Table S3: Proteins and metabolites found differentially expressed in the comparison of INS-1E β cells treated with palmitate+GLP-1 vs cells without treatment (grey lines when fold change ≥1.5).

Fold palm+GLP-1/ctrl	ID	Name	Function	Location
-1.66	Q8K3P6	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25	channels and transporter	mito
+3.13	Q05962	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	channels and transporter	mito
+3.13	P81155	voltage-dependent anion channel 2	channels and transporter	mito
-1.53	P29410	adenylate kinase 2	kinase/phosphatases	mito
-1.40	Q9WUS0	adenylate kinase 4	kinase/phosphatases	mito
-1.58	P10888	cytochrome c oxidase subunit IV isoform 1	krebs cycle/ATP production	mito
-1.32	Q6AYQ8	fumarylacetoacetate hydrolase domain containing 1	krebs cycle/ATP production	mito
-1.31	P20788	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	krebs cycle/ATP production	mito
-1.25	P56574	isocitrate dehydrogenase 2 (NADP+), mitochondrial	krebs cycle/ATP production	mito
-1.20	P62898	cytochrome c, somatic	krebs cycle/ATP production	mito
+1.25	P15999	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	krebs cycle/ATP production	mito
+1.39	Q06647	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	krebs cycle/ATP production	mito
+1.47	P11507	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	krebs cycle/ATP production	mito
+1.64	P29419	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit E	krebs cycle/ATP production	mito
-1.71	P18886	carnitine palmitoyltransferase 2	Lipid metabolism	mito
-1.54	P15650	acyl-CoA dehydrogenase, long chain	Lipid metabolism	mito
-1.32	Q60587	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	Lipid metabolism	mito
-1.23	Q6P6R2	dihydrolipoamide dehydrogenase	Lipid metabolism	mito
-1.03	HMDB00552	3-methylglutarylcarnitine	Lipid metabolism	mito
+1.13	HMDB13130	glutarylcarnitine	Lipid metabolism	mito
+1.96	P56720	sterol regulatory element binding transcription factor 1	Lipid metabolism	mito
-2.52	Q561S0	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	mitochondrial enzymes	mito

-2.32	P12007	isovaleryl-CoA dehydrogenase	mitochondrial enzymes	mito
-1.74	P19643	monoamine oxidase B	mitochondrial enzymes	mito
-1.25	Q8VHF5	citrate synthase	mitochondrial enzymes	mito
-1.20	P19234	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa	mitochondrial enzymes	mito
+1.16	P07895	superoxide dismutase 2, mitochondrial	mitochondrial enzymes	mito
-1.54	P85834	Tu translation elongation factor, mitochondrial	mitochondrial protein processing	mito
-1.38	Q3KR86	inner membrane protein, mitochondrial	mitochondrial protein processing	mito
-1.32	P67779	prohibitin	mitochondrial protein processing	mito
-1.23	Q6AXV4	SAMM50 sorting and assembly machinery component	mitochondrial protein processing	mito
+1.28	D4A7N1	coiled-coil-helix-coiled-coil-helix domain containing 6	mitochondrial protein processing	mito
+1.32	Q5XIH7	prohibitin 2	mitochondrial protein processing	mito
-2.66	Q5XHZ0	TNF receptor-associated protein 1	other/unknown function	mito
-1.26	Q9R063	peroxiredoxin 5	oxidative stress/apoptosis	mito
-3.26	Q6TUG0	DnaJ (Hsp40) homolog, subfamily B, member 11	protein synthesis/translation regulation/protein folding/ER stress	mito
+1.47	P48721	heat shock 70kDa protein 9 (mortalin)	protein synthesis/translation regulation/protein folding/ER stress	mito
+2.63	P0C2N5	suppressor of variegation 4-20 homolog 1 (Drosophila)	epigenetic regulation	nucleus
-1.40	Q6LED0	histone cluster 1, H3e	other/unknown function	nucleus
-1.35	P84245	H3 histone, family 3A	other/unknown function	nucleus
-1.25	Q00715	histone cluster 1, H2bl	other/unknown function	nucleus
+1.49	P21807	peripherin	cytoskeleton related proteins	plasma membrane
-1.31	P14562	lysosomal-associated membrane protein 1	Proteasoma/Lysosoma/Autophagy	plasma membrane
-1.41	P47819	glial fibrillary acidic protein	cytoskeleton related proteins	cyto
+1.45	P68370	tubulin, alpha 1a	cytoskeleton related proteins	cyto
+1.79	P60711	actin, beta	cytoskeleton related proteins	cyto
-1.80	P04797	glyceraldehyde-3-phosphate dehydrogenase	glucose metabolism	cyto
-1.60	P04764	enolase 1, (alpha)	glucose metabolism	cyto
+1.75	Q9ESV6	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	glucose metabolism	cyto
+1.27	Q62812	myosin, heavy chain 9, non-muscle	other/unknown function	cyto
+1.30	Q9Z2Q4	5-methyltetrahydrofolate-homocysteine methyltransferase	posttranslational modification/ubiquitination	cyto
+1.30	P62986	ubiquitin A-52 residue ribosomal protein fusion product 1	posttranslational modification/ubiquitination	cyto
+1.27	P63102	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.28	P62630	eukaryotic translation elongation factor 1 alpha 1	protein synthesis/translation	cyto

