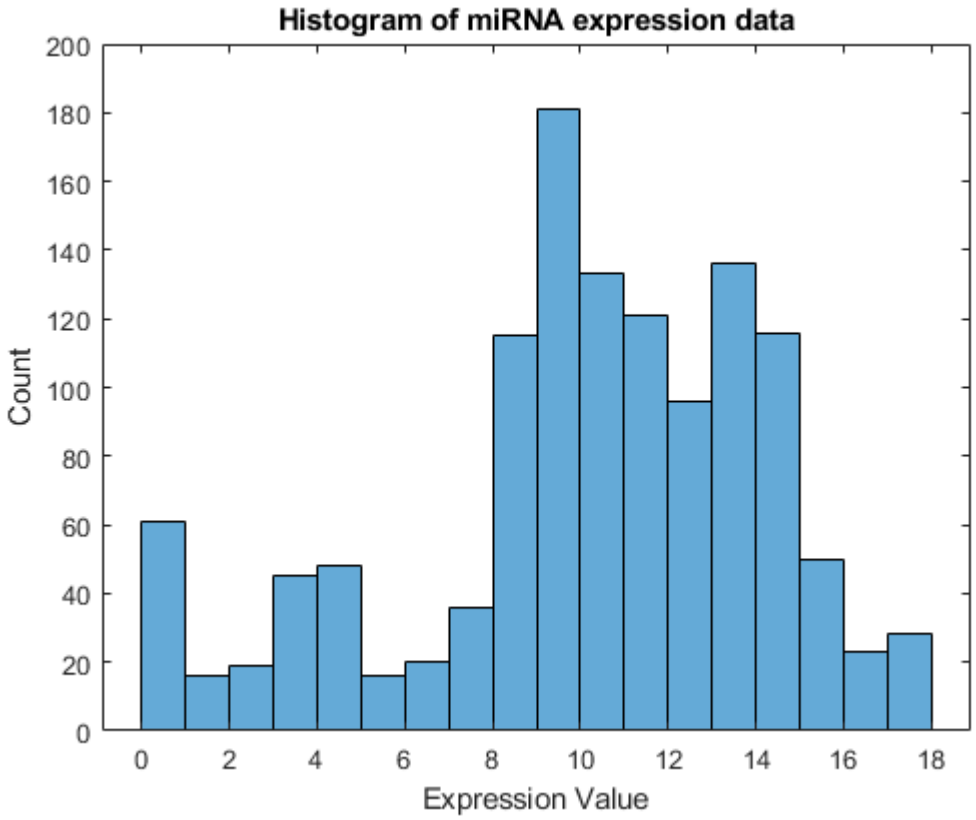
Unsupervised Learning In-Class Practice: Answer Key

Loading and examining the data

```
% Load the dataset
miRNA = readtable('miRNA_data.xlsx');
% Create a variable for patient IDs
patient_ID = miRNA.Patient_ID;
% Create a variable for patient health status
health_stat = miRNA.Health_Status;
% Create a variable for gene names
genes = miRNA.Properties.VariableNames(3:end);
% Create a variable for gene expression data
miRNA_data = table2array(miRNA(:,3:end));

% Histogram of expression data
histogram(miRNA_data)
xlabel('Expression Value'); ylabel('Count')
title('Histogram of miRNA expression data')
```



Answer: The data is left-skewed.

Determining optimal k value using KMC

```
% Create a vector of k values ranging from 2 to 10
k_values = 2:10;
```

```
% For-loop to calculate the silhouette statistic for different k values
n = length(k_values);       % number of k values
s_score = zeros(n,1);       % variable to store silhouette statistic values
for i = 1:n
    % Use the kmeans function to cluster patients into k clusters
    [idx,~] = kmeans(miRNA_data,k_values(i));
    % Use the silhouette function to calculate silhouette values
    s = silhouette(miRNA_data,idx);
    % Calculate the silhouette score by taking the mean
    s_score(i) = mean(s);
end
max(s_score)
```

