

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

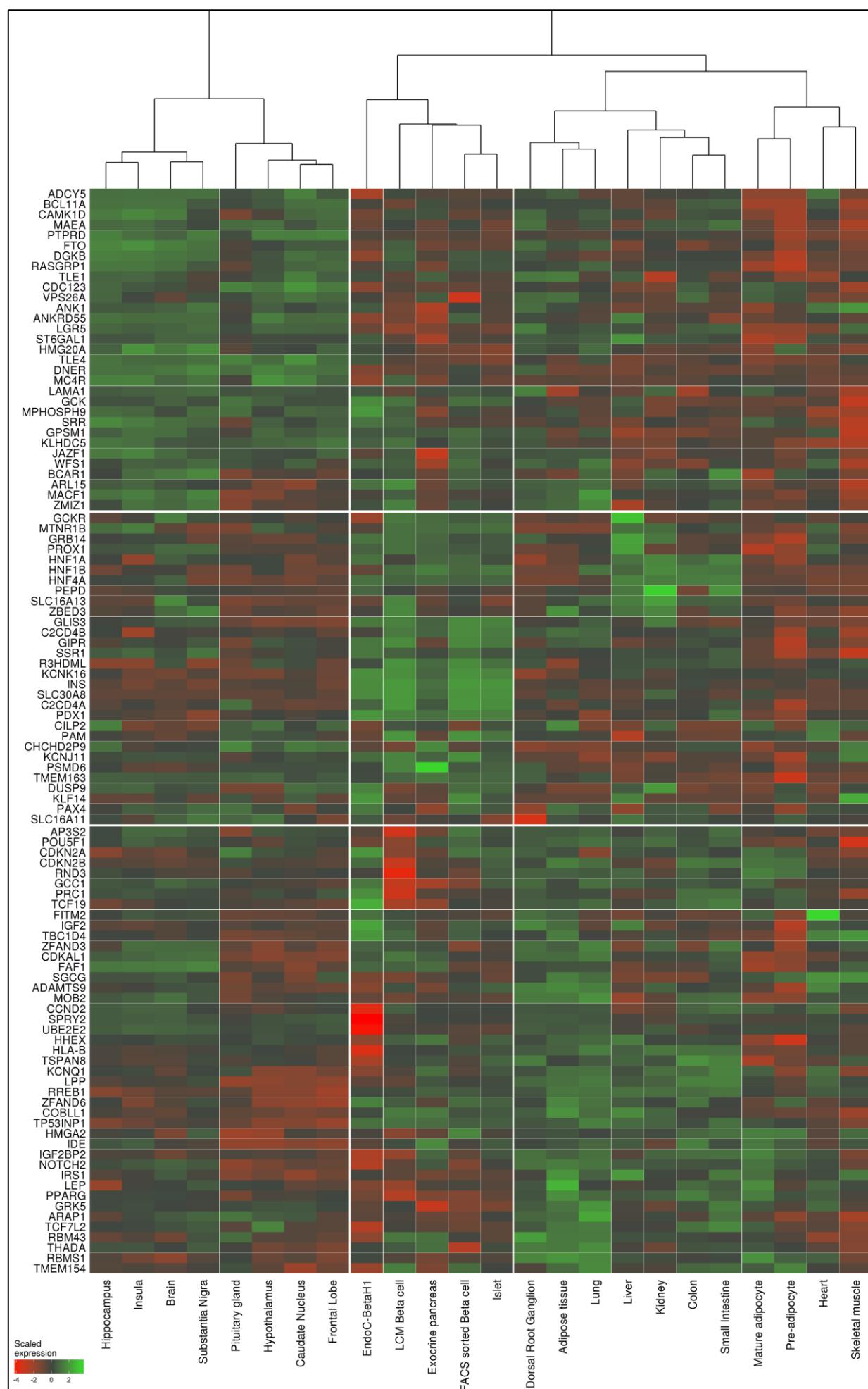


Figure B. (1) Heat map representing the expression of three genes known to be highly expressed in gut in the panel of human organs, tissues and cells; (2) Enrichment analysis of gut markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p-value of 0.05.

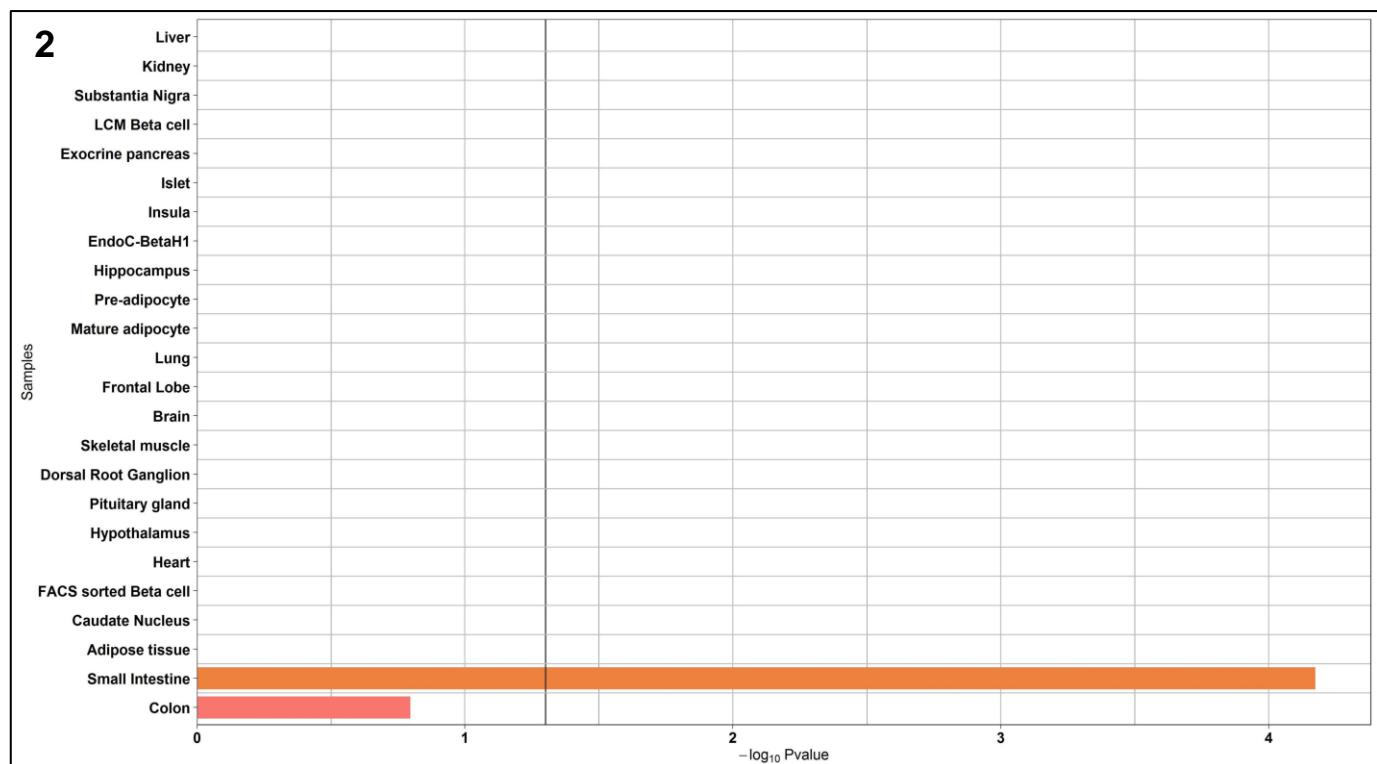
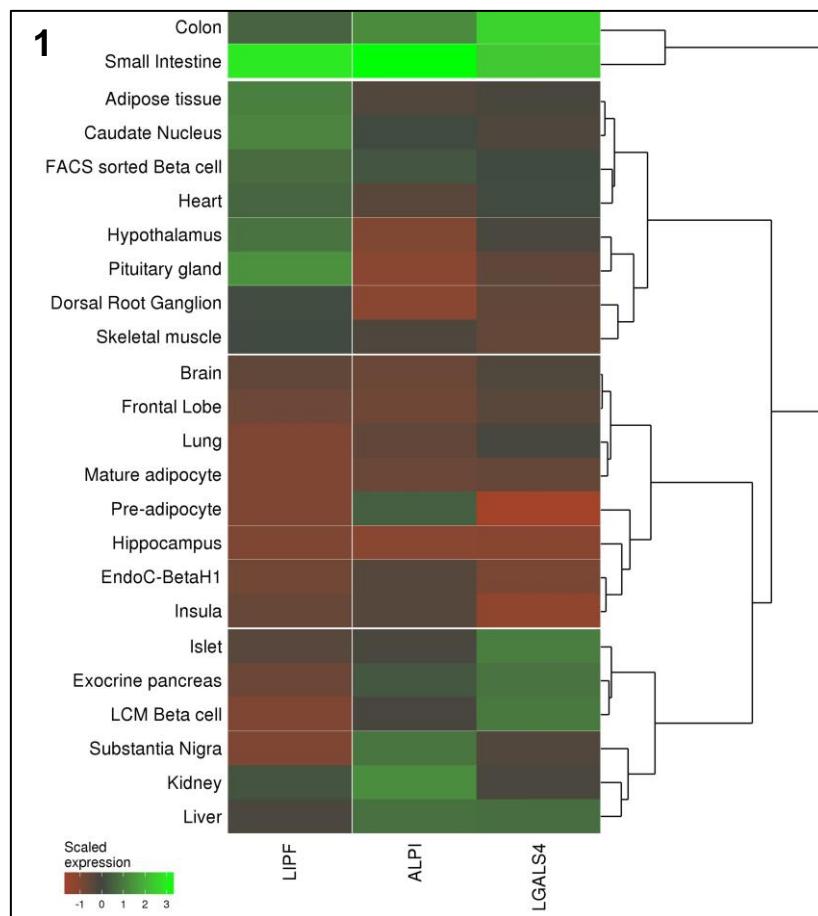