			regulation/protein folding/ER stress	
+1.33	P34058	heat shock protein 90kDa alpha (cytosolic), class B member 1	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.39	P62425	ribosomal protein L7a	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.49	P61983	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.92	P17077	ribosomal protein L9	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.41	P10536	RAB1B, member RAS oncogene family	vescicle transport/signal transduction	cyto
+1.41	Q63942	RAB3D, member RAS oncogene family	vescicle transport/signal transduction	cyto
+1.45	Q62636	RAP1B, member of RAS oncogene family	vescicle transport/signal transduction	cyto
-1.41	P25235	ribophorin II	metabolism/miscellaneous	ER
+1.47	Q9JK11	reticulon 4	other/unknown function	ER
-1.51	P04785	prolyl 4-hydroxylase, beta polypeptide	posttranslational modification/ubiquitination	ER
-1.49	P18418	calreticulin	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.39	P52555	endoplasmic reticulum protein 29	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.37	Q63081	protein disulfide isomerase family A, member 6	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.35	Q63617	hypoxia up-regulated 1	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.35	P38659	protein disulfide isomerase family A, member 4	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.25	P11598	protein disulfide isomerase family A, member 3	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.24	P06761	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	protein synthesis/translation regulation/protein folding/ER stress	ER
+1.75	P35565	calnexin	protein synthesis/translation regulation/protein folding/ER stress	ER
-2.49	P28576	platelet-derived growth factor alpha polypeptide	hormones/growth factors/receptors/neuropeptides	Extracellular Space
-1.22	P01323	insulin	hormones/growth factors/receptors/neuropeptides	Extracellular Space
-1.22	P01322	insulin I	hormones/growth factors/receptors/neuropeptides	Extracellular space

+2.04	P08426	RIKEN cDNA 2210010C04 gene	other/unknown function	extracellular space
-1.28	P0C5H9	mesencephalic astrocyte-derived neurotrophic factor	protein synthesis/translation regulation/protein folding/ER stress	extracellular space
-1.43	HMDB00517	L-arginine	aminoacid metabolism	other
-1.19	HMDB00182	L-lysine	aminoacid metabolism	other
-1.15	HMDB00687	L-leucine	aminoacid metabolism	other
-1.12	HMDB00148	L-glutamic acid	aminoacid metabolism	other
-1.09	HMDB00159	L-phenylalanine	aminoacid metabolism	other
-1.08	541-15-1	L-carnitine	aminoacid metabolism	other
-1.08	HMDB00161	L-alanine	aminoacid metabolism	other
-1.05	HMDB00162	L-proline	aminoacid metabolism	other
-1.03	HMDB00158	L-tyrosine	aminoacid metabolism	other
+1.08	HMDB00883	L-valine	aminoacid metabolism	other
+1.16	HMDB00168	L-asparagine	aminoacid metabolism	other
+1.17	HMDB00177	L-histidine	aminoacid metabolism	other
+1.24	HMDB00214	L-ornithine	aminoacid metabolism	other
+1.29	HMDB00123	glycine	aminoacid metabolism	other
+1.38	HMDB00187	L-serine	aminoacid metabolism	other
+1.40	HMDB00191	L-aspartic acid	aminoacid metabolism	other
+1.40	HMDB00696	L-methionine	aminoacid metabolism	other
+1.61	HMDB00167	L-threonine	aminoacid metabolism	other
+1.49	Q64119	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle-like	other/unknown function	other
+1.39	P63018	heat shock 70kDa protein 8	protein synthesis/translation regulation/protein folding/ER stress	other