

Figure A. Heat map representing the expression of each T2D-susceptibility gene in the panel of human organs, tissues and cells.

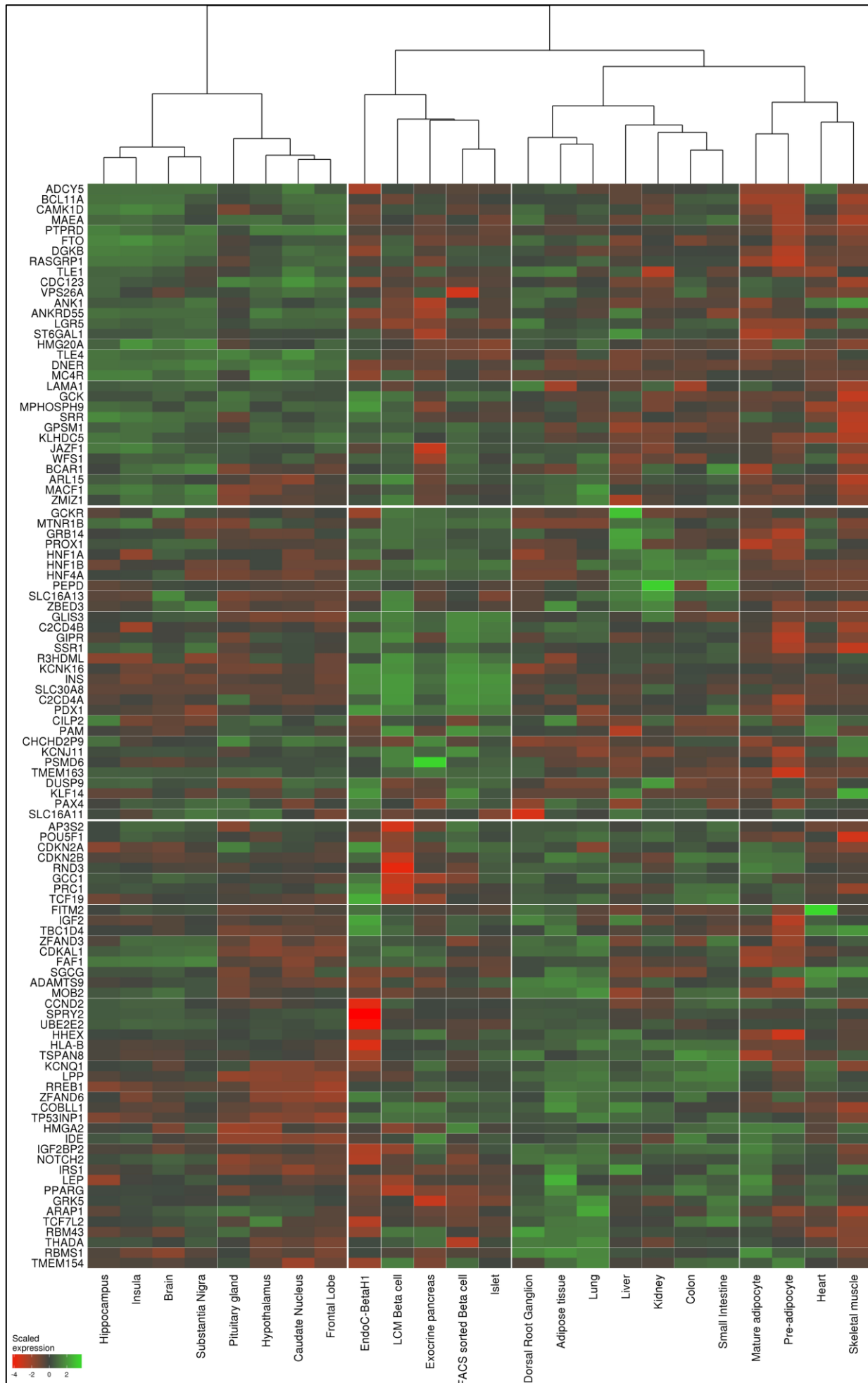


Figure B. (1) Heat map representing the expression of three genes known to be highly expressed in gut in the panel of human organs, tissues and cells; (2) Enrichment analysis of gut markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of 0.05.

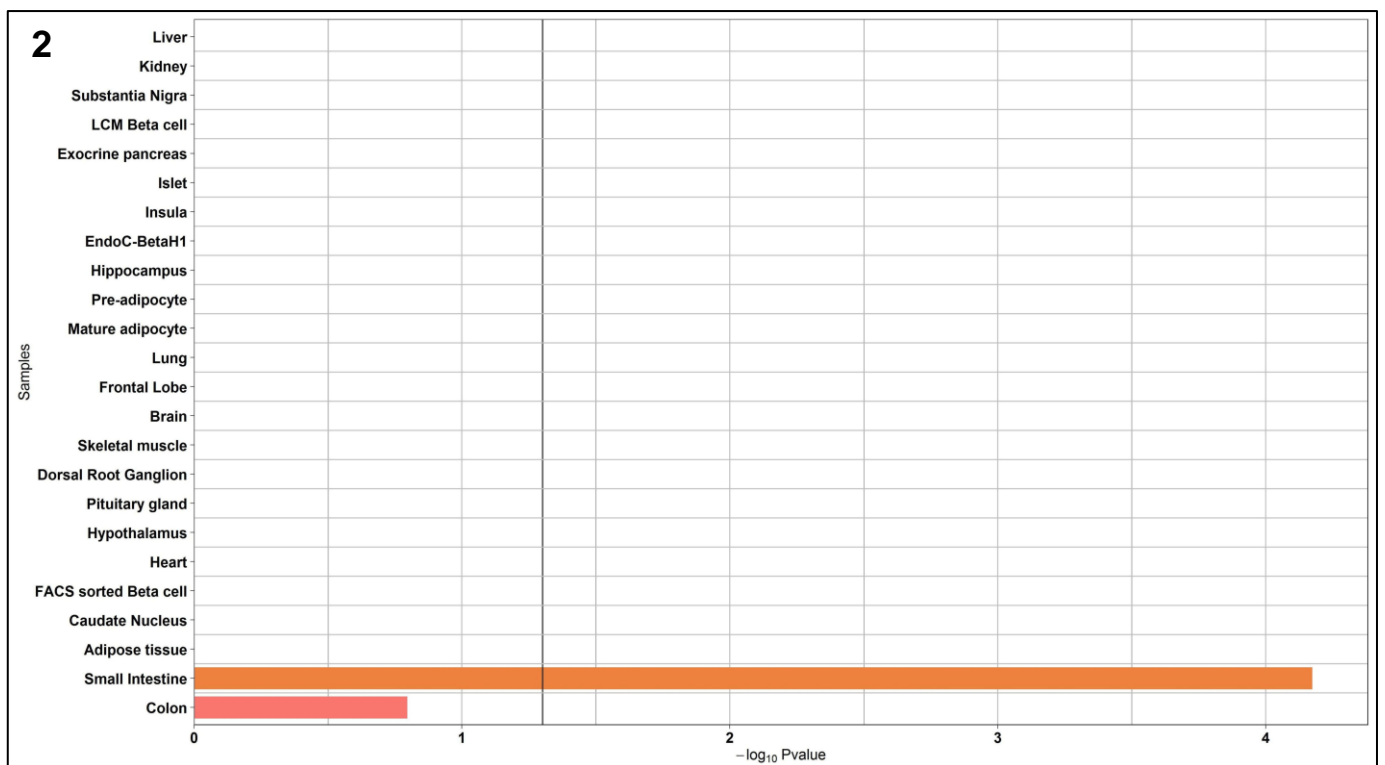
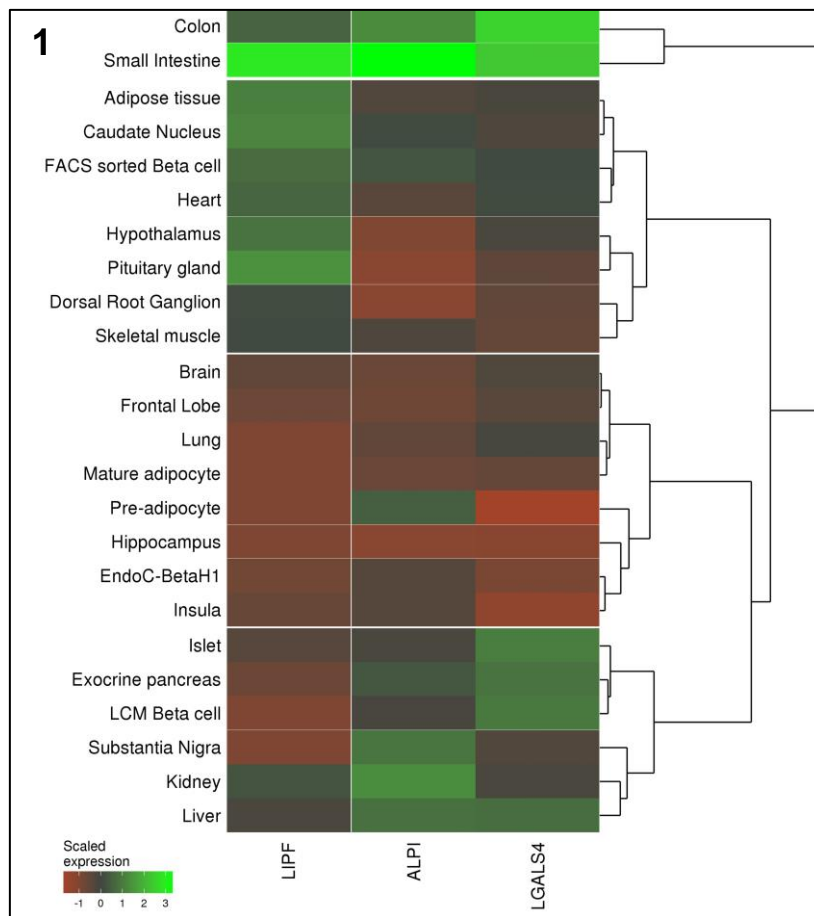


Figure C. (1) Heat map representing the expression of three genes known to be highly expressed in adipose tissue in the panel of human organs, tissues and cells; (2) Enrichment analysis of adipose tissue markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of 0.05.

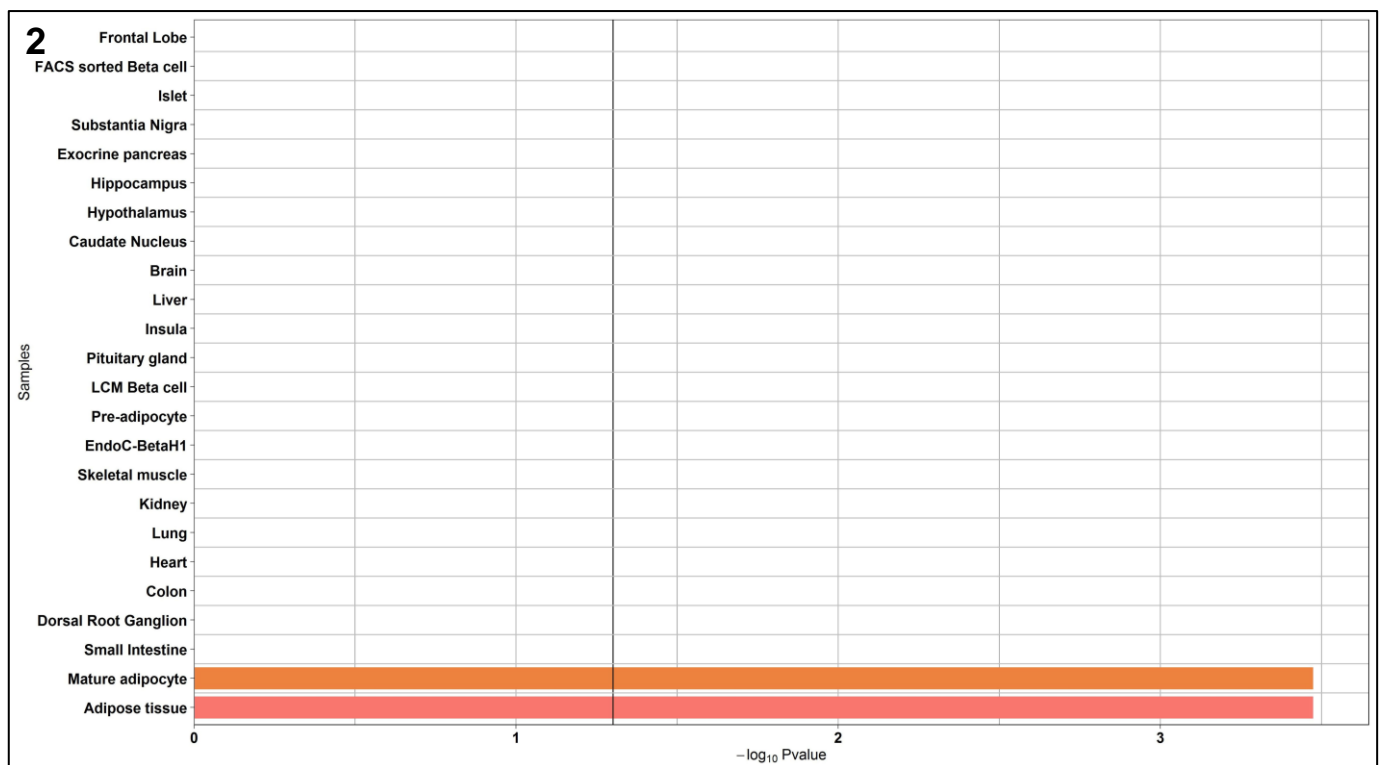
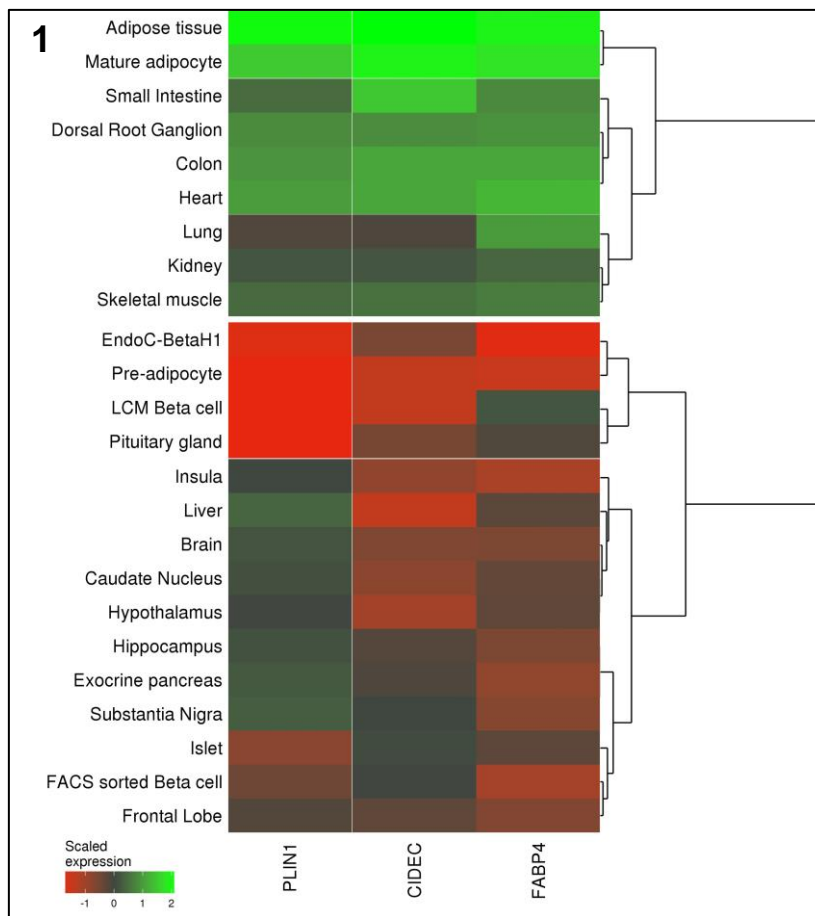


Figure D. (1) Heat map representing the expression of four genes known to be highly expressed in kidney in the panel of human organs, tissues and cells; (2) Enrichment analysis of kidney markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of 0.05.

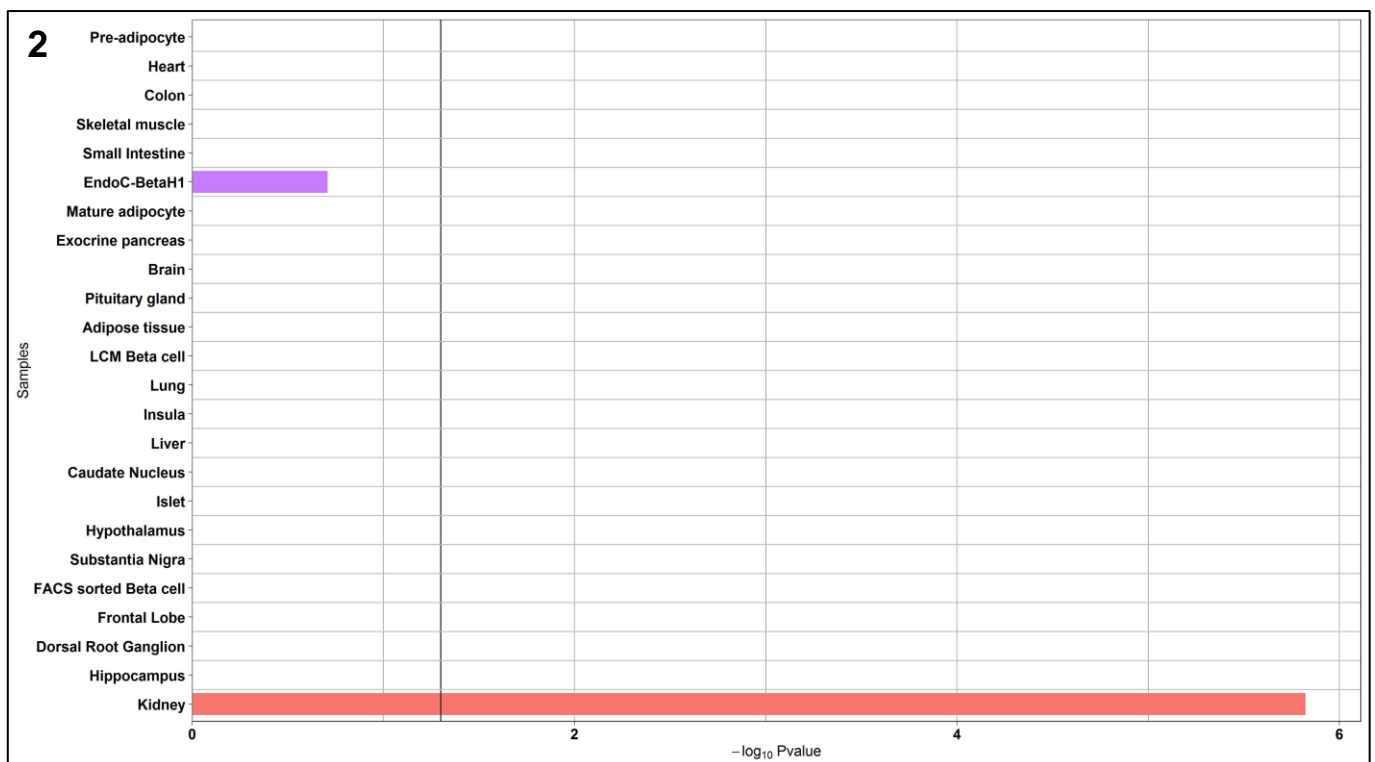
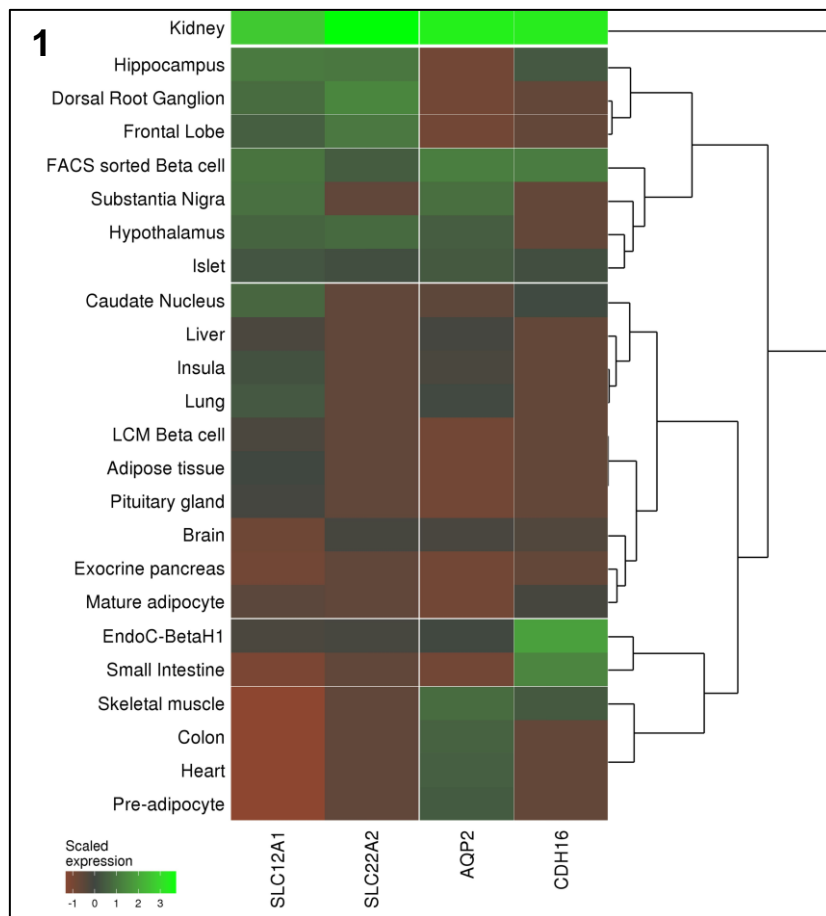


Figure E. (1) Heat map representing the expression of three genes known to be highly expressed in lung in the panel of human organs, tissues and cells; (2) Enrichment analysis of lung markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of 0.05.

