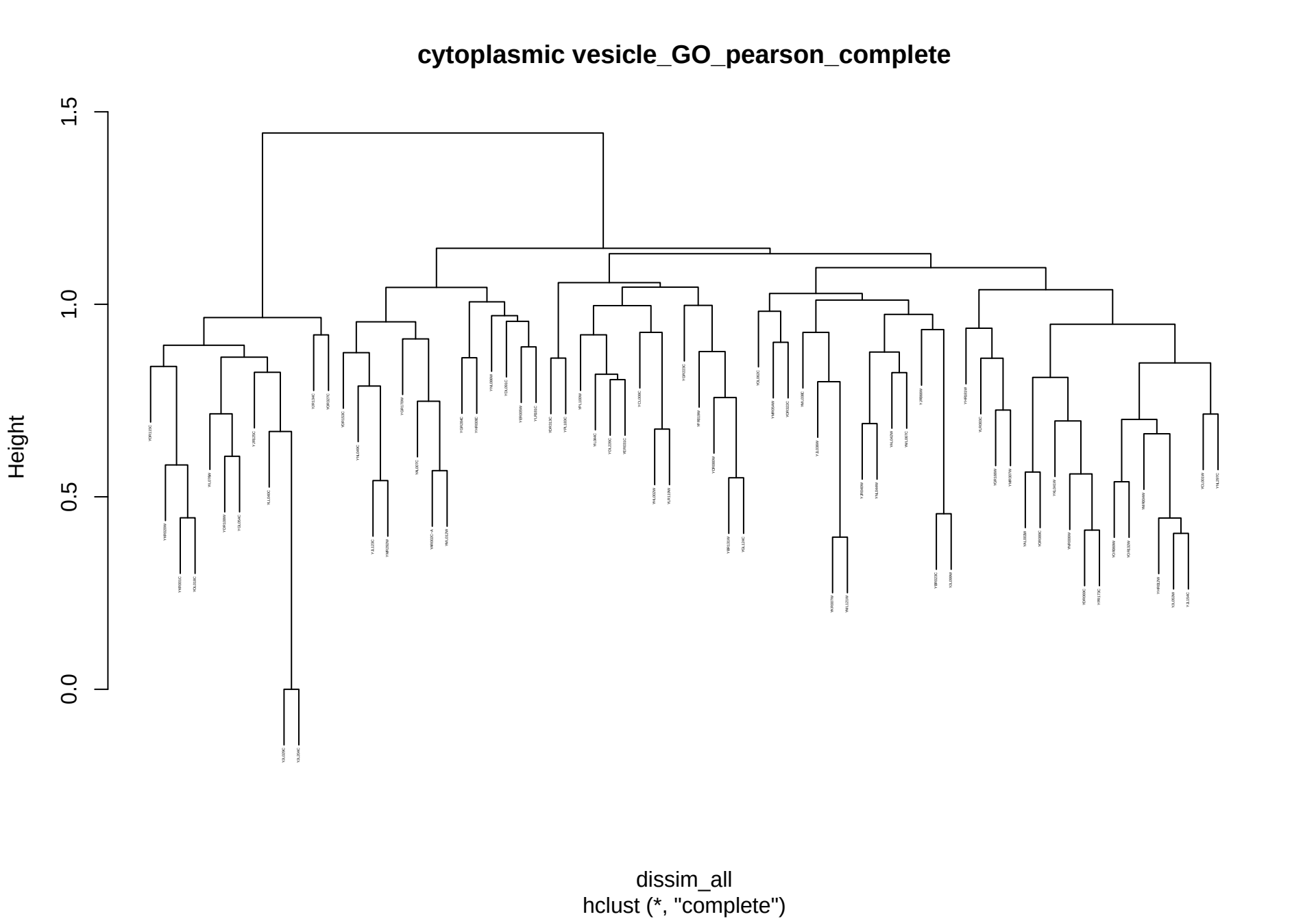

nucleolus_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

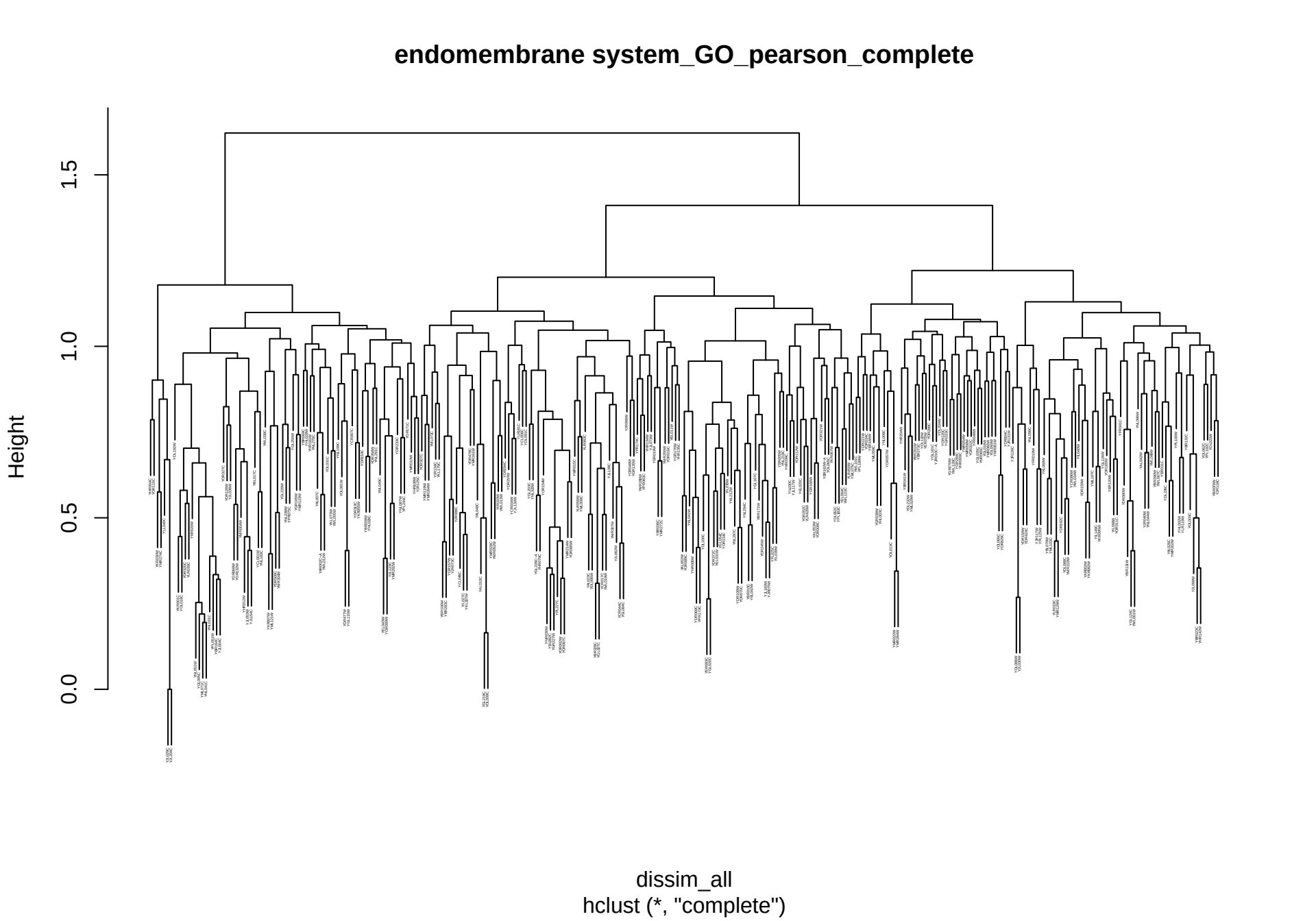

protein targeting_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")

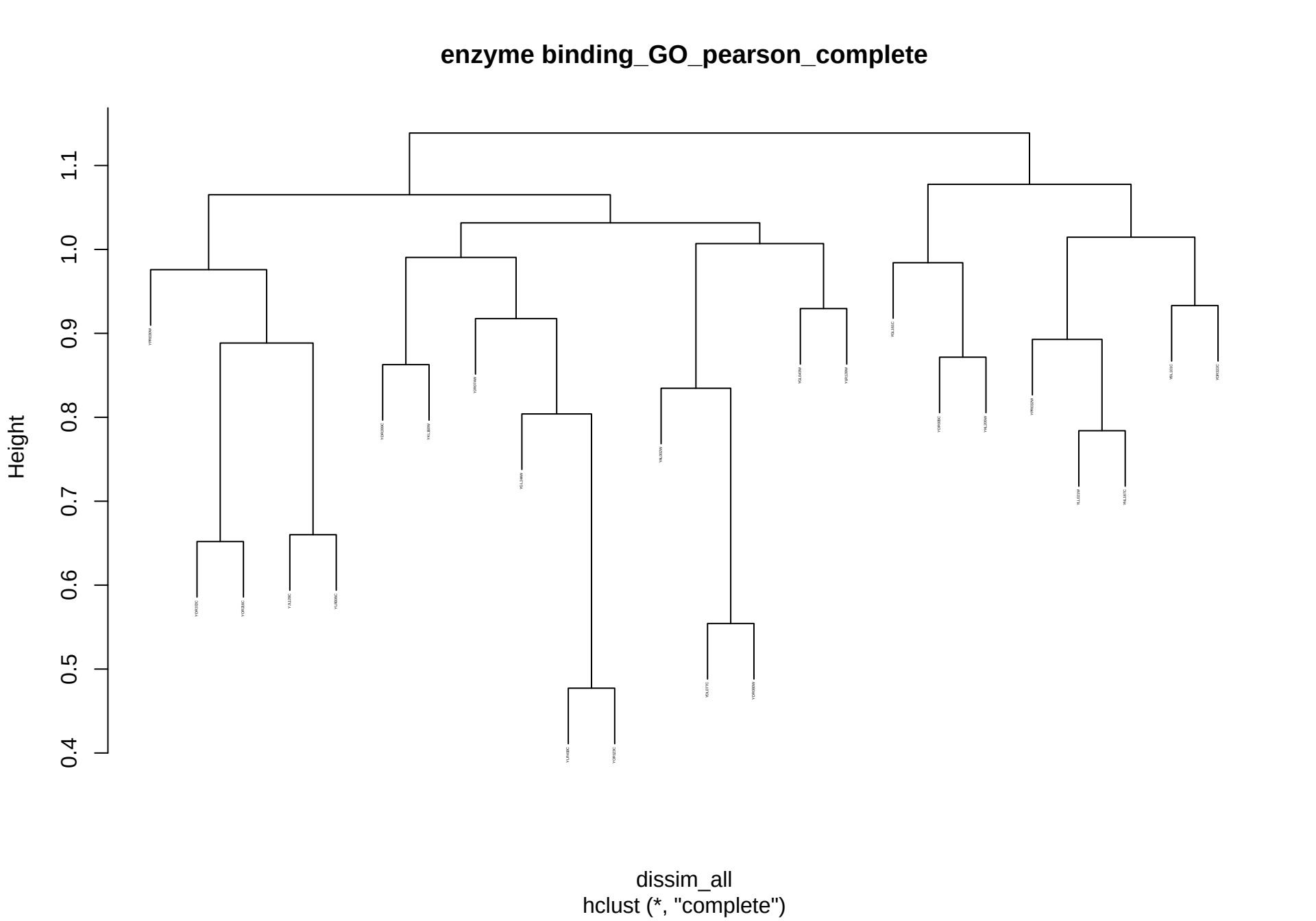

chromosome_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

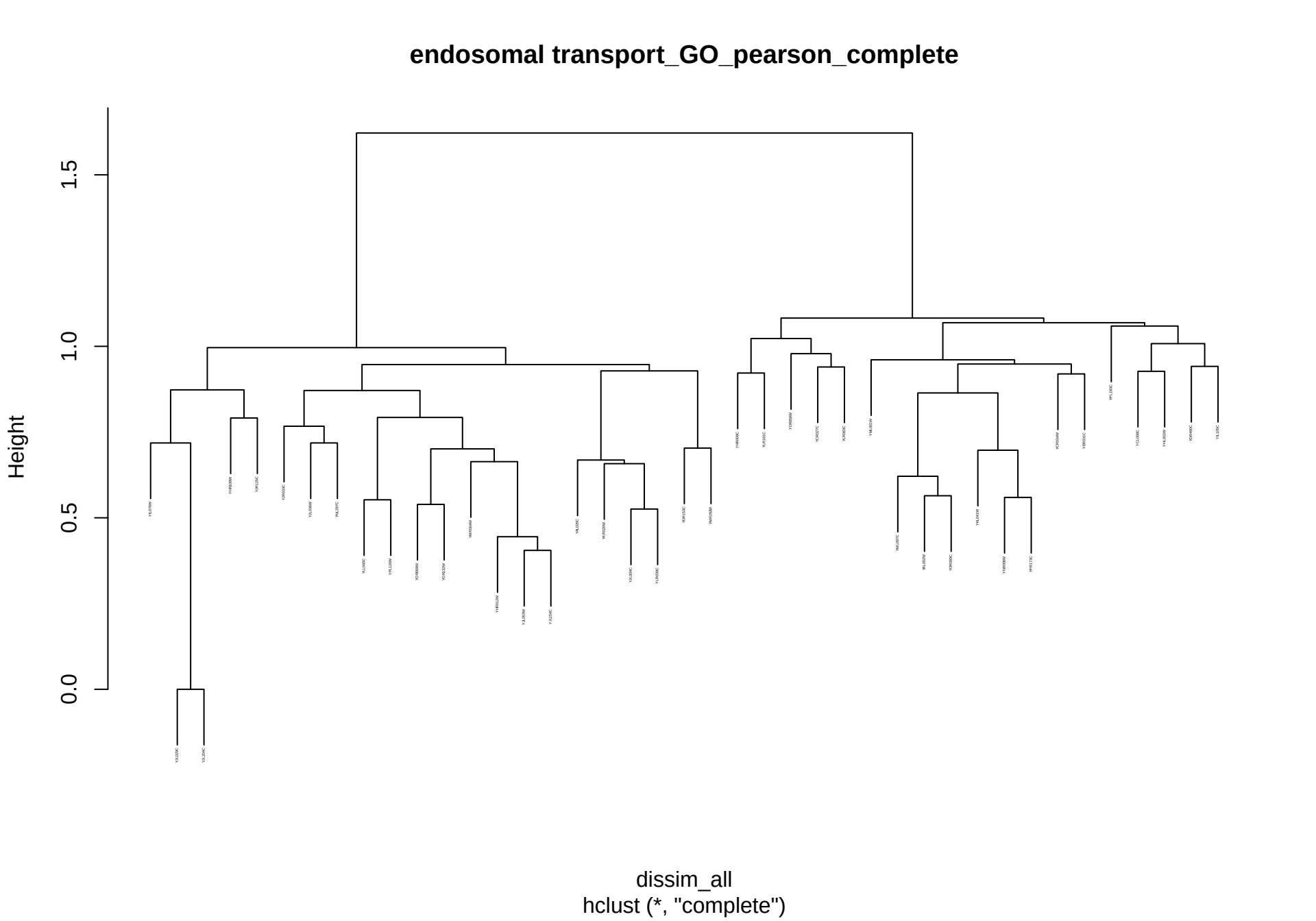

nucleic acid binding transcription factor activity_GO_pearson_complete
Height
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

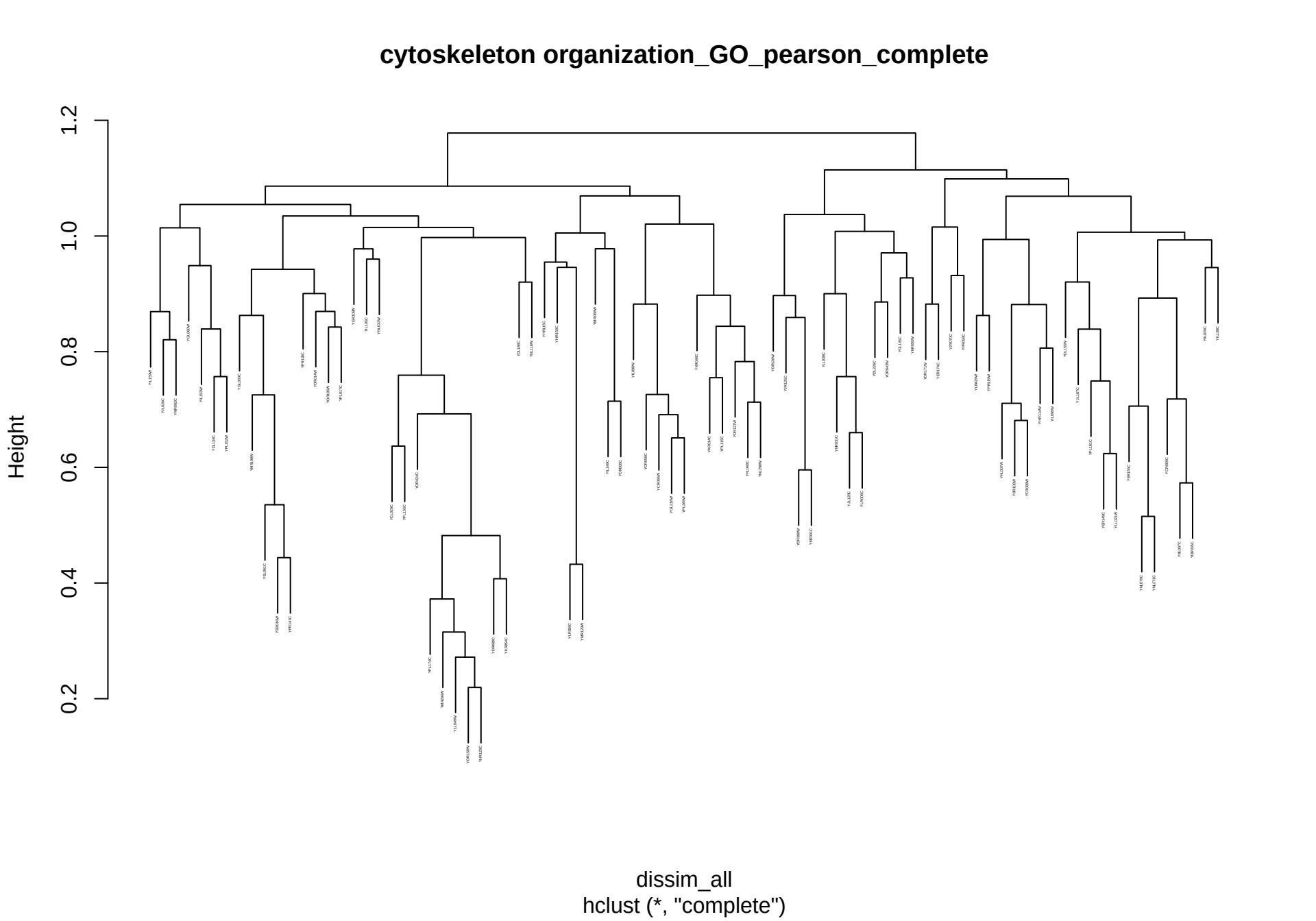

transcription factor activity, protein binding_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

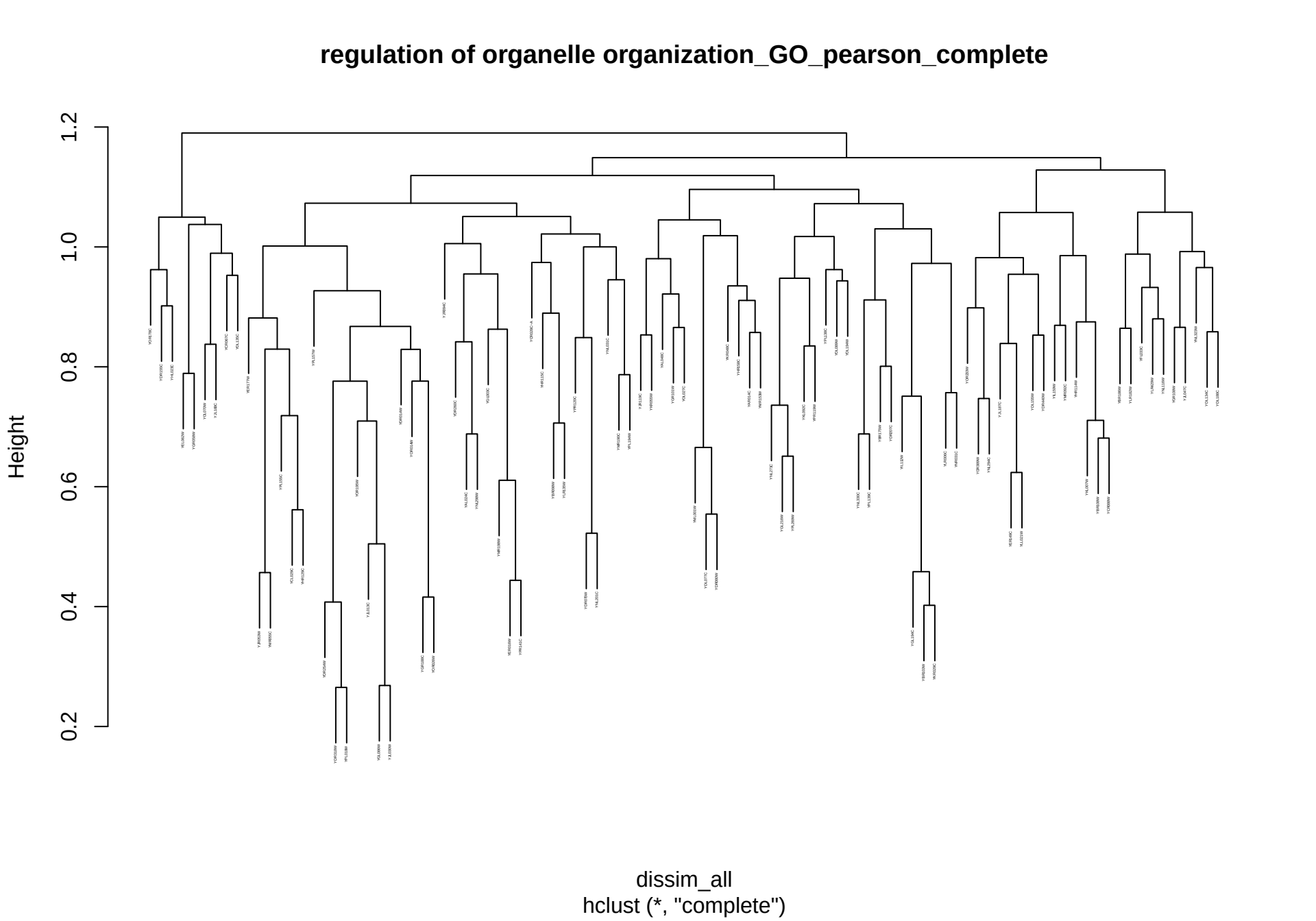

cytoplasmic vesicle_GO_pearson_complete
Height
1.5
1.0
0.5
0.0
dissim_all
hclust (*, "complete")

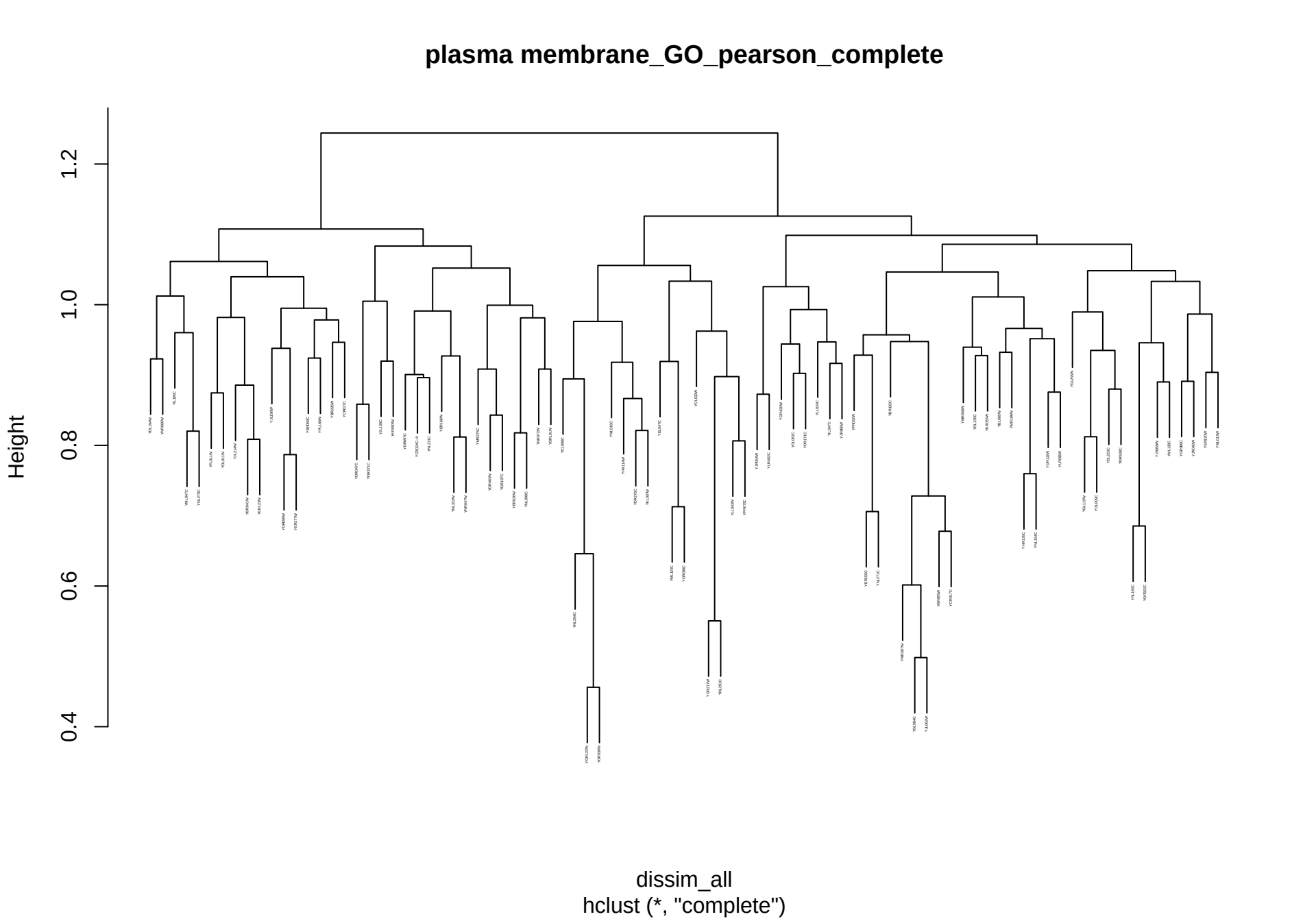

endomembrane system_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")

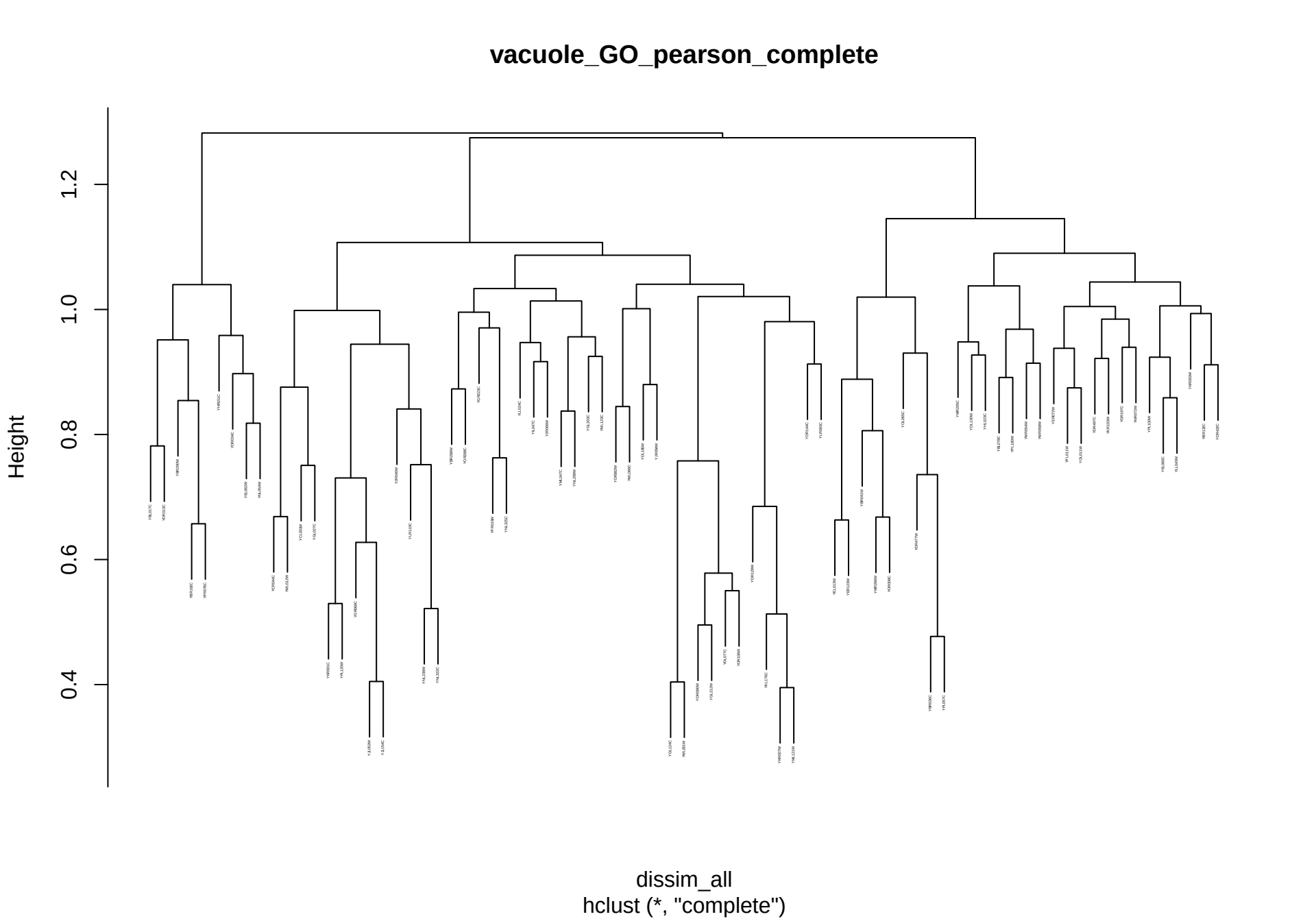

enzyme binding_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

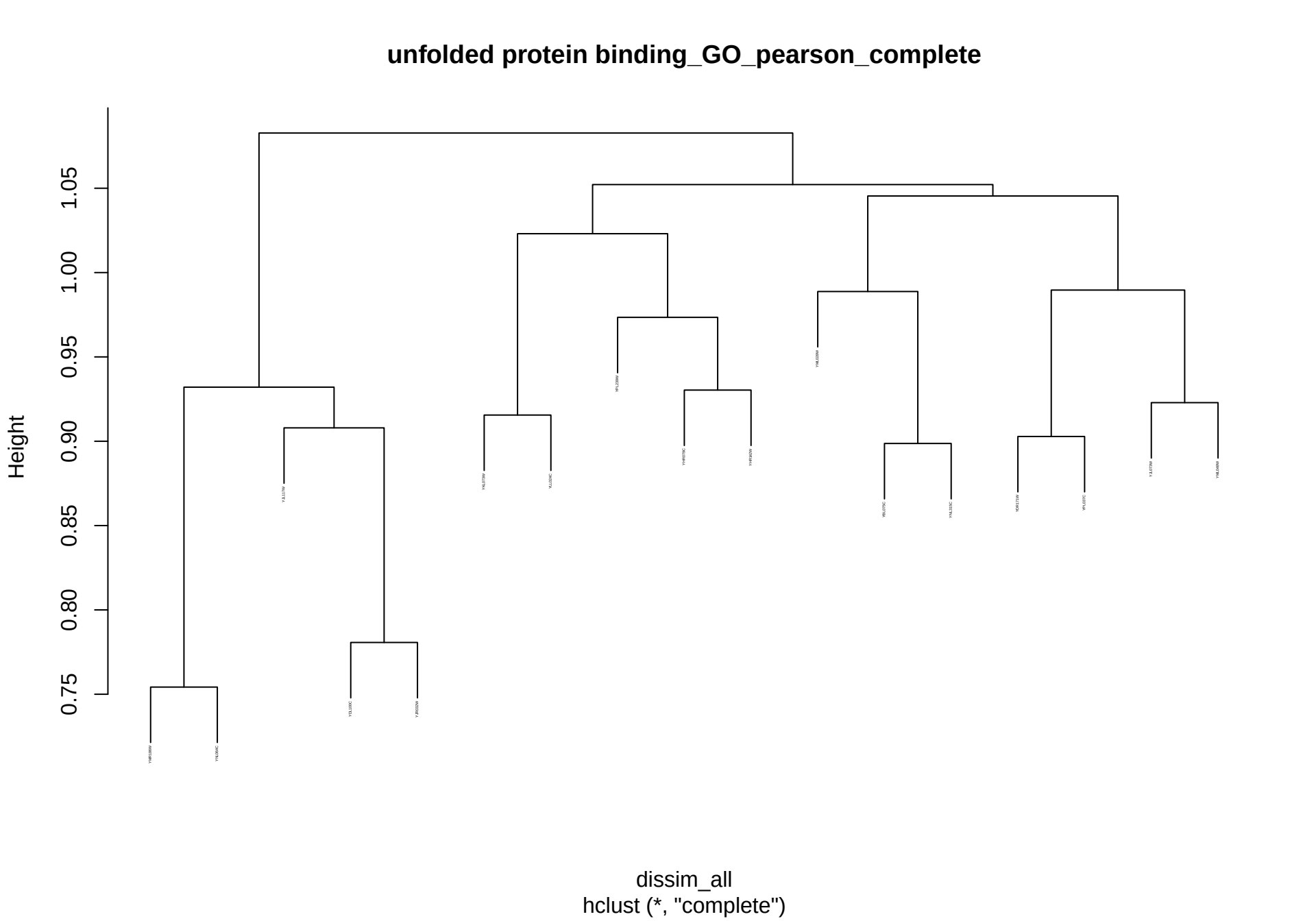

endosomal transport_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")

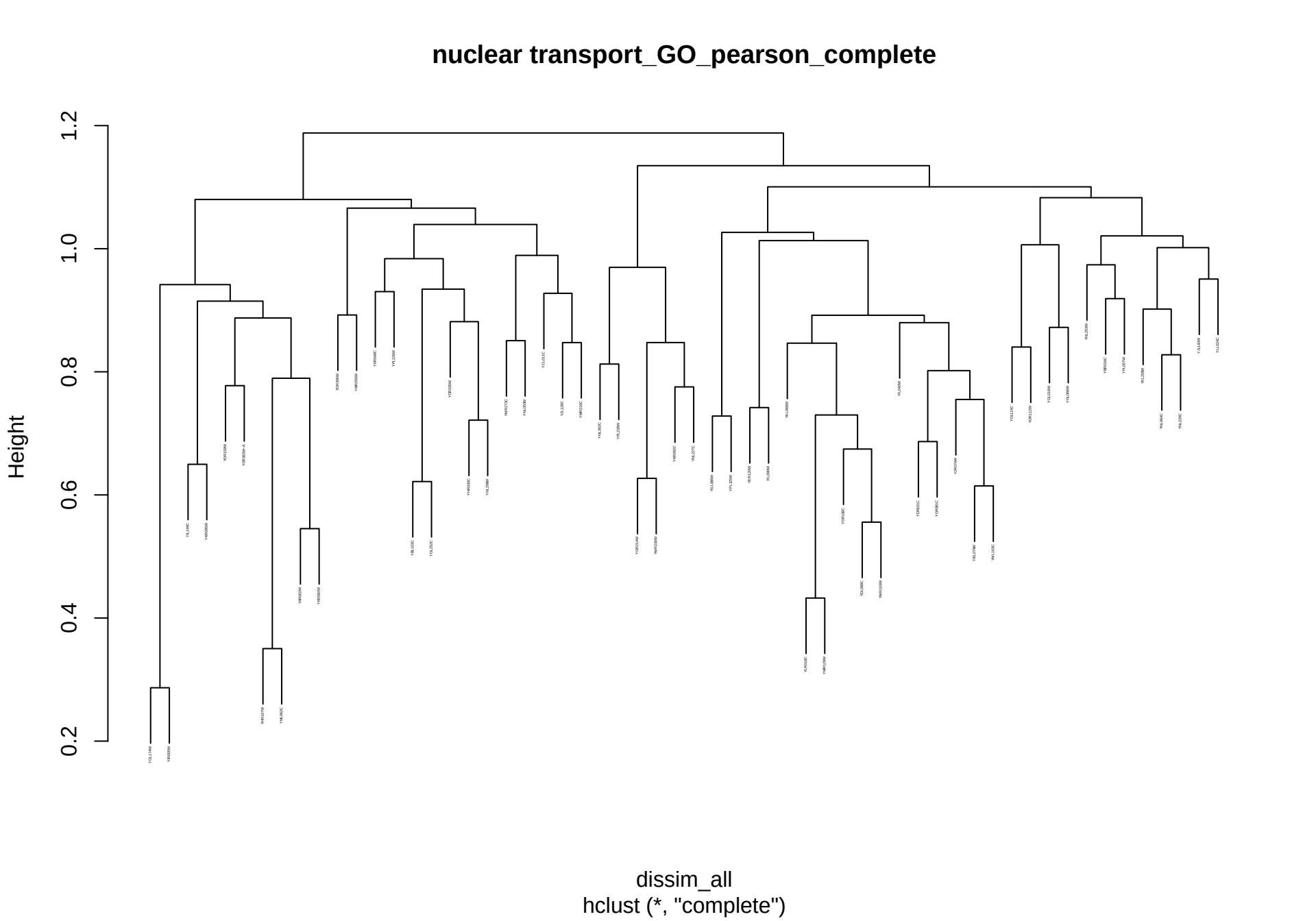

cytoskeleton organization_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

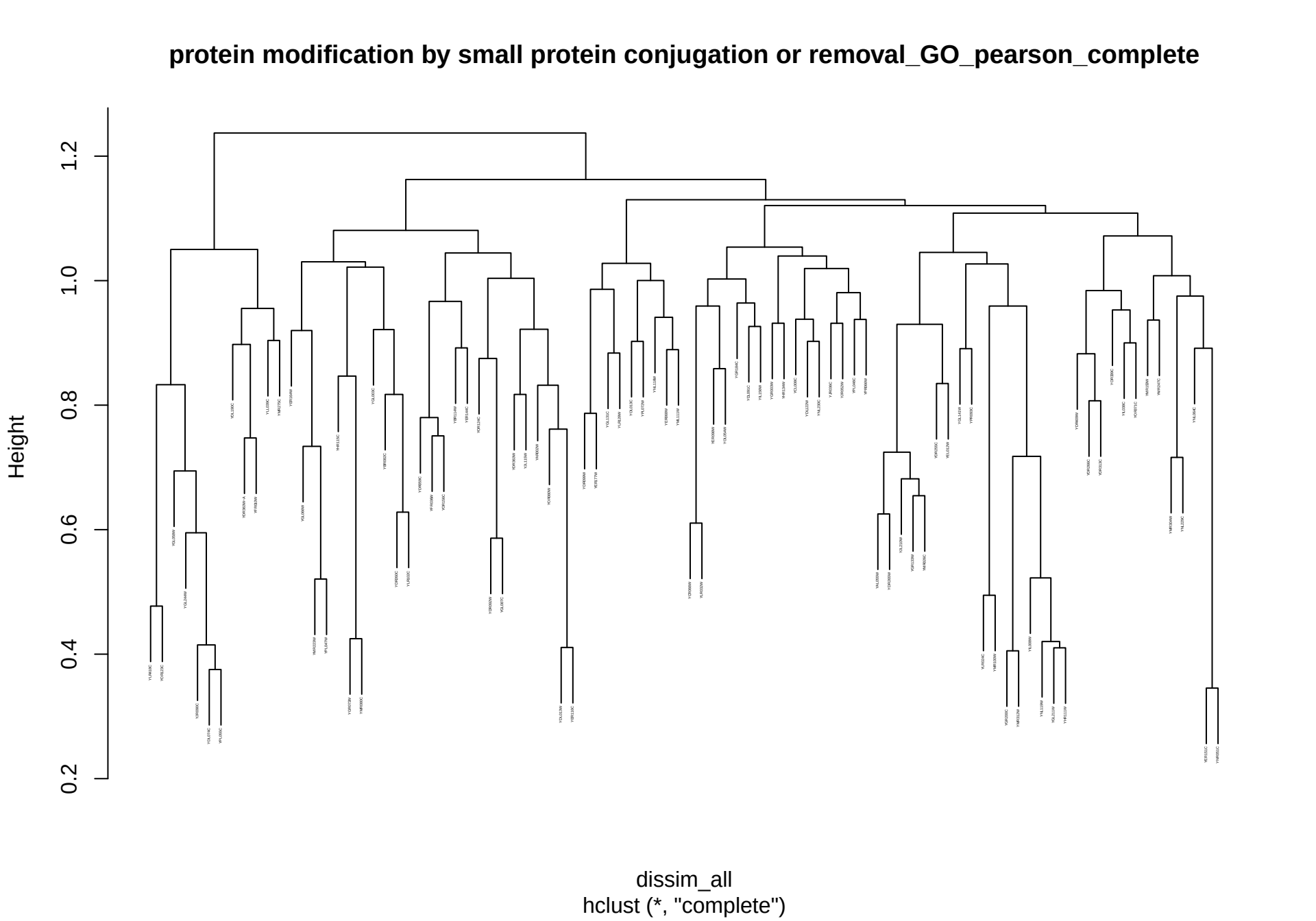

regulation of organelle organization_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

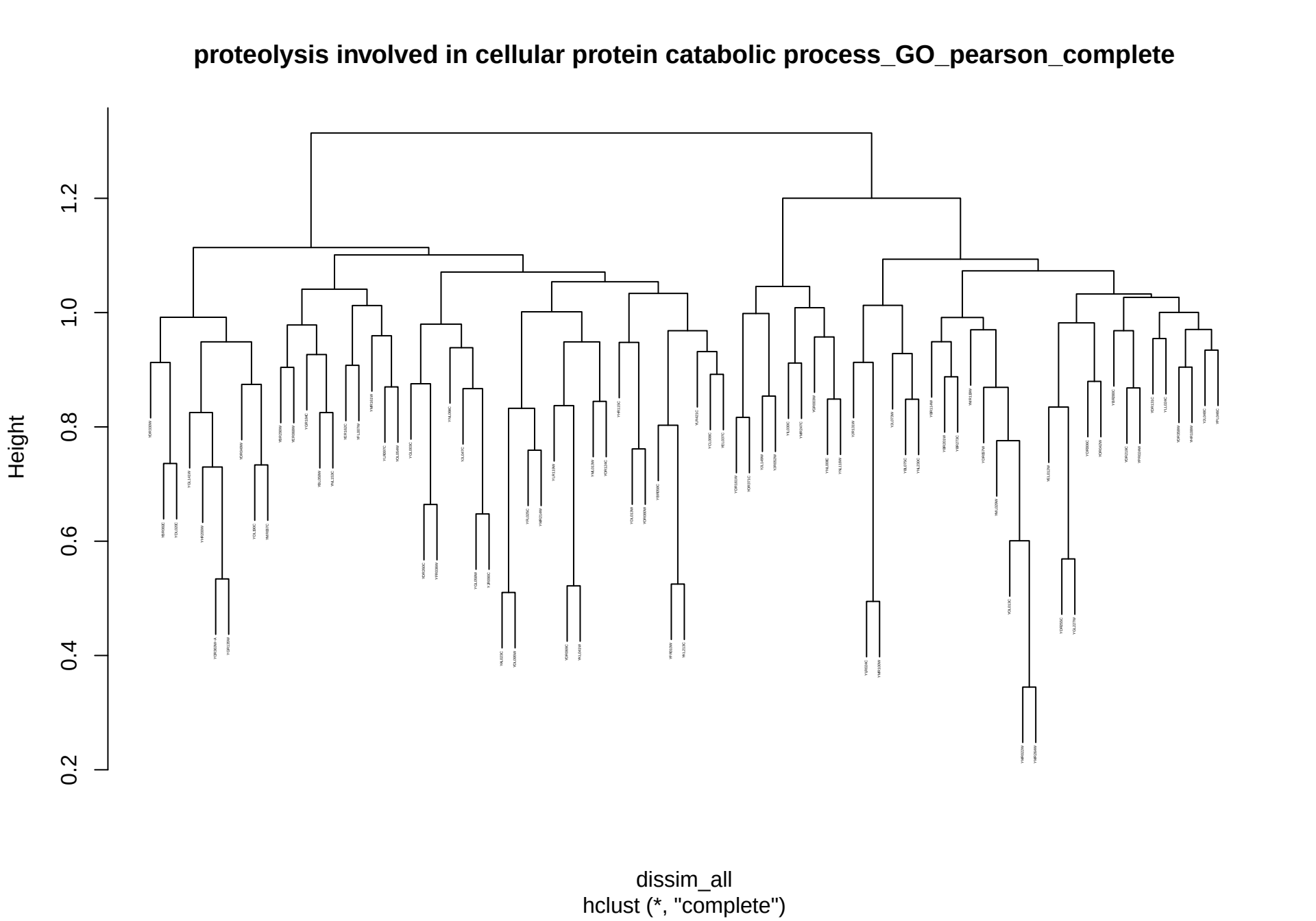

plasma membrane_GO_pearson_complete
Height
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

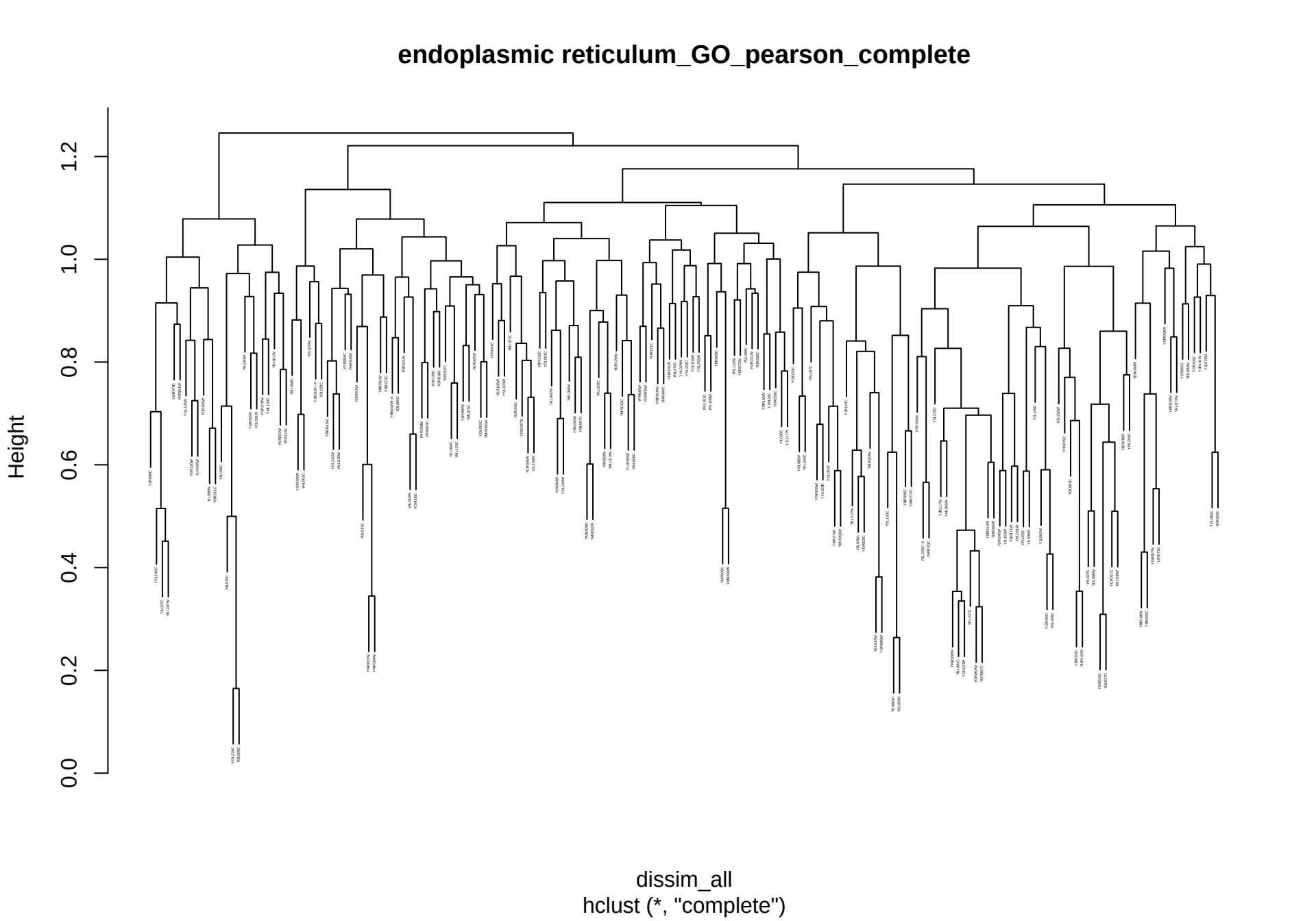

vacuole_GO_pearson_complete
Height
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

