

Supplementary Information for

**Altered glycolysis triggers impaired mitochondrial metabolism and mTORC1 activation in diabetic  $\beta$ -cells**

by

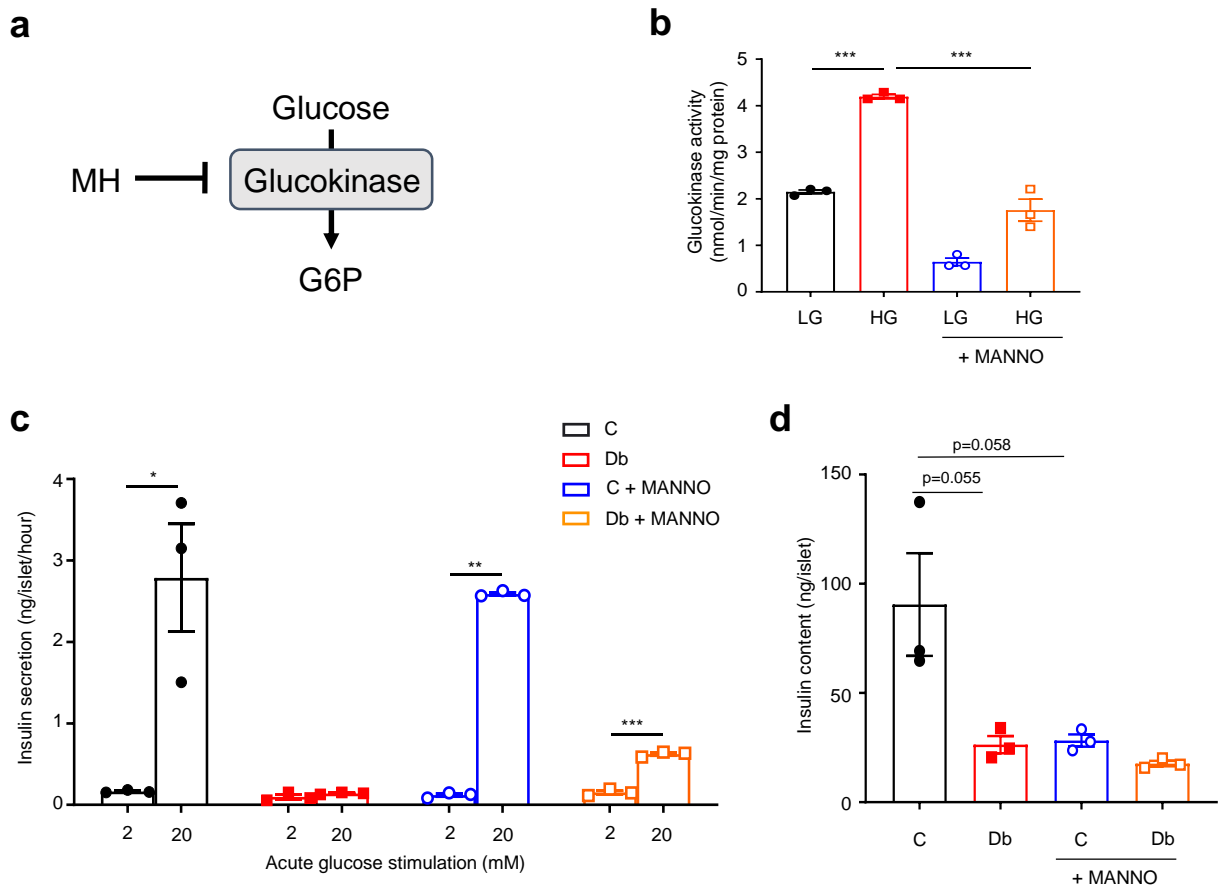
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Supplementary Figures 1-7

Table 1A

Table 1B

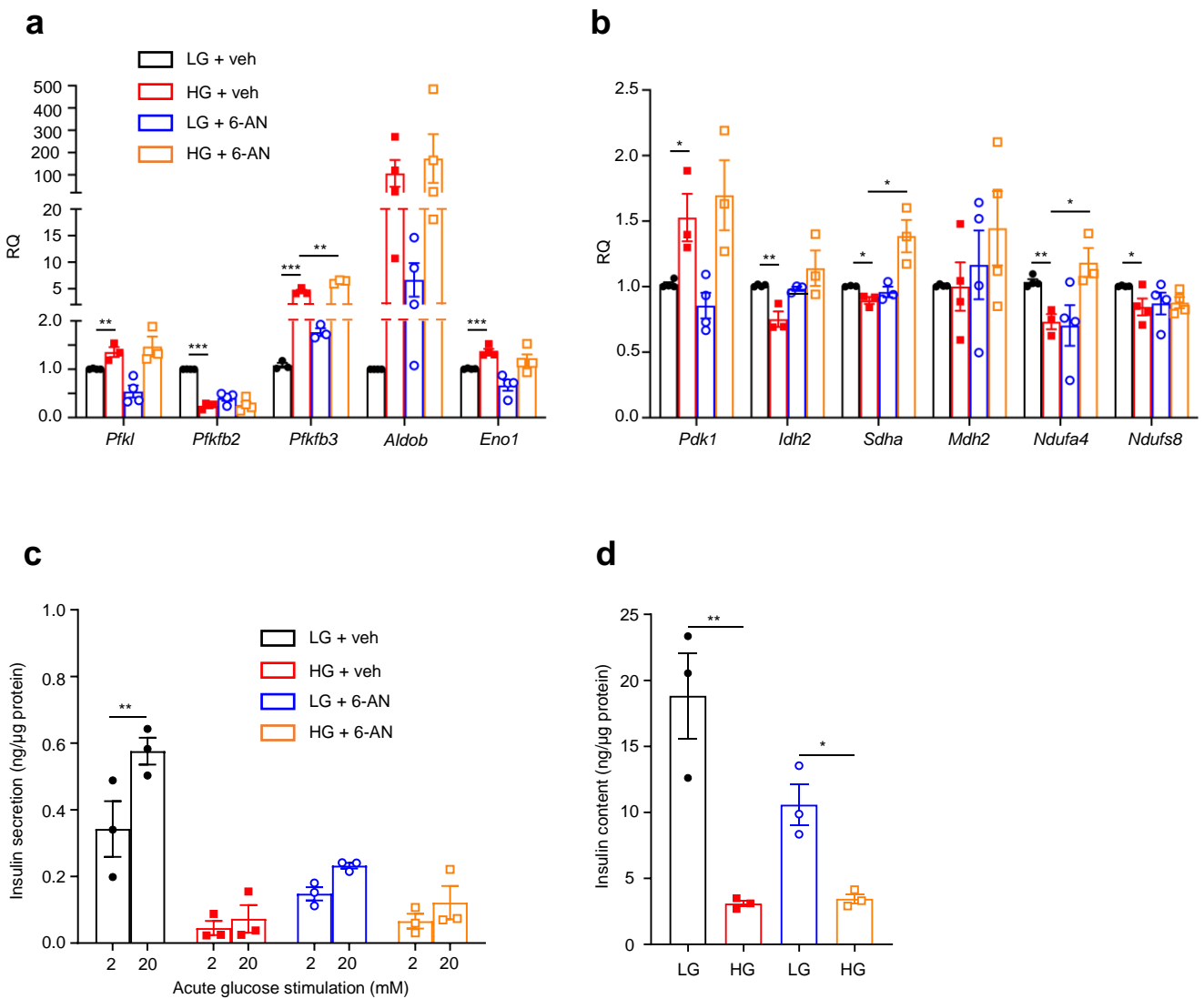
Uncropped blots for Supplementary Figures 4 and 5