Figure C. (1) Heat map representing the expression of three genes known to be highly expressed in adipose tissue in the panel of human organs, tissues and cells; (2) Enrichment analysis of adipose tissue markers expression in the panel of human organs, tissues and cells. The black vertical line denotes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

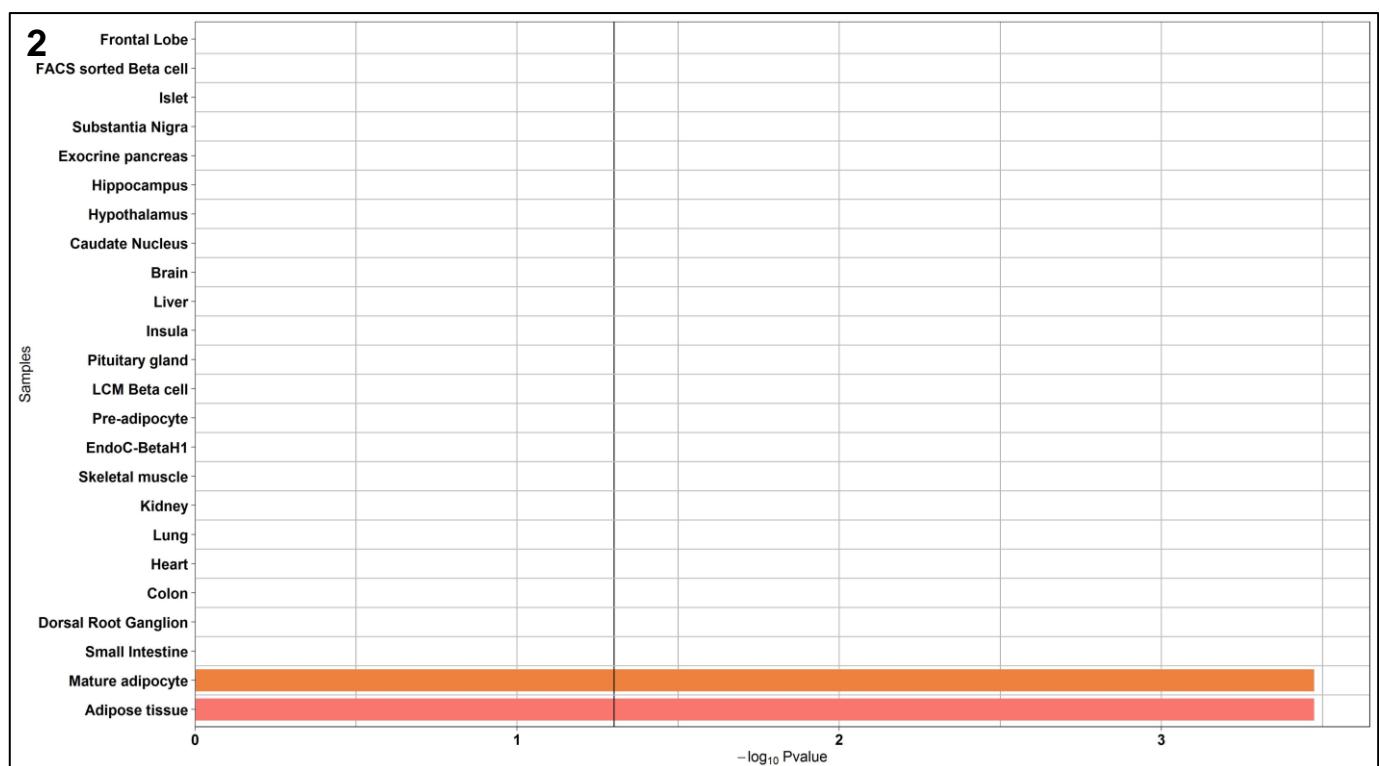
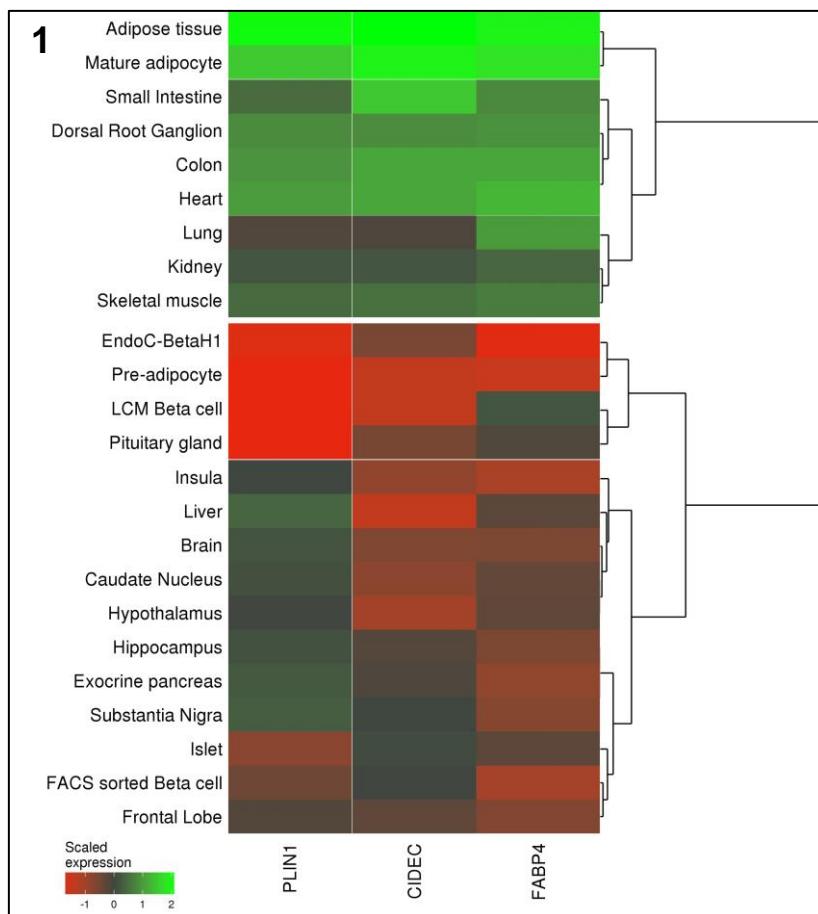


