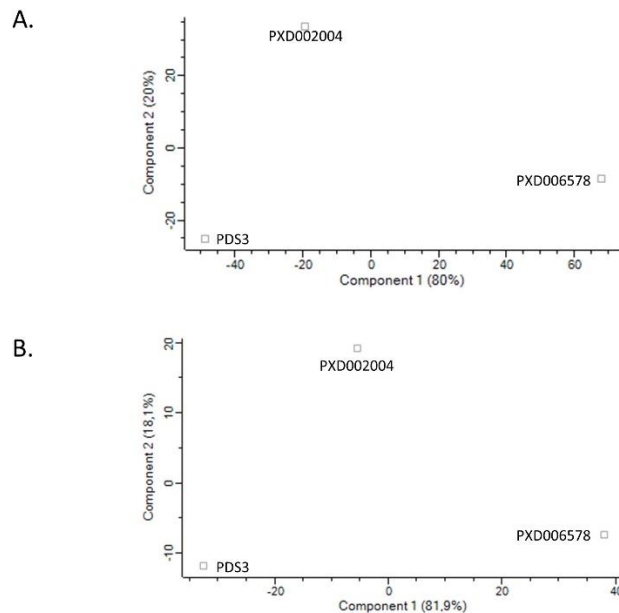


# Integrative analysis of multi-omics data to identify deregulated molecular pathways and druggable targets in Chronic Lymphocytic Leukemia

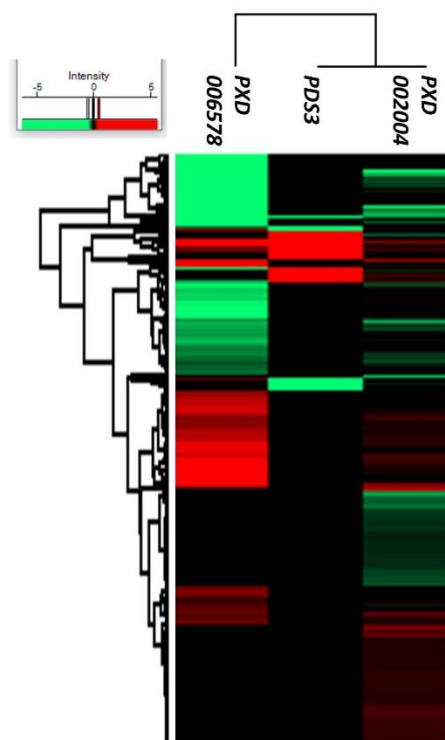
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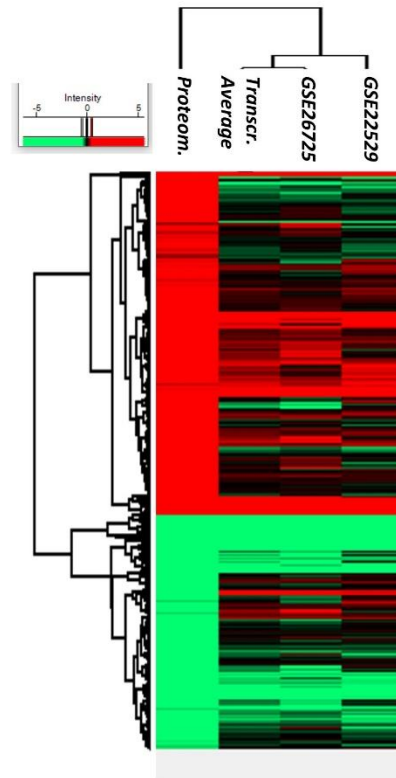
**Supplemental Figure S1:** PCA of the three proteomic datasets (A) in all the proteins identified and (B) in the common differentially expressed proteins. It is observed that no one dataset is particularly related to another one both in the total proteins identified and in the common differentially expressed proteins, each dataset has a distinct profile showing the importance of each dataset in the holistic unbiased approach to proteomics. As it makes sense in common differentially expressed proteins the datasets become more relevant.

## Supplementary Figures



**Supplemental Figure S2:** Heatmap of the total proteins identified in the three datasets. Not all proteins were detected in all datasets and there are some proteins that do not be expressed in the same way in all studies.

## Supplementary Figures



**Supplemental Figure S3:** Heatmap of the common identifiers between the transcriptomic datasets and the means of common differentially expressed proteins. Another diagram that visualizes once again the different regulation of genetic information between proteomics and transcriptomics.