SUPPLEMENTAL FIGURE LEGENDS

Figure.S1: **Viability in stable INS1E clones.** Apoptosis was measured by annexin V-FITC plus PI staining and FACS analysis. Bars show the percentages of cells that were viable ($Annexin^-/PI^-$), early apoptotic ($Annexin^+/PI^-$) or late apoptotic/dead ($Annexin^+/PI^+$) (n= 3). Results are expressed as mean ± SEM.

Figure.S2**: mRNA levels of mitochondrial, K_{ATP} channels and ER stress related genes in stable INS1E clones**. mRNA levels of stable INS1E cell lines were detected by real time PCR. The data were normalized to TBP1 mRNA and presented relative to control cells (n=6). Results are expressed as mean ± SEM.

Figure.S3: **Mitochondrial content in stable INS1E clones**. Mitochondrial content was estimated as the ratio between copy numbers of mtDNA (cytochrome c oxidase 1, COI) *versus* nuclear DNA (CCAAT-enhancer-binding proteins-β, C/EBP-β) (n=4). Results are expressed as mean ± SEM.

Figure.S4: **Protein levels of mitochondrial respiratory chain subunits stable INS1E clones**. Representative immunoblotting revealing protein levels of the mitochondrial complex subunits (I, II, III, IV, V) of stable INS1E clones using a monoclonal anti-total OXPHOS antibody cocktail. Actin was used as a control of protein quantity (n=7).

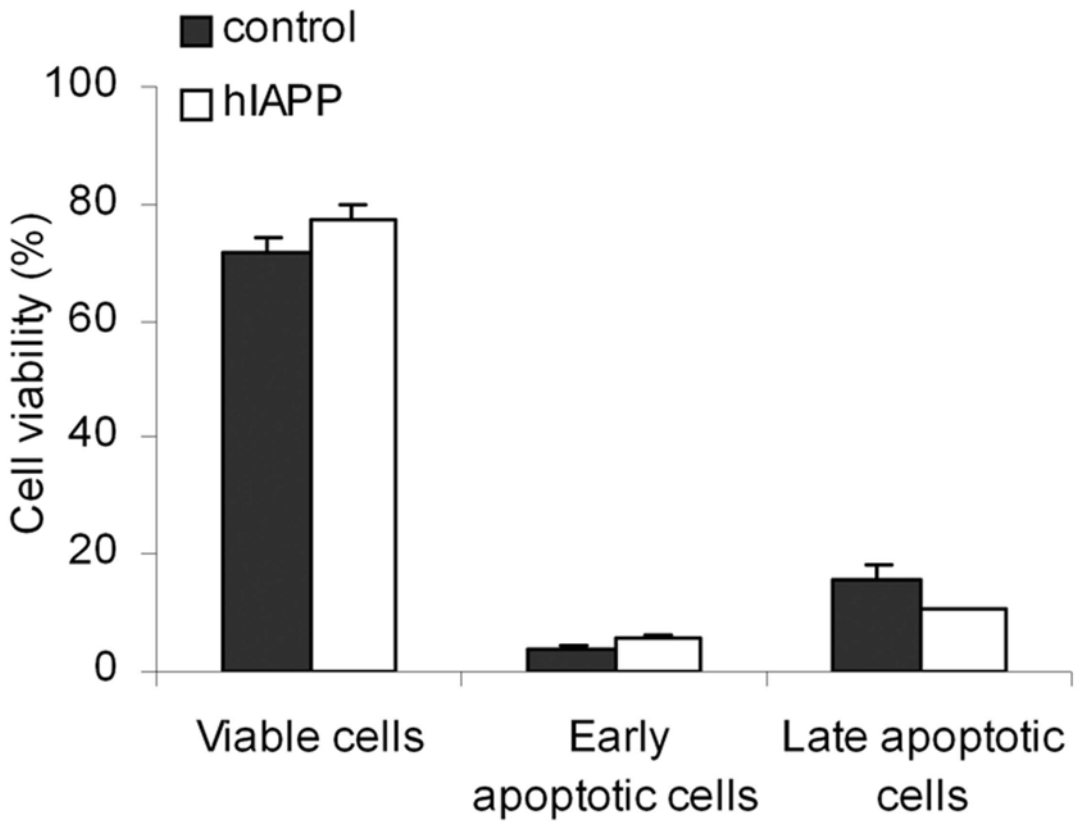
control
hIAPP
100
80
60
40
20
0
Cell viability (%)
Viable cells
Early apoptotic cells
Late apoptotic cells

