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mTORC1 to AMPK Switching Underlies β -Cell Metabolic Plasticity During Maturation and Diabetes

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Abstract

Pancreatic beta cells (β -cells) differentiate during fetal life, but only postnatally acquire the capacity for glucose-stimulated insulin secretion (GSIS). How this happens is not clear. In exploring what molecular mechanisms drive the maturation of β -cell function, we found that the control of cellular signaling in β -cells fundamentally switched from the nutrient sensor target of rapamycin (mTORC1) to the energy sensor 5'-adenosine monophosphate-activated protein kinase (AMPK), and that this was critical for functional maturation. Moreover, AMPK was activated by the dietary transition taking place during weaning, and this in turn inhibited mTORC1 activity to drive the adult β -cell phenotype. While forcing constitutive mTORC1 signaling in adult β -cells relegated them to a functionally immature phenotype with characteristic transcriptional and metabolic profiles, engineering the switch from mTORC1 to AMPK signaling was sufficient to promote β -cell mitochondrial biogenesis, a shift to oxidative metabolism, and functional maturation. We also found that type 2 diabetes, a condition marked by both mitochondrial degeneration and dysregulated GSIS, was associated with a remarkable reversion of the normal AMPK-dependent adult β -cell signature to a more neonatal one characterized by mTORC1 activation. Manipulating the way in which cellular nutrient signaling pathways regulate β -cell metabolism may thus offer new targets to improve β -cell function in diabetes.

Introduction

During the neonatal period, pancreatic islets progressively lose their proliferative capacity and develop instead the capacity for highly sensitive and robust glucose-stimulated insulin secretion (GSIS) (1). This functional maturation is complex, involving both metabolic and transcriptional remodeling of pancreatic β -cells (2, 3). However, the specific cues and responsive molecular mechanisms mediating this cellular remodeling remain poorly understood.

Previous studies suggest that β -cell maturation and the capacity for GSIS are regulated by a diverse set of factors. First, altered macronutrient consumption initiated upon weaning is associated with changes in islet microRNA (miRNA) levels (4, 5). Next, the transition induced during weaning is associated with enhanced glucose-stimulated oxidative phosphorylation and insulin secretion (6), the induction of key β -cell-specific transcription factors promoting mitochondrial function and oxidative metabolism (3, 7, 8), and expression of UCN3, an essential marker of mature β -cells (1). Weaning is also associated with methylation-dependent repression of transcripts involved in anaerobic glycolytic metabolism (2). Together, these changes support the notion that the induction of GSIS, and the corresponding attenuation of proliferation, among β -cells are associated with a remodeling of cellular metabolism. However, the signaling hierarchy, in particular master regulators, in charge of this remodeling remains elusive.

mTOR (the mammalian target of rapamycin) is a nutrient-sensitive kinase critical for the regulation of postnatal pancreatic β -cell proliferation and growth (9,

10). Two mTOR complexes exist, mTORC1 and mTORC2, reflecting differences in regulation and subunit composition (11). Several reports show that mTORC1 promotes β -cell proliferation in utero and during the neonatal period (12, 13) through the regulation of cyclins D2 and D3, and CDK4 (9). Furthermore, β -cell-specific ablation of TSC1 or TSC2 (the upstream inhibitors of mTOR) results in increased postnatal β -cell mass (10, 14, 15). On the other hand, β -cell-specific deletion of mTORC1 in mice results in severe glucose intolerance due to underdeveloped β -cell mass (16-18). Collectively, these data indicate that mTORC1 expression is required for the development and growth of β -cells during embryonic and early postnatal life.

AMPK (5' adenosine monophosphate-activated protein kinase) is a master sensor of cellular energy status (19) and a potent inhibitor of mTORC1 activity (20, 21). Its kinase activity is regulated by the intracellular ratio of ATP vs. AMP/ADP, serving as a key sensor for energy stress (22). In opposition to mTORC1, AMPK has an evolutionarily conserved role in restraining cellular growth and proliferation in response to limitations in cellular energy availability (22). Moreover, deleting LKB1 (an upstream AMPK activator) increases β -cell proliferation and mass by inducing the mTORC1 pathway, resulting in enhanced insulin output (23-25). Furthermore, work from our group and others using mice lacking both AMPK α 1 and α 2 highlights the importance of AMPK for a mature β -cell phenotype, including adult-like insulin secretory characteristics (25-27).

Here we show, using both genetic and nutritional approaches, that a concerted switch from mTORC1- to AMPK-dependent cellular signaling mediates

the manifestation of several features that define functional β -cell maturation. Furthermore, we show that this same switch, when engaged in the reverse direction, underlies a process leading to β -cell dysfunction in driving type 2 diabetes (T2D). In sum, the reciprocal opposition between mTORC1 and AMPK determines whether β -cells adopt a more proliferative, immature phenotype, or the mature, highly insulin-responsive phenotype essential for postnatal life.

Results

β -cells switch from mTORC1 to AMPK-dependent signaling during postnatal maturation.

To identify pathways critical for β -cell maturation, we performed RNAseq on neonatal and adult β -cells from mouse pancreata. Islets from MIP-GFP mice were harvested at both postnatal days 6 and 45, dispersed, and β -cells were isolated by fluorescence-activated cell sorting (FACS) (Figure 1A). Principal components analysis (PCA) of these RNAseq data showed that the neonatal (P6) β -cell replicates cluster together, away from the adult (P45) replicates (Supplemental Figure 1A). Gene Set Enrichment Analysis (GSEA) (28) showed that the neonatal β -cell transcriptome is enriched for pathways regulating the cell cycle, whereas adult β -cell transcriptomes are enriched for genes comprising the citrate (TCA) cycle and mitochondrial electron transport chain (Supplemental Figure 1C).

Analysis of specific genes related to either β -cell proliferation (*Nek2*, *Cenpf*, *Cenpe*, *Mki67*, *Cdk1*, *Rfc5*, *Ccna2*, *Pole*) or β -cell maturation (*Ins1*, *Ins2*, *Ucn3*, *G6pc2*, *Ero1lb*, *Syt4*, *Pcsk1*, *Mafb*) confirmed that immature neonatal β -cells have relatively higher mRNA levels of proliferation markers, and that by adulthood this phenotype switches to one characterized by the induction of mRNA encoding indicators of maturation (Supplemental Figure 1D). This clearly evident switch confirmed the quality and reliability of our RNAseq datasets.

Further analysis of the RNAseq data revealed that the levels of mRNA encoding AMPK and mTORC1 pathway-regulated transcripts were markedly

different between neonatal and adult β -cells. Specifically, the expression of mTORC1 activator and effector genes was elevated in neonatal β -cells, whereas genes in the AMPK pathway (*Prkaa2*) were induced in adult β -cells (Figure 1B).

We next assessed the activation of mTORC1 in pancreatic islets by immunofluorescence using the Ser240/244 phosphorylation of its downstream target rpS6 as readout. We found that mTORC1 is highly active in neonatal β -cells, but that this activation is dramatically decreased around P18 and is undetectable in adult β -cells (Figure 1C). FACS analysis confirmed this observation, showing that cells doubly positive for insulin and phospho-rpS6 (p-rpS6) comprised 20% of the cells in neonatal islets, but only 5% of the cells in adult islets (Figure 1D).

Of note, we also observed heterogeneous mTORC1 activity in cell types surrounding the islets of both neonatal and adult mice. Indeed, mTORC1 is a common controller of cellular energy metabolism, and its activation in exocrine cell types has been shown (18, 29), suggesting this observation was to be expected.

To further dissect the process of β -cell maturation and the mechanism underlying mTORC1 inhibition in adult islets, we assessed the expression and activity of AMPK, an upstream regulator and inhibitor of mTORC1 (20, 21) in both neonatal and adult islets. In line with the RNAseq data, immunoblotting showed that total AMPK catalytic α subunit protein abundance is substantially lower in neonatal islets than adult islets (figure 1E). Additionally, although AMPK activity (α subunit p-Thr-172) in cultured islets was generally reduced by increasing extracellular glucose concentration (2.8 mM to 16.7 mM) as described (30, 31), both total and p-AMPK were consistently elevated in the β -cells of adult vs.

neonatal islets (Figure 1E). These data indicate that that β -cells, which represent 60-80% of mouse pancreatic islets (32) undergo a pronounced induction of both AMPK expression and activity during the neonatal-to-adult transition.

Moreover, the pattern of AMPK activity in the context of isolated islets was reciprocal to that of mTORC1. For example, whereas total and phospho-AMPK were increased in adult vs. neonatal islets, the opposite was true for phospho-rpS6 (Figure 1E). Moreover, whereas phospho-AMPK was relatively reduced by switching adult islets from low to high glucose, mTORC1 activity measured concomitantly was relatively increased by this switch (Figure 1E and Supplemental Figure 1E).

We also measured levels of p-AMPK (Thr-172) in pancreatic sections, a convenient proxy for in situ AMPK activation, though we note that AMPK is also regulated by AMP, ADP, and direct allosteric mechanisms (19). Whereas no neonatal β -cells stained for p-AMPK (n=30 islets; 4 mice per group), adult β -cells were robustly positive for p-AMPK by comparison (Figure 1F). All of these data together highlight the intriguing concept that the transition of pancreatic β -cells from neonatal to adult life occurs in the context of a fundamental switch from mTORC1 to AMPK-dependent signaling.

Weaning from maternal milk induces the switch from mTORC1 to AMPK signaling in β -cells.

To investigate what regulates the reciprocal relationship between mTORC1 and AMPK signaling in maturing β -cells, we analyzed both adult human and adult

mouse islets that were treated for 12 hours with either everolimus (an mTORC1 inhibitor) or 5-aminoimidazole-4-carboxamide-1-beta-d-ribofuranoside (AICAR, an AMPK activator) (19). As expected, everolimus treatment inhibited mTORC1 activity in β -cells, as revealed by a dramatic reduction in specific rpS6 phosphorylation, but hardly altered AMPK phosphorylation. By contrast, AICAR treatment was sufficient to both activate AMPK and completely abrogate mTORC1 phosphorylation in both mouse and human islets (Figures 2A & 2B, with associated quantifications in Supplemental Figures 2A & 2B). Taken together, these findings indicate that inhibiting mTORC1 activity is not sufficient on its own to activate AMPK in β -cells, but that activating AMPK is sufficient to repress mTORC1. This unidirectional relationship supports the concept that AMPK, as in other systems, is a key repressor of mTORC1 in β -cells. Indeed, its activation is responsible for shutting off mTORC1 signaling, triggering a key step in β -cell maturation.

The process of weaning, which in mice starts in the third week of life, is associated with decreased reliance on the consumption of fat-rich maternal milk in favor of an adult-type diet with a more carbohydrate-rich macronutrient composition (33). Given the role of mTORC1 as a nutrient-sensing kinase, we hypothesized that postnatal β -cell maturation may represent an adaptation to the cessation of milk consumption, and that mTORC1 repression through AMPK activation may act as a physiological mediator of this process.

