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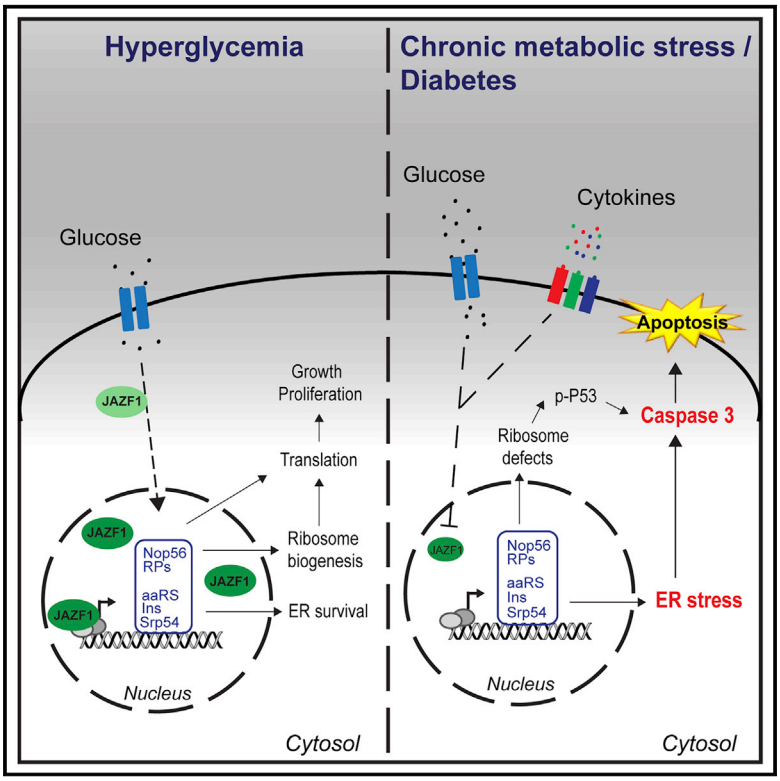
# The Diabetes Gene *JAZF1* Is Essential for the Homeostatic Control of Ribosome Biogenesis and Function in Metabolic Stress

## Graphical Abstract




## Highlights

- JAZF1 localizes in the nucleus in high-glucose and metabolic stress conditions
- JAZF1 mediates metabolic stress via endoplasmic reticulum and p53 stress pathways
- JAZF1 regulates ribosome biogenesis and aminoacyl-tRNA synthetases
- JAZF1 is a direct negative regulator of insulin gene transcription

## Authors

Ahmad Kobiita, Svenja Godbersen, Elisa Araldi, ..., Giatgen Spinas, Holger Moch, Markus Stoffel

## Correspondence

stoffel@biol.ethz.ch

## In Brief

JAZF1 has been identified in several GWASs as a type 2 diabetes susceptibility gene. Kobiita et al. demonstrate that JAZF1 is a transcriptional regulator that is translocated in the nucleus upon metabolic stress and in diabetes. The study also reveals numerous functions of JAZF1 in the regulation of genes involved in ribosome biogenesis and protein translation, including insulin gene transcription.

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# The Diabetes Gene *JAZF1* Is Essential for the Homeostatic Control of Ribosome Biogenesis and Function in Metabolic Stress

Ahmad Kobiita,[1] Svenja Godbersen,[1] Elisa Araldi,[1] Umesh Ghoshdastider,[1] Marc W. Schmid,[2] Giatgen Spinas,[3] Holger Moch,[4] and Markus Stoffel[1,5,6,*]

[1]Institute of Molecular Health Sciences, ETH Zurich, Otto-Stern-Weg 7, HPL H36, 8093 Zürich, Switzerland
[2]MWSchmid GmbH, Möhrlistrasse 25, 8006 Zurich, Switzerland
[3]Klinik für Endokrinologie, Diabetologie und Klinische Ernährung, Universitäts-Spital Zürich, Rämistrasse 100, 8091 Zürich, Switzerland
[4]Department of Pathology and Molecular Pathology, University and University Hospital Zürich, Schmelzbergstrasse 12, 8091 Zürich, Switzerland
[5]Medical Faculty, University of Zurich, Zurich, Switzerland
[6]Lead Contact
*Correspondence: stoffel@biol.ethz.ch
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## SUMMARY

The ability of pancreatic β-cells to respond to increased demands for insulin during metabolic stress critically depends on proper ribosome homeostasis and function. Excessive and long-lasting stimulation of insulin secretion can elicit endoplasmic reticulum (ER) stress, unfolded protein response, and β-cell apoptosis. Here we show that the diabetes susceptibility gene *JAZF1* is a key transcriptional regulator of ribosome biogenesis, global protein, and insulin translation. JAZF1 is excluded from the nucleus, and its expression levels are reduced upon metabolic stress and in diabetes. Genetic deletion of *Jazf1* results in global impairment of protein synthesis that is mediated by defects in ribosomal protein synthesis, ribosomal RNA processing, and aminoacyl-synthetase expression, thereby inducing ER stress and increasing β-cell susceptibility to apoptosis. Importantly, JAZF1 function and its pleiotropic actions are impaired in islets of murine T2D and in human islets exposed to metabolic stress. Our study identifies JAZF1 as a central mediator of metabolic stress in β-cells.

## INTRODUCTION

Glucose-induced insulin secretion (GSIS) from pancreatic β-cells plays a key role in glucose homeostasis. Functional and sufficient β-cells are required to maintain normoglycemia. Genetic and environmental factors as well as aging are major risk factors for the gradual decline in insulin secretion. Genome-wide association studies (GWASs) have revealed a variety of type 2 diabetes (T2D) susceptibility genes, many of which appear to primarily be involved in β-cell differentiation and function (Bonnefond et al., 2010). Three defects have consistently been reported in patients with T2D: gradual decline in β-cell function and dedifferentiation and a reduction in β-cell mass (Accili et al., 2016). The molecular mechanisms of β-cell failure in T2D are incompletely understood, but several lines of evidence suggest that mitochondrial dysfunction (Mulder, 2017), oxidative and endoplasmic reticulum (ER) stress (Keane et al., 2015), dysfunctional fatty acid metabolism (Prentki et al., 2013), glucolipotoxicity (Poitout and Robertson, 2008), and amyloid deposition (Hull et al., 2004) contribute to functional β-cell alterations and loss of β-cell mass by apoptosis and compromised proliferation. The functional adaptation of β-cells and the response to chronic metabolic stress have been linked to ER stress and the unfolded protein response (UPR) (Back and Kaufman, 2012).

Proinsulin biosynthesis is regulated by nutrients, most notably glucose. Short-term glucose stimulation (≤2h) leads to a rapid (~2-fold) increase in total protein synthesis and an ~20-fold increase in proinsulin synthesis (Itoh and Okamoto, 1980). This process is mediated almost entirely by enhanced translation of preexisting mRNAs that are translocated from an inert cytosolic pool to translationally active membrane-bound polysomes on the rough ER, and ultimately through an augmented rate of initiation, facilitated through increased availability of the translational ternary complex and brought about by the dephosphorylation of eIF2α (Scheuner et al., 2005; Sonenberg and Hinnebusch, 2009). Prolonged glucose stimulation also leads to increases in preproinsulin mRNA levels (~2-fold), increased insulin mRNA stability, and a corresponding increase in proinsulin translation (≥10-fold) (Brunstedt and Chan, 1982). However, chronic overproduction of insulin per se (i.e., in insulin resistance) or genetic mutations (e.g., in the insulin gene) can lead to the formation of misfolded proteins that may generate ER stress (Arunagiri et al., 2018). This in turn can trigger intracellular signaling events that ultimately activate transcription of ER chaperones, oxidoreductases, and ER-associated protein degradation (ERAD) components.

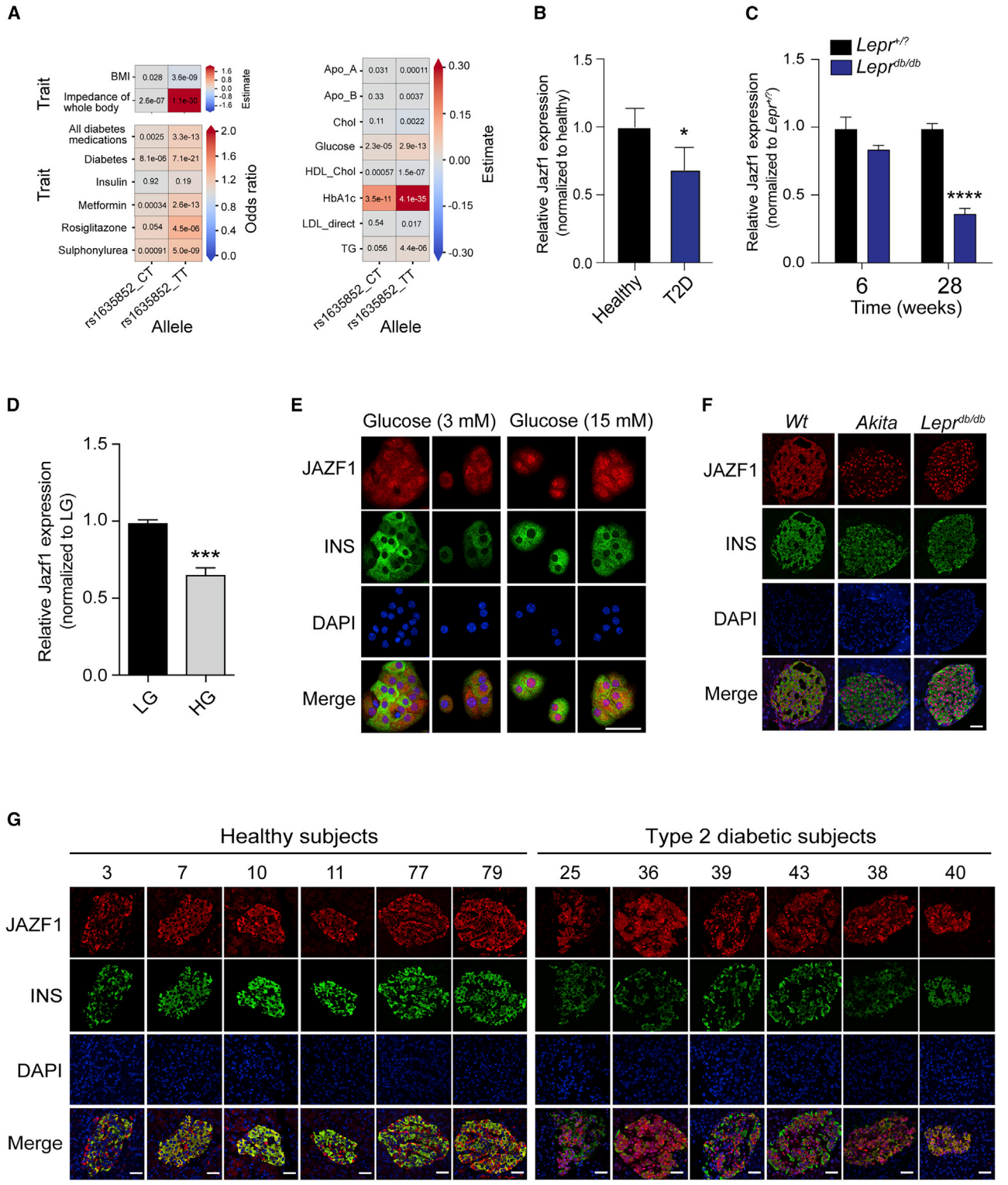


**Figure 1. Jazf1 Levels and Localization of β-Cells in Normoglycemia and in T2D**

(A) Association analyses of indicated phenotypes and quantitative traits in European-ancestry participants of UK Biobank. p values of associations are indicated, while odds ratio or estimates are color-coded. p values < 5e-8 are significant. Number of participants analyzed per trait ranged between 354,259 and 487,867. (B–D) Expression levels of Jazf1 in islets from healthy humans and T2D patients (n = 5) (B), islets from *Lepr*$^{db/db}$ and control littermate mice at 6 and 28 weeks (n = 3) (C), and mouse islets cultured in 3 mM (LG) and 24 mM (HG) glucose for 24 h (n = 3) (D).

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Normally, this response enhances the cell's capacity to sustain protein secretion during times of high demands. If adaptive UPR outputs are effective, this will lead to a reduction of unfolded proteins and restoration of homeostasis. However, if ER stress persists, the UPR switches its physiological output from promoting adaptation to instead promoting self-destruction, usually through apoptosis (Papa, 2012). The regulation of β-cell gene expression in response to metabolic stress has been extensively studied at the transcriptional level, but regulation of mRNA translation, including ribosome biogenesis and rRNA processing, has received less attention. Likewise, how these processes are regulated transcriptionally and how they may be linked to ER stress and the UPR pathways during the development of T2D is not understood.

Juxtaposed with another zinc finger (ZnF) protein 1, JAZF1 (TIP27, ZNF802) encodes a 27 kDa protein with three C2H2-type ZnFs and functions as a repressor of DNA response element 1 (DR1)-dependent transcription of nuclear receptor subfamily 2, group C, member 2 (NR2C2, TR4) (Nakajima et al., 2004). JAZF1 represses NR2C2 transcriptional activity via direct binding to the ligand-binding domain (LBD) of NR2C2 (Omori et al., 2005; Lee et al., 1997; Tanabe et al., 2007).

GWASs have identified gene variants in that are linked to insulin secretion and increased susceptibility to develop T2D (Grarup et al., 2008; Zeggini et al., 2008). JAZF1 levels are decreased in pancreatic islet of T2D patients, and increased transcript levels are associated with higher insulin secretion (Taneera et al., 2012). Gene variants involving JAZF1 are also associated with height (Manolio, 2010), risk for prostate cancer (Thomas et al., 2008), and endometrial stromal tumors (Koontz et al., 2001). Although NR2C2 may have functions in energy homeostasis and inflammation (Liu et al., 2007; Kang et al., 2011; Yang et al., 2014; Meng et al., 2018), no studies have explored its role in pancreatic β-cells, except a recent study demonstrating allele-specific transcriptional activity at T2D-associated single-nucleotide polymorphisms in regions of open chromatin at the JAZF1 locus (Fogarty et al., 2013).

In this study we used genetic, molecular, biochemical, and physiological approaches to investigate the role of JAZF1 in islet gene regulation and report a previously unrecognized role as an essential regulator of mRNA translation through coordinating protein gene expression, ribosome biogenesis, and rRNA processing. We further show that impaired JAZF1 function in T2D contributes to ribosomal and ER stress, activation of apoptosis pathways, and ultimately β-cell demise.

