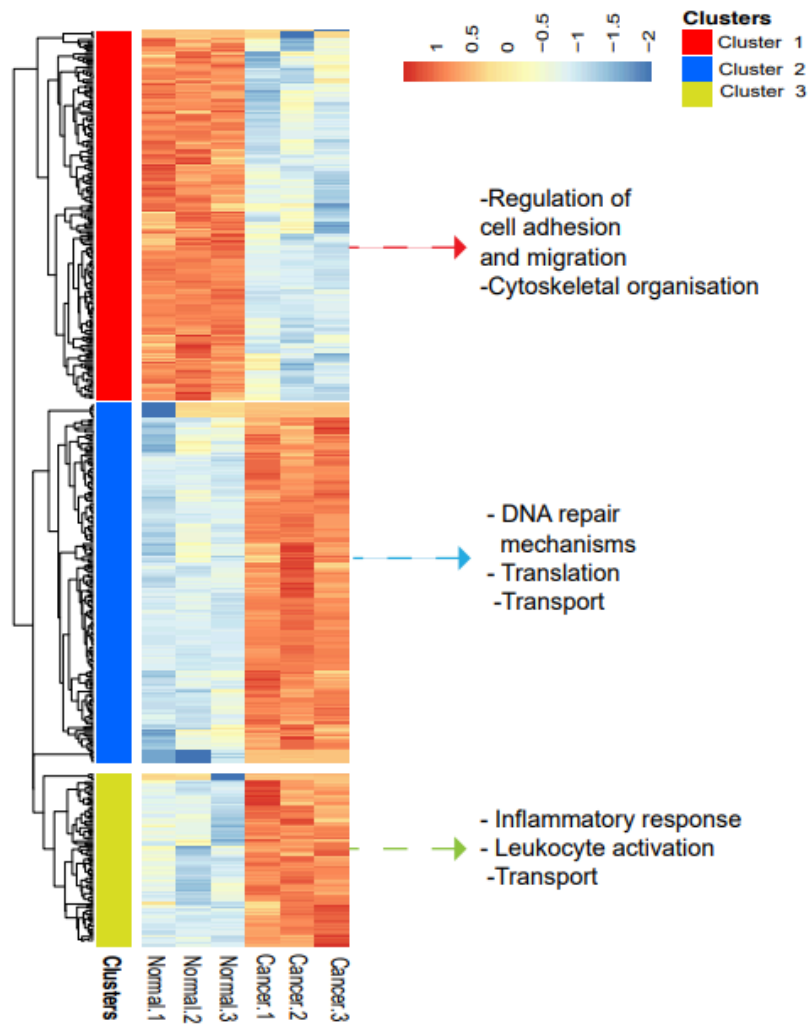
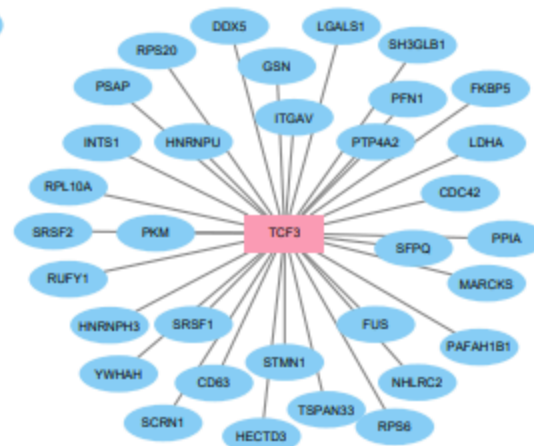
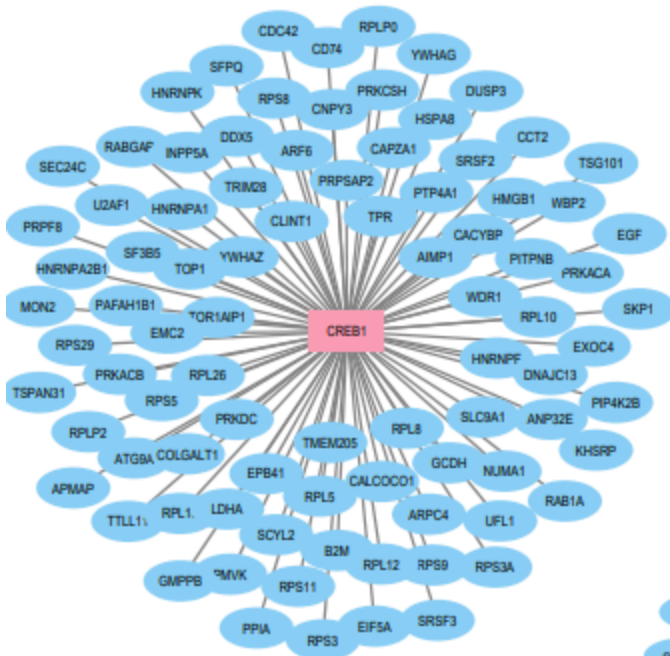
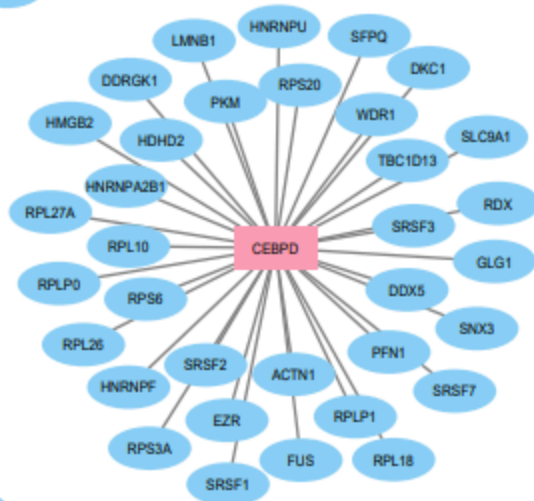
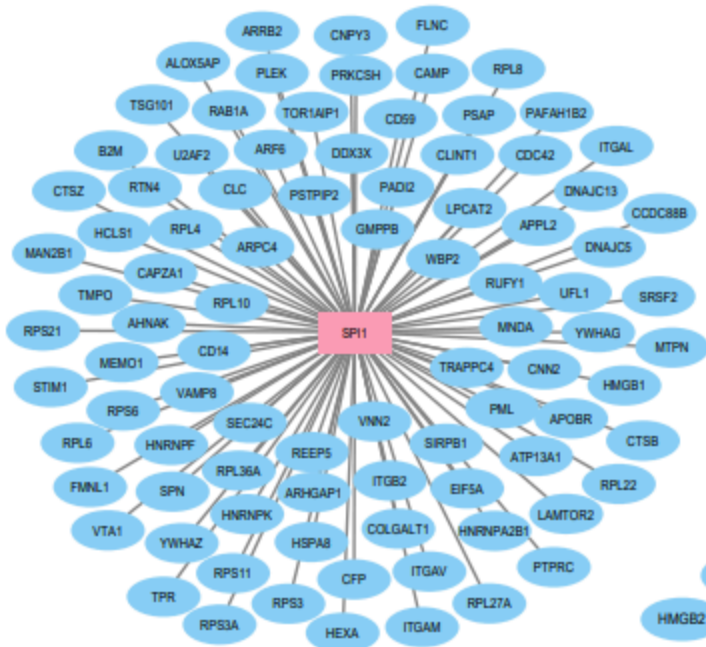
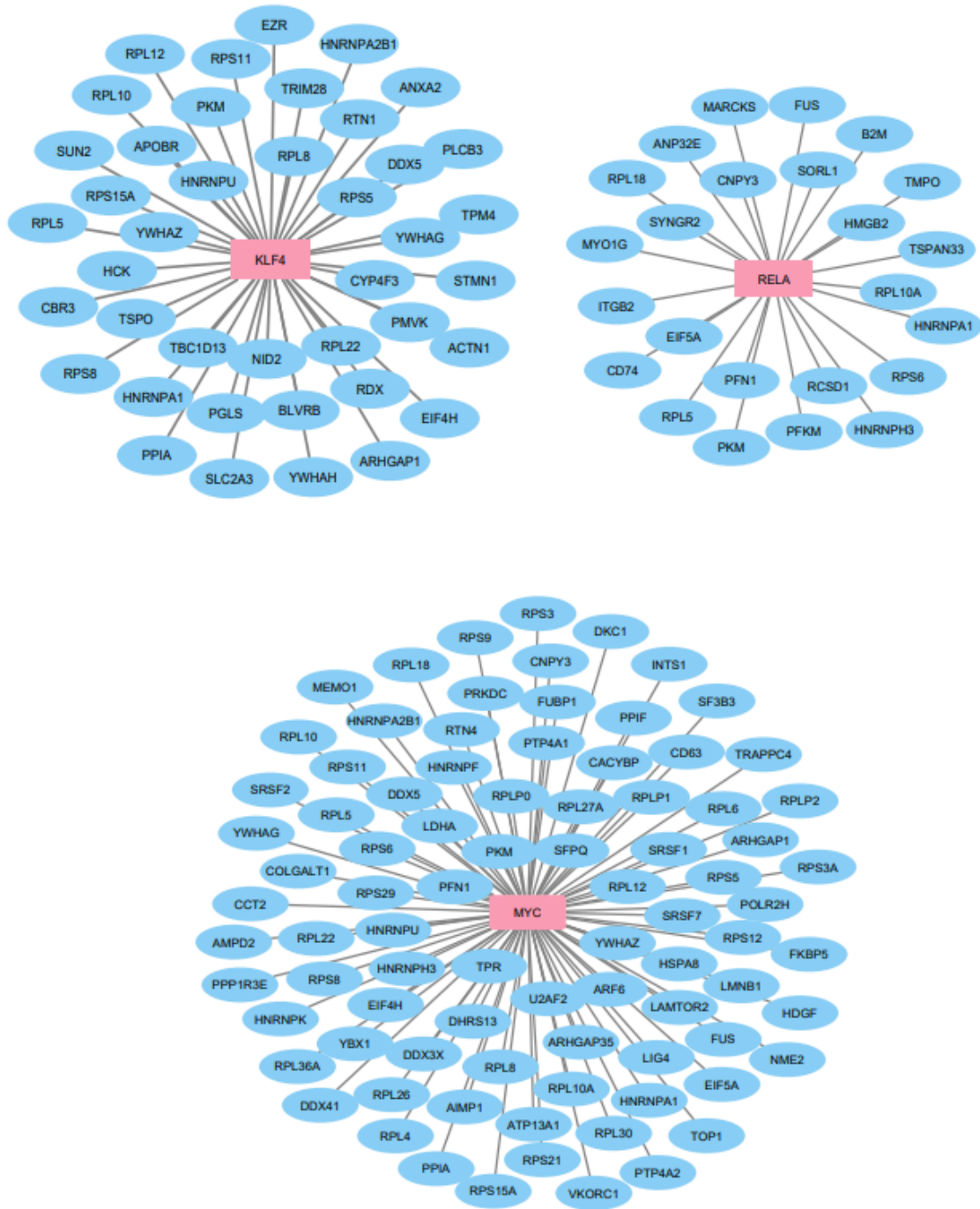


Supplementary figure S1: The principal component analysis of the proteins identified from the cancer-control samples using DIA-MS method for quantitative proteomic analysis.



Supplementary figure S2: The cluster map depicting the hierarchical clustering of differentially expressed proteins and their associated biological process and pathways.





Supplementary figure S3 : The figure illustrates potential transcription factors enriched from differentially expressed proteins and their corresponding protein targets. The transcription factor is depicted in the center, surrounded by its associated protein targets.