To test this hypothesis, we enabled mice to continue to consume a diet highly enriched for milk fat by giving them access to a milk fat-rich diet and supplementing this with daily milk fat gavage, beginning at P11-P13 and continuing

through adulthood (P40). This allowed us to maintain high milk fat consumption in the mice during the period over which weaning normally occurs. Remarkably, allowing mice to continue assimilating milk fat throughout their entry into adulthood, a period during which this is usually declining, was sufficient to allow β -cells to maintain neonatal levels of mTORC1 activity, which was otherwise completely repressed in the control mice (Figure 2C).

We next assessed the expression and phosphorylation of β -cell AMPK and rpS6 in the islets of these mice. Unlike the AMPK activation seen in the islets of adult mice weaned onto standard chow, islets from mice that continued milk fat consumption past weaning displayed a marked suppression of AMPK phosphorylation, although not all the way to neonatal levels, despite the entry into adulthood (Figure 2D). Similarly, extending milk fat consumption past weaning tended to produce higher levels of p-rpS6 within the islets of adult mice, though this trend was not significant (Figure 2D and Supplemental Figure 2C).

We also examined whether continuing milk fat consumption from the neonatal period into adulthood in mice impacts β -cells function. Mice provided with milk fat by gavage from P11 into adulthood had lower serum glucose levels than did vehicle-treated control mice, both at baseline and during a glucose tolerance test, indicative of constitutively enhanced glucose clearance (Figure 2E & supplemental Figure 2D). Supporting this, β -cell (INS⁺) area tended to be higher in milk fat-supplemented mice than in controls, though this trend was not statistically significant (Supplemental Figure 2E). Moreover, the percentage of proliferating (Ki67⁺) β -cells was higher in the mice provided milk fat than it was in control mice

(Figure 2F). We also found that mRNA levels for the maturity markers *Ins1*, *Ins2*, and *Mafa* were lower in the islets of the mice provided milk fat (Supplemental Figure 2F). Islet mRNA levels of *Ucn3*, by contrast, were not affected, although this is not surprising given that ~93% of β -cells already express *Ucn3* by P13, which is prior to weaning (1).

These data together highlight that continuing milk fat consumption from the neonatal period into adulthood in mice is sufficient to maintain an immature β -cell phenotype, and strongly support the concept that shifting from fat to carbohydrate consumption during weaning is a previously unrecognized mechanistic driver of mTORC1 to AMPK switching and consequent functional β -cell maturation.

mTORC1 maintains the immature phenotype of pancreatic β -cells.

To definitively test whether mTORC1 is responsible for maintaining the immature phenotype of neonatal pancreatic β -cells, we generated Rip-Cre:*Tsc1*^{F/F} mice (β TSC1 KO), where TSC1, the upstream negative regulator of mTORC1, is deleted, leading to a constitutive activation of mTORC1 in β -cells (Figure 3A). β TSC1 KO mice also carry a YFP allele, having been crossed onto a ROSA26-stop-EYFP line, with the latter serving as a lineage tracing tool to assess Cre expression and genomic recombination. All subsequent experiments were performed using β TSC1 KO mice or littermate (*Tsc1*^{F/F}; or *Tsc1*^{+/+}, Cre⁺) controls. We confirmed that Cre expression in β TSC1 KO mice is restricted to pancreatic β -cells by demonstrating co-localization of insulin and YFP staining (data not shown). Transcriptional analysis confirmed that *Tsc1* mRNA is significantly reduced in islets

from β TSC1 KO mice versus those from control mice (Figure 3B). Confirming the direct consequence of deleting TSC1 specifically in β -cells, ~85% of pancreatic β -cells in β TSC1 KO mice had increased specific p-rpS6 staining intensity, indicative of upregulated β -cell mTORC1 activity (Supplemental Figures 3A & 3B). Measuring pancreatic INS⁺ area histologically showed that constitutive activation of mTORC1 in adult β TSC1 KO mice increases β -cell mass (Figure 3C), mirroring what was seen in response to milk-fat gavage.

To more fully determine whether constitutively activating mTORC1 recapitulates an immature islet phenotype in adult mice, we performed RNAseq on islets from adult β TSC1 KO and control mice. We first explored a list of β -cell disallowed genes that are known to be upregulated in neonatal islets (2, 34). Gene set enrichment analysis (GSEA) showed that adult β TSC1 KO islets were enriched for the expression of such genes (Figure 3D). Moreover, expression of key maturation genes (*Ins1*, *Ins2*, *Unc3*, *G6pc2*, *Erol1b*, *Syt4*, *Pcsk1*, *Mafa*) was concomitantly reduced in adult β TSC1 KO islets when compared to control islets (Figure 3E). Assessment of MafA by immunostaining mirrored the transcriptional data, as MafA expression was reduced in the islets of β TSC1 KO vs. control mice (Supplemental Figure 3C). Together, these data indicate that forcing β -cell-specific mTORC1 activation in mice results in the expression of a transcriptional pattern, including critical genes, that is typical of neonatal islets.

In addition to sharing a transcriptional signature with neonatal β -cells, β TSC1 KO islets were also functionally immature. For example, serum insulin levels in β TSC1 KO mice were higher, both after fasting and after glucose

stimulation when compared to those of control mice (Supplemental Figure 3D). Correspondingly, β TSC1 KO mice had relatively lower fasting blood glucose levels (mean value of 83 mg/dL in β TSC1 KO vs. 109 mg/dl in control) and cleared injected glucose faster (Supplemental Figures 3E & 3F). Furthermore, analysis of dynamic insulin secretion ex vivo showed that β TSC1 KO islets have increased basal insulin secretion at low glucose concentrations but fail to significantly increase this secretion in response to glucose challenge, a behavior seen in immature β -cells (Figure 3F).

To further confirm the ability of mTORC1 to elicit an immature phenotype in adult pancreatic β -cells, we also crossed *Tsc1^{F/F}* mice with those expressing the inducible MIP1-CreER driver in order to generate iTSC1 KO mice (Fig 3G). We first noted that treating adult iTSC1 KO mice with tamoxifen was sufficient to markedly induce p-rpS6 staining among β -cells in pancreatic islets (57% stained for p-rpS6), indicative of strong mTORC1 activation (Supplemental Figure 3G). In assessing β -cell function we noted that, similar to what was seen in both β TSC1 KO mice and WT mice maintained on dietary milk fat during their entry into adulthood, fasting blood glucose levels were lower after 3 weeks of tamoxifen administration in iTSC1 KO mice than in *Tsc1^{F/F}* (no Cre) littermates (Supplemental Figure 3H). Moreover, serum insulin levels were higher, both after fasting and after 30 minutes of glucose stimulation, and injected glucose was correspondingly cleared more rapidly in iTSC1 KO mice versus controls (Figures 3H & 3I). Together, these data show that inducing mTORC1 activation in adult β -cells is

sufficient to spontaneously revert them to an immature, neonatal-type functional state.

AMPK activation triggers a switch to oxidative metabolism in mature islets.

In line with data from Yoshihara et al. (3), analysis of our RNAseq data from neonatal and adult pancreatic β -cells (Supplemental Figure 1C) revealed an induction of TCA cycle and electron transport chain pathway genes during the transition to adulthood. Intriguingly, 9 out of the total 13 genes encoded by mitochondrial DNA (mtDNA) were up-regulated in adult pancreatic β -cells during this transition. This included the genes encoding cytochrome c oxidase subunits I, II, and III; the NADH dehydrogenases 1, 2, 4, 5, and 6, and the ATP synthase F_0 subunit 6. The expression of other genes, including *Uqcrrh*, *Uqcrrq*, *Cox5b*, and *Cox6a2*, which are part of the mitochondrial respiratory chain, was also increased in adult versus neonatal pancreatic β -cells (Figure 4A). Together, these data suggest that the maturation of pancreatic β -cells is orchestrated in conjunction with increased mitochondrial function and oxidative metabolism.

To address the mechanism(s) leading to increased expression of mitochondrial genes, we assessed the ratio of mtDNA copy number per genomic DNA copy number by qPCR. mtDNA copy number in adult islets (mean of 444/cell) was ~2 times higher than in neonatal ones (mean of 218/cell) (Figure 4B), suggesting that β -cell maturation is tied to increased mitochondrial mass. Consistent with this concept, mRNA levels of two regulators of mitochondrial biogenesis, *Ppargc1a* (PGC1 α) and *Ppargc1b* (PGC1 β), were also higher in adult

vs. neonatal islets, suggesting that mitochondrial biogenesis is important for β -cell maturation (Figure 4C).

Given that the abundance of mtDNA is tightly correlated with cellular respiratory activity (35), we sought to directly assess mitochondrial function by measuring oxygen consumption in neonatal and adult islets using a bioenergetic analyzer (Seahorse XF). The glucose-stimulated increase in oxygen consumption was markedly higher in isolated adult vs. neonatal islets, as was maximal oxygen consumption, which can be measured after treating islets with the mitochondrial uncoupler carbonyl cyanide-4-(trifluoromethoxy) phenylhydrazone (FCCP) (Figure 4D). These data confirm that the increase in β -cell mitochondrial mass seen during the transition from neonatal to adult life is commensurate with a pronounced induction of mitochondrial activity.

AMPK activation is known to promote oxidative metabolism (36). We therefore hypothesized that AMPK activation might be responsible for the increase in β -cell mitochondrial number and function that we saw during islet maturation. To investigate this possibility, we simultaneously eliminated both AMPK1 and AMPK2 (AMPKdKO) expression selectively in pancreatic β -cells by crossing *Prkaa1^{F/F}/Prkaa2^{F/F}* mice with Ins-Cre (26) or Rip-Cre (37) mice. RNAseq of islets from adult AMPKdKO (Ins-Cre) and floxed (no Cre) control mice showed that the transcriptomic signatures of AMPKdKO islets were similar to those of WT neonatal islets, importantly including down-regulation of the same set of mtDNA-encoded and respiratory pathway genes induced during normal adult β -cell maturation (Figure 4E). Monitoring mitochondrial numbers by electron microscopy confirmed

that adult AMPKdKO (Rip-Cre) islets have fewer and smaller mitochondria than those of controls (Figures 4F and 4G). We also treated adult islets from WT mice with compound C, an AMPK inhibitor (38) to confirm our findings in AMPKdKO mice. Remarkably, compound C treatment for 24 hours reduced the number of mitochondria in adult islets, recapitulating the knockout phenotype (Figure 4H).

The importance of AMPK regulation during β -cell maturation was also evident in our studies with milk fat supplementation. For example, WT mice that continued to consume milk fat throughout the period when weaning normally occurs had lower islet mRNA levels of *Ppargc1a* (no difference for *Ppargc1b*) than did mice weaned onto regular chow in a normal manner (Figure 4I). Taken together, our findings highlight the important role of cellular AMPK activation as a switch that is flipped in response to shifting patterns of macronutrient consumption and that turns on β -cell oxidative metabolism, a hallmark of their adult phenotype.

T2D induces increased β -cell mTORC1 activity and a reversion of pancreatic islets to an immature phenotype.