## RESULTS

### Genetic *JAZF1* Variance, Decreased JAZF1 Expression, and Nuclear JAZF1 Localization in Pancreatic β-Cells Are Associated with T2D and Metabolic Stress

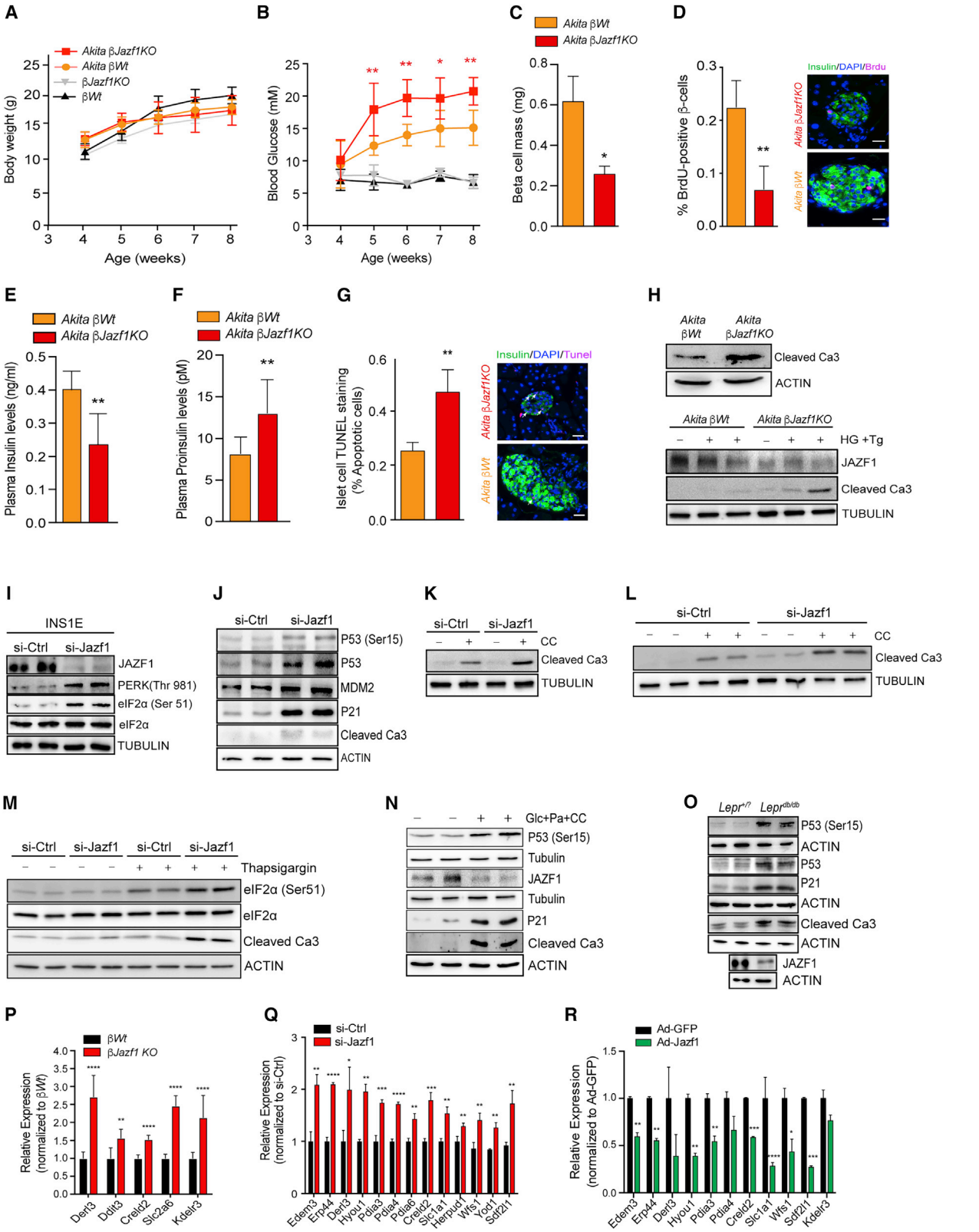
We studied an intronic variant in the *JAZF1* gene (rs1635852; pairwise $R^2 < 0.01$, minor allele frequency in dataset 49.63%), that has been shown to display allelic differences in enhancer activity with the T2D risk allele T showing lower transcriptional activity (Fogarty et al., 2013). Genotypes from ~400,000 European-ancestry participants from UK Biobank, a U.K. population-based cohort of people 40–69 years of age (Bycroft et al., 2018), were analyzed to confirm that variations in the *JAZF1* genomic locus predispose to T2D, as shown by significant associations of the rs1635852_TT genotype with diabetes phenotypes and traits. Interestingly, the association of the risk genotype with lower body mass index indicates that JAZF1 may have a key role in β-cell function rather than in organs regulating insulin sensitivity and energy homeostasis (Figure 1A).

We first examined the expression of Jazf1 across metabolic tissues in mice fed with a chow diet. We found that Jazf1 transcript levels were most abundant in pancreatic islets, followed by adipose tissue, where expression was previously reported to be highest in all tissues (Figure S1A) (Ho et al., 2013; Yang et al., 2015).

Several studies have shown that Jazf1 mRNA is decreased in T2D islets and that increased transcript levels are associated with higher insulin secretion (Taneera et al., 2012). Indeed, we found reduced JAZF1 expression in human islets from T2D organ donors compared with healthy donors (Figure 1B). Furthermore, in $Lepr^{db/db}$ compared with control $Lepr^{+/?}$ mice, Jazf1 transcript levels were slightly decreased at 6 weeks of age and reduced by more than 2-fold at 28 weeks of age, at which time $Lepr^{db/db}$ mice became profoundly diabetic (Figure 1C). Pancreatic mouse islets from wild-type (WT) mice cultured in high-glucose conditions also had decreased Jazf1 levels (Figure 1D). Last, we found that Jazf1 expression was decreased in islets of patients with type 1 diabetes (T1D) and in a mouse model of T1D (NOD) (Figures S1B–S1D).

Jazf1 has a putative nuclear localization sequence (NLS), located within the second ZnF motif (Figure S1E). We noticed a significant homology of the C-terminal ZnF motif between JAZF1 and yeast Sfp1 (Figure S1F), a transcription factor that controls the expression of more than 60 genes involved in ribosome biogenesis, cell cycle G2/M transition, and DNA damage response (Fingerman et al., 2003; Albert et al., 2019). Immunofluorescence staining revealed nuclear localization in transformed rat and human β-cell lines exposed to low and high glucose, indicating a role in proliferation (Figures S1G and S1H), a notion that was supported by reduced cell division when Jazf1 was silenced (Figure S1I). In primary β-cells, JAZF1 was localized mostly in the cytosol at low glucose but translocated to the nucleus at high glucose levels (Figure 1E). Similarly, we observed a predominant cytosolic distribution of JAZF1 in WT mice fed *ad libitum* a chow diet. In contrast, JAZF1 was located mainly in the nuclei of β-cells from hyperglycemic *Akita* and $Lepr^{db/db}$ mice, in which T2D develops as a result of ER stress due to a mutation in *Ins2* and severe insulin resistance, respectively (Figure 1F). This finding was confirmed by subcellular fractionation and immunoblotting experiments in islets of $Lepr^{db/db}$ and control mice (Figure S1J).

(E–G) Immunohistochemistry of isolated mouse β-cells cultured in low (3 mM) and high (15 mM) glucose for 1 h (E), pancreatic sections of wild-type (WT), *Akita*, and $Lepr^{db/db}$ mice (24 weeks of age) (F), and pancreatic biopsies of six healthy and six T2D human subjects (G), stained for JAZF1, Insulin, and DNA (DAPI). Scale bars: 25 μm (E) and 100 μm (E–G). Numbers in (E) and (G) represent anonymized identifiers. Clinical data of human subjects (G) is shown in Figure S1K. Data are presented as mean ± SD. *$p \leq 0.05$, **$p \leq 0.01$, and ***$p \leq 0.001$ by Student's t test.

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We also found that JAZF1 was preferentially localized in the nuclei of β-cells in pancreatic tissue sections of human T2D subjects, whereas it localized mainly to the cytosol of non-diabetic controls (Figures 1G and S1K). Last, in contrast to JAZF1, NR2C2 was always associated with the nucleus, irrespective of the glucose levels, in primary β-cells or in *Akita* mice (Figures S1L and S1M). These results demonstrate that JAZF1 expression levels and cellular compartmentalization are regulated by metabolic stress conditions, leading to a nuclear localization in response to elevated glucose concentrations.

## Increased Susceptibility of JAZF1-Depleted β-Cells to ER Stress-Induced Apoptosis

To study the function of JAZF1, we generated β-cell-specific Jazf1 knockout mice by crossing *Jazf1*$^{fl/fl}$ mice with *RIP-Cre* transgenic mice that express Cre-recombinase under the control of the rat insulin 2 promoter (called *βJazf1KO*). PCR and western blot analysis confirmed the specific ablation of Jazf1 in islets but not in other metabolic tissues (Figures S2A–S2C). *βJazf1KO* mice were indistinguishable from control *Jazf1*$^{fl/fl}$ littermates (called *βWt*) with regard to weight, blood glucose, and GSIS in isolated islets (Figures S2D–S2F). Pancreatic insulin content and β-cell mass were reduced in *βJazf1KO* mice at age 16 weeks compared with *βWt* mice, with a similar percentage of Ki-67-positive β-cells (Figures S2G–S2I). Challenging animals with a high-fat diet (HFD) for 12 weeks resulted in a similar phenotype with regard to weight, blood glucose, and glucose tolerance (Figures S2J–S2L). Similar to chow-fed mice, *βJazf1KO* animals on the HFD had reduced β-cell mass and displayed lower β-cell proliferation compared with *βWt* mice (Figures S2M and S2N).

We next studied the consequences of genetic *Jazf*1 ablation in *Akita* mice, a well-characterized genetic T2D model, due to unresolved ER stress and β-cell apoptosis (Yoshioka et al., 1997; Wang et al., 1999). *Akita βJazf1KO* mice exhibited similar body weight but higher blood glucose levels compared with *Akita βWt* mice (Figures 2A and 2B). The β-cell mass was reduced by 50% in *Akita βJazf1KO* mice (Figure 2C), and measurements of β-cell proliferation by *in vivo* BrdU assays showed a ~70% reduction compared with *Akita βWt* mice (Figure 2D). Furthermore, plasma insulin levels were decreased and proinsulin levels increased in *Akita βJazf1KO* animals (Figures 2E and 2F), with no changes in the levels of insulin-processing genes (Pcsk1, Pcsk2, Cpe) (Figure S2O).

Unresolved ER stress can lead to β-cell death through the activation of p53-dependent apoptotic pathways in murine (Hoshino et al., 2014) and human (Tornovsky-Babeay et al., 2014) T2D. We performed TUNEL staining and cleaved caspase-3 assays and found that β-cell apoptosis was increased in 8-week-old *Akita βJazf1KO* mice compared with *Akita* control animals (Figures 2G and 2H). A similar response was observed when challenging islets of *Akita βJazf1KO* with high glucose for 24 h, followed by thapsigargin (TG) treatment for 5 h (Figure 2H). Interestingly, knockdown of Jazf1 in INS1E cells was sufficient to activate ER stress genes PERK and eIF2a (Figure 2I) as well as the p53 pathway, as measured by increased phosphorylation of p53(Ser15), p53 accumulation, and activation of its targets P21 and MDM2, in unstressed conditions (Figure 2J).

We next studied the response of Jazf-depleted INS1E and MIN6 cells to various stresses: treatment of cells with a cytokine cocktail (CC) or TG, which are known to induce ER dysfunction and initiate cell death (Cardozo et al., 2005; Lerner et al., 2012), led to increased Ser51 phosphorylation of eIF2a and more apoptosis as shown by higher levels of cleaved caspase-3 compared with si-Ctrl-transfected cells (Figures 2K–2M). Of note, the expression of JAZF1 protein levels decreased in human primary islets exposed to a diabetogenic milieu (high glucose, palmitic acid, and cytokines) (Figure 2N). Furthermore, JAZF1 levels also decreased in islets exposed to ER stress (Figure 2H) and to INS1E cells treated with TG (Figure S2P). These results are also consistent with increased ER stress markers in islets from *Lepr*$^{db/db}$ mice that are known to undergo ER stress-induced apoptosis (Figures 2O and S2Q). Interestingly, silencing Nr2c2 in β-cells conferred protection to ER stress (Figures S2R and S2S). Of note, Nr2c2 levels were unaffected in β-cells with induced ER stress (Figure S2T). Taken together, these data provide a link between JAZF1/NR2C2 complex and ER stress in pancreatic β-cells.

When protein production exceeds the ER processing capacity or mutant proteins such as *Ins2Akita C96Y* are not properly folded, they can activate a signaling network called the UPR. The transcriptome analysis of islets from *βJazf1KO* and *βWt* mice identified increased levels of several UPR genes that

**Figure 2. Loss of JAZF1 Function in β-Cells Exacerbates ER Stress and Apoptosis *In Vivo* and *In Vitro***

(A–G) Body weight (A), blood glucose levels (B), pancreatic β-cell mass (C), TUNEL staining of insulin-positive islet cells (D), percentage of BrdU-positive β-cells (E), plasma insulin levels (F), and proinsulin levels (G) in mice with indicated genotypes. Islet measurements (C–G) were carried out in 8-week-old mice. In (A), (B), (F), and (G), n = 6 for each group; in (D) and (E)( n = 3). Scale bar: 25 μm.

(H) Immunoblot analysis of cleaved caspase in isolated islets from *Akita βJazf1KO* and *Akita βWt* littermates of 8-week-old animals (top) and after culturing in 24 mM glucose (HG) and TG for 5 h (bottom). Anti-tubulin antibodies were used as a loading control (n = 3). Scale bar: 25 μm.

(I and J) Immunoblot analysis of indicated (phospho) proteins from INS1E cells transfected with siRNAs targeting Jazf1 (si-Jazf1) or control (si-Ctrl) to measure ER stress (I) and p53 pathway activation and apoptosis (J).

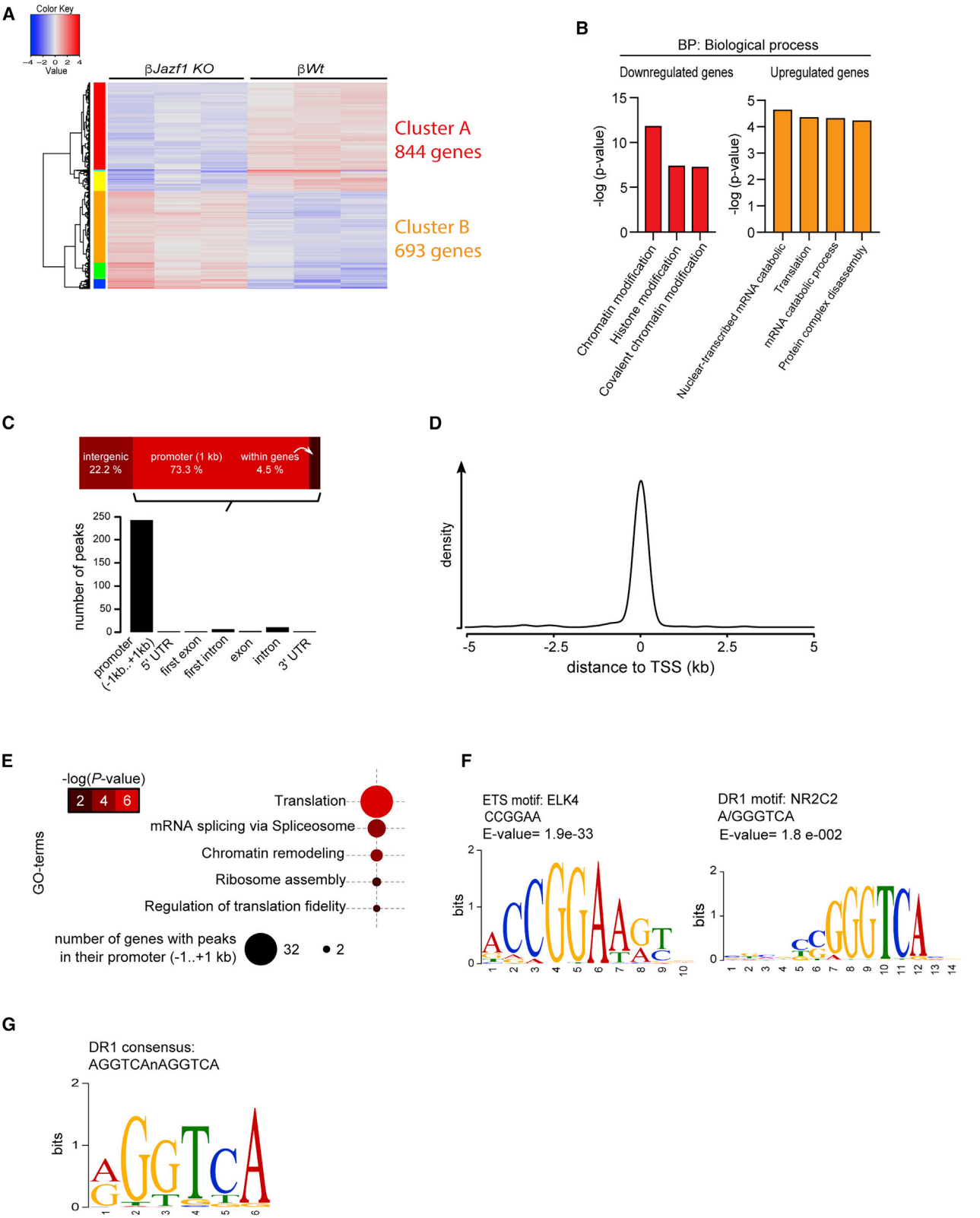
(K–M) Immunoblot analysis of cleaved caspase-3 from INS1E (K) and MIN6 (L and M) cells transfected with siRNAs targeting Jazf1 and exposed to a cytokine cocktail (CC; IL-1β, IFN-γ, and TNF-α) for 24 h (K and L) or thapsigargin (M) for 5 h.

(N) Immunoblot analysis of indicated proteins from human pancreatic islets that were exposed to high glucose (Glc), palmitic acid (Pa), and a cytokine cocktail (CC) for 72 h.

(O) Western blot analysis of indicated proteins from isolated pancreatic islets of 28-week-old *db/db* (*Lepr*$^{db/db}$) or control (*Lepr*$^{+/?}$) mice. Each line represents pooled islets from three mice.

(P–R) Transcript levels of UPR-related genes from isolated islets of *βJazf1KO* and control mice (P), INS1E cells transfected with siRNAs targeting Jazf1 (si-Jazf1) or control (si-Ctrl) (Q), or INS1E cells infected with control or Jazf1-expressing adenoviruses (R). n = 3 per group.

Data are presented as mean ± SD. *p ≤ 0.05, **p ≤ 0.01, and ***p ≤ 0.001 by two-way ANOVA with Holm-Sidak multiple-comparisons test (A and B) or Student's t test (C–G and P–R).