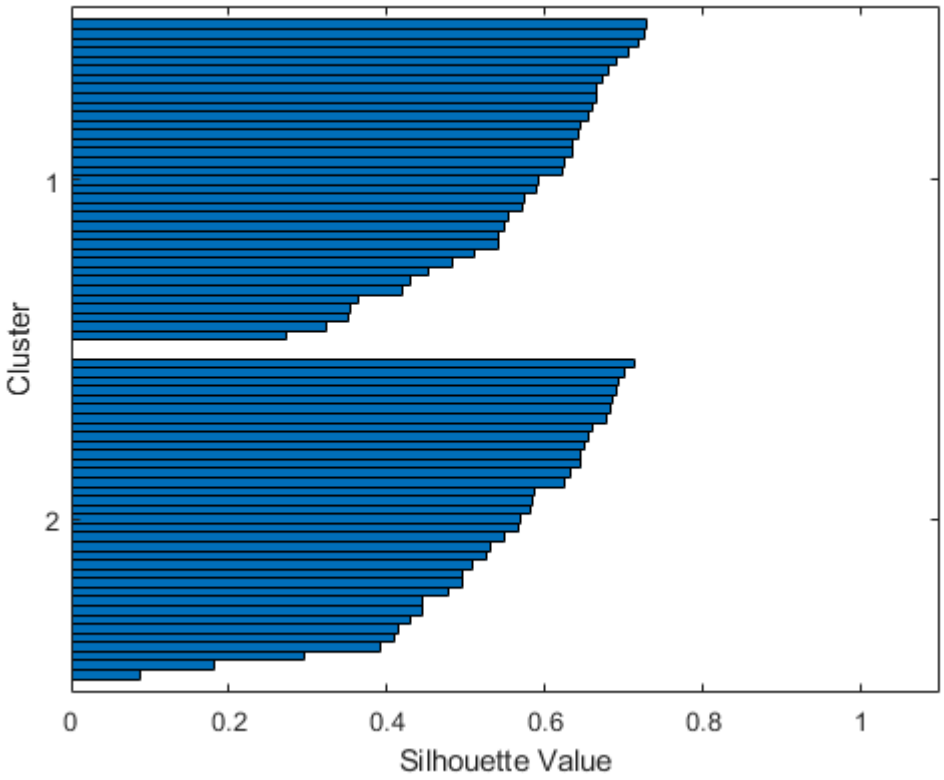
```
ans = 0.5539
```

```
k = find(s_score==max(s_score))+1
```

```
k = 2
```

Answer: The max silhouette statistic is equal to 0.5539, and this corresponds with k = 2.

```
% Silhouette plot based on best k value
[idx,~] = kmeans(miRNA_data,k);
silhouette(miRNA_data,idx)
```



Answer: No negative values are present, but a negative silhouette value would imply that its associated observation was not well-placed into its assigned cluster.

```
cluster_1 = health_stat(idx == 1)
```

```
cluster_1 = 35×1 cell array
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
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    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'healthy' }
    {'diseased'}
    {'diseased'}
    {'diseased'}
    {'diseased'}
```

```
cluster_2 = health_stat(idx == 2)
```

