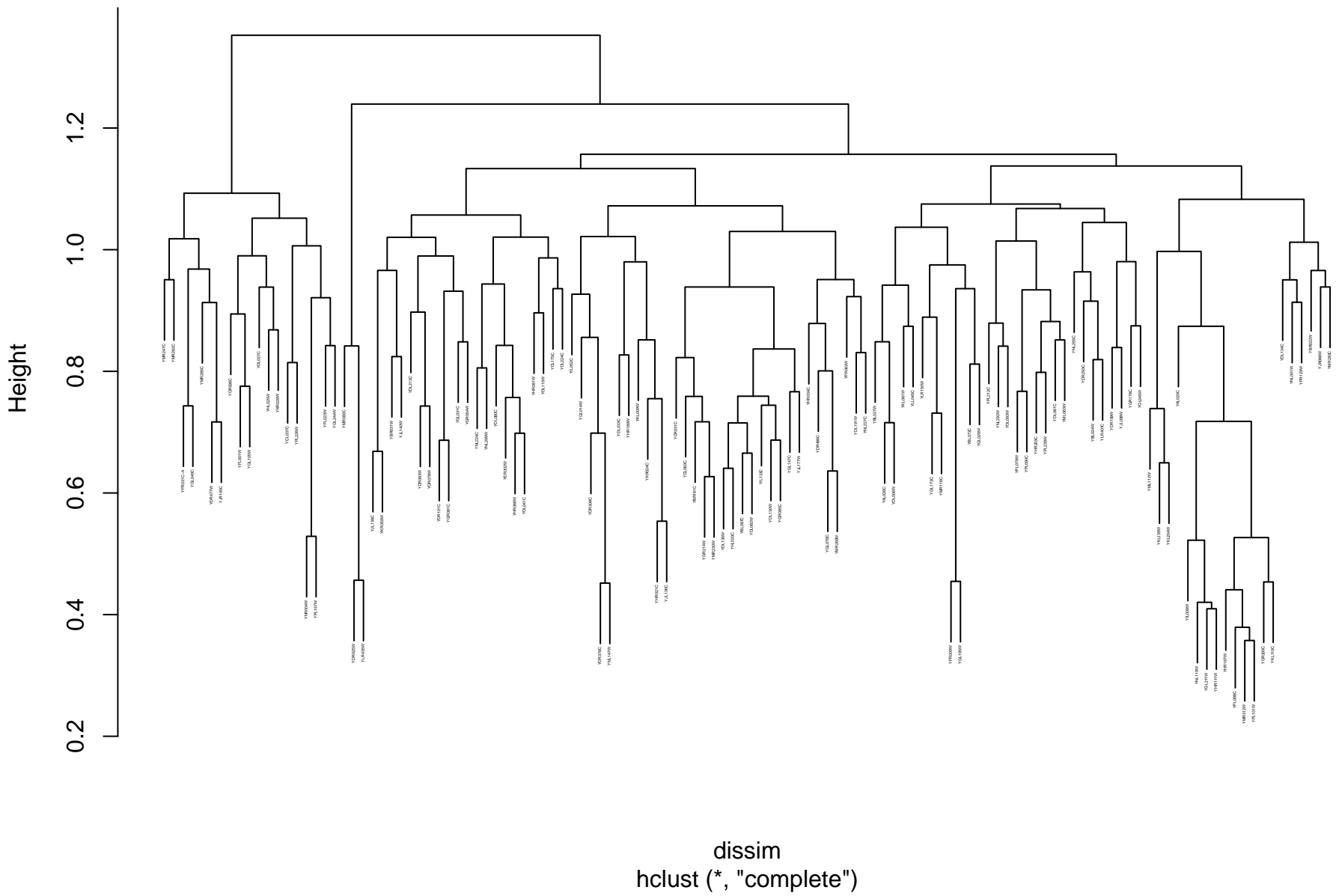
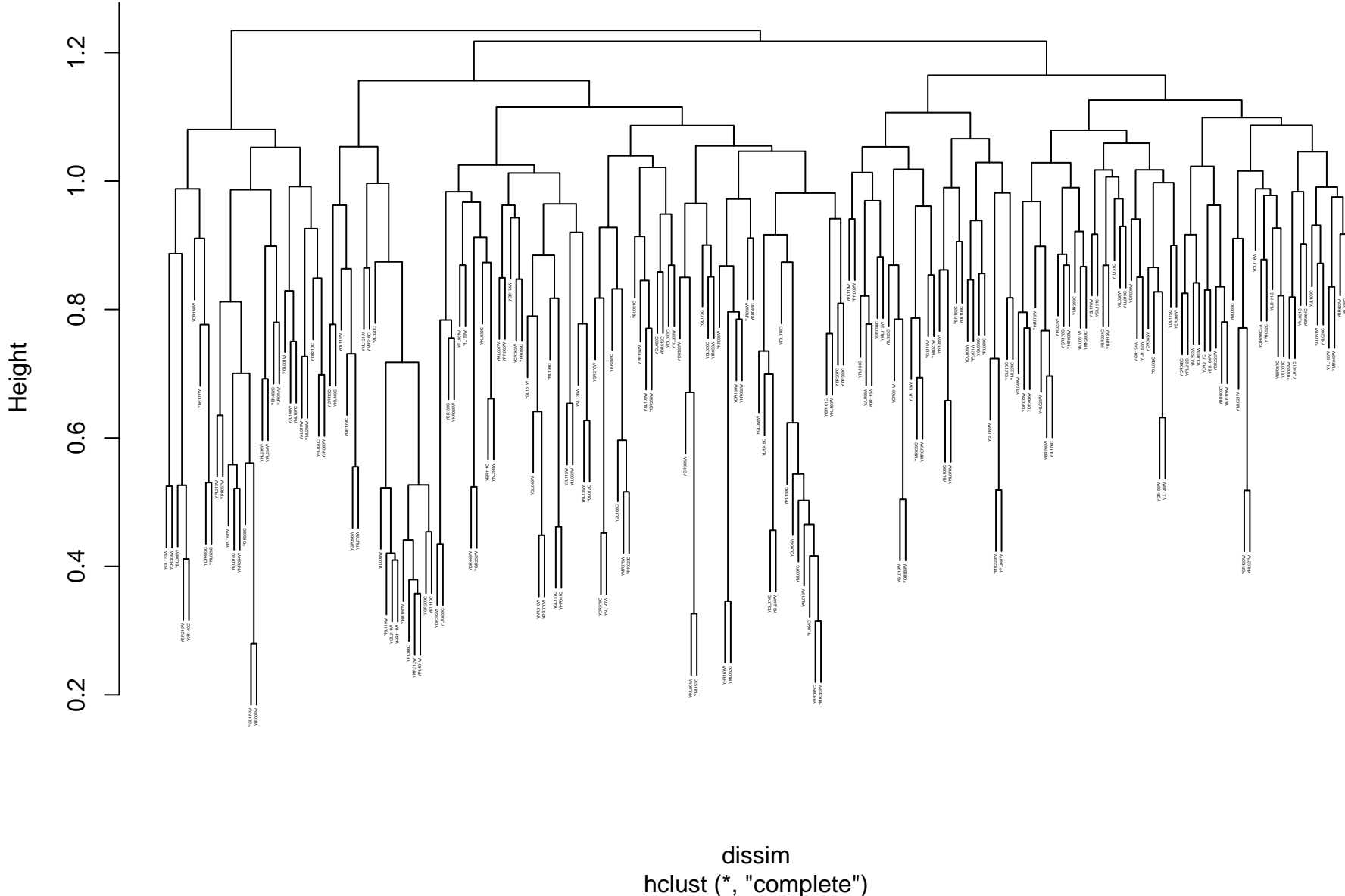


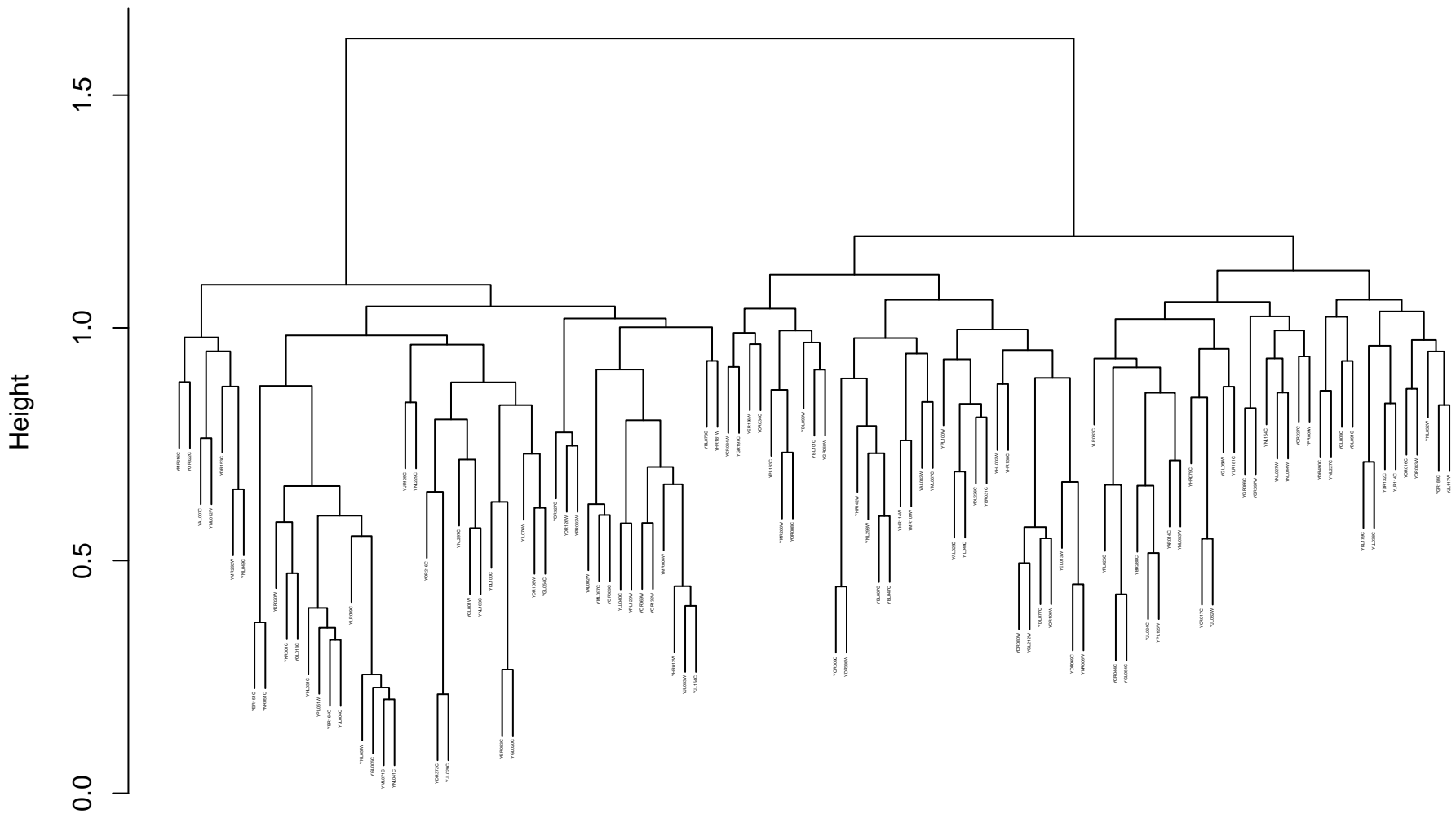
ribosome\_GO\_pearson\_complete



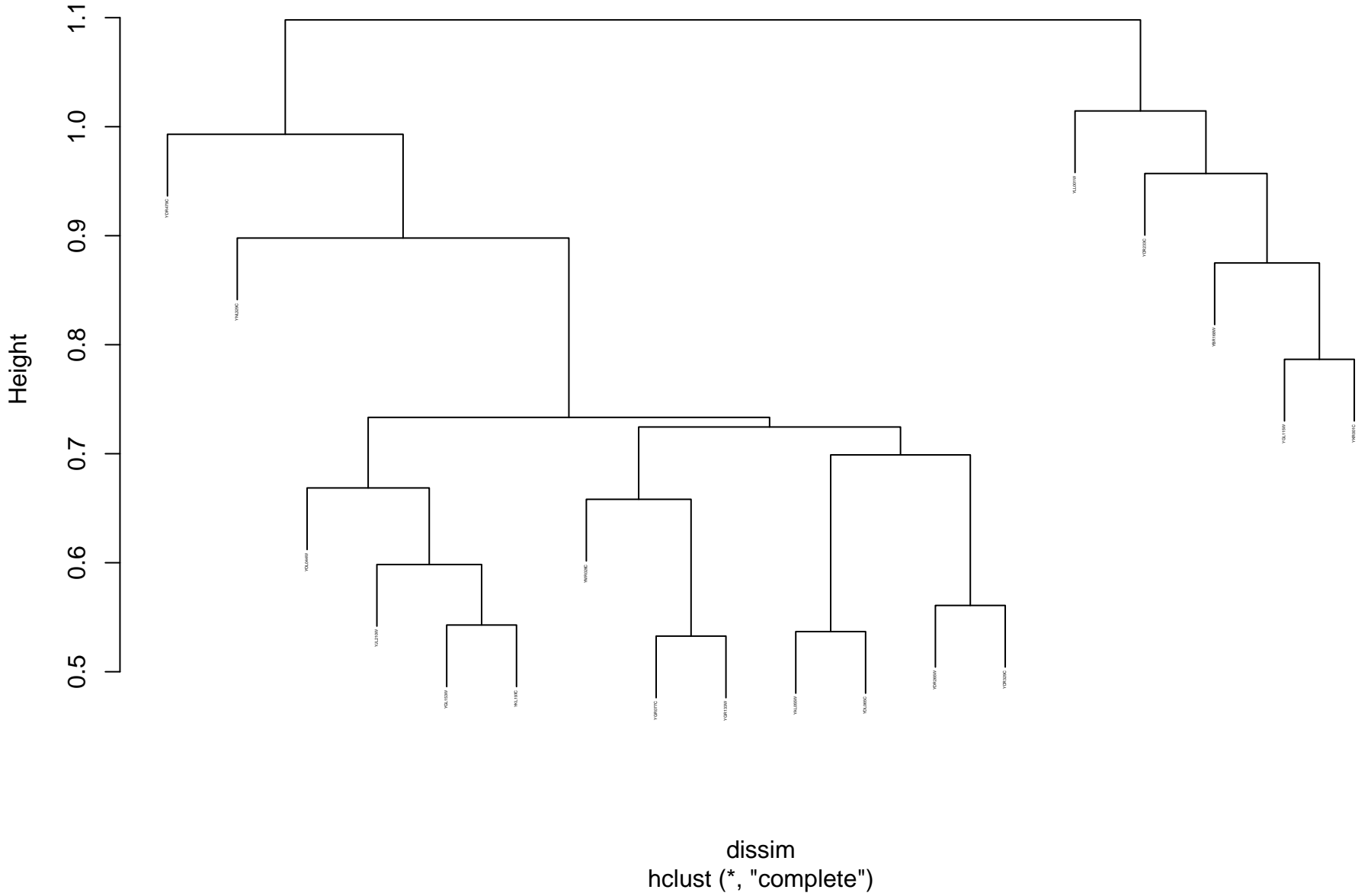
transcription and mRNA processing\_GO\_pearson\_complete



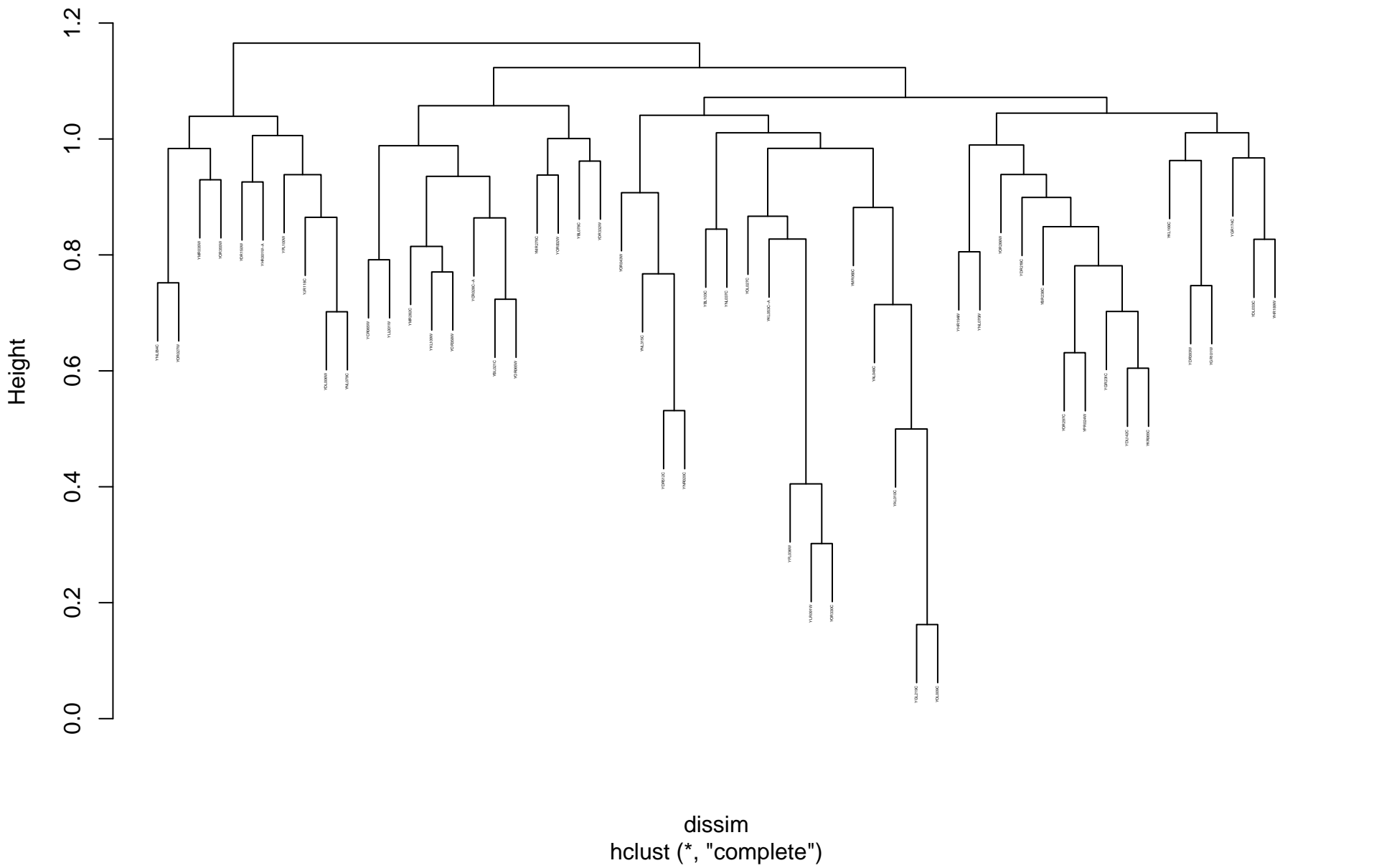
```
dissim
hclust (*, "complete")
```



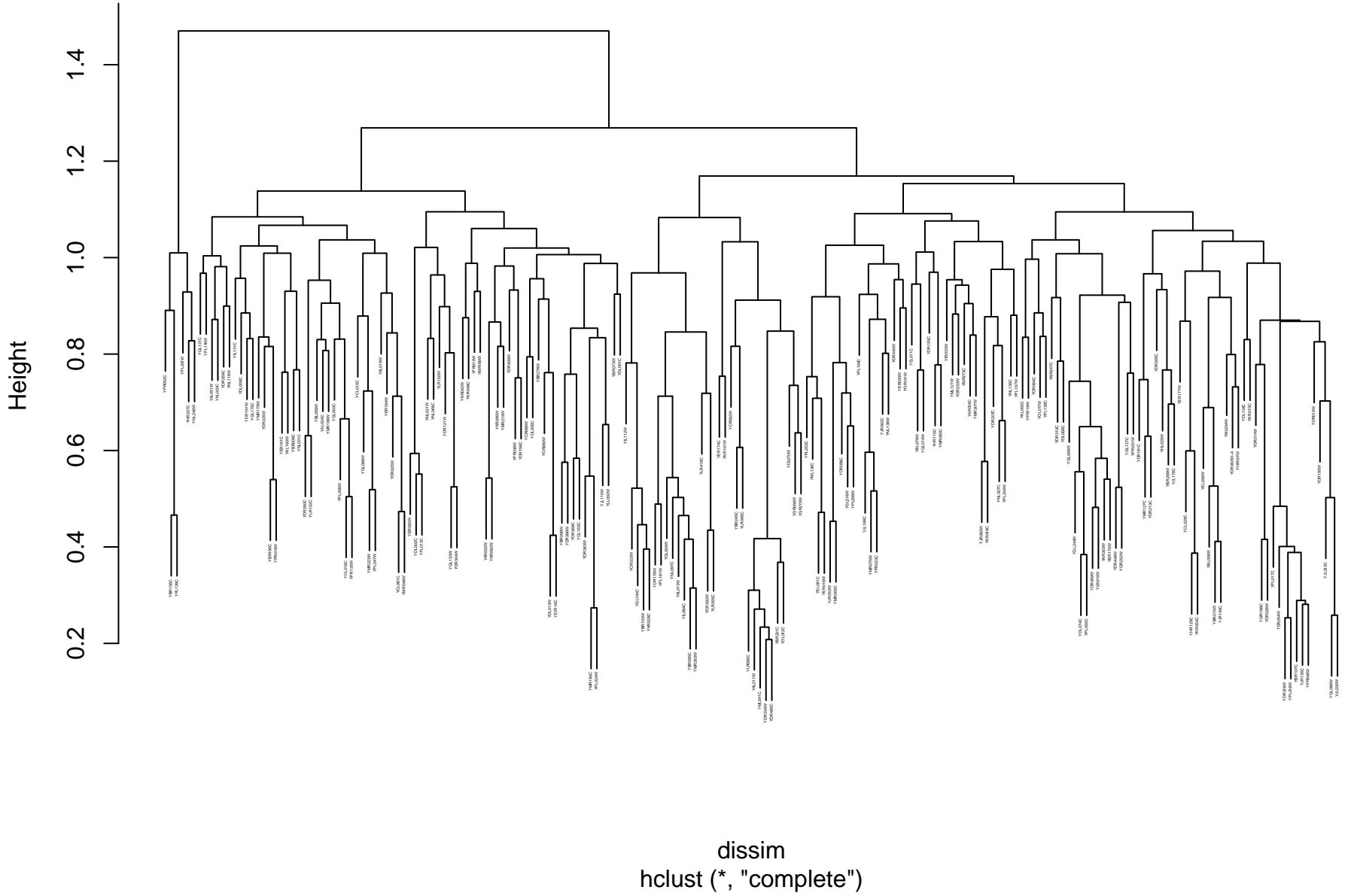
**peroxisome\_GO\_pearson\_complete**



# mitochondrion\_GO\_pearson\_complete



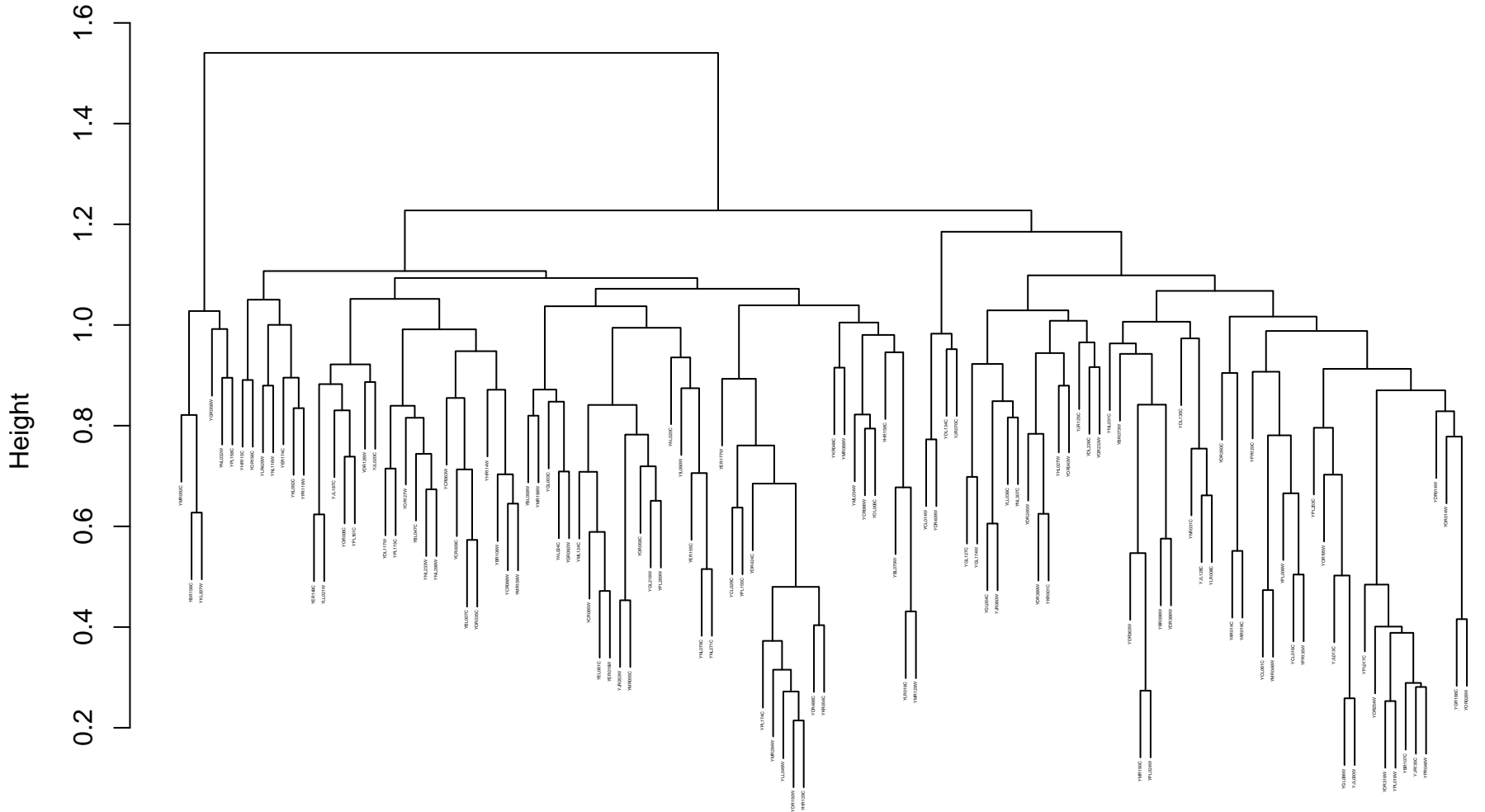
**chromatin\_GO\_pearson\_complete**



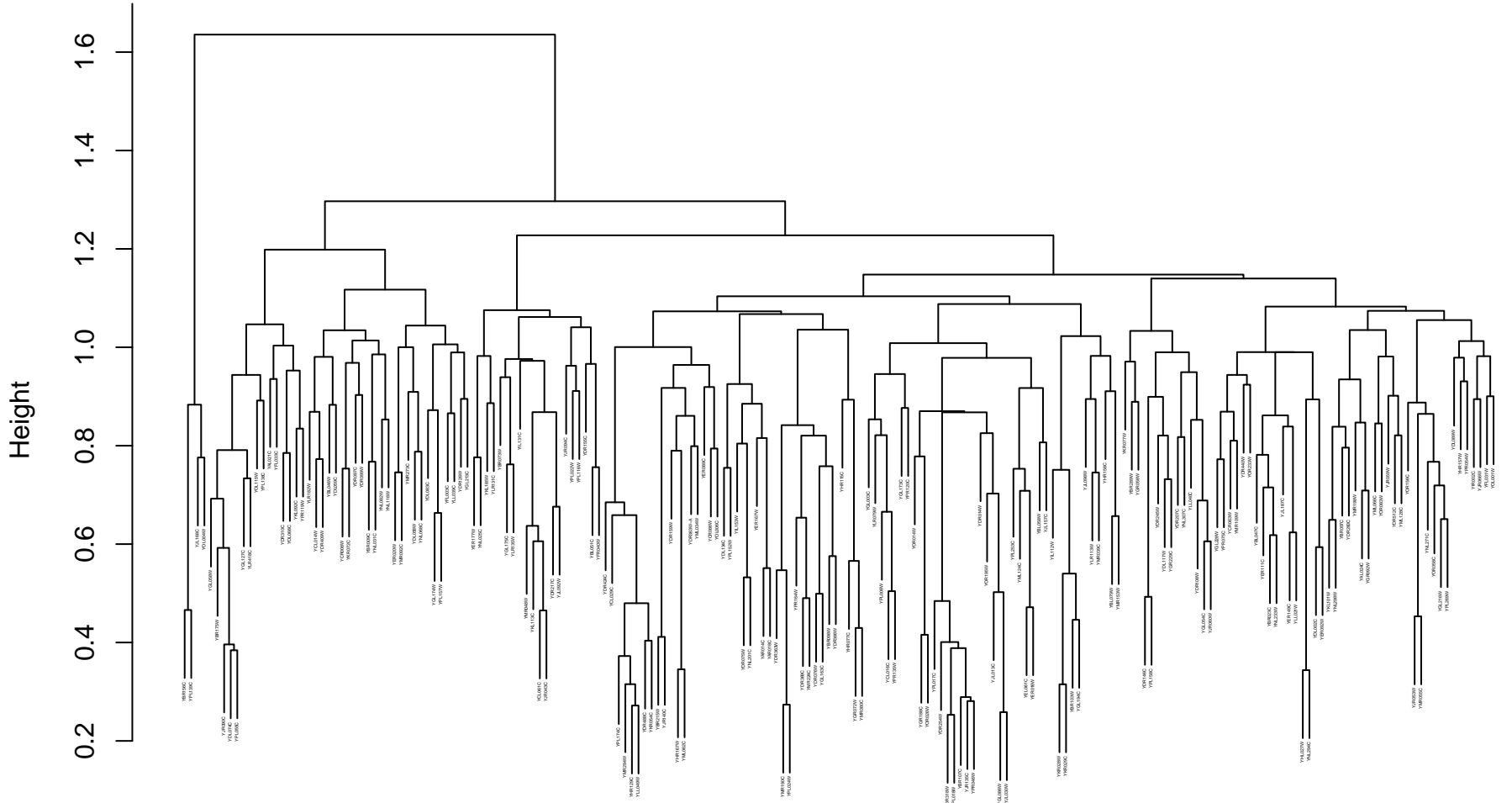
```

dissim
hclust (*, "complete")

