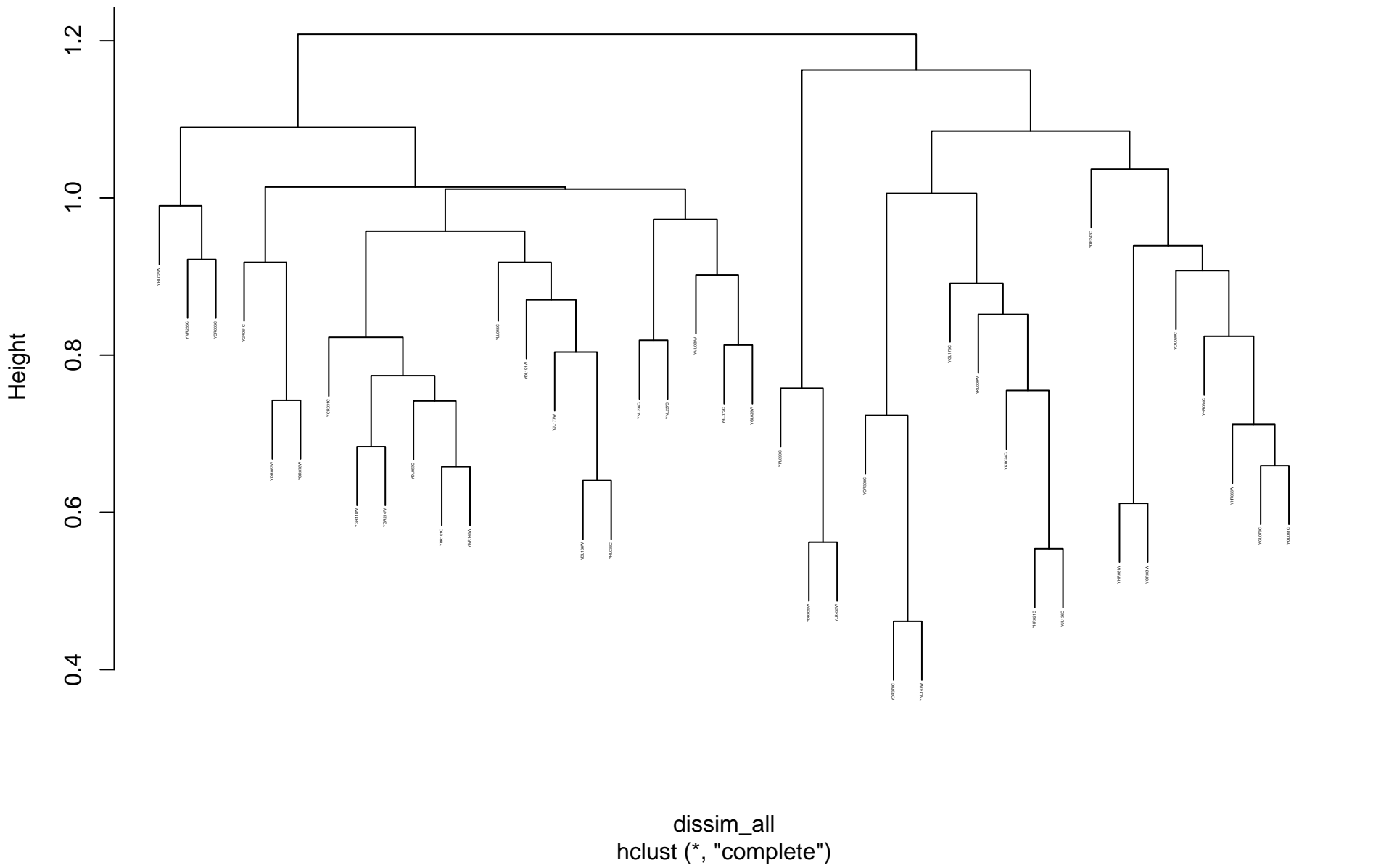
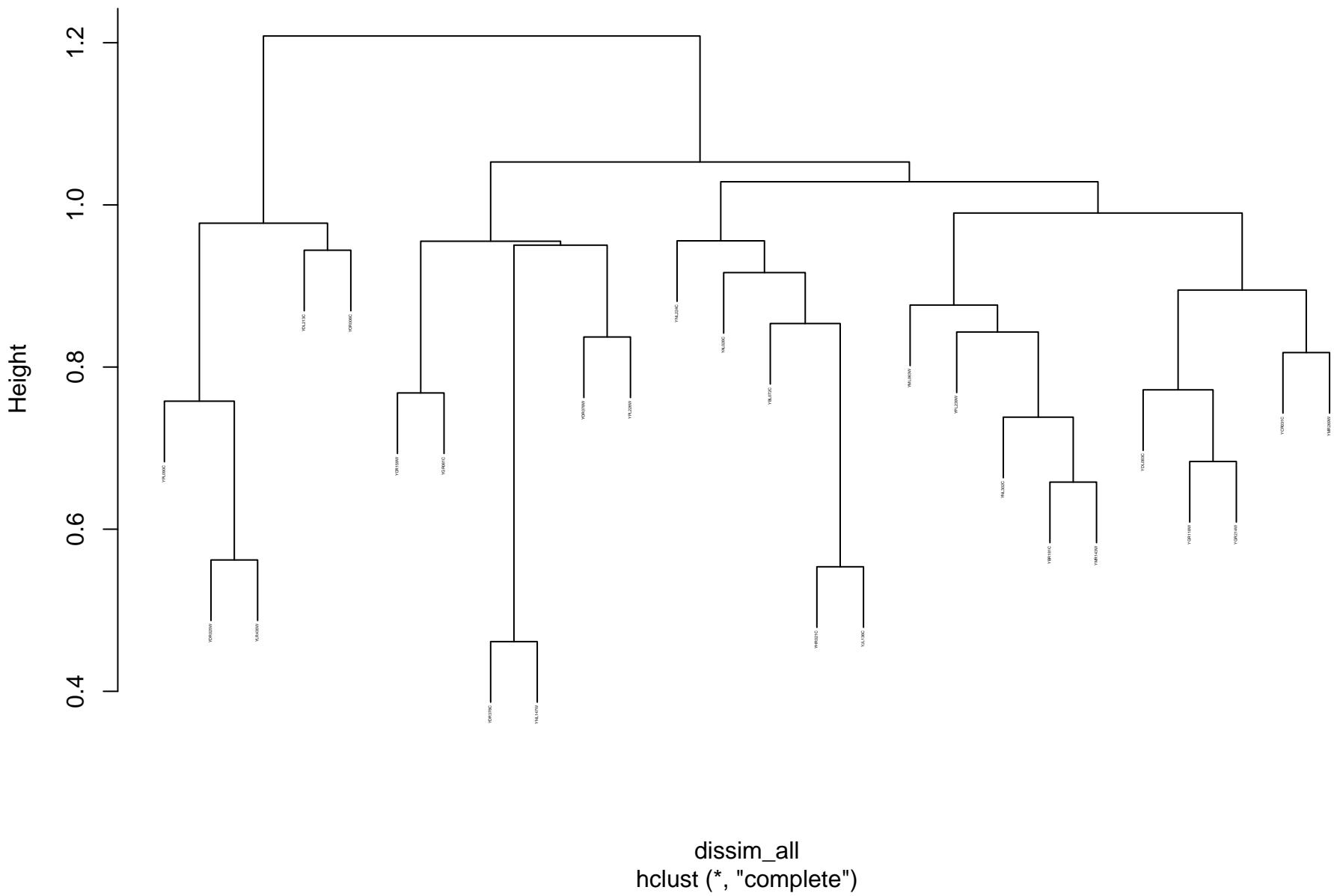


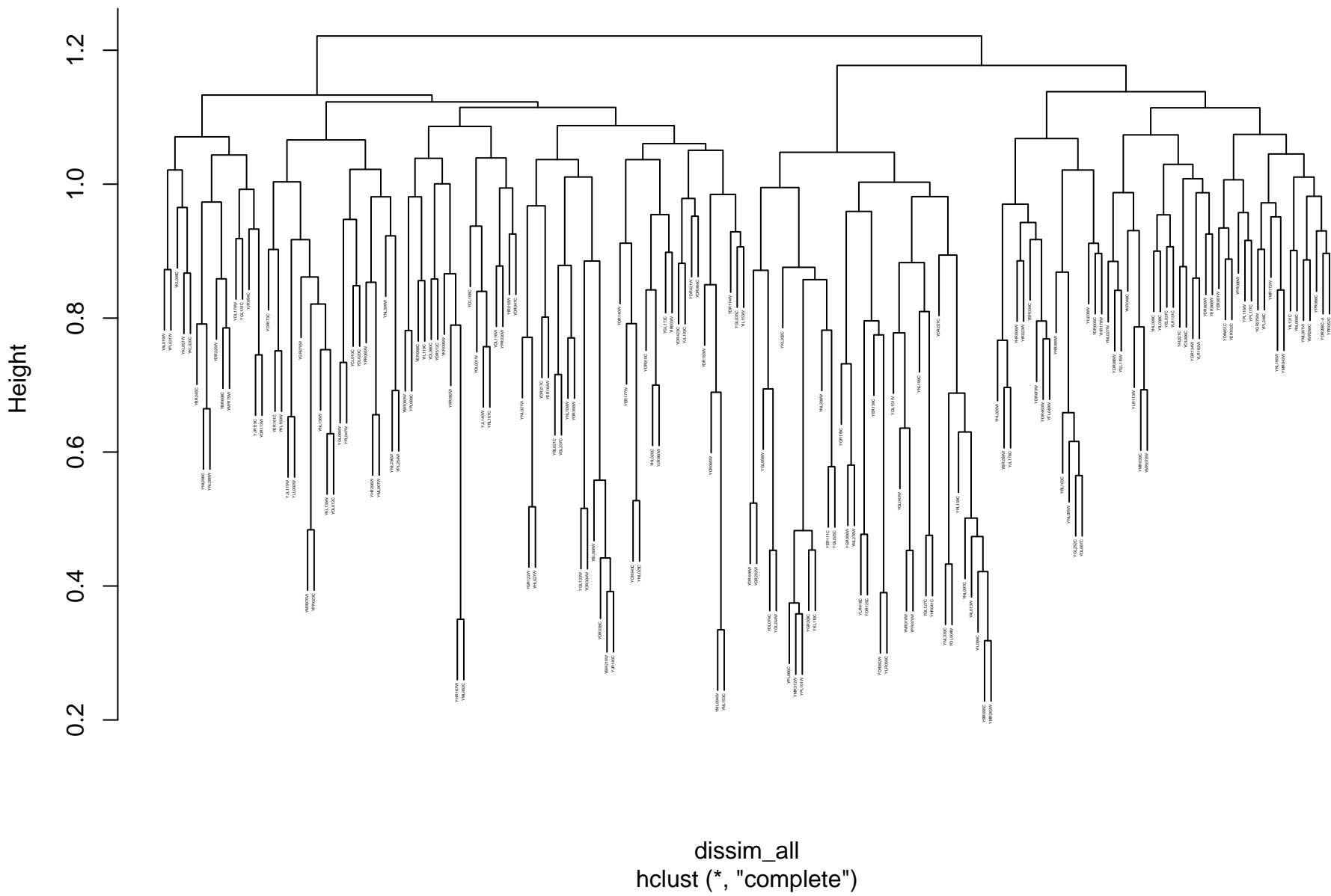
rRNA processing_GO_pearson_complete



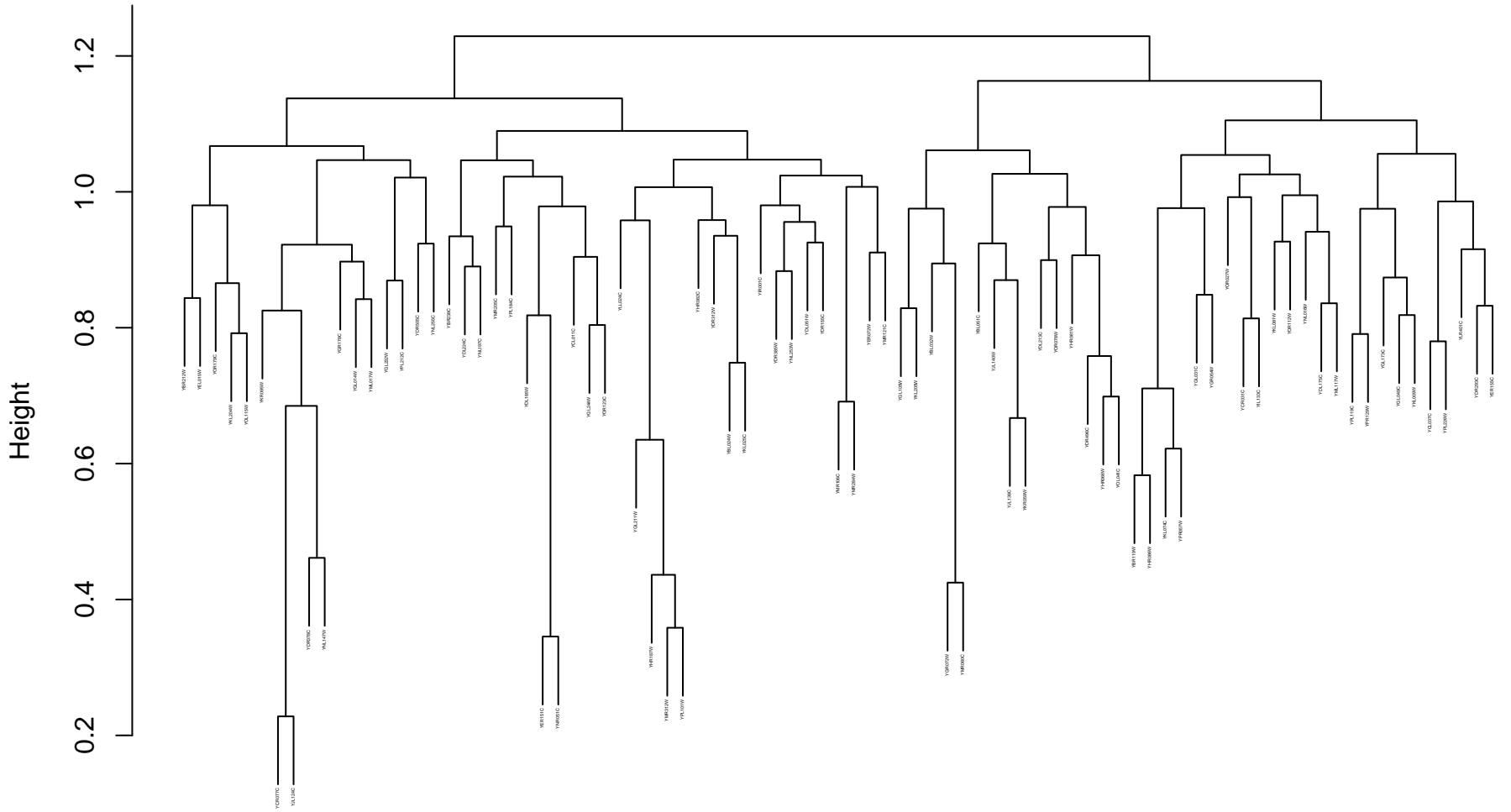
ribosomal small subunit biogenesis_GO_pearson_complete



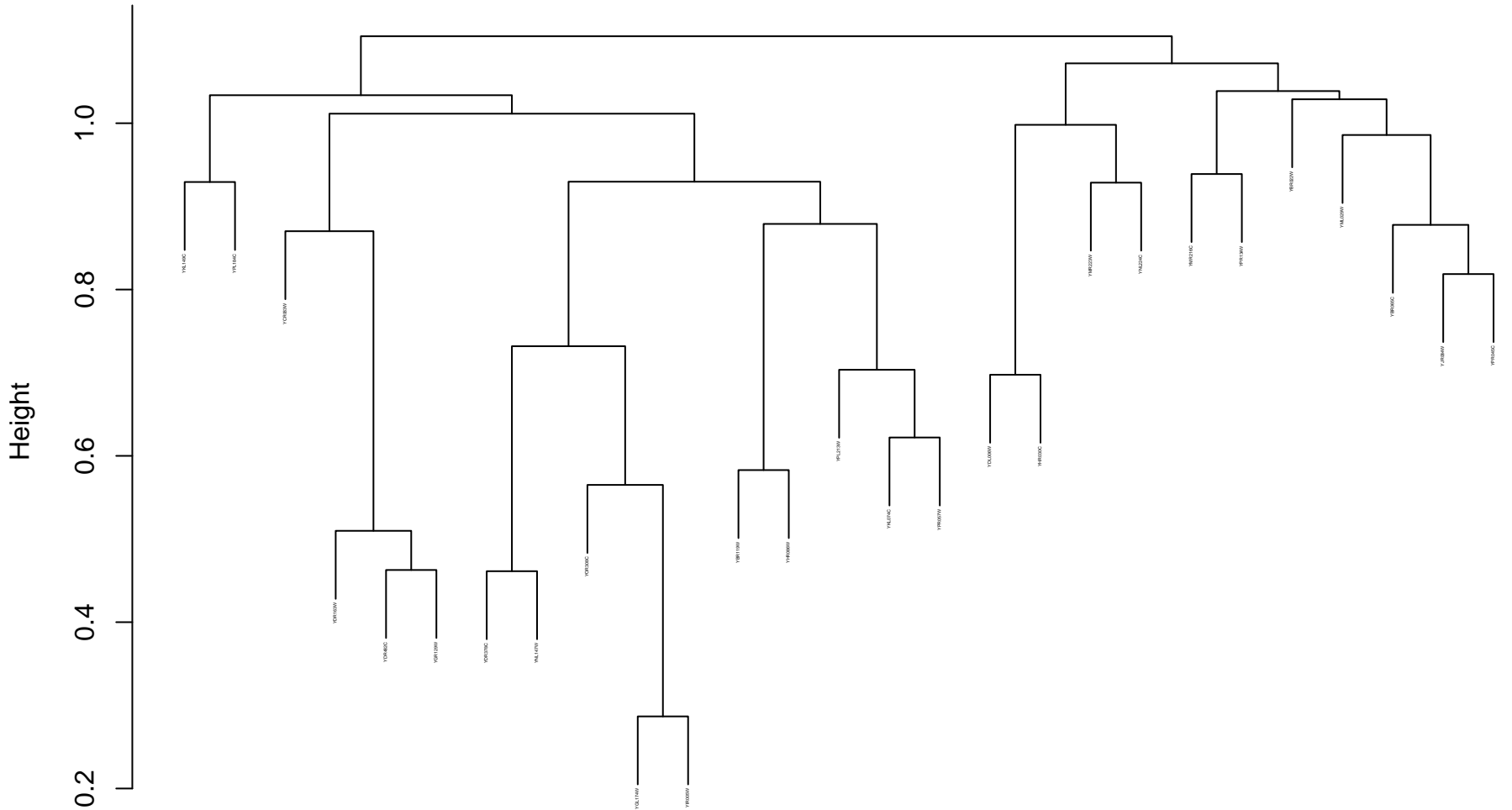
transcription from RNA polymerase II promoter_GO_pearson_complete



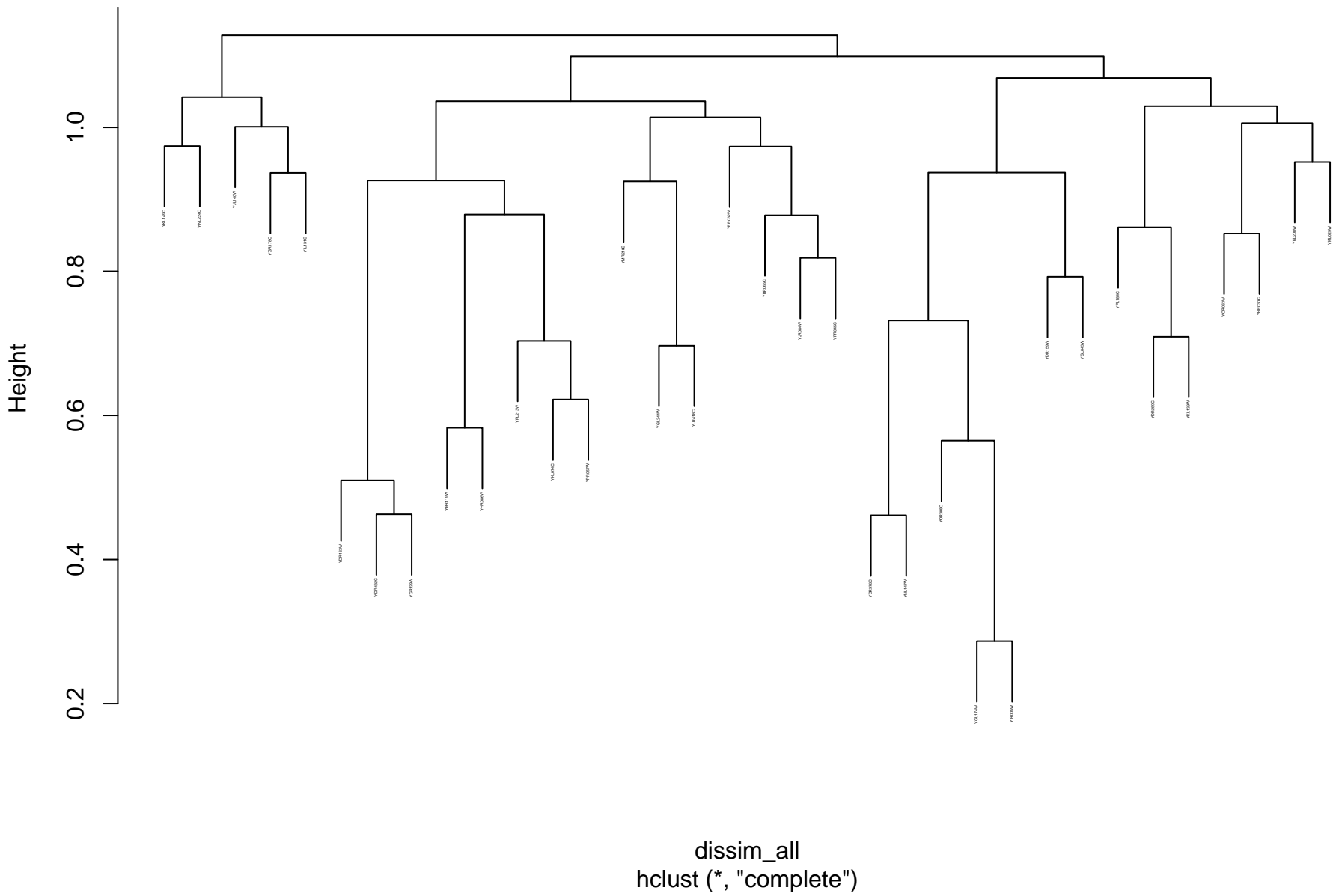
```
dissim_all
hclust (*, "complete")
```



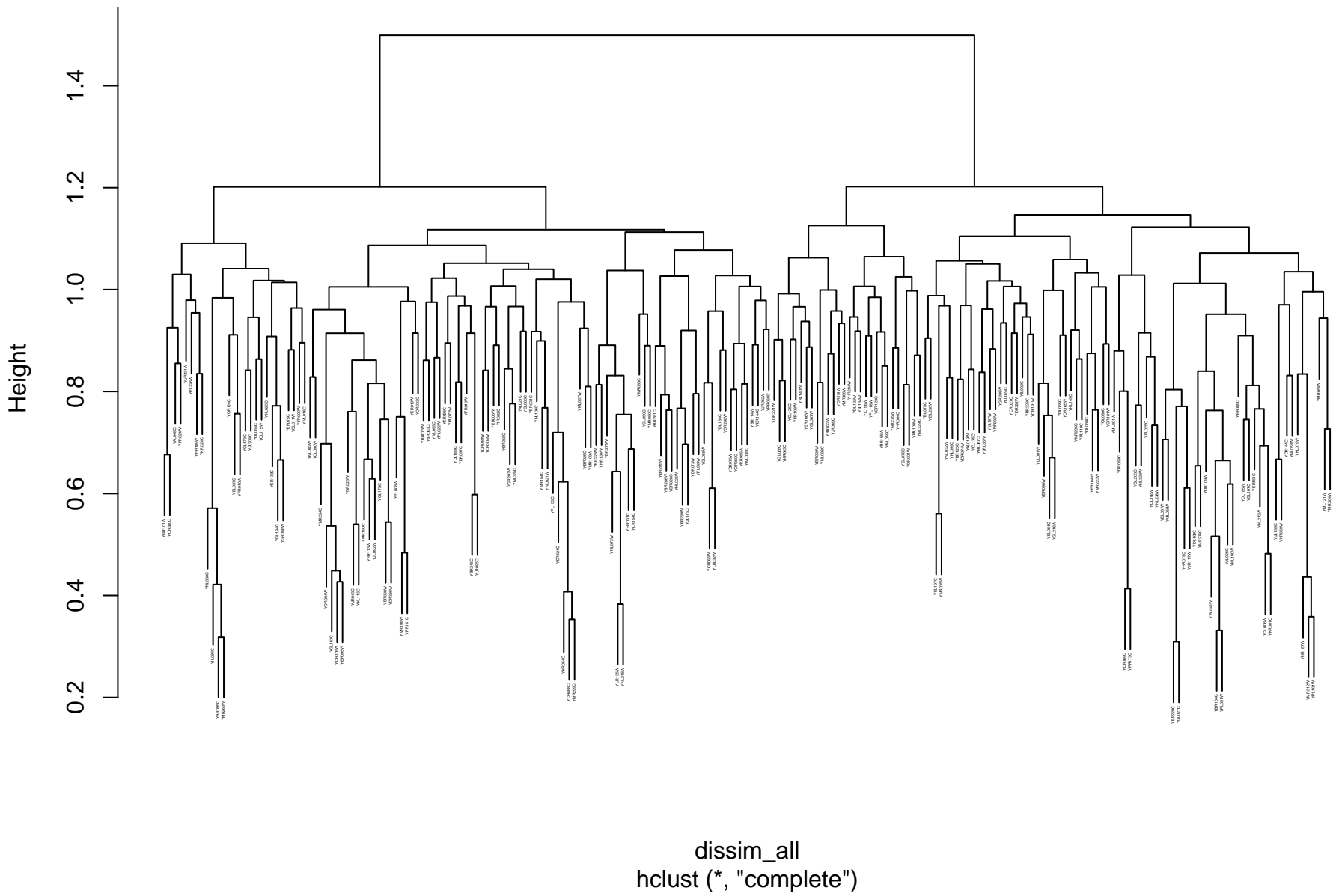
```
dissim_all
hclust (*, "complete")
```



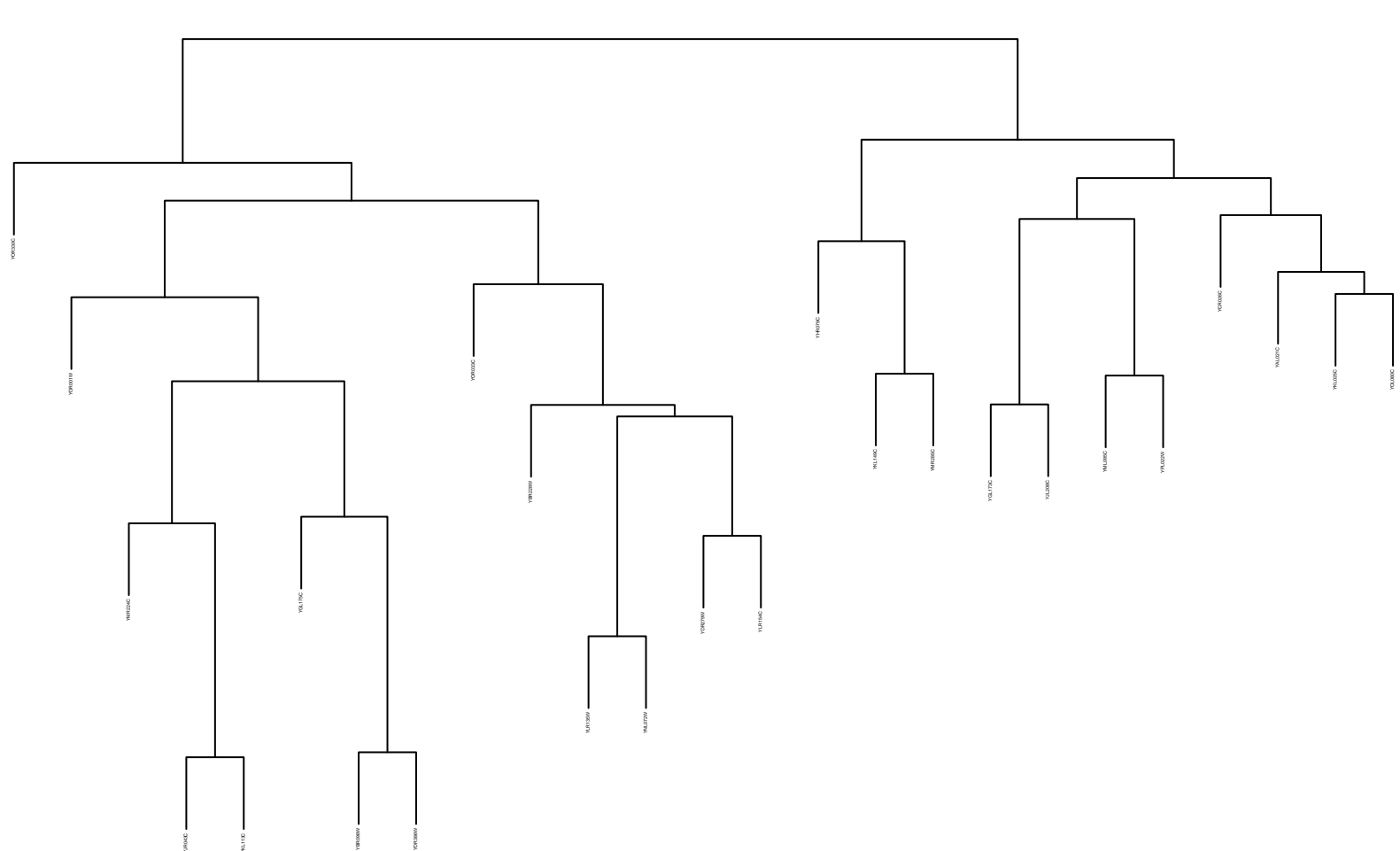
mRNA processing_GO_pearson_complete



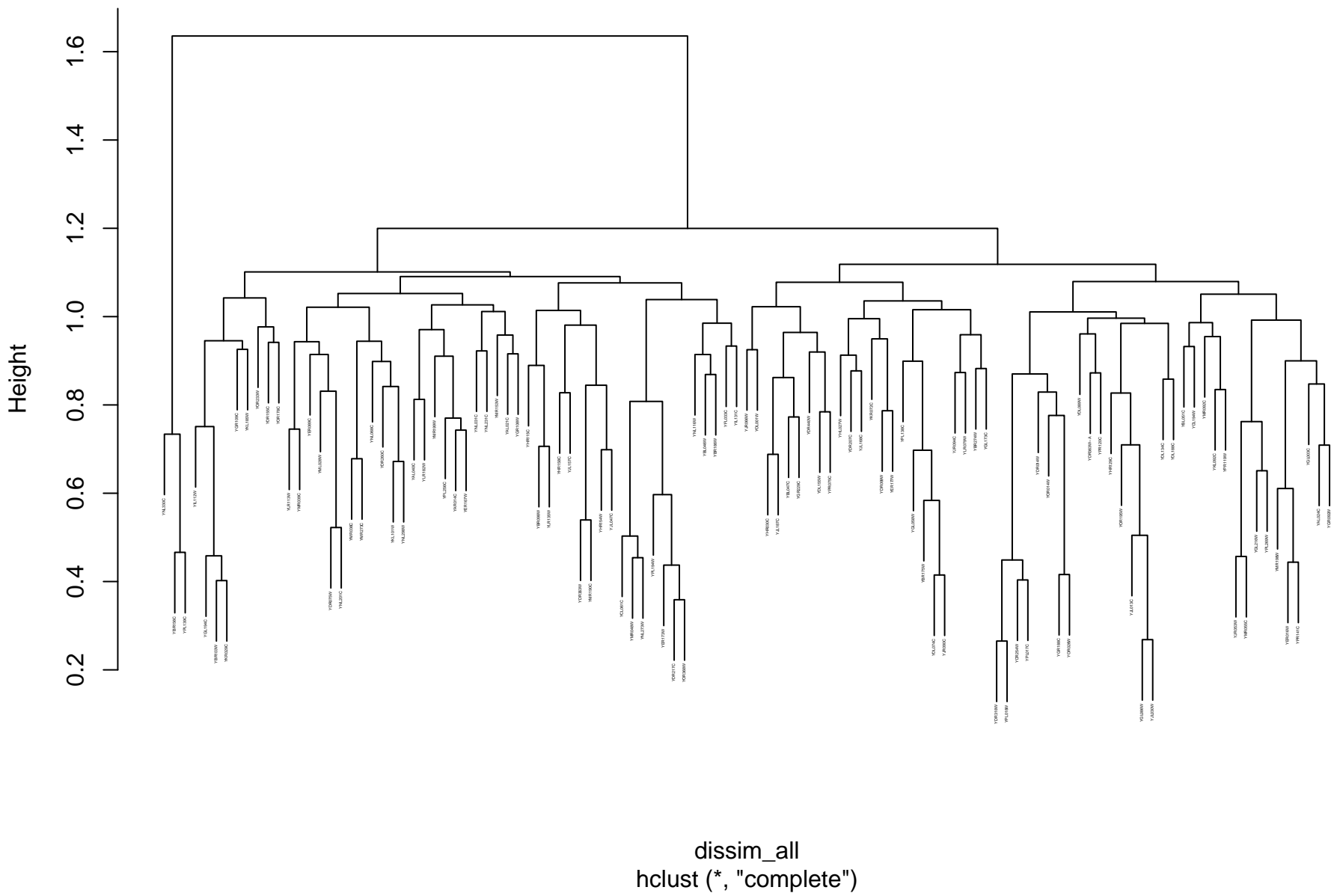
hydrolase activity_GO_pearson_complete



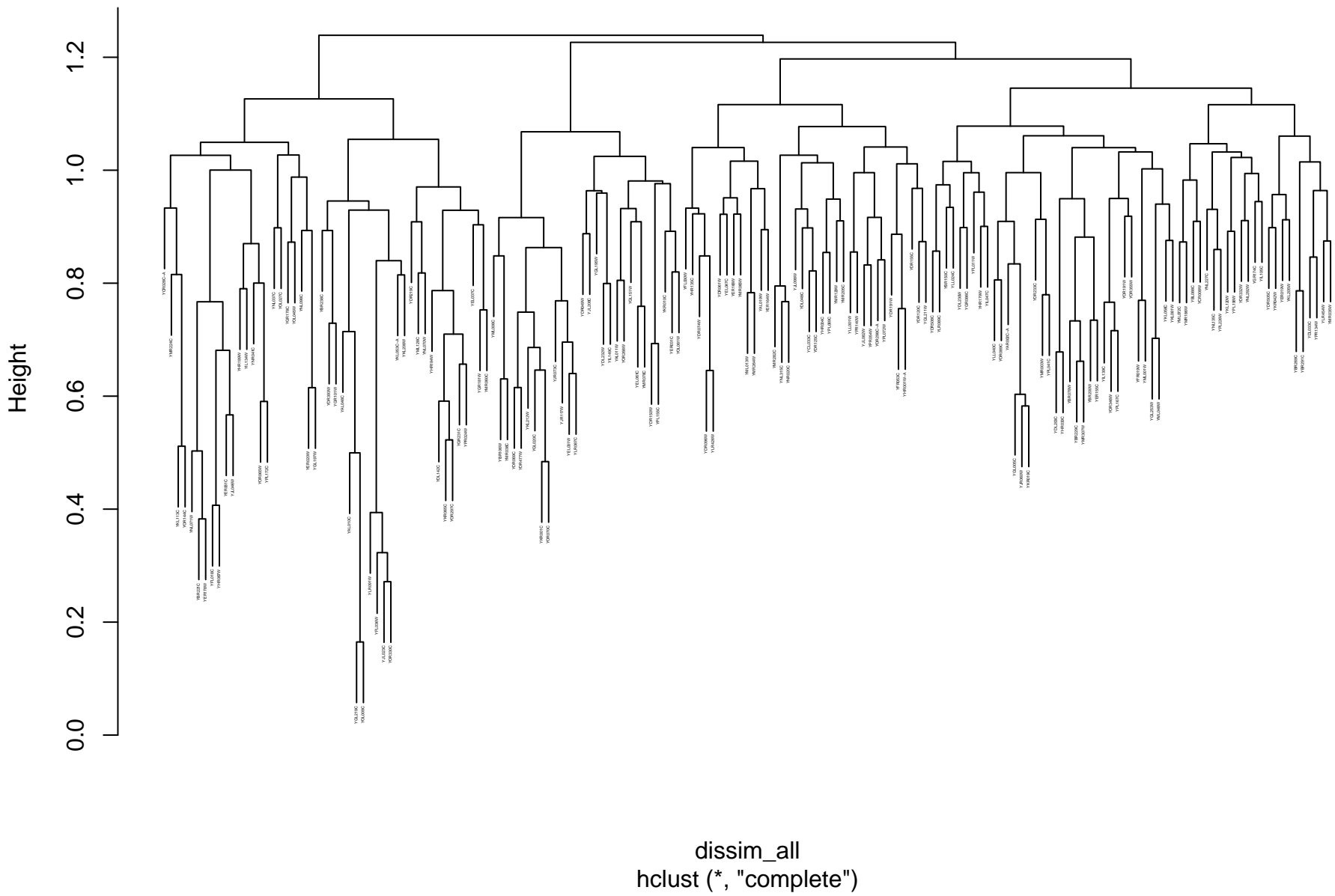
```
dissim_all
hclust (*, "complete")
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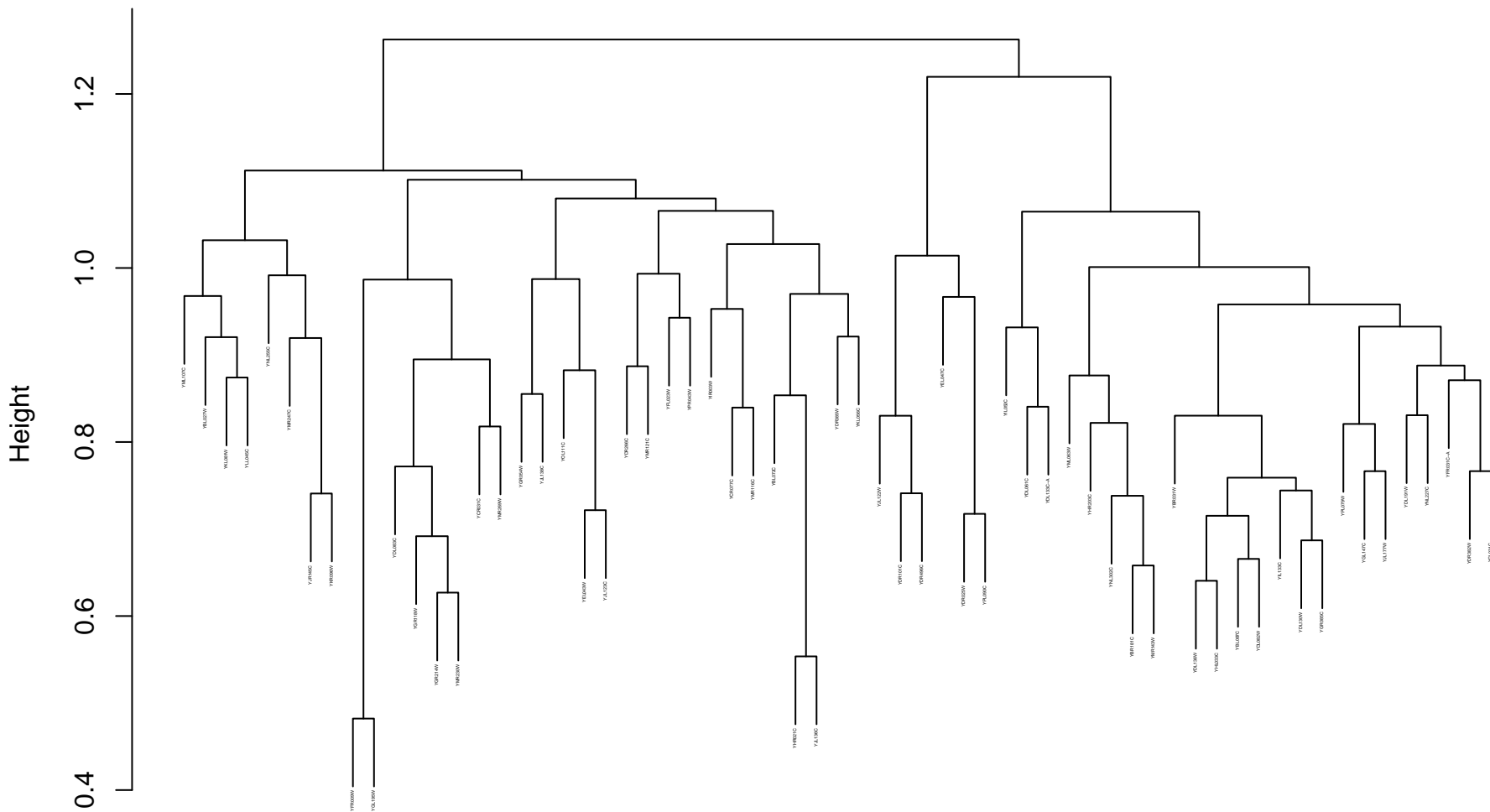
regulation of cell cycle_GO_pearson_complete



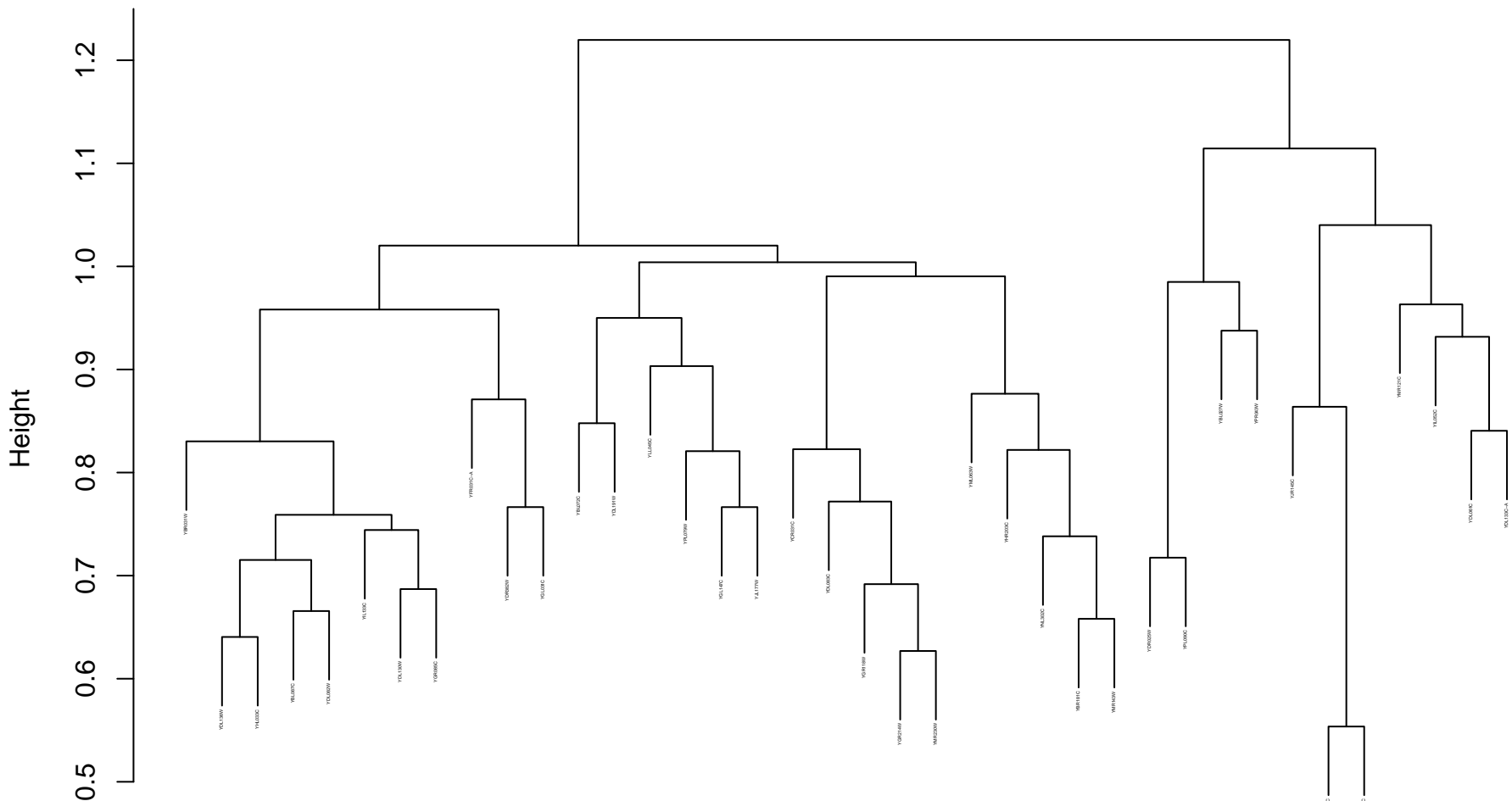
mitochondrion_GO_pearson_complete



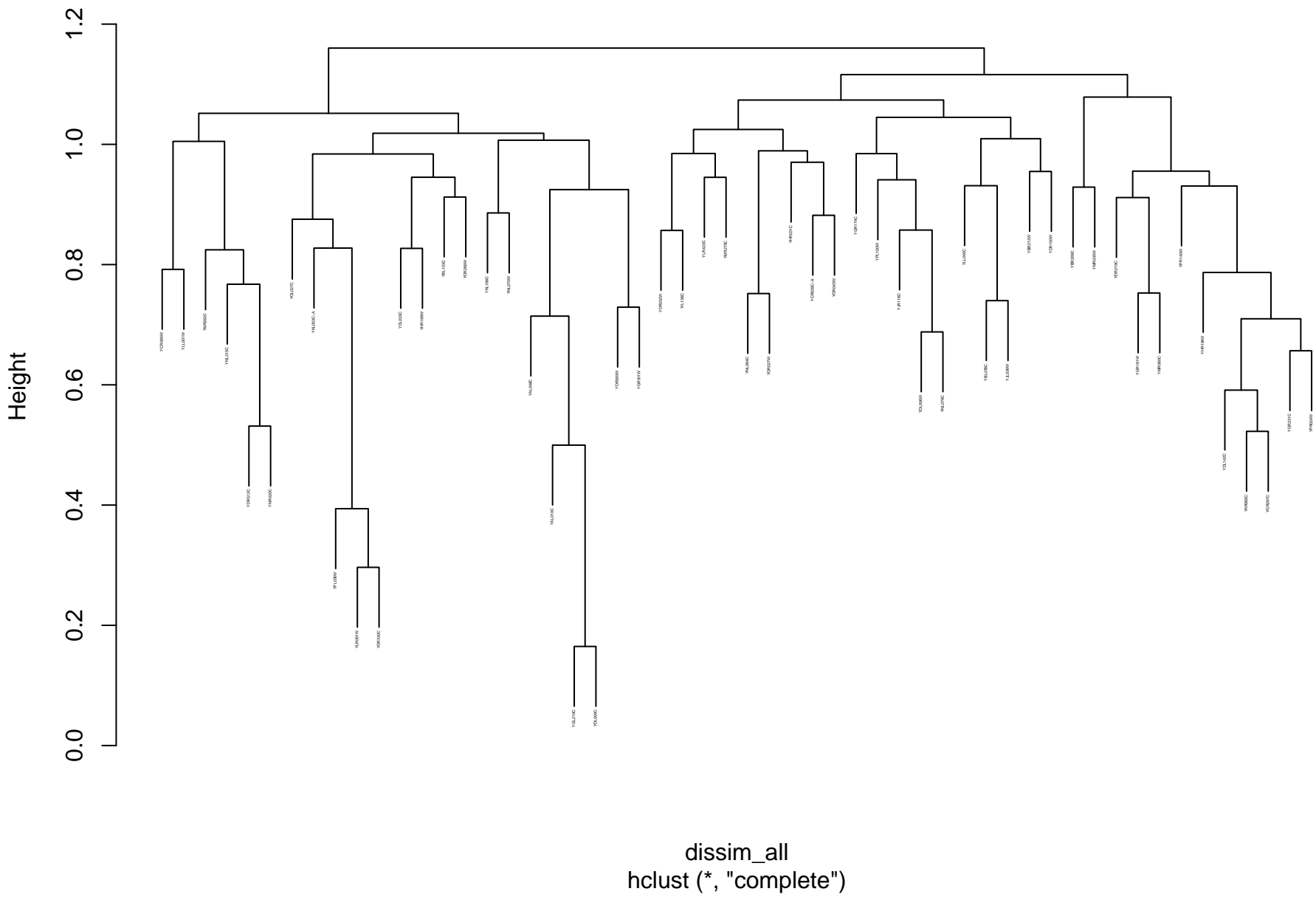
ribosome_GO_pearson_complete



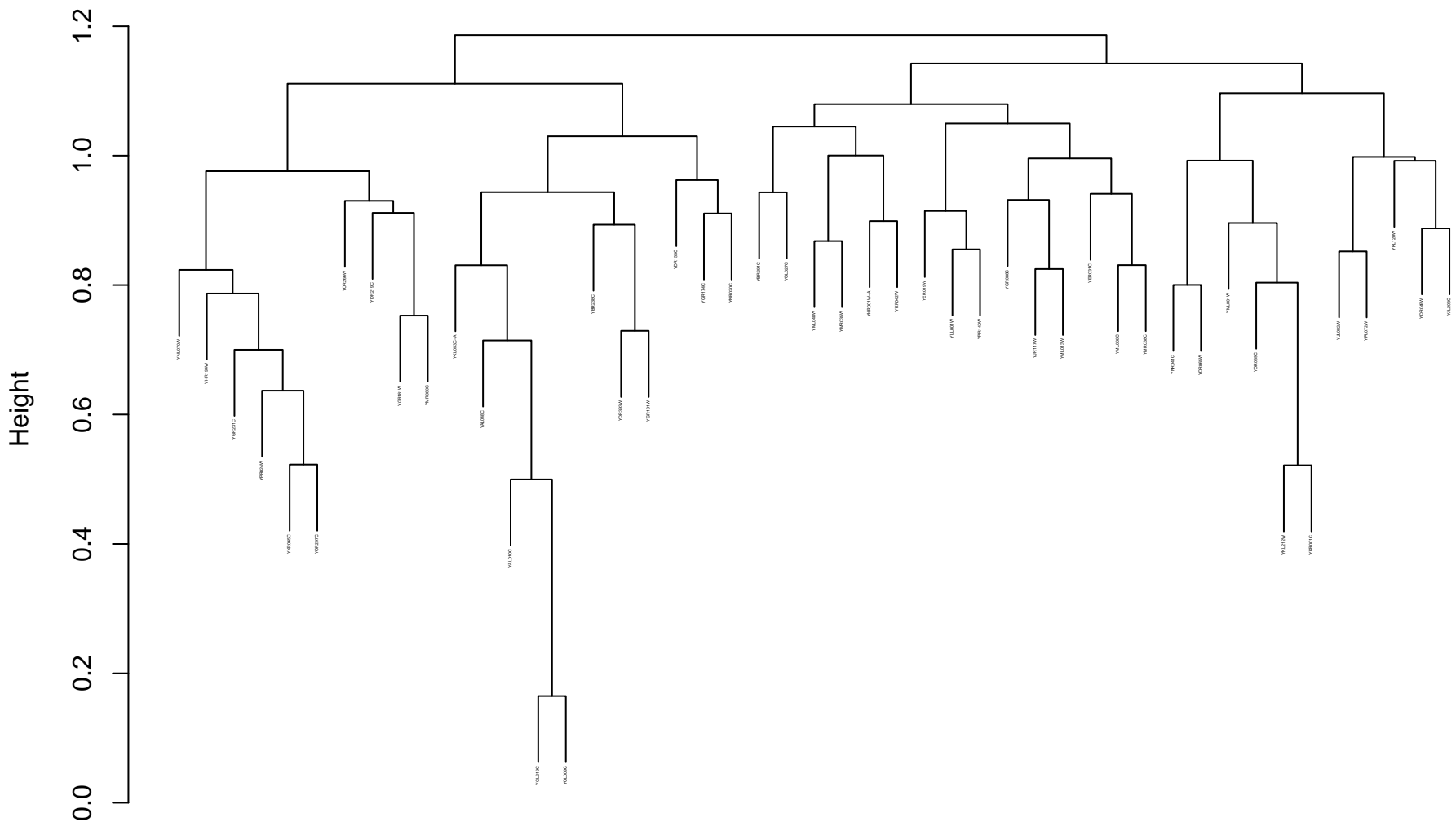
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dissim_all
hclust (*, "complete")
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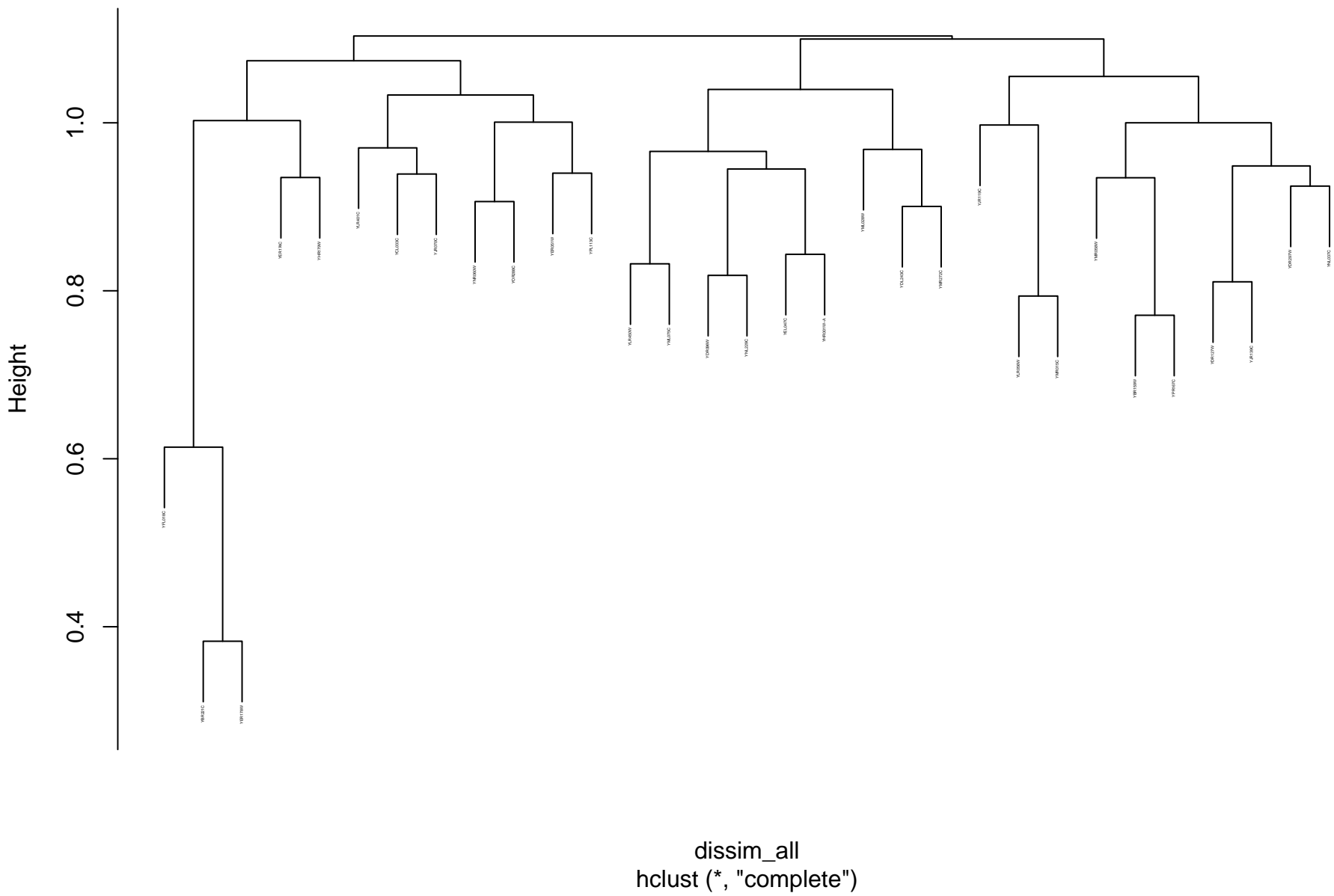
mitochondrion organization_GO_pearson_complete



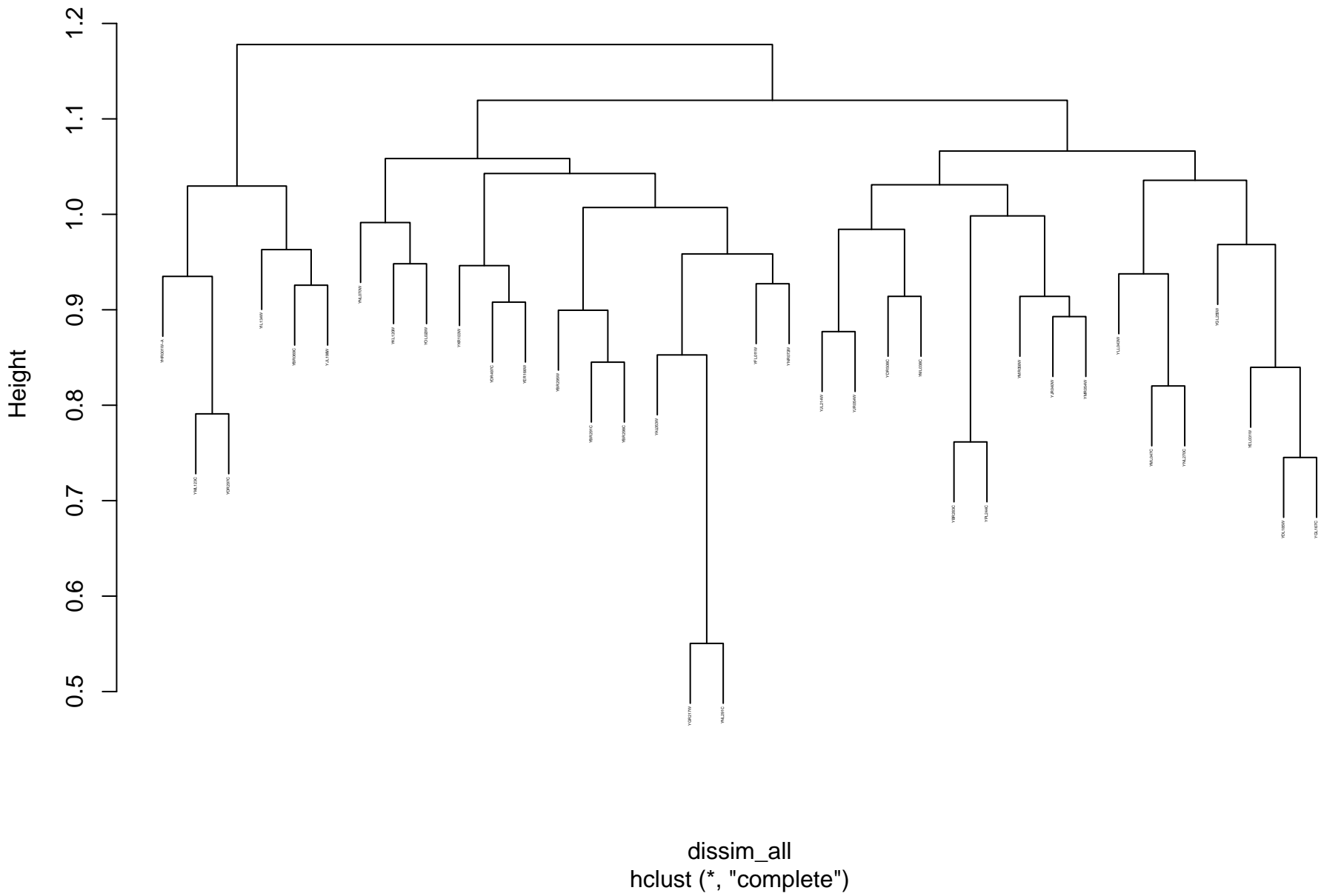
```
dissim_all
hclust (*, "complete")
```



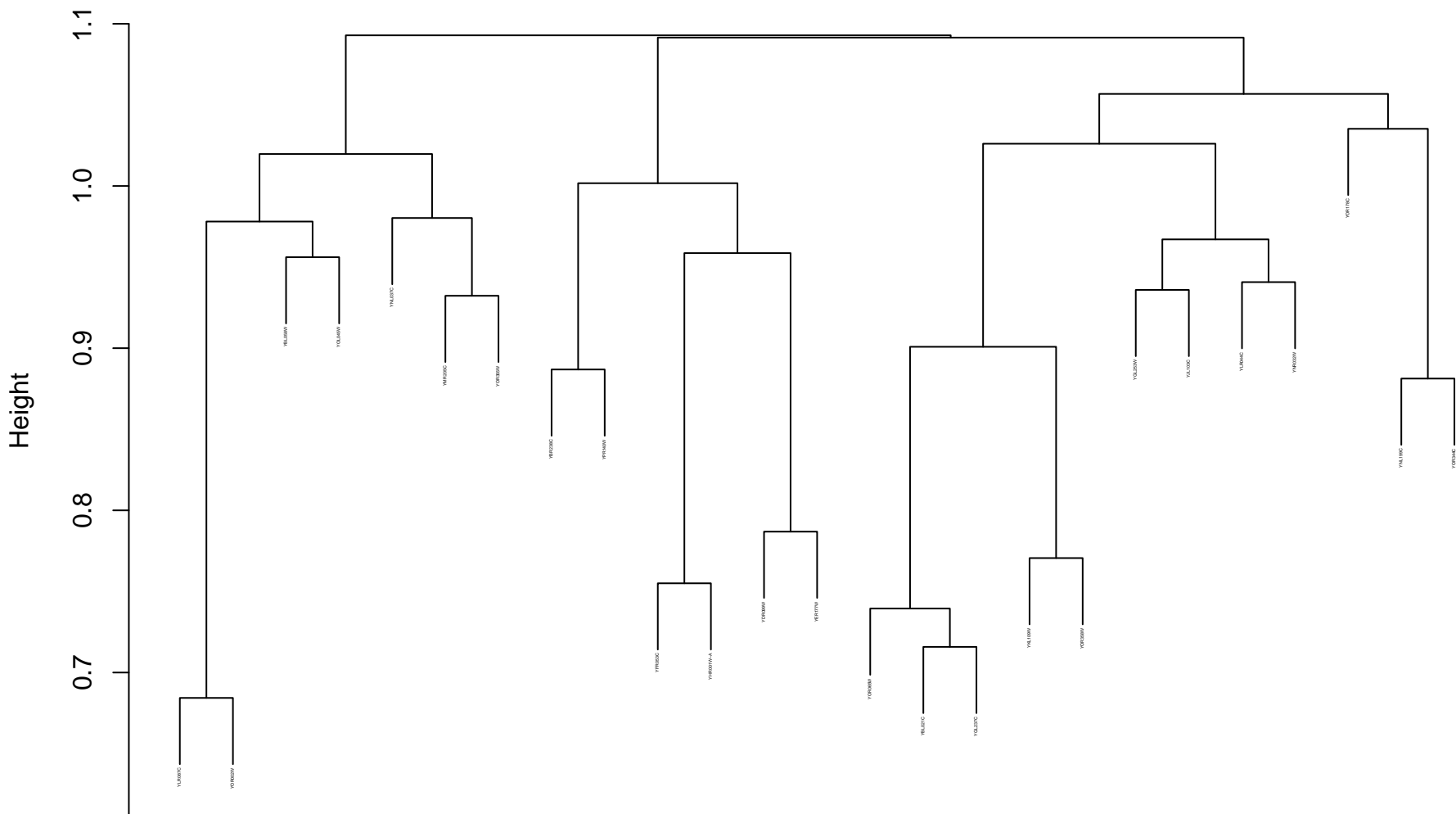
oxidoreductase activity_GO_pearson_complete



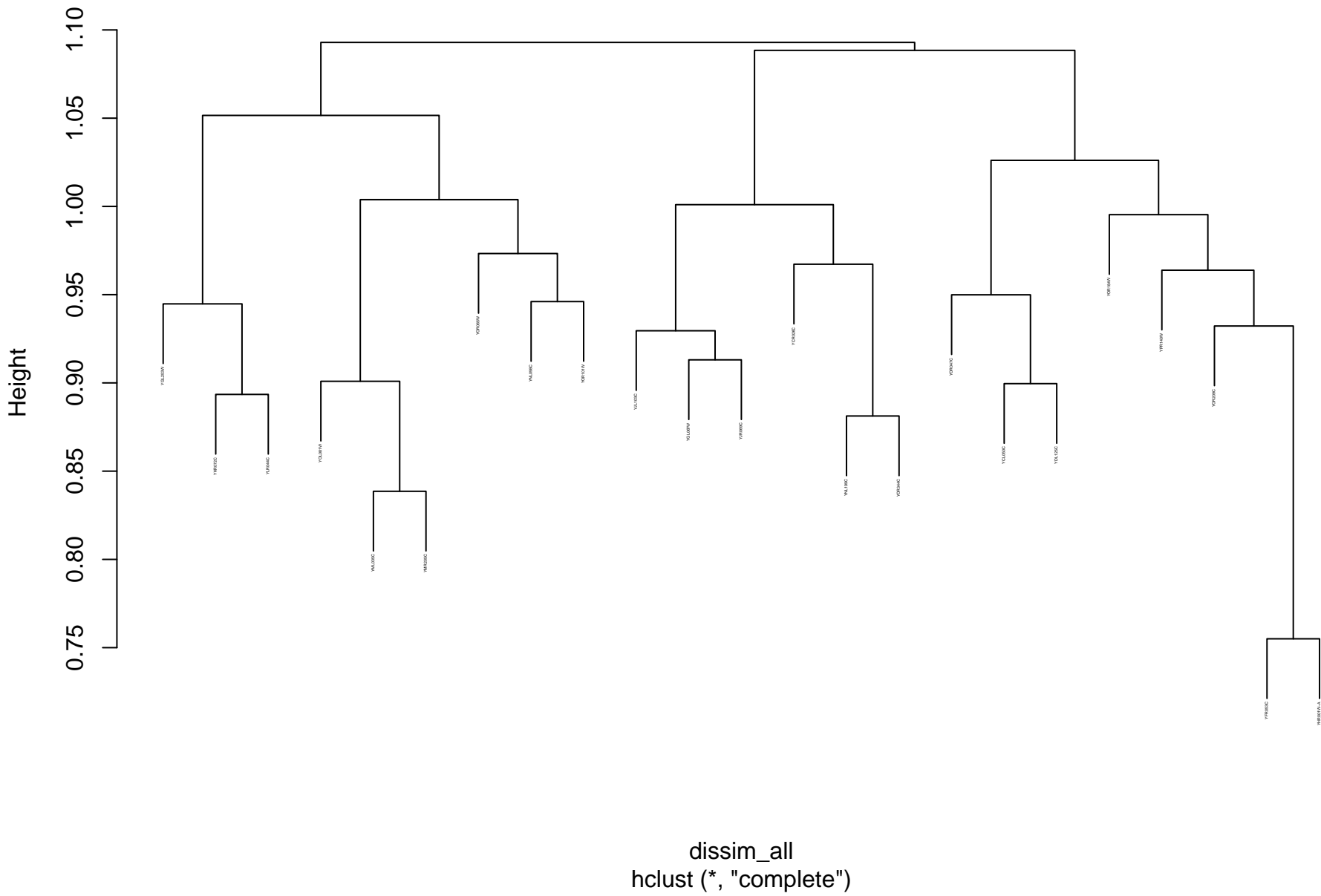
transmembrane transporter activity_GO_pearson_complete



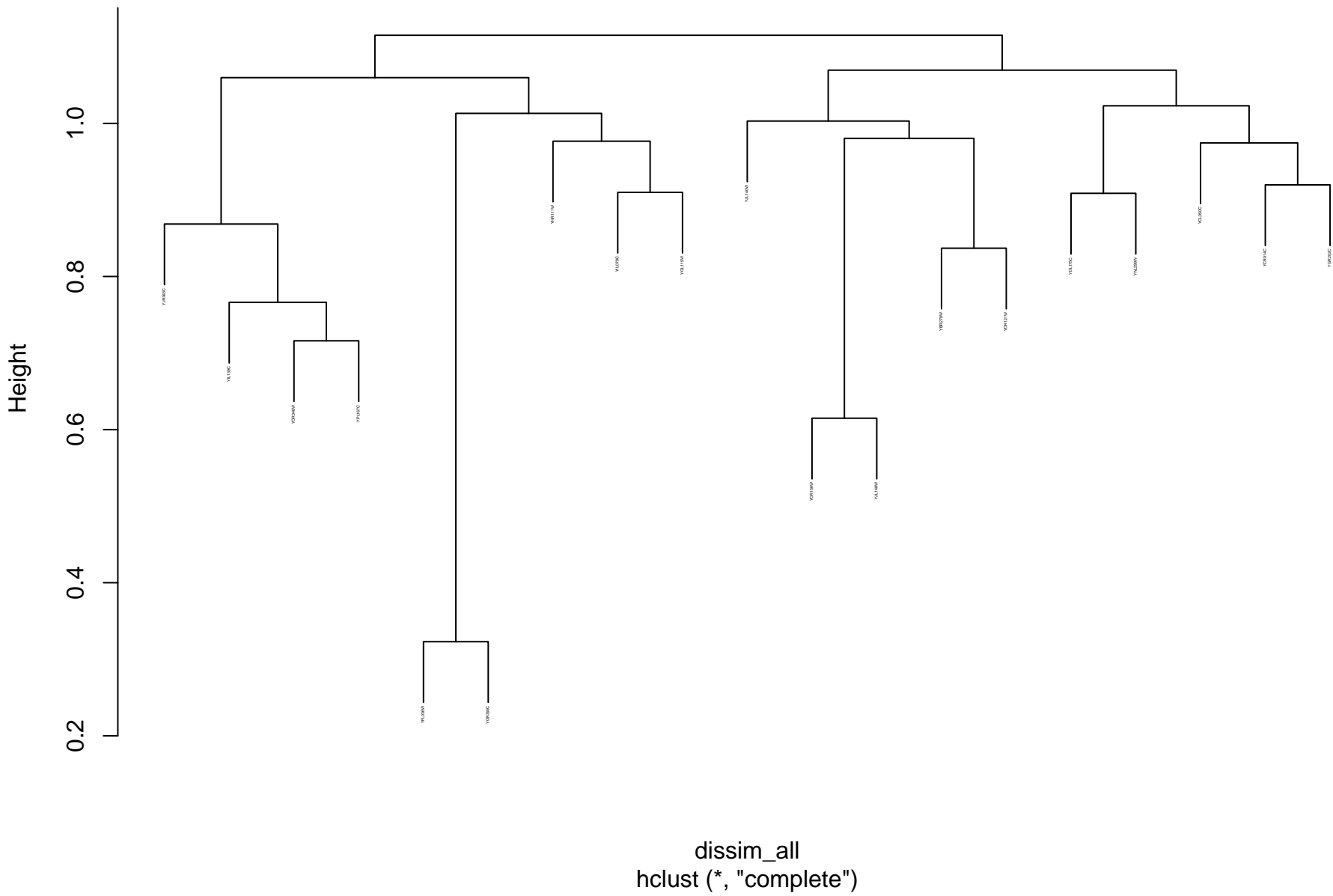

