Data in Brief 5 (2015) 226–240

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Dataset for the quantitative proteomics analysis of the primary hepatocellular carcinoma with single and multiple lesions

Xiaohua Xing [a,b], Yao Huang [c], Sen Wang [a,b], Minhui Chi [a,b,c], Yongyi Zeng [a,b,c], Lihong Chen [a,b,c], Ling Li [a,b,c], Jinhua Zeng [a,b,c], Minjie Lin [a,b], Xiao Han [d], Jingfeng Liu [a,b,c], Xiaolong Liu [a,b,*]

[a] The Liver Center of Fujian Province, Fujian Medical University, Fuzhou 350025, People's Republic of China
[b] The United Innovation of Mengchao Hepatobiliary Technology Key Laboratory of Fujian Province, Mengchao Hepatobiliary Hospital of Fujian Medical University, Fuzhou 350025, People's Republic of China
[c] Liver Disease Center, The First Affiliated Hospital of Fujian Medical University, Fuzhou 350007, People's Republic of China
[d] Biotechnology Research Institute, Chinese Academy of Agricultural Sciences, Beijing 100081, People's Republic of China

ARTICLE INFO

Article history:
Received 18 August 2015
Received in revised form
27 August 2015
Accepted 28 August 2015
Available online 8 September 2015

ABSTRACT

Hepatocellular Carcinoma (HCC) is one of the most common malignant tumor, which is causing the second leading cancer-related death worldwide. The tumor tissues and the adjacent noncancerous tissues obtained from HCC patients with single and multiple lesions were quantified using iTRAQ. A total of 5513 proteins (FDR of 1%) were identified which correspond to roughly 27% of the total liver proteome. And 107 and 330 proteins were dysregulated in HCC tissue with multiple lesions (MC group) and HCC tissue with a single lesion (SC group), compared with their noncancerous tissue (MN and SN group) respectively. Bioinformatics analysis (GO, KEGG and IPA) allowed these data to be organized into distinct categories. The data accompanying the manuscript on this approach (Xing et al., J. Proteomics (2015), http://dx.doi.org/10.1016/j.jprot.2015.08.007 [1]) have been deposited to the iProX with identifier IPX00037601.

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2015.08.007
* Correspondence to: The Liver Center of Fujian Province, Fujian Medical University, Fuzhou 350025, People's Republic of China.
E-mail address: xiaoloong.liu@gmail.com (X. Liu).

http://dx.doi.org/10.1016/j.dib.2015.08.036

Specifications table

Subject area	Biology
More specific subject area	Proteomics on the Hepatocellular Carcinoma
Type of data	List of identified proteins as tables (.xls), raw data in website
How data was acquired	The data was acquired by Liquid chromatography mass spectrometry in tandem (LC–MS/MS).The samples were separated by a Acquity UPLC system (Waters Corporation, Milford, MA) and detected by a Nano-Aquity UPLC system (Waters Corporation, Milford, MA) connected to a quadrupole-Orbitrap mass spectrometer (Q-Exactive) (Thermo Fisher Scientific, Bremen, Germany).
Data format	Filtered and analyzed
Experimental factors	Non-applied
Experimental features	Proteins were extracted from tumor tissues of HCC patients with single and multiple lesions, iTRAQ labeled and then prepared for liquid chromatography-mass spectrometry (LC–MS/MS) analysis.
Data source location	Fuzhou, China, Mengchao Hepatobiliary Hospital of Fujian Medical University
Data accessibility	Filtered and analyzed data are supplied here and raw data have also been deposited to the integrated Proteome resources (iProX) with identifier IPX00037601 (http://www.iprox.org/index).

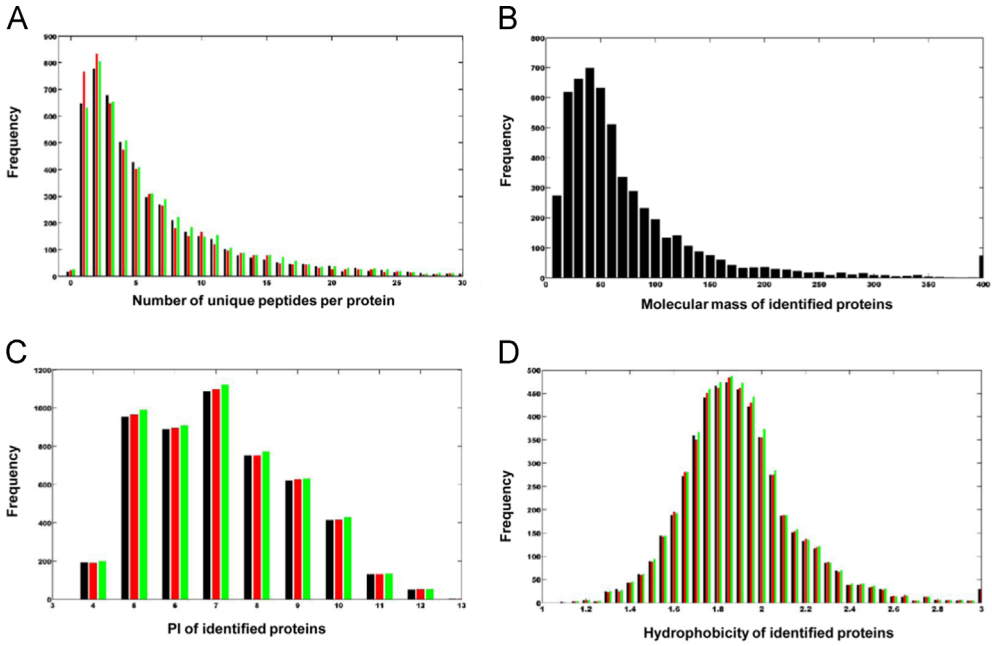

Fig. 1. The qualities of the proteome dataset. (A) Frequency distribution of the identified proteins with ≥ 1 unique peptides. (B) Molecular weight distribution of identified proteins proved that there is no bias in the protein extraction process. (C) Isoelectric point distribution of the identified proteins to show the unbias of the protein extraction. (D) Protein hydrophobicity distribution of the identified proteins.