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Data Article

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



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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. Trugilho, 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

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

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Specifications Table

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

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

Table 1

List of 54 differentially abundant proteins for statistics between HepG2 x pcDNA3.

Locus	Fold Change	pValue	Signal+ (pcDNA3)	Signal- (HepG2)	Description
splP20674l COX5A_HUMAN	7.52	0.04600	1.29E-03	1.72E-04	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2
splP39656l OST48_HUMAN	6.45	0.00016	9.18E-04	1.42E-04	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4
splQ71UI9IH2AV_HUMAN	4.20	0.02071	5.62E-03	1.34E-03	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3
splP0C0S5IH2AZ_HUMAN	4.18	0.02251	5.58E-03	1.34E-03	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2
splP02768IALBU_HUMAN	3.40	0.01591	6.34E-04	1.87E-04	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
triB4DLR8l B4DLR8_HUMAN	3.32	0.01500	2.00E-03	6.04E-04	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1
splP15559lNQO1_HUMAN	3.27	0.01639	1.45E-03	4.45E-04	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1; triH3BNV2IH3BNV2_HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1
splP13073l COX4I_HUMAN	3.16	0.04534	5.81E-04	1.84E-04	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1; triH3BP0IH3BP0_HUMAN Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment) OS=Homo sapiens GN=COX4I1 PE=1 SV=1
splQ9UBX3lDIC_HUMAN	3.14	0.02829	6.89E-04	2.19E-04	Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2
triG3V576l G3V576_HUMAN	3.13	0.01342	1.92E-03	6.15E-04	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V575lG3V575_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V555lG3V555_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1
splP07910l HNRPC_HUMAN	3.13	0.01342	1.45E-03	4.64E-04	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4
triB4DY08l B4DY08_HUMAN	3.13	0.01342	1.54E-03	4.93E-04	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V4W0lG3V4W0_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V251lG3V251_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V3K6lG3V3K6_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V5X6lG3V5X6_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V4M8lG3V4M8_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1; triG3V2H6lG3V2H6_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=1 SV=1
triG3V2Q1l G3V2Q1_HUMAN	3.13	0.01342	1.46E-03	4.66E-04	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1
triG3V4C1l G3V4C1_HUMAN	3.13	0.01342	1.52E-03	4.87E-04	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=1
splO15173l PGRC2_HUMAN	3.11	0.00180	7.94E-04	2.55E-04	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRC2 PE=1 SV=1

spiP05787IK2C8_HUMAN	3.02	0.01302	8.22E-03	2.72E-03	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7: triF8VUG2IF8VUG2_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens GN=KRT8 PE=1 SV=1: triF8VP67IF8VP67_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens GN=KRT8 PE=1 SV=1: triF8VRG4IF8VRG4_HUMAN Keratin, type II cytoskeletal 8 (Fragment) OS=Homo sapiens GN=KRT8 PE=1 SV=1
spiP61353IRL27_HUMAN	2.98	0.03444	9.43E-04	3.17E-04	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2: triK7EQQ9IK7EQQ9_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=1
triK7ELC7I K7ELC7_HUMAN	2.98	0.03444	8.91E-04	2.99E-04	60S ribosomal protein L27 (Fragment) OS=Homo sapiens GN=RPL27 PE=1 SV=1
triE9PCY7I E9PCY7_HUMAN	2.81	0.02643	1.33E-03	4.74E-04	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1: triH0YBG7I H0YBG7_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1: triD6RBM0ID6RBM0_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1: triE5RGH4IE5RGH4_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1: triD6RIU0ID6RIU0_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1: triD6RFM3I D6RFM3_HUMAN Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1
triE7EMC6I E7EMC6_HUMAN	2.77	0.00863	5.78E-04	2.08E-04	Annexin OS=Homo sapiens GN=ANXA6 PE=1 SV=1
spiP37108ISRP14_HUMAN	2.71	0.01021	8.50E-04	3.14E-04	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2: triH0YLW0I H0YLW0_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=1
spiQ53GQ0I DHB12_HUMAN	2.42	0.01385	6.34E-04	2.62E-04	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2
spiP04040ICATA_HUMAN	2.42	0.00728	7.06E-04	2.92E-04	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3
triF8VVM2I F8VVM2_HUMAN	2.41	0.00909	8.74E-04	3.62E-04	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=1
triHOYLA2I HOYLA2_HUMAN	2.30	0.00896	8.54E-04	3.71E-04	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=1
spiP22087IFBRL_HUMAN	2.21	0.01012	8.83E-04	4.00E-04	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2: triM0R299IM0R299_HUMAN rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=1 SV=1
triH3BNX8I H3BNX8_HUMAN	0.75	0.04600	1.27E-03	1.68E-04	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=1
triHOY449I HOY449_HUMAN	-1.11	0.00212	2.27E-04	2.52E-03	Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens GN=YBX1 PE=1 SV=1
triH3BRN4I H3BRN4_HUMAN	-1.70	0.00099	4.66E-04	7.91E-04	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=1: spiP80404I GABT_HUMAN 4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3
spiP16401IH15_HUMAN	-1.74	0.04345	2.18E-04	3.79E-03	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3
triH3BNQ7I H3BNQ7_HUMAN	-2.14	0.00576	3.69E-04	7.89E-04	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=1
triAOA087WYT3I AOA087WYT3_HUMAN	-2.22	0.00267	4.43E-04	9.82E-04	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=4 SV=1
spiQ15185ITEBP_HUMAN	-2.37	0.00333	4.54E-04	1.08E-03	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1
spiO14979I HNRDL_HUMAN	-2.55	0.01357	1.96E-04	5.01E-04	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3