```
dissim_all
hclust (*, "complete")
```



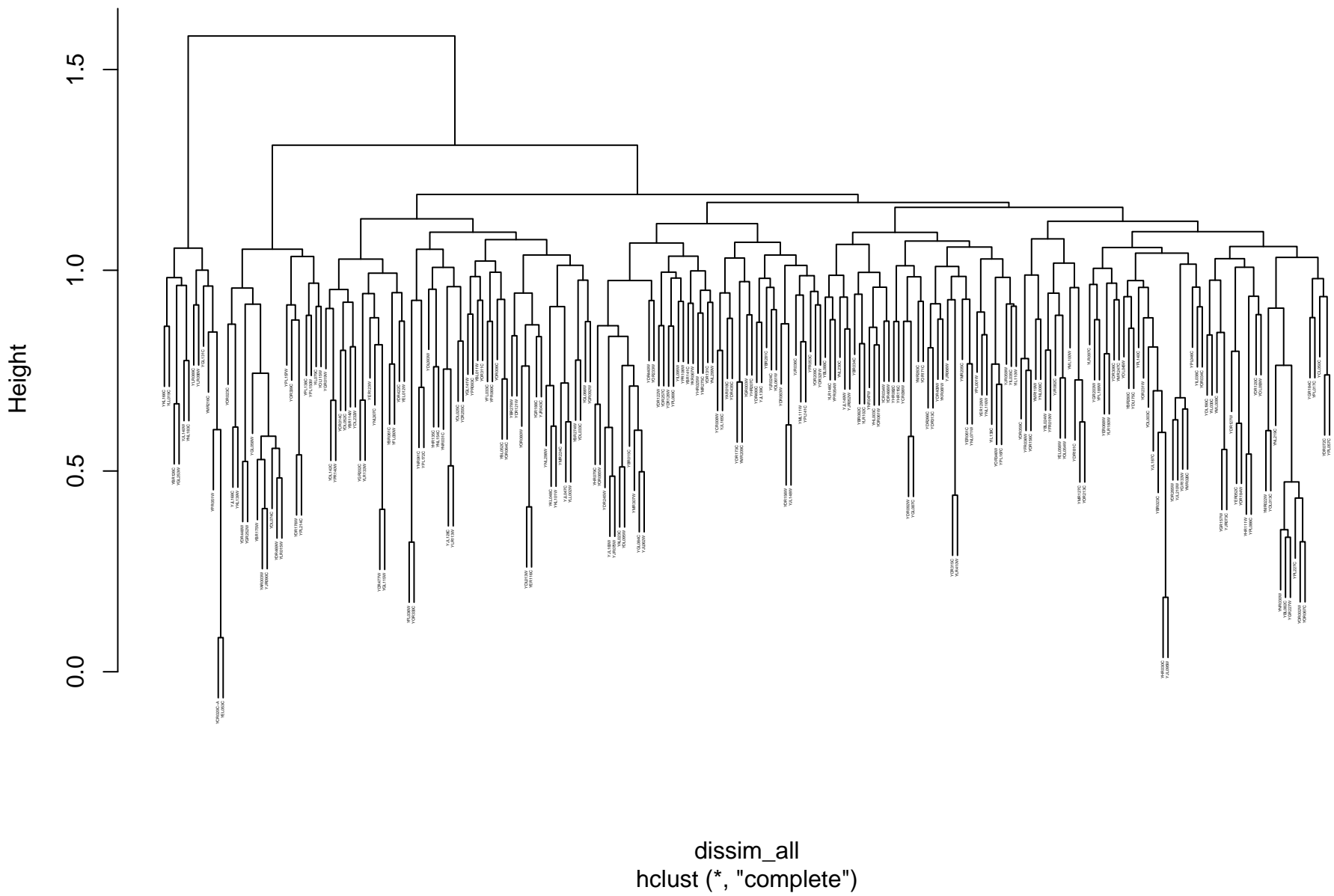
nucleobase-containing small molecule metabolic process_GO_pearson_complete



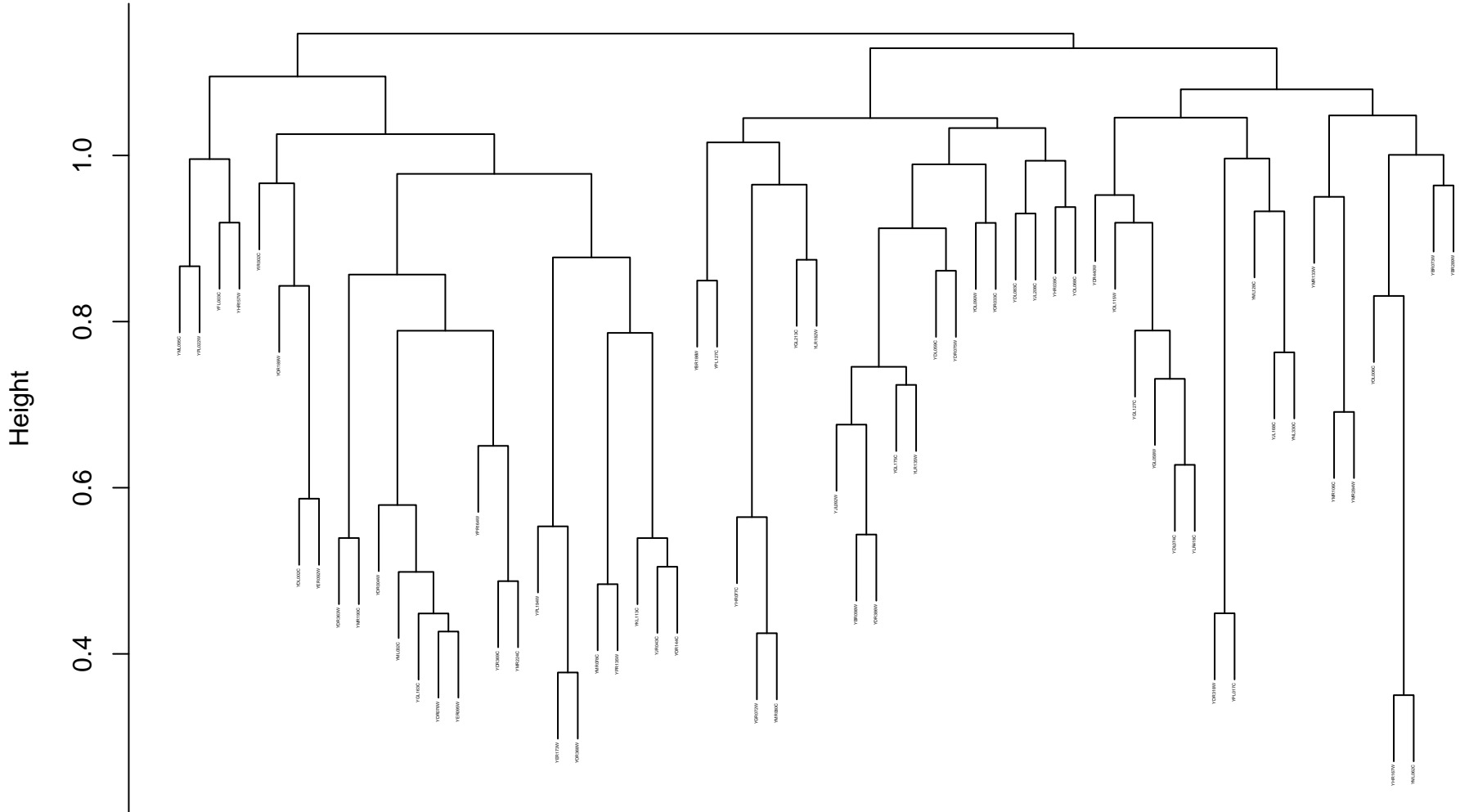
nucleotidyltransferase activity_GO_pearson_complete



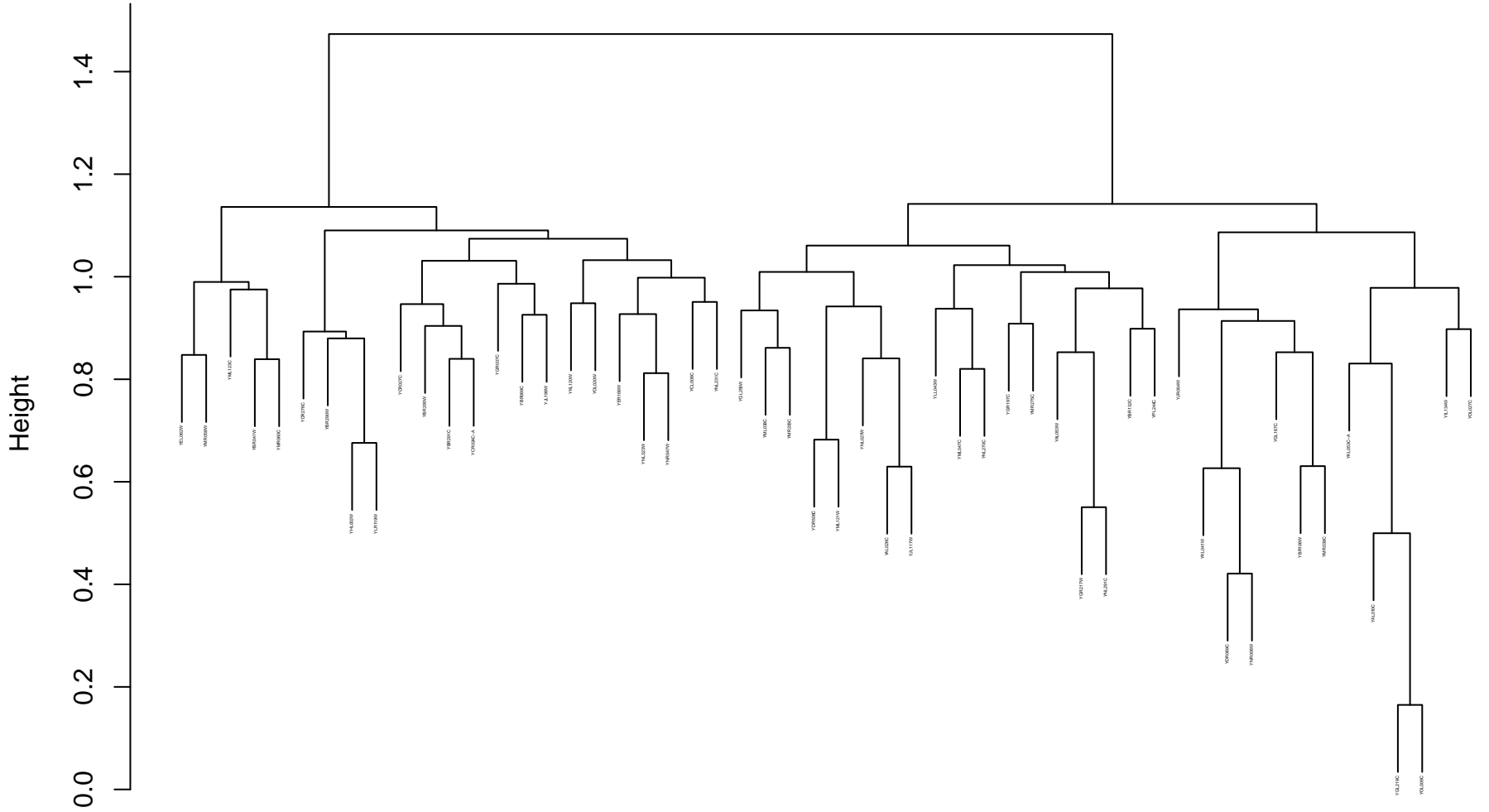
transferase activity_GO_pearson_complete



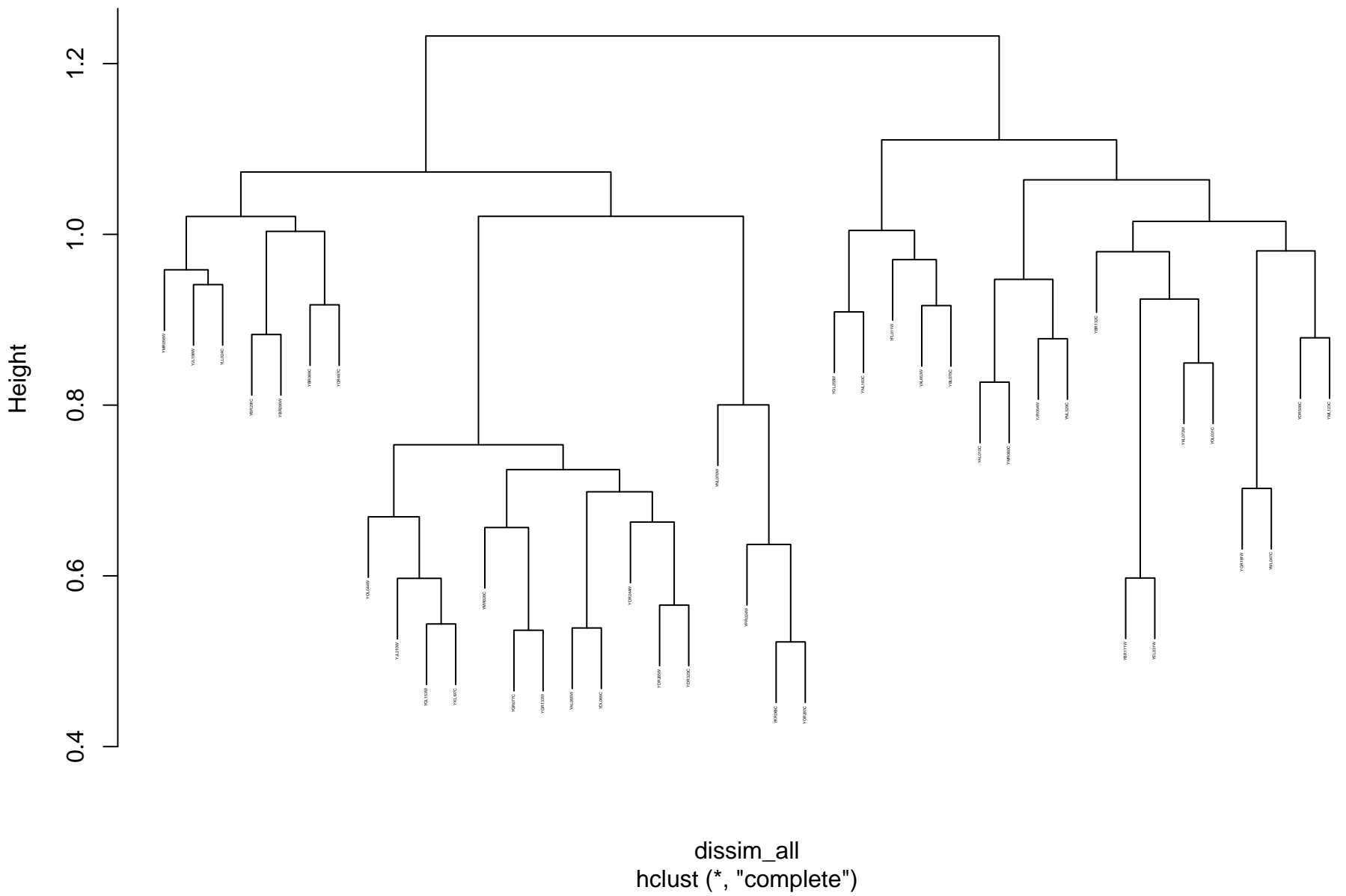
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dissim_all
hclust (*, "complete")
```