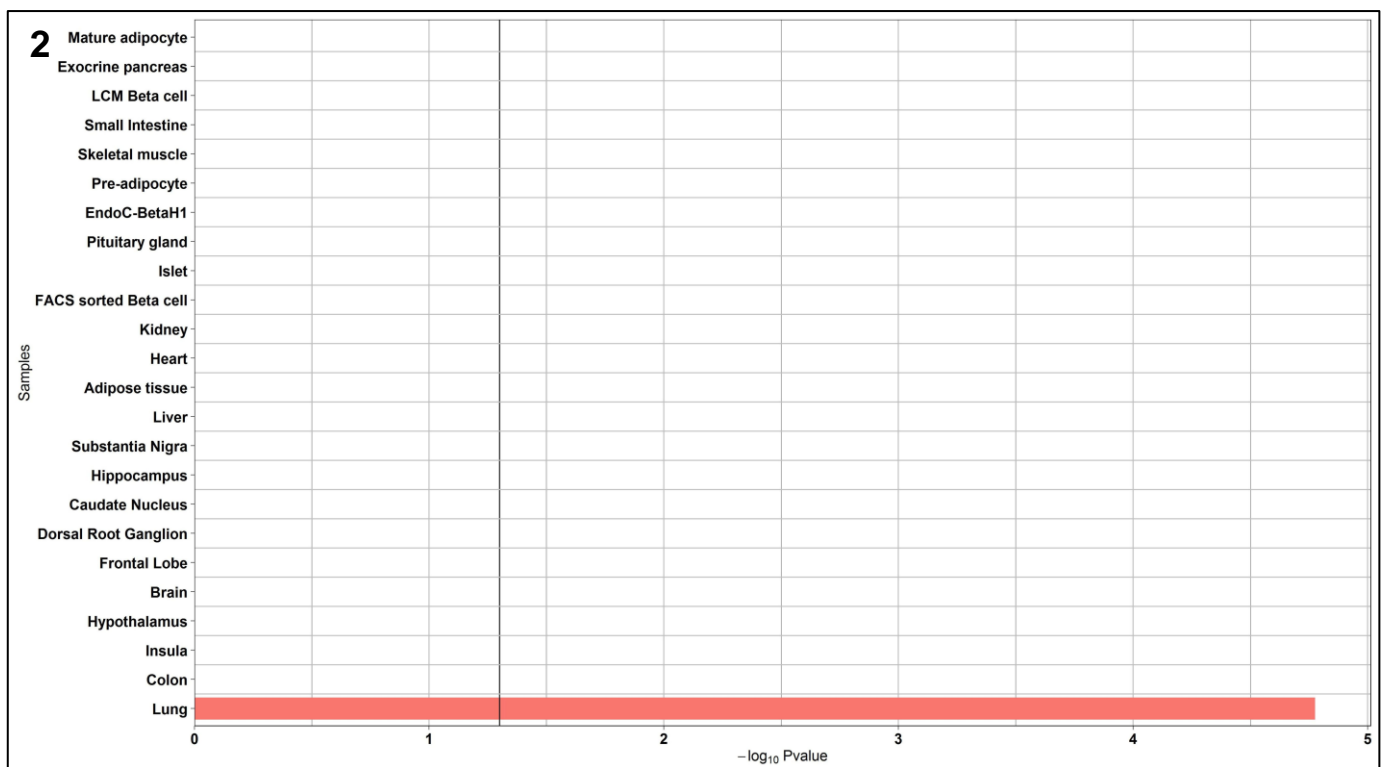
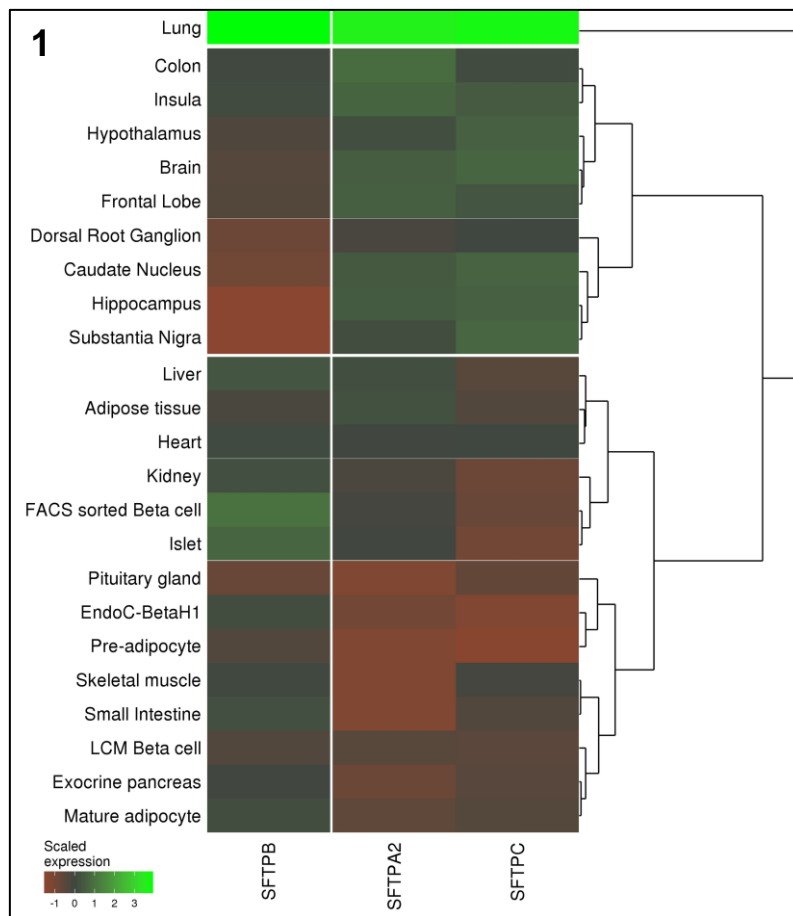


Figure F. (1) Heat map representing the expression of 13 genes known to be highly expressed in pancreatic islets in the panel of human organs, tissues and cells; (2) Enrichment analysis of pancreatic islet markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of 0.05.

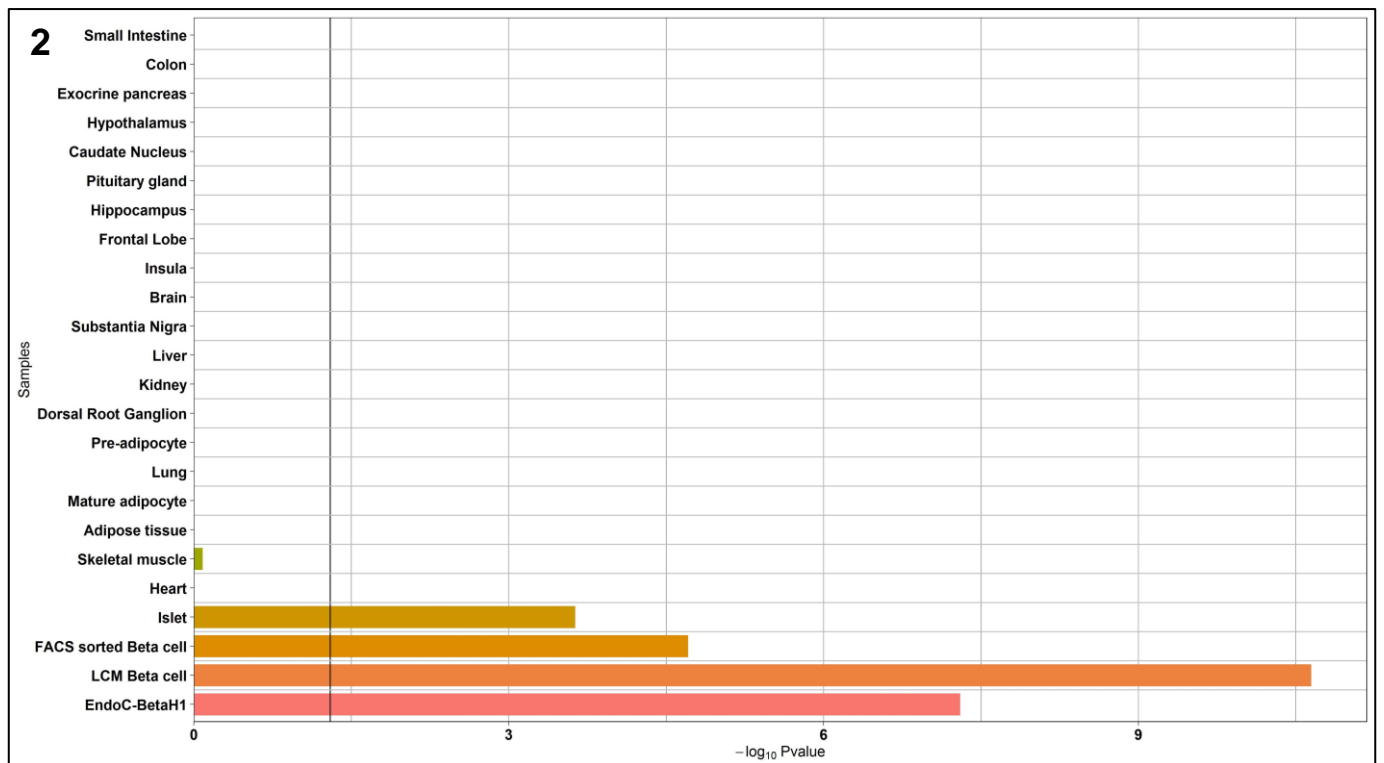
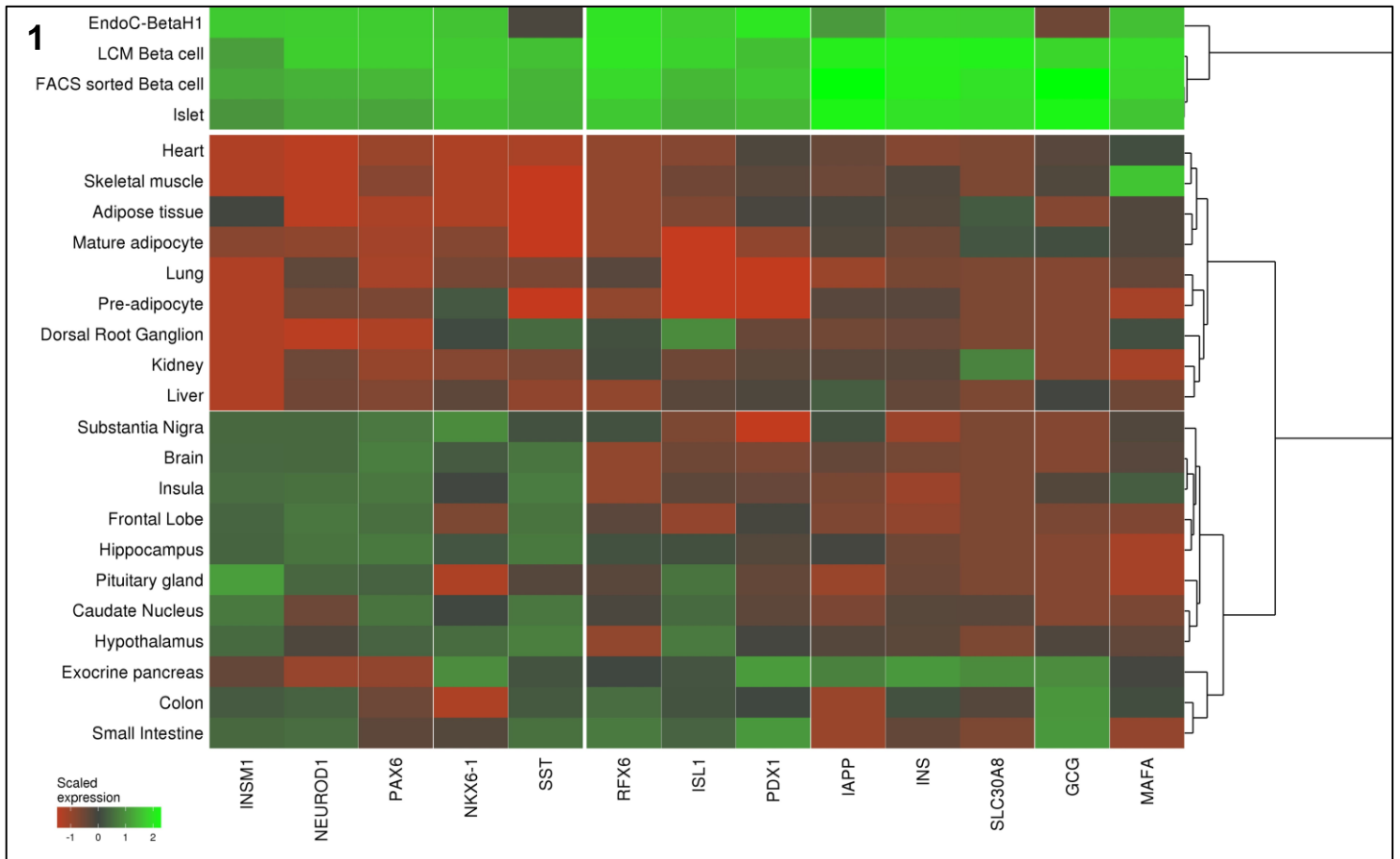


Figure H. Decreased expression of target genes in EndoC-βH1 cells. EndoC-βH1 cells were transfected with control non-targeting pool siRNA (siNTP) or target gene siRNA, and were analyzed 72 hours post-transfection. The mRNA expression of target genes and *INS* (encoding insulin) was determined by real-time quantitative PCR. Results are presented relative to gene expression in siNTP-transfected cells. *PSMB2* was used as endogenous control. Data from at least three independent transfections are presented.

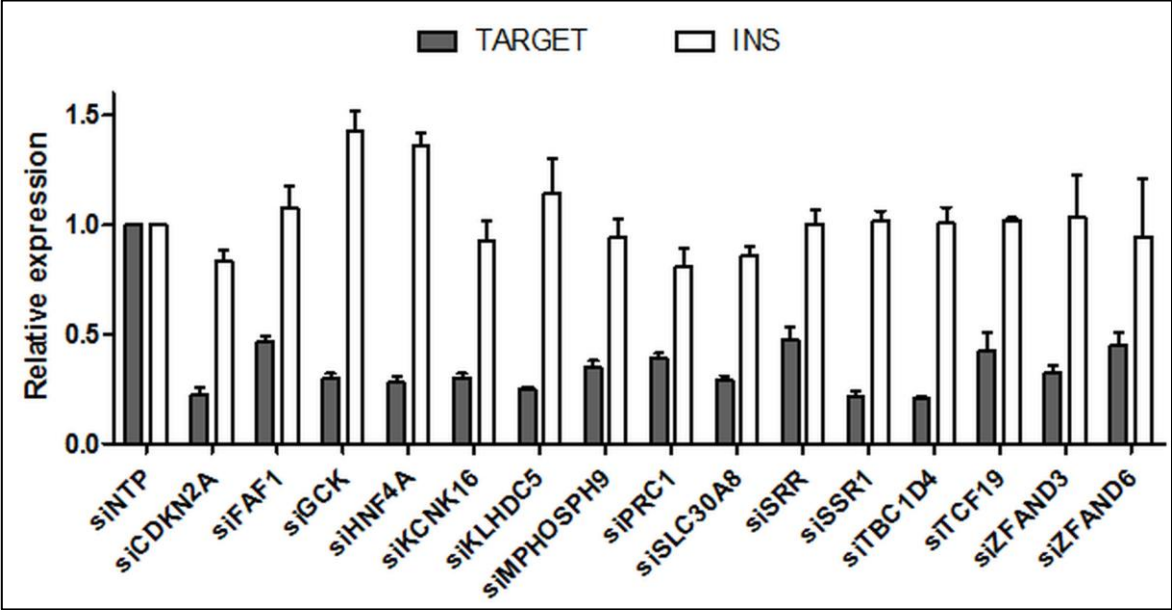


Figure I. Decreased expression of *MPHOSPH9* (1), *SSR1* (2), *FAF1* (3) or *KLHDC5* (4) do not lead to impaired insulin secretion from EndoC- β H1 cells. EndoC- β H1 cells were transfected with control non-targeting pool siRNA (siNTP) or target gene siRNA, and were analyzed 72 hours post-transfection. Insulin secretion (percentage of secretion of the total insulin content) was analyzed in response to 60 minutes incubation with 0.5 mM glucose (\pm 0.5 mM IBMX), followed by 60 minutes incubation with 16.7 mM glucose (\pm 0.5 mM IBMX). Data are mean values \pm SEM of at least three independent experiments. *ns*, not significant. *Glc*, glucose; *IBMX*, phosphodiesterase inhibitor 3-isobutyl-1-methylxanthine.