Table 1 (continued)

Locus	Fold Change	pValue	Signal+ (pcDNA3)	Signal- (HepG2)	Description
triA0A087WUK21 A0A087WUK2_HUMAN	-2.55	0.01357	2.27E-04	5.79E-04	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=4 SV=1
spiP01009A1A1AT_HUMAN	-2.74	0.02442	2.45E-04	6.73E-04	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3; triG3V2B9IG3V2B9_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=1 SV=1; triG3V544IG3V544_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=1 SV=1; triG3V387IG3V387_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=1 SV=1; triG3V5R8IG3V5R8_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=1 SV=1; triG3V4I7IG3V4I7_HUMAN Short peptide from AAT (Fragment) OS=Homo sapiens GN=SERPINA1 PE=4 SV=1
spiP05455ILA_HUMAN	-2.88	0.02516	2.26E-04	6.52E-04	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2; triE7ERC4IE7ERC4_HUMAN Lupus La protein (Fragment) OS=Homo sapiens GN=SSB PE=1 SV=1; triE9PGX9IE9PGX9_HUMAN Lupus La protein (Fragment) OS=Homo sapiens GN=SSB PE=1 SV=1
spiP10599ITHIO_HUMAN	-3.01	0.04302	2.14E-04	6.44E-04	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3
triE7EMB3I E7EMB3_HUMAN	-3.13	0.04674	6.16E-04	1.93E-03	Calmodulin OS=Homo sapiens GN=CALM2 PE=1 SV=1
triHOY7A7I HOY7A7_HUMAN	-3.13	0.04674	6.45E-04	2.02E-03	Calmodulin (Fragment) OS=Homo sapiens GN=CALM2 PE=1 SV=1
triE7ETZ0I E7ETZ0_HUMAN	-3.13	0.04674	8.05E-04	2.52E-03	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=1
spiP62158ICALM_HUMAN	-3.16	0.04206	8.10E-04	2.56E-03	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2; triQ96HY3IQ96HY3_HUMAN CALM1 protein OS=Homo sapiens GN=CALM3 PE=1 SV=1; triG3V361IG3V361_HUMAN Calmodulin (Fragment) OS=Homo sapiens GN=CALM1 PE=1 SV=1
triJ3QQX2I J3QQX2_HUMAN	-3.54	0.00702	2.84E-04	1.00E-03	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1A PE=1 SV=1; triJ3KTF8IJ3KTF8_HUMAN Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDI1A PE=1 SV=3; triJ3KS60IJ3KS60_HUMAN Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1A PE=1 SV=1
spiP52565I GDIR1_HUMAN	-3.59	0.00515	3.27E-04	1.17E-03	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1A PE=1 SV=3
spiP39687I AN32A_HUMAN	-3.84	0.01529	1.68E-04	6.45E-04	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1
spiP25787IPSA2_HUMAN	-4.00	0.02378	3.39E-04	1.36E-03	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2
spiP17174IAATC_HUMAN	-4.13	0.01587	2.65E-04	1.09E-03	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3
triK7ER90I K7ER90_HUMAN	-4.13	0.03401	1.33E-04	5.49E-04	Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=1 SV=1
spiP06748INPM_HUMAN	-4.20	0.02188	8.93E-04	3.75E-03	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2; triE5RI98IE5RI98_HUMAN Nucleophosmin (Fragment) OS=Homo sapiens GN=NPM1 PE=1 SV=1
triJ3QLC8I J3QLC8_HUMAN	-4.24	0.01244	1.73E-04	7.34E-04	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=1
	-5.72	0.01114	6.04E-04	3.45E-03	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HINT1 PE=1 SV=2

spIP49773						
HINT1_HUMAN						
spIQ86SX6	- 6.14	0.04372	2.79E-04	1.71E-03	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2	
GLRX5_HUMAN						
spIQ15181 IPYR_HUMAN	- 6.55	0.03416	8.78E-05	5.75E-04	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	
triHOYCY6	- 7.66	0.00032	7.86E-05	6.02E-04	FAD-AMP lyase (cyclizing) (Fragment) OS=Homo sapiens GN=DAK PE=1 SV=1	
HOYCY6_HUMAN						

Table 2

List of 41 differentially abundant proteins for statistics between pcDNA3 x pcENS1.

