**Supplementary Table 1. Dysregulated proteins in the HEP-G2 hepatocyte cells induced by hyperlipidemic serum.**

**Fatty-acid degradation pathway (hsa00071)**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No** | **Gene name** | **Accession code** | **Protein name** | **Unique peptides** | **Score sequest** | **Abundance ratio:**  **A/C** | **Abundance ratio:**  **At/C** | ***p*-value: A/C** | ***p*-value: At/C** |
| 1 | ACADS8 | P45954 | Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial | 11 | 253.66 | 0.175 | 0.157 | 2.28E-13 | 1.79E-13 |
| 2 | ACADS | P16219 | Short-chain specific acyl-CoA dehydrogenase, mitochondrial | 4 | 130.02 | 2.878 | 2.601 | 2.35E-08 | 3.35E-08 |
| 3 | HADHA | P40939 | Trifunctional enzyme subunit alpha, mitochondrial | 20 | 477.51 | 0.218 | 0.194 | 2.28E-13 | 1.79E-13 |
| 4 | HADH | Q16836-1 | Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial | 6 | 64.35 | 0.255 | 0.232 | 2.62E-13 | 1.80E-13 |
| 5 | ACAT1 | P24752 | Acetyl-CoA acetyltransferase, mitochondrial | 15 | 371.16 | 0.01 | 0.01 |  | 1.79E-13 |
| 6 | ACAT2 | Q9BWD1 | Acetyl-CoA acetyltransferase, cytosolic | 7 | 322.53 | 0.182 | 0.186 | 2.28E-13 | 1.79E-13 |
| 7 | ECHS1 | P30084 | Enoyl-CoA hydratase, mitochondrial | 4 | 197.84 | 0.118 | 0.122 | 3.99E-13 | 1.41E-12 |
| 8 | ACADL | P28330 | Long-chain specific acyl-CoA dehydrogenase, mitochondrial | 6 | 133.13 | 3.219 | 2.878 | 8.43E-13 | 1.06E-12 |
| 9 | ALDH9A1 | P49189 | 4-trimethylaminobutyraldehyde dehydrogenase | 4 | 171.21 | 2.952 | 2.32 | 4.72E-10 | 3.37E-07 |
| 10 | ALDH7A1 | P49419 | Alpha-aminoadipic semialdehyde dehydrogenase | 5 | 101.39 | 0.025 | 0.025 | 2.28E-13 | 1.79E-13 |
| 11 | ALDH2 | P05091 | Aldehyde dehydrogenase, mitochondrial | 21 | 1677.14 | 1.875 | 1.499 | 1.17E-11 | 2.59E-07 |
| 12 | ALDH1B1 | P30837 | Aldehyde dehydrogenase X, mitochondrial | 11 | 386.19 | 0.036 | 0.043 | 2.28E-13 | 1.79E-13 |
| 13 | ADH5 | P11766 | alcohol dehydrogenase class-3 | 7 | 111.7 | 0.338 | 0.521 | 7.36E-13 | 9.05E-09 |
| 14 | ACAA2 | P42765 | 3-ketoacyl-CoA thiolase, mitochondrial | 10 | 138.42 | 0.547 | 0.515 | 2.32E-07 | 2.61E-07 |
| 15 | ACOX1 | Q15067 | Peroxisomal acyl-coenzyme A oxidase 1 | 11 | 140.95 | 0.117 | 0.128 | 2.28E-13 | 1.79E-13 |

**Glycolysis/Gluconeogenesis pathway (hsa00010)**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No** | **Gene name** | **Accession code** | **Protein name** | **Unique peptides** | **Score sequest** | **Abundance ratio:**  **A/C** | **Abundance ratio:**  **At/C** | ***p-*value:**  **A/C** | ***p*-value:**  **At/C** |
| 1 | ALDH9A1 | P49189 | 4-trimethylaminobutyraldehyde dehydrogenase | 4 | 171.21 | 2.952 | 2.32 | 4.72E-10 | 3.38E-07 |
| 2 | ALDH7A1 | P49419 | Alpha-aminoadipic semialdehyde dehydrogenase | 5 | 101.39 | 0.025 | 0.025 | 2.29E-13 | 1.8E-13 |
| 3 | ALDH1B1 | P30837 | Aldehyde dehydrogenase X, mitochondrial | 11 | 386.19 | 0.036 | 0.043 | 2.29E-13 | 1.8E-13 |
| 4 | ADH5 | P11766 | alcohol dehydrogenase class-3 | 7 | 111.7 | 0.338 | 0.521 | 7.36E-13 | 9.06E-09 |
| 5 | ALDH2 | P05091 | Aldehyde dehydrogenase, mitochondrial | 21 | 1677.14 | 1.875 | 1.499 | 1.17E-11 | 2.6E-07 |
| 6 | AKR1A1 | P14550 | alcohol dehydrogenase [NADP(+)] | 6 | 271.68 | 1.389 | 1.588 | 2.65E-08 | 1.2E-12 |
| 7 | PDHA1 | P08559 | Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial | 13 | 465.88 | 0.712 | 0.608 | 0.000122 | 1.12E-05 |
| 8 | PKM | P14618 | Pyruvate kinase PKM | 46 | 8021.82 | 1.643 | 1.653 | 2.29E-13 | 1.8E-13 |
| 9 | PGAM1 | P18669 | Phosphoglycerate mutase 1 | 24 | 6621.56 | 1.538 | 1.785 | 1.67E-09 | 1.4E-11 |
| 10 | ENO2 | P09104 | Gamma-enolase | 3 | 1533.52 | 1.666 | 1.872 | 1.38E-06 | 9.84E-07 |
| 11 | GPI | P06744 | glucose-6-phosphate isomerase | 19 | 659.96 | 0.429 | 0.475 | 3.04E-13 | 9.8E-13 |
| 12 | PFKP | Q01813 | ATP-dependent 6-phosphofructokinase, platelet type | 6 | 365.04 | 2.562 | 2.325 | 2.29E-13 | 1.82E-13 |
| 13 | HK3 | P52790 | Hexokinase-3 | 6 | 260.98 | 3.044 | 2.115 | 6.05E-13 | 5.81E-10 |

