

Gene symbol	Gene title	P16 ^a	P19 ^a	P32 ^a
Stress/injury				
<i>Pap</i>	pancreatitis-associated protein	11.2	26.0	ns
<i>Pap</i>	pancreatitis-associated protein	7.2	13.0	ns
<i>Reg3g</i>	regenerating islet-derived 3 gamma	7.6	18.4	3.2
<i>Reg3a</i>	regenerating islet-derived 3 alpha	3.2	11.3	ns
<i>Reg2</i>	regenerating islet-derived 2	4.1	5.3	0.5
<i>Hspa1a / Hsp70-3</i>	heat shock protein 1A	10.5	-	-
<i>Hspa1b / Hsp70-1</i>	heat shock protein 1B	12.6	2.8	ns
<i>Hspa1b / Hsp70-1</i>	heat shock protein 1B	8.5	2.6	2.3
<i>Hspa1b / Hsp70-1</i>	heat shock protein 1B	6.5	2.5	ns
<i>Hsp105</i>	heat shock protein 105	ns	7.5	ns
<i>1810009J06Rik</i>	trypsinogen	ns	4.3	3.2
<i>Ctrc</i>	chymotrypsin C (caldecrin)	4.9	ns	0.2
<i>Cox7a1</i>	cytochrome c oxidase, subunit VIIa 1	-	2.6	5.3
<i>Cp</i>	ceruloplasmin	ns	ns	4.9
Inflammation/immune				
<i>Mac-2 / Lgals3</i>	lectin, galactose binding, soluble 3	ns	5.7	4.6
<i>Mmp12</i>	matrix metalloproteinase 12	-	14.9	55.7
<i>Scya6 / Ccl6</i>	chemokine (C-C motif) ligand 6	2.0	4.9	3.5
<i>Lcn2</i>	lipocalin 2	2.8	ns	4.3
<i>Lip1</i>	lysosomal acid lipase 1	ns	4.9	ns
<i>Hexb</i>	hexosaminidase B (lysosome)	ns	3.0	5.3
<i>Serpine2</i>	serine (or cysteine) proteinase inhibitor, E2	ns	2.0	4.3
<i>Socs3</i>	suppressor of cytokine signaling 3	ns	ns	6.5
<i>Ambp</i>	alpha 1 microglobulin/bikunin	ns	ns	4.3
<i>Tlr3</i>	toll-like receptor 3	ns	9.8	-
<i>Pld1</i>	phospholipase D1	ns	-	7.5
Matrix/cytoskeleton				
<i>Bgn</i>	biglycan	-	7.0	7.5
<i>Vwf</i>	Von Willebrand factor homolog	-	12.1	-
<i>GpnmB</i>	glycoprotein (transmembrane) nmb	-	-	7.0
<i>Cldn2</i>	claudin 2	-	-	4.6
<i>Cnn3</i>	calponin 3, acidic	5.8	3.2	ns
<i>Tagln</i>	transgelin	-	4.3	-
<i>Pfn2</i>	profilin 2	ns	ns	4.3
Growth-related				
<i>Tgfb1</i>	transforming growth factor, beta induced	4.1	-	-
<i>Acvrin1</i>	activin receptor interacting protein 1	6.2	-	ns
<i>Pdgfra</i>	platelet derived growth factor receptor alpha	ns	4.9	ns
Others				
<i>Galgt1</i>	beta-1,4 N-acetylgalactosaminyltransferase	-	ns	11.3
<i>Gif</i>	gastric intrinsic factor	-	-	9.2
<i>Ms4a7</i>	membrane-spanning 4-domains, A7	-	-	8.6

<i>Ms4a11</i>	membrane-spanning 4-domains, A11	ns	8.0	2.0
<i>Thoc4</i>	THO complex 4	ns	7.5	ns
<i>Trim30</i>	tripartite motif protein 30	ns	4.0	ns
<i>Tm7sfl</i>	transmembrane 7 superfamily member 1	ns	9.2	7.5
<i>Tm7sfl</i>	transmembrane 7 superfamily member 1	-	ns	7.5
<i>Tmem45a</i>	transmembrane protein 45a	-	ns	7.5
<i>Tspan1</i>	tetraspan 1	-	-	26.0
<i>I700029I01Rik</i>	RIKEN cDNA 1700029I01 gene	ns	ns	5.7
<i>I110021E09Rik</i>	weakly similar to splicing factor, arginineserine-rich 4	ns	ns	6.1
-	weakly similar to env polyprotein, retrovirus-related	-	ns	8.0
-	expressed sequence AI594671	5.7	-	-

Table S1. Summary of microarray data for genes that showed increased expression levels in the mutant pancreata. Fold change in the mutant expression levels as compared to the wild-type levels. “-”, the expression was not detectable at a significant level; “ns,” the expression was detectable but was less than 2-fold change between mutant and wild-type samples significant level (i.e., less than 2-fold change). Repeated appearance of the same gene in the tables indicates multiple detections by different Affymetrix probes for the same gene. For P16 samples, RNA from a single pancreas was used per array, and each genotype had two biological replicates. For data analysis, signals of the replicates were averaged for each probe within a genotype for calculation of a ratio (i.e., mutant average signal / wild-type average signal). Genes identified by the software as “Present” in at least one array out of a total of 4 arrays were selected for further analyses, and those with ratios ≤ 0.5 or ≥ 2.0 were considered as differentially expressed genes at a significant level. For P19 and P32 experiments, cDNA sample was similarly generated from total pancreatic RNA (10 μ g) from single animals and then, equivalent amounts of two samples of the same genotype were pooled prior to cRNA and hybridization to a single array. Genes identified as “Present” in at least one of the two arrays (mutant and wild-type) were selected for further analyses. The genes that showed an increase difference of ≥ 2.0 fold in the magnitude (i.e., Signal Log Ratio ≥ 1.0 or ≤ -1.0) were considered as differentially expressed genes at a significant level. Repeat appearance of the same gene in the tables indicates multiple detections by different Affymetrix probes for the same gene.