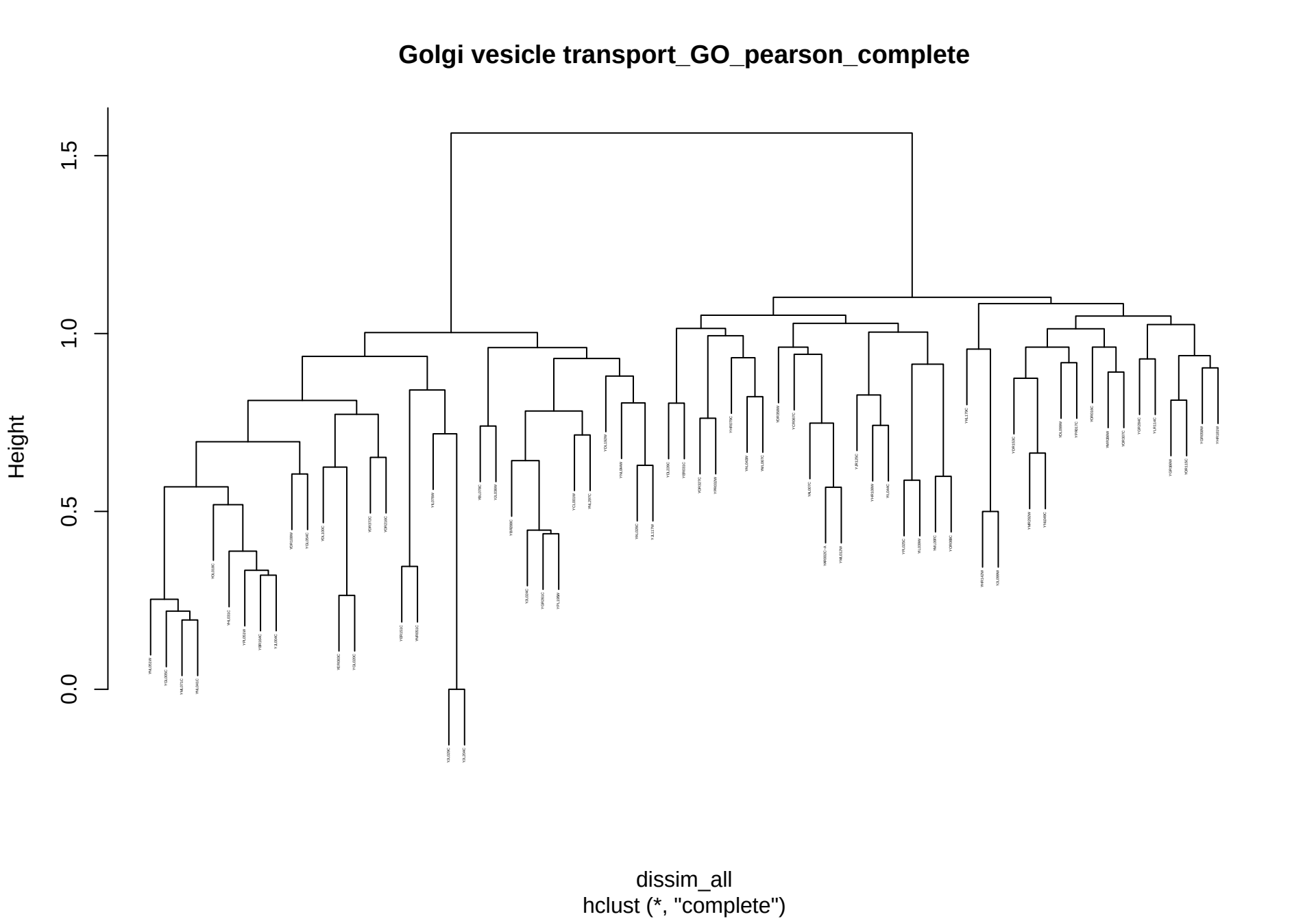

unfolded protein binding_GO_pearson_complete
Height
0.75
0.80
0.85
0.90
0.95
1.00
1.05
dissim_all
hclust (*, "complete")

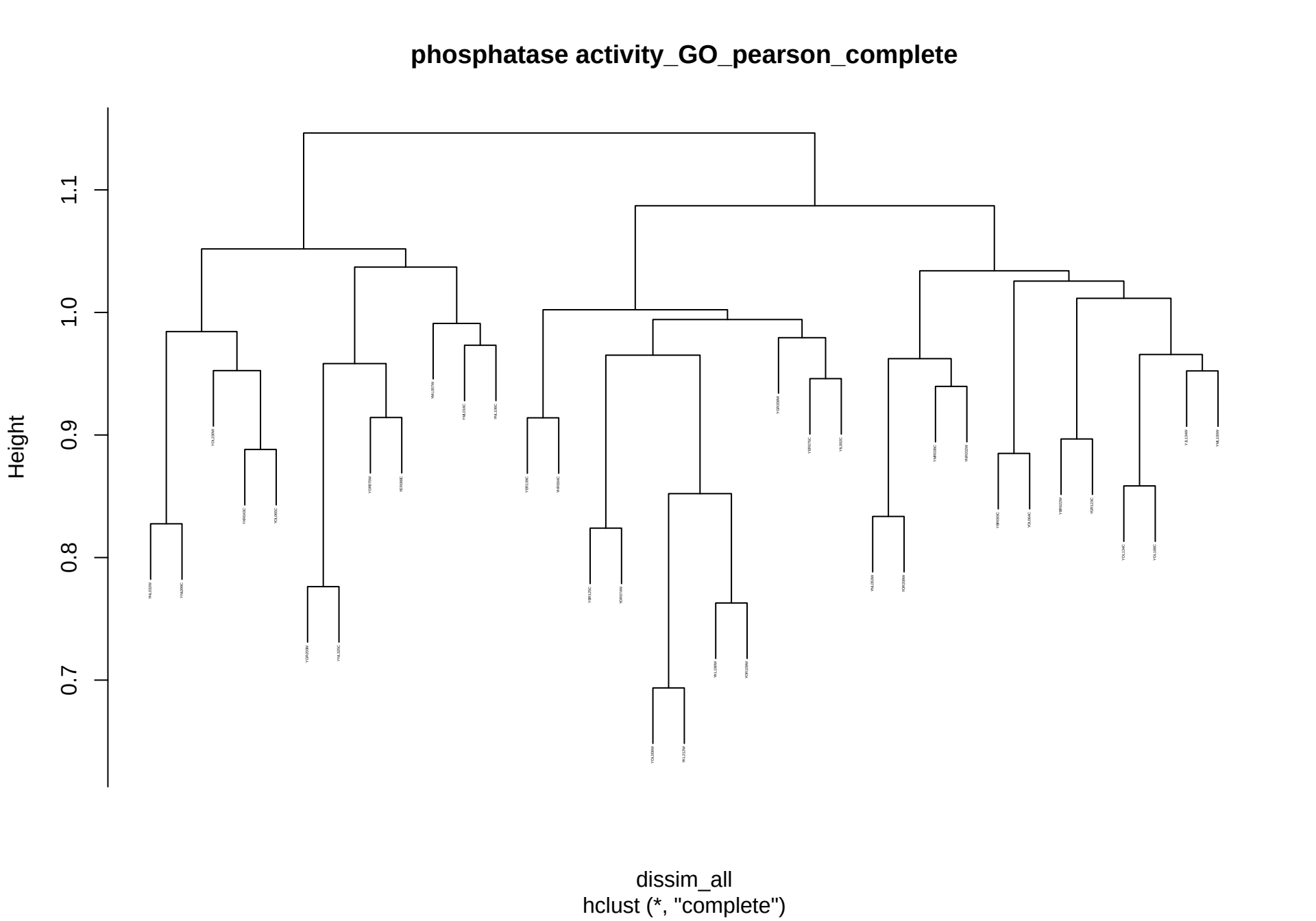

nuclear transport_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

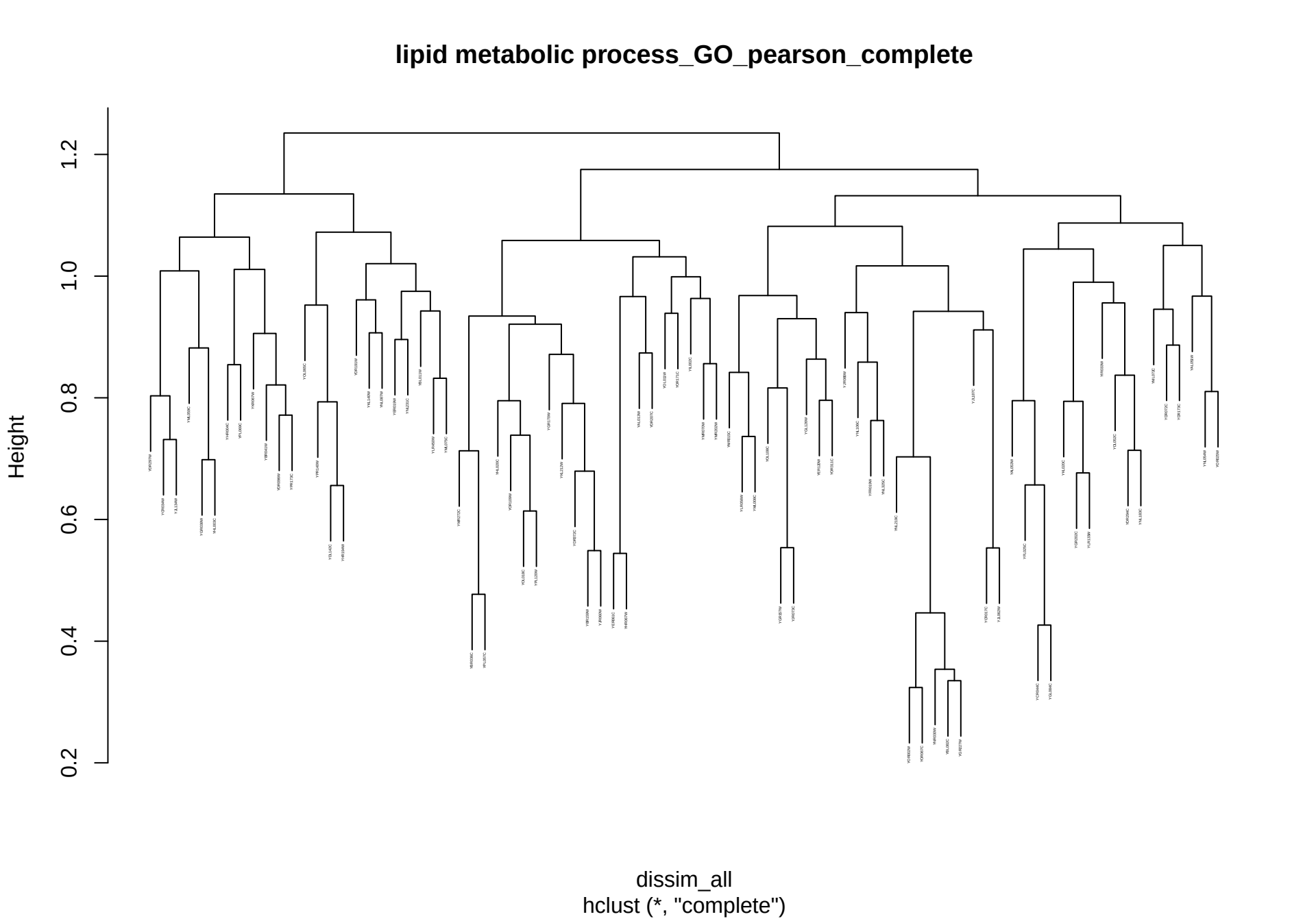

protein modification by small protein conjugation or removal_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

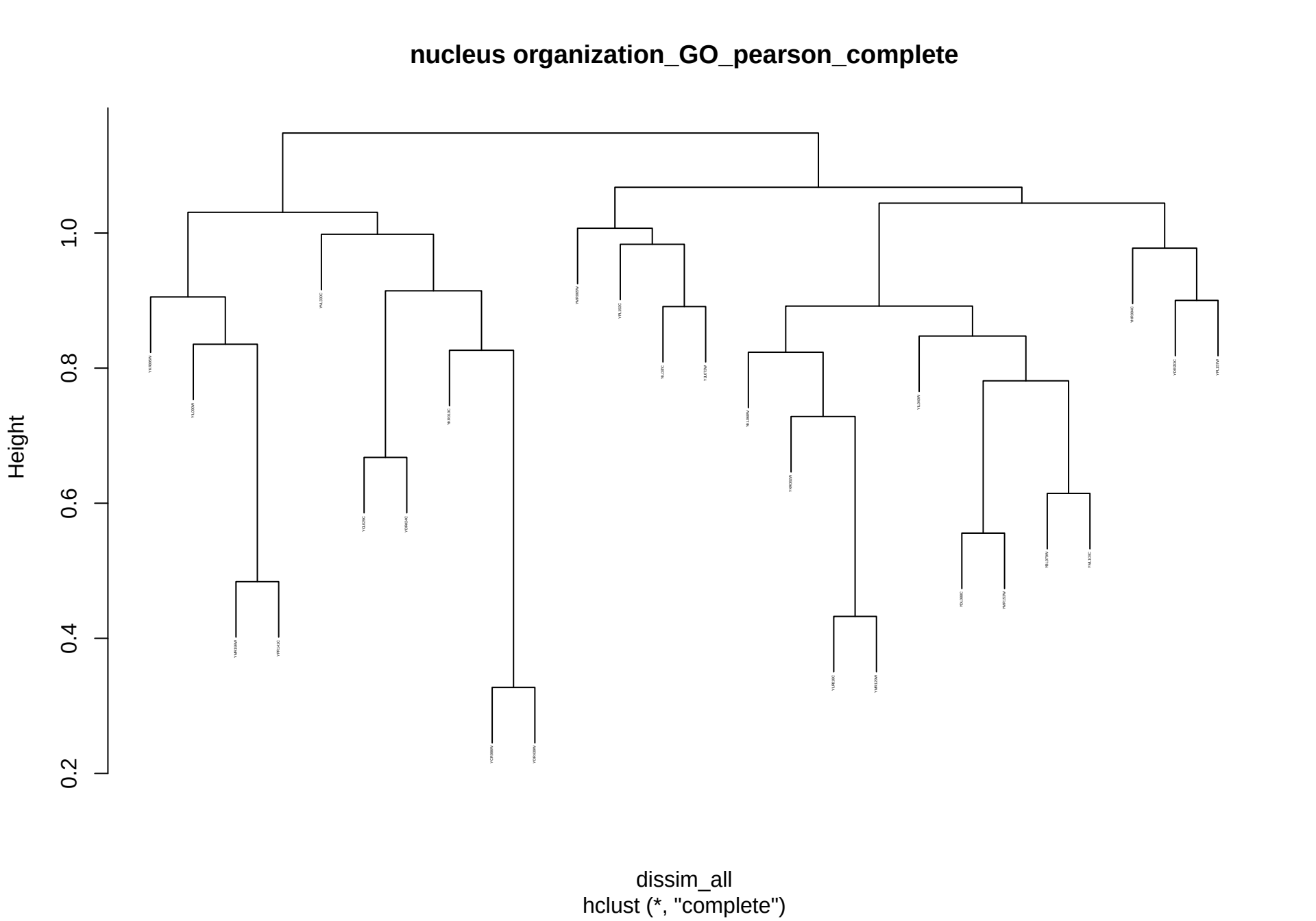

proteolysis involved in cellular protein catabolic process_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

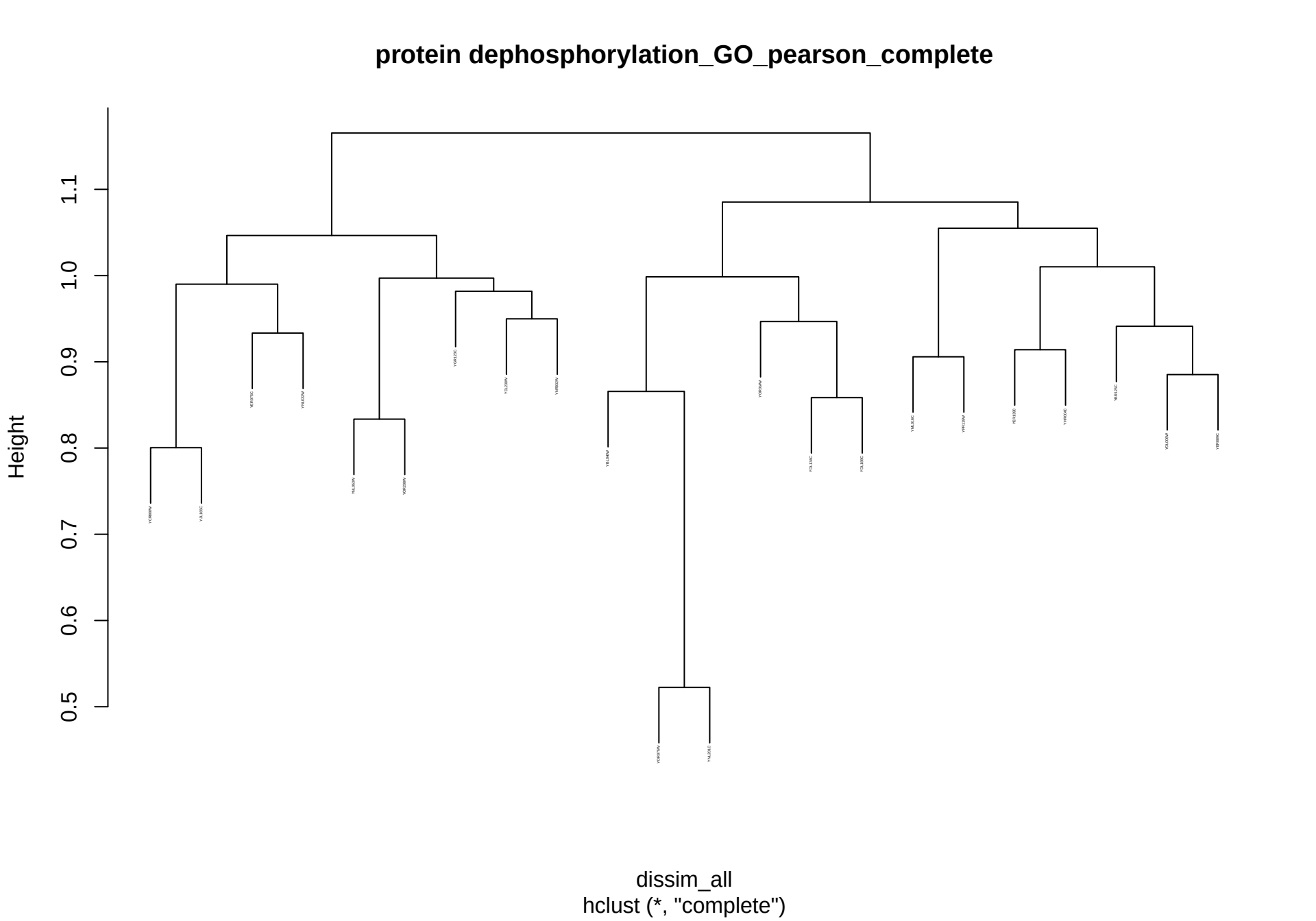

endoplasmic reticulum_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

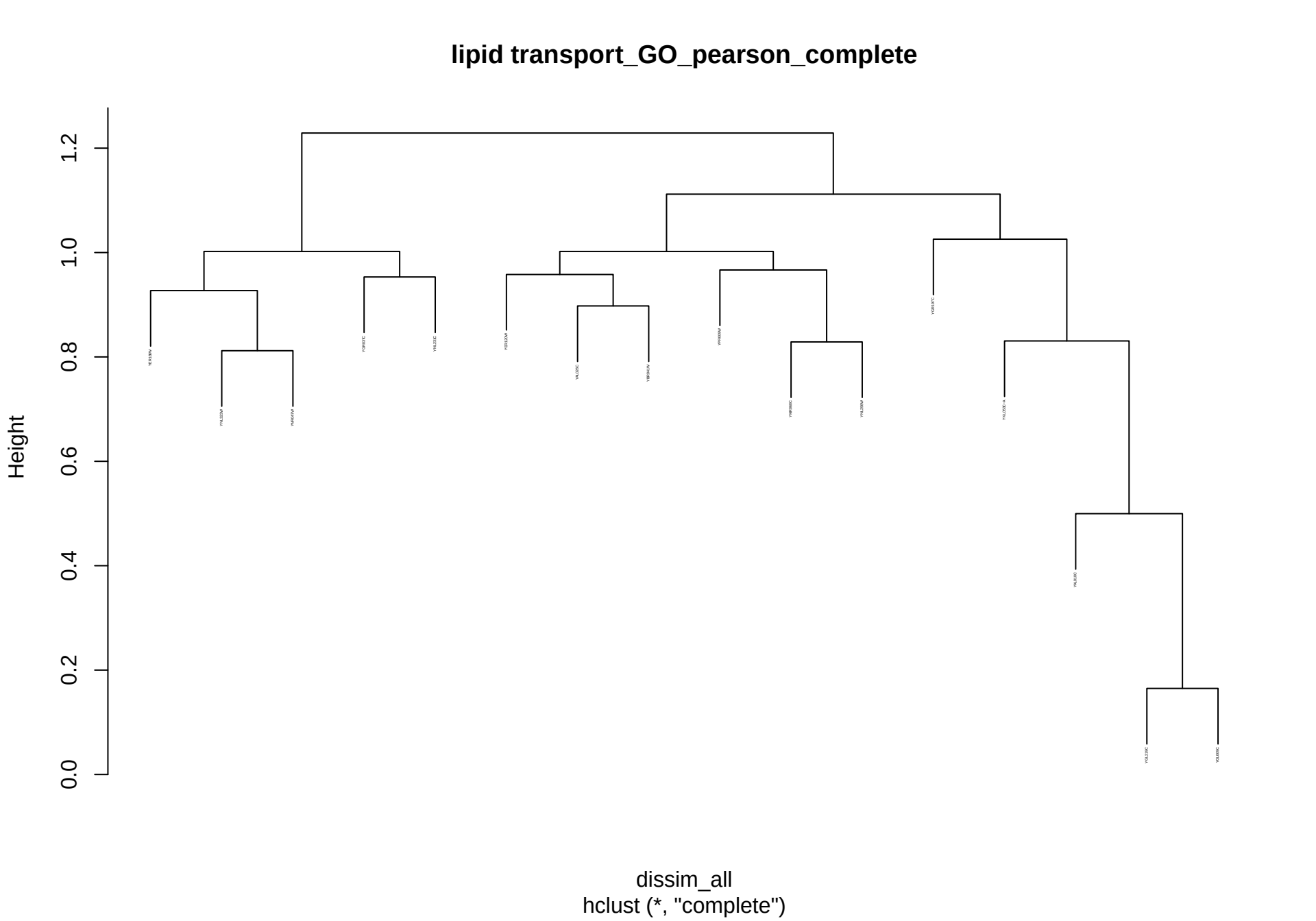

Golgi vesicle transport_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")

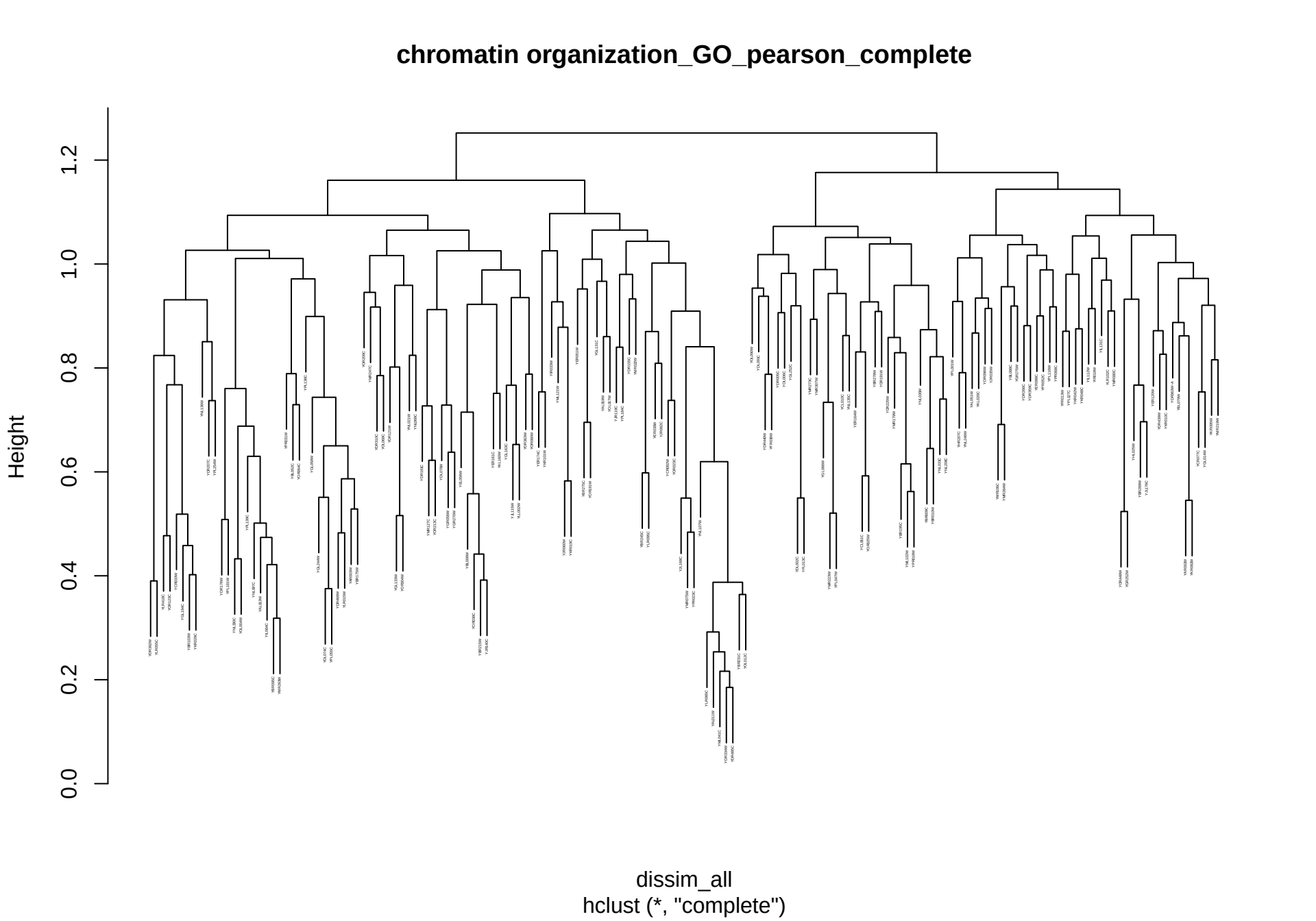

phosphatase activity_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
dissim_all
hclust (*, "complete")

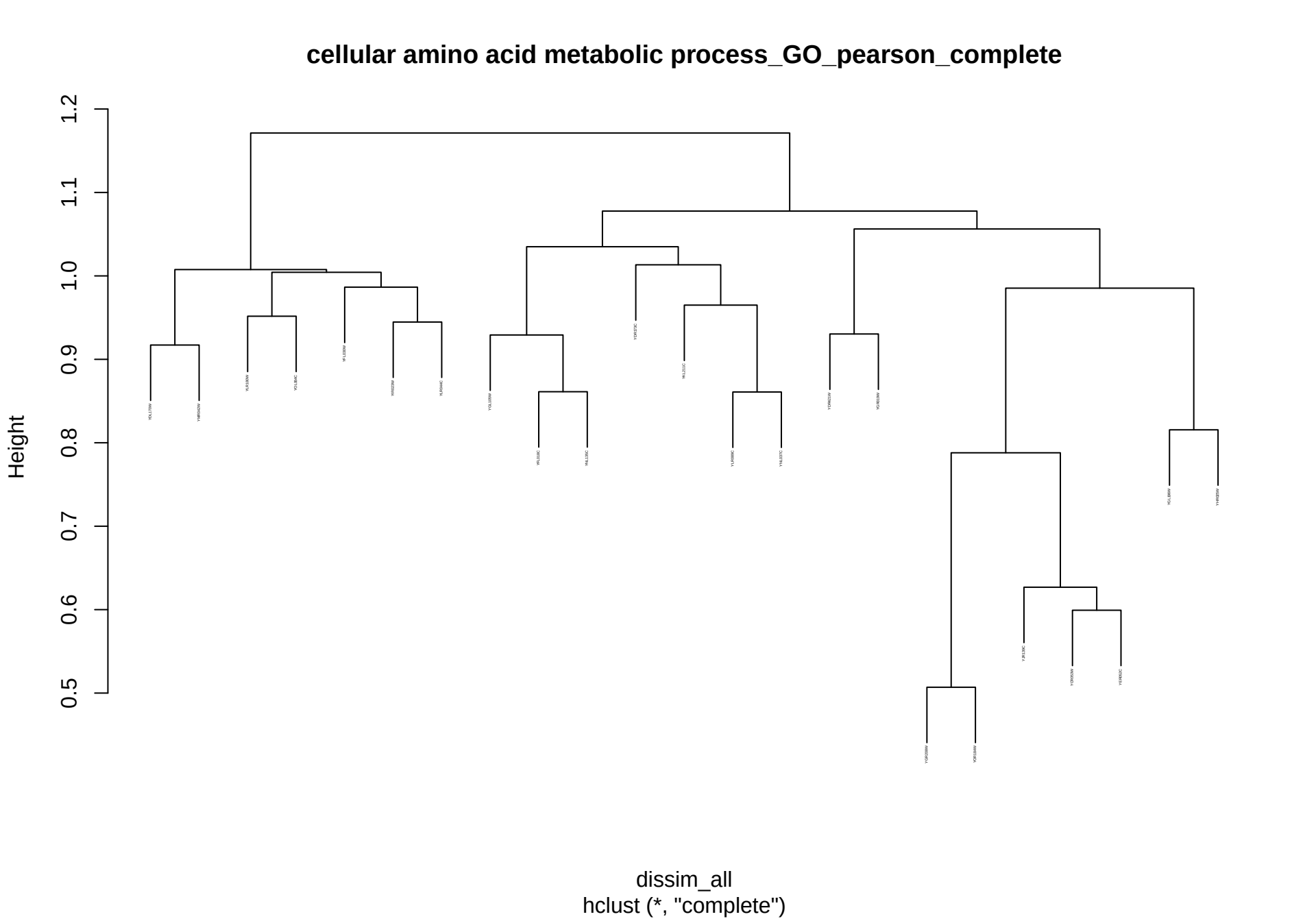

lipid metabolic process_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

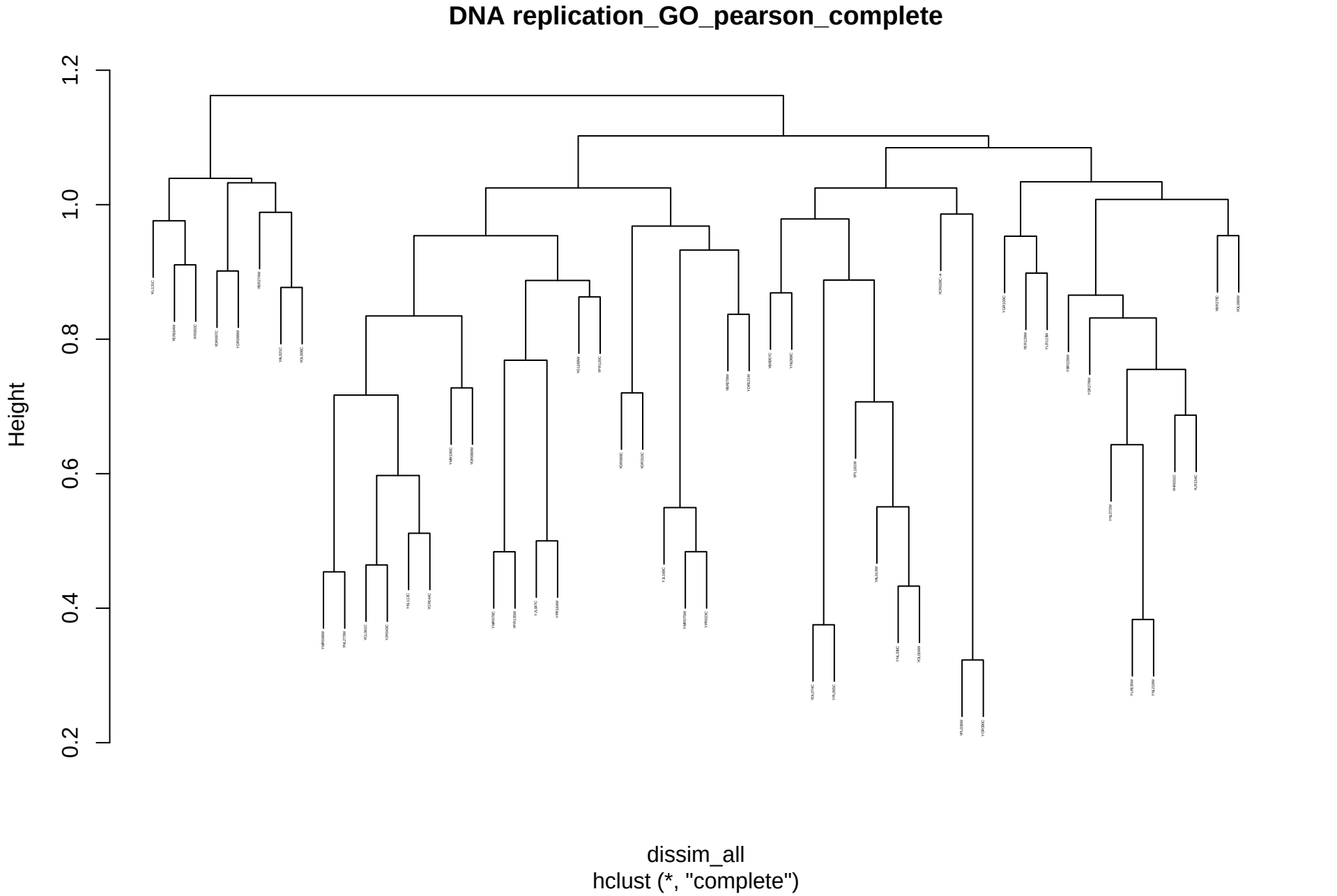

nucleus organization_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")

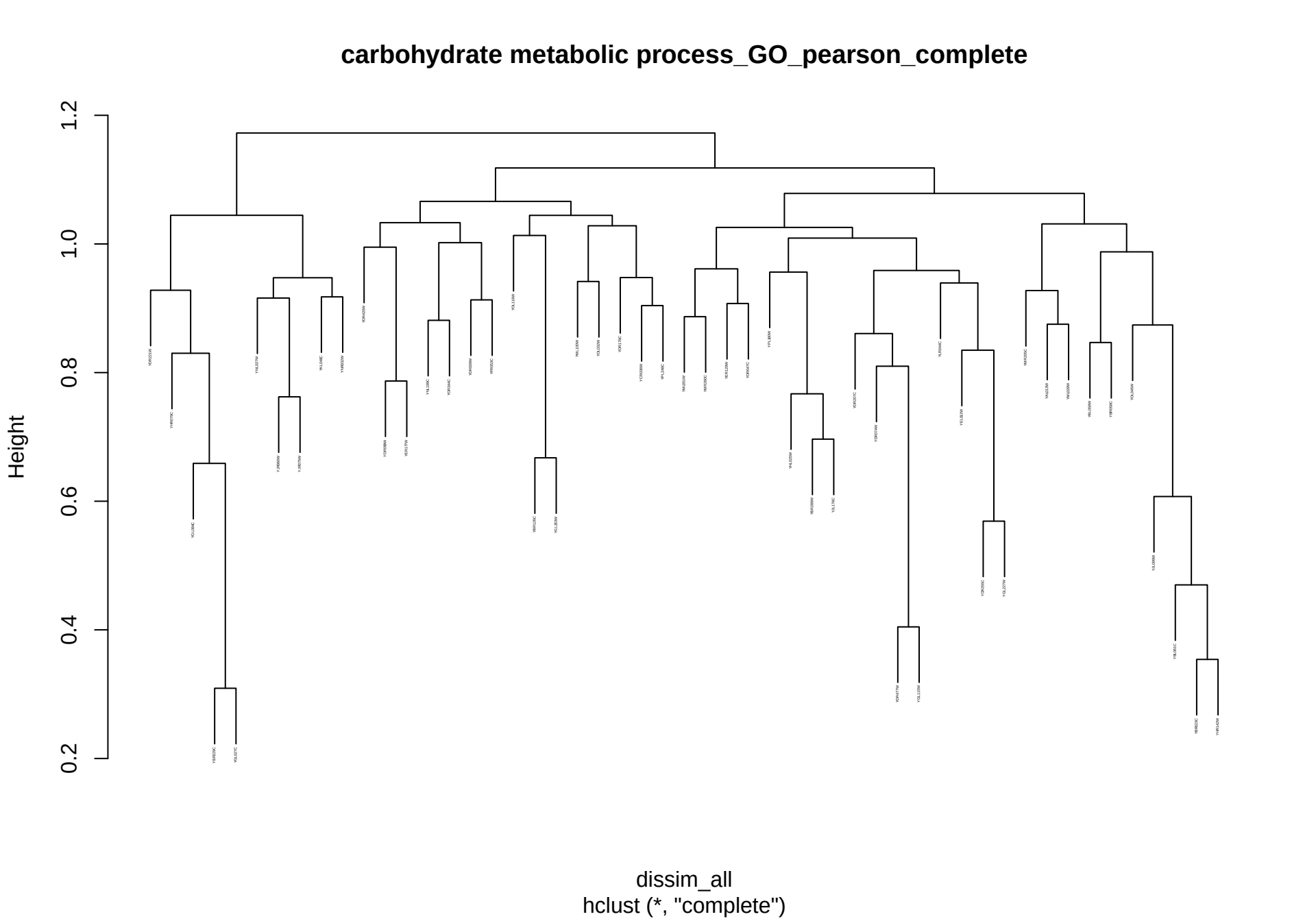

protein dephosphorylation_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
0.5
dissim_all
hclust (*, "complete")

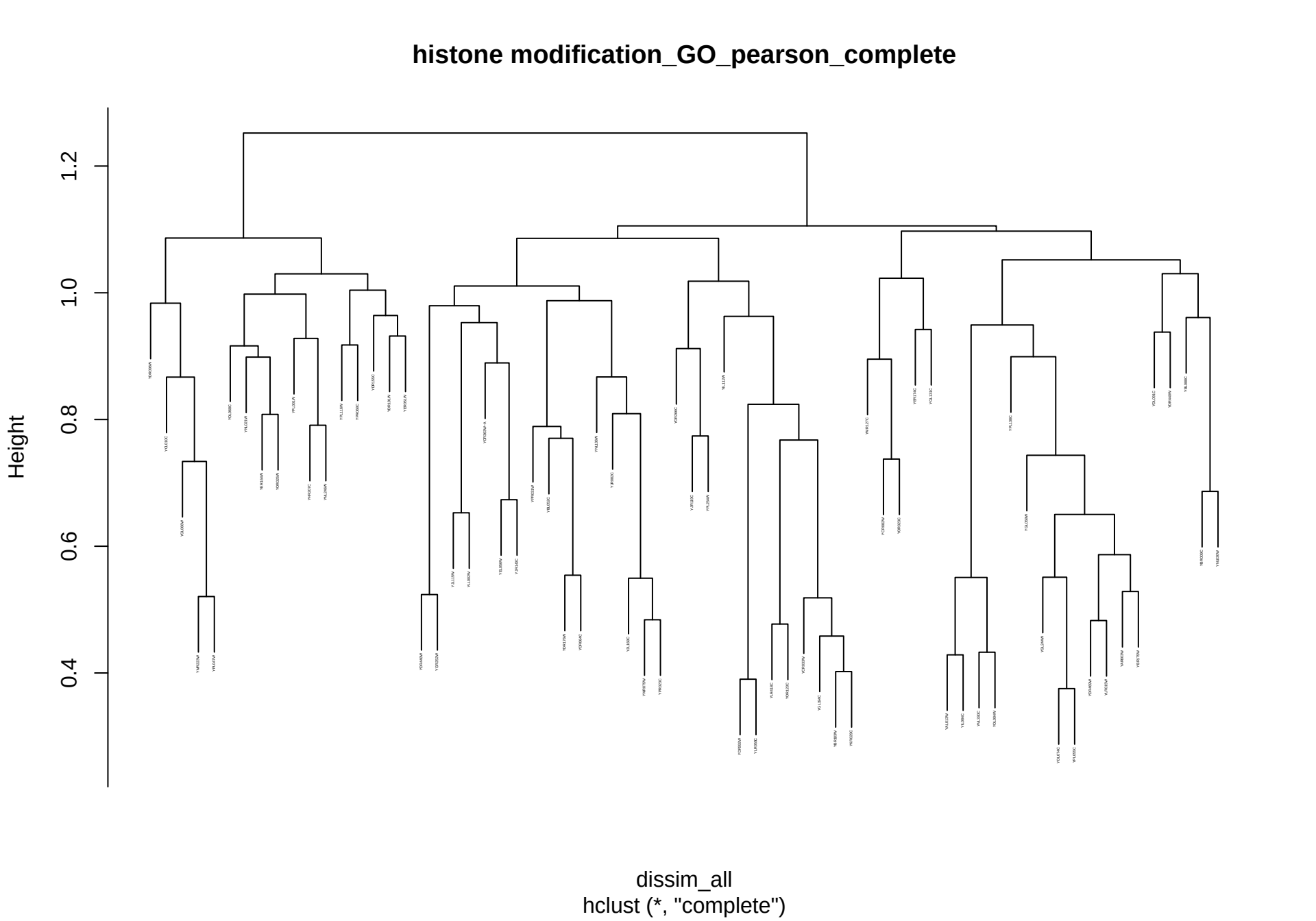

lipid transport_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

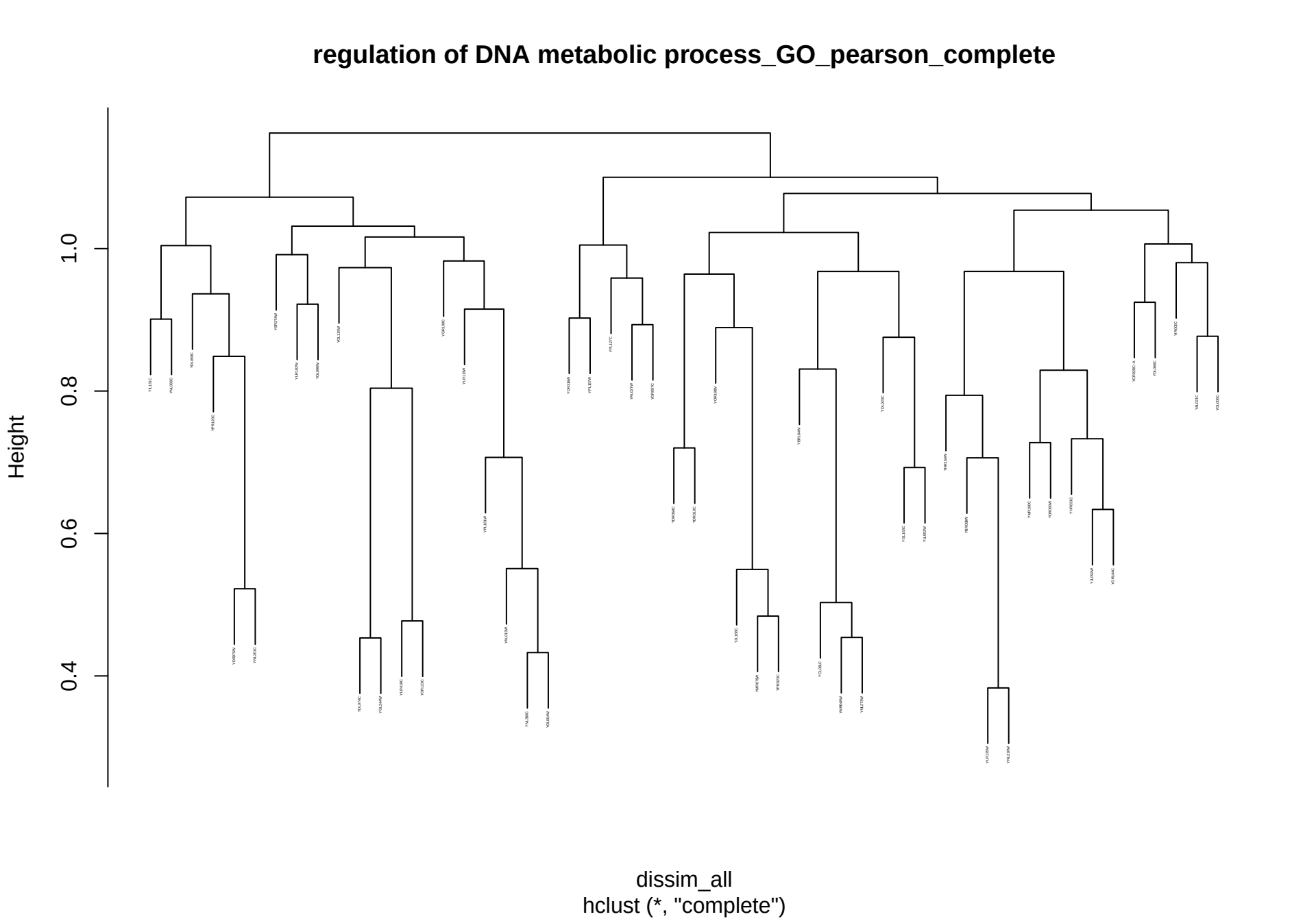

chromatin organization_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

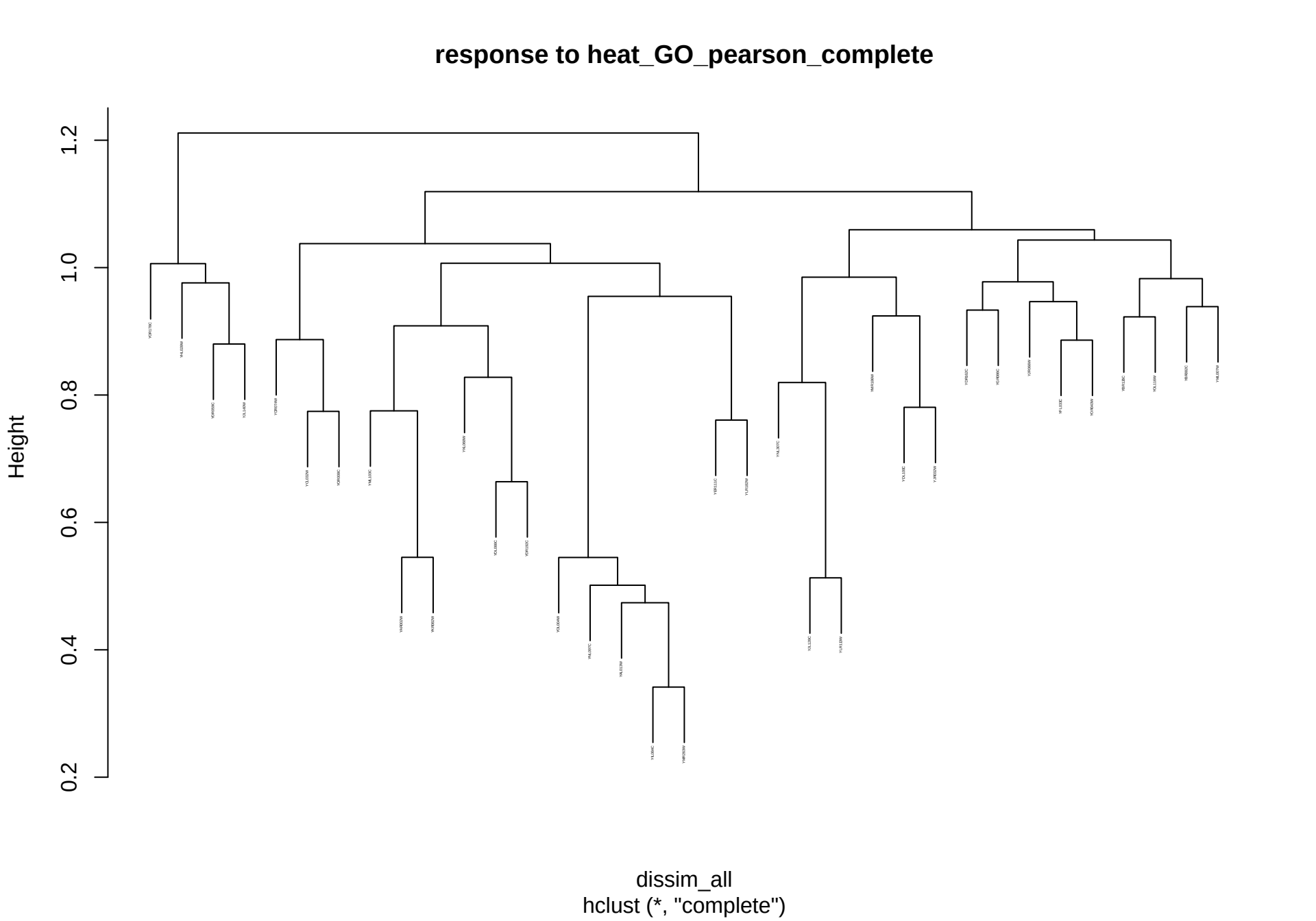

cellular amino acid metabolic process_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
dissim_all
hclust (*, "complete")

