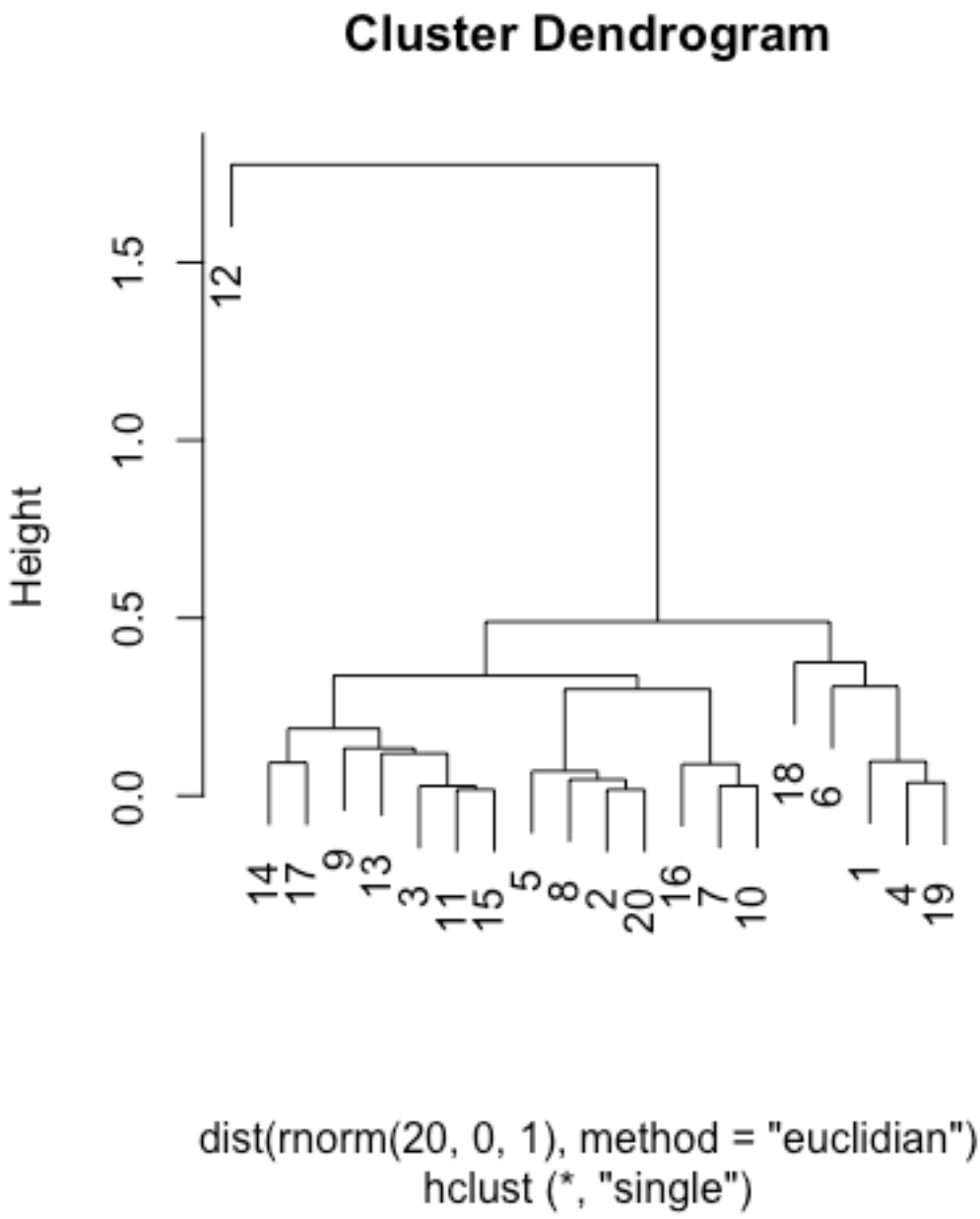
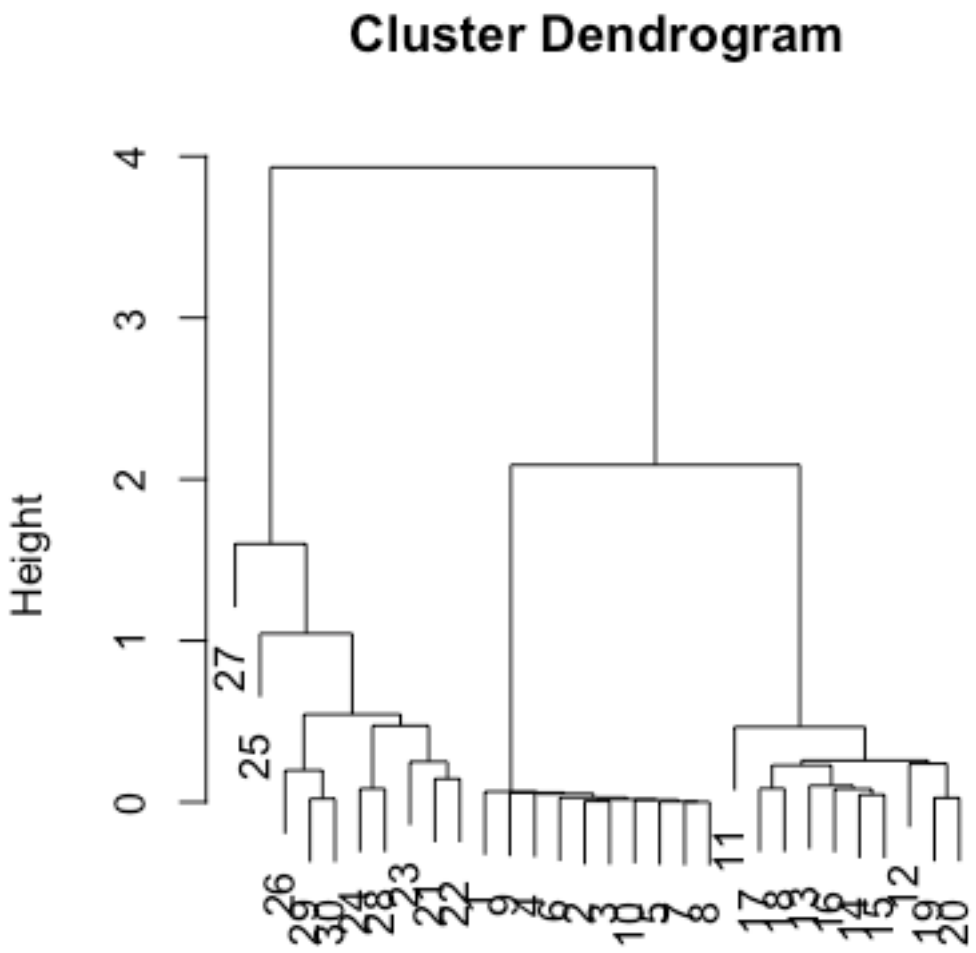
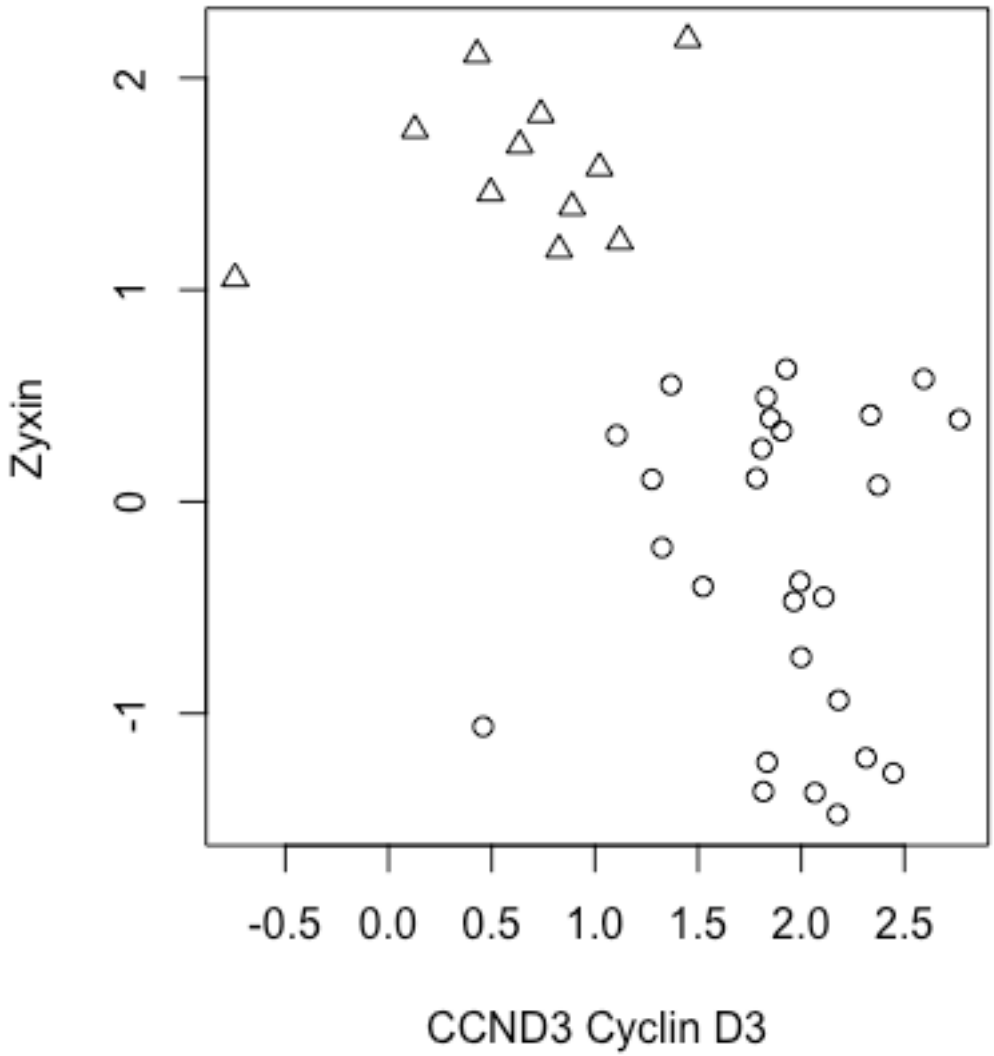
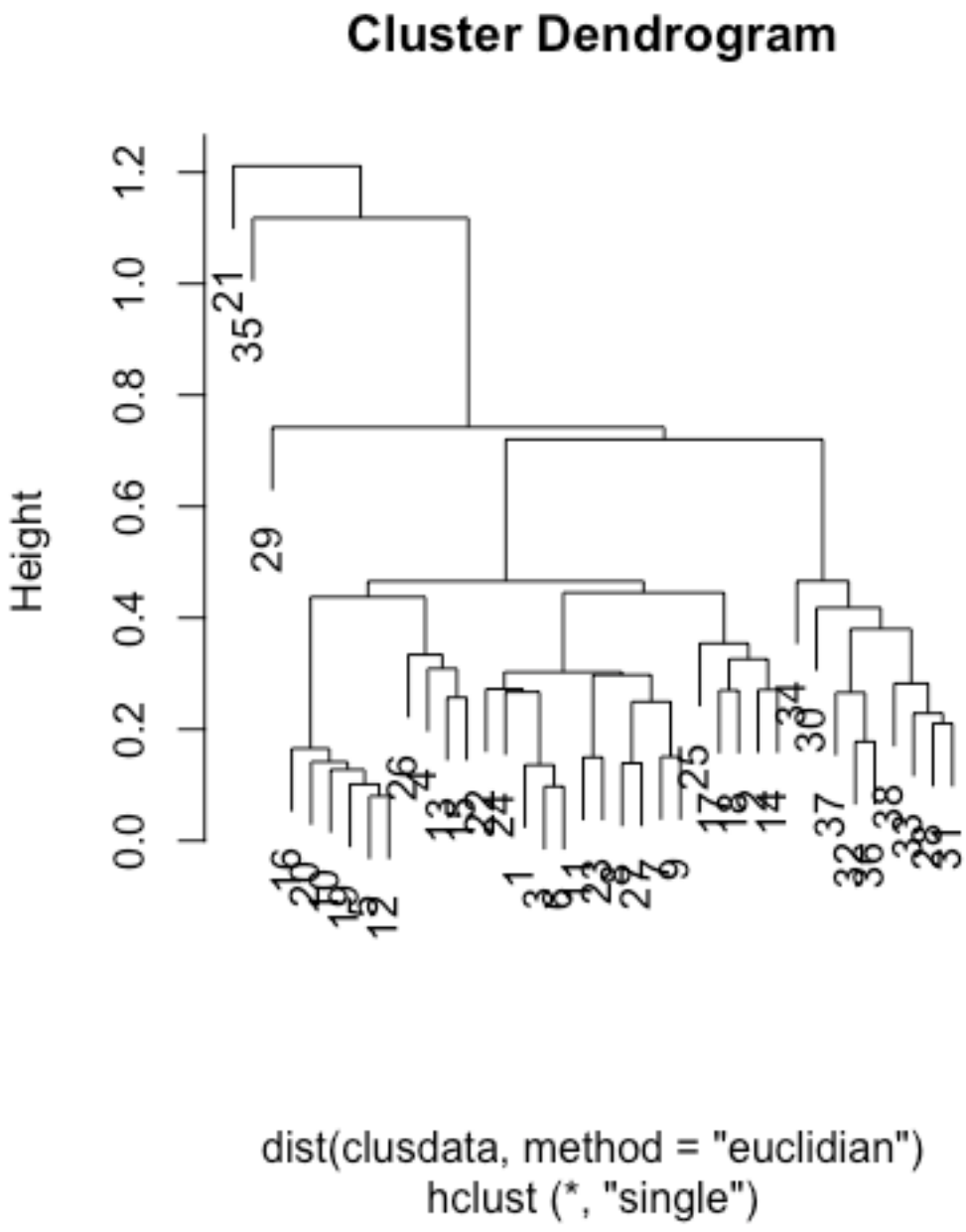