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included Derl3, Creld2, Kdelr3, and the ER stress gene Ddit3 (Chop) (Figure 2P). One of the most upregulated ER stress-related genes was Derlin-3, which is essential for the machinery of the ERAD pathway by targeting misfolded proteins upon ER stress (Oda et al., 2006). We measured increased levels of several UPR-related genes upon knockdown of Jazf1 in INS1E cells in untreated as well as TG-treated cells (Figures 2Q and S2U). Importantly, overexpression of Jazf1 in primary dispersed mouse islets (Figure 2R) or in INS1E cells (Figure S2V) in high-glucose conditions revealed the opposite transcriptional response. Furthermore, the same genes were upregulated in islets of diabetic *db/db* mice (Figure S2W). These results demonstrate a role of JAZF1 in ER stress responses and indicate that decreased JAZF1 expression in β-cells may contribute to the activation of ER stress pathways and ultimately apoptosis.

## Genome-wide Identification of JAZF1 Targets by RNA and ChIP Sequencing

In search of a molecular explanation for the ER stress/apoptosis susceptibility of *Jazf1*-deficient β-cells, we performed RNA sequencing (RNA-seq) on isolated islets of *βJazf1KO* and *βWt* mice (Table S1). The transcriptome analysis identified 2,637 significantly regulated genes with mild gene expression changes ($\log_2$ fold change $\leq$ 0.5, p $\leq$ 0.01, false discovery rate [FDR] < 0.05) upon deletion of *Jazf1* (Figure S3A). Hierarchical clustering on the basis of RNA levels identified two major gene sets (Figure 3A), with 844 downregulated genes (cluster A) and 693 upregulated genes (cluster B) in *βJazf1KO* islets compared with *β Wt* littermates. Gene Ontology (GO) analysis of cluster A identified enriched annotated gene products relating to histone and chromatin modification (Figure 3B). Gene set B showed GO enrichment in nuclear-transcribed mRNAs, mRNA catabolic processes, and protein translation (Figure 3B). These results are consistent with JAZF1 as a principal transcriptional regulator of ribosome biogenesis and functional ortholog of Sfp1.

To confirm the transcriptional role of JAZF1 at the chromatin level, we performed a genome-wide chromatin immunoprecipitation (ChIP) sequencing (ChIP-seq) analysis of JAZF1 in pancreatic β-cells. Because no suitable antibody for ChIP was available, we infected cells with a recombinant adenovirus expressing HA-tagged JAZF1 at a low MOI to perform ChIP. After 24 h, Jazf1 transcript and protein levels were increased ~2.5-fold compared with endogenous Jazf1 levels (Figures S3B and S3C). ChIP analysis identified 316 target genes that were enriched mainly for proximal promoter regions (Figure 3C), as shown by the majority of JAZF1 peaks occurring within 1 kb relative to the transcription start site (TSS) (Figure 3D; Table S2). To identify putative biological processes for JAZF1 targets, we carried out an enrichment analysis for GO and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis and found that Jazf1 targets were enriched for biological processes such as translation, ribosome, mRNA splicing, chromatin remodeling, and regulation of translation fidelity (Figures 3E and S3D). In line with our RNA-seq data, the ChIP-seq analysis also supported JAZF1's role as a transcriptional regulator of ribosome biogenesis and protein synthesis. Because sequence-specific DNA binding domains for JAZF1 have not been identified, we used the *de novo* motif discovery program MEME-ChIP (Machanick and Bailey, 2011) to identify sequence motifs that are overrepresented in JAZF1 binding sites. The most significant JAZF1-associated motifs corresponded to consensus binding sites for the ETS domain family transcription factors (E26 transformation specific), which are unique to metazoans (Degnan et al., 1993). Of the 243 JAZF1 promoter binding sites, 63% contain at least one ETS consensus motif CCGGAA (Figure 3F). ETS family transcription factors interact with a multitude of co-regulatory partners to elicit gene-specific responses and drive distinct biological processes such as development, cell cycle, proliferation, and apoptosis (Oikawa and Yamada, 2003). Additionally, JAZF1 has been shown to function as a repressor of the direct repeat DNA element (DR1)-dependent transcriptional regulation by Nr2c2 through interaction with its LBD (Nakajima et al., 2004). Nr2c2 has been implicated in both transcriptional activation and repression and comprises the most abundant nuclear hormone receptor (NHR) in pancreatic islets (Bookout et al., 2006; Chuang et al., 2008). To examine the potential interaction between JAZF1 and NR2C2, we performed immunoprecipitation followed by mass spectrometry (IP-MS) in INS1E cells. IP-MS identified only NR2C2 interacting with JAZF1 (Figure S2E; Table S3), a finding that was validated with co-immunoprecipitation assays (Figure S2F). To identify NR2C2 elements in the promoters of JAZF1 target, we used the NHR computational analysis program "NHR-scan" to predict NHR binding sites in genomic sequences (Sandelin and Wasserman, 2005). This analysis revealed that the DR1 motif was overrepresented in the promoters of JAZF1 targets, with 29% of the peaks compared with other NHR motifs (Figure 3G). The DR1 motif in JAZF1 binding sites was also confirmed with MEME analysis (Figure 3F) and confirms ChIP-seq studies of NR2C2 in four different non-β-cell lines that identified a DR1 motif in 30% of peaks (O'Geen et al., 2010). Furthermore, GO analysis of NR2C2 target genes was enriched in ribosome, translation, and RNA processing, similar to our ChIP analysis of JAZF1 targets. Together, the integration of experimental MS-IP, RNA-seq, and ChIP-seq data of JAZF1 and published NR2C2 ChIP data (O'Geen et al., 2010) demonstrates that the JAZF1/NR2C2 complex is a key transcriptional regulator of ribosome biogenesis and protein translation.

**Figure 3. JAZF1 Regulates Ribosomal Proteins and Aminoacyl-tRNA Synthetases**

(A) Heatmap for hierarchical clustering of differential gene expression in isolated pancreatic islets from *βJazf1KO* and *βWt* mice (n = 3).

(B) Functional enrichment analysis of JAZF1 target genes on the basis of Gene Ontology terms for biological process (BP) of clusters A and B of RNA-seq data from isolated islets from *βJazf1KO* and *βWt* mice.

(C) Representative diagram indicating the distribution of JAZF1 peaks in the genome.

(D) Distribution profile of peak distances relative to the transcription start site (TSS).

(E) Gene Ontology analysis of JAZF1 target genes.

(F and G) Motif analysis of JAZF1 binding site using MEME (F) and NHR scan analysis (G).

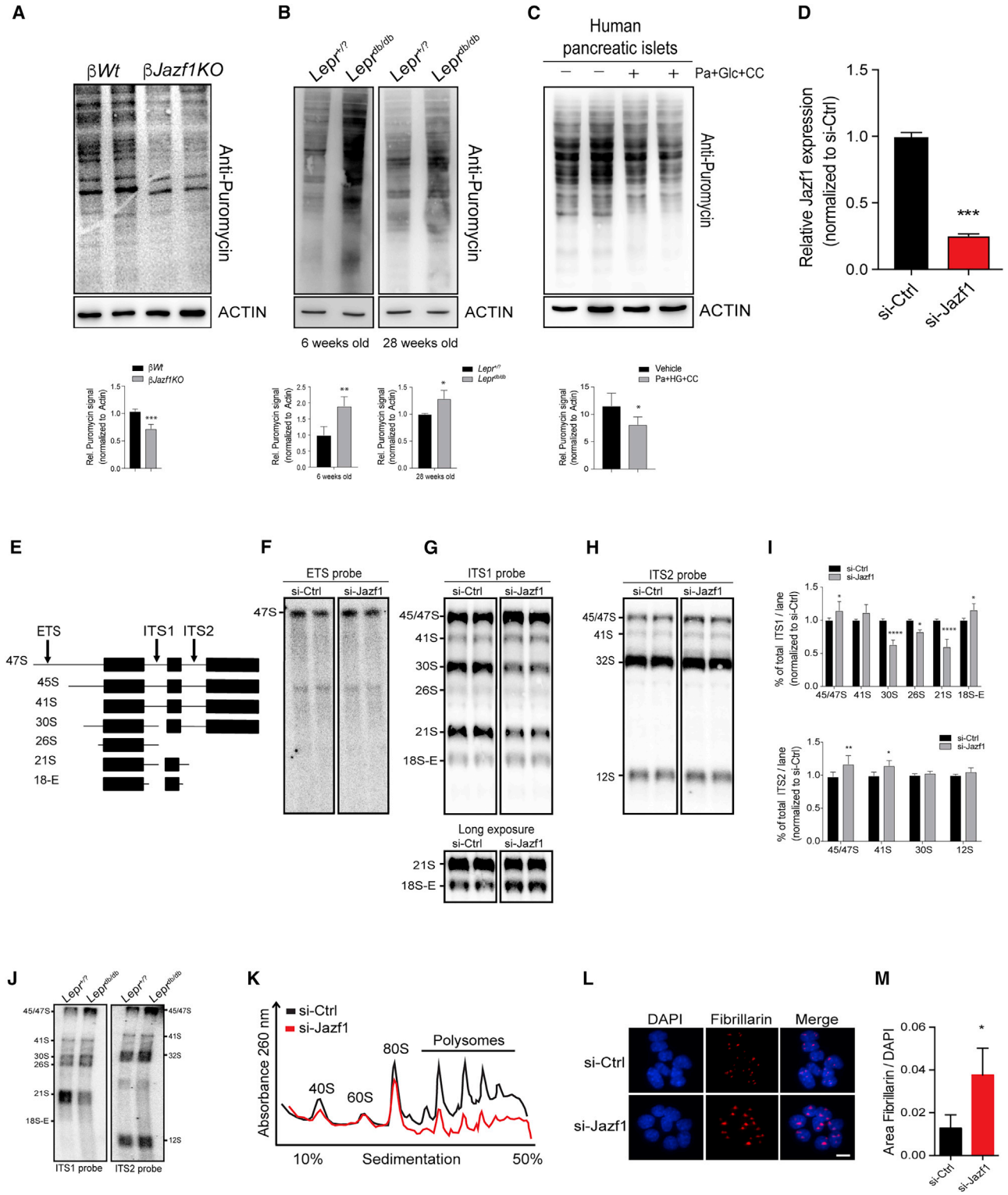


**Figure 4. Loss of JAZF1 Function Leads to Impaired Protein Synthesis and rRNA Processing**

(A–C) Protein synthesis, assessed via puromycin labeling, in islets of *βJazf1KO* and *βWt* control mice (A), *Lepr*$^{db/db}$ and littermate controls at 6 and 28 weeks of age (B), and human pancreatic islets cultured in the presence or absence of palmitate and cytokines (IL-1β, IFN-γ, and TNF-α) for 72 h (C). Quantifications of total puromycin protein levels normalized to actin; a total of four replicates (A and C) and three replicates (B) are shown below the images.

(D) Jazf1 expression in MIN6 cells following siRNA transfection and determined by qPCR (n = 3).

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### Impaired Protein Synthesis and rRNA Processing in *Jazf1*-Null Mice

To investigate JAZF1's involvement in protein synthesis and ribosome biogenesis, we treated islets of *βJazf1KO* and control mice with puromycin and measured the rate of protein synthesis on the basis of the incorporation of puromycin to newly synthesized proteins (Schmidt et al., 2009). Western blot analysis showed decreased levels of translation in islets of *βJazf1KO* compared with *βWt* mice (Figure 4A). We also studied islets of prediabetic and diabetic $Lepr^{db/db}$ mice at the ages of 6 and 28 weeks, respectively, and found increased protein synthesis at 6 weeks of age, when β-cells compensate for insulin resistance by hypersecretion of insulin and β-cell replication (Cavaghan et al., 2000; Rhodes, 2005). However, at 28 weeks of age, the ratio of protein synthesis in $Lepr^{db/db}$ islets was decreased compared with 6-week-old $Lepr^{db/db}$ mice (Figure 4B). These age-dependent alterations in protein synthesis correlate with the well-known compensatory and decompensatory phases of β-cells in diabetes development (Weir and Bonner-Weir, 2004). The data are also in consistent with the profound decrease in protein translation when β-cells are exposed to experimental ER stress (Figure S4A). Protein synthesis was also decreased in human islets that were exposed palmitic acid and a CC and high-glucose conditions for 72 h (Figure 4C). These results demonstrate that JAZF1 expression or activity is required for normal translation of β-cell proteins in physiological and metabolic stress conditions.

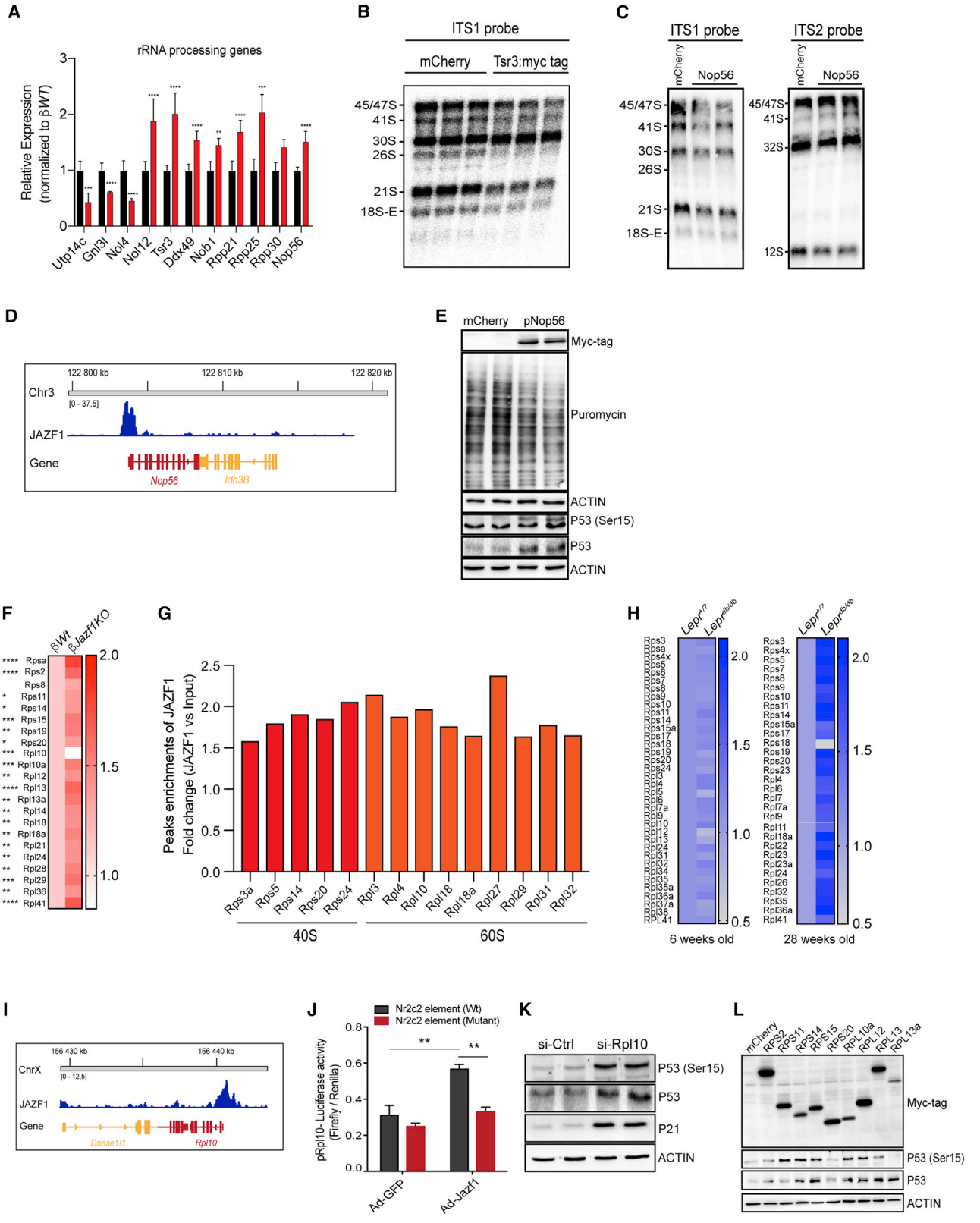
We next asked whether JAZF1 might be involved in ribosome biogenesis, thereby providing mechanistic insights linking loss of JAZF1 function and altered protein synthesis. This possibility was tested by silencing JAZF1 in MIN6 cells using small interfering RNAs (siRNAs), leading to a ~80% reduction of Jazf1 transcript levels (Figure 4D), and assessing the processing of the ribosomal subunit precursor RNAs by northern blotting using three different probes: ETS (transcription of 47S rRNA), ITS1 (processing of 18S), and ITS2 (processing of 28S) (Figure 4E). We found that the transcription of 47S rRNA was not affected in Jazf1-depleted cells versus control cells (Figure 4F), but the ITS1 probe revealed a significant accumulation of 45/47S and 41S pre-rRNAs and decreased levels of 30S and 21S pre-rRNAs (Figure 4G). Furthermore, we noted a significant accumulation of 18S-E pre-rRNA in Jazf1-depleted cells, indicating that the last step of 18S rRNA processing was impaired. Similar results were found with the ITS2 probe, revealing an enrichment of 45S and 41S pre-rRNAs but not the 12S pre-rRNA precursor following knockdown of Jazf1 (Figures 4G–4I). Importantly, we found a similar defect in rRNA processing in islets of $Lepr^{db/db}$ mice compared with $Lepr^{+/?}$ islets (Figure 4J), suggesting that rRNA processing may be impaired in T2D. In order to determine the impact of this alteration at the level of the ribosome, we performed a polysome profiling analysis in MIN6 cells in which Jazf1 levels were reduced by RNAi. JAZF1-depleted cells exhibited a lower abundance of free 40S subunits, which contains mature 18S rRNA, and a consequent decrease of 80S ribosomes and polysomes compared with control siRNA-transfected cells (Figure 4K). As alterations in ribosome biogenesis are often associated with changes in the morphology of nucleoli (Mélèse and Xue 1995; Boulon et al., 2010), we stained cells with anti-fibrillarin, a nucleolar protein involved in pre-rRNA processing, to monitor the nucleolus size. Silencing of Jazf1 resulted in larger nucleoli, as determined by an increased ratio between nucleolar and nuclear areas, suggesting a direct correlation between nucleolar size and rRNA processing upon Jazf1 knockdown (Figures 4L and 4M). Collectively, these results indicate that JAZF1 plays an important role in pre-rRNA processing by facilitating the formation of 18S rRNA and ribosomal 40S subunits and thereby regulating protein synthesis.

