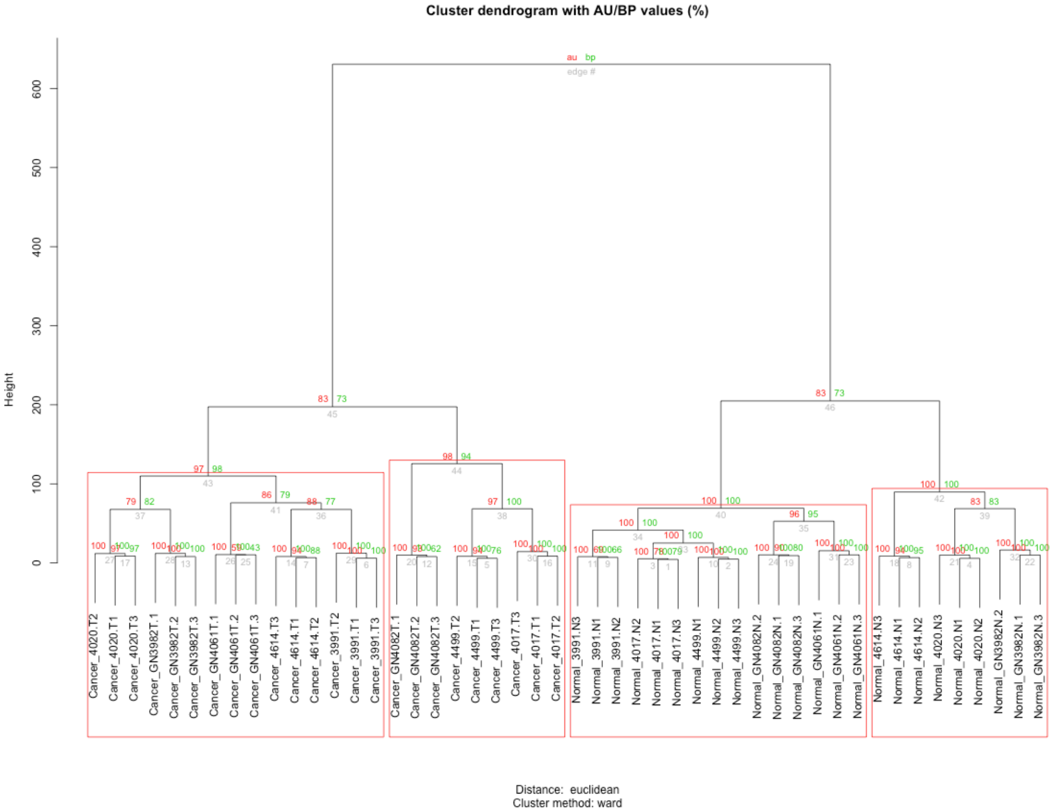
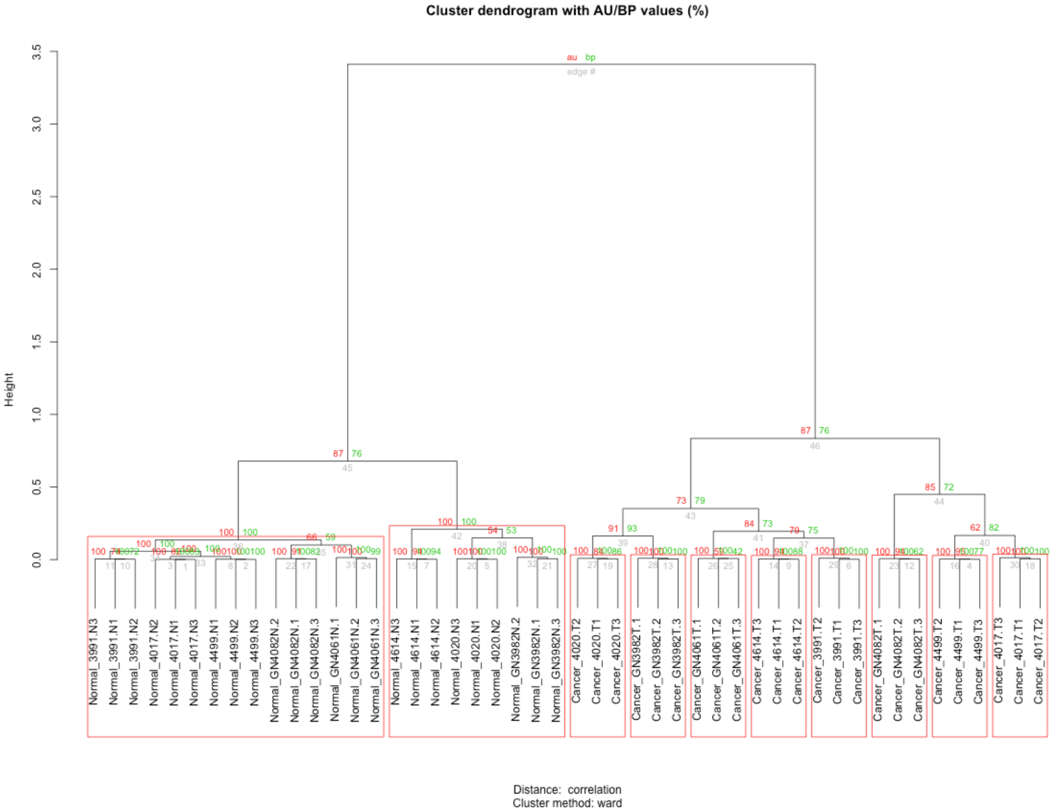
Hierarchical clustering analysis of tissues based on their global protein profiles

