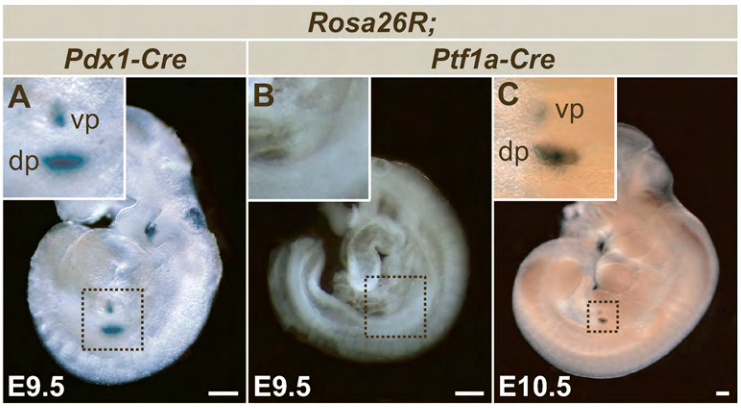

Fig. S1. *Pdx1-Cre* and *Ptf1a-Cre* are active in the pancreas by E9.5 and E10.5, respectively. (**A-C**) X-Gal staining for β-gal activity from the recombined *Rosa26R* reporter allele reveals *Pdx1-Cre* to be active in the dorsal (dp) and ventral (vp) pancreatic buds by E9.5 (A) while *Ptf1a-Cre* is not active until E10.5 (B,C). Scale bars: 250 µm.

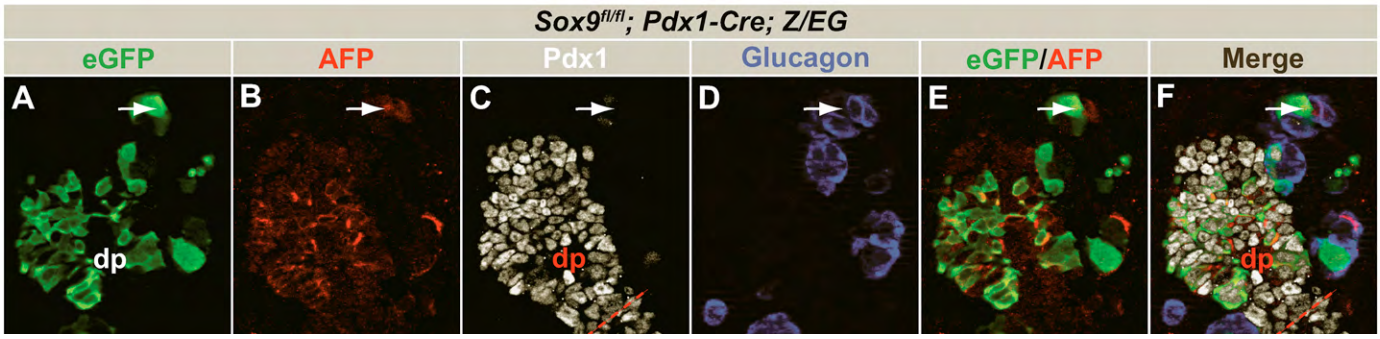

Fig. S2. AFP$^+$ cells arise from Pdx1$^+$ progenitors in *Sox9*-deficient pancreata. (**A-F**) eGFP induced by *Pdx1-Cre*-driven recombination of the *Z/EG* reporter allele (A) labels Pdx1$^+$ cells and their progeny in the dorsal pancreas (dp) (A,F). AFP$^+$ cells (B), including AFP$^+$ Pdx1$^-$ cells (arrows in A-F), are eGFP$^+$, showing their derivation from *Pdx1*-expressing pancreatic progenitors in *Sox9*-deleted pancreata (E,F). Most first-wave glucagon$^+$ endocrine cells (D) are also eGFP$^+$ and are thus derived from *Sox9*-deleted pancreatic progenitors (F). Broken line indicates the boundary between dorsal pancreas and duodenum (duo). Scale bar: 20 µm.

