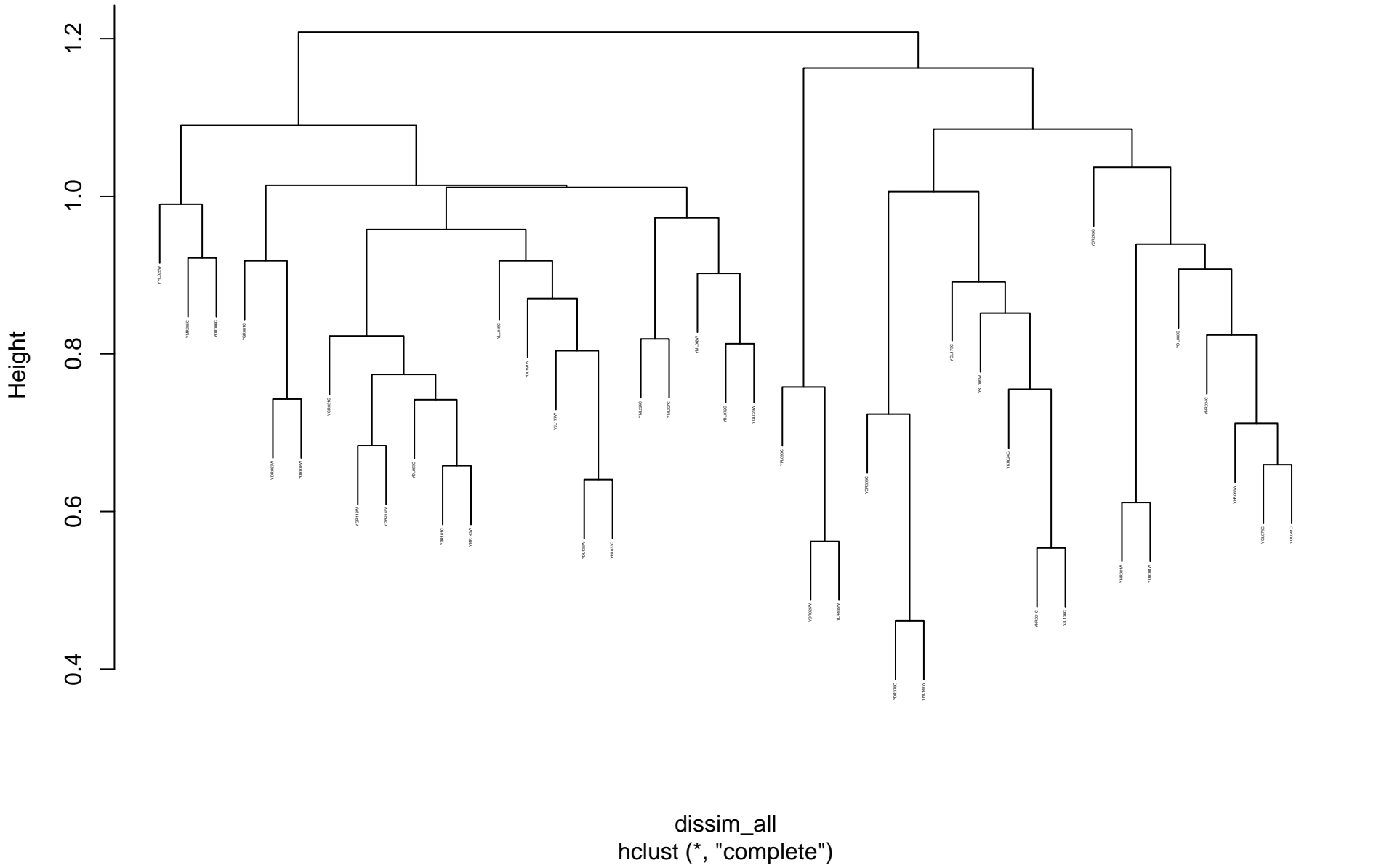
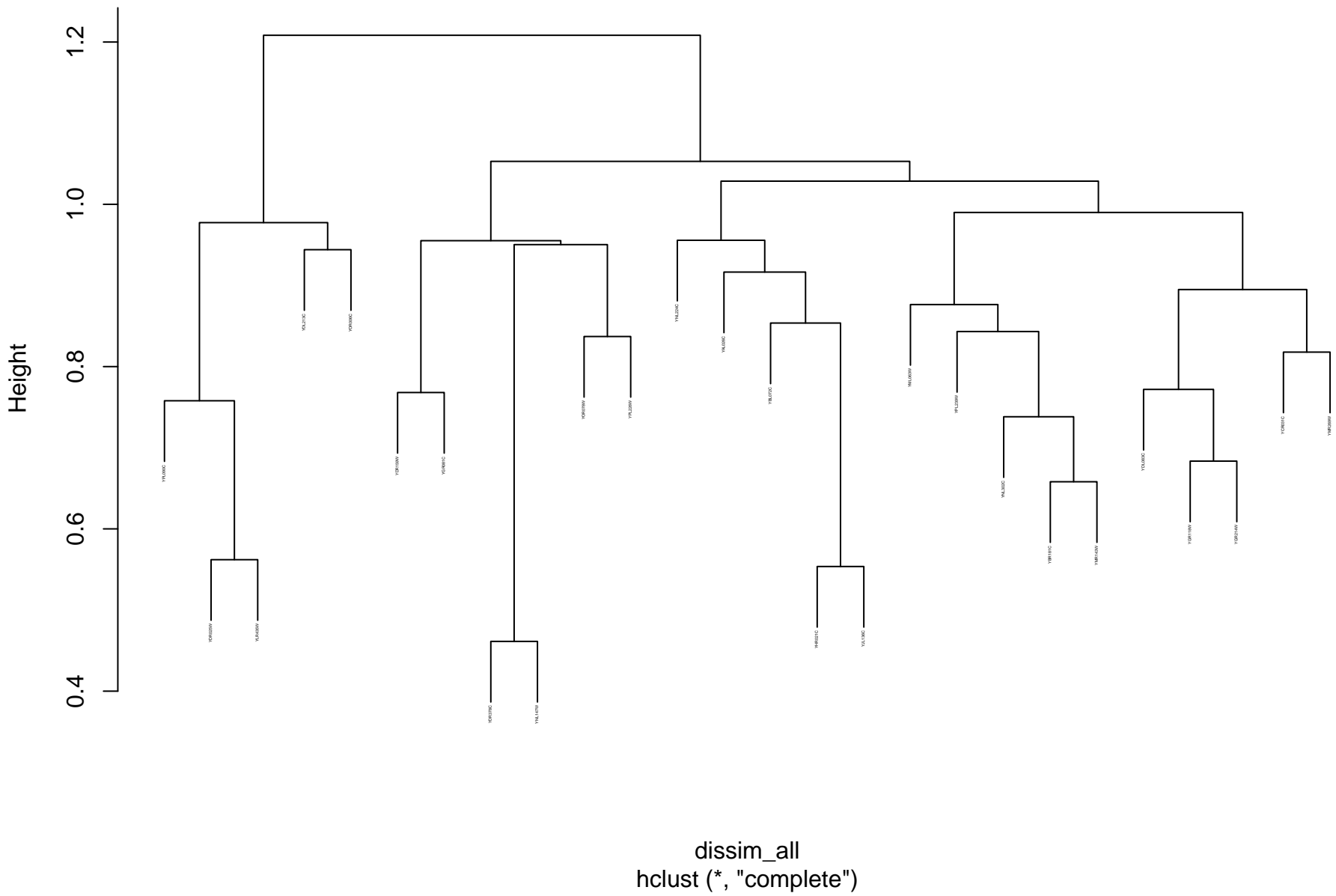


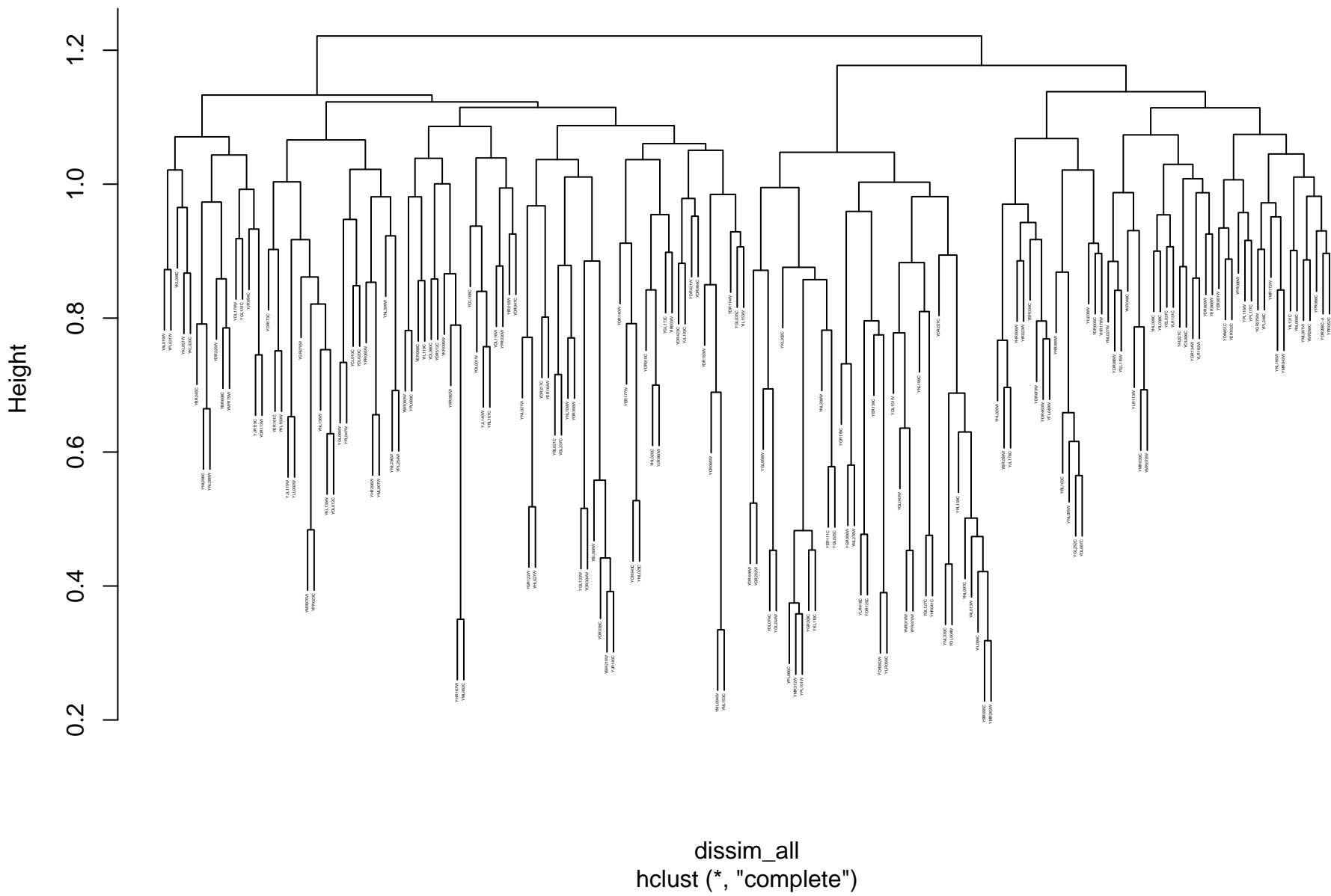
rRNA processing_GO_pearson_complete



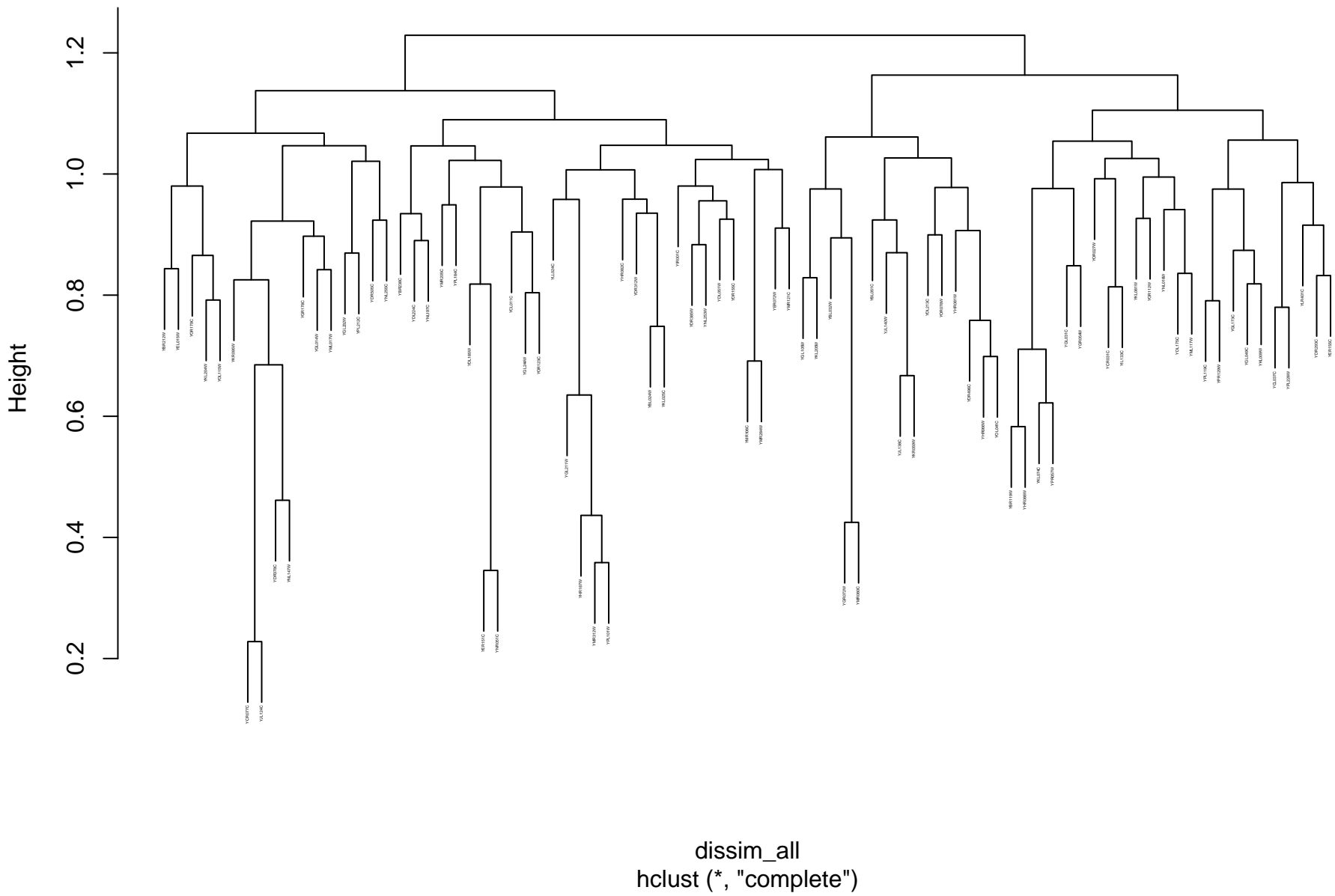
ribosomal small subunit biogenesis_GO_pearson_complete



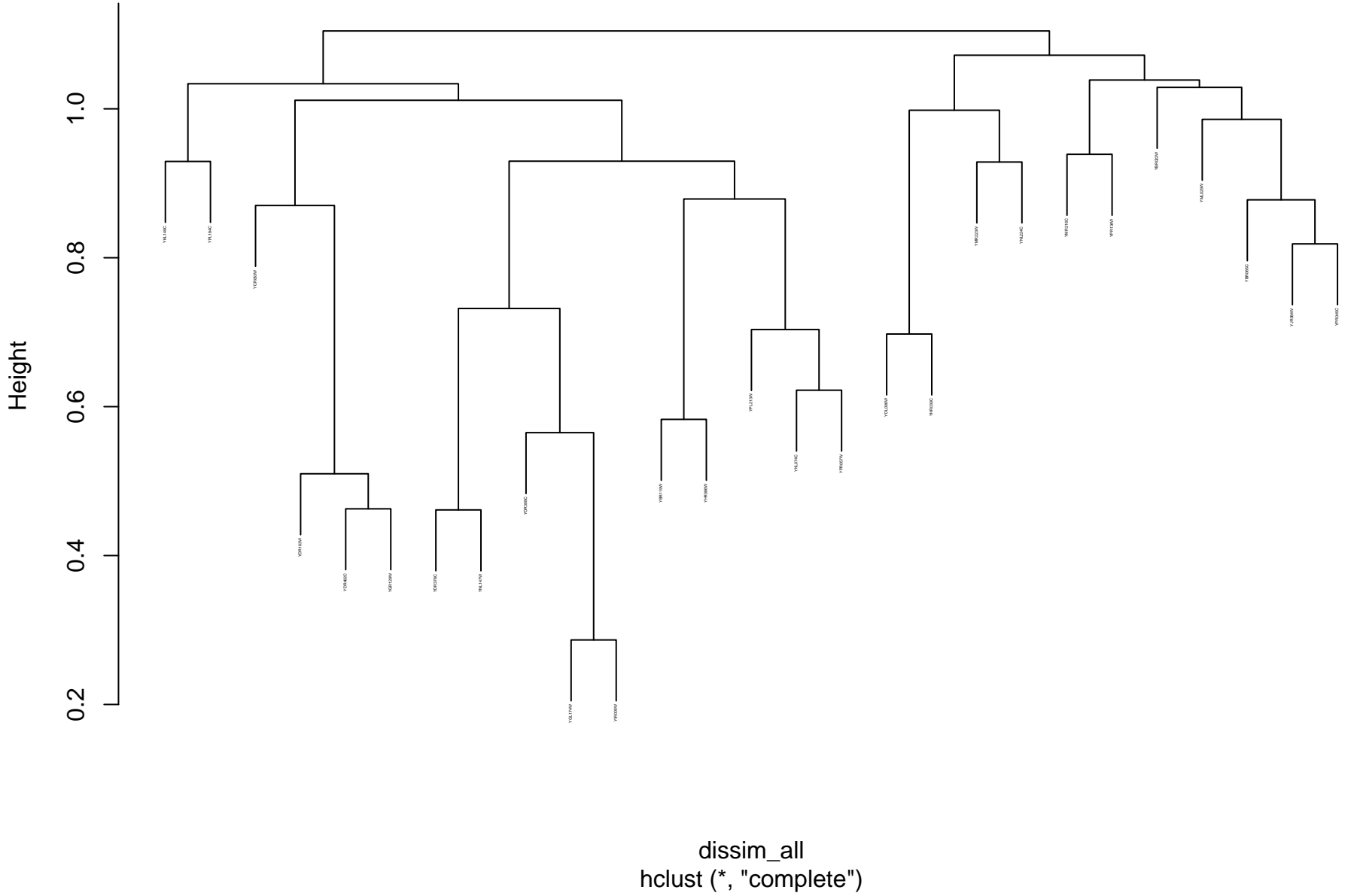
transcription from RNA polymerase II promoter_GO_pearson_complete



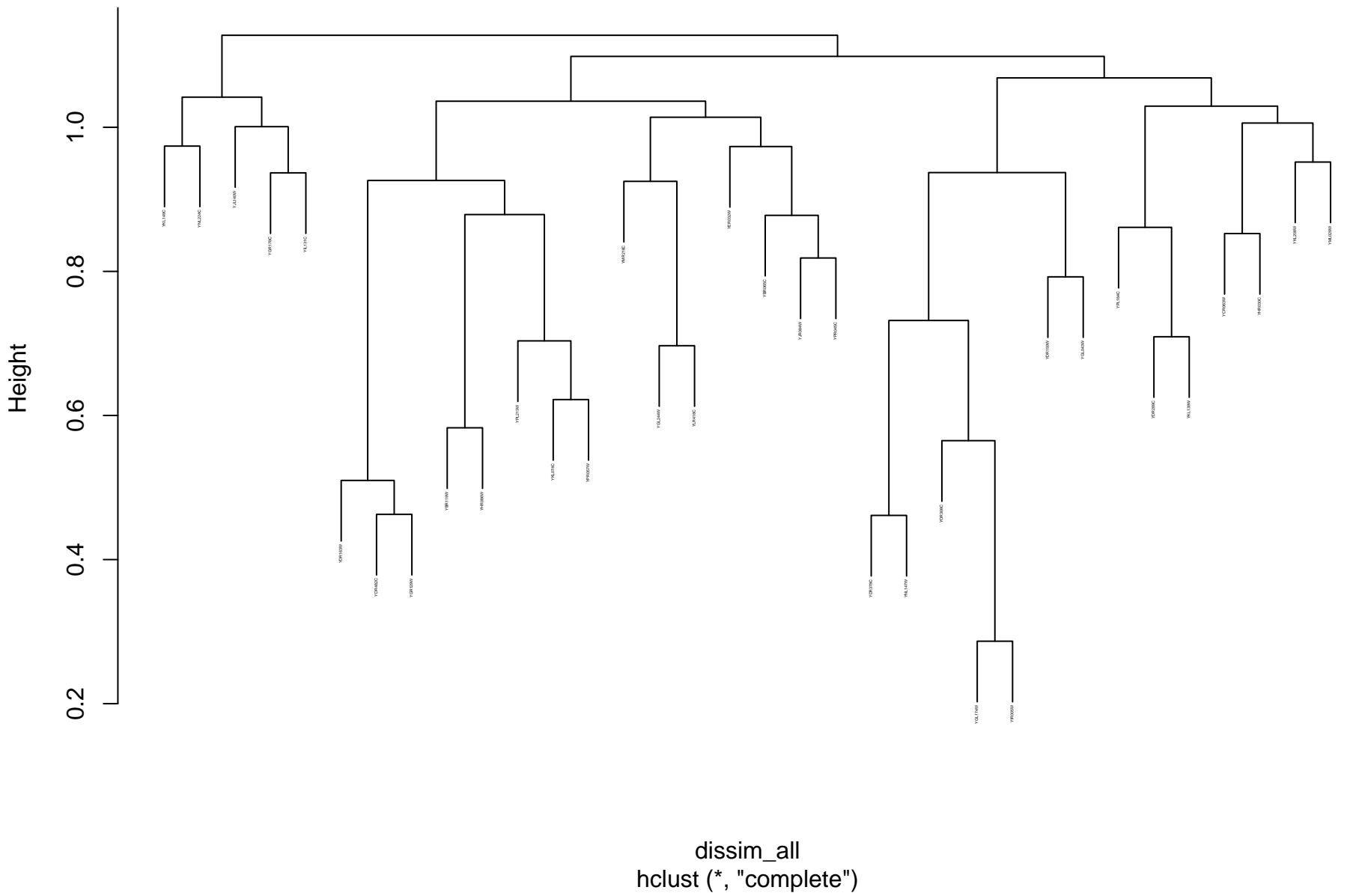
RNA binding_GO_pearson_complete



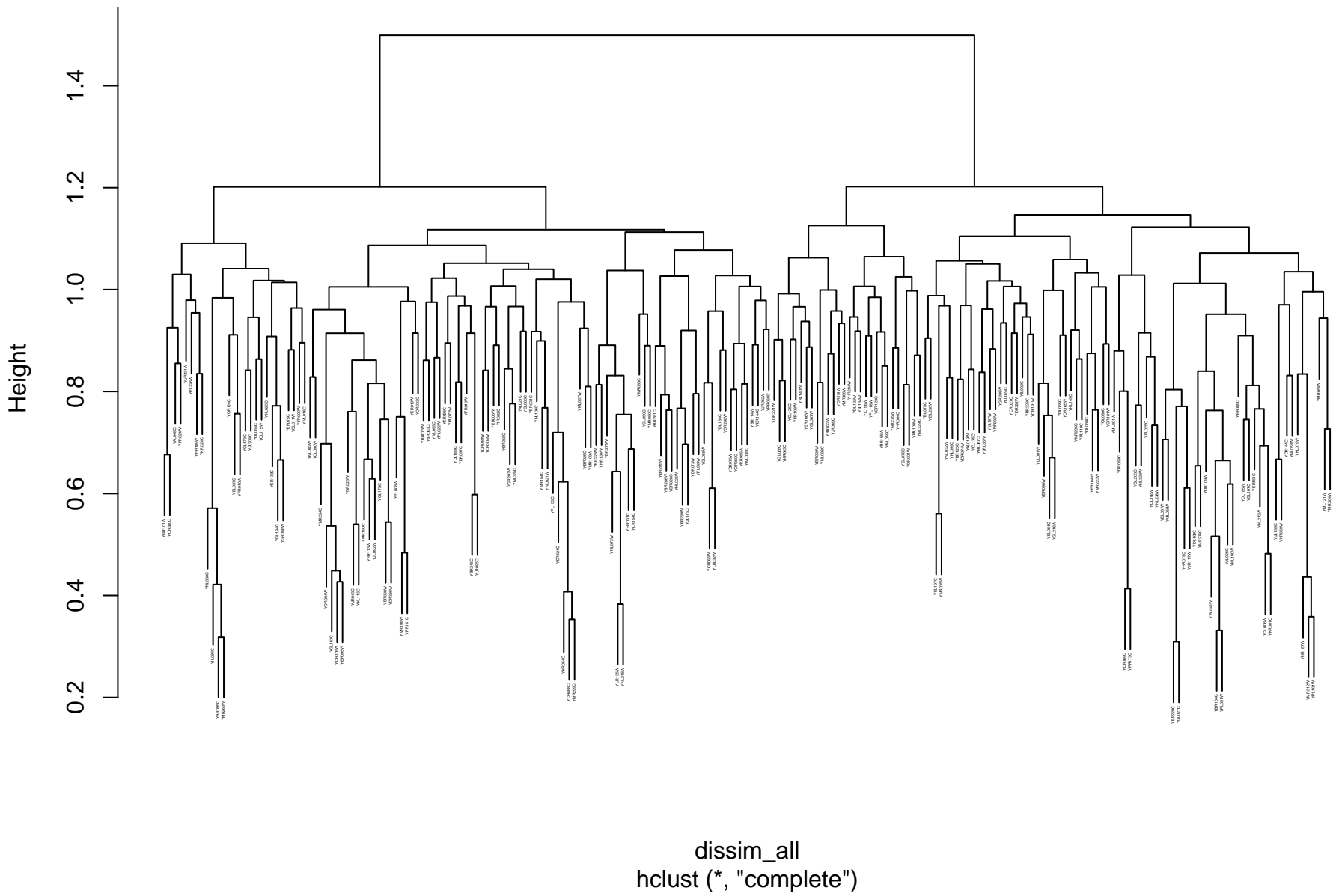
RNA splicing_GO_pearson_complete



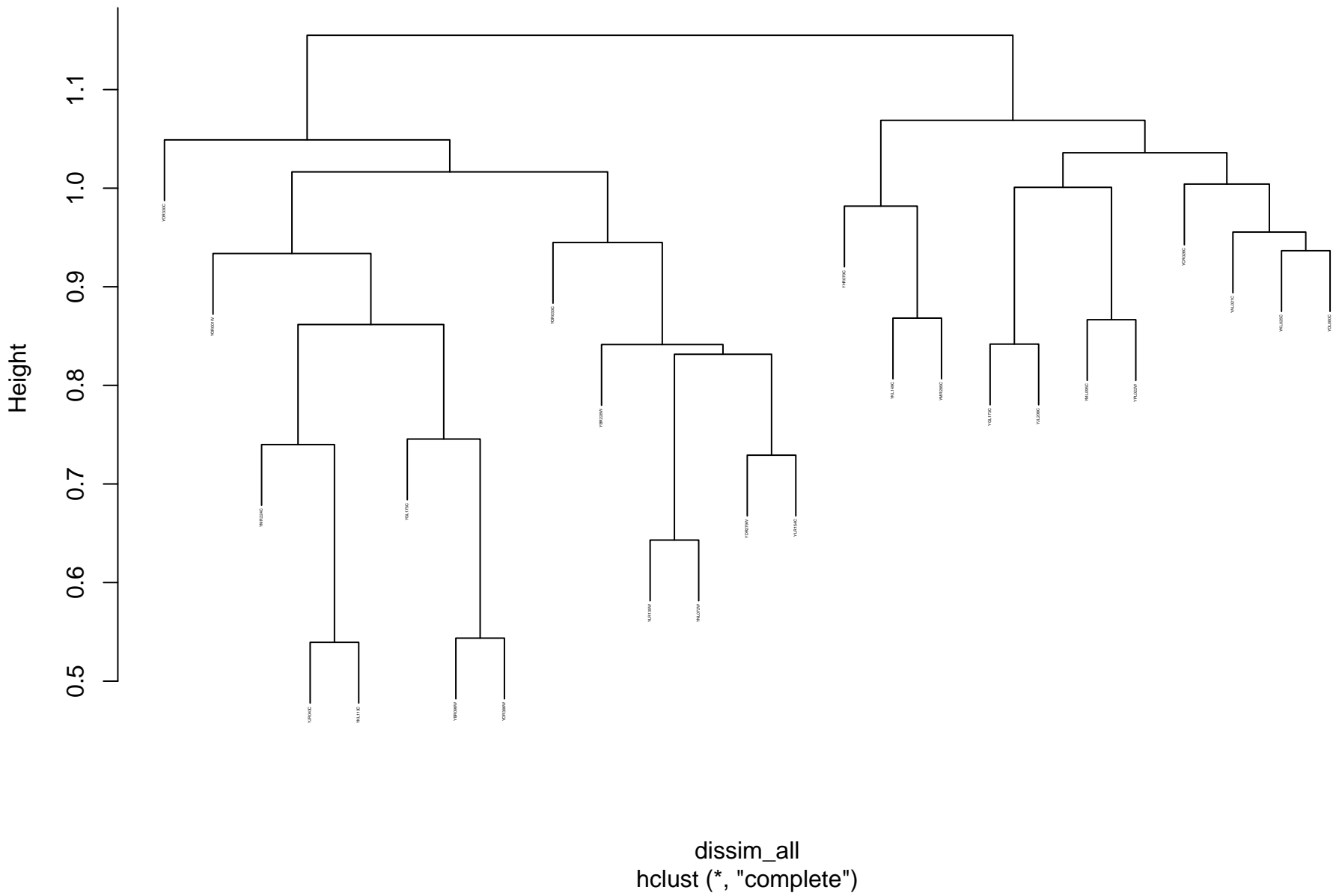
mRNA processing_GO_pearson_complete



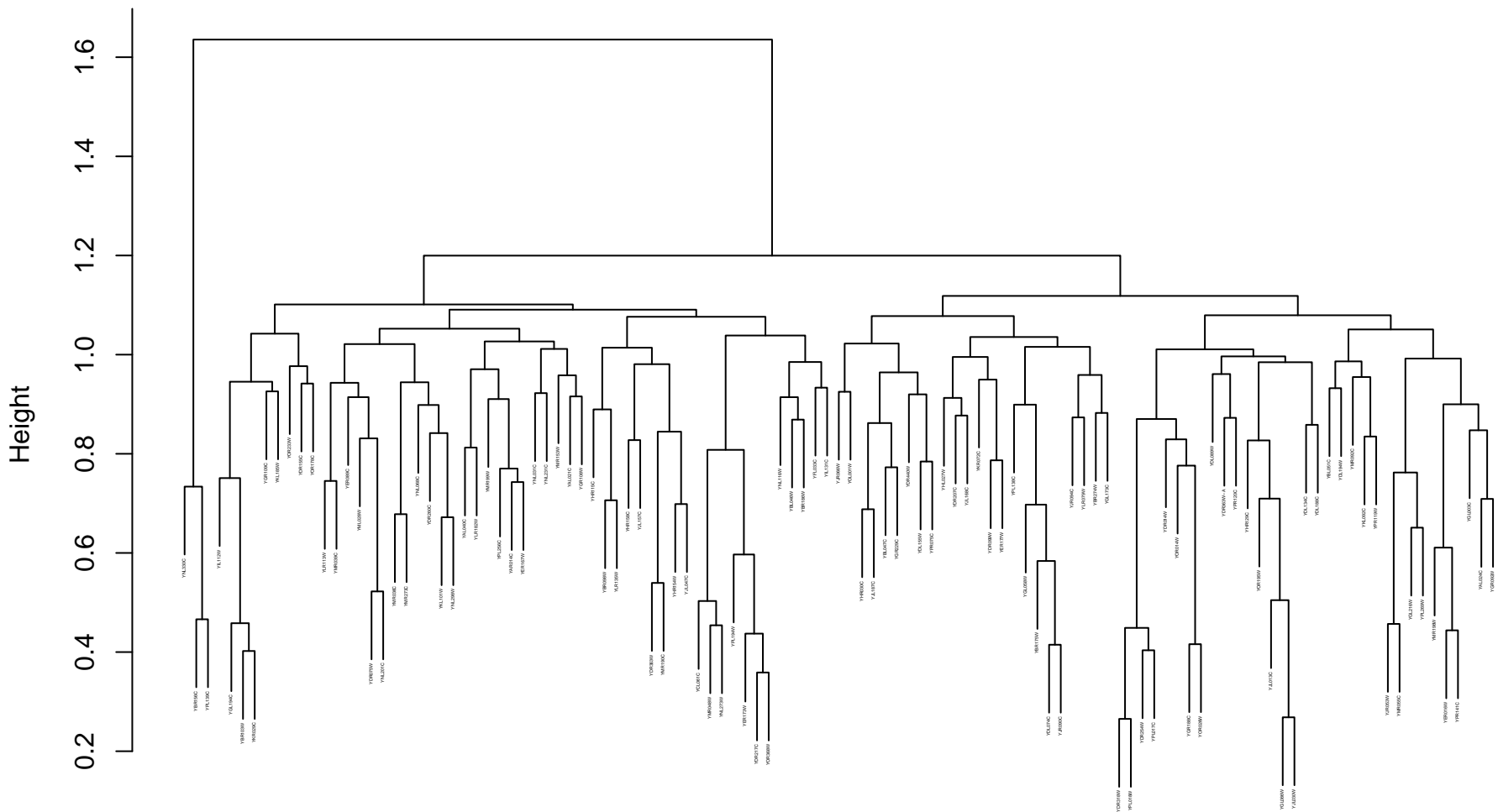
hydrolase activity_GO_pearson_complete



nuclease activity_GO_pearson_complete

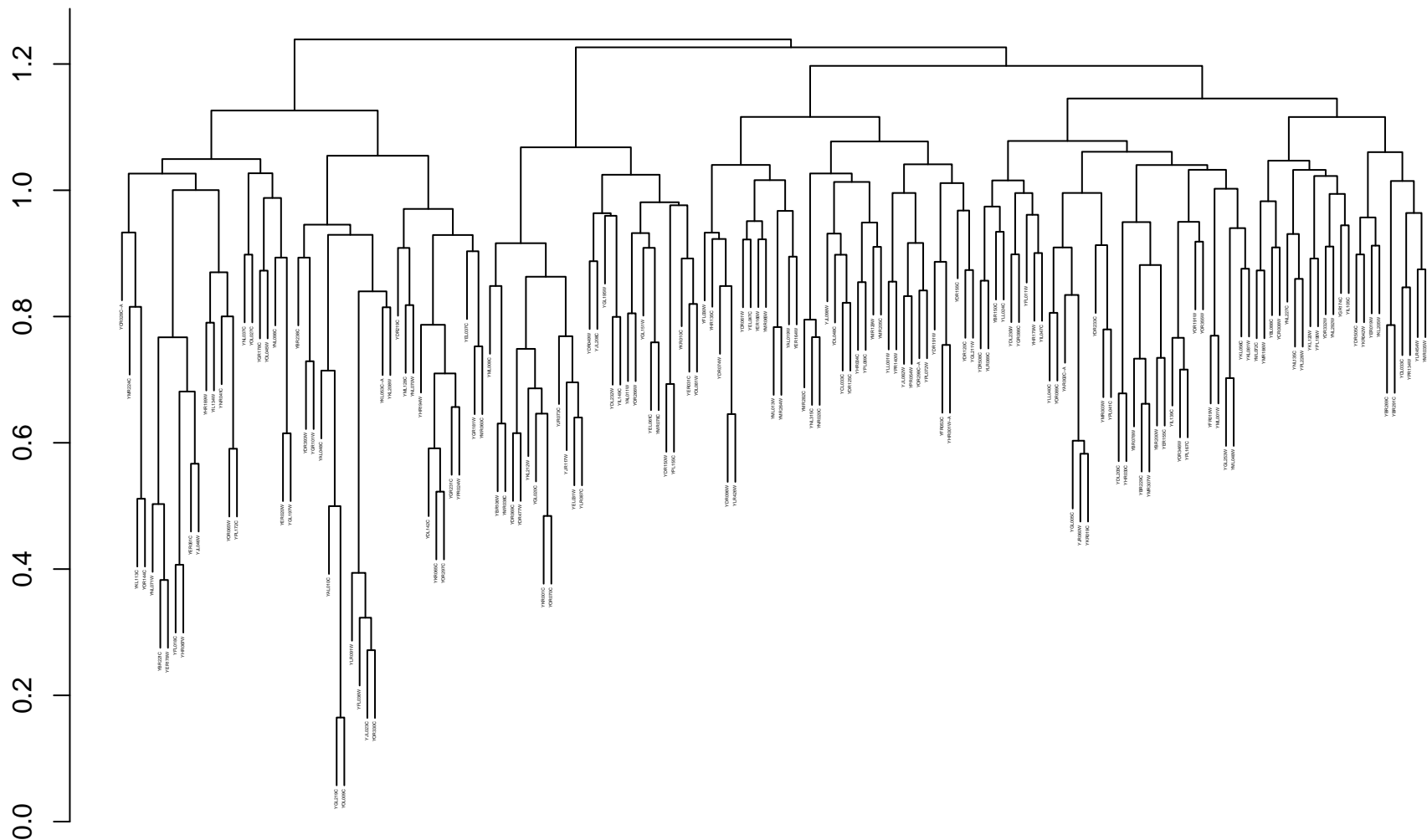



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dissim_all
hclust (*, "complete")
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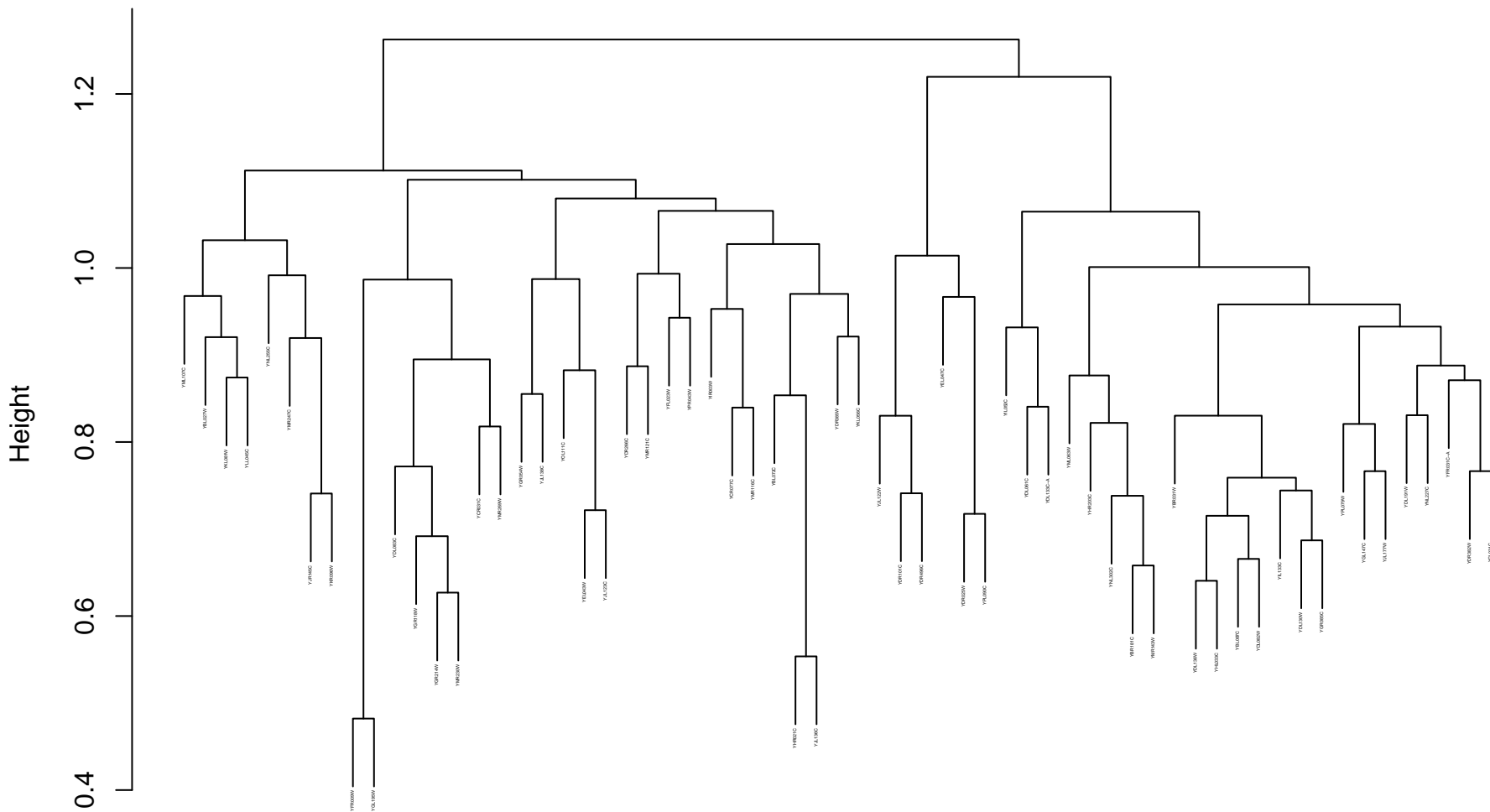
mitochondrion_GO_pearson_complete

Height

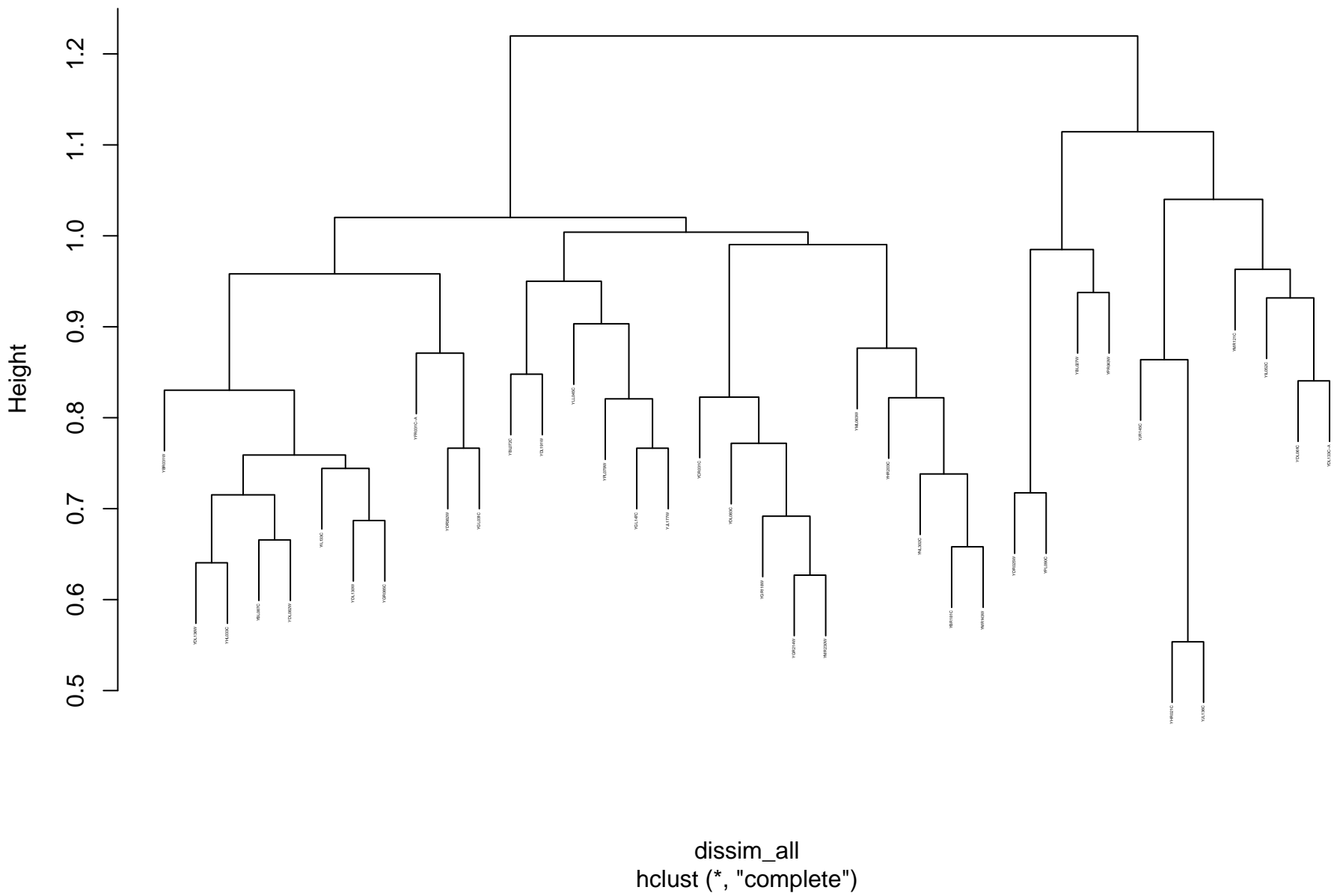


dissim_all
hclust (*, "complete")

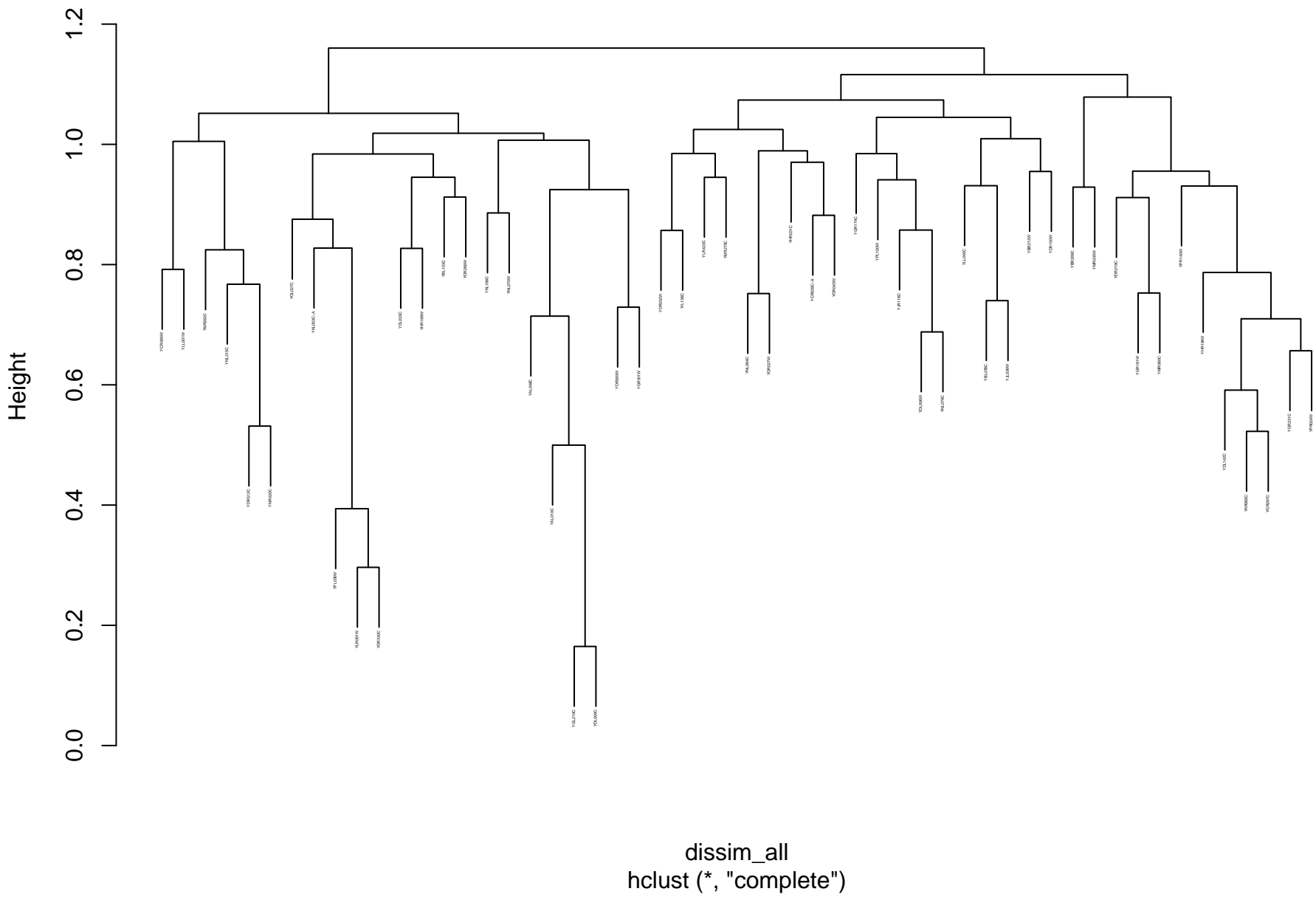
ribosome_GO_pearson_complete



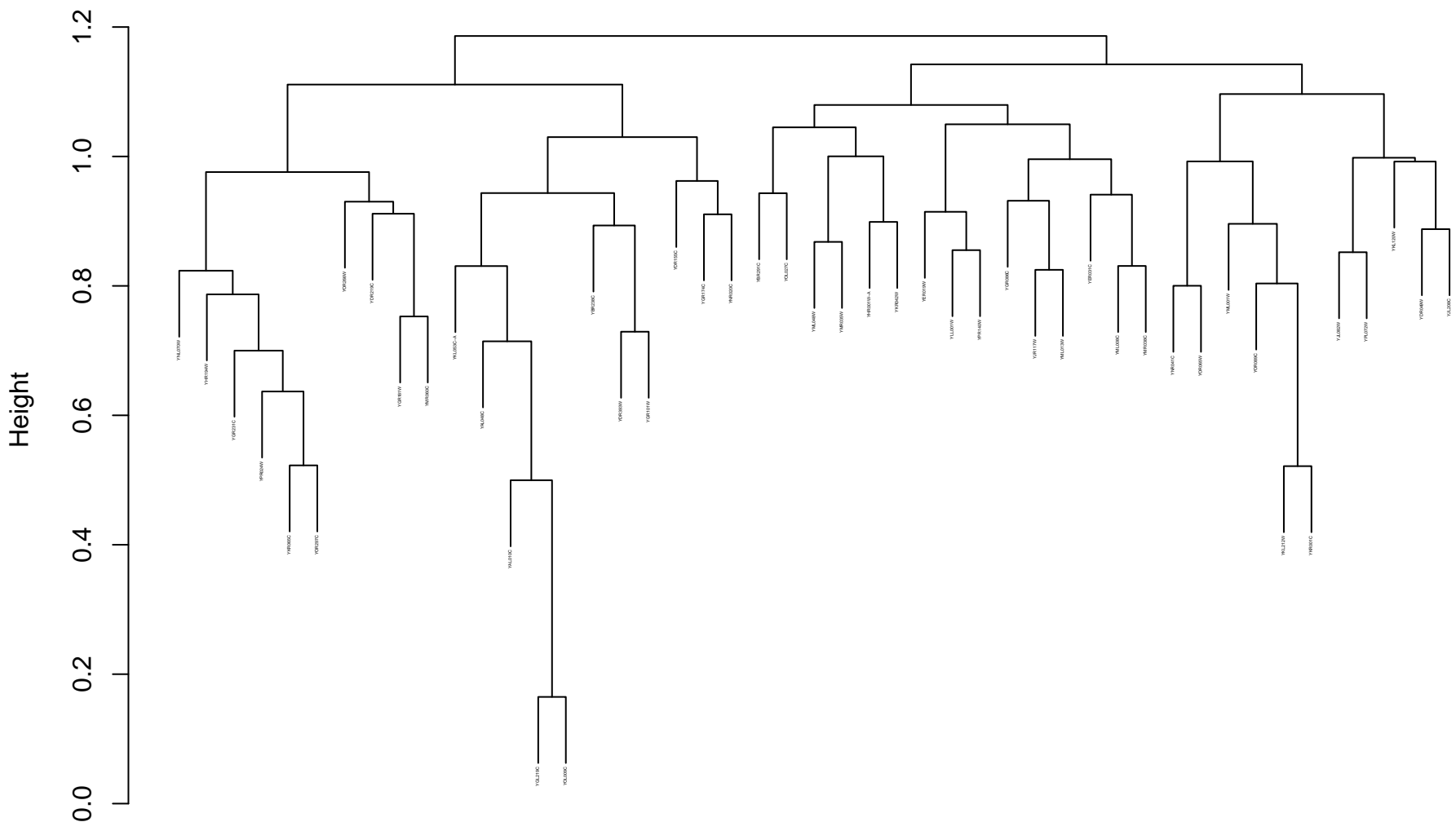
structural constituent of ribosome_GO_pearson_complete



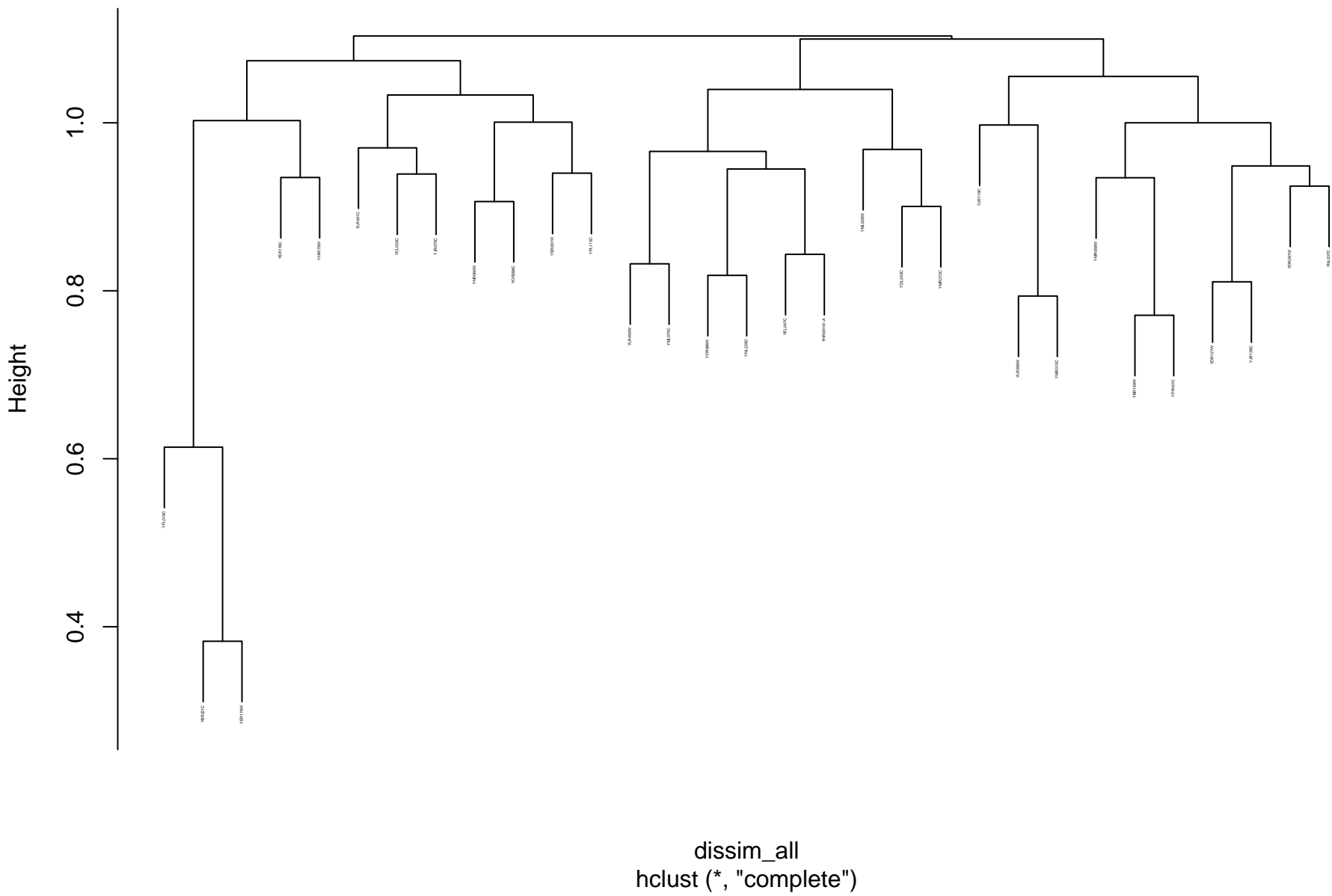
mitochondrion organization_GO_pearson_complete



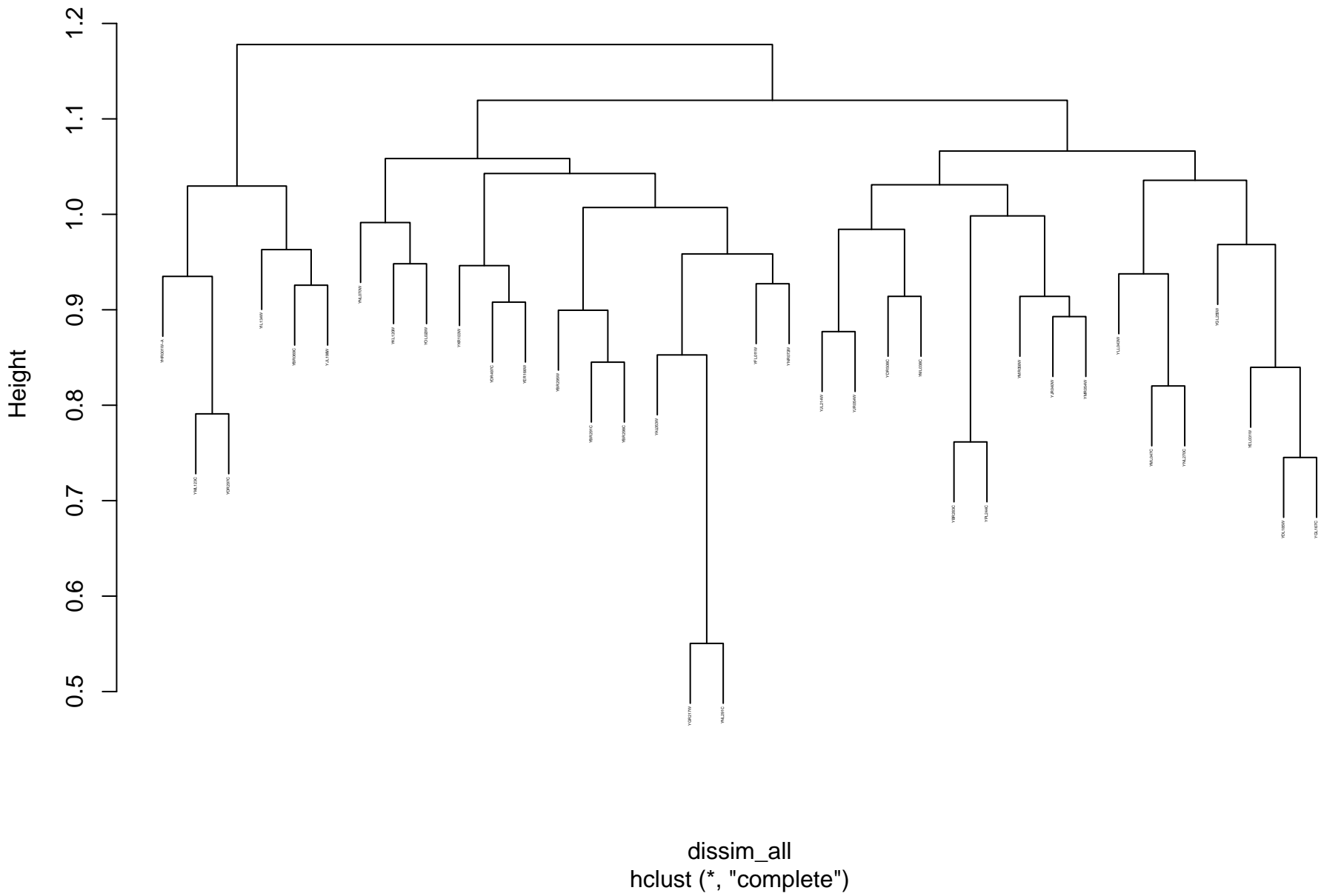
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dissim_all
hclust (*, "complete")
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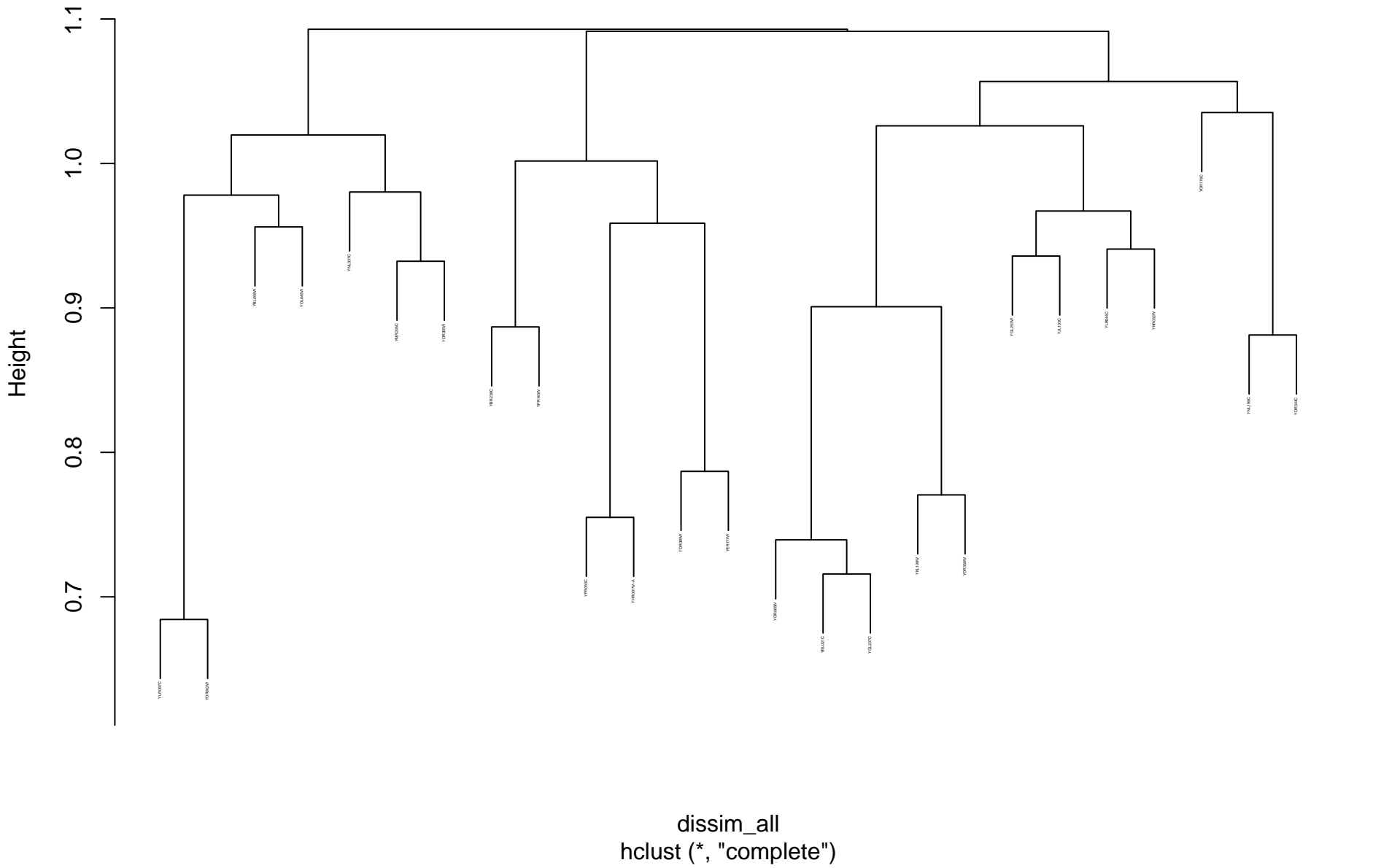
oxidoreductase activity_GO_pearson_complete