Insulin resistance, a precursor of T2D, stimulates β -cell proliferation in conjunction with hyperinsulinemia (39). Mice lacking functional leptin receptors (*db/db*) are profoundly obese and develop severe, symptomatic hyperglycemia that is often used to model T2D. Notably, *db/db* mice also exhibit a period of compensatory hyperinsulinemia prior to developing overt T2D (40, 41). Given that neonatal islets are also hyperproliferative and display increased insulin secretion, we wondered whether the phenotype of *db/db* mice might involve a reversion of

pancreatic β -cells back to a relatively immature phenotype. If so, we further wondered whether this reversion could stem from a switch between AMPK and mTORC1 signaling in the opposite direction from that seen during normal β -cell maturation.

To test these hypotheses, we performed RNAseq on islets isolated from 4 week-old *db/db* mice and their WT littermates. We found that, in a manner reminiscent of neonatal islets, the expression of mTORC1 activators and mTORC1 effector genes were increased, while the expression of mTORC1 inhibitors and in particular *Prkaa1*, the gene encoding the AMPK alpha-1 subunit, were repressed in *db/db* islets vs. controls (Figure 5A). Moreover, islet immunostaining (p-rpS6 at Ser240/244) showed that mTORC1 activity was higher in β -cells from *db/db* mice than control mice (Figure 5B).

To more deeply probe the phenotype of islets in the context of T2D, the transcriptomes of *db/db* and control islets were analyzed using GSEA against a curated list of maturation genes (e.g. *Ins2*, *Ucn3*, *G6pc2*, *Erol1b*, *Pcsk1n*). Each of these genes was down-regulated in *db/db* versus control islets (Figure 5A). Together, these data support the concept that, as hyperglycemia emerges in *db/db* mice, mTORC1 activity increases and AMPK activity falls, leading to the downregulation of genes normally expressed in functionally mature β -cells. These observations points to T2D as being a state characterized by a reversion of β -cells towards an immature phenotype. Consistent with this view, *db/db* islets secreted more insulin than control islets (Figure 5C) and had both lower glucose-stimulated

and maximal OCR than did control islets, indicating reduced oxidative respiratory capacity in line with downregulated AMPK activity (Figure 5D).

To further explore the roles of AMPK and mTORC1 in diabetic islets, we used both everolimus and AICAR to modulate the activity of AMPK and mTORC1, respectively, in *db/db* islets from 12-week-old mice, and then assessed GSIS. Inhibiting mTORC1 with everolimus had no effect on insulin secretion from *db/db* mouse islets. By contrast, repressing mTORC1 activity by activating AMPK with AICAR resulted in enhanced insulin secretion at both 2.8mM and 16.7mM extracellular glucose (Figure 5E).

We also examined whether the relationship between mTORC1 and AMPK in islets translated to human subjects, including healthy individuals and those with T2D. Immunostaining for p-rpS6 (Ser240/244) revealed increased mTORC1 activation in islets from individuals with T2D (Figure 5F), a reactivation consistent with reversion to an immature phenotype, and matching observations in islets from *db/db* mice. We simultaneously assessed mTORC1 activation in isolated β -cells sorted as previously described (42) from islets dispersed from the pancreata of healthy subjects and those with T2D. Immunoblots of this β -cell-enriched population showed that whereas total rpS6 levels were similar between control samples and those from individuals with T2D, levels of p-rpS6 (Ser240/244) were increased in the context of T2D, mirroring what was seen by islet immunostaining. We similarly assessed activation of AMPK in sorted β -cells and found that although there was less total AMPK in the context of T2D ($p=0.045$, $n=3$), levels of p-AMPK (Th172) were specifically reduced as well (Figure 5G). These data reveal a new

mechanism, involving reactivation of a neonatal signaling pattern in β -cells, that underlies β -cell dysfunction in T2D spanning from mouse models to human subjects. Indeed, we show that islets from individuals with T2D are characterized by relative mTORC1 activation and AMPK inhibition.

Discussion

β -cell maturation entails the acquisition of GSIS capability and a loss of proliferative capacity. The principal aims of this study were to explore what governs these dynamic changes, an important issue given that a reversal of functional β -cell maturity may contribute to deficient glucose responsiveness in T2D (43) and, conceivably, to the failure of residual β -cells in Type 1 diabetes (44). We show using multiple approaches that a switch from mTORC1- to AMPK-dependent signaling in β -cells controls this process, both in mice and humans.

Relative mTORC1 activation in neonatal islets is associated β -cell proliferation and constitutive insulin secretion, as compared to less proliferative and more specifically glucose responsive adult islets. Remarkably, artificially reactivating mTORC1 in adult islets could recapitulate the neonatal phenotype, as it was sufficient to both reduce the expression of maturity-defining β -cell genes and impair normal GSIS. Others have demonstrated a similar effect by activating mTORC1 via β -cell-selective deletion of Raptor, which also decreases β -cell mass and size, and reduces GSIS (18).

Our work probing the TSC1/2 complex in β -cells further supports the importance of mTORC1 signaling in maintaining β -cell immaturity. Importantly, these findings also agree with data from earlier studies (9, 10, 14, 45). For example, constitutively activating mTORC1 signaling by inactivating TSC1 or TSC2 leads to an expansion of β -cell mass via enhanced cell division (14) and hypertrophy (10, 46).

Our ability to induce an mTORC1-dependent subsidence of normal GSIS may involve altered expression of genes involved in glucose sensing, for example upregulation of the low K_M hexokinase (HK1) and de-repression of “disallowed” genes including *Ldha*, in line with previous reports (26, 47). Such alterations would enhance glycolytic ATP generation, leading to closure of ATP-sensitive K^+ channels and constitutive insulin release even at low extracellular glucose levels (30). Inducing mTORC1-dependent β -cell immaturity may also compromise both triggering (48) and amplifying (49, 50) pathways needed for appropriate GSIS in response to increasing extracellular glucose levels. The consequence of this mTORC1-driven regime is to prompt basal insulin secretion but impair glucose responsiveness.

This all indicates that a repression of mTORC1-dependent signaling is required to license β -cells to undergo transcriptional and functional maturation. We show here that AMPK, a known inhibitor of mTORC1 in other contexts, is responsible for exerting this repressive effect. Indeed, prior work showed a tight reciprocal relationship between AMPK activity and mTORC1 signaling in clonal mouse β -cells (51). Moreover, deleting the upstream AMPK kinase LKB1 markedly increases mTORC1 signaling in islets, an effect likely due, at least in part, to AMPK inhibition (24, 25). Although we show ample evidence supporting the reciprocal relationship between AMPK and mTORC1 in maturing β -cells here, we did not clearly see increased mTORC1 signaling in islets from mice lacking both AMPK α subunits (results not shown). However, this probably reflects effects related to deleting AMPK chronically and during development.

Beyond its direct effects on modulating the phosphorylation state of mTORC1 (11), AMPK may potentiate β -cell maturation in other ways as well. For example, AMPK may act to repress the expression of disallowed genes (26). Although the precise mechanism by which this might occur is unknown, there is evidence suggesting that AMPK can regulate β -cell miRNA levels (26, 27) and potentially induce epigenetic changes that alter chromatin accessibility at relevant genomic loci (unpublished data).

Importantly, several of the phenotypic features of immaturity inducible in β -cells and islets by forcing either mTORC1 activation or AMPK inhibition could be reproduced by maintaining high milk fat consumption in mice emerging from the neonatal period. Indeed, our data support the concept that AMPK activation, and consequent mTORC1 inhibition among β -cells during the transition from neonatal to adult life are driven by specific shifts in macronutrient consumption that take place when animals wean from near-constant consumption of a relatively high-fat milk diet and begin to consume a mixed diet that is relatively carbohydrate-rich in a diurnally recurring manner. This dietary shift might significantly lower the time-averaged intracellular ATP vs. ADP/AMP ratios in β -cells due to decreased overall oxidative flux through the TCA cycle. Such a reduction would be expected to activate AMPK via both well-defined posttranslational modifications (phosphorylation of α subunits at Thr-172) and potentially by other transcriptional and/or translational mechanisms.

We also show that AMPK activation in adult islets likely promotes mitochondrial biogenesis, as mitochondrial genes (and nuclear-encoded genes

involved in mitochondrial function) were clearly repressed in AMPKdKO mouse islets. This repression correlates with the concomitant switch we observed away from ATP generation via oxidative phosphorylation.

Other changes concomitant with β -cell maturation include a characteristic shift in islet polarization, islet compaction, and their organization into rosette-like structures around islet capillaries, concordant with their ability to sense glucose and secrete appropriate amounts of insulin into the blood (52). These changes occur during the postnatal period, increase significantly by P11, and reach a maximum during the entry into adulthood (53).

The Wnt/planar cell polarity (PCP) pathway, conserved across mammals, regulates islet polarity and compaction, through its effector Flattop, to promote β -cell maturation and function (53). The ratios of Flattop-negative to Flattop-positive β -cells are similar to the ratios we quantified for p-rpS6-positive to -negative β -cells, suggesting that the process driving islet polarization and compaction may be linked to the β -cell mTORC1-AMPK signaling switch we highlight. Interestingly, LKB1-AMPK signaling is known to be important in establishing pancreatic β -cell polarity. For example, deleting LKB1, an AMPK activator, leads to the inappropriate positioning of nuclei around capillaries, and altered localization of cilia at the center of rosettes (24). Thus, mTORC1-AMPK switching may orchestrate multiple interconnected aspects of β -cell and islet maturation.

Our findings indicate, strikingly, that mTORC1 activation in models of T2D (mouse and human) may both initiate and drive changes in β -cell signaling, phenotype, and function that are part of both the transient compensatory response

to systemic insulin resistance, as well as the subsequent deterioration that ultimately produces T2D. Indeed, mTORC1 activation was increased in islets of both *db/db* mice and human subjects with T2D, when compared with relevant controls. Similar findings were recently reported by Yuan et al, who observed a decrease in mTORC2 activation in islets from diabetic subjects (54). The former studies, however, did not provide any insights into the regulation of mTORC1 or mTORC2 activity.

We suggest that lowered AMPK activity is likely to be a major driver of increased mTORC1 signaling in T2D islets, driving β cells to a more immature state. Indeed, previous work (55) reported lowered AMPK activation in T2D islets, although specific reductions in levels of AMPK α subunits was not observed. Likewise, Solimena et al (56) report that AMPK and insulin/IGF-1 signaling in islets are specifically affected in people with T2D, using laser capture microdissection to show changes in pancreatic mRNA levels of both *PRKAB2* (AMPK β 2) and *PRKAG2* (AMPK γ 2).

How AMPK activity is reduced in T2D remains an open question. When measured in vitro at equal glucose concentrations, glucose oxidation is lowered in the islets of those with T2D vs. those of control subjects (55). This is somewhat puzzling, as the hyperglycemia characterizing T2D might be expected to increase metabolic flux in β -cells and, in turn, increase intracellular ATP vs. ADP ATP/AMP ratios, which is not what has been reported. At any rate, altered energetic flux likely underlies the reduction in phosphorylation of catalytic AMPK α subunits that takes place in the context of T2D. Resolving this issue will require precise measurements

of adenine nucleotides, as well as the activity of other AMPK regulators including the relevant upstream kinases and phosphatases (22) in T2D β -cells.