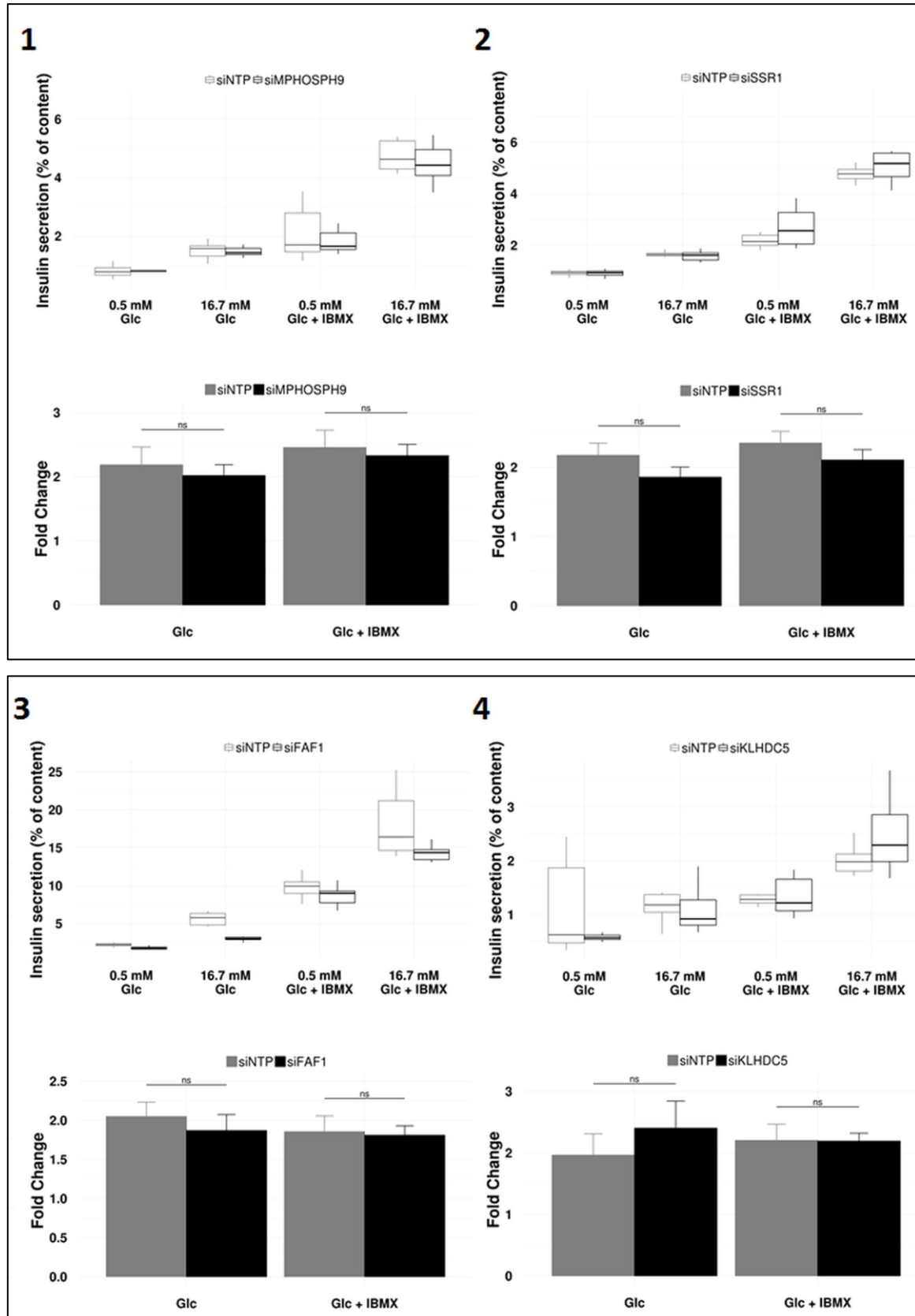


Figure J. SRR (1) and ZFAND6 (2) are expressed in pancreatic islets. Representative images of immunofluorescence staining for SRR (green; A), ZFAND6 (green, B) and insulin (red) performed on fixed tissue sections from normal human pancreases. Yellow (merged images) indicates co-localization of SRR or ZFAND6 with insulin. Blue, DAPI.

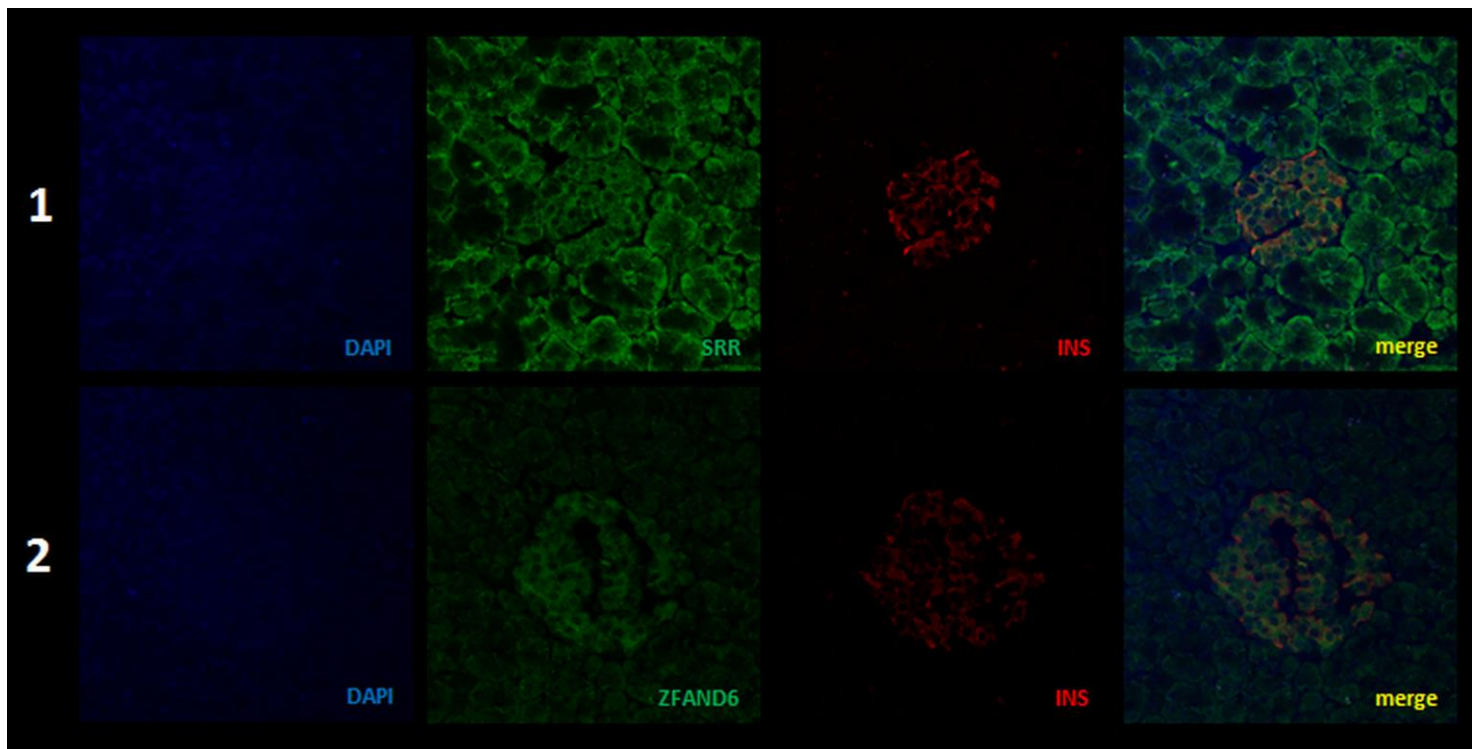
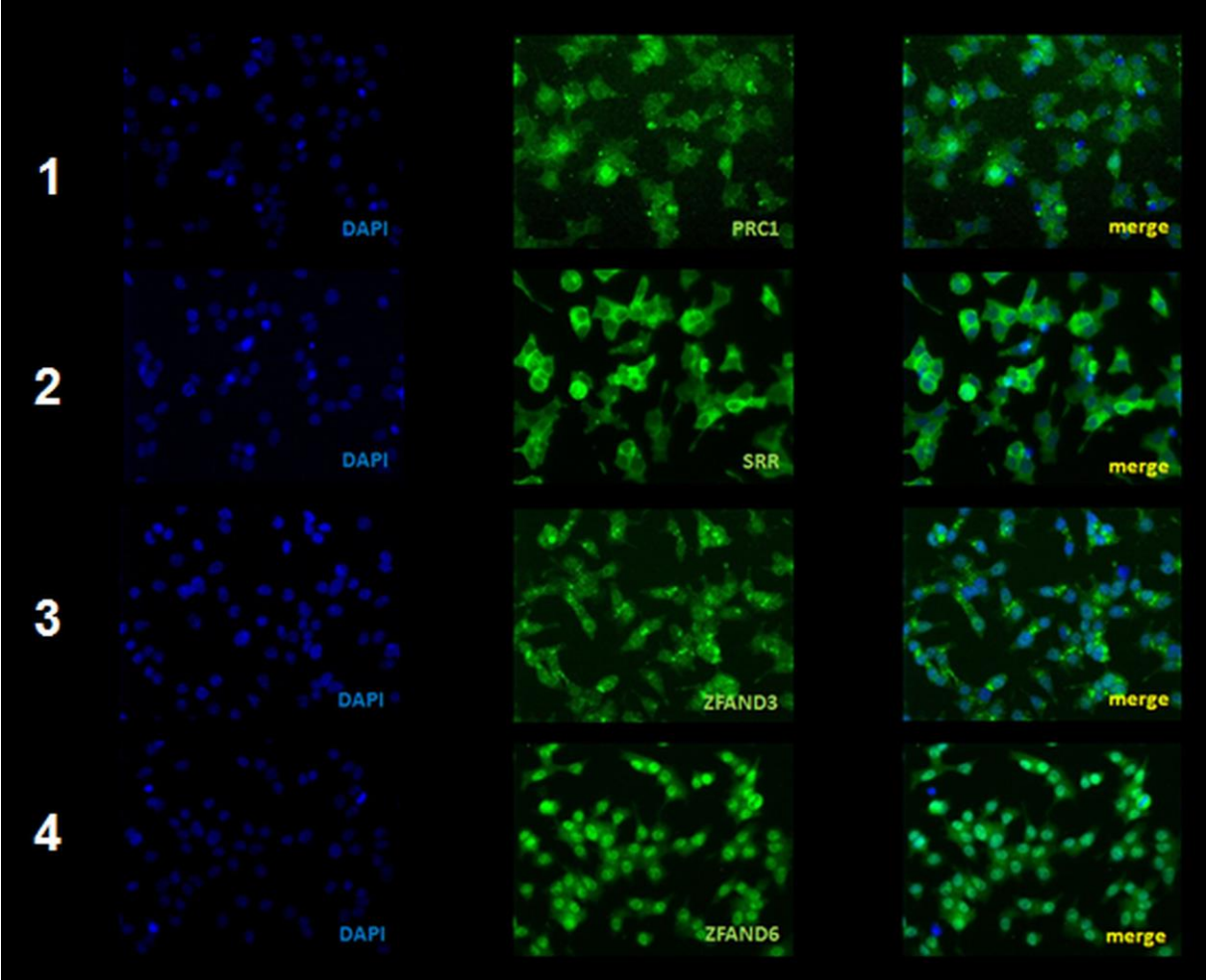


Figure K. PRC1 (1), SRR (2), ZFAND3 (3) and ZFAND6 (4) are expressed in EndoC-βH1 cells. Representative images of immunofluorescence staining for PRC1 (green; 1), SRR (green; 2), ZFAND3 (green; 3), ZFAND6 (green, 4) performed on fixed EndoC-βH1 cells. Blue, DAPI.



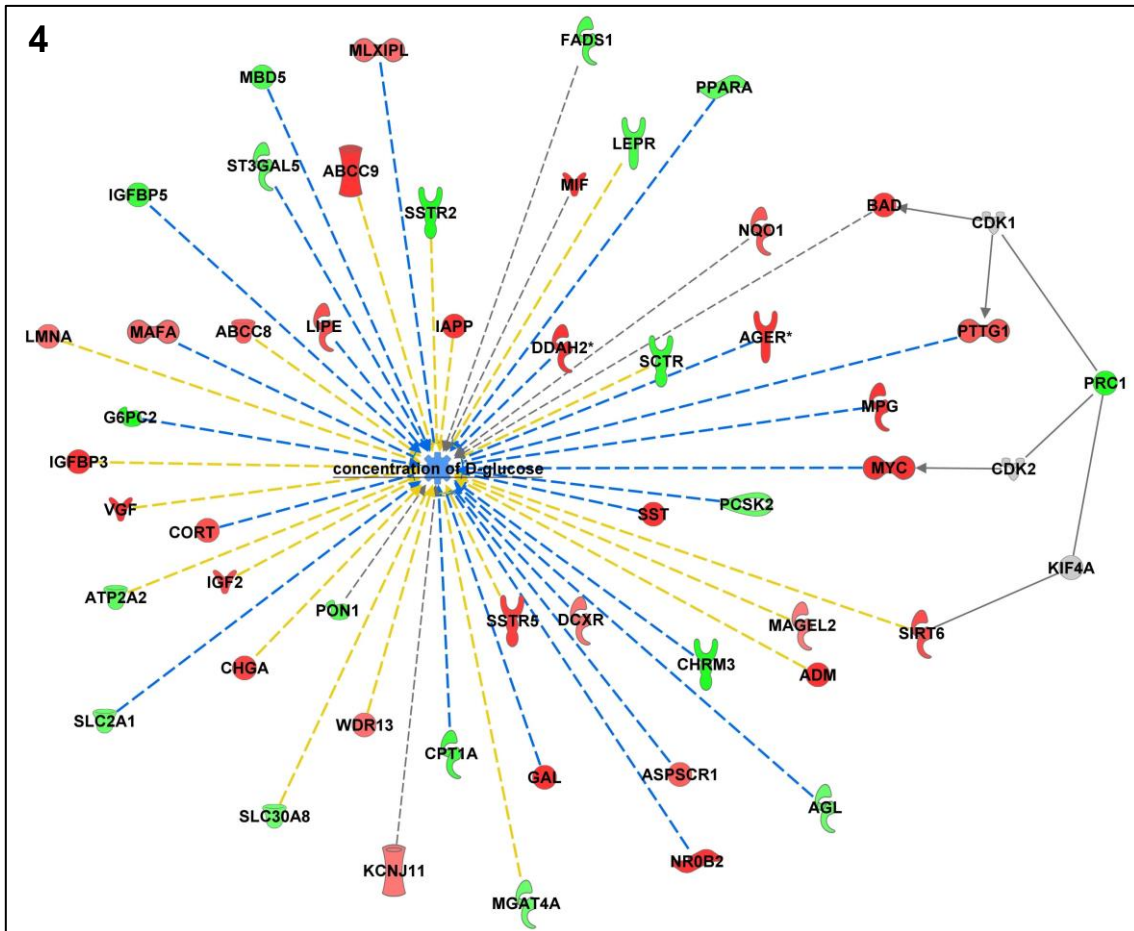
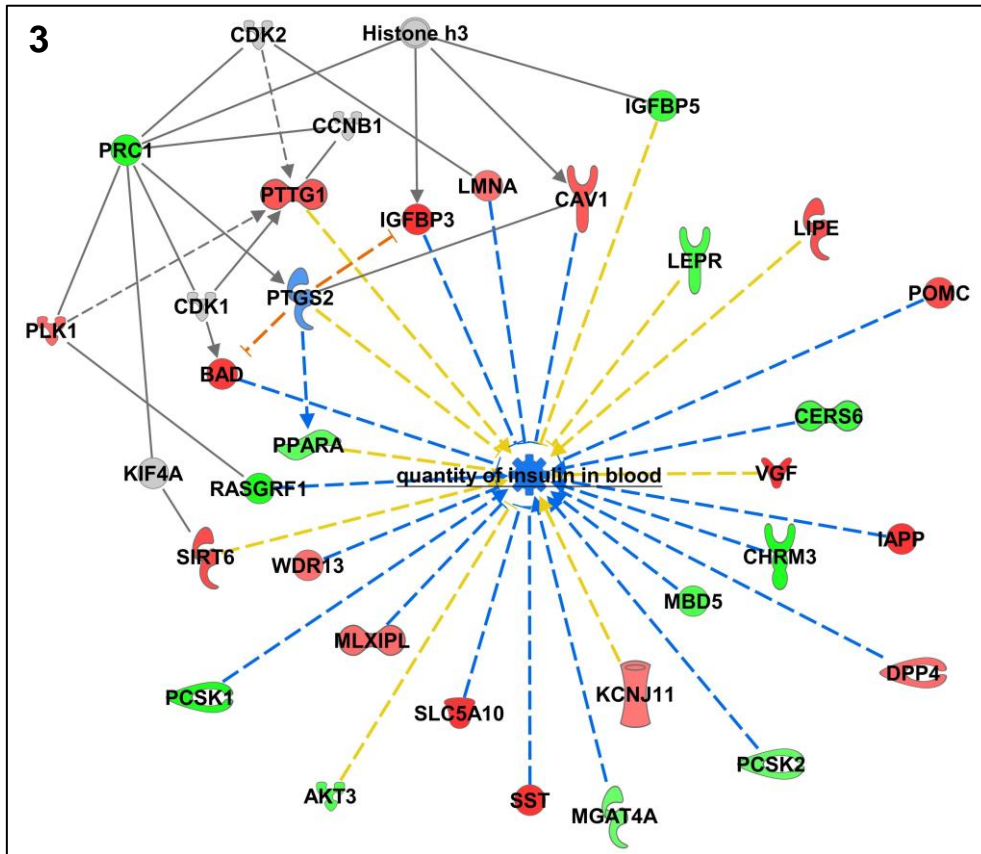
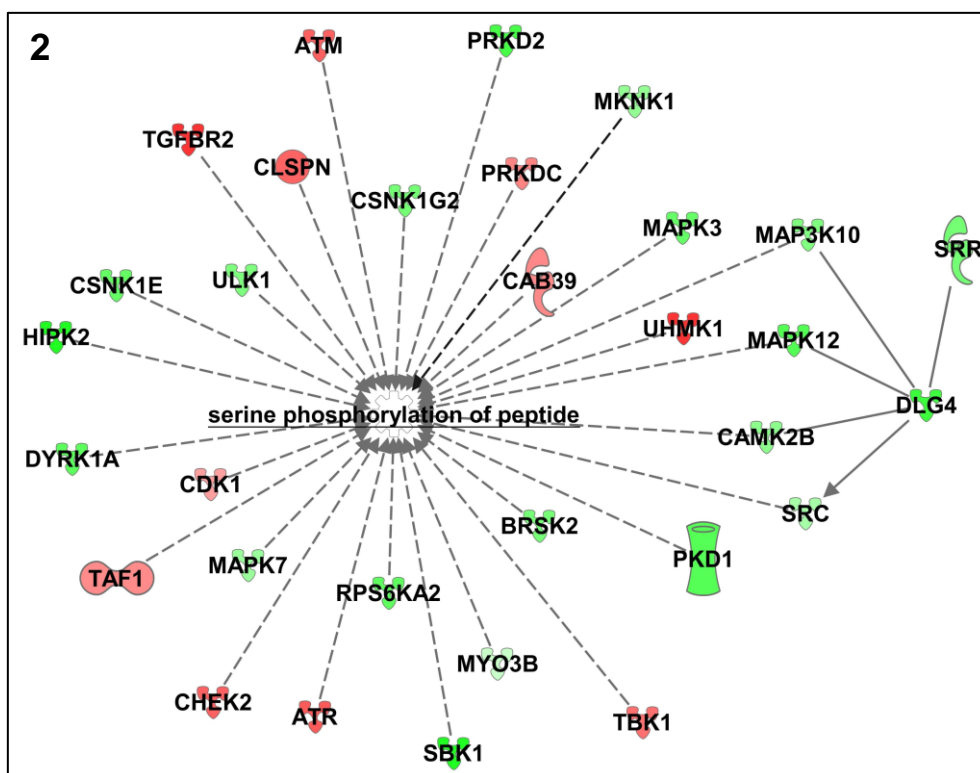
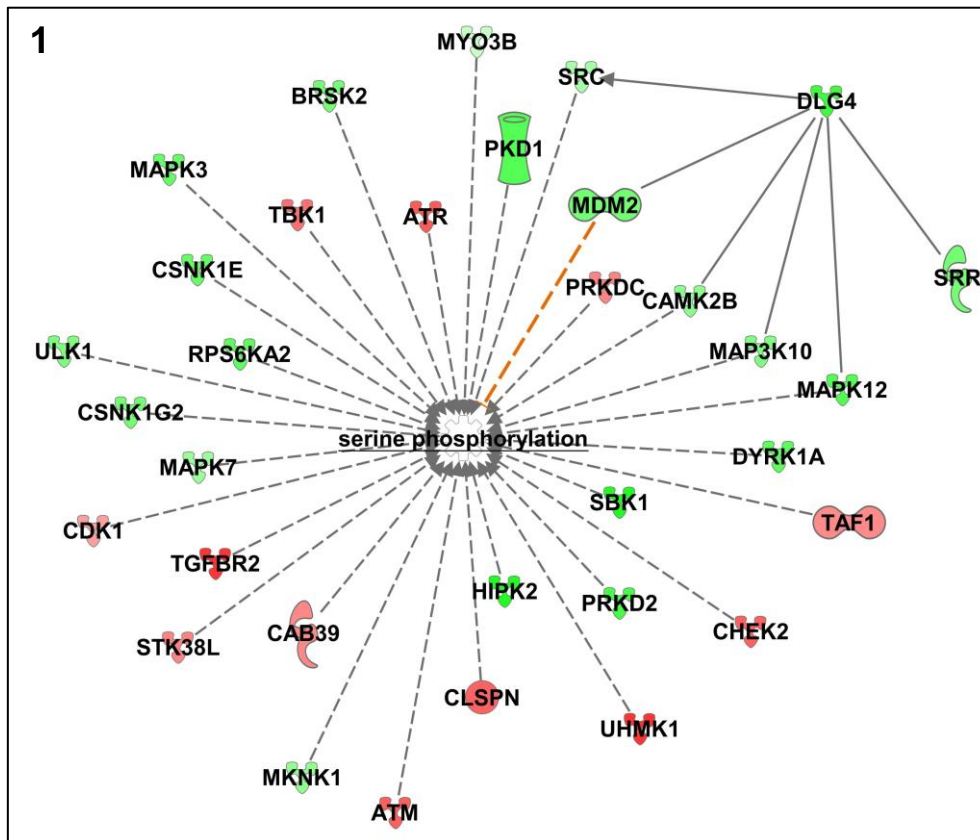


Figure M. Decreased *SRR* expression in EndoC- β H1 cells emphasizes several networks found by IPA: (1) a network related to serine phosphorylation; (2) a network related to serine phosphorylation of peptide; (3) a network related to endoplasmic reticulum stress response; (4) a network related to congenital disorders of glycosylation. The legends used in each figure are denoted in Figure 7.



