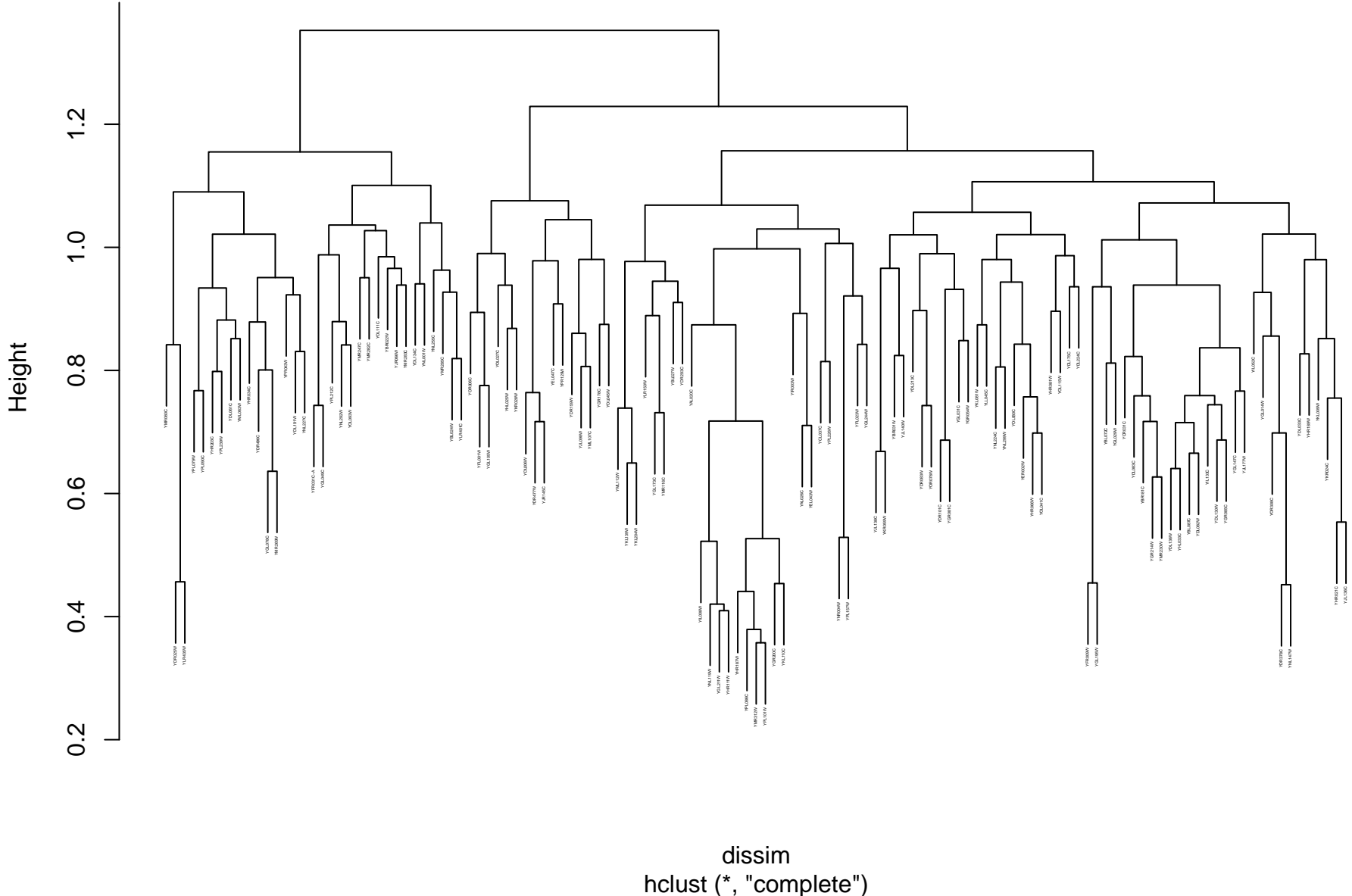
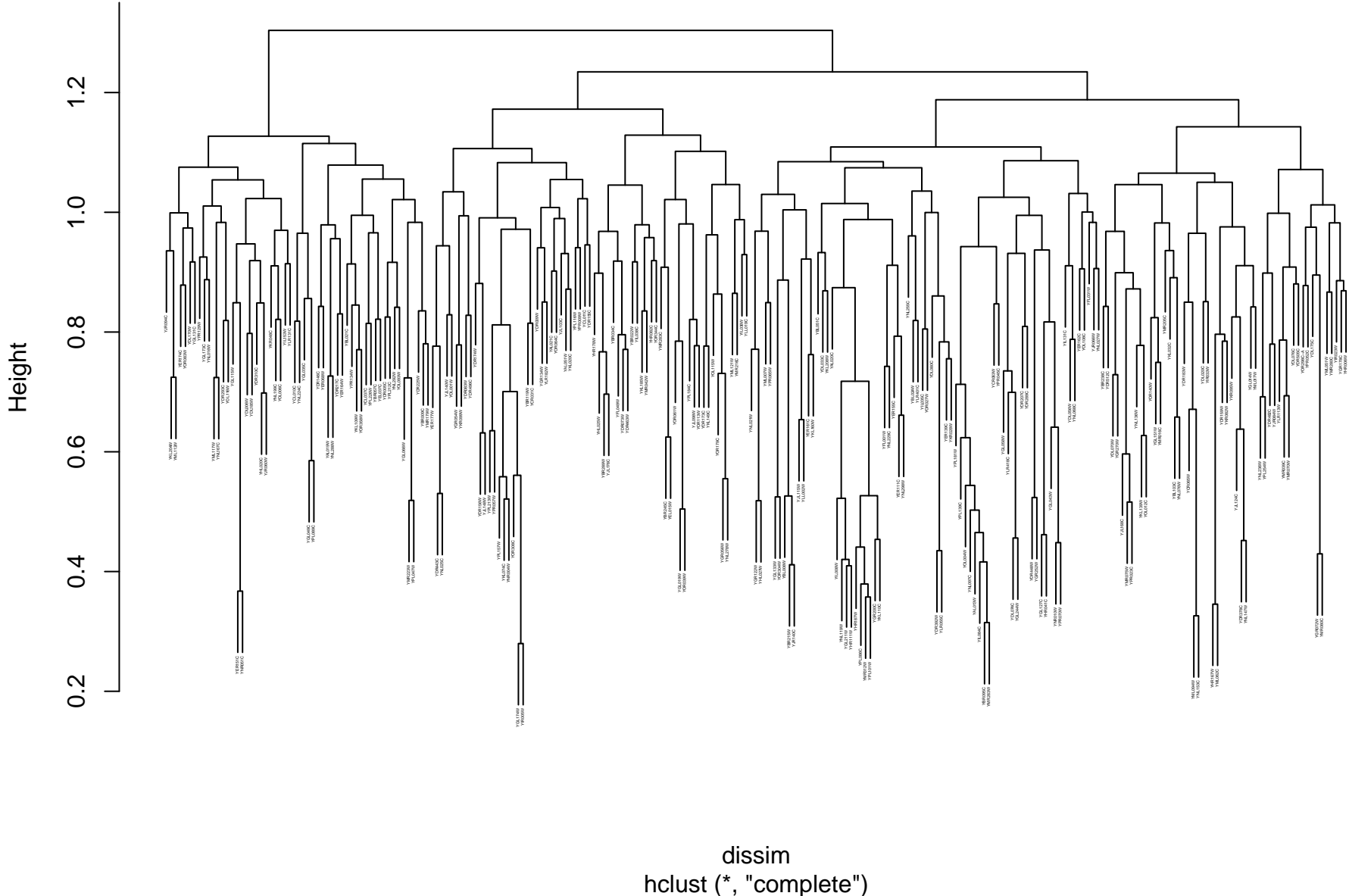


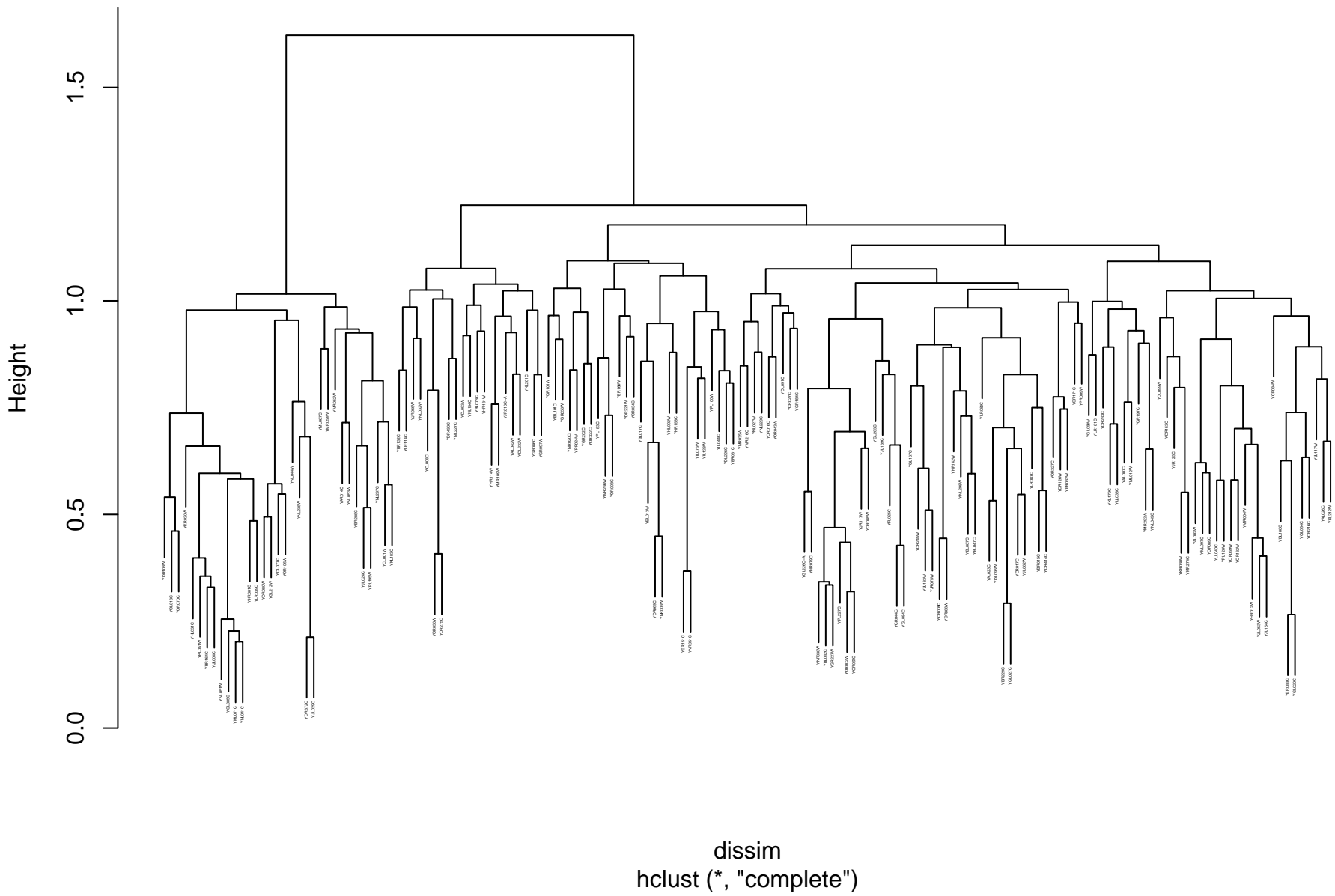
ribosome_GO_pearson_complete



transcription and mRNA processing_GO_pearson_complete



Golgi and ER_GO_pearson_complete



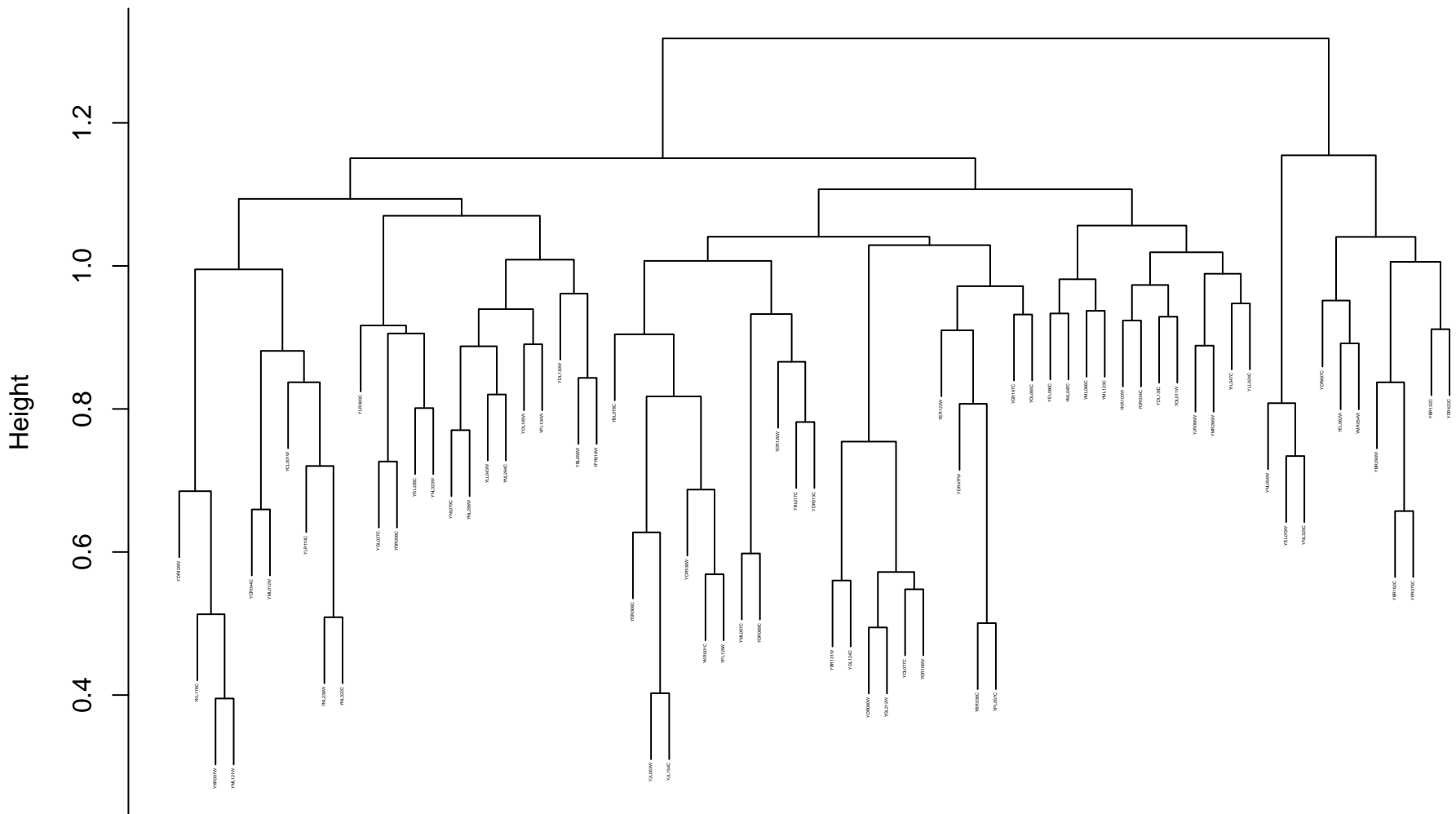
```

dissim
hclust (*, "complete")

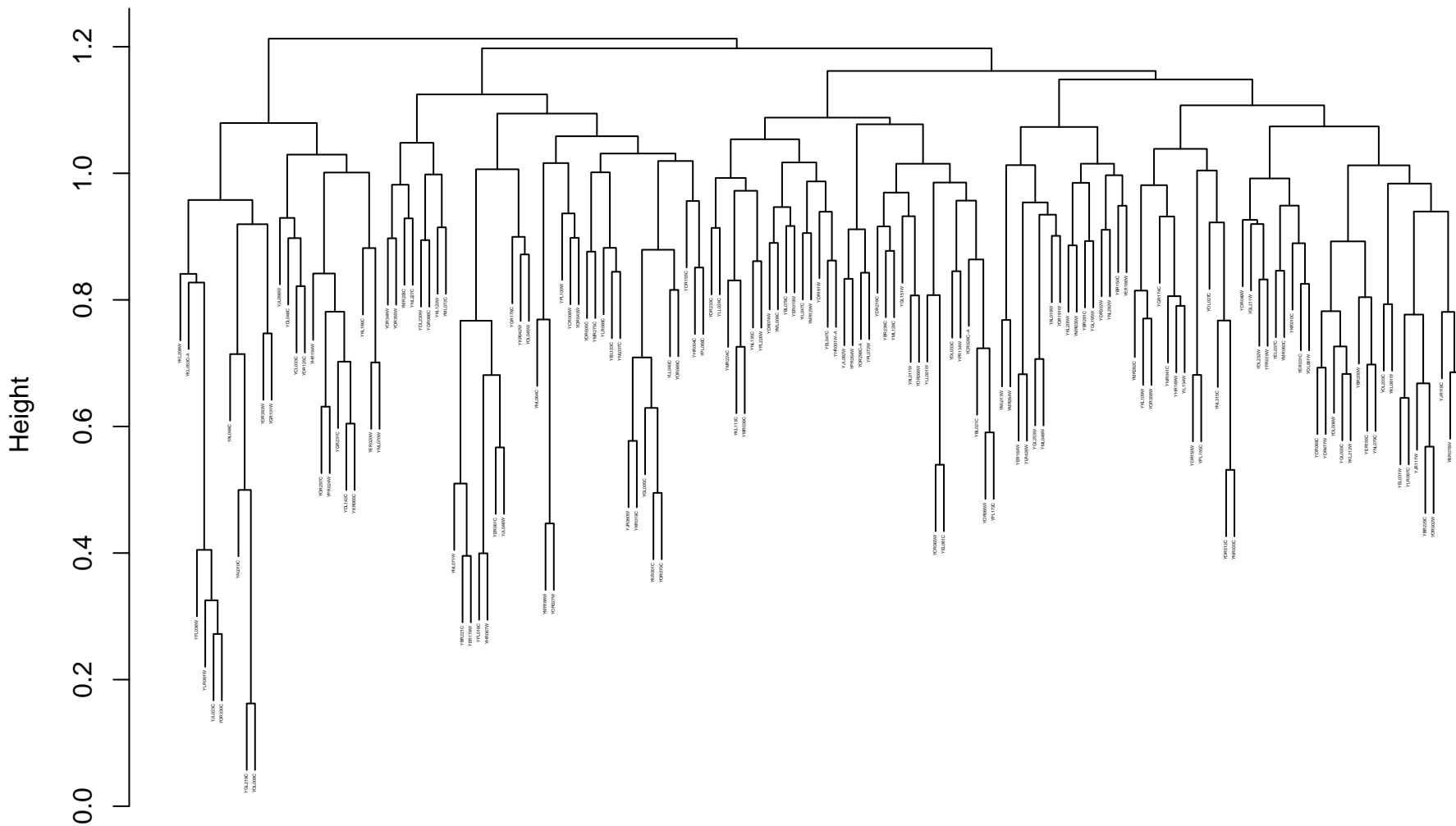
```



