**Table S1** Characteristics of the protein spots identified by mass spectrometry in the *longissimus* muscle of pigletsa

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 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 |
| A02 | tr|F1SB60|F1SB6 | 142 | 100 | 9/14 | 39 | 92 | 100 | Superoxide dismutase (mitochondrial) | SOD2 | 24.9 | 8.59 | 0.03 |
| A04 | sp|A1XQU1|PSB7 | 268 | 100 | 14/44 | 24 | 216 | 100 | Proteasome (prosome, macropain) subunit, beta type, 7 | PSMB7 | 30.3 | 6.90 | 0.02 |
| A07 | tr|F1S073|F1S07 | 1140 | 100 | 35/15 | 70 | 891 | 100 | Annexin A2 | ANXA2 | 38.8 | 6.92 | 0.01 |
| A09 | tr|F1RUN2|F1RUN | 1140 | 100 | 48/24 | 67 | 662 | 100 | Serum album | ALB | 71.6 | 5.98 | 0.05 |
| A10 | sp|Q0QF01|DHSA | 936 | 100 | 36/37 | 49 | 708 | 100 | Succinate dehydrogenase complex, subunit A, flavoprotein (Fp) | SDHA | 73.8 | 7.29 | <0.01 |
| A11 | sp|Q6S4N2|HS71B | 981 | 100 | 38/35 | 52 | 727 | 100 | Heat shock 70 kDa protein 1B | HSPA1B | 70.3 | 5.60 | 0.04 |
| A12 | tr|F1S0V3|F1S0V | 483 | 100 | 30/34 | 47 | 304 | 100 | Annexin A6 | ANXA6 | 59.7 | 5.48 | 0.03 |
| A13 | tr|F1S232|F1S23 | 176 | 100 | 18/57 | 24 | 100 | 100 | Aldehyde dehydrogenase 9 family, member A1 | ALDH9A1 | 66.1 | 8.71 | 0.01 |
| A14 | tr|F1RTN3|F1RTN | 454 | 100 | 31/47 | 40 | 313 | 100 | Moesin | MSN | 67.9 | 6.18 | <0.001 |
| A16 | tr|G3H1L8|G3H1L | 94 | 100 | 10/49 | 17 | 76 | 100 | Arginase-2 (mitochondrial) | ARG2 | 33.6 | 5.01 | 0.01 |
| A17 | tr|D2XN65|D2XN6 | 319 | 100 | 21/27 | 44 | 215 | 100 | Glycerol-3-phosphate dehydrogenase 1 | GPD1 | 38.4 | 6.01 | 0.09 |
| A18 | sp|Q5S1U1|HSPB1 | 329 | 100 | 12/26 | 32 | 267 | 100 | Heat shock 27 kDa protein 1 | HSPB1 | 23.0 | 6.23 | 0.02 |
| A19 | tr|F1S8R2|F1S8R | 106 | 100 | 7/43 | 14 | 90 | 100 | Pyrroline-5-carboxylate reductase 1 | PYCR1 | 33.8 | 8.20 | 0.05 |
| A21 | tr|H9F6L1|H9F6L | 493 | 100 | 14/25 | 36 | 438 | 100 | Thioredoxin-dependent peroxide reductase (mitochondrial) | PRDX3 | 22.2 | 5.70 | 0.09 |
| A29 | sp|Q75NG9|TNNT3 | 598 | 100 | 20/41 | 33 | 516 | 100 | Troponin T type 3 (skeletal, fast) | TNNT3 | 32.2 | 6.05 | 0.05 |
| A32 | tr|Q0PY11|Q0PY1 | 435 | 100 | 20/31 | 39 | 341 | 100 | Eukaryotic translation elongation factor 1 alpha 1 | EEF1A1 | 50.5 | 9.10 | 0.06 |
| A33 | tr|I3LK59|I3LK5 | 425 | 100 | 23/26 | 47 | 303 | 100 | Enolase 1 (alpha) | ENO1 | 38.2 | 8.93 | 0.07 |
| A34 | tr|F1RS36|F1RS3 | 497 | 100 | 21/54 | 28 | 404 | 100 | Heat shock 70 kDa protein 5 (glucose-regulated protein, 78kDa) | HSPA5 | 70.3 | 5.21 | 0.09 |
| A36 | tr|G0Z3A1|G0Z3A | 882 | 100 | 36/28 | 56 | 593 | 100 | Phosphoglucomutase 1 | PGM1 | 62.0 | 6.07 | 0.09 |
| A37 | tr|F1RUK8|F1RUK | 383 | 100 | 30/30 | 50 | 221 | 100 | Rab GDP dissociation inhibitor beta | GDI2 | 50.8 | 5.79 | 0.07 |
