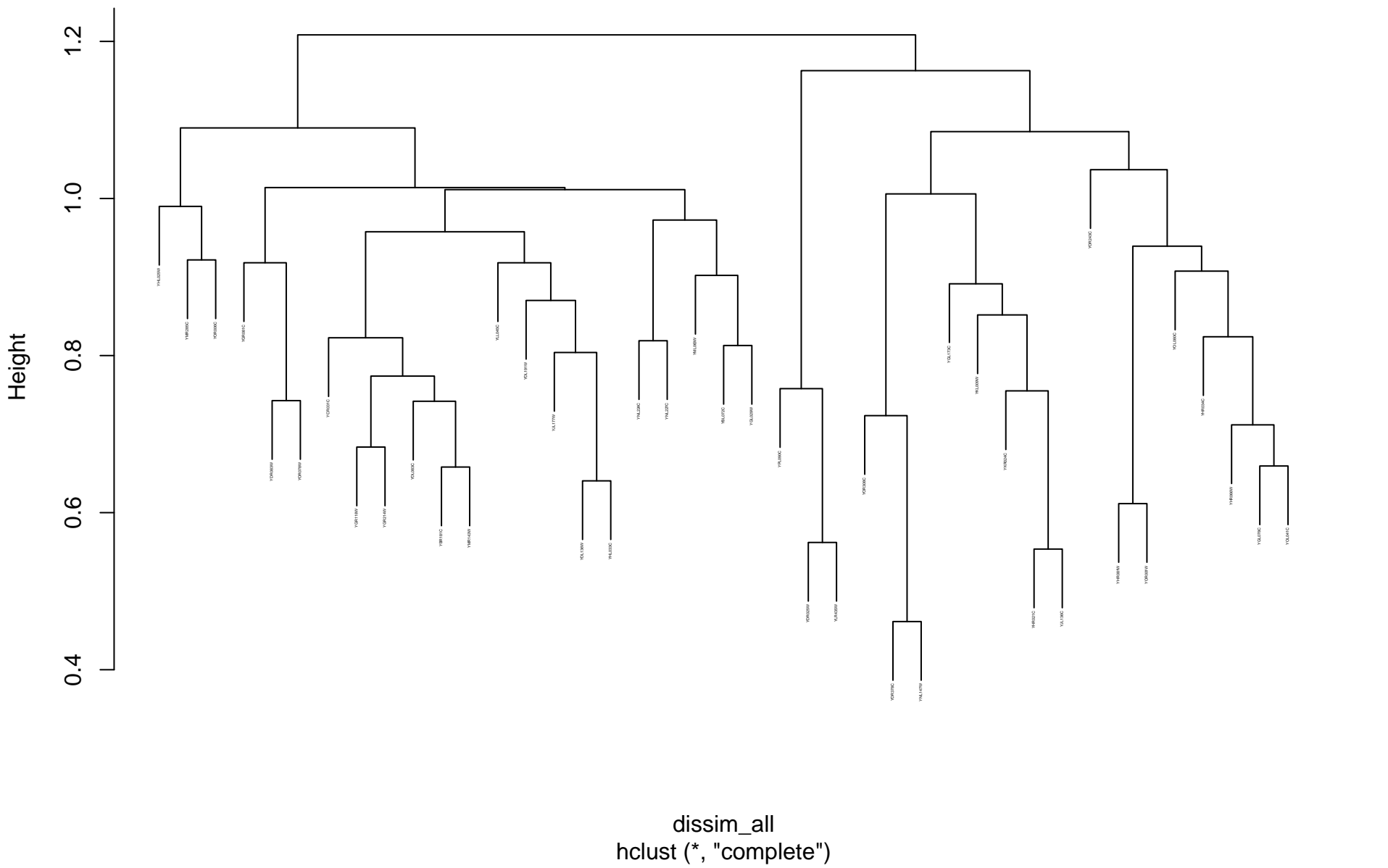
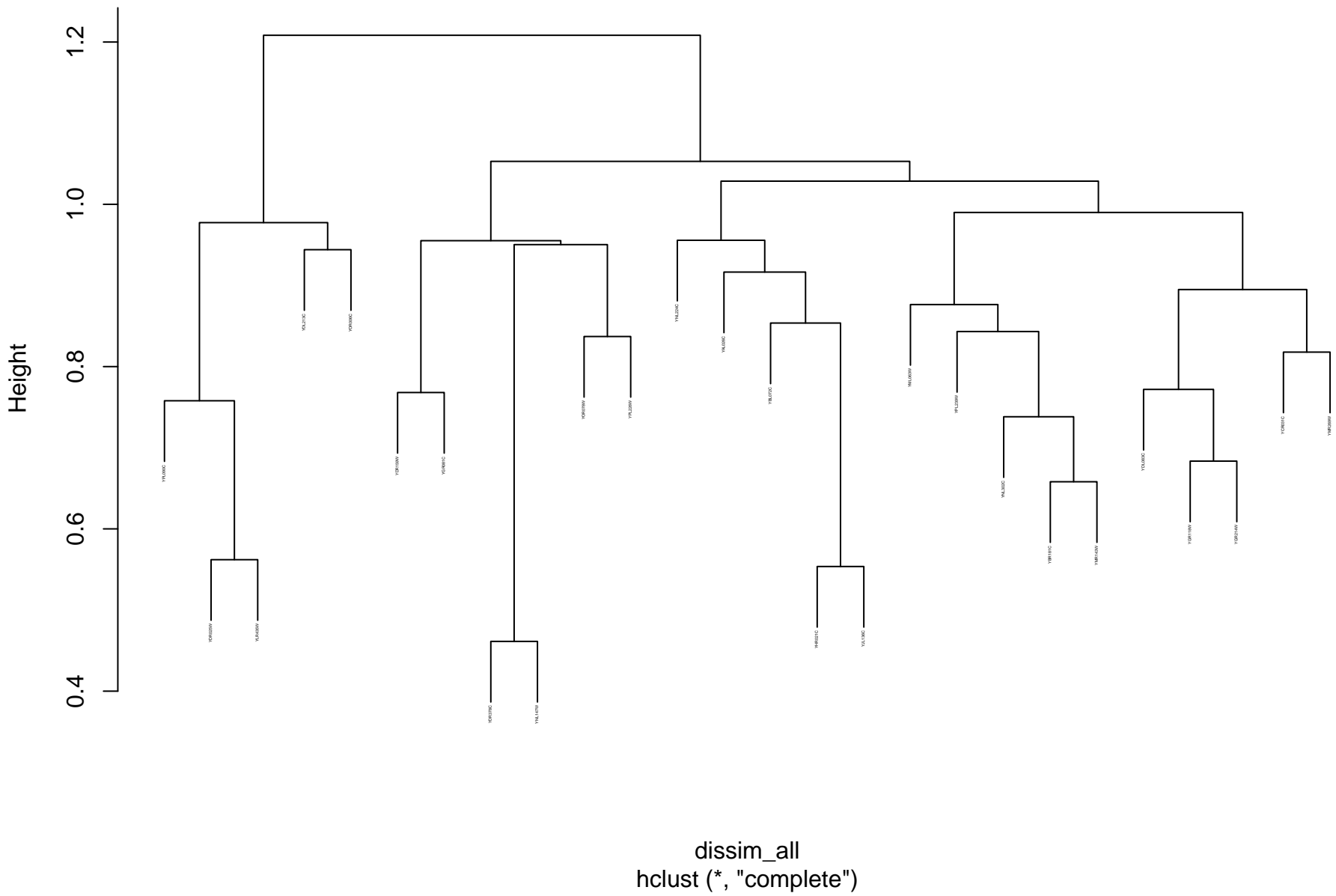


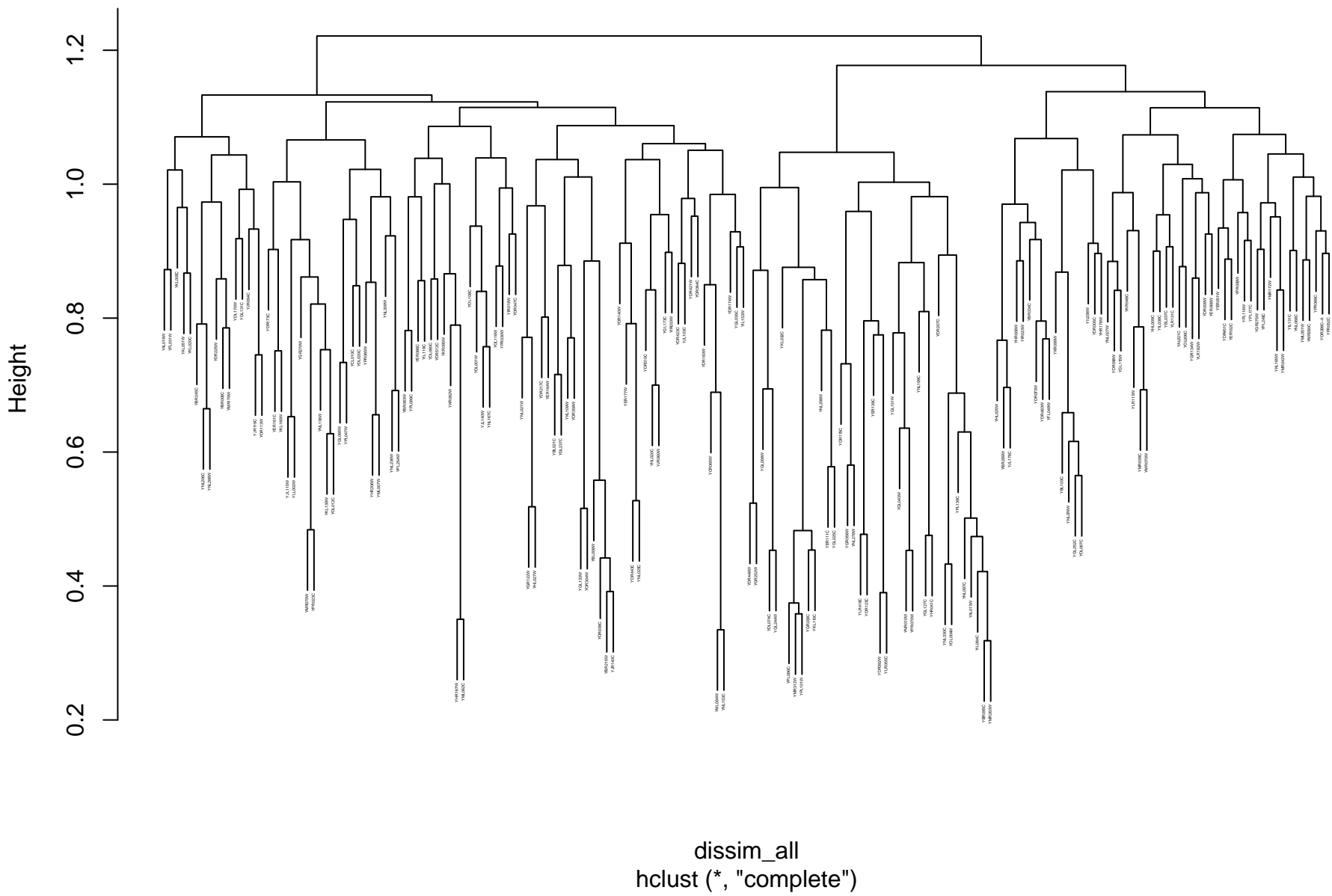
rRNA processing_GO_pearson_complete



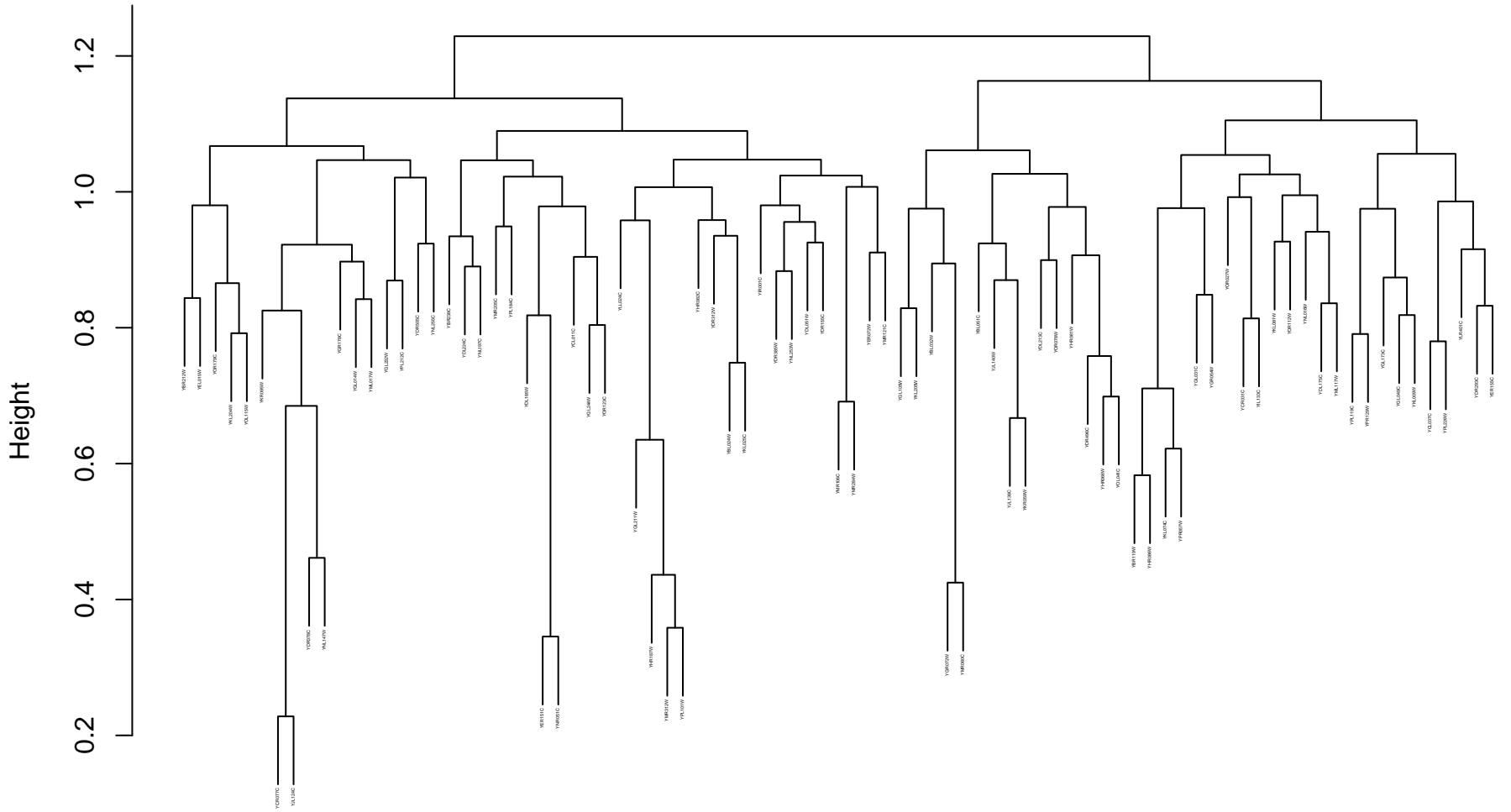
ribosomal small subunit biogenesis_GO_pearson_complete



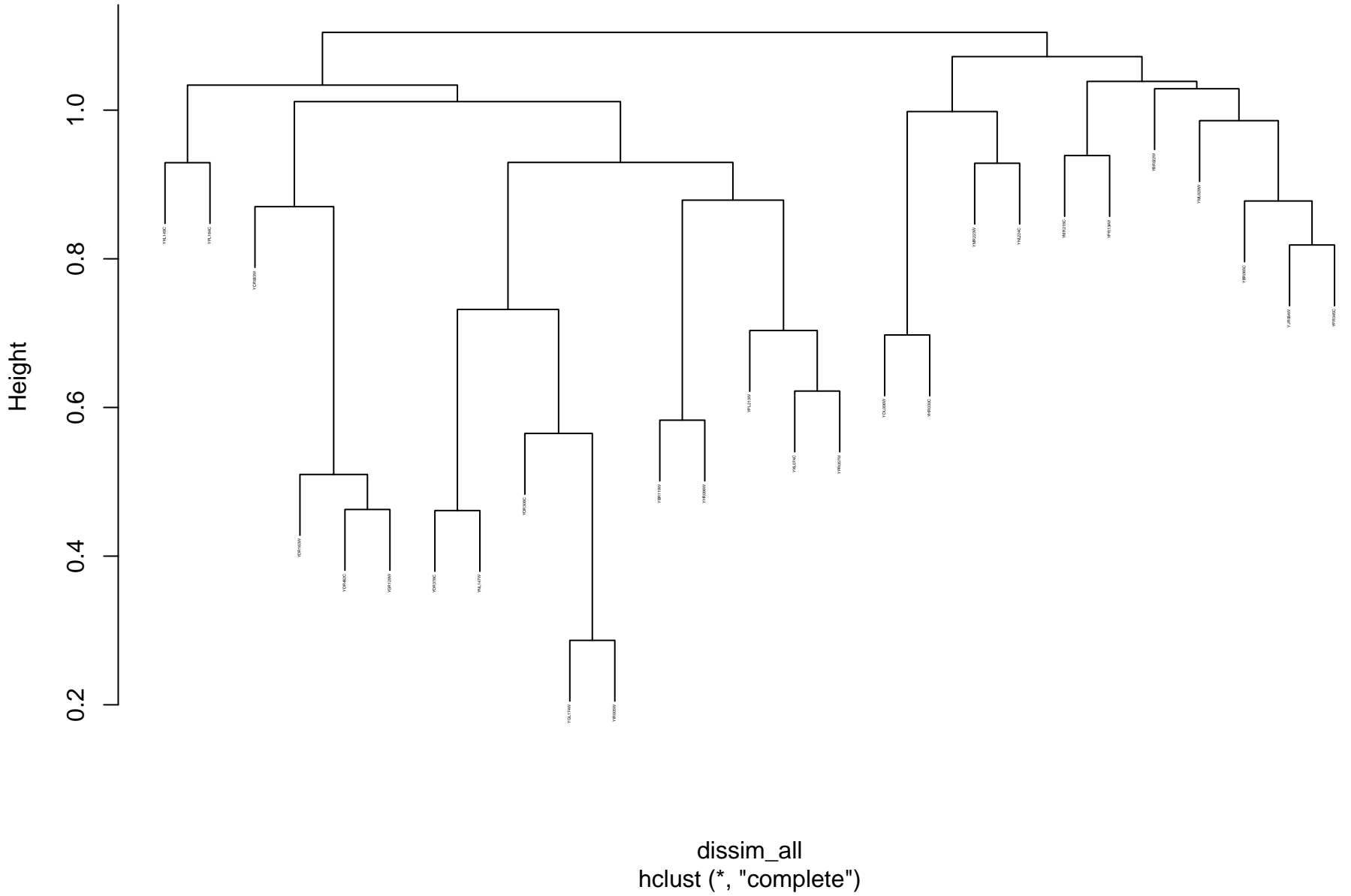
transcription from RNA polymerase II promoter_GO_pearson_complete



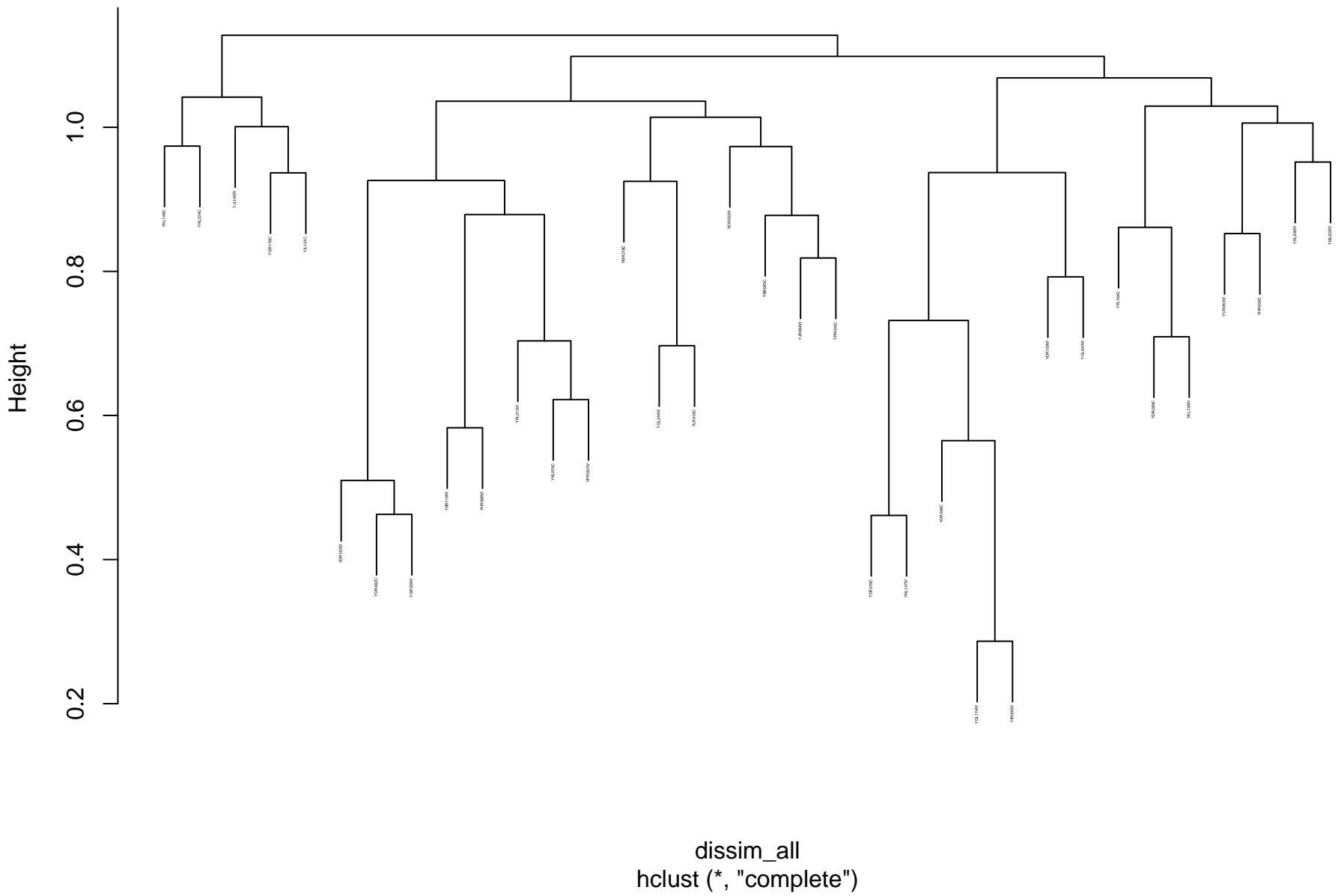
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dissim_all
hclust (*, "complete")
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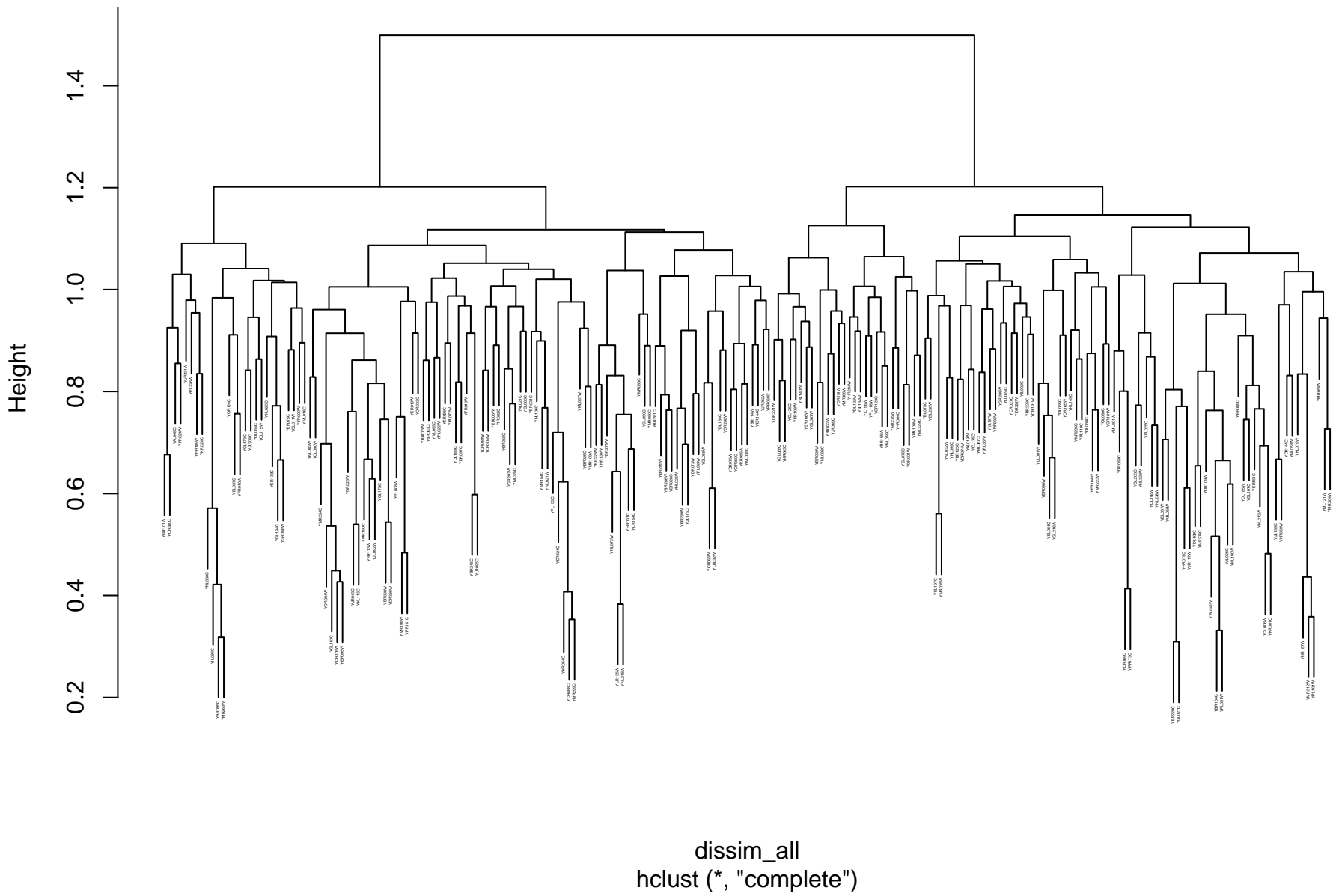
RNA splicing_GO_pearson_complete



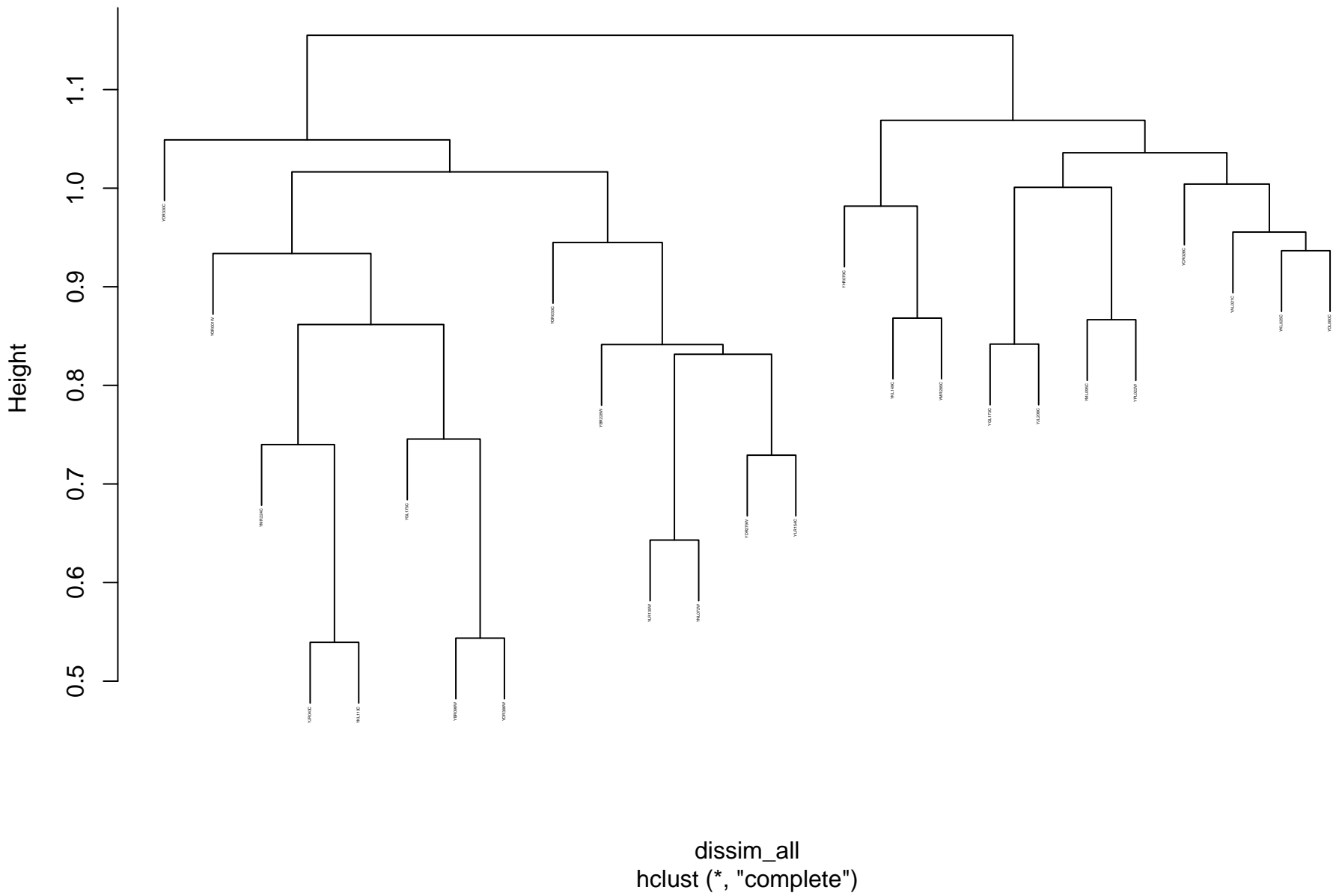
mRNA processing_GO_pearson_complete



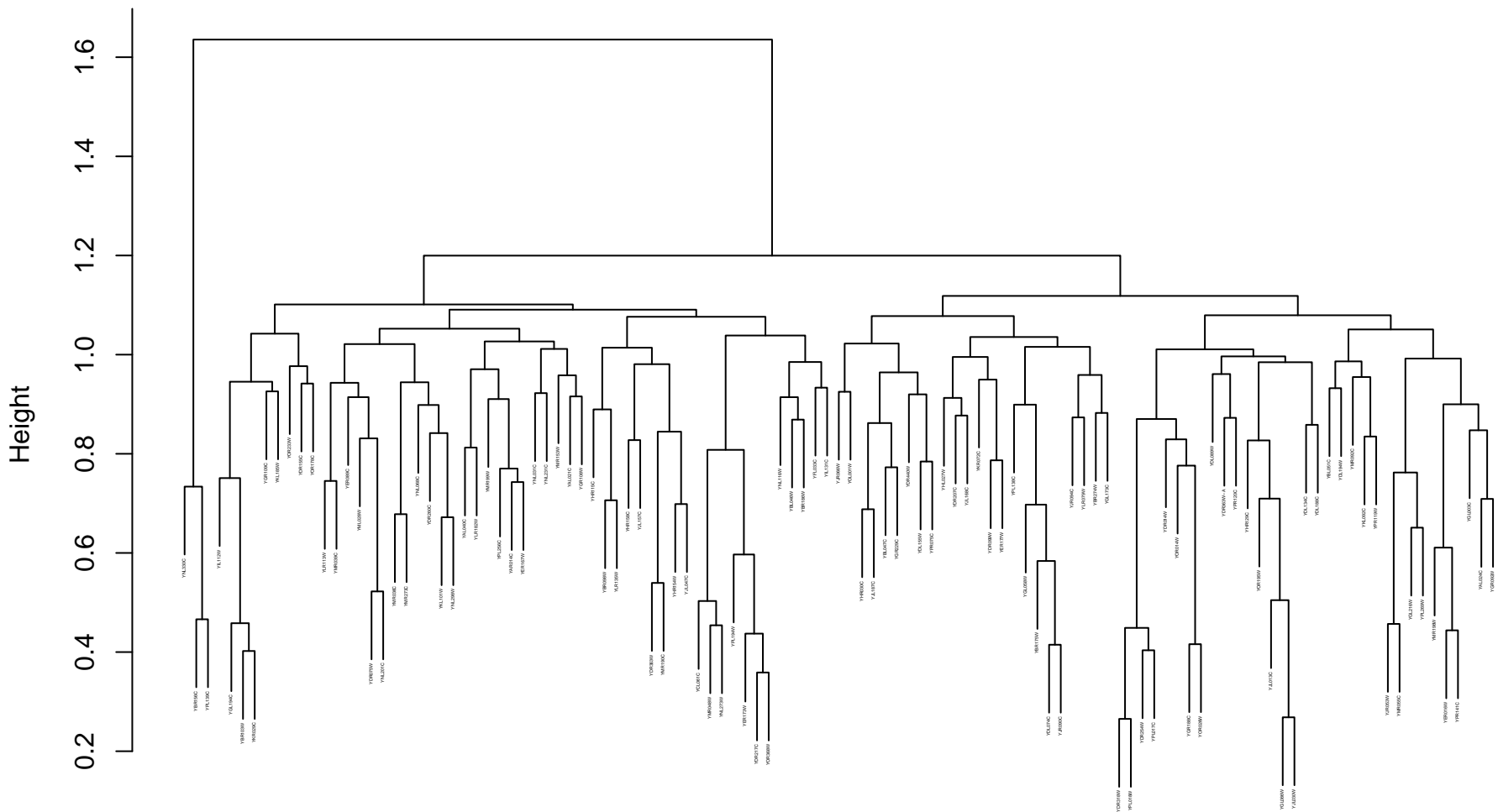
hydrolase activity_GO_pearson_complete



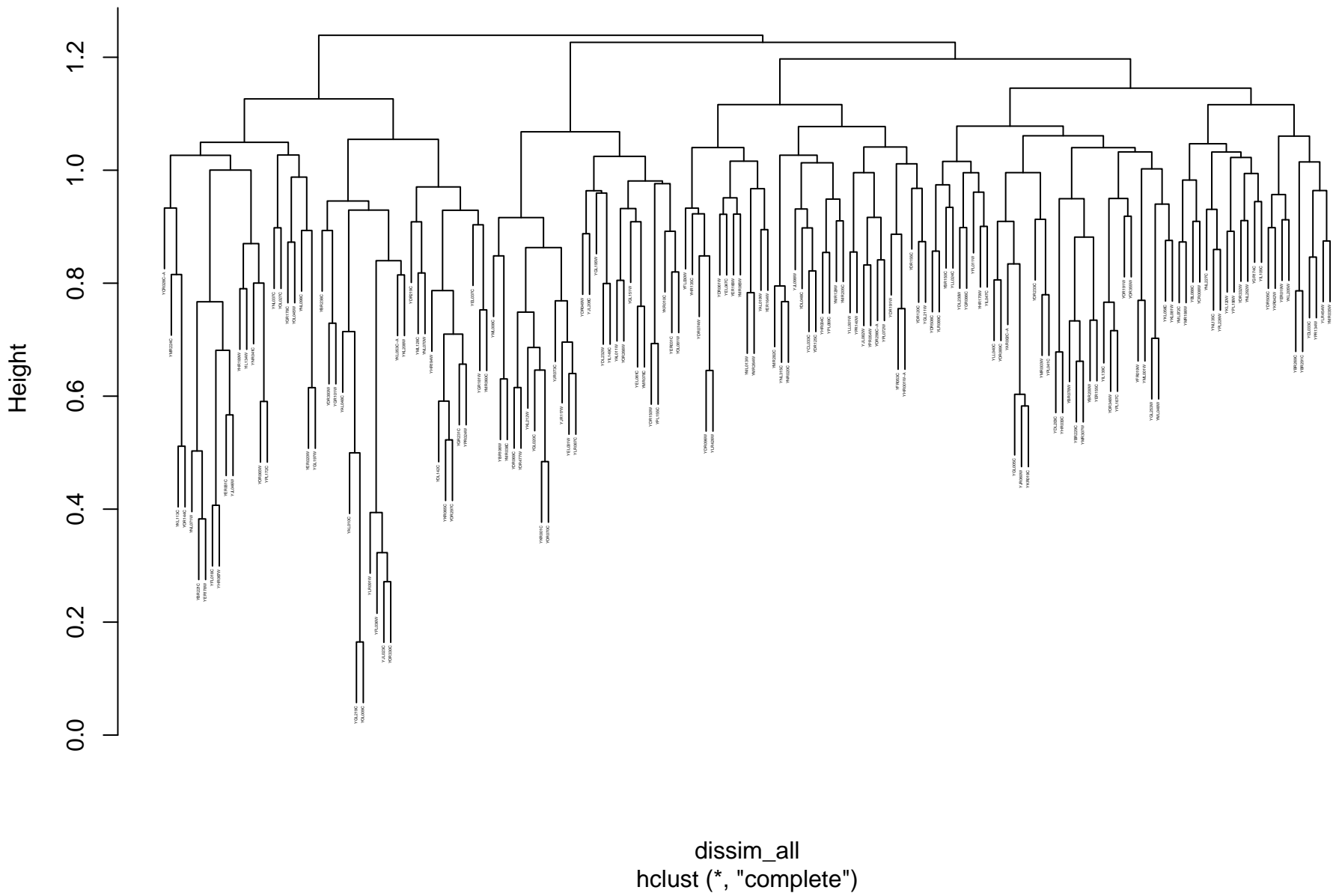
nuclease activity_GO_pearson_complete



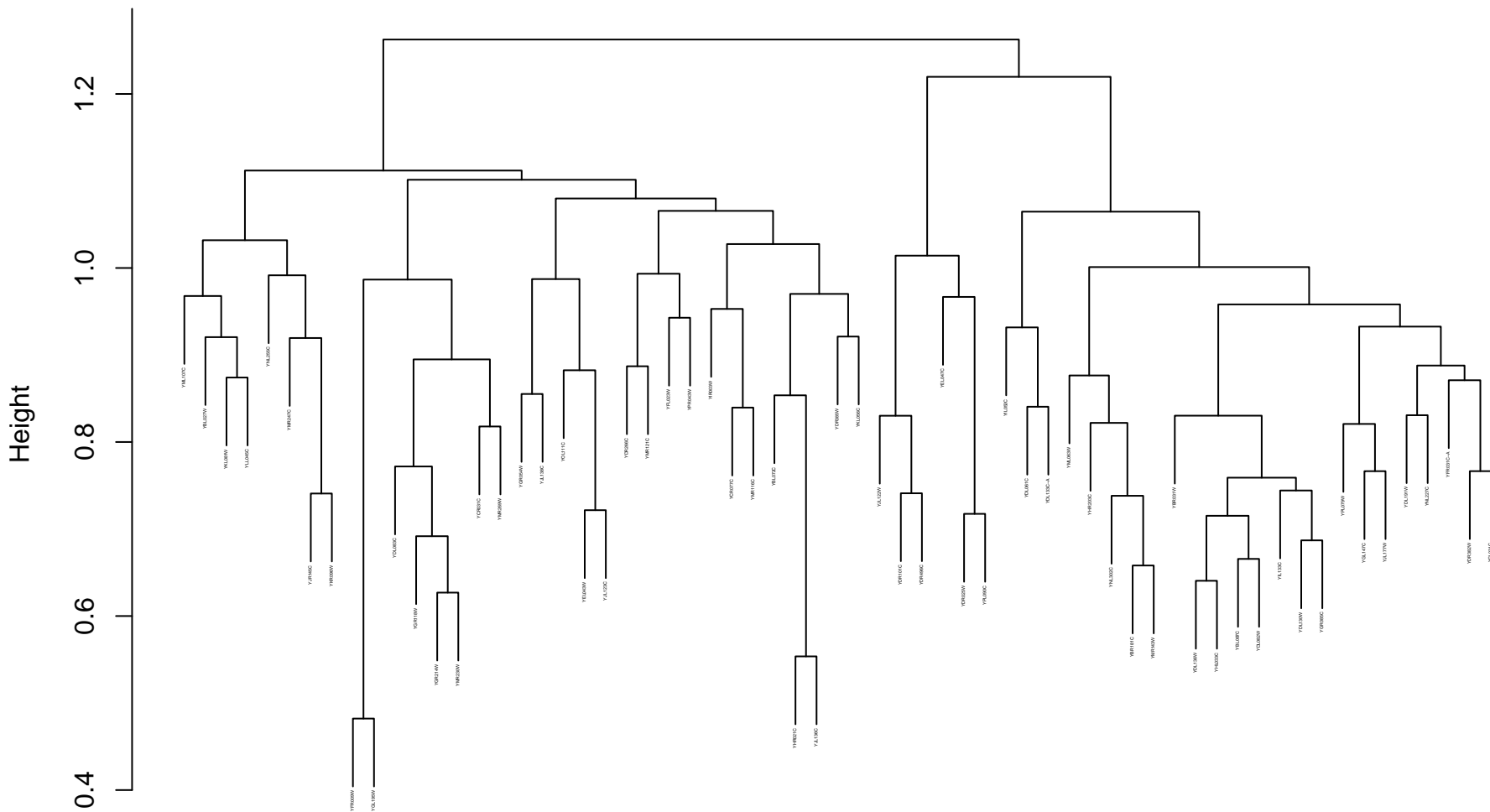

```
dissim_all
hclust (*, "complete")
```



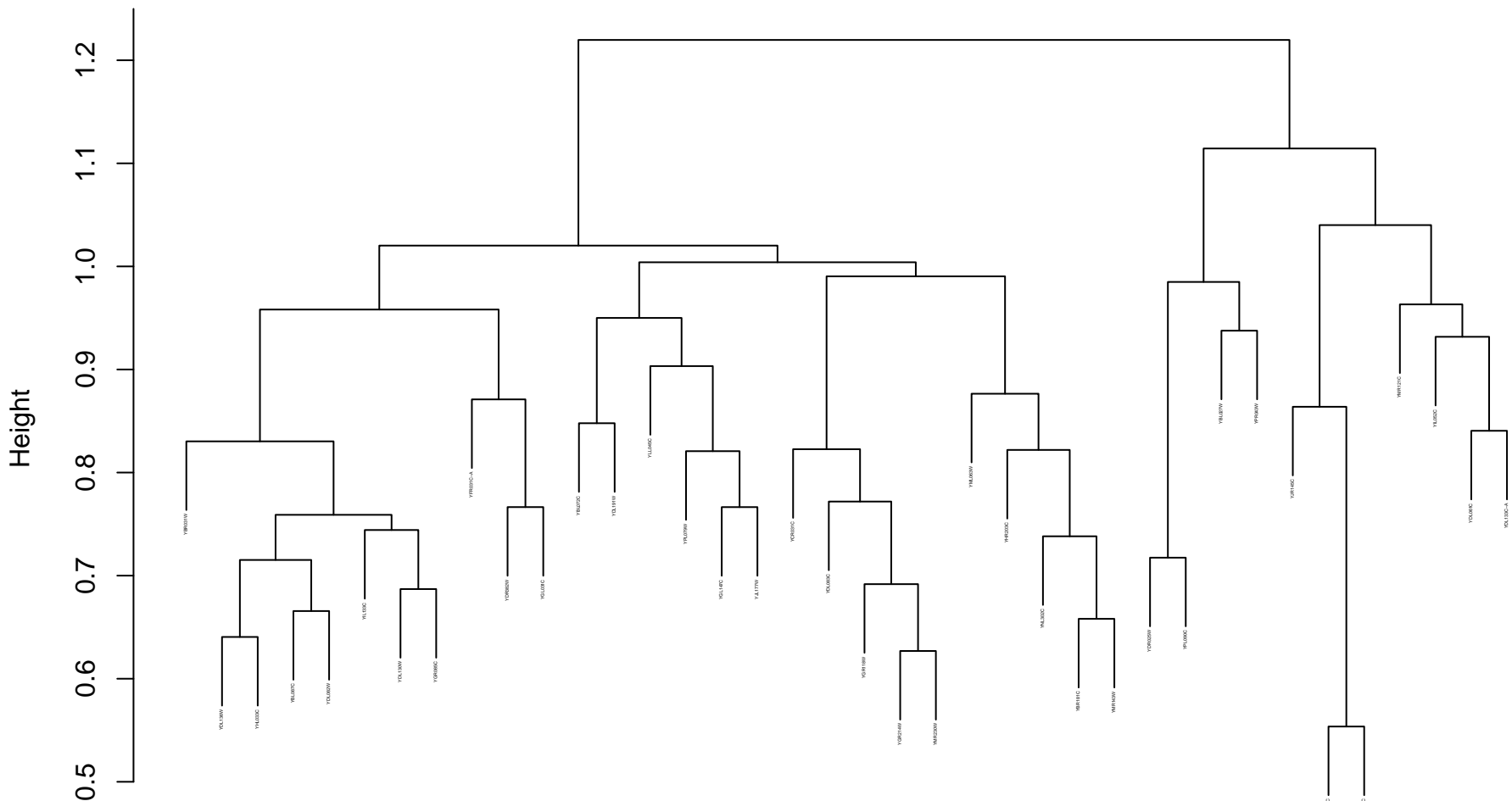
mitochondrion_GO_pearson_complete



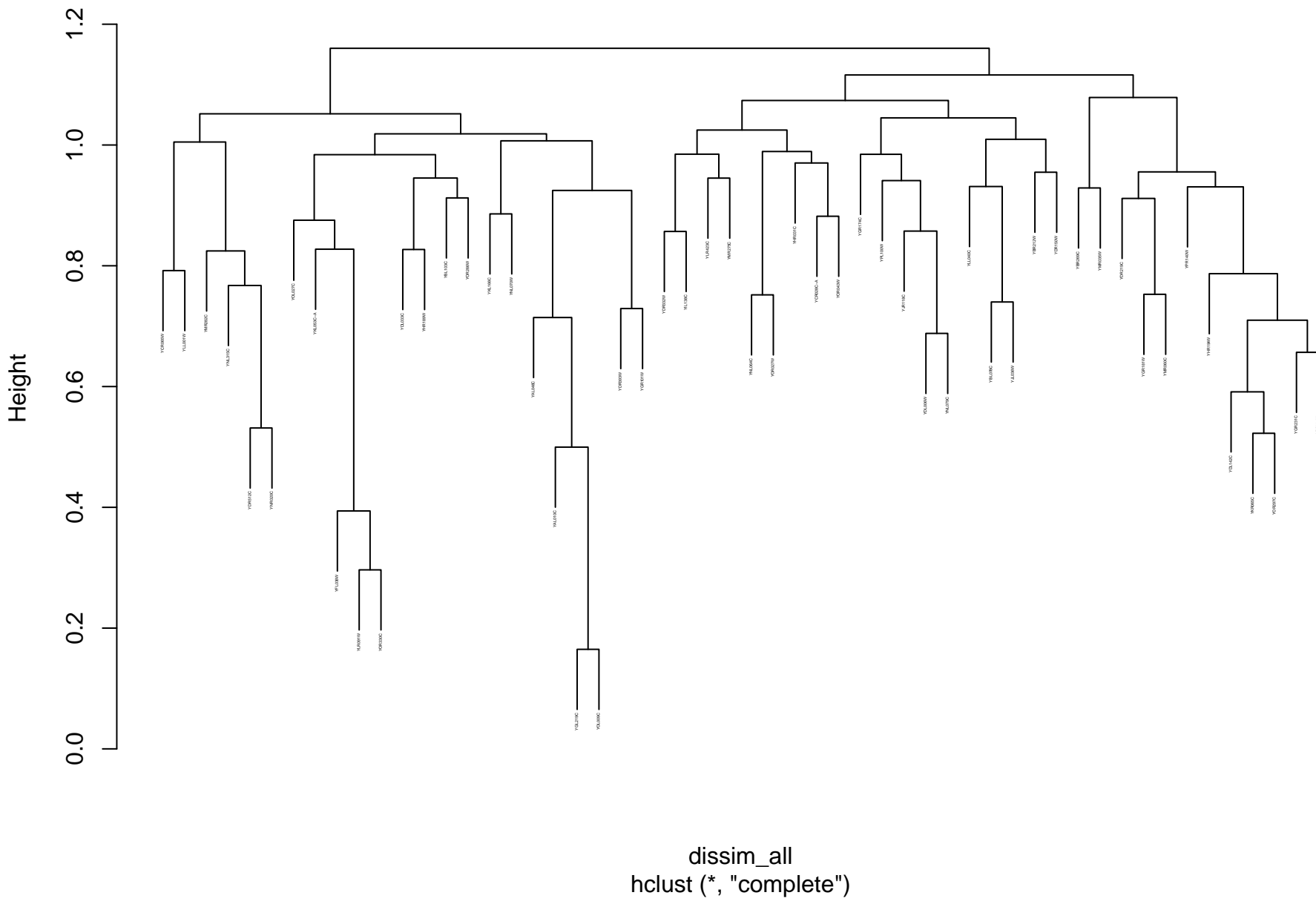
ribosome_GO_pearson_complete



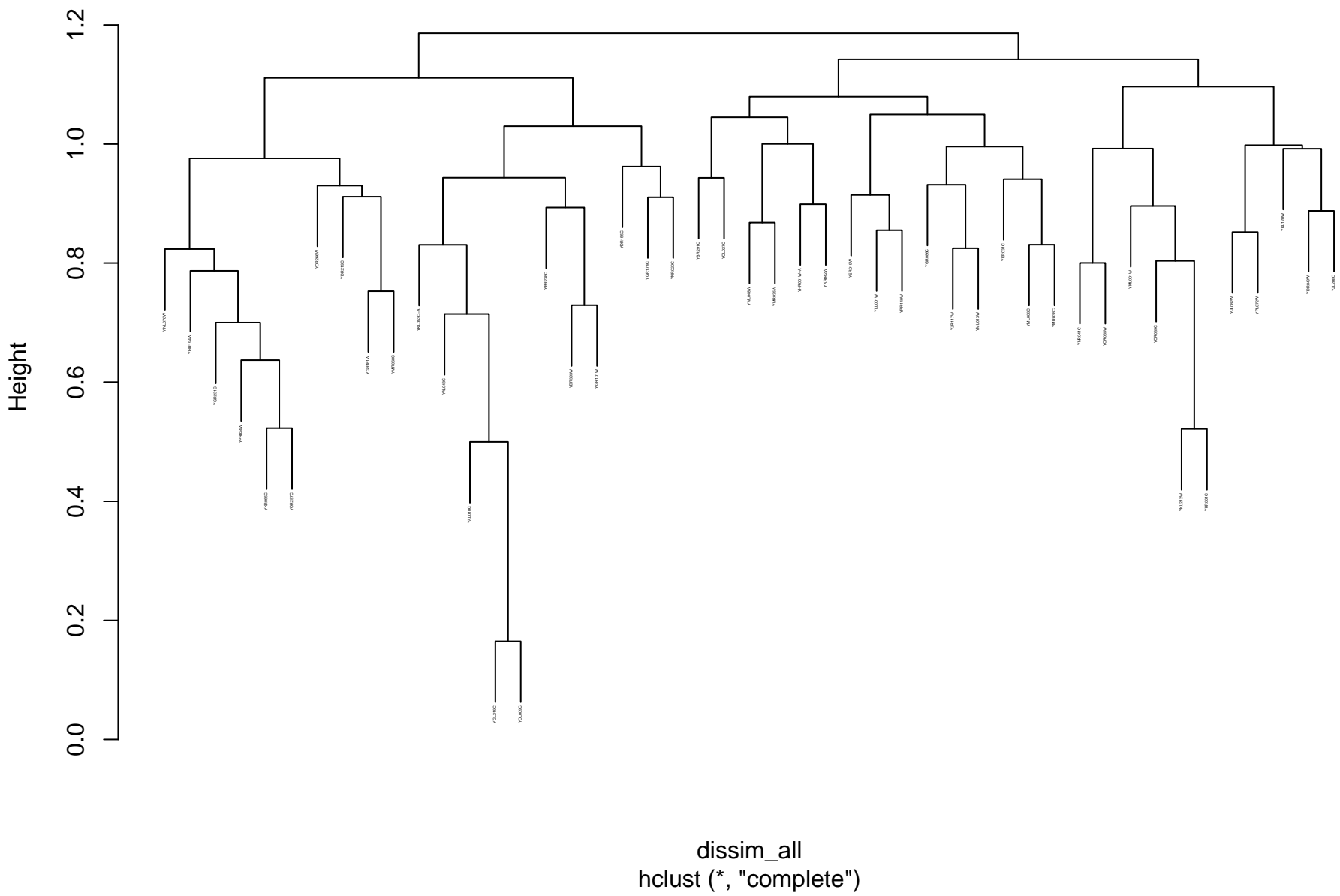
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dissim_all
hclust (*, "complete")
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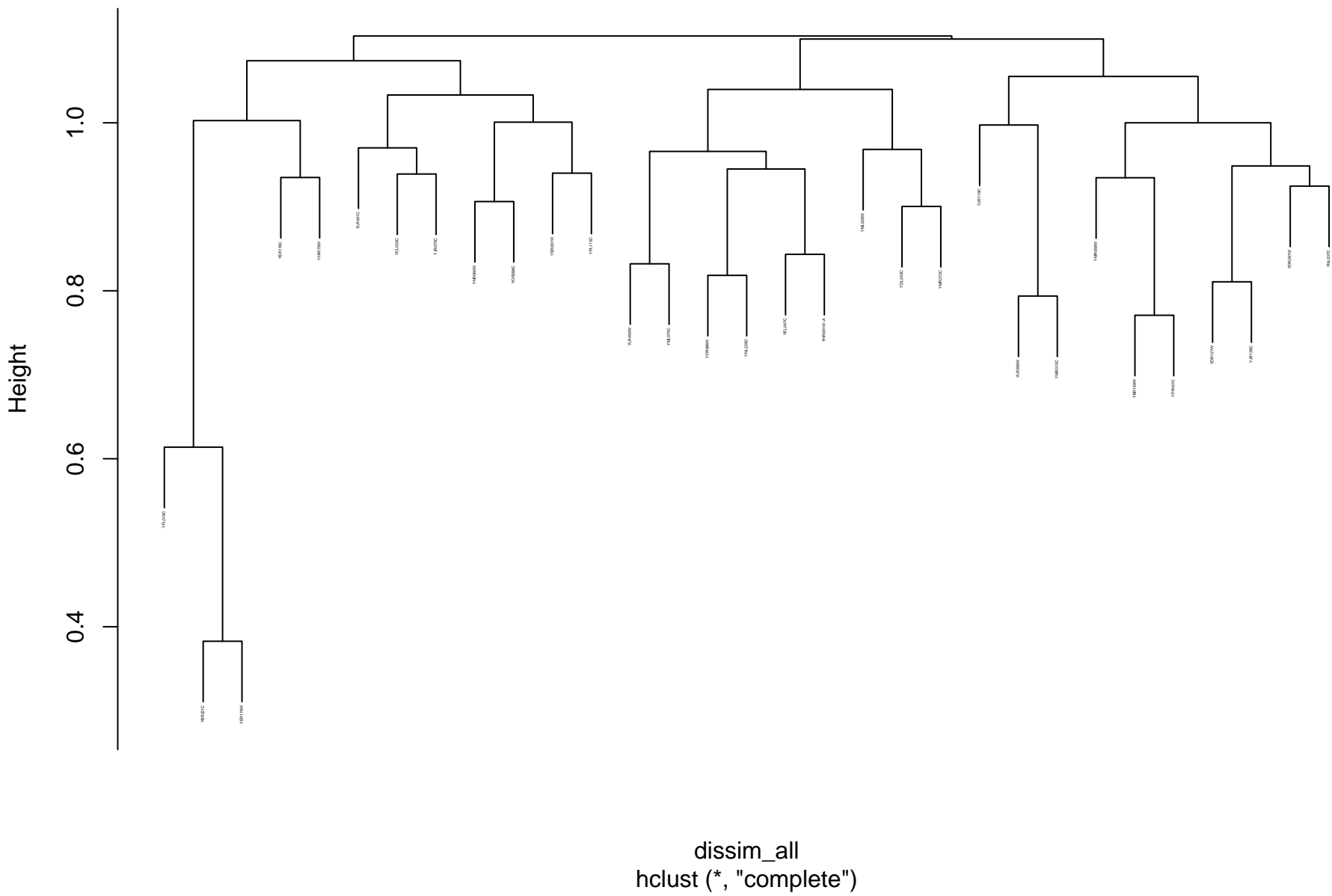
mitochondrion organization_GO_pearson_complete



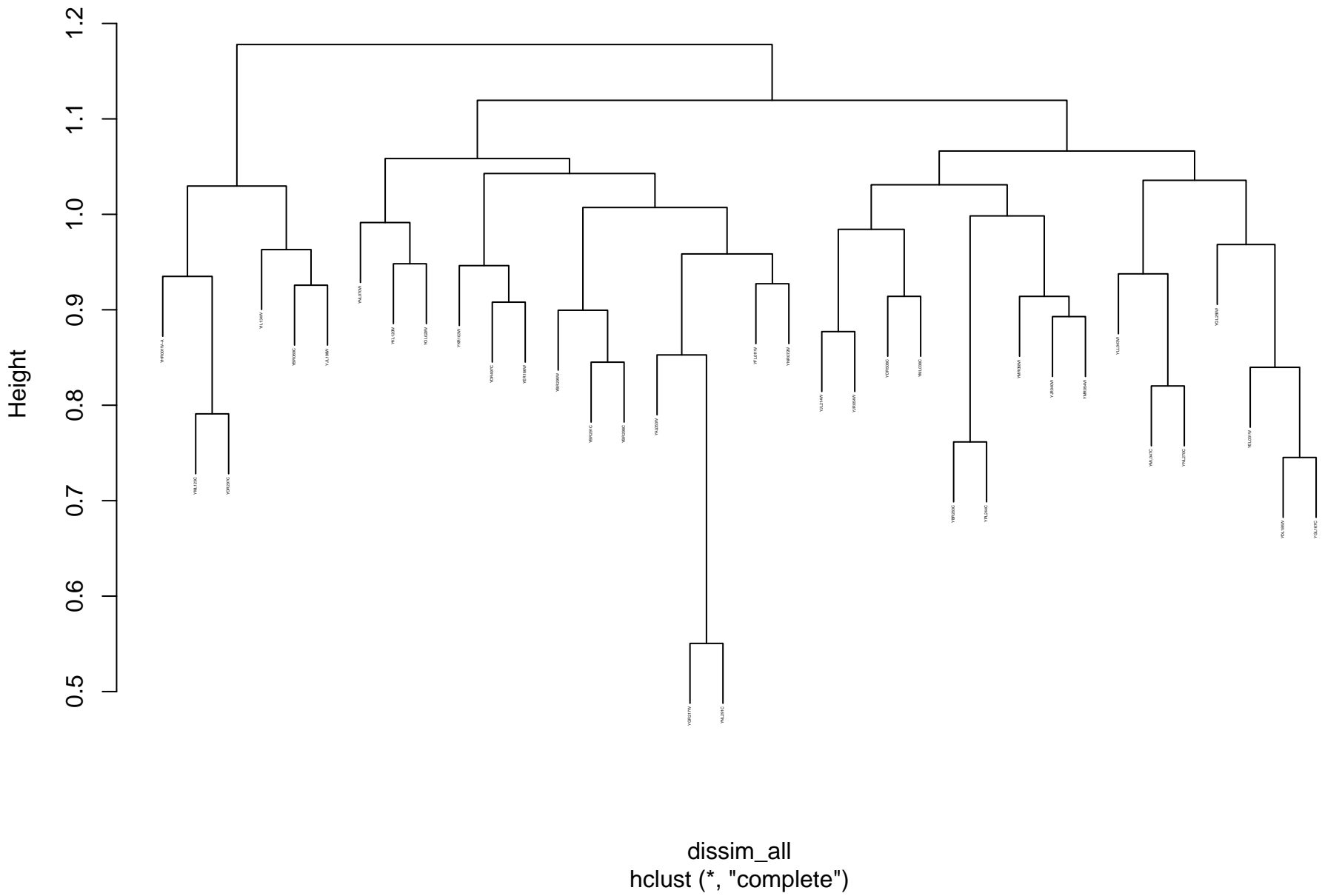
mitochondrial envelope_GO_pearson_complete



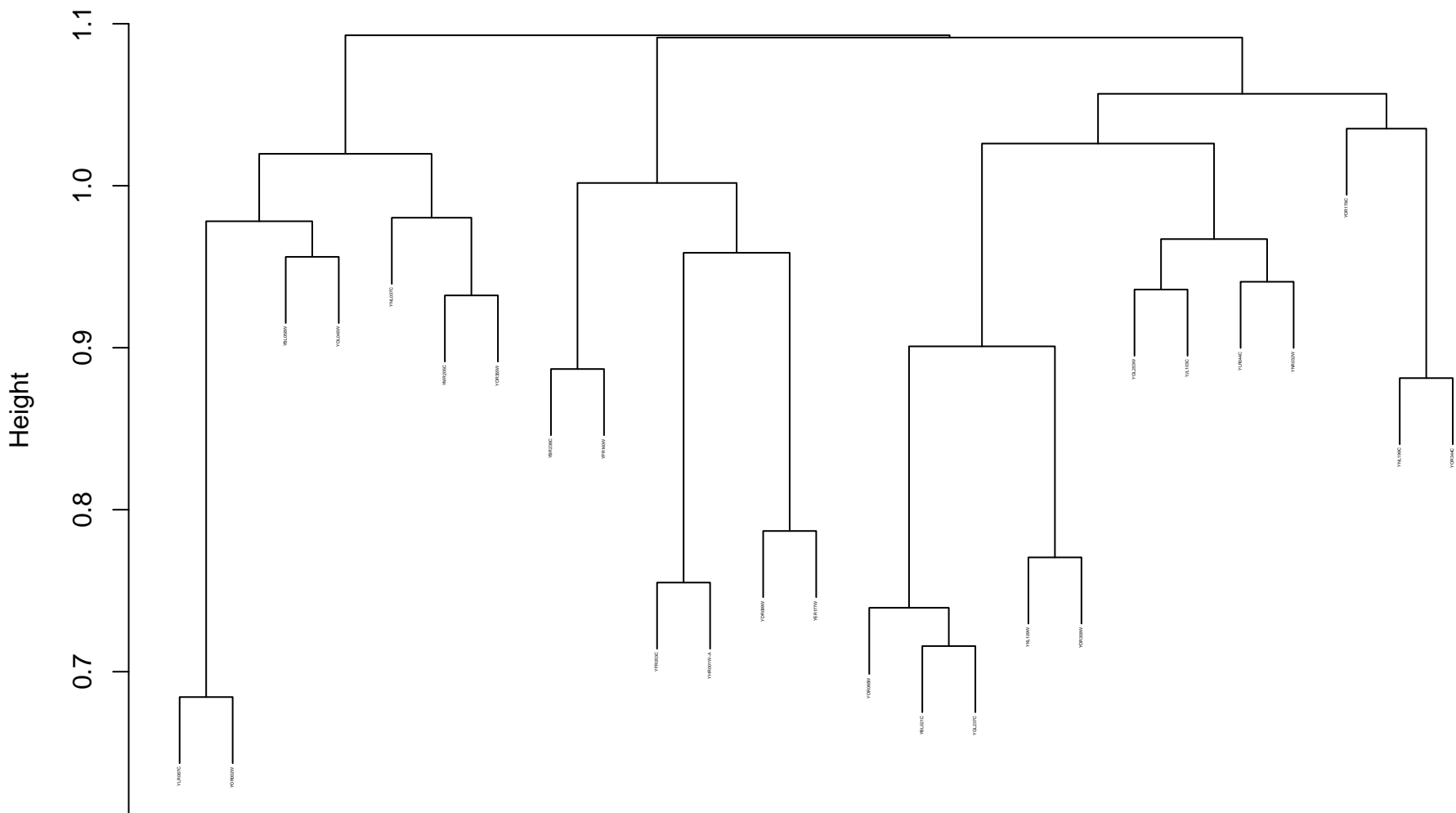
oxidoreductase activity_GO_pearson_complete