Our study provides comprehensive evidence indicating mTORC1 and AMPK form a reciprocally coupled switch that is controlled by metabolic and nutritional factors and that is central to the maturation of the pancreatic β -cell. Remarkably, this same switch becomes defective, operating in a reverse direction and promoting β -cell immaturity and consequent functional impairment in T2D. Therapeutic approaches to stimulate AMPK activity in the β -cell may thus provide valuable new tools to improve insulin output in this disease, complementing the recently-reported actions of such drugs in insulin-sensitive tissues (57, 58).

Materials and Methods

Mouse studies

MIP-GFP (B6.Cg-Tg(Ins1-EGFP)1Hara/J) mice were used to sort pancreatic β -cells and perform RNAseq on a pure pancreatic β -cell population. C57BL/6J mice were used to assess pancreatic β -cell maturation and confirm the data obtained from RNAseq. β TSC1 KO and iTSC1 KO mice were generated by crossing Rip-Cre mice (B6N.Cg-Tg(Ins2-Cre)25Mgn/J) and MIP1-CreER (B6.Cg-Tg(Ins1-Cre/ERT)1Lphi/J) mice, respectively, with mice expressing conditional alleles of *Tsc1*^{F/F} (*Tsc1*^{F/F}; *Tsc1*tm1Djk/J). AMPKDKO mice were generated as previously described (26, 37). All these mice, including *db/db* mice (BKS.Cg-Dock7m +/+ Leprdb/J), were purchased from The Jackson Laboratory.

MIP-GFP and Rip-Cre mice express a human growth hormone (hGH) mini-gene (59), a fact that could cause confusion when interpreting results obtained using either model. To avoid confounds and associated ambiguity in our data analysis, we used a series of controls to confirm the validity of the data we obtained using both MIP-GFP and Rip-Cre mice. MIP-GFP mice were used to facilitate easy sorting of pancreatic β -cells, and thus simplify performing RNAseq on a highly pure β -cell population. Note that because we compared neonatal vs. adult MIP-GFP mice, both groups had β cells expressing the same mini-gene. Thus we compared between chronological ages while spreading the impact, if any, of the mini-gene evenly across groups. This fact reduces the likelihood that any differences we observed were due to the presence of the hGH mini-gene *per se*.

We further confirmed the validity of the RNAseq data obtained using MIP-GFP mice in C57BL/6 mice, which do not express the mini-gene at all. For example, the RNAseq data obtained from the β -cells of MIP-GFP mice supported a relative activation of mTORC1 in neonatal pancreatic β -cells and relative activation of AMPK in adult β cells. Each of these findings were rigorously confirmed in C57BL/6 mice by immunofluorescence histology, β -cell FACS, and immunoblot.

Moreover, the RNAseq experiment on MIP-GFP β -cells revealed a switch in cellular metabolism and an increase in the expression of mitochondrial genes. We confirmed these data too by assessing mitochondrial number, the relative mRNA levels of *Ppargc1a* and *Ppargc1b*, and cellular oxygen consumption all independently in islets from C57BL/6 mice. Taken together, these controls offer considerable evidence to support the contention that our findings in β cells using the MIP-GFP model are not a consequence of the hGH mini-gene in the construct used to make the mice.

Rip-Cre mice were used for crossing with *Tsc1^{F/F}* mice to generate Rip-Cre-dependent TSC1-deficient mice (β TSC1 KO mice). However, in our studies, we compared *Tsc1^{F/F}* mice (Cre-negative), Rip-Cre mice (no flox), and β TSC1 KO mice (Cre⁺). In this comparison, we found no differences between mice that expressed TSC1 but either did (Rip-Cre, no flox) or did not (*Tsc1^{F/F}*) express the hGH mini-gene. As such, we can confidently conclude that the differences we found are due to the forced activation of mTORC1, and not due to off-target effects resulting from the mini-gene. Moreover, we also used a completely separate inducible Cre model (MIP1-CreER), which does not express the hGH mini-gene,

to activate mTORC1 in adult mice (iTSC1 KO). iTSC1 KO mice (no mini-gene) had a phenotype similar to the one seen in β TCS1 KO mice, which expressed the mini-gene. As Rip-Cre mice were also used to generate AMPKDKO mice in order to assess the number of mitochondria per β -cell area, and mitochondrial volume density per β -cell. The controls used in these experiments are heterozygous mice ($Prkaa1^{+/F}/Prkaa2^{+/F}$; Rip-Cre⁺) in order to again spread the presence of the hGH mini-gene equally across groups.

Mice were fed *ad libitum* and housed under a 12-hour light/12-hour dark cycle. Genotyping was performed by Transnetyx on tail snips using a PCR-based protocol. For tamoxifen inducible mice, we injected adult mice (8 weeks old) with 75 mg/kg of tamoxifen i.p. for 5 consecutive days.

In order to maintain milk fat as a principal source of nutrients and to reduce consumption of carbohydrates, Newborn pups (males and females) were provided oral milk fat (1% v/w) or vehicle by daily gavage beginning at P11-P13 while remaining with their nursing mothers in the presence of dietary pellets containing 42% of calories from milk fat (Western diet). At P21, control pups were weaned on a standard rodent chow diet with vehicle gavage, whereas the milk fat group was weaned onto a Western diet while continuing to receive daily milk fat gavage. All mice were maintained in this manner until they were analyzed at P40.

Metabolic and physiological analyses.

Fasting blood glucose concentrations in mice were determined using a handheld glucometer (Freestyle Lite) after 6 hours of fasting. For in vivo glucose

challenges, mice were fasted for 6 h, after which serum insulin and blood glucose were collected by sub-mandibular bleeding prior to and 30 minutes following an i.p. injection of glucose (2g/kg); serum was collected by centrifugation and insulin levels measured by ELISA (Mercodia). For glucose tolerance tests, blood glucose levels were measured before, and 15, 30, 60, and 120 minutes following an i.p. injection of glucose (2g/kg).

An automated perfusion system (BioRep Technologies, Miami FL) was used to measure dynamic insulin secretion by islets. 20-30 size-matched islets per mouse were immobilized in Bio-Gel P-4 Gel (Bio-Rac, Hercules CA) that was maintained at 37°C in a temperature-controlled chamber. Islets were perfused at 100uL/min with Krebs-Ringer bicarbonate buffer supplemented with 0.25% BSA (KRB buffer) and containing 2.8mM glucose for a preincubation period of 30 minutes. Islets were next perfused in sequence with KRB buffer containing 2.8mM glucose for 20 minutes, following by KRB buffer containing 16.7mM glucose for 30 minutes, and finally KRB buffer containing 30mM KCl for 10 minutes. Flow-through was collected every minute during the three perfusion steps of the assay. Islets were next recovered from the chambers and insulin content was extracted by overnight incubation in acid/ethanol solution. For static measurements of GSIS by *db/db* islets, the newly isolated islets were first incubated overnight in medium with 11mM glucose, after which they were preincubated in KRB buffer containing 2.8mM glucose with or without 1mM AICAR or 40uM everolimus for 1 hour. The islets were next incubated in KRB buffer containing 2.8mM glucose for 30 minutes, 16.7mM glucose for another 30 minutes, and then KCl as above, with respective

AICAR or everolimus treatment maintained during steps. The supernatant was collected after each incubation. Total Insulin content was then extracted from islets by overnight incubation with acid ethanol solution. Insulin in the supernatants and islet extracts was then measured by ELISA.

Flow cytometry and β -cell sorting

Islets from neonatal (P6) or post-weaning (P45) mice were dissociated, fixed, permeabilized and stained for p-rpS6 and insulin (#5018 or #9008, respectively, Cell Signaling Technology) for FACS analysis using a LSRFortessa X20Dual machine. FACS data were analyzed with FlowJo software.

Islets from MIP-GFP mice were digested into a single-cell suspension and sorted for GFP by FACS to 85%–95% average purity. Sorted cells were then processed for RNA extraction.

Human islet samples were obtained from both healthy adult organ donors and adult donors with T2D. Islets were dissociated using Accumax for 7-8 minutes and washed 3 times with PBS containing 2% BSA and 2.8mM glucose. Cells were next incubated for 30 minutes at 4°C in the presence of the pancreatic marker antibodies HPi2 (#77-HPi2-PU-0.1 clone HIC1-2B4, ALPCO) and HPa3 (kindly provided by Dr. Markus Grompe). After washing, samples were incubated at room temperature for an additional 30 minutes in presence of fluorescent-coupled secondary antibodies. Cells were next washed and resuspended in PBS containing 2% BSA and 2.8mM glucose. Before sorting, DAPI stain was added to

distinguish live vs. dead cells. The details of gating strategy are shown in Supplemental Figure 4A.

Transmission electron microscopy (EM) analysis

Pancreatic islets (~30) were fixed in 2.5% [wt./vol.] glutaraldehyde in 0.1 M phosphate buffered saline, pH 7.3 (PBS) at 4°C. After being washed in PBS, islets were post-fixed in 0.1% [w/v] osmium tetroxide in PBS and dehydrated in a graded series of ethanol. The islets were then rapidly transferred to propylene oxide and embedded in PolyBed 812 (Polysciences, Inc).

Ultrathin sections were cut with a diamond knife, stained with uranyl acetate and lead citrate, and observed under a Zeiss 902 transmission electron microscope. β -cells were identified under EM by their distinct morphology including dense core granules (60). β -cells were considered dead based on a loss of plasma membrane integrity, fragmentation into discrete bodies, or engulfment of the cell corpse or its fragments by an adjacent cell (61). The presence of marked chromatin condensation and/or of blebs were considered signs of apoptosis, whereas massive vacuole accumulation and absence of chromatin condensation were considered signs of autophagy (62).

For morphometric studies, volume density values were derived from the evaluation of 3-5 different islets for each pancreas. 12 photomicrographs were taken of each islet at $10^5 \times$ magnification. A graticule (11x11 cm) composed of 169 points was placed on the micrographs, and the number of points intersecting the autophagic vacuoles and mitochondria was counted. Volume density of

intracellular organelles was calculated according to the formula: $VD = P_i/P_t$, where P_i is the number of points within the subcellular component and P_t is the total number of points within the cells, and expressed in ml/100ml of tissue (ml%) (63).

Assessments of cellular metabolism and mitochondrial number.

The oxygen consumption rate (OCR) of β -cells was measured in real time using a Seahorse XF24 analyzer (Seahorse Bioscience). Batches of 30 islets were loaded into islet capture microplates and covered with a mesh to prevent movement of the islets during the assay. This was followed by incubation in a non- CO_2 incubator at 37°C for 1 hour. 3-5 measurements in 2.8 mM glucose were taken, followed by replacement with 16.7mM glucose and sequential addition of 5 μ M Oligomycin, 1 μ M FCCP, 5 μ M Rotenone and 5 μ M Antimycin A. OCR was normalized to the average baseline measurement in 2.8mM glucose, and expressed as a percentage changes from this baseline during the assay. After the experiment, the islets underwent DNA extraction, and the number of mitochondria was determined by qPCR as a ratio of mtDNA copy number per genomic DNA copy number using the following primers: For mtDNA: Forward gagcatcttatccacgcttcc, Reverse ggtgtactcccgtgtaaa. For genomic DNA: Forward cttccccactggcctcaag Reverse ccaaaacccagtgatccagc.

