

Figure S1: Sequences of WT and KO clones of *DKK3*, *SLC22A1* and *CSRP3*. KOs were validated using Synthego's "TIDER" online tool and double checked by hand.

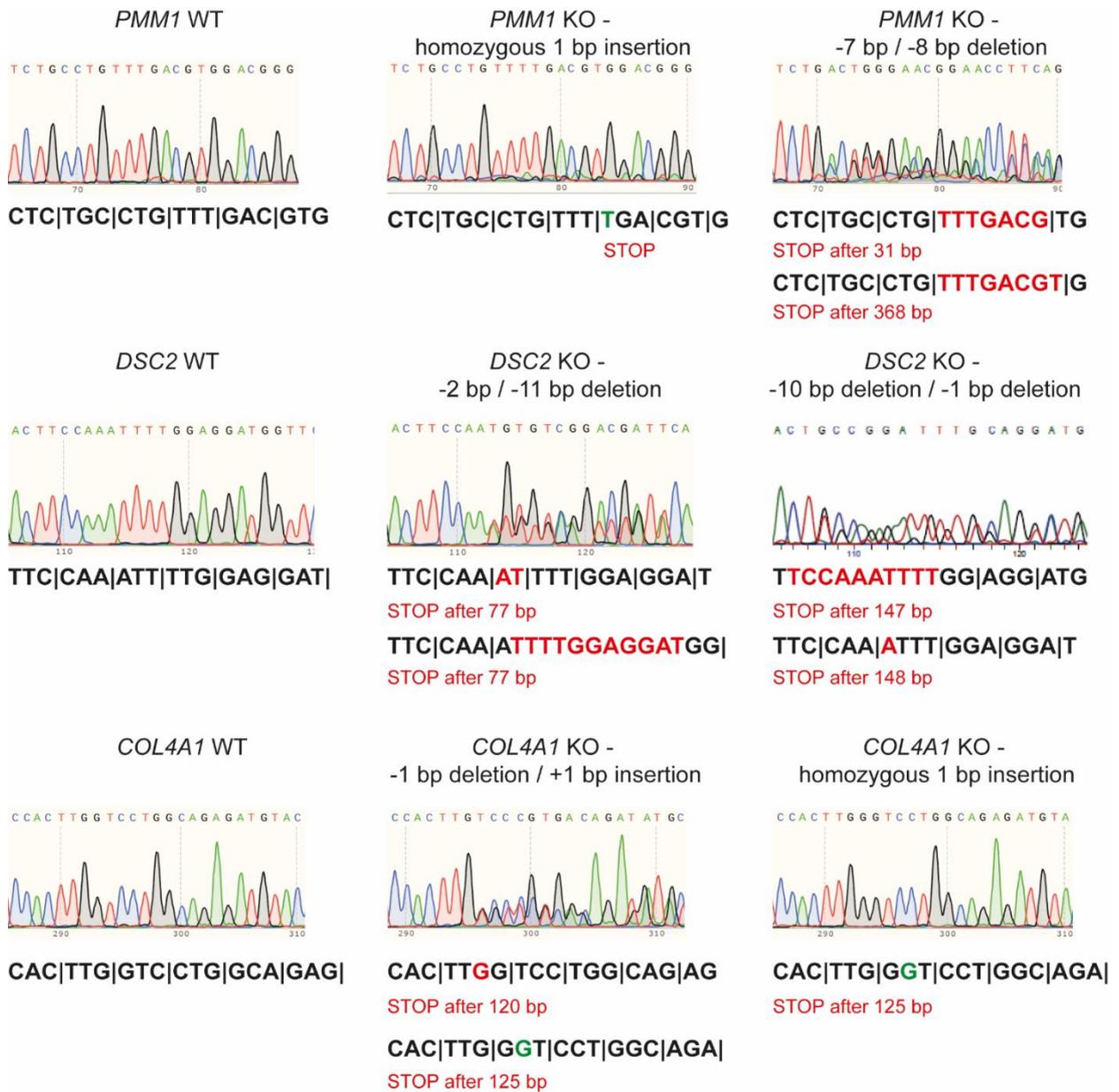


Figure S2: Sequences of WT and KO clones of PMM1, DSC2 and COL4A1. KOs were validated using Synthego's "TIDER" online tool and double checked by hand.

