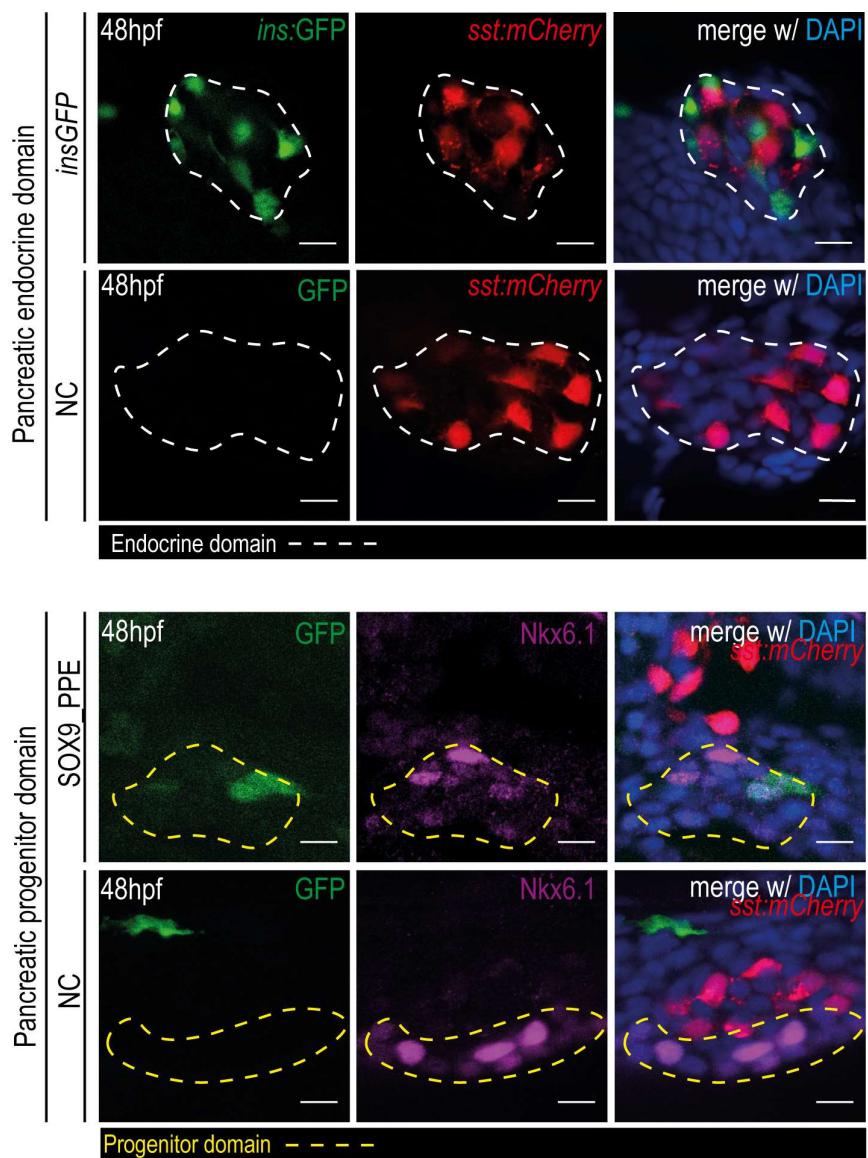
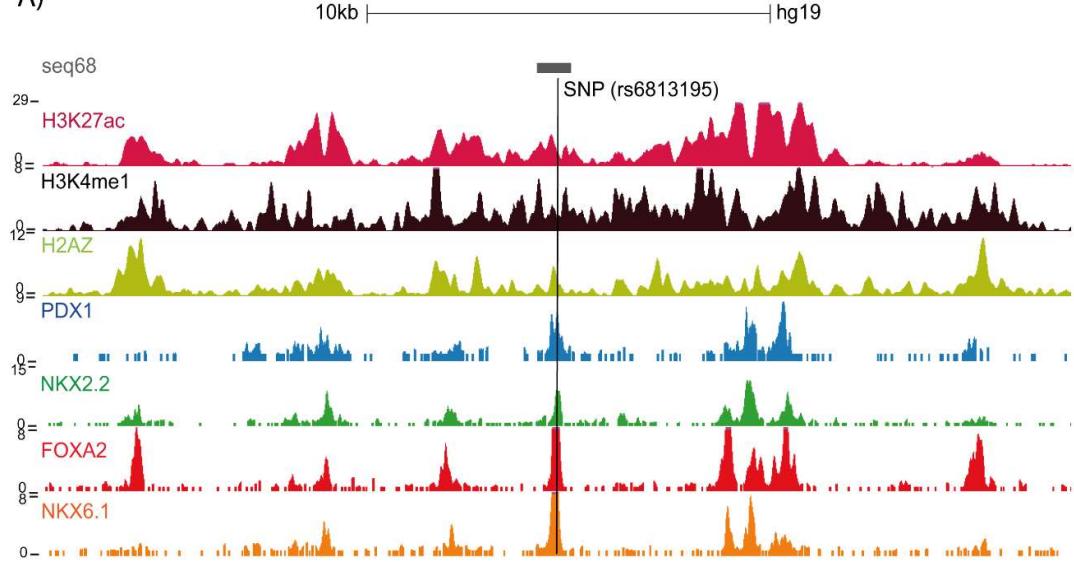


Online Supplemental Material

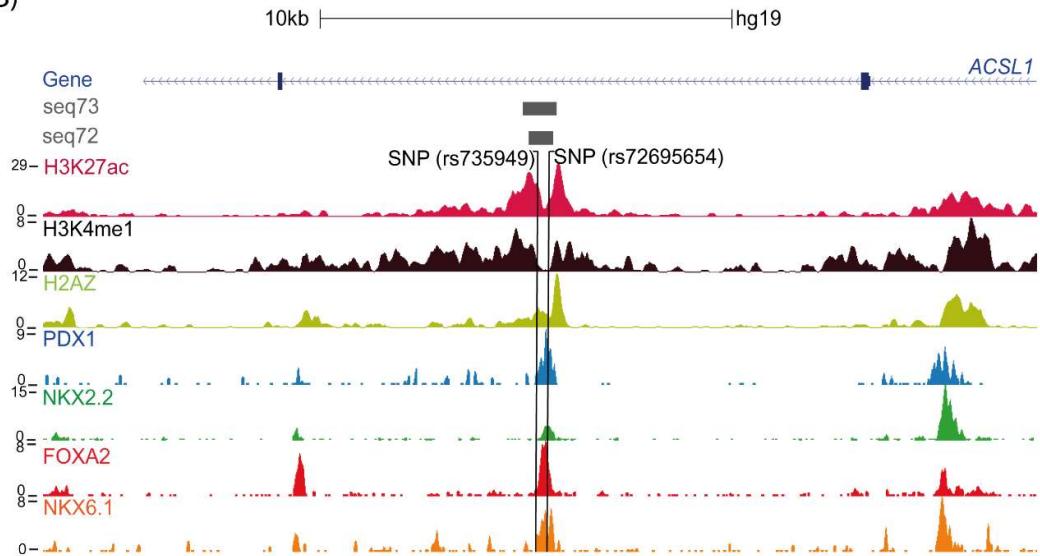


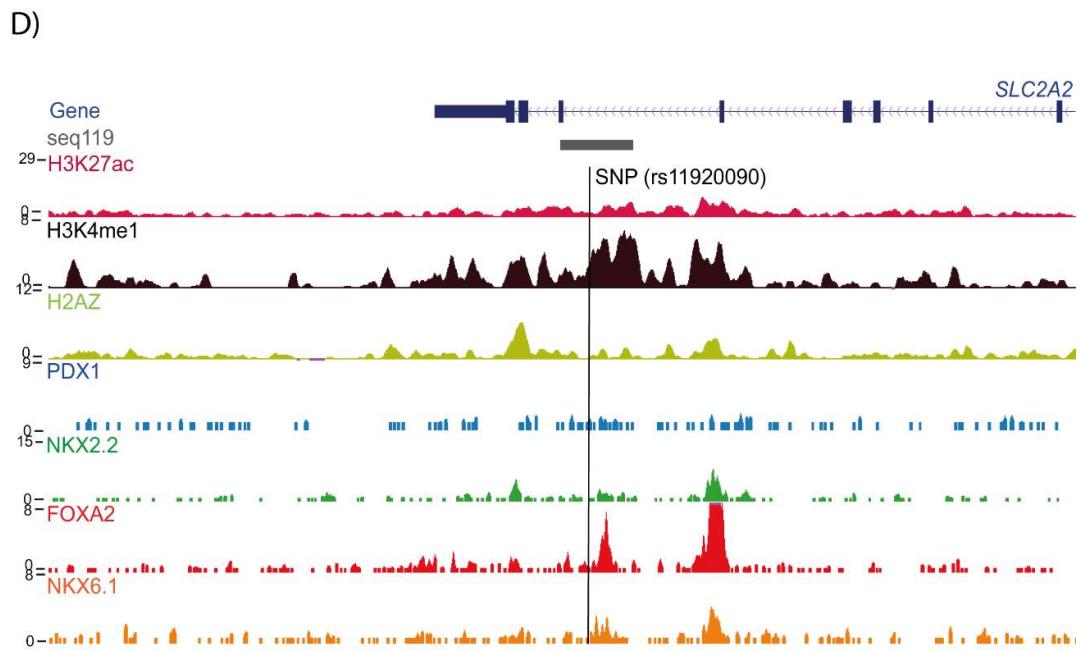
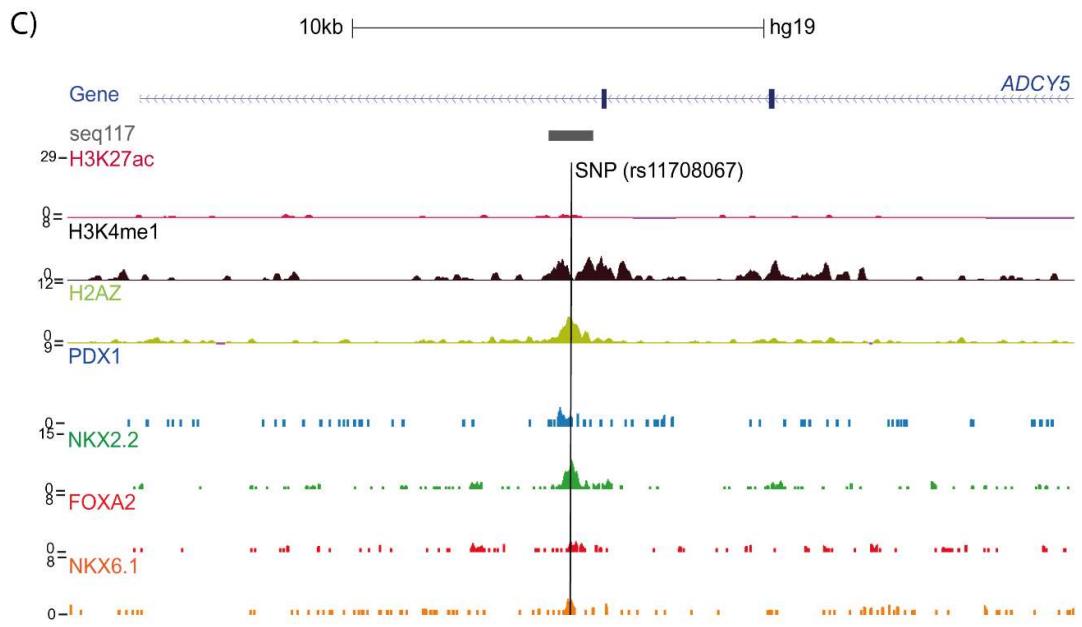
Supplementary Fig.1 - Top: Representative confocal images resulted from the injection of *ins:GFP* vector, showing GFP expression in endocrine pancreatic domain (white dashed line) defined by the *sst:mCherry* reporter line. The NC did not show GFP positive cells in endocrine pancreatic domain. The 48hpf embryos were stained with DAPI (blue). Scale bar, 10 μ m. Bottom: Confocal images from Z48 vector containing a pancreatic progenitor enhancer (SOX9_PPE), showing GFP positive cells co-localization with the progenitor domain (yellow dashed line) defined by the Nkx6.1 staining (purple). The NC was not able to drive GFP expression in the pancreatic progenitor domain. The 48 hpf embryos were stained with DAPI (blue) and Nkx6.1 (purple). Scale bar, 10 μ m.

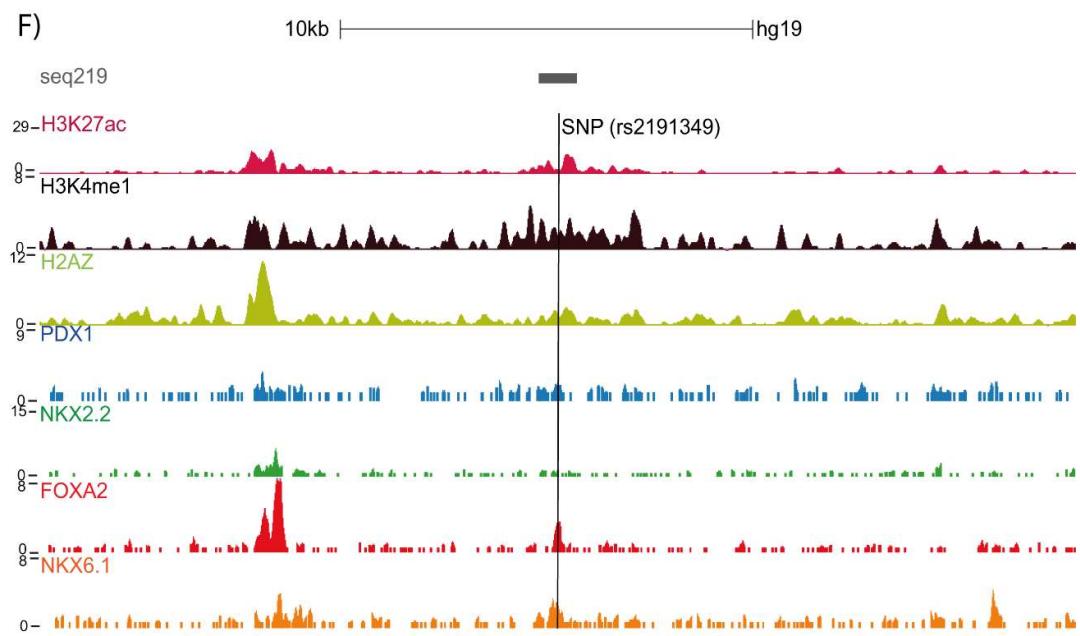
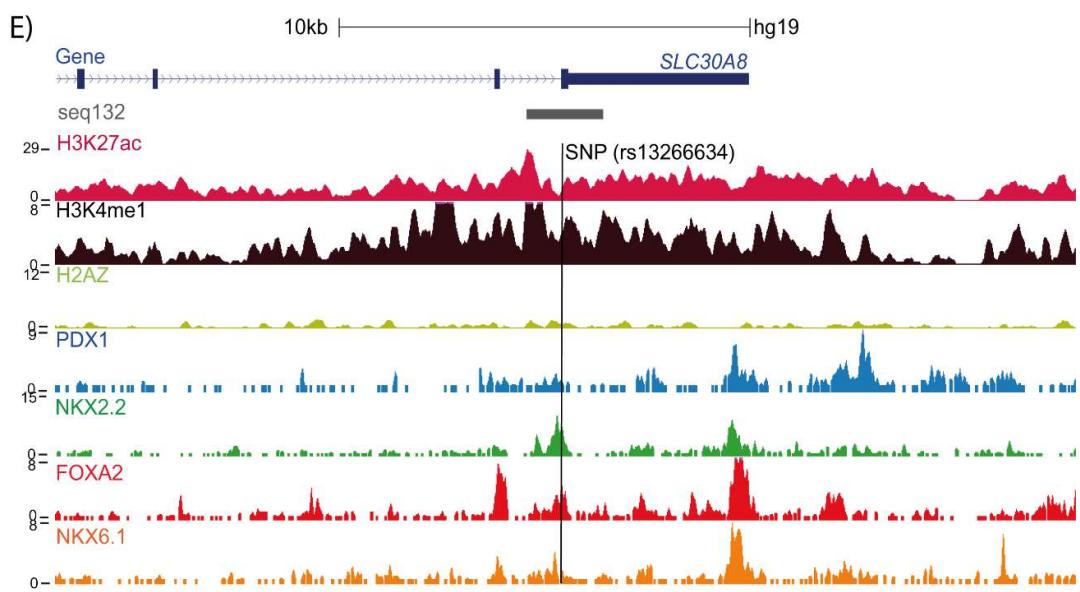
A)