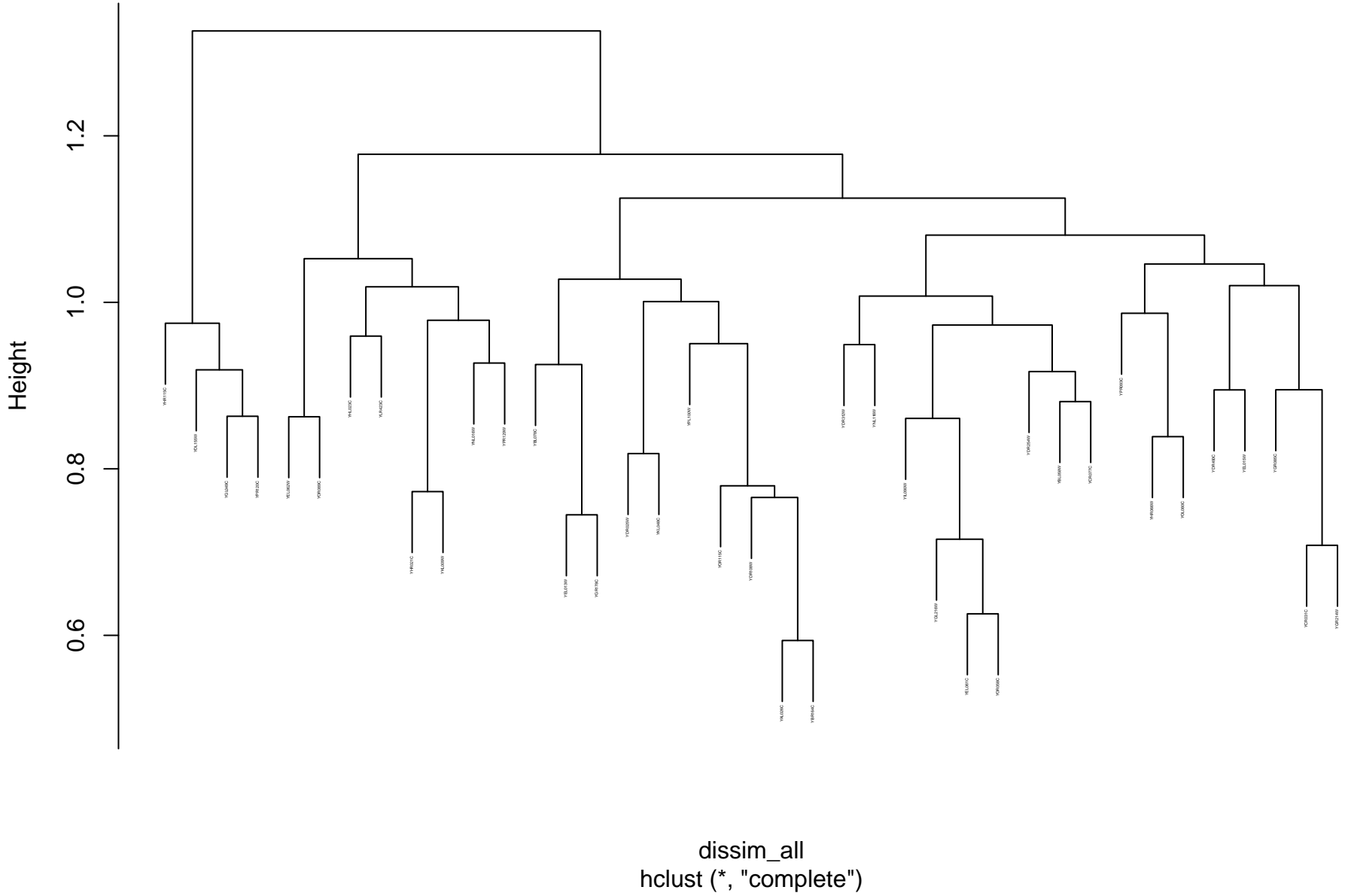
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dissim_all
hclust (*, "complete")
```



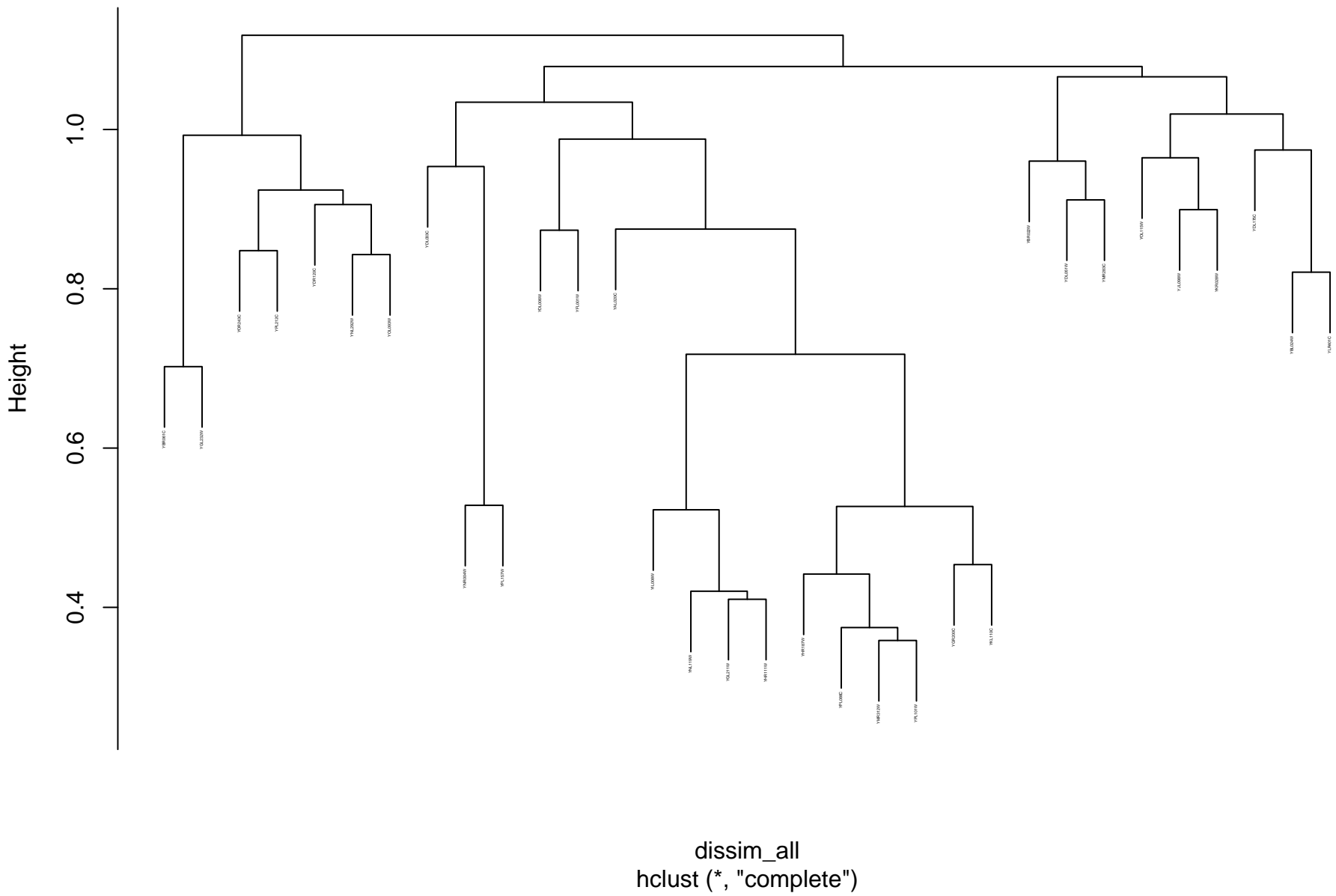
transmembrane transport_GO_pearson_complete



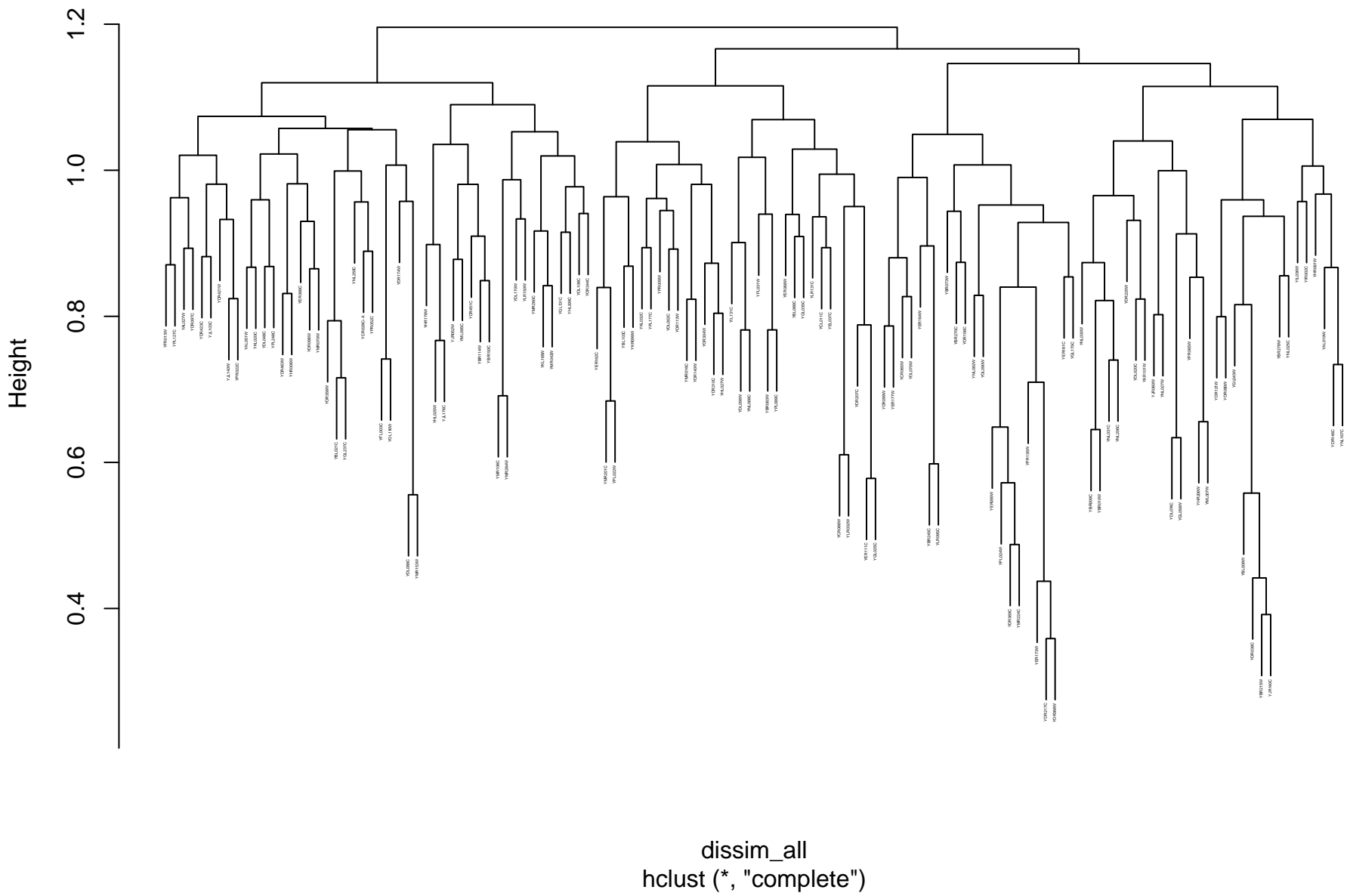
organelle assembly_GO_pearson_complete



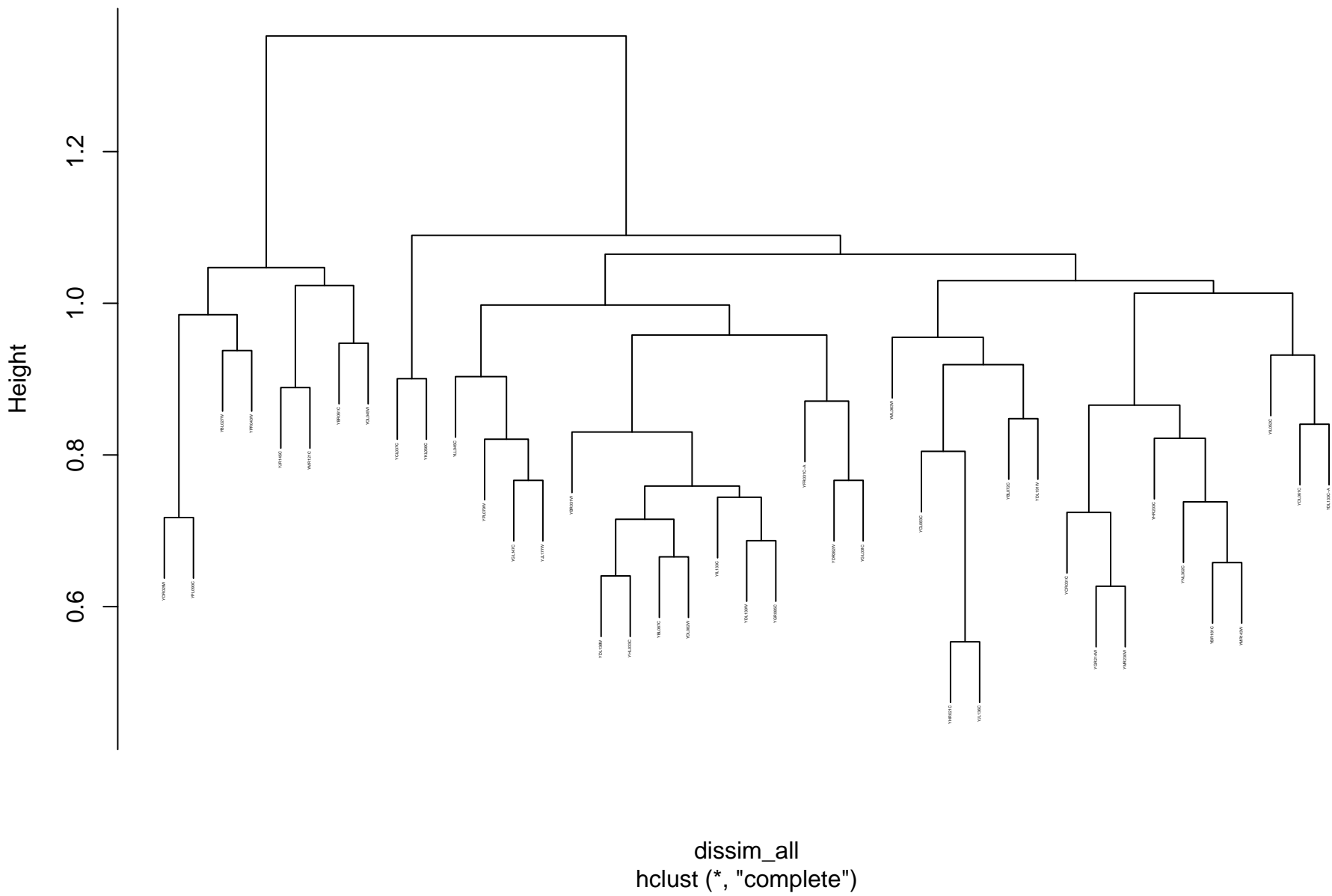
tRNA processing_GO_pearson_complete



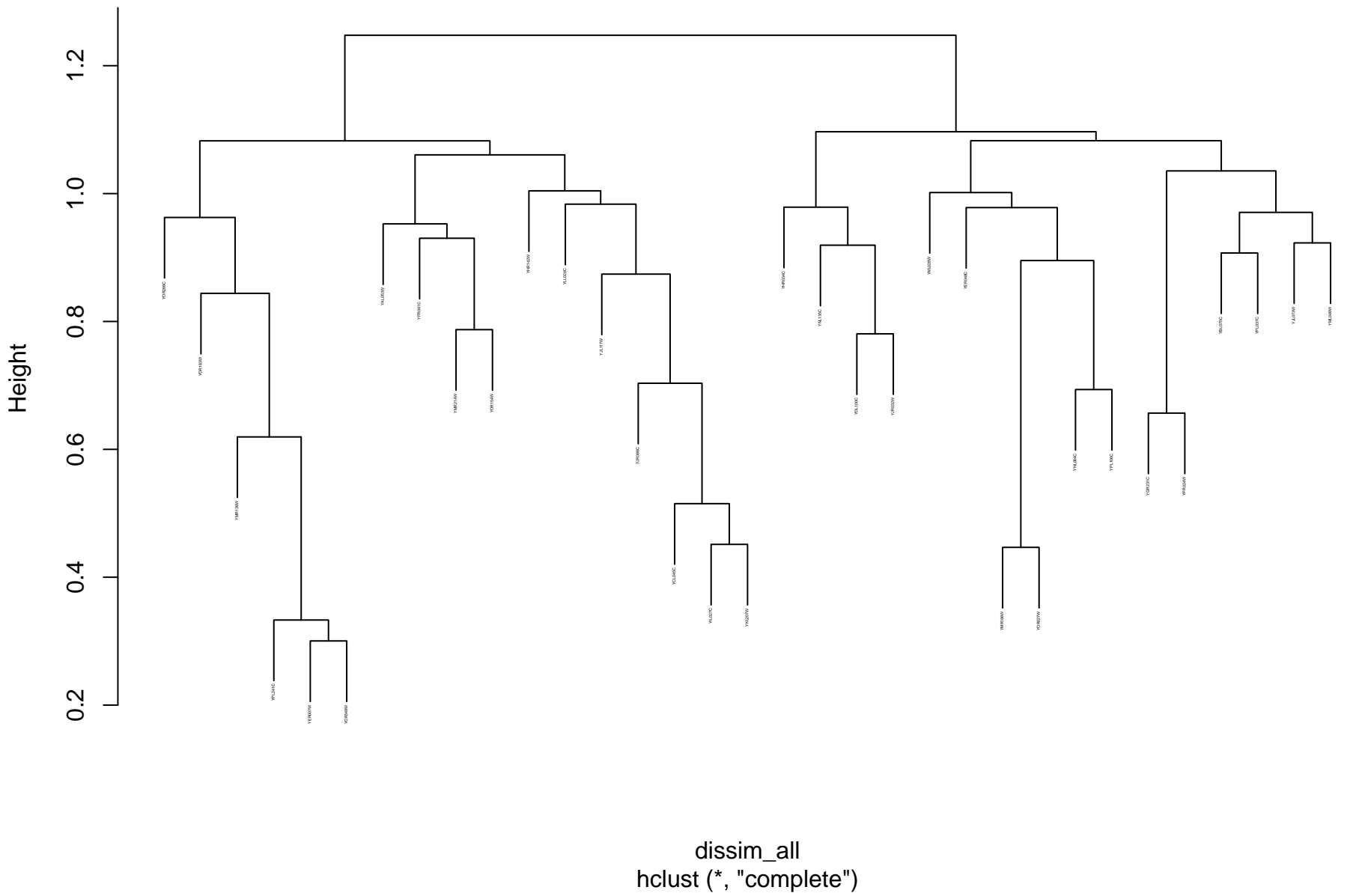
DNA binding_GO_pearson_complete



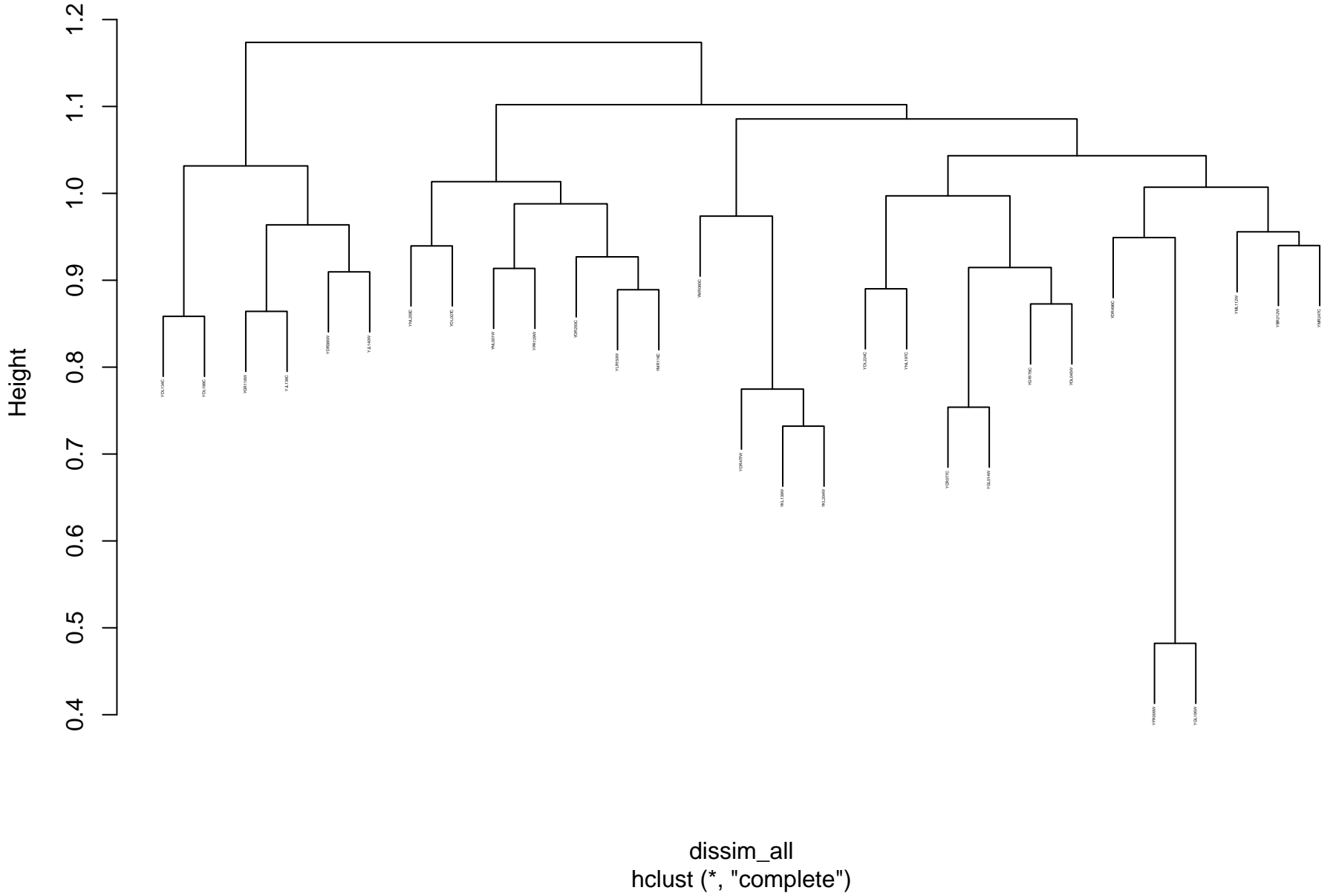
cytoplasmic translation_GO_pearson_complete



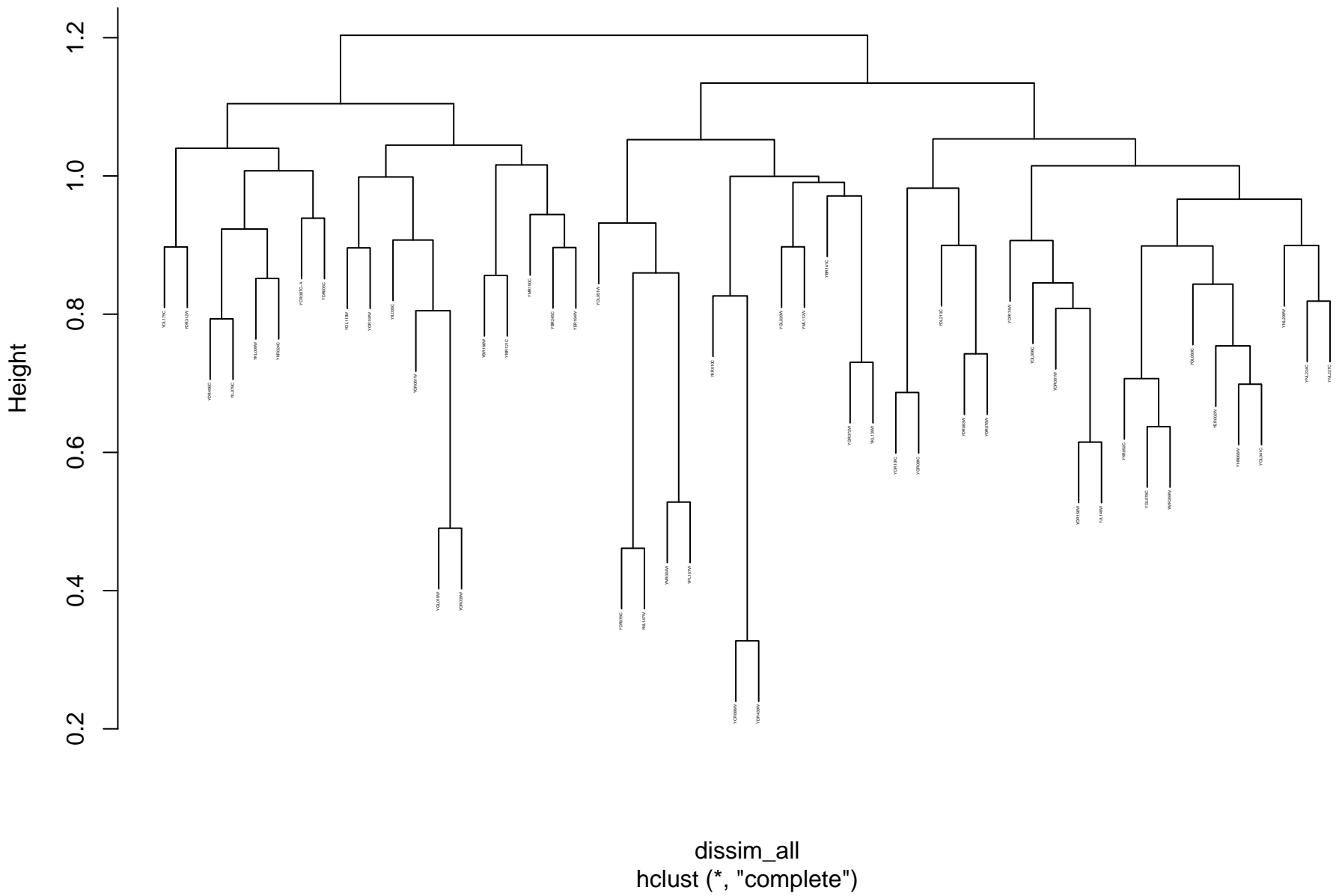
protein folding_GO_pearson_complete



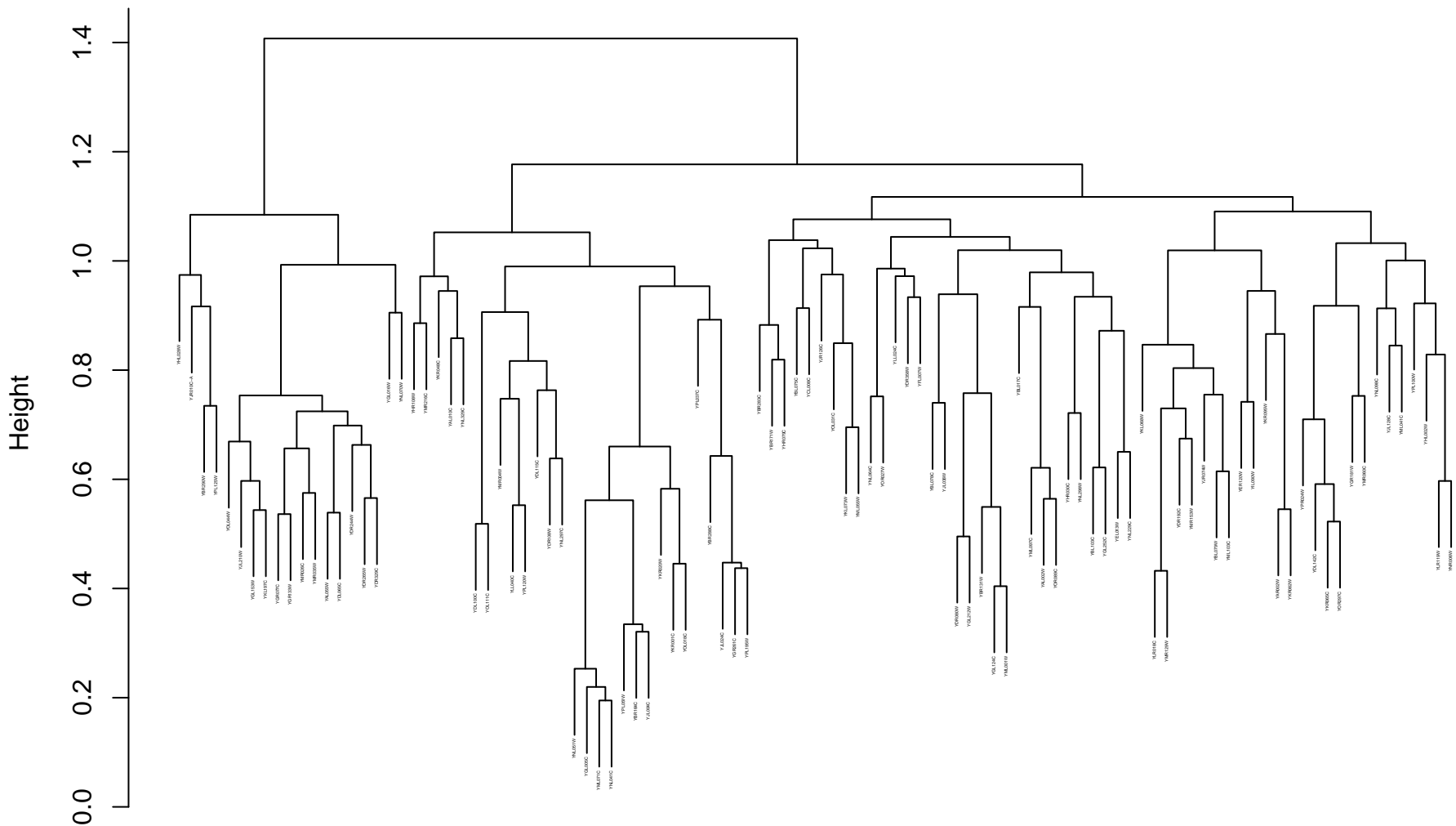
regulation of translation_GO_pearson_complete



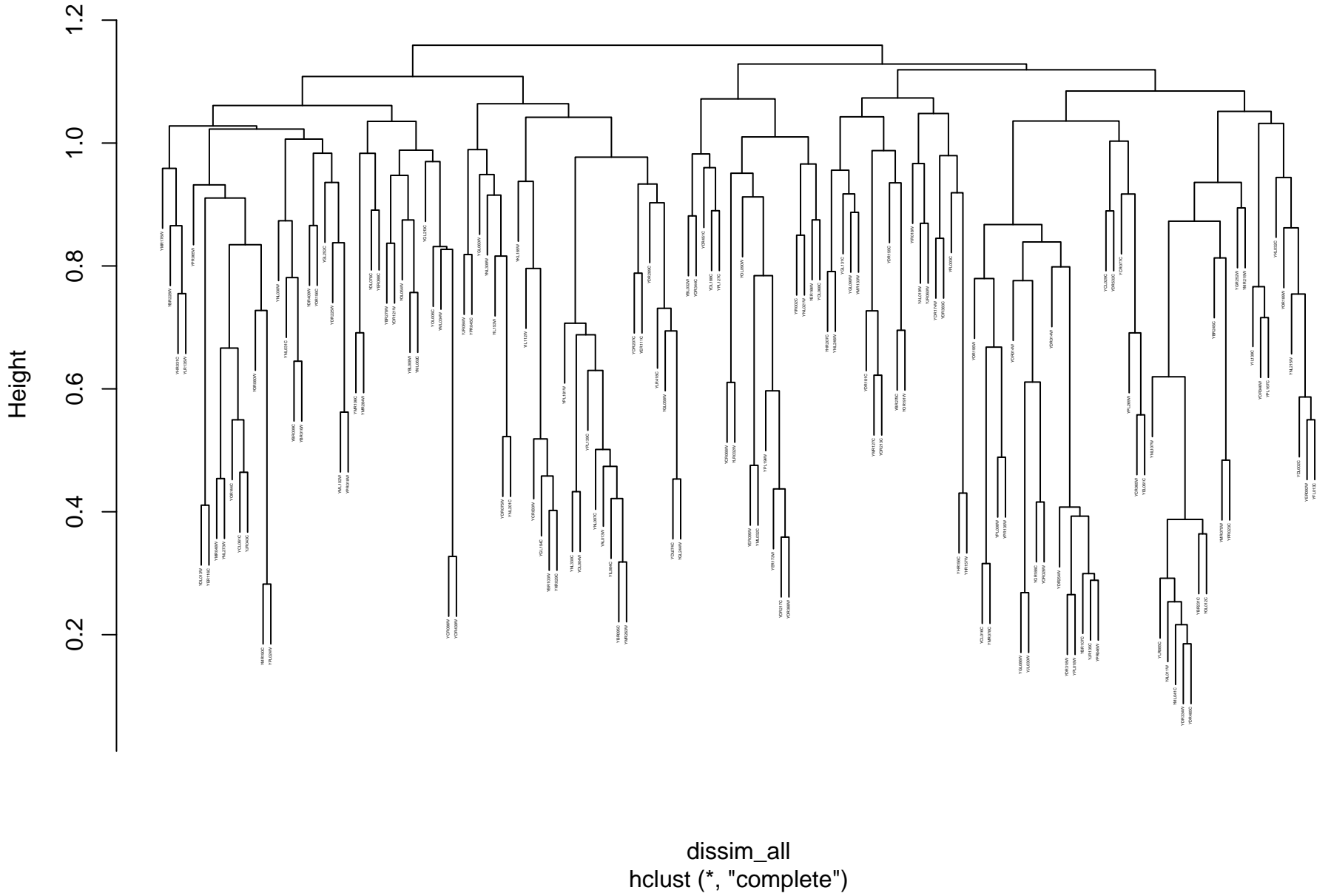
nucleolus_GO_pearson_complete



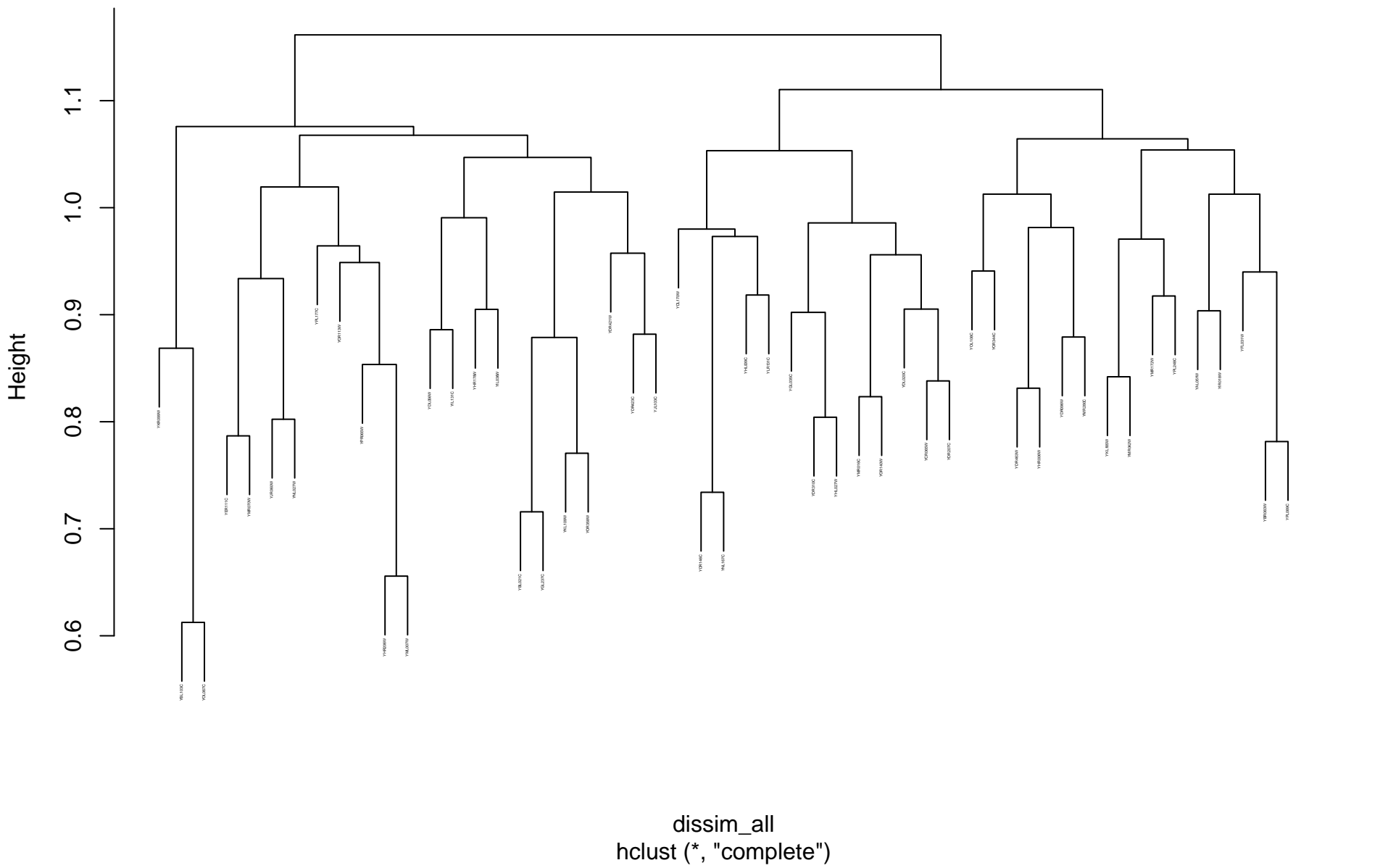
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dissim_all
hclust (*, "complete")
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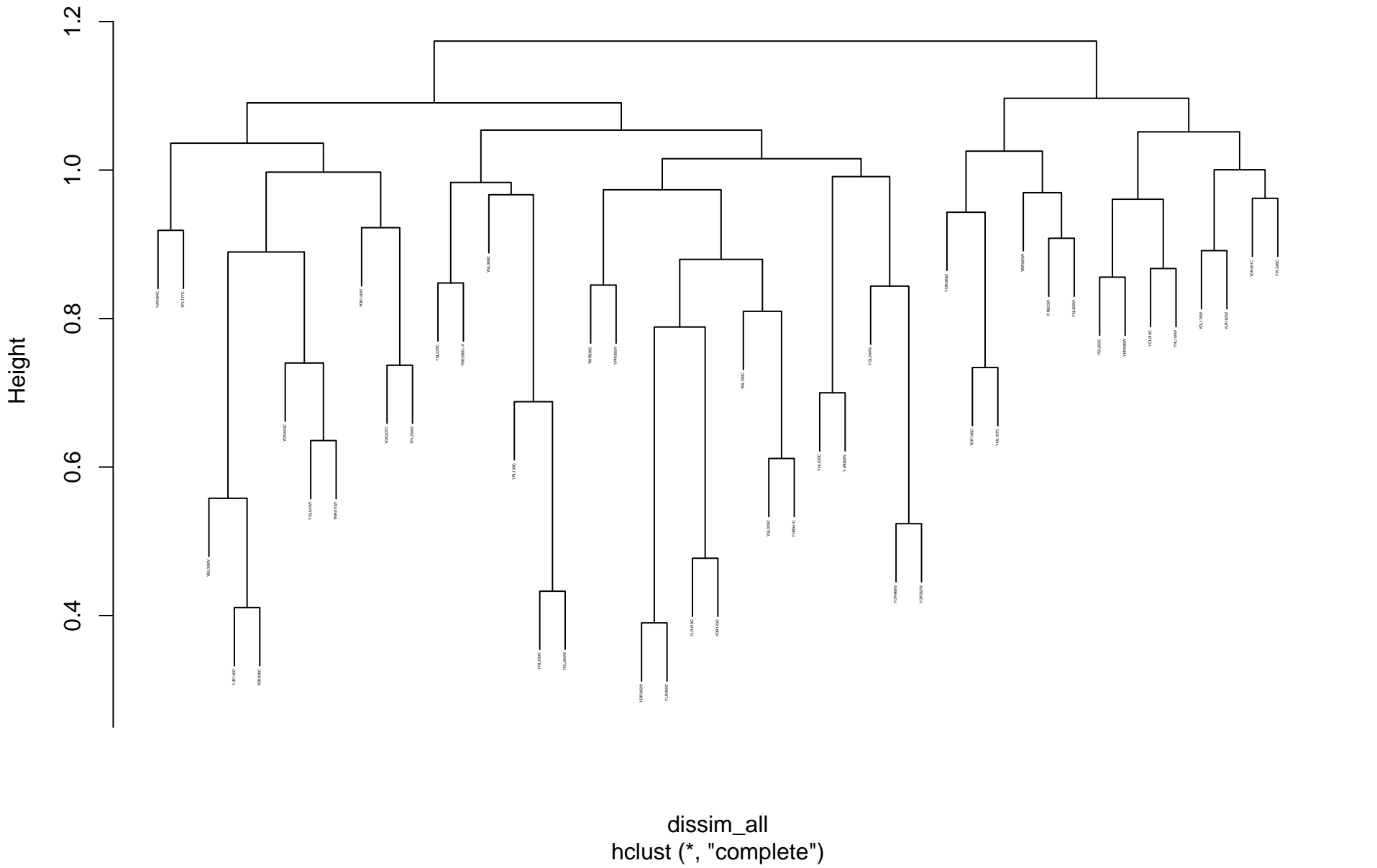
chromosome_GO_pearson_complete



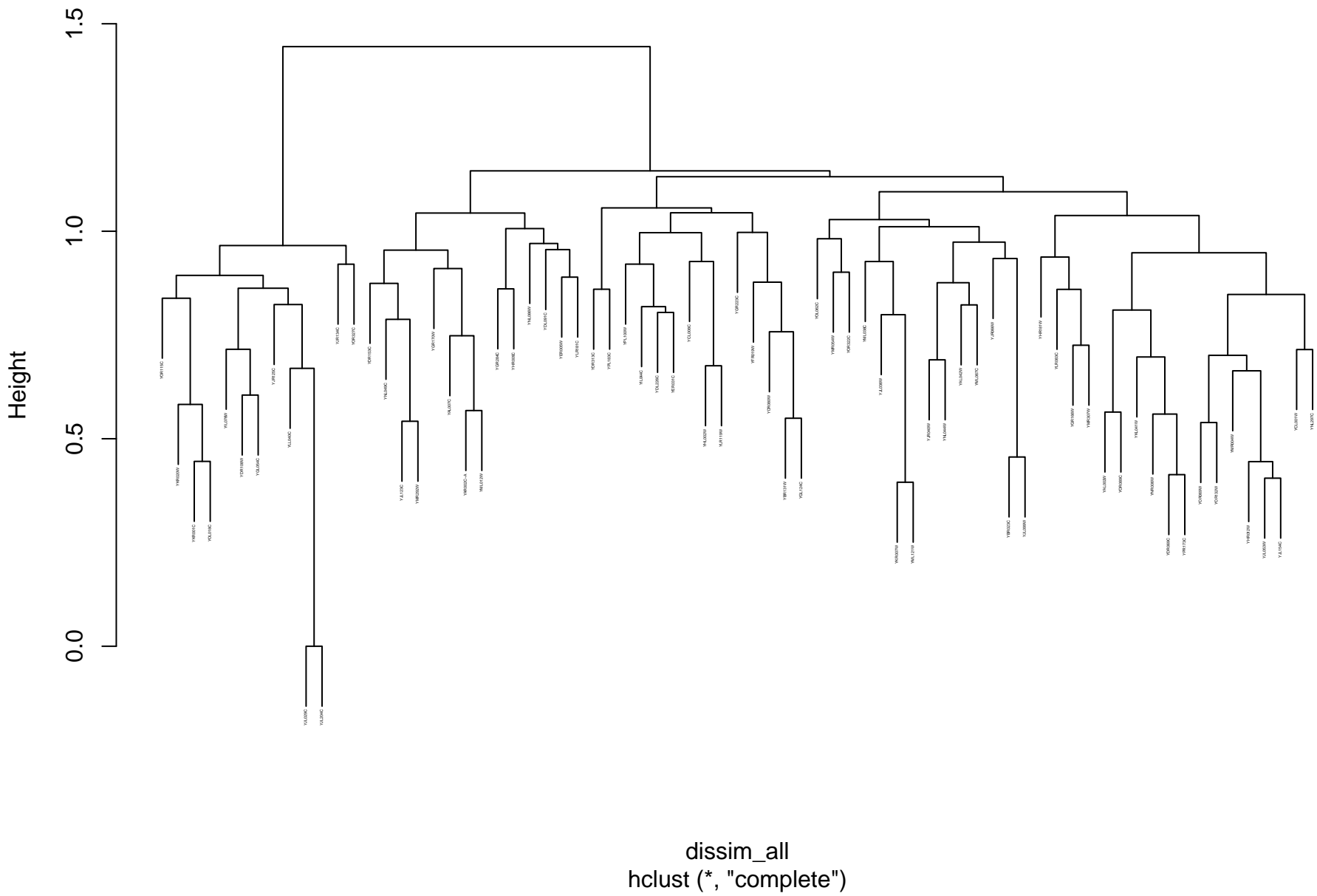
nucleic acid binding transcription factor activity_GO_pearson_complete



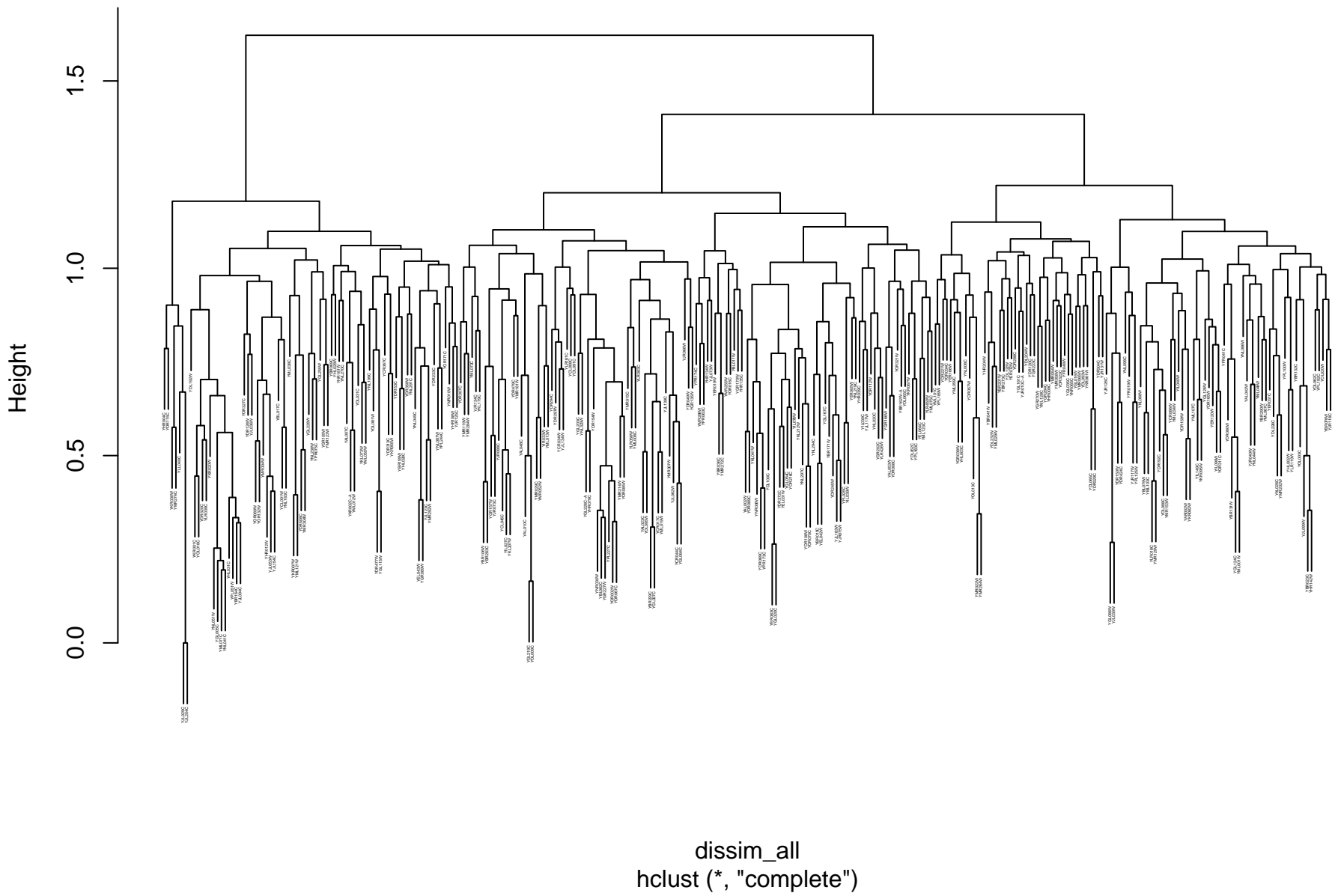
transcription factor activity, protein binding_GO_pearson_complete



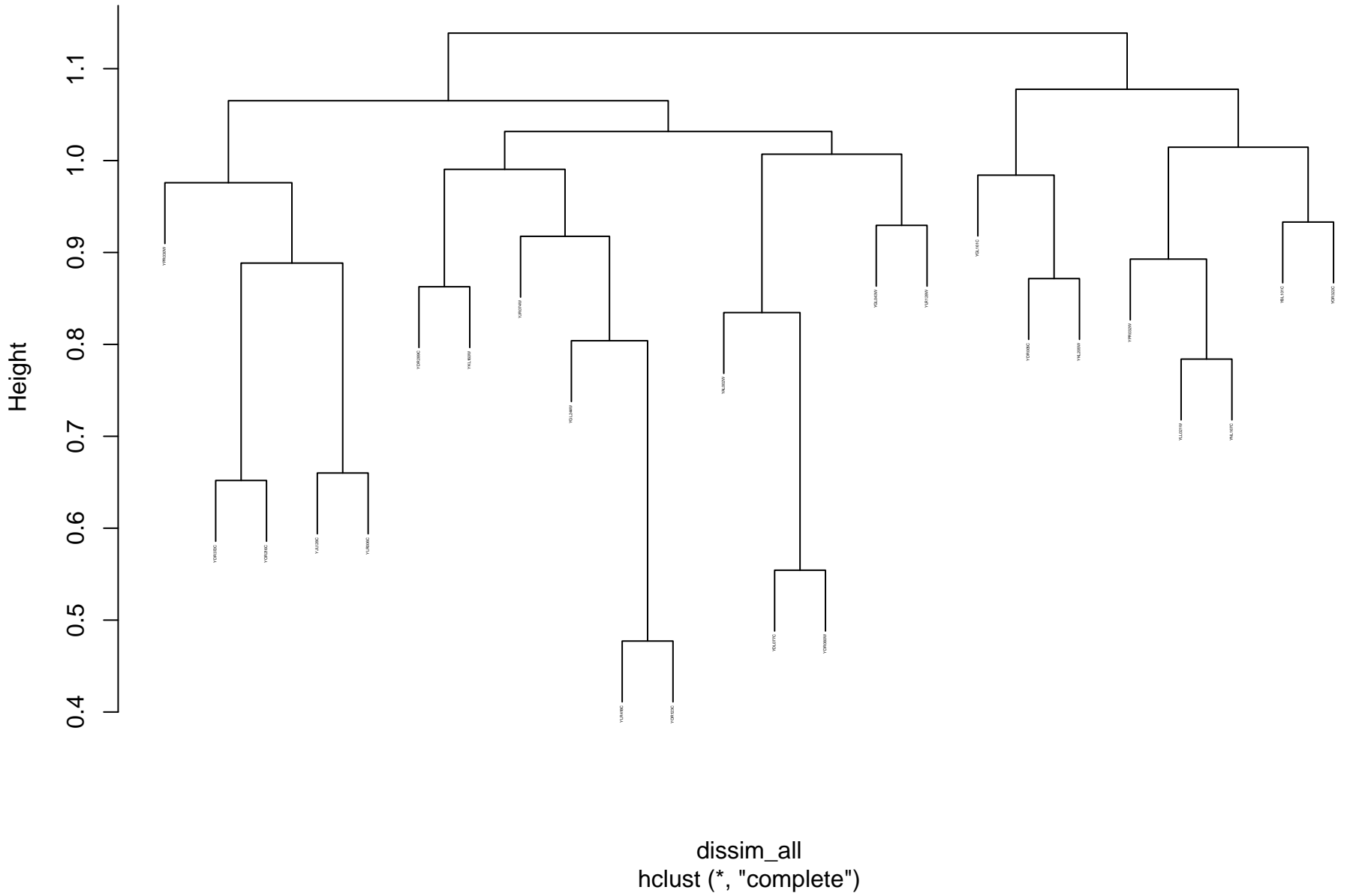
cytoplasmic vesicle_GO_pearson_complete



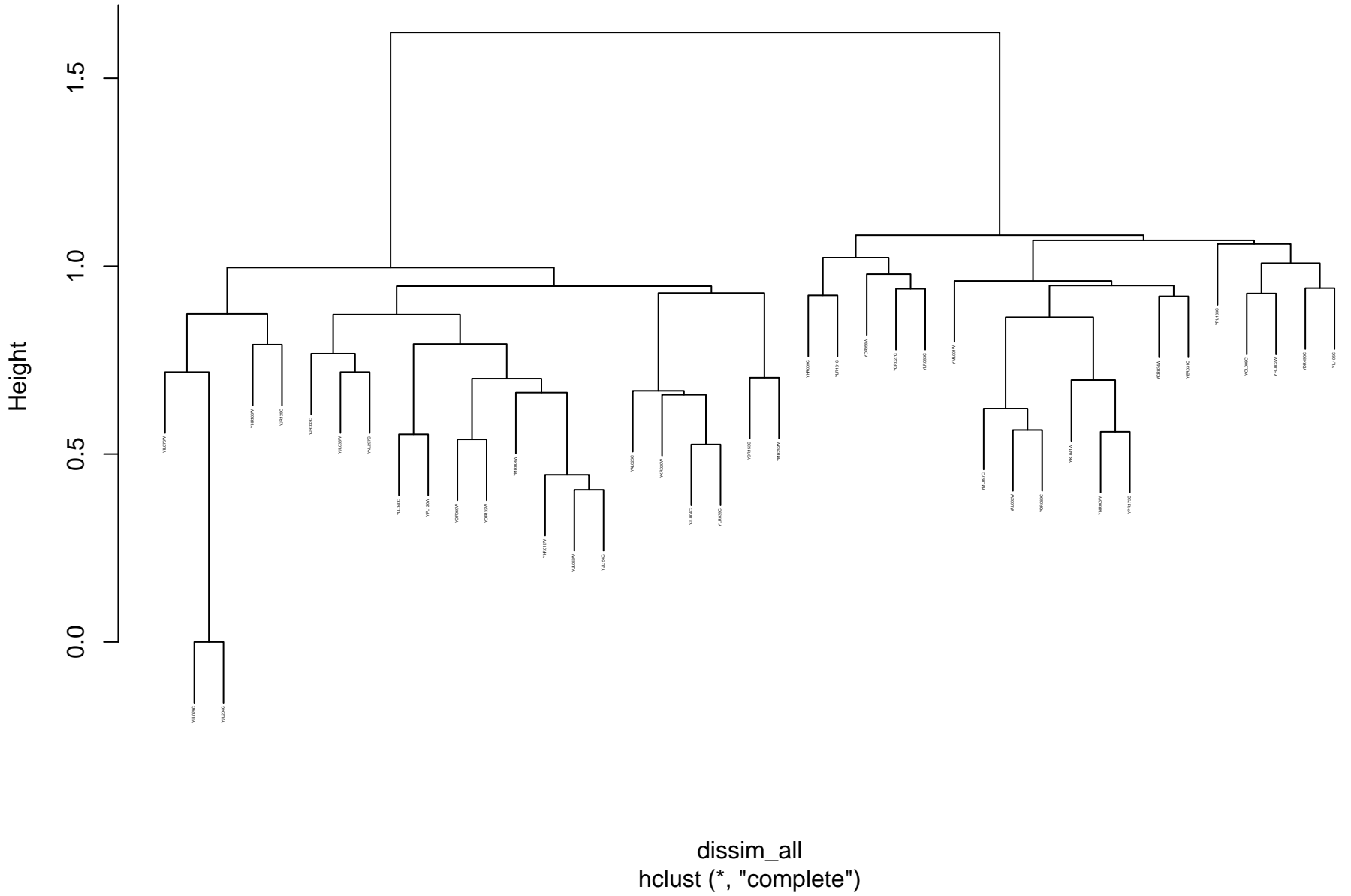
endomembrane system_GO_pearson_complete



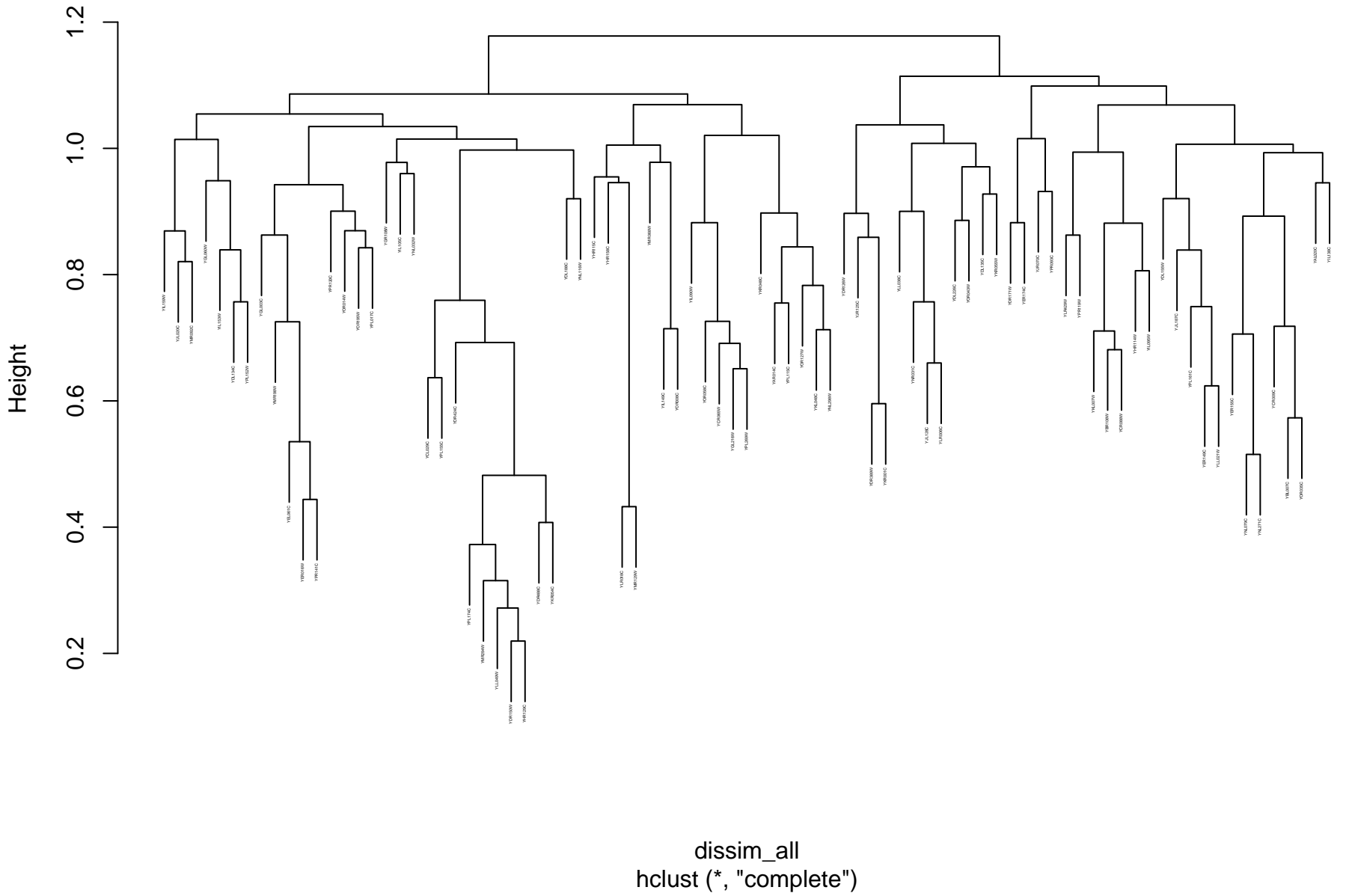
enzyme binding_GO_pearson_complete



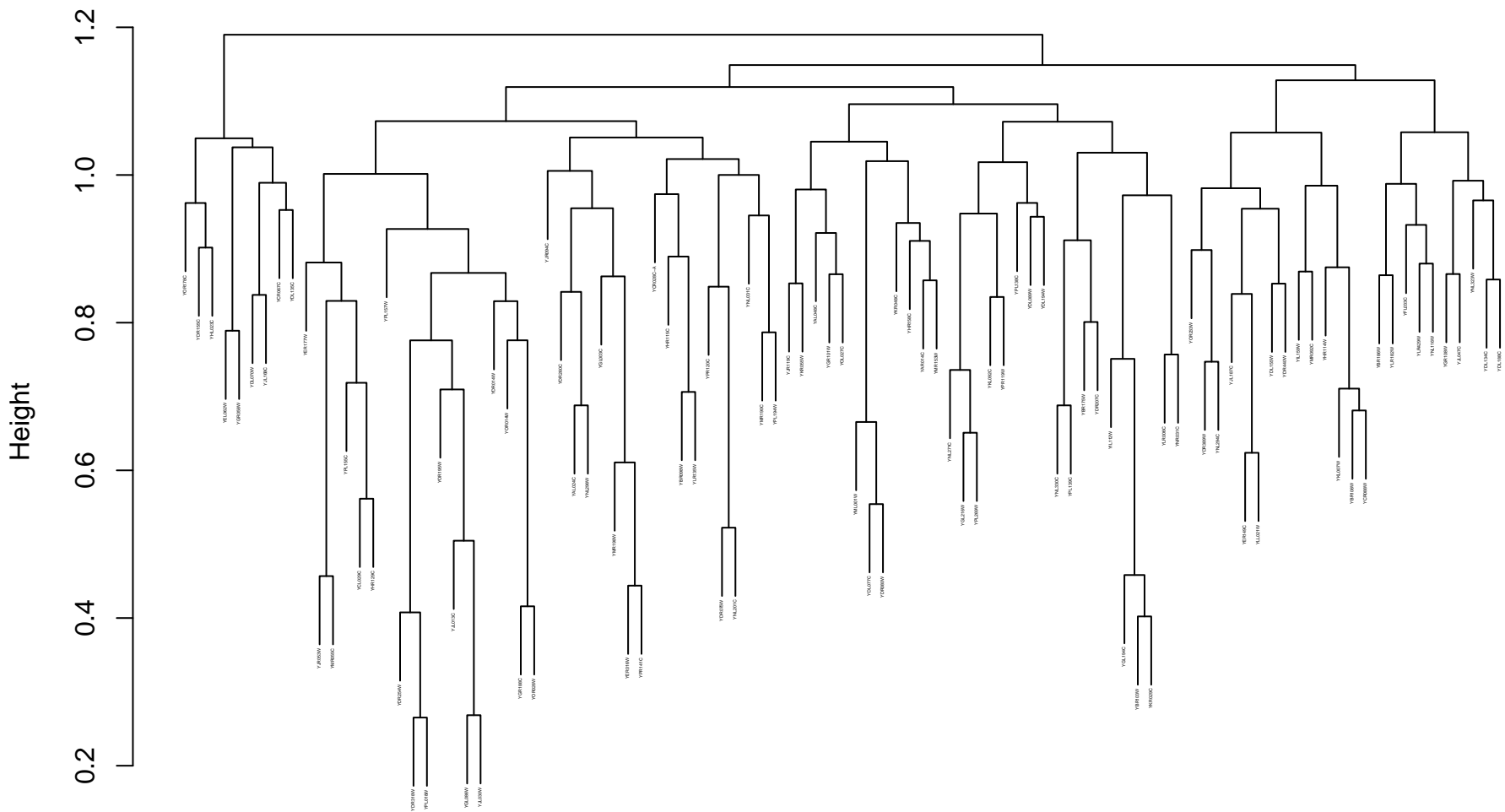
endosomal transport_GO_pearson_complete



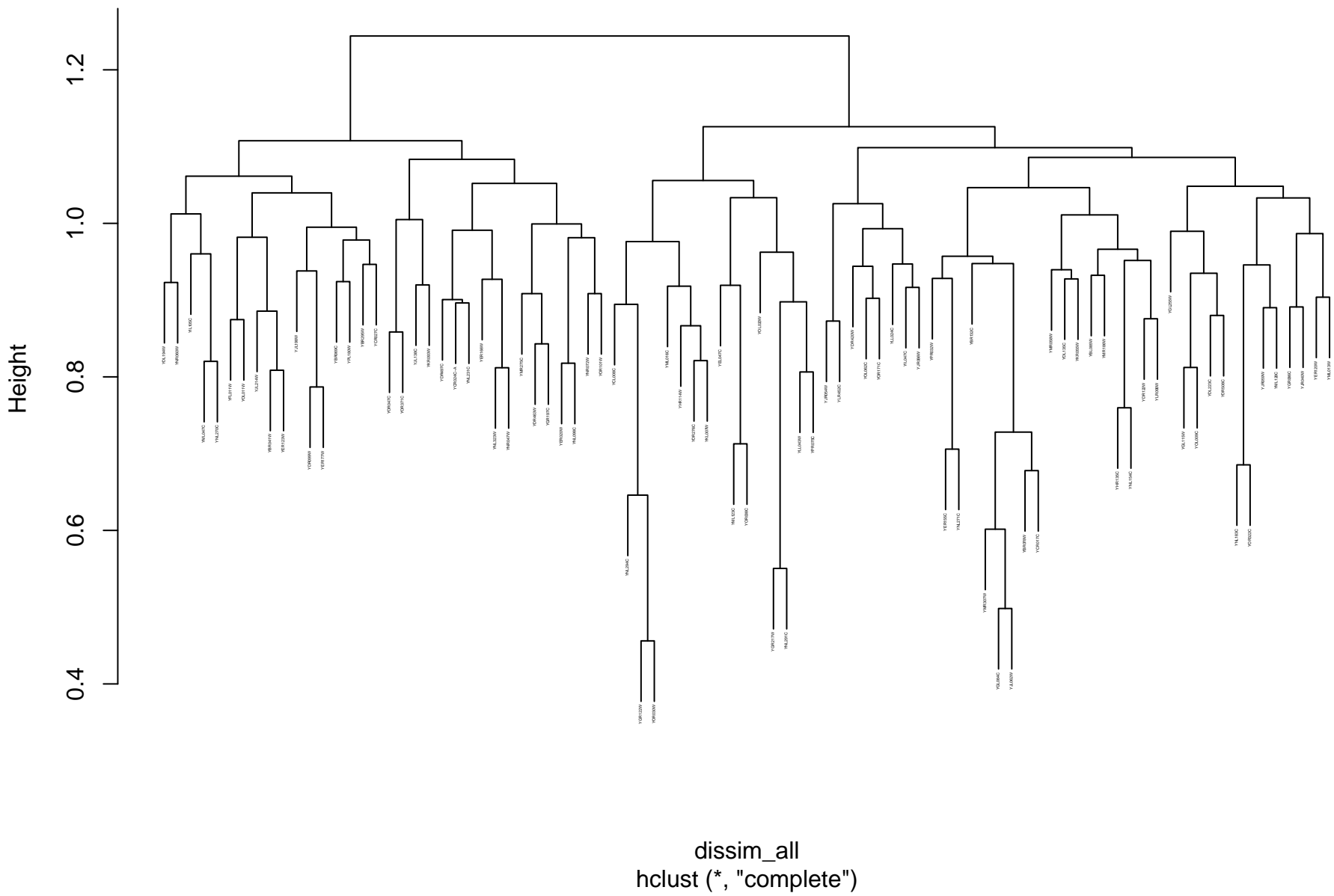
cytoskeleton organization_GO_pearson_complete



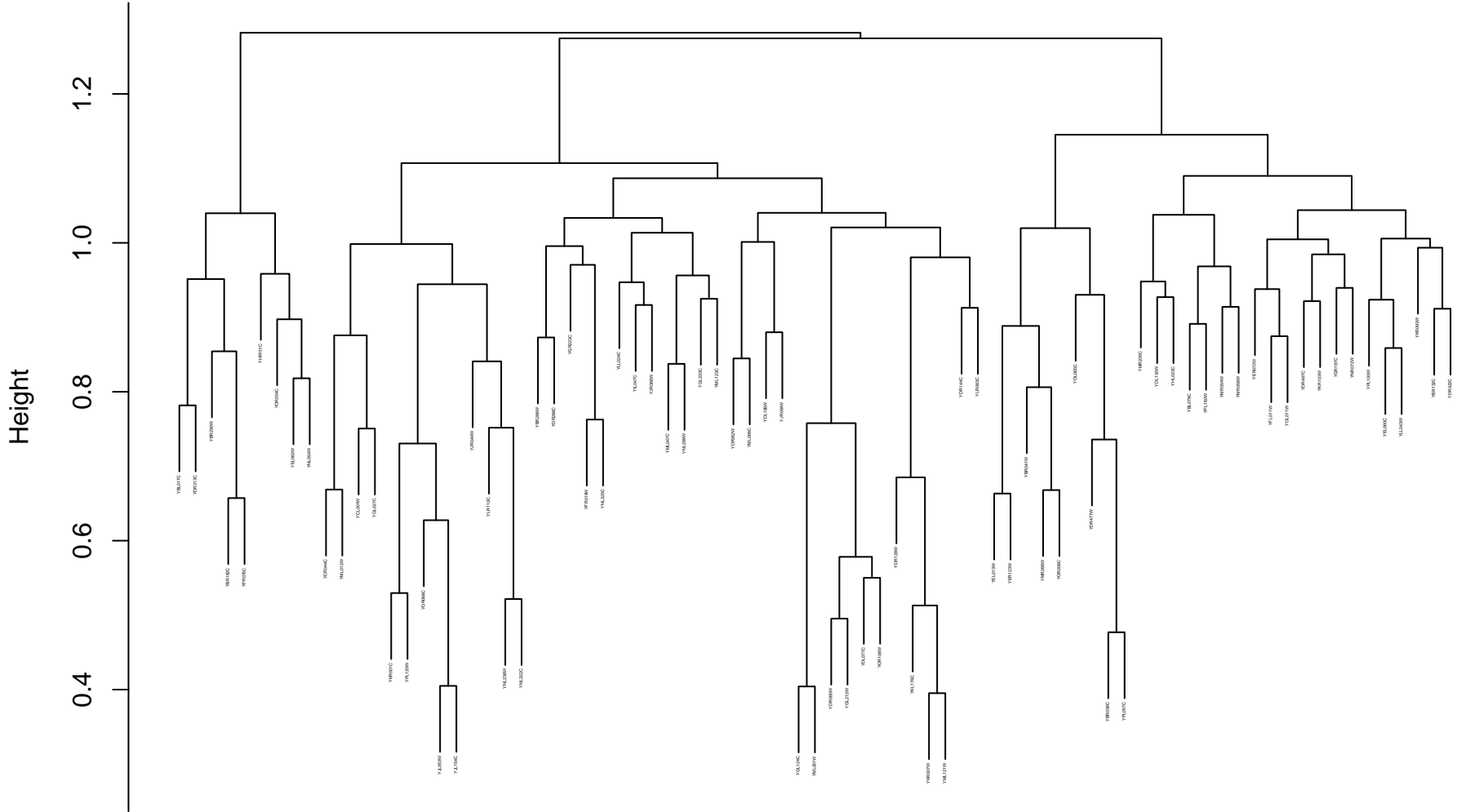
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dissim_all
hclust (*, "complete")
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plasma membrane_GO_pearson_complete

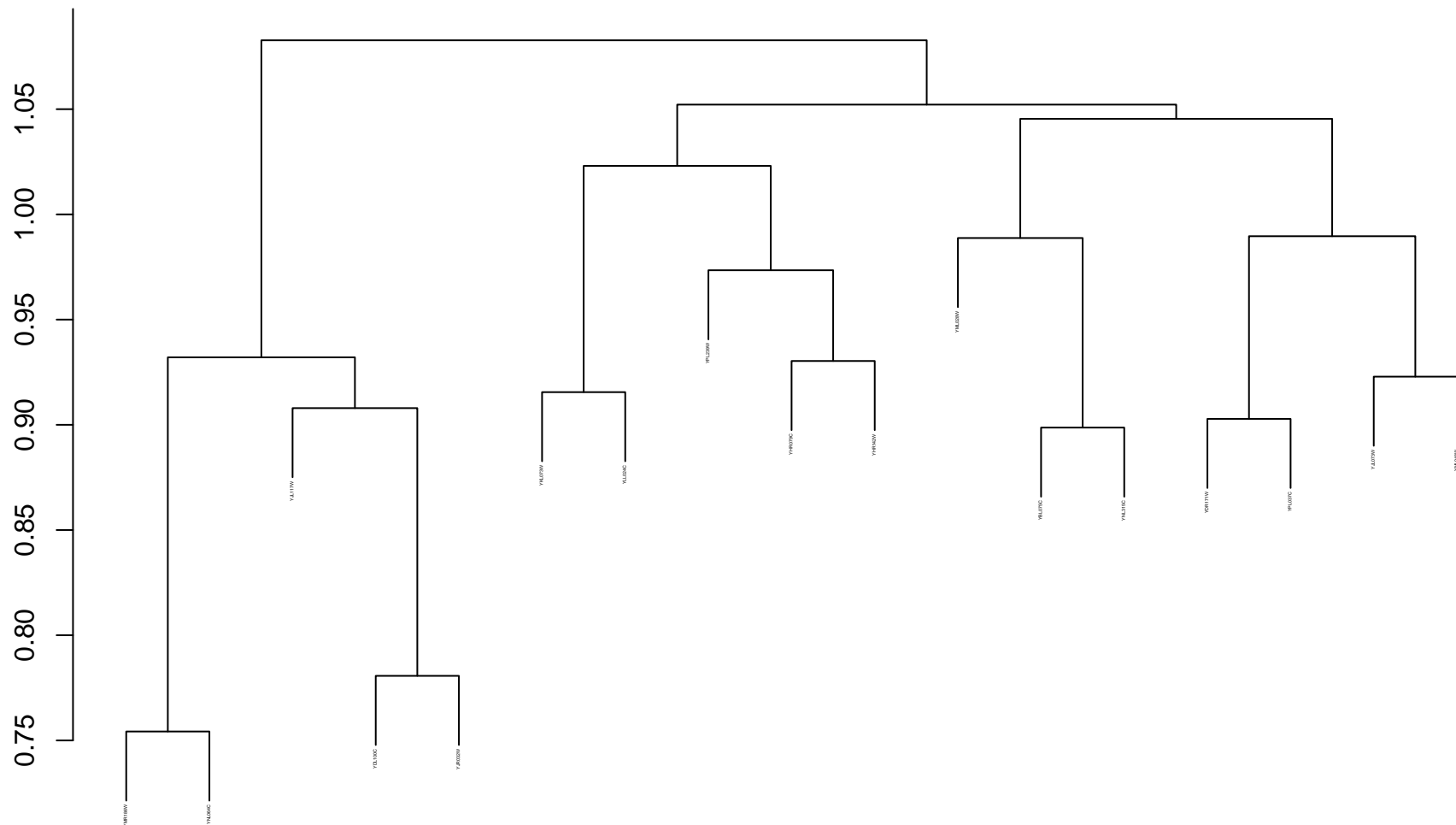


vacuole_GO_pearson_complete



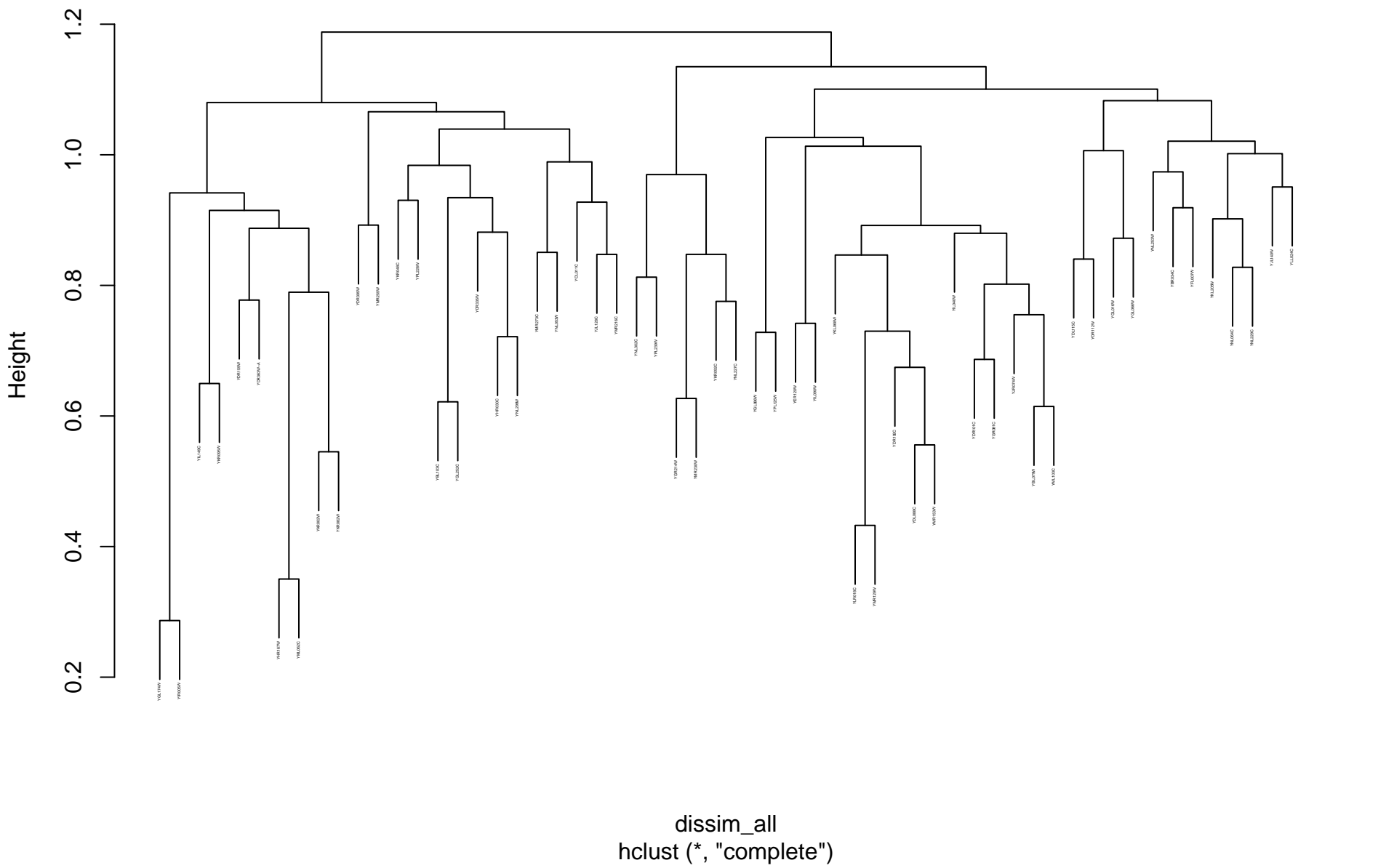
unfolded protein binding_GO_pearson_complete

Height

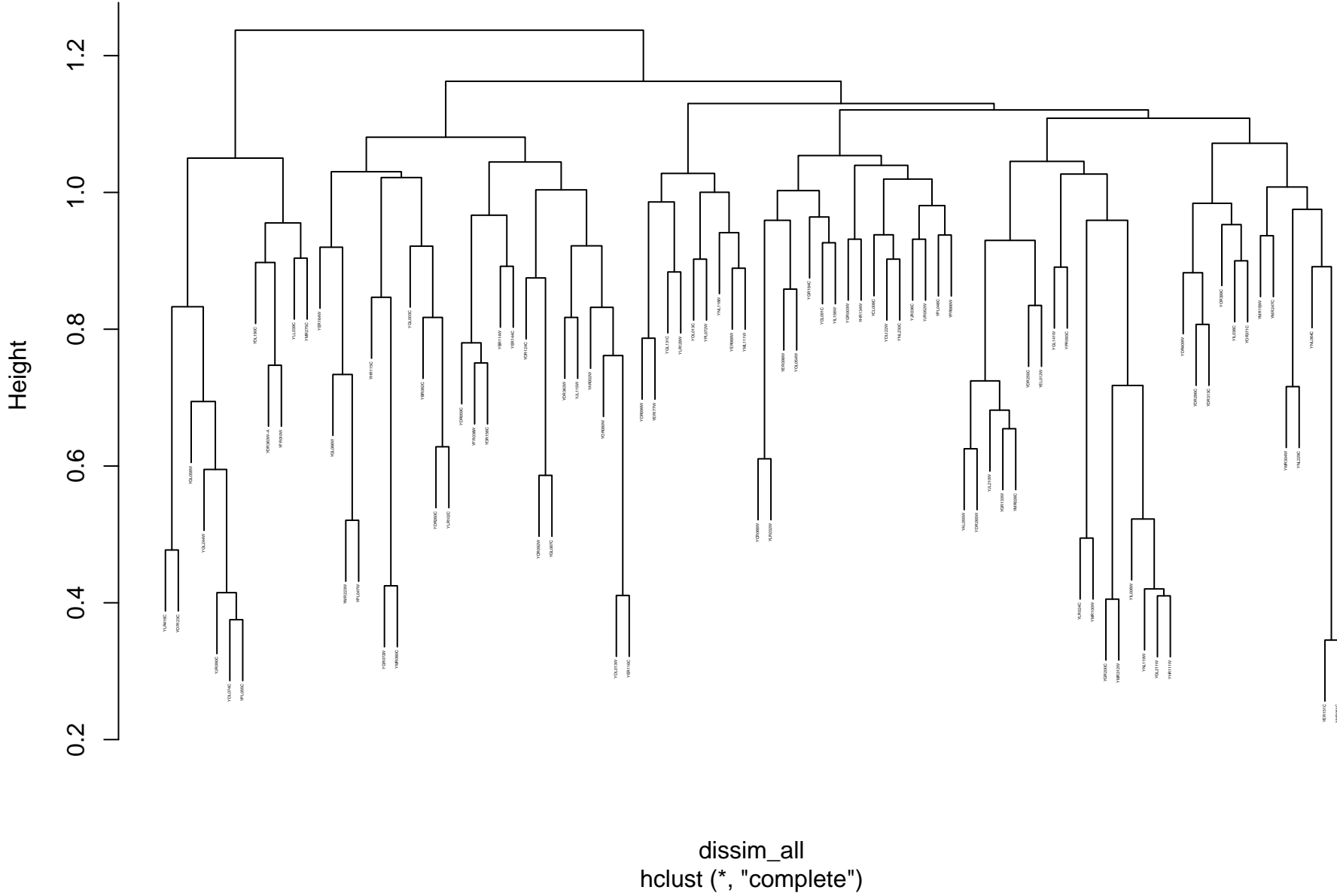


dissim_all
hclust (*, "complete")

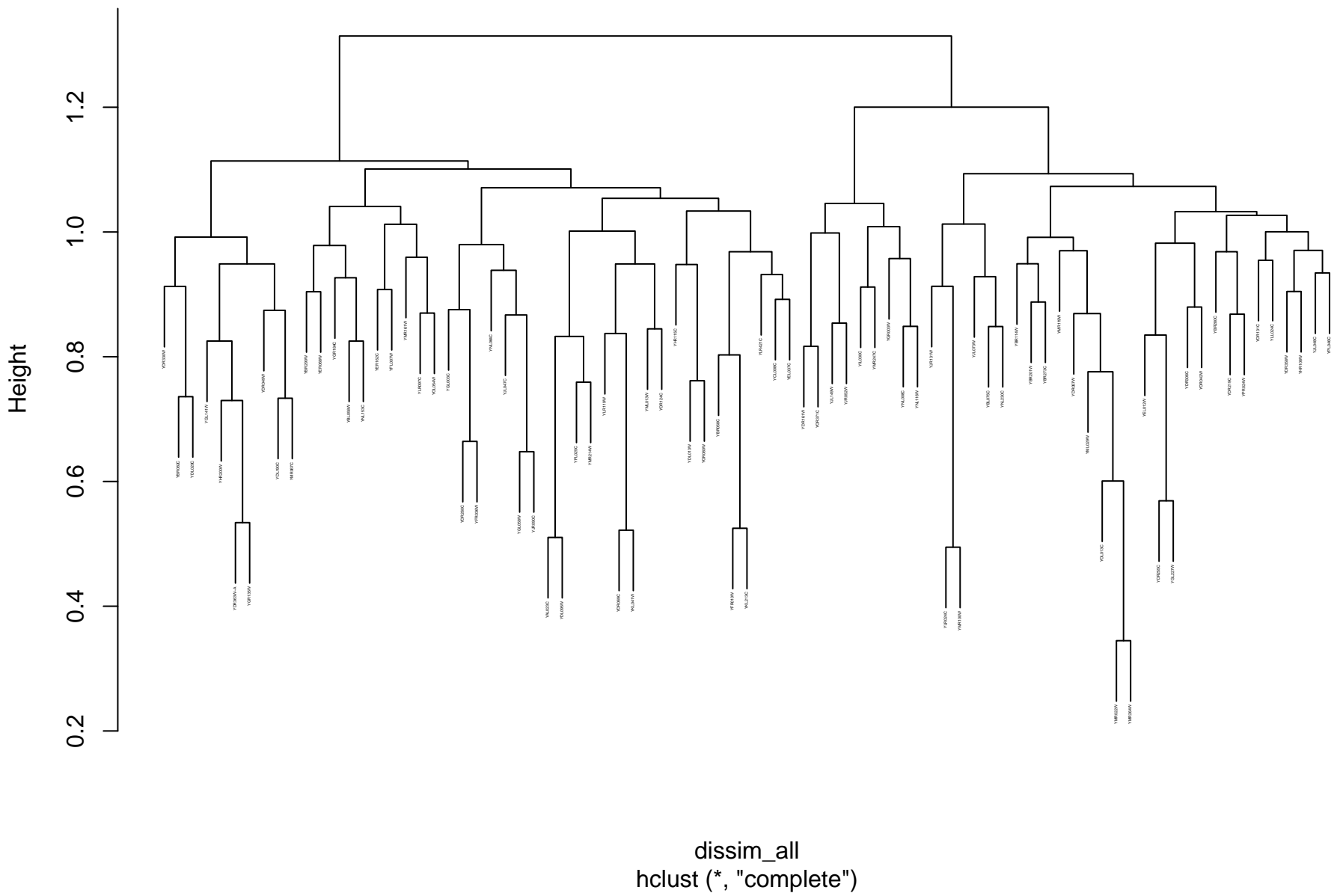
nuclear transport_GO_pearson_complete



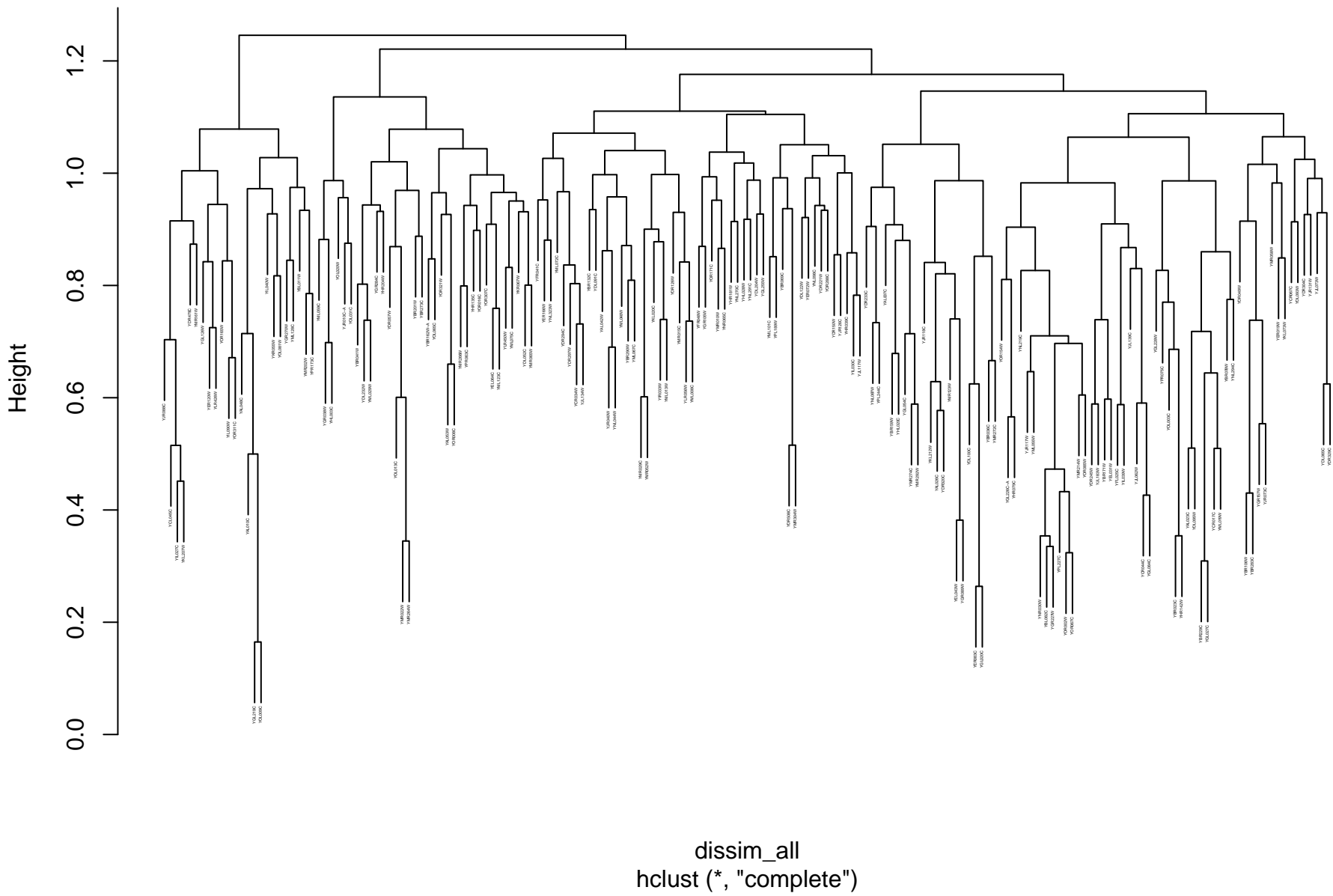
protein modification by small protein conjugation or removal_GO_pearson_complete



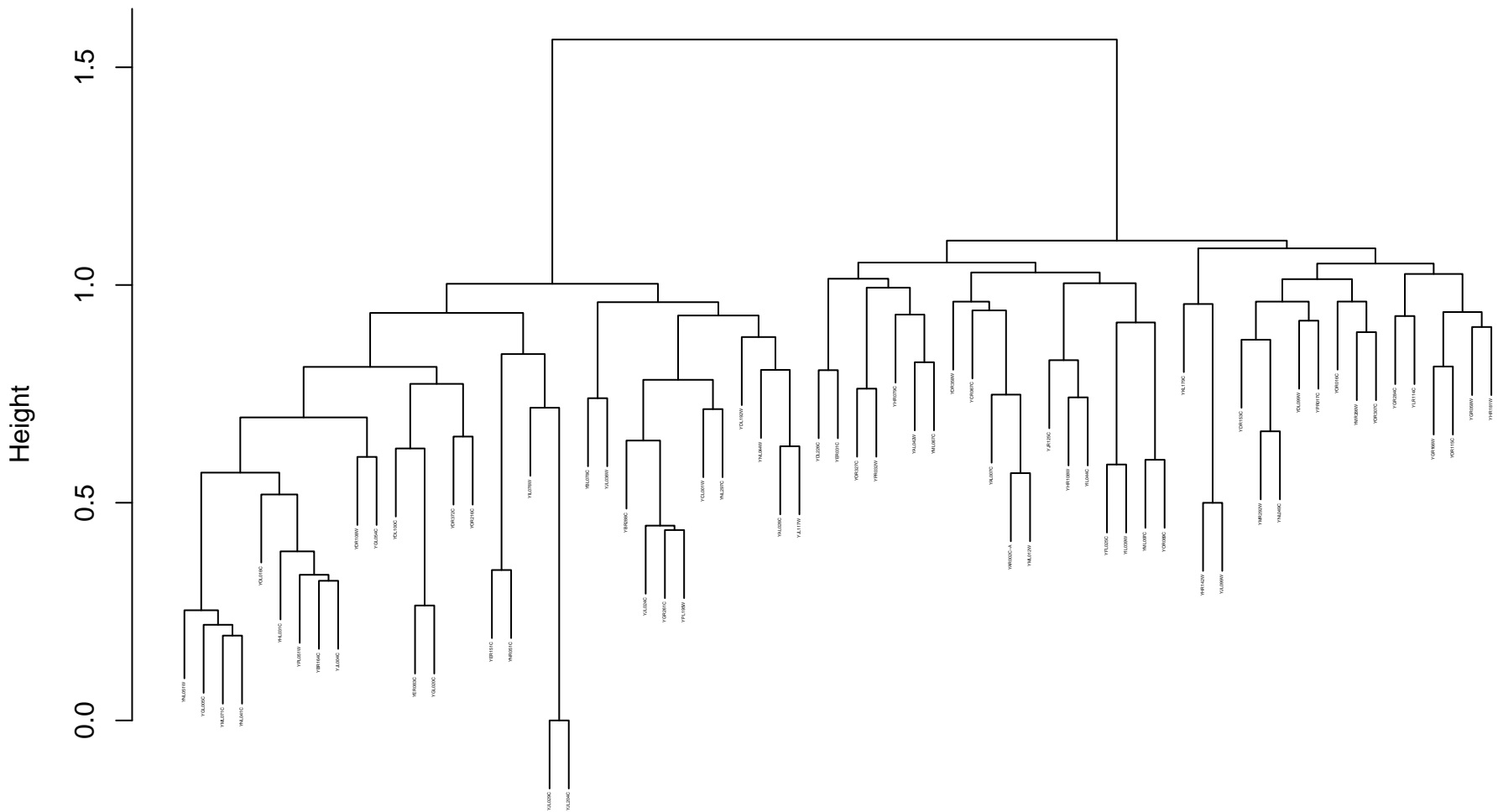
proteolysis involved in cellular protein catabolic process_GO_pearson_complete



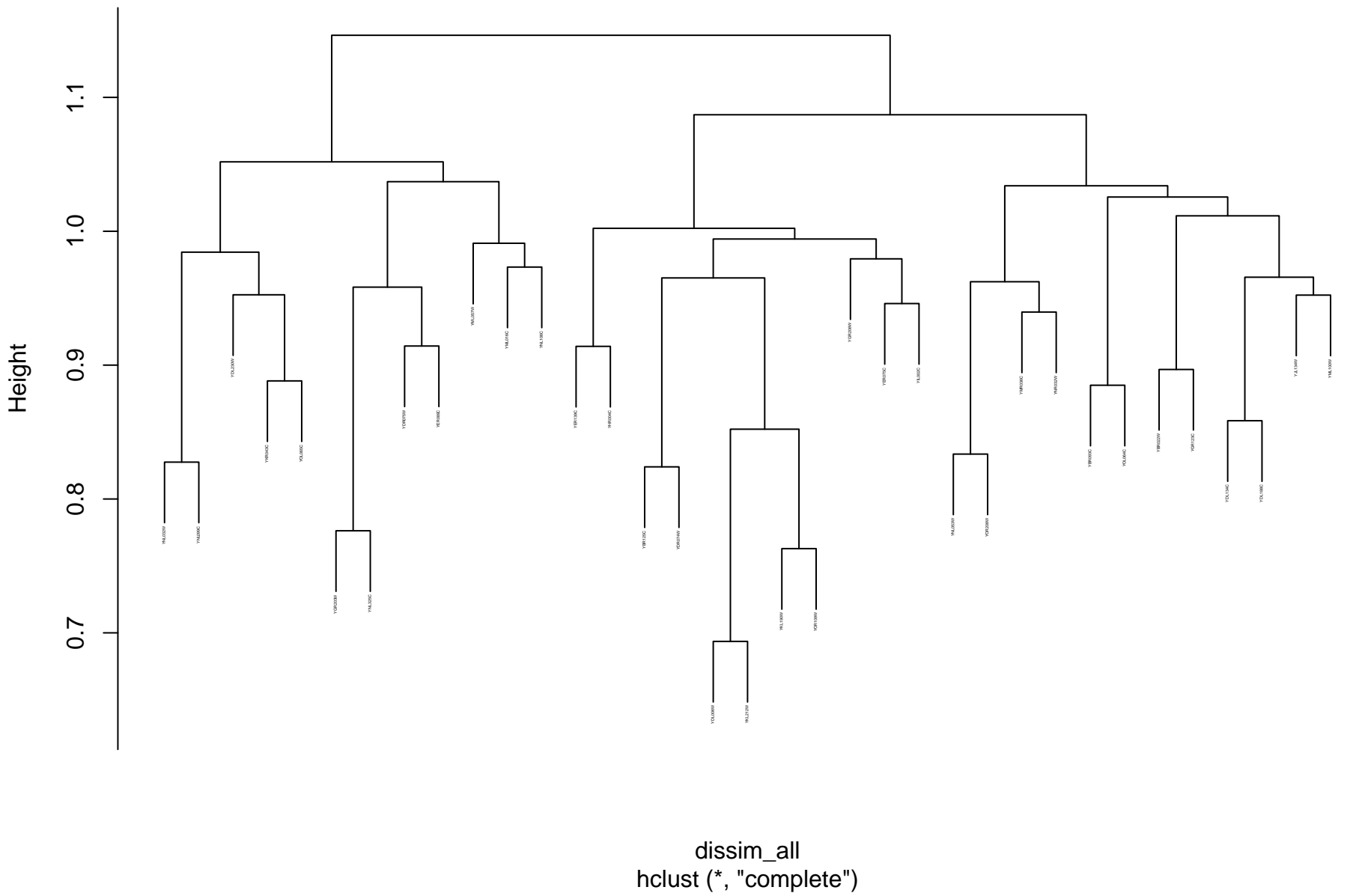
endoplasmic reticulum_GO_pearson_complete



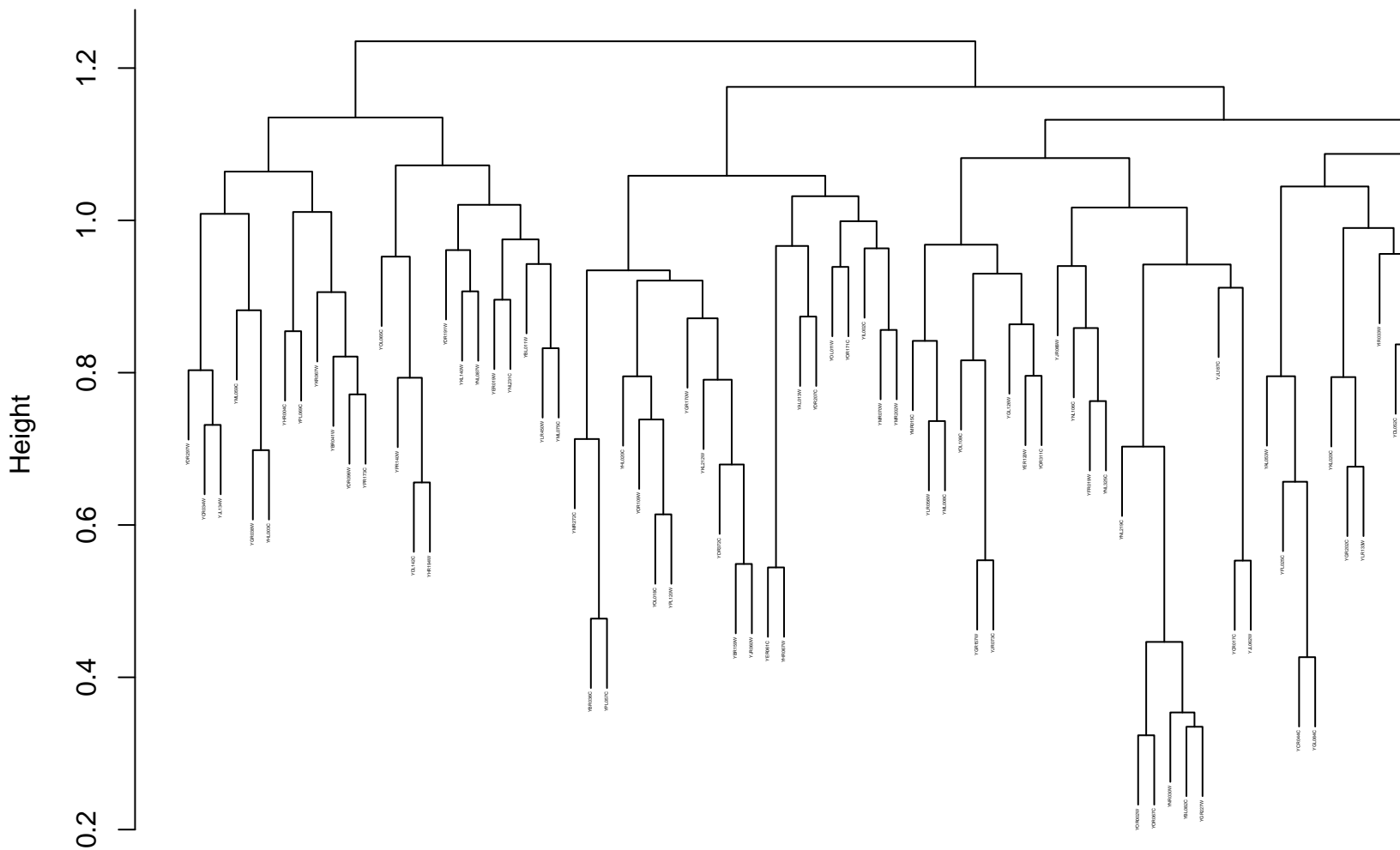
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dissim_all
hclust (*, "complete")
```



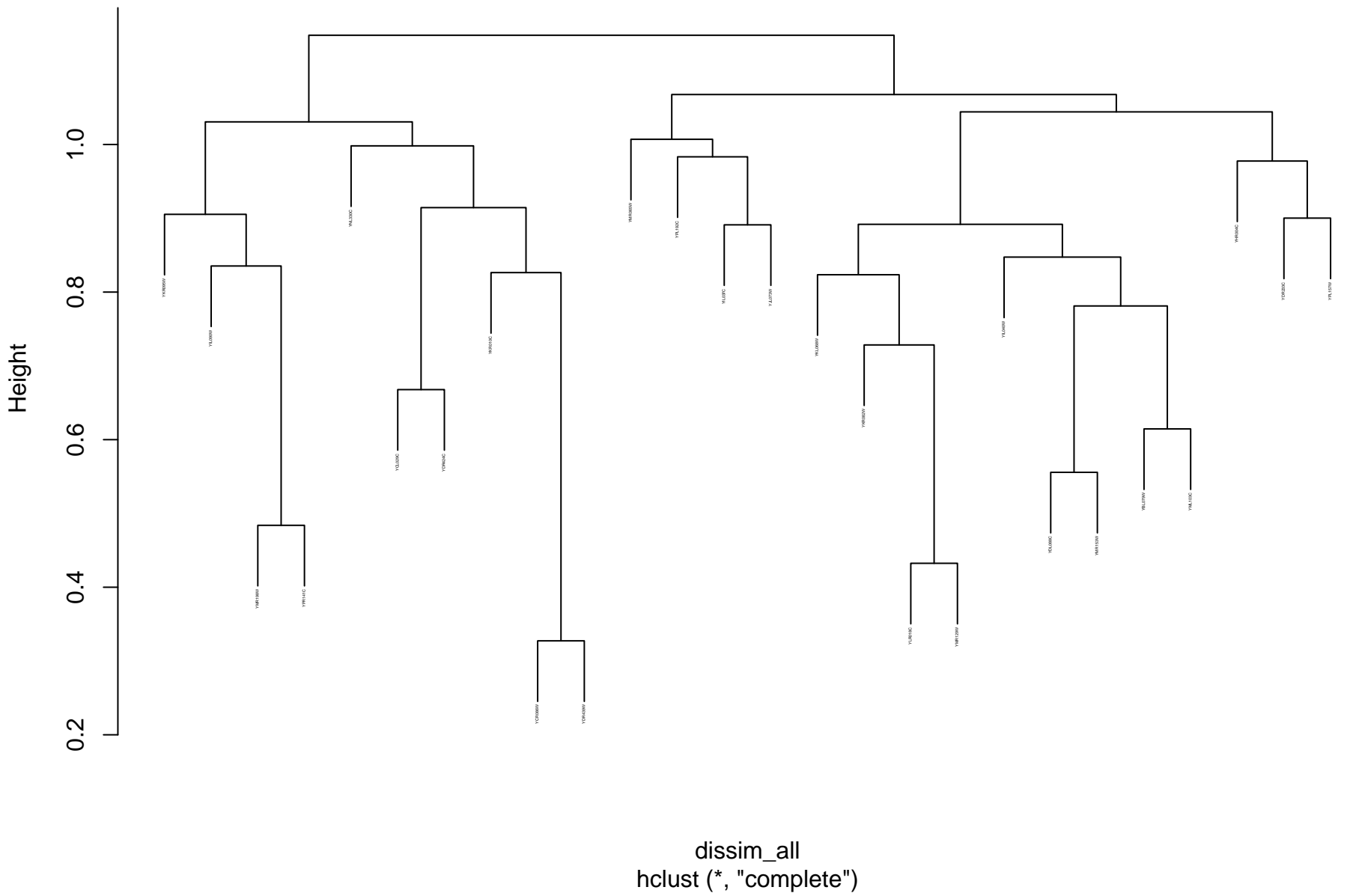
phosphatase activity_GO_pearson_complete