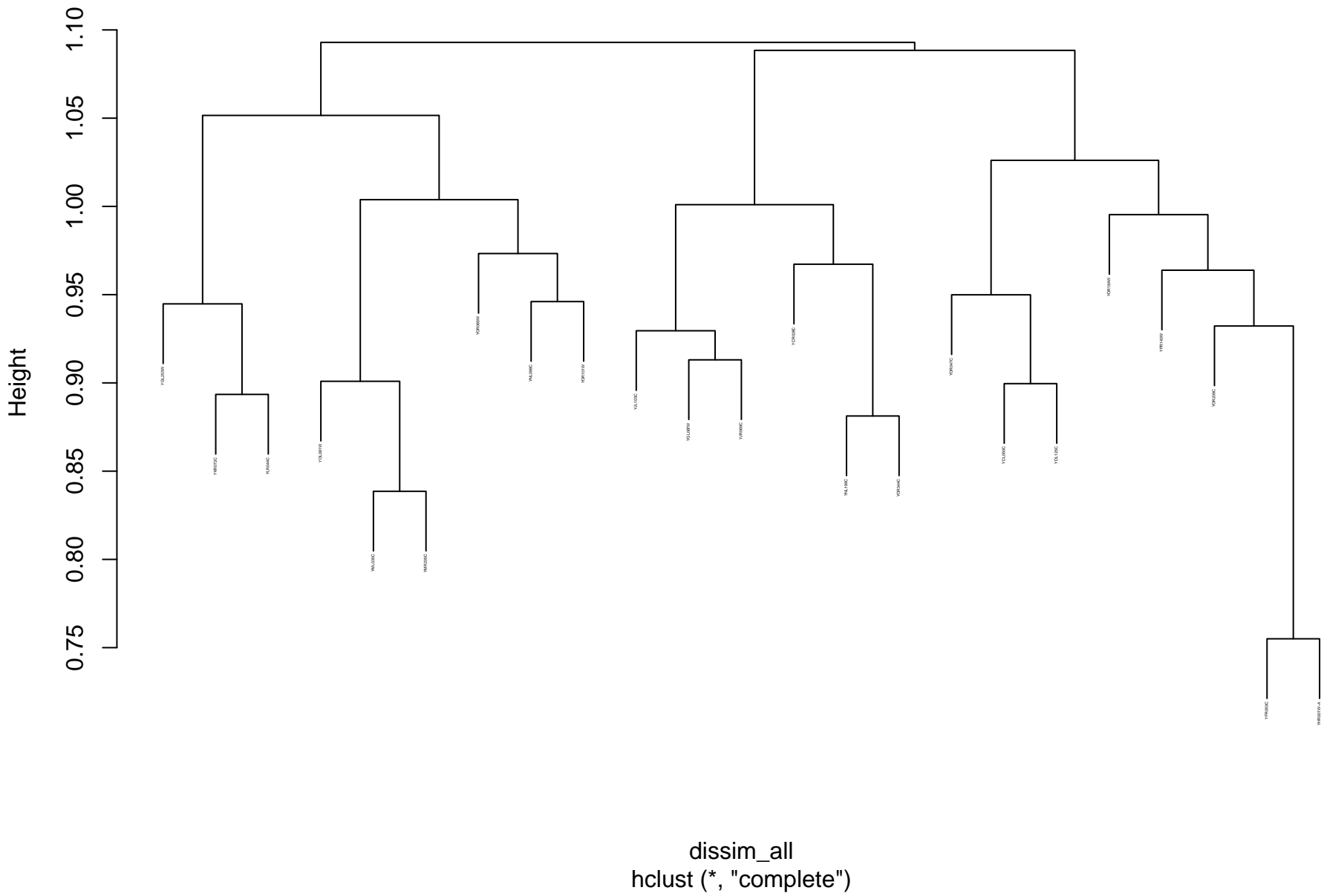
transmembrane transporter activity_GO_pearson_complete



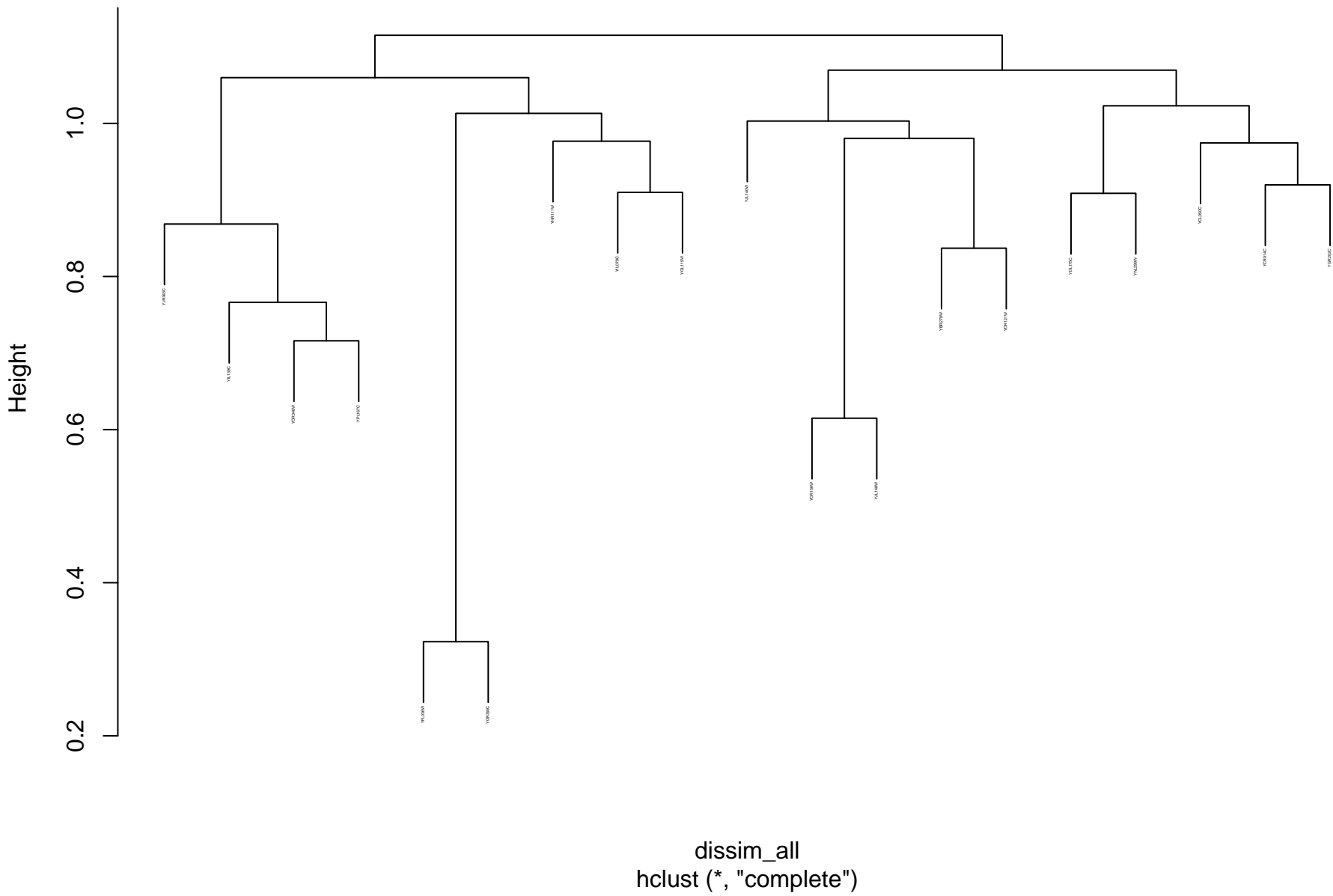
generation of precursor metabolites and energy_GO_pearson_complete



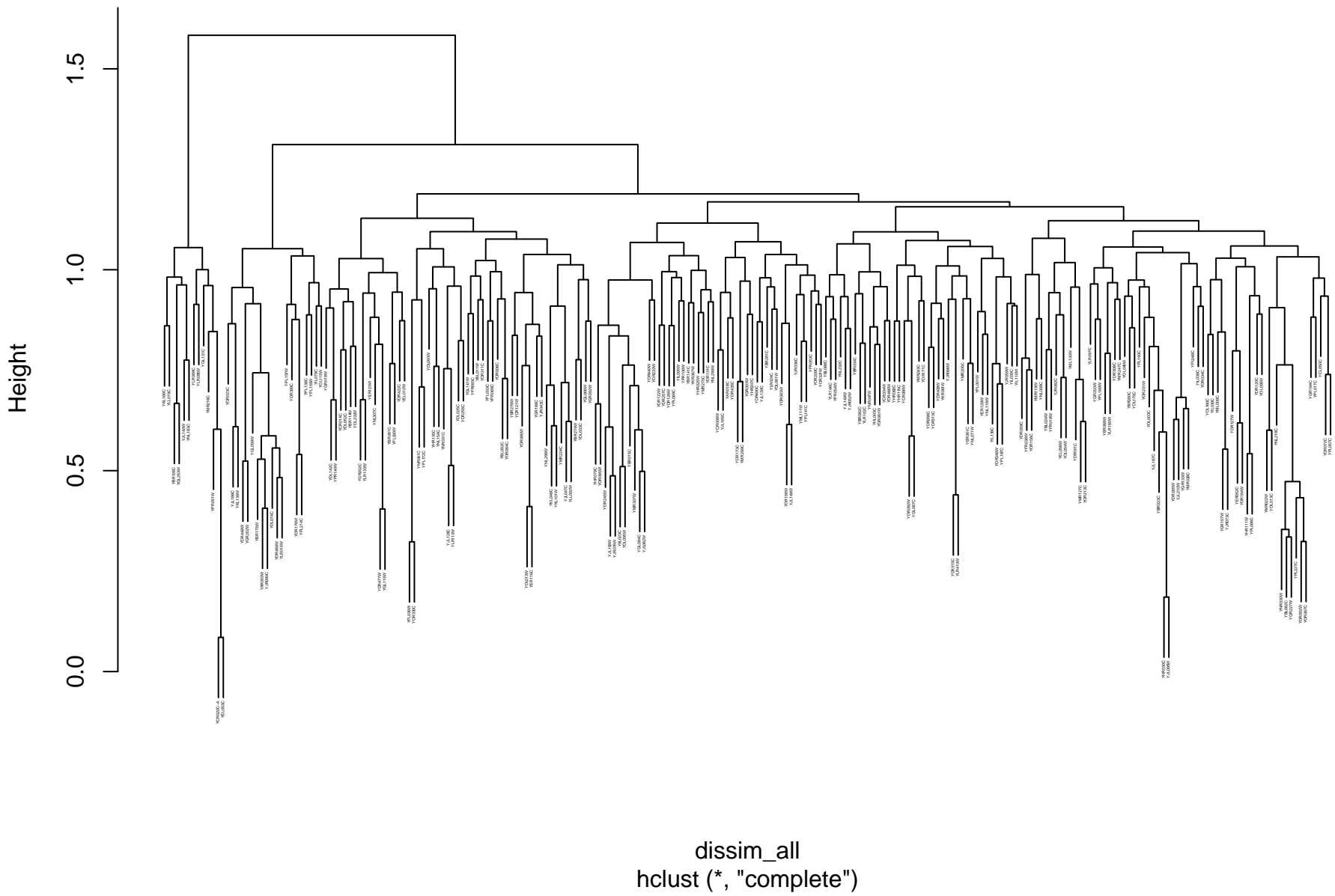
nucleobase-containing small molecule metabolic process_GO_pearson_complete



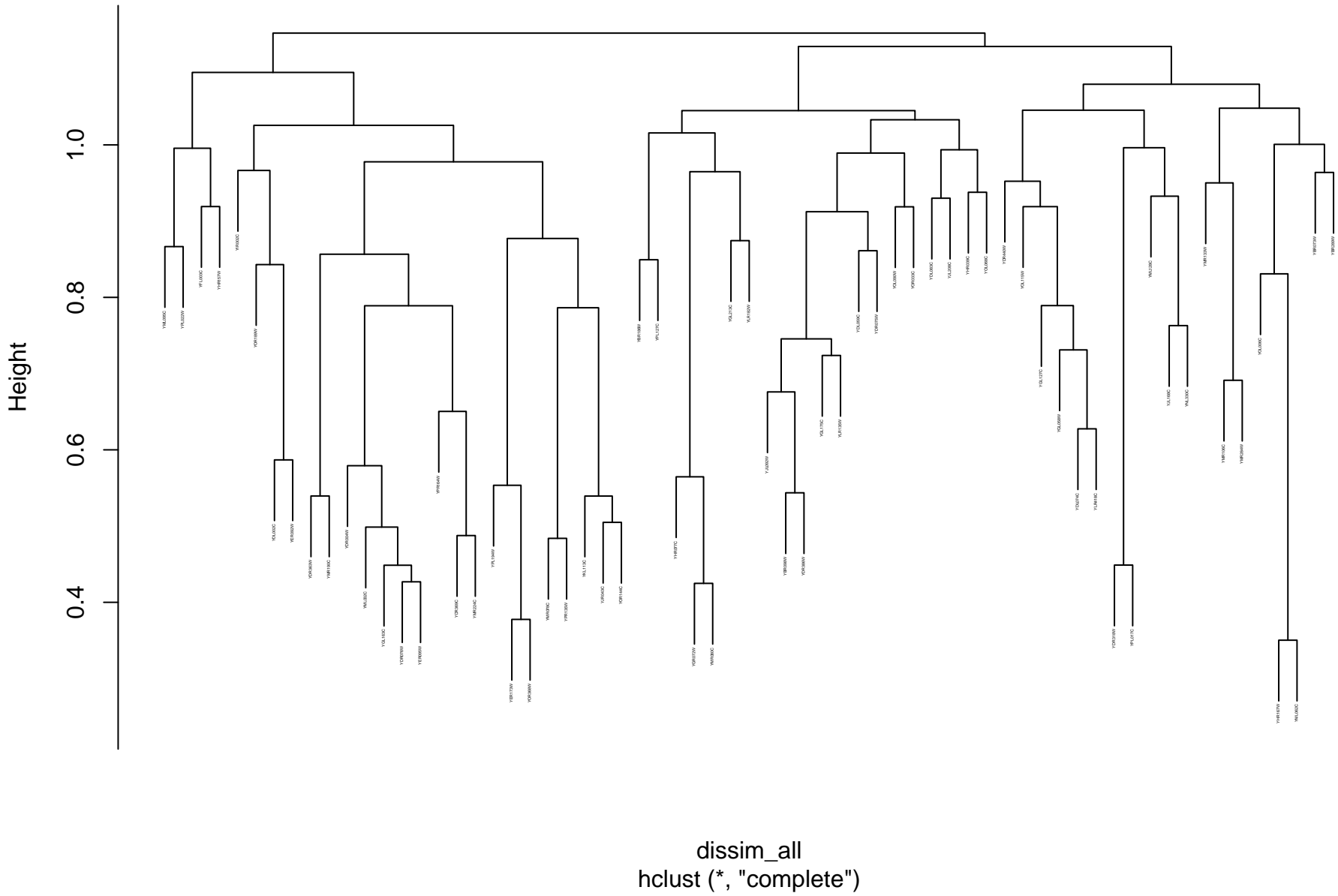
nucleotidyltransferase activity_GO_pearson_complete



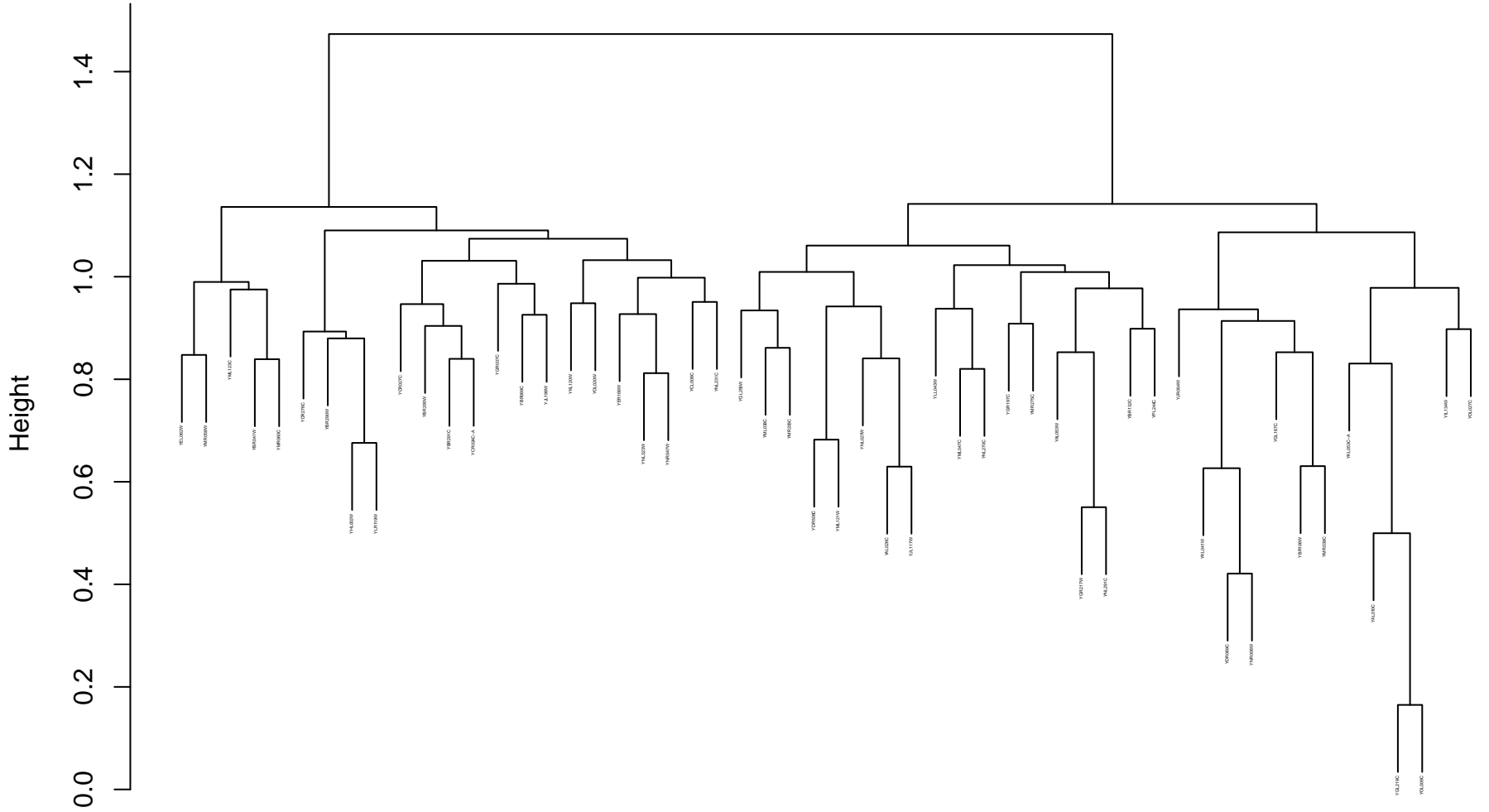
transferase activity_GO_pearson_complete



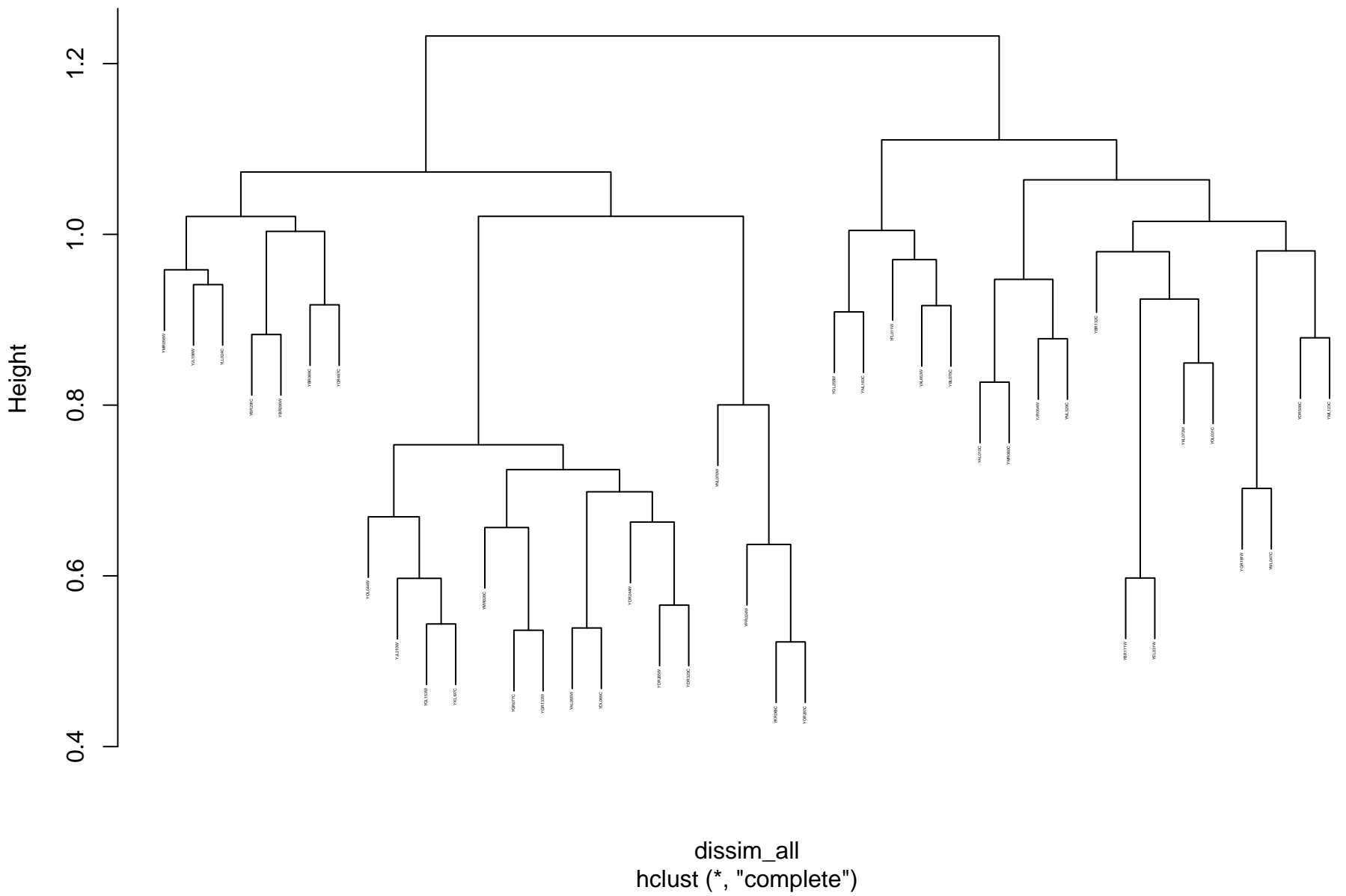
DNA recombination_GO_pearson_complete



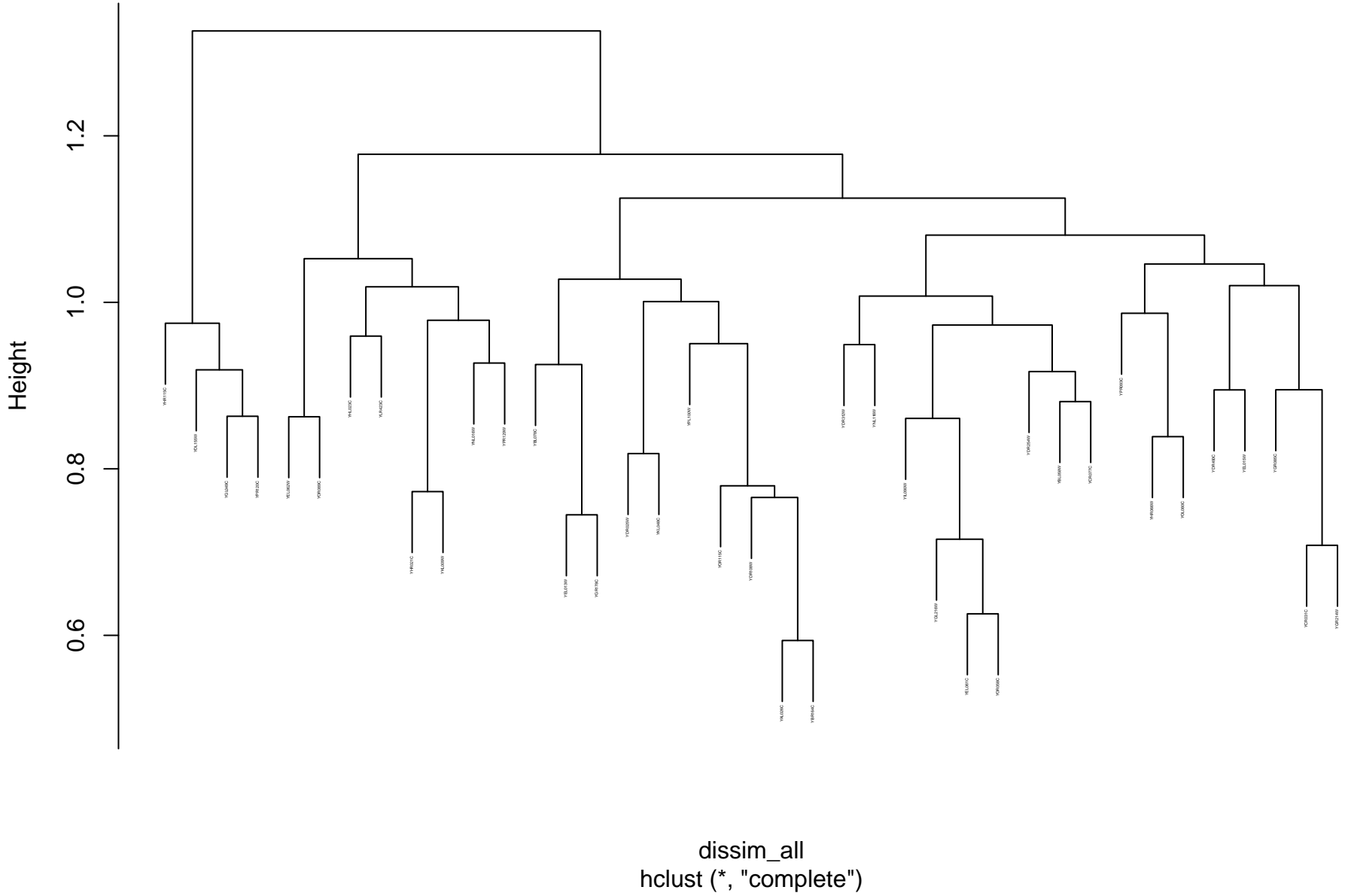
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dissim_all
hclust (*, "complete")
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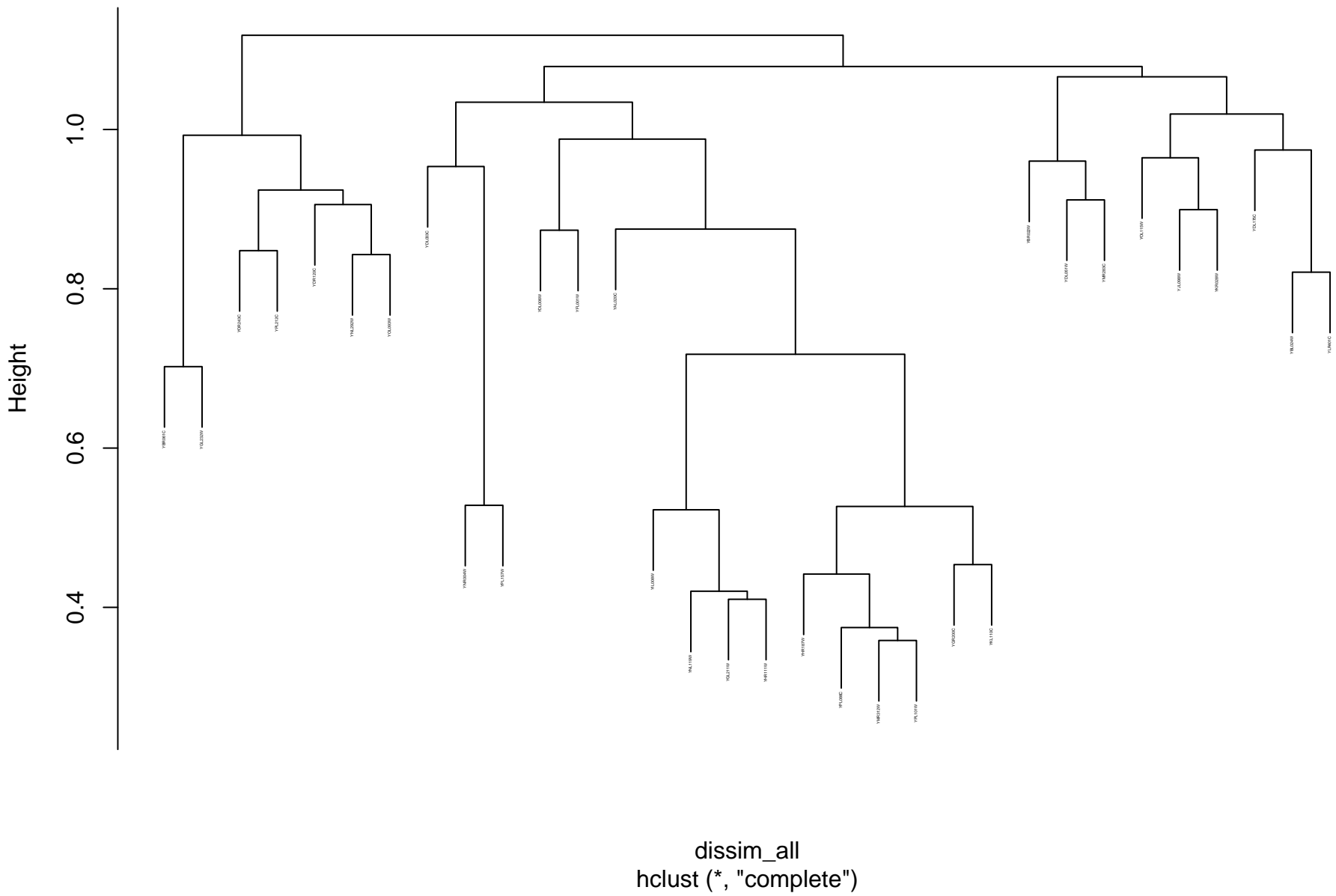
transmembrane transport_GO_pearson_complete



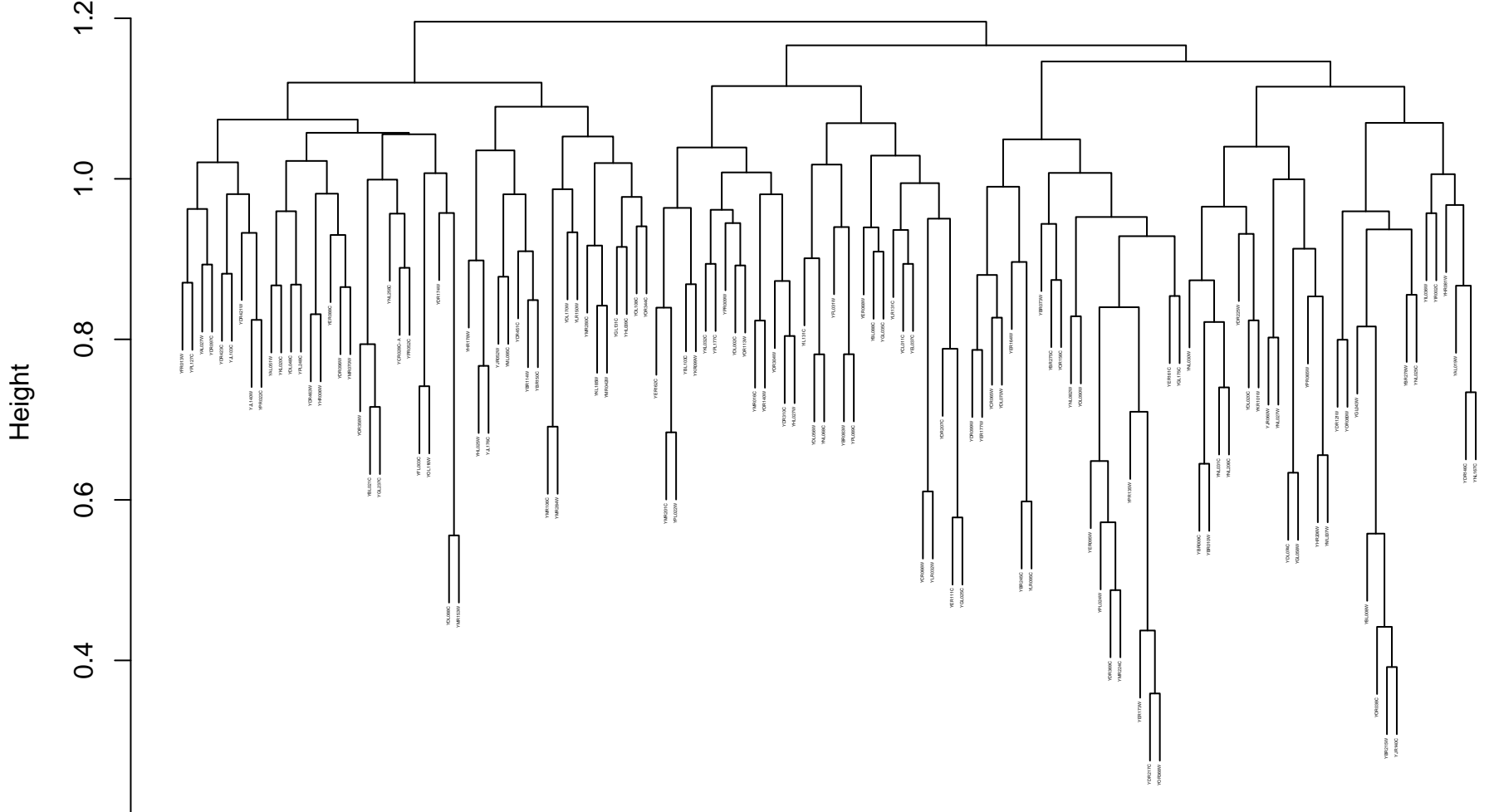
organelle assembly_GO_pearson_complete



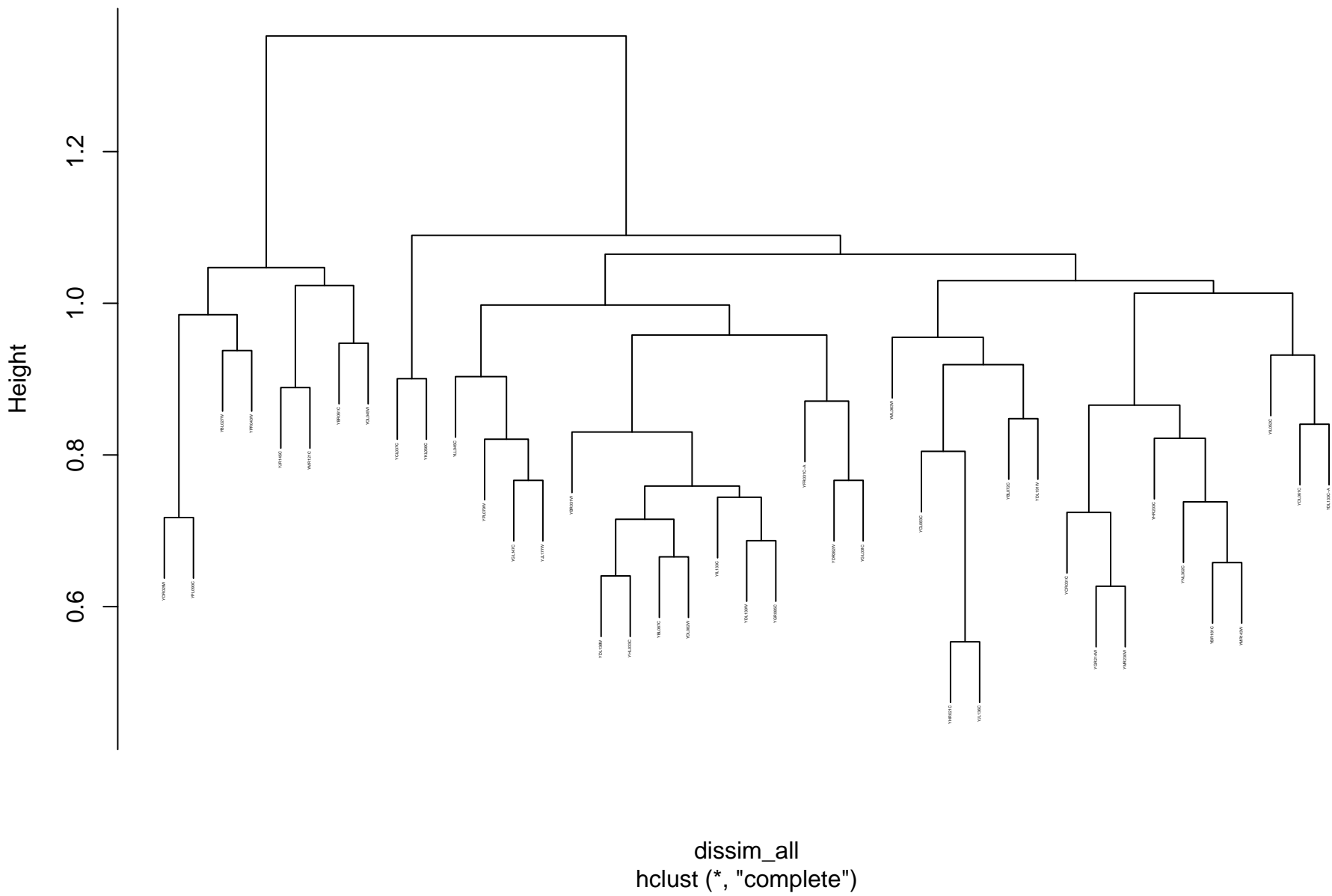
tRNA processing_GO_pearson_complete



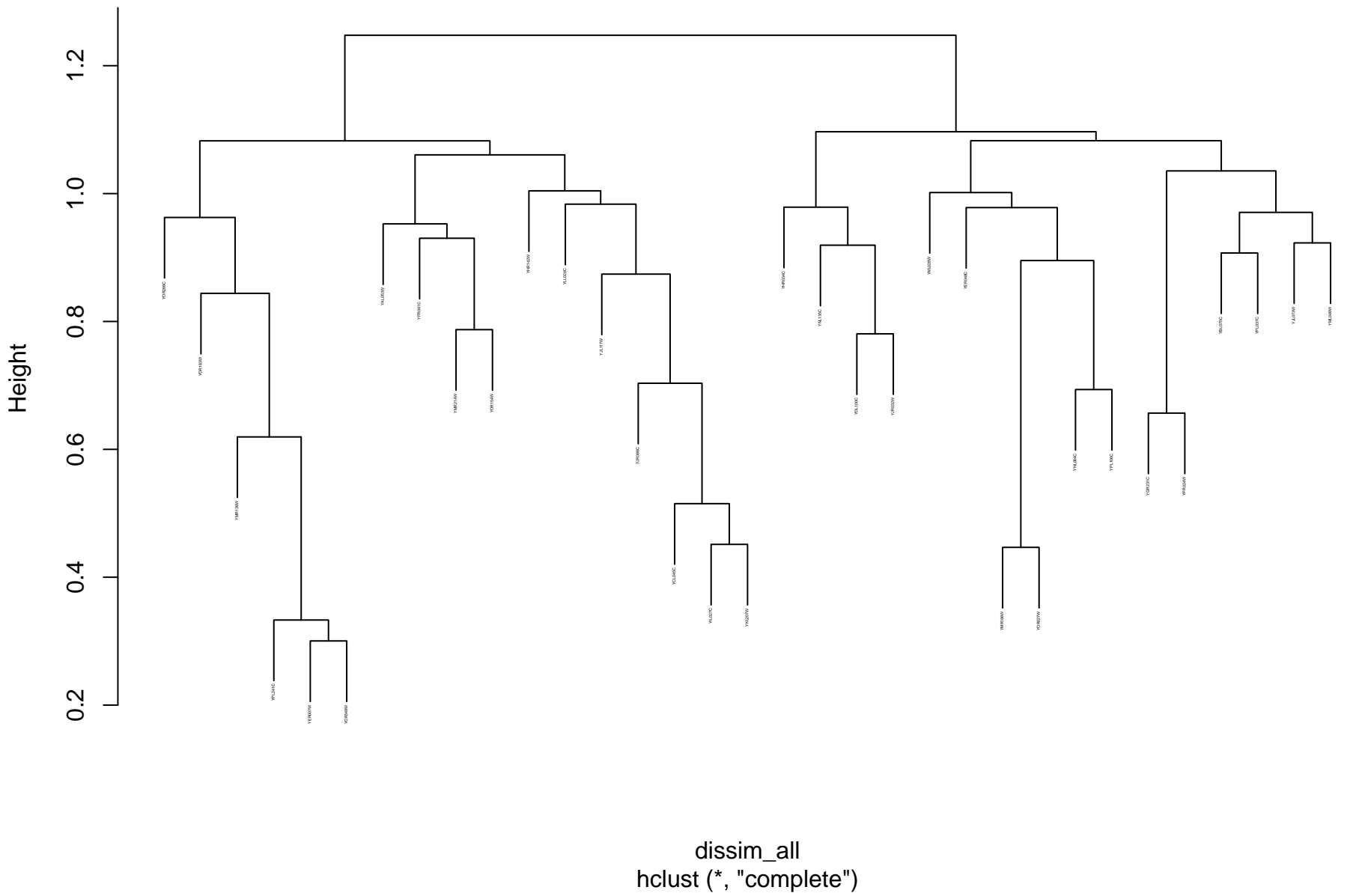
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dissim_all
hclust (*, "complete")
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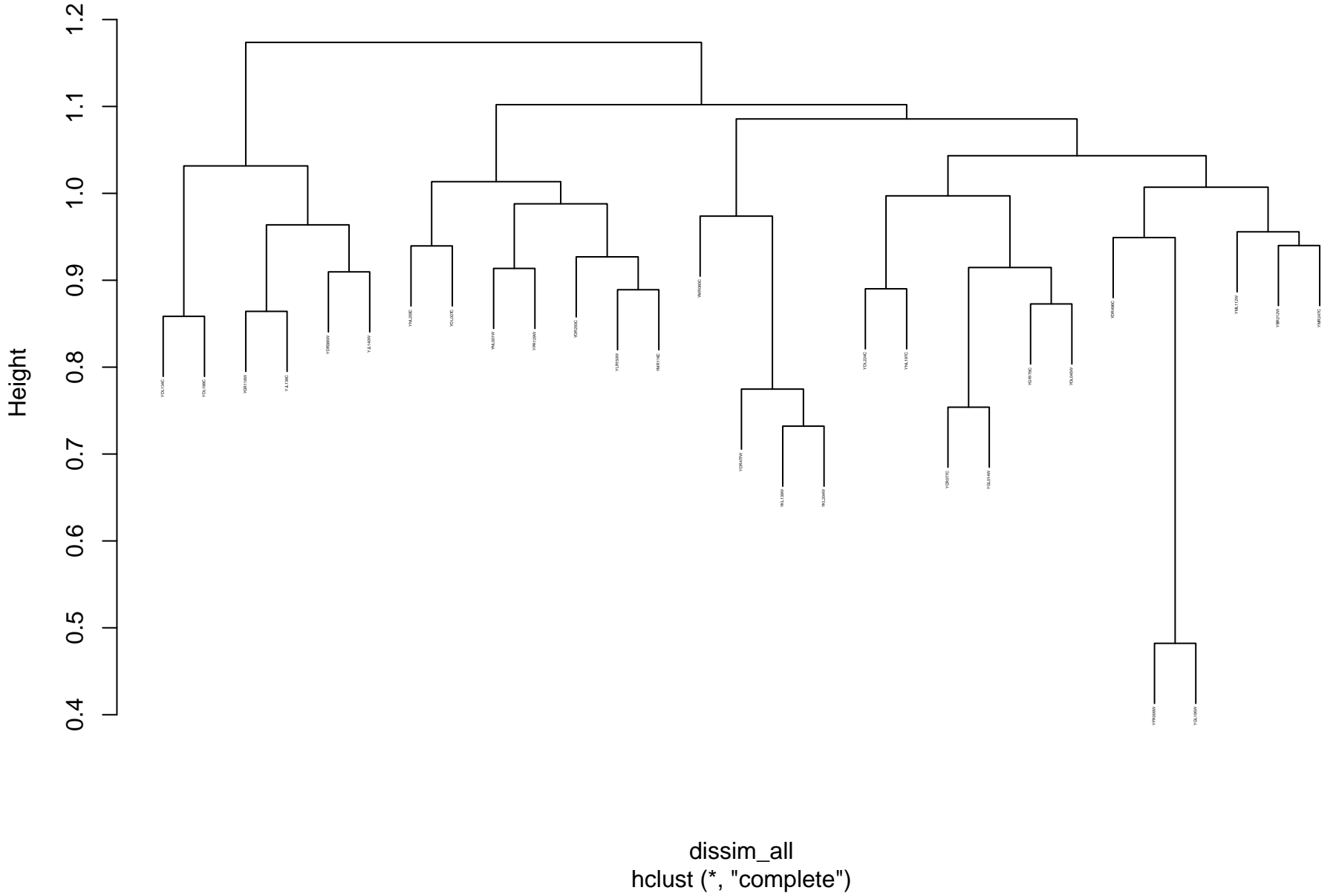
cytoplasmic translation_GO_pearson_complete



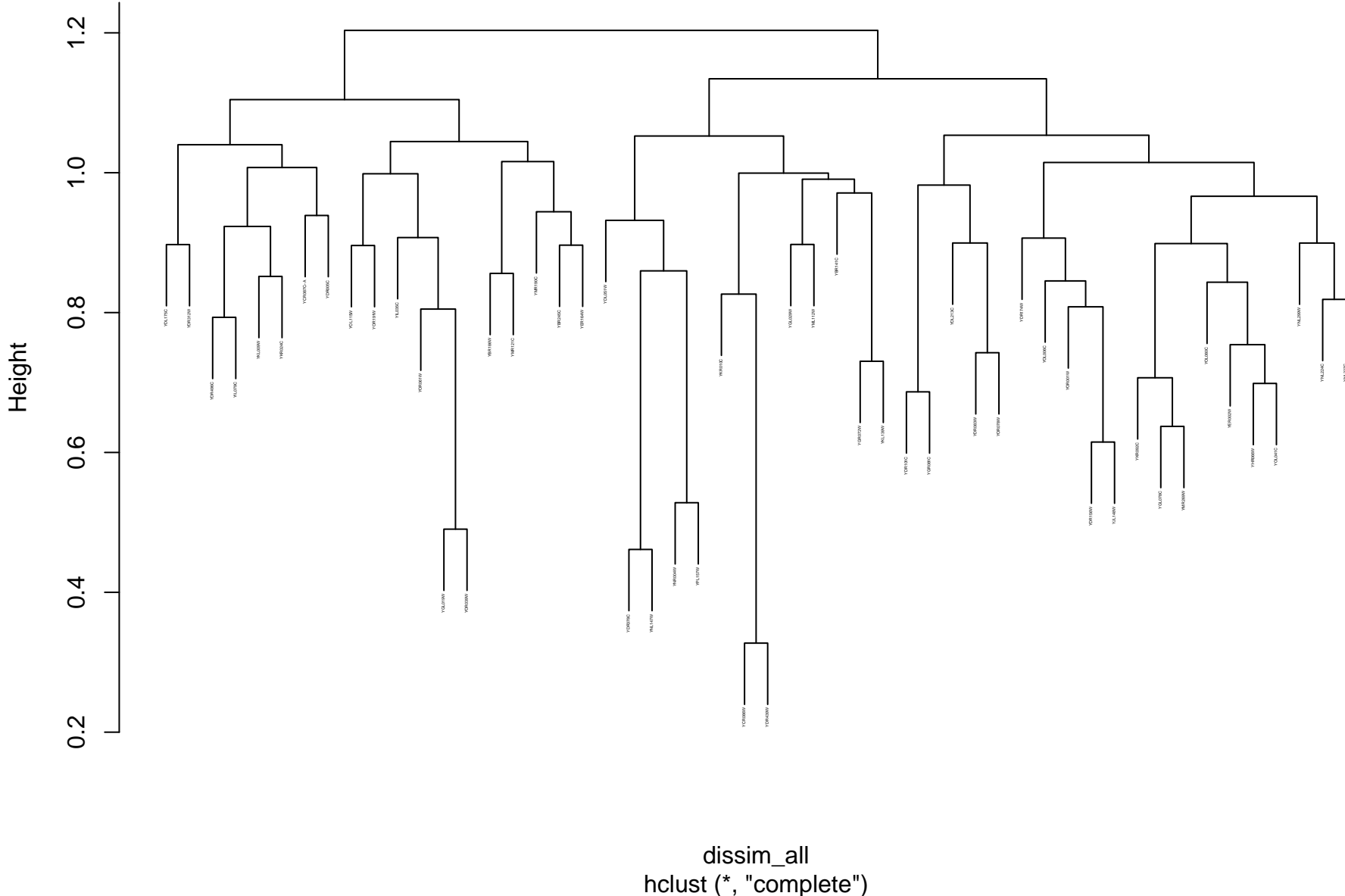
protein folding_GO_pearson_complete



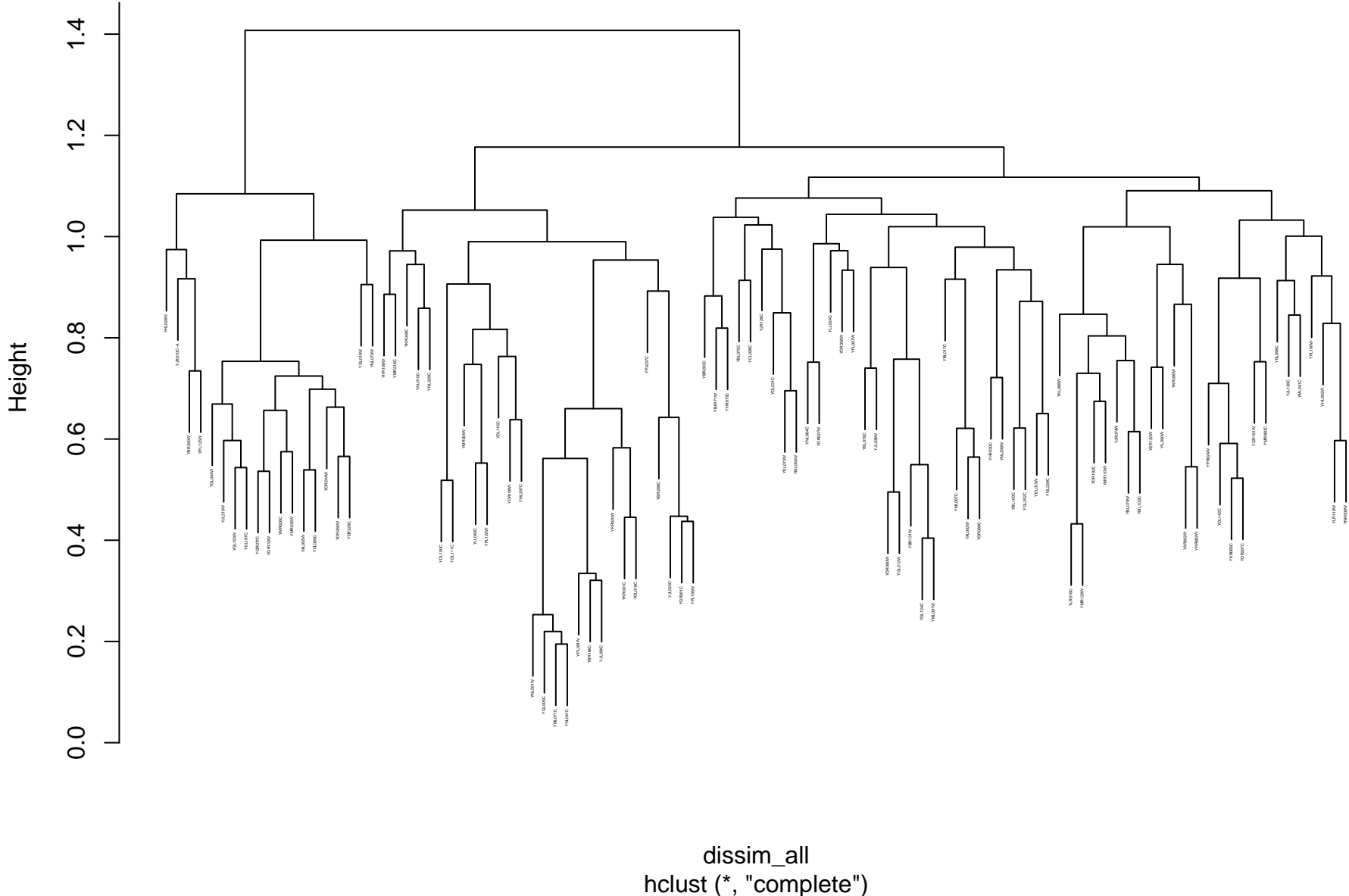
regulation of translation_GO_pearson_complete



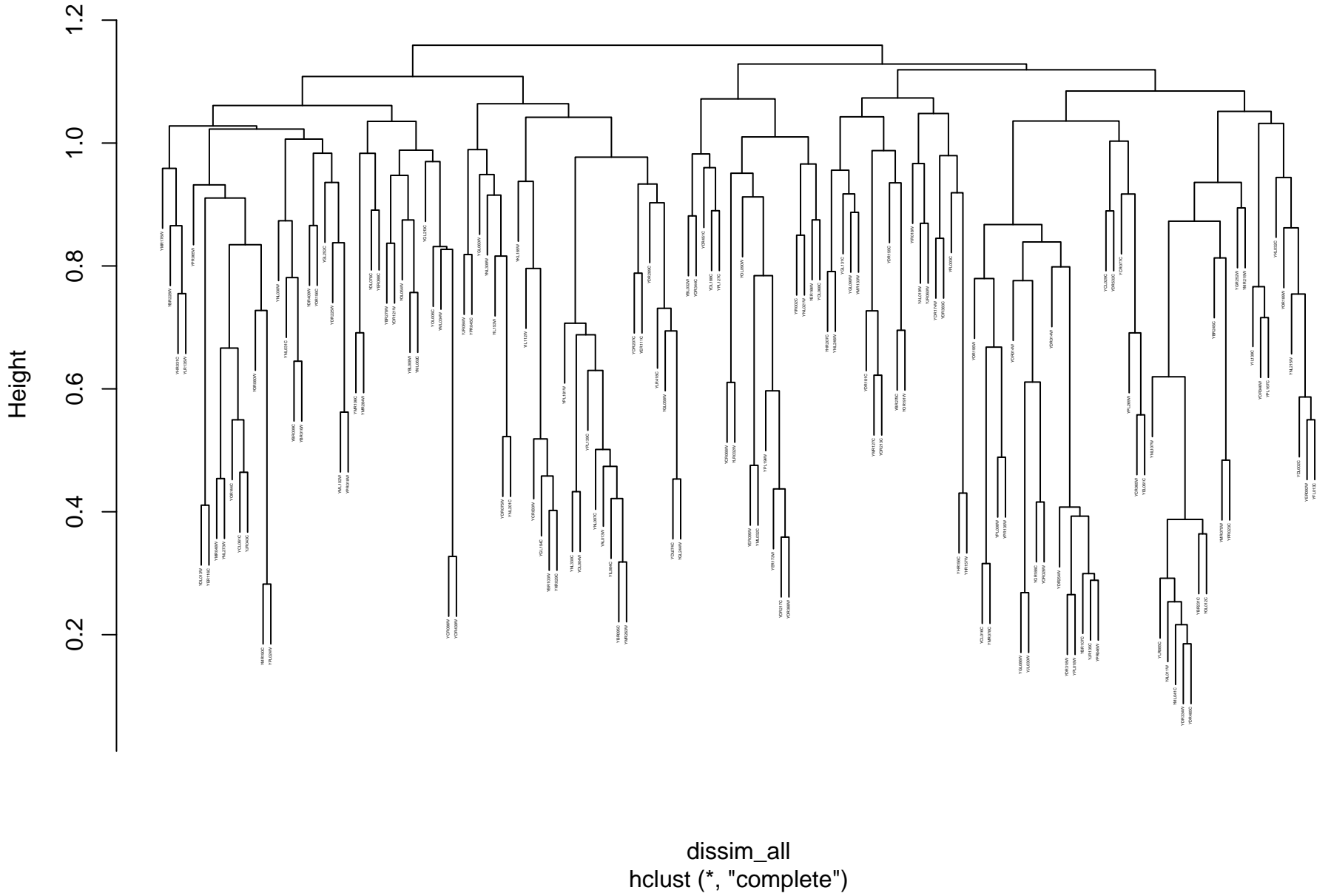
nucleolus_GO_pearson_complete



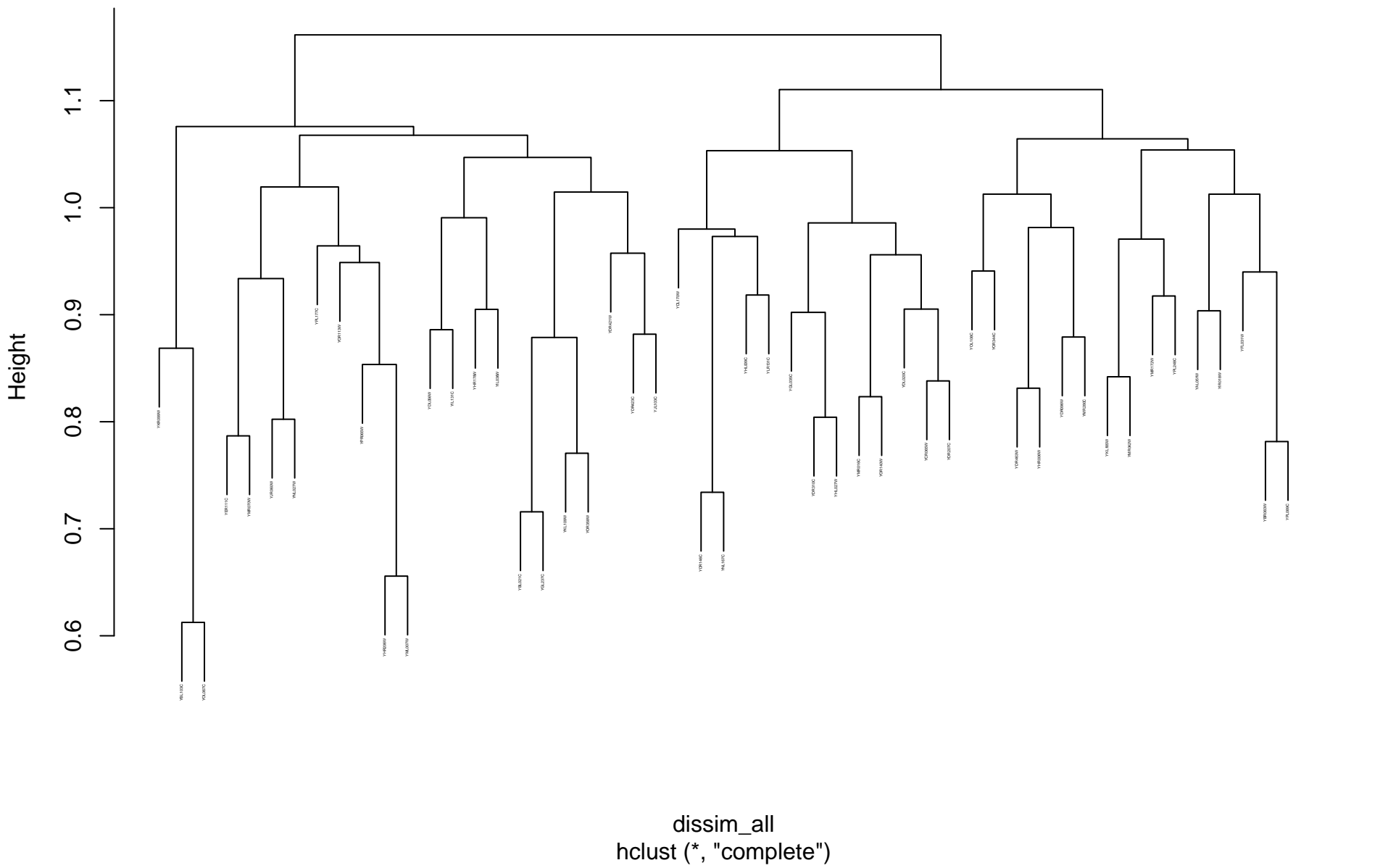
protein targeting_GO_pearson_complete



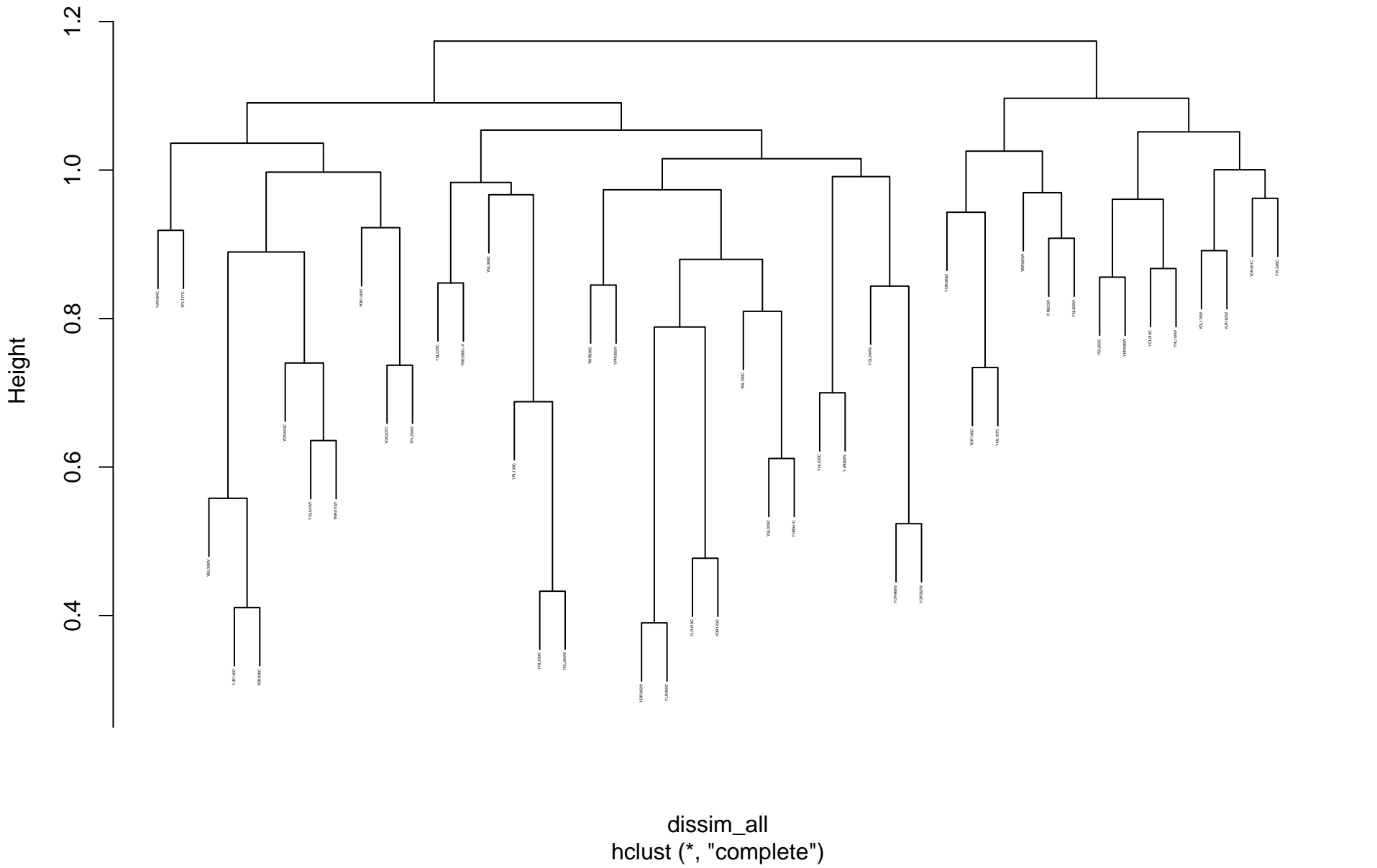
chromosome_GO_pearson_complete



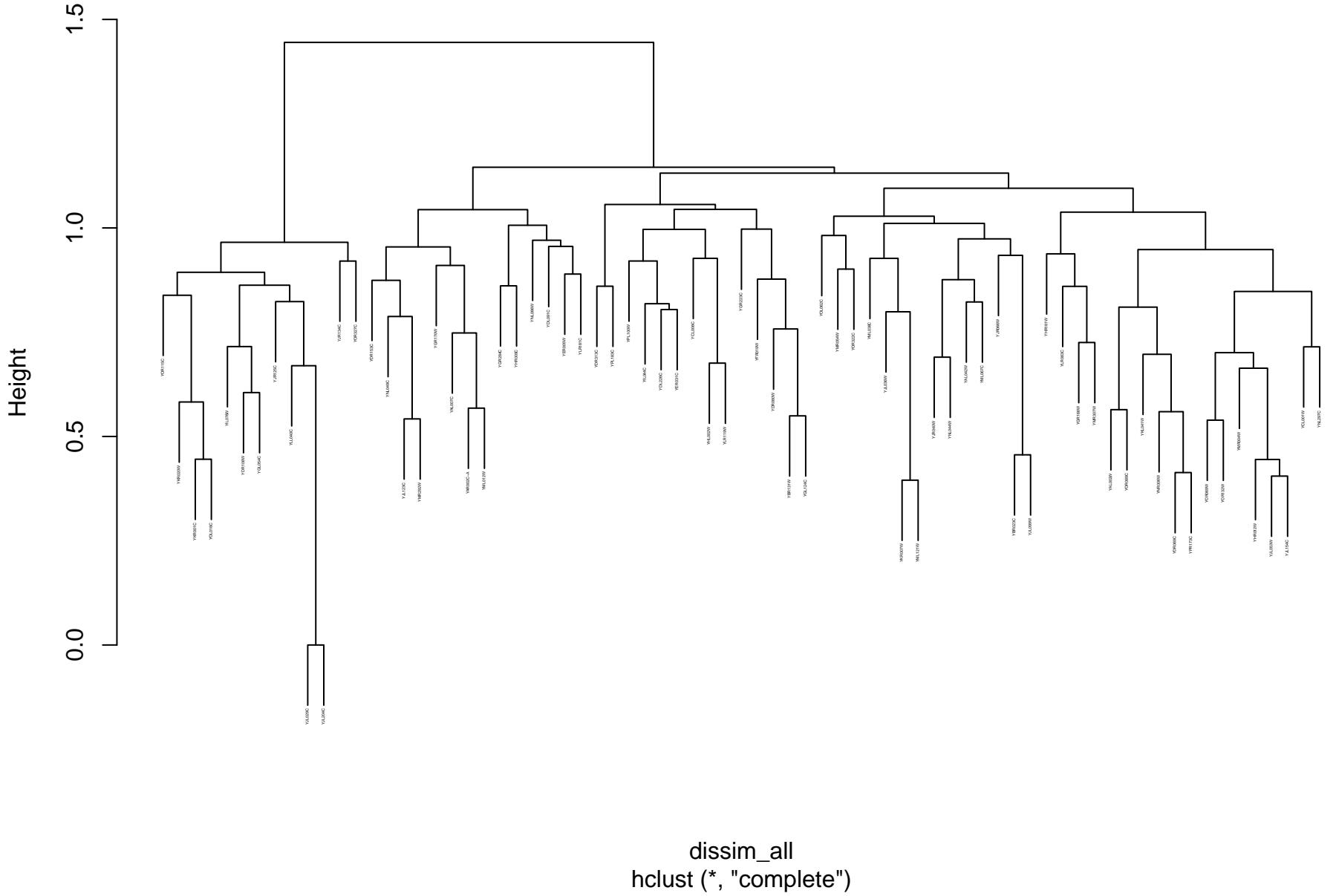
nucleic acid binding transcription factor activity_GO_pearson_complete