Figure D. (1) Heat map representing the expression of four genes known to be highly expressed in kidney in the panel of human organs, tissues and cells; (2) Enrichment analysis of kidney markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a p -value of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

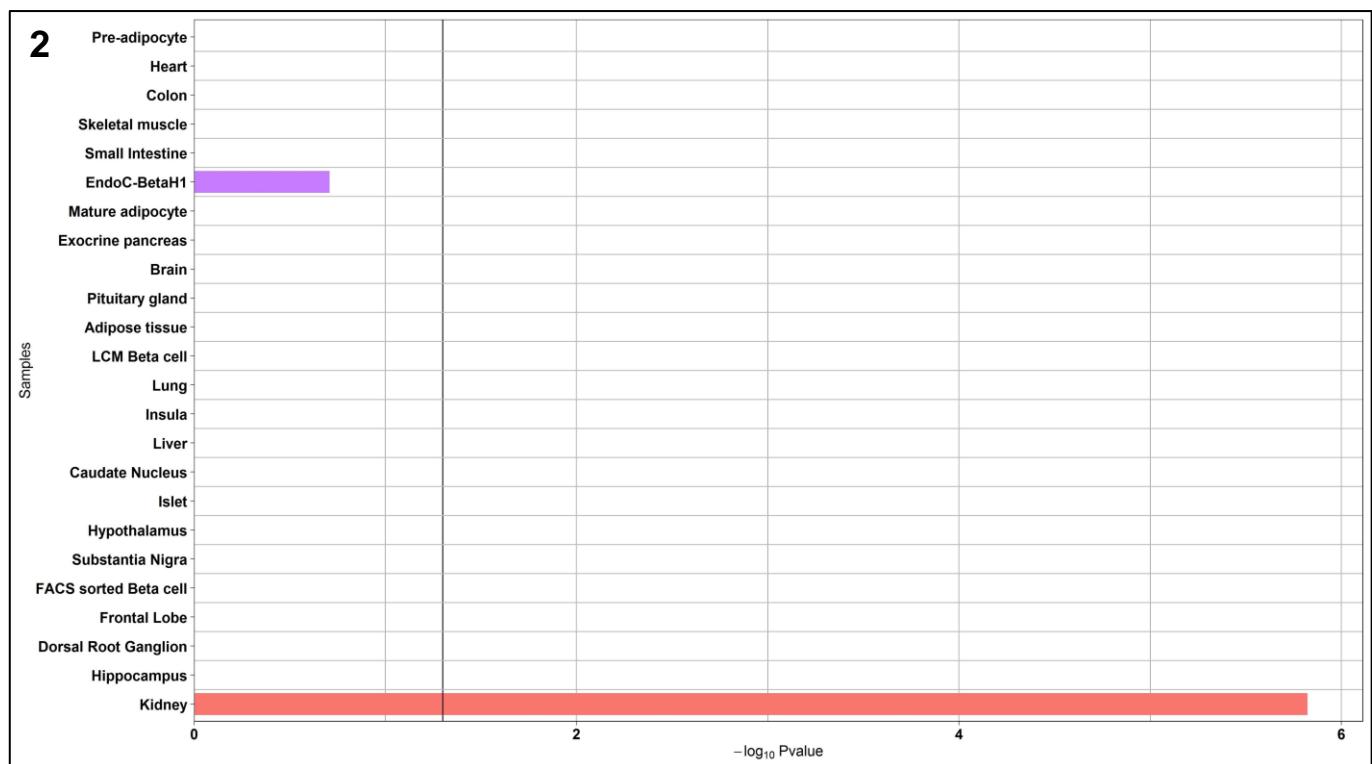
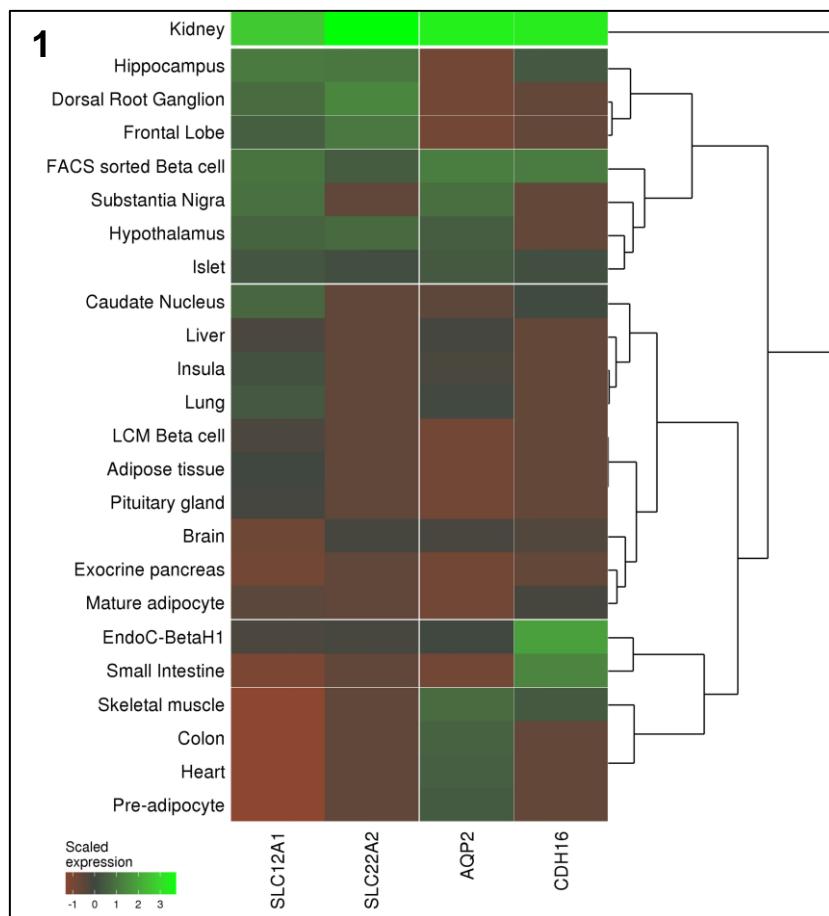


Figure E. (1) Heat map representing the expression of three genes known to be highly expressed in lung in the panel of human organs, tissues and cells; (2) Enrichment analysis of lung markers expression in the panel of human organs, tissues and cells. The black vertical line denotes a *p*-value of 0.05.