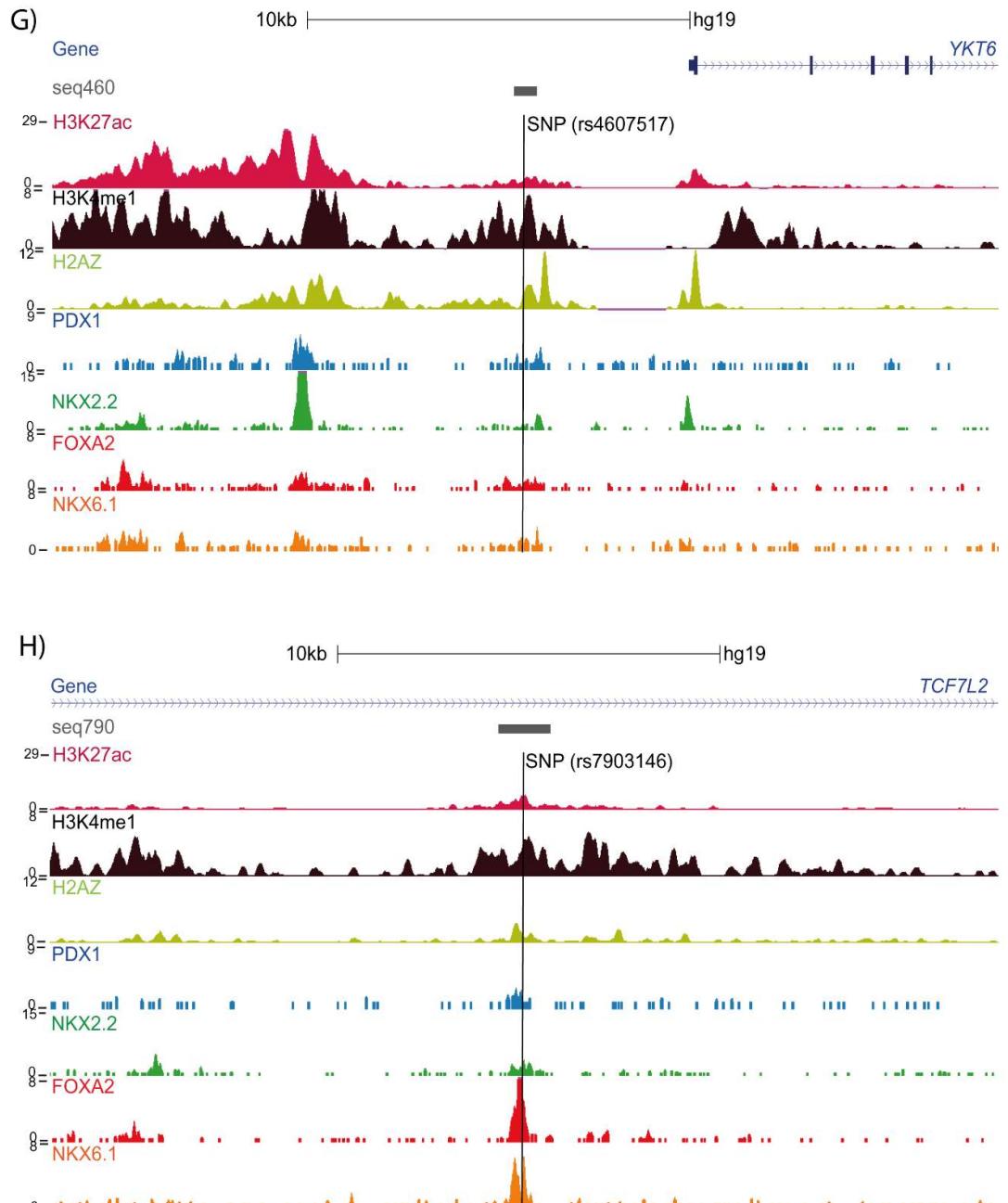


B)

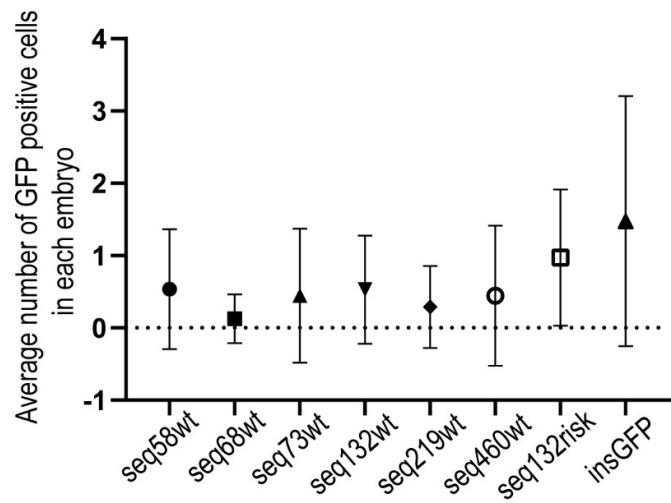






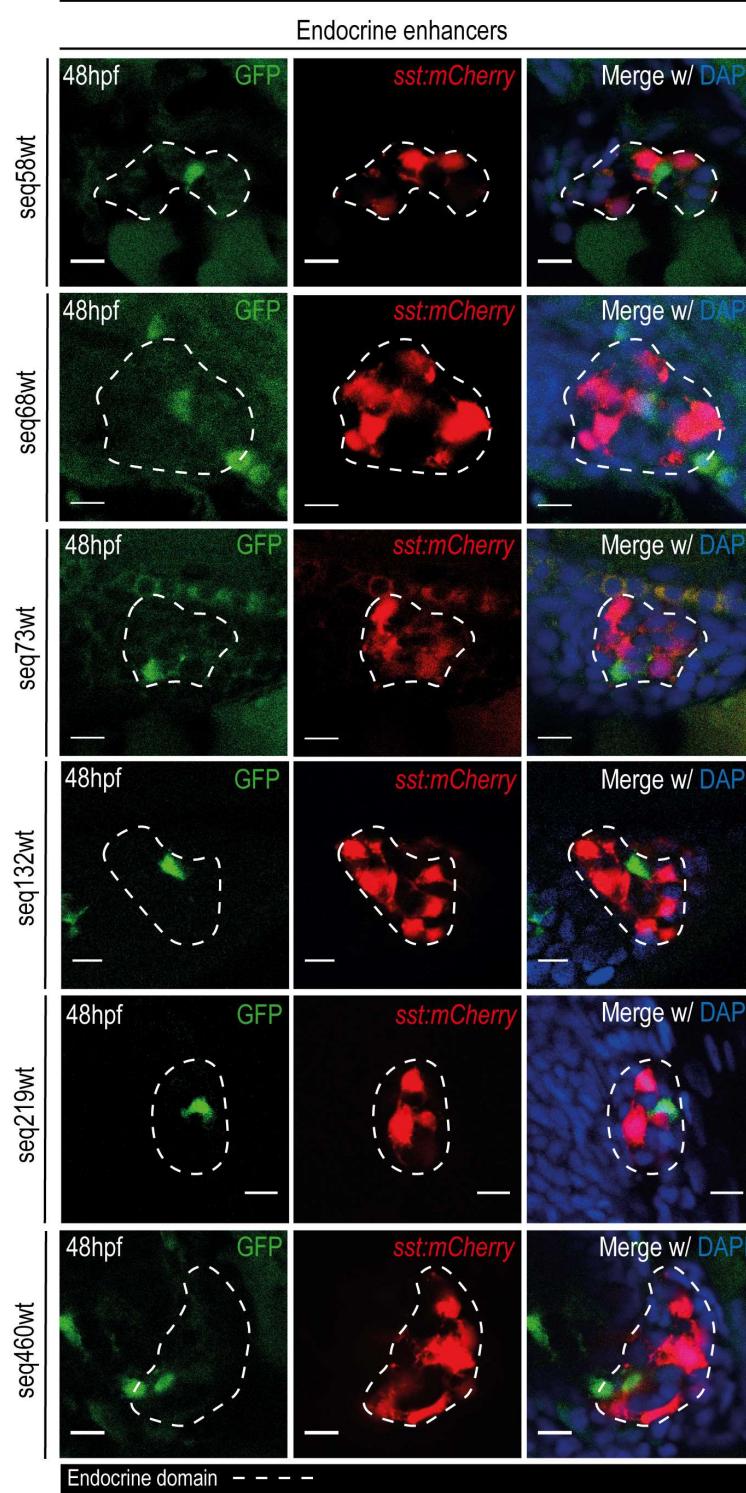


Supplementary Fig.2 Genomic landscapes of the putative enhancers seq68 (A), seq72 (B), seq73 (B), seq117 (C), seq119 (D), seq132 (E) seq219 (F), seq460 (G) and seq790 (H) (represented in grey). Tracks represent H3K27ac (pink), H3K4me1 (black), histone variant H2A.Z (light green) and TF binding (PDX1 - blue, NKX2.2 - dark green, FOXA2 - red and NKX6.1 - orange) from ChIP-seq data for human endocrine pancreas samples. The location of the type 2 diabetes associated SNPs (rs6813195, rs735949, rs72695654, rs11708067, rs11920090, rs13266634, rs2191349, rs4607517 and rs7903146) is represented as a vertical black line.



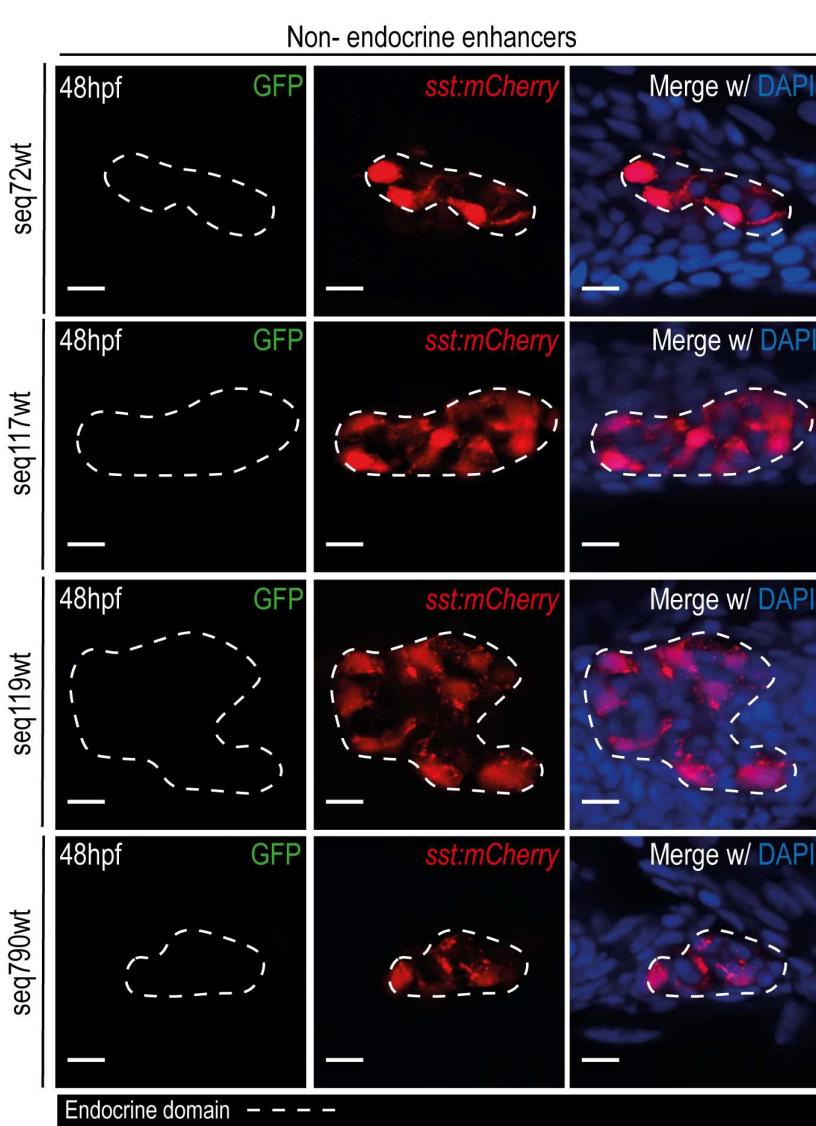
Supplementary Fig. 3 – Graph representing the average number of GFP positive cells per embryo per sequence and in insGFP promoter vector. Data are mean \pm SD.

Endocrine enhancer assays *in vivo*

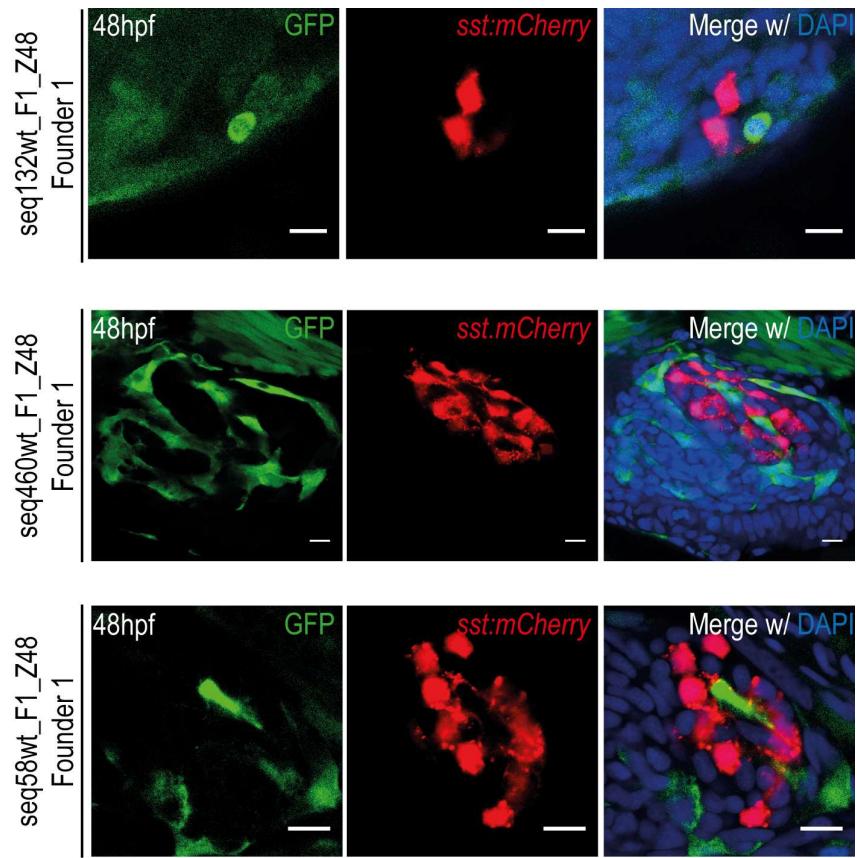


Supplementary Fig.4 - Representative confocal images for seq58wt, seq68wt, seq73wt, seq132wt, seq219wt and seq460wt. All six sequences showed GFP positive cells in endocrine pancreatic domain (white dashed line) defined by the *sst:mCherry* reporter line. The 48 hpf embryos were stained with DAPI (blue). Scale bar, 10 μ m.