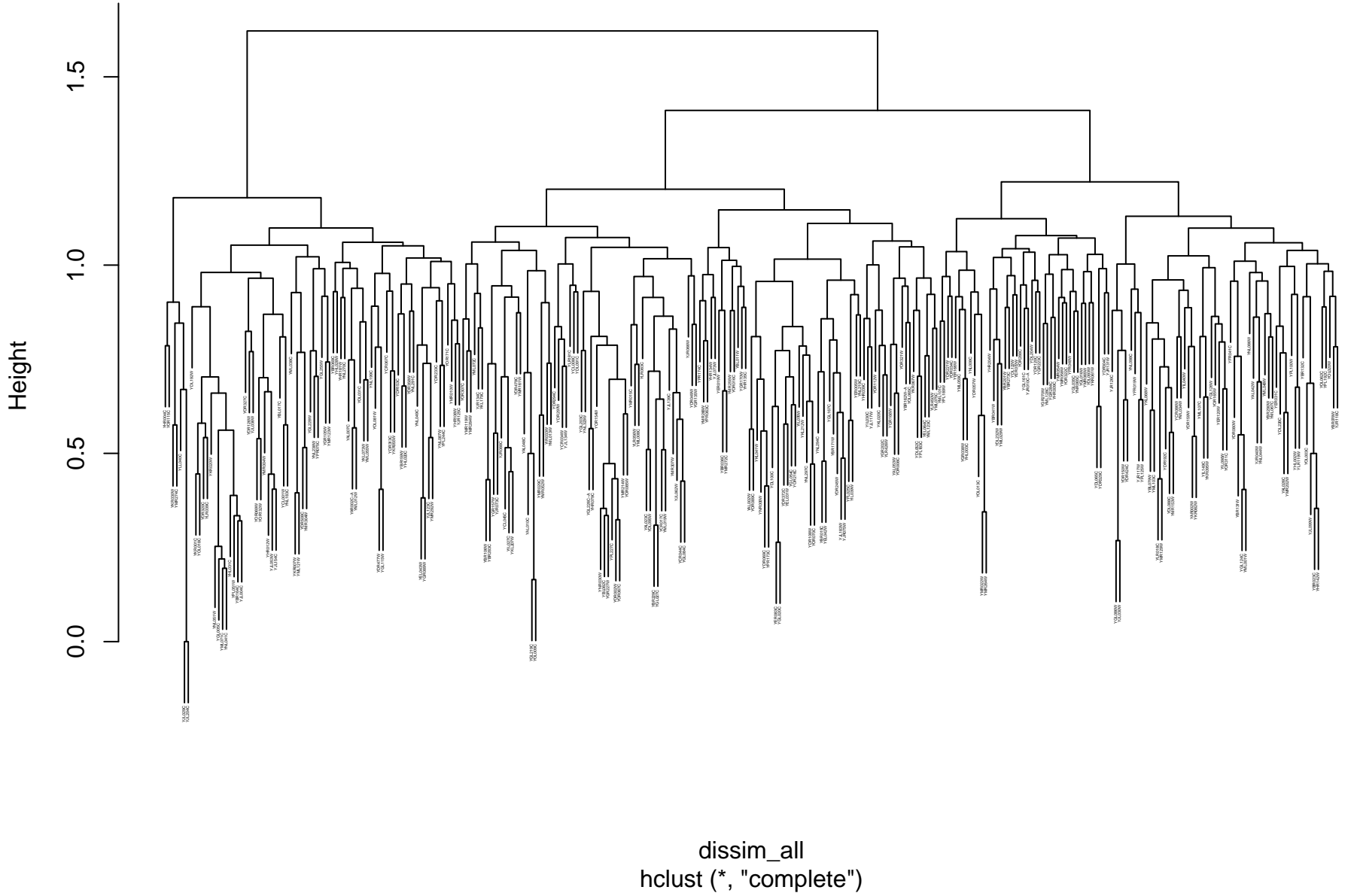
transcription factor activity, protein binding_GO_pearson_complete



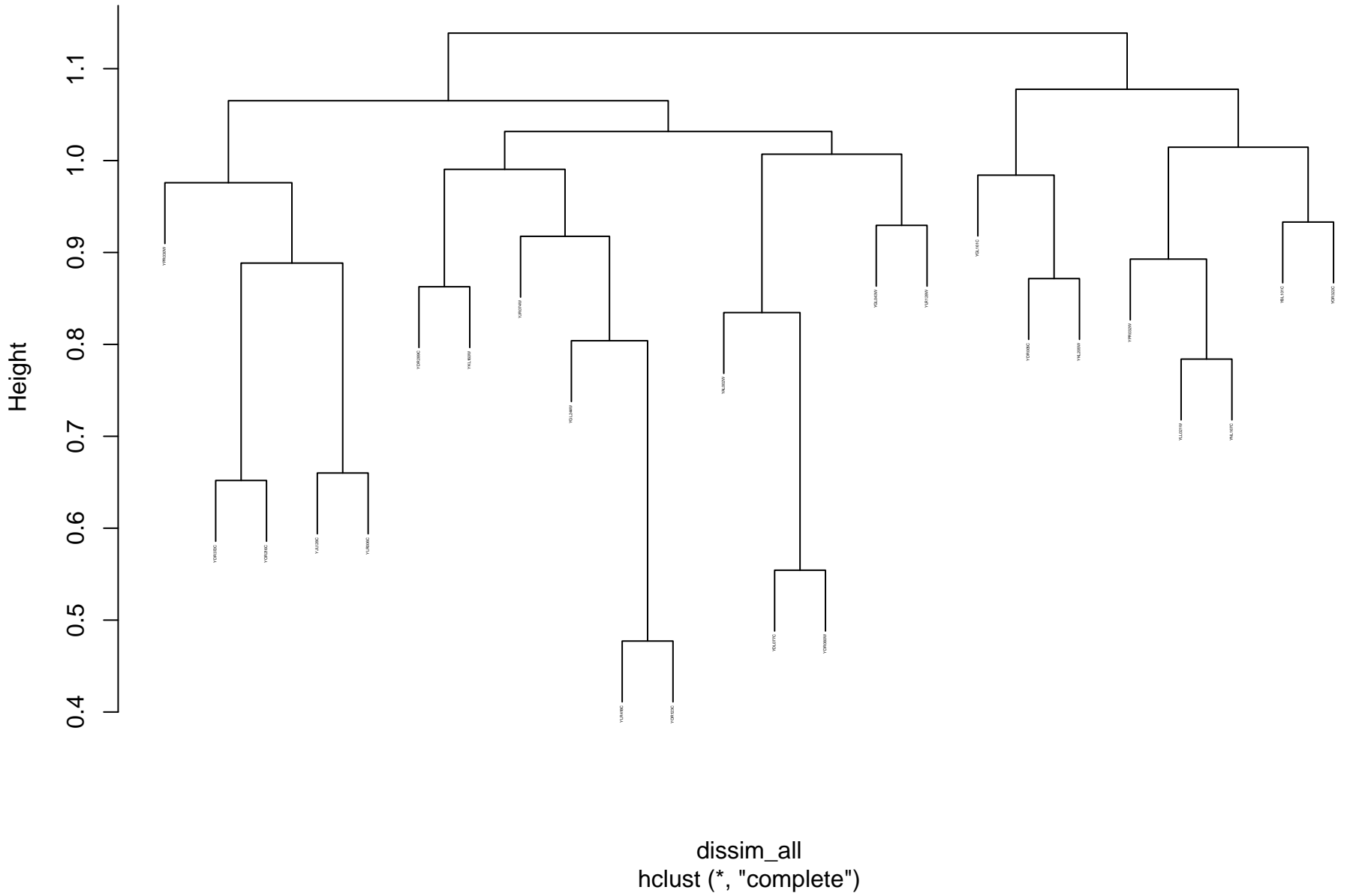
cytoplasmic vesicle_GO_pearson_complete



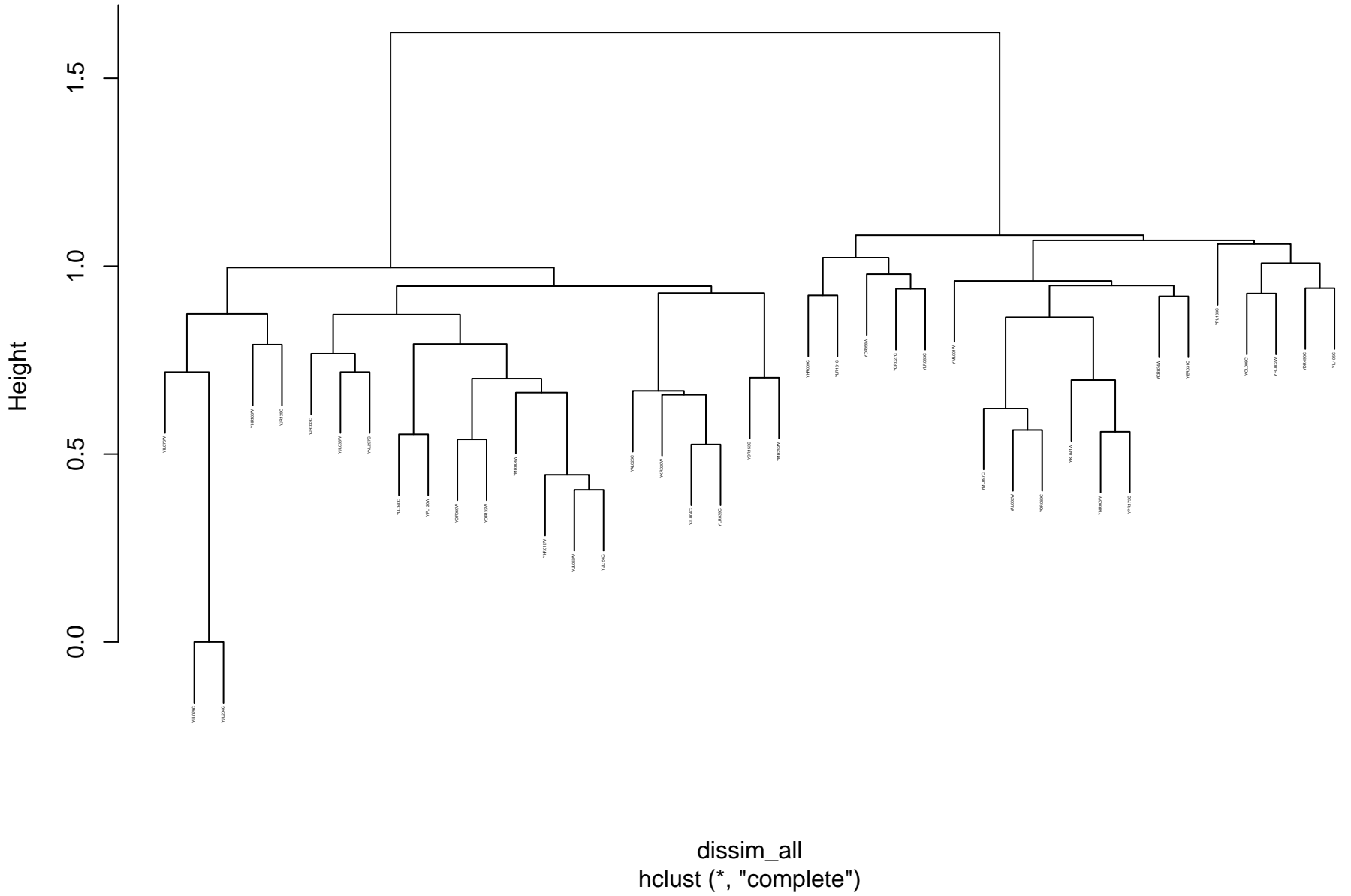
endomembrane system_GO_pearson_complete



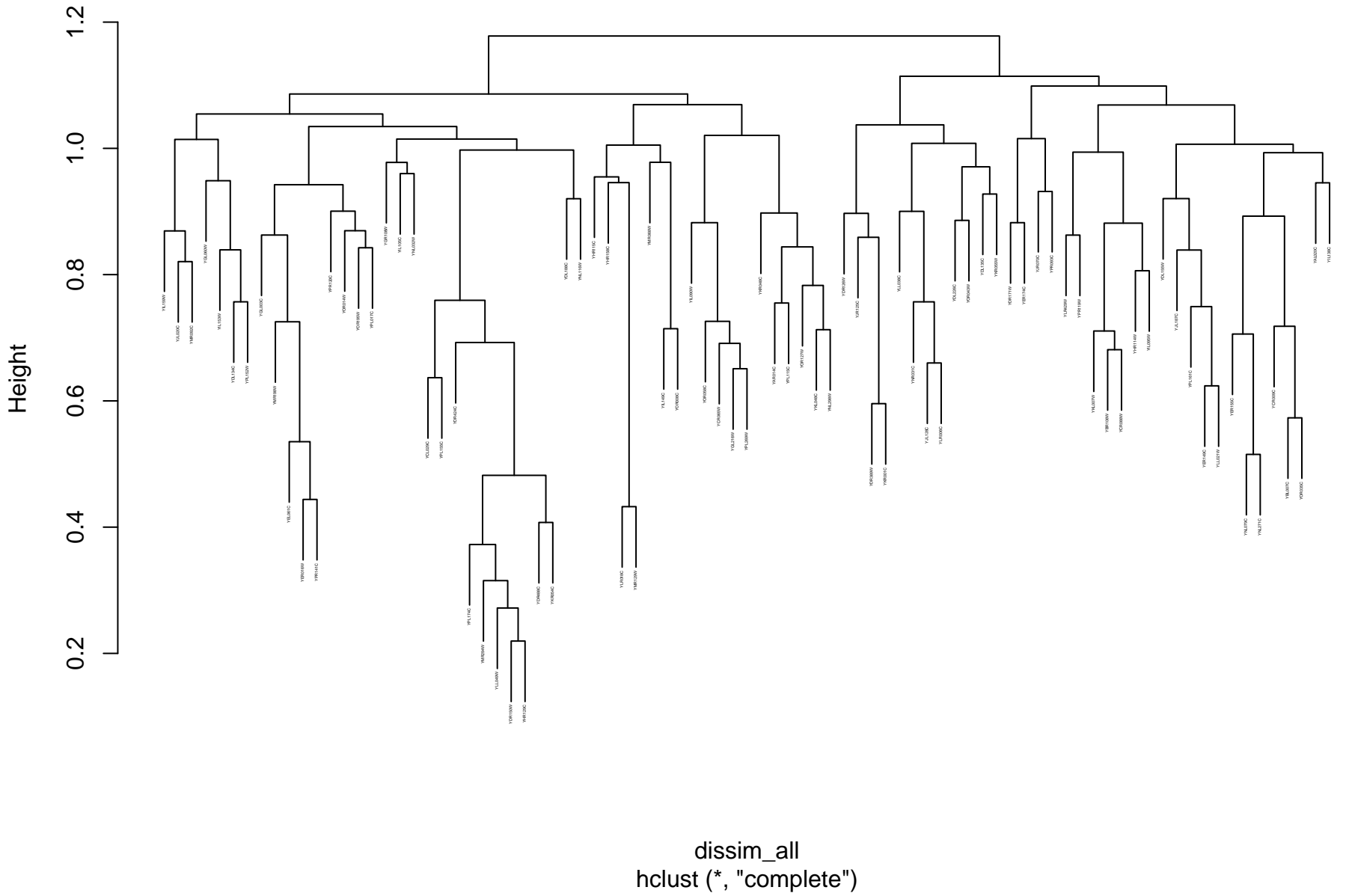
enzyme binding_GO_pearson_complete



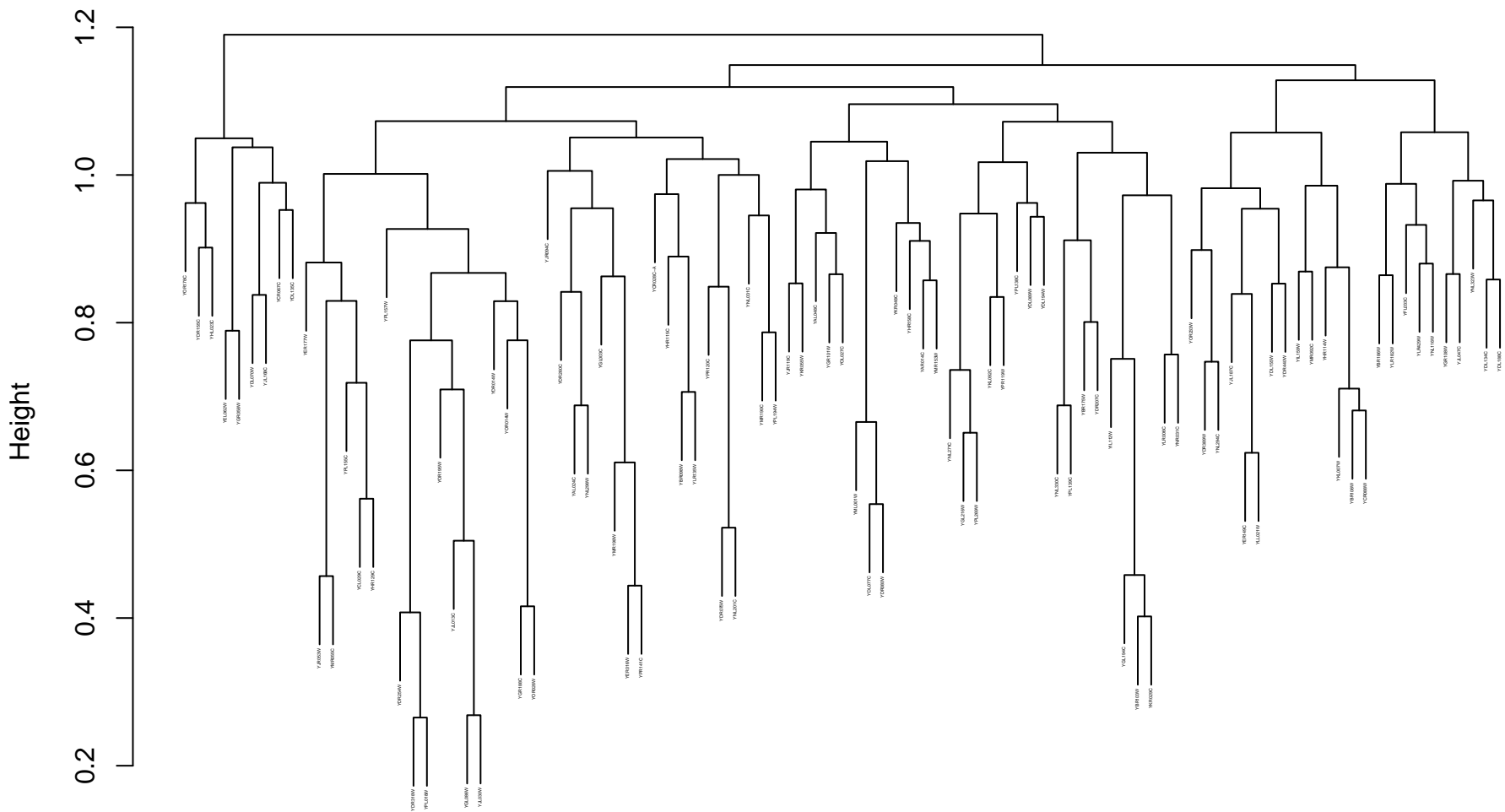
endosomal transport_GO_pearson_complete



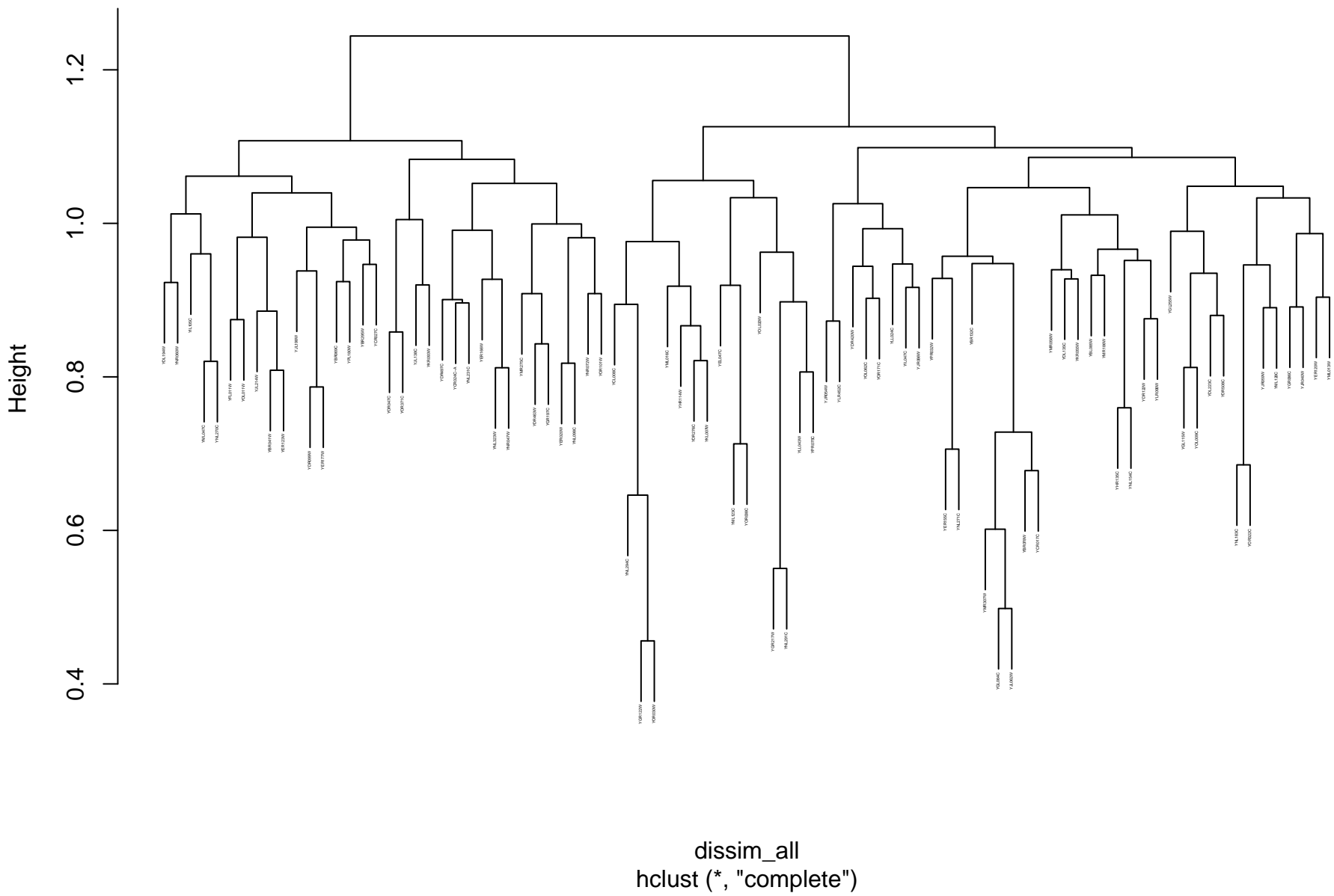
cytoskeleton organization_GO_pearson_complete



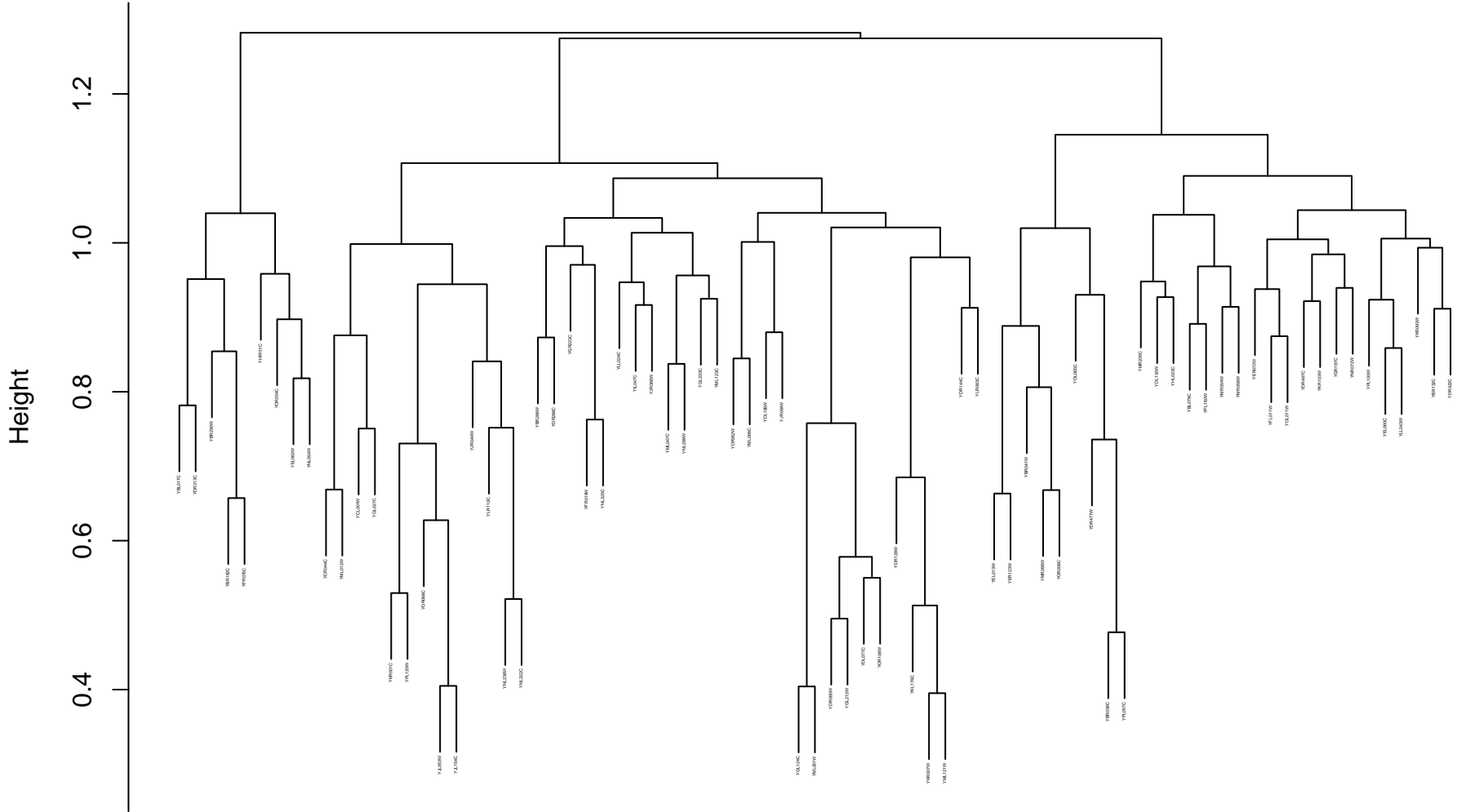
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dissim_all
hclust (*, "complete")
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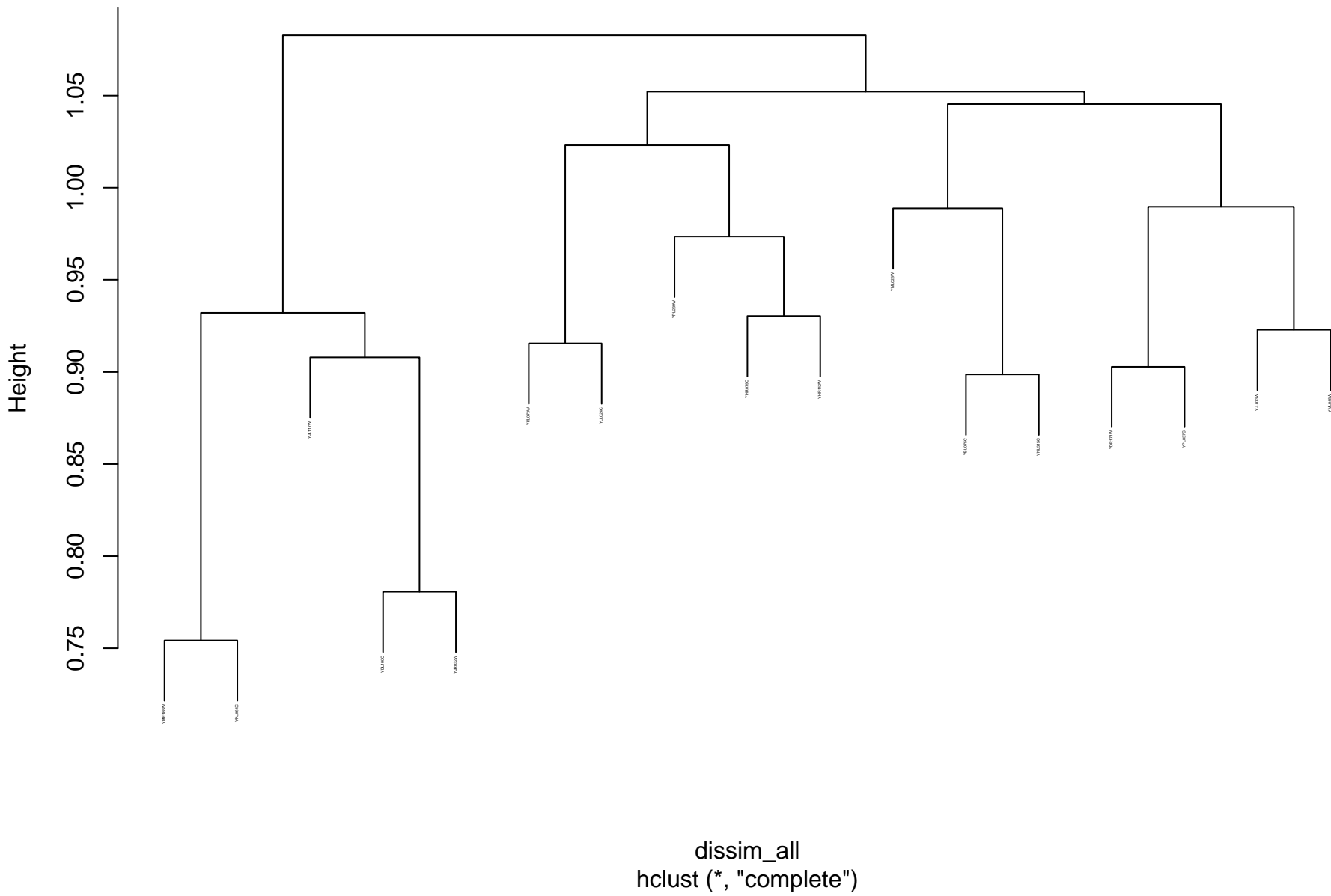
plasma membrane_GO_pearson_complete



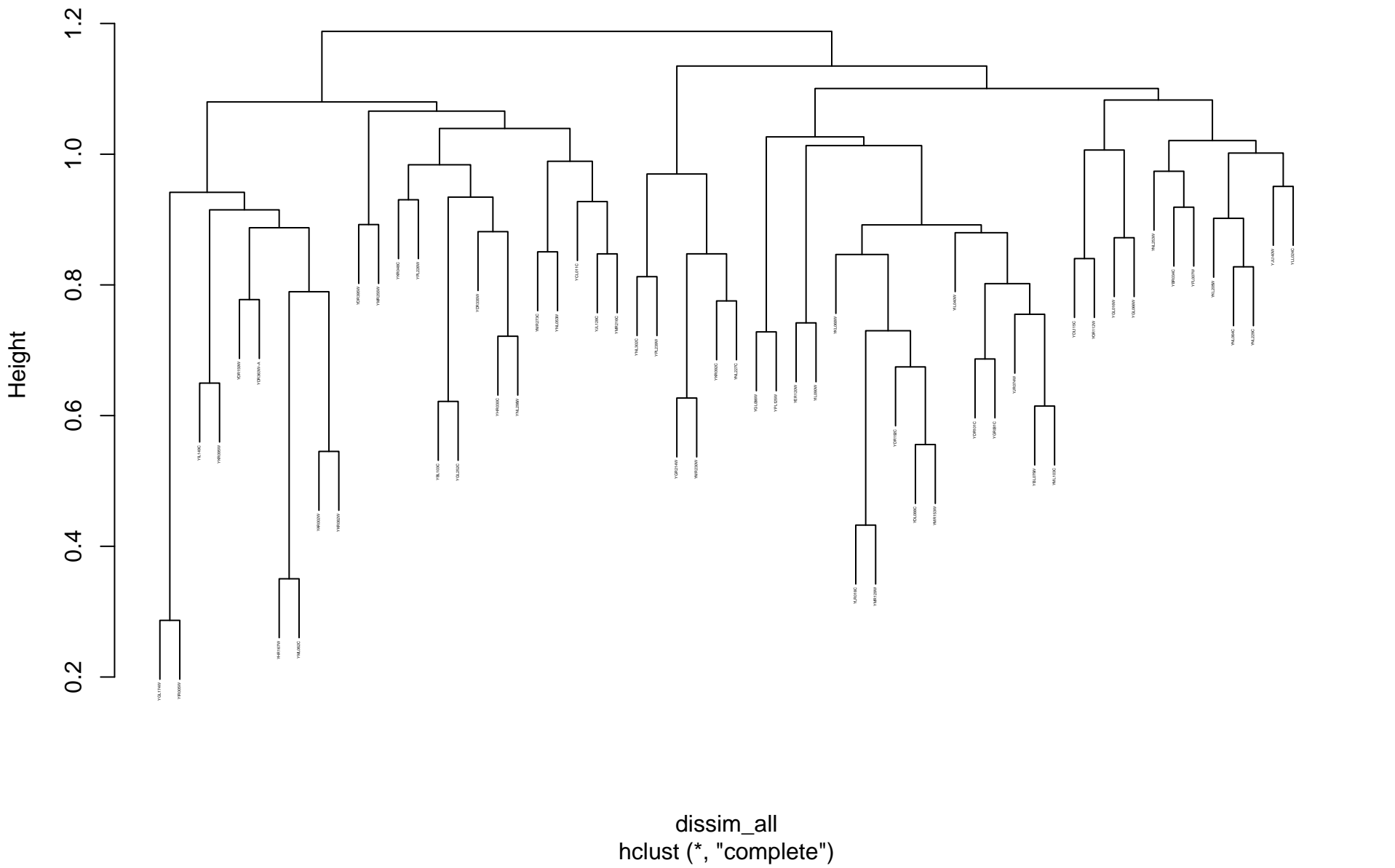
vacuole_GO_pearson_complete



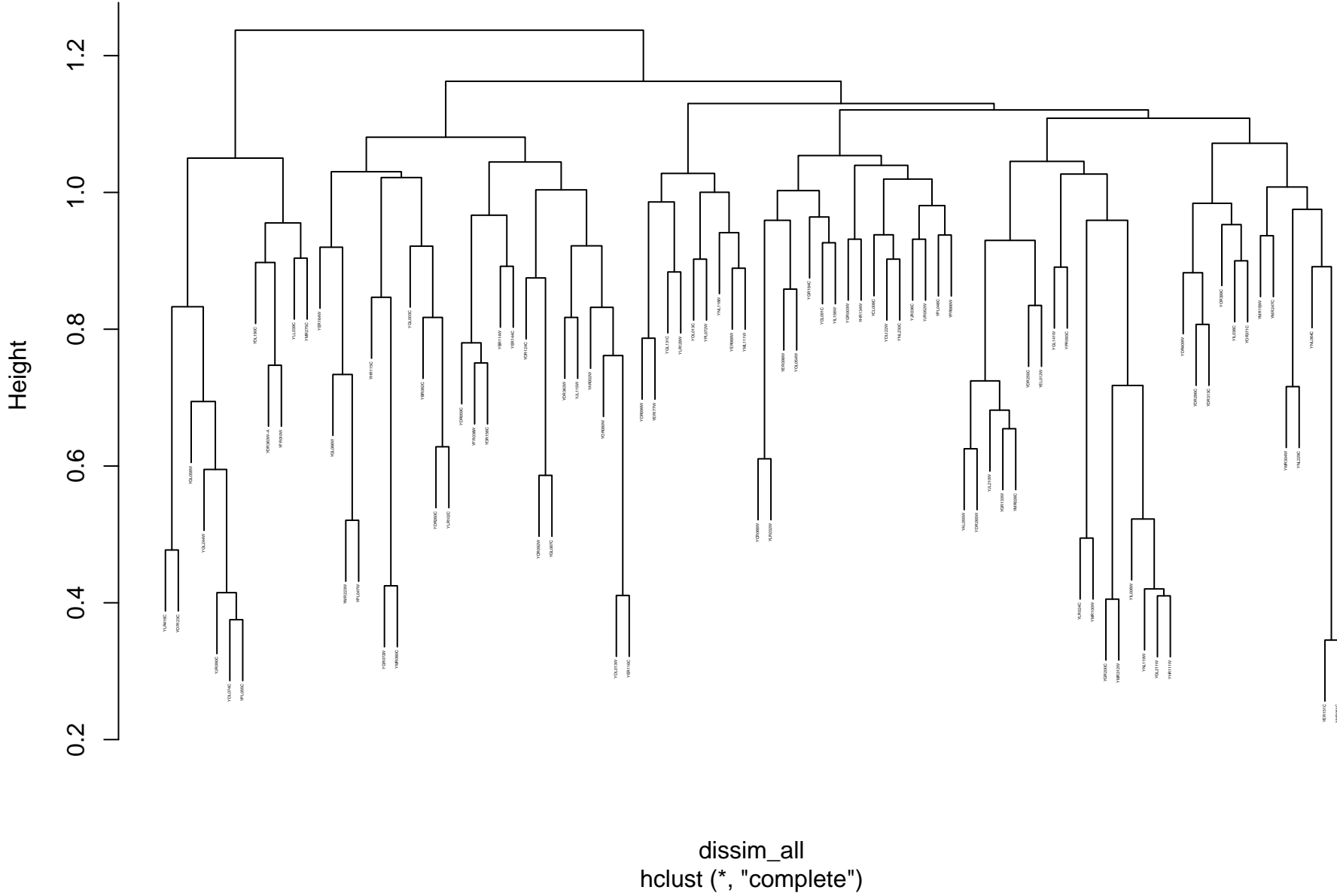
unfolded protein binding_GO_pearson_complete



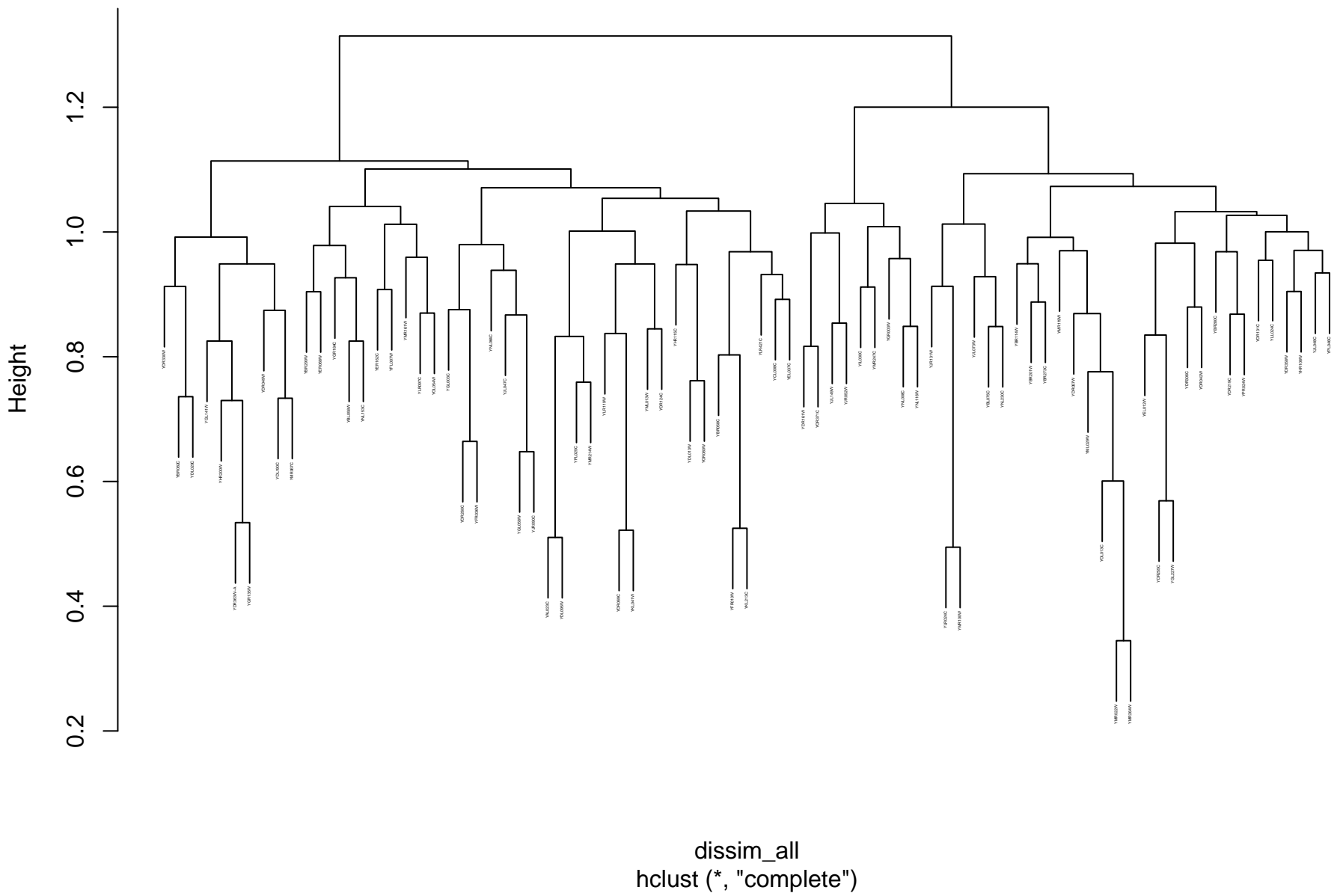
nuclear transport_GO_pearson_complete



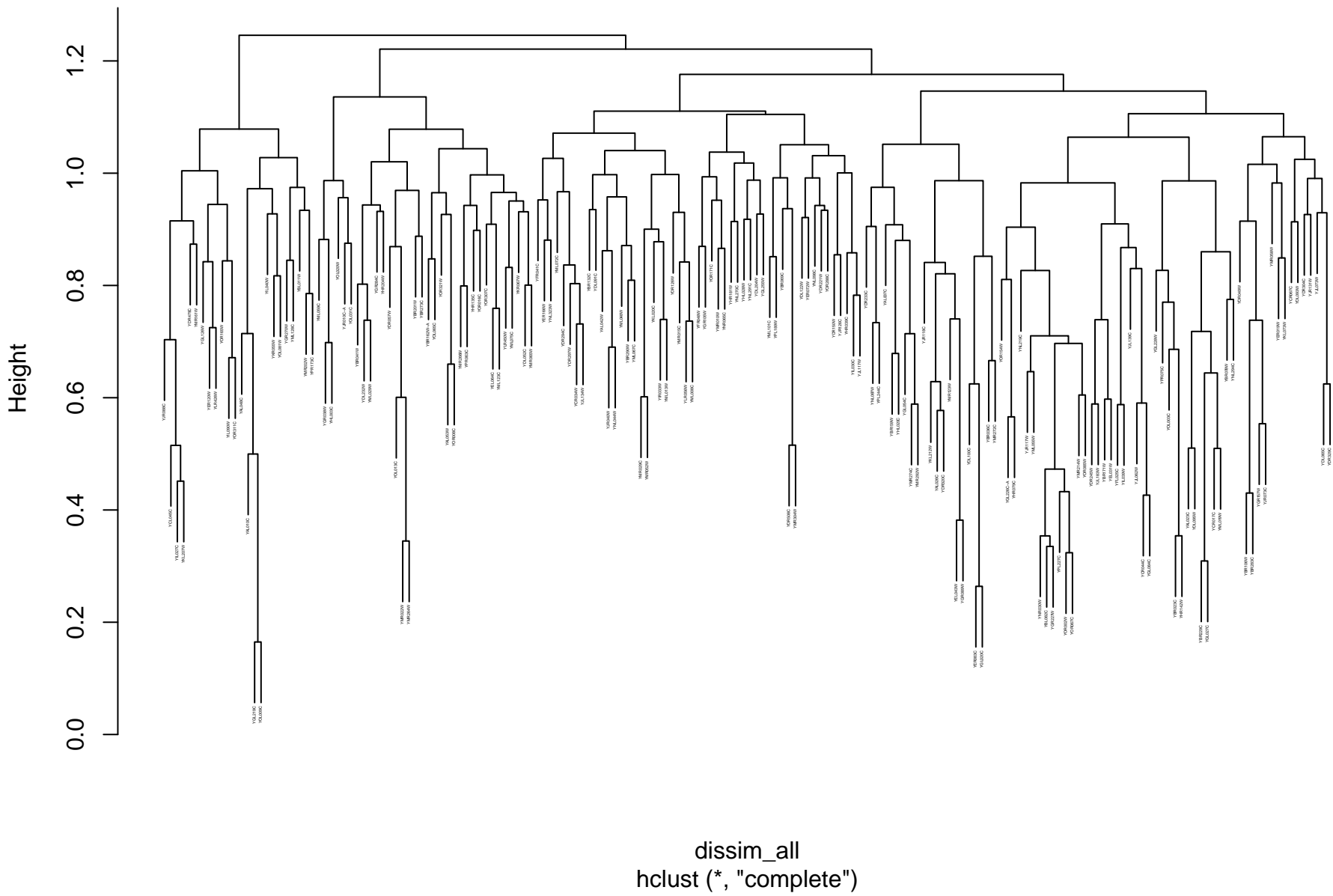
protein modification by small protein conjugation or removal_GO_pearson_complete



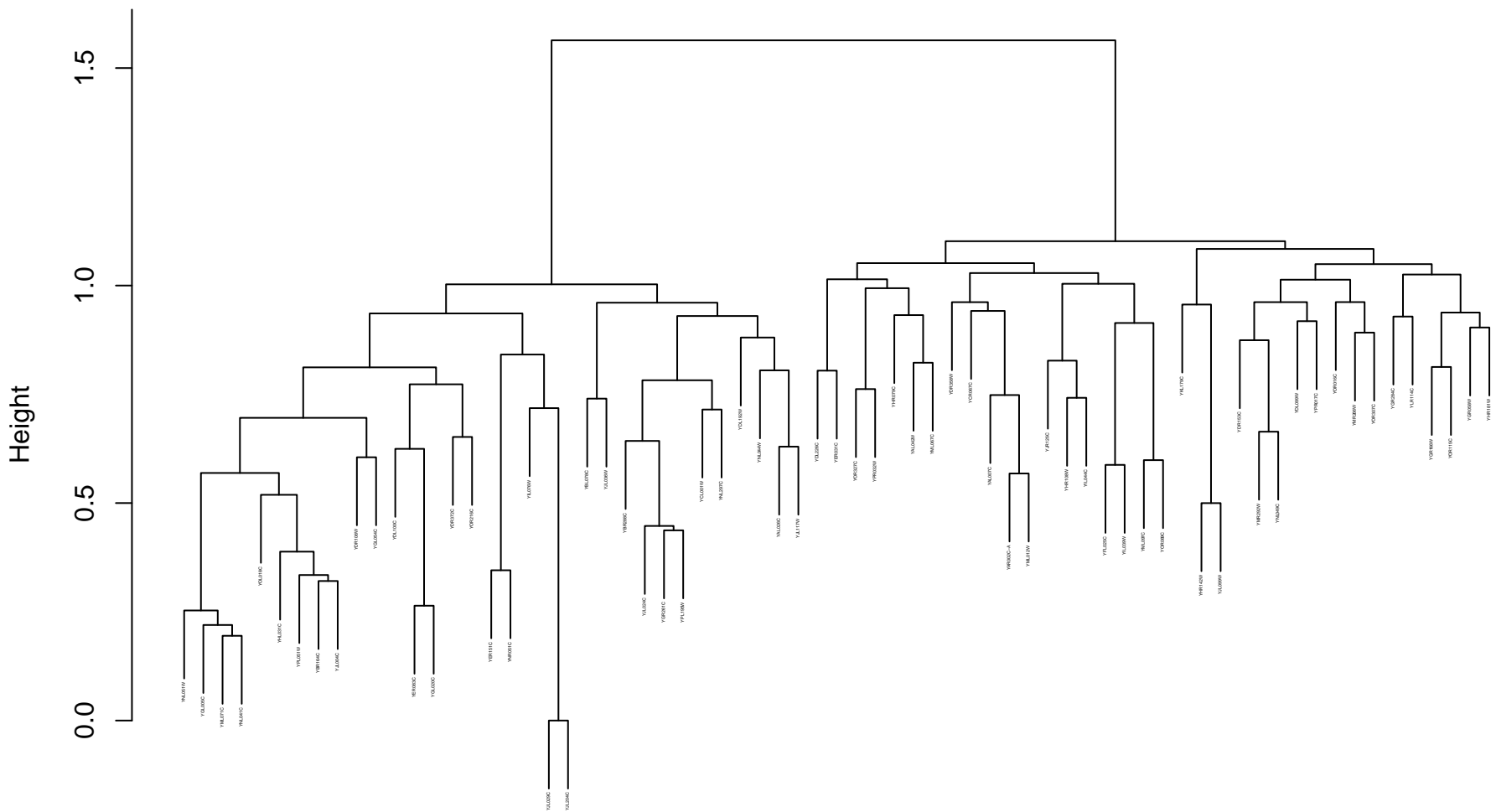
proteolysis involved in cellular protein catabolic process_GO_pearson_complete



endoplasmic reticulum_GO_pearson_complete

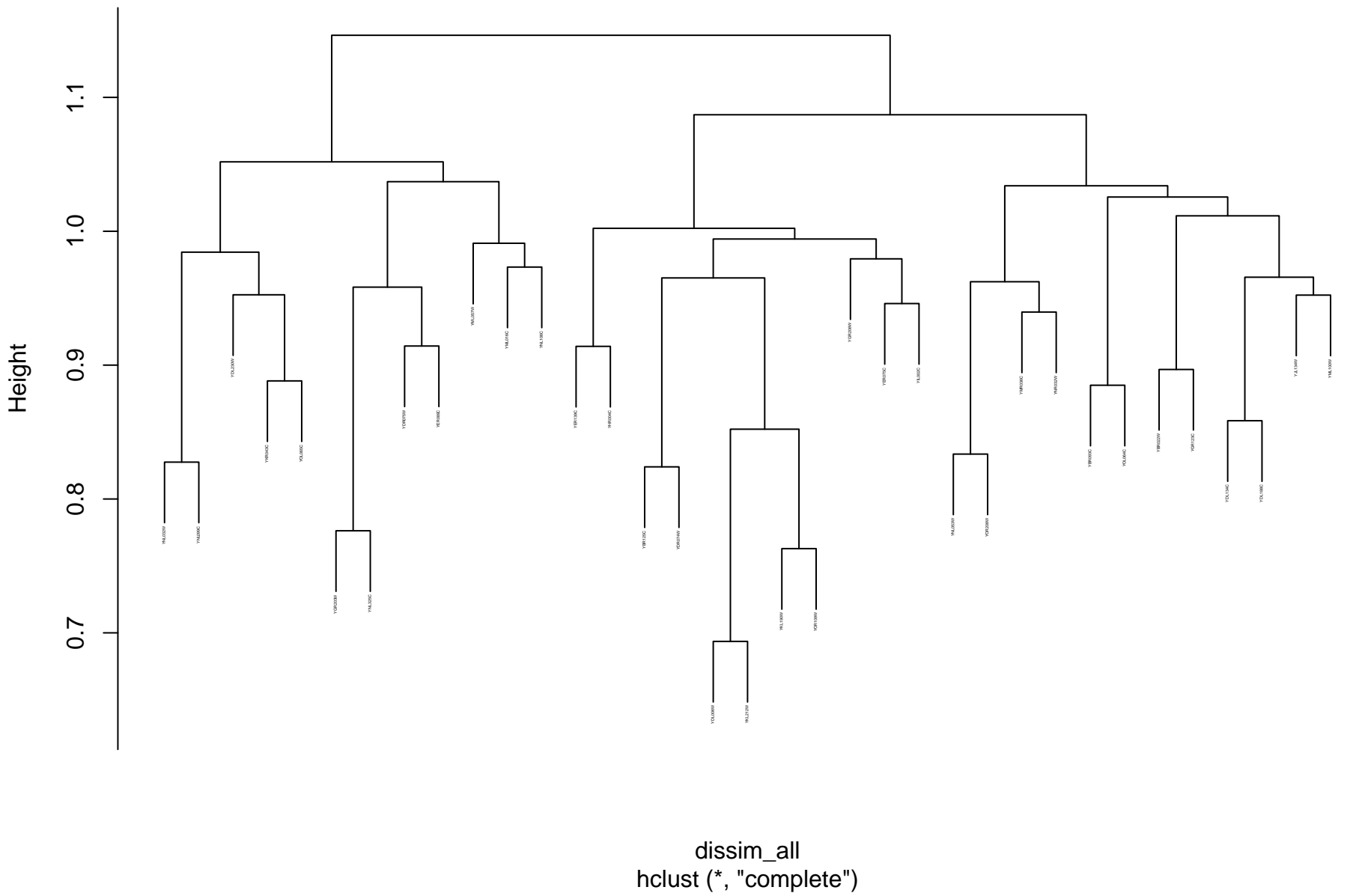


Golgi vesicle transport_GO_pearson_complete

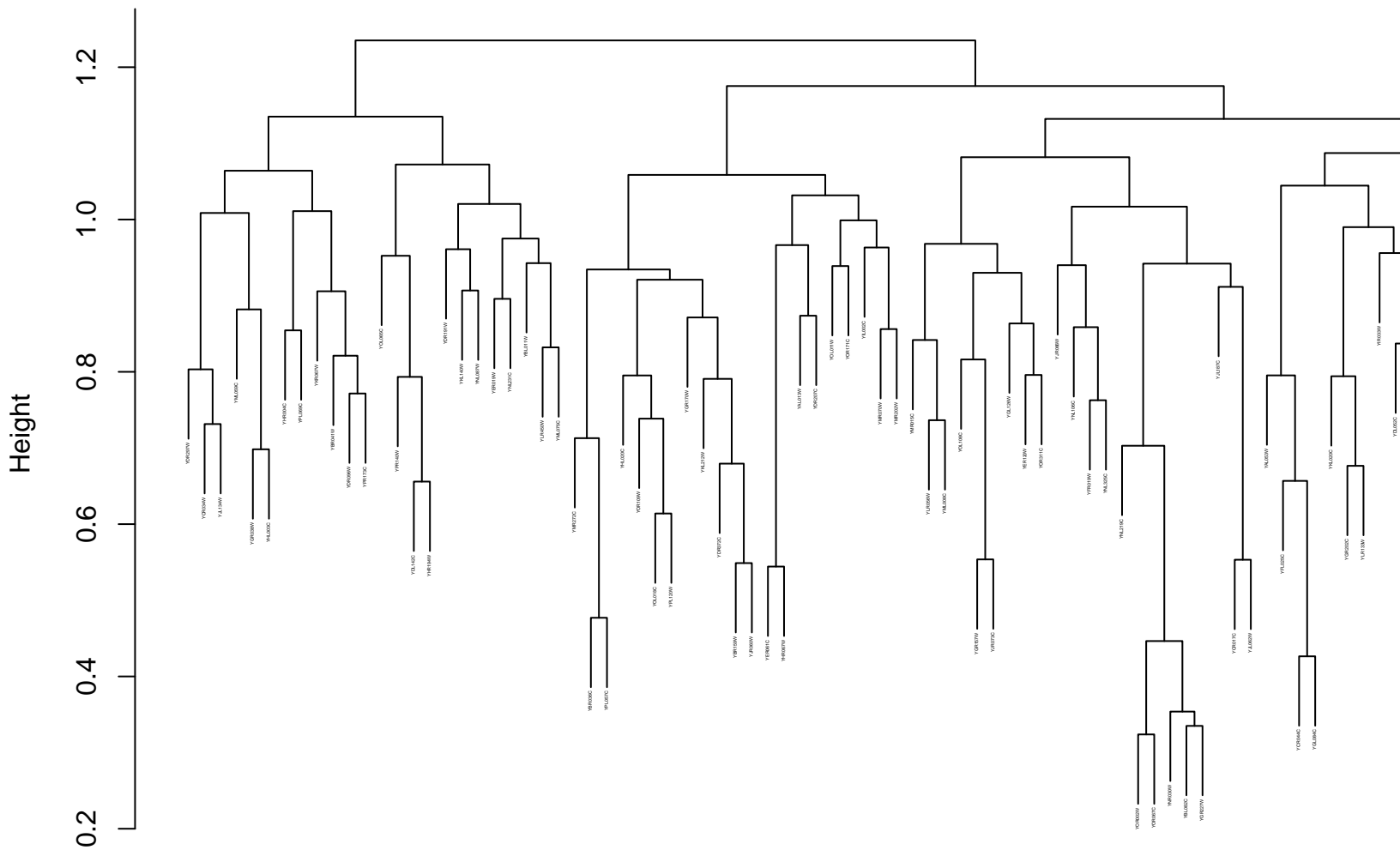


dissim_all
hclust (*, "complete")

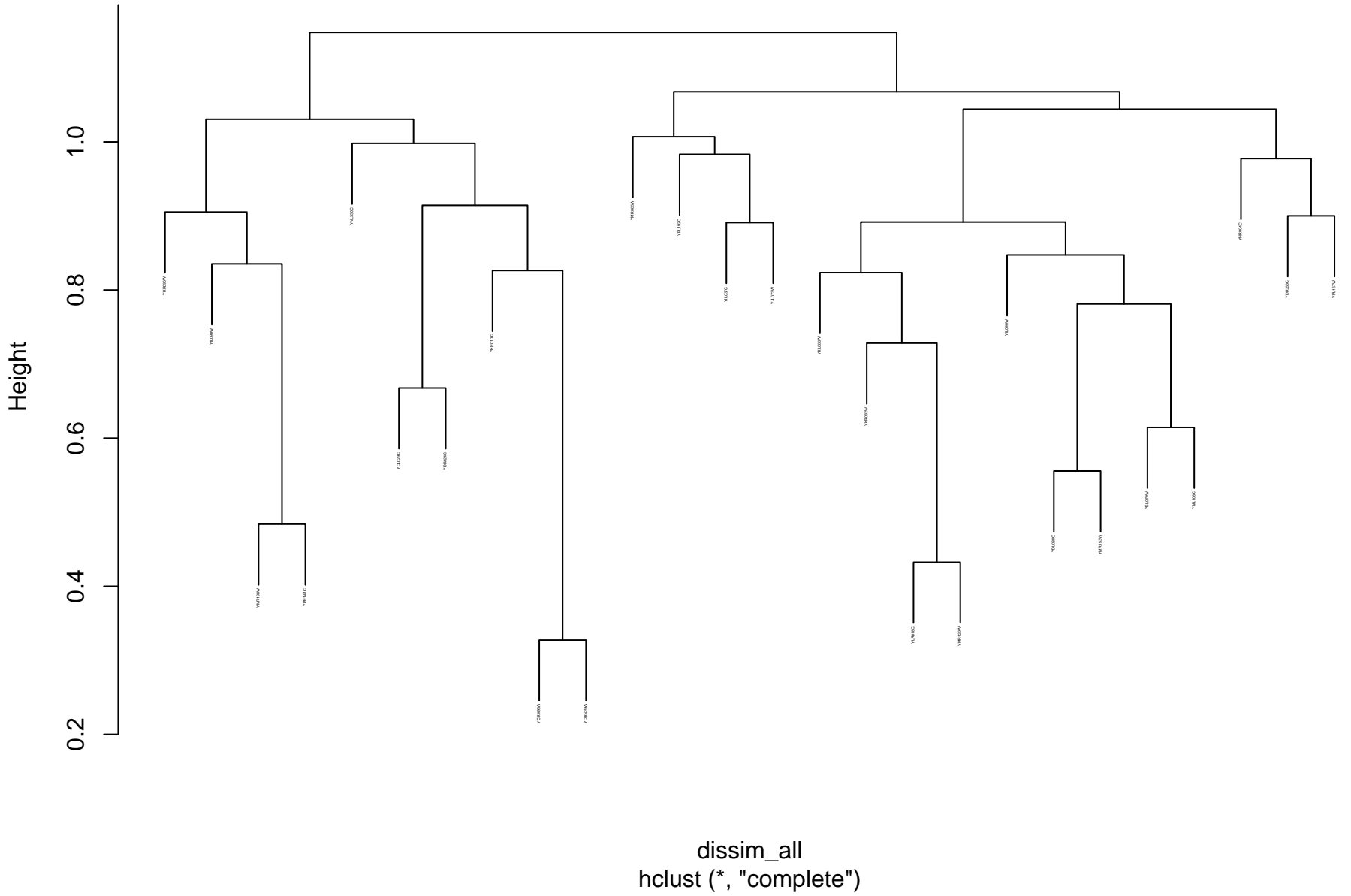
phosphatase activity_GO_pearson_complete