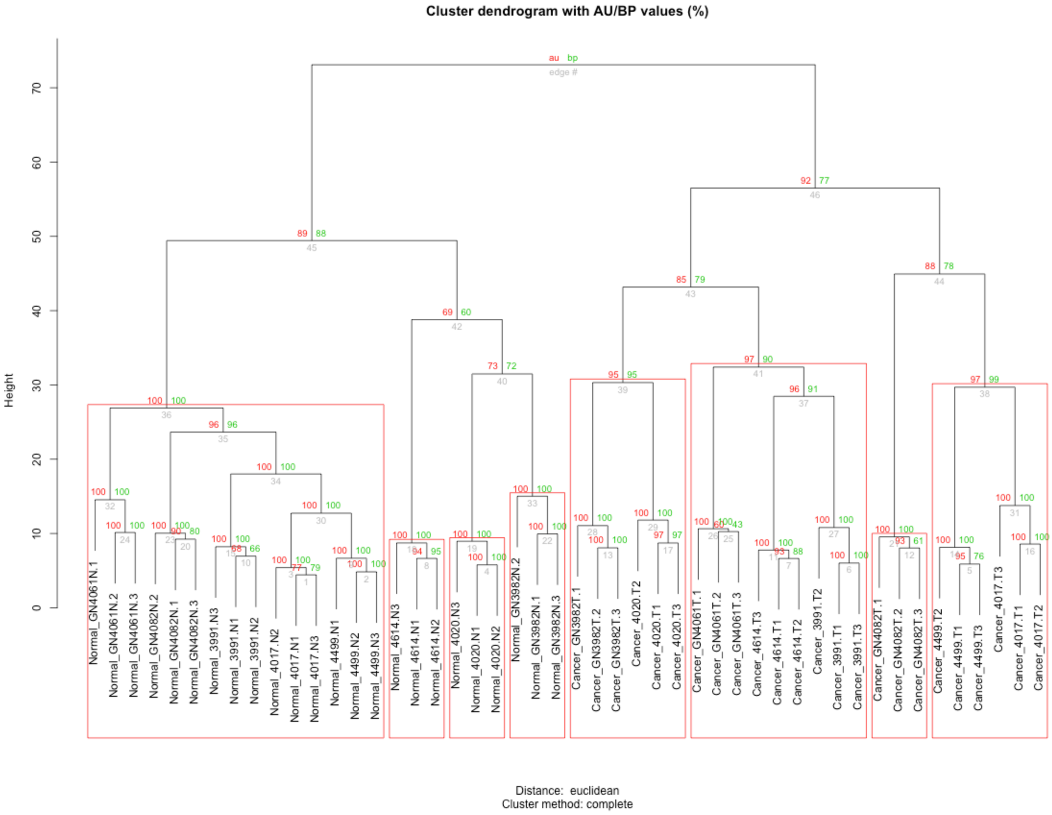
A)