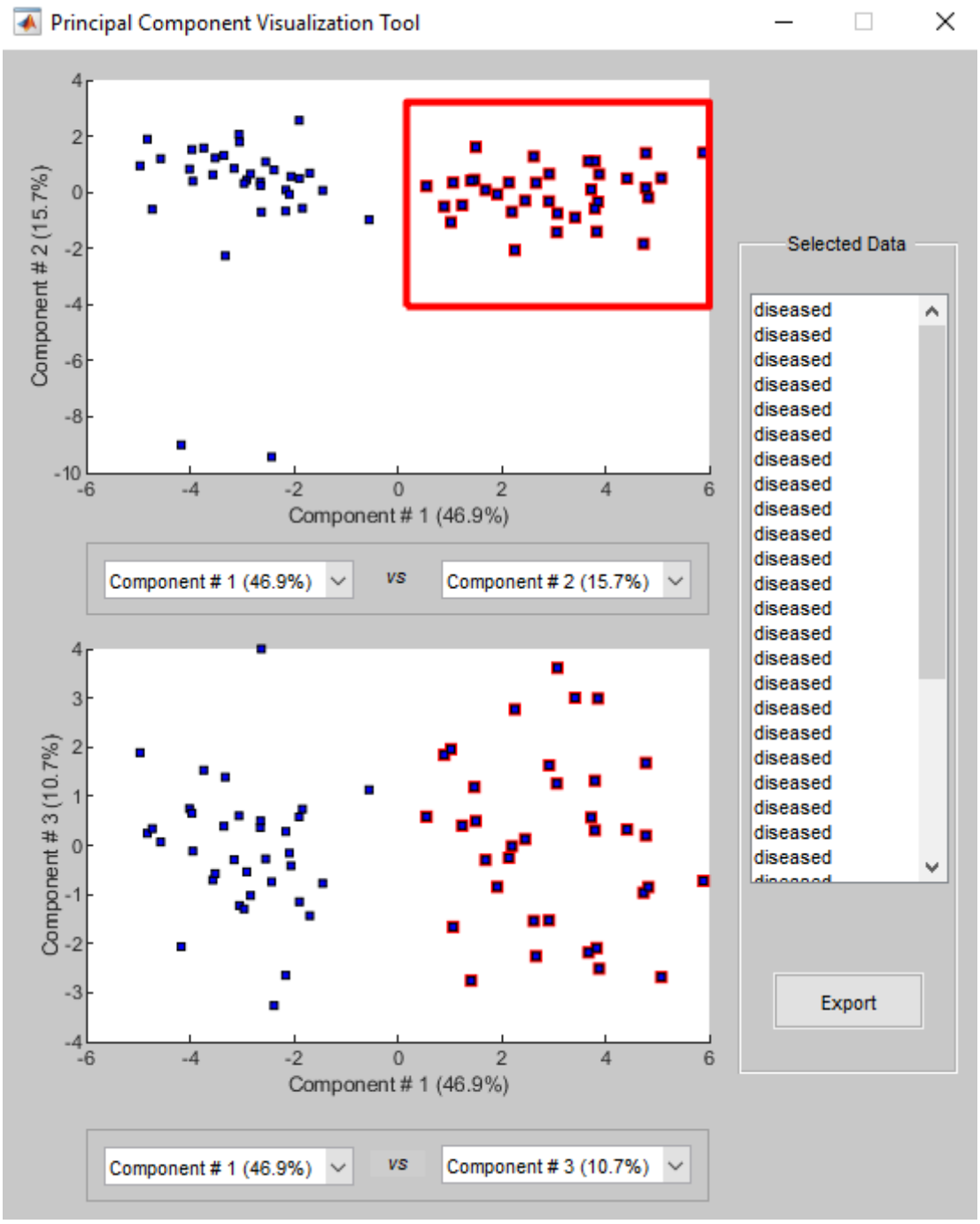
```
cluster_2 = 35×1 cell array
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'diseased'}
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
    {'healthy' }
```

```
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
{'healthy' }
```

Answer: The patients cluster based on health status (for the most part).

Visualizing data in lower dimension using PCA

```
% Visualize miRNA data in component space (use patient health status for labeling)
mapcaplot(miRNA_data,health_stat)
```



Answer: There seems to be two distinct clusters with two outliers. PC1 and PC2 account for 62.6% of the variance.

Answer: Yes, it seems like the clusters we see from PCA match with our results from k-means clustering.

```
% Determine coefficient matrix using PCA
[coeff,scores] = pca(miRNA_data);
% Create table of genes matched to coefficients of best PC
pc1_coeff = coeff(:,1);
table(genes',pc1_coeff)
```