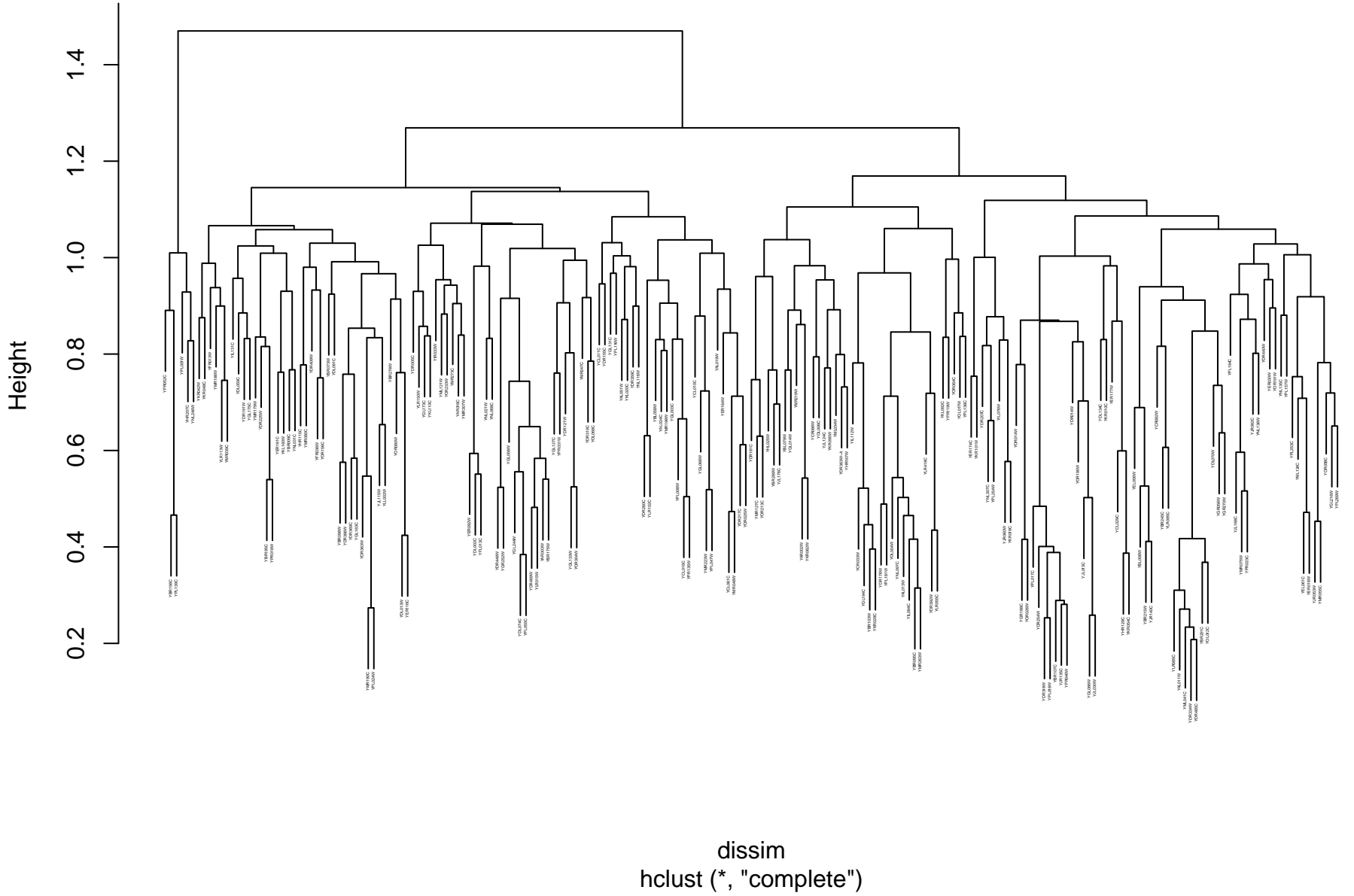
```
dissim
hclust (*, "complete")
```



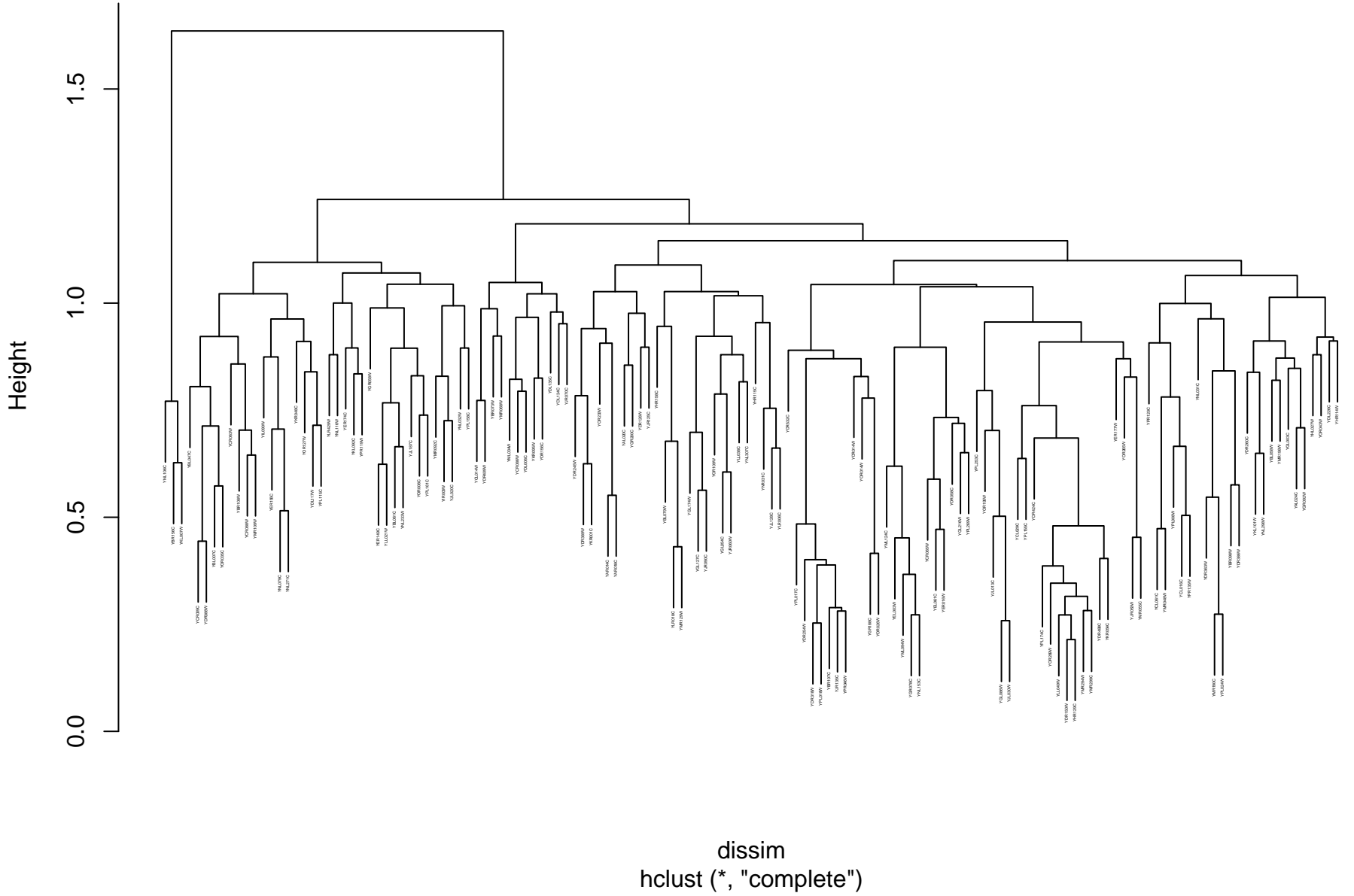
```
dissim
hclust (*, "complete")
```



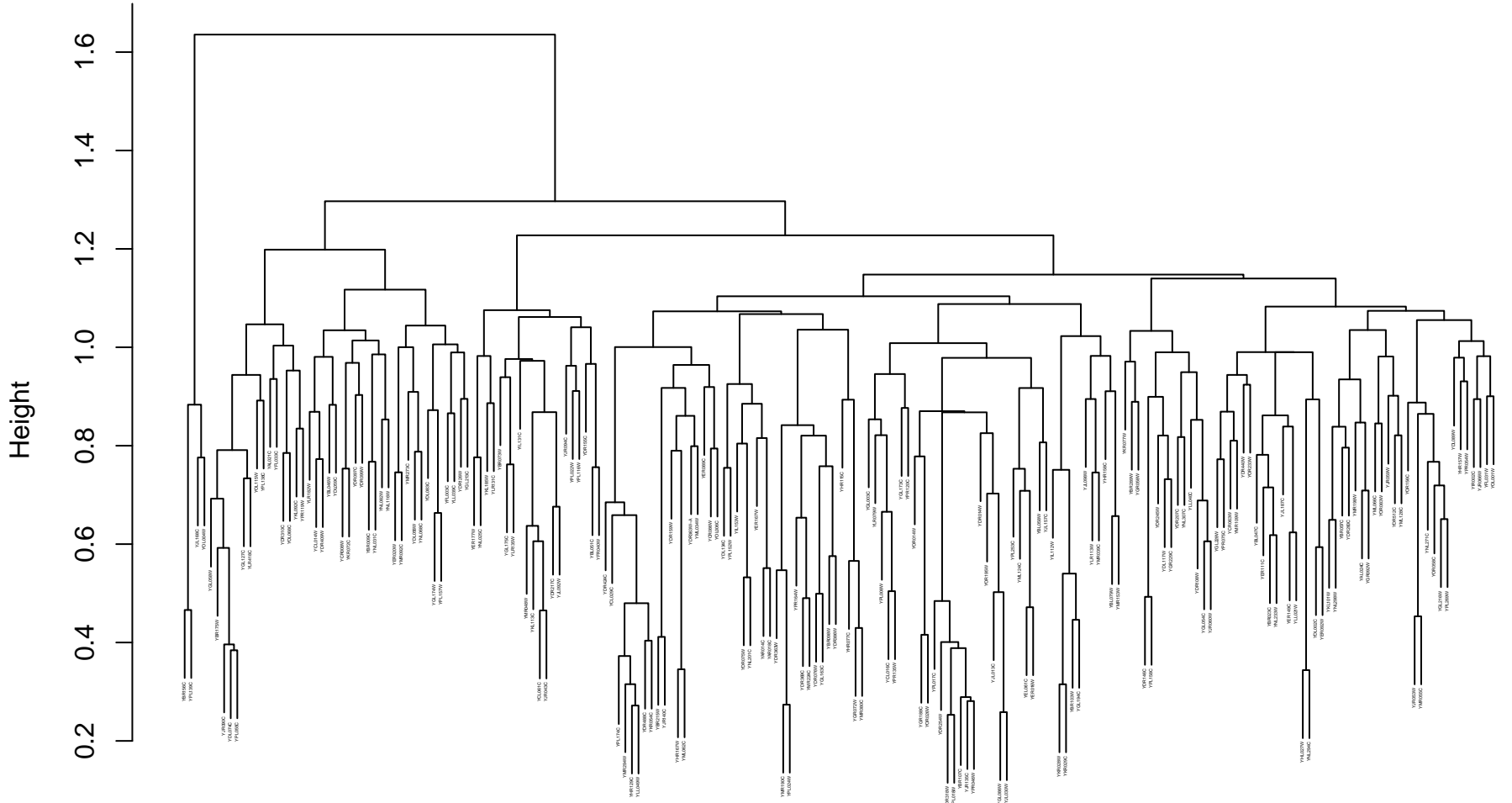
```
dissim
hclust (*, "complete")
```



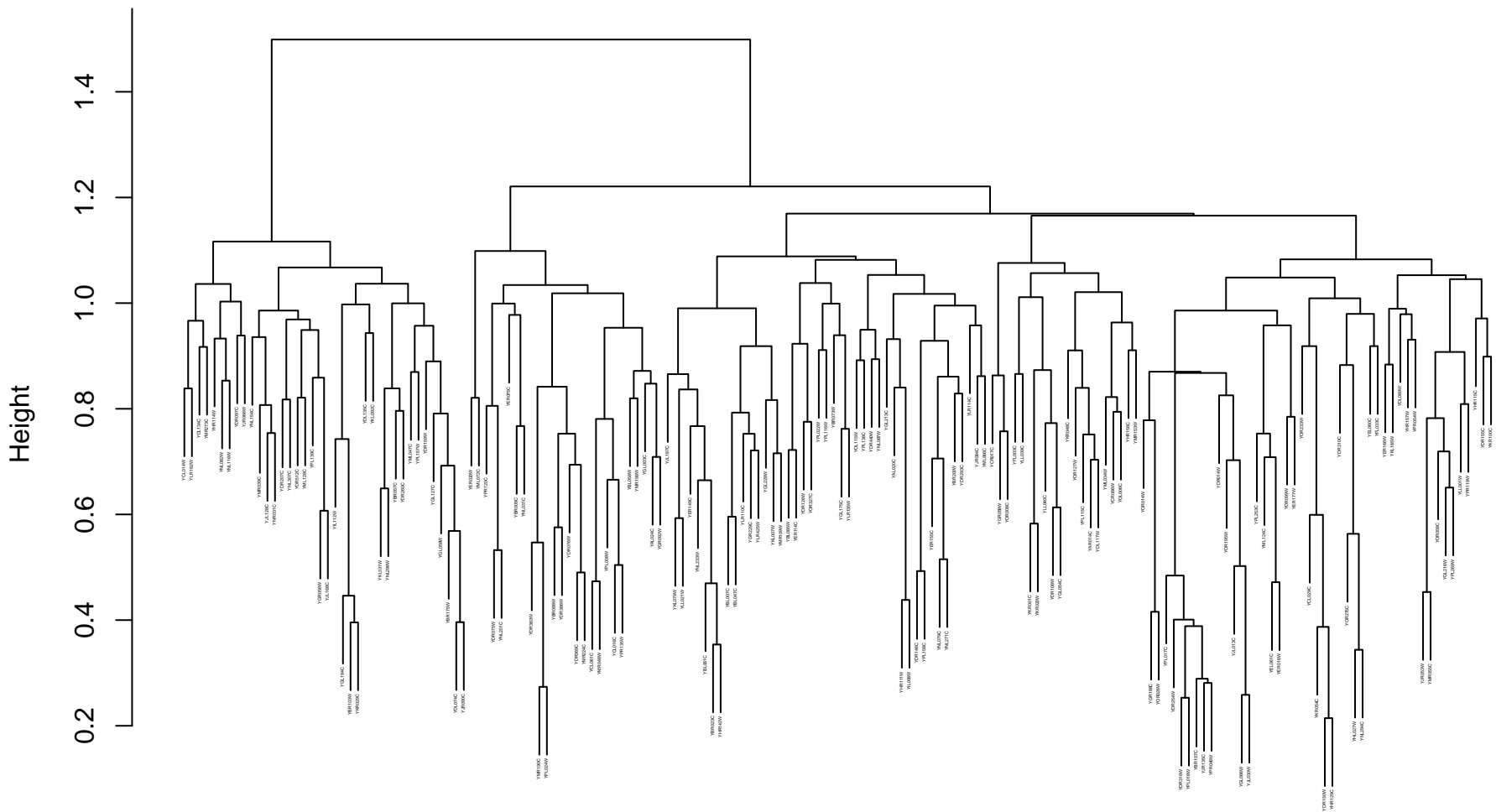
cytoskeleton_GO_pearson_complete




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



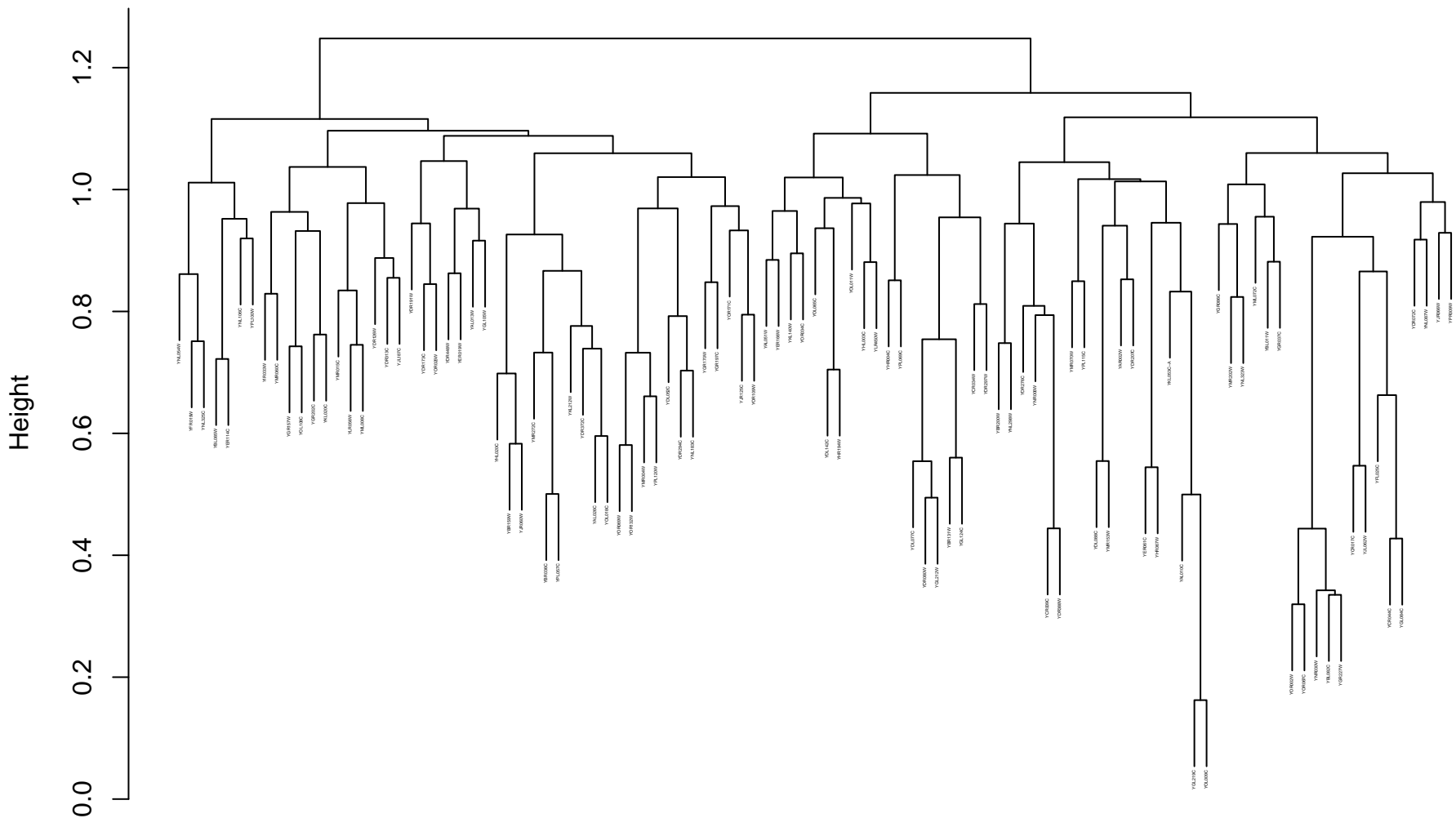
```
dissim
hclust (*, "complete")
```



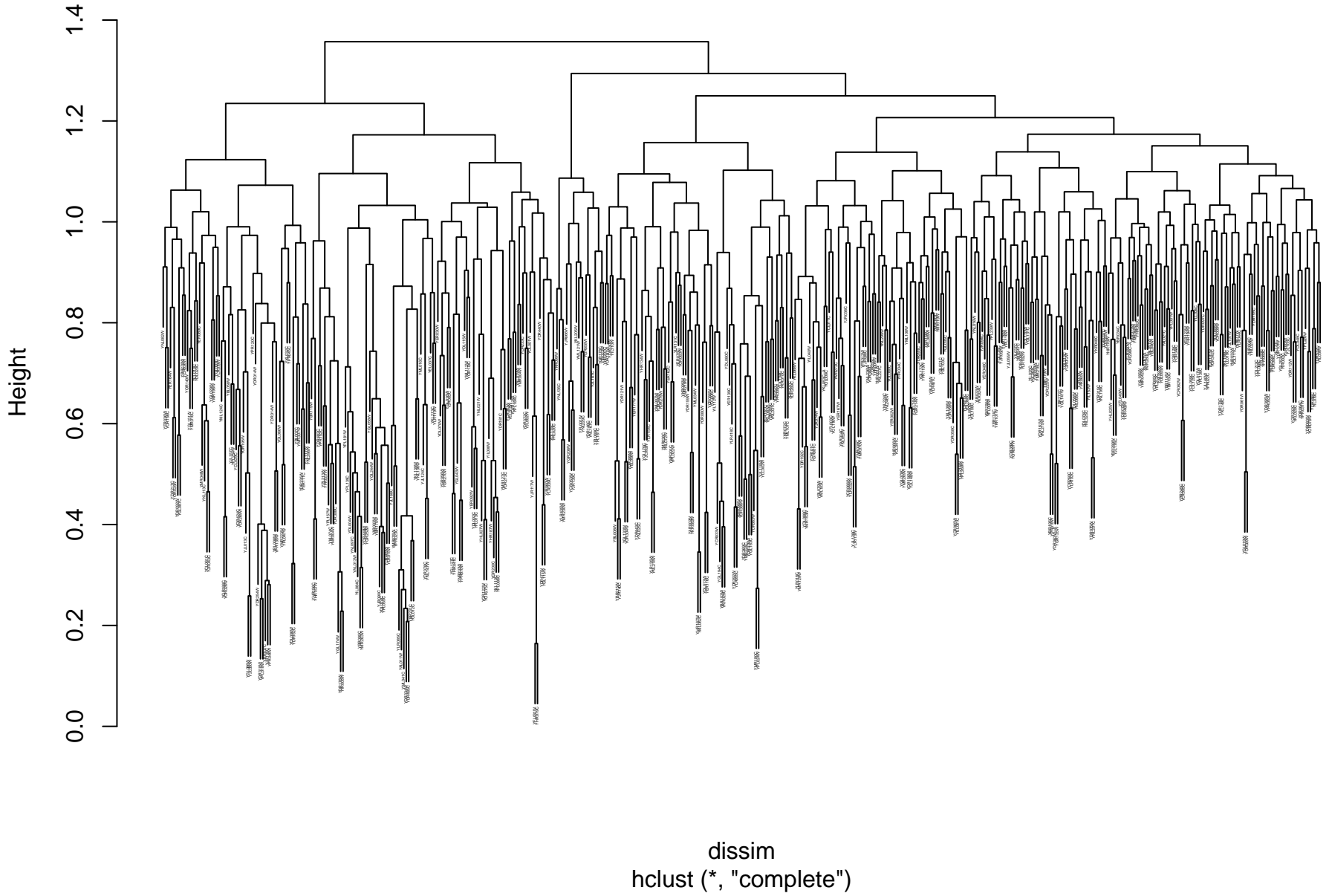
```

dissim
hclust (*, "complete")

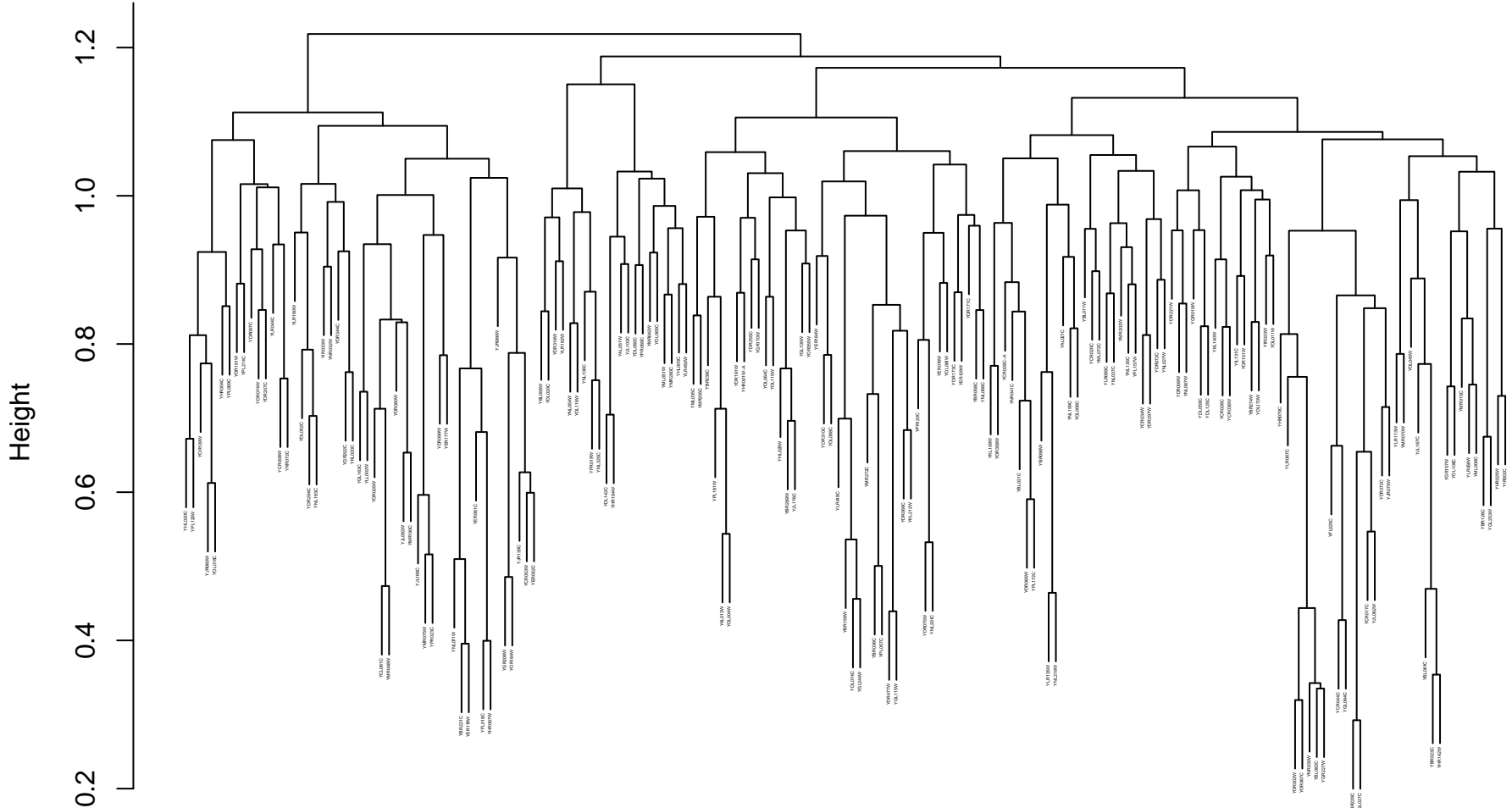
```



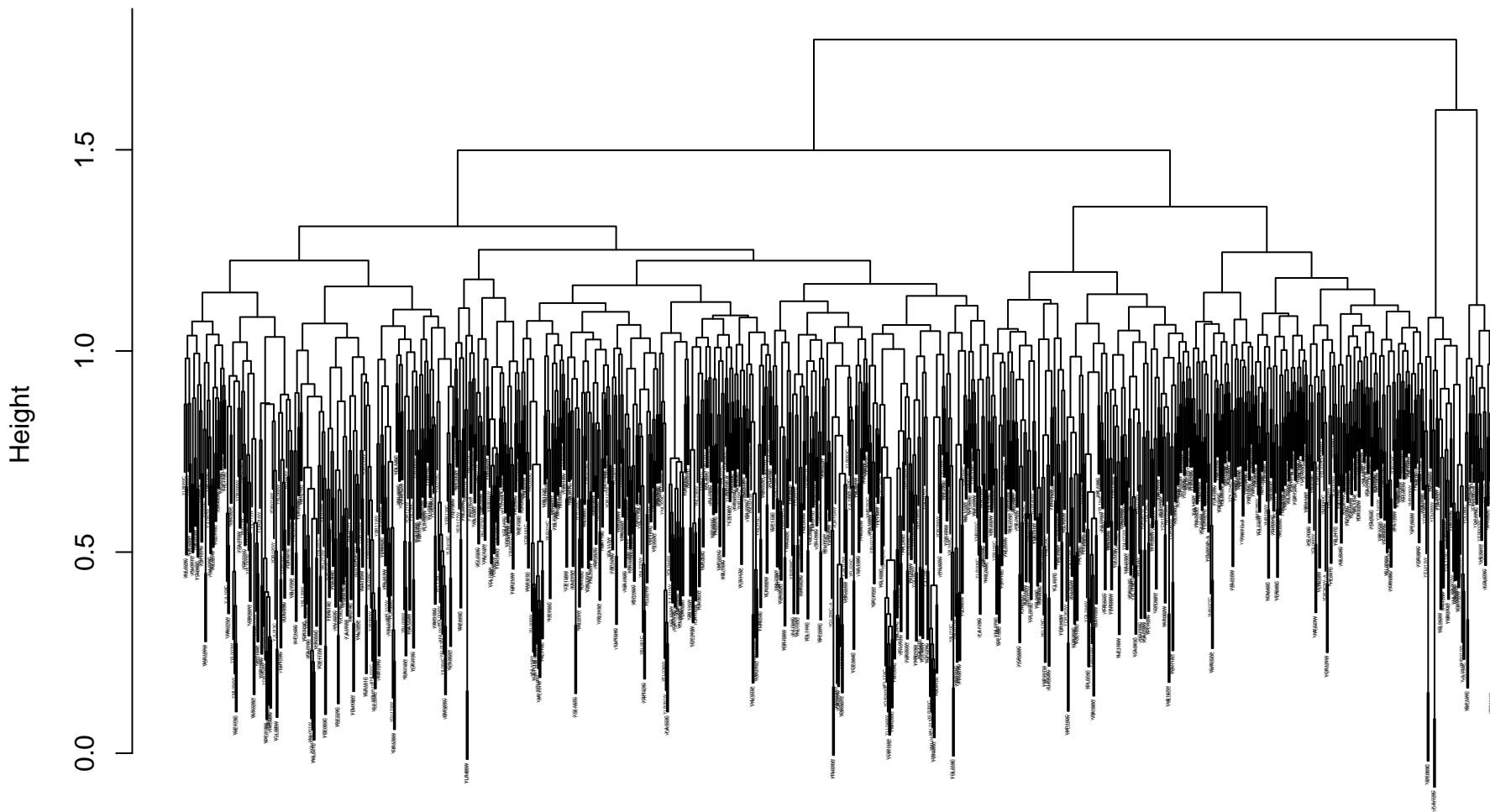
nuclear transport_GO_pearson_complete



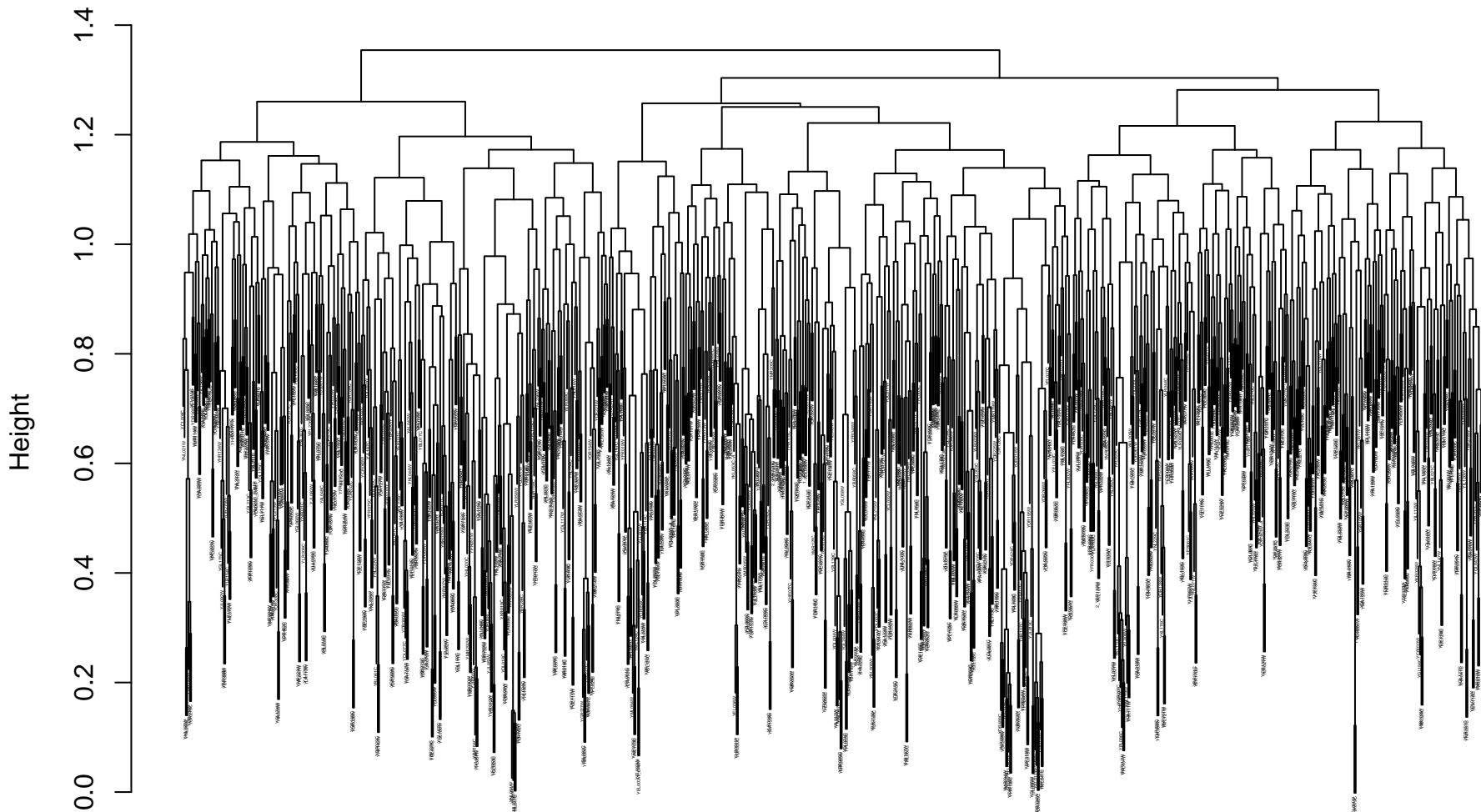
metabolic_GO_pearson_complete



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



gene_pearson_complete

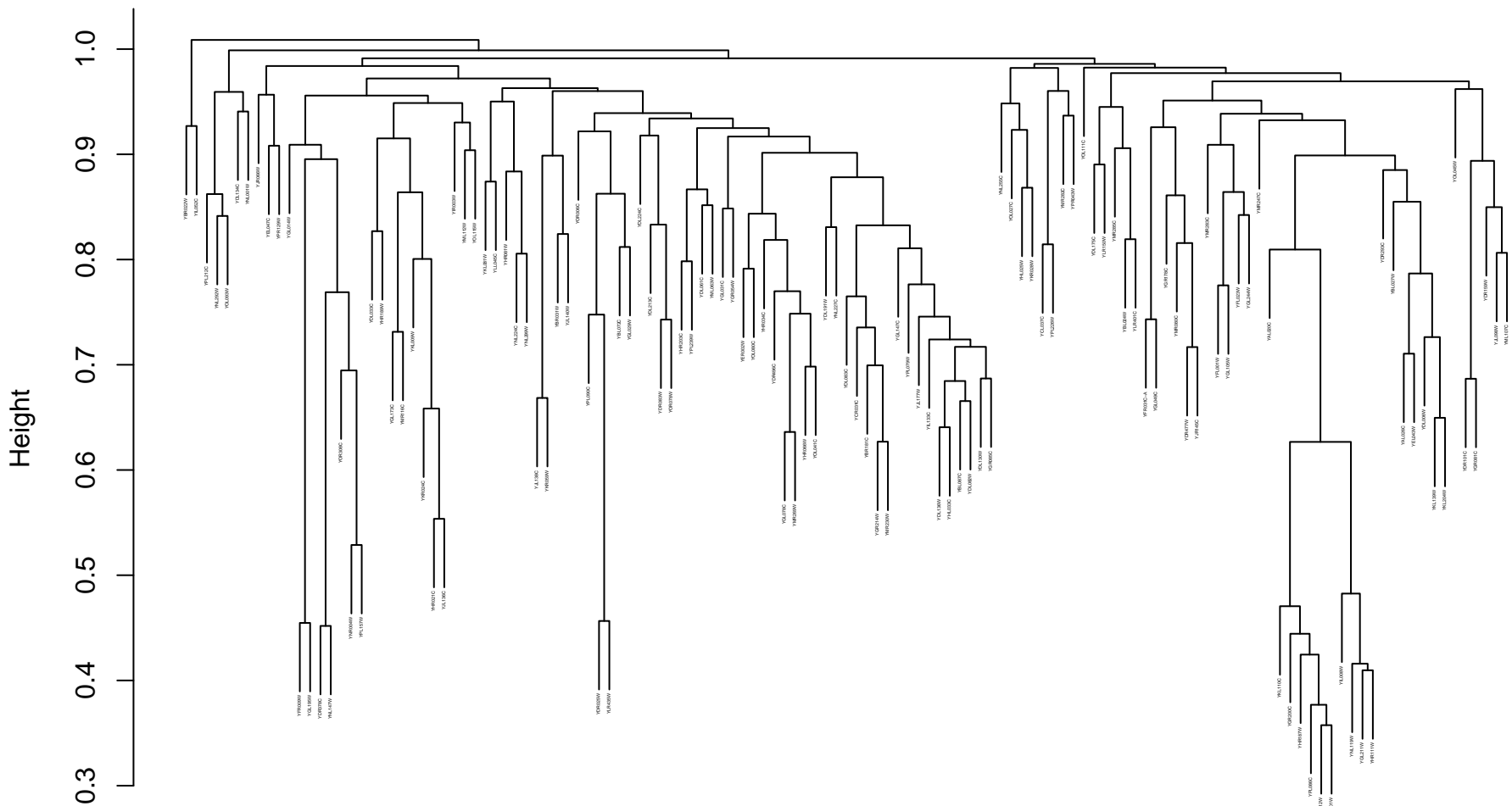


dissim
hclust (*, "complete")

```

dissim
hclust (*, "average")

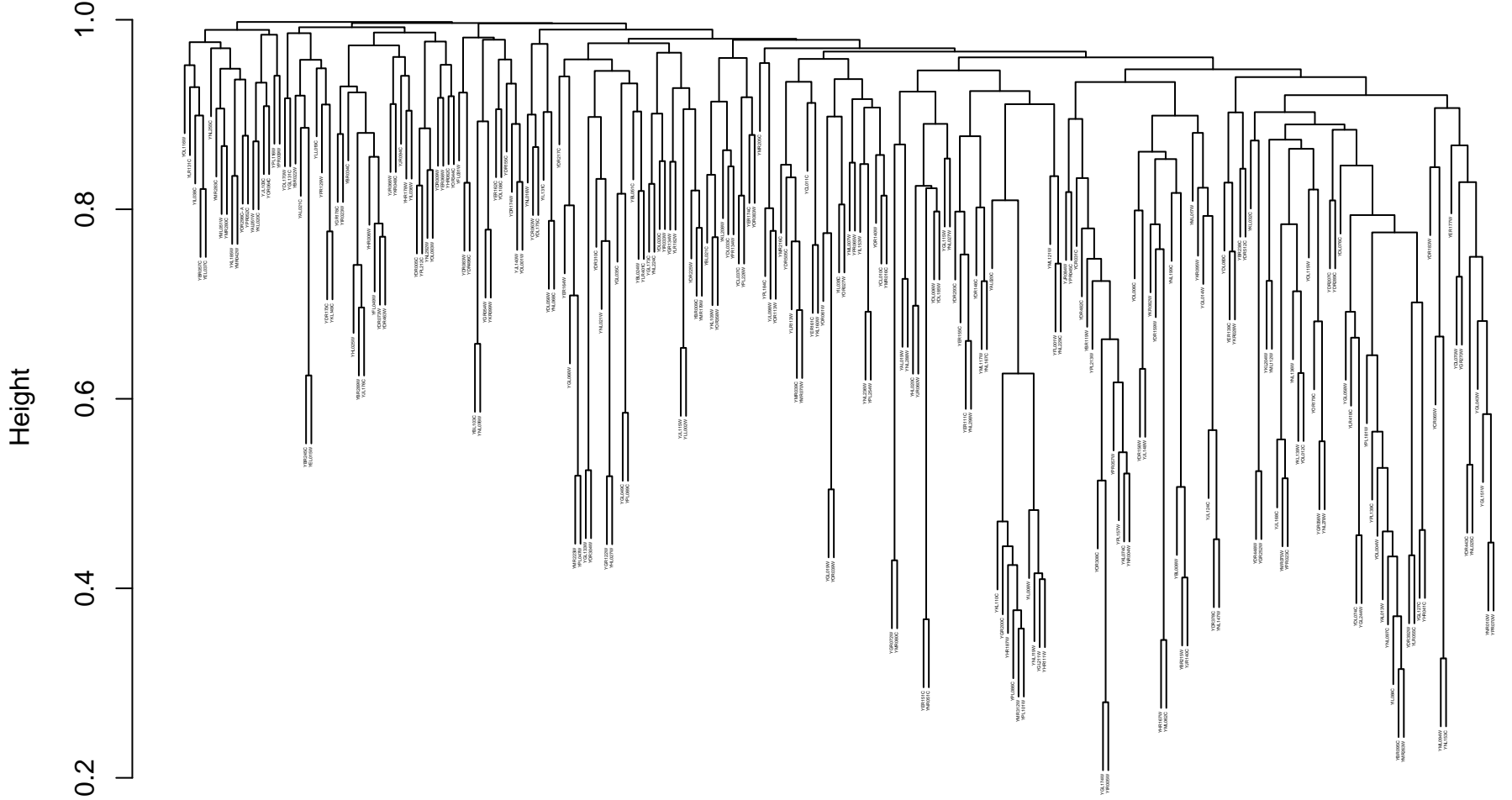
```



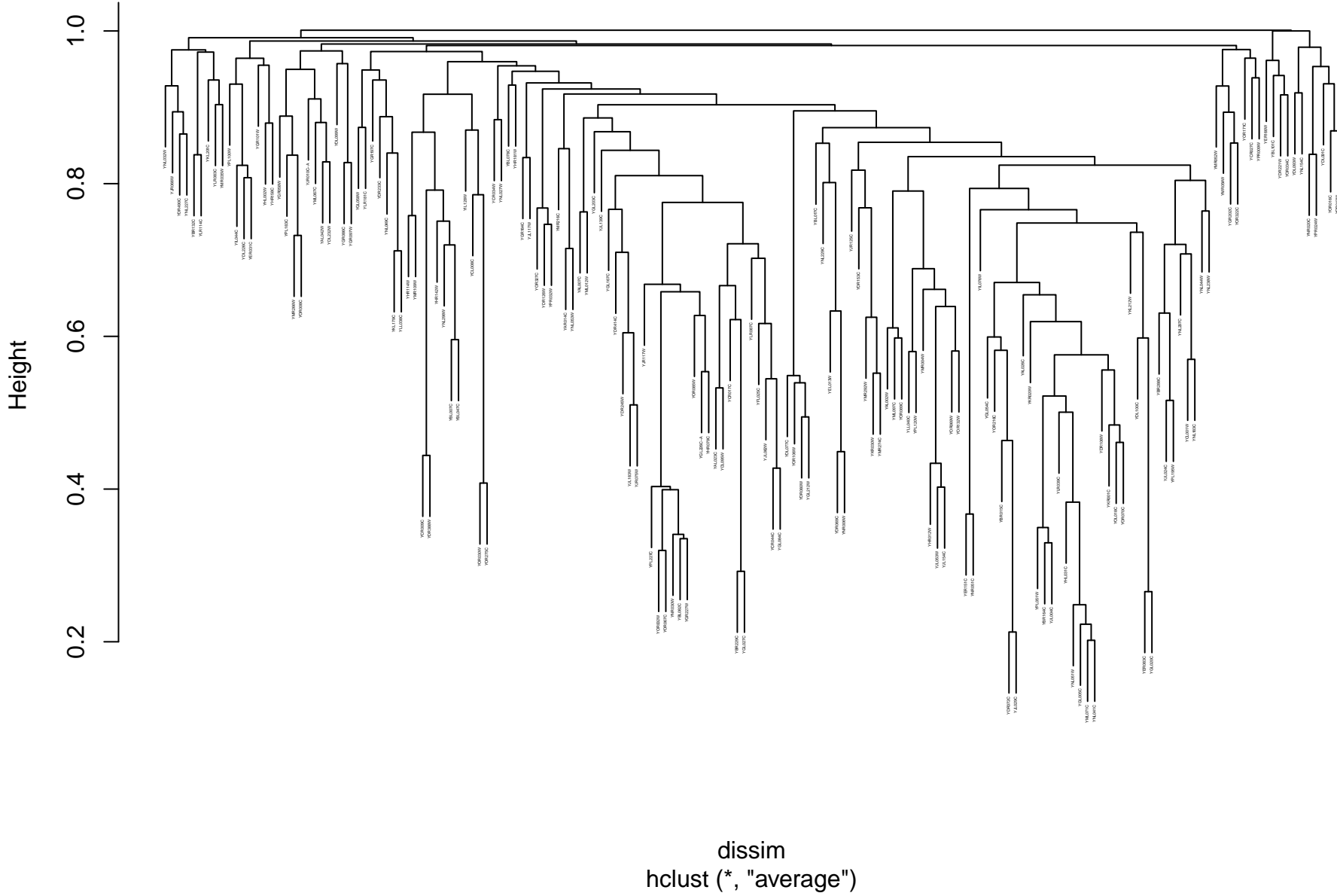

```

dissim
hclust (*, "average")

```



Golgi and ER_GO_pearson_average



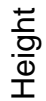
```

dissim
hclust (*, "average")

```

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

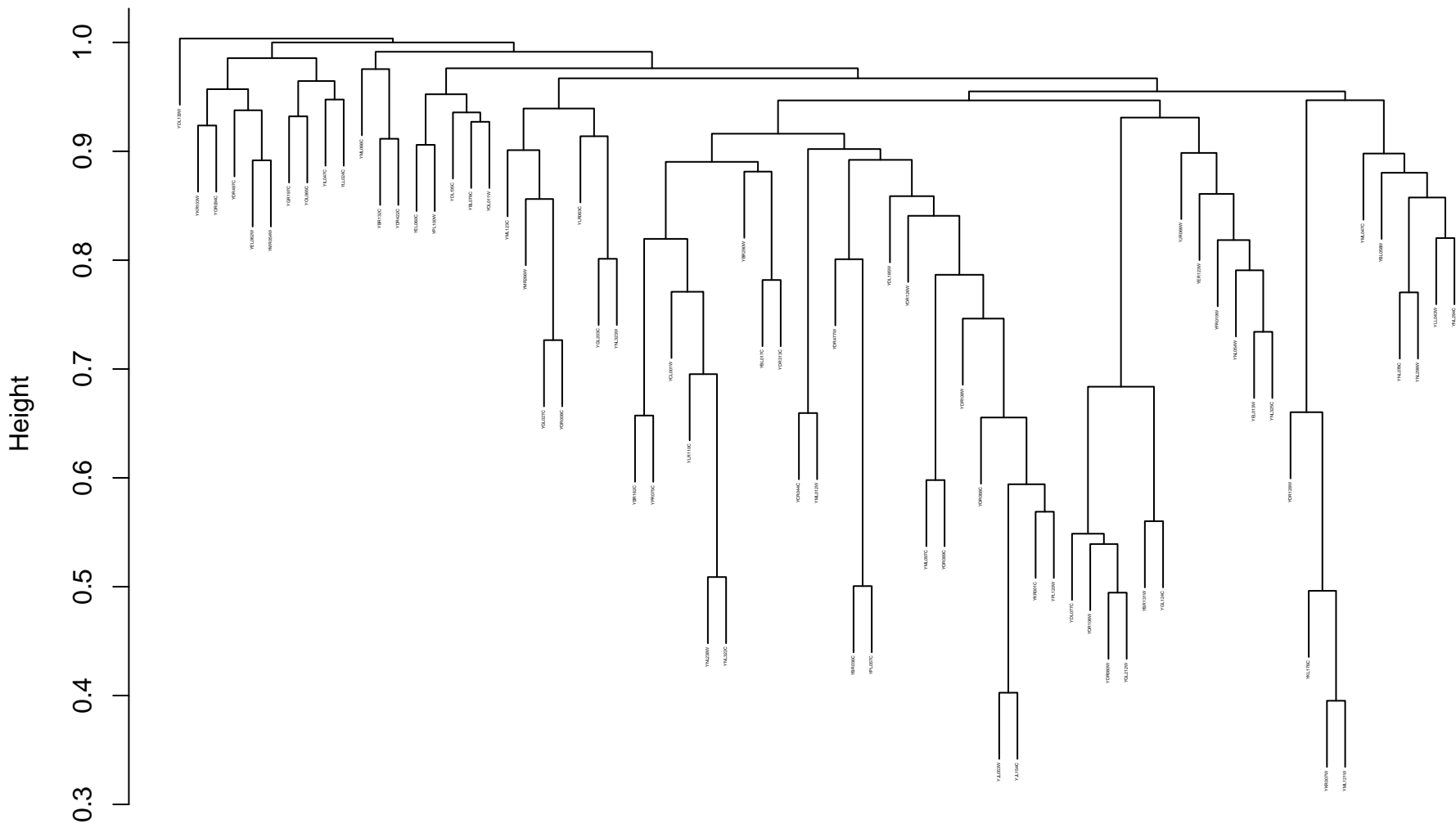
```
hclust (*, "average")
```



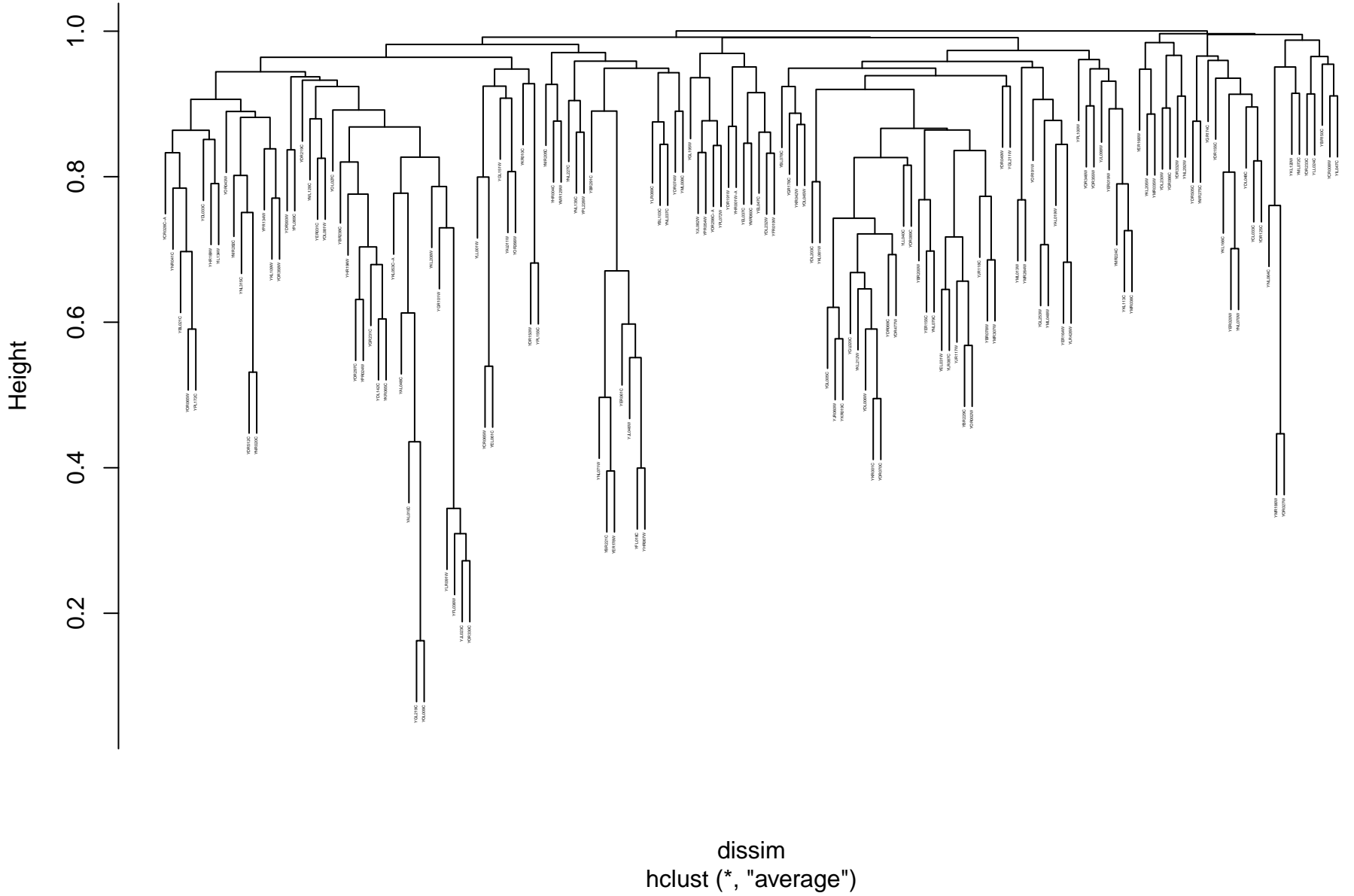
```

dissim
hclust (*, "average")