### JAZF1 Regulates the Expression of rRNA Processing and Ribosomal Protein Genes and Influences p53-Dependent Stress Responses

To identify the genes that could mediate the defect in rRNA processing, we queried RNA-seq data from *βJazf1KO* and *βWt* mice for expression changes in transcripts encoding ribosome biogenesis factors. We found significantly dysregulated genes that are involved in rRNA processing (Figure 5A). We examined two factors, respectively, that are upregulated (Tsr3, Nop56) and downregulated (Nol4, UTP14C) in islets of *βJazf1KO* mice. Silencing of Nol4 and UTP14C in MIN6 cells had no effect on rRNA processing (Figure S5A). Tsr3 overexpression led to abnormal 18S rRNA processing compared with control cells (mCherry) when probed with ITS1 (Figures 5B and S5B). Similar defects in pre-rRNA processing were found when we overexpressed Nop56 in MIN6 cells (Figure 5C). Tsr3 catalyzes the base modification of 18S rRNA (Meyer et al., 2016), whereas Nop56 is a component of the box C/D small nucleolar ribonucleoprotein complexes that direct 2-prime-O-methylation of pre-rRNAs during its maturation and therefore may function in an early to middle step of pre-rRNA processing (Hayano et al., 2003). Whereas we did not detect an enrichment of JAZF1 at the *Tsr3* promoter, our ChIP analysis revealed that JAZF1 binds to the promoter region of *Nop56* (Figure 5D).

Defects of rRNA modifications or processing enzymes often lead to disturbed ribosome biogenesis or assembly (King et al., 2003; Liang et al., 2009). This in turn can activate cellular stress responses, including activation of the p53 pathway, a process

(E) Schematic illustration of pre-rRNA processing. Cleavage sites to remove external and internal spacers (ETS/*ITS1/2*) are indicated.
(F–H) Northern blot analysis of MIN6 cells transfected with si-Jazf1 and control siRNAs and hybridized with ETS (F), ITS1 (G), or ITS2 (H) probes.
(I) Densitometric analysis of the pre-rRNA of 18S (ITS1 probe) and 28S (ITS2 probe) of MIN6 cells transfected with si-Jazf1 and control siRNAs (n = 4).
(J) Northern blot analysis of isolated islets from $Lepr^{db/db}$ and wild-type mice, hybridized with the indicated probes.
(K) Polysome profiling analysis of MIN6 cells transfected with si-Jazf1 and control siRNAs.
(L and M) Immunohistochemical staining of nucleolar protein fibrillarin and DNA (DAPI) in MIN6 cells transfected with si-Jazf1 and control si-RNAs (L) and quantification of stained fibrillarin/DAPI area (M). Scale bar: 10 μm (n = 3).
Data are presented as mean ± SD; *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$, and ****$p \leq 0.0001$ by two-way ANOVA (Sidak's multiple-comparison test) (I) or Student's t test (A–D and M).

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named "ribosomal stress" (Boulon et al., 2010; Wang et al., 2015). We elicited ribosomal stress by treating MIN6 cells with low doses of actinomycin D, known to selectively inhibit RNA polymerase I (Perry and Kelley, 1970), which resulted in decreased protein translation and a strong activation of p53 and apoptosis (Figure S5C). Interestingly, increased Nop56 expression was sufficient to impair protein translation and activate p53 and its target p21 (Figure 5E), whereas Tsr3 overexpression had no effect on protein translation but was sufficient to activate p53 (Figures S5D and S5E). These data show that JAZF1 directly and indirectly regulates rRNA biogenesis factors that alter pre-rRNA processing and stimulate ribosomal stress responses.

Our transcriptomic analysis in *βJazf1KO* mice revealed increased levels of several 40S and 60S ribosomal protein (RP) genes compared with *βWt* mice (Figure 5F). In line with the RNA-seq data, ChIP-seq analysis showed that JAZF1 binds to the promoters of five small (40S) and nine large (60S) RP genes (Figure 5G). Interestingly, the levels of RPs are not affected in islets of prediabetic $Lepr^{db/db}$ mice, when Jazf1 expression is unchanged, but in older diabetic $Lepr^{db/db}$ mice, when Jazf1 expression was reduced by 50%, RPs were significantly increased compared with WT controls (Figures 1C and 5H). These findings are consistent with recent studies showing increased expression of RP genes in islets from $Lepr^{db/db}$ mice (El Ouaamari et al., 2015).

We next studied the transcriptional regulation of selected JAZF1-targeted RPs by perturbing JAZF1 levels using luciferase reporter assays. We first confirmed the reduced levels of Rpl10 in islets of *βJazf1KO* mice (Figure S5F) and found that overexpression of JAZF1 resulted in increased Rpl10 promoter activity. This regulation was dependent on an intact Nr2c2 element in the promoter of Rpl10 and supports the negative regulation of JAZF1 on this promoter (Figures 5I and 5J). Conversely, the Rps14, which is also a direct JAZF1 target and overexpressed in islets of *βJazf1KO* mice (Figures 5F and S5G), showed decreased transcript levels when Jazf1 was overexpressed and increased expression upon silencing of Jazf1 (Figure S5H), which corroborates the upregulation in islets of diabetic $Lepr^{db/db}$ mice (Figure 5H). This JAZF1 transcriptional control was also dependent on an Nr2c2 element in the Rps14 promoter (Figure S5I).

The observed ribosome defects in *βJazf1KO* mice led us to hypothesize that the "disturbance" of ribosome subunit components induces an "imbalance state" in the cell, activating the p53 pathway and consequently cell-cycle arrest, thereby influencing proliferation and apoptosis (Zhang and Lu, 2009; Warner and McIntosh, 2009). To explore if the silencing of Rpl10 and overexpression of various RPs in *βJazf1KO* islets can activate the p53 pathway, we knocked down Rpl10 and overexpressed RPs of the small and large subunit in INS1E cells. Both silencing of Rpl10 and overexpression of Rps-11, Rps-14, Rps-15, Rpl10a, and Rpl12 activated the p53 pathway (Figures 5K and 5L). These findings indicate that JAZF1 is required for tight control of rRNA processing and RP transcription and for the coordination of these processes with cell survival pathways.

## JAZF1 Regulates Aminoacyl-tRNA Synthetases

Our ChIP-seq analysis demonstrated that JAZF1 binds to the promoters of seven aminoacyl-tRNA synthetase genes (aaRSs) (Figure 6A), consistent with the KEGG analysis of JAZF1 target genes revealing that "aaRSs" ranked second in the enrichment gene sets after "ribosome" (Figure S3D). aaRSs are composed of 20 different ligases that catalyze the ligation of a specific amino acid to its cognate tRNA, thereby ensuring the fidelity of protein synthesis (Ibba and Söll, 2000). The expression levels of two aaRSs, aspartyl-tRNA synthetase (Dars) and glycyl-tRNA synthetase (Gars), were decreased in islets from *βJazf1KO* compared with *βWt* mice (Figure 6B) and JAZF1 was found in ChIP studies to bind to their respective promoter regions (Figures 6C and 6D). Moreover, silencing of Jazf1 in INS1E cells resulted in lower mRNA levels of Gars and Dars compared with si-control-transfected cells (Figure 6E). Adenoviral overexpression of Jazf1 elicited the opposite transcriptional regulation of Dars and Gars compared with Ad-GFP-infected cells (Figure 6F). Furthermore, transcript levels of Dars and Gars were significantly decreased in islets of diabetic $Lepr^{db/db}$ mice (Figure 6G). Of note, in humans, the mRNA levels of Gars are the most highly expressed in pancreas compared with other tissues (Antonellis et al., 2003) and further enriched in β-cells (Park et al., 2010). To investigate if reduced expression of Dars and Gars can be linked to ER stress and activation of cell death pathways, we silenced these aaRSs in the presence and absence of ER stress.

**Figure 5. JAZF1 Regulates rRNA Processing and Ribosomal Protein Transcription**

(A) Expression levels of pre-rRNA processing genes in islets of *βJazf1KO* and *βWt* control mice (n = 3).

(B and C) Northern blot analysis of MIN6 cells transfected with expression plasmids for Tsr3 (B) and Nop56 (C) and hybridized with indicated probes. mCherry plasmid was used as a control.

(D) Genome Browser tracks of ChIP-seq peaks in INS1E cells. Region spanning the Nop56/Idh3B genes on chromosome 3 is shown. ChIP-seq peaks are presented after normalizing to input.

(E) Western blot analysis of indicated proteins in MIN6 cells transfected with Nop56 and control (mCherry) expression plasmids. Protein synthesis was assessed using puromycin labeling.

(F) Heatmap of ribosomal gene expression in islets of *βJazf1KO* and *βWt* mice.

(G) Peak enrichment of JAZF1 on promoters of indicated ribosomal proteins of 40S and 60S subunits in INS1E cells.

(H) Heatmap of relative ribosomal gene expression in islets of $Lepr^{db/db}$ and control mice at 6 and 28 weeks of age.

(I) Genome Browser tracks of ChIP-seq peaks in INS1E cells. Region spanning the Dnase1l1/Rpl10 genes on the X chromosome is shown.

(J) Luciferase reporter assay of INS1E cells transfected with plasmids containing wild-type (WT) Rpl10 promoter or a mutated Nr2c2 site (mutant) and infected with either a control or Jazf1-expressing adenovirus (Ad-Jazf1). Levels are relative to Renilla luciferase activity (n = 5).

(K and L) Western blot analysis of indicated proteins in INS1E cells transfected with si-Rpl10 or control siRNAs (K) or expression plasmids of indicated myc-tagged ribosomal genes (L).

Data are presented as mean ± SD; *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$, and ****$p \leq 0.0001$ by two-way ANOVA (Sidak's multiple-comparison test) (J) or Student's t test (A).

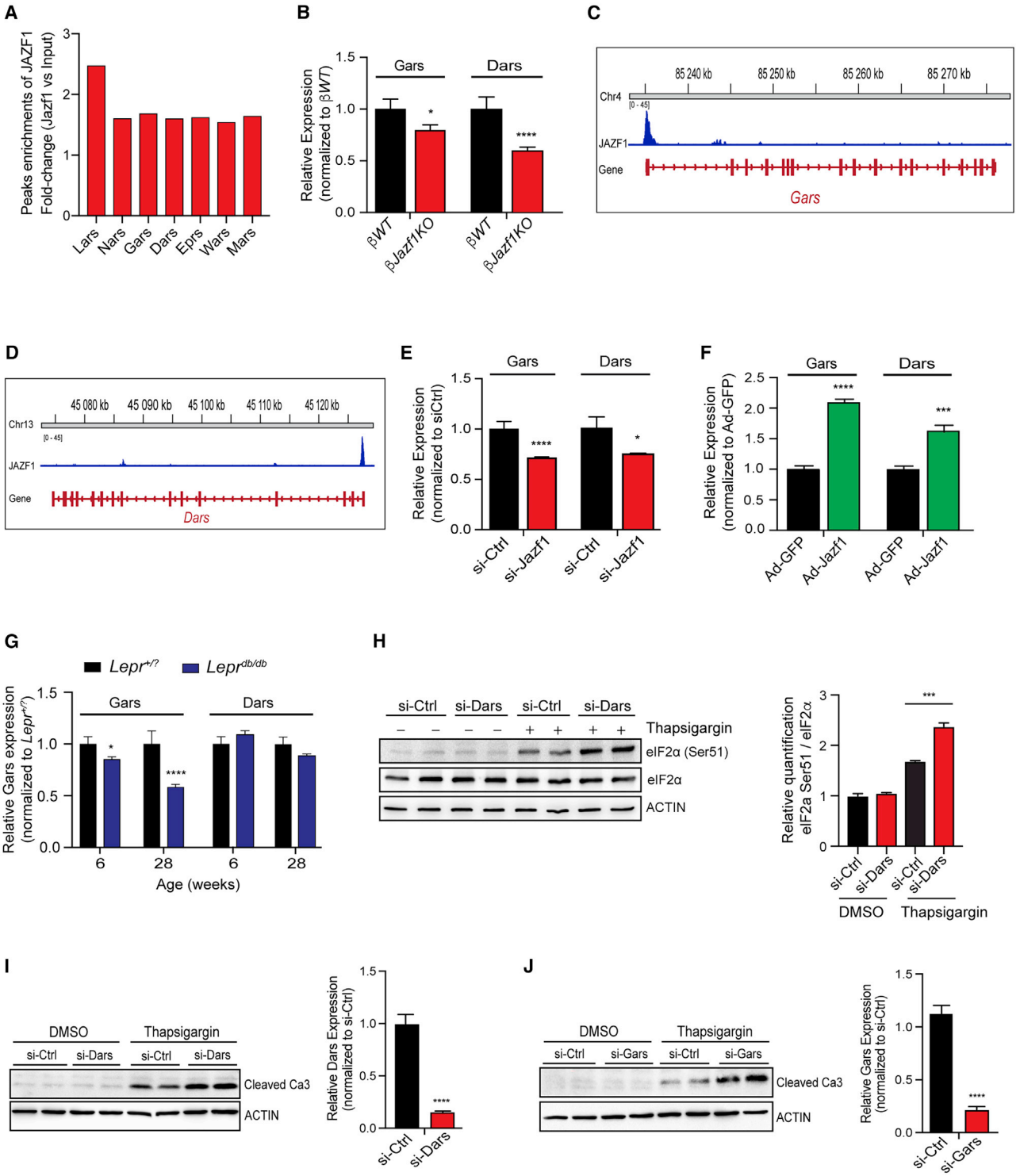


**Figure 6. JAZF1 Regulates the Expression of Aminoacyl-tRNA Synthetase Genes**

(A) Peak enrichment of JAZF1 in ChIP-seq analysis of INS1E cells on promoters of indicated aminoacyl-tRNA synthetase genes.

(B) Relative expression levels of Gars and Dars in islets of *βJazf1KO* and *βWt* control mice (n = 3).

(C and D) Genome Browser tracks of ChIP-seq peaks in INS1E cells. Regions spanning the Gars (C) and Dars (D) genes, respectively, are shown. ChIP-seq peaks were normalized to input.

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No evidence for ER stress was observed upon Gars knockdown, but we measured increased phosphorylation of eIF2α when Dars was silenced (Figure 6H). This finding underlines recent reports suggesting that deficiency states of aaRSs are linked to the ER stress response (Krokowski et al., 2013; Fröhlich et al., 2017). Moreover, knockdown of Dars and Gars rendered the susceptibility to apoptosis upon exposure to ER stress (Figures 6I and 6J). Together, these findings show that JAZF1 is a positive and direct transcriptional regulator of aaRSs, which play a crucial role in translation and ER stress-mediated apoptosis of pancreatic β-cells.