```



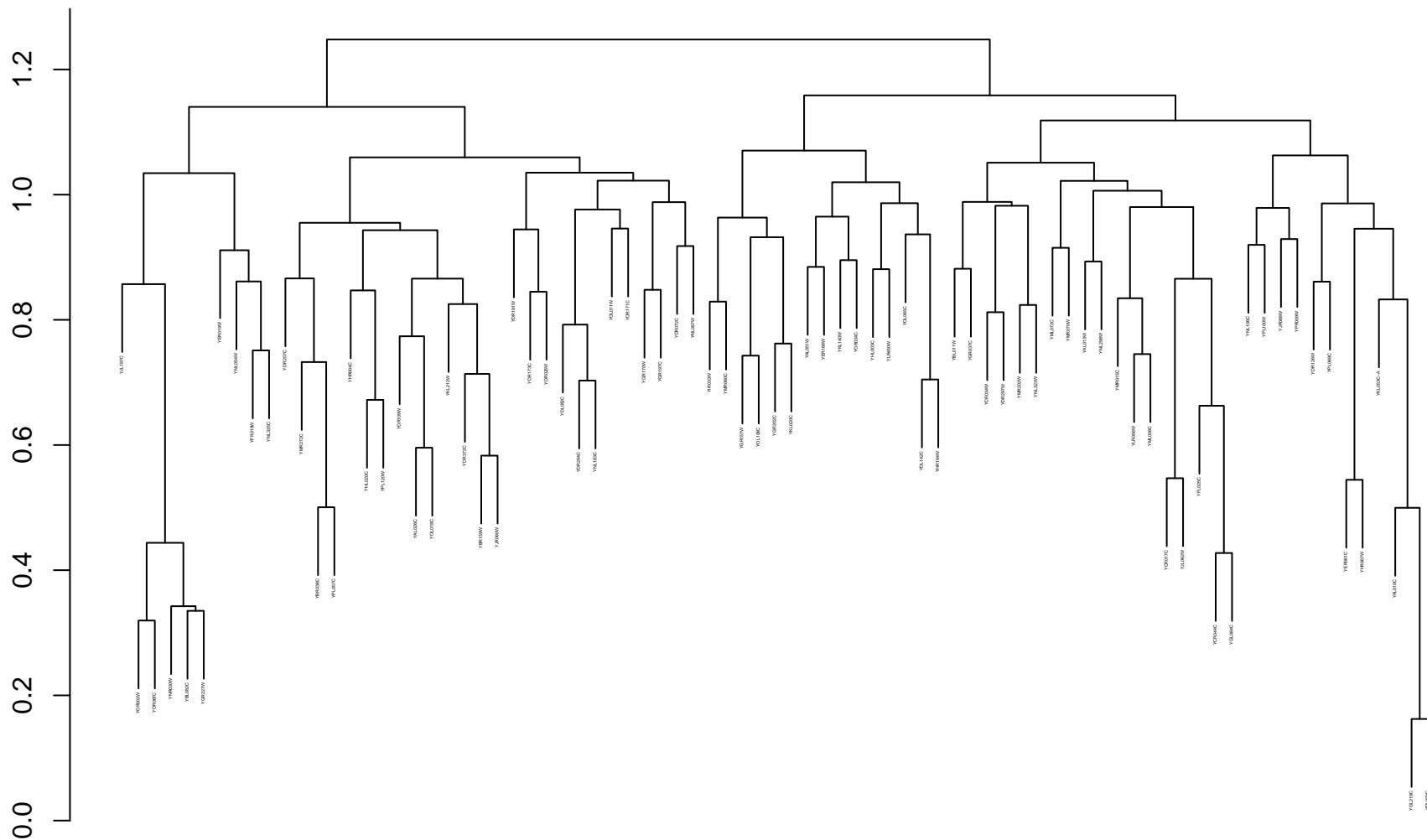
```
dissim
hclust (*, "complete")
```



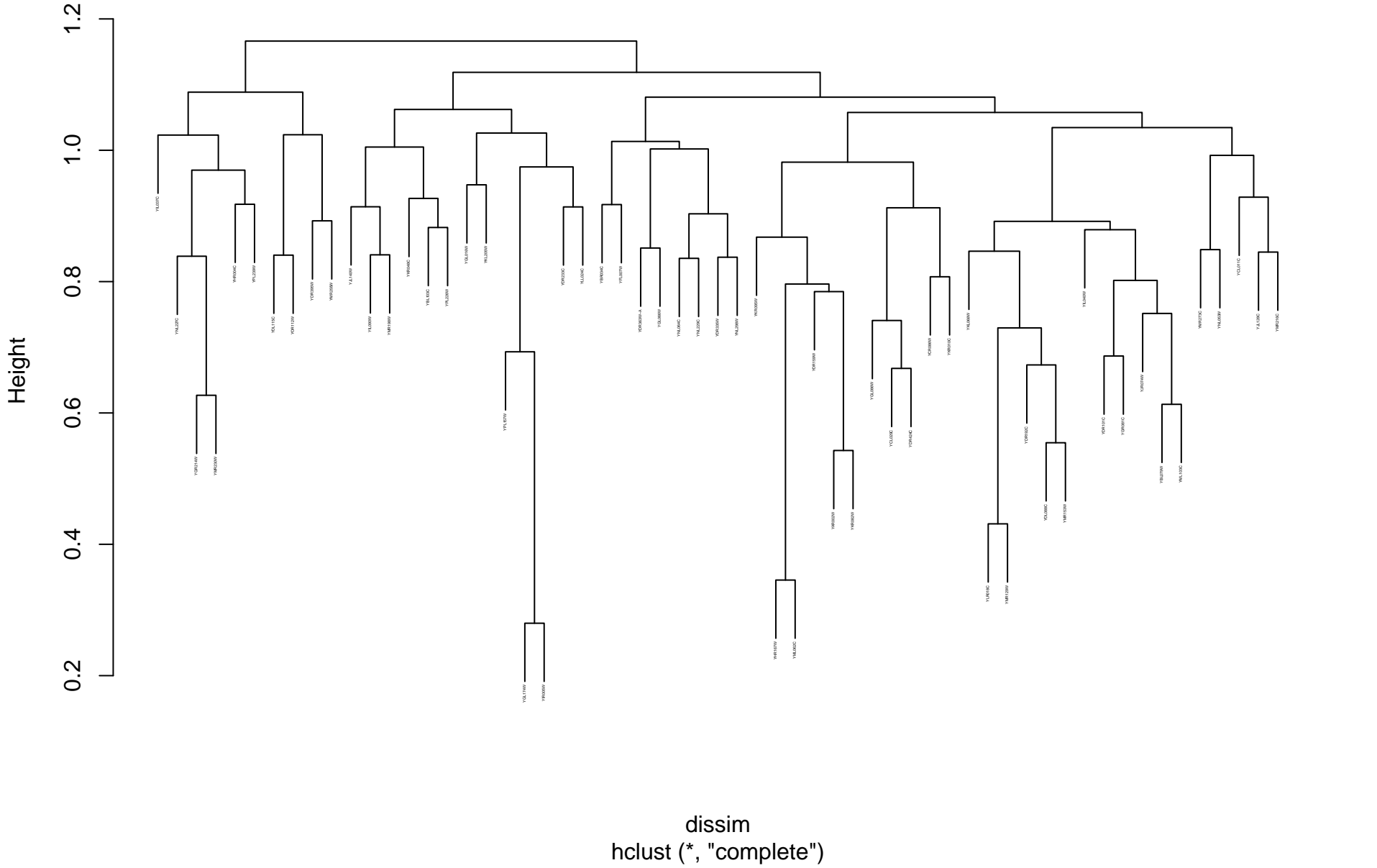


```
dissim
hclust (*, "complete")
```

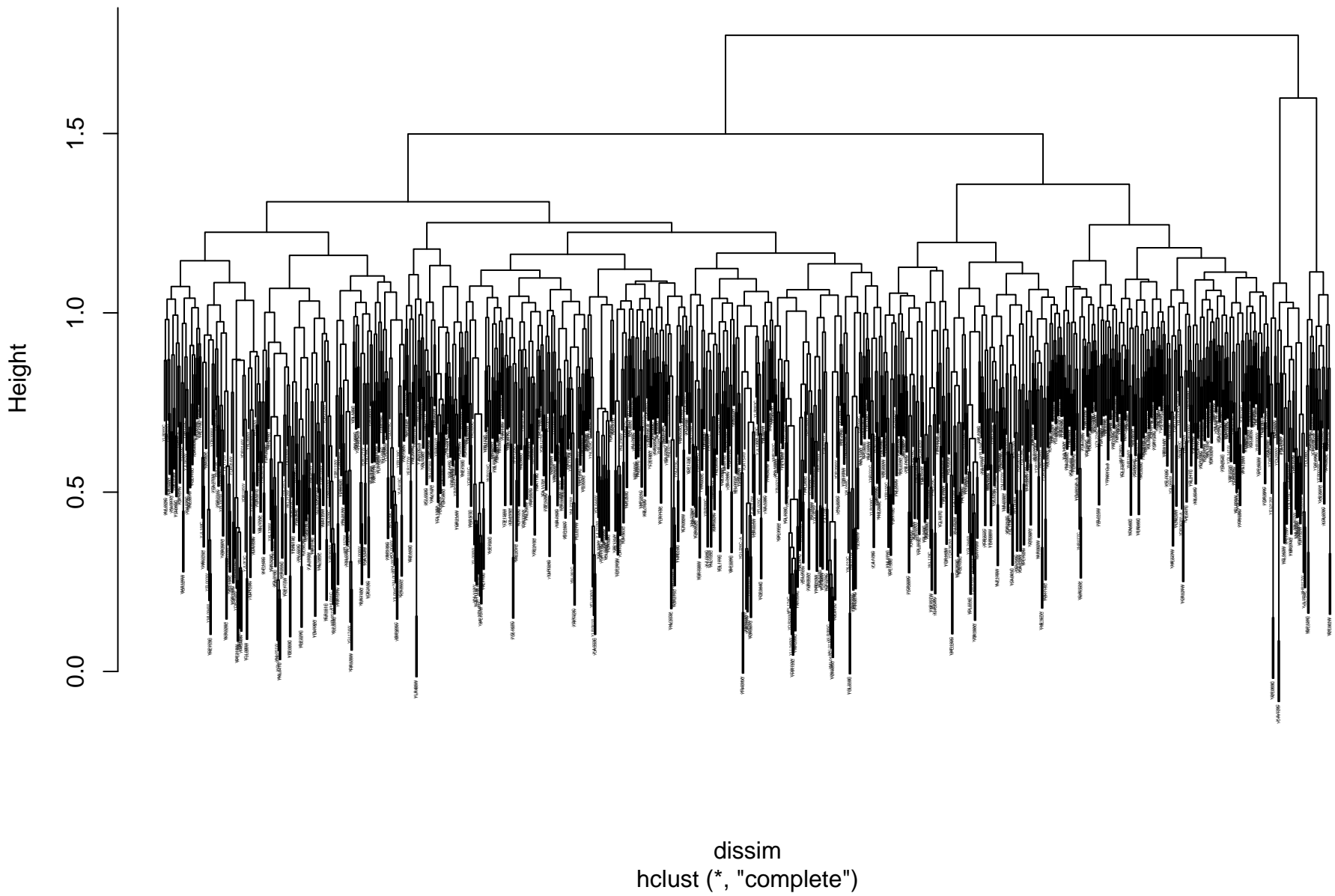
```
dissim
hclust (*, "complete")
```



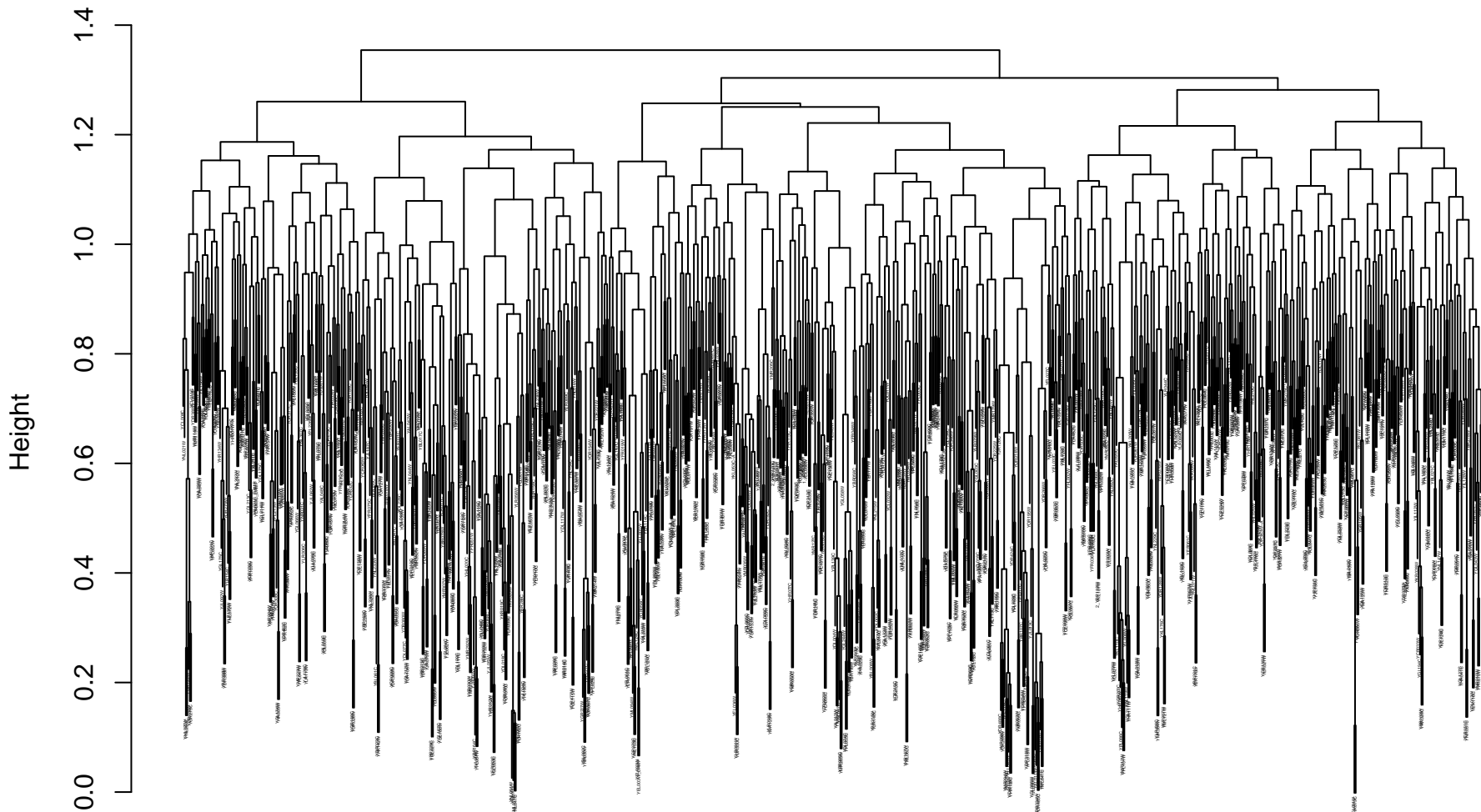
## nuclear transport\_GO\_pearson\_complete



# library\_pearson\_complete



**gene\_pearson\_complete**

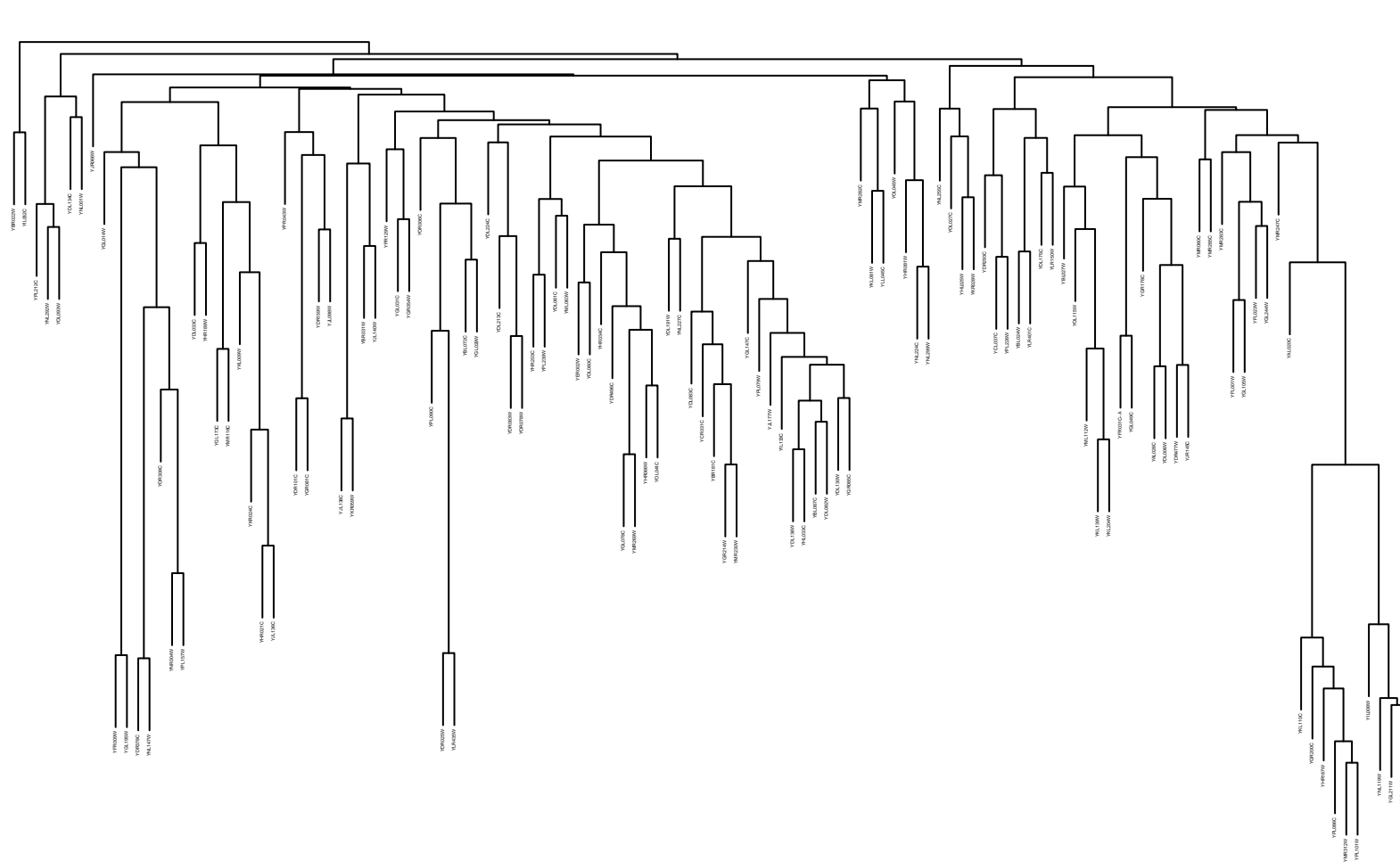


```
dissim
hclust (*, "complete")
```

# ribosome\_GO\_pearson\_average

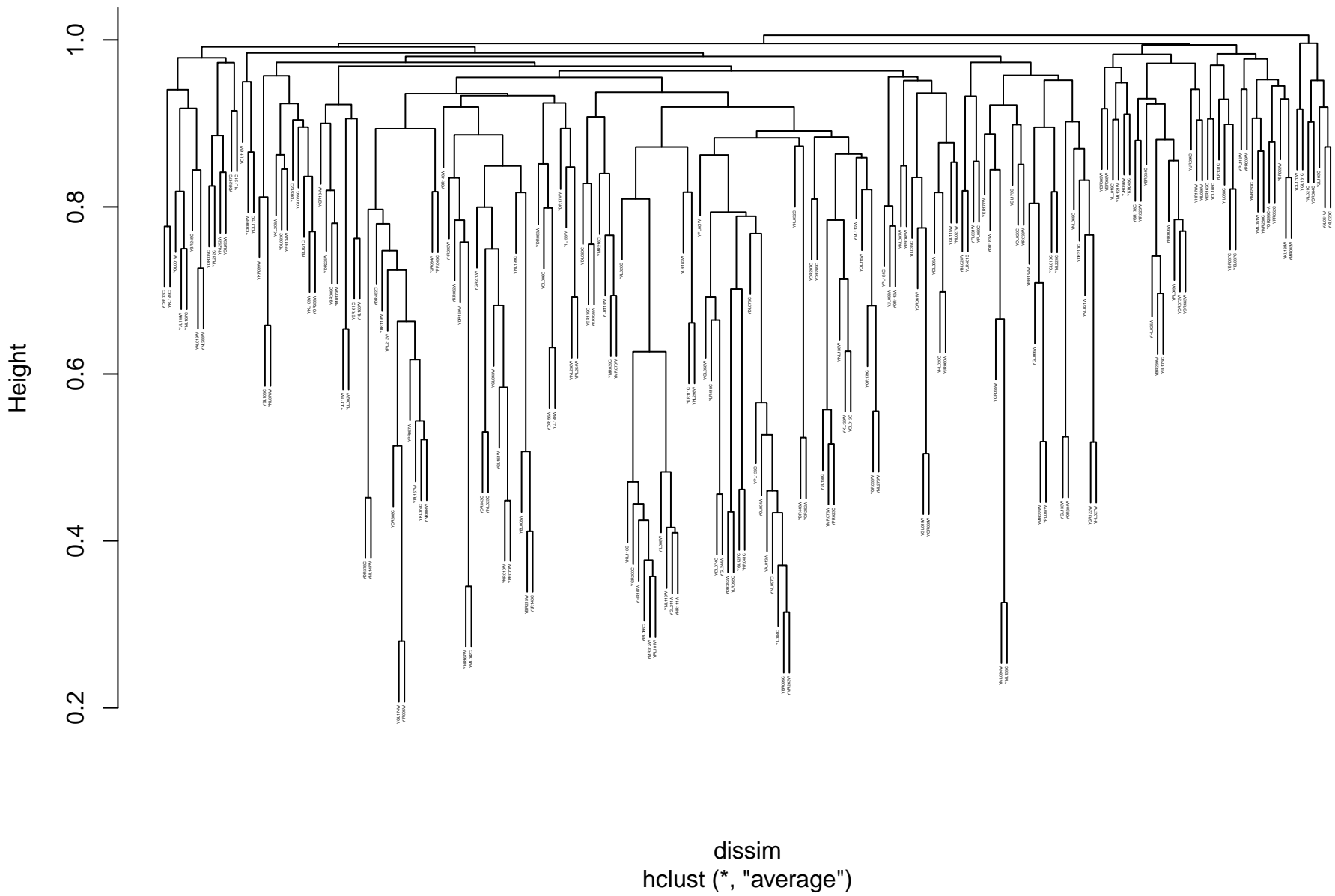
Height

1.0  
0.9  
0.8  
0.7  
0.6  
0.5  
0.4  
0.3



dissim  
hclust (\*, "average")

# transcription and mRNA processing\_GO\_pearson\_average



```

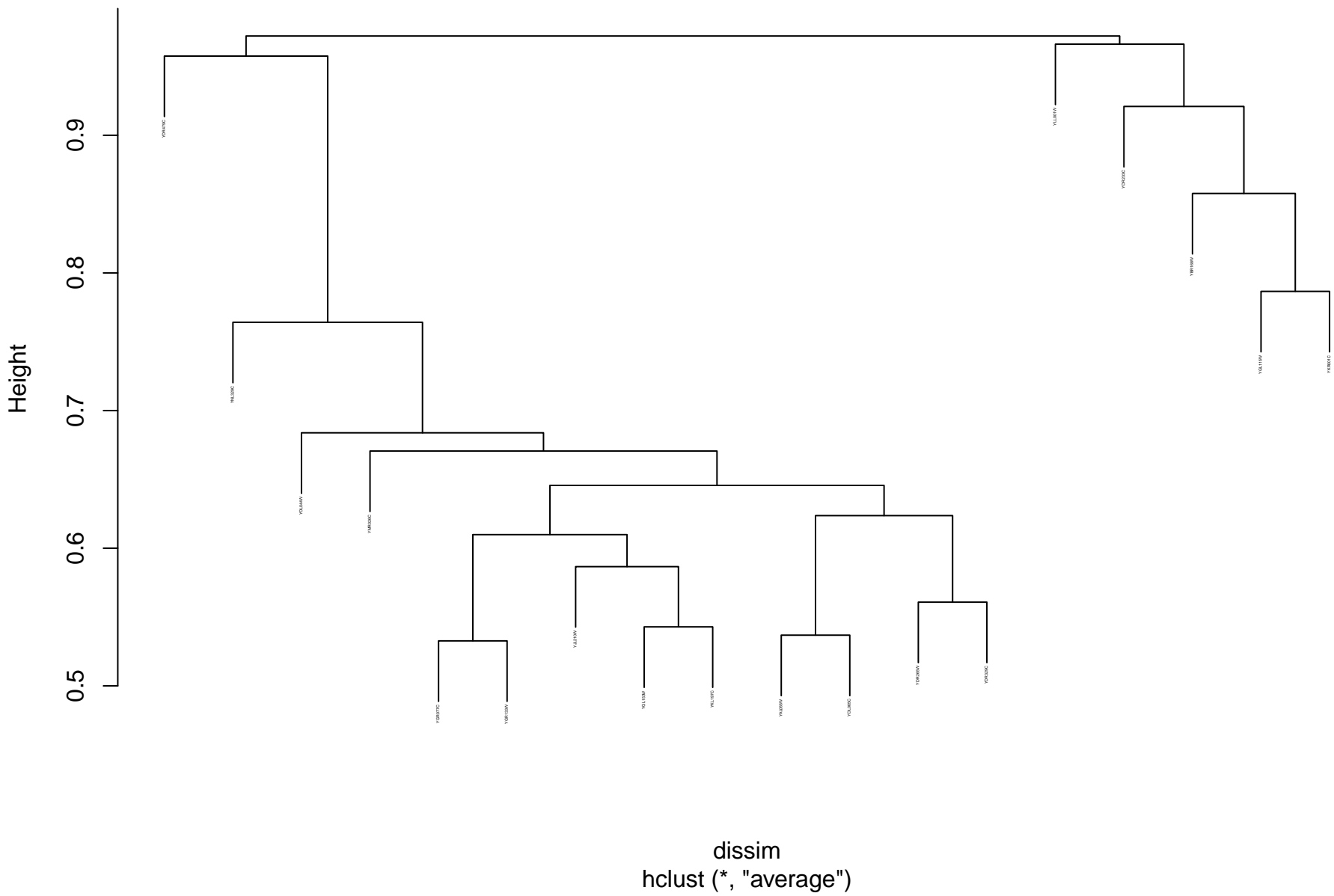
dissim
hclust (*, "average")

```



```
hclust (*, "average")
```

# peroxisome\_GO\_pearson\_average

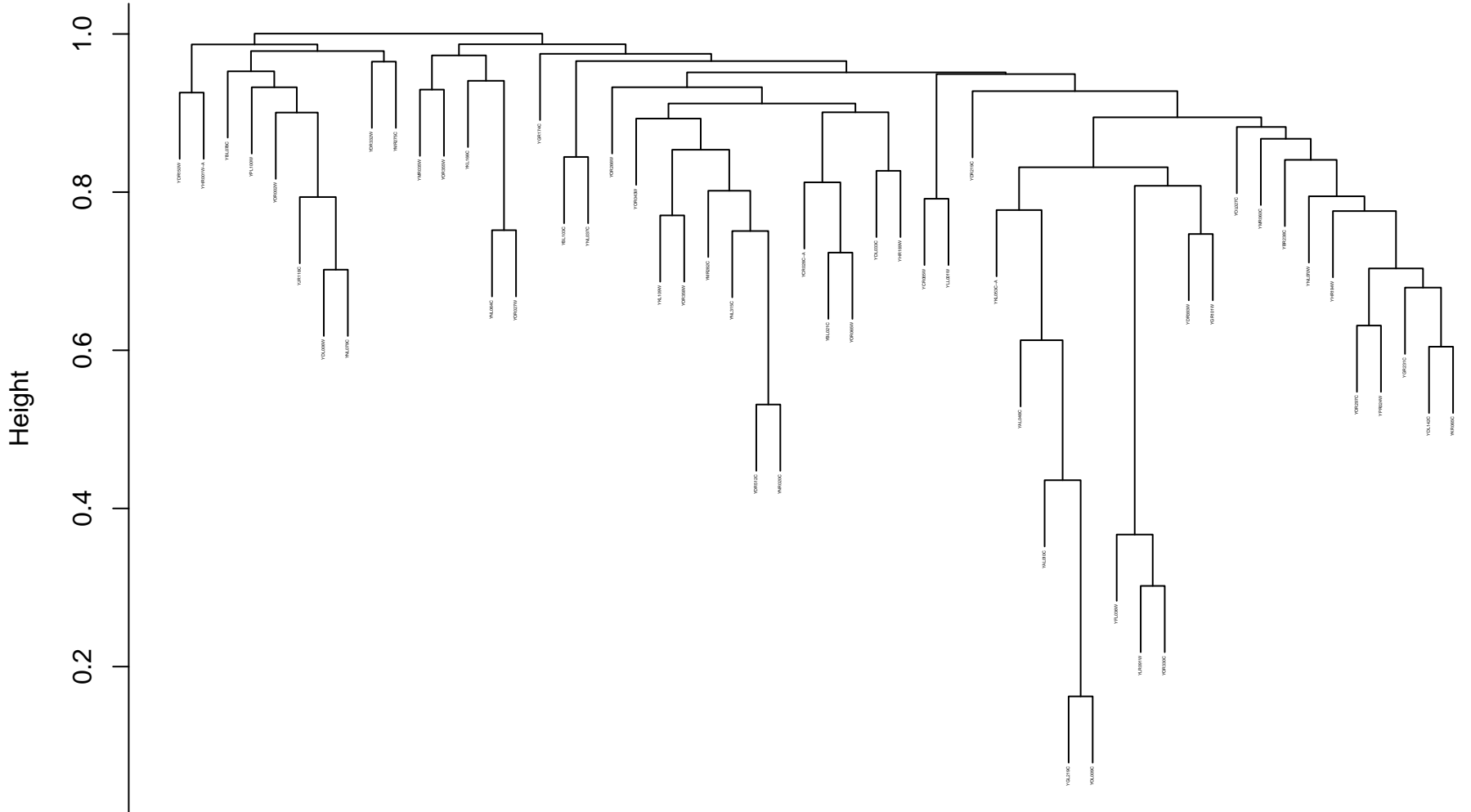




```

dissim
hclust (*, "average")

