**Table S2**: Proteins and metabolites found differentially expressed in the comparison of INS-1E β cells treated with palmitate vs cells without treatment (grey lines when fold change ≥1.5).

| Fold palm/ctrl | ID | Name | Function | Location |
|---|---|---|---|---|
| -1.48 | P10860 | glutamate dehydrogenase 1 | aminoacid metabolism | mito |
| -1.21 | Q05962 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 | channels and transporter | mito |
| +1.43 | P81155 | voltage-dependent anion channel 2 | channels and transporter | mito |
| +1.54 | Q8K3P6 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 | channels and transporter | mito |
| +1.61 | P29410 | adenylate kinase 2 | kinase/phosphatases | mito |
| +2.22 | Q9WUS0 | adenylate kinase 4 | kinase/phosphatases | mito |
| -1.69 | P00507 | glutamic-oxaloacetic transaminase 2 | krebs cycle/ATP production | mito |
| -1.35 | P21571 | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6 | krebs cycle/ATP production | mito |
| -1.23 | P32551 | ubiquinol-cytochrome c reductase core protein II | krebs cycle/ATP production | mito |
| -1.21 | Q9ER34 | aconitase 2, mitochondrial | krebs cycle/ATP production | mito |
| +1.28 | P35435 | ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 | krebs cycle/ATP production | mito |
| +1.30 | P10719 | ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide | krebs cycle/ATP production | mito |
| +1.61 | P13803 | electron-transfer-flavoprotein, alpha polypeptide | krebs cycle/ATP production | mito |
| +1.70 | P15999 | ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle | krebs cycle/ATP production | mito |
| +2.00 | P20788 | ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 | krebs cycle/ATP production | mito |
| +2.27 | P29419 | ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E | krebs cycle/ATP production | mito |
| -1.15 | HMDB00552 | 3-methylglutarylcarnitine | Lipid metabolism | mito |
| +1.04 | HMDB13130 | glutarylcarnitine | Lipid metabolism | mito |
| +1.25 | P18886 | carnitine palmitoyltransferase 2 | Lipid metabolism | mito |
| +1.45 | P15650 | acyl-CoA dehydrogenase, long chain | Lipid metabolism | mito |
| +1.75 | O35547 | acyl-CoA synthetase long-chain family member 4 | Lipid metabolism | mito |
| +1.96 | P56720 | sterol regulatory element binding transcription factor 1 | Lipid metabolism | mito |
| -1.43 | P07153 | ribophorin I | metabolism/miscellaneous | mito |
| +1.11 | Q561S0 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, | mitochondrial enzymes | mito |

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|---|---|---|---|---|
| | | 42kDa | | |
| +1.47 | P12007 | isovaleryl-CoA dehydrogenase | mitochondrial enzymes | mito |
| +2.00 | Q6AYQ8 | fumarylacetoacetate hydrolase domain containing 1 | mitochondrial enzymes | mito |
| +2.63 | P07895 | superoxide dismutase 2, mitochondrial | mitochondrial enzymes | mito |
| +1.18 | Q6AXV4 | SAMM50 sorting and assembly machinery component | mitochondrial protein processing | mito |
| +1.24 | P85834 | Tu translation elongation factor, mitochondrial | mitochondrial protein processing | mito |
| +1.28 | Q4FZT0 | stomatin (EPB72)-like 2 | mitochondrial protein processing | mito |
| +1.43 | P67779 | prohibitin | mitochondrial protein processing | mito |
| +1.79 | P56571 | ES1 protein homolog, mitochondrial | other/unknown function | mito |
| -1.29 | Q6TUG0 | DnaJ (Hsp40) homolog, subfamily B, member 11 | protein synthesis/translation regulation/protein folding/ER stress | mito |
| +1.43 | P48721 | heat shock 70kDa protein 9 (mortalin) | protein synthesis/translation regulation/protein folding/ER stress | mito |
| +1.64 | P0C2N5 | suppressor of variegation 4-20 homolog 1 (Drosophila) | epigenetic regulation | nucleus |
| +1.56 | P84245 | H3 histone, family 3A | other/unknown function | nucleus |
| +1.82 | A9UMV8 | H2A histone family, member J | other/unknown function | nucleus |
| +1.54 | P17046 | lysosomal-associated membrane protein 2 | Proteasoma/Lysosoma/Autophagy | plasma membrane |
| +1.30 | P59215 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O | signal transduction | plasma membrane |
| +1.30 | P04897 | guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 | signal transduction | plasma membrane |
| +1.37 | P69897 | tubulin, beta class I | cytoskeleton related proteins | cyto |
| +1.49 | P47819 | glial fibrillary acidic protein | cytoskeleton related proteins | cyto |
| +1.56 | P68370 | tubulin, alpha 1a | cytoskeleton related proteins | cyto |
| +1.69 | P60711 | actin, beta | cytoskeleton related proteins | cyto |
| +1.32 | P04764 | enolase 1, (alpha) | glucose metabolism | cyto |
| +1.49 | P04797 | glyceraldehyde-3-phosphate dehydrogenase | glucose metabolism | cyto |
| +2.00 | Q9ESV6 | glyceraldehyde-3-phosphate dehydrogenase, spermatogenic | glucose metabolism | cyto |
| -1.65 | Q5RJR8 | leucine rich repeat containing 59 | other/unknown function | cyto |
| +2.08 | Q63716 | peroxiredoxin 1 | oxidative stress/apoptosis | cyto |
| +1.67 | P62986 | ubiquitin A-52 residue ribosomal protein fusion product 1 | posttranslational modification/ubiquitination | cyto |
| -1.24 | P34058 | heat shock protein 90kDa alpha (cytosolic), class B member 1 | protein synthesis/translation regulation/protein folding/ER stress | cyto |
| +1.25 | Q07984 | signal sequence receptor, delta | protein synthesis/translation regulation/protein folding/ER stress | cyto |
| +1.28 | P62630 | eukaryotic translation elongation factor 1 alpha 1 | protein synthesis/translation regulation/protein | cyto |