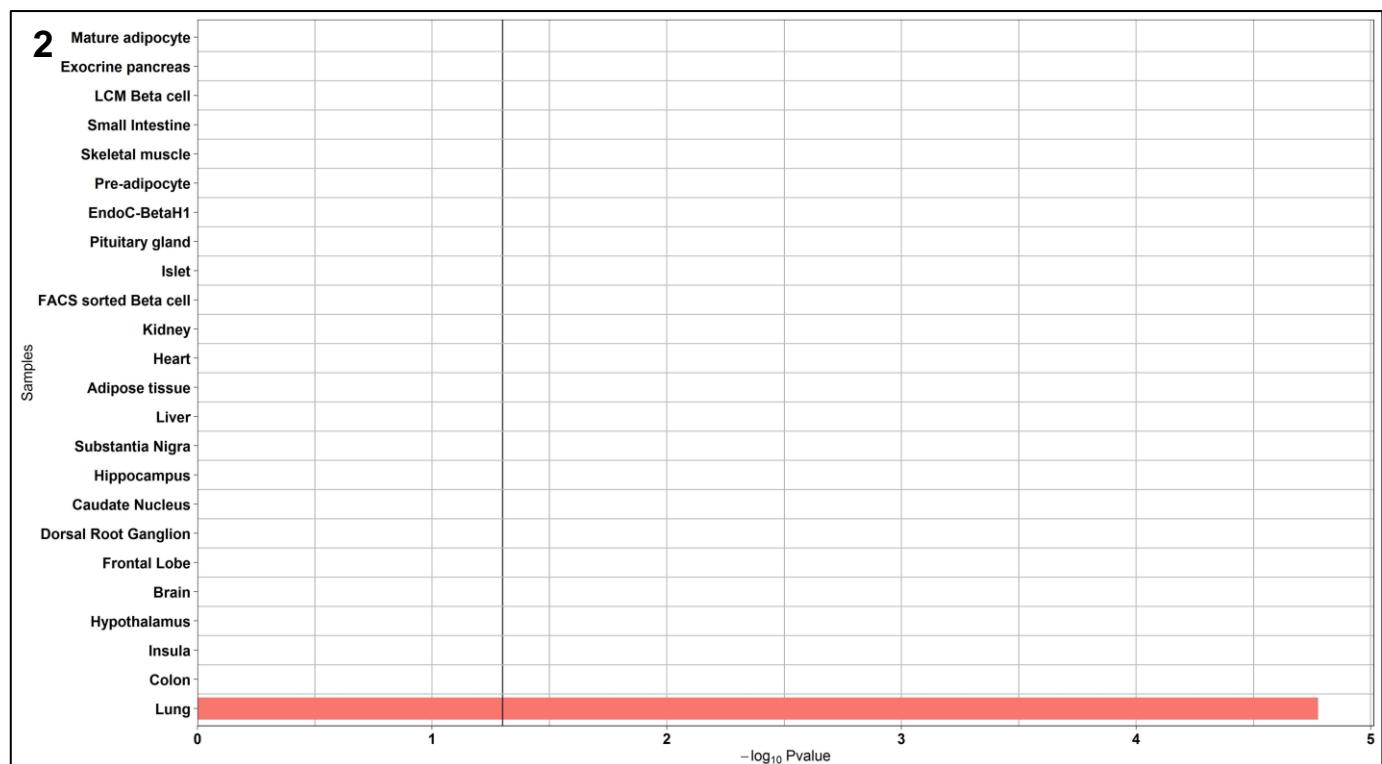
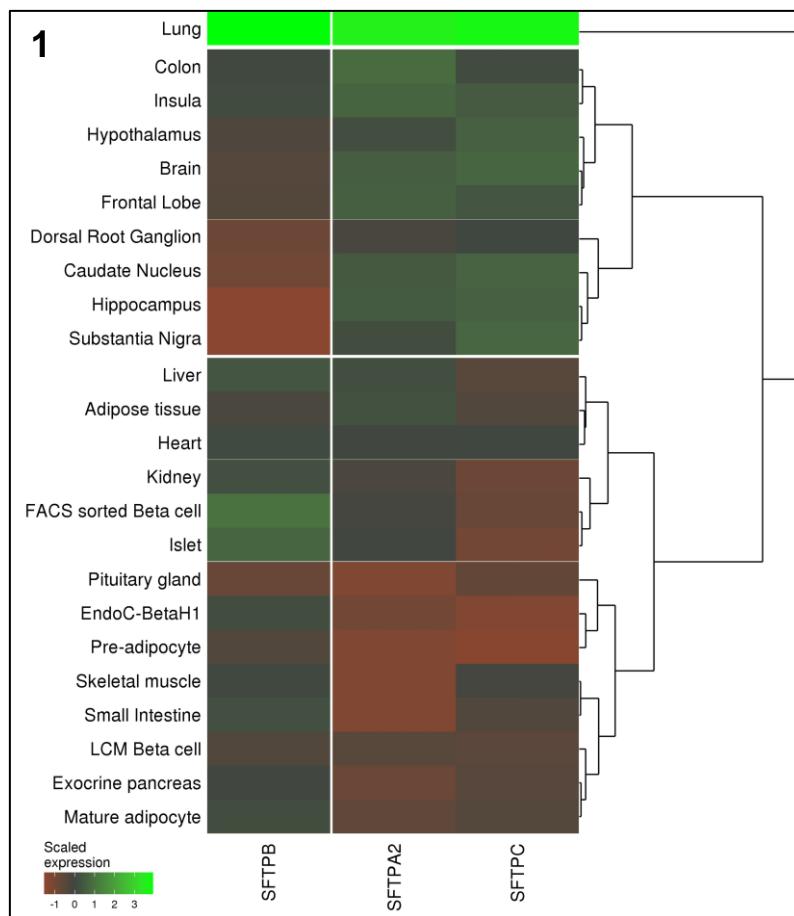


Figure F. (1) Heat map representing the expression of 13 genes known to be highly expressed in pancreatic islets in the panel of human organs, tissues and cells; (2) Enrichment analysis of pancreatic islet markers expression in the panel of human organs, tissues and cells. The black vertical line denotes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