```

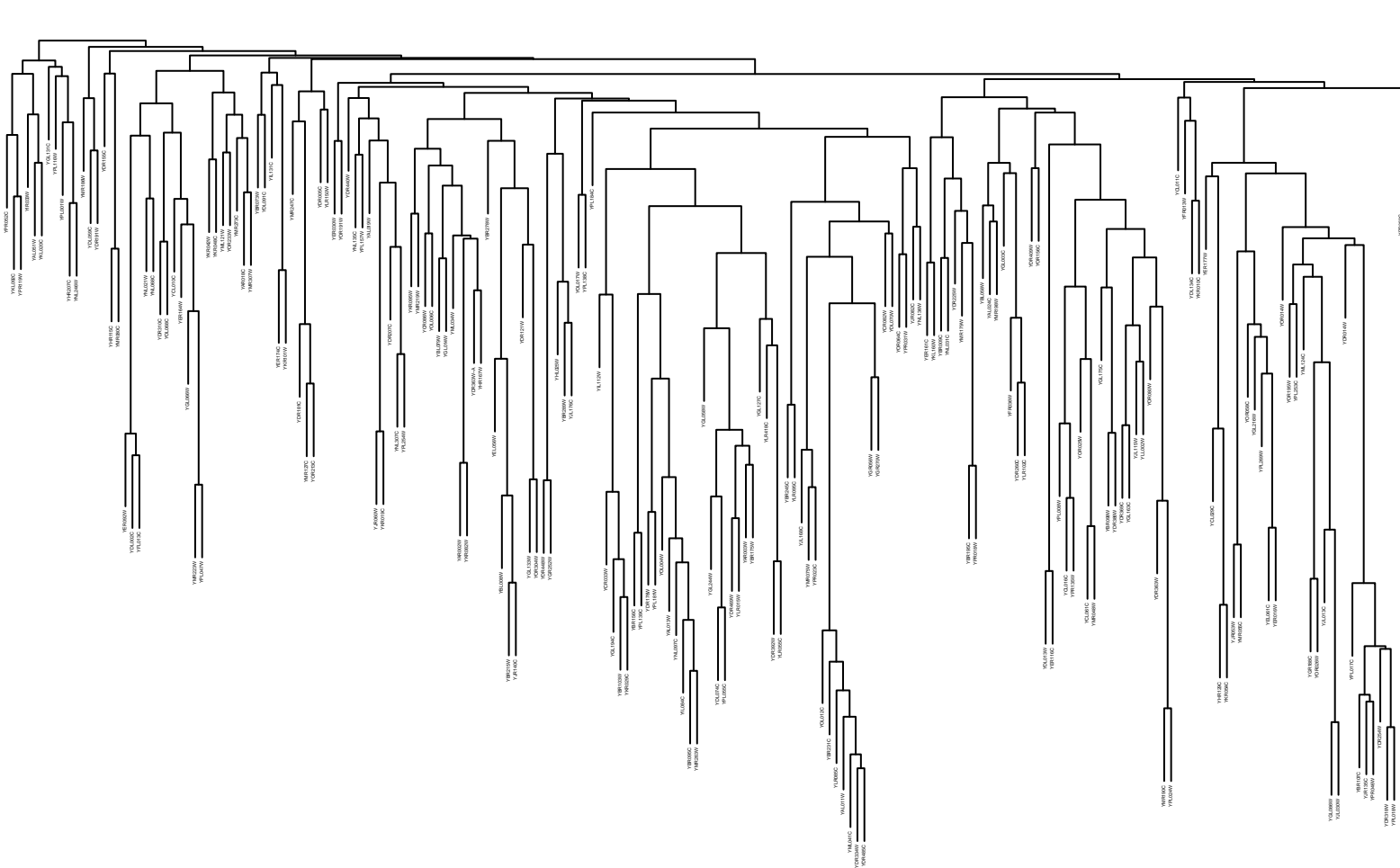


# chromatin\_GO\_pearson\_average

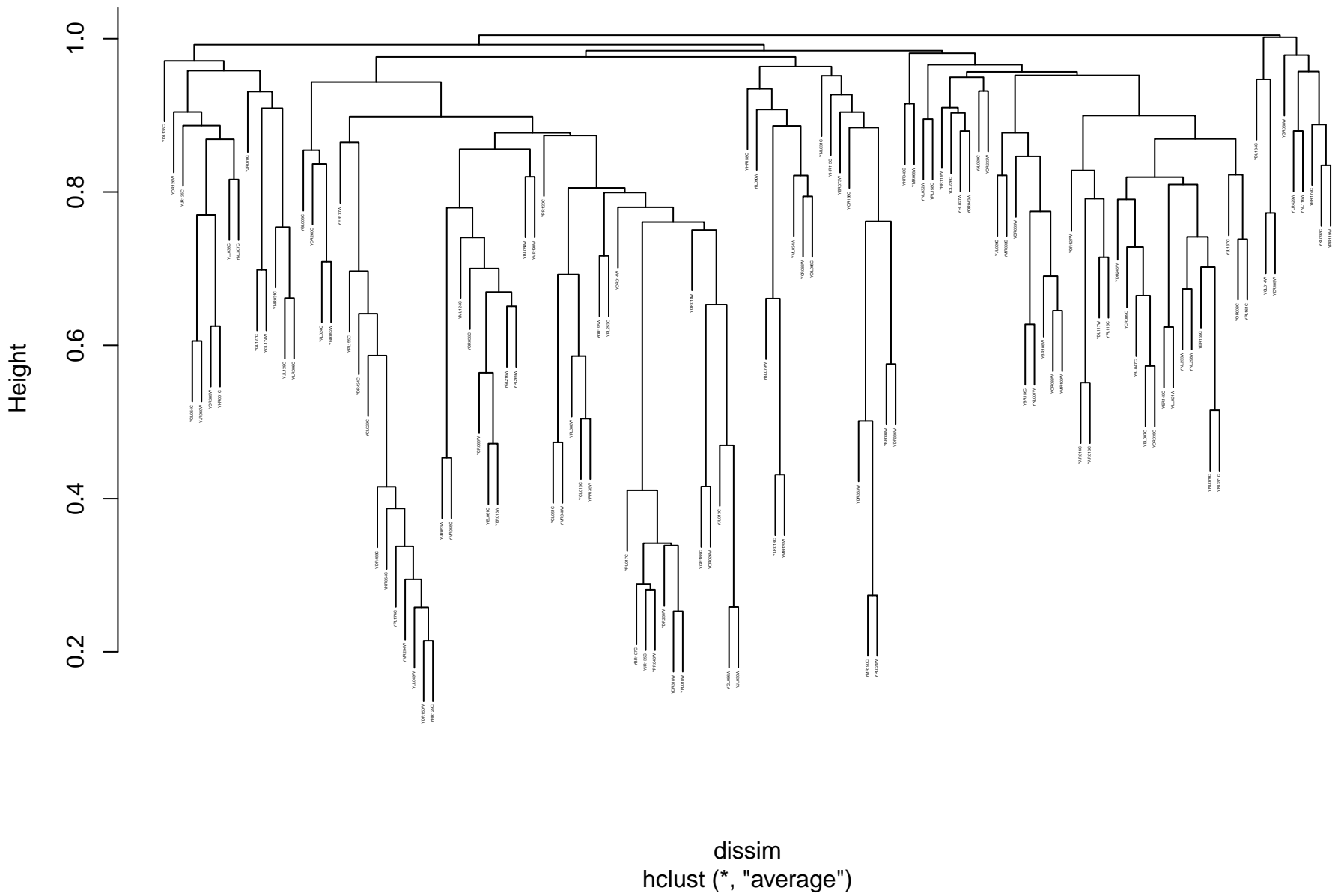
Height

1.0  
0.8  
0.6  
0.4  
0.2

dissim  
hclust (\*, "average")

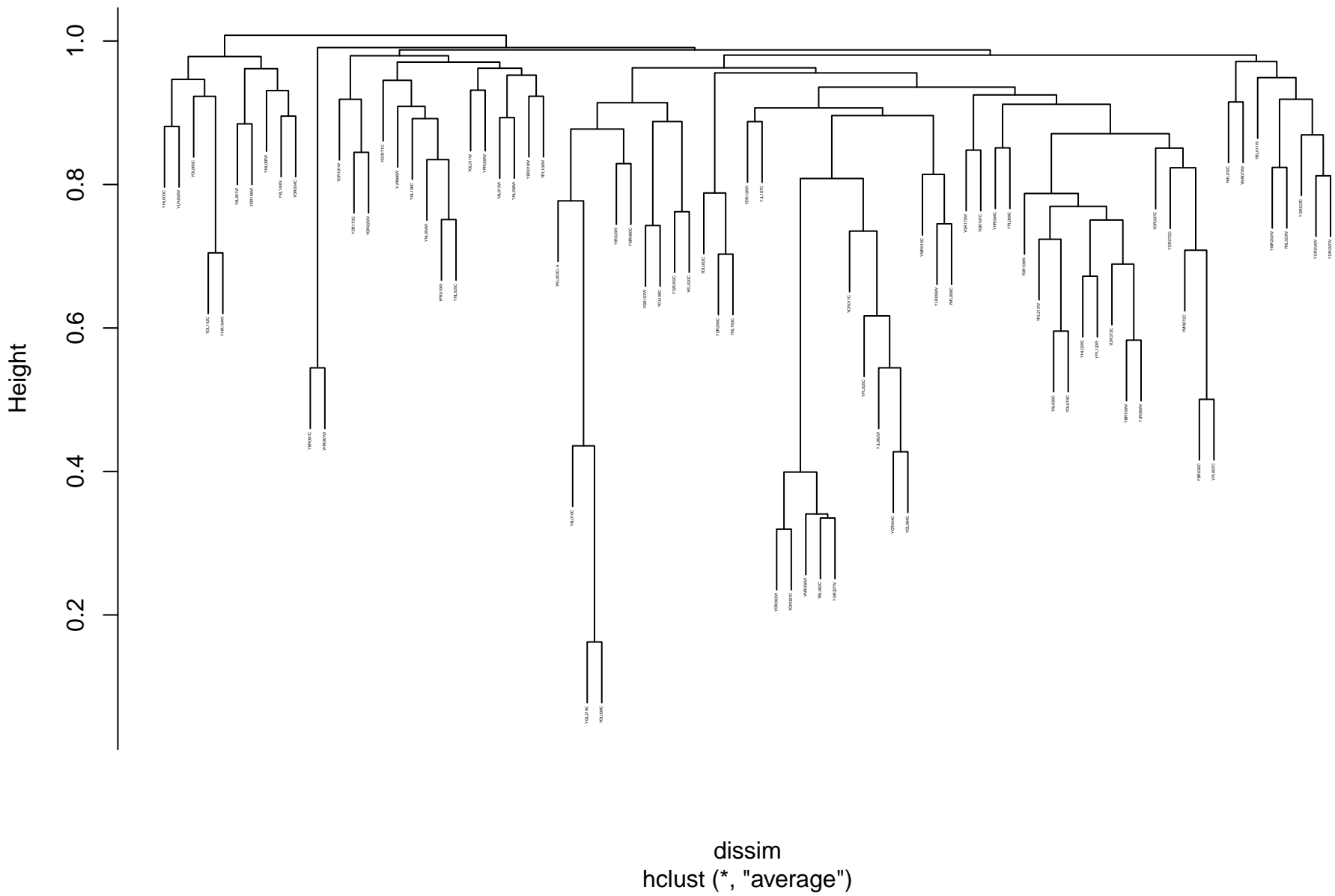


# cytoskeleton\_GO\_pearson\_average

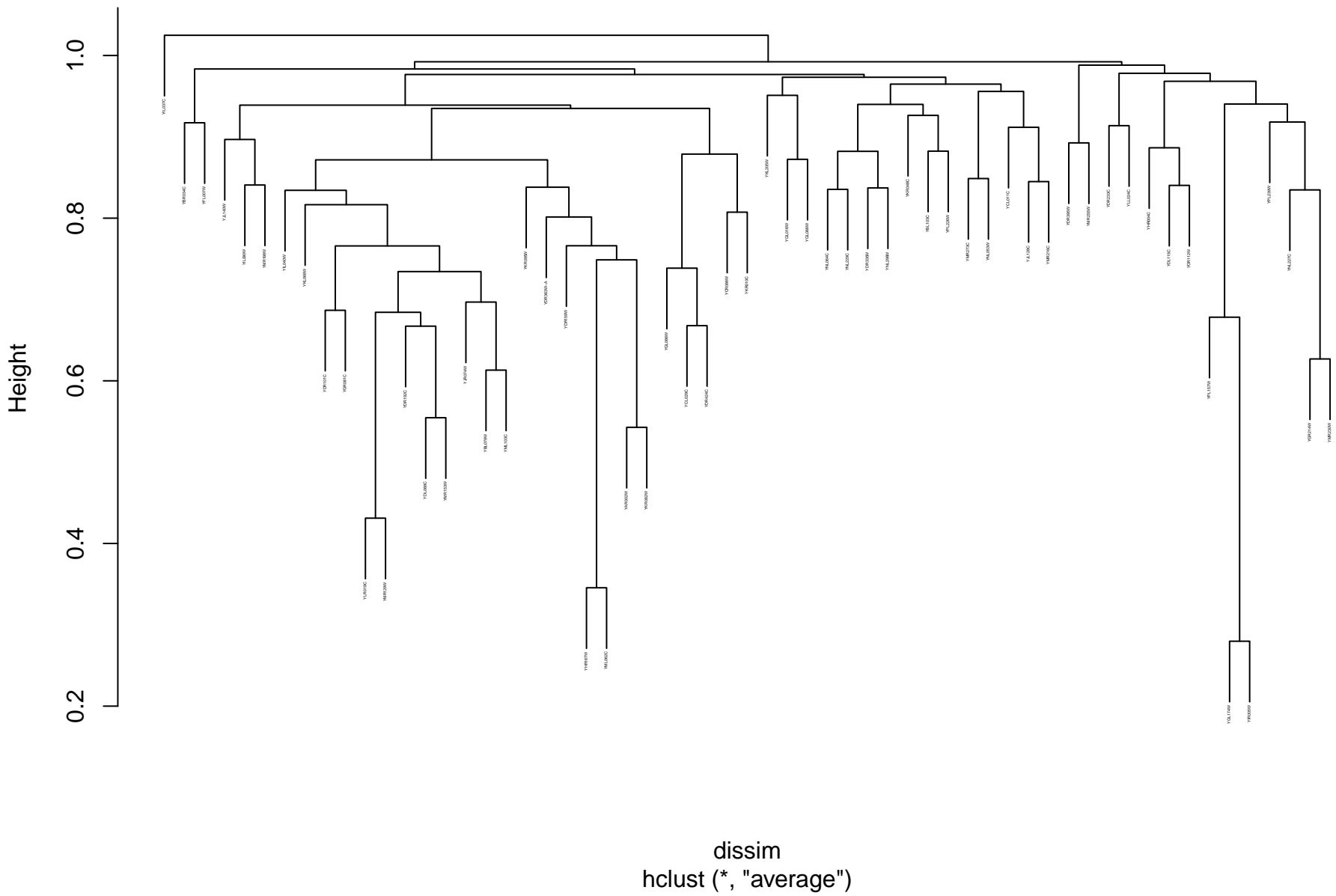




# lipids\_GO\_pearson\_average

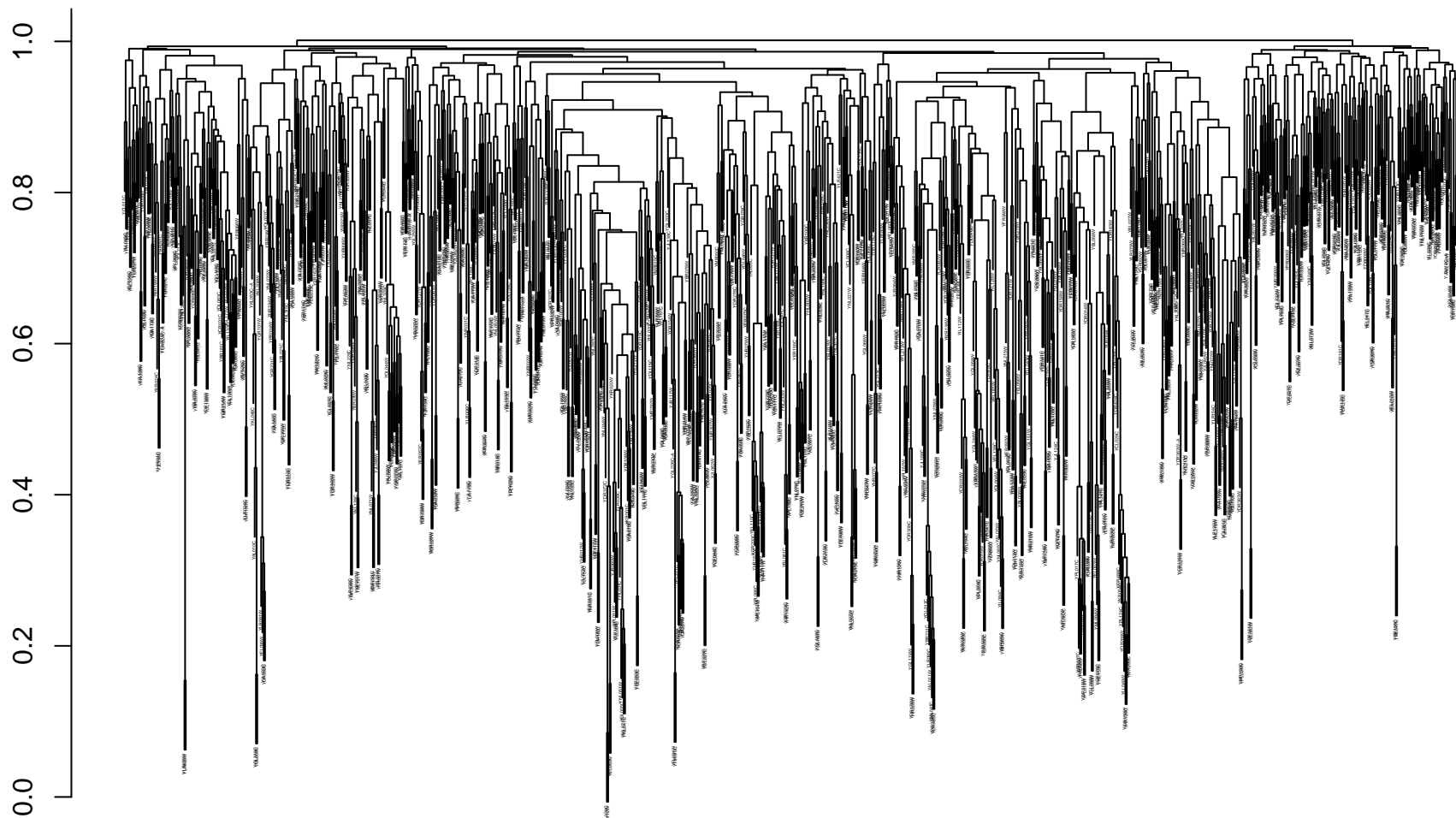


nuclear transport\_GO\_pearson\_average



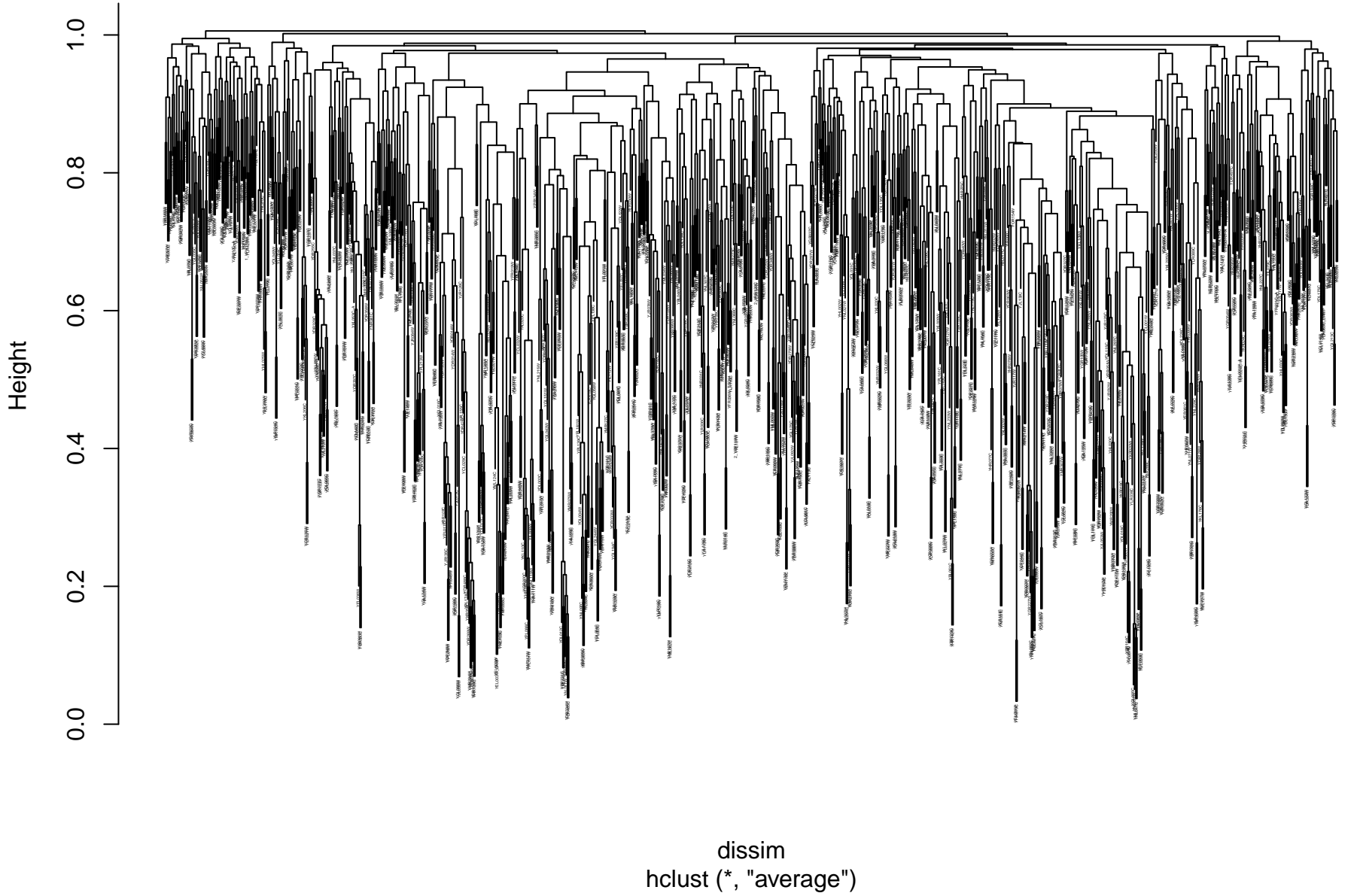
Height

library\_pearson\_average



dissim  
hclust (\*, "average")

**gene\_pearson\_average**

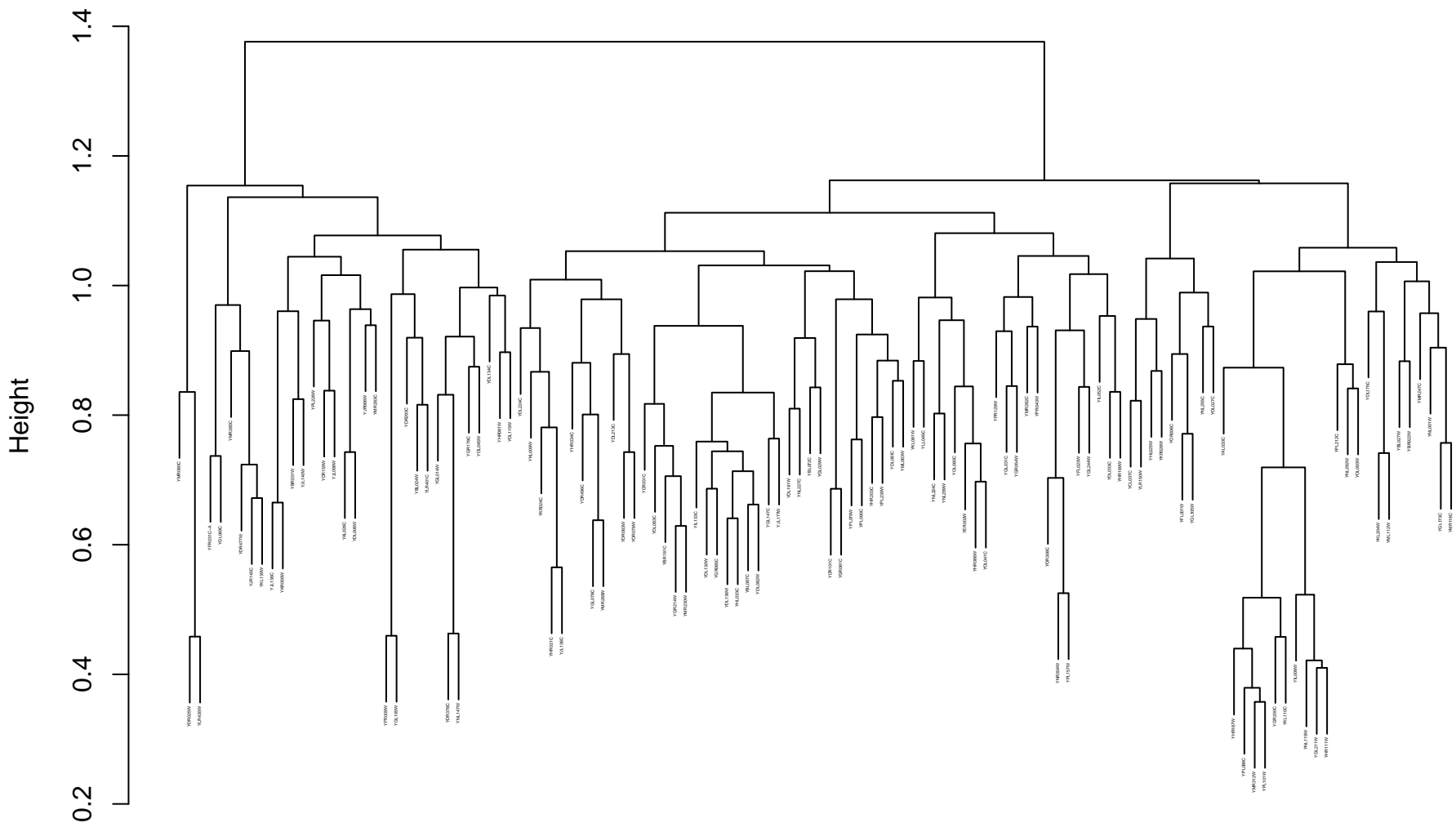




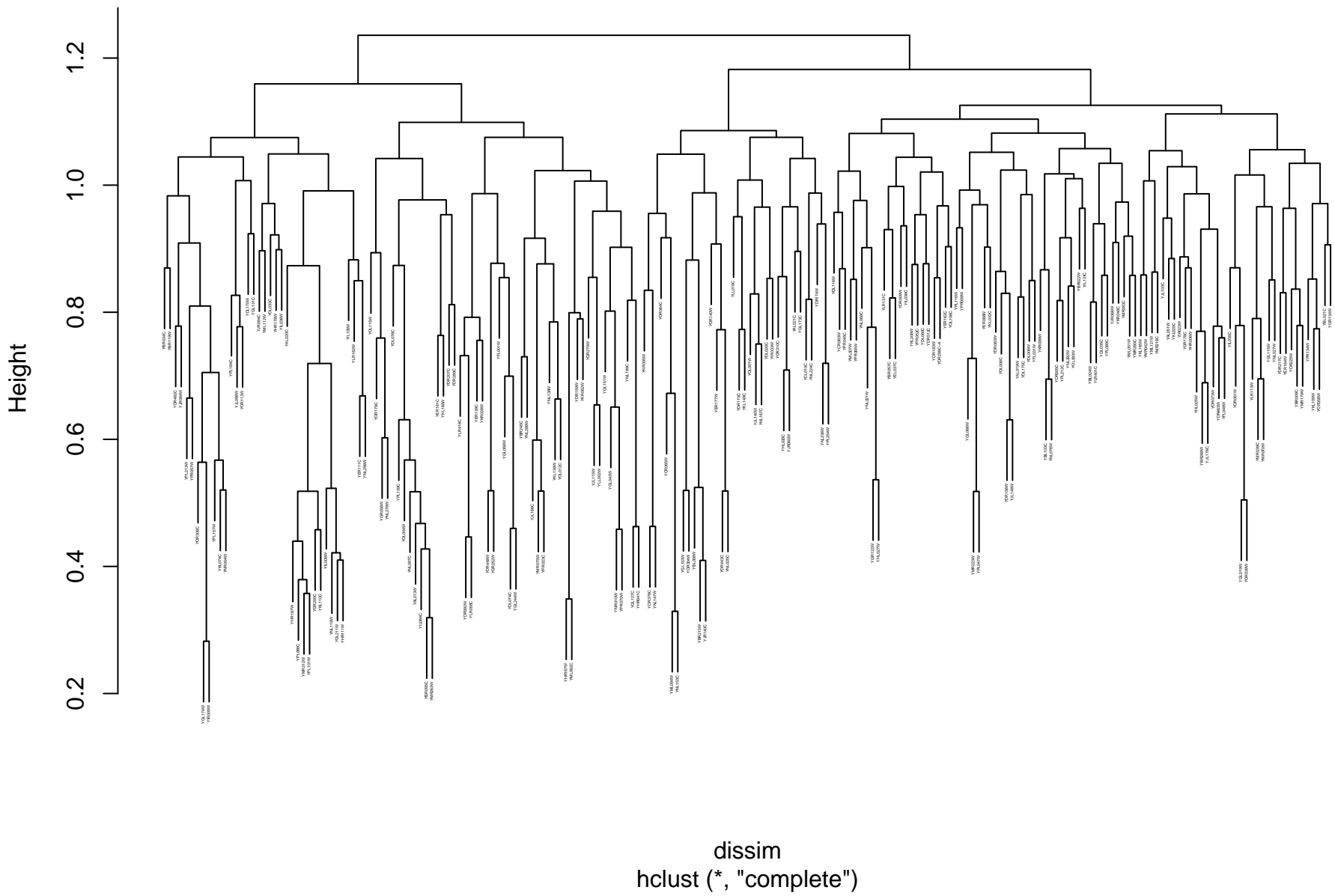
```

dissim
hclust (*, "complete")

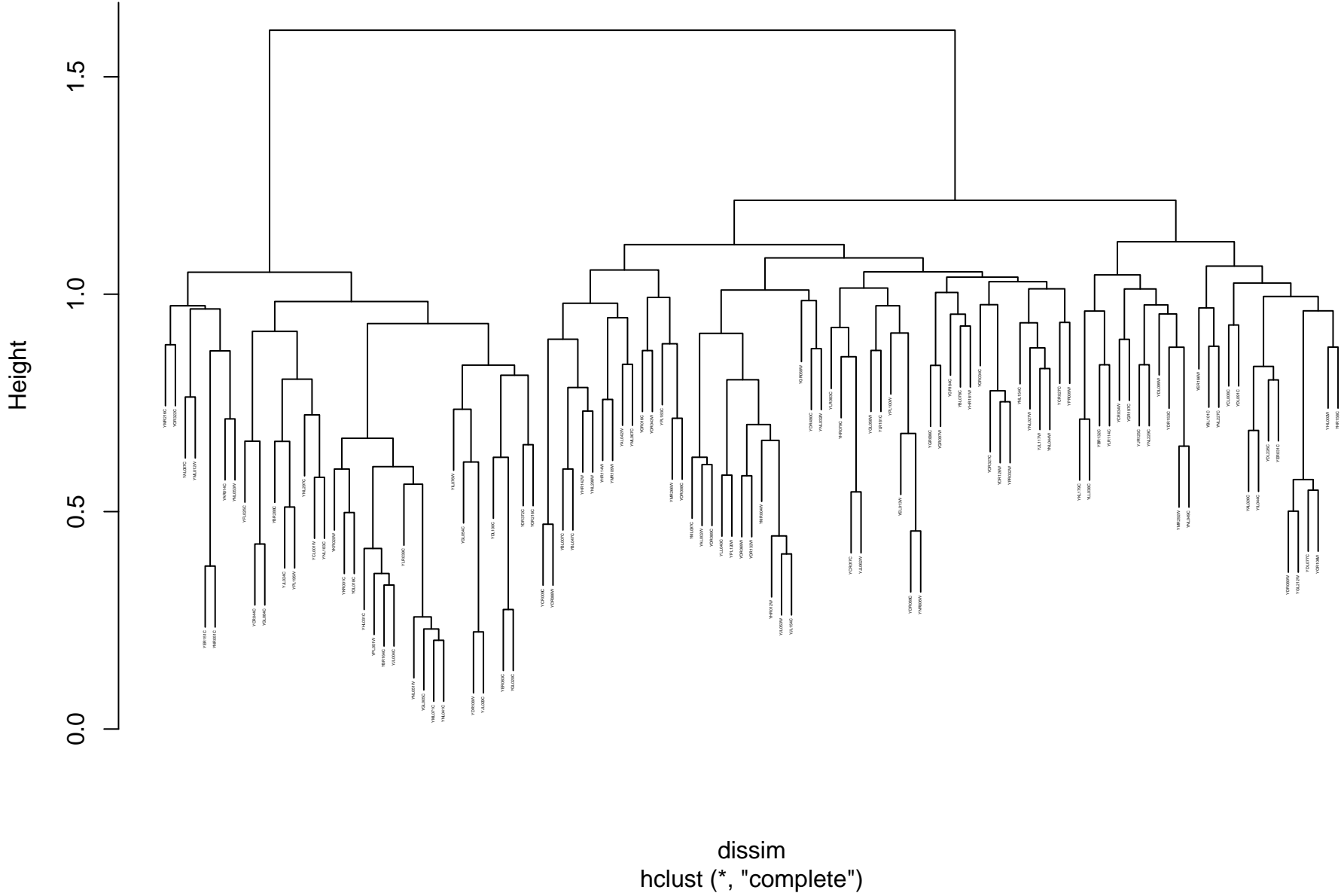
```