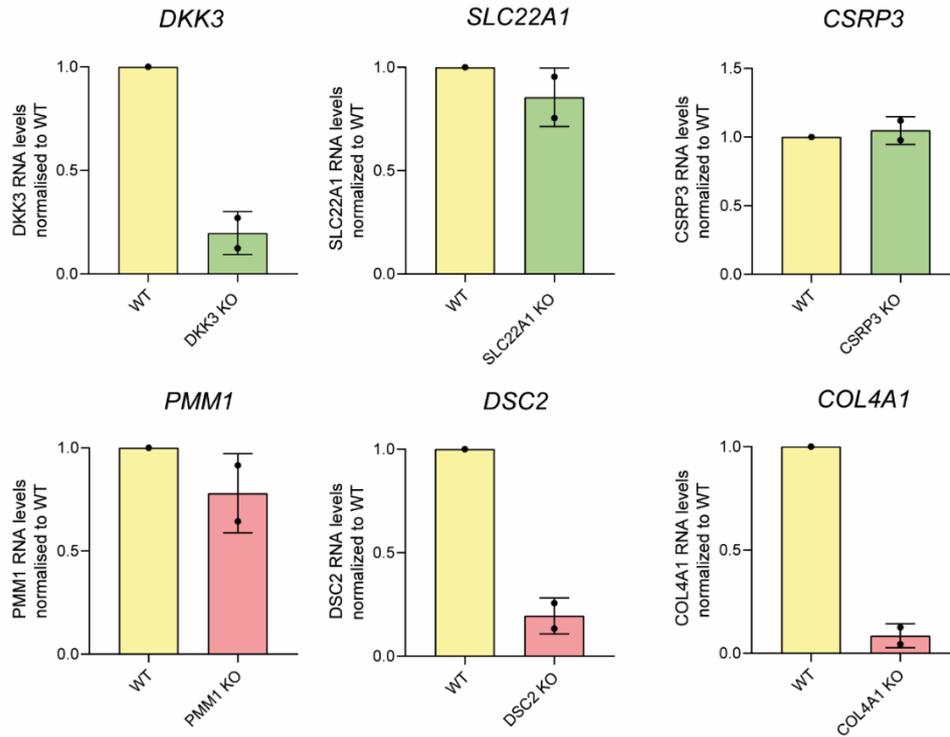
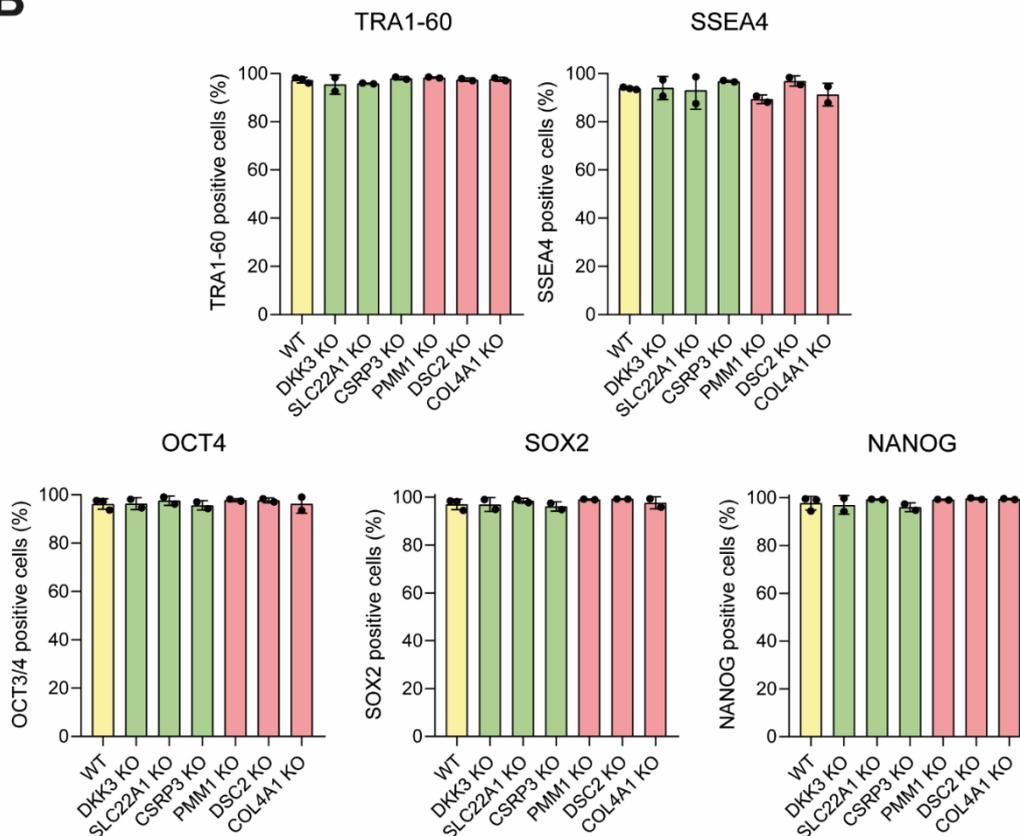
A**B**