**Supplementary Figure 1. Mannoheptulose partially restores insulin secretion in diabetic islets**

- (a) Diagram showing where mannoheptulose (MH) inhibits glucose metabolism.
- (b) Summed activity of all hexokinases measured in LG- or HG-cells incubated for 48hr ± 10mM mannoheptulose. Activity was measured at 20mM glucose, where glucokinase activity predominates, in the continued presence of 10mM mannoheptulose (MANNO) (n=3 biologically independent experiments).
- (c,d). Insulin secretion (c) and insulin content (d) in control (C) and diabetic (Db) islets incubated for 48hr ± 10mM mannoheptulose and then measured at 2mM or 20mM glucose for 1h in the absence of mannoheptulose (n=3 animals/genotype).

All panels show individual data points and mean ± s.e.m. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, two-tailed unpaired Student's t-test. Control (black), diabetic (red), control + MANNO (blue), diabetic + MANNO (orange). Source data are provided in the Supplementary Source Data file.

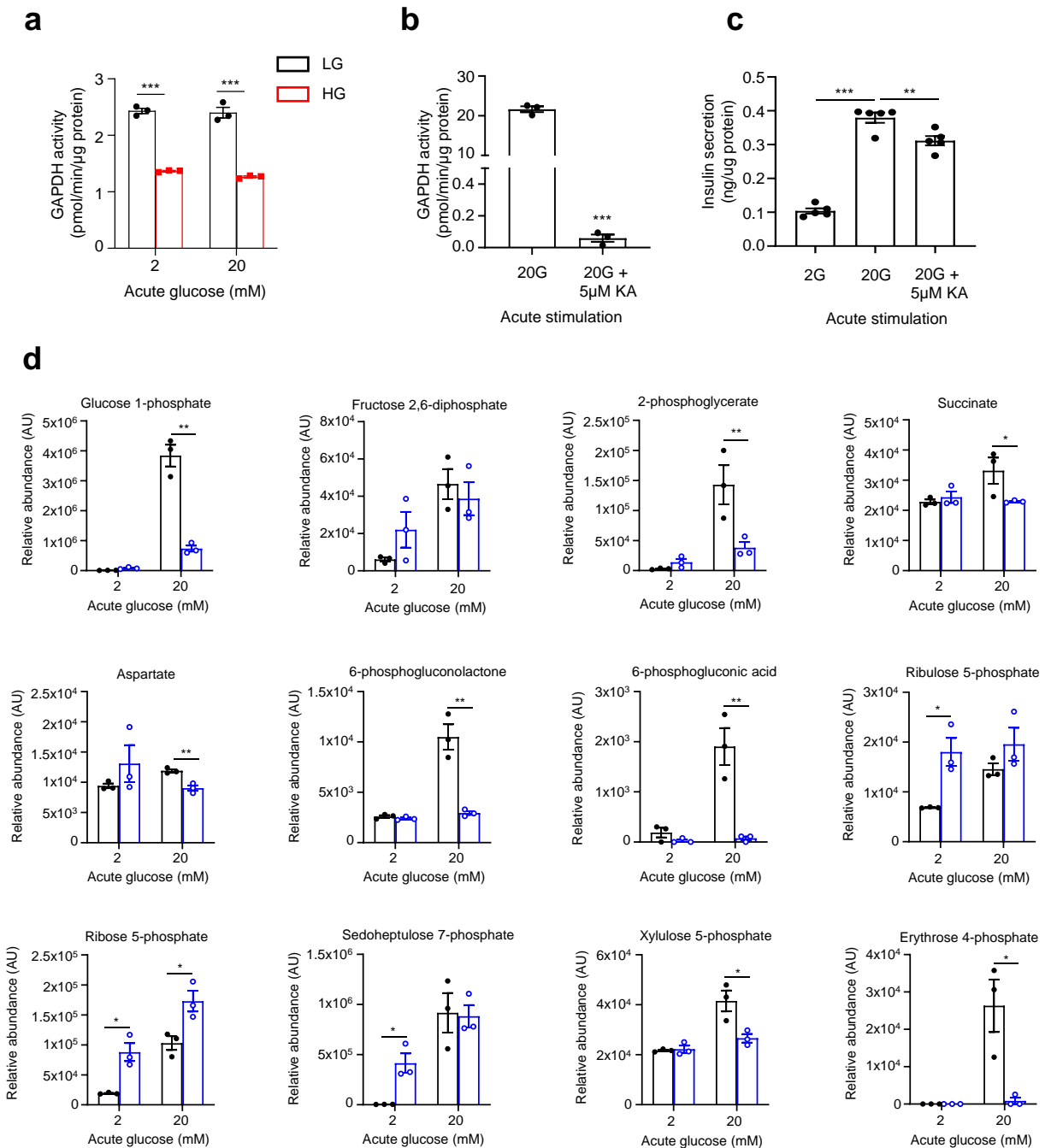


**Supplementary Figure 2. Inhibition of the pentose phosphate pathway does not prevent gene changes and loss of insulin secretion in HG-cells.**

**(a,b)** mRNA levels of the indicated genes involved in glycolytic **(a)** and mitochondrial **(b)** metabolism assessed by qPCR in LG-cells and HG-cells cultured for 48hrs + 0.1% DMSO (veh) or 100μM 6-aminonicotinamide (6-AN). *Pfkfb2*, *Aldob*, *Eno1*, *Mdh2*, *Ndufs8*, n=4 independent experiments; *Pfkfb3*, *Idh2*, *Sdha*, n=3 biologically independent experiments; *Pfk1*, *Pdk1*, *Ndufa4*, n=4 biologically independent experiments for LG and LG+6-AN, but n=3 biologically independent experiments for HG and HG+6-AN.