```



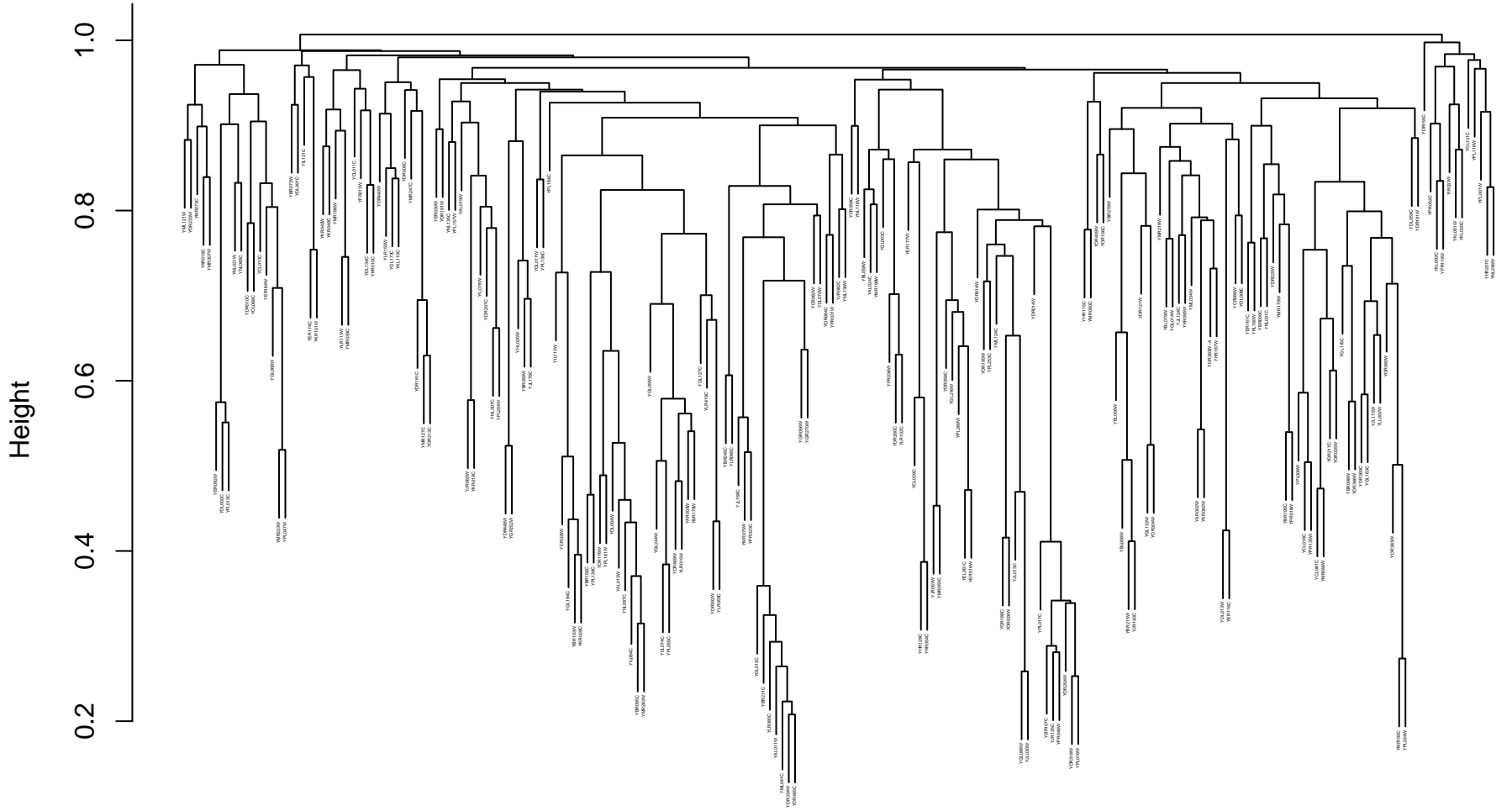
mitochondrion_GO_pearson_average



```

dissim
hclust (*, "average")

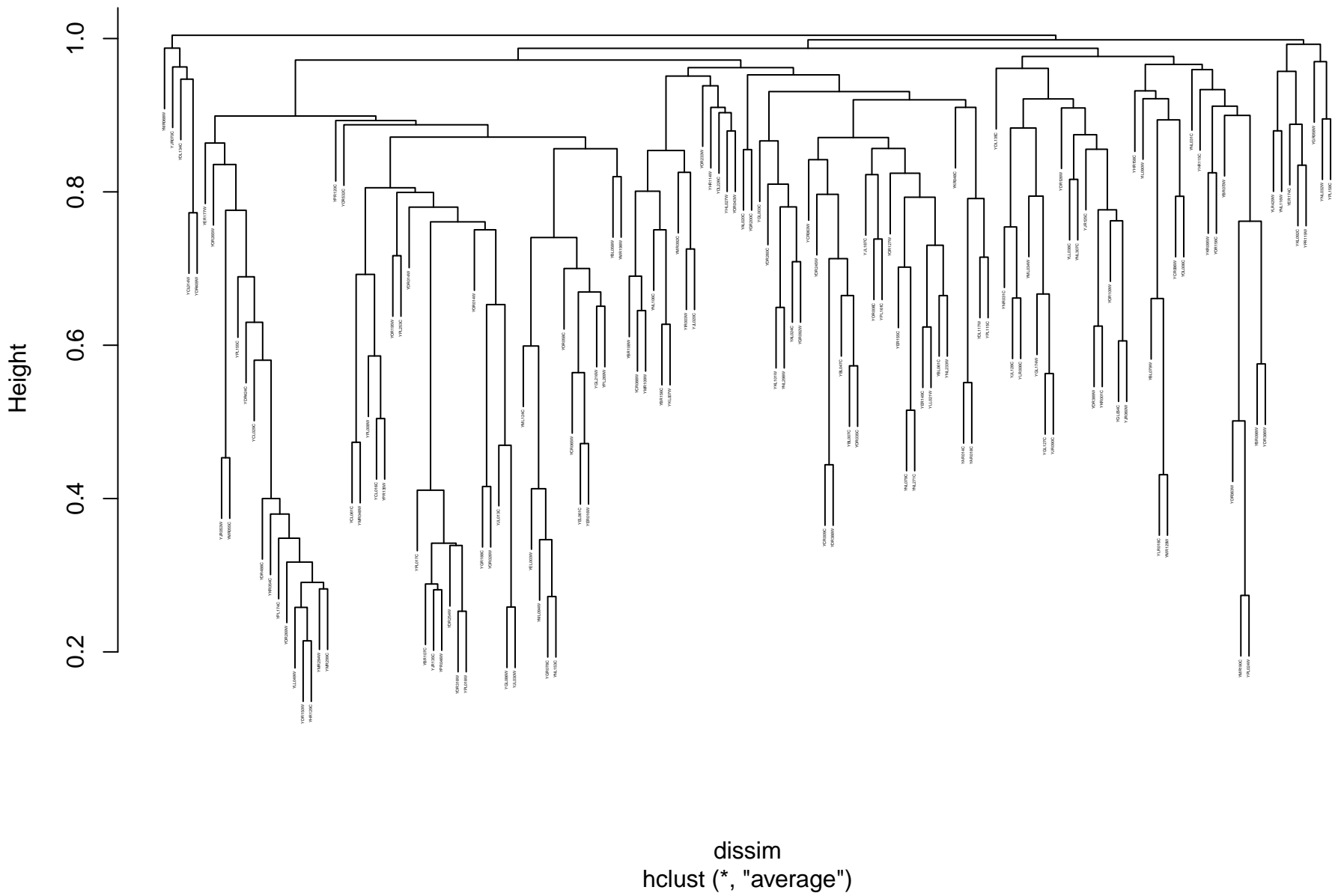
```



```

dissim
hclust (*, "average")

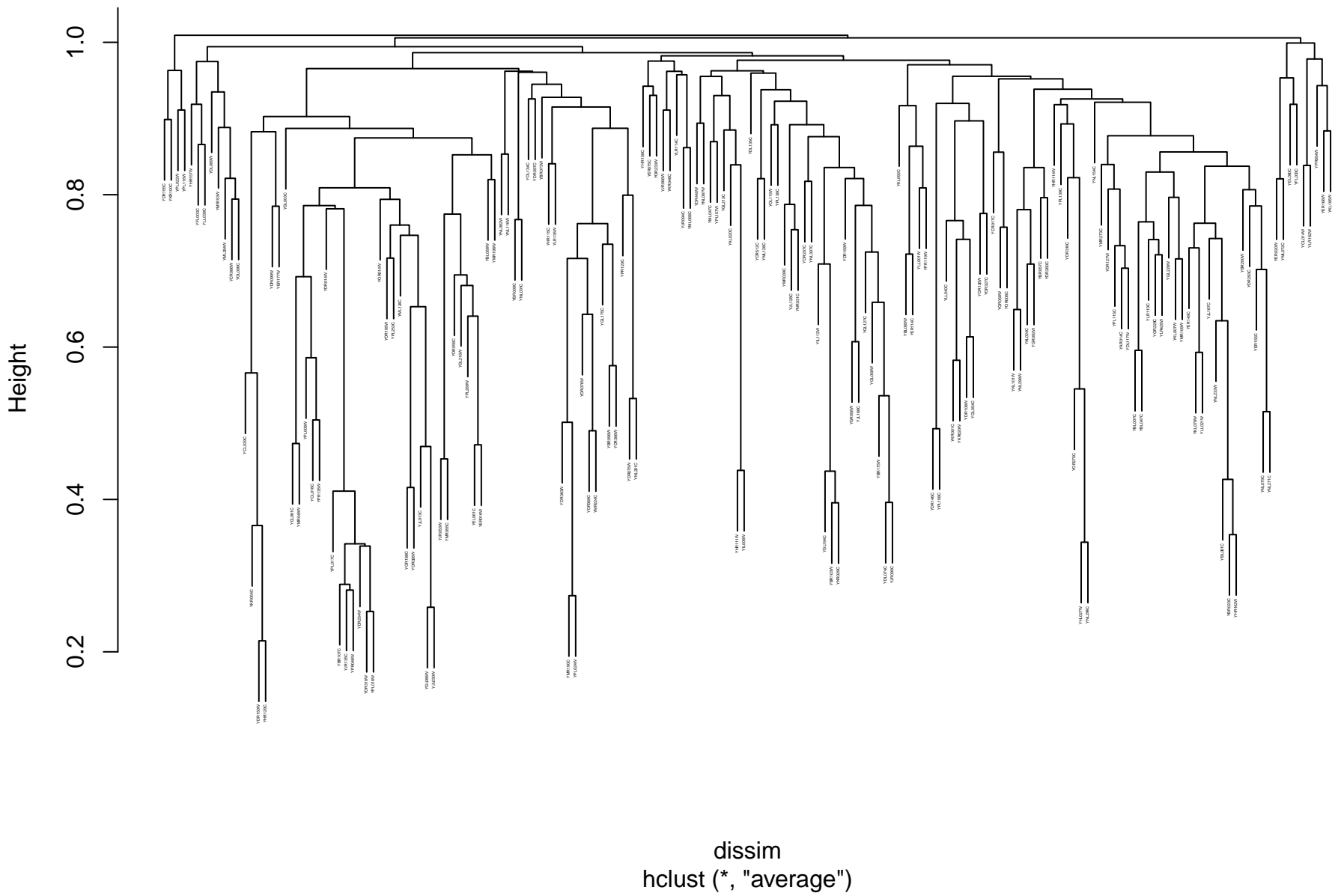
```




```

dissim
hclust (*, "average")

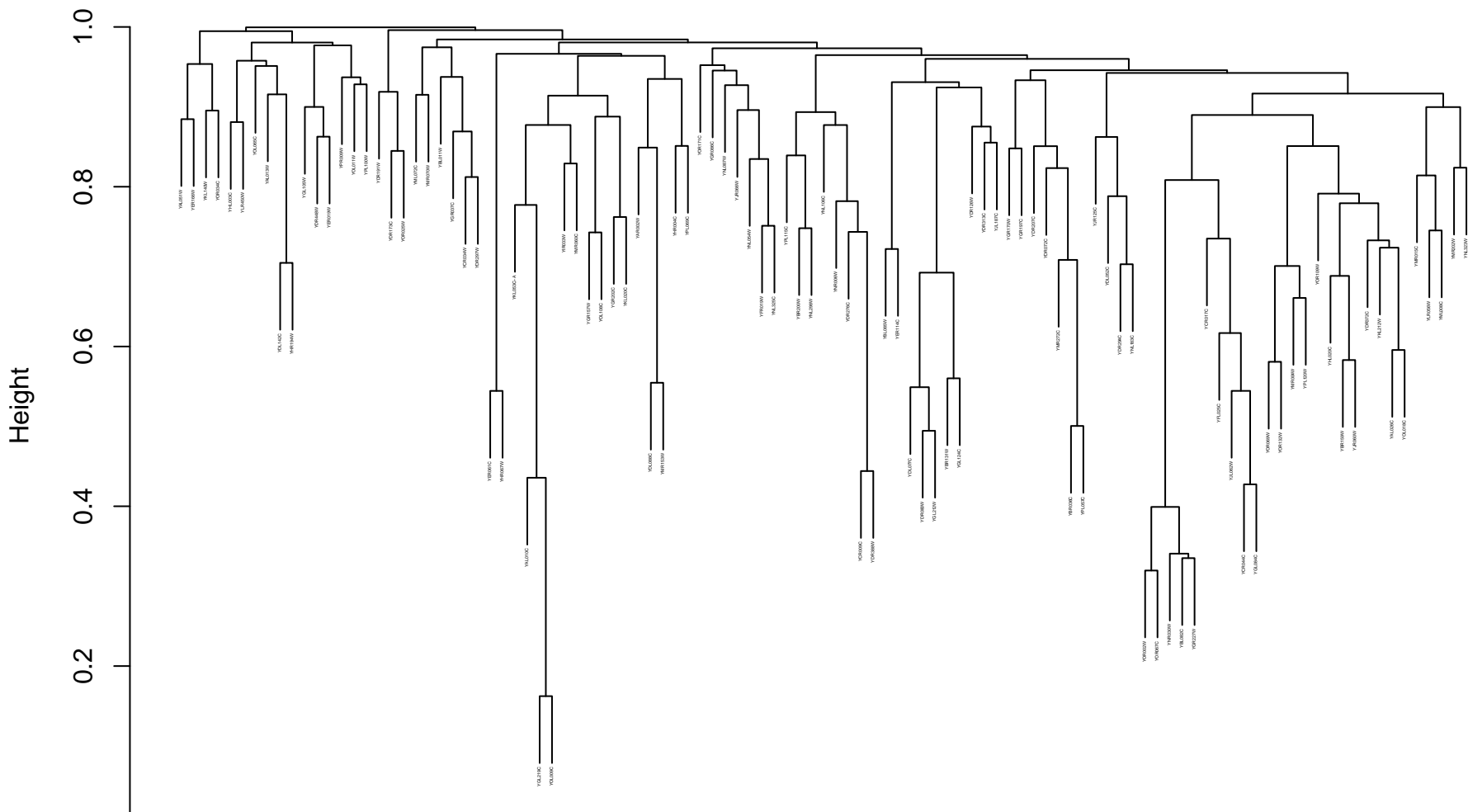
```



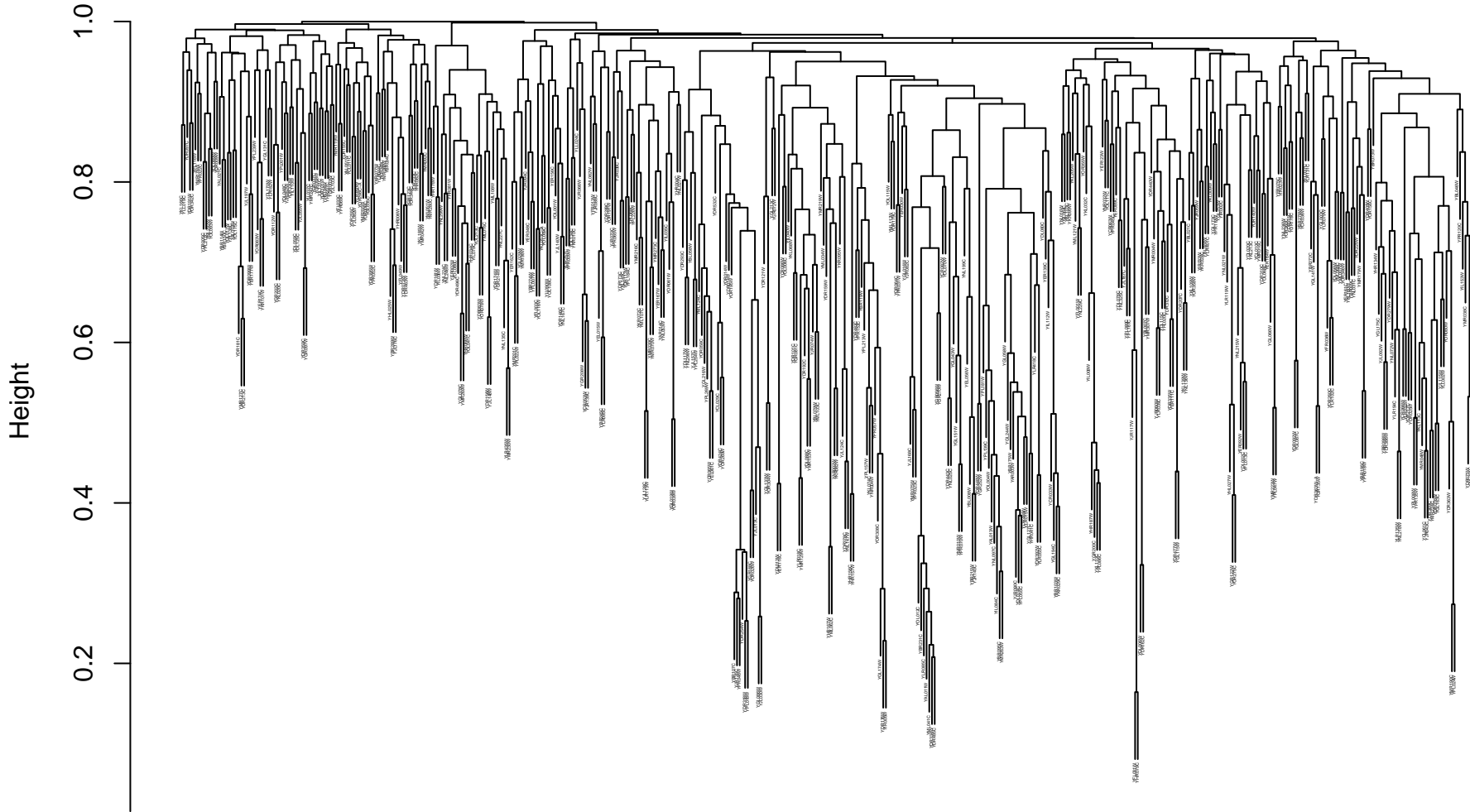
```

dissim
hclust (*, "average")

```



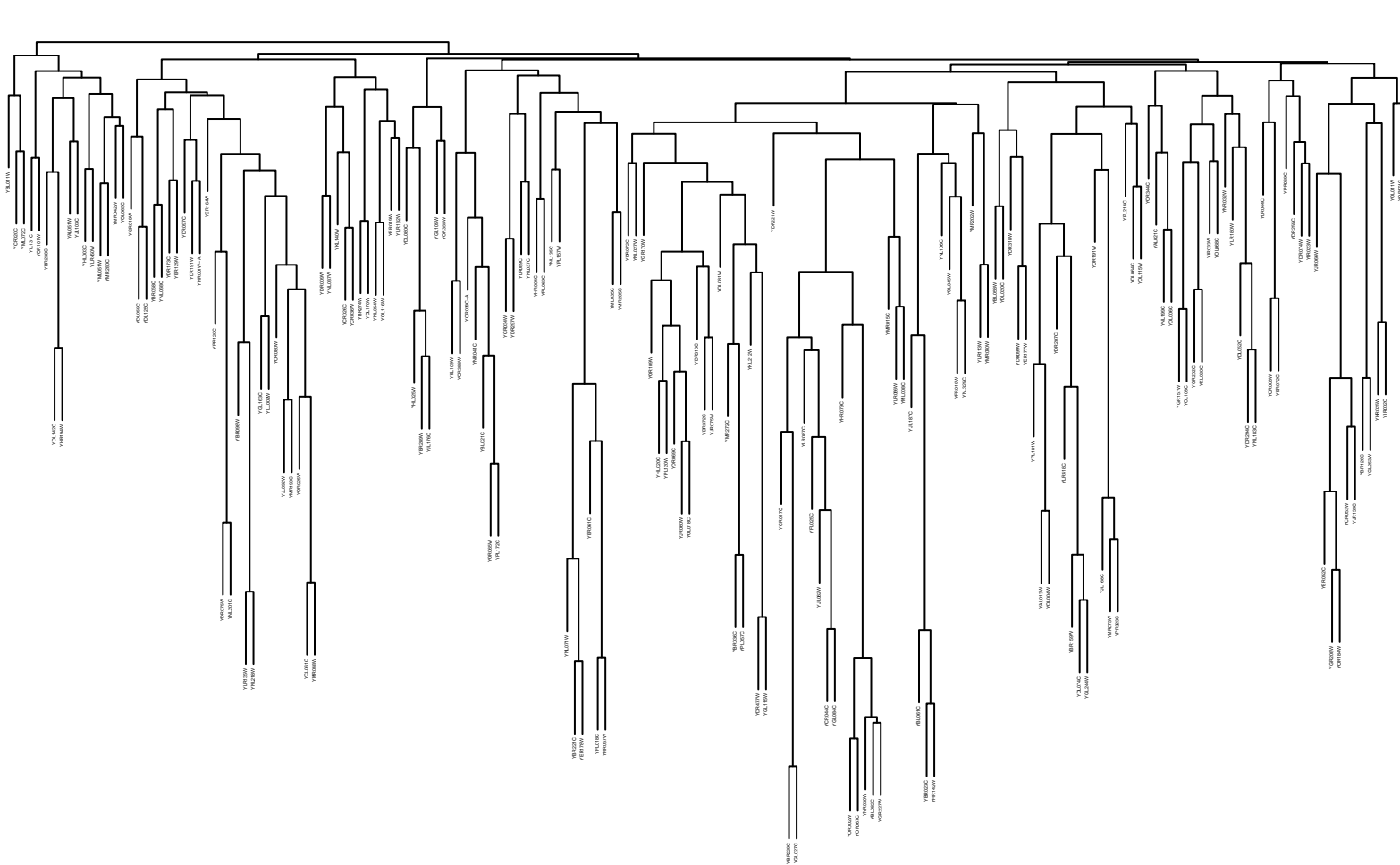
nuclear transport_GO_pearson_average



metabolic_GO_pearson_average

Height

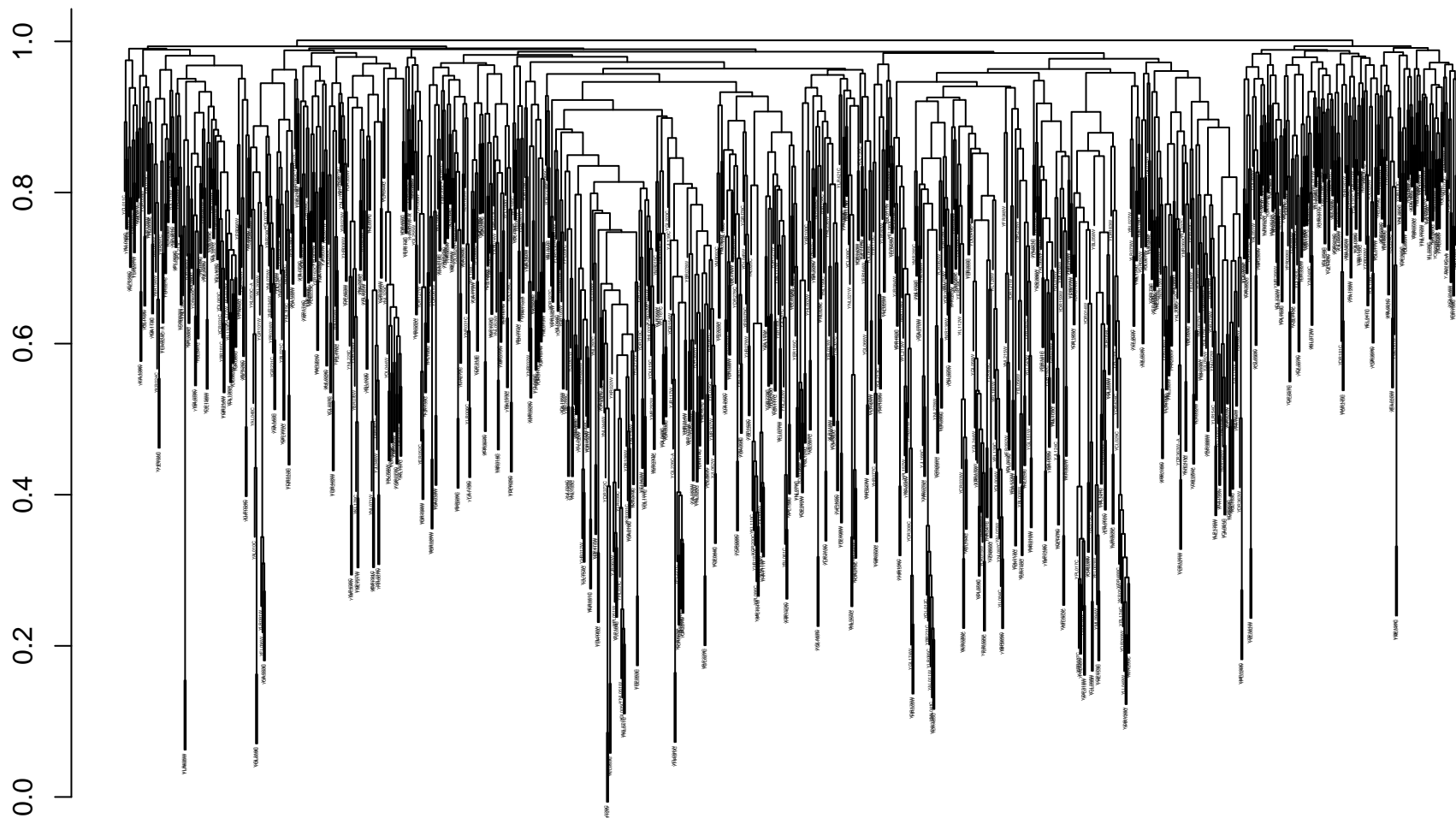
1.0
0.8
0.6
0.4
0.2



dissim
hclust (*, "average")

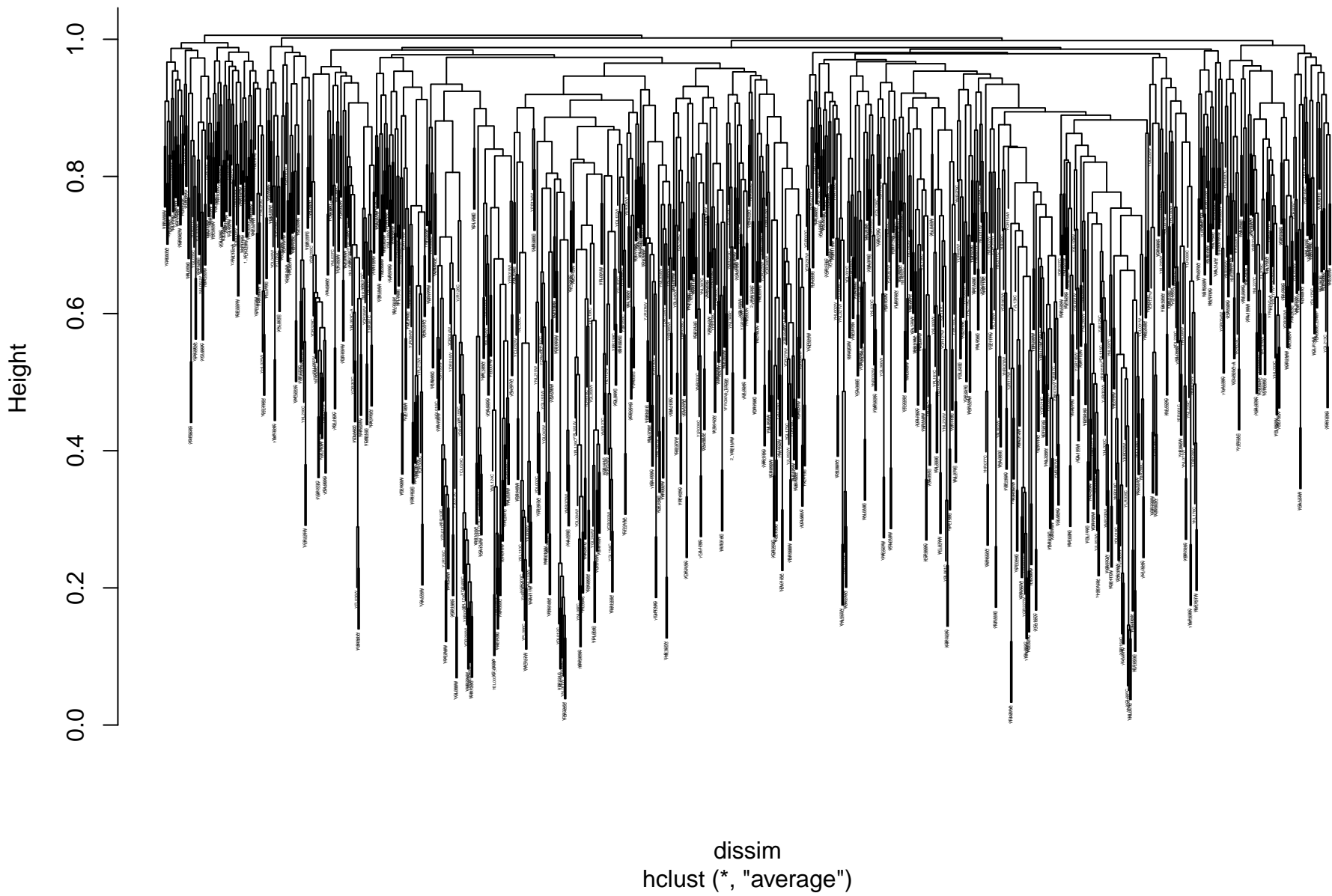
Height

library_pearson_average

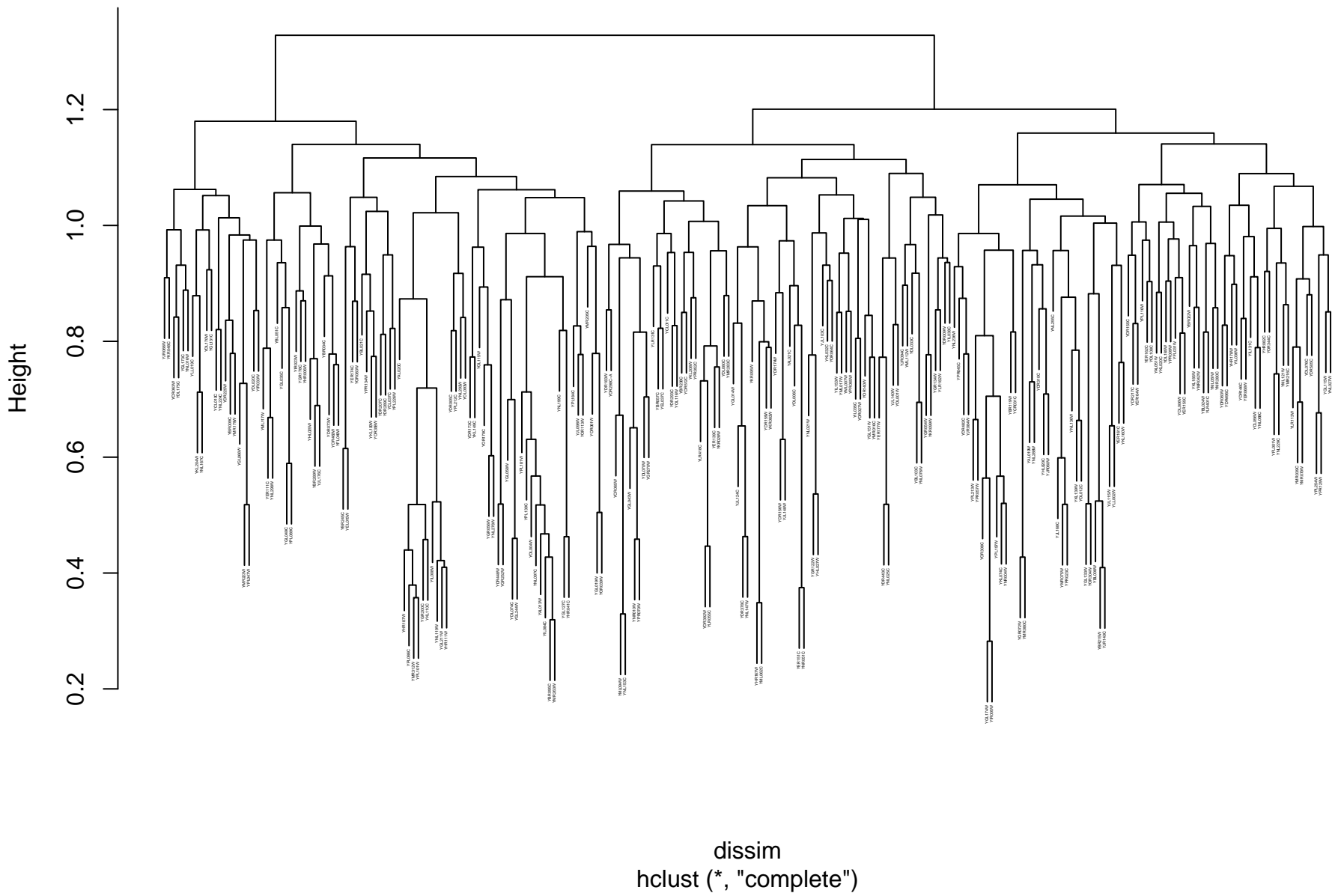


dissim
hclust (*, "average")

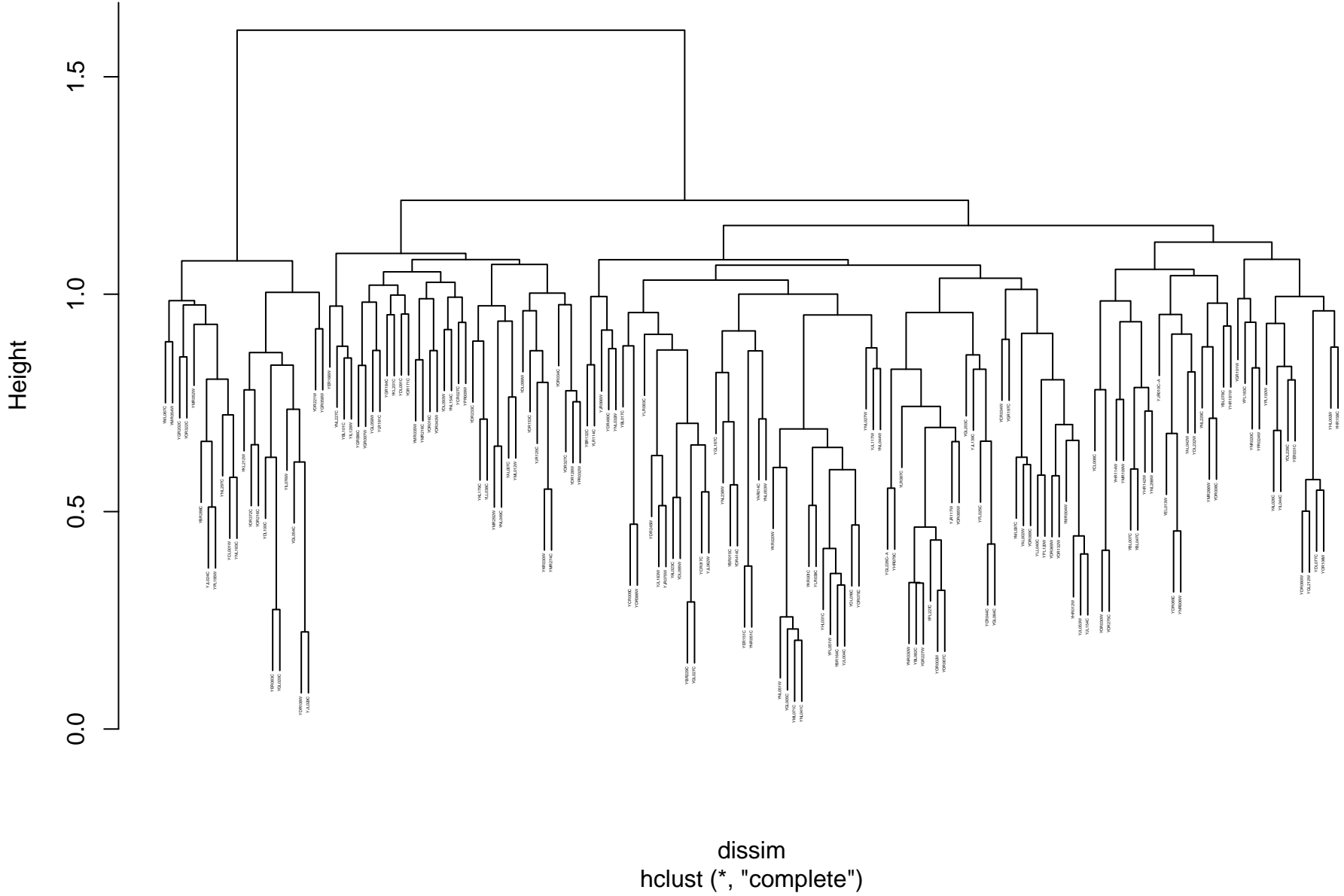
gene_pearson_average



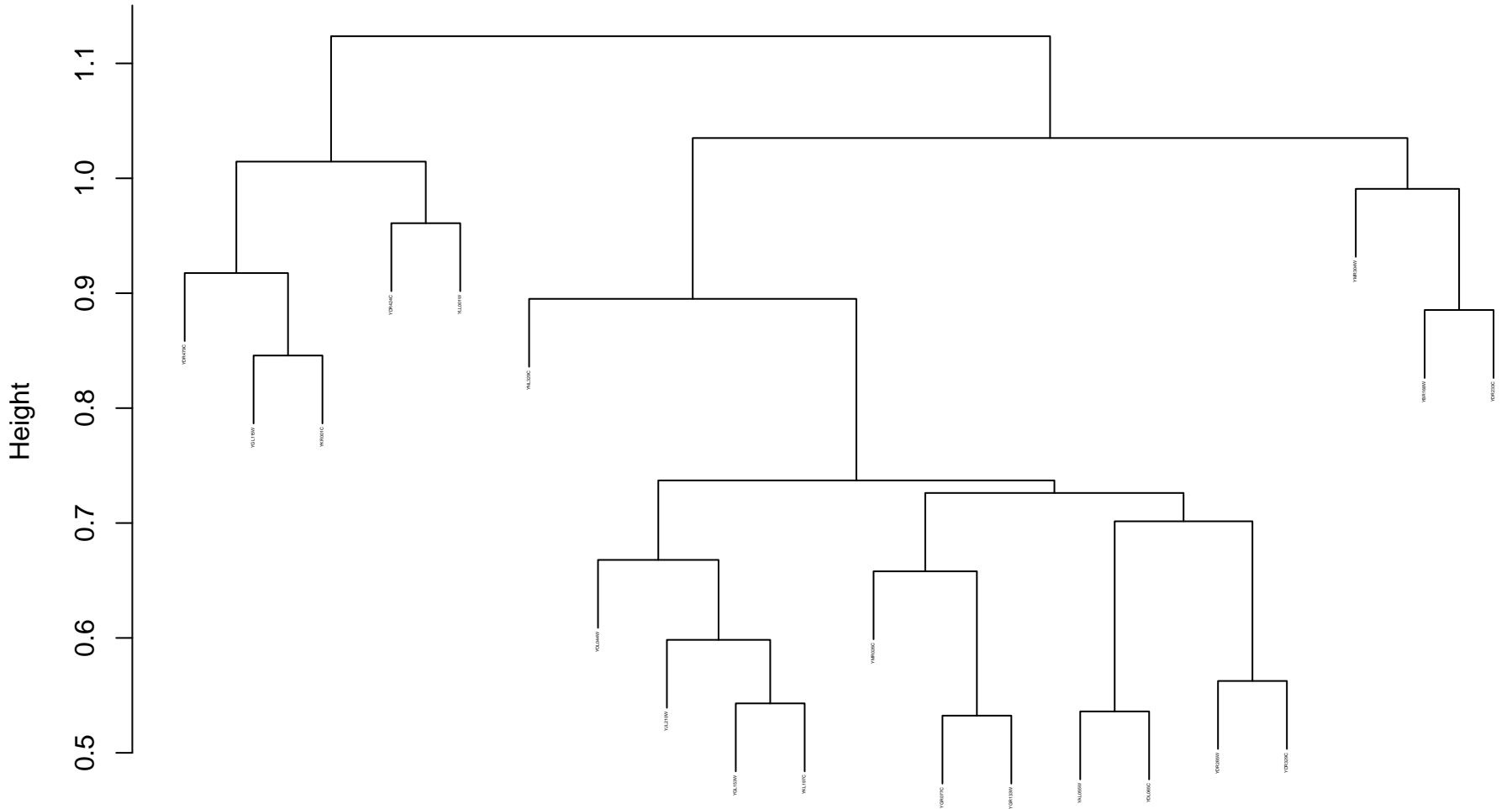
transcription and mRNA processing_GO_correlation_complete