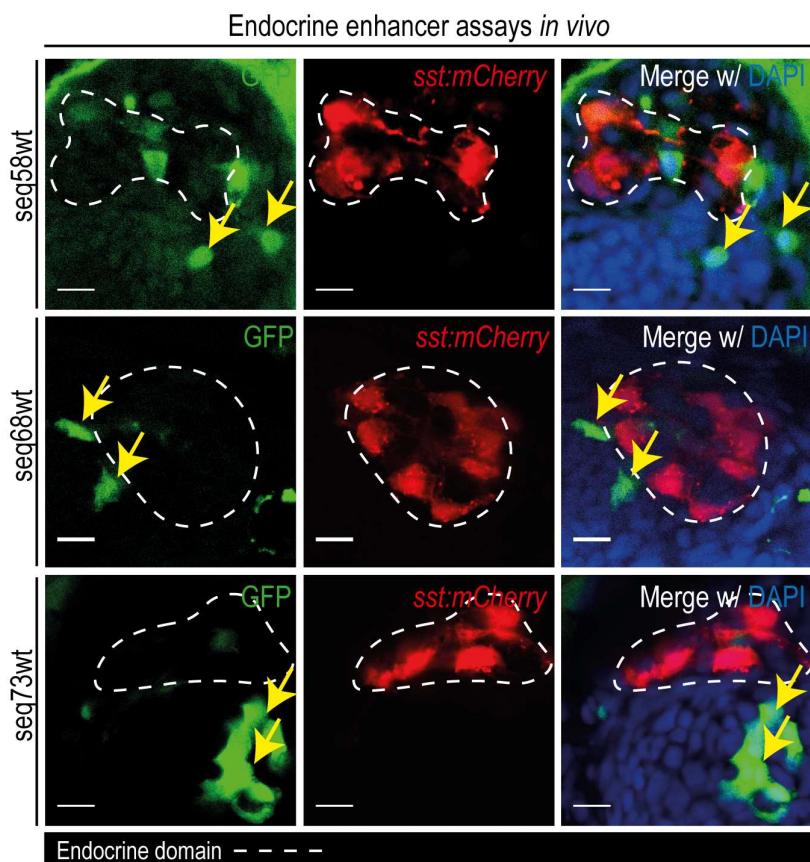
Endocrine enhancer assays *in vivo*



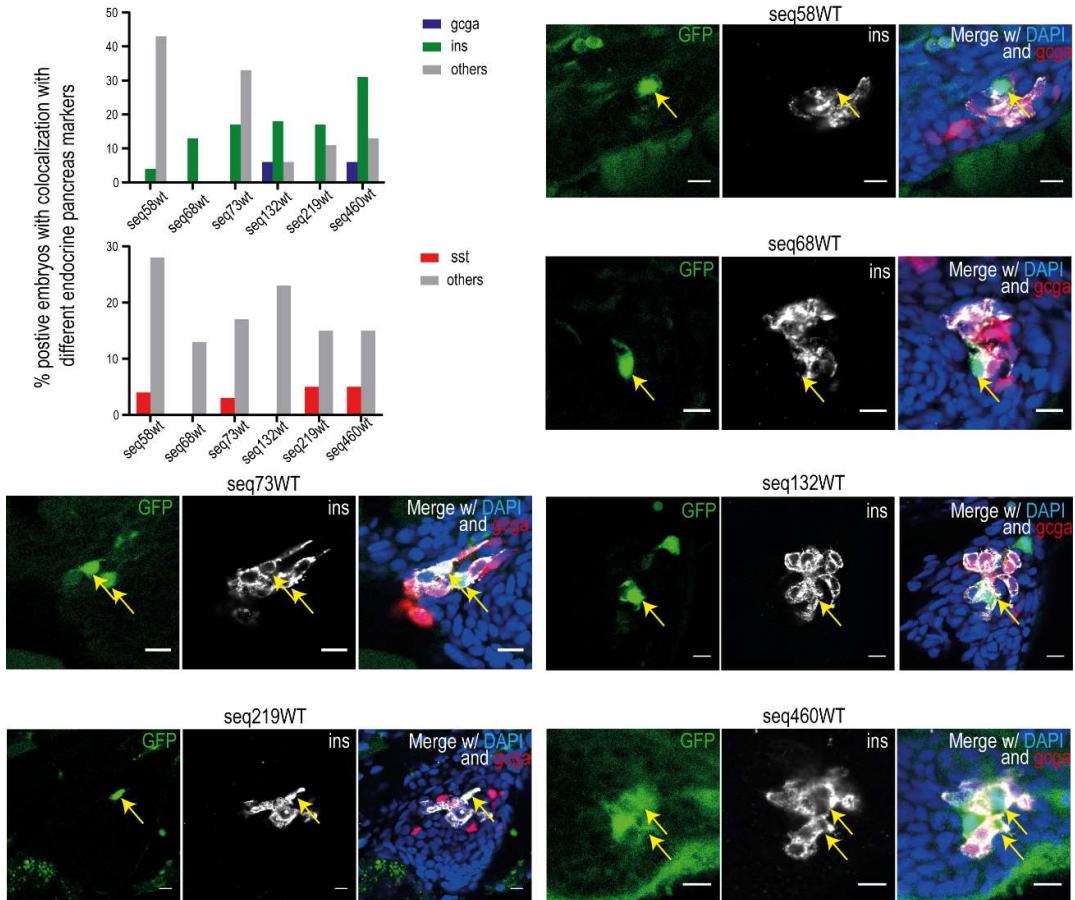
Supplementary Fig.5 - Representative confocal images of seq72wt, seq117wt, seq119wt and seq790wt. All four sequences did not show GFP positive cells in endocrine pancreatic domain (white dashed line) defined by the *sst:mCherry* reporter line. The 48 hpf embryos were stained with DAPI (blue). Scale bar, 10 μ m.



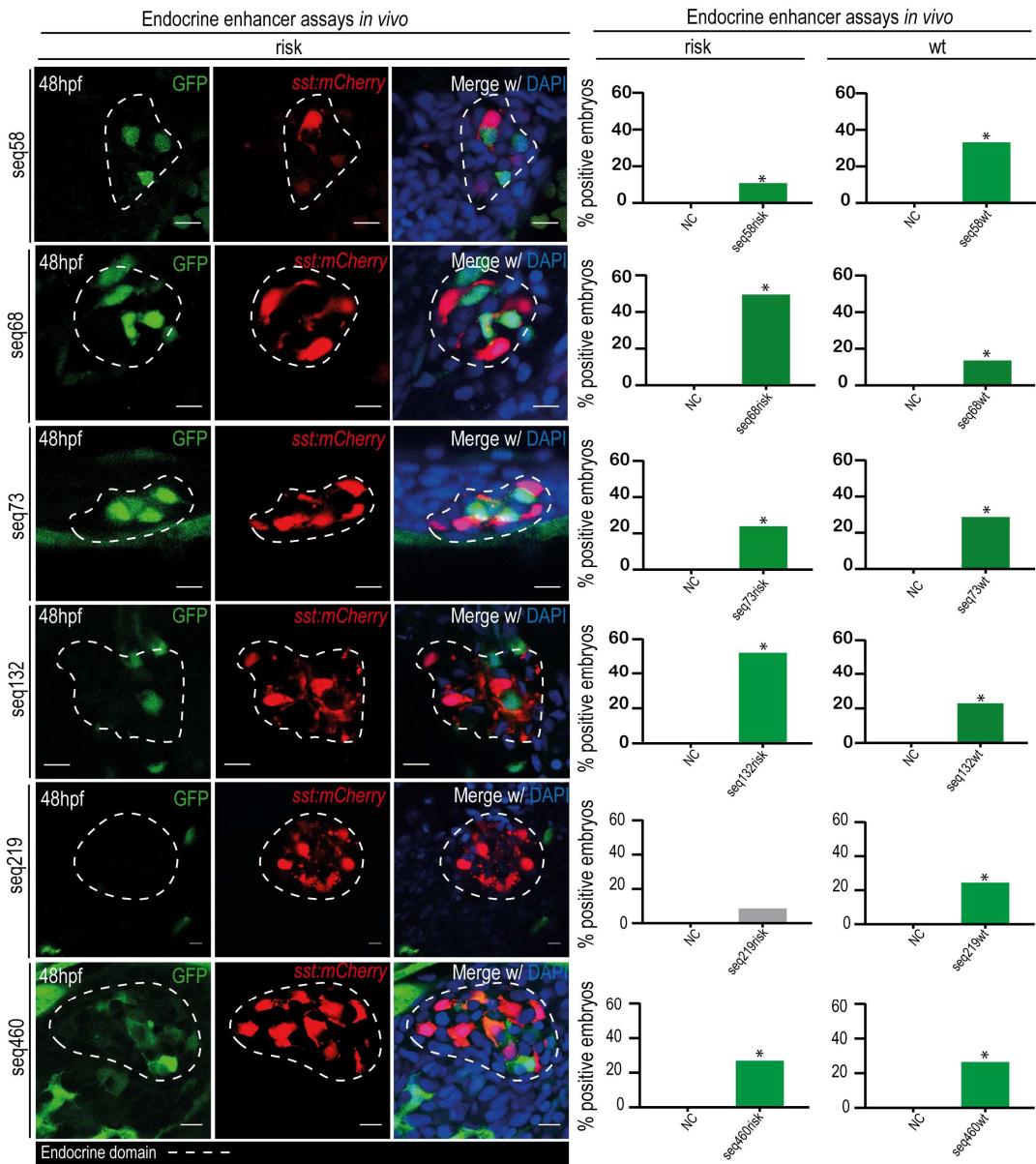
Supplementary Fig.6 - Representative confocal images of stable transgenic lines from seq132wt, seq460wt and seq58wt. All 3 sequences presented GFP positive cells within endocrine pancreatic domain, defined by *sst:mCherry* reporter line. The 48hpf embryos were stained with DAPI. Scale bar: 10 μ m.



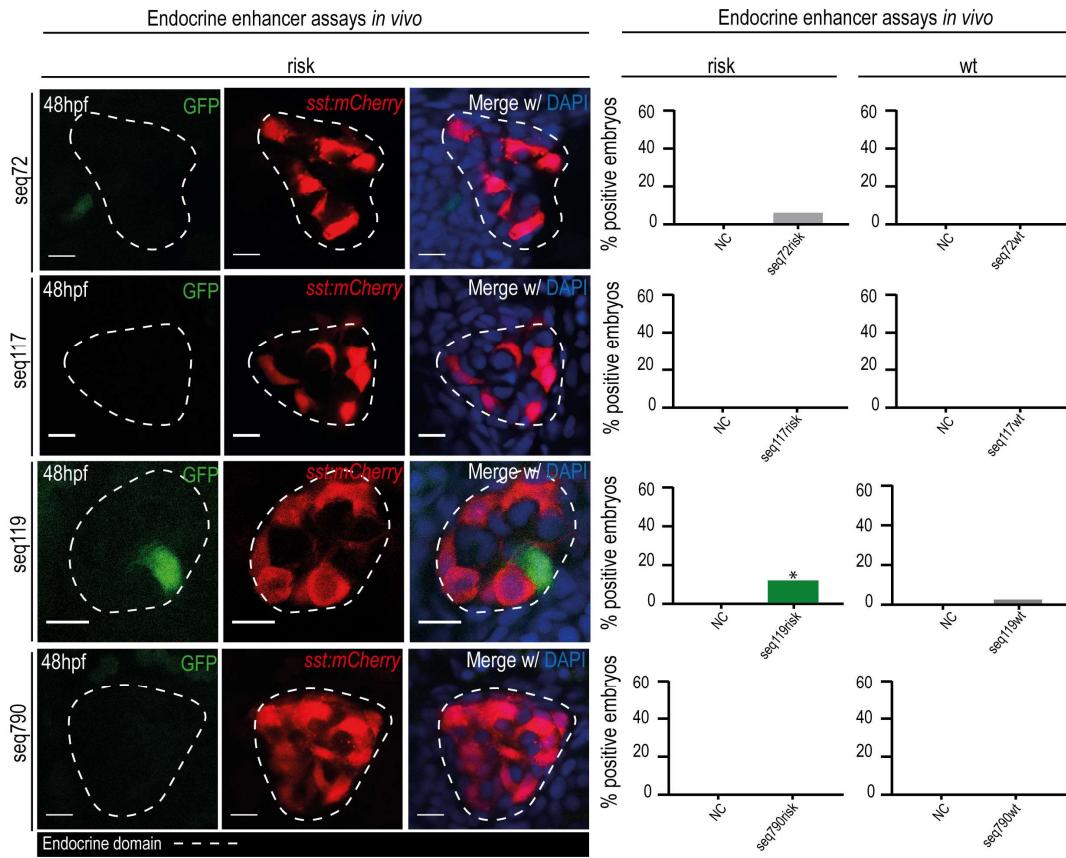
Supplementary Fig.7 - Representative confocal images of seq58wt, seq68wt and seq73wt. These three sequences presented GFP positive cells in adjacent area to the endocrine domain defined by the *sst:mCherry* reporter line. The 48 hpf embryos were stained with DAPI (blue). Scale bar, 10 μ m.



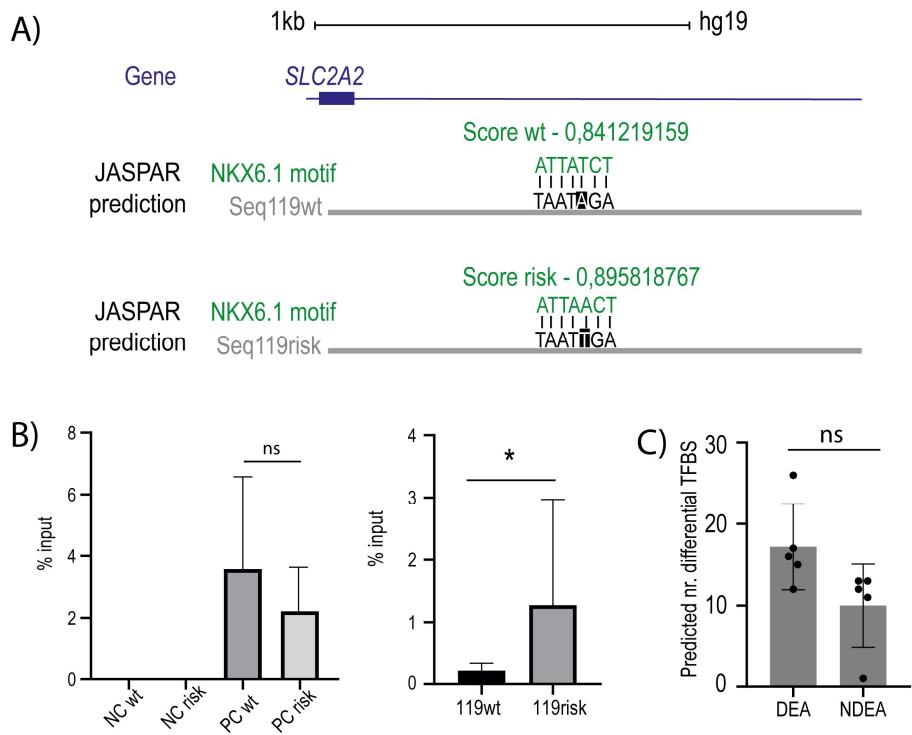
Supplementary Fig. 8 - Graphs representing the percentage of the number of embryos with GFP positive cells colocalizing with somatostatin (sst), glucagon (gcga) and insulin (ins) secreting cells. Representative confocal images resulted from the injection of seq58wt (n=24), seq68wt (n=15), seq73wt (n=12), seq132wt (n=16), seq219wt (n=18) and seq460wt (n=16). The endocrine pancreatic domain (white dashed line) is defined by the *gluc:mCherry* reporter line. The yellow arrows indicate GFP colocalizing with insulin. The 48 hpf embryos were stained with DAPI (blue) and insulin (white). Scale bar, 10 μ m.