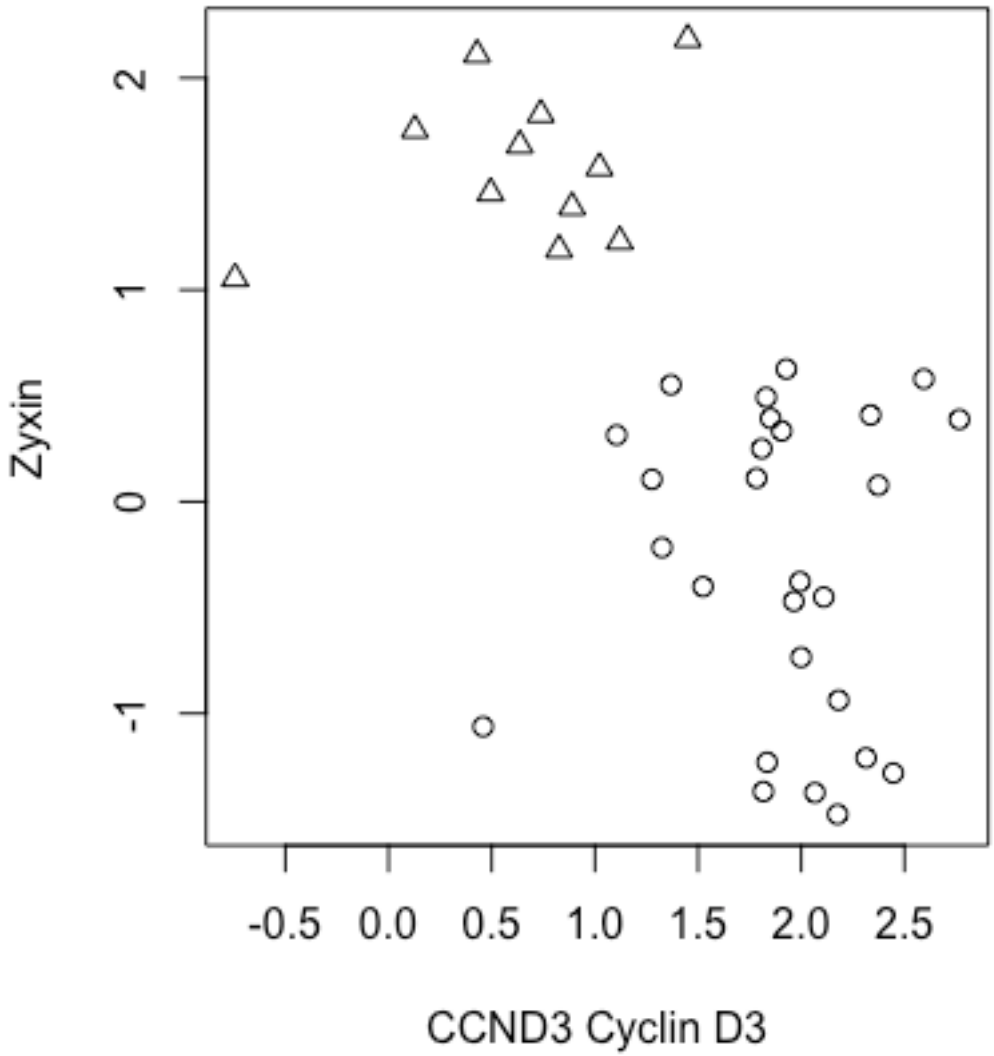
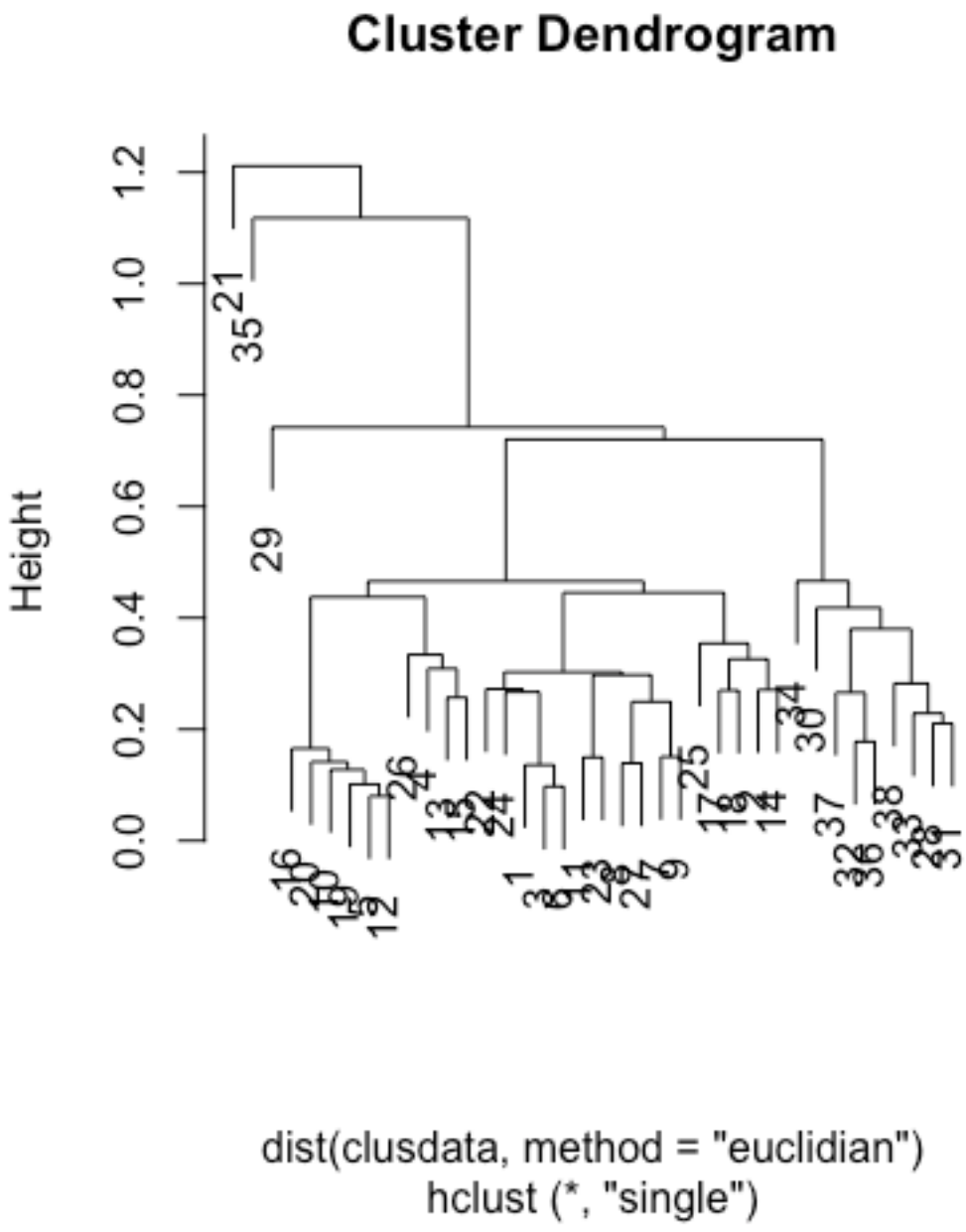

Cluster Dendrogram
Height
0.0
0.5
1.0
1.5
12
14
17
9
13
3
11
15
5
8
2
20
16
7
10