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|---|---|---|---|---|
| | | | folding/ER stress | |
| +1.37 | P19944 | ribosomal protein, large, P1 | protein synthesis/translation regulation/protein folding/ER stress | cyto |
| +1.41 | P62890 | ribosomal protein L30 | protein synthesis/translation regulation/protein folding/ER stress | cyto |
| +1.29 | P38406 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type | signal transduction | cyto |
| +1.40 | P10536 | RAB1B, member RAS oncogene family | vescicle transport/signal transduction | cyto |
| +1.47 | Q63942 | RAB3D, member RAS oncogene family | vescicle transport/signal transduction | cyto |
| +1.40 | Q9WVB1 | RAB6A, member RAS oncogene family | vescicle transport/signal transduction | cyto |
| -1.28 | Q9JK11 | reticulon 4 | other/unknown function | ER |
| +1.67 | P61621 | Sec61 alpha 1 subunit (S. cerevisiae) | other/unknown function | ER |
| -1.26 | P85007 | Immediate early response 3-interacting protein 1 | oxidative stress/apoptosis | ER |
| -1.24 | P04785 | prolyl 4-hydroxylase, beta polypeptide | posttranslational modification/ubiquitination | ER |
| -1.41 | Q63617 | hypoxia up-regulated 1 | protein synthesis/translation regulation/protein folding/ER stress | ER |
| -1.40 | P18418 | calreticulin | protein synthesis/translation regulation/protein folding/ER stress | ER |
| -1.28 | P38659 | protein disulfide isomerase family A, member 4 | protein synthesis/translation regulation/protein folding/ER stress | ER |
| +1.24 | P28576 | platelet-derived growth factor alpha polypeptide | hormones/growth factors/receptors/neuropeptides | extracellular space |
| +1.29 | P01323 | insulin | hormones/growth factors/receptors/neuropeptides | extracellular space |
| +2.13 | P01322 | insulin I | hormones/growth factors/receptors/neuropeptides | extracellular space |
| +2.08 | P08426 | RIKEN cDNA 2210010C04 gene | other/unknown function | extracellular Space |
| -1.41 | HMDB00182 | L-lysine | aminoacid metabolism | other |
| -1.38 | HMDB00158 | L-tyrosine | aminoacid metabolism | other |
| -1.37 | HMDB00687 | L-leucine | aminoacid metabolism | other |
| -1.33 | HMDB00517 | L-arginine | aminoacid metabolism | other |
| -1.28 | HMDB00148 | L-glutamic acid | aminoacid metabolism | other |
| -1.28 | HMDB00159 | L-phenylalanine | aminoacid metabolism | other |
| -1.27 | HMDB00168 | L-asparagine | aminoacid metabolism | other |
| -1.12 | HMDB00162 | L-proline | aminoacid metabolism | other |
| -1.11 | HMDB00214 | L-ornithine | aminoacid metabolism | other |

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|---|---|---|---|---|
| -1.09 | HMDB00161 | L-alanine | aminoacid metabolism | other |
| -1.09 | HMDB00883 | L-valine | aminoacid metabolism | other |
| +1.06 | HMDB00177 | L-histidine | aminoacid metabolism | other |
| +1.09 | 541-15-1 | L-carnitine | aminoacid metabolism | other |
| +1.11 | HMDB00187 | L-serine | aminoacid metabolism | other |
| +1.16 | HMDB00696 | L-methionine | aminoacid metabolism | other |
| +1.17 | HMDB00191 | L-aspartic acid | aminoacid metabolism | other |
| +1.39 | HMDB00167 | L-threonine | aminoacid metabolism | other |
| +1.43 | HMDB00123 | glycine | aminoacid metabolism | other |
| +1.25 | Q64119 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle-like | other/unknown function | other |
| -1.21 | P63018 | heat shock 70kDa protein 8 | protein synthesis/translation regulation/protein folding/ER stress | other |