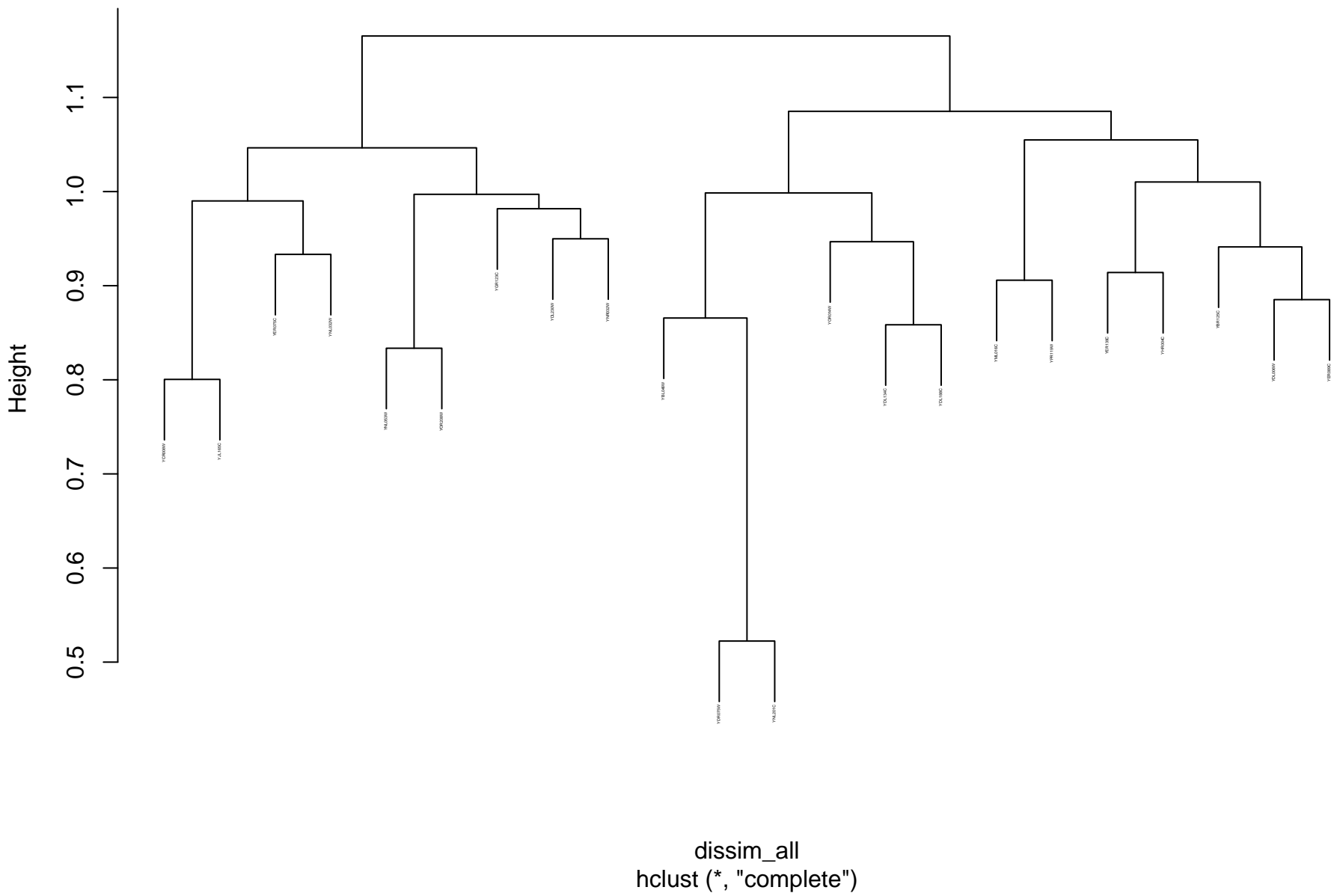
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dissim_all
hclust (*, "complete")
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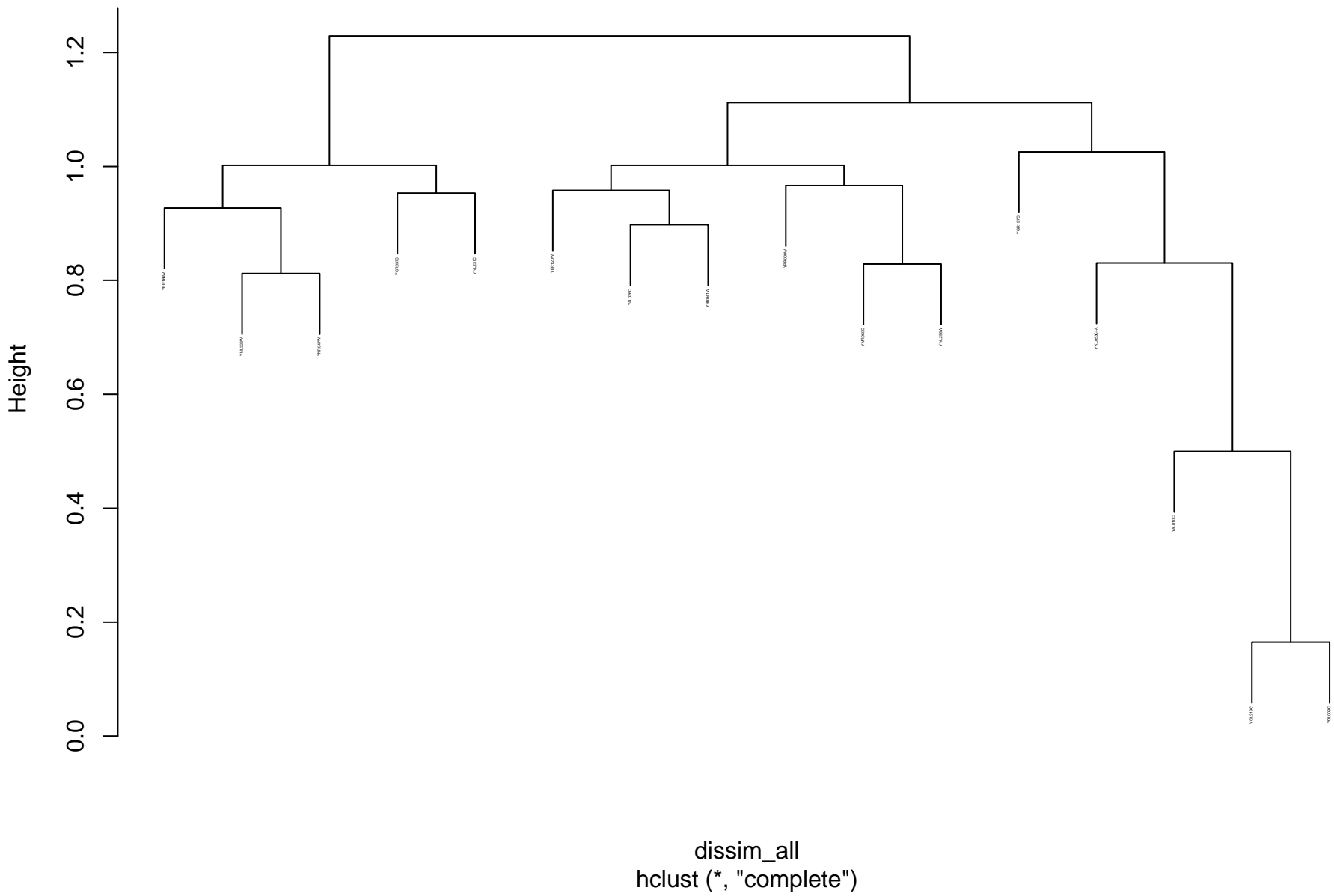
nucleus organization_GO_pearson_complete



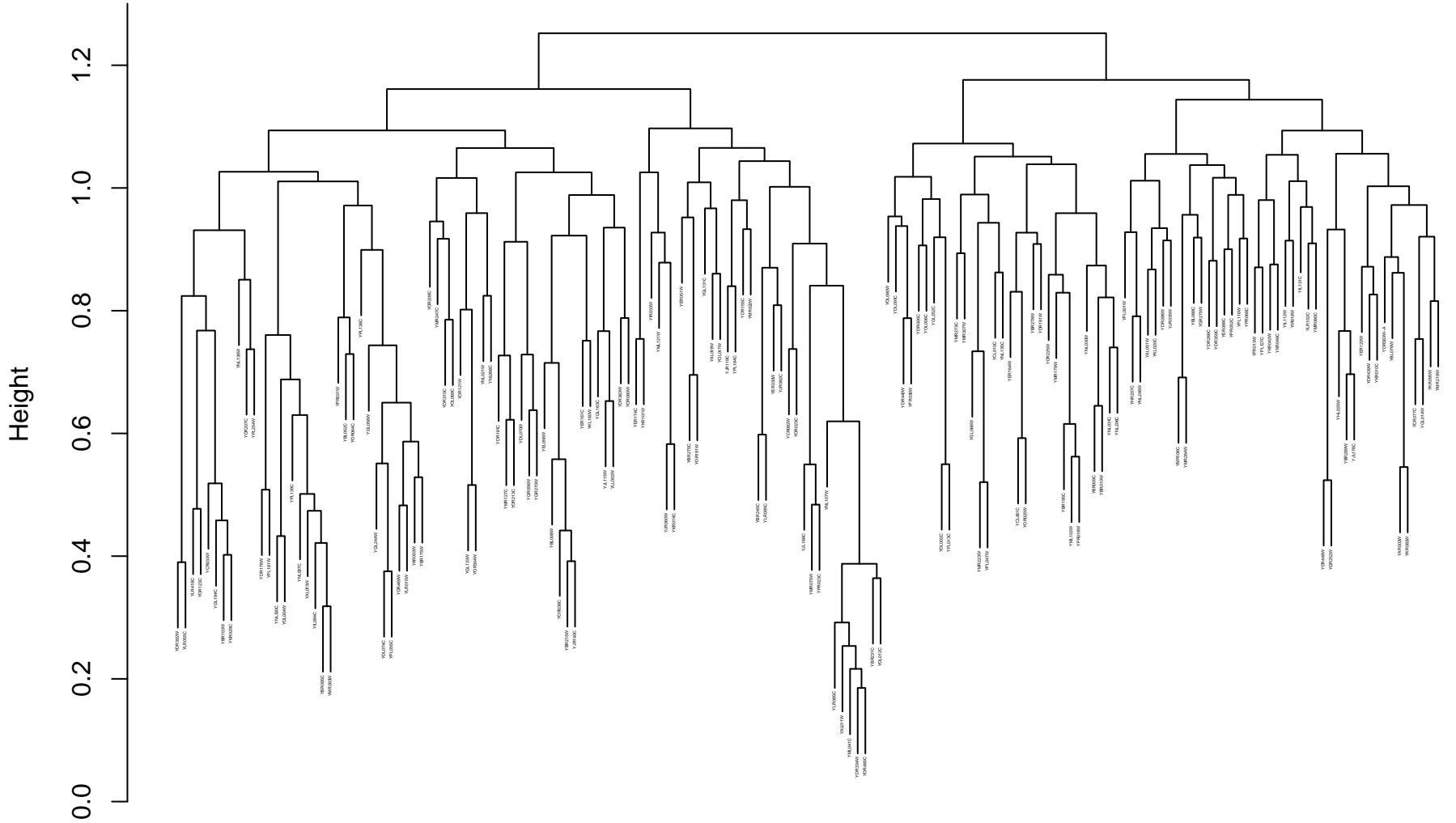
protein dephosphorylation_GO_pearson_complete



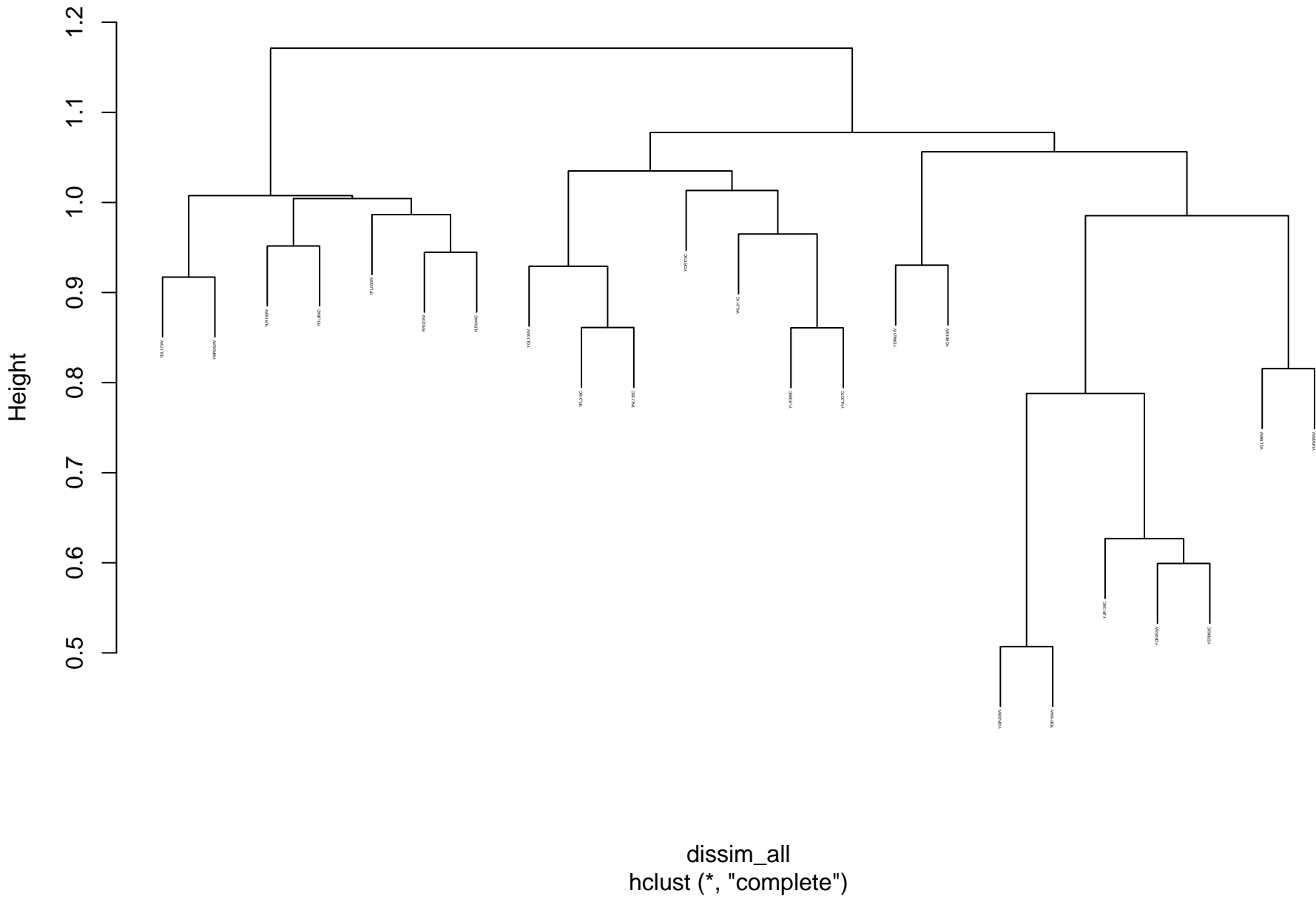
lipid transport_GO_pearson_complete



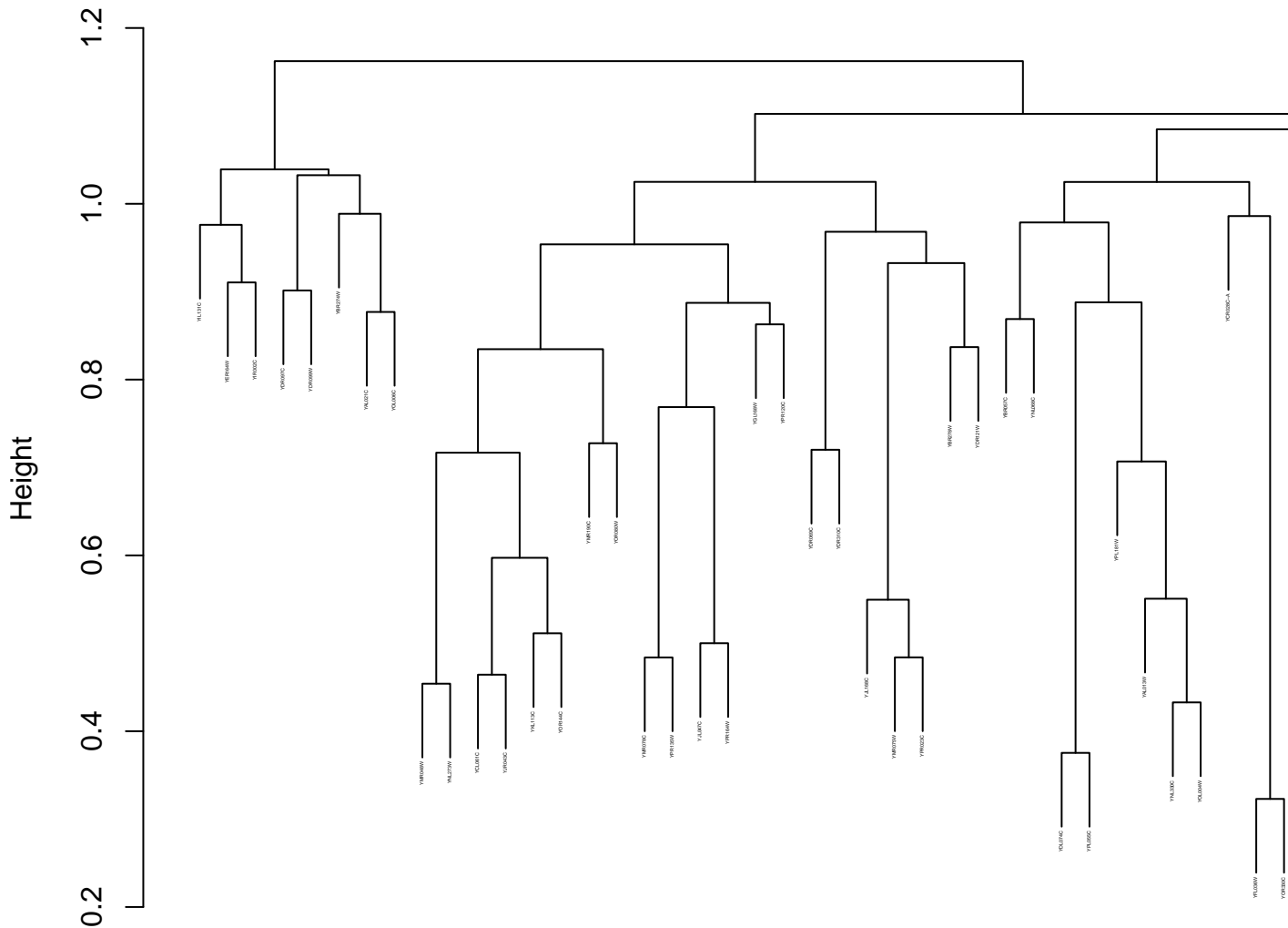
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dissim_all
hclust (*, "complete")
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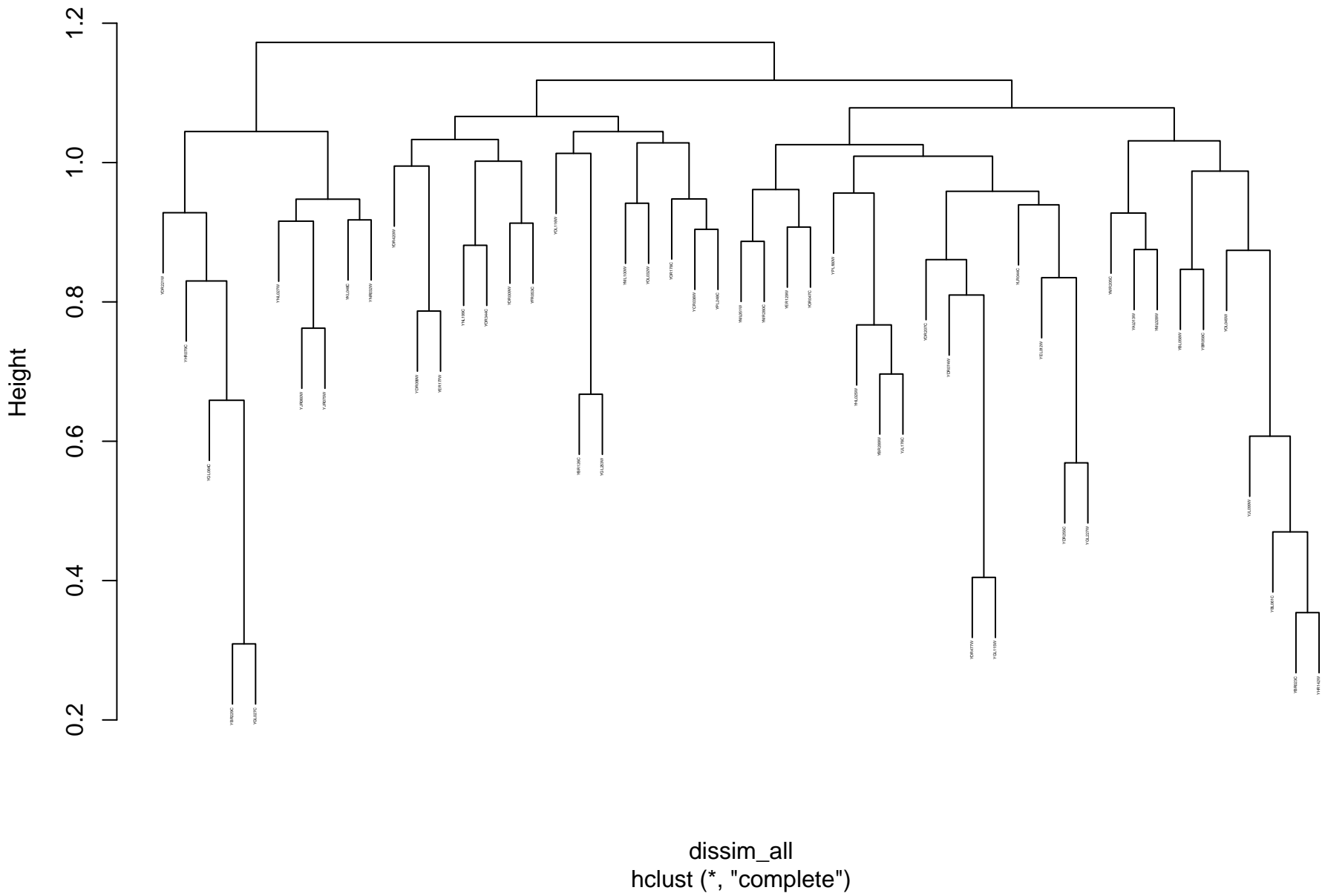
cellular amino acid metabolic process_GO_pearson_complete



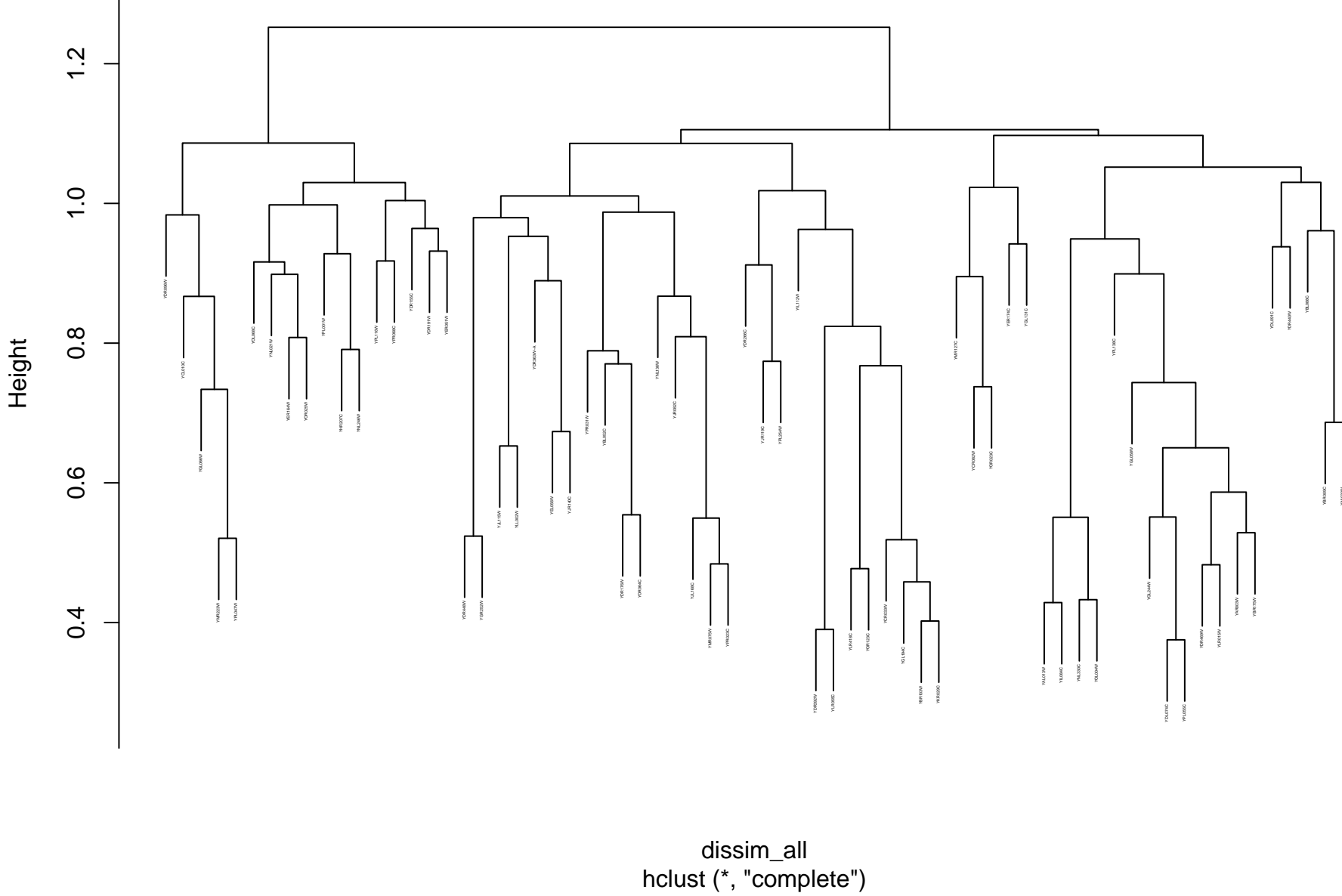
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dissim_all
hclust (*, "complete")
```



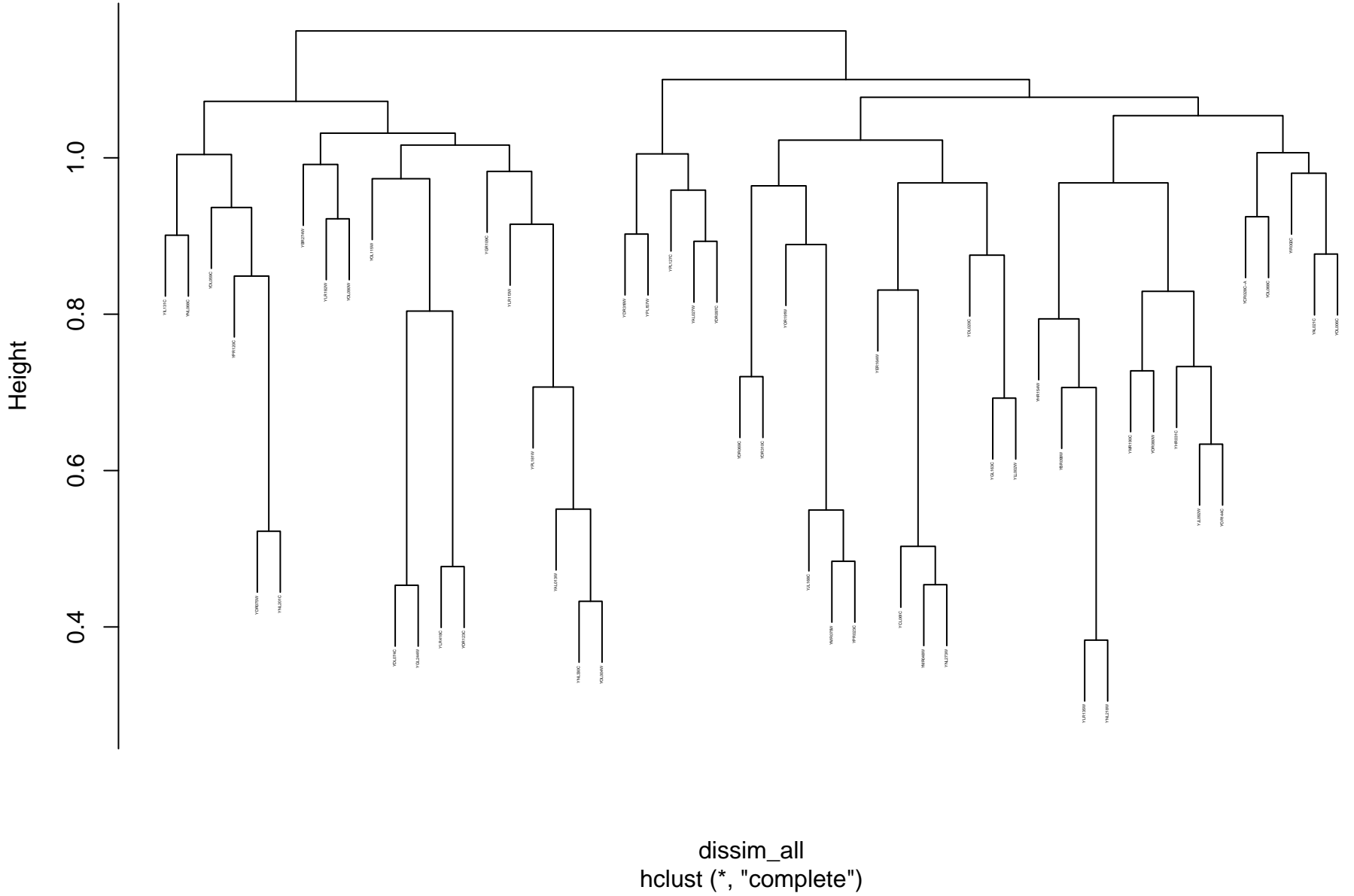
carbohydrate metabolic process_GO_pearson_complete



histone modification_GO_pearson_complete

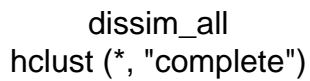


regulation of DNA metabolic process_GO_pearson_complete

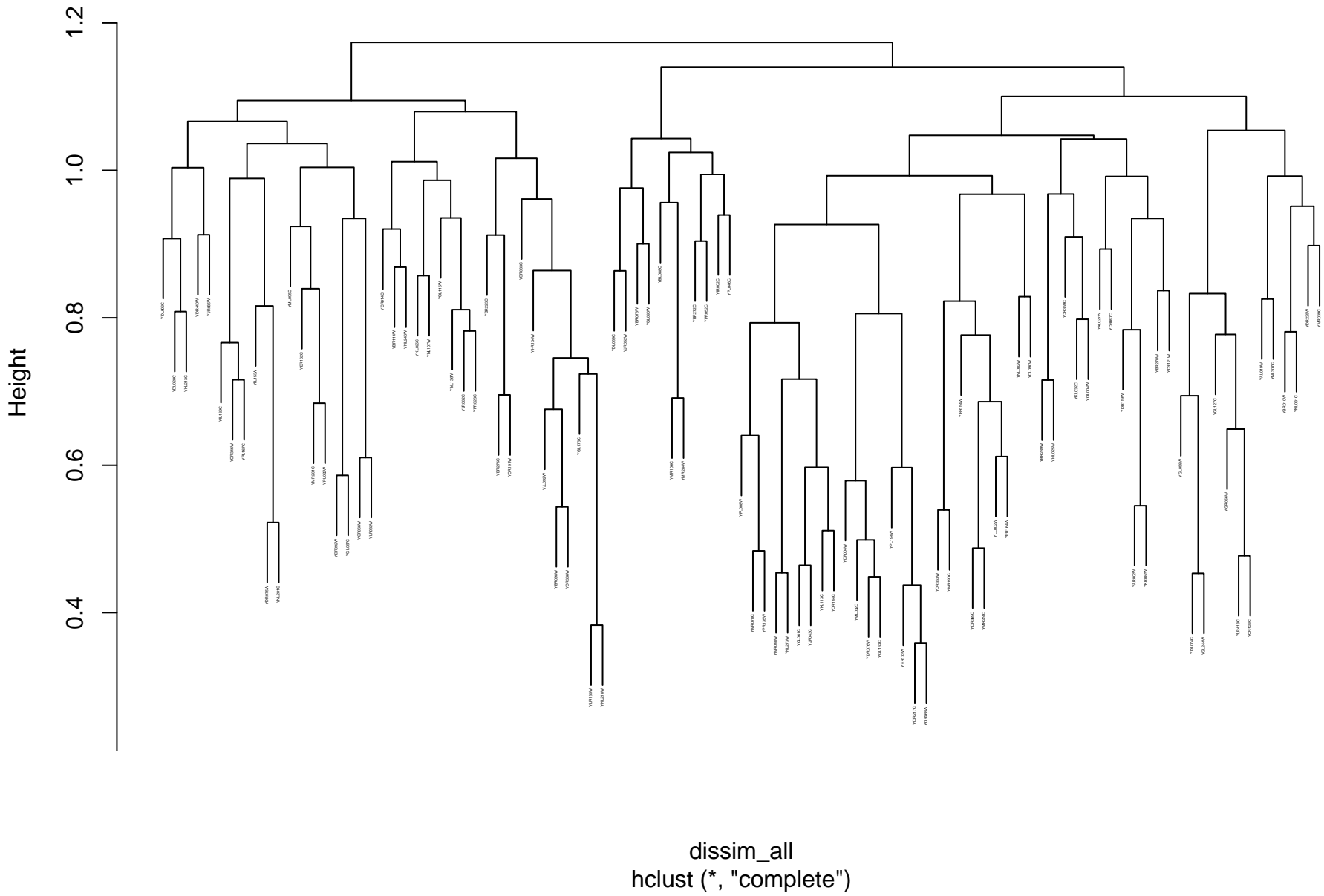


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dissim_all
hclust (*, "complete")
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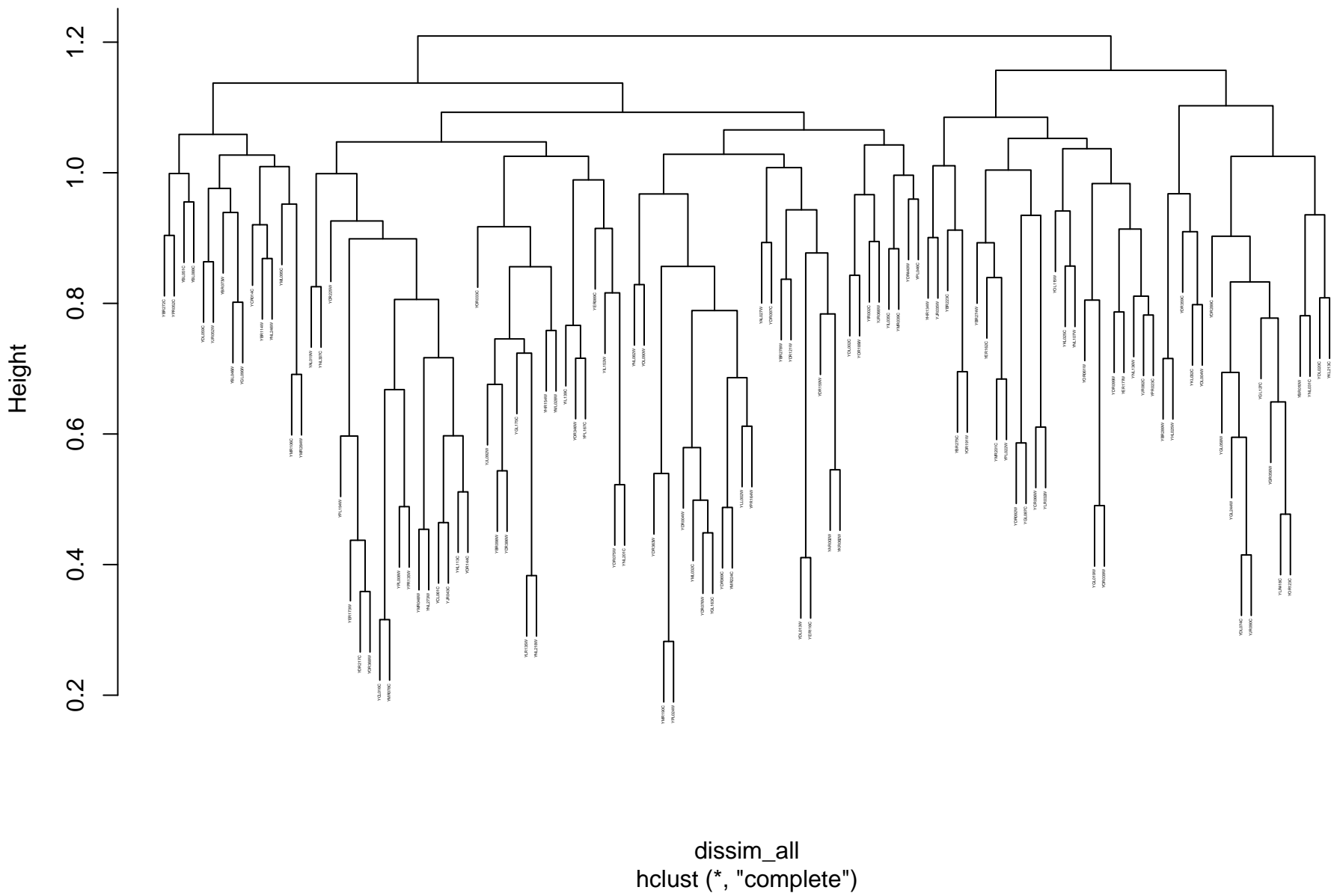
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dissim_all
hclust (*, "complete")
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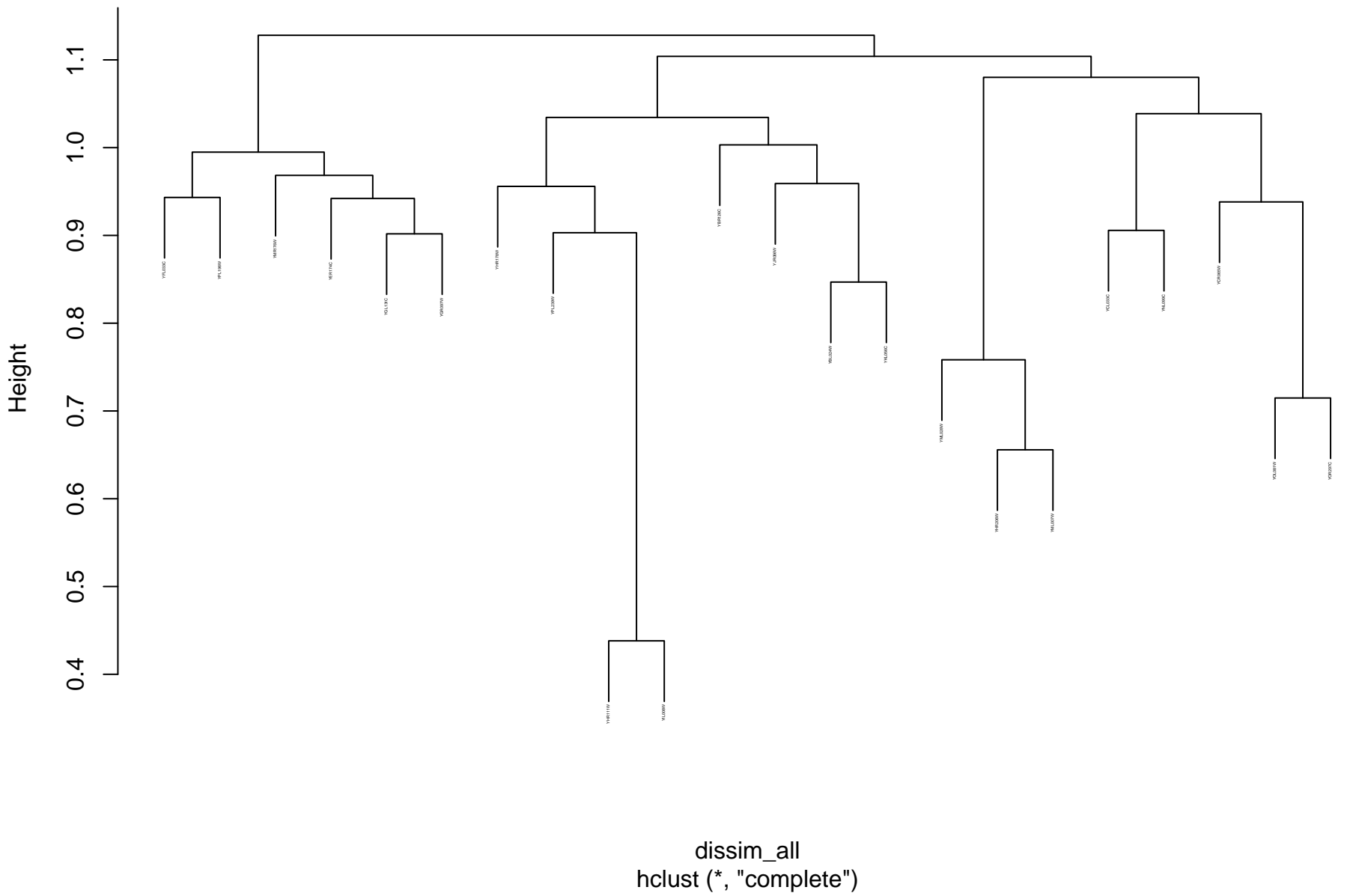
DNA repair_GO_pearson_complete



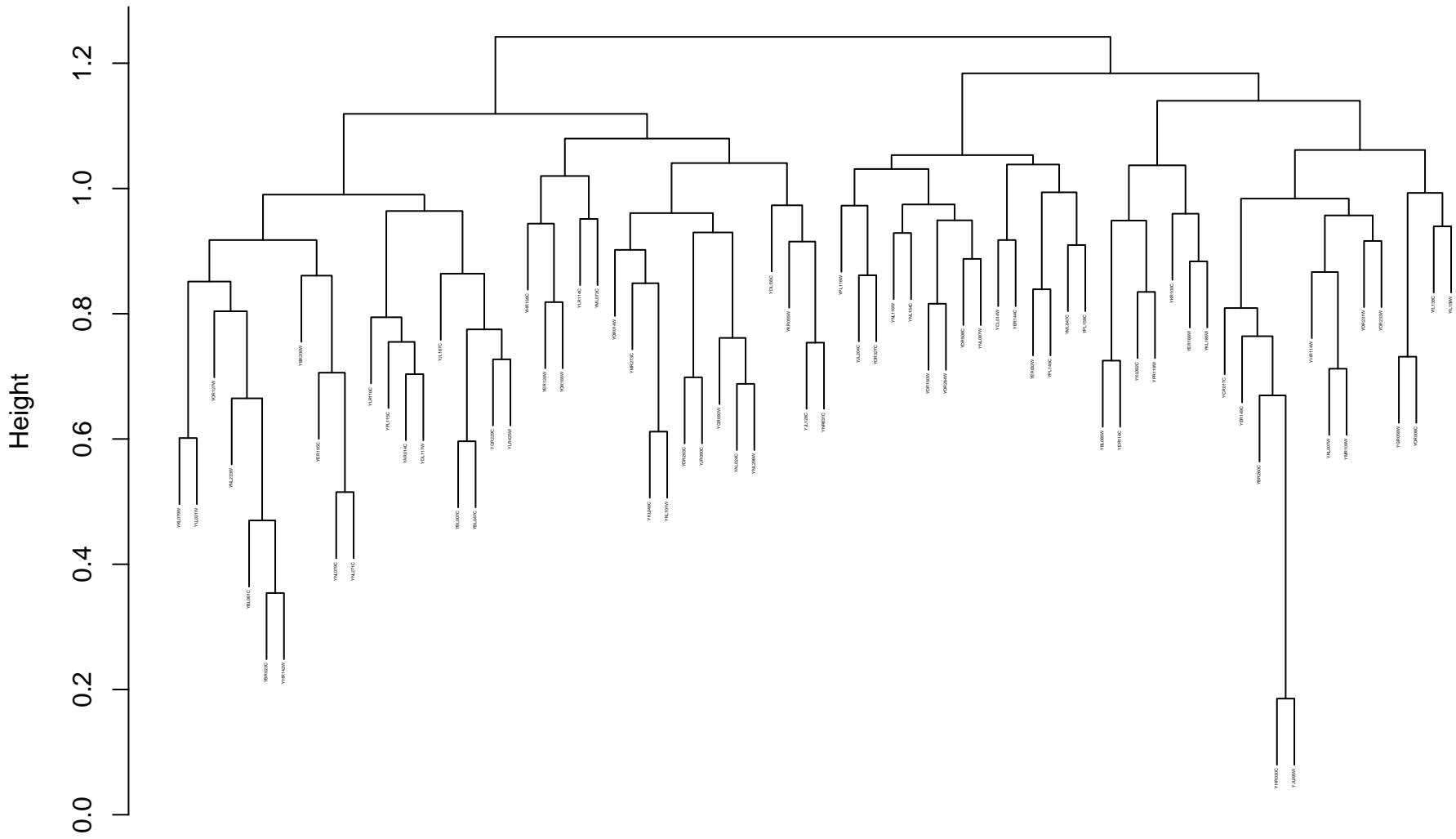
cellular response to DNA damage stimulus_GO_pearson_complete



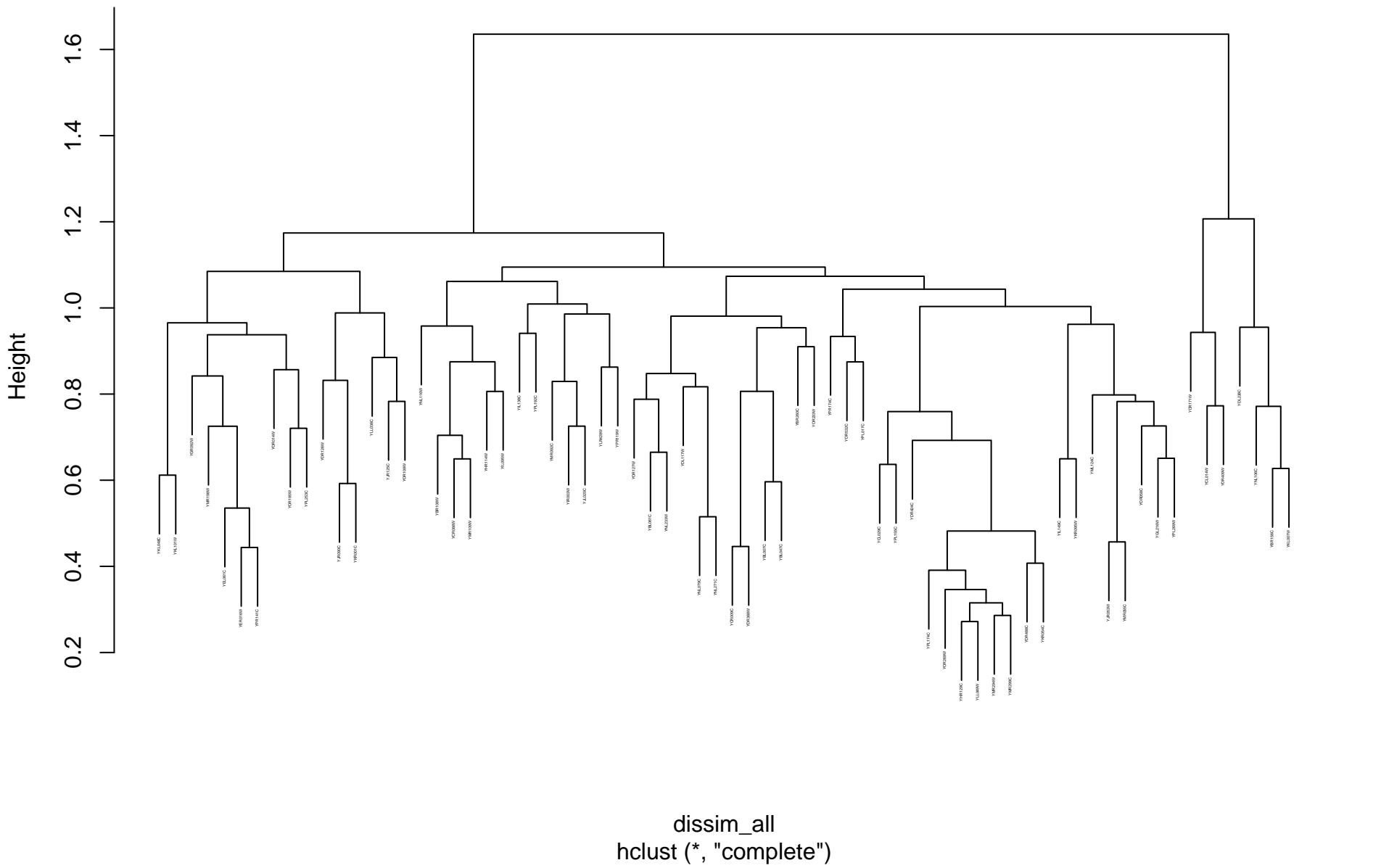
response to oxidative stress_GO_pearson_complete



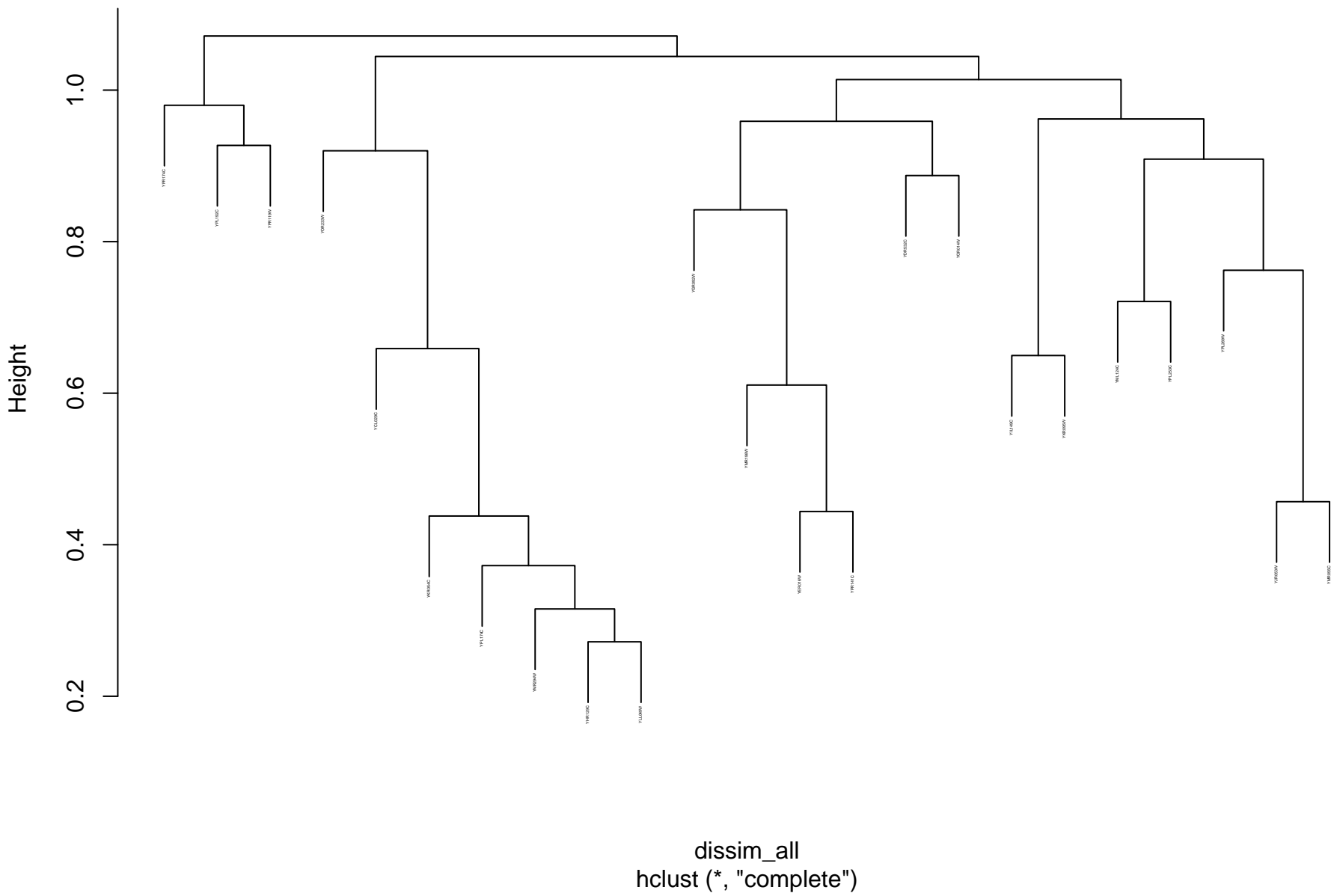
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dissim_all
hclust (*, "complete")
```



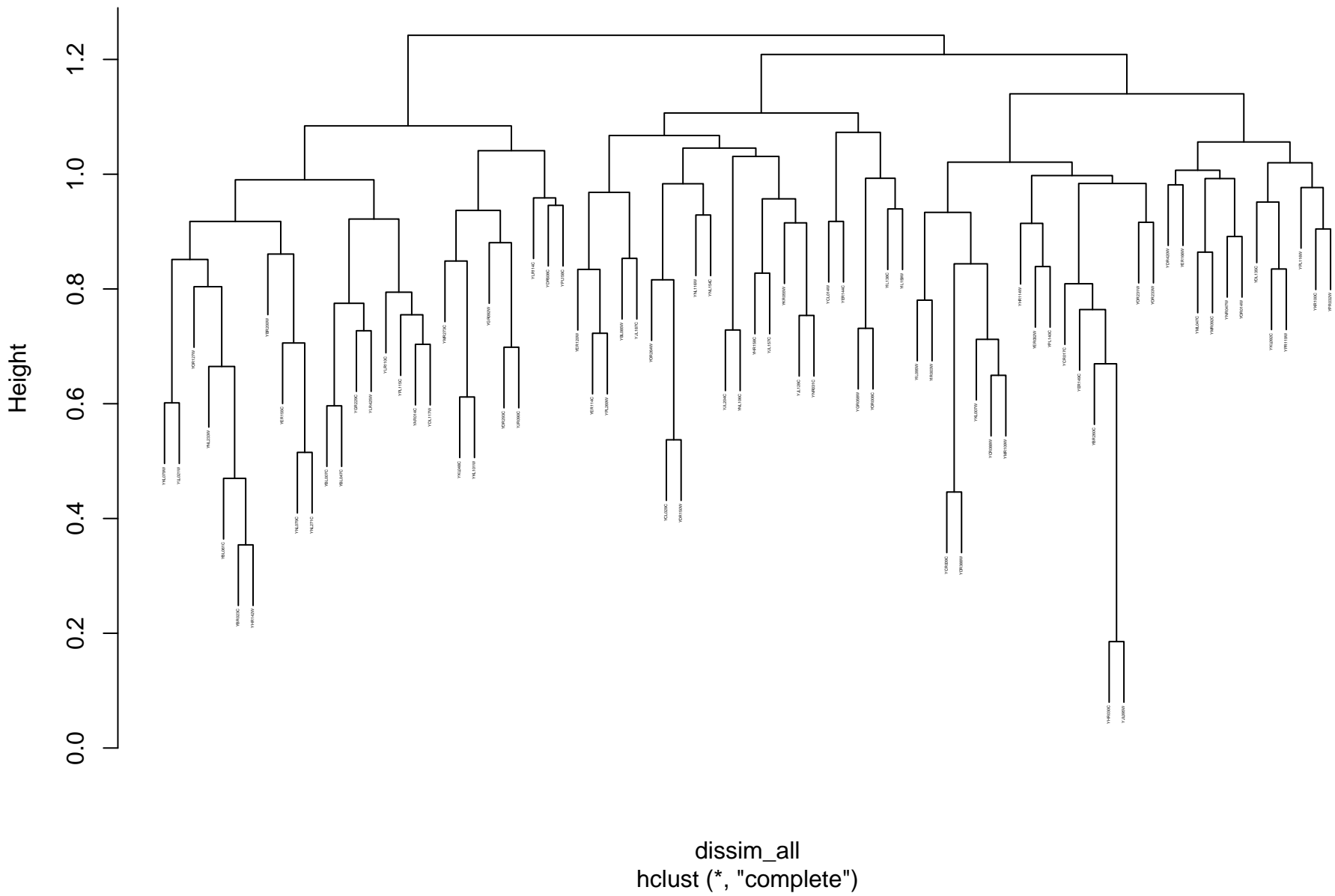
cytoskeleton_GO_pearson_complete



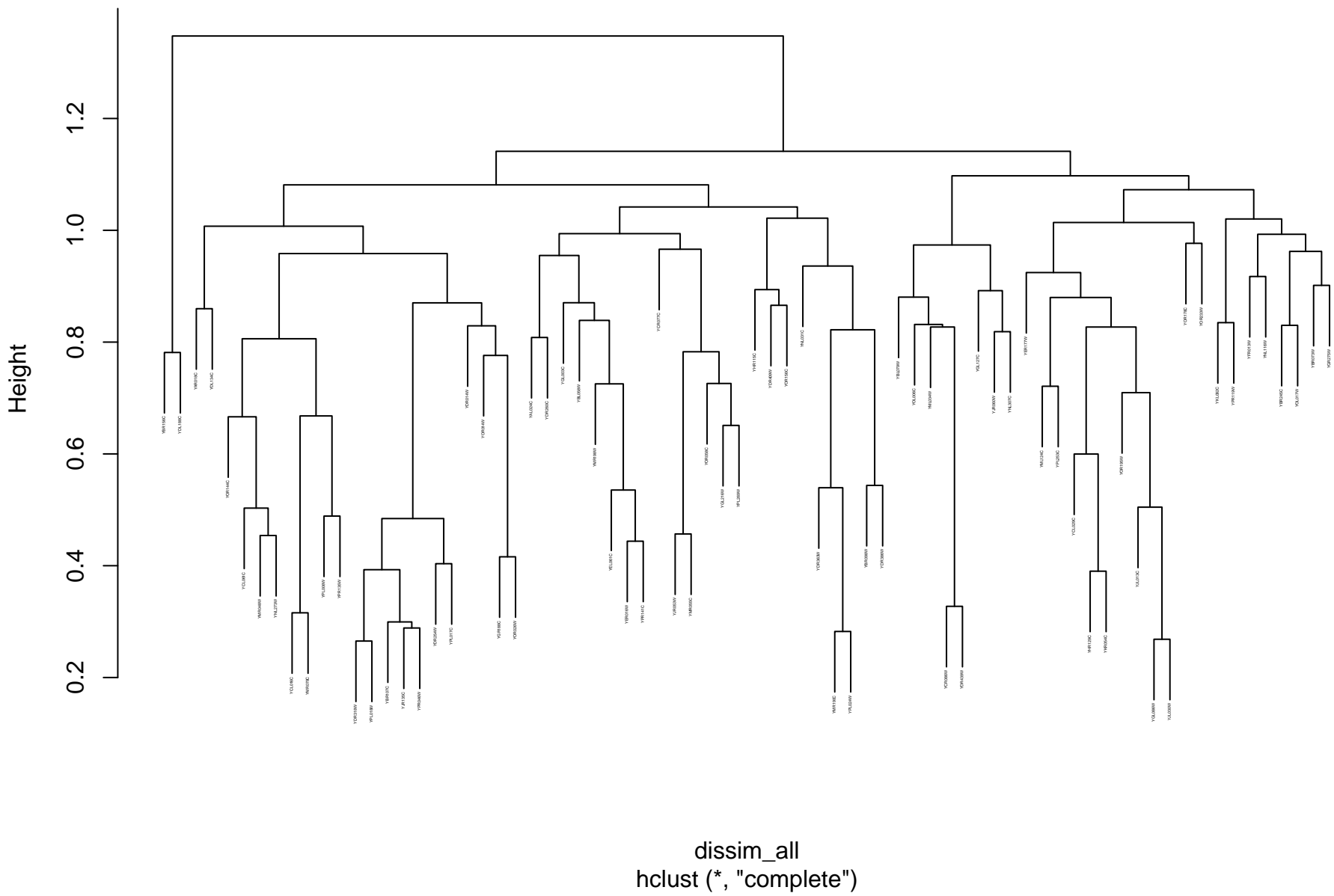
microtubule organizing center_GO_pearson_complete



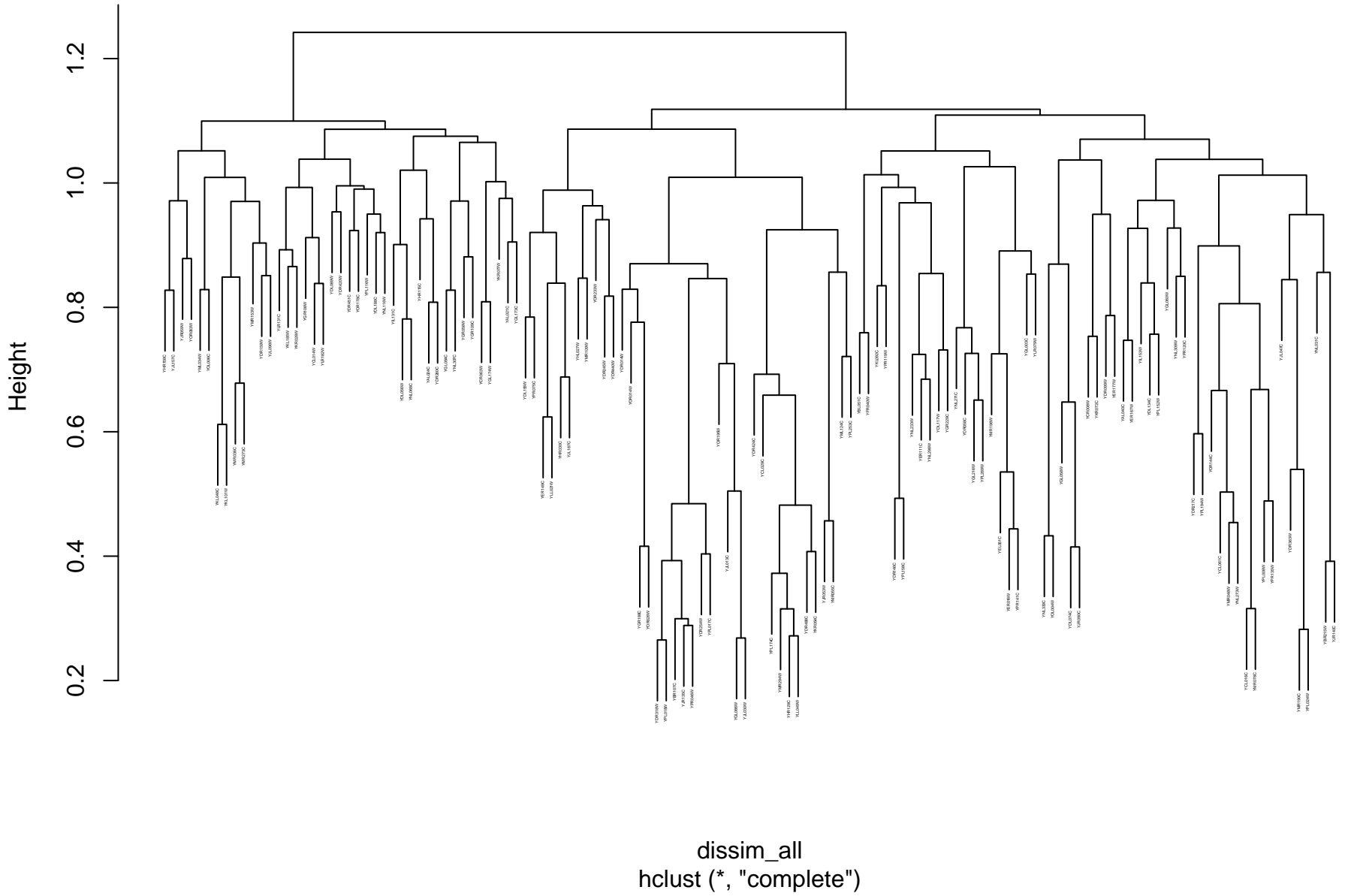
site of polarized growth_GO_pearson_complete



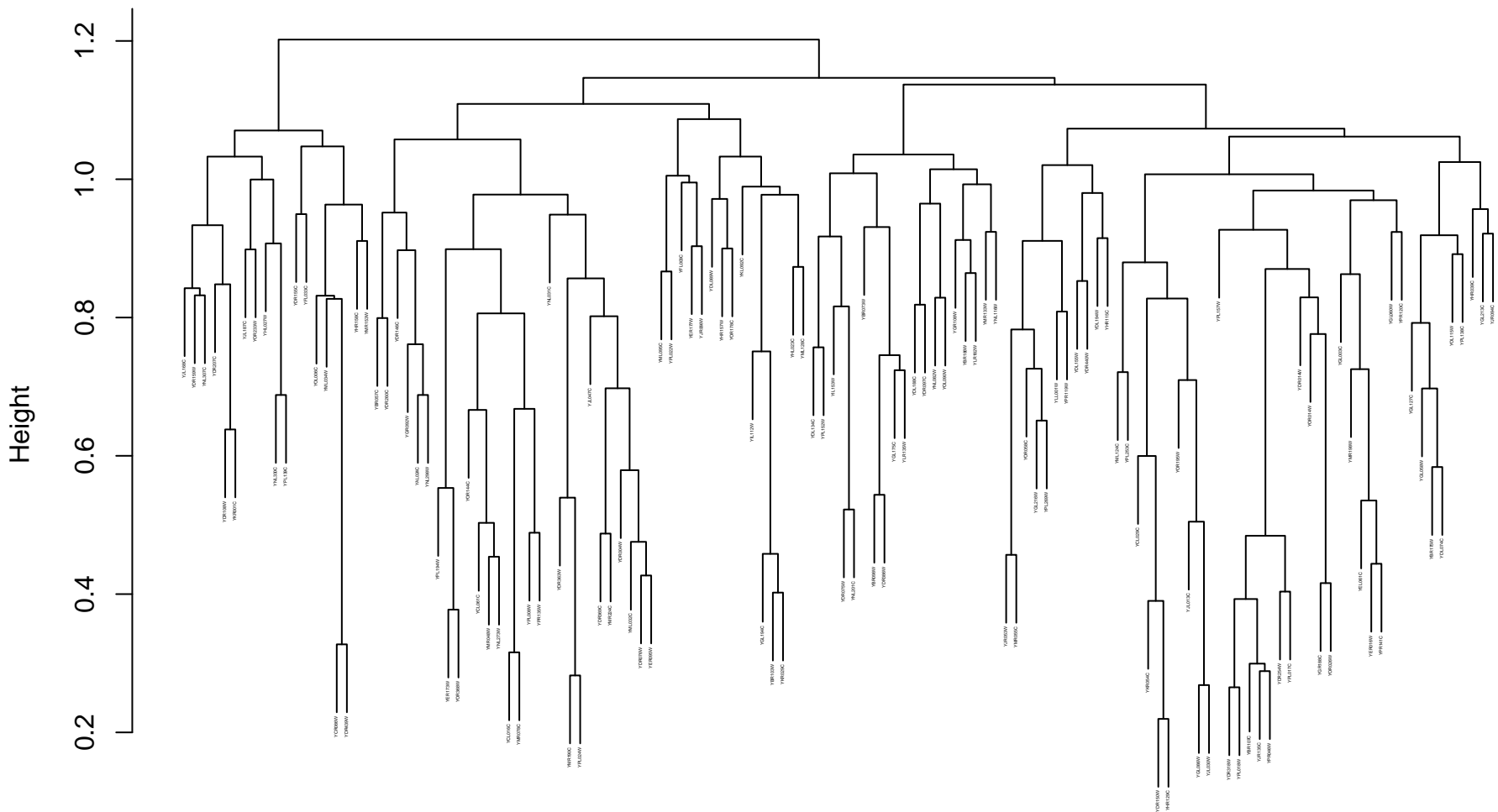
chromosome segregation_GO_pearson_complete