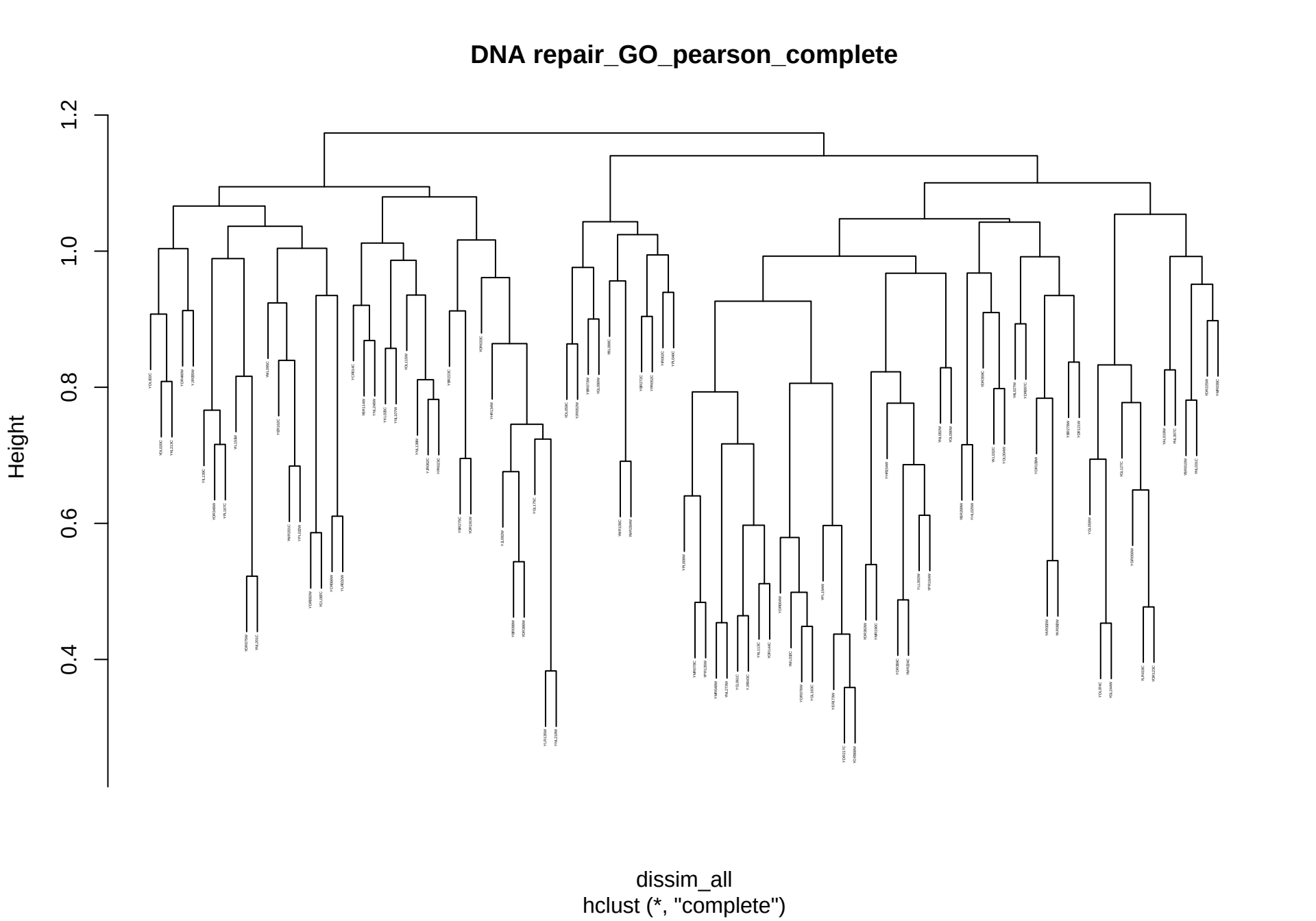

DNA replication_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

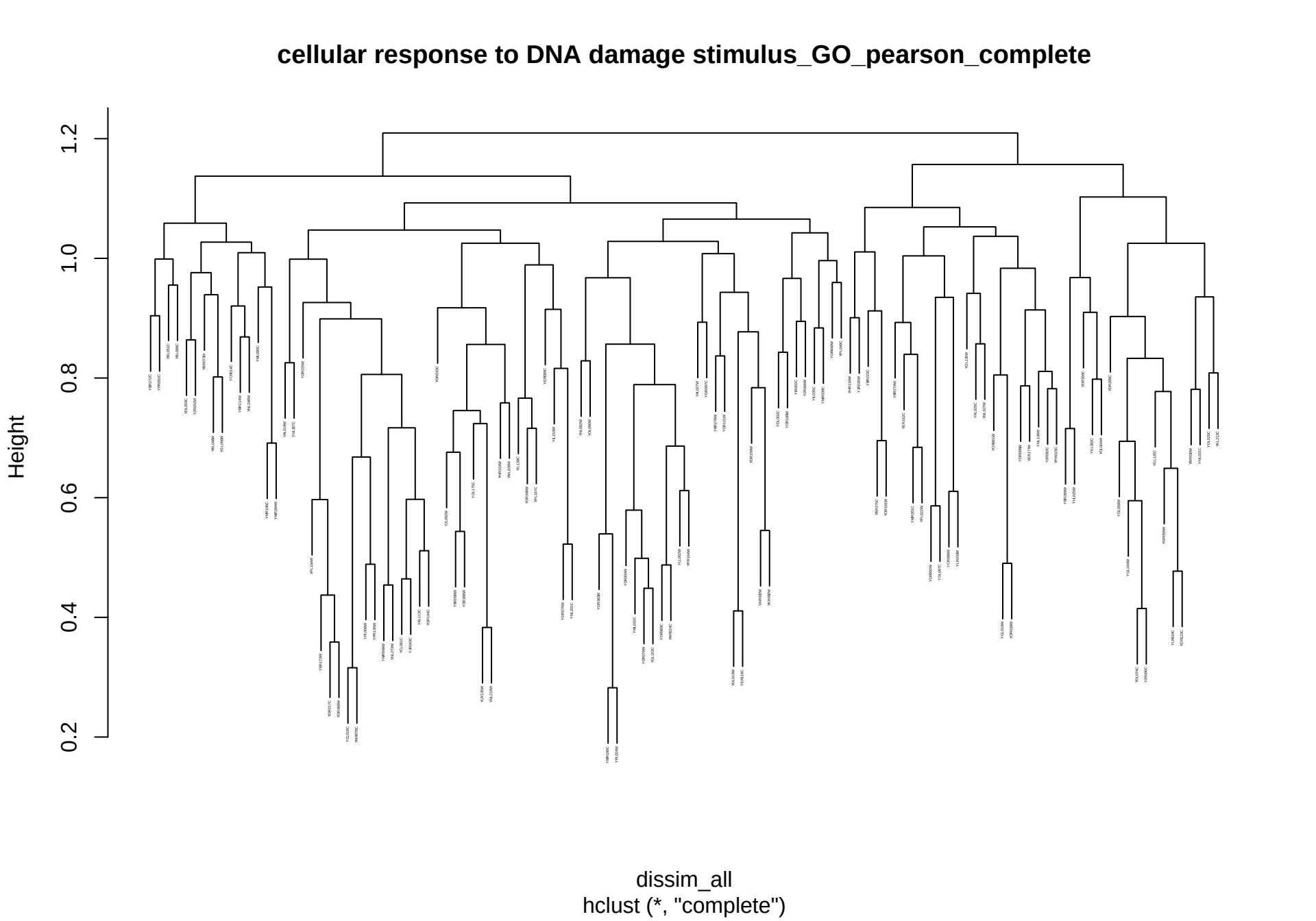

carbohydrate metabolic process_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

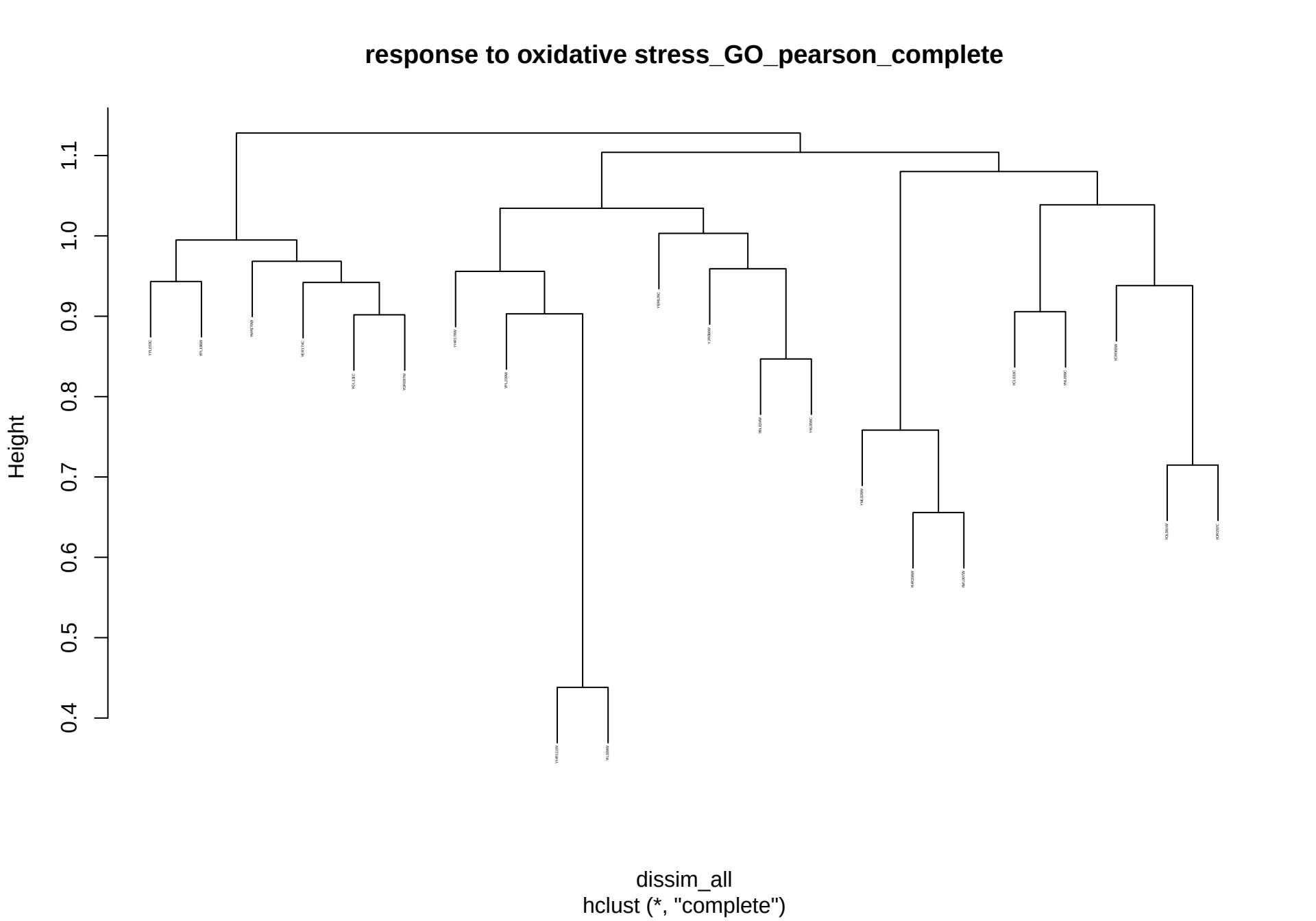

histone modification_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

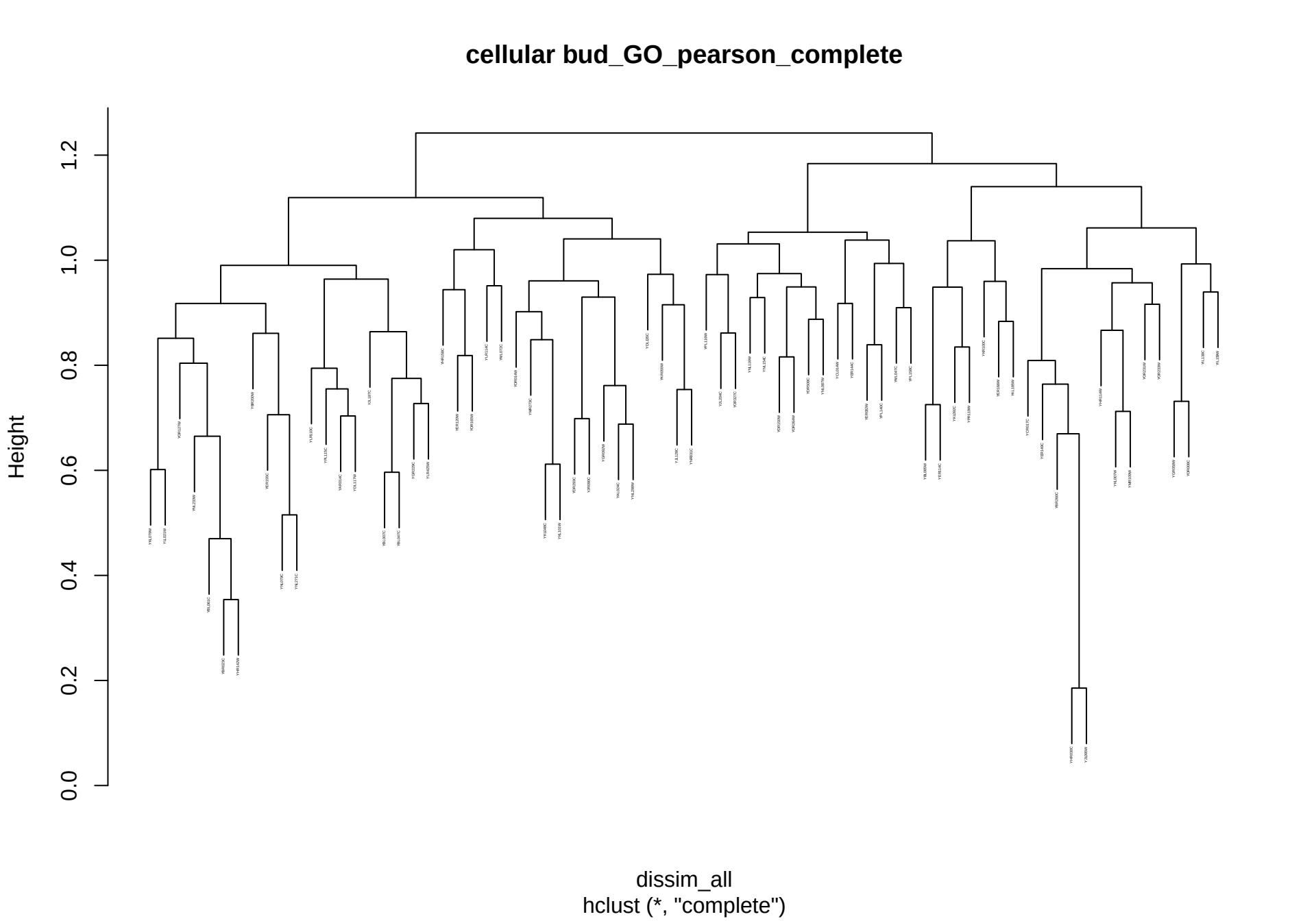

regulation of DNA metabolic process_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

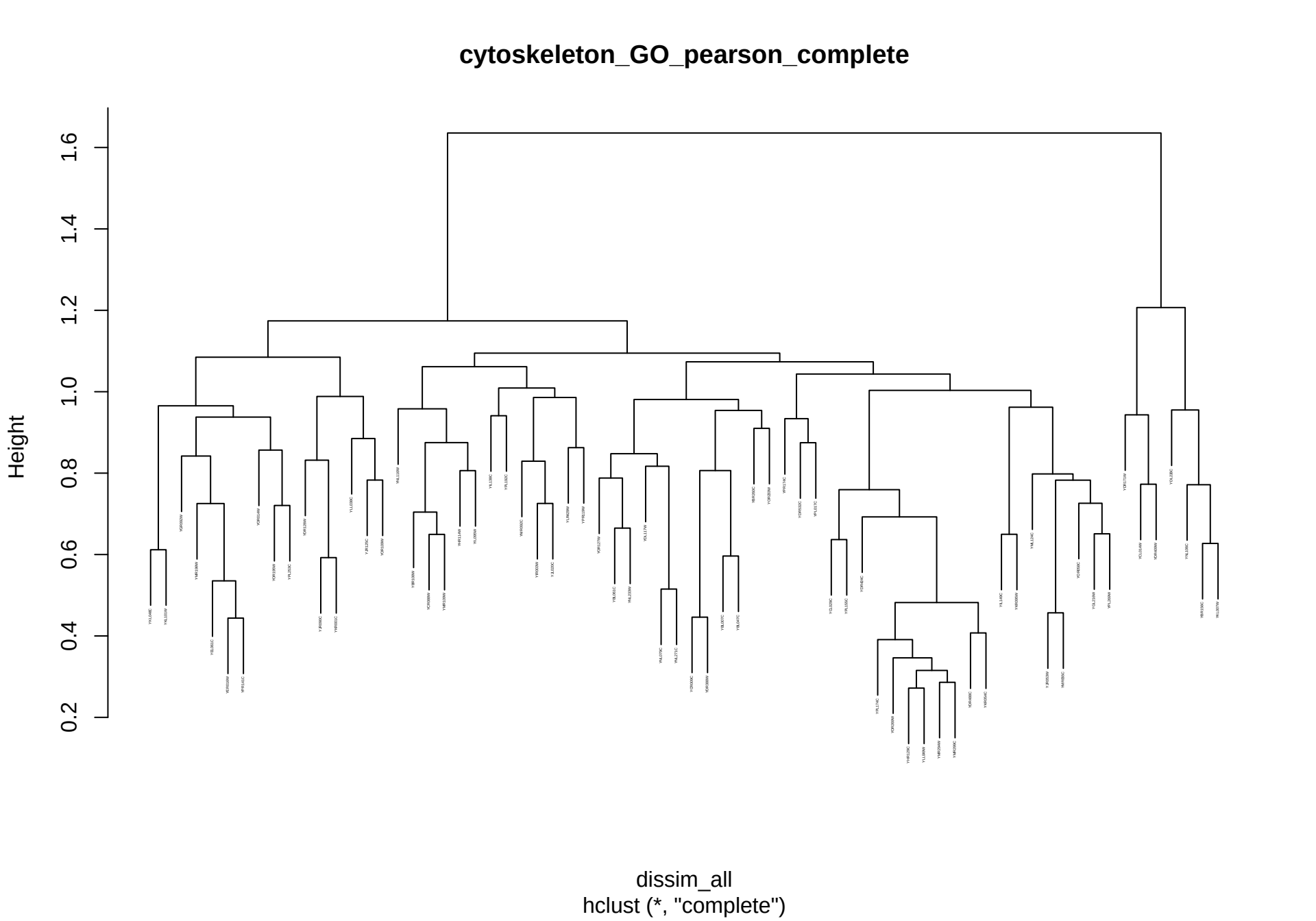

response to heat_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

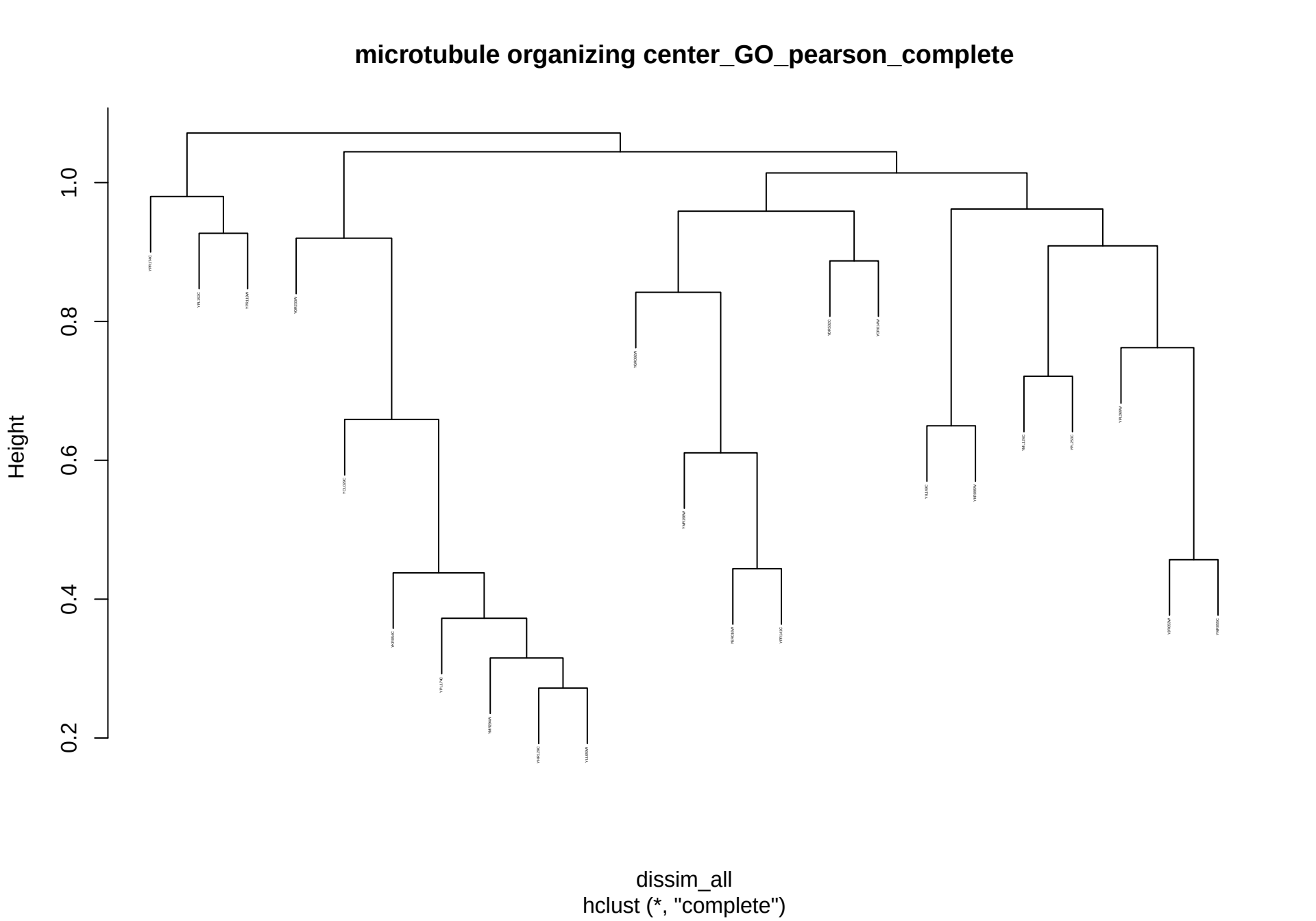

DNA repair_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

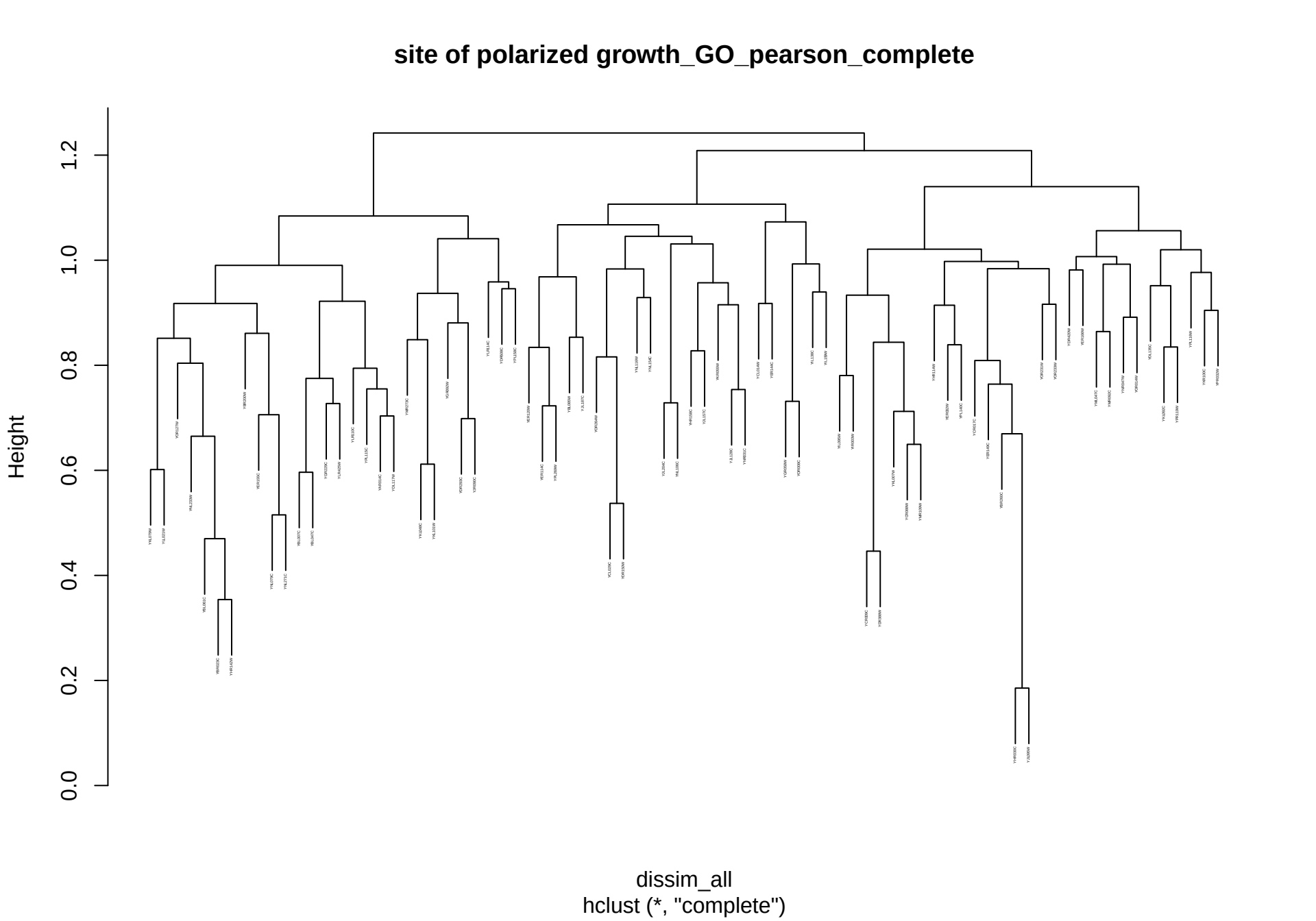

cellular response to DNA damage stimulus_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

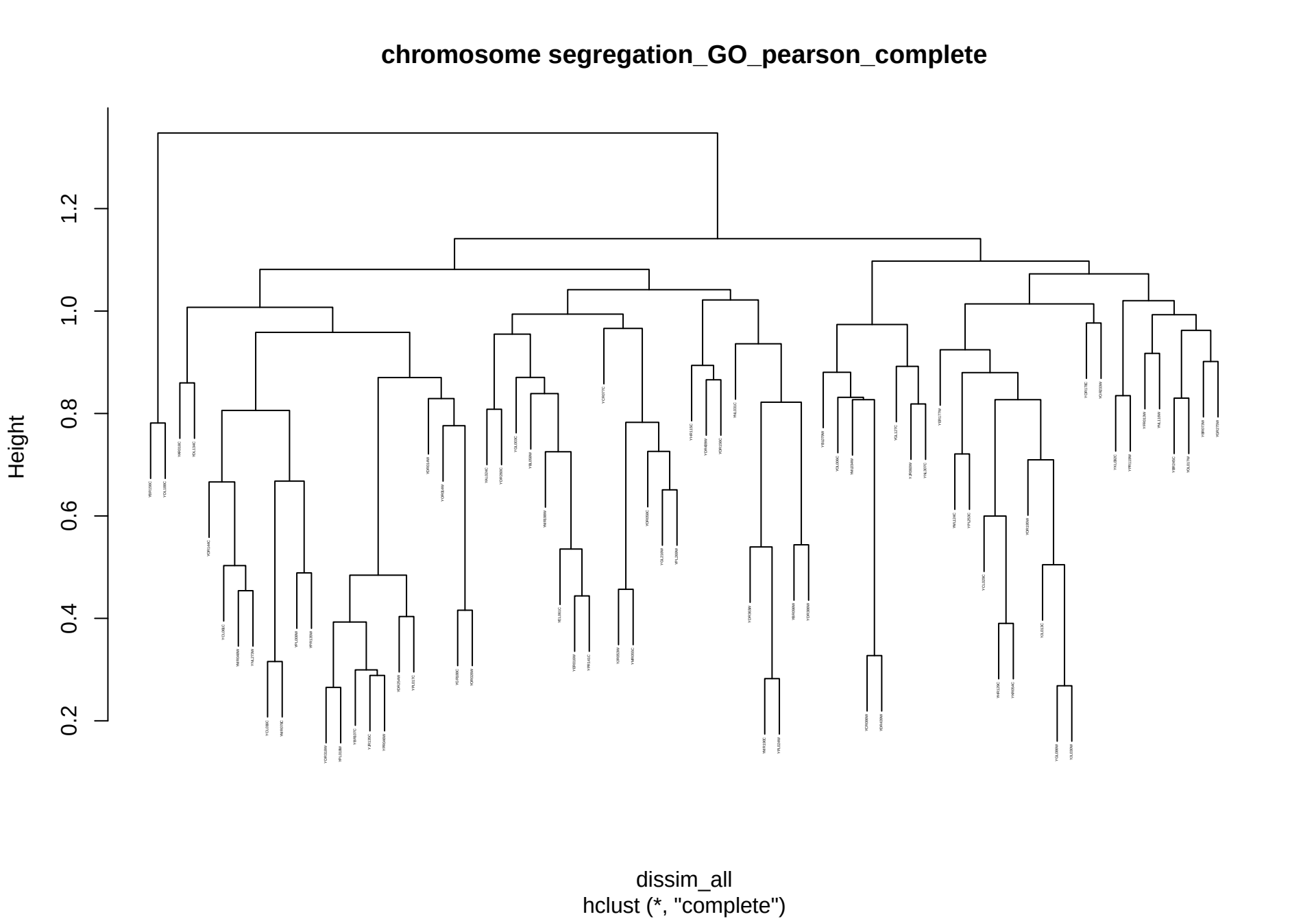

response to oxidative stress_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

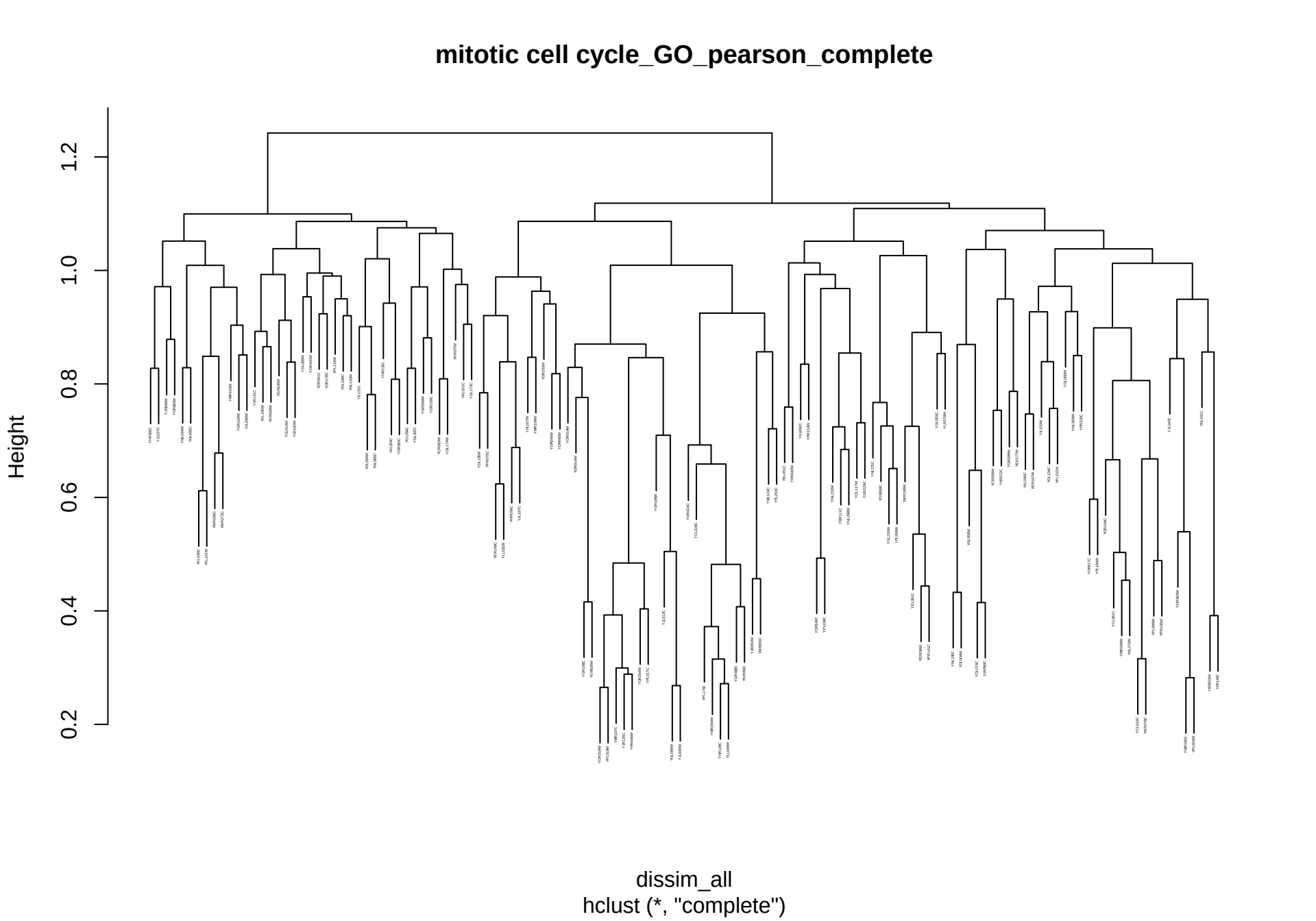

cellular bud_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

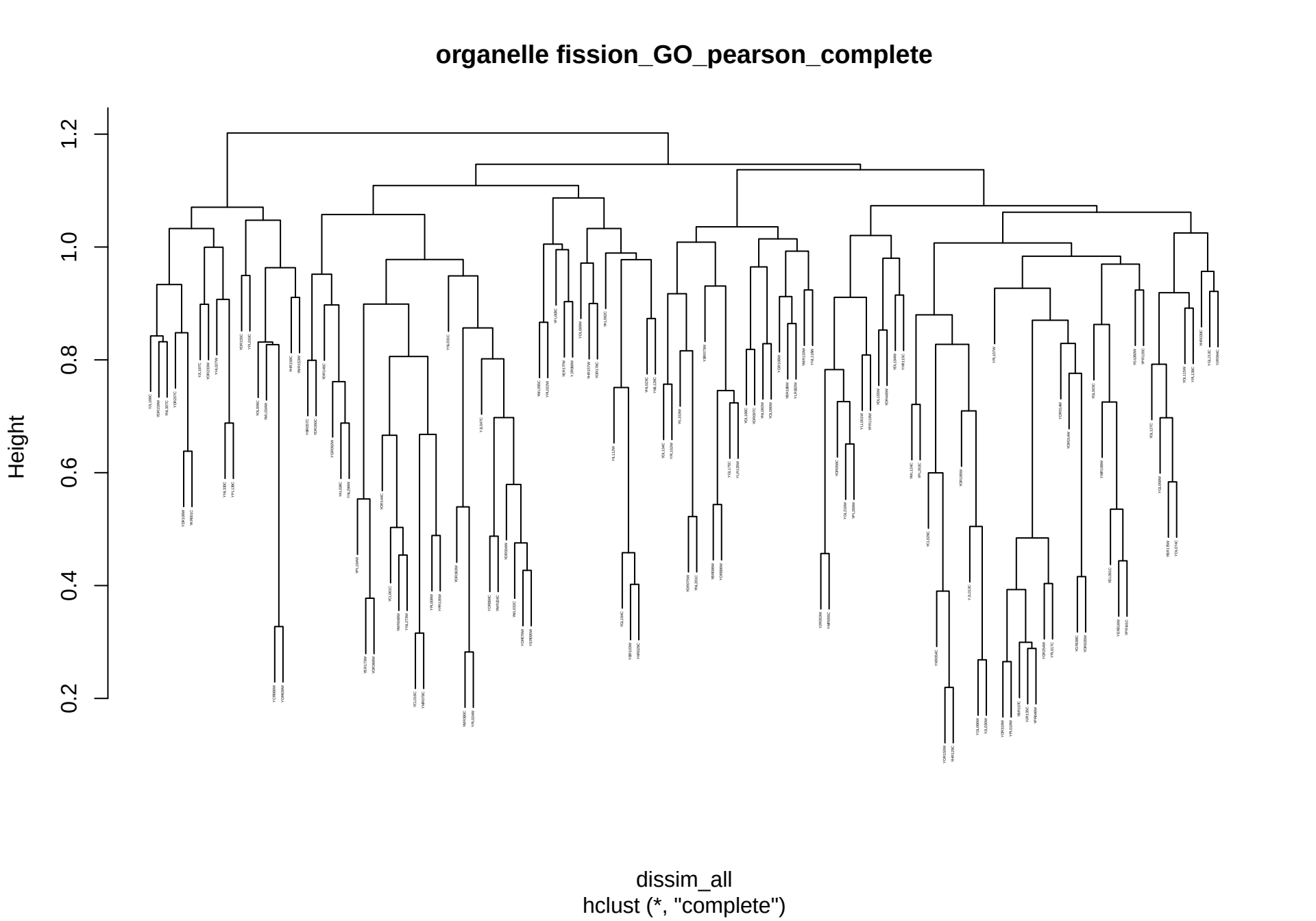

cytoskeleton_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
dissim_all
hclust (*, "complete")

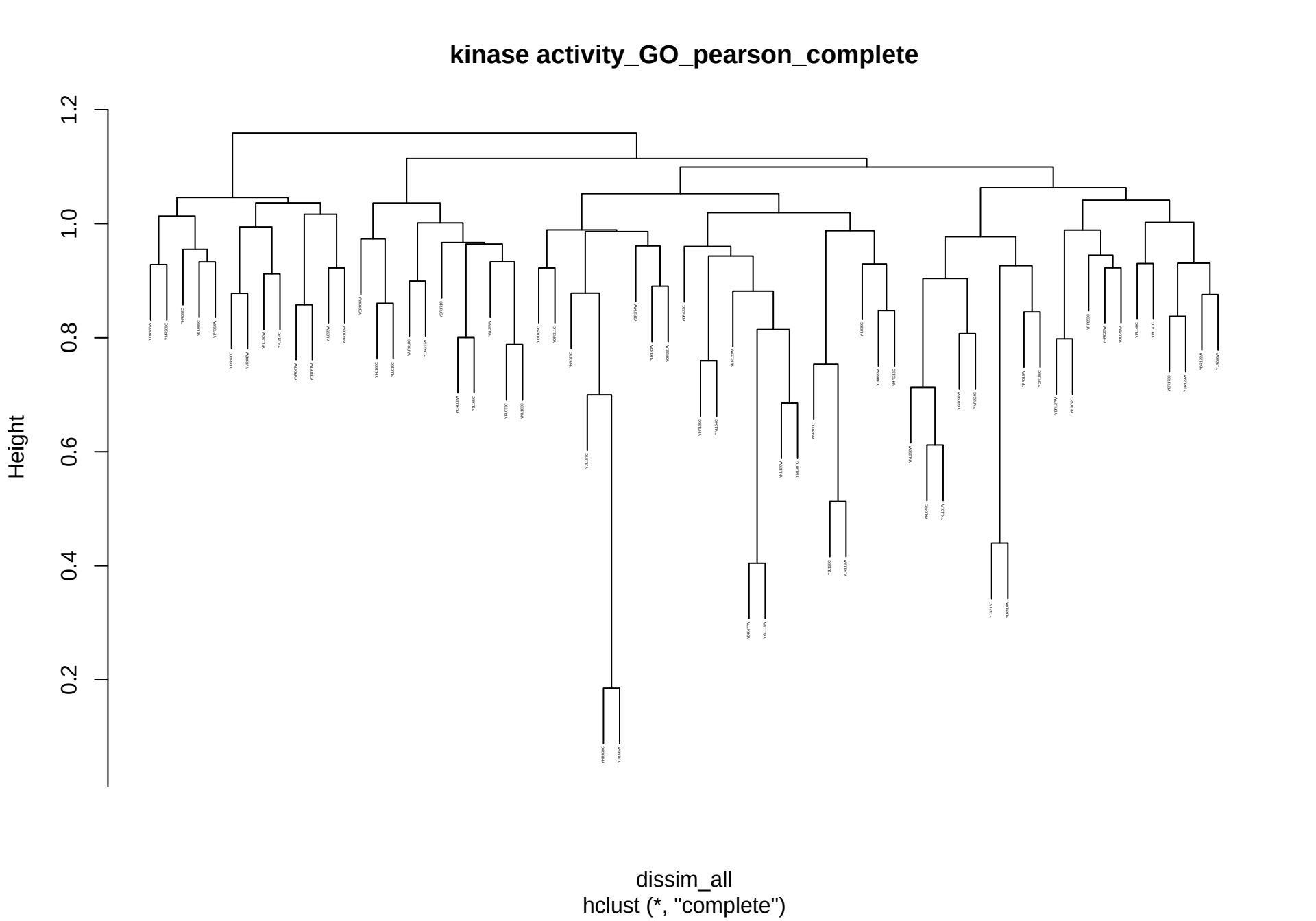

microtubule organizing center_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