Golgi and ER_GO_correlation_complete



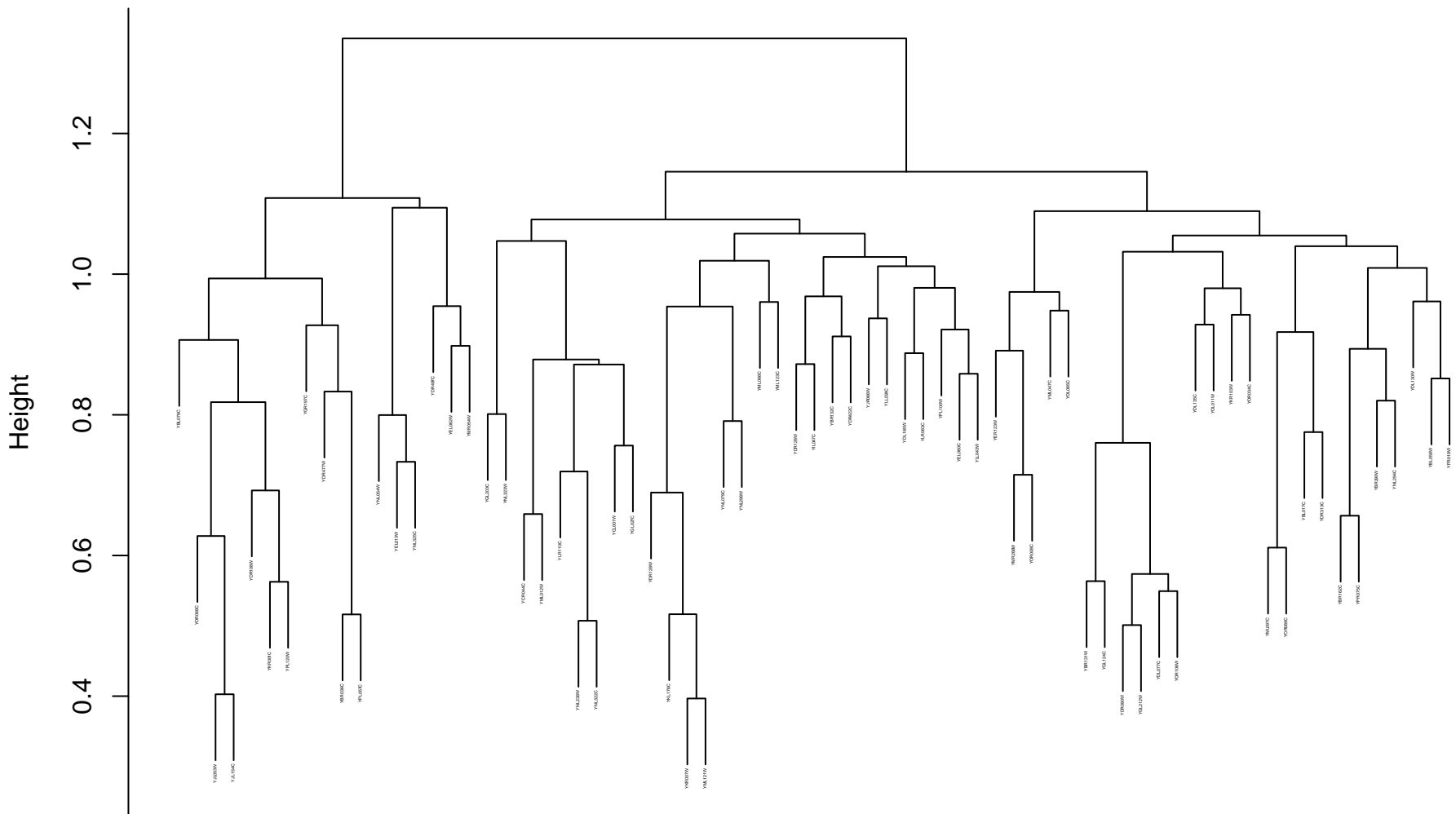
```
dissim
hclust (*, "complete")
```



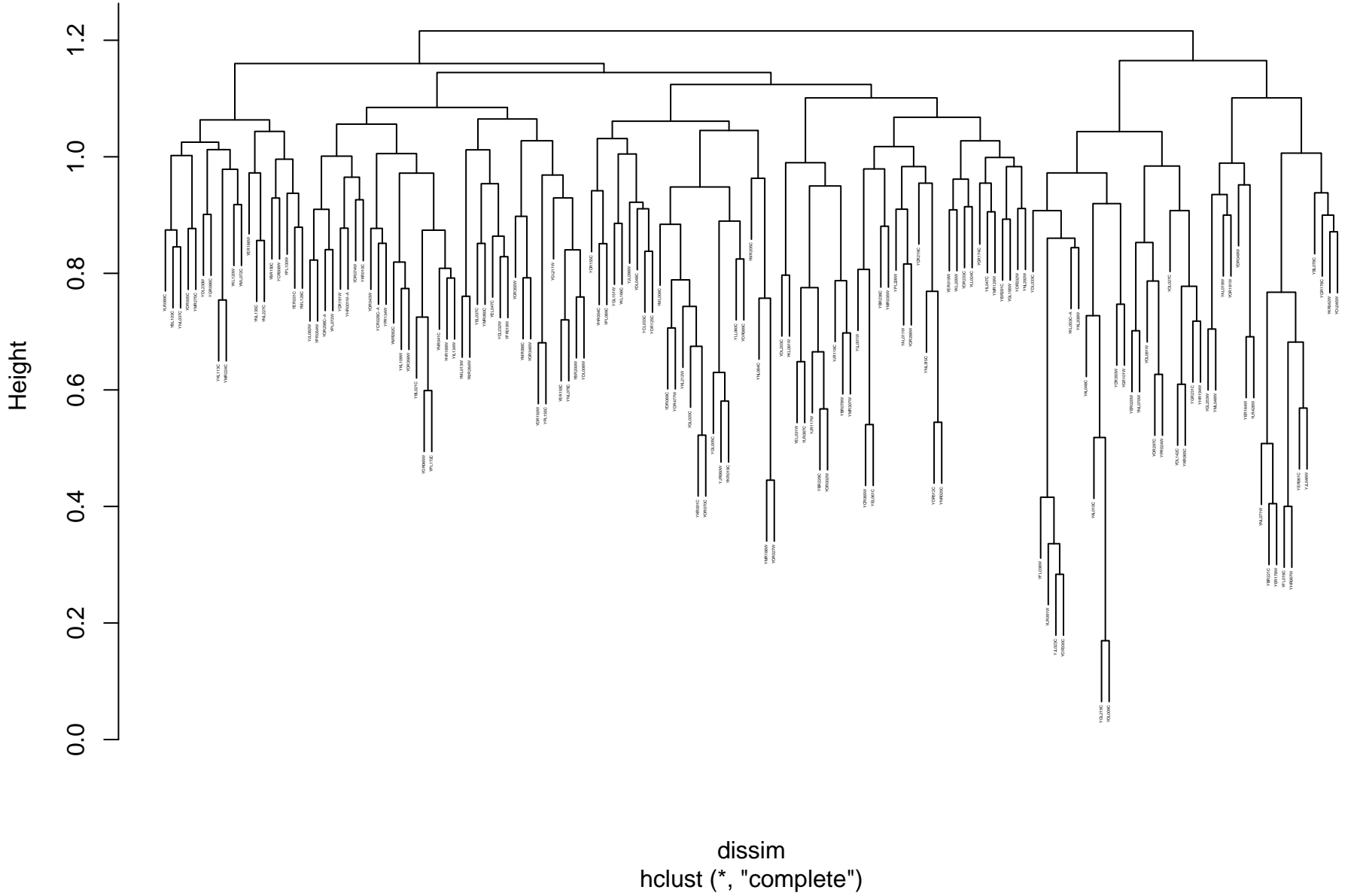
```

dissim
hclust (*, "complete")

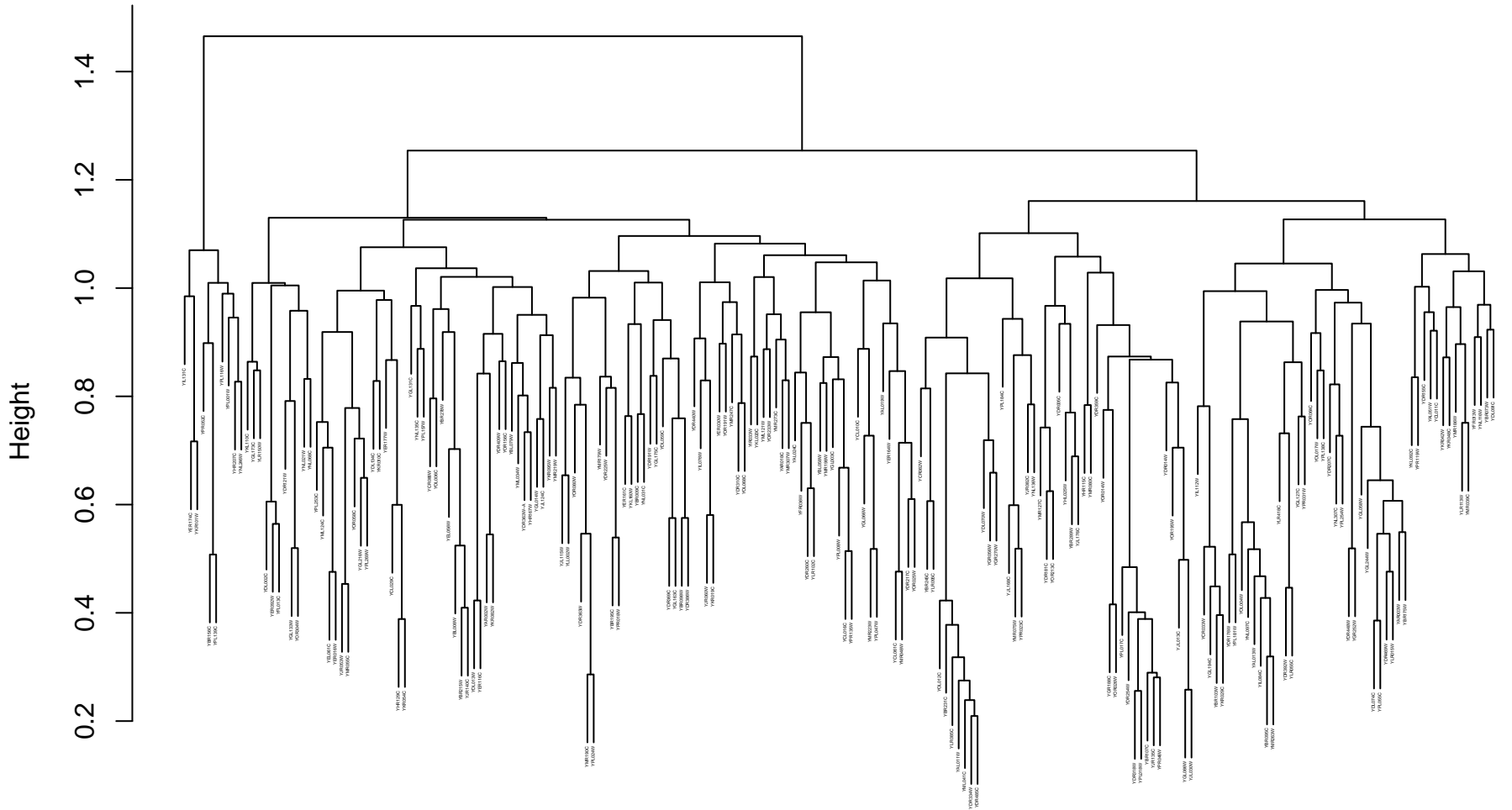
```



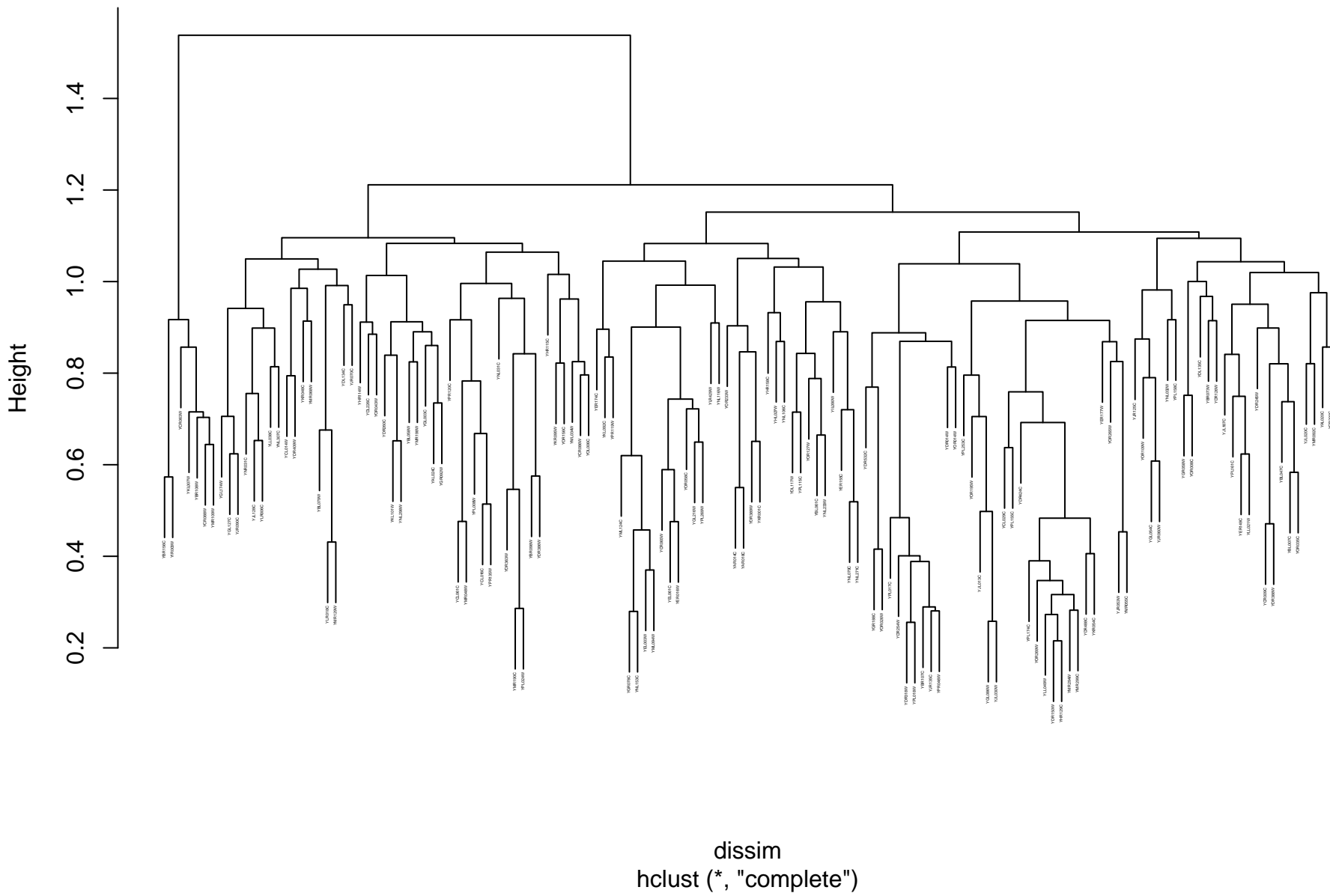
mitochondrion_GO_correlation_complete



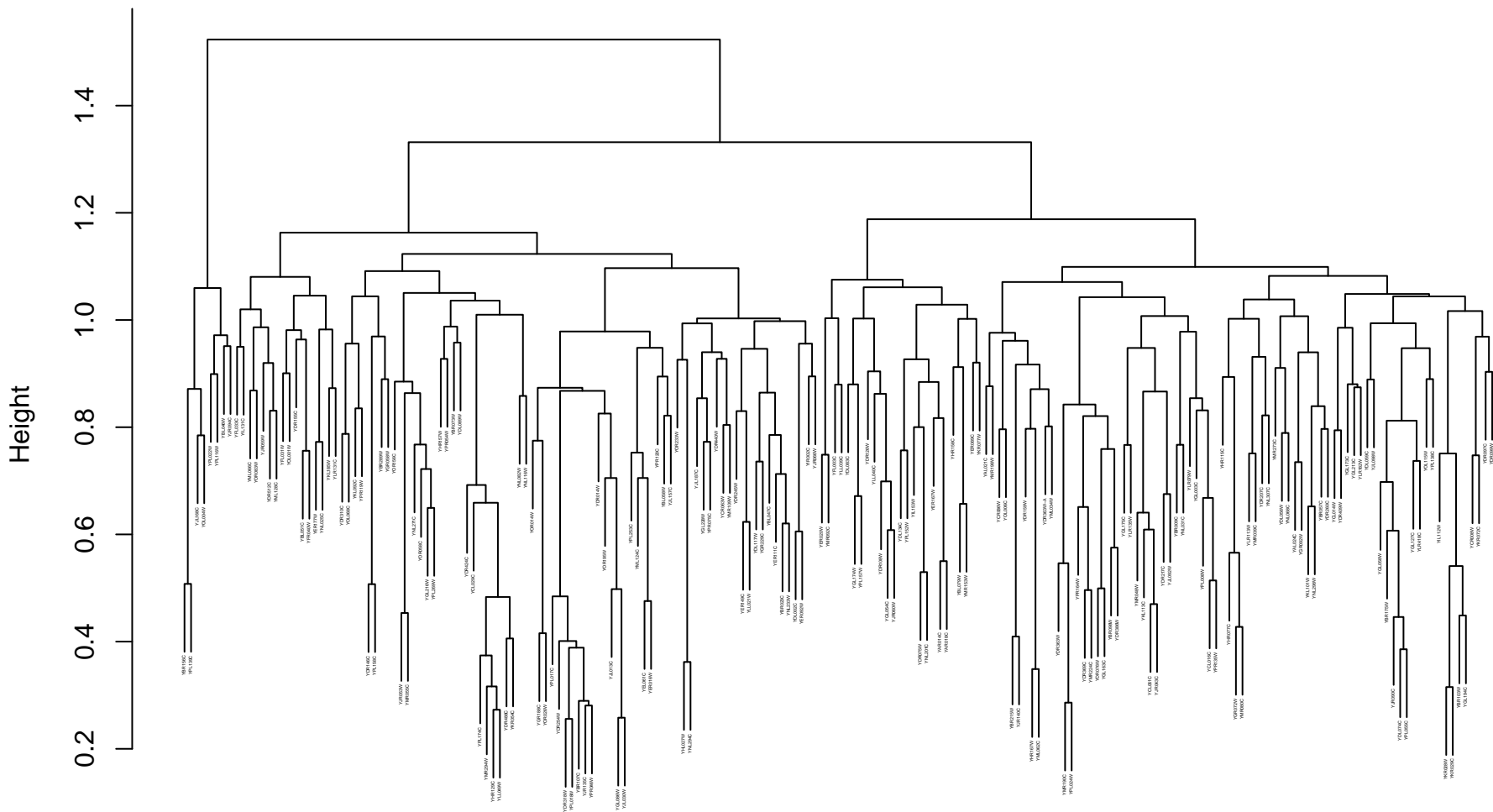
```
dissim
hclust (*, "complete")
```



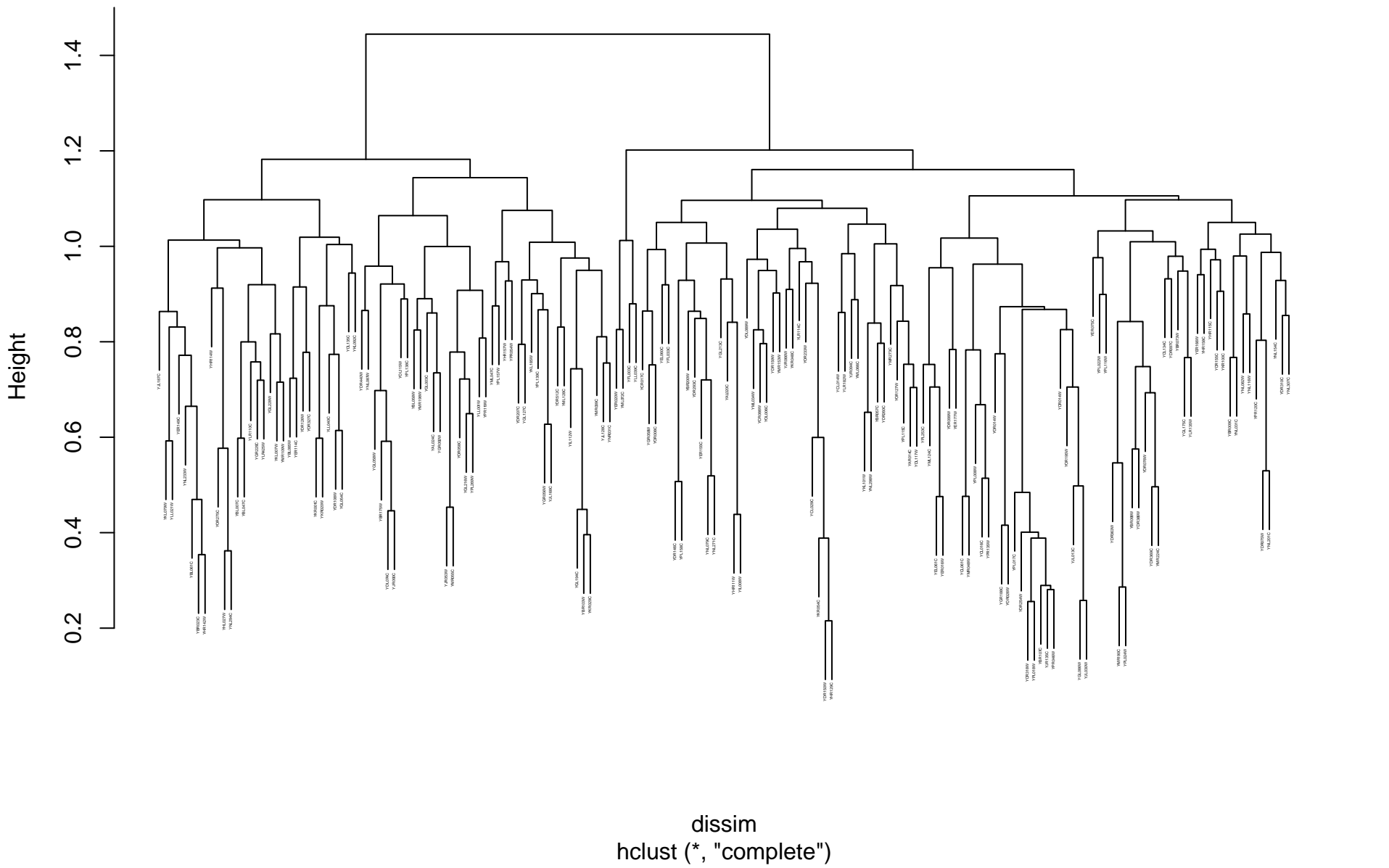
cytoskeleton_GO_correlation_complete



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



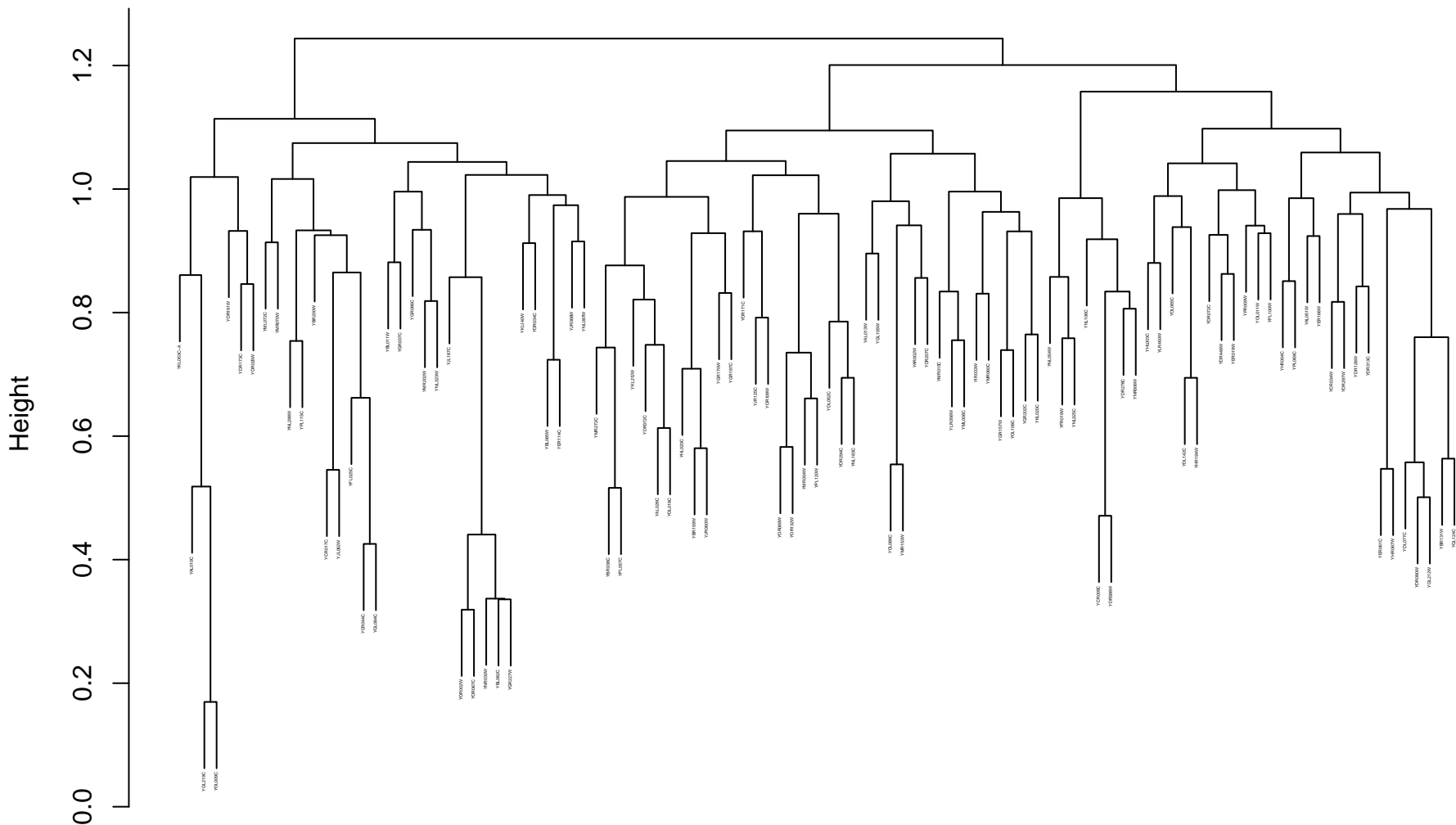
budding_GO_correlation_complete



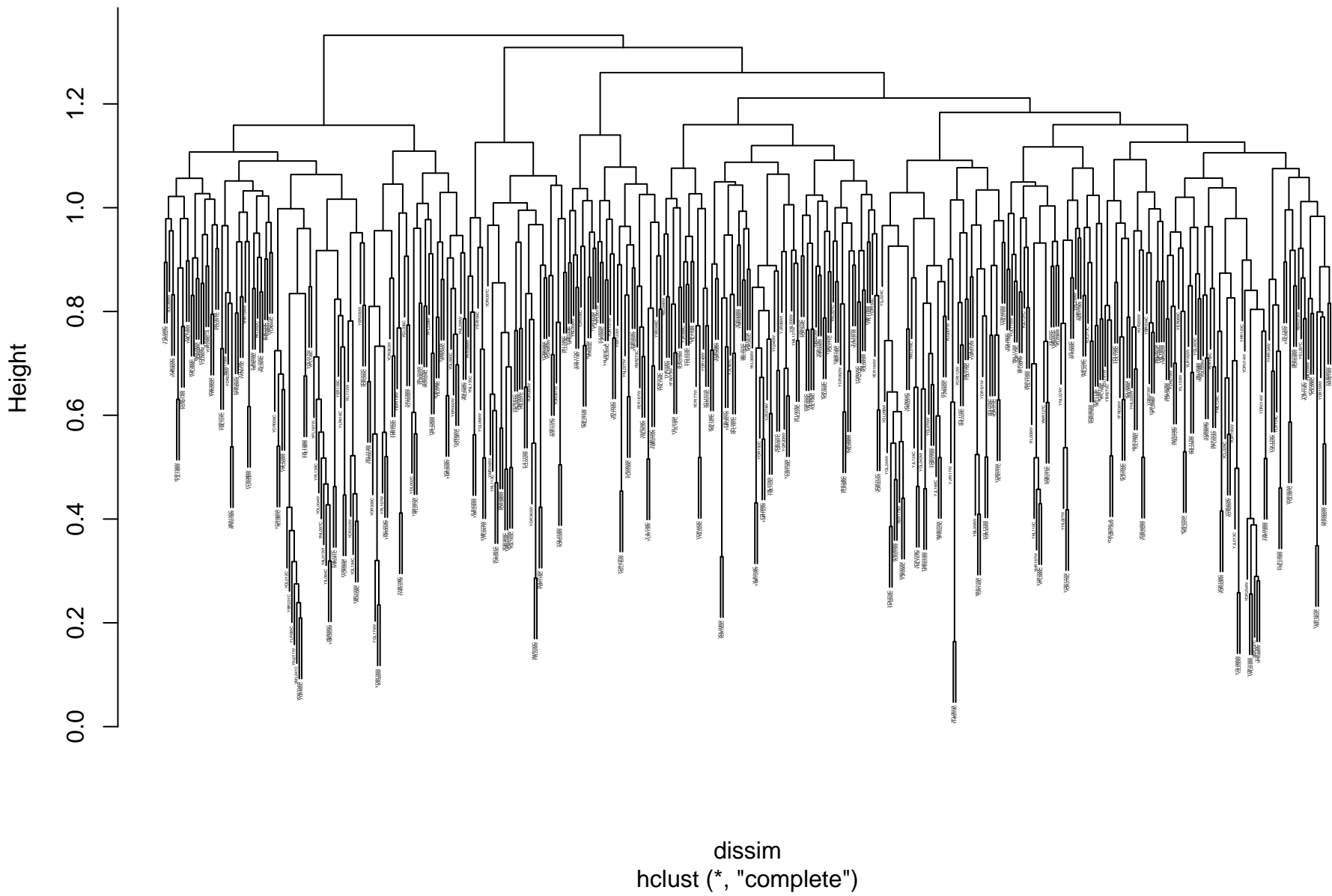

```

dissim
hclust (*, "complete")

```



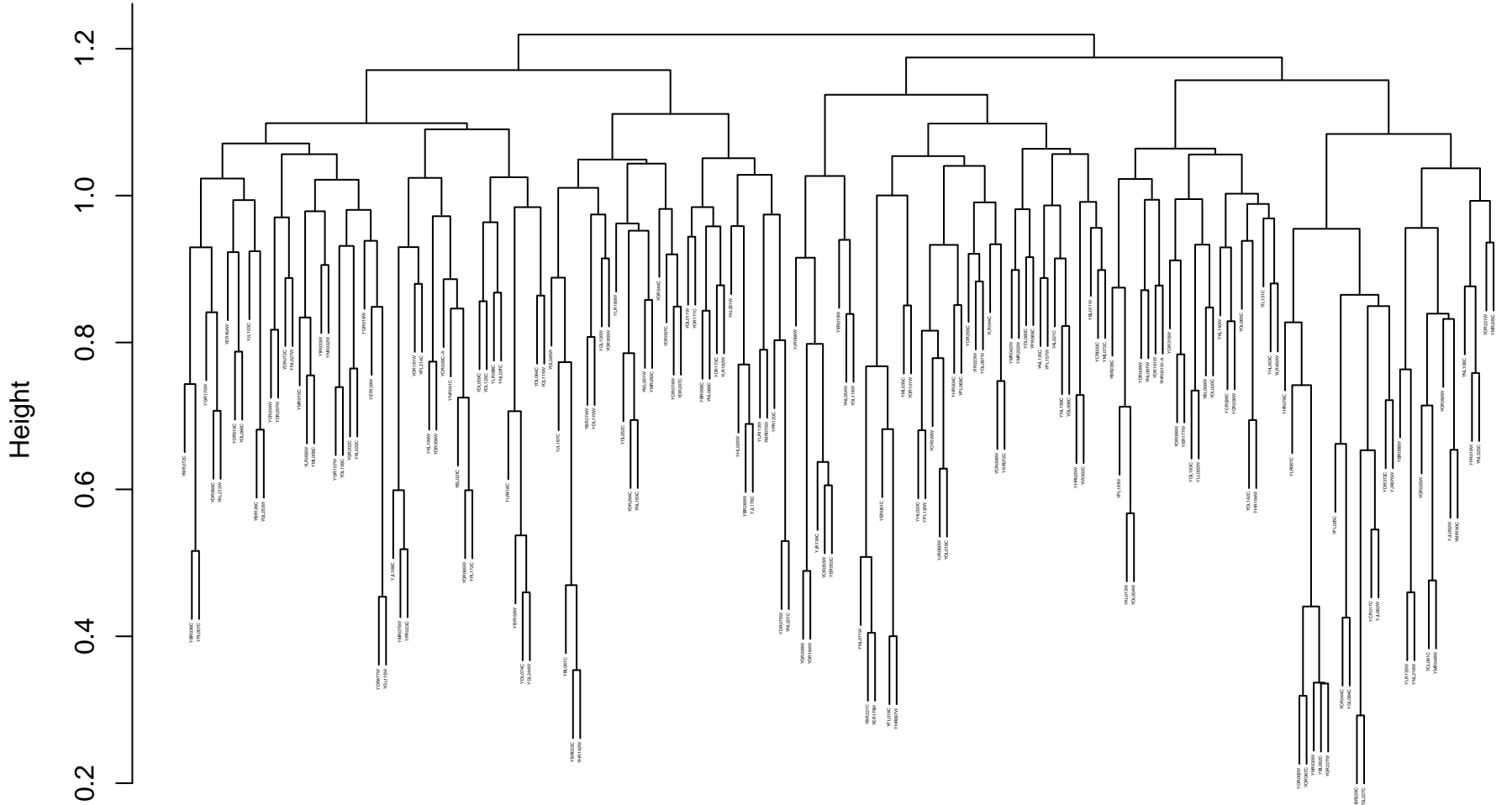
nuclear_transport_GO_correlation_complete



```

dissim
hclust (*, "complete")