### Srp54a and Insulin Are Direct Targets of JAZF1

SRP54a is a key component of the ribonucleoprotein complex that interacts with ribosomes to bring the translocation of secretory and membrane proteins to the ER (Focia et al., 2004). We noted that Srp54a transcript levels were 2-fold lower in islets of *βJazf1KO* mice compared with controls (Figure 7A). Our ChIP-seq data further demonstrated that JAZF1 binds to the Srp54a promoter region (Figure 7B). Recently, it has been shown that mutations in *SRP54a* cause Shwachman-Bodian-Diamond syndrome, a recessive disease characterized by exocrine pancreatic insufficiency, bone marrow failure, and skeletal dysplasia, but may also present with early infancy diabetes (Kamoda et al., 2005). Loss-of-function mutations and knockdown of *SRP54a* have been shown to induce ER stress and are associated with apoptosis in human bone marrow cells (Bellanné-Chantelot et al., 2018). Interestingly, we found that Srp54a levels are increased and reduced in islets from prediabetic and diabetic $Lepr^{db/db}$ mice, respectively, compared with control mice (Figure 7C). Moreover, knockdown of Srp54a in INS1E cells induced the phosphorylation of eIF2α and increased levels of cleaved caspase-3 (Figure 7D). These data indicate that JAZF1 participates in the regulation of SRP54a expression, which plays a crucial role in ER stress-mediated apoptosis of β-cells.

Our ChIP-seq data also identified enriched binding of JAZF1 at the proximal promoter region of the *Ins1* gene (Figure 7E). Furthermore, the NHR scan analysis identified a direct repeat (DR1) Nr2c2 element located at −61 to −49 bp relative to the TSS and contained the consensus hexanucleotide sequence AGGTCA. Importantly, this element is conserved among mouse, rat, and human genomes (Figure S6A). In the human promoter, it is located between nucleotide positions −276 and −264 bp relative to the TSS. Of note, this motif is located in the previously described glucose-responsive element (Z element) (−292 to −243 bp) that acts both as a glucose-responsive enhancer in primary cultured islet cells and as a transcriptional repressor in immortalized β- and non-β-cells (Sander et al., 1998; Pino et al., 2005).

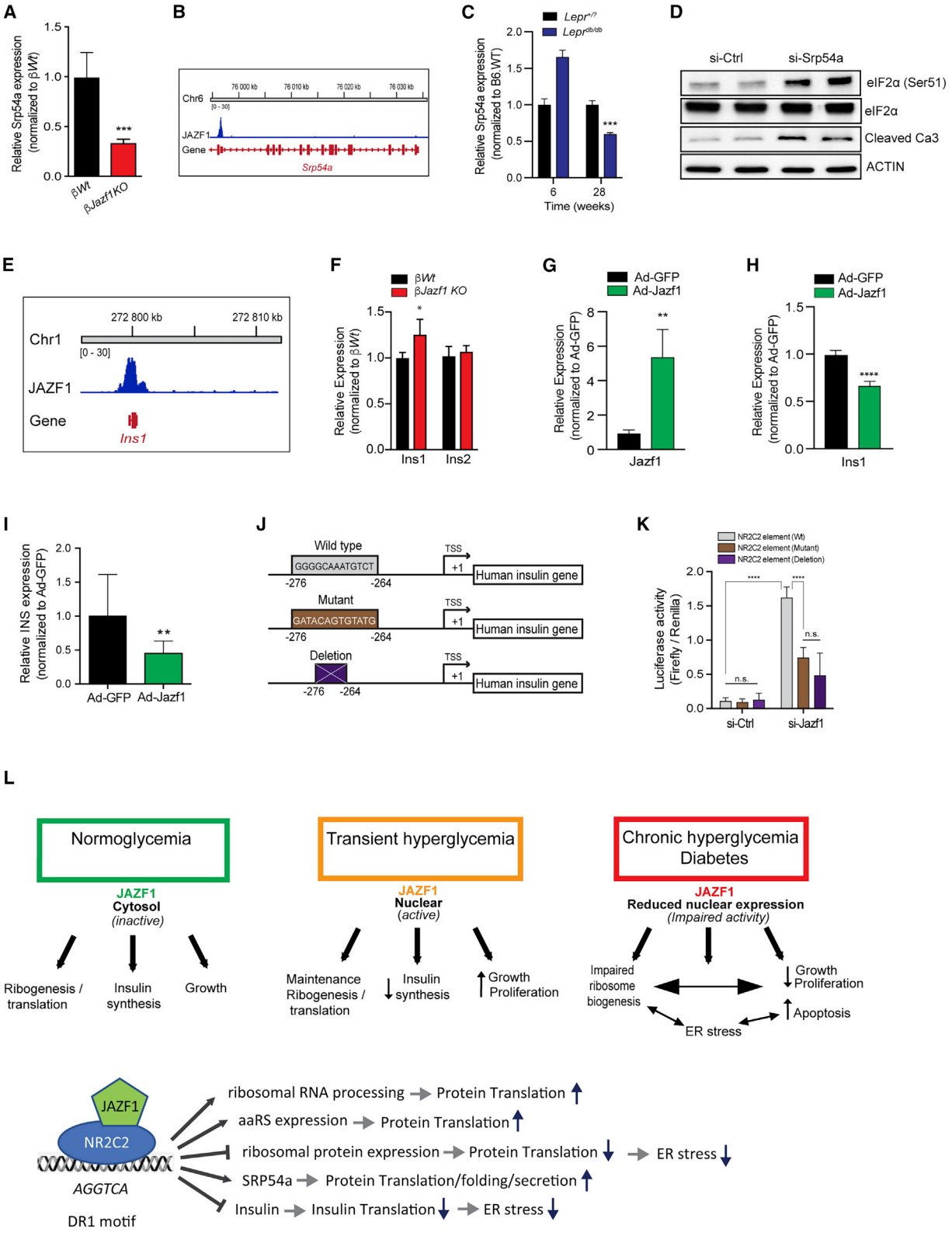
Our RNA-seq and qPCR analysis revealed that the transcript levels of *Ins1* were increased in islets of *βJazf1KO* compared with *βWt* mice, whereas Ins2 mRNA levels were unchanged (Figure 7F). In addition, INS1E cells infected with a Jazf1-expressing adenovirus had reduced levels of Ins1 compared with cells infected with a control virus (Figures 7G and 7H). Overexpression of Jazf1 in dispersed human islet cells resulted in decreased *INS* transcript levels compared with control (Ad-GFP) infected cells (Figure 7I), indicating that the transcriptional regulation of the *INS* gene by JAZF1 is conserved between rodents and human.

To determine if JAZF1 regulates human insulin gene transcription through the NR2C2 DR1 element, we generated three luciferase reporters with upstream human insulin promoter sequences (WT), or identical constructs harboring point mutations (mutant), or a deletion of the NR2C2 DR1 motif (Figure 7J). These reporter constructs were transfected into EndoC-βH2 human cells in which JAZF1 was either present or silenced by RNAi. The basal activity of the human insulin promoter was increased in Jazf1-depleted cells. Remarkably, this activation was abolished in reporter plasmids harboring a NR2C2 mutant or deletion element (Figure 7K), indicating that the DR1 element is required for the regulation of the human insulin gene by JAZF1. Of note, *βJazf1KO* mice exhibited higher levels of serum proinsulin compared with *βWt* animals, an observation that is in agreement with the higher proinsulin levels found in human and rodent T2D. These results demonstrate key roles for JAZF1 in protein translation by transcriptional regulation of Srp54a, a protein that links three key elements of the SRP complex (i.e., the 7SL RNA, the signal sequence of the nascent ribosome-bound polypeptide chain, and the signal peptide receptor on the ER membrane), as well as the insulin gene through a conserved negative regulatory element (NRE) containing a DR1 site in the *INS* promoter, whose mechanistic basis of repression has remained elusive.

## DISCUSSION

In this study we confirm in a large cohort that the SNP rs1635852, located in intron X of *JAZF1*, is a T2D susceptibility gene. Rs1635852 is located in a key region of a β-cell enhancer and mediates allele-specific differences in JAZF1 expression, with the T2D risk allele T exhibiting lower transcriptional activity than the nonrisk allele C. Furthermore, the risk allele also mediates increased binding to protein complexes involving JAZF1, suggesting that it functions as part of a transcriptional repressor complex (Fogarty et al., 2013). Our study also demonstrates that JAZF1 is a key factor in pancreatic β-cells for sensing metabolic stress signals and for mediating a dynamic and coordinated transcriptional response that regulates protein translation in response to increased insulin demand. JAZF1 is enriched in β-cells and dynamically distributed in the cytoplasm and nucleus, with a predominantly cytosolic localization with low glucose in mice and healthy human subjects and a nuclear presence upon stimulation with high glucose and in different murine models (*Akita*, *db/db*) and in pancreatic sections of patients with

(E–G) Expression levels of Gars and Dars in INS1E cells upon silencing using siRNAs (E) or overexpression of Jazf1 (Ad-Jazf1) compared with control cells (Ad-GFP) (F) and in islets of $Lepr^{db/db}$ and control mice ($Lepr^{+/?}$) at 6 and 28 weeks of age (G). n = 3 per group.
(H–J) Western blot analysis of eIF2α (Ser51), eIF2α (H) and cleaved caspase-3 (I and J) in INS1E cells following transfection of siRNAs targeting Dars (H and I) or Gars (J) in response to thapsigargin (TG) for 5 h. Quantification of band intensities by densitometry are shown on right. All data are in duplicates.
Data are presented as mean ± SD; *p ≤ 0.05, **p ≤ 0.01, ***p ≤ 0.001, and ****p ≤ 0.0001 by Student's t test.

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T2D. Although our mouse genetic studies show that JAZF1 is dispensable for normal β-cell function, it is clear that during increased insulin demand or β-cell growth, JAZF1 translocates to the nucleus, thereby influencing the transcription and the expression of its target genes. The mechanisms by which JAZF1 translocates to the nucleus during metabolic stress may be mediated by increased $Ca^{2+}$ levels, induced by high glucose and/or cytokine signaling, or by a calcineurin-mediated process that dephosphorylates JAZF1, thereby exposing nuclear import signals leading to translocation in the nucleus, where Jazf1 regulates transcription (Cartwright and Helin, 2000). This model is supported by several conserved phosphorylated serine and tyrosine residues in JAZF1. It will be important to determine the kinases and phosphatases that regulate stress- and glucose-mediated nuclear import in pancreatic β-cells. We show that in diabetic states, the nuclear shuttling of JAZF1 in β-cells is intact, but the overall expression levels are significantly reduced in diabetic rodents, in islets of T2D patients, and in islets exposed to chronic metabolic stress, findings that support a study reporting reduced JAZF1 levels in human islets of hyperglycemic donors (Taneera et al., 2012). These results indicate that in chronic stress conditions, JAZF1 function is impaired, contributing to progressive β-cell dysfunction as shown in *Akita βJazf1KO* mice that have a markedly accelerated disease progression due to increased β-cell apoptosis and decreased proliferation (Figure 7L).

Our analysis of ChIP-seq and RNA-seq revealed that JAZF1 is a transcriptional mediator of ribosome biogenesis, including 40S and 60S subunit genes, rRNA processing, and aaRSs, and that these processes are impaired in murine T2D (Figure 7L). These findings are consistent with RNA-seq analysis from islets of human T2D showing ribosome biogenesis transcripts as the most enriched gene set (De Jesus et al., 2019; Li et al., 2018). Our data are also consistent with JAZF1 being an ortholog of yeast Sfp1, a master transcriptional regulator of ribosome biogenesis in yeast (De Virgilio and Loewith, 2006).

Our morphometric analysis of nucleoli revealed that their size is enlarged in Jazf1-depleted β-cells, and their shape remained intact. This appearance resembles what has been seen in aging cell culture models and in senescent cells (BeMiller and Lee, 1978; Bowmann et al., 1976). Conversely, small nucleoli are a cellular hallmark of longevity in mutant as well as calorie-restricted organisms, which also exhibit decreased expression of ribosomal RNA and proteins, including fibrillarin (Tiku et al., 2017). Recent evidence suggests additional roles for nucleoli as key hubs for sensing and reacting to various stress stimuli such as induction of senescence, DNA damage by activating the p53 pathways, cell-cycle arrest, and apoptosis (Deisenroth et al., 2016). Furthermore, nucleolar stress and p53 activation, both present in islets of diabetic *βJazf1KO* mice, have also been associated with increased nucleoli size (James et al., 2014). The increased nucleolar size in β-cells that are depleted in JAZF1 are therefore consistent with these published reports but may be attributed to the increased synthesis of RP, as ~1/3 of all nucleolar proteins detected by mass spectrometry are composed of RPs (Boisvert et al., 2007; Lam et al., 2010).

One of the most striking results of our study is the finding that in response to experimental conditions of ER stress, Jazf1 transcripts and nuclear protein levels are reduced, leading to increased ER stress and susceptibility to apoptosis. Data from mutant *Jazf1* mice also show that JAZF1 contributes to ER homeostasis. Previous studies have shown that increased protein synthesis can lead to upregulation of the UPR pathway through accumulation of misfolded proteins (Harding et al., 2000a, 2000b; Ron, 2002). We found that deletion of *Jazf1* induces the expression of UPR-related genes, whereas Jazf1 overexpression elicits the opposite transcriptional response. We implicate three processes in leading to the activation of ER stress in the absence of JAZF1: impaired rRNA processing, abnormal RP expression, and defective transcriptional regulation of tRNAs. The observed defect in rRNA processing upon in *βJazf1KO* mice can be predicted to affect ribosome assembly and protein production. Moreover, we uncover a previously unrecognized defect in rRNA processing and translation in islets from *db/db* mice at the decompensation stage. Our RNA-seq and ChIP-seq analysis further indicate that the gene encoding Nop56, which is a direct JAZF1 target, is responsible for the impairment in rRNA processing, as overexpression of Nop56 in β-cells led to

**Figure 7. JAZF1 Is a Transcriptional Regulator of the *SRP54a* and *INS* Genes**

(A) Srp54a transcript levels of *βJazf1KO* and *βWt* control mice. n = 3 per group.

(B) Genome Browser tracks of ChIP-seq peaks in INS1E cells. Region spanning the *Srp54a* gene and its promoter is shown. ChIP-seq peaks are presented after normalizing to input.

(C) Expression of Srp54a in islets of 6- and 28-week-old $Lepr^{db/db}$ and wild-type control mice.

(D) Western blot of indicated proteins in INS1E cells following transfection with si-Srp54a or si-Ctrl. Actin was used as a loading control.

(E) Genome Browser tracks of ChIP-seq peaks in INS1E cells. Approximately 20 kb region spanning the murine Ins1 locus is shown on chromosome 1. ChIP-seq peaks are presented after normalizing to input.

(F) Relative expression levels of *Ins1* and *Ins2* in islets of *βJazf1KO* and *βWt* mice.

(G–I) Relative expression of Jazf1 (G) and Ins1 (H) in INS1E cells, and INS (I) in dispersed human islets following Ad-Jazf1 or control Ad-GFP infection. n = 3 per group.

(J) Schematic representation of reporter plasmids harboring the human insulin promoter with wild-type, mutant, or a deleted DR1 element site. TSS, transcription start site.

(K) Luciferase activity assays in Endoc-βH2 cells transfected with firefly luciferase reporter constructs shown in (J). Data are normalized to Renilla luciferase. n = 5 for each group.

(L) Illustration of model depicting the role of JAZF1 in normal (green) conditions and in response to short (orange) and chronic (red) exposure to metabolic stress. Bottom: illustration of model showing the molecular function of JAZF1 in active (nuclear) conditions.

Data are presented as mean ± SD; *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$, and ****$p \leq 0.0001$ by two-way ANOVA (Sidak's multiple-comparison test) (K) or Student's t test (A, C, and F–I).

defect in 18S and 28S processing. This finding is in line with a recent study demonstrating that knockdown or overexpression of Nop56 results in defects in pre-rRNA processing (Lykke-Andersen et al., 2018).