**(c,d)** Insulin secretion **(c)** and insulin content **(d)** in LG-cells and HG-cells cultured for 48hrs + 0.1% DMSO (veh) or 100μM 6-aminonicotinamide (6-AN) and then exposed to 2mM or 20mM glucose for 1 hr (n=3 biologically independent experiments).

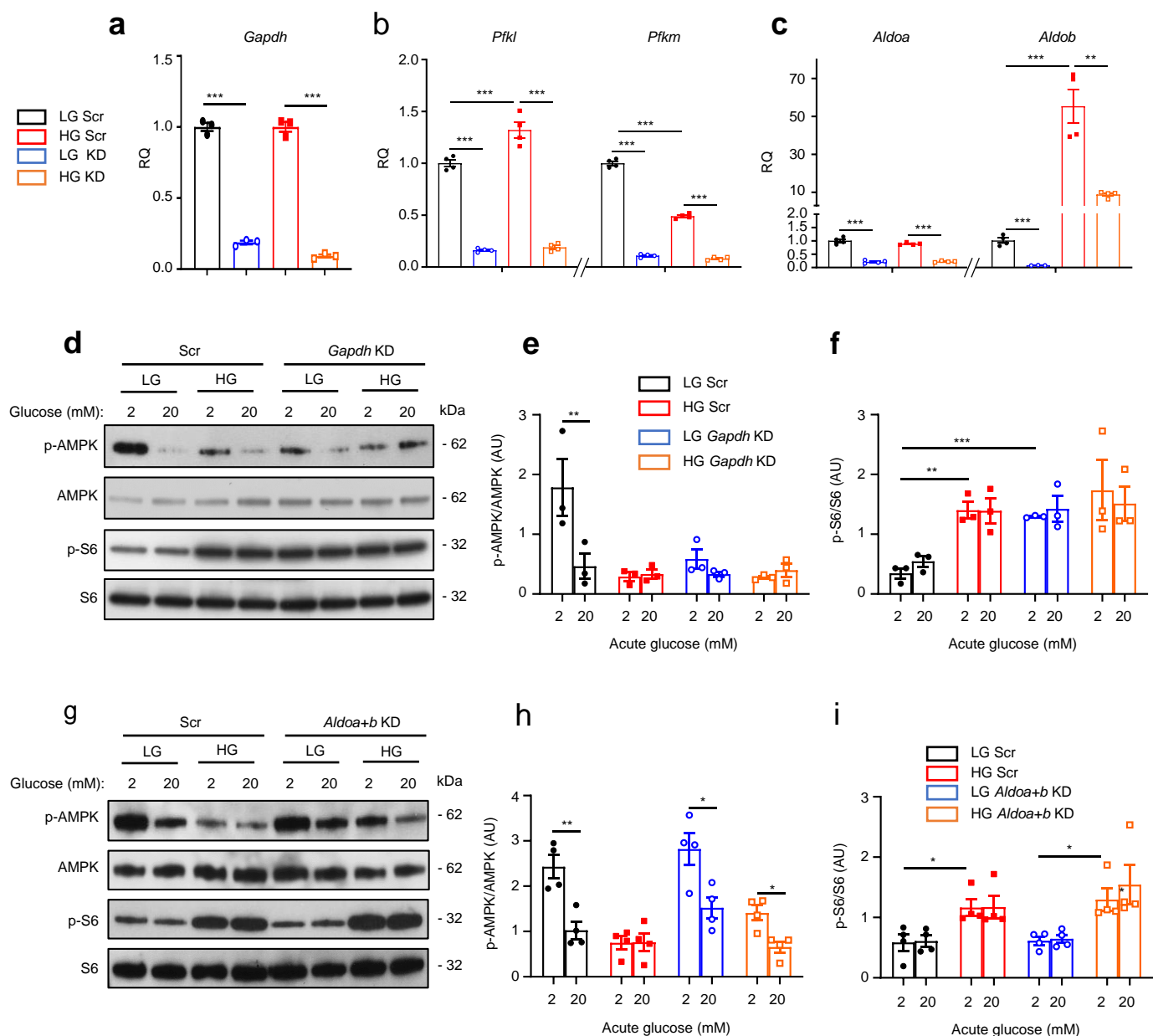
All panels show individual data points and mean ± s.e.m. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, two-tailed unpaired Student's t-test. Source data are provided in the Supplementary Source Data file.



**Supplementary Figure 3. Inhibition of GAPDH induces gene changes to similar those induced by chronic hyperglycaemia**

- (a) GAPDH activity in LG-cells (black) and HG-cells (red) (n=3 biologically independent experiments).
- (b,c) Acute effects of 5μM koniginic acid (KA) on GAPDH activity (b, n=3 independent experiments) and insulin secretion (c, n=5 biologically independent experiments). LG-cells were exposed to KA for 30mins.
- (d) Metabolite abundances in LG-cells cultured for 48 hr in the absence (black) or presence (blue) of 5μM koniginic acid (KA) and subsequently stimulated with 2mM or 20mM glucose for 1h in the absence of KA (n=3 biologically independent experiments).

All panels show individual data points and mean ± s.e.m. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, two-tailed unpaired Student's t-test. Source data are provided in the Supplementary Source Data file.



**Supplementary Figure 4. Effects of GADPH and Aldolase knockdown on AMPK and mTOR**

(a) *Gapdh* mRNA level in LG-cells and HG-cells cultured for 48hrs with either scrambled siRNA (Scr) or *Gapdh* siRNA (KD) (n=3 biologically independent experiments).

