

Article

Proteomic-Based Analysis of Hypoxia- and Physioxia-Responsive Proteins and Pathways in Diffuse Large B-Cell Lymphoma

Kamila Duś-Szachniewicz , Katarzyna Gdesz- Birula , Krzysztof Zduniak , and Jacek R. Wiśniewski

Supplementary Figures

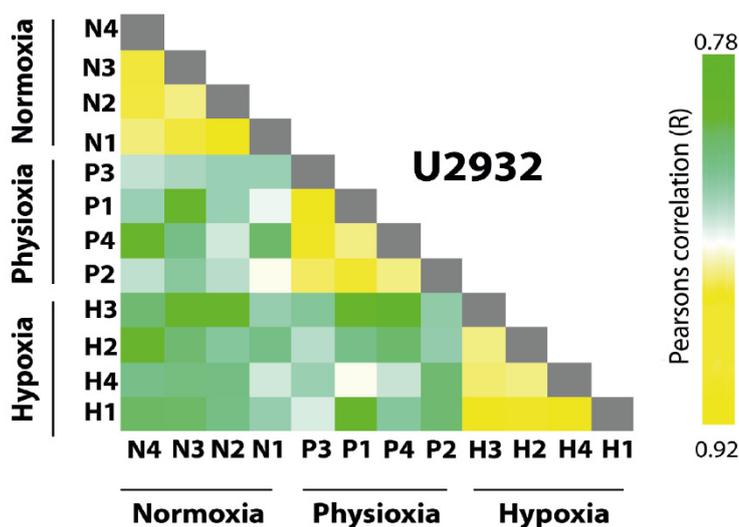


Figure S1. The heatmaps of the correlation coefficients of protein intensities after normalization showing reproducibility between biological replicates of U2932 proteomes under hypoxia (H, 1% of O₂), physioxia (P, 5% of O₂), and normoxia (N, 21% of O₂). Scale bar represents the range of the correlation coefficients (R) displayed. .