We also discovered that JAZF1 is a prominent regulator of numerous RPs and demonstrate that JAZF1 is responsible for maintaining the balance between the components of ribosomal subunits (rRNA and RPs) for optimal ribosome synthesis. Ablation of *Jazf1* in islets revealed increased levels of many RP transcripts, accompanied by a reduction in the 40S subunit, indicating that JAZF1 is primarily a negative transcriptional regulator of RPs. Our data therefore offer a mechanistic explanation for a recent study reporting increased levels of subsets of RPs in a rat T2D model compared with control islets using unbiased quantitative proteomic analysis (Hou et al., 2017). An emerging body of literature suggests that rRNA processing and ribosome biogenesis are tightly orchestrated processes and that imbalances in synthesis or turnover can affect signaling pathways and disease development. Furthermore, these pathways are linked to p53 activation as a general response to defective ribosome function (Barlow et al., 2010; Dutt et al., 2011). For example, Rps6 haploinsufficiency activates the p53 pathway in mouse embryonic cells and T lymphocyte cells (Sulic et al., 2005). Zebrafish with a heterozygous Rpl11 mutation exhibit increased glucose levels and upregulated preproinsulin transcript level (Danilova et al., 2011). Furthermore, conditional inactivation of Rps14 in mice leads to a p53-dependent erythroid differentiation defect (Schneider et al., 2016). Interestingly, overexpression or silencing of single RPs is sufficient to affect ribosome biogenesis and induce activation of the p53 pathway (Lohrum et al., 2003; Zhou et al., 2013). We show that silencing or overexpression of the JAZF1 targets Rpl10 and Rps14 is sufficient to perturb protein synthesis and induce p53 activation and apoptosis. Of note, GWASs have identified an association between p53 and T2D susceptibility (Gaulton et al., 2008; Burgdorf et al., 2011), which is consistent with our and other studies showing evidence of DNA damage and p53 activation in islets of *db/db* mice and human T2D subjects (Tornovsky-Babeay et al., 2014; Belgardt et al., 2015). Together, our study describes a previously unrecognized mechanism in T2D in which defective ribosome synthesis during metabolic stress activates p53 and apoptosis in β-cells.

In this study, we show that JAZF1 is a direct transcriptional activator of genes encoding aminoacyl tRNA synthetases. Mutations in tRNA ligases frequently give rise to diseases with neuronal pathologies and autoimmune and metabolic disorders. Specifically, mutations in glycine tRNA ligase (GARS) are associated with childhood neuropathological diseases alongside altered mitochondrial protein and respiratory chain subunit expression (Boczonadi et al., 2018). Our finding that GARS levels are reduced by 50% in *db/db* mice and that silencing of Gars and Dars renders β-cells more sensitive to ER stress-mediated apoptosis corroborates phenotypic traits in mice with mutated tRNA synthetase exhibiting impaired translational fidelity, protein misfolding, and induction of ER stress (Lee et al., 2006).

Our study demonstrates that JAZF1 is a direct transcriptional activator of Srp54a, a component of the signal recognition particle complex that is recognized by the signal sequence of the nascent polypeptide on the ribosome and docked to the ER membrane via the conjugate receptors. In β-cells, Srp54a binds to the preproinsulin signal sequence appearing from the ribosome and slows down protein synthesis, which can prevent the premature initiation of preproinsulin folding prior to nascent peptide to the ER membrane (Eskridge and Shields, 1983; Walter and Blobel, 1983). We show that deletion of Srp54a leads to increased phosphorylated eIF2$\alpha$ levels and induces apoptosis. Importantly, Srp54a levels were decreased in absence of JAZF1; furthermore, Srp54a expression was reduced in islets of *db/db* mice where chronic ER stress is induced. Interestingly, five mutations located in the preproinsulin signal peptide have been reported to cause diabetes in humans (Støy et al., 2007; Garin et al., 2010). Collectively, we propose that under chronic insulin demand, in conditions of partial or absolute JAZF1 deficiency, JAZF1 contributes to ER stress through increasing insulin transcription directly and through defective expression of Srp54, which can lead to cytosolically misassembled, misfolded, and mislocalized proteins (Bellanné-Chantelot et al., 2018).

Insulin is a major ER client protein in β-cells, and high levels of misfolded insulin protein can affect the protein folding capacity and elicit ER stress. Interestingly, the serum proinsulin level and proinsulin/insulin ratio were higher in *Akita βJazf1KO* mice compared with *Akita βWt* mice. Previously, it has been shown that the proinsulin/insulin ratio is increased in *Akita* mice, which exhibit high levels of ER stress in β-cells (Winnay et al., 2014). This observation is consistent with elevated proinsulin/insulin ratios in human T2D (Ward et al., 1987; Vangipurapu et al., 2015) and with studies demonstrating that proinsulin misfolding is an early feature in the progression of prediabetes (Liu et al., 2005; Arunagiri et al., 2019). Furthermore, transgenic insulin-overexpressing mice exhibit glucose intolerance in the absence of obesity (Shanik et al., 2008), and insulin-knockout mice are partially protected from chronic ER stress in β-cells (Szabat et al., 2016). These data indicate that JAZF1 can alleviate ER stress by reducing insulin synthesis, a notion that is supported by the phenotype of transgenic Jazf1 mice that have reduced fasting plasma insulin levels and enhanced glucose tolerance (Yuan et al., 2015).

In this context and on the basis of our gene expression analysis from mutant JAZF1 in human and rodent islets and further supported by the JAZF1 ChIP-seq analysis, it is relevant that we also found the insulin promoter to be a direct JAZF1 target. JAZF1 binds to a conserved DR1 site in the *Ins1* promoter, which is absent in Ins2 due to a nucleotide substitution. These observations are consistent with the transcriptional regulation of *Ins1* but not *Ins2*. Interestingly, in humans, we identified a DR1 site in the insulin promoter within a previously described inhibitory sequence (−279 to −258), also referred to as the NRE (Boam et al., 1990; Clark et al., 1995). This element also lies within the glucose-sensing Z element (−243 to −292) (Sander et al., 1998; Pino et al., 2005), which functions as an enhancer in primary islet cells but represses transcription in immortalized β-cells. Furthermore, the direct regulation of the insulin gene by JAZF1 might contribute to the low insulin content of transformed β-cell lines and act as a protective mechanism to counteract glucose toxicity by downregulating insulin secretion

during chronic hyperglycemia and thereby relieving ER stress and facilitating cell survival.

In summary, our study reveals JAZF1 as an important regulator of ER stress and ribosome biogenesis via a feedback action preventing the activation of ER and p53 stress-mediated β-cell apoptosis. These findings further highlight the crucial influence of JAZF1 on β-cell function. Finally, modulating JAZF1 activity may be a potential pharmacological strategy to alleviate β-cell stress and promote β-cell survival in T2D.

## STAR★METHODS

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## SUPPLEMENTAL INFORMATION

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## AUTHOR CONTRIBUTIONS

A.K. and M.S. designed the study. A.K. and S.G. performed most of the experiments. A.K. analyzed and interpreted data and wrote the manuscript. E.A. and U.G. provided the UK Biobank analysis. M.W.S. performed the ChIP-seq analysis. The human pancreatic sections of healthy and T2D subjects were made available by G.S. and H.M. M.S. supervised the project and wrote the manuscript. All authors read the manuscript.

## DECLARATION OF INTERESTS

The authors declare no competing interests.

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## STAR★METHODS

### KEY RESOURCES TABLE

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|---|---|---|
| Antibodies | | |
| Monoclonal Rabbit Anti-Jazf1 | This paper | N/A |
| Monoclonal Mouse Anti-Jazf1 | Santa Cruz | Cat# sc-376503, RRID: AB_11149923 |
| Polyclonal Rabbit Nr2c2 | Sigma | Cat#HPA006313, RRID: AB_1079503 |
| Monoclonal Rabbit Anti-Phospho eIF2α (ser51) | Cell signaling | Cat#3398, RRID: AB_10829234 |
| Monoclonal Rabbit Anti-eIF2α | Cell signaling | Cat# 5324, RRID: AB_10692650 |
| Polyclonal Rabbit Anti-Phospho Perk (Thr981) | Santa Cruz | Cat# sc-32577, RRID: AB_2293243 |
| Monoclonal Rabbit Anti-BiP | Cell signaling | Cat#3177, RRID: AB_2119845 |
| Monoclonal Mouse Anti-Ki67 | BD Biosciences | Ca#556003, RRID: AB_396287 |
| Monoclonal Rat Anti-BrdU | Abcam | Cat#ab6326, RRID: AB_305426 |
| Polyclonal Rabbit Anti-Cleaved Caspase 3 | Cell Signaling | Cat#9661, RRID: AB_234118 |
| Polyclonal Rabbit Anti-phospho p53 (Ser15) | Cell Signaling | Cat#12571S, RRID: AB_2714036 |
| Monoclonal Mouse Anti-p53 | Santa Cruz | Cat#sc-126 RRID: AB_628082 |
| Monoclonal Mouse Anti-γ-Tubulin | Sigma | Cat#T6557, RRID: AB_477584 |
| Monoclonal Rabbit Anti-β-Actin | Cell Signaling | Cat#4970, RRID: AB_2223172 |
| Monoclonal Rabbit Anti-P21 | Abcam | Cat#ab109199, RRID: AB_10861551 |
| Monoclonal Mouse Anti-Puromycin | Merck Millipore | Cat#MABE343, RRID: AB_2566826 |
| Polyclonal Rabbit Anti-Myc-tag | Cell Signaling | Cat#2272, RRID: AB_10692100 |
| Monoclonal Mouse Anti-Mdm2 | Santa Cruz | Cat#sc-965, RRID: AB_627920 |
| Polyclonal Guinea Pig Anti-Insulin | Dako | Cat#A056401 RRID: AB_2617169 |
| Hoechst 33342 | Thermo Fischer Scientific | Cat#H3570 |
| Chemicals, Peptides, and Recombinant Proteins | | |
| D-glucose anhydrous | Sigma | Cat#49139 |
| BrdU | Sigma | Cat# B5002 |
| Insulin solution | Sigma | Cat#I9278 |
| Histopaque-1077 | Sigma | Cat#10771 |
| Liberase | Sigma | Cat#05401127001 |
| Lipofectamine 2000 | Invitrogen | Cat#11668500 |
| Lipofectamine RNAiMAX | Invitrogen | Cat#13778-075 |
| Trypsin | Promega | Cat#V5111 |
| Phosphatase inhibitor | Thermo Fisher | Cat# 78427 |
| Protease Inhibitor | Sigma | Cat#5056489001 |
| Actinomycin D | Sigma | Cat#A1410 |
| Puromycin | Sigma | Cat#P8833 |
| Thapsigargin | Sigma | Cat#T9033 |
| Cycloheximide | Sigma | Cat#C4859 |
| Sucrose | Sigma | Cat#84100 |
| Anti-HA Magnetic Beads | Thermo Fisher | Cat#88836 |
| IL-1β | Sigma | Cat#I5271 |
| TNF-α | Sigma | Cat#T7539 |
| Interferon-γ | Sigma | Cat#I3265 |
| Sodium Palmitate | Sigma | Cat#P9767 |
| BSA (Fatty acid Free) | Sigma | Cat#A8806 |

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| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|---|---|---|
| γ32P-ATP | Perkin Elmer | NEG035C00MC |
| Nitrocellulose membrane | Perkin Elmer | NBA083C001EA |
| Amersham Hybond-N+ | GE healthcare | RPN2023B |
| Commercial Assays | | |
| Insulin ELISA | ALPCO | Cat#80-INSRTU-E10-AL |
| Proinsulin ELISA | Mercodia | Cat#10-1232-01 |
| TUNEL Assay | Millipore | Cat#S7165 |
| Deposited Data | | |
| RNA sequencing | This paper | PRJNA595139 |
| ChIP sequencing | This paper | PRJNA595471 |
| Experimental Models: Cell Lines | | |
| MIN6 | Provided by Dr. C. Wolheim | N/A |
| INS1E 832/13 with low passage number | Provided by Boehringer Ingelheim GmbH | N/A |
| ENDOC-βH2 | Univercell biosolutions | N/A |
| Experimental Models: Organisms/Strains | | |
| Mouse.C57BL/6.Jazf1:tm1a(EUCOMM) Wtsi | KOMP repository | Clone ID: 637131 |
| Mouse. B6.RIP-Cre | Provided by Prof. P. Herrera | N/A |
| FLPe knock in/ROSA26 (FLP1 Deleter) | The Jackson Lab | Stock No:009086 |
| Mouse Diabetic db/db B6.BKS(D)-*Lepr$^{db}$*/J | The Jackson Laboratory | Stock No. 000697 |
| Mouse.Akita mice: C57BL/6-Ins2$^{Akita}$/J | The Jackson Laboratory | JAX: 003548 |
| Oligonucleotides | | |
| siRNA: Human Jazf1 | Dharmacon | L-018012-01-0005 |
| siRNA: Mouse Jazf1 | Dharmacon | L-055638-01-0005 |
| siRNA: Rat Jazf1 | Dharmacon | L-108949-00-0005 |
| siRNA: Srp54a | Dharmacon | L-099583-02-0005 |
| siRNA: Dars | Dharmacon | L-096367-02-0005 |
| siRNA: Gars | Dharmacon | L-095034-02-0005 |
| siRNA: Rpl10 | Dharmacon | L-095634-02-0005 |
| siRNA: Scramble | Dharmacon | D-001810-10 |
| Sequence-Based Reagents | | |
| Primers for PCR, RT-qPCR and probes for Northen blot analysis are listed in Table S4 | This paper | N/A |
| Recombinant DNA | | |
| Jazf1 adenovirus: Ad: Jazf1-HA-tagged | This paper | N/A |
| Gfp adenovirus: Ad:GFP | This paper | N/A |
| Nop56 (Myc-DDK-tagged) | Origene | MR209091 |
| Tsr3 (Myc-DDK-tagged) | Origene | MR204683 |
| Rps2 (Myc-DDK-tagged) | Origene | MR204027 |
| Rps11 (Myc-DDK-tagged) | Origene | MR216516 |
| Rps14 (Myc-DDK-tagged) | Origene | RC203889 |
| Rps15 (Myc-DDK-tagged) | Origene | MR200959 |
| Rps20 (Myc-DDK-tagged) | Origene | MR200561 |
| Rpl10a (Myc-DDK-tagged) | Origene | MR200782 |
| Rpl12 (Myc-DDK-tagged) | Origene | MR201323 |
| Rpl13 (Myc-DDK-tagged) | Origene | MR202263 |
| Rpl13a (Myc-DDK-tagged) | Origene | MR202103 |

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*Continued*

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|---|---|---|
| Software and Algorithms | | |
| Prism 8 | GraphPad | https://www.graphpad.com/scientific-software/prism/ |
| Progenesis QI for proteomics | Nonlinear Dynamics | http://www.nonlinear.com/progenesis/qi-for-proteomics/ |
| Fiji | Fiji ImageJ | https://fiji.sc/ |
| Integrative Genomics Viewer (IGV) tool version 2.4 | Robinson et al., 2010 | N/A |
| (Enrichr) Enrichment analysis | Kuleshov et al., 2016 | http://amp.pharm.mssm.edu/Enrichr/ |
| MEME suite | Machanick and Bailey 2011 | N/A |
| NHR-scan | Sandelin et al.,2004 | N/A |
| FGCZ Heatmap | Generated by SUSHI | http://fgcz-shiny.uzh.ch/fgcz_heatmap_app/ |
| Other | | |
| Normal Chow Diet | KLIBA NAFAG | 3437 |
| High Fat Diet | SAFE | 260HF |

## RESOURCE AVAILABILITY

### Lead Contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, MS (stoffel@biol.ethz.ch).

### Materials Availability

The *Jazf1*$^{fl/fl}$ mouse line (Jazf1tm1a (EUCOMM) Wtsi) is deposited at the European Conditional Mouse Mutagenesis Program Eucomm.

### Data and Code Availability

The accession numbers for the RNA-seq and ChIP-seq data reported in this paper are ArrayExpress: PRJNA595139 and ArrayExpress: PRJNA595471, respectively.

## EXPERIMENTAL MODEL AND SUBJECT DETAILS

### Mouse models

All animals were housed in a pathogen-free animal facility at the Institute of Molecular Health Sciences at ETH Zurich. Mice were maintained on a 12-h light/ dark cycle (lights on from 6:00 to 18:00). Mice were given *ad libitum* access to a standard laboratory chow or HFD (SAFE, 260HF) containing 20% protein, 36% lipids and 36.7% carbohydrate, and water. Male mice were used for all experiments shown (except Akita) and the age of mice was above 8-12 weeks unless otherwise indicated in Figures. All mice were maintained on a pure C57BL/6N background. Genotypings of *Jazf1*$^{fl/fl}$, *Rip-Cre* or *Akita* mice were performed by PCR with primers listed in Table S4. All animal experiments were in accordance with institutional guidelines and approved by the kantonale Veterinäramt Zürich.

### Generation of βJazf1KO mice

#### *Mouse.C57BL/6.Jazf1:tm1a(EUCOMM)Wtsi*

Mice carrying the Jazf1 mutation (Jazf1tm1a (EUCOMM) Wtsi) were obtained from the Knockout Mouse Project (KOMP) repository (https://www.komp.org/ProductSheet.php?cloneID=637131). Briefly, Jazf1tm1a (EUCOMM)Wtsi mice contain an IRES:LacZ trapping cassette and a floxed promoter-driven neo cassette inserted. Jazf1tm1a(EUCOMM)Wtsi mice were initially crossed with Flp-1 trangenic line (Jackson Lab) to remove the FRT-flanked lacZ-neo cassette, converting the ''knockout-first'' allele to a conditional allele (*Jazf1*$^{fl/fl}$). To generate the beta cell-specific knockout animals *(βJazf1KO)*, Jazf1 floxed mice were crossed with RIP-Cre transgenic mice leading to exon 3 deletion. RIP-Cre Jazf1 KO mice were maintained on a C57BL/6N background.