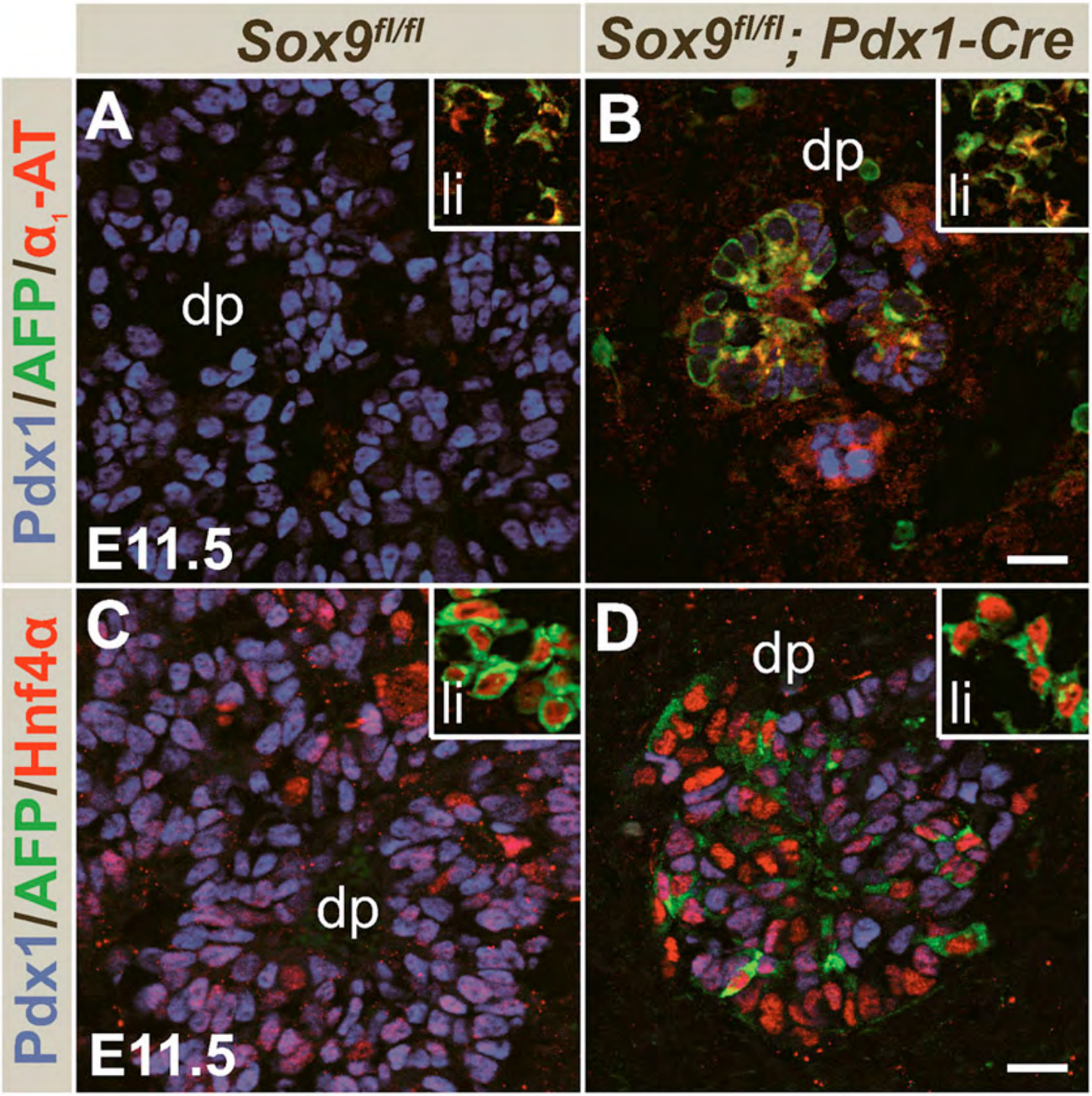

Fig. S3. *Sox9*-deleted pancreatic progenitors activate a bona fide hepatic program. (**A**,**B**) Immunodetection reveals almost complete absence of AFP or α_1-antitrypsin (α_1-AT) in the E11.5 control *Sox9$^{fl/fl}$* dorsal pancreas (dp) (A), but abundant expression in *Sox9$^{fl/fl}$; Pdx1-Cre* pancreas (B). (**C**,**D**) Although low-level Hnf4α nuclear expression is seen in Pdx1$^+$ pancreatic progenitors in E11.5 control pancreas (C), high-level Hnf4α expression is evident in AFP$^+$ cells of *Sox9$^{fl/fl}$; Pdx1-Cre* pancreas (D), similar to that seen in the liver (li) (C,D). Scale bars: 20 μm.