18
6
1
4
19
dist(rnorm(20, 0, 1), method = "euclidian")
hclust (*, "single")

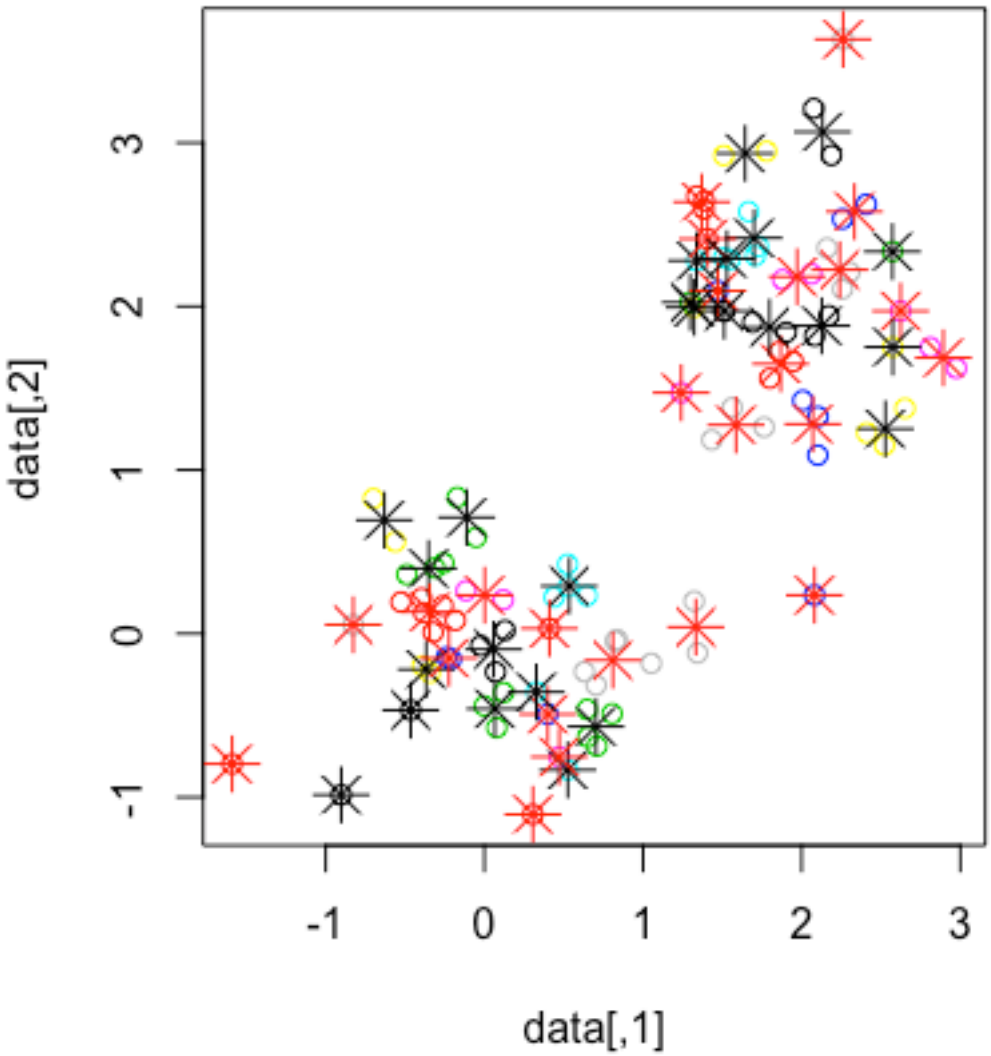

Cluster Dendrogram
Height
0
1
2
3
4
27
25
11
