Supporting Information

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SI Materials and Methods

Antisera. Anti-Meis1, -Meis2, and-Flag (M2) were from Sigma. Anti-RNA polymerase II was obtained from Abcam.

q-PCR Primers. Ndfip1-F: 5-TTCGGAAGATGCCAGAAACT-3 R: 5-GAAGCCTTTGCCAGAAAACA-3

Bnip3-F: 5-AAAGGGGGAATTTTCTCAGC-3

R: 5-TCCAATGTAGATCCCCAAGC-3 Ceng1-F: 5-CGGTCCCTCAAGTCTTTCTG-3 R: 5-GCAAGGTGCTGAGGTTTCTC-3

Proximal Pdpk1 promoter (for RNA polymerase II ChIP):

F: 5-AACCCGGAA ATACGGCTCT-3 R: 5-TCTCGCCCATTGGTCAGTAT-3

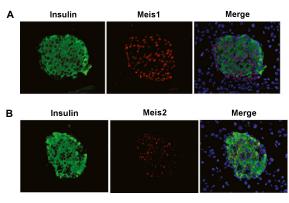


Fig. S1. Expression of Meis1 and Meis2 in adult pancreas islets. Representative image of adult mouse pancreatic islets following immunofluorescence for insulin (green), Meis1 (red in *A*) or Meis2 (red in *B*). (*A* and *B*, *Right*) Merged image of insulin, Meis, and DAPI (blue).

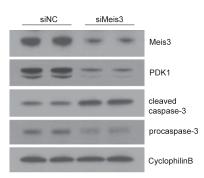
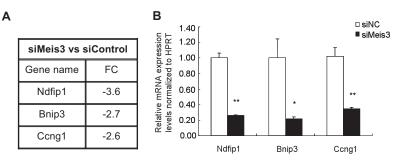
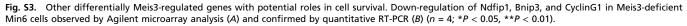


Fig. S2. Meis3 regulation of PDK1 and cell survival in β-HC9 cells. Representative Western blot analysis of PDK1 and cleaved caspase-3 protein levels in siRNA-transfected β-HC9 cells, performed in duplicate.





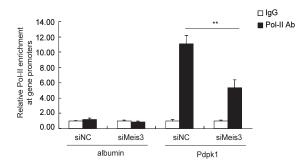


Fig. S4. Effect of Meis3 on the RNA polymerase II recruitment at Pdpk1 promoter. RNA polymerase II occupancy at Pdpk1 promoter was assessed by chromatin immunoprecipitation (ChIP) following the 72 h transfection with Meis3-targeted siRNA in Min6 cells. DNA enrichments are presented as fold change compared with control IgG binding. Four independent ChIP experiments were performed for both Meis3 antiserum and IgG, **P < 0.01.

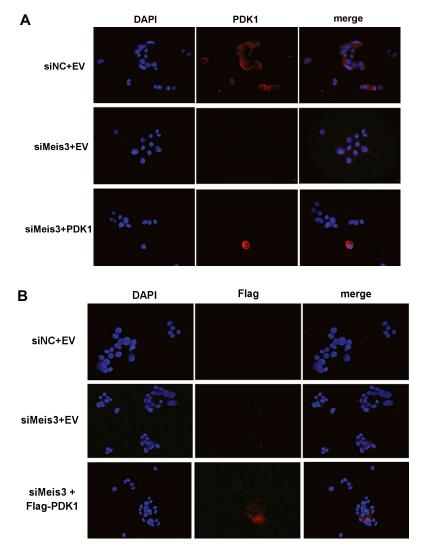


Fig. S5. Immunostaining for the overexpressed PDK1 in Min6 cells. Min6 cells were conucleofected (Amaxa Biosystems) with 1 nmol of siRNA and 600 ng of empty vector or PDK1 expression plasmid. Transfected Min6 cells were plated in the glass chamber slides followed by immunofluorescence staining for PDK1 (*A*) or Flag (*B*), respectively. Nuclei were counterstained with DAPI.

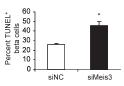


Fig. S6. Quantification of TUNEL staining in isolated primary islets. Insulin-positive nuclei and TUNEL-positive cells were counted by iVision software (BioVision Technologies) using the counting tool. Percent TUNEL-positive cells were quantified in 300 insulin-positive nuclei per group (n = 3, *P < 0.01 relative to siNC control).

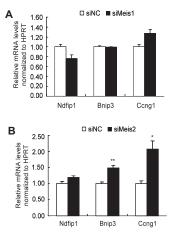


Fig. S7. The expression levels of Ndfip1, Bnip3, and CyclinG1 in Meis1- or Meis2-deficient Min6 cells. RT-QPCR analysis of relative mRNA levels of indicated genes in siRNA-transfected cells. *n* = 3, **P* < 0.05, ***P* < 0.01 compared with values of the mRNA levels in nontargeted control siRNA (siNC)-transfected cells.

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