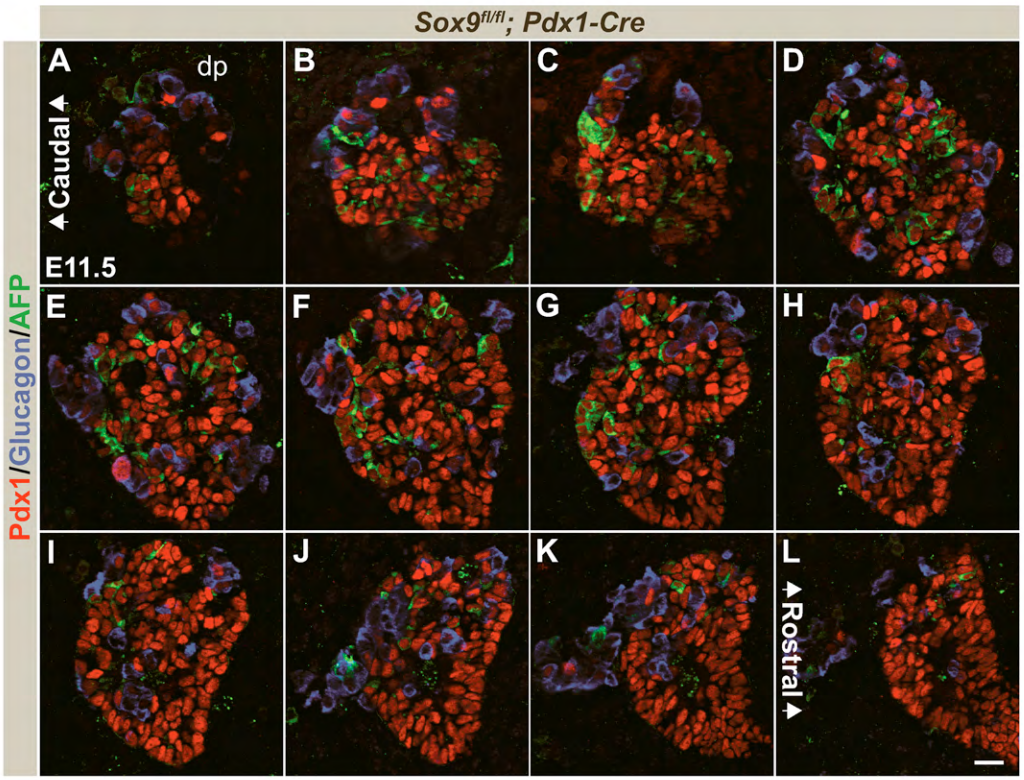

Fig. S4. Variable ratios of mutually exclusive AFP⁺ and glucagon⁺ populations. (**A-L**) Immunodetection on 12 sequentially ordered (rostral to caudal) serial sections through a single E11.5 *Sox9$^{fl/fl}$; Pdx1-Cre* dorsal pancreas (dp) shows both glucagon⁺ cells and AFP⁺ cells to occur in clusters. Glucagon and AFP expression are mutually exclusive. The ratio of glucagon⁺ cells:AFP⁺ cells:Pdx1⁺ cells varies greatly between different sections of the same *Sox9$^{fl/fl}$; Pdx1-Cre* pancreas. Scale bar: 20 µm.