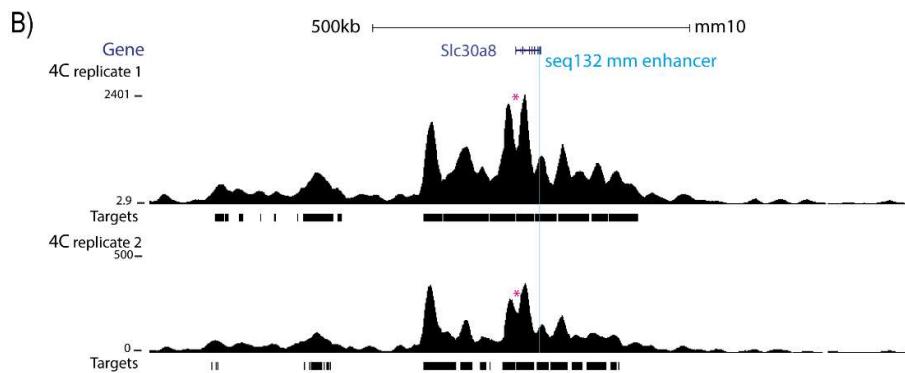
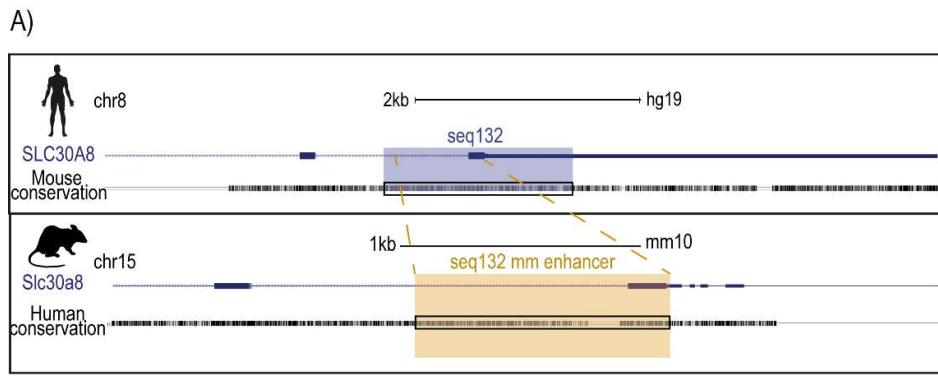
Supplementary Fig.9 - Left: Representative confocal images for all the risk alleles of the identified endocrine pancreatic enhancers: seq58risk, seq68risk, seq73risk, seq132risk, seq219risk and seq460risk. The endocrine pancreatic domain is represented by the white dashed line and it is defined by the *sst:mCherry* reporter line. The 48hpf embryos were stained with DAPI (blue). Scale bar, 10 μ m. Right: Graphs showing the total percentage of positive embryos for wt and risk alleles of the aforementioned sequences seq58 wt/risk (36%, n=56 / 12%, n=43), seq68 wt/risk (13%, n=47 / 50%, n=32), seq73 wt/risk (28%, n=47 / 22%, n=36), seq132 wt/risk (23%, n=34 / 56%, n=36), seq219wt//risk (24%, n=38 / 6%, n=35) seq460 wt/risk (27%, n=36 / 27%, n=30) Chi-square test: p<0,05 (*).



Supplementary Fig.10 - Left: Representative confocal images from all the risk alleles of the wt sequences that previously tested negative for enhancer activity (non-endocrine pancreatic enhancers): seq72risk, seq117risk, seq119risk and seq790risk. The endocrine pancreatic domain is represented by the white dashed line and it is defined by the *sst:mCherry* reporter line. The 48hpf embryos were stained with DAPI (blue). Scale bar, 10 µm. Right: Graphs showing the total percentage of positive embryos in wt and risk alleles of the identified endocrine pancreatic enhancers: seq72 wt/risk (0%, n=27 / 6%, n=30), seq117 wt/risk (0%, n=21 / 0%, n=8), seq119 wt/risk (4%, n=27 / 14%, n=28) and seq790 wt/risk (0%, n=20 / 0%, n=14). Chi-square test: p<0,05 (*).



Supplementary Fig.11 –(A) Jaspar relative score prediction of differential Nkx6.1 binding in wt and risk variants (Score wt: 0,841219159; Score risk: 0,895818767). **(B)** **Left:** Graph representing the negative (*cryaa* promoter) and positive (*hnf1α* promoter) control regions used in ChIP, showing no enrichment and a higher enrichment in both alleles, respectively. **Right:** ChIP enrichment for Nkx6.1 in MIN6 stable lines with human seq119wt and seq119risk. Data are mean \pm SD. Mann Whitney test: p<0,05 (*). **(C)** Graph representing the number of differential predicted TFBS within the group of enhancers with (DEA) and without differential enhancer activity (NDEA). The two groups were compared by unpaired t-test. p<0,05.



Supplementary Fig.12 –(A) Sequence conservation of seq132 between human (top) and mouse (bottom). The seq132 and seq132mm are highlighted. **(B)** Genomic landscape of mouse gene *slc30a8* (blue) showing the 2 replicates from 4C performed in MIN6 cell line (black). The viewpoint, *Slc30a8* promoter, is represented in pink (asterisk).

Sequence	Coordinates (GRCh37/hg19)	SNP	wt/risk allele	P-value	Disease related	r2 from the lead SNP	Credible set SNPs (<80%PPA)(34)	Putative enhancer state (5)	Chromatin state (5)	TFBS (5)
seq58	chr6:37,775,193-37,776,330	rs5869265	C / A	2.00E-10 (Lead SNP)	Type 2 diabetes	1000 Genomes Project CEU $r^2 = 0.96$ (LD with rs9470794)	no	Weak	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq68	chr4:153,519,496-153,521,069	rs6813195	T / C	4.00E-14	Type 2 diabetes	Lead SNP	no	Weak	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq72	chr4:185,716,034-185,716,803	rs72695654	G / T	3.70E-06 (Lead SNP)	Fasting glucose and type 2 diabetes	1000 Genomes Project CEU $r^2 = 0.94$ (LD with rs735949)	no	Strong	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq73	chr4:185,715,954-185,716,970	rs735949	C / T	3.70E-06	Fasting glucose and type 2 diabetes	Lead SNP	no	Strong	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq117	chr3:123,065,139-123,066,383	rs11708067	G / A	5.00E-32	Type 2 diabetes Homeostasis model assessment of beta-cell function	Lead SNP	yes	Weak	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq119	chr3:170,716,833-170,718,562	rs11920090	A / T	8.00E-13	Type 2 diabetes	Lead SNP	no	Strong	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq132	chr8:118,183,960-118,185,784	rs13266634	T / C	1.00E-47	Type 2 diabetes	Lead SNP	yes	Weak	H3K27ac, H3K4me1, H2AZ	PDX1, NKX2.2, FOXA2, NKX6.1
seq219	chr7:15,063,701-15,064,872	rs2191349	G / T	3.00E-44	Fasting blood glucose and type 2 diabetes	Lead SNP	no	Other	H3K27ac, H3K4me1, H2AZ	MAFB, PDX1, NKX6.1
seq460	chr7:44,235,330-44,236,228	rs4607517	G / A	7.00E-92	Type 2 diabetes	Lead SNP	no	Strong	H3K27ac, H3K4me1, H2AZ	NKX2.2
seq790	chr10:1,14,757,655-11,759,128	rs7903146	C / T	6.00E-447	Peak insulin response	Lead SNP	yes	Strong	H3K27ac, H3K4me1	FOXA2,

PPA: Posterior probability of association

Supplementary Table 1 –List of the selected putative enhancer sequences. The respective coordinates, overlapping type 2 diabetes associated SNPs, wt and risk alleles, p-values, disease related, r2 from the lead SNP, chromatin states, and the overlapping TFBSs with strong ChIP-seq peak, are discriminated for each sequence. The SNPs that are part of the credible set are discriminated (31). The rs5869265 and rs72695654 are in high linkage disequilibrium (100 Genomes Project CEU $r^2 > 0.8$) with lead SNPs reported in GWAS catalog, being considered the risk alleles A and T respectively.

Supplementary Table 2 – Total list of the primers used in this study.

Seq58

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
NEUROD1	GAACAGATGGCAG	16,1826	9,90078	0,995050964	0,875148484	wt	1
BHLH15	CCATCTGT	11,6381	4,64482	0,963409531	0,832620322	wt	1
YY1	AAAGATGCCAG	6,93956	15,3079	0,825561041	0,946979791	risk	1
OLIG3	AACAGATGGC	9,28684	6,4711	0,898049606	0,851225106	wt	0
Tcf12	AACAGATGGCA	8,04759	0	0,893235401	0	wt	1
Gata4	TCTTTCTCCC	0	8,17506	0	0,889325094	risk	1
TCF4	GCCATCTGTT	5,89183	0	0,877538534	0	wt	1
Tcf3	GCCATCTGTT	6,89191	0	0,87692178	0	wt	0
GATA3	AGAAAAGA	0	6,5876	0	0,872653708	risk	1
GATA6	GGGGAAAAAGATG	0	8,71767	0	0,859319004	risk	1
Myc	CCATCTTTC	5,37231	0	0,853670959		wt	1
MAX	GAACAGATGG	4,81313	0	0,842786913	0	wt	1
HNF4G	GGAGAACAGATGGCA	6,94403	0	0,838750612	0	wt	0
Ascl2	GCCATCTGTT	7,3974	0	0,828244302	0	wt	1
Rxra	CAGATGGCAGC	4,30832	0	0,826386987	0	wt	0
Tfec	AACAGATGGC	6,42627		0,82423229		wt	0
RORC	AAAAAGATGGCA	0	6,31808	0	0,82119829	risk	1
TFAP4	AACAGATGGC	5,62338	0	0,818700149	0	wt	1
NFAT5	CTTTCTCCC	0	5,26747	0	0,817415415	risk	1
ZEB1	CATCTG	4,56217	4,38815	0,813430428	0,806522192	wt	0
HNF4A	CTGCCATCTGTTCTC	5,29646	0	0,805371839	0	wt	1
FOXO3	GGAGAACAA	6,25847	0	0,80235975	0	wt	1
ASCL1	AGAACAGATGGCA	5,9011	0	0,800782542	0	wt	1

Seq68

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
NFIX	TGCGGAAG	0	5,48411	0	0,874615693	risk	1
NFE2L2	GTGATGCAGCA	10,8334	8,37657	0,870973071	0,80990749	wt	1
Rxra	GCAAGGCCAGT	6,28014	6,28014	0,854789085	0,854789085	wt	0
CEBPA	GCTGCATCACT	2,70475	0,579997	0,830392604	0,804937845	wt	1
Mafb	GCTGCATC	5,51425	0	0,827417498	0	wt	1
Esrng	GCAAGGCCAG	4,14226	4,14226	0,817111519	0,817111519	wt	1
MEIS1	TTGCCGC	1,59862	0	0,814599111	0	risk	1
JUNB	CA GTGATGCAG	1,88779	0	0,814286261	0	wt	1
JUND	AGTGTGCGAC	0,248792	0	0,80933893	0	wt	1
ETS1	CTTGCT	3,65816	0	0,809079322	0	wt	1
HOXA2	CCGCATCACT	3,35648	0	0,806317854	0	risk	1
CEBPB	CCTTGCTGCAT	-1,54594	0	0,803734637	0	wt	1
NR2F2	GCAAGGCCAGT	5,97343	5,97343	0,802707635	0,802707635	wt	1

Seq73

TF	Binding site	Score WT	Score risk	Relative score WT	Relative score risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
FOXH1	ACAAATACACA	11,5433	3,03764	0,93501129	0,815358964	wt	0
FOXD2	ACAAACAA	6,94322	8,35322	0,900266554	0,930169815	risk	1
FOXP3	ACAAACAA	6,1809	8,5041	0,8711956	0,929646506	risk	0
NR3C1	GGAAACATGTGTATT	13,3344	10,1148	0,91454486	0,874464368	wt	0
FOXL1	TACAAATA	6,4764	0	0,898546012	0	wt	0
FOXO6	ATACACA	5,96965	0	0,875240106	0	wt	1
Foxa2	CAATGTGTATT	9,70117	9,54966	0,872638676	0,868758253	wt	1
NR3C2	TGGAACAAATGTGTATT	10,3632	7,05619	0,87035699	0,839105275	wt	1
FOXO4	ATACACA	6,0096	0	0,867463112	0	wt	1
FOXC1	AAATGTGTA	5,08571	0	0,866539251	0	wt	1
Neurog1	ACAAATGTGT	5,67924	6,96099	0,834583127	0,864345402	risk	0
Foxd3	CAATGTGTGT	8,6765	9,20803	0,842668731	0,853272957	risk	0
Foxq1	CAATGTGTATT	9,6916	0	0,850163839	0	wt	1
FOXG1	ATACACAT	5,92499	0	0,846162563	0	wt	0
HOXA5	CACACATT	0	5,42911	0	0,844085516	risk	1
Myc	CAATGTGTAT	4,1004	3,5073	0,835002487	0,826297332	wt	1
FOXK2	AAATACACATT	7,11292	0	0,831751967	0	wt	1
MEF2C	TTCCTACAAATACAC	7,22312	0	0,829959064	0	wt	0
NEUROD2	TACACATTGT	3,81787	0	0,827157388	0	wt	0
ZNF354C	ATACAC	4,82832	0	0,821096857	0	wt	1
Foxj2	ATACACAT	4,5094	0	0,81784419	0	wt	1
NKX2-8	GTATTTGTA	2,43163	0	0,814510374	0	wt	0
STAT1	AAATTCCTACAAACA	7,88368	7,97238	0,808911597	0,81034354	risk	1

Seq132

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
Tcf3	CCCAAGCTGGCT	12,555	0	0,952250391	0	wt	0
TCF4	CCCAAGCTGGC	8,45918	0	0,916803022	0	wt	1
Myog	GCCAGCTGGGA	8,92548	0	0,913604247	0	wt	0
Myod1	CCCAAGCTGGTGC	8,713	0	0,902220172	0	wt	1
FIGLA	CCCAAGCTGGC	8,92208	0	0,893885428	0	wt	0
Tcf12	GCCAGCTGGGA	7,86887	0	0,890740198	0	wt	1
PAX5	ACAGCACGCCAGCGGGGA	11,2341	13,7514	0,858808679	0,888219183	risk	1
TFAP2A	GCCAGCCGG	0	6,77176	0	0,881869392	risk	1
NEUROD1	AGCCAGCTGGGAC	9,74202	0	0,872118038	0	wt	1
Pax2	TGTCCTCGG	0	5,41577	0	0,85666724	risk	1
RBPJ	GCTGGACAG	6,29924	0	0,855183015	0	wt	1
Neurog1	GCCAGCTGGG	6,37768	0	0,850800832	0	wt	0
ASCL1	CAGCCAGCTGGGA	8,27687	0	0,840690936	0	wt	1
PAX9	TGTCCCCGCTGGCTGCT	0	8,50939	0	0,831403104	risk	0
TFAP4	GCCAGCTGGG	6,30787	0	0,829728315	0	wt	1
STAT3	CAGCTGGGACA	1,32493	0,586987	0,813605668	0,804665821	wt	1
ZBTB18	CAGCCAGCTGGGA	4,742	0	0,812298861	0	wt	1
Atoh1	GCCAGCTGGG	4,69235	0	0,810347344	0	wt	0
NHLH1	GCCAGCTGGG	5,58268	0	0,809935213	0	wt	0
MYB	CCCAGCTGGC	3,78195	0	0,808536243	0	wt	1
Ascl2	GCCAGCTGGG	6,17312	0	0,803928059	0	wt	0
TFDP1	AGCGGGACAG	0	6,17637	0	0,803288255	risk	1
SP1	CCGGCTGGCT	0	6,14518	0	0,801216595	risk	1