```



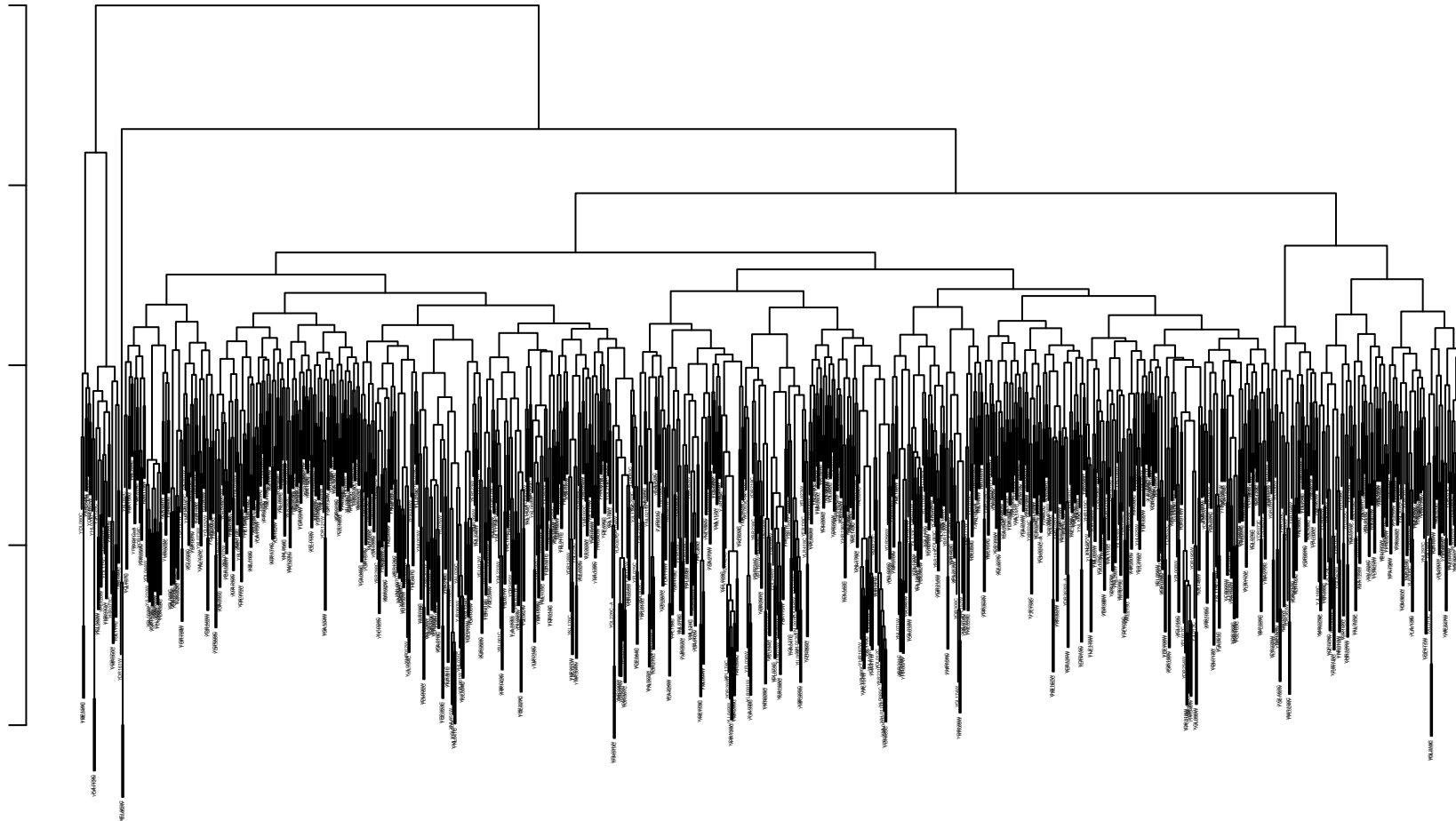
library_correlation_complete

Height

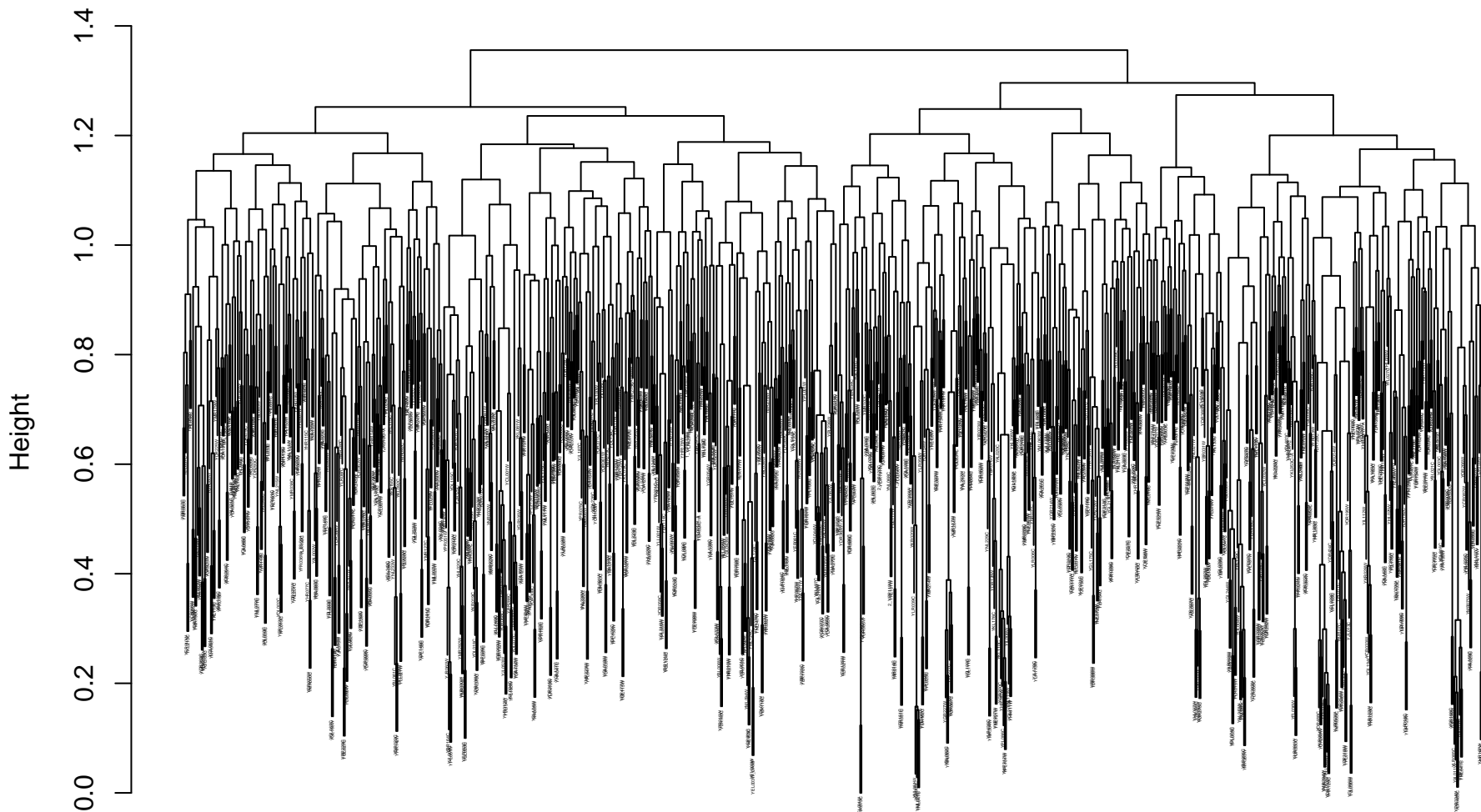
-6.017409e-14

1.000000e+00

2.000000e+00



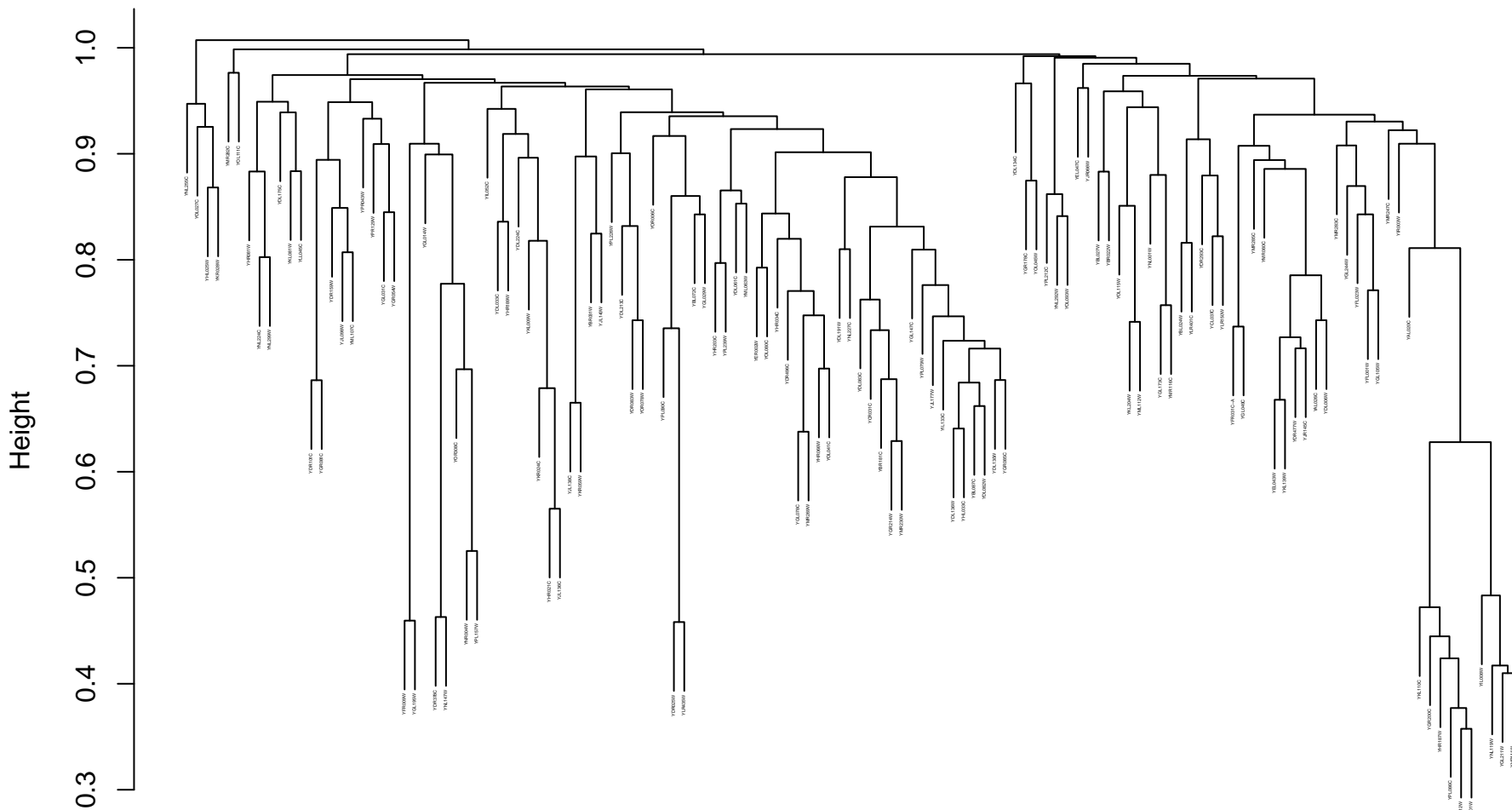
gene_correlation_complete



```

dissim
hclust (*, "average")

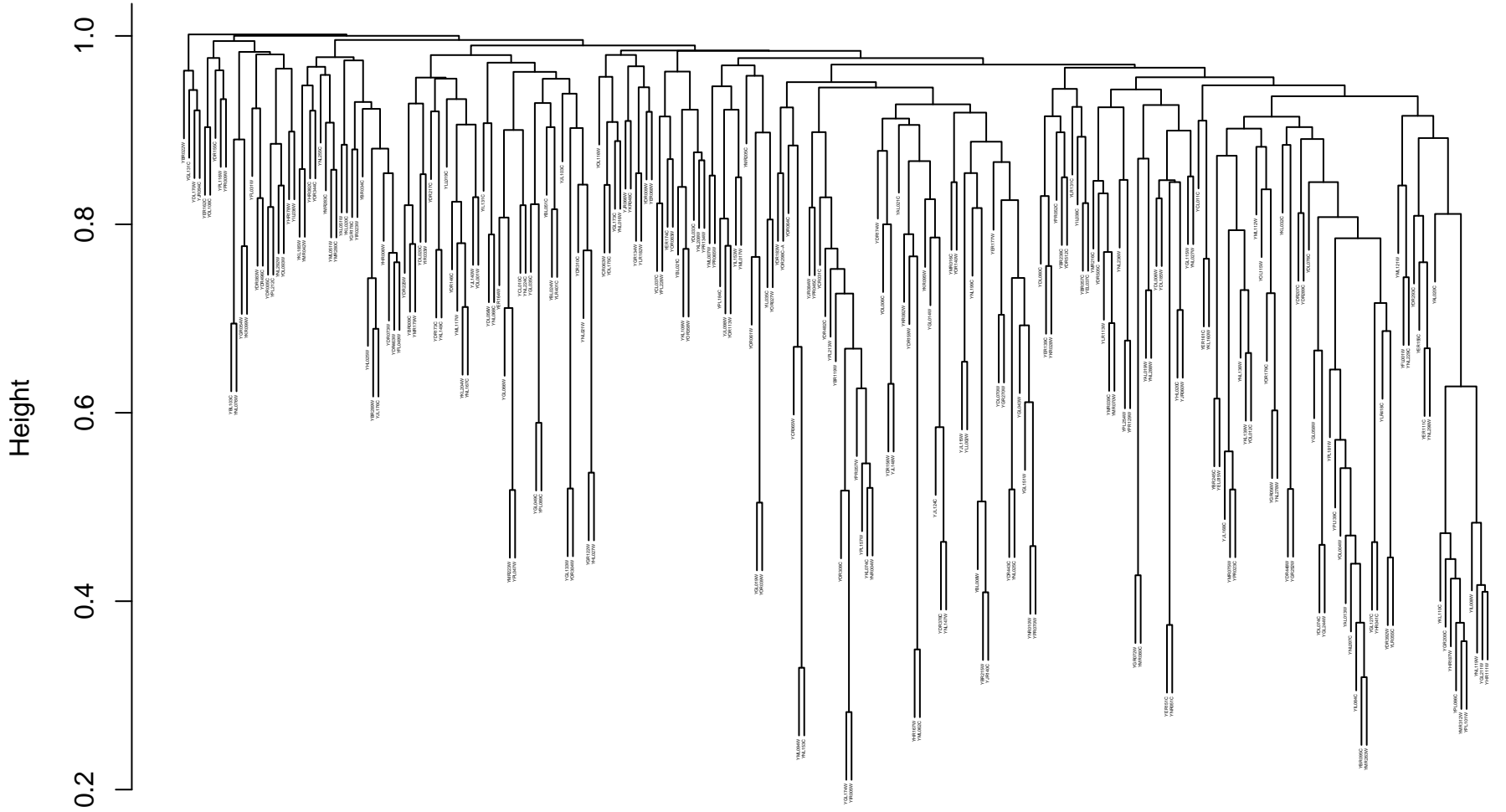
```



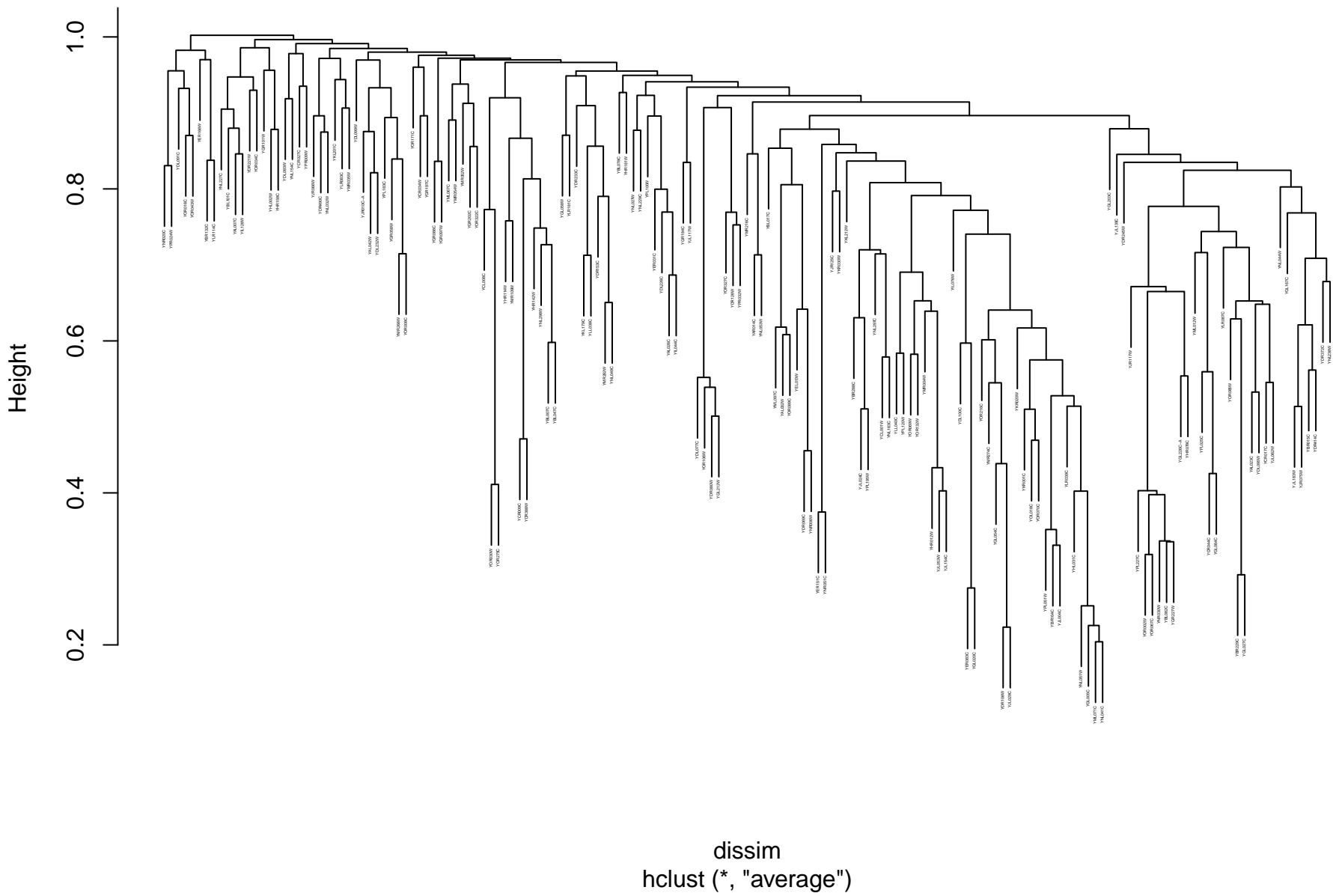
```

dissim
hclust (*, "average")

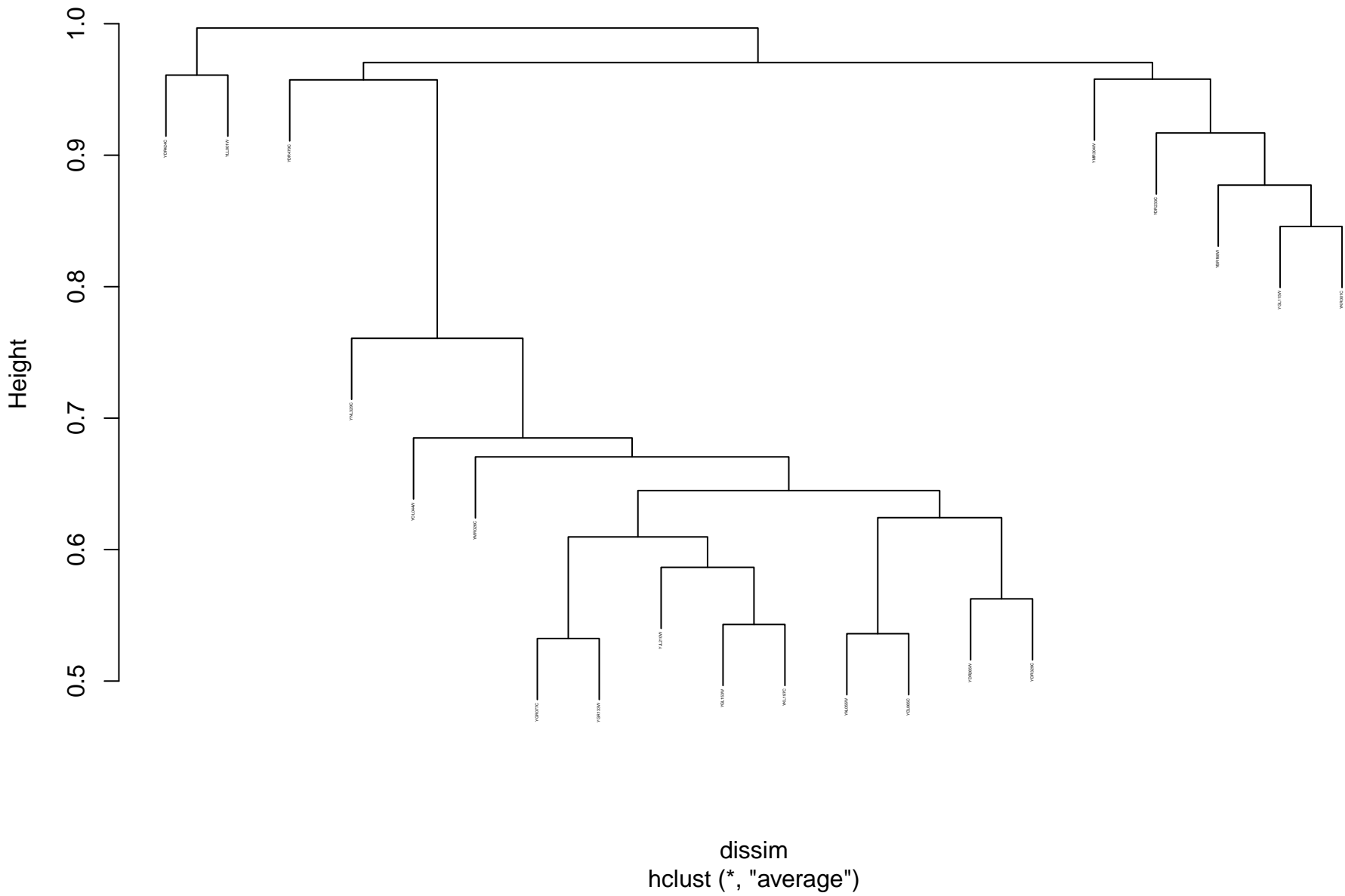
```



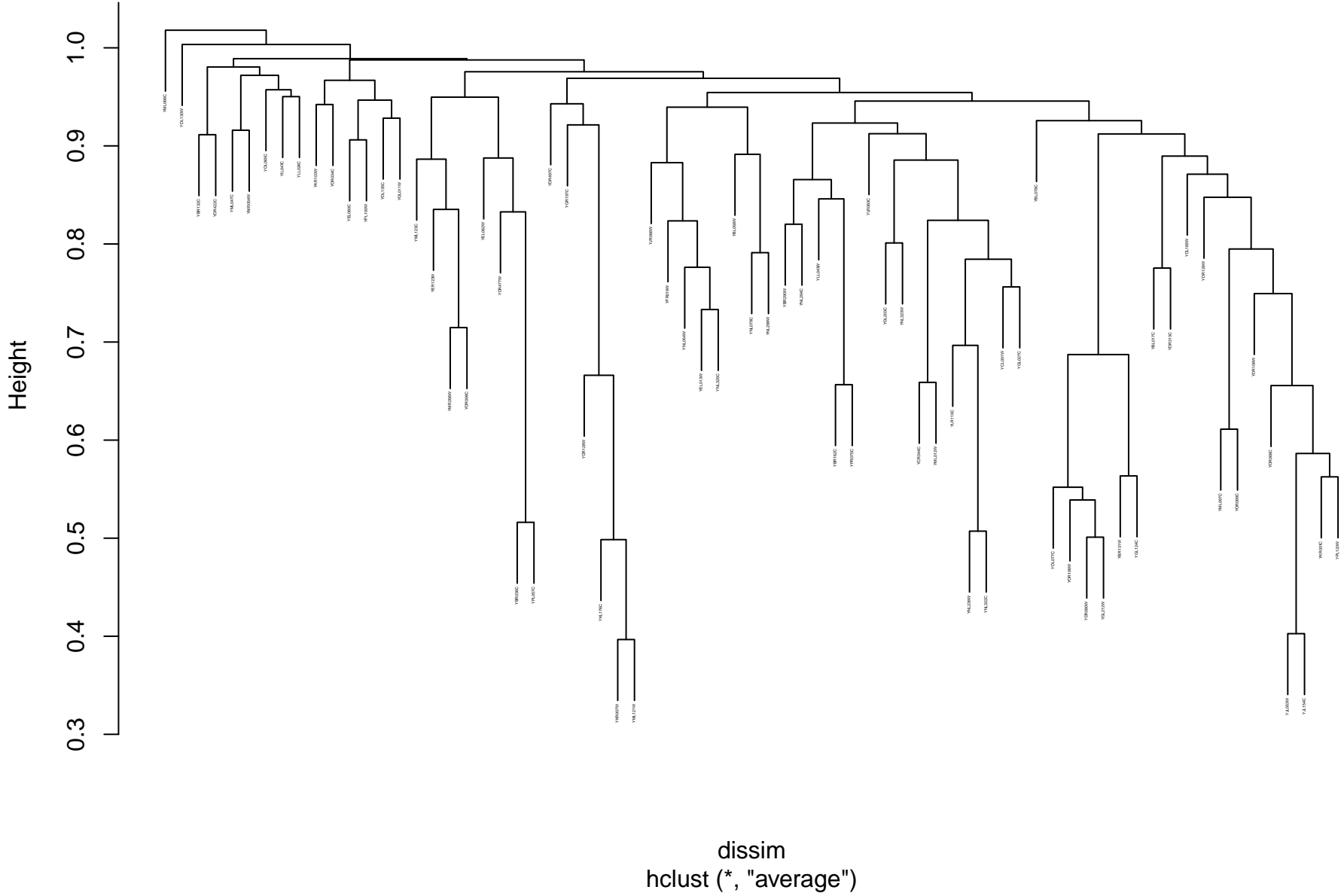
Golgi and ER_GO_correlation_average



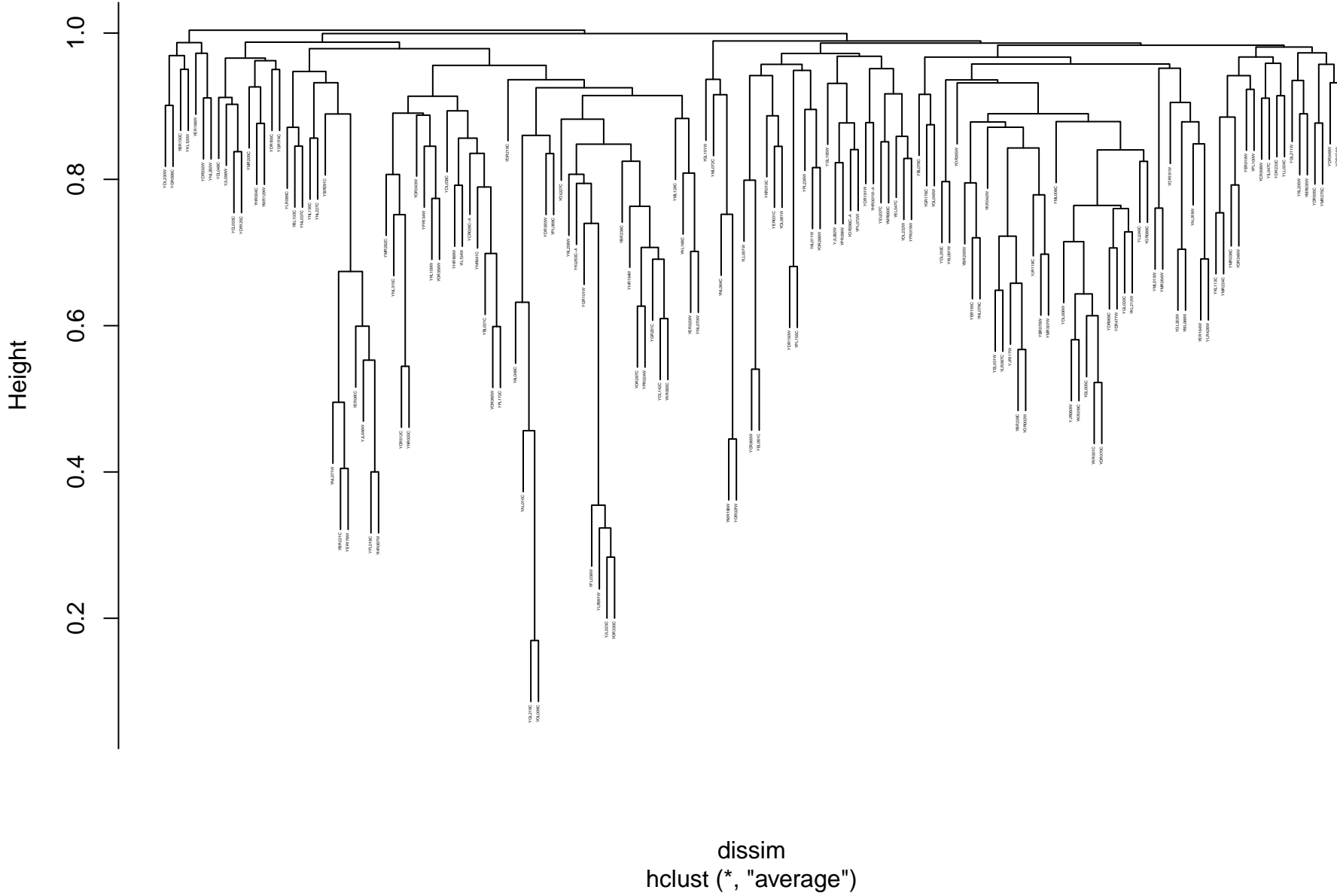
peroxisome_GO_correlation_average



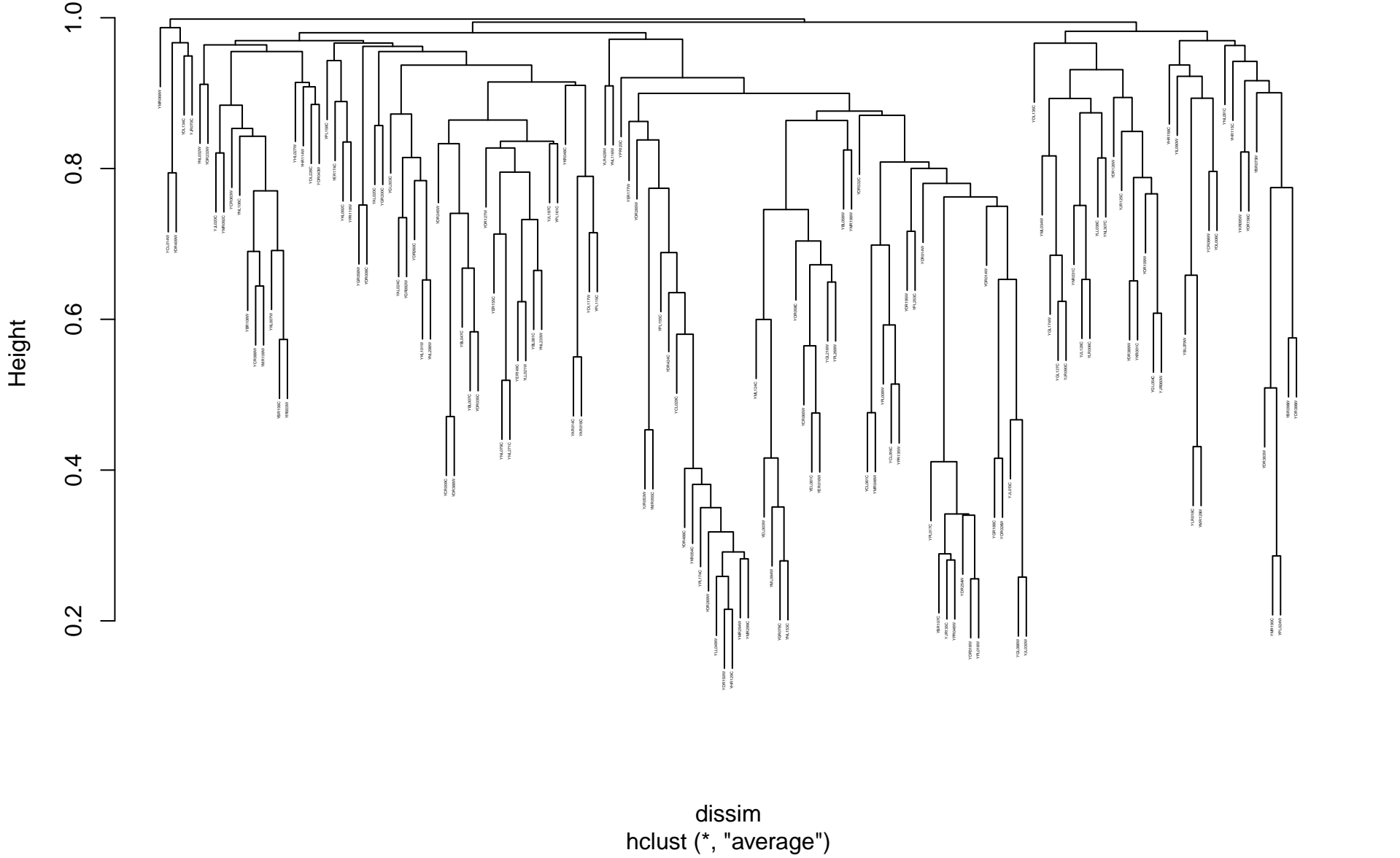
vacuole_GO_correlation_average



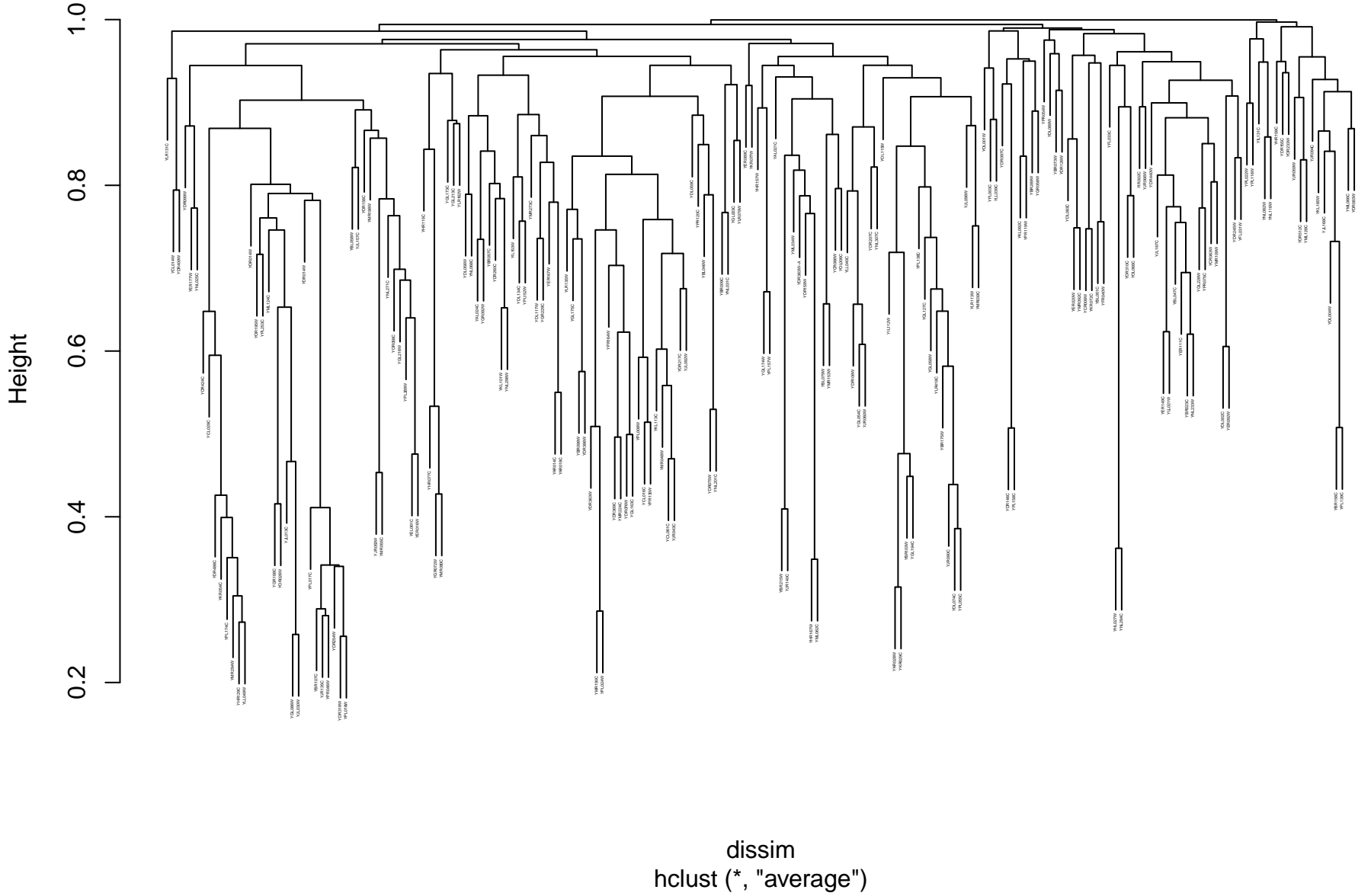
mitochondrion_GO_correlation_average



cytoskeleton_GO_correlation_average



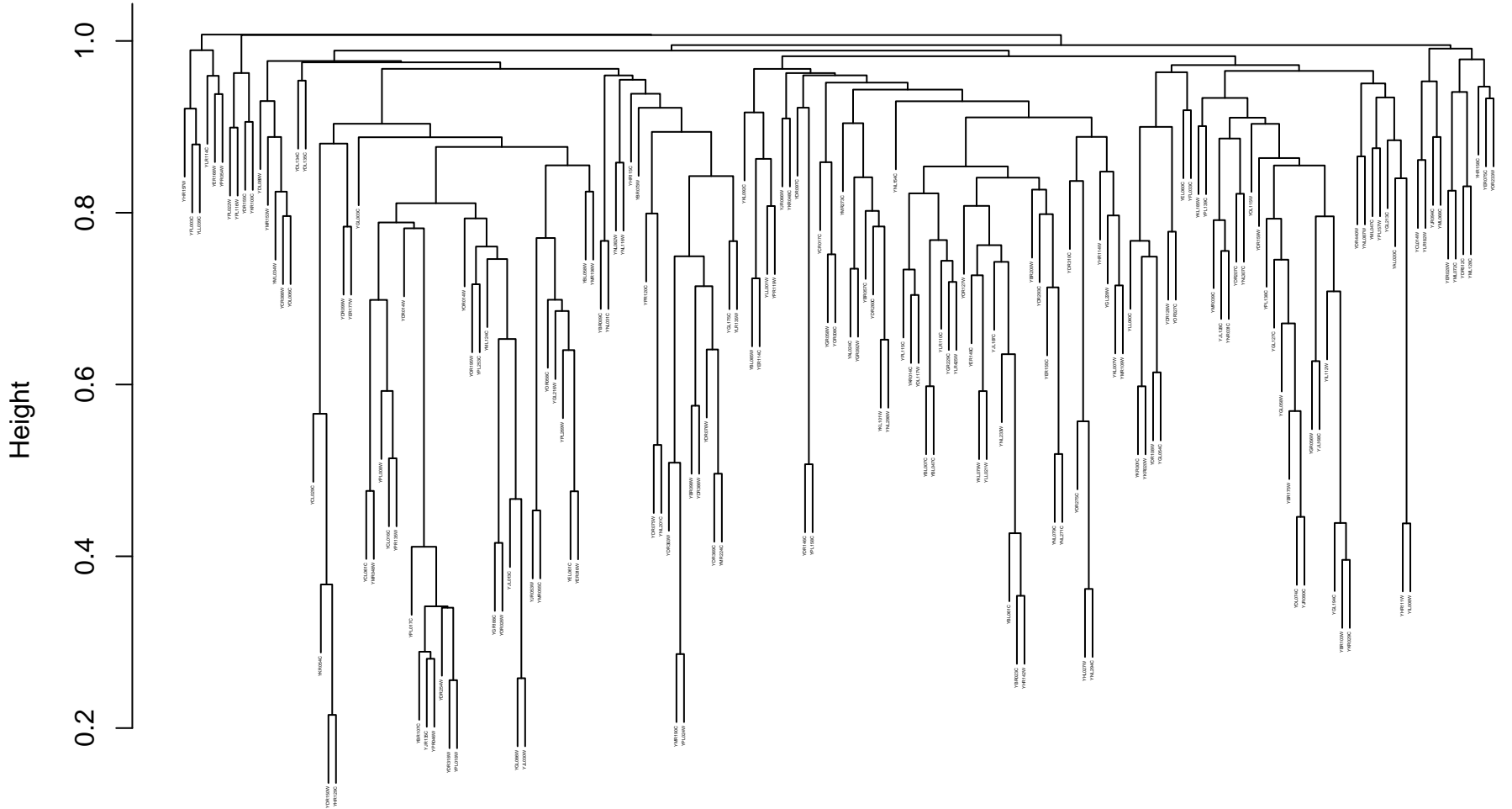
cell cycle_GO_correlation_average



```

dissim
hclust (*, "average")

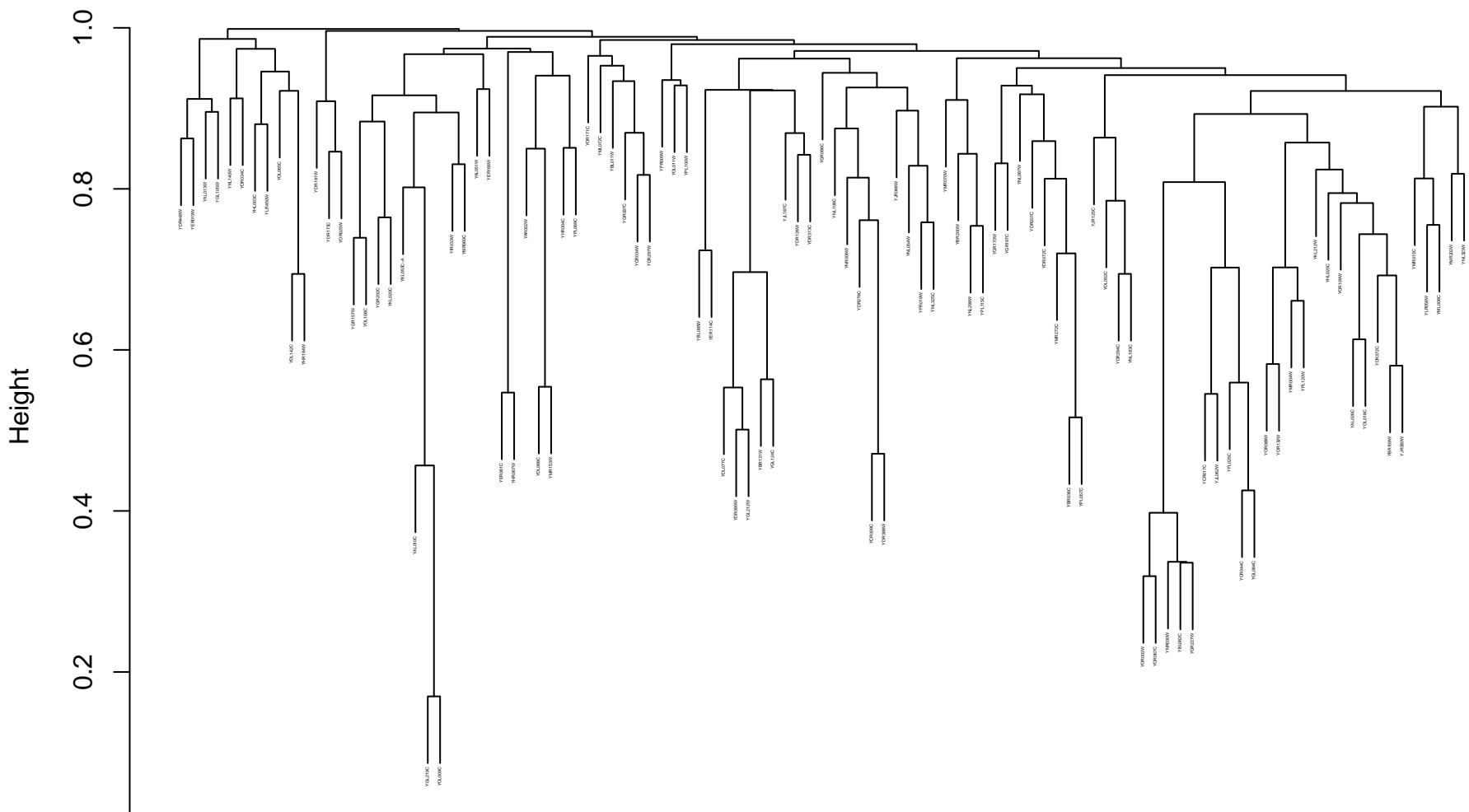
```



