

SUPPLEMENTARY DATA

Supplementary Table 1. Human donor information

Donor Age	Ethnicity/Race	Gender	BMI	Cause of Death	Tissue Source
3 months	Caucasian	M	17.4	Anoxia	NDRI
10 months	Caucasian	F	16.1	CVA	NDRI
19 months	Hispanic	F	12.9	Head Trauma	NDRI
4 years	Caucasian	F	19.0	Head Trauma	IIAM
5 years	African American	F	15.9	Anoxia	NDRI
10 years	Caucasian	M	19.3	Head Trauma	NDRI

NDRI – National Disease Research Interchange

IIAM – International Institute for the Advancement of Medicine

CVA – Cerebrovascular accident

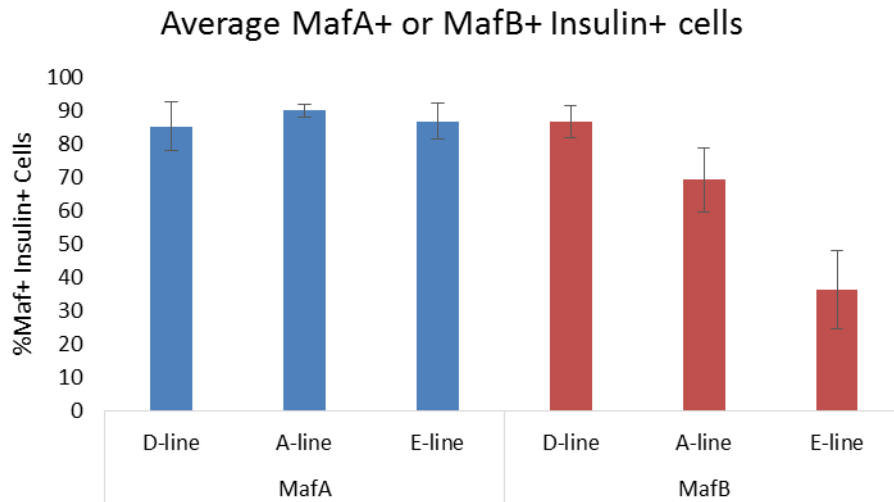
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Supplementary Table 2. Primers used for islet gene expression

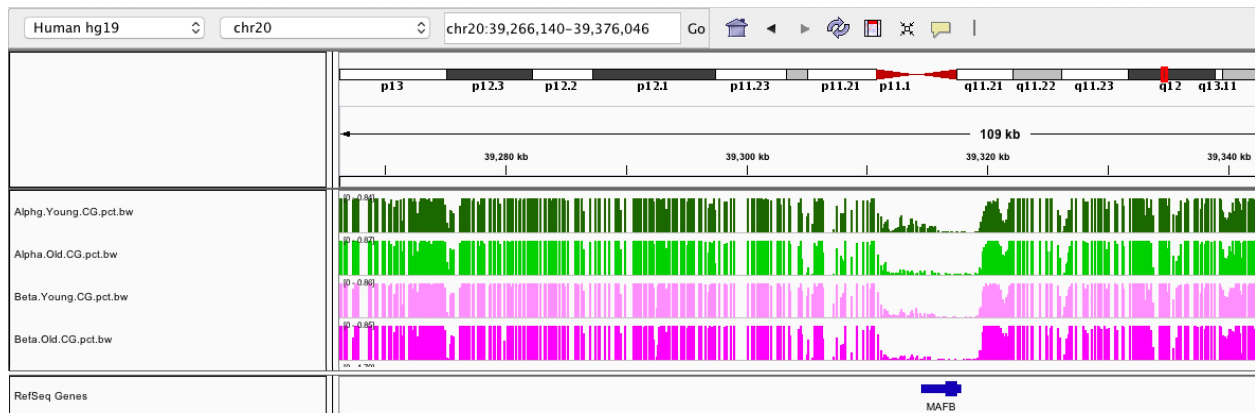
Gene	Sequence
Atp2a2 F	AGCCAGAGAGATGCCTGCTTAAA
Atp2a2 R	AGAGCAGGAGCATCATTCACACCA
Ccnd2 F	GAGTGGGAACCTGGTAGTGTG
Ccnd2 R	CGCACAGAGCGATGAAGGT
Cldn8 F	GCAACCTACGCTCTTCAAATGG
Cldn8 R	TTCCCAGCGGTTCTCAAACAC
Ddc F	TAGCTGACTATCTGGATGGCAT
Ddc R	GTCCTCGTATGTTTCTGGCTC
G6pc2 F	ACCTGGTCCTTTCTGTGGAGTGTT
G6pc2 R	TTCAAAGGCCTCGGCTACTAGCAT
Gcg F	CATTCACCAGCGACTACAGCAA
Gcg R	TCATCAACCACTGCACAAAATCT
Htr1d F	ATCACCGATGCCCTGGAGTA
Htr1d R	GCCAGAAGAGTGGAGGGATG
Htr2b F	GAACAAAGCACAACTTCTGAGC
Htr2b R	CCGCGAGTATCAGGAGAGC
Htr3a F	CCTGGCTAACTACAAGAAGGGG
Htr3a R	TGCAGAAACTCATCAGTCCAGTA
Ins2 F	GGCTTCTTCTACACACCCAT
Ins2 R	CCAAGGTCTGAAGGTCACCT
Mafa F	CCTGTAGAGGAAGCCGAGGAA
Mafa R	CCTCCCCCAGTCGAGTATAGC
Mafb 3' UTR F	CGAGGTCCGGGAGTAACTTTT
Mafb 3' UTR R	CTTGGCGACTCCTTGGAATAA
Mafb F	AACGCGTCCAGCAGAAACA
Mafb R	AGCTGCTCCACCTGCTGAAT
Prlr F	CACTTGCTTACATGCTGCTTG
Prlr R	CAGGTGGTGA CTGTCCATTCA
Slc18a1 F	GTCCCGGAAGCTGGTGTG
Slc18a1 R	ACAGTGAGCAGCATATTGTCC
Slc2a2 F	GTAAATGGCAGCTTTCCGGTC
Slc2a2 R	CAGTTCGGCTATGACATCGGT
Slc30a8 F	AGCTTCCTGTGTTTCTAGGCCAT
Slc30a8 R	AATCTATTCCGACGGCTGCCTCAT
Tph1 F	AACAAAGACCATTTCCTCCGAAAG
Tph1 R	TGTAACAGGCTCACATGATTCTC
Tph2 F	TCGAAATCTTCGTGGACTGCG
Tph2 R	CGGATTCAGGGTCA CAATGGT

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Supplementary Figure 1. The three β MafBTg mouse lines characterized varied in their production of MafB within the islet β cell population. The number islet MafA⁺ Insulin⁺ and MafB⁺ Insulin⁺ cells were divided by the total number of Insulin⁺ cells to obtain the percent of MafA⁺ and MafB⁺ β cells within the total β cell population in the D-, A-, and E-lines. The D-line was the focus of subsequent experimentation because of the higher percentage of MafB⁺ β cells.



Supplementary Figure 2. The methylation status of the 5'- and 3'- flanking region surrounding the human *MAFB* gene. Note the similarity in the methylation state between young and old MAFB⁺ α and β cells, with hypomethylation proximal to the *MAFB* gene.



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Supplementary Figure 3. Transgenic MafB expression is elevated at e15.5 and 2-months. *MafA^{fl/fl}* and β MafBTg RNA analyzed to delineate the endogenous *MafB* 3' untranslated region (UTR) and coding (endogenous + transgenic) qPCR signals. qPCR normalized to *Gapdh* expression. n=3-5, *p<0.05.