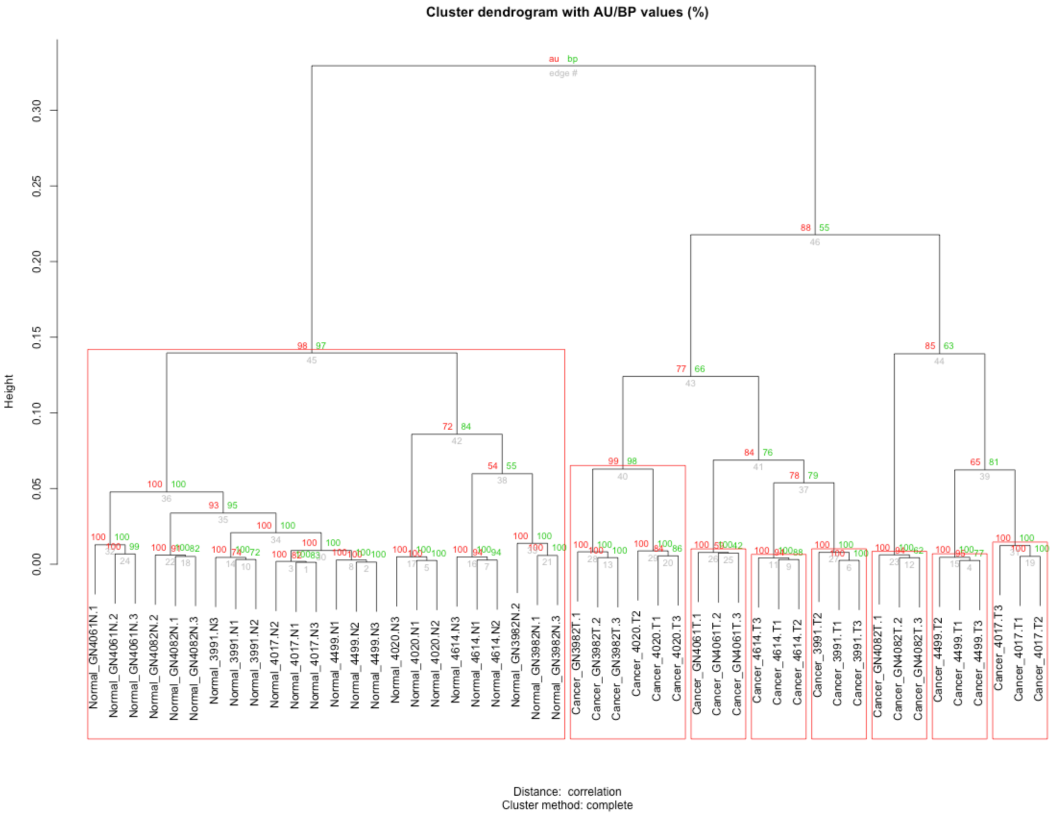
B)