Seq219

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
FOXC1	atcatgt	5,4601	0	0,887481988	0	WT	1
GRHL2	gtaaaggatgttaa	12,4502	10,9803	0,879806296	0,853364284	WT	1
Pax2	gatcgat	5,84664	5,00666	0,87358725	0,840602054	WT	1
Lhx4	tcatttaa	0	6,2302	0	0,867647007	Risk	0
HLF	tcttacatgtac	7,1943	0	0,863221714	0	WT	1
DBP	gatcgatgttga	6,09006	0	0,860332187	0	WT	1
TEF	tcttacatgtac	6,74804	0	0,857210797	0	WT	1
JUNDvar.2	aaggatcgatgttga	4,87603	0	0,847713259	0	WT	1
VAX2	taataatgt	0	5,7904	0	0,84714633	Risk	1
HOXB3	gatccatttaa	0	4,82217	0	0,84610076	Risk	1
ISL2	tcattttaa	0	5,93316	0	0,841852634	Risk	1
HOXB2	gatccatttaa	0	5,00057	0	0,840874055	Risk	1
JUN	aggatcgatgttga	4,85199	0	0,840563509	0	WT	1
Dlx4	tcatttaa	0	4,9254	0	0,839239544	Risk	1
NFIL3	tcatgttggac	8,83467	0	0,83897551	0	WT	1
Pax6	ttaaggatcatt	0	10,9967	0	0,837270028	Risk	1
GSC	catgttcctt	5,76966	5,16334	0,830352106	0,817054565	WT	1
NKX6-1	tcatttaa	0	4,26911	0	0,829643585	Risk	1
Arid3a	attttaa	0	5,399	0	0,826577908	Risk	1
Arid3b	gtctttaaaatgttga	0	6,72959	0	0,822961343	Risk	1
Bhlhe40	cttacatgtac	2,91117	0	0,822486649	0	WT	1
LIN54	tcttaaatgt	0	4,2698	0	0,822270435	Risk	1
LBX2	atcattttaatgt	0	5,41535	0	0,821581912	Risk	1
VENTX	atcattttaa	0	3,33065	0	0,8214111748	Risk	0
ATF4	ggatcgatgttga	6,64264	0	0,813569591	0	WT	1
HOXA2	gatccatttaa	0	3,5678	0	0,811095483	Risk	1
Prrx2	tcatttaa	0	4,52469	0	0,804040681	Risk	0
FOXD2	ttaaatgt	0	2,29556	0	0,801698956	Risk	1
HLTF	gatccatttaa	0	3,40649	0	0,800223744	Risk	1

Seq460

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
Pax2	Tgtcaact	5,06043	8,09328	0,842713818	0,96180982	risk	1
ISL2	tcactcaa	0	6,74948	0	0,863090898	risk	0

Seq72

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter - 1; inactive promoter - 0)
NR2F2	TAAAGGTCACT	0	13,5291	0	0,966059123	risk	1
Esmg	TAAAGGTCACT	4,04628	11,8595	0,815699532	0,930637668	risk	1
Rxra	TAAAGGTCACT	2,70904	10,9064	0,803350977	0,921424841	risk	1
ESRRa	TAAAGGTCACT	7,2383	12,6831	0,806915622	0,912014985	risk	1
RORA	CTAACGGTCA	0	10,643	0	0,89723706	risk	1
NR2F1	TAAAGGTCACTAC	0	10,2106	0	0,884776523	risk	0
HNF4A	GTGACCTTTAGCTTT	6,26925	10,1082	0,818320526	0,8694205	risk	1
NR1H4	GTAGTGACCTT	0	9,93038	0	0,869246518	risk	1
Nr5a2	AAGCTAAAGGTCACT	0	11,4836	0	0,859419351	risk	1
HNF4G	AAAAGCTAAAGGTCC	8,22637	0	0,855273743	0	wt	0
Pax2	GGTCACTA	0	5,01899	0	0,841086371	risk	1
Nr2f6	AAAGCTAAAGGTCA	0	11,6441	0	0,834649752	risk	1
MNX1	GGTCACTACA	0	4,34715	0	0,808772596	risk	1
FOXA1	TCTGTAGTAGCCTT	0	0,795672	0	0,800124752	risk	1

Seq117

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter -1; inactive promoter -0)
VDR	AGAGTCGA	0	7.57674		0	0.879535949	risk
CEBPA	AGTGCAAAATC	0	6.16935		0	0.871898783	risk
ISL2	GCACTTA	0	7.04119		0	0.870680299	risk
CEBPB	GAGTGCAAAAT	0	3.95144		0	0.861358913	risk
NFAT5	ATTTGCACT	0	6.443		0	0.841377938	risk
NFATC2	TTTGC	0	6.9943		0	0.838994417	risk
NFIA	AGTGCAAAAT	0	2.84446		0	0.835788317	risk
E2F3	AATAGAGCGAAAAATC	8.24254	0	0.81806109	0	wt	1
ETS1	TTTGC	3.82245	0	0.816657782	0	wt	1
Gnbe1	GATTGGCGCTCTATTA	6.63759	0	0.815722909	0	wt	0
NFATC1	ATTTGCACT	5.28505	5.80683	0.800501023	0.815372467	risk	1
NFATC3	ATTTGCACT	0	5.89827	0	0.808852865	risk	1
E2F4	GAGCGAAAAAT	3.48749	0	0.800038631	0	wt	1

Seq119

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter -1; inactive promoter -0)
Prrx2	AATTA	5.58756	9.12437	0.838048459	0.999999981	Risk	0
Dlx4	TCAATTAT	5.68314	9.4114	0.859912623	0.961628714	Risk	1
HESX1	GATAATTGAA	3.34856	11.3415	0.805953711	0.959513688	Risk	0
MIXL1	TTCATTATTC	4.90977	9.55679	0.832996443	0.953935619	Risk	1
LBX2	TTCATTATTC	0	9.14439		0	0.924059323	Risk
VSX1	TCAATTAT	0	8.95335		0	0.920612325	Risk
HOXB2	TTCATTATTC	3.45078	7.73966	0.800614667	0.912028513	Risk	1
HOXB3	TTCATTATTC	4.07366	7.50279	0.828678707	0.908536693	Risk	1
VAX2	TCAATTAT	0	8.10382		0	0.908303252	Risk
HOXA2	TTCATTATTC	0	7.57297		0	0.901646588	Risk
NKX8-1	ATAATTGA	4.8019	7.31493	0.841219159	0.895818767	Risk	1
Lhx4	ATAATTGA	4.70094	7.41615	0.832474118	0.894923879	Risk	1
VENTX	TTCATTAT	3.25782	6.81217	0.820202239	0.879232284	Risk	0
VDR	TTGGTCA	0	7.43784	0	0.875575509	Risk	1
CEBPA	ATTGTATAATA	5.53487	4.87453	0.864297673	0.856386755	WT	1
HNF4G	AATTATCAAATTCCA	6.645	7.40642	0.834897627	0.8440708587	Risk	0
LHX6	GATAATTGAA	0	5.571	0	0.844078596	Risk	1
RHOXF1	TTGACCA		1.90526	0.803733662	0.841008099	Risk	0
SRF	AGAACCAAAATAGGCC	10.146	9.09013	0.840880715	0.828168717	WT	1
BARHL2	AATTATCAA	0	2.50809	0	0.813281927	Risk	0
PDX1	ATAATTGA	2.24364	2.26688	0.809382437	0.809847369	Risk	1
MNX1	AATTATCAA	0	4.32515	0	0.808268525	Risk	1

Seq790

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity allele	Expression in endocrine pancreas (active promoter -1; inactive promoter -0)
DBP	aattatataata	5.55267	13.7444	0.853285763	0.960698744	risk	1
HLF	aattatataata	0	12.8054	0	0.9512252	risk	1
TEF	aattatataata	5.72107	12.4399	0.84390711	0.93094498	risk	1
NFIL3	ttatataataat	8.52783	11.927	0.831126032	0.918084591	risk	0
CEBPB	attatataat	0	6.37874	0	0.871215647	risk	1
CEBD	attatataat	0	6.29609	0	0.861146811	risk	1
ZEB1	gcacagctg	5.88416	0	0.845306775	0	wt	1
CEBPA	attatataata	0	3.35271	0	0.838155202	risk	1
Arid3a	tatata	0	5.399	0	0.826577908	risk	1
Prrx2	tatta	0	4.91772	0	0.825515567	risk	1
HOXB3	agatatata	0	3.83659	0	0.823157828	risk	1
CEBPG	attatataat	0	3.26846	0	0.817915184	risk	1
TEAD1	tagatactat	4.39783	0	0.812735256	0	wt	1
Dlx4	gatattat	0	3.50408	0	0.800462443	risk	1

Seq132wt vs seq132PDX1

TF	Binding site	Score WT	Score Risk	Relative score WT	Relative score Risk	Highest affinity binidig site	Expression in endocrine pancreas (active promoter - 1; inactive promoter -0)
Pdx1	CTAATG	8.72988		0	0.965432864	0	
HOXB3	ACACATTAGG	8.23982		0	0.925700529	0	PDX1 A 1
HOXB2	ACACATTAGG	7.39411		0	0.90305208	0	PDX1 A 1
HOXA2	ACACATTAGG	7.13602		0	0.891767719	0	PDX1 A 1
HLTF	ACACATTGGG	0	5.99807	0	0.891560658	No PDX1 G	1
VENTX	ACACATTAG	7.26487		0	0.886750634	0	PDX1 A 0
Sox17	CACATTGGG	0	7.40552	0	0.862559299	No PDX1 G	0
NF1X	GCAGCCCCAA	0	4.44073	0	0.850051973	No PDX1 G	1
Prrx2	CATTA	5.34257	0	0.843137572	0	PDX1 A	1
Neurog1	CCAATGTGTT	0	5.87923	0	0.839227048	No PDX1 G	0
Lhx4	CACATTAG	4.50603	0	0.827991314	0	PDX1 A	1
VAX2	CACATTAG	4.94313	0	0.824748192	0	PDX1 A	1
MAX	TAACACATTG	0	3.37815	0	0.822677822	No PDX1 G	1
NFIC	TGGCCT	0	4.18303	0	0.81530306	No PDX1 G	1
Dlx4	CACATTAG	3.95614	0	0.812795645	0	PDX1 A	1
Sox6	CCAATGTGTT	0	5.08245	0	0.811390272	No PDX1 G	1
TFEC	AACACATTAG	5.78176	0	0.806881079	0	PDX1 A	0
THAP1	CAGCCCAAT	0	4.49031	0	0.805059037	No PDX1 G	1
RUNX1	TAATGTGTTAT	6.66952	0	0.802184621	0	PDX1 A	0

Supplementary Table 3 – List of the predicted TFBS for pancreatic TFs. The wt and risk alleles were analyzed using 719 specific position weight matrices for TFs in vertebrates. The score and relative score are represented for each allele pair. In each row, the allele for which the TF is predicted to bind preferentially is discriminated. Included also, are the seq132wt and seq132wtPDX1, where the nucleotide change resides in a putative binding site for PDX1.

Wt /risk sequences alignments

Seq58

Query = wt

Sbjct = risk

Query 1	CTCTGAGAAGGAAATTGAACGCAATAGTTGAATTCTCAATGTTCATGTTCCCCGTA	60
Sbjct 1	CTCTGAGAAGGAAATTGAACGCAATAGTTGAATTCTCAATGTTCATGTTCCCCGTA	60
Query 61	TGTGCGTGCGCATGCACATATAAACACATCTAGCTTCACACCTGTGTACTCACACCTG	120
Sbjct 61	TGTGCGTGCGCATGCACATATAAACACATCTAGCTTCACACCTGTGTACTCACACCTG	120
Query 121	TGTGTACACACTCCTCCTGTACATGTGTACACGCACACCCTCCCACCGCATGAGCAG	180
Sbjct 121	TGTGTACACACTCCTCCTGTACATGTGTACACGCACACCCTCCCACCGCATGAGCAG	180
Query 181	TATGTGGATTTTCTTCCAGCAGCCCTTCAAGAACATACACAGATGGGATTGGGTCT	240
Sbjct 181	TATGTGGATTTTCTTCCAGCAGCCCTTCAAGAACATACACAGATGGGATTGGGTCT	240
Query 241	GCTACATGACTGAGCAGCCCCACATCAGAAAGTCATCATCATTGAATCCATCATGTGGT	300
Sbjct 241	GCTACATGACTGAGCAGCCCCACATCAGAAAGTCATCATCATTGAATCCATCATGTGGT	300
Query 301	GCAGCCTTGGCAAGGGCACAGCTCCTCGTCTGCCAATGGGCCGTGGAGGAATGCCCTC	360
Sbjct 301	GCAGCCTTGGCAAGGGCACAGCTCCTCGTCTGCCAATGGGCCGTGGAGGAATGCCCTC	360
Query 361	TCCTCCAGAGCAGAGAGCAGATATGGCAGGCAGTTGCCAGGCAGTTGAGCCGGAGAA	420
Sbjct 361	TCCTCCAGAGCAGAGAGCAGATATGGCAGGCAGTTGCCAGGCAGTTGAGCCGGAGAA	420
Query 421	AGATGGCAGCTGCACAGCCTCTTAGCCCAGTTCCCTGGCTGCCGGGAAGGAGTTGC	480
Sbjct 421	AGATGGCAGCTGCACAGCCTCTTAGCCCAGTTCCCTGGCTGCCGGGAAGGAGTTGC	480
Query 481	AGGCGGCAAGGATCCTGCAGAAACGCCCTCCCTATAACAGGCCATCTGCCCTATCC	540
Sbjct 481	AGGCGGCAAGGATCCTGCAGAAACGCCCTCCCTATAACAGGCCATCTGCCCTATCC	540

Query 541 TCTTACTGGGCTTGGAGGTCCAATCCTGCCCTGGTCACCACCTGTGTGGCTTACCAA 600
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TCTTACTGGGCTTGGAGGTCCAATCCTGCCCTGGTCACCACCTGTGTGGCTTACCAA 600

Query 601 GCTGTGCAACTGGGGCAGGATGAATATCCTGAGTGCTGGTACTAGAACTCTAATTCTCT 660
||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 GCTGTGCAACTGGGGCAGGATGAATATCCTGAGTGCTGGTACTAGAACTCTAATTCTCT 660

Query 661 AATCTCAGTTAACCTCAAGTCTGCTCCTTACTCCTAACAGAACACTAGCCTTA 720
||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 AATCTCAGTTAACCTCAAGTCTGCTCCTTACTCCTAACAGAACACTAGCCTTA 720

Query 721 CCTGATTAATCATGACCTTAGGAAGAAACCCCTGGATAATTTAGCAAATATCACATCTC 780
||||||||||||||||||||||||||||||||||||||||||||
Sbjct 721 CCTGATTAATCATGACCTTAGGAAGAAACCCCTGGATAATTTAGCAAATATCACATCTC 780

Query 781 TCAAATCTACACACACACATTGTCCTCAGGTAGGAGACACTGTAGATGCCAGTCTGGT 840
||||||||||||||||||||||||||||||||||||||||
Sbjct 781 TCAAATCTACACACACACATTGTCCTCAGGTAGGAGACACTGTAGATGCCAGTCTGGT 840