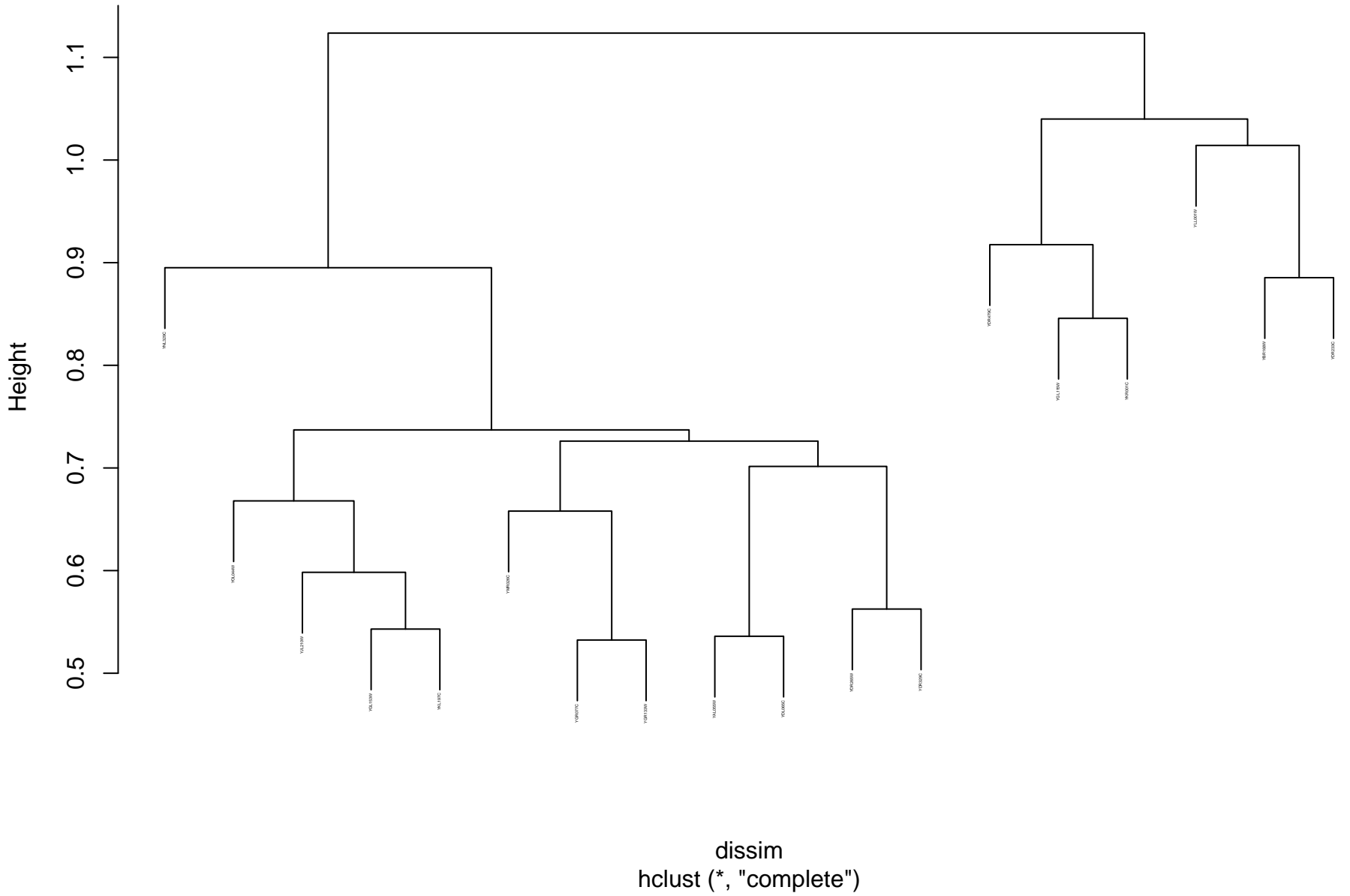
# transcription and mRNA processing\_GO\_correlation\_complete



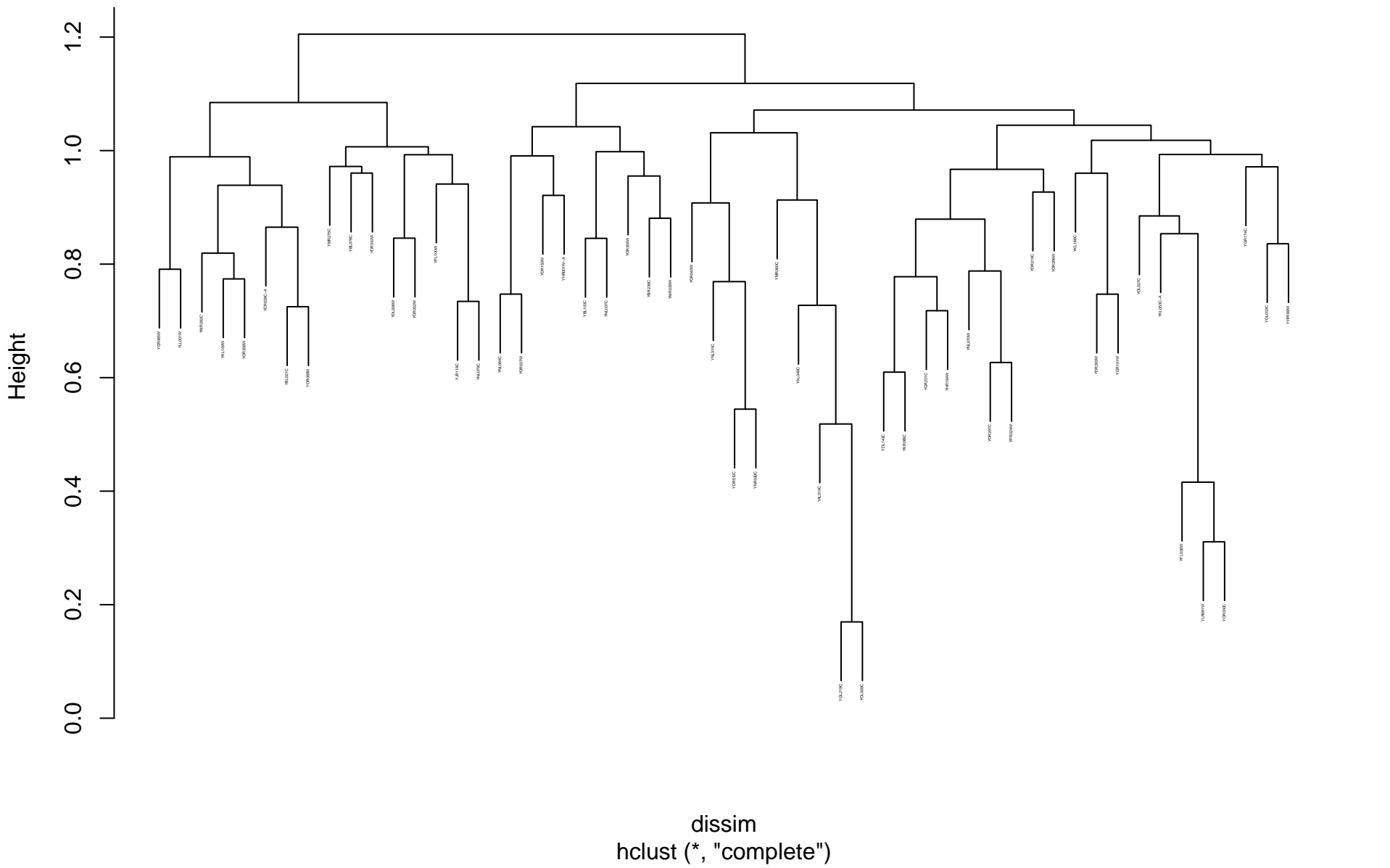
Golgi and ER\_GO\_correlation\_complete



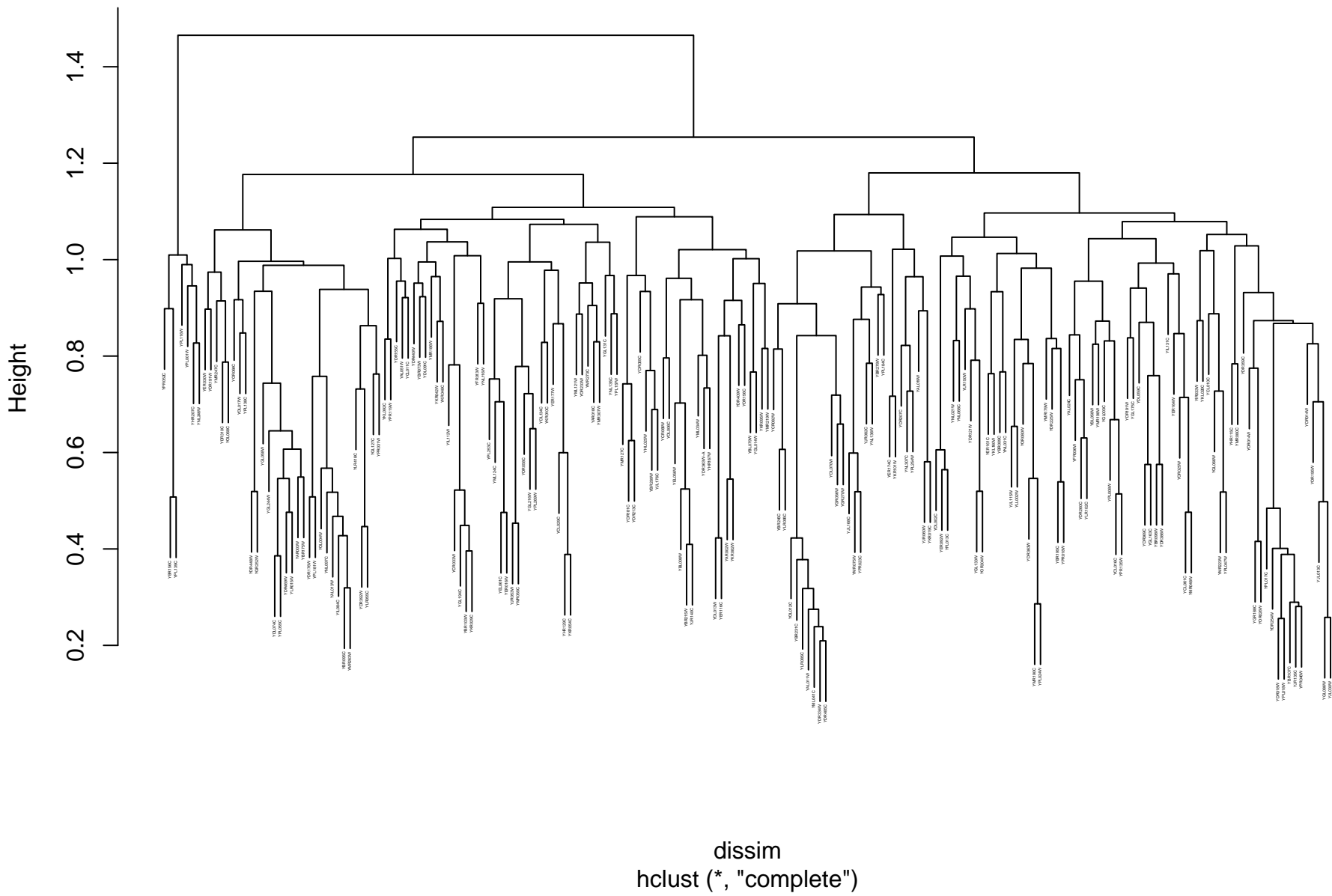
**peroxisome\_GO\_correlation\_complete**



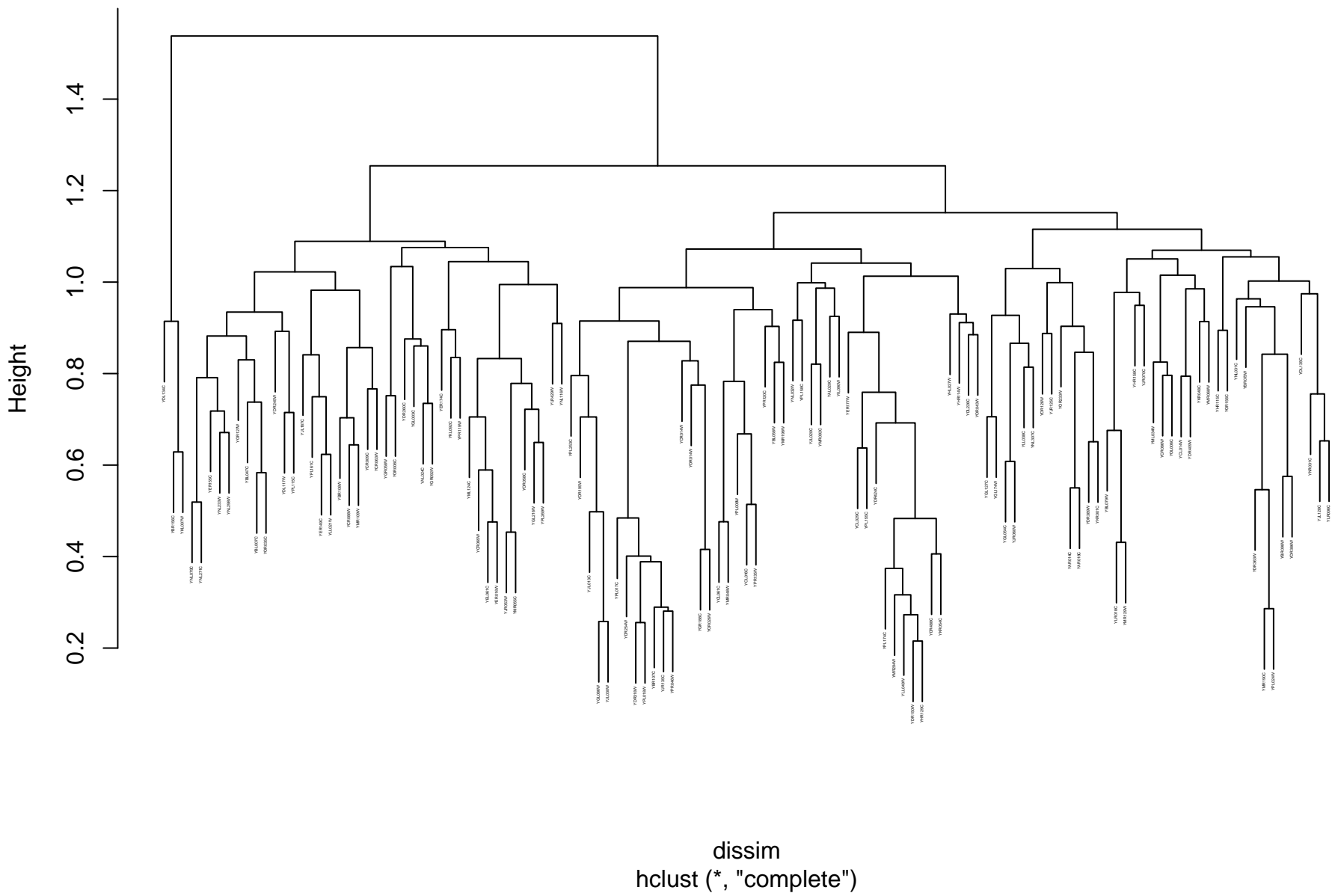
# mitochondrion\_GO\_correlation\_complete



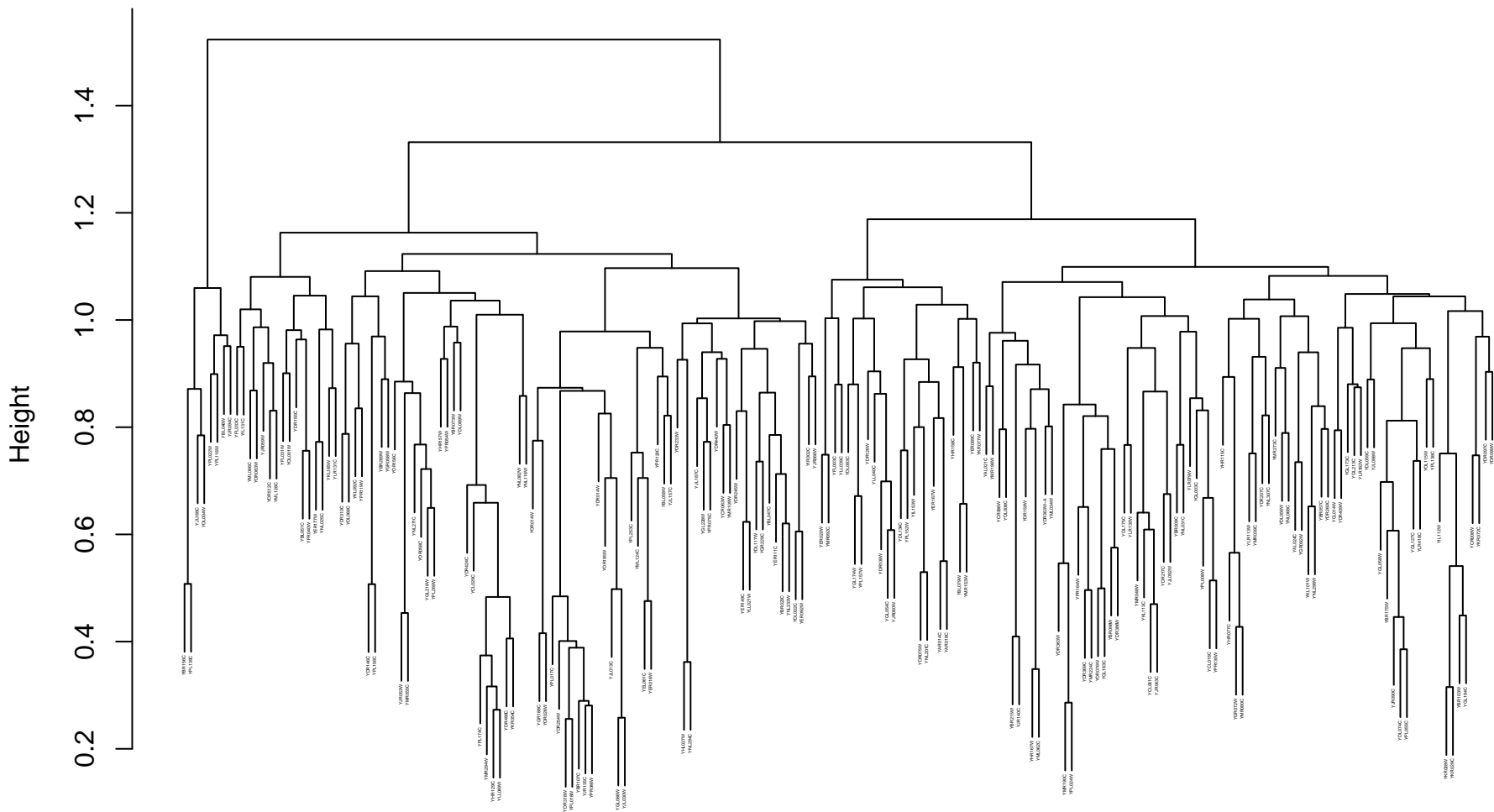
# chromatin\_GO\_correlation\_complete



**cytoskeleton\_GO\_correlation\_complete**

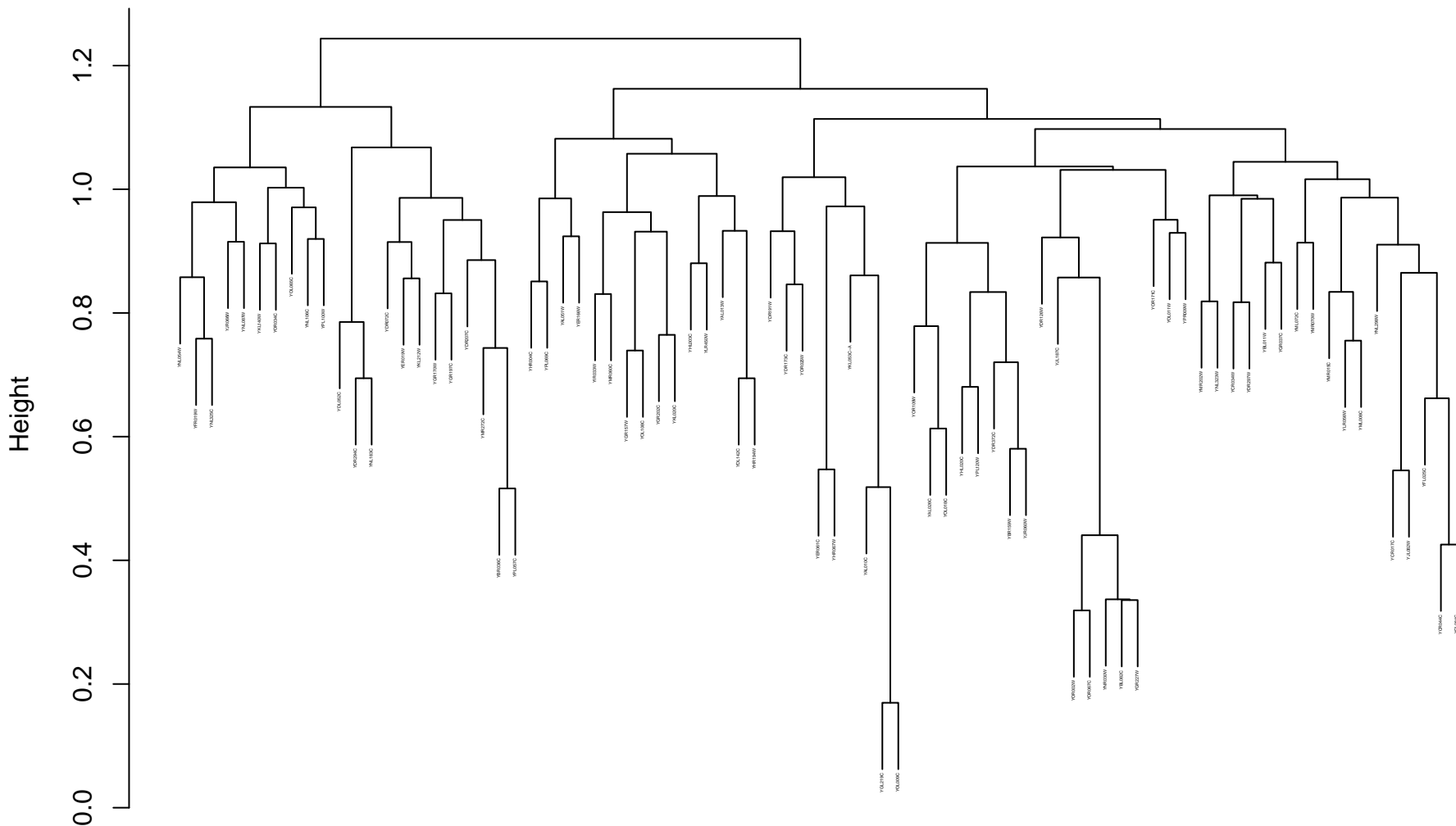


```
dissim
hclust (*, "complete")
```

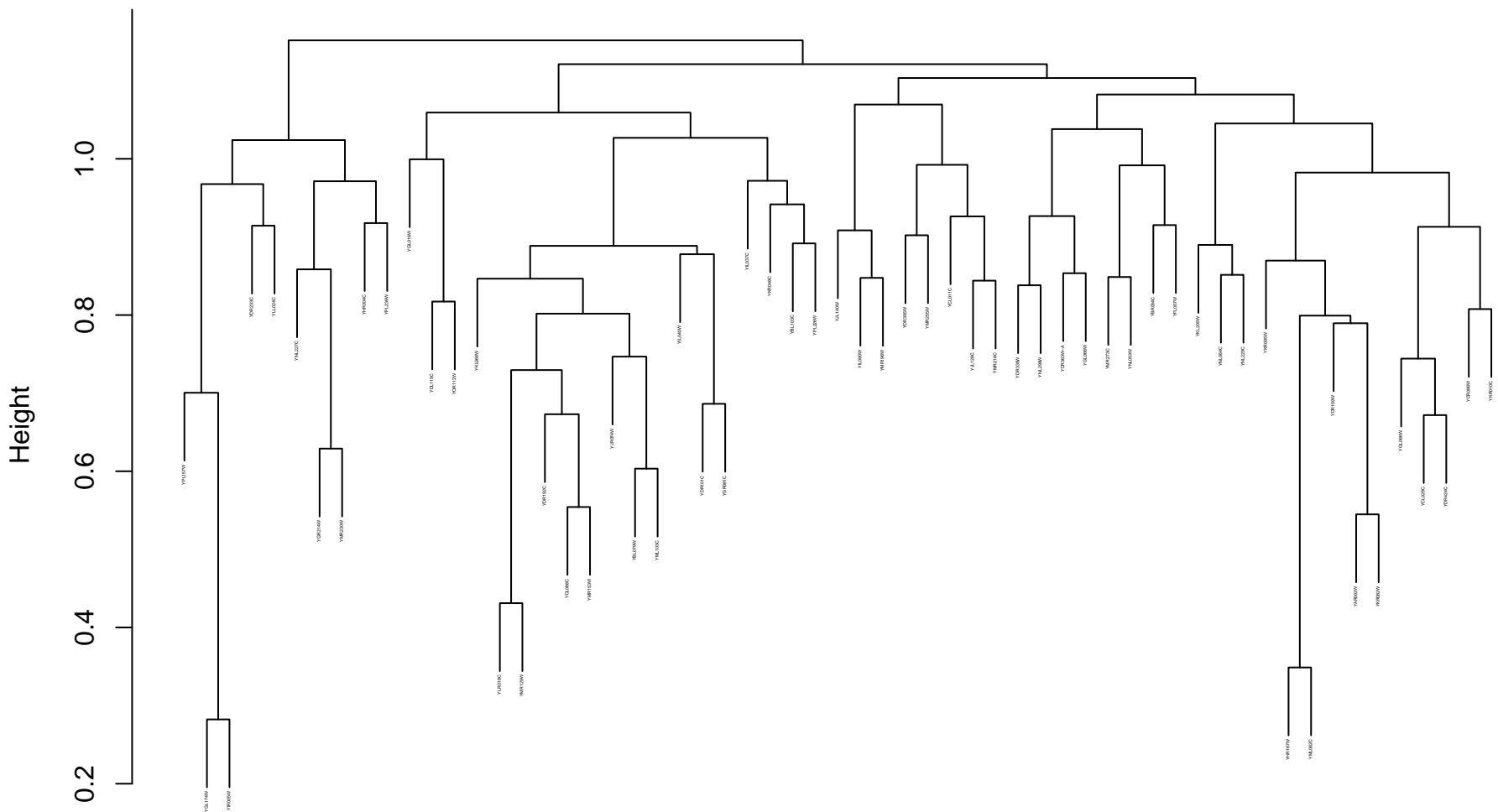




```
dissim
hclust (*, "complete")
```