Locus	Fold Change	pValue	Signal+ (pcENS1)	Signal- (pcDNA3)	Description
spiQ9UK22iFBX2_HUMAN	2.887204251	0.00294	0.000565646	0.000195915	F-box only protein 2 OS=Homo sapiens GN=FBXO2 PE=1 SV=2
triF2Z2V0i	2.448891458	0.01885	0.000415618	0.000169717	Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=1 SV=1
F2Z2V0_HUMAN					
spiP05386iRLA1_HUMAN	2.20861757	0.01819	0.002338141	0.001058645	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1
spiP43243i	2.106781667	0.00112	0.000626087	0.000297177	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2: triB3KM87iB3KM87_HUMAN Matrin-3
MATR3_HUMAN					OS=Homo sapiens GN=MATR3 PE=1 SV=1
triA8MXP9i	2.106781667	0.00112	0.000592509	0.000281239	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1
A8MXP9_HUMAN					
spiP51149iRAB7A_HUMAN	1.938939554	0.00429	0.000768084	0.000396136	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1: triC9J592iC9J592_HUMAN
					Ras-related protein Rab-7a (Fragment) OS=Homo sapiens GN=RAB7A PE=1 SV=1
spiQ9P035i	1.842287267	0.00587	0.00044159	0.000239697	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1
HACD3_HUMAN					SV=2
spiP52926i	-0.002597139	0.02916	0.000932861	0.002422769	High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1
HMGA2_HUMAN					
triF5H2A4i	-0.002597139	0.02916	0.00086171	0.002237981	High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1
F5H2A4_HUMAN					
triF5H6H0i	-0.002597139	0.02916	0.000691713	0.001796475	High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1
F5H6H0_HUMAN					
triJ3QRW1i	-0.018702242	0.00638	0.000248201	0.000464192	26S protease regulatory subunit 8 (Fragment) OS=Homo sapiens GN=PSMC5 PE=1 SV=1
J3QRW1_HUMAN					
spiP00338iLDHA_HUMAN	-0.267759962	0.03438	0.000722573	0.001934761	> L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2: triF5GXY2i
					F5GXY2_HUMAN l-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens GN=LDHA PE=1
					SV=3
spiP02765iFETUA_HUMAN	-0.475079452	0.0123	0.000111731	0.00053081	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1
spiP08238iHS90B_HUMAN	-1.523033786	0.0036	0.002236377	0.003406078	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4
spiP02545iLMNA_HUMAN	-1.560530275	0.00312	0.000879213	0.001372039	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1
spiP39023iRL3_HUMAN	-2.033045505	0.00327	0.000226732	0.000460956	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2: triG5E9G0iG5E9G0_HUMAN
					60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=1: triB5MCW2iB5MCW2_HU-
					MAN 60S ribosomal protein L3 (Fragment) OS=Homo sapiens GN=RPL3 PE=1 SV=1
spiP02768iALBU_HUMAN	-2.302973671	0.00479	0.000275409	0.000634261	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
spiP26373iRL13_HUMAN	-2.352456304	0.0203	0.000324859	0.000764216	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4: triH3BUK8iH3BUK8_HU-
					MAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=1 SV=1: triJ3QSB4i
					J3QSB4_HUMAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 PE=1 SV=1
triA0A087X1S2i	-2.401479196	0.00478	0.000370535	0.000889831	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=4 SV=1
A0A087X1S2_HUMAN					
triA0A087WZH7i	-2.408424932	0.00411	0.000303789	0.000731652	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1
A0A087WZH7_HUMAN					

