Table S1. Transcription factors or transcriptional regulators upregulated in Ngn3-positive islet progenitor cells

AffyID	Gene symbol	Gene title	FC	FDR
1436092_at	*Mafa*	Transcribed locus, moderately similar to XP_574723.1 PREDICTED: similar to LRRGT00097 (*Rattus norvegicus*)	386.55	0.007
1419271_at	*Pax6*	paired box gene 6	275.2	0.008
1426413_at	*Neurod1*	neurogenic differentiation 1	171.99	0.011
1425886_at	*Fev*	FEV (ETS oncogene family)	139.22	0.011
1455123_at	*St18*	suppression of tumorigenicity 18	130.74	0.009
1450042_at	*Arx*	aristaless related homeobox gene (Drosophila)	119	0.011
1451598_at	*Pax4*	paired box gene 4	87.63	0.011
1419185_a_at	*Mlxipl*	MLX interacting protein-like	75.37	0.012
1457613_at	*Rfxdc1/Rfx6*	regulatory factor X domain containing 1	65.73	0.011
1421399_at	*Insm1*	insulinoma-associated 1	61.65	0.010
1422773_at	*Myt1*	myelin transcription factor 1	53.62	0.010
1422165_at	*Pou3f4*	POU domain, class 3, transcription factor 4	52.83	0.012
1418176_at	*Vdr*	vitamin D receptor	51.53	0.012
1447174_at	*Dach1*	Dachshund 1 (Drosophila)	49.16	0.029
1450428_at	*Lhx1*	LIM homeobox protein 1	42.43	0.008
1451716_at	*Mafb*	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	38.73	0.012
1426298_at	*Irx2*	Iroquois related homeobox 2 (Drosophila)	37.8	0.012
1460299_at	*Hlxb9*	homeobox gene HB9	34.41	0.012
1429573_at	*Dmrtc1a*	DMRT-like family C1a	30.05	0.012
1436600_at	*Tnrc9*	trinucleotide repeat containing 9	29.82	0.012
1432034_at	*Neurog3*	neurogenin 3	28.41	0.012
1422720_at	*Isl1*	ISL1 transcription factor, LIM/homeodomain	28.26	0.022
1425828_at	*Nkx6.1*	NK6 transcription factor related, locus 1 (Drosophila)	24.18	0.036
1421112_at	*Nkx2.2*	NK2 transcription factor related, locus 2 (Drosophila)	23.87	0.013
1449967_at	*Sim1*	single-minded homolog 1 (Drosophila)	15.11	0.020
1422174_at	*Ipf1*	insulin promoter factor 1, homeodomain transcription factor	12.36	0.032
1419224_at	*Cecr6*	cat eye syndrome chromosome region, candidate 6 homolog (human)	11.22	0.023
1440439_at	*AI591476*	Expressed sequence AI591476	10.99	0.039
1441484_at	*Tcf2*	Transcription factor 2	10.75	0.043
1448272_at	*Btg2*	B-cell translocation gene 2, anti-proliferative	10	0.030
1429269_at	*BC068157*	cDNA sequence BC068157	9.46	0.041
1440870_at	*Prdm16*	PR domain containing 16	7.23	0.045
1448928_at	*Hdac6 /// LOC669168*	histone deacetylase 6 /// similar to Histone deacetylase 6 (HD6) (Histone deacetylase mHDA2)	6.89	0.043
1430353_at	*Glis3*	GLIS family zinc finger 3	6.88	0.045
1436483_at	*Myt1l*	myelin transcription factor 1-like	6.54	0.029
1433894_at	*AI591476*	expressed sequence AI591476	6.53	0.047
1418582_at	*Cbfa2t3h*	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 homolog (human)	6.45	0.020
1429633_at	*Lcor*	ligand dependent nuclear receptor corepressor	6.36	0.043
1434777_at	*Mycl1*	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	5.92	0.036
1437894_at	*Prox1*	prospero-related homeobox 1	5.84	0.042
1456824_at	*Zfp612*	zinc finger protein 612	5.52	0.047
1416983_s_at	*Foxo1*	forkhead box O1	5.19	0.032
1456021_at	*Atf6*	activating transcription factor 6	4.74	0.045
1450684_at	*Etv1*	ets variant gene 1	4.49	0.023
1435236_at	*A630018P17Rik*	RIKEN cDNA A630018P17 gene	4.23	0.017
1455944_at	*Zfp516*	zinc finger protein 516	3.33	0.048
1425484_at	*Tox*	thymocyte selection-associated HMG box gene	2.57	0.044

Comparison of gene expression profiles in Ngn3-positive versus Ngn3-negative cells (E15.5 pancreas). Probe sets found upregulated in Ngn3-positive cells with an FDR>5% were selected and transcriptional regulators were identified using GO annotations (biological process and molecular function) containing transcription. Results are sorted by fold-change (FC). *Mafa* and *Insm1* were hand-annotated as transcription factors. Excluded transcriptional regulators (FDR>5% and <10%) include: *Atf6*, *Rfx3*, *Dach2*, *Zfp568*, *Hhex*, *Zfp354b*, *Tshz1*.