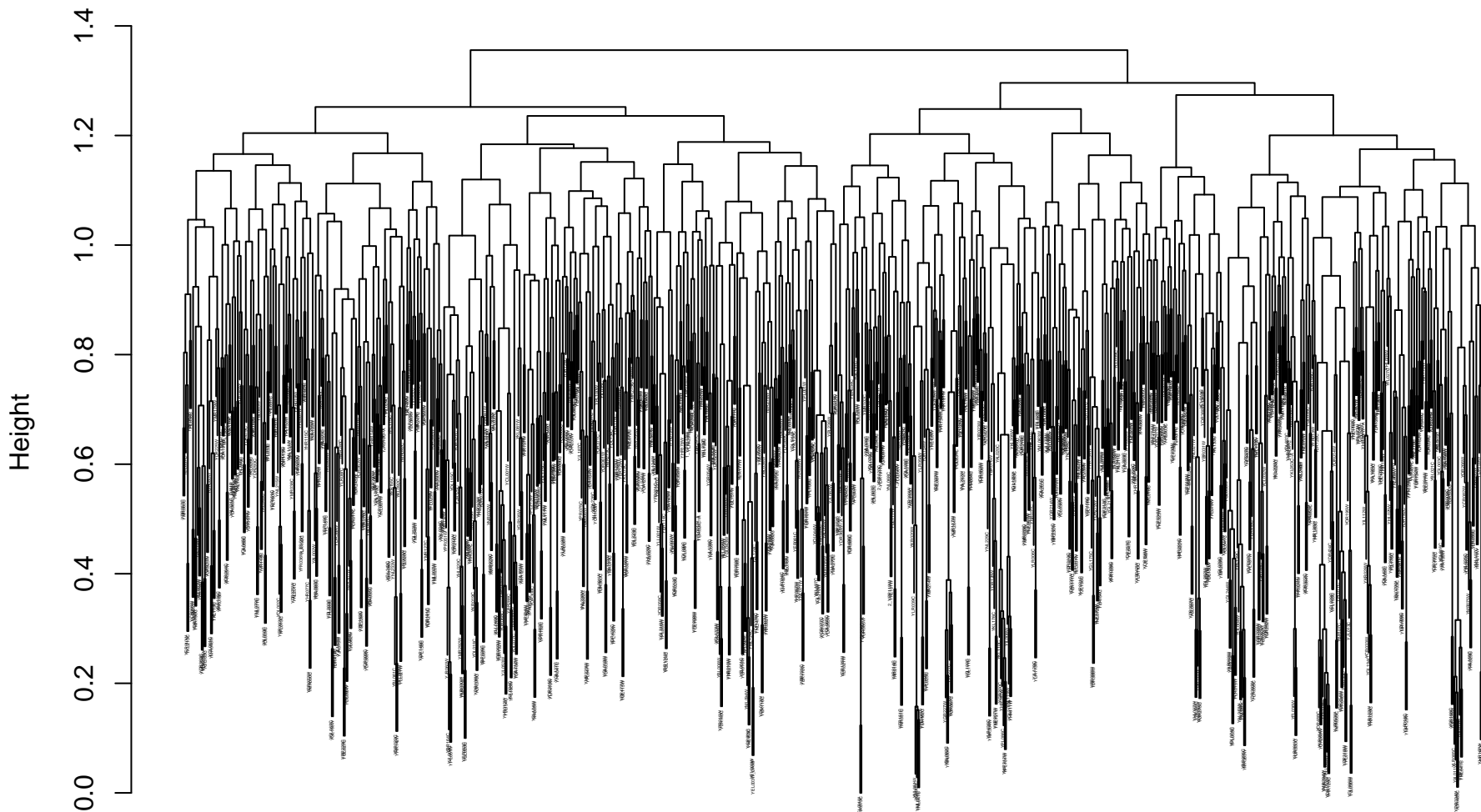


```
dissim
hclust (*, "complete")
```





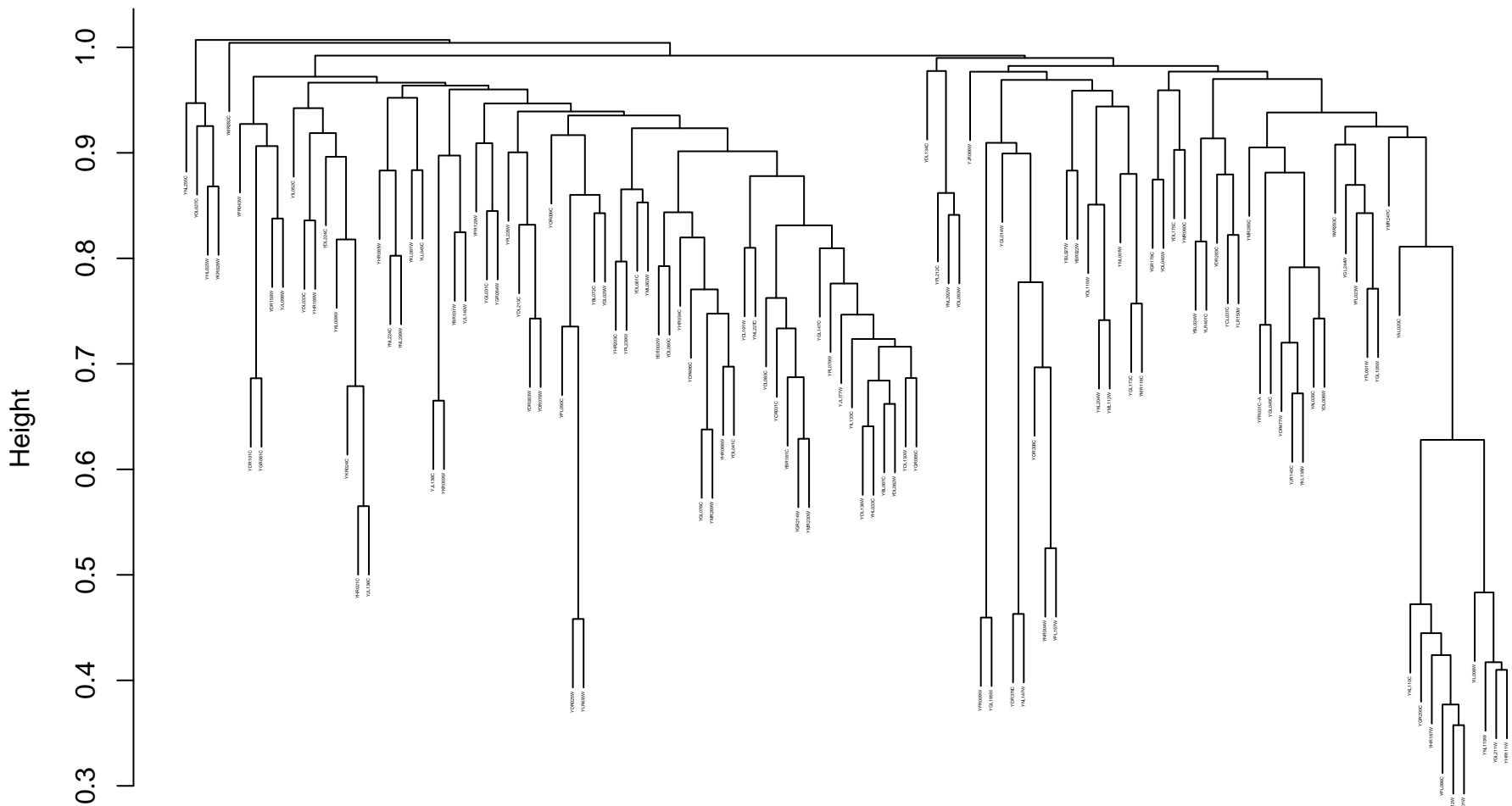
gene\_correlation\_complete



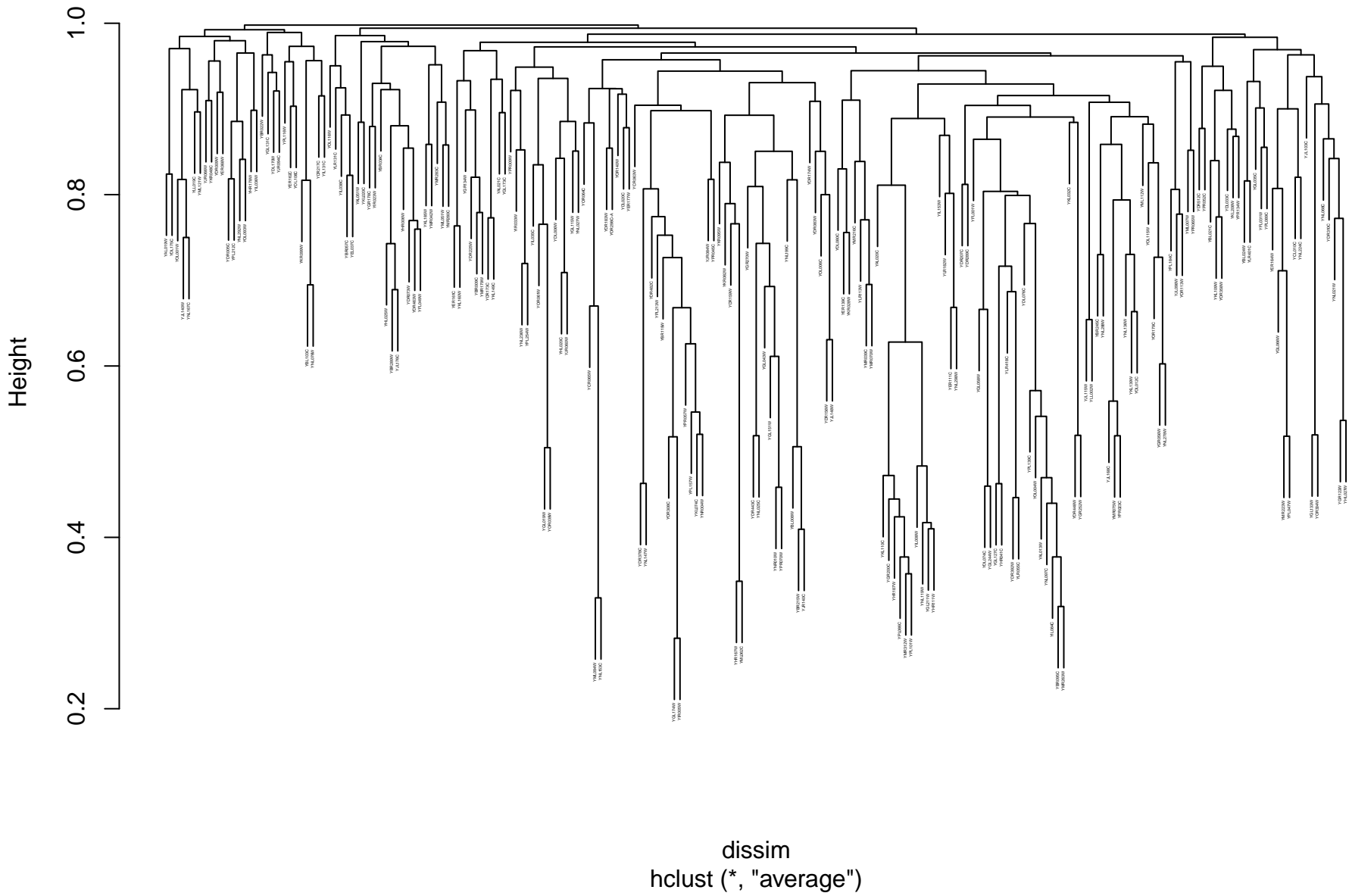
```

dissim
hclust (*, "average")

```



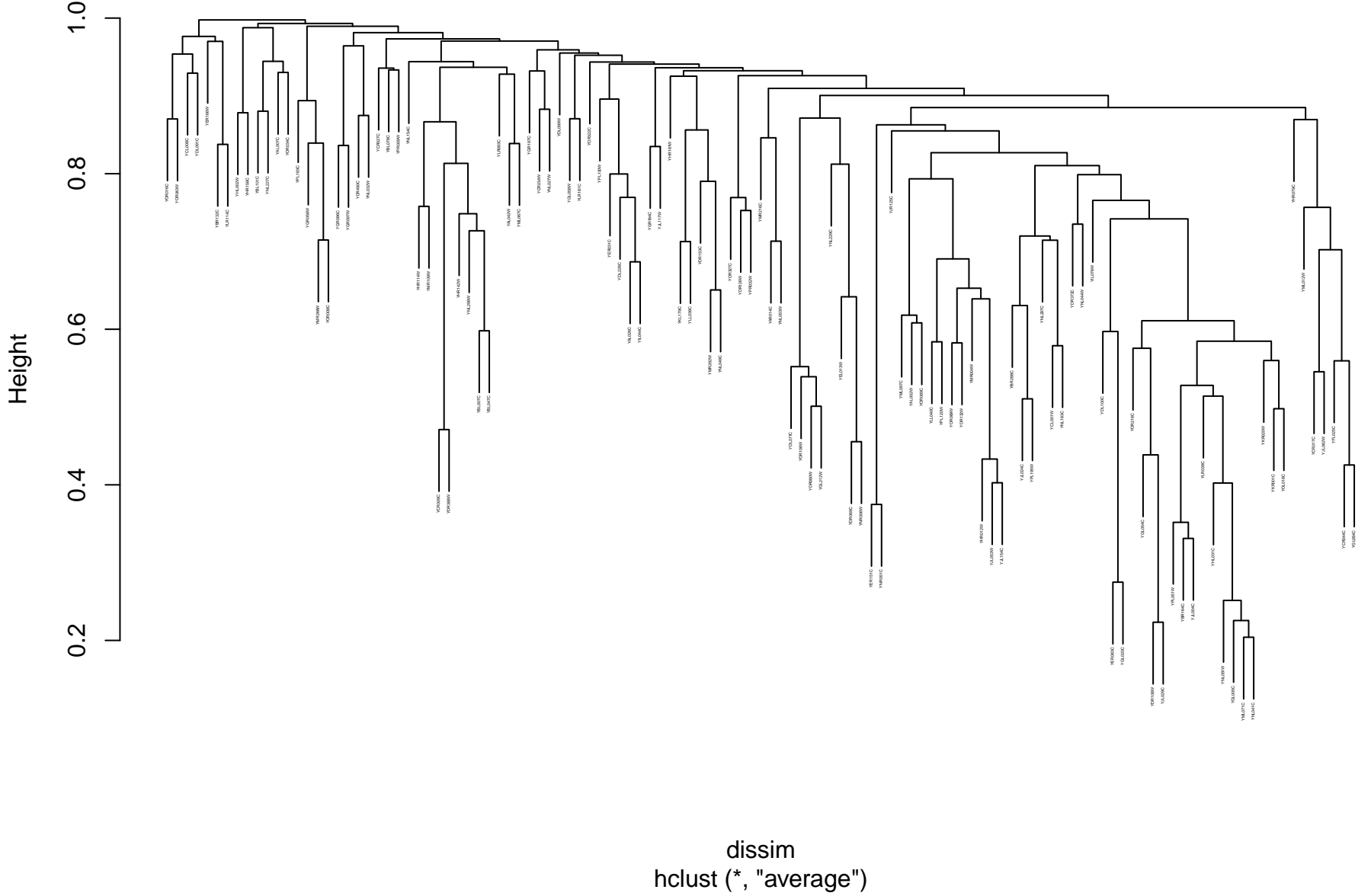
transcription and mRNA processing\_GO\_correlation\_average



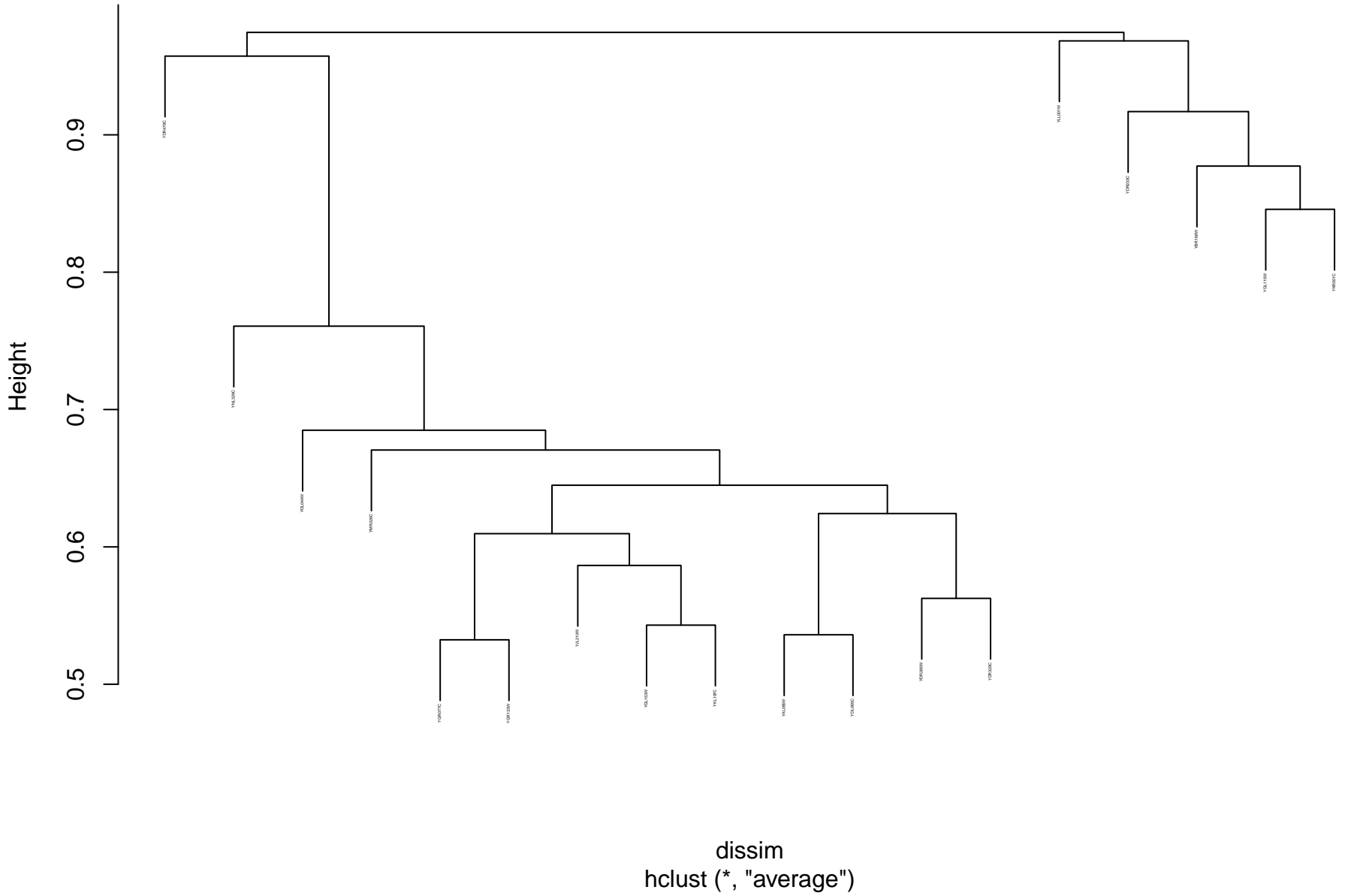
```

dissim
hclust (*, "average")

```



**peroxisome\_GO\_correlation\_average**





```

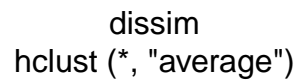
dissim
hclust (*, "average")

```

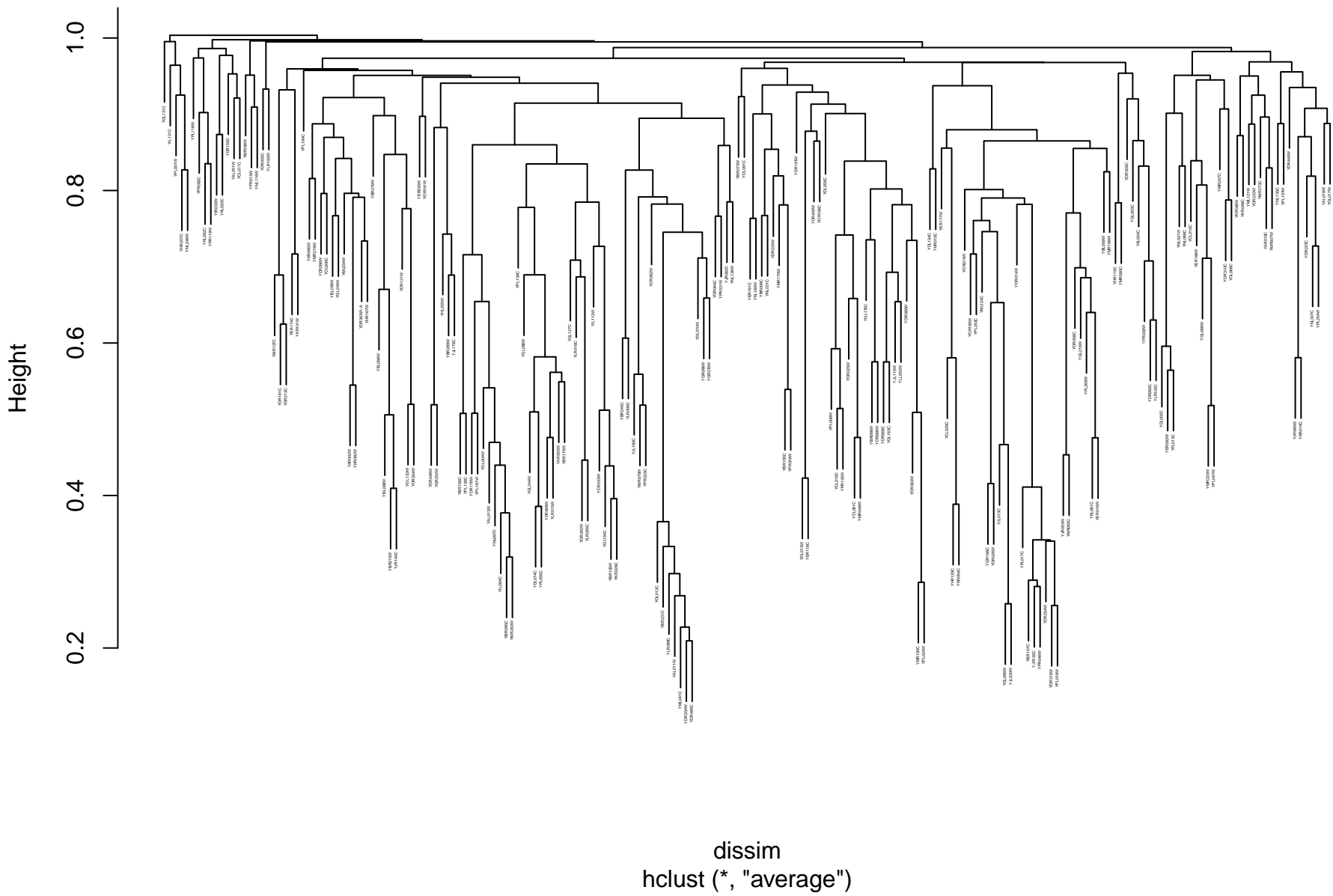
```

dissim
hclust (*, "average")

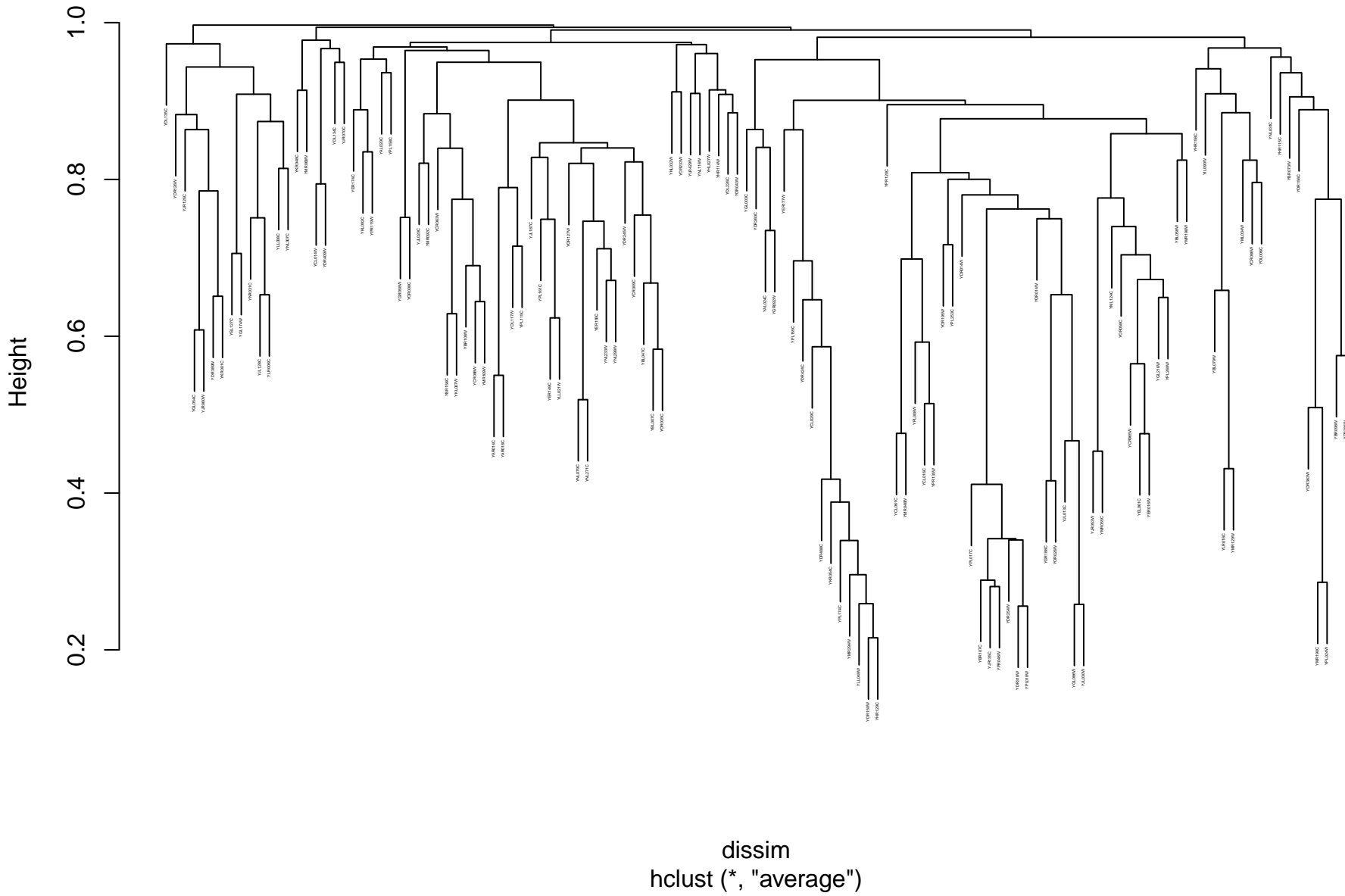
```



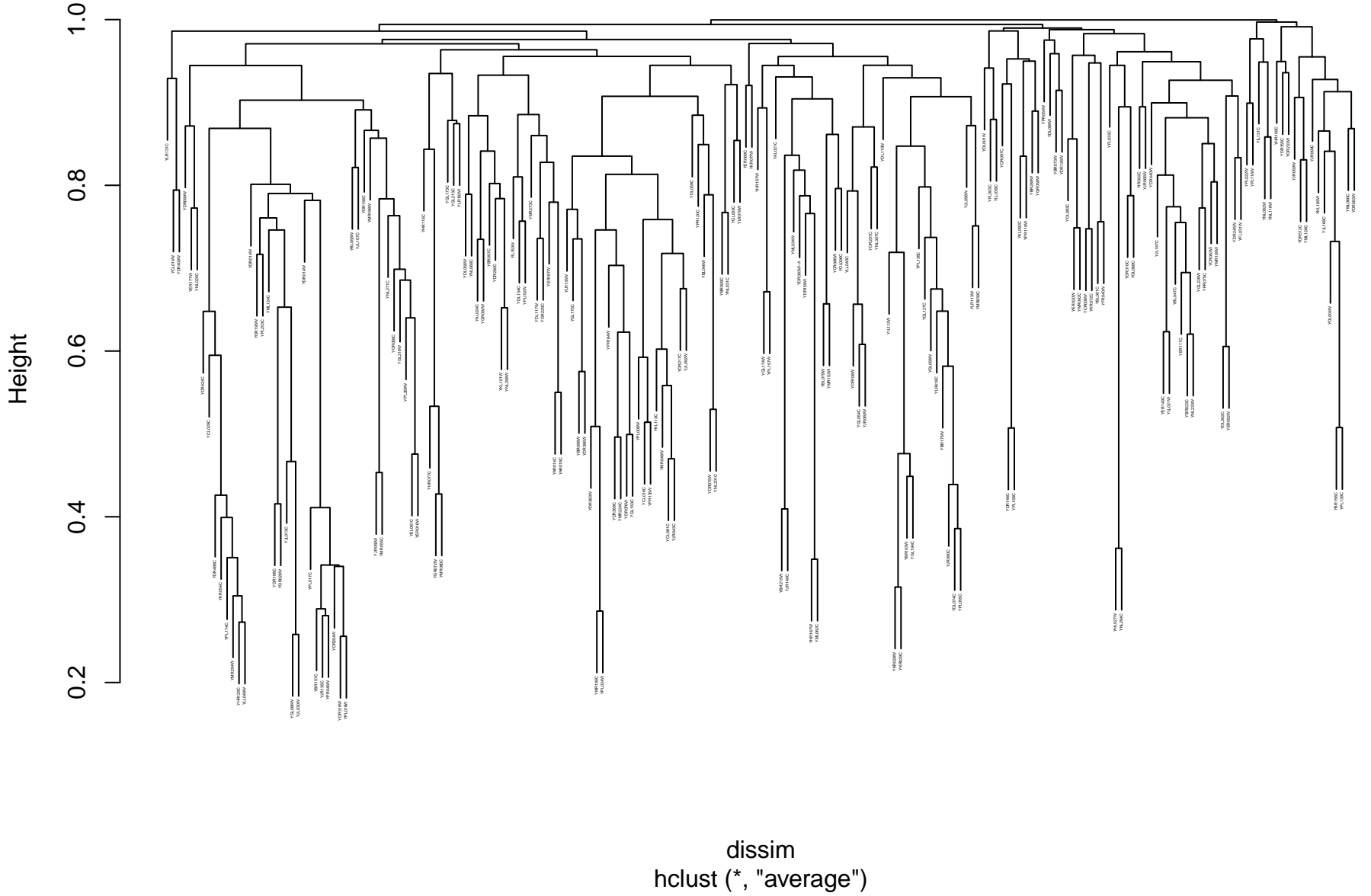
# chromatin\_GO\_correlation\_average



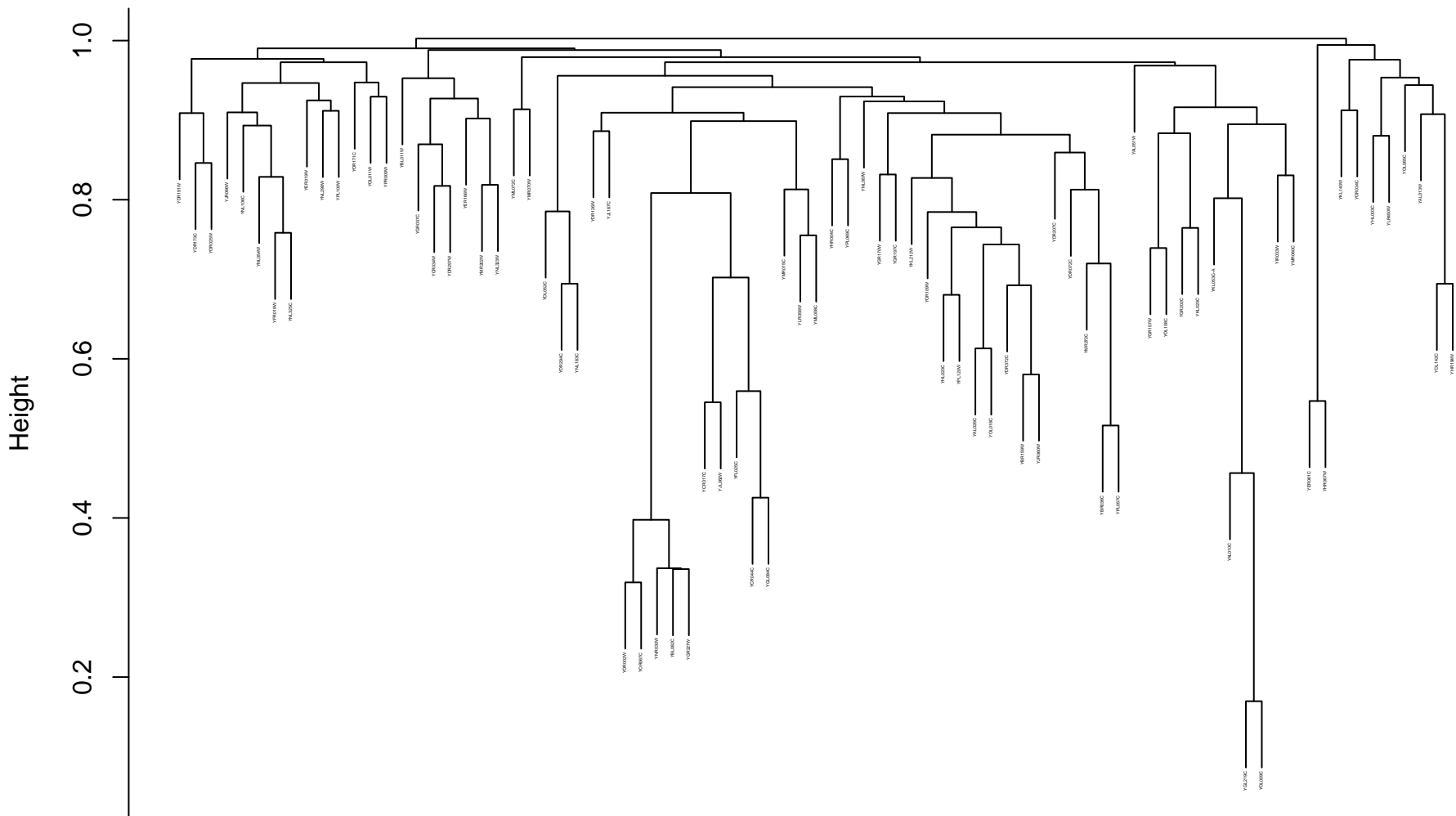
cytoskeleton\_GO\_correlation\_average



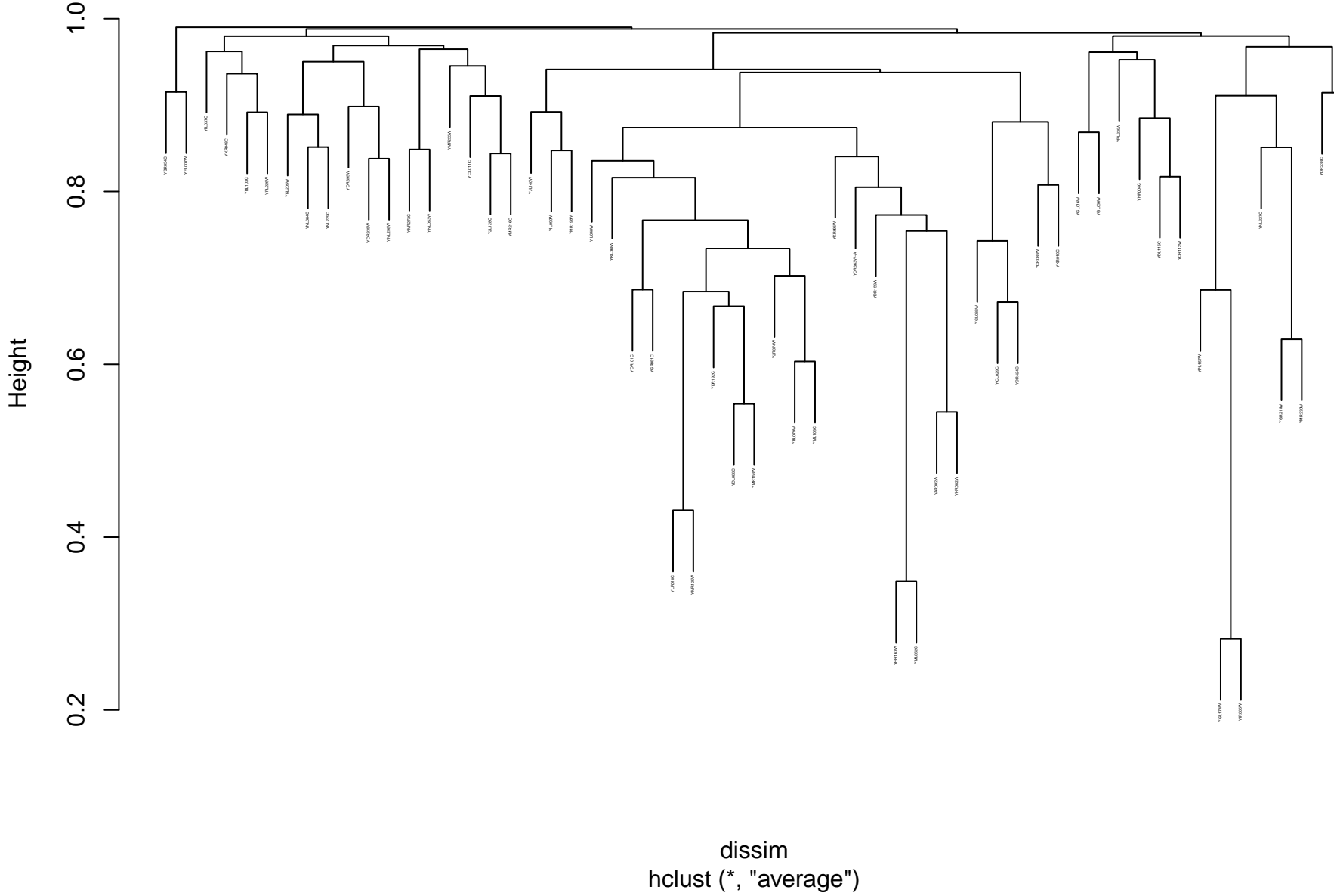
**cell cycle\_GO\_correlation\_average**



```
dissim
hclust (*, "average")
```