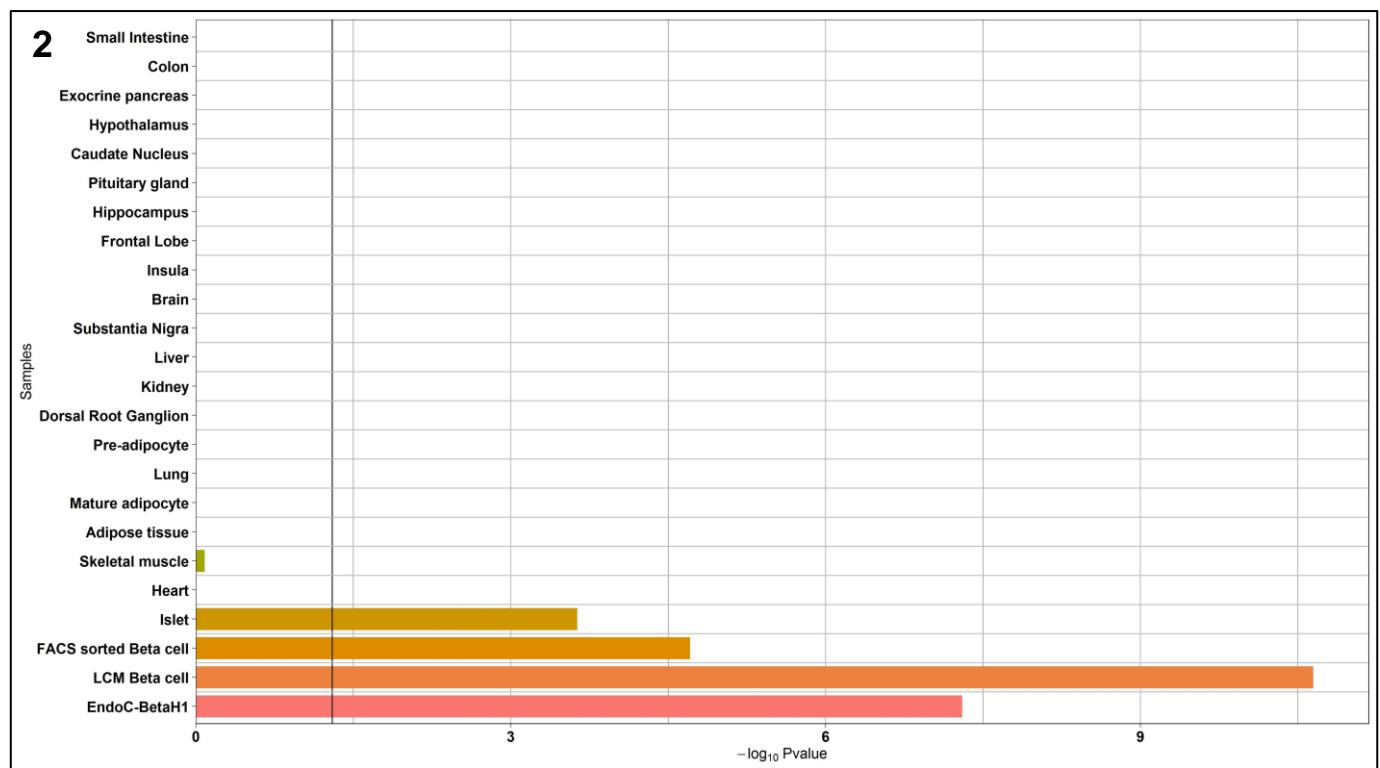
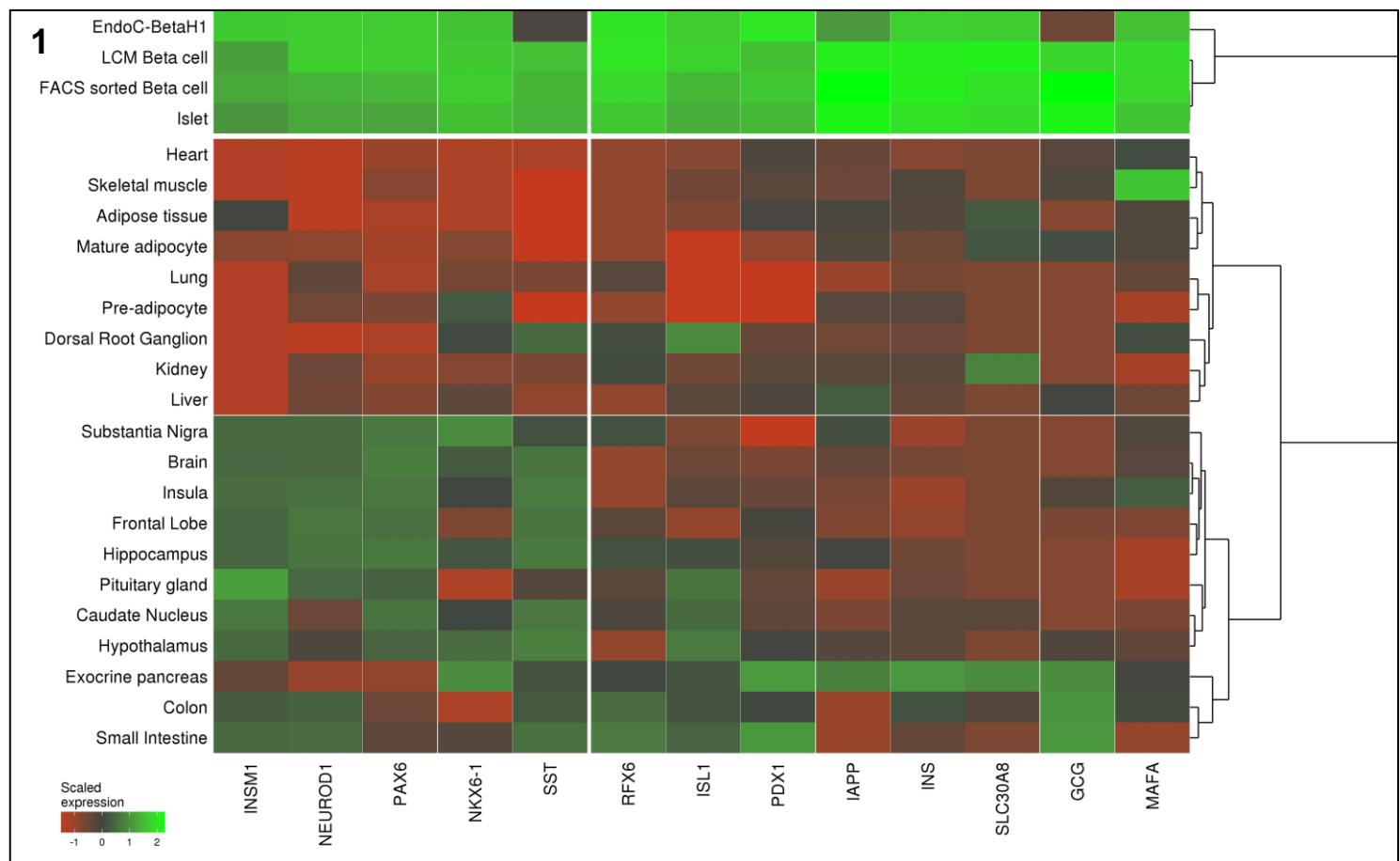


Figure G. Heat map representing the expression of genes causing monogenic diabetes in the panel of human organs, tissues and cells.

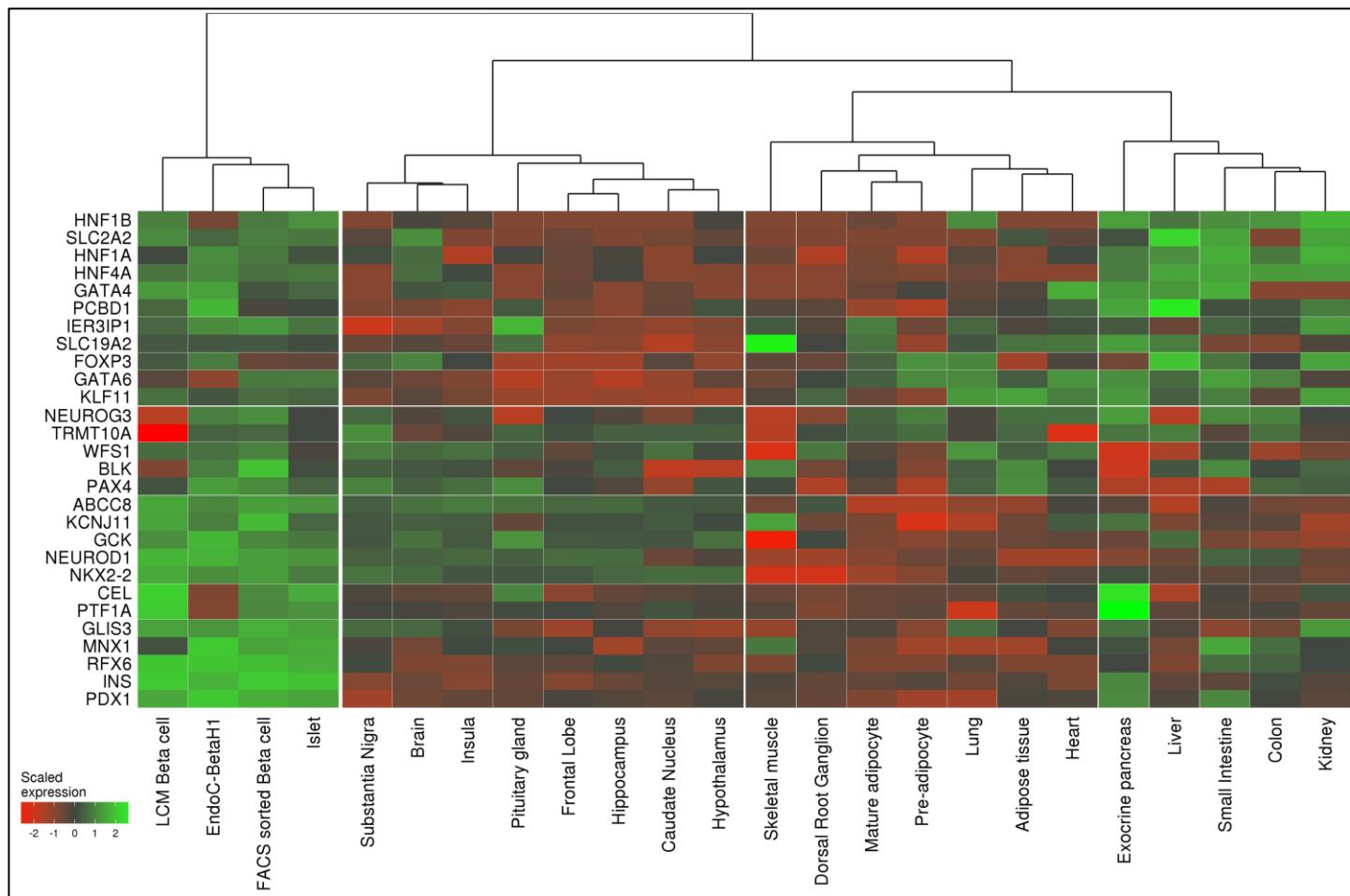


Figure H. Decreased expression of target genes in EndoC-βH1 cells. EndoC-βH1 cells were transfected with control non-targeting pool siRNA (siNTP) or target gene siRNA, and were analyzed 72 hours post-transfection. The mRNA expression of target genes and *INS* (encoding insulin) was determined by real-time 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.