triA0A087WWU81 A0A087WWU8_HUMAN	-2.440187743	0.00449	0.000253765	0.000619234	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=4 SV=1
spiP299661 MARCS_HUMAN	-2.684863748	0.00191	0.00026381	0.000708295	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4
spiQ9GZT3ISLIRP_HUMAN	-2.730197953	0.00514	0.000172275	0.000470346	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1
triG3V2S91 G3V2S9_HUMAN	-2.730197953	0.00514	0.000151436	0.000413449	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1
triHOYJ40IHOYJ40_HUMAN	-2.730197953	0.00514	0.000195604	0.000534038	SRA stem-loop-interacting RNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=SLIRP PE=1 SV=1
triA0A087WUN71 A0A087WUN7_HUMAN	-2.730197953	0.00514	0.000204109	0.000557257	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=4 SV=1
triG3V4X61 G3V4X6_HUMAN	-2.730197953	0.00514	0.000191612	0.00052314	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1
spiP53004BIEA_HUMAN	-2.899141374	0.03897	0.000143578	0.000416253	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2: triC9J1E1IC9J1E1_HUMAN Biliverdin reductase A (Fragment) OS=Homo sapiens GN=BLVRA PE=1 SV=1
triH3BT361 H3BT36_HUMAN	-3.082880329	0.02293	0.000536524	0.001654038	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=4 SV=1
spiP62269RS18_HUMAN	-3.304625932	0.02144	0.000280286	0.000926242	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3: triJ3JS69J3JS69_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=1
triB7WNR01 B7WNR0_HUMAN	-3.482472238	0.0473	0.000142247	0.00049537	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1
triD6RHD51 D6RHD5_HUMAN	-3.482472238	0.0473	0.000153093	0.000533143	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1
triHOYA551 HOYA55_HUMAN	-3.482472238	0.0473	0.000154779	0.000539015	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=1 SV=1
triH7C3671 H7C367_HUMAN	-3.818005689	0.03869	0.000206727	0.000789284	Non-POU domain-containing octamer-binding protein (Fragment) OS=Homo sapiens GN=NONO PE=1 SV=3
triA0A087X0X31 A0A087X0X3_HUMAN	-3.895589738	0.04525	0.000131893	0.000513803	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=4 SV=1
spiQ5VTE0IEF1A3_HUMAN	-4.17671178	0.00362	0.001520654	0.006351333	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1
triC9J0J7IC9J0J7_HUMAN	-4.228640752	0.01546	0.000141501	0.000598356	Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=1
triC9JQ45IC9JQ45_HUMAN	-4.228640752	0.01546	0.00011706	0.000495003	Profilin OS=Homo sapiens GN=PFN2 PE=1 SV=1
triQ5TA011 Q5TA01_HUMAN	-4.374529519	0.01927	0.000236106	0.001032853	Glutathione S-transferase omega-1 (Fragment) OS=Homo sapiens GN=GSTO1 PE=1 SV=1
spiQ9H9B41 SFXN1_HUMAN	-4.423436439	0.01596	0.000148649	0.000657539	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4: triD6RFI0ID6RFI0_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=1 SV=3
spiP25786IPSA1_HUMAN	-9.640254654	0.00328	4.97959E-05	0.000480045	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1: triF5GX11I F5GX11_HUMAN Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1

Table 3

List of 81 differentially abundant proteins for statistics between pMAXGFP x pcENS1.

Locus	Fold Change	pValue	Signal+ (pcENS1)	Signal- (pMAXGFP)	Description
triE9PIZ4 E9PIZ4_HUMAN	4.27	0.02884	5.1564100956E-04	1.2067638747E-04	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=1
triHOYMI6 HOYMI6_HUMAN	2.63	0.04622	3.6248916762E-04	1.3785223116E-04	Proteasome subunit alpha type (Fragment) OS=Homo sapiens GN=PSMA4 PE=1 SV=1
spiP60900 PSA6_HUMAN	2.51	0.01497	6.5820719273E-04	2.6200153475E-04	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1
triG3V295 G3V295_HUMAN	2.51	0.01497	7.9763039119E-04	3.1749939680E-04	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1
triG3V311 G3V311_HUMAN	2.51	0.01497	1.0940470906E-03	4.3548903750E-04	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1
triG3V3U4 G3V3U4_HUMAN	2.51	0.01497	1.5132613964E-03	6.0235866869E-03	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1
triG3V5Z7 G3V5Z7_HUMAN	2.51	0.01497	6.4253559290E-04	2.5576340297E-04	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1
spiP61626 LYSC_HUMAN	2.46	0.00250	8.0788085952E-04	3.2813609299E-04	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1
spiP62081 RS7_HUMAN	2.07	0.00203	4.7837342096E-04	2.3069960621E-04	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1
spiO43175 SERA_HUMAN	2.05	0.02052	3.5415580623E-04	1.7288143062E-04	> D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4
triM0R210 M0R210_HUMAN	1.88	0.03982	1.8803502747E-03	1.0008461759E-03	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=1
spiP62249 RS16_HUMAN	1.84	0.03469	1.6295554871E-03	8.8430929241E-04	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2
triA0A087WZ27 A0A087WZ27_HUMAN	1.84	0.03469	1.6295554871E-03	8.8430929241E-04	Zinc finger protein 90 OS=Homo sapiens GN=ZNF90 PE=4 SV=1
spiP46782 RS5_HUMAN	1.82	0.04115	1.3188765458E-03	7.2344215749E-04	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4: triM0R0F0 M0R0F0_HUMAN
spiP50395 GDIB_HUMAN	1.82	0.04377	7.3807276416E-04	4.0635192954E-04	40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=1 SV=1 Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2: triV9GYF8 V9GYF8_HUMAN Rab GDP dissociation inhibitor beta (Fragment) OS=Homo sapiens GN=GDI2 PE=1 SV=1
spiP62136 PP1A_HUMAN	1.81	0.04937	7.1055348515E-04	3.9154015764E-04	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1
triK7ERG4 K7ERG4_HUMAN	1.79	0.03148	9.9775810350E-04	5.5628189049E-04	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1
triM0R0R2 M0R0R2_HUMAN	1.79	0.04224	1.1751143601E-03	6.5592088945E-04	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1