nuclear transport\_GO\_correlation\_average



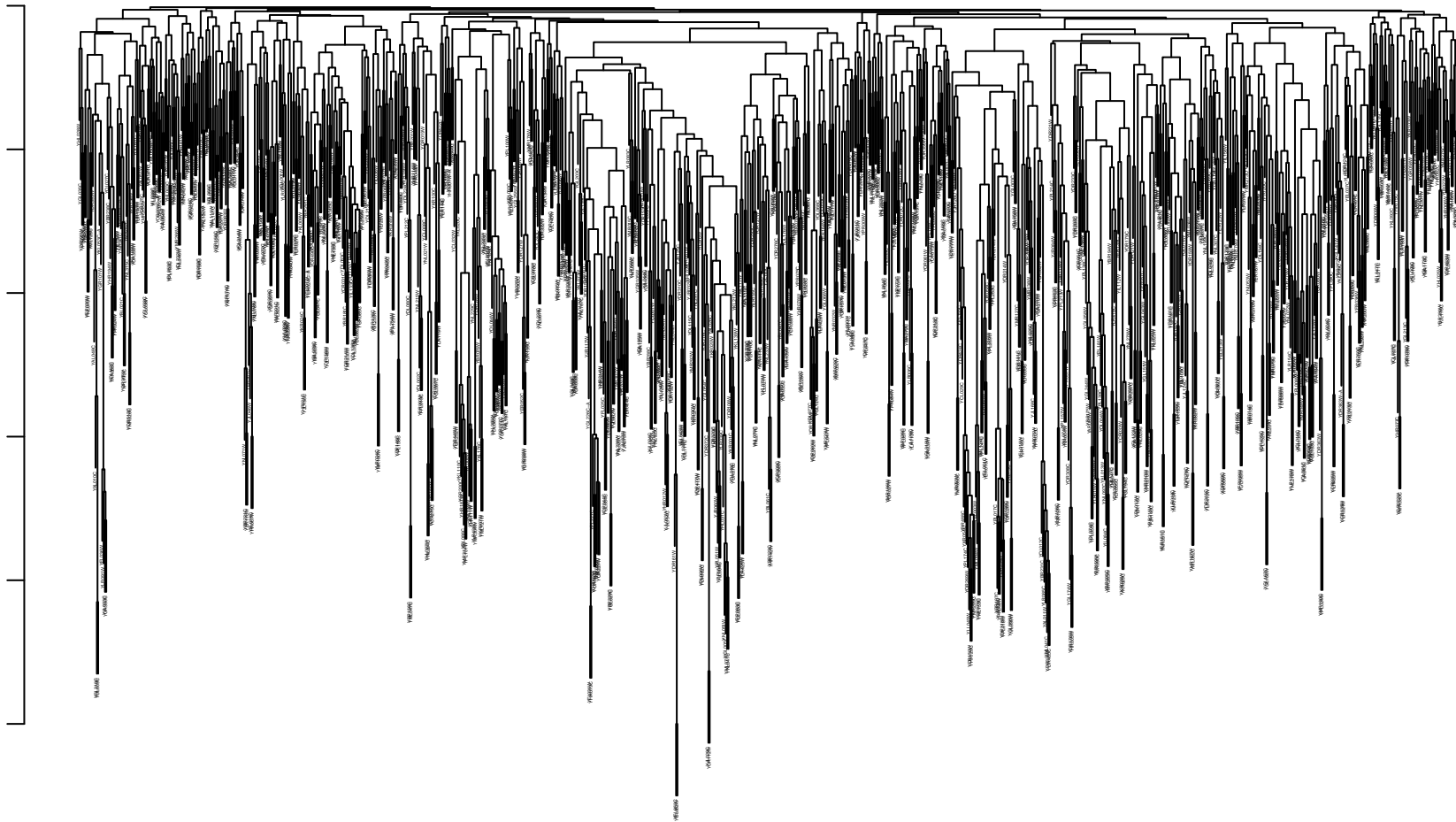
Height

library\_correlation\_average

8.000000e-01

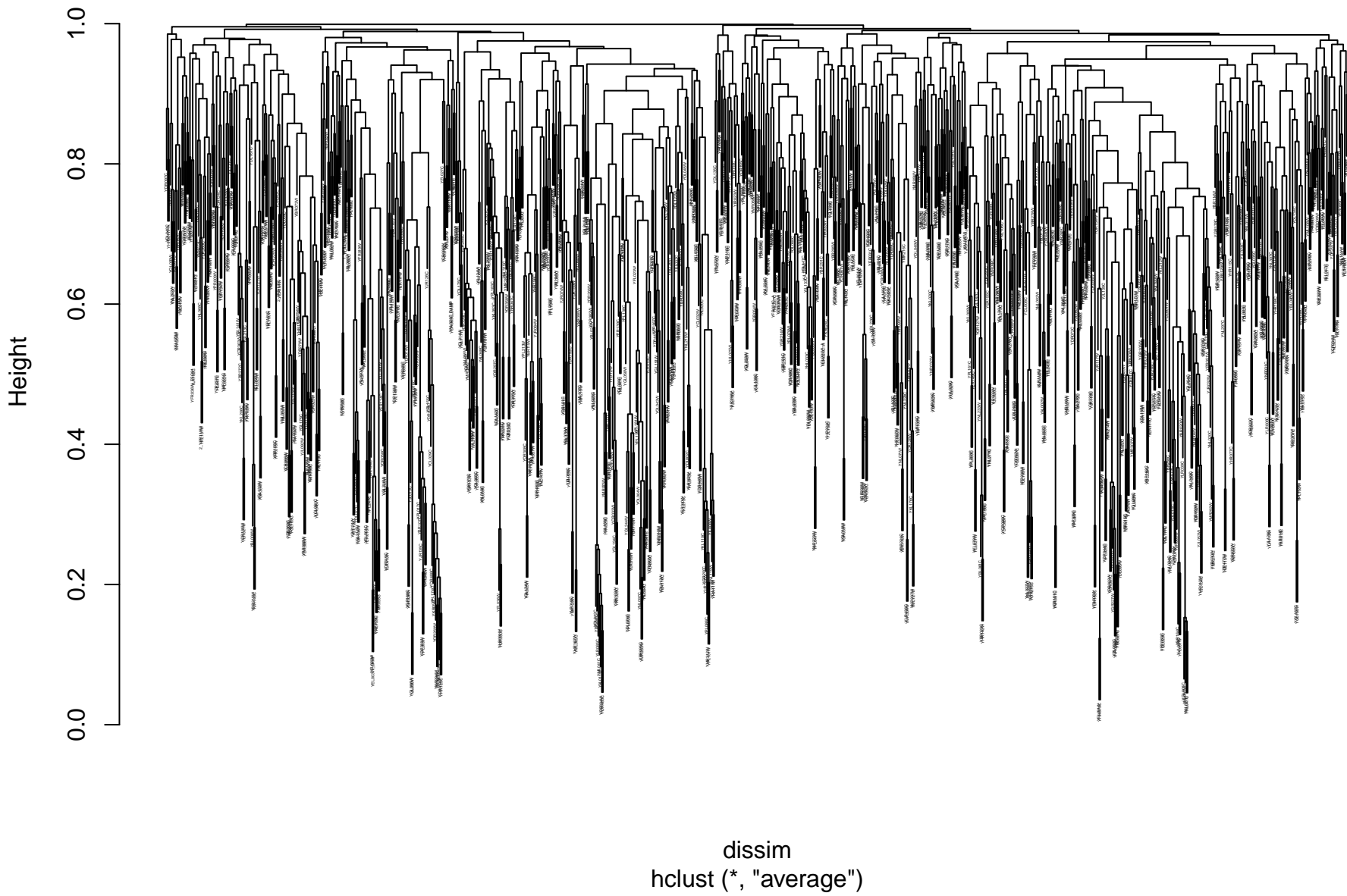
4.000000e-01

-6.017409e-14



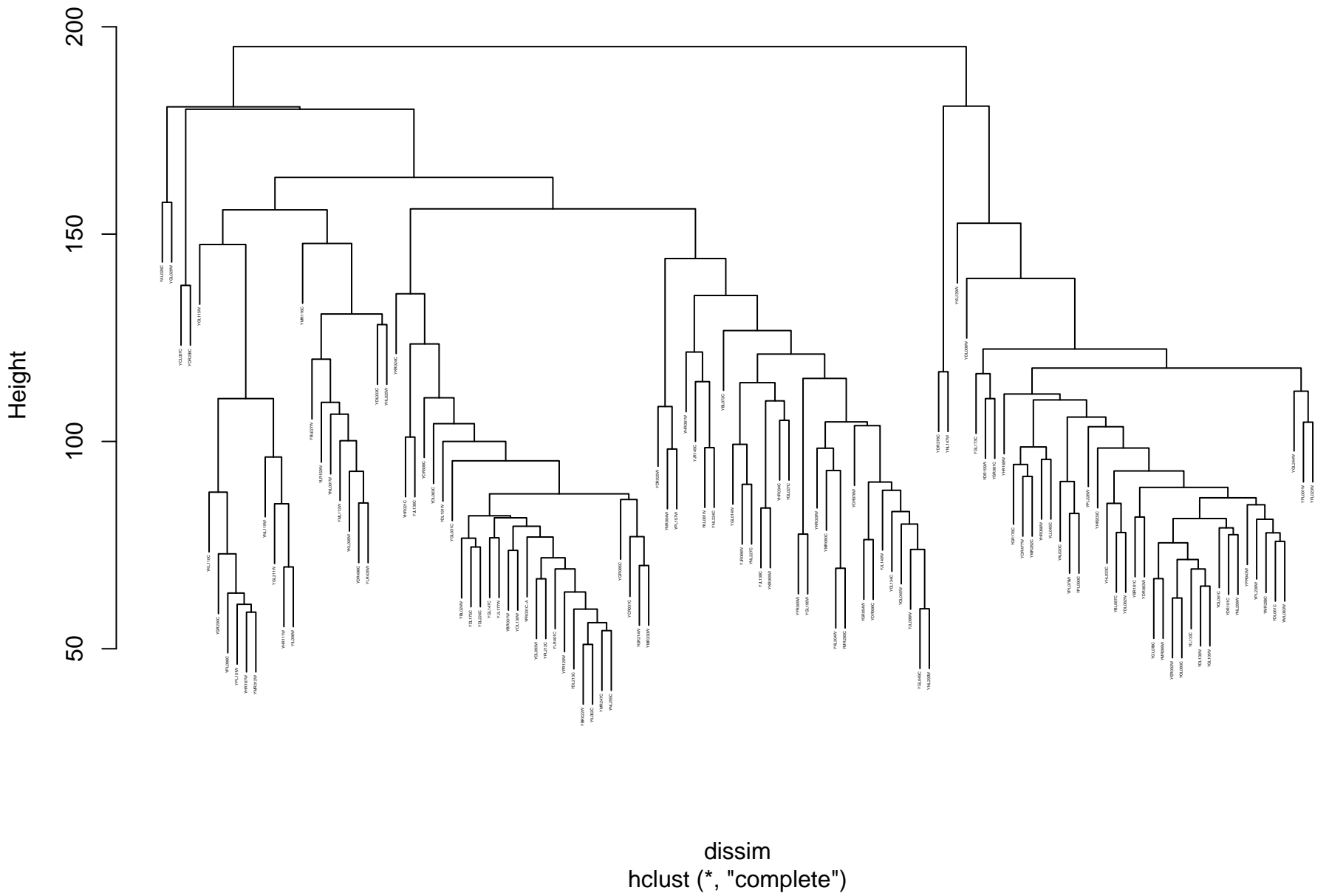
dissim  
hclust (\*, "average")

# gene\_correlation\_average

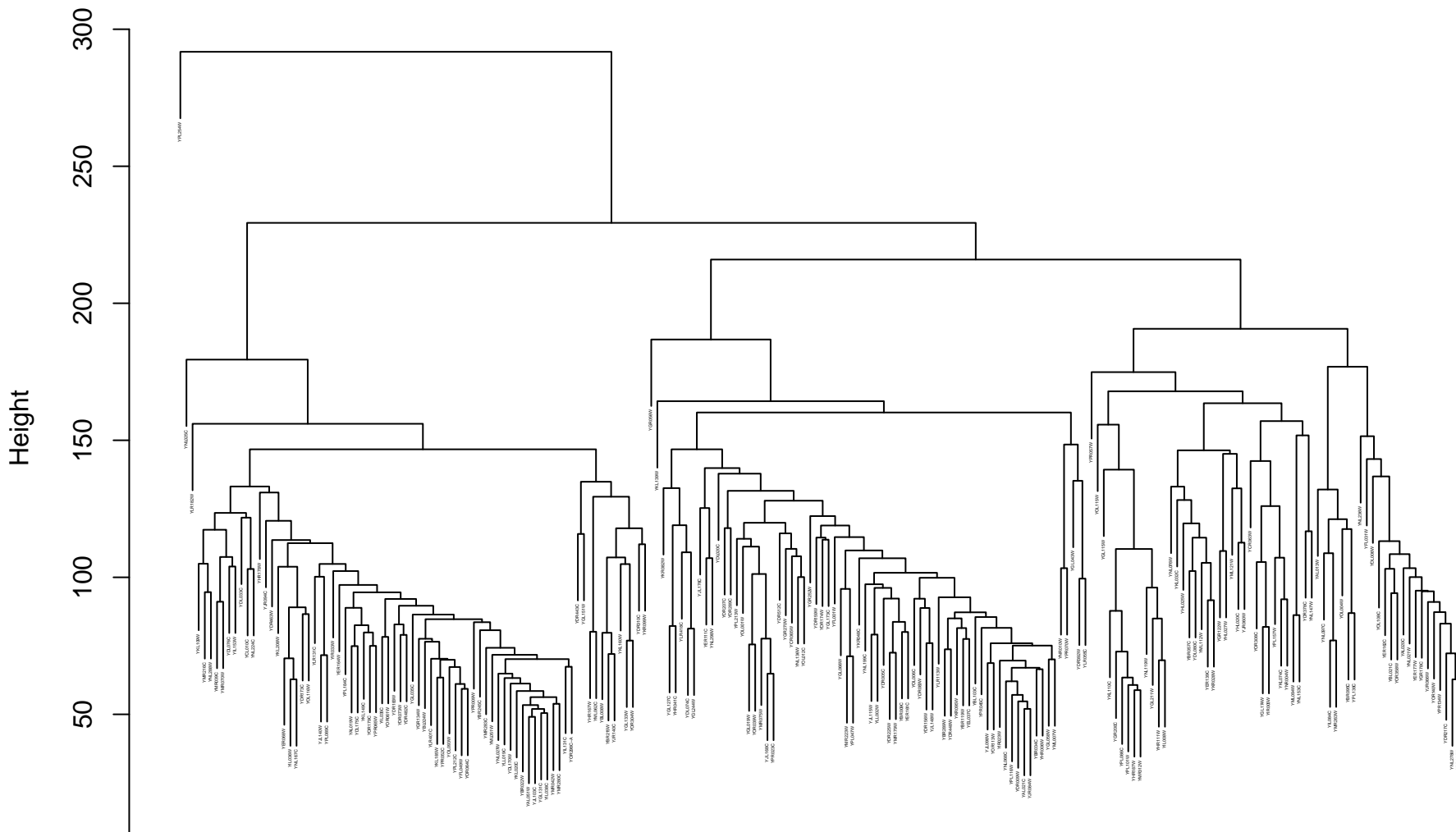




# ribosome\_GO\_euclidean\_complete



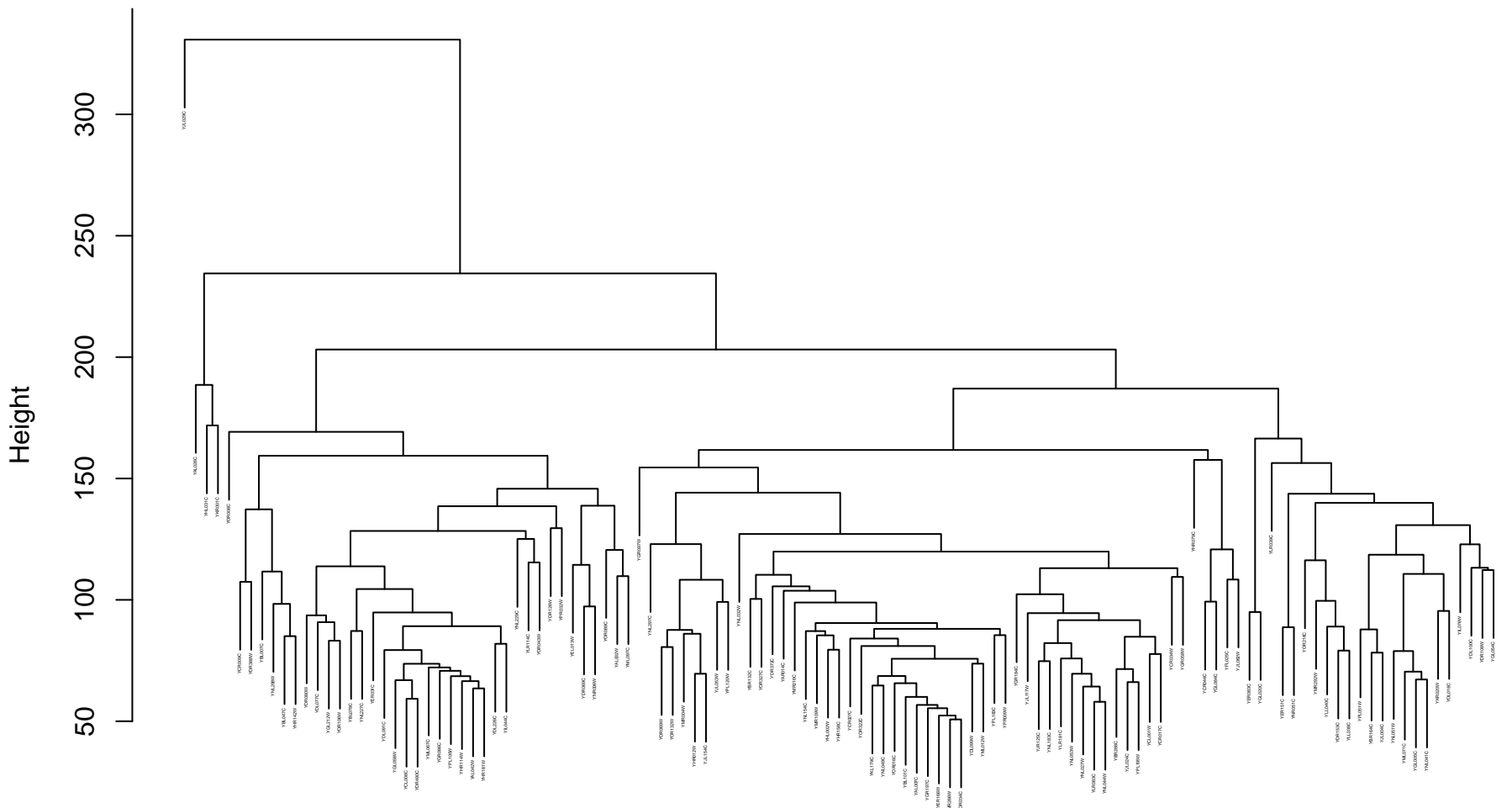
```
dissim
hclust (*, "complete")
```



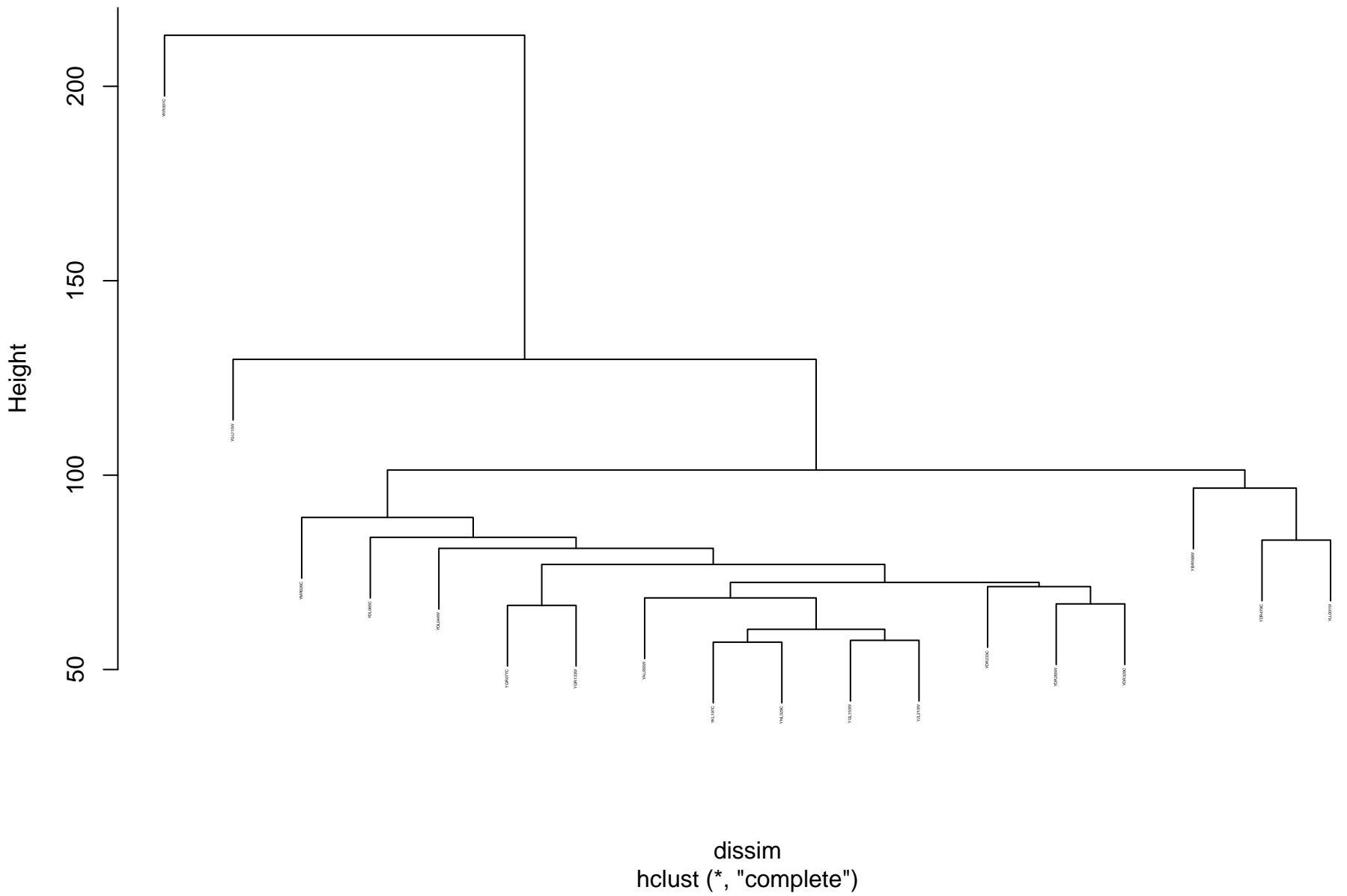
```

dissim
hclust (*, "complete")

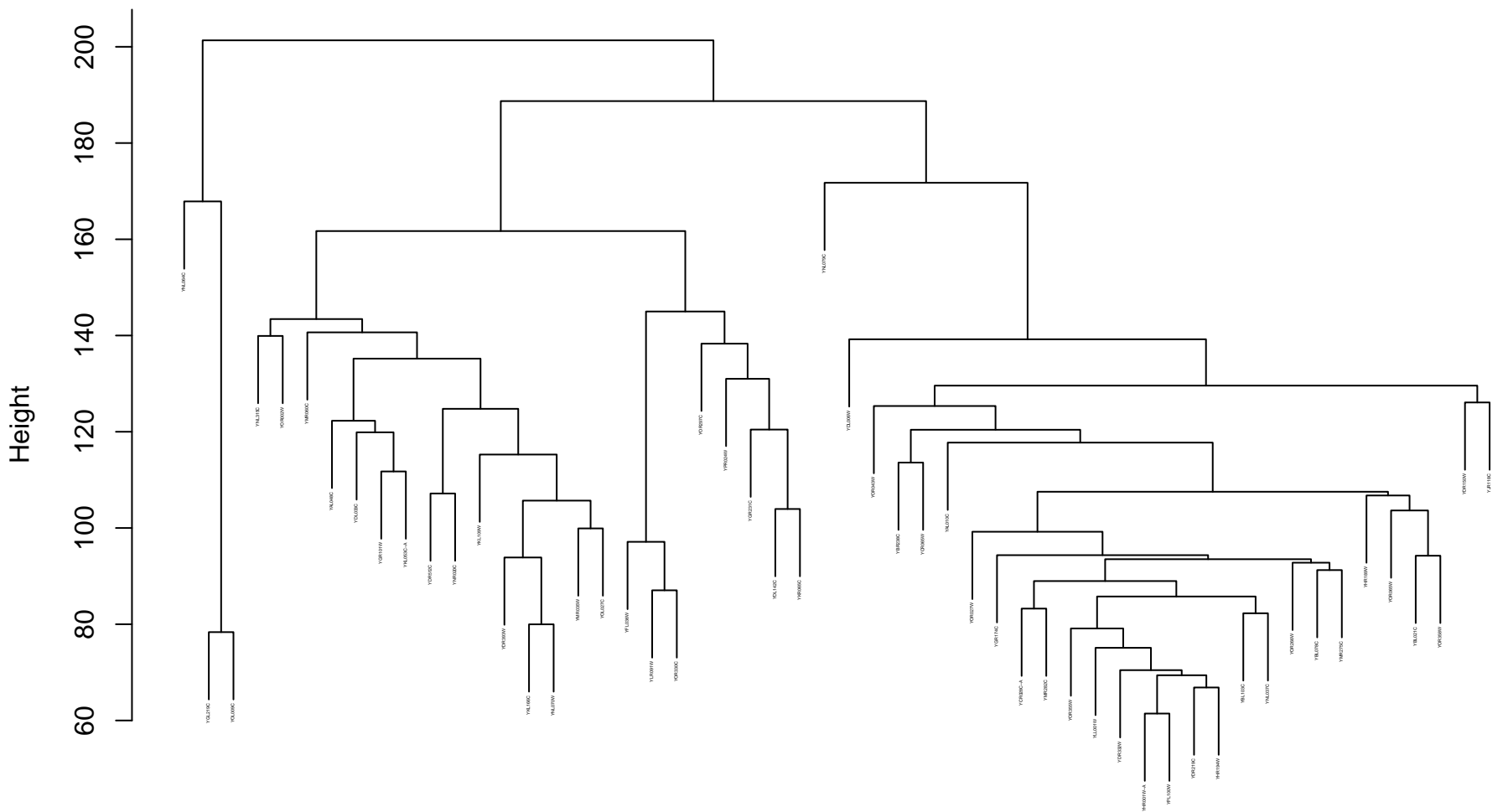
```