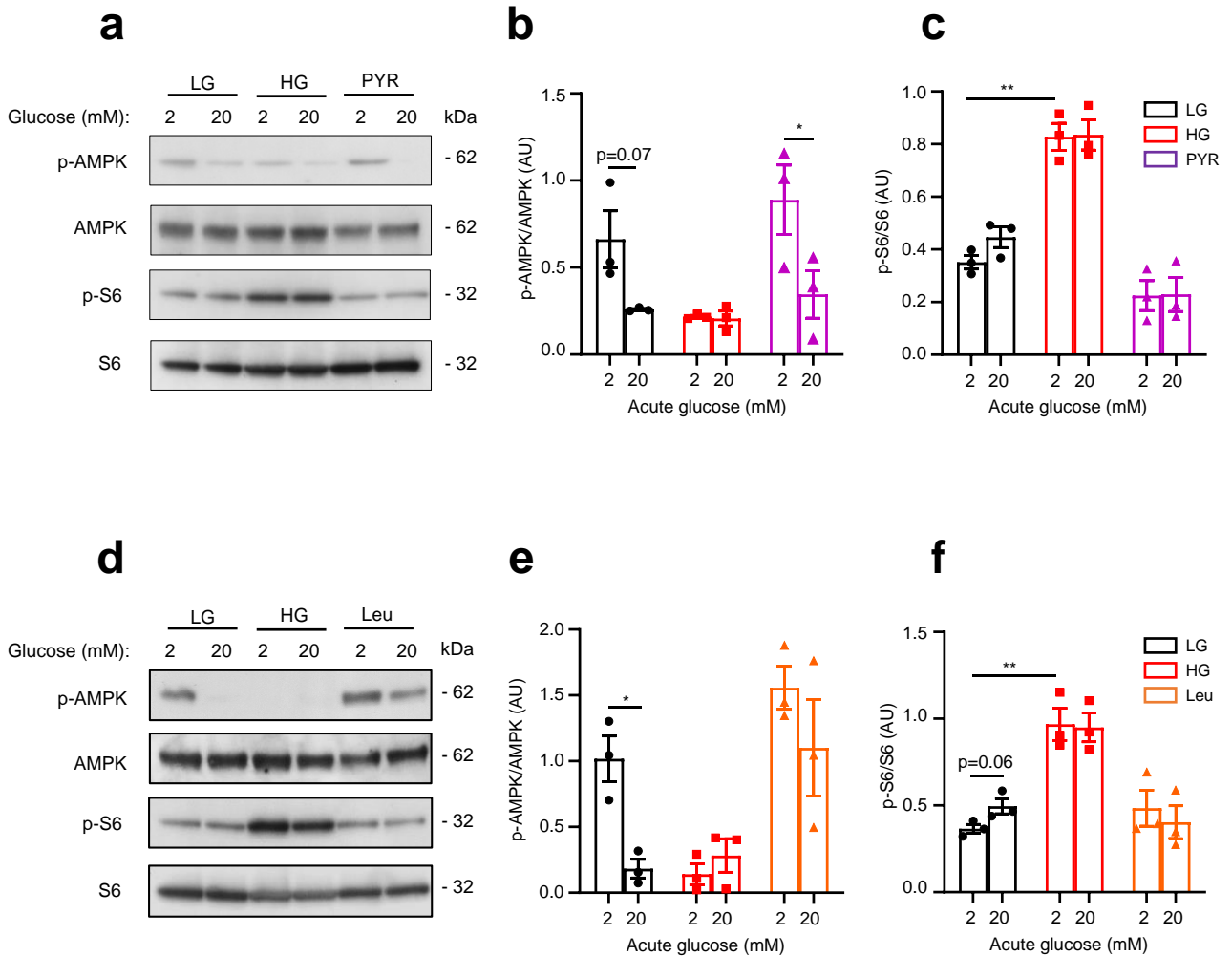
(b) *Pfkf1* and *Pfkf2* mRNA levels in LG-cells and HG-cells cultured for 48hrs with either scrambled siRNA (Scr) or both *Pfkf1* and *Pfkf2* siRNAs (KD) (n=4 biologically independent experiments).

(c) *Aldoa* and *Aldob* mRNA levels in LG-cells and HG-cells cultured for 48hrs with either scrambled siRNA (Scr) or both *Aldoa* and *Aldob* siRNAs (KD) (n=4 biologically independent experiments).

(d) Representative Western blot of lysates from cells transfected with scrambled siRNA (Scr) or *Gapdh* siRNA (*Gapdh* KD) and cultured at low (LG) or high (HG) glucose for 48h. Cells were subsequently stimulated with 2mM or 20mM glucose for 1h. Phosphorylated (p) and total AMPK and S6. (e, f) Quantitative densitometry analysis of p-AMPK/AMPK (e, n=3 independent experiments) and p-S6/S6 (f, n=3 biologically independent experiments).