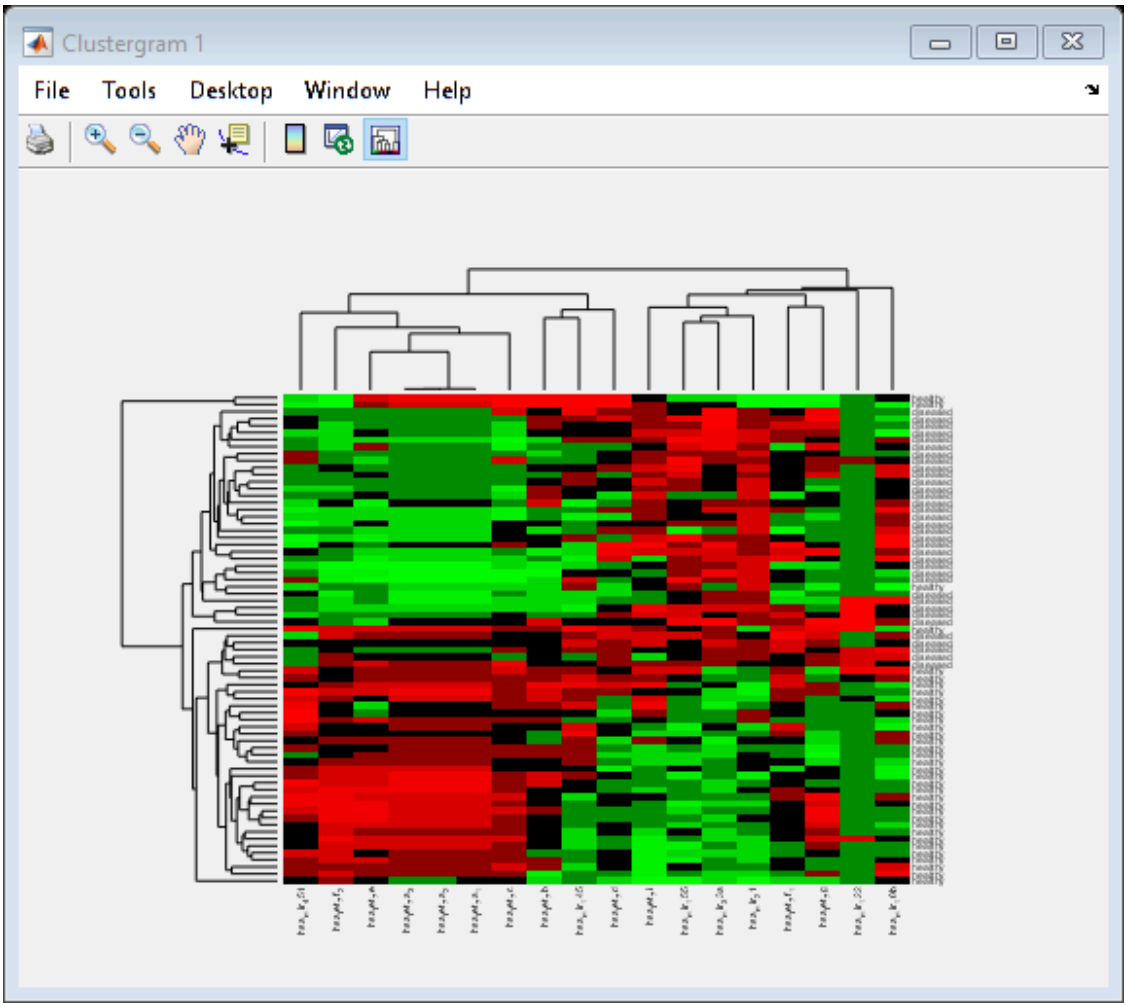
```
ans = 18×2 table
```

	Var1	pc1_coeff
1	'hsa_let_...	-0.2578
2	'hsa_let_...	-0.2587
3	'hsa_let_...	-0.2564
4	'hsa_let_7b'	-0.1416
5	'hsa_let_7c'	-0.3000
6	'hsa_let_7d'	0.0070
7	'hsa_let_7e'	-0.2214
8	'hsa_let_...	0.0300
9	'hsa_let_...	-0.2845
10	'hsa_let_7g'	0.0058

