Supporting information

Mass Spectrometry-Based Analysis of Rat Liver and Hepatocellular Carcinoma Morris Hepatoma 7777 Plasma Membrane Proteome

Lulu Cao[1], James G. Clifton[3], Werner Reutter[4], Djuro Josic[2,5]*

[1]Proteomics Core, COBRE Center for Cancer Research Development, Rhode Island Hospital, Providence, RI 02903 USA

[2]Department of Medicine, Warren Alpert Medical School, Brown University, Providence, RI 02903, USA

[3]Department of Molecular Pharmacology, Physiology and Biotechnology, Brown University, Providence, RI 02903, USA

[4]Institut für Laboratoriumsmedizin und Klinische Chemie, Charité- Universitätsmedizin Campus Benjamin Franklin, D-14195 Berlin, Germany

[5]Department of Biotechnology, University of Rijeka, HR-51000 Rijeka, Croatia

*Corresponding author: Djuro_Josic@brown.edu, djosic@biotech.uniri.hr

TABLE OF CONTENTS

I. Figure S1: Distribution of GRAVY scores versus molecular weight (MW) of proteins identified from normal rat liver and Morris hepatoma 7777 plasma membranes using different treatments.

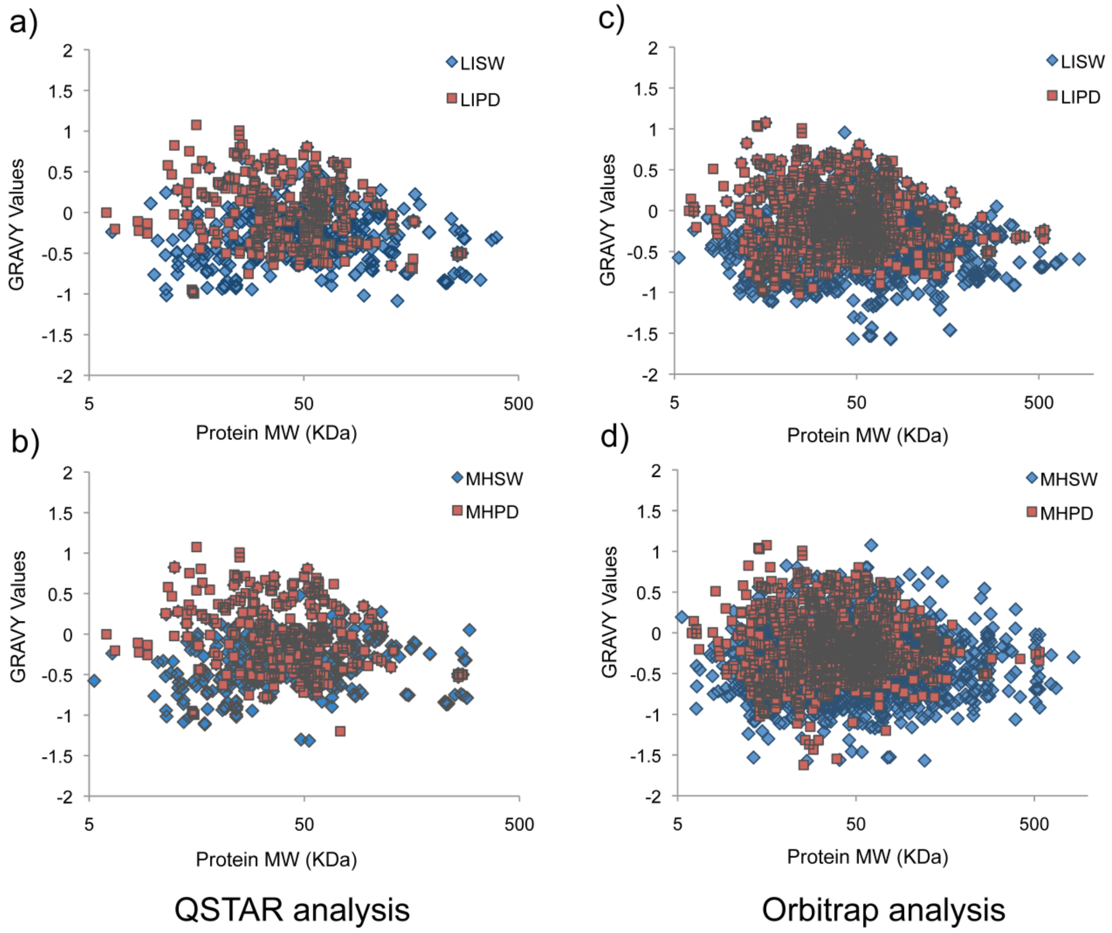

Figure S1. Distribution of GRAVY scores versus molecular weight (MW) of proteins identified from normal rat liver and Morris hepatoma 7777 plasma membranes using different treatments. The grand average hydrophobicity (GRAVY) values were calculated for each identified protein as the arithmetic mean of the sum of the hydropathy values of all the amino acids in a protein sequence. Proteins with positive GRAVY values are considered to be hydrophobic, and those with negative values, hydrophilic. Both data acquired by a QSTAR XL mass spectrometer (left) and an Orbitrap Velos mass spectometer (right) are shown for comparison. Comparisons of distribution of GRAVY scores are represented for a) c) LISW and LIPD, b) d) MHSW and MHPD.