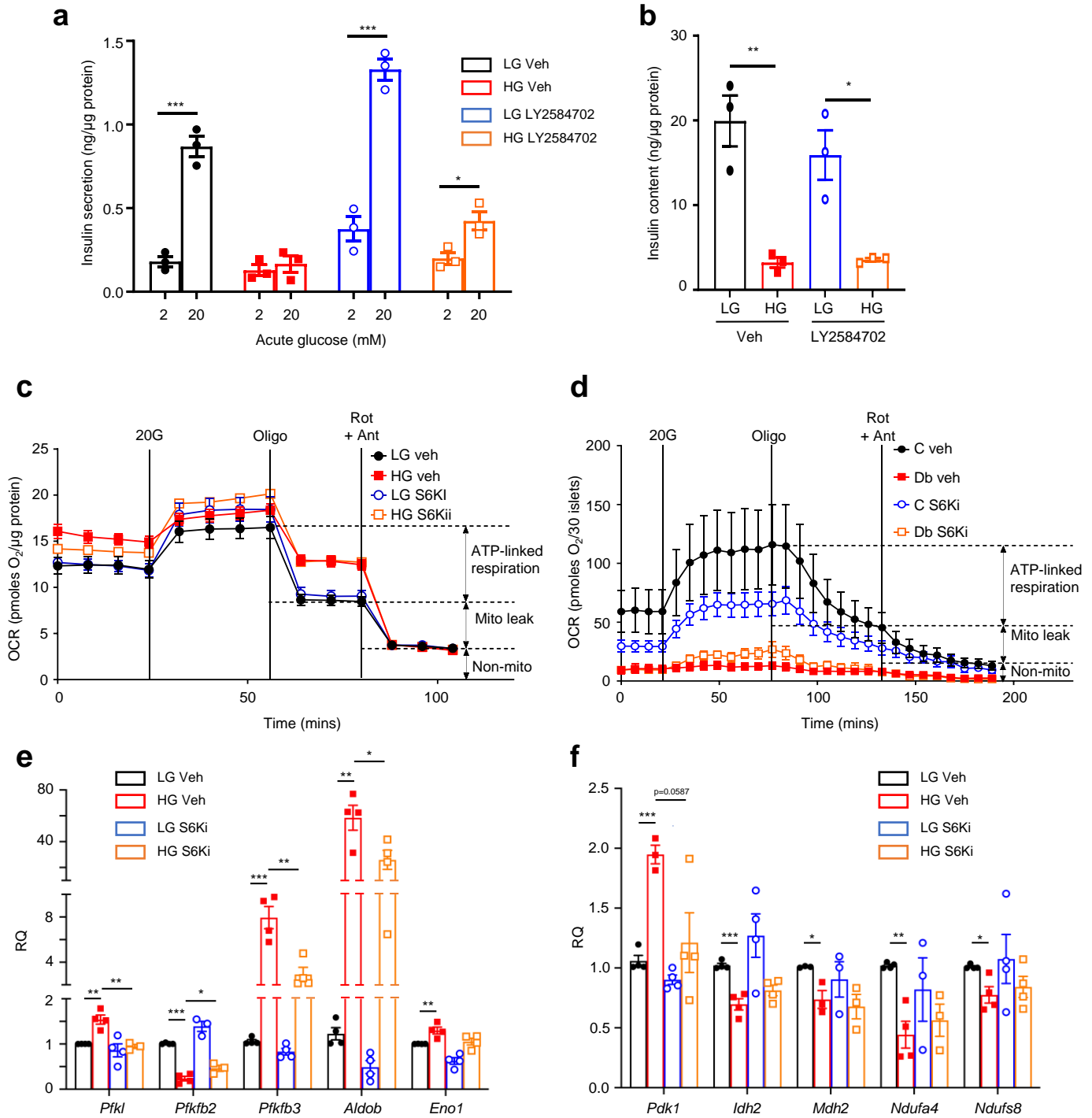
(g) Representative Western blot of lysates from cells transfected with scrambled siRNA (Scr) or *Aldoa* and *Aldob* siRNA (*Aldoa+b* KD) and cultured at low (LG) or high (HG) glucose. Cells were subsequently stimulated with 2mM or 20mM glucose for 1h. Phosphorylated (p) and total AMPK and S6. (h,i) Quantitative densitometry analysis of p-AMPK/AMPK (h, n=4 biologically independent experiments) and p-S6/S6 (i, n=4 biologically independent experiments).

All panels show individual data points and mean  $\pm$  s.e.m. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, two-tailed unpaired Student's t-test. Uncropped Western blots are provided at the end of this file. Source data are provided in the Supplementary Source Data file.



**Supplementary Figure 5. Effects of chronic Me-pyruvate and leucine on AMPK and mTOR**

- (a) Representative Western blot of lysates from LG-cells, HG-cells and cells cultured for 48hr in 20mM Me-pyruvate (PYR), and then stimulated with 2mM or 20mM glucose for 1hr. Phosphorylated (p) and total AMPK and S6.
- (b,c) Quantitative densitometry analysis of p-AMPK/AMPK (b, n=3 biologically independent experiments) and p-S6/S6 (c, n=3 biologically independent experiments). LG-cells (black), HG-cells (red), 20mM Me-pyruvate (purple).
- (d) Representative Western blot of lysates from LG-cells, HG-cells and cells cultured for 48hr in 20mM leucine (Leu), then stimulated with 2mM or 20mM glucose for 1hr. Phosphorylated (p) and total AMPK and S6.
- (e,f) Quantitative densitometry analysis of p-AMPK/AMPK (e, n=3 biologically independent experiments) and p-S6/S6 (f, n=3 biologically independent experiments). LG-cells (black), HG-cells (red), 20mM leucine (orange).
- Data are individual data points plus mean±sem. \*p < 0.05, \*\*p < 0.01, two-tailed unpaired Student's t-test. Uncropped Western blots are provided at the end of this file. Source data are provided in the Supplementary Source Data file.



**Supplementary Figure 6. Inhibition of S6 kinase partially prevents the effects of chronic hyperglycaemia**

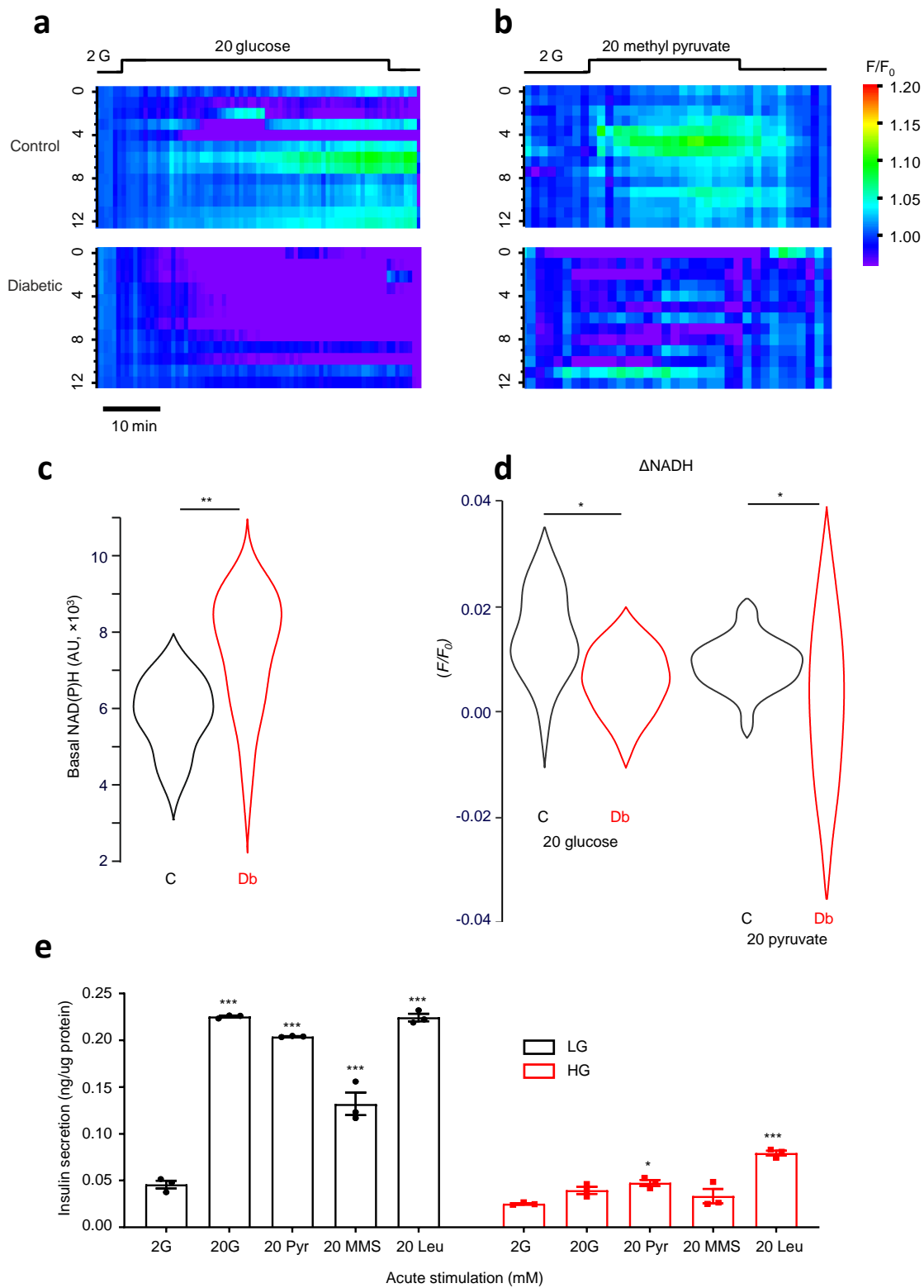
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**Supplementary Figure 6. Inhibition of S6 kinase partially prevents the effects of chronic hyperglycaemia**