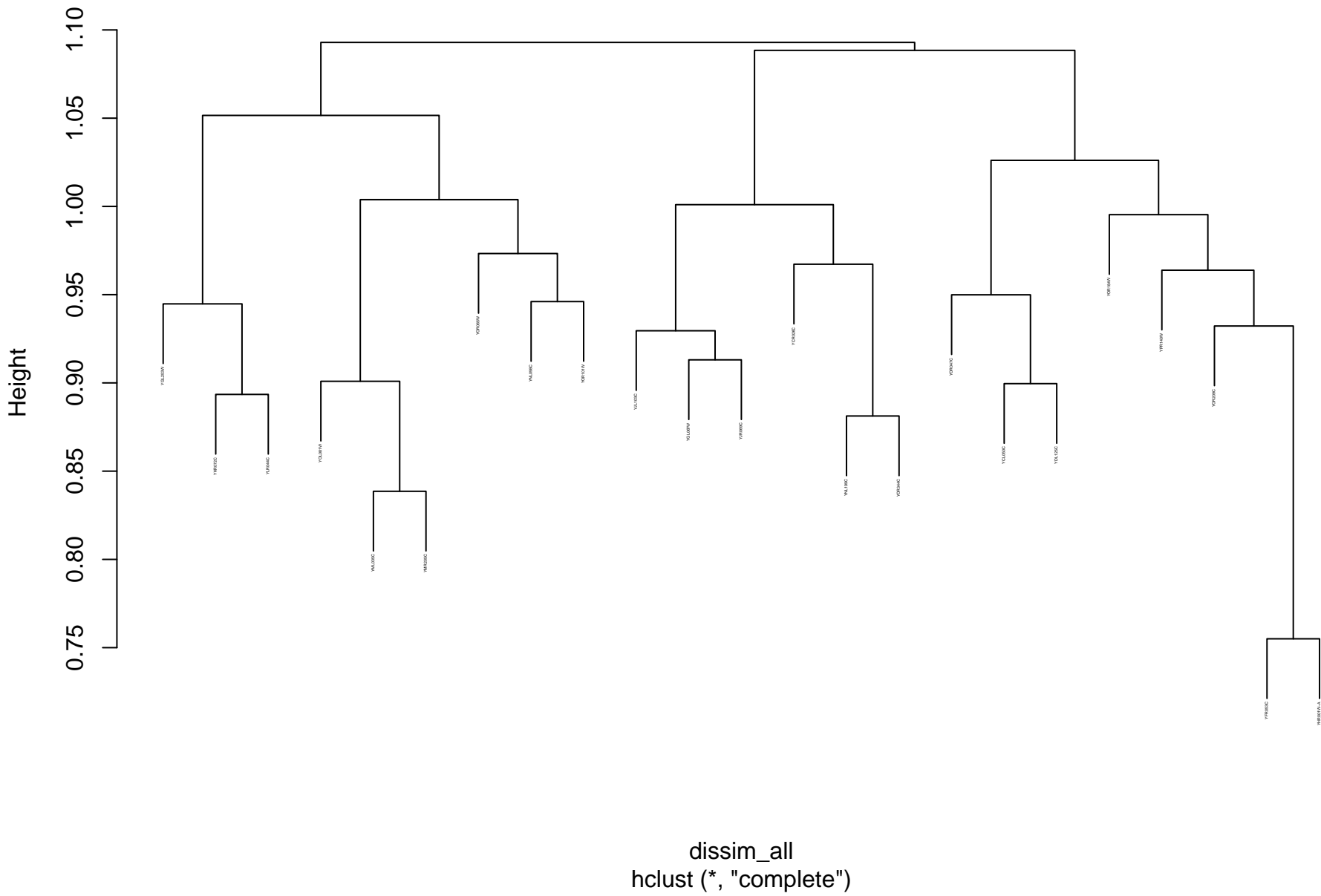
transmembrane transporter activity_GO_pearson_complete



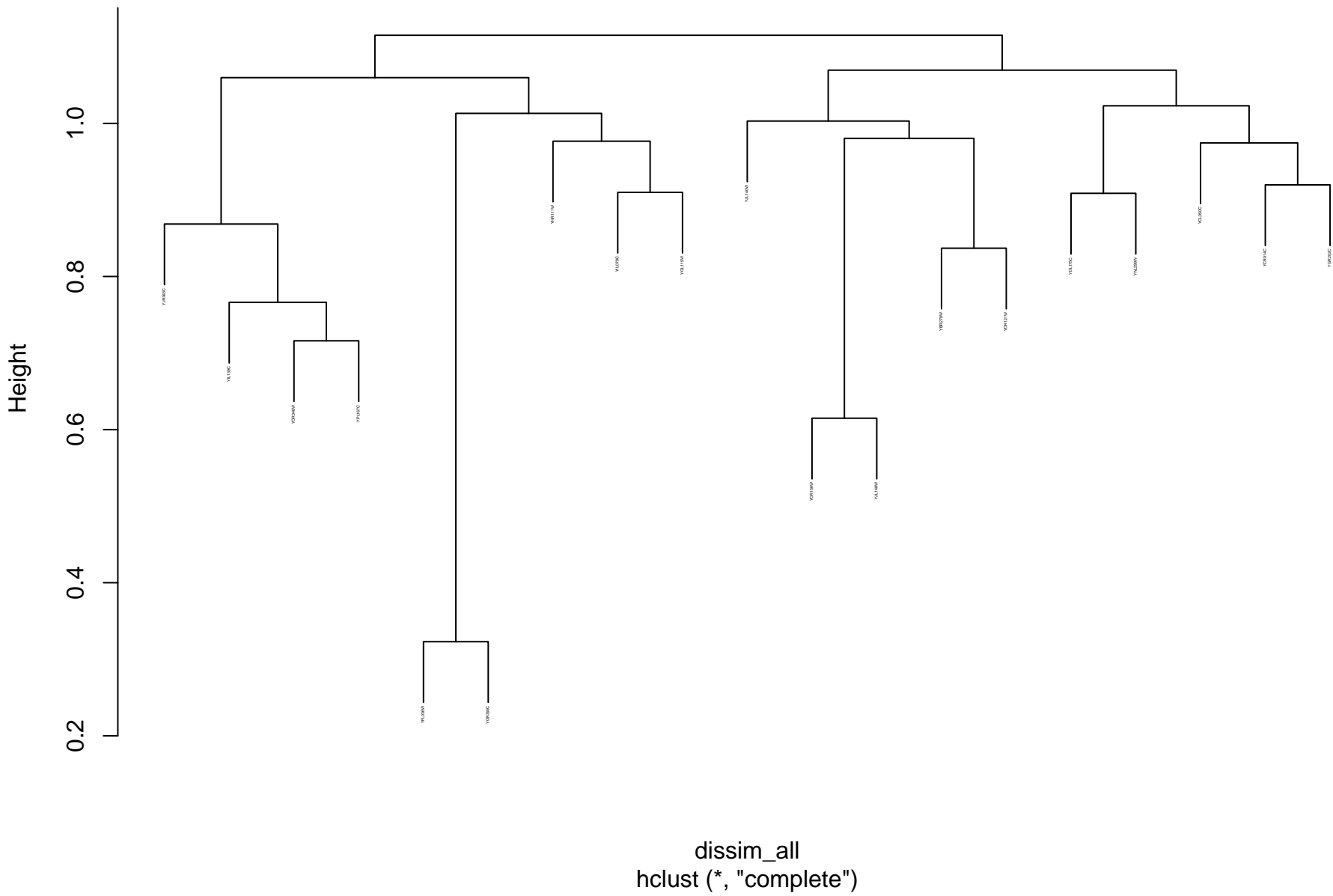

```
dissim_all
hclust (*, "complete")
```



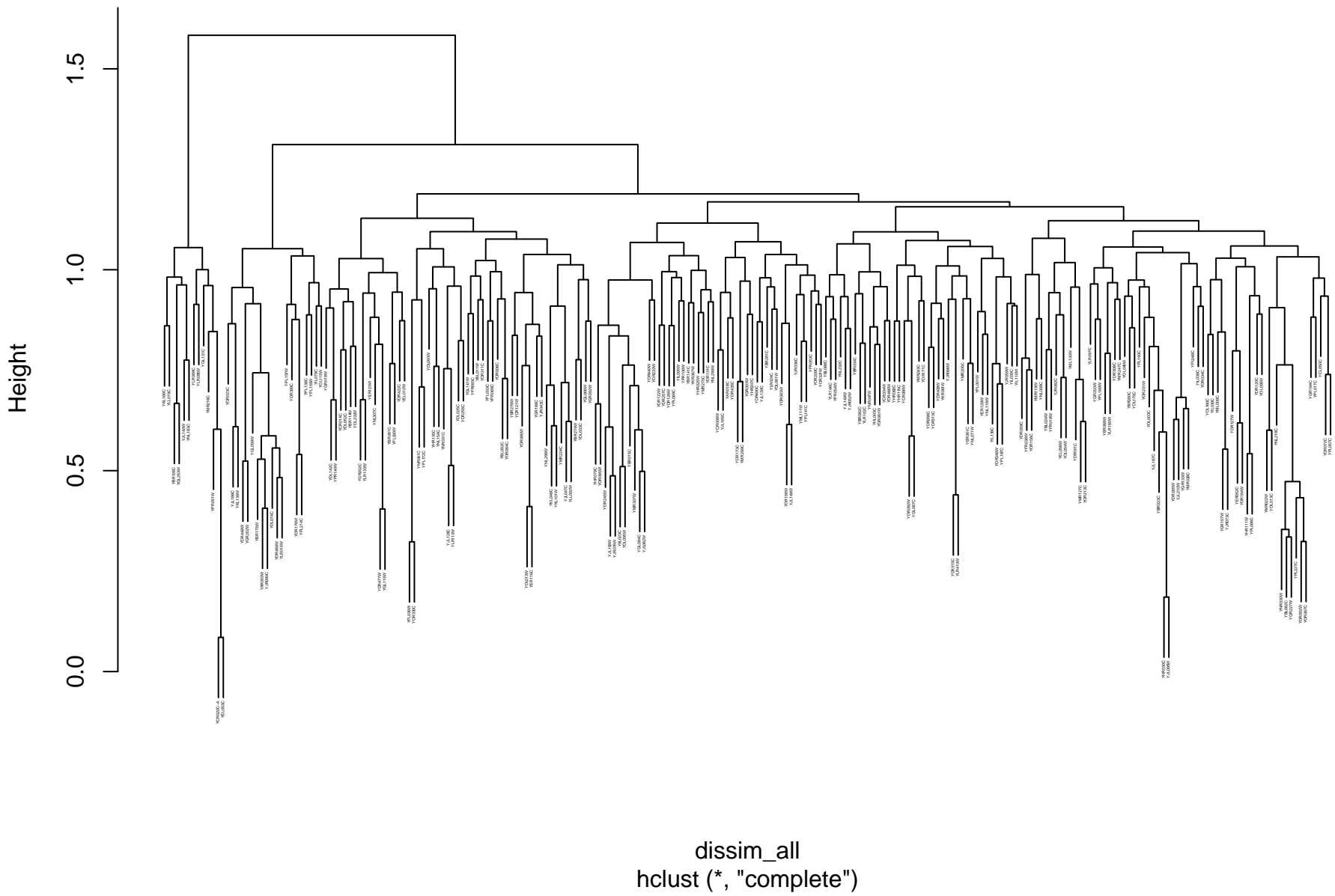
nucleobase-containing small molecule metabolic process_GO_pearson_complete



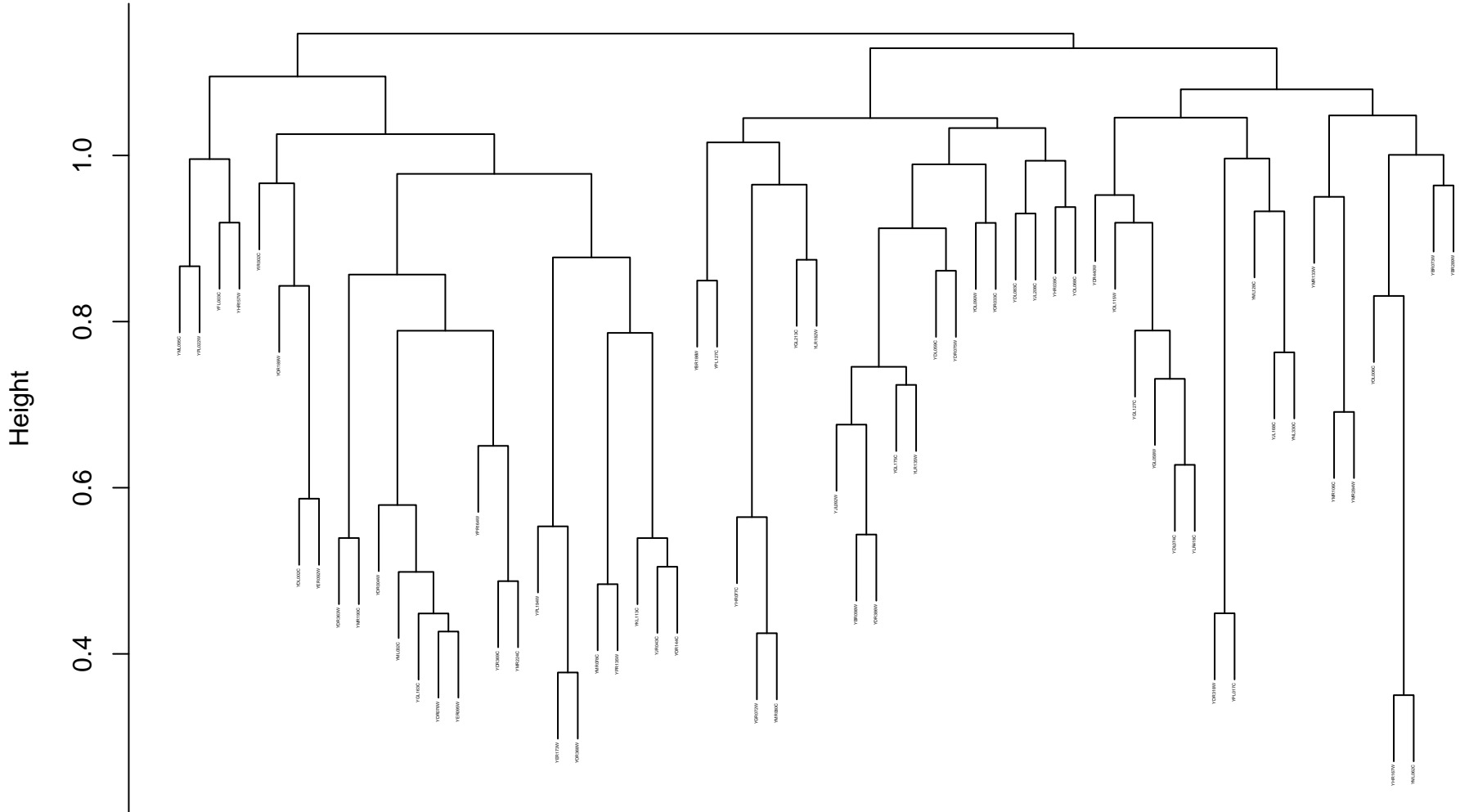
nucleotidyltransferase activity_GO_pearson_complete



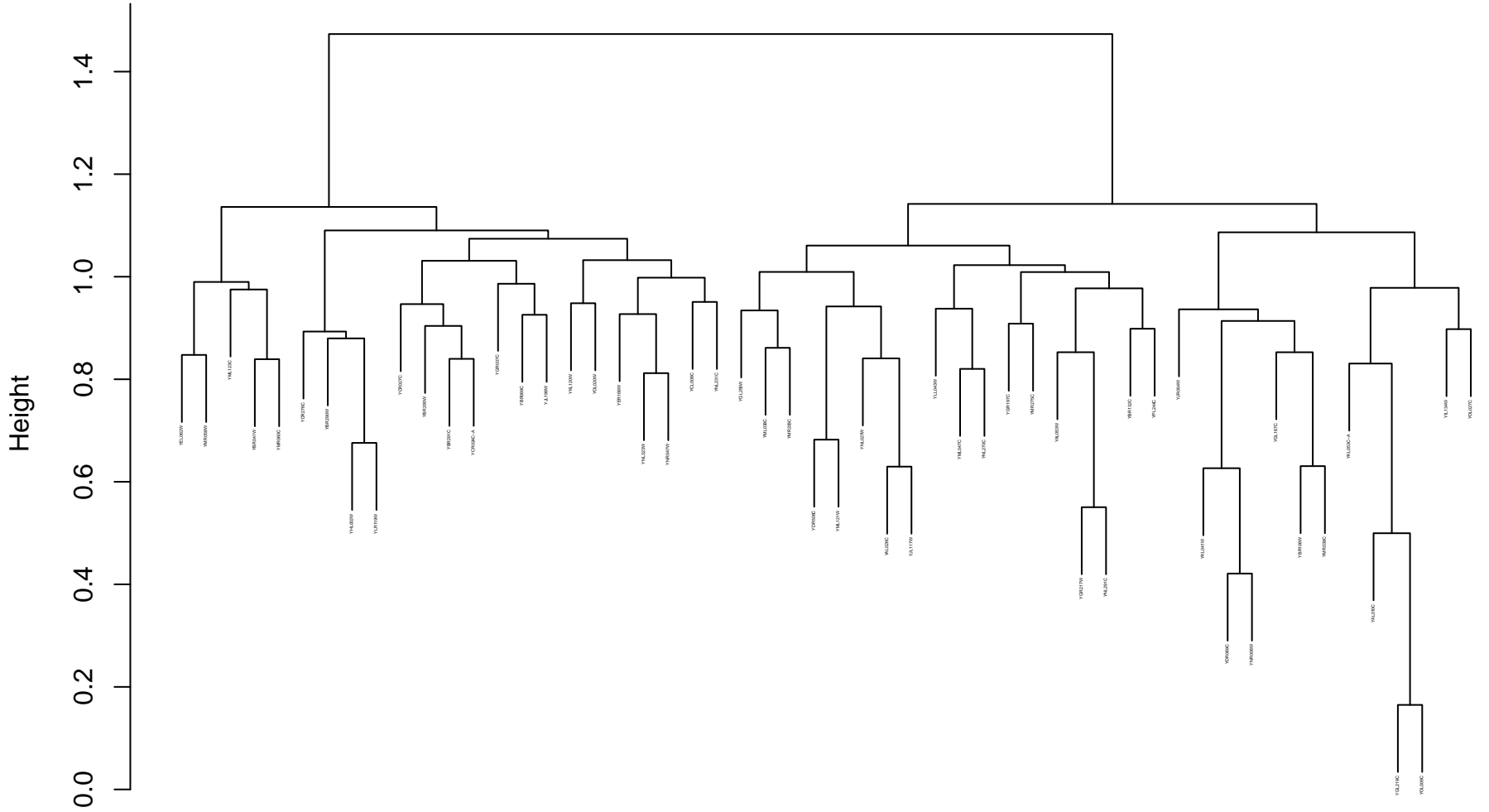
transferase activity_GO_pearson_complete



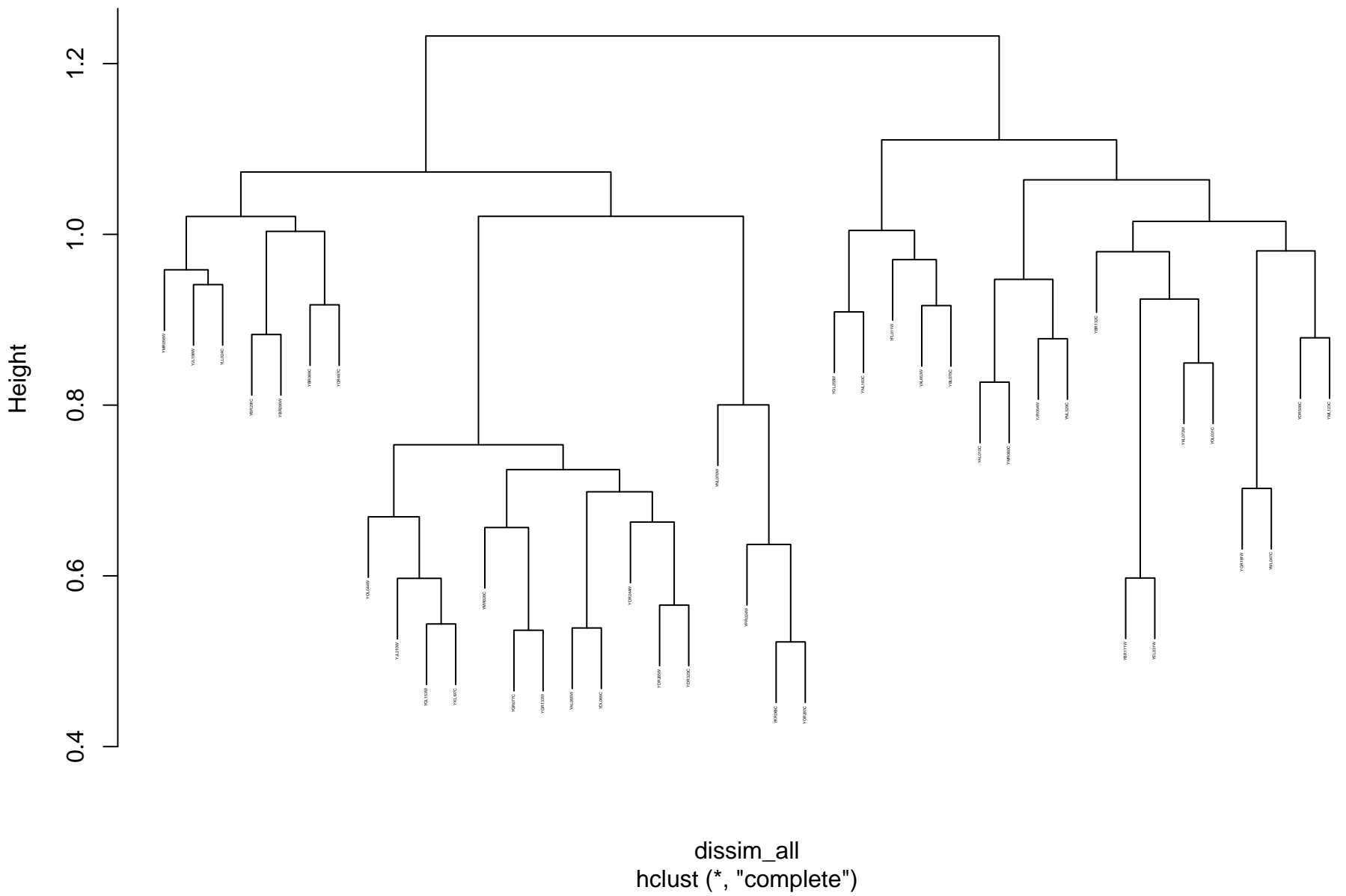
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dissim_all
hclust (*, "complete")
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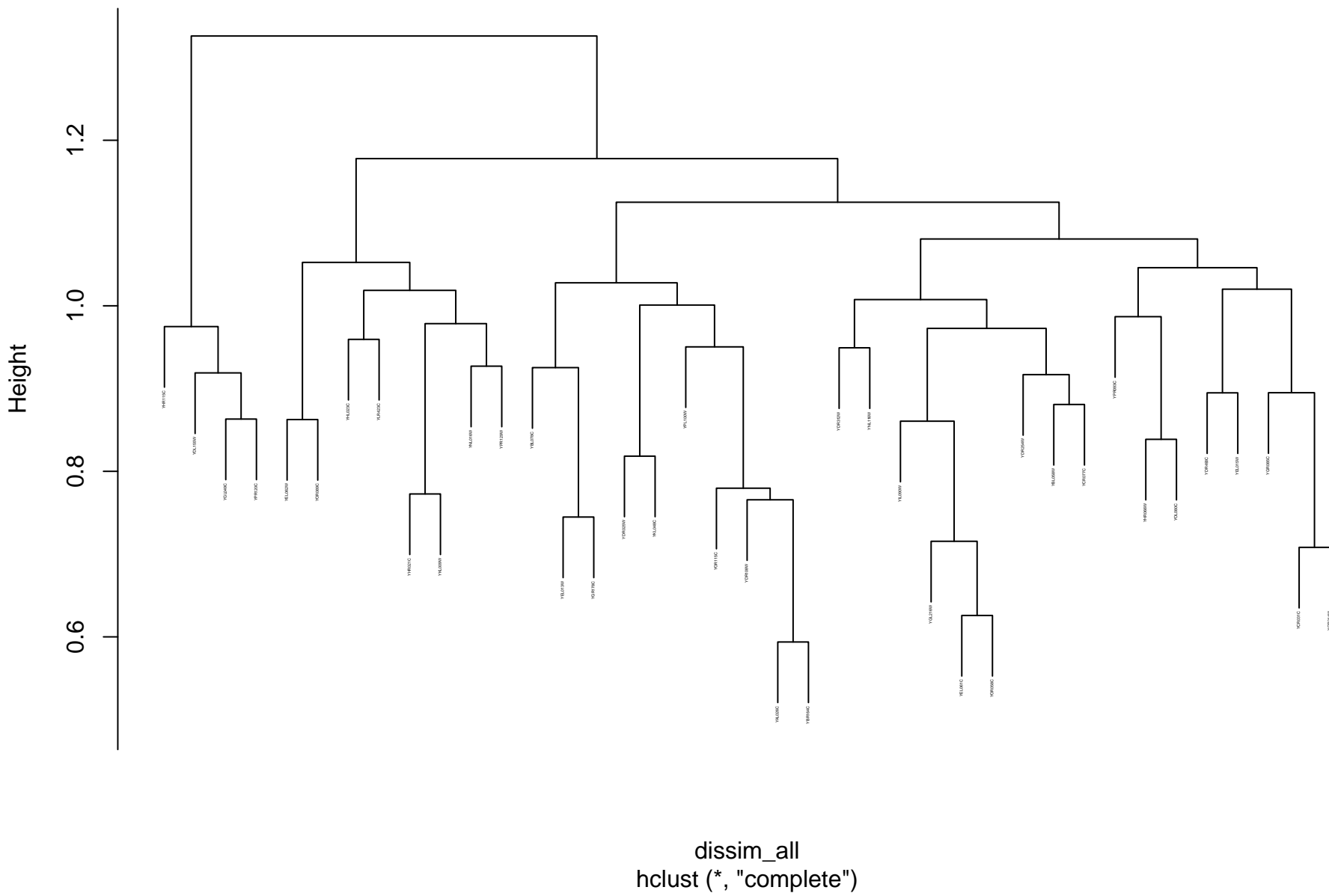
```
dissim_all
hclust (*, "complete")
```



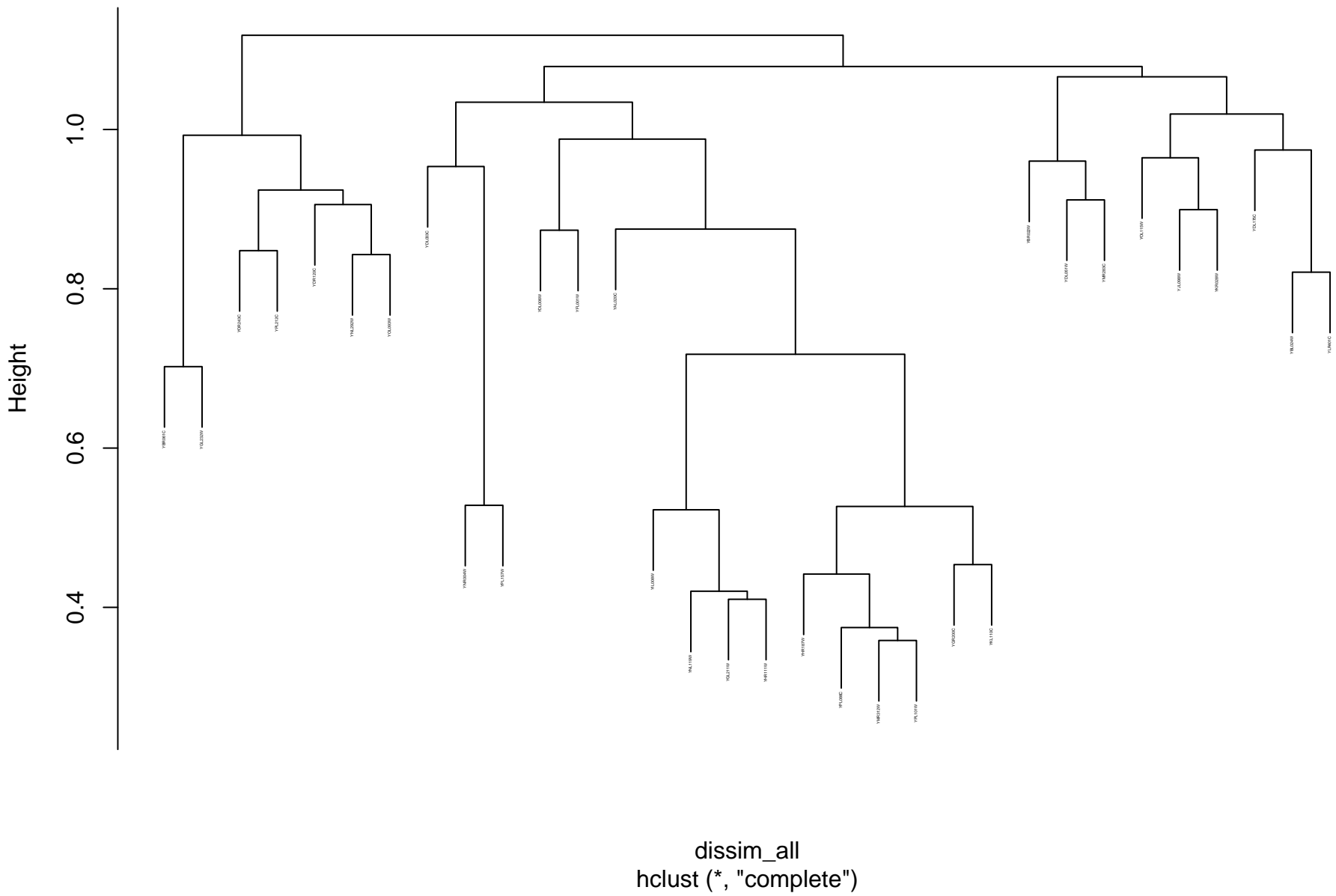
transmembrane transport_GO_pearson_complete



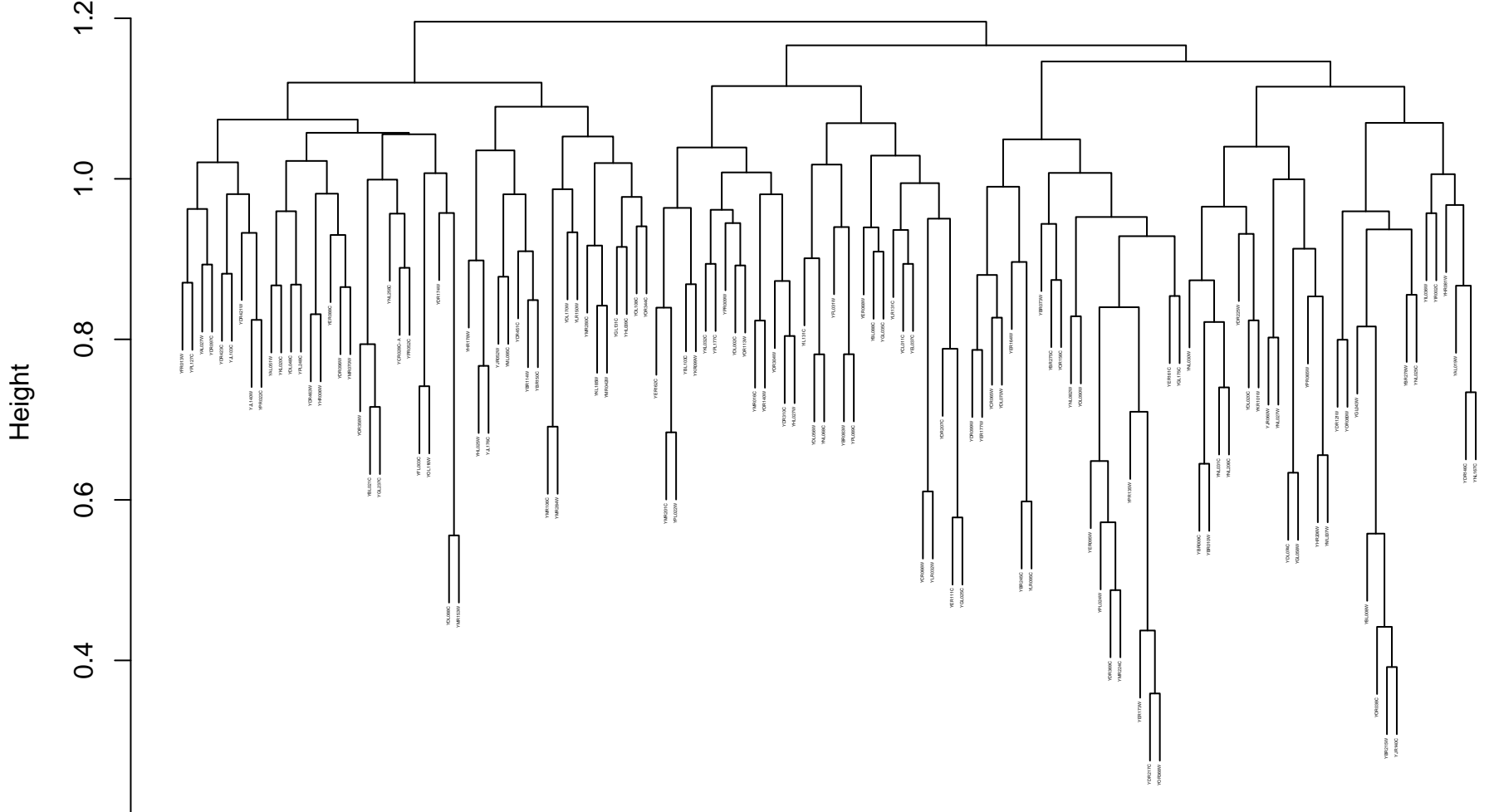
organelle assembly_GO_pearson_complete



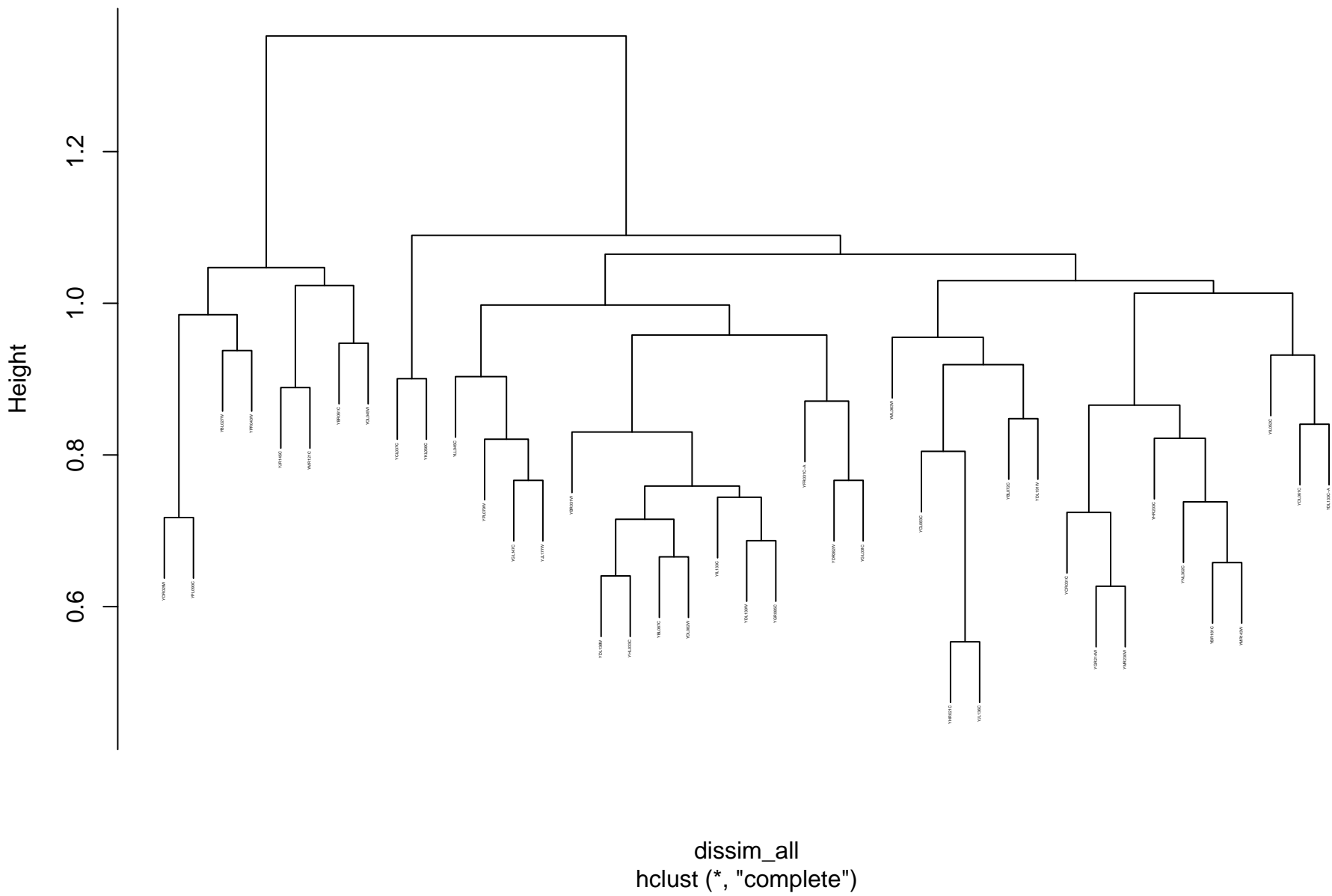
tRNA processing_GO_pearson_complete



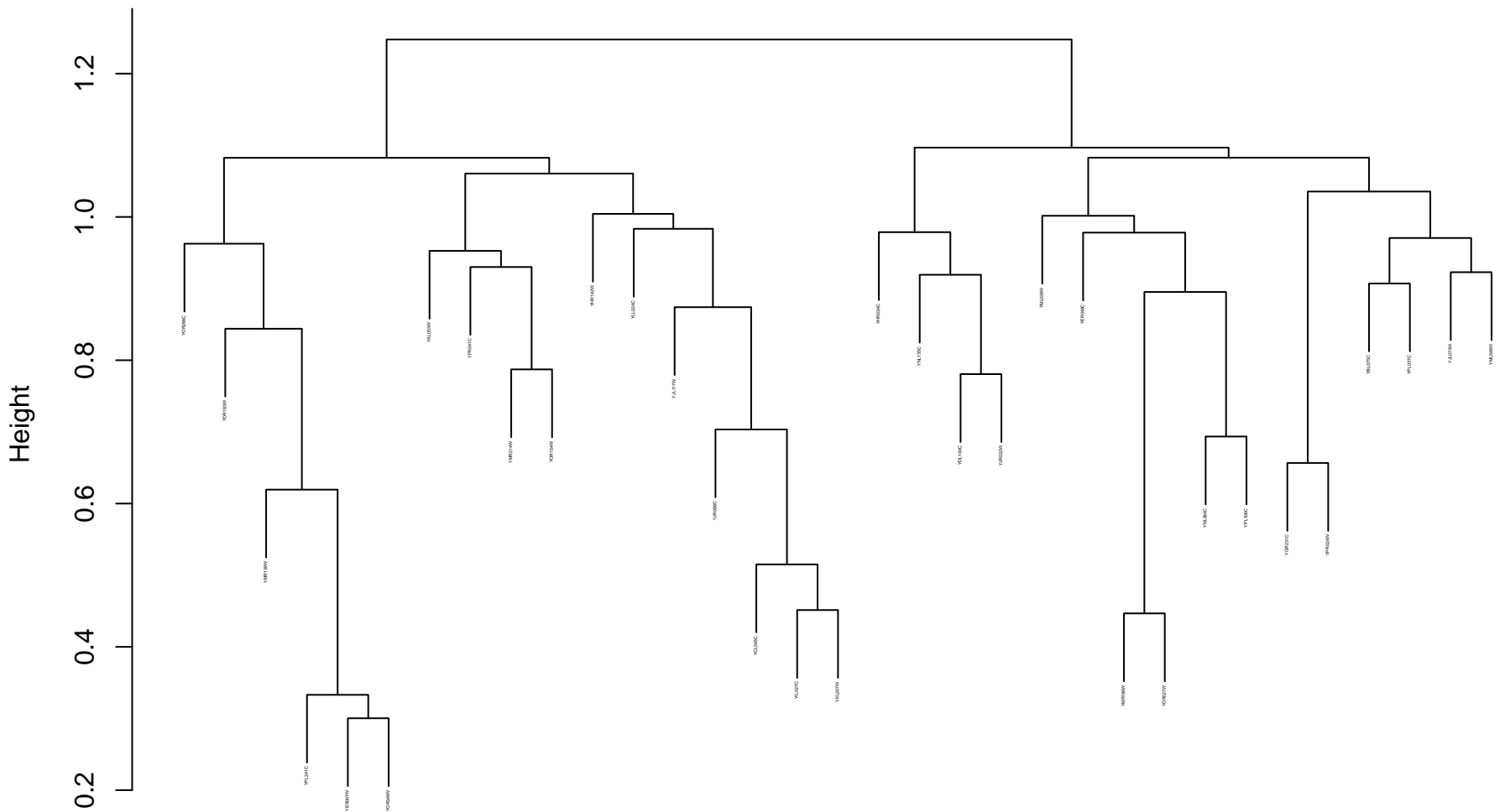
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dissim_all
hclust (*, "complete")
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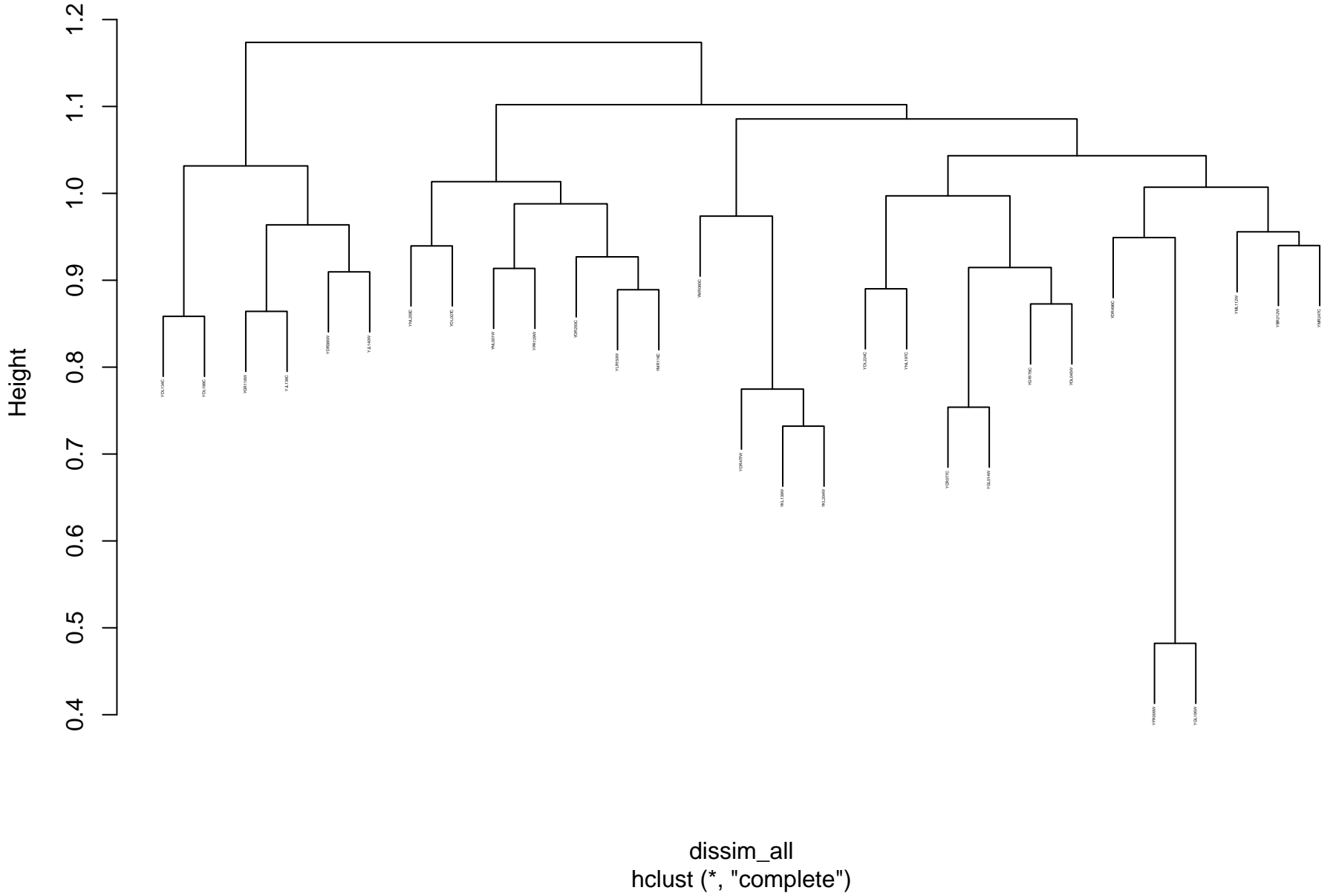
cytoplasmic translation_GO_pearson_complete



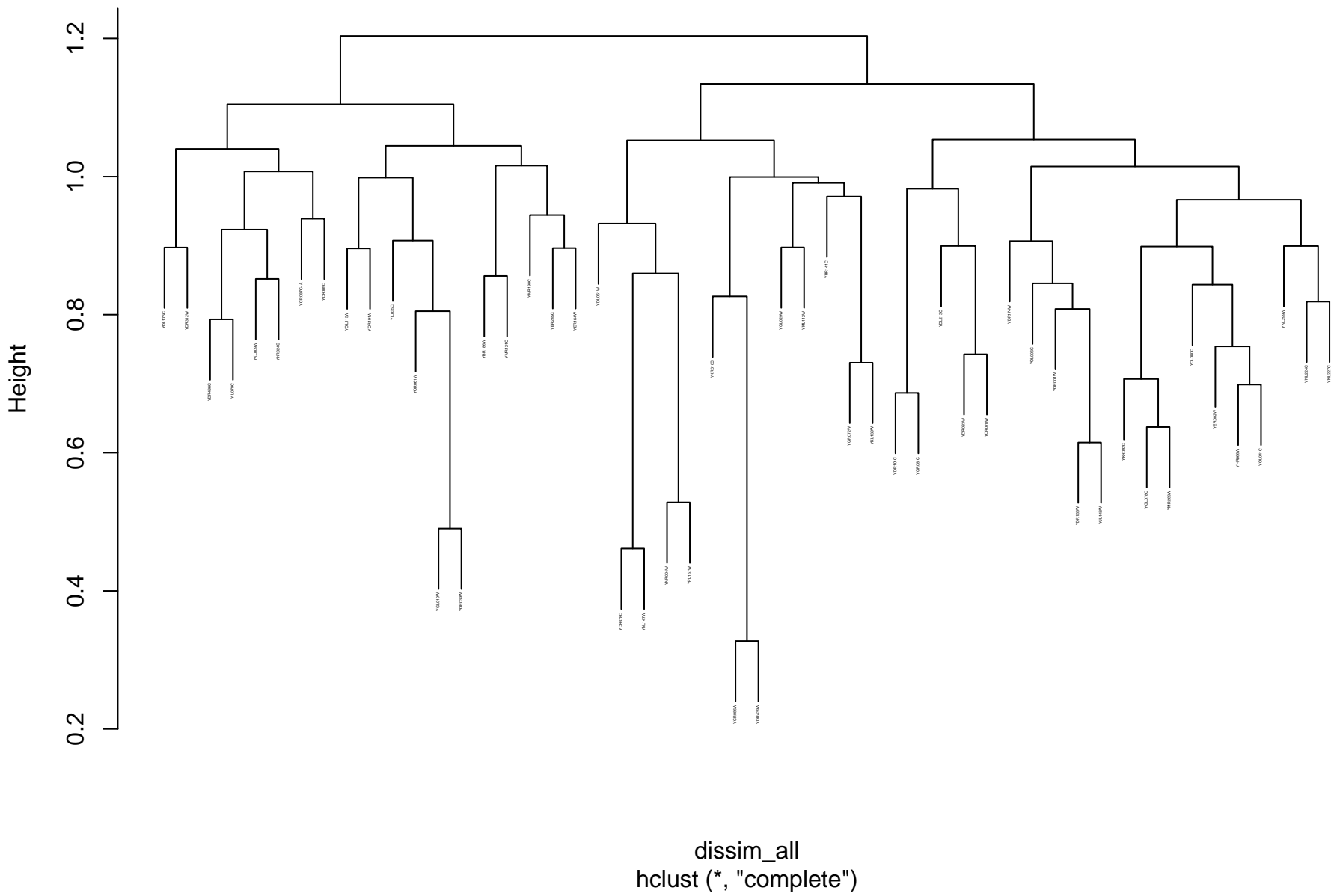
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dissim_all
hclust (*, "complete")
```



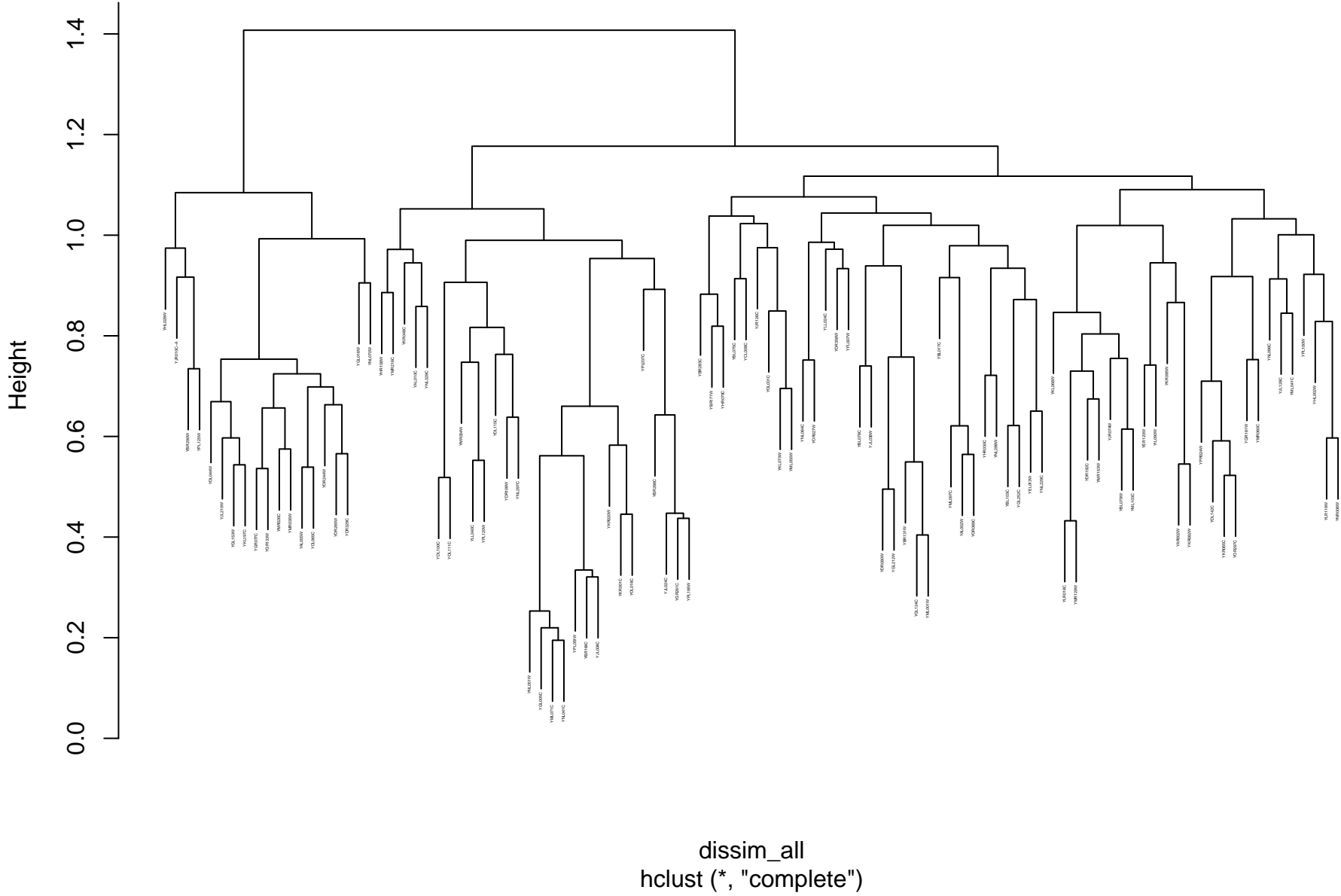
regulation of translation_GO_pearson_complete



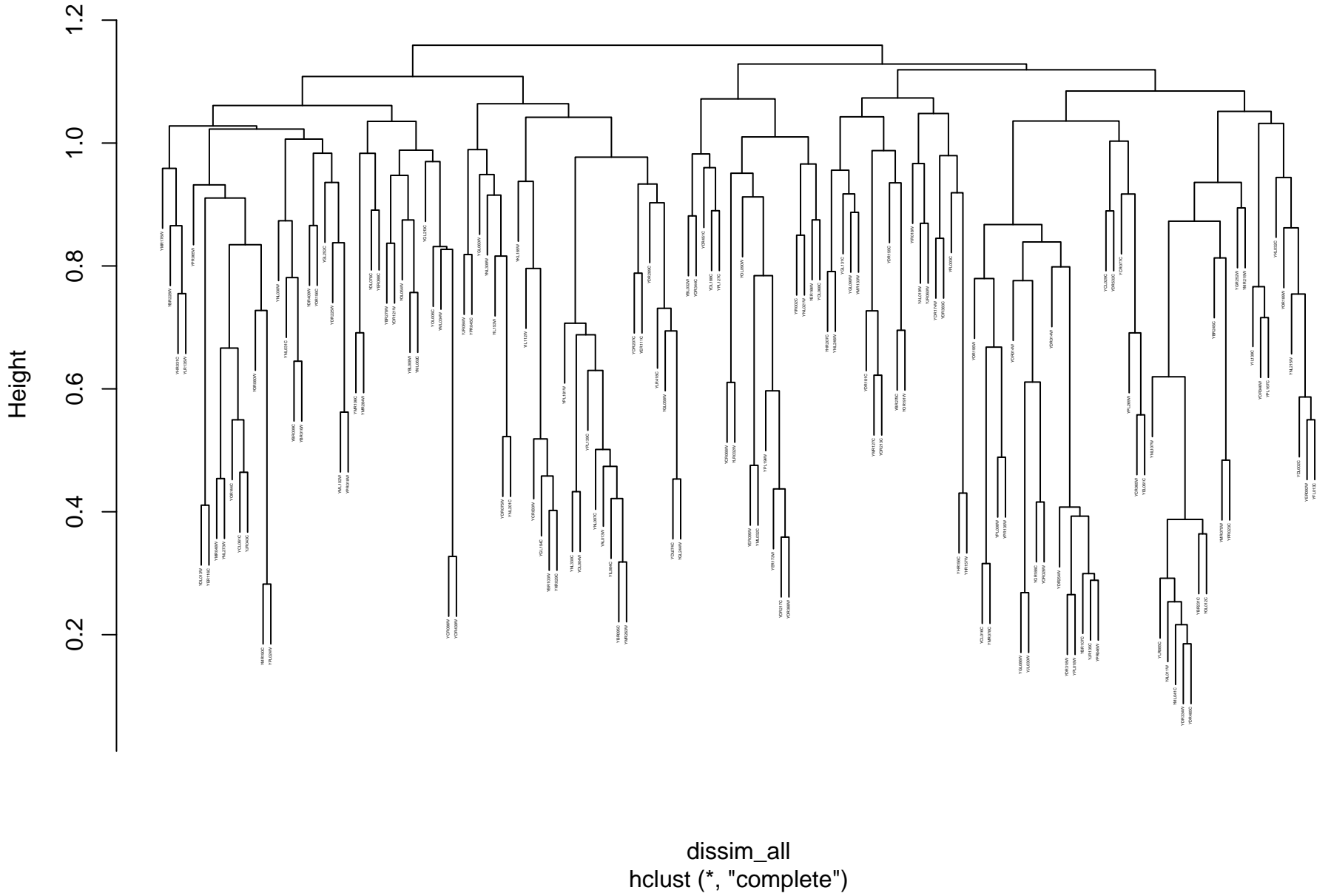
nucleolus_GO_pearson_complete



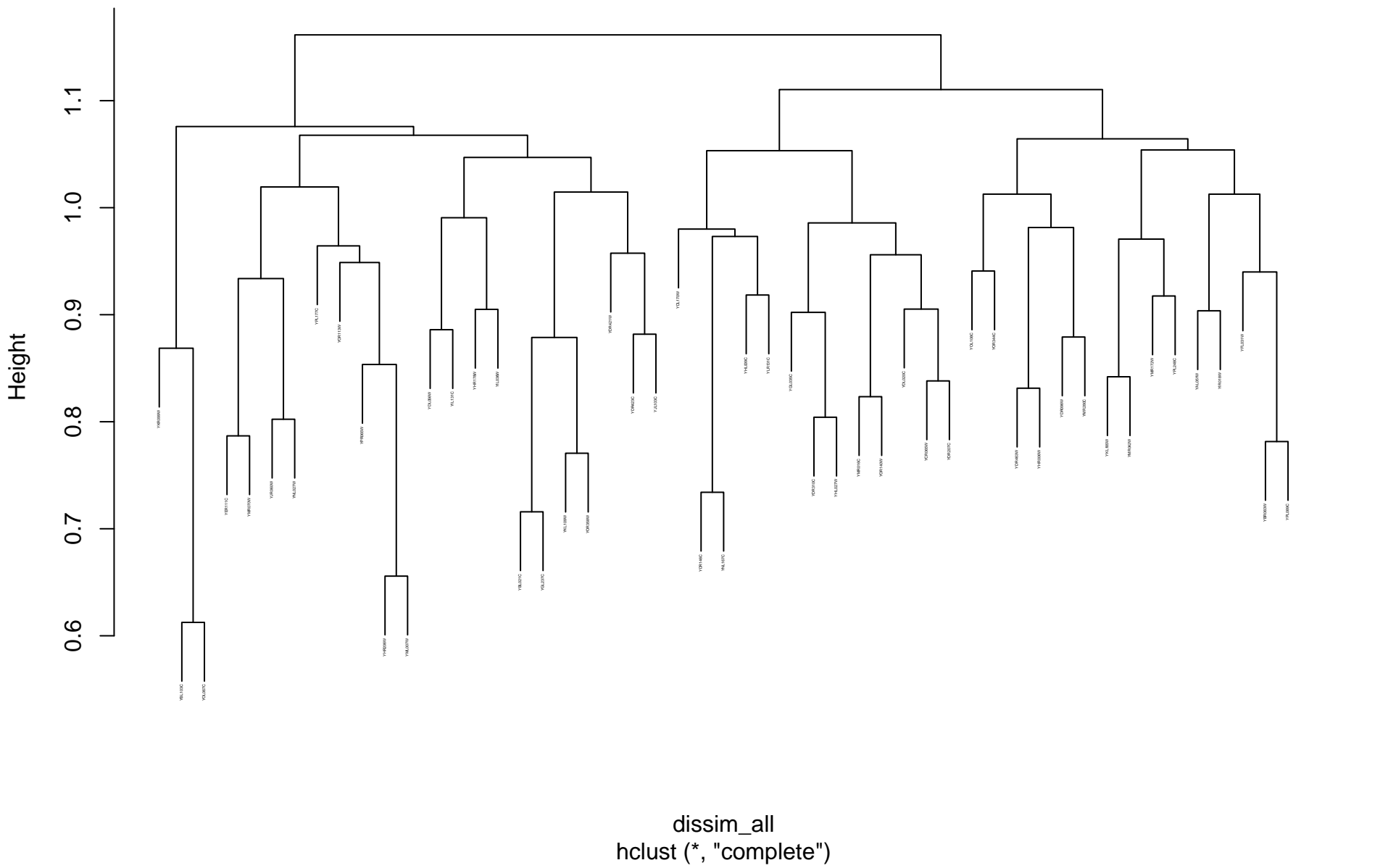
protein targeting_GO_pearson_complete



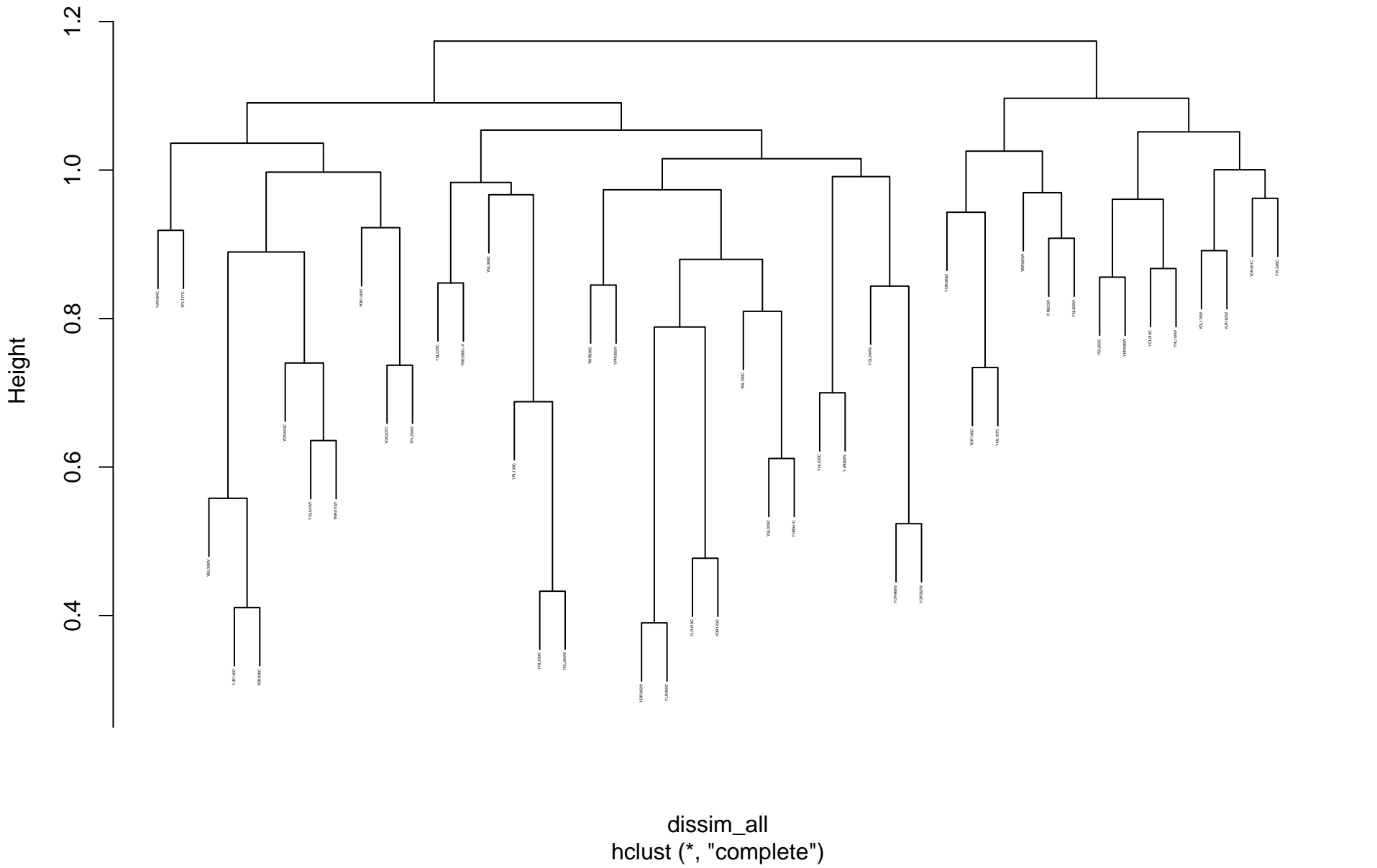
chromosome_GO_pearson_complete



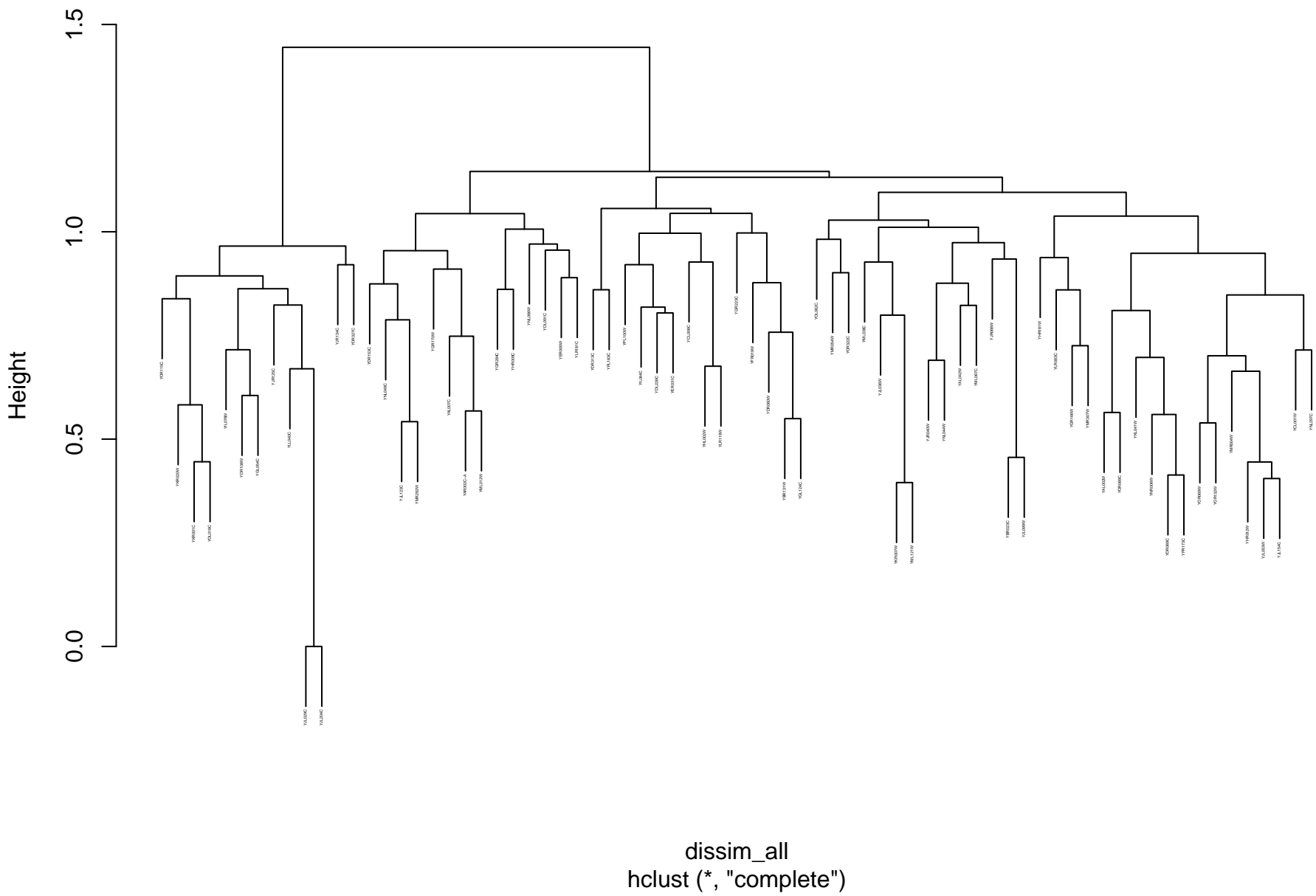
nucleic acid binding transcription factor activity_GO_pearson_complete



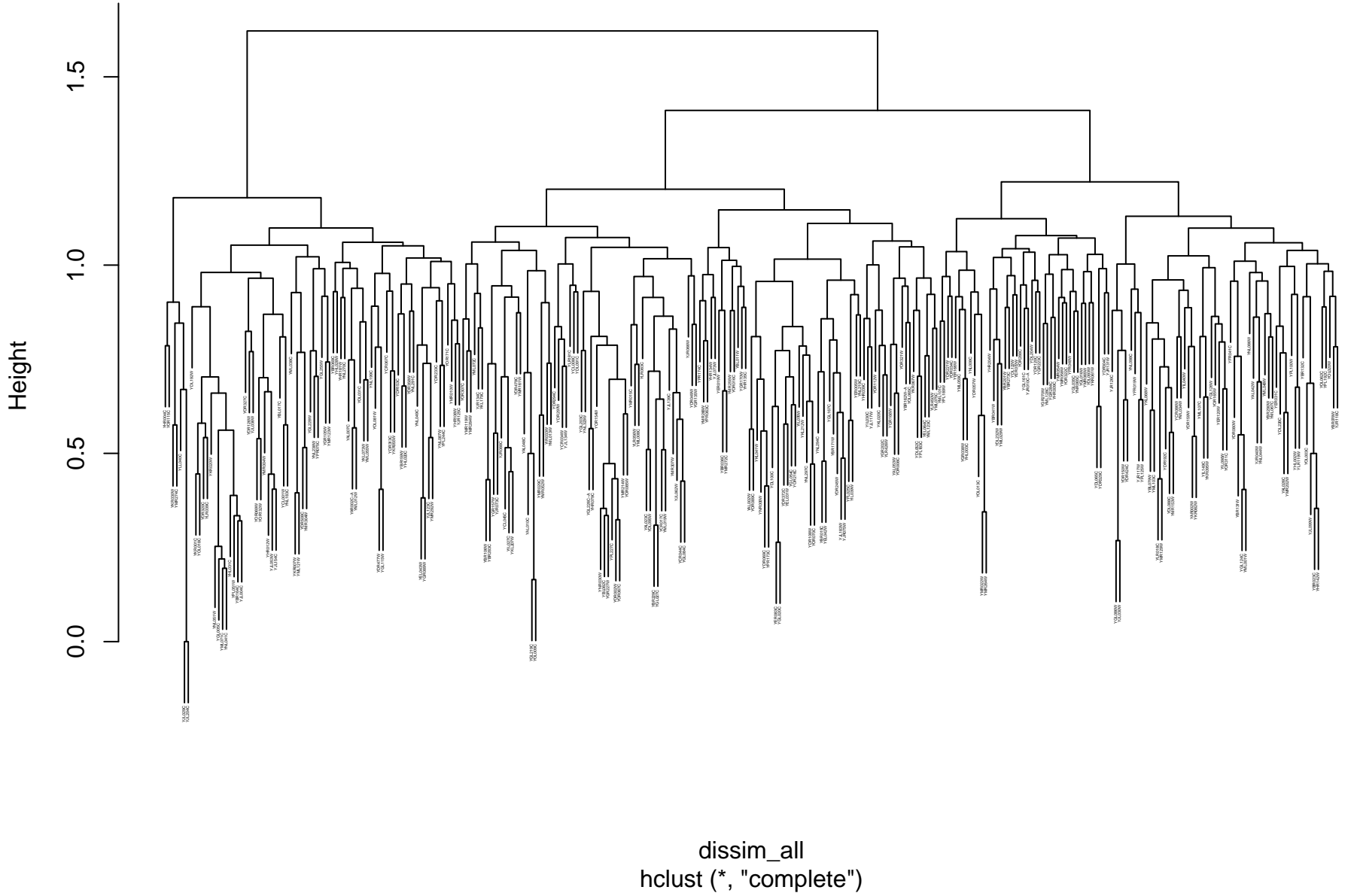
transcription factor activity, protein binding_GO_pearson_complete



cytoplasmic vesicle_GO_pearson_complete

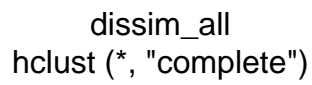


endomembrane system_GO_pearson_complete

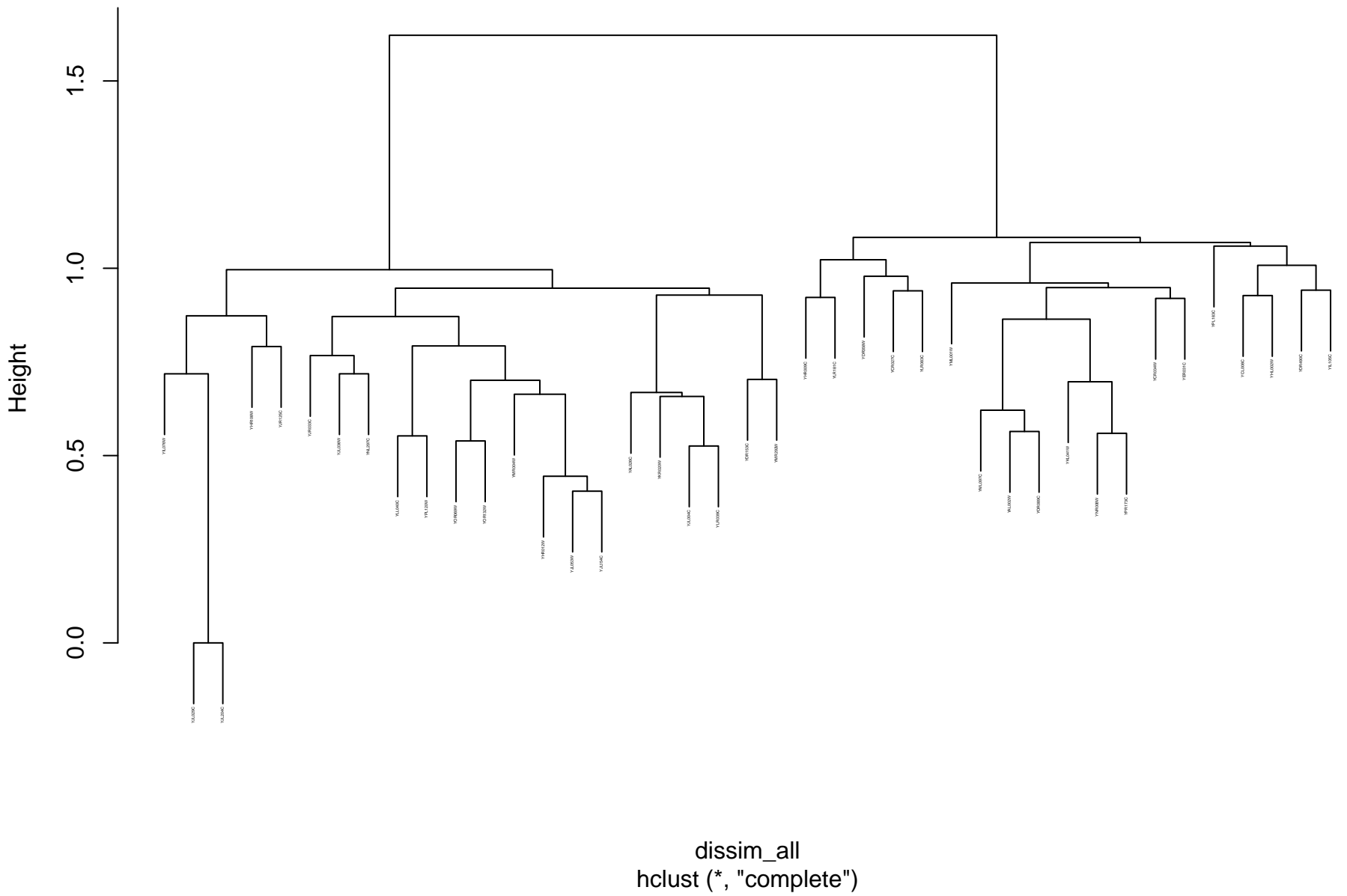


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dissim_all
hclust (*, "complete")
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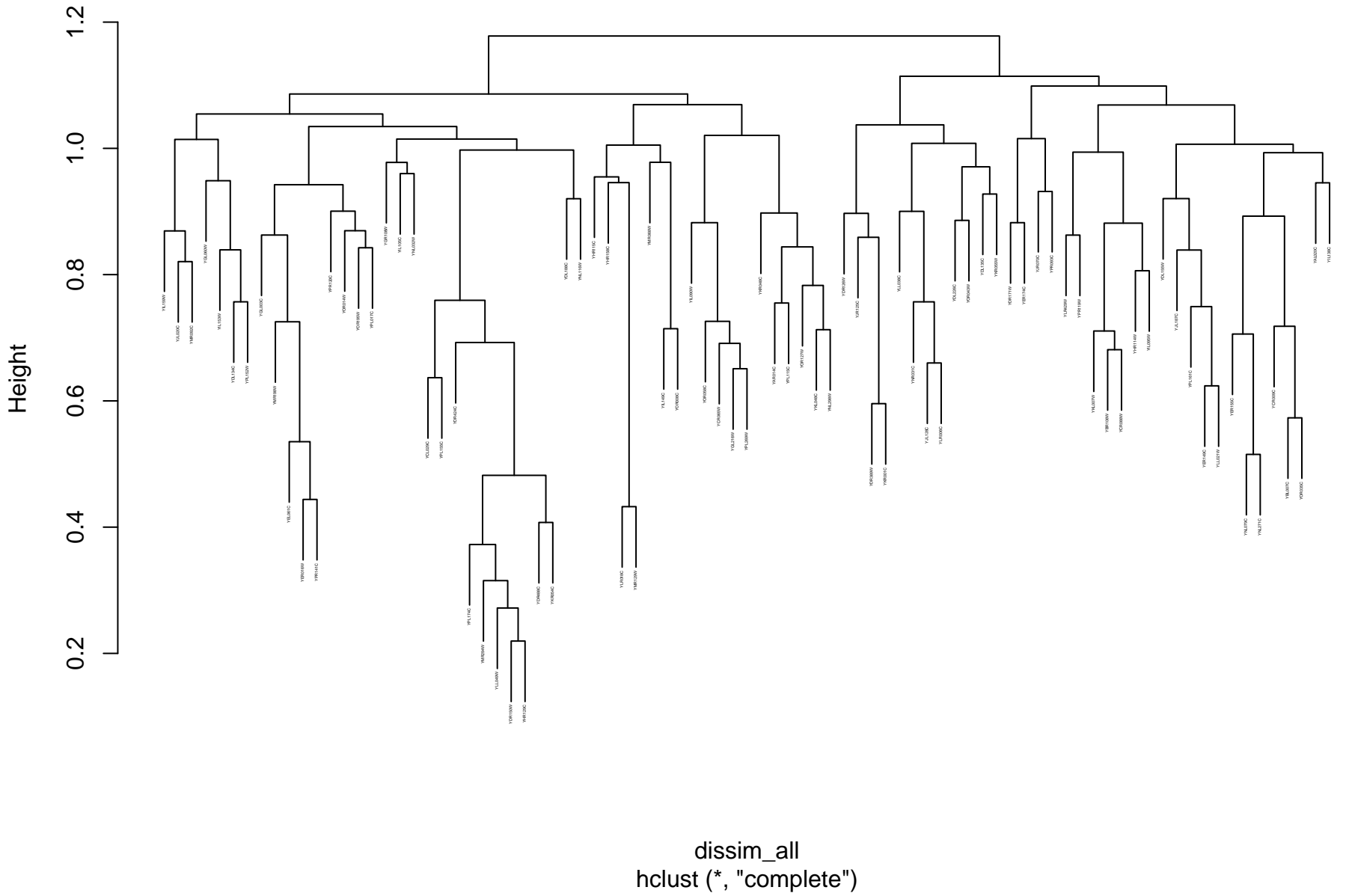
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dissim_all
hclust (*, "complete")
```