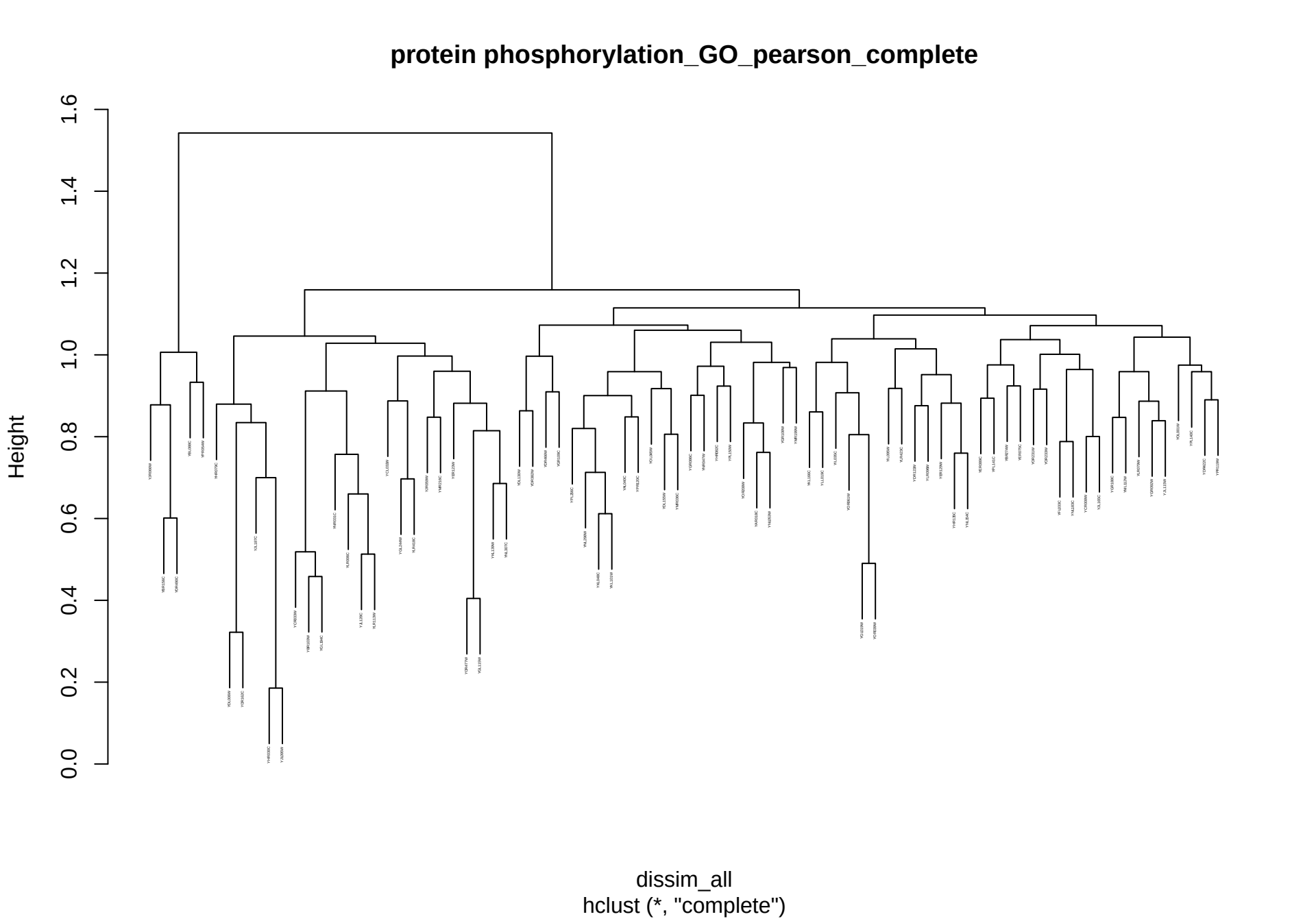

site of polarized growth_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

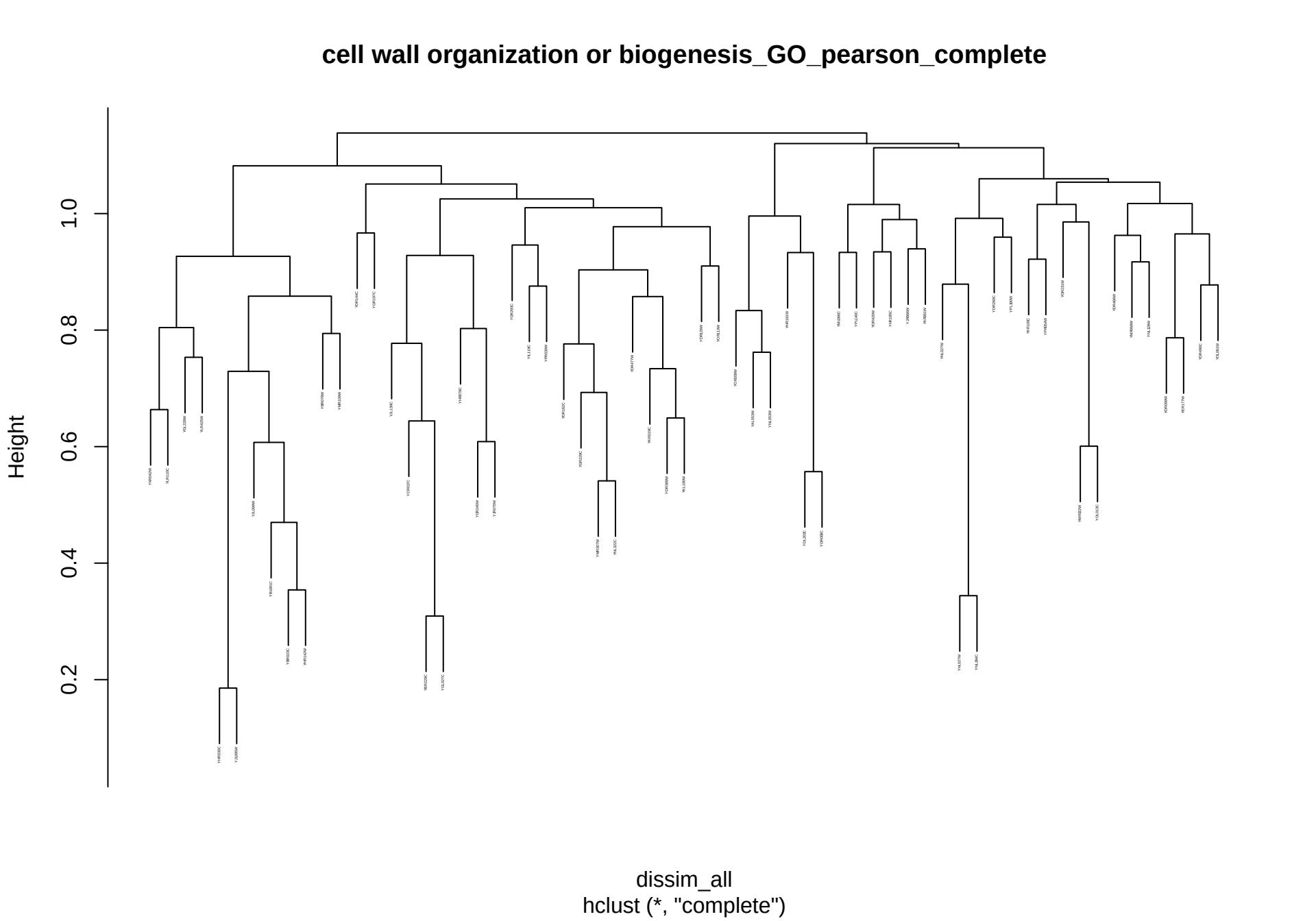

chromosome segregation_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

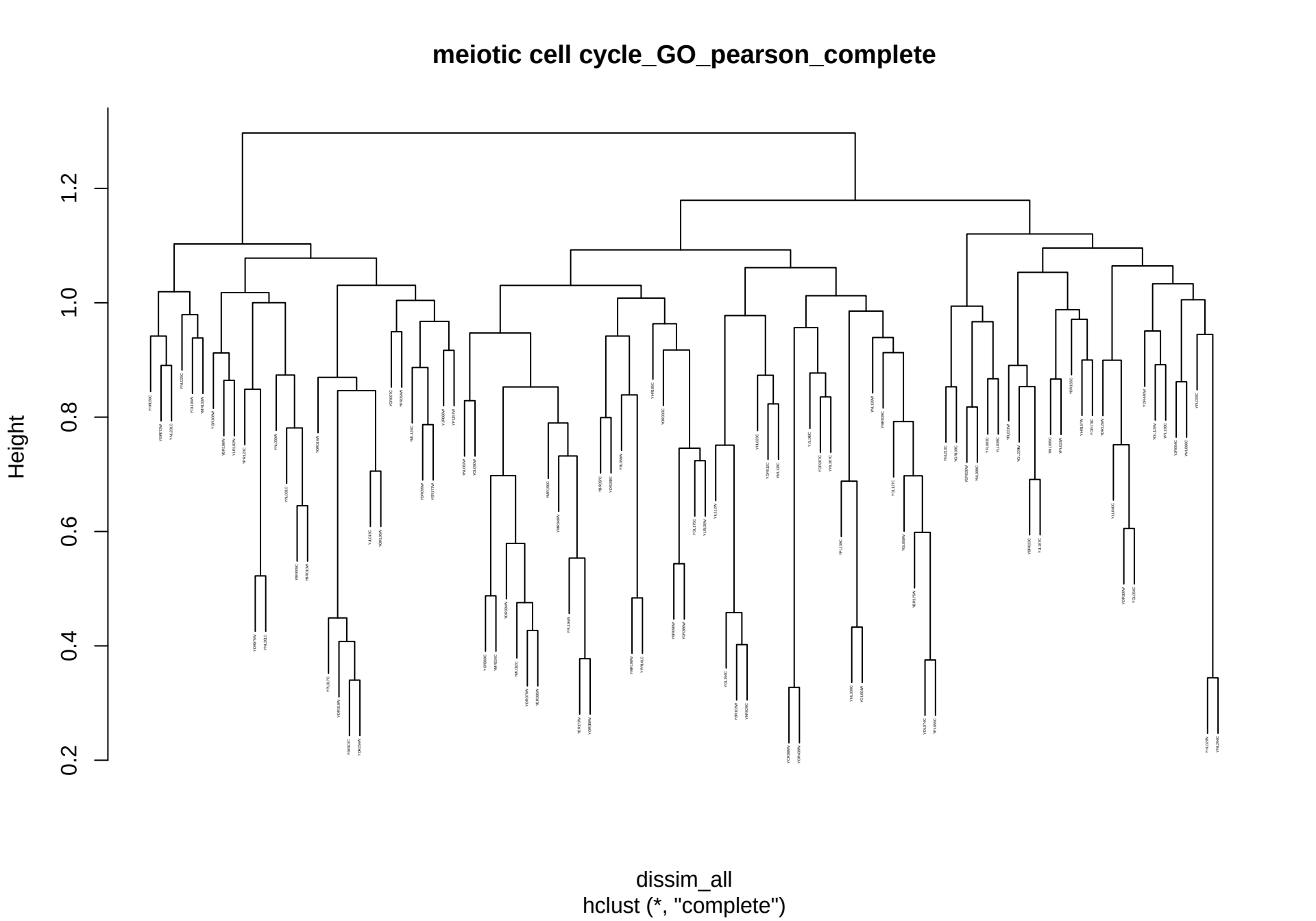

mitotic cell cycle_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

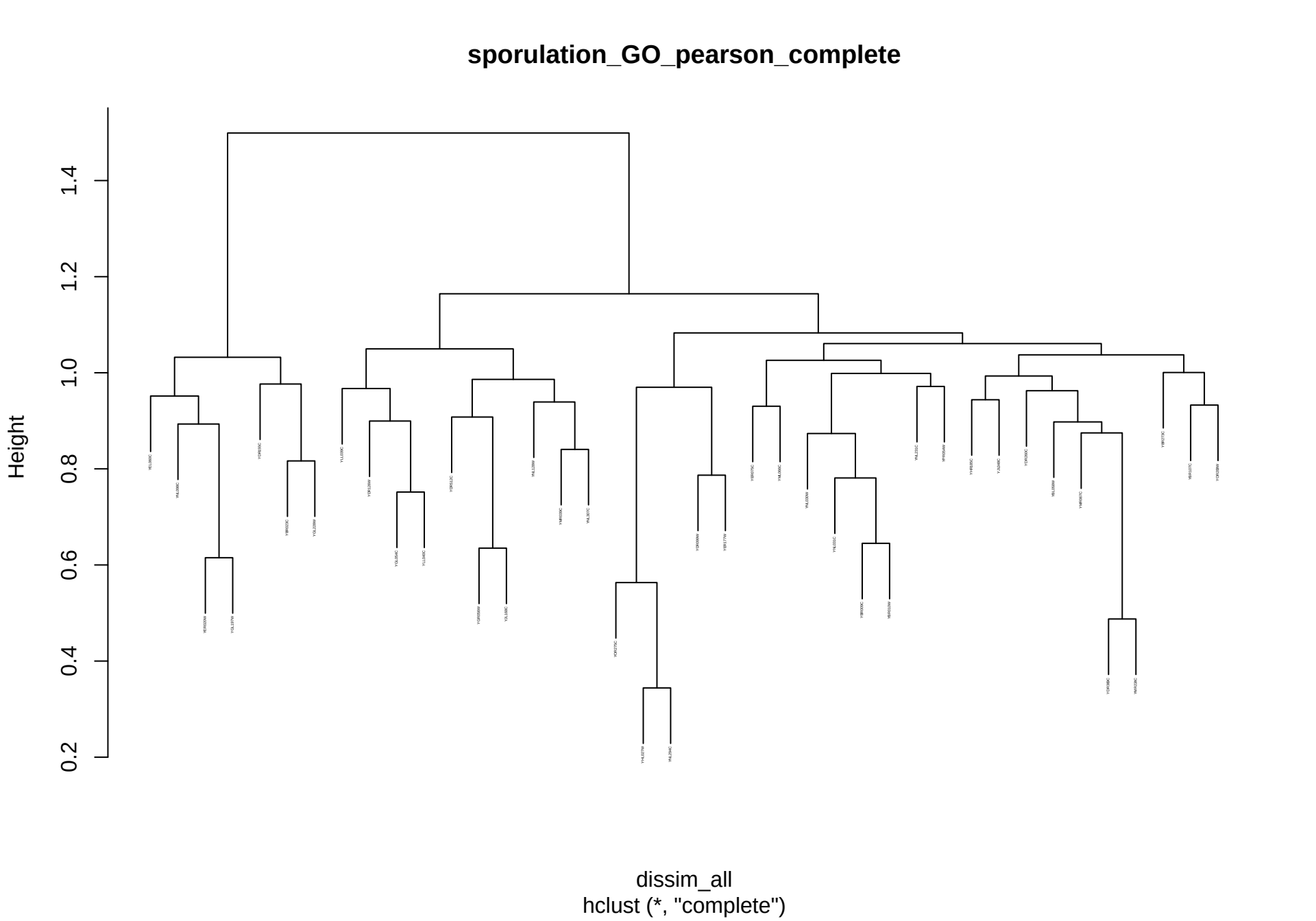

organelle fission_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

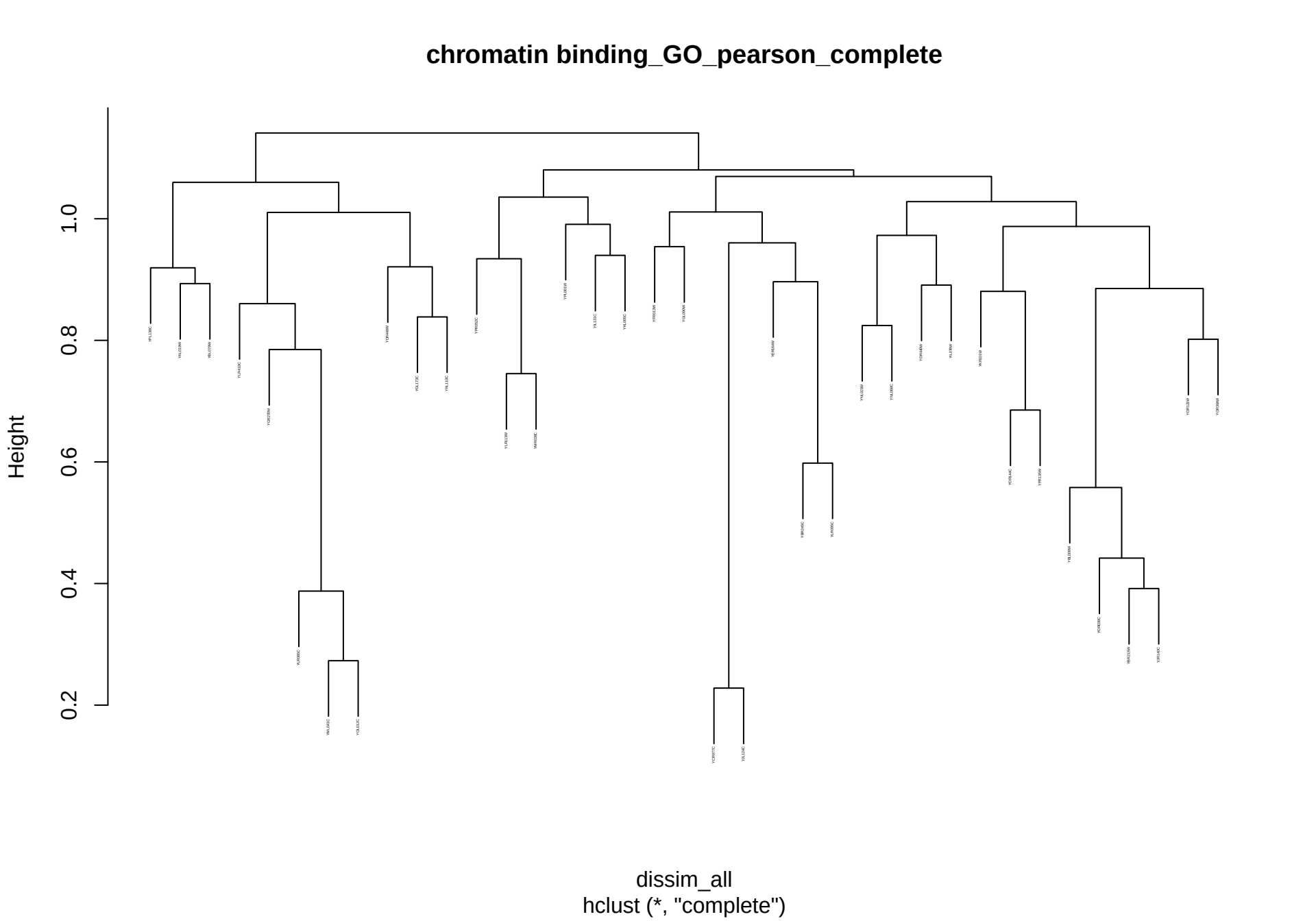

kinase activity_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")


protein phosphorylation_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
dissim_all
hclust (*, "complete")

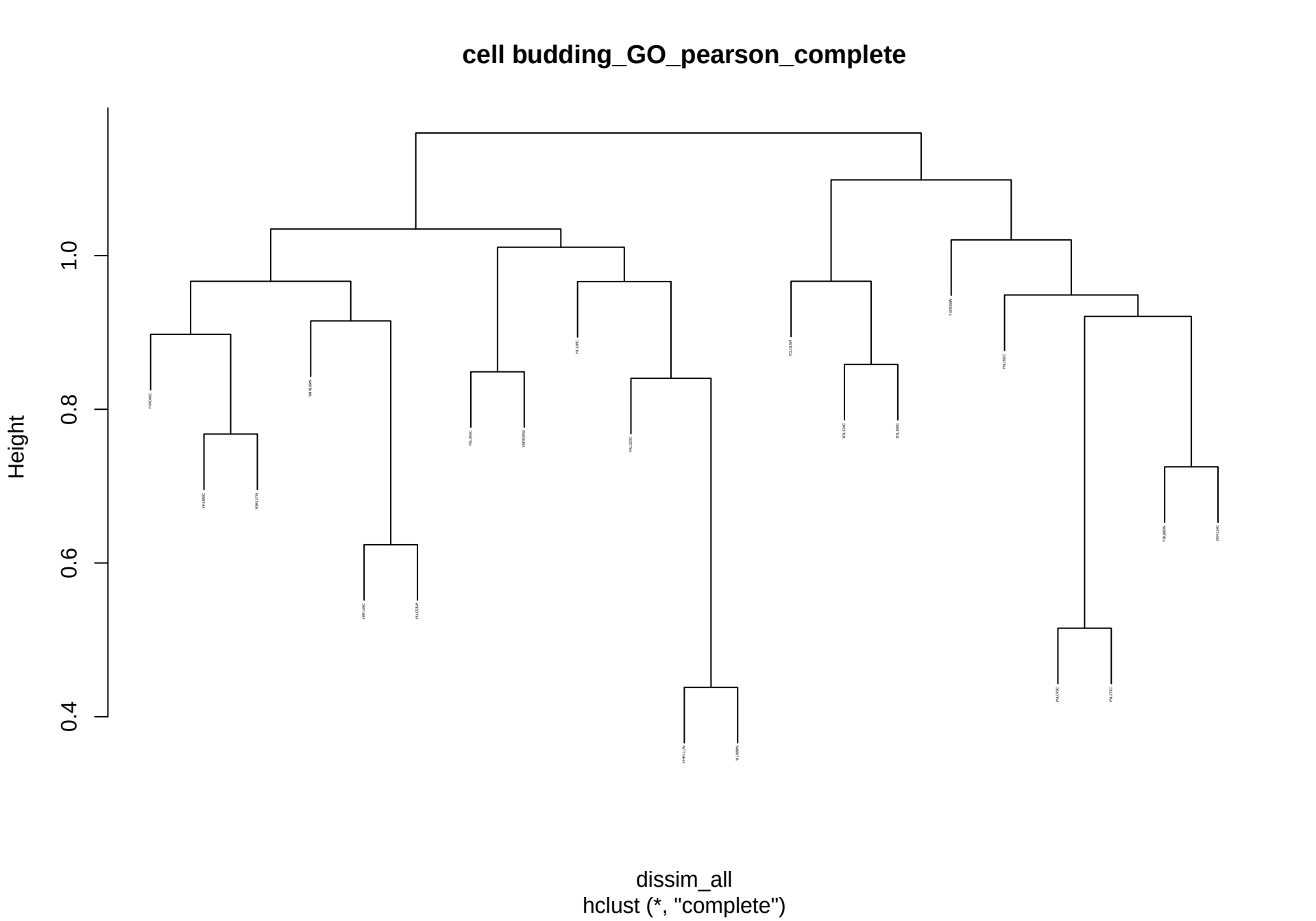

cell wall organization or biogenesis_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")

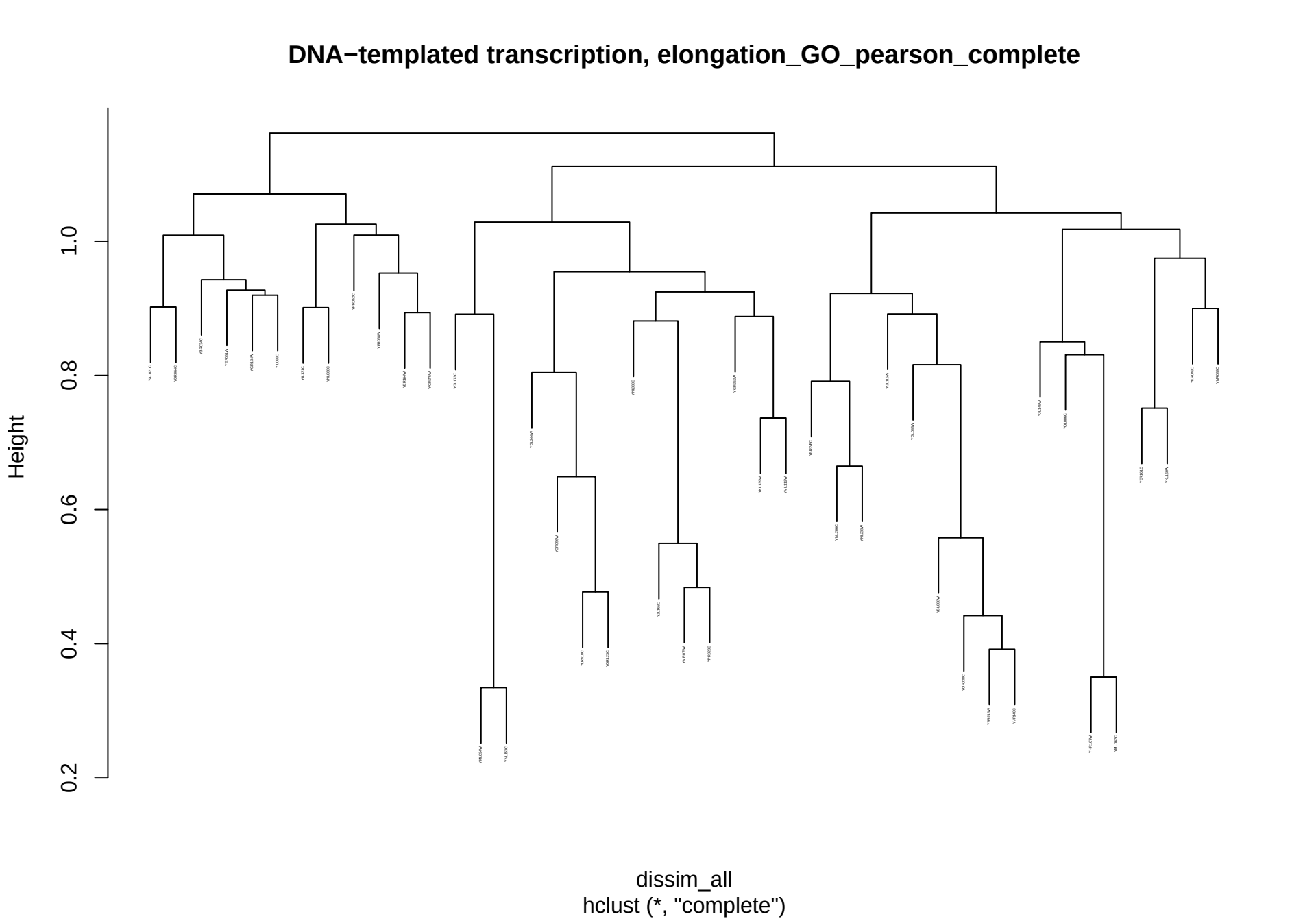

meiotic cell cycle_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

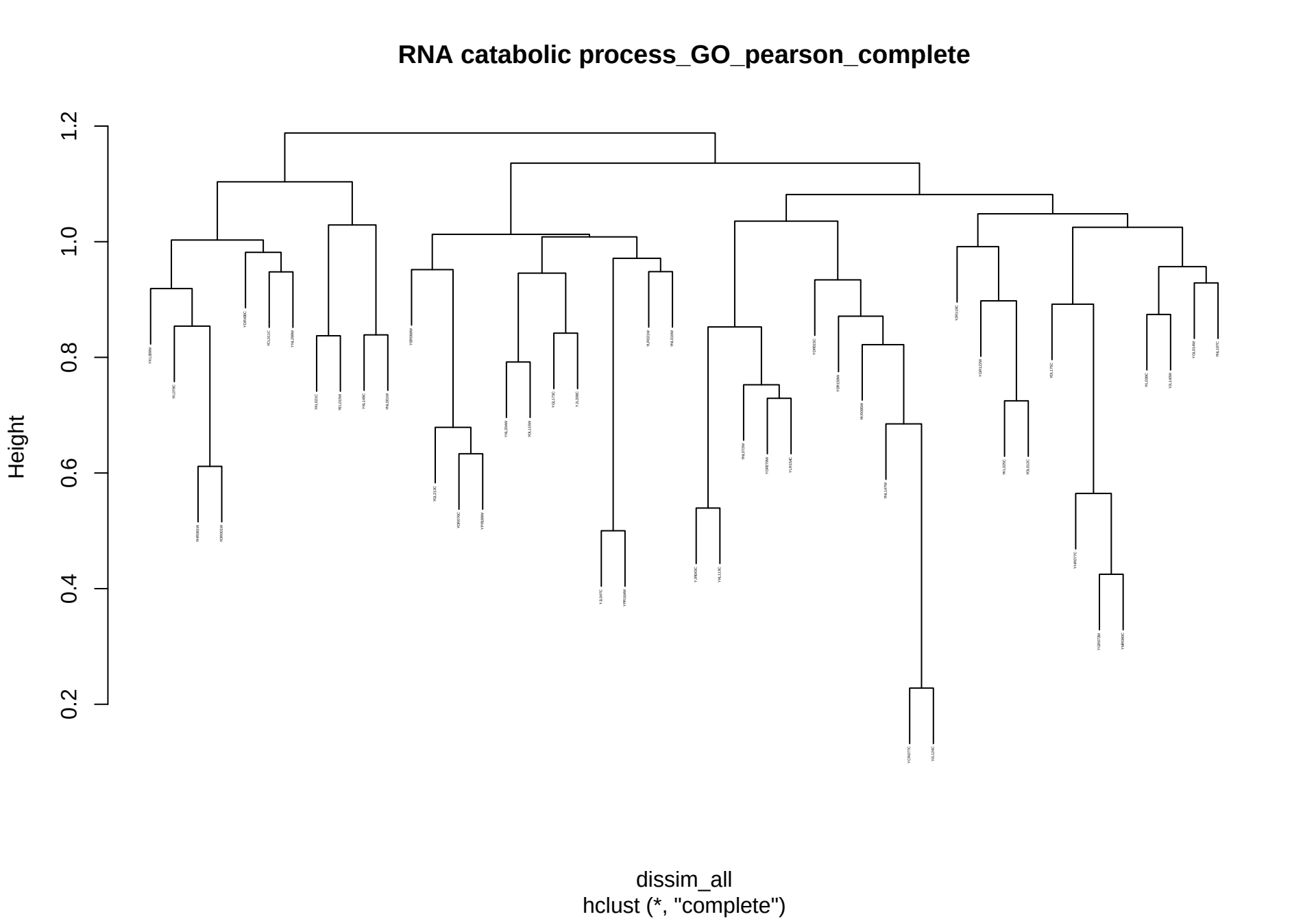

sporulation_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")

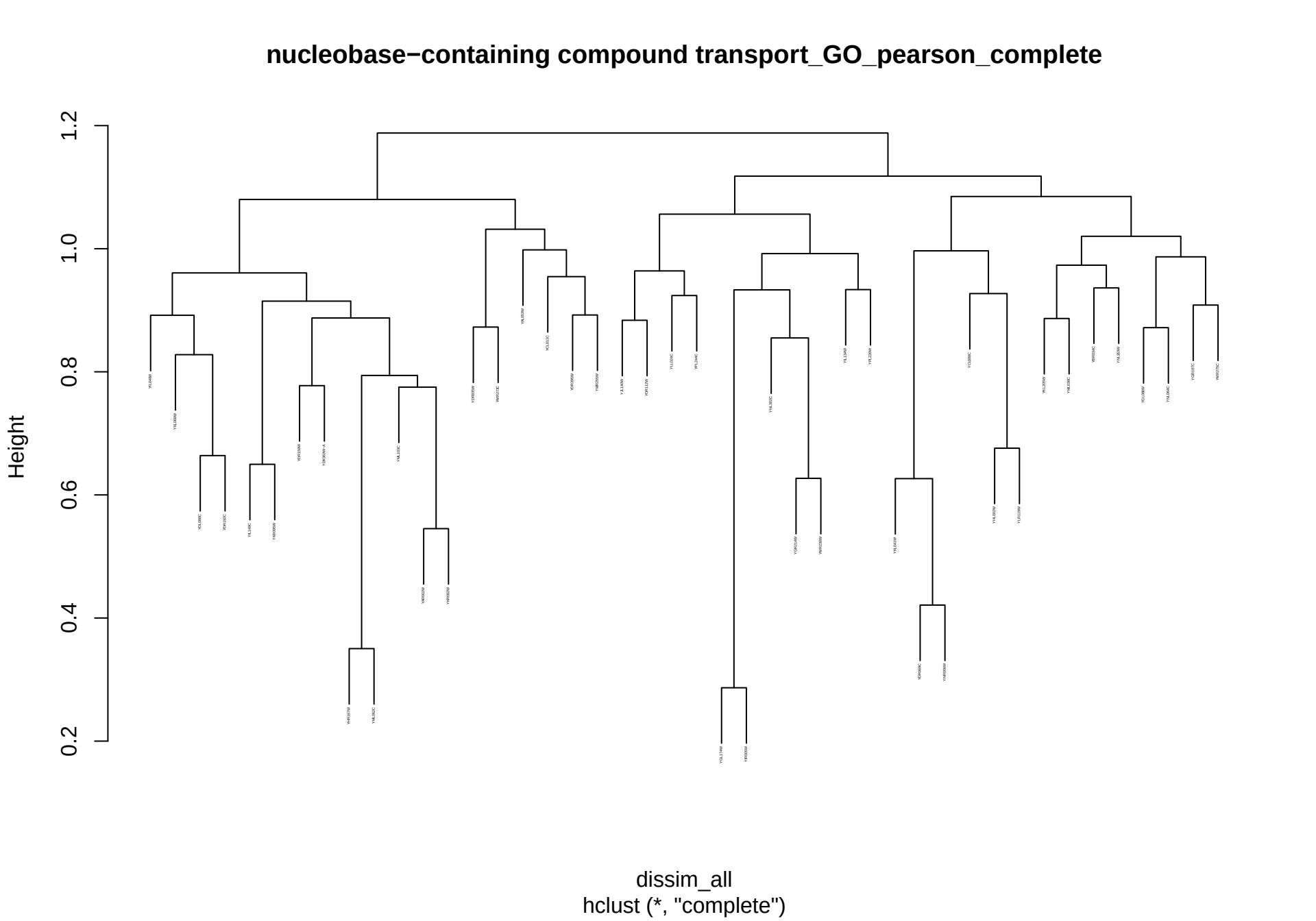

chromatin binding_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

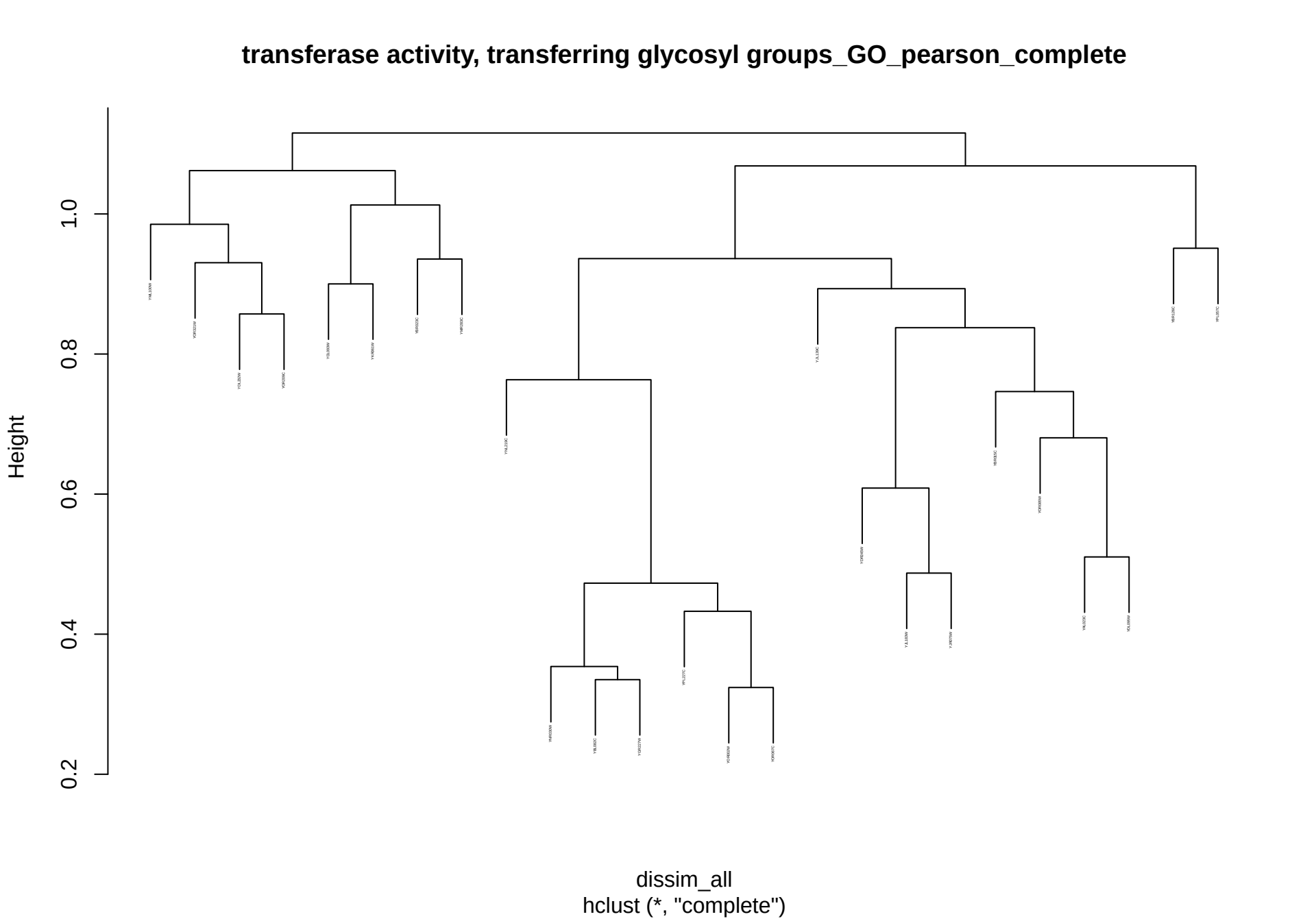

RNA modification_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

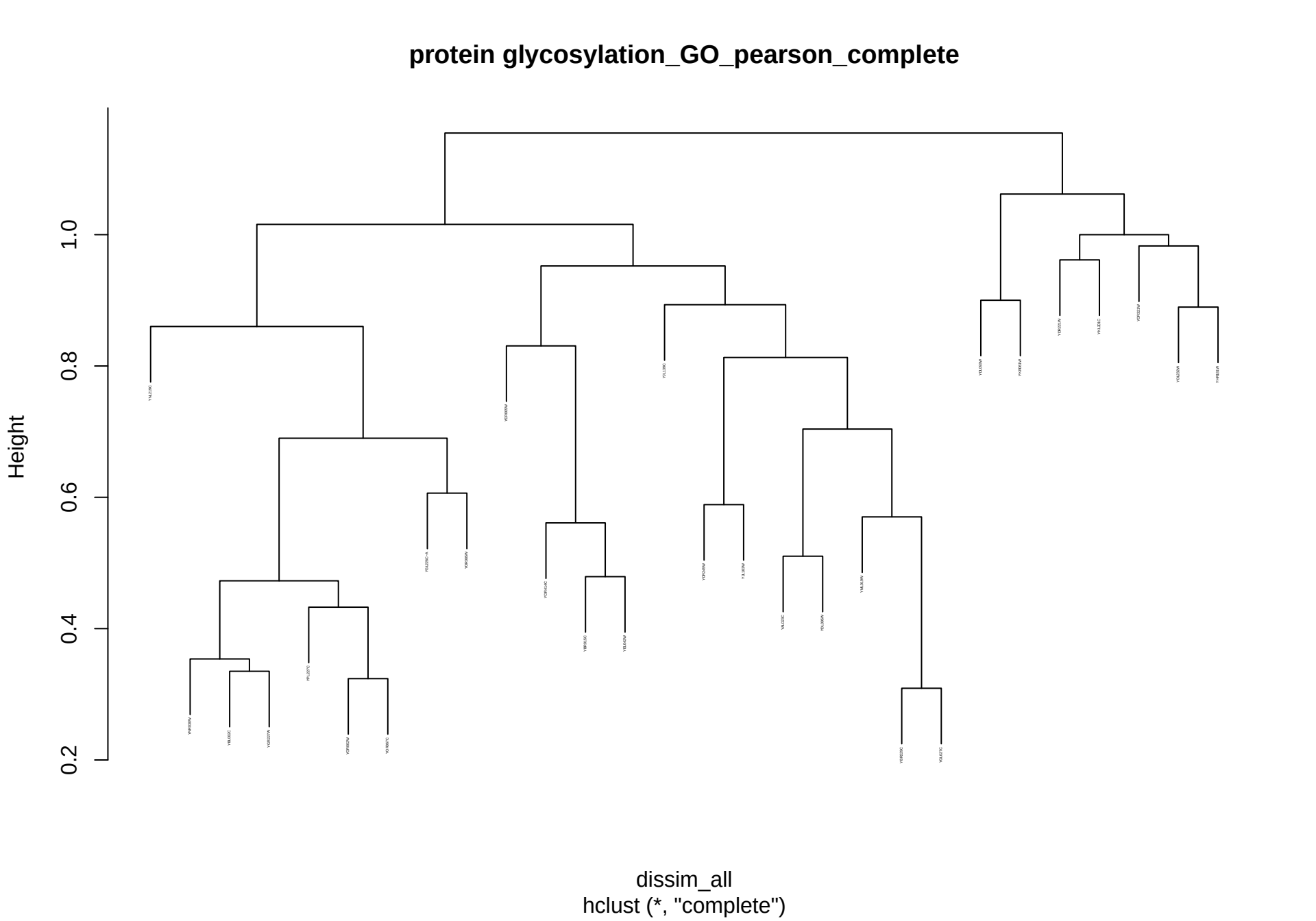

cell budding_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

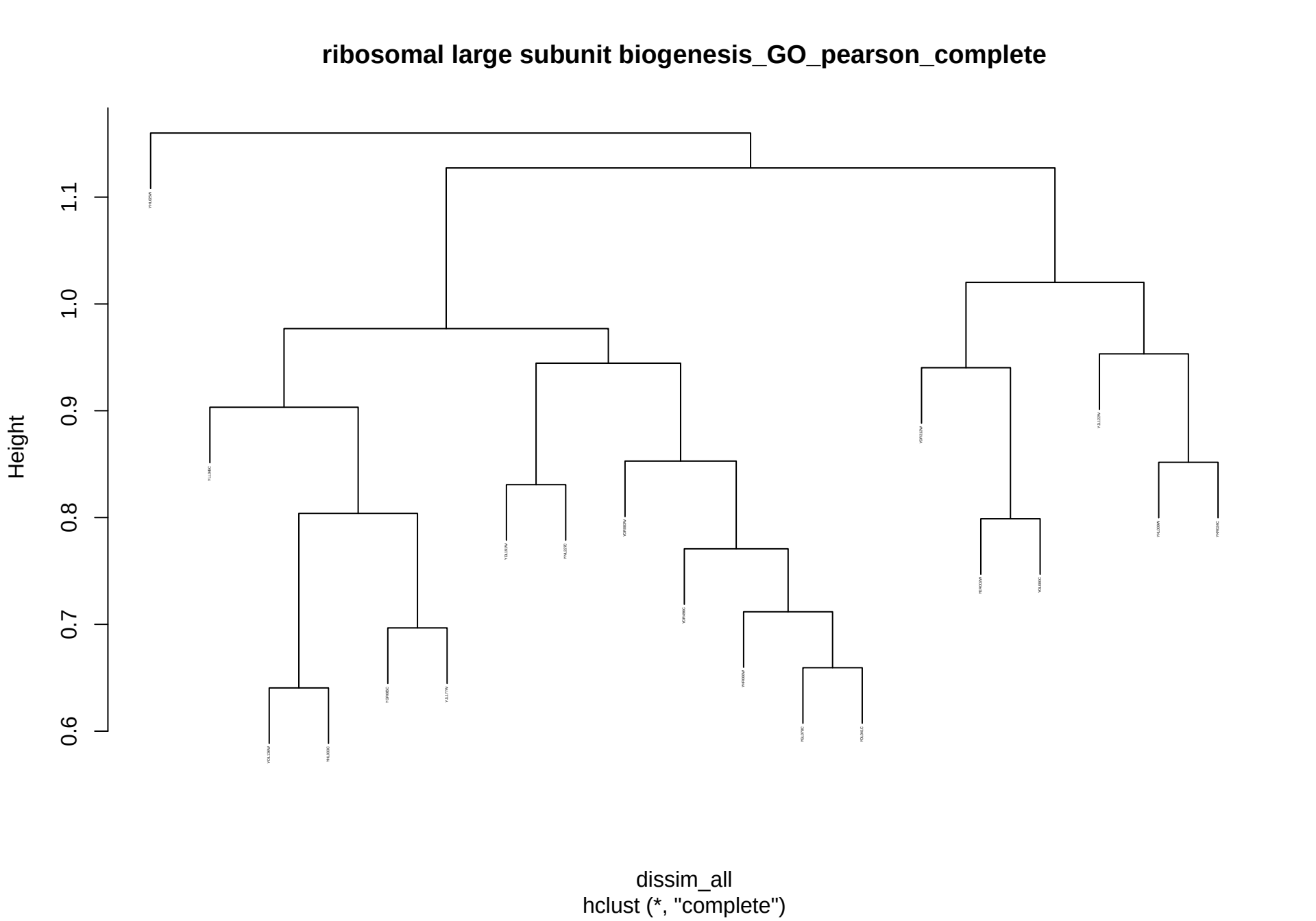

DNA−templated transcription, elongation_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

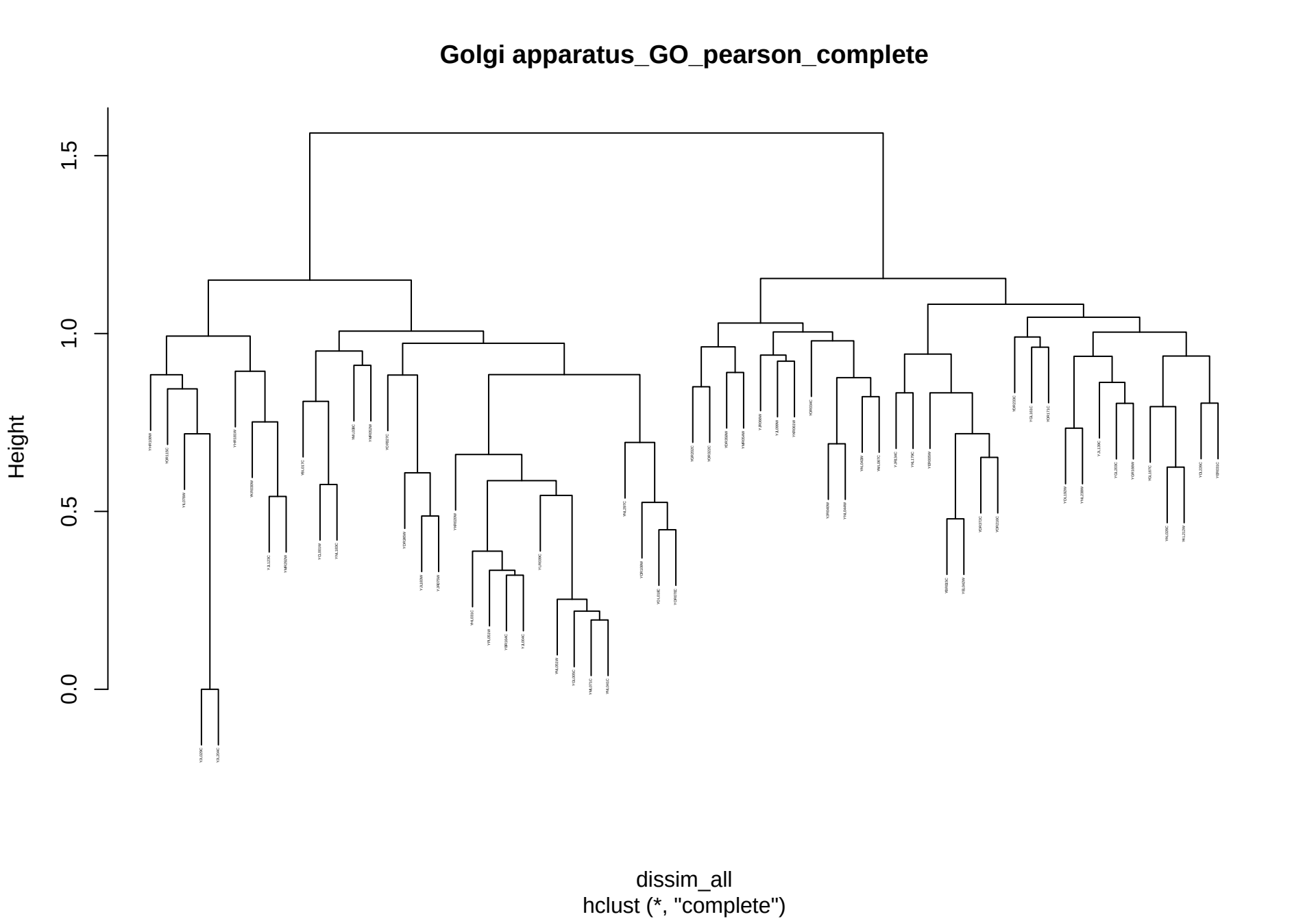

RNA catabolic process_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

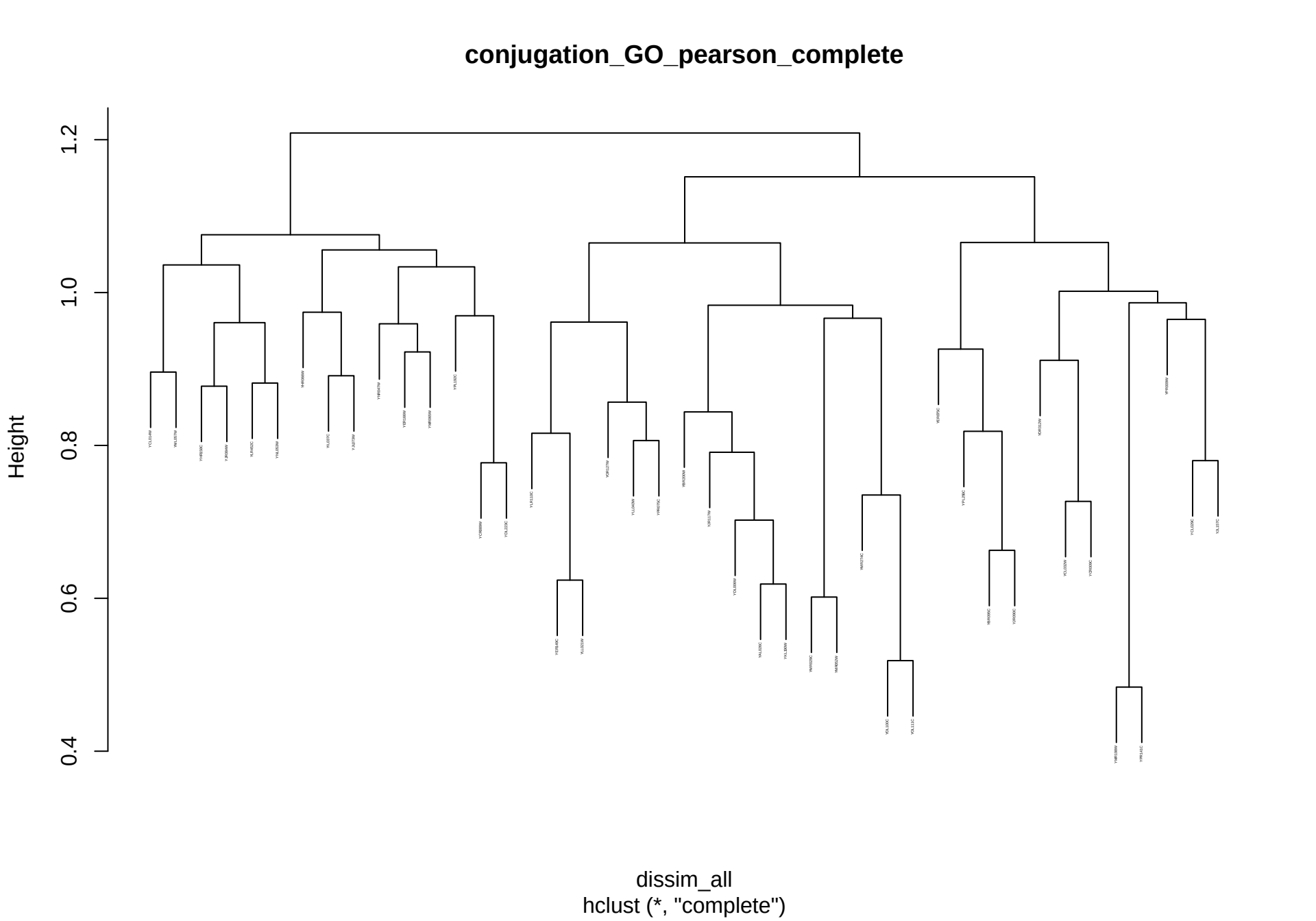

nucleobase−containing compound transport_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

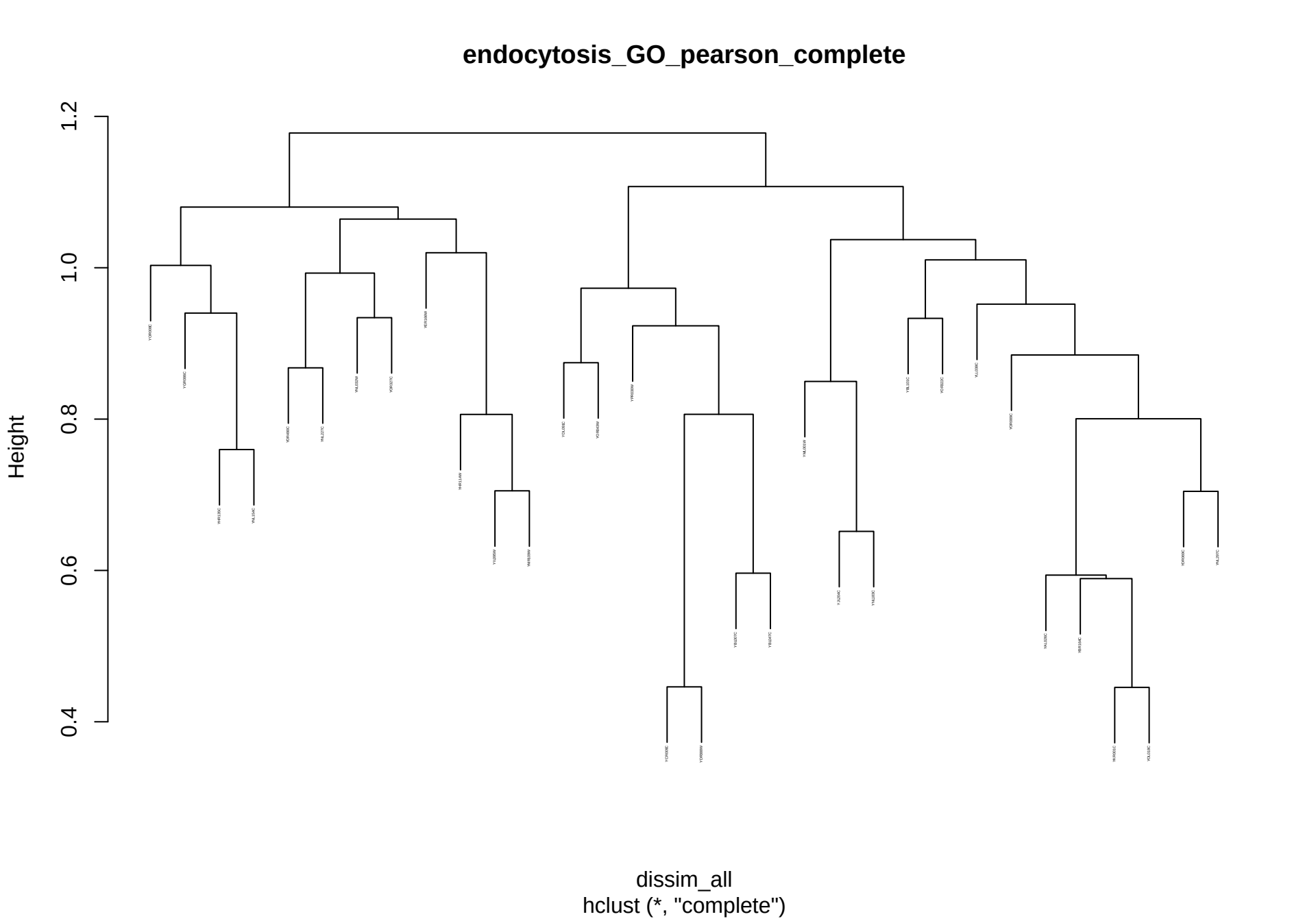

transferase activity, transferring glycosyl groups_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