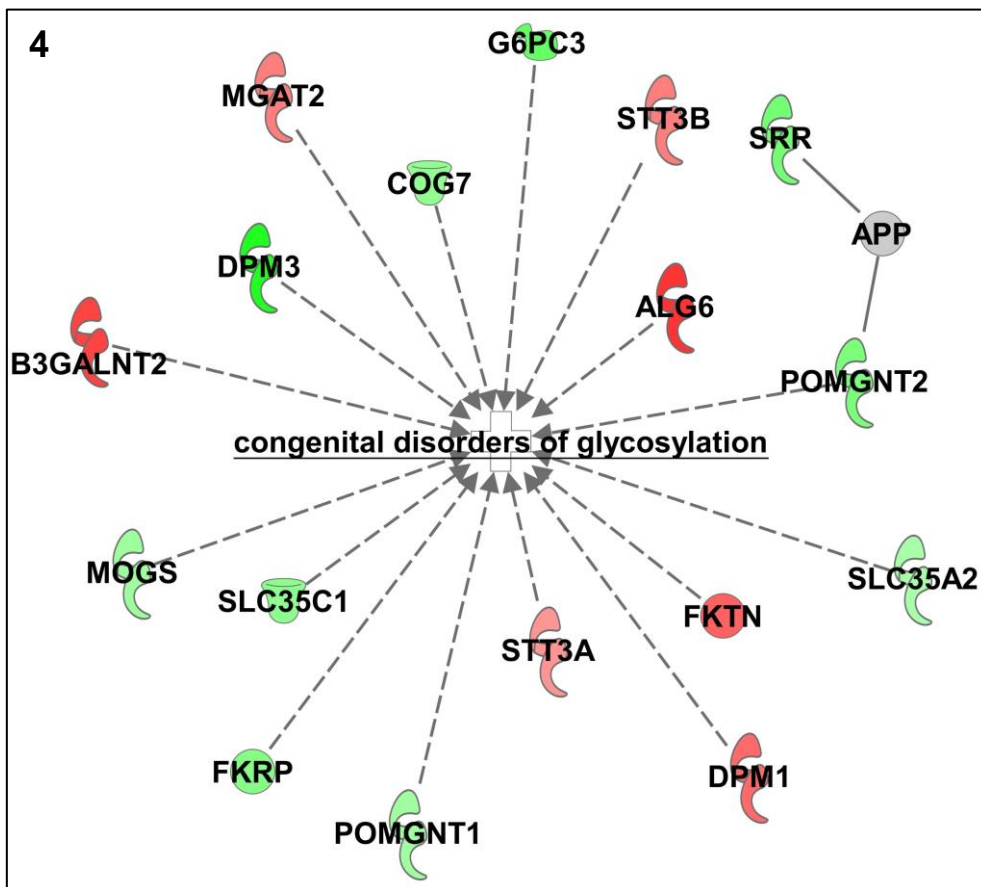
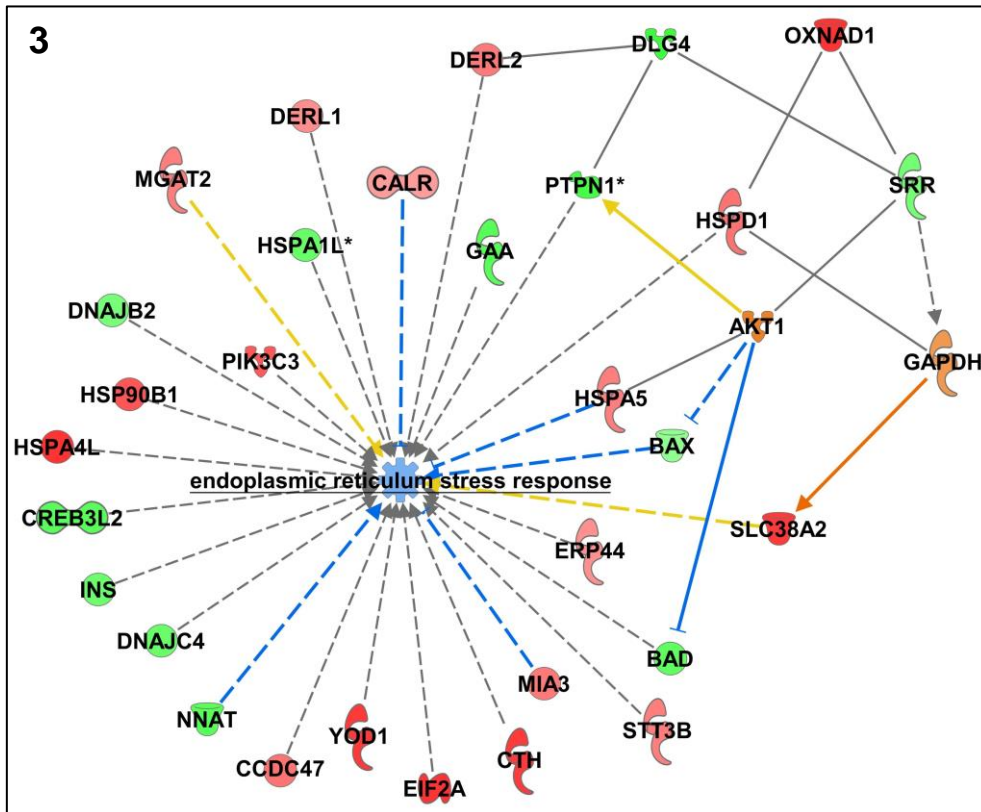
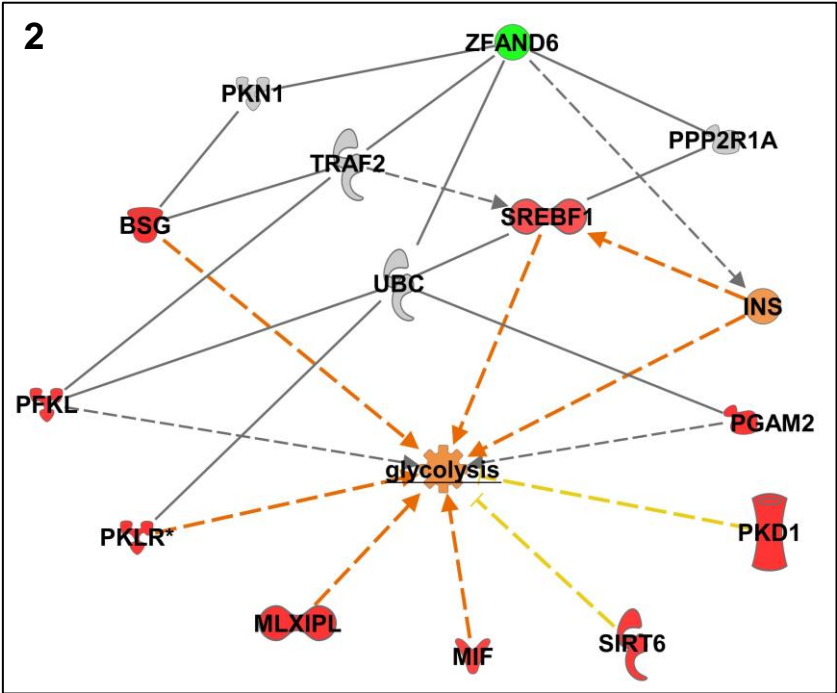
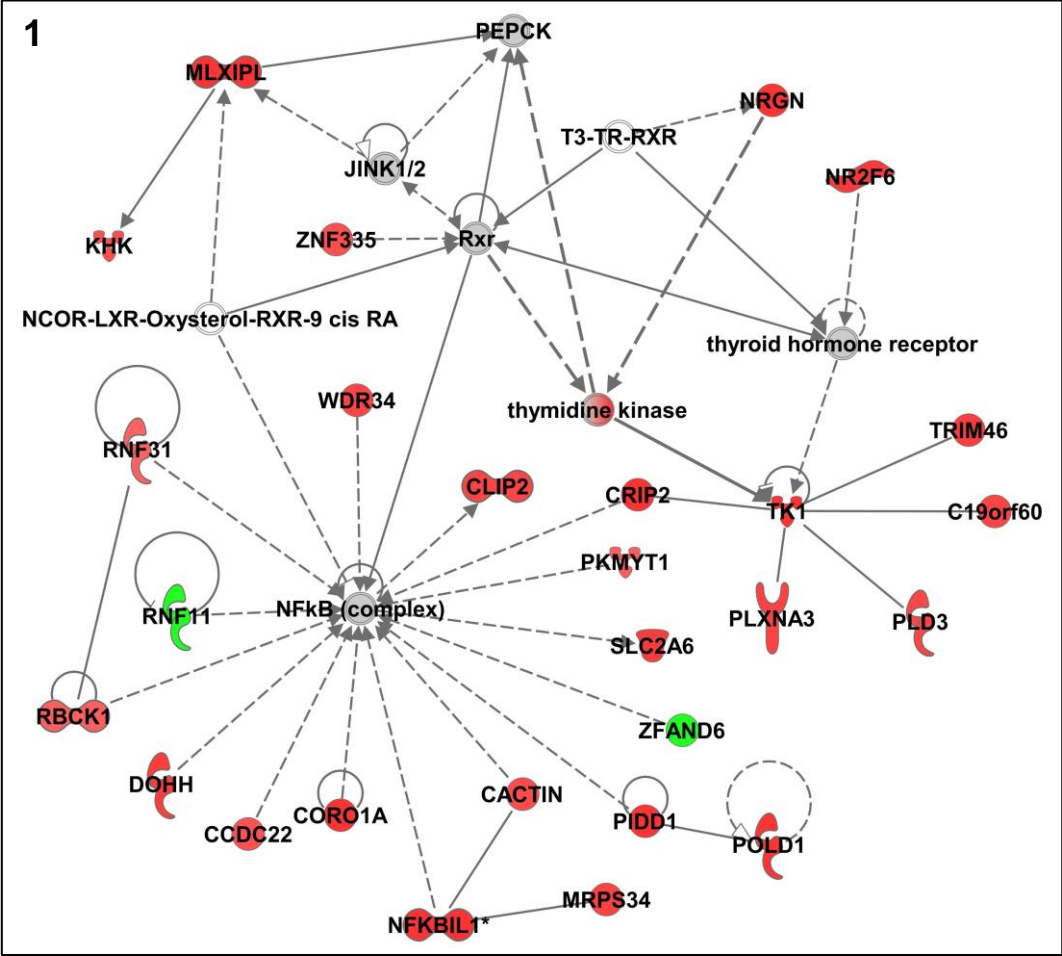


Figure N. Decreased *ZFAND6* expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network of 27 molecules entitled “Cell Signaling, Lipid Metabolism, Small Molecule Biochemistry”; (2) a network related to glycolysis; (3) a network related to the quantity of insulin in blood; (4) a network related to abnormal morphology of pancreas; (5) a network related to abnormal morphology of small islets of Langerhans. The legends used in each figure are denoted in Figure 7.



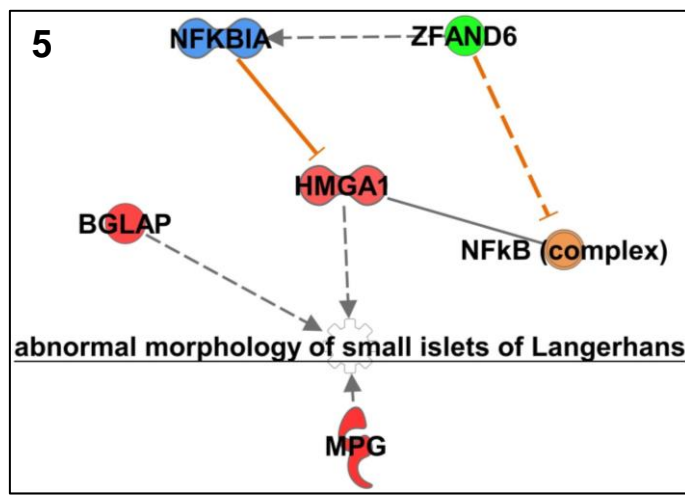
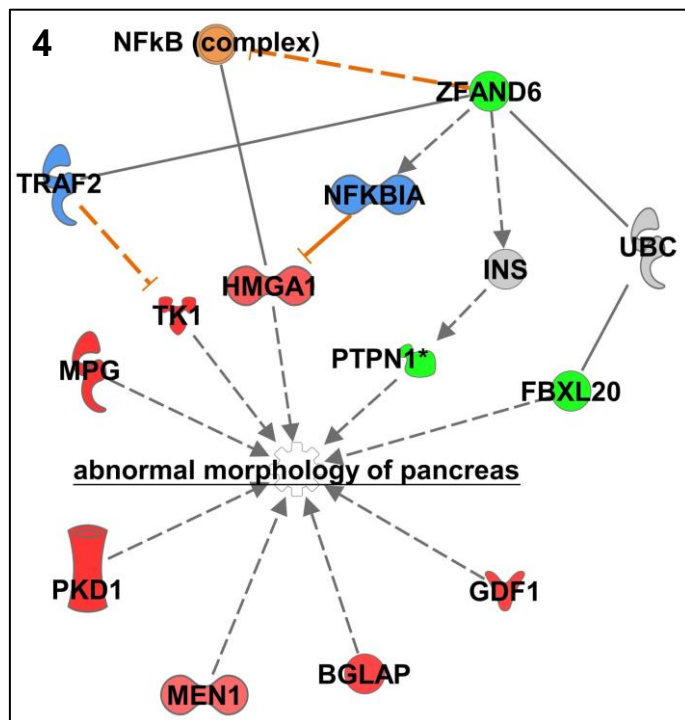
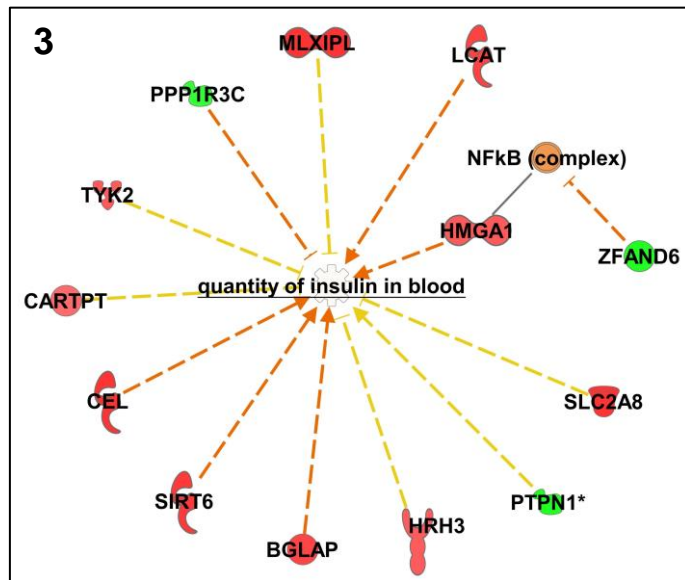


Figure O. Decreased ZFAND3 expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network of 16 molecules entitled “Cellular Assembly and Organization, Lipid Metabolism, Molecular Transport”; (2) a network related to the transport of alpha-amino acid. The legends used in each figure are denoted in Figure 7.

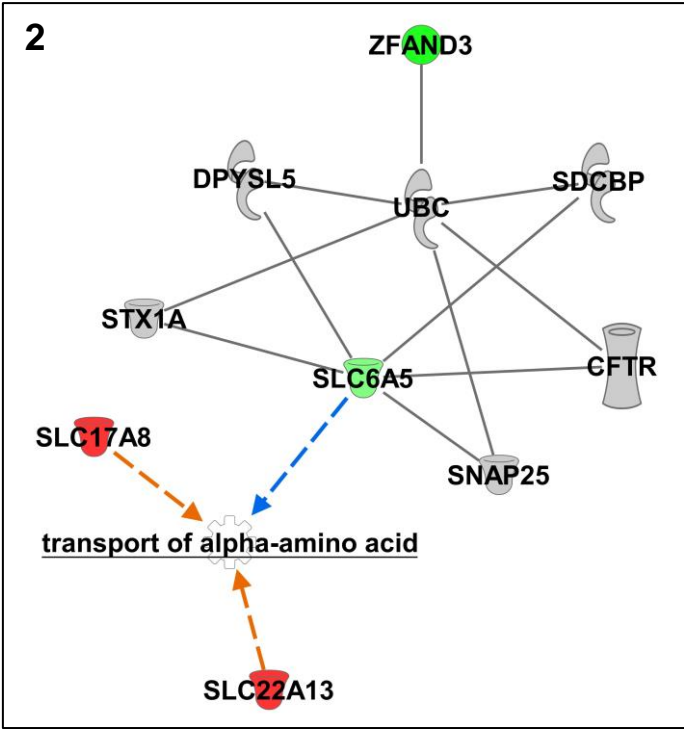
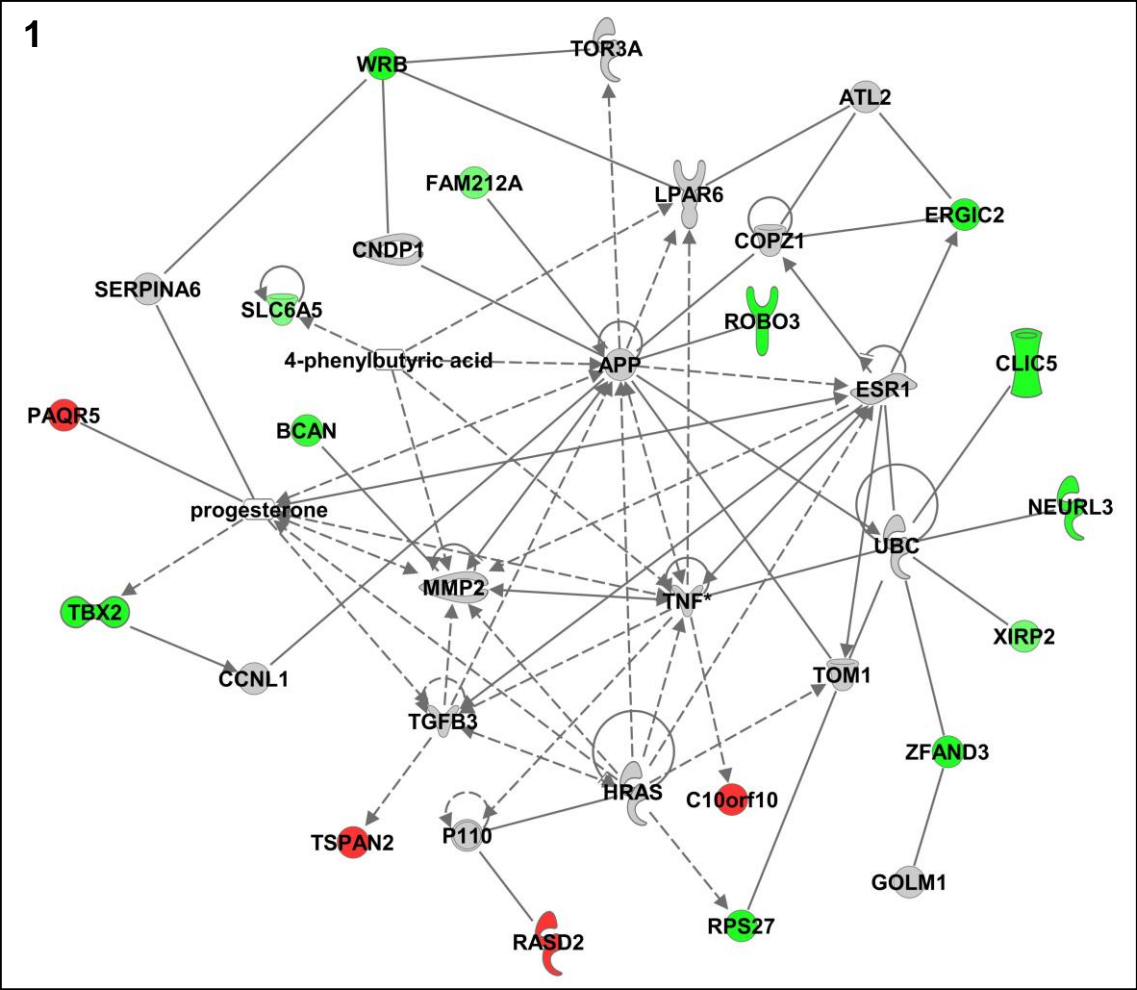


Figure P. Positive correlation between the expression of *Ins2* and the expression of *Prc1*, *Srr*, *Zfand6* and *Zfand3* in mouse pancreatic islets with altered beta-cell function. The expression of the five genes were investigated through quantitative RT-PCR (housekeeping genes: *Actb*) in pancreatic islets from mouse models with altered pancreatic beta-cell function due to STZ treatment (two pools of pancreatic islets treated or not with STZ from eight 10-week old mice; **P1**, **P2**) or to a non-sense mutation in the leptin gene in *ob/ob* mice (pancreatic islets from five 5-week old mice or from five 8-week old mice; **P3**, **P4**). Data represent mean values \pm SD. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; ns, not significant; STZ, streptozotocin; wk, week.