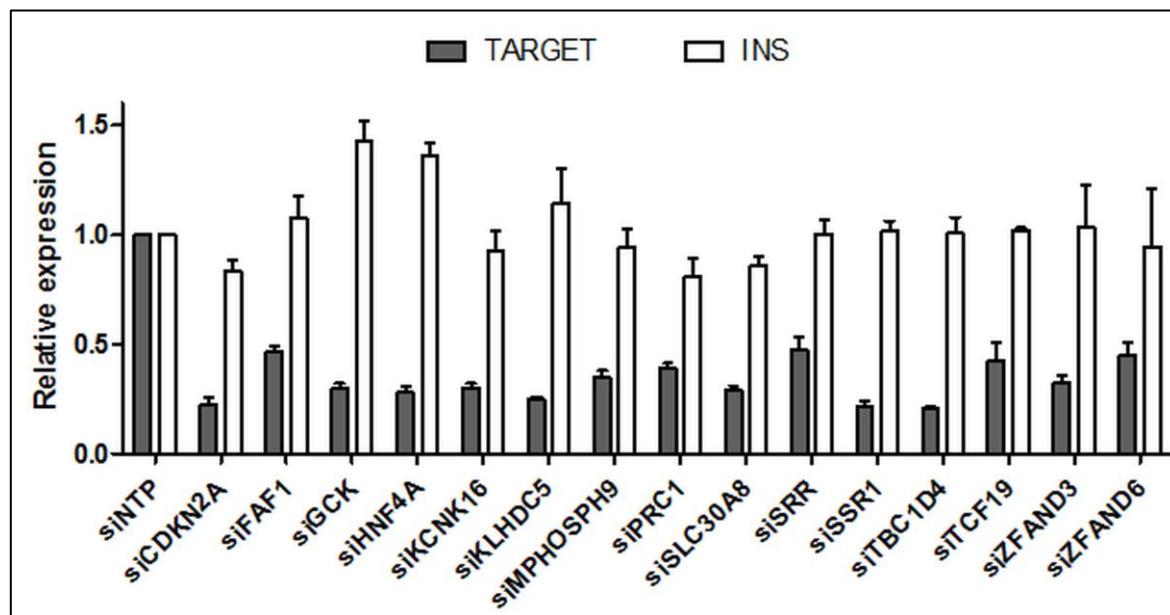


Figure I. Decreased expression of *MPHOSPH9* (1), *SSR1* (2), *FAF1* (3) or *KLHDC5* (4) do not lead to impaired insulin secretion from EndoC-βH1 cells. EndoC-βH1 cells were transfected with control non-targeting pool siRNA (siNTP) or target gene siRNA, and were analyzed 72 hours post-transfection. Insulin 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.

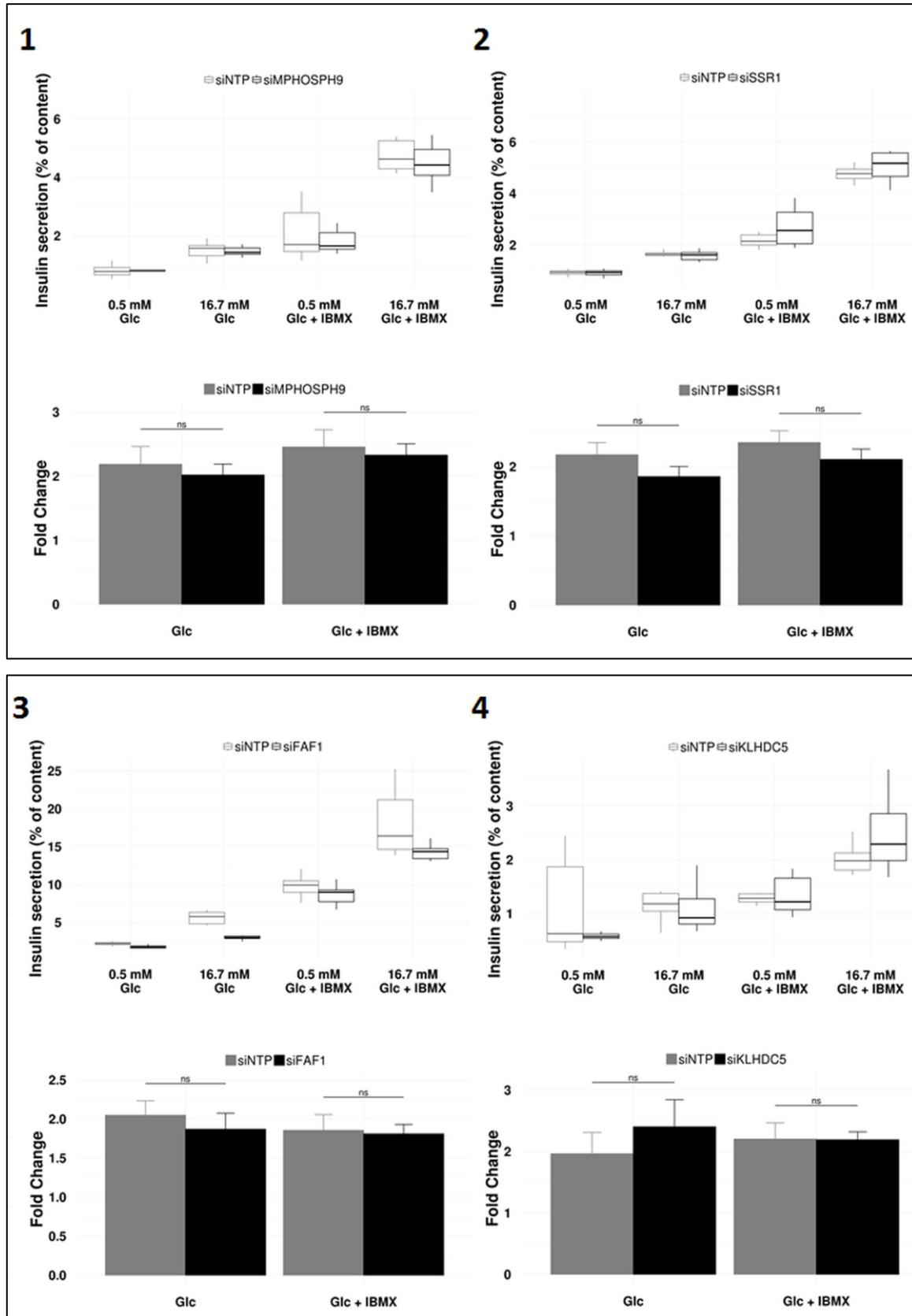


Figure J. SRR (1) and ZFAND6 (2) are expressed in pancreatic islets. Representative images of immunofluorescence staining for SRR (green; A), ZFAND6 (green, B) and insulin (red) performed on fixed tissue sections from normal human pancreases. Yellow (merged images) indicates co-localization of SRR or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

