Comparative proteomic profiling of Hodgkin lymphoma cell lines

Supplementary Table 1. List of antibodies used in western blotting and flow-cytometry.		
Western blotting		
Antibody name	**Company**	**Dilution**
Anti-Cofilin	Santa Cruz Biotechnology (sc-33779)	1:1000
Anti-phospho Cofilin (ser3)	Santa Cruz Biotechnology (sc-21867-R)	1:1000
Anti-Ezrin	Santa Cruz Biotechnology (sc-20773)	1:1000
Anti-phospho Ezrin (Tyr354)	Santa Cruz Biotechnology (sc-101678)	1:500
Anti-LDHB	Santa Cruz Biotechnology (sc-133731)	1:1000
Anti-Monocarboxylate transporter 1	Abcam (NBP2-17242)	1:2000
Anti-HSP70	Sigma (H51747)	1:2000
Anti-Peroxiredoxin 1	Santa Cruz Biotechnology (sc-7381)	1:1000
Anti-Peroxiredoxin 2	Santa Cruz Biotechnology (sc-33572)	1:1000
Anti-Peroxiredoxin 6	Santa Cruz Biotechnology (sc-393024)	1:1000
Anti-Rock	Santa Cruz Biotechnology (sc-5560)	1:1000
Anti-Src	Cell Signaling (2110)	1:1000
Anti-α Tubulin	Santa Cruz Biotechnology (sc-23948)	1:2000
Flow cytometry		
Antibody name	**Company**	**Dilution**
Anti-CD19-FITC	BD Biosciences (clone SJ25C1)	1:5
Anti-CD20-FITC	BD Biosciences (clone L27)	1:5
Anti-CD25-APC	BD Biosciences (clone 2A3)	1:20
Anti-CD32-APC	BD Biosciences (clone FLI8.26)	1:5
Anti-CD38-FITC	BD Biosciences (clone HB7)	1:5
Anti-CD44-APC	BD Biosciences (clone G44-26)	1:5
Anti-CD44v6-APC	R&D Systems (clone 2F10)	1:10
Anti-CD58-APC	Miltenyi Biotec (clone TS2/9)	1:11
Anti-CD90-FITC	BD Biosciences (clone 5E10)	1:5
Anti-CD99-FITC	BD Biosciences (clone TÜ12)	1:5
Anti-CD123-FITC	BD Biosciences (clone 7G3)	1:5

Supplementary Table 2. Node Explorer by NetworkAnalyst.

UNIPROT ID	Name	Degree	Betweeness
P19338	Nucleolin (NCL)	51	1534.81
P15311	Ezrin (EZR)	27	1061.51
P08865	40S ribosomal protein SA (RPSA)	36	1040.16
P63104	14-3-3 protein zeta/delta (YWHAZ)	27	979.04
P07237	Protein disulfide-isomerase (P4HB)	30	923.53
P13639	Elongation factor 2 (EEF2)	41	901.19

NOTE: highly interconnected hub nodes are shown. NetworkAnalyst provides two widely used topological measures—degree and betweenness centrality. The degree of a node is the number of connections it has to other nodes. The betweenness centrality measures number of shortest paths going through the node.

Supplementary Figure 1. Graphical representation of the experimental workflow. The overall process consists of a number of steps, which include protein separation by 2-DE, identification by MS/MS, and analysis by flow cytometry. Data were processed by bioinformatics tools to identify significant enriched pathways or networks.

Supplementary Figure 2. Proteasome KEGG pathway map. List of identified members include: Proteasome subunit beta type-3 (PSB3), Proteasome activator complex subunit 2

(PSME2), Proteasome subunit beta type-2 (PSB2), Proteasome subunit beta type-8 (PSB8), and 26S proteasome regulatory subunit 7 (PRS7).

Supplementary Figure 3. Hematopoietic cell lineage KEGG pathway map. List of identified members include: CD19 molecule, CD38 molecule, CD44 molecule, CD25 molecule (interleukin 2 receptor, alpha), CD123 molecule (interleukin 3 receptor, alpha), CD20 molecule (membrane-spanning 4-domains, subfamily A, member 1).

Supplementary Figure 4. NetworkAnalyst network of differentially expressed proteins. a) Main hub nodes are highlighted. b) A zoom in of the ezrin node is shown.