spiP477551 CAZA2_HUMAN	1.76	0.00907	3.8503391537E-04	2.1892360270E-04	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3
triA8MXQ1 A8MXQ1_HUMAN	1.58	0.00171	1.8271019599E-03	1.1545048441E-03	Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1IP PE=4 SV=1
spiP432431 MATR3_HUMAN	1.56	0.00335	6.2608664580E-04	4.0083578369E-04	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2: triB3KM87IB3KM87_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1
triA8MXP9 A8MXP9_HUMAN	1.56	0.00335	5.9250881452E-04	3.7933844557E-04	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1
triE9PSD5 E9PSD5_HUMAN	0.43	0.02884	4.9845297591E-04	1.1665384122E-04	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=1
spiP180851ARF4_HUMAN	0.18	0.01873	1.0283317157E-03	5.6312821438E-04	ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3: triC9JPM4IC9JPM4_HUMAN ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens GN=ARF4 PE=1 SV=1
triAOA087X1Z3 AOA087X1Z3_HUMAN	-0.20	0.00919	2.9662475890E-04	5.9412009618E-04	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=4 SV=1
triHOYM70 HOYM70_HUMAN	-0.20	0.00919	3.3045038930E-04	6.6187063346E-04	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=1: triHOYKU2I HOYKU2_HUMAN Proteasome activator complex subunit 2 (Fragment) OS=Homo sapiens GN=PSME2 PE=1 SV=1
triH3BT71 H3BT71_HUMAN	-0.22	0.03725	3.6164761545E-04	7.8828832196E-04	RNA-binding motif protein, X chromosome, N-terminally processed OS=Homo sapiens GN=RBMX PE=1 SV=1
triHOYMF4 HOYMF4_HUMAN	-0.24	0.01281	4.5610249693E-04	1.0891334963E-03	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1
spiQ92928 RAB1C_HUMAN	-0.33	0.00379	1.7941339393E-04	5.9502701116E-04	Putative Ras-related protein Rab-1C OS=Homo sapiens GN=RAB1C PE=5 SV=2
spiQ9H0U4 RAB1B_HUMAN	-0.33	0.00379	1.7941339393E-04	5.9502701116E-04	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1
spiP08238 HS90B_HUMAN	-1.19	0.00037	2.2363769567E-03	2.6541184171E-03	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4
spiP15531 NDKA_HUMAN	-1.38	0.00005	1.9216269100E-03	2.6508648328E-03	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1
spiP22570ADRO_HUMAN	-1.40	0.00127	4.9680105400E-04	6.9510914113E-04	NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=3
spiP02545 LMNA_HUMAN	-1.41	0.00262	8.7921299898E-04	1.2356451265E-03	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1
spiQ8NBS9 TXND5_HUMAN	-1.55	0.01047	4.3710044382E-04	6.7551841613E-04	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2
triK7ES89 K7ES89_HUMAN	-1.57	0.00284	3.3391802783E-04	5.2383721696E-04	Dual-specificity protein phosphatase 3 (Fragment) OS=Homo sapiens GN=DUSP3 PE=1 SV=1
spiP60953 CDC42_HUMAN	-1.59	0.01599	5.7952351298E-04	9.2218098533E-04	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2: triQ5JYX0I Q5JYX0_HUMAN Cell division control protein 42 homolog (Fragment) OS=Homo sapiens GN=CDC42 PE=1 SV=1
triE3W990 E3W990_HUMAN	-1.74	0.00295	2.0678393968E-04	3.6029249723E-04	Sequestosome-1 (Fragment) OS=Homo sapiens GN=SQSTM1 PE=1 SV=1
	-1.79	0.01080			

Table 3 (continued)

Locus	Fold Change	pValue	Signal+ (pcENS1)	Signal- (pMAXGFP)	Description
spiQ148471 LASP1_HUMAN			5.3129711808E-04	9.5247256550E-04	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2: tr(C9J9W2) C9J9W2_HUMAN LIM and SH3 domain protein 1 (Fragment) OS=Homo sapiens GN=LASP1 PE=1 SV=1
triG3V1V01 G3V1V0_HUMAN	−1.80	0.01301	4.6887694121E-04	8.4429729734E-04	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform CRA_c OS=Homo sapiens GN=PDE6H PE=4 SV=1: tr(F8W1R7IF8W1R7_HUMAN Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1
spiP606601MYL6_HUMAN	−1.80	0.01301	4.9992839427E-04	9.0021102564E-04	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2
triB7Z6Z41 B7Z6Z4_HUMAN	−1.80	0.01301	3.1718146023E-04	5.7114228937E-04	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=2 SV=1
triF8VPF31 F8VPF3_HUMAN	−1.80	0.01301	5.8068605796E-04	1.0456297298E-03	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma (Fragment) OS=Homo sapiens GN=PDE6H PE=4 SV=1
triG8JLA21 G8JLA2_HUMAN	−1.80	0.01301	4.9663939168E-04	8.9428858468E-04	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1
triJ3KND31 J3KND3_HUMAN	−1.80	0.01301	4.9663939168E-04	8.9428858468E-04	Retinal cone rhodopsin-sensitive cGMP 3',5'-cyclic phosphodiesterase subunit gamma OS=Homo sapiens GN=PDE6H PE=4 SV=1
spiP003381LDHA_HUMAN	−1.91	0.04007	7.2257279358E-04	1.3809825096E-03	> L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2: tr(F5GXY2) F5GXY2_HUMAN L-lactate dehydrogenase A chain (Fragment) OS=Homo sapiens GN=LDHA PE=1 SV=3
spiO952921VAPB_HUMAN	−1.92	0.02424	2.7412268027E-04	5.2623836772E-04	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3
triH7C2111 H7C211_HUMAN	−1.99	0.01036	2.1368459062E-04	4.2559598943E-04	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1: spiQ998731 ANM1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2: tr(E9PKG1E9PKG1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1
spiQ9UL461 PSME2_HUMAN	−2.00	0.00919	3.1524137556E-04	6.3140796832E-04	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4
triA0A087WZH71 A0A087WZH7_HUMAN	−2.05	0.01540	3.0378860599E-04	6.2309294752E-04	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=4 SV=1
spiQ9NX631 MIC19_HUMAN	−2.06	0.04956	2.1744009773E-04	4.4818711141E-04	MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1
triC9JRZ61 C9JRZ6_HUMAN	−2.06	0.04956	2.1275388873E-04	4.3852790643E-04	MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1
spiQ926881 AN32B_HUMAN	−2.16	0.04445	2.5741410440E-04	5.5640940806E-04	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1: tri(Q5T6W8I)Q5T6W8_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member B (Fragment) OS=Homo sapiens GN=ANP32B PE=1 SV=1
triHOY6E71 HOY6E7_HUMAN	−2.18	0.03725	3.6660169237E-04	7.9908679213E-04	RNA-binding motif protein, X chromosome, N-terminally processed (Fragment) OS=Homo sapiens GN=RBMX PE=1 SV=2

