Table S1: Proteins and metabolites found differentially expressed in the comparison of INS-1E β cells treated with GLP-1 vs cells without treatment (grey lines when fold change ≥1.5).

Fold GLP-1/ctrl	ID	Name	Function	Location
+1.25	P10860	glutamate dehydrogenase 1	aminoacid metabolism	mito
+1.32	Q05962	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	channels and transporter	mito
+1.54	P81155	voltage-dependent anion channel 2	channels and transporter	mito
-1.13	Q9WUS0	adenylate kinase 4	kinase/phosphatases	mito
-1.25	P31399	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d	krebs cycle/ATP production	mito
-1.24	P15999	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	krebs cycle/ATP production	mito
-1.24	P35434	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	krebs cycle/ATP production	mito
-1.23	P10888	cytochrome c oxidase subunit IV isoform 1	krebs cycle/ATP production	mito
-1.08	P13803	electron-transfer-flavoprotein, alpha polypeptide	krebs cycle/ATP production	mito
+1.30	P11507	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	krebs cycle/ATP production	mito
+1.32	P06685	ATPase, Na+/K+ transporting, alpha 1 polypeptide	krebs cycle/ATP production	mito
+1.32	P06687	ATPase, Na+/K+ transporting, alpha 3 polypeptide	krebs cycle/ATP production	mito
-1.25	Q60587	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), beta subunit	Lipid metabolism	mito
-1.09	P18886	carnitine palmitoyltransferase 2	Lipid metabolism	mito
+1.04	HMDB00552	3-methylglutarylcarnitine	Lipid metabolism	mito
+1.39	HMDB13130	glutarylcarnitine	Lipid metabolism	mito
-1.32	P19643	monoamine oxidase B	mitochondrial enzymes	mito
-1.31	P00388	P450 (cytochrome) oxidoreductase	mitochondrial enzymes	mito
-1.11	P12007	isovaleryl-CoA dehydrogenase	mitochondrial enzymes	mito
-1.10	Q561S0	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	mitochondrial enzymes	mito
+1.25	P25809	creatine kinase, mitochondrial 1B	mitochondrial enzymes	mito
+1.37	P07895	superoxide dismutase 2, mitochondrial	mitochondrial enzymes	mito
-1.41	Q4FZT0	stomatin (EPB72)-like 2	mitochondrial protein processing	mito
-1.40	P67779	prohibitin	mitochondrial protein processing	mito
-1.39	P85834	Tu translation elongation factor, mitochondrial	mitochondrial protein processing	mito

-1.37	Q6AXV4	SAMM50 sorting and assembly machinery component	mitochondrial protein processing	mito
+1.52	D4A7N1	coiled-coil-helix-coiled-coil-helix domain containing 6	mitochondrial protein processing	mito
-1.40	Q5XHZ0	TNF receptor-associated protein 1	protein synthesis/translation regulation/protein folding/ER stress	mito
-1.21	P48721	heat shock 70kDa protein 9 (mortalin)	protein synthesis/translation regulation/protein folding/ER stress	mito
+1.39	P0C2N5	suppressor of variegation 4-20 homolog 1	epigenetic regulation	nucleus
-1.43	P84245	H3 histone, family 3A	other/unknown function	nucleus
-1.29	A9UMV8	H2A histone family, member J	other/unknown function	nucleus
-1.27	Q00715	histone cluster 1, H2bl	other/unknown function	nucleus
+1.37	P60711	actin, beta	cytoskeleton related proteins	cyto
-1.25	P04764	enolase 1, (alpha)	glucose metabolism	cyto
-1.18	P04797	glyceraldehyde-3-phosphate dehydrogenase	glucose metabolism	cyto
-1.17	Q9ESV6	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	glucose metabolism	cyto
-1.25	Q6AYR6	haloacid dehalogenase-like hydrolase domain containing 2	other/unknown function	cyto
+1.21	Q63716	peroxiredoxin 1	oxidative stress/apoptosis	cyto
-1.54	P63018	heat shock 70kDa protein 8	protein synthesis/translation regulation/protein folding/ER stress	cyto
+1.39	P61983	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma	protein synthesis/translation regulation/protein folding/ER stress	cyto
-1.20	P25235	ribophorin II	metabolism/miscellaneous	ER
+1.33	Q9JK11	reticulon 4	other/unknown function	ER
-1.35	Q641Y0	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit (non-catalytic)	posttranslational modification/ubiquitination	ER
-1.21	Q6TUG0	DnaJ (Hsp40) homolog, subfamily B, member 11	protein synthesis/translation regulation/protein folding/ER stress	ER
+1.33	Q63617	hypoxia up-regulated 1	protein synthesis/translation regulation/protein folding/ER stress	ER
+1.52	P18418	calreticulin	protein synthesis/translation regulation/protein folding/ER stress	ER
+1.61	P35565	calnexin	protein synthesis/translation regulation/protein folding/ER stress	ER
-1.16	P28576	platelet-derived growth factor alpha polypeptide	hormones/growth factors/receptors/neuropeptides	extracellular space
+1.43	P01323	insulin	hormones/growth factors/receptors/neuropeptides	extracellular space
+1.43	P01322	insulin I	hormones/growth	extracellular

			factors/receptors/neuropeptides	space
-1.81	HMDB00517	L-arginine	aminoacid metabolism	other
-1.35	HMDB00158	L-tyrosine	aminoacid metabolism	other
-1.30	HMDB00687	L-leucine	aminoacid metabolism	other
-1.28	HMDB00177	L-histidine	aminoacid metabolism	other
-1.26	HMDB00159	L-phenylalanine	aminoacid metabolism	other
-1.25	HMDB00182	L-lysine	aminoacid metabolism	other
-1.24	HMDB00162	L-proline	aminoacid metabolism	other
-1.17	HMDB00148	L-glutamic acid	aminoacid metabolism	other
-1.02	HMDB00883	L-valine	aminoacid metabolism	other
-1.01	541-15-1	L-carnitine	aminoacid metabolism	other
+1.03	HMDB00161	L-alanine	aminoacid metabolism	other
+1.05	HMDB00696	L-methionine	aminoacid metabolism	other
+1.09	HMDB00191	L-aspartic acid	aminoacid metabolism	other
+1.10	HMDB00214	L-ornithine	aminoacid metabolism	other
+1.15	HMDB00168	L-asparagine	aminoacid metabolism	other
+1.25	HMDB00123	glycine	aminoacid metabolism	other
+1.26	HMDB00167	L-threonine	aminoacid metabolism	other
+1.64	HMDB00187	L-serine	aminoacid metabolism	other