26
29
30
24
28
23
21
22
9
4
6
2
3
10
5
7
8
17
18
13
16
14
15
12
19
20
dist(x, method = "euclidian")
hclust (*, "single")

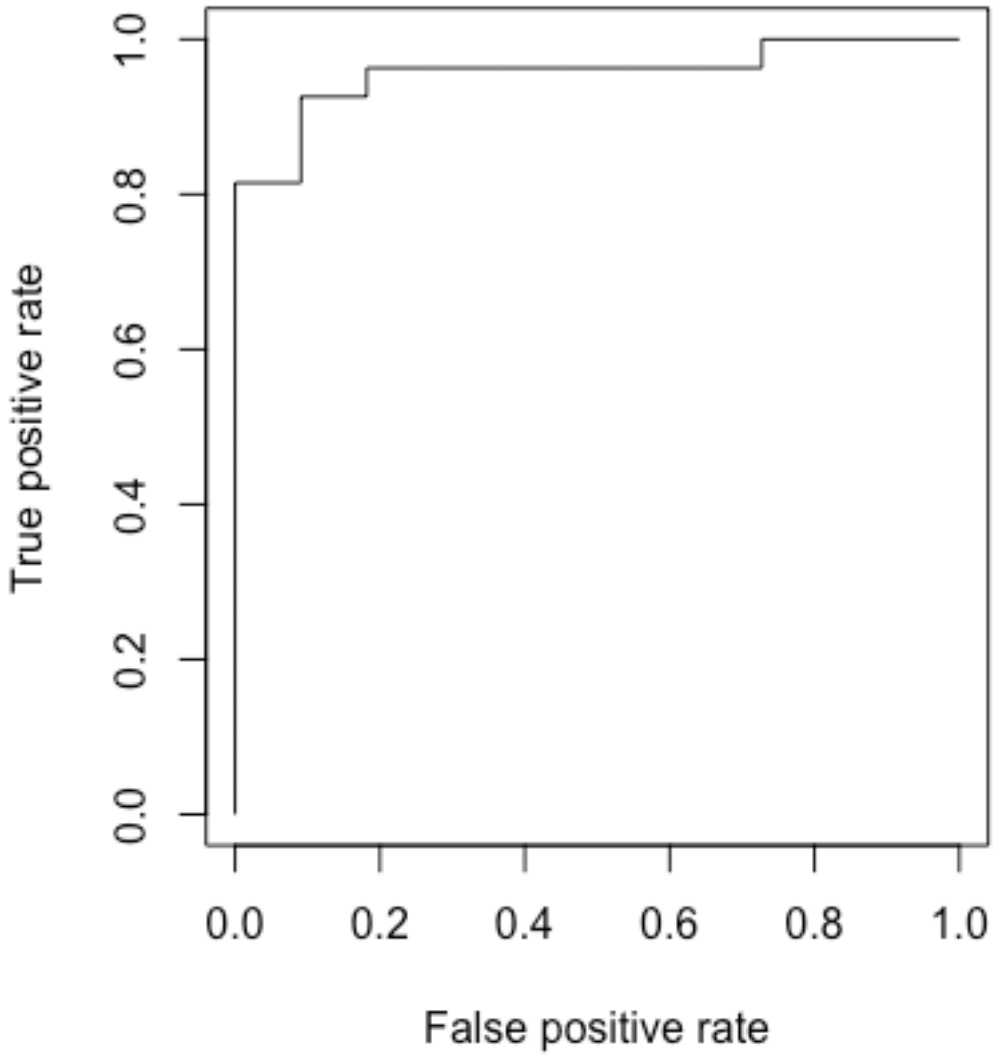