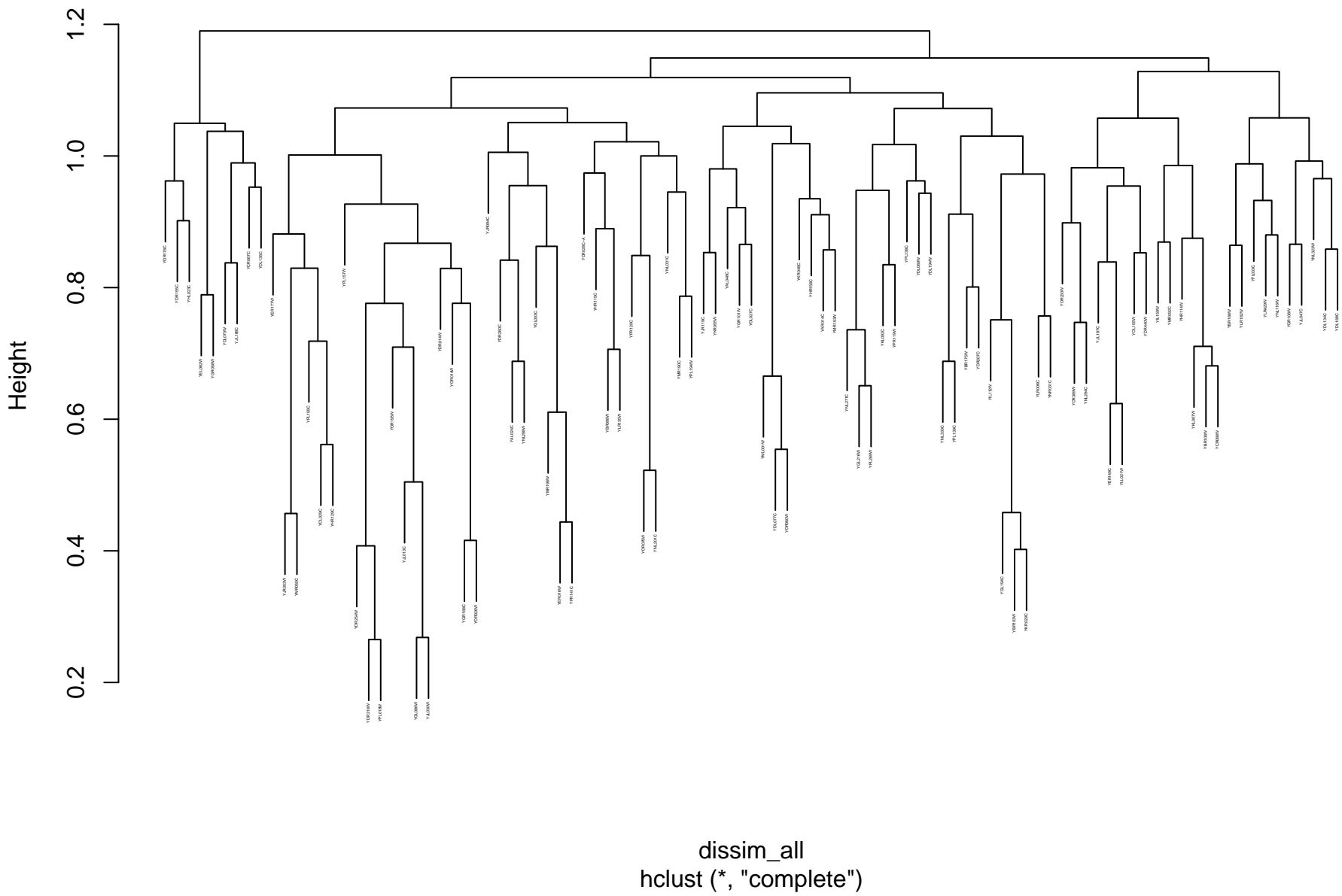
endosomal transport_GO_pearson_complete



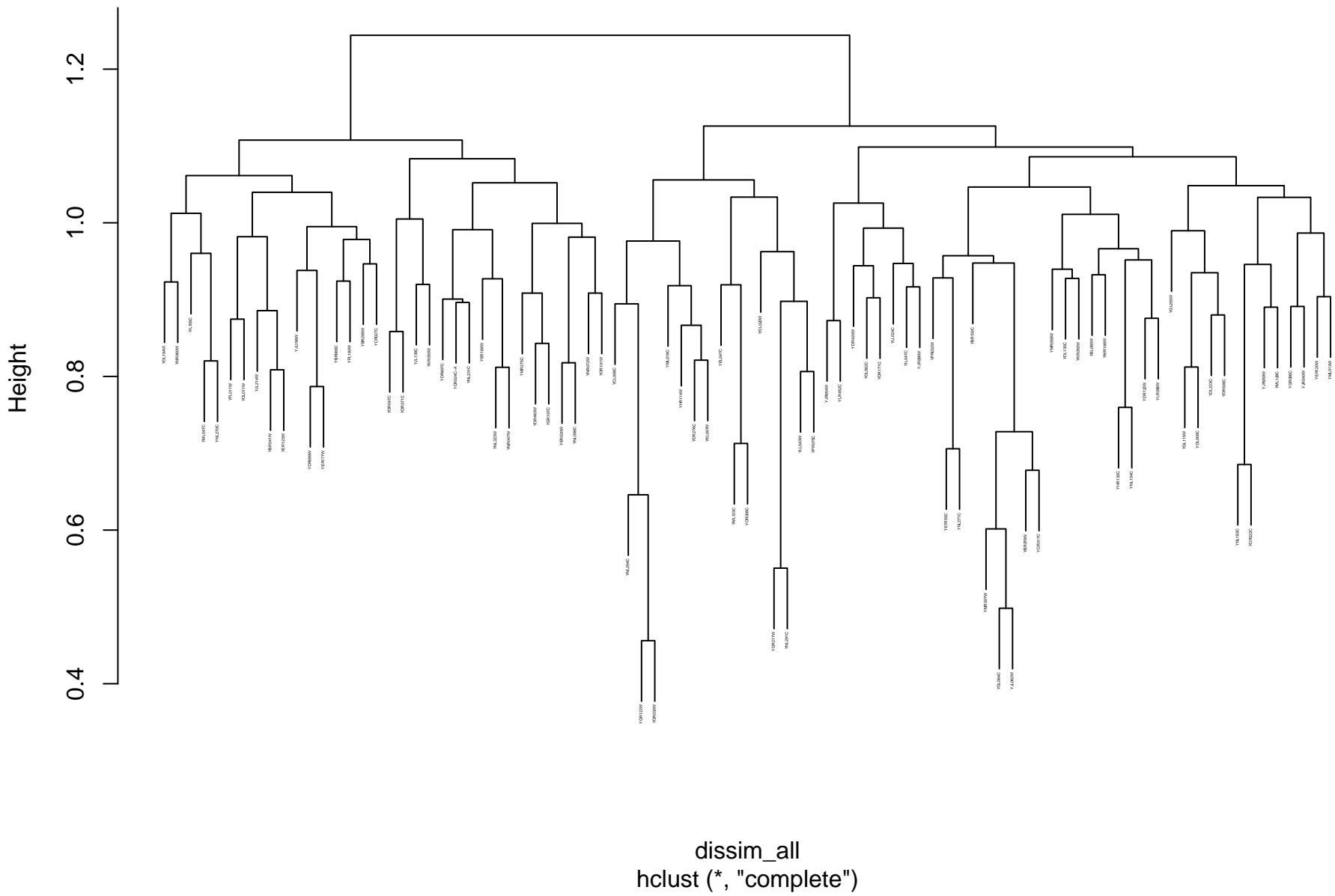
cytoskeleton organization_GO_pearson_complete



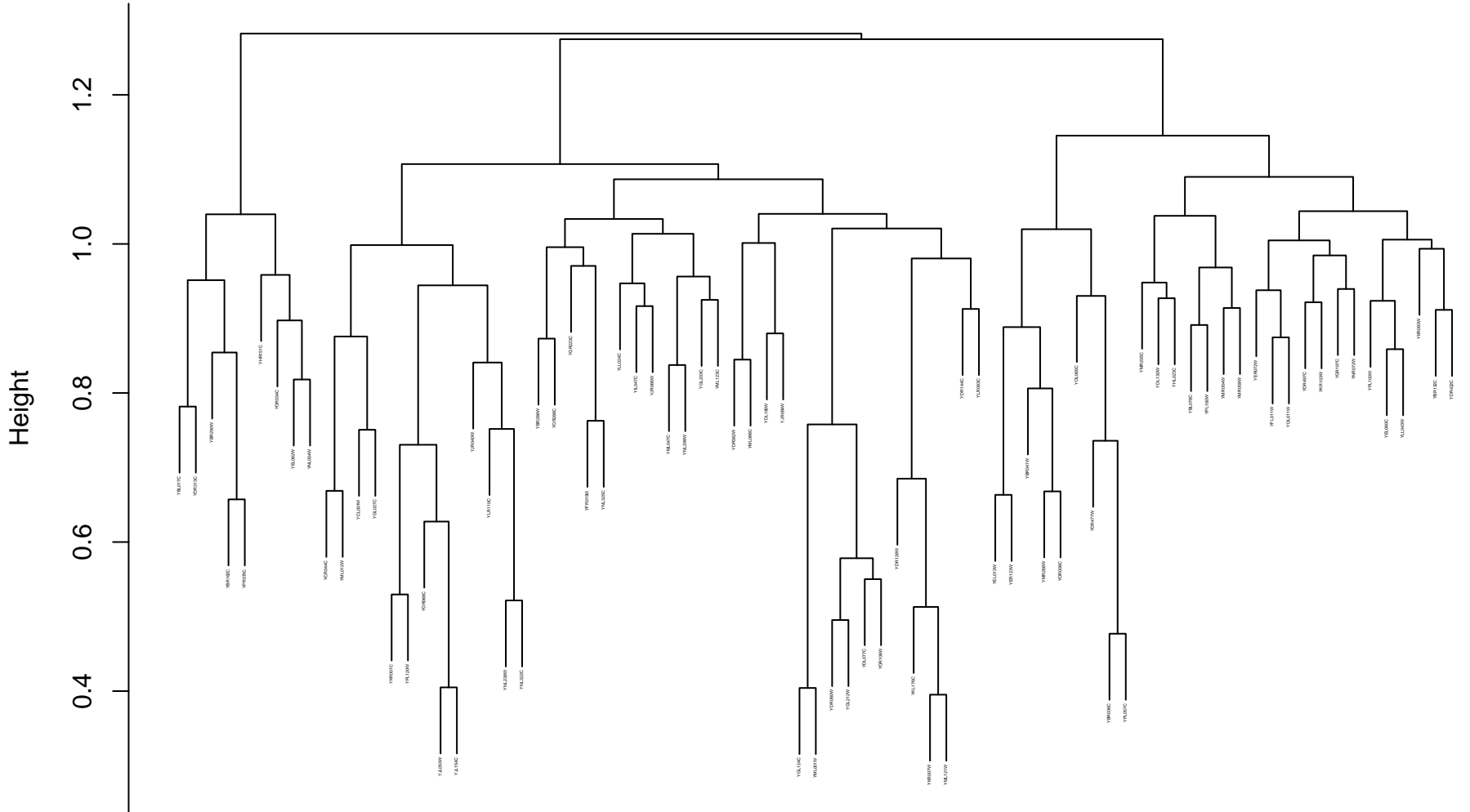
regulation of organelle organization_GO_pearson_complete



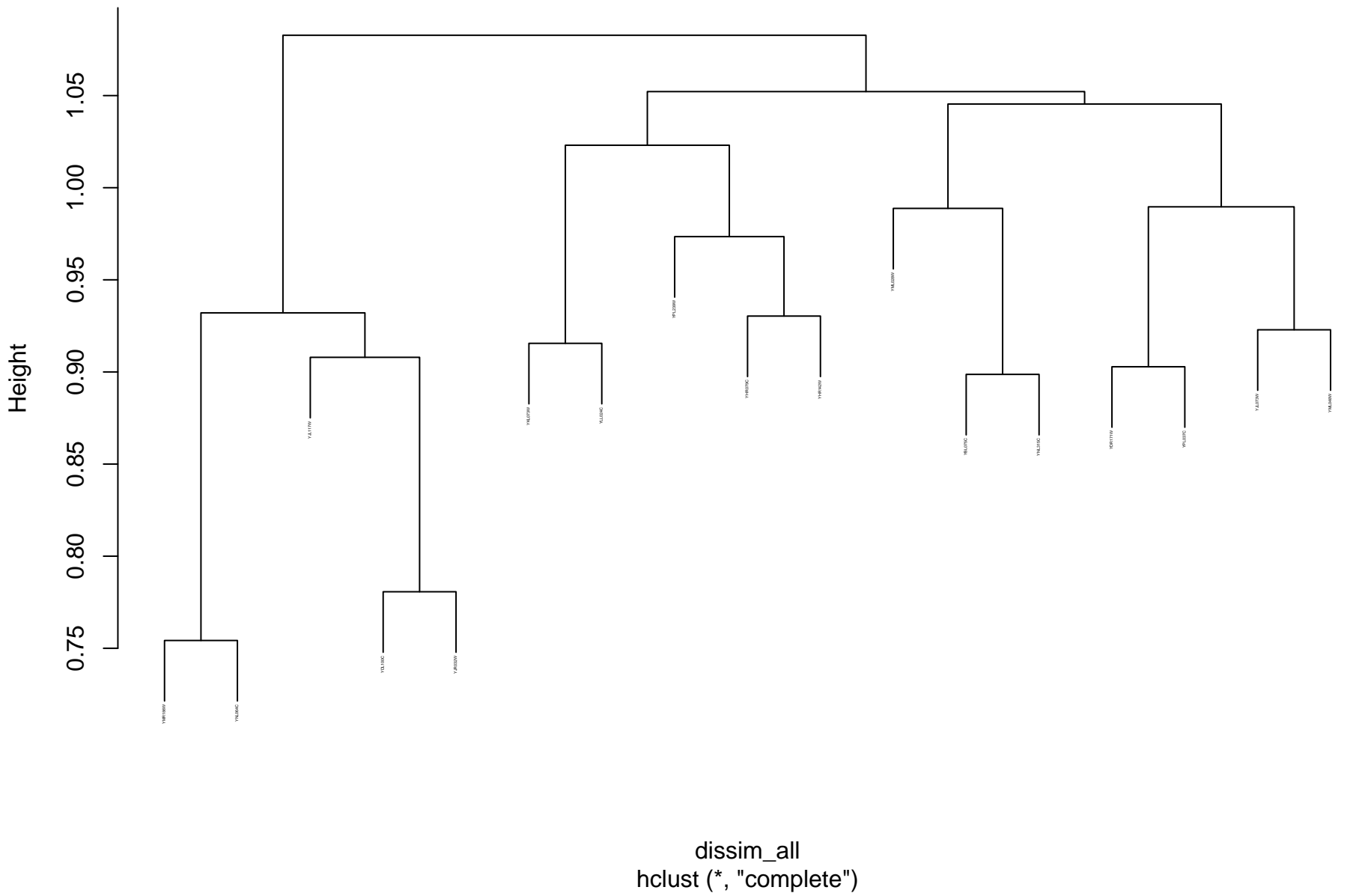
plasma membrane_GO_pearson_complete



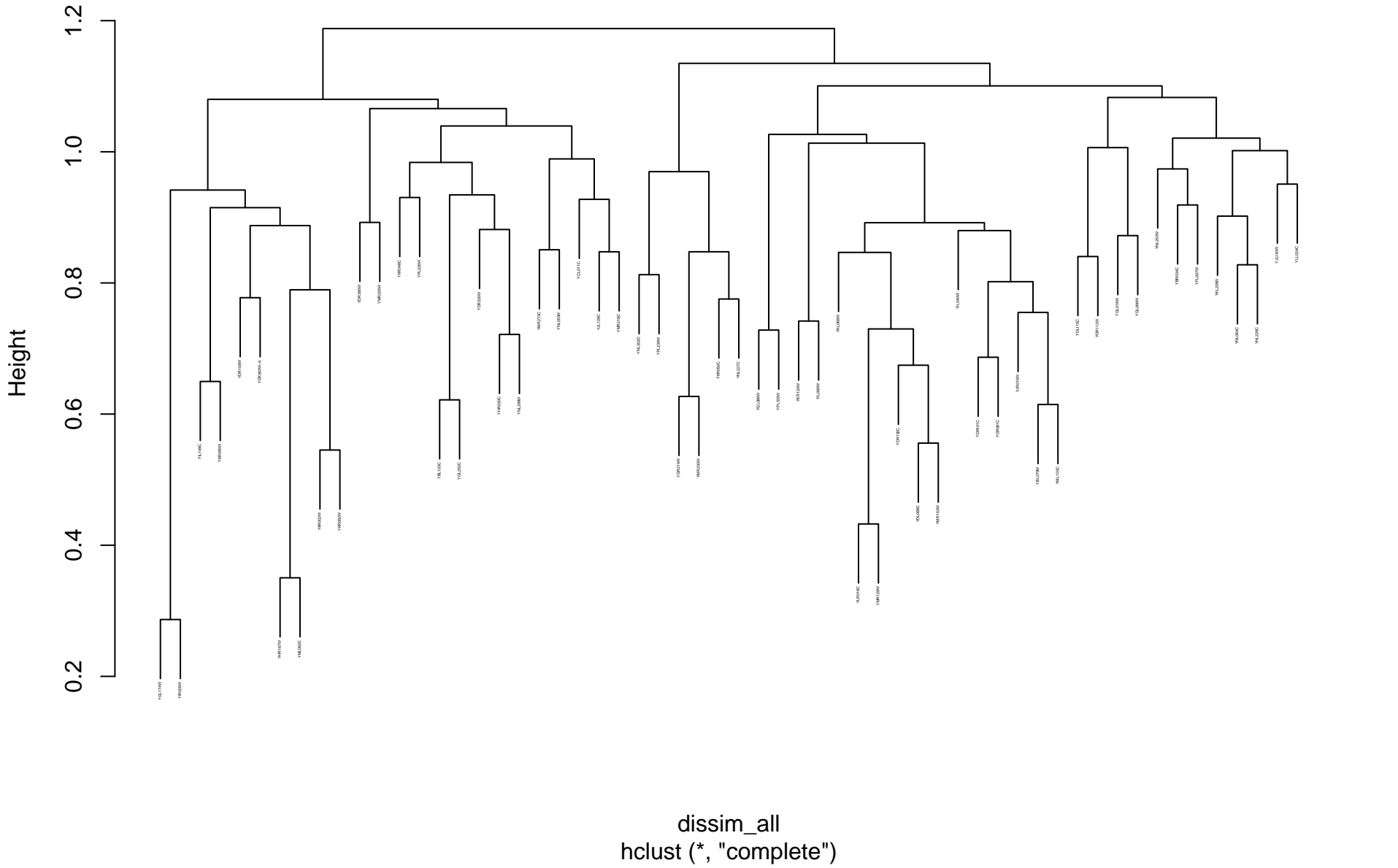
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dissim_all
hclust (*, "complete")
```



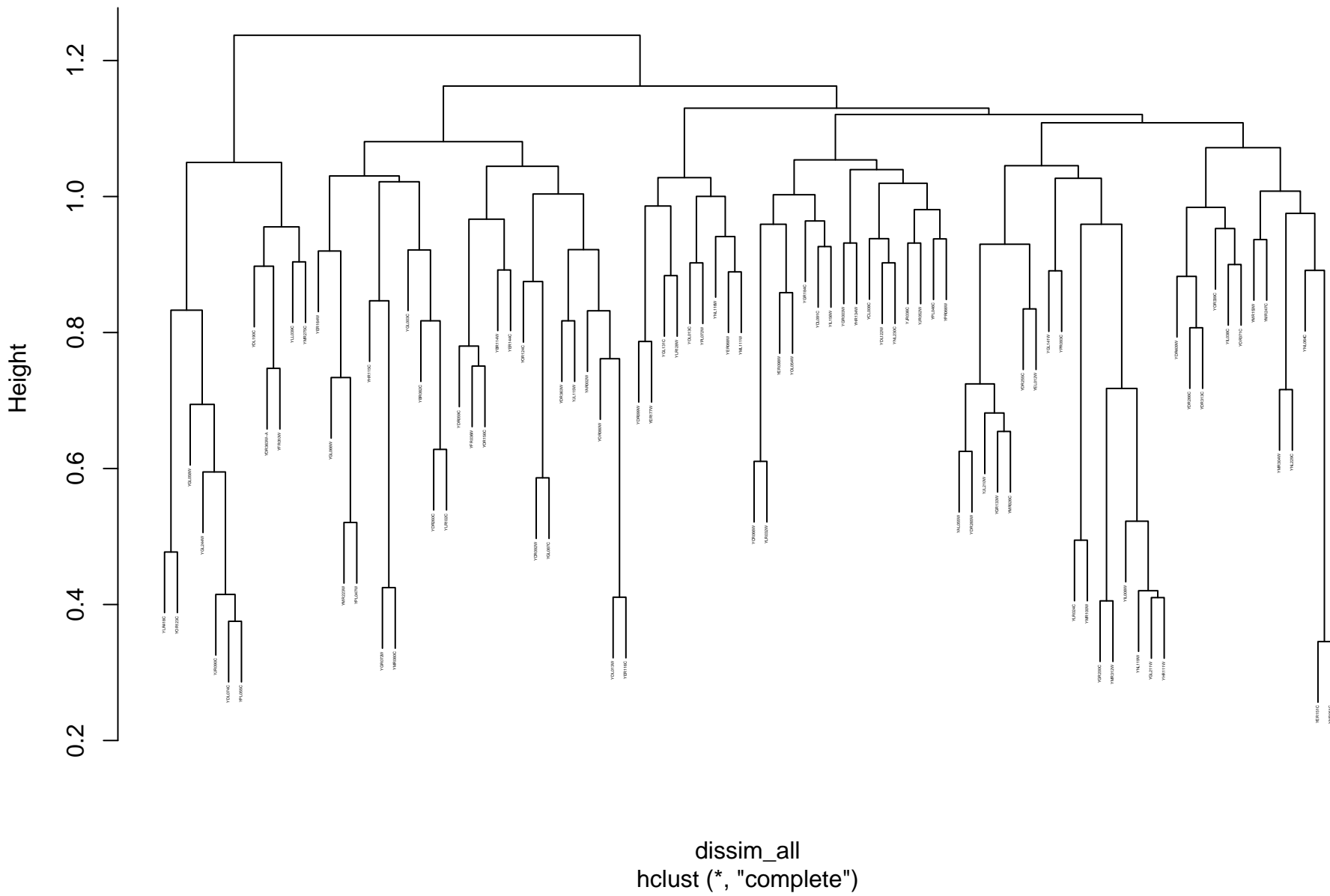
unfolded protein binding_GO_pearson_complete



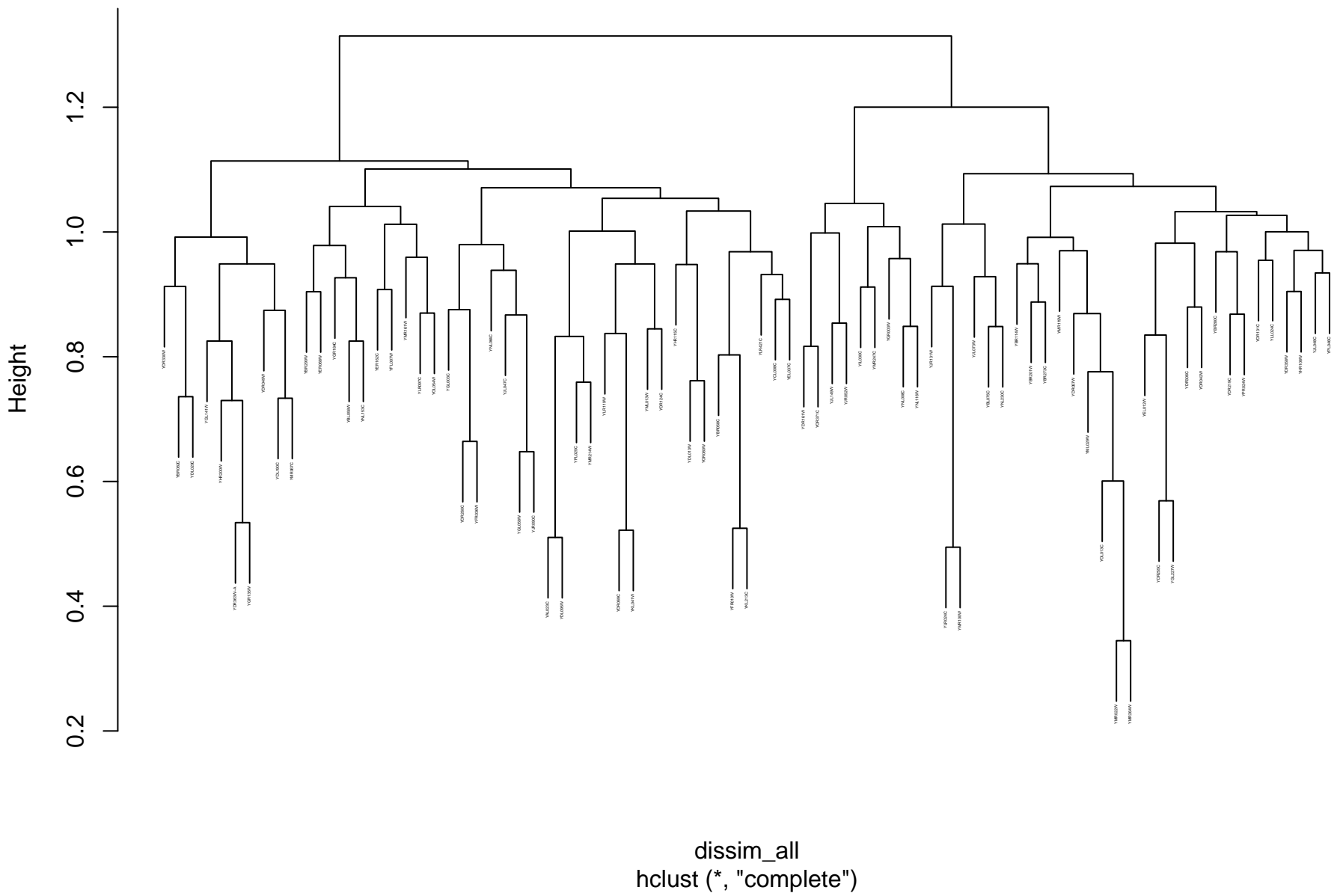
nuclear transport_GO_pearson_complete



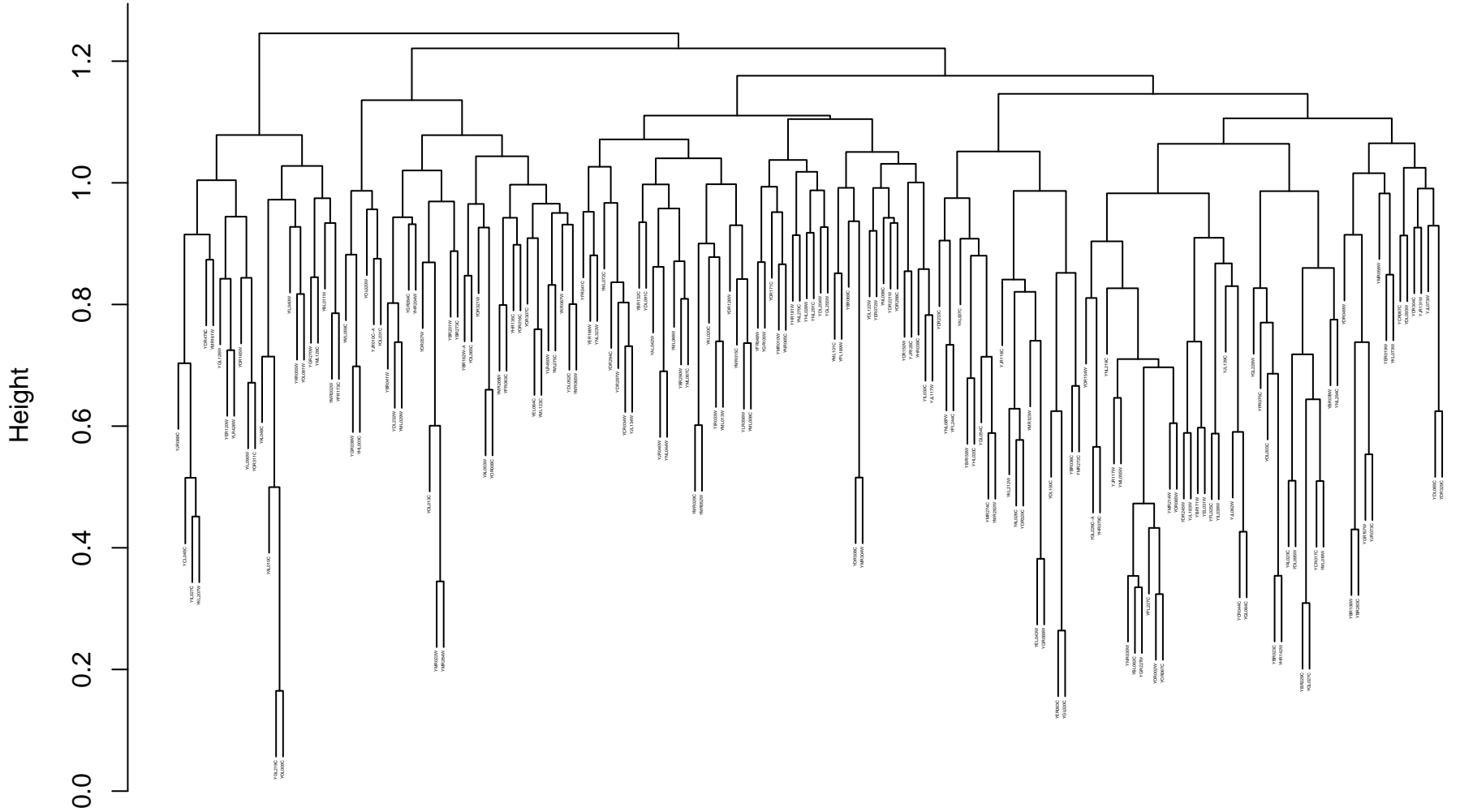
protein modification by small protein conjugation or removal_GO_pearson_complete



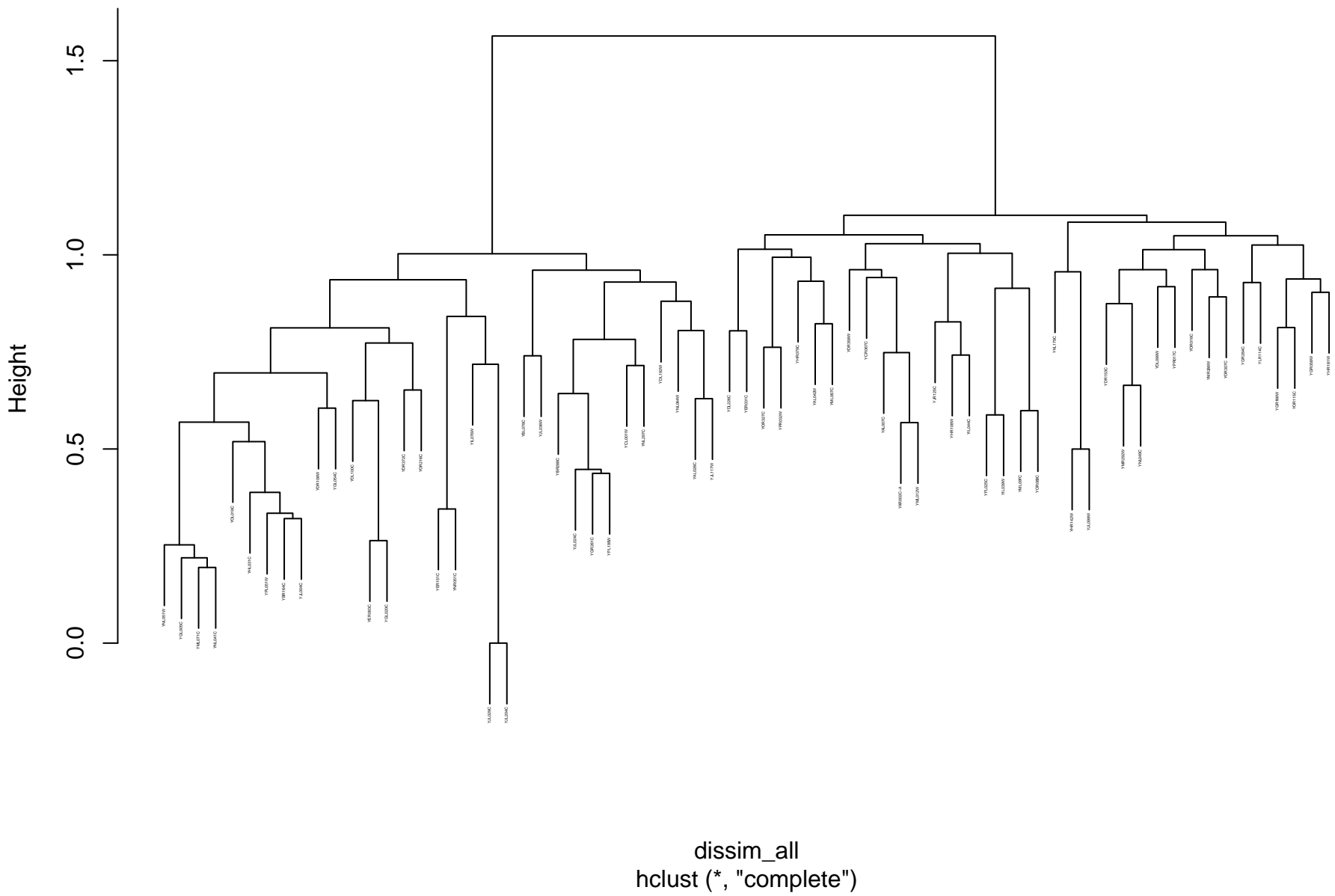
proteolysis involved in cellular protein catabolic process_GO_pearson_complete



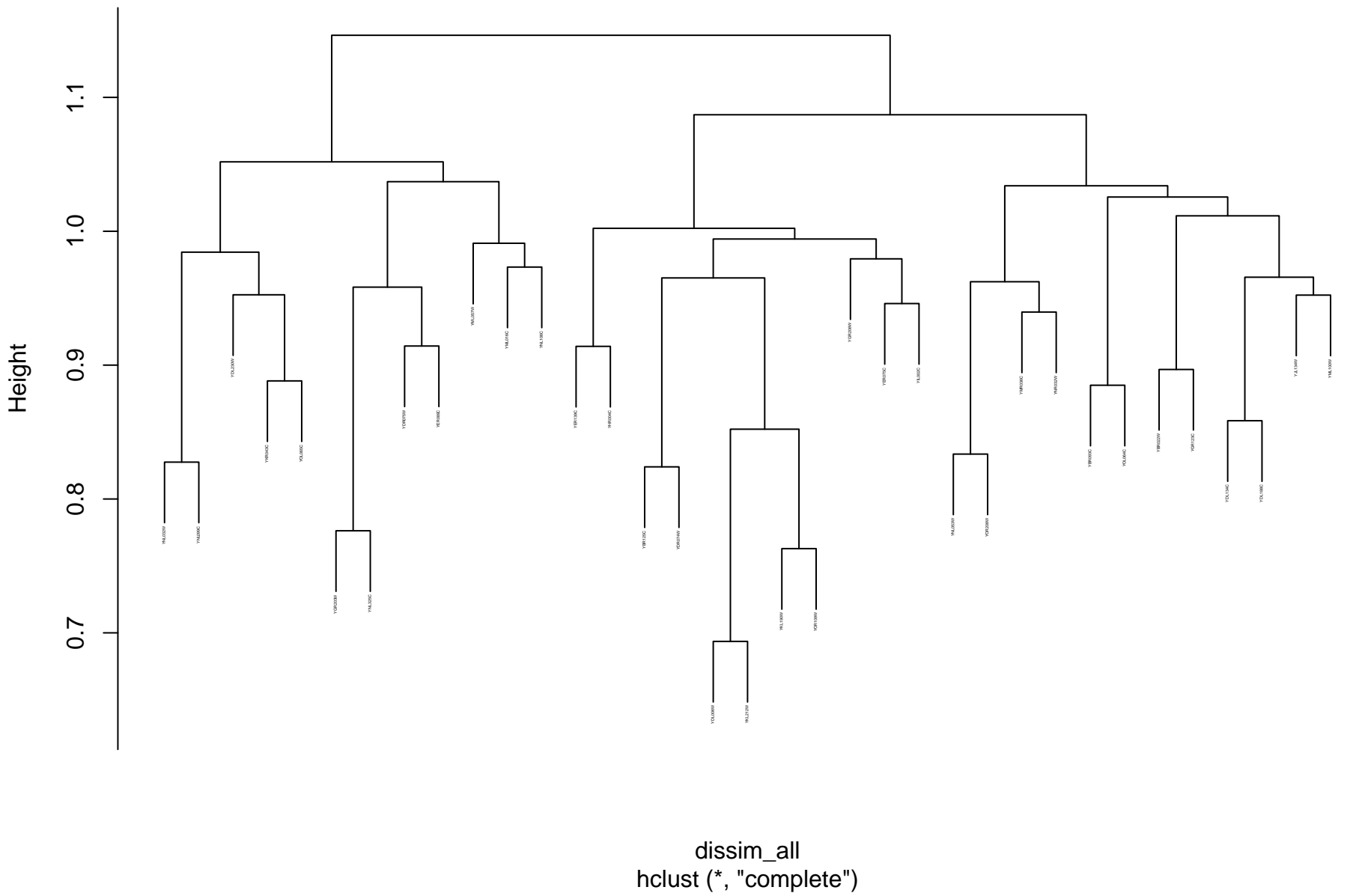
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dissim_all
hclust (*, "complete")
```



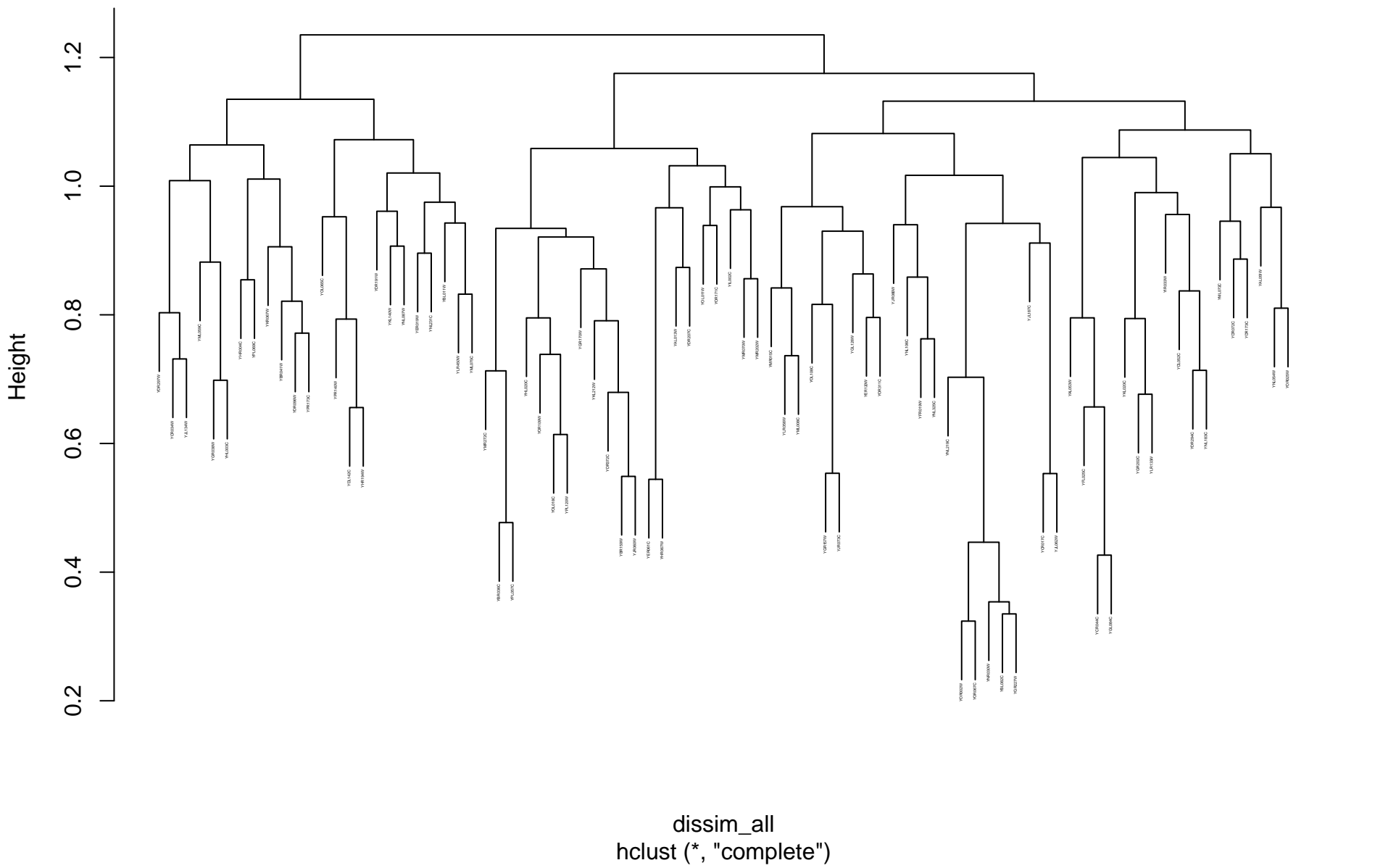
Golgi vesicle transport_GO_pearson_complete



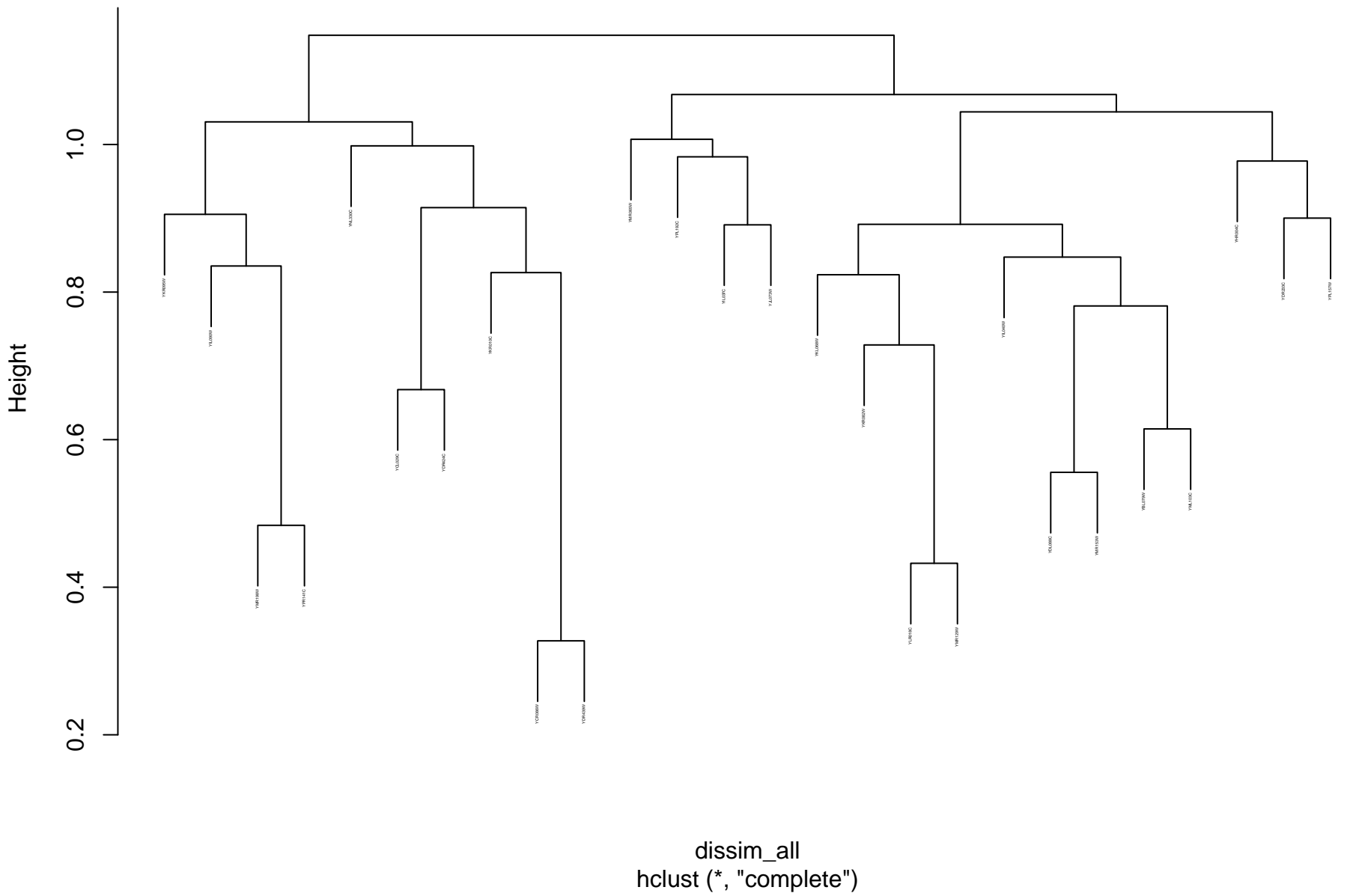
phosphatase activity_GO_pearson_complete