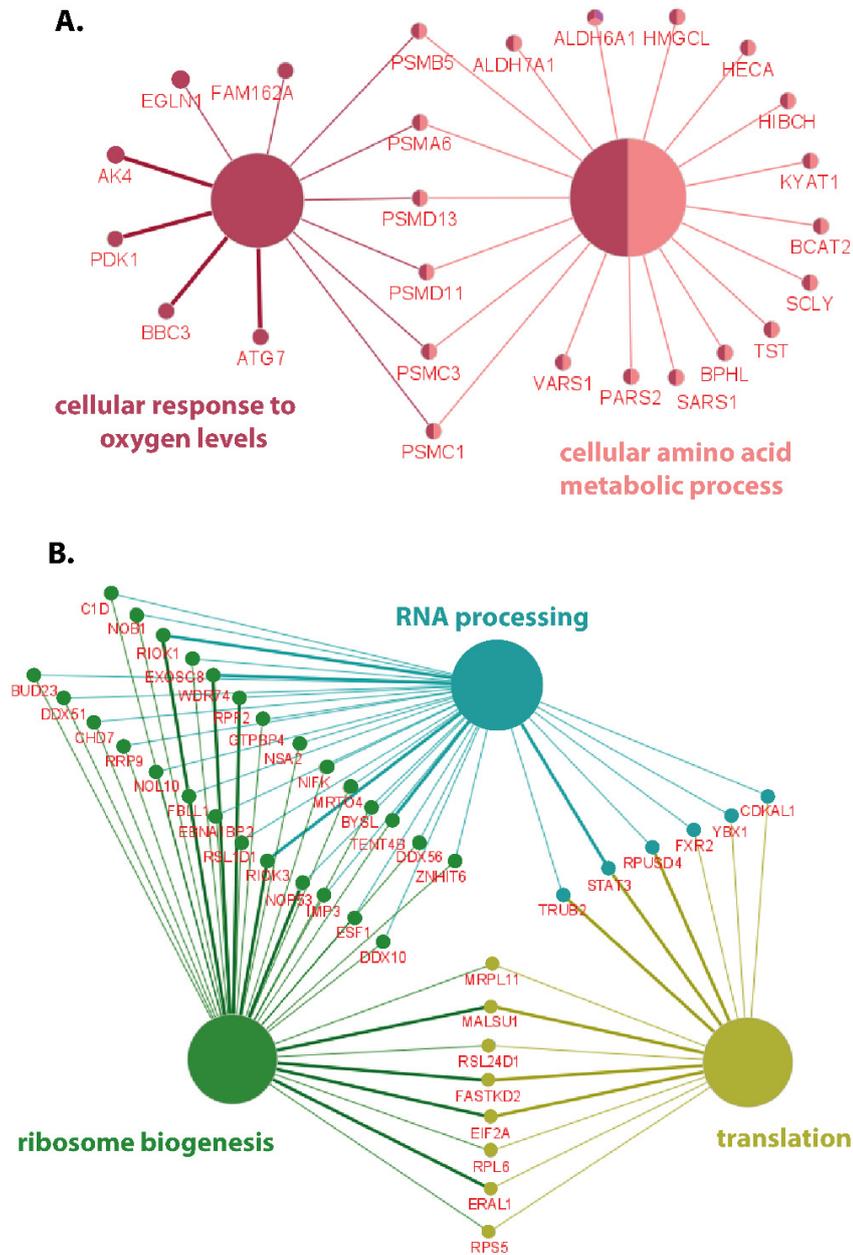


Figure S2. Cytoscape based ClueGo/CluePedia pathway visualization of (A) up-regulated, and (B) down-regulated proteins in Ri-1 cell line. Enriched pathways were obtained from the Gene Ontology- Biological Processes database. The size of the nodes corresponds to the significance of the GO pathway.

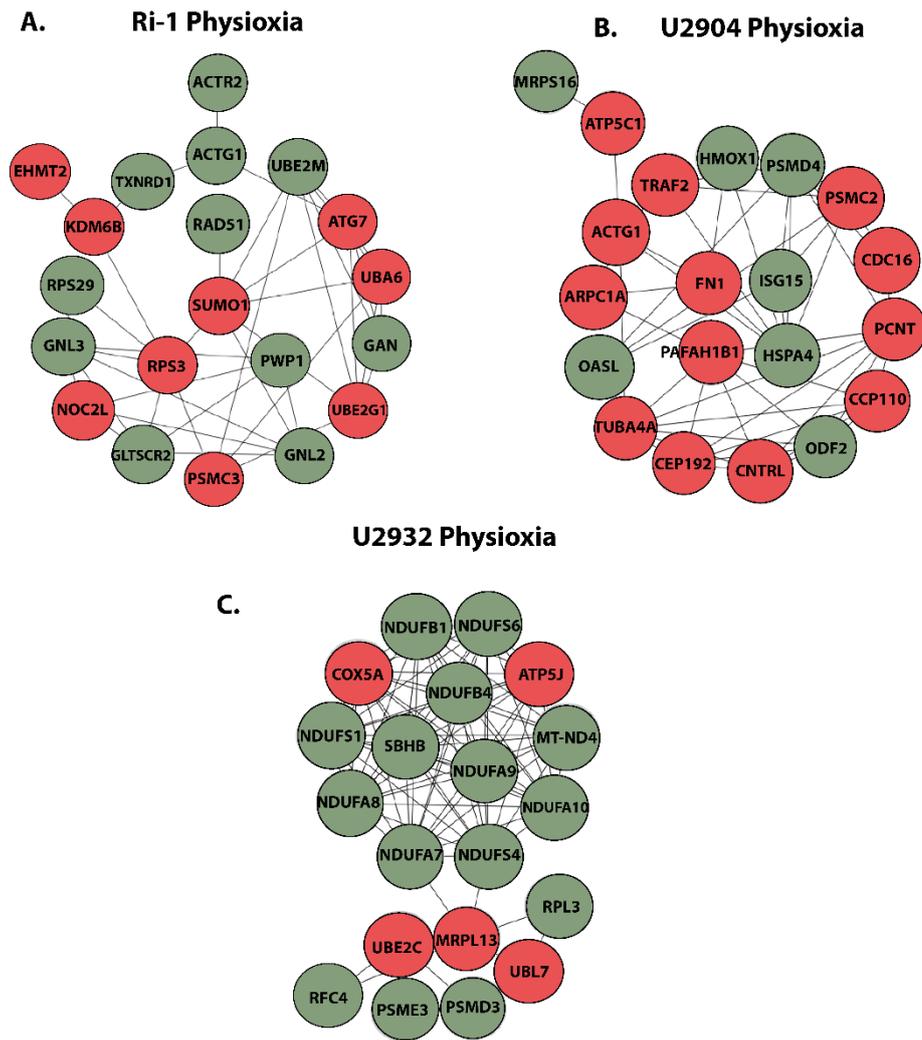


Figure S3. Top 20 hub proteins identified in (A) Ri-1, (B) U2904, and (C) U2932 cell lines under physioxia (5% O₂) based on the highest Degree score. Analyzed and generated by cytoHubba App of Cytoscape. Red and green nodes represent up- and down-regulated proteins, respectively.