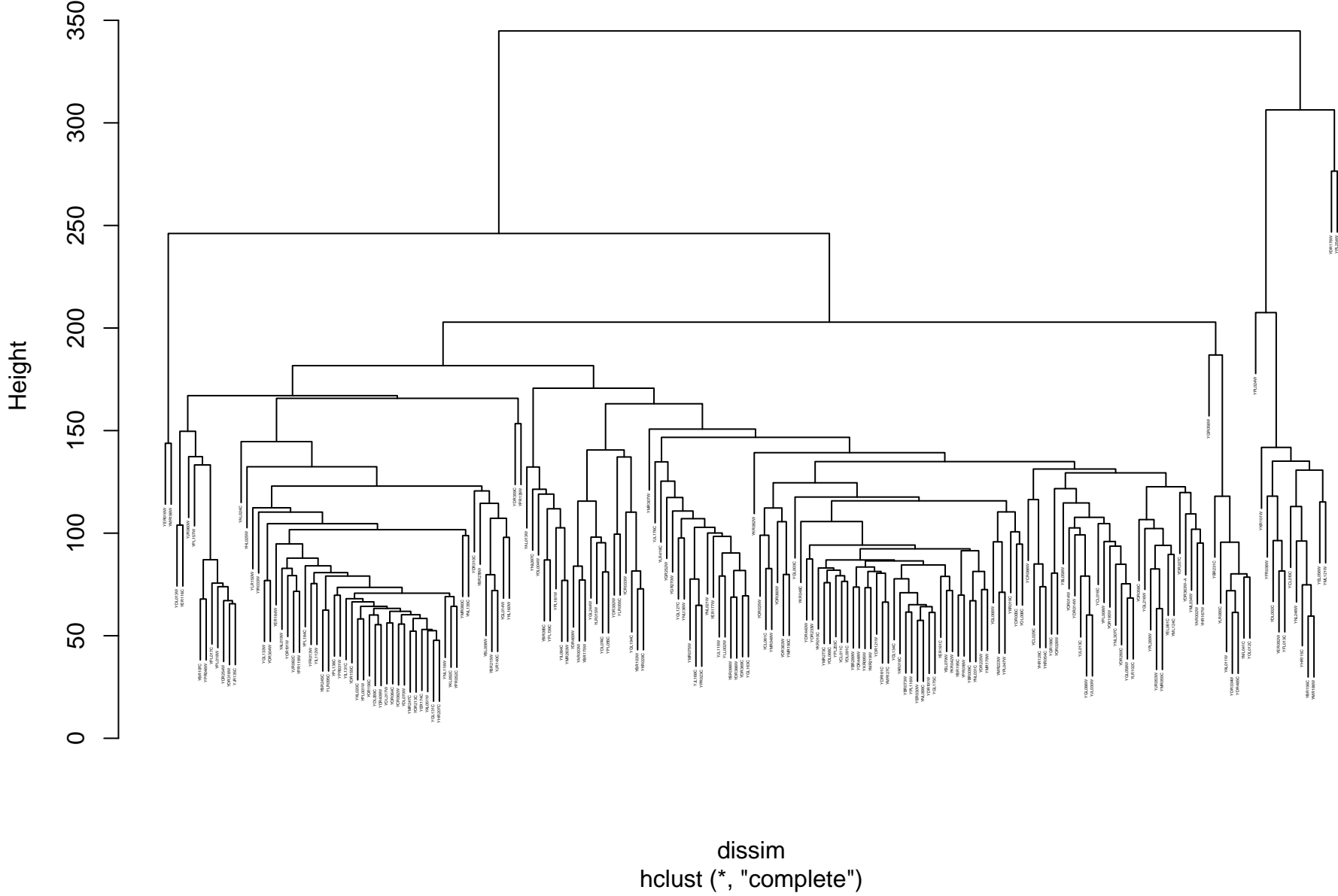
# peroxisome\_GO\_euclidean\_complete



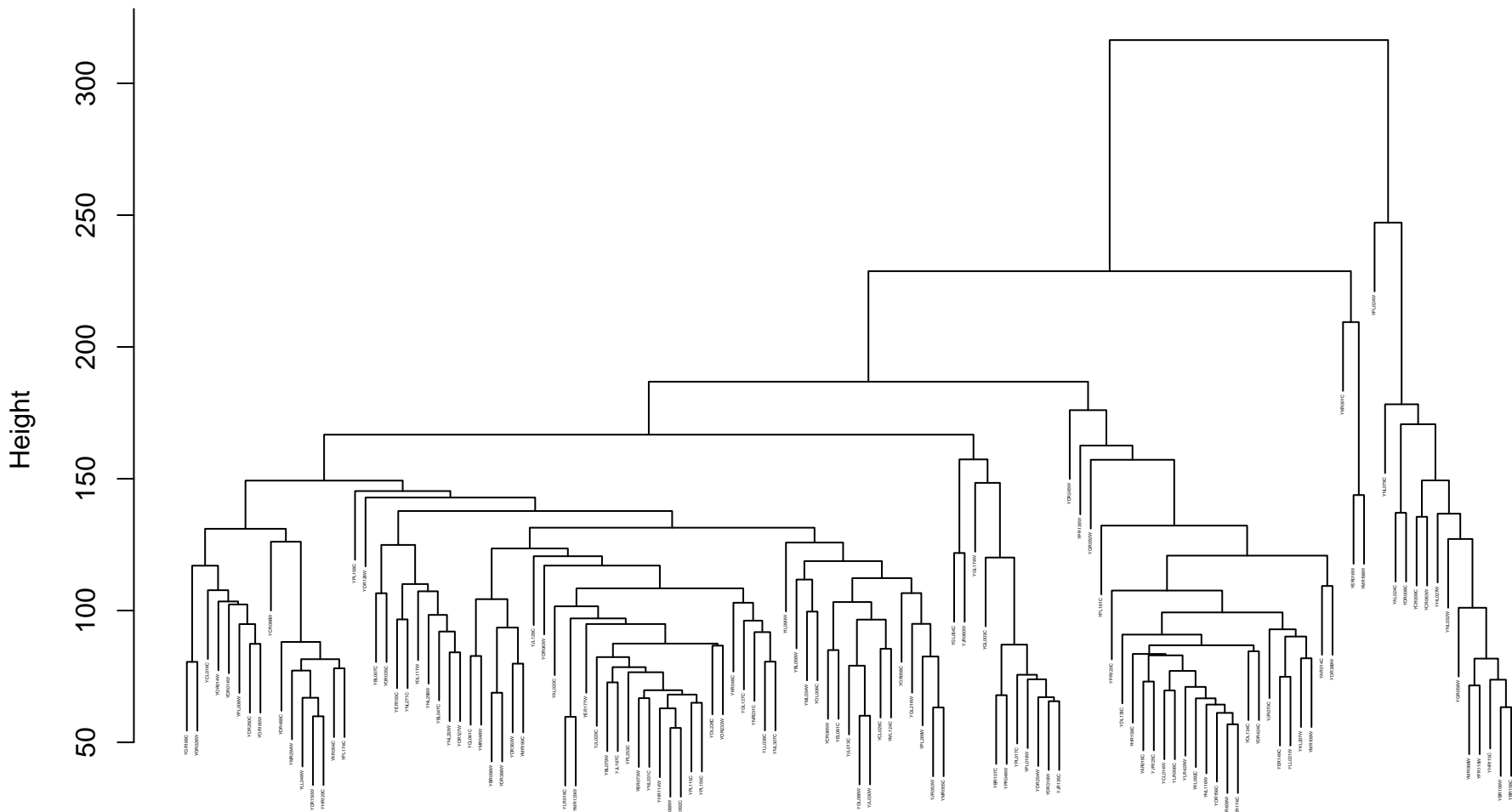
```
dissim
hclust (*, "complete")
```



chromatin\_GO\_euclidean\_complete

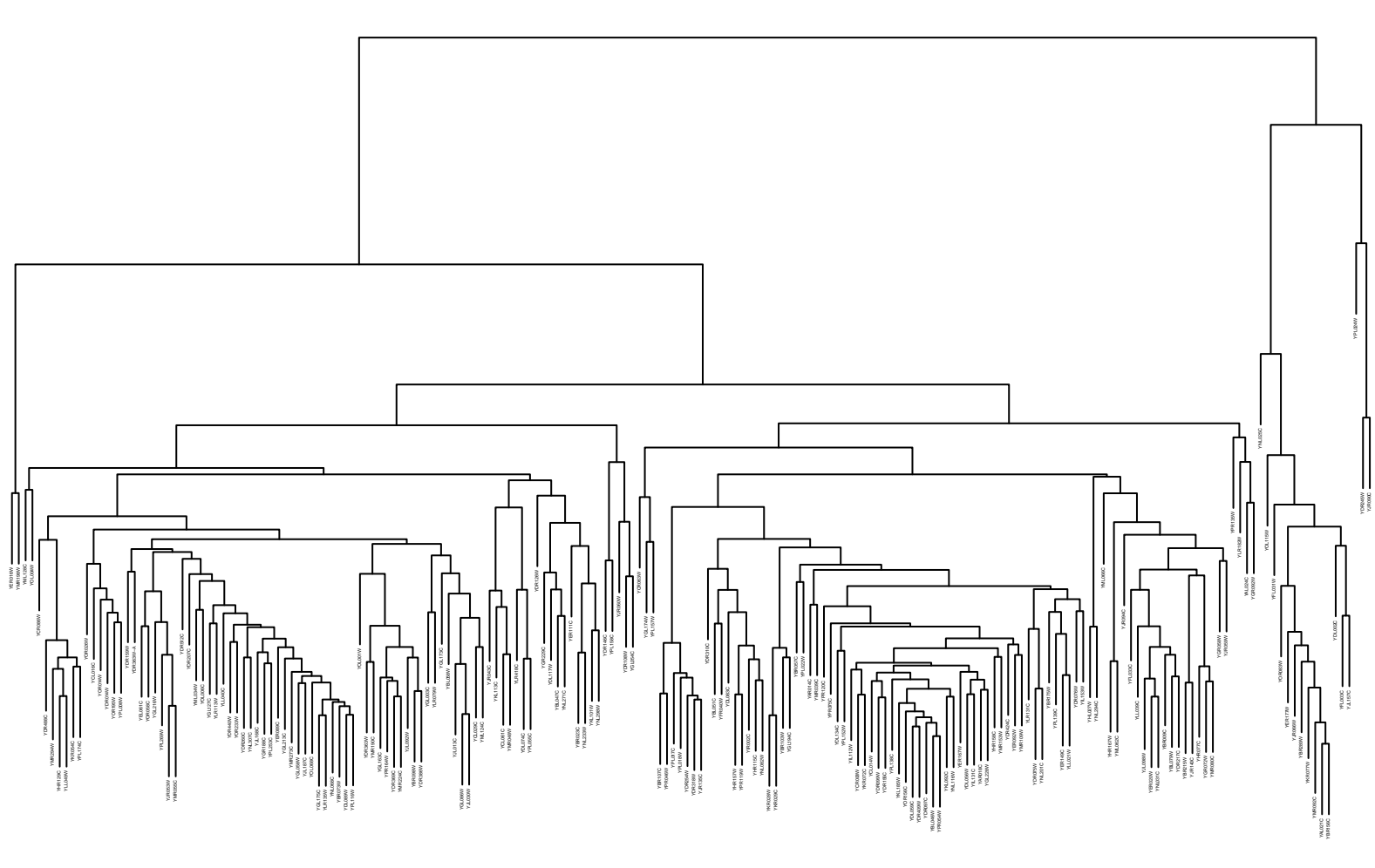


```
dissim
hclust (*, "complete")
```



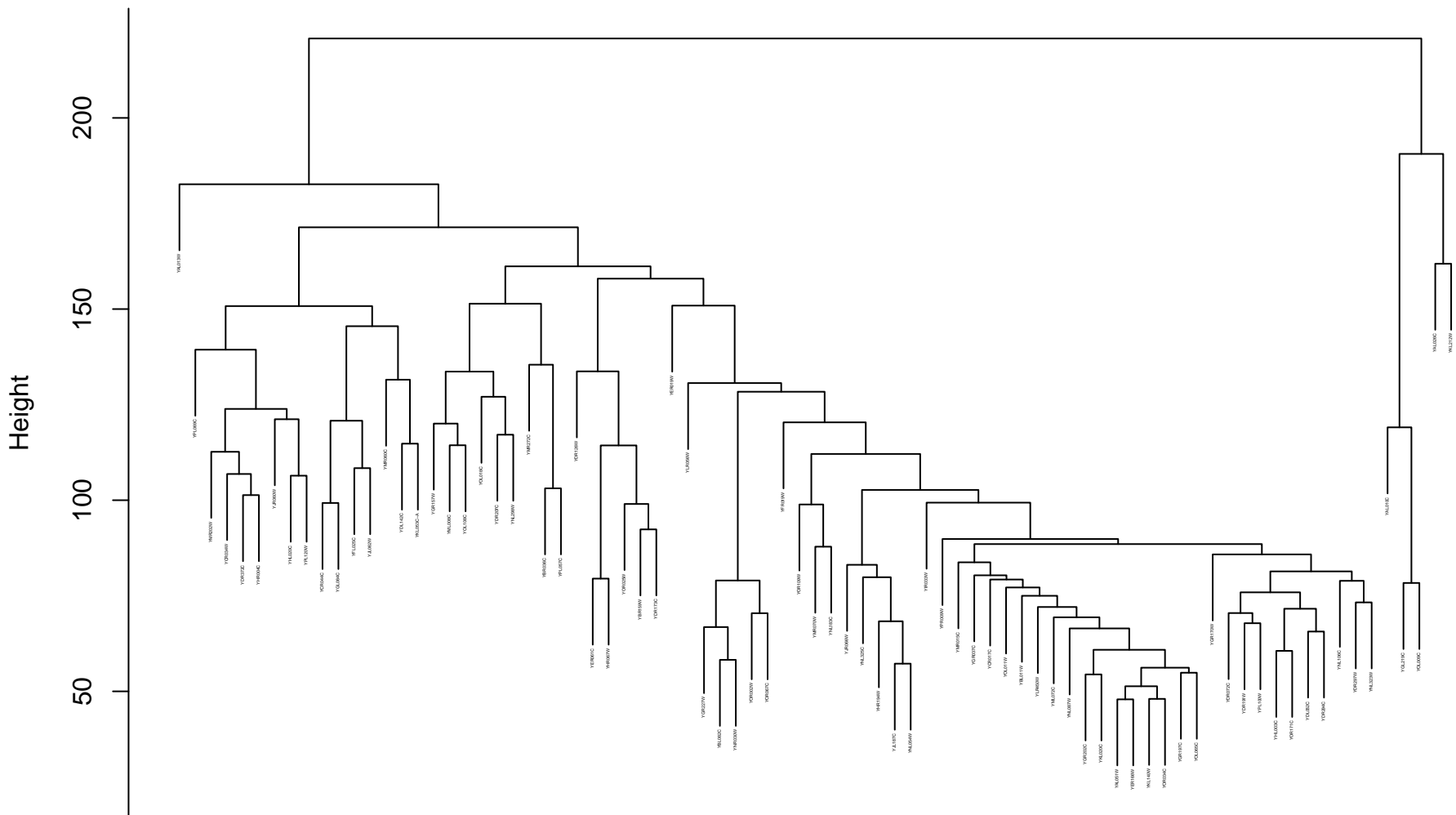
```
dissim
hclust (*, "complete")
```

Figure 1 is a line graph showing the number of cases per 100,000 population over time. The y-axis represents the number of cases per 100,000 population, ranging from 0 to 300. The x-axis represents time, with labels for 50, 100, 150, 200, 250, and 300. The graph shows a sharp increase in cases starting around day 50, peaking at approximately 280 cases per 100,000 around day 200, and then declining to about 150 cases per 100,000 by day 300.