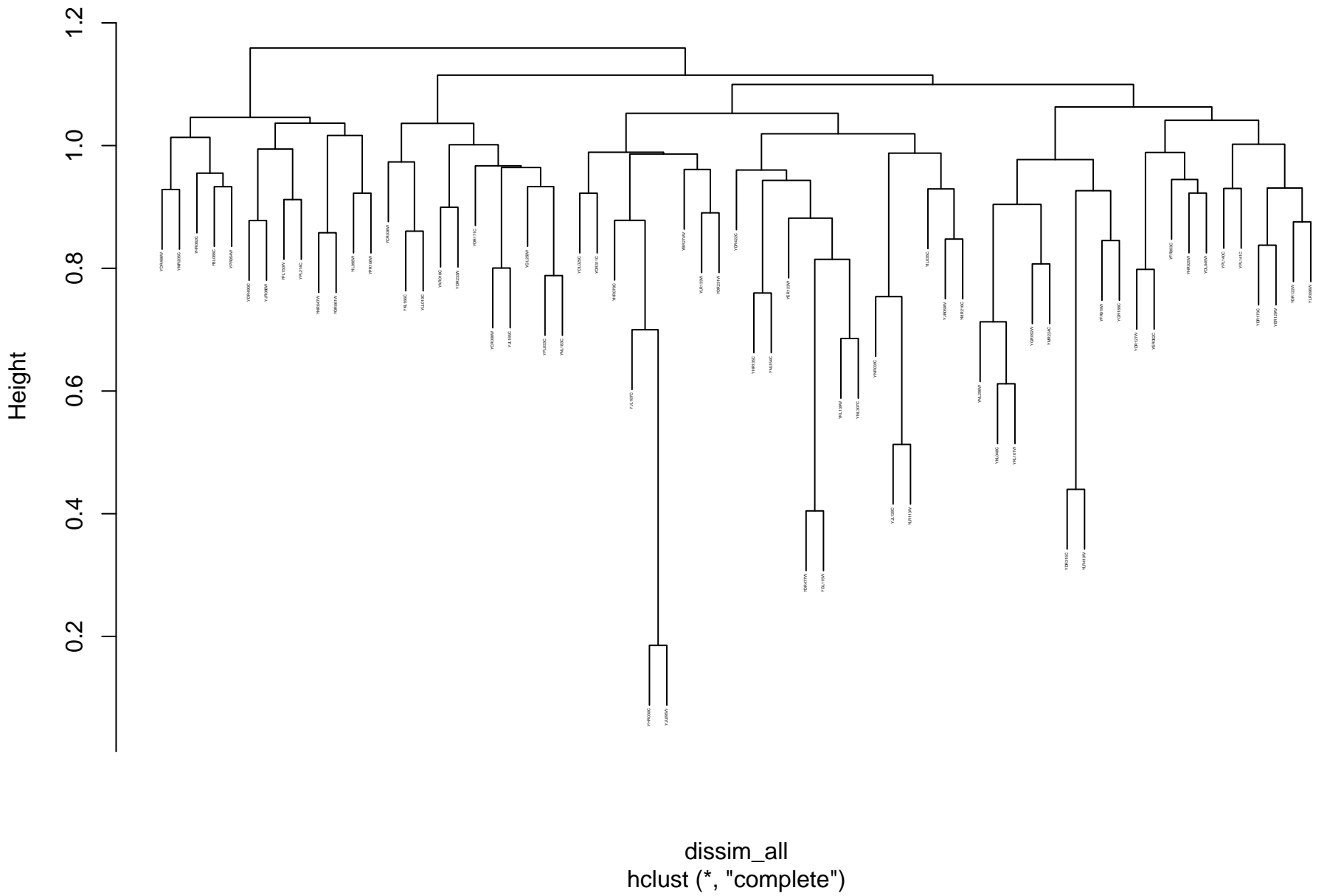
mitotic cell cycle_GO_pearson_complete



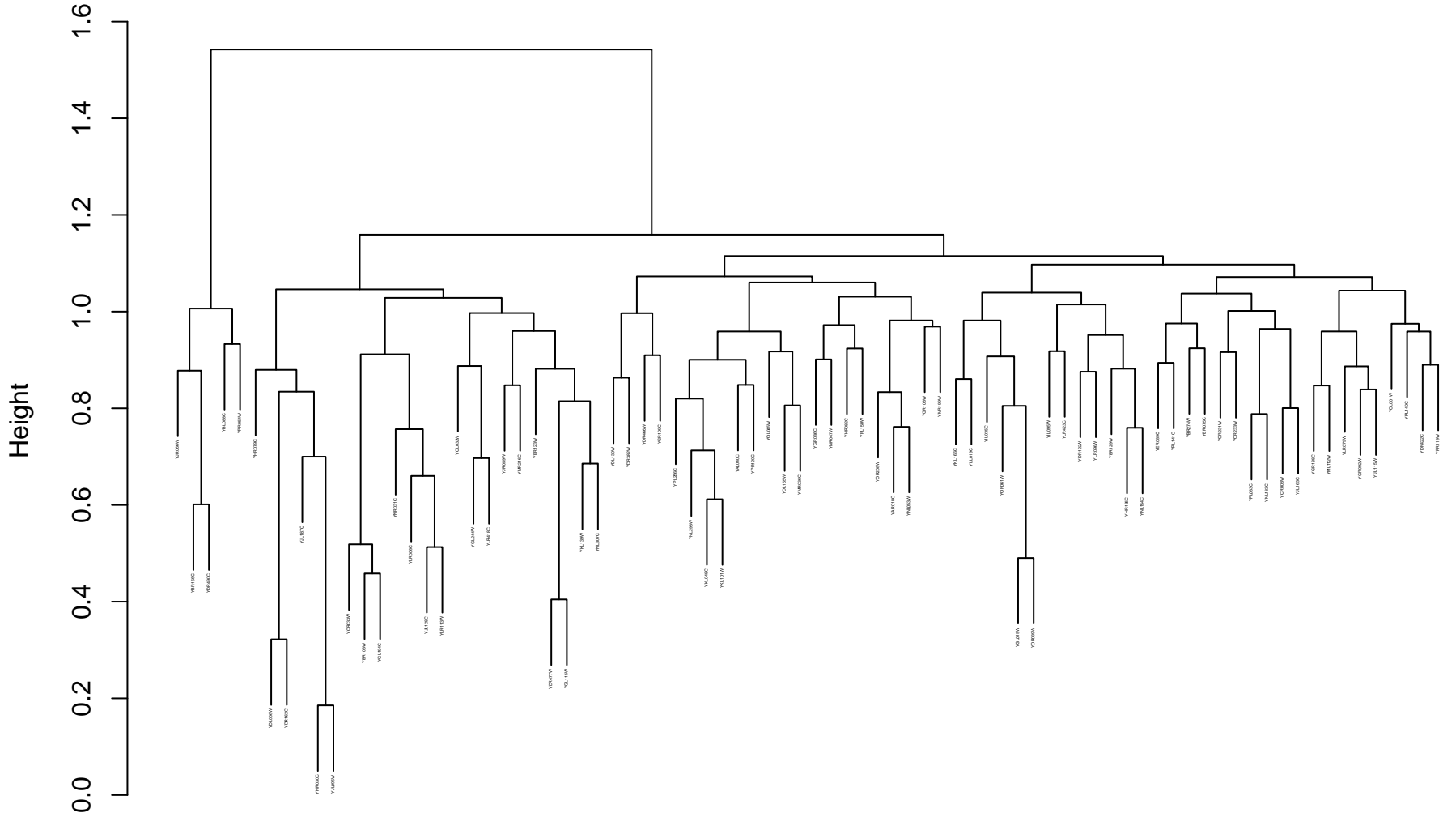
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dissim_all
hclust (*, "complete")
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kinase activity_GO_pearson_complete

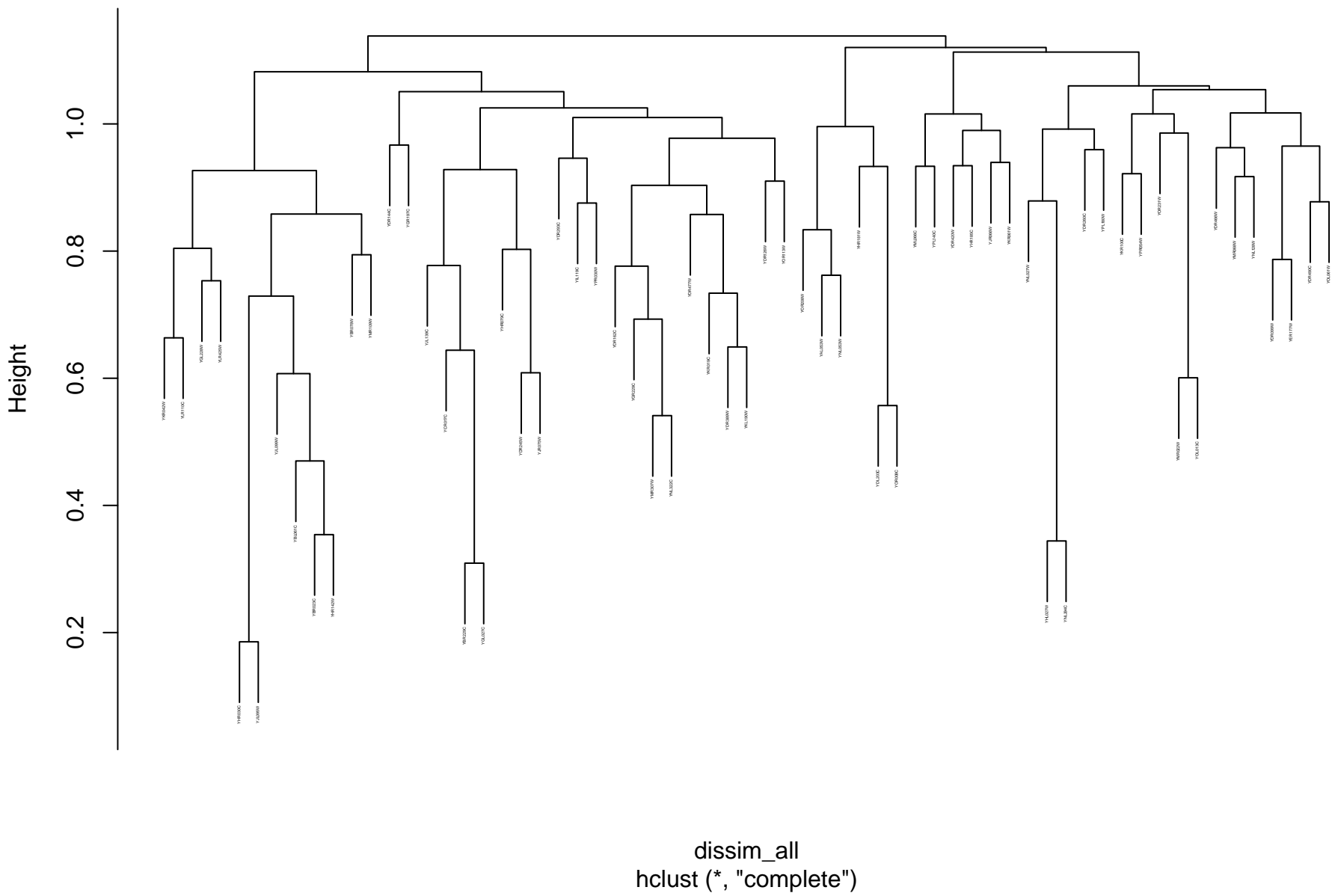


protein phosphorylation_GO_pearson_complete

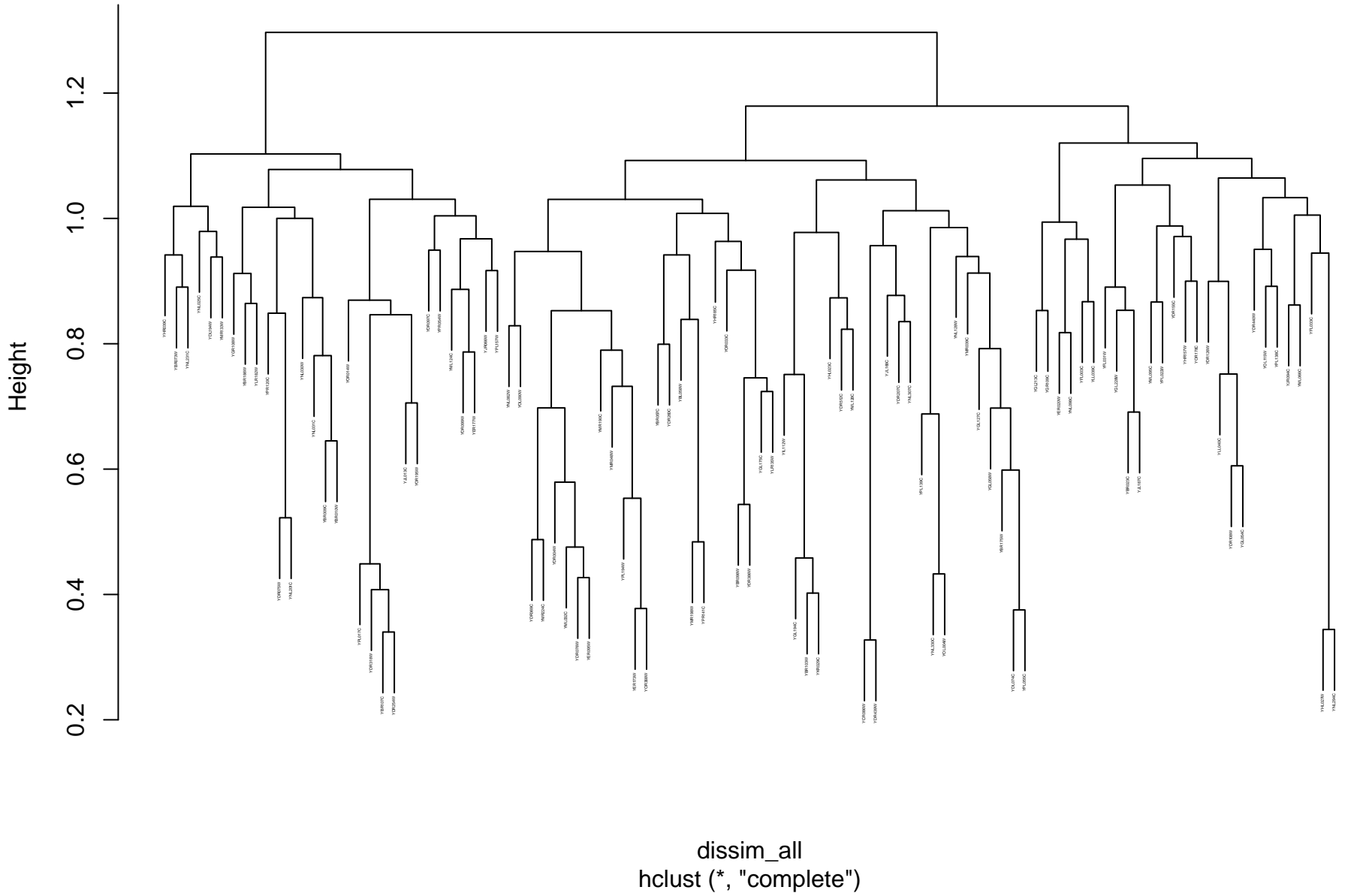


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dissim_all
hclust (*, "complete")
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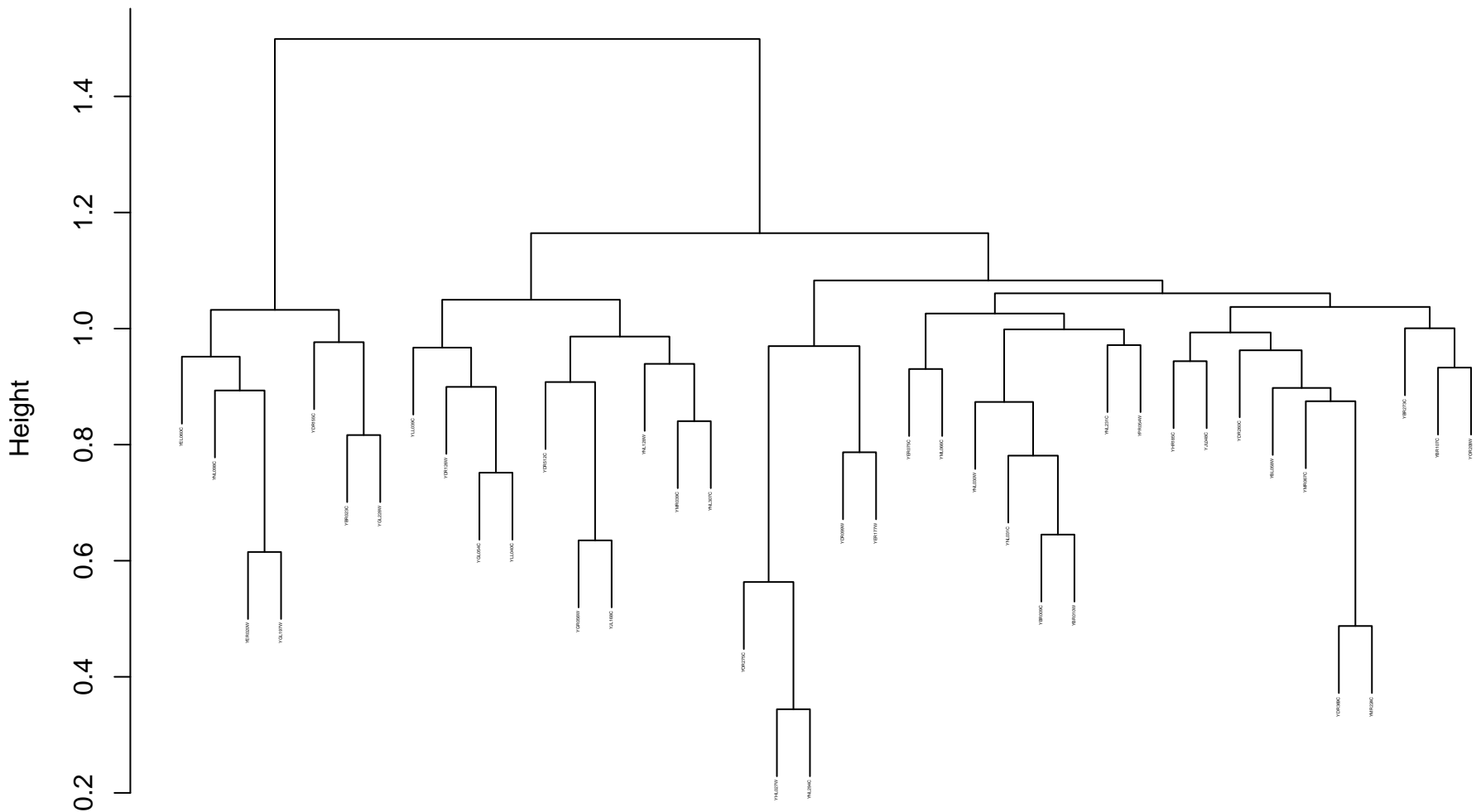

cell wall organization or biogenesis_GO_pearson_complete



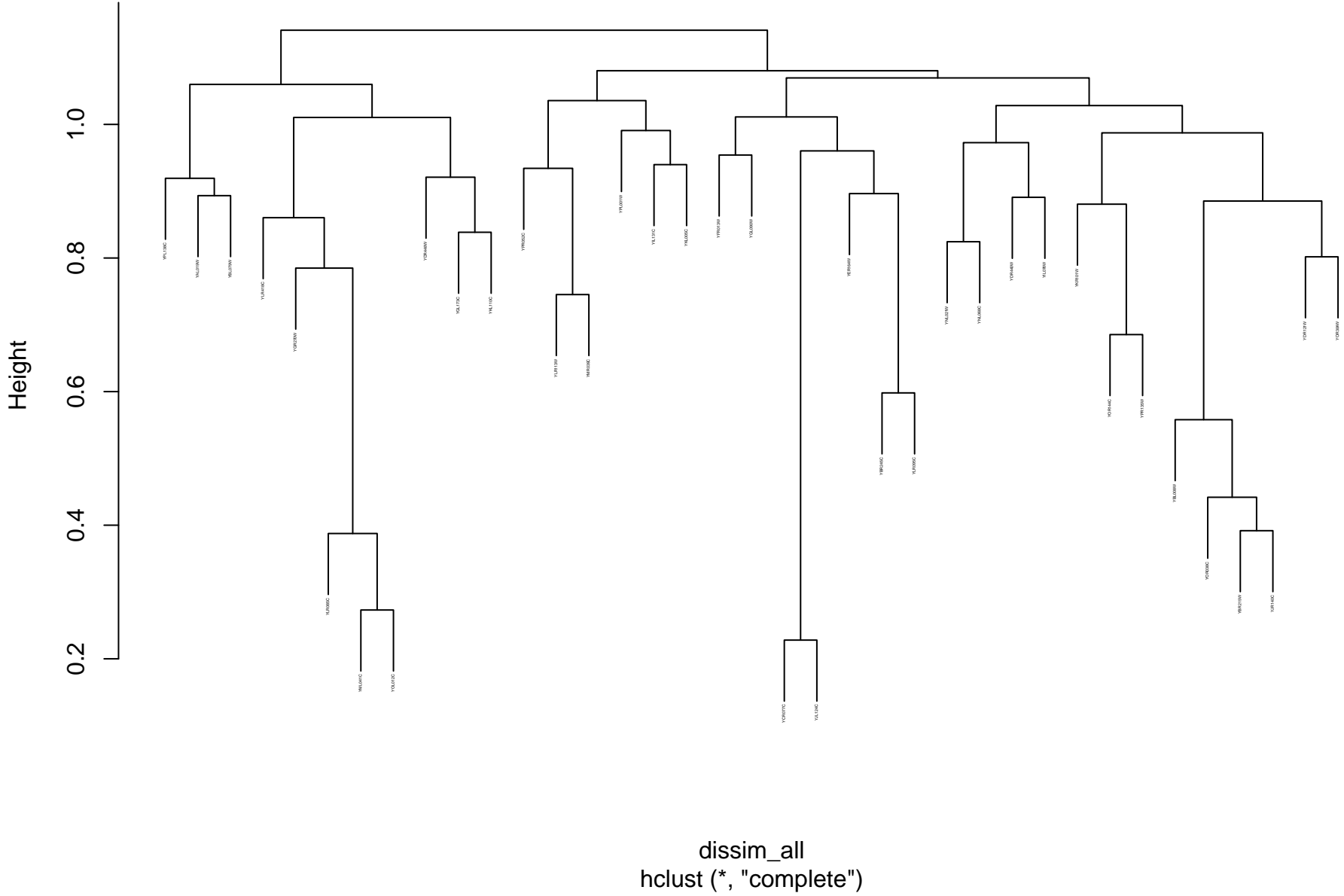
meiotic cell cycle_GO_pearson_complete



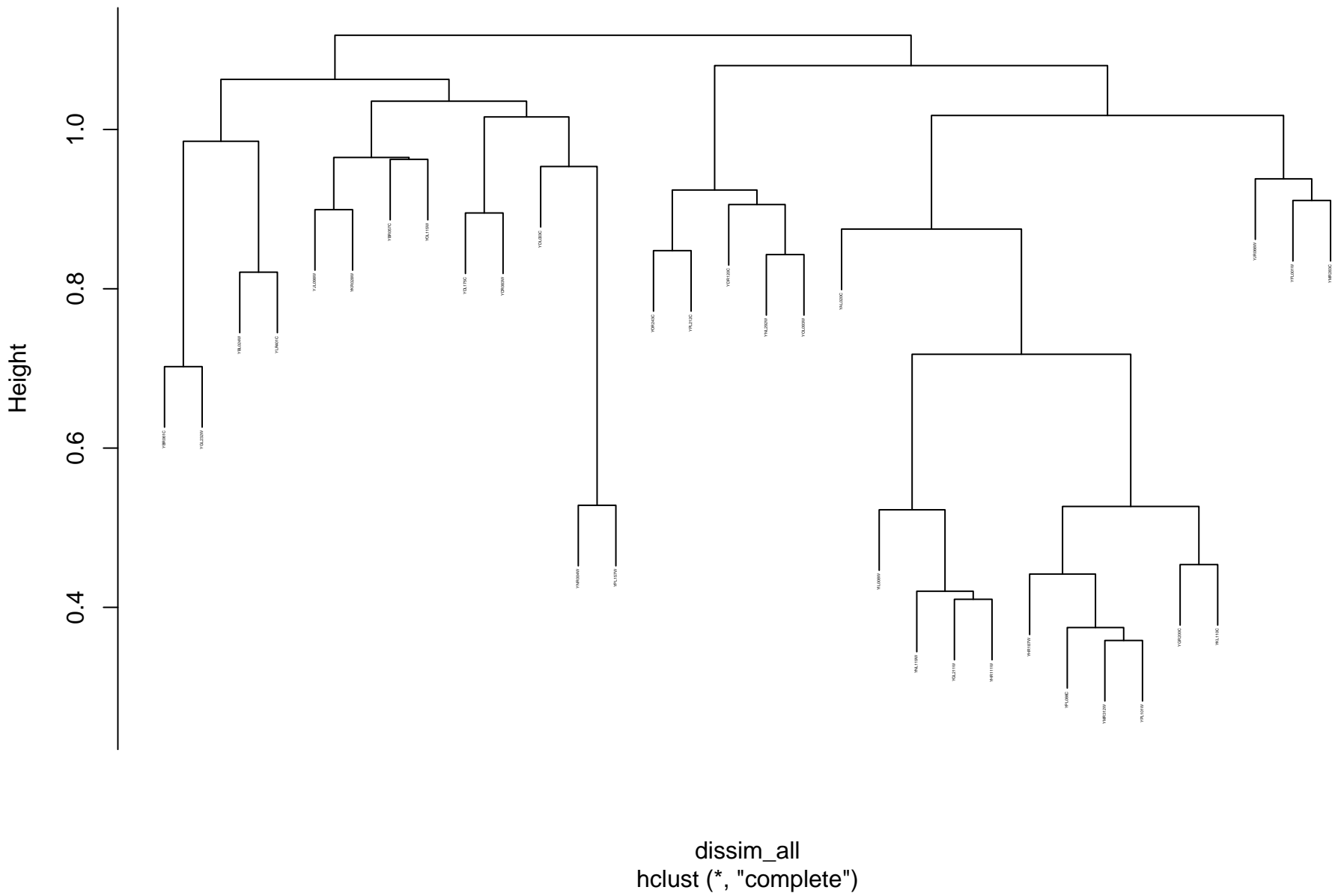
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dissim_all
hclust (*, "complete")
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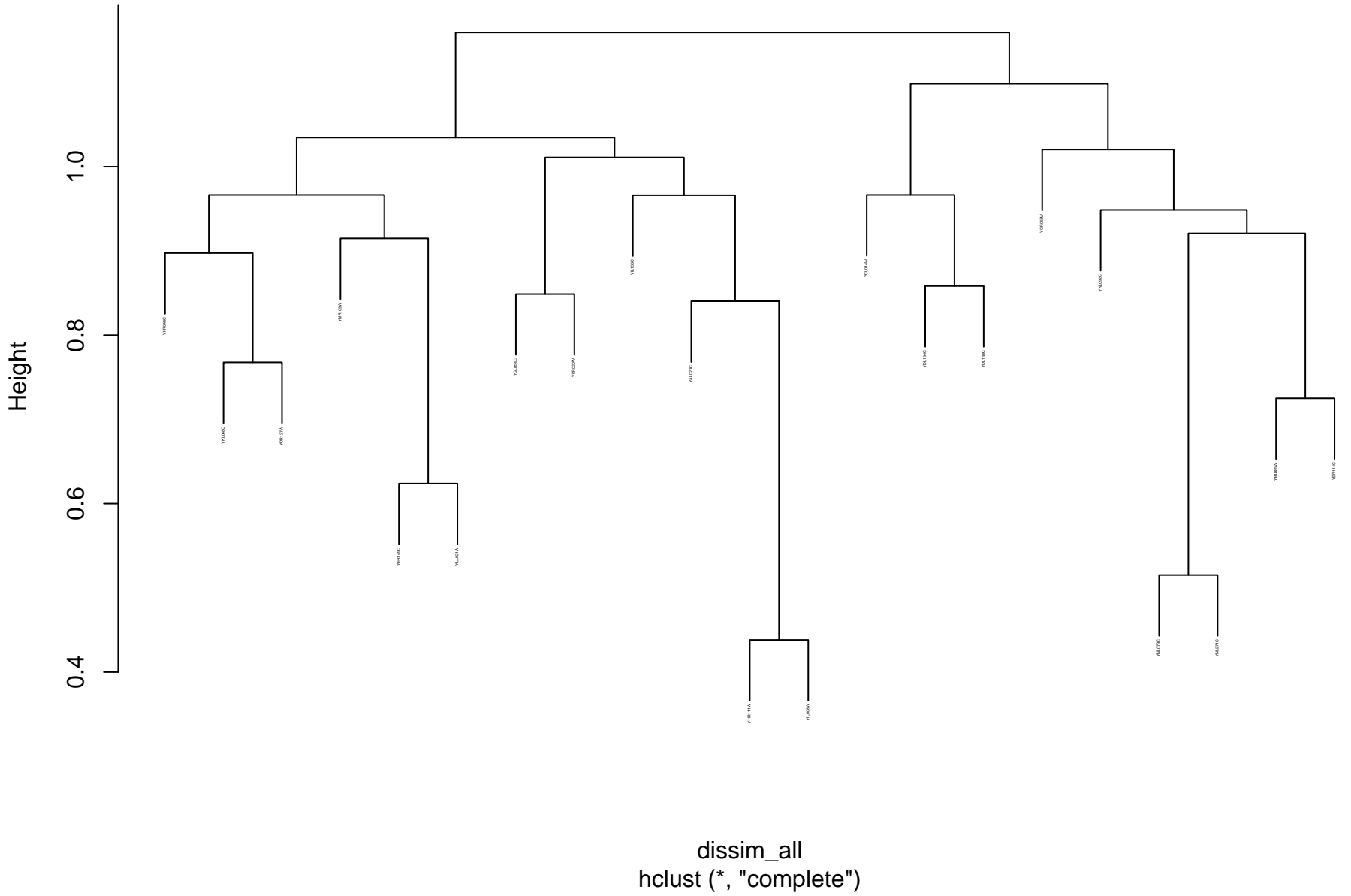
chromatin binding_GO_pearson_complete



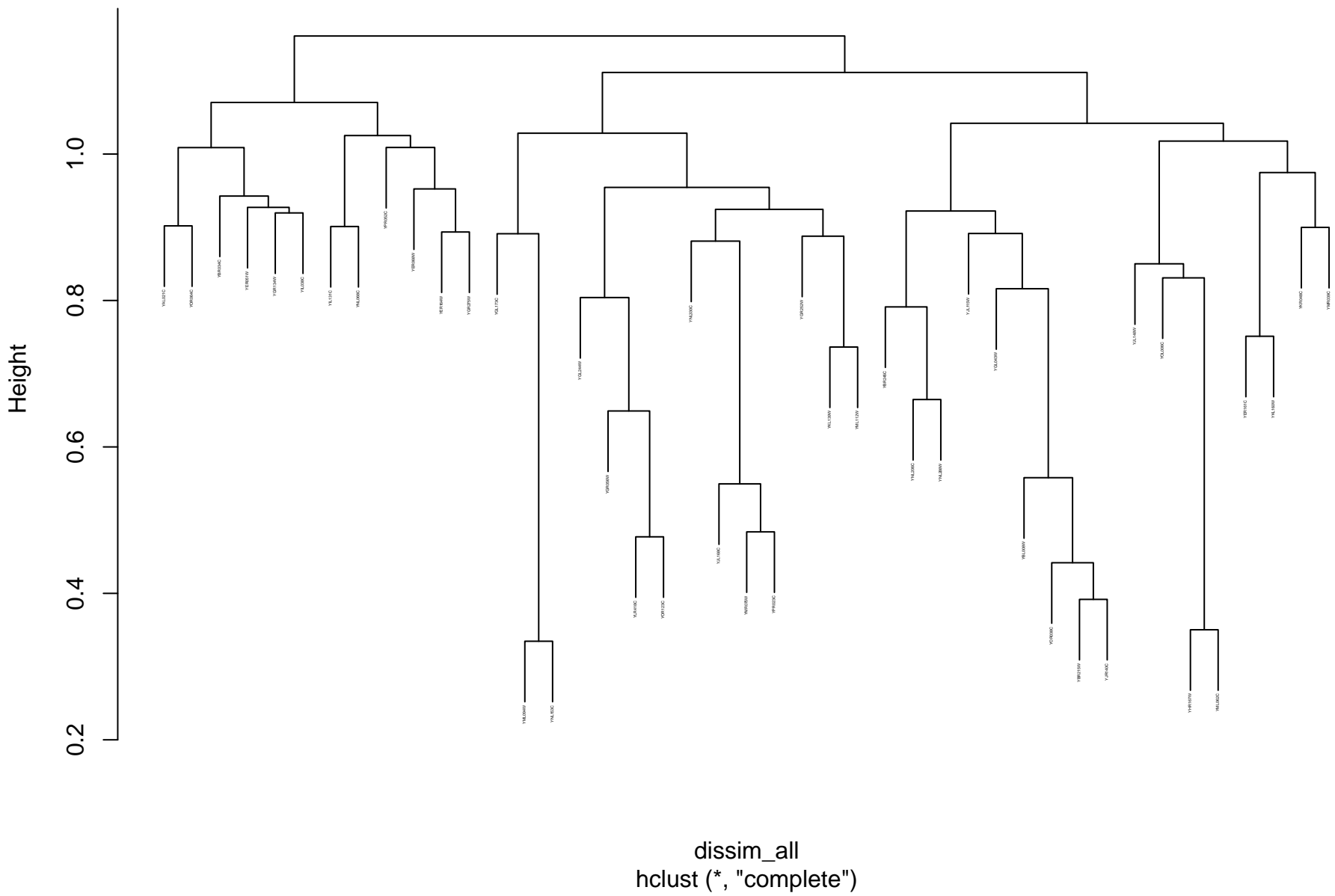
RNA modification_GO_pearson_complete



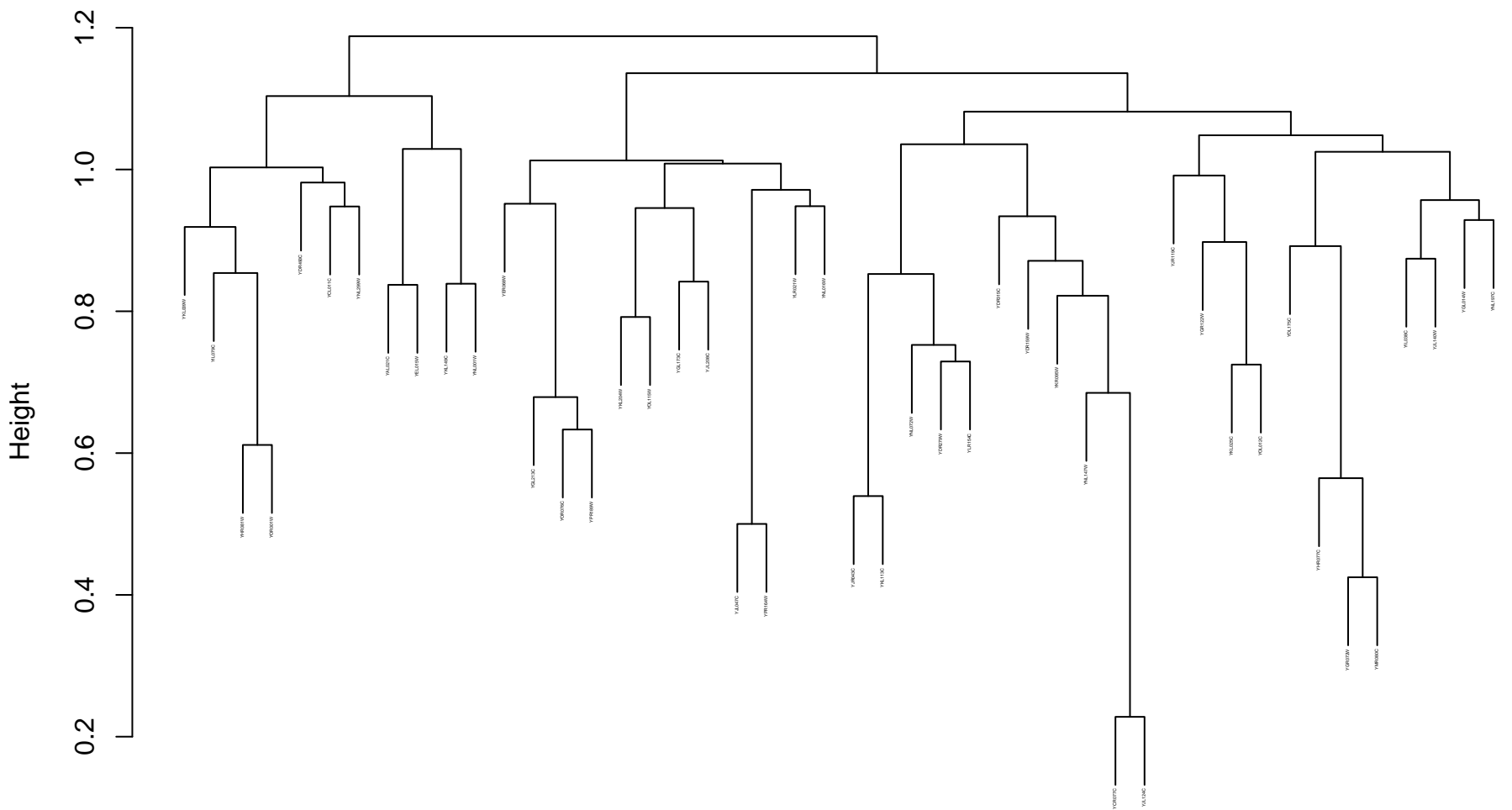
cell budding_GO_pearson_complete



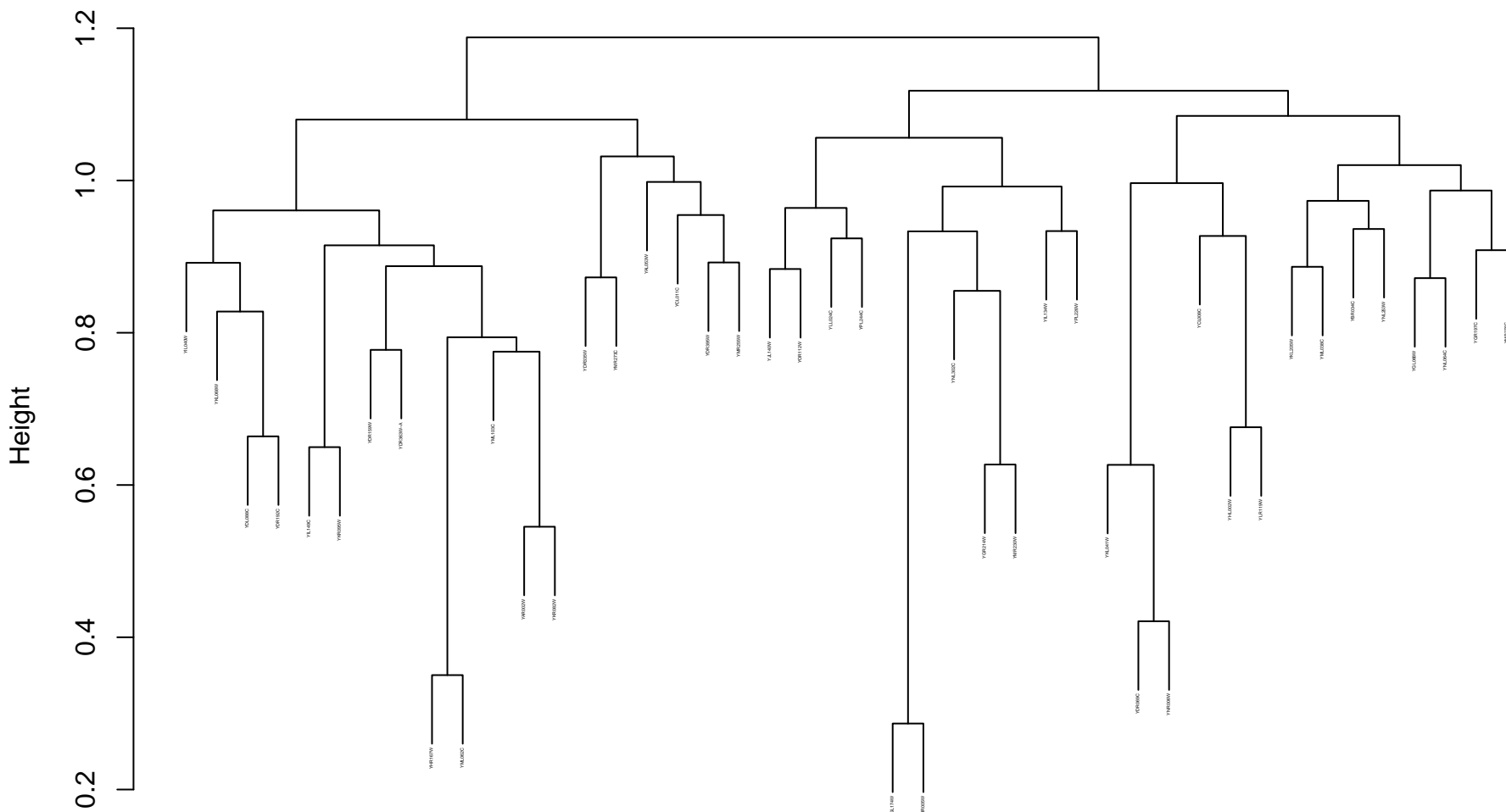
DNA-templated transcription, elongation_GO_pearson_complete



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dissim_all
hclust (*, "complete")
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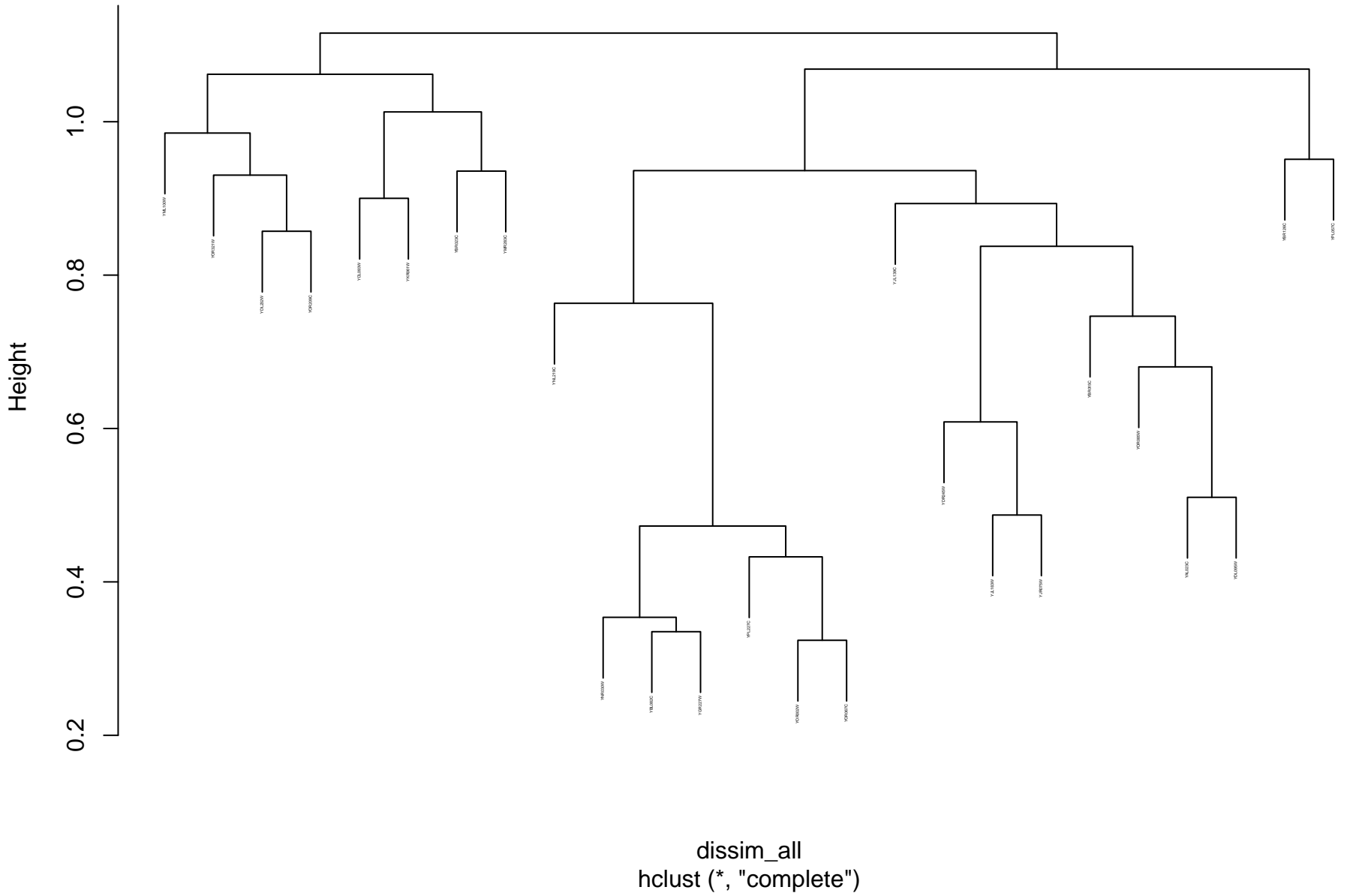


nucleobase-containing compound transport_GO_pearson_complete

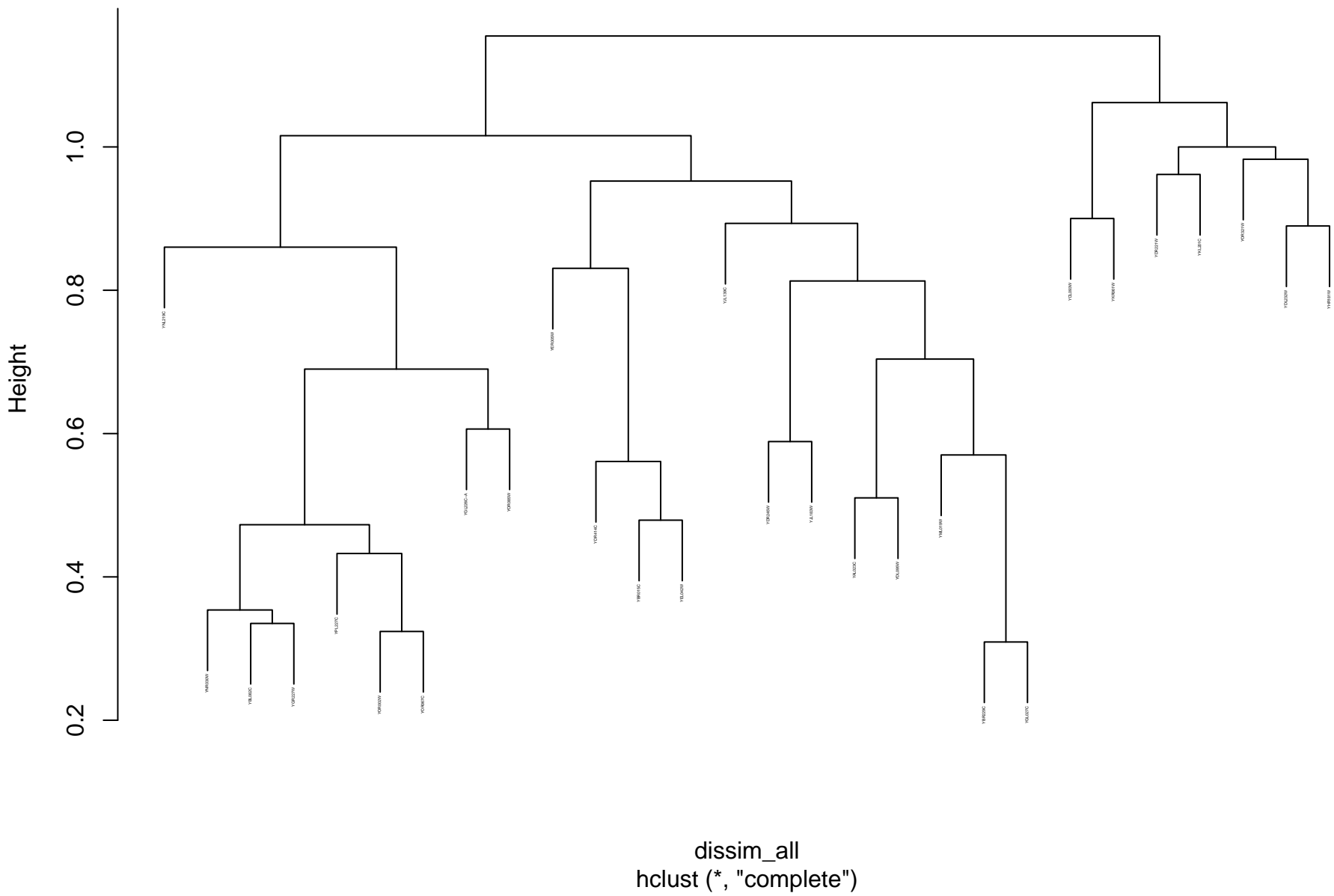


dissim_all
hclust (*, "complete")

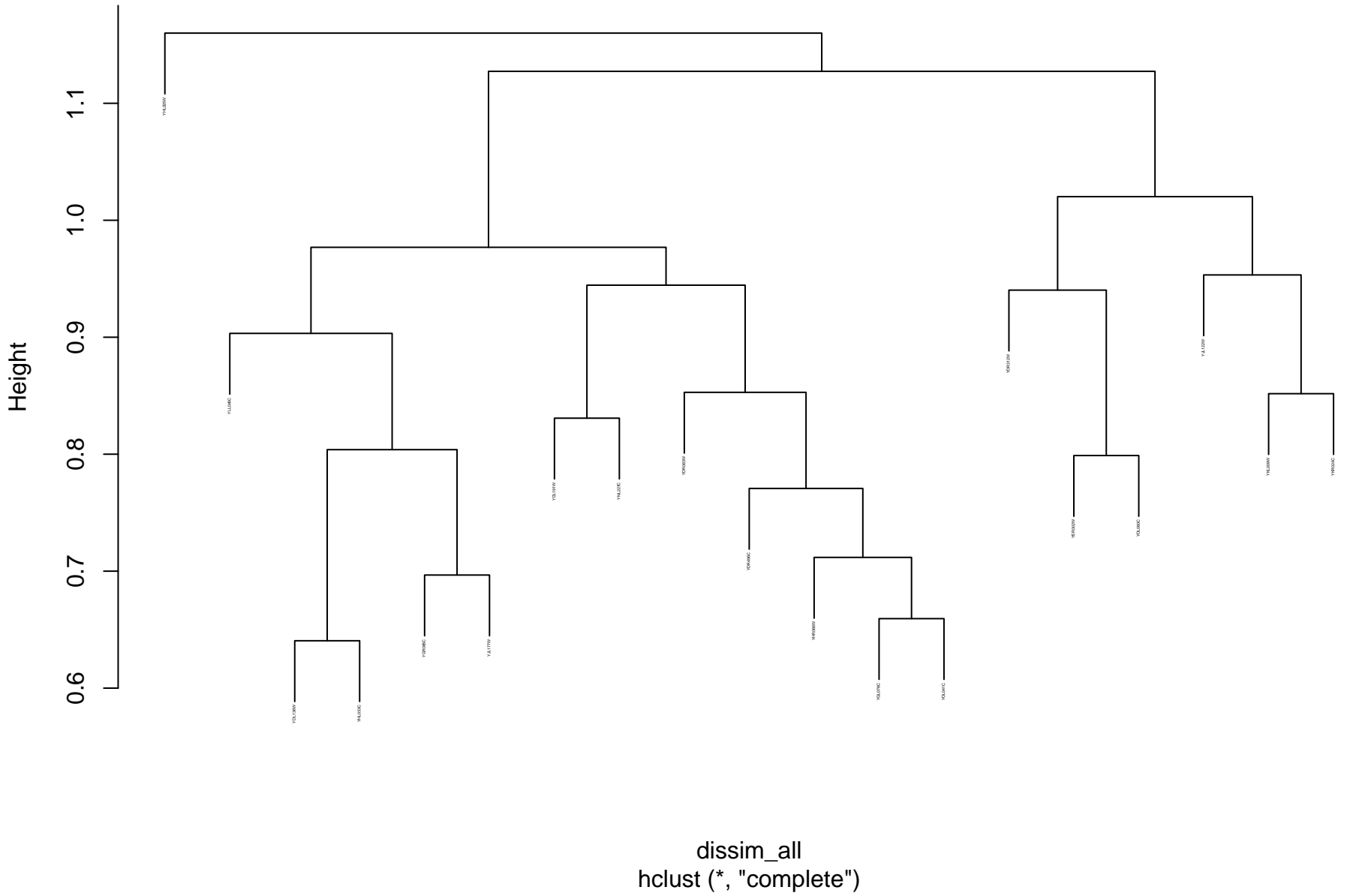
transferase activity, transferring glycosyl groups_GO_pearson_complete



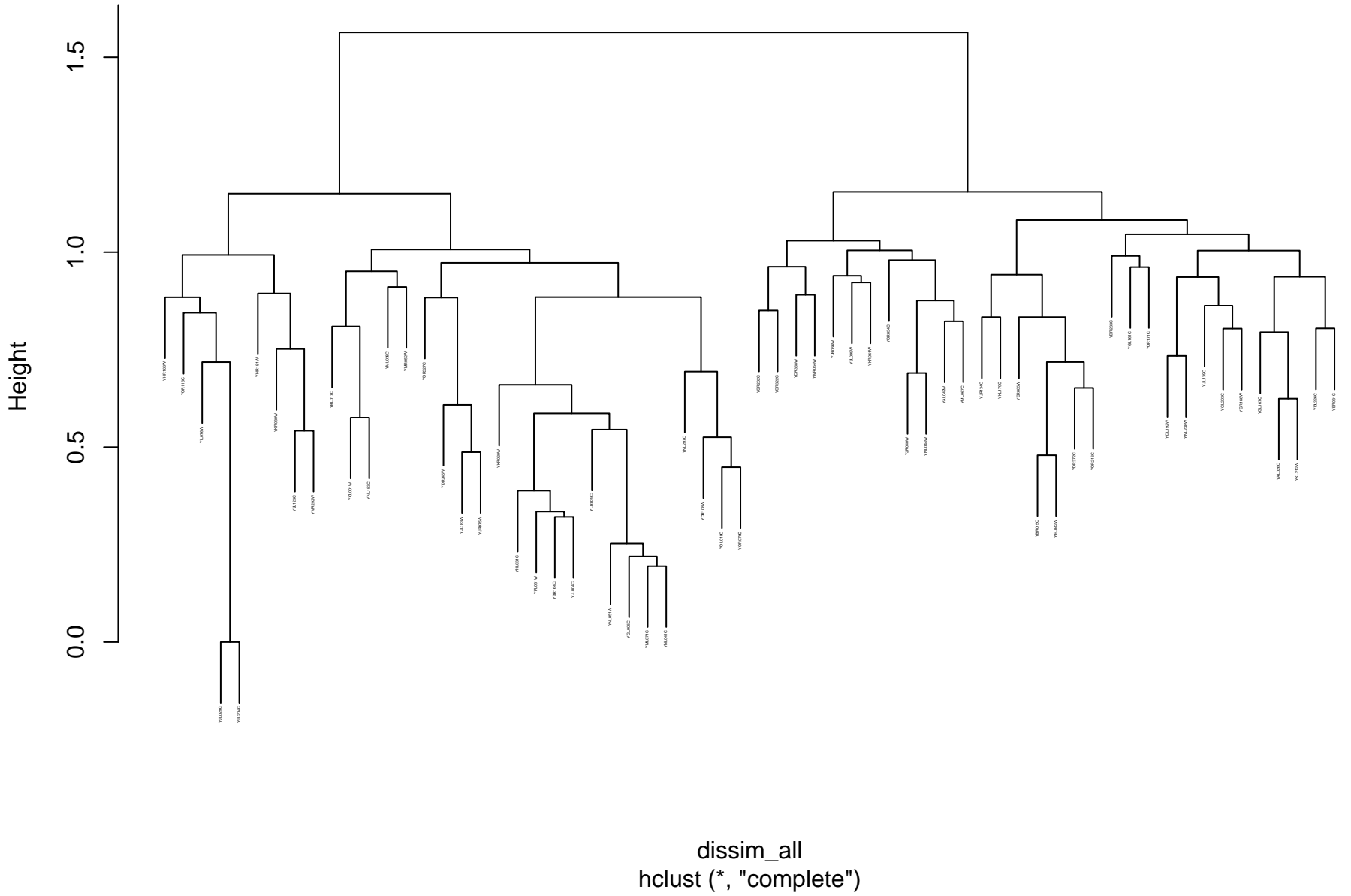
protein glycosylation_GO_pearson_complete