Immunofluorescence staining and morphometric analysis of islets.

A standard immunofluorescence protocol was performed to stain paraffin sections of fixed human and mouse pancreata using the following primary

antibodies: anti-phospho-Ser240/244-rpS6 (#5364, cell signaling technologies), anti-phospho-Thr172-AMPK (#2535S, cell signaling technology) anti-insulin (A056401-2, Agilent), anti-Pdx1 (F109-D12, Developmental Studies Hybridoma Bank), anti-MafA (NBP1-00121, Novus biologicals). Briefly, pancreatic tissue was flushed with PBS, dissected, fixed in buffered zinc formalin fixative (Z-Fix, Anatech Ltd) overnight, dehydrated in grades of ethanol, and processed for paraffin embedding. 5µm sections were heated, de-waxed, and rehydrated through a series of ethanol dilutions then placed in distilled H₂O. Heat-induced epitope retrieval was performed by immersion in antigen unmasking solution (H-3300, Vector) and microwave heating. After blocking with antibody diluent (DAKO), sections were incubated with a primary antibody and then with appropriate Alexa 488- or 555-coupled secondary antibodies (Jackson Research). Nuclei were counterstained using DAPI. To stain with anti-p-AMPK (Thr172), PBS-flushed pancreata were perfused in vivo with 4% PFA via intracardiac catheter prior to dissection in order to fix the pancreas as fast as possible. The pancreata were then dissected and incubated for 2h in 4% PFA and then conserved in OCT at -80c until sectioning. Cyrosections were then washed with PBS followed by the antigen retrieval and blocking steps as described above.

RNA isolation, RT-PCR, and real-time PCR.

RNA was isolated using Direct-zol (zymo research) and digested with RNase-free DNase to eliminate DNA. RNA (50-200ng) was used for preparation of cDNA using Superscript IV Reverse transcriptase (Invitrogen) by the oligo(dT)

priming method. qPCR was performed using the 1× Fast SYBR Green Mix (Applied Biosystems) in an ABI7900HT system (Applied Biosystems). The expression levels of each transcript were normalized to the housekeeping gene RPLP19. The primer sequences used are listed in Supplemental Table 1.

RNAseq library generation

For neonatal vs adult, β TSC1 KO vs control, and *db/db* vs control RNAseq analyses, Total RNA was isolated from the appropriate prep using Direct-zol RNA MicroPrep plus (Zymo Research), following the manufacturer's instructions. Sequencing libraries were prepared from 10-25 ng of total RNA using the SMARTer Stranded RNAseq Kit (Clontech) according to the manufacturer's protocol. Briefly, after rRNA depletion, remaining RNA was used for first-stranded cDNA synthesis and purification, after which the samples were ligated to unique adapters and PCR amplified. Libraries were then validated using a 2100 BioAnalyzer (Agilent), normalized, and pooled for sequencing using the UCSF Institute for Human Genetics core service.

To process RNAseq libraries, adaptor sequences were trimmed using Cutadapt version 1.13 (64), requiring a length greater than 20 nt after trimming, and quality-filtered by requiring all bases to have a minimum score of 20 (-m 20 -q 20). Only reads that passed the quality or length threshold on both strands were considered for mapping. Reads were mapped with the spliced-read mapper GSNAP (version 2016-08-10) (65) using default parameters. Reads were aligned against the NCBI37 (mm9) genome build release 67 downloaded from

Ensemble. Reads mapping to the genes of interest were counted using HTseq (v.0.7.1) (66) in the union mode. Differential expression analysis was performed in R using DESeq2 (v.1.16.0) (67) with the default parameters, including the Cook's distance treatment to remove outliers. AMPKDKO RNAseq data were obtained as previously described (26).

RNA-seq data that support the findings of this study have been deposited in the Gene Expression Omnibus (GEO) under accession code GSE132261. From Kone et al, data for RNA-Seq are available at the European Molecular Biology Laboratory–European Bioinformatics Institute (EMBL-EBI) ArrayExpress website accession number E-MTAB-2791.

Immunoblotting

Cells were lysed in ice-cold RIPA Buffer containing a cocktail of protease and phosphatase inhibitors. Lysates were kept on ice for 5 minutes and cleared by centrifugation. Protein concentrations were determined using the Pierce 660nm Protein Assay, and immunoblotting was performed using the Bolt mini-gel and iBlot2 system. Membranes were next blocked with 5% BSA and incubated overnight with the primary antibody, anti-p-rpS6 (Ser240/244, 1:1000, #5364), anti-p-AMPK (Ser172, 1:1000, #2535S), anti-rpS6 (#2217S, 1:1000), and anti-AMPK (#5831S, 1:1000), all from Cell Signaling Technology, and both anti- β -tubulin (ab11307, 1:5000) and anti-GAPDH (ab8245, 1:5000) from Abcam. Primary incubation was followed by a 1-hour incubation with the secondary antibody at room temperature, after which the blots were revealed using the ECL system. We

routinely used both GAPDH and tubulin as loading controls. Rarely, as was the case for the data presented in Figure 5G, we were unable to effectively blot for tubulin. In this case, GAPDH served as the sole loading control.

Statistics

Statistical analyses performed for specific data sets are described in the figure legends. All statistical tests were performed using GraphPad Prism software v8. Data are presented as mean \pm SEM and subjected to two-tailed unpaired t-test (Student's t-test). For multiple comparison unpaired t-tests were corrected using the Holm-Sidak method. Significance was assessed using p-value cutoffs indicated as follows: * $p < 0.05$, ** $0.001 < p < 0.01$, *** $0.0001 < p < 0.001$, and **** $p < 0.0001$.

Study approval

All animal experiments were performed in accordance with NIH policies on the use of laboratory animals and approved by The University of California San Francisco Institutional Animal Care and Use Committee (IAAUC).

Author contributions

R.J., S.T., G.A.R., S.K. and A.B. conceived of and designed the research. R.J., S.T, A.S., G.S., M.M., M.V., and A.S. performed the experiments. R.J., S.T., S.G., P.M., M.M, A.S., A.M., M.H., Y.D., G.A.R, S.K., and A.B. analyzed the data and interpreted the results. R.J., S.K., and A.B. prepared the figures and drafted the manuscript. R.J, S.T, A.S., G.S., P.M., M.M., A.S., S.G., E.B.M., A.M., M.H., Y.D., G.A.R., S.K., and A.B. edited and revised the manuscript. All authors reviewed the final manuscript.

Figure Legends

Figure 1. β -cells switch from mTORC1 to AMPK-dependent signaling during postnatal maturation. **A.** Experimental paradigm for RNAseq on sorted pancreatic β -cells in mice at P6 and P45. **B.** Heatmap, showing the expression profile of genes related to mTORC1/AMPK signaling in β -cells at P6 and P45. In the comparison, deepening colors represent progressively lower (blue) or higher (red) mRNA levels for any given gene ($p < 0.05$). **C.** Representative pancreatic sections from WT mice at P6, P18 and 2 months of age stained for insulin (green) and p-rpS6 (red). DAPI (blue) counter-stains the nuclei, scale bar: 50 μ m. **D.** Quantification (FACS) of the number of cells positive for both insulin and p-rpS6 in P7 and 2-month-old WT mice. Data shown are representative of 3 separate experiments. $*p = 0.0178$ (two-tailed unpaired t-test). **E.** Immunoblot representing an experiment repeated three times ($n = 3$ for each), showing total rpS6, p-rpS6 (Ser240/244), p-AMPK (Thr172), and total AMPK in neonatal and adult islets treated with either 2.8mM or 16.7mM glucose. β -tubulin was used as loading control. Corresponding p-AMPK and total AMPK normalized to tubulin quantifications are adjacent. 5-7 P6 mice and 1 adult mouse was used for each replicate. $*p < 0.01$ (unpaired t-test corrected for multiple comparison using the Holm-Sidak method). **F.** Representative pancreatic sections from WT mice at P6 and 2 months of age stained for Pdx1 (green) and p-AMPK (red), with DAPI (blue) counter-staining the nuclei (scale bar: 50 μ m).

Figure 2. Weaning from maternal milk induces the switch from mTORC1 to AMPK signaling in β -cells. **A.** and **B.** Representative immunoblots showing p-AMPK, p-rpS6, total AMPK, total rpS6, and tubulin in **(A)** adult human islets and **(B)** adult mouse islets after treatment with 1mM AICAR or 40 μ M Everolimus for the indicated time (n=3 for both human and mouse islets except only for the 3-hour AICAR treatment condition, where n=2). **C.** Experimental paradigm for the milk fat-supplemented diet (MFD), and immunostaining for insulin (green) and p-rpS6 (red) in representative pancreatic sections from P40 mice otherwise fed either standard chow (control) or the milk fat-supplemented diet (MFD). DAPI (blue) counter-stains the nuclei (scale bar: 50 μ m). **D.** Experimental paradigm for the milk fat-supplemented diet (MFD) and associated representative immunoblots, showing p-AMPK, p-rpS6, total S6, and total AMPK in control and milk fat-supplemented diet (MFD) mice. β -tubulin was used as loading control. Quantification of p-AMPK/AMPK and AMPK/ β -tubulin is shown below. **p=0.0062 (Unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** IPGTT in control and MFD mice (n=7). *p<0.05 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **F.** Percentage of KI67⁺ and insulin⁺ cells in control and MFD islets (n=3-5). ***p=0.0002 (two-tailed unpaired t-test).

Figure 3. mTORC1 maintains the immature phenotype of pancreatic β -cells.