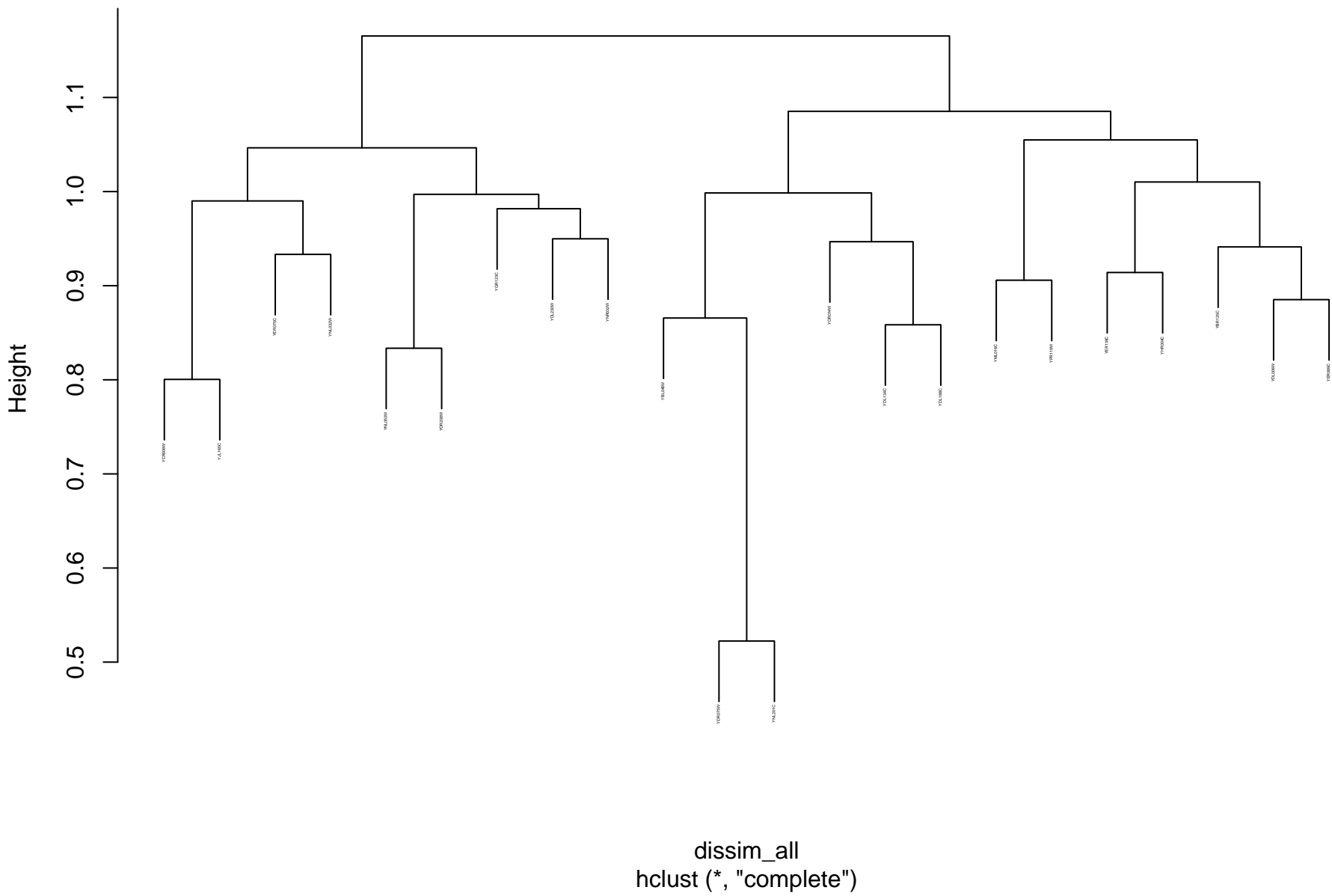
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dissim_all
hclust (*, "complete")
```



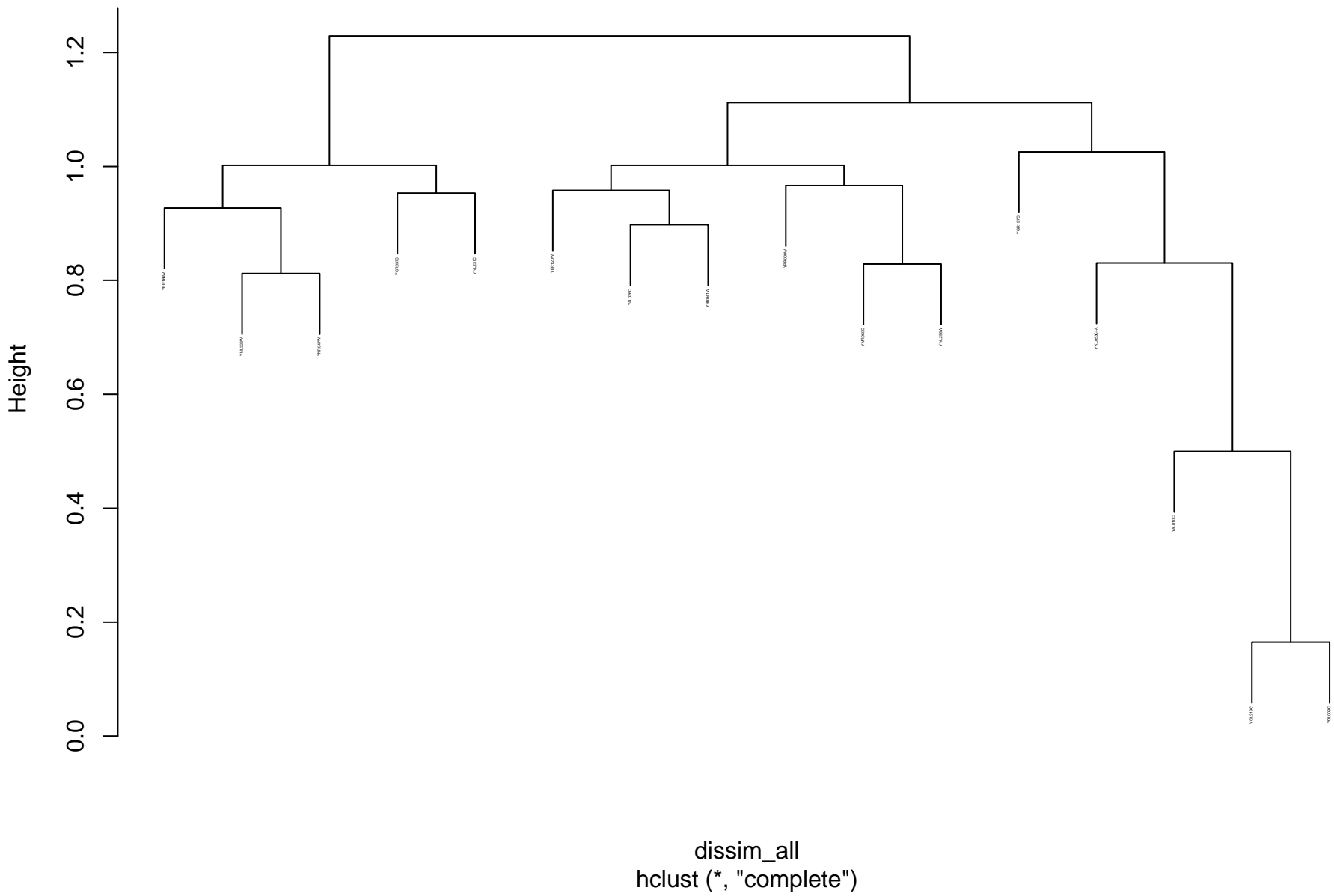
nucleus organization_GO_pearson_complete



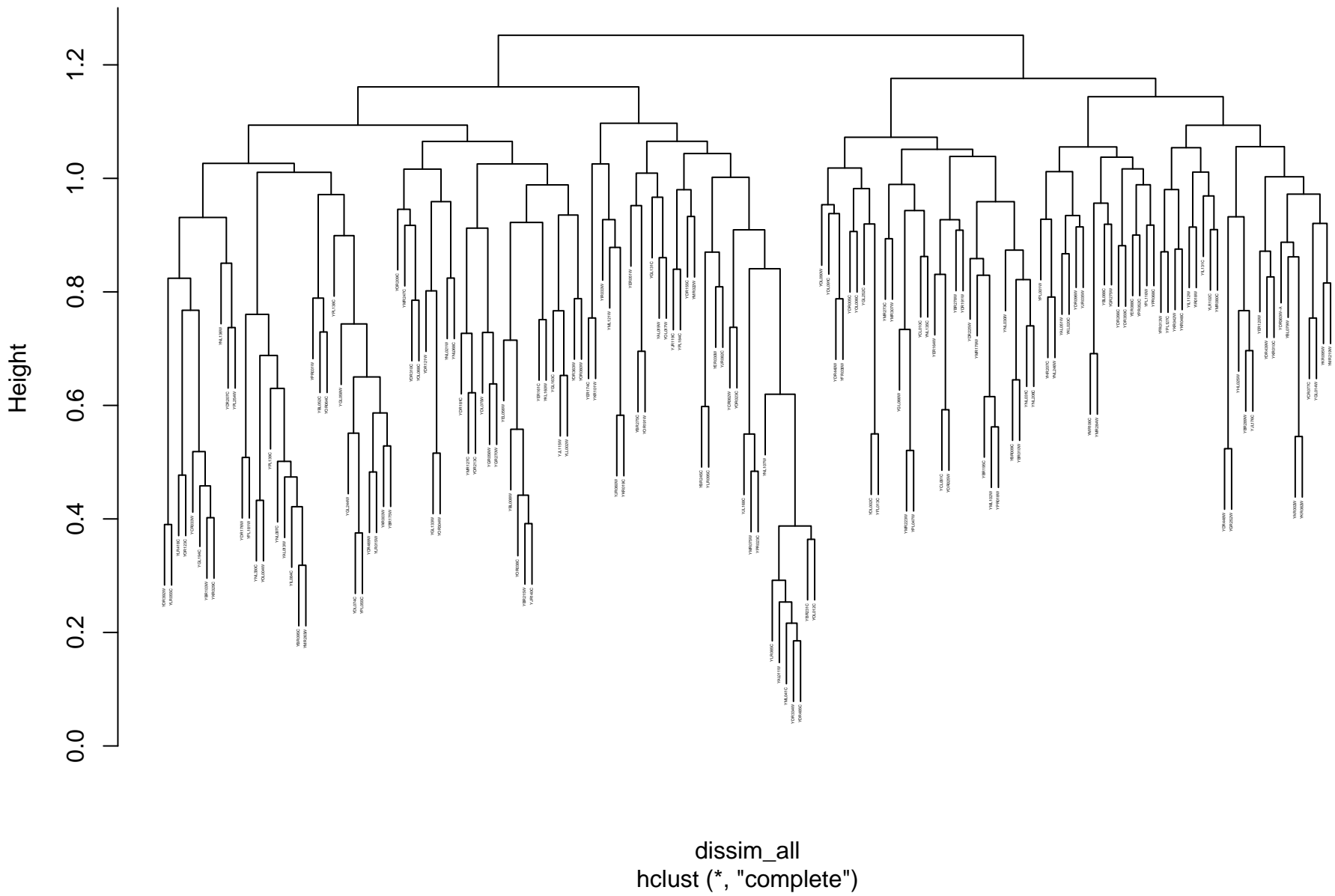
protein dephosphorylation_GO_pearson_complete



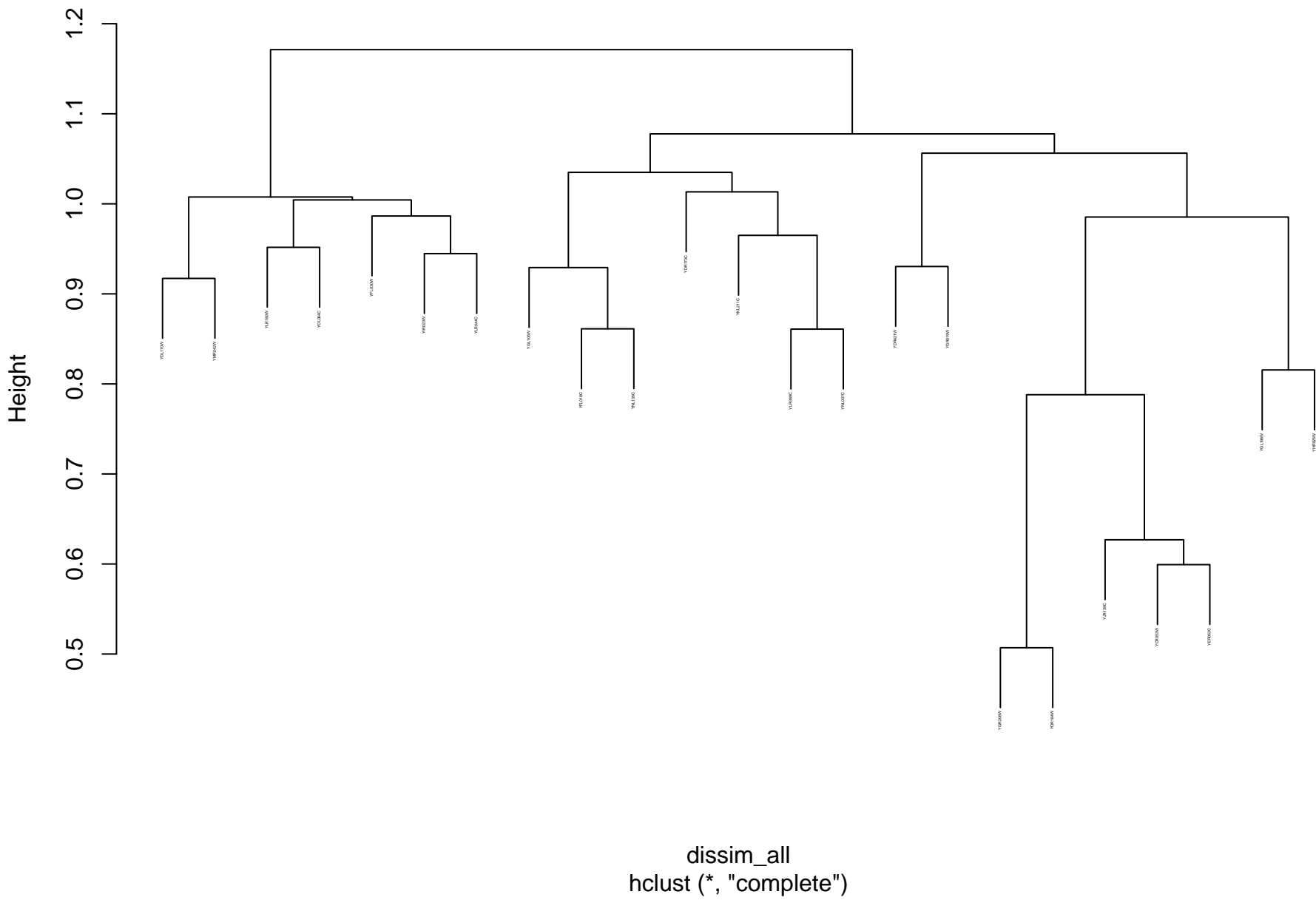
lipid transport_GO_pearson_complete



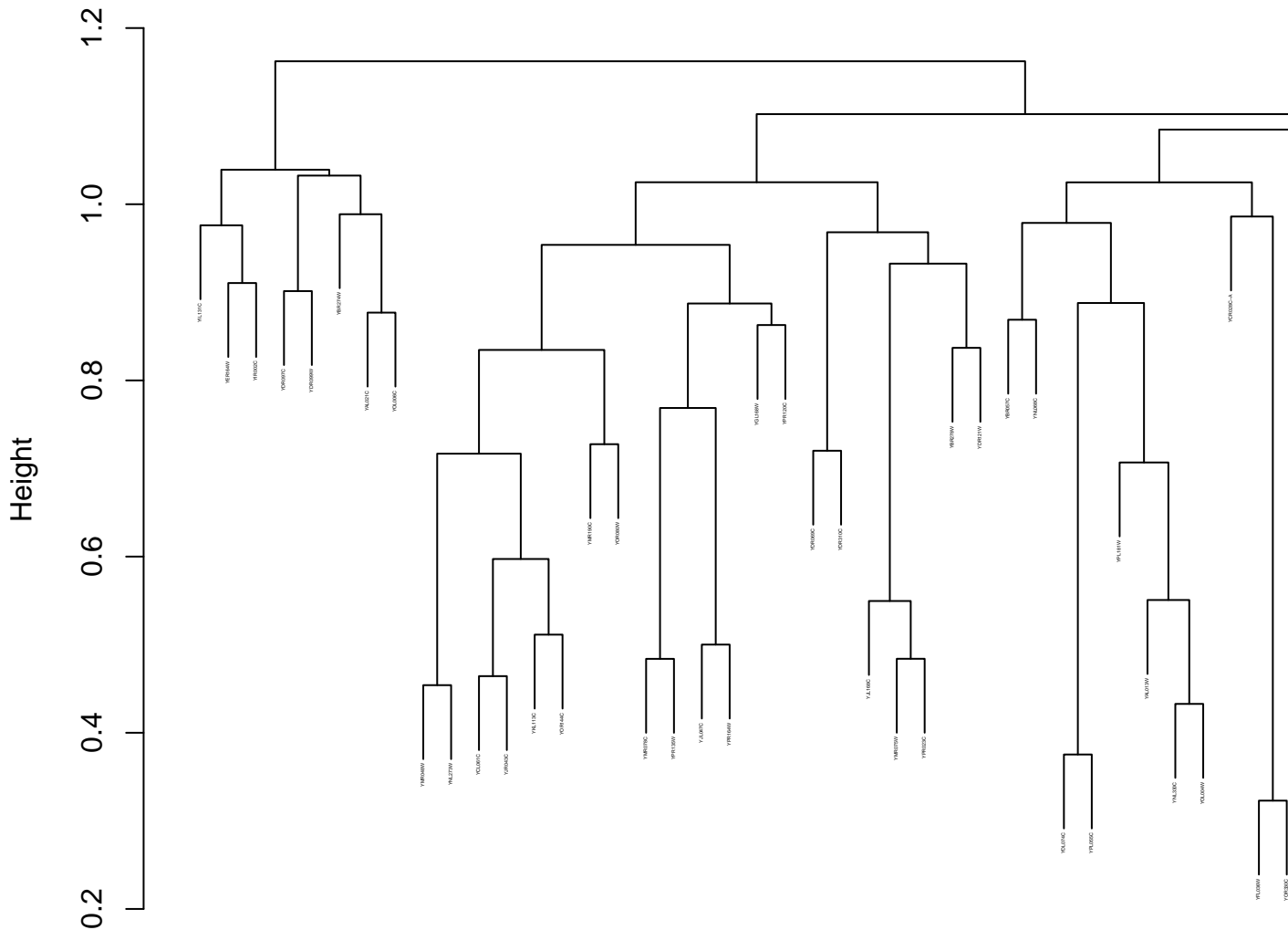
chromatin organization_GO_pearson_complete



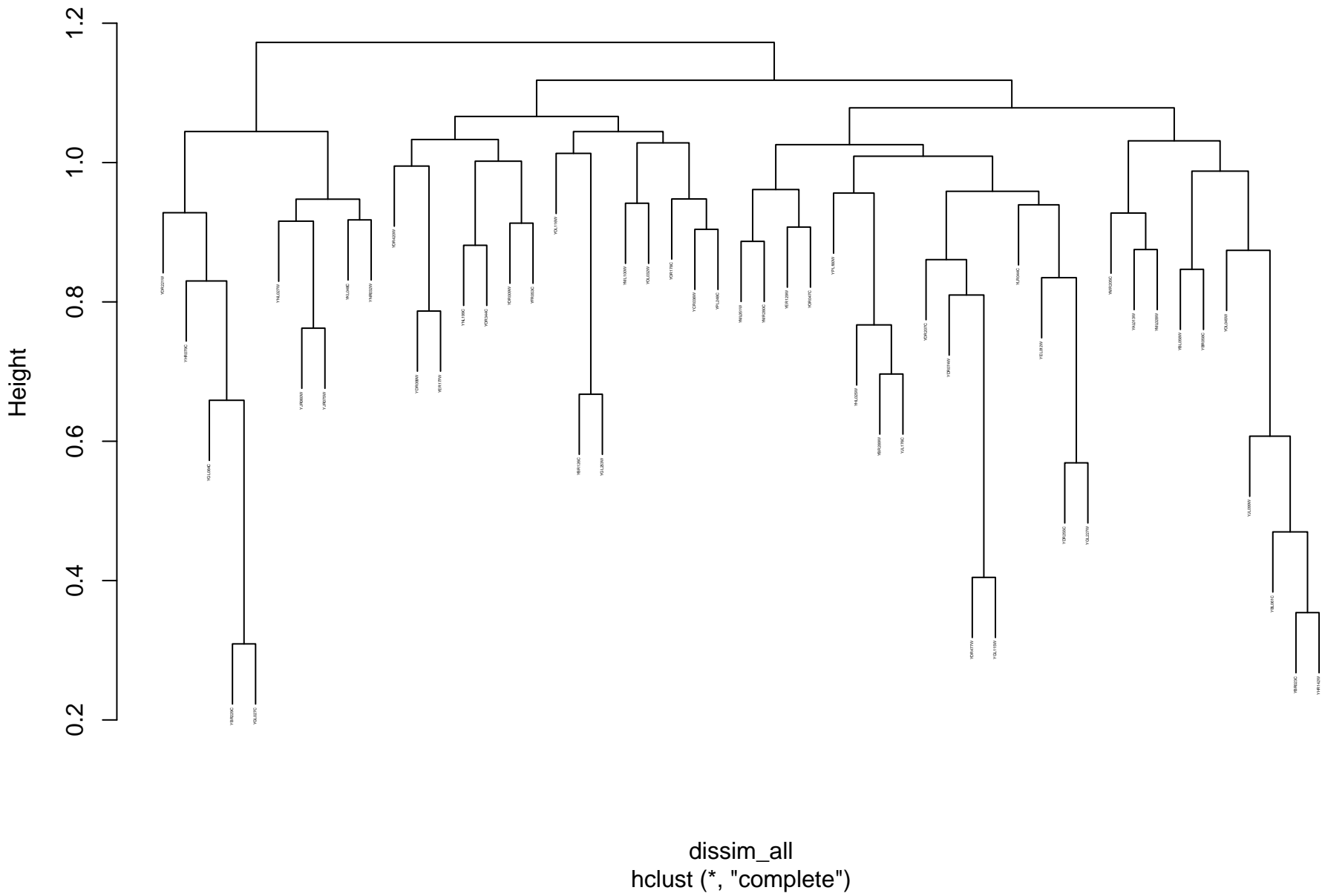
cellular amino acid metabolic process_GO_pearson_complete



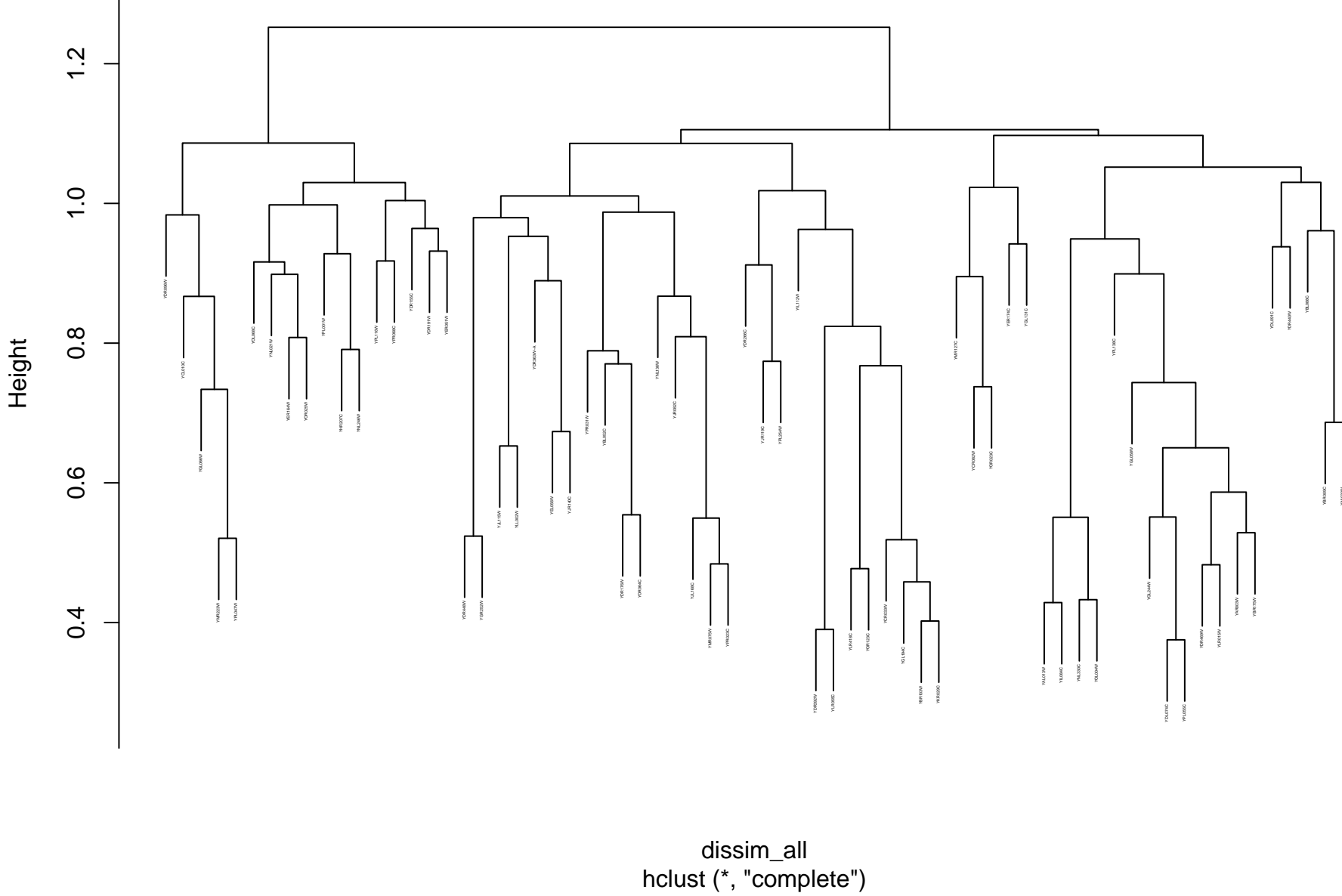
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dissim_all
hclust (*, "complete")
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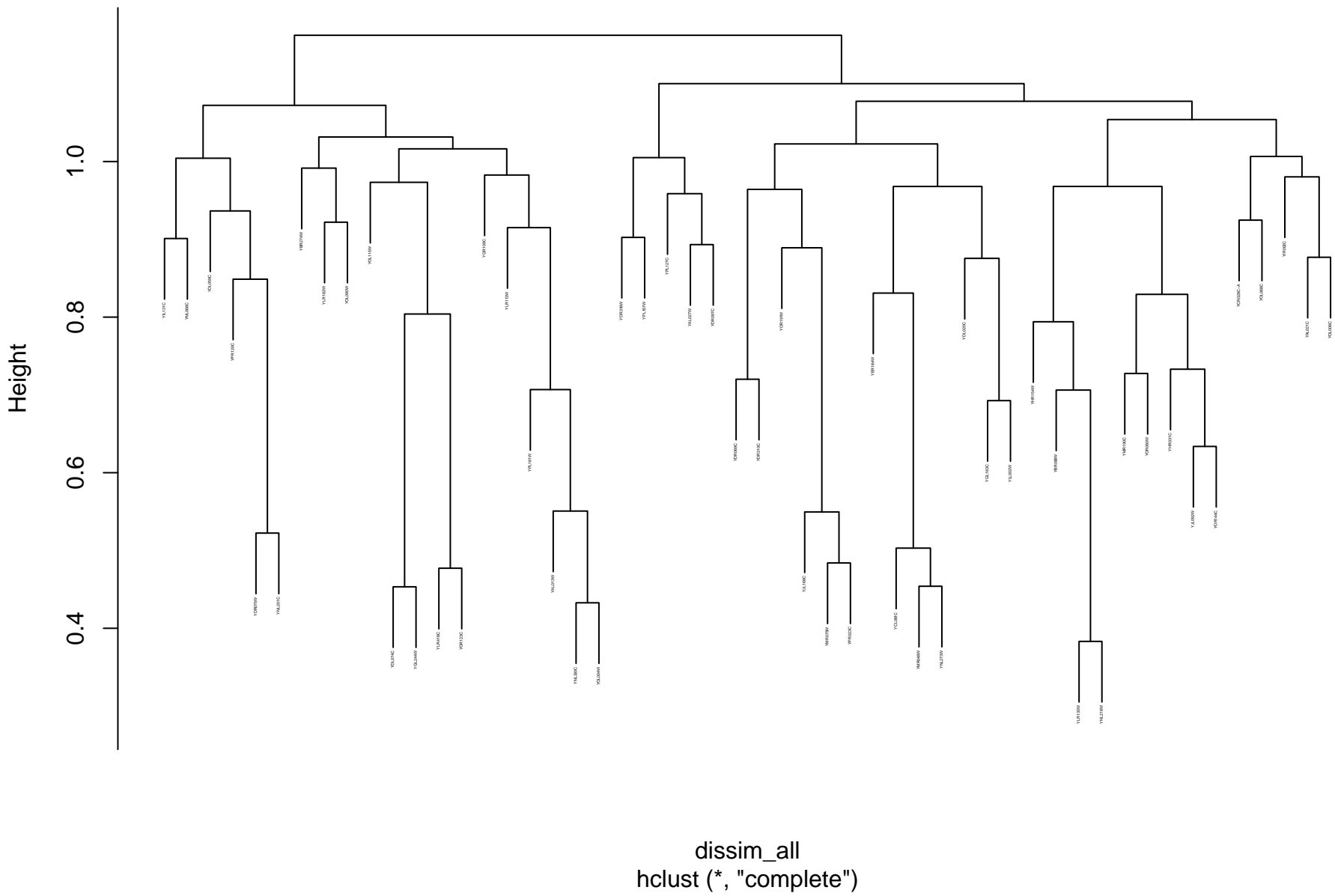
carbohydrate metabolic process_GO_pearson_complete



histone modification_GO_pearson_complete

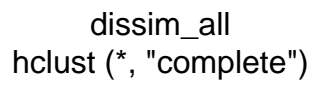


regulation of DNA metabolic process_GO_pearson_complete

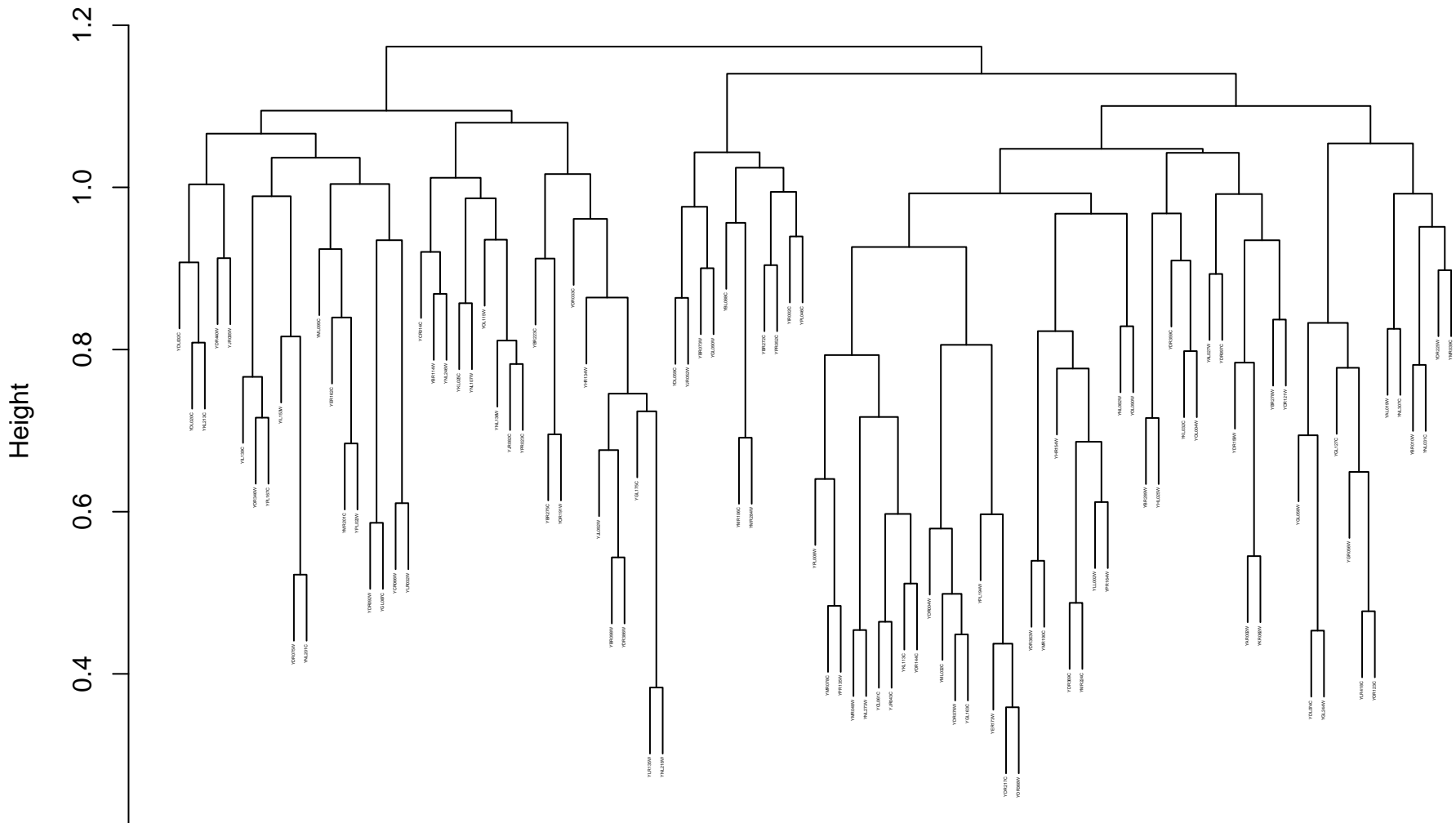


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dissim_all
hclust (*, "complete")
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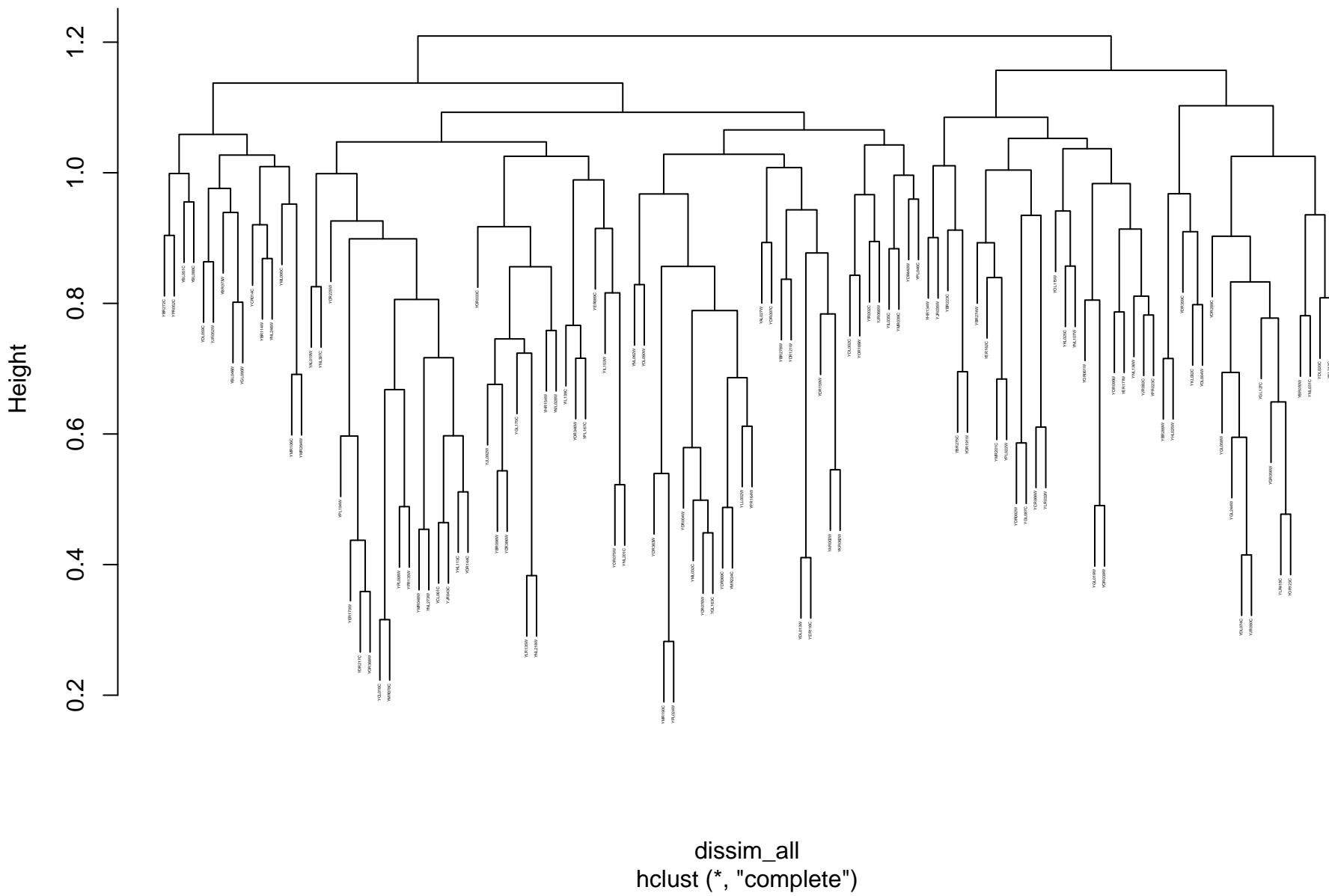
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dissim_all
hclust (*, "complete")
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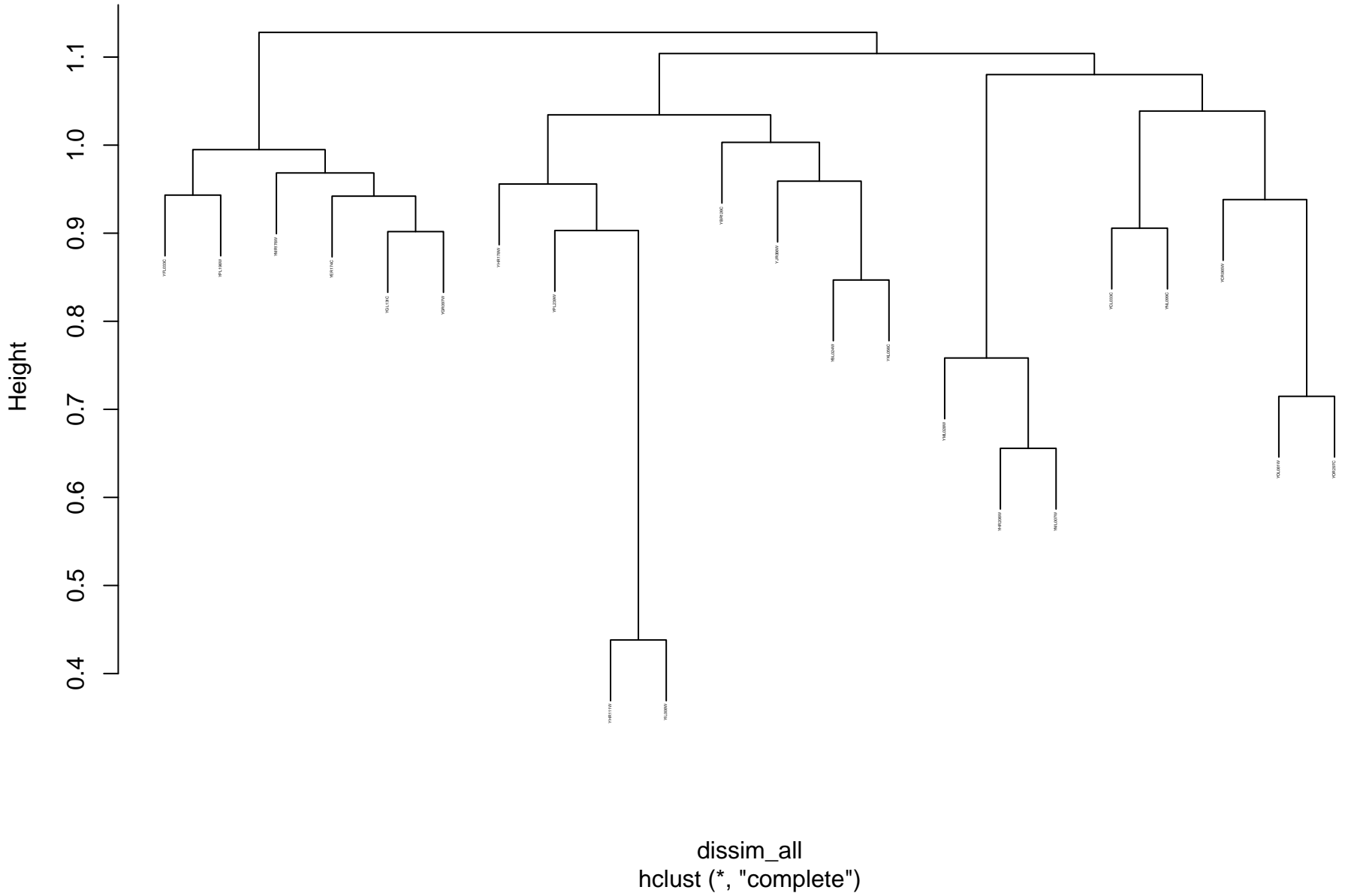


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dissim_all
hclust (*, "complete")
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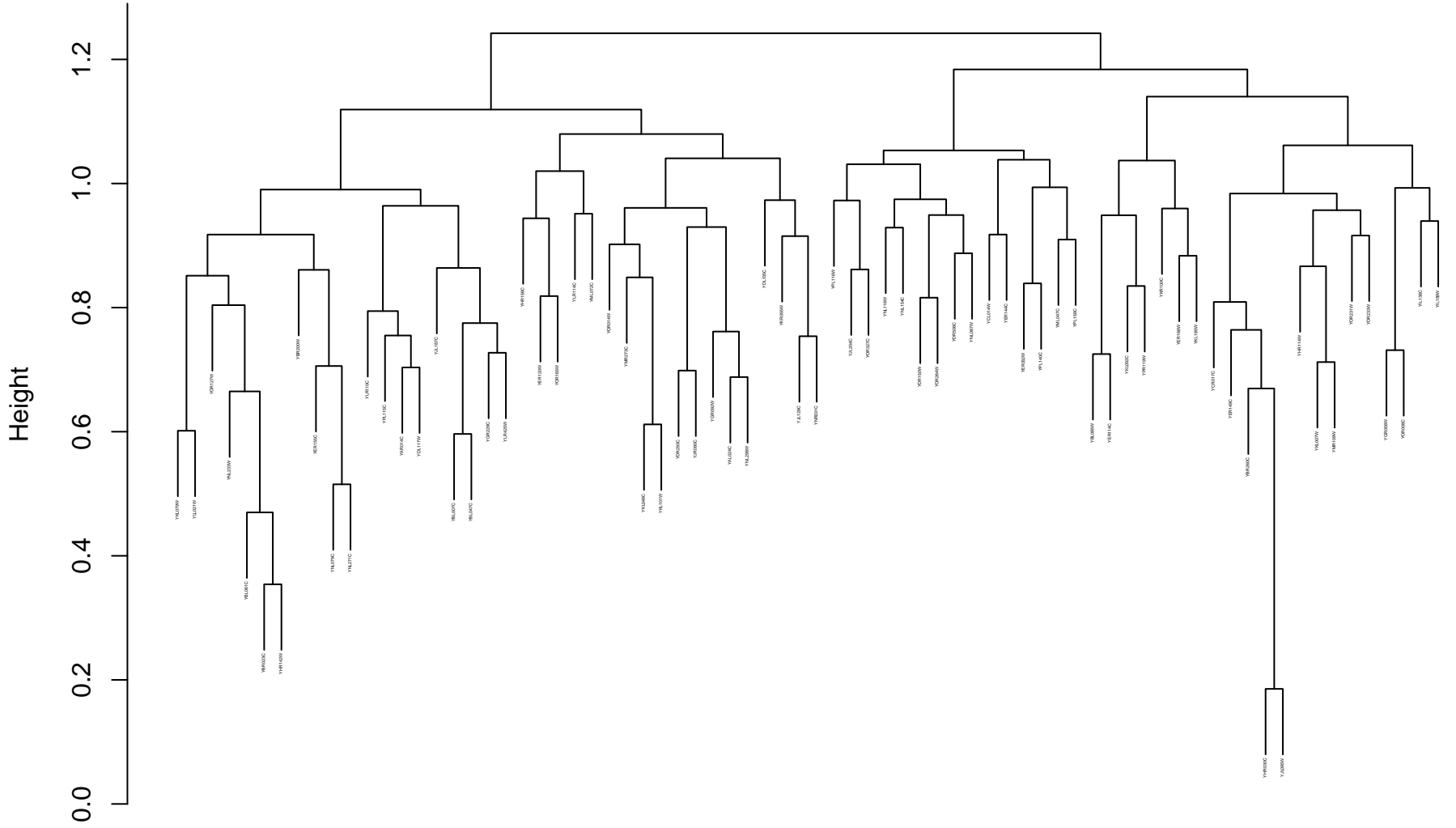


cellular response to DNA damage stimulus_GO_pearson_complete

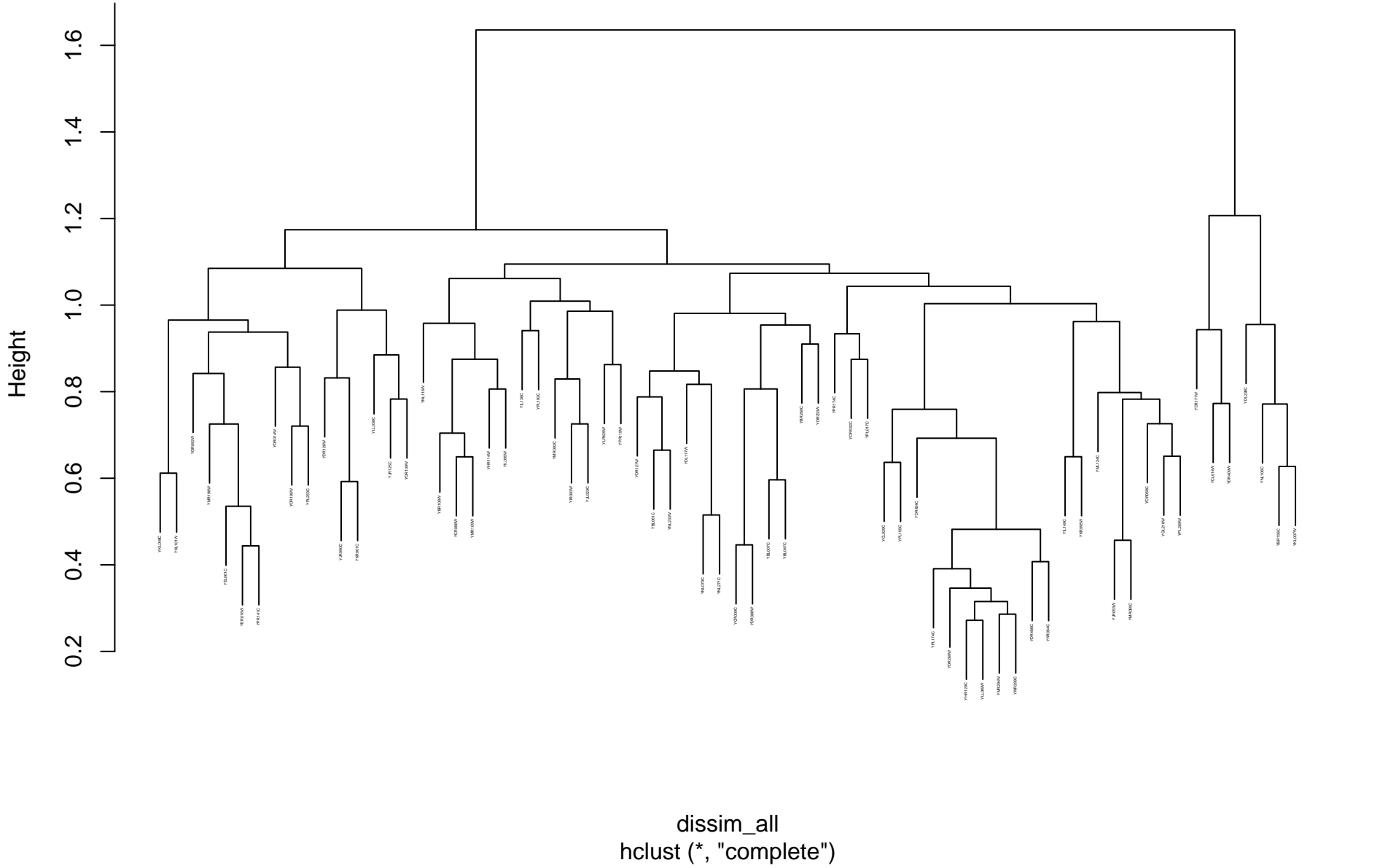


response to oxidative stress_GO_pearson_complete

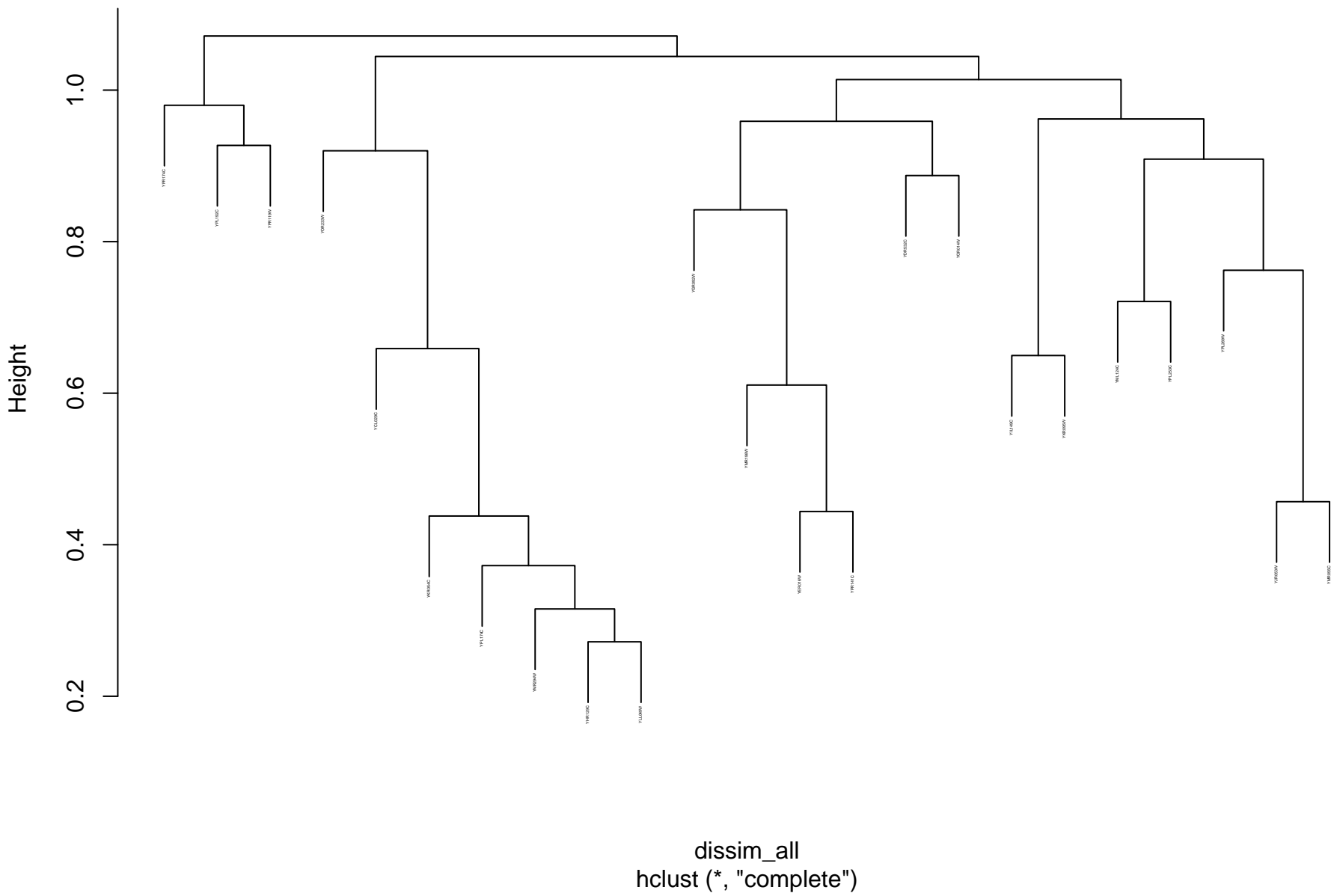
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dissim_all
hclust (*, "complete")
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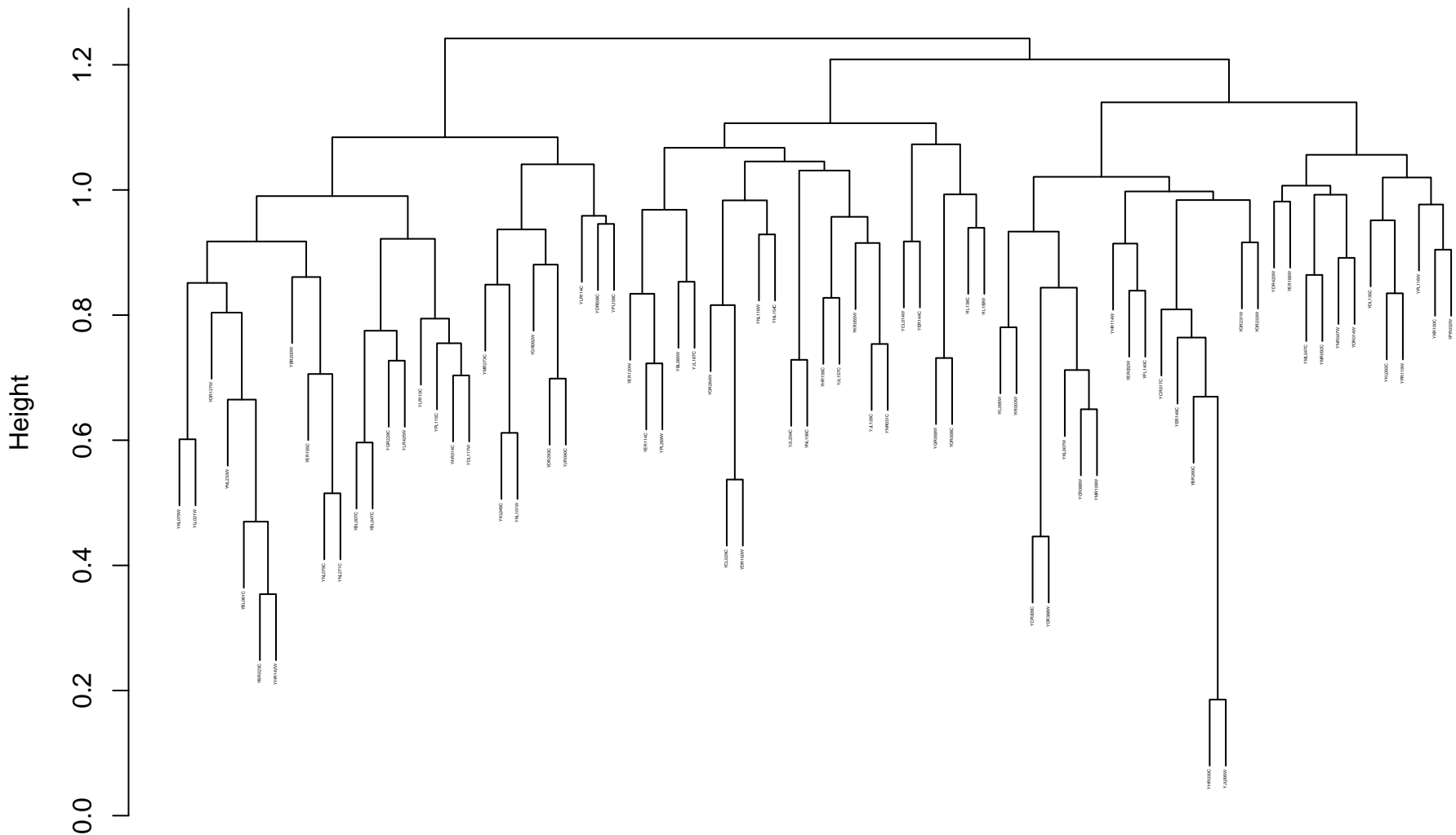

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dissim_all
hclust (*, "complete")
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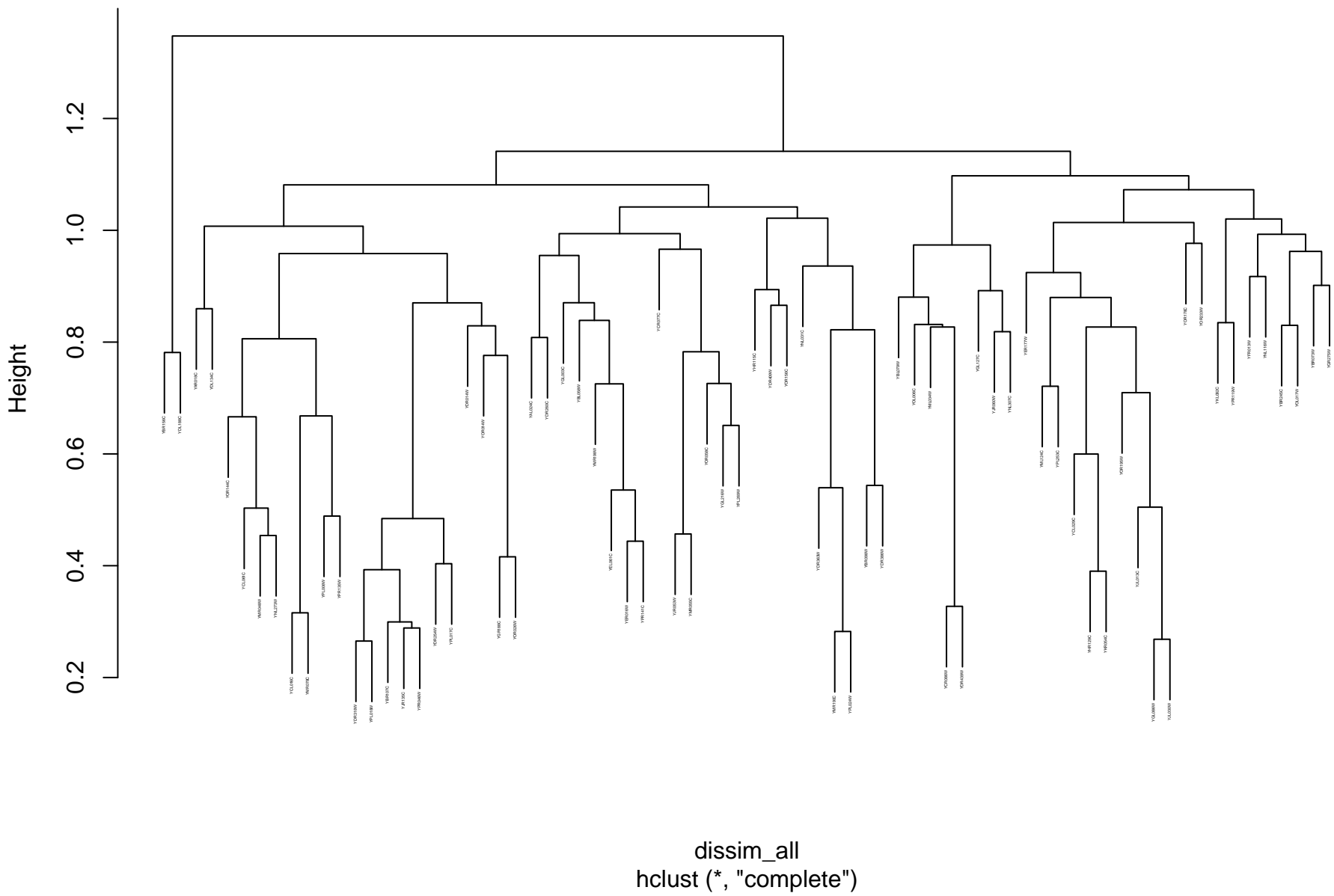
microtubule organizing center_GO_pearson_complete



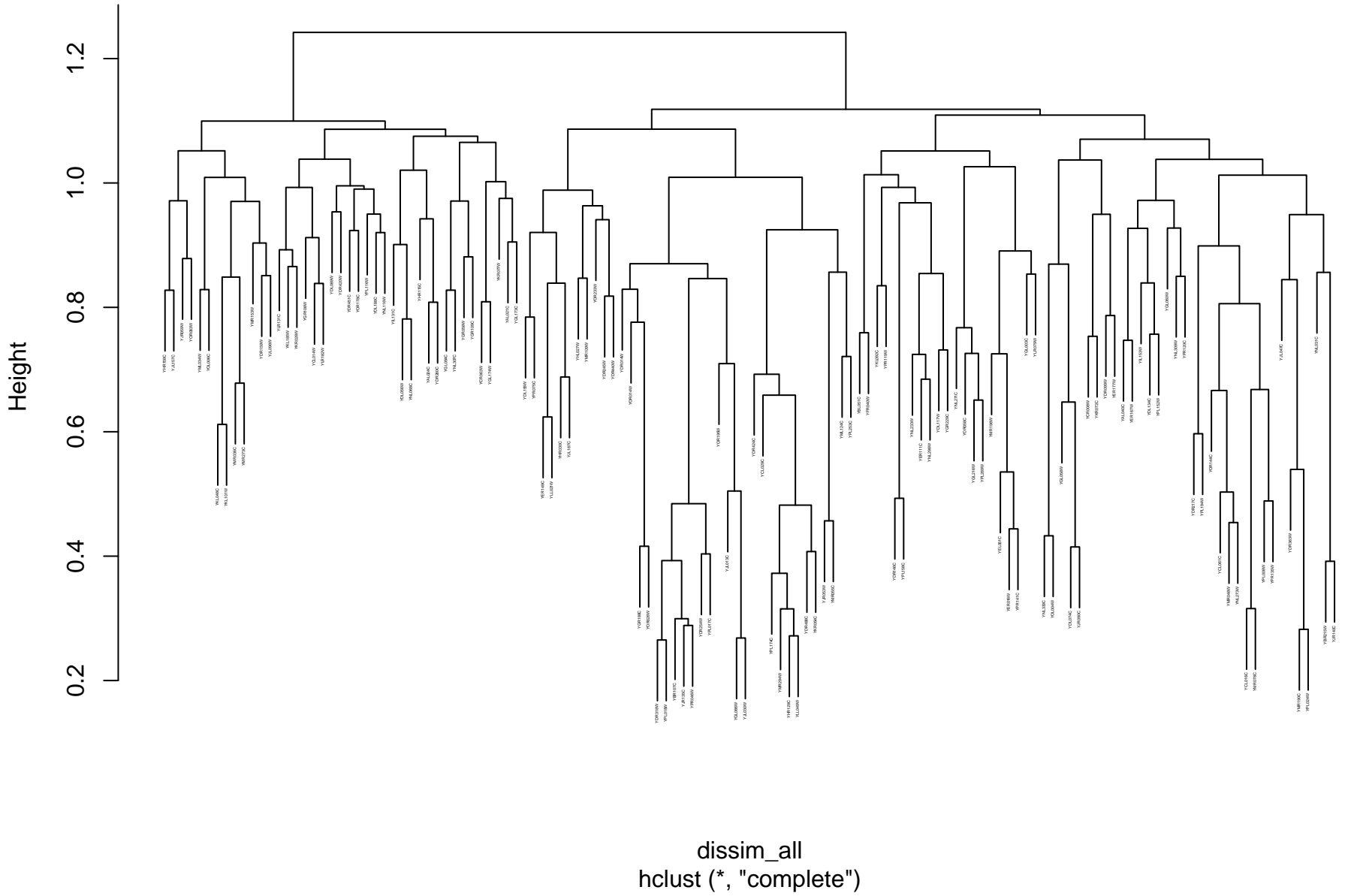
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dissim_all
hclust (*, "complete")
```