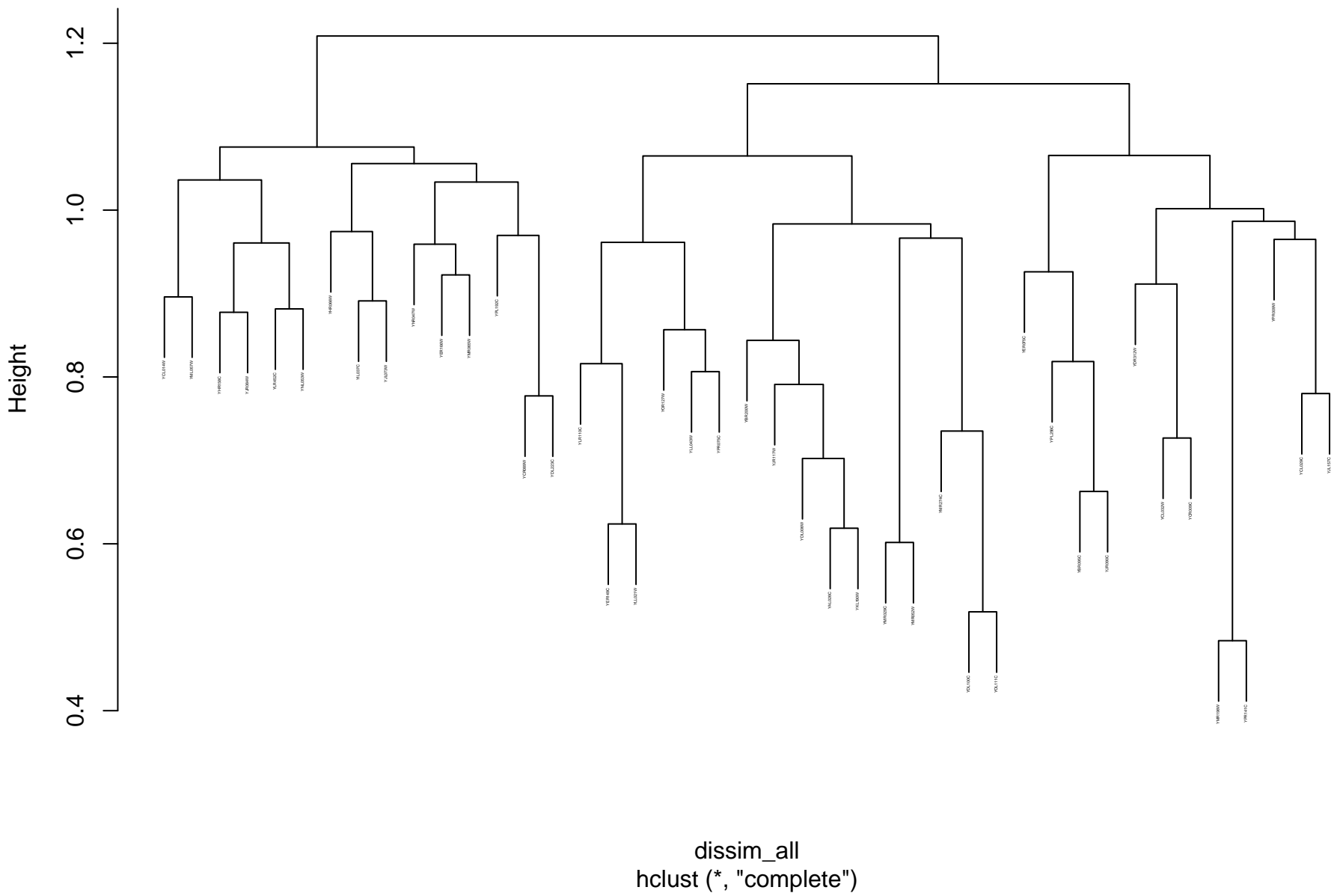


ribosomal large subunit biogenesis_GO_pearson_complete

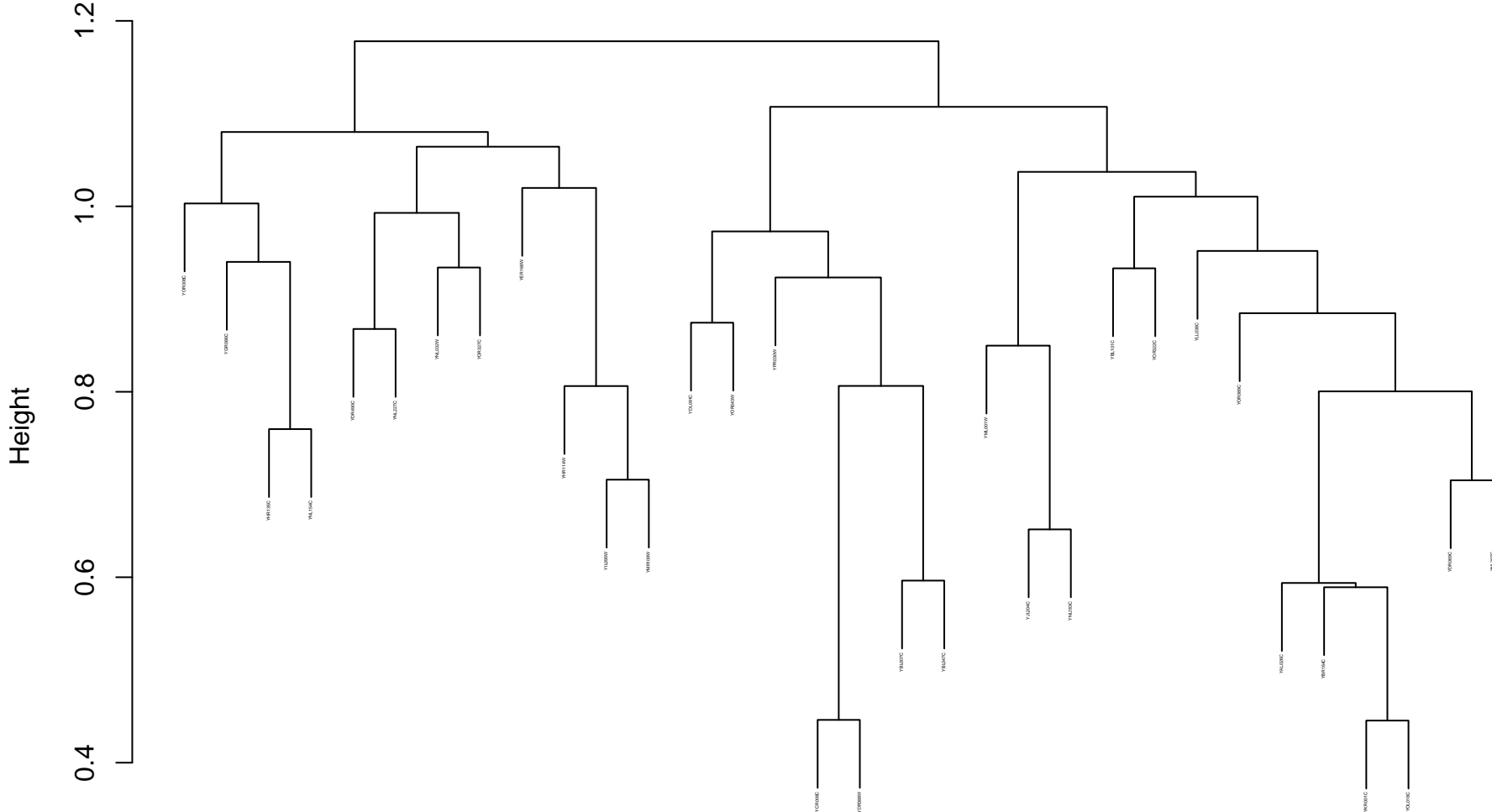


Golgi apparatus_GO_pearson_complete



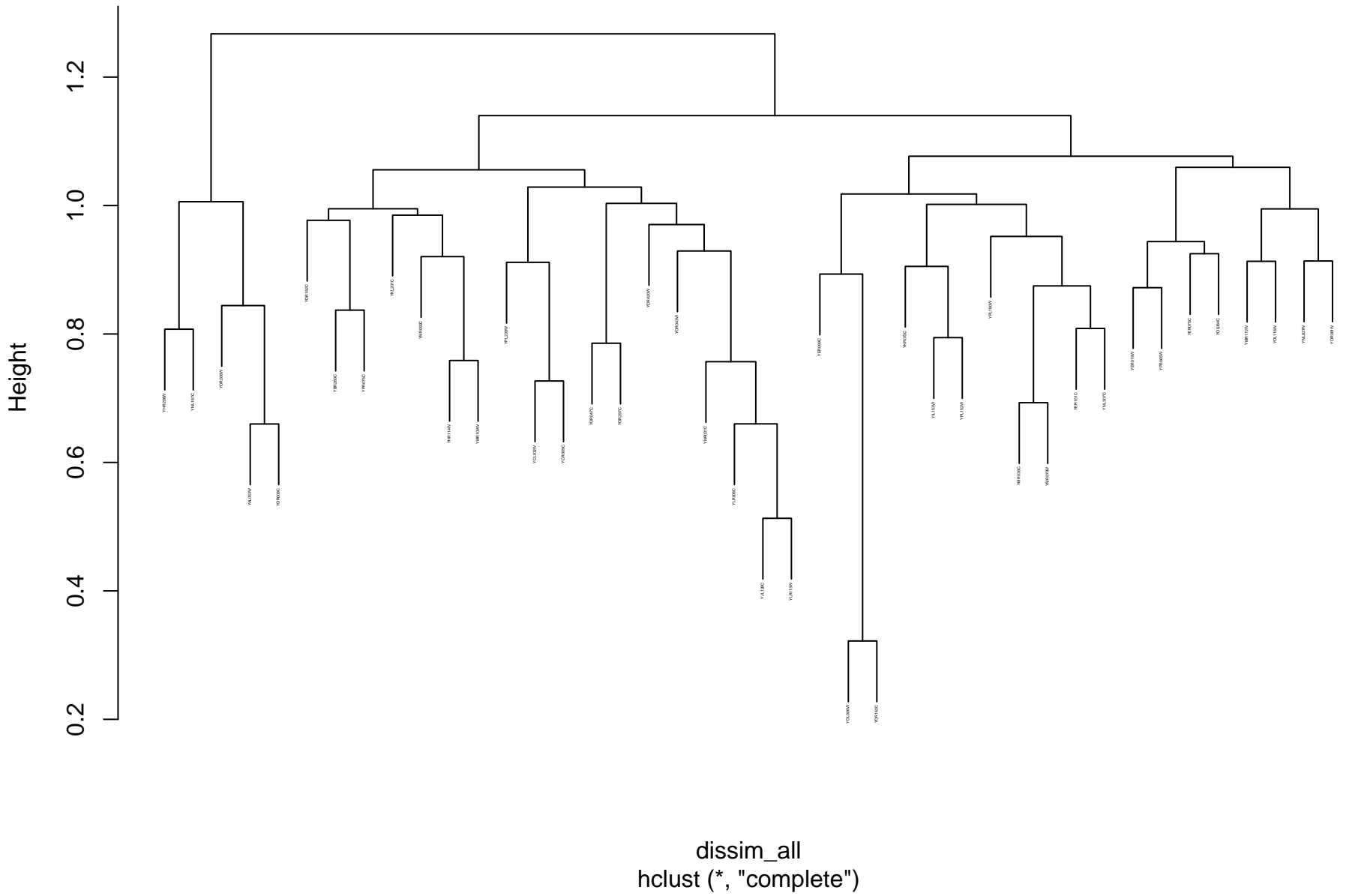
conjugation_GO_pearson_complete

endocytosis_GO_pearson_complete

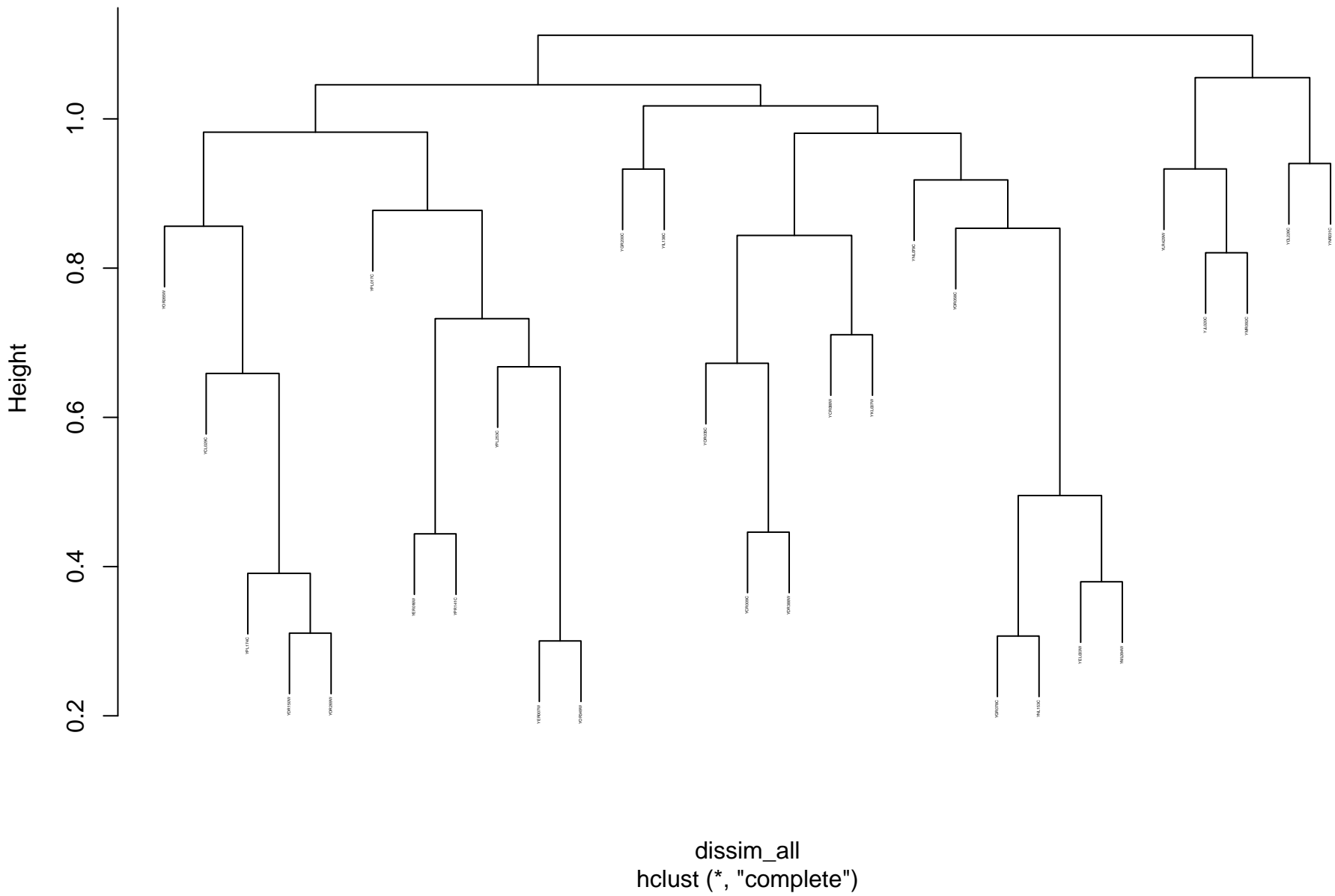


dissim_all
hclust (*, "complete")

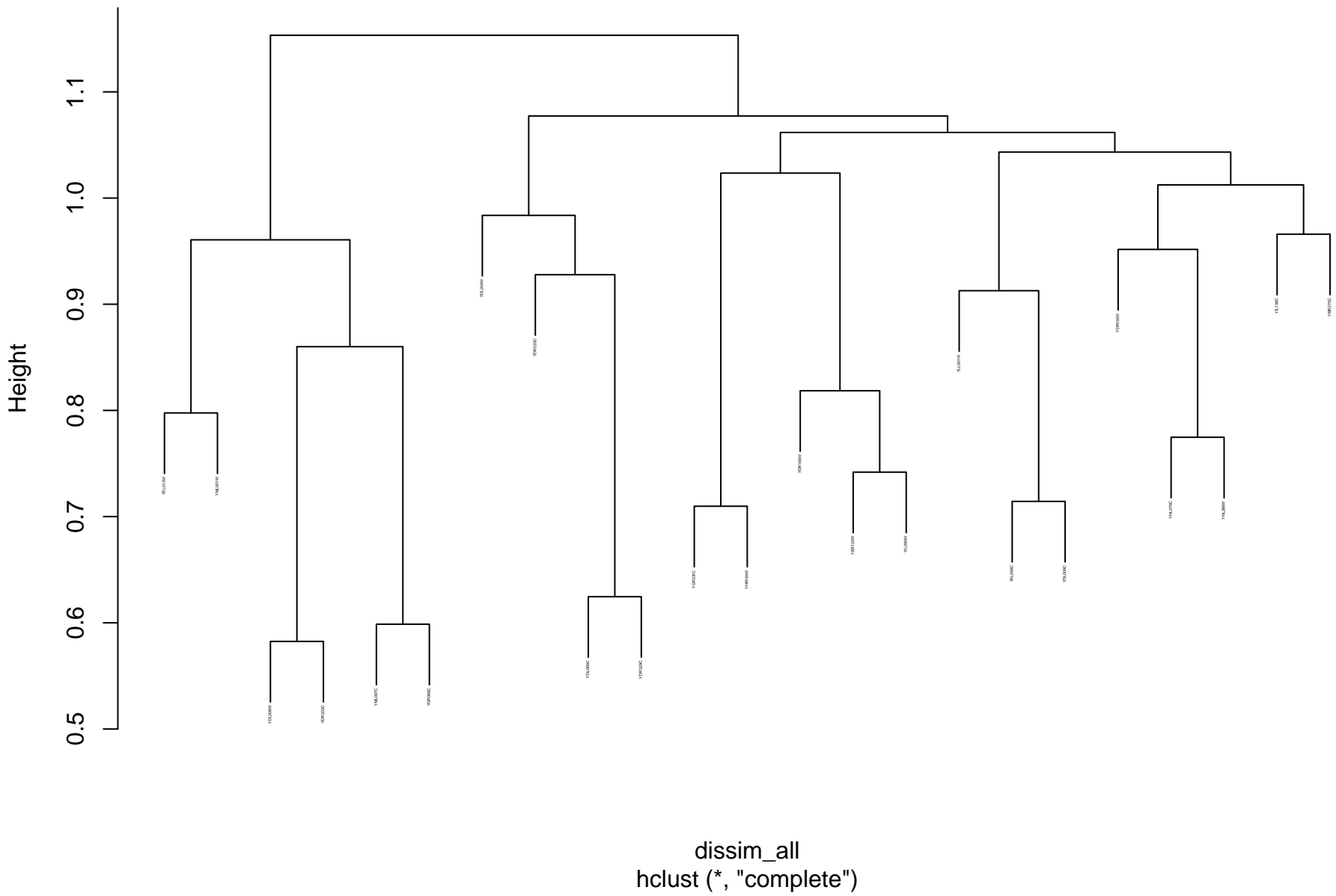
response to osmotic stress_GO_pearson_complete



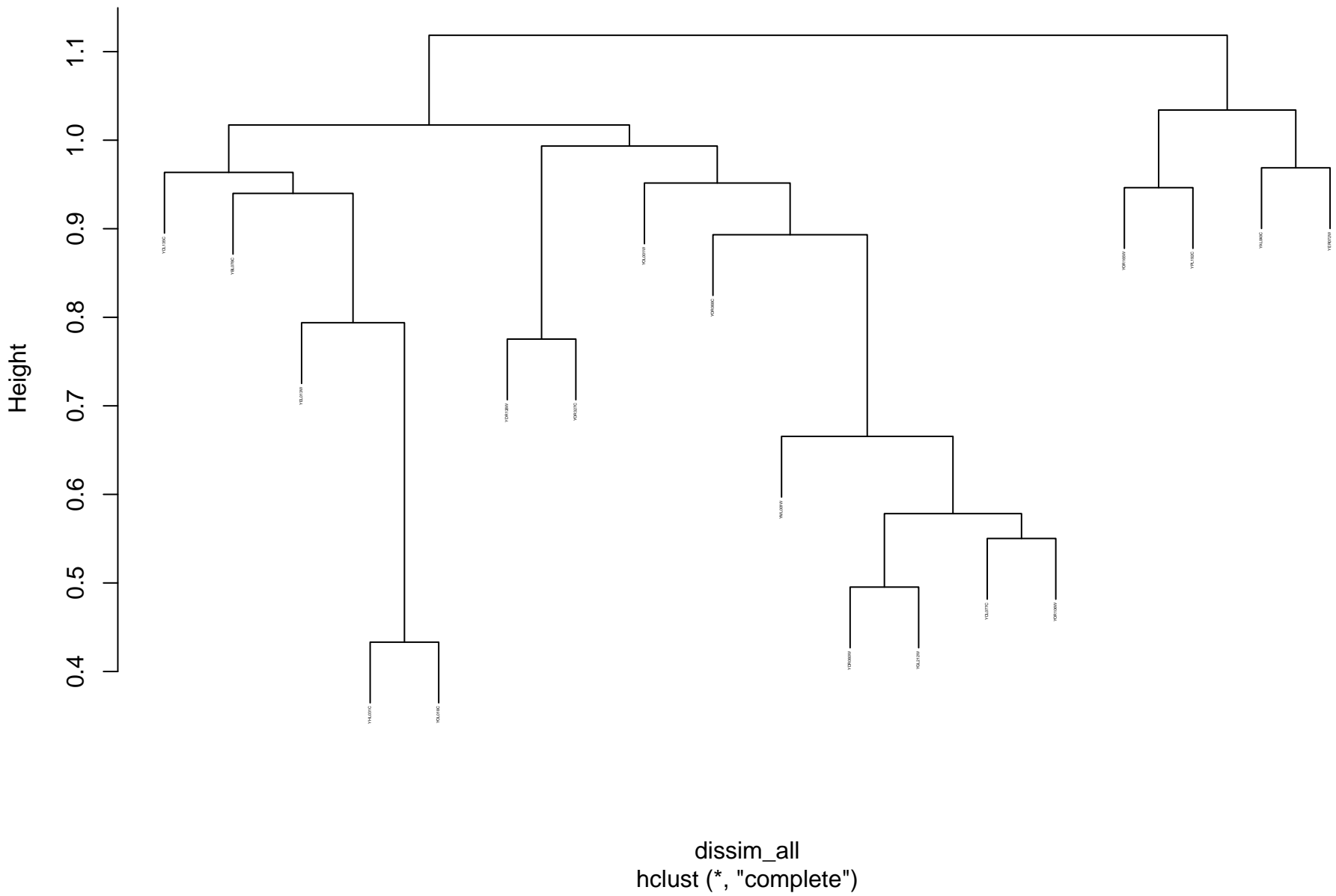
cytoskeletal protein binding_GO_pearson_complete



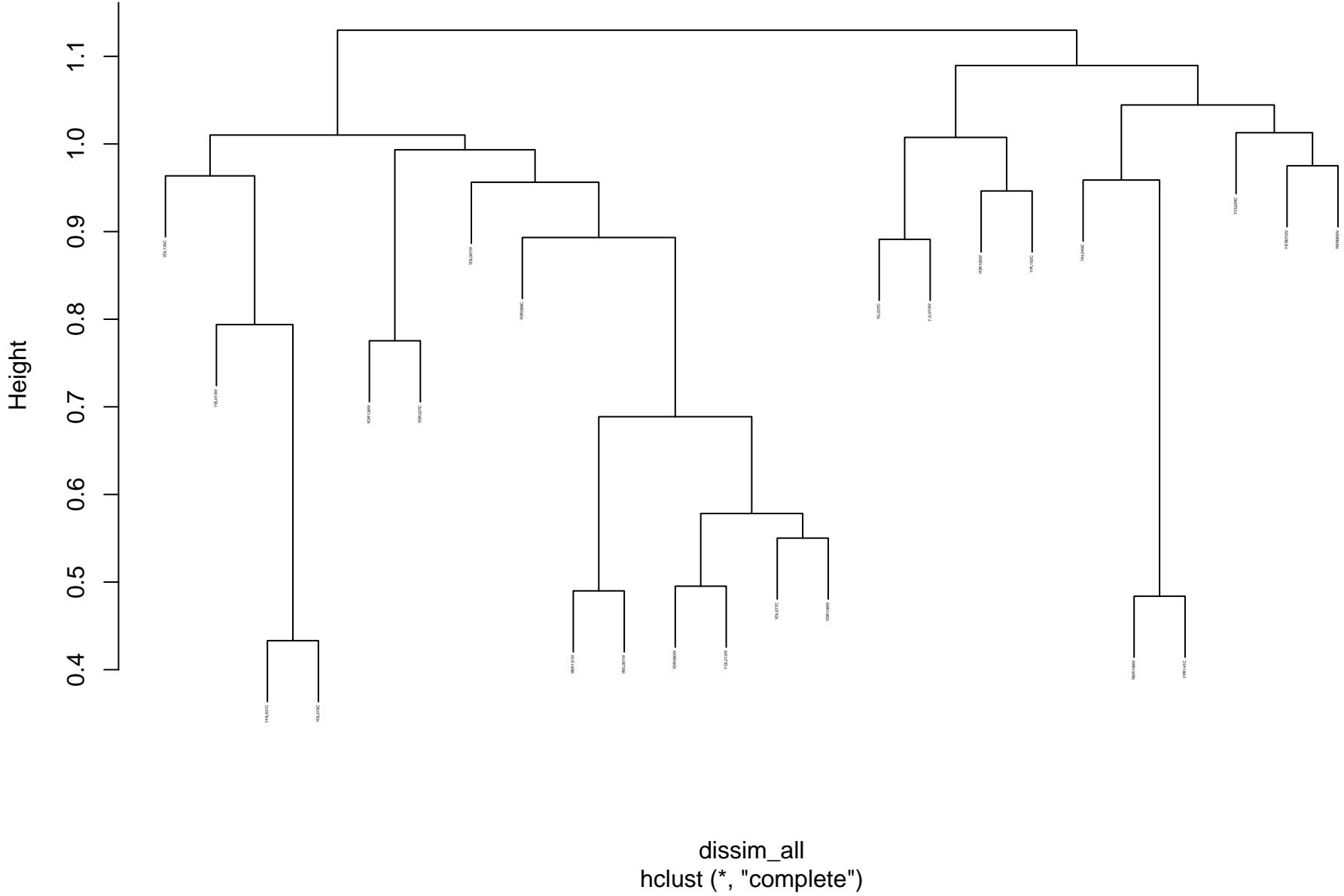
organelle inheritance_GO_pearson_complete



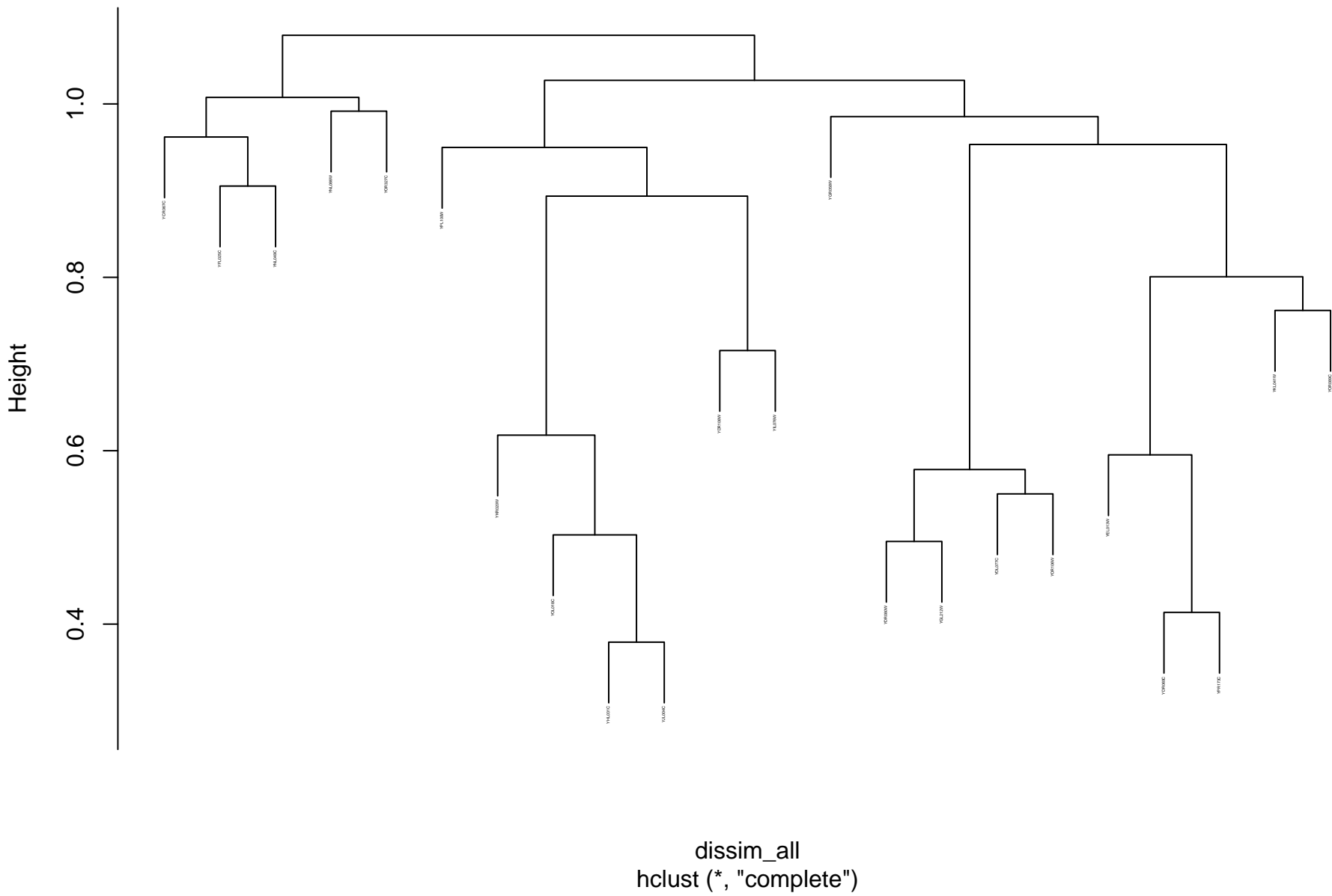
membrane fusion_GO_pearson_complete



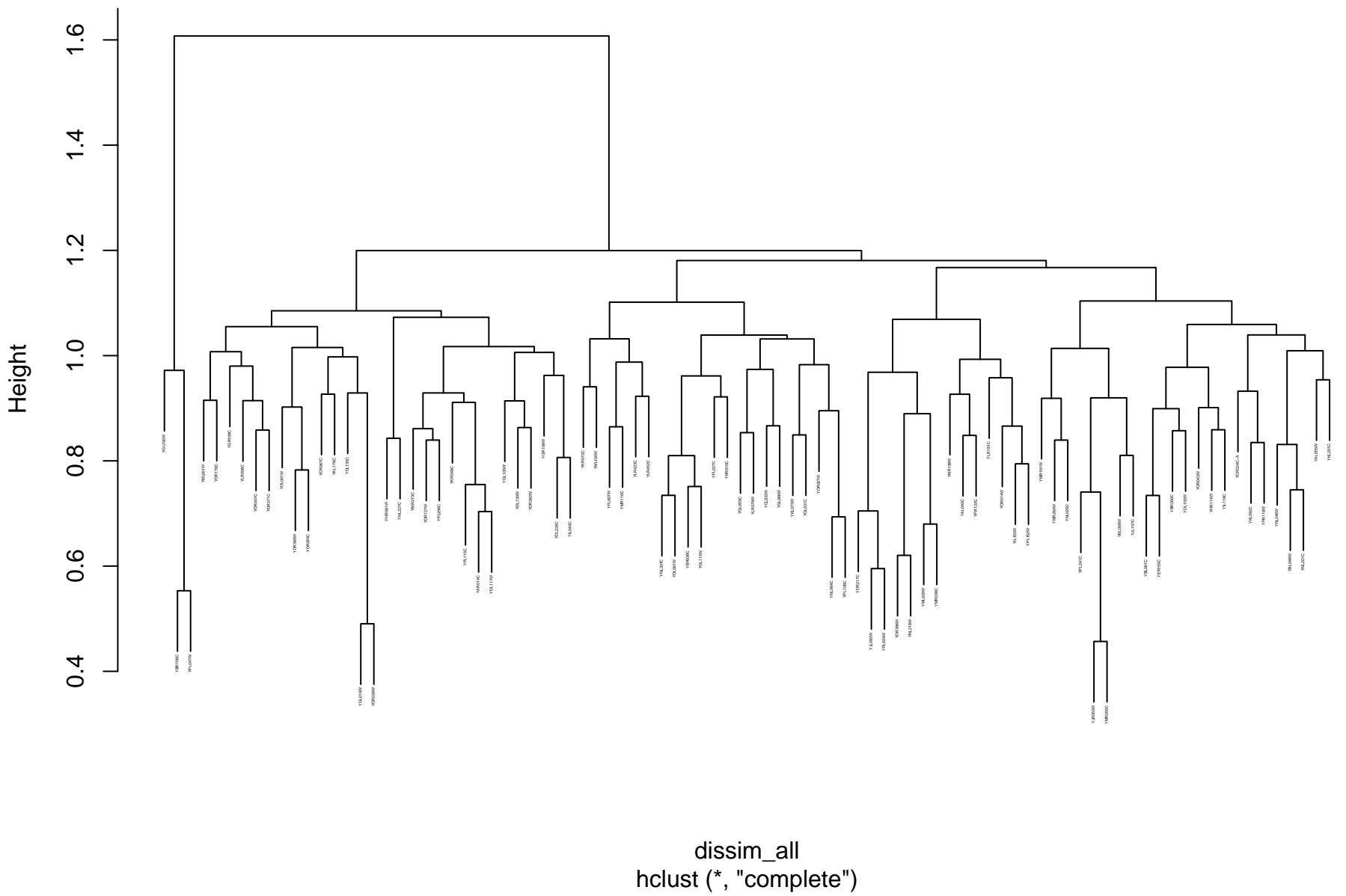
organelle fusion_GO_pearson_complete



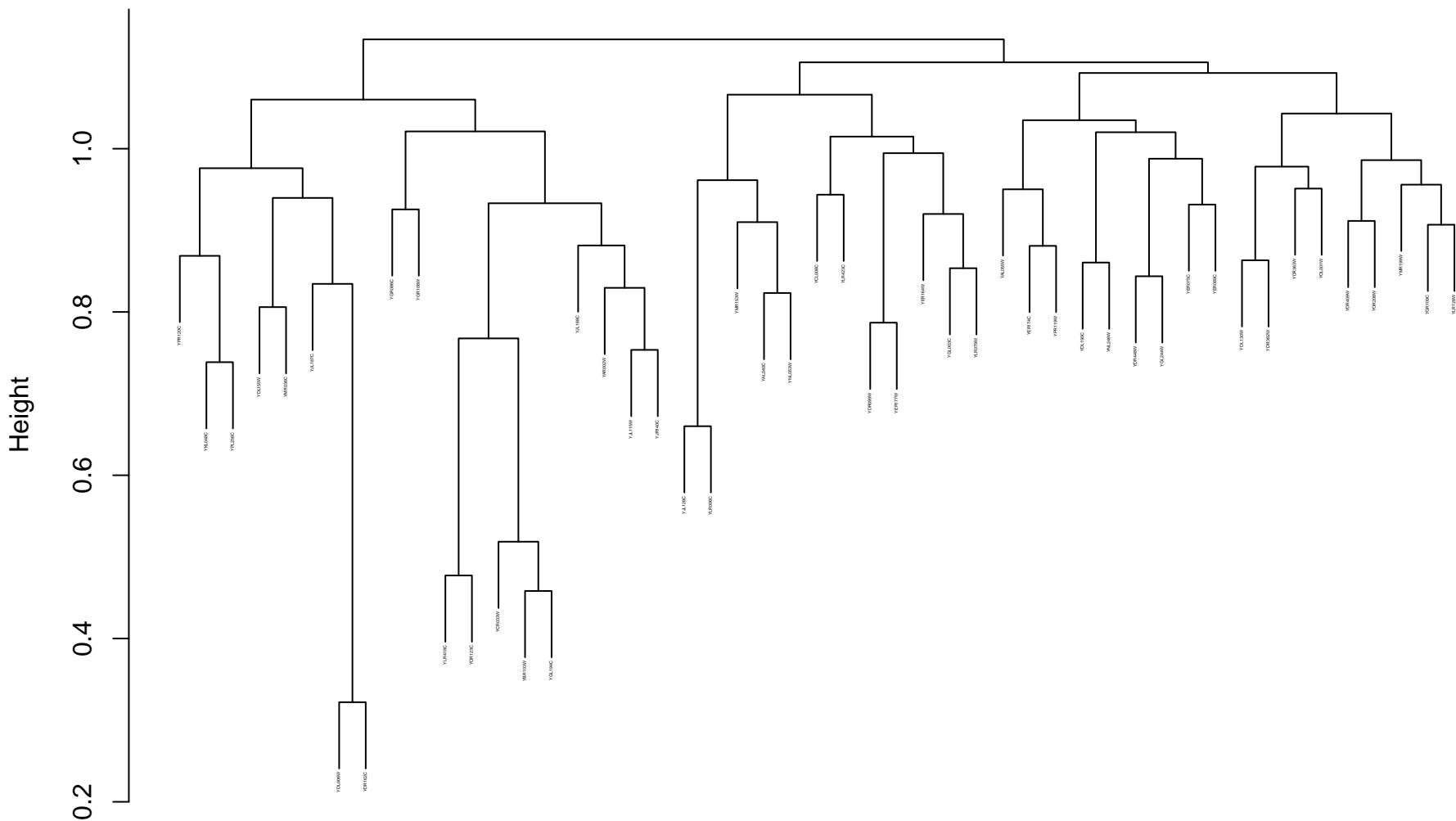
vesicle organization_GO_pearson_complete



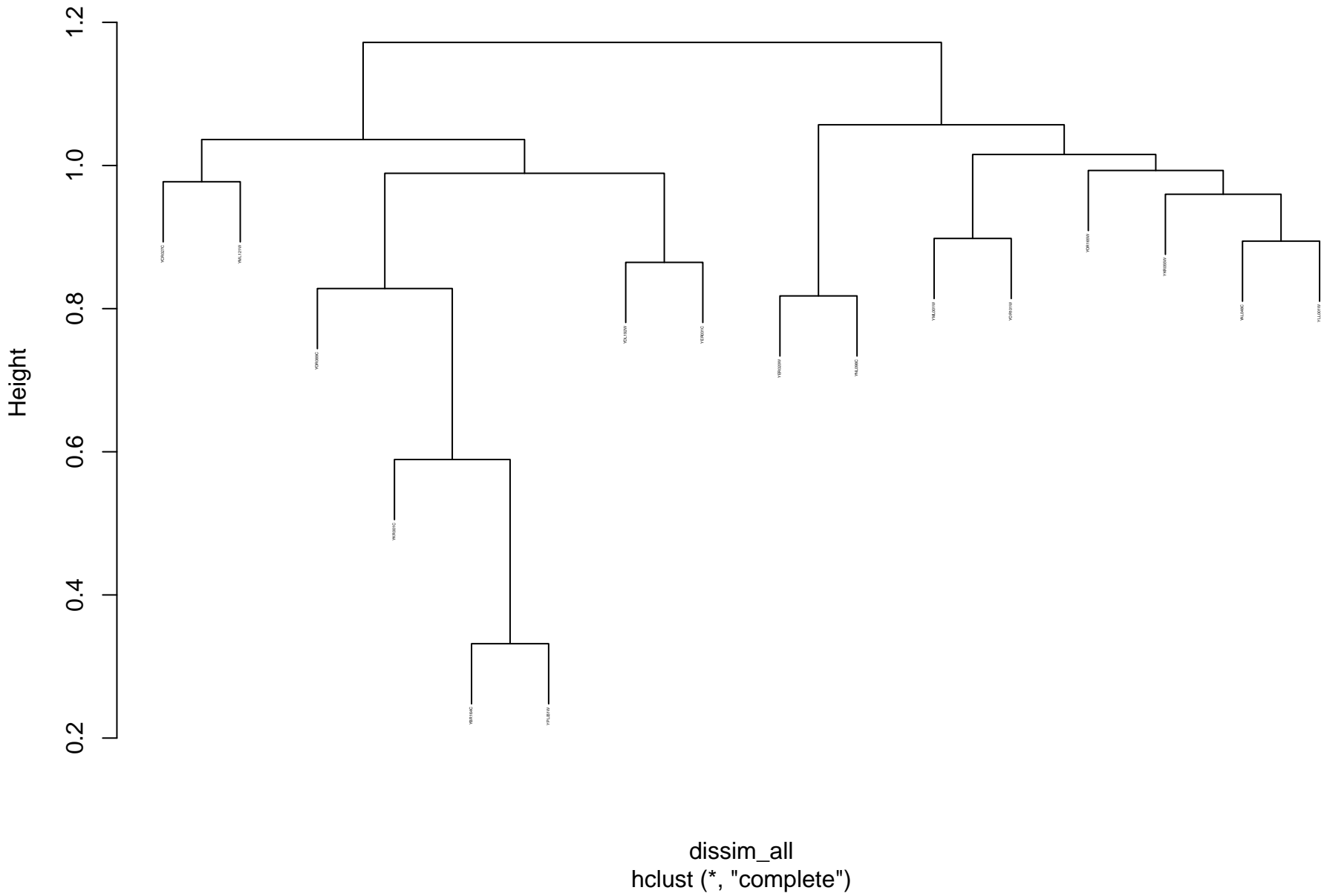
enzyme regulator activity_GO_pearson_complete



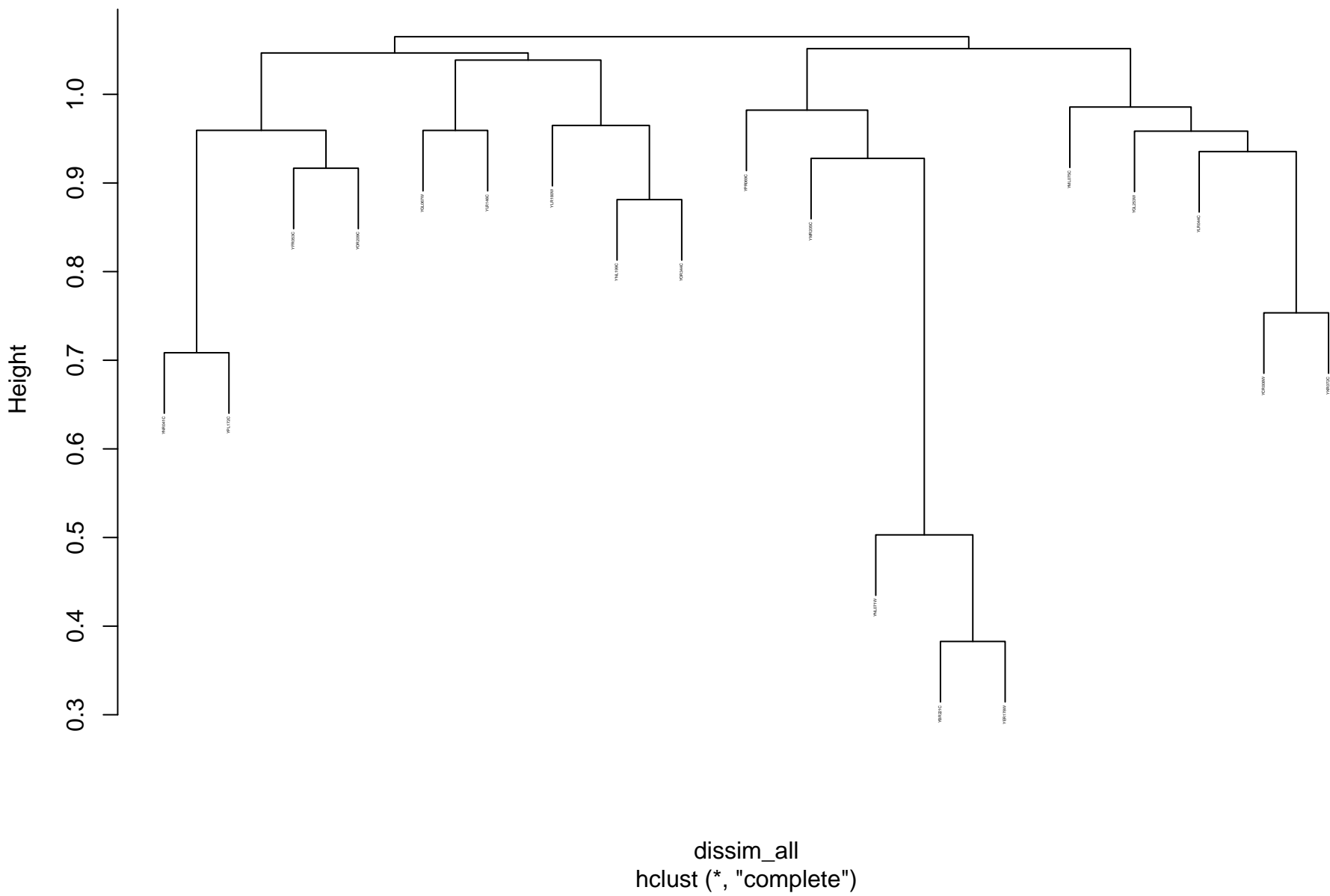
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dissim_all
hclust (*, "complete")
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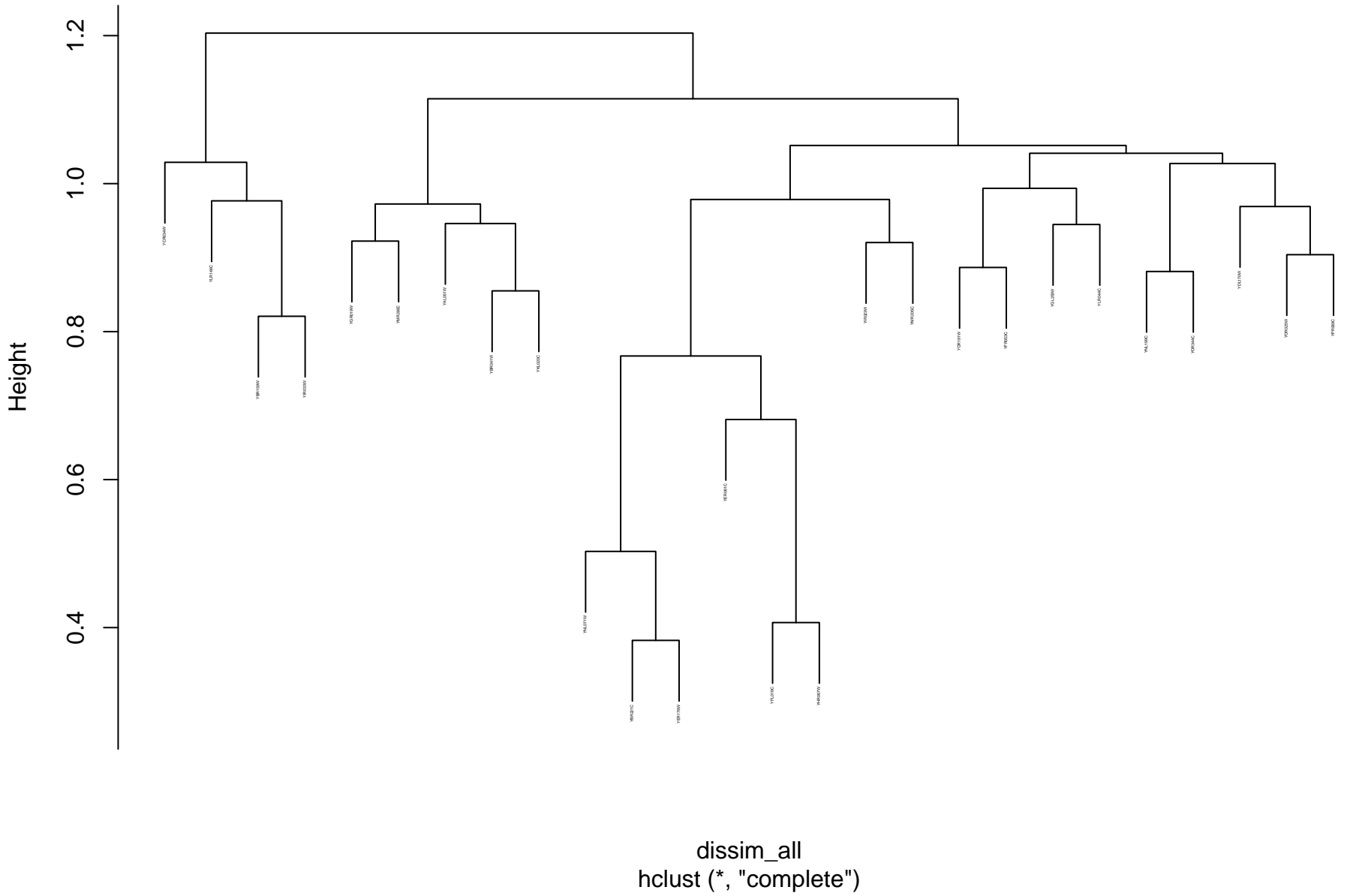
GTPase activity_GO_pearson_complete



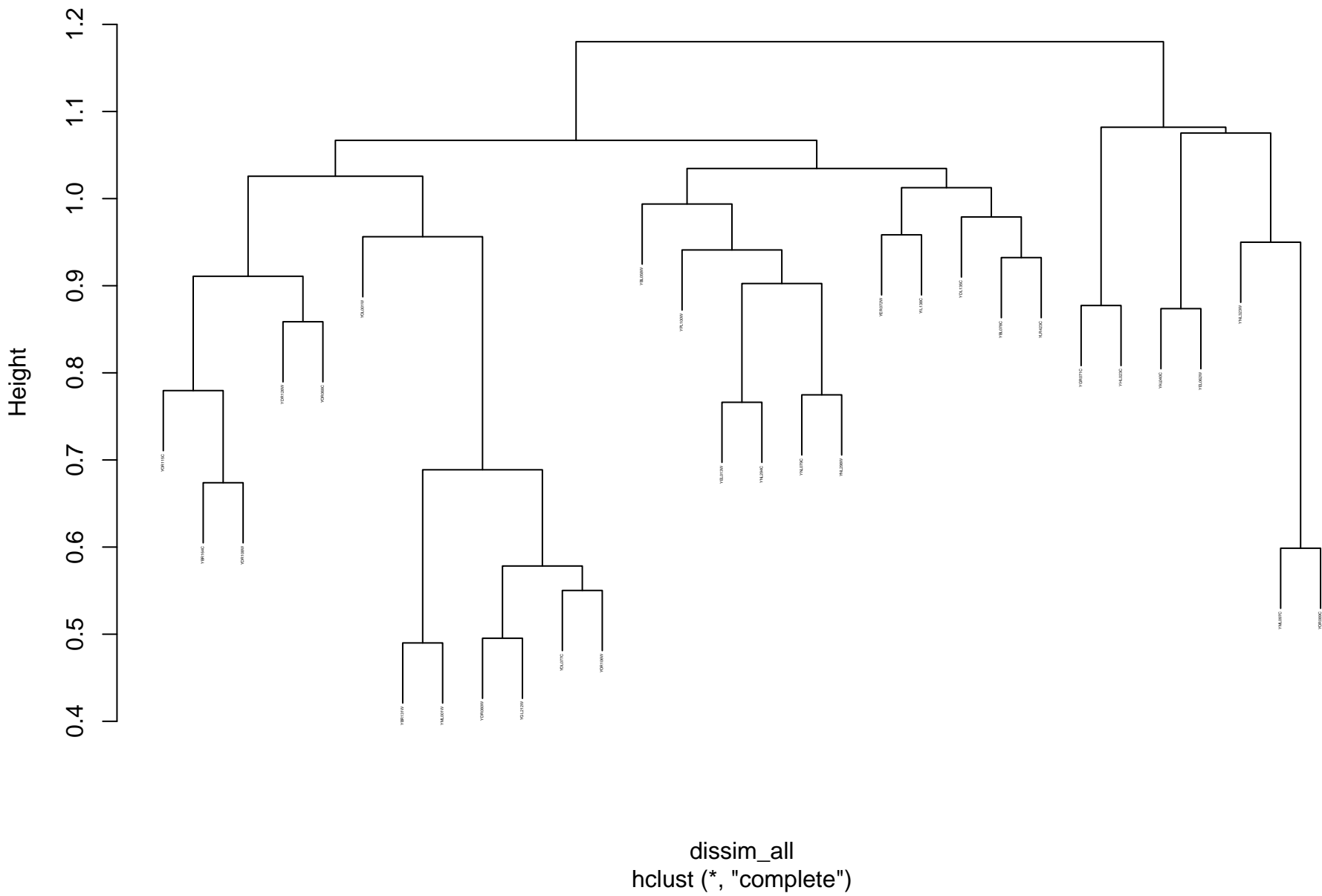
cofactor metabolic process_GO_pearson_complete



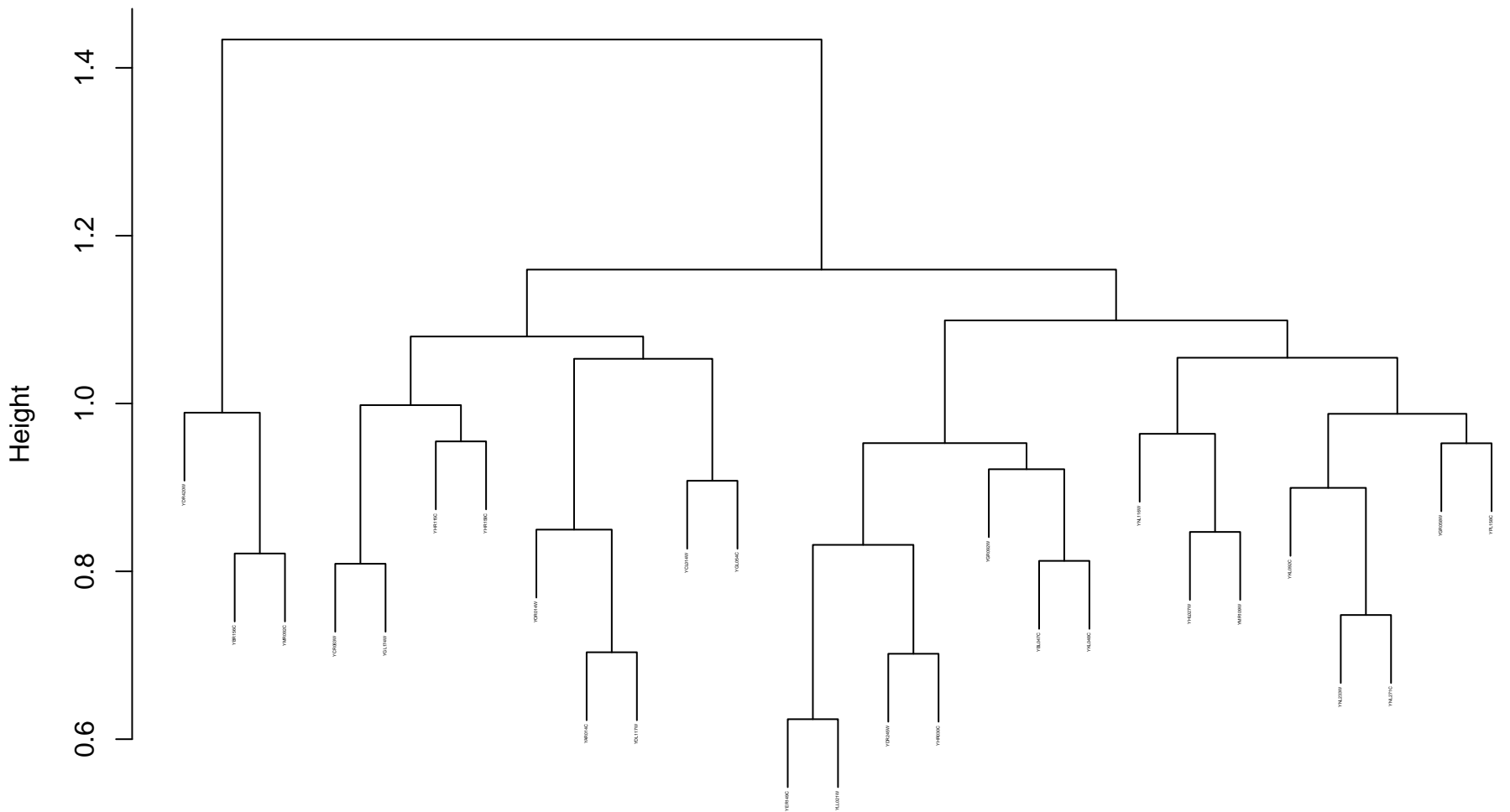
monocarboxylic acid metabolic process_GO_pearson_complete



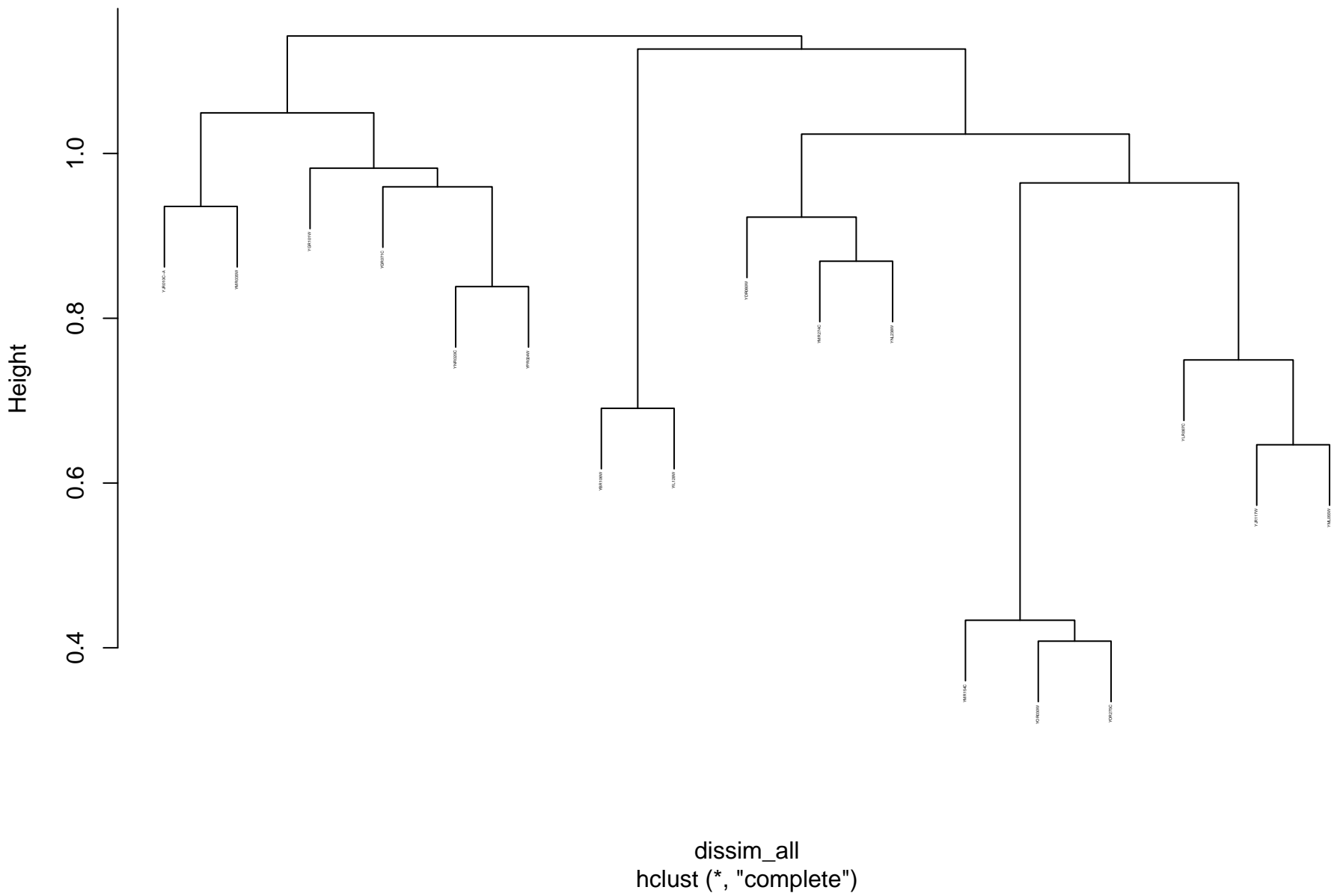
vacuole organization_GO_pearson_complete



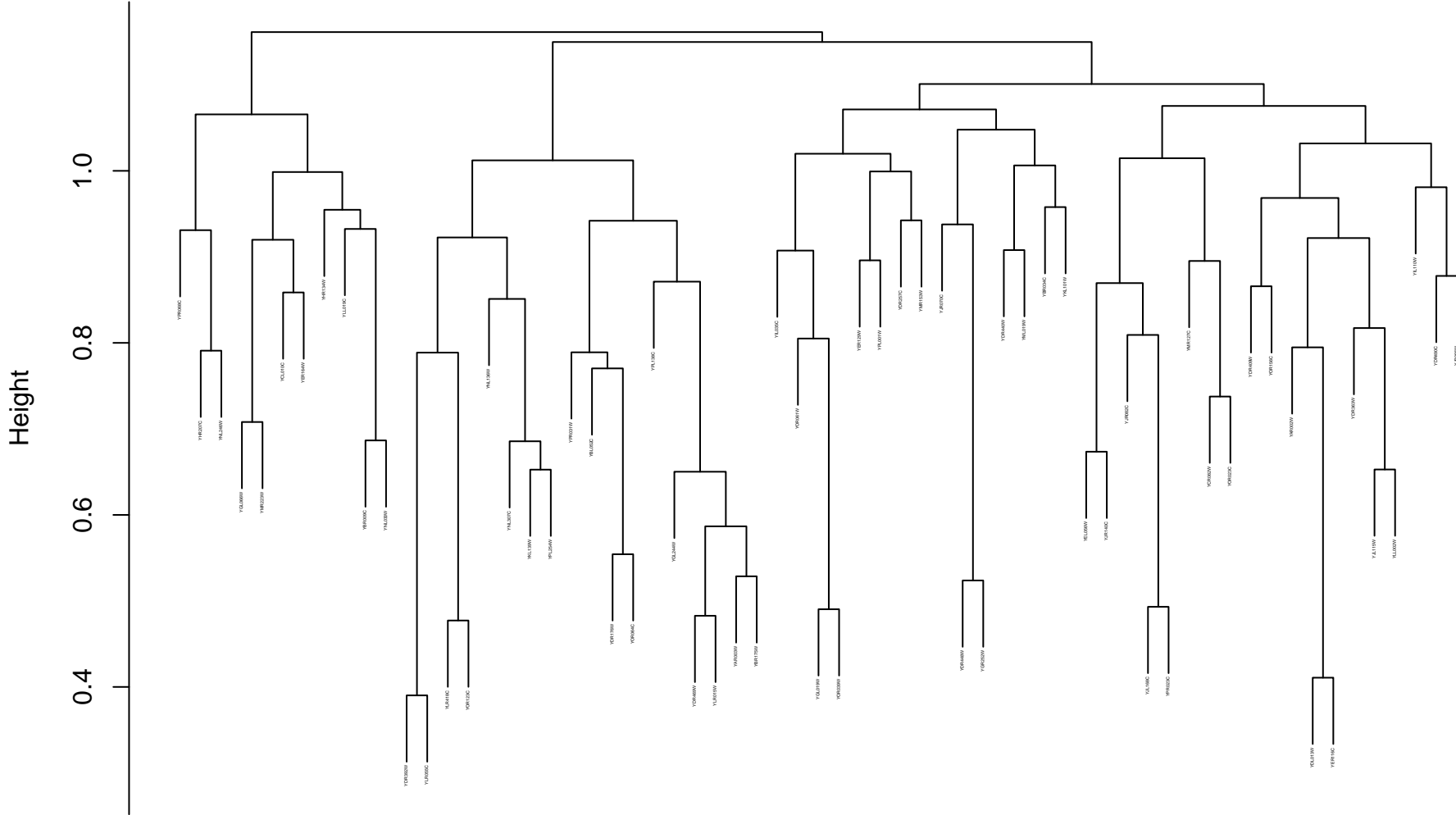
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dissim_all
hclust (*, "complete")
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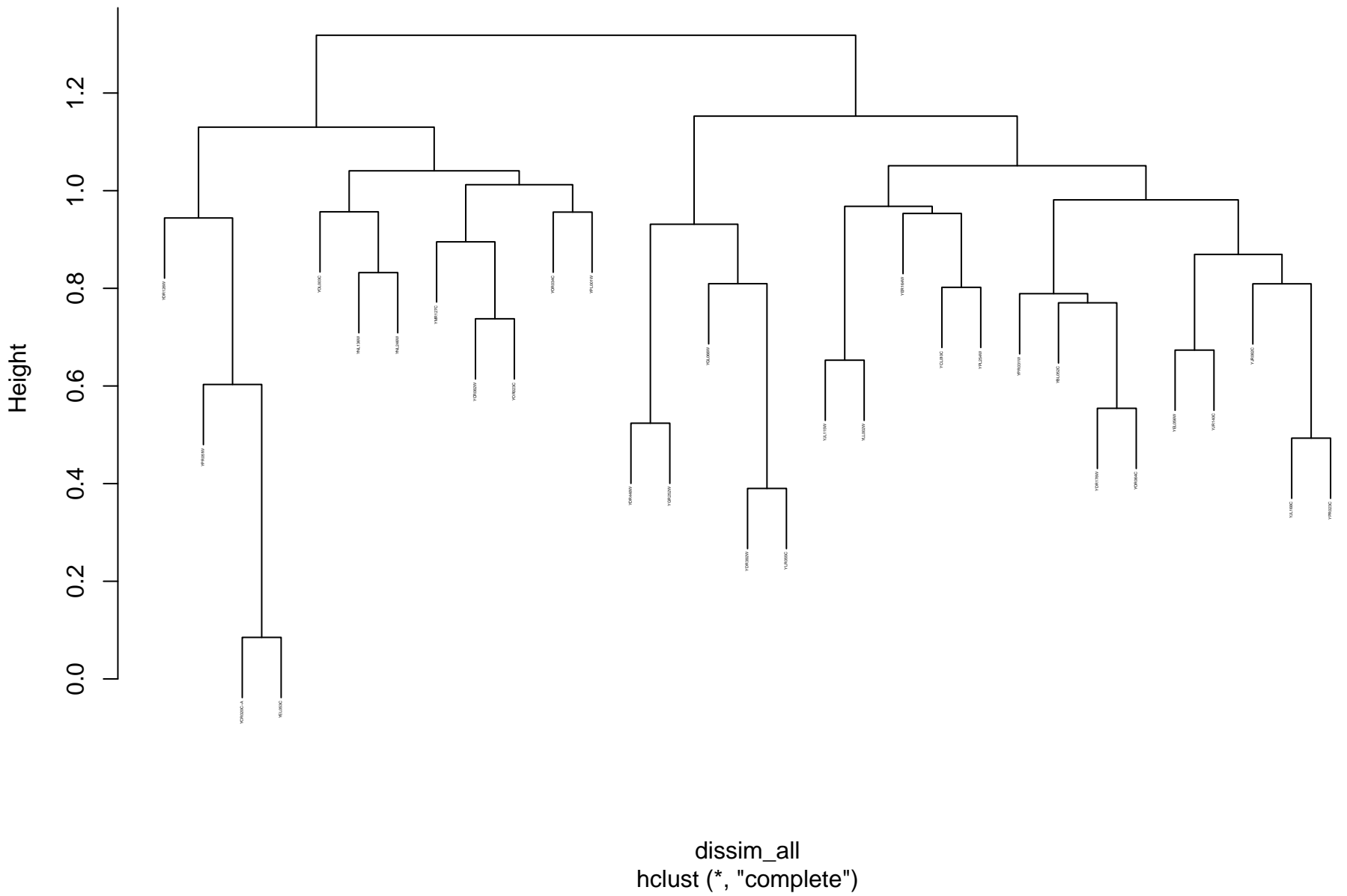
protein maturation_GO_pearson_complete



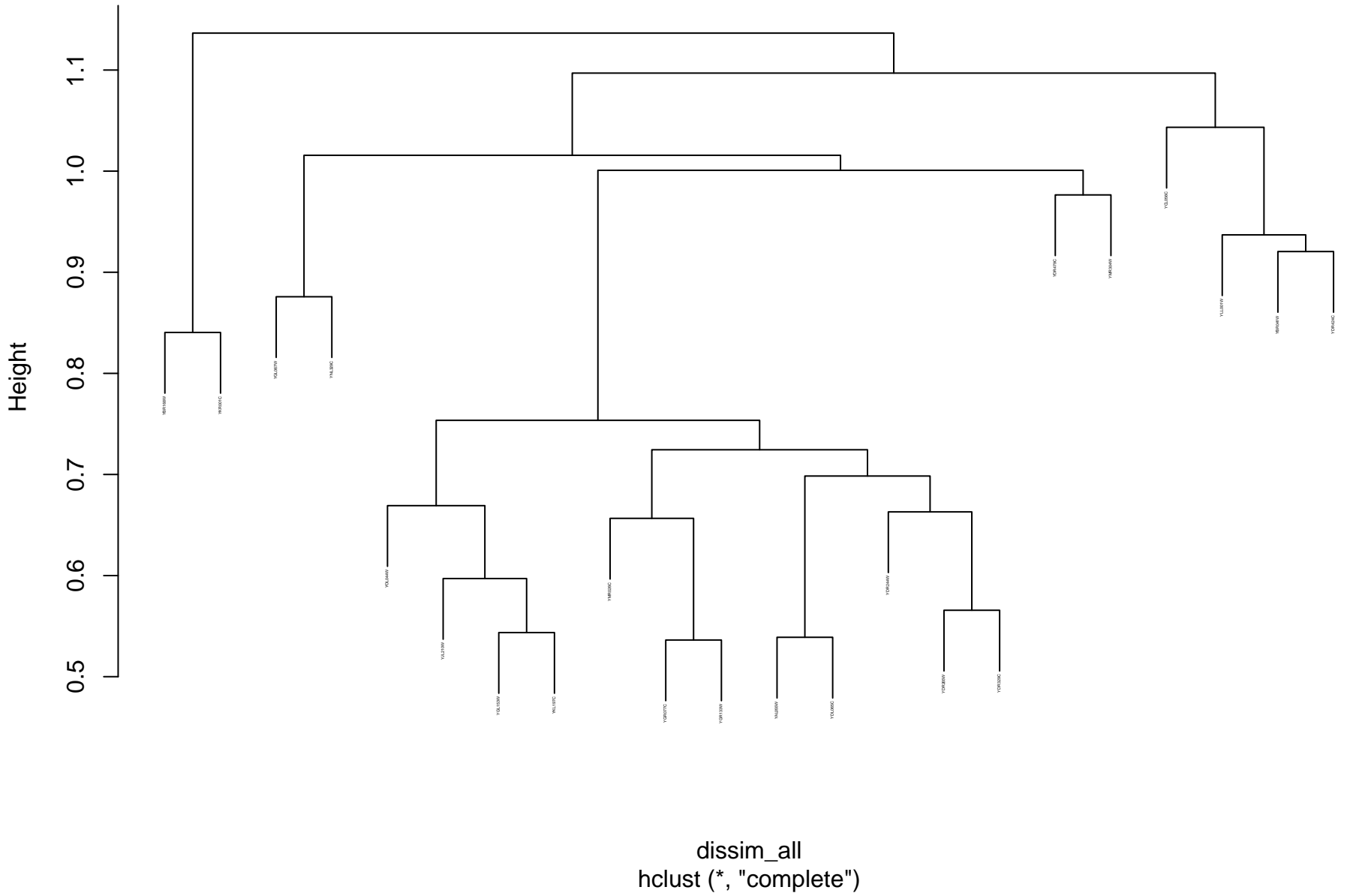
peptidyl-amino acid modification_GO_pearson_complete