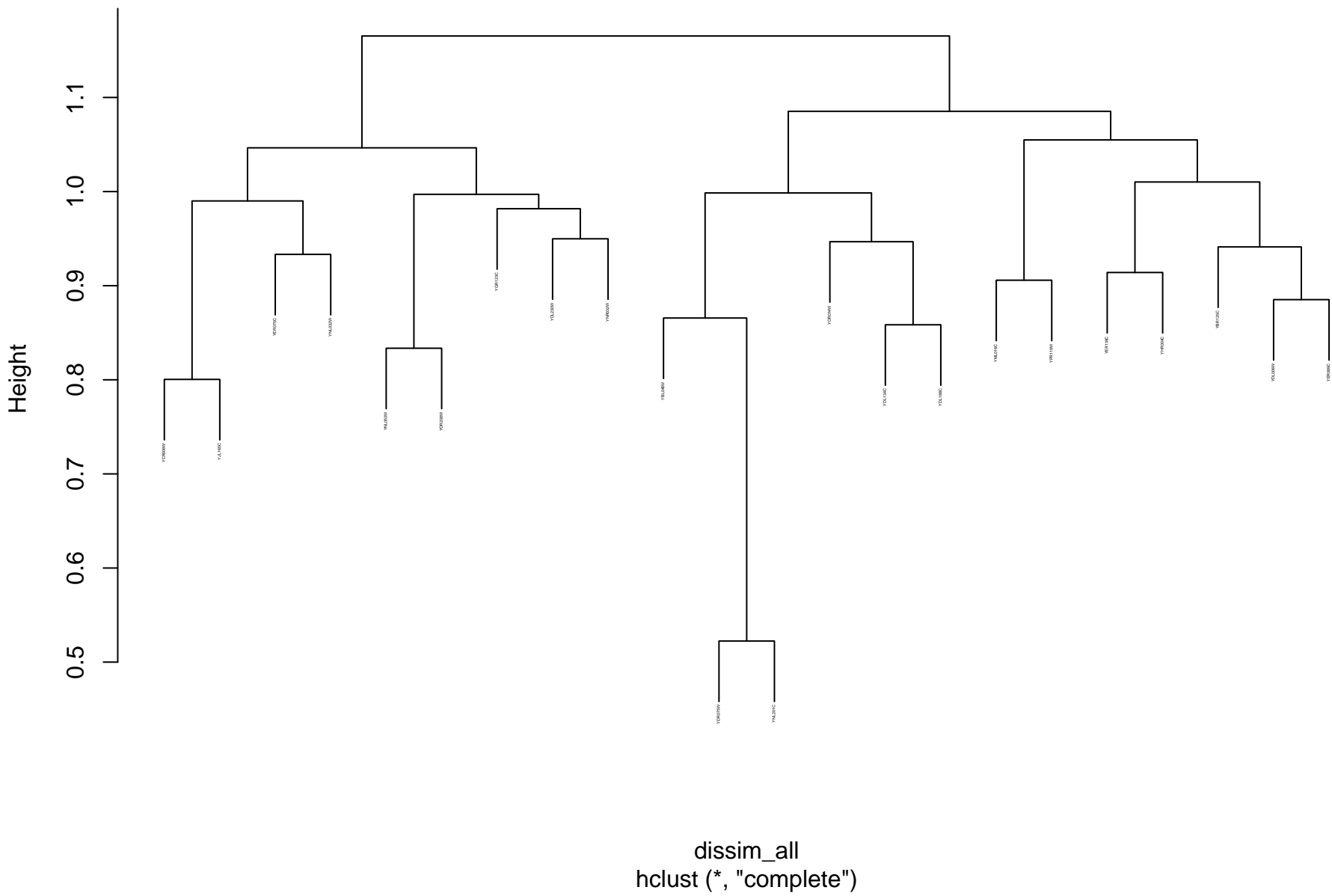
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dissim_all
hclust (*, "complete")
```



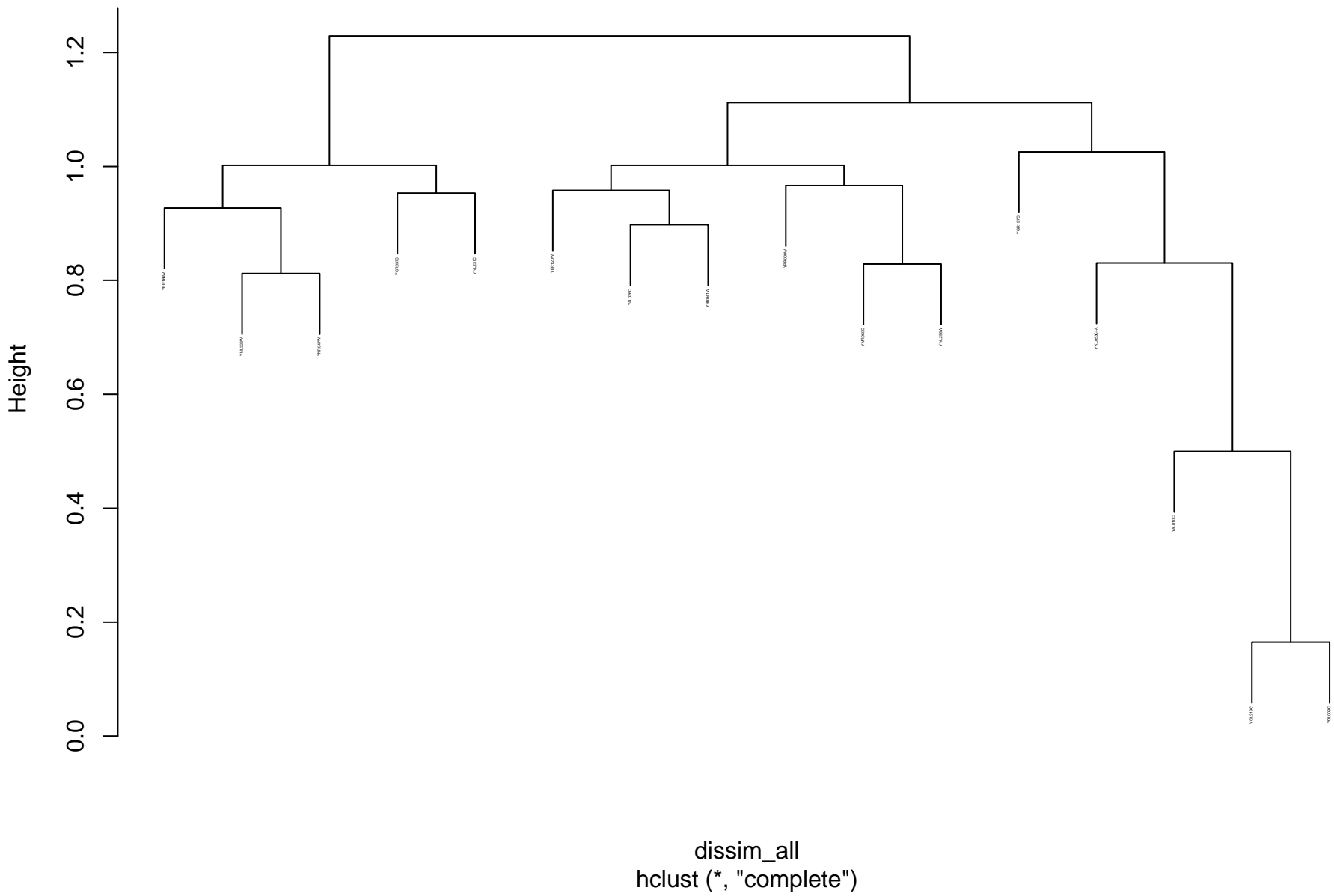
nucleus organization_GO_pearson_complete



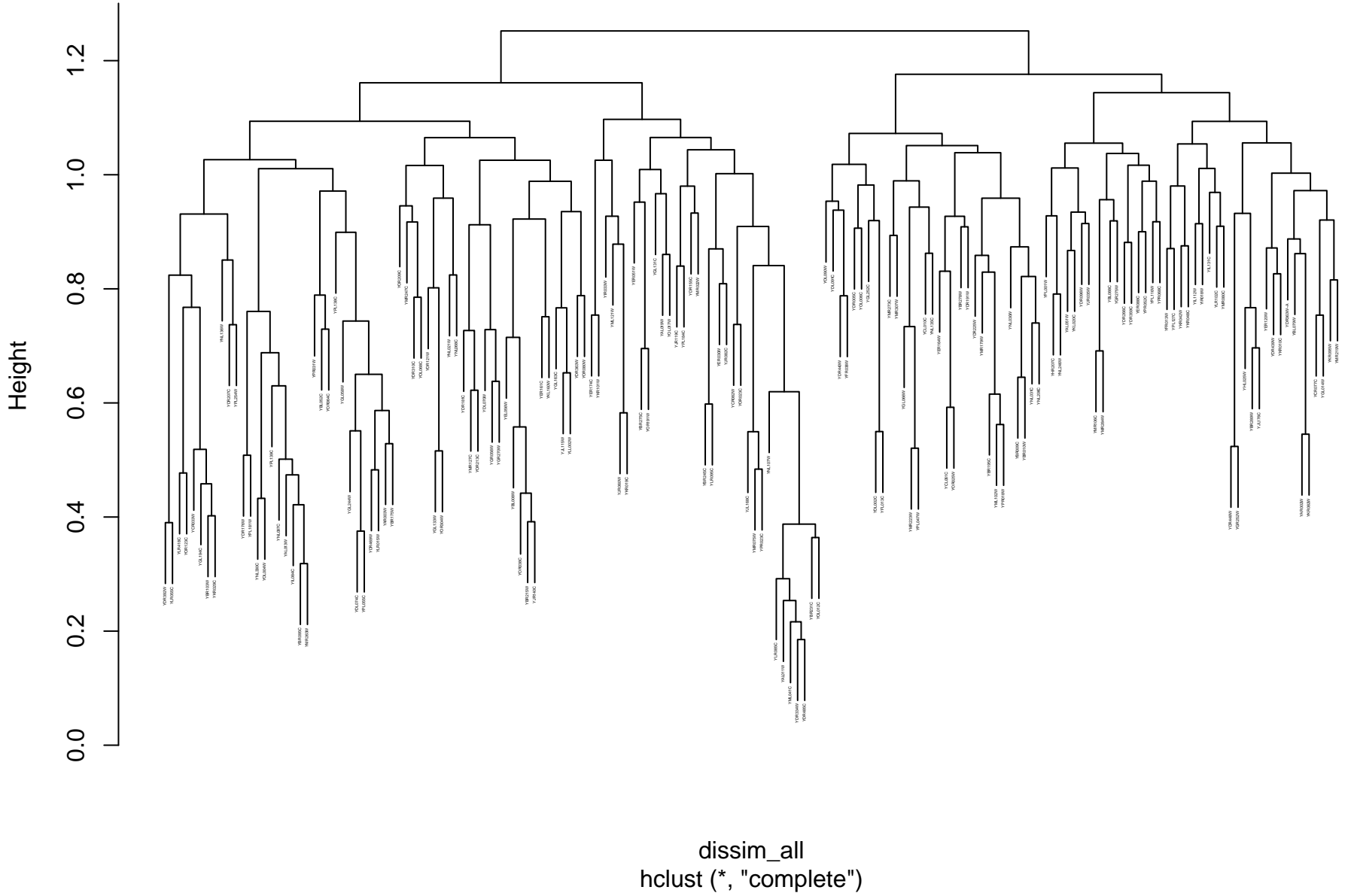
protein dephosphorylation_GO_pearson_complete



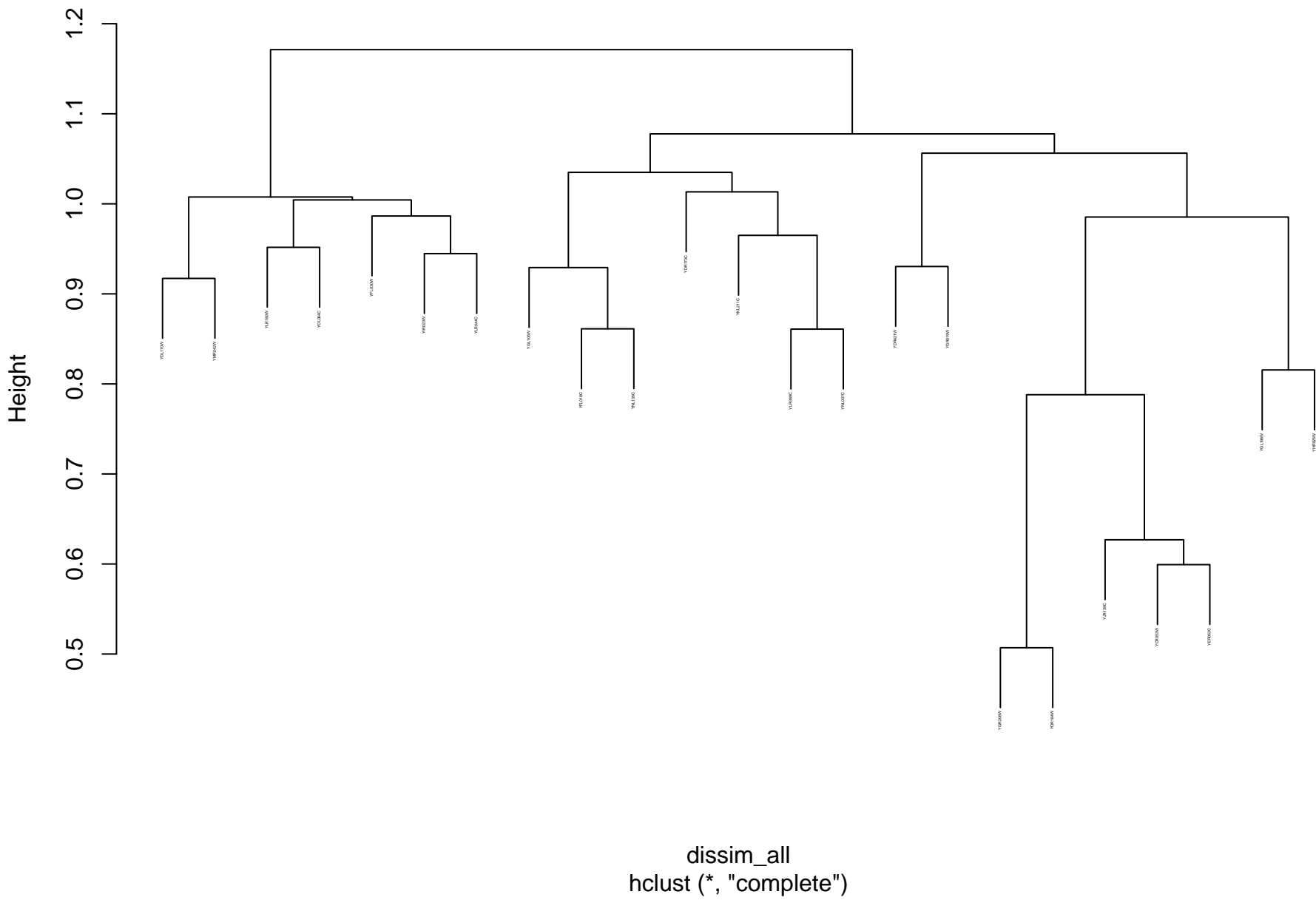
lipid transport_GO_pearson_complete



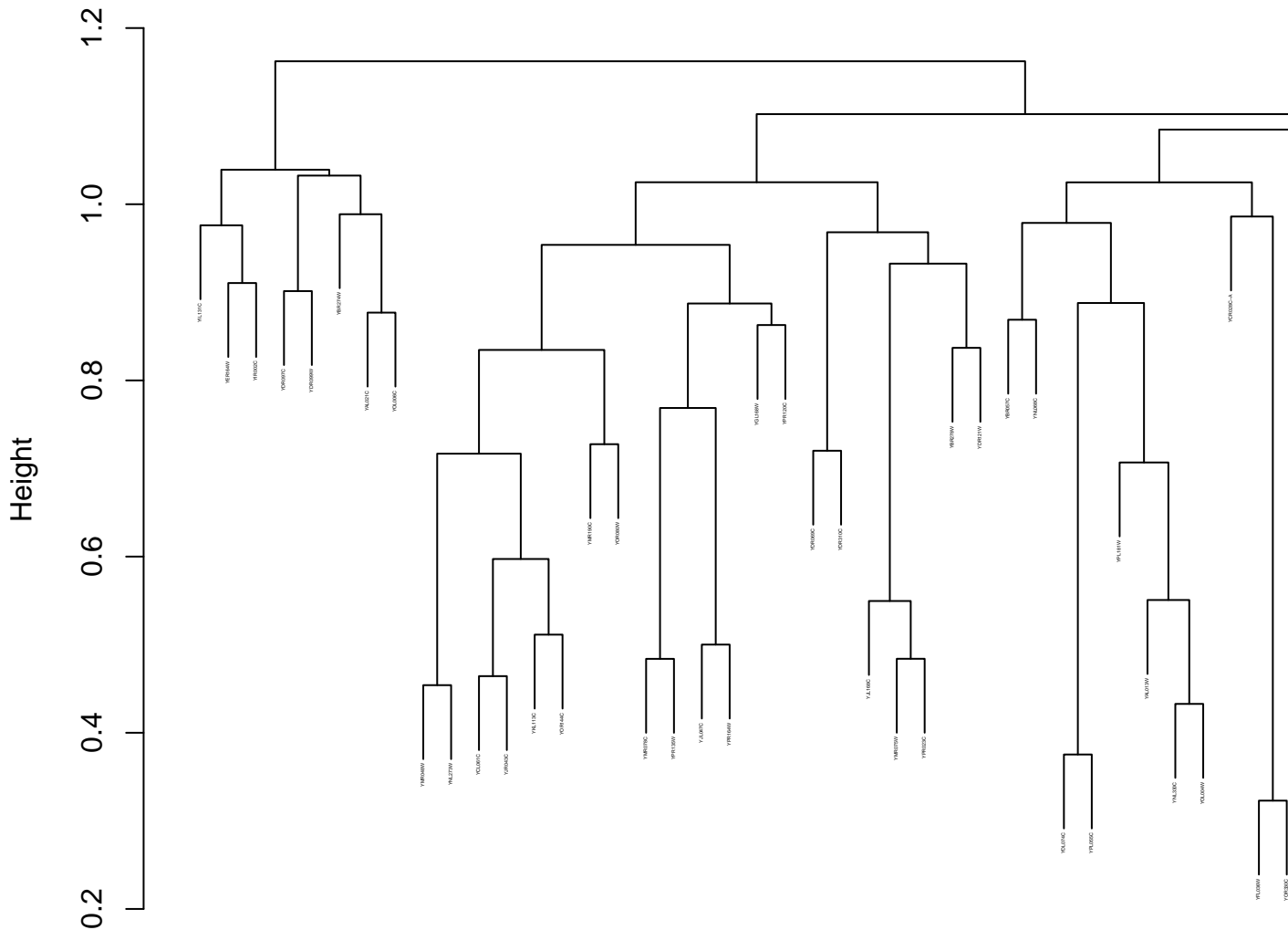
chromatin organization_GO_pearson_complete



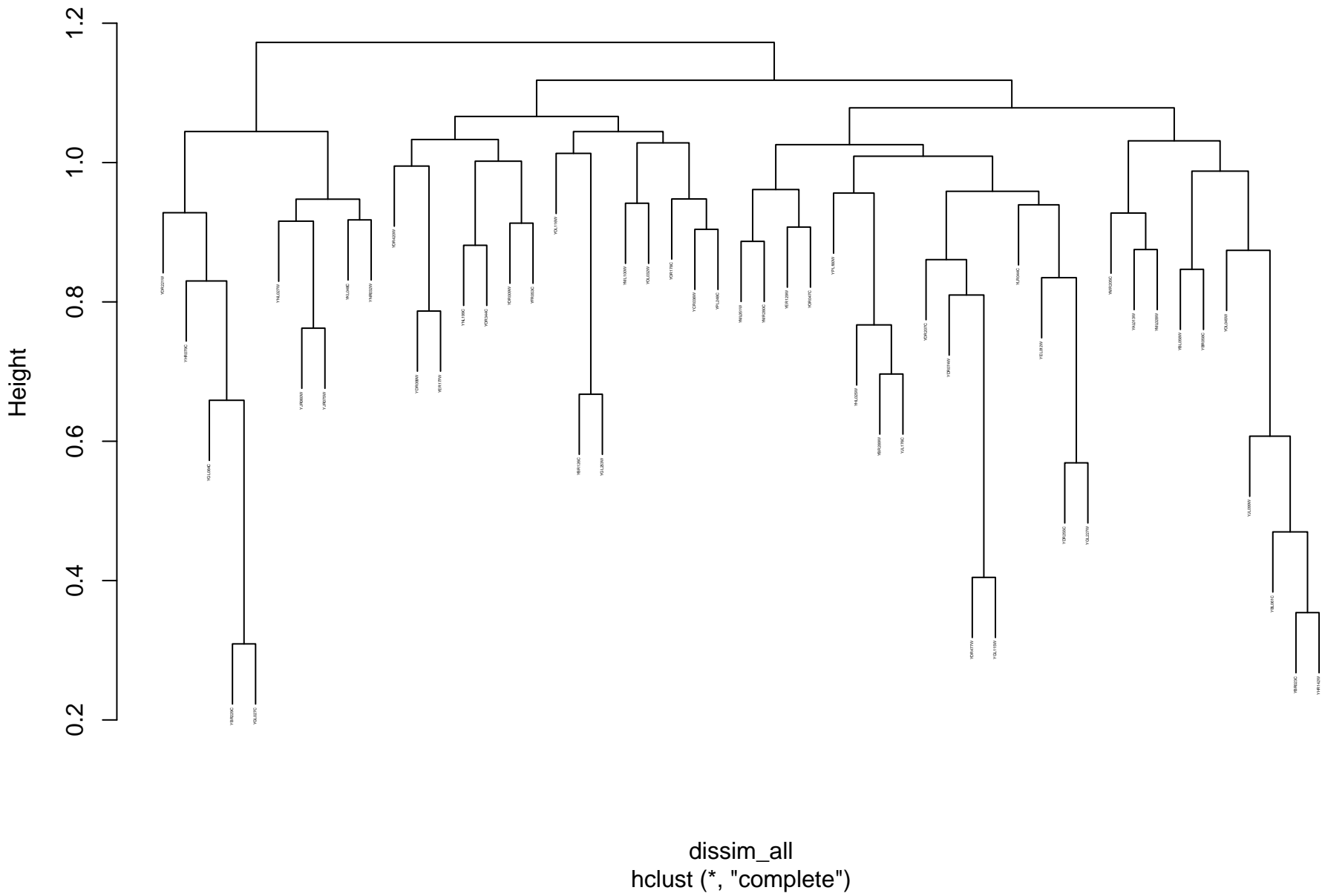
cellular amino acid metabolic process_GO_pearson_complete



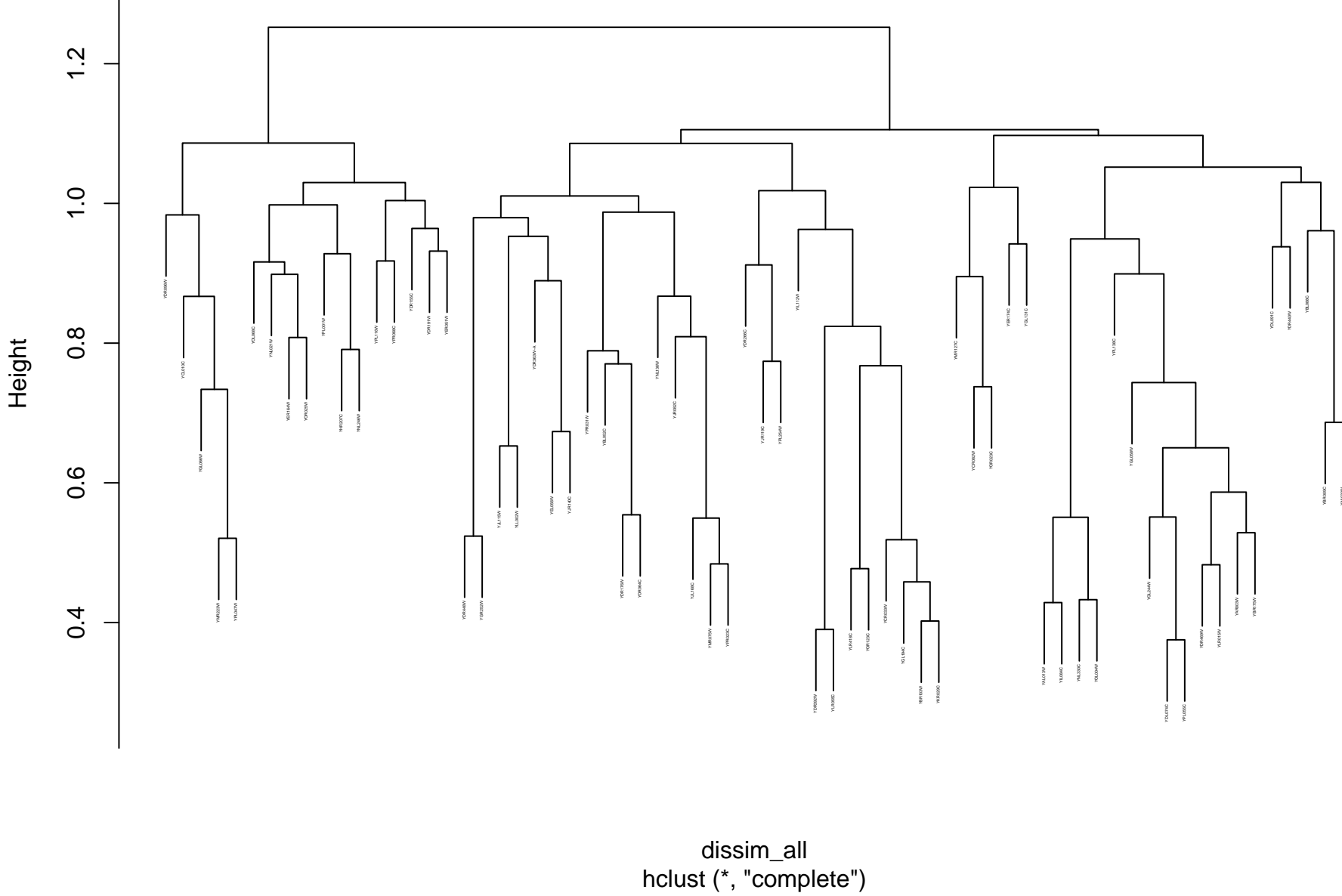
```
dissim_all
hclust (*, "complete")
```



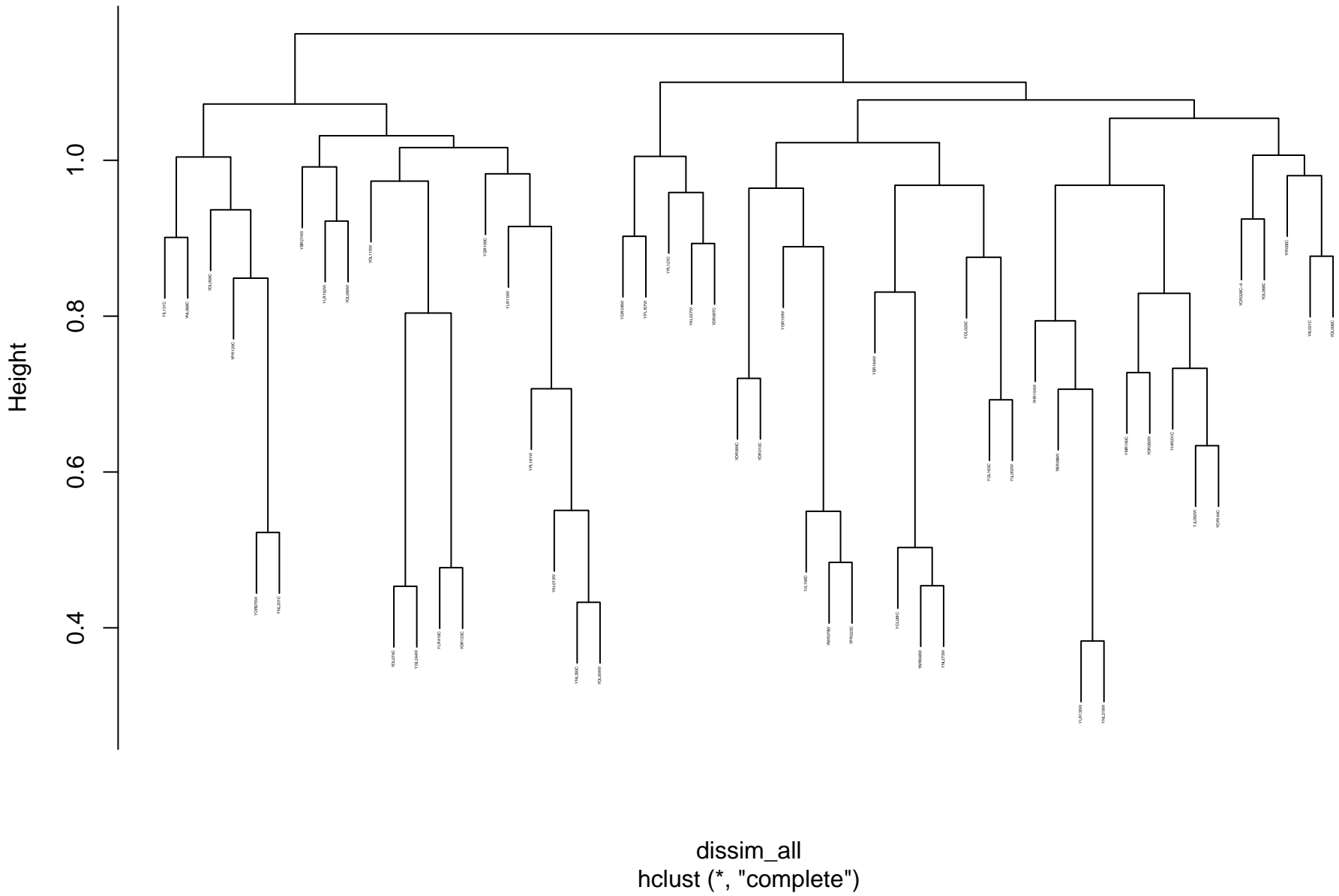
carbohydrate metabolic process_GO_pearson_complete



histone modification_GO_pearson_complete

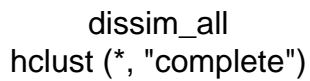


regulation of DNA metabolic process_GO_pearson_complete

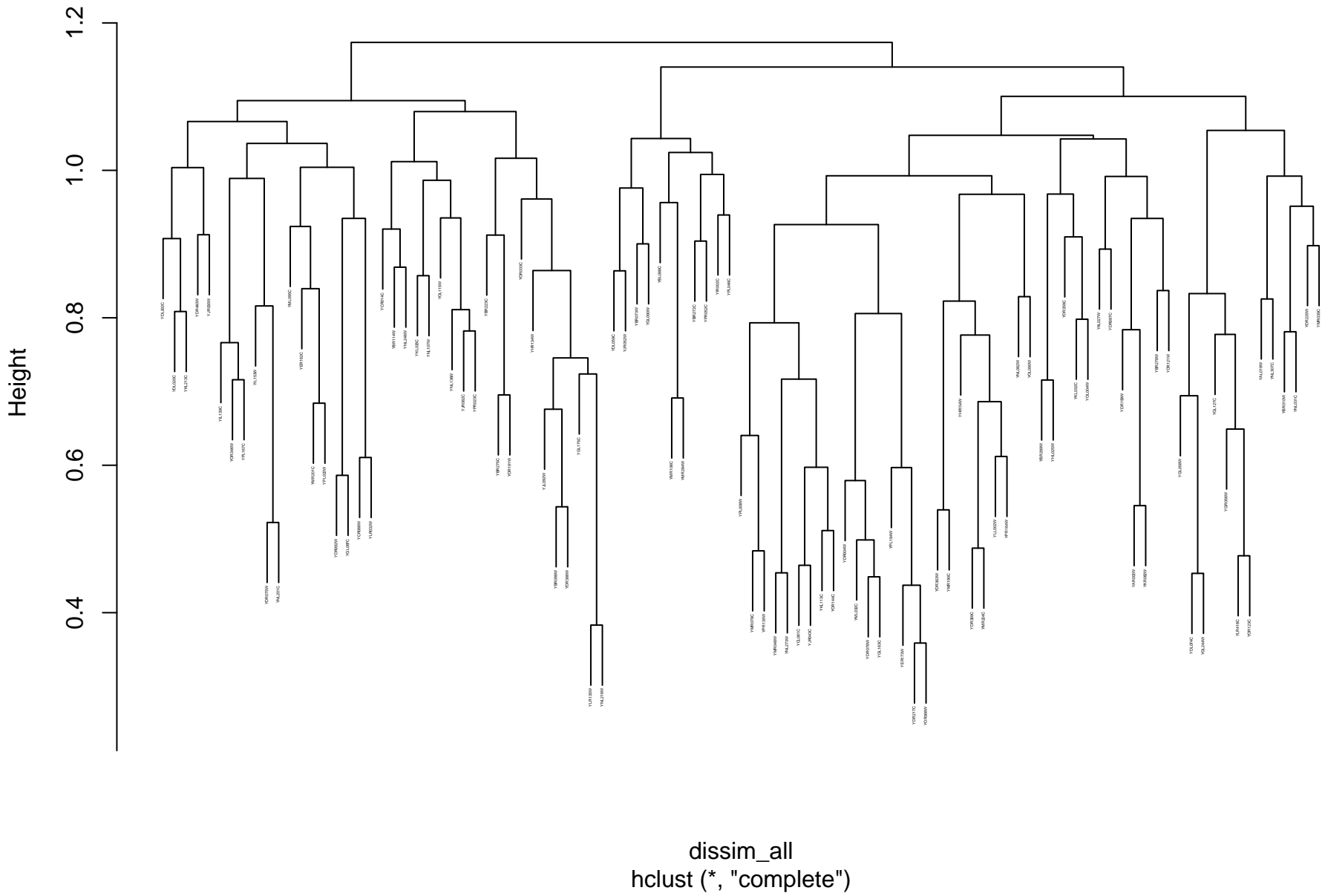


```
dissim_all
hclust (*, "complete")
```

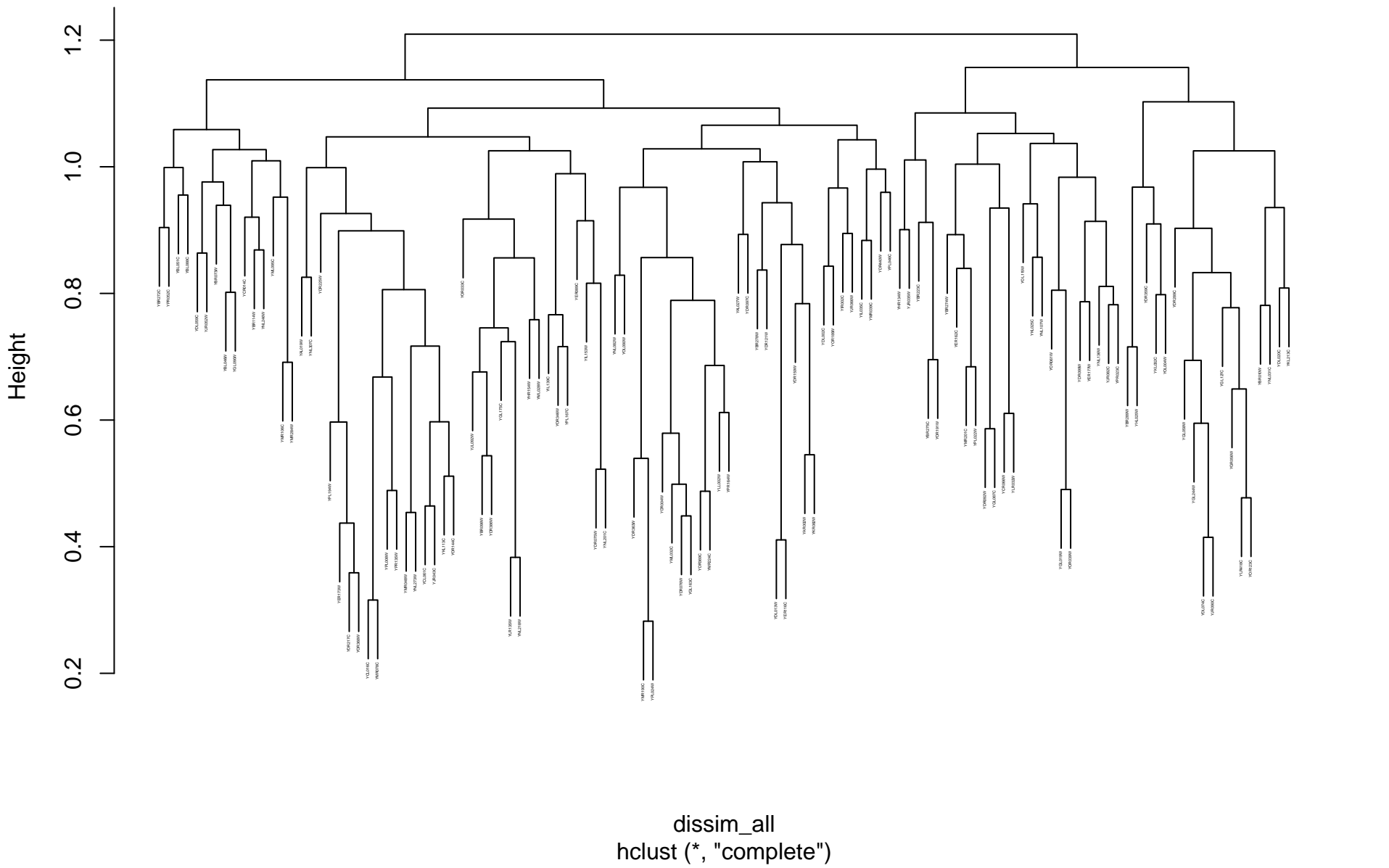
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dissim_all
hclust (*, "complete")
```



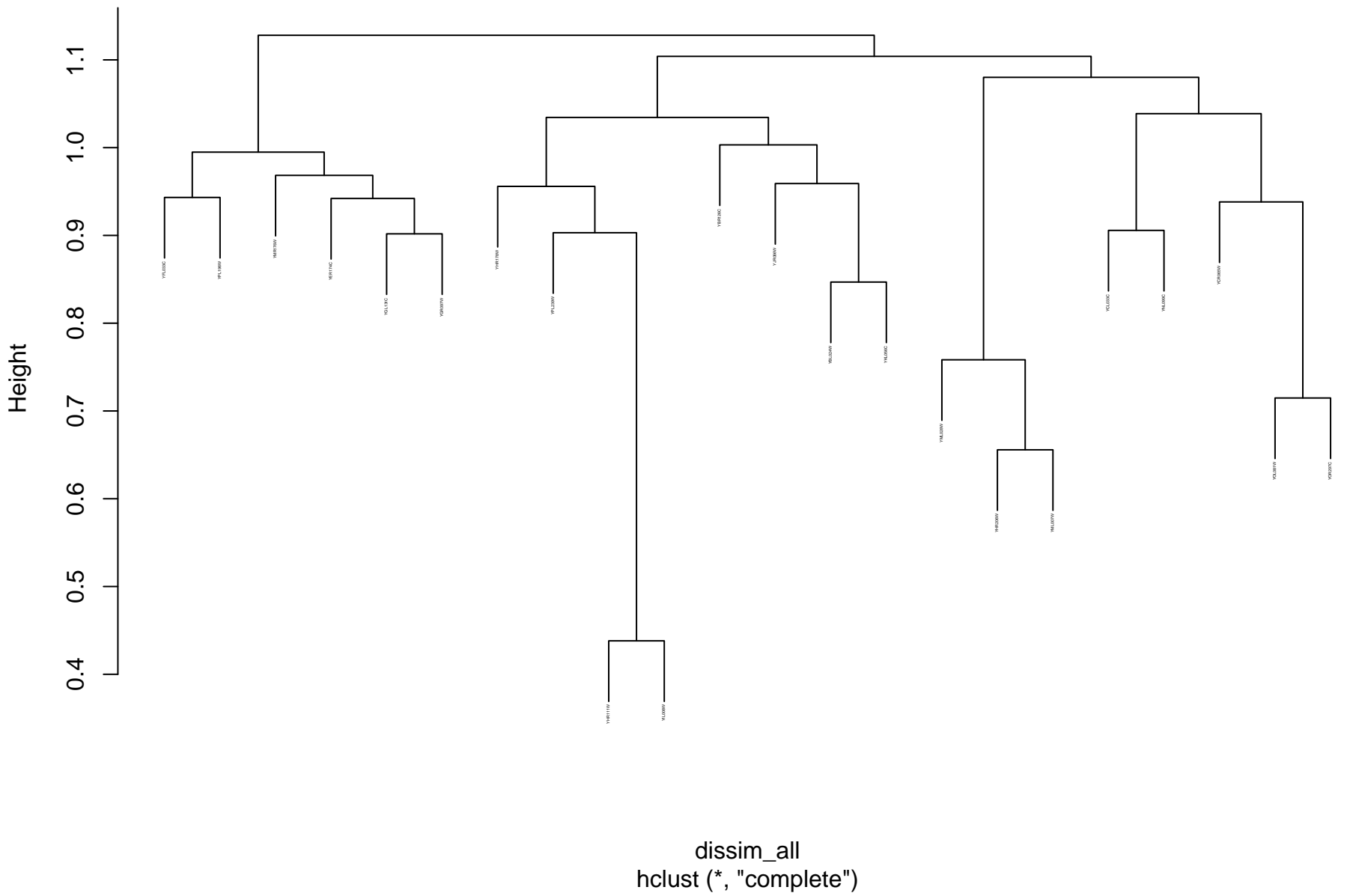
DNA repair_GO_pearson_complete



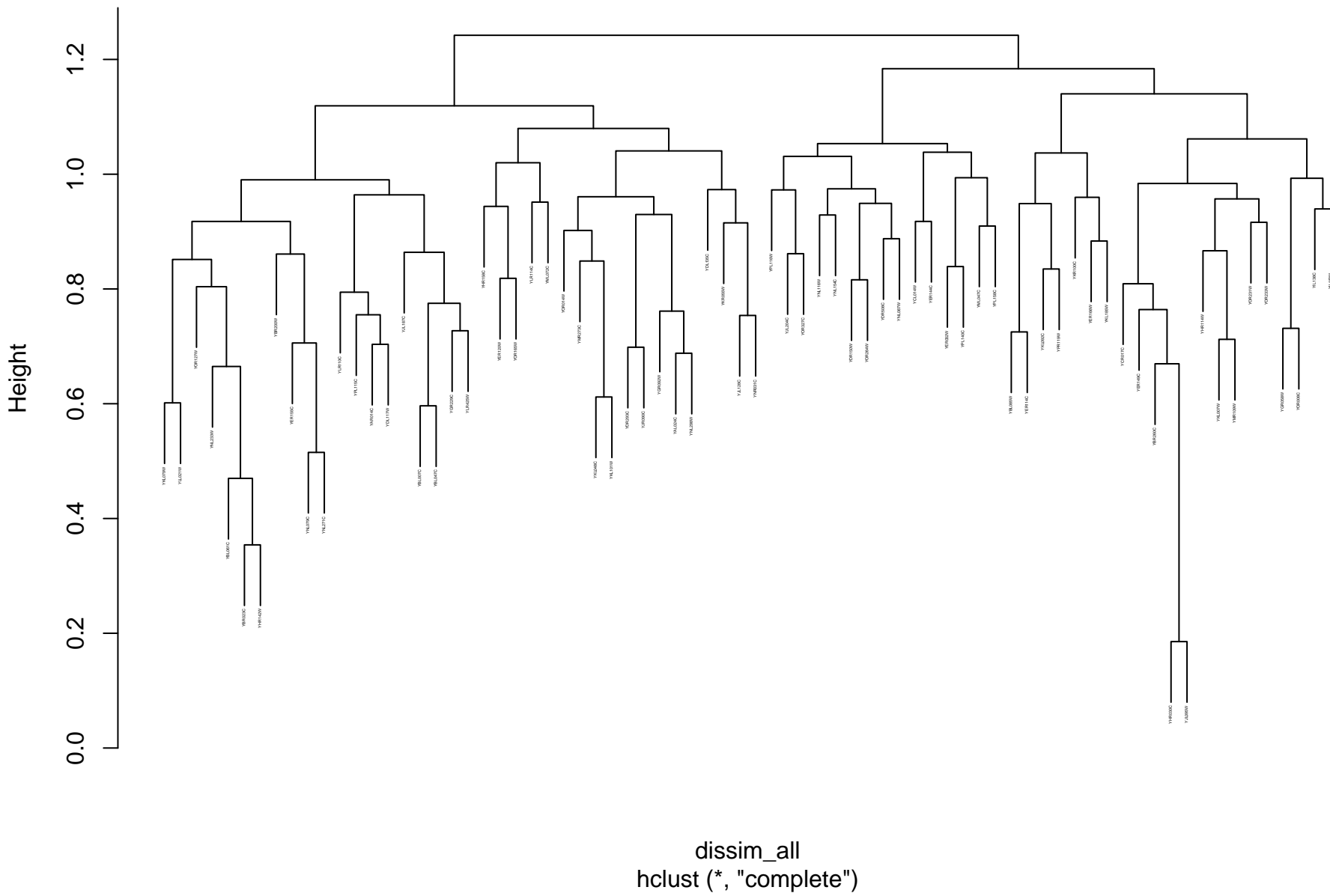
cellular response to DNA damage stimulus_GO_pearson_complete



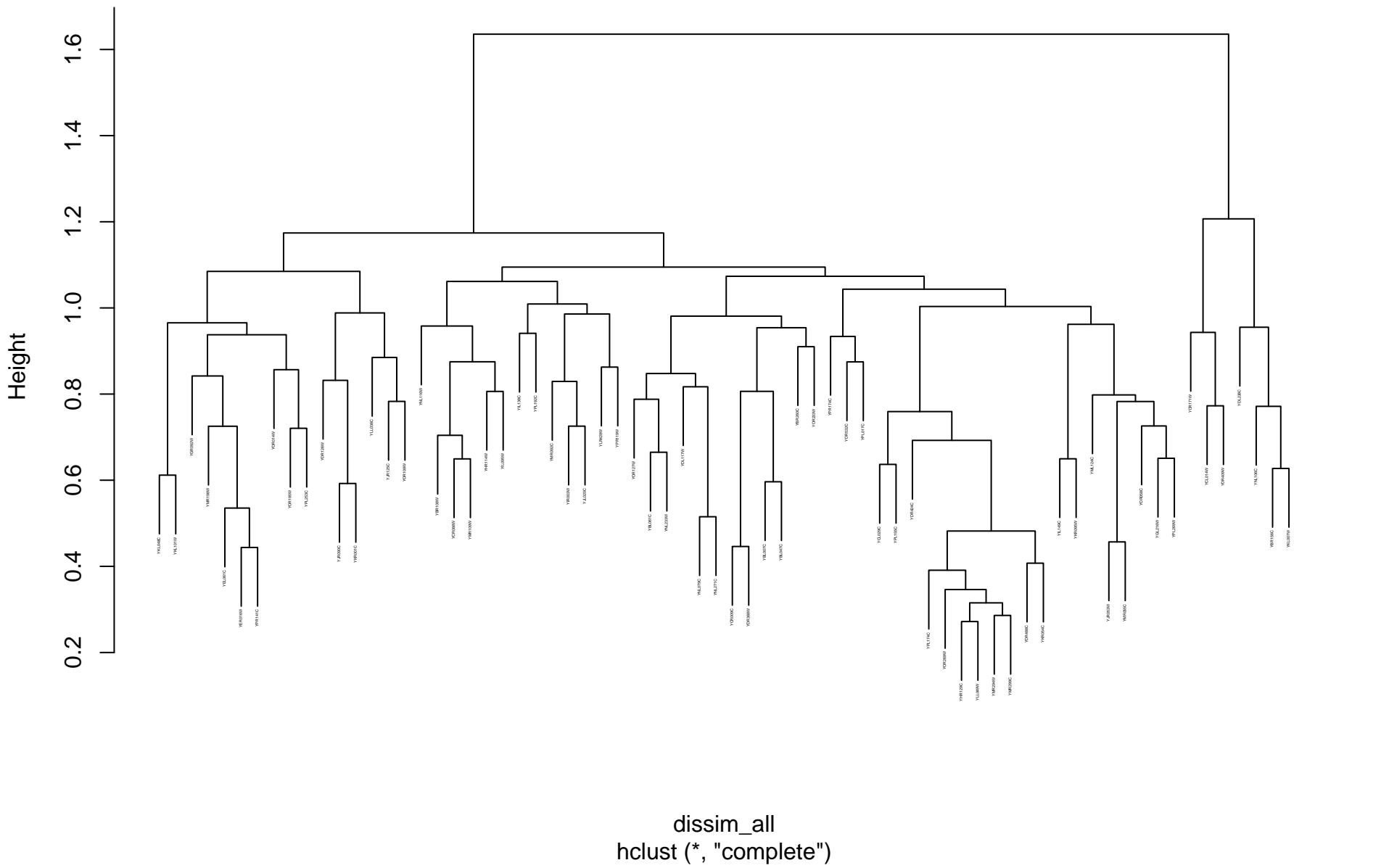
response to oxidative stress_GO_pearson_complete



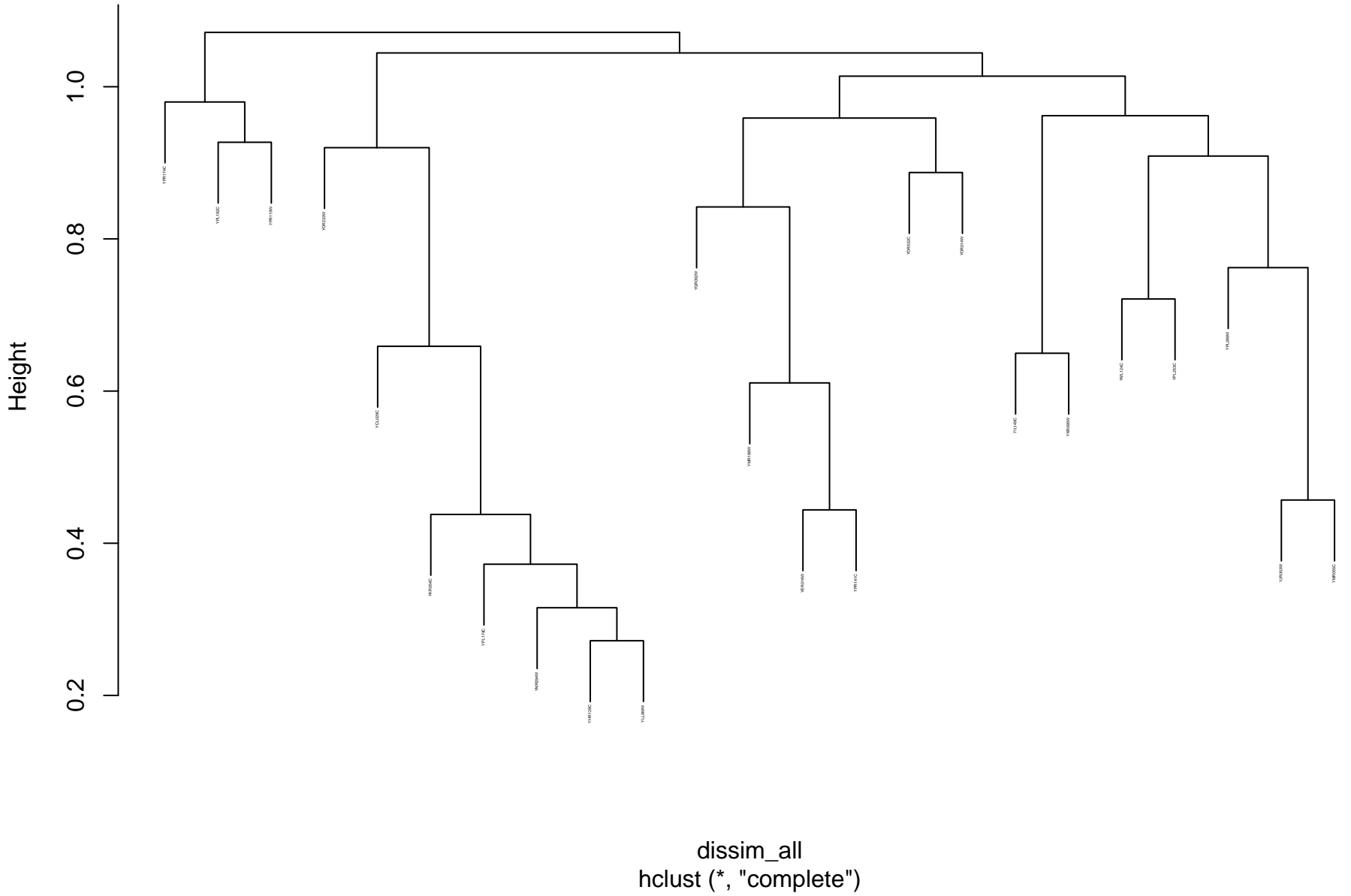
cellular bud_GO_pearson_complete



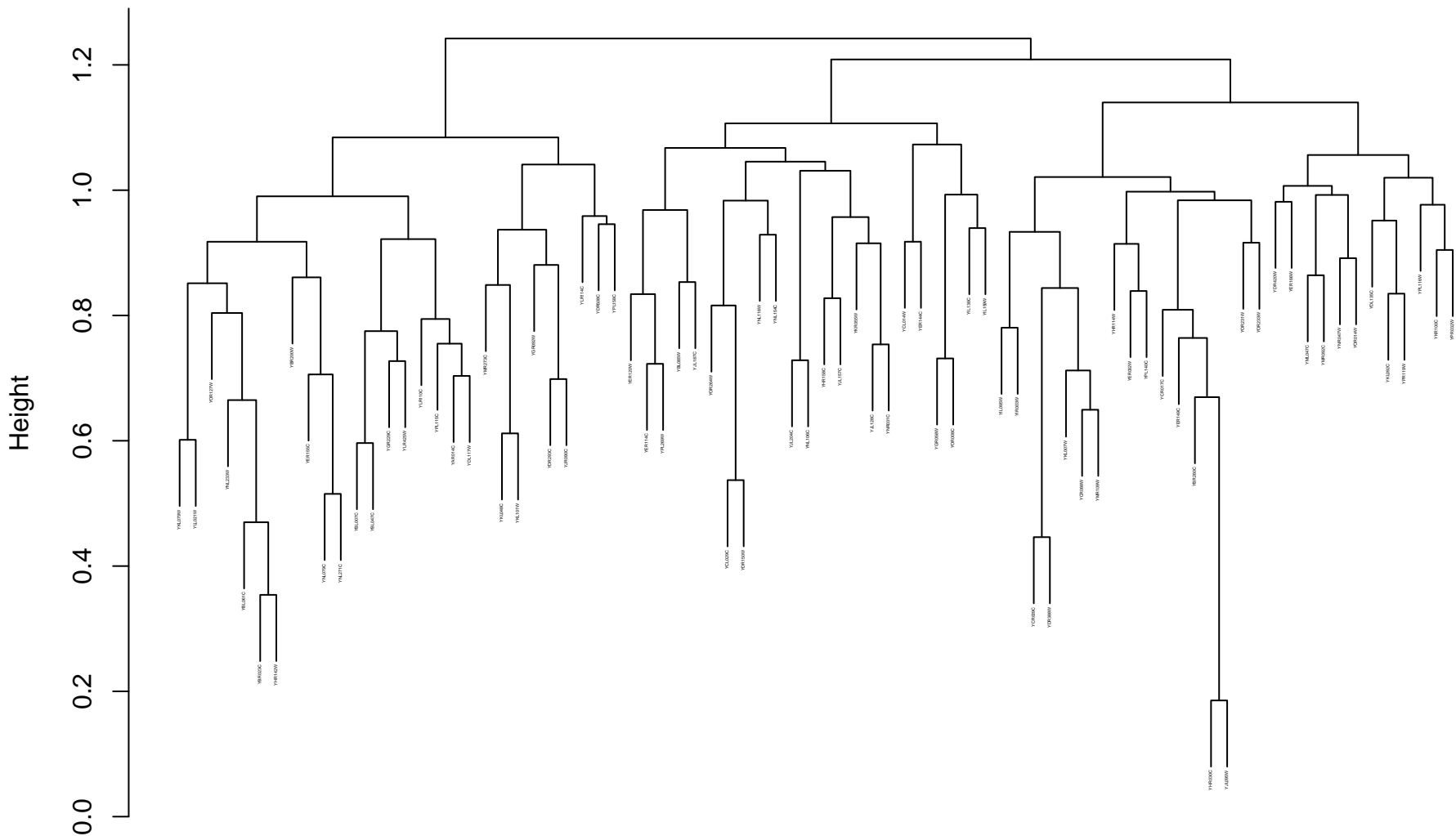
cytoskeleton_GO_pearson_complete



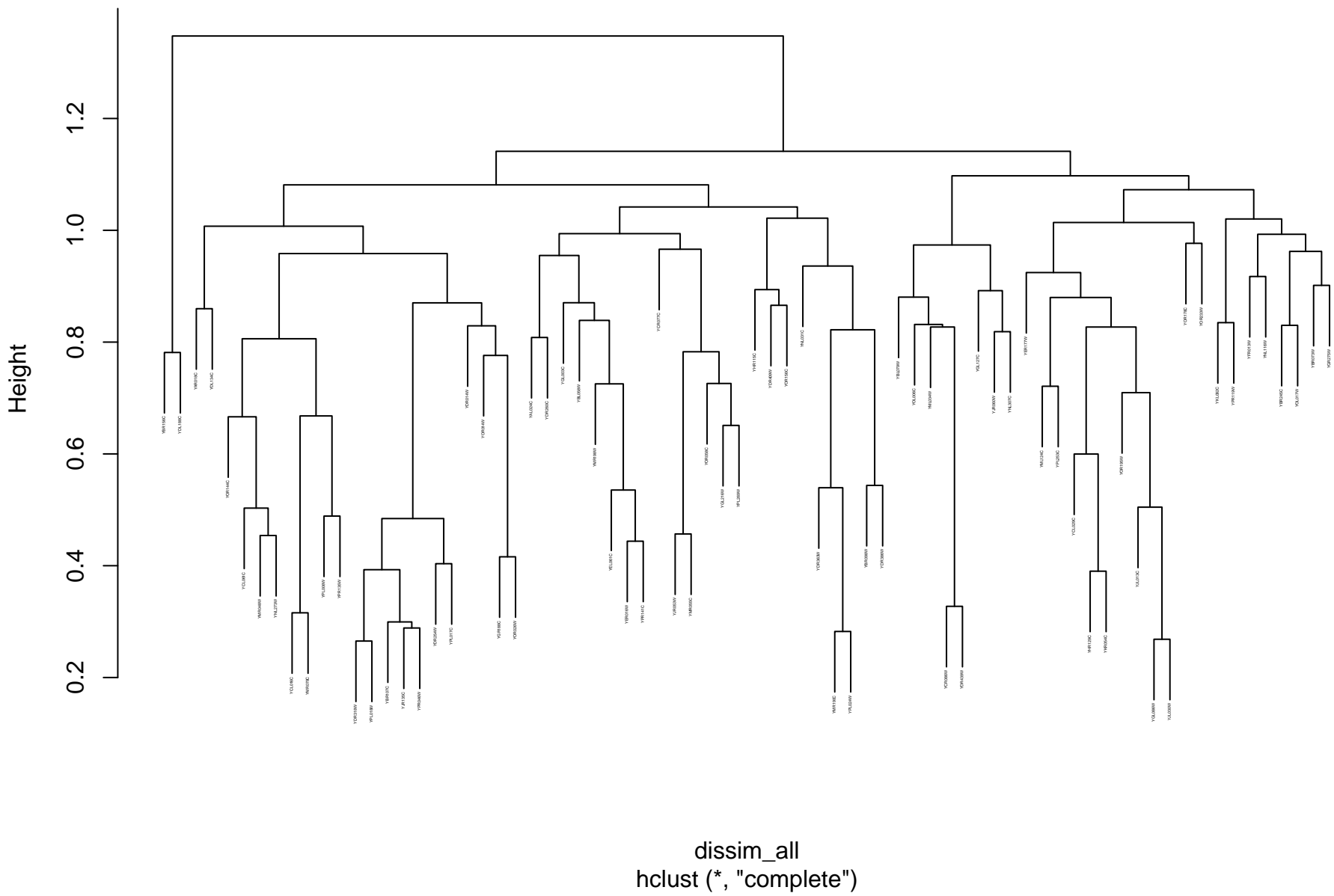
microtubule organizing center_GO_pearson_complete