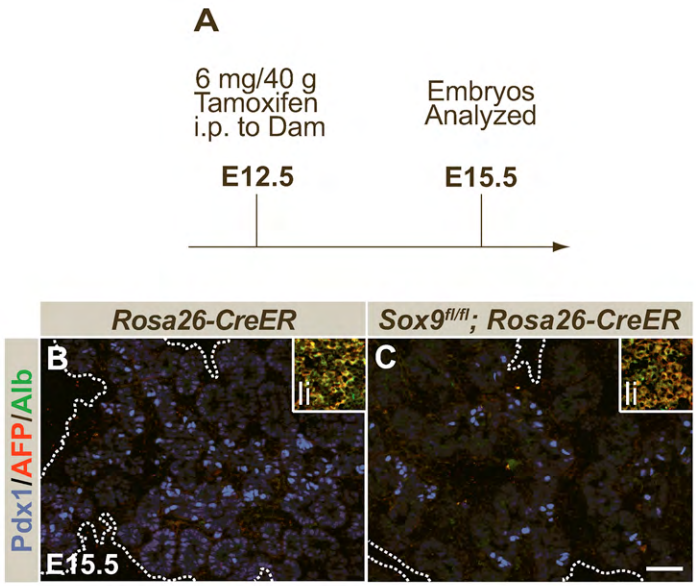

Fig. S5. Competence window for *Sox9*-deleted pancreatic progenitors to adopt hepatic fates closes by E12.5. (**A-C**) AFP⁺ or albumin⁺ cells are not detected in the E15.5 *Sox9$^{fl/fl}$; Rosa26-CreER* pancreatic epithelium (indicated by broken lines in B,C) after intraperitoneal (i.p.) tamoxifen-induced *Sox9* deletion at E12.5. li, liver. Scale bar: 50 µm.