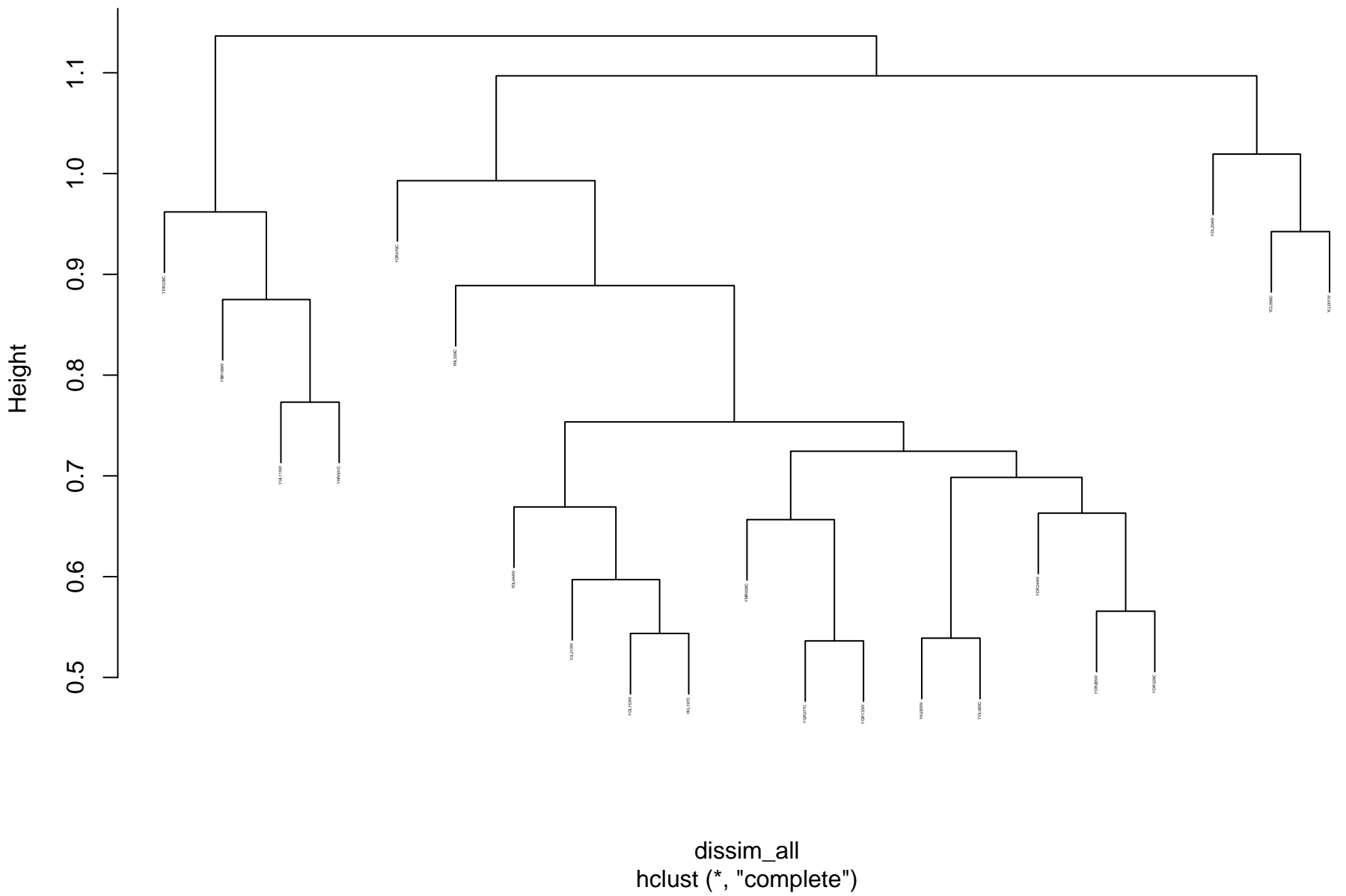
protein acylation_GO_pearson_complete



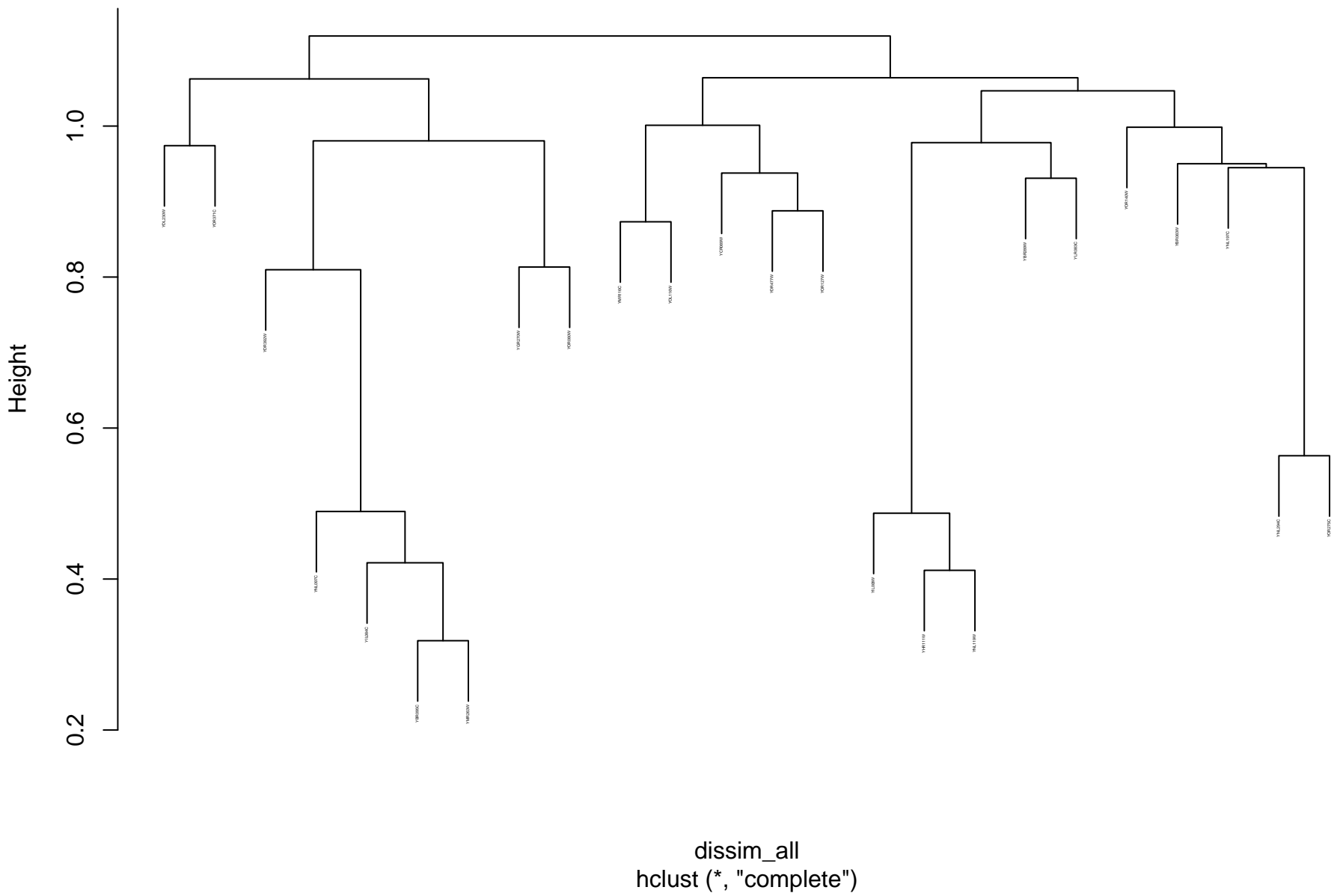
peroxisome_GO_pearson_complete



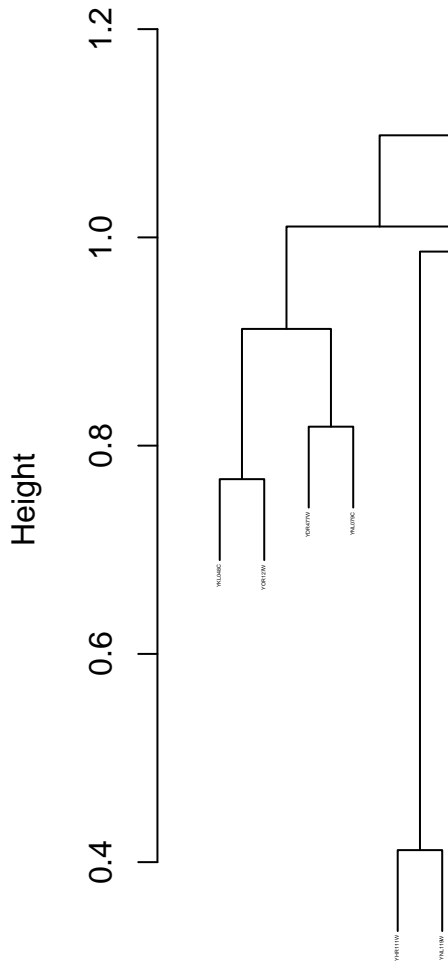
peroxisome organization_GO_pearson_complete



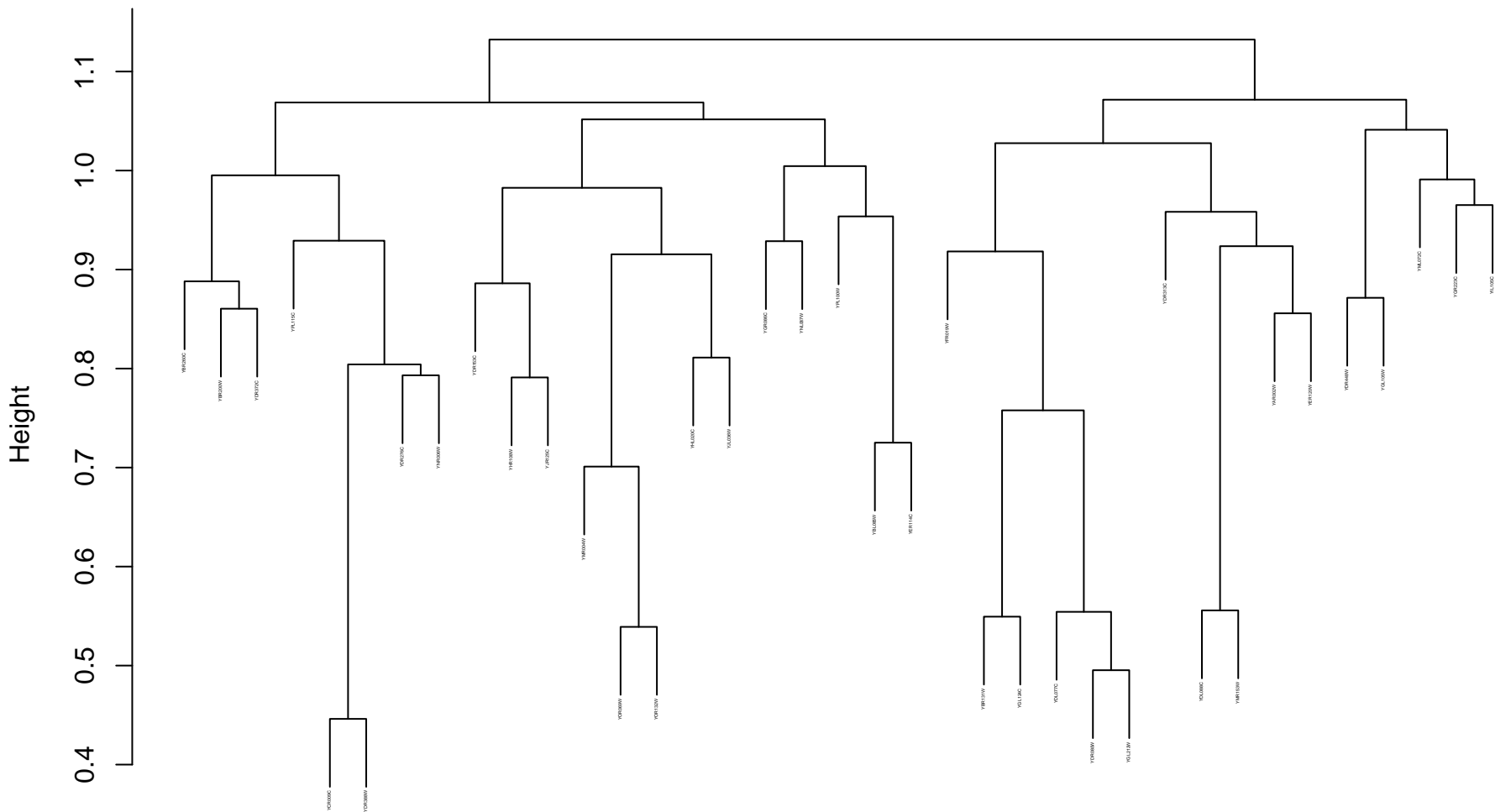
invasive growth in response to glucose limitation_GO_pearson_complete



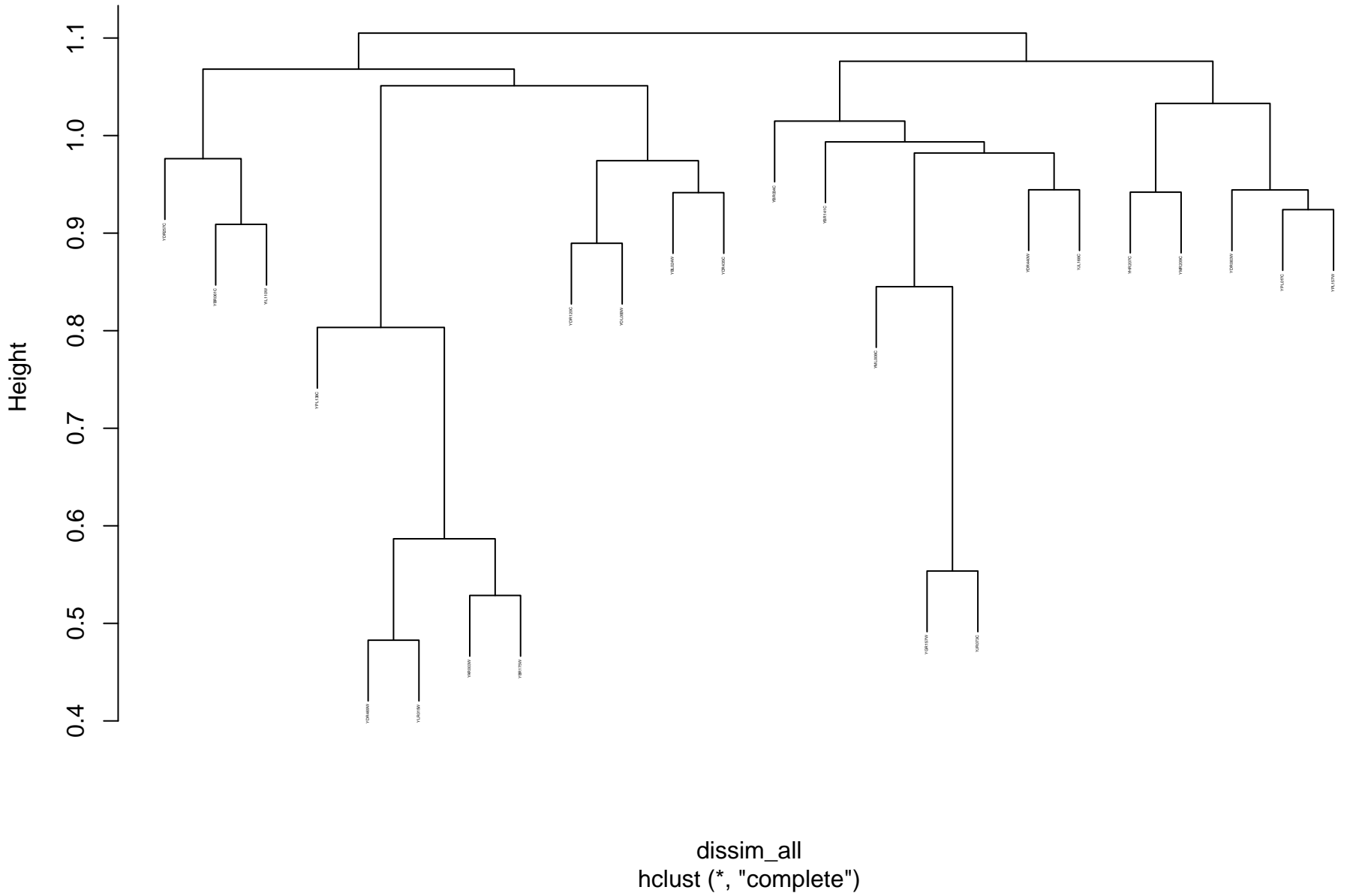
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dissim_all
hclust (*, "complete")
```



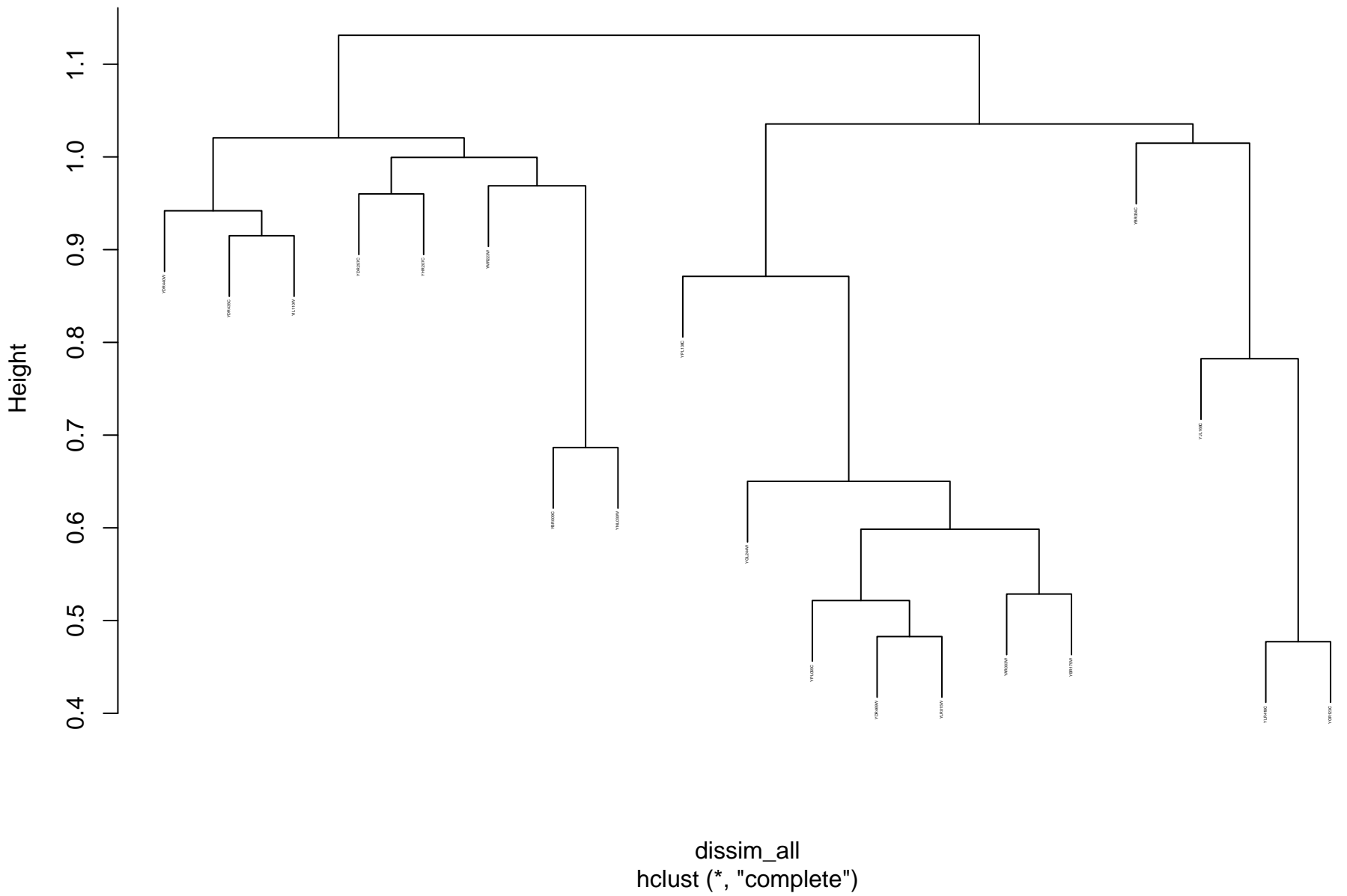
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dissim_all
hclust (*, "complete")
```



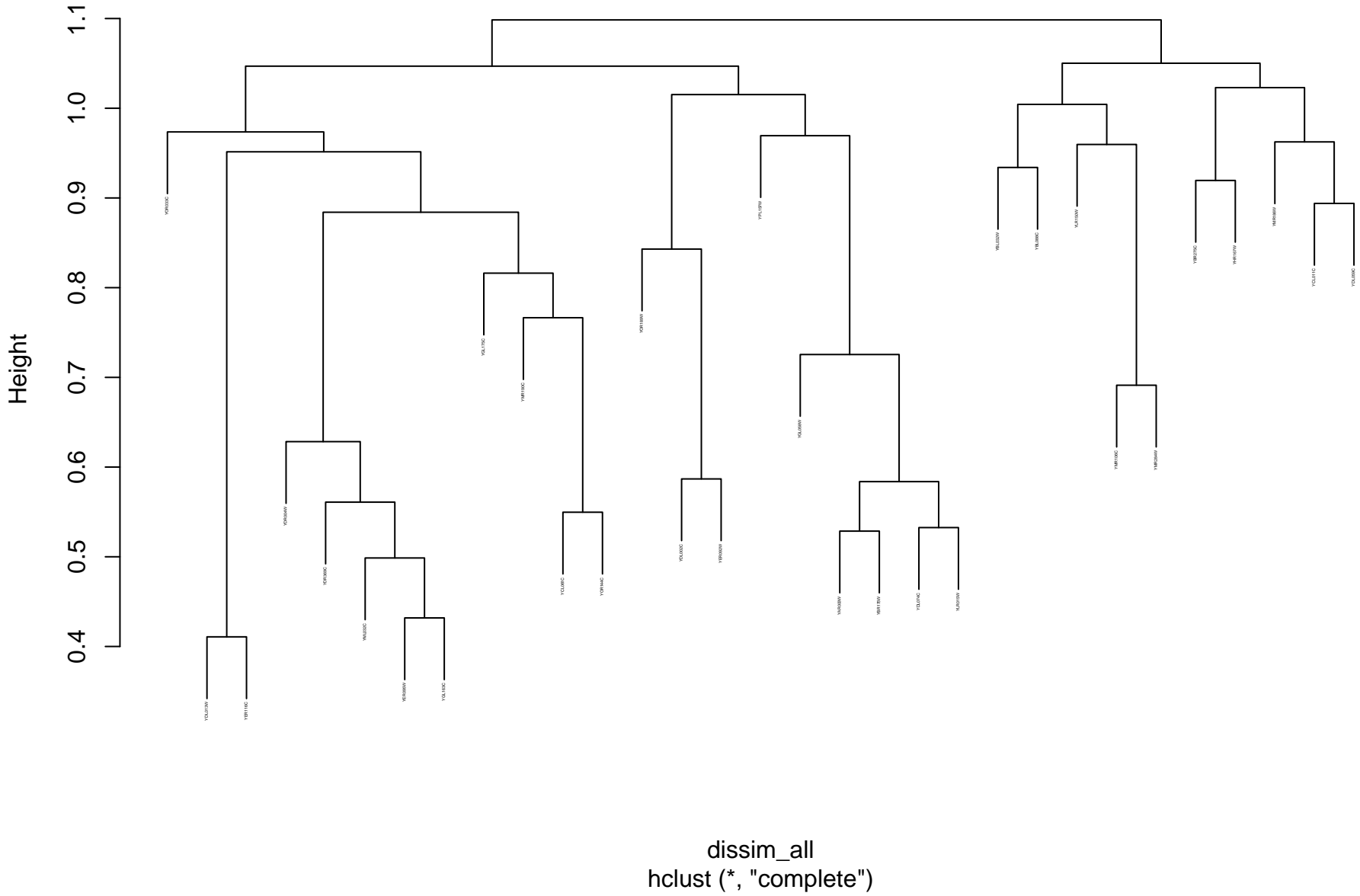
methyltransferase activity_GO_pearson_complete



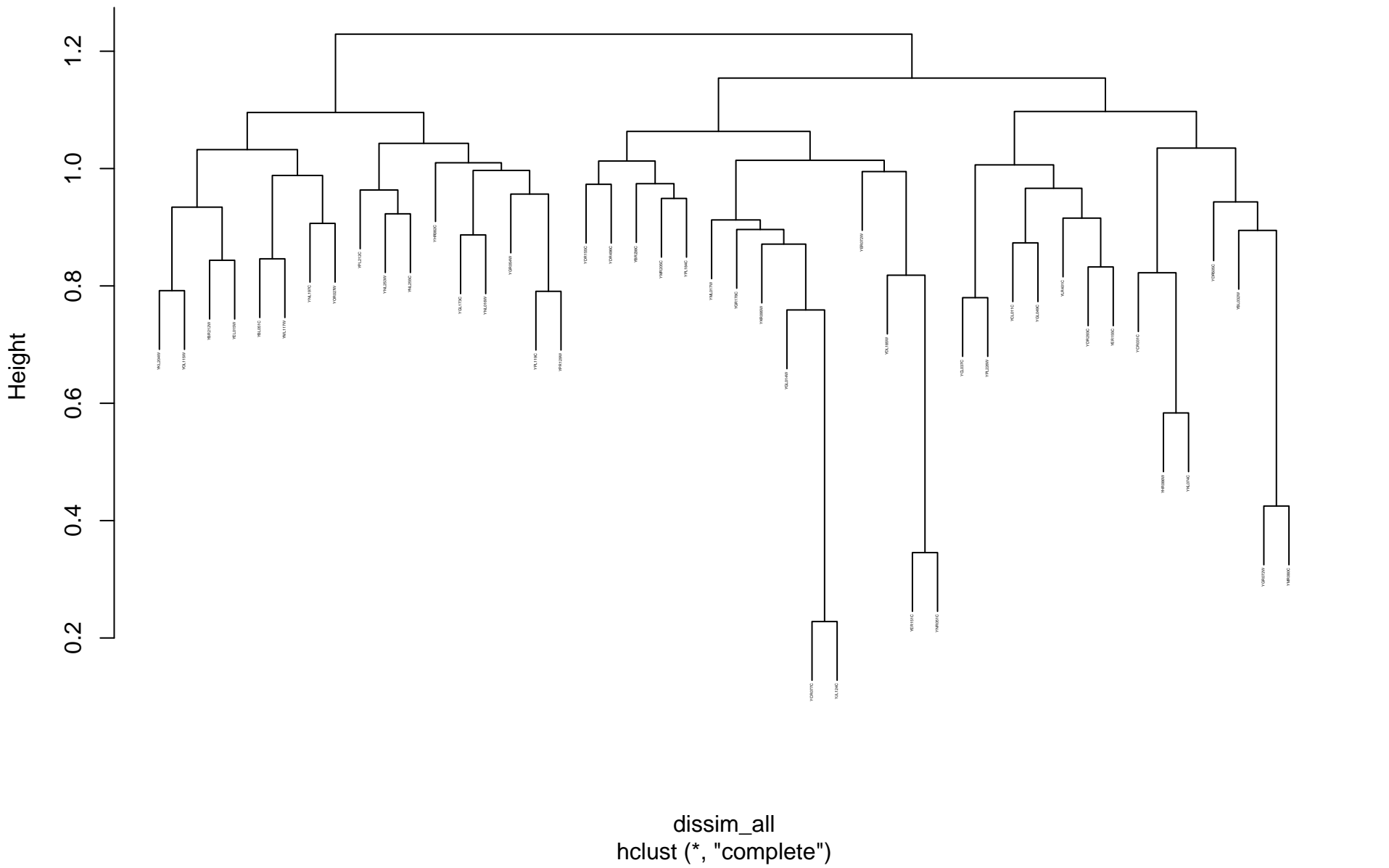
protein alkylation_GO_pearson_complete



telomere organization_GO_pearson_complete

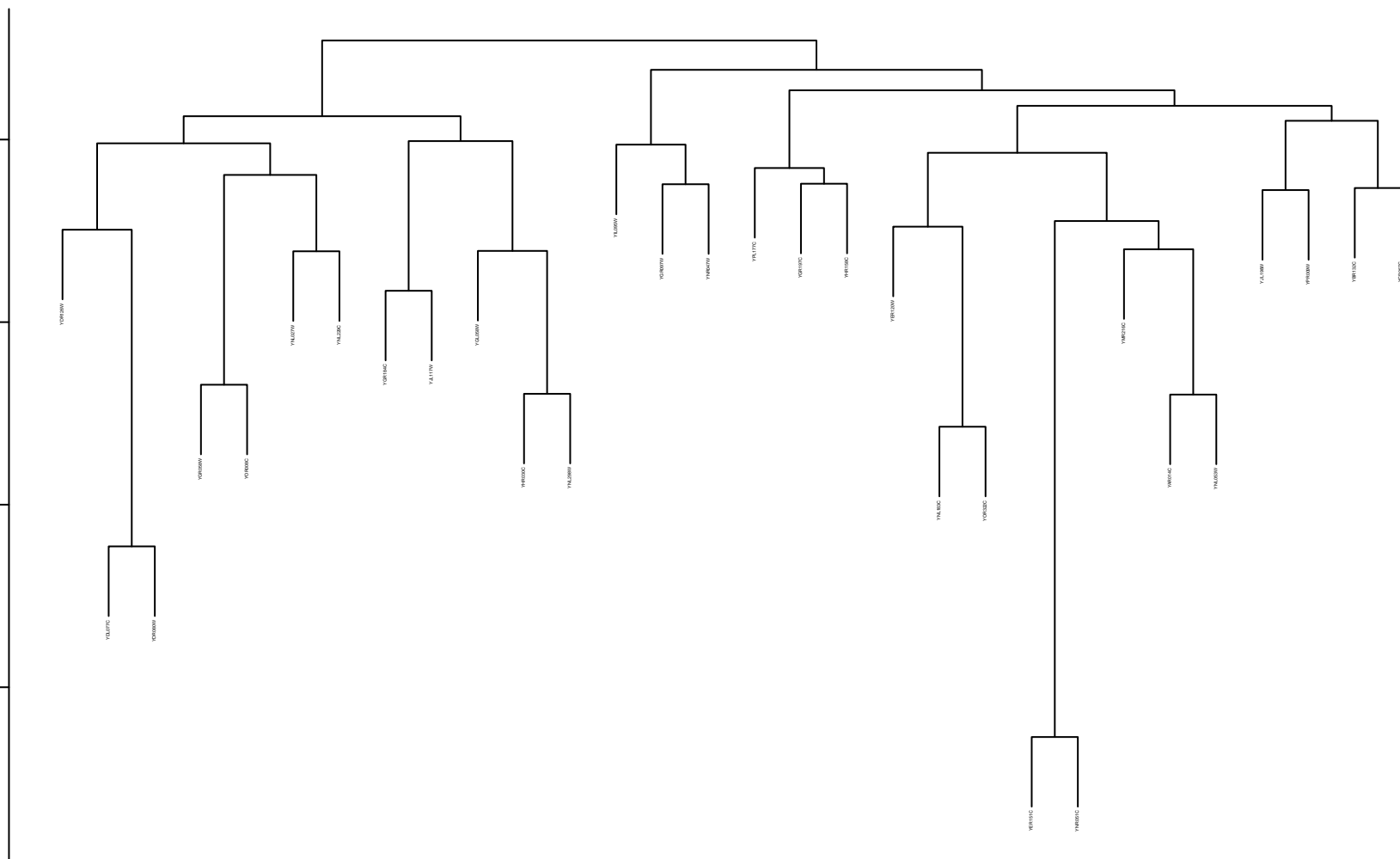


mRNA binding_GO_pearson_complete

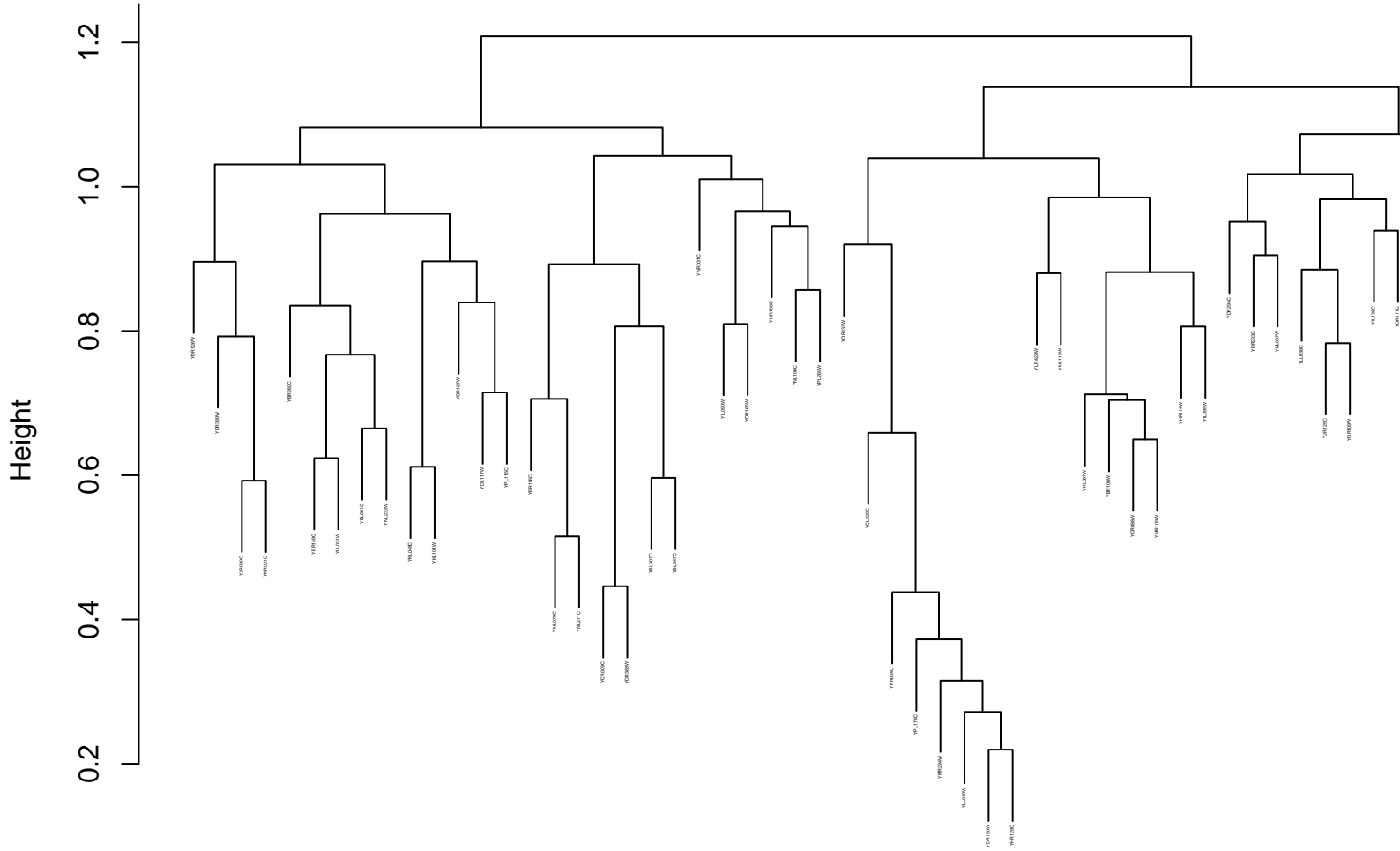



```
dissim_all
hclust (*, "complete")
```

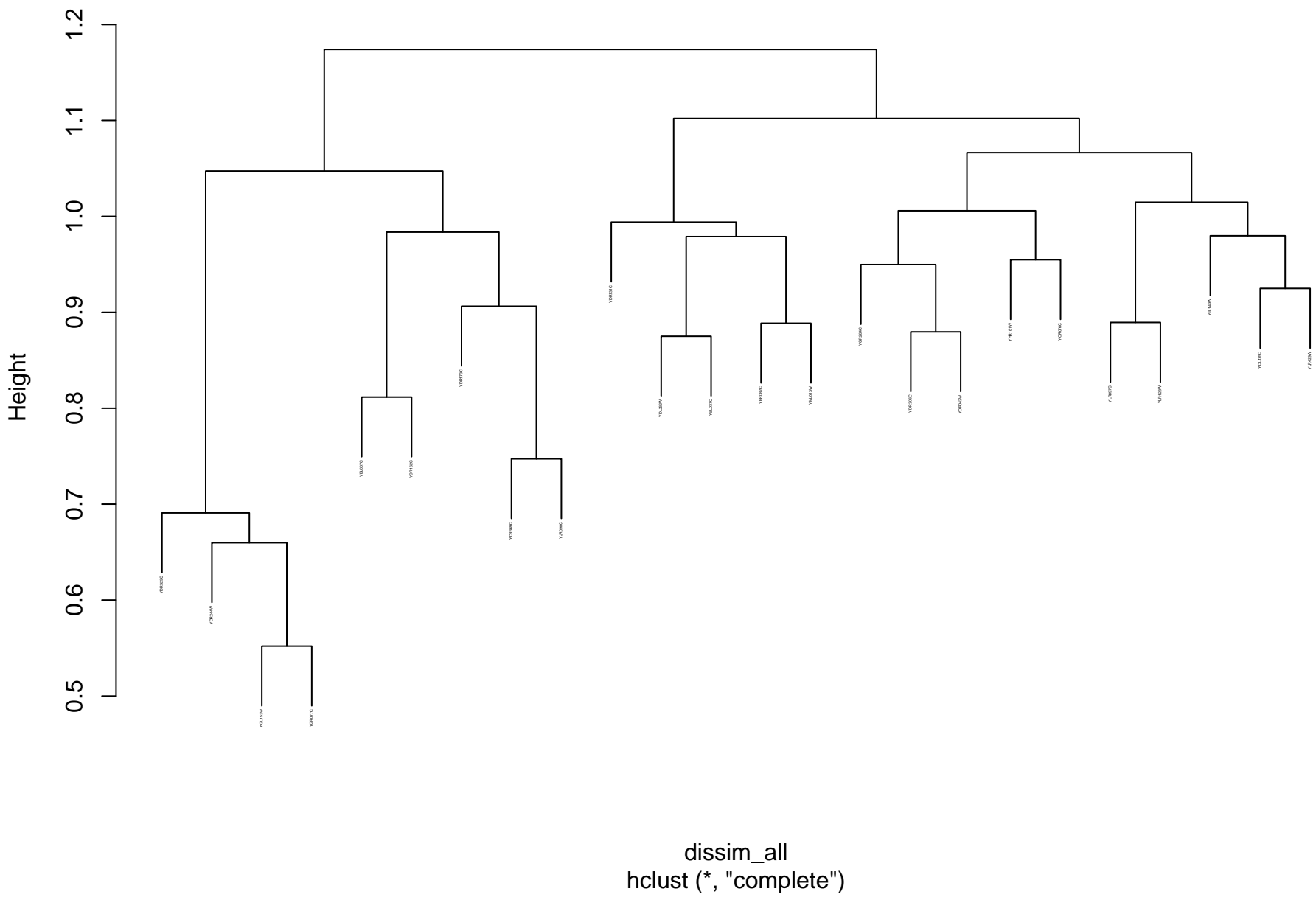
0.4 0.6 0.8 1.0



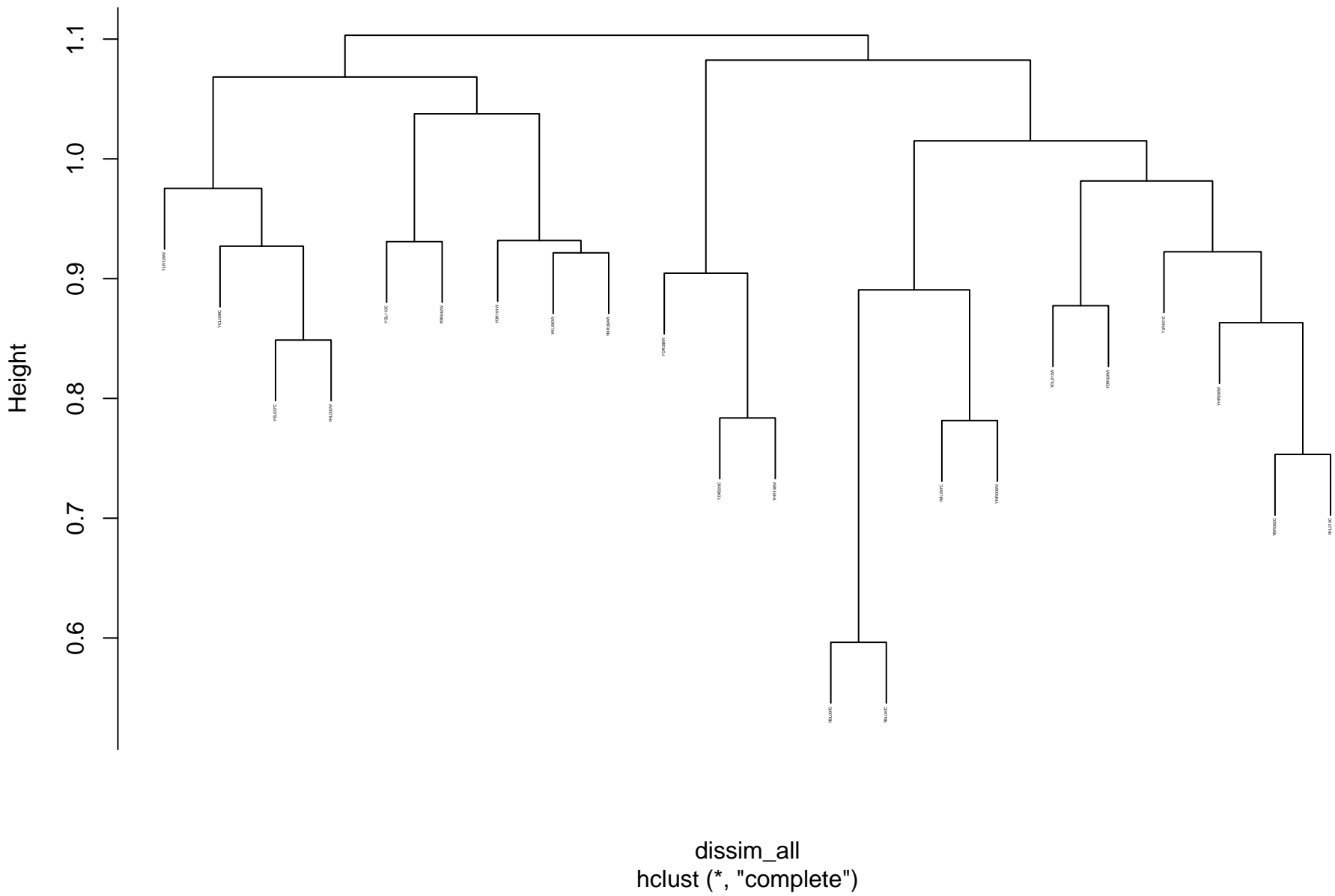
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dissim_all
hclust (*, "complete")
```



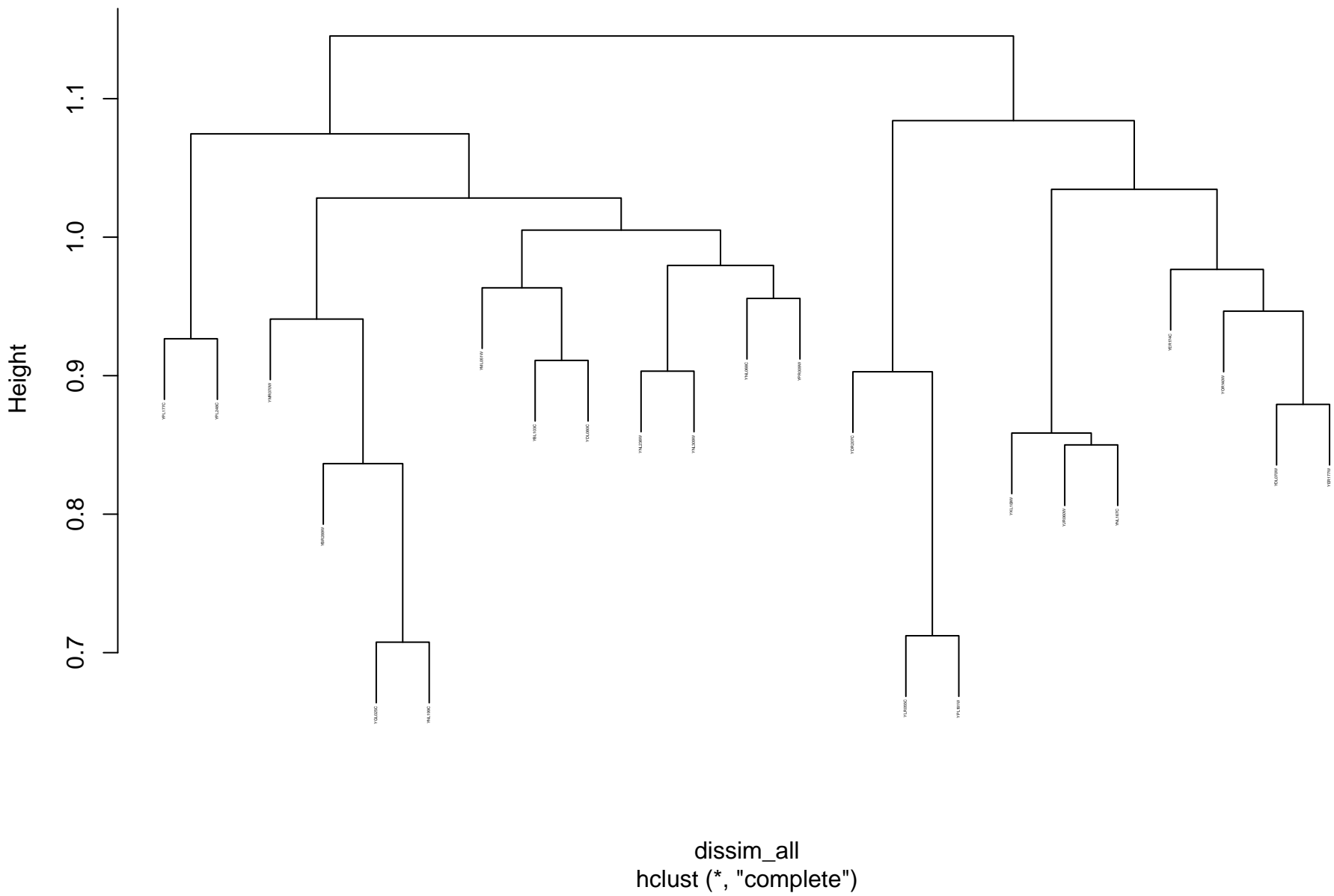
protein binding, bridging_GO_pearson_complete



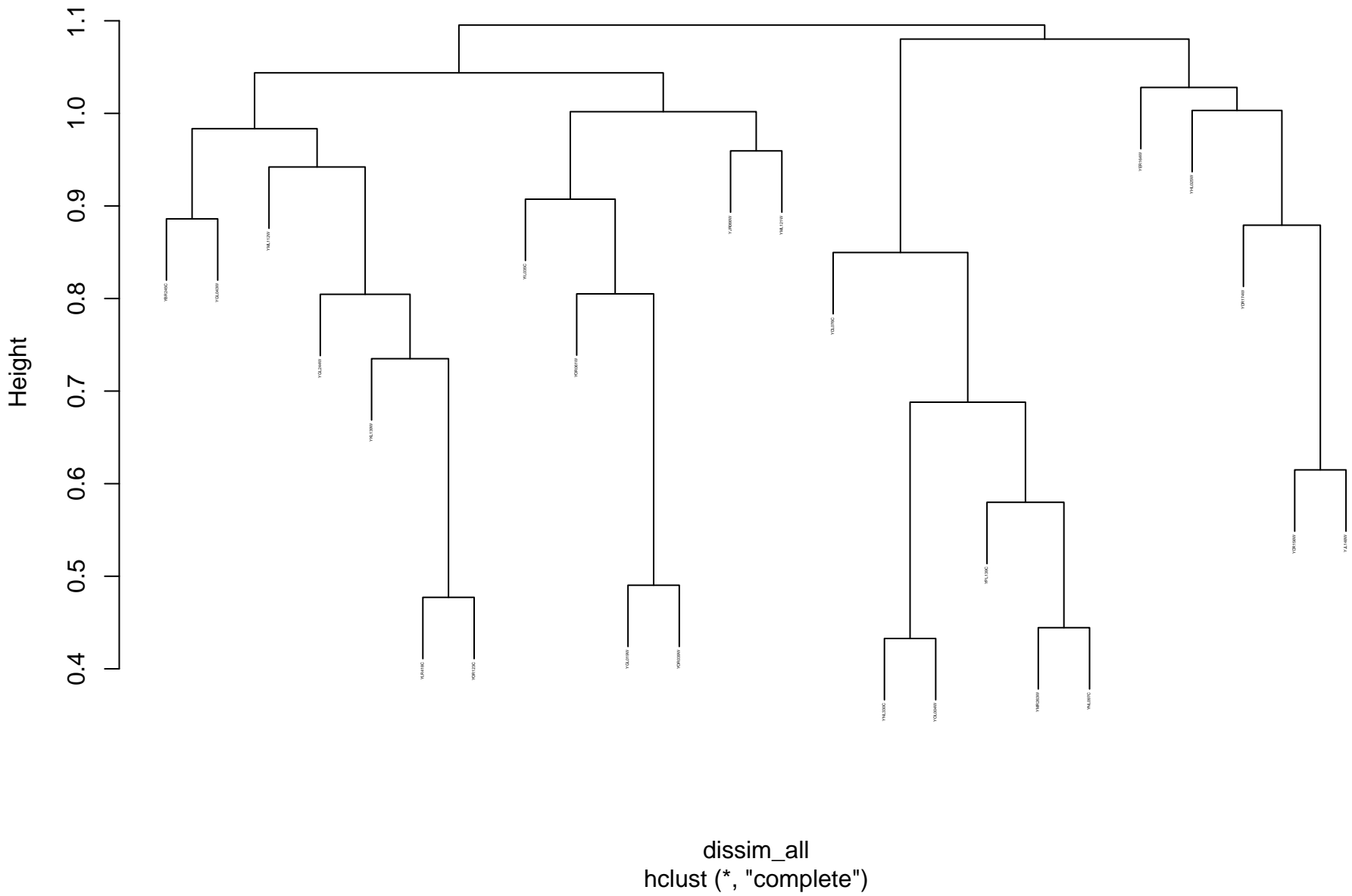
ubiquitin-like protein binding_GO_pearson_complete



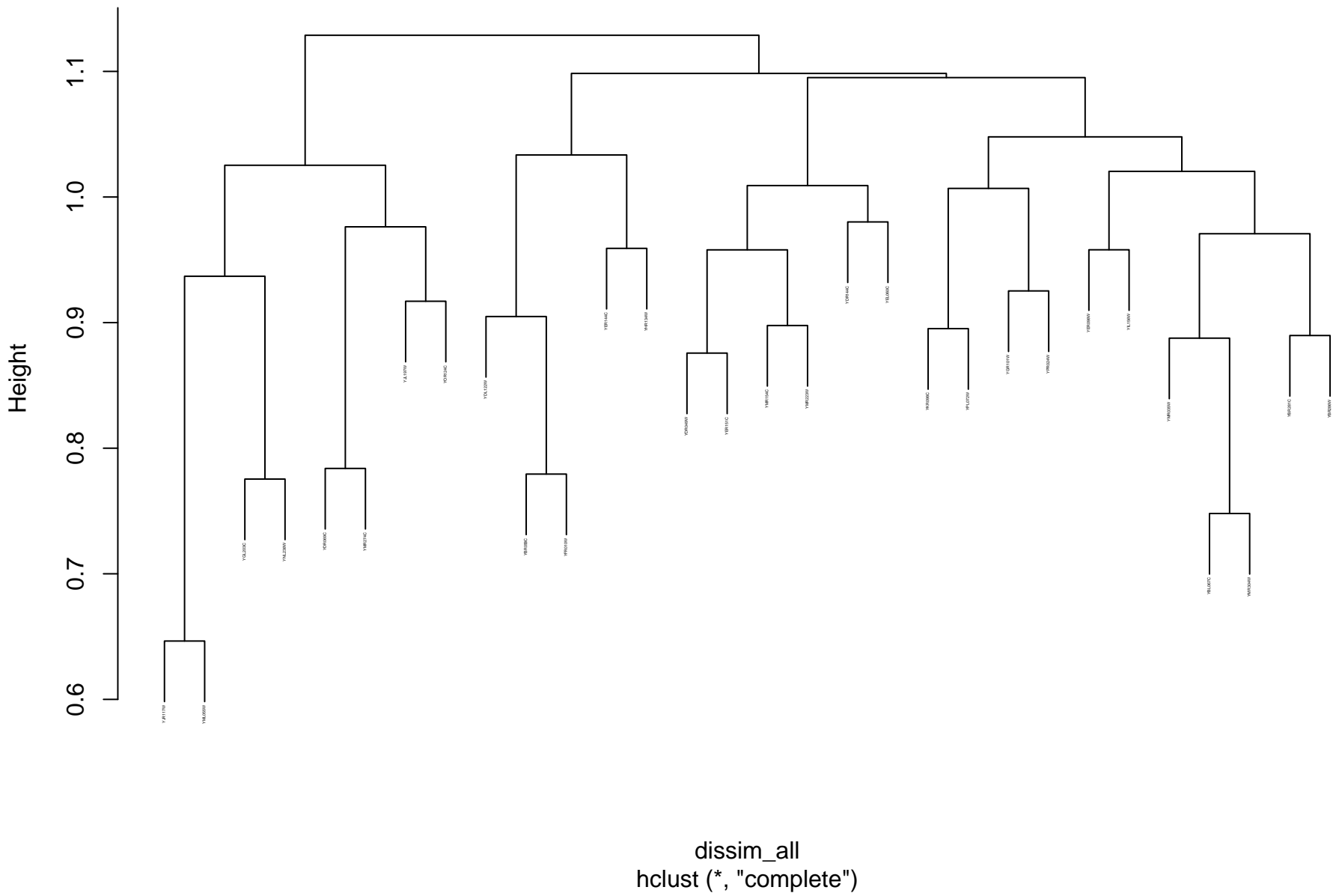
transcription factor binding_GO_pearson_complete



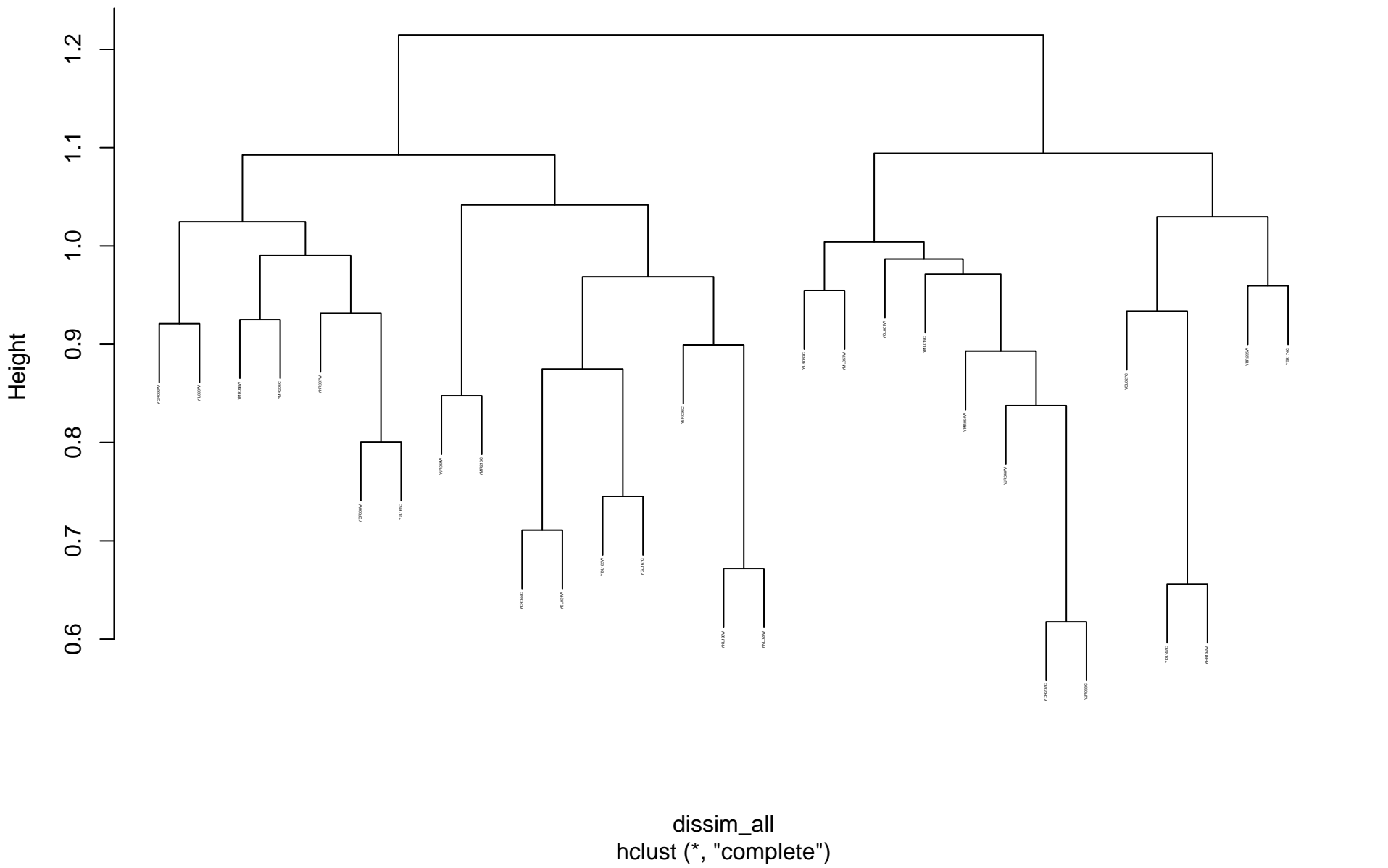
transcription from RNA polymerase I promoter_GO_pearson_complete



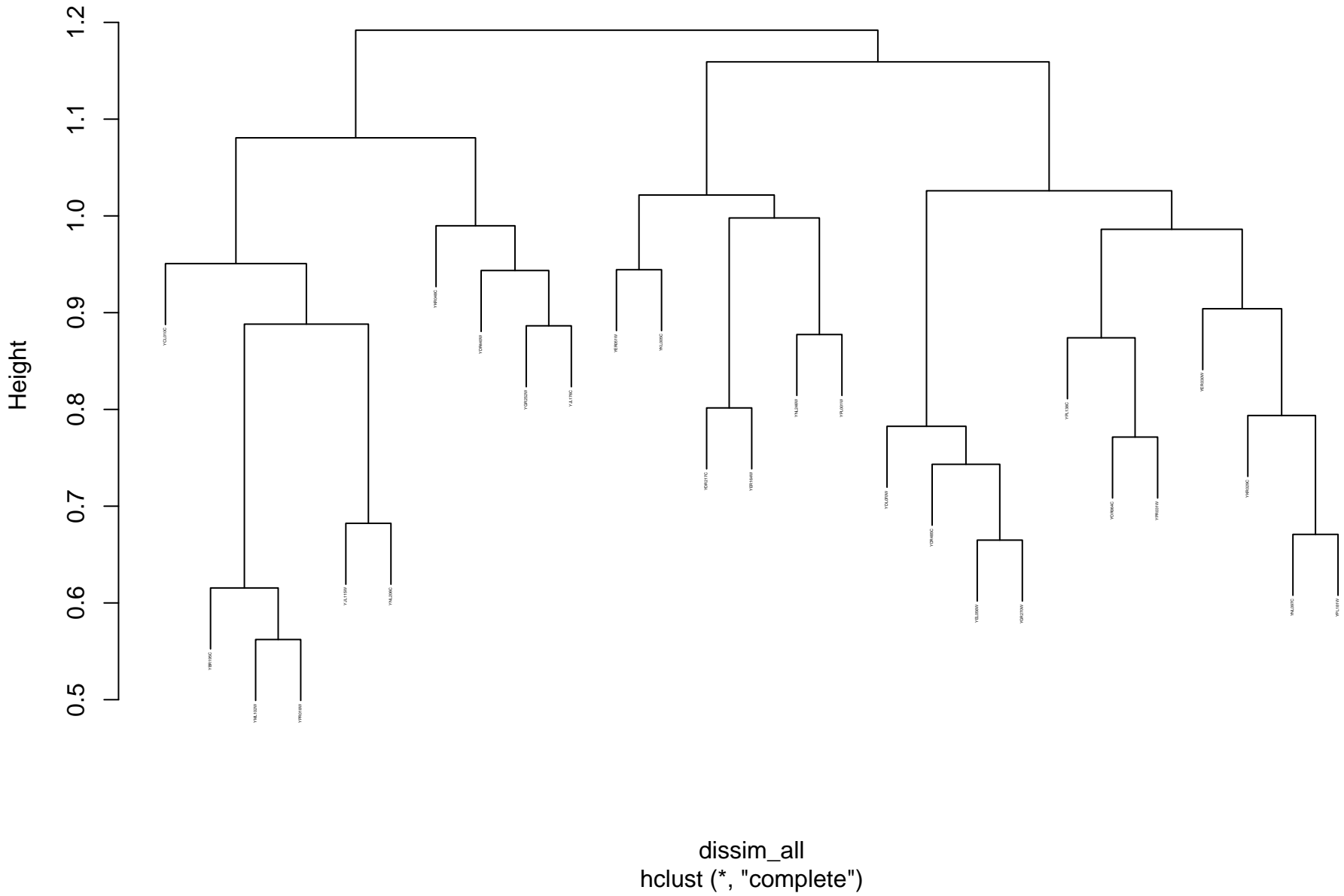
peptidase activity_GO_pearson_complete



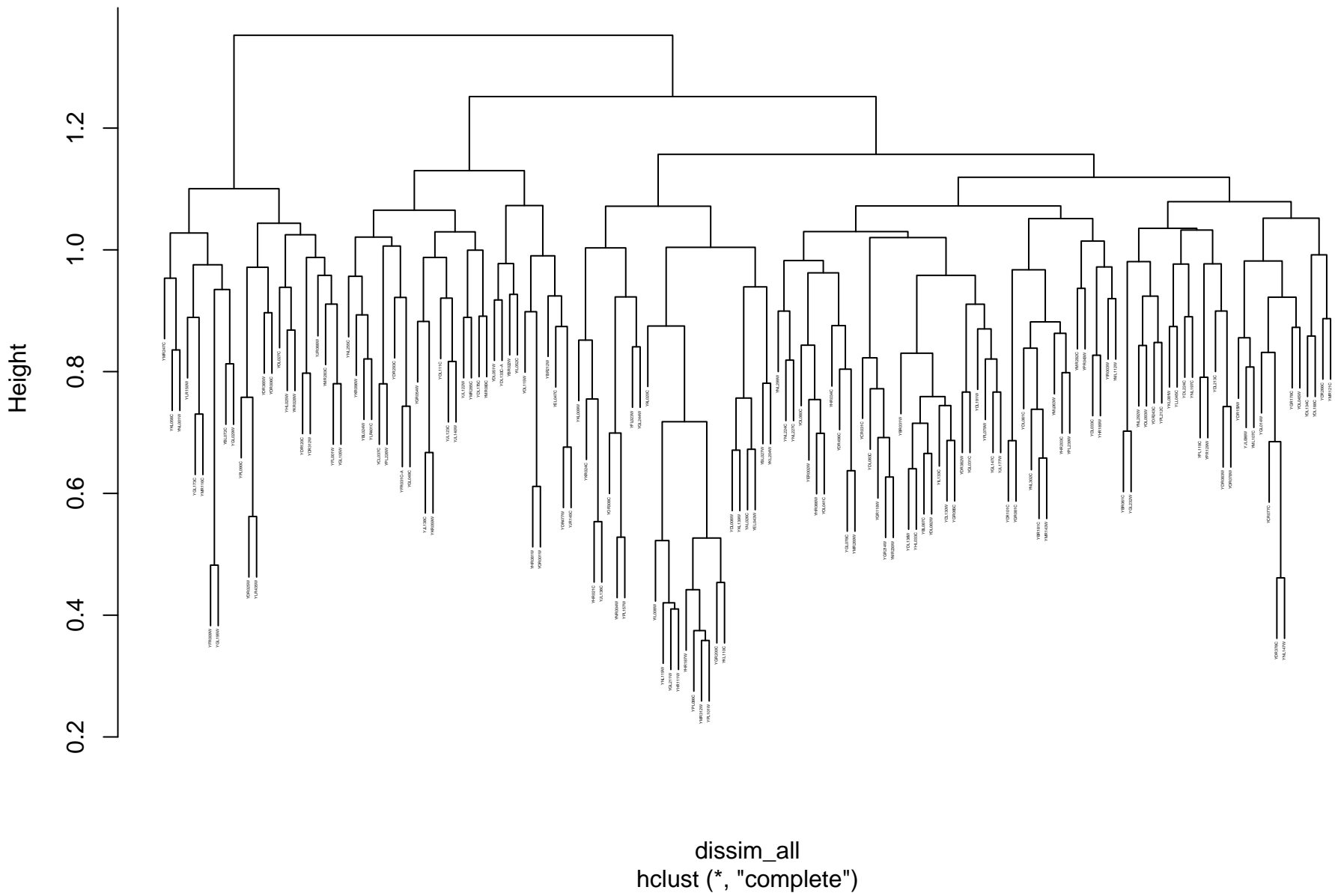
cellular ion homeostasis_GO_pearson_complete



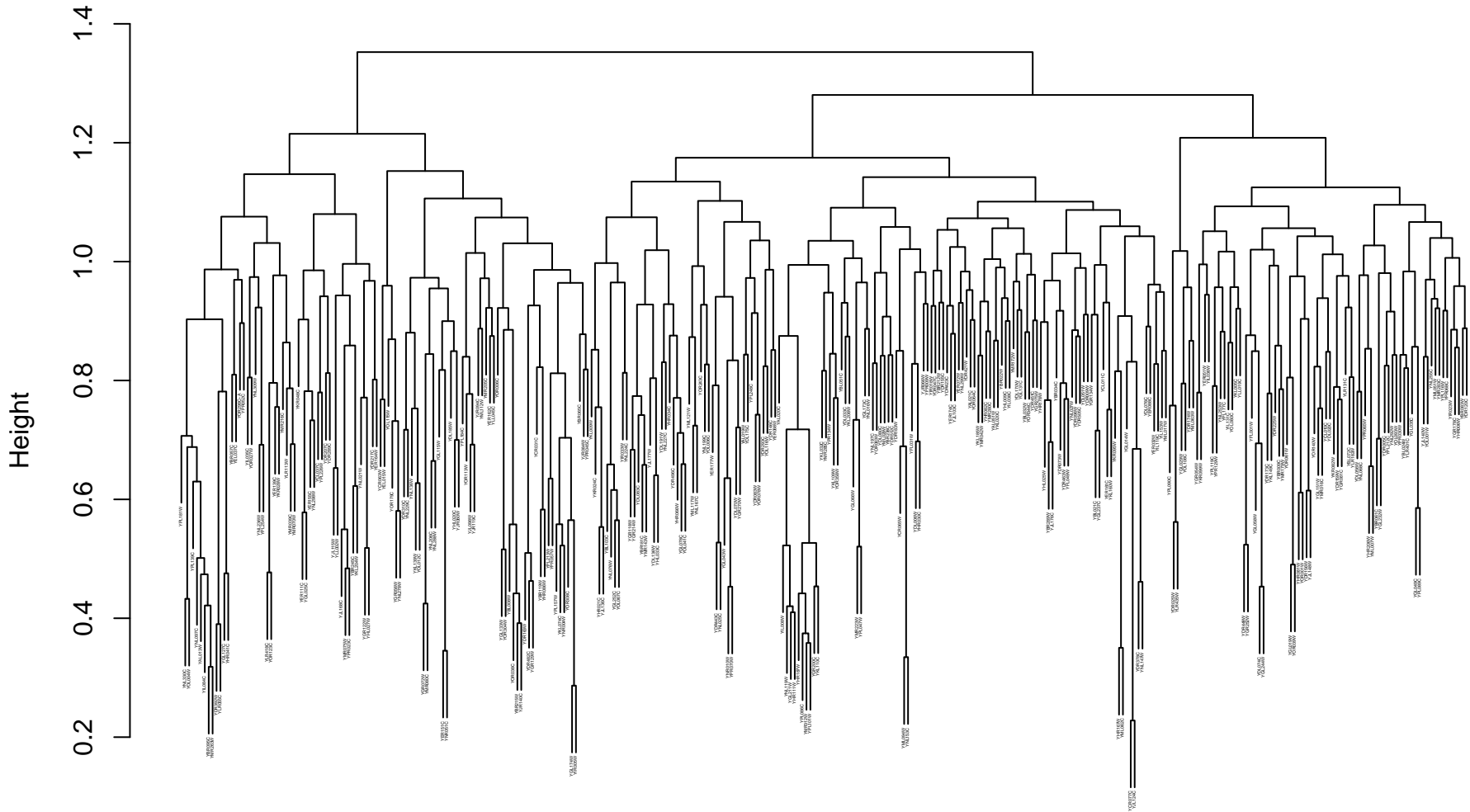
histone binding_GO_pearson_complete



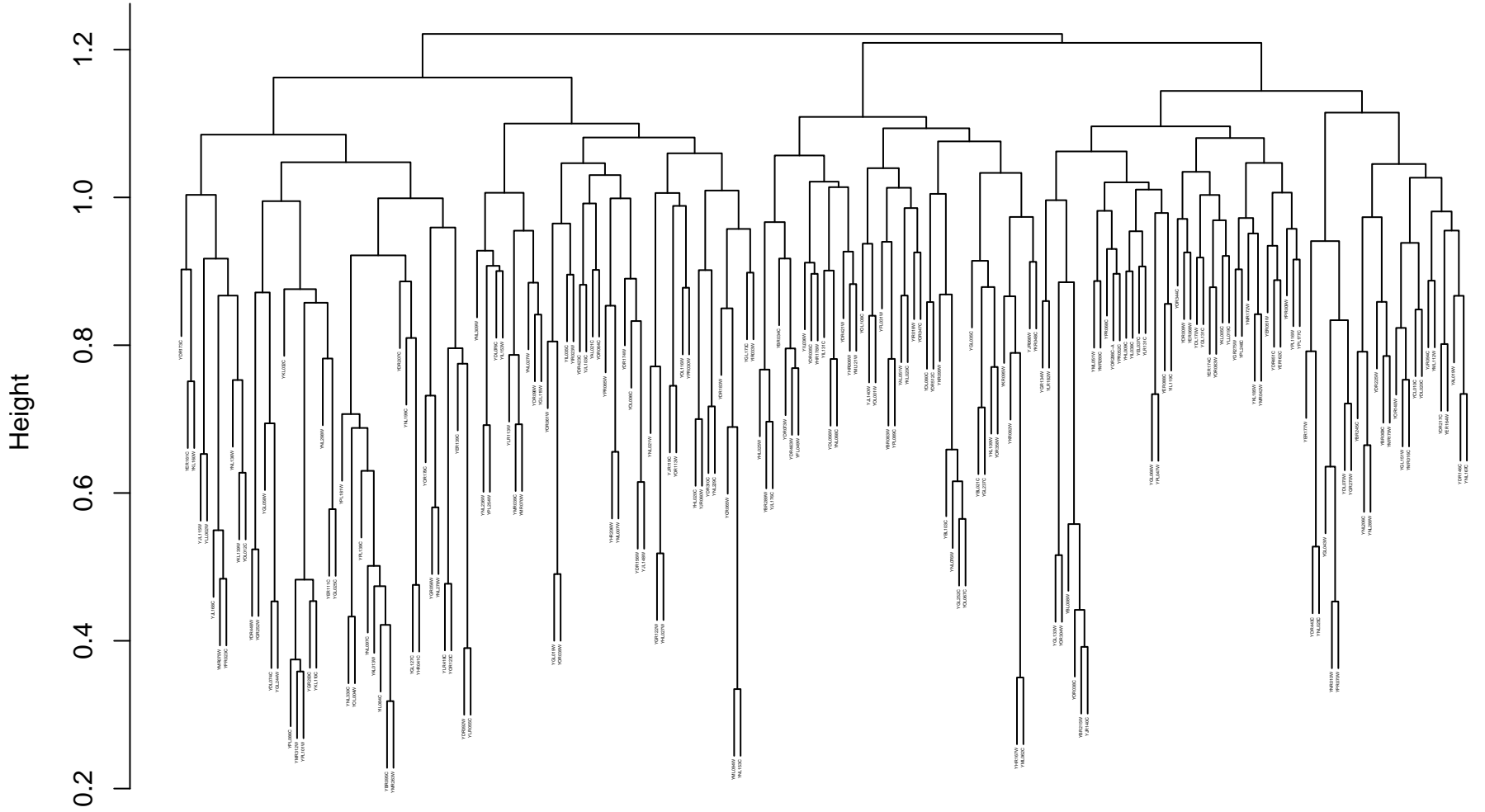
ribosomes and translation_GO_pearson_complete



transcription and mRNA processing_GO_pearson_complete

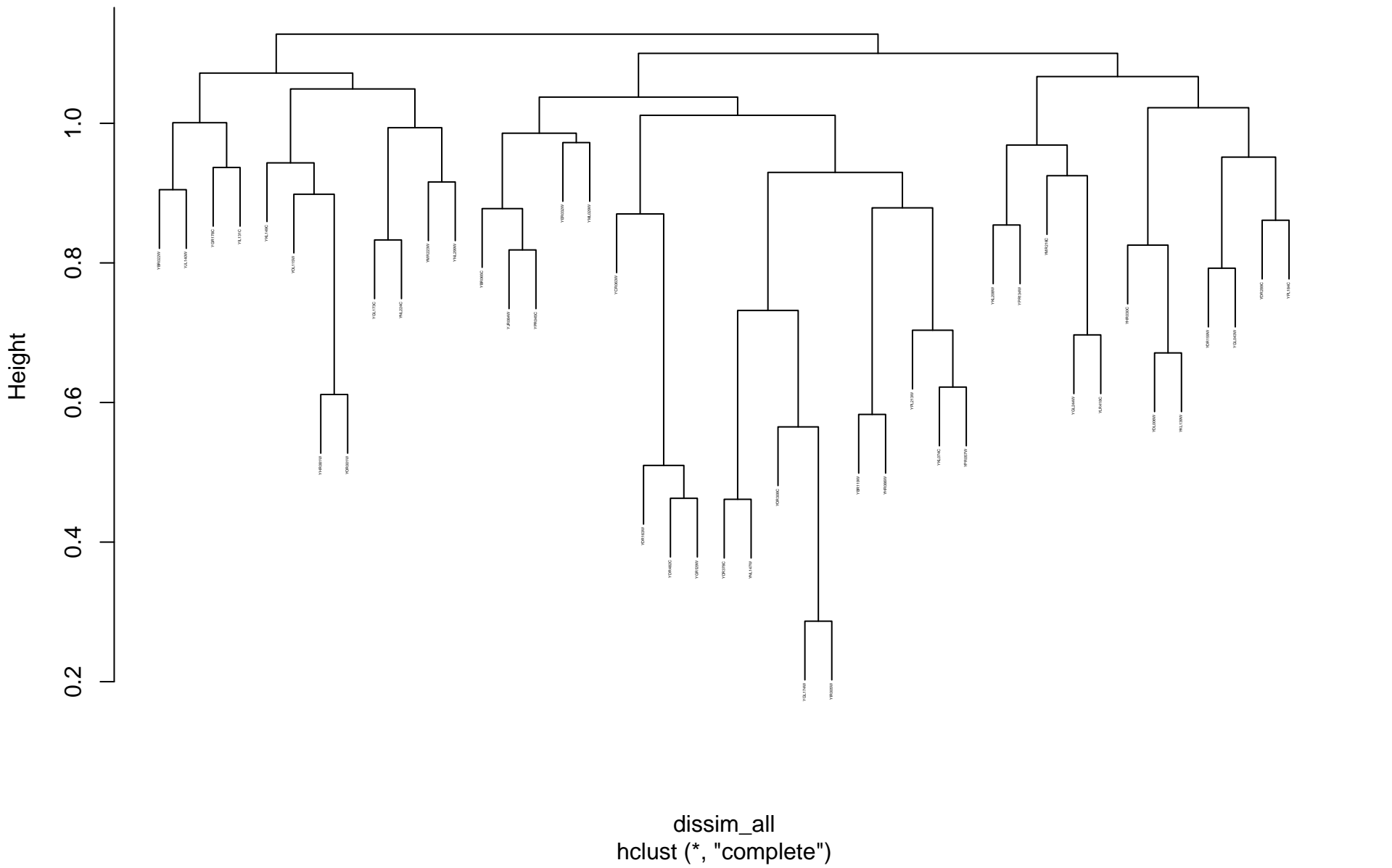


transcription_GO_pearson_complete

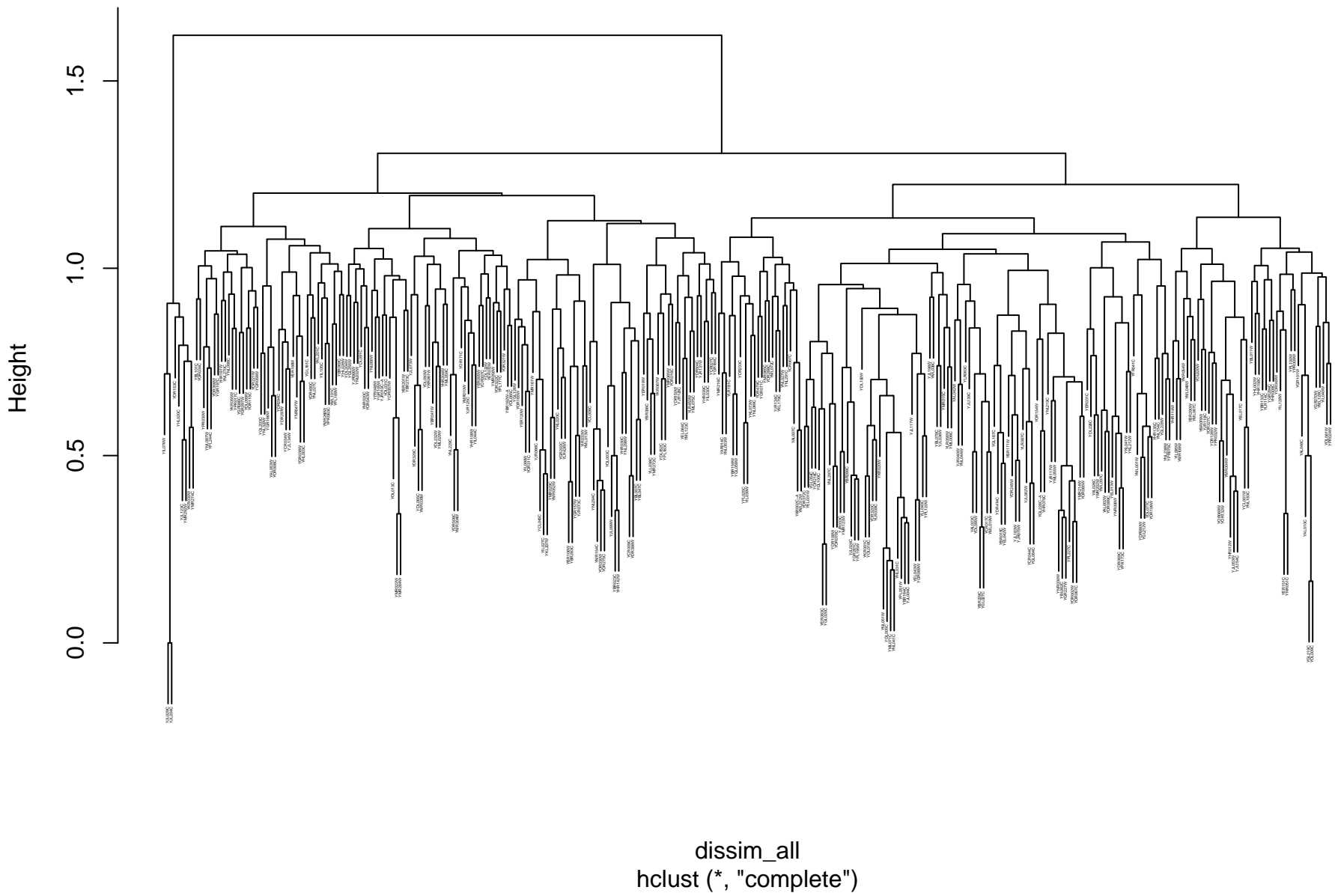