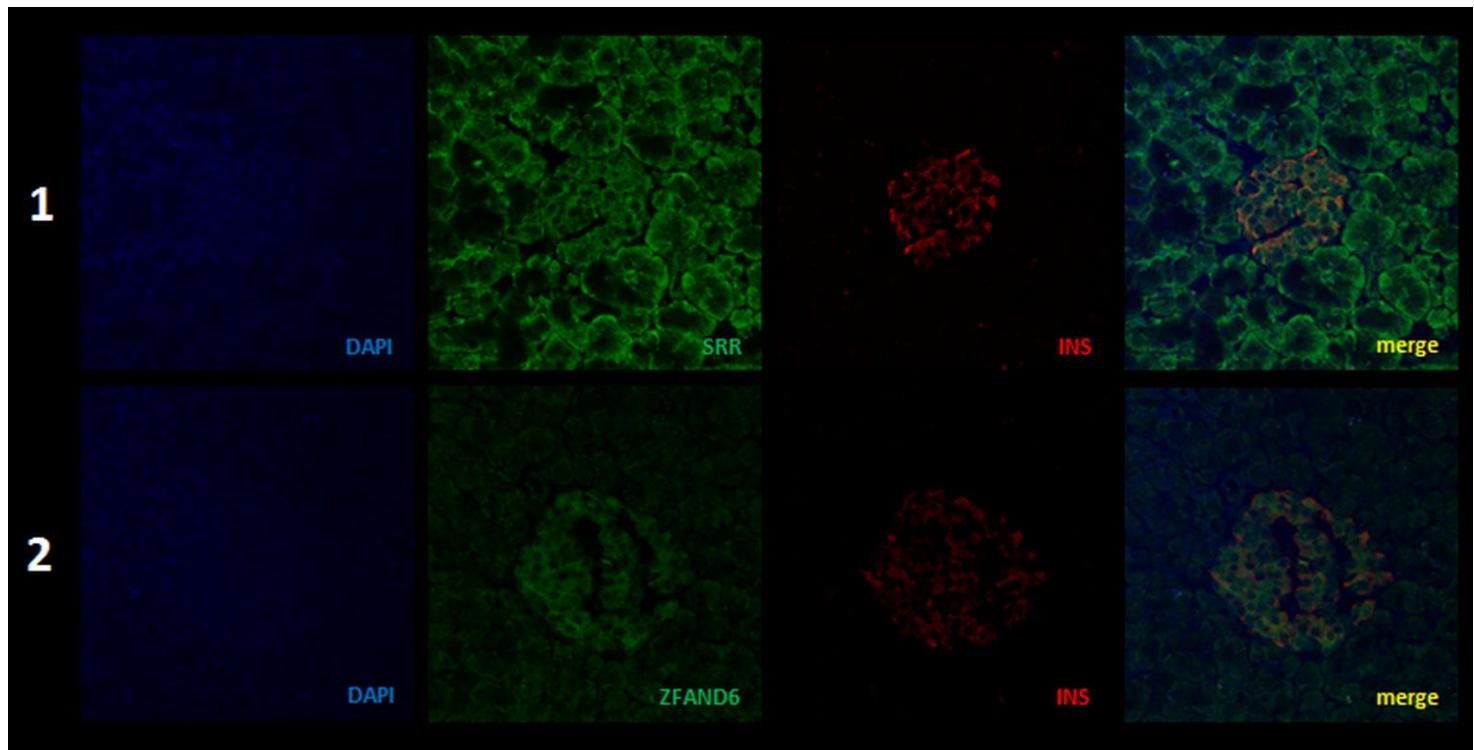


Figure K. PRC1 (1), SRR (2), ZFAND3 (3) and ZFAND6 (4) are expressed in EndoC- β H1 cells. Representative images of immunofluorescence staining for PRC1 (green; 1), SRR (green; 2), ZFAND3 (green; 3), ZFAND6 (green; 4) performed on fixed EndoC- β H1 cells. Blue, DAPI.

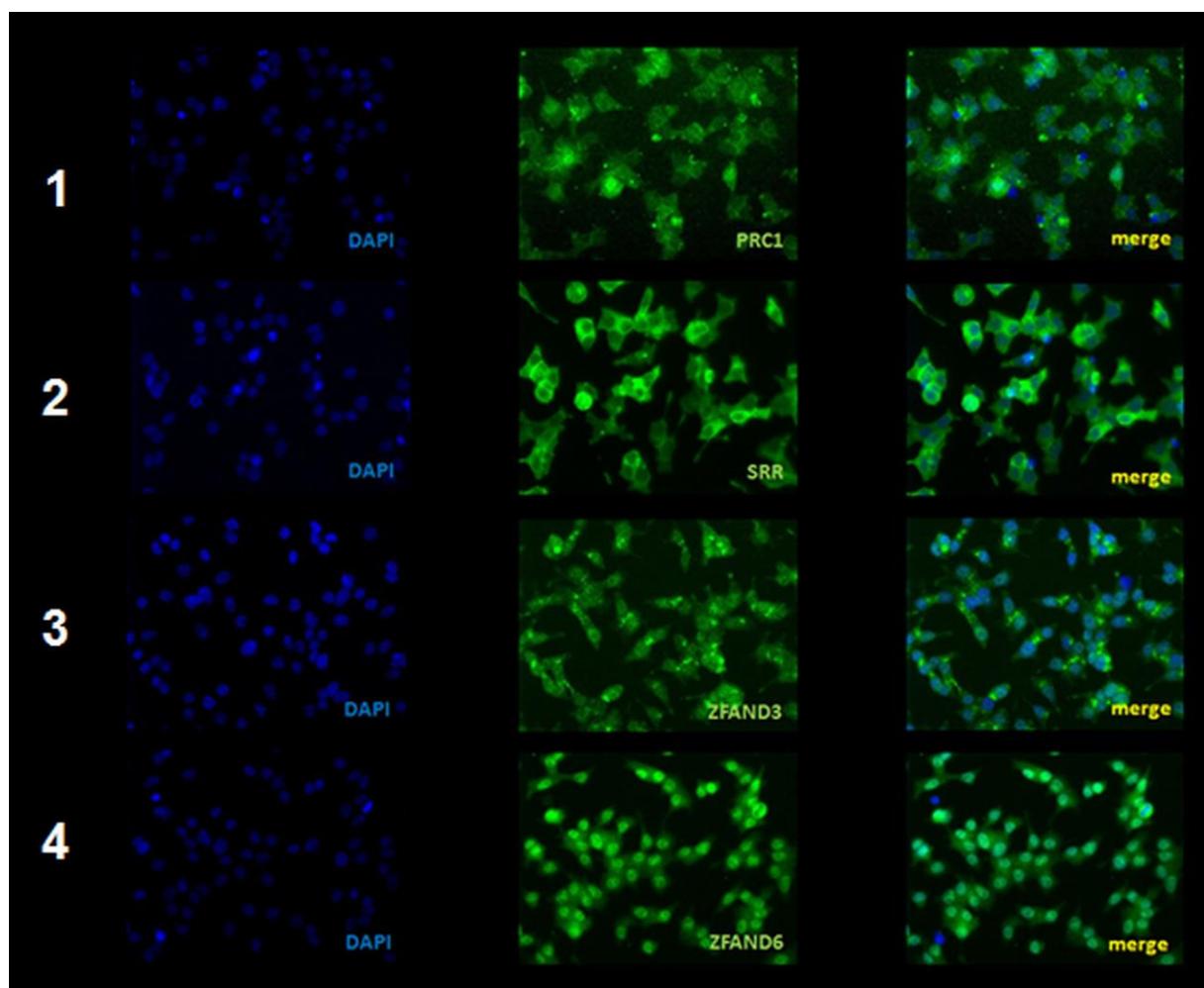
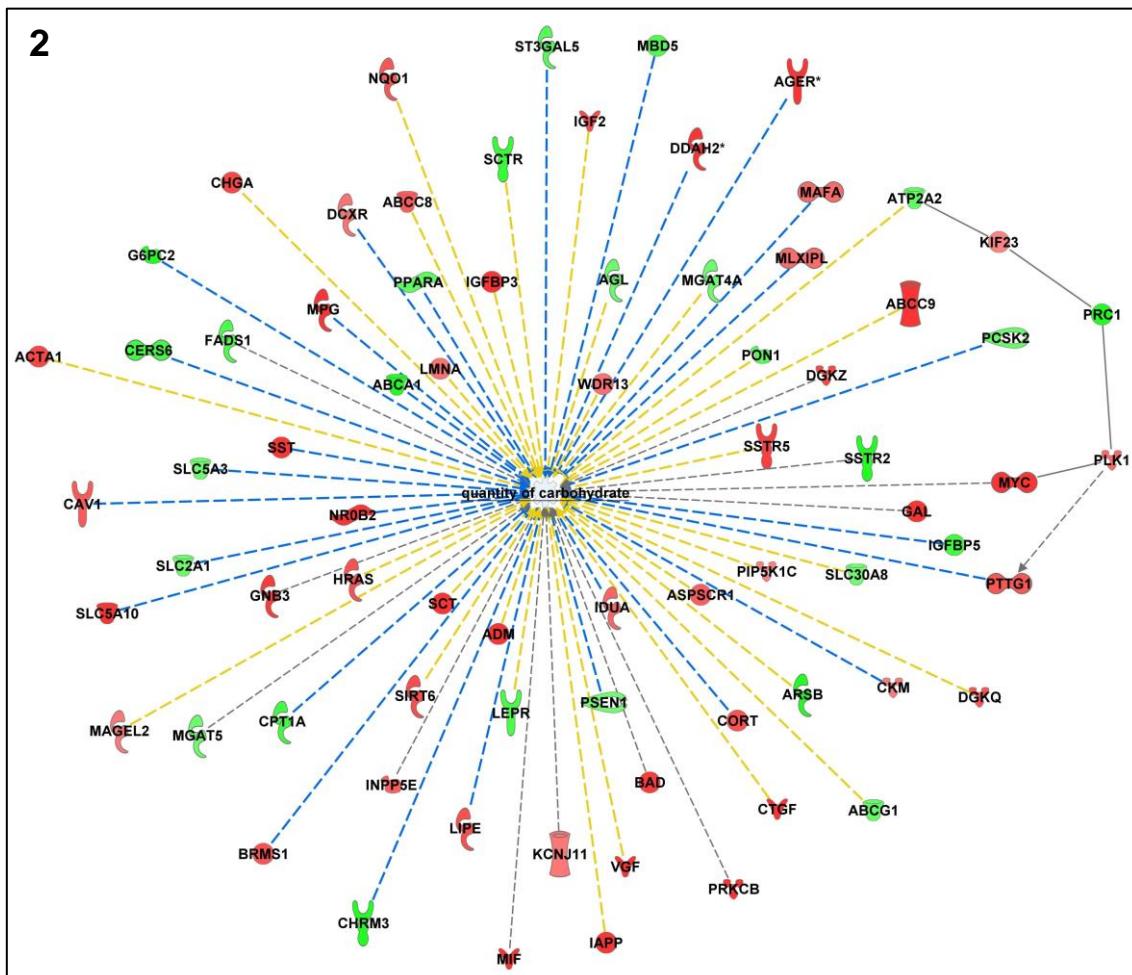
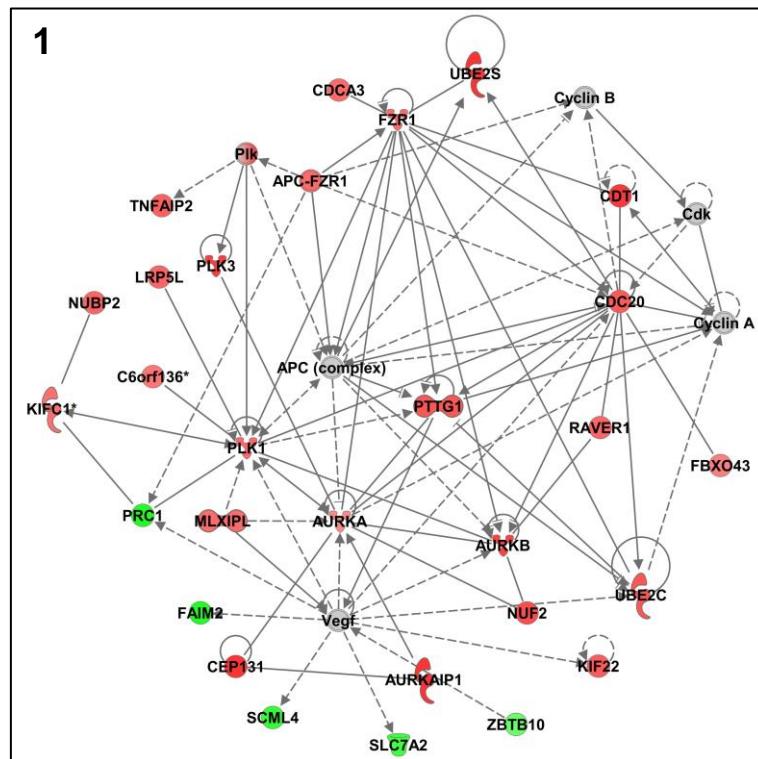