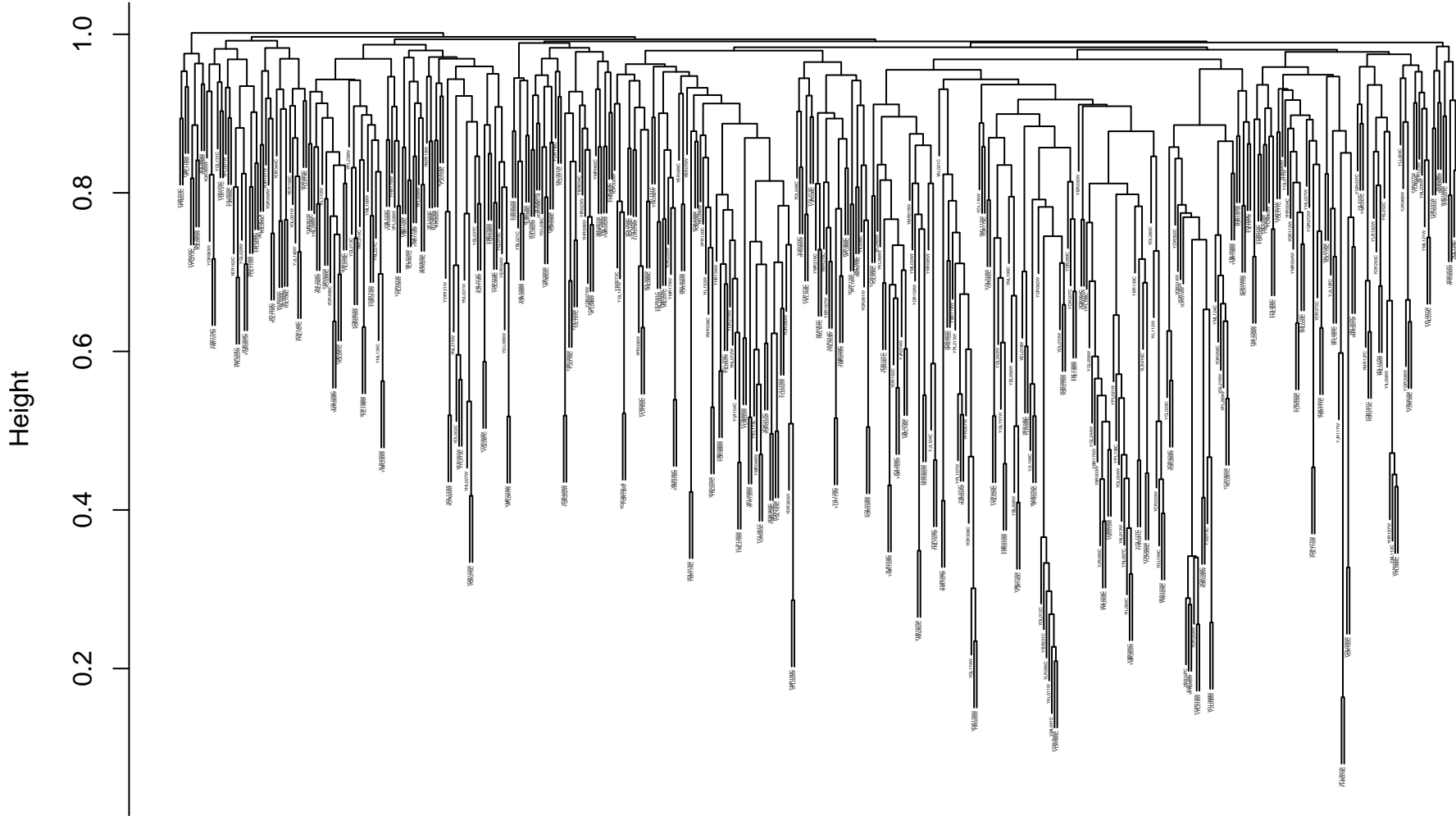
```

dissim
hclust (*, "average")

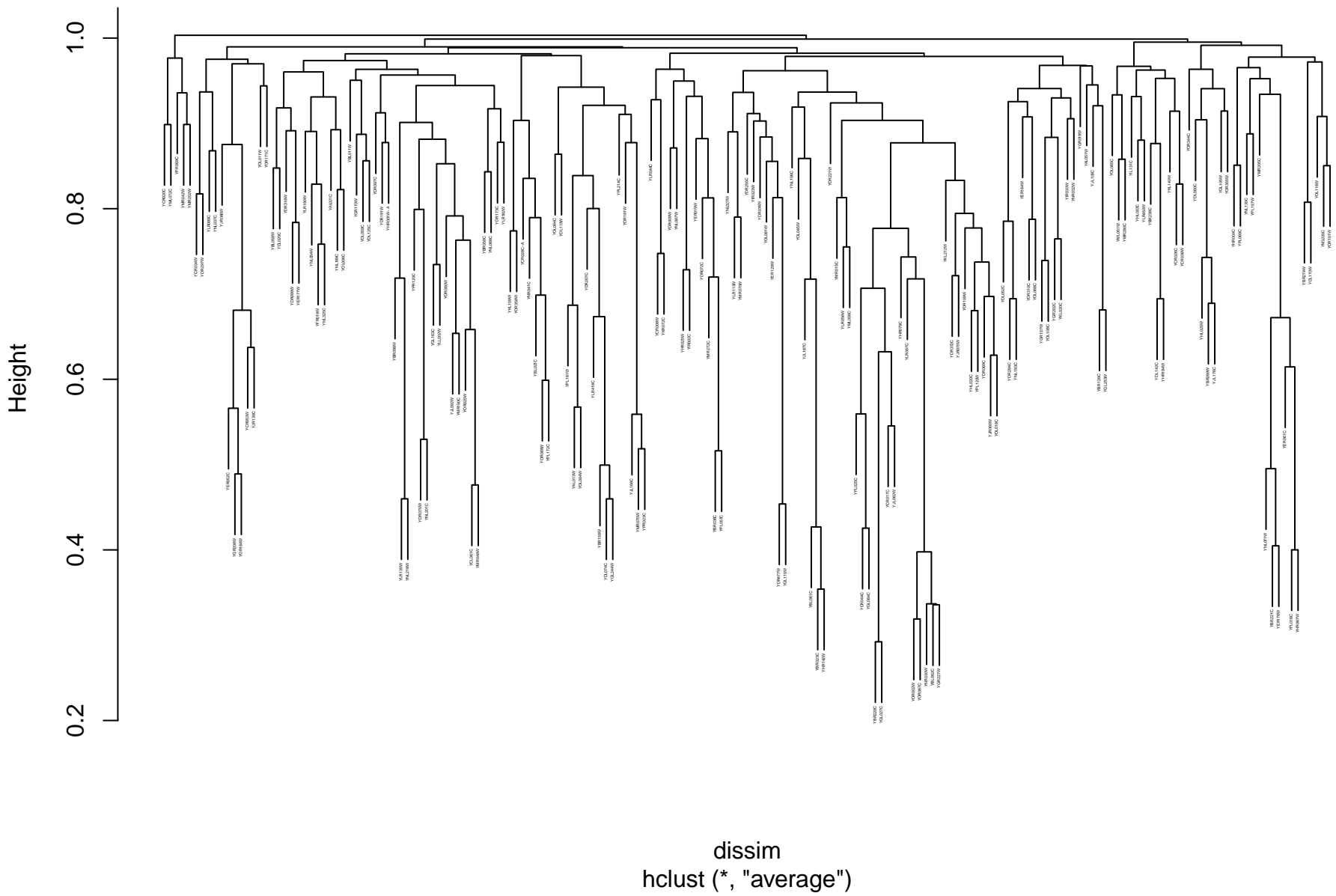
```



nuclear transport_GO_correlation_average



metabolic_GO_correlation_average



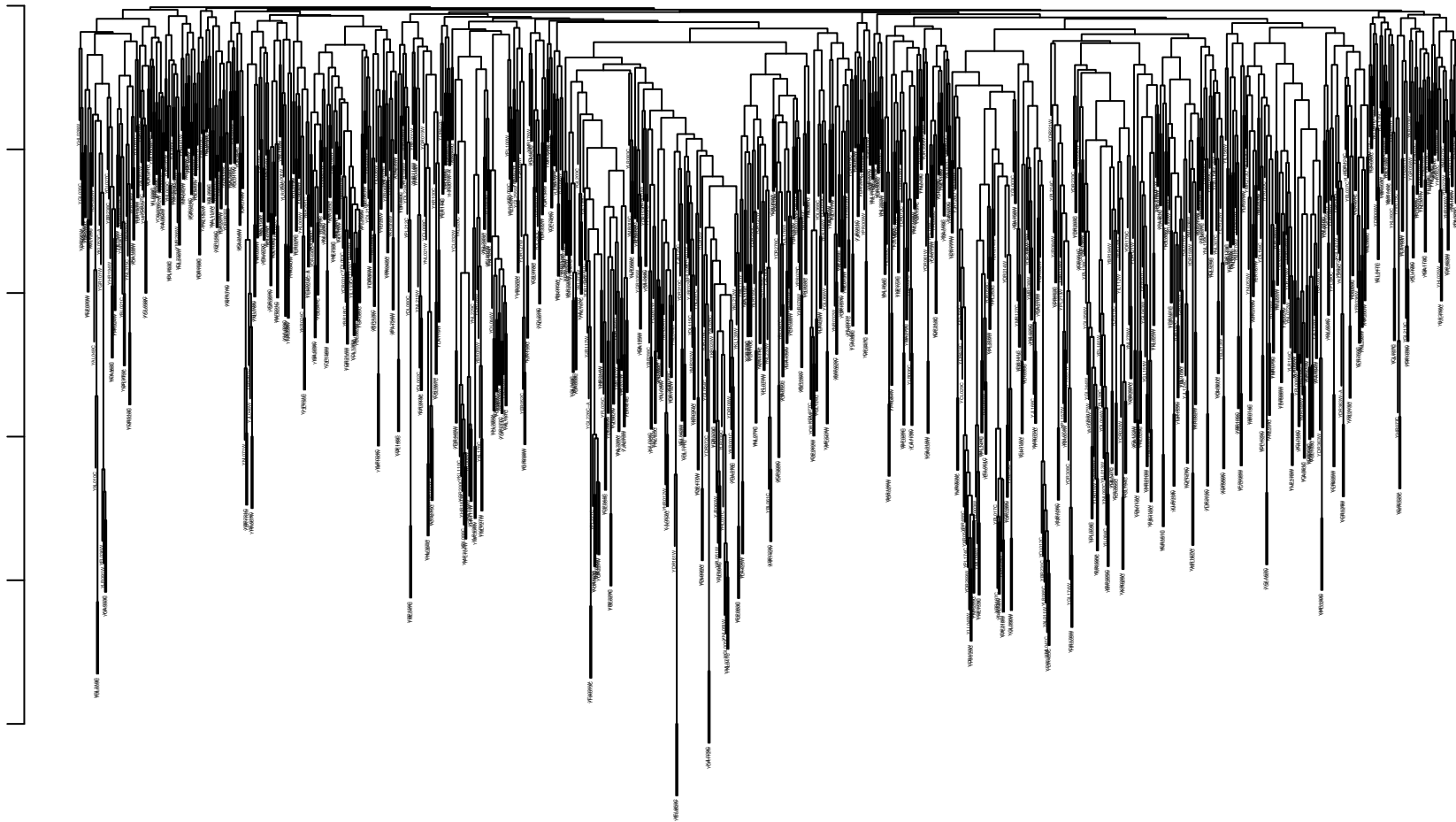
Height

library_correlation_average

8.000000e-01

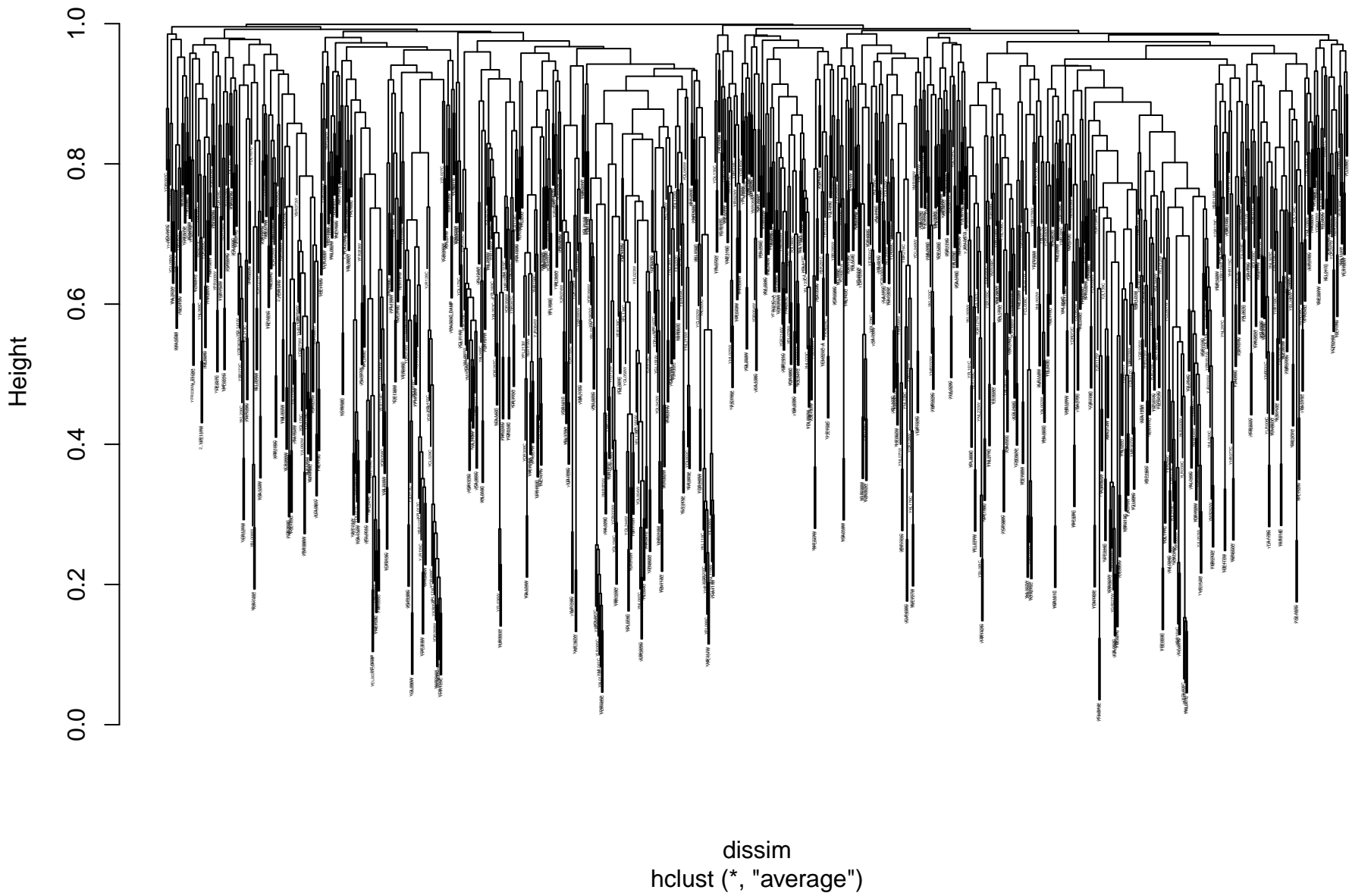
4.000000e-01

-6.017409e-14

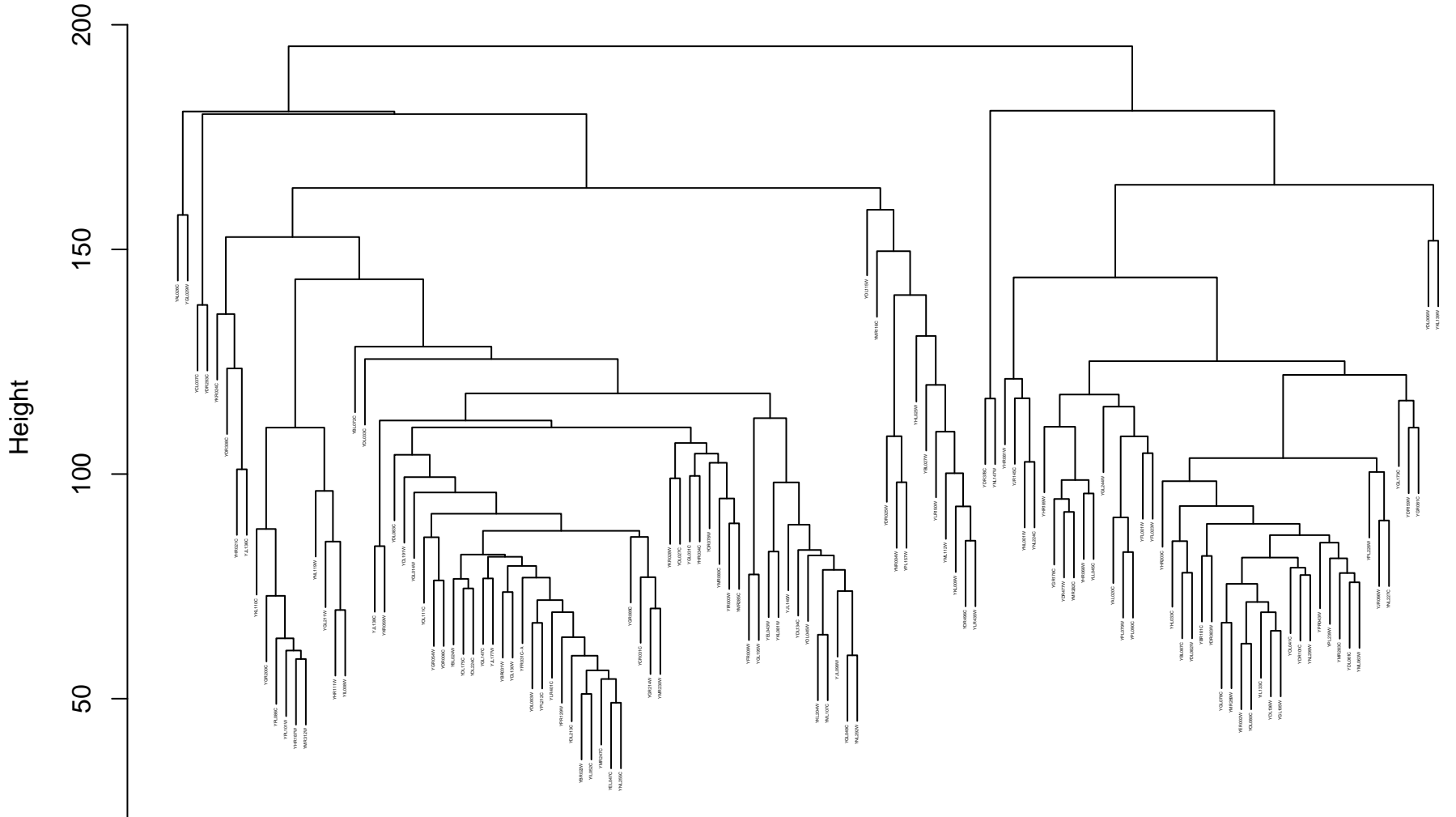


dissim
hclust (*, "average")

gene_correlation_average



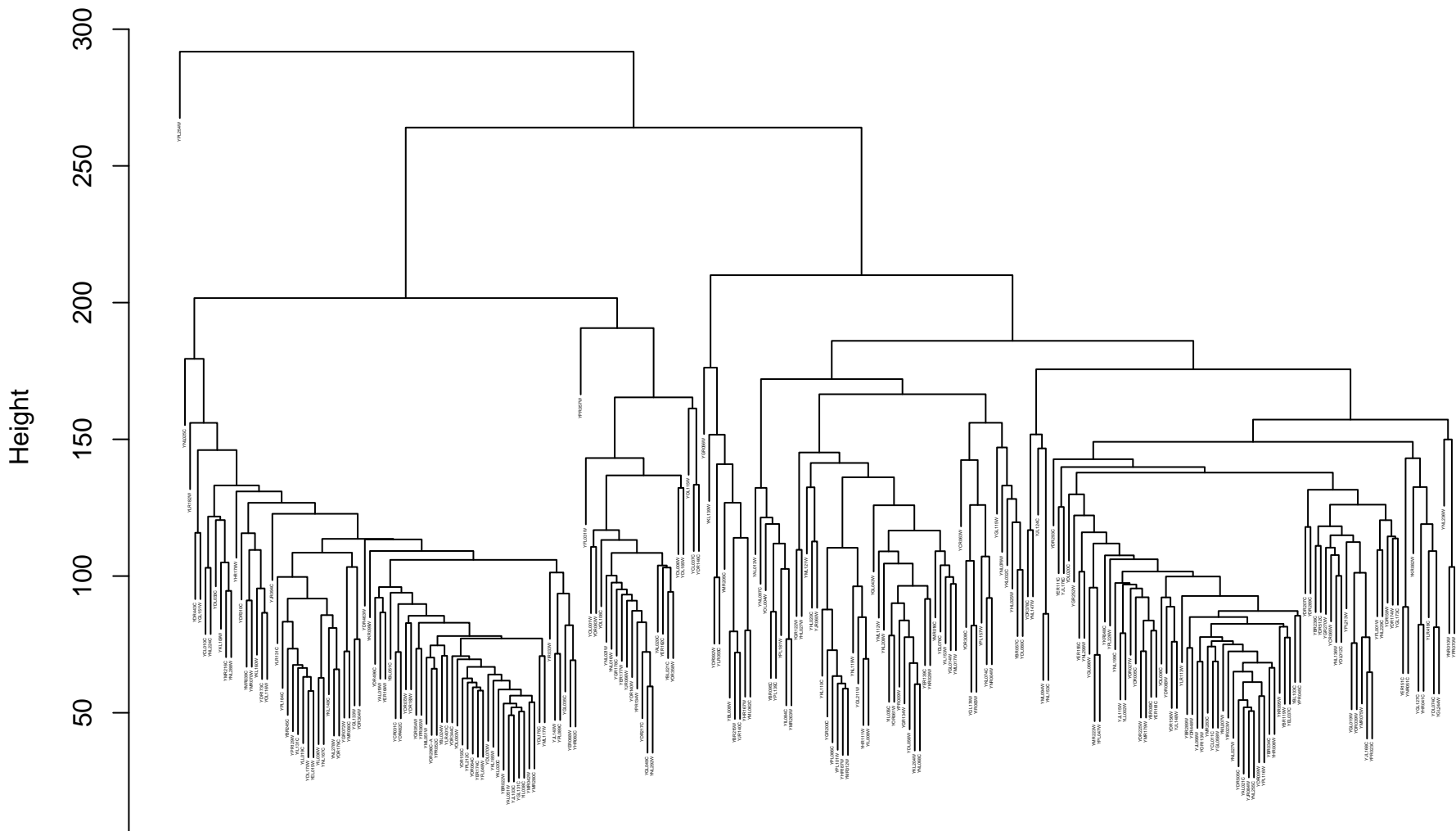
```
dissim
hclust (*, "complete")
```



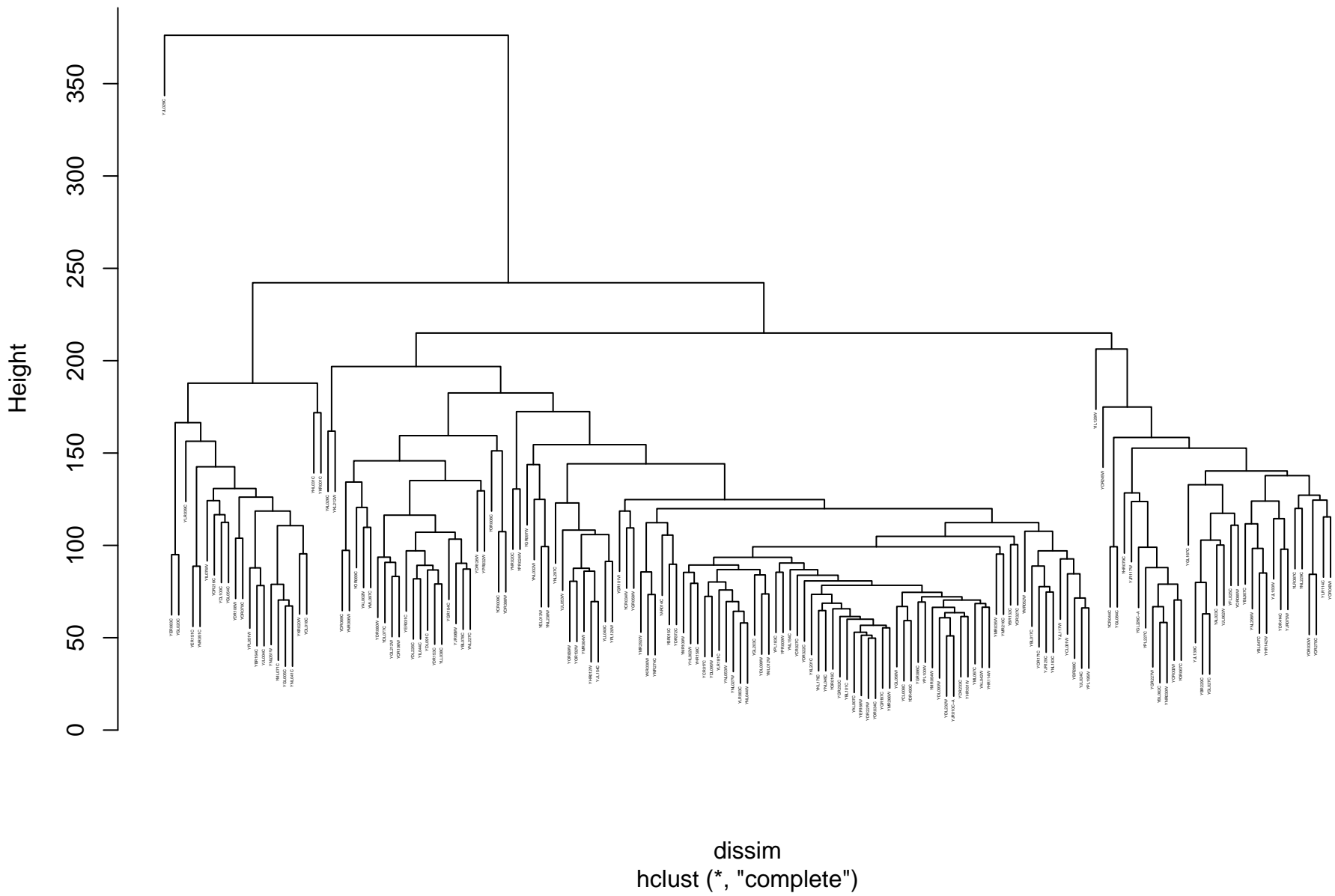
```

dissim
hclust (*, "complete")

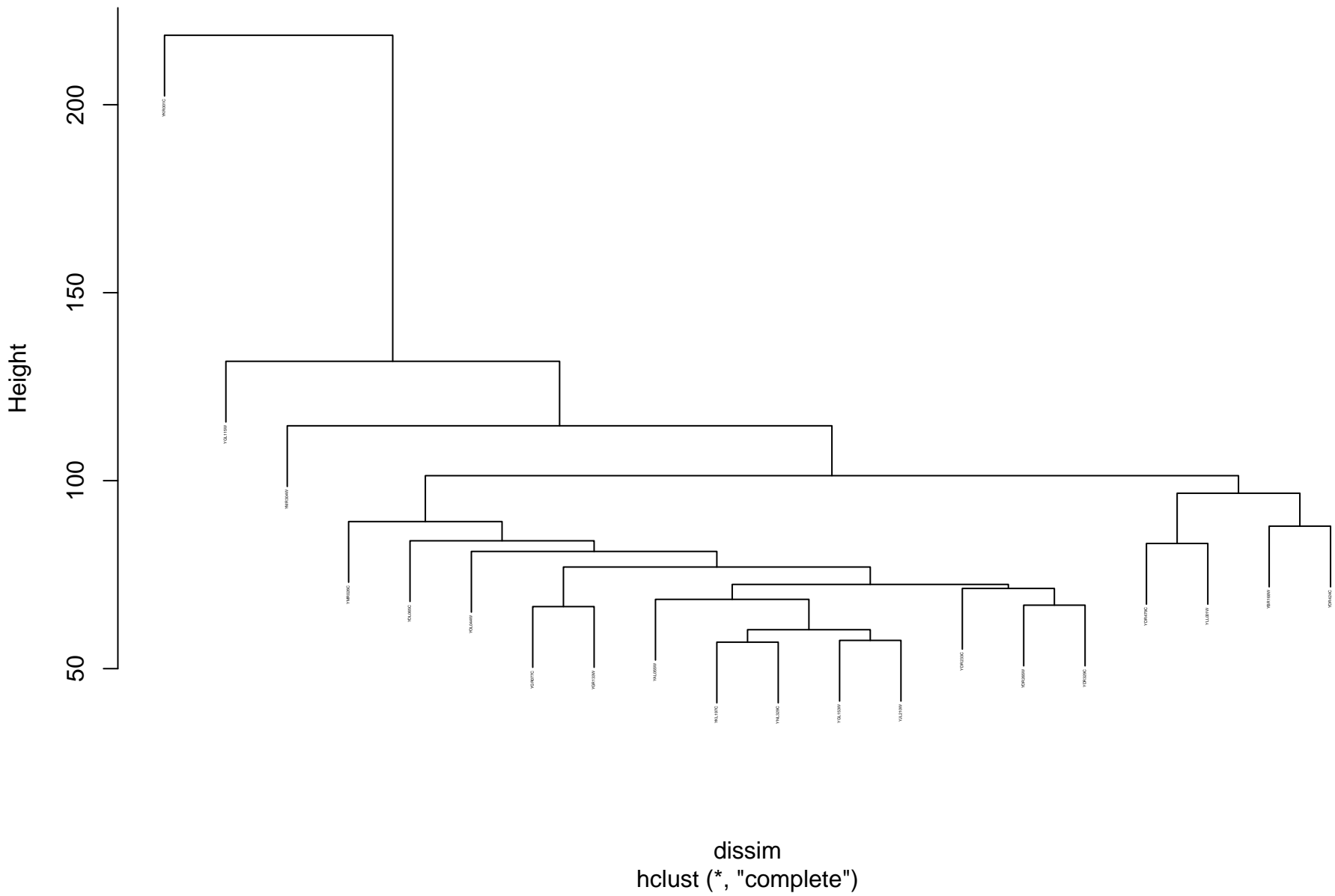
```



Golgi and ER_GO_euclidean_complete



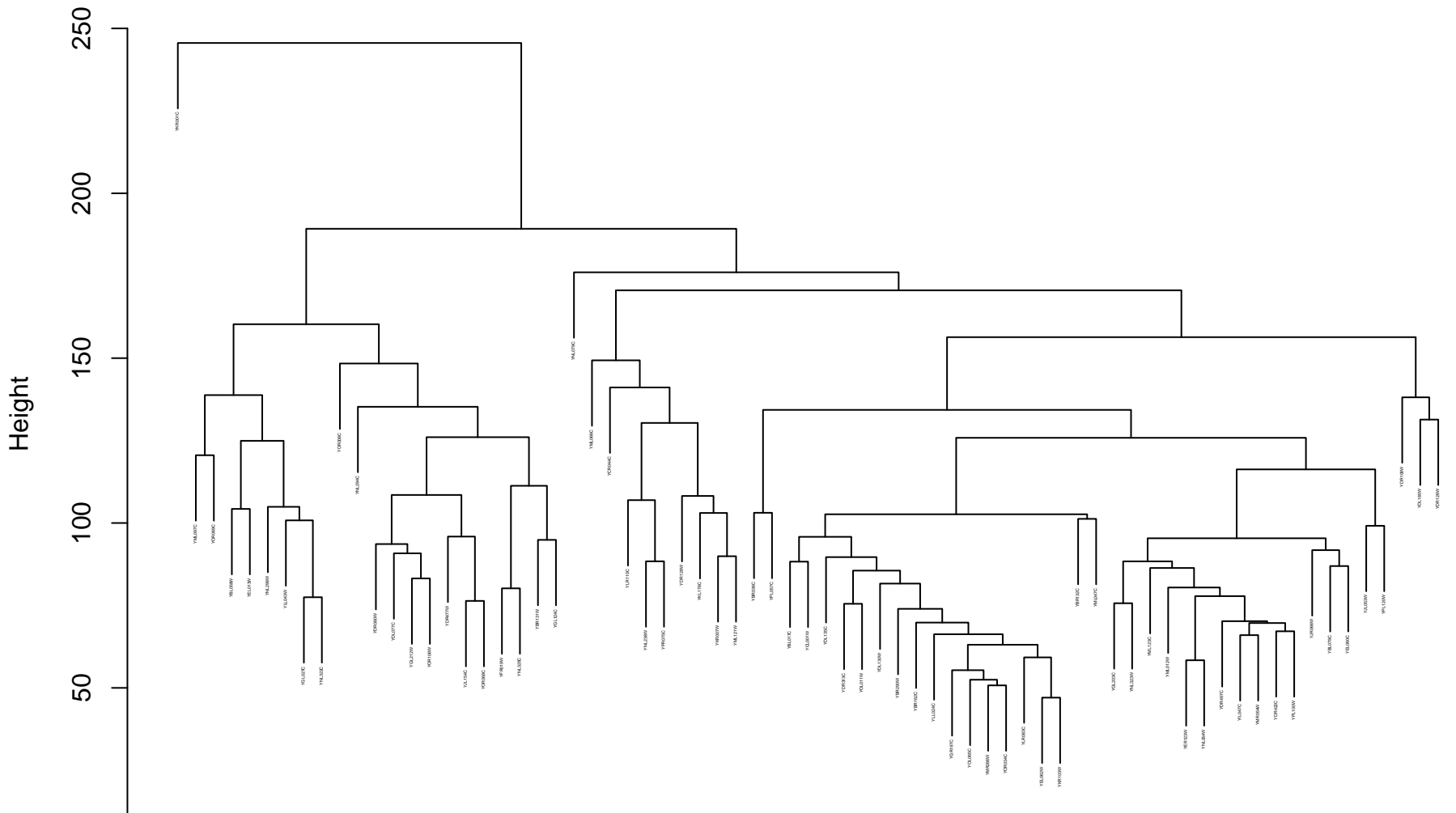
peroxisome_GO_euclidean_complete



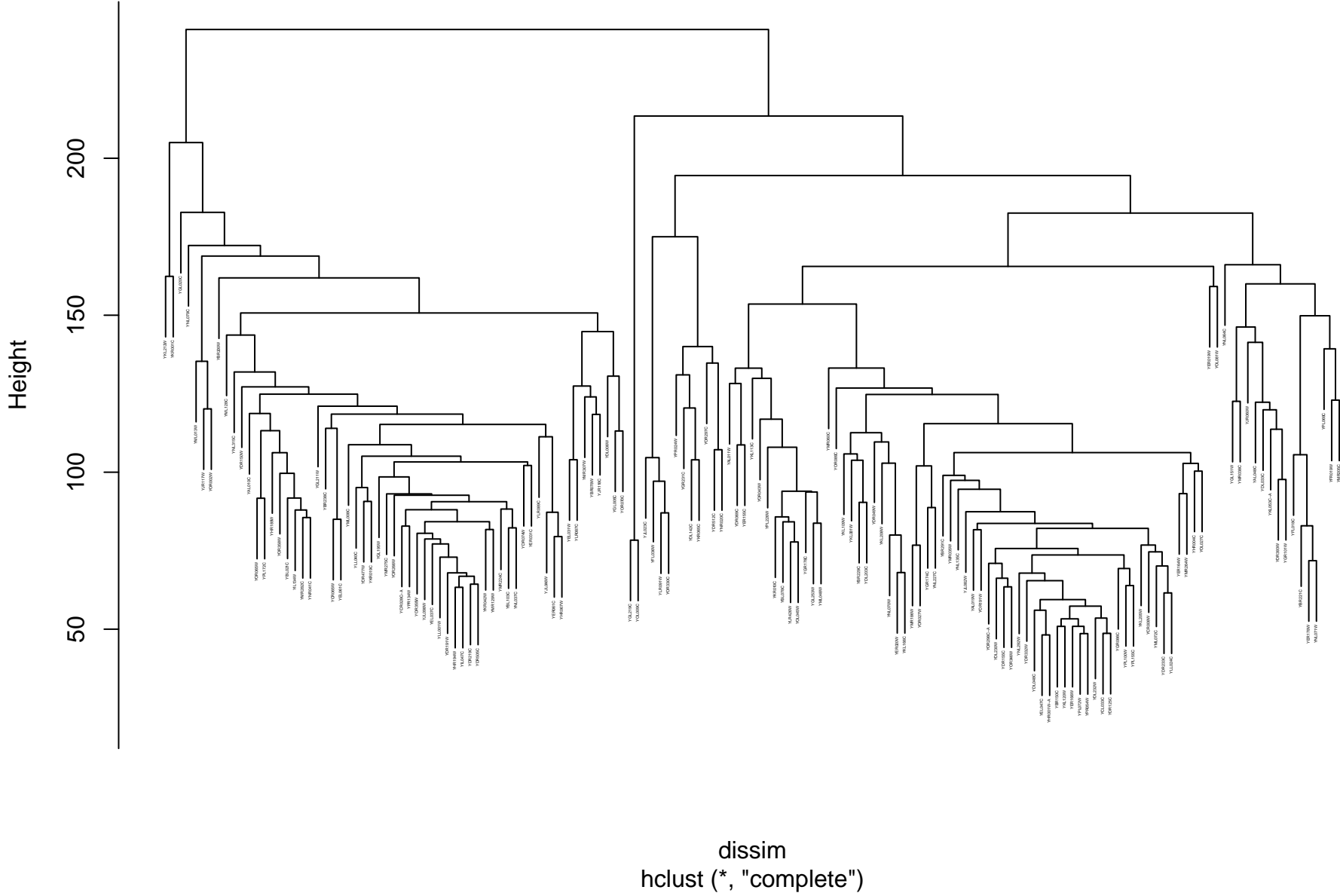

```

dissim
hclust (*, "complete")

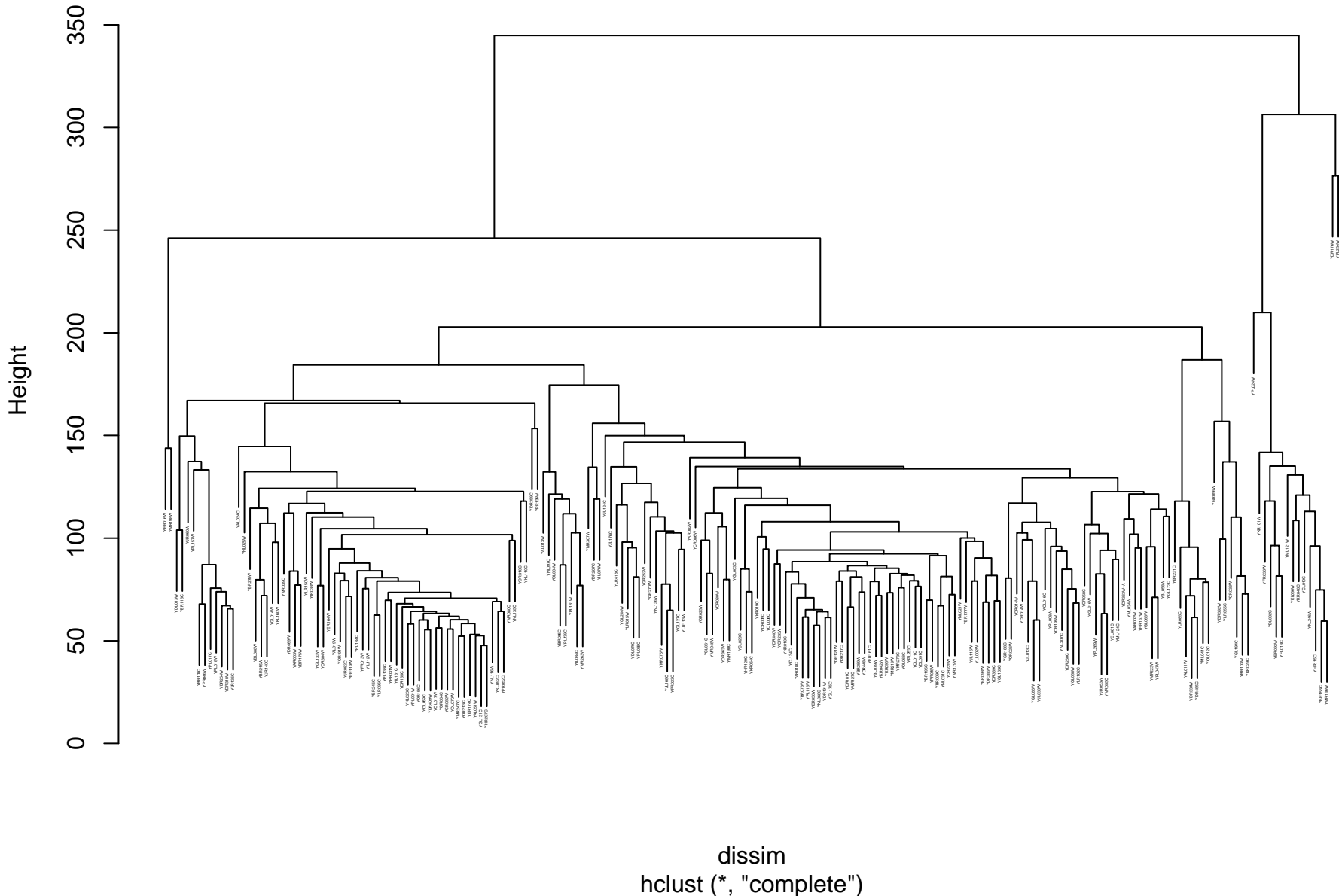
```