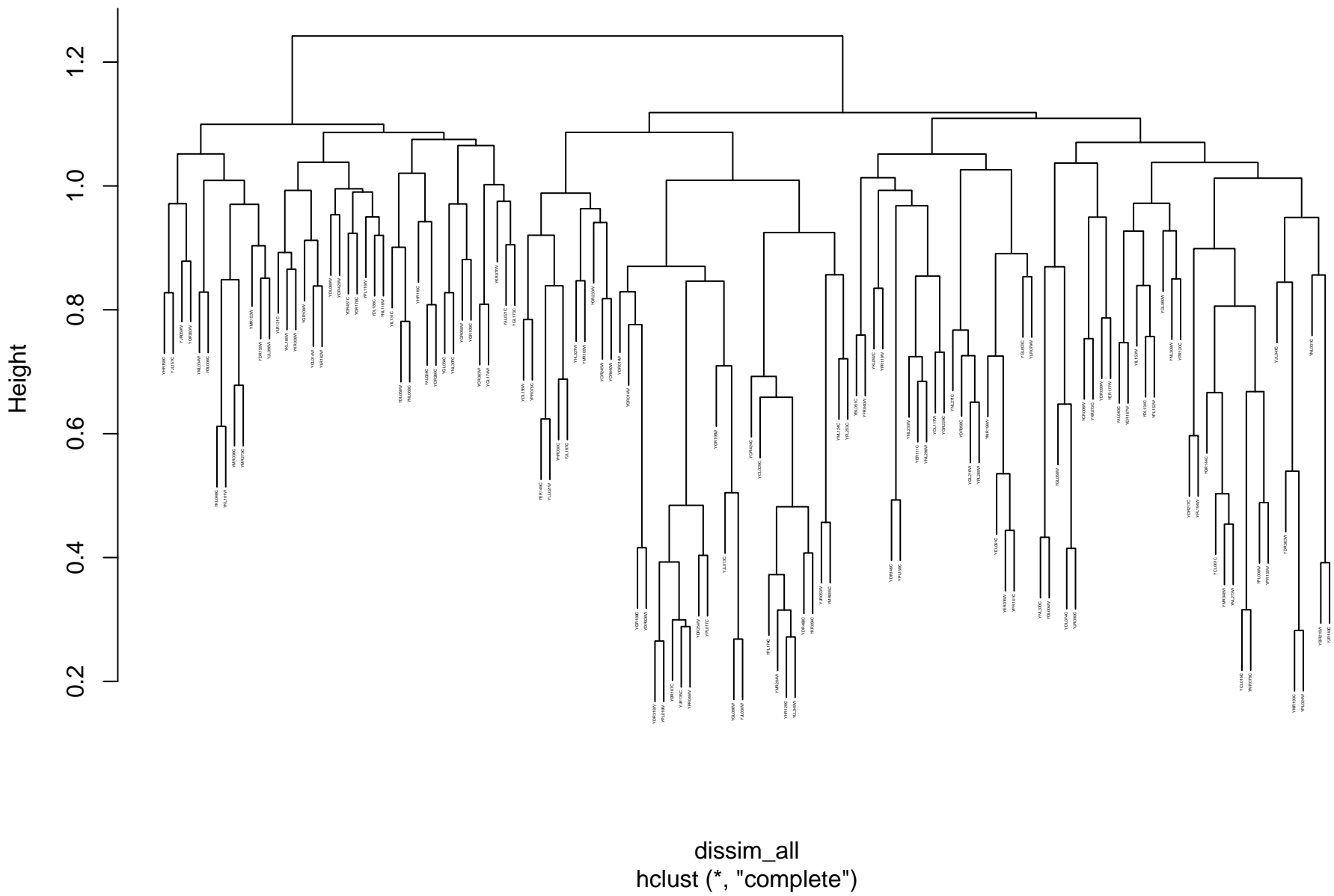
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dissim_all
hclust (*, "complete")
```



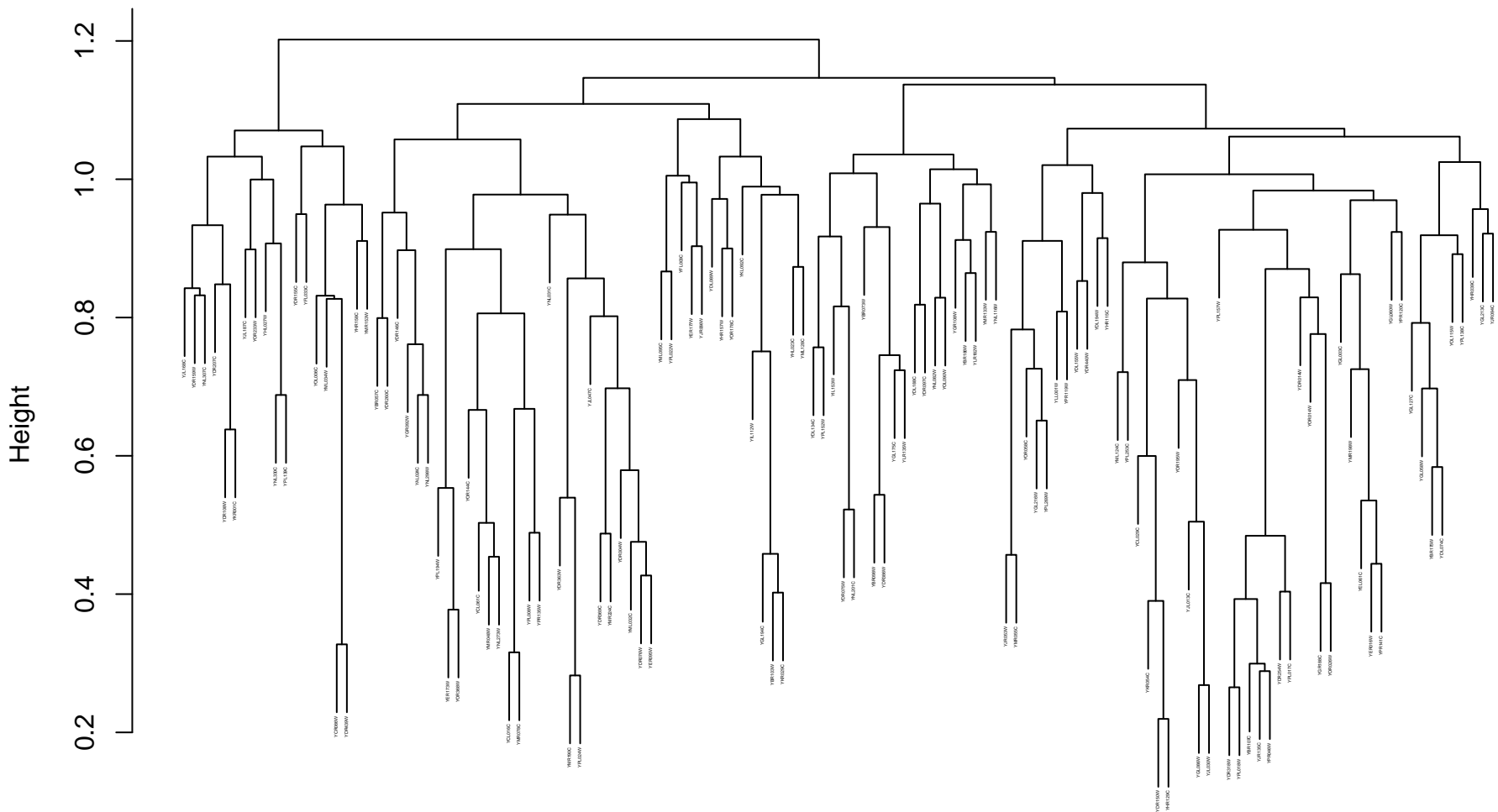
chromosome segregation_GO_pearson_complete



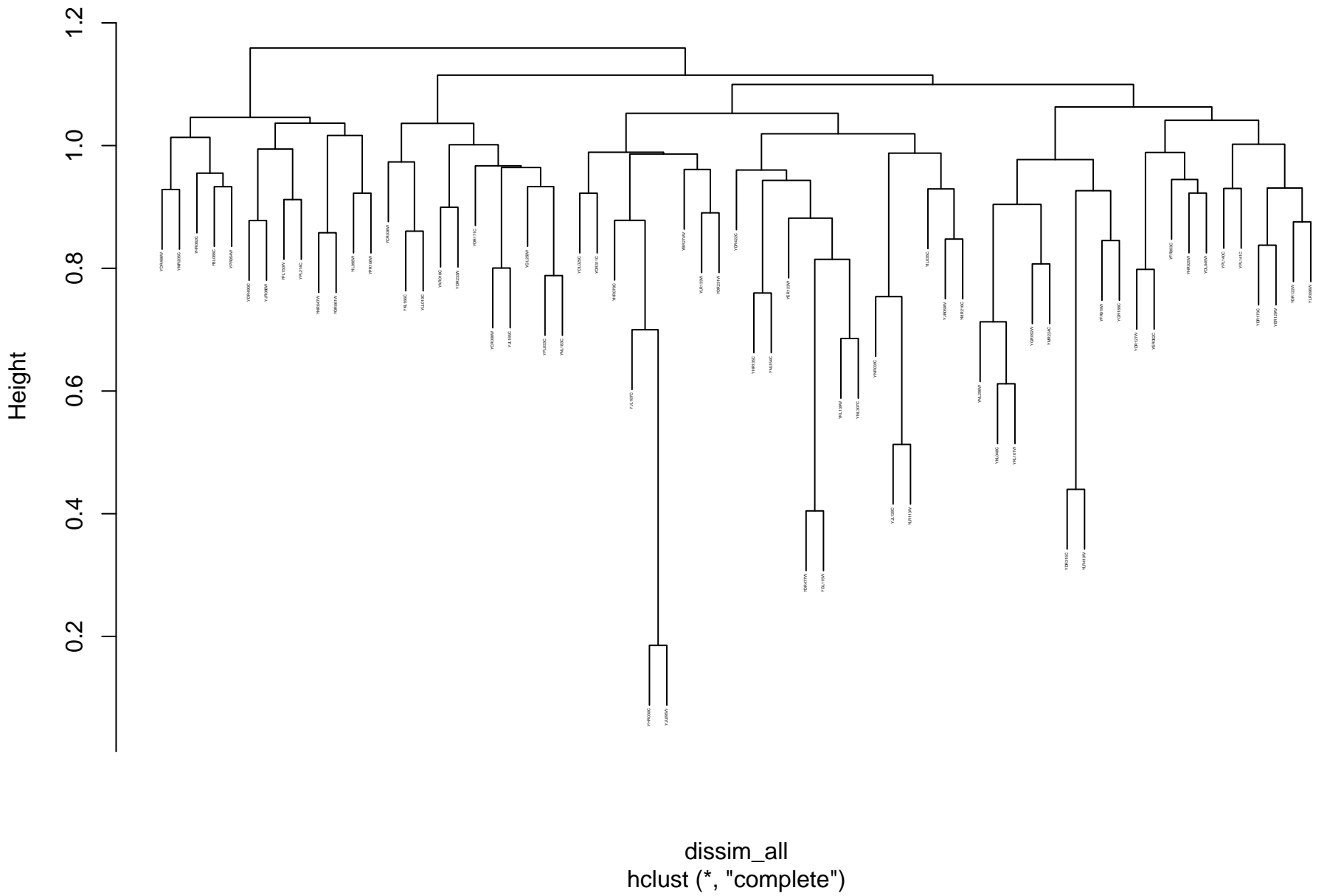
mitotic cell cycle_GO_pearson_complete



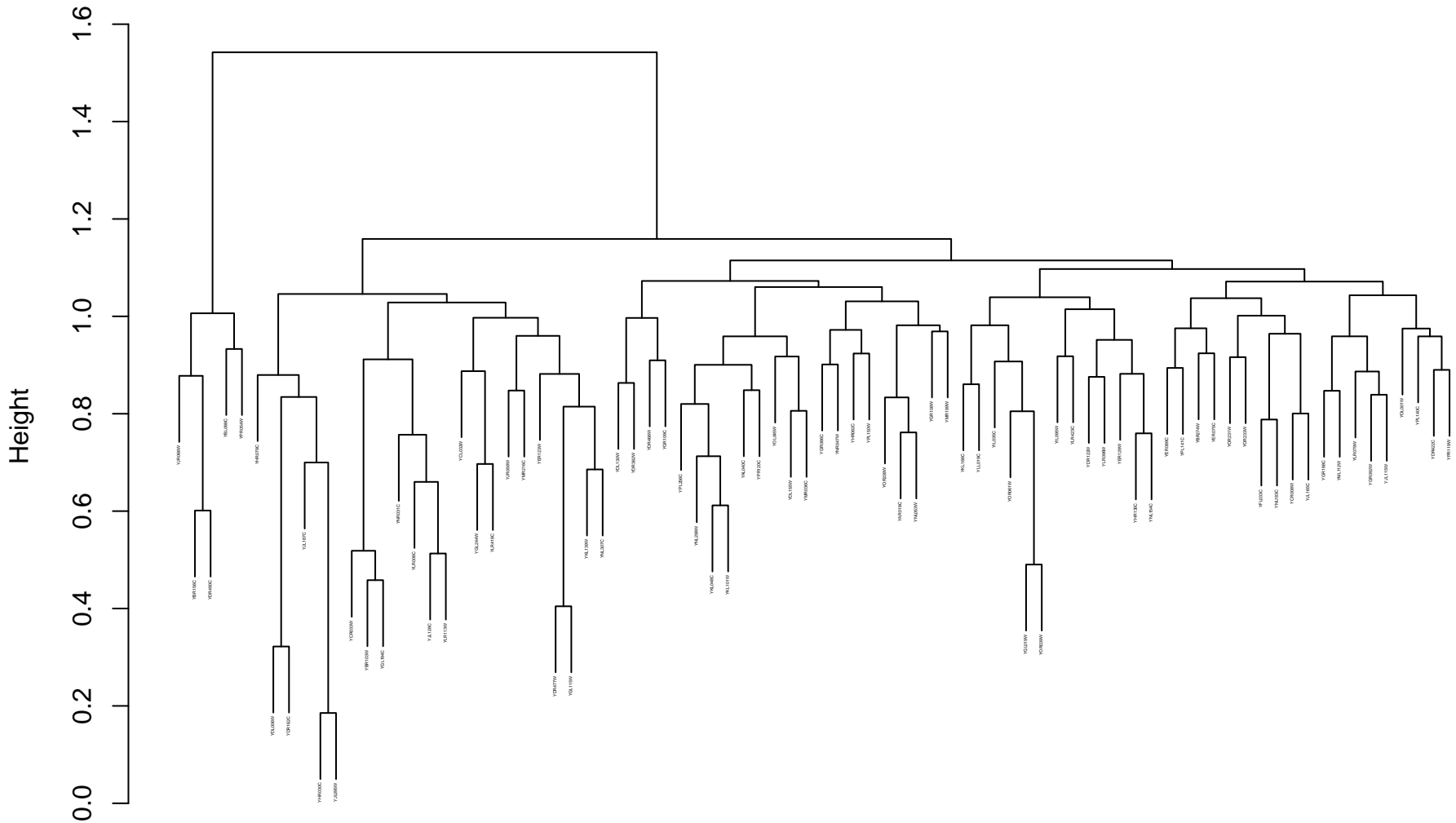
```
dissim_all
hclust (*, "complete")
```



kinase activity_GO_pearson_complete

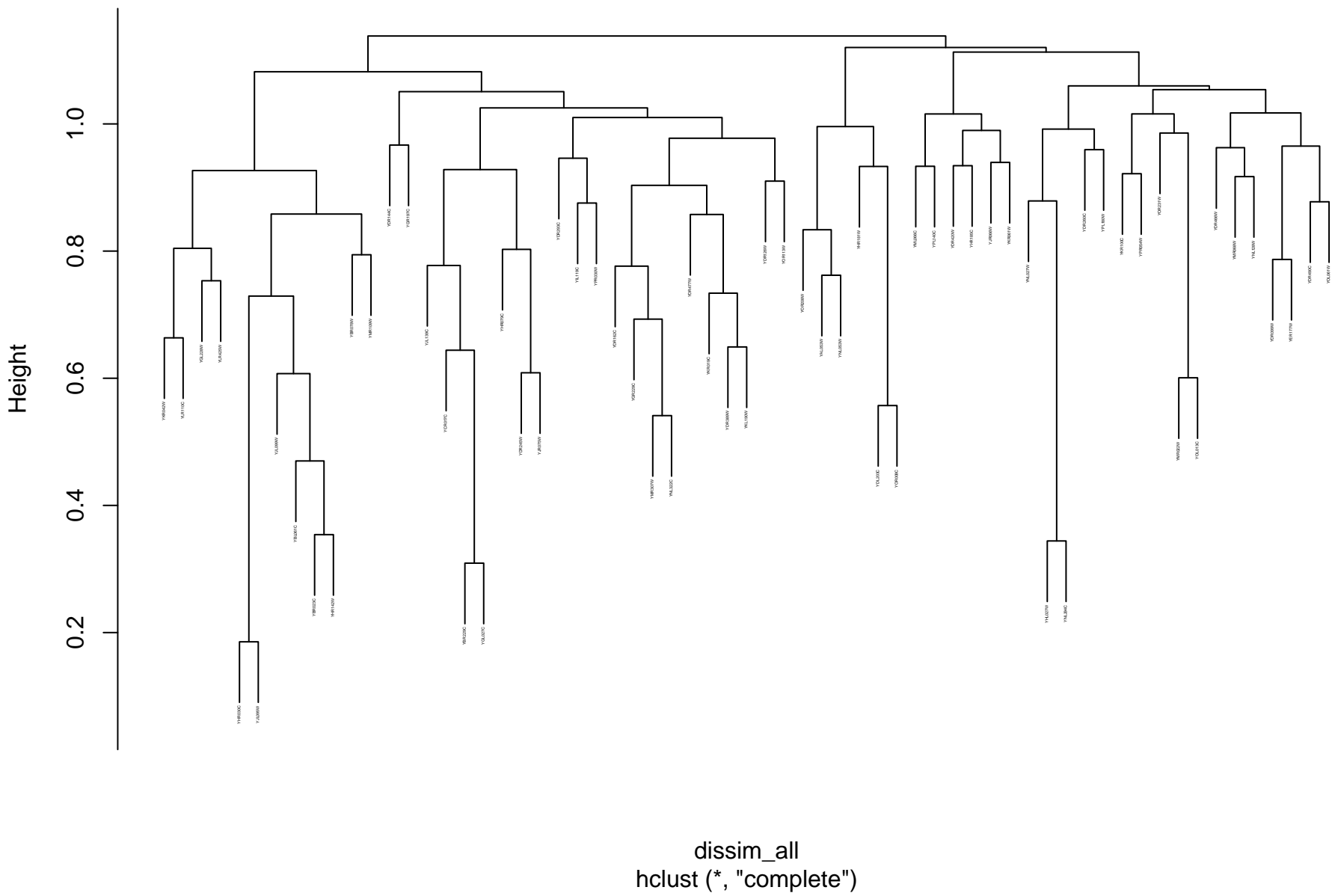


protein phosphorylation_GO_pearson_complete

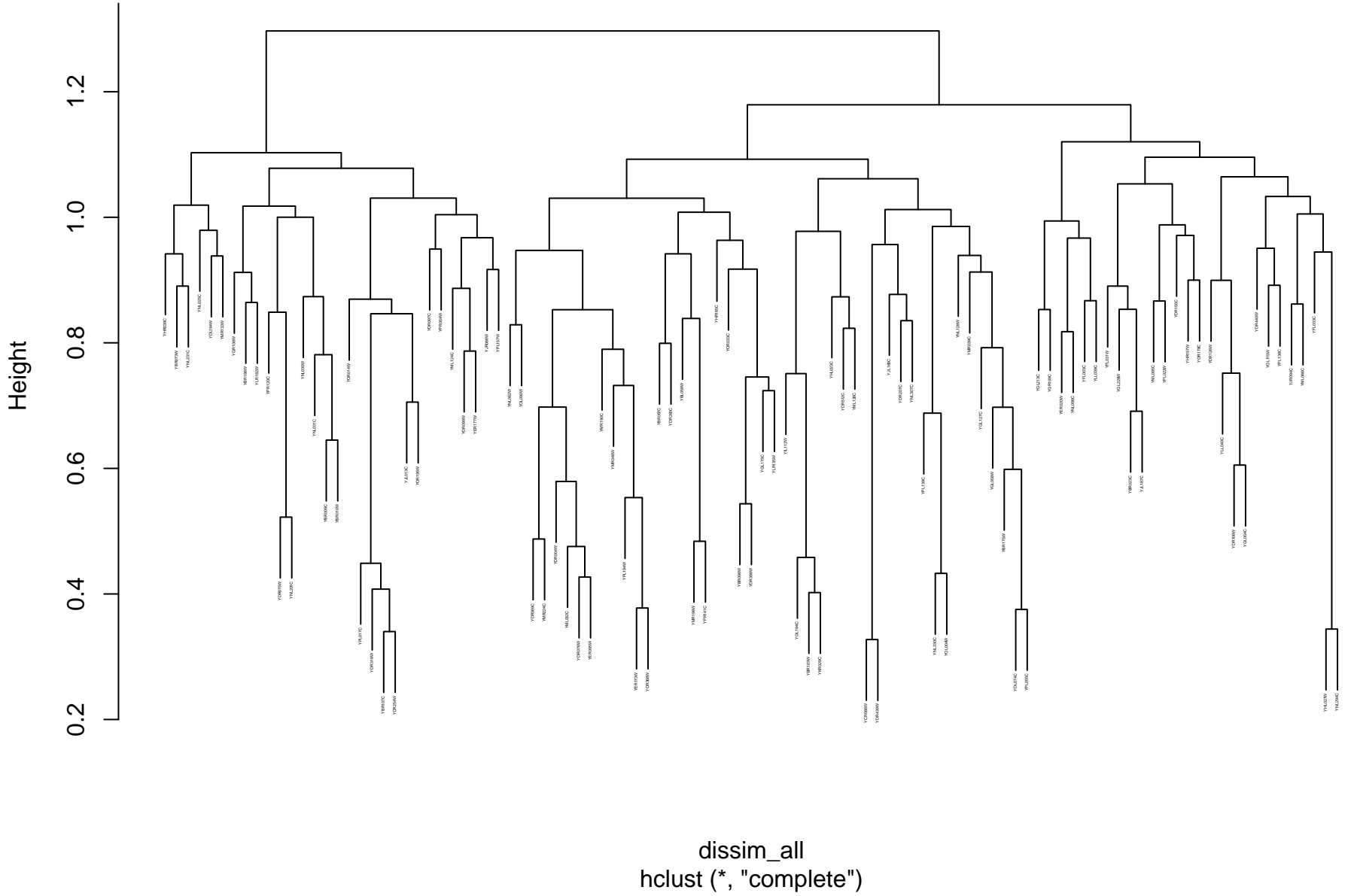


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dissim_all
hclust (*, "complete")
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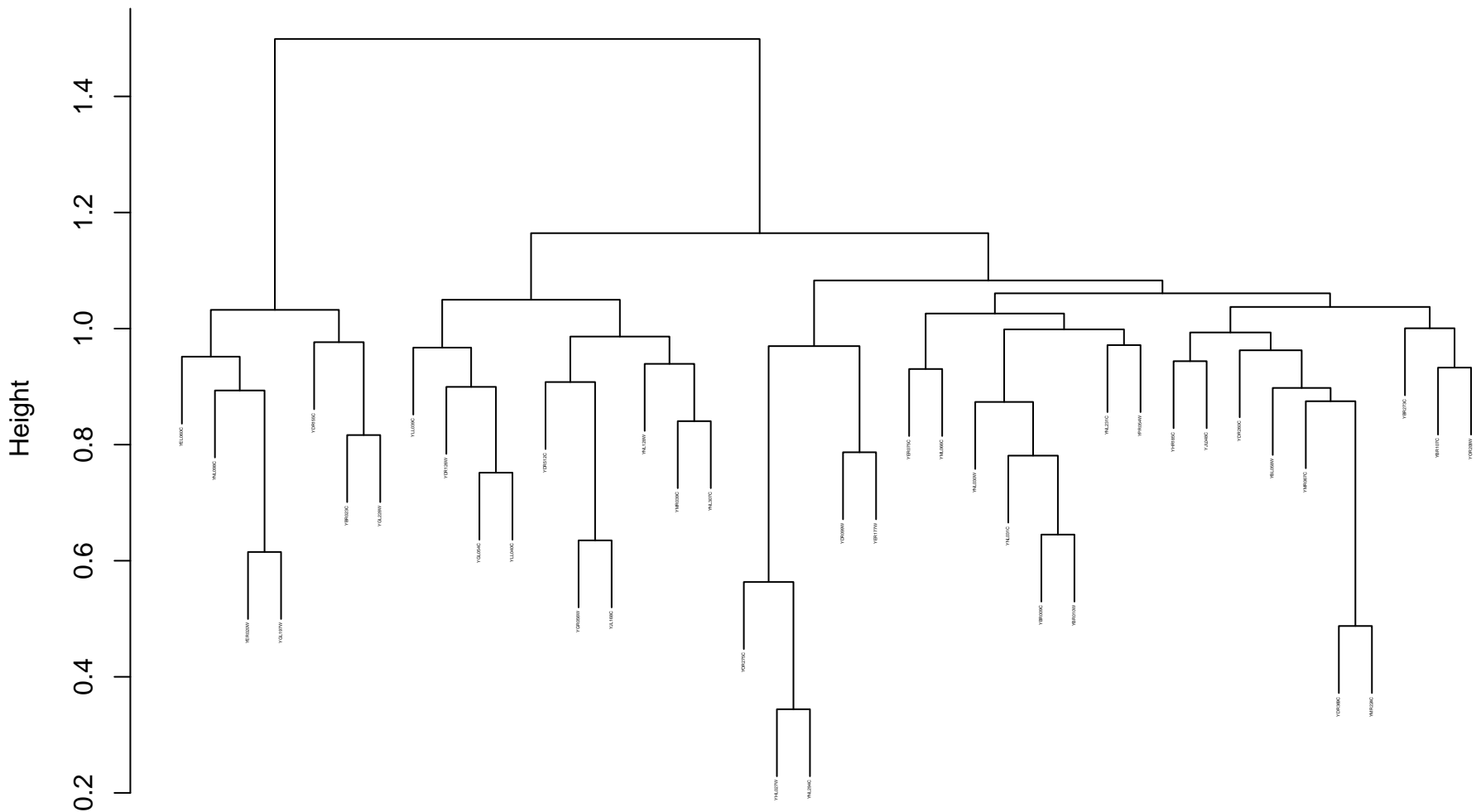

cell wall organization or biogenesis_GO_pearson_complete



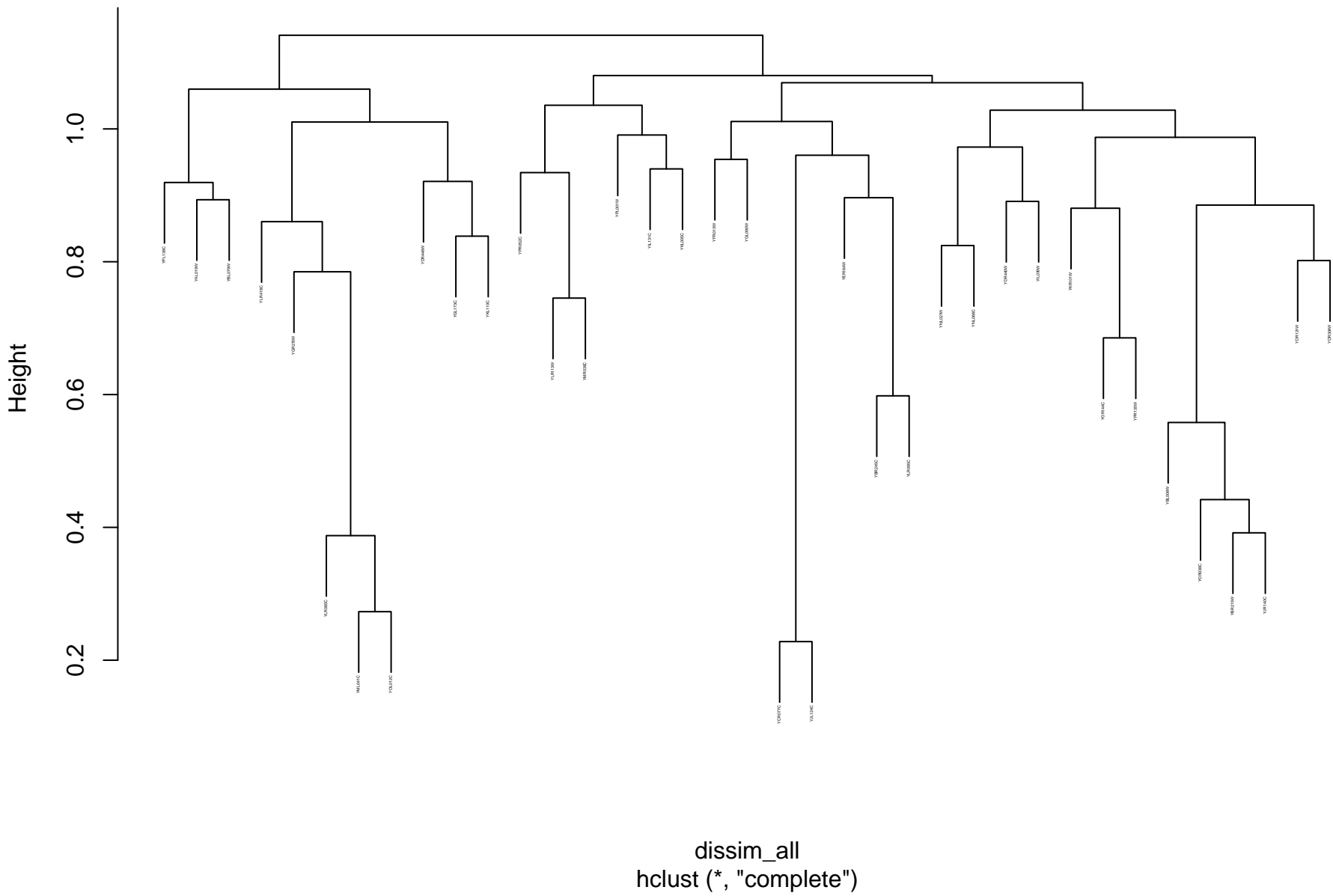
meiotic cell cycle_GO_pearson_complete



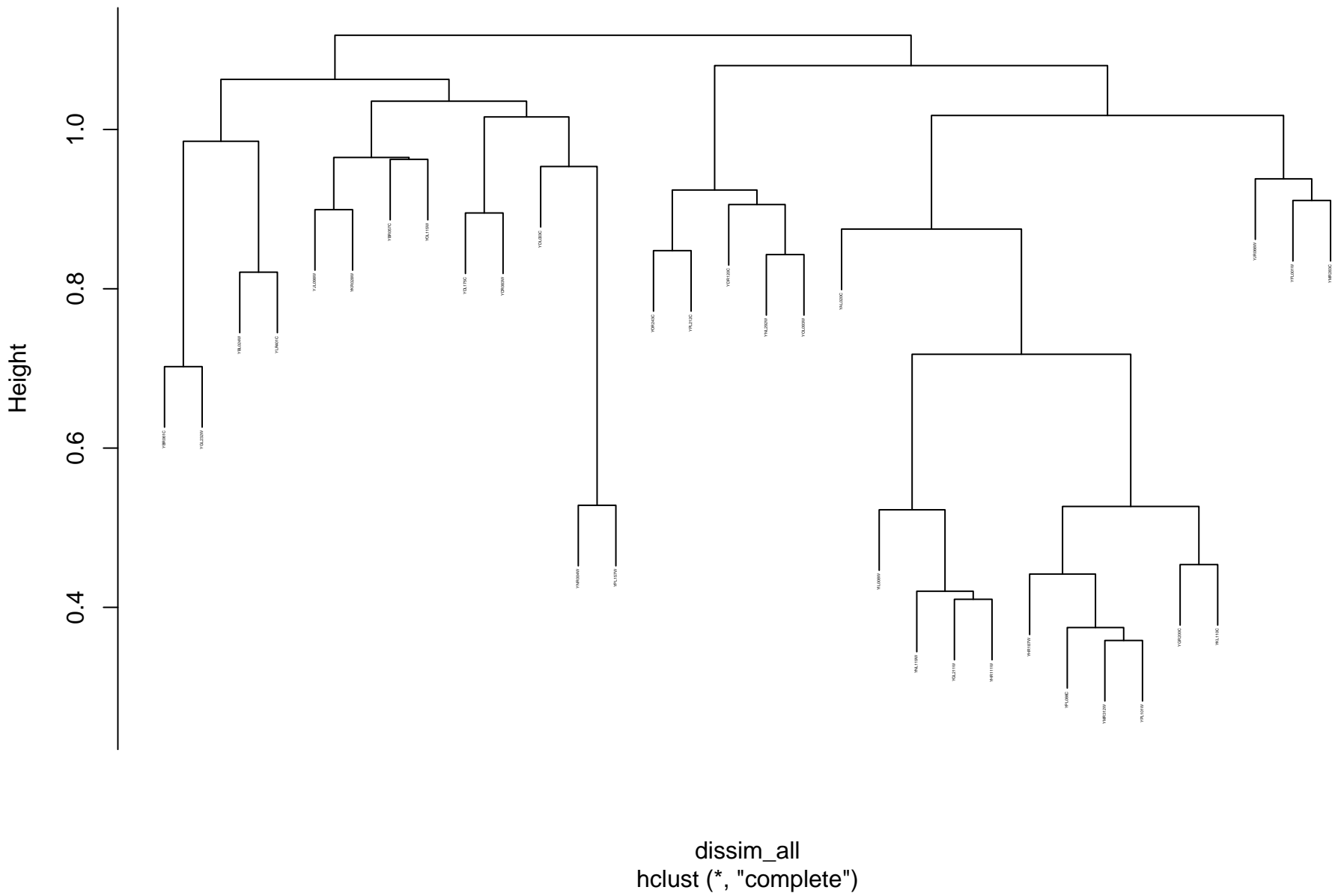
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dissim_all
hclust (*, "complete")
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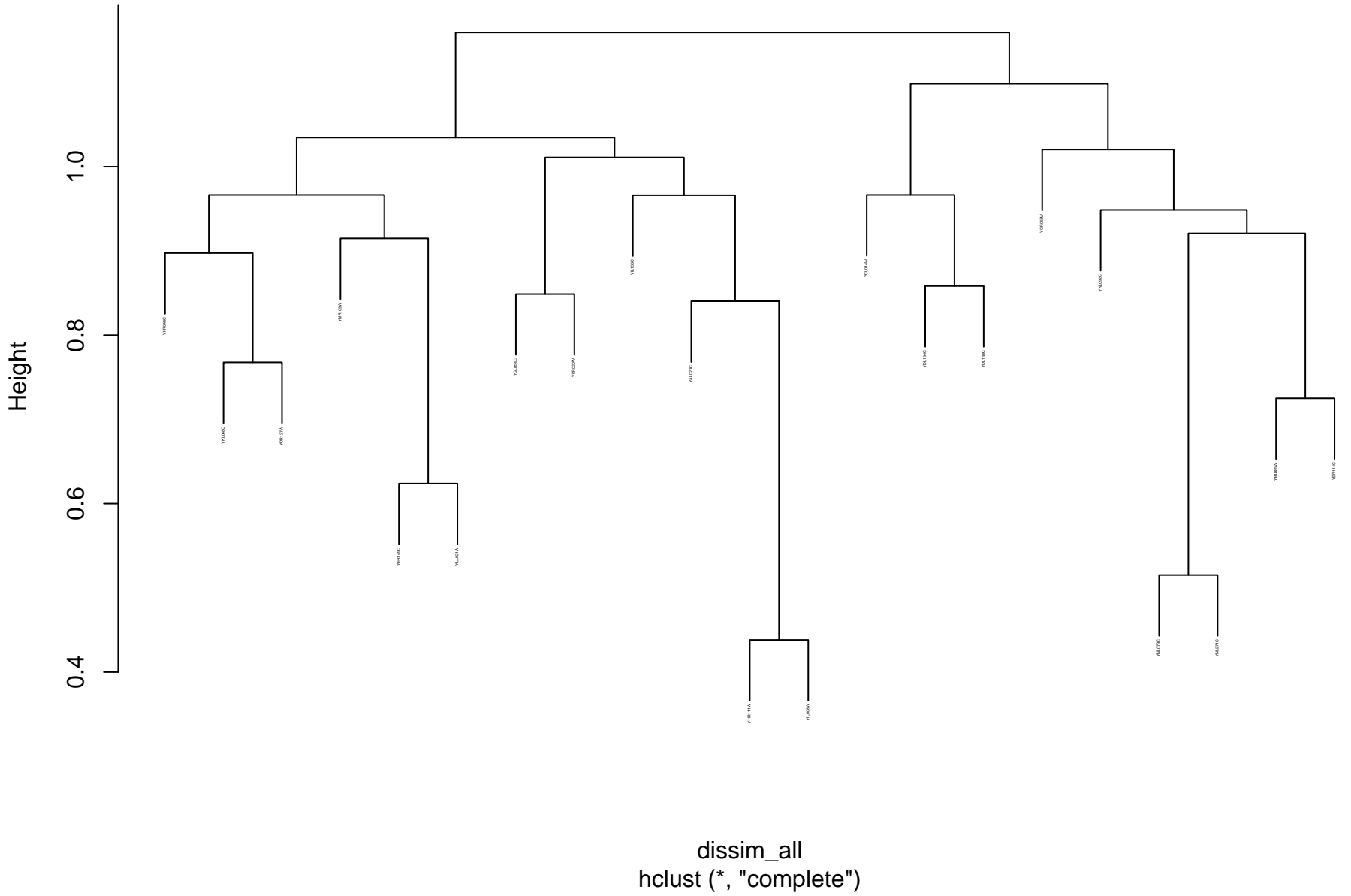
chromatin binding_GO_pearson_complete



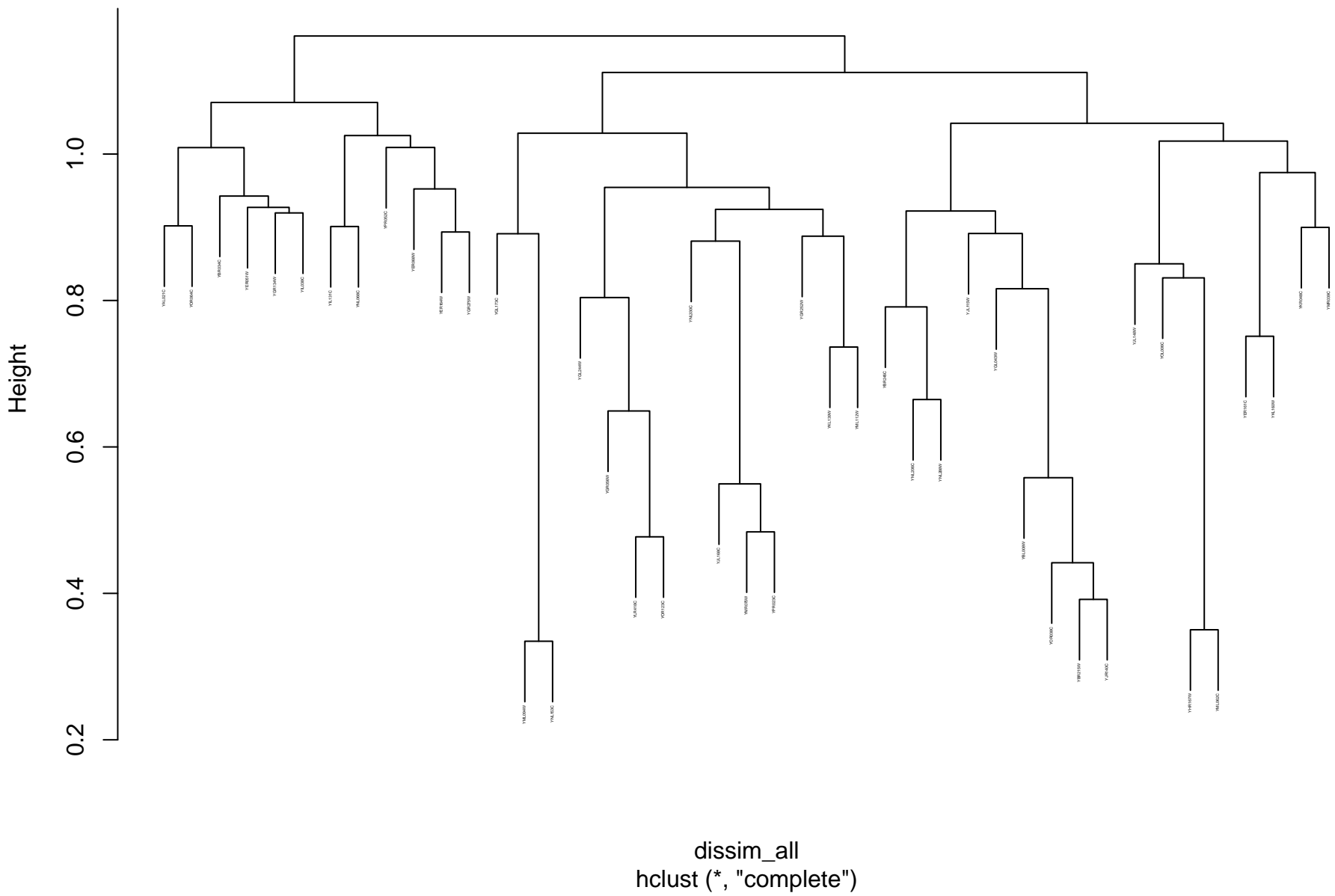
RNA modification_GO_pearson_complete



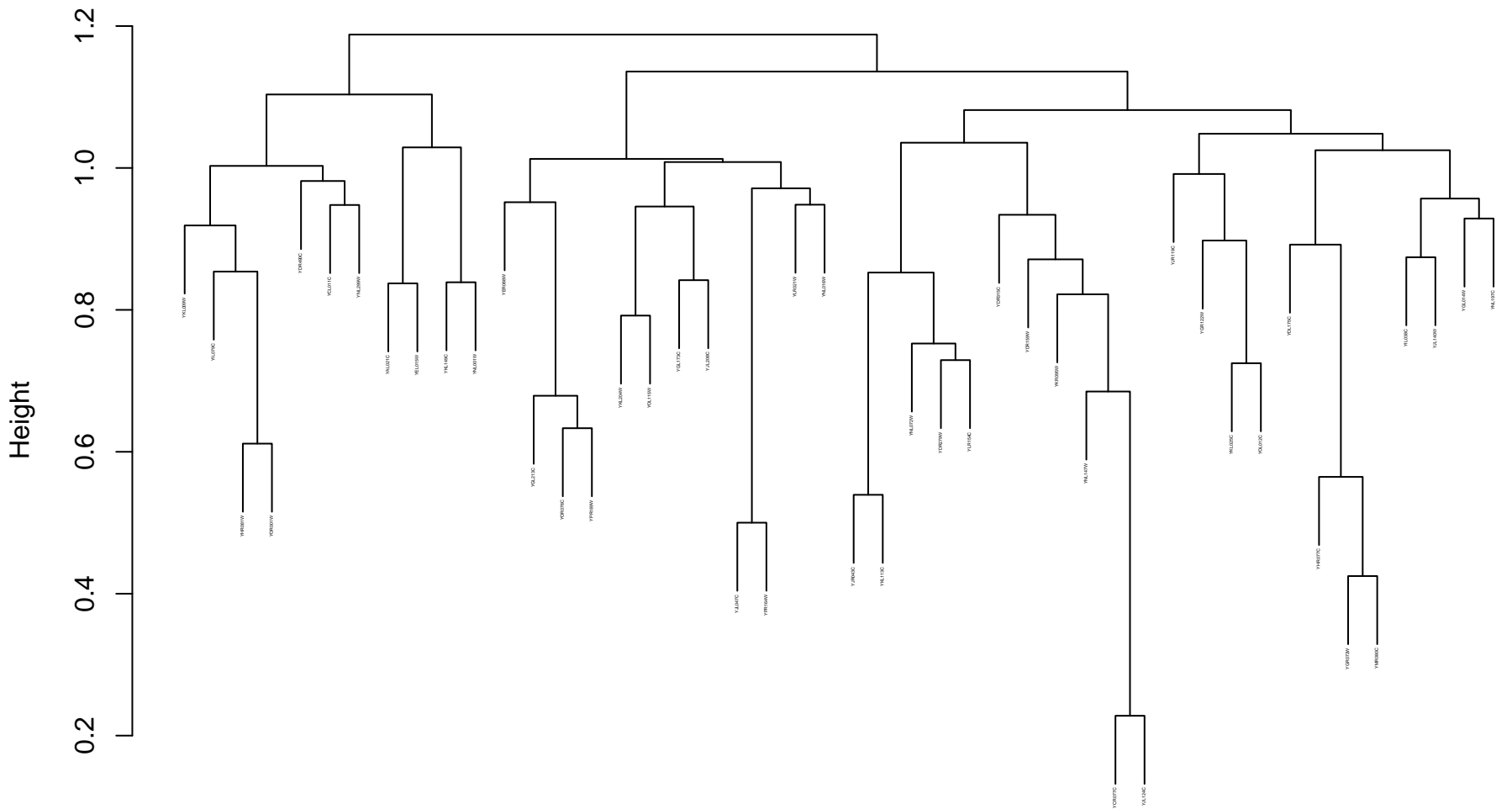
cell budding_GO_pearson_complete



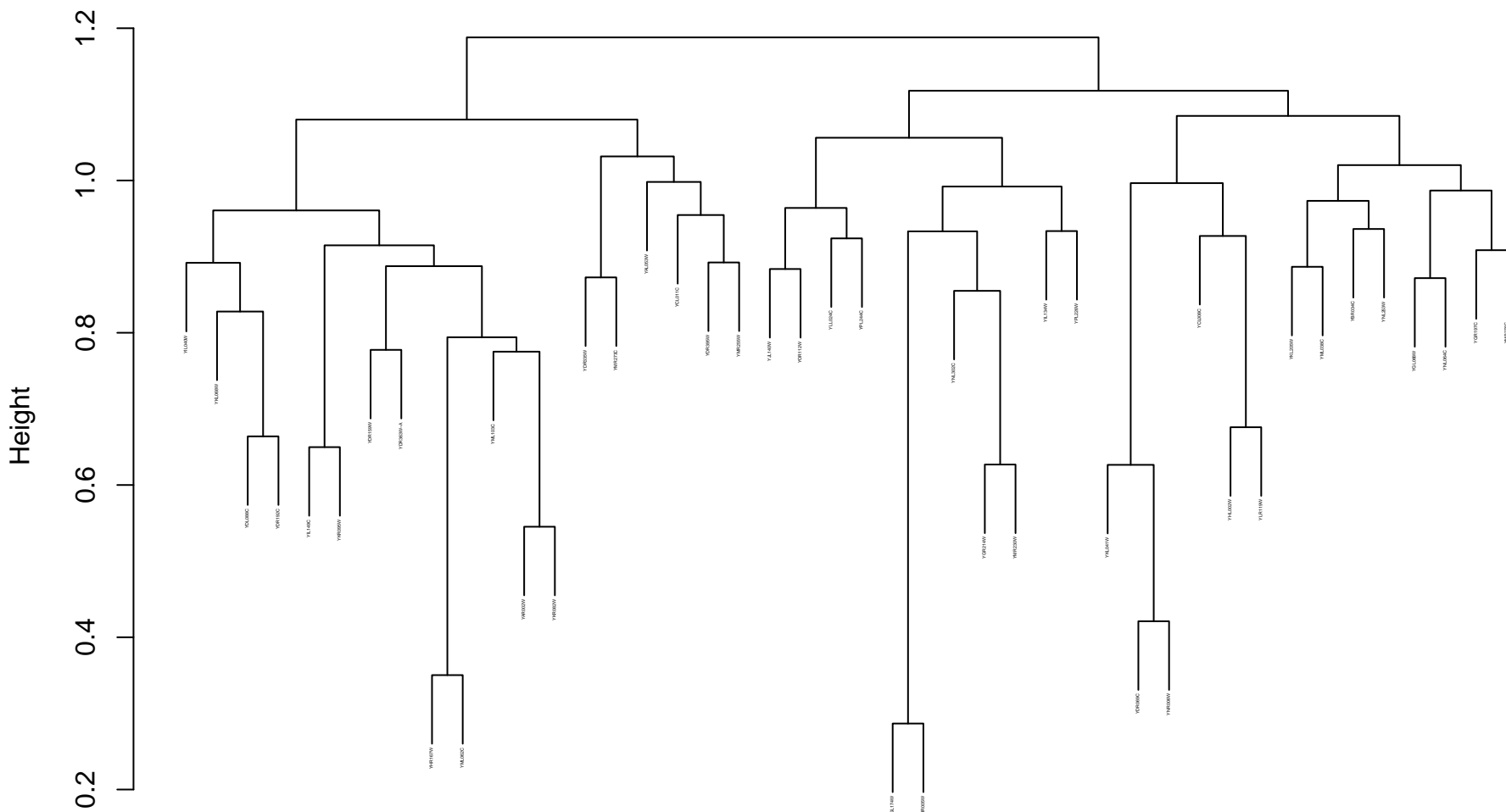
DNA-templated transcription, elongation_GO_pearson_complete



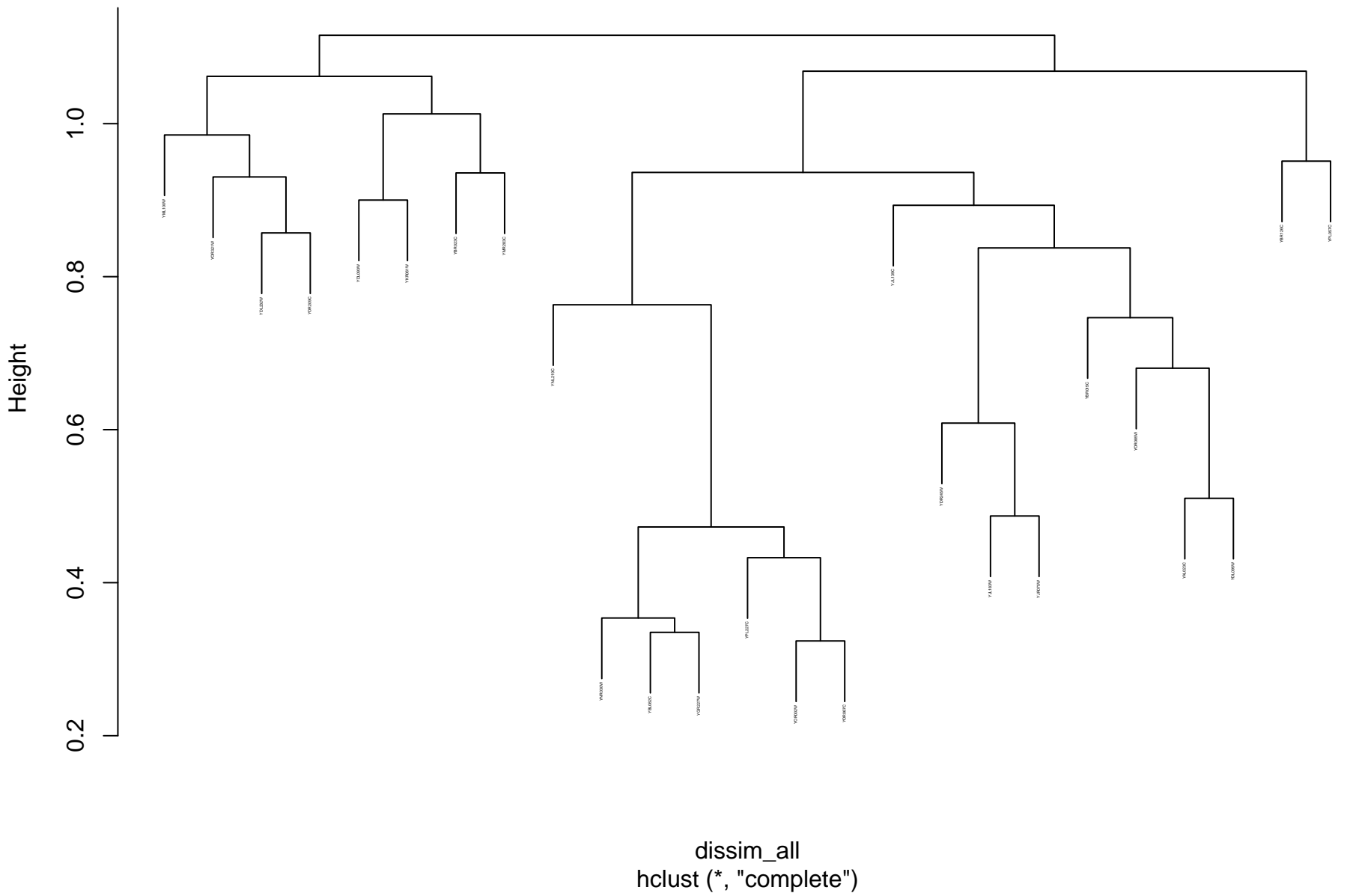
```
dissim_all
hclust (*, "complete")
```



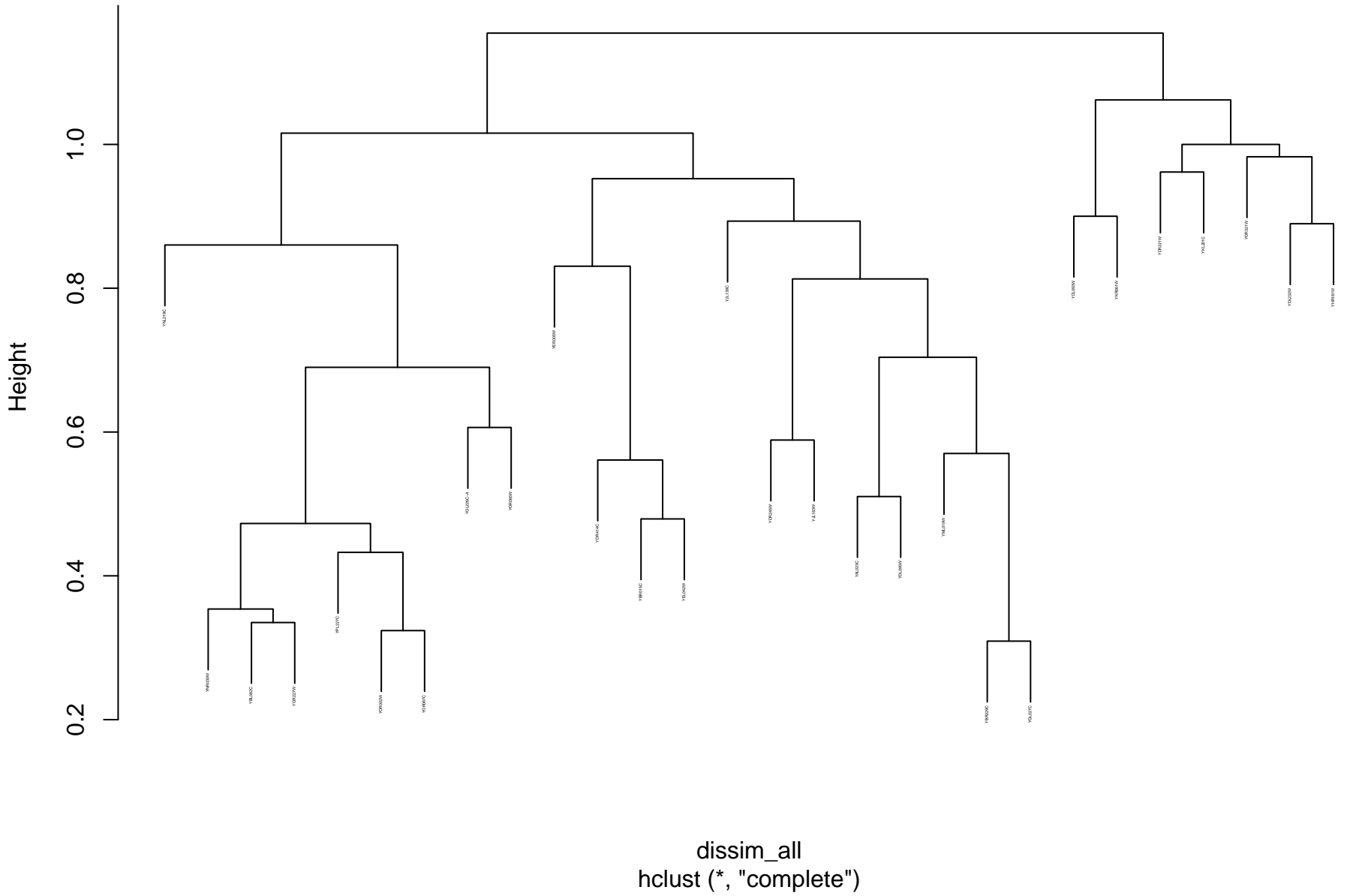

```
dissim_all
hclust (*, "complete")
```



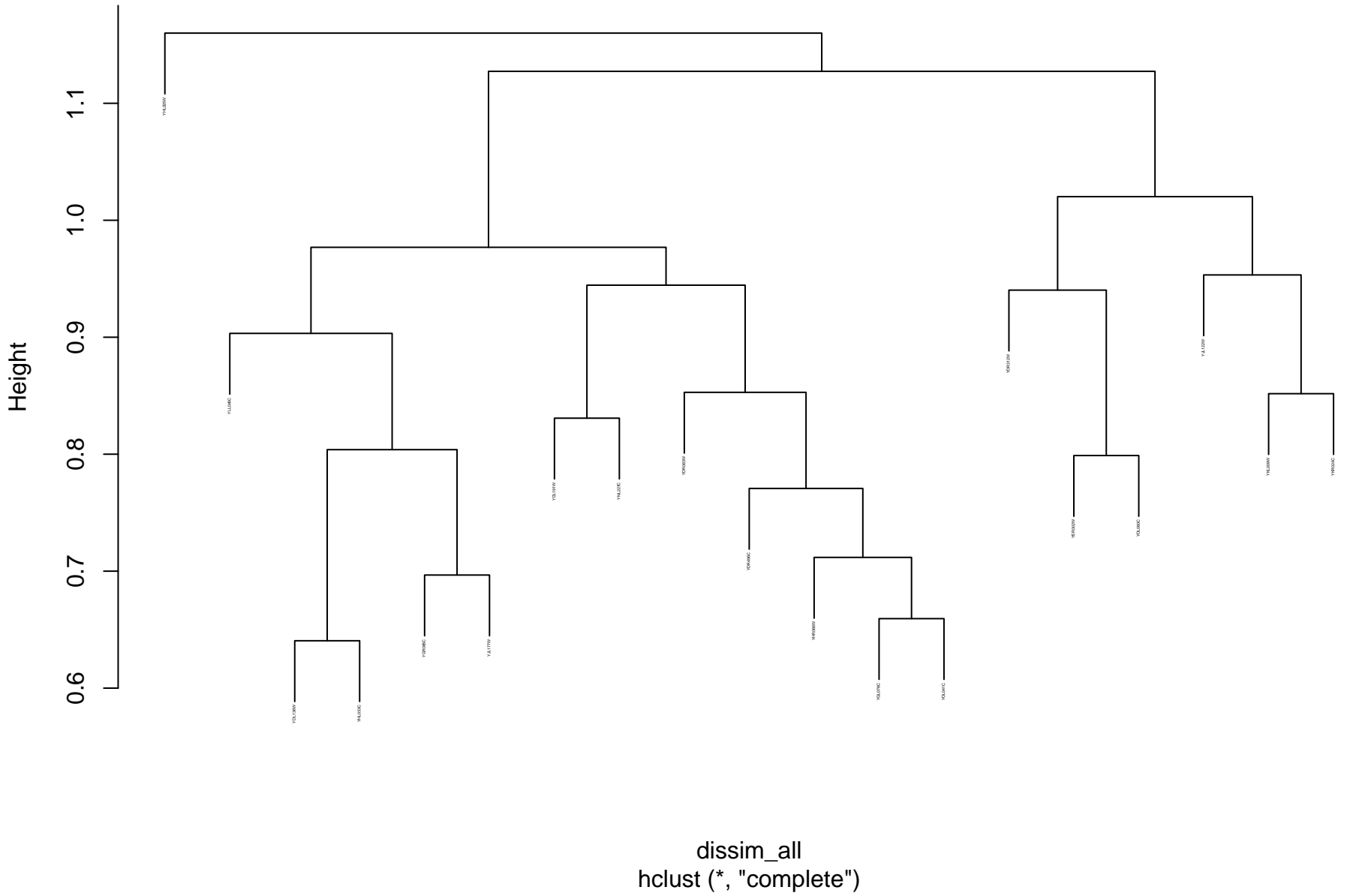
transferase activity, transferring glycosyl groups_GO_pearson_complete



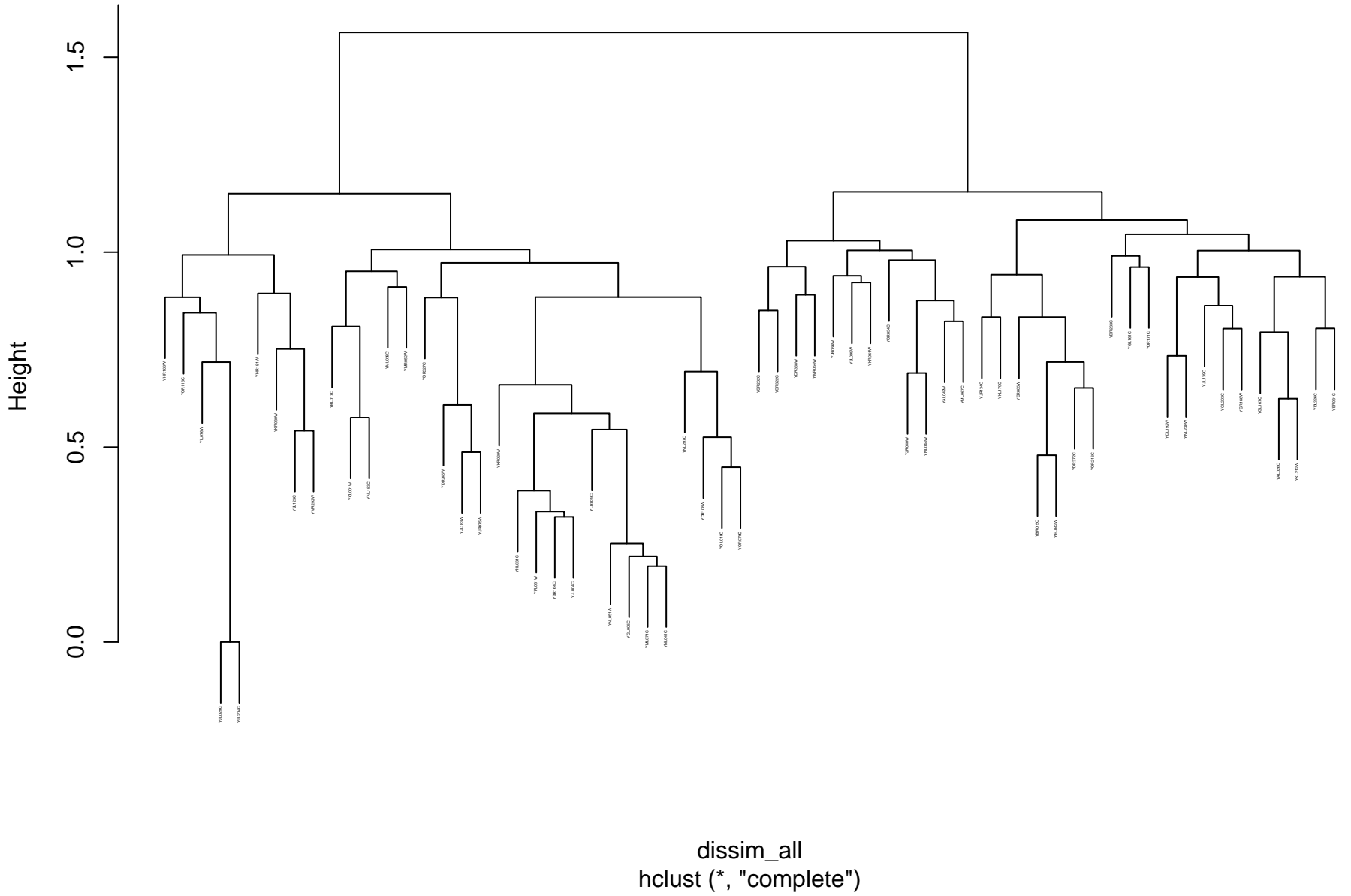
protein glycosylation_GO_pearson_complete

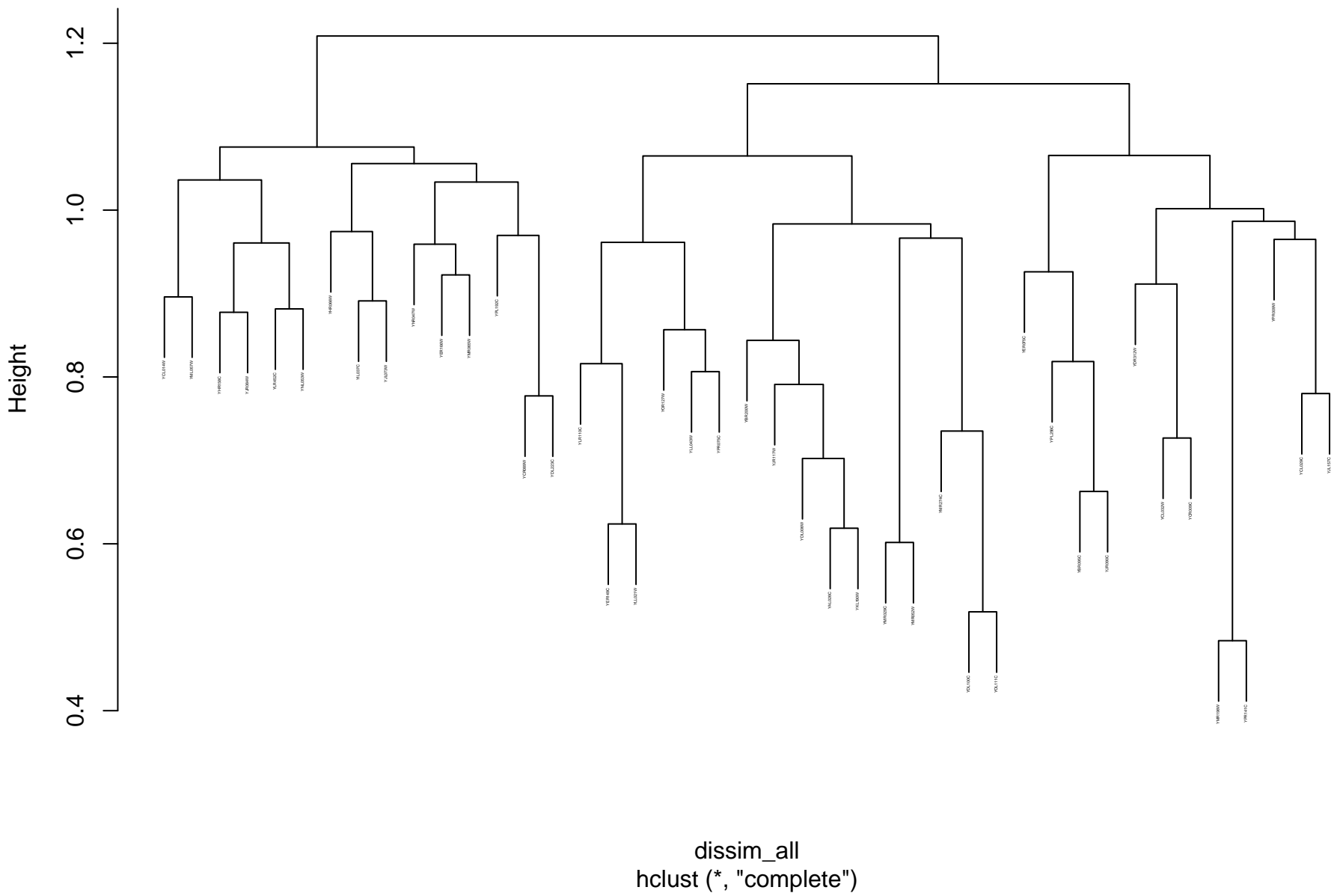


ribosomal large subunit biogenesis_GO_pearson_complete

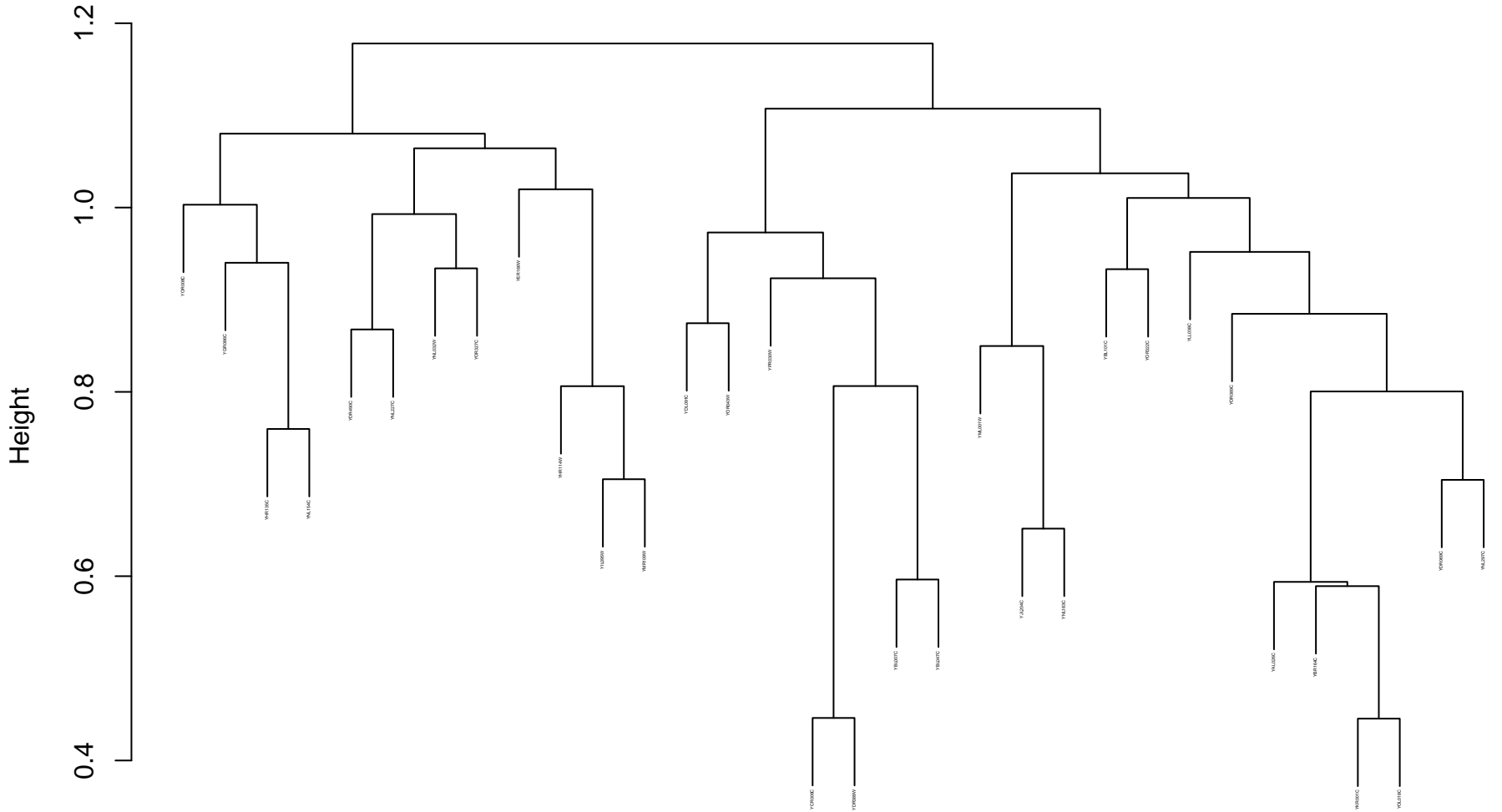


Golgi apparatus_GO_pearson_complete

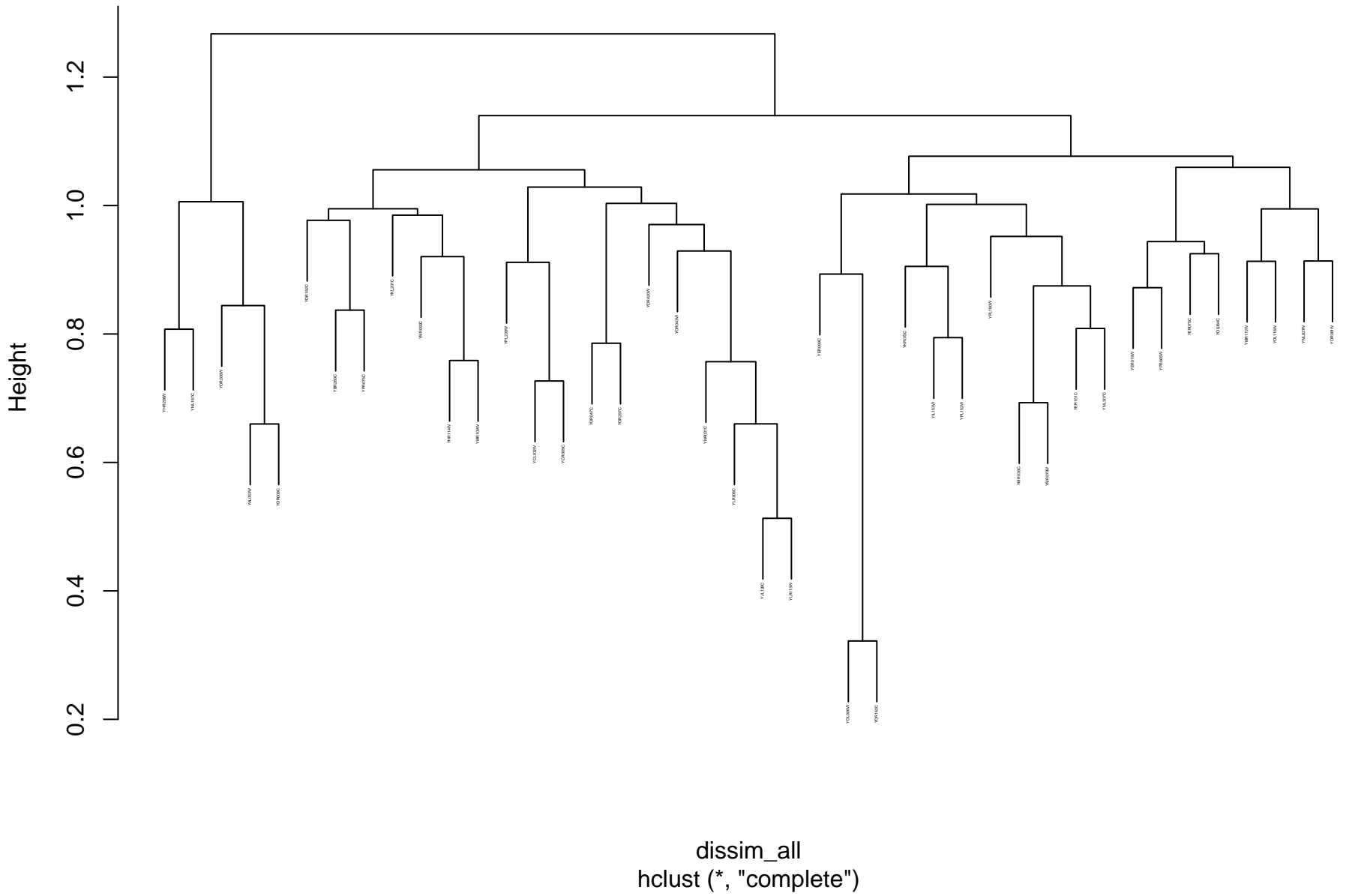


conjugation_GO_pearson_complete

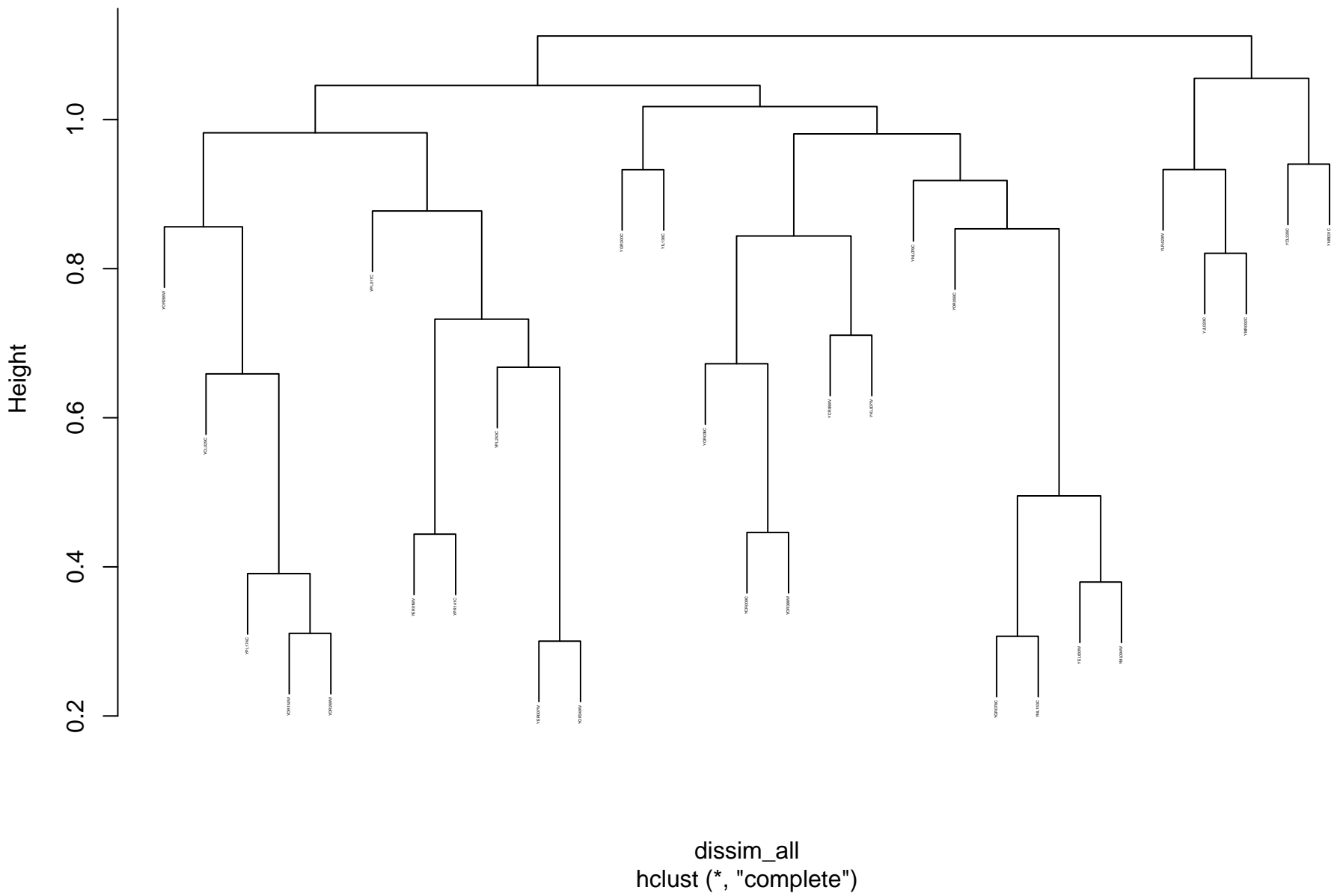
```
dissim_all
hclust (*, "complete")
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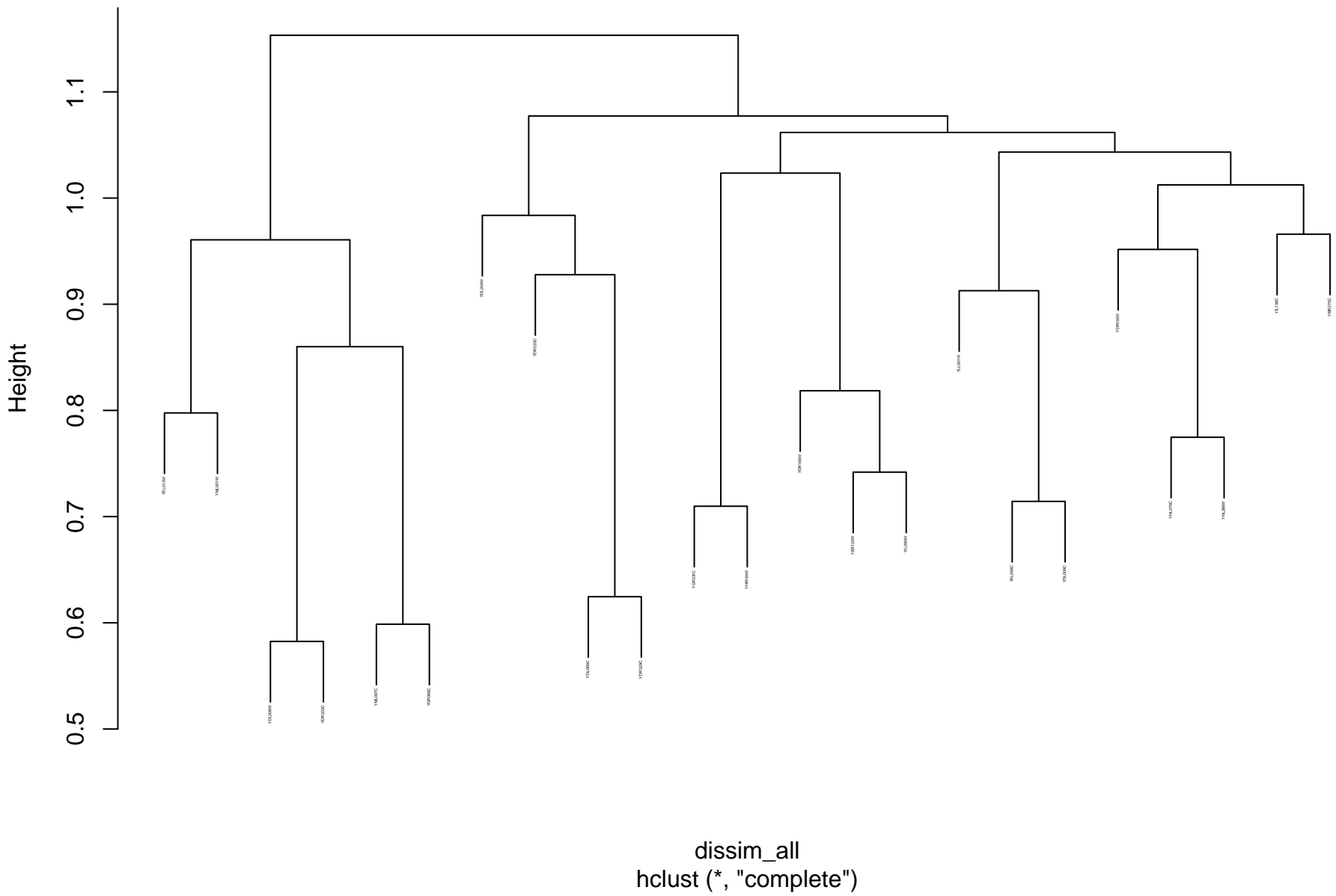
response to osmotic stress_GO_pearson_complete