Fig. S1

	genes	control	hIAPP
Mitochondria biogenesis	*TFAM*	1.00±0.13	0.92±0.24
	NRF1	1.00±0.27	0.89±0.07
KATP channel subunits	*Kir 6.2*	1.00±0.09	1.09±0.15
	Sur1	1.00±0.09	0.83±0.07
ER stress	*Bip*	1.00±0.15	0.87±0.16
	CHOP	1.00±0.24	0.85±0.22

Fig. S2

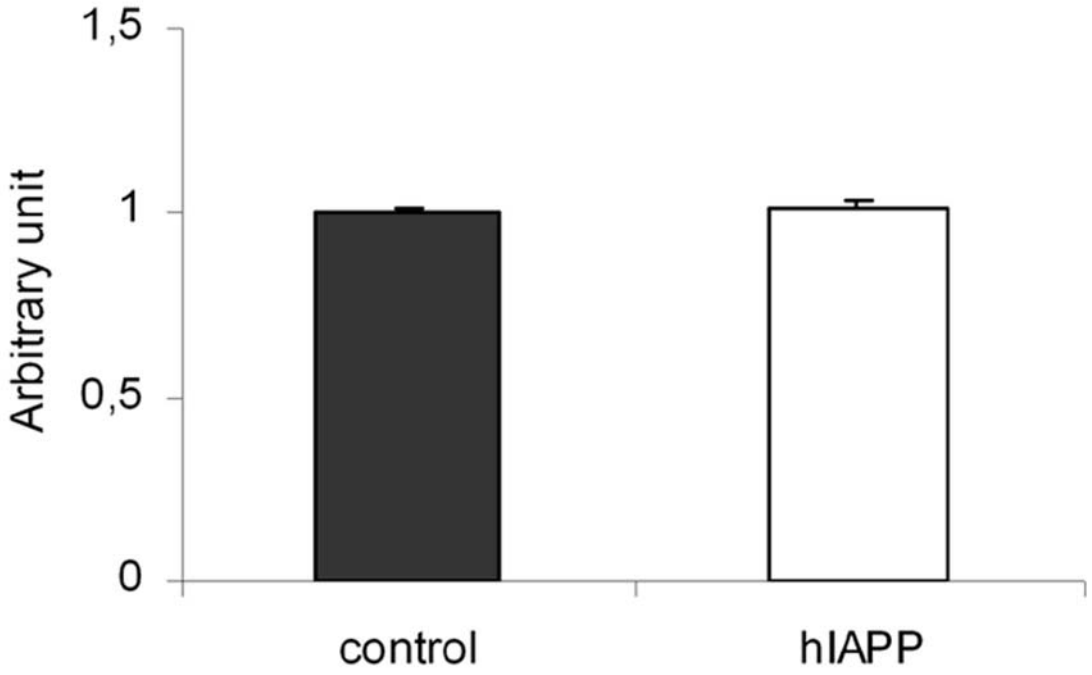

Fig. S3

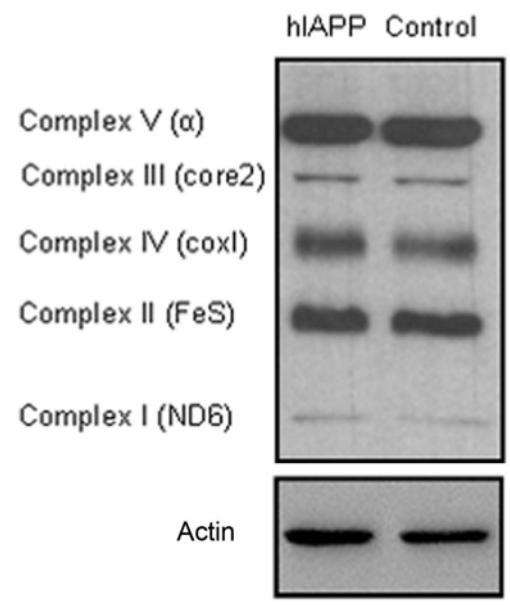
hIAPP
Control
Complex V (α)
Complex III (core2)
Complex IV (coxI)
Complex II (FeS)
Complex I (ND6)
Actin

Fig. S4