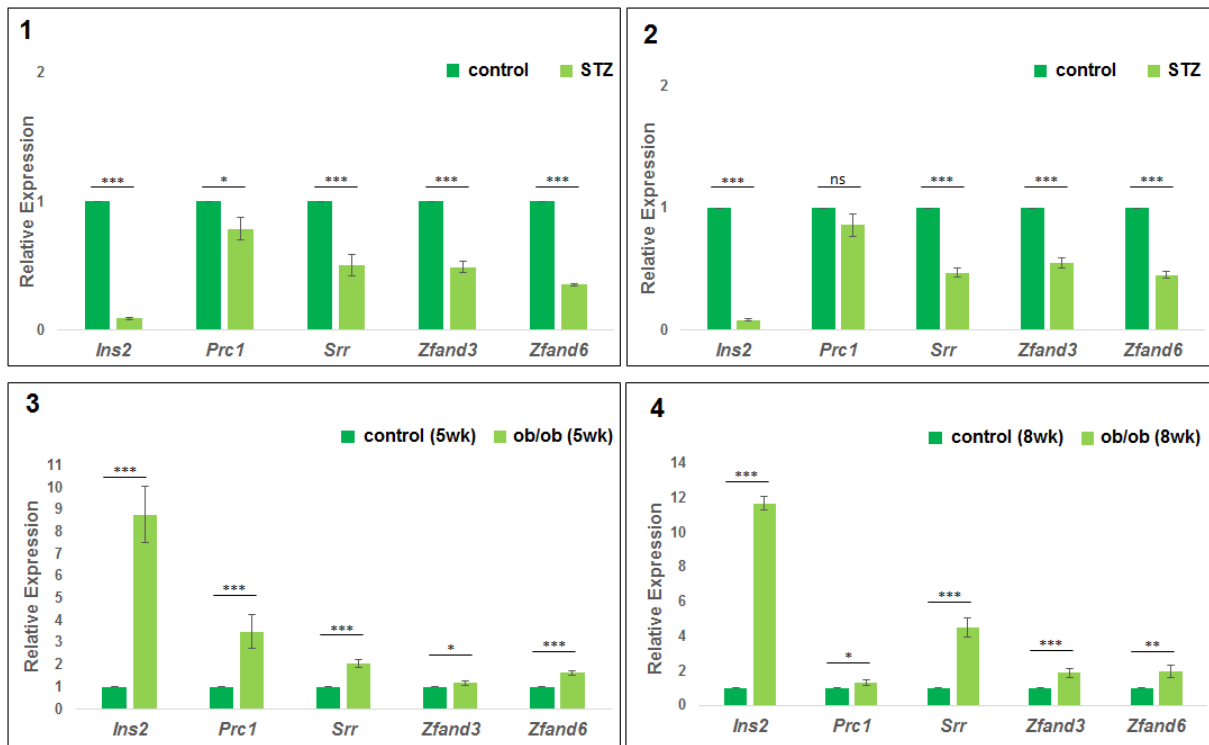
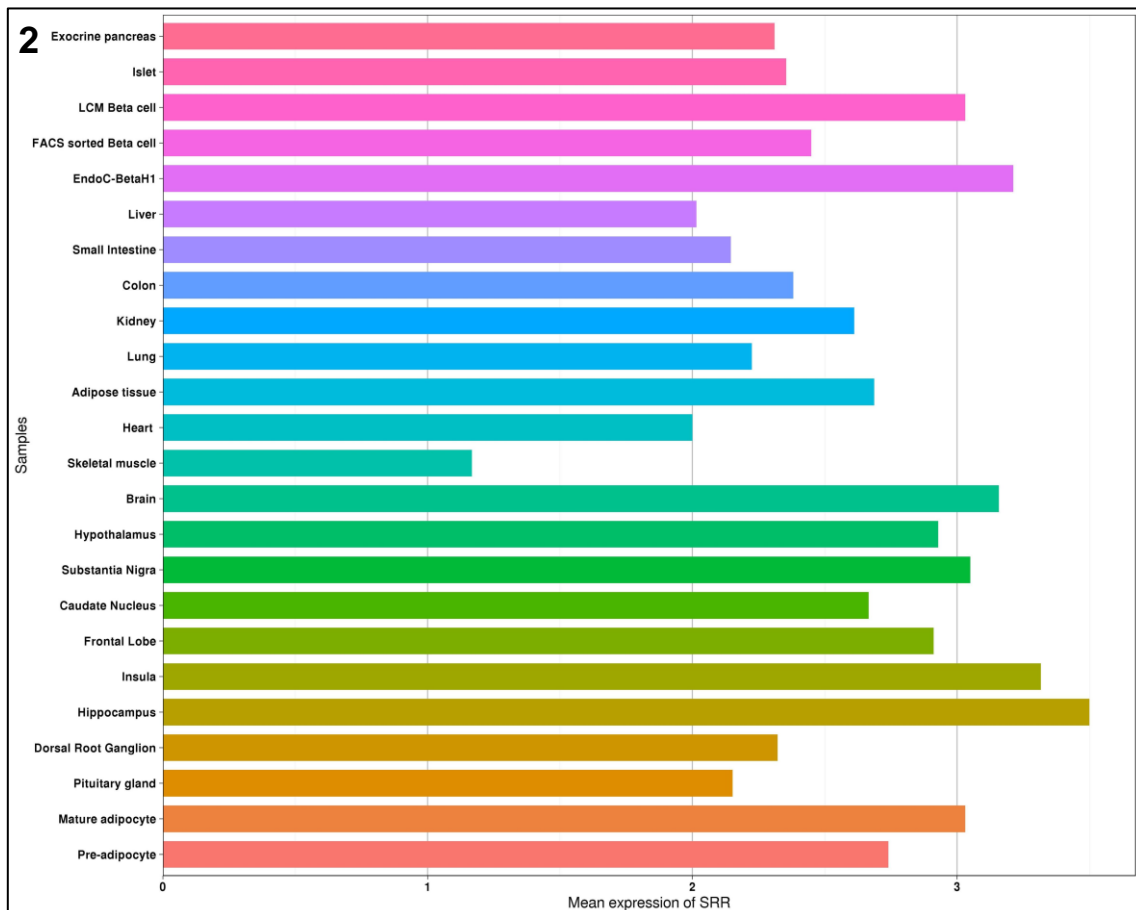
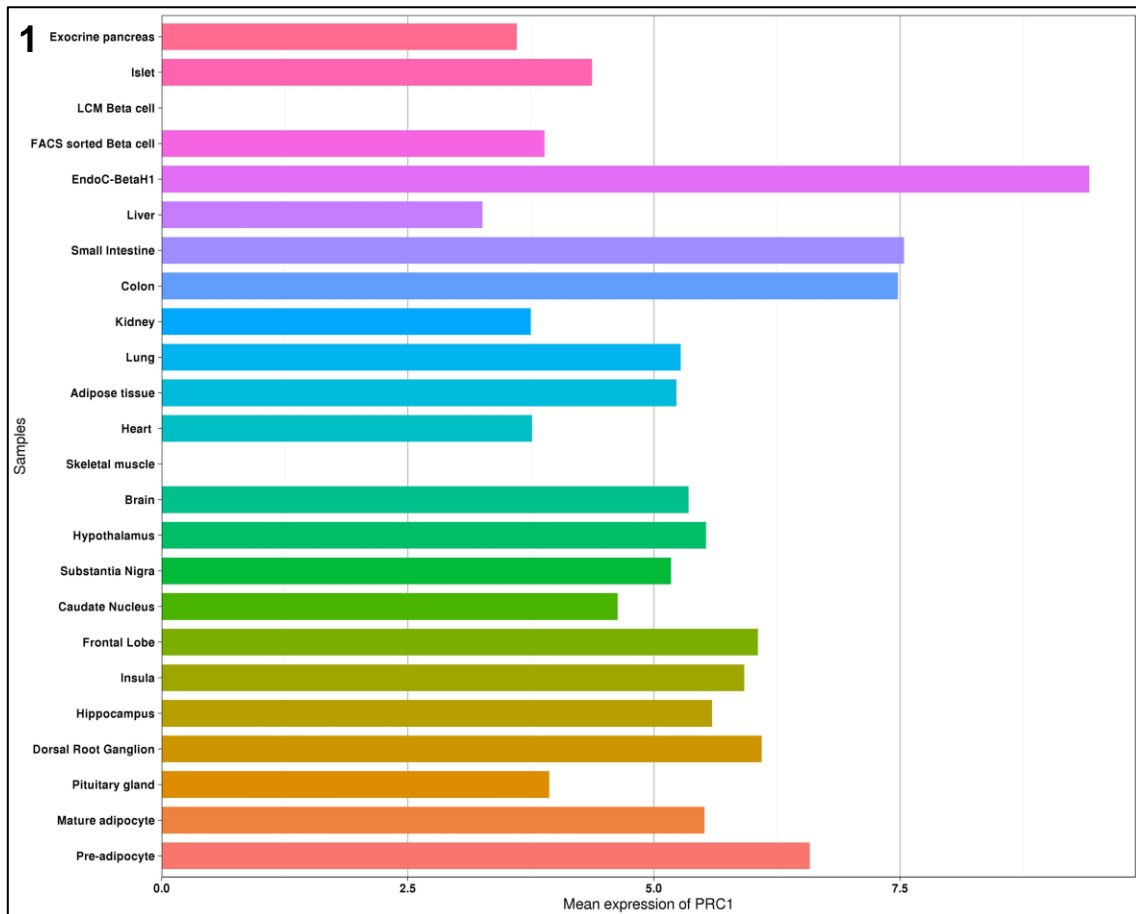


Figure Q. *PRC1* (1), *SRR* (2), *ZFAND6* (3) and *ZFAND3* (4) are ubiquitously expressed in our panel of human tissues.



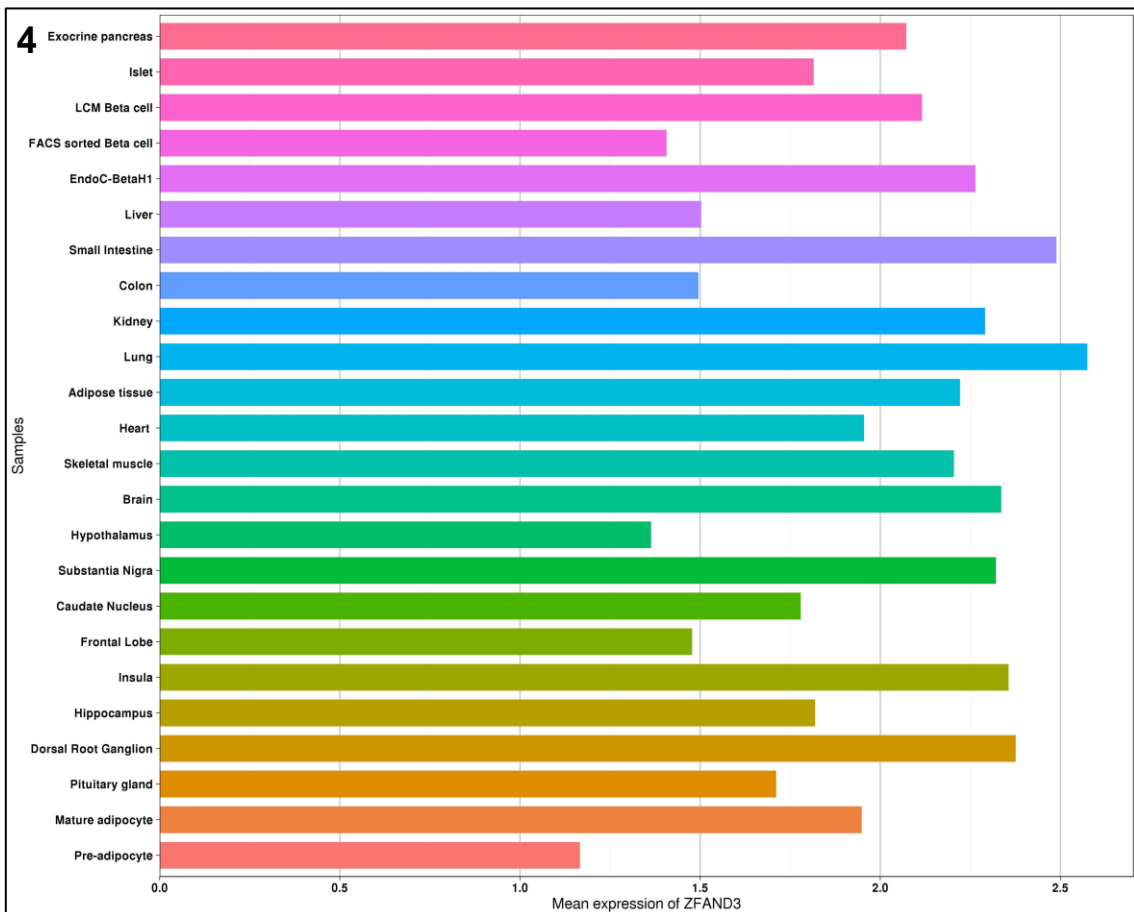
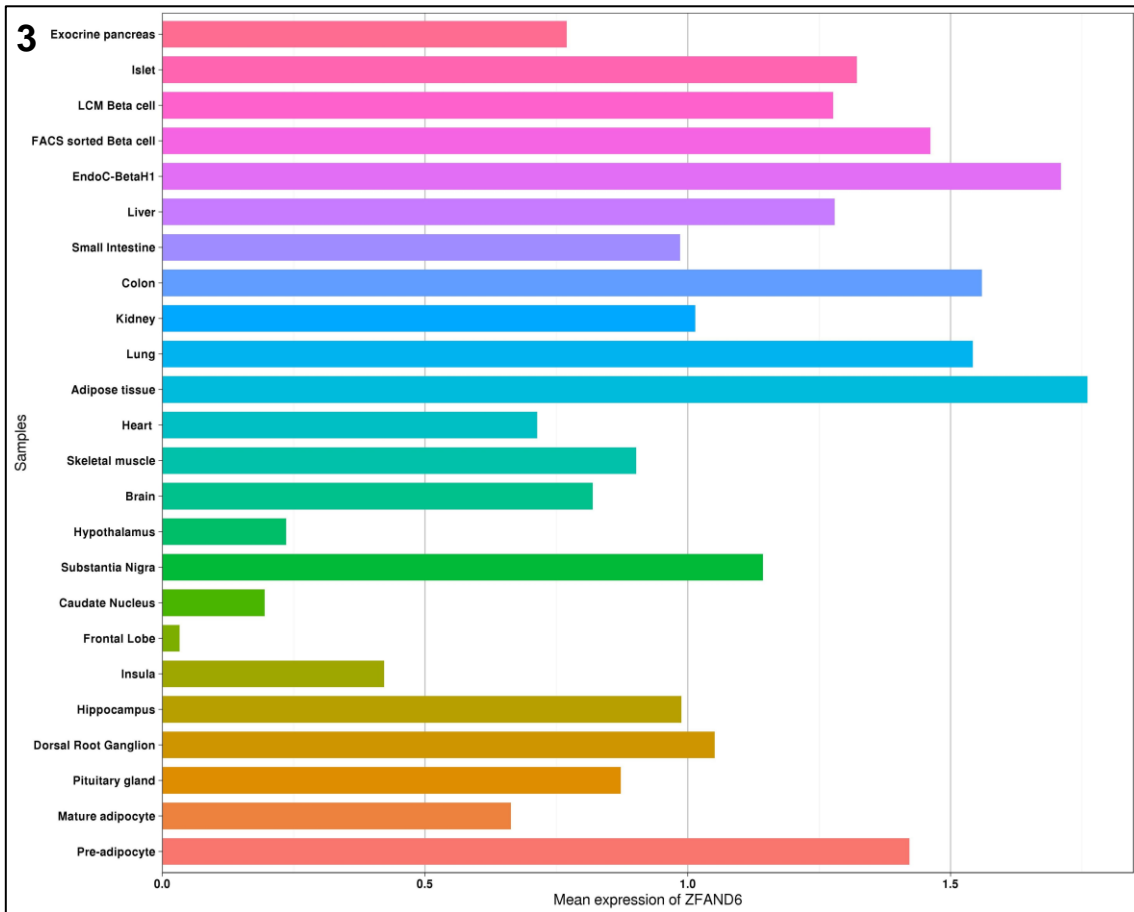


Table A. Probe design and selection for the expression study.