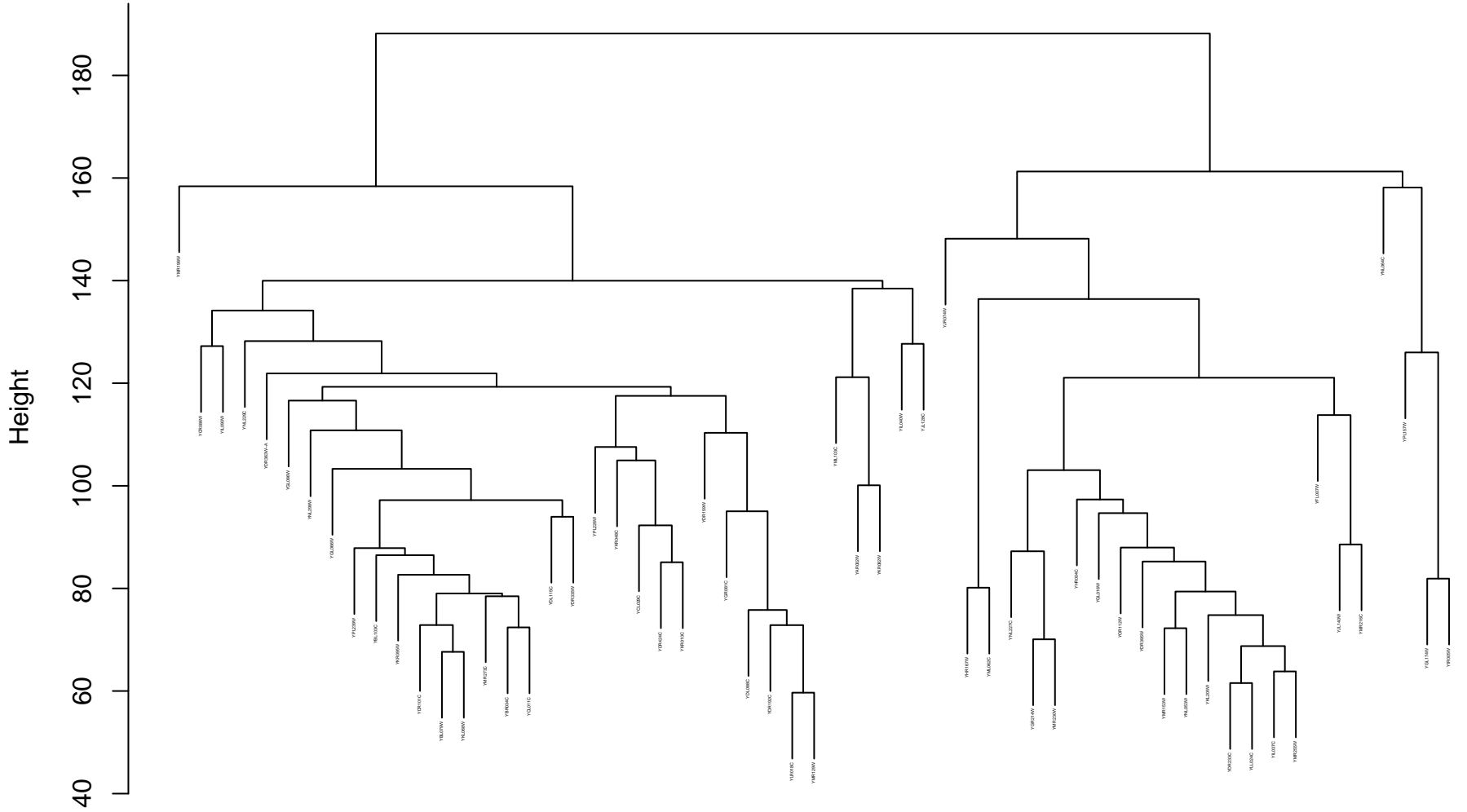


```
dissim
hclust (*, "complete")
```

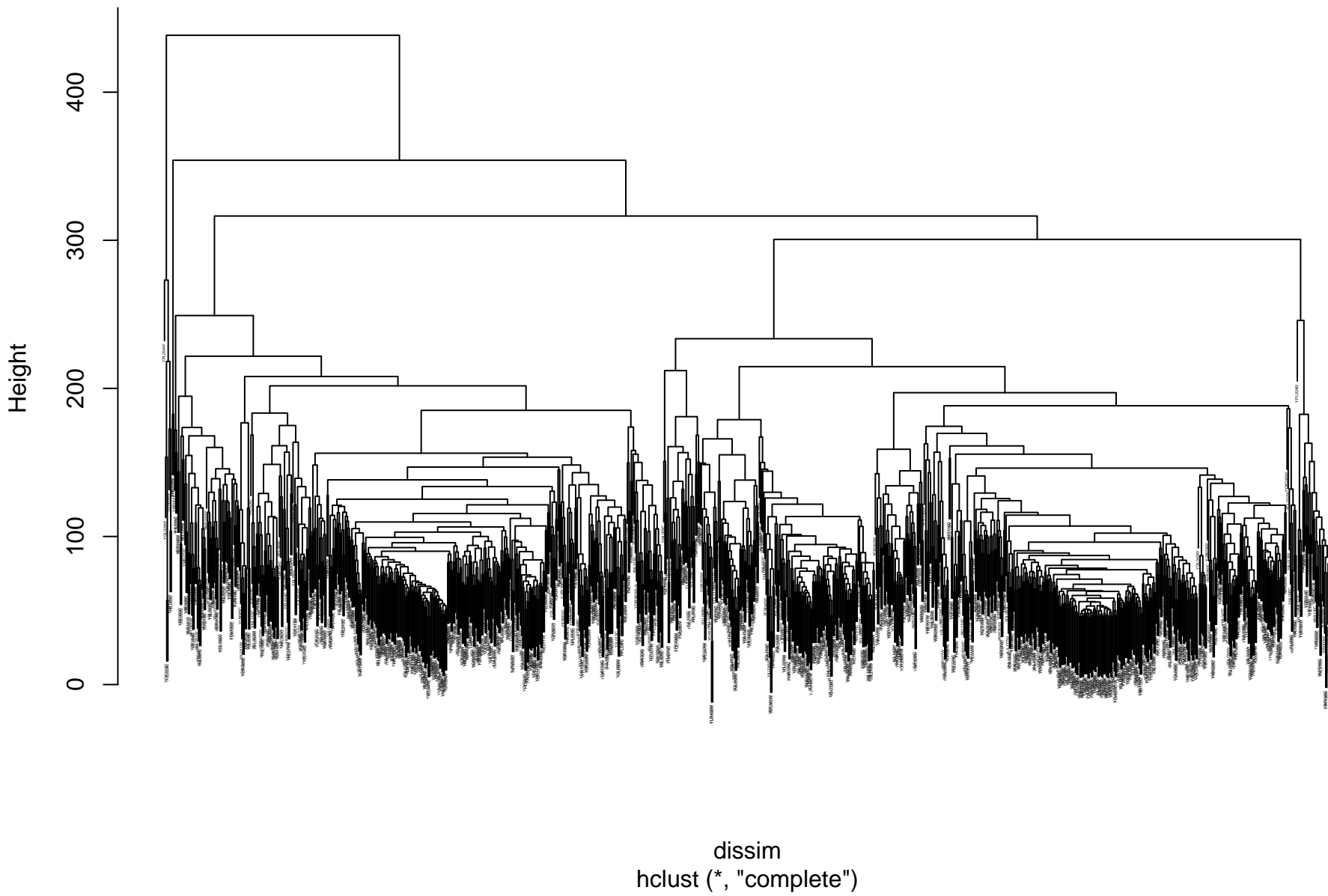


```
dissim
hclust (*, "complete")
```

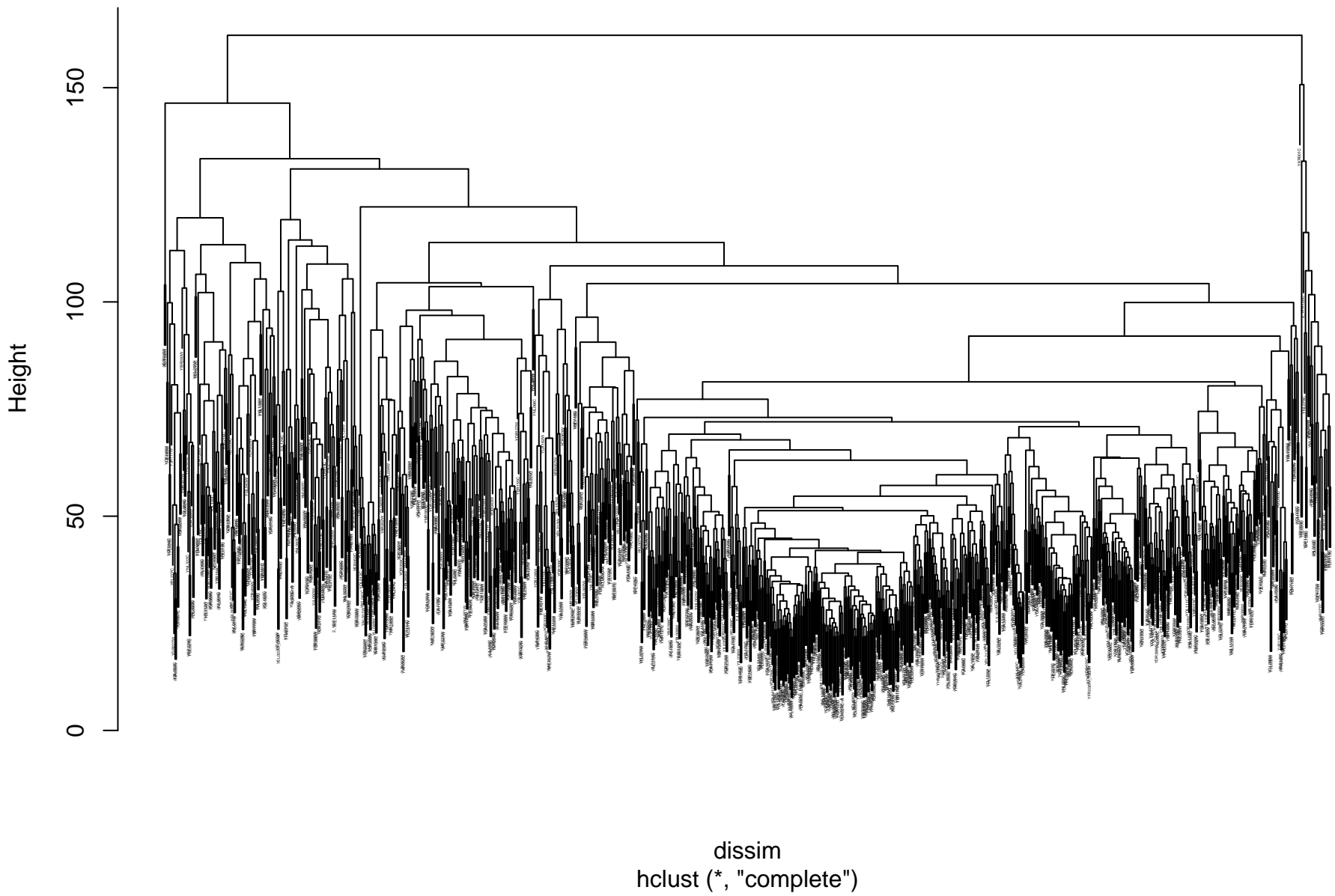
```
dissim
hclust (*, "complete")
```



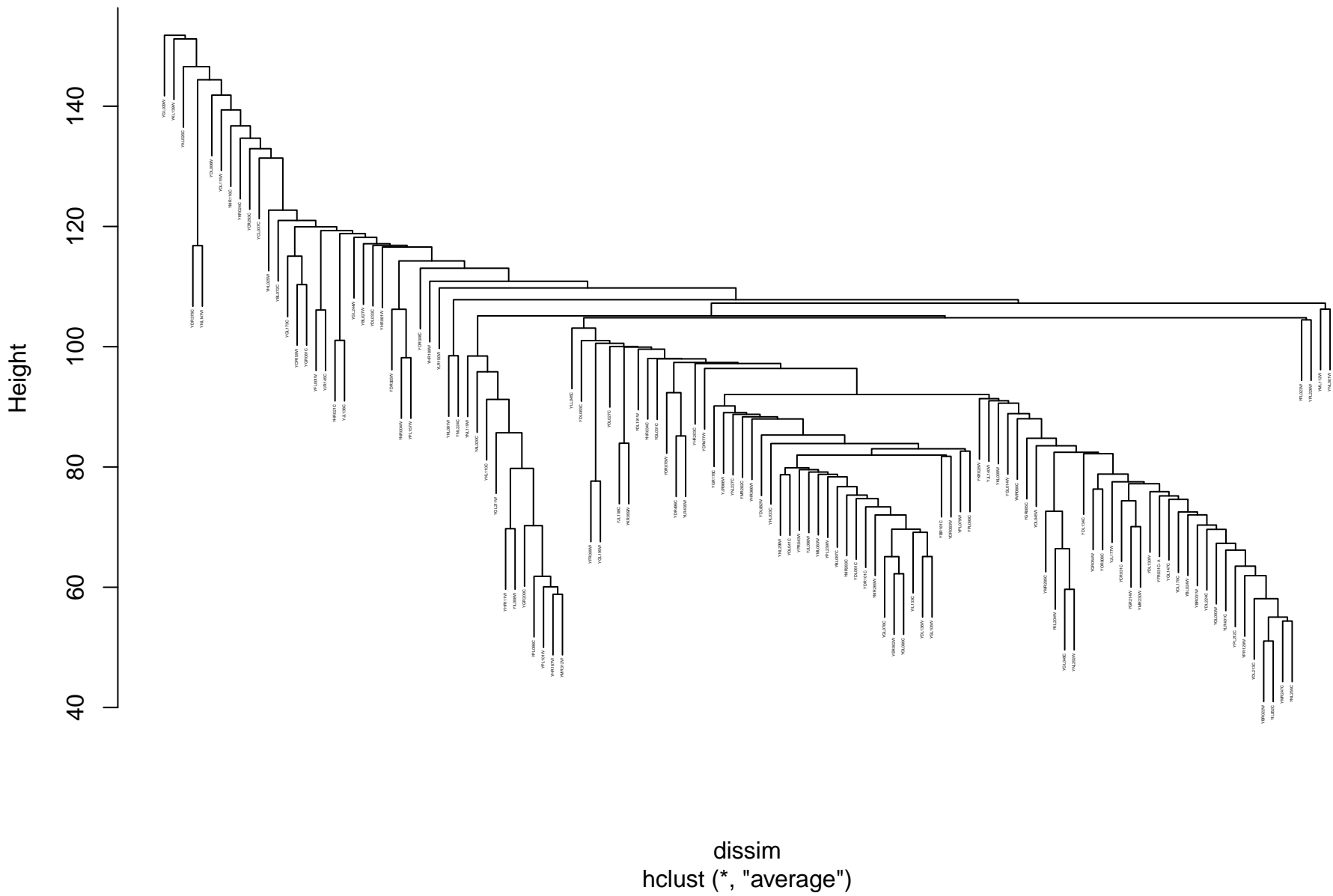
# library\_euclidean\_complete



**gene\_euclidean\_complete**



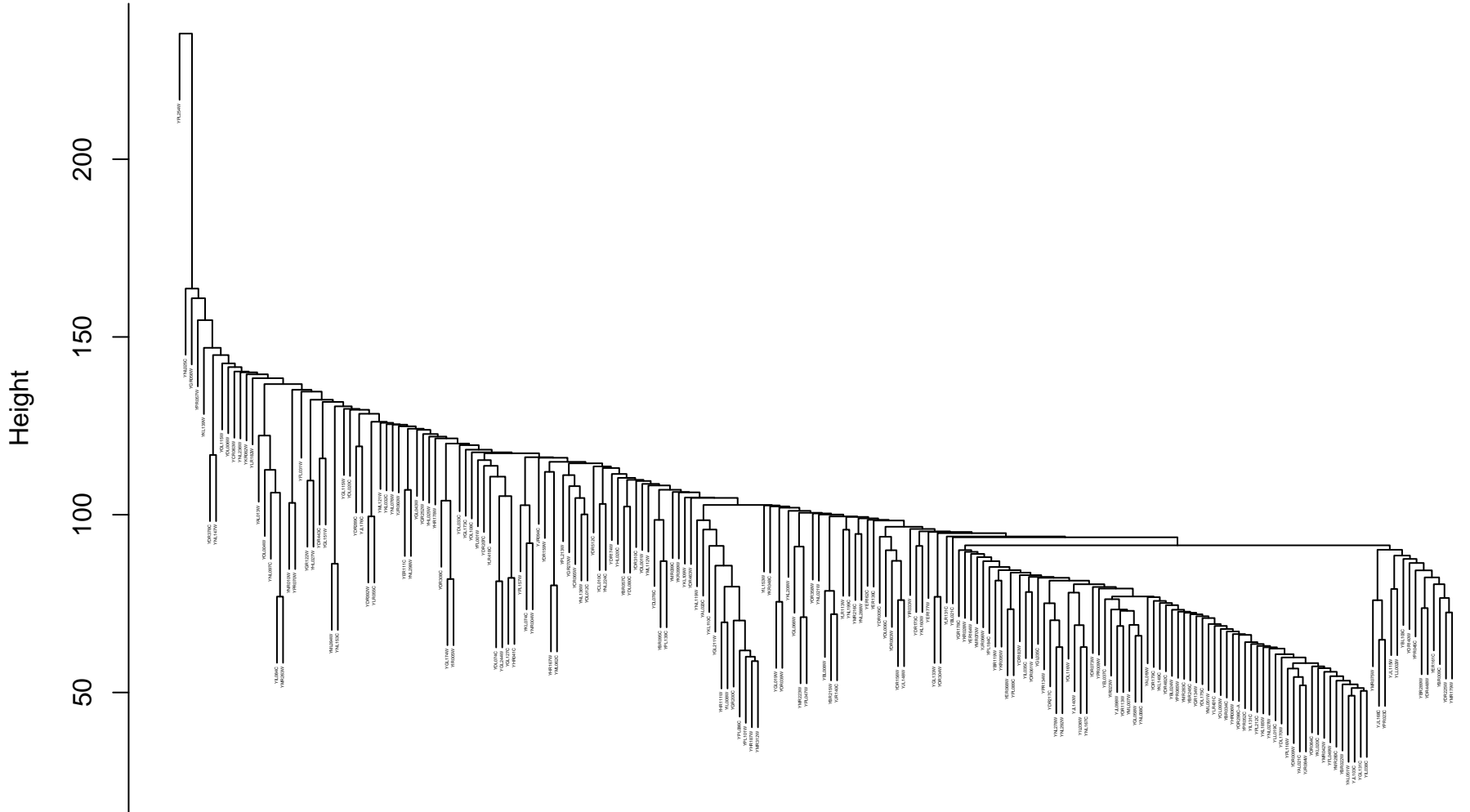
ribosome\_GO\_euclidean\_average



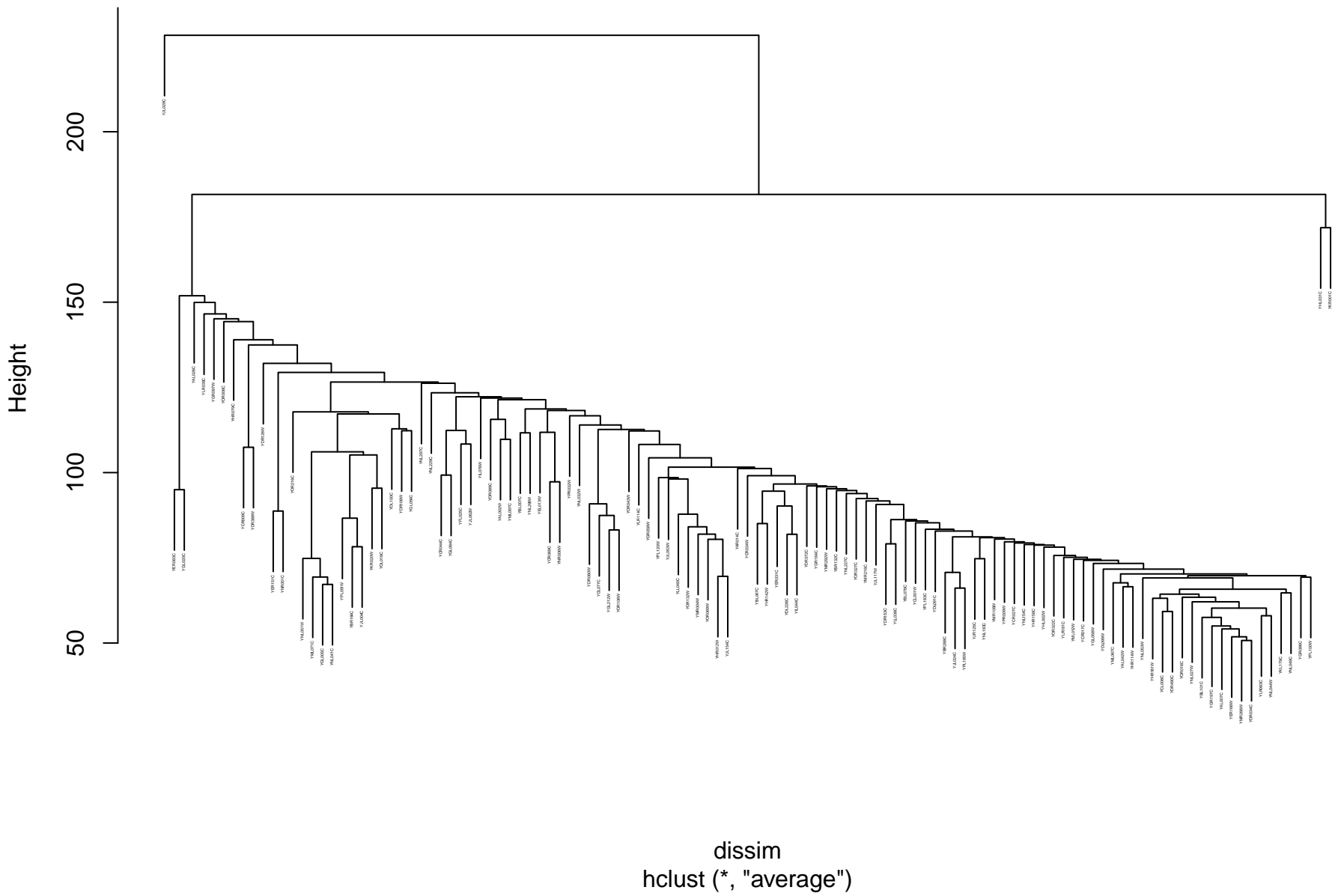
```

dissim
hclust (*, "average")

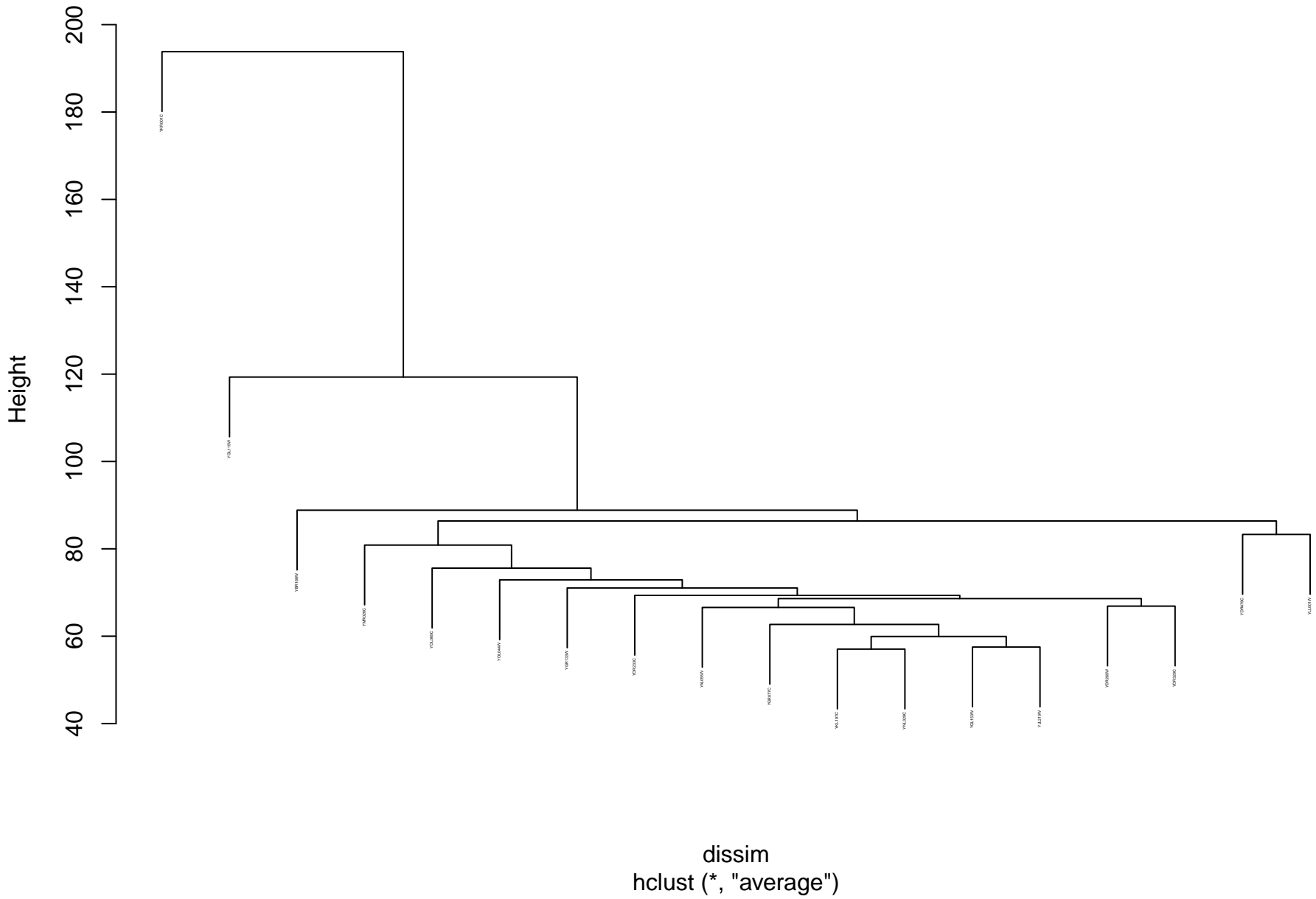
```



# Golgi and ER\_GO\_euclidean\_average



peroxisome\_GO\_euclidean\_average

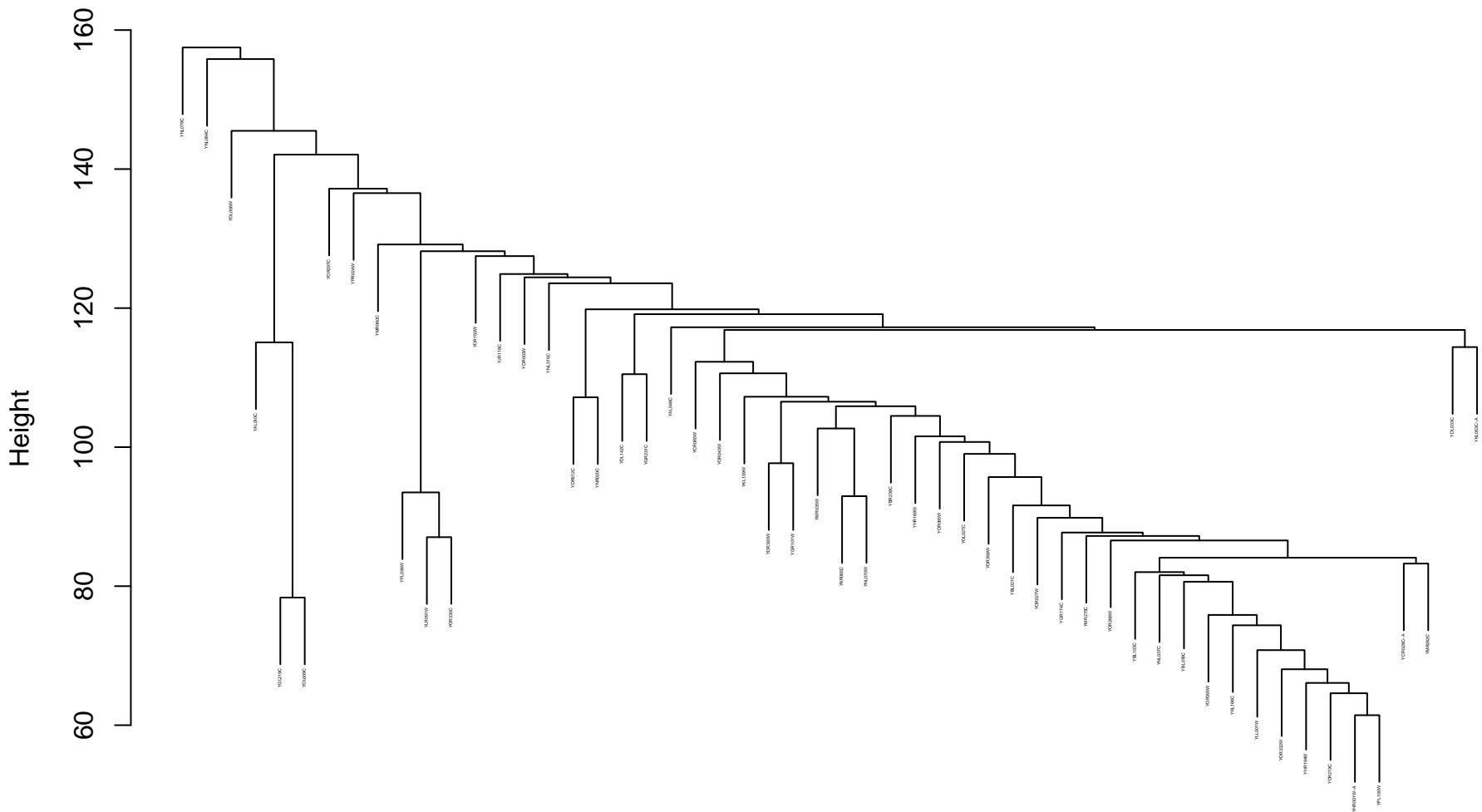




```

dissim
hclust (*, "average")

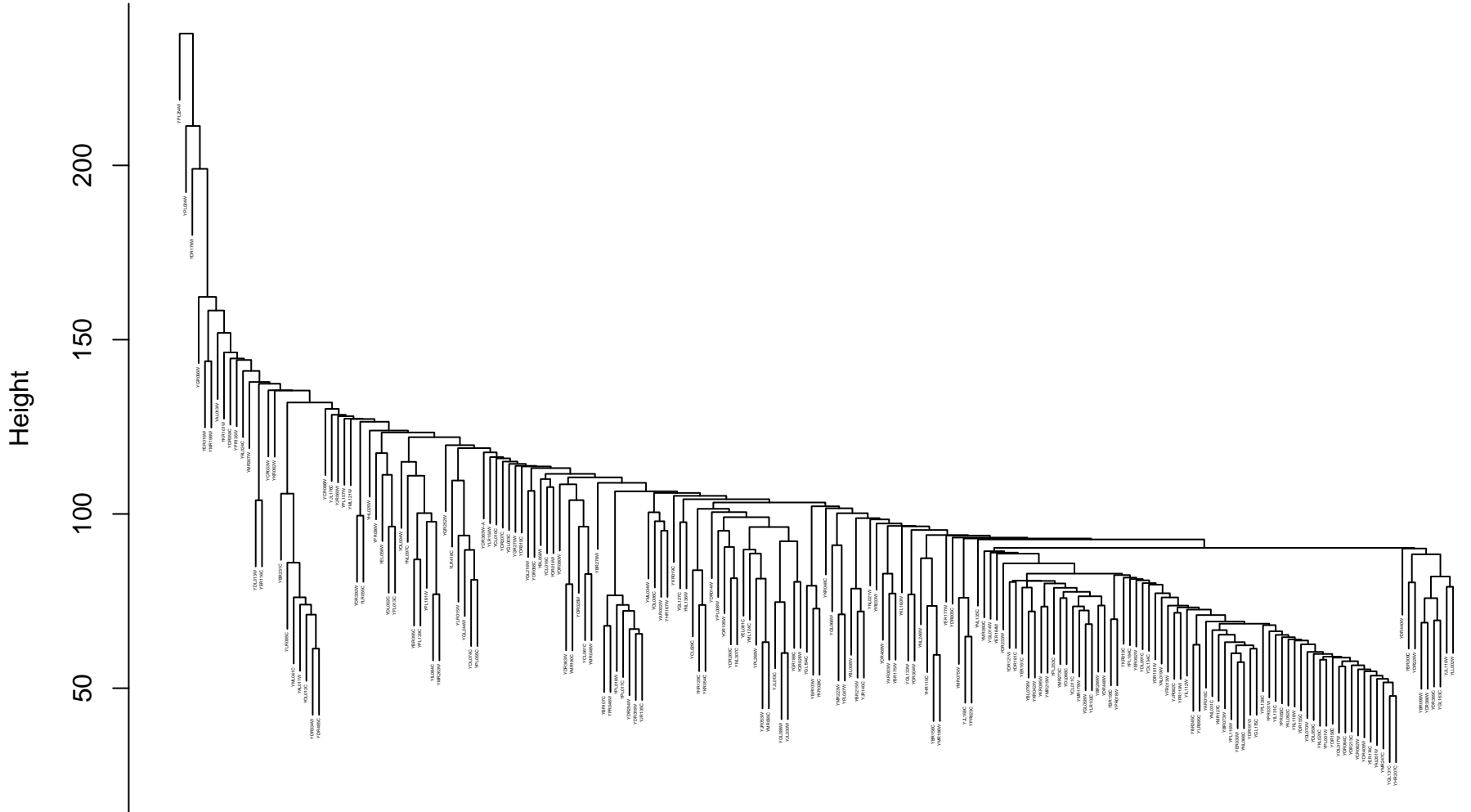
```



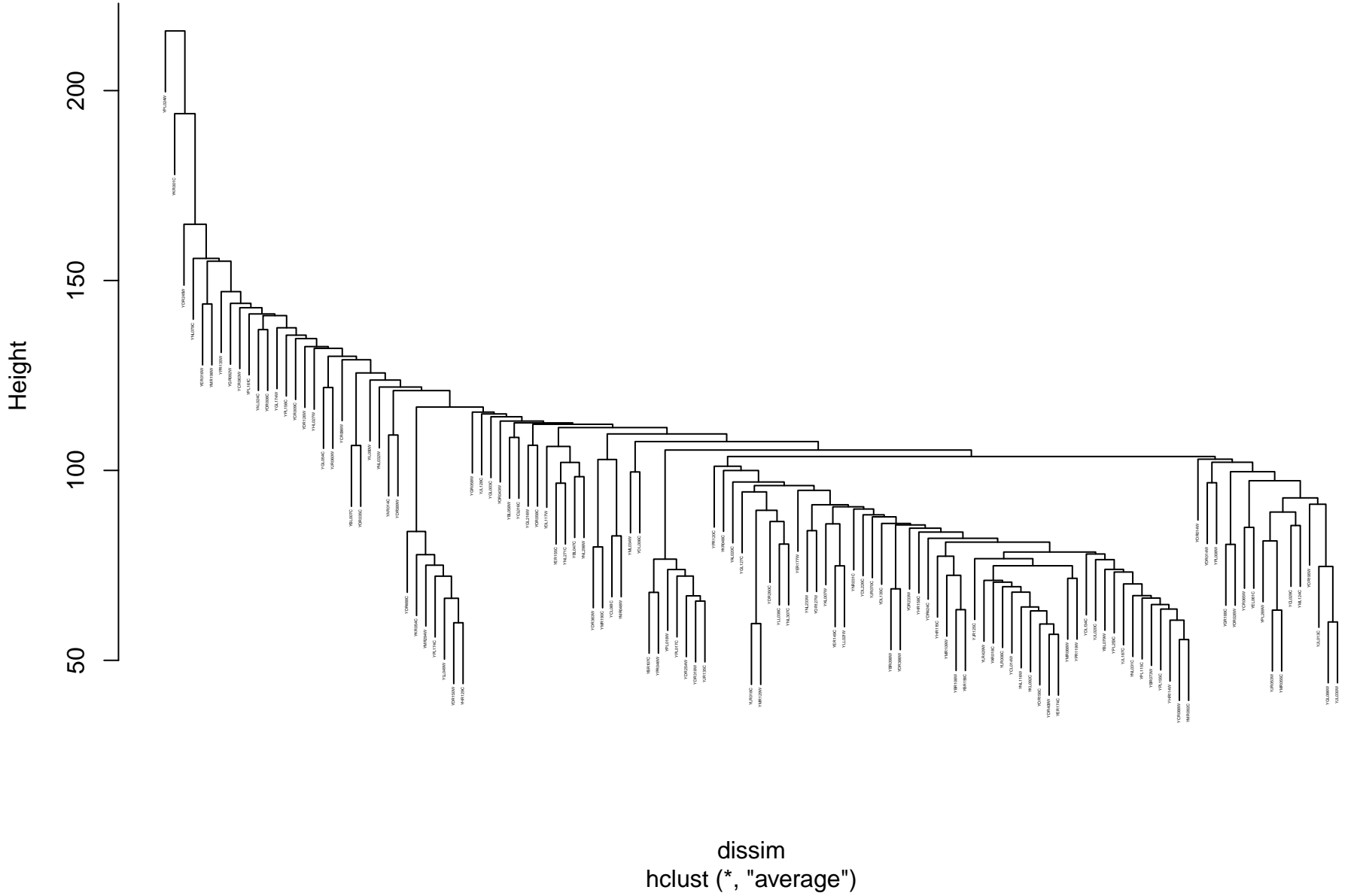
```

dissim
hclust (*, "average")

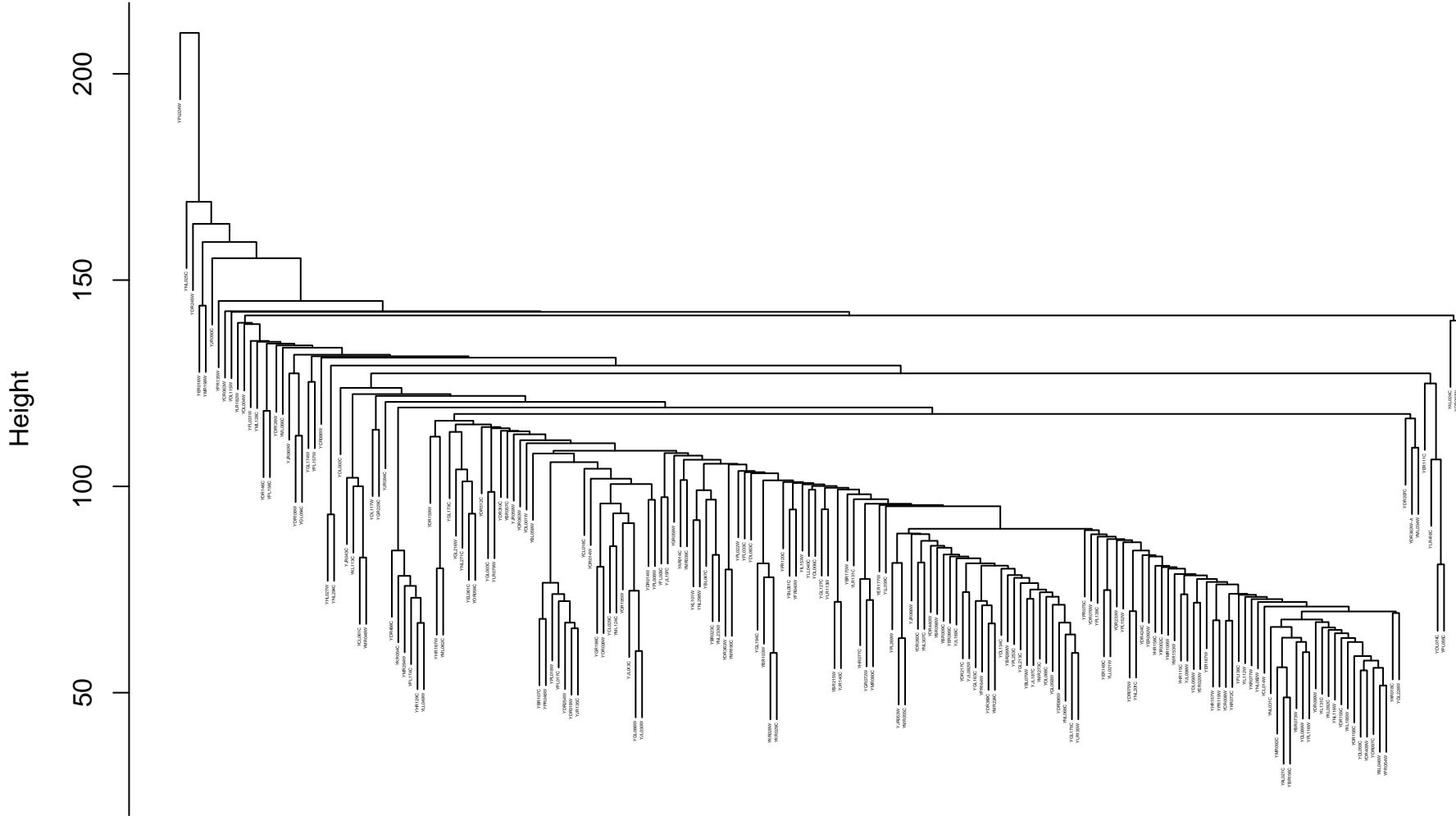
```



# cytoskeleton\_GO\_euclidean\_average



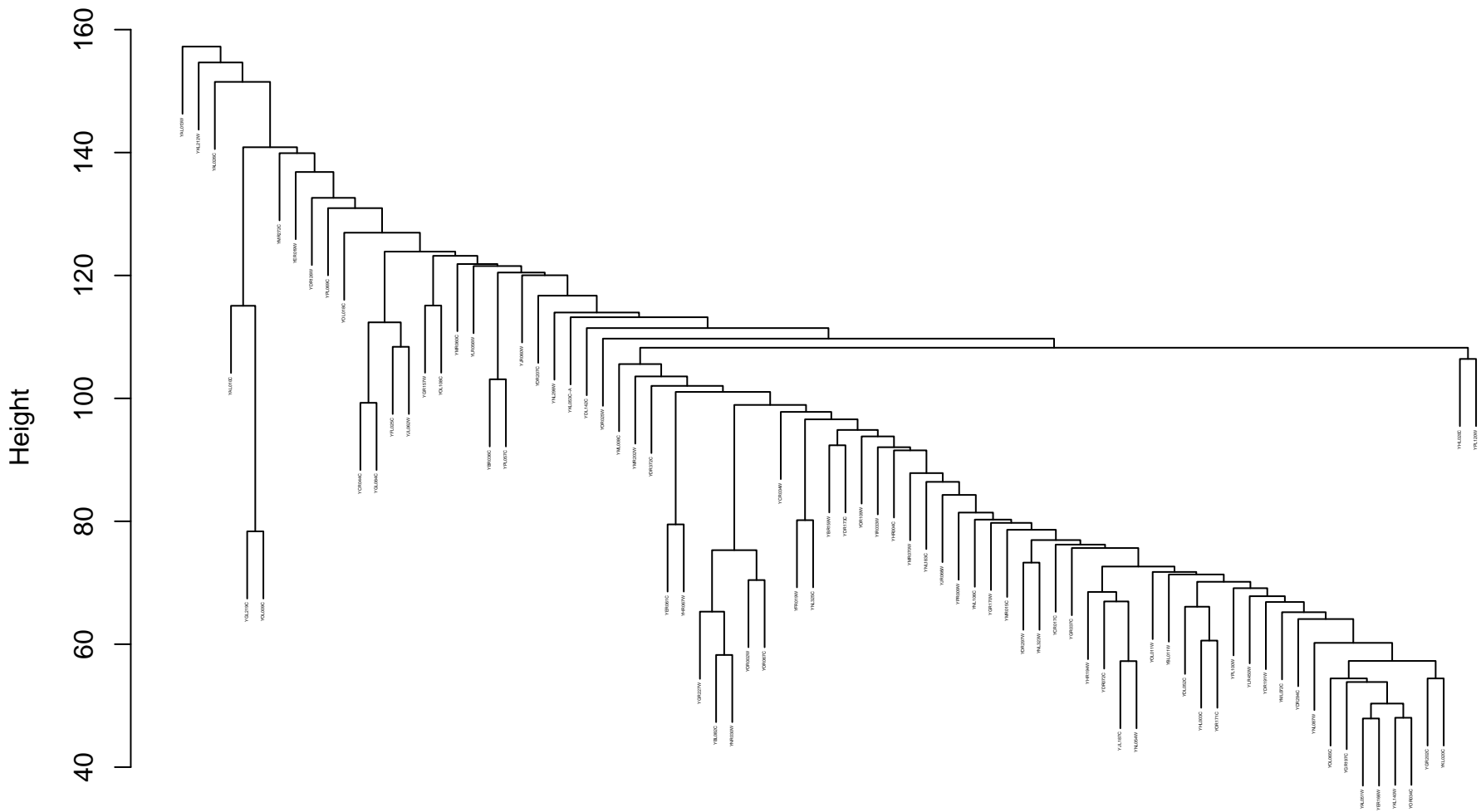
cell cycle\_GO\_euclidean\_average



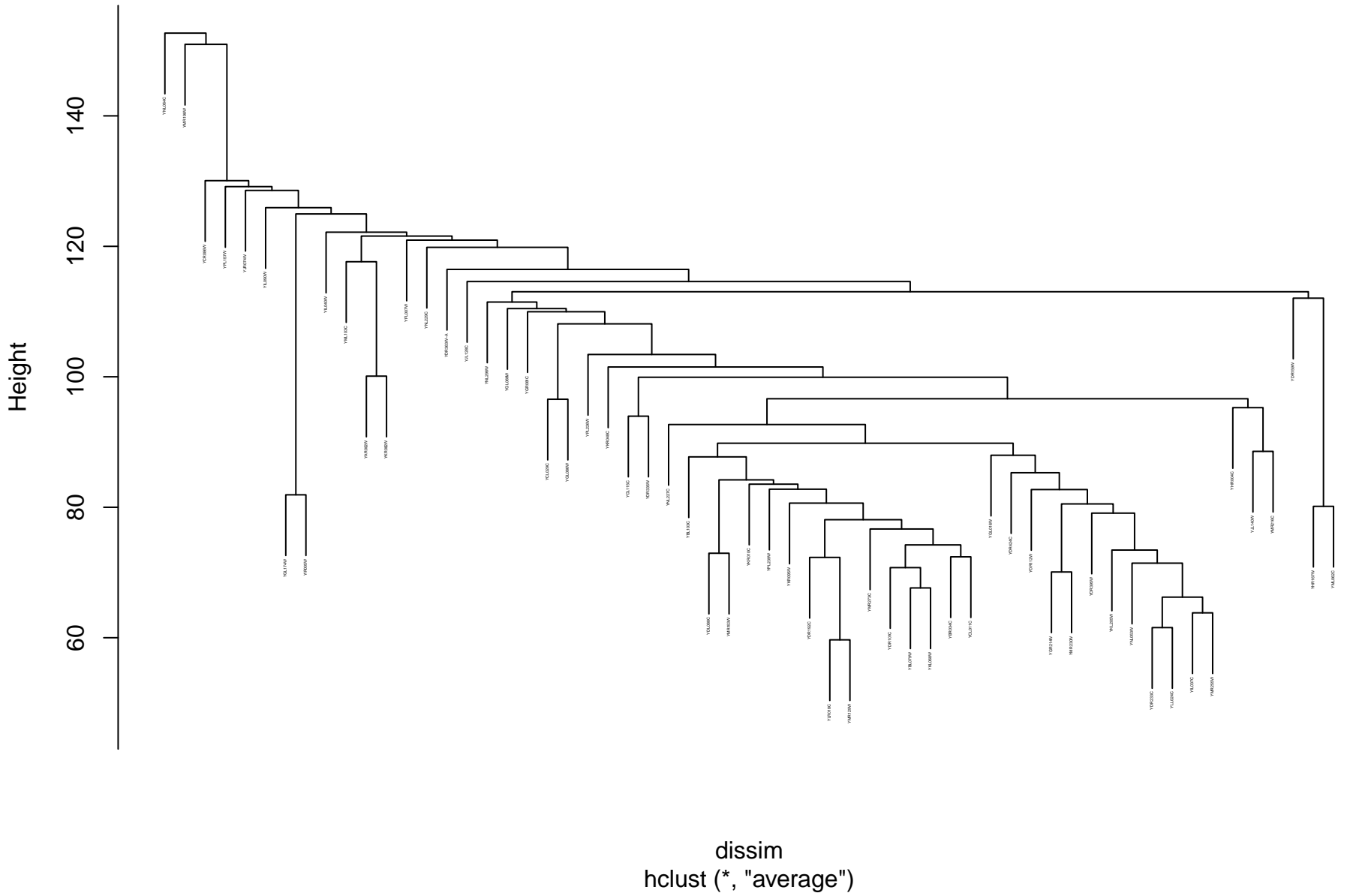
```

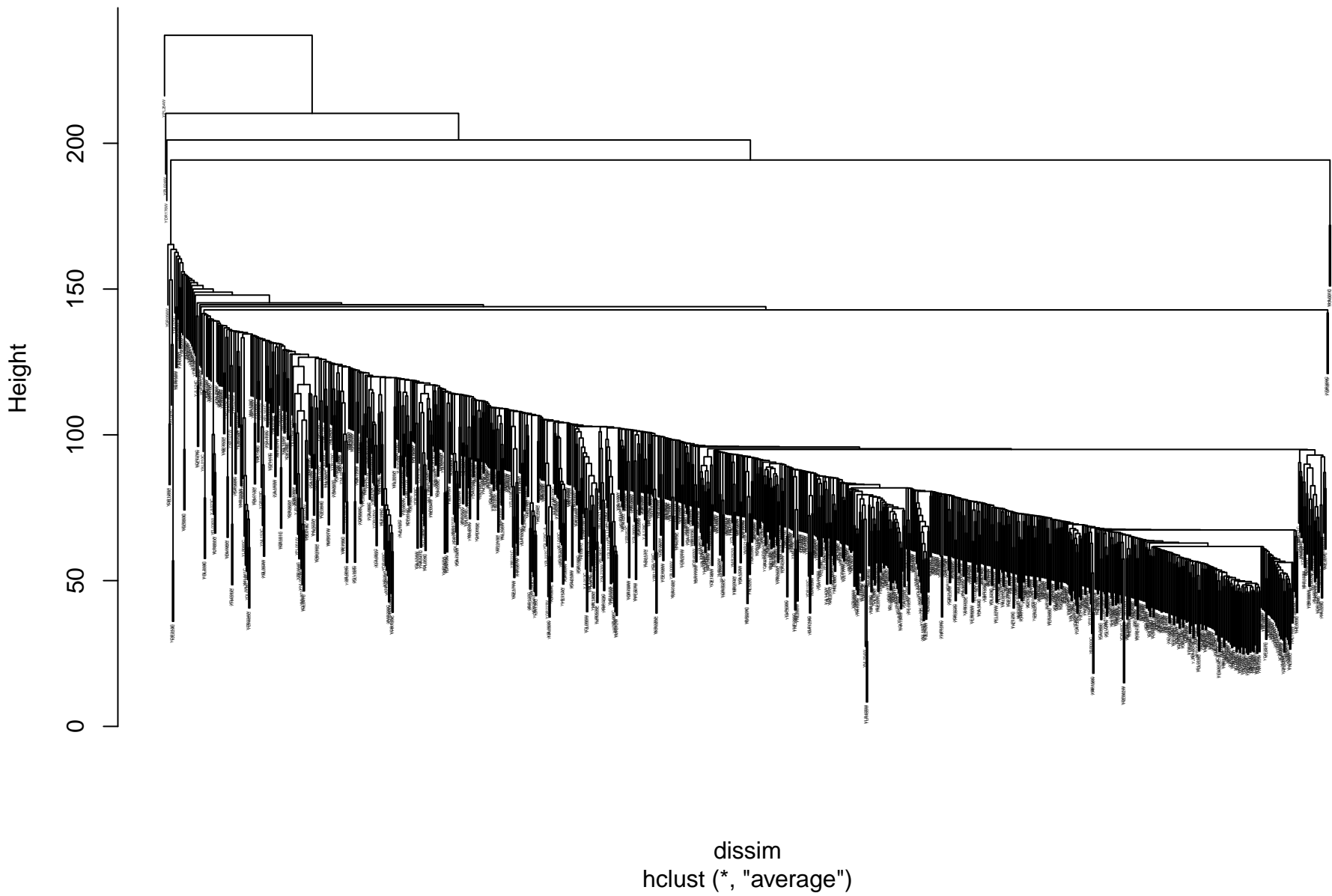
dissim
hclust (*, "average")

```



# nuclear transport\_GO\_euclidean\_average



**library\_euclidean\_average**

gene\_euclidean\_average