Cluster dendrogram with AU/BP values (%)
Height
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
au
bp
edge #
87
76
45
87
76
46
73
79
43
85
72
44
91
93
39
84
73
41
62
82
40
100
100
66
59
54
53
Normal_3991.N3
Normal_3991.N1
Normal_3991.N2
Normal_4017.N2
Normal_4017.N1
Normal_4017.N3
Normal_4499.N1
Normal_4499.N2
Normal_4499.N3
Normal_GN4082N.2
Normal_GN4082N.1
Normal_GN4082N.3
Normal_GN4061N.1
Normal_GN4061N.2
Normal_GN4061N.3
Normal_4614.N3
Normal_4614.N1
Normal_4614.N2
Normal_4020.N3
Normal_4020.N1
Normal_4020.N2
Normal_GN3982N.2
Normal_GN3982N.1
Normal_GN3982N.3
Cancer_4020.T2
Cancer_4020.T1
Cancer_4020.T3
Cancer_GN3982T.1
Cancer_GN3982T.2
Cancer_GN3982T.3
Cancer_GN4061T.1
Cancer_GN4061T.2
Cancer_GN4061T.3
Cancer_4614.T3
Cancer_4614.T1
Cancer_4614.T2
Cancer_3991.T2
Cancer_3991.T1
Cancer_3991.T3
Cancer_GN4082T.1
Cancer_GN4082T.2
Cancer_GN4082T.3
Cancer_4499.T2
Cancer_4499.T1
Cancer_4499.T3
Cancer_4017.T3
Cancer_4017.T1
Cancer_4017.T2
Distance: correlation
Cluster method: ward

C)


Cluster dendrogram with AU/BP values (%)
Height
0
10
20
30
40
50
60
70
au
bp
edge #
89
88
45
92
77
46
100
100
36
69
60
42
85
79
43
88
78
44
96
96
35
73
72
40
95
95
39
97
90
41
97
99
38
100
100
34
96
91
37
Normal_GN4061N.1
Normal_GN4061N.2
Normal_GN4061N.3
Normal_GN4082N.2
Normal_GN4082N.1
Normal_GN4082N.3
Normal_3991.N3
Normal_3991.N1
Normal_3991.N2
Normal_4017.N2
Normal_4017.N1
Normal_4017.N3
Normal_4499.N1
Normal_4499.N2
Normal_4499.N3
Normal_4614.N3
Normal_4614.N1
Normal_4614.N2
Normal_4020.N3
Normal_4020.N1
Normal_4020.N2
Normal_GN3982N.2
Normal_GN3982N.1
Normal_GN3982N.3
Cancer_GN3982T.1
Cancer_GN3982T.2
Cancer_GN3982T.3
Cancer_4020.T2
Cancer_4020.T1
Cancer_4020.T3
Cancer_GN4061T.1
Cancer_GN4061T.2
Cancer_GN4061T.3
Cancer_4614.T3
Cancer_4614.T1
Cancer_4614.T2
Cancer_3991.T2
Cancer_3991.T1
Cancer_3991.T3
Cancer_GN4082T.1
Cancer_GN4082T.2
Cancer_GN4082T.3
Cancer_4499.T2
Cancer_4499.T1
Cancer_4499.T3
Cancer_4017.T3
Cancer_4017.T1
Cancer_4017.T2
Distance: euclidean
Cluster method: complete

D)



Supplementary Figure 1: Hierarchical clustering analysis dendrograms of cancer and non-cancer renal tissue samples based on their global protein abundance levels.
The analysis was performed using R package ‘pvclust’ (http://www.is.titech.ac.jp/~shimo/prog/pvclust). To estimate p-values for the clusters, 100,000 bootstrap resampling were used to cluster the dataset iteratively. Each cluster shows two types of p-values in percentage scale: AU (Approximately Unbiased) in red and BP (Bootstrap Probability) in green. Clusters with AU larger than 95% are highlighted by rectangles, which are strongly supported by data with significance level of 0.05. The clustering was performed using Pearson’s correlation or Euclidean distance metrics and complete linkage or Ward agglomeration methods.

A) Hierarchical clustering of samples using Euclidean distance and Ward agglomeration method
B) Hierarchical clustering of samples using correlation distance and Ward agglomeration method
C) Hierarchical clustering of samples using Euclidean distance and complete linkage agglomeration method
D) Hierarchical clustering of samples using correlation distance and complete linkage agglomeration method