Rip-Cre mice (Tg(Ins2-cre)23Herr) were kindly provided by P. Herrera. A 0.6 kb fragment containing the rat insulin promoter was adjoined to the Cre recombinase coding sequence to drive expression in pancreatic cells. The insertion of the transgene is unknown.

## Animal procedures

### *High fat diet*

Male mice were fed a HFD starting at 5 weeks old for 12 weeks.

## Blood glucose measurements IPGTT and BrdU injection

Mice were fasted for 6 h and injected intraperitoneally with D-glucose (Sigma, 49139) solution (2.5 g/kg dose for chow diet mice and 1.5 g/kg for HFD mice) for IPGTT experiment. Blood glucose values were measured with a Bayer Contour XT glucometer at 0, 15, 30, 45, 60, and 120 min after injection.

For β-cell proliferation study, mice were injected intraperitoneally with Brdu (100 mg/kg) (Sigma, B5002) for 2 days before mouse dissection.

## Cell culture and transfections

### *INS1E*

Initial stocks of the clonal INS1E 832/13 were provided by Boehringer Ingelheim GmbH with passage number 85 (P85) and cultured in RPMI 1640 supplemented with 11.1 mM D-glucose, 10% (v/v) fetal bovine serum (FBS), 10 mM HEPES, 1 mM Pyruvate, 50 μM beta-mercaptoethanol, 2 mM Glutamax (GlutaMAX, Invitrogen) and 10,000 units/mL penicillin and 10 mg/mL streptomycin. Cells were incubated at 37°C in 5% $CO_2$, 95% air. All experiments used cells harvested between passages P88-90.

## MIN6

The initial stock of the clonal MIN6 cell line was obtained by Prof. C. Wolheim. Cells were cultured in DMEM supplemented with 20% (v/v) FBS, 2 mM Glutamax (GlutaMAX, Invitrogen), 30 μM beta-mercaptoethanol and 10,000 units/mL penicillin and 10 mg/mL streptomycin.

## EndoC-βH2:

Cells were obtained from Univercell biosolutions company. Cells were culture in complete medium culture (Reference: OPTIβ1 ®)

INS1E, MIN6 and EndoC-βH2 cell lines were authenticated in-lab by performing GSIS assays and by RT-PCR of beta-cell specific genes. Cells are routinely tested twice annually for the presence of Mycoplasma and found negative.

**INS1E**, **MIN6, EndoC-βH2 cells** were maintained at 37 C in a humidified incubator with 5% CO2 in air.

## Expression and purification of recombinant Zinc finger domains

To prepare pure GST proteins, BL21(DE3) cells were grown at 37 C in a fermentor to an A600 of ~0.5. Protein expression was induced with isopropyl 1-thio-β-D-galactopyranoside (0.5 mM) and protein allowed to accumulate for an additional 4h. Following centrifugation, a pellet from 6 l of culture was resuspended in ZnF buffer (10 mM $NaH_2PO_4$, pH 7.4, 150 mM NaCl, 5 mM β-ME, 10 μM $ZnCl_2$). All purification steps were performed at 4°C. Bacteria were lysed by sonication and the lysate was centrifuged (40,000 x g for 30 min) to remove insoluble debris. GST-ZF23 and GST-JAZF1 was recovered from the lysate by affinity chromatography using a GSTPrep FF 16/10 affinity column (Amersham Biosciences). Bound protein was washed with 10 column volumes of ZnF buffer and eluted with 20 mM glutathione in 50 mM HEPES, pH 7.4, 5 mM β-ME, and 10 μM $ZnCl_2$. Purification of MBP-fusion proteins were done in a similar manner.

## Antibody production

Protein fragments corresponding to amino acids 1-243 and 170-243 of JAZF1 fused to glutathione *S*-transferase (GST) were expressed, purified using glutathione Sepharose 4B (Amersham Biosciences) and used to raise JAZF1- N64 antibodies. JAZF1 antibodies were raised in rabbits immunized seven times with 500 μg of the GST-fusion protein (Davids Biotechnoligie GmbH (Germany)). JAZF1 specific antibodies were purified from 50 mL of serum in PBS on a Sepharose 2B column containing identical JAZF1 fragments fused to maltose-binding protein (MBP) coupled to CNBr activate Sepharose 2B beads and eluted with 0.1 M glycine (pH 2.5).

## Recombinant adenoviruses

Recombinant Adenovirus were generated by cloning the murine Jazf1 cDNA into pVQAd CMV K-NpA (pVQAd, Viraquest). Ad-Ctrl was based on the same vector backbone (with a GFP) but lacked the *Jazf1* transgene.

For virus infection experiments, cells were infected with Ad-Jazf1 or Ad-GFP at a MOI 5 for cells and a MOI 20 for dispersed islets.

## Human islets and pancreatic sections

Human islets were obtained from Prodo Laboratories Inc. Pancreatic biopsy specimens from Caucasian patients were obtained postmortem at the University Hospital, Zurich. Pancreatic specimens were formaldehyde fixed for histopathological examination. Informed consent was obtained in accordance with the regulations of the Ethics Committee of the Canton Zurich.

Isolated Islets were from healthy and T2D donors (see table below). The islet preparation of donors consisted of 2,500 – 10,000 islet equivalents with a purity of >80% and a viability of >90%. Pancreatic islets were handpicked under a microscope and cultured in CMRL-1066 medium containing 5.6 mM glucose, 10% FBS, 100 IU/ml penicillin/streptomycin and glutamax.

| Donor | Gender | Age | Diagnosis | Cause of death | BMI |
|---|---|---|---|---|---|
| 1 | M | 29 | N | Stroke | 42.2 |
| 2 | M | 45 | T2D | Stroke | 27.3 |
| 3 | M | 60 | N | Stroke | 27.4 |
| 4 | F | 53 | N | CVD | 32 |
| 5 | M | 48 | T2D | Gunshot | 43.7 |
| 6 | M | 43 | T2D | Stroke | 27.6 |
| 7 | M | 59 | T2D | Stroke | 32.5 |
| 8 | M | 37 | N | Stroke | 25.4 |
| 9 | M | 57 | N | Stroke | 29.4 |
| 10 | F | 41 | T2D | Stroke | 43.1 |

### Mouse pancreatic islet

Mouse pancreatic islets were isolated from male mice as previously described (Zmuda et al., 2011) with slight modifications. A total of 2 mL of Liberase (5 mg/ml) (Sigma 05401127001, diluted in HBSS buffer, GIBCO, 14170-112) was injected through the common bile duct to perfuse the whole pancreas. The perfused pancreas was dissected and incubated at 37°C for 17 min. Digested exocrine cells and intact islets were separated via centrifugation (2400 × rpm for 20 min with very slow acceleration and no braking) over Histopaque-1077 (Sigma, 10771), and intact islets were manually picked under the microscope. Islets were cultured in RPMI 1640 with 10% FBS and 100 U/ml penicillin/streptomycin.

## METHOD DETAILS

### Immunohistochemistry and β-cell mass measurements

Whole pancreas or pancreatic buds were fixed with 4% paraformaldehyde (PFA) and embedded in paraffin, and the cut sections were antigen-retrieved by boiling them in citrate buffer (10 mM Citric Acid, 0.05% Tween 20, pH 6.6). Cells or dispersed islets were fixed with 2% PFA for 15 min. The sections or cells were permeabilized and blocked in PBS containing 0.1% Triton X-100, 1% BSA and 5% goat serum. Primary antibody binding was performed overnight at 4°C, while secondary antibody incubation was carried out at room temperature (21°C) for 1h. Leica TCS SP8 confocal microscope was used for fluorescent imaging.

For β-cell mass, Ki-67 or BrdU labeling and Tunel assay, 3.5 mm sections were cut and 5 sections that were at least 500mm apart were taken from each mouse and stained for insulin and DNA (Hoechst). Entire pancreatic sections were scanned using Panoramic 250 Slide scanner (3D Histech). The fraction of insulin positive area compared to total pancreatic area (stained with Hoechst) was analyzed using Fiji software (https://fiji.sc/), and β-cell mass was calculated by multiplying this fraction by the initial pancreatic weight.

For nucleolar and nuclear area, MIN6 cells are transfected with Jazf1 or scramble siRNAs for 48h. Cells are fixed with 2% PFA for 15 min then are permeabilized and blocked in PBS containing 0.1% Triton X-100, 1% BSA and 5% goat serum. The nucleolus was detected by Fibrillarin antibody, and the nucleus was detected by Hoechst staining and fluorescence images were observed using a Zeiss Apotome 2 microscope. The area of the nucleolar and nuclear regions was quantified using Fiji software (https://fiji.sc/).

For cell proliferation assay, INS1E cells were transfected by a reverse transfection with Jazf1 or scramble siRNAs for 48 h. Cells were fixed with 2% PFA for 15 min, then permeabilized and blocked in PBS containing 0.1% Triton X-100, 1% BSA and 5% goat serum. The nucleus was detected by Hoechst staining and fluorescence images were observed using a Zeiss Apotome 2 microscope.

### Insulin and Proinsulin

To determine mouse serum insulin or Proinsulin levels, blood was obtained from the tail vein and centrifuged for serum separation. Insulin was measured by Insulin ELISA Kit (ALPCO, 80-INSRTU-E10-AL) and Proinsulin was measured by ELISA Kit (Mercodia, 10-1232-01). To measure total pancreatic insulin content, insulin was extracted by acid-ethanol buffer (HCl:Ethanol 1:49, 0.1% Triton) from total pancreas. For islet insulin content, insulin was extracted by acid-ethanol buffer (HCl:Ethanol 1:49, 0.1% Triton) from 80 size matched islets. Hormones were then assessed by Insulin ELISA Kit.

### Dispersed islets experiments

Islets were digested by 0.05% trypsin at 37°C for 5 min, and then centrifuged and resuspended. Cells were seeded into a 96-well plate which was coated overnight with medium from 804G cell line culture (Langhofer et al., 1993). Dispresed islets were cultured in low or high glucose. Leica TCS SP8 confocal microscope was used for fluorescent imaging.

### Transfections

For knockdown experiments cells, INS1E or MIN6 were plated in 6 well plates and transfected the next day at 60%–70% confluency. For each well to be transfected, an RNAi duplex-Lipofectamine® RNAiMAX complexes was prepared as follows: 30 nM (final concentration) RNAi duplex was diluted in Opti-MEM® reduced Serum Medium. 7 μl of Lipofectamine® RNAiMAX was diluted in Opti-MEM®, and mixed gently. The diluted RNAi duplex was combined the diluted Lipofectamine® RNAiMAX and mixed gently. The RNAi duplex-Lipofectamine® RNAiMAX complexes were incubated for 10 min at room temperature before transferring them to each well containing cells. The medium was changed after 6 h and cells were incubated for 48 h at 37°C in a $CO_2$ incubator.

For transient plasmid transfections INS1E or MIN6 cells were plated in 6 well plates with growth medium without antibiotics overnight and transfected the next day at 60%–80% confluency. Using a DNA (ug) to Lipofectamine 2000 (ul) ration of 1:3. The liquid was gently mixed by rocking the plate back and forth and incubated at 37°C in a $CO_2$ incubator. The medium was changes after 6 h and incubated for 42 h before harvesting the cells. Successful transfection and expression of vector in cells was assessed by RT-qPCR and or western blotting.

### Treatment with reagents

Cells or islets are treated with 5nM of Actinomycin D (Ribosome stress) or 500 nM thapsigargin (ER stress), cytokines cocktail (10 ng/ml IL-1β, 100 ng/ml IFN-γ and 25 ng/ml TNF-α), low glucose (3mM), high glucose (15mM) or chronic high glucose (25mM). The duration of treatments is indicated in the figure legends for each experiment.

### Stress induction of human islets with glucose, palmitate, and cytokines

Islets were from donors. The islet preparation of donors consisted of 2,500 islet equivalents with a purity of >80% and a viability of >90%. Pancreatic islets were handpicked under a microscope and cultured in CMRL-1066 medium containing 5.6 mM glucose, 10% FBS, 100 IU/ml penicillin/streptomycin and glutamax; then islets were challenged with 25 mM glucose, cytokines (10 ng/ml IL-1β, 100 ng/ml IFN-γ and 25 ng/ml TNF-α) and 100 uM of palmitate-BSA conjugate. Medium was renewed every 24 h. Islets were collected for experiments after 72 h.

### RNA isolation and quantification

TRIzol reagent (Invitrogen, 15596-026) was used for RNA isolation according to the manufacturer's protocol. RNA was reverse transcribed using High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, 4368813). Quantitative PCR was performed in an LC480 II Lightcycler (Roche) and using gene specific primers and Sybr Fast 2x Universal Master mix (Kapa biosystems, KK4611). Results were normalized to 36b4 or Gapdh mRNA levels. The sequences of primers pairs of respective transcripts are shown in Table S4.

### Northern blot

Total RNA from indicated cells or islets were extracted by TRIzol (Invitrogen). RNA samples (3-5μg) were heated in RNA loading buffer contains 62.5% deionized formamide, 1.14 M formaldehyde, 200 μg/ml bromphenol blue, 200 μg/ml xylene cyanole, in MOPS-EDTA-sodium acetate at 1.25x working concentration (Sigma-Aldrich R1386) and were electrophoresed in 0.8% formaldehyde-agarose gels (0.8 % agarose – 2.2 M formaldehyde gel) in 1XMOPS buffer at 4∼5 V/cm and transferred onto Hybond N+ membranes (Amersham) with 10 x SSC. ETS, ITS1 and ITS2 probes (sequences indicated in Table S4) used to generate α-$^{32}$P dCTP-labeled probes. Probes were purified over nucleotide purification columns (Zymo Research) prior to hybridization. Membranes were prehybridized for 1 hr at 65°C in 50% formamide, 5 × SSPE, 5 × Denhardt's solution, 1% w/v SDS, 200 μg/ml salmon sperm DNA. The $^{32}$P-labeled oligonucleotide probe was added and incubated overnight at 50°C. Blots were developed on PhosphorImager screens and developed on a Typhoon Imager. Northern blot quantification based on densitometry of bands was performed in ImageJ.

### Luciferase assay

Wild-type, mutant, and deletion of NR2C2 element in the promoters region of the human *Ins*, rat *Rps14* and *Rpl10* genes were generated by *de novo* DNA synthesis (Gene Universal) and cloned to a luciferase reporters (pGL4.25[luc2CP/minP] Vector (Promega cat#: E8411).

INS1E or ENDOC-βH2 cells were grown in until cells were 60%–80% confluent. Cells were cultured in 96-well plates and transfected with 30 nM si-RNA of si-Jazf1 or si-Scramble. After 24h, cells are transfected with 200 ng of a luciferase reporters vector under the control of the wild-type and mutants promoters and with 100 ng of pRL *Renilla* luciferase control reporter vector (Promega cat#: E2411) as an internal control for transfection efficiency. The complex of DNA/lipofectamine 2000 are used 1:3 ratio. One day after transfection, cells were harvested and assayed using the Dual-Luciferase Reporter Assay System (Promega).

### Polysome profiling

MIN6 cells were treated with 0.1 mg/mL cycloheximide (Sigma-Aldrich) for 5 min at 37 °C, washed twice with 0.1 mg/mL cycloheximide in 1X PBS. Polysome lysis buffer composed of 15 mM Tris HCl pH 7.4, 15 mM $MgCl_2$, 300 mM NaCl, 100 μg/mL cycloheximide, 1% Triton X-100, 40 U/μL RNase and protease inhibitors. The lysis buffer was used to resuspend cells, followed by 10 min incubation on ice and 5 min centrifugation at 13,000 rpm at 4 °C. Clear supernatants (1,5mg of protein) from lysed cells were loaded into the 10 to

50% sucrose gradient. After centrifugation for 4h at 32′000 rpm at 4°C in a SW41 rotor (Beckman Coulter), gradients were analyzed at OD254 with a Foxy Jr. Gradient collector (Teledyne Isco).

### Proteomic studies

$10^7$ INS1E cells were used per IP sample. Proteins were extracted by NP-40 buffer with protease inhibitors. Protein samples were digested to peptides with Filter-aided Sample Preparation (FASP) method (Wiśniewski et al., 2009). Peptide enrichment was performed after FASP with Ti-IMAC (Resyn Biosciences, MR-TIM002). Enriched peptides were dissolved in 10 μl LC-MS solvent (3% acetonitrile, 0.1% formic acid) after C18 ZipTip (Millipore, ZTC18S096) desalting.