- (a,b)** Insulin secretion **(a)** and insulin content **(b)** in LG-cells and HG-cells cultured for 48hr in the presence of absence of 10 $\mu$ M of the S6 kinase inhibitor, LY2584702 (n=3 independent experiments). **(b)** Oxygen consumption rate (OCR) of LG- and HG-cells cultured for 48hr  $\pm$  10 $\mu$ M of the S6 kinase inhibitor PF-4708671 (S6Ki). OCR is shown at 2mM glucose and after sequential addition of 20mM glucose (20G), 1  $\mu$ M oligomycin (Oligo) and 0.5 $\mu$ M rotenone + 0.5 $\mu$ M antimycin A (Rot+Ant) (n=5 biologically independent experiments/group).
- (c)** Oxygen consumption rate (OCR) of control and diabetic islets cultured for 48hr  $\pm$  10 $\mu$ M S6Ki. OCR is shown at 2 mM glucose and after sequential addition of 20mM glucose (20G), 5  $\mu$ M oligomycin (Oligo) and 5  $\mu$ M rotenone + 5  $\mu$ M antimycin A (Rot+Ant). Control islets (black, n=7 mice examined over 7 independent experiments), Diabetic islets (red, n=7 animals examined over 7 independent experiments), Control islets + S6Ki (blue, n=7 mice examined over 10 independent experiments), Diabetic islets + S6Ki (orange, n=7 mice examined over 8 independent experiments).
- (e,f)** mRNA levels for the indicated genes involved in glycolytic **(e)** and mitochondrial **(f)** metabolism assessed by qPCR in LG-cells and HG-cells cultured for 48hrs  $\pm$  10 $\mu$ M of the S6-kinase inhibitor PF-4708671 (S6Ki). *Pfkfb3*, *Aldob*, *Eno1*, *Idh2*, n=4 biologically independent experiments for all conditions; *Mdh2*, n=3 biologically independent experiments for all conditions; *Pfkfb2*, *Ndufa4*, n=4 biologically independent experiments for LG+Veh and HG+Veh but n=3 biologically independent experiments for LG+S6Ki and HG+S6Ki; *Pfkl*, n=4 biologically independent experiments for LG+Veh, HG+Veh and LG+S6Ki but n=3 biologically independent experiments for HG+S6Ki. *Pdk1*, n=4 biologically independent experiments for LG+Veh, LG+S6Ki and HG+S6Ki but n=3 biologically independent experiments for HG+Veh

All panels show mean  $\pm$  s.e.m. \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001; two-tailed unpaired Student's t-test. Source data are provided in the Supplementary Source Data file.





**Supplementary Figure 7**  
For legend see next page

**Supplementary Figure 7. Diabetic islets display an attenuated response to glycolytic and mitochondrial substrates**

- (a,b)** Representative heatmaps of the time course of NADH autofluorescence in islets isolated from control and  $\beta$ V59M diabetic mice, as indicated, in response to **(a)** a glycolytic (20 mM glucose, 20G) or **(b)** a mitochondrial (20 mM methyl-pyruvate) substrate.
- (c,d)** Quantification of the magnitude of NADH autofluorescence for control (C) and diabetic (Db) islets. **(c)** Basal (2 mM glucose) autofluorescence of NAD(P)H in arbitrary units.  $n = 71$  control islets and  $n=140$  diabetic islets. As control and diabetic islets were imaged in the same field arbitrary units can be compared. **(d)** Fold change in NAD(P)H fluorescence intensity induced by 20 mM glucose ( $n=83$  control islets and  $n=150$  diabetic islets) or 20 mM methyl pyruvate ( $n=54$  control and  $n=78$  diabetic islets).
- (e)** Insulin secretion in LG-cells and HG-cells stimulated for 1h with 2mM glucose or 20mM glucose (G), 20mM methyl pyruvate (MeP), 20mM monomethyl succinate (MMS) or 20mM leucine (leu) ( $n=3$  biologically independent experiments).
- All panels show mean  $\pm$  s.e.m. \* $p < 0.05$ , \*\* $p < 0.01$ ; (c-d), two-tailed unpaired Student's t-test. (e), two-way ANOVA with Bonferroni post hoc corrections. Source data are provided at the end of this file.