⋮

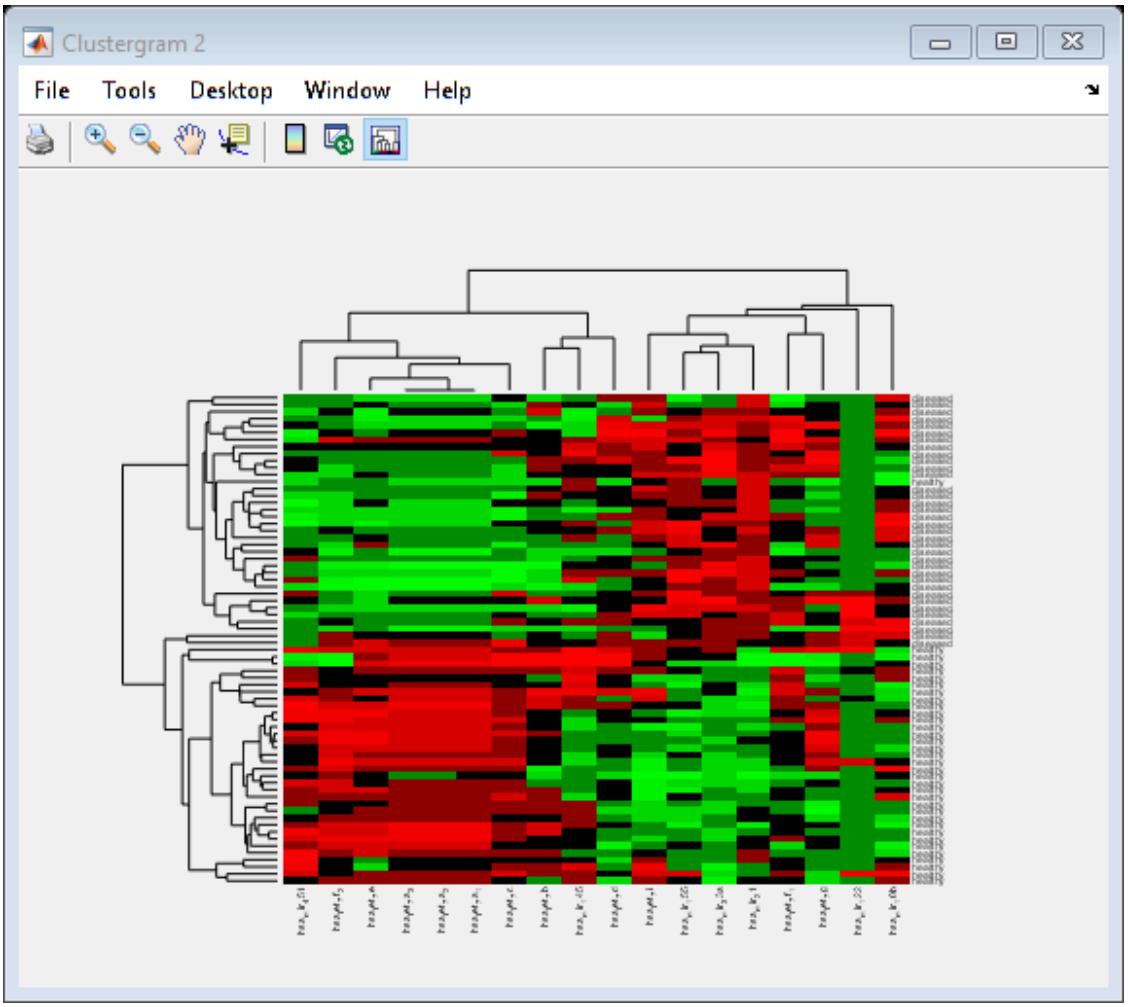
Identifying disease using HC

```
% Create clustergram (label rows, label columns, and standardize by
% columns)
miRNA_cg = clustergram(miRNA_data,...
    'RowLabels',health_stat,...
    'ColumnLabels',genes,...
    'Standardize','column');
```



Answer: It seems that the outliers were picked out at the edges, but the two clusters we've seen before are not clearly separated.

```
% Clustergram with redbluecmap
miRNA_cg_corr_rbc = clustergram(miRNA_data,...
    'RowLabels',health_stat,...
    'ColumnLabels',genes,...
    'Standardize','column',...
    'RowPDist','correlation',...
    'ColumnPDist','correlation');
```



Answer: As opposed to before, this clustergram better separates patients according to their health status. This matches closer to our previous results from KMC and PCA.

Answer: Some signature miRNAs might be miR-451, *Let*-7, miR-155, miR-33, and miR-21. Refer to associated disease in signature miRNA table for potential disease that could be represented.