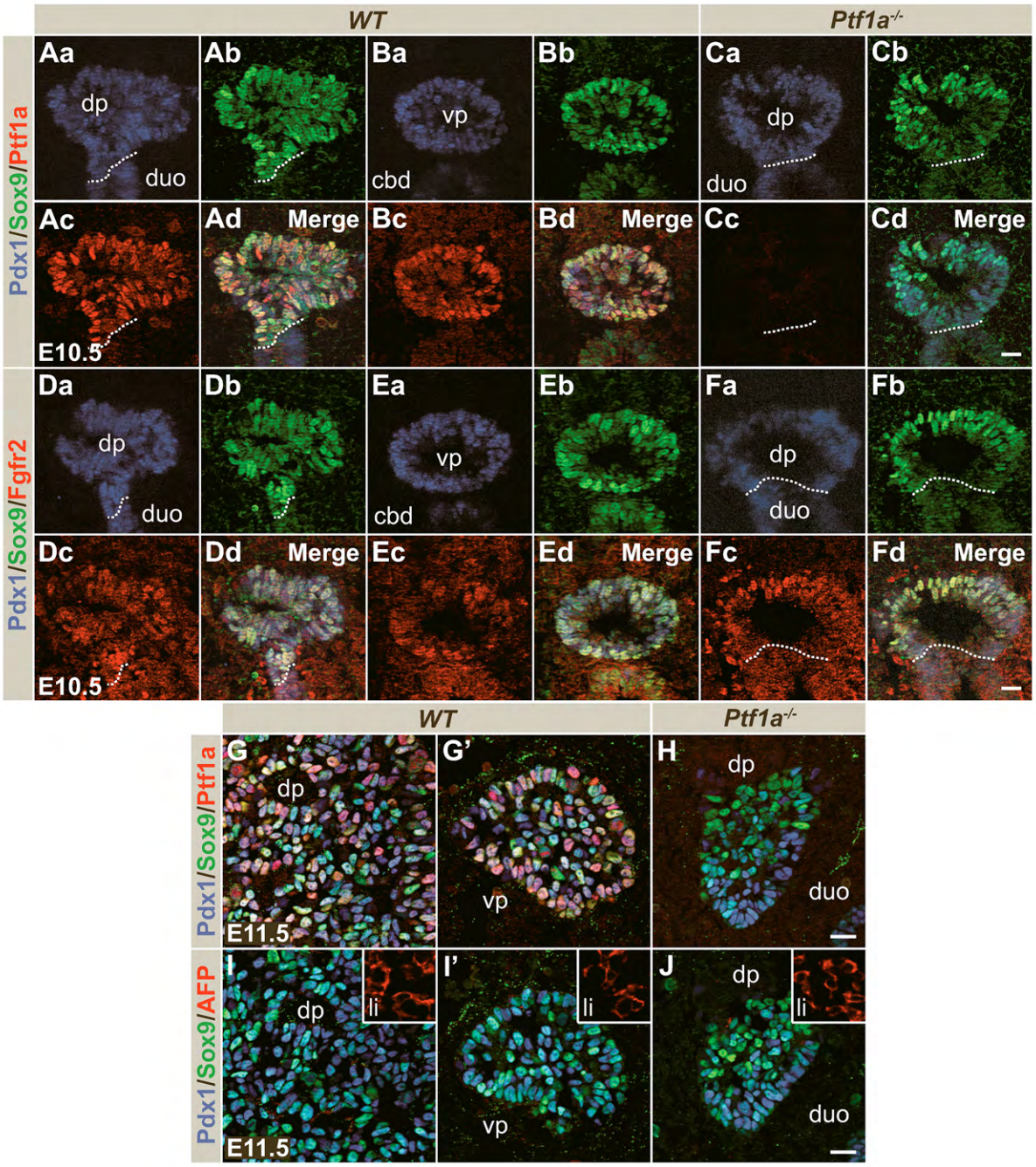

Fig. S6. *Ptf1a*-deficient pancreatic progenitors retain pancreatic identity. (**Aa-Cd**) Pancreatic progenitors in E10.5 wild-type (*WT*) dorsal (Aa-Ad) and ventral (Ba-Bd) pancreas express Pdx1, Sox9 and Ptf1a; both Pdx1 and Sox9 are expressed in dorsal pancreas of *Ptf1a*$^{-/-}$ mice (Ca-Cd). (**Da-Fd**) Like Pdx1 and Sox9, Fgfr2 expression persists in the *Ptf1a*$^{-/-}$ dorsal pancreas (Fa-Fd) as in dorsal (Da-Dd) and ventral (Ea-Ed) wild-type pancreata. (**H-J**) At E11.5, both Sox9 and Pdx1 are maintained in *Ptf1a*$^{-/-}$ dorsal pancreas (H,J), as in wild-type dorsal (G,I) and ventral (G′,I′) pancreata. AFP is not detected in E11.5 wild-type dorsal (I) and ventral (I′) pancreata or dorsal pancreas of *Ptf1a*$^{-/-}$ mice (J). *Ptf1a*$^{-/-}$ ventral pancreas is not shown as it is histologically undetectable by E11.5. Broken line demarcates the boundary between the dorsal pancreas and duodenum (Aa-Ad,Ca-Cd,Da-Dd,Fa-Fd). dp, dorsal pancreas; vp, ventral pancreas; duo, duodenum; cbd, common bile duct; li, liver. Scale bars: 20 μm.

Table S1. Sequences of primers used for mRNA quantification by qRT-PCR

Primer	Forward	Reverse
Sox9	5'-GAGCCGGATCTGAAGAGGGA-3'	5'-GCTTGACGTGTGGCTTGTTC-3'
AFP	5'-CTTCCCTCATCCTCCTGCTAC-3'	5'-ACAAACTGGGTAAAGGTGATGG-3'
Albumin	5'-TGCTTTTTCCAGGGGTGTGTT-3'	5'-TTACTTCCTGCACTAATTTGGCA-3'
Transferrin	5'-TGGGGGTTGGGTGTACGAT-3'	5'-AGCGTAGTAGTAGGTCTGTGG-3'
G-6-P	5'-CGACTCGCTATCTCCAAGTGA-3'	5'-GTTGAACCAGTCTCCGACCA-3'
Fgfr2b	5'-CCCATCCTCCAAGCTGGACTG-3'	5'-CAGAGCCAGCACTTCTGCATTG-3'
Fgfr2c	5'-CCCATCCTCCAAGCTGGACTG-3'	5'-TCTCACAGGCGCTGGCAGAAC-3'
Fgfr4	5'-TTGGCCCTGTTGAGCATCTTT-3'	5'-GCCCTCTTTGTACCAGTGACG-3'