Antibody	Source	Dilution
Rabbit anti-phospho-AMPK $\alpha$ -T172 antibody	Cell Signaling Technology, cat. #2535	1:1000
Rabbit anti-AMPK $\alpha$ antibody	Cell Signaling Technology, cat. #2532	1:1000
Rabbit anti-phospho-S6-S240/244 antibody	Cell Signaling Technology, cat. #5364	1:4000
Rabbit anti-S6 antibody	Cell Signaling Technology, cat. #2217	1:4000
Rabbit anti-phospho-PDHe1 $\alpha$ -S293	Cell Signaling Technology, cat. #31866	1:1000
Rabbit anti- $\alpha$ tubulin antibody	Cell Signaling Technology, cat. #2144S	1:1000
Rabbit anti-phospho-Raptor (Ser792) Antibody	Cell Signaling Technology, cat. #2083	1:1000
Rabbit anti-Raptor Antibody	Cell Signaling Technology, cat. #2280	1:1000
Rabbit anti-phospho-4E-BP1 (Thr37/46) Antibody	Cell Signaling Technology, cat. #2855	1:1000
Rabbit anti-4E-BP1 Antibody	Cell Signaling Technology, cat. #9644	1:1000

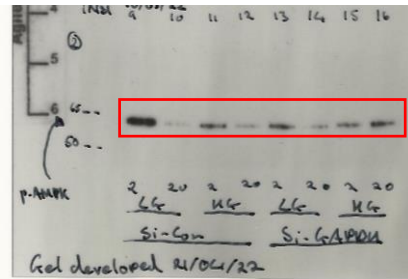
**Supplementary Table 1 A. Western blot antibodies**

Gene	Catalogue number (Applied Biosystems)
<i>Actb</i>	Rn00667869_m1
<i>Aldoa</i>	Rn00820577_g1
<i>Aldob</i>	Rn01768292_m1
<i>Eno1</i>	Rn01518942_gH
<i>Gapdh</i>	Rn01775763_g1
<i>Hprt1</i>	Rn01527840_m1
<i>Hspa8</i>	Rn00821191_g1
<i>Idh2</i>	Rn01478119_m1
<i>Mdh2</i>	Mm00725890_s1
<i>Ndufa4</i>	Mm00809672_s1
<i>Ndufs8</i>	Mm00523063_m1
<i>Pdk1</i>	Mm00554306_m1
<i>Pfkfb2</i>	Mm00435575_m1
<i>Pfkfb3</i>	Rn00678825_m1
<i>Pfkl</i>	Mm00435587_m1
<i>Pfkm</i>	Mm01309576_m1
<i>Sdha</i>	Rn00590475_m1

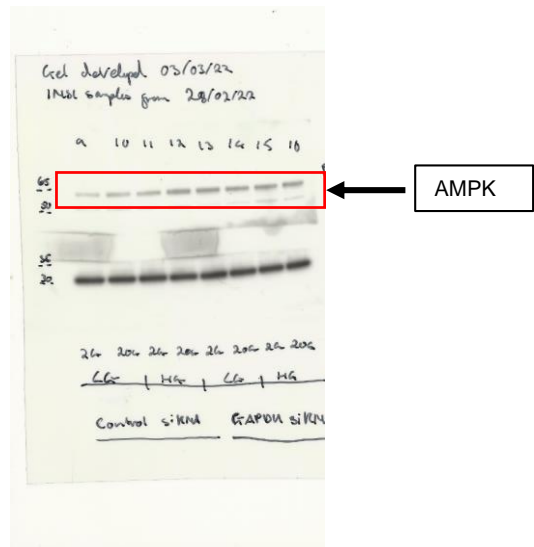
**Supplementary Table 1B. Taqman probes**

# Uncropped western blots for Supplementary Fig.4d

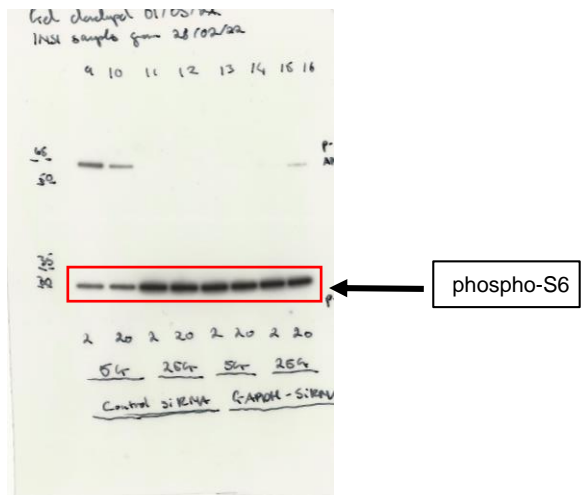
phospho-AMPK (red box refers to bands in Fig.S4d)



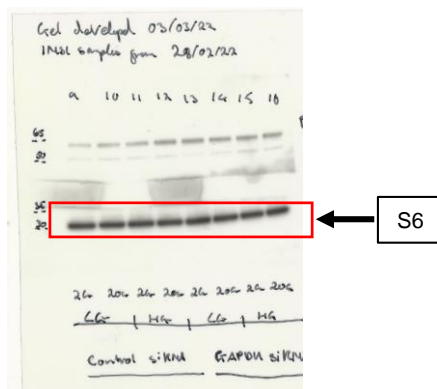
AMPK (red box refers to bands in Fig.S4d)



phospho-S6 (red box refers to bands in Fig.S4d, bands at 62 kDa are from different antibody)

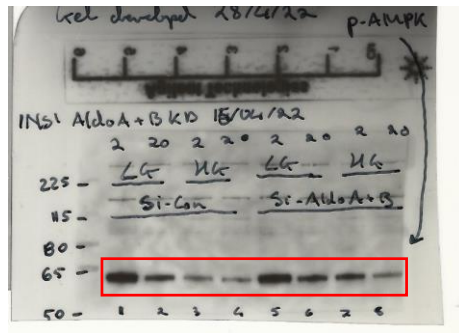


S6 (red box refers to bands in Fig.S4d)

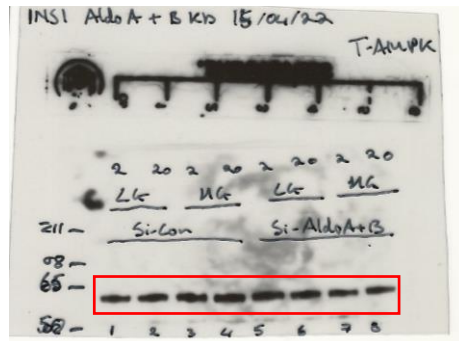


## Uncropped western blots for Supplementary Fig.4g

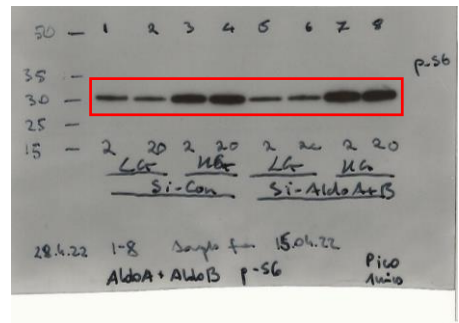
phospho-AMPK (red box refers to bands in Fig.S4g)