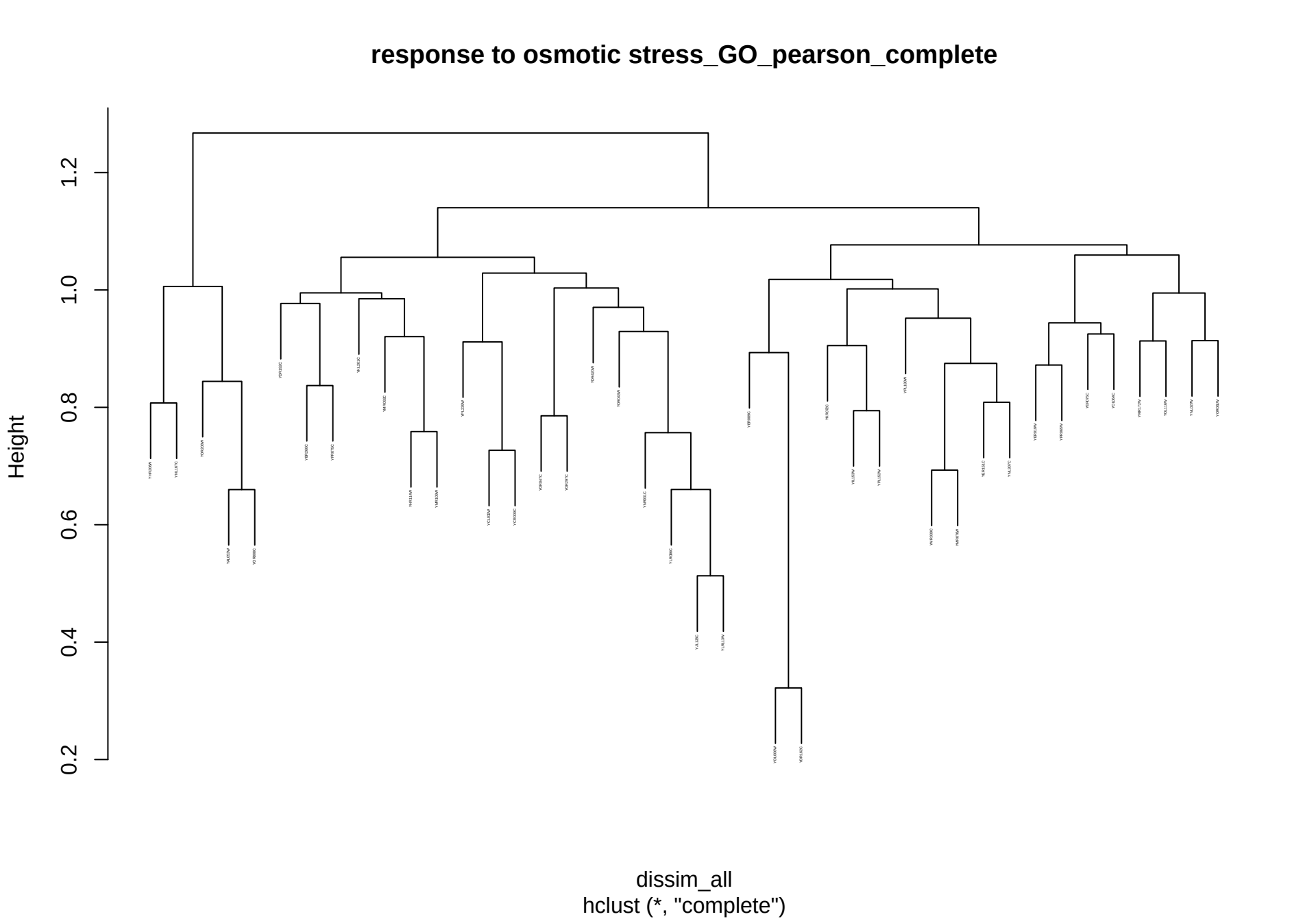

protein glycosylation_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")

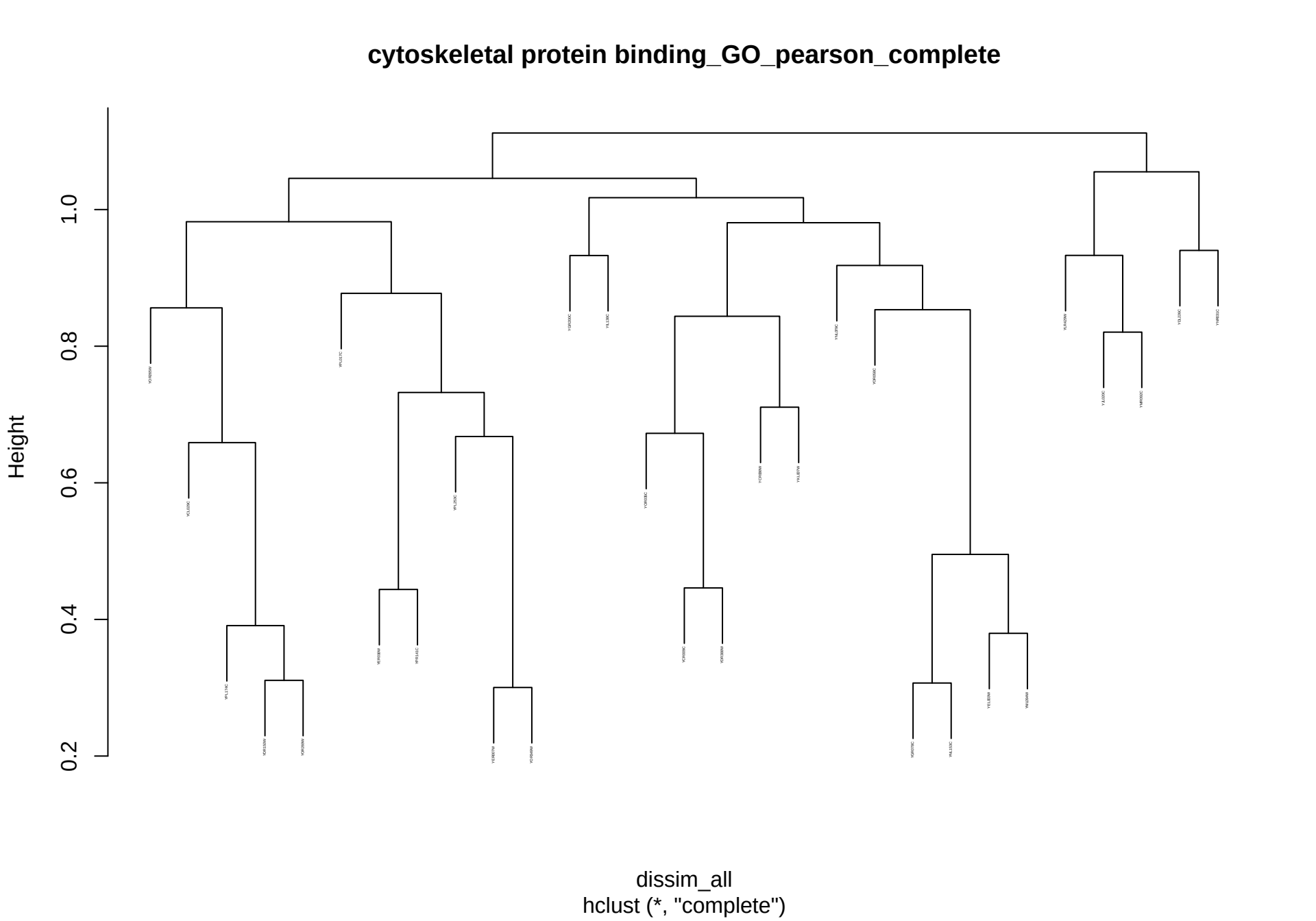

ribosomal large subunit biogenesis_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
dissim_all
hclust (*, "complete")

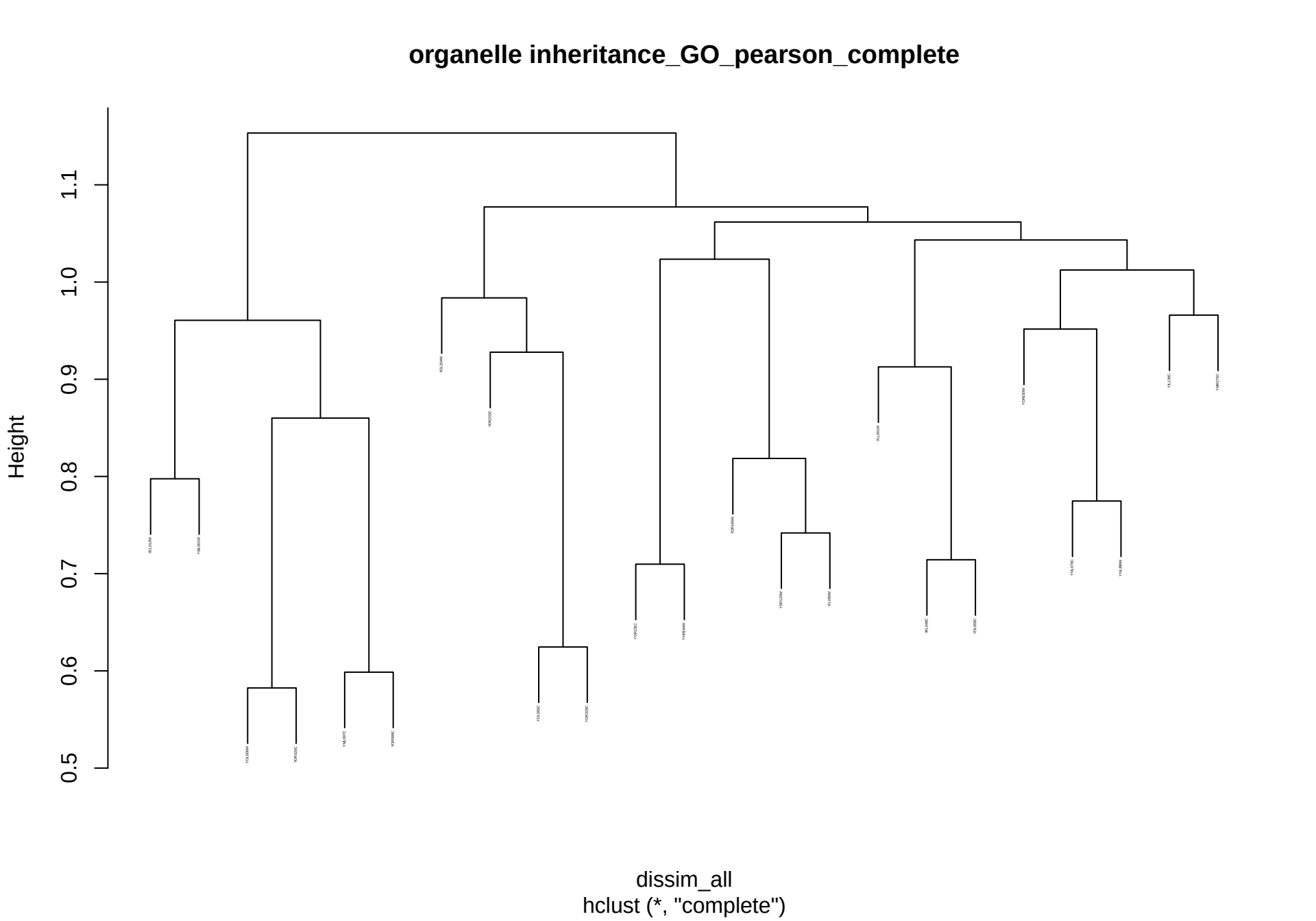

Golgi apparatus_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")

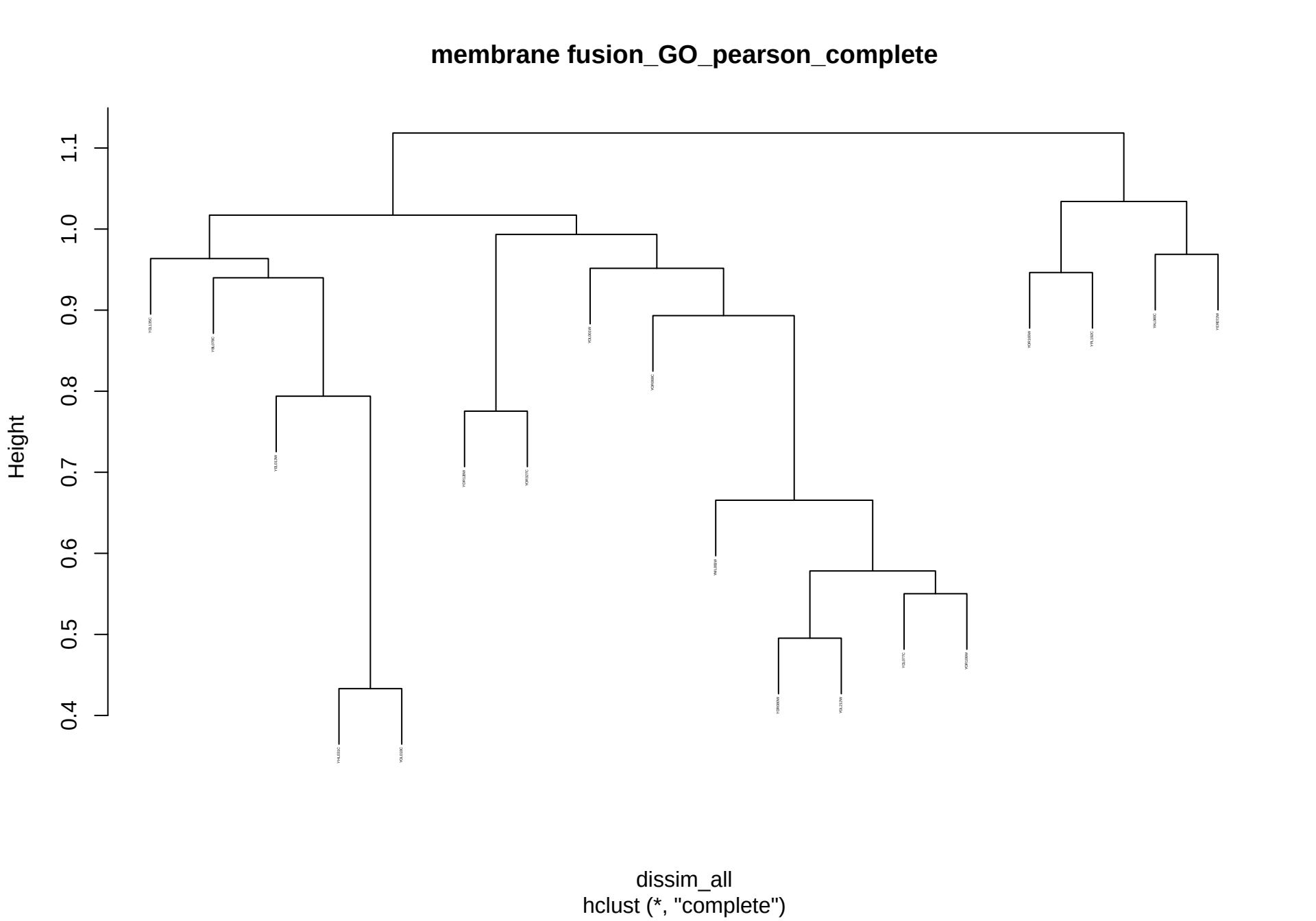

conjugation_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

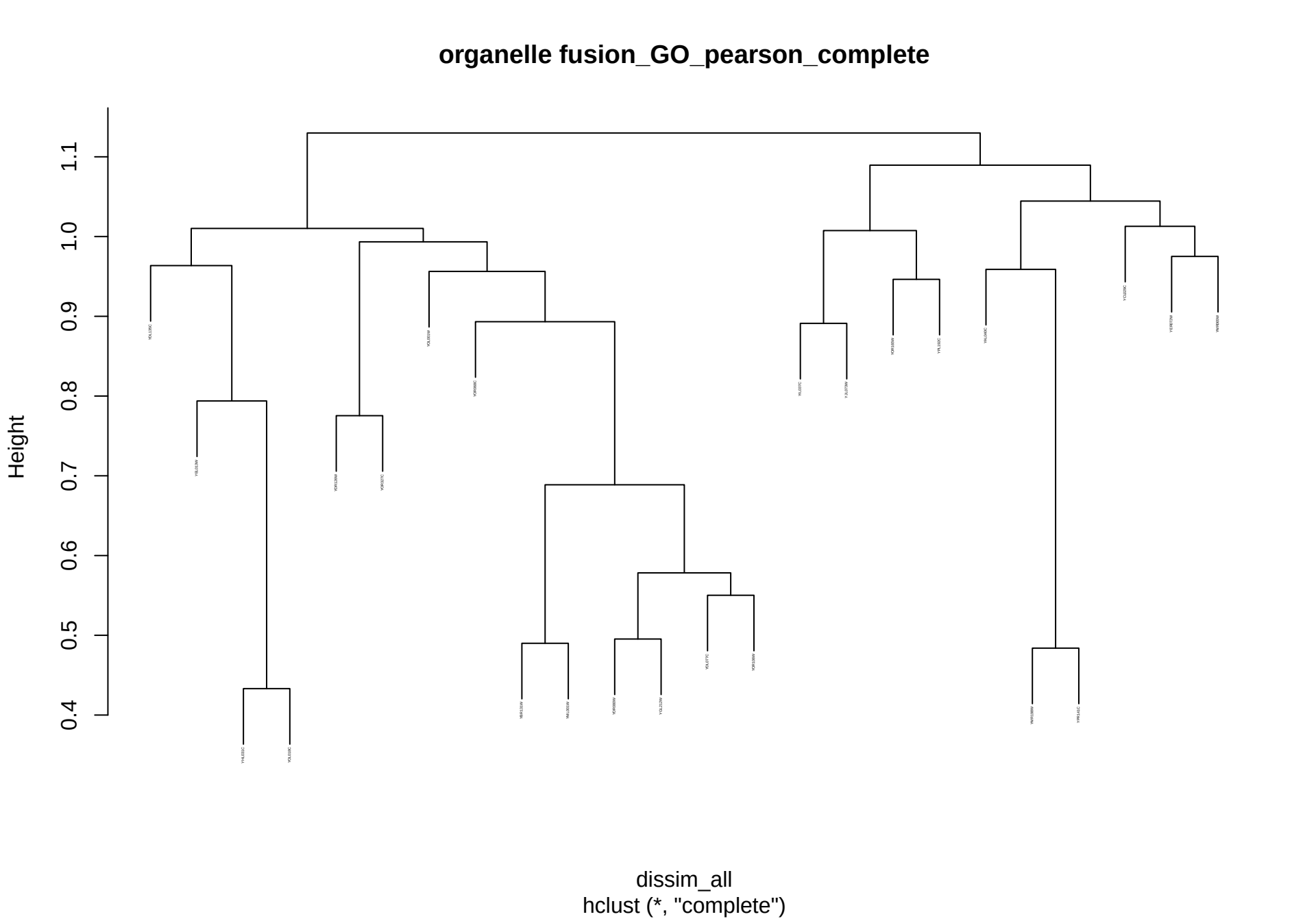

endocytosis_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

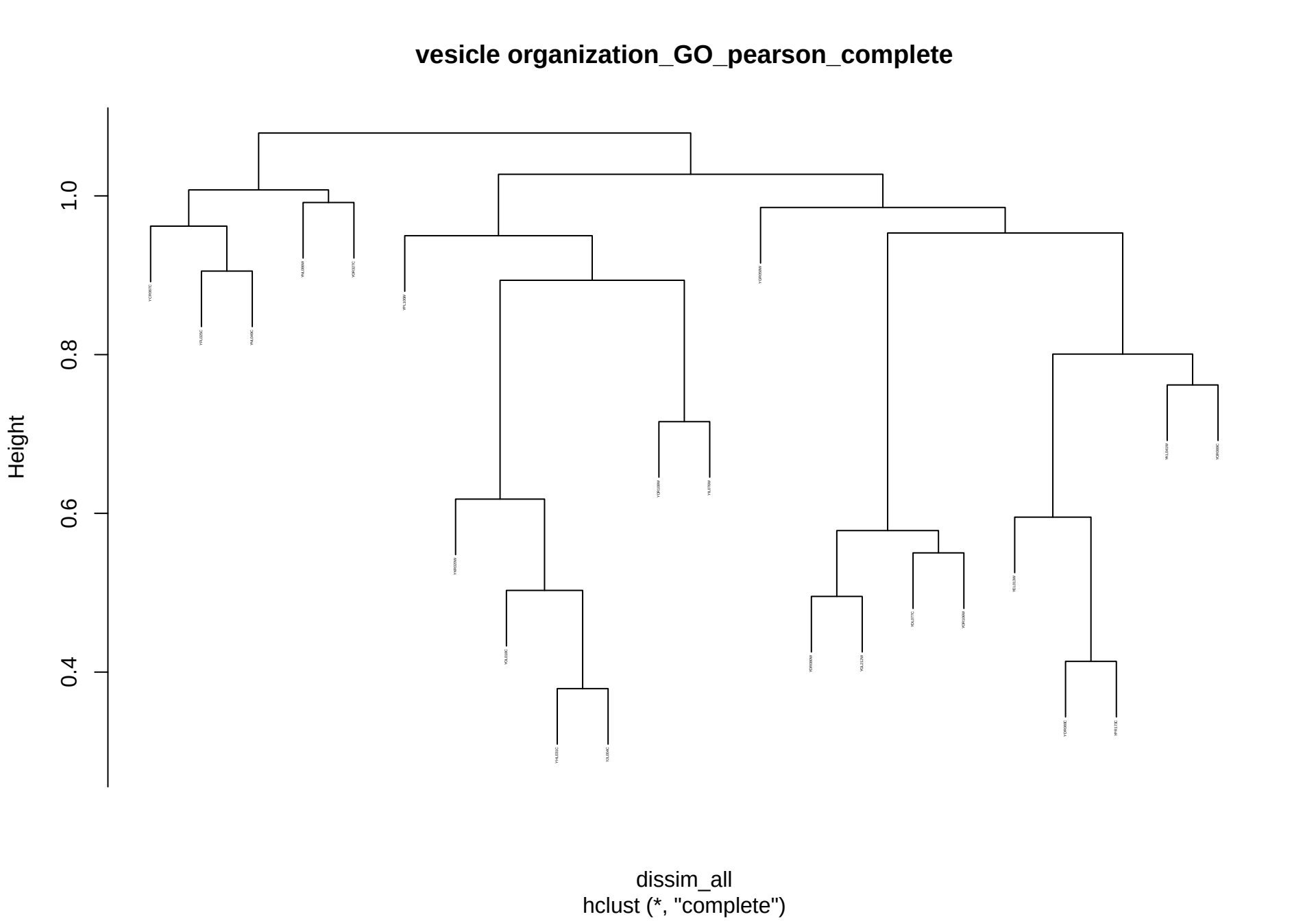

response to osmotic stress_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

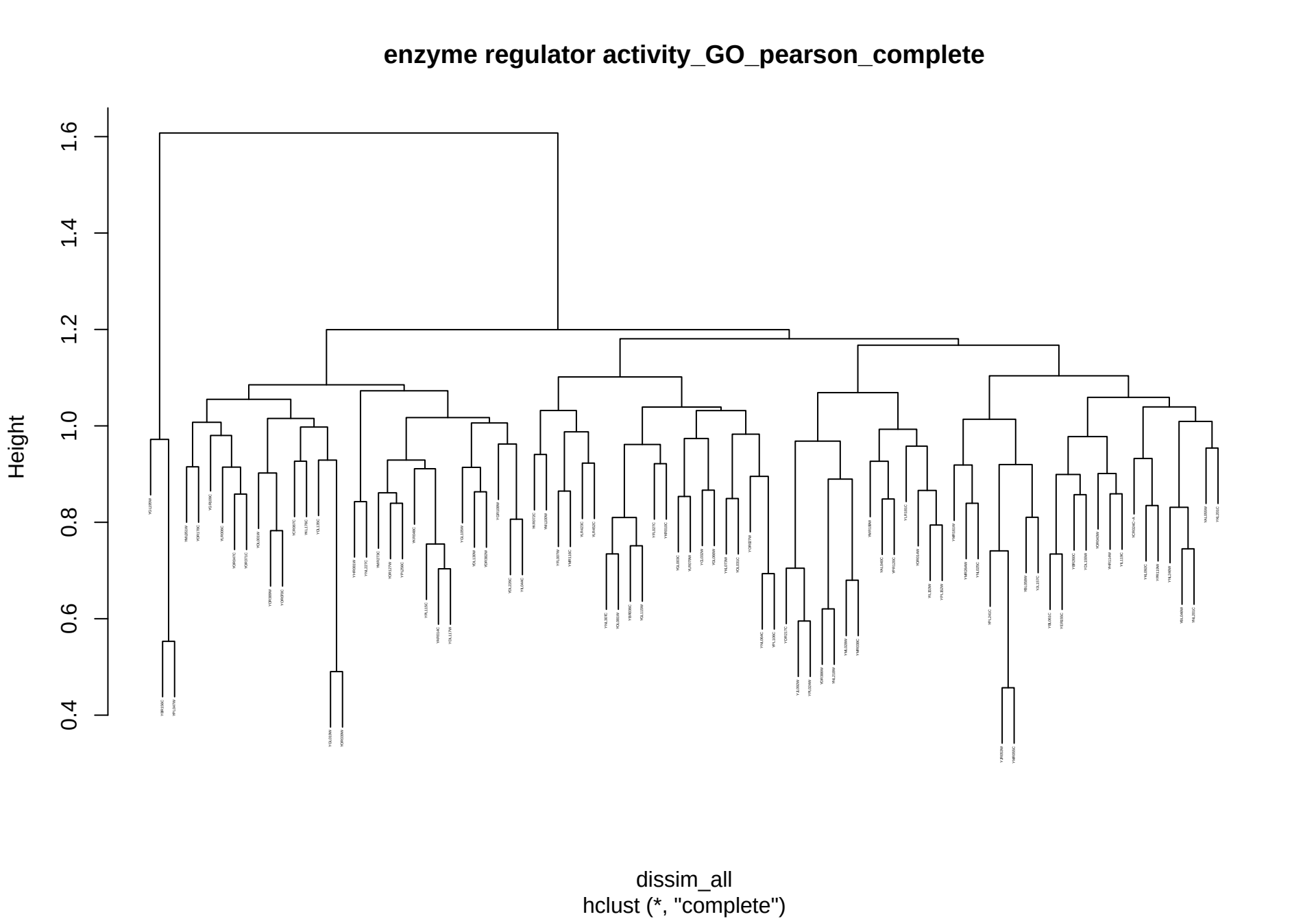

cytoskeletal protein binding_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")

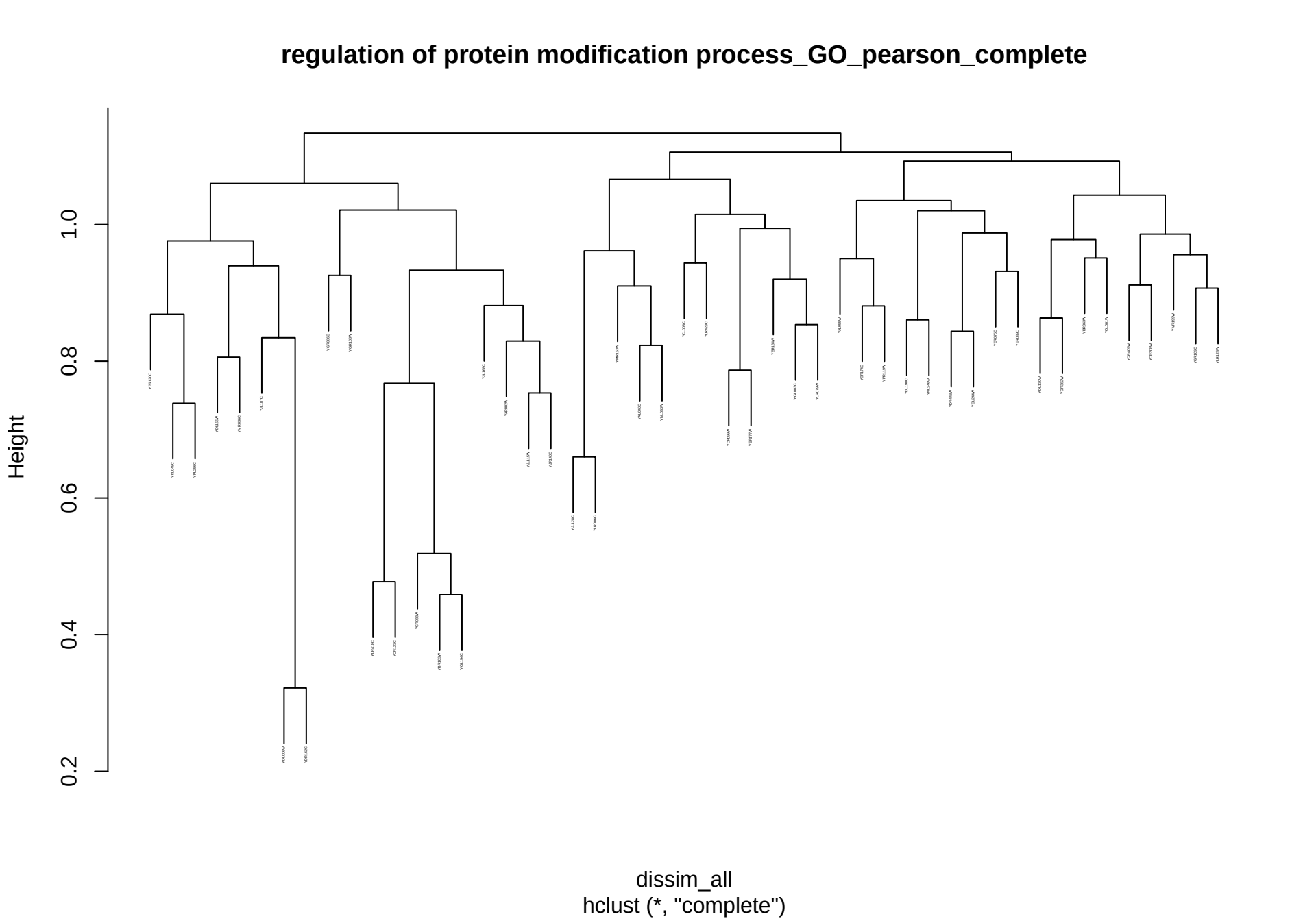

organelle inheritance_GO_pearson_complete
Height
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

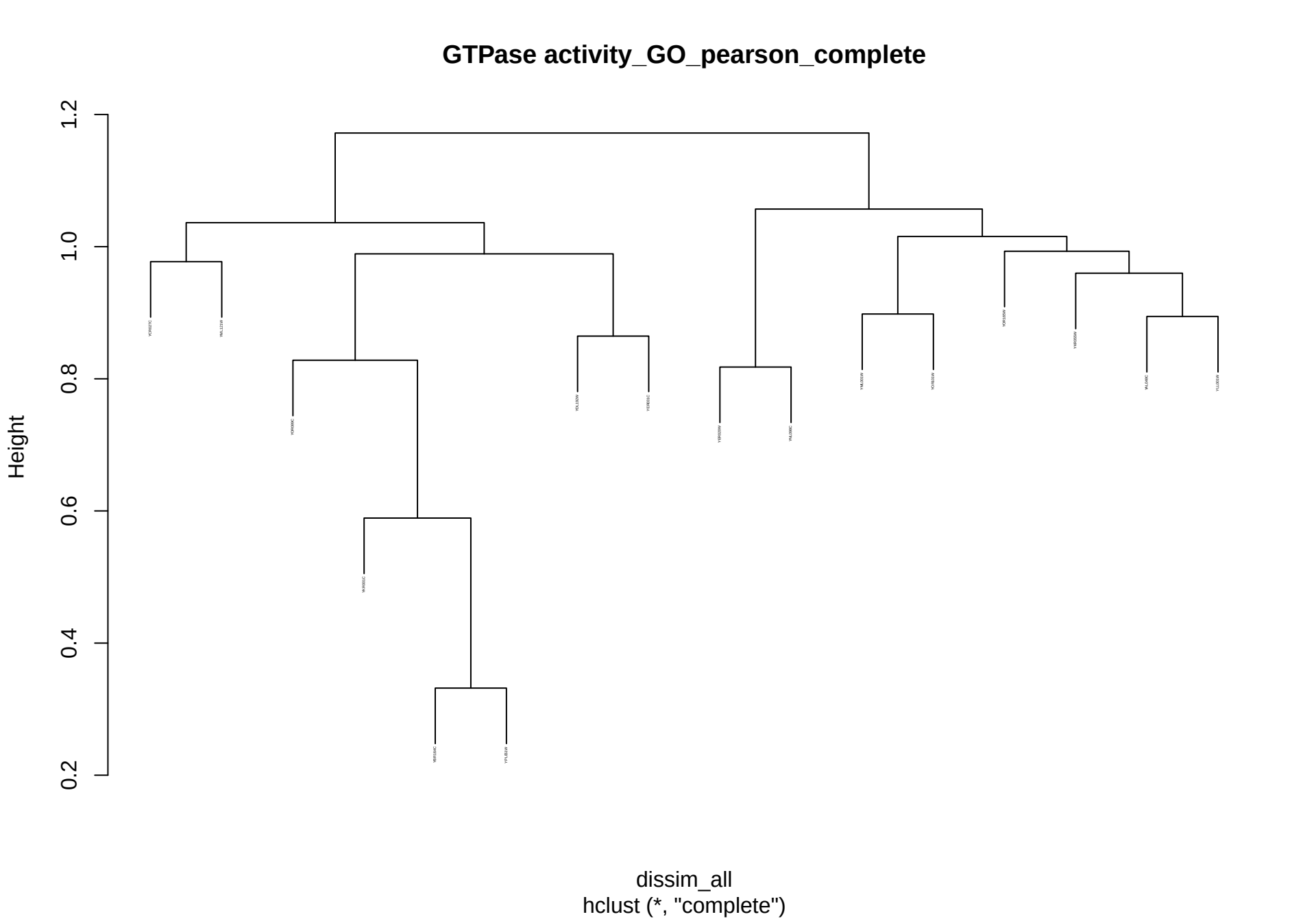

membrane fusion_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

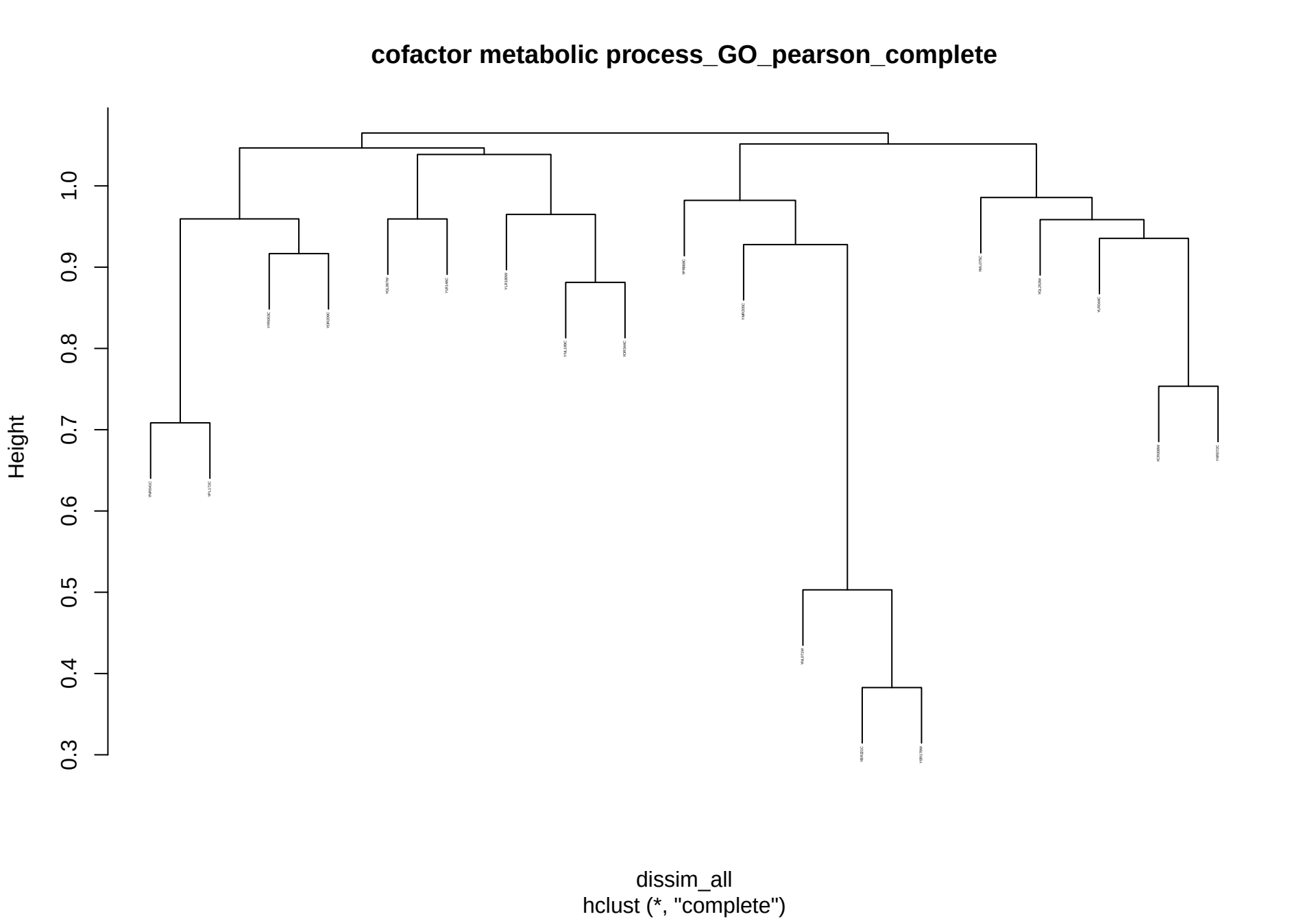

organelle fusion_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

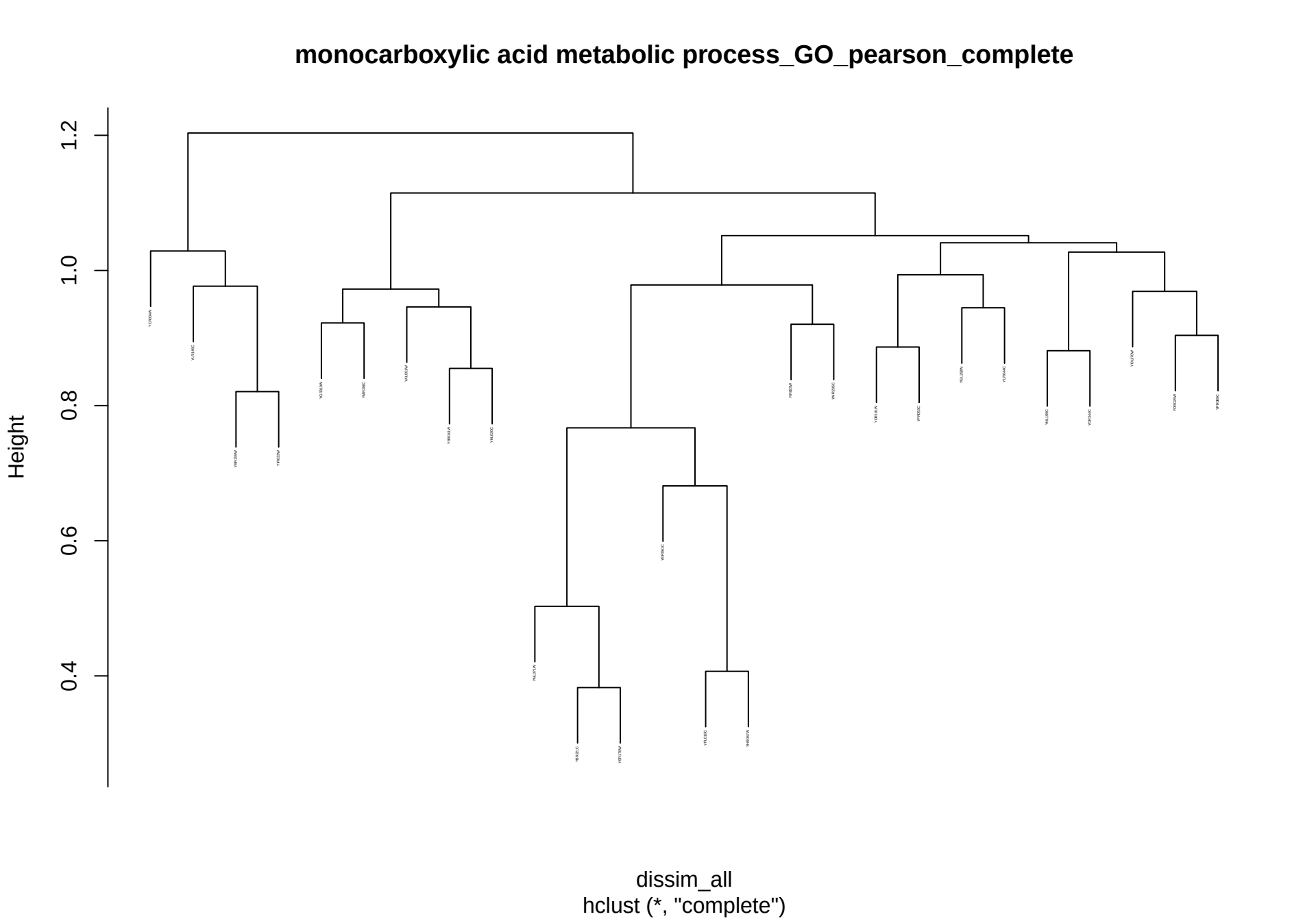

vesicle organization_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

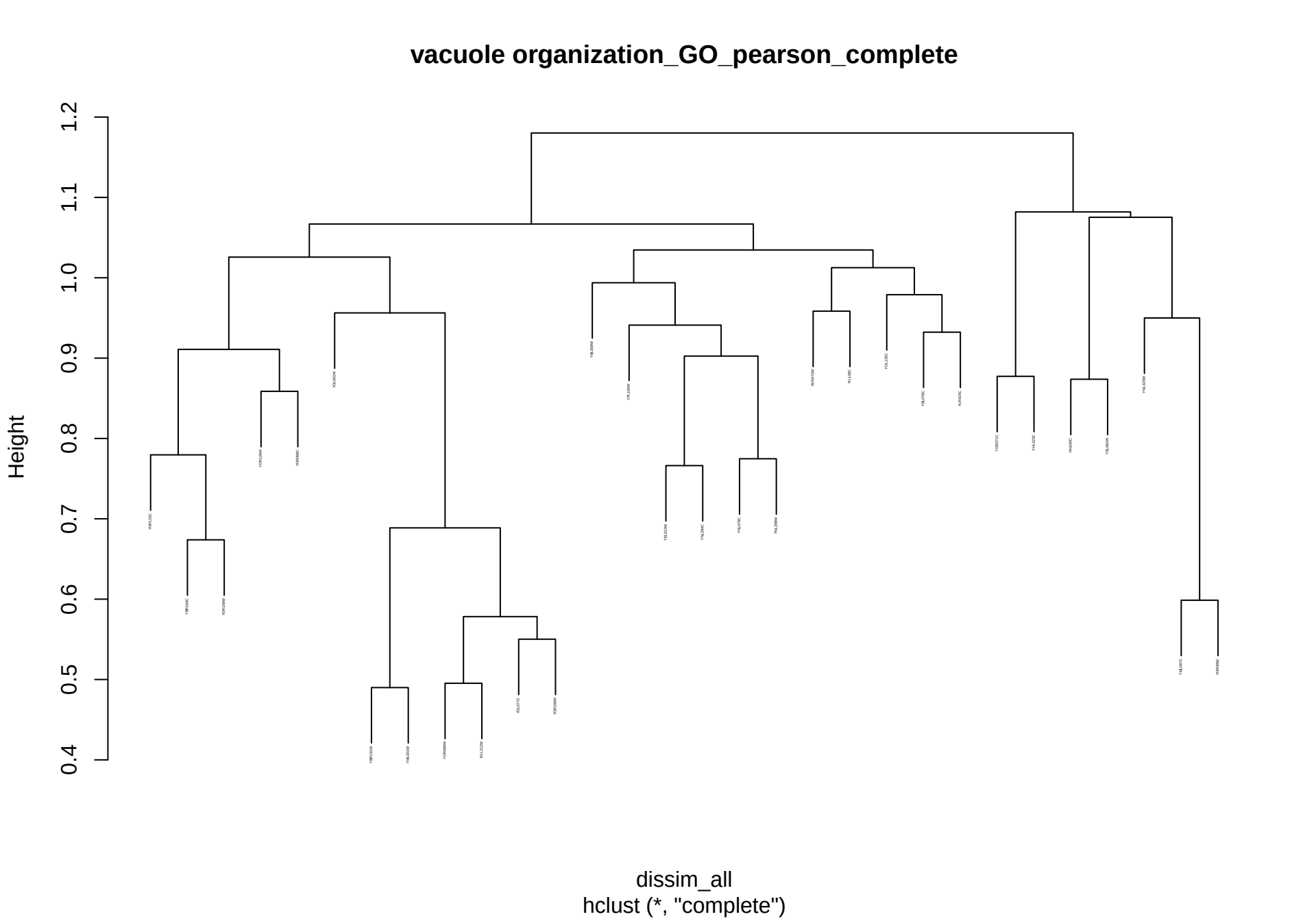

enzyme regulator activity_GO_pearson_complete
Height
0.4
0.6
0.8
1.0
1.2
1.4
1.6
dissim_all
hclust (*, "complete")

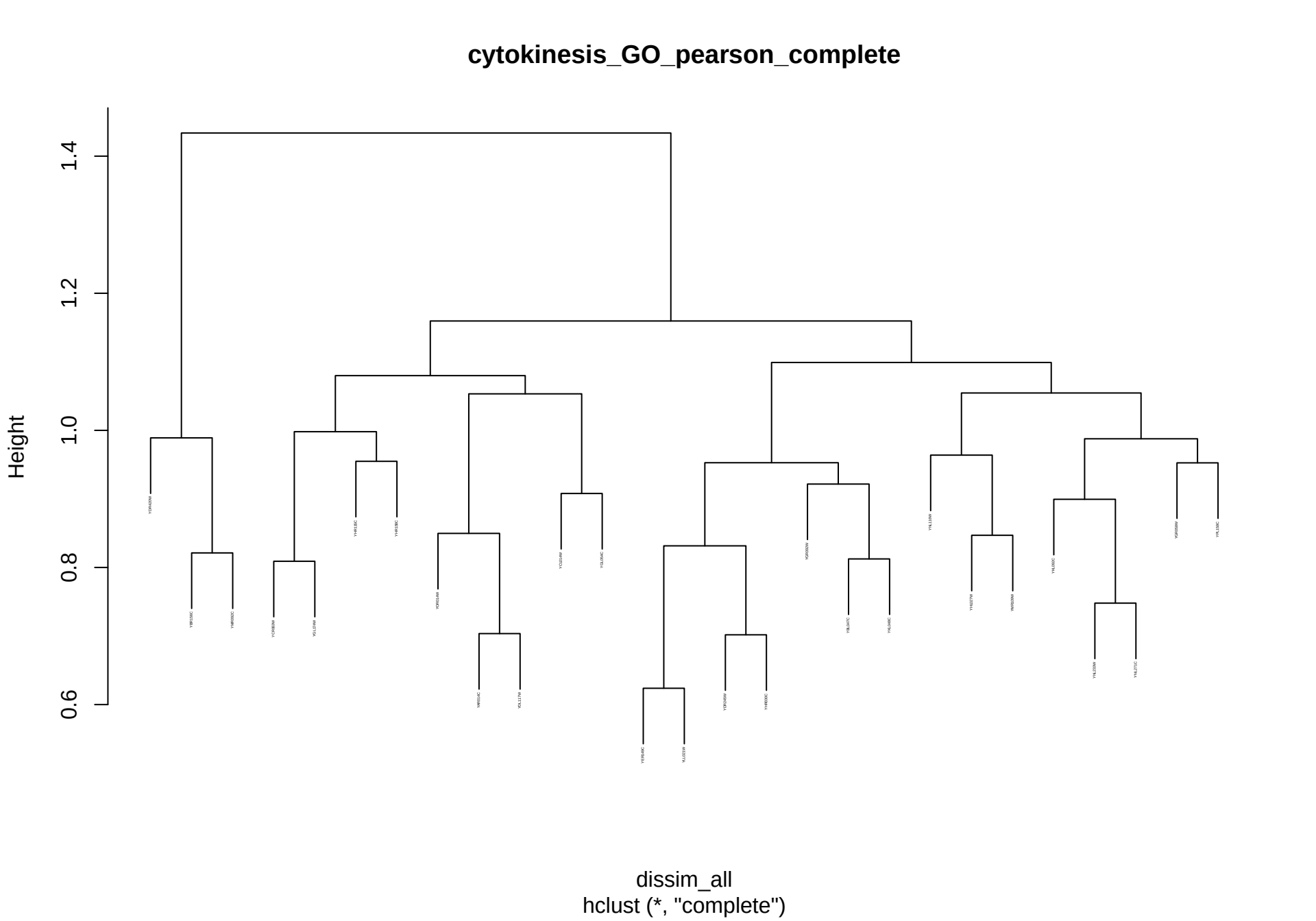

regulation of protein modification process_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")