| A38 | tr|F2Z594|F2Z59 | 270 | 100 | 15/15 | 50 | 177 | 100 | High mobility group box 1 | HMGB1 | 25.1 | 5.62 | 0.07 |
| A39 | sp|Q9GJT2|ESTD\_ | 206 | 100 | 12/16 | 43 | 148 | 100 | S-formylglutathione hydrolase | ESD | 32.0 | 6.54 | 0.10 |
| A40 | tr|G3RNX8|G3RNX | 292 | 100 | 24/10 | 70 | 240 | 100 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 8 | NDUFA8 | 20.3 | 6.60 | 0.05 |
| A42 | sp|A5A8V7|HS71L | 95 | 100 | 12/43 | 22 | 41 | 100 | Heat shock 70 kDa protein 1-like | HSPA1L | 70.7 | 6.01 | 0.04 |
| A43 | sp|Q3SYR3|ABEC2 | 286 | 100 | 9/22 | 29 | 253 | 100 | Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2 | APOBEC2 | 26.2 | 4.84 | 0.06 |
| A44 | sp|O19069|SUCA\_ | 264 | 100 | 10/20 | 33 | 220 | 100 | Succinyl-CoA ligase (ADP/GDP-forming) subunit alpha (mitochondrial) | SUCLG1 | 36.5 | 9.35 | 0.09 |
| Proteins decreased in abundance in piglets fed TSAA– diet |
| A05 | tr|Q1AG05|Q1AG0 | 142 | 100 | 11/11 | 50 | 69 | 100 | Calsarcin-3 | MYOZ3 | 26.5 | 6.86 | 0.01 |
| A06 | sp|Q4PS85|MYOZ1 | 141 | 100 | 9/36 | 20 | 123 | 100 | Myozenin-1 | MYOZ1 | 31.6 | 7.86 | 0.01 |
| A15 | sp|Q99PR8|HSPB2 | 185 | 100 | 7/13 | 35 | 151 | 100 | Heat shock 27 kDa protein 2 | HSPB2 | 20.4 | 5.27 | 0.04 |
| A20 | sp|P62936|PPIA\_ | 583 | 100 | 23/8 | 74 | 470 | 100 | Peptidyl-prolyl cis-trans isomerase A (cyclophilin A) | PPIA | 18.1 | 8.34 | 0.10 |
| A23 | sp|Q29380|VDAC3 | 382 | 100 | 20/18 | 52 | 256 | 100 | Voltage-dependent anion channel 1 | VDAC3 | 30.9 | 8.85 | 0.09 |
| A24 | sp|P63246|GBLP\_ | 964 | 100 | 29/8 | 79 | 768 | 100 | guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 | GNB2L1 | 35.5 | 7.60 | 0.05 |
| A25 | tr|Q5XIG1|Q5XIG | 318 | 100 | 22/27 | 45 | 223 | 100 | LIM domain binding 3 | LDB3 | 31.0 | 9.17 | 0.06 |
| A27 | sp|P00339|LDHA\_ | 485 | 100 | 34/6 | 85 | 262 | 100 | Lactate dehydrogenase A | LDHA | 36.9 | 8.18 | 0.06 |
| A31 | sp|Q5XLD3|KCRM\_ | 784 | 100 | 34/18 | 66 | 570 | 100 | Creatine kinase, muscle | CKM | 43.3 | 6.61 | 0.06 |
| Unidentified proteins |
| A01 | - | 32 | 21 | 0 | 10 | - | - | - | - | 75.2 | 7.00 | 0.01 |
| A03 | - | 36 | 69 | 45/55 | 45 | 25 | 57 | - | - | 9.2 | 9.24 | 0.03 |
| A35 | - | 58 | 100 | 9/27 | 74 | - | - | - | - | 85.1 | 5.93 | 0.06 |

aPiglets were fed a diet deficient (TSAA−) or sufficient (TSAA+) in total sulfur amino acids from 42 to 52 days of age. Spot numbers as presented in Fig. 1.

bCorresponds to the nucleotide sequence entries retrieved after the analysis of each protein by two dimensional gel electrophoresis in combination with mass spectrometry (MS/MS). Searches were made using MASCOT as a search engine.

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