Nurul F Jufri et al., J Proteomics Bioinform 2014, 7:8
http://dx.doi.org/10.4172/0974-276X.S1.074

OMICS Group Conferences
Accelerating Scientific Discovery

4th International Conference on
Proteomics & Bioinformatics
August 04-06, 2014 Hilton-Chicago/Northbrook, Chicago, USA

Excessive magnitude of tensile stretch revealed stress effect to endothelial cell

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Chronic lymphocytic leukaemia (CLL) is incurable disease with heterogeneous clinical outcomes. Identification of proteins expressed in CLL cells has the potential to better our understanding of the disease. A cellular fractionation method was developed to extract cytosolic proteins enriched fraction and nuclear proteins enriched fraction (termed NP40 fraction and SDS fraction respectively) from CLL patients samples. Protein fractions were independently subjected to trypsin- digestion followed by separation using two-dimensional nano liquid chromatography (2D nano-LC) and peptide identification by matrix-assisted laser desorption/ionization time of flight tandem mass spectrometry (MALDI TOF/TOF MS). We report the largest and most conserved protein set identified in primary CLL cells; 900 proteins were detected with false discovery rate (FDR) < 1%. Of these proteins 625 were identified using 2 or more different peptides (ion score ≥ 95% C.I.) and 375 proteins were identified based on single peptides (ion score > 99% C.I.). From the NP40 fractions 729 proteins were detected and 326 proteins were identified in the SDS fractions; 221 proteins were common in both fractions. Protein localisation analysis using Gene Ontology data and Quick GO-EBI tool showed that 50% of the proteins found in the NP40 fractions was cytosolic proteins, while 82% of proteins detected in the SDS fractions was nuclear proteins. This study showed the benefit of proteomics especially when combined with cellular fractionation to identify proteins associated with a disease.

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