Query 841 CCGTATCCCTCAGCCCTTACCACTTCAGTGATCCCACCAAATTCAAATGGCCCGTCTCG 900
||||||||||||||||||||||||||||||||||||||||
Sbjct 841 CCGTATCCCTCAGCCCTTACCACTTCAGTGATCCCACCAAATTCAAATGGCCCGTCTCG 900

Query 901 CATGTCTTGCCCTGAGGGTTTCTCTGAAACCAGAGAACGCTGTTTGCCTGCAAAGGCA 960
||||||||||||||||||||||||||||||||||||
Sbjct 901 CATGTCTTGCCCTGAGGGTTTCTCTGAAACCAGAGAACGCTGTTTGCCTGCAAAGGCA 960

Query 961 GGCTGAAGTGCAATGATCTATGTCAACTATTGATGGAAGTGGGTATATAAAACTCAGTGT 1020
||||||||||||||||||||||||||||||||
Sbjct 961 GGCTGAAGTGCAATGATCTATGTCAACTATTGATGGAAGTGGGTATATAAAACTCAGTGT 1020

Query 1021 GCCACCTCCCCGACTCCTCAGATGGATGGCTTAATGTGAGGTTT 1068
||||||||||||||||||||||||||||
Sbjct 1021 GCCACCTCCCCGACTCCTCAGATGGATGGCTTAATGTGAGGTTT 1068

Seq68

Query = wt

Sbjct = risk

Query 541 AAATTTAAAATTCTGGTTCATGATTCTATATTGCAAATGAGGAAATGAGGTGCAAAGG 600
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 AAATTTAAAATTCTGGTTCATGATTCTATATTGCAAATGAGGAAATGAGGTGCAAAGG 600

Query 601 CGTTTAAATGCC█ACTCCAAGTTCAAAAAGTGATATTACAGCAGGATTAAGCTCAAATCG 660
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 CGTTTAAATGCC█ACTCCAAGTTCAAAAAGTGATATTACAGCAGGATTAAGCTCAAATCG 660

Query 661 AAGCCTCCTGGTTCCTAGCATAGTAGCTAGGCCAAACAAAGCCAGTCAGAAGGTTAAGG 720
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 AAGCCTCCTGGTTCCTAGCATAGTAGCTAGGCCAAACAAAGCCAGTCAGAAGGTTAAGG 720

Query 721 GGAATTAAATTGCAATAAAATACATCAACAGCAAAAGGGAGAGGAAGCAAGTAAACAA 780
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 721 GGAATTAAATTGCAATAAAATACATCAACAGCAAAAGGGAGAGGAAGCAAGTAAACAA 780

Query 781 GAACTGATGCTGTAAATACTGGCCTTGC█GCATCACTGGCTAGACAGAGCAGGAGTGTGG 840
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 781 GAACTGATGCTGTAAATACTGGCCTTGC█GCATCACTGGCTAGACAGAGCAGGAGTGTGG 840

Query 841 TTGCCATGGTAATGCAACC ACTGAGTCCTGAGGTTTTAAAAAATTGCAGATCAGGT 900
|||||||||||||||||||||||||||||||||||||||||||
Sbjct 841 TTGCCATGGTAATGCAACC ACTGAGTCCTGAGGTTTTAAAAAATTGCAGATCAGGT 900

Query 901 GCAGTGGCTCATGCCTGTAATCCCAGCACTTGGAGACCGAGGTGGACAGATTGCCTGA 960
|||||||||||||||||||||||||||||||||||||||||||
Sbjct 901 GCAGTGGCTCATGCCTGTAATCCCAGCACTTGGAGACCGAGGTGGACAGATTGCCTGA 960

Query 961 GTTCAGGAGTTCAAGACCAGCCTGGCAACATGACAAA ACTCTGTCTCCACAAAAAATAC 1020
|||||||||||||||||||||||||||||||||||||||
Sbjct 961 GTTCAGGAGTTCAAGACCAGCCTGGCAACATGACAAA ACTCTGTCTCCACAAAAAATAC 1020

Query 1021 AAAAATTAAACCGGGCATGGTGGTACATGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGC 1080
|||||||||||||||||||||||||||||||||||||||||||
Sbjct 1021 AAAAATTAAACCGGGCATGGTGGTACATGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGC 1080

Query 1081 ACGAGAATCACTGAAACCCGGGAGGCAGAGGTTGCACTGAGCTGAGATCATGCCACTGCA 1140
|||||||||||||||||||||||||||||||||||||||

Sbjct 1081 ACGAGAATCACTTGAACCCGGGAGGCAGAGGTTGCACTGAGCTGAGATCATGCCACTGCA 1140

Query 1141 TCCTGGACAGGGTACAGGGTAAGAGACCCCTGCCTCCAAAAGAAAAAAAAAGAAA 1200
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1141 TCCTGGACAGGGTACAGGGTAAGAGACCCCTGCCTCCAAAAGAAAAAAAAAGAAA 1200

Query 1201 AAGCAAAAAATGTTAAATATCTCTAACCTTAAGTGAACGGATGGGAGGTGTTAAAATG 1260
|||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1201 AAGCAAAAAATGTTAAATATCTCTAACCTTAAGTGAACGGATGGGAGGTGTTAAAATG 1260

Query 1261 GCCAAGAGGCCCTGTCTGATTCACTGTGGCATTCACTCAGTCAGGACAGCCACTAGAA 1320
|||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1261 GCCAAGAGGCCCTGTCTGATTCACTGTGGCATTCACTCAGTCAGGACAGCCACTAGAA 1320

Query 1321 ATAAGCCATGGCTCTAGATGCAATCTGAGTTGC 1353
|||||||||||||||||||||||||

Sbjct 1321 ATAAGCCATGGCTCTAGATGCAATCTGAGTTGC 1353

Seq72

Query = wt

Sbjct = risk

Query 1 TTGCAAAACATCTCATCACAGAAAAAAATCAGCTGACCACAAACCCGCTCAATGAA 60
|||||||||||||||||||||||||||||||||||||

Sbjct 1 TTGCAAAACATCTCATCACAGAAAAAAATCAGCTGACCACAAACCCGCTCAATGAA 60

Query 61 AGGGAAGAAAATTGAAAGTCACAATGTCCAATTCTACAAACACACATTGTTCCAGAAA 120
|||||||||||||||||||||||||||||

Sbjct 61 AGGGAAGAAAATTGAAAGTCACAATGTCCAATTCTACAAACACACATTGTTCCAGAAA 120

Query 121 ATAGGACTGCCGTAGAAATTACATGCCAACCATTTGAATATACAAGGCATCTGCTTCA 180
|||||||||||||||||||||||||||||

Sbjct 121 ATAGGACTGCCGTAGAAATTACATGCCAACCATTTGAATATACAAGGCATCTGCTTCA 180

Query 181 CTTCTGCCTAGTTCAAAGGGAGCCACATTCCCATCTACTACCTTGGTCAGCTTGGAC 240
|||||||||||||||||||||||||||||

Sbjct 181 CTTCTGCCTAGTTCAAAGGGAGCCACATTCCCATCTACTACCTTGGTCAGCTTGGAC 240

Query 241 AATGGGTGCTGAAGGTGTTTGTCAGAAAACACAGCCTACGCTGGCATTTCATTGG 300
|||||||||||||||||||||||||||||

Sbjct 241 AATGGGTGCTGAAGGTGTTTGTCAGAAAACACAGCCTACGCTGGCATTTCATTGG 300

```

Query  301  CACCAGTTGGTCCATCTGGCTATTTAACATAAGTAAATTACAGCACGCATTC  360
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CACCAGTTGGTCCATCTGGCTATTTAACATAAGTAAATTACAGCACGCATTC  360

Query  361  GTCCTTATGCGTTCTGTCAACACGTTCTGTTAATGAAGCCTGTGAGAACG  420
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTCCTTATGCGTTCTGTCAACACGTTCTGTTAATGAAGCCTGTGAGAACG  420

Query  421  ACATCATTTGACAAAATCAAATTGTGTTTCAGACCTGCTTATCATATTCCAT  480
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACATCATTTGACAAAATCAAATTGTGTTTCAGACCTGCTTATCATATTCCAT  480

Query  481  TCTGTAG[GACCTTAGCTTTCTGGTAAAGAGAGCCTGGAAATAGTTTTAA  540
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TCTGTAG[GACCTTAGCTTTCTGGTAAAGAGAGCCTGGAAATAGTTTTAA  540

Query  541  ATATAACAATCAACCTTTCTTAAATTCTAACGCCAGGCACTTAATACTCCTG  600
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ATATAACAATCAACCTTTCTTAAATTCTAACGCCAGGCACTTAATACTCCTG  600

Query  601  GGCCTGGCTTGGCATAAAGATCAGAAACTCTGCCTCAGTTCTCACCTG  651
|||||||||||||||||||||||||||||||||||||||||||
Sbjct  601  GGCCTGGCTTGGCATAAAGATCAGAAACTCTGCCTCAGTTCTCACCTG  651

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Seq73

Query = wt

Sbjct = risk

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Query  1    TCACCTGTGCCTGGCTGGTTCTGATTTCAACACTTGCTCTAACCTCAGAACCT  60
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Sbjct  1    TCACCTGTGCCTGGCTGGTTCTGATTTCAACACTTGCTCTAACCTCAGAACCT  60

Query  61    TTTTCTTTCTTCATTCTAGTCCATCTCCAGTTCCAACCTCCGGCTCCACTATCCCA  120
|||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTTTCTTTCTTCATTCTAGTCCATCTCCAGTTCCAACCTCCGGCTCCACTATCCCA  120

Query  121   GAGGATTGCTGAAGAGGGACGGGGTAGGGTAGGAGGCTGACACGGTACTTCGCAAAA  180
|||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGGATTGCTGAAGAGGGACGGGGTAGGGTAGGAGGCTGACACGGTACTTCGCAAAA  180

Query  181   CATCTCATCACCAGAAAAAAATCAGCTGACCACAAACCCGCCTCAATGAAAGGAAGAA  240
|||||||||||||||||||||||||||||||||||||||
Sbjct  181   CATCTCATCACCAGAAAAAAATCAGCTGACCACAAACCCGCCTCAATGAAAGGAAGAA  240

Query  241   AATTGAAAGTCACAATGTCAAATTCTACAAA[ACACATTGTTCCAGAAAATAGGACTG  300
|||||||||||||||||||||||||||||||||||

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|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241 AATTTGAAGTCACAATGTCCAATTCTACAA[REDACTED]ACACATTGTTCCAGAAAATAGGACTG 300

Query  301 CCCGTAGAAATTACATGCCAACCATTTGAATATAAAGGCATCTGCTTCACTTCTGCCT 360
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301 CCCGTAGAAATTACATGCCAACCATTTGAATATAAAGGCATCTGCTTCACTTCTGCCT 360

Query  361 AGTTCAAAGGGAGGCCACATTCCCACACTACCTTGGTCAGCTTGGACAATGGGTGC 420
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361 AGTTCAAAGGGAGGCCACATTCCCACACTACCTTGGTCAGCTTGGACAATGGGTGC 420

Query  421 TGAAGGTGTTTGTCAGAACACAGCCTACGCTGGTCATTTTCATTGGCACCGATTG 480
|||||||||||||||||||||||||||||||||||||||||||
Sbjct  421 TGAAGGTGTTTGTCAGAACACAGCCTACGCTGGTCATTTTCATTGGCACCGATTG 480

Query  481 GTTCCATCTGGCTATTTAACATAAGTAAATATTACAGCACGCATTCGTCTTAT 540
|||||||||||||||||||||||||||||||||||||||
Sbjct  481 GTTCCATCTGGCTATTTAACATAAGTAAATATTACAGCACGCATTCGTCTTAT 540

Query  541 GCGTTCTGTCATCAAACACGTTCTGTAAATGAAGCCTGTGAGAACGACATCATT 600
|||||||||||||||||||||||||||||||||||||||
Sbjct  541 GCGTTCTGTCATCAAACACGTTCTGTAAATGAAGCCTGTGAGAACGACATCATT 600

Query  601 GTACAAAATCAAATTGTGTTTCAGACCTGTTATCATATTCCCTA[REDACTED]GTATCTGTAGGG 660
|||||||||||||||||||||||||||||||||||||||
Sbjct  601 GTACAAAATCAAATTGTGTTTCAGACCTGTTATCATATTCCCTA[REDACTED]GTATCTGTAGGG 660

Query  661 ACCTTAGCTTTCTCCTGGTAAAGAGAGCCGGAAATAGTTTAAATATAACAA 720
|||||||||||||||||||||||||||||||||||
Sbjct  661 ACCTTAGCTTTCTCCTGGTAAAGAGAGCCGGAAATAGTTTAAATATAACAA 720

Query  721 TCAACCTCTTCTTAAATTCTAACGCCAGGCACCTAACACTCCTGTGGCTGGTC 780
|||||||||||||||||||||||||||||||||||
Sbjct  721 TCAACCTCTTCTTAAATTCTAACGCCAGGCACCTAACACTCCTGTGGCTGGTC 780

Query  781 TTGGCATAAAGATCAGAAACTCTGCCTTCAGTTCTCACCTGCAGGCCACCCAC 835
|||||||||||||||||||||||||||||||||||
Sbjct  781 TTGGCATAAAGATCAGAAACTCTGCCTTCAGTTCTCACCTGCAGGCCACCCAC 835

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Seq117

Query = wt

Sbjct = risk

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Query  1      CTTCCCGGATGTGGAGATTCAAGCCAGGGCAGCCTTCTGGAGACCAAGGTGACTG 60
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Sbjct	1	CTTCCCGGATGTGGAGATTCAGCCAGGGCAGCCTCTCCTGGGAGACCAAGGTGACTG 60
Query	61	CTGCCTACACTGTCCCTACCTGACAGAGAACGATGGGGGTTGGGAGACCCCCAAACTG 120
Sbjct	61	CTGCCTACACTGTCCCTACCTGACAGAGAACGATGGGGGTTGGGAGACCCCCAAACTG 120
Query	121	GGGGCCAATGTGTTATGCAGATAACATGTCCTCTAAAGGCTTAGAGTCTCAGTTTGAG 180
Sbjct	121	GGGGCCAATGTGTTATGCAGATAACATGTCCTCTAAAGGCTTAGAGTCTCAGTTTGAG 180
Query	181	AGACAGATGGAAGACATGCAGTCAGGATCCACAGTCTGGATCCCAGGGCAGACTGGGA 240
Sbjct	181	AGACAGATGGAAGACATGCAGTCAGGATCCACAGTCTGGATCCCAGGGCAGACTGGGA 240
Query	241	ACTGGGCAGTTCTCATTCTGCCTGAAGAAAACAGTGCTCCCTACCCCTACTGCTGTCA 300
Sbjct	241	ACTGGGCAGTTCTCATTCTGCCTGAAGAAAACAGTGCTCCCTACCCCTACTGCTGTCA 300
Query	301	GCCTCACCTGTGTGTATGTGTGT 360
Sbjct	301	GCCTCACCTGTGTGTATGTGTGT 360
Query	361	GTGTGTGAGAGAGAGAGATAATTGCACTATTCACCTAATCACTTCTTGAAAACGCAG 420
Sbjct	361	GTGTGTGAGAGAGAGAGATAATTGCACTATTCACCTAATCACTTCTTGAAAACGCAG 420
Query	421	GCCAAGCCTCCAAAGAGTCCTTTACACCAACCTCAGAGGACTCGTAGTCCTAGGGAA 480
Sbjct	421	GCCAAGCCTCCAAAGAGTCCTTTACACCAACCTCAGAGGACTCGTAGTCCTAGGGAA 480
Query	481	ACTTGCTGGGAGAAGGAACTCTCGGAAGGAAACACAGCAGCTCTTTCTGGCAT 540
Sbjct	481	ACTTGCTGGGAGAAGGAACTCTCGGAAGGAAACACAGCAGCTCTTTCTGGCAT 540
Query	541	ATGGGAGGATTATCAGGCTCTCAGGAAGGCCATGCTGGATGAAGGCCACTGTATCGCTTC 600
Sbjct	541	ATGGGAGGATTATCAGGCTCTCAGGAAGGCCATGCTGGATGAAGGCCACTGTATCGCTTC 600
Query	601	GTGTCCCCGTGGAACTCATAAGCAGATTTGCCTCTATTAAATCTACATCTGTTGCACG 660
Sbjct	601	GTGTCCCCGTGGAACTCATAAGCAGATTTGCCTCTATTAAATCTACATCTGTTGCACG 660
Query	661	TCCCTGCTGTCAAGCAGCTCTGTCTAGGGAGGCGCAAACACGCAGTGAAAGGAGCGTGG 720
Sbjct	661	TCCCTGCTGTCAAGCAGCTCTGTCTAGGGAGGCGCAAACACGCAGTGAAAGGAGCGTGG 720