Gene	Accession	Target sequence	Tm _{CP}	Tm _{RP}	PN (CP;RP)	Group
<i>ABCC8</i>	NM_000352.3	ACCTCCGTGGTCTACTATCACA ACATCGAGACTTCCAACCTCCC CAAGCTGCTAATTGCCCTGCTG GTGTATTGGACCCTGGCCTTCA TCACCAAGACCA	81	82	309041; 209041	Monogenic diabetes gene
<i>ADAMTS9</i>	NM_182920.1	AGTGAAATTATTAGAGACCCTGA GCGAATACGAAATCGTGTCTCC CATCCGAGTGAACGCTCTCGGA GAACCCTTTCCCACGAACGTCC ACTTCAAAGA	80	83	350001; 250001	T2D gene
<i>ADCY5</i>	NM_183357.2	CCCCTCCATATTCATGCTCAGC TTCTACCTGACCTGTTCCCTGCT GCTGACCTTGGTGGTGTGGTGTG TCTGTGATCTACTCCTGCGTAAA GCTCTTCCC	83	80	350002; 250002	T2D gene
<i>ALPI</i>	NM_001631.3	CAGCAAGGCTCAGGACAGCAAA GCCTACACGTCCATCCTGTACG GCAATGGCCCCGGGCTACGTGTT CAACTCAGGCGTGCACAGAC GTGAATGAGAGC	85	85	386252; 286252	Marker of gut
<i>ANK1</i>	NM_020477.2	CAGGGTACTTTTTCCCAACCTCA TCTGTCAGAAATCCATGTGGGC TTCCTGGAAAGAAAAAAAAAAAA AAGAAAAGTGGCATGAAATCA GTTTAAACACC	80	79	374572; 274572	T2D gene
<i>ANKRD55</i>	NM_024669.2	GCACAGCAGCAGAAGAGAGTGA ACATTCTGCCAACCCACCAGT GATGAAAATTAAGTGTGGGCA CTCGCTGCAGAAATGTAGATGA ATATGTATTTTC	85	77	351314; 251314	T2D gene
<i>AP3S2</i>	NM_005829.4	GGTGCTAGGGCTCGTGAGCGC CGGGGCCAAGTTTCCGAGTGCC GCTCTCAGCAGCGCACCAACCG GAAGTGATCGTGTGGGCGGA AGGAGGAGCTTTC	85	85	355827; 255827	T2D gene
<i>AQP2</i>	NM_000486.5	GTCTCACAGGTAGTATATGGTG GAGCCAACACTTGAAGTCAAGAC CTTTTACACAAAATCCCATGAT TTTTCCACTGAGACAAATCCTAG GCTCCTGGGA	80	82	365408; 265408	Marker of kidney
<i>ARAP1</i>	NM_001040118.2	GGCCACAGTGAAGGCCCTTATC AGCCACCTGTACTGTGTTCAAGT GCTTCTCAGACACGAACAGAT GAACGTGCACAACCTGGCAATT GTGTTTGGGCCC	83	83	370135; 270135	T2D gene
<i>ARL15</i>	NM_019087.2	AATGCCATCTTGAATGTAAAAGA ACTTGGAGGGCTGATAACATC CGGAAATACTGGAGCCGCTACT ACCAAGGATCTCAAGGGGTAAT ATTTGTATTAG	84	81	300047552; 200047552	T2D gene
<i>BCAR1</i>	NM_001170717.1	CTGGCCCCGGGCACCCTGTACG ATGTGCCCCCGTGAACGGGTGCT TCCTCCTGAGGTGGCTGATGGT GGCGTGGTCGACAGTGGTGTGT ATGCGGTGCCTCC	85	86	374085; 274085	T2D gene
<i>BCL11A</i>	NM_022893.3	TACACATGTACAACCTGCAAACA GCCATTACCAAGTGCATGGTTT CTCTTGCAACACGCACAGAACA CTCATGGATTAAGAATCTACTTA GAAAGCGAAC	79	83	335334; 235334	T2D gene
<i>BLK</i>	NM_001715.2	AGCTTCTTGCTCCAATCAACAAG GCCGGCTCCTTTCTTATCAGAG AGAGTGAAACCAACAAGGTGC CTTCTCCCTGTCTGTGAAGGAT GTCACCACCCA	78	81	304841; 204841	Monogenic diabetes gene
<i>C1orf43</i>	NM_015449.2	ATTCGACTCTCCAGGGTTCAGG ATATCAAGTATGAGCCCCAGCT CCTTGCAGATGATGATGCTAGA CTACTACAACCTGGAAACCCAGG GAAATCAAAGTT	84	84	300000629; 200000629	Housekeeping gene

<i>C2CD4A</i>	NM_207322.2	GCATTTTGTTTAAGACCCCGGAT AAGAAAATGAGGGCAAAAGAGG TGAAGTGAATTGTCCAAGATCA ACAGTGAATTATTAGTTGGAACG CCAGCCTGAT	81	80	310209; 210209	T2D gene
<i>C2CD4B</i>	NM_001007595.2	AGGATGCGGCTCCTCGAGAAAC TCTGTTCCCTCGGCCGAGGCAG CTCCGCGCCGAAGCCCGCCTTC GCCAAAGTGCTCACGCCGAATC GCATCCCCGAAT	86	86	335228; 235228	T2D gene
<i>CAMK1D</i>	NM_020397.2	AAAGAGACCCTCGGAACCGGG GCCTTTTCCGAAGTGGTTTTAGC TGAAGAGAAGGCAACTGGCAAG CTCTTTGCTGTGAAGTGTATCCC TAAGAAGGCGC	79	81	305079; 205079	T2D gene
<i>CCND2</i>	NM_001759.3	TGTGAGGAACAGAAGTGCGAAG AAGAGGTCTTCCCTCTGGCCAT GAATTACCTGGACCGTTTCTTG GCTGGGGTCCCAGACTCCGAAGT CCCATCTGCAAC	85	86	340263; 240263	T2D gene
<i>CDC123</i>	NM_006023.2	TTGGTGAAGTCACAGATTCCT GCTGTTCCACTGGGAAGAACTG ATATCTGAGAACAACCTAAACGG CGATTTTAGTGAAGTTGACGCTC AAGAGCAGGA	83	81	300039699; 200039699	T2D gene
<i>CDH16</i>	NM_004062.2	GCCACGTGAACACATAATCCCC GTGGTGGTCAGCCACAATGCC AGATGTGGCAGCTCCTGGTTCC AGTGATCGTGTGTCGCTGCAAC GTGGAGGGGCGAG	82	81	308452; 208452	Marker of kidney
<i>CDKAL1</i>	NM_017774.2	GGTCACTCTGTGAGACTGCTGG GTCAGAAAAAGGATAATGGAAG GCGGCTTGGGGGAGCACGATT GGATTTGCCGAAGATTAGGAAG AATCCAATGATAG	82	82	306459; 206459	T2D gene
<i>CDKN2A</i>	NM_000077.3	AAGCGCACATTCATGTGGGCAT TTCTTGCGAGCCTCGCAGCCTC CGGAAGCTGTGCACTTCATGAC AAGCATTTTGTGAAGTAGGGAA GCTCAGGGGGGT	82	81	302810; 202810	T2D gene
<i>CDKN2B</i>	NM_004936.3	CACTTGGGTGACGGCAGTCGAT GCGTTCACTCCAATGTCTGCTG AGGAGTTATGGTGAACCCACAA CTTAGGCCCTAGCGGCAGAAAG GAAAACCTGAAG	82	81	301731; 201731	T2D gene
<i>CEL</i>	NM_001807.3	GGTTCGTGGAAGGCGTCAATAA GAAGCTCGGCCCTCTGGGTGAC TCTGTGGACATCTTCAAGGGCA TCCCCTTCGCAGCTCCCACCAA GGCCCTGGAAAA	85	84	348673; 248673	Monogenic diabetes gene
<i>CHCHD2P9</i>	ENST0000046172 6.1	CTTCTATGGGATCAAACAGTTTC TGGAGTGTGCCAGAACCAGG GCGACATCAAGCTCTGTGAGGA TTTCAGTAAGGTGCTGAAACAG TGCCGACTTGCA	86	84	300093539; 200093539	T2D gene
<i>CIDEA</i>	NM_022094.2	GACAAGGATGGAATACGCCATG AAGTCCCTTAGCCTTCTCTACCC CAAGTCCCTCTCCAGGCATGTG TCAGTGCGTACCTCTGTGGTGA CCCAGCAGCTG	84	85	343264; 243264	Marker of adipose tissue
<i>CILP2</i>	NM_153221.2	CCGCTCCCAGCTCAGAAGCCGT CTCTGACTTCTCGTGCATTTTT GACCCTGATTTCAATCTTCTACC CTTGGGAGTTCTGGCGTTTGGC ACAAAGTCCC	83	79	300060271; 200060271	T2D gene
<i>COBLL1</i>	NM_014900.3	AGTTTTTTTCAACGCAGTAAGAA AAAGCGAGACCAAACCTGCAAGT GCCCTGCAACCCCTCTAGTAA ATAAGCACCGCCCAACTTTTACA AGGTCCAATA	80	82	313525; 213525	T2D gene
<i>DGKB</i>	NM_004080.1	TCCACTTCTGTGCTCCTGGGC TTAGAAAATAACGTGAAGGATG ATGGACAGCACGTGTGGCGACT GAAGCACTTTAACAAACCTGCC TATTGCAACCTT	78	79	302687; 202687	T2D gene

<i>DNER</i>	NM_139072.3	CCTCTACATCATCATTGGAGCC CTCTGCGTGGCCTTCATCCTTAT GCTGATCATCCTGATCGTGGGG ATTTGCCGCATCAGCCGCATTG AATACCAGGGT	82	83	350100; 250100	T2D gene
<i>DUSP9</i>	NM_001395.2	CCCATCTCCGACCACTGGAGCC AGAACCTGTCGCGGTTCTTTCC GGAGGCCATTGAGTTCATTGAT GAGGCCTTGTCCCAGAACTGCG GGGTGCTCGTCC	85	84	347657; 247657	T2D gene
<i>FABP4</i>	NM_001442.2	GGTGAATGCGTCATGAAAGGC GTCACCTCCACGAGAGTTTATG AGAGAGCATAAGCCAAGGGACG TTGACCTGGACTGAAGTTCGCA TTGAACTCTACA	83	83	311558; 211558	Marker of adipose tissue
<i>FAF1</i>	NM_007051.2	GCTTTTCAAGAGGCCTTCTATGT GAAAGCCCGAGATAGAAAGCTT CTTGCTATCTACCTCCACCATGA TGAAAGTGTGTTAACCAACGTG TTCTGCTCAC	81	80	314945; 214945	T2D gene
<i>FITM2</i>	NM_001080472.1	CTTGTCCCAGAAGGTGTTGGC ACCTTGTTTGGTTTGCTGAGCTG GTACGGGACATACGGGTTTTGG TATCCGAAAGCCTTTTCCCAG GACTTCCTCCC	79	82	300022375; 200022375	T2D gene
<i>FOXP3</i>	NM_014009.3	GGGCCATCCTGGAGGCTCCAG AGAAGCAGCGGACACTCAATGA GATCTACCACTGGTTCACACGC ATGTTTGCCTTCTTCAGAAACCA TCCTGCCACCTG	81	79	310104; 210104	Monogenic diabetes gene
<i>FTO</i>	NM_001080432.2	AAAGTGAGGATGACTCTCATCT CGAAGGCAGGGATCCTGATATT TGGCATGTTGGTTTTAAGATCTC ATGGGACATAGAGACACCTGGT TTGGCGATACC	84	80	344638; 244638	T2D gene
<i>GATA4</i>	NM_002052.3	GACTTCTTTCCCAAGATGTCCTT GTCCCCTGCGTTCCCACCTGTG GCCTAGACCGTGGGTTTTGCAT TGTGTTTCTAGCACCGAGGATC TGAGAACAAGC	83	81	311568; 211568	Monogenic diabetes gene
<i>GATA6</i>	NM_005257.3	GACAGTGGCGACTGCGCTGACA GAACGTGATTCTCGTGCCTTTAT TTTAAAAGAGATGTTTTTCCCAA GAGGCTTGCTGAAAGAGTGAGA GAAGATGGAA	80	83	311617; 211617	Monogenic diabetes gene
<i>GCC1</i>	NM_024523.5	TACAGCAGGAAATGAGAAAGAC AGCTCTTGCAGAGGATCAACTC CGTCAGCAATCTCAGGTAGAAG AACAGAGGGTGGCAGCCCTGG AGAATCAAATATC	82	81	300572; 200572	T2D gene
<i>GCG</i>	NM_002054.2	TGGACTCCAGGCGTGCCCAAGA TTTTGTGCAGTGGTTGATGAATA CCAAGAGGAACAGGAATAACAT TGCCAAACGTCACGATGAATTT GAGAGACATGC	84	83	311569; 211569	Marker of pancreatic islet
<i>GCK</i>	NM_000162.3	CCACCTTTCTCGCTGGAATCAAT TTCCCAGAAGGGAGTTGCTCAC TCAGGACTTTGATGCATTTCCAC ACTGTCAGAGCTGTTGGCCTCG CCTGGGCCCA	82	83	311750; 211750	T2D gene & Monogenic diabetes gene
<i>GCKR</i>	NM_001486.3	TGGGTGCTGAATACAGTGAGTA CAGGTGCTCATGTGCTTCTTGG TAAGATCCTACAAAACCATGT TGGACCTTCGGATTAGCAACTC CAAGCTCTTCT	84	82	349899; 249899	T2D gene
<i>GIPR</i>	NM_000164.2	CCCTGTCTCTCGCCACACTGCT GCTAGCCCTGCTCATCTTGAGT TTGTTCCAGGCGGCTACATTGCA CTAGAAACTATATCCACATCAAC CTGTTACGTC	82	79	302954; 202954	T2D gene
<i>GLIS3</i>	NM_001042413.1	CCCGGGACATCCATGTCCAGCA ATAGTGTCTCTAACTCATTACCA TCCTACCTTTTTGGCACGAAA GTAGCCACTCTCCTTACCCTAGT CCTCGGCACT	82	83	300021627; 200021627	T2D gene & Monogenic diabetes gene

<i>GPSM1</i>	NM_001145638.1	GGCCACGGCGAGCCCCAGGAG CCGGGGGACGACTTCTTCAACA TGCTCATCAAGTACCAGTCCTC CAGGATCGATGACCAGCGCTGC CCGCCACCTGACG	84	84	374380; 274380	T2D gene
<i>GRB14</i>	NM_004490.2	ACAGCTGGACCCTTTTTGAGCA CCTGCCTCACATAGGTGTAGAA AGAACAATAGAAGACCACGAAC TGGTGATTGAAGTGCTATCCAA CTGGGGGATAGA	83	82	302690; 202690	T2D gene
<i>GRK5</i>	NM_005308.2	GTTCTCCACGGGCTCTGTGTCC ATCCCATGGCAAACGAGATGA TAGAAACAGAATGCTTTAAGGA GCTGAACGTGTTTGGACCTAAT GGTACCCTCCCG	79	78	303130; 203130	T2D gene
<i>HHEX</i>	NM_002729.4	GCACTATCACTTAGTACCTGTTT GACCAAGGTGTTAAGGGGATAG TACCTCCAATTCAAGCAGAGA AACTGACCTGACTAAAGTTAATC GCAGATGAAC	82	83	311692; 211692	T2D gene
<i>HLA-B</i>	NM_005514.6	CCCTGAGATGGGAGCCGCTCTTC CCAGTCCACCGTCCCCATCGTG GGCATTGTTGCTGGCCTGGCTG TCCTAGCAGTTGTGGTCATCGG AGCTGTGGTCCG	86	86	329226; 229226	T2D gene
<i>HMG20A</i>	NM_018200.2	TATACATCTCCATTTTCTGACCT CTGGACTAACTGGTTGCTCAGC AAGGTTCTGAAGGAGAGTTTCT TGCATTGGACAGGCCAGTCTT CTCCCATCATT	81	80	348437; 248437	T2D gene
<i>HMGA2</i>	NM_003484.1	GAGGAGGAATTCTTTCCCGCC TAACATTTCAAGGGACACAATTC ACTCCAAGTCTCTTCCCTTTCCA AGCCGCTTCCGAAGTGCTCCCG GTGCCCGCAA	81	85	370307; 270307	T2D gene
<i>HNF1A</i>	NM_000545.4	GGGGGTCGTGGAGAGCTAGGA GCAAAGCCTGTTTCATGGCAGAT GTAGGAGGGACTGTCGCTGCTT CGTGGGATACAGTCTTCTTACTT GGAAGTGAAGGG	82	82	310561; 210561	T2D gene & Monogenic diabetes gene
<i>HNF1B</i>	NM_000458.1	ACGTCCTGCTGGCACCTCAGAC AATCCACTCTCAGGAGCGCAGC CCGAAGCCCAGTTTCCCTTCTAT GCAGTATTGCCACAATGCCTCT CCCACGATGTC	82	79	300034; 200034	T2D gene & Monogenic diabetes gene
<i>HNF4A</i>	NM_178850.1	CCTTGACAGCATCACCTGGCA GATGATCGAGCAGATCCAGTTC ATCAAGCTCTTCGGCATGGCCA AGATTGACAACCTGTTGCAGGA GATGCTGCTGGG	83	83	360741; 260741	T2D gene & Monogenic diabetes gene
<i>IAPP</i>	NM_000415.1	ATTCTCTCATCTACCAACGTGGG ATCCAATACATATGGCAAGAGG AATGCAGTAGAGTTTTAAAGA GAGAGCCACTGAATTACTTGCC CCTTTAGAGGA	83	81	311536; 211536	Marker of pancreatic islet
<i>IDE</i>	NM_004969.3	AACTGATCGCACAGAAGAGTG GTATGGAACCCAGTACAAACAA GAAGCTATACCGGATGAAGTCA TCAAGAAATGGCAAATGCTGA CCTGAATGGGAA	83	83	300039130; 200039130	T2D gene
<i>IER3IP1</i>	NM_016097.3	GGGAACAGACCAGGGAATTGGT GGATTTGGAGAAGAGCCGGGAA TTAAATCACAGCTAATGAACCTT ATTCGATCTGTAAGAACCGTGAT GAGAGTGCCA	84	81	343083; 243083	Monogenic diabetes gene
<i>IGF2</i>	NM_001127598.1	ACACACACTCATGCGCAGCACA TACATGAACACAGCTCACAGCA CACAAACACGCAGCACACACGT TGACACGCAAGCACCCACCTG CACACACACATG	87	88	322178; 222178	T2D gene
<i>IGF2BP2</i>	NM_001007225.1	GAACAAAAGCGAAACACACAAA CCAGCCTCAACTTACACTTGGTT ACTCAAAAAGAACAAGAGTCAAT GGTACTTGTCTAGCGTTTTGG AAGAGGAAAAC	84	81	366890; 266890	T2D gene

<i>INS</i>	NM_000207.2	GGGTCCCTGCAGAAGCGTGCC ATTGTGGAACAATGCTGTACCA GCATCTGCTCCCTCTACCAGCT GGAGAACTACTGCAACTAGACG CAGCCCCGAGGCA	85	86	350253; 250253	T2D gene & Monogenic diabetes gene & Marker of pancreatic islet
<i>INSM1</i>	NM_002196.2	AAGCCTCCCCTTGCCGGGGAG AAGCTTTTTTCTTGCTAGTATT CGCTGTGTTTCATGGTCTAGAAAT GCGGTCTGGTCTCGCCTCGCCT ACCAATCTCTG	79	83	311571; 211571	Marker of pancreatic islet
<i>IRS1</i>	NM_005544.2	CCCTGGGCAGCGGTGAGAGCA GCTCCACCCGCCGCTCAAGTGA GGATTTAAGCGCCTATGCCAGC ATCAGTTTCCAGAAGCAGCCAG AGGACCGTCAGTA	83	83	300093750; 200093750	T2D gene
<i>ISL1</i>	NM_002202.2	CTTACAGGCTAACCCAGTGGAA GTACAAAGTTACCAGCCACCTT GGAAAGTACTGAGCGACTTCGC CTTGACAGAGTGACATAGATCAG CCTGCTTTTCAG	79	83	308799; 208799	Marker of pancreatic islet
<i>JAZF1</i>	NM_175061.3	CCTGGACCACAGAGAGTGCCAT CAGCTCCGAAGCCATCCTCAGC TCCATGTGCATGAATGGAGGGG AAGAGAAGCCTTTTGCCTGCC AGTTCCTGGATG	82	82	310734; 210734	T2D gene
<i>KCNJ11</i>	NM_000525.3	CTCATCCAGGGTGTTACAAGGC ACTTGTCACTATGCTATTTCTGG CCTCAGCAGGAACCTGTACTGG GTTATTTTTGTCCCTGCTCCTCC CAACCCAATT	81	81	349841; 249841	T2D gene & Monogenic diabetes gene
<i>KCNK16</i>	NM_001135105.1	CTGGTCATTCTCATCTTCCCACC CATGGTCTTCAGCCATGTGGAG GGCTGGAGCTTCAGCGAGGGC TTCTACTTTGCTTTCATCACTCT CAGCACCATTG	83	80	300029232; 200029232	T2D gene
<i>KCNQ1</i>	NM_181798.1	CAGACGTGGGTCGGGAAGACC ATCGCCTCCTGCTTCTCTGCTT TGCCATCTCCTTCTTTGCGCTCC CAGCGGGGATTCTTGGCTCGGG GTTTGGCCCTGA	83	83	311680; 211680	T2D gene
<i>KLF11</i>	NM_001177716.1	TCATCACCTCTAGCCAAAAGTGT GTCCCTCAGGTAGACTTTTCCC GAAGGAGGAACTATGTTTGCAG CTTCCCAGGTTGCCGGAAGACC TACTTCAAAG	83	83	349892; 249892	Monogenic diabetes gene
<i>KLF14</i>	NM_138693.2	CAGGCCGTTGTCCCTGCTTTCT CTCTGCCCATCCTTCTTTCCCAG AGTCATTACACCAAGGCACAGA CTGGTTCCTCTGCTCTGAGGGT GGTCCAGGCA	80	86	349984; 249984	T2D gene
<i>KLHDC5</i>	NM_020782.1	CCACCGCTTTTTAAGGAGGCA TTATGAATGAGTGCAGCATTCT GTCCTCTGTGCCAGGATTTGGT CTTAGAATCCATGTCAGATTGGT GCTTCCAGAC	78	79	300533; 200533	T2D gene
<i>LAMA1</i>	NM_005559.2	CAGTTGCACCAAAATGCCACCC TTGAACTCAAGGCTGCTGAAGA TTTATTGTACAAATTCAGGAAA ATTACCAGAAGCCGCTGGAAGA ATTGGAGGTAT	81	82	311620; 211620	T2D gene
<i>LEP</i>	NM_000230.2	GTAGTTCTTGTCTGATTGGCTCA CCCAAGCAAGGCCAAAATTACC AAAAATCTTGGGGGGTTTTACT CCAGTGGTGAAGAAAATCCTT TAGCAGGTGG	80	81	316749; 216749	T2D gene
<i>LGALS4</i>	NM_006149.3	AGAAGATCACCCACAACCCATT TGGTCCCGGACAGTTCTTTGAT CTGTCCATTGCTGTGGCTTGG ATCGCTTCAAGGTTTACGCCAAT GGCCAGCACCT	82	84	344872; 244872	Marker of gut
<i>LGR5</i>	NM_003667.2	CTTATGCTTACCAGTGTGTGCA TTTGGAGTGTGTGAGAATGCCT ATAAGATTTCTAATCAATGGAAT AAAGGTGACAACAGCAGTATGG ACGACCTTCA	79	79	344720; 244720	T2D gene