**Nonalcoholic fatty liver disease pathway (hsa04932)**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **No** | **Gene name** | **Accession** | **Protein name** | **Unique peptides** | **Score sequest** | **Abundance ratio:**  **A/C** | **Abundance ratio**  **At/C** | ***p*-value:**  **A/C** | ***p*-value: At/C** |
| 1 | NDUFA7 | O95182 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 | 4 | 136.46 | 0.608 | 0.523 | 8.41E-08 | 7.16E-11 |
| 2 | NDUFA13 | Q9P0J0 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 | 5 | 144.58 | 0.414 | 0.339 | 2.29E-13 | 1.8E-13 |
| 3 | NDUFB10 | O96000 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 | 3 | 63.55 | 0.209 | 0.197 | 9.15E-12 | 3.29E-11 |
| 4 | NDUFV1 | P49821 | NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial | 3 | 16.01 | 0.281 | 0.234 | 9.29E-13 | 1.99E-13 |
| 5 | NDUFB4 | O95168-1 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 | 3 | 14.42 | 1.83 | 1.949 | 6.57E-06 | 1.7E-07 |
| 6 | NDUFB8 | O95169 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial | 1 | 44 | 1.501 | 1.721 | 0.00285 | 7.94E-05 |
| 7 | COX6C | P09669 | Cytochrome c oxidase subunit 6C | 3 | 48.84 | 0.033 | 0.032 | 2.29E-13 | 1.8E-13 |
| 8 | COX4I1 | P13073 | Cytochrome c oxidase subunit 4 isoform 1, mitochondrial | 2 | 59.09 | 0.087 | 0.01 | 2.29E-13 |  |
| 9 | COX6A1 | P12074 | Cytochrome c oxidase subunit 6A1, mitochondrial | 1 | 174.51 | 1.565 | 1.244 | 2.8E-06 | 0.004729 |
| 10 | COX5B | P10606 | Cytochrome c oxidase subunit 5B, mitochondrial | 6 | 115.77 | 0.191 | 0.194 | 2.29E-13 | 1.8E-13 |
| 11 | UQCRH | P07919 | Cytochrome b-c1 complex subunit 6, mitochondrial | 3 | 87.55 | 0.038 | 0.01 | 2.29E-13 |  |
| 12 | UQCRB | P14927 | Cytochrome b-c1 complex subunit 7 | 5 | 185.3 | 0.237 | 0.238 | 2.59E-13 | 2.31E-13 |
| 13 | UQCRC2 | P22695 | Cytochrome b-c1 complex subunit 2, mitochondrial | 13 | 301.3 | 0.113 | 0.138 | 2.29E-13 | 2.1E-13 |
| 14 | UQCRC1 | P31930 | Cytochrome b-c1 complex subunit 1, mitochondrial | 9 | 333.54 | 0.725 | 0.577 | 1.86E-05 | 2.4E-08 |
| 15 | UQCRFS1 | P47985 | cytochrome b-c1 complex subunit Rieske, mitochondrial | 10 | 197.74 | 0.433 | 0.507 | 0.000127 | 0.004613 |
| 16 | CYCS | P99999 | cytochrome c | 8 | 556.15 | 2.062 | 2.161 | 2.3E-13 | 1.8E-13 |
| 17 | BAX | Q07812 | Apoptosis regulator BAX | 3 | 270.19 | 1.747 | 1.942 | 7.26E-07 | 6.12E-09 |
| 18 | MT-CO2 | P00403 | Cytochrome c oxidase subunit 2 | 3 | 58.83 | 0.285 | 0.01 | 3.24E-09 |  |