```

Query 721 GCTCTGGAGCGGCCACTTGGGTGCAGCCTGGCTGTACCACTGCTGGCTGGGACCTTGA 780
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 721 GCTCTGGAGCGGCCACTTGGGTGCAGCCTGGCTGTACCACTGCTGGCTGGGACCTTGA 780

Query 781 GCCCTTGAGTCTTTAATCTAGAACATGCCATCCCCACCCCTTTCTTCATGACTGG 840
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 781 GCCCTTGAGTCTTTAATCTAGAACATGCCATCCCCACCCCTTTCTTCATGACTGG 840

Query 841 CTTTTAAAGAGTACACAATGTAGACTGTCCCACGTTCTGGATTGTCAGTTGTTCTT 900
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 841 CTTTTAAAGAGTACACAATGTAGACTGTCCCACGTTCTGGATTGTCAGTTGTTCTT 900

Query 901 GGTGATGTGTTTTCTTAAACTTTTATTACAGAAAATTCAAATAGAGTACATG 960
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 901 GGTGATGTGTTTTCTTAAACTTTTATTACAGAAAATTCAAATAGAGTACATG 960

Query 961 AAGTAAATAGCATACATGAGCCATCTATCAACCGGGTGTGTTGATAAAGGTAGCTGGCTT 1020
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 961 AAGTAAATAGCATACATGAGCCATCTATCAACCGGGTGTGTTGATAAAGGTAGCTGGCTT 1020

Query 1021 GCAGTGCTGTCAGGAGGACTGGTGATAAGGTGGCAGAGCCTGGCCAGTGCCTGGACG 1080
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1021 GCAGTGCTGTCAGGAGGACTGGTGATAAGGTGGCAGAGCCTGGCCAGTGCCTGGACG 1080

Query 1081 CACTGGCTTAGGAGGCATGGAAGCTGCCAGATGGTGGTAAGATGAGATGATGGTGGTGA 1140
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1081 CACTGGCTTAGGAGGCATGGAAGCTGCCAGATGGTGGTAAGATGAGATGATGGTGGTGA 1140

Query 1141 CATTCGGGTCCCAGTCTATGCTTCCATCTCTCTGGTAGGCTAGGAGCTCCTCCCCAAA 1200
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1141 CATTCGGGTCCCAGTCTATGCTTCCATCTCTCTGGTAGGCTAGGAGCTCCTCCCCAAA 1200

Query 1201 GCGGCTGGTGGCTTCCTCCTTCTCCTCC 1231
|||||||||||||||||||||||||||
Sbjct 1201 GCGGCTGGTGGCTTCCTCCTTCTCCTCC 1231

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Seq119

Query = wt

Sbjct = risk

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Query 1 ATGAAGATGGCACAAACAAACATCCCACTCATCCAATTAGAAAGAGAGAACGTCGCCCT 60
|||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 ATGAAGATGGCACAAACAAACATCCCACTCATCCAATTAGAAAGAGAGAACGTCGCCCT 60

```

Query 61 GCCTTCTCCACAAGGAATACCTAGGACAATTAAAGAAATTATCTCAGTTGTGAGTC 120
||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 GCCTTCTCCACAAGGAATACCTAGGACAATTAAAGAAATTATCTCAGTTGTGAGTC 120

Query 121 ACAAAATATTGACTGTTACTTAAATCATTTACTGCCAAGAGGTCAAGGTGGGAG 180
||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 ACAAAATATTGACTGTTACTTAAATCATTTACTGCCAAGAGGTCAAGGTGGGAG 180

Query 181 ATAACAGATAAGAGGCATTCATCCTCCATTTACAGGAGTGAGATCAAGGTGGGAG 240
||||||||||||||||||||||||||||||||||||||||
Sbjct 181 ATAACAGATAAGAGGCATTCATCCTCCATTTACAGGAGTGAGATCAAGGTGGGAG 240

Query 241 TGACTCTAGCCCCAGGTGGCAGAGCTAGTTCACTGGACAGCGGGTAATGATCAAATATC 300
||||||||||||||||||||||||||||||||||||||||
Sbjct 241 TGACTCTAGCCCCAGGTGGCAGAGCTAGTTCACTGGACAGCGGGTAATGATCAAATATC 300

Query 301 TGCTTAATTAGTCACATTGGTTGAATAGACCATTATAGAGATAGAACATAATGTTAC 360
||||||||||||||||||||||||||||||||||||||||
Sbjct 301 TGCTTAATTAGTCACATTGGTTGAATAGACCATTATAGAGATAGAACATAATGTTAC 360

Query 361 CACTACTCCAGGATTATCACTTGGGTACAATATTCACAGACTGTACAGCTGGGTCTCT 420
||||||||||||||||||||||||||||||||||||
Sbjct 361 CACTACTCCAGGATTATCACTTGGGTACAATATTCACAGACTGTACAGCTGGGTCTCT 420

Query 421 TCCAATAGATGCTGTACATTAAAATTGAAGGTTCCACATTAAACATGACATTAAC 480
||||||||||||||||||||||||||||||||||||
Sbjct 421 TCCAATAGATGCTGTACATTAAAATTGAAGGTTCCACATTAAACATGACATTAAC 480

Query 481 TTATTTCTAATAGTTATCTTAAGTTAAATTACAAGGGCTGTGCACTATTGACACCGG 540
||||||||||||||||||||||||||||||||||||
Sbjct 481 TTATTTCTAATAGTTATCTTAAGTTAAATTACAAGGGCTGTGCACTATTGACACCGG 540

Query 541 AAACAGTACAACGTTCAGGTGTCAACTATTCTCATCCAATTCTCACTGCTTAATAAA 600
||||||||||||||||||||||||||||||||
Sbjct 541 AAACAGTACAACGTTCAGGTGTCAACTATTCTCATCCAATTCTCACTGCTTAATAAA 600

Query 601 GTCCTATTATGACCACTCACCTAGAACATGTGAATTGATAAT█GAACCAAAATAGGC 660
||||||||||||||||||||||||||||||||
Sbjct 601 GTCCTATTATGACCACTCACCTAGAACATGTGAATTGATAAT█GAACCAAAATAGGC 660

Query 661 CTGCATTTCTGGTATGCTTAATTGTATCTTGTGCTGGGAGTGAACATTGTTAAA 720
||||||||||||||||||||||||||||||||
Sbjct 661 CTGCATTTCTGGTATGCTTAATTGTATCTTGTGCTGGGAGTGAACATTGTTAAA 720

Query 721 AGTTAGCACTTAAAGCAAAGGGTAAATGCTTCTTATCTTAAGTGGAGATACGTC 780

||||||||||||||||||||||||||||||||||||||||||||
Sbjct 721 AGTTAGCACTTAAAGCAAAGGGTAAATGCTTCTTACTGAGGAGATACTGTC 780

||||||||||||||||||||||||||||||||||||||||
Query 781 ATTGATTCCCTTAGTTGTGGACCTTGCATTAATGGTTAAGTTACAATTAGCCAAG 840

||||||||||||||||||||||||||||||||||||
Sbjct 781 ATTGATTCCCTTAGTTGTGGACCTTGCATTAATGGTTAAGTTACAATTAGCCAAG 840

||||||||||||||||||||||||||||||||||||
Query 841 ACCAGAGTTGTTACTCTGCCTGATCCTGGAATATTACCAAGGCTGGTGAGTCAC 900

||||||||||||||||||||||||||||||||||||
Sbjct 841 ACCAGAGTTGTTACTCTGCCTGATCCTGGAATATTACCAAGGCTGGTGAGTCAC 900

||||||||||||||||||||||||||||||||||||
Query 901 CTCCCCCTCACCCCCCACAAAACCTCCTGTCATAATTCTCACTTGGCACCTGGTGAGC 960

||||||||||||||||||||||||||||||||||||
Sbjct 901 CTCCCCCTCACCCCCCACAAAACCTCCTGTCATAATTCTCACTTGGCACCTGGTGAGC 960

||||||||||||||||||||||||||||||||
Query 961 AAGTTGGCTGGCTCATCAGCCTATCAGTAAATCAATAGCAATCCAATGTCTTAGTATAG 1020

||||||||||||||||||||||||||||||||
Sbjct 961 AAGTTGGCTGGCTCATCAGCCTATCAGTAAATCAATAGCAATCCAATGTCTTAGTATAG 1020

||||||||||||||||||||||||||||||||
Query 1021 TGAGCTCTGGCTCTGAAGACATCTTAGAACATTCACCTACAGTGAAGCCTGTTCTC 1080

||||||||||||||||||||||||||||||||
Sbjct 1021 TGAGCTCTGGCTCTGAAGACATCTTAGAACATTCACCTACAGTGAAGCCTGTTCTC 1080

||||||||||||||||||||||||||||||||
Query 1081 AGAGGCACACTCATATCAGAGTTAAATCACTTCAGATAAGATGATAAGCTAACAGCAC 1140

||||||||||||||||||||||||||||||||
Sbjct 1081 AGAGGCACACTCATATCAGAGTTAAATCACTTCAGATAAGATGATAAGCTAACAGCAC 1140

||||||||||||||||||||||||||||
Query 1141 ATATTTAATTATTGAGAAGGAAGTTGGAAAAACAGACTTTCTCAAGTCATTAATT 1200

||||||||||||||||||||||||||||
Sbjct 1141 ATATTTAATTATTGAGAAGGAAGTTGGAAAAACAGACTTTCTCAAGTCATTAATT 1200

||||||||||||||||||||||||||||
Query 1201 CTCTCTATATTTAACTCTTTATTATGATGTTCAAAACTGGCTTGGGCCACCACGTCA 1260

||||||||||||||||||||||||||||
Sbjct 1201 CTCTCTATATTTAACTCTTTATTATGATGTTCAAAACTGGCTTGGGCCACCACGTCA 1260

||||||||||||||||||||||||||||
Query 1261 AGCTACCAAGAAAATAGAACGATTTCTTGTGAATAAGCTCCCTACTATAAACTCTAA 1320

||||||||||||||||||||||||||||
Sbjct 1261 AGCTACCAAGAAAATAGAACGATTTCTTGTGAATAAGCTCCCTACTATAAACTCTAA 1320

||||||||||||||||||||||||||||
Query 1321 ACTGAACATCTGAAAATTGAGTTGGCCTCTGTCCTGAGGCCTGGTACACTCAGGAT 1380

||||||||||||||||||||||||||||
Sbjct 1321 ACTGAACATCTGAAAATTGAGTTGGCCTCTGTCCTGAGGCCTGGTACACTCAGGAT 1380

||||||||||||||||||||||||||||
Query 1381 GAGTGTGACAAGGAGTGAGACATGGTCAGTGGCTGGAGATGCTTCCCAATTAGAACGCT 1440

||||||||||||||||||||||||||||
Sbjct 1381 GAGTGTGACAAGGAGTGAGACATGGTCAGTGGCTGGAGATGCTTCCCAATTAGAACGCT 1440

```

Query 1441 CATCTTGCCTCAGGGCCTCACGCAAATCCTGGCTCTAGTTCAATTGGTAGTCACC 1500
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 1441 CATCTTGCCTCAGGGCCTCACGCAAATCCTGGCTCTAGTTCAATTGGTAGTCACC 1500

Query 1501 GCTTCTTCTCAGTGTACCTGCTTCAGATCCCTCCATTTCTGCTTTTC 1560
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 1501 GCTTCTTCTCAGTGTACCTGCTTCAGATCCCTCCATTTCTGCTTTTC 1560

Query 1561 TCTCAAGATTACAGGCCCTCTTCTACCAGCCCATTAGT 1598
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 1561 TCTCAAGATTACAGGCCCTCTTCTACCAGCCCATTAGT 1598

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Seq132

Query = wt

Sbjct = risk

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Query 1 GCATTTACTGCCTCAAGAGAAAGCTCAGGCCAAGGATAACACATTAGGCTGCTAAAAAAT 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 1 GCATTTACTGCCTCAAGAGAAAGCTCAGGCCAAGGATAACACATTAGGCTGCTAAAAAAT 60

Query 61 GACTCAAGGAGTTACTTAGGGCAGGGACAGGAACACTAGTGACGGTCATTTGAAAATC 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 61 GACTCAAGGAGTTACTTAGGGCAGGGACAGGAACACTAGTGACGGTCATTTGAAAATC 120

Query 121 GTGCTTCTCAGACATCGTCATCTCTCGAAGGGGCTTAGGTCTGACTTGAGGAATTAA 180
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 121 GTGCTTCTCAGACATCGTCATCTCTCGAAGGGGCTTAGGTCTGACTTGAGGAATTAA 180

Query 181 CAGCATTCACTATGCCAATTTCACTGCAAATGGAAGAACAGTTGACGGTTG 240
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 181 CAGCATTCACTATGCCAATTTCACTGCAAATGGAAGAACAGTTGACGGTTG 240

Query 241 CTATGGAGGAGACTTACAGCCTGCTGATAGCATTTGGACAGGAAAAAATGGCAGTGA 300
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 241 CTATGGAGGAGACTTACAGCCTGCTGATAGCATTTGGACAGGAAAAAATGGCAGTGA 300

Query 301 GGGTTGCTGCTCTAAGAAAGGTCTGTGGGAGCTCTAACGCTCCTGGTCTGCACT 360
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 301 GGGTTGCTGCTCTAAGAAAGGTCTGTGGGAGCTCTAACGCTCCTGGTCTGCACT 360