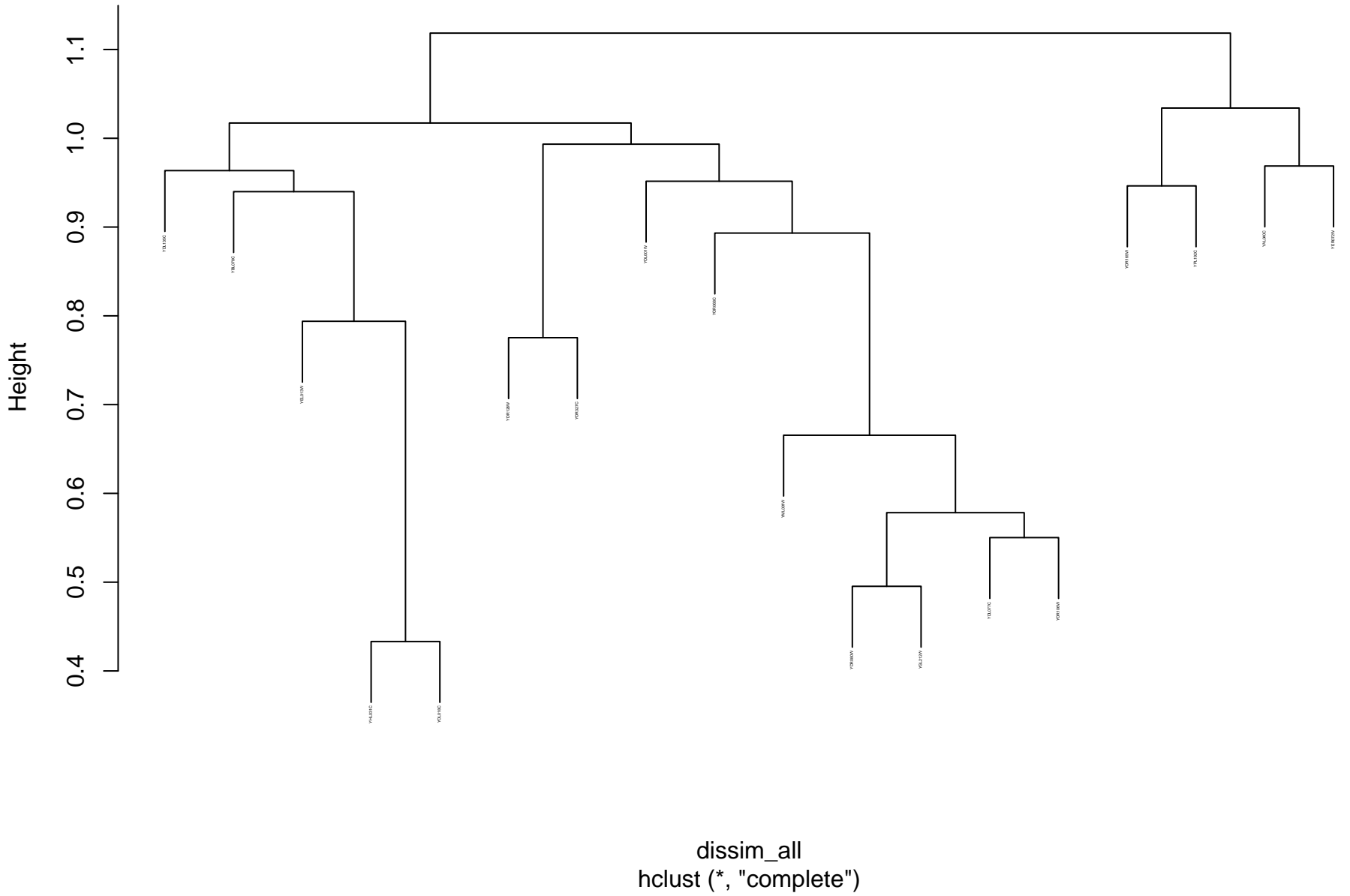
cytoskeletal protein binding_GO_pearson_complete



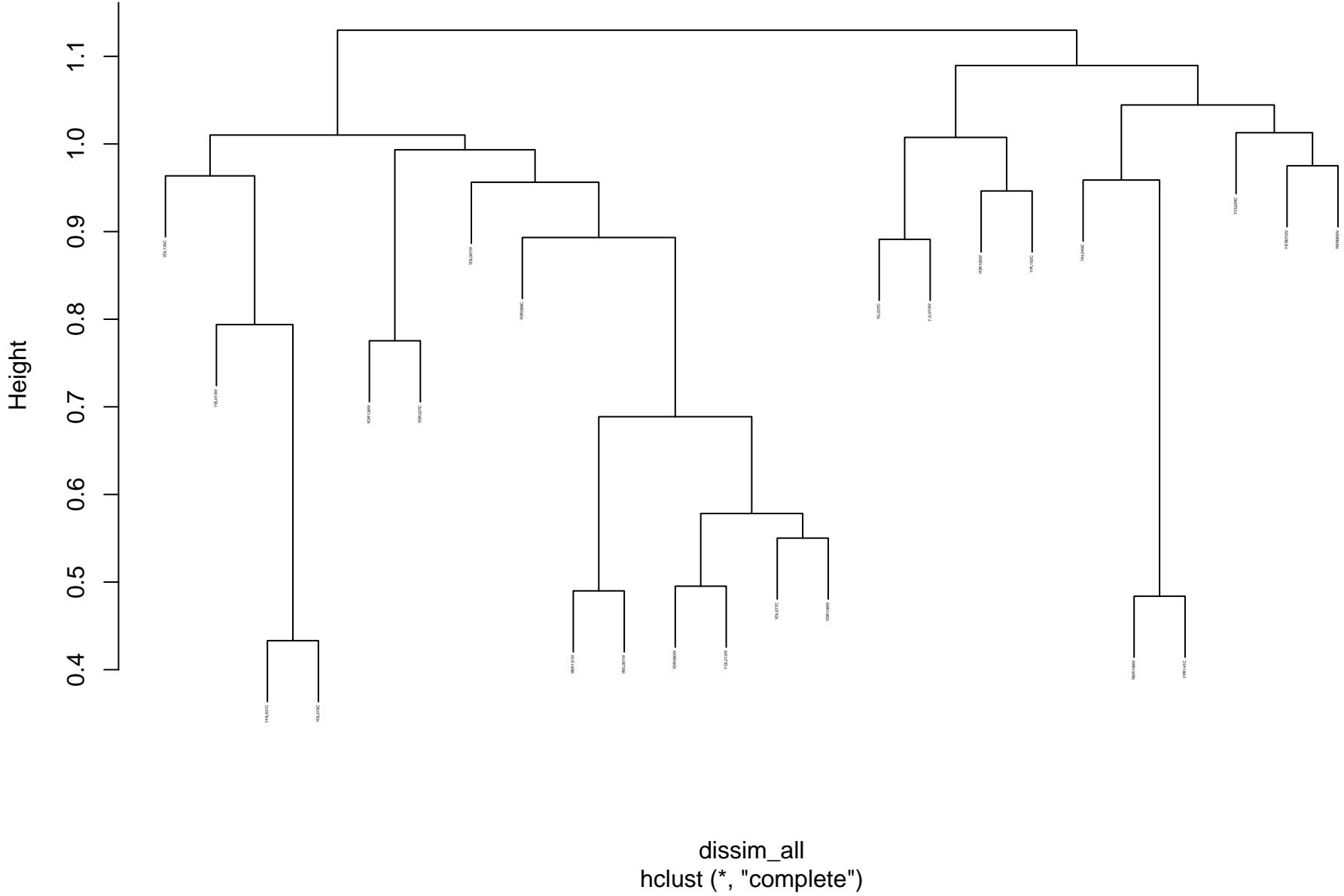
organelle inheritance_GO_pearson_complete



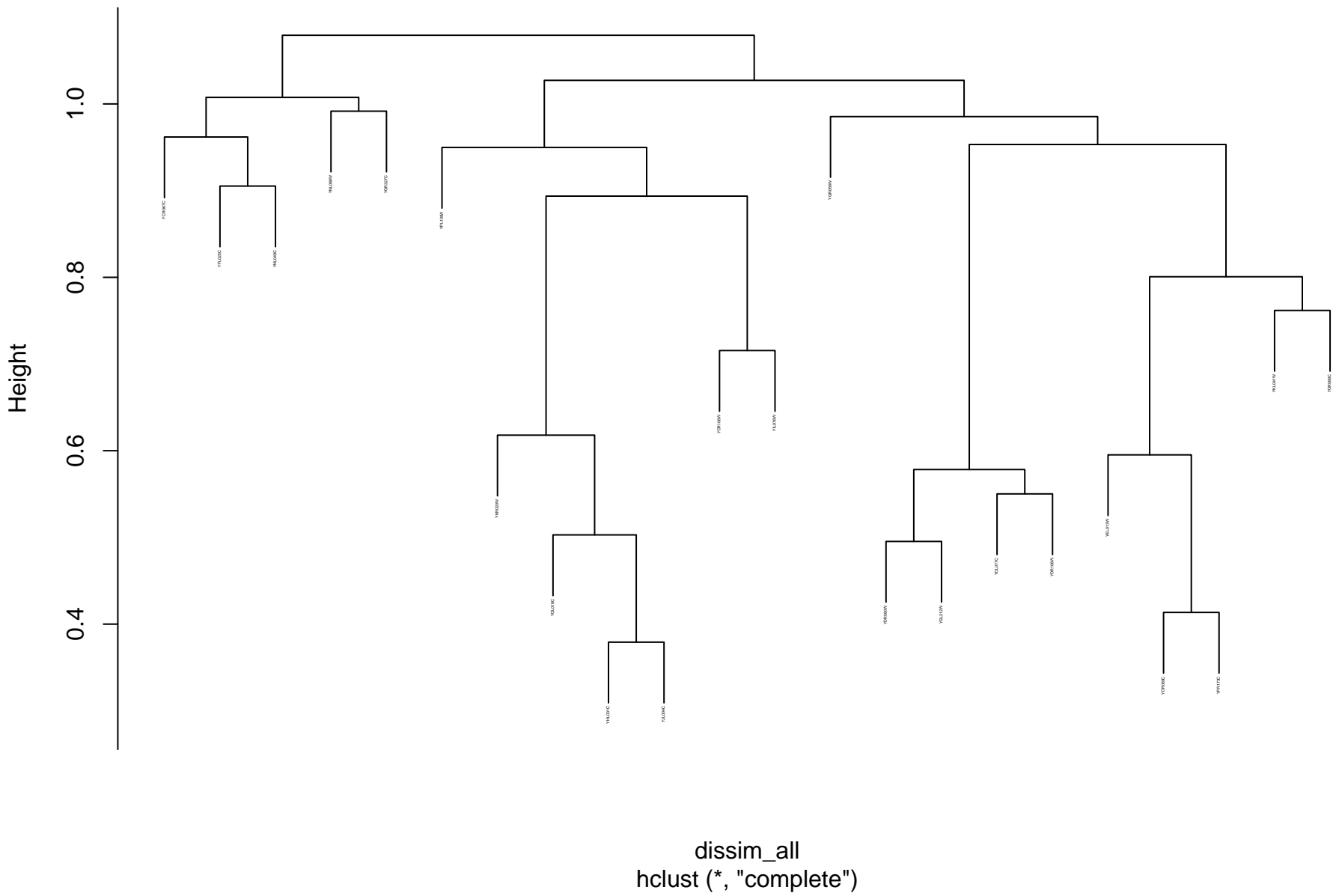
membrane fusion_GO_pearson_complete



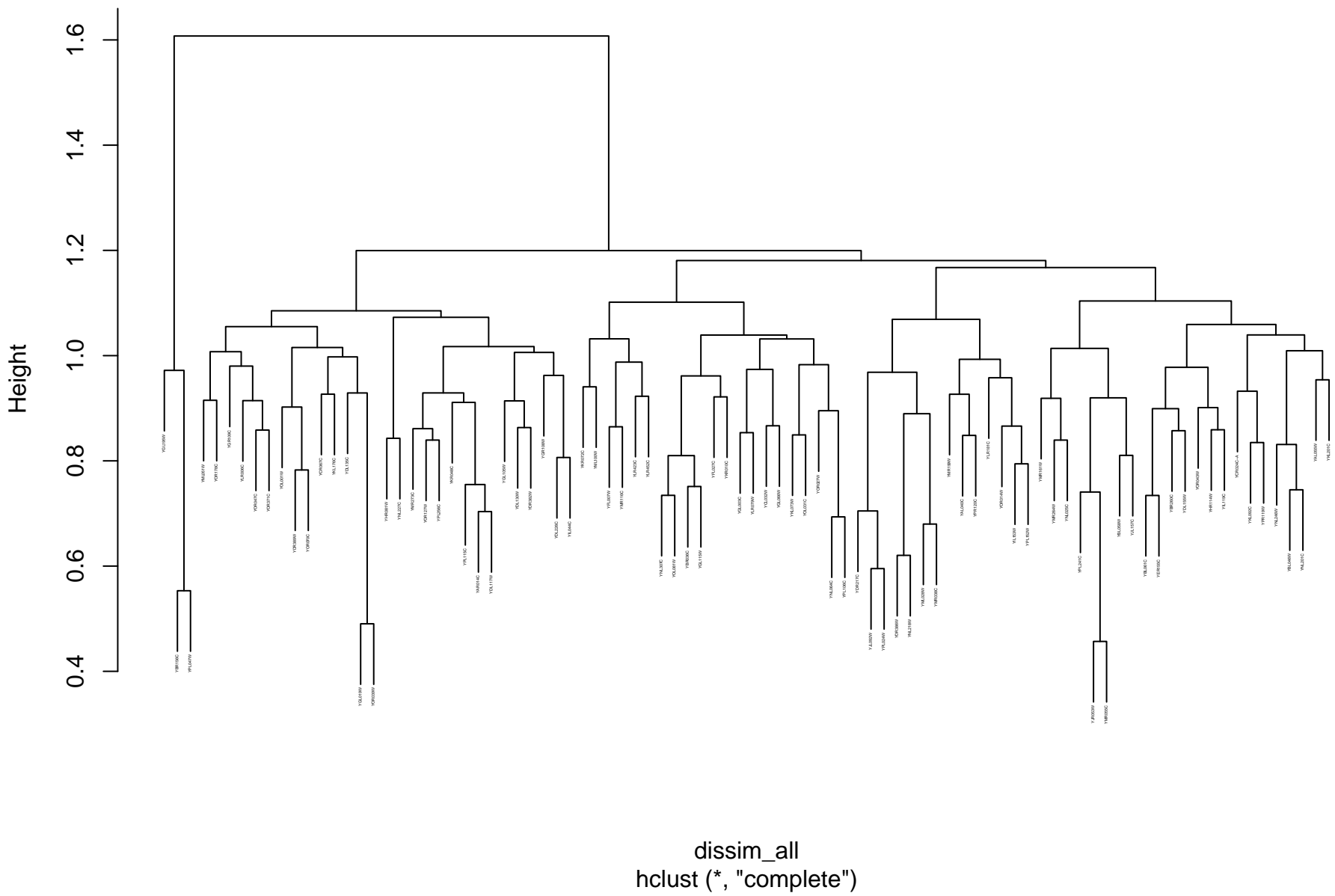
organelle fusion_GO_pearson_complete



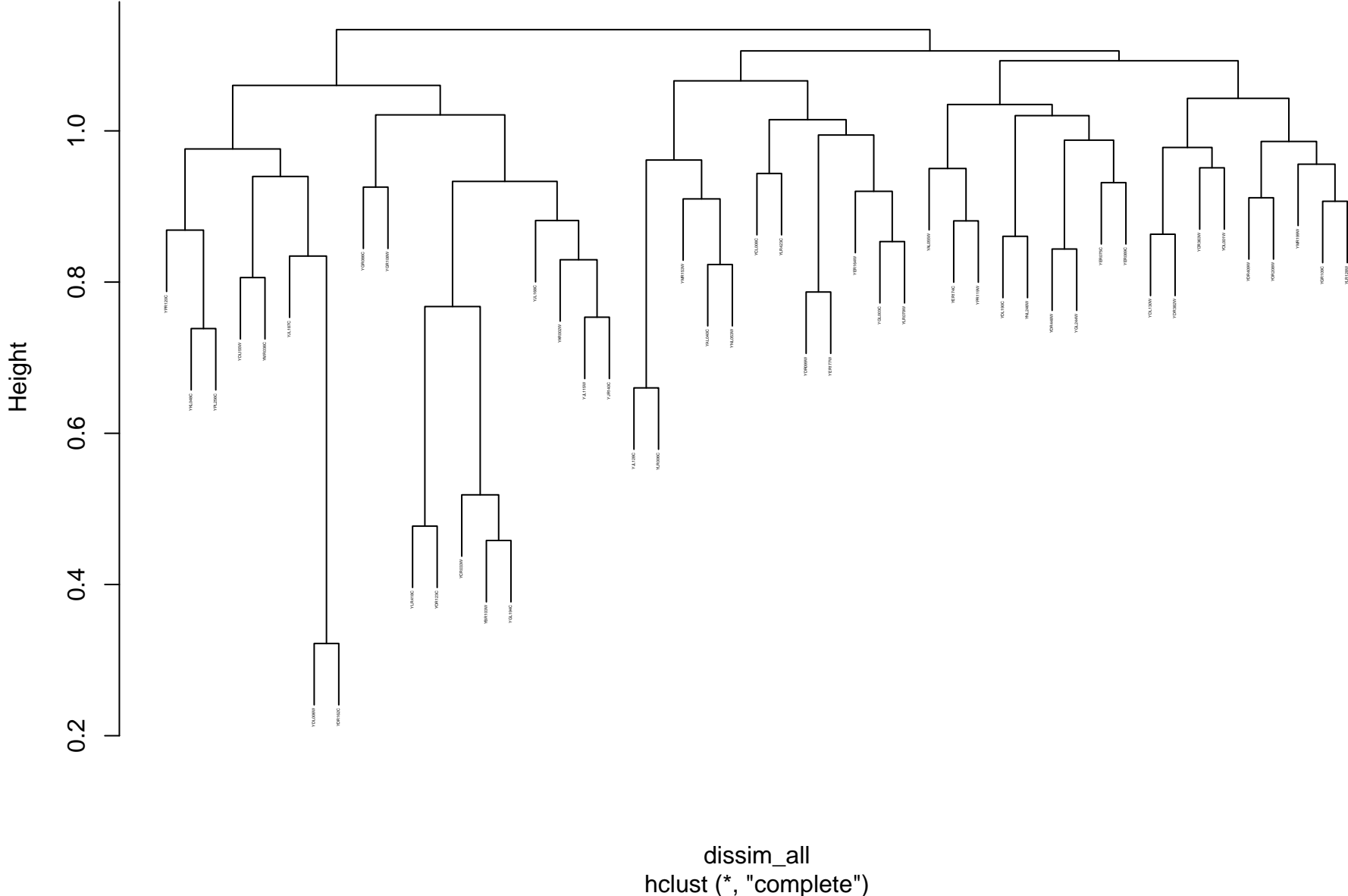
vesicle organization_GO_pearson_complete



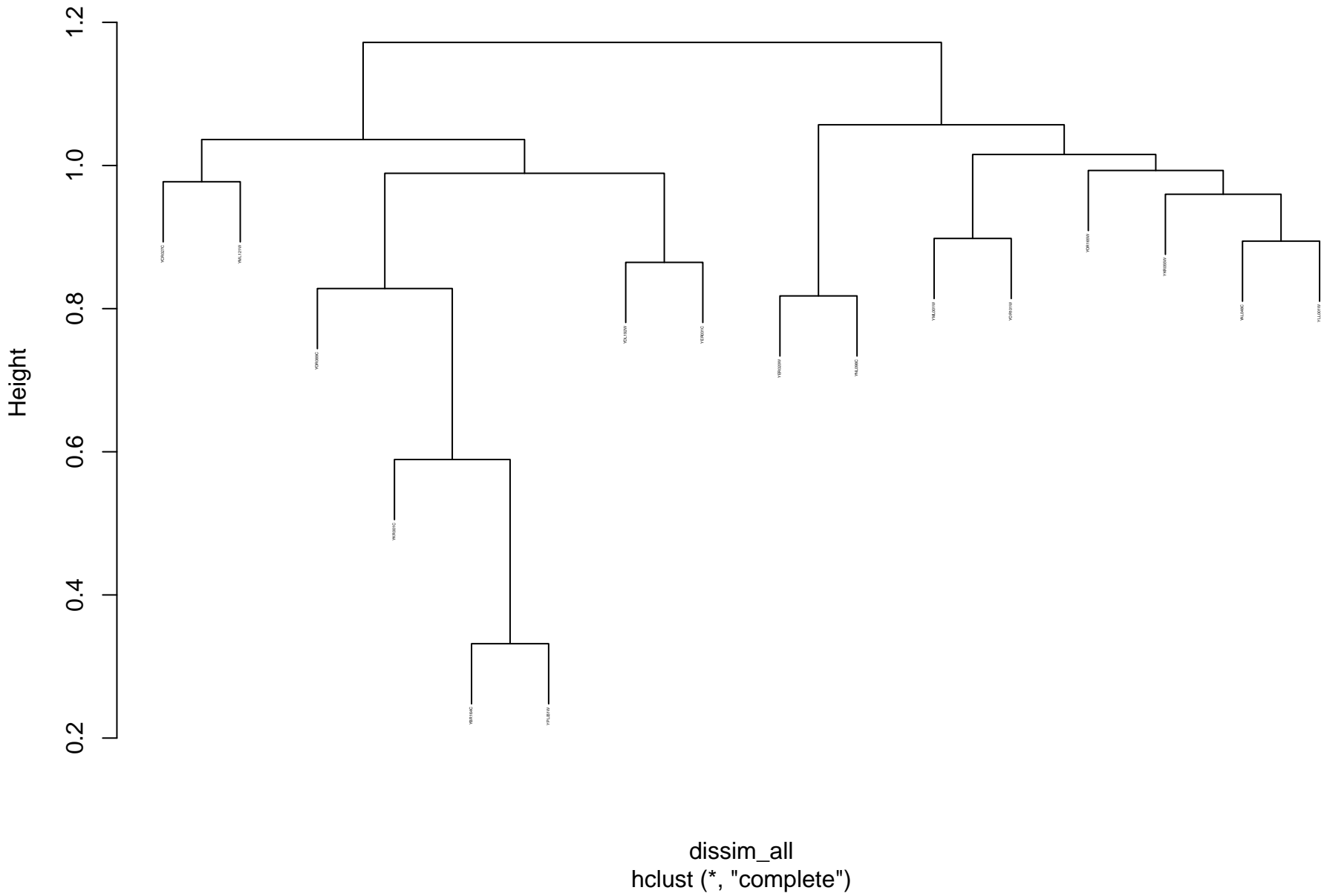
enzyme regulator activity_GO_pearson_complete

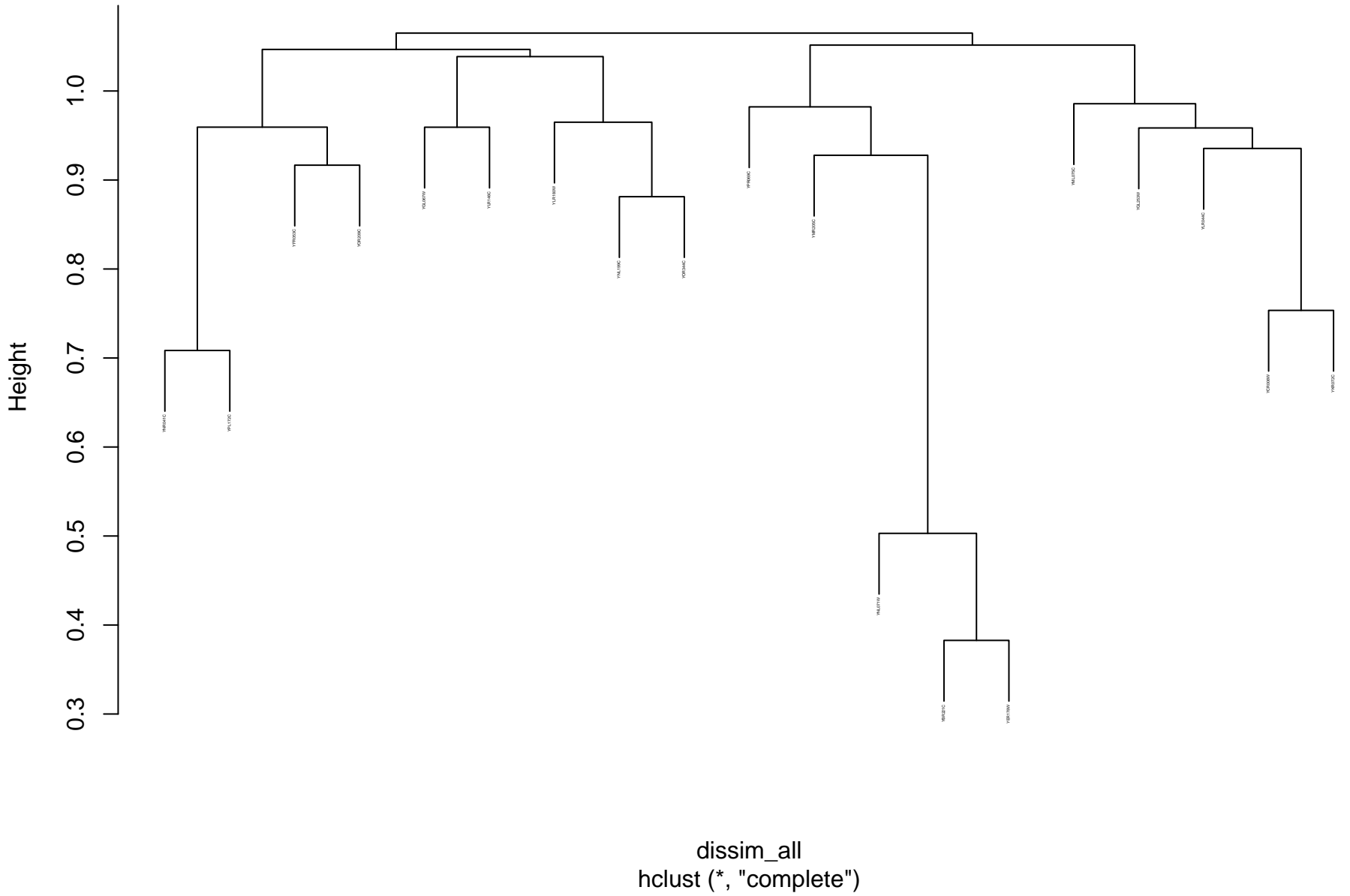


regulation of protein modification process_GO_pearson_complete

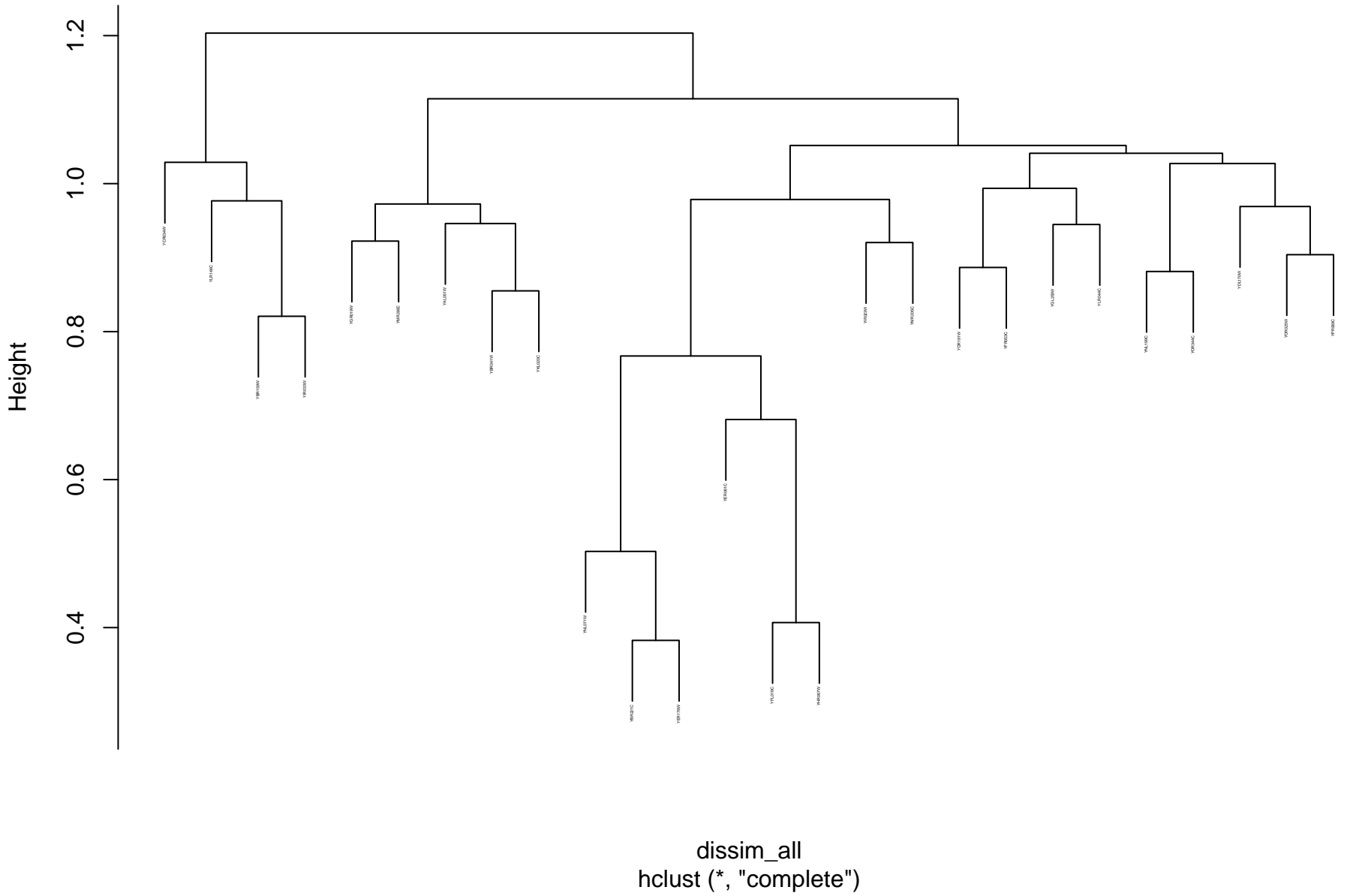


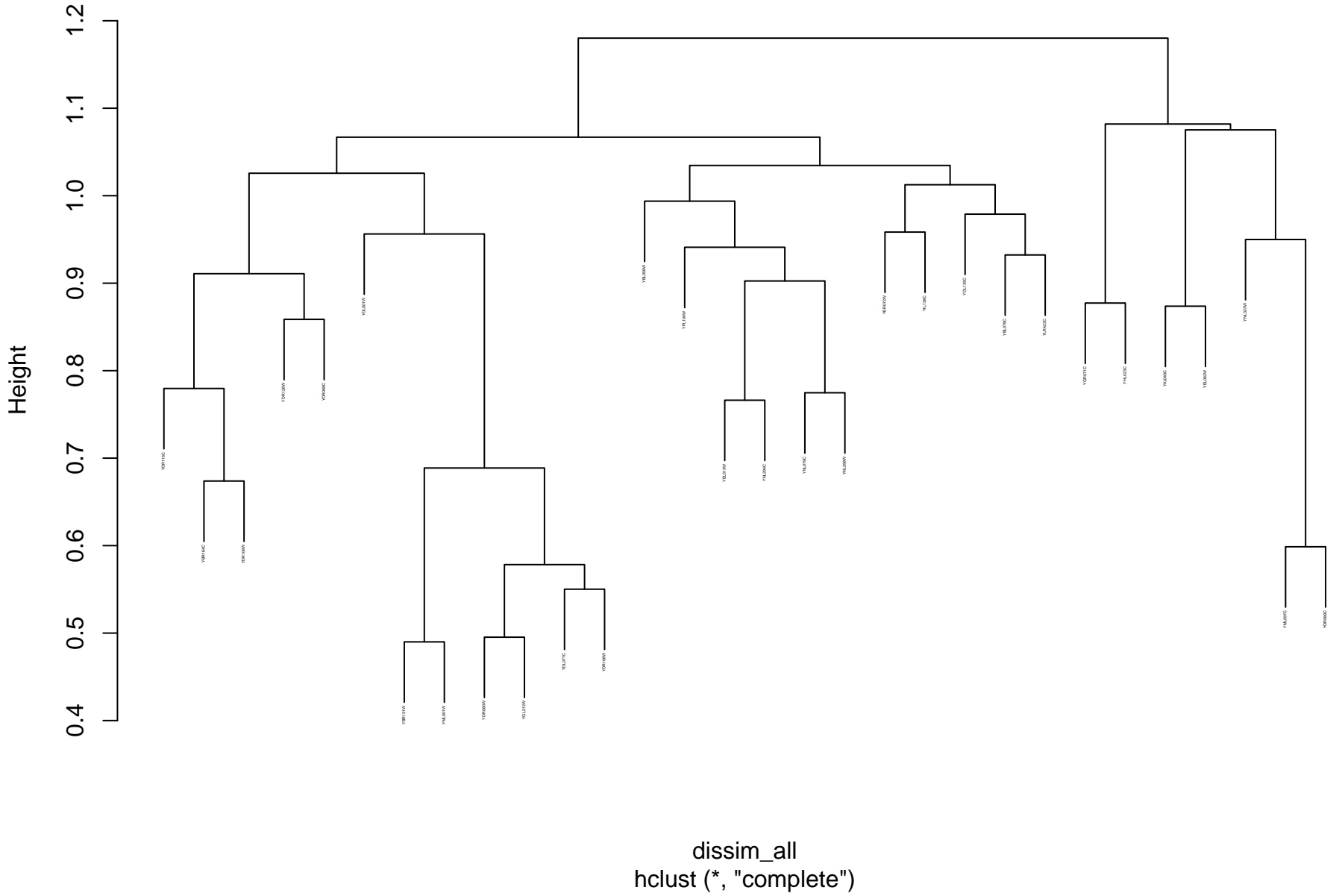
GTPase activity_GO_pearson_complete



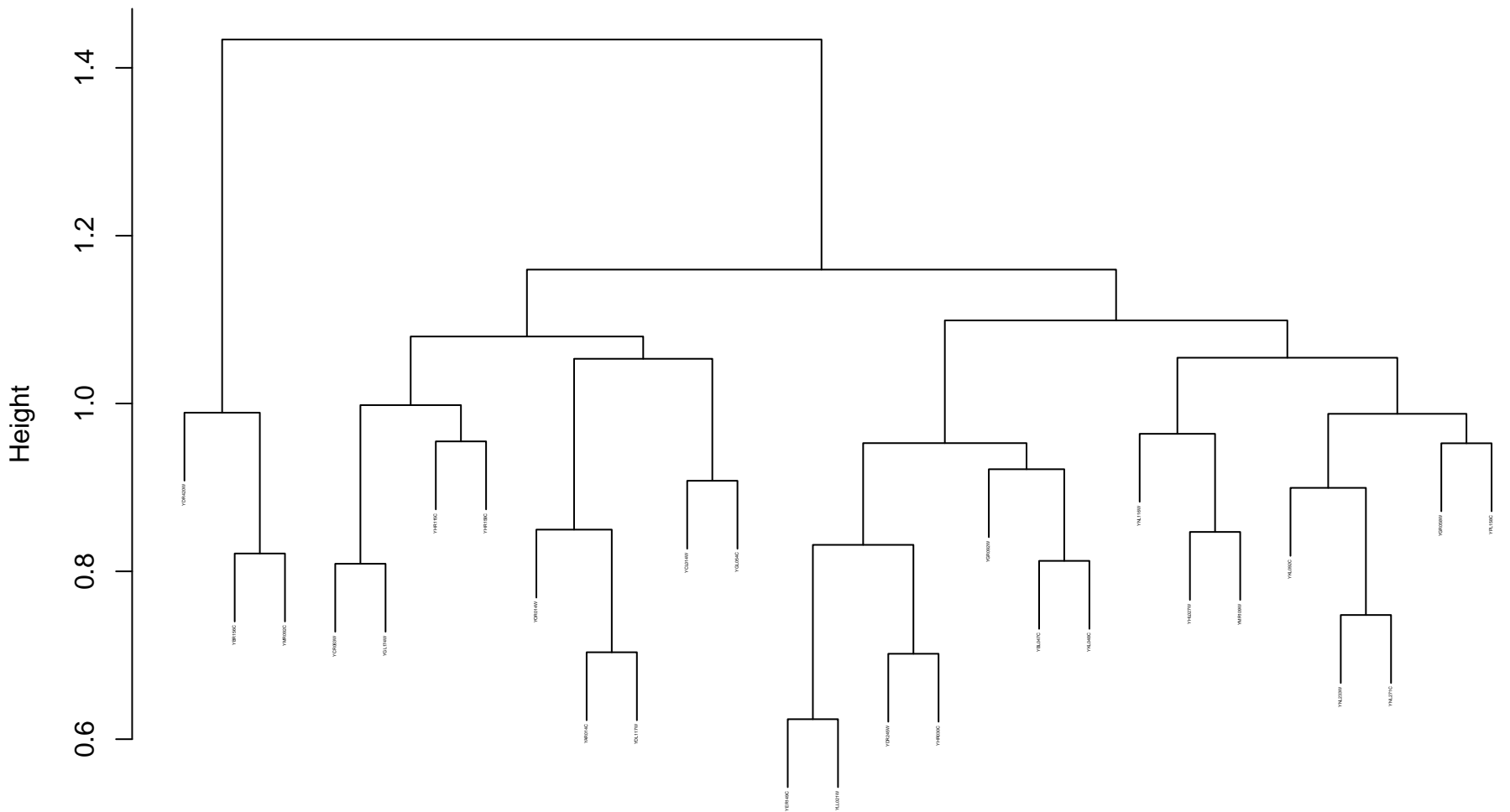
cofactor metabolic process_GO_pearson_complete

monocarboxylic acid metabolic process_GO_pearson_complete

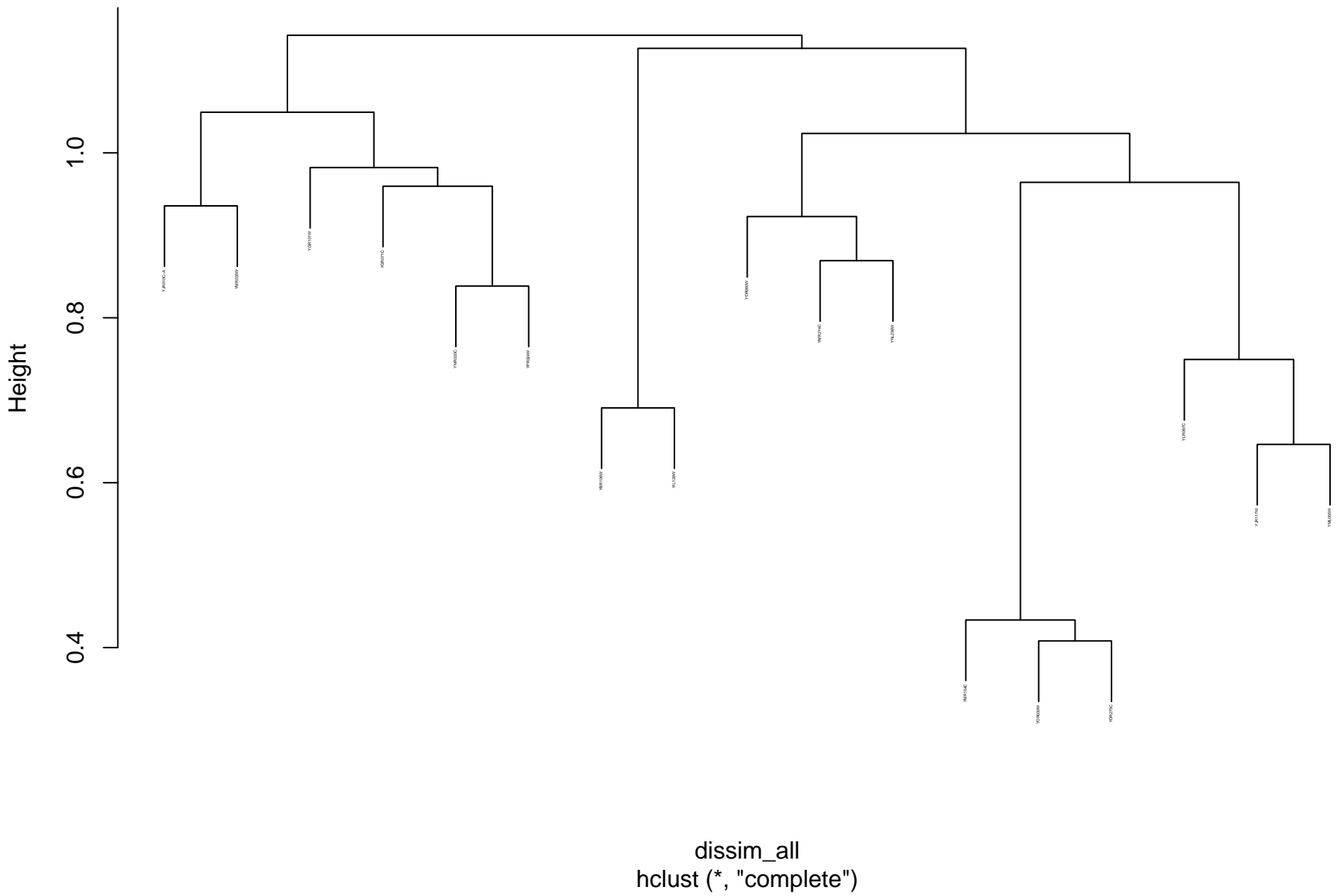


vacuole organization_GO_pearson_complete

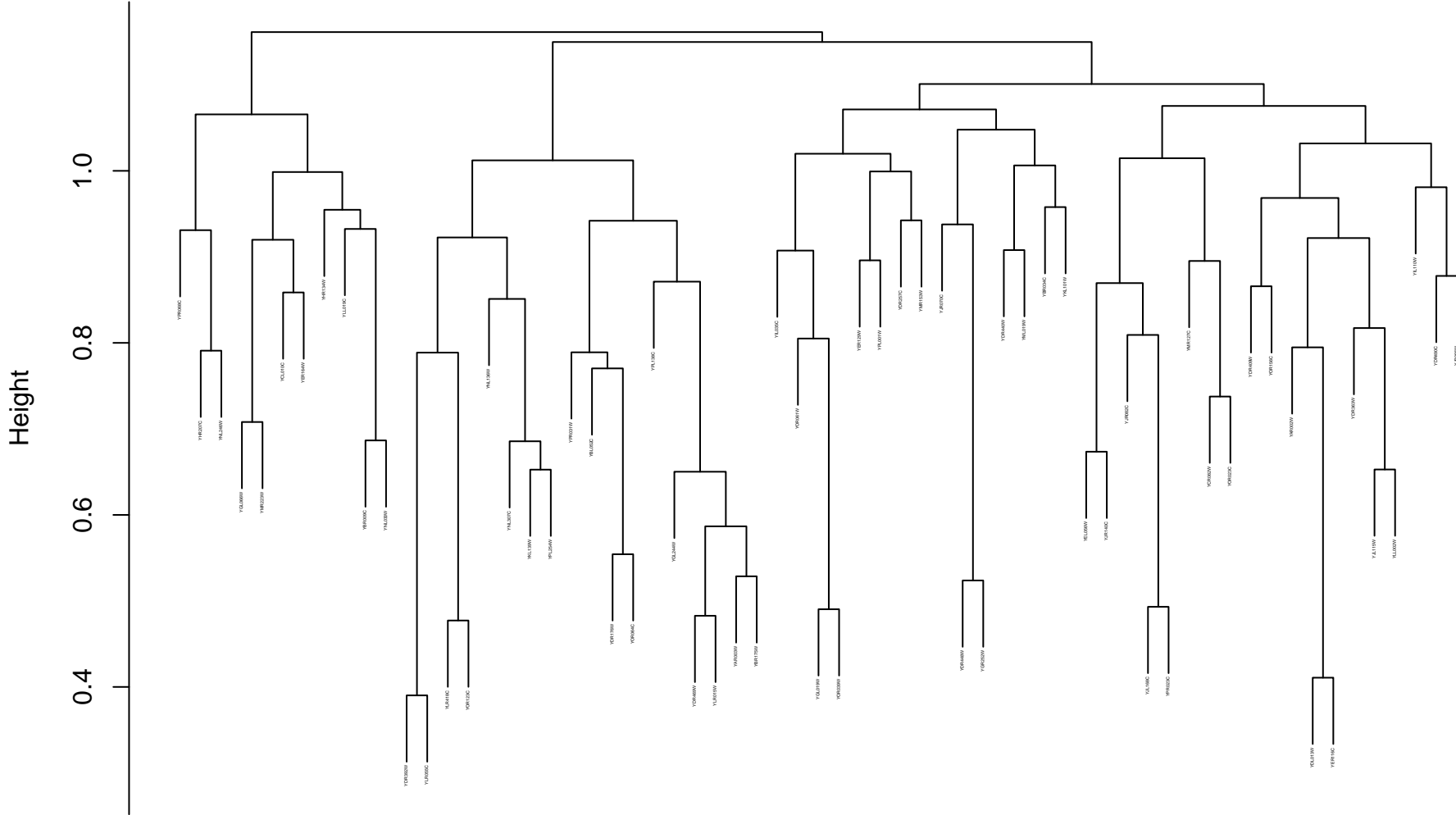
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dissim_all
hclust (*, "complete")
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protein maturation_GO_pearson_complete

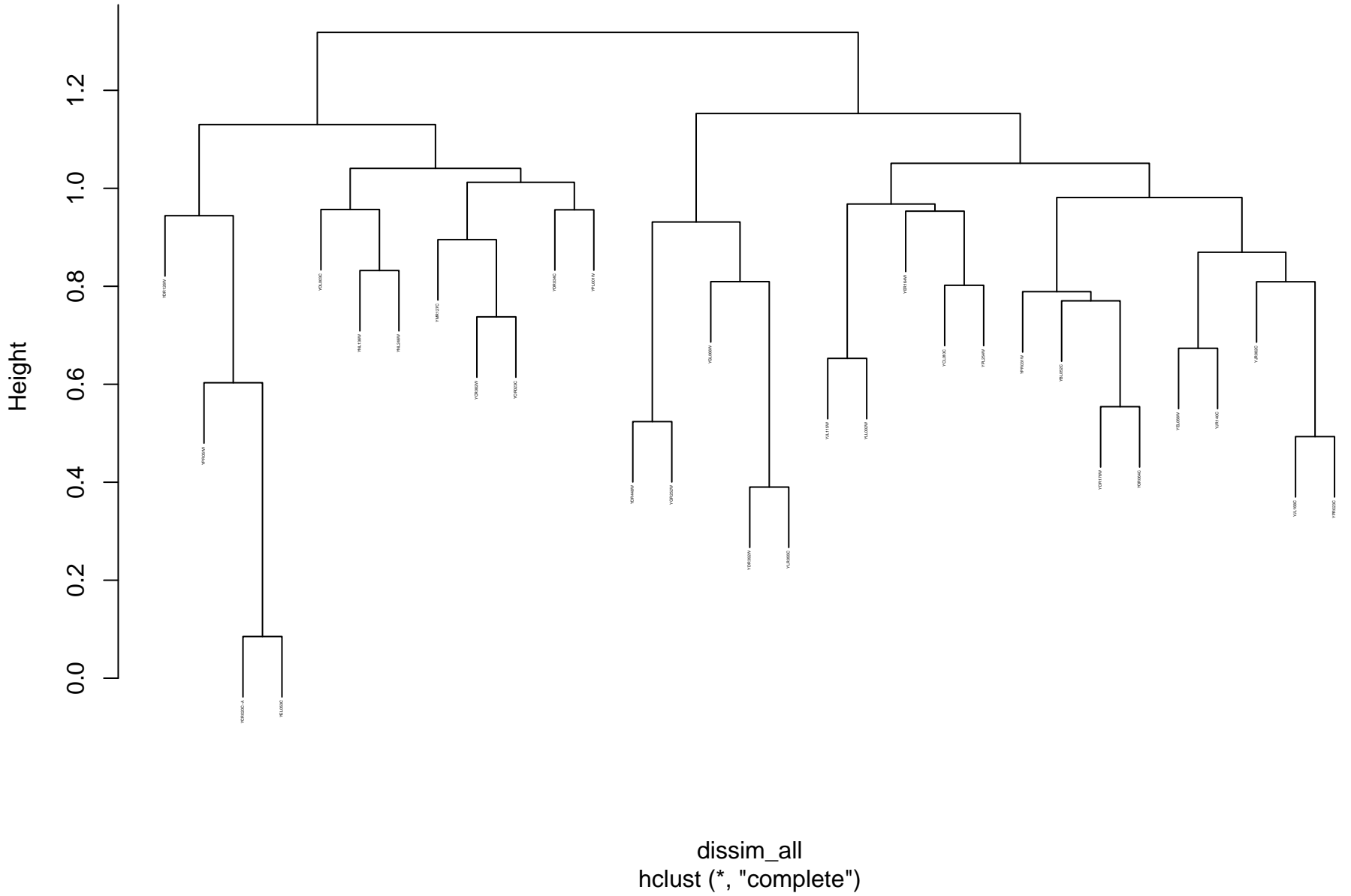


peptidyl-amino acid modification_GO_pearson_complete

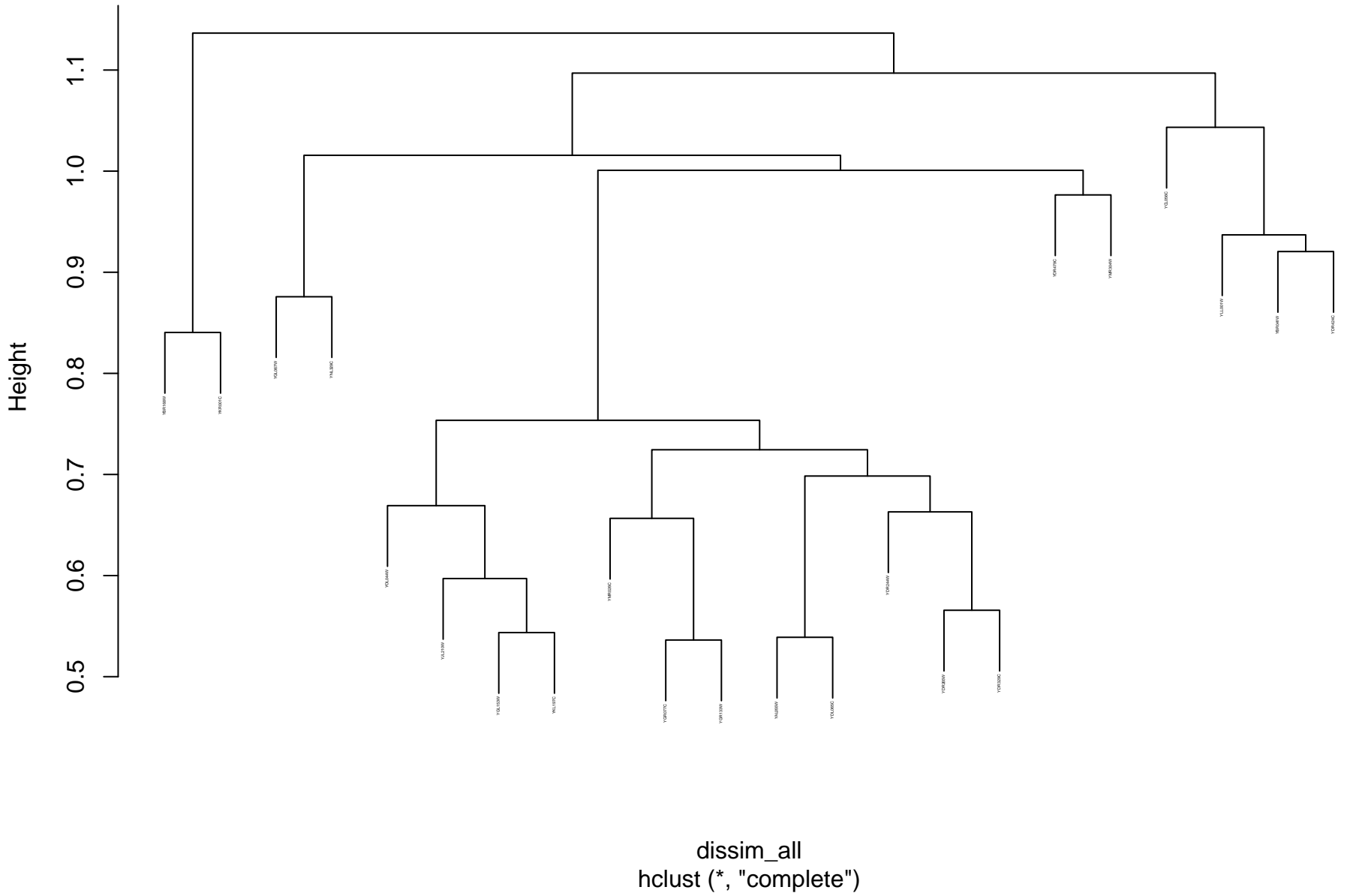


dissim_all
hclust (*, "complete")