Zyxin
2
1
0
-1
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
CCND3 Cyclin D3

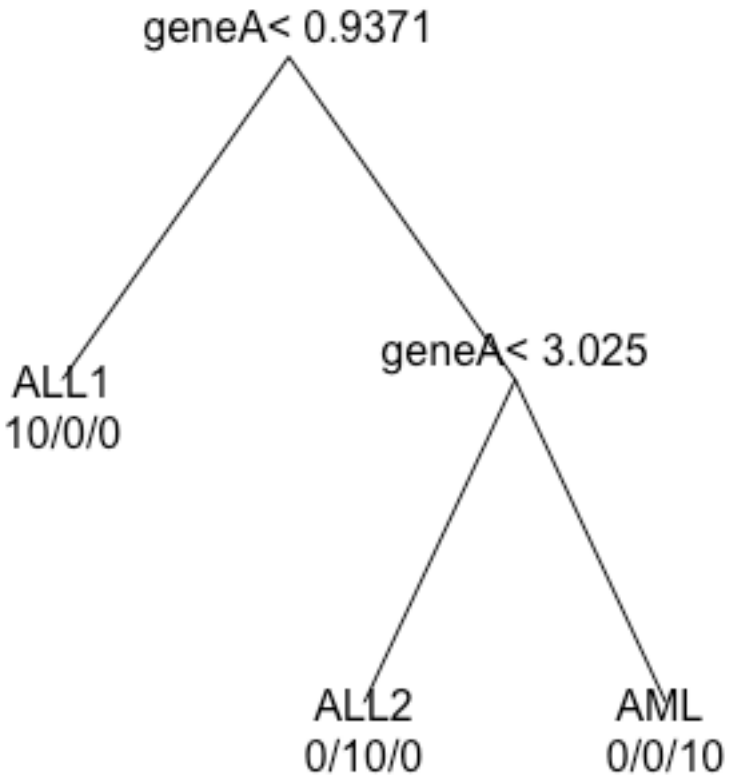

Cluster Dendrogram
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dist(clusdata, method = "euclidian")
hclust (*, "single")


Zyxin
2
1
0
-1
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
CCND3 Cyclin D3


Cluster Dendrogram
Height
0.0
0.2
0.4
0.6
0.8
1.0
1.2
dist(clusdata, method = "euclidian")
hclust (*, "single")


data[,2]
3
2
1
0
-1
-1
0
1
2
3
data[,1]


True positive rate
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0
False positive rate


geneA< 0.9371
ALL1
10/0/0
geneA< 3.025
ALL2
0/10/0
AML
0/0/10