Query 361 ATCCTTGATATAAATTCTGATTACATACAAAGCCTGCAACCCAGAGATCCCTGGAGCTG 420
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Sbjct 361 ATCCTTGATATAAATTCTGATTACATACAAAGCCTGCAACCCAGAGATCCCTGGAGCTG 420

```

Query	421	GTGAGCAGGGCTGTATAAGAAATAATAGTCTGTCTGGCTTTCCAGGGCTGTCTCC	480
Sbjct	421	GTGAGCAGGGCTGTATAAGAAATAATAGTCTGTCTGGCTTTCCAGGGCTGTCTCC	480
Query	481	CCTTCATAGTAAGCTCCTAGGAATGCCAGACTCCAGAGATAACAGTGGACAGAAAGAGT	540
Sbjct	481	CCTTCATAGTAAGCTCCTAGGAATGCCAGACTCCAGAGATAACAGTGGACAGAAAGAGT	540
Query	541	TCCCCATAGCGACAGGGCACTTGCTGCACTAGAGTTCCCTGCCTGTGTGAATG	600
Sbjct	541	TCCCCATAGCGACAGGGCACTTGCTGCACTAGAGTTCCCTGCCTGTGTGAATG	600
Query	601	TAGCTGATTATCAGAGCAAACGTGGCTCCTCTGAGTGCCTGCCTGTGTGAATG	660
Sbjct	601	TAGCTGATTATCAGAGCAAACGTGGCTCCTCTGAGTGCCTGCCTGTGTGAATG	660
Query	661	CAGGTCAAAGACAAAGTACTTGAAGTTGGAGTCAGAGCAGTCGCCATGCGTGTCAATC	720
Sbjct	661	CAGGTCAAAGACAAAGTACTTGAAGTTGGAGTCAGAGCAGTCGCCATGCGTGTCAATC	720
Query	721	AGTGCTAATCTCCCTGTGCTCTTATCAACAGCAGCCAGC G GGGACAGCCAAGTGGTTC	780
Sbjct	721	AGTGCTAATCTCCCTGTGCTCTTATCAACAGCAGCCAGC G GGGACAGCCAAGTGGTTC	780
Query	781	GGAGAGAAATTGCTAAAGCCCTAGCAAAGCTTACGATGCACTCACTCACCATTCAGA	840
Sbjct	781	GGAGAGAAATTGCTAAAGCCCTAGCAAAGCTTACGATGCACTCACTCACCATTCAGA	840
Query	841	TGGAATCTCCAGTTGACCAGGACCCGACTGCCTTCTGTGAAGACCCCTGTGACTAGC	900
Sbjct	841	TGGAATCTCCAGTTGACCAGGACCCGACTGCCTTCTGTGAAGACCCCTGTGACTAGC	900
Query	901	TCAGTCACACCGTCAGTTCCAAATTGACAGGCCACCTCAAACATGCTATGCAG	960
Sbjct	901	TCAGTCACACCGTCAGTTCCAAATTGACAGGCCACCTCAAACATGCTATGCAG	960
Query	961	TTTCTGCATCATAGAAAATAAGGAACCAAGGAAGAAATTGATGTCATGGTGCA G TCAC	1020
Sbjct	961	TTTCTGCATCATAGAAAATAAGGAACCAAGGAAGAAATTGATGTCATGGTGCA G TCAC	1020
Query	1021	ATTTTATCTATTTATTAGTTGCATTCAACATGAAGGAAGAGGCAGTGAGATCCATCAAT	1080
Sbjct	1021	ATTTTATCTATTTATTAGTTGCATTCAACATGAAGGAAGAGGCAGTGAGATCCATCAAT	1080
Query	1081	CAATTGGATTATATACTGATCAGTAGCTGTGTTCAATTGAGGAATGTGTATAGATTA	1140

||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1081 CAATTGGATTATATACTGATCAGTAGCTGTGTTCAATTGCAGGAATGTGTATAGATTA 1140

Query 1141 TTCTTGAGTGGAGCCGAAGTAACAGCTGTTGTAACTATCGCAATACCAAATTCATCTC 1200
||||||||||||||||||||||||||||||||||||||||

Sbjct 1141 TTCTTGAGTGGAGCCGAAGTAACAGCTGTTGTAACTATCGCAATACCAAATTCATCTC 1200

Query 1201 CCTTCCAATAATGCATCTTGAGAACACATAGGAAATTGAACTCAGGAAAGTCTTACTA 1260
||||||||||||||||||||||||||||||||||||||||

Sbjct 1201 CCTTCCAATAATGCATCTTGAGAACACATAGGAAATTGAACTCAGGAAAGTCTTACTA 1260

Query 1261 GAAATCAGTGGAGGGACAAATAGTCACAAAATTACCAAAACATTAGAAACAAAAAAT 1320
||||||||||||||||||||||||||||||||||||||||

Sbjct 1261 GAAATCAGTGGAGGGACAAATAGTCACAAAATTACCAAAACATTAGAAACAAAAAAT 1320

Query 1321 AAGGAGAGCCAAGTCAGGAATAAAAGTGACTCTGTATGCTAACGCCACATTAGAACTTGG 1380
||||||||||||||||||||||||||||||||||||

Sbjct 1321 AAGGAGAGCCAAGTCAGGAATAAAAGTGACTCTGTATGCTAACGCCACATTAGAACTTGG 1380

Query 1381 TTCTCTCACCAAGCTGTAATGTGATTTTTTCTACTCTGAATTGAAATATGTATGAA 1440
||||||||||||||||||||||||||||||||||||

Sbjct 1381 TTCTCTCACCAAGCTGTAATGTGATTTTTTCTACTCTGAATTGAAATATGTATGAA 1440

Query 1441 TATACAGAGAAGTGCTTACAACATAAATTTTACTTGTACATTGTCACATTGGCAATAATCC 1500
||||||||||||||||||||||||||||||||||||

Sbjct 1441 TATACAGAGAAGTGCTTACAACATAAATTTTACTTGTACATTGTCACATTGGCAATAATCC 1500

Query 1501 CTCTTATTCCTAAATTCTAACCTGTTATTCAAAACTTATATAATCACTGTTCAAAAG 1560
||||||||||||||||||||||||||||||||

Sbjct 1501 CTCTTATTCCTAAATTCTAACCTGTTATTCAAAACTTATATAATCACTGTTCAAAAG 1560

Query 1561 GAAATATTTCACCTACCAGAGTGCTTAAACACTGGCACCCAGCCAAAGAATGTGGTTGTA 1620
||||||||||||||||||||||||||||||||

Sbjct 1561 GAAATATTTCACCTACCAGAGTGCTTAAACACTGGCACCCAGCCAAAGAATGTGGTTGTA 1620

Query 1621 GAGACCCAGAAGTCTTCAAGAACAGCCGACAAAACATTGAGTTGACCCCACCAAGTTG 1680
||||||||||||||||||||||||||||||||

Sbjct 1621 GAGACCCAGAAGTCTTCAAGAACAGCCGACAAAACATTGAGTTGACCCCACCAAGTTG 1680

Query 1681 TTGCCAC 1687
|||||||

Sbjct 1681 TTGCCAC 1687

Seq219

Query = wt

Sbjct = risk

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Sbjct 601 ATTAAGACCGTAAATCAAACATCTAGCGGTGGGTCTGAGCCTCACTAAAATGAAAA 660

Query 661 AGCTTCCCAGCTGAGTCAGGCCAGACCTGCGGAAGCCATTCTCATTCCATTATGGAAGG 720
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 AGCTTCCCAGCTGAGTCAGGCCAGACCTGCGGAAGCCATTCTCATTCCATTATGGAAGG 720

Query 721 GCCAGGTGTTGCCAAGGCCACACACTTGACATTCTAGTCCCCTGGATTCAATATATAAA 780
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 GCCAGGTGTTGCCAAGGCCACACACTTGACATTCTAGTCCCCTGGATTCAATATATAAA 780

Query 781 ACTTAGTGATATGTCCTCAGCTGCTATAGTGAATGGTATGTAGCTGTGCAAGGATTA 840
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 ACTTAGTGATATGTCCTCAGCTGCTATAGTGAATGGTATGTAGCTGTGCAAGGATTA 840

Query 841 AACCTGAAACAAAATAATGATGCAAGACAATCCTTGAGCTTGTGAAACCCAACTCTAG 900
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 841 AACCTGAAACAAAATAATGATGCAAGACAATCCTTGAGCTTGTGAAACCCAACTCTAG 900

Query 901 CTTTCAGCTGGCTGAATGTGTTCAAGCCAGGTATGGAGGTGCCAAGGGTTAGCAGCCA 960
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 901 CTTTCAGCTGGCTGAATGTGTTCAAGCCAGGTATGGAGGTGCCAAGGGTTAGCAGCCA 960

Query 961 CAAGGAACAACTTCCTCATATATTGGTCAACACAGTAATCACAATGAATAGAACTC 1020
||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 961 CAAGGAACAACTTCCTCATATATTGGTCAACACAGTAATCACAATGAATAGAACTC 1020

Query 1021 AAGAGTAAAATGAATTCTGTCAATCAACCAGTCCTGTTGTCAGATAATCATCATCACCT 1080
||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1021 AAGAGTAAAATGAATTCTGTCAATCAACCAGTCCTGTTGTCAGATAATCATCATCACCT 1080

Query 1081 TTGAGGACAATAGCTTGGCTTAATGGATCTTGAAGGGAAAGCCAGACCATGAATATAGAG 1140
||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1081 TTGAGGACAATAGCTTGGCTTAATGGATCTTGAAGGGAAAGCCAGACCATGAATATAGAG 1140

Query 1141 GCCCTGGAGGA 1151
||||||||||

Sbjct 1141 GCCCTGGAGGA 1151

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Seq460

Query = wt

Sbjct = risk

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Query 1 GCCTATCTTCAAATCTACTTCCCAGATGCCTCCACCCCTATGATTAATAATCCT 60
||||||||||||||||||||||||||||||||||||||||||

Sbjct 1 GCCTATCTTCAAATCTACTTCCCAGATGCCTCCACCCCTATGATTAATAATCCT 60

```

Query 61 TTTCTTCATTAATGAGAAGACAAATAATTACTGTTACCTGTTAACATCAACAATGA 120
||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 TTTCTTCATTAATGAGAAGACAAATAATTACTGTTACCTGTTAACATCAACAATGA 120

Query 121 CTAGAGCTTGTAAATATAATGTTTATTATTCCAAACAAACATTCTATGGAAAGAATATT 180
||||||||||||||||||||||||||||||||||||||||
Sbjct 121 CTAGAGCTTGTAAATATAATGTTTATTATTCCAAACAAACATTCTATGGAAAGAATATT 180

Query 181 TTCTAGTTTATAGATAAAAACAAAAGGAGACTCAGGGAGGTAATGGTTGCTCACTTT 240
||||||||||||||||||||||||||||||||||||
Sbjct 181 TTCTAGTTTATAGATAAAAACAAAAGGAGACTCAGGGAGGTAATGGTTGCTCACTTT 240

Query 241 GTGATTTGTGATGTGTCAGTGCTGGACTGAATCCAAGTTGGACAGCTGGCGAT 300
||||||||||||||||||||||||||||||||||||
Sbjct 241 GTGATTTGTGATGTGTCAGTGCTGGACTGAATCCAAGTTGGACAGCTGGCGAT 300

Query 301 GCAGCGAGGAGGTCTGCTTTGGTAACACAGTGAGCTGGAAAGTCTGCAACCAC 360
||||||||||||||||||||||||||||||||
Sbjct 301 GCAGCGAGGAGGTCTGCTTTGGTAACACAGTGAGCTGGAAAGTCTGCAACCAC 360

Query 361 ATGACTATGAATGAGGCTTCTGGAACAGTAGAGGCTGAGTGAGGCCAGAGAGGCAGG 420
||||||||||||||||||||||||||||
Sbjct 361 ATGACTATGAATGAGGCTTCTGGAACAGTAGAGGCTGAGTGAGGCCAGAGAGGCAGG 420

Query 421 AAGAGTTGCCAGGAGTGGCTGCATGACAGTTGTTAACAGCTTCACTGTTGACATCTGA 480
||||||||||||||||||||||||||||
Sbjct 421 AAGAGTTGCCAGGAGTGGCTGCATGACAGTTGTTAACAGCTTCACTGTTGACATCTGA 480

Query 481 ACCCCAACTCTGTCCTTACCAACCATCTCCTAAATTGAATCTCAGTCTCTATGTCTGT 540
||||||||||||||||||||||||||||
Sbjct 481 ACCCCAACTCTGTCCTTACCAACCATCTCCTAAATTGAATCTCAGTCTCTATGTCTGT 540

Query 541 AGGGTGGCAATAATATTCCCCTGTTTGAGGATTAATGATGTGGCACATGGAAA 600
||||||||||||||||||||||||
Sbjct 541 AGGGTGGCAATAATATTCCCCTGTTTGAGGATTAATGATGTGGCACATGGAAA 600

Query 601 GTACTTGGCATAAGGTAAACTTGGACAGCCACTATAATGTGTCAGTGGATACTGA 660
||||||||||||||||||||||||
Sbjct 601 GTACTTGGCATAAGGTAAACTTGGACAGCCACTATAATGTGTCAGTGGATACTGA 660

Query 661 AATTATTCATCCAAGCGCTGCTTCTGATC 693
||||||||||||||||||||
Sbjct 661 AATTATTCATCCAAGCGCTGCTTCTGATC 693

Seq790

Query = wt

Sbjct = risk

Sbjct 601 TGCCGTATGAGGCACCCTAGTTTCAGACGAGAAACCACAGTTACAGGGAAGGCAAGTA 660

Query 661 ACTTAGTCAATGTCAGATAACTAGGAAAAGGTTAGAGGGGCCCTGGACACAGGCCTGTGT 720
||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 661 ACTTAGTCAATGTCAGATAACTAGGAAAAGGTTAGAGGGGCCCTGGACACAGGCCTGTGT 720

Query 721 GACTGAGAAGCTGGGCACCTCACTGCTACATTCATCTTCGCTATAAACATTAGC 780
||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 721 GACTGAGAAGCTGGGCACCTCACTGCTACATTCATCTTCGCTATAAACATTAGC 780

Query 781 TTTTTGTGTTGCTGACTGGCAACAATACATAGTGAAGTTCTAATAATTGTAATGCTT 840
||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 781 TTTTTGTGTTGCTGACTGGCAACAATACATAGTGAAGTTCTAATAATTGTAATGCTT 840

Query 841 TTGCATGTCTTGATTTCTGGTATCACATCACATCAAATTAAGATACTGATCAGC 900
||||||||||||||||||||||||||||||||||||||||||||

Sbjct 841 TTGCATGTCTTGATTTCTGGTATCACATCACATCAAATTAAGATACTGATCAGC 900

Query 901 AGTGTGAGAGGTTATTTCCATGTCCTTCATTAGTGTAGCTTGTGGATGGATTGA 960
||||||||||||||||||||||||||||||||||||||||||||

Sbjct 901 AGTGTGAGAGGTTATTTCCATGTCCTTCATTAGTGTAGCTTGTGGATGGATTGA 960

Query 961 GGCTCTCTGTGCTTCCCCCAGCAAAGTGAATACCAGACTTCCTATTAAAAAAAGTAT 1020
||||||||||||||||||||||||||||||||||||||||||||

Sbjct 961 GGCTCTCTGTGCTTCCCCCAGCAAAGTGAATACCAGACTTCCTATTAAAAAAAGTAT 1020

Query 1021 TTTATTTTCAGAGACAGGGCTCATCTGTCTCCAGGCTGGAGTGCAGTGGACAATC 1080
||||||||||||||||||||||||||||||||||||||||

Sbjct 1021 TTTATTTTCAGAGACAGGGCTCATCTGTCTCCAGGCTGGAGTGCAGTGGACAATC 1080

Query 1081 ATAGCCCCACTGCAGCCTCCAACCTTGGGTTCAAATGATCCTCCTGCCTCAGCCTCTTT 1140
||||||||||||||||||||||||||||||||||||||||

Sbjct 1081 ATAGCCCCACTGCAGCCTCCAACCTTGGGTTCAAATGATCCTCCTGCCTCAGCCTCTTT 1140

Query 1141 AAGCAGTGCCTTCCCCATTCTCATGGACTTCCAATCCATGAGATACTTGCTGCAGG 1200
||||||||||||||||||||||||||||||||||||||||

Sbjct 1141 AAGCAGTGCCTTCCCCATTCTCATGGACTTCCAATCCATGAGATACTTGCTGCAGG 1200

Query 1201 GAAGCCCTGTCTGTCCAGGCCTGTGTAATAGACGACTTCACATGGCCTGTGTTGTT 1260
||||||||||||||||||||||||||||||||||||||||

Sbjct 1201 GAAGCCCTGTCTGTCCAGGCCTGTGTAATAGACGACTTCACATGGCCTGTGTTGTT 1260

Query 1261 TGCCTTCTGTGTGGCTAAGTTCCATGACCTGGTG 1295
||||||||||||||||||||||||||||||||

Sbjct 1261 TGCCTTCTGTGTGGCTAAGTTCCATGACCTGGTG 1295

wt allele

risk variant

common variant