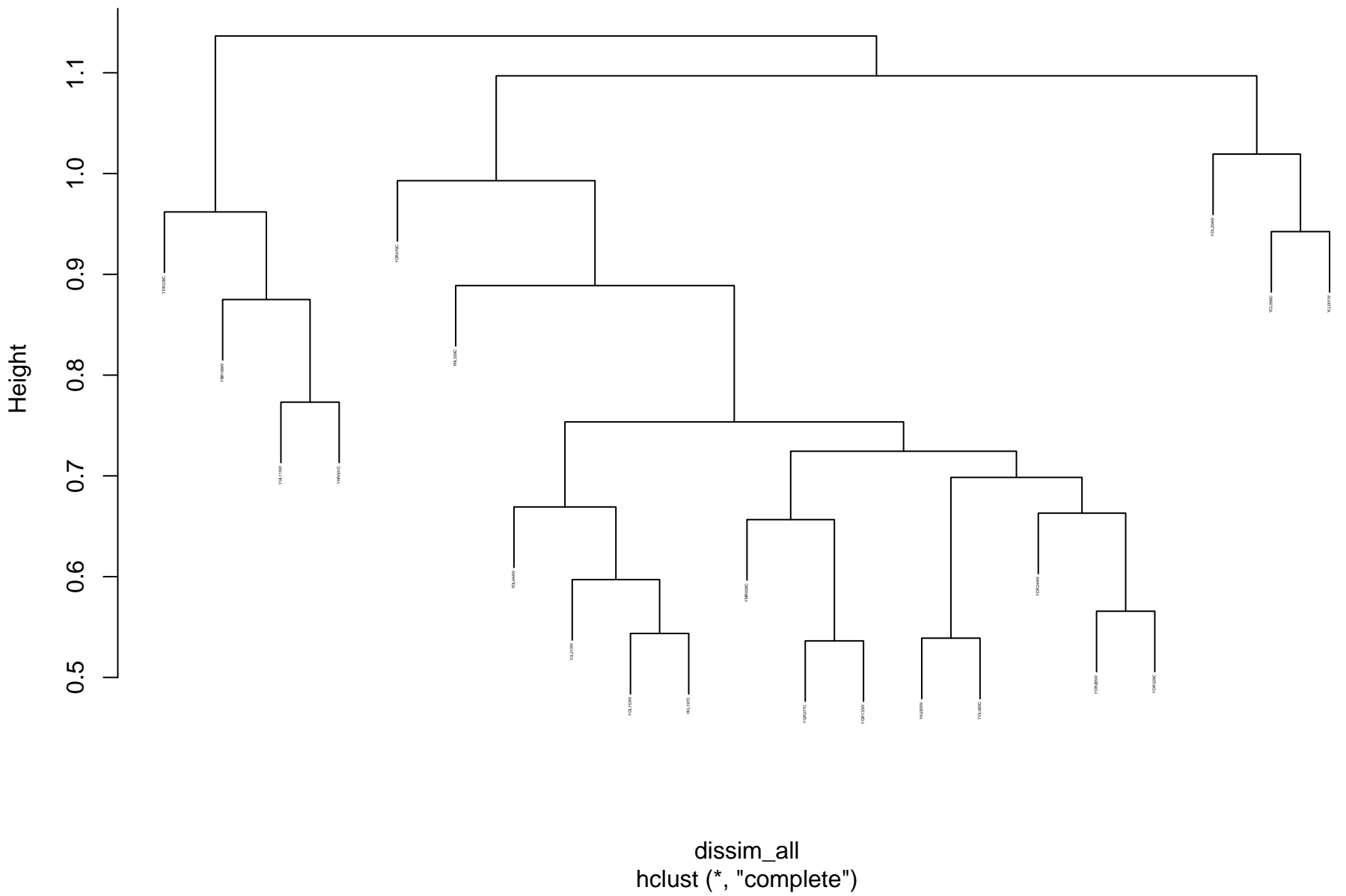
protein acylation_GO_pearson_complete



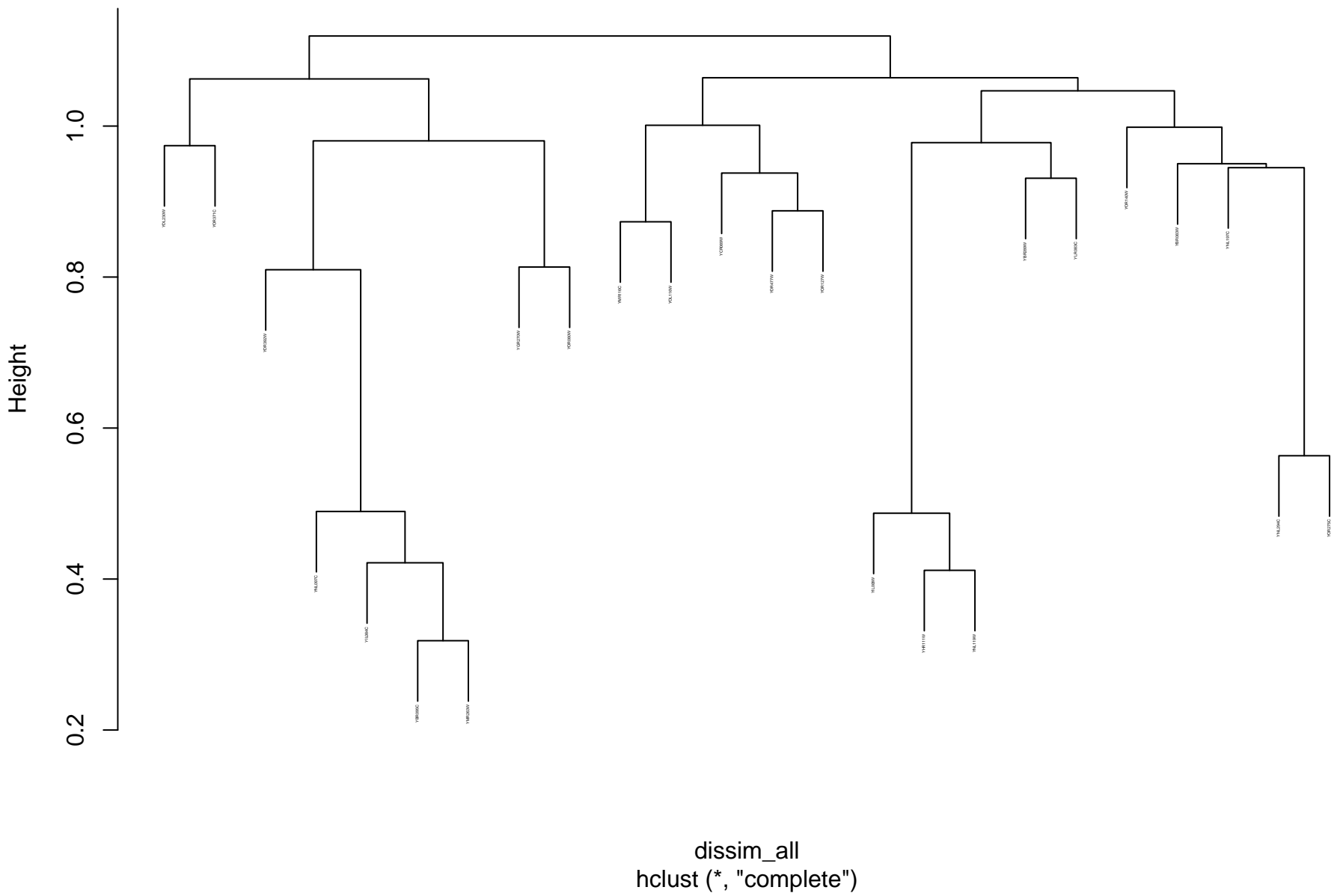
peroxisome_GO_pearson_complete



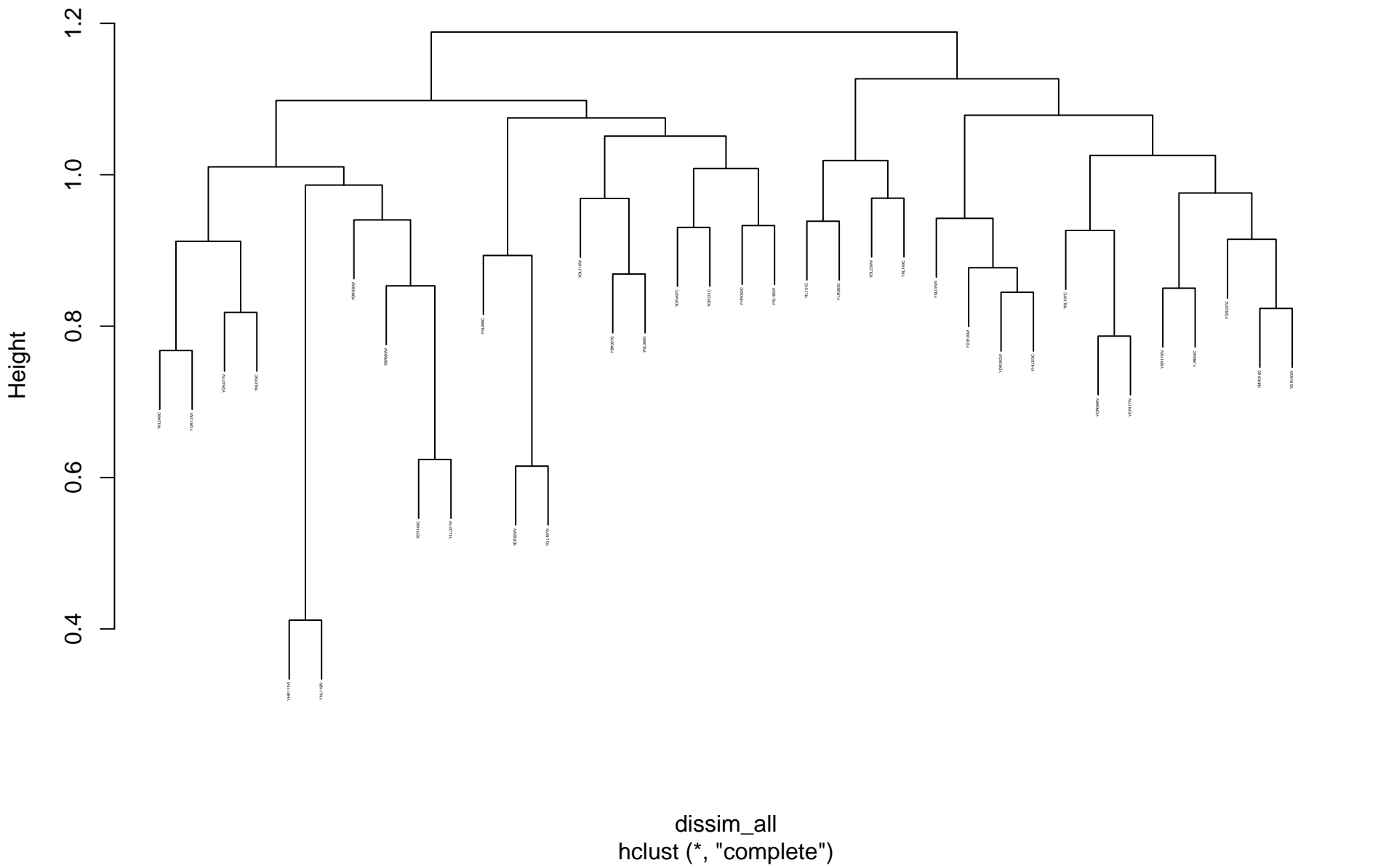
peroxisome organization_GO_pearson_complete



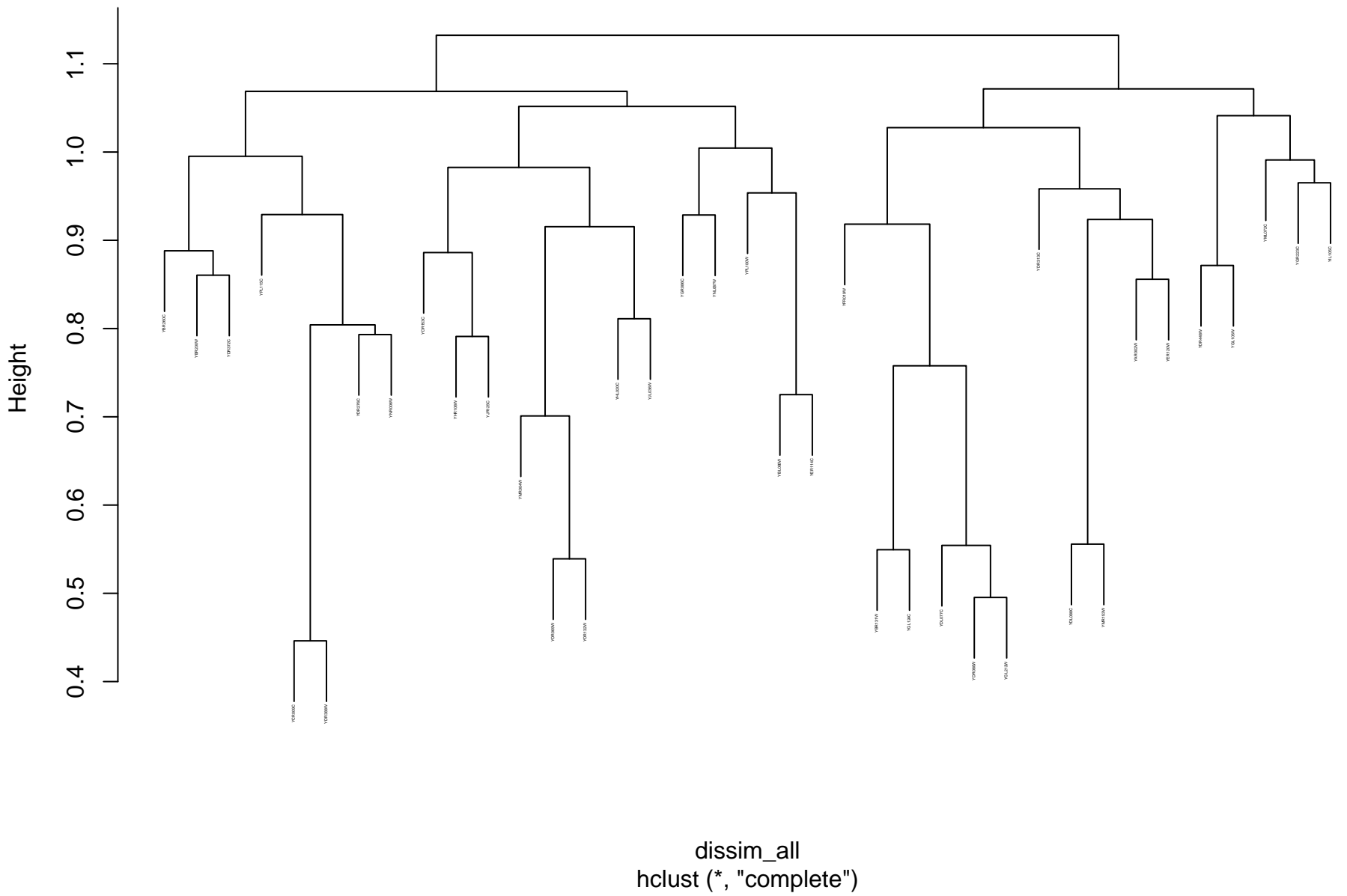
invasive growth in response to glucose limitation_GO_pearson_complete



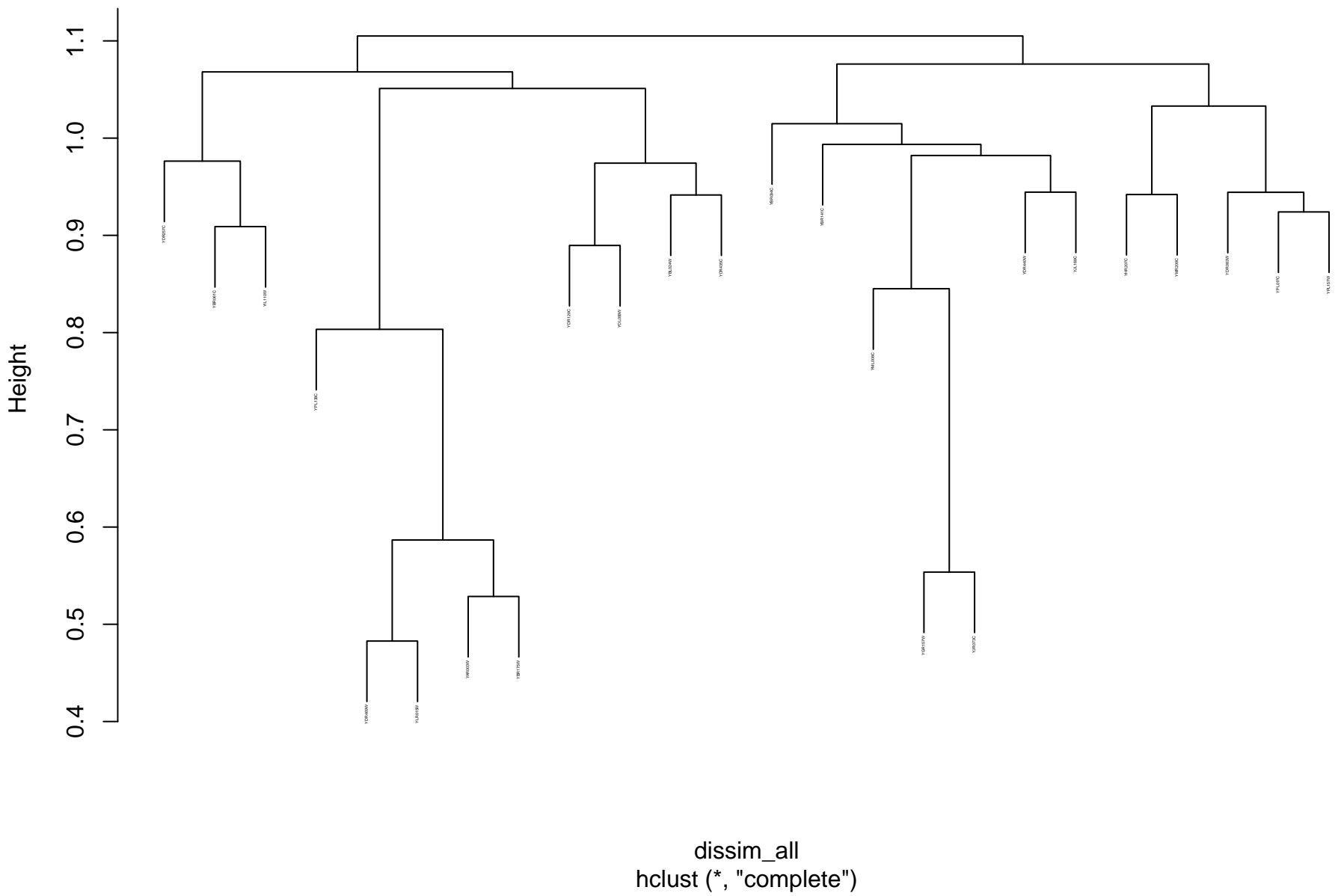
pseudohyphal growth_GO_pearson_complete



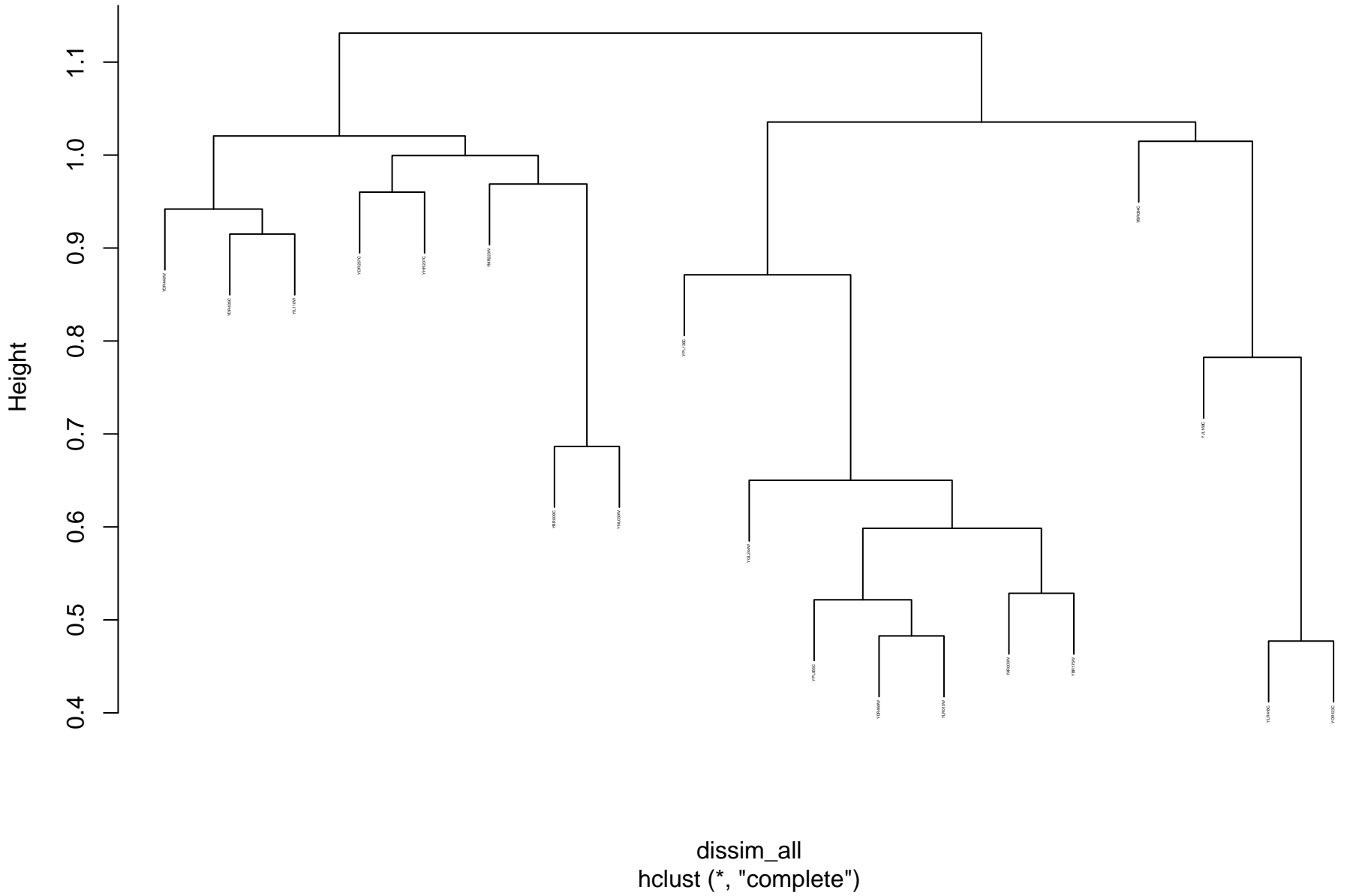
lipid binding_GO_pearson_complete



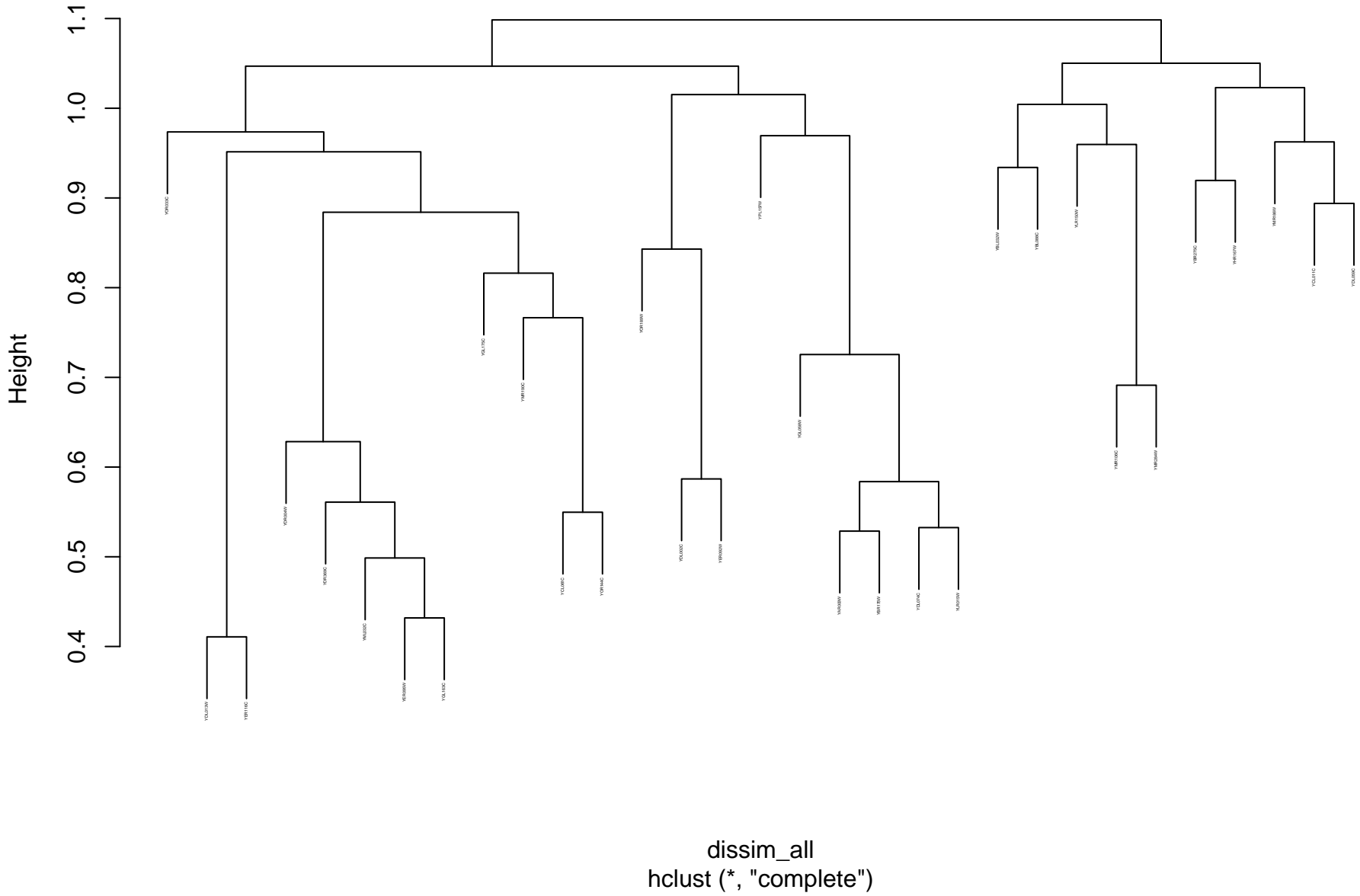
methyltransferase activity_GO_pearson_complete



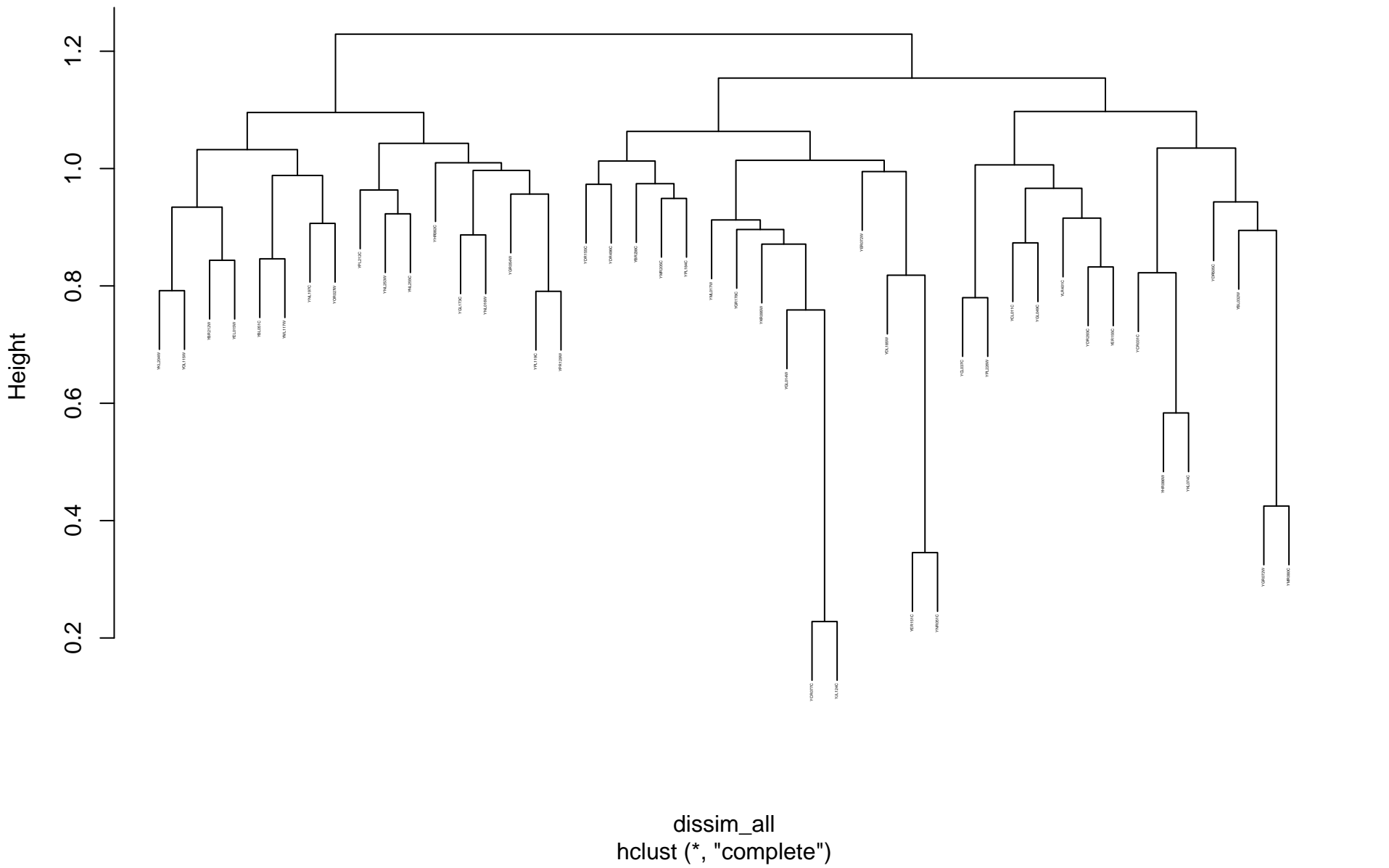
protein alkylation_GO_pearson_complete



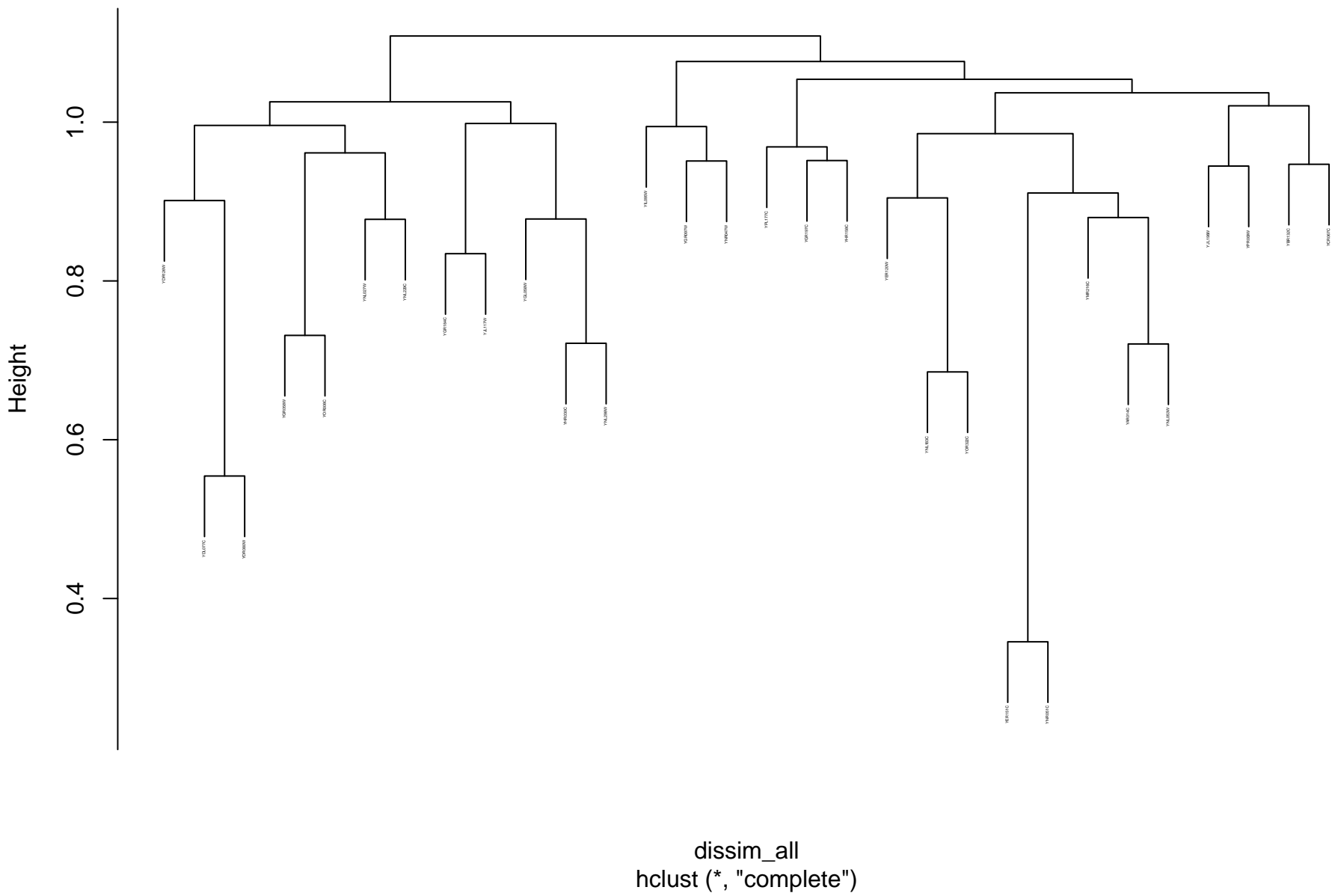
telomere organization_GO_pearson_complete



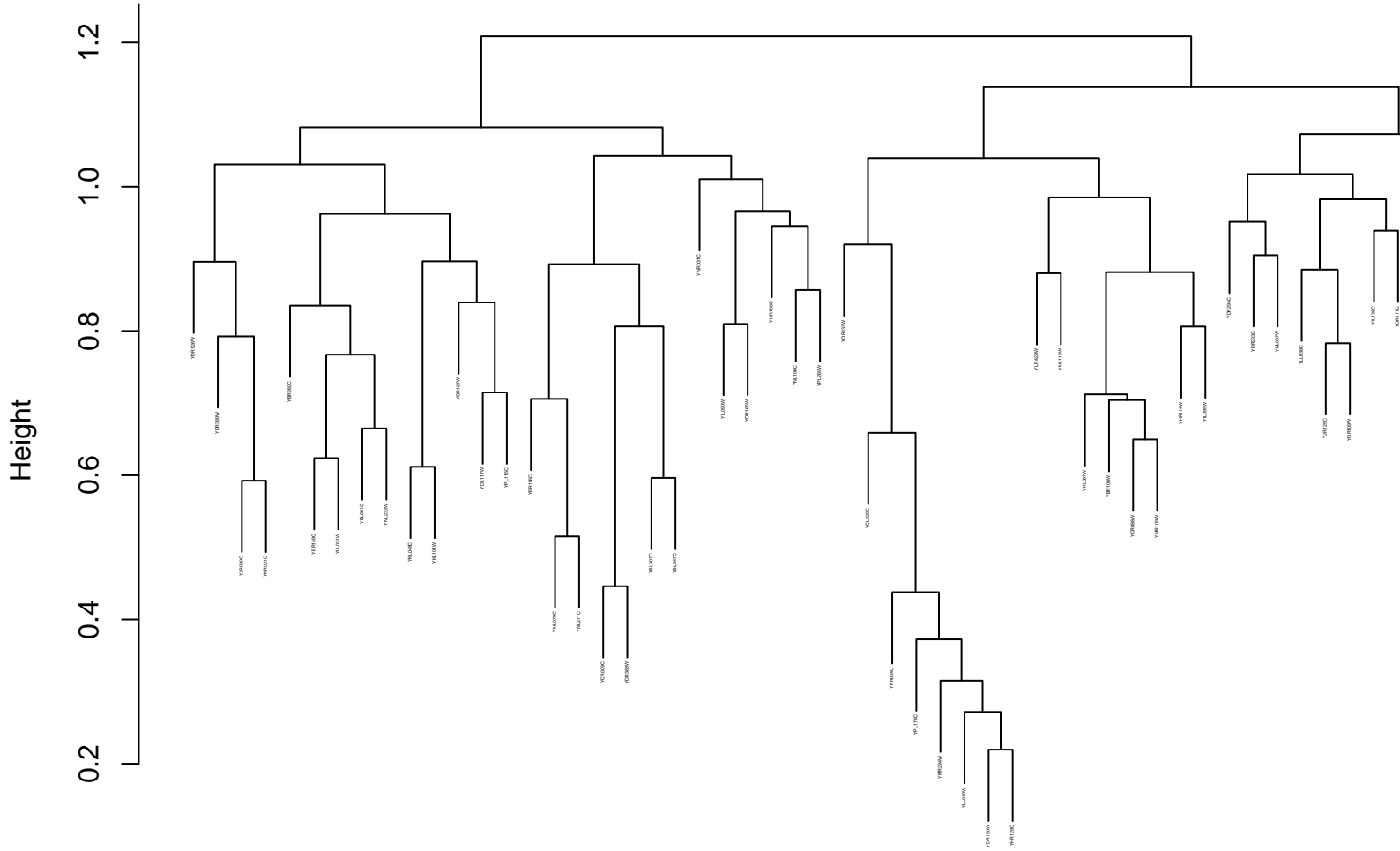
mRNA binding_GO_pearson_complete



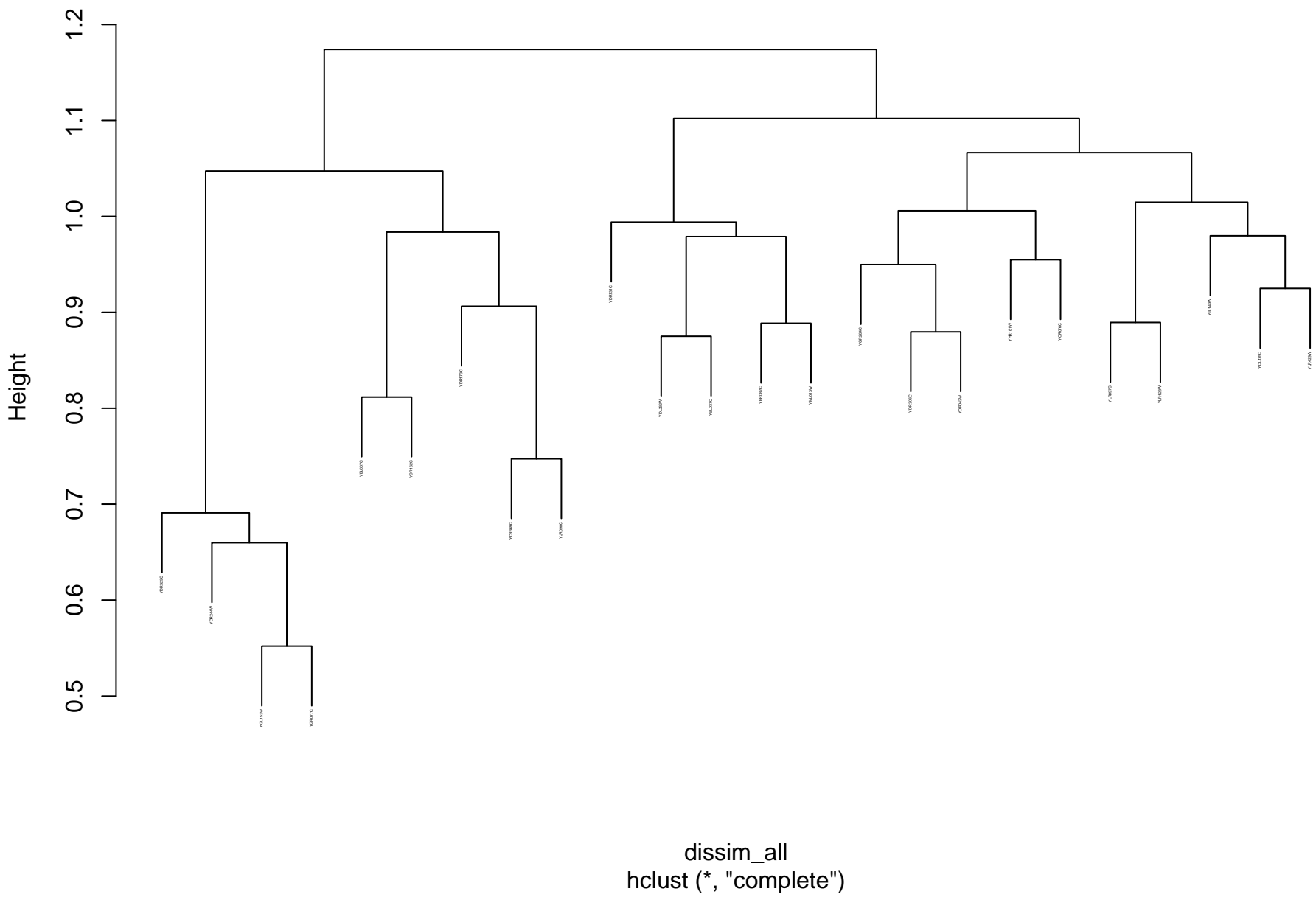
regulation of transport_GO_pearson_complete



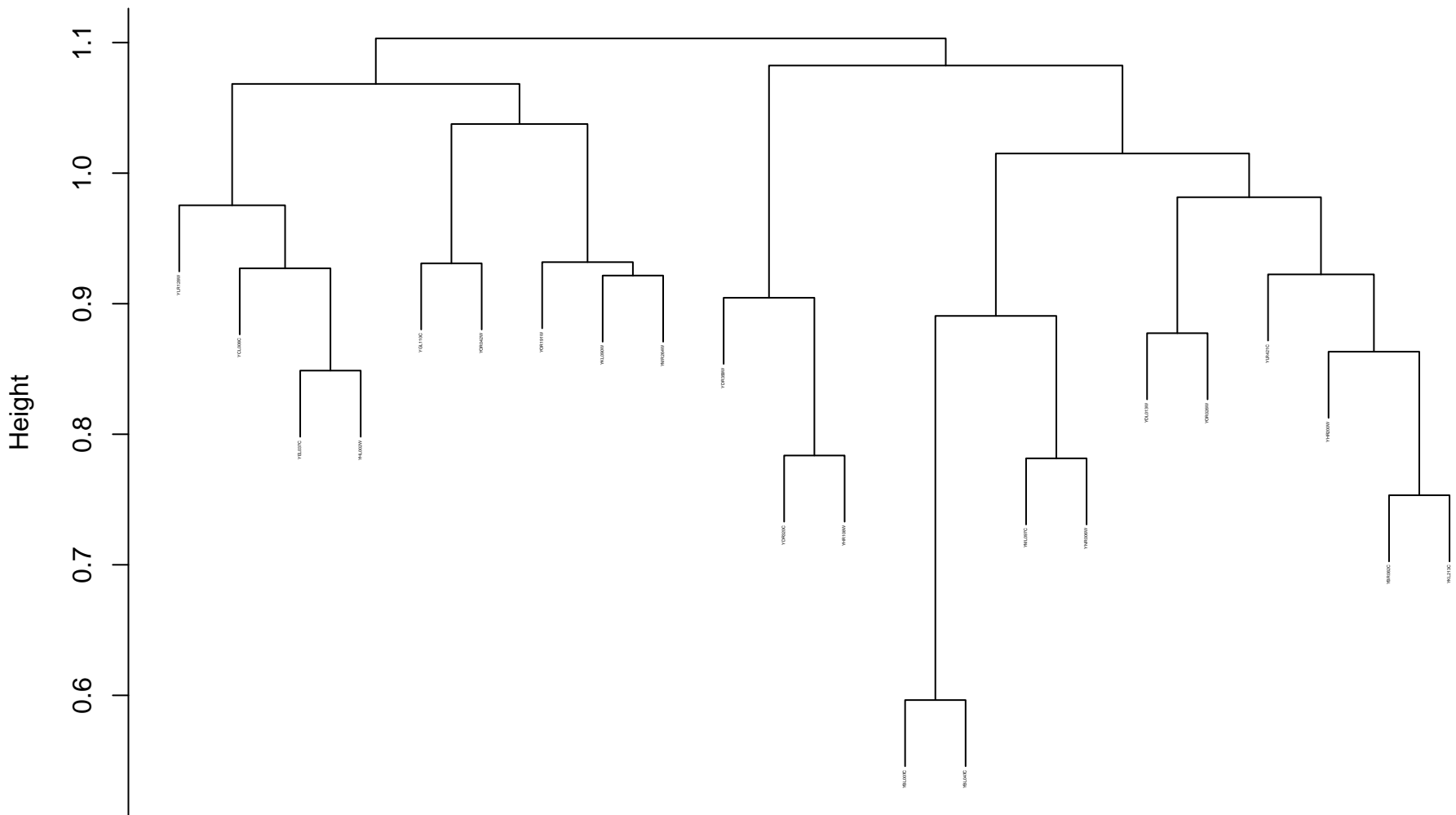
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dissim_all
hclust (*, "complete")
```



protein binding, bridging_GO_pearson_complete

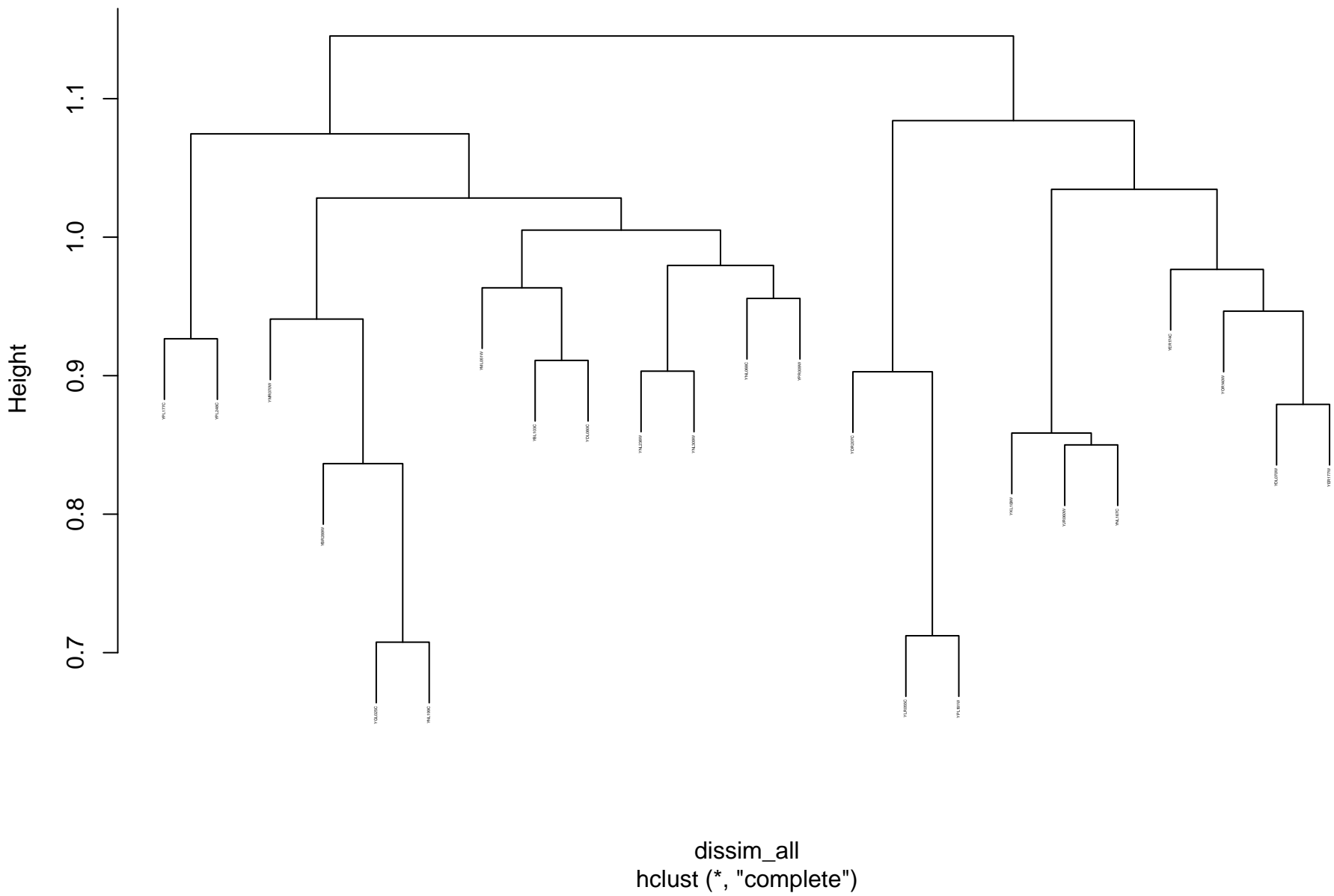


ubiquitin-like protein binding_GO_pearson_complete

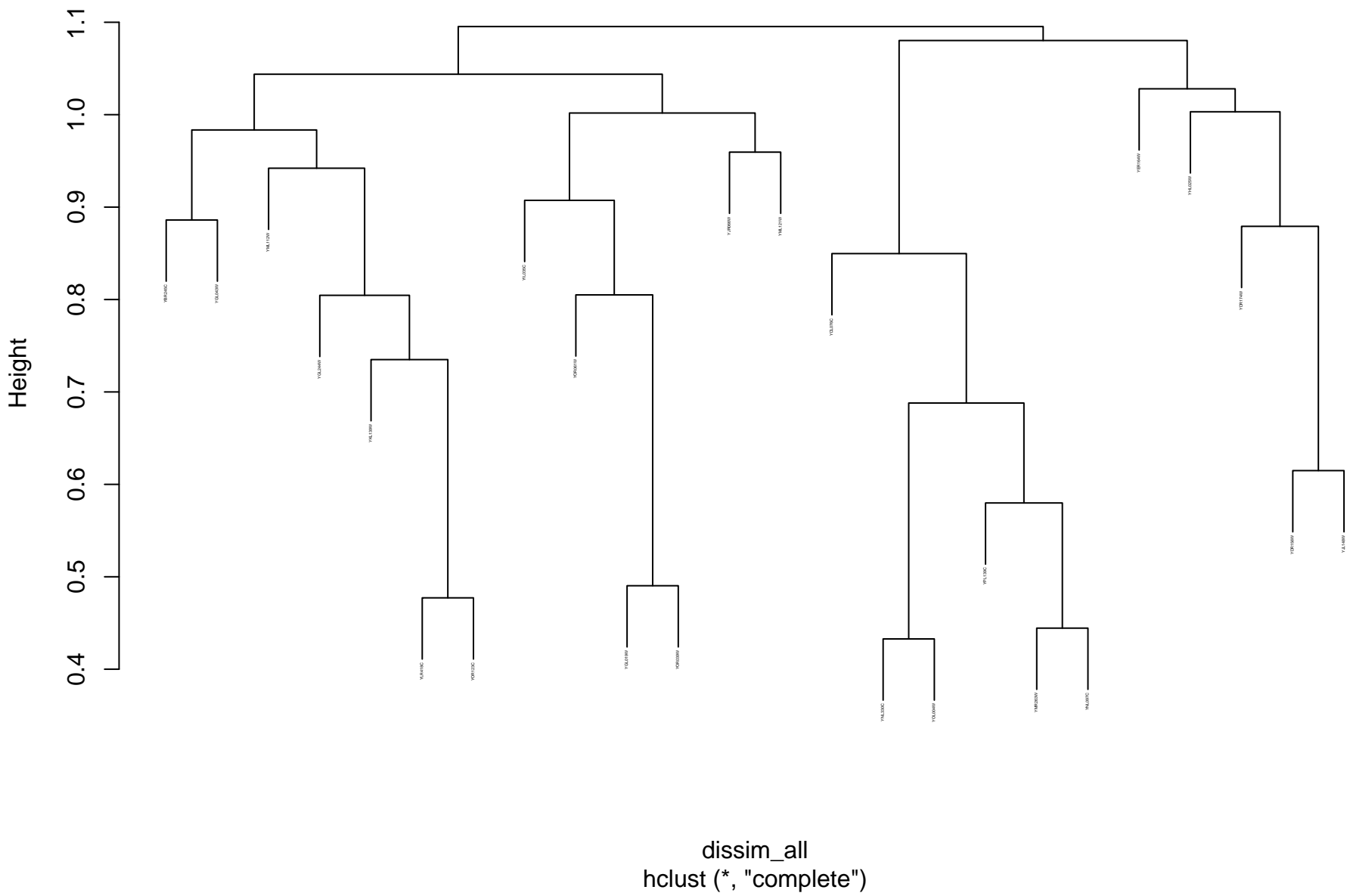