A. Genetic model for constitutive activation of mTORC1 **B.** mRNA levels of *Tsc1* in islets from control and β -TSC1KO mice (n=7-9). p=0.0002 (two-tailed unpaired t-test). **C.** Relative β -cell areas in pancreatic sections from control and β -TSC1KO

mice, measured as the ratio of insulin⁺ area/insulin⁺ cell number (n=37-38 islets/group). ****p<0.0001 (two-tailed unpaired t-test). **D.** GSEA, showing enrichment of disallowed genes in RNAseq data from β -TSC1KO islets (*p<0.05). **E.** Heatmap, showing the transcriptoinal profile of β -cell maturity markers in β -TSC1KO and control mice (p<0.05). **F.** Insulin secretion (percent of insulin content) in a perfusion assay on β -TSC1KO and control islets exposed to 3mM and 16mM glucose, respectively (n=4-5). *p<0.05 and **p<0.01 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **G.** Model for inducing mTORC1 activation in adult mice. **H.** Plasma insulin levels after glucose challenge in iTSC1 KO and control mice (n=8-9). *p=0.017 and **p=0.0012 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **I.** IPGTT in iTSC1 KO and control mice (n=10-11). *p<0.05, **p<0.01, ***p<0.001, and ****p<0.0001 (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

Figure 4. AMPK activation triggers a switch to oxidative metabolism in mature islets. **A.** Heatmap, profiling mitochondrial genes and genes related to ox-phos metabolism in P6 and P45 β -cells (p<0.05). **B.** qPCR, showing the ratio of mtDNA over nuclear DNA in P6 and adult islets (n=4-5). ****p<0.0001 (two-tailed unpaired t-test). **C.** Relative *Ppargc1a* and *Ppargc1b* mRNA levels in P6 and adult islets (n= 4). *p=0.016, **p=0.0029 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **D.** Oxygen consumption rates for cultured neonatal and adult islets (Seahorse XF), with data presented relative to baseline (n=7-8). *p<0.01, **p<0.001, ***p<0.0001 (unpaired t-test corrected for multiple

comparison using Holm-Sidak method). **E.** Heatmap, showing the transcriptional profile of mitochondrial genes those related to ox-phos metabolism in AMPKDKO control islets ($p < 0.05$). **F.** and **G.** Morphometric analysis of mitochondria in AMPKDKO and control β -cells, showing (**F**) the number of mitochondria per $70 \mu\text{m}^2$ area $n=32-36$, and (**G**) the volume density (ml%). $n=29-33$ β -cells per group, **** $p < 0.0001$ (two-tailed unpaired t-test). **H.** qPCR, showing the ratio of mtDNA to nuclear DNA in WT adult islets treated with $10 \mu\text{M}$ compound C ($n=3$). *** $p = 0.0003$ (two-tailed unpaired t-test). **I.** *Ppargc1a* and *Ppargc1b* mRNA levels in the islets of control mice vs. those receiving milk fat throughout their development into adulthood ($n=3$). ** $p = 0.0013$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

Figure 5. T2D induces increased β -cell mTORC1 activity and a reversion of pancreatic islets to an immature phenotype. **A.** Heatmap, showing the transcriptional profile of genes in the AMPK/mTORC1 pathway and those involved in β -cell maturation in islets from *db/db* and control mice ($p < 0.05$). **B.** Immunostaining for insulin (green), p-rpS6 (red), and DAPI (nuclei) in representative pancreatic sections from 4-week-old *db/db* and control mice (Scale bar: $50 \mu\text{m}$). **C.** Insulin secretion (% of insulin content) in a perifusion assay on islets from 4 week-old *db/db* or control mice in presence of 3mM and 16mM glucose, respectively ($n=4$) **** $p < 0.0001$, and * $p < 0.05$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **D.** Oxygen consumption rates for *db/db* and control islets presented relative to baseline ($n=9-10$ per group).

****p<0.01, ***p<0.001** (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** GSIS by control and *dbdb* islets treated with 40μM everolimus or 1mM AICAR. n=3 *p<0.05 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **F.** Immunostaining for insulin (green), p-rpS6 (red), and DAPI (nuclei) in representative pancreatic sections from human donors with or without T2D (Scale bar: 50 μm). **G.** Representative immunoblots for p-AMPK, p-rpS6, total AMPK, and total rpS6 in healthy donors (n=4) or those with T2D (n=3). GAPDH was used as loading control. Quantifications of p-AMPK and p-rpS6 normalized total AMPK and rpS6, respectively, and total AMPK or rpS6 normalized to GAPDH are shown below. **p<0.001 and *p<0.05 (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

Supplemental Figures

Supplemental Figure 1. **A.** Principal components analysis (PCA) of RNAseq libraries from P6 and P45 pancreatic β -cells. **B.** Plot of normalized mean expression counts vs. log2-fold change for P6 vs. P45 β -cells. **C.** GSEA of RNAseq data, showing enrichment by reactome cell cycle pathway genes in neonatal β -cells, and instead, enrichment by reactome TCA cycle and respiratory electron transport chain genes in adult β -cells ($p < 0.05$). **D.** Heatmap, showing β -cell transcriptional profiles including relative upregulation of genes related to proliferation at P6 and maturation at P45 ($p < 0.05$). **E.** Quantification of data in Figure 1E, with p-rpS6 normalized to total rpS6 (top) and total rpS6 normalized to tubulin (bottom). ** $p = 0.006$ * $p = 0.0109$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

Supplemental Figure 2. **A.** Quantification of the immunoblots in Figure 2A for p-rpS6 and p-AMPK performed on mouse islets treated for 12 hours with 40 μ M everolimus (left) or 1mM AICAR (right) normalized to total rpS6 or total AMPK, respectively ($n=3$ per group). * $p = 0.0104$, **** $p < 0.0001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **B.** Quantification of the immunoblots in Figure 2B for p-rpS6 and p-AMPK performed on human islets treated for 12 hours with 40 μ M everolimus (left) or 1mM AICAR (right) normalized to total rpS6 or total AMPK, respectively ($n=3$ per group). ** $p = 0.0051$ ** $p = 0.0018$, and **** $p < 0.0001$ (unpaired t-test corrected for multiple comparison using Holm-

Sidak method). **C.** Quantification of data in Figure 2D, showing p-rpS6 normalized to total rpS6 and total rpS6 normalized to tubulin. **D.** Figure 2E corresponding area under the curve $n=7$. $*p=0.011$ (two-tailed unpaired t-test). **E.** Calculated β -cell area in islets from control mice and MFD mice ($n=5-6$). $p=0.4720$ (two-tailed unpaired t-test). **F.** qPCR, showing relative mRNA levels of β -cell maturation markers in control and MFD mice $n=3-4$. $**p=0.008$, $****p<0.0001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

Supplemental Figure 3. **A.** Immunostaining for insulin (green), p-rpS6 (red), and DAPI (blue) in representative pancreatic sections from control and β -TSC1KO mice (scale bar: 50 μm). **B.** Percentage of β -cells positive for both p-rpS6 and insulin in adult β -TSC1KO and control mice ($n=4-5$). $****p<0.0001$ (two-tailed unpaired t-test). **C.** Immunostaining for insulin (green), MafA (red) and DAPI (blue) in representative pancreatic sections from adult β -TSC1KO and control mice (scale bar: 50 μm). **D.** Plasma insulin levels after glucose challenge in β -TSC1KO and control mice ($n=5$), $***p=0.0009$ and $***p=0.00015$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** Fasting blood glucose levels in β -TSC1KO mice and littermate controls ($n=17-38$) $****p<0.0001$ (two-tailed unpaired t-test). **F.** IPGTTs for β -TSC1 KO mice and littermate controls ($n=4-11$). $**p<0.01$, $***p<0.0001$, and $****p<0.0001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **G.** Percentage of cells positive for both p-rpS6 and insulin in islets from β -TSC1KO and control mice ($n=4$). $****p<0.0001$ (two-tailed unpaired t-test). **H.** Fasting blood glucose levels in

iTSC1KO mice and littermate controls (n=6). **p=0.0173 (two-tailed unpaired t-test).

Supplemental Figure 4. Gating strategy for sorting β -cells from human islets.

Supplemental Tables

Supplemental Tables 1-6.

Log2-fold changes and associated p-values for genes presented in the heatmaps shown in supplemental Figure 1D, Figures 1B, 3E, 4A, 4E, 5A.

Supplemental table 7.

qPCR primer sequences.

Supplemental table 8.

List of disallowed genes.

Acknowledgements

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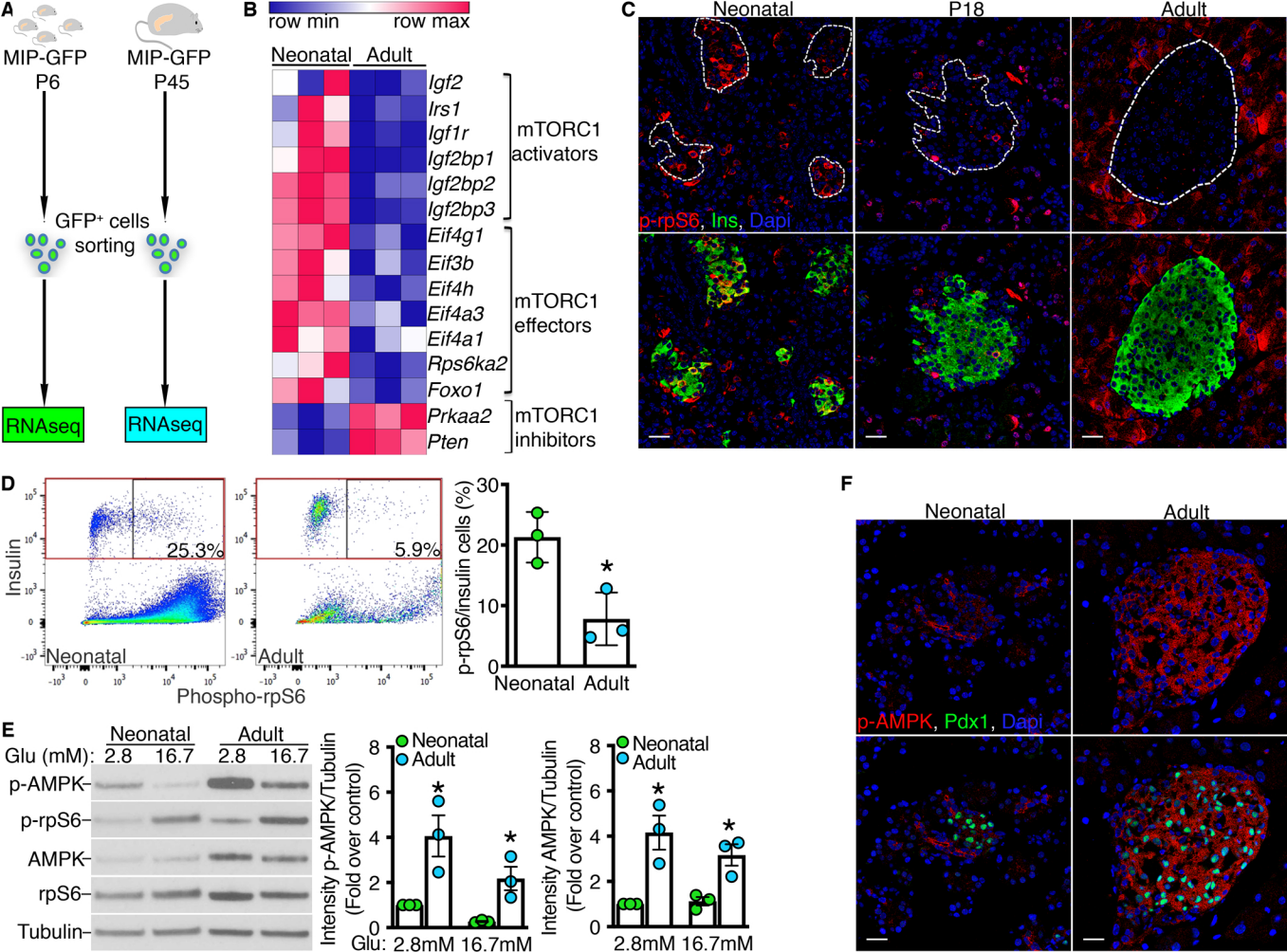


Figure 1. β -cells switch from mTORC1 to AMPK-dependent signaling during postnatal maturation. **A.** Experimental paradigm for RNAseq on sorted pancreatic β -cells in mice at P6 and P45. **B.** Heatmap, showing the expression profile of genes related to mTORC1/AMPK signaling in β -cells at P6 and P45. In the comparison, deepening colors represent progressively lower (blue) or higher (red) mRNA levels for any given gene ($p < 0.05$). **C.** Representative pancreatic sections from WT mice at P6, P18 and 2 months of age stained for insulin (green) and p-rpS6 (red). DAPI (blue) counter-stains the nuclei, scale bar: 50 μ m. **D.** Quantification (FACS) of the number of cells positive for both insulin and p-rpS6 in P7 and 2-month-old WT mice. Data shown are representative of 3 separate experiments. * $p = 0.0178$ (two-tailed unpaired t-test). **E.** Immunoblot representing an experiment repeated three times ($n = 3$ for each), showing total rpS6, p-rpS6 (Ser240/244), p-AMPK (Thr172), and total AMPK in neonatal and adult islets treated with either 2.8mM or 16.7mM glucose. β -tubulin was used as loading control. Corresponding p-AMPK and total AMPK normalized to tubulin quantifications are adjacent. 5-7 P6 mice and 1 adult mouse was used for each replicate. * $p < 0.01$ (unpaired t-test corrected for multiple comparison using the Holm-Sidak method). **F.** Representative pancreatic sections from WT mice at P6 and 2 months of age stained for Pdx1 (green) and p-AMPK (red), with DAPI (blue) counter-staining the nuclei (scale bar: 50 μ m).