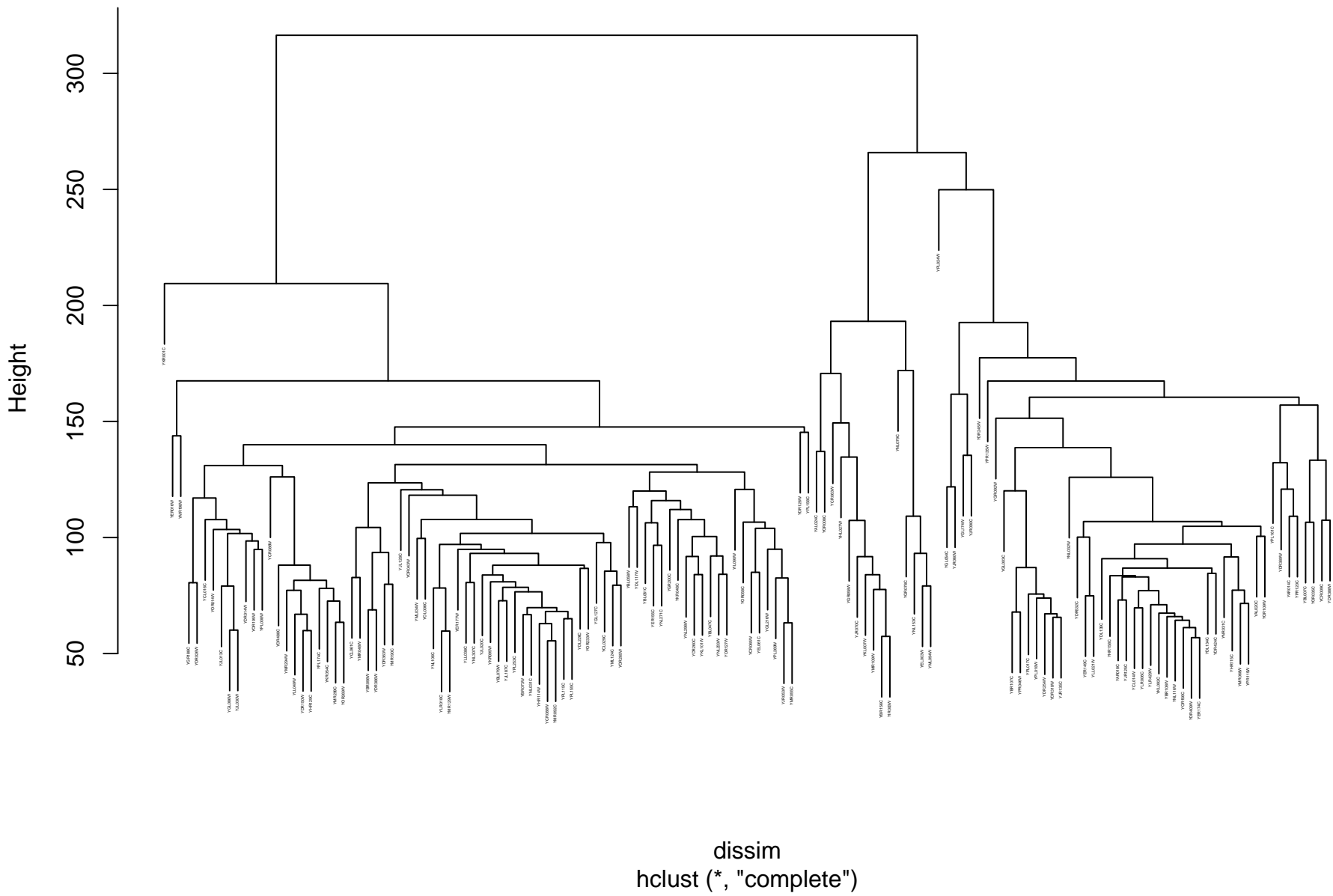
mitochondrion_GO_euclidean_complete



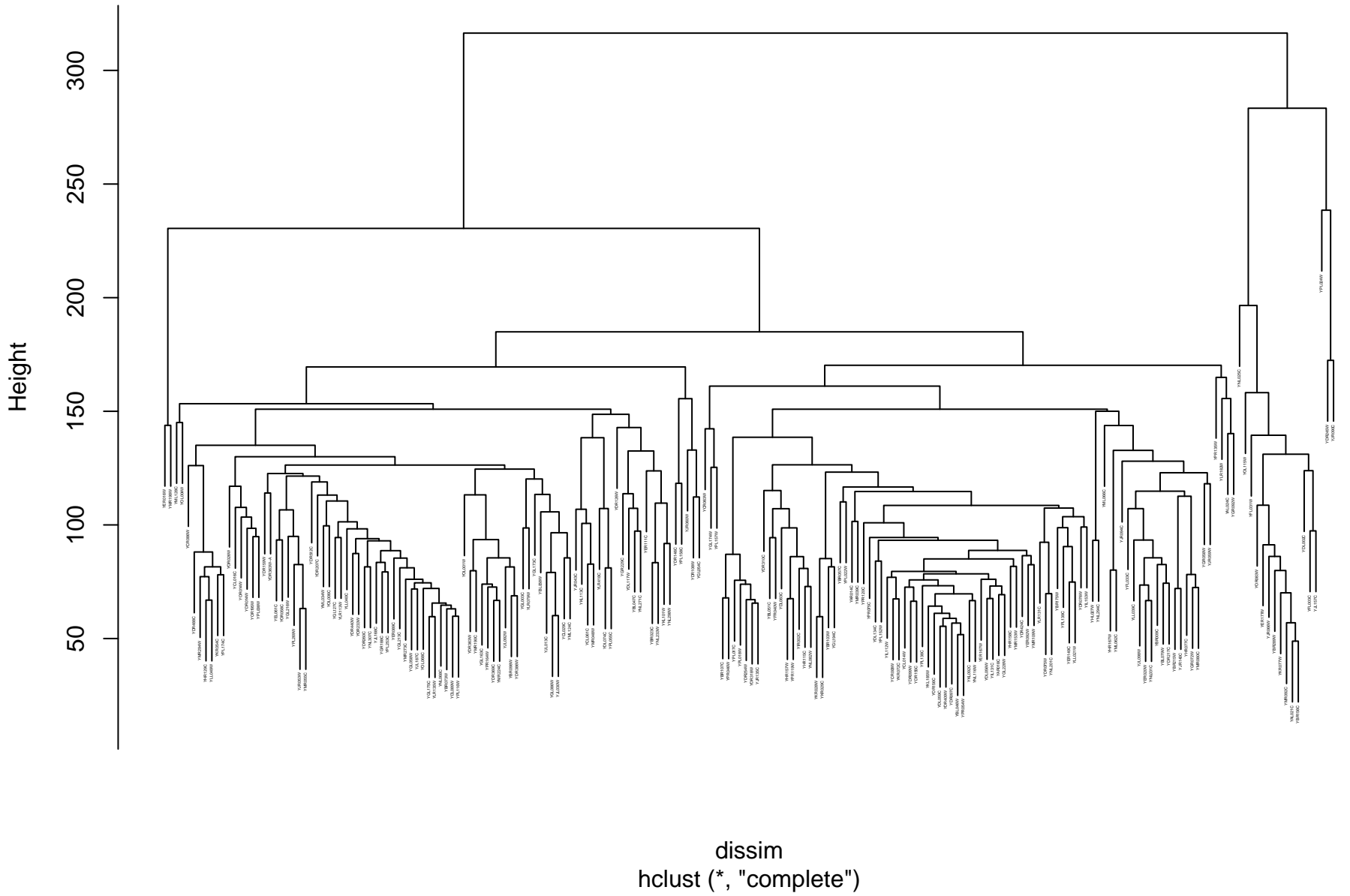
chromatin_GO_euclidean_complete



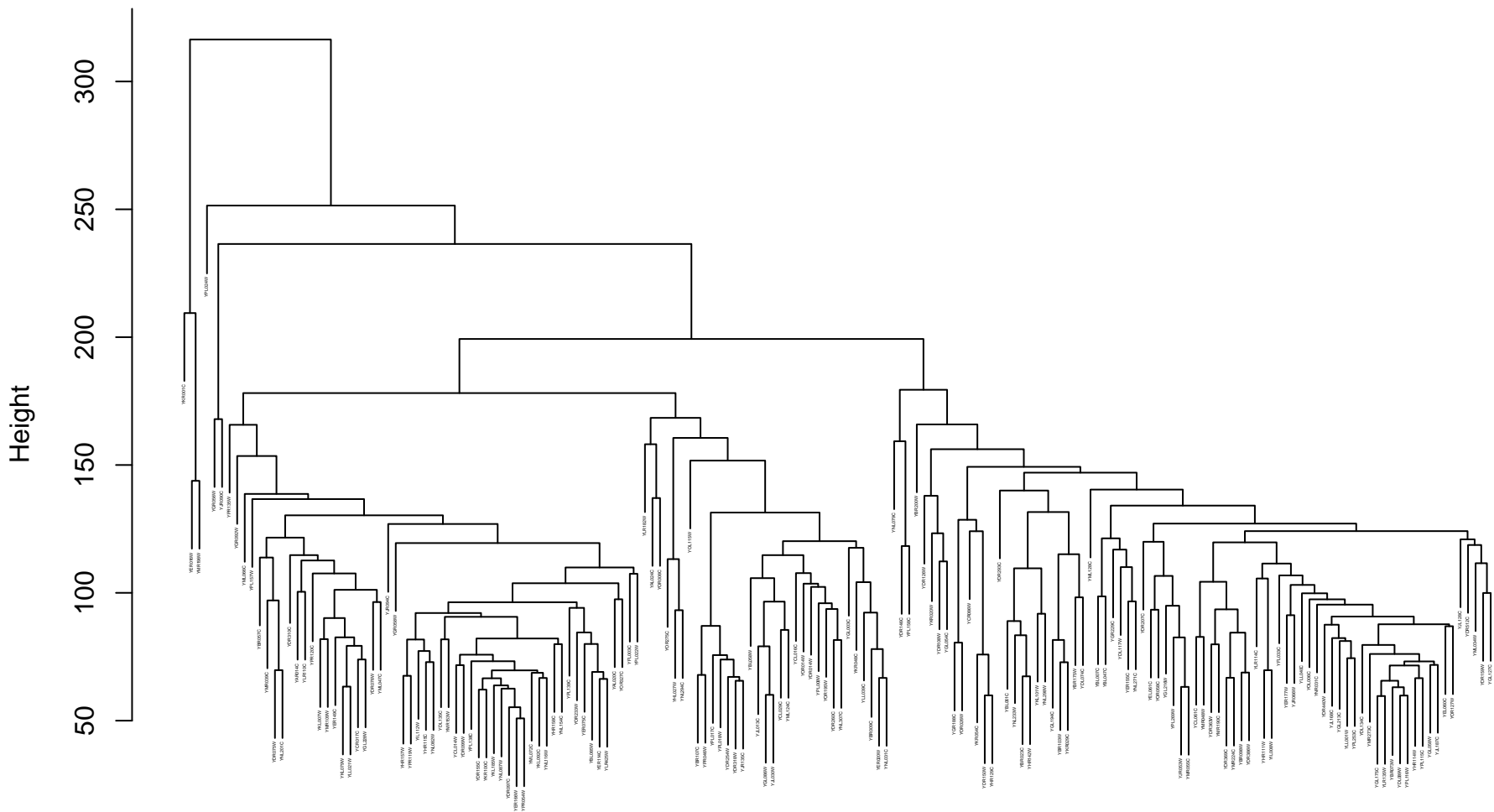
cytoskeleton_GO_euclidean_complete



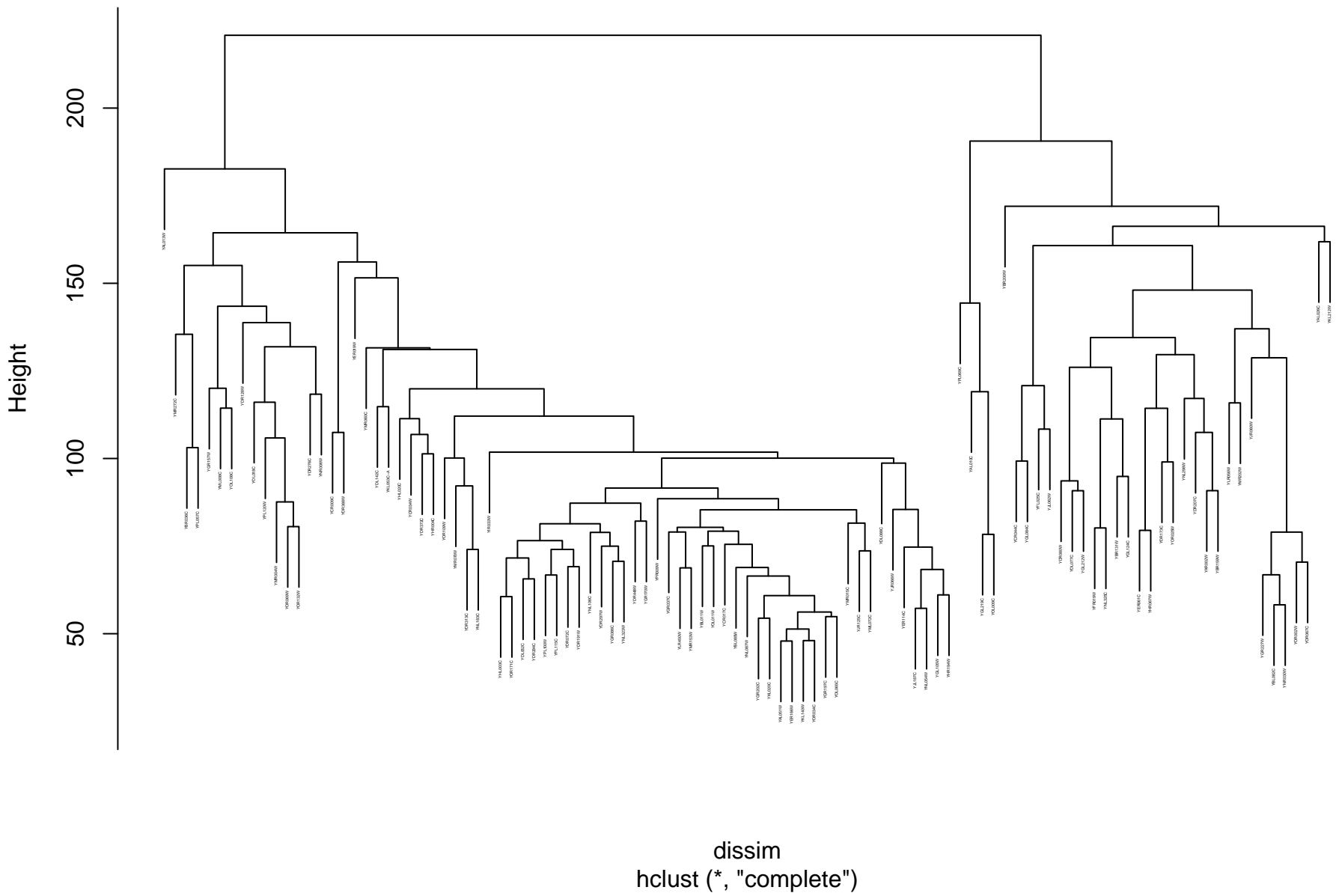
cell cycle_GO_euclidean_complete



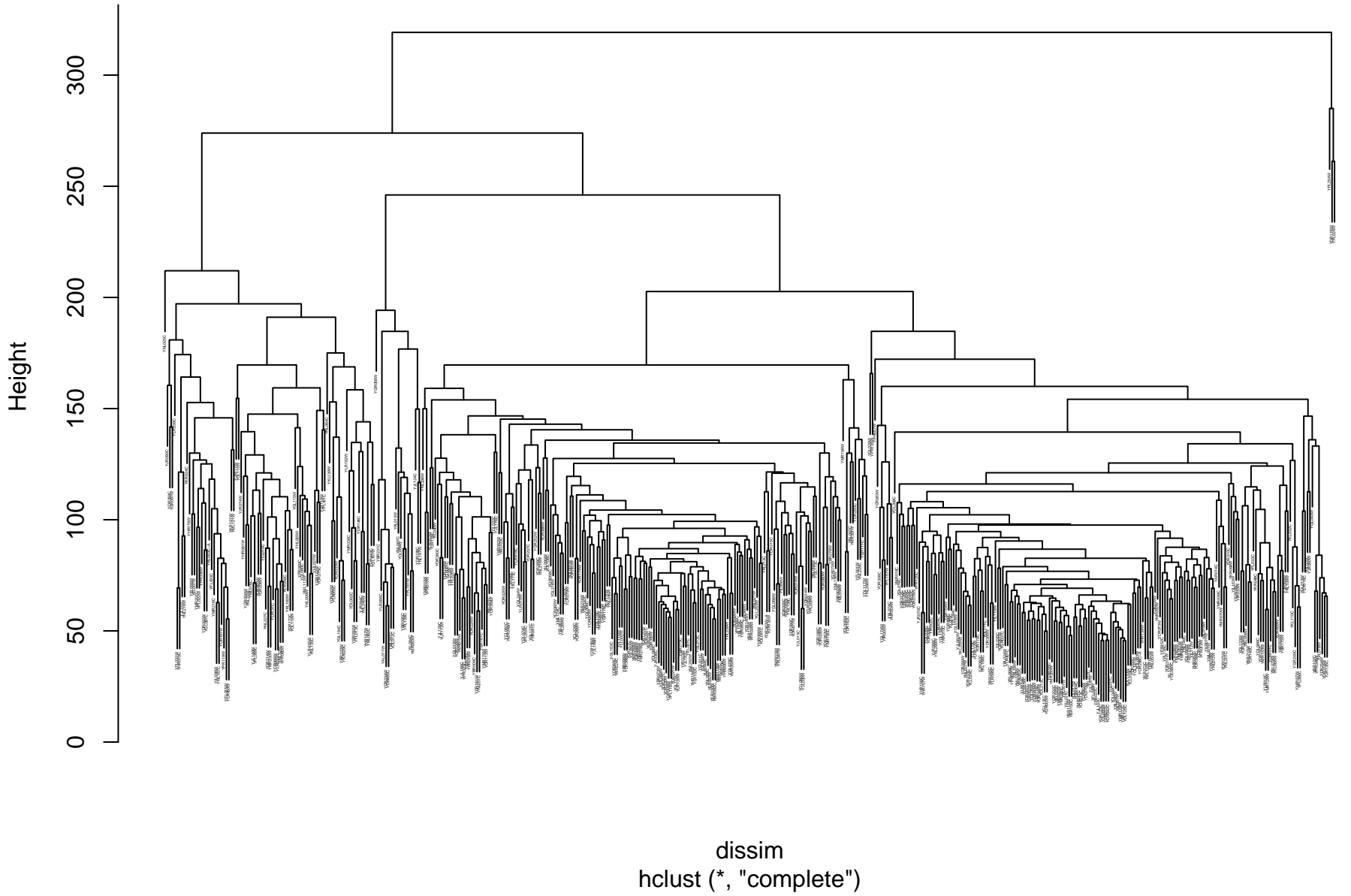
```
dissim
hclust (*, "complete")
```



lipids_GO_euclidean_complete



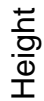
nuclear transport_GO_euclidean_complete



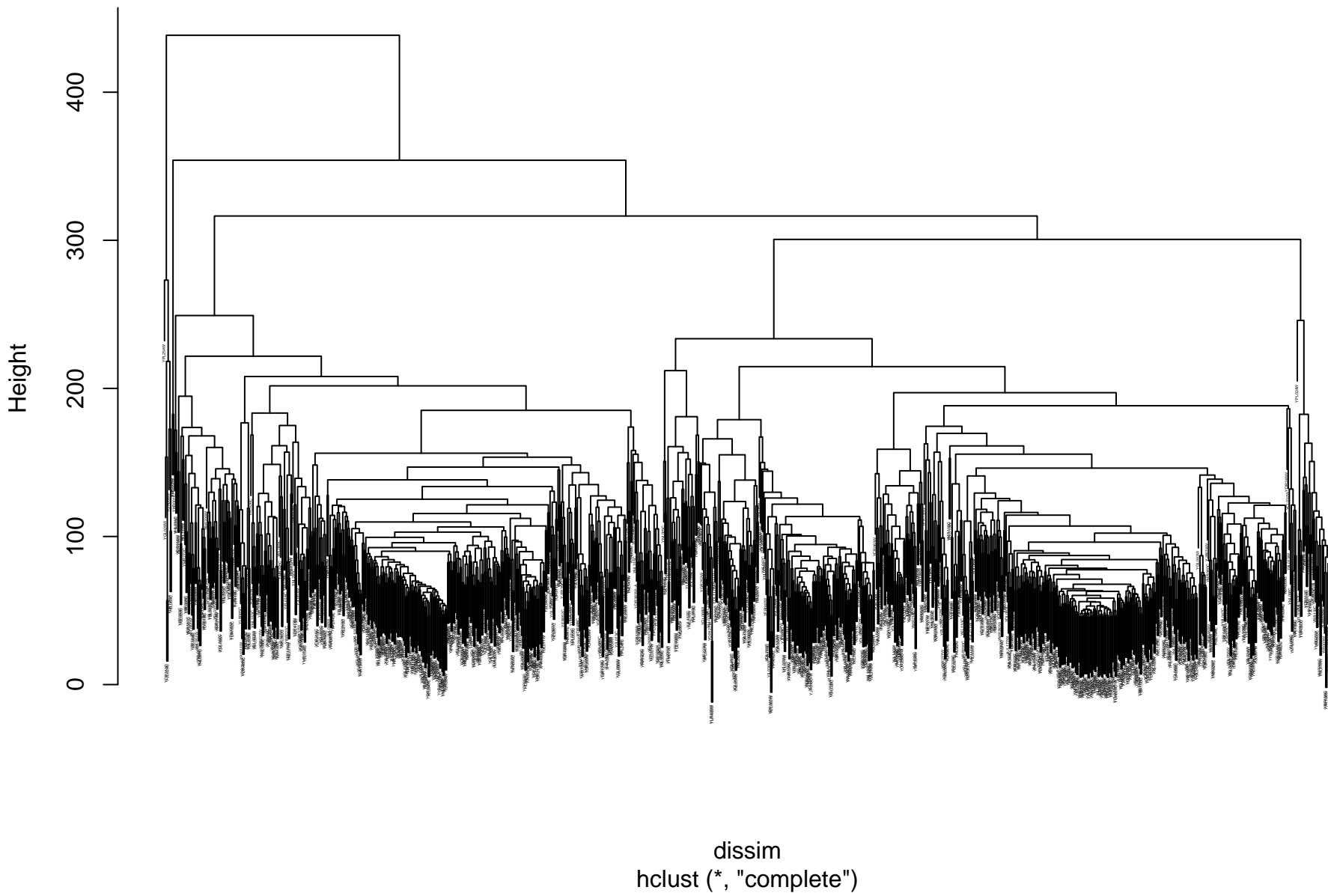

```

dissim
hclust (*, "complete")

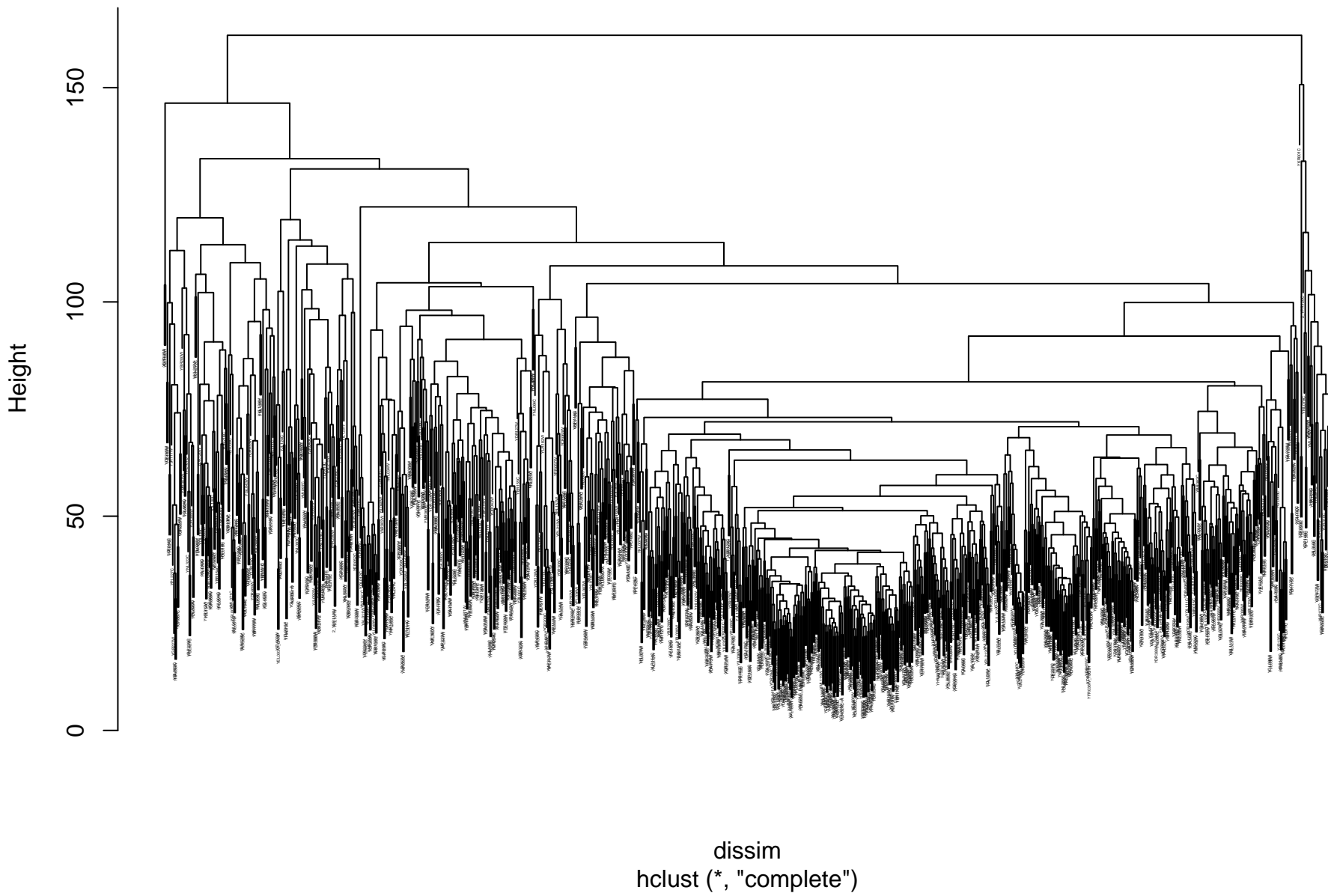
```



library_euclidean_complete



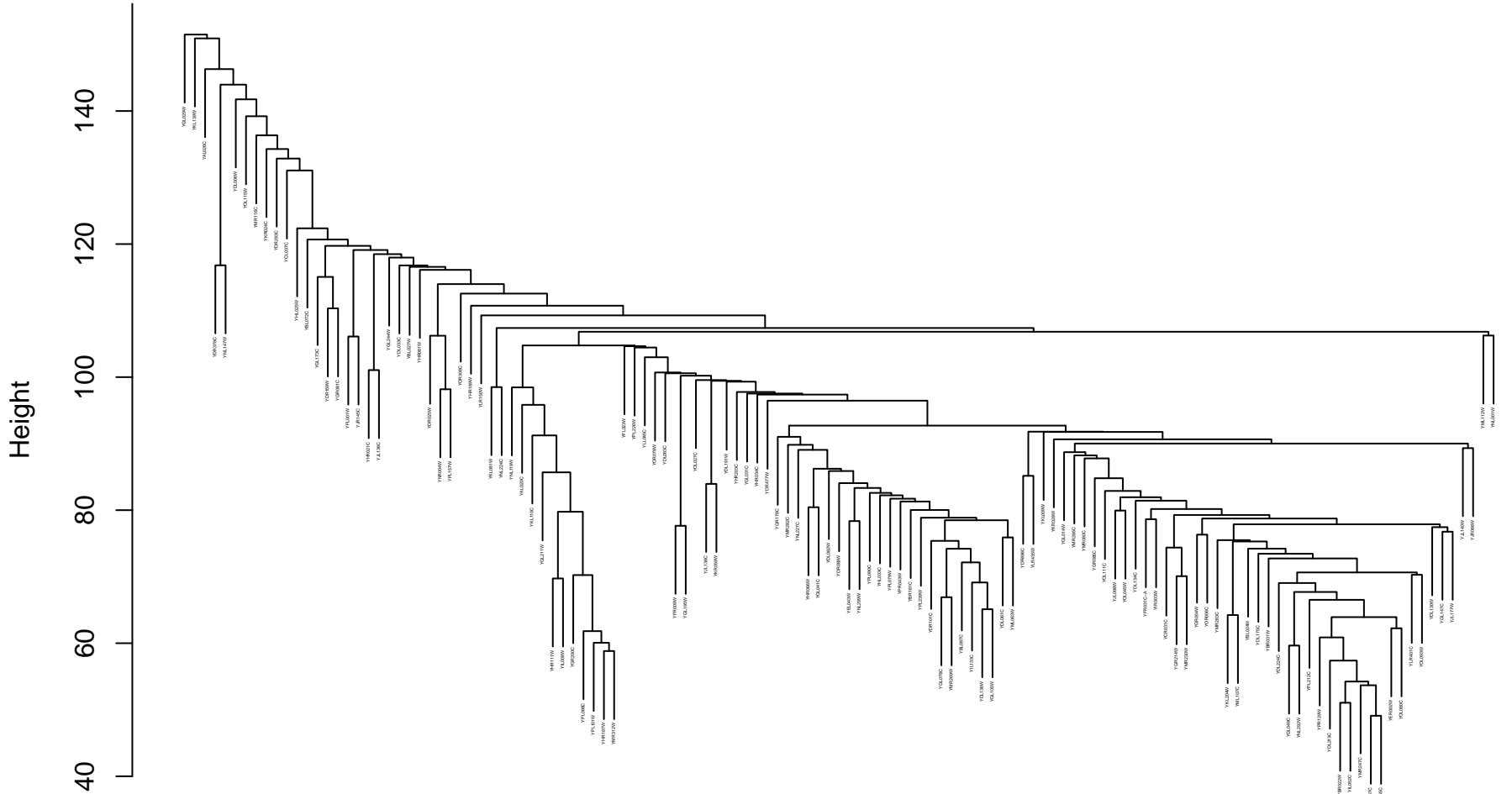
gene_euclidean_complete



```

dissim
hclust (*, "average")

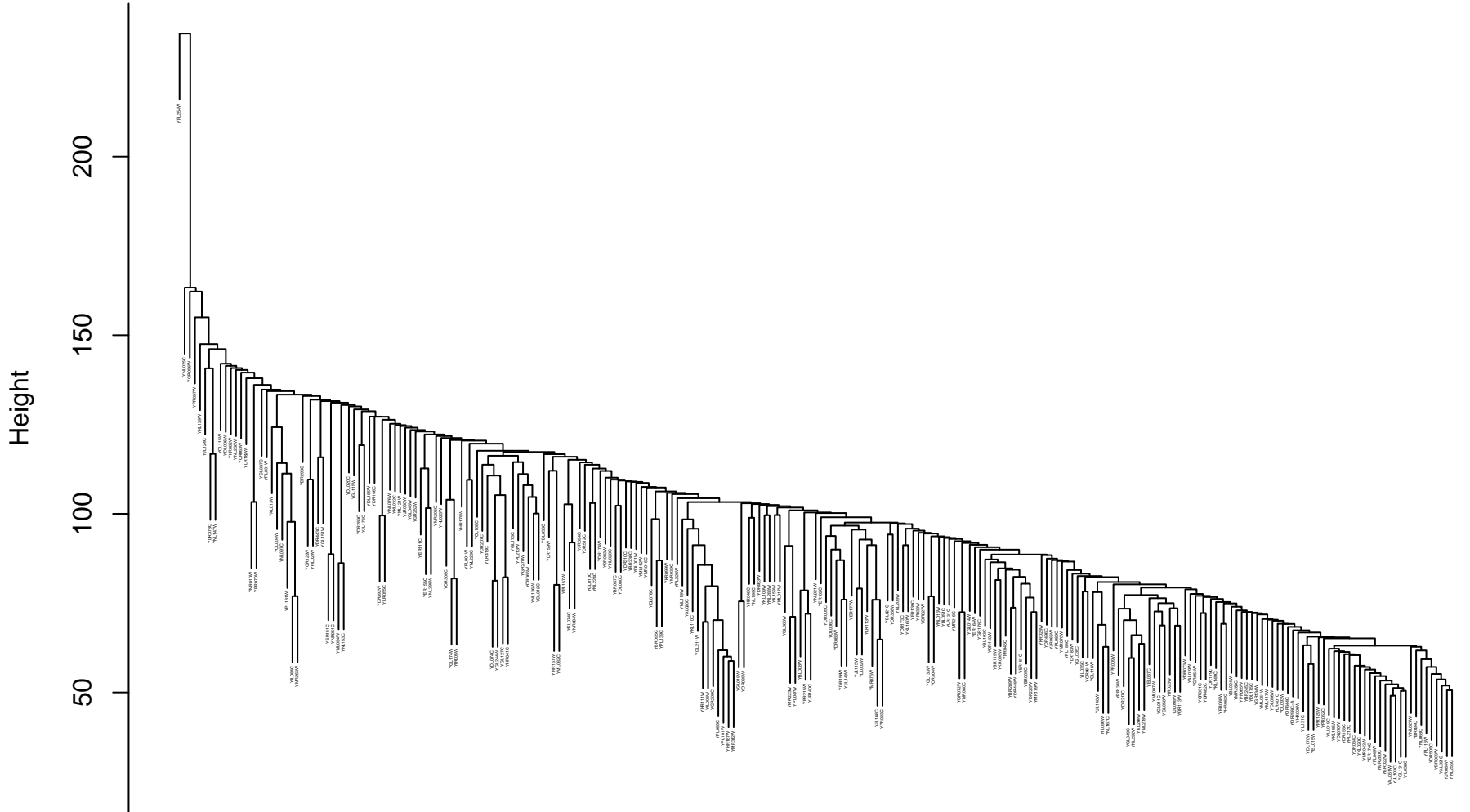
```



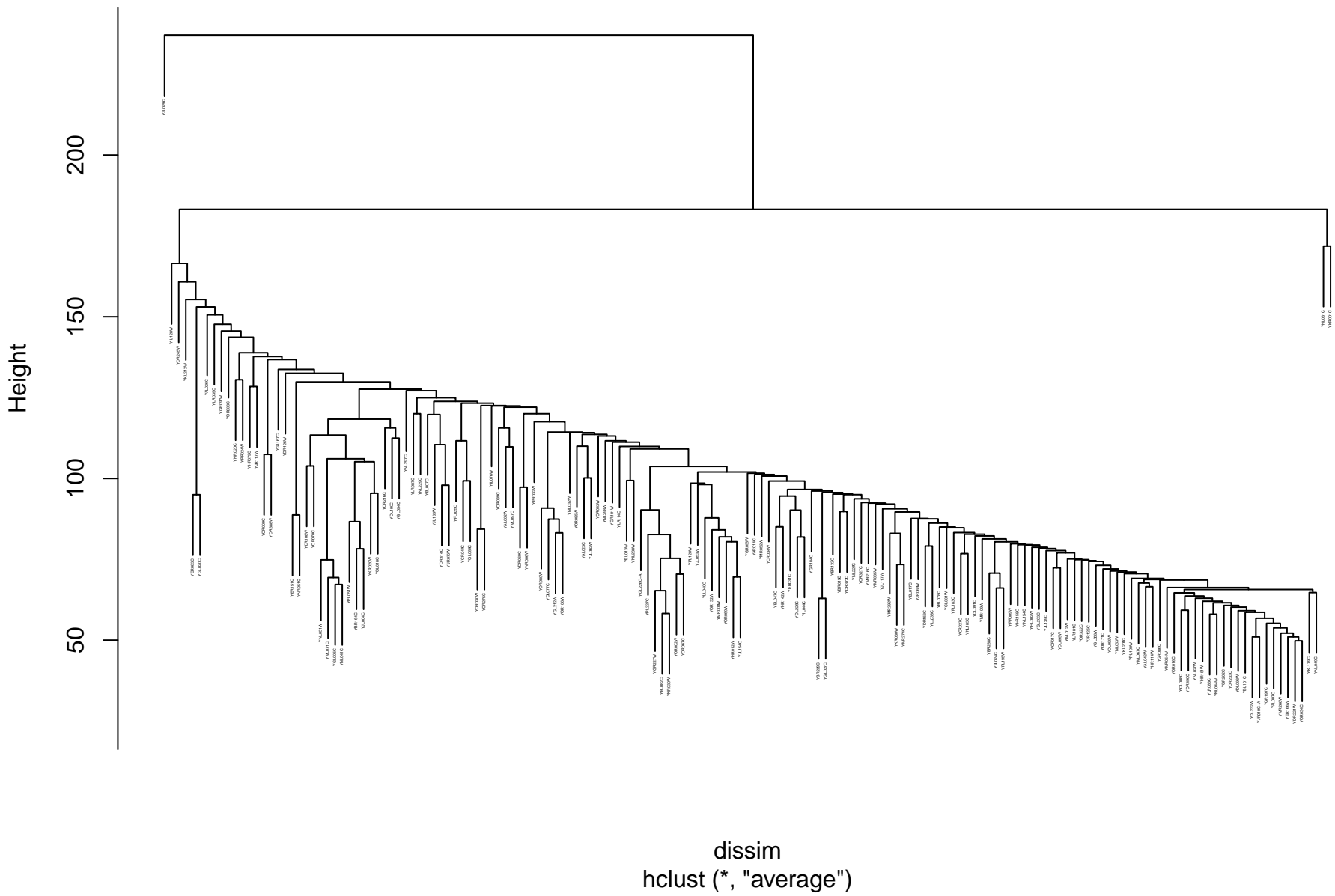
```

dissim
hclust (*, "average")

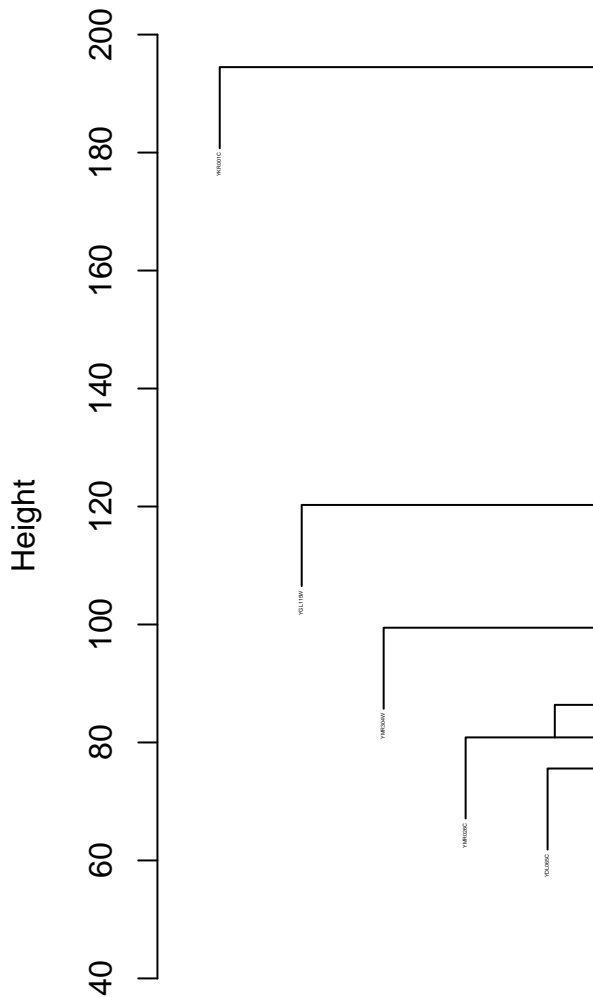
```