```
dissim_all
hclust (*, "complete")
```

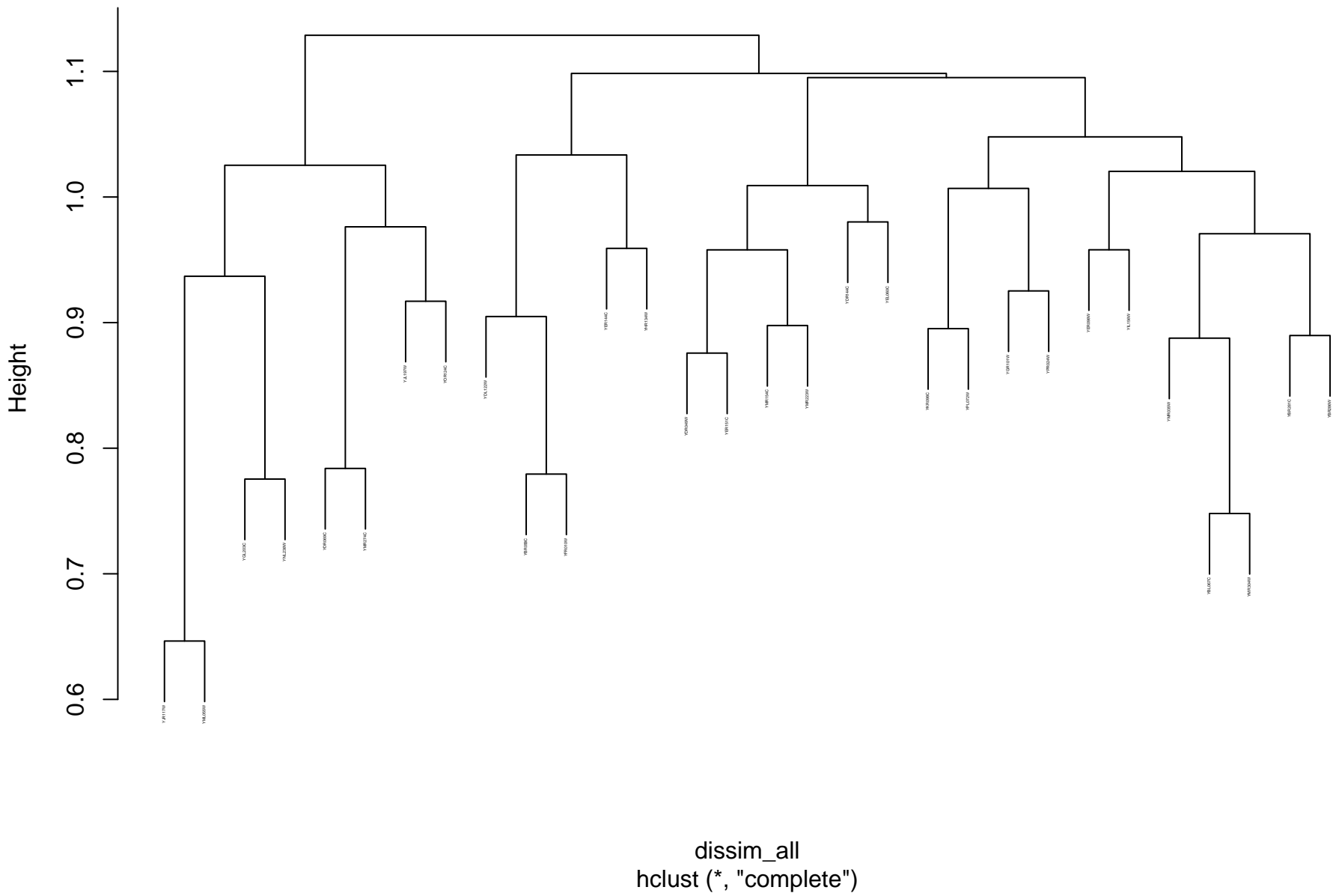
transcription factor binding_GO_pearson_complete



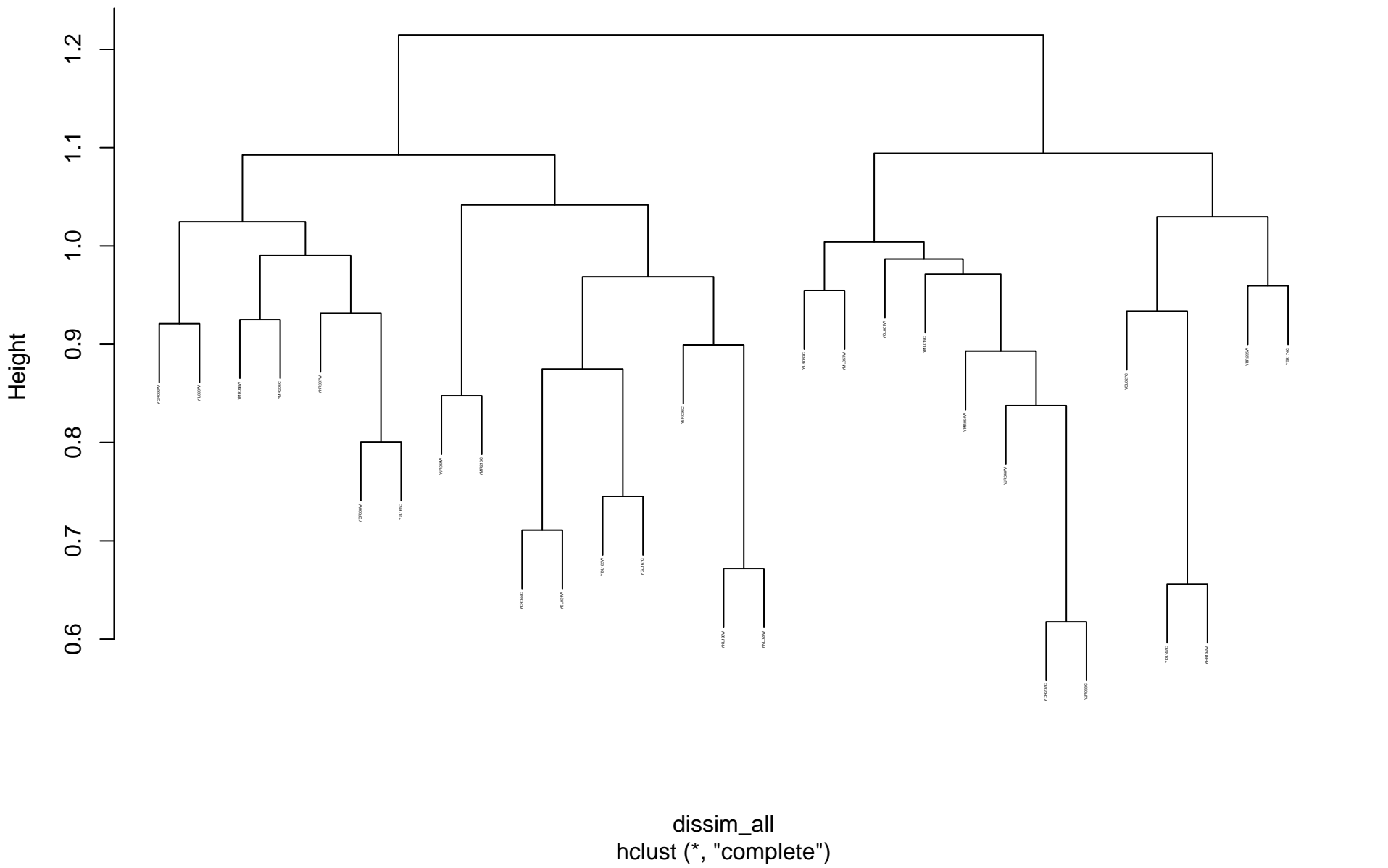
transcription from RNA polymerase I promoter_GO_pearson_complete



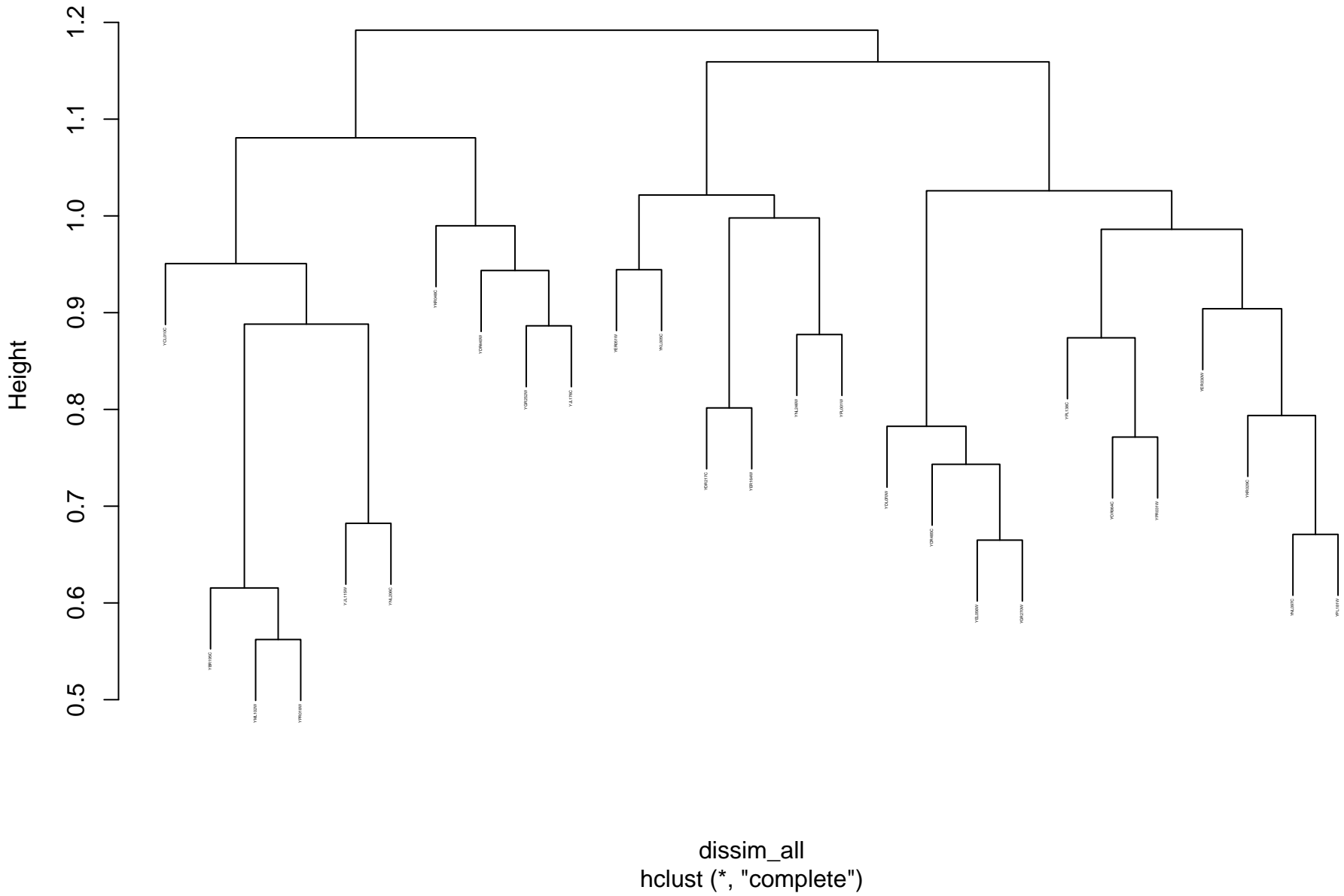
peptidase activity_GO_pearson_complete



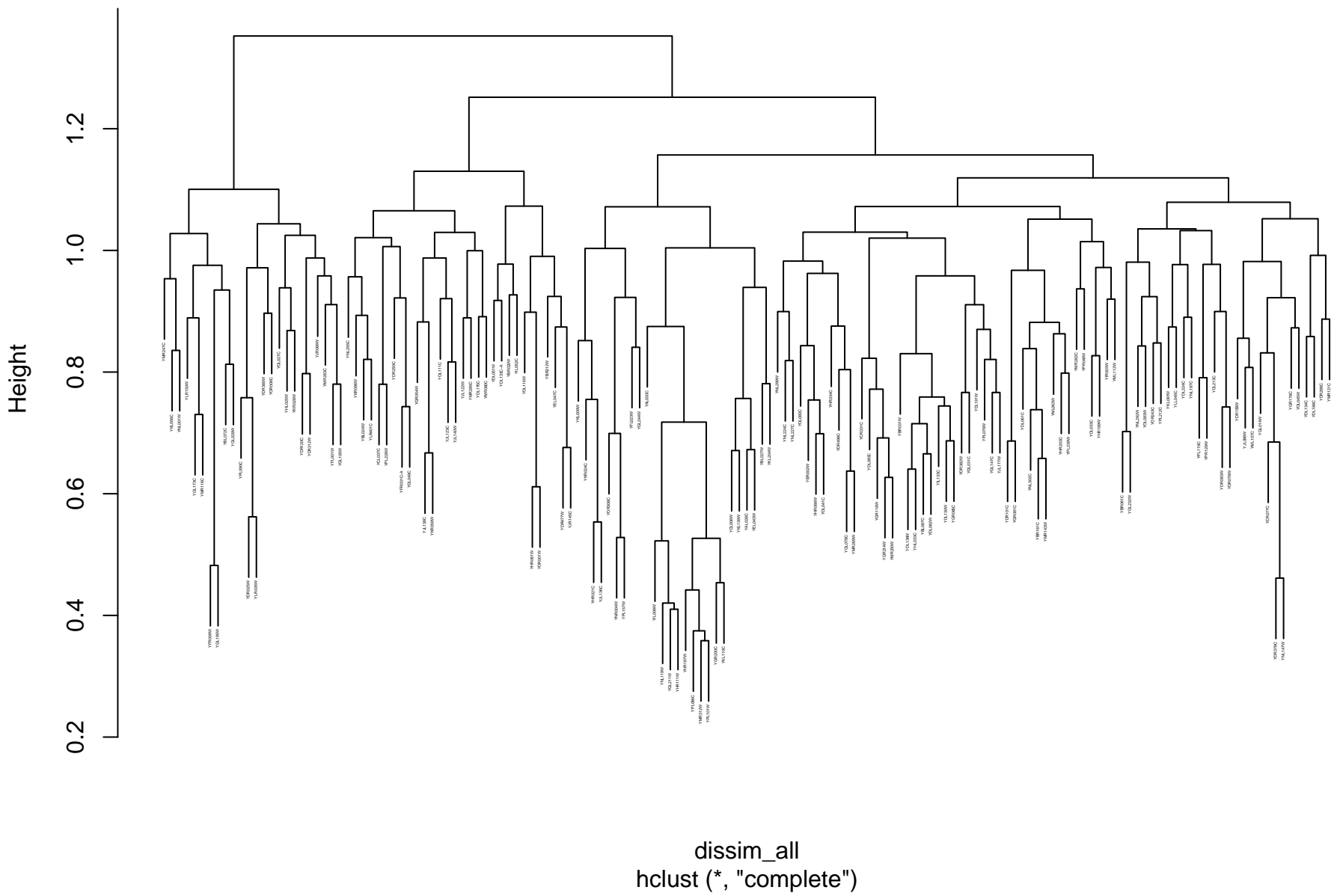
cellular ion homeostasis_GO_pearson_complete



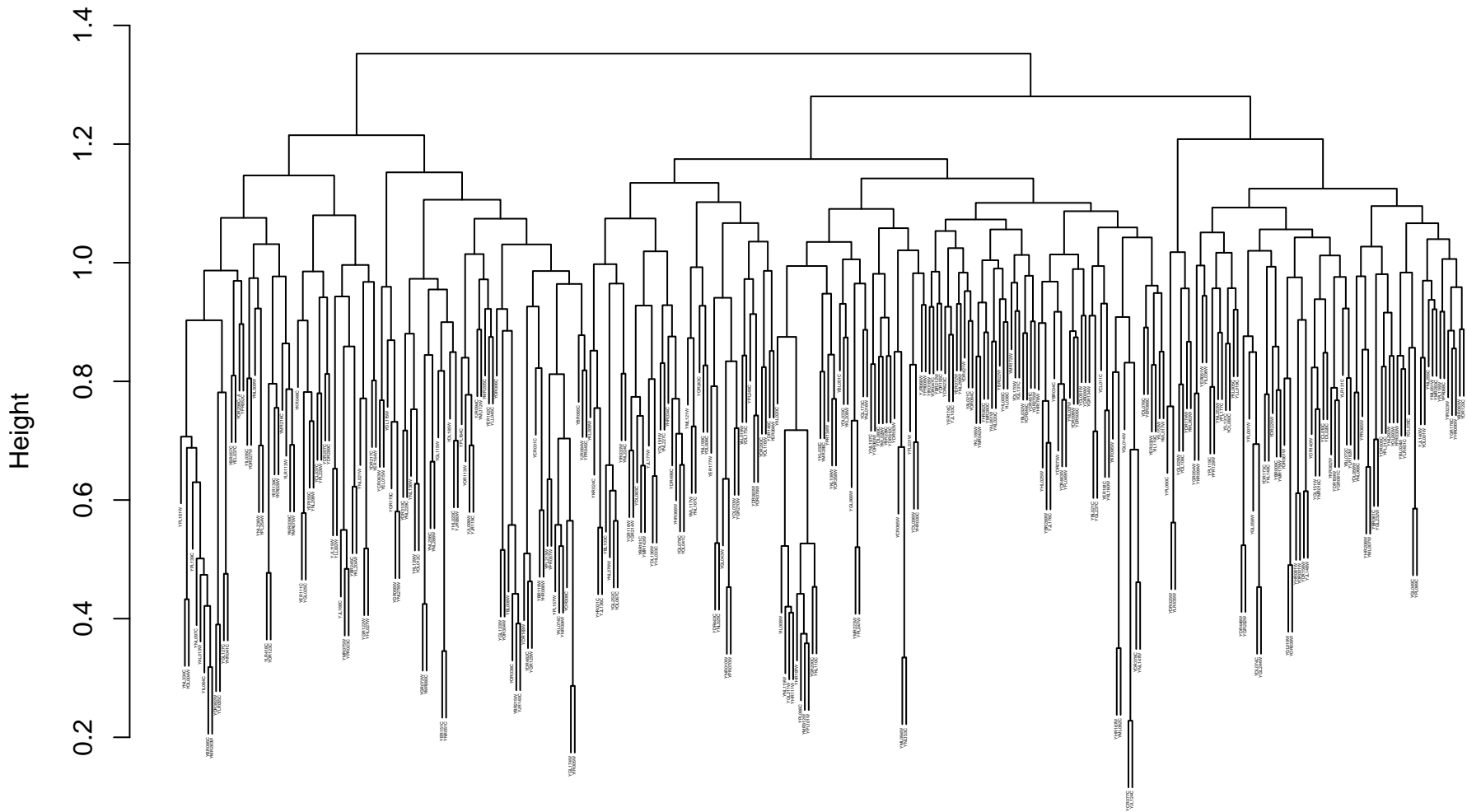
histone binding_GO_pearson_complete



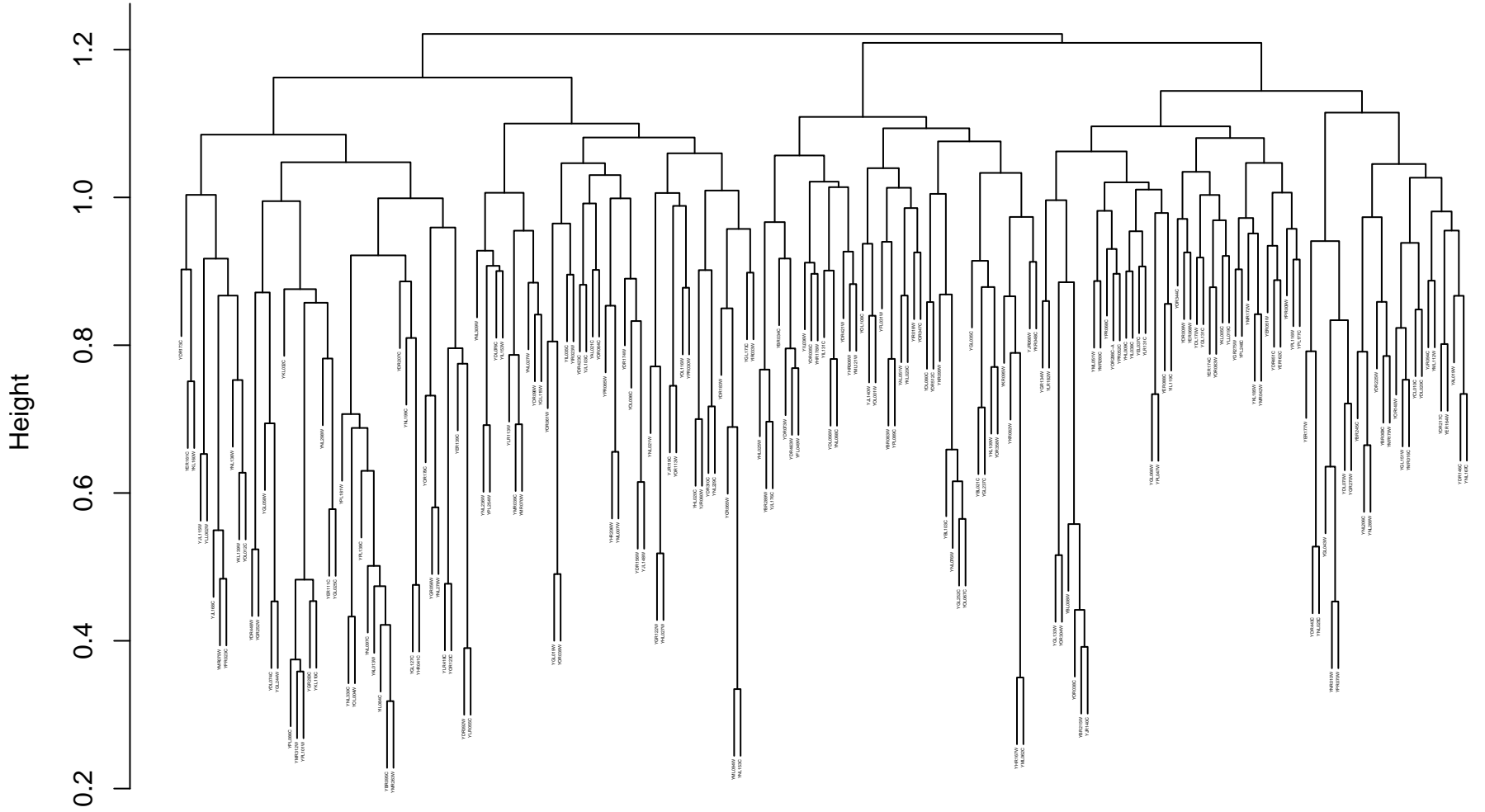
ribosomes and translation_GO_pearson_complete



transcription and mRNA processing_GO_pearson_complete

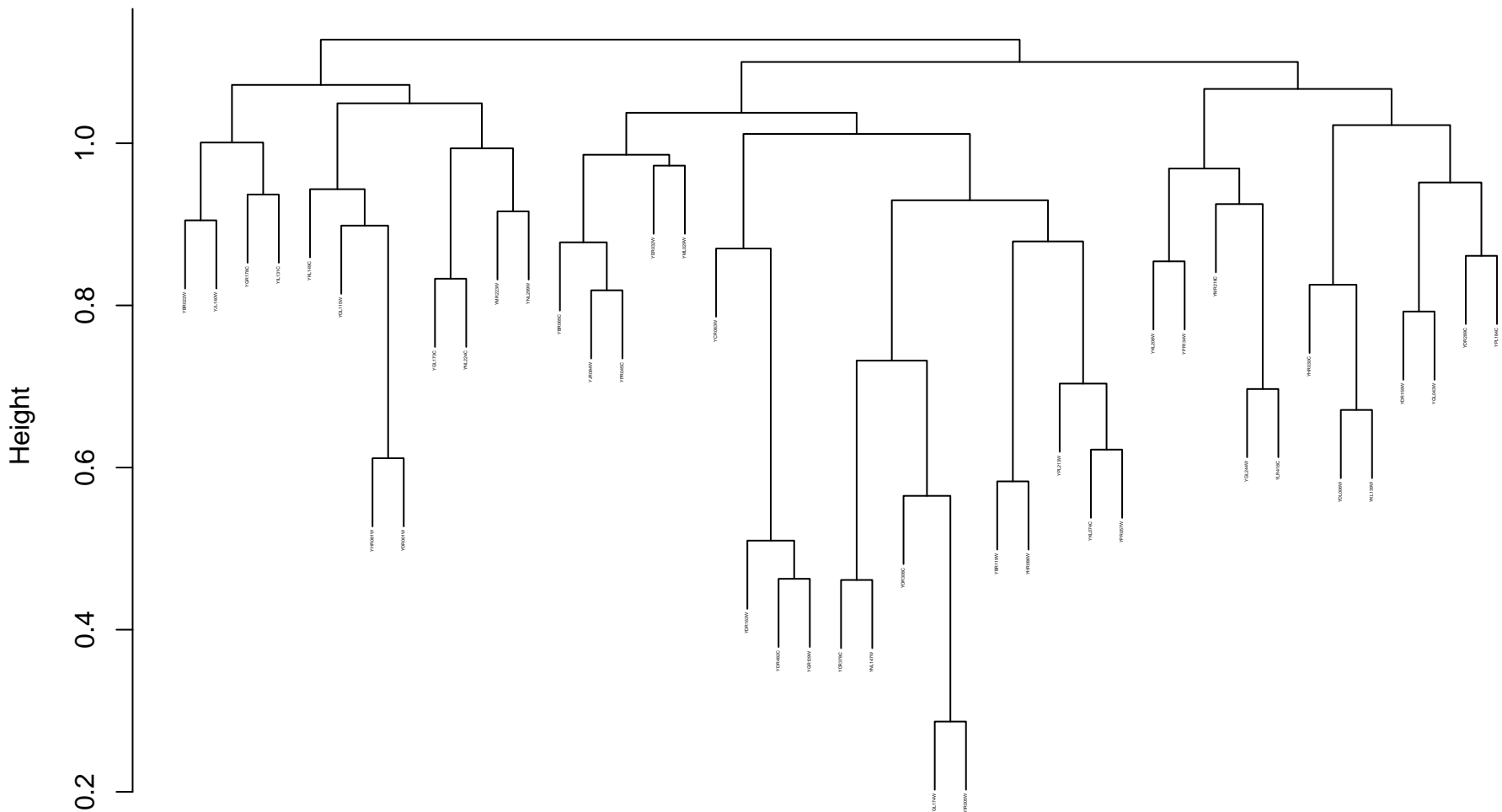


transcription_GO_pearson_complete

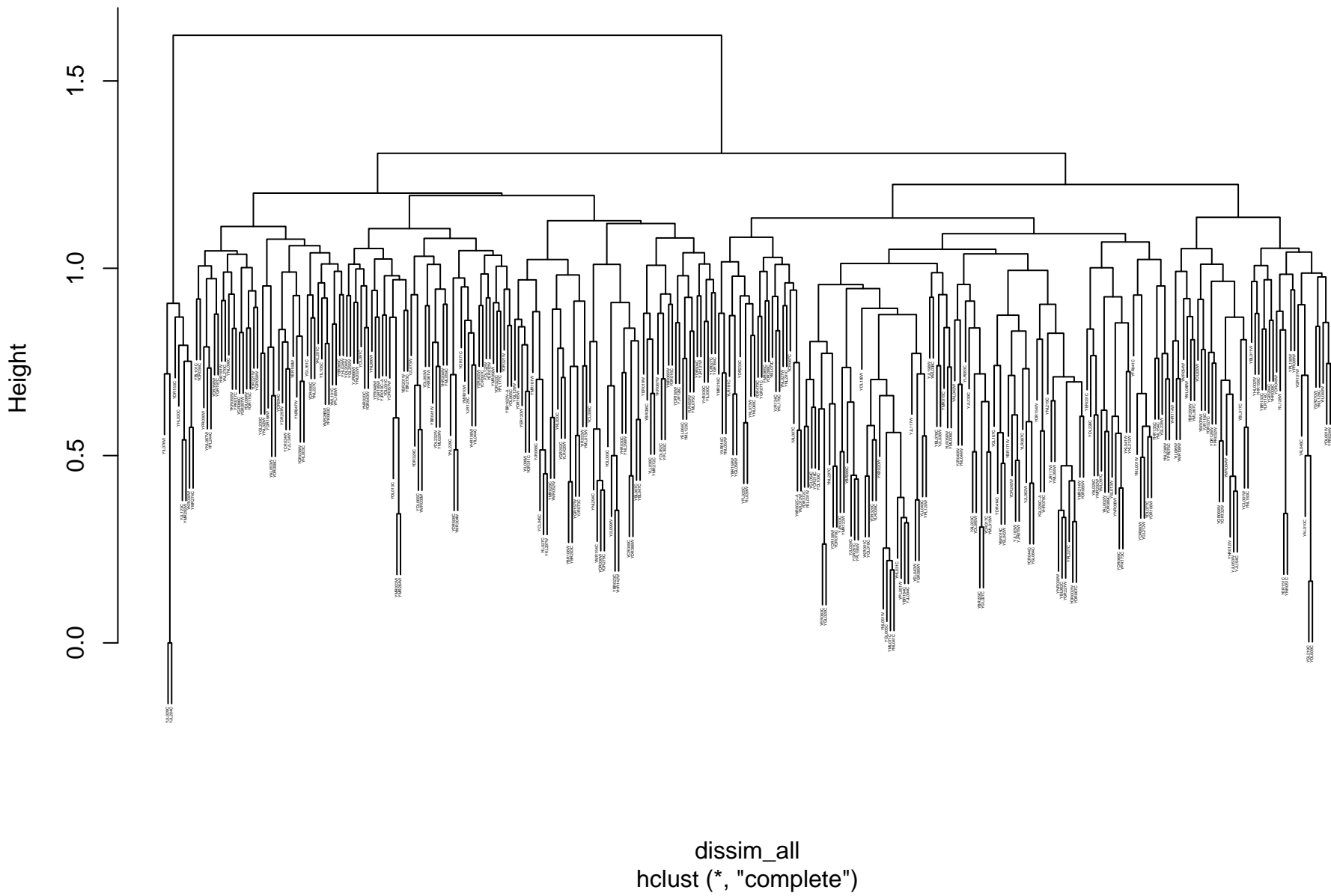


```
dissim_all
hclust (*, "complete")
```

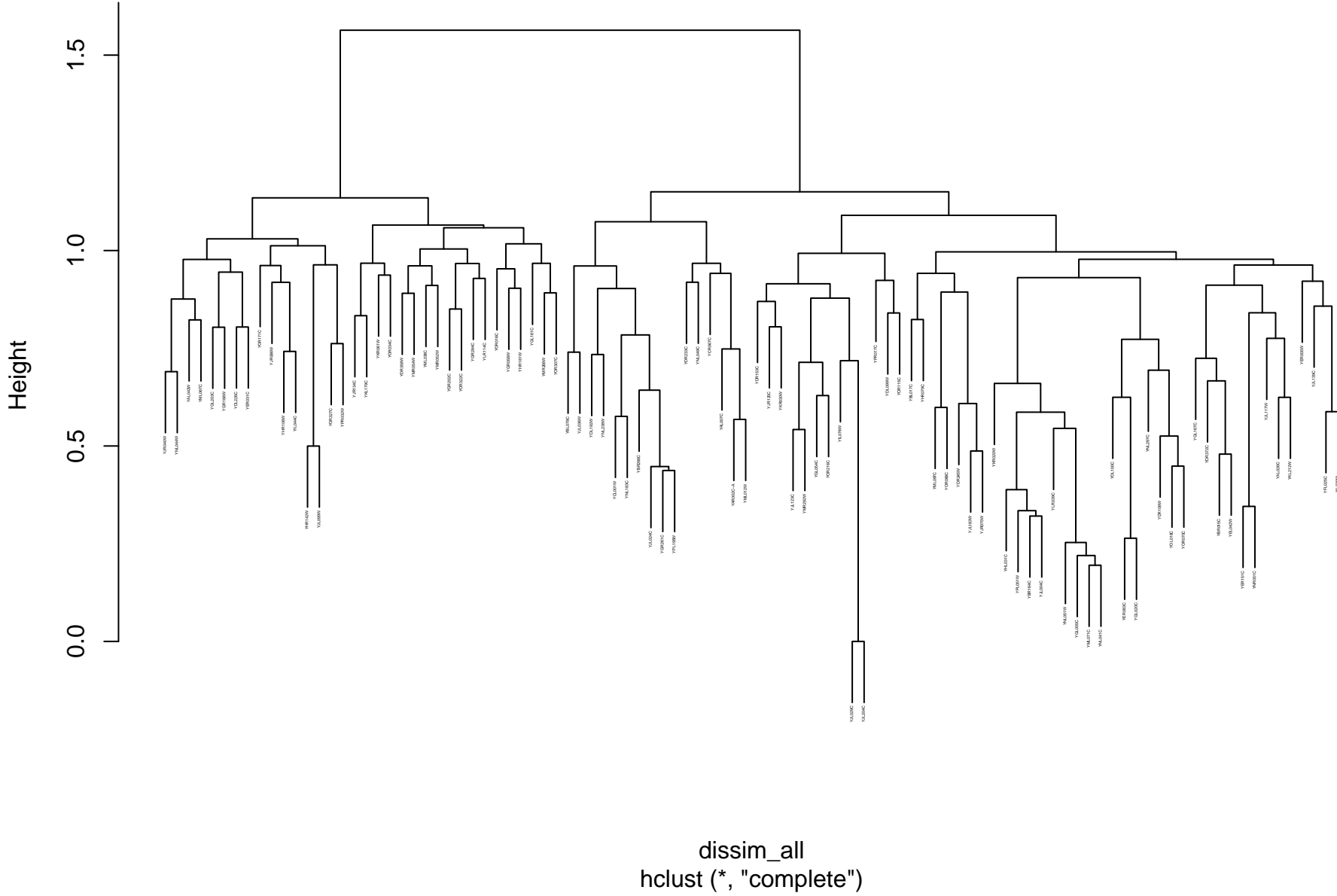
```
dissim_all
hclust (*, "complete")
```



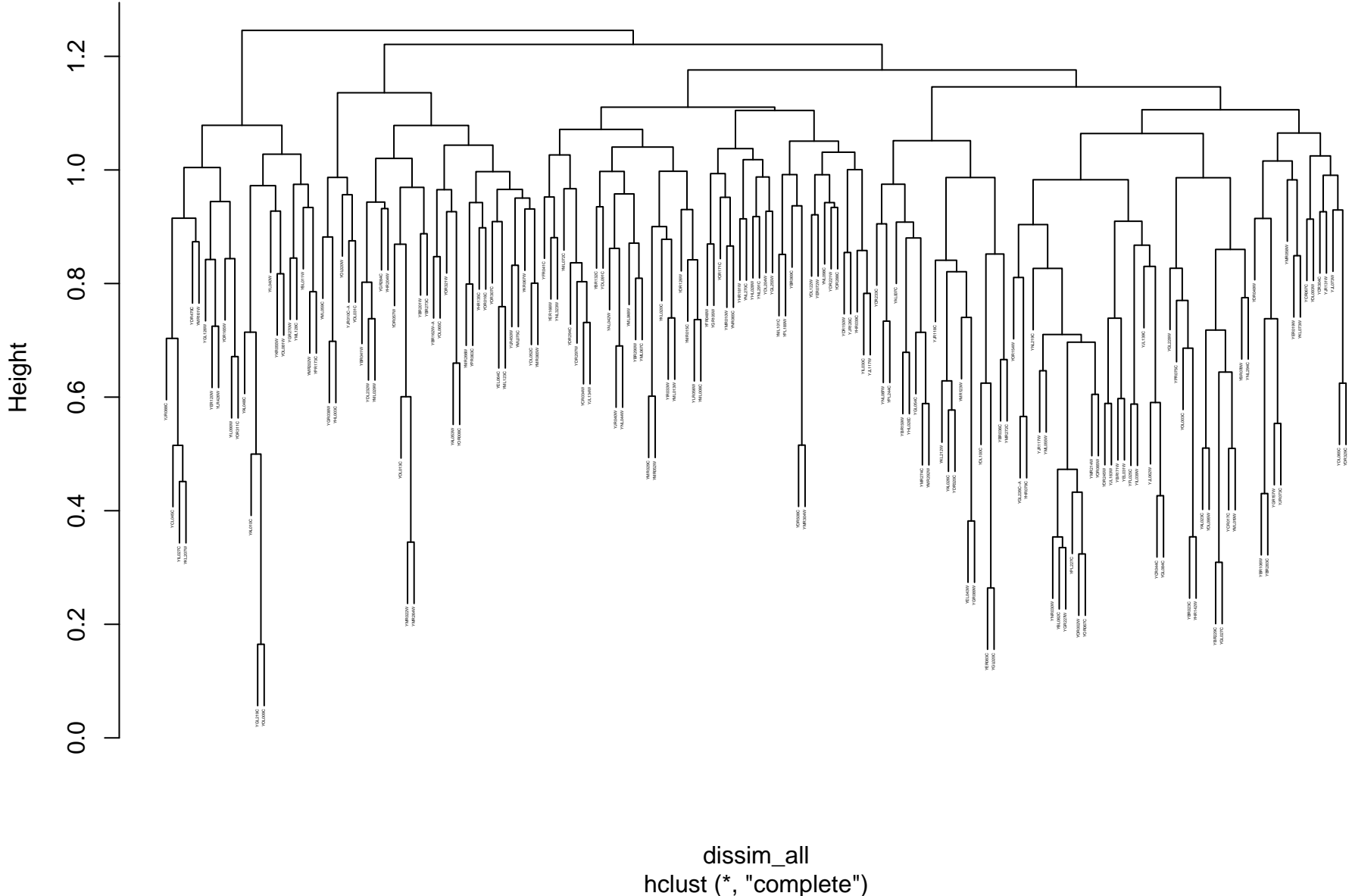
Golgi and ER_GO_pearson_complete



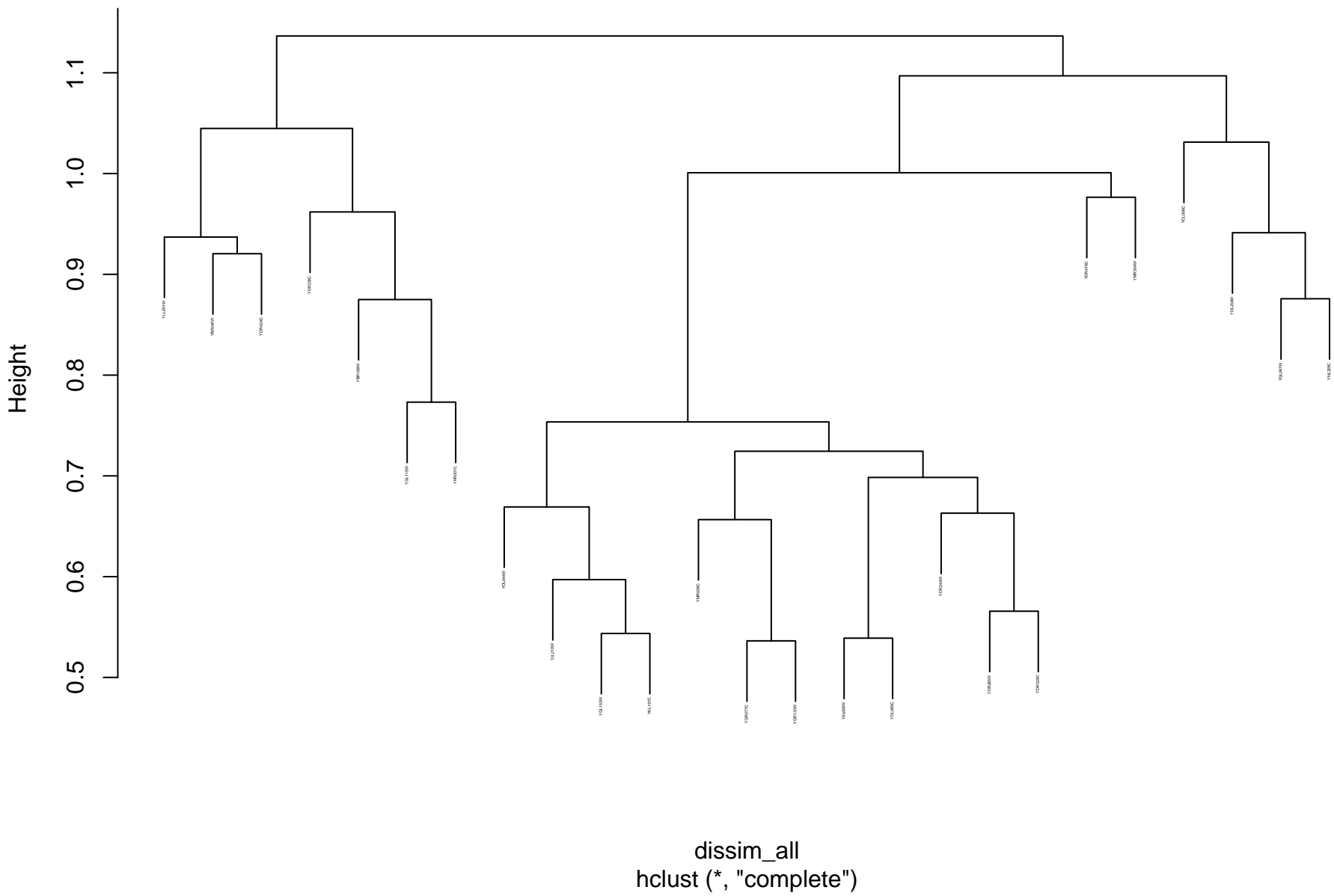
Golgi_GO_pearson_complete



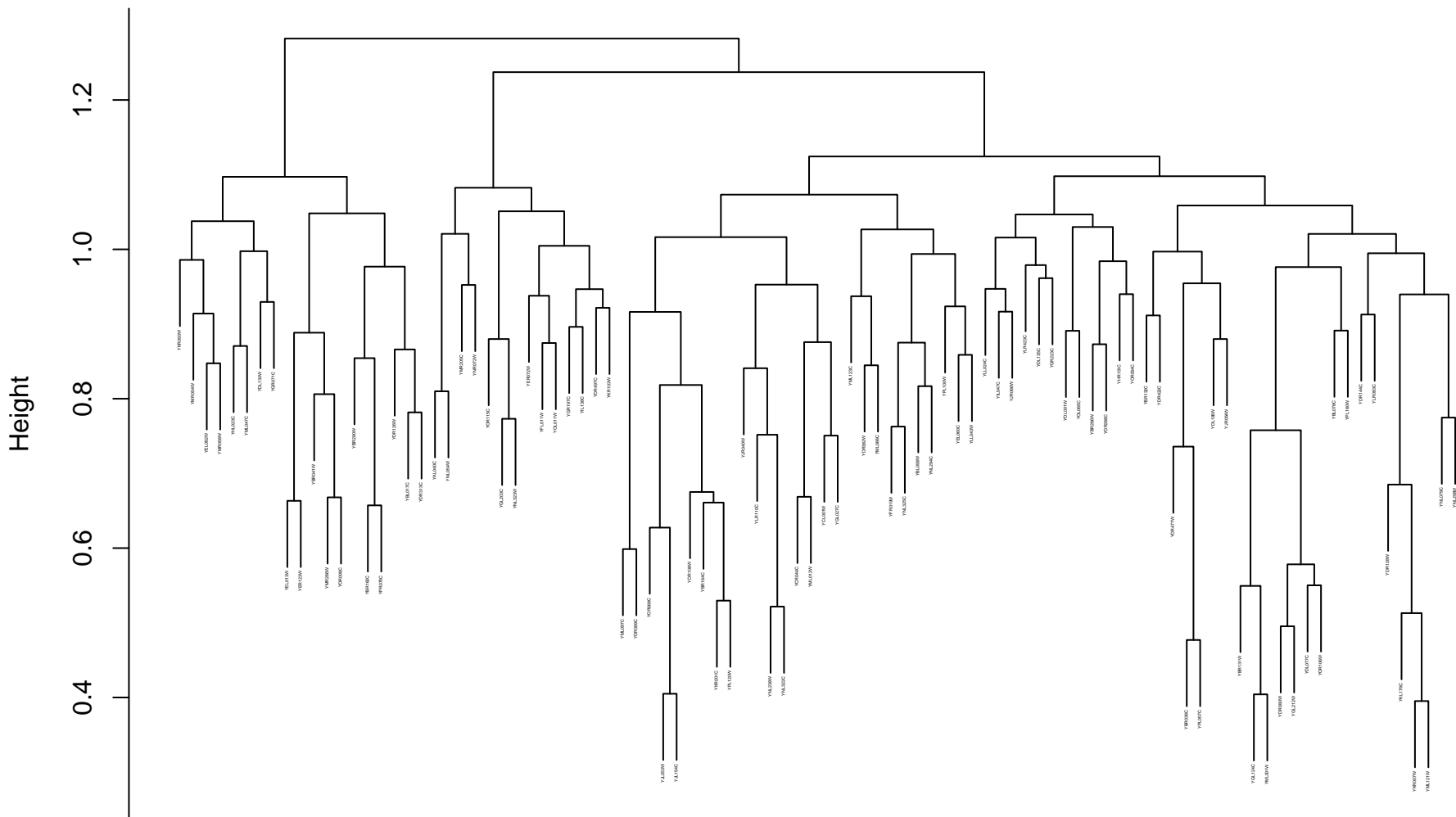
ER_GO_pearson_complete



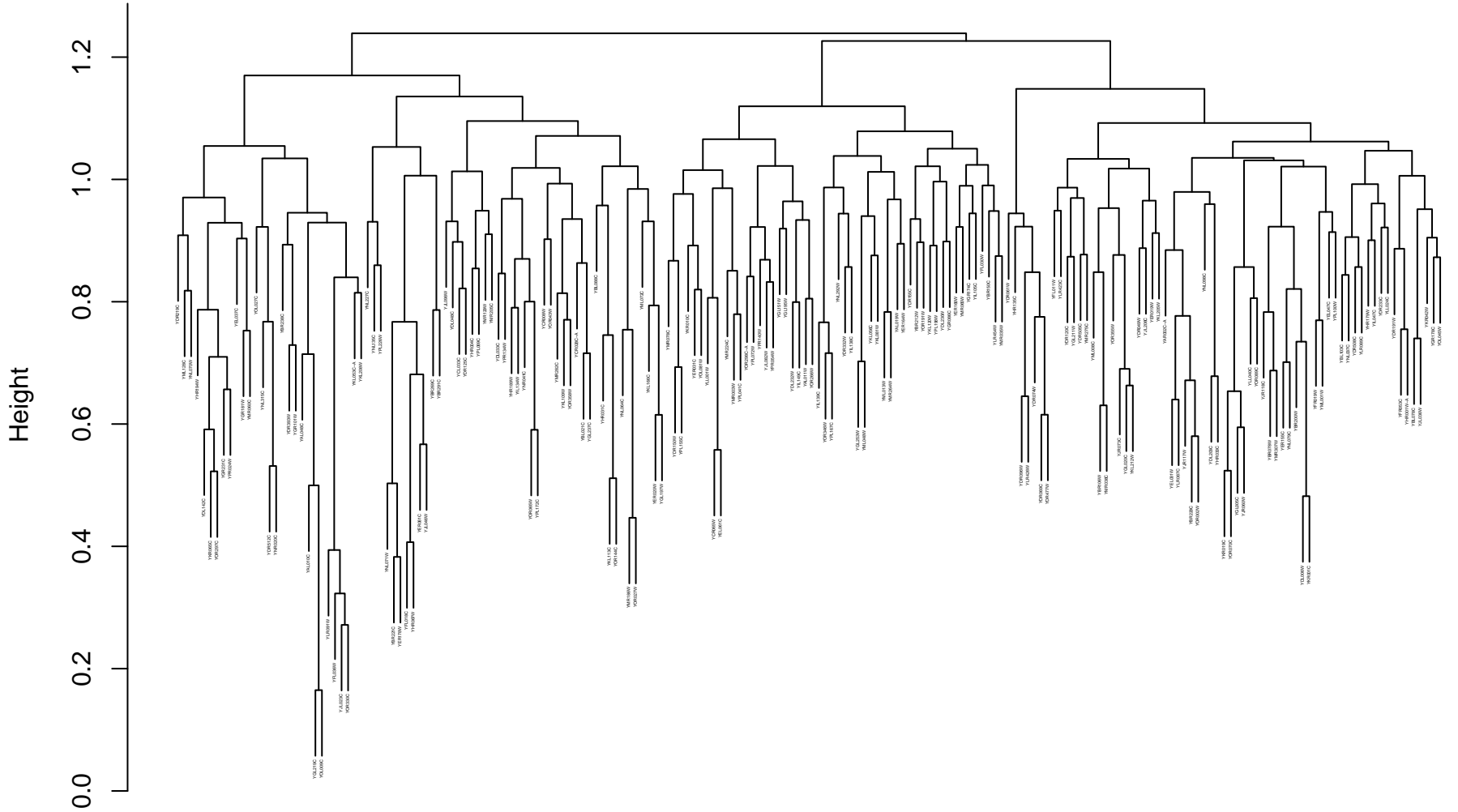
peroxisomes_GO_pearson_complete



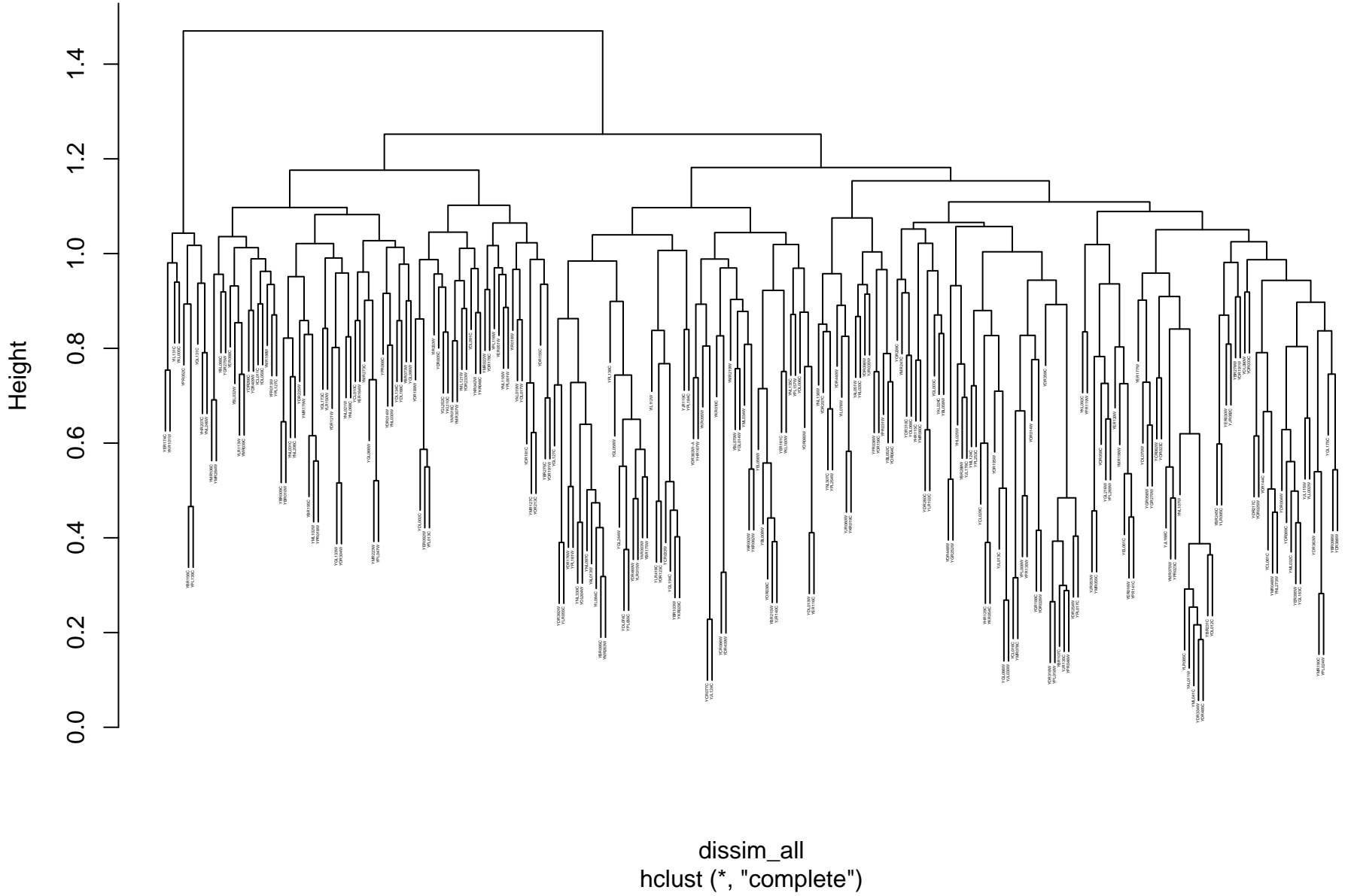
vacuoles_GO_pearson_complete



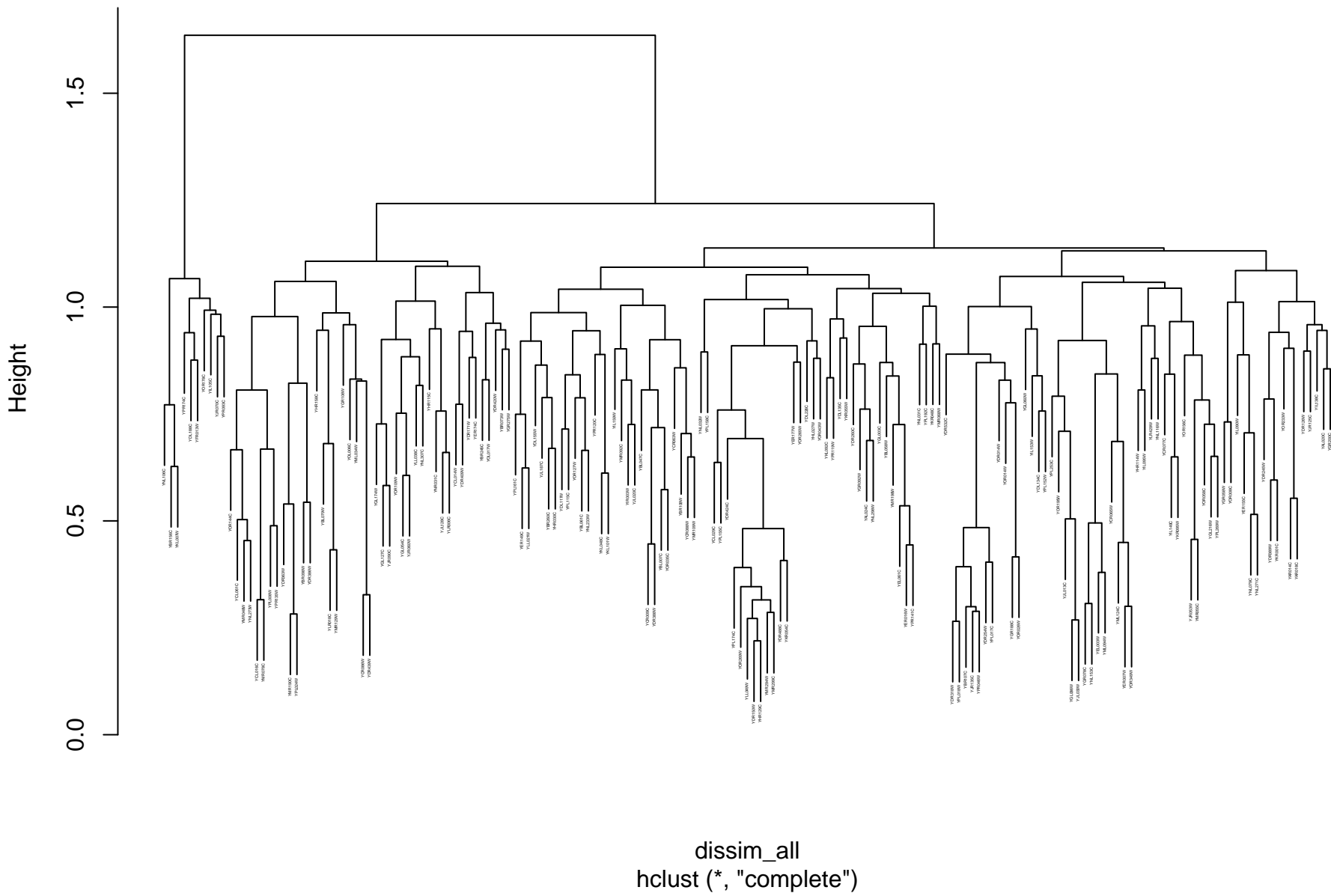
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dissim_all
hclust (*, "complete")
```



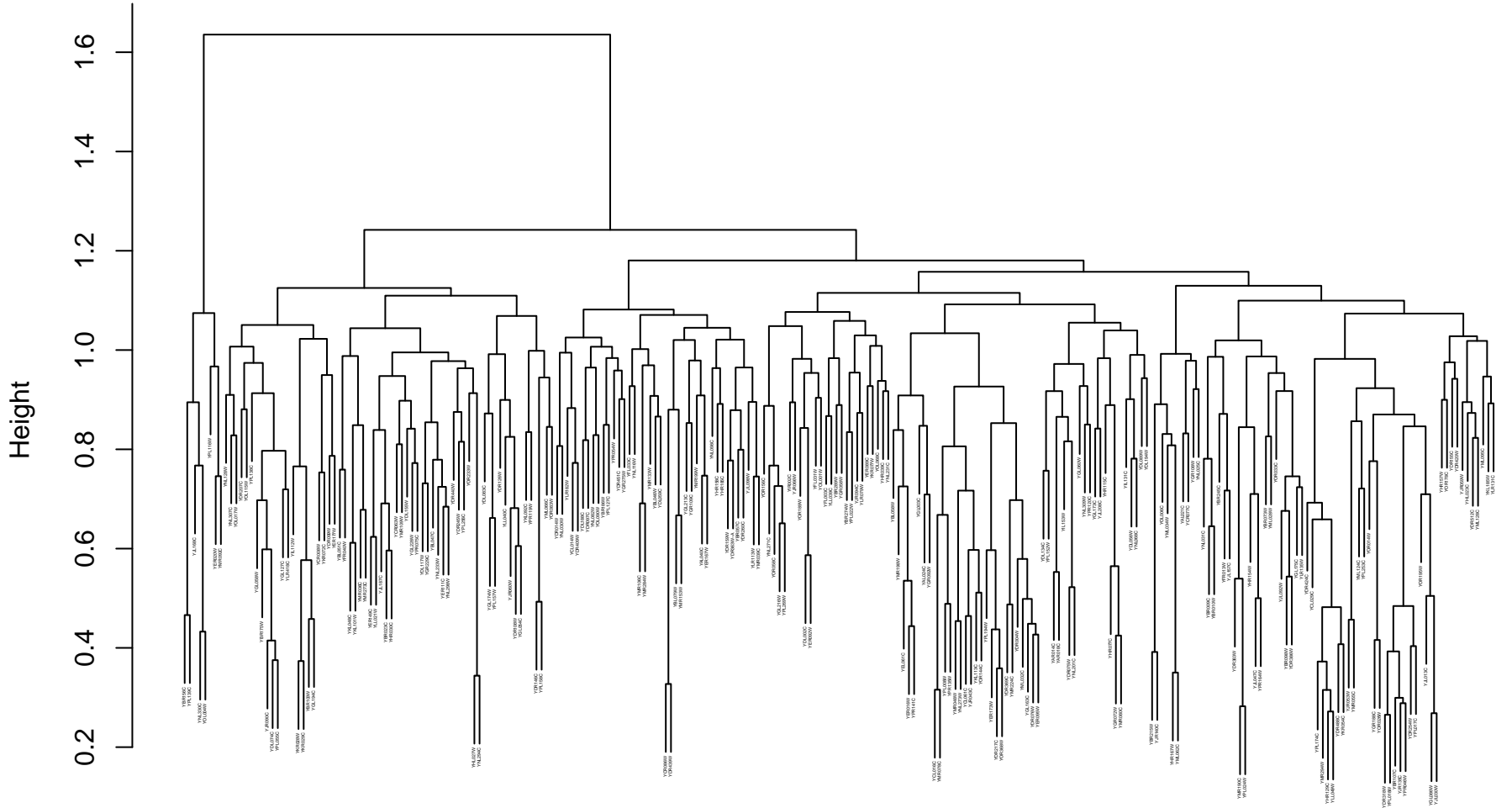
chromatin_GO_pearson_complete



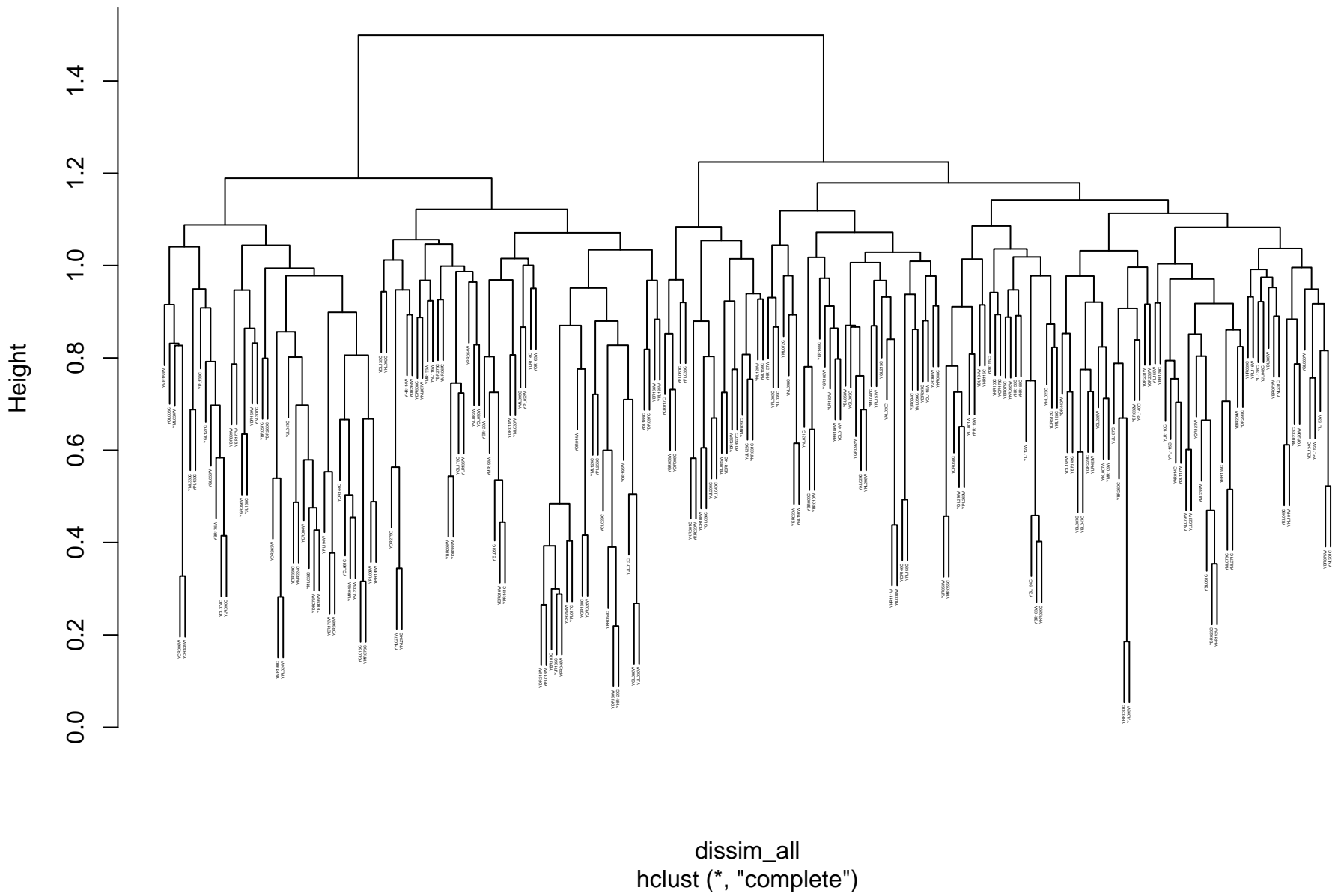
cytoskeleton and microtubules_GO_pearson_complete



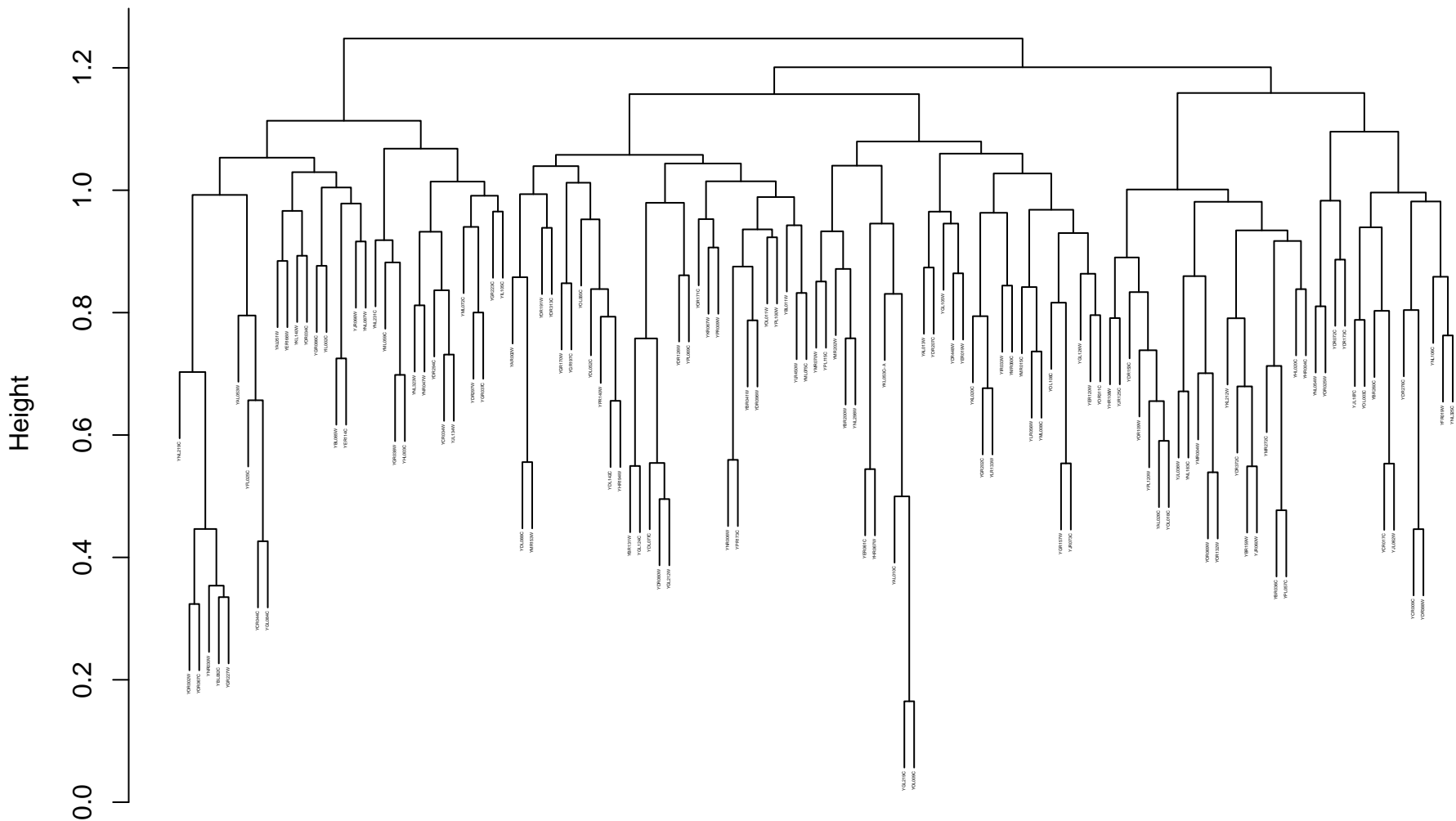
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dissim_all
hclust (*, "complete")
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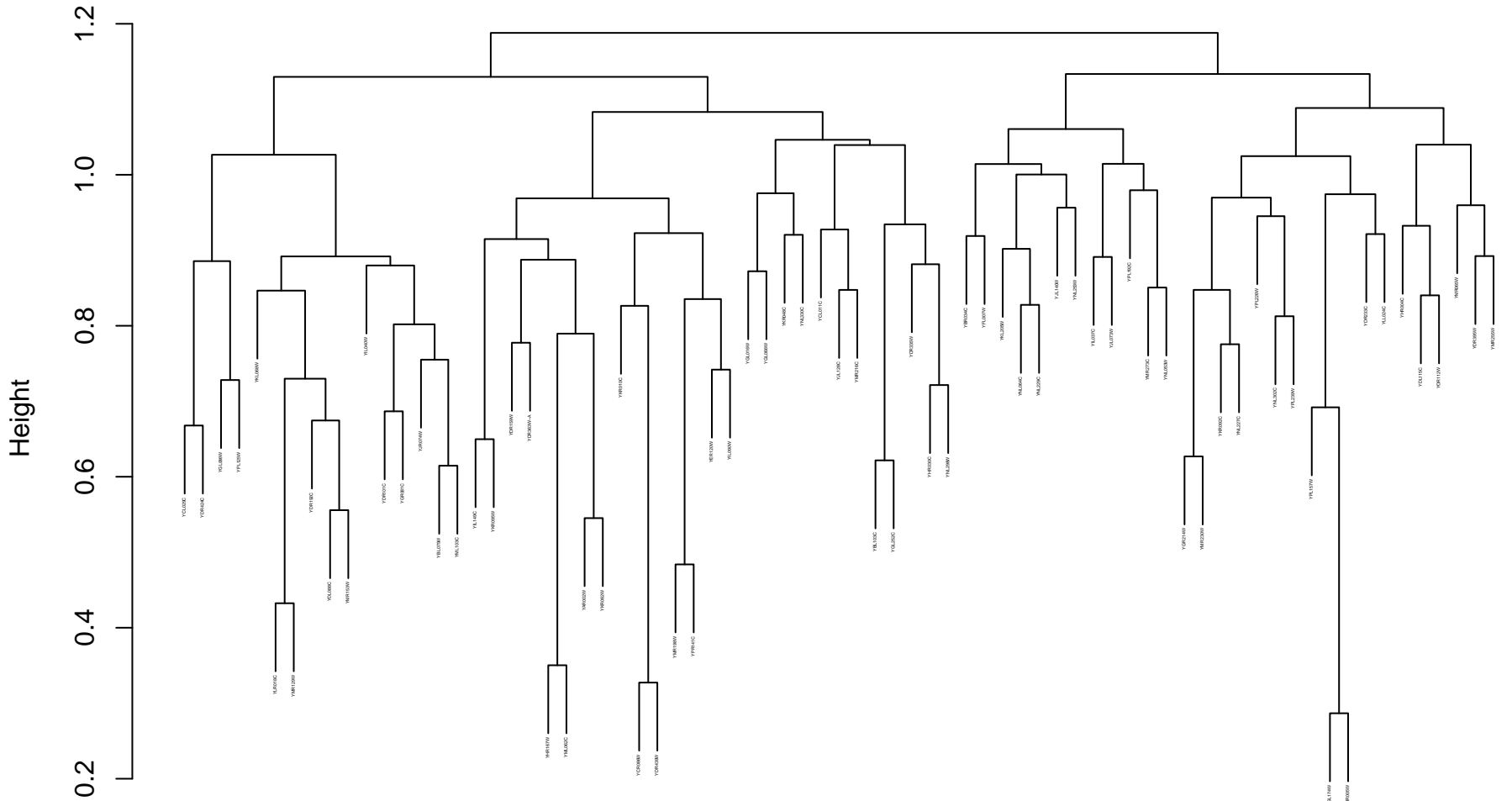
budding_GO_pearson_complete



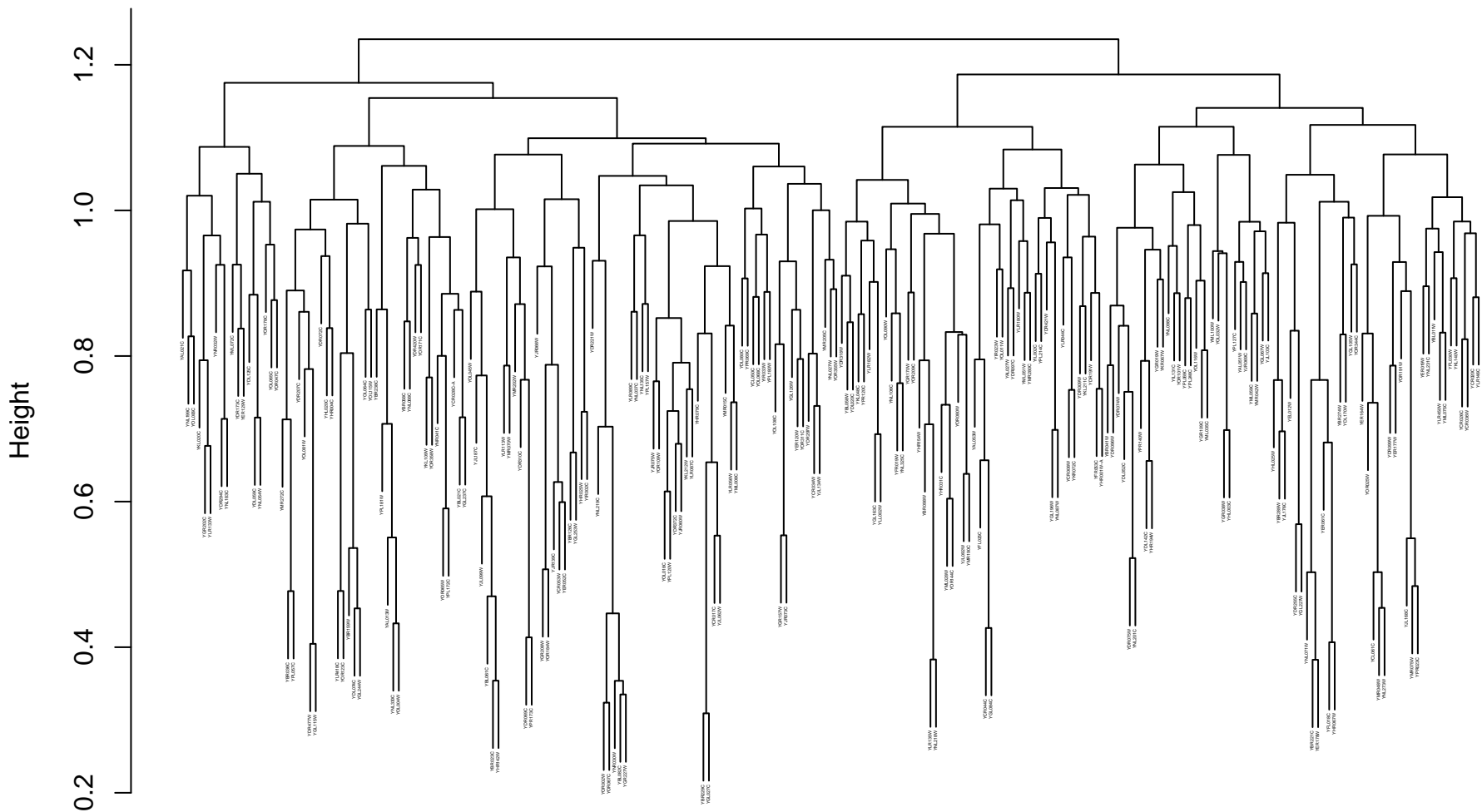
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dissim_all
hclust (*, "complete")
```



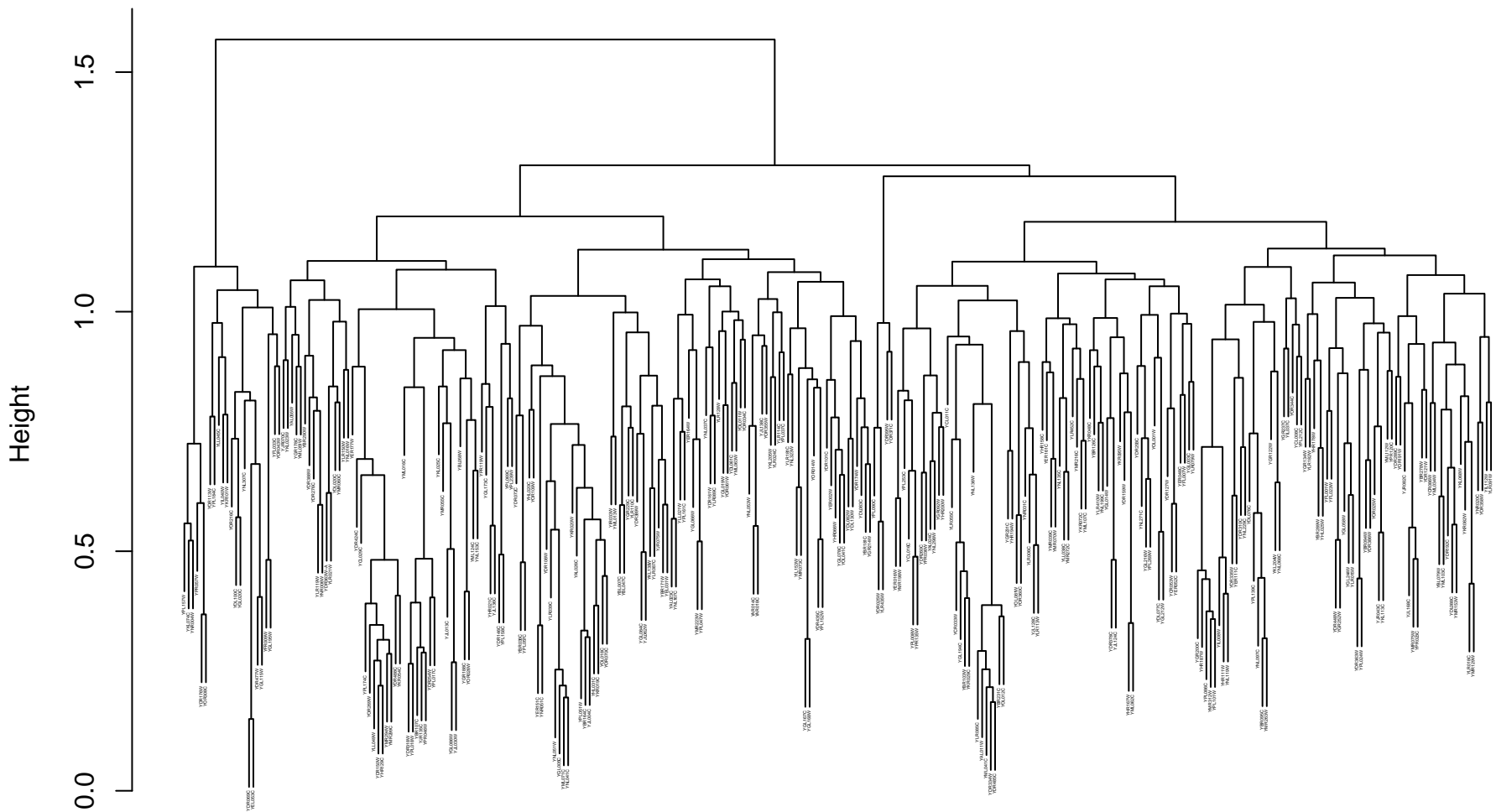

```
dissim_all
hclust (*, "complete")
```



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



sig_Gsp1_Gl_pearson_complete



dissim_all
hclust (*, "complete")

whole_library_pearson_complete