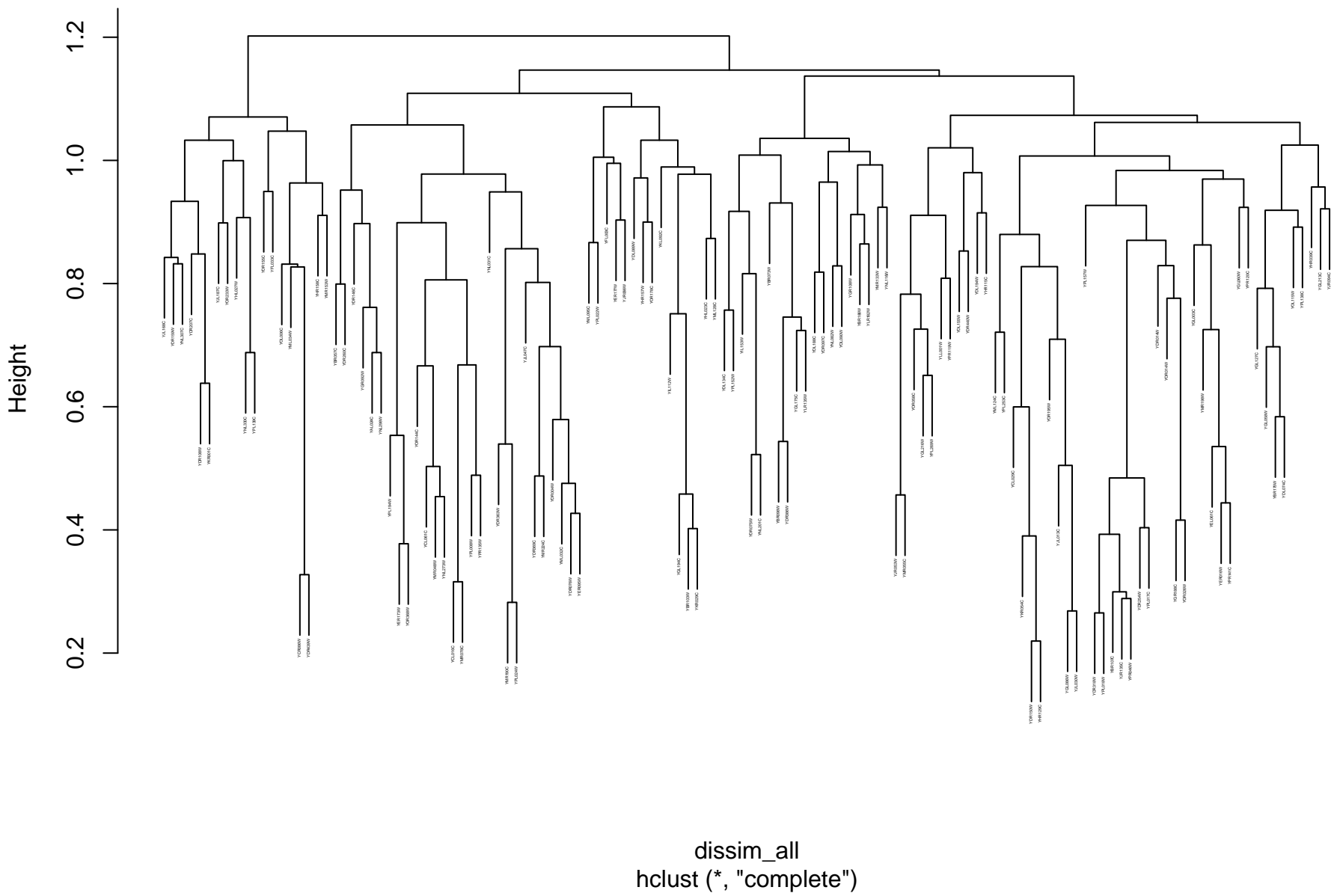
chromosome segregation_GO_pearson_complete



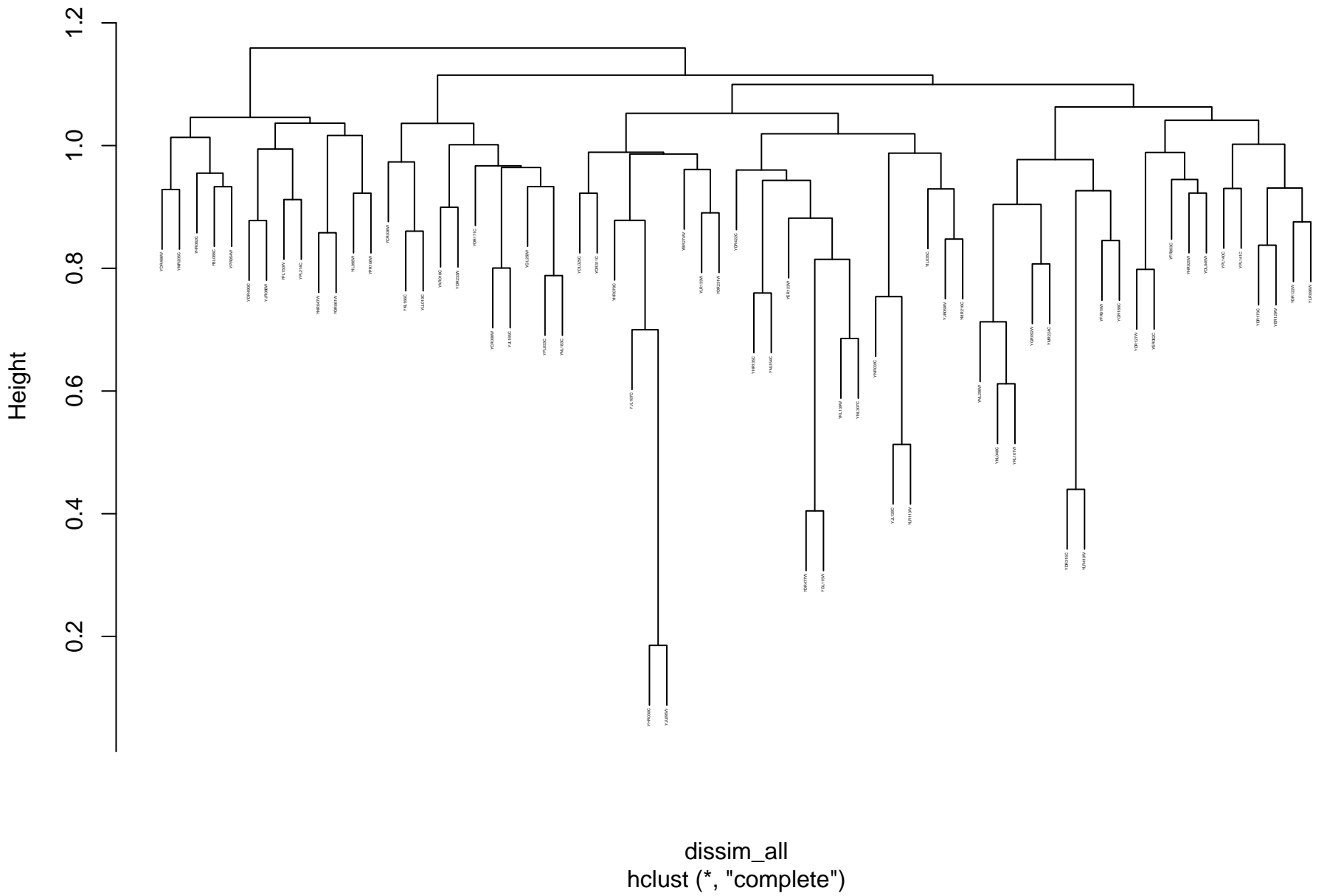
mitotic cell cycle_GO_pearson_complete



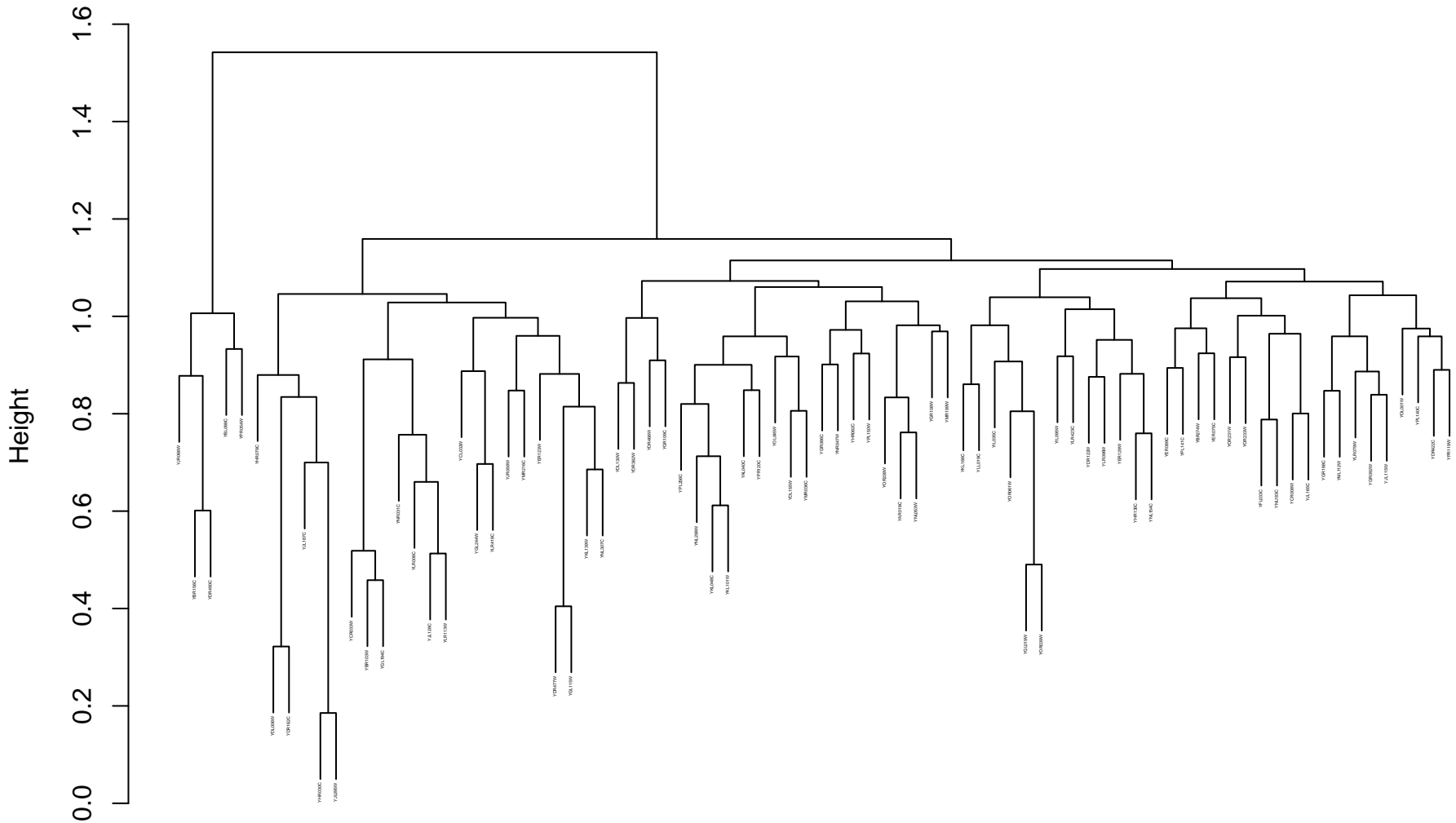
organelle fission_GO_pearson_complete



kinase activity_GO_pearson_complete

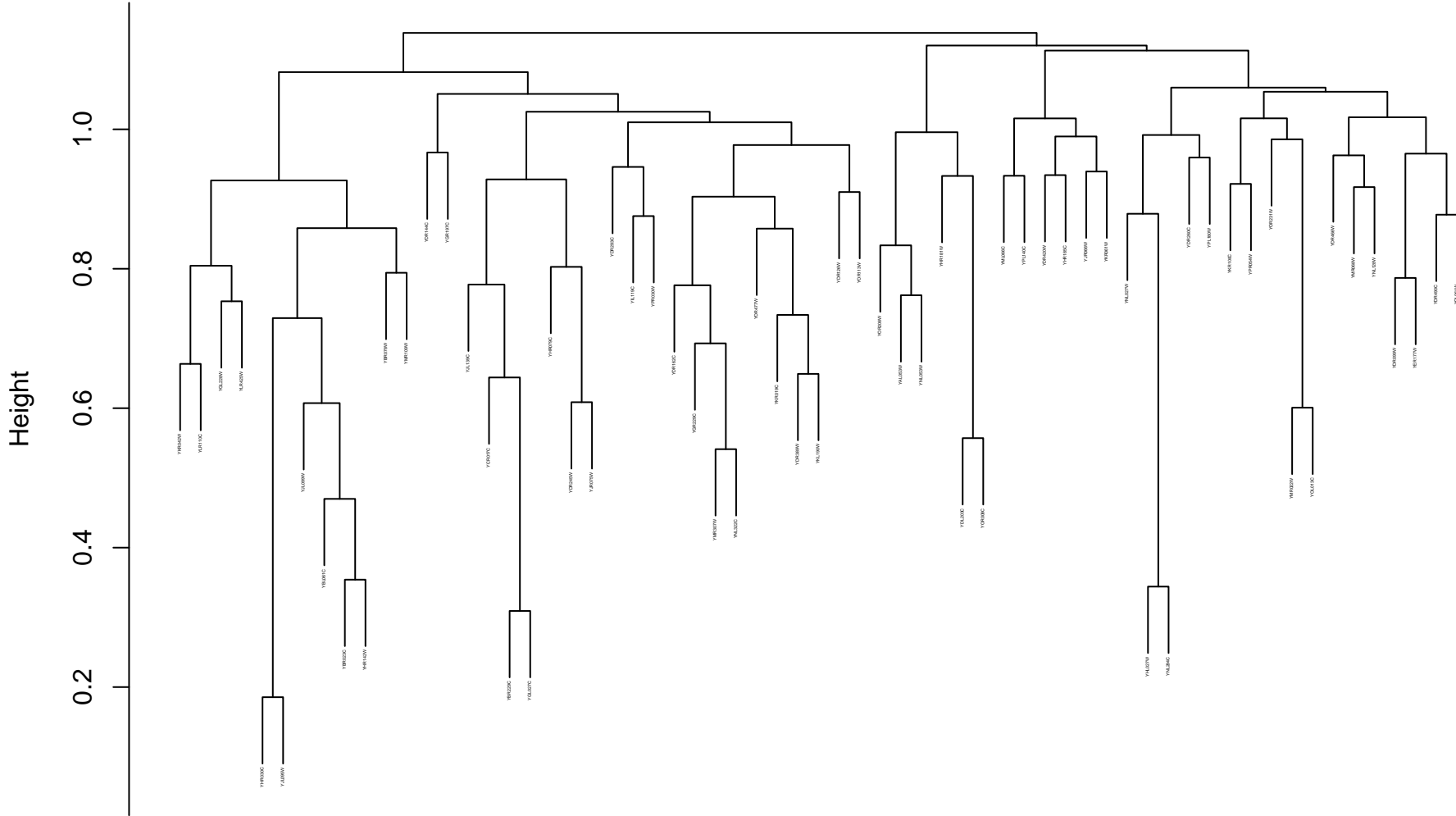


protein phosphorylation_GO_pearson_complete



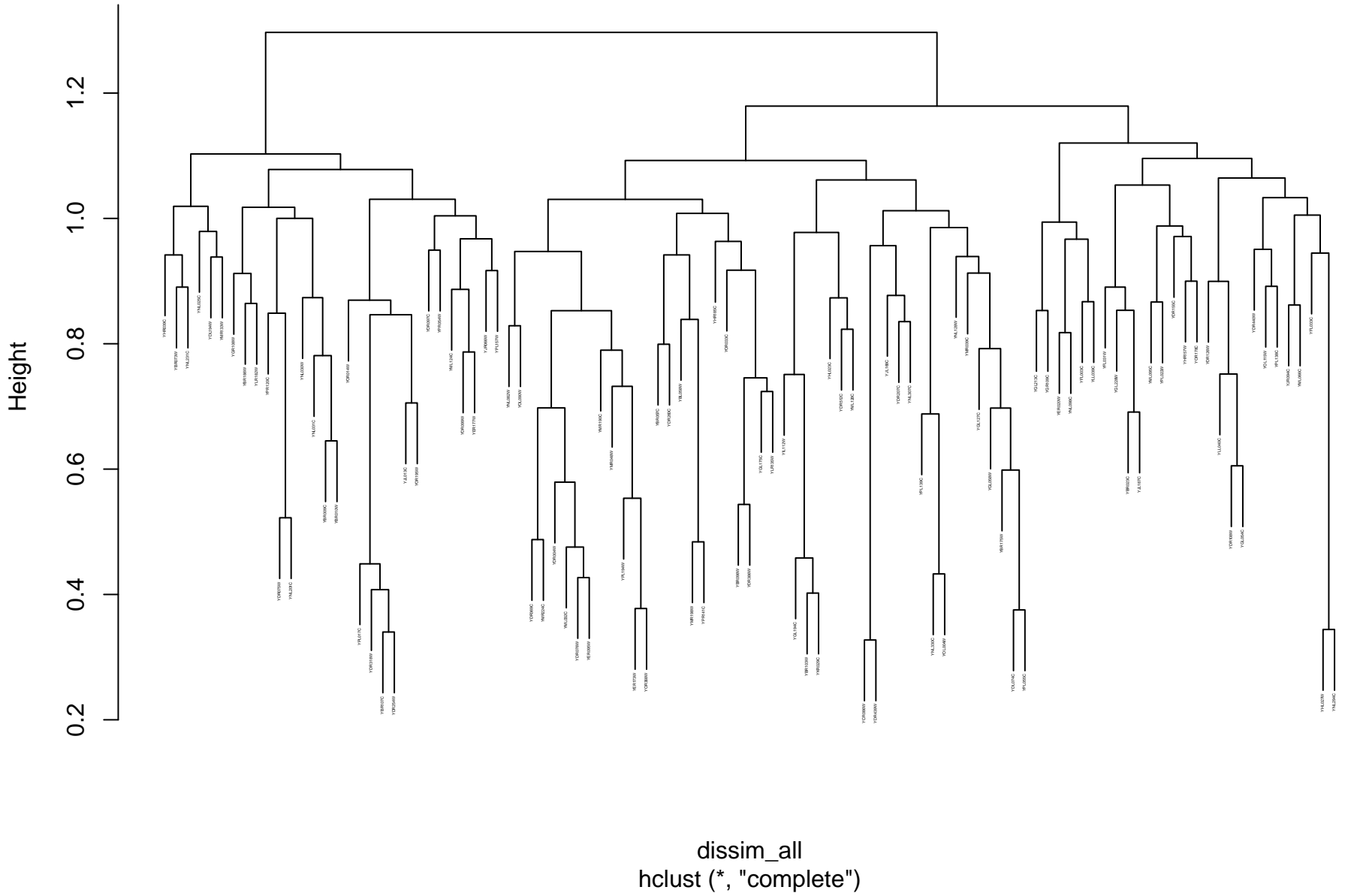
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dissim_all
hclust (*, "complete")
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cell wall organization or biogenesis_GO_pearson_complete

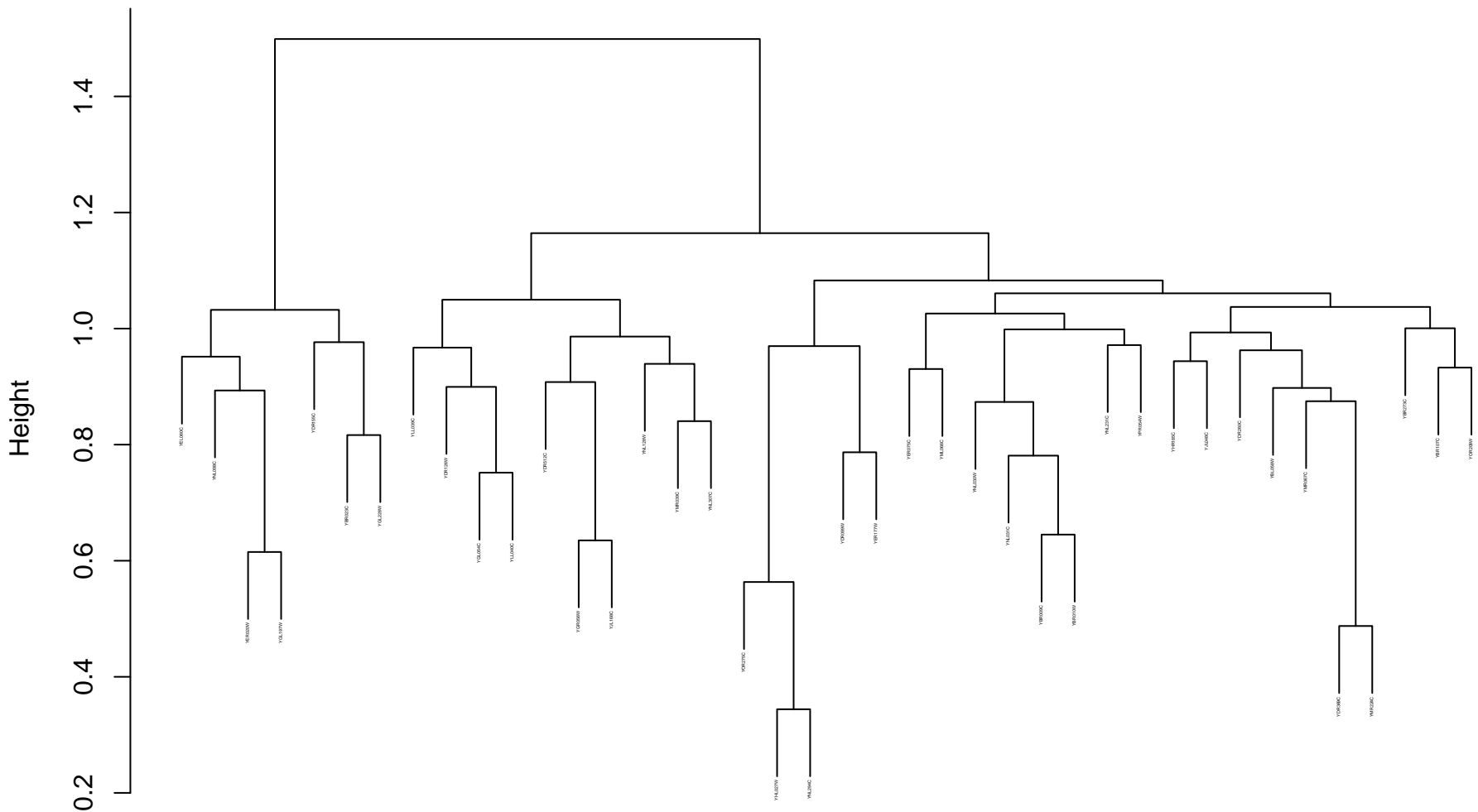


dissim_all
hclust (*, "complete")

meiotic cell cycle_GO_pearson_complete

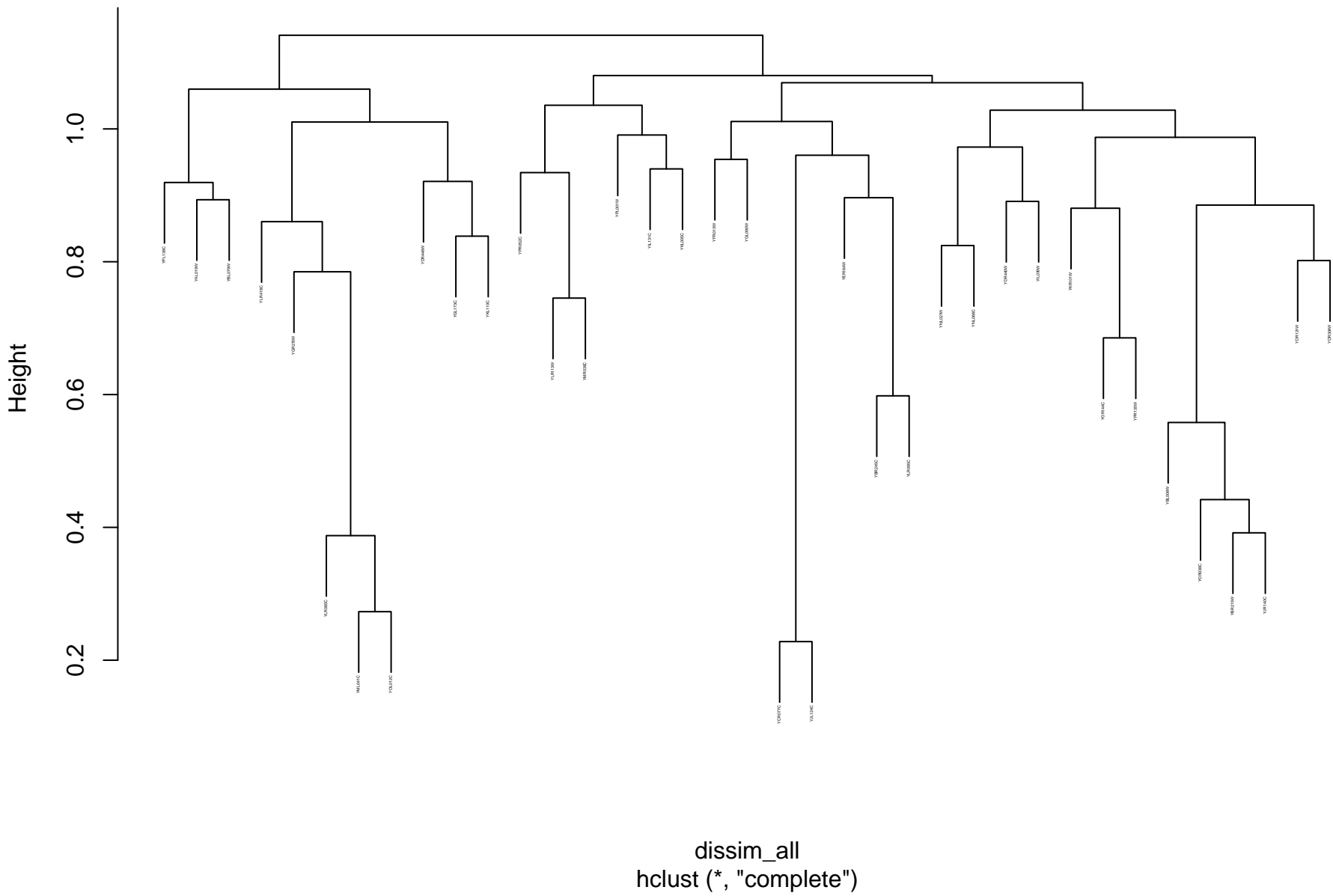


sporulation_GO_pearson_complete

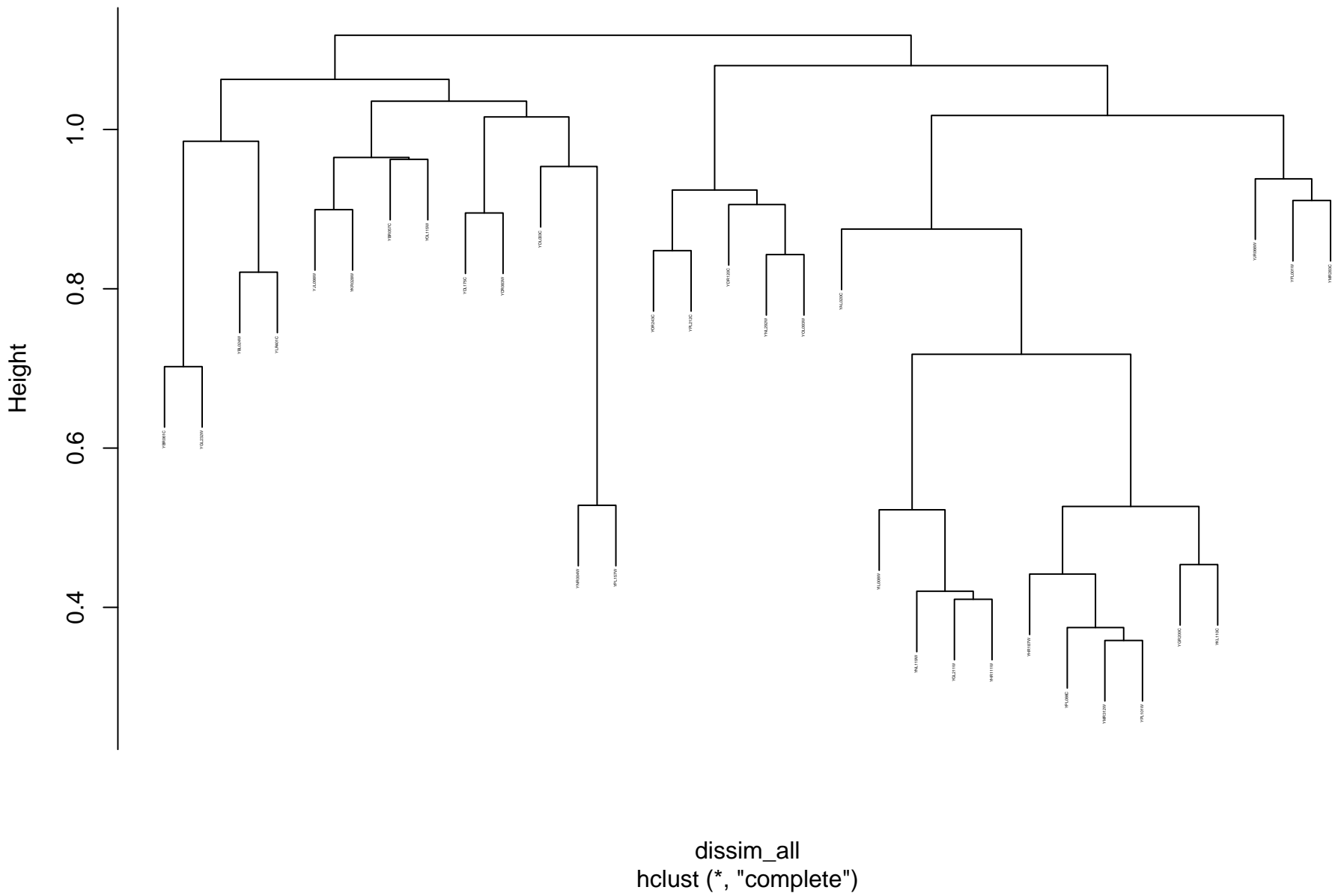


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dissim_all
hclust (*, "complete")
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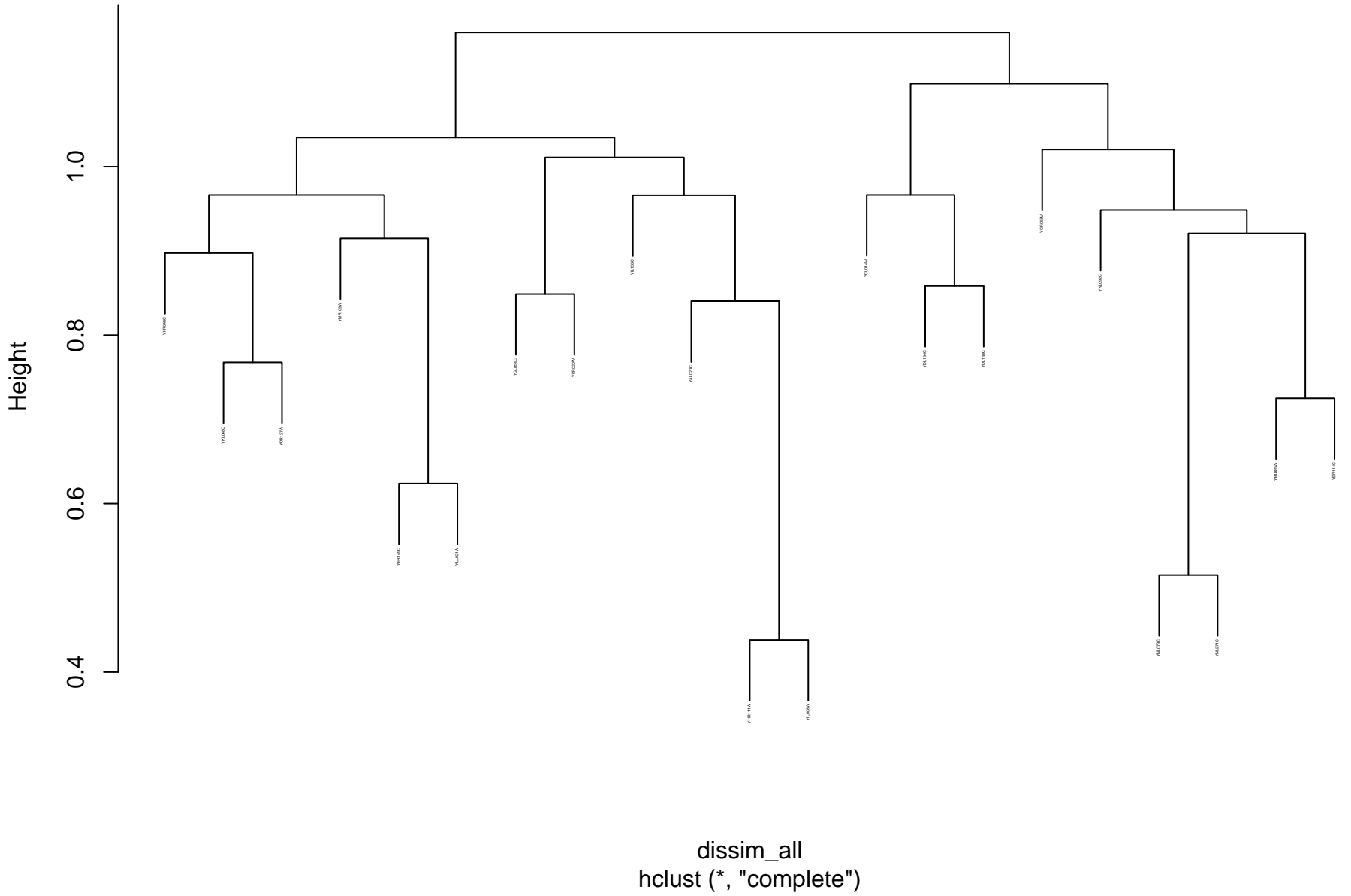
chromatin binding_GO_pearson_complete



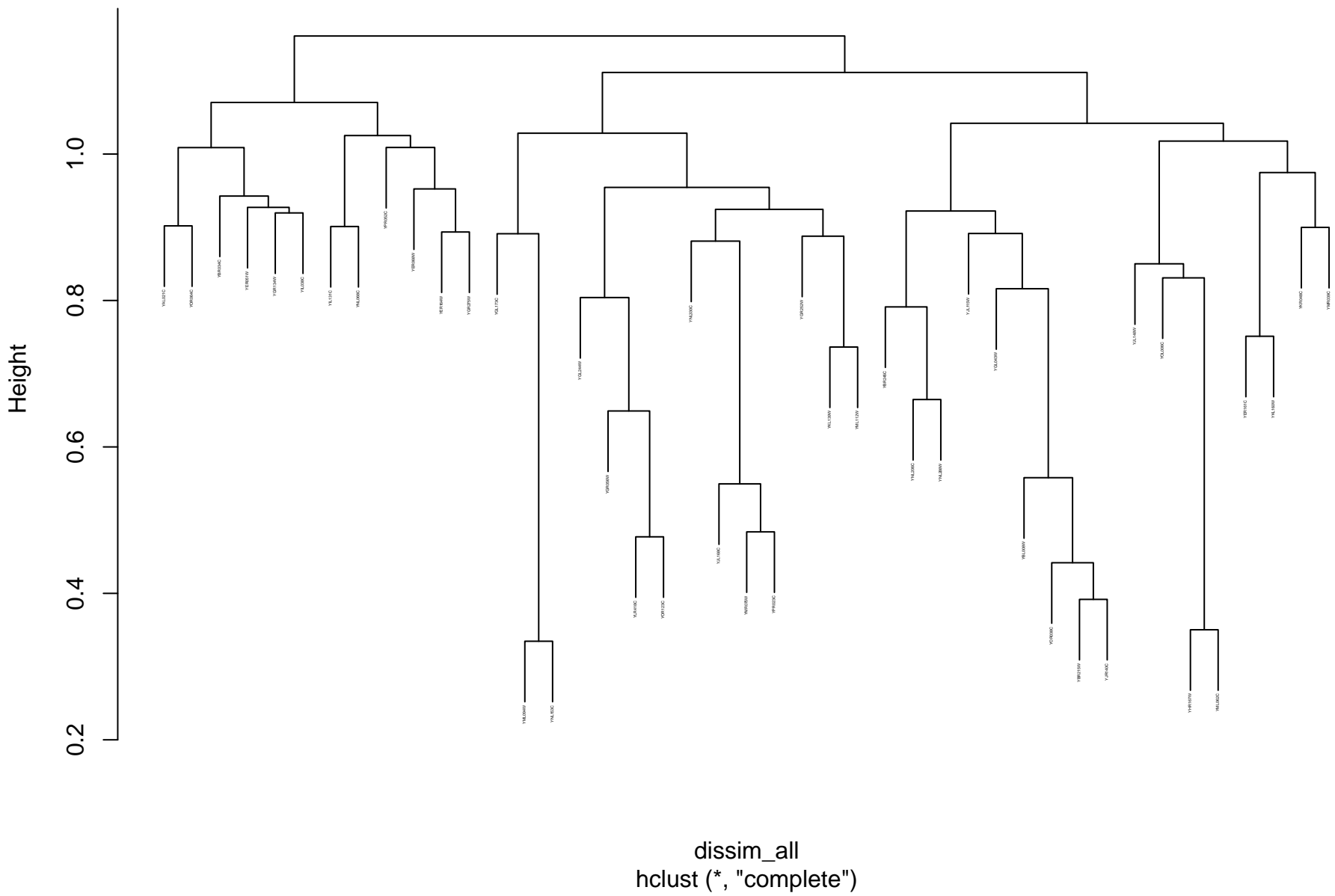
RNA modification_GO_pearson_complete



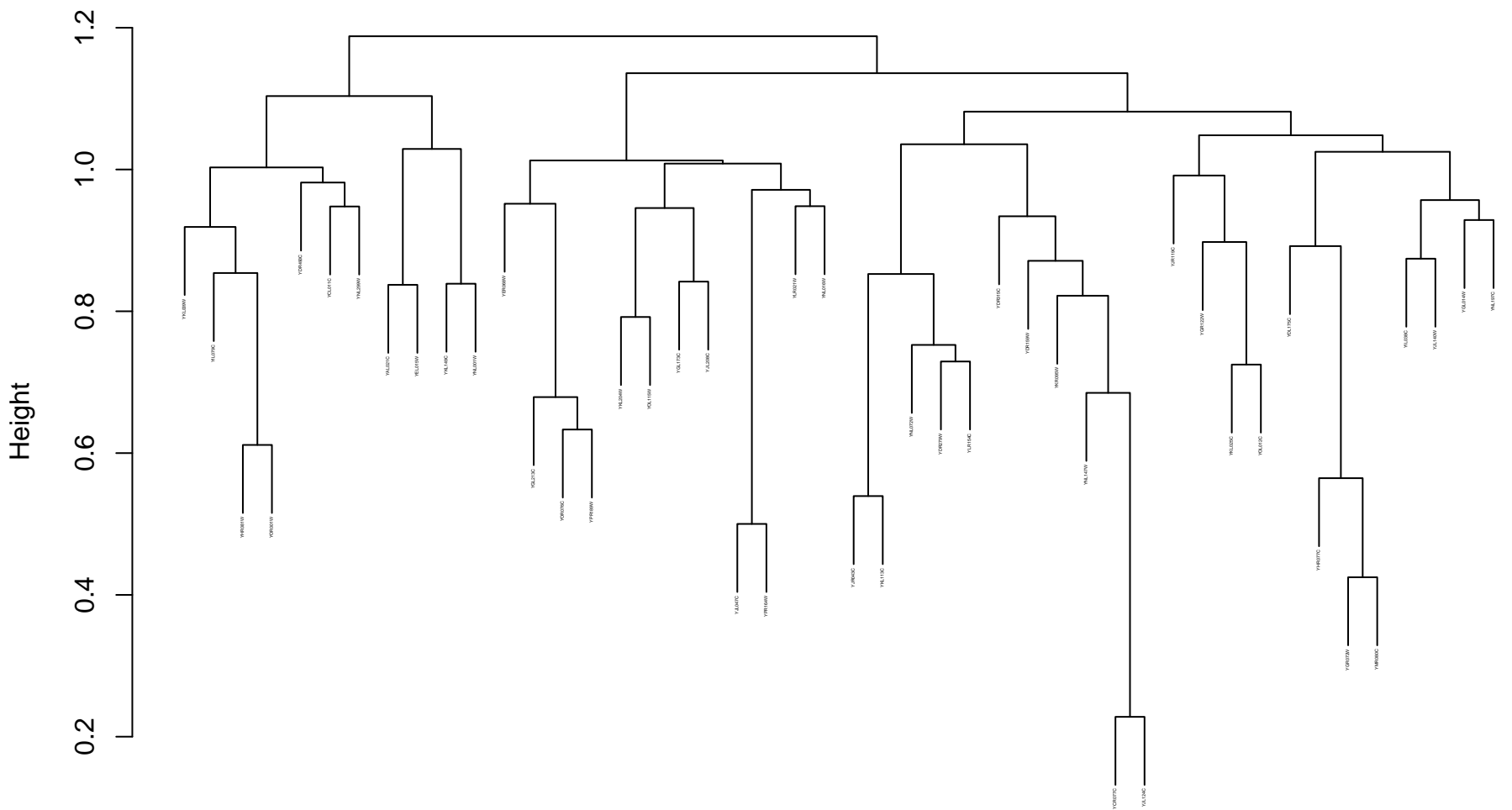
cell budding_GO_pearson_complete



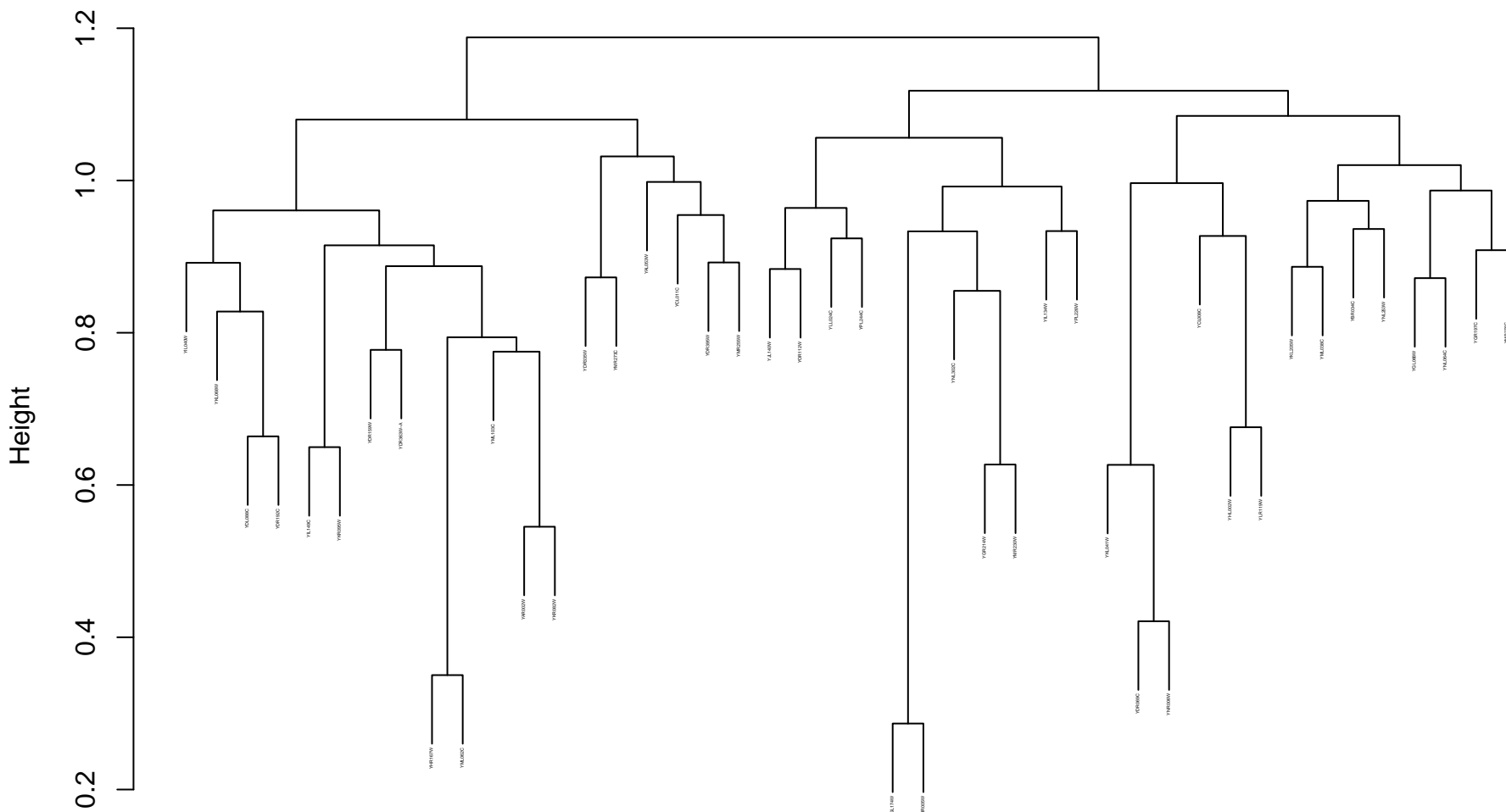
DNA-templated transcription, elongation_GO_pearson_complete



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

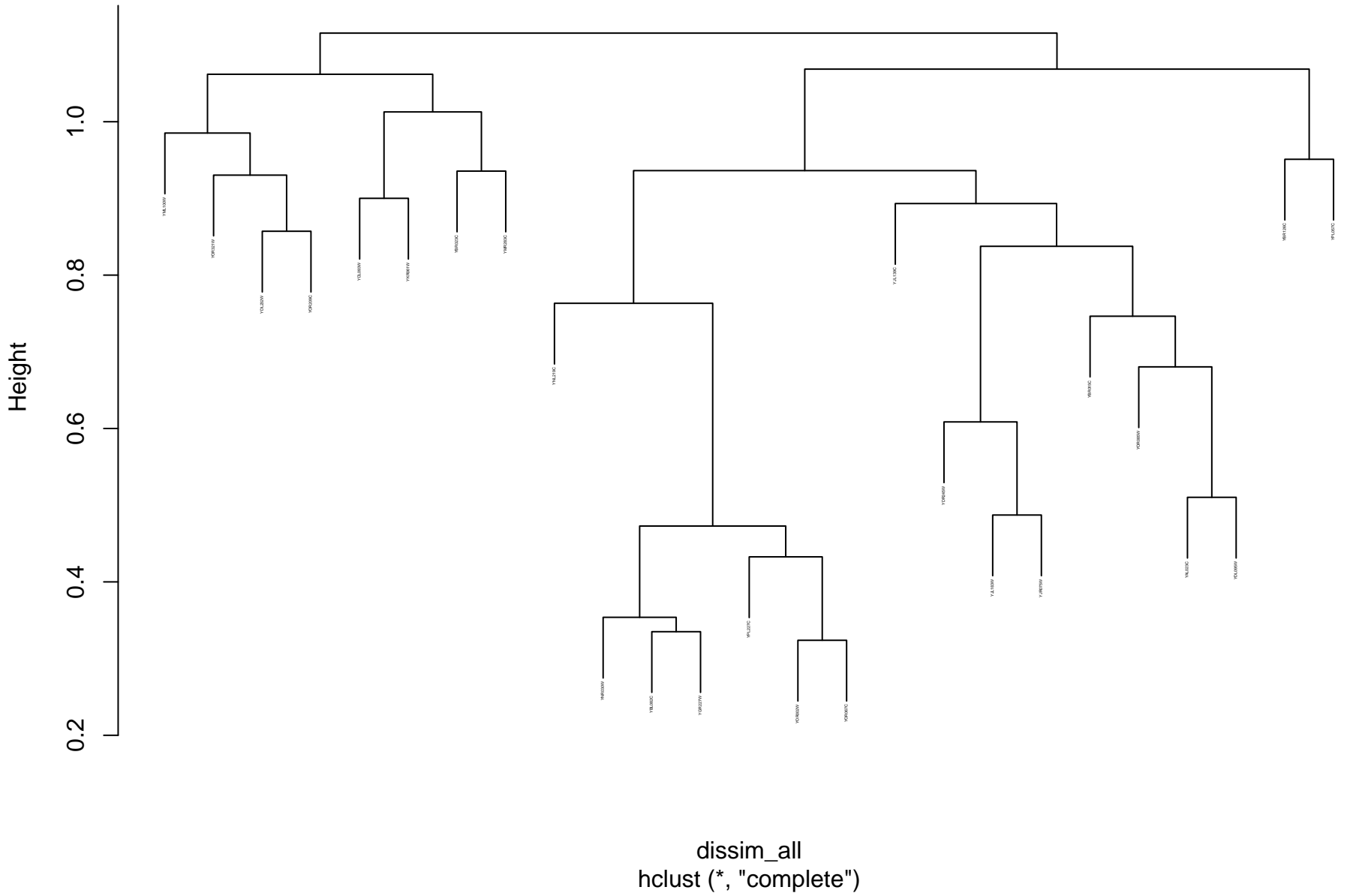


nucleobase-containing compound transport_GO_pearson_complete

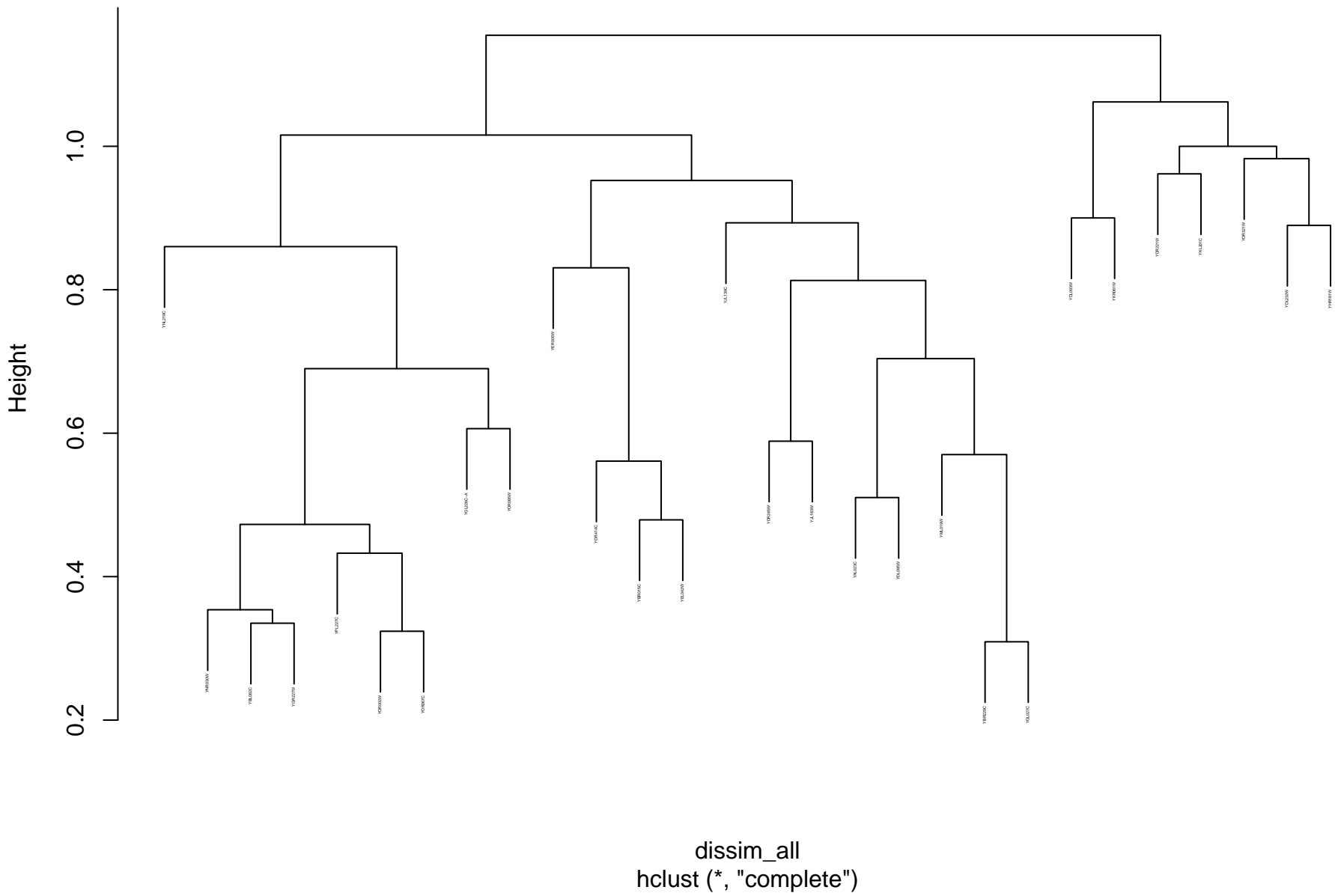


dissim_all
hclust (*, "complete")

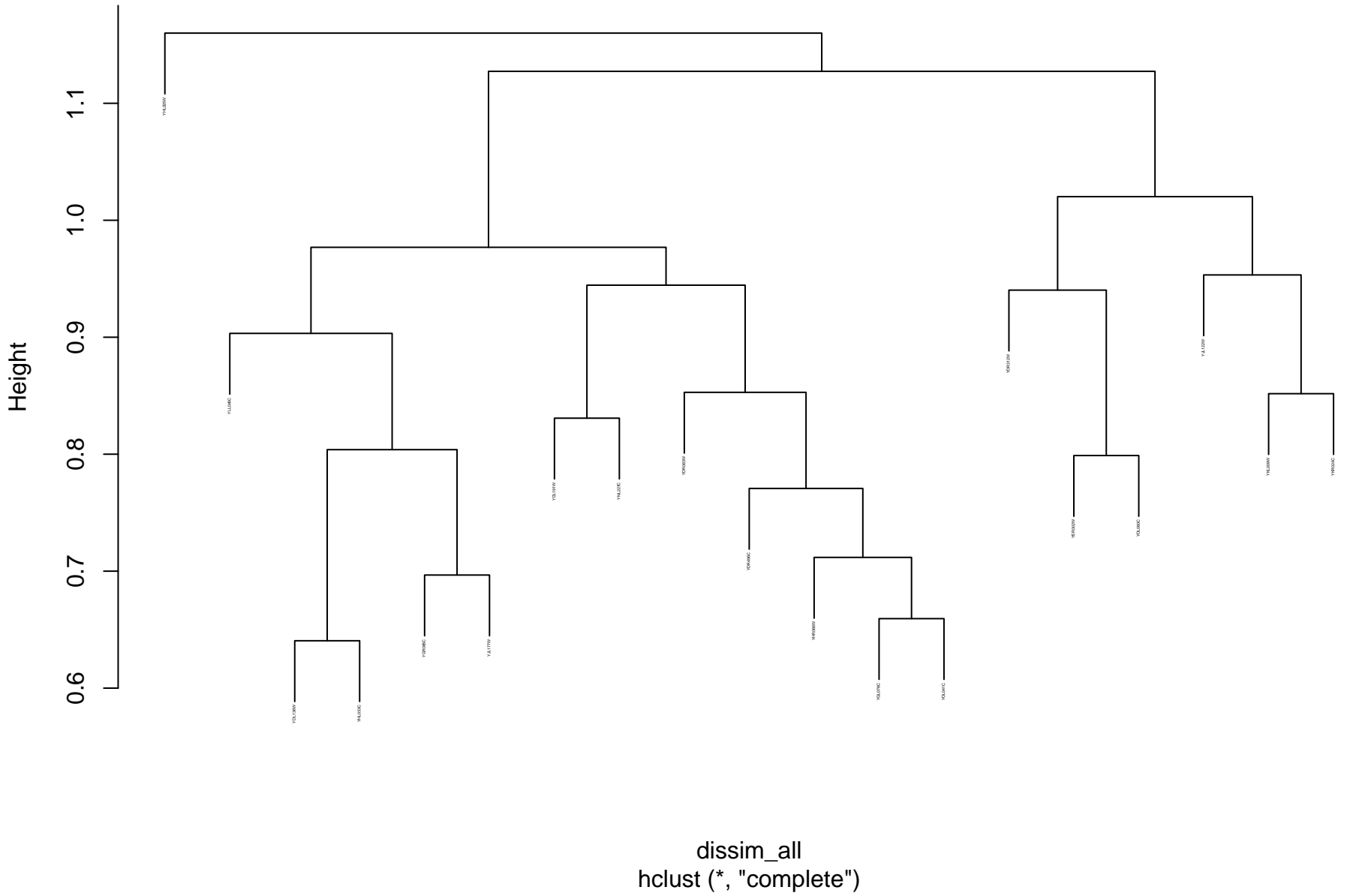
transferase activity, transferring glycosyl groups_GO_pearson_complete