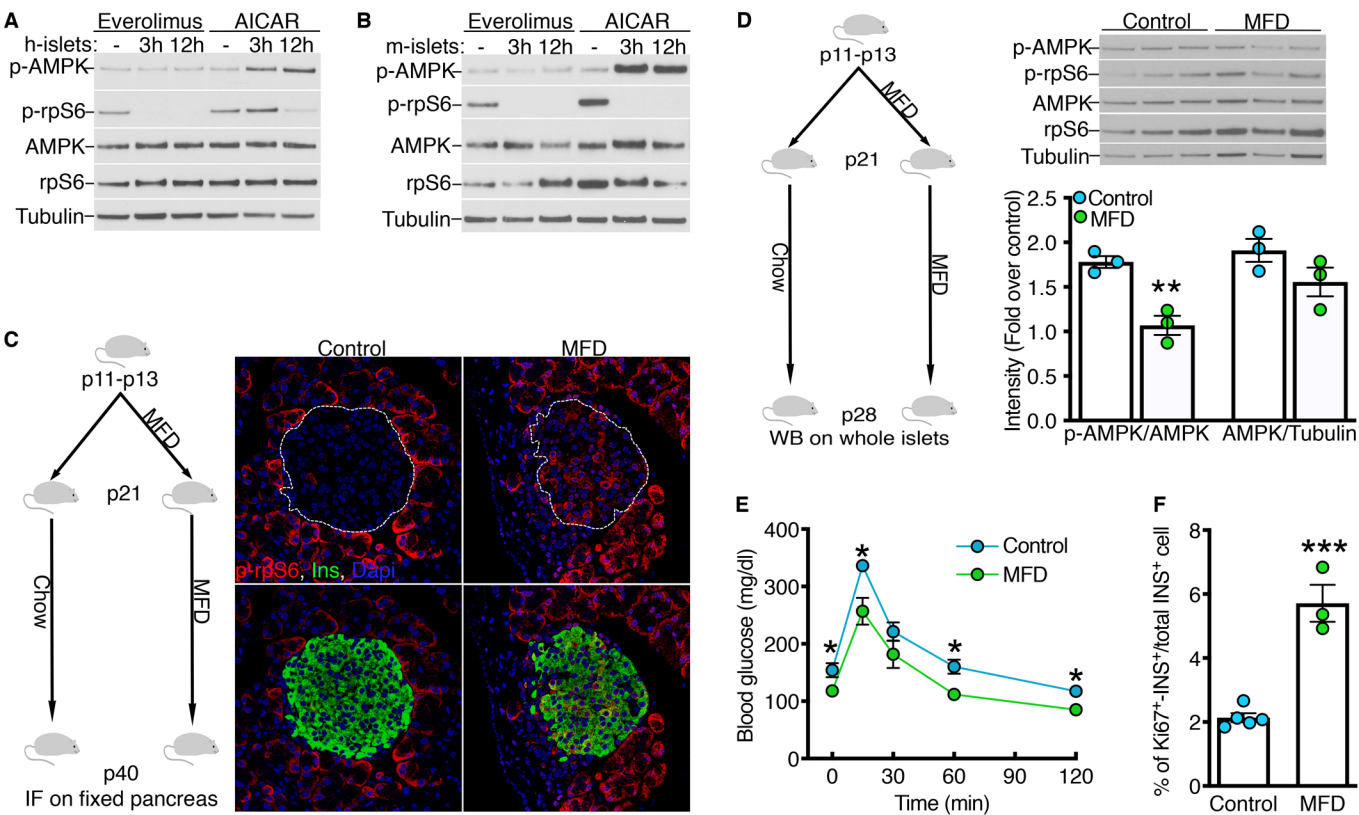


Figure 2. Weaning from maternal milk induces the switch from mTORC1 to AMPK signaling in β -cells. **A.** and **B.** Representative immunoblots showing p-AMPK, p-rpS6, total AMPK, total rpS6, and tubulin in **(A)** adult human islets and **(B)** adult mouse islets after treatment with 1mM AICAR or 40 μ M Everolimus for the indicated time (n=3 for both human and mouse islets except only for the 3-hour AICAR treatment condition, where n=2). **C.** Experimental paradigm for the milk fat-supplemented diet (MFD), and immunostaining for insulin (green) and p-rpS6 (red) in representative pancreatic sections from P40 mice otherwise fed either standard chow (control) or the milk fat-supplemented diet (MFD). DAPI (blue) counter-stains the nuclei (scale bar: 50 μ m). **D.** Experimental paradigm for the milk fat-supplemented diet (MFD) and associated representative immunoblots, showing p-AMPK, p-rpS6, total S6, and total AMPK in control and milk fat-supplemented diet (MFD) mice. β -tubulin was used as loading control. Quantification of p-AMPK/AMPK and AMPK/ β -tubulin is shown below. **p=0.0062 (Unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** IPGTT in control and MFD mice (n=7). *p<0.05 (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **F.** Percentage of Ki67⁺ and insulin⁺ cells in control and MFD islets (n=3-5). ***p=0.0002 (two-tailed unpaired t-test).

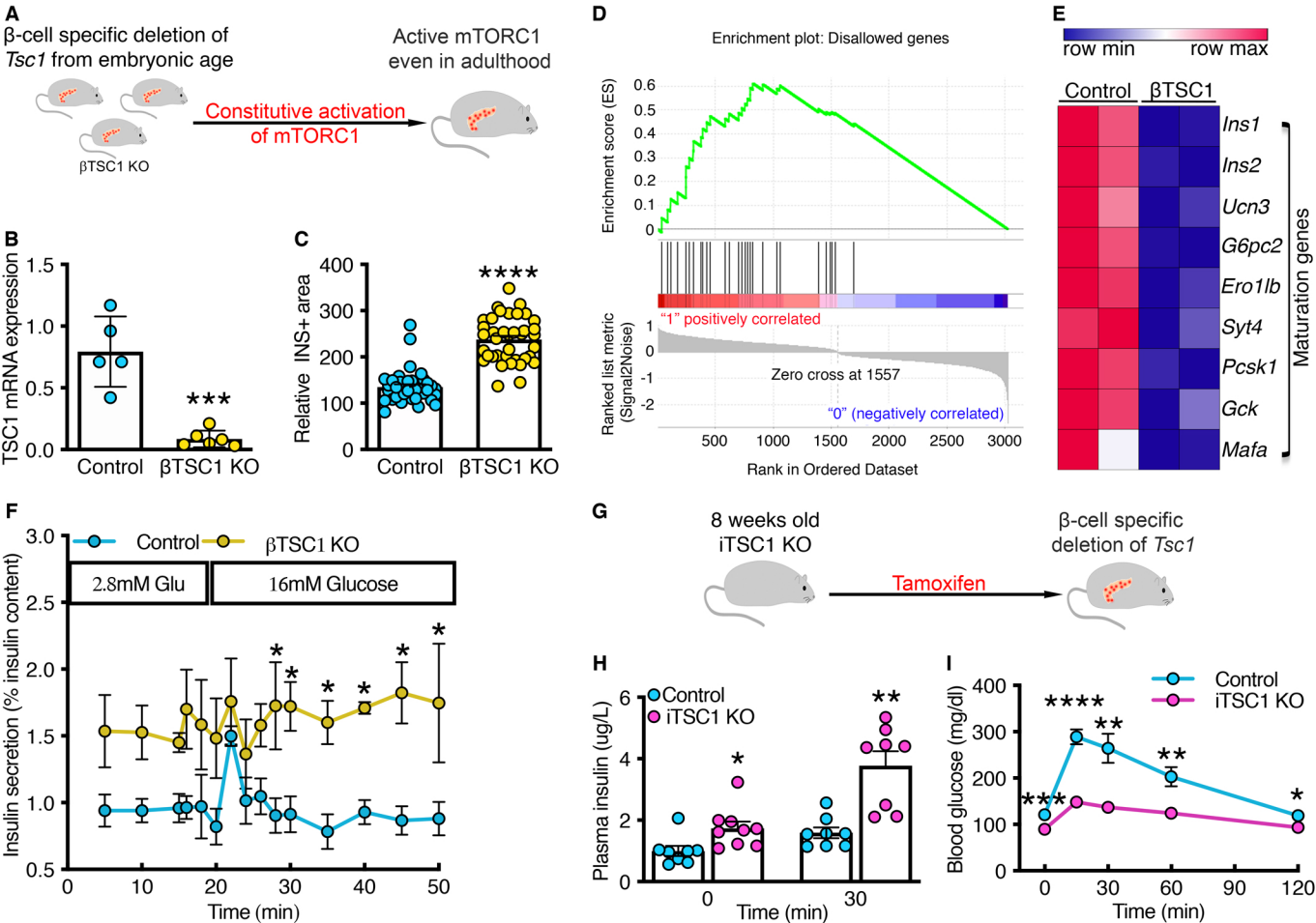


Figure 3. mTORC1 maintains the immature phenotype of pancreatic β -cells. **A.** Genetic model for constitutive activation of mTORC1. **B.** mRNA levels of *Tsc1* in islets from control and β -TSC1KO mice ($n=7-9$). $p=0.0002$ (two-tailed unpaired t-test). **C.** Relative β -cell areas in pancreatic sections from control and β -TSC1KO mice, measured as the ratio of insulin⁺ area/insulin⁺ cell number ($n=37-38$ islets/group). **** $p < 0.0001$ (two-tailed unpaired t-test). **D.** GSEA, showing enrichment of disallowed genes in RNAseq data from β -TSC1KO islets (* $p < 0.05$). **E.** Heatmap, showing the transcriptoinal profile of β -cell maturity markers in β -TSC1KO and control mice ($p < 0.05$). **F.** Insulin secretion (percent of insulin content) in a perfusion assay on β -TSC1KO and control islets exposed to 3mM and 16mM glucose, respectively ($n=4-5$). * $p < 0.05$ and ** $p < 0.01$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **G.** Model for inducing mTORC1 activation in adult mice. **H.** Plasma insulin levels after glucose challenge in iTSC1 KO and control mice ($n=8-9$). * $p=0.017$ and ** $p=0.0012$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **I.** IPGTT in iTSC1 KO and control mice ($n=10-11$). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, and **** $p < 0.0001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