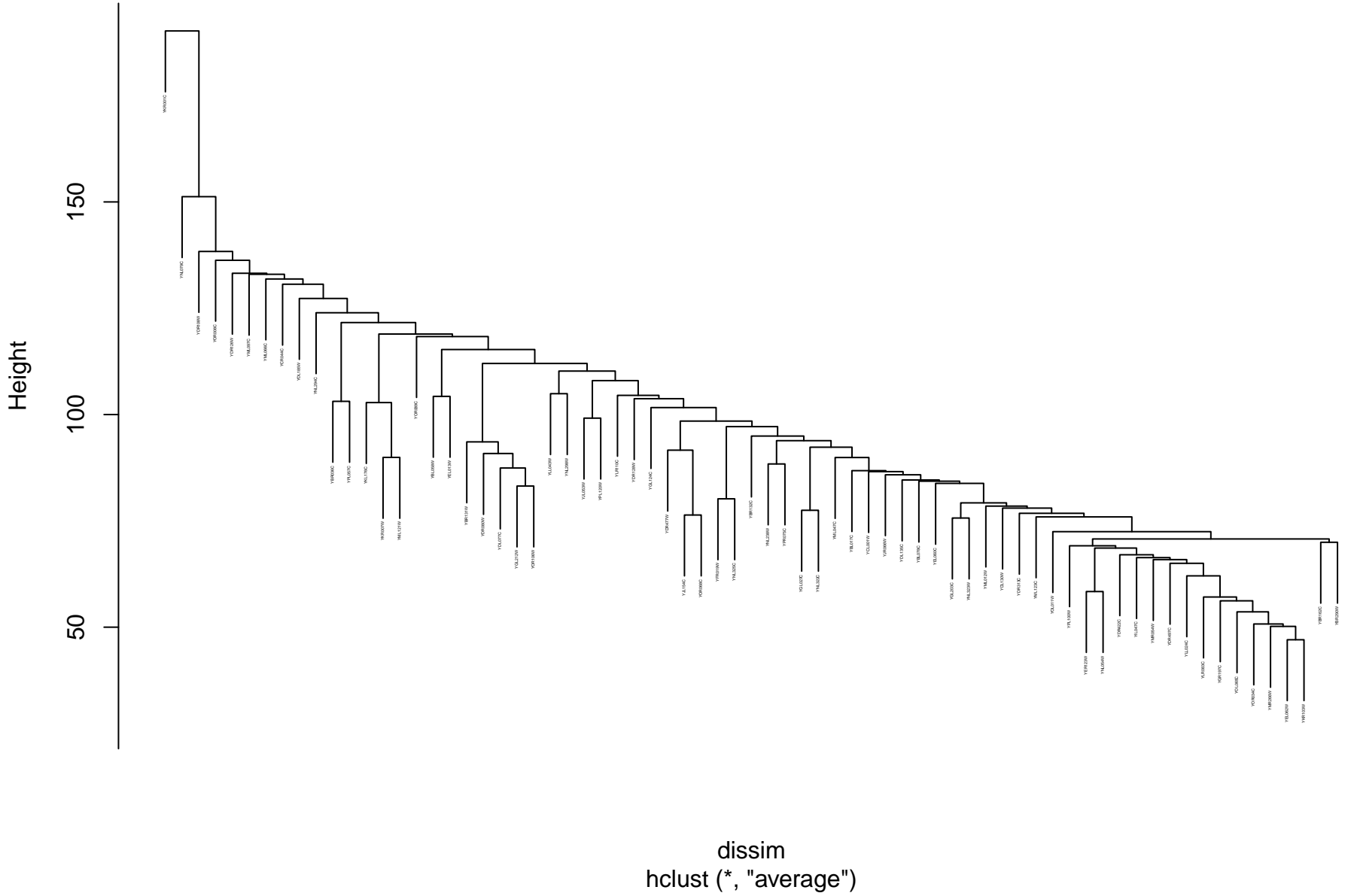
Golgi and ER_GO_euclidean_average



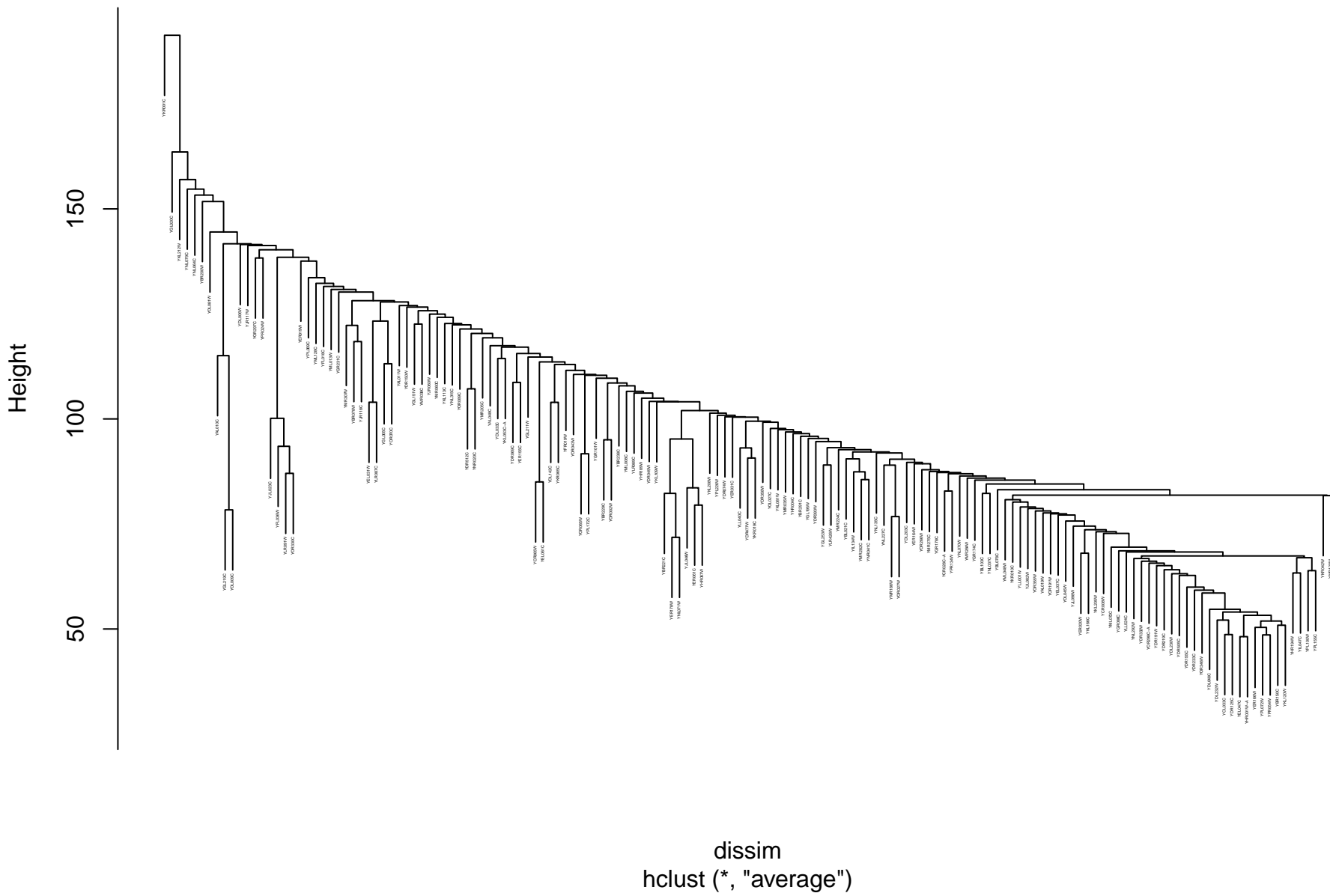
```
dissim
hclust (*, "average")
```

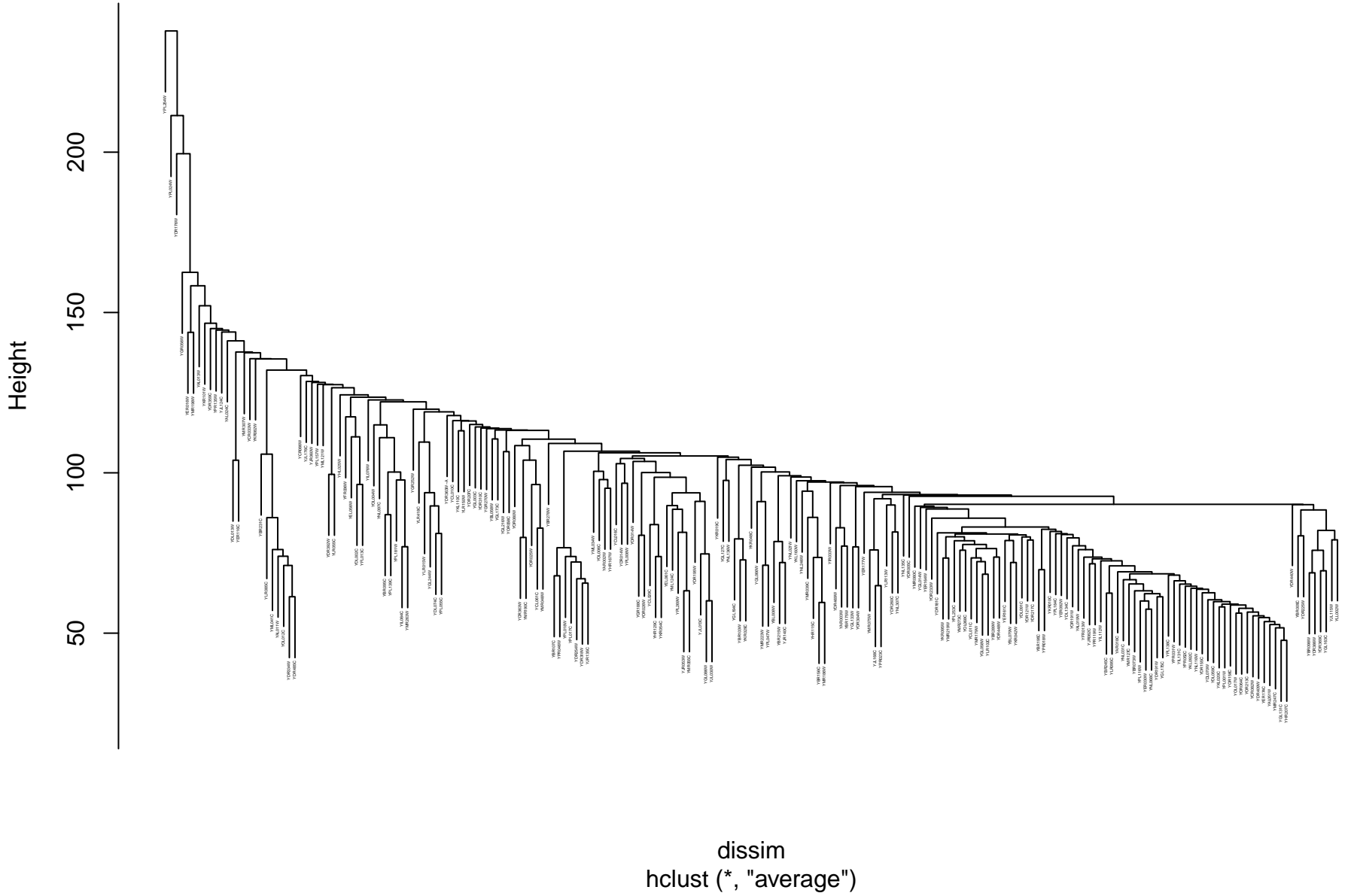


vacuole_GO_euclidean_average



mitochondrion_GO_euclidean_average

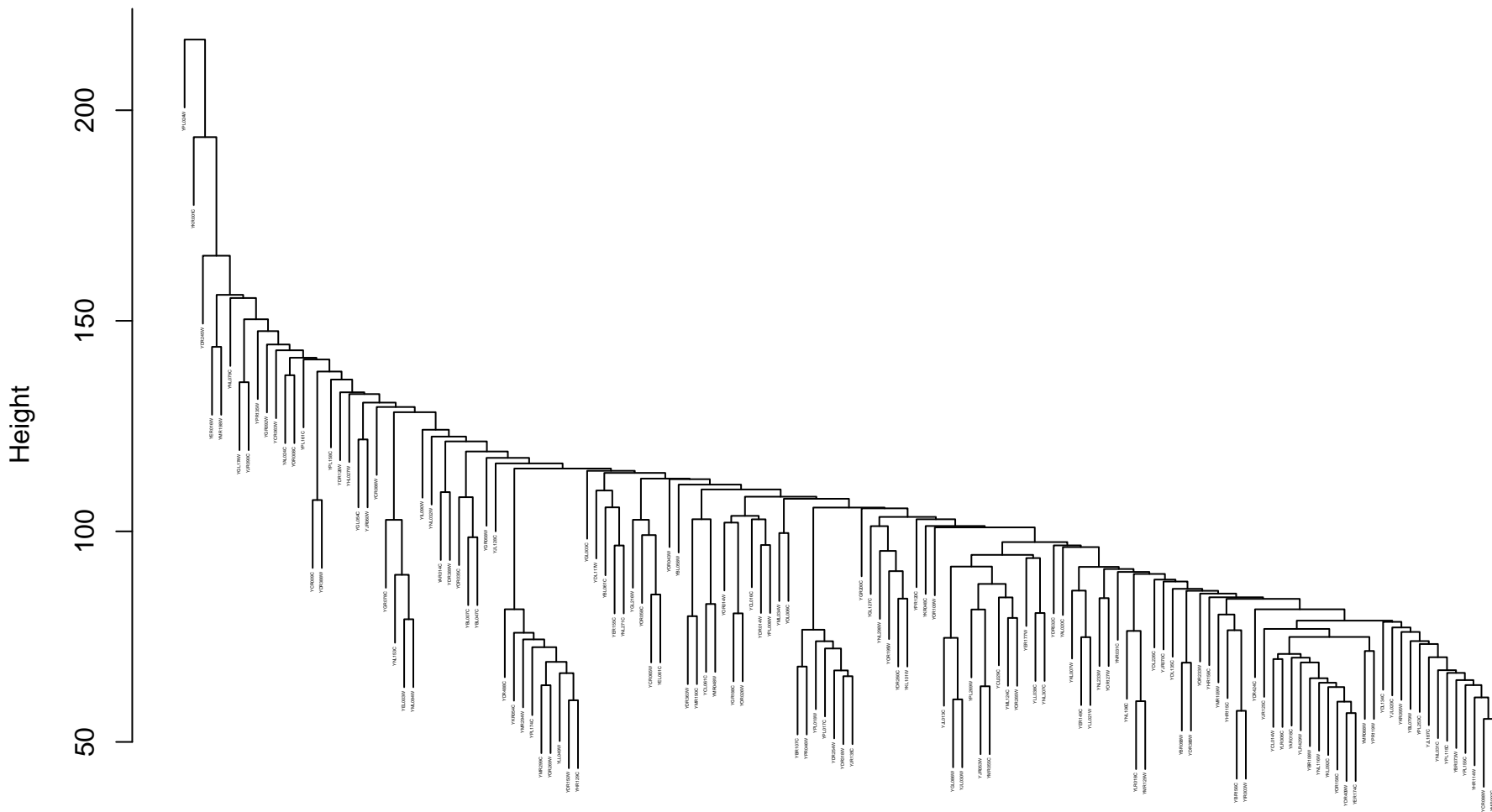


chromatin_GO_euclidean_average

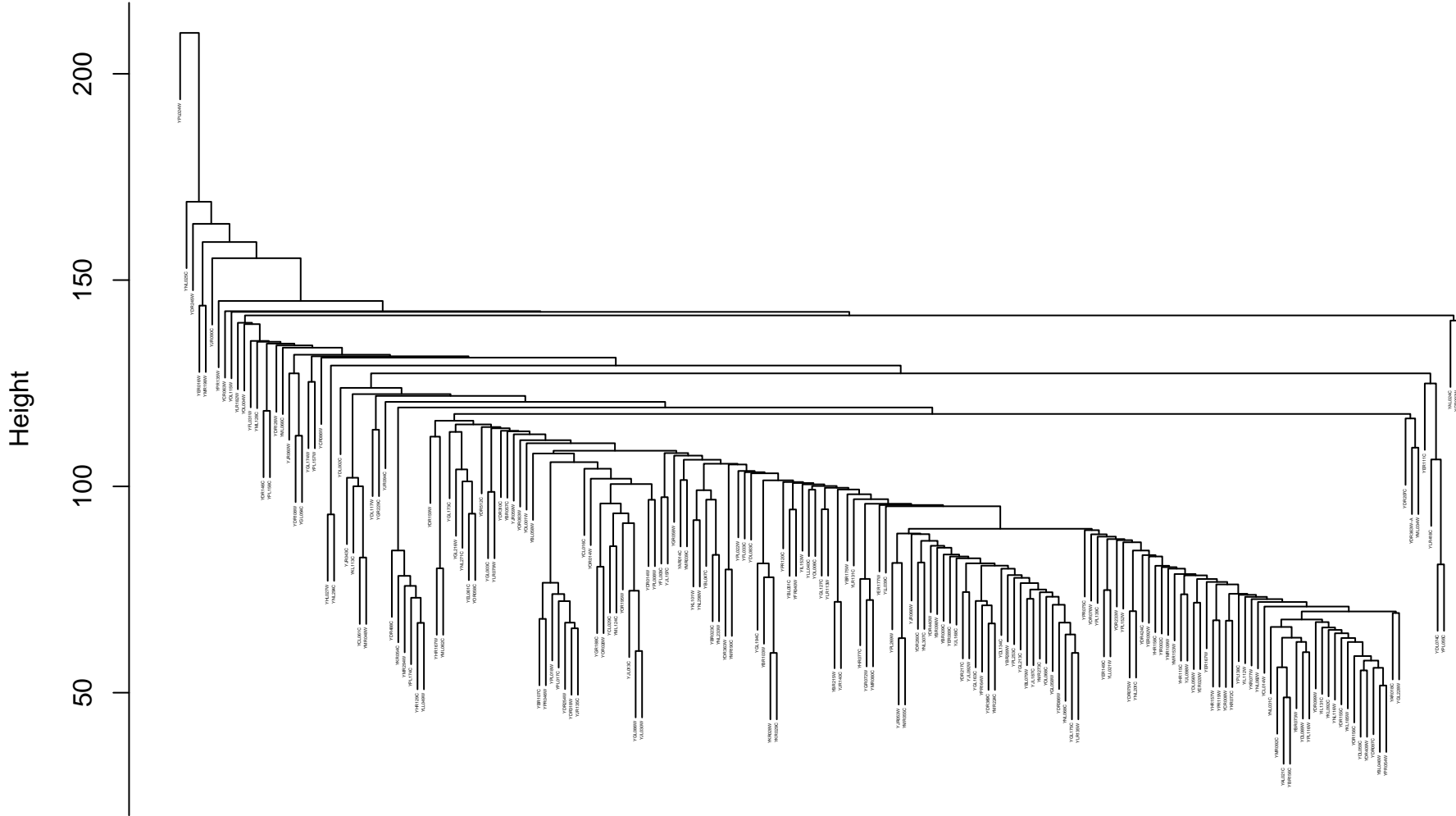
```

dissim
hclust (*, "average")

```

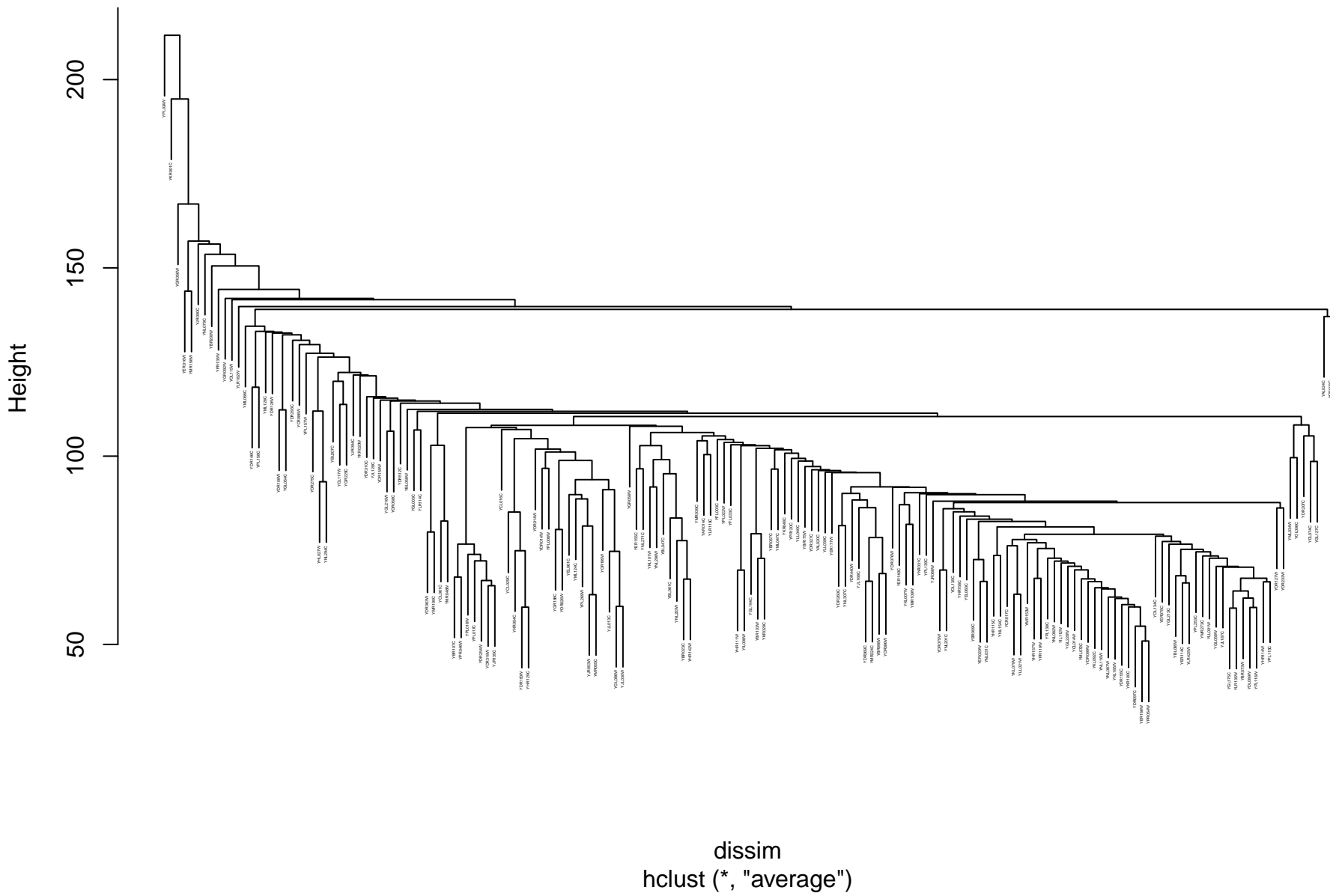


cell cycle_GO_euclidean_average

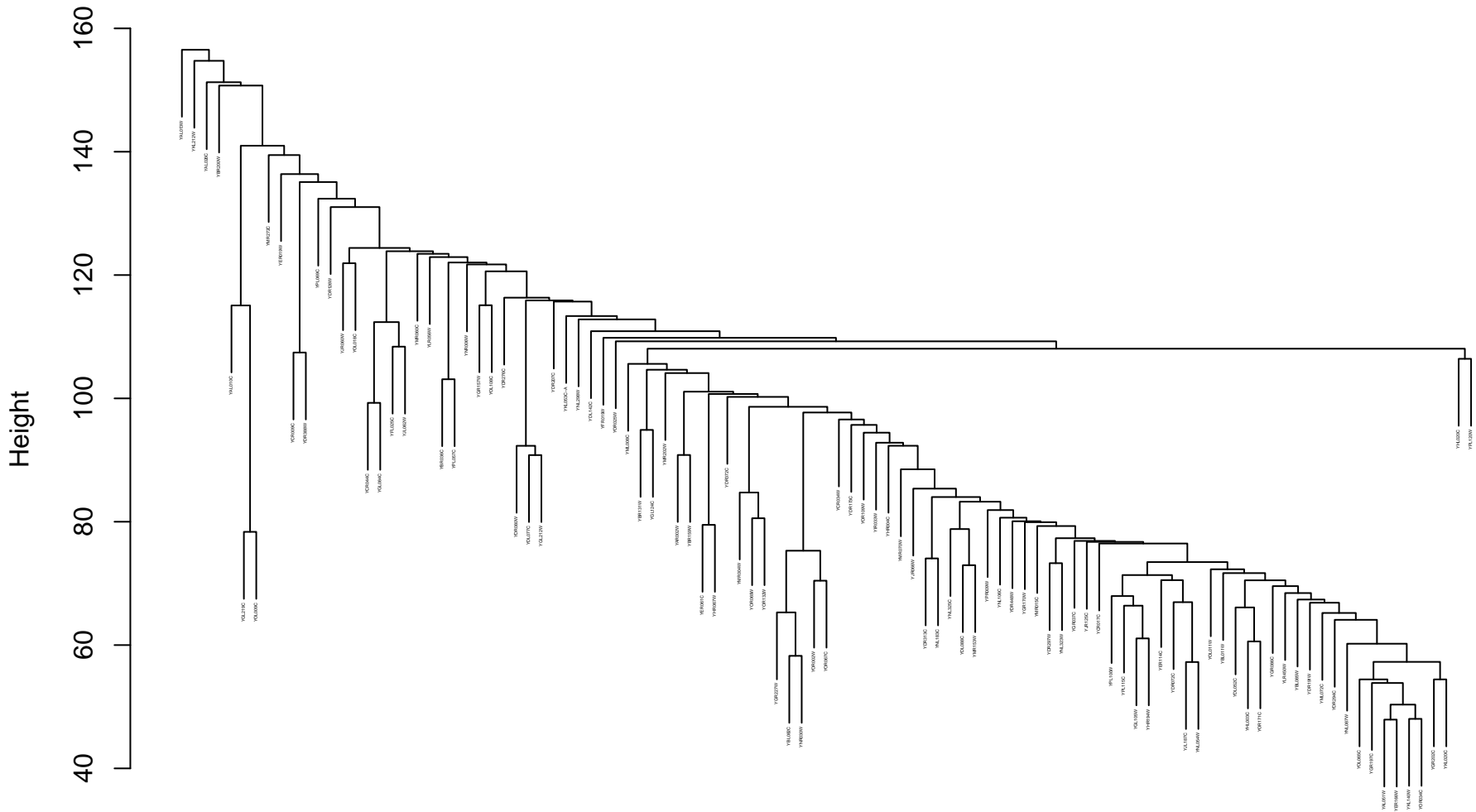


dissim
hclust (*, "average")

budding_GO_euclidean_average



lipids_GO_euclidean_average

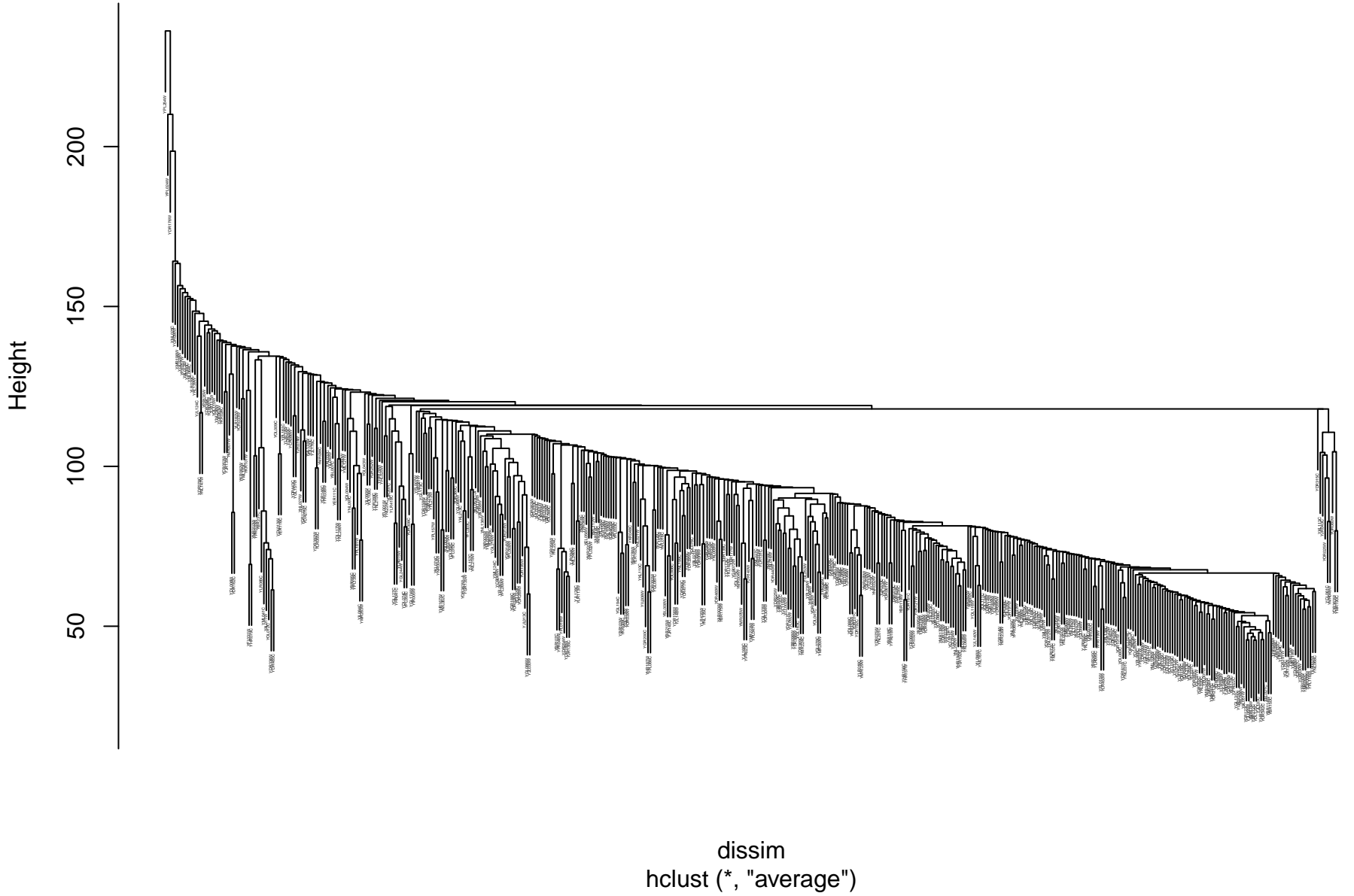


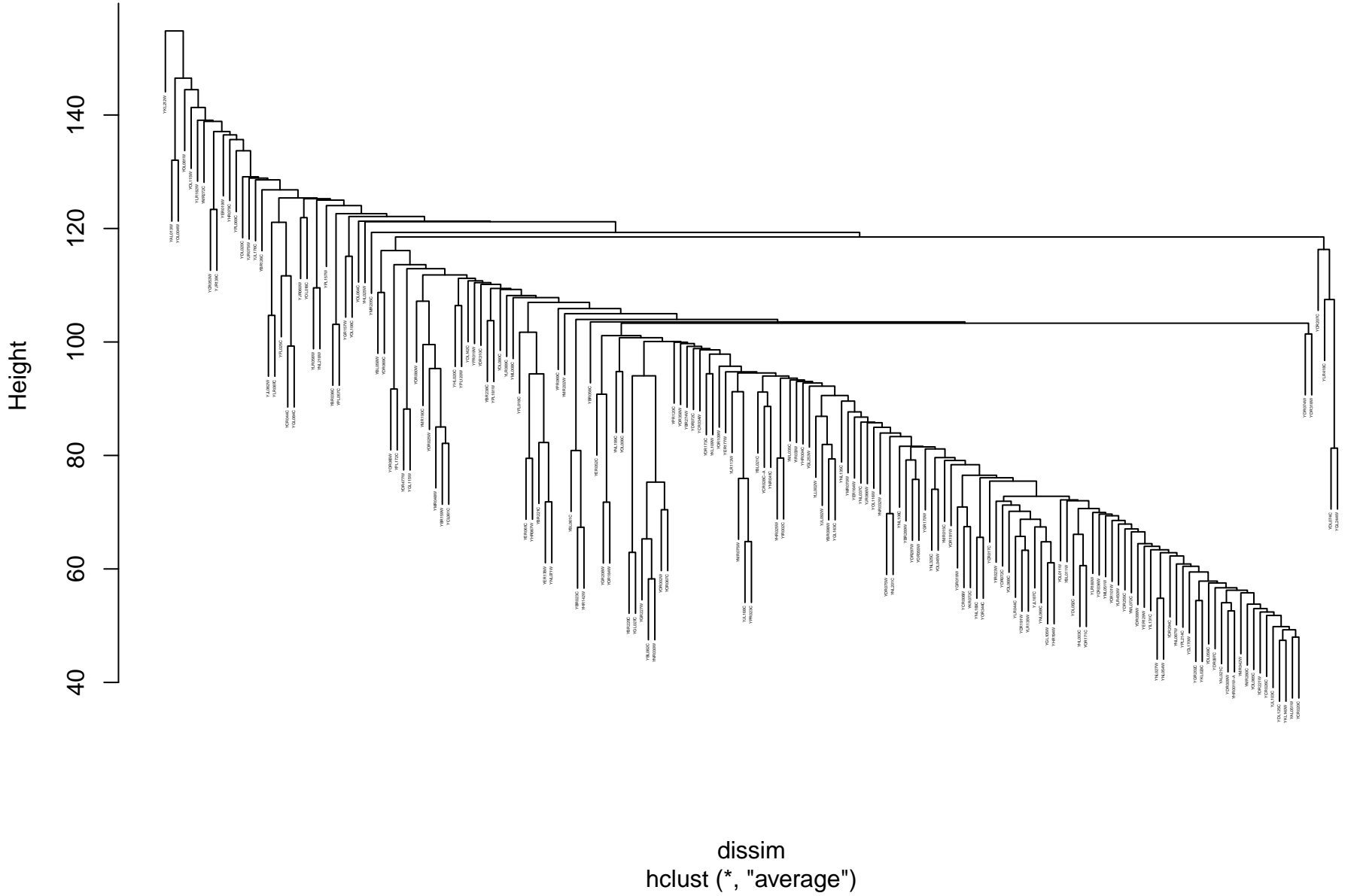
```

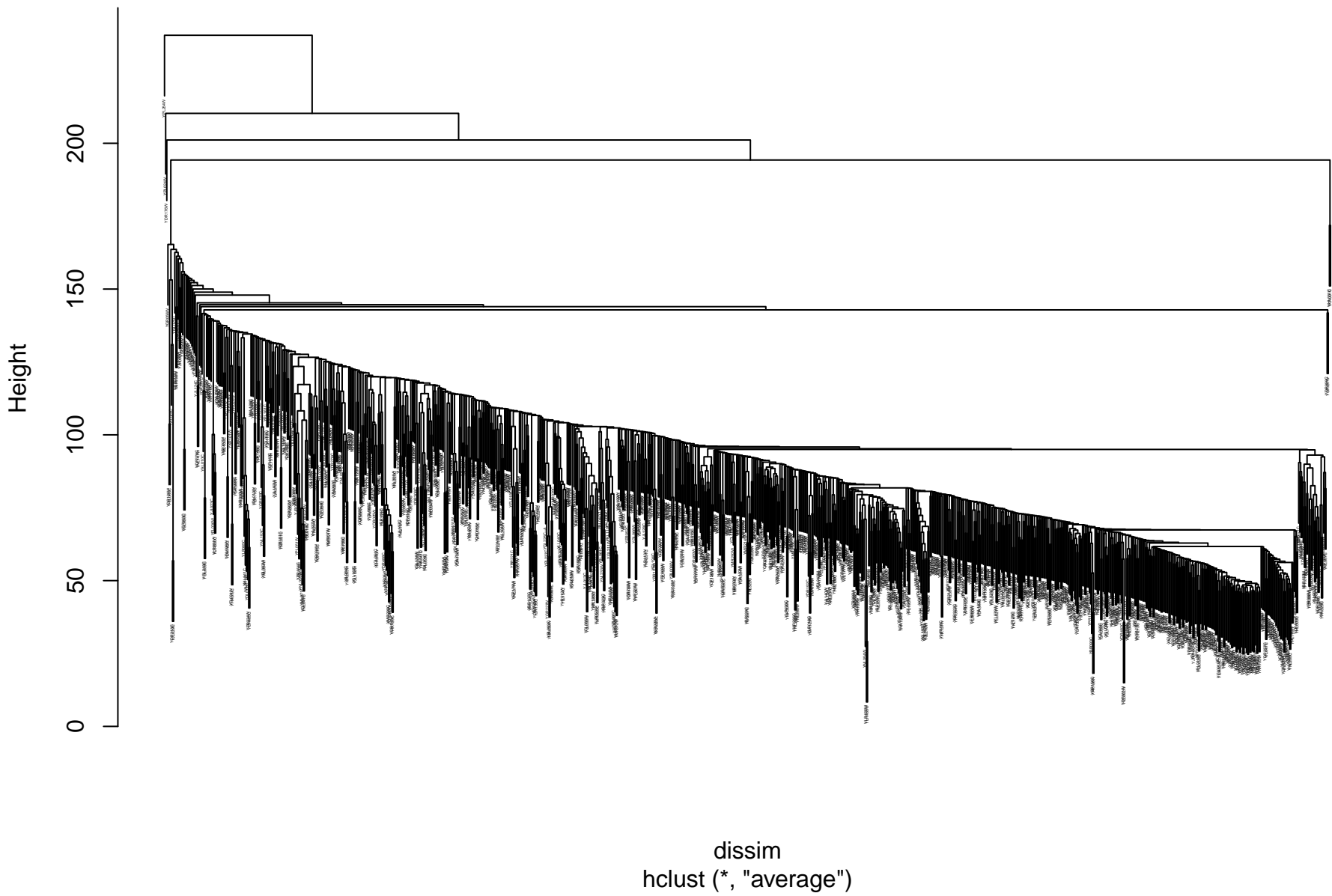
dissim
hclust (*, "average")

```

nuclear transport_GO_euclidean_average



metabolic_GO_euclidean_average

library_euclidean_average

gene_euclidean_average