Mass spectrometry analysis was performed on an Orbitrap Fusion Tribrid mass spectrometer (Thermo Scientific, San Jose, CA), which was connected to an Easy-nLC 1000 HPLC system (Thermo Scientific). Liquid chromatography solvent compositions in channels A and B were 0.1% formic acid in water and 0.1% formic acid in acetonitrile, respectively. 4 μl of the sample in LC-MS solvent was loaded onto a frit column (inner diameter 75 μm, length 15 cm) packed with reverse phase material (C18-AQ, particle size 1.9 μm, pore size 120 Å, Dr. Maisch GmbH, Germany), and separated at a flow rate of 300 nL per min. The following LC gradient was applied: 0 min: 1% buffer B, 80 min: 30% B, 90 min: 50% B, 95 min: 98% B, 100 min: 98% B.

Survey scans were recorded in the Orbitrap mass analyzer in the range of m/z 350-1800, with a resolution of 60000, and AGC target value of 200,000 and a maximum injection time of 50 ms. Higher energy collisional dissociation (HCD) spectra were acquired in the linear ion trap analyzer, using a normalized collision energy of 30%. A maximum injection time of 100 ms, and an AGC target value of 30,000 were applied. The precursor ion isolation width was set to m/z 2,0. Charge state screening was enabled, and only precursor ions with charge states 2-7 were included. The threshold for signal intensities was 5000, and precursor masses already selected for MS/MS acquisition were excluded from further selection during 45 s.

### Immunoblot analysis

Cells or islets were collected and lysed by RIPA Buffer (50 mM Tris pH 7.5, 1% NP-40, 0,5% Na-Deoxycholate, 0.1% SDS, 150 mM NaCl, 1 mM EDTA pH 8.0, supplemented with protease and phosphatase inhibitors. Protein concentrations were determined by Bicinchonic Acid (BCA) assay. 30-50 μg of total protein lysates were mixed with Laemmli buffer and boiled for 5 min. 10%–14% SDS-PAGE gel was used for protein separation. Membranes were blocked by 5% milk/TBS-T or 5% BSA/TBS-T (for phosphorylation antibodies) for 1 h after electrotransfer to nitrocellulose membranes (NBA083C001EA, Perkin Elmer) and incubated with appropriate antibodies overnight at 4°C. Membranes were exposed to secondary antibodies for 1 h at room temperature and developed using ECL Western Blotting Substrate (Thermo, 32106). Immunoblotting quantification based on densitometry of bands was performed in ImageJ

### Cellular fractionation

Freshly isolated islets were digested with trypsin into single cells and washed with PBS. Cell pellet was re-suspended in Hypotonic Lysis Buffer (HLB, 10 mM HEPES, 1.5 mM $MgCl_2$, 10 mM KCl, 1 mM DTT and fresh protease inhibitor) and incubated on ice for 30 min. 6 μL 10% NP40 per 100 μL HLB was added after the incubation and vortexed for 10 s, then centrifuged immediately for 30 s. Supernatant was saved as cytosolic extract. The nuclei were then washed with 1 mL of HLB to remove any contaminating cytoplasm and re-sedimented. Pellet was re-suspended in Nuclear Lysis Buffer (NLB, 10 Mm HEPES, 100 mM KCl, 3 mM $MgCl_2$, 0.1 mM EDTA, 1 mM DTT and fresh protease inhibitor) and incubated on ice for 30 min. Extra 1/10th volume of 4 M $(NH_4)_2SO_4$ was added over 30 min. Solution was centrifuged and the supernatant was saved as nuclear extract.

Protein concentrations were determined by bicinchoninic acid (BCA) assay and equal amounts of protein were loaded for immunoblotting.

### Co-Immunoprecipitation assay

$10^7$ INS1E cells are used per IP sample. Cells are whased twice in cold 1x PBS. Cells are lysed in NP-40 buffer (20 mM Tris HCl pH 8,137 mM NaCl, 1% NP-40, 2 mM EDTA) for 30 min in ice. Cellular debris were removed by centrifugation at 4°C for 10 min and transfer the supernatant to a new 2 mL tube. Save 4% of the lysate as an input control, the remaining lysate were adjusted to the volume of 1.5 mL with pre-cold lysis buffer. Add 70 ul of anti HA magnetics beads against the HA tagged Jazf1 protein. Incubate the tubes on a tube rotator 4h at 4°C. (same for IgG mouse: negative control). Wash 5 times the beads with the lysis buffer. After washing, resuspend the beads in 30 μL of 2x Laemmli buffer, boil for 5 min, and analyze by immunoblot analysis.

### Puromycin analysis

The cells or isolated pancreatic islets were treated with puromycin (1 μg/ml) for 30 min in fresh medium. The cells were lysed and protein synthesis was detected with anti-puromycin antibodies by western blot.

### Illumina RNA sequencing

Total RNA was isolated from islets using PicoPure® RNA Isolation Kit (Invitrogen, KIT0204). Sequencing libraries were prepared from 100-500 ng total RNA using the TruSeq RNA Sample Preparation Kit v2 (Illumina) according to the manufacturer's protocol. Briefly, total RNA samples (100–1,000 ng) were polyA selected and reverse transcribed into double-stranded cDNA. Then cDNA samples

were fragmented, end repaired, and polyadenylated before ligation of TruSeq adaptors containing the index for multiplexing fragments on both ends were selectively enriched with PCR. The quality and quantity of the enriched libraries were validated using Qubit (1.0) Fluorometer and the Caliper GX LabChip GX (Caliper Life Sciences). The product is a smear with an average fragment size of approximately 260 bp. The libraries were normalized to 10 nM in Tris-Cl 10 mM, pH 8.5 with 0.1% Tween-20.

The quality of RNA-seq reads were checked with fastqc, which computes various quality metrics for the raw reads. Reads were aligned to the genome and transcriptome with TopHat v. 1.3.3 (https://ccb.jhu.edu/software/tophat/manual.shtml). Before mapping, the low-quality ends of the reads were clipped (three bases from the read start and 10 bases from the read end). TopHat was run with default options. The 'fragment length' parameter was set to 100 bases with a standard deviation of 100 bases. On the basis of these alignments, the distribution of the reads across genomic features was assessed. Isoform expression was quantified with the RSEM algorithm (Li and Dewey 2011) with the option for estimation of the read start position distribution turned on. Transcripts were defined using the Ensemble annotations over protein-coding mRNAs. Differential expression analysis of mapped RNA-seq data were performed using EdgeR (Robinson et al., 2010).The raw sequencing data were deposited at NCBI Sequence Read Archive (SRA, https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA595139) and are accessible through the accession number PRJNA595139.

### Jazf1 expression in islets from human and mouse T1D model

RNA-seq dataset from islets of human T1D (Mastracci et al.,2018: Accession number GSE102371). RNA-seq dataset from islets of B10.RagKO and NOD.RagKO mice (Dooley et al., 2016: Accession number GSE56507). Array expression data from islets of NOD mice. (Carrero et al., 2013: Accession number GSE41203).

The expression data of individual samples were merged, transcript expression was converted to gene expression and ensembl gene ids were mapped to HGNC symbols. Differential gene expression analysis was carried out by DESeq2.The data were processed using in-house Python and R scripts. The Affymetrix MoGene IDs were annotated to ensembl IDs, gene symbols, chromosome loci etc. by the Biomart R package.

### ChIP-Seq assay

$10^7$ INS1E cells are used per IP. Cells were crosslinked with 1% formaldehyde for 10 min at room temperature, crosslinking was stopped by addition of 2M Glycine (0.125M final concentration) at room temperature for 5 min. Cells are washed twice in cold 1x PBS. Cells are lysed into ice-cold lysis buffer (50 mM Tris-HCl, pH 8.1, 1% SDS, 10 mM EDTA, 1X protease inhibitors) for 1h in ice. Following cell lysis, the samples were sonicated (Bioruptor Plus, Diagenode) to generate fragments of average length of 300-100 base pairs. Cellular debris were removed by centrifugation at 4°C for 10 min (10,000 g), 10 % of the lysate was stored as the source of ''Input'' and the remaining lysate was diluted 8 times in dilution buffer (final concentration: 16.7 mM Tris-HCl, pH 8.1, 0.01 SDS, 1.1% Triton X-100, 1.2 mM EDTA, 16.7 mM NaCl, protease inhibitor), in presence of 70 μL of anti-HA Magnetic beads were then incubated at 4°C with rotating for overnight.

Beads were washed extensively at 4°C in Low salt buffer (20mM Tris-HCl, pH 8.1, 0.1% SDS, 1%Triton X-100, 2mM EDTA, 150 mM NaCl), in High salt buffer (20mM Tris-HCl, pH 8.1, 0.1% SDS, 1%Triton X-100, 2mM EDTA, 500mM NaCl), and in LiCl buffer (10mM Tris-HCl, pH 8.1, 250mM LiCl, 1% NP-40, 1% sodium deoxycholate, 1mM EDTA), and finally in 1ml of TE buffer (10mM Tris-HCl, pH 8.0, 1mM EDTA). The bound chromatin was released from the beads by vortexing at room temperature in 200 μL elution buffer (1% SDS and 100 mM NaHCO3). 1 μL of 10mg/ml RnaseA and 5M NaCl (200mM final concentration) was added to the eluate and incubated O/N at 65°C, and then treated with Proteinase K for 1 hr at 55°C; DNA was purified using QIAGEN PCR purification kit.

### ChIP-seq data processing

Short reads generated in this study were deposited at NCBI Sequence Read Archive (SRA, https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA595471) and are accessible through the accession number

PRJNA595471. Adaptor sequences and low quality stretches within the reads were removed with TrimGalore (options –illumina, version version 0.4.0, www.bioinformatics.babraham.ac.uk/projects/trim_galore). Reads were then aligned to the rat reference genome (ensembl93) with bowtie2 keeping only unique alignments with a mapping quality greater than 10 (version 2.8.2, Langmead and Salzberg, 2012). For each sample, coverage peaks were identified with MACS (version 2.1.1; Zhang et al., 2008) with a Q-value threshold of 0.05 for the identification of broad peaks. Peaks of the two batch 1 and the four batch 2 replicates were merged with MULTOVL and only peaks identified in at least two batch 1 or at least three batch 2 replicates were kept (version 1.3, options -m 3 -u; Aszódi,2012). Reads overlapping with at least 30 bases with the peaks were counted with featureCounts (version 1.6.0, multiple overlaps allowed, Liao, Smyth, and Shi,2014). Peaks not mapped by at least five reads in any of the samples were excluded from further analyses. Peak regions were mapped to the genomic context (e.g., promoter or intergenic) with Homer (version 4.10, Heinz et al., 2010) and the rn6 annotation.

### Differential binding

Variation in sequence counts between IP and control conditions was analyzed with a general linear model in R with the package DESeq2 (version 1.14.1, (Love, Huber, and Anders, 2014)). We first fitted a factor to account for batch effects (~batch + treatment). p

values were adjusted for multiple testing (Benjamini-Hochberg), and peaks with an adjusted p value (false discovery rate, FDR) below 0.05 and a minimal log2 fold-change (i.e., the difference between the log2 transformed, normalized sequence counts) of 0 were considered to be significantly bound by Jaz1. Normalized sequence counts were calculated accordingly with DESeq2 and log2(x+1) transformed.

### Functional characterization with GO terms

To functionally characterize genes with a significantly Jaz1-bound peak in their promoter (1 kb up- and downstream of the transcriptional start site), we tested for enrichment of gene ontology (GO) terms with topGO (version 2.28 Alexa, Rahnenführer, and Lengauer, 2006) in conjunction with the GO annotation from Ensembl available through biomaRt (Durinck et al., 2009). Analysis was based on gene counts using the "weight" algorithm with Fisher's exact test (both implemented in topGO). A term was identified as significant if the p value was below 0.05.

Enrichment of KEGG pathways in gene sets was tested with clusterProfiler (version 3.12.0, Yu et al., (2012)) using the gene to pathway mappings available through biomaRt (Durinck et al., 2009) and the package org.Rn.eg.db (version 3.8.2, Carlson, 2019).

### Motif discovery

To search for known and novel motifs we used MEME-ChIP and 2 kb sequences centered around significantly Jaz1-bound peaks (version 5.0.2 with the parameters -meme-mod zoops -meme-minw 6 -meme-maxw 30 -meme-nmotifs 10 -dreme-e 0.05 -centrimo-score 5.0 -centrimo-ethresh 10.0, Machanick and Bailey (2011)). The percentage of peaks with a motif similar to CCGGAA was extracted from the CentriMo output (part of the MEME-ChIP pipeline). To further search for the presence of nuclear hormone receptor binding sites in significantly Jaz1-bound peaks in promoter (1 kb up- and downstream of the transcriptional start site) and intergenic regions we used NHRscan with default settings (available at nhrscan.genereg.net, accessed at the 24th of November 2019, Sandelin and Wasserman, 2005).

### UK BioBank data processing

The genotype data from rs1635852 (affy30273931) was obtained through UK Biobank application number 48008. The data were extracted and filtered for missing data using in-house scripts implemented with python 3.6 (python.org) and pandas (https://pandas.pydata.org/). The cleaned initial dataset included 241196 participants with the C T genotype, 125147 participants with the T T genotype, 121524 participants with the C C genotype. The diabetic participants were 26740 (5.481% of the whole dataset). We applied general linear model (GLM) to identify the association between the SNPs and phenotypes. In case of continuous phenotypes, GLM with Gaussian link function was used. To analyze binary phenotypes like diabetes, we append GLM with logit link function of binomial distribution. The p values and effect sizes (beta coefficient in case of linear regression and odds ratio in case of logistic regression) were used to assess the magnitude of the SNP effect on a given phenotype.

The Linear Regression used here can be written in the following form:

$$Y = \beta_0 + snp_*\beta_1 + age_*\beta_2 + sex_*\beta_3 + pc1_*\beta_4 + \ldots + pc10_*\beta_{13} + \varepsilon$$

The Logistic Regression we applied may be written in the following form:

$$Y = 1/(1 + \exp - (\beta_0 + \mathrm{snp}_*\beta_1 + \mathrm{age}_*\beta_2 + \mathrm{sex}_*\beta_3 + \mathrm{pc1}_*\beta_4 + \ldots + \mathrm{pc10}_*\beta_{13} + \mathrm{e}))$$

Generalized linear regression analysis was conducted on blood biochemical data (fields: 30630-0.0 Apolipoprotein A, 30640-0.0 Apolipoprotein B, 30690-0.0 Cholesterol, 30740-0.0 Glucose, 30760-0.0 HDL cholesterol, 30750-0.0 Glycated haemoglobin (HbA1c), 30780-0.0 LDL direct, 30870-0.0 Triglycerides), biometric measurements (fields: 21001-0.0 BMI, 23106-0.0 Impedance of whole body) using rs1635852 (affy30273931), age, sex, and genetic Principal Component 1-10 (field 31-0.0 sex, field 21022-0.0 age at recruitment, field 22008-0.0 through 22008-0.10 for genetic principal components) as covariates. The reference genotype used for analysis was C C. The blood biochemical data were available for 467,929 participants, while BMI and impedance for 485887 and 478818 participants, respectively. The additional covariates were included to account for the unwanted source of variation within the population age, sex, ethnic diversity etc.

Logistic regression analysis was conducted on diabetes diagnosed by a doctor (field 2443-0.0, for 487,867 participants) and medication use (Treatment/medication code fields 20003-0.0 through 20003-0.47, for 354,259 participants) using rs1635852 (affy30273931), age, sex, and genetic Principal Component 1-10 (field 31-0.0 sex, field 21022-0.0 age at recruitment, field 22008-0.0 through 22008-0.10 for genetic principal components) as covariates. The reference genotype used for analysis was CC. Medications were grouped according to ATC pharmacological subgroups within therapeutic subgroup A10 (Wu et al., 2019). Medications with different UK Biobank code but identical ATC subcode were grouped in the same category (A10A Insulin, A10BA metformin, A10BB sulfonylurea, A10BG rosiglitazone, A10BD Metformin |Rosiglitazone, A10BF Acarbose, A10BX Meglitinide). The all_diabetes_medication data were obtained by calculating if a participant takes any diabetes medication, regardless of the quantity.

R programming language (https://www.r-project.org/) with tidyverse library (https://www.tidyverse.org/) were used to conduct the statistical analysis.

## QUANTIFICATION AND STATISTICAL ANALYSIS

### Statistical analysis

Statistical parameters including the exact value of n, precision measures (mean ± SD) and statistical significance are reported in the Figures and Figure Legends. Two-tailed unpaired Student's t test was applied for comparisons between two groups. ANOVA was used on comparisons that involved multiple groups. Statistical differences are indicated as (*: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$; ****: $p < 0.0001$). $p < 0.05$ was considered significant. Samples were not systematically blinded before every experiment. Biological or technical replicates are indicated in the figure legends. Statistical analyses were performed using GraphPad Prism 8 software.

## ADDITIONAL RESOURCES

None