<i>LIPF</i>	NM_001198828.1	AGAAGCAGCTACACTATGTTGG CCATTCCCAGGGCACCACCATT GGTTTTATTGCCTTTTCCACCAA TCCCAGCCTGGCTAAAAGAATC AAAACCTTCTA	84	79	387771; 287771	Marker of gut
<i>LPP</i>	NM_005578.2	GCTGTATGACATGGAAAATCCA CCTGCTGACGAATACTTTGGCC GCTGTGCTCGCTGTGGAGAAAA CGTAGTTGGGAAGGTACAGGA TGCACTGCCATG	81	82	308346; 208346	T2D gene
<i>MACF1</i>	NM_012090.5	CATGGATGAAAAGGAGCAGCTT ATACAGTCCAAGAGTTCCGTTG CCAGTCTCGTTGGGAGATCAAA AACCATCGTTCAGCTAAAACCA CGCAGTCCAGAC	83	83	300043617; 200043617	T2D gene
<i>MAEA</i>	NM_001017405.2	CCCTGCCCATGGCCCACTGTGC CAACTCCCGCCTGGTCTGCAAG ATTTCTGGCGACGTGATGAACG AGAACAATCCGCCCATGATGCT GCCAACGGCTA	83	83	300089574; 200089574	T2D gene
<i>MAFA</i>	NM_201589.2	AGCTGCCCAGCAGCCCGCTGG CCATCGAGTACGTAACGACTT CGACCTGATGAAGTTCGAGGTG AAGAAGGAGCCTCCCGAGGCC GAGCGCTTCTGCCA	85	86	311743; 211743	Marker of pancreatic islet
<i>MC4R</i>	NM_005912.1	TGGAGGGTGCTACGAGCAACTT TTGTCTCTCCTGAGGTGTTTGT GACTCTGGGTGTCATCAGCTTG TTGGAGAATATCTTAGTGATTGT GGCAATAGCC	80	78	303291; 203291	T2D gene
<i>MXN1</i>	NM_005515.3	CCTGGGCGCTTCCCTTTTAAAGC AAGGGCGCCTCACCTGCTCTTC AAGAAACAGCGAGAGGGAGAC CCAGGGGGCTGAAACTTGAACT CTGGTTCTTTTAA	80	82	310646; 210646	Monogenic diabetes gene
<i>MOB2</i>	NM_053005.3	CCACATCAACCTGCAGTATAGC ACCATCTCGGAGTTCTGCACAG GAGAGACGTGTCAGACGATGGC CGTGTGCAACACACAGTACTAC TGGTATGACGAG	84	84	340815; 240815	T2D gene
<i>MPHOSPH9</i>	NM_022782.3	AGCCTGGGAGAAGAATAAATCA GTTAGCTACGAACAGTGTAAAGC CGGTTTCAGTCACTCCACAGGG GAATGATTTTGAATATACAGCAA AAATTCGGACC	83	80	300049787; 200049787	T2D gene
<i>MTNR1B</i>	NM_005959.3	ATCCCTGAGGGGCTATTTGTCA CTAGCTACTTACTGGCTTATTTT AACAGCTGCCTGAATGCCATTG TCTATGGGCTCTTGAACCAAAA CTTCCGCAGGG	78	79	302238; 202238	T2D gene
<i>NEUROD1</i>	NM_002500.2	GTGCCCAGCTCAATGCCATATTT CATGATTAGAGGCACGCCAGTT TCACCATTTCCGGGAAACGAAC CCACTGTGCTTACAGTACTGT CGTGTTTACAA	81	79	311578; 211578	Monogenic diabetes gene & Marker of pancreatic islet
<i>NEUROG3</i>	NM_020999.2	CGCGCGAAGTGGGCATTGCAAA GTGCGCTCATTTTAGGCCTCCT CTCTGCCACCACCCATAATCT CATTCAAAGAATACTAGAATGGT AGCACTACCCG	83	82	311658; 211658	Monogenic diabetes gene
<i>NKX2-2</i>	NM_002509.3	TAATTATTATTATGGAGTCGAGT TGACTCTCGGCTCCACTAGGGA GGCGCCGGGAGGTTGCCTGCG TCTCCTTGGAGTGGCAGATTCC ACCCACCCAGCT	82	83	383978; 283978	Monogenic diabetes gene
<i>NKX6-1</i>	NM_006168.2	CTGGCCTGTACCCCTCATCAAG GATCCATTTTGTGGACAAAGAC GGGAAGAGAAAACACACGAGAC CCACTTTTTCCGGACAGCAGAT CTTCGCCCTGG	84	83	311629; 211629	Marker of pancreatic islet
<i>NOTCH2</i>	NM_024408.3	AAGAGTCACCAAATTTTGAGAGT TATACTTGCTTGTGTGCTCCTGG CTGGCAAGGTGACGGGTGTACC ATTGACATTGACGAGTGTATCTC CAAGCCCTG	79	83	347789; 247789	T2D gene

<i>PAM</i>	NM_000919.2	TCATATATACCAGGCTTGCTCTT TGCAGTGAATGGGAAGCCTCAT TTTGGGGACCAAGAACCTGTAC AAGGATTTGTGATGAACTTTTCC AATGGGGAAA	79	82	335097; 235097	T2D gene
<i>PAX4</i>	NM_006193.2	TGTCCAGCCCTCTTTGCCTGGG AAATCCAACGCCAGCTTTGTGC TGAAGGGCTTTGCACCCAGGAC AAGACTCCCAGTGTCTCCTCCA TCAACCGAGTCC	83	84	300039793; 200039793	T2D gene & Monogenic diabetes gene
<i>PAX6</i>	NM_000280.3	GAACATCCTTTACCCAAGAGCA AATTGAGGCCCTGGAGAAAGAG TTTGAGAGAACCCATTATCCAGA TGTGTTTGCCCGAGAAAGACTA GCAGCCAAAAT	84	83	366937; 266937	Marker of pancreatic islet
<i>PCBD1</i>	NM_000281.2	GGGCTGTGGGGTGAATGAGC TGGAAGGCCGTGATGCCATCTT CAAGCAGTTTCATTTCAAAGACT TCAACAGGGCCTTTGGGTTTCAT GACAAGAGTGGC	83	78	300015261; 200015261	Monogenic diabetes gene
<i>PDX1</i>	NM_000209.3	TGACCTCTTTCTTCTCCTCCTC CTCCTTCTACCTCCCCTTCTCAT CCCTCCTCTTCTTCTCTAGC TGCACACTTCACTACTGCACATC TTATAACT	78	79	311526; 211526	T2D gene & Monogenic diabetes gene & Marker of pancreatic islet
<i>PEPD</i>	NM_000285.3	ACGATCCAGAATGGGGATATGT GCCTGTTGACATGGGCGGTGA GTATTACTGCTTCGCTTCCGACA TCACCTGCTCCTTTCCCGCCAA CGGCAAGTTCA	83	82	300015263; 200015263	T2D gene
<i>PLIN1</i>	NM_001145311.1	CATCTCCACCCGCCTCCGCAGT GCCAGAAACAGCATCAGCGTTC CCATCGCGAGCACTTCAAGACAA GGTCTGGGGGCCGCTTTGGC CGGGTGGAGCTT	82	84	362927; 262927	Marker of adipose tissue
<i>POU5F1</i>	NM_002701.4	AAGTTCTTCACTAAGGAAG GAATTGGGAACACAAGGGTGG GGGCAGGGGAGTTTGGGGCAA CTGTTGGAGGGAAGGTGAAGT TCAATGATGCTC	78	82	308193; 208193	T2D gene
<i>PPARG</i>	NM_015869.3	GAGCAAAGAGGTGGCCATCCG CATCTTTCAGGGCTGCCAGTTT CGCTCCGTGGAGGCTGTGCAG GAGATCACAGAGTATGCCAAAA GCATTCTGGTTTT	81	81	300811; 200811	T2D gene
<i>PRC1</i>	NM_199413.1	ACAGAAAGTCTGCTCCAGCTCC ACGATGCTGAGATTGTGCGGTT AAAAAATACTATGAAGTTCACA AGGAACTCTTTGAAGGTGTCCA GAAGTGGGAAG	84	82	336825; 236825	T2D gene
<i>PROX1</i>	NM_002763.3	TCTCCTTGTCGCTCATAAAGTCC GAGTGCGGCGATCTTCAAGATA TGTCTGAAATATCACCTTATTCG GGAAGTGCAATGCAGGAAGGAT TGTCACCCAA	79	82	311583; 211583	T2D gene
<i>PSMB2</i>	NM_002794.4	AGCAATATTGTCCAGATGAAGG ACGATCATGACAAGATGTTTAAG ATGAGTGAAAAGATATTACTCCT GTGTGTTGGAGAGGCTGGAGAC ACTGTACAGT	79	85	300093536; 200093536	Housekeeping gene
<i>PSMB4</i>	NM_002796.2	GGACACAGCTATAGTCCTAGAG CTATTCATTCATGGCTGACCAG GGCCATGTACAGCCGGCGCTC GAAGATGAACCCCTTTGTGGAAC ACCATGGTCATCG	87	86	300093534; 200093534	Housekeeping gene
<i>PSMD6</i>	NM_001271780.1	ATAGGTCATTAACCCTTGGCTAT ATGGCAGAAGCGTTTGGTGTG GTGTGGAATTCATTGATCAGGA ACTGTCCAGTTTATTGCTGCC GGGAGACTACA	79	81	365106; 265106	T2D gene
<i>PTF1A</i>	NM_178161.2	CAACAGCAAATCTTCTTCAACA ACATAGAAAACGAACCACCATTT GAGTTTGTGTCCTGAGAAGTCC CAGACTCGGCTGAAGATCTGAT TATGTCTCTG	78	82	311732; 211732	Monogenic diabetes gene

<i>PTPRD</i>	NM_001040712.2	TTTTAGTTAAACAAAGGGGGTCA GACAGACATTGCATCATCCAGA CATGCCTTGTTGGACATGTAGA ATCCGATGGAGCACTGCACACC AGAATGATTGG	80	84	341816; 241816	T2D gene
<i>R3HDML</i>	NM_178491.2	CCAGGTACCGCCGGAAGCGCC ACATCTCTGTGAGAGACATGAA TGCCTTACTGGATTATCACAACC ACATCCGGGCCAGTGTGTACCC ACCTGCCGCCAA	84	84	325372; 225372	T2D gene
<i>RASGRP1</i>	NM_005739.3	ACGATCTCATTGACAGCTGCATT CAATCTTTTGATGCAGATGGAAA CCTGTGTGCGAAGTAACCAACTG TTGCAAGTCATGCTGACCATGC ACCGAATTGT	78	82	335283; 235283	T2D gene
<i>RBM43</i>	NM_198557.2	CAGCAATATAGTCATAAGGGCT GCTTTCTCTTGCTGAGCAGTGA CCATTGCCATGAATGAGGCTAG CTTTACACACCGTATCTCATGAA TCCTTATAGTC	81	78	355924; 255924	T2D gene
<i>RBMS1</i>	NM_016839.2	ATCTGTCACTAGGCAGCACCGG AACATACATGCCTGCAACGTCA GCTATGCAAGGAGCCTACTTGC CACAGTATGCACATATGCAGAC GACAGCGGTTCC	82	82	309308; 209308	T2D gene
<i>RFX6</i>	NM_173560.2	AGCAGTGCATATTACCACTCCG TTTATTCTGGAAAGGGCTTGACA AGGTTTTCTGGAAGCAAGCTAA AGAATGAGGGTGGCTTCACTCG TAAATATTCCG	80	82	336282; 236282	Monogenic diabetes gene & Marker of pancreatic islet
<i>RND3</i>	NM_005168.3	GGAACAAATCACAGAGGCCAC AAAGCGGATTTACACATGCCT AGCAGACCAGAACTCTCGGCAG TTGCTACGGACTTACGAAAGGA CAAAGCGAAGAG	82	80	308797; 208797	T2D gene
<i>RREB1</i>	NM_001003698.2	TTCGAACACATCGAGGACTGCT GCGTCACAACGCGCTTGCCAC AAACAACCTCCAGGGATGCAA TGGGCAGACCTTTCATACAGAA CAACCCTTCAAT	79	80	310505; 210505	T2D gene
<i>SFTPA2</i>	NM_001098668.2	CCATCTCTCCAGCTAGCAAAATT ACTACCAGAGCCGTTACTACAC ACAAAGGCTATTGACCGAGCAC ATACCATGTGCCACACACCTTG ACAAAATCTTT	83	83	390536; 290536	Marker of lung
<i>SFTPB</i>	NM_000542.3	CACACACAGGATCTCTCCGAGC AGCAATTCCTTCTCTCCCC TATTGCTGGCTCTGCAGGGCTC TGATCAAGCGGATCCAAGCCAT GATCCCAAGG	83	86	344205; 244205	Marker of lung
<i>SFTPC</i>	NM_003018.2	TTCCCTGCTGCCAGTGCACCT GAAACGCCTTCTTATCGTGGTG GTGGTGGTGGTCCCTCATCGTCG TGGTGATTGTGGGAGCCCTGCT CATGGGTCTCCA	81	81	301927; 201927	Marker of lung
<i>SGCG</i>	NM_000231.2	ACACTGAGTGTTGAGTTGCCGT GTGGAGTTAATGTATGACGCTC CACTGTGGATATCTAATGCCCT GTTGAGAGTAGCCTTGCTCAGT ACTAAAATGCC	82	84	345859; 245859	T2D gene
<i>SLC12A1</i>	NM_000338.2	CCAAGTTCGACTGAATGAACTC TTACAGGAGCACTCCAGAGCTG CTAATCTCATTGTCCTGAGCCTT CCCCTGGCAAGAAAGGGATCCA TATCGGATTG	83	81	300015293; 200015293	Marker of kidney
<i>SLC16A11</i>	NM_153357.1	CGGCCTGAGTCTGTTACACGCG CGGGCCTTCTCAATCTTTGCTCT AGGCACAGCCCTGGTTGGGGG CGGGTACTTCGTTCCCTTACGTG CACTTGGCTCCC	82	83	365403; 265403	T2D gene
<i>SLC16A13</i>	NM_201566.2	GGTGCTCTCAGCGTTCTTCCAG TCGGCGCTTGTGTTTGGGGTGC TCCGCTCCTTTGGGGTCTTCTTC GTGGAGTTTGTGGCGGCGTTTG AGGAGCAGGCA	84	82	365405; 265405	T2D gene

<i>SLC19A2</i>	NM_006996.1	CCTGTGGGAGAAAGTGATGCCT TCTCGCTATGCTGCTATCTATAA TGGTGGCGTGGAGGCCGTTTCA ACCTTACTGGGTGCTGTTGCTG TGTTTGCACTT	80	80	300323; 200323	Monogenic diabetes gene
<i>SLC22A2</i>	NM_003058.2	CTAACATCTGGCTTGAGCTCCC GCTGATGGTTTTCGGCGTGCTT GGCTTGGTTGCTGGAGGTCTGG TGCTGTTGCTTCCAGAACTAAA GGGAAAGCTTT	82	84	320257; 220257	Marker of kidney
<i>SLC2A2</i>	NM_000340.1	CAATTATGGAATATAGTTCTGA TGGGTCCCAAAGCTTAGCAGG GTGCTAACGTATCTCTAGGCTG TTTTCTCCACCAACTGGAGCACT GATCAATCCT	81	82	311532; 211532	Monogenic diabetes gene
<i>SLC30A8</i>	NM_173851.2	CAGATGCAACCAATTCATTCAGT CCACGAGCATGATGTGAGCACT GCTTTGTGCTAGACATTGGGCT TAGCATTGAAACTATAAAGAGGA ATCAGACGCA	80	83	349995; 249995	T2D gene & Marker of pancreatic islet
<i>SPRY2</i>	NM_005842.2	GCCGTTTTAACTGATATGCTTGT TAGAACTCAGCTAATGGAGCTC AAAGTATGAGATACAGAACTTG GTGACCCATGTATTGCATAAGC TAAAGCAACAC	77	84	368417; 268417	T2D gene
<i>SRR</i>	NM_021947.1	ACAATTGCCCTGGAAGTGCTGA ACCAGGTTCCCTTTGGTGGATGC ACTGGTGGTACCTGTAGGTGGA GGAGGAATGCTTGCTGGAATAG CAATTACAGTTA	82	81	301964; 201964	T2D gene
<i>SSR1</i>	NM_003144.3	ACATTGCCTGGGTCTCAGTAAG CCGCTTAAGTGACTGCTCTCATT TTCGCTGTAAAGCACCATACTGT AATAACATCCCATGAAGCATGG GGCGGGGAAG	79	81	308324; 208324	T2D gene
<i>SST</i>	NM_001048.3	AGCTGCTGTCTGAACCCAACCA GACGGAGAATGATGCCCTGGAA CCTGAAGATCTGTCCAGGCTG CTGAGCAGGATGAAATGAGGCT TGAGCTGCAGAG	82	82	301249; 201249	Marker of pancreatic islet
<i>ST6GAL1</i>	NM_003032.2	ATGATGACGCTGTGTGACCAGG TGGATATTTATGAGTTCCTCCA TCCAAGCGCAAGACTGACGTGT GCTACTACTACCAGAAGTTCTTC GATAGTGCCT	81	82	361087; 261087	T2D gene
<i>TBC1D4</i>	NM_014832.2	GCAGTTTCTGGCTTTACAGTACC GACTCAGACACAGATTGCCTAA TAAACAACAGCCTCCTGACATAT CCTATAAGGAACTTTTGAAGCA GCTCACTGCT	81	83	344936; 244936	T2D gene
<i>TCF19</i>	NM_001077511.1	TTGCAAGTCGGCTTAACCAATTT TGCATTGAGTCCTAGGCTGCTT GCACTCTGAATTTGGGCTATTCA GGTAGTGTGCTCAAAGTTGAAA CCGCATACAG	79	79	300022149; 200022149	T2D gene
<i>TCF7L2</i>	NM_001146274.1	ATATGGTCCCACCACATCATA GCTACACACGACGGCATTCCG CATCCGGCCATAGTCACACCAA CAGTCAAACAGGAATCGTCCCA GAGTGATGTCGG	86	86	362160; 262160	T2D gene
<i>THADA</i>	NM_001083953.1	CCAGAATCTTCTGATGGATTATT GACGGTGGAGCAGGTAAAAGAA ATAGGAGATTACTTTAACAACA CCTTTTGCAGTCCAGGCACAGA GGAGCATTTG	81	78	329955; 229955	T2D gene
<i>TLE1</i>	NM_005077.3	CCGACTCACATGACAGCCATT CTTTCTTTCTGGGTGATCTGGG GATCACGCCTTGCCCAAGTGTG AGATTACCTTTCTGTTCTTGCA GTTACCTCAC	82	79	311859; 211859	T2D gene
<i>TLE4</i>	NM_007005.3	AAAACAAGGACAGCAGAGGAGG GTTTGCAGAGACCTCCCTCTGA AAAACAAAAGAATGGACTCTCT CCTGGGATGAGGACTTGCTTTC TTTACCTCCGG	81	79	309013; 209013	T2D gene