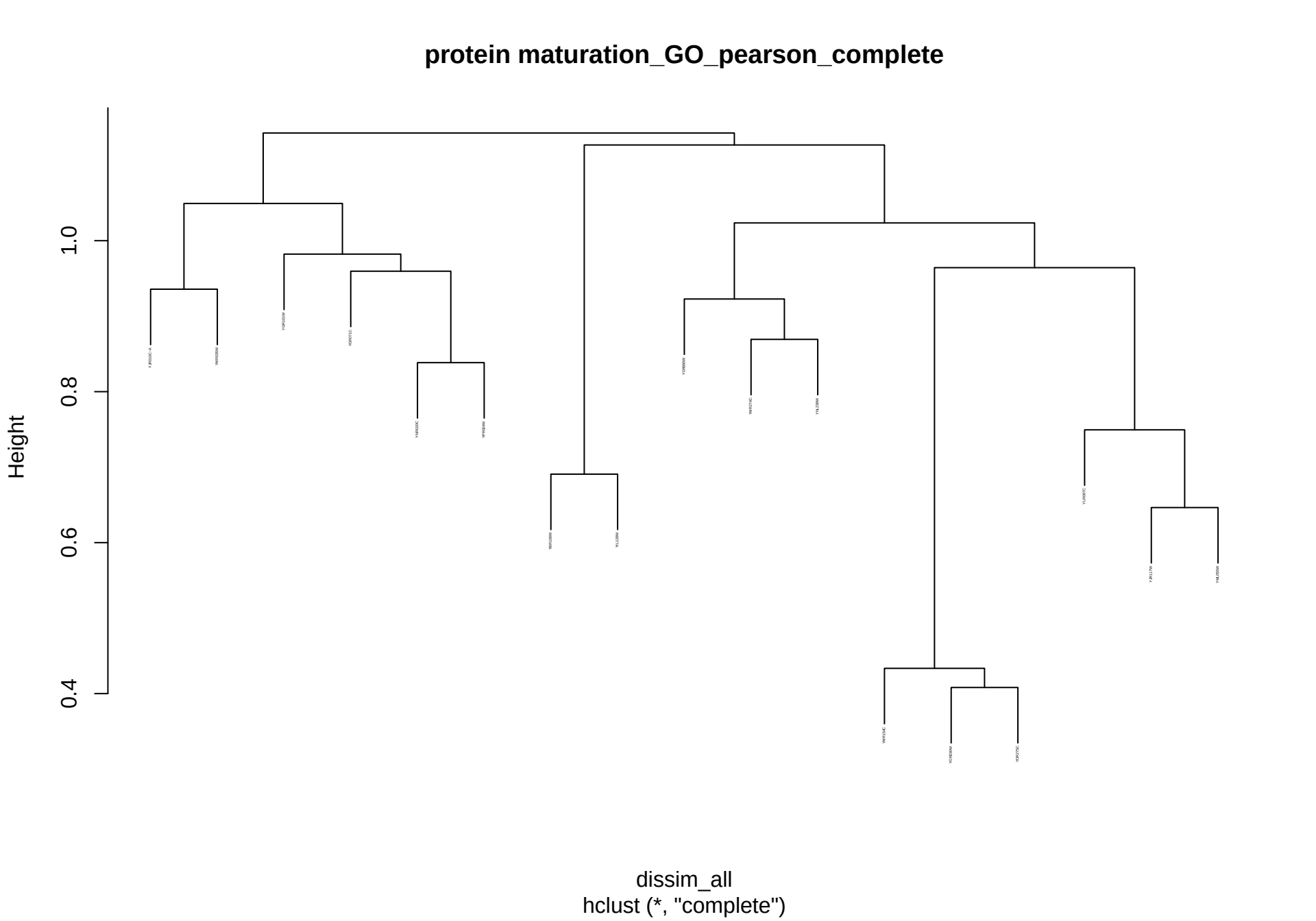

GTPase activity_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

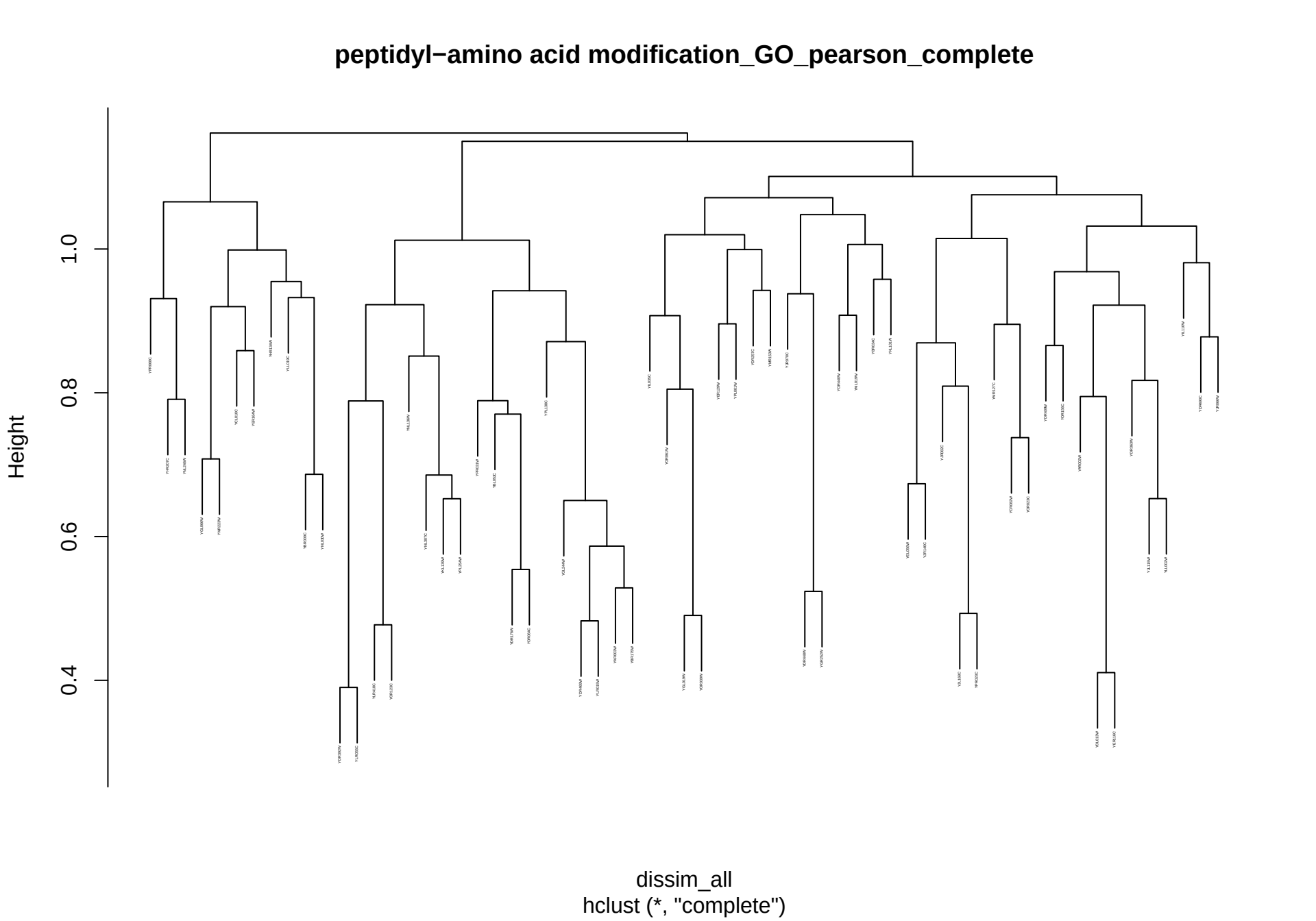

cofactor metabolic process_GO_pearson_complete
Height
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
dissim_all
hclust (*, "complete")

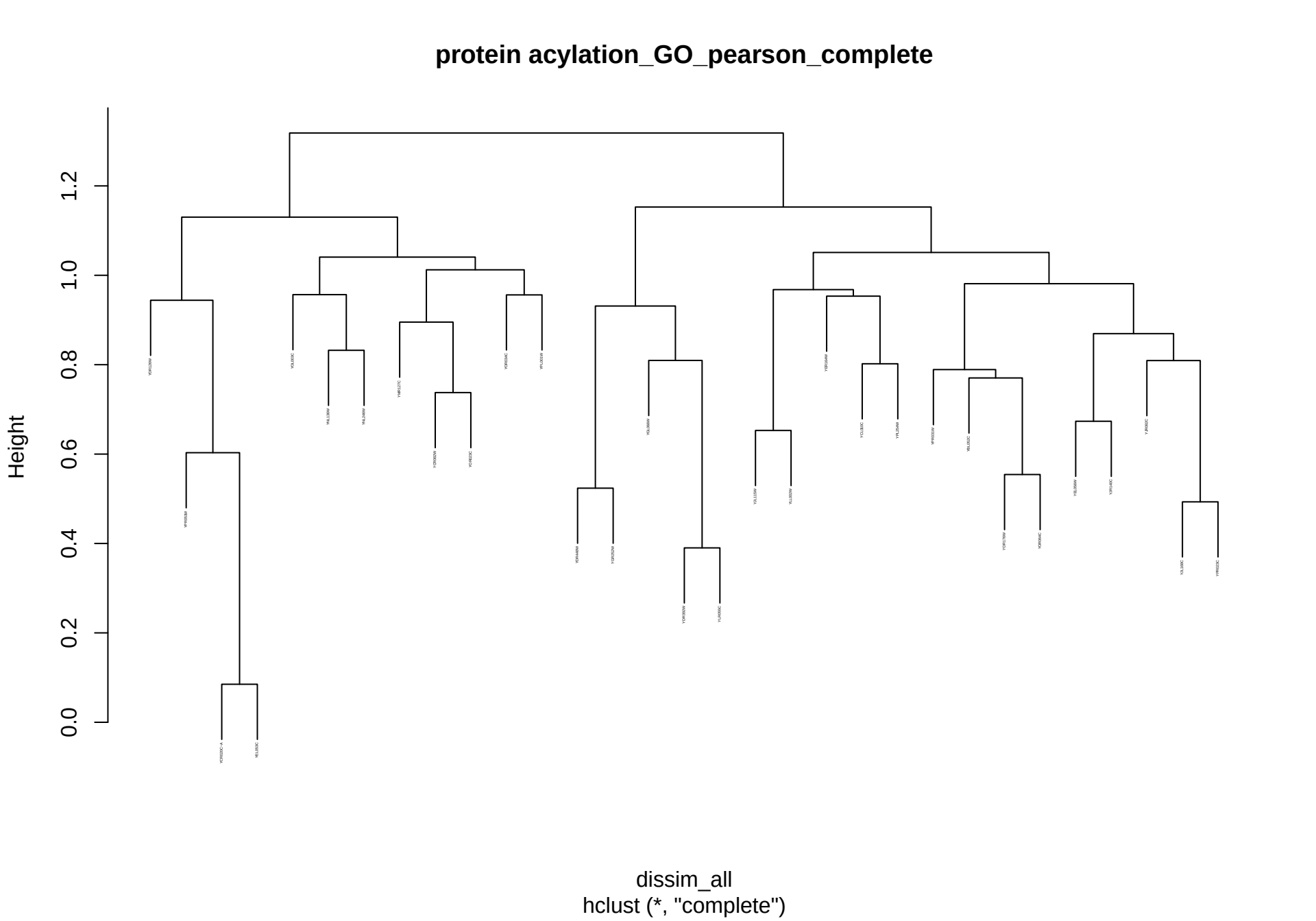

monocarboxylic acid metabolic process_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

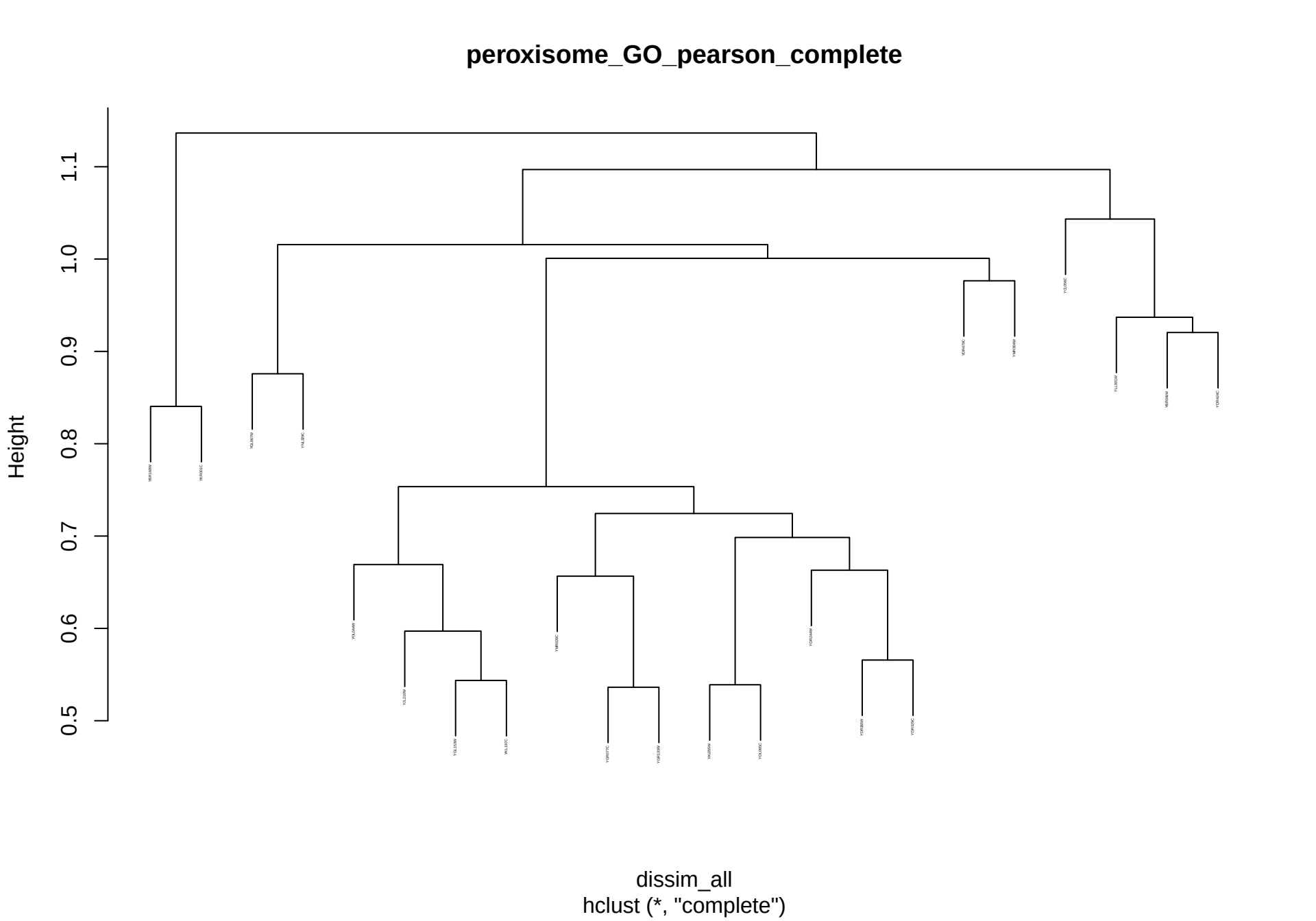

vacuole organization_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
dissim_all
hclust (*, "complete")

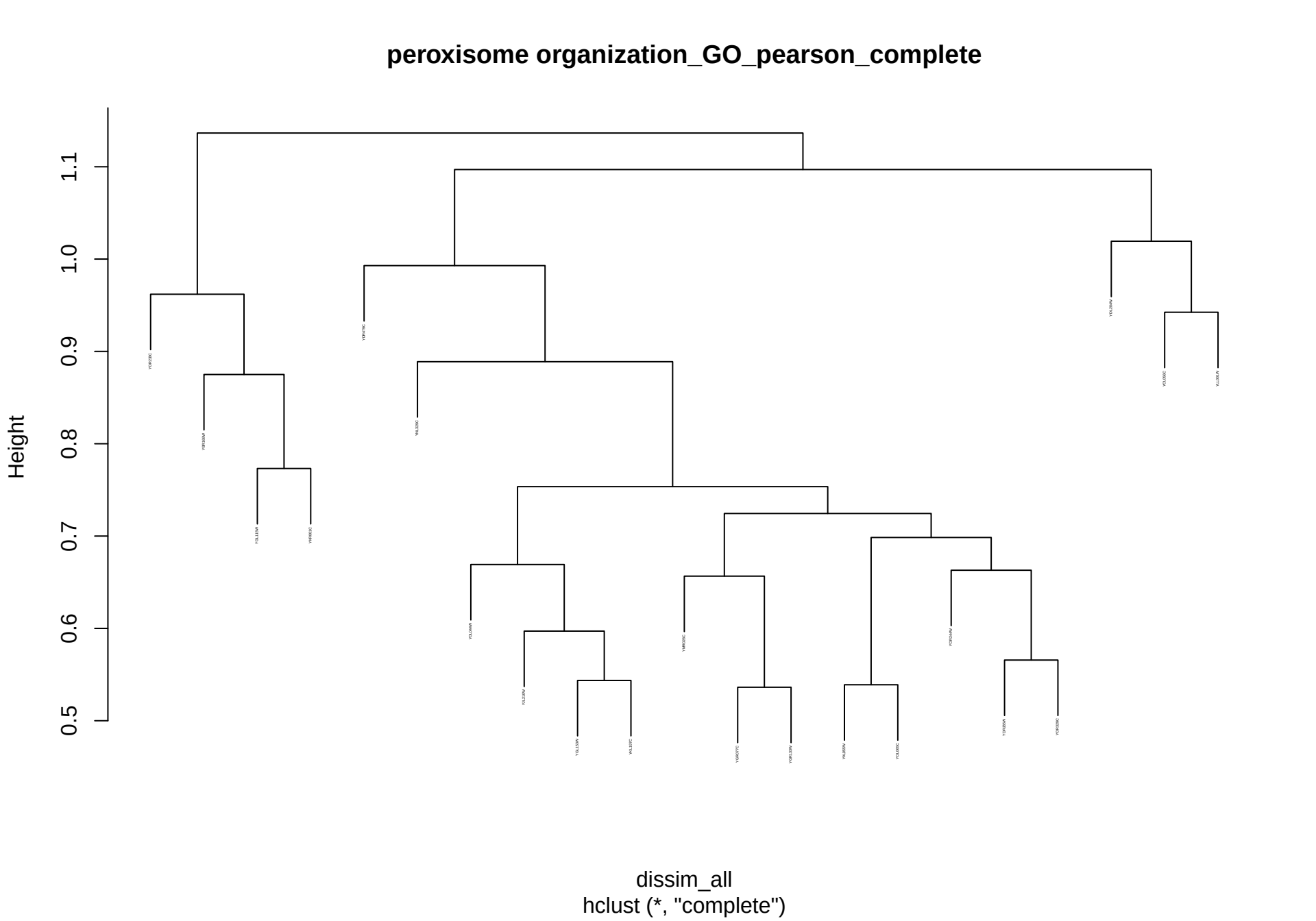

cytokinesis_GO_pearson_complete
Height
1.4
1.2
1.0
0.8
0.6
dissim_all
hclust (*, "complete")

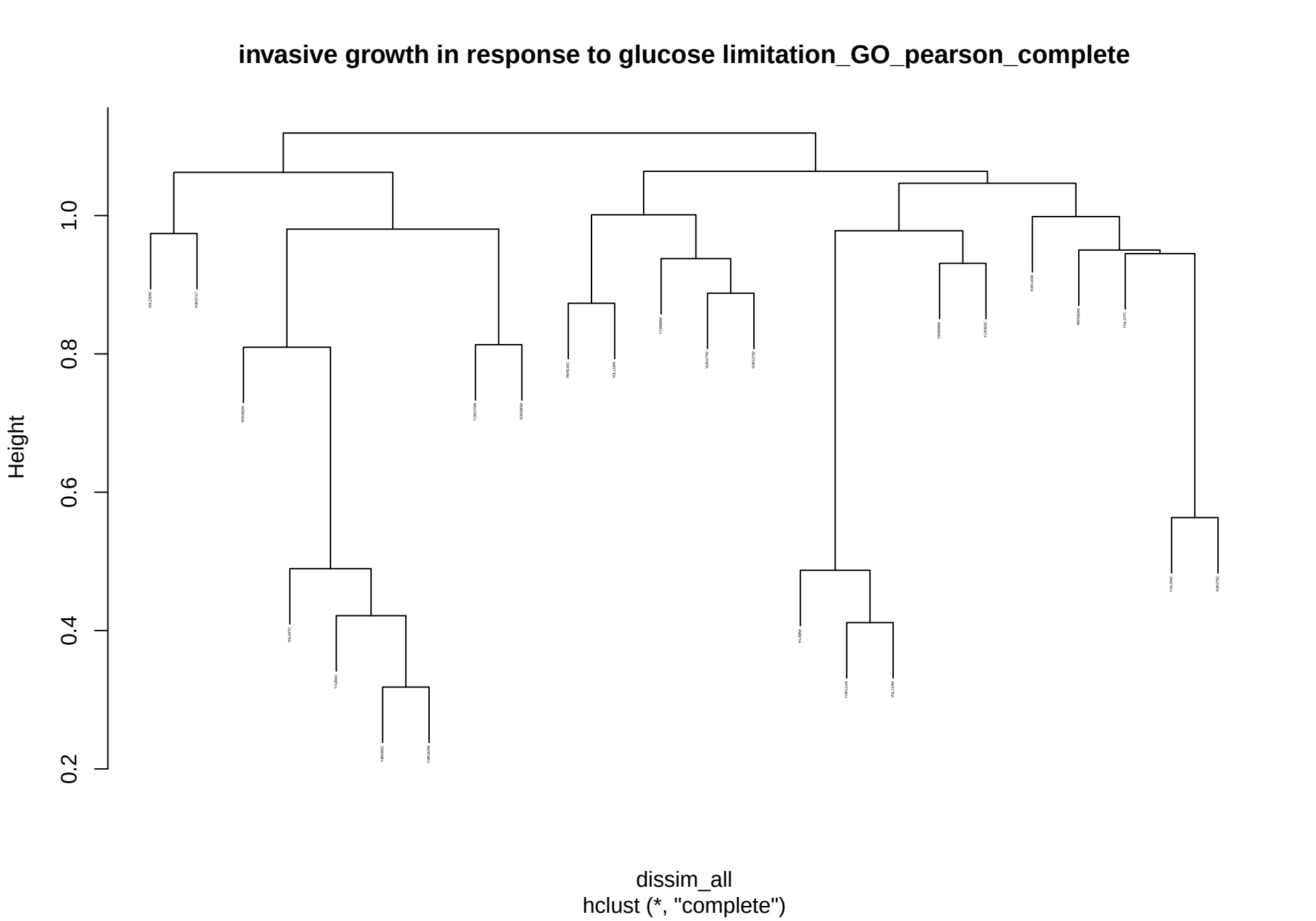

protein maturation_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

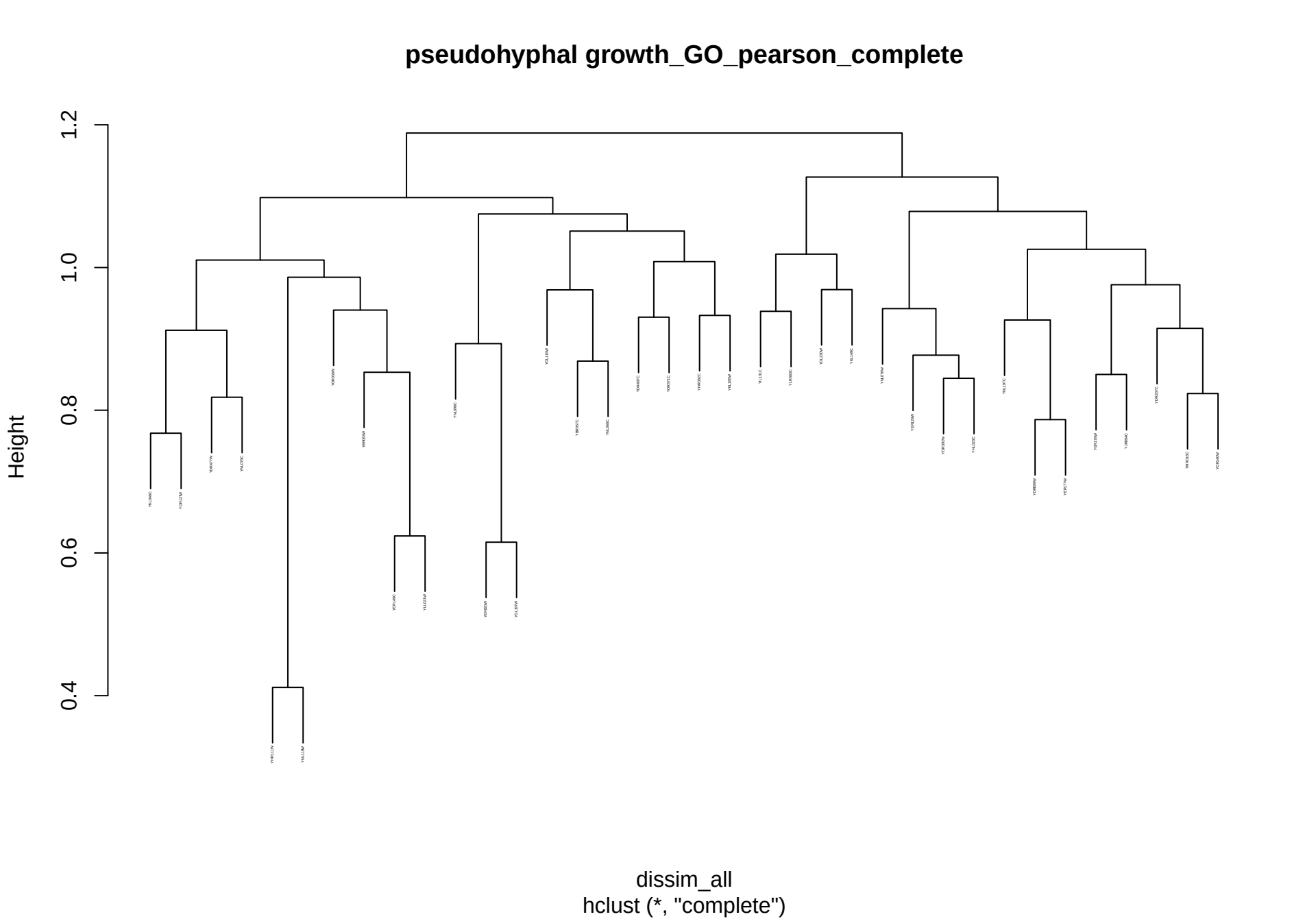

peptidyl−amino acid modification_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

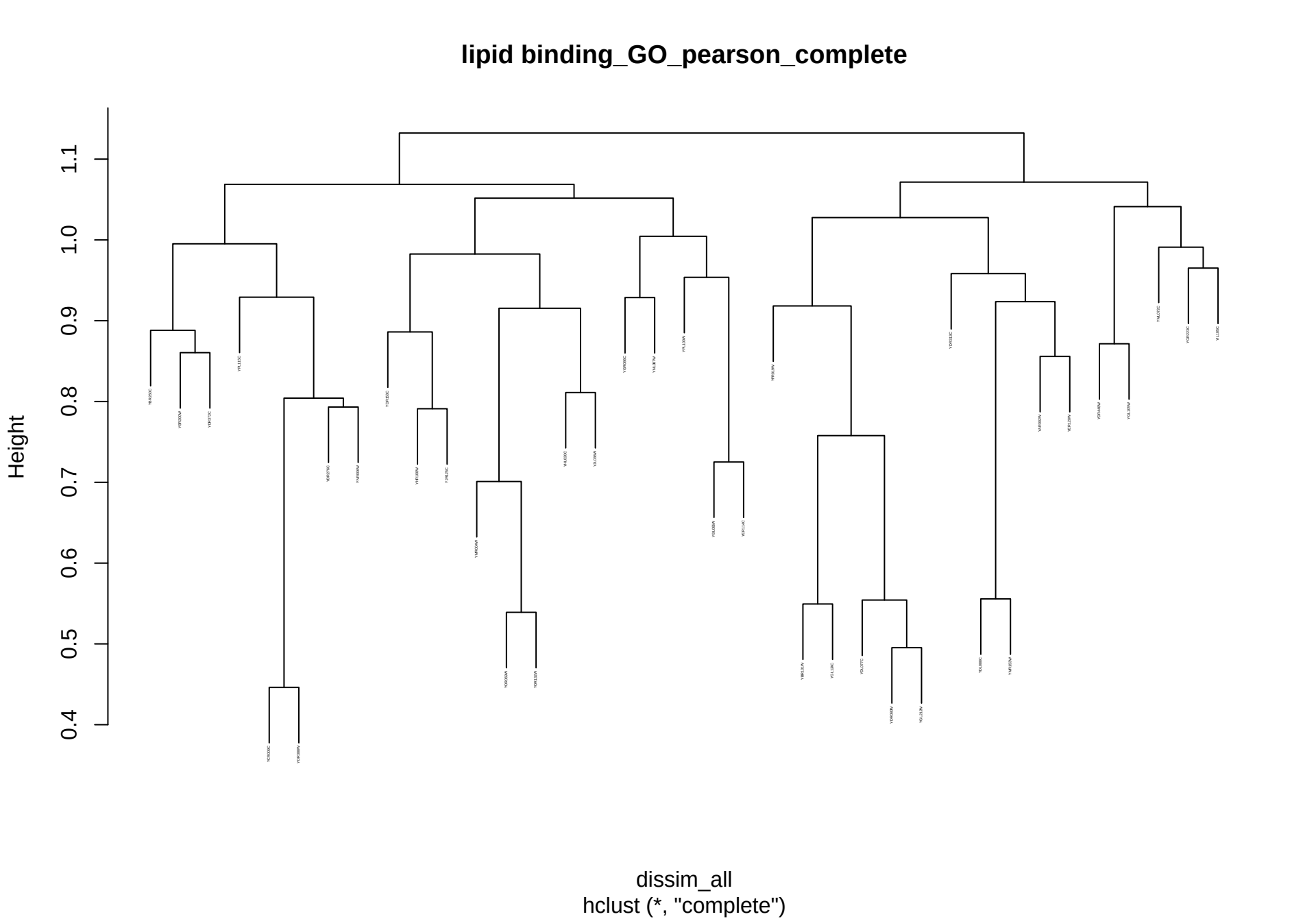

protein acylation_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

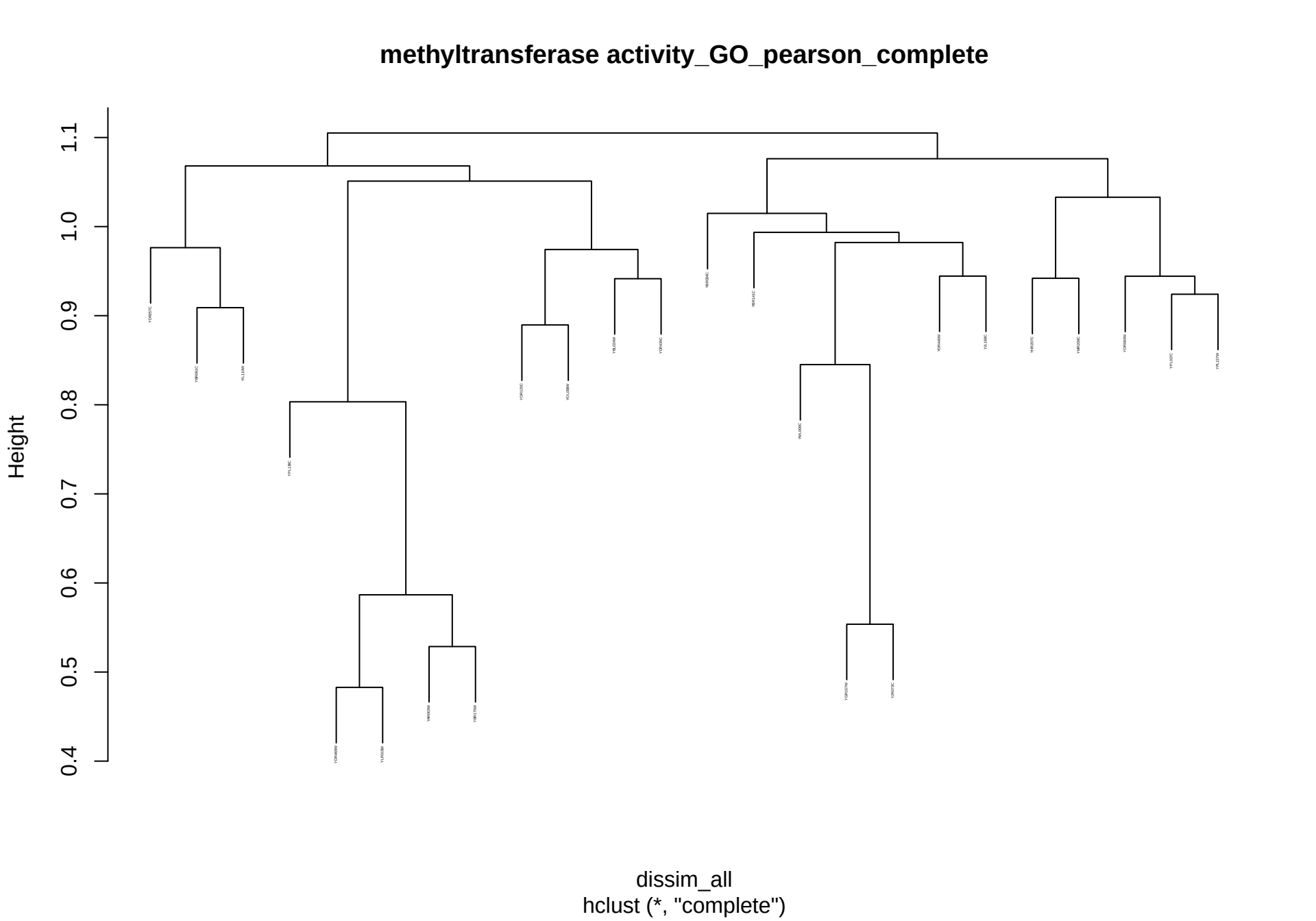

peroxisome_GO_pearson_complete
Height
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

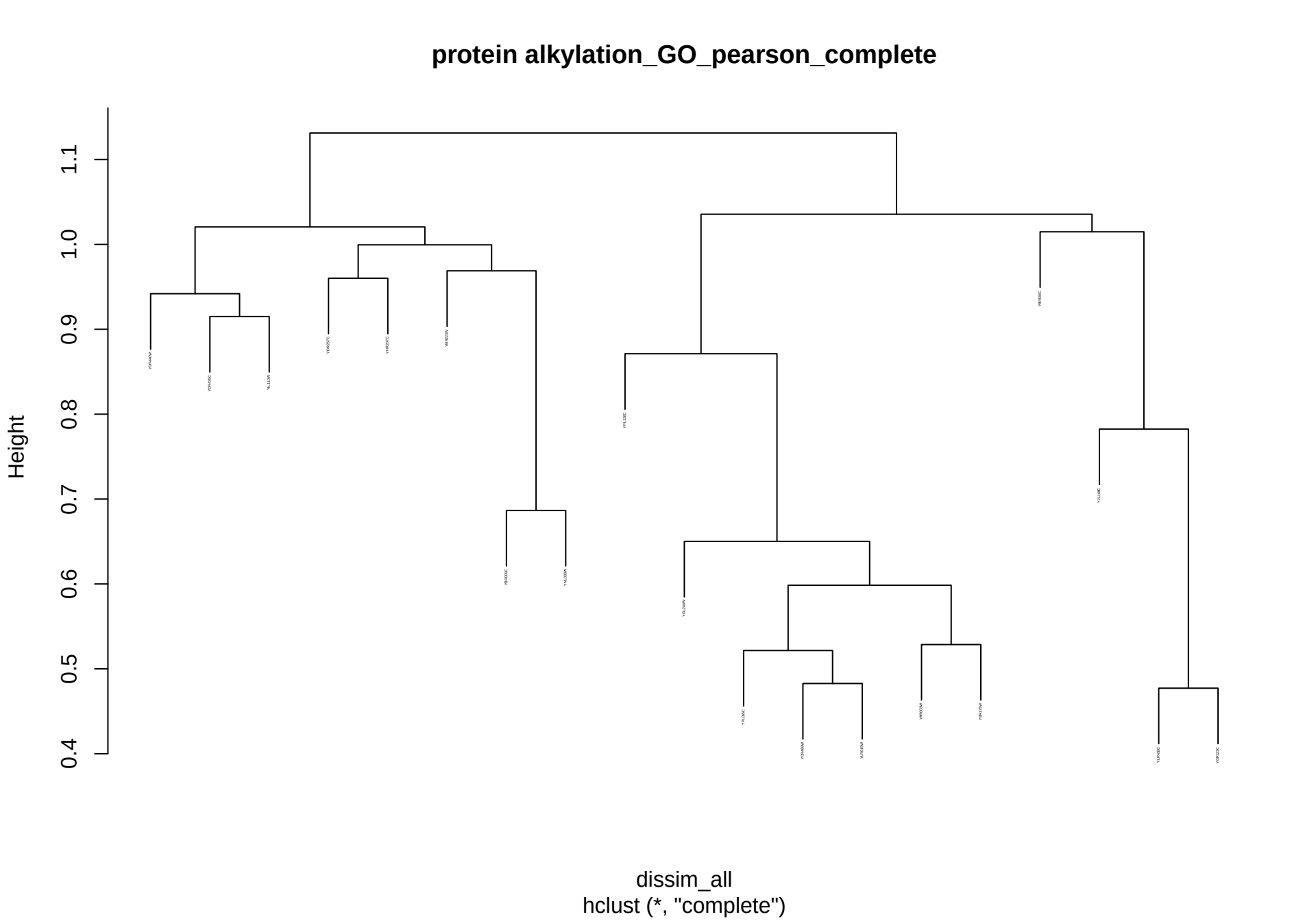

peroxisome organization_GO_pearson_complete
Height
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

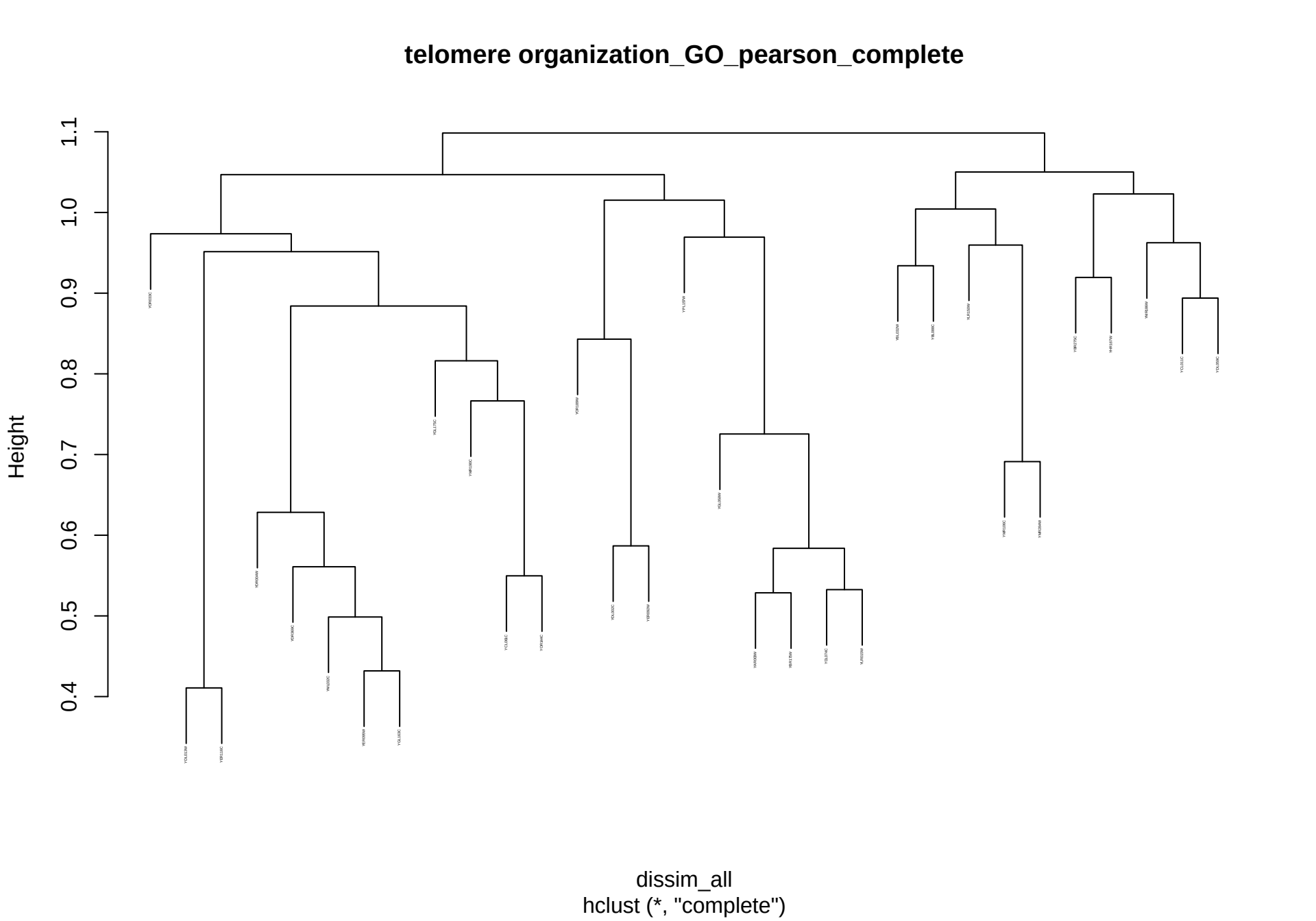

invasive growth in response to glucose limitation_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")

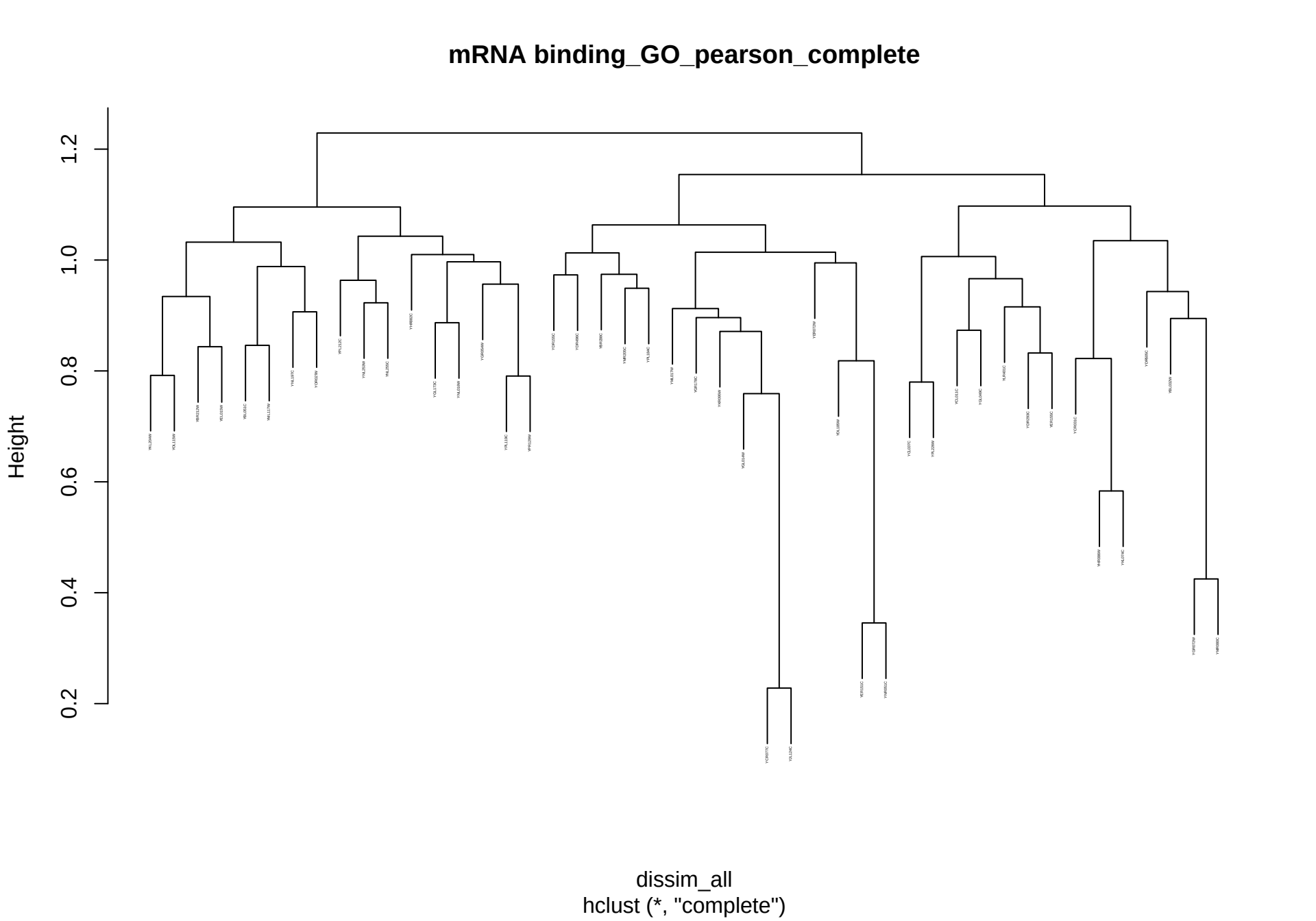

pseudohyphal growth_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

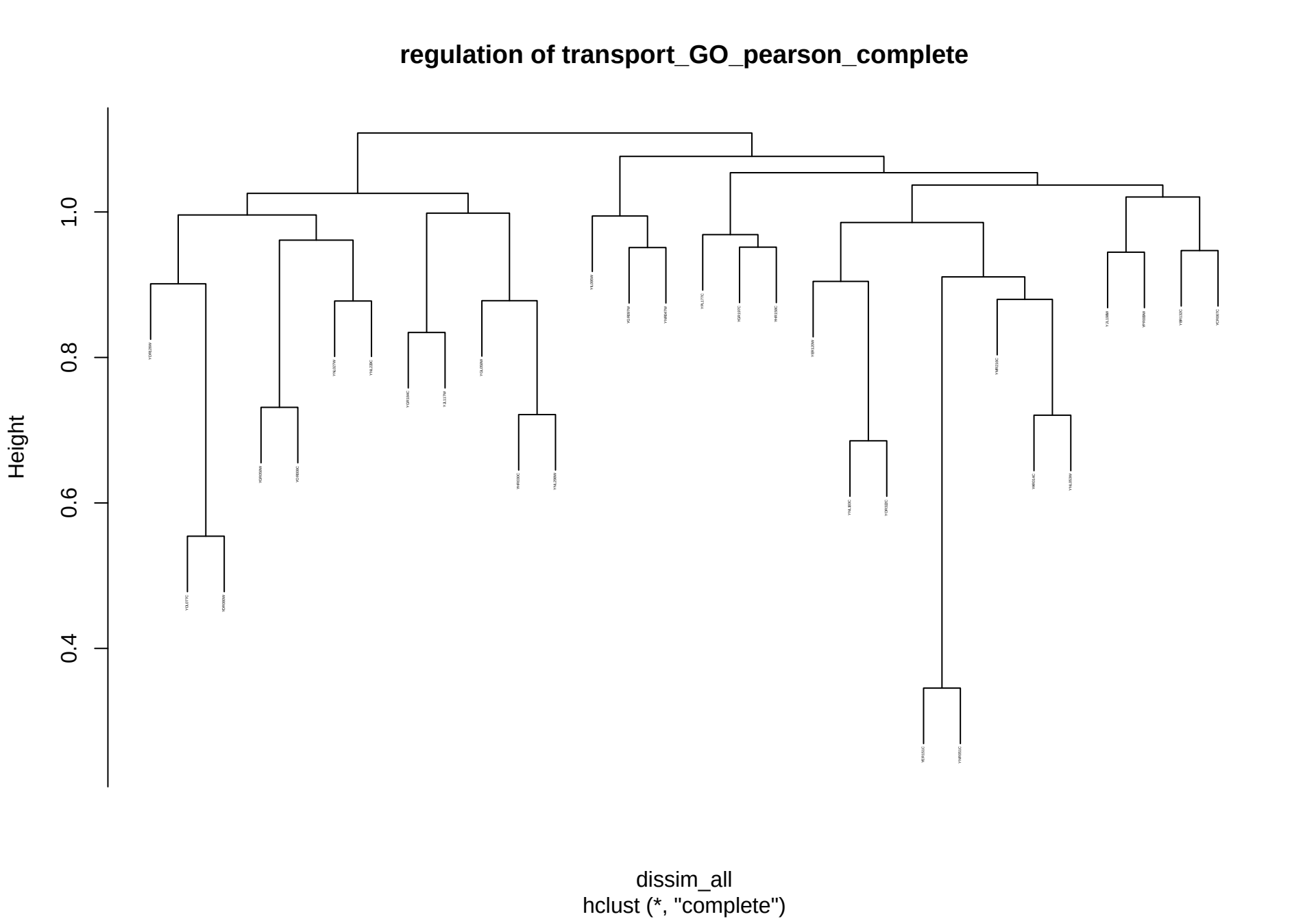

lipid binding_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

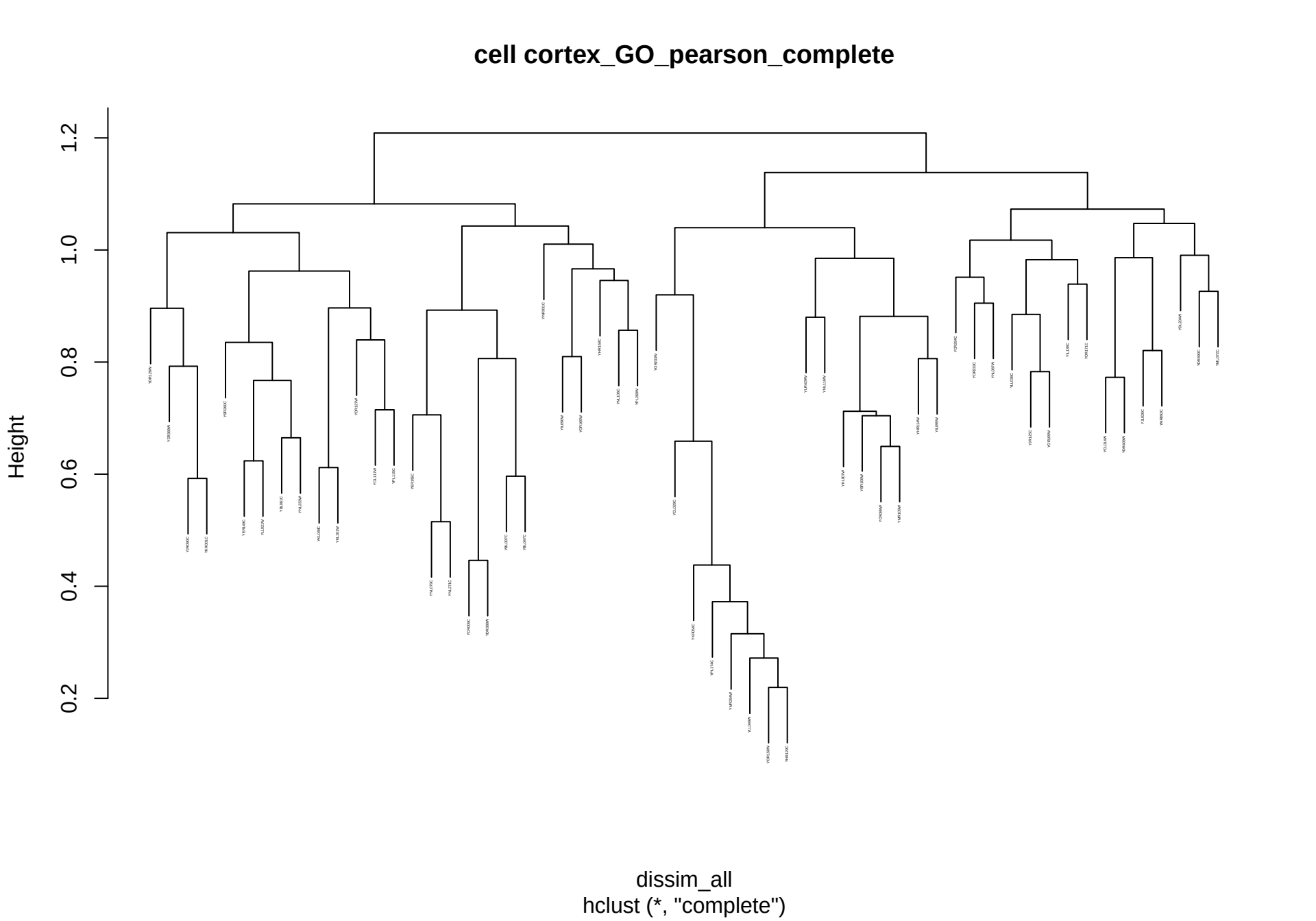

methyltransferase activity_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
dissim_all
hclust (*, "complete")