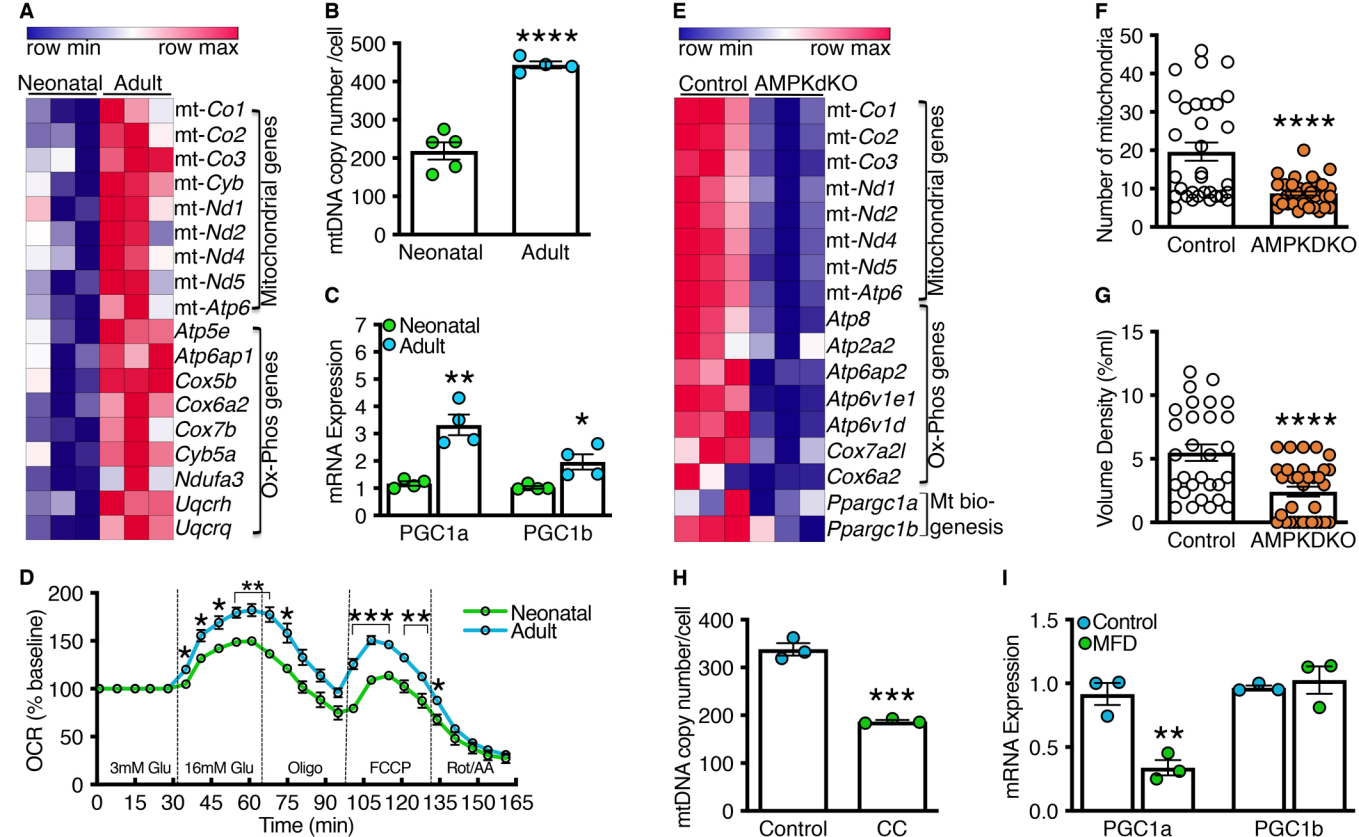


Figure 4. AMPK activation triggers a switch to oxidative metabolism in mature islets. **A.** Heatmap, profiling mitochondrial genes and genes related to ox-phos metabolism in P6 and P45 β -cells ($p < 0.05$). **B.** qPCR, showing the ratio of mtDNA over nuclear DNA in P6 and adult islets ($n = 4-5$). **** $p < 0.0001$ (two-tailed unpaired t-test). **C.** Relative *Pparg1a* and *Pparg1b* mRNA levels in P6 and adult islets ($n = 4$). * $p = 0.016$, ** $p = 0.0029$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **D.** Oxygen consumption rates for cultured neonatal and adult islets (Seahorse XF), with data presented relative to baseline ($n = 7-8$). * $p < 0.01$, ** $p < 0.001$, *** $p < 0.0001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** Heatmap, showing the transcriptional profile of mitochondrial genes and genes related to ox-phos metabolism in AMPKDKO control islets ($p < 0.05$). **F.** and **G.** Morphometric analysis of mitochondria in AMPKDKO and control β -cells, showing (F) the number of mitochondria per $70 \mu\text{m}^2$ area $n = 32-36$, and (G) the volume density (ml%). $n = 29-33$ β -cells per group, **** $p < 0.0001$ (two-tailed unpaired t-test). **H.** qPCR, showing the ratio of mtDNA to nuclear DNA in WT adult islets treated with 10 μM compound C ($n = 3$). *** $p = 0.0003$ (two-tailed unpaired t-test). **I.** *Pparg1a* and *Pparg1b* mRNA levels in the islets of control mice vs. those receiving milk fat throughout their development into adulthood ($n = 3$). ** $p = 0.0013$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).

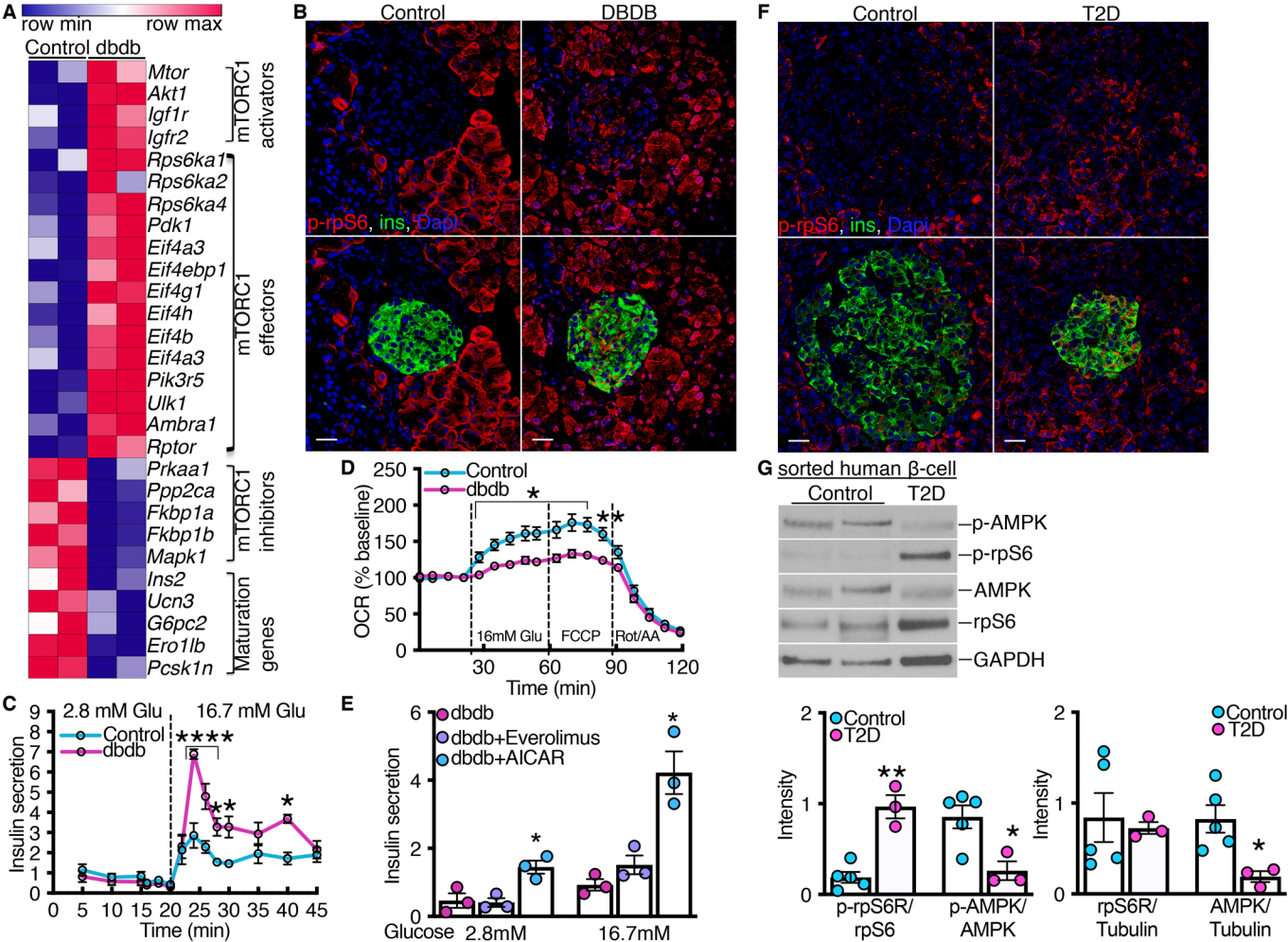


Figure 5. T2D induces increased β-cell mTORC1 activity and a reversion of pancreatic islets to an immature phenotype. **A.** Heatmap, showing the transcriptional profile of genes in the AMPK/mTORC1 pathway and those involved in β-cell maturation in islets from *db/db* and control mice ($p<0.05$). **B.** Immunostaining for insulin (green), p-rpS6 (red), and DAPI (nuclei) in representative pancreatic sections from 4-week-old *db/db* and control mice (Scale bar: 50 μ m). **C.** Insulin secretion (% of insulin content) in a perfusion assay on islets from 4-week-old *db/db* or control mice in presence of 3mM and 16mM glucose, respectively ($n=4$) **** $p<0.0001$, and * $p<0.05$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **D.** Oxygen consumption rates for *db/db* and control islets presented relative to baseline ($n=9-10$ per group). ** $p<0.01$, *** $p<0.001$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **E.** GSIS by control and *dbdb* islets treated with 40 μ M everolimus or 1mM AICAR. $n=3$ * $p<0.05$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method). **F.** Immunostaining for insulin (green), p-rpS6 (red), and DAPI (nuclei) in representative pancreatic sections from human donors with or without T2D (Scale bar: 50 μ m). **G.** Representative immunoblots for p-AMPK, p-rpS6, total AMPK, and total rpS6 in healthy donors ($n=4$) or those with T2D ($n=3$). GAPDH was used as loading control. Quantifications of p-AMPK and p-rpS6 normalized total AMPK and rpS6, respectively, and total AMPK or rpS6 normalized to GAPDH are shown below. ** $p<0.001$ and * $p<0.05$ (unpaired t-test corrected for multiple comparison using Holm-Sidak method).