<i>TMEM154</i>	NM_152680.2	GCGCAGCCCTAGTCTTCGCCCT GGTGATCGCGCTCGTTCCCGTC GGCCGGGGTAATTATGAGGAAT TAGAAAACCTCAGGAGATACAAC TGTGGAATCTGA	85	81	373634; 273634	T2D gene
<i>TMEM163</i>	NM_030923.4	TGGGGGTGATATTCCTTCTGTC ATCCATATGTATAGTGGTCAAAG CCATCCATGACCTCTCAACTAG GCTGCTCCCAGAAGTGGACGAT TTCCTGTTCCAG	79	83	388351; 288351	T2D gene
<i>TP53INP1</i>	NM_033285.3	CCAAGAGCTTTCCGCCCTTCCCA GTGGATAAAAAGAACACAGTGAA AGACAGCCTCTTAACAGAAATA GCCTTCGTCGCCAAAATCTTAC CAGGGATTGCCA	83	80	348825; 248825	T2D gene
<i>TRMT10A</i>	NM_001134665.1	CCCACAGACAAAGCCTGTGAAA GTGCTTCTCATGACAATCAGTCT GTCAGGATGGAGGAAGGTGGAT CGGACAGTGATTCCAGTGAGGA GGAATATAGCA	84	83	383028; 283028	Monogenic diabetes gene
<i>TSPAN8</i>	NM_004616.2	CTGGCTATGTGGTATCTTGATCC TAGCATTAGCAATATGGGTACG AGTAAGCAATGACTCTCAAGCA ATTTTTGGTTCTGAAGATGTAGG CTCTAGCTCC	79	79	317600; 217600	T2D gene
<i>UBE2E2</i>	NM_152653.3	GTGAAAGTGTTCAAGCAAGAACC AGAAAGAGAACAAGTTCAGCCC AAGAAAAAGGAGGGAAAAATAT CCAGCAAACCGCTGCTAAATT GTCAACTAGTGC	84	83	368035; 268035	T2D gene
<i>VCP</i>	NM_007126.3	AGATGGATCTCATTGACCTAGA GGATGAGACCATTGATGCCGAG GTCATGAACTCTCTAGCAGTTAC TATGGATGACTTCCGGTGGGCC TTGAGCCAGAG	85	87	300093533; 200093533	Housekeeping gene
<i>VPS26A</i>	NM_004896.3	TGGCACTTTGATAAAATGGTCA GGAACCAACTTTACTGGCAAAA GGGTCCATGTACCACCATGTGC TGGAGCATCTGTTCTACATGTG GATATCTATGAA	84	81	300039091; 200039091	T2D gene
<i>VPS29</i>	NM_016226.4	AGTGGTCACCTATGTGTATCAG CTAATTGGAGATGATGTGAAAG TAGAACGAATCGAATACAAAAA CCTTAAAGCCAGGCCTGTCTTG ATGATTTTTGG	81	76	300093535; 200093535	Housekeeping gene
<i>WFS1</i>	NM_006005.3	GTCAGCAACCTCACCATCGACT TCTCGCCTTCTTCATCCCCTG GTCATCTTCTACCTGTCCTTCAT CTCCATGGTGATCTGCACCCTC AAGGTGTTCC	80	81	326714; 226714	T2D gene & Monogenic diabetes gene
<i>ZBED3</i>	NM_032367.2	GGGCTGGGAACCCGAACCTGG TGACTTTGAAAGGATAGAGCTT CATTCCATACCAAAGACTTATCA CACCATGTGCCTATACACCAG CAGCCCAAGGTG	83	83	349968; 249968	T2D gene
<i>ZFAND3</i>	NM_021943.2	ACAGCCAGACGATGATTCCGCT CCAAGTACAAGTAACAGCCAAT CAGATTTGTTTTCCGAAGAGAC CACCAGTGACAACAACAATACC TCGATAACCAG	84	83	343067; 243067	T2D gene
<i>ZFAND6</i>	NM_001242919.1	AAGTGCCTATGCTTTGTTCCACT GGCTGTGGATTTTATGGAAACC CTCGTACAAATGGCATGTGTTT AGTATGCTATAAAGAACATCTTC AAAGACAGAA	79	78	363380; 263380	T2D gene
<i>ZMIZ1</i>	NM_020338.3	CCACGGTCAACATGGGGCAGTA TTACAAGCCAGAACAGTTTAATG GACAAAATAACACGTTCTCGGG AAGCAGCTACAGTAACTACAGC CAAGGGAATGT	84	83	300048334; 200048334	T2D gene

CP, capture probe; **RP**, reporter probe; **PN (CP;RP)**, NanoString part number for the probe pair; **T_m**, melting temperature.

Table B. List of deregulated genes emphasized by the decreased expression of *PRCI* in EndoC- β H1 cells, within the network related to apoptosis.

Gene	Log2 Fold Change	Standard Error	P-Value
<i>AAMDC</i>	0.52	0.23	0.026521
<i>AATK</i>	0.45	0.23	0.048149
<i>ABCA1</i>	-0.73	0.26	0.004842
<i>ABCG1</i>	-0.42	0.21	0.047317
<i>ACVR1C</i>	-0.69	0.24	0.003253
<i>ADM</i>	0.68	0.25	0.005929
<i>AES</i>	0.44	0.21	0.03579
<i>AGAP2</i>	0.57	0.25	0.020592
<i>AGER</i>	0.70	0.23	0.002415
<i>AKT3</i>	-0.46	0.19	0.017728
<i>ANO6</i>	-0.46	0.20	0.019754
<i>ANTXR1</i>	-0.62	0.25	0.013917
<i>ANXA2</i>	0.69	0.25	0.006579
<i>APH1B</i>	-0.45	0.20	0.023689
<i>AQP3</i>	0.81	0.22	0.000178
<i>ARAF</i>	0.44	0.21	0.034539
<i>ARC</i>	0.68	0.27	0.010949
<i>ARHGDI A</i>	0.74	0.22	0.000681
<i>ARHGDI B</i>	0.72	0.27	0.007243
<i>ARSB</i>	-0.59	0.21	0.004996
<i>ASCL1</i>	-0.69	0.25	0.005143
<i>ASIC1</i>	-0.55	0.21	0.008409
<i>ASTN1</i>	-0.53	0.26	0.041322
<i>ATAD3A</i>	0.67	0.25	0.00736
<i>ATP1A2</i>	-0.66	0.26	0.010295
<i>ATP2B4</i>	-0.65	0.20	0.001412
<i>AURKA</i>	0.40	0.20	0.04257
<i>AURKB</i>	0.63	0.22	0.004344
<i>BAD</i>	0.65	0.24	0.007457
<i>BCL2L12</i>	0.53	0.25	0.031085
<i>BIRC5</i>	0.55	0.20	0.004569
<i>BMP5</i>	-0.48	0.22	0.025444
<i>BOK</i>	0.47	0.23	0.044972
<i>BRMS1</i>	0.57	0.22	0.009569
<i>CAPRIN1</i>	-0.39	0.20	0.049352
<i>CASR</i>	-0.45	0.22	0.04326
<i>CAV1</i>	0.55	0.26	0.038241
<i>CCDC47</i>	-0.40	0.20	0.044883
<i>CCNG1</i>	-0.44	0.21	0.041519
<i>CDC20</i>	0.55	0.21	0.008527
<i>CDC25B</i>	0.49	0.21	0.022689
<i>CDK3</i>	0.60	0.23	0.0087
<i>CDKN2D</i>	0.66	0.21	0.001588
<i>CDKN3</i>	0.44	0.20	0.030734
<i>CERS6</i>	-0.51	0.21	0.014281
<i>CHTF18</i>	0.93	0.23	7.5E-05
<i>COX8A</i>	0.49	0.22	0.027924
<i>CRABP2</i>	0.54	0.27	0.047503
<i>CTGF</i>	0.82	0.26	0.001622
<i>DDAH2</i>	0.93	0.23	5.88E-05
<i>DKK3</i>	-0.59	0.21	0.005361
<i>DLL1</i>	0.69	0.23	0.002325
<i>DOT1L</i>	0.43	0.21	0.037789
<i>DPM3</i>	0.67	0.26	0.011948
<i>DPP4</i>	0.49	0.20	0.013016
<i>DUSP6</i>	1.05	0.26	4.82E-05
<i>DVL1</i>	0.53	0.24	0.026796

<i>E4F1</i>	0.52	0.21	0.014491
<i>EEF1D</i>	0.58	0.24	0.013565
<i>EMD</i>	0.43	0.21	0.042982
<i>EPHA4</i>	-0.57	0.20	0.004588
<i>ERF</i>	0.47	0.21	0.027617
<i>ETS1</i>	-0.50	0.20	0.013281
<i>ETV5</i>	1.02	0.22	2.47E-06
<i>FABP1</i>	0.42	0.20	0.039304
<i>FAIM2</i>	-0.80	0.26	0.002387
<i>FAU</i>	0.51	0.24	0.03122
<i>FBLIM1</i>	0.60	0.21	0.005009
<i>FBXO32</i>	-0.54	0.24	0.02366
<i>FDXR</i>	0.46	0.23	0.048941
<i>FKBP8</i>	0.51	0.23	0.027115
<i>FN1</i>	-0.82	0.22	0.000224
<i>GADD45B</i>	0.54	0.25	0.027072
<i>GADD45GIP1</i>	0.59	0.25	0.018306
<i>GAL</i>	2.05	0.27	3.14E-14
<i>GJC1</i>	-0.48	0.22	0.028607
<i>GJD2</i>	-0.49	0.22	0.029174
<i>GLI1</i>	0.49	0.20	0.012469
<i>GLI3</i>	0.54	0.27	0.041923
<i>GLIS2</i>	0.53	0.20	0.007872
<i>GLTSCR2</i>	0.53	0.24	0.025619
<i>GMDS</i>	0.41	0.21	0.048503
<i>GREM1</i>	-0.40	0.21	0.049667
<i>H2AFX</i>	0.92	0.25	0.00023
<i>HES1</i>	0.57	0.27	0.032923
<i>HEY1</i>	0.71	0.23	0.001658
<i>HIC1</i>	0.55	0.23	0.019566
<i>HIP1</i>	-0.61	0.24	0.01004
<i>HIP1R</i>	0.43	0.21	0.041477
<i>HIPK1</i>	-0.79	0.22	0.000272
<i>HIST1H1C</i>	0.50	0.24	0.035005
<i>HLA-G</i>	-0.54	0.26	0.039708
<i>HMGA2</i>	0.87	0.25	0.000585
<i>HMGCR</i>	-0.46	0.21	0.026645
<i>HMGN5</i>	0.57	0.25	0.020766
<i>HRAS</i>	0.58	0.24	0.014624
<i>HSPA1A</i>	0.57	0.24	0.016413
<i>HSPA1B</i>	0.56	0.24	0.019072
<i>IAPP</i>	0.67	0.25	0.006894
<i>IER3</i>	0.84	0.22	0.000131
<i>IGF2</i>	0.59	0.20	0.002566
<i>IGFBP3</i>	0.95	0.24	5.24E-05
<i>IGFBP5</i>	-0.52	0.25	0.038864
<i>IL6R</i>	-0.58	0.21	0.005117
<i>INPP5E</i>	0.53	0.24	0.02983
<i>IRF3</i>	0.58	0.24	0.014547
<i>IRF7</i>	0.69	0.26	0.008565
<i>ITGB1</i>	-0.47	0.24	0.045799
<i>JMY</i>	-0.47	0.20	0.017757
<i>JUNB</i>	0.83	0.22	0.000179
<i>KCNJ11</i>	0.45	0.20	0.025037
<i>KRT18</i>	0.73	0.21	0.000496
<i>KRT8</i>	0.73	0.23	0.001301
<i>LAG3</i>	0.54	0.27	0.047092
<i>LEPR</i>	-0.49	0.24	0.039331
<i>LHX4</i>	-0.60	0.22	0.007397
<i>LMNA</i>	0.47	0.20	0.021663
<i>LRP6</i>	-0.42	0.22	0.049416

<i>LYPLA1</i>	-0.41	0.21	0.046869
<i>LYPLA2</i>	0.53	0.23	0.023191
<i>MAP1LC3A</i>	0.48	0.23	0.03904
<i>MAP1S</i>	0.56	0.22	0.012016
<i>MAP3K10</i>	0.49	0.22	0.0239
<i>MAP4K1</i>	0.55	0.27	0.040423
<i>MAPK11</i>	0.53	0.21	0.013492
<i>MAPK12</i>	0.49	0.23	0.031358
<i>MAPK7</i>	0.46	0.21	0.026399
<i>MAPT</i>	-0.50	0.22	0.026513
<i>MC1R</i>	0.62	0.23	0.007596
<i>MET</i>	-0.56	0.21	0.008706
<i>MICAL1</i>	0.51	0.22	0.020053
<i>MIF</i>	0.73	0.26	0.00422
<i>MME</i>	-0.46	0.20	0.020296
<i>MMP2</i>	-0.48	0.22	0.032016
<i>MPG</i>	0.82	0.24	0.000518
<i>MRPL41</i>	0.57	0.27	0.030625
<i>MSH6</i>	-0.49	0.19	0.011544
<i>MYBL2</i>	0.63	0.21	0.00238
<i>MYC</i>	0.97	0.27	0.000287
<i>NAA38</i>	0.62	0.24	0.010331
<i>NDRG1</i>	-0.41	0.20	0.040641
<i>NDUFA13</i>	0.62	0.22	0.004797
<i>NFKBID</i>	0.62	0.23	0.006925
<i>NINJ1</i>	0.51	0.23	0.027097
<i>NME3</i>	0.79	0.26	0.002277
<i>NME4</i>	0.45	0.20	0.026162
<i>NQO1</i>	0.56	0.22	0.008878
<i>NR0B2</i>	0.91	0.22	3.14E-05
<i>NR1H2</i>	0.61	0.24	0.009835
<i>NRGN</i>	0.65	0.23	0.00515
<i>NUDT1</i>	0.66	0.25	0.008246
<i>NUF2</i>	0.59	0.20	0.002504
<i>OSGIN1</i>	0.65	0.25	0.008131
<i>PAFAH1B3</i>	0.48	0.22	0.030455
<i>PAM16</i>	0.44	0.22	0.040561
<i>PCSK2</i>	-0.41	0.19	0.033134
<i>PDE5A</i>	-0.40	0.20	0.043578
<i>PDLIM7</i>	0.58	0.22	0.008612
<i>PHLDA1</i>	0.63	0.24	0.009764
<i>PIDD1</i>	0.63	0.26	0.01402
<i>PIM3</i>	0.75	0.23	0.001312
<i>PLCE1</i>	-0.42	0.21	0.042433
<i>PLK1</i>	0.50	0.19	0.00978
<i>PLK3</i>	0.65	0.22	0.003874
<i>POMC</i>	0.59	0.25	0.01925
<i>POU3F1</i>	0.55	0.27	0.043455
<i>PPARA</i>	-0.43	0.20	0.035315
<i>PQBP1</i>	0.52	0.21	0.013244
<i>PRKCB</i>	2.19	0.27	6.11E-16
<i>PRR13</i>	0.49	0.21	0.01766
<i>PRR7</i>	0.53	0.27	0.047617
<i>PSEN1</i>	-0.39	0.19	0.044557
<i>PTPRZ1</i>	-0.50	0.22	0.025283
<i>PTTG1</i>	0.56	0.20	0.006187
<i>RAC3</i>	0.60	0.25	0.015065
<i>RAD9A</i>	0.69	0.24	0.003309
<i>RB1</i>	-0.49	0.21	0.019312
<i>RBCK1</i>	0.54	0.23	0.018173
<i>RBPJ</i>	-0.60	0.19	0.001993

<i>RHOC</i>	0.53	0.21	0.012576
<i>ROR1</i>	-0.67	0.24	0.005216
<i>RPRM</i>	0.52	0.26	0.047254
<i>RPS19</i>	0.49	0.23	0.034511
<i>RPS6KA5</i>	-0.48	0.22	0.030225
<i>RTN4R</i>	0.61	0.27	0.021813
<i>RUVBL2</i>	0.48	0.23	0.036673
<i>S100A11</i>	0.66	0.26	0.010635
<i>S100A6</i>	0.55	0.24	0.024644
<i>S1PR3</i>	-0.63	0.26	0.016902
<i>SAT1</i>	0.63	0.20	0.001506
<i>SATB1</i>	-0.48	0.21	0.026124
<i>SCN3B</i>	-0.43	0.19	0.02628
<i>SDF2L1</i>	0.73	0.25	0.00364
<i>SIRT6</i>	0.59	0.24	0.012135
<i>SLC18A3</i>	0.64	0.26	0.012553
<i>SLC2A1</i>	-0.39	0.19	0.041783
<i>SLC39A10</i>	-0.46	0.20	0.01861
<i>SLC39A6</i>	-0.44	0.22	0.048108
<i>SLC6A6</i>	-0.45	0.20	0.02347
<i>SMAD5</i>	-0.57	0.21	0.005689
<i>SOX5</i>	-0.90	0.22	3.79E-05
<i>SPOCK1</i>	-0.45	0.21	0.038062
<i>SST</i>	1.30	0.21	3.35E-10
<i>SSTR2</i>	-0.62	0.19	0.001131
<i>ST3GAL1</i>	-0.52	0.26	0.044856
<i>ST6GAL1</i>	-0.67	0.19	0.000472
<i>STC1</i>	0.62	0.26	0.017674
<i>STUB1</i>	0.49	0.22	0.024207
<i>SULF1</i>	-0.76	0.21	0.000259
<i>TACC3</i>	0.67	0.22	0.002058
<i>TCF4</i>	-0.54	0.20	0.008119
<i>TEX11</i>	-0.50	0.20	0.013485
<i>TFDP2</i>	-0.40	0.19	0.042089
<i>TFPT</i>	0.49	0.23	0.034336
<i>THBD</i>	-0.58	0.25	0.021691
<i>TIAM1</i>	-0.43	0.20	0.03475
<i>TIMP3</i>	-0.62	0.22	0.004322
<i>TK1</i>	0.59	0.23	0.010718
<i>TMBIM6</i>	-0.41	0.19	0.031823
<i>TMEFF2</i>	-0.64	0.23	0.005074
<i>TNFAIP2</i>	0.52	0.24	0.031759
<i>TNFAIP8L1</i>	0.57	0.23	0.013299
<i>TNFRSF11B</i>	0.71	0.25	0.004933
<i>TNFRSF12A</i>	0.68	0.22	0.001925
<i>TNFRSF6B</i>	0.66	0.27	0.012419
<i>TNNI3</i>	0.57	0.27	0.032266
<i>TP53I3</i>	0.47	0.21	0.025102
<i>TREX2</i>	0.53	0.25	0.033846
<i>TRIM32</i>	-0.50	0.20	0.012077
<i>UGT8</i>	-0.95	0.19	1.11E-06
<i>VCAN</i>	0.61	0.27	0.022184
<i>VCL</i>	-0.52	0.19	0.006984
<i>WNT5A</i>	-0.61	0.20	0.002646
<i>ZBED6</i>	-0.53	0.25	0.035941
<i>ZBTB17</i>	0.48	0.22	0.030132
<i>ZFP36</i>	0.81	0.21	0.000108