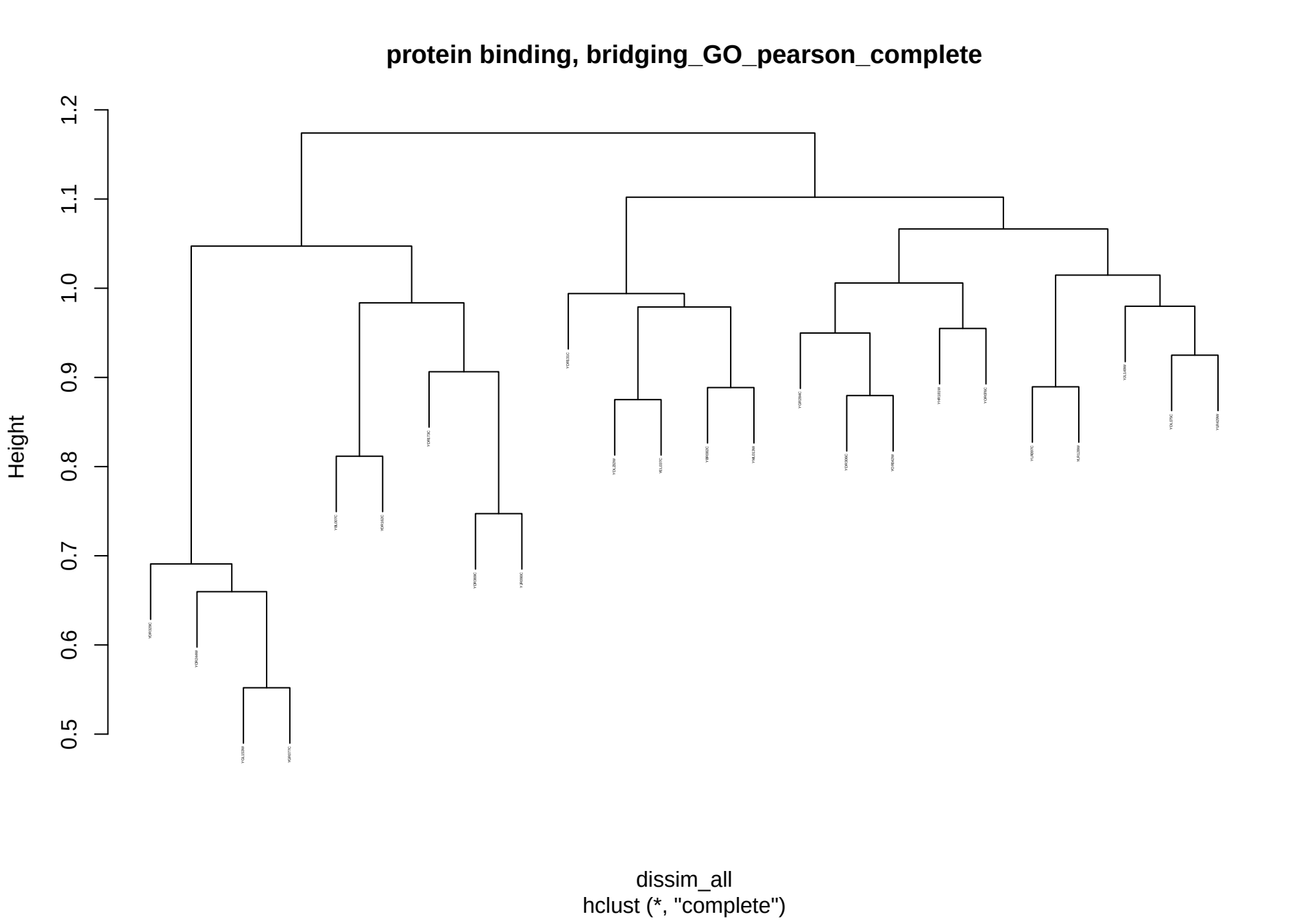

protein alkylation_GO_pearson_complete
Height
0.4
0.5
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

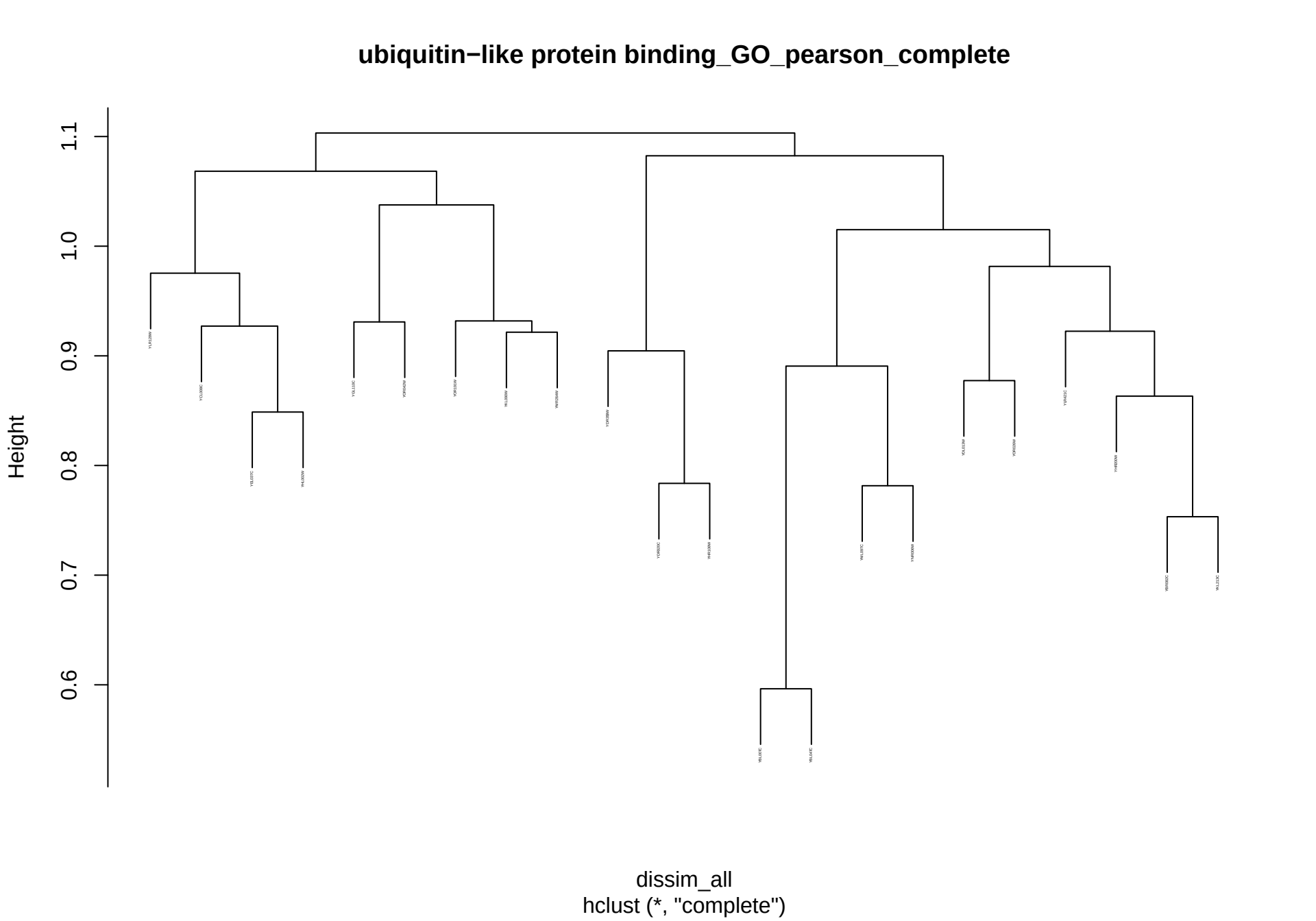

telomere organization_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
dissim_all
hclust (*, "complete")

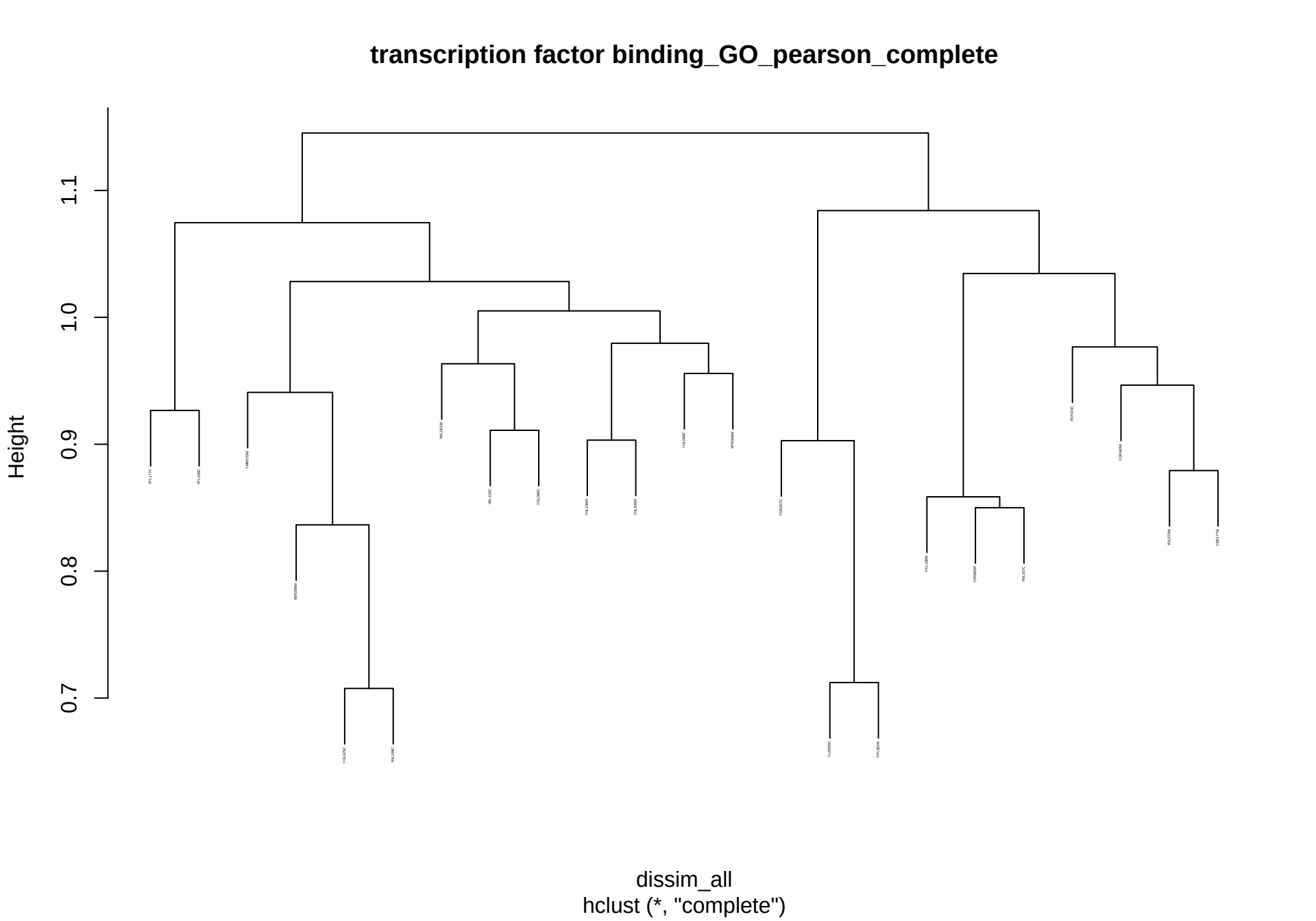

mRNA binding_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

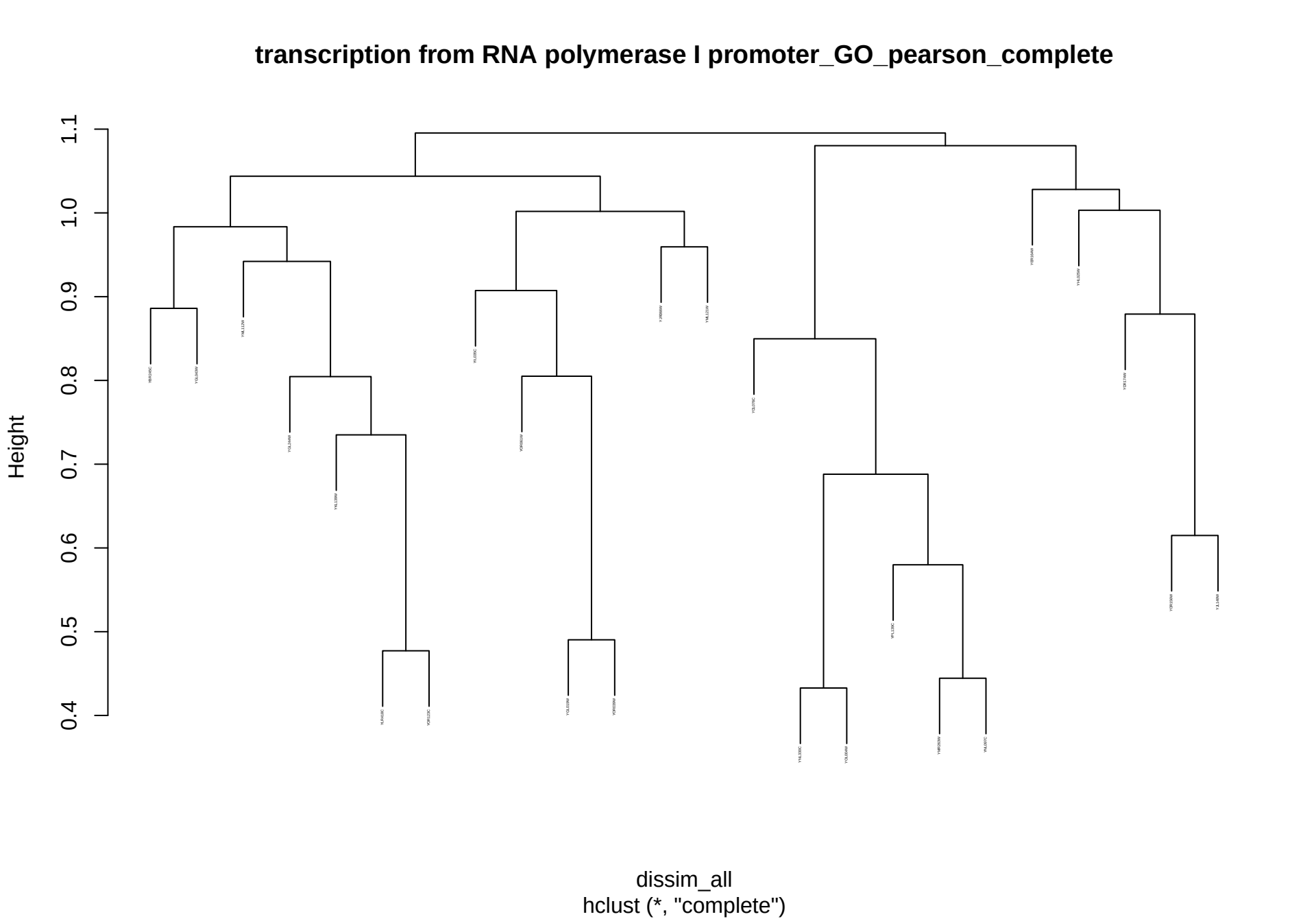

regulation of transport_GO_pearson_complete
Height
1.0
0.8
0.6
0.4
dissim_all
hclust (*, "complete")

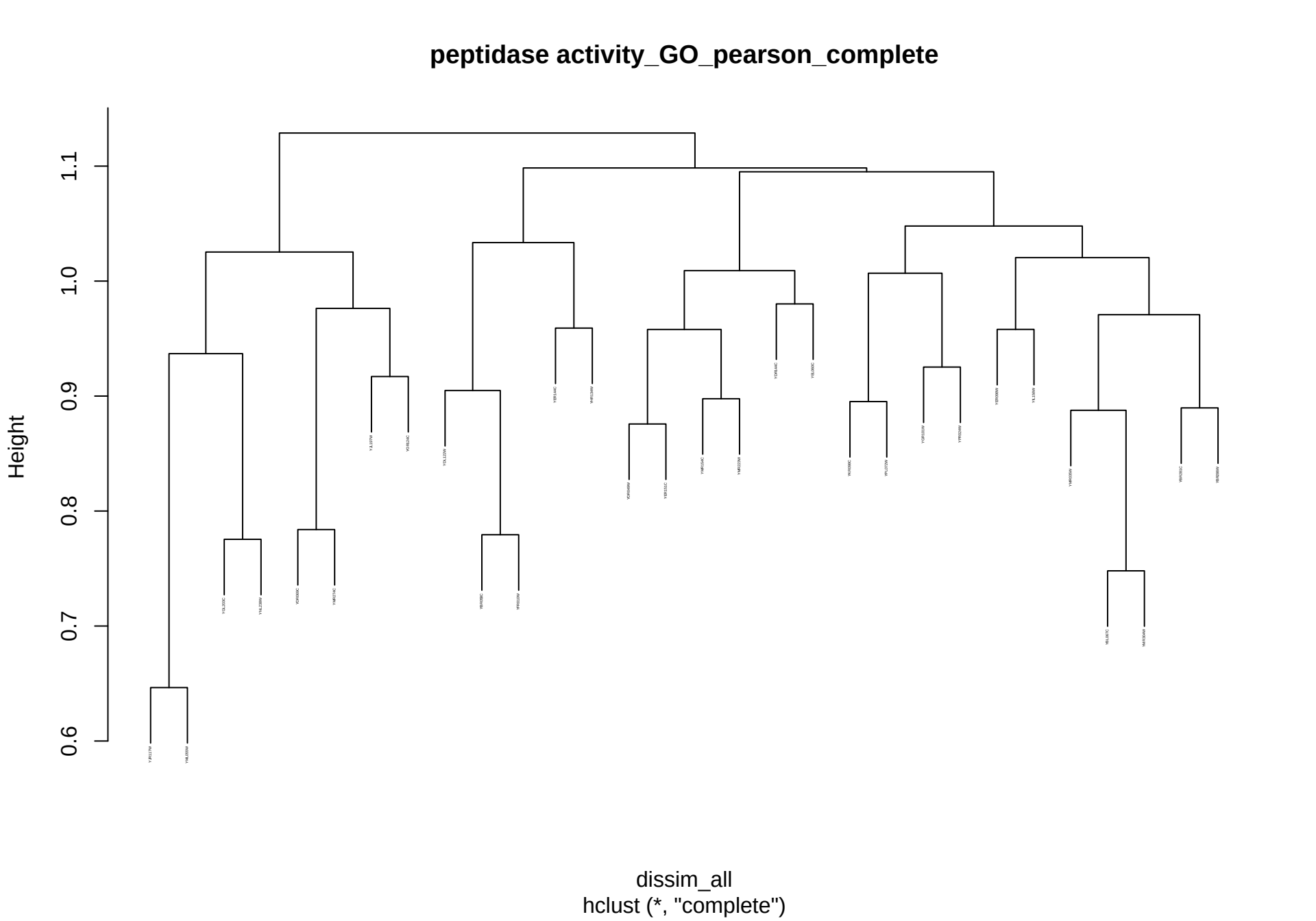

cell cortex_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

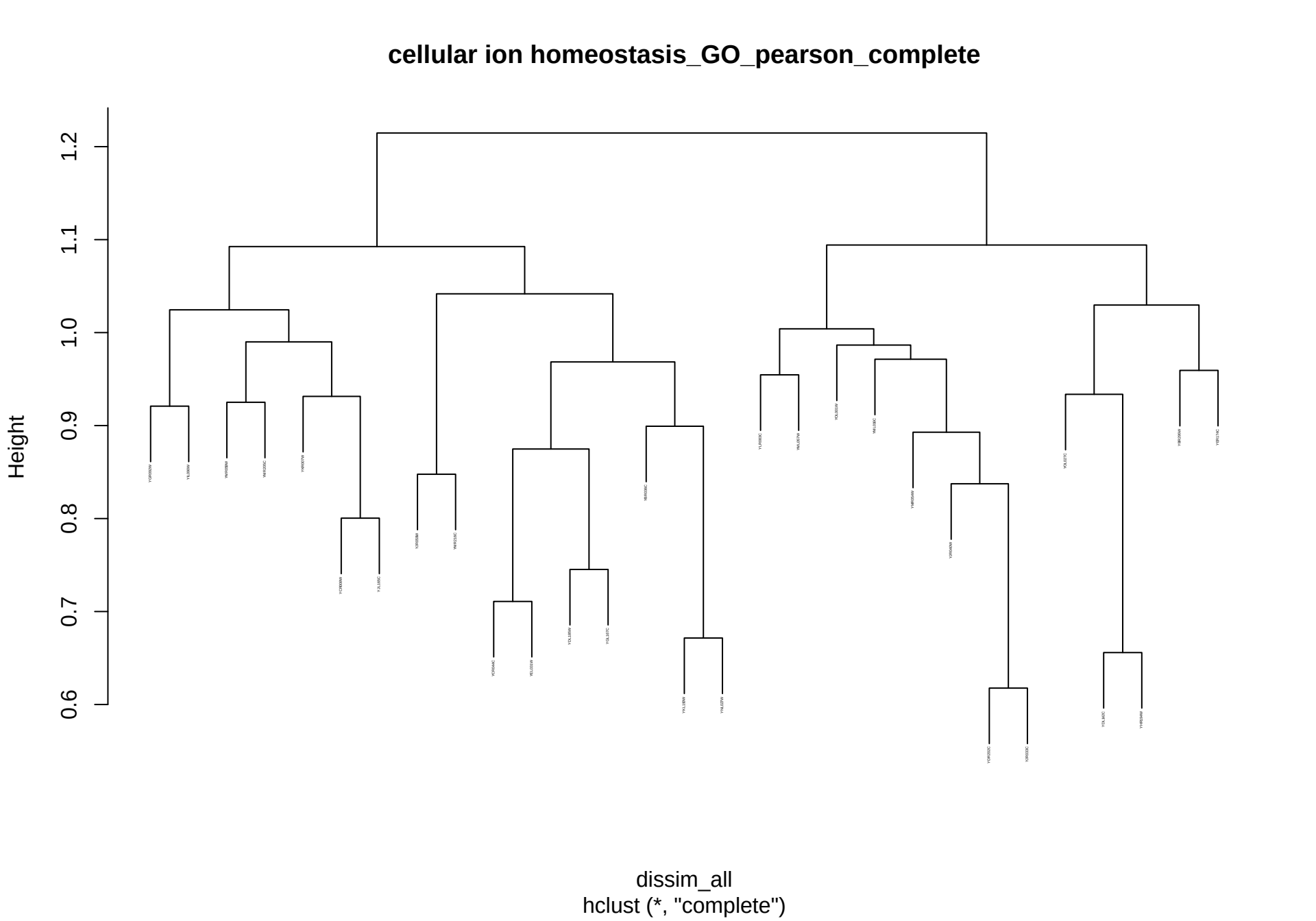

protein binding, bridging_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
dissim_all
hclust (*, "complete")

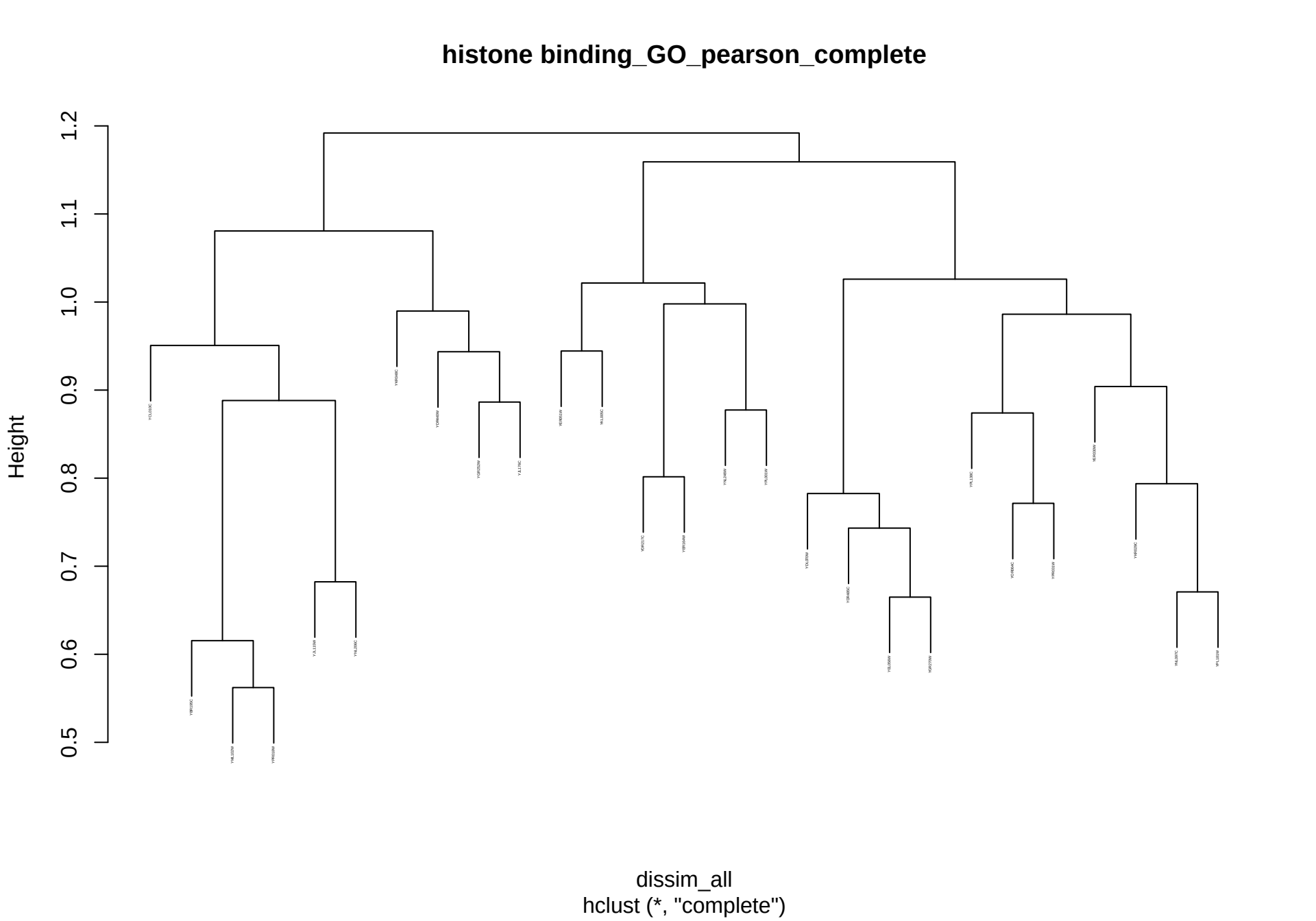

ubiquitin−like protein binding_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
dissim_all
hclust (*, "complete")

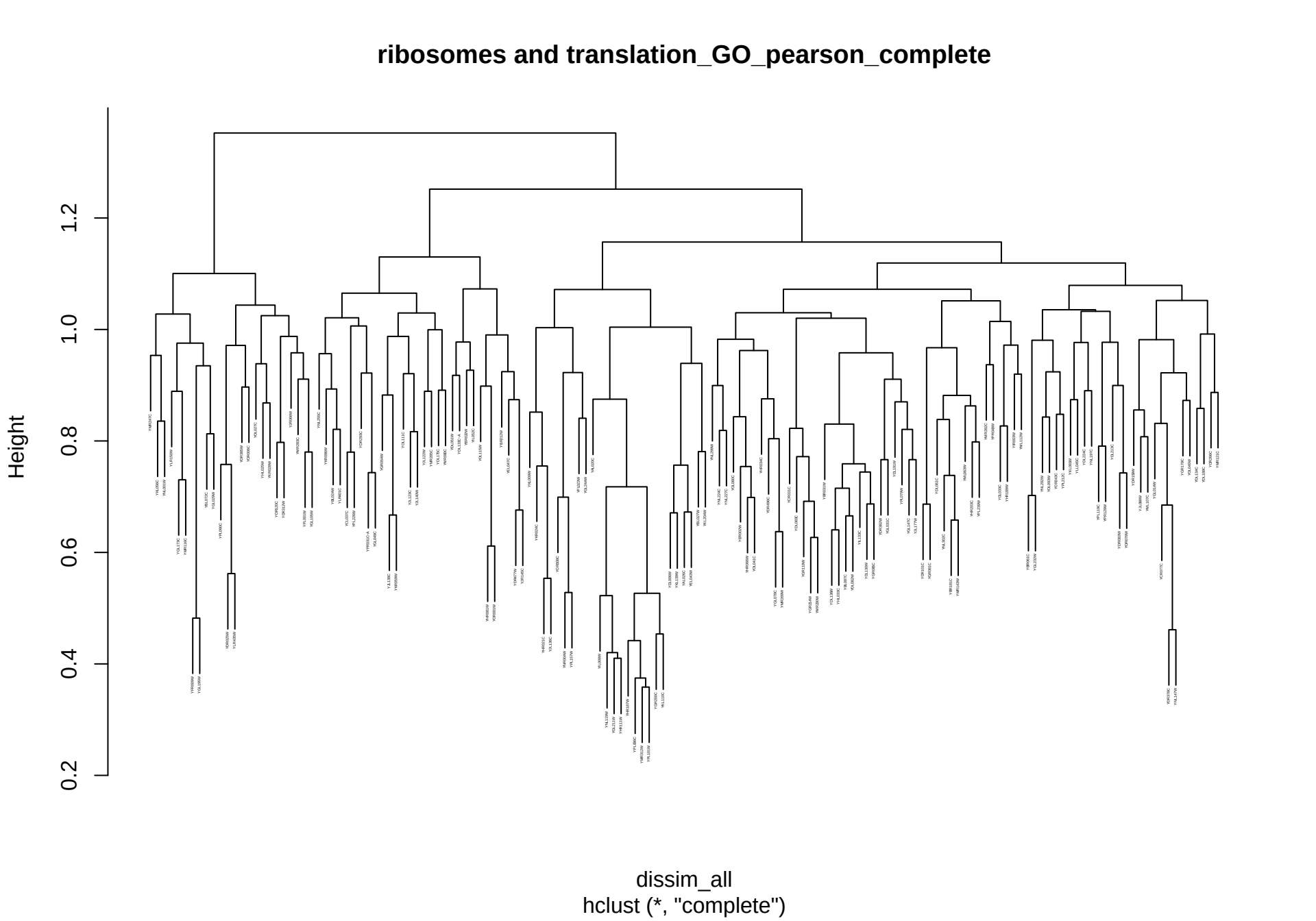

transcription factor binding_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
dissim_all
hclust (*, "complete")


transcription from RNA polymerase I promoter_GO_pearson_complete
Height
1.1
1.0
0.9
0.8
0.7
0.6
0.5
0.4
dissim_all
hclust (*, "complete")

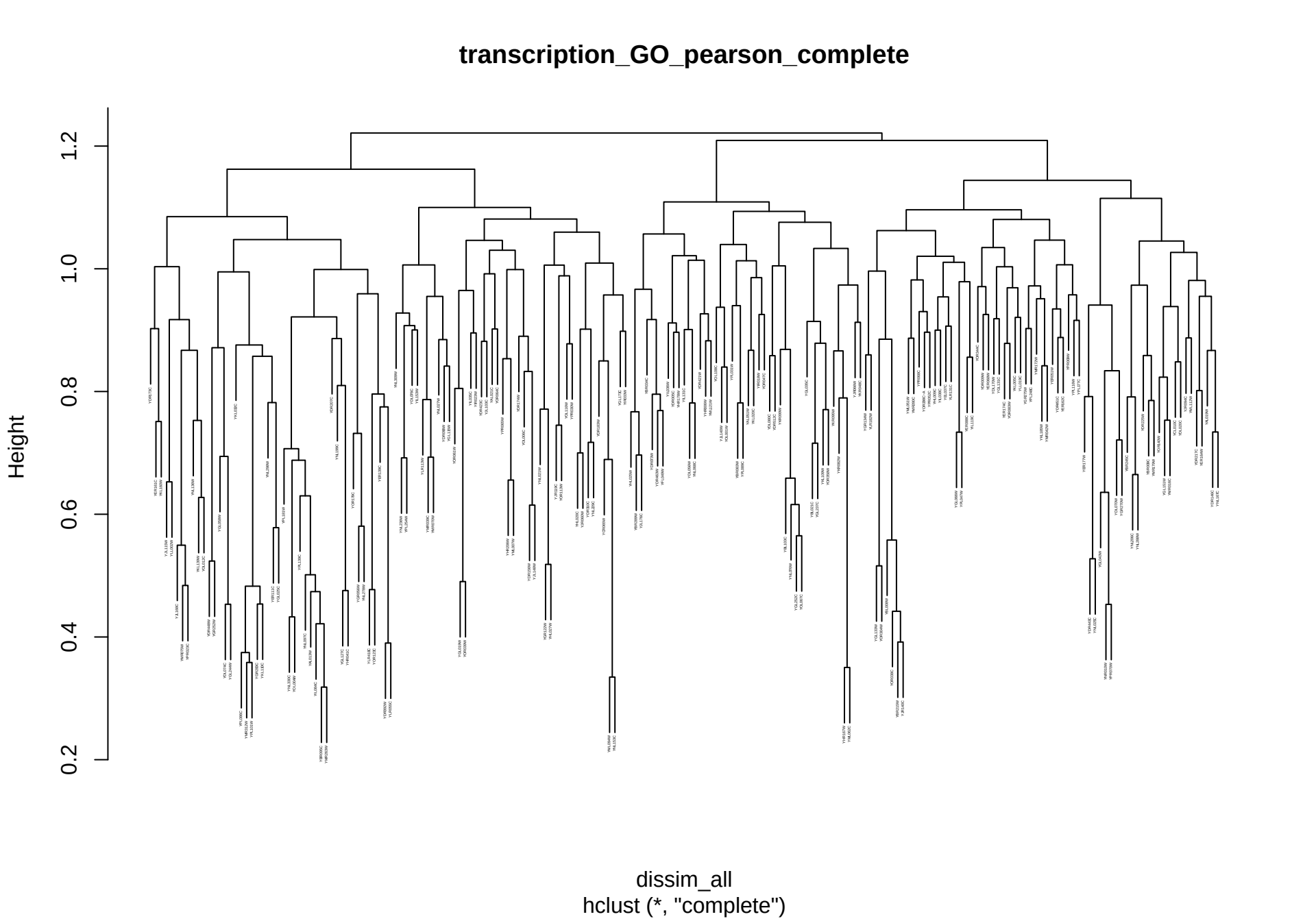

peptidase activity_GO_pearson_complete
Height
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")

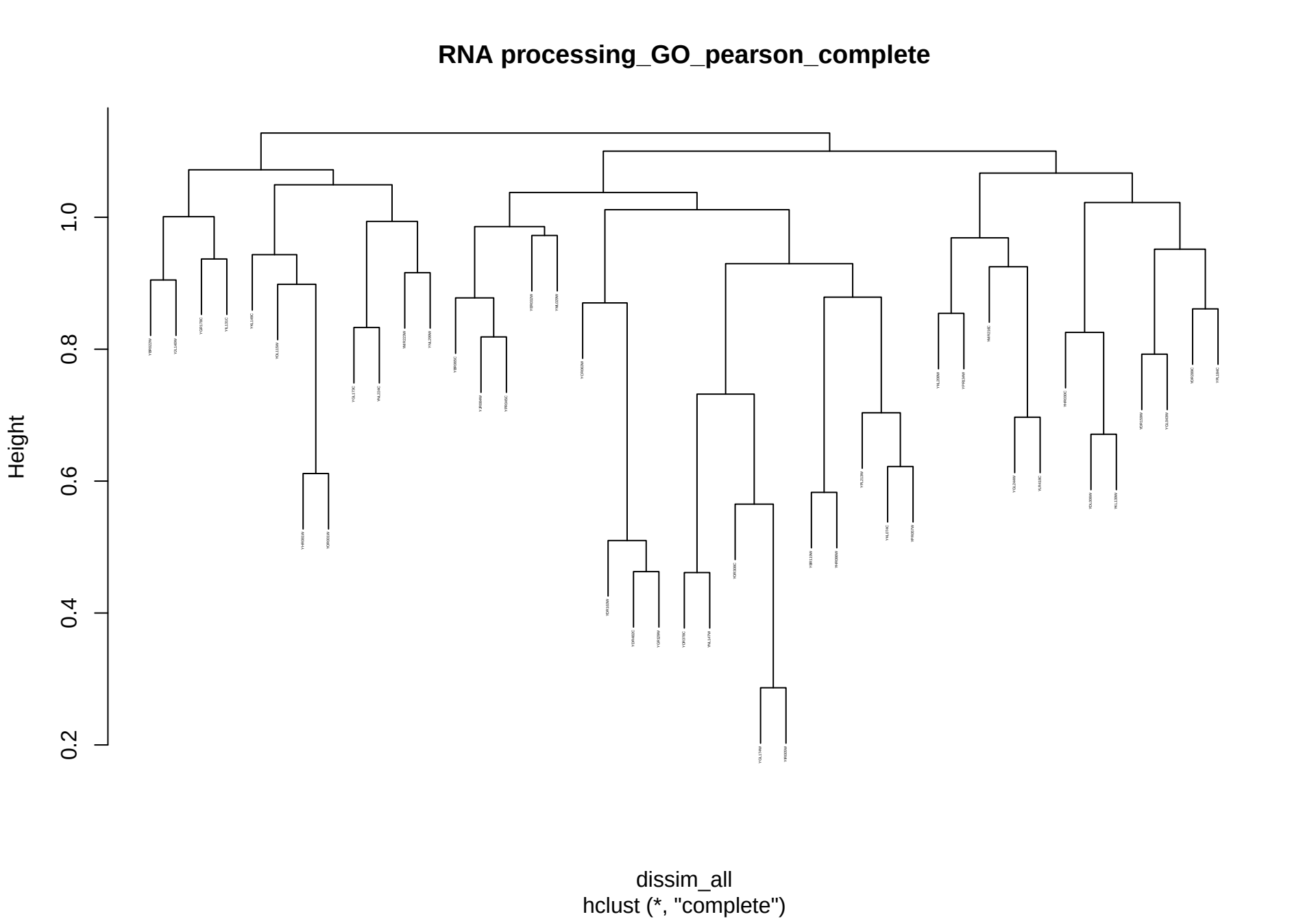

cellular ion homeostasis_GO_pearson_complete
Height
0.6
0.7
0.8
0.9
1.0
1.1
1.2
dissim_all
hclust (*, "complete")

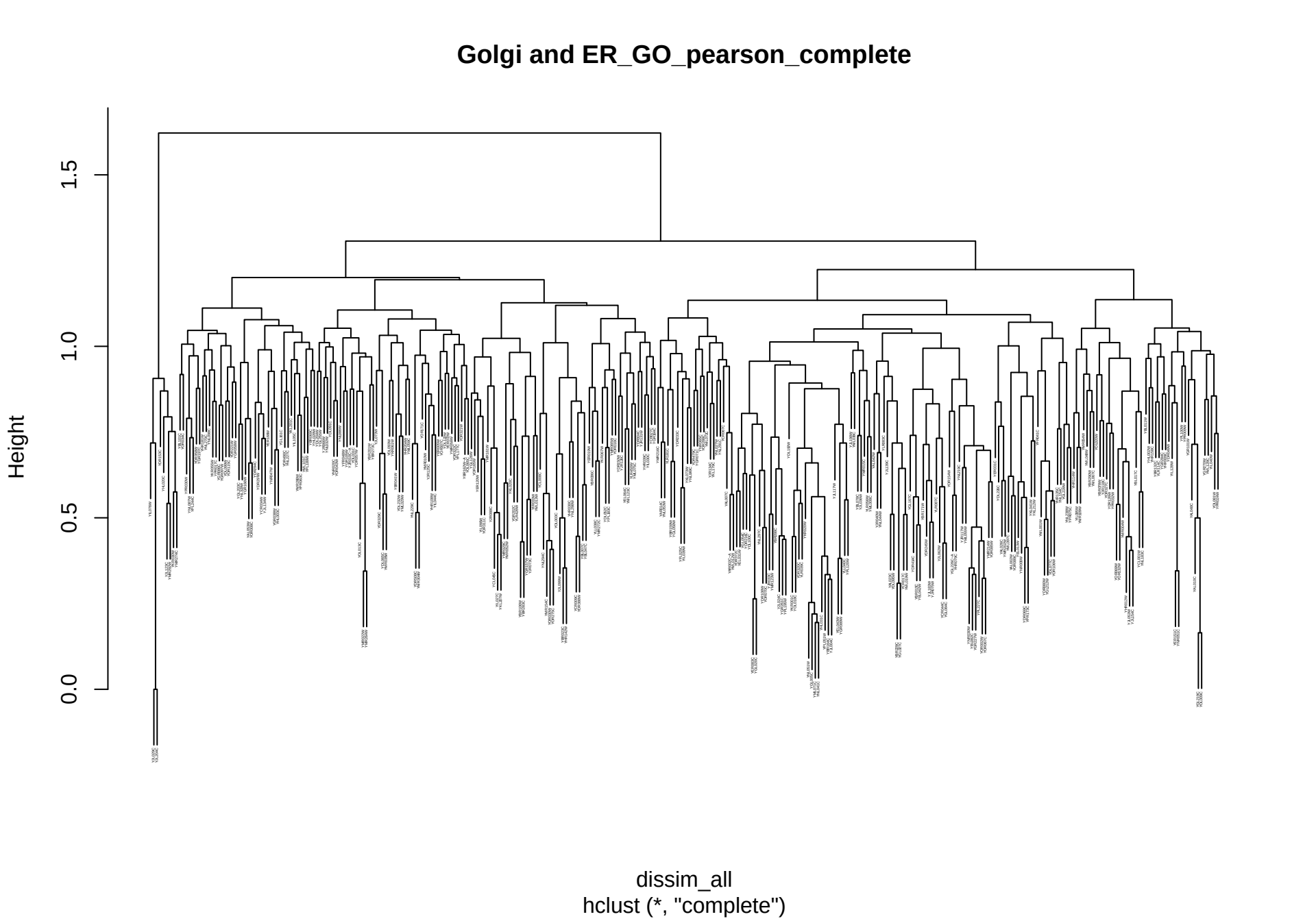

histone binding_GO_pearson_complete
Height
1.2
1.1
1.0
0.9
0.8
0.7
0.6
0.5
dissim_all
hclust (*, "complete")

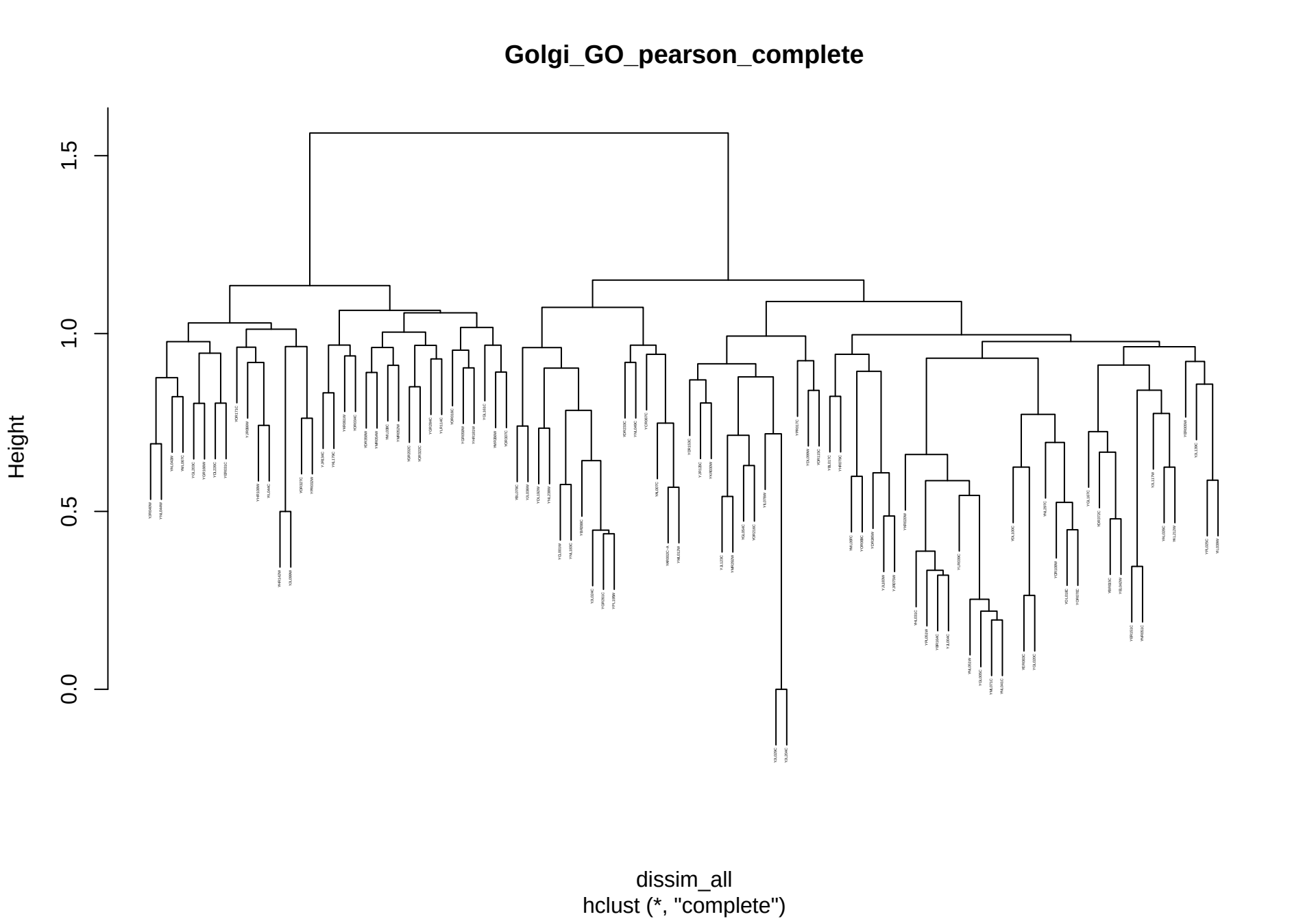

ribosomes and translation_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")