Figure S3: Reduced RNA levels of KO genes are observed via qPCR and pluripotency markers are retained after genome editing. A) qPCR performed with RNA from pancreatic progenitor cells shows a decrease in RNA after gene editing (n=1 experiment, 2 clones per genotype in technical duplicates). B) Expression of pluripotency markers was validated by flow cytometry (n=1 experiment, 2 clones per genotype).

Table S1: List of all hits shown in Figure 2B –
d0 vs. d5 CXCR4 negative cells

Gene	shRNA ID	Log2 fold change
<i>PDCD6</i>	V2LHS_71869	12,569
<i>CPD</i>	V2LHS_113166	11,993
<i>GATM</i>	V2LHS_33446	11,097
<i>ATP5J2</i>	V2LHS_263664	11,085
<i>PMM1</i>	V2LHS_170159 10	10,766
<i>LYN</i>	V2LHS_134144	10,614
<i>JUNB</i>	V2LHS_235957	9,723
<i>STMN4</i>	V2LHS_116885	9,424
<i>Matr3</i>	V2LHS_22224	8,686
<i>USMG5</i>	V2LHS_177355	8,113
<i>AHR</i>	V2LHS_132480	7,921
<i>CLDN7</i>	V2LHS_113182	7,894
<i>HIP2</i>	V2LHS_37619	7,866
<i>DKK1</i>	V2LHS_19944	7,698
<i>TIMM10</i>	V2LHS_43241	7,696
<i>CDKN2B</i>	V2LHS_51831	7,440
<i>APOA4</i>	V2LHS_93246	6,910
<i>PLA2G10</i>	V2LHS_2651	6,699
<i>SLC7A3</i>	V2LHS_177606	6,620
<i>PTGIS</i>	V2LHS_131518	5,111
<i>CPN1</i>	V2LHS_113187	4,398
<i>PMM1</i>	V2LHS_170160 3	3,974
<i>ITM2A</i>	V2LHS_67751	3,749
<i>RBP7</i>	V2LHS_118309	3,625
<i>XPA</i>	V2LHS_92694	3,470
<i>SLC7A7</i>	V2LHS_46447	2,664
<i>DSC2</i>	V2LHS_62044 2	2,546
<i>NR1H3</i>	V2LHS_239181	2,022
<i>PDZK1</i>	V2LHS_169832	2,017
<i>IGFBP6</i>	V2LHS_32798	1,876
<i>SFRS2IP</i>	V2LHS_36802	1,791
<i>NGDN</i>	V2LHS_76266	1,727
<i>VIL1</i>	V2LHS_197376	1,723
<i>MAP3K5</i>	V2LHS_2204	1,641
<i>FOXA2</i>	V2LHS_86206	1,515
<i>BTBD1</i>	V2LHS_196030	1,515
<i>TFPI2</i>	V2LHS_198390	1,433
<i>CA4</i>	V2LHS_112199	1,427
<i>COL4A1</i>	V2LHS_150714 1	1,406
<i>INA</i>	V2LHS_177282	1,396
<i>F10</i>	V2LHS_93365	1,389
<i>RNF7</i>	V2LHS_13708	1,353
<i>LTA</i>	V2LHS_227733	1,350
<i>CITED1</i>	V2LHS_173199	1,276
<i>GLRA1</i>	V2LHS_82866	1,241
<i>FGFBP1</i>	V2LHS_49795	1,223
<i>EPHA2</i>	V2LHS_17961	1,207
<i>ROCK1</i>	V2LHS_70607	1,194
<i>COL4A1</i>	V2LHS_150713 1	1,170