triC9J4S4iC9J4S4_HUMAN	-2.19	0.00627	4.4976713953E-04	9.8605217655E-04	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1
spiO15143i ARPC1B_HUMAN	-2.20	0.00773	1.6888176270E-04	3.7175544430E-04	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3: triC9JFG9iC9JFG9_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3: triC9J6C8iC9J6C8_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3: triC9JQM8iC9JQM8_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3: triC9JEY1iC9JEY1_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=1: triF8VXW2iF8VXW2_HUMAN Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=2: triC9J4Z7iC9J4Z7_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=1: triC9K057iC9K057_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=1: triC9JBj7iC9JBj7_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=1: triC9JTT6iC9JTT6_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=1 SV=3
triK7ELC7i K7ELC7_HUMAN	-2.22	0.03550	3.7971620398E-04	8.4465213197E-04	60S ribosomal protein L27 (Fragment) OS=Homo sapiens GN=RPL27 PE=1 SV=1
spiP29966i MARCS_HUMAN	-2.30	0.00963	2.6381044628E-04	6.0621816617E-04	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4
triH3BT36i H3BT36_HUMAN	-2.45	0.00347	5.3652366733E-04	1.3139040782E-03	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=4 SV=1
spiP46779iRL28_HUMAN	-2.59	0.00655	3.4415463721E-04	8.9038650796E-04	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3
triHOYKD8i HOYKD8_HUMAN	-2.59	0.00655	2.7734814881E-04	7.1754677406E-04	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1
triHOYLP6i HOYLP6_HUMAN	-2.59	0.00655	5.2976612693E-04	1.3705949617E-03	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1
spiO00483i NDUA4_HUMAN	-2.74	0.03035	3.7754188433E-04	1.0331761575E-03	Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1
spiQ15274i NADC_HUMAN	-2.75	0.00691	2.0572201432E-04	5.6661625682E-04	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3: triC9JCj5iC9JCj5_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=5
triH7BZ11i H7BZ11_HUMAN	-3.07	0.00710	2.2555444718E-04	6.9288128636E-04	Protein RPL36A-HNRNPH2 OS=Homo sapiens GN=RPL36A-HNRNPH2 PE=3 SV=2
triJ3KQN4i J3KQN4_HUMAN	-3.07	0.00710	1.8743256878E-04	5.7577459007E-04	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=1: spiP83881iRL36A_HUMAN 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2: triR4GN19iR4GN19_HUMAN 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=4 SV=1
spiQ969Q0i RL36L_HUMAN	-3.07	0.00710	2.5108891290E-04	7.7132067726E-04	60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3
triHOY5B4i HOY5B4_HUMAN	-3.07	0.00710	2.3763772114E-04	7.2999992670E-04	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=3 SV=2
triD6RHD5i D6RHD5_HUMAN	-3.10	0.01904	1.5309327240E-04	4.7403637068E-04	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1
	-3.10	0.01904			Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1

Table 3 (continued)