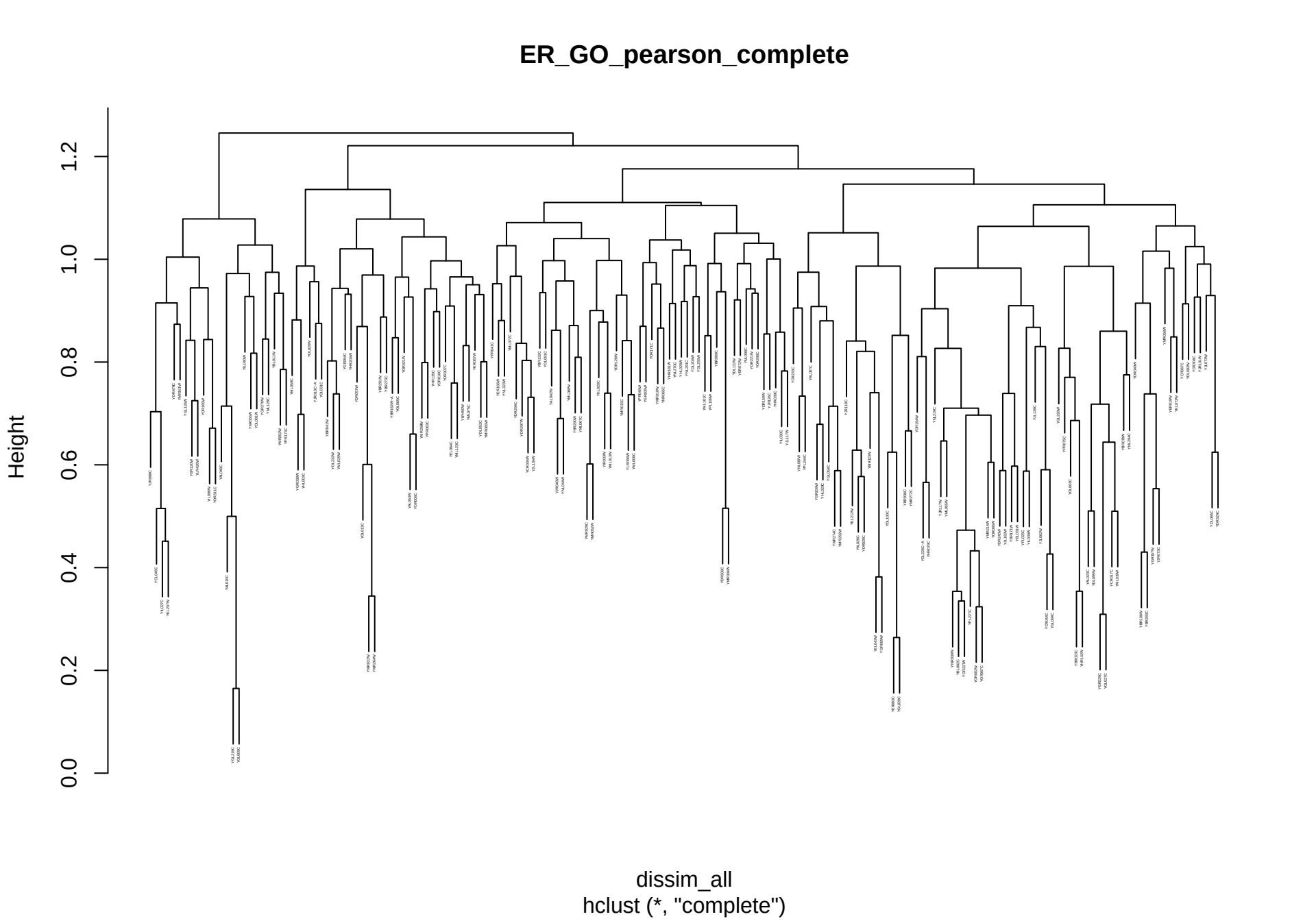
transcription and mRNA processing_GO_pearson_complete

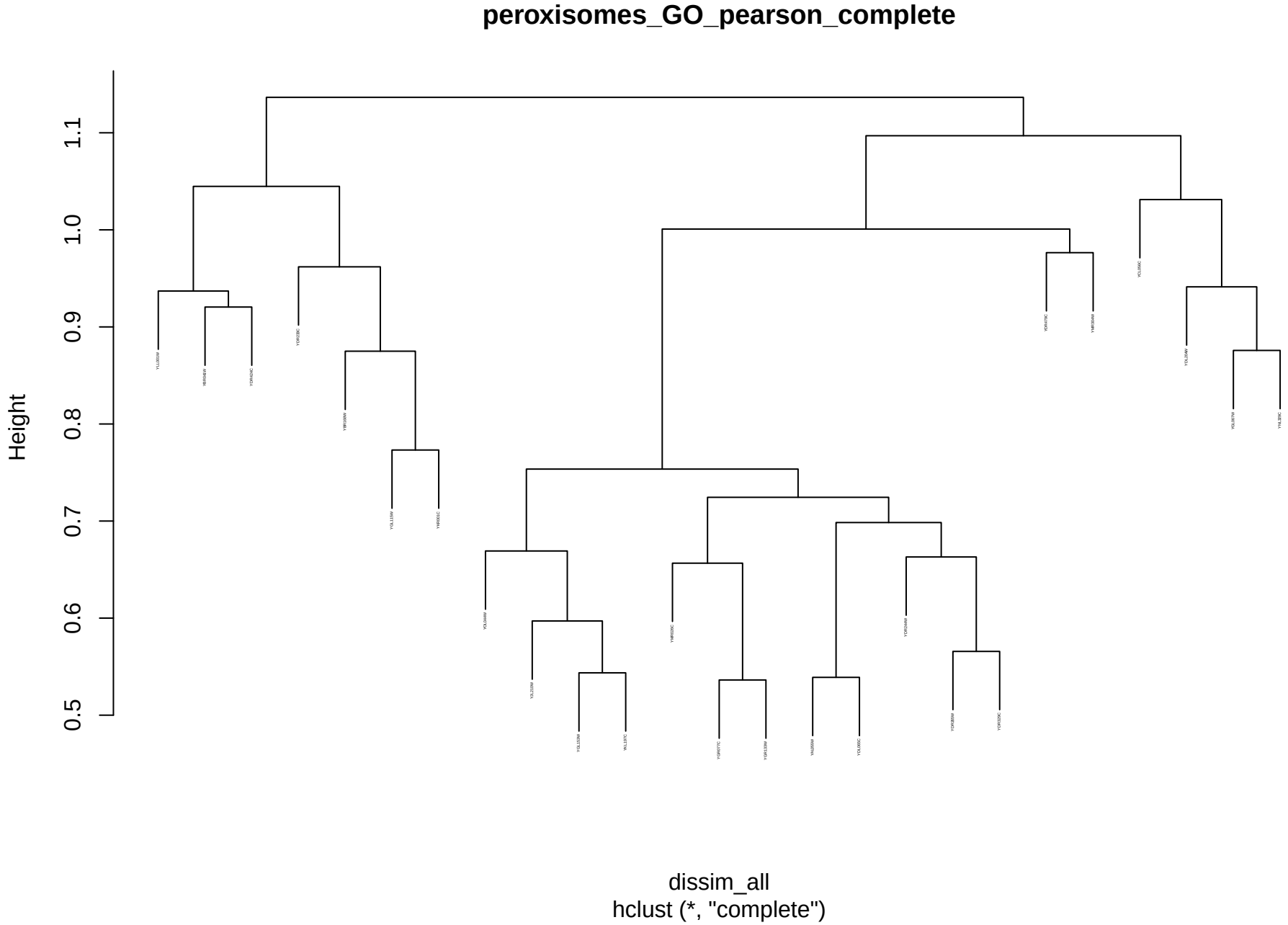

transcription_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


RNA processing_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
dissim_all
hclust (*, "complete")


Golgi and ER_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")


Golgi_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")


ER_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


peroxisomes_GO_pearson_complete
Height
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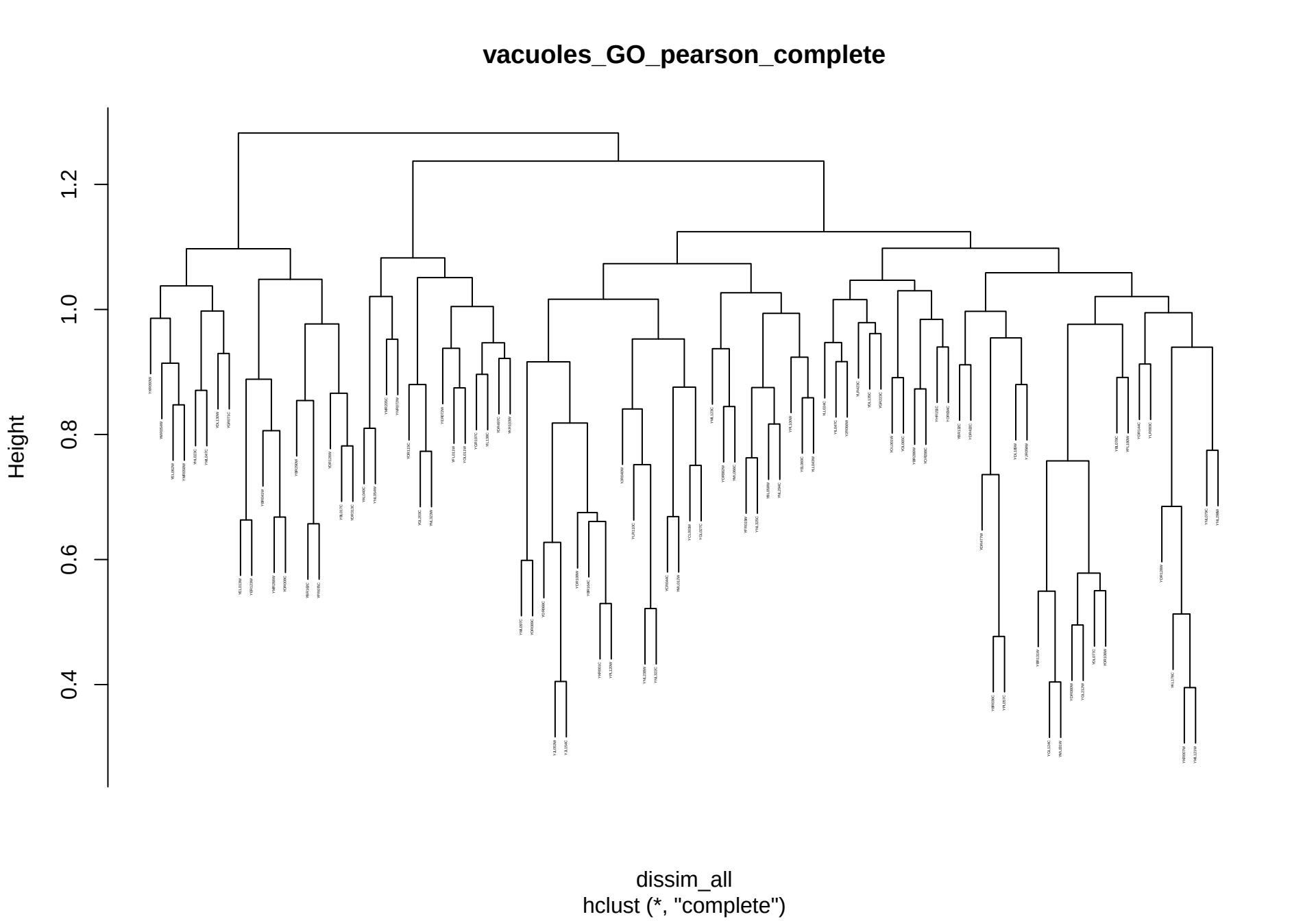
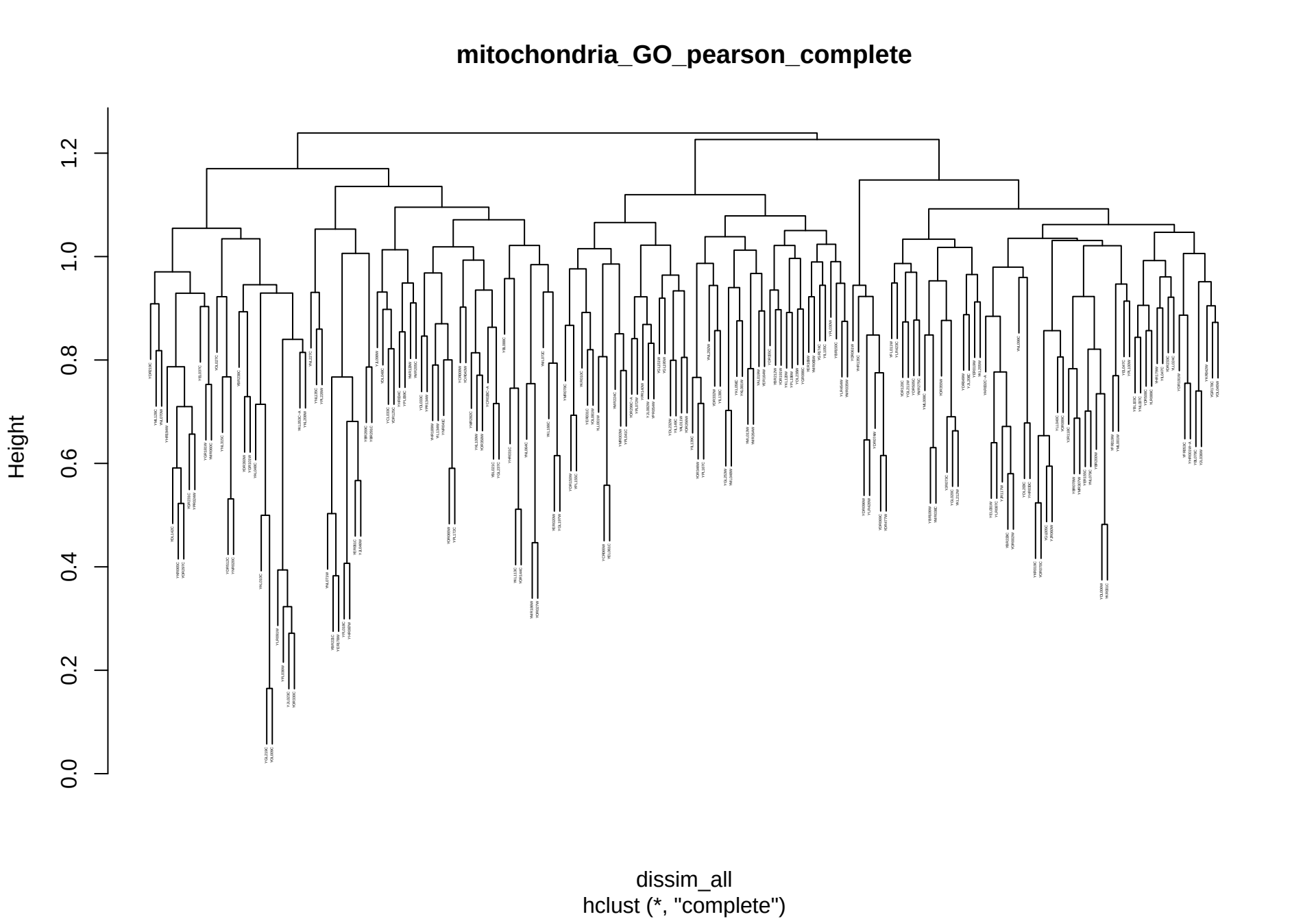
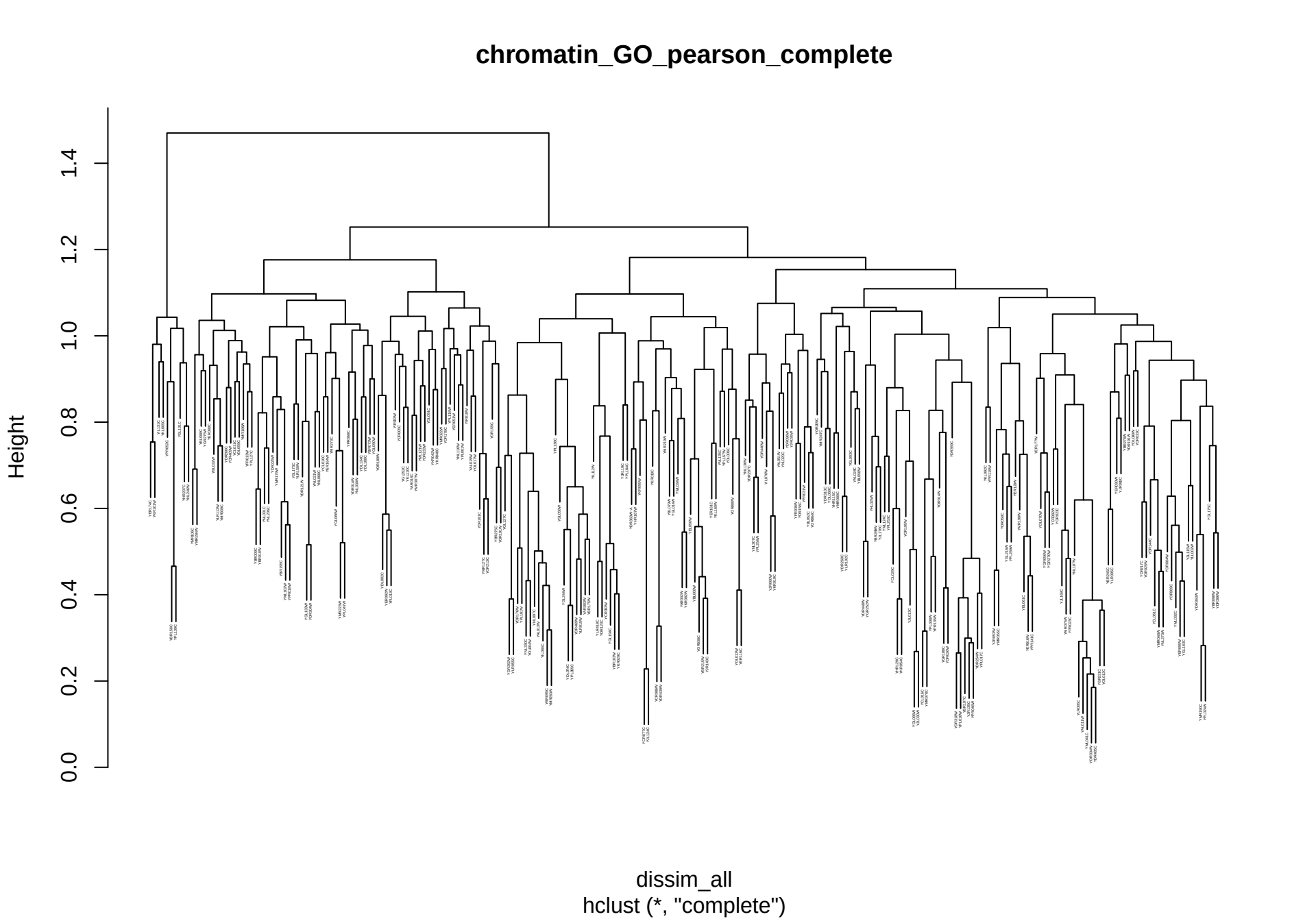
0.6
0.7
0.8
0.9
1.0
1.1
dissim_all
hclust (*, "complete")


vacuoles_GO_pearson_complete
Height
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


mitochondria_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


chromatin_GO_pearson_complete
Height
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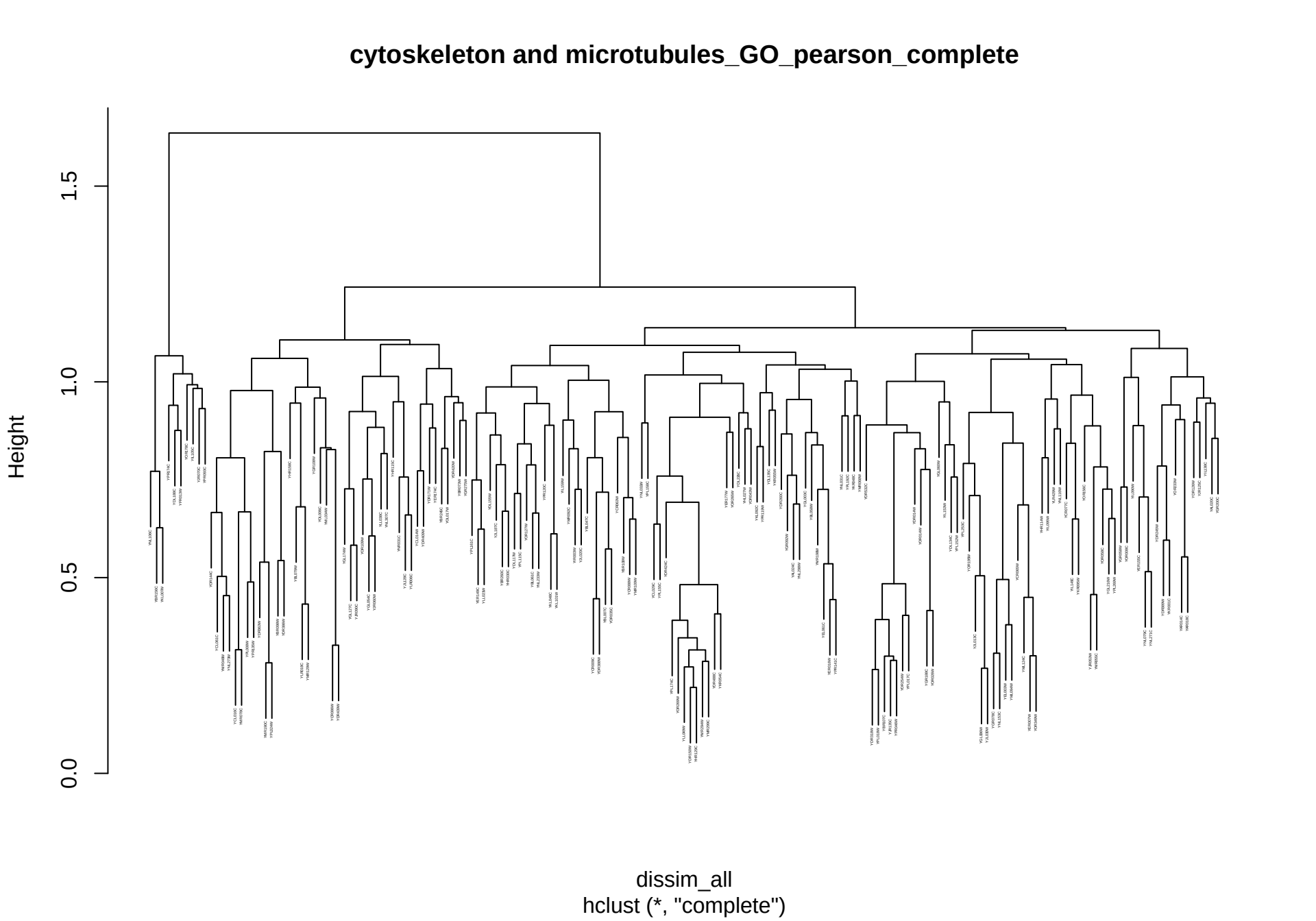
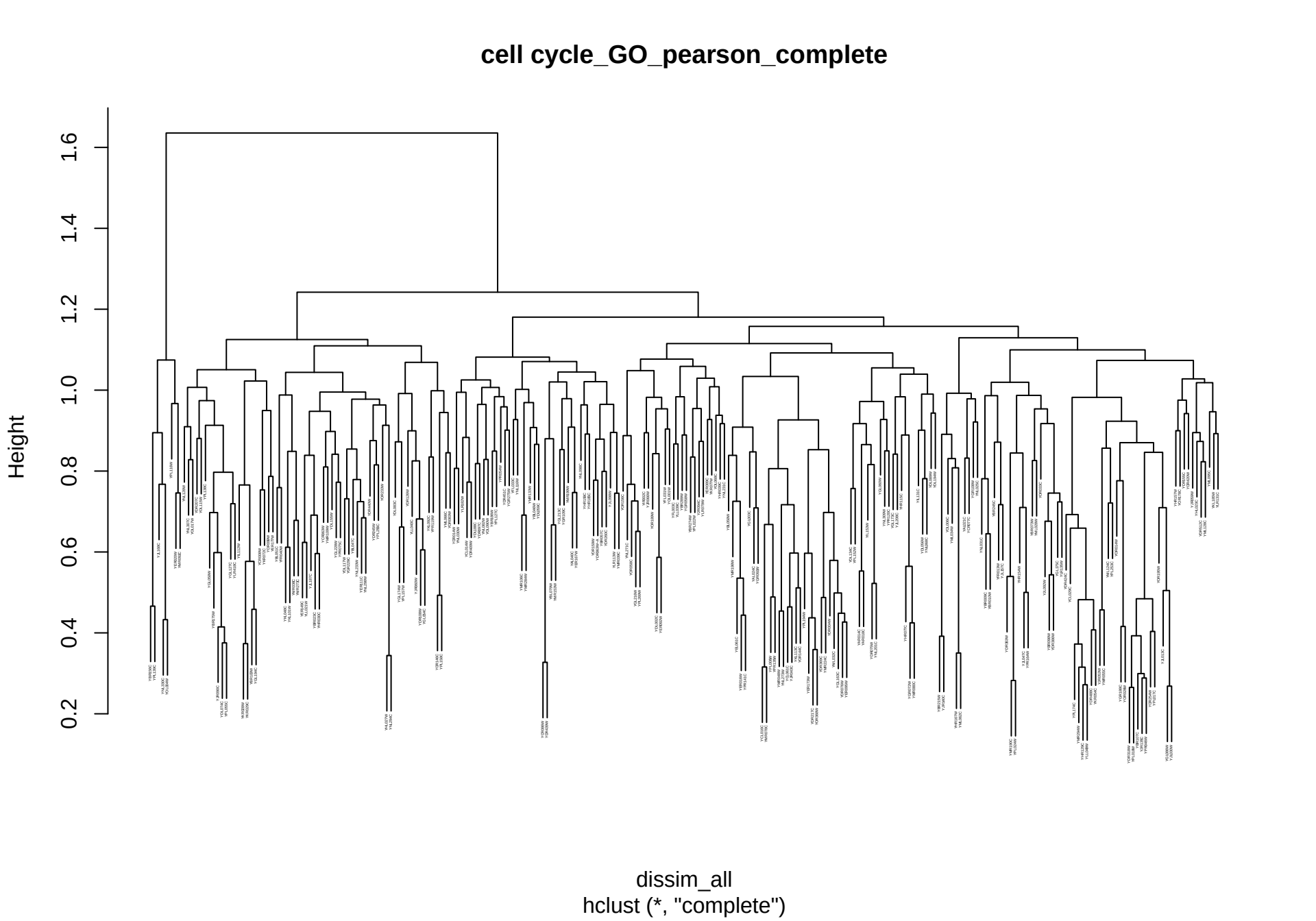
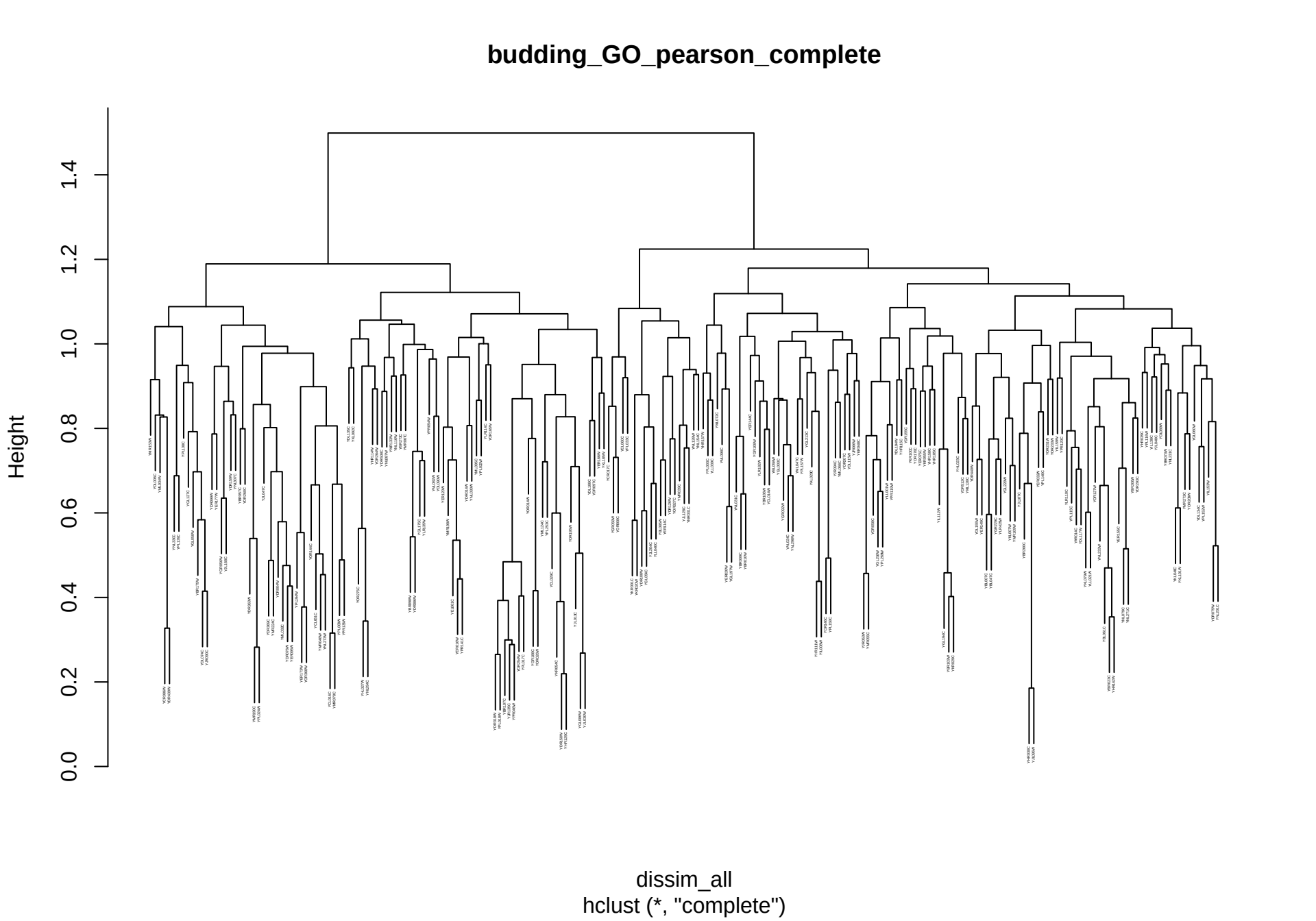
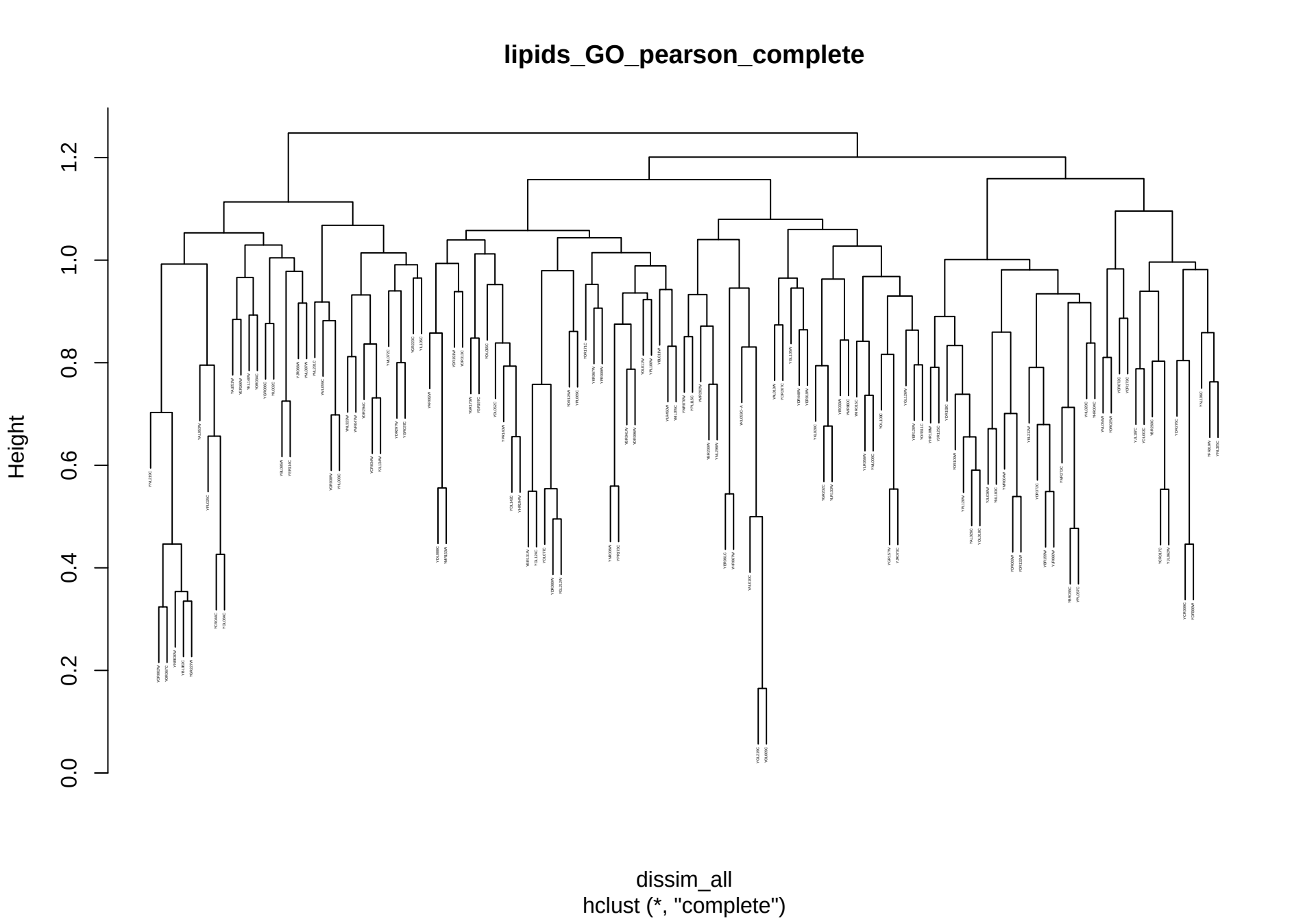
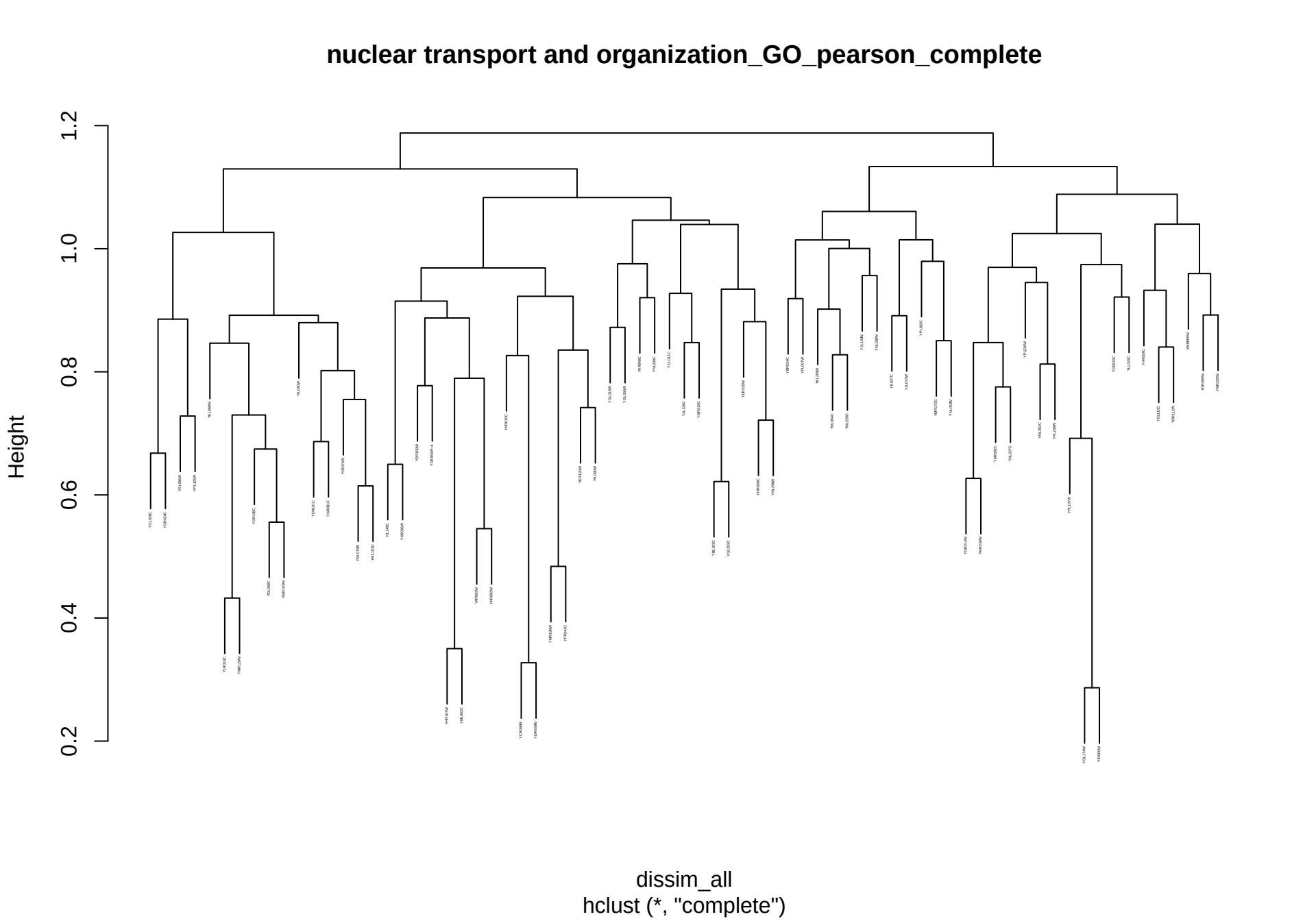
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")

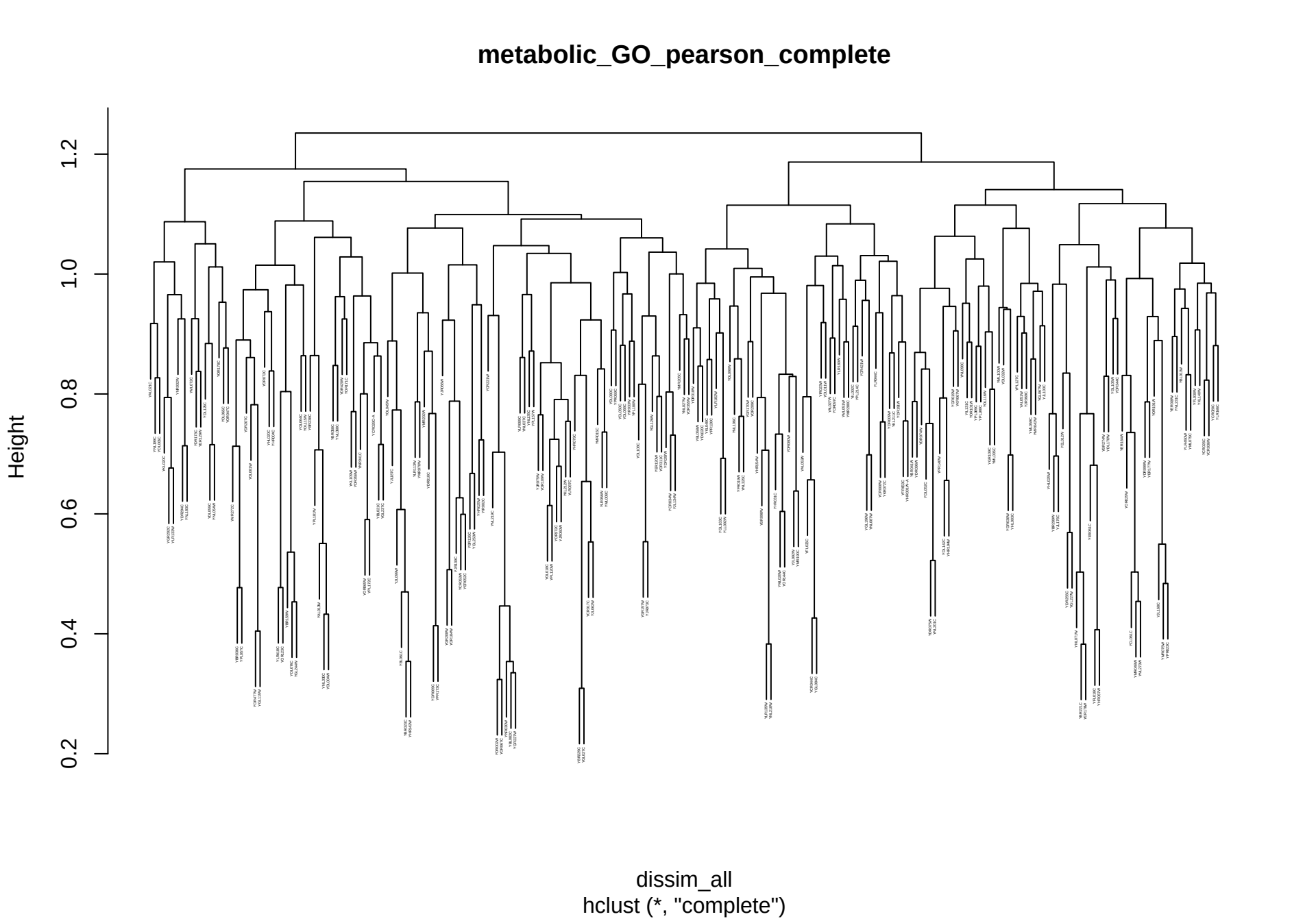

cytoskeleton and microtubules_GO_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")

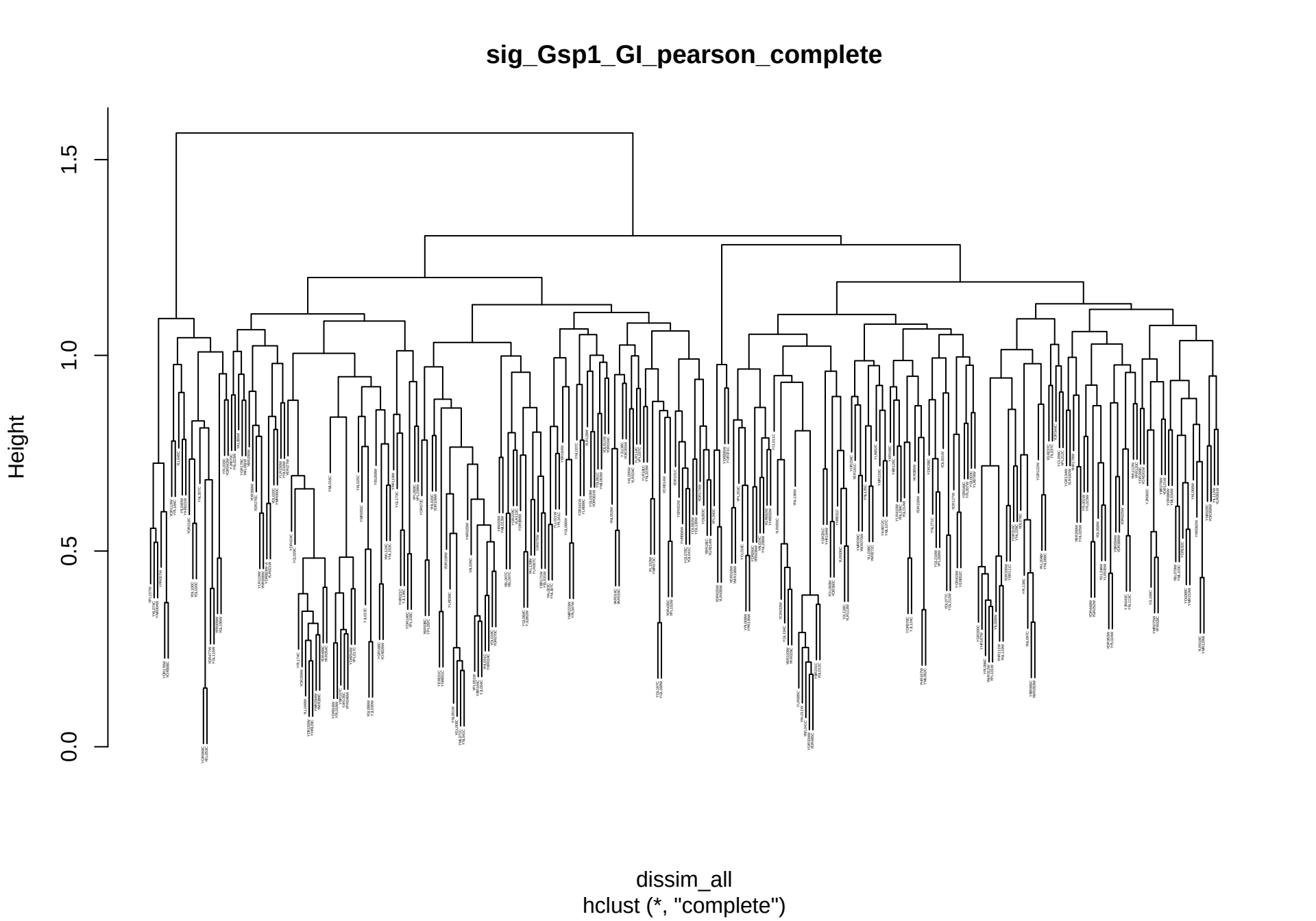

cell cycle_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
dissim_all
hclust (*, "complete")

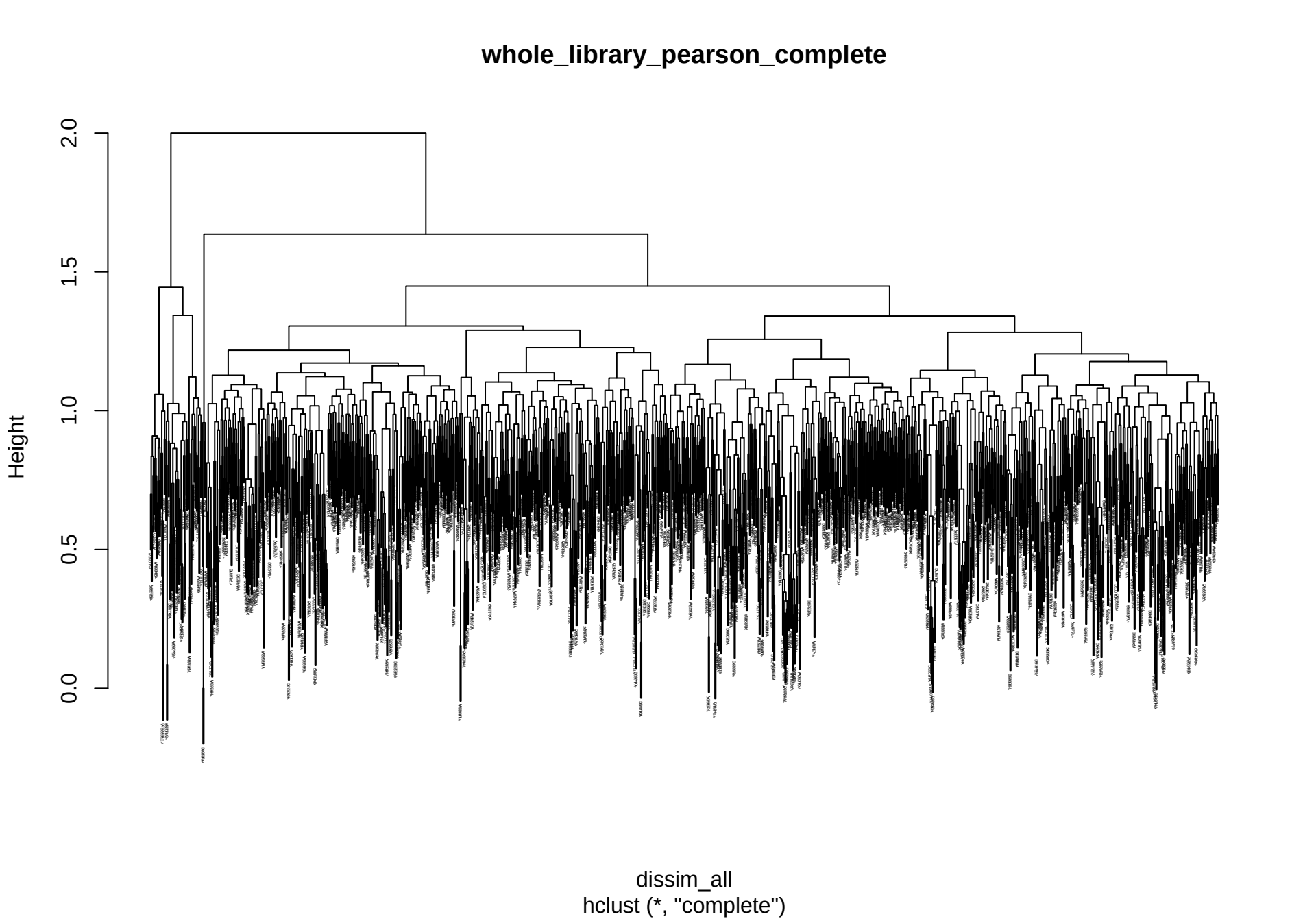

budding_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
dissim_all
hclust (*, "complete")


lipids_GO_pearson_complete
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


nuclear transport and organization_GO_pearson_complete
Height
1.2
1.0
0.8
0.6
0.4
0.2
dissim_all
hclust (*, "complete")


metabolic_GO_pearson_complete
Height
0.2
0.4
0.6
0.8
1.0
1.2
dissim_all
hclust (*, "complete")


sig_Gsp1_GI_pearson_complete
Height
0.0
0.5
1.0
1.5
dissim_all
hclust (*, "complete")


whole_library_pearson_complete
Height
0.0
0.5
1.0
1.5
2.0
dissim_all
hclust (*, "complete")