<i>BCHE</i>	V2LHS_259891	1,151
<i>DSC2</i>	V2LHS_62042 1	1,138
<i>CYP26A1</i>	V2LHS_112498	1,133
<i>DAB2</i>	V2LHS_150163	1,130
<i>CHRD2</i>	V2LHS_136912	1,079
<i>LRP10</i>	V2LHS_59766	1,063
<i>PDCD6IP</i>	V2LHS_64525	1,049
<i>BCAT1</i>	V2LHS_64327	1,035
<i>PRG1</i>	V2LHS_170386	1,031
<i>SLC22A1</i>	V2LHS_153077	-1,012
<i>SLC22A1</i>	V2LHS_279379	-1,041
<i>PREPL</i>	V2LHS_118927	-1,042
<i>DKK3</i>	V2LHS_71314	-1,042
<i>POU1F1</i>	V2LHS_230873	-1,045
<i>DKK3</i>	V2LHS_71317	-1,045
<i>CXCL12</i>	V2LHS_111679	-1,054
<i>PBOV1</i>	V2LHS_200991	-1,082
<i>DIO2</i>	V2LHS_225563	-1,134
<i>NMI</i>	V2LHS_4367	-1,194
<i>PHGDH</i>	V2LHS_91258	-1,214
<i>CETN3</i>	V2LHS_14771	-1,230
<i>CSRP2BP</i>	V2LHS_100125	-1,267
<i>CTS2</i>	V2LHS_113325	-1,404
<i>CSRP3</i>	V2LHS_172436	-1,508
<i>FOLR1</i>	V2LHS_135471	-1,540
<i>PON2</i>	V2LHS_231553	-1,603
<i>LN2</i>	V2LHS_159554	-1,609
<i>FHL1</i>	V2LHS_131742	-1,637
<i>SLC16A10</i>	V2LHS_176201	-1,683
<i>LRP8</i>	V2LHS_160292	-1,794
<i>RAE1</i>	V2LHS_27966	-1,867
<i>ABC2</i>	V2LHS_270743	-2,423
<i>PIGK</i>	V2LHS_68405	-2,442
<i>RRBP1</i>	V2LHS_47386	-2,510
<i>CPA3</i>	V2LHS_150836	-2,983

Table S2: List of all hits –
d0 vs. d5 CXCR4 positive cells

Gene	shRNA ID	Log2 fold change
EPHA8	V2LHS_65935	8,375
DKK3	V2LHS_71317	2,457
GPC1	V2LHS_114228	1,422
CLDN7	V2LHS_113182	1,082
GADD45B	V2LHS_114575	1,063
CSRP3	V2LHS_172436	1,032
PTGIS	V2LHS_131518	-1,119
Matr3	V2LHS_22224	-1,297
ZFP37	V2LHS_172098	-1,340
PDZK1	V2LHS_169832	-1,435
CDKN2B	V2LHS_51831	-1,768
PMM1	V2LHS_170159	-1,969
SCEL	V2LHS_16720	-1,999
HIP2	V2LHS_37619	-2,994
USMG5	V2LHS_177355	-4,689
DKK1	V2LHS_19944	-6,195
CKB	V2LHS_150588	-6,211