Locus	Fold Change	pValue	Signal+ (pcENS1)	Signal- (pMAXGFP)	Description
triB7WNR01 B7WNR0_HUMAN			1.4224658306E-04	4.4045079786E-04	
triHOYA551 HOYA55_HUMAN	-3.10	0.01904	1.5477932166E-04	4.7925703555E-04	Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=1 SV=1
spiQ9HAV71 GRPE1_HUMAN	-3.24	0.02180	1.2662540785E-04	4.1001496166E-04	GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2
spiP622691RS18_HUMAN	-3.24	0.01564	2.8028634126E-04	9.0884462029E-04	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3: triJ3JS691J3JS69_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=1
triC9JQB31 C9JQB3_HUMAN	-3.26	0.01641	1.1866193463E-04	3.8718514857E-04	Ras-related protein Ral-B (Fragment) OS=Homo sapiens GN=RALB PE=1 SV=1
triE9PLD01 E9PLD0_HUMAN	-3.70	0.04512	1.5238542031E-04	5.6381042429E-04	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=3 SV=1
spiQ9UN861 G3BP2_HUMAN	-3.81	0.00228	1.1344218542E-04	4.3192164871E-04	Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2: triD6RB17ID6RB17_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1: triD6RAC7ID6RAC7_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1: triD6RGJ4ID6RGJ4_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1: triD6RBM9ID6RBM9_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1: triD6R9A4ID6R9A4_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1: triD6R9X5ID6R9X5_HUMAN Ras GTPase-activating protein-binding protein 2 (Fragment) OS=Homo sapiens GN=G3BP2 PE=1 SV=1
triMOQXU71 MOQXU7_HUMAN	-3.82	0.03844	9.5943708277E-05	3.6629063166E-04	Mitochondrial import inner membrane translocase subunit TIM44 (Fragment) OS=Homo sapiens GN=TIMM44 PE=1 SV=1
spiQ9H9B41 SFXN1_HUMAN	-4.04	0.00033	1.4864899148E-04	6.0096890241E-04	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4: triD6RFI0ID6RFI0_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=1 SV=3
triJ3KRE21 J3KRE2_HUMAN	-4.63	0.02210	1.0372838583E-04	4.8012684663E-04	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=1
spiP041791 SODM_HUMAN	-5.14	0.00047	1.1732492605E-04	6.0335127872E-04	Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2

under humid atmosphere with 5% CO₂. In all experiments, cells were transfected between 86 and 89 cell passages with 70–80% confluence.

2.2. Plasmids

The recombinant plasmid pcENS1 was previously constructed in our laboratory [2], using the pcDNA3 mammalian expression vector (Invitrogen). It contains the sequence of 63 nucleotides that encodes 21 amino acids from the C-terminal portion of the DENV2 envelope (E) protein and the full length DENV2 *ns1* gene. The vector pcDNA3 was used as a negative control, while the plasmid pMAXGFP (Amaxa), which encodes the green fluorescent protein (GFP) from *Pontellina plumata* copepod, was used as a control for expression of a DENV non-related protein.

2.3. Transfection

Transfection was performed by nucleofection with the Nucleofector V™ kit (Amaxa), according to manufacturer's recommendation. Briefly, HepG2 cells were seeded on 75 cm² bottles, harvested after 4 or 5 days with the aid of cell scrapers in 3 ml of CMF solution (8 g/L of NaCl; 0.4 g/L of KCl; 0.1 g/L of Na₂SO₄; 0.39 g/L of Na₂HPO₄·12H₂O; 0.15 g/L of KH₂PO₄; 1.1 g/L of glucose; 0.0025 g/L of phenol red, pH 7.4), centrifuged at 500 g for 5 min and suspended in the nucleofection solution (Amaxa). Cell suspension with 5 µg of DNA plasmids (10⁶ cells/100 µl/cuvettes) was submitted to an electric shock in the Nucleofector 6 equipment (Amaxa), using the T-28 program. Nine cuvettes were used for each sample (pcDNA3, pcENS1 or pMAXGFP). After shock, cells received 500 µL of DMEM with 10% FBS and were immediately transferred to microcentrifuge tubes containing another 500 µL DMEM with 10% FBS. Cells were seeded on 25 cm² flasks, incubated in humid atmosphere with 5% CO₂ at 37 °C for 24 h.

2.4. Proteomic sample preparation

Cells were centrifuged at 500 g for 10 min and suspended in 50 mM ammonium bicarbonate buffer containing 0.2% of RapiGest™ SF (Waters). The protein concentration was determined using Qubit 2.0[®] kit (Invitrogen) following the manufacturer's instructions. A total of 50 µg protein was used for each sample. Samples were treated with 5 µL of 100 mM dithiothreitol for reduction, incubated for 3 h at 37 °C. After reaching room temperature, samples were alkylated with 5 µL of 400 mM iodoacetamide for 15 min, in the dark. Trypsin (Promega) was added in the ratio 1:50 enzyme/substrate and digestion was performed for 20 h, at 37 °C. The reaction was stopped after adding formic acid to final concentration of 1%. Aliquots from this digestion were desalted by using POROS R2 C8–18 resin (Invitrogen), packaged in micropipette tips (Millipore) and equilibrated in TFA 1%. After washing with 0.1% TFA, peptides were eluted in 0.1% TFA with 70% acetonitrile and completely dried in the vacuum centrifuge.