Figure L. Decreased *PRC1* expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network of 28 molecules entitled “Cell Cycle, Cellular Movement, Cellular Assembly and Organization”; (2) a network related to the quantity of carbohydrates; (3) a network related to the quantity of insulin in blood; (4) a network related to the concentration of D-glucose. The legends used in each figure are denoted in Figure 7.



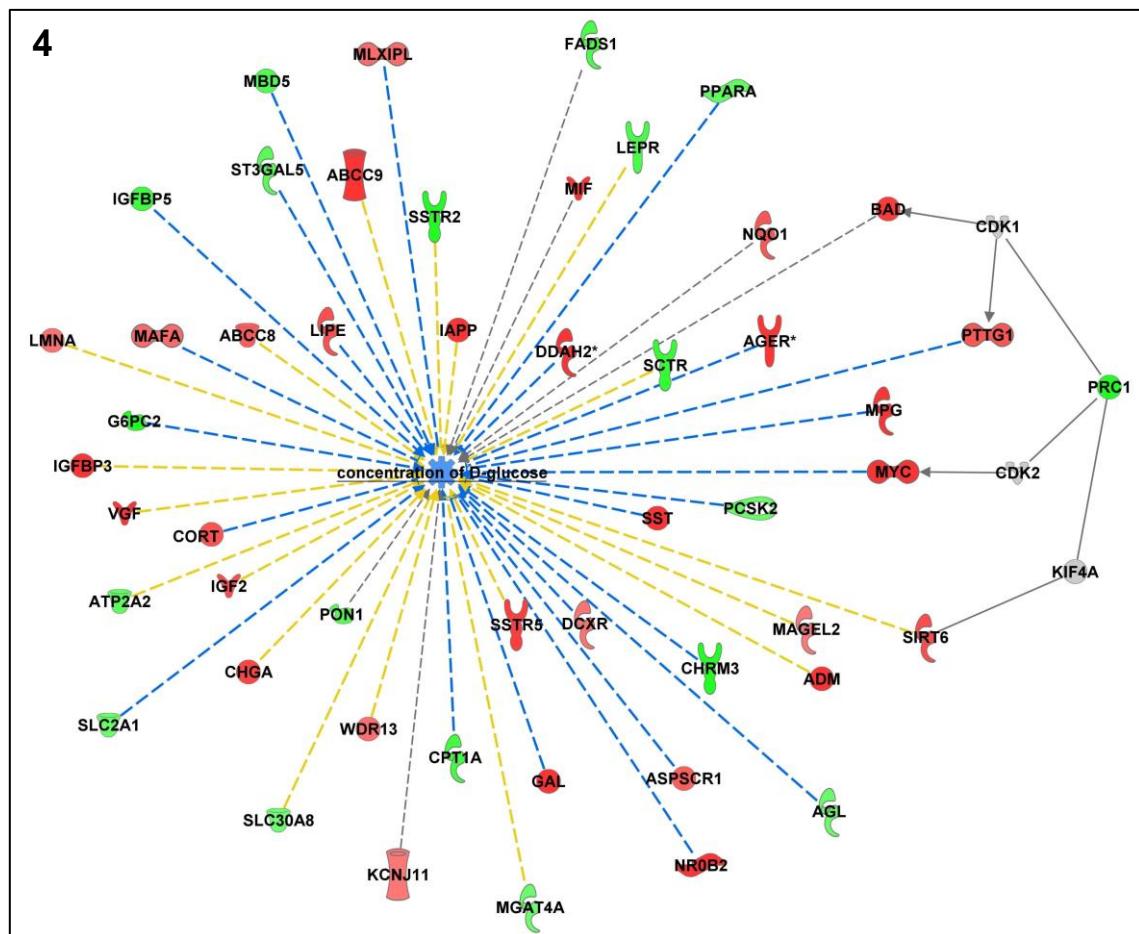