```
dissim_all
hclust (*, "complete")
```

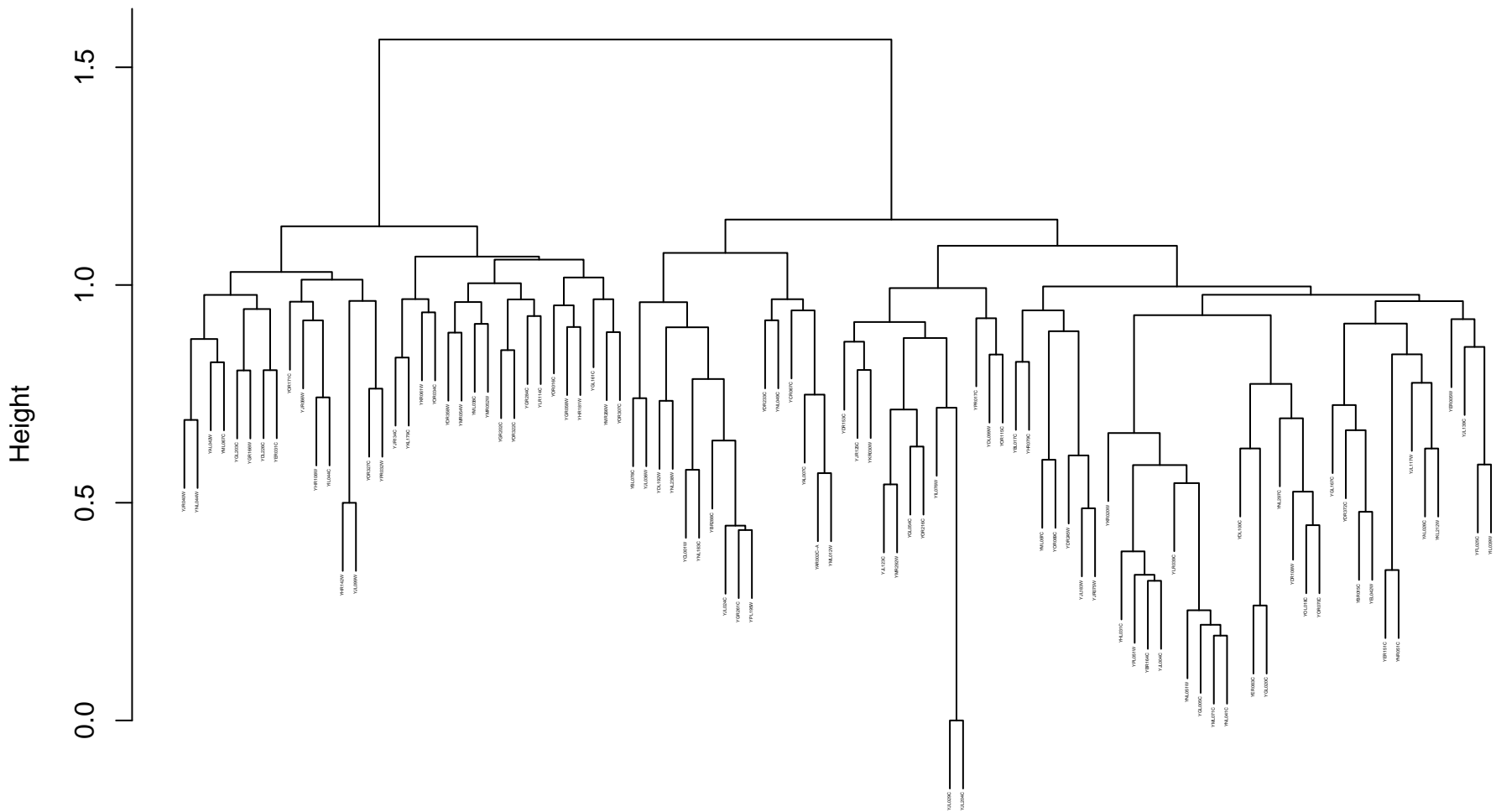
RNA processing_GO_pearson_complete



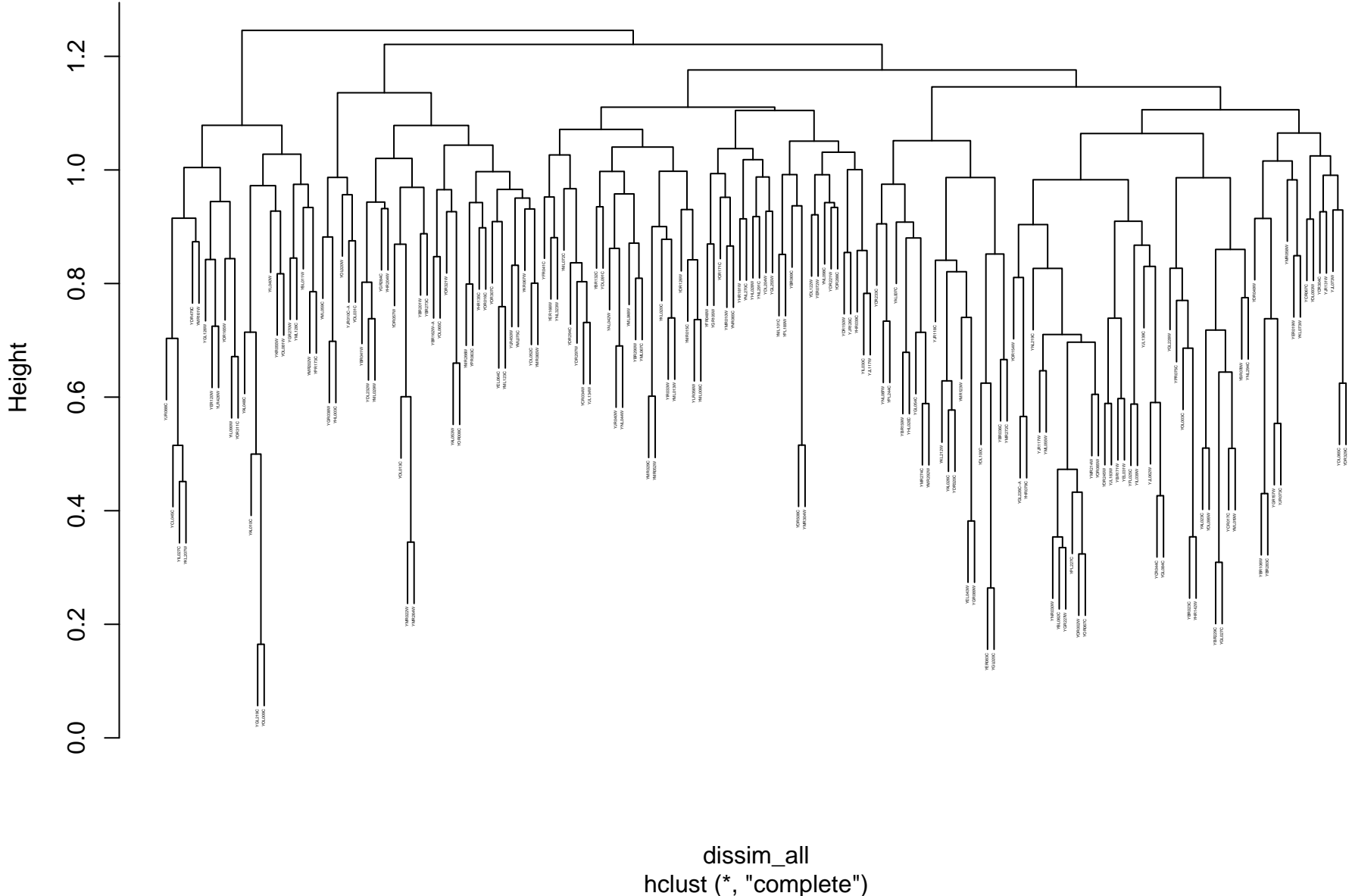
Golgi and ER_GO_pearson_complete



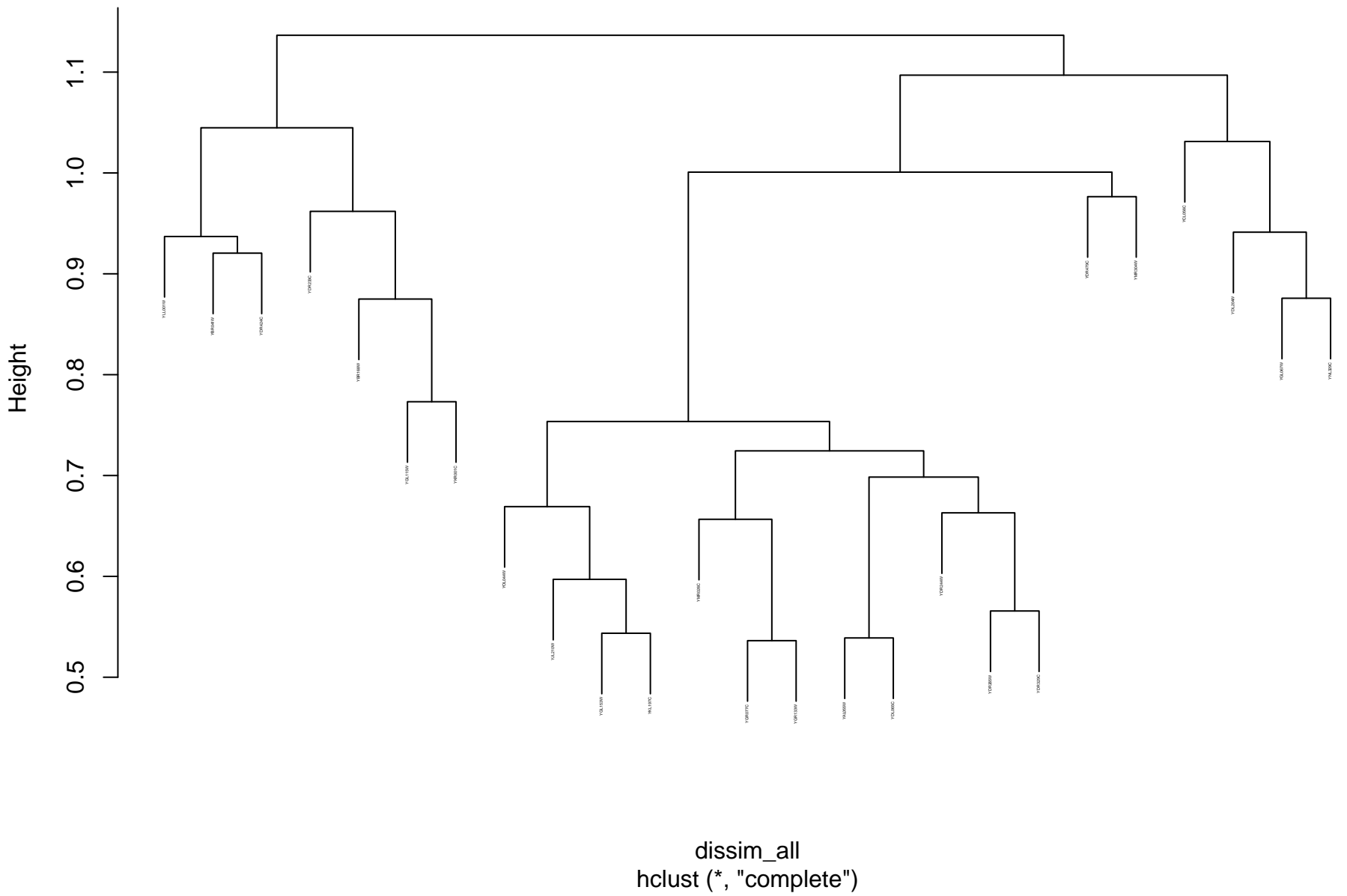
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dissim_all
hclust (*, "complete")
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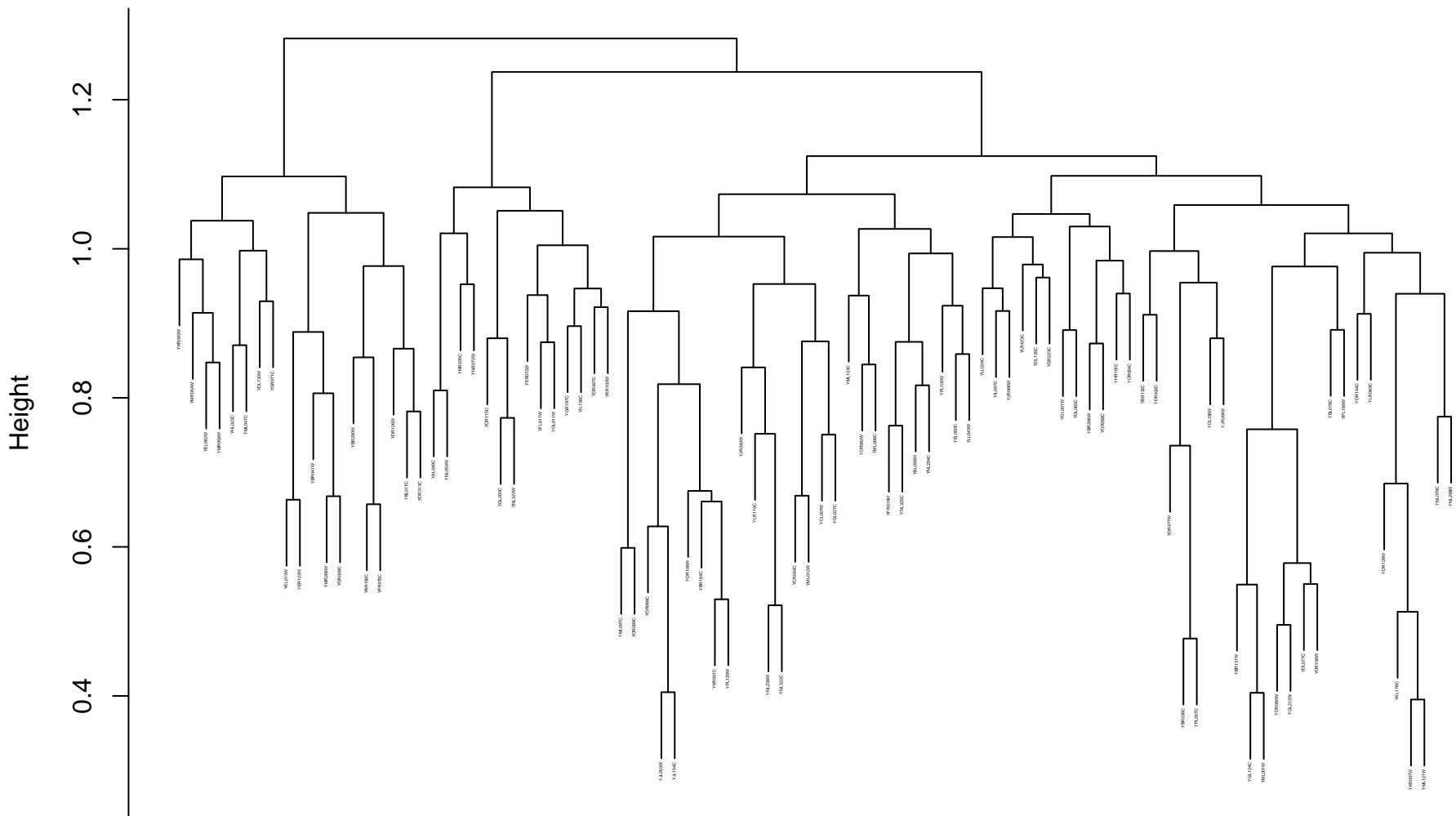
ER_GO_pearson_complete



peroxisomes_GO_pearson_complete

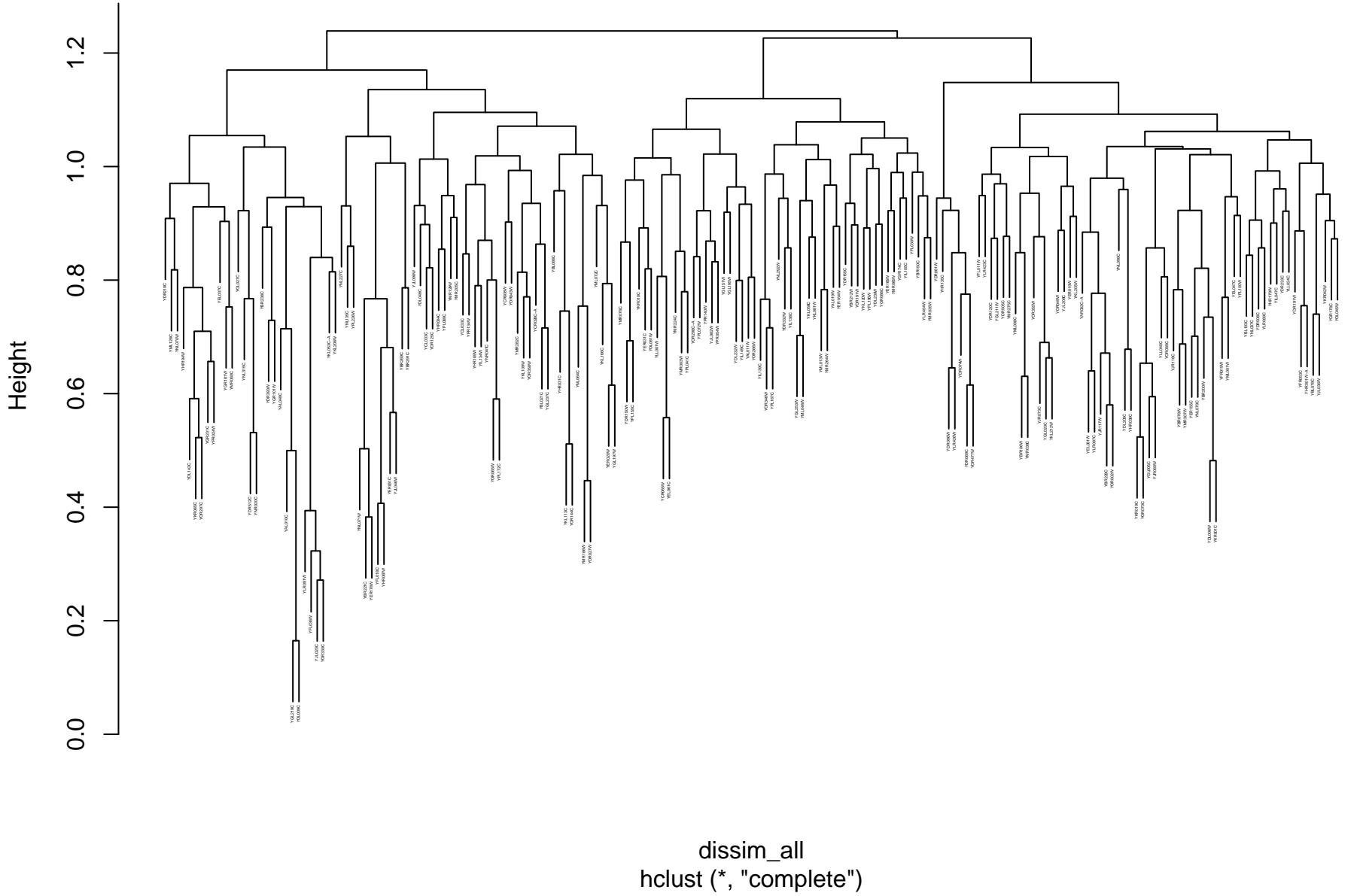


vacuoles_GO_pearson_complete

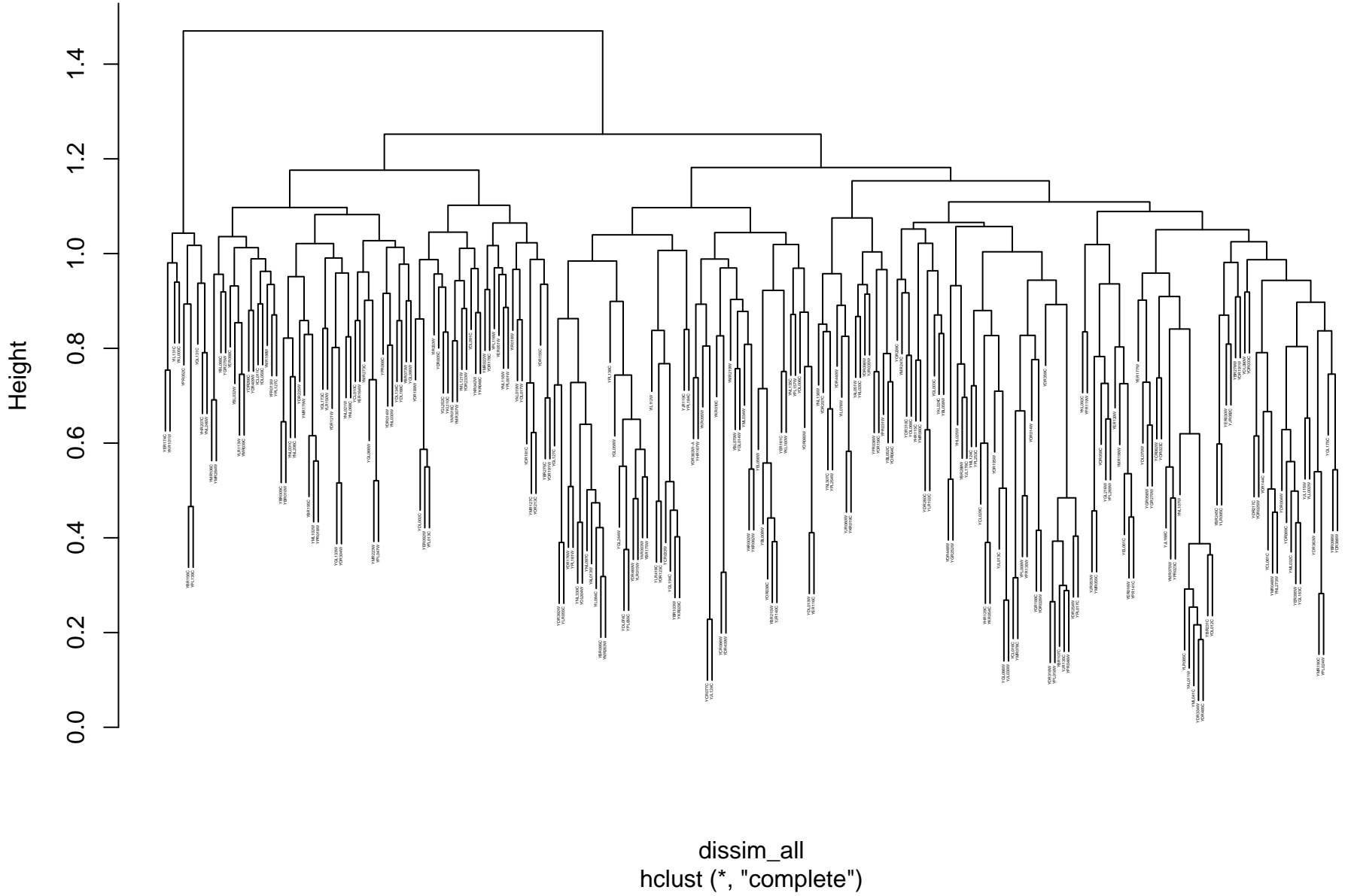


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dissim_all
hclust (*, "complete")
```

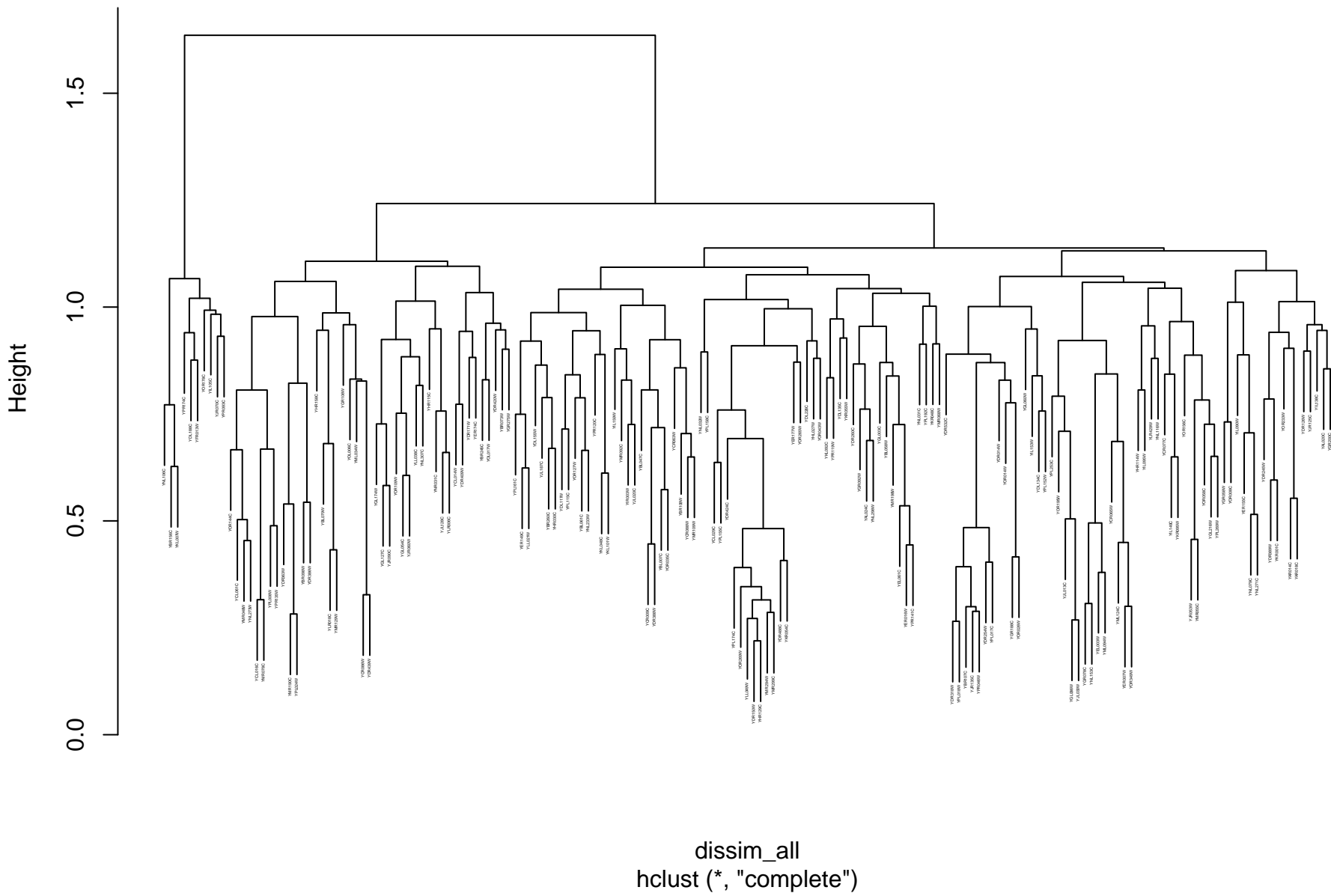
mitochondria_GO_pearson_complete



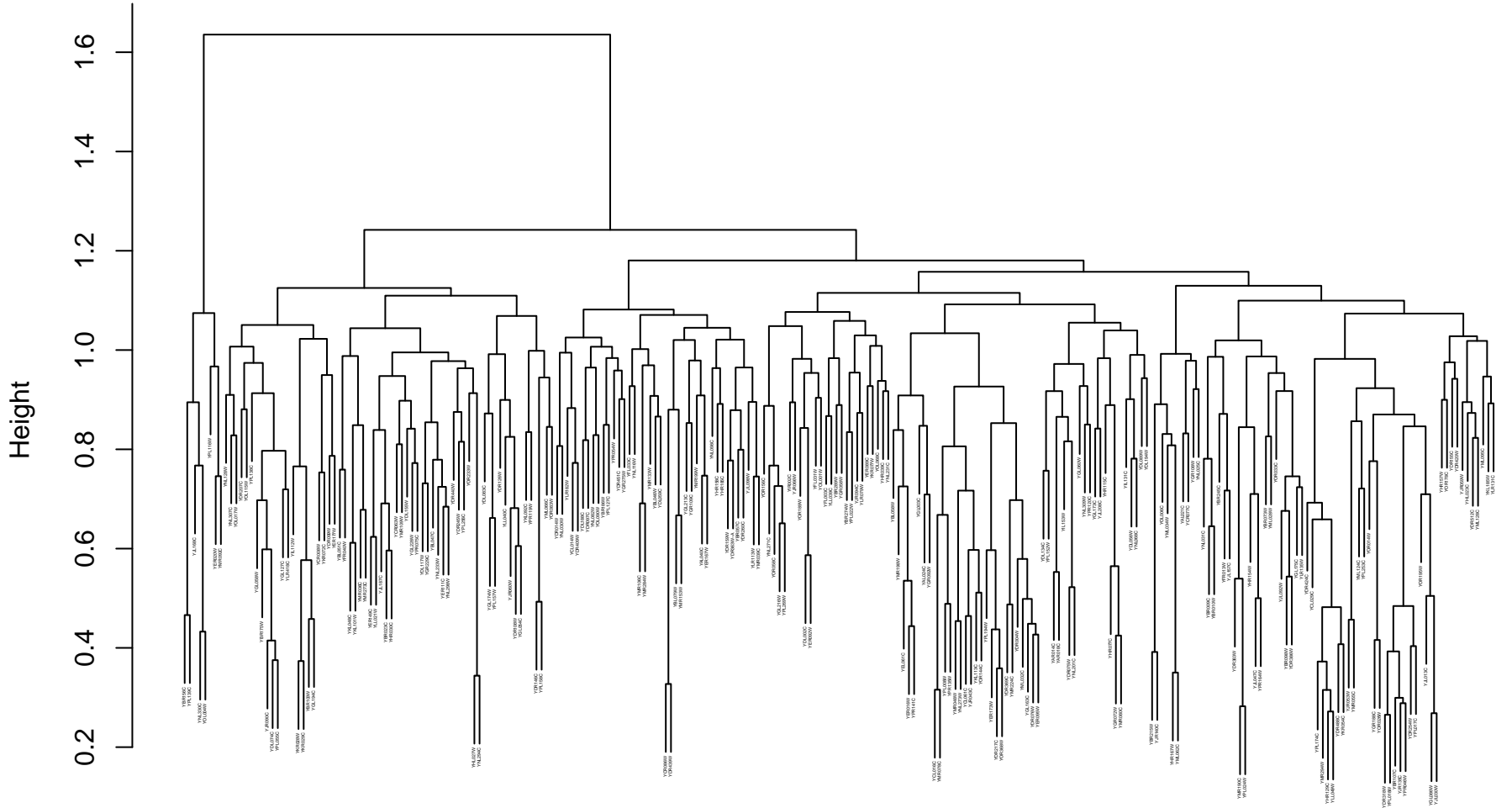
chromatin_GO_pearson_complete



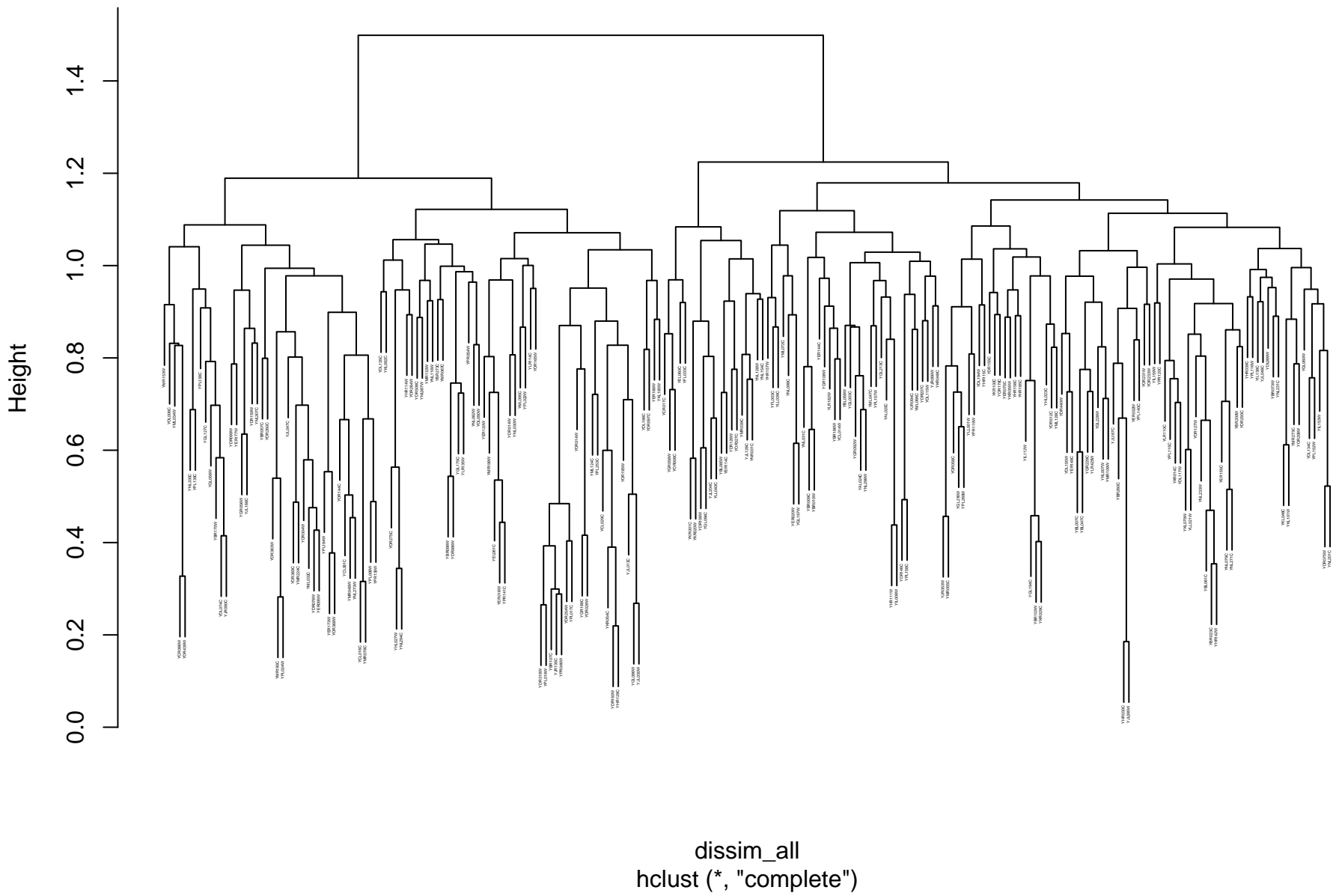
cytoskeleton and microtubules_GO_pearson_complete



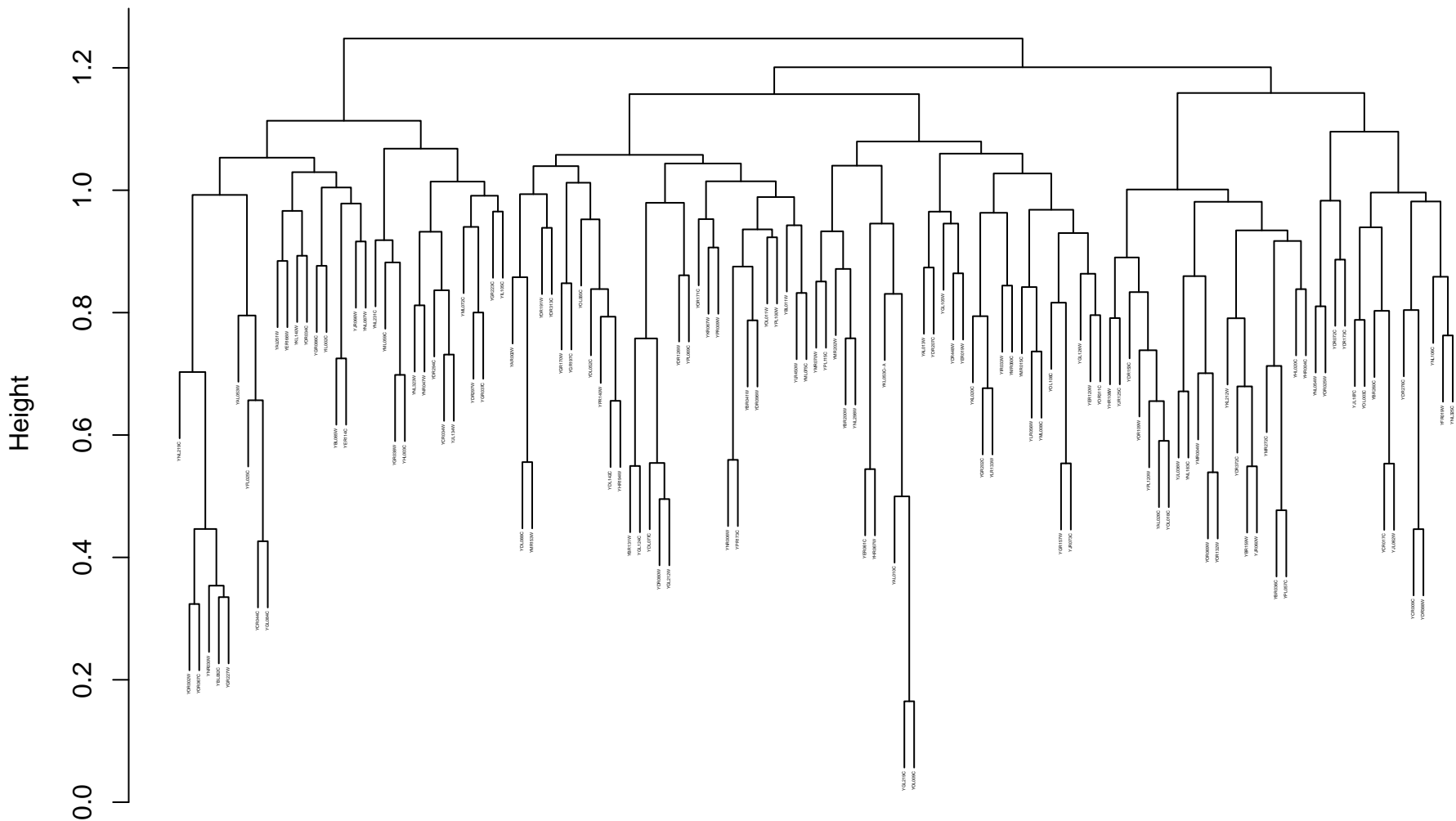
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dissim_all
hclust (*, "complete")
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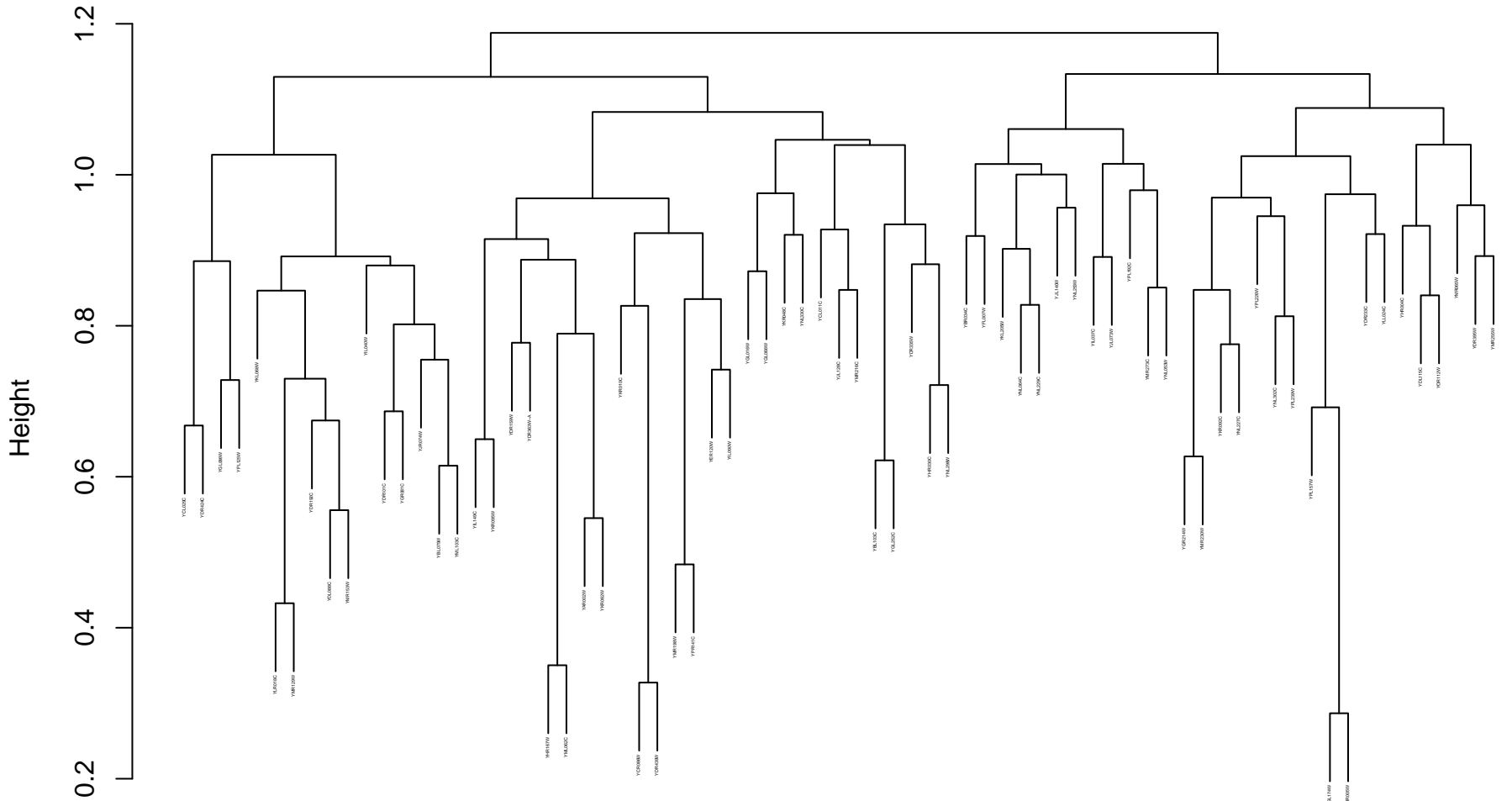
budding_GO_pearson_complete



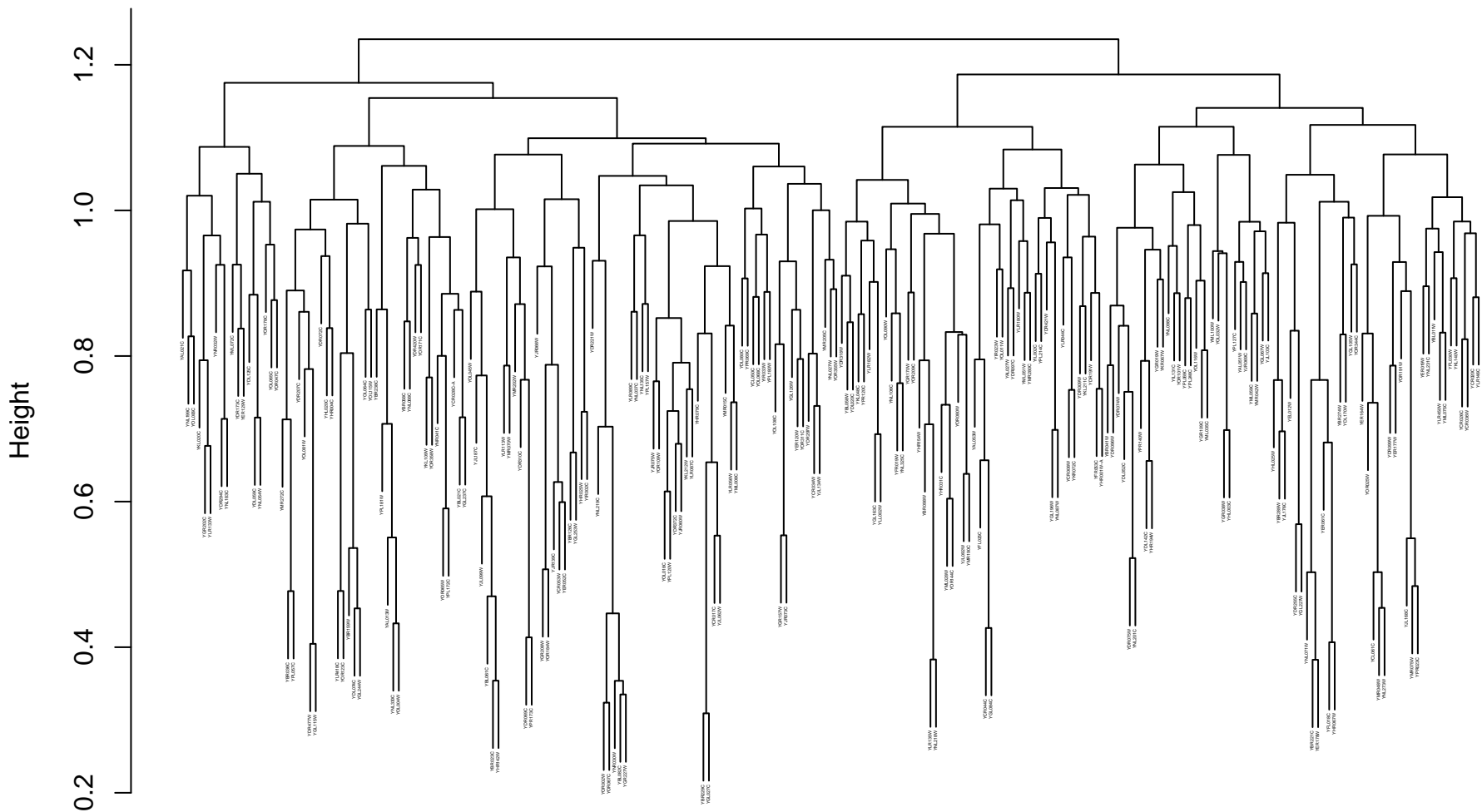
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dissim_all
hclust (*, "complete")
```



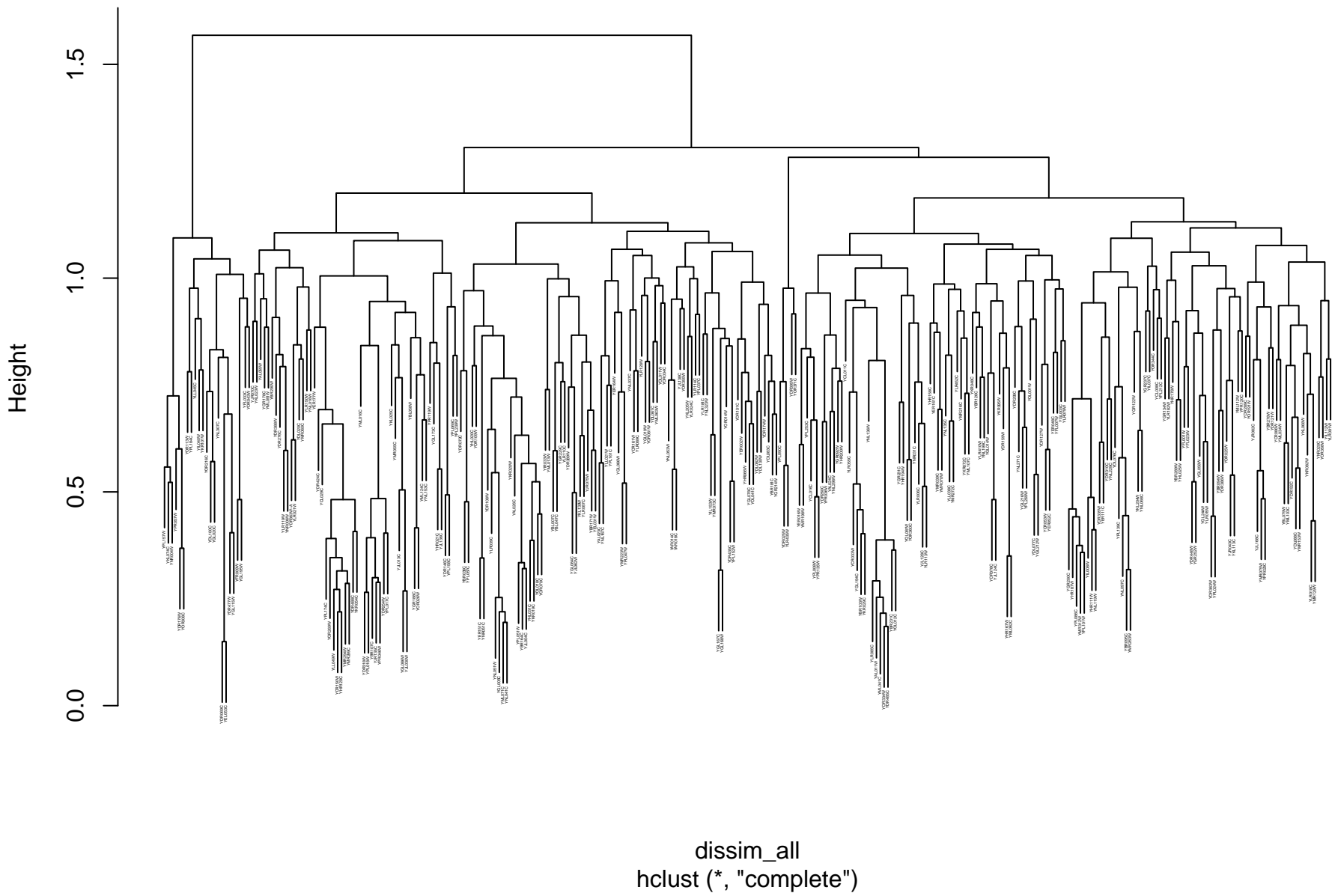

```
dissim_all
hclust (*, "complete")
```



```
dissim_all
hclust (*, "complete")
```



sig_Gsp1_Gl_pearson_complete



whole_library_pearson_complete