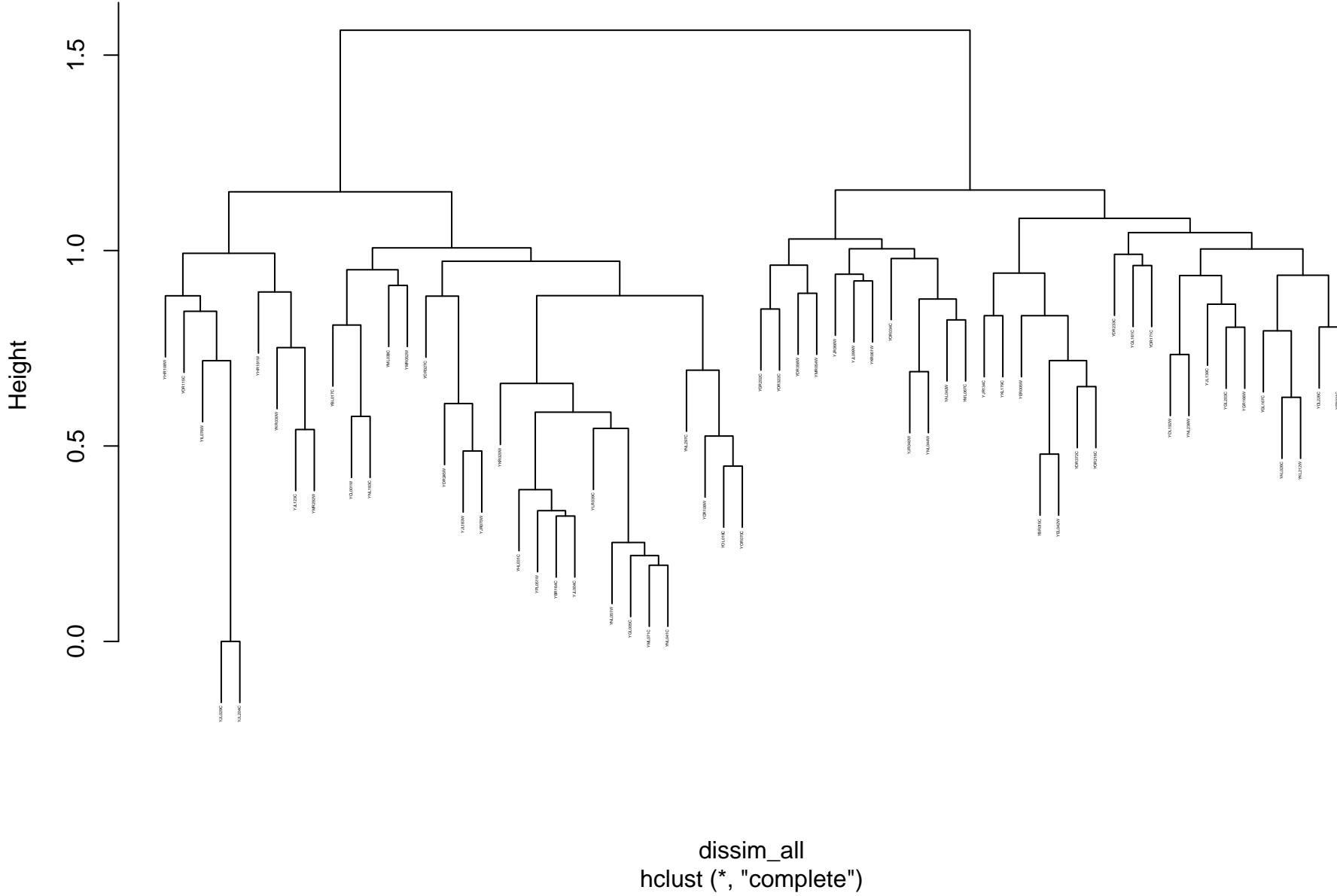
protein glycosylation_GO_pearson_complete



ribosomal large subunit biogenesis_GO_pearson_complete

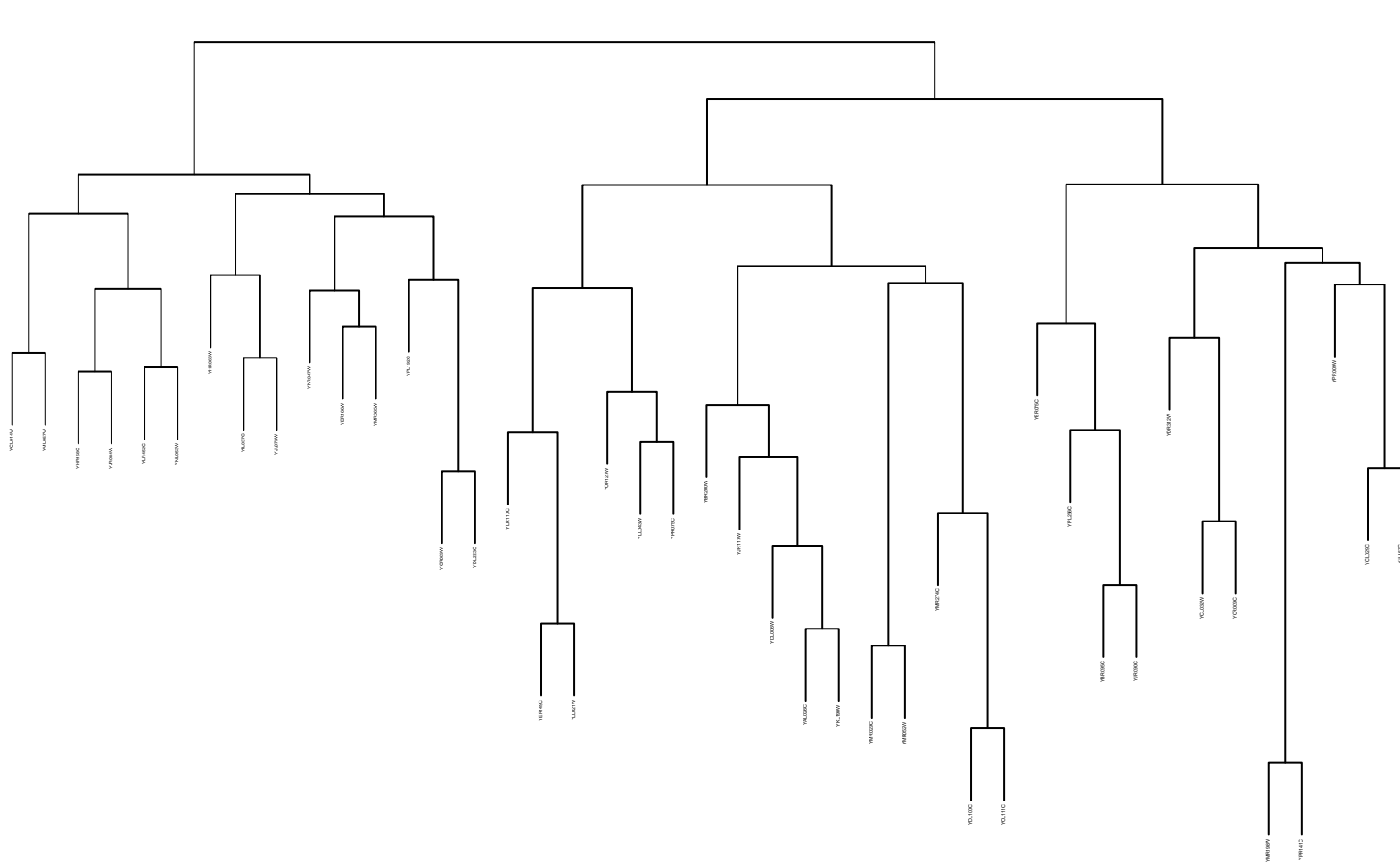


Golgi apparatus_GO_pearson_complete

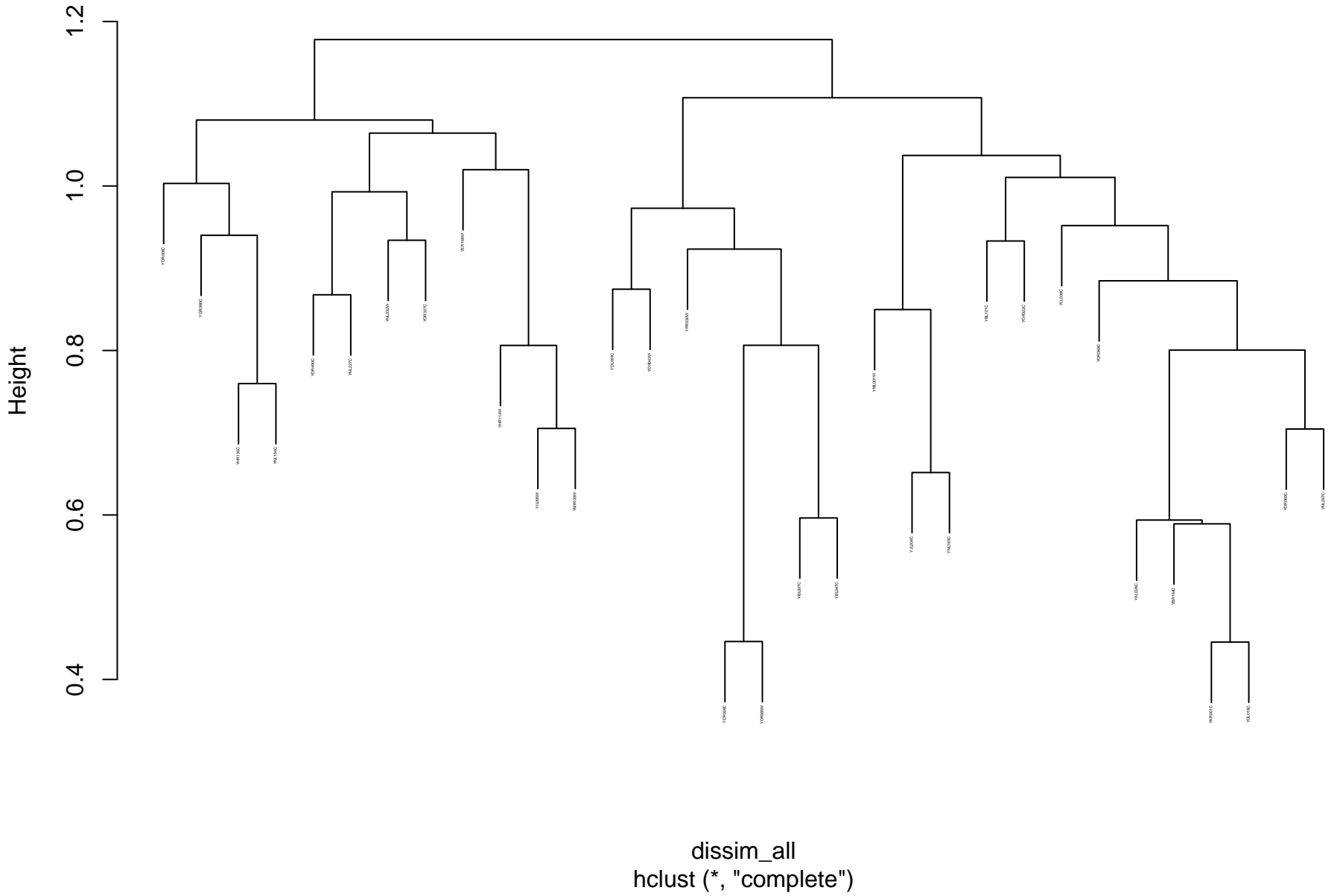


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dissim_all
hclust (*, "complete")
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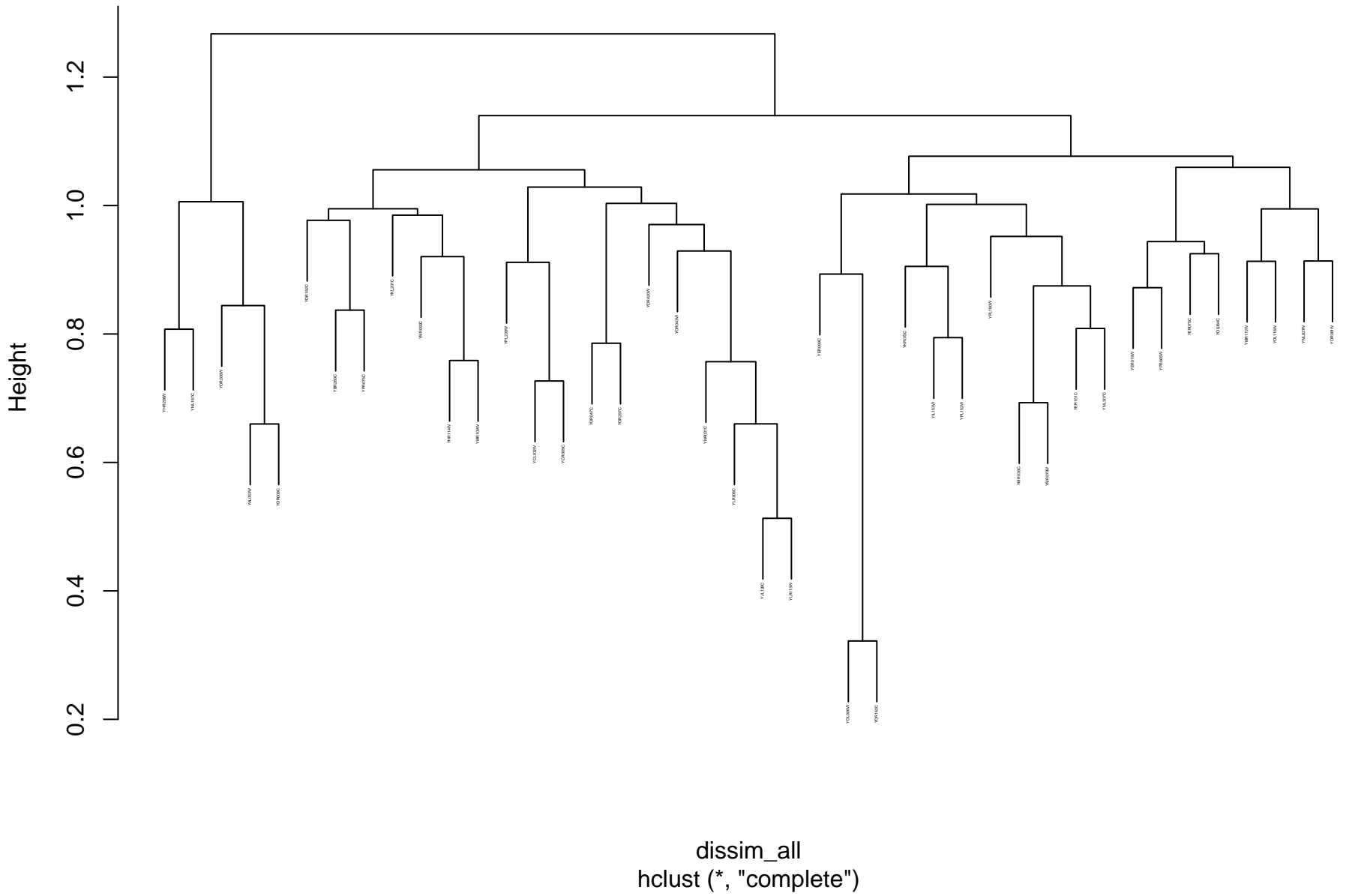
0.4 0.6 0.8 1.0 1.2



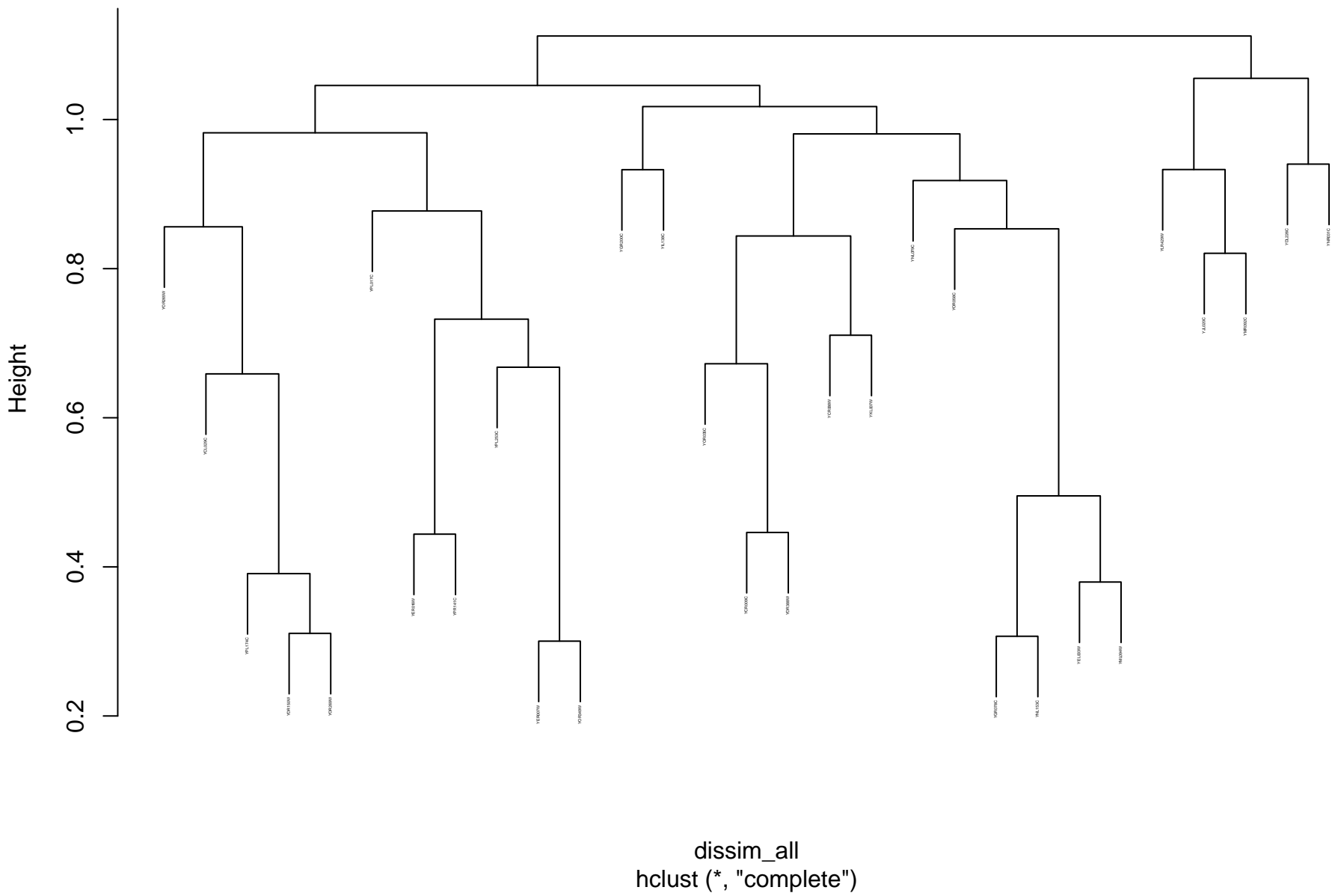
endocytosis_GO_pearson_complete



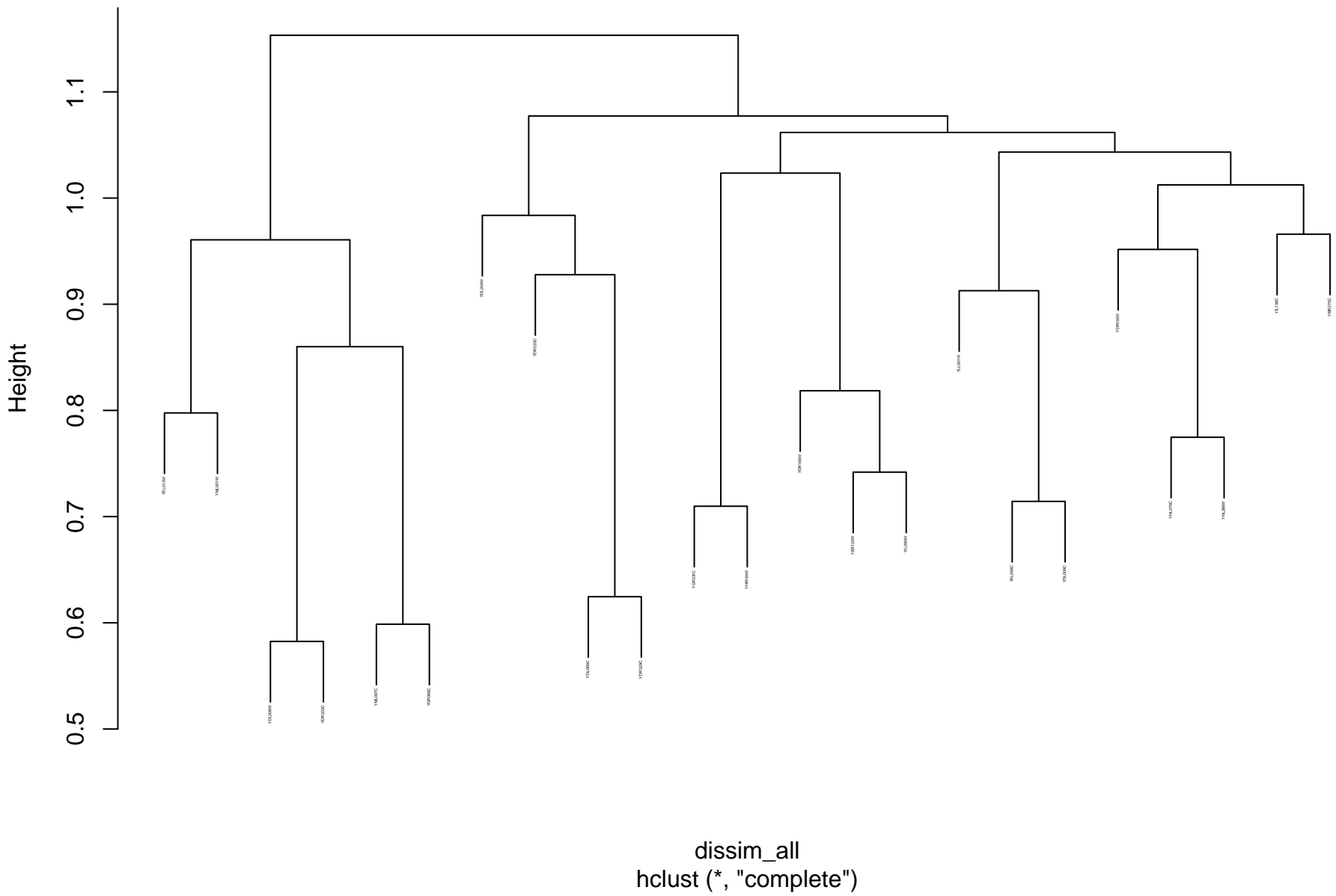
response to osmotic stress_GO_pearson_complete



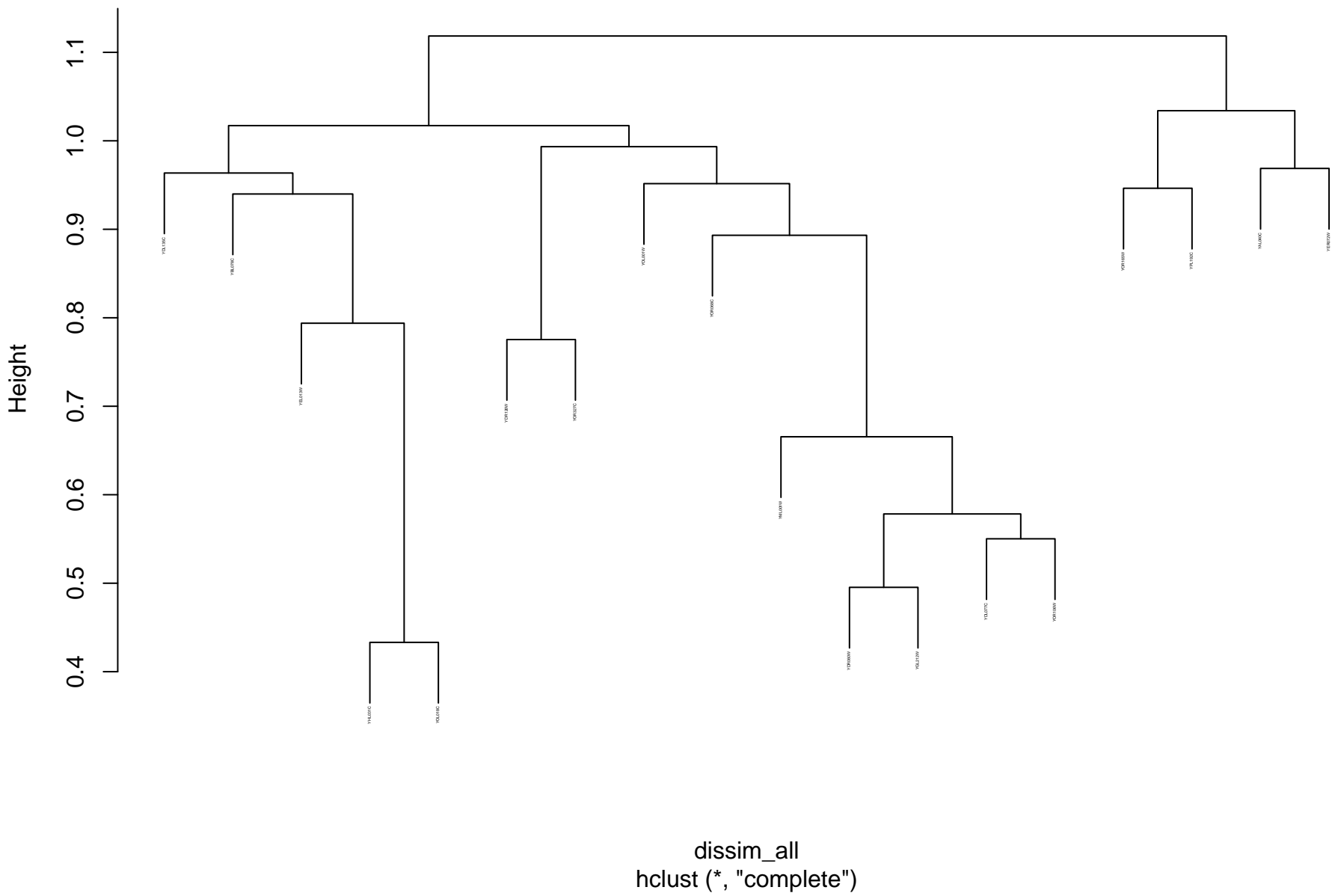
cytoskeletal protein binding_GO_pearson_complete



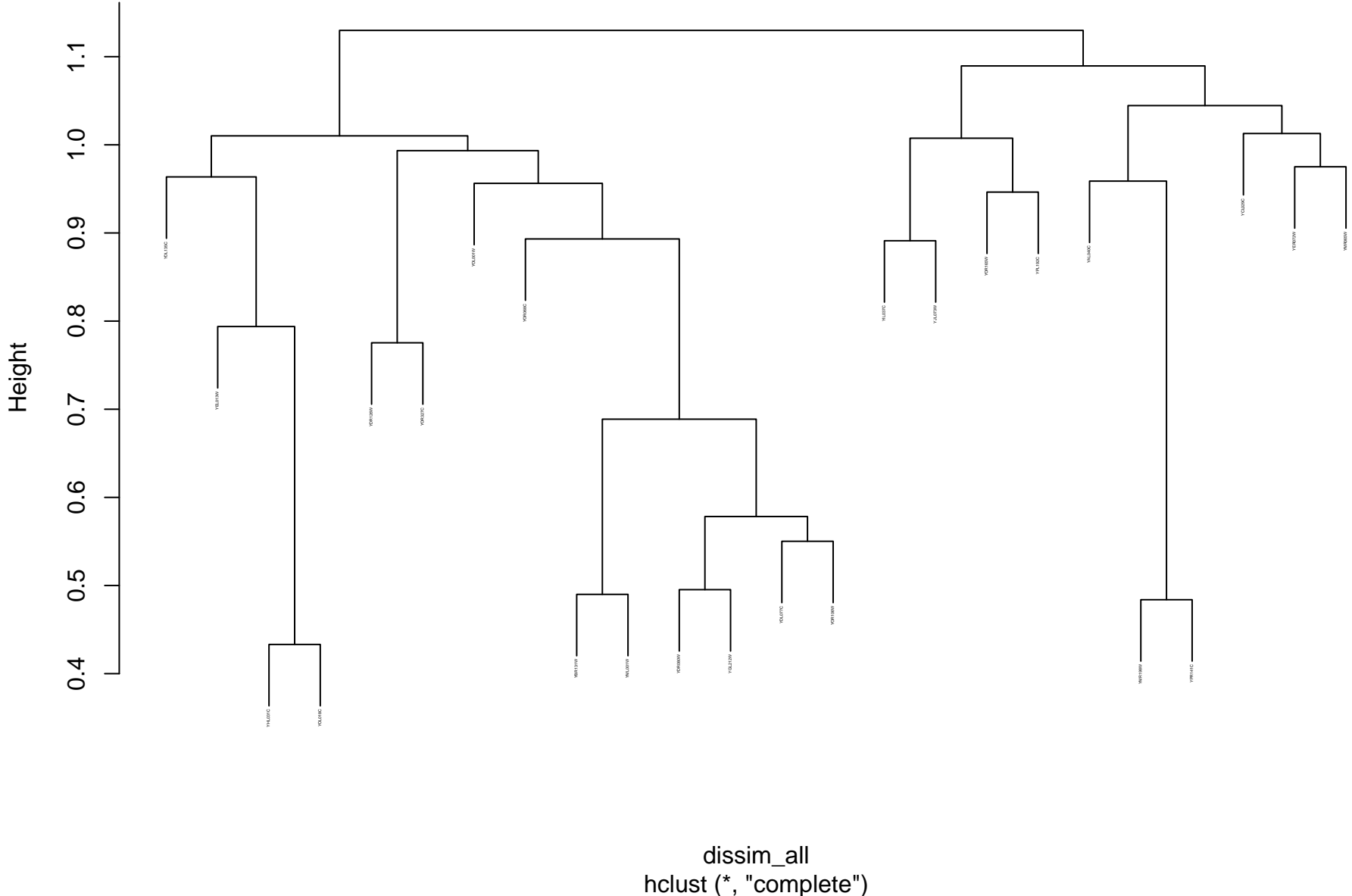
organelle inheritance_GO_pearson_complete



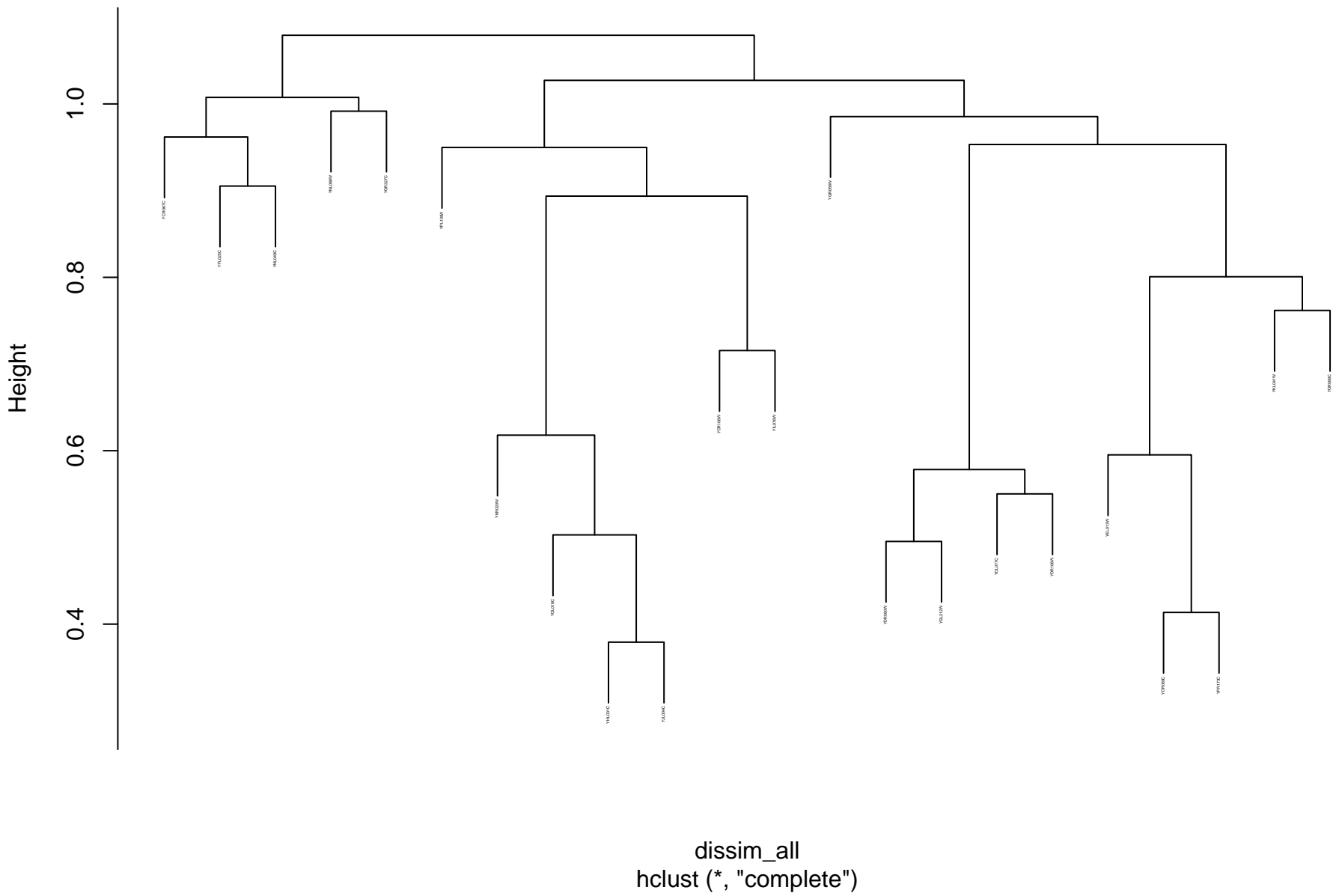
membrane fusion_GO_pearson_complete



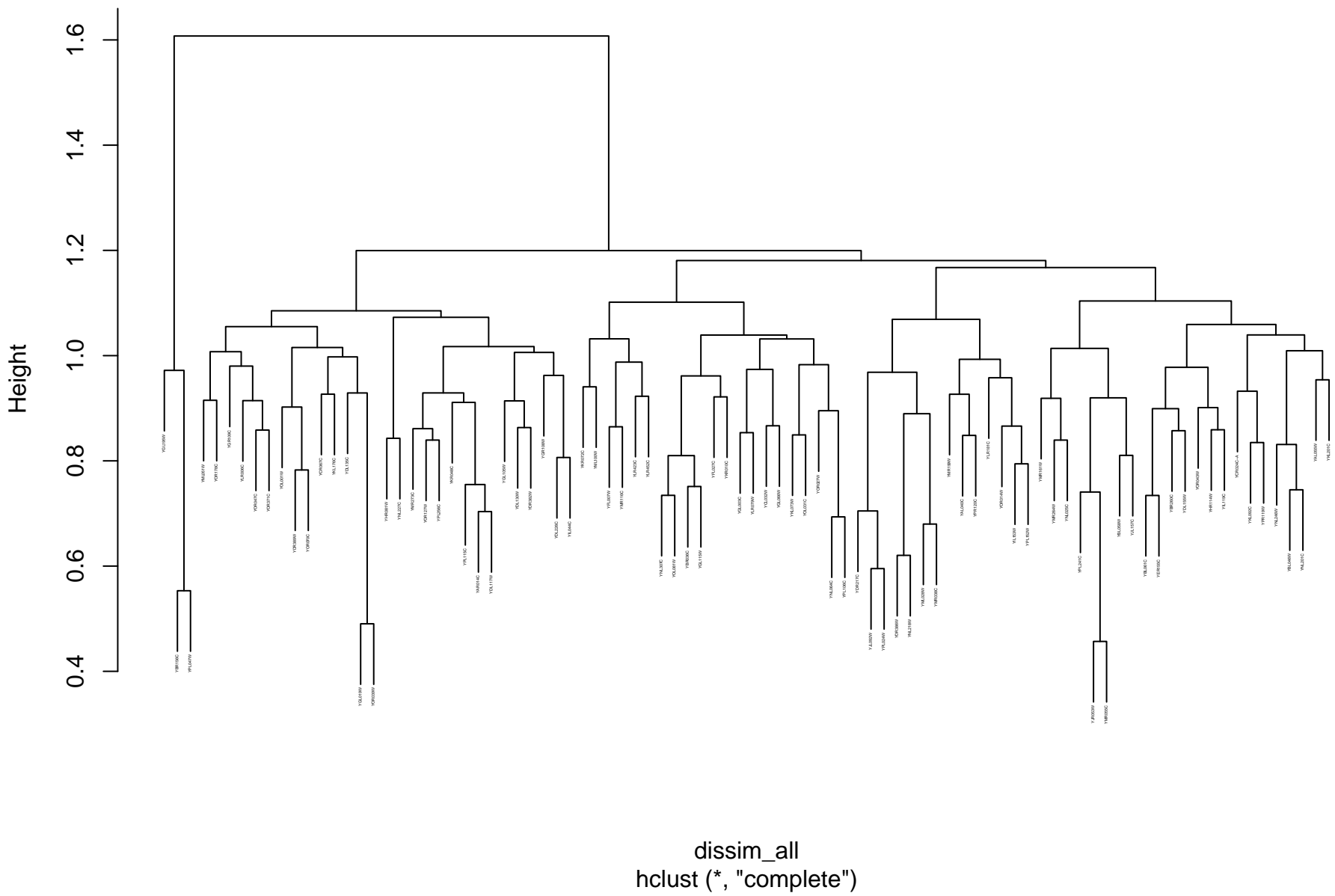
organelle fusion_GO_pearson_complete



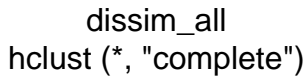
vesicle organization_GO_pearson_complete



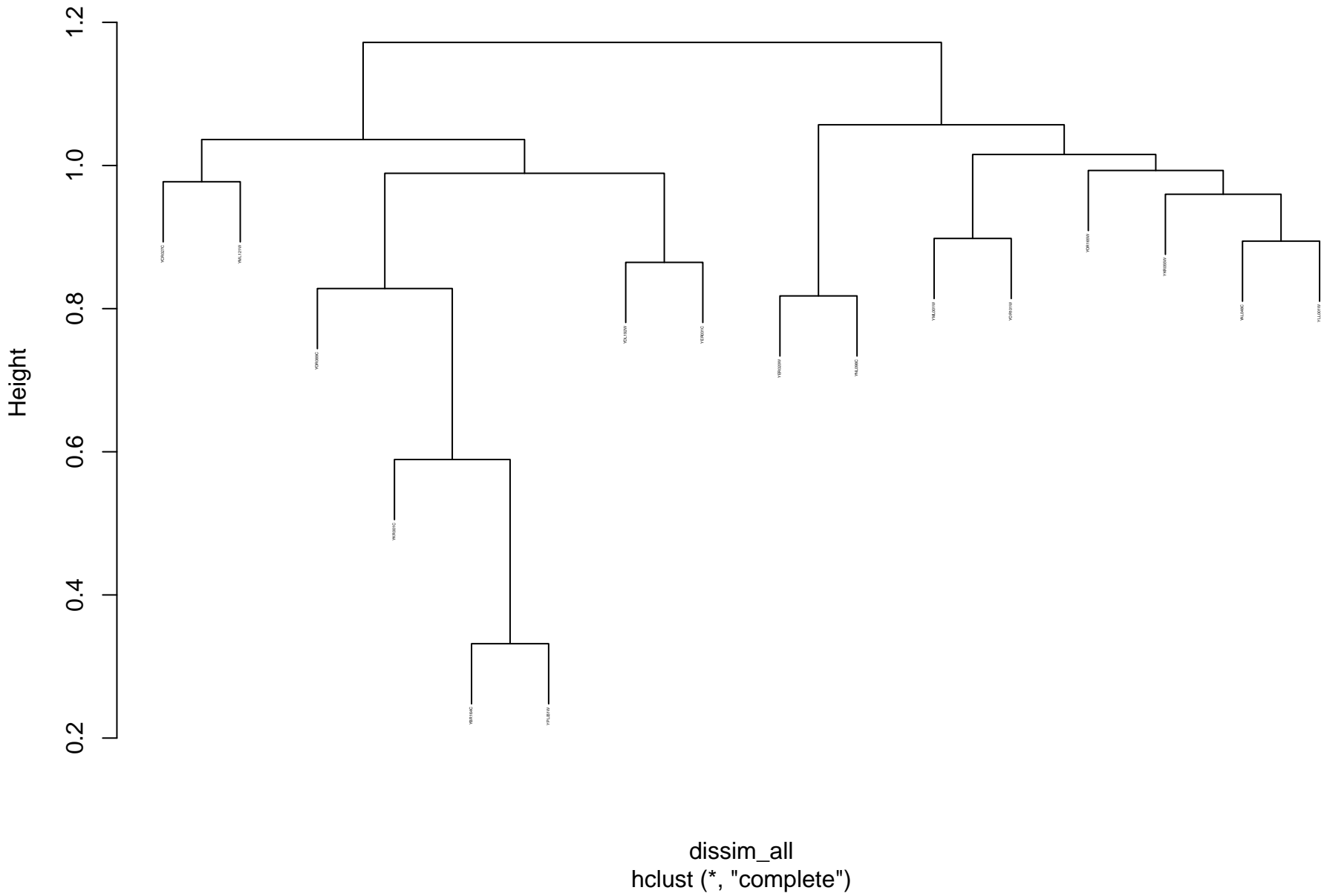
enzyme regulator activity_GO_pearson_complete

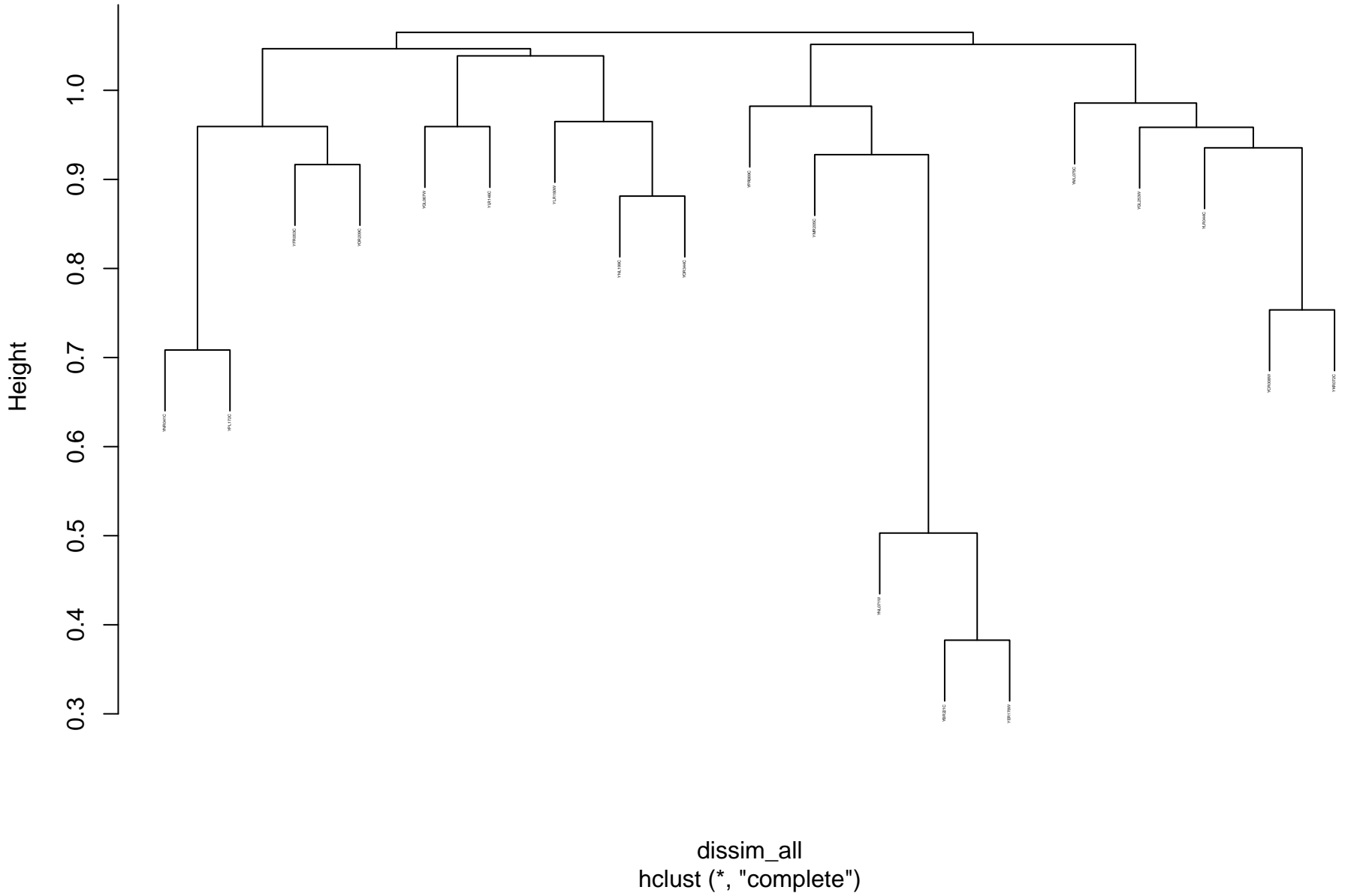


regulation of protein modification process_GO_pearson_complete

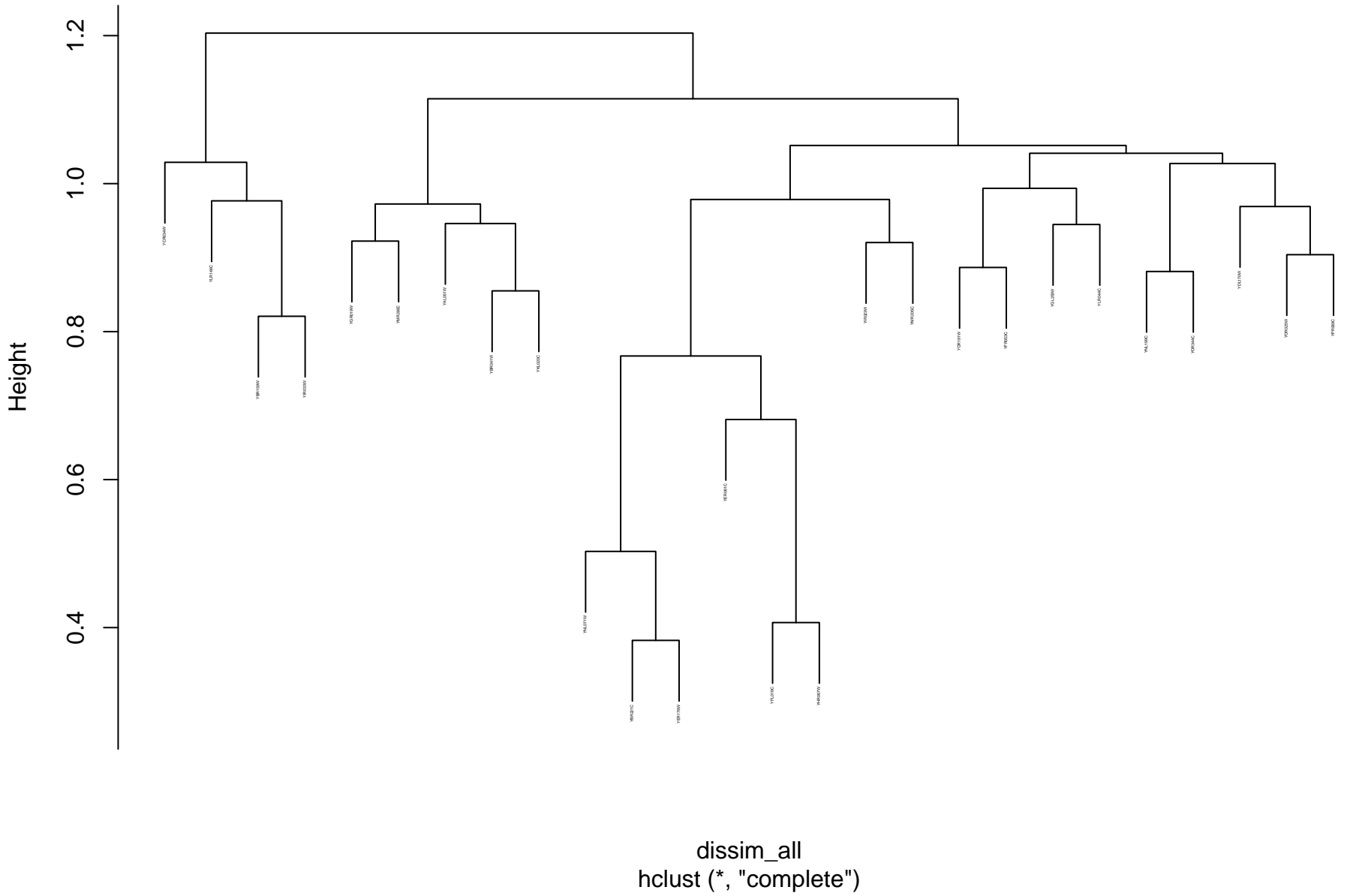


GTPase activity_GO_pearson_complete

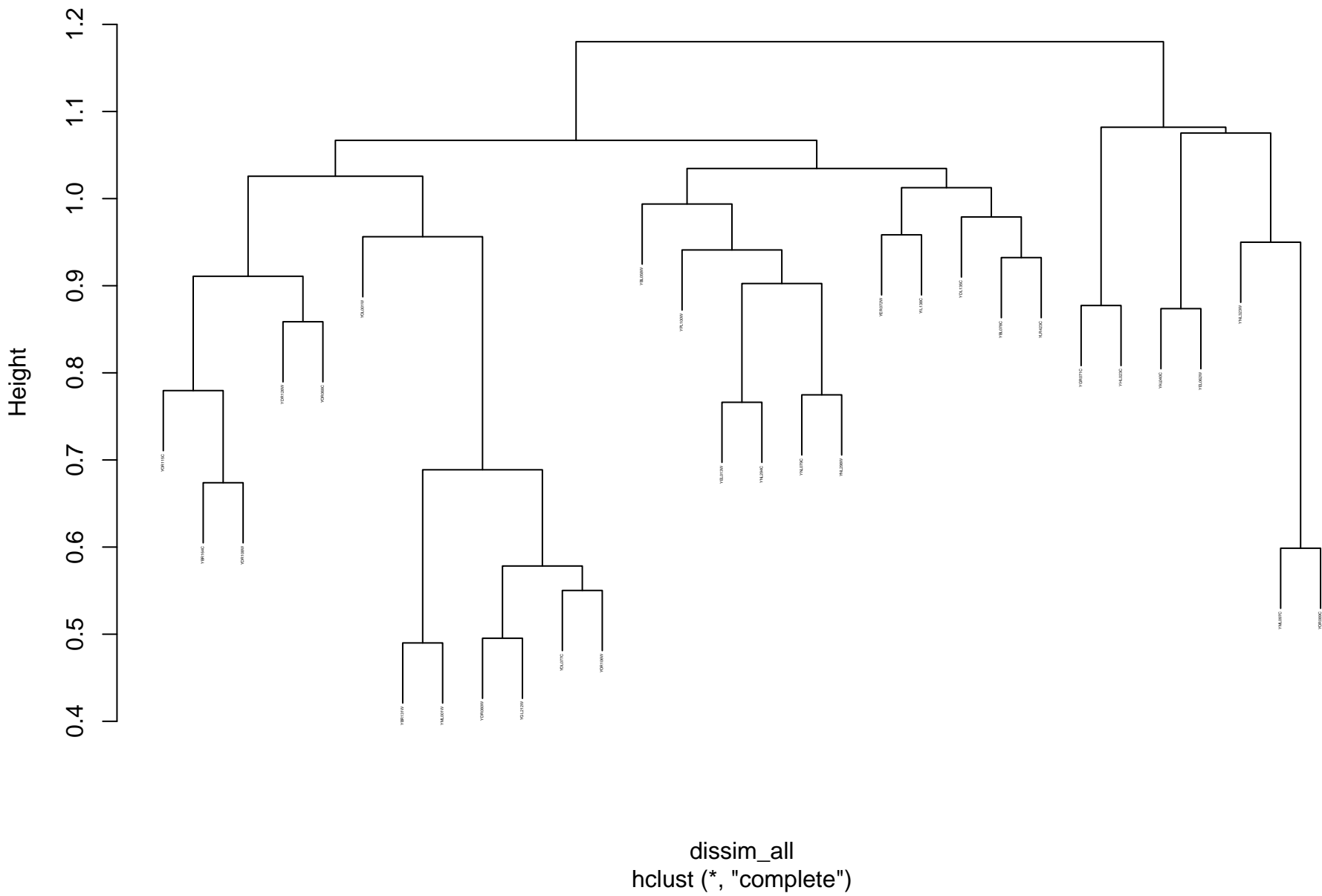


cofactor metabolic process_GO_pearson_complete

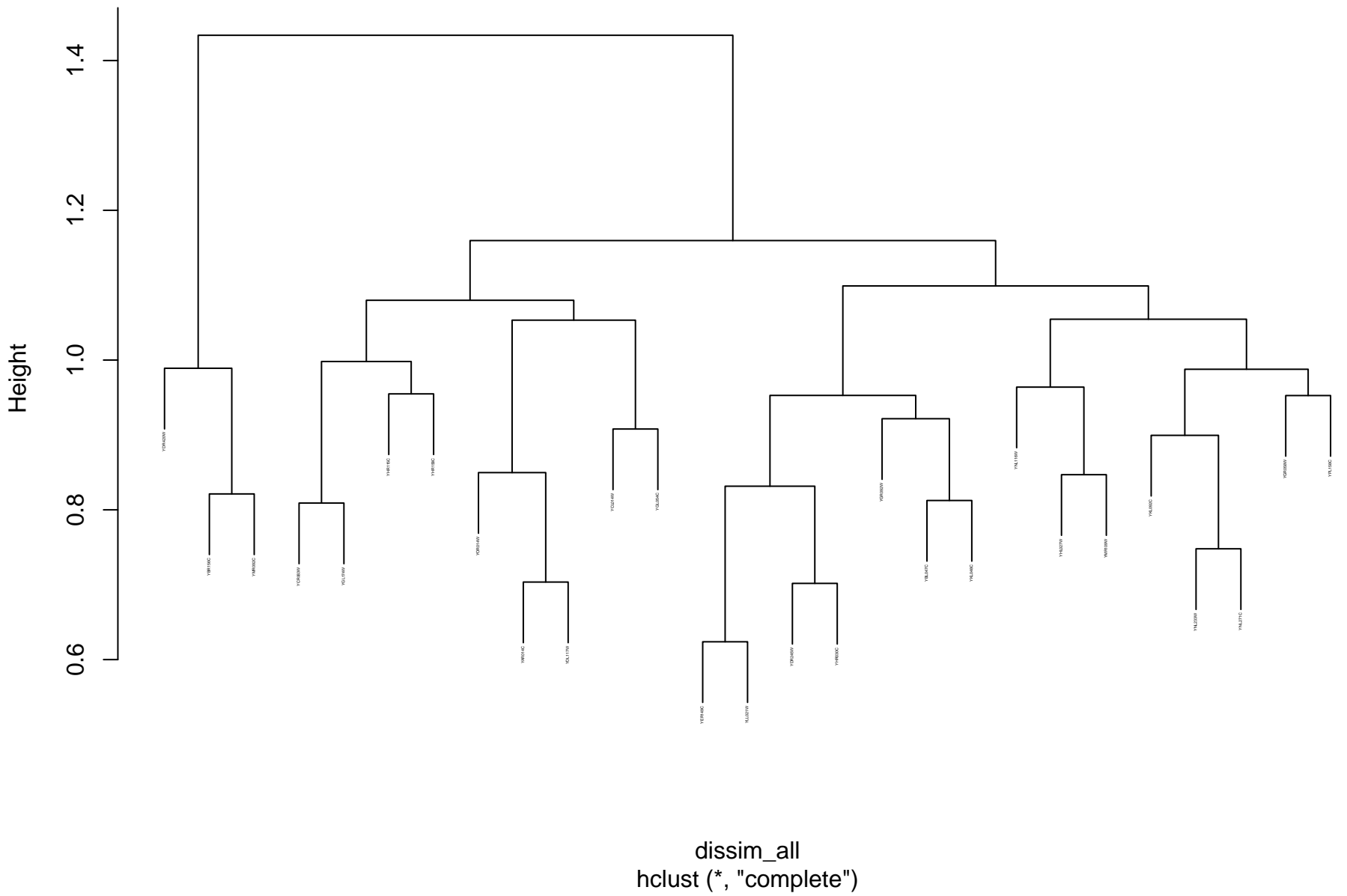
monocarboxylic acid metabolic process_GO_pearson_complete



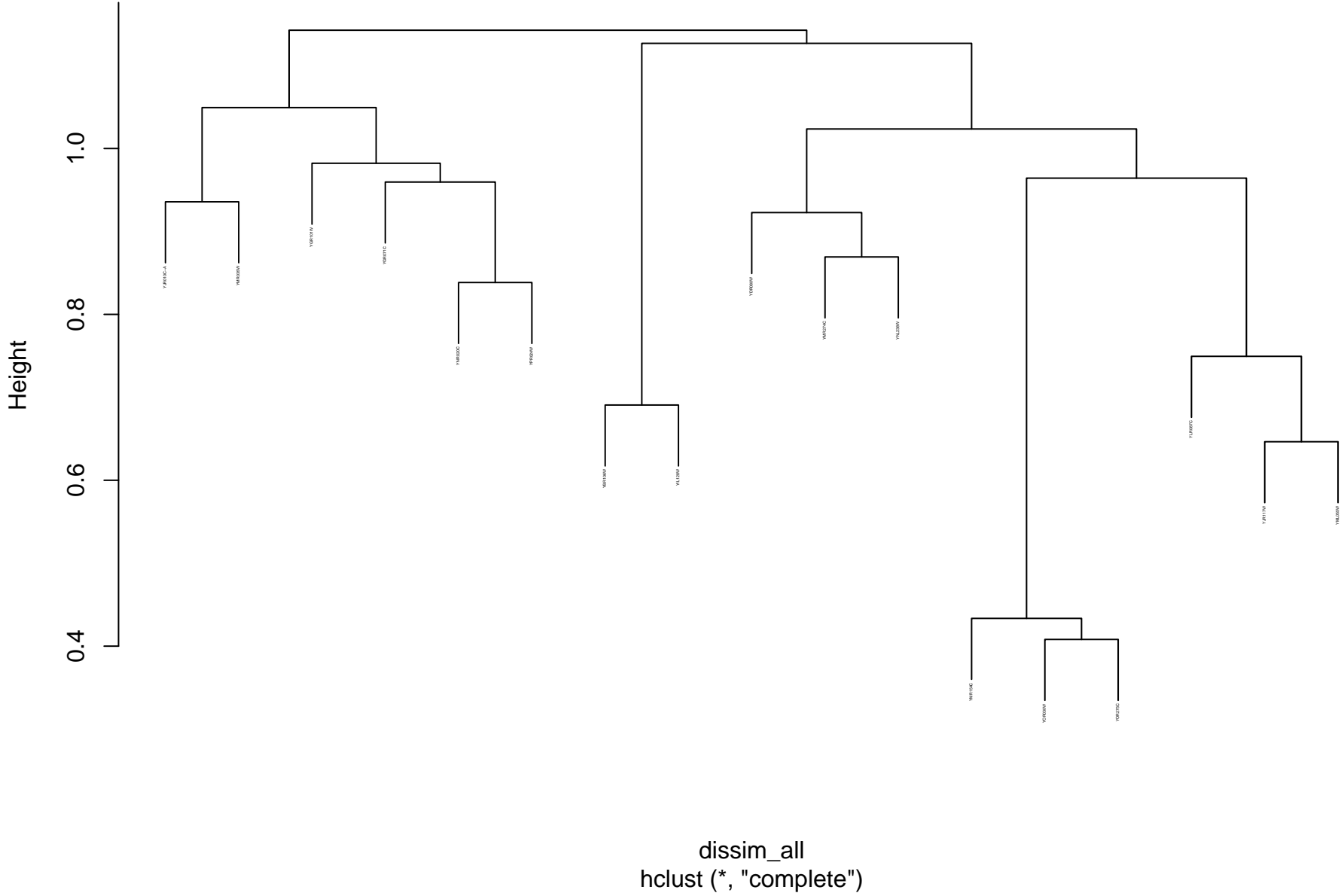
vacuole organization_GO_pearson_complete



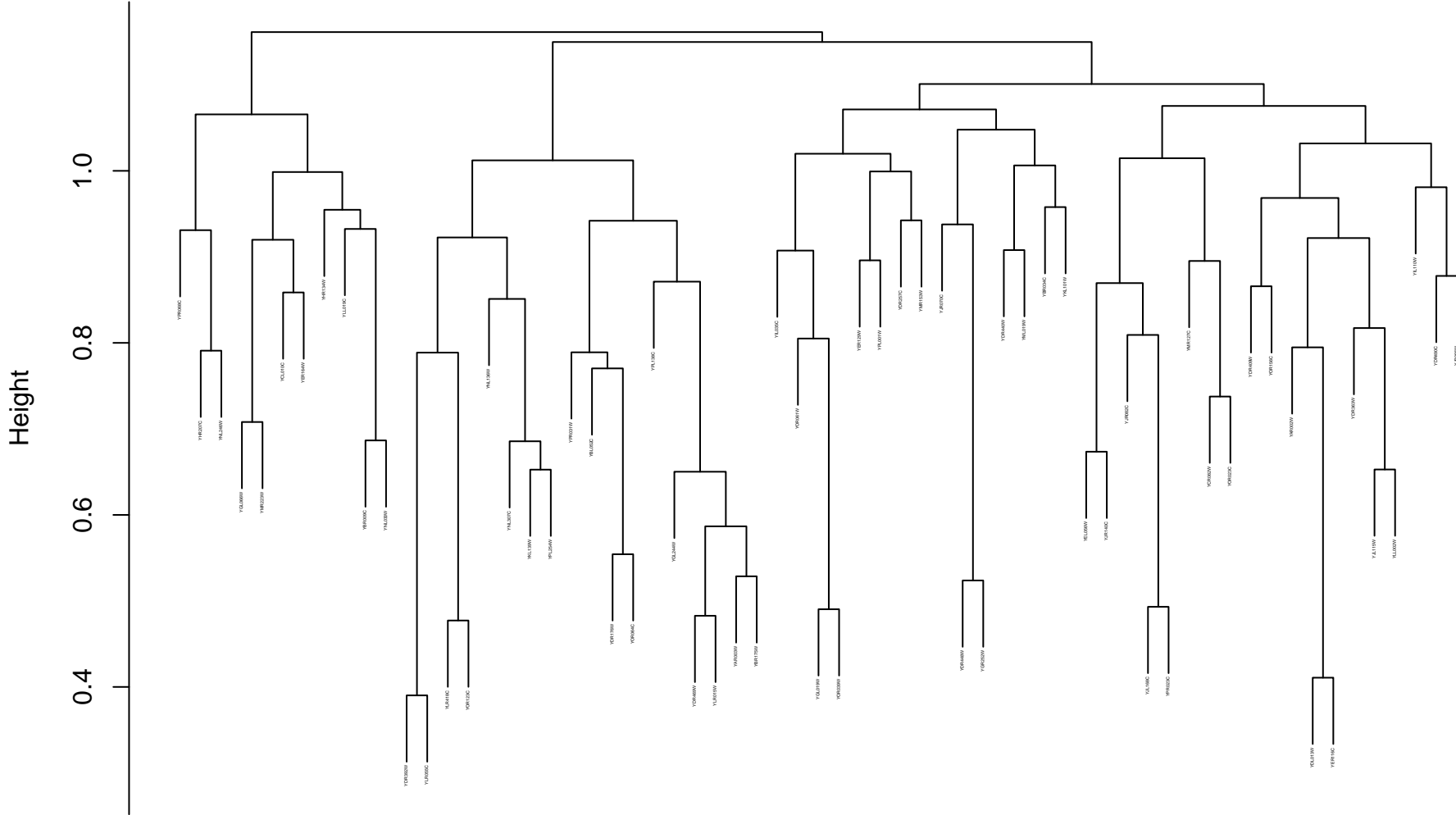
cytokinesis_GO_pearson_complete



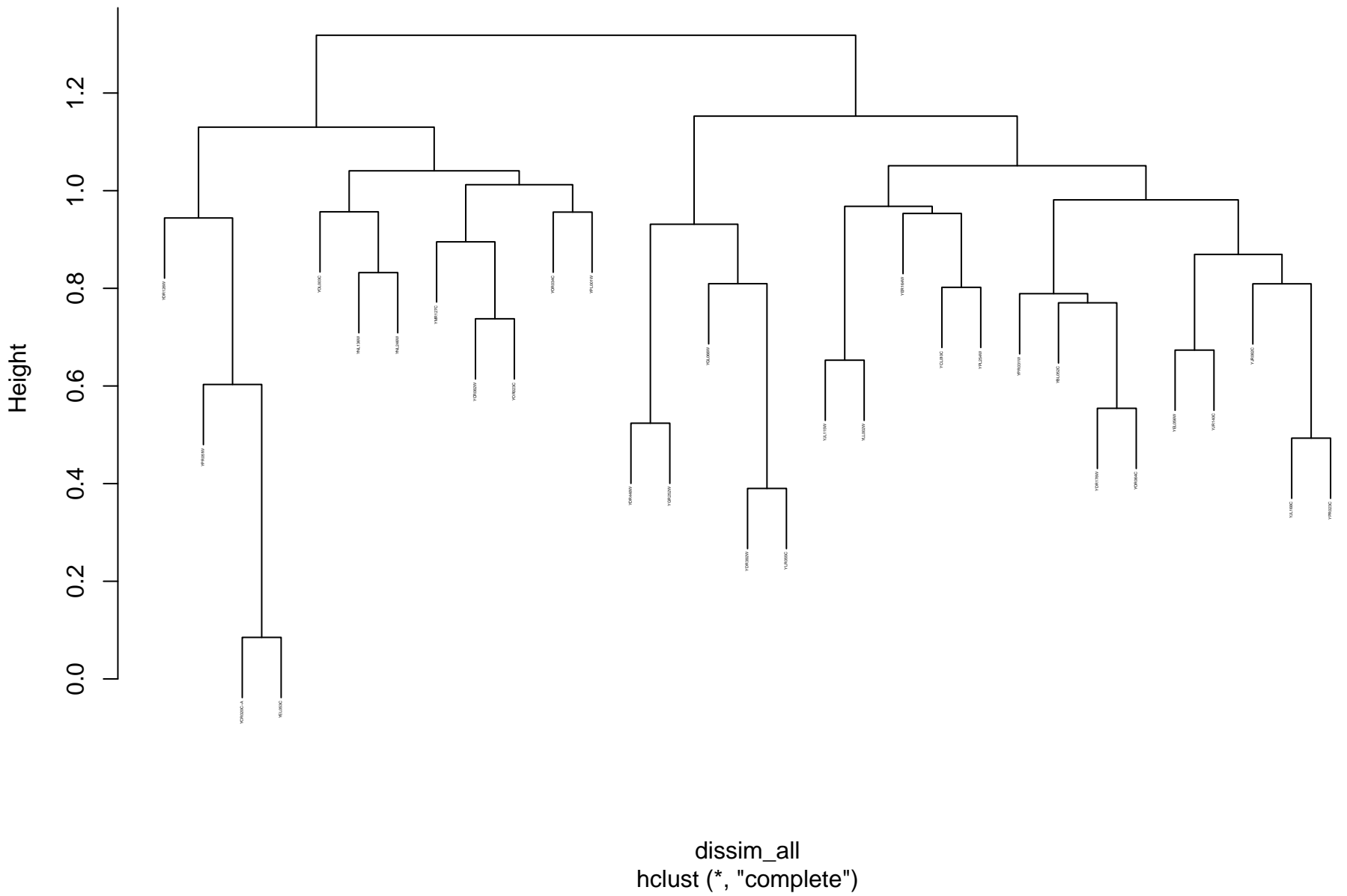
protein maturation_GO_pearson_complete



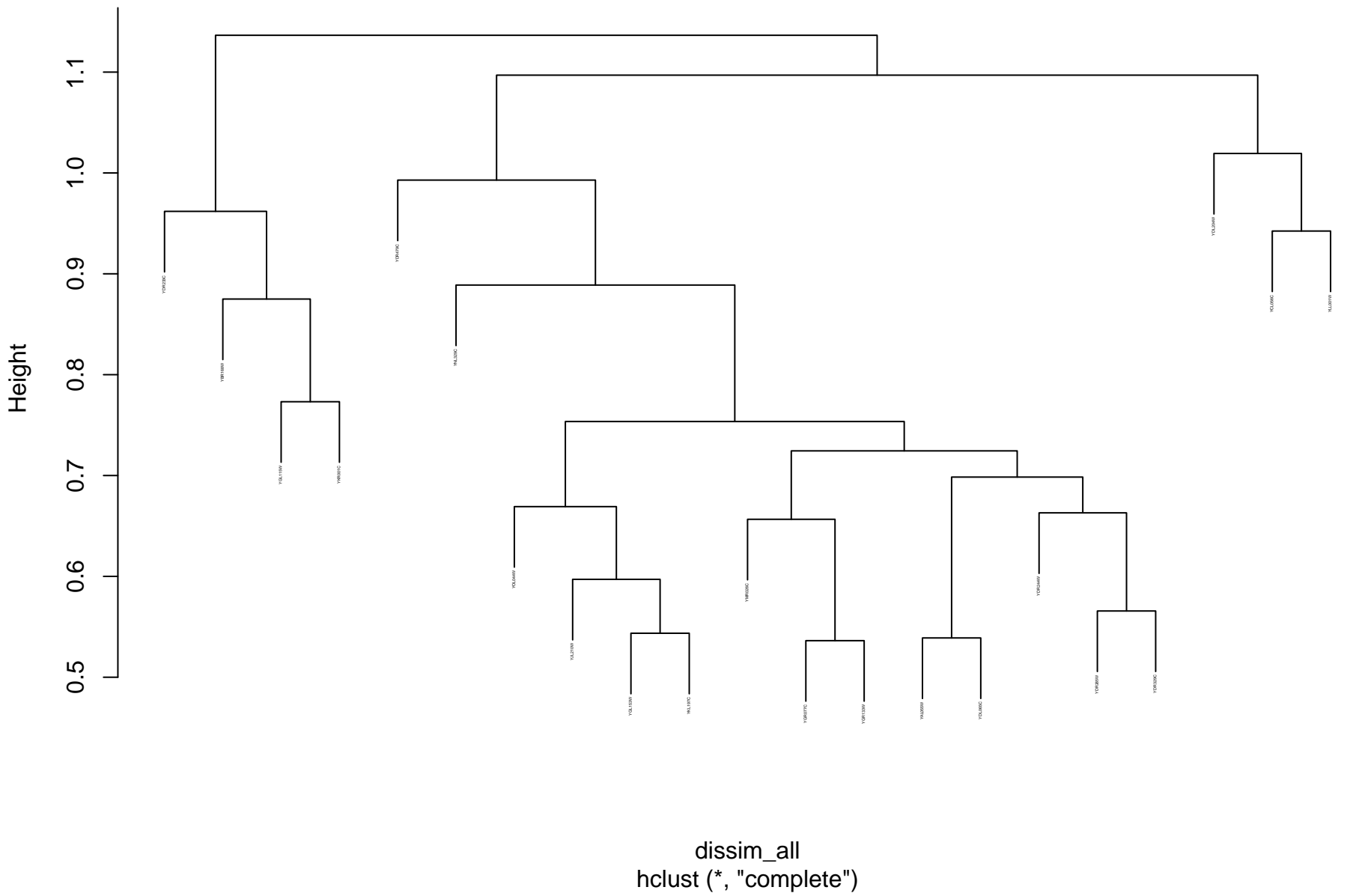
peptidyl-amino acid modification_GO_pearson_complete