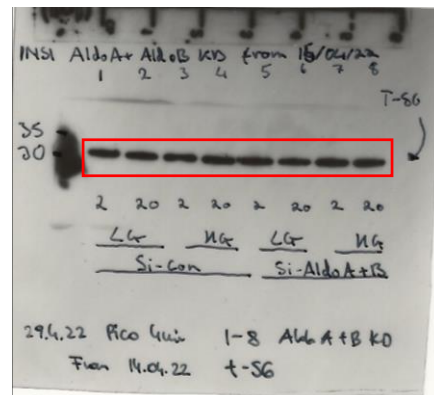
AMPK (red box refers to bands in Fig.S4g)



phospho-S6 (red box refers to bands in Fig.S4g)

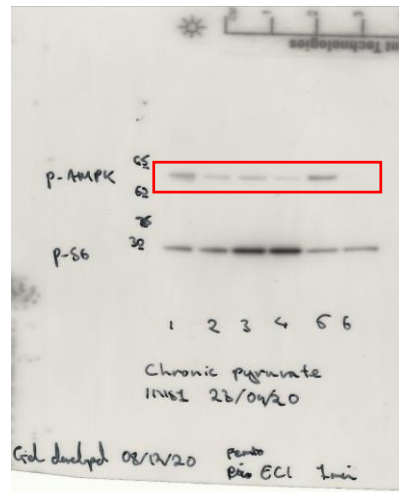


S6 (red box refers to bands in Fig.S4g)

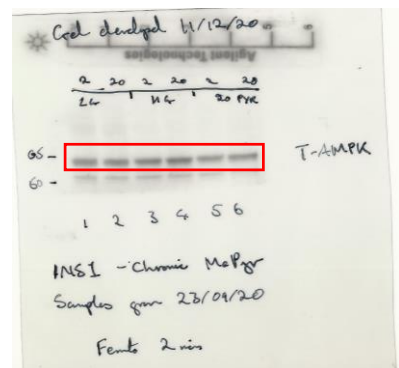


Uncropped western blots for Supplementary Fig.5a

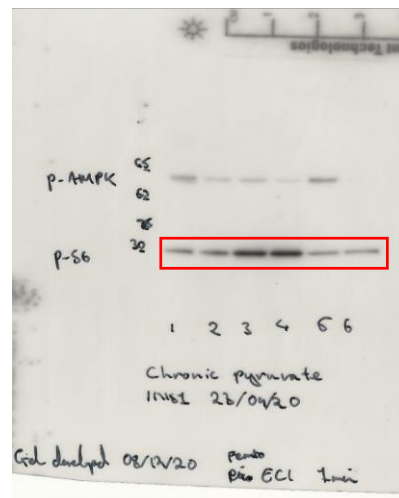
phospho-AMPK (red box refers to bands in Fig.S5a, bands at 32 kDa are from separate antibody on separate membrane)



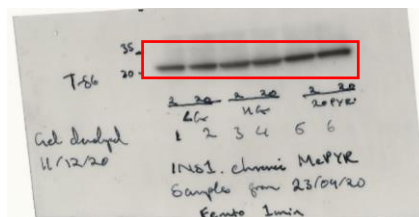
AMPK (red box refers to bands in Fig.S5a)



phospho-S6 (red box refers to bands in Fig.S5a, bands at 62 kDa are from separate antibody on separate membrane)

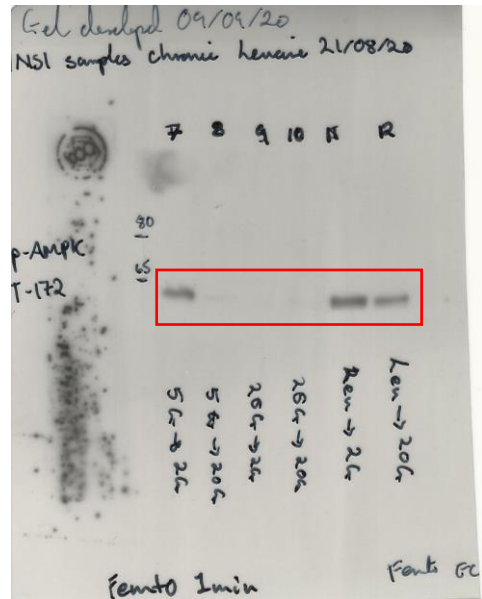


S6 (red box refers to bands in Fig.S5a)

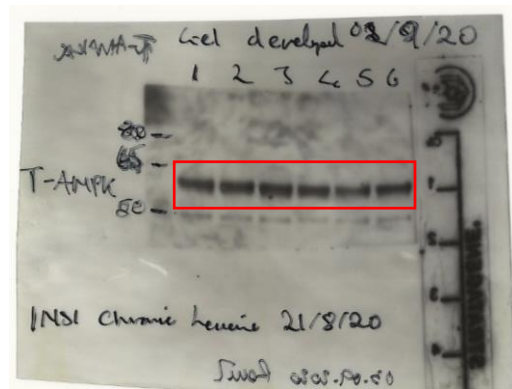


Uncropped western blots for Supplementary Fig.5d

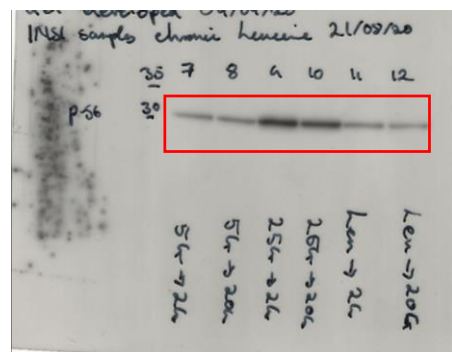
phospho-AMPK (red box refers to bands in Fig.S5d)



AMPK (red box refers to bands in Fig.S5d)



phospho-S6 (red box refers to bands in Fig.S5d)



S6 (red box refers to bands in Fig.S5d, bands at 62 kDa are from separate antibody on separate membrane)

