Data in Brief 10 (2017) 248–263

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Dataset of proteins mapped on HepG2 cells and those differentially abundant after expression of the dengue non-structural 1 protein

Kíssila Rabelo [a,1], Monique R.O. Trugilho [b,1,2], Simone M. Costa [a], André T.S. Ferreira [b], Paulo C. Carvalho [c], Jonas Perales [b], Ada M.B. Alves [a,*]

[a] Laboratory of Biotechnology and Physiology of Viral Infections, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil
[b] Laboratory of Toxinology, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil
[c] Laboratory for Proteomics and Protein Engineering, Carlos Chagas Institute, Fiocruz, Paraná, Brazil

ARTICLE INFO

Article history:
Received 3 November 2016
Received in revised form
17 November 2016
Accepted 23 November 2016
Available online 6 December 2016

Keywords:
Mass spectrometry
NS1
DENV
HepG2 cells

ABSTRACT

The data supplied in this article are related to the research article entitled "The effect of the dengue non-structural 1 protein expression over the HepG2 cell proteins in a proteomic approach" (K. Rabelo, M.R. Trugillo, S.M. Costa, B.A. Pereira, O.C. Moreira, A.T. Ferreira et al., 2016) [1]. The present article provides the inventory of peptides and proteins mapped in a hepatocyte cell line (HepG2) by mass spectrometry in the presence of the non-structural protein 1 (NS1) of Dengue 2 virus (DENV2). Cells were transfected with pcENS1 plasmid, which encodes the DENV2 NS1 protein, or the controls pcDNA3 (negative control) or pMAXGFP, encoding the

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2016.11.001
* Corresponding author.
E-mail address: ada@ioc.fiocruz.br (A.M.B. Alves).
[1] Both authors contributed equally to this work.
[2] Current address: Center for Technological Development in Health (CDTS), Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil.

http://dx.doi.org/10.1016/j.dib.2016.11.083

green fluorescent protein (GFP), a protein unrelated to dengue. Differentially abundant protein lists were obtained by comparing cells transfected with pcENS1 and controls.

Specifications Table

Subject area	*Biology*
More specific subject area	*Proteomics, Virology*
Type of data	*Table*
How data was acquired	*Mass spectrometry*
Data format	*Raw and analyzed*
Experimental factors	*HepG2 cells were transfected with plasmids expressing different proteins, lysed, trypsinized and submitted to Orbitrap*
Experimental features	*All samples were analyzed LTQ-Orbitrap XL mass spectrometer*
Data source location	*Oswaldo Cruz Foundation, Brazil*
Data accessibility	*Within this article*

Value of the data

- These data describe the use of quantitative mass spectrometry-based proteomic experiments to assess the biological significance of cell alterations caused by DENV NS1 protein.
- 4756 proteins were mapped and we identify 41 or 81 differentially abundant proteins in the presence of NS1, comparing to controls.
- The data open new perspectives to identify the molecular mechanisms involving DENV NS1 protein in infected cells.

1. Data

HepG2 cells were transfected with the plasmids: pcENS1, pcDNA3 and pMAXGFP. To produce accurate data, we used three independent experimental biological replicates and samples were submitted to LTQ-Orbitrap XL (Thermo Scientific). Data analysis, using the PatternLab for Proteomics software, identified 14,138 peptides which mapped to 4756 proteins, from all conditions (HepG2 transfected with the three different plasmids and non-transfected cells) (Supplementary Table S1a–h). Applying the maximum parsimony principle we found 2314 proteins (Supplementary Table S1g). Using the Tfold module we generate the differential abundance distribution when comparing: non-transfected HepG2 x cell transfected with pcDNA3 (Table 1); HepG2 transfected with pcDNA3 x pcENS1 (Table 2) and cells transfected with pMAGFP x pcENS1 (Table 3)[1].

2. Experimental design, materials and methods

2.1. Cell culture

HepG2 cells (ATCC) were cultivated in Dulbecco's modified Eagle's medium (DMEM) (SIGMA) supplemented with 10% fetal bovine serum (FBS) (Invitrogen). Cells were maintained at 37° C and