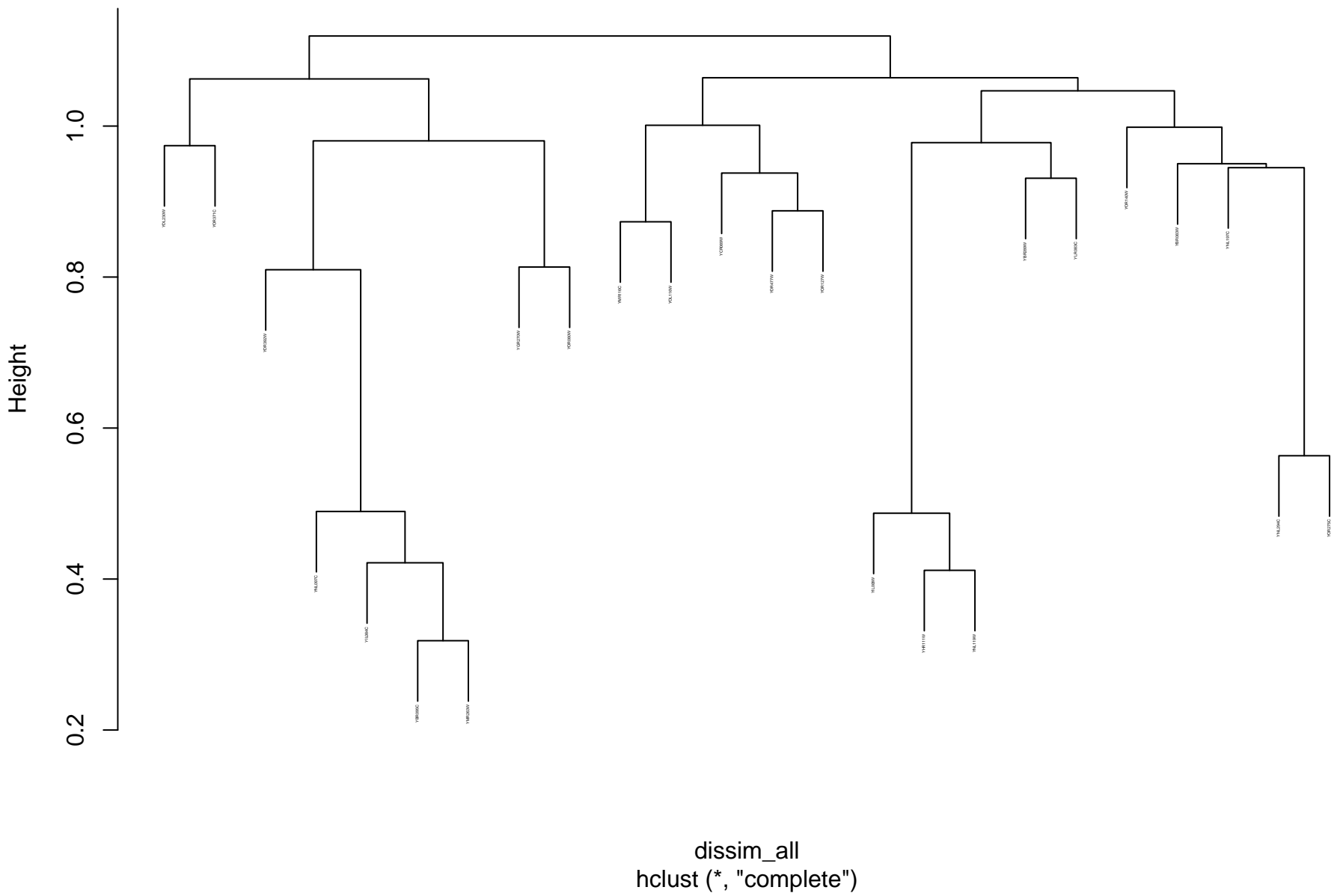
protein acylation_GO_pearson_complete



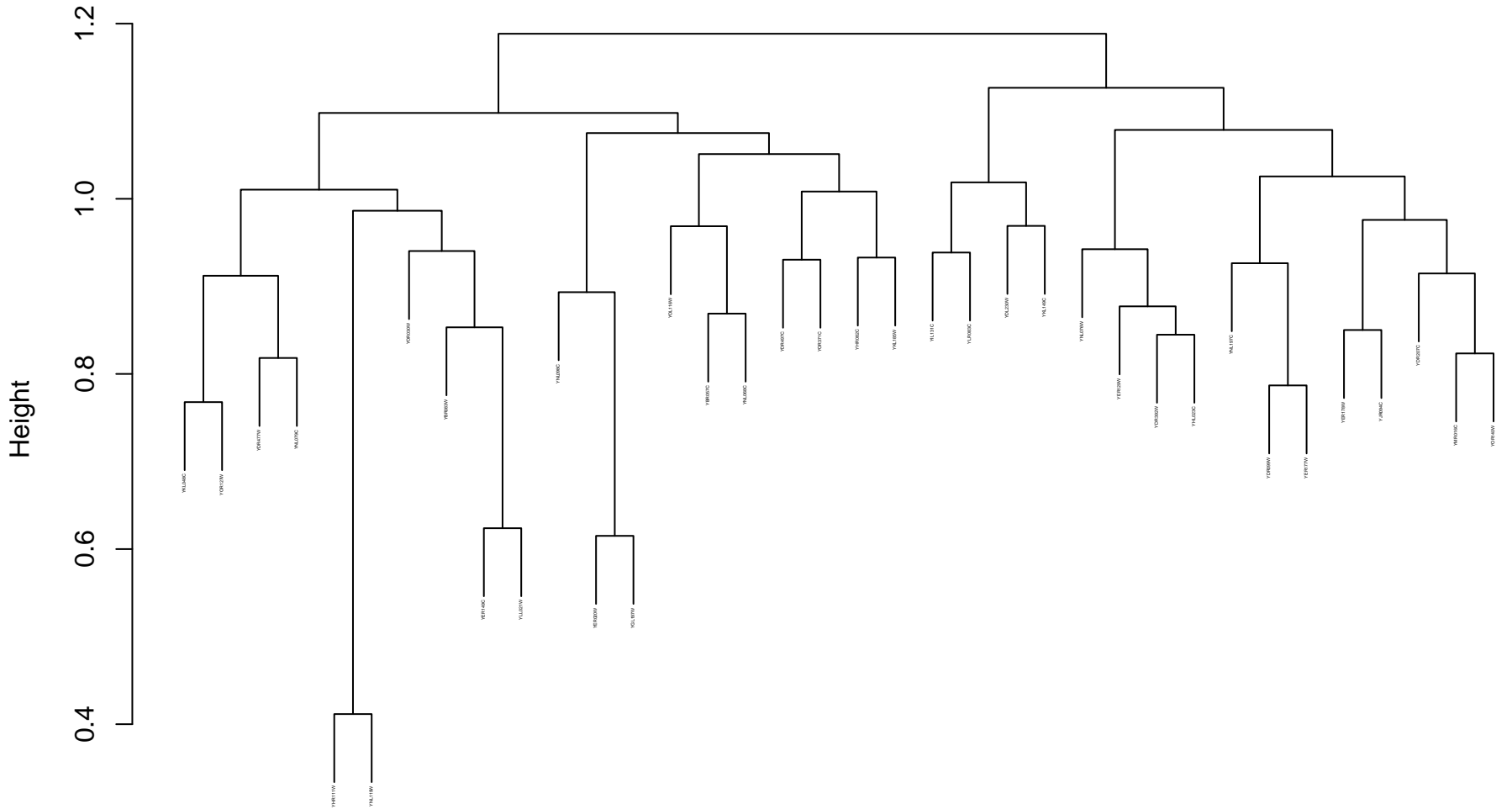
peroxisome organization_GO_pearson_complete



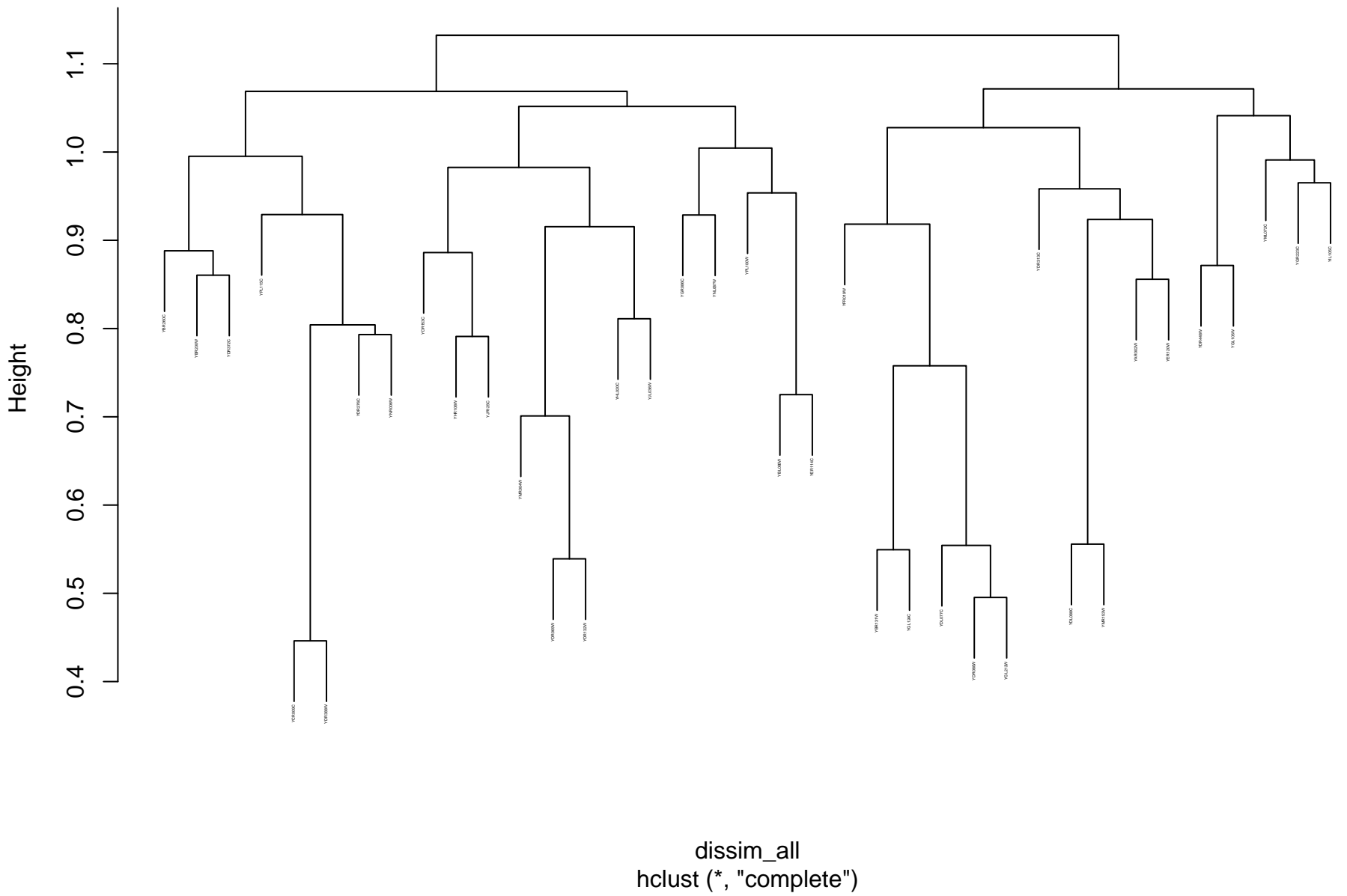
invasive growth in response to glucose limitation_GO_pearson_complete



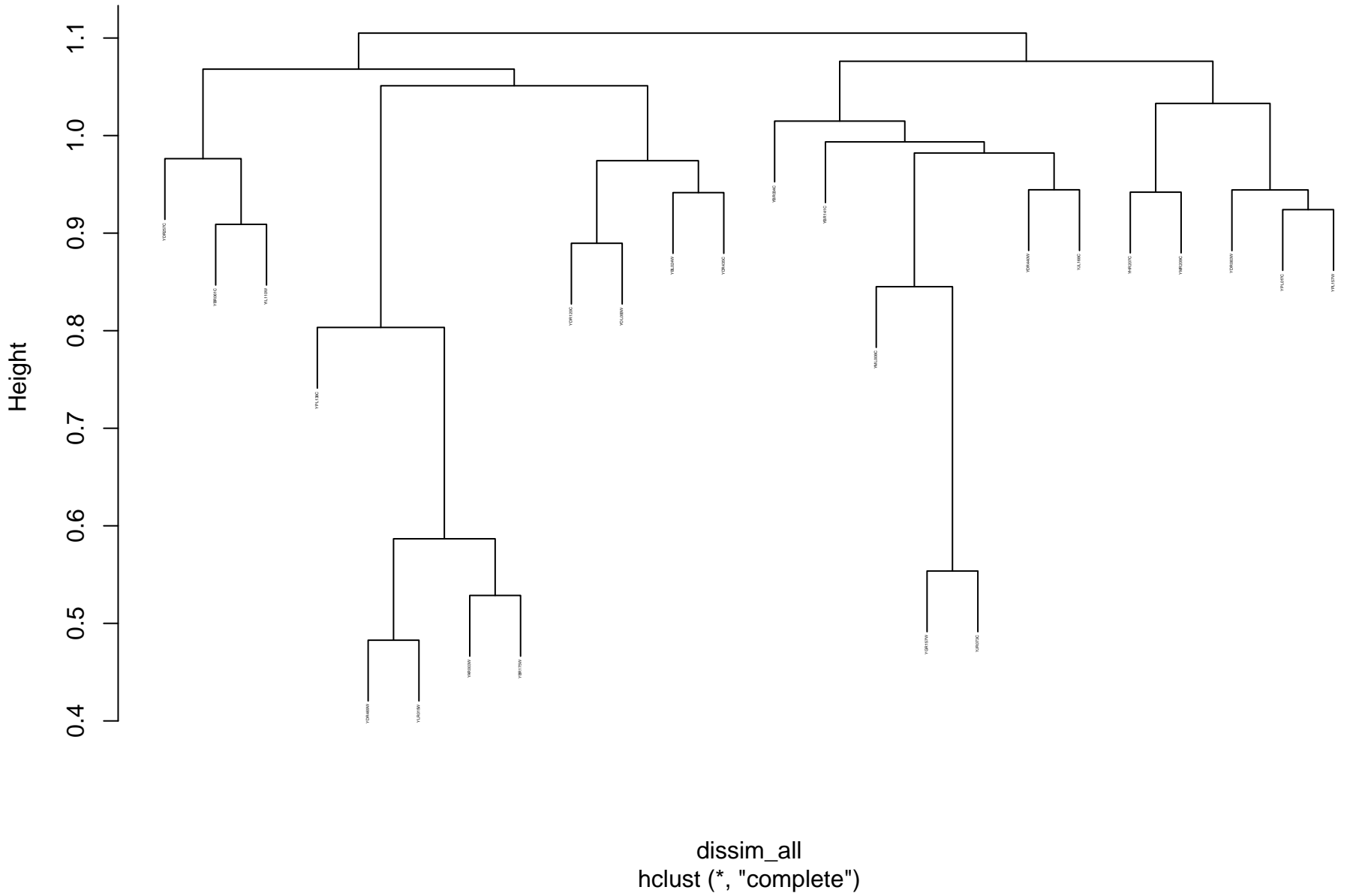
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dissim_all
hclust (*, "complete")
```



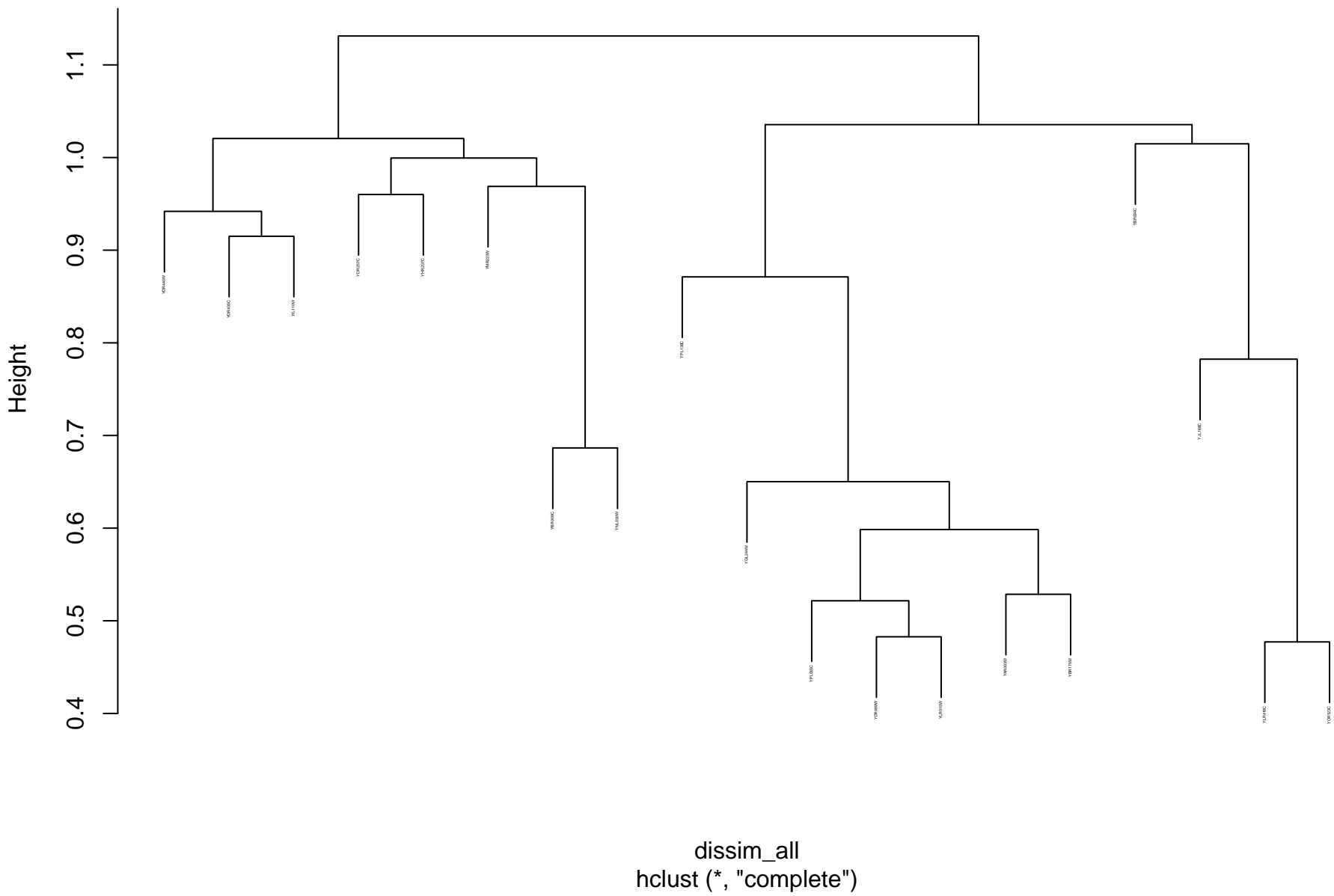
lipid binding_GO_pearson_complete



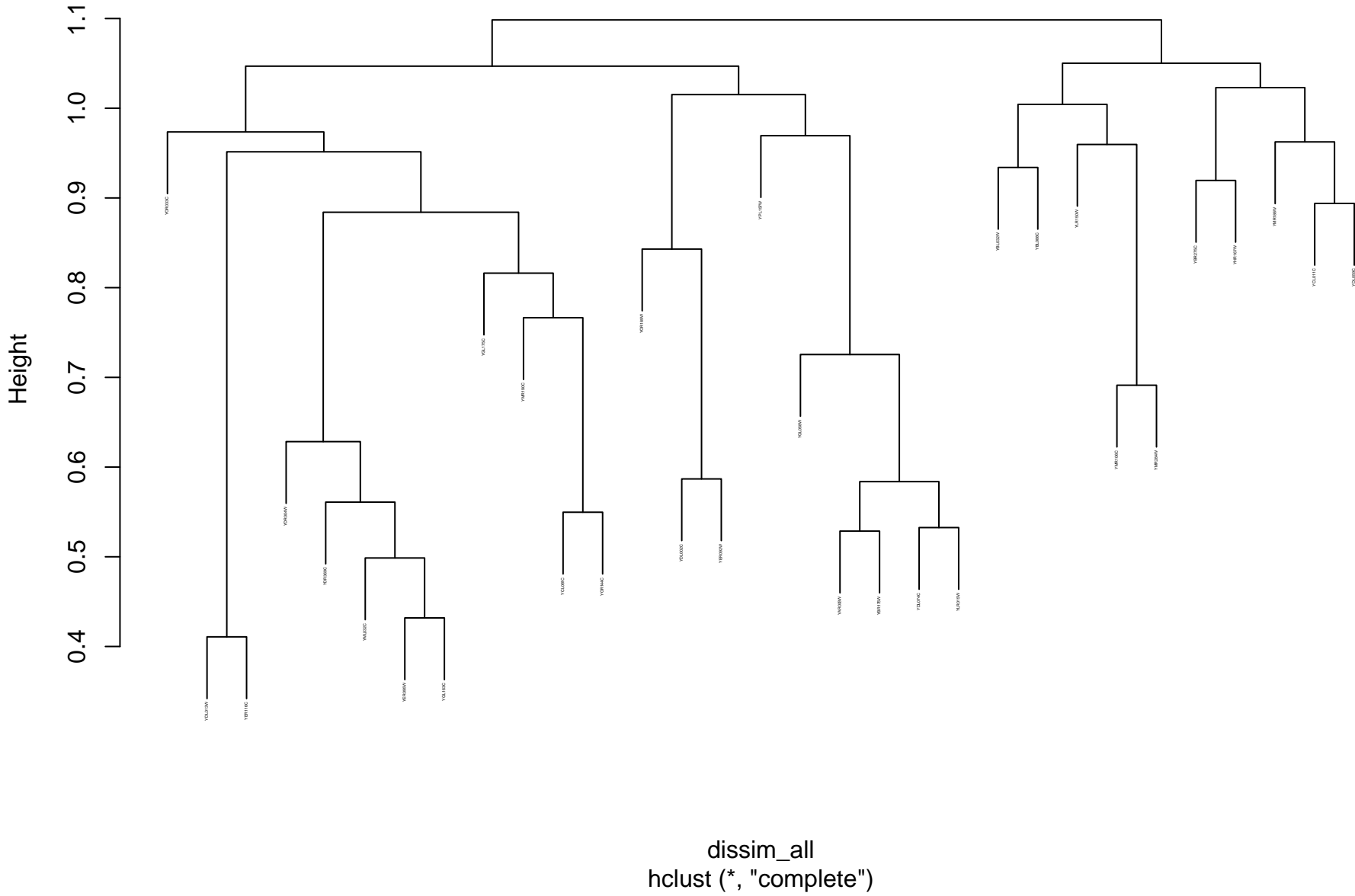
methyltransferase activity_GO_pearson_complete



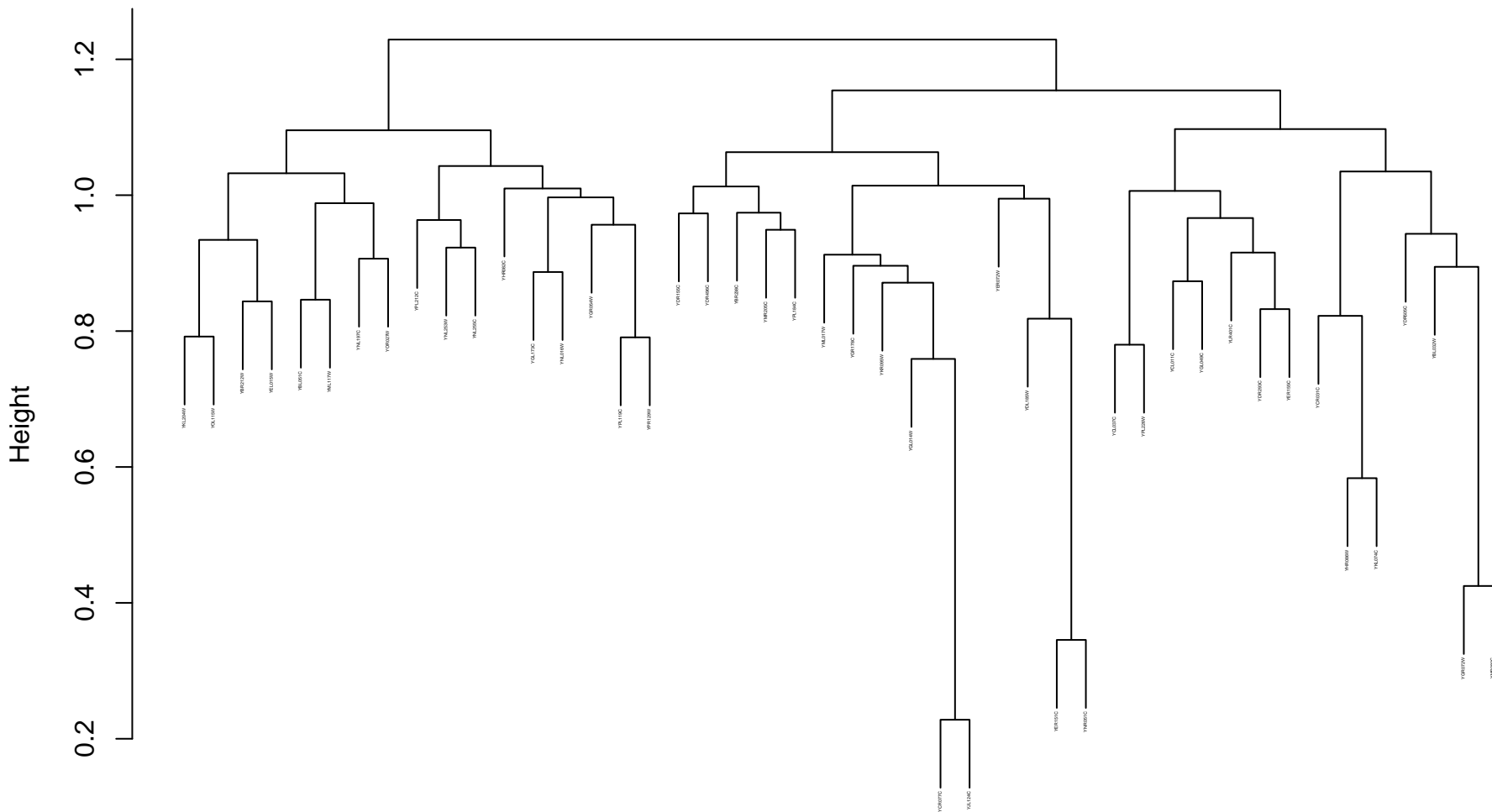
protein alkylation_GO_pearson_complete



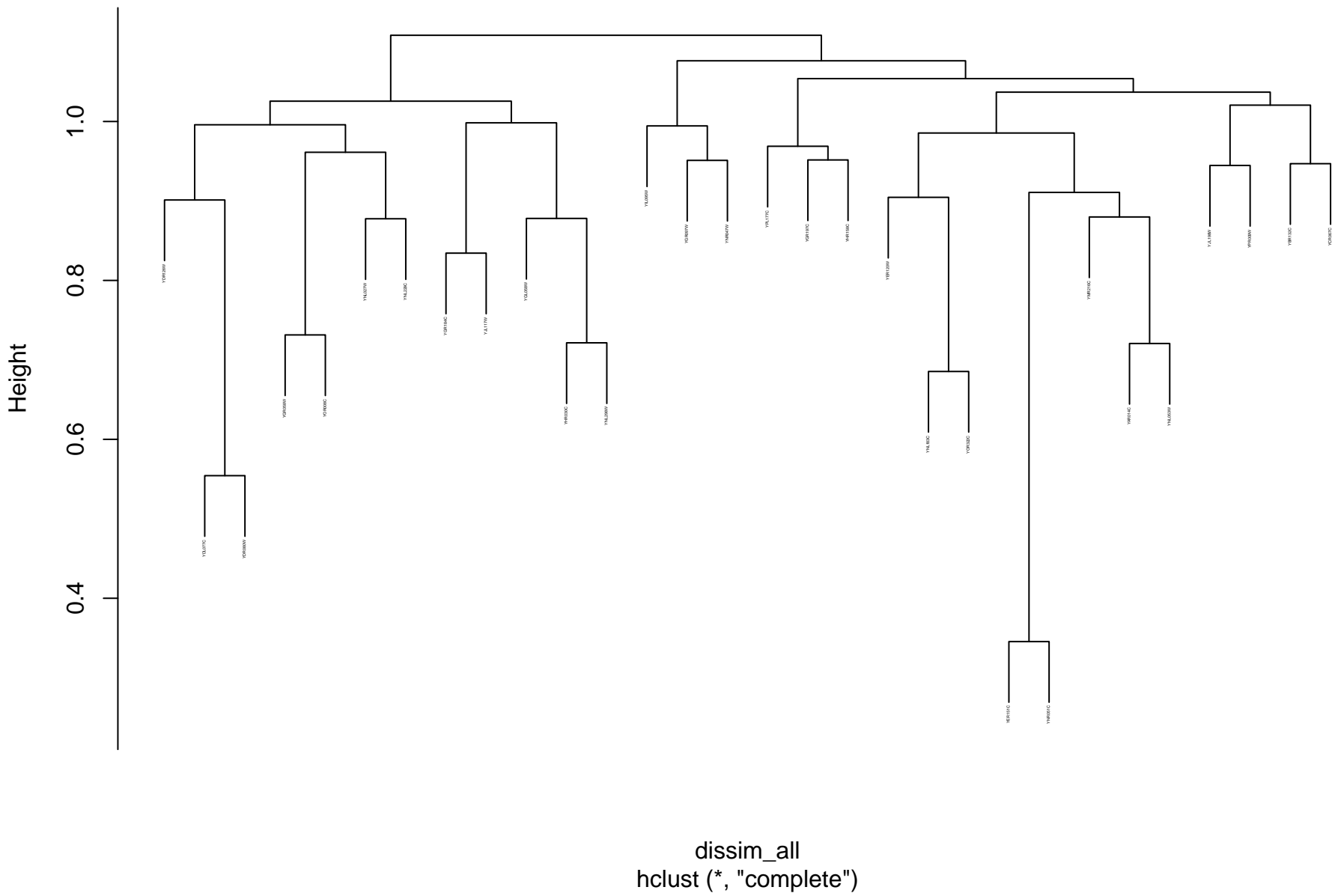
telomere organization_GO_pearson_complete



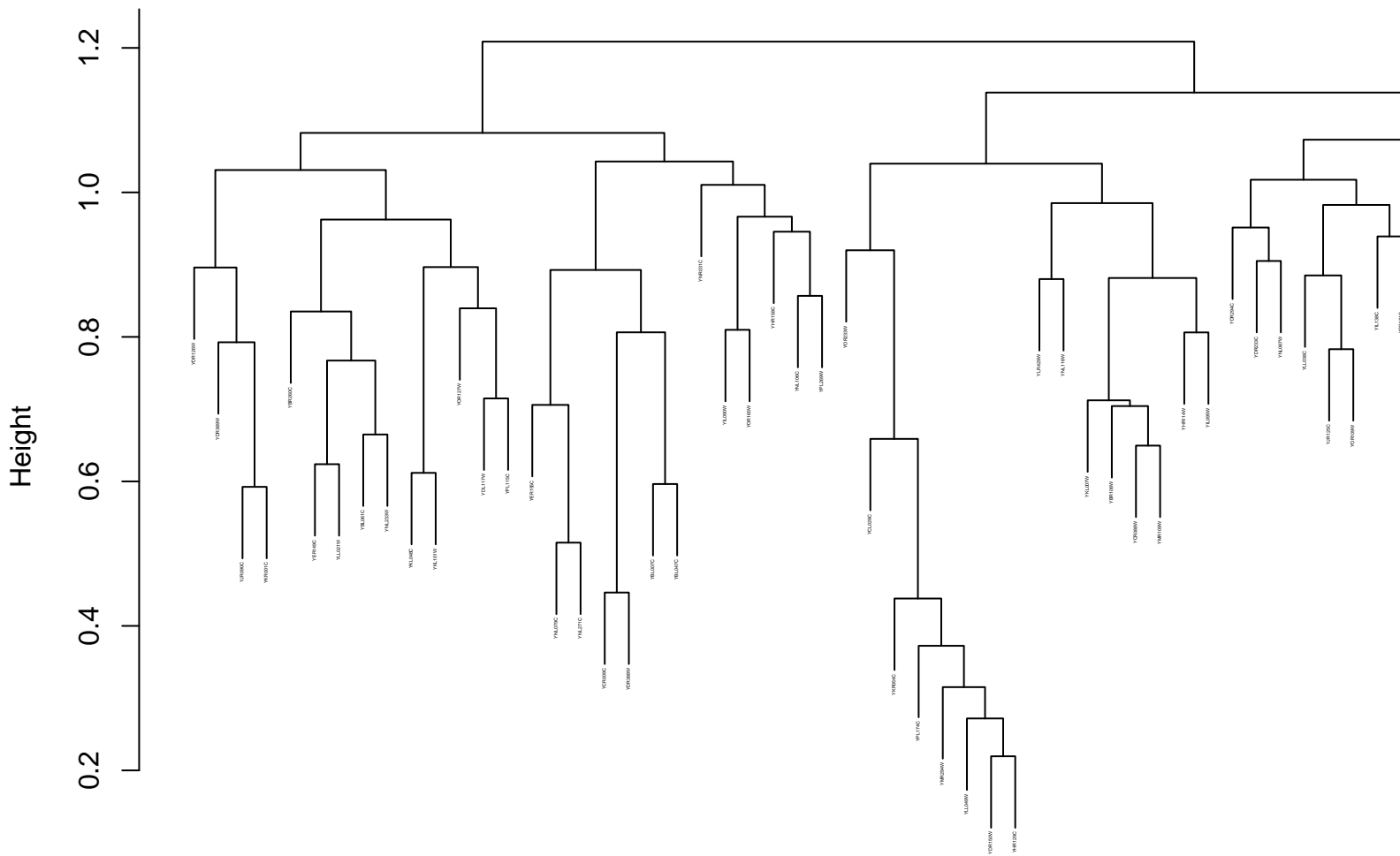
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dissim_all
hclust (*, "complete")
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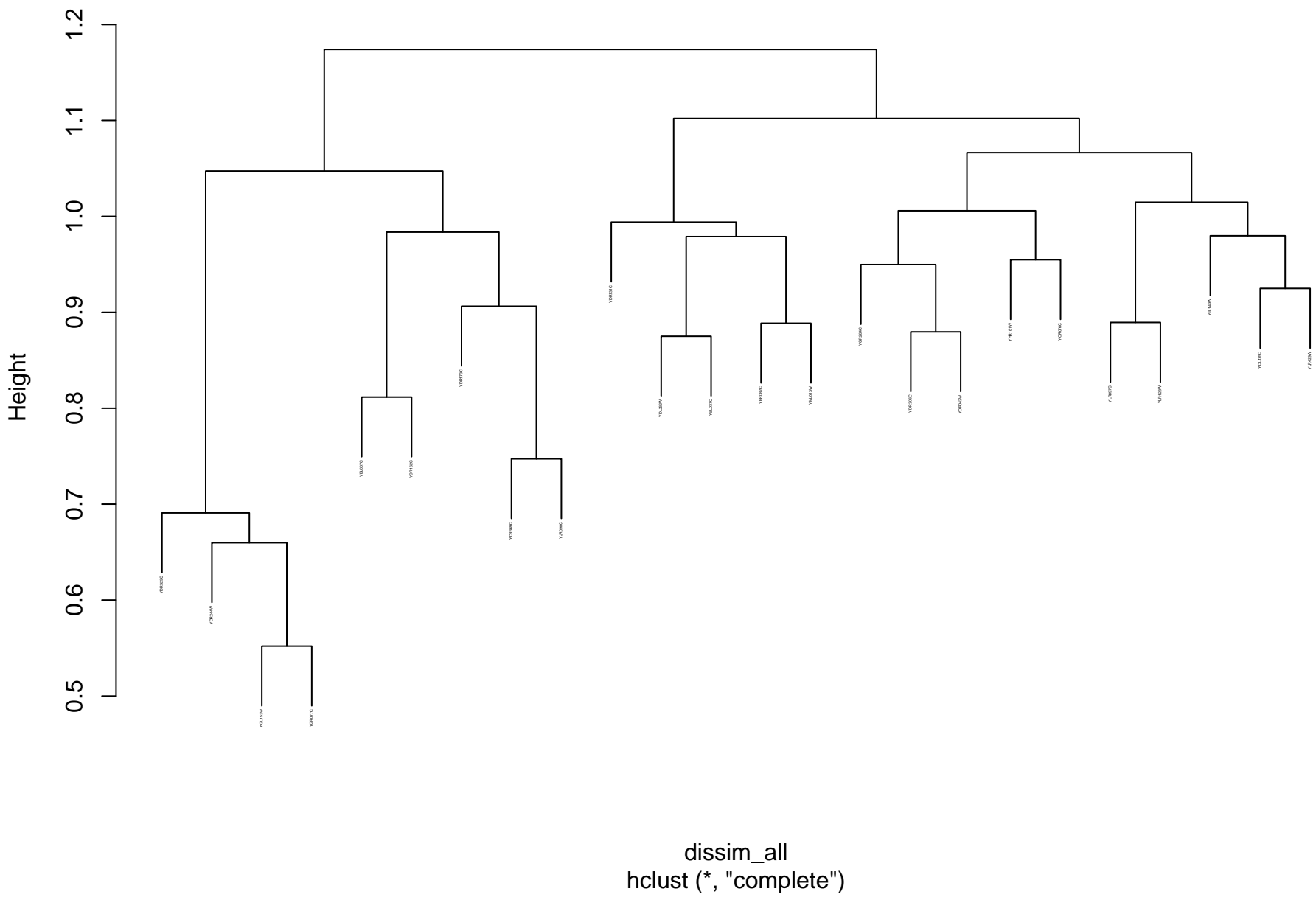
regulation of transport_GO_pearson_complete



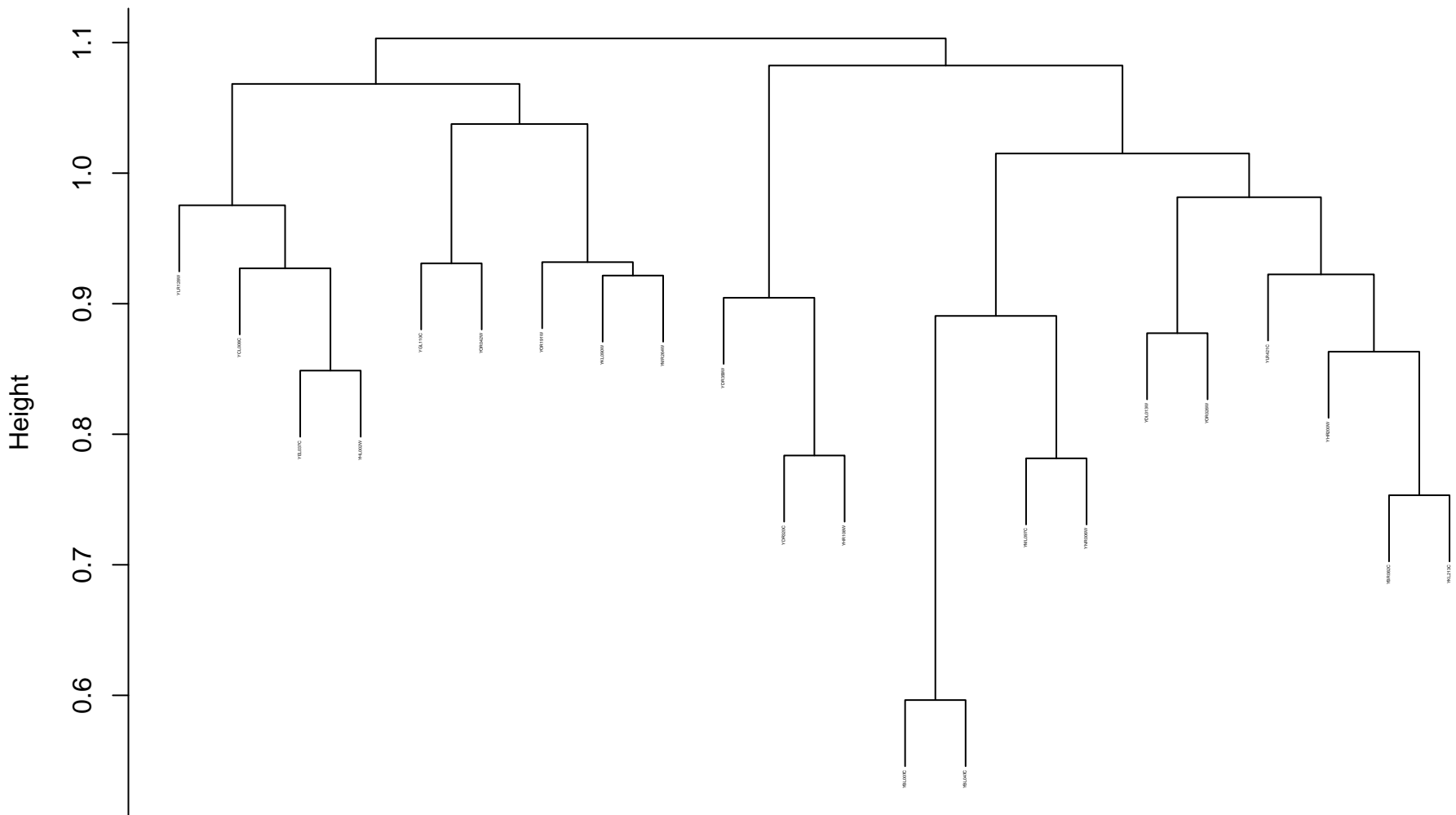
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dissim_all
hclust (*, "complete")
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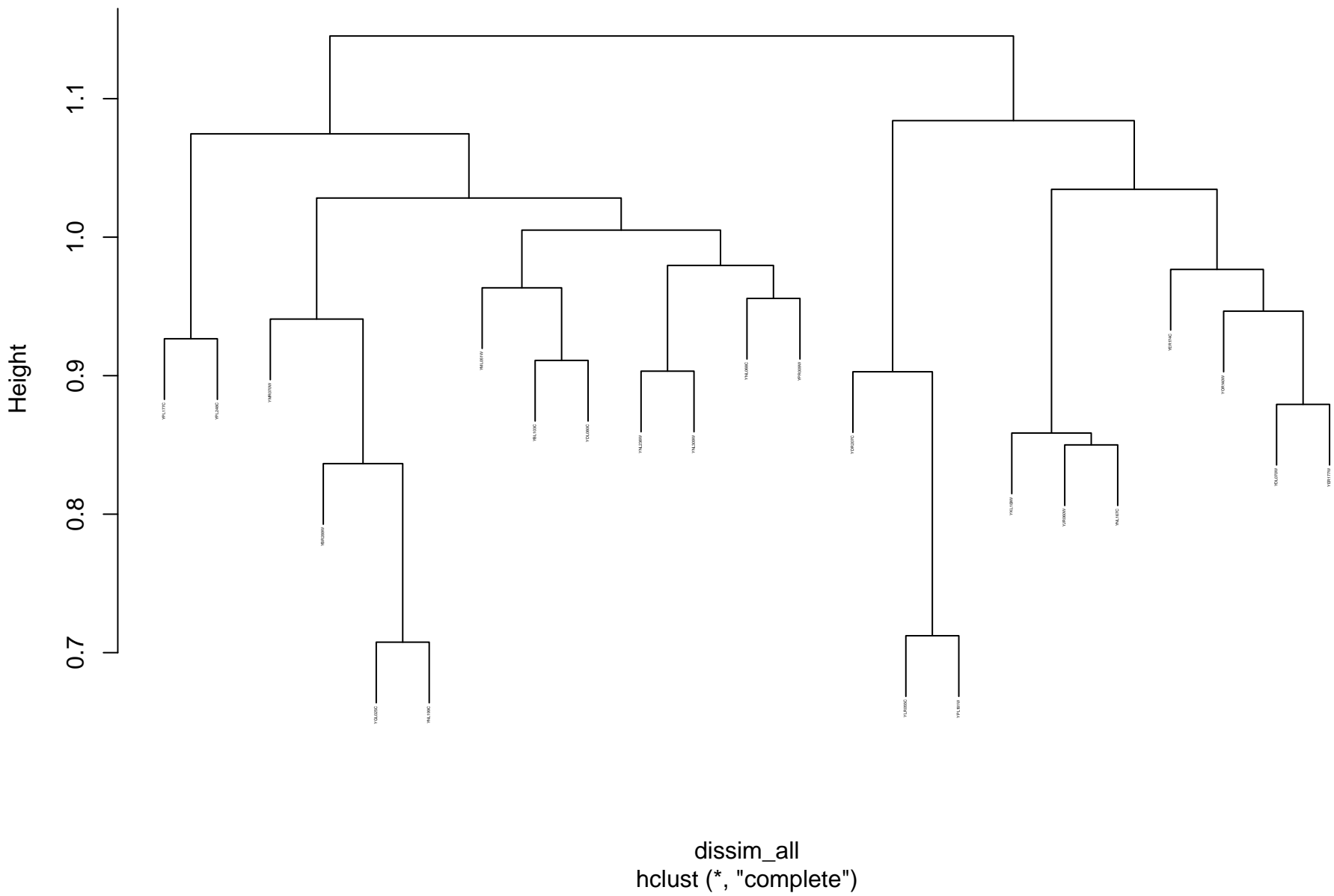
protein binding, bridging_GO_pearson_complete



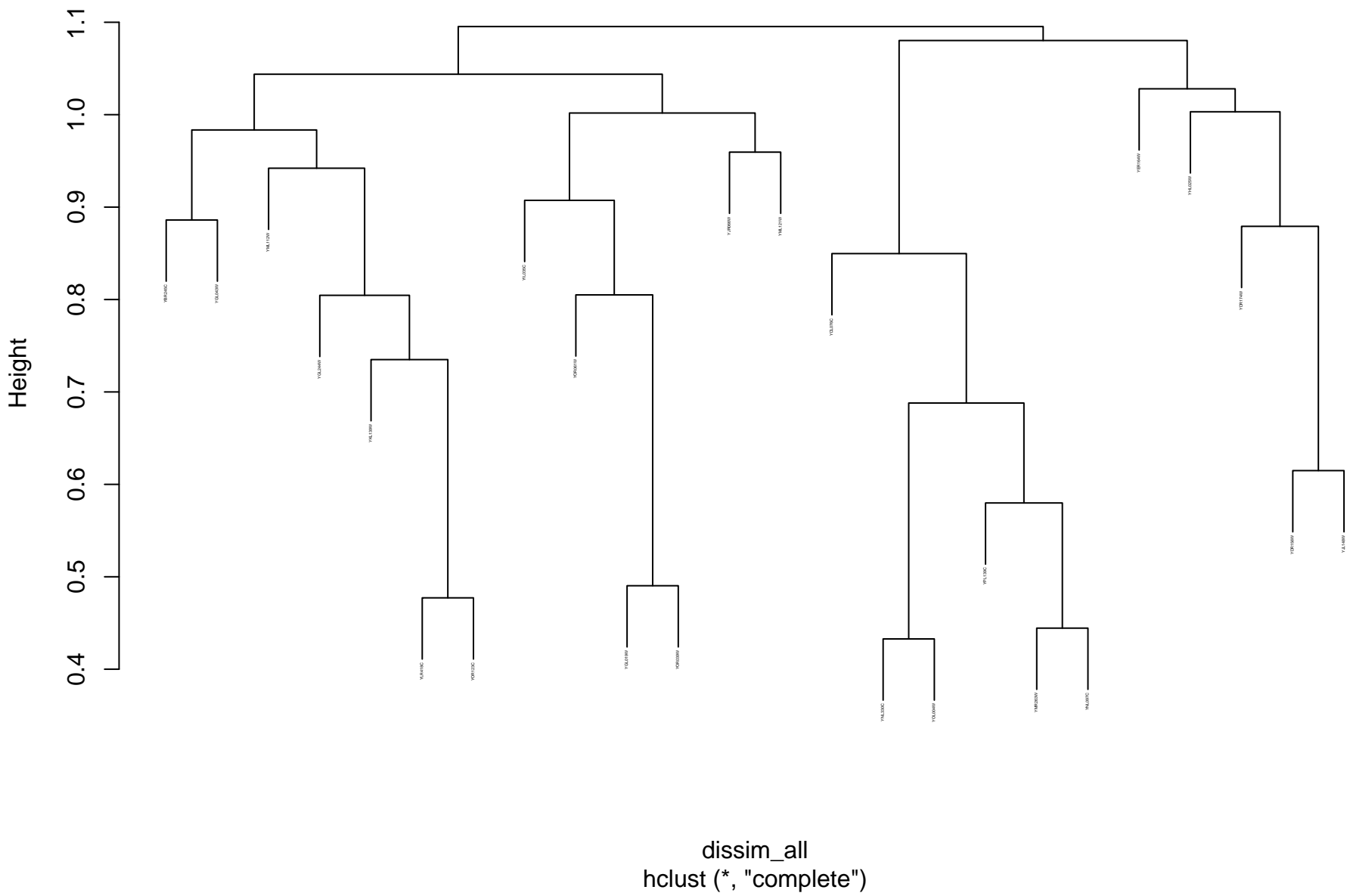
ubiquitin-like protein binding_GO_pearson_complete



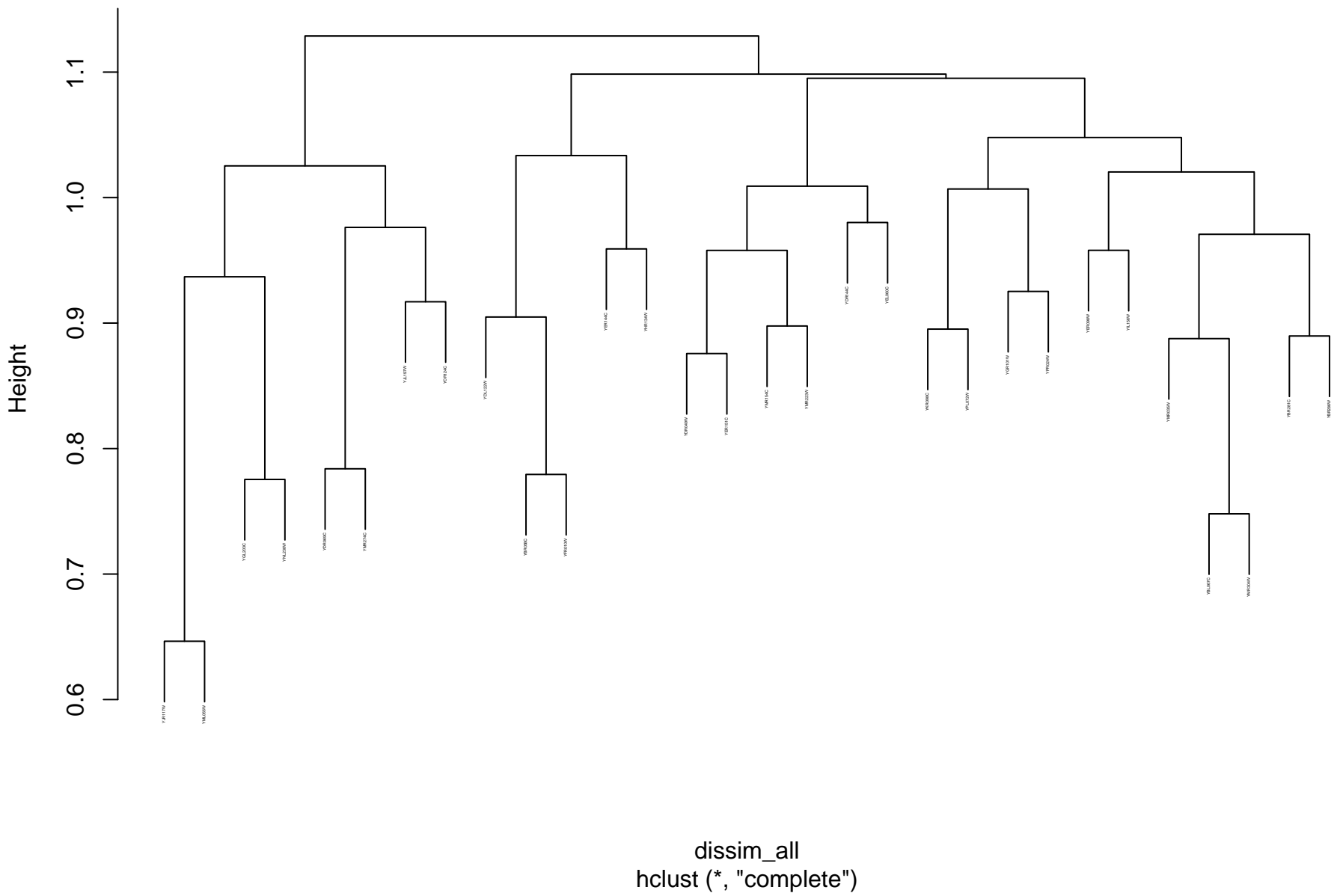
transcription factor binding_GO_pearson_complete



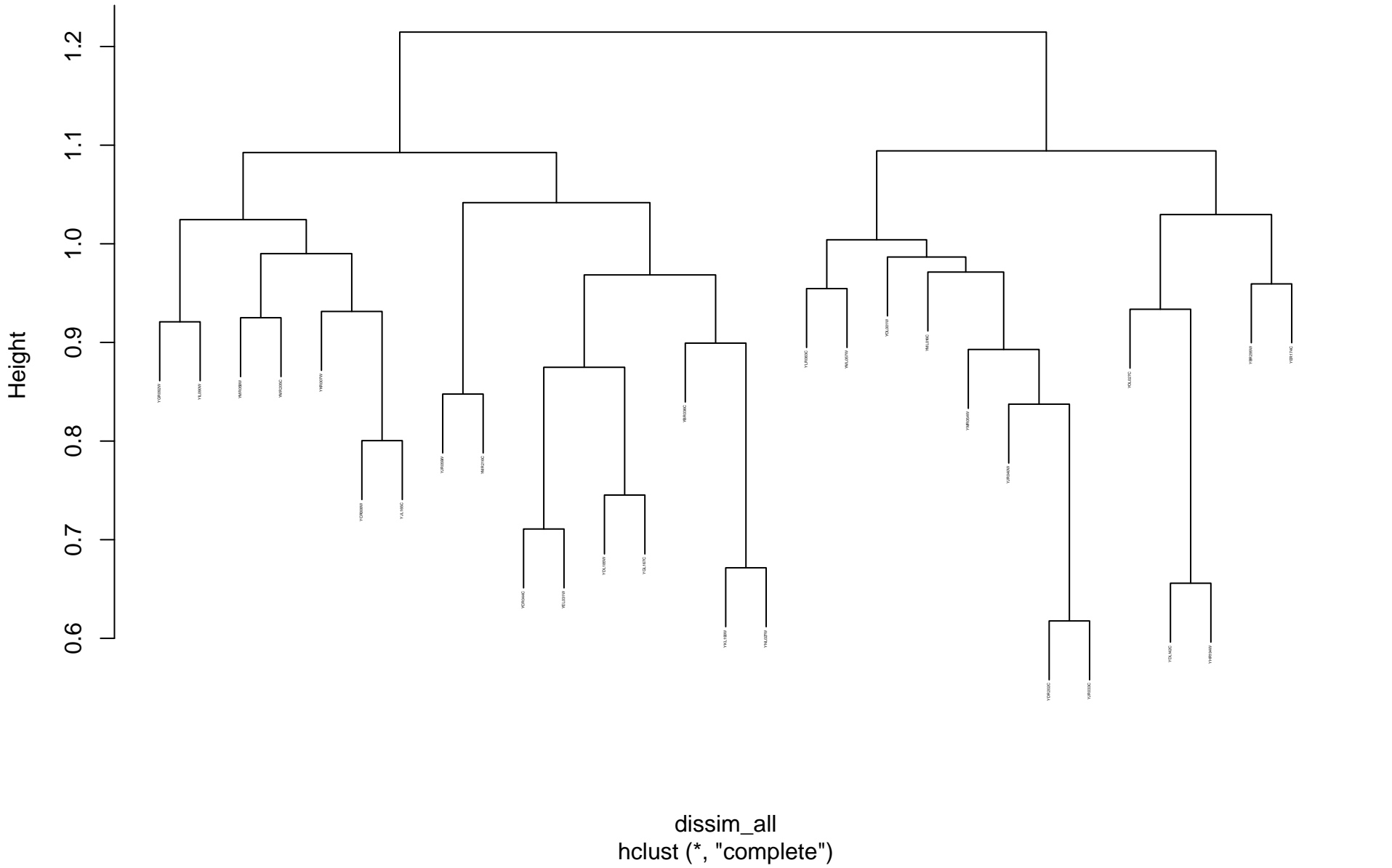
transcription from RNA polymerase I promoter_GO_pearson_complete



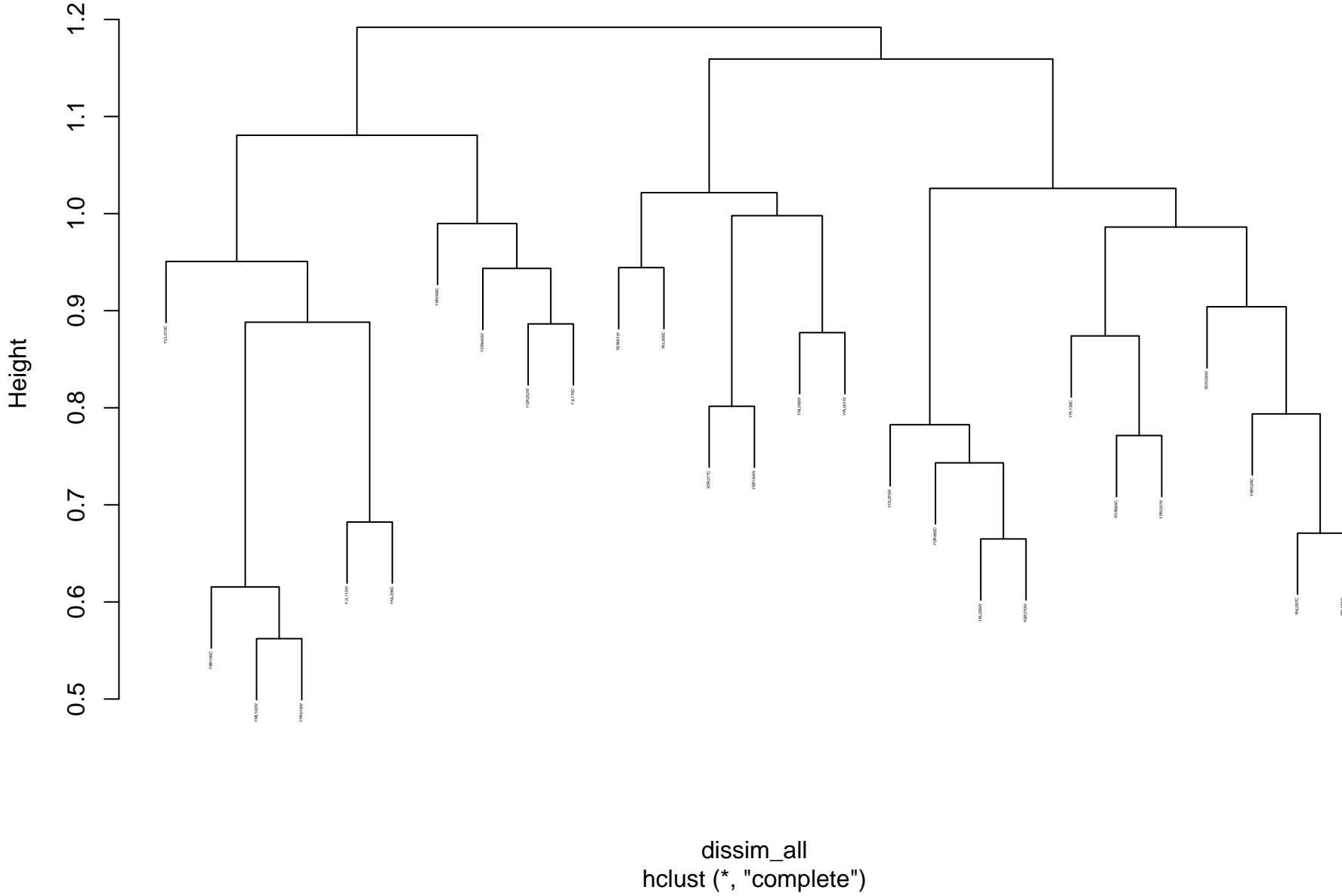
peptidase activity_GO_pearson_complete



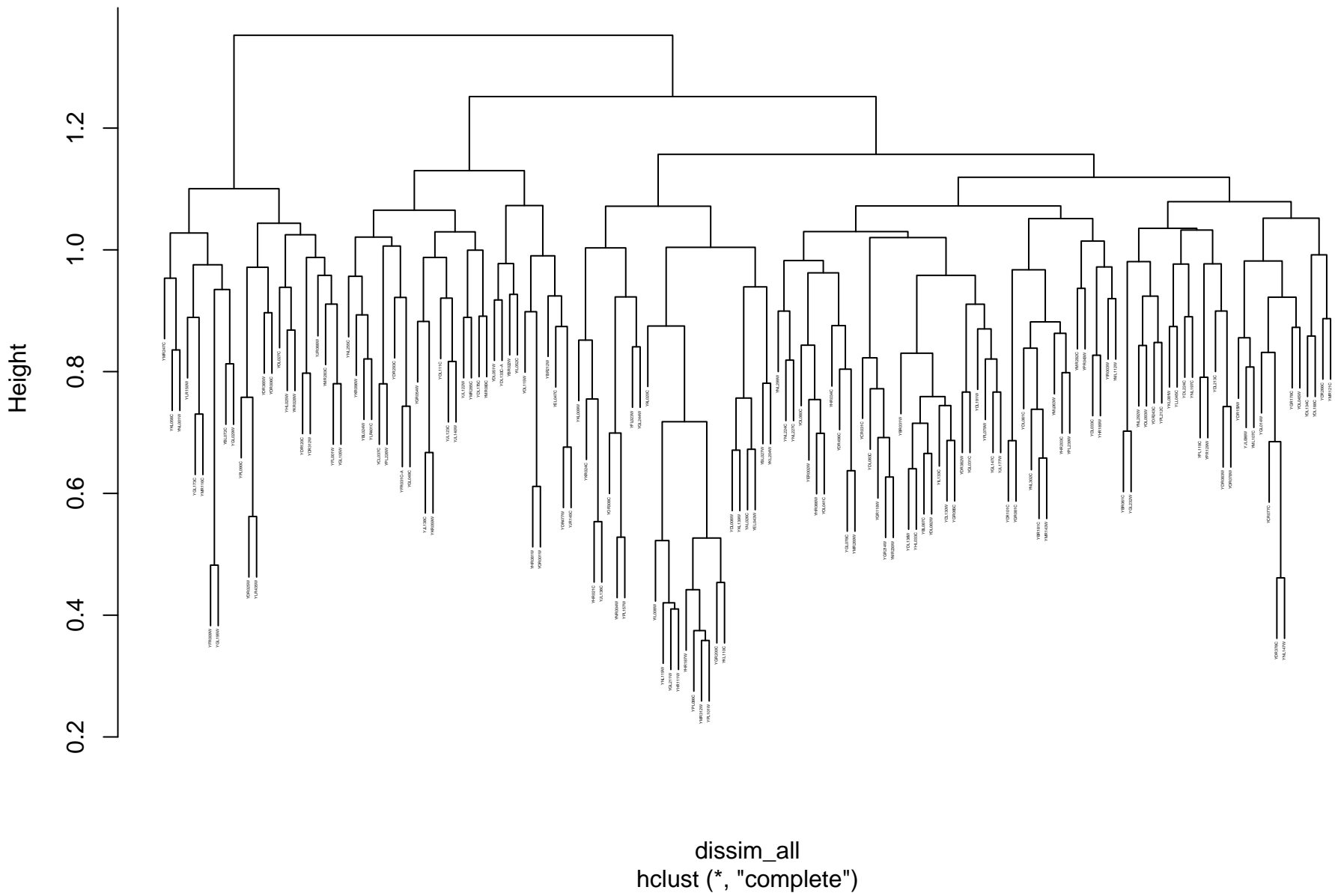
cellular ion homeostasis_GO_pearson_complete



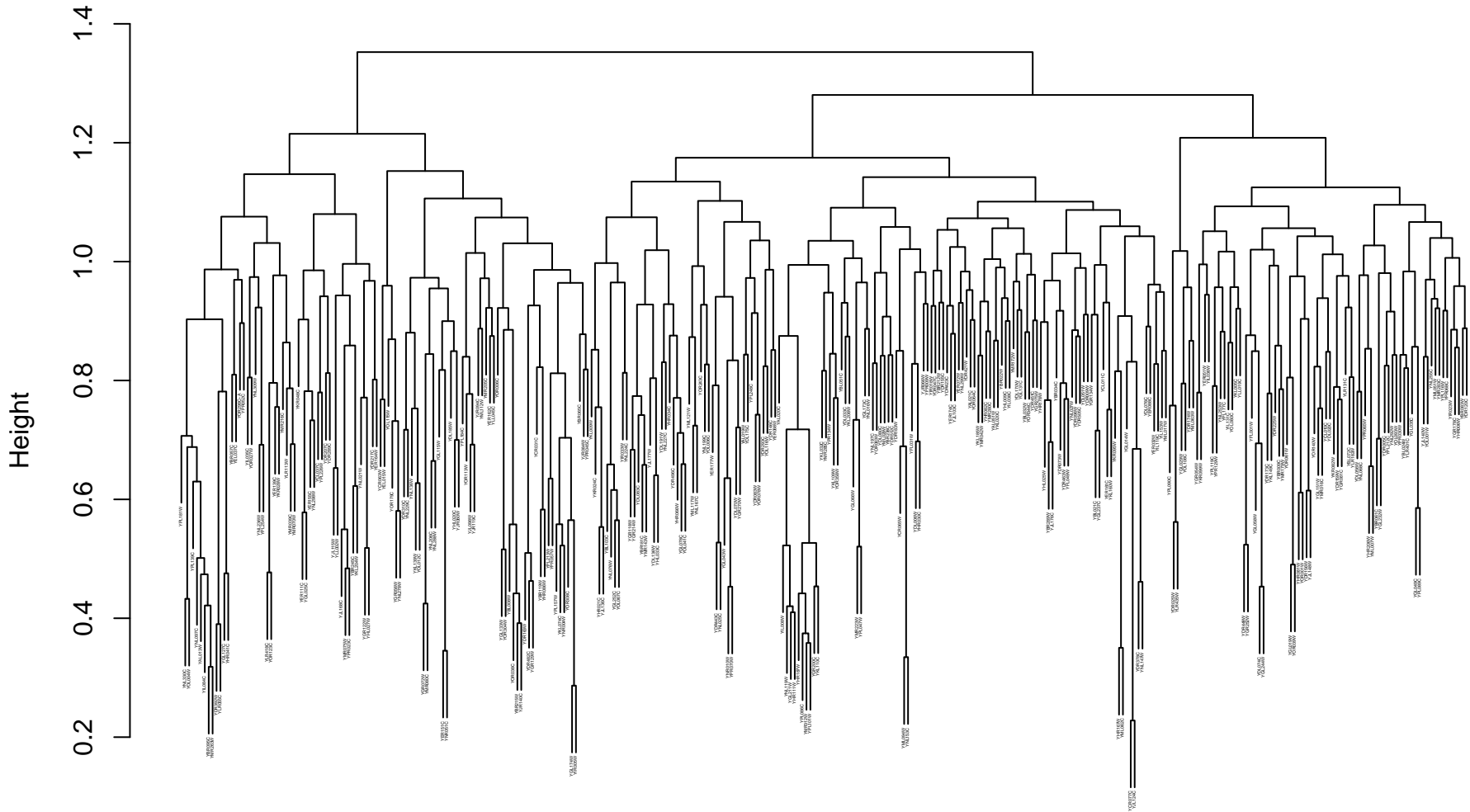
histone binding_GO_pearson_complete



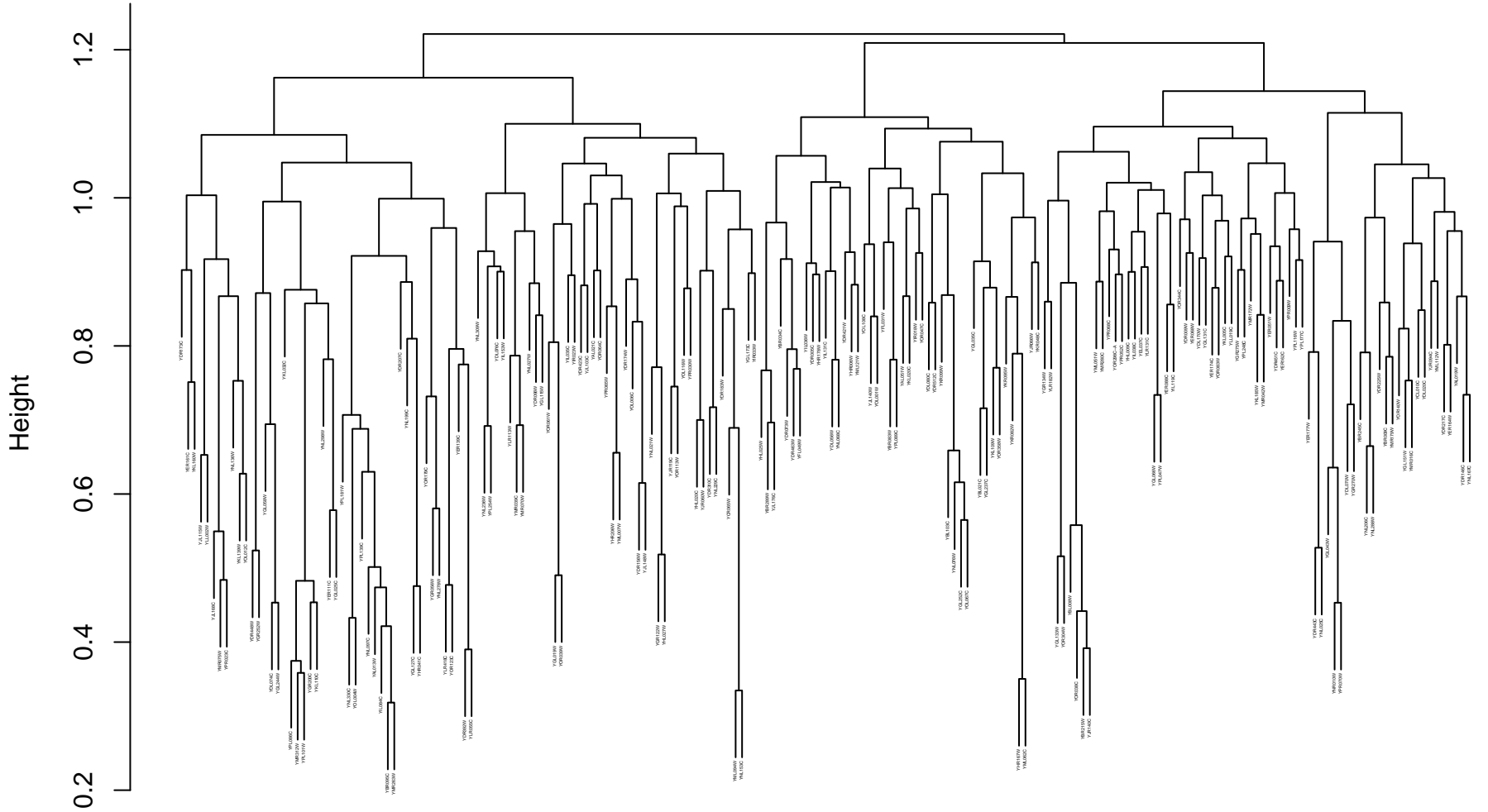
ribosomes and translation_GO_pearson_complete



transcription and mRNA processing_GO_pearson_complete

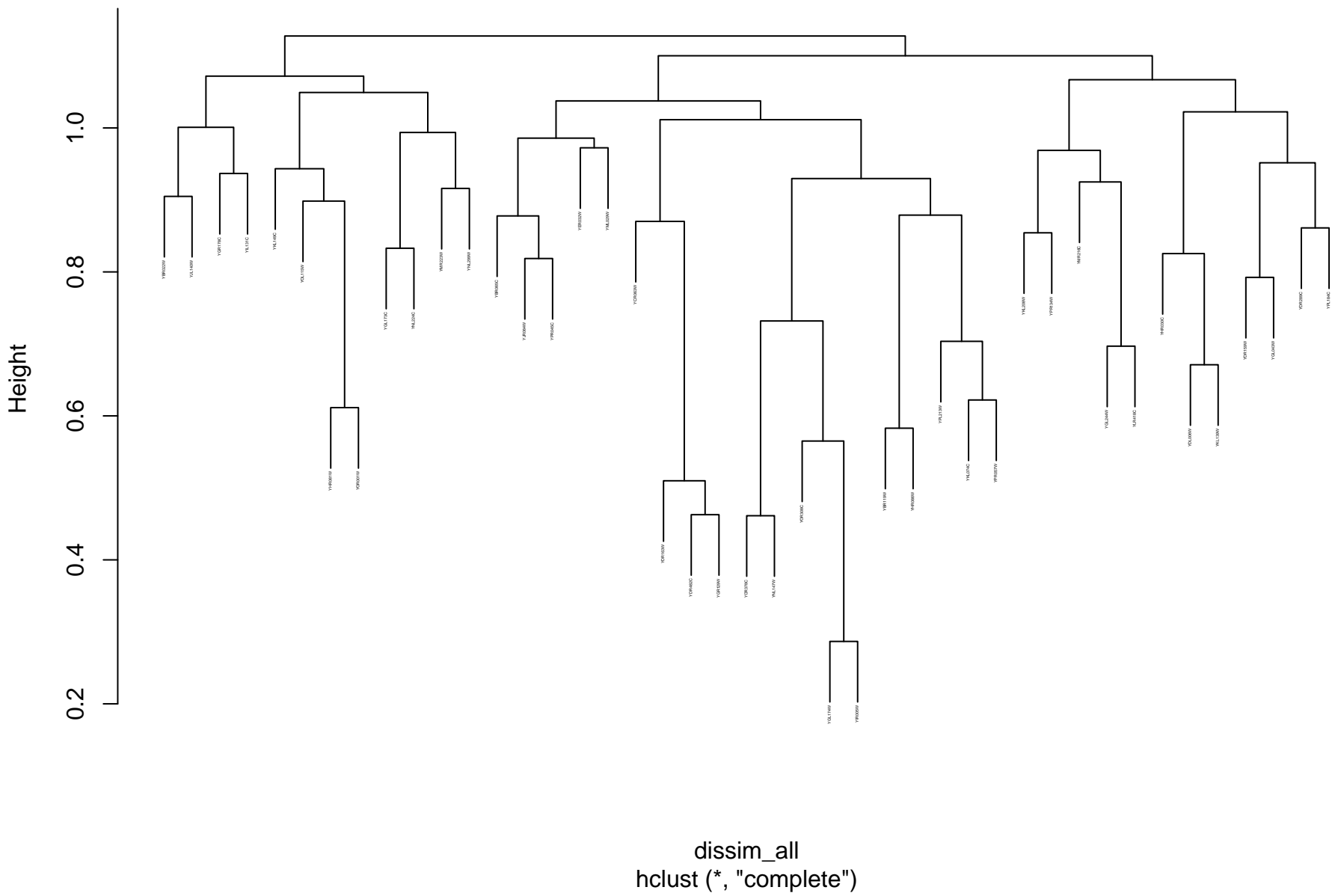


transcription_GO_pearson_complete

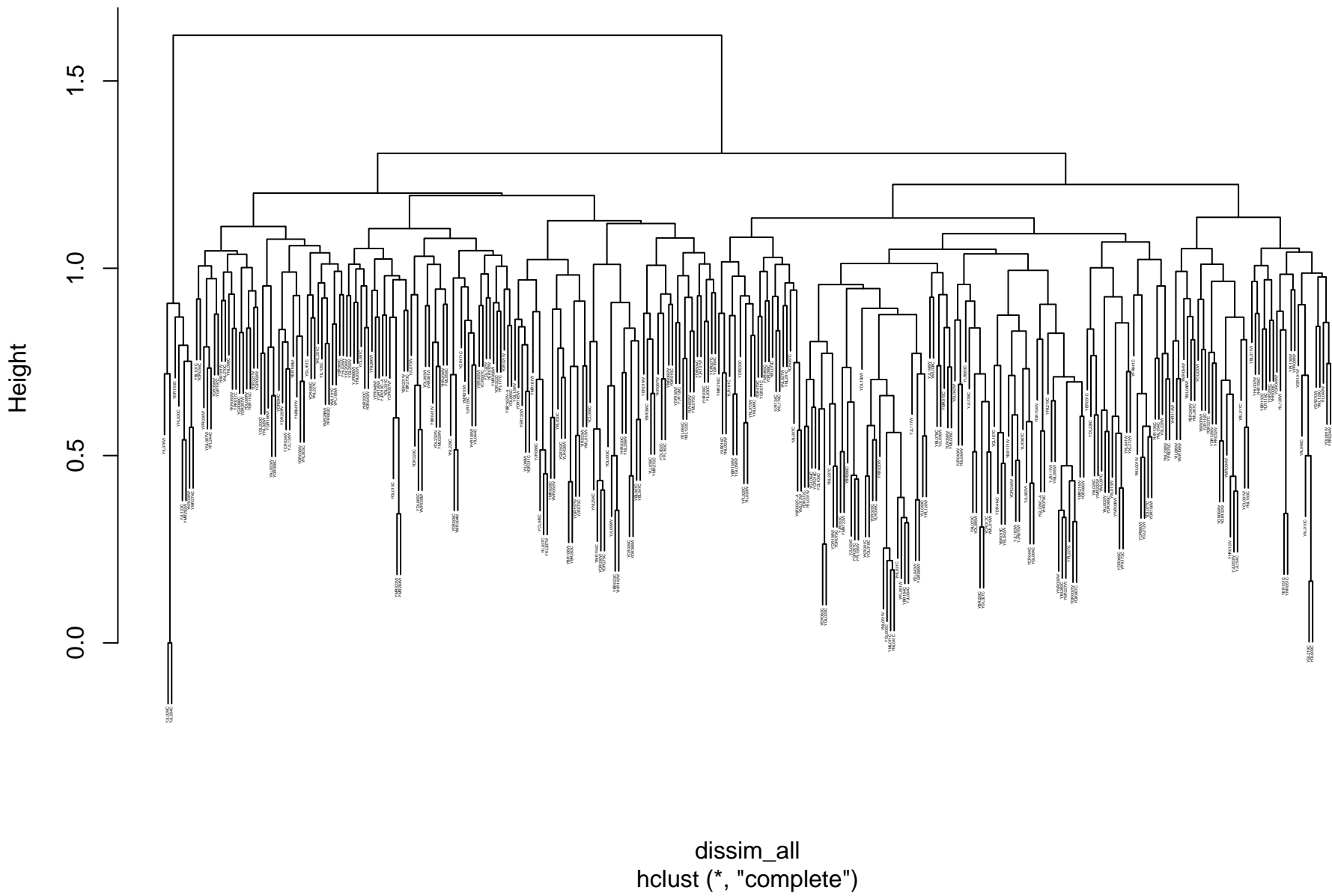


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dissim_all
hclust (*, "complete")
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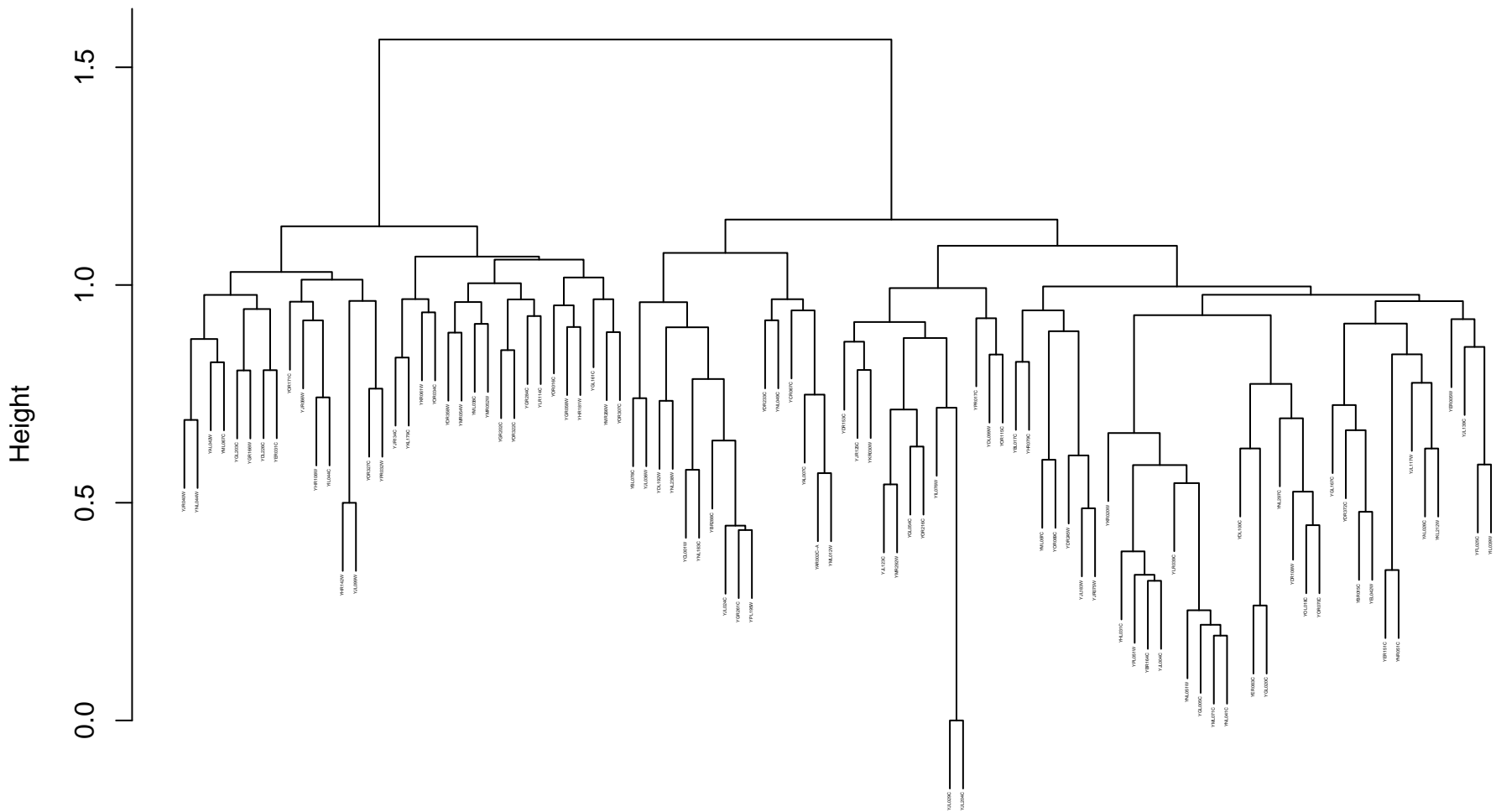
RNA processing_GO_pearson_complete



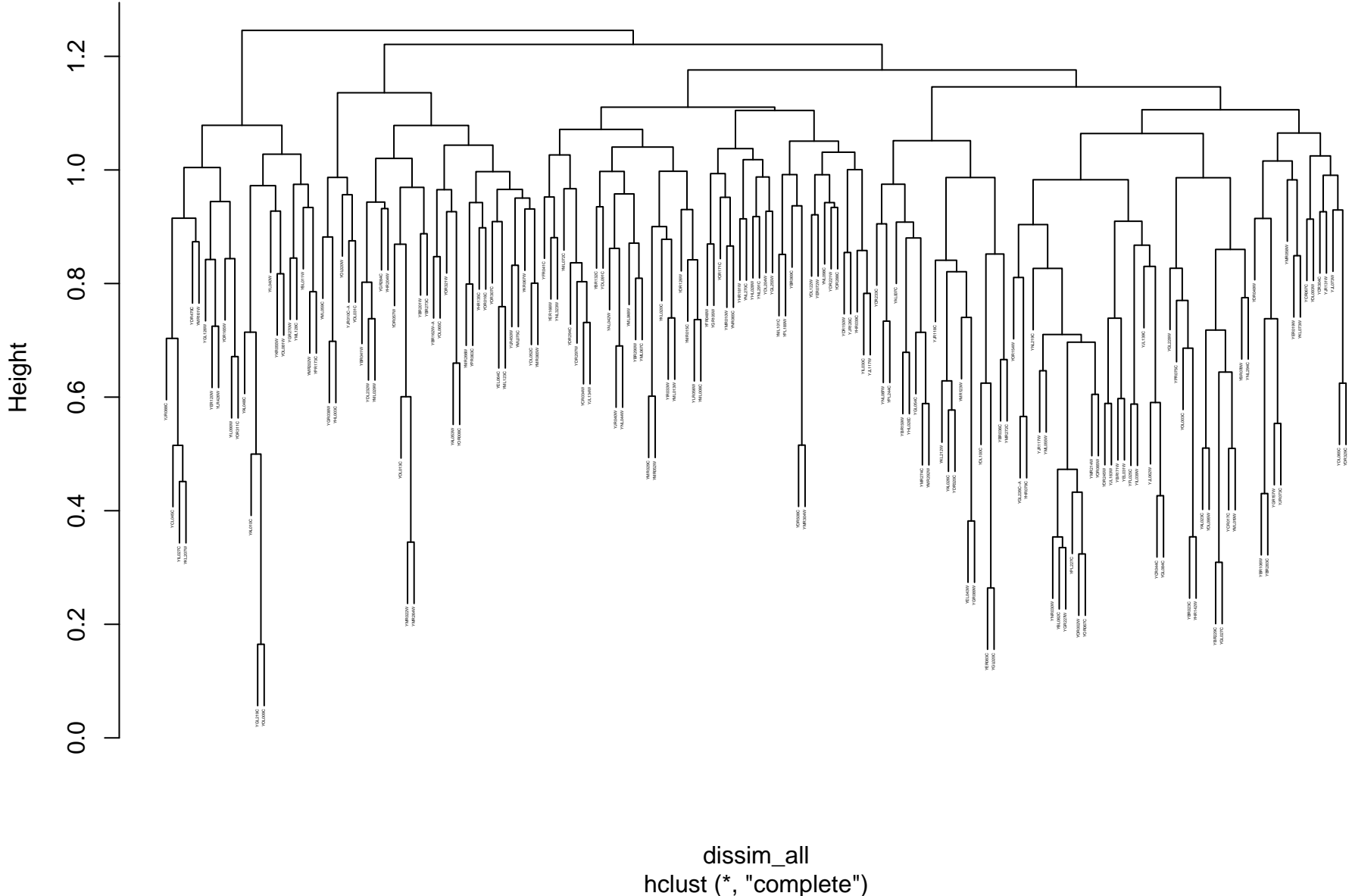
Golgi and ER_GO_pearson_complete



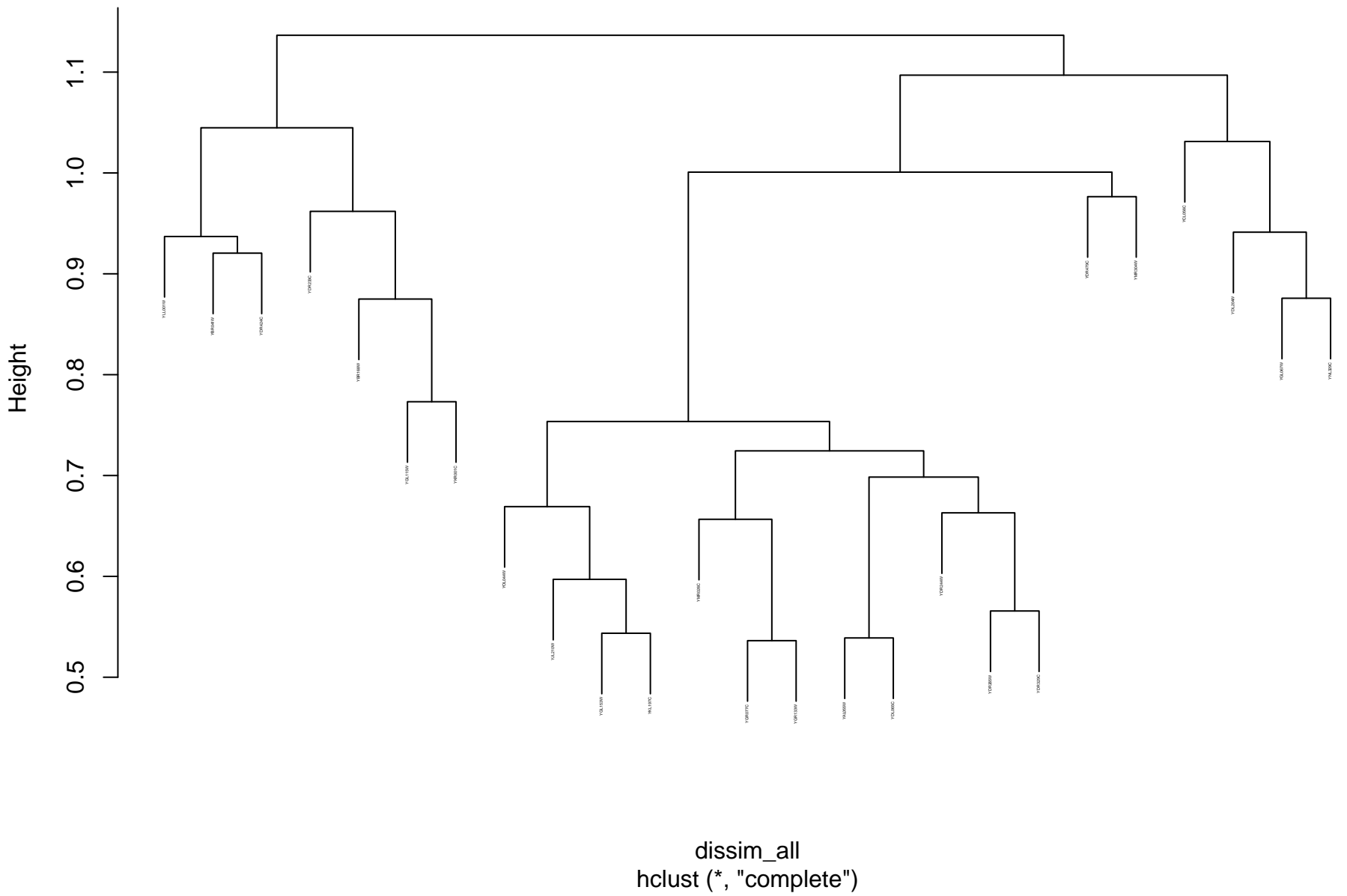
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dissim_all
hclust (*, "complete")
```



