**Table S2** Characteristics of the protein spots identified by mass spectrometry in the *rhomboideus* muscle of pigletsa

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Spota | Accession numberb | Protein scorec | Protein score CI (%)c | Matched peptides/ Unmatched peaks | Total % of sequence coveragec | Total ion scorec | Total ion CI%c | Protein name | Derived HUGOd | MW kDae | pIe | *P* |
| Proteins increased in abundance in piglets fed TSAA– diet |
| A45 | sp|P62936|PPIA\_ | 659 | 100 | 27/9 | 74 | 517 | 100 | Peptidyl-prolyl cis-trans isomerase A (cyclophilin A) | PPIA | 18.1 | 8.34 | 0.09 |
| A46 | tr|F5CI18|F5CI1 | 425 | 100 | 14/20 | 41 | 357 | 100 | Phosphatidylethanolamine binding protein | PEBP1 | 21.0 | 7.01 | 0.01 |
| A47 | tr|I3LAB6|I3LAB | 626 | 100 | 17/23 | 43 | 555 | 100 | Proteasome (prosome, macropain) subunit, alpha type, 4 | PSMA4 | 26.0 | 6.92 | 0.02 |
| A48 | tr|Q7YSF4|Q7YSF | 610 | 100 | 32/13 | 71 | 434 | 100 | Troponin I type 1 (skeletal, slow) | TNNI1 | 21.8 | 9.61 | 0.00 |
| A55 | tr|F1SB60|F1SB6 | 570 | 100 | 17/21 | 45 | 460 | 100 | Superoxide dismutase (mitochondrial) | SOD2 | 24.9 | 8.59 | 0.08 |
| A56 | sp|Q9MZ16|VDAC1 | 966 | 100 | 27/9 | 74 | 751 | 100 | Voltage-dependent anion channel 1 | VDAC1 | 30.8 | 8.62 | 0.06 |
| A62 | sp|Q6S4N2|HS71B | 1010 | 100 | 41/44 | 48 | 743 | 100 | Heat shock 70 kDa protein 1B | HSPA1B | 70.3 | 5.60 | 0.07 |
| A66 | tr|Q5XIG1|Q5XIG | 357 | 100 | 24/21 | 53 | 234 | 100 | LIM domain binding 3 | LDB3 | 31.0 | 9.17 | 0.03 |
| A67 | tr|Q2HYU1|Q2HYU | 1010 | 100 | 38/31 | 55 | 761 | 100 | Creatine kinase, mitochondrial 2 (sarcomeric) | CKMT2 | 48.0 | 8.47 | 0.05 |
| A72 | tr|F1RPS8|F1RPS | 125 | 100 | 8/28 | 22 | 95 | 100 | ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit | ATP5E | 57.7 | 8.85 | 0.09 |
| Proteins decreased in abundance in piglets fed TSAA– diet |
| A49 | sp|P20788|UCRI\_ | 614 | 100 | 20/29 | 41 | 508 | 100 | Cytochrome b-c1 complex subunit Rieske, mitochondrial | UQCRFS1 | 29.7 | 9.04 | 0.05 |
| A51 | sp|Q4PS85|MYOZ1 | 416 | 100 | 18/10 | 64 | 320 | 100 | Myozenin 1 | MYOZ1 | 31.6 | 7.86 | 0.01 |
| A52 | sp|Q75NG9|TNNT3 | 216 | 100 | 9/26 | 26 | 181 | 100 | Troponin T type 3 (skeletal, fast) | TNNT3 | 32.2 | 6.05 | 0.04 |
| A53 | sp|Q29236|TCPZ\_ | 154 | 100 | 22/28 | 44 | 131 | 100 | T-complex protein 1 subunit zeta | CCT6A | 10.9 | 6.23 | 0.02 |
| A54 | sp|Q148N0|ODO1\_ | 534 | 100 | 39/91 | 30 | 306 | 100 | Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) | OGDH | 116.9 | 6.28 | 0.03 |
| A58 | sp|P00339|LDHA\_ | 689 | 100 | 38/20 | 65 | 412 | 100 | L-lactate dehydrogenase A chain | LDHA | 36.9 | 8.18 | 0.08 |
| A60 | tr|G0Z3A1|G0Z3A | 999 | 100 | 45/42 | 52 | 659 | 100 | Phosphoglucomutase 1 | PGM1 | 62.0 | 6.07 | 0.07 |
| A61 | sp|Q5XLD3|KCRM | 797 | 100 | 36/27 | 57 | 550 | 100 | Creatine kinase, muscle | CKM | 43.3 | 6.61 | 0.06 |
| A63 | tr|F1MS05|F1MS0 | 444 | 100 | 24/56 | 30 | 339 | 100 | Cytoplasmic aconitate hydratase | ACO1 | 98.7 | 8.11 | 0.07 |
| A64 | tr|G9F6X9|G9F6X | 924 | 100 | 37/29 | 56 | 701 | 100 | Dihydropyrimidinase-like 2 | DPYSL2 | 62.7 | 5.78 | 0.06 |
| A65 | tr|I3LP41|I3LP4 | 202 | 100 | 14/19 | 43 | 123 | 100 | Malate dehydrogenase 2, NAD (mitochondrial) | MDH2 | 36.0 | 8.93 | 0.06 |
| A68 | tr|F1RW89|F1RW8 | 878 | 100 | 32/36 | 47 | 686 | 100 | Electron-transferring-flavoprotein dehydrogenase | ETFDH | 69.3 | 7.08 | 0.03 |
| A69 | tr|F1RQQ8|F1RQQ | 720 | 100 | 48/46 | 51 | 376 | 100 | Phosphorylase, glycogen, muscle | PYGM | 97.7 | 6.65 | 0.00 |
| A71 | tr|D2KPI8|D2KPI | 534 | 100 | 31/22 | 58 | 358 | 100 | Adenylosuccinate lyase | ADSL | 55.8 | 6.45 | 0.06 |
| Unidentified protein |
| A50 | - | 41 | 89 | 11/35 | 24 | - | - | - | - | 42.6 | 5.98 | 0.03 |

aPiglets were fed a diet deficient (TSAA−) or sufficient (TSAA+) in total sulfur amino acids from 42 to 52 d of age. Spots numbers as presented in Fig. 2.

bCorresponds to the nucleotide sequence entries retrieved after the analysis of each protein by two dimensional gel electrophoresis in combination with MS/MS. Searches were made using Mascot as a search engine (Matrix Science Ltd., London; http://www.matrixscience.com).

cProtein score, protein score confidence intervals (CI), total ion scores and total ion score confidence intervals (CI) are reported for the combined search of MALDI-TOF/TOF MS and MS/MS data.

dWhere applicable, a corresponding gene alias was assigned to each protein using Human Gene Ontology (HUGO).

eThe theoretical molecular weight (MW) and isoelectric point (pI) are given for each protein.