2.5. Isoelectric focalization of peptides (OFFGEL)

Twenty five micrograms of peptides were solubilized in 1.8 mL of 0.01% ampholytes (OFFGEL buffer pH 3–10) containing 4% (*v/v*) glycerol and was submitted to the 3100 OFFGEL Fractionator with the OFFGEL Low Res Kit pH 3–10 (Agilent Technologies) immobilized pH gradient (IPG) DryStrips, following the Agilent's instructions. The peptides were also separated according to the manufacturer's instruction and optimized as described in Hubner et al. [3]. Twelve well fractionations were focused for 20 kV with a maximum current of 50 mA and power of 200 mW for 24 h. Each fraction was separately desalted as previously described and suspended in 40 µL of 1% formic acid. All fractions were analyzed on 10 cm reversed phase (RP) column coupled to an LTQ-Orbitrap XL mass spectrometer.

2.6. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis

Desalted peptides fractions were loaded separately onto a 10 cm RP column coupled to the mass spectrometer by using a Proxeon easy-nLC-System (Thermo Scientific Easy-nLC II). Four microliters were initially applied to a 2 cm long (100 μm internal diameter) trap column packed with 5 μm , 200 \AA Magic C18 AQ matrix (Michrom Bioresources) followed by separation on a 10 cm long (75 μm internal diameter) separation column packed with the same matrix directly on a self-pack 5–15 μm Tip empty column (New Objective). Samples were loaded onto the trap column at 2 $\mu\text{L}/\text{min}$ while chromatographic separation occurred at 200 nL/min. Mobile phase A consisted of 0.1% formic acid in water while mobile phase B consisted of 0.1% formic acid in acetonitrile. Peptides were eluted with a gradient of 2–40% of B over 32 min followed by up to 80% B in 4 min, maintaining at this concentration for 2 min more, before column equilibration. The HPLC system was coupled to the LTQ-Orbitrap XL via a nanoscale LC interface (Thermo Scientific). Source voltage was set to 1.9 kV, the temperature of heated capillary was set to 200 $^{\circ}\text{C}$ and tube lens voltage to 48 and 100 V, respectively. The target precursor specters were acquired in ion trap full scan MS with 60,000 while FWHM full AGC target was set to 500,000. MS1 spectra were acquired on the Orbitrap analyzer (300–1700 m/z) at a 60,000 resolution (for m/z 445.1200). For each spectrum, the 10 most intense ions were submitted to CID fragmentation (minimum signal required of 10,000; isolation width of 2.5; normalized collision energy of 35.0; activation Q of 0.25 and activation time of 30 s, followed by MS2 acquisition on the linear trap quadrupole analyzer. Dynamic exclusion option was enabled and set with the following values for each parameter: repeat count = 1; repeat duration = 30 s; exclusion list size = 500; exclusion duration = 45 s and exclusion mass width = 10 ppm. Data were acquired in technical triplicates using the Xcalibur software (version 2.0.7).

2.7. Protein identification

The raw data files were processed and quantified using PatternLab for Proteomics software v 3.2 [4] (available at: <http://max.ioc.fiocruz.br/mtrugilho/RabeloK2016/>). Peptide sequence matching (PSM) was performed using the Comet algorithm [5] against the UniProt database (<http://www.uniprot.org/>) with human proteins entries downloaded January 2015, plus a FASTA file containing Dengue virus and GFP sequences, retrieved from the NCBI database. A target-reverse strategy was employed for increased confidence in protein identifications [6]. The search considered tryptic and semi-tryptic peptide candidates. The cysteine carbamidomethylation and oxidation of methionine were considered as fixed and variable modifications, respectively. The Comet search engine considered a precursor mass tolerance of 40 ppm and bins of 1.0005 for the MS/MS. The validity of the peptide spectrum matches were assessed using PatternLab's Search Engine Processor (SEPro) module [7]. Briefly, identifications were grouped by charge state (+2 and > +3) and then by tryptic status (i.e., tryptic or semi-tryptic), resulting in four distinct subgroups. For each result, the XCorr, DeltaCN and Secondary Score values were used to generate a Bayesian discriminator. SEPro then automatically established a cutoff score to accept a false-discovery rate (FDR) of 1% based on the number of decoys, independently performed on each data subset, resulting in a false-positive rate that was independent of tryptic status or charge state [7]. Additionally, a minimum sequence length of 6 amino acid residues was required. Then, only PSMs with less than 5 ppm were considered to compose a final list of proteins supported by at least three independent evidences (e.g., identification of a peptide in different charge states, modified and non-modified version of the same peptide, or different peptides). All identification results are reported with less than 1% FDR, both peptide and protein level, by PatternLab's SEPro module. Spectral counting for estimation of protein copy number was accomplished using the normalized spectral abundance factor (NSAF) [8]. These conditions generate 14,138 peptides which mapped to 4756 proteins, from all samples (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). Differentially abundant proteins were pinpointed (Table 2a–c) using PatternLab's TFold module with a Benjamini–Hochberg q -value of 0.05 [9].

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Transparency document. Supporting Material

Transparency data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.11.083>.

Appendix A. Supporting Material

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.11.083>.

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