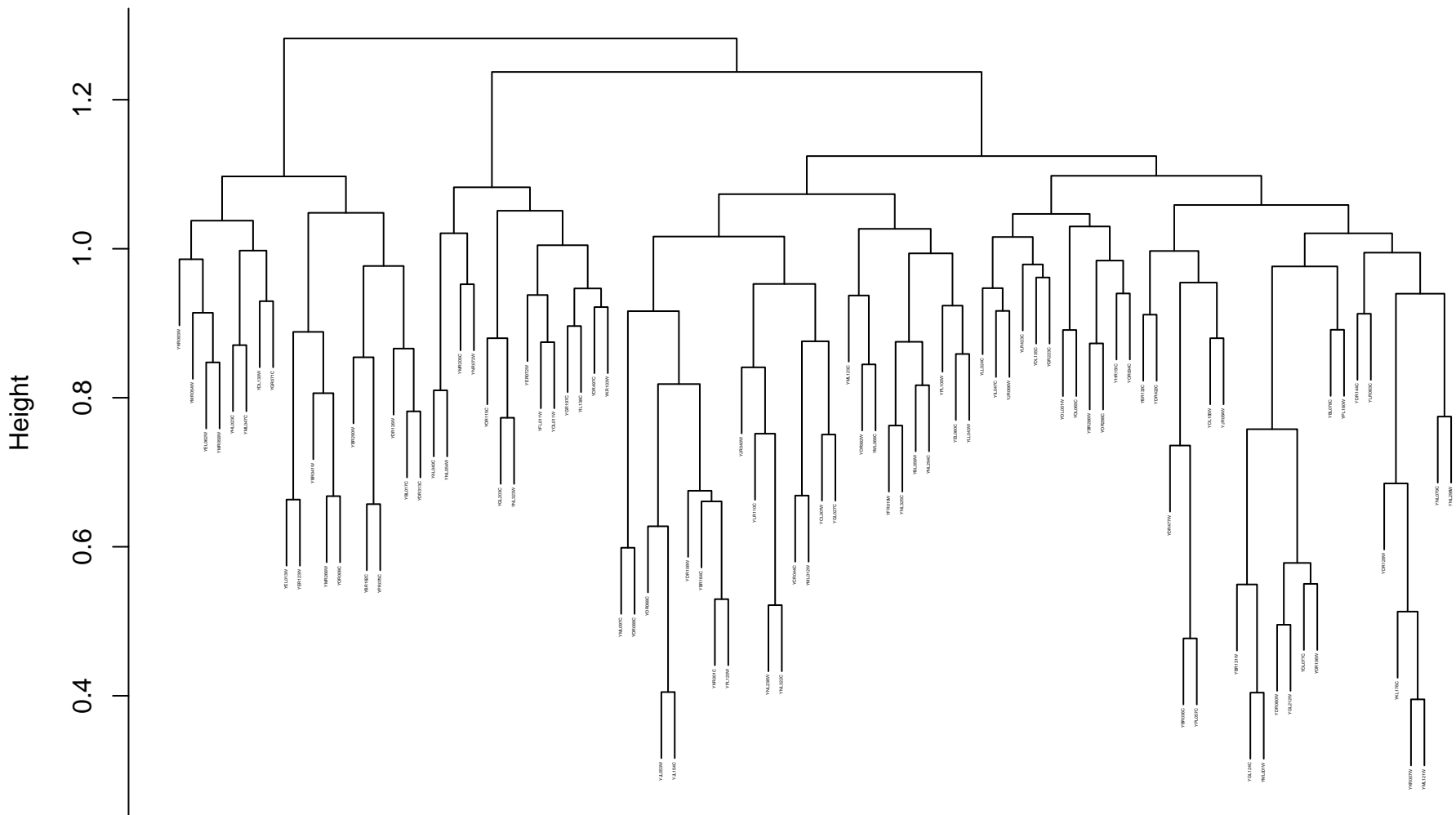
ER_GO_pearson_complete



peroxisomes_GO_pearson_complete

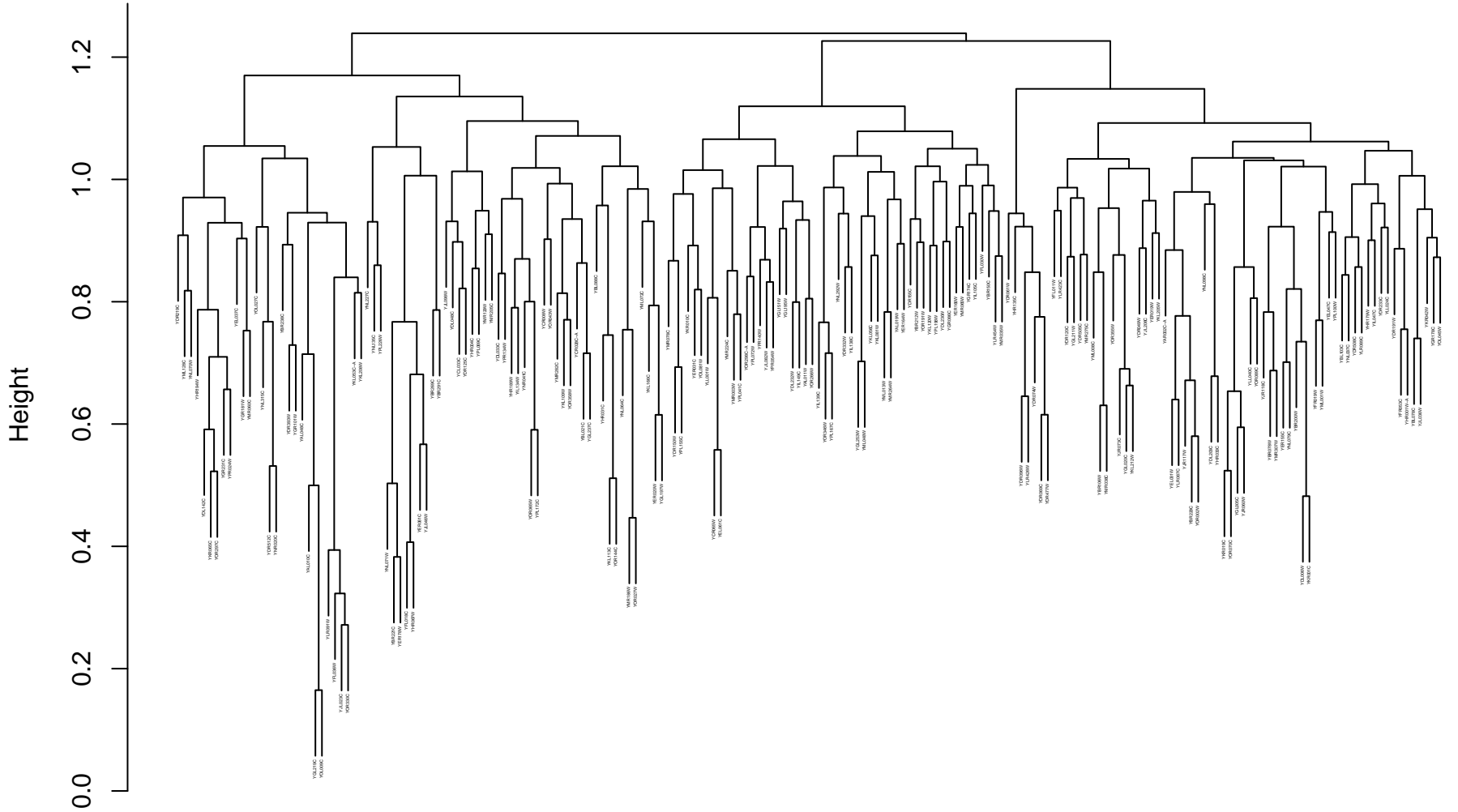


vacuoles_GO_pearson_complete

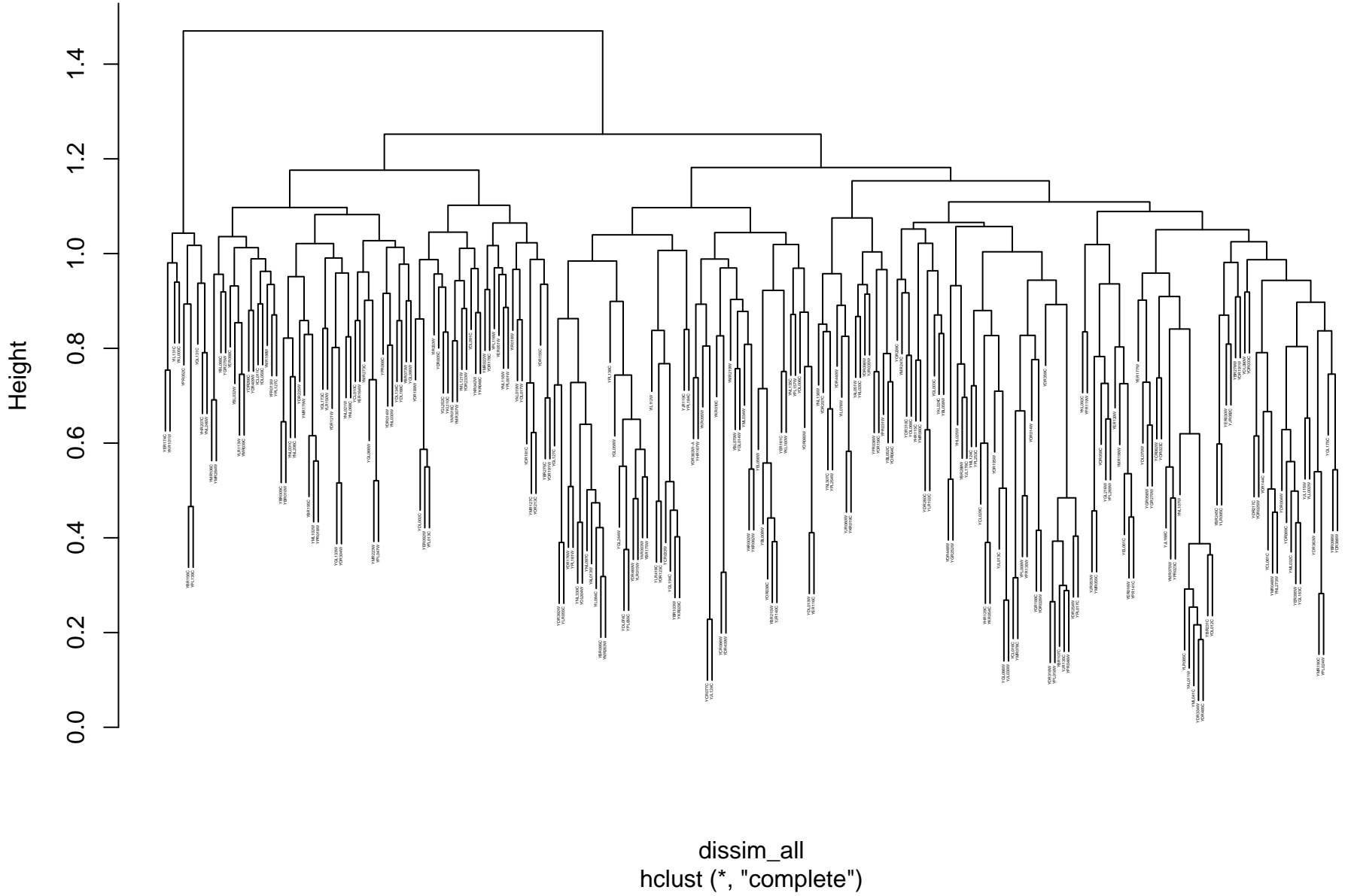


```
dissim_all
hclust (*, "complete")
```

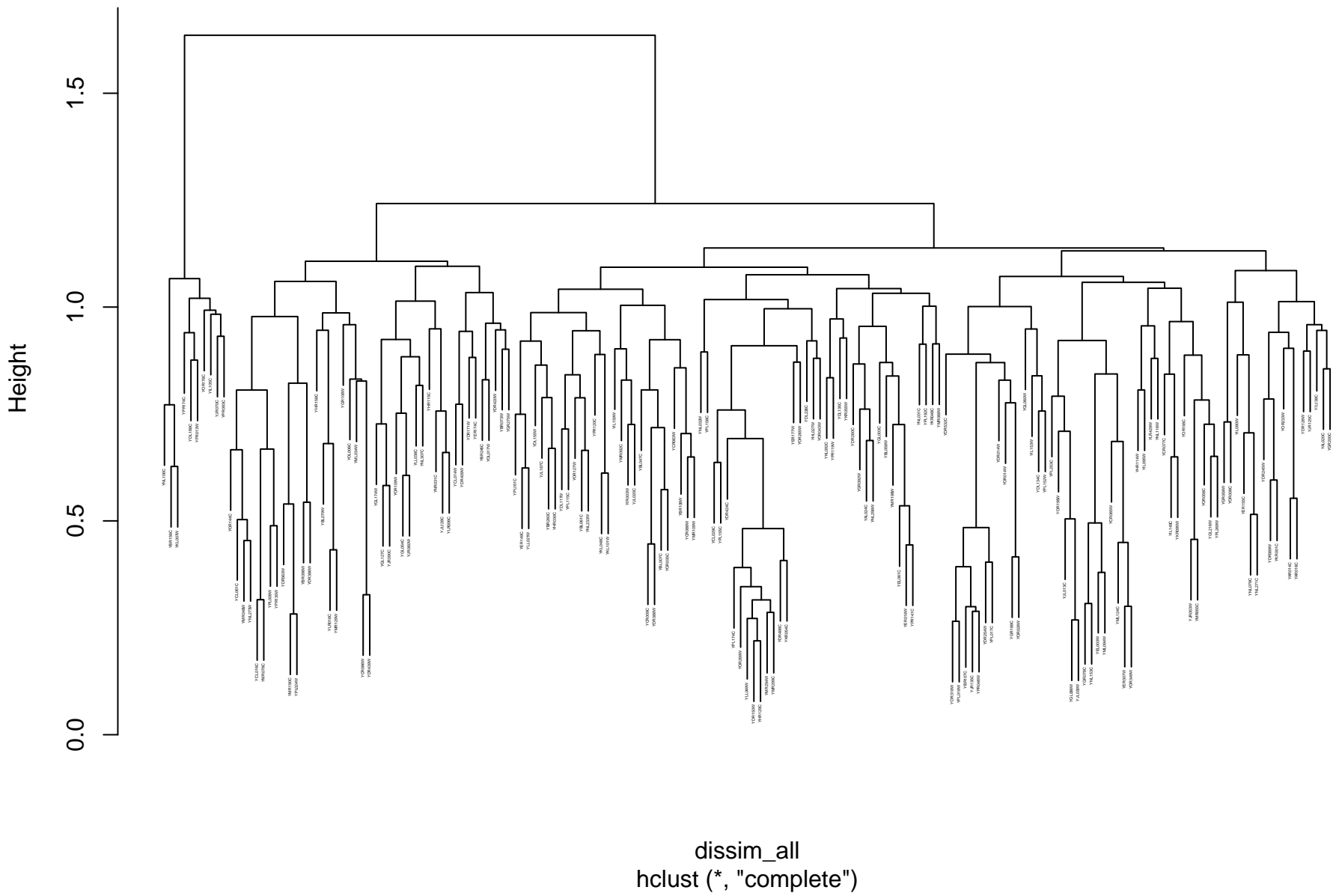
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dissim_all
hclust (*, "complete")
```



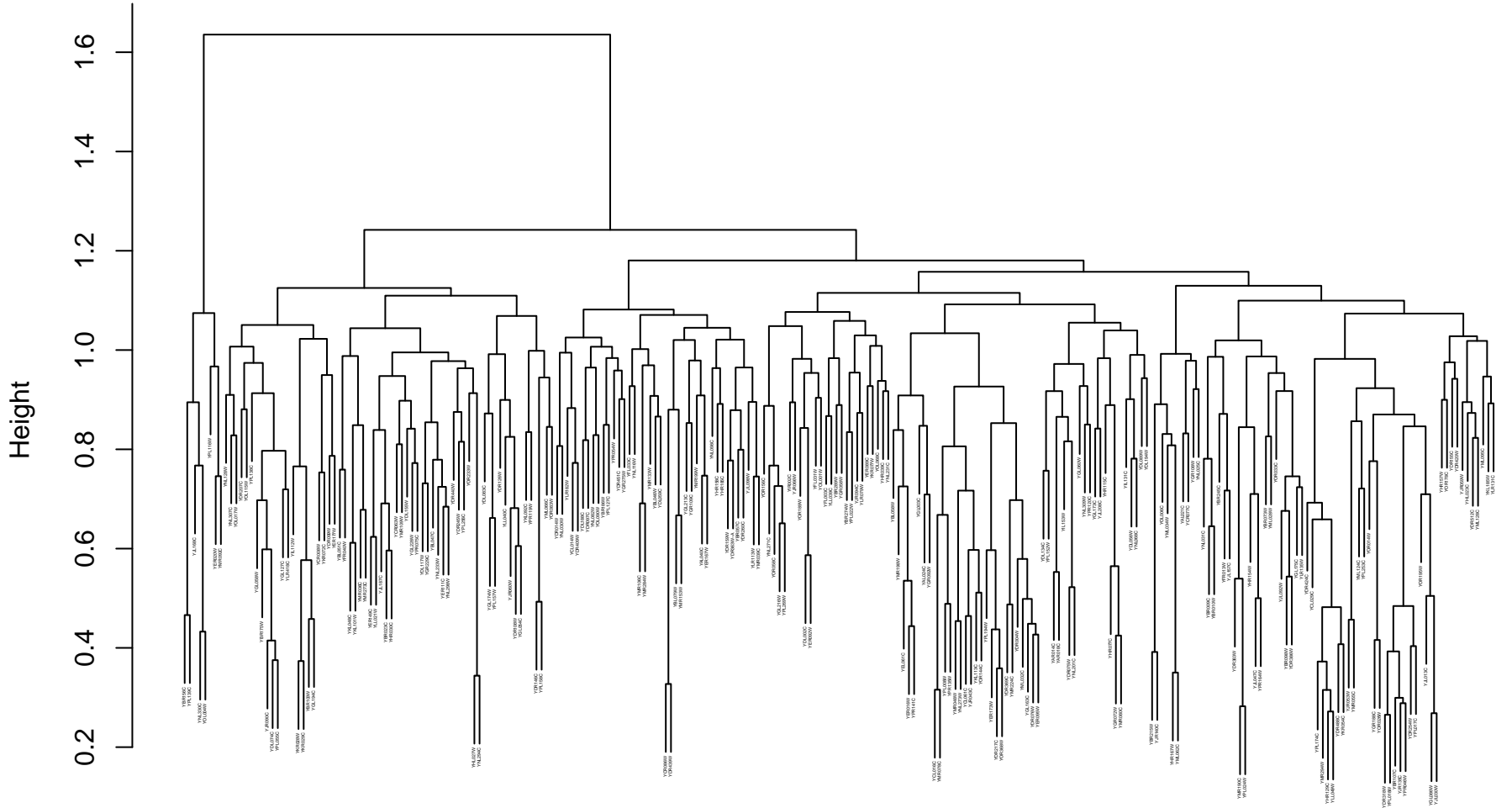
chromatin_GO_pearson_complete



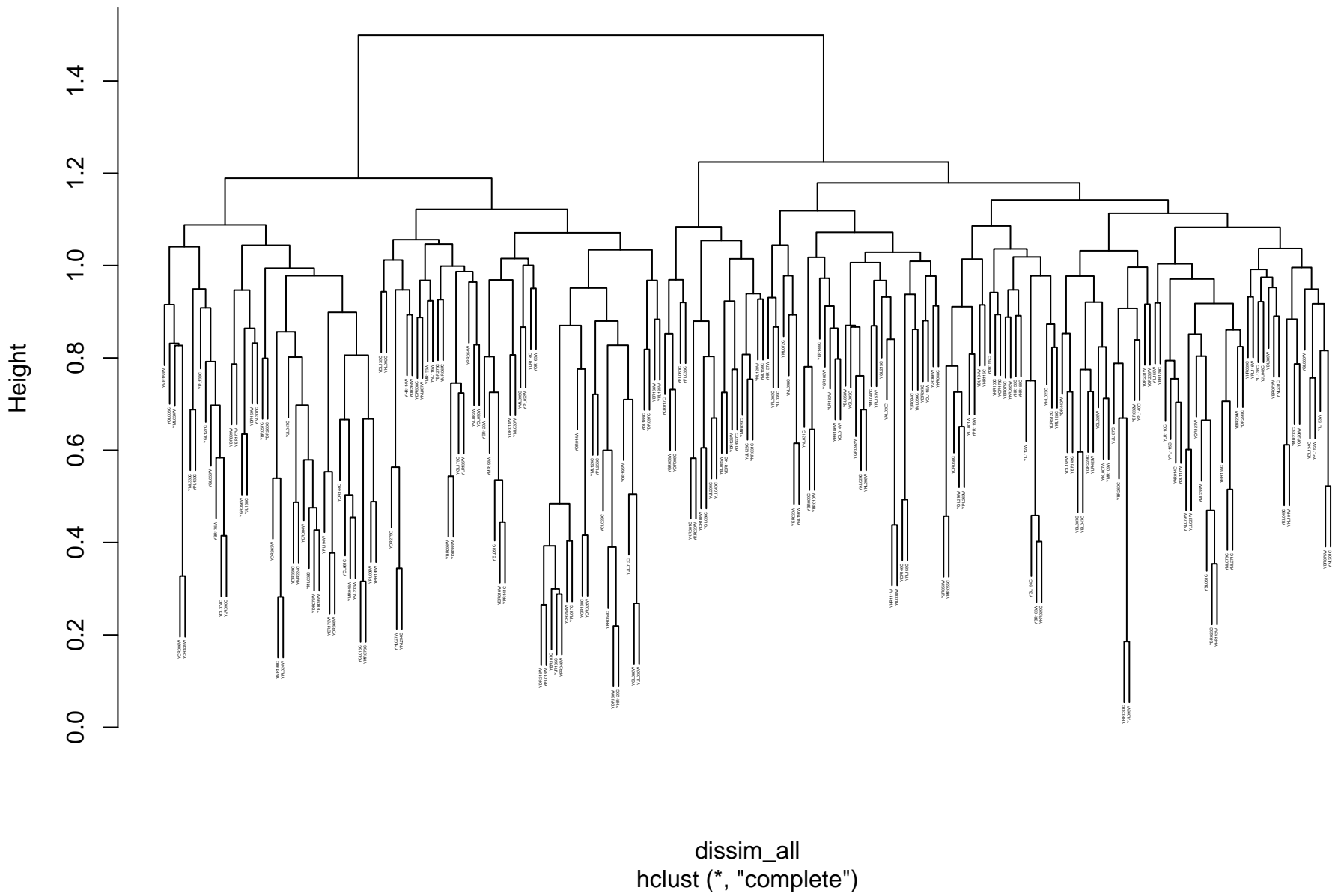
cytoskeleton and microtubules_GO_pearson_complete



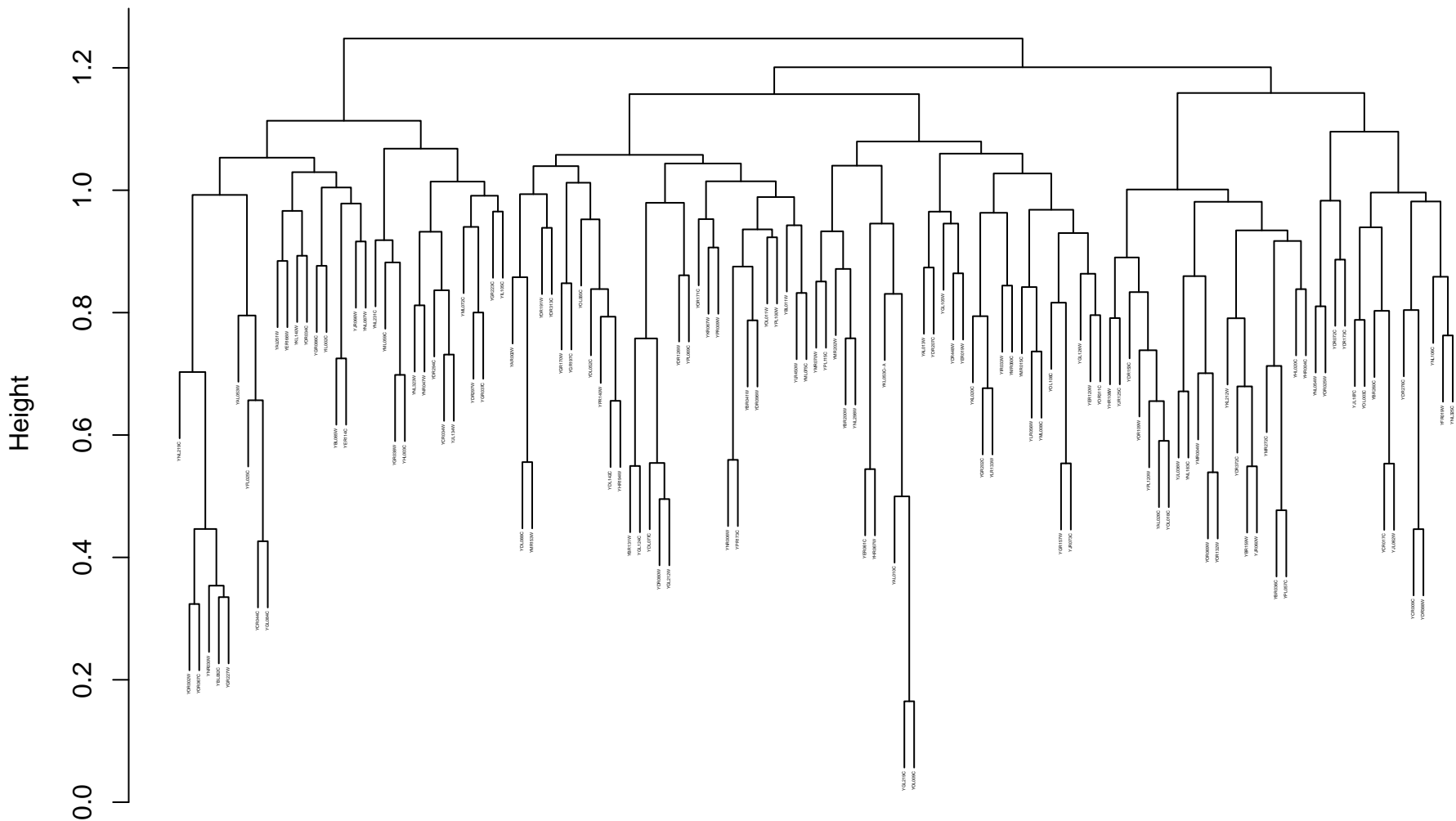
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dissim_all
hclust (*, "complete")
```



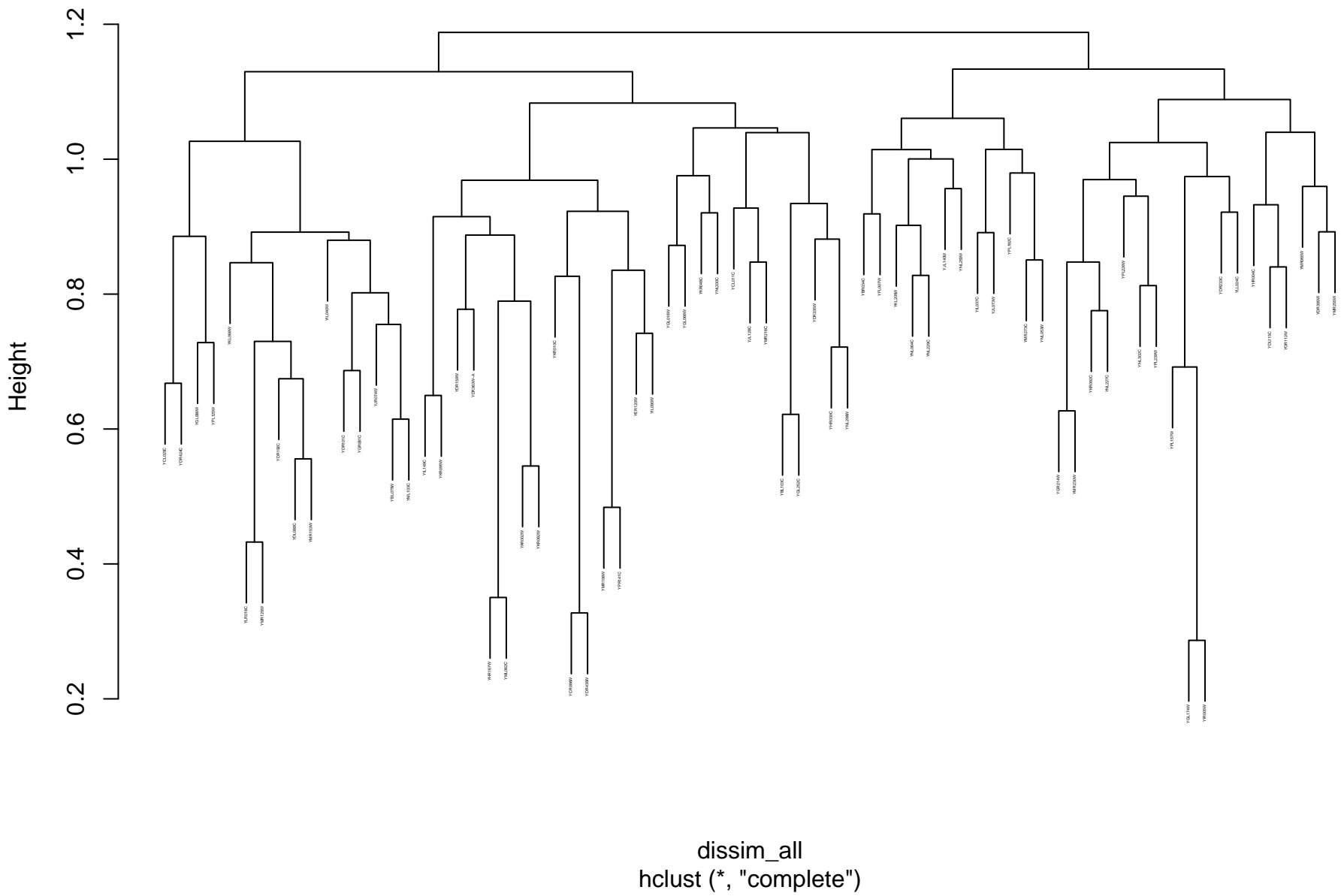
budding_GO_pearson_complete



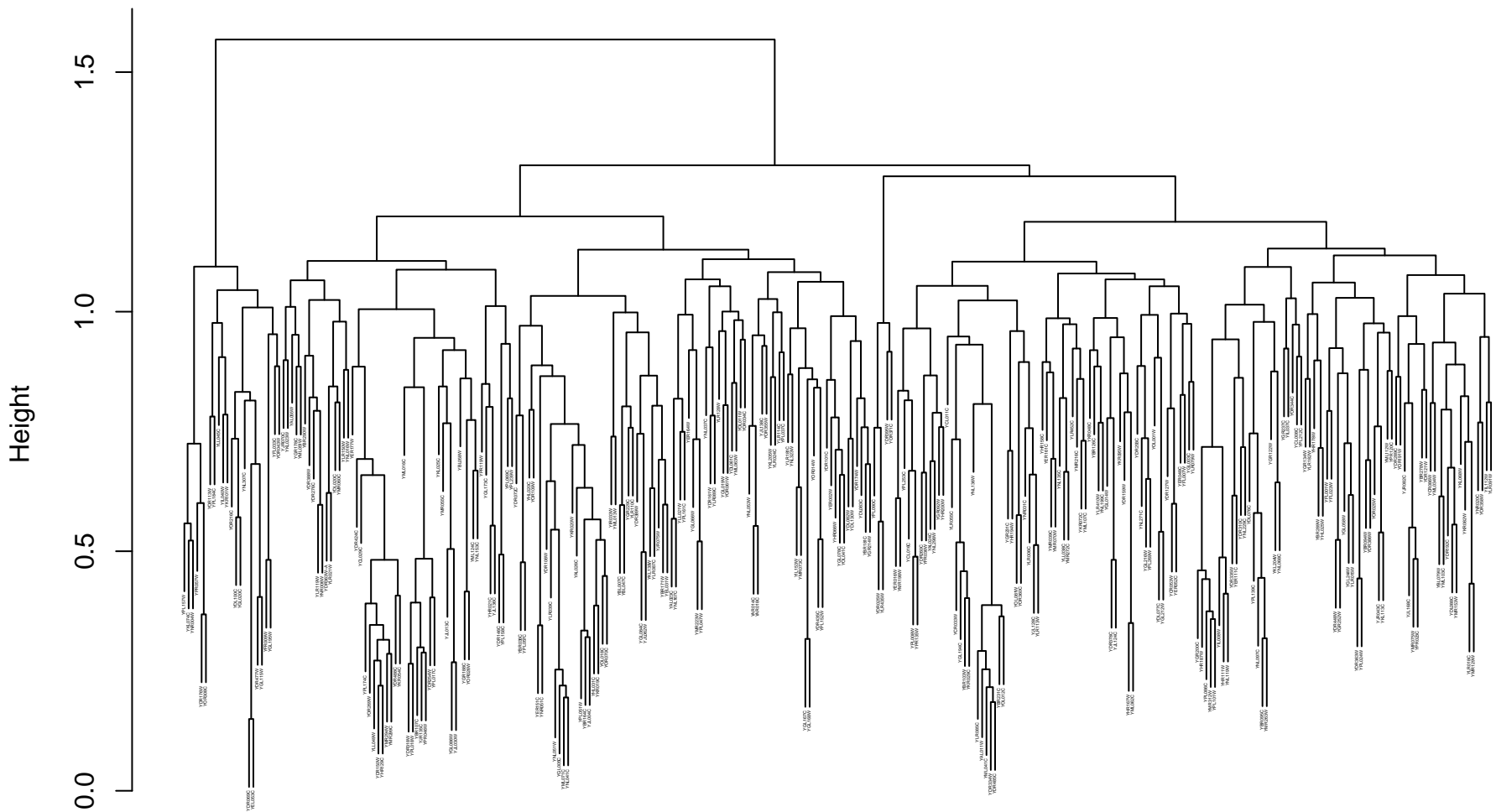
```
dissim_all
hclust (*, "complete")
```



nuclear transport and organization_GO_pearson_complete



sig_Gsp1_Gl_pearson_complete



dissim_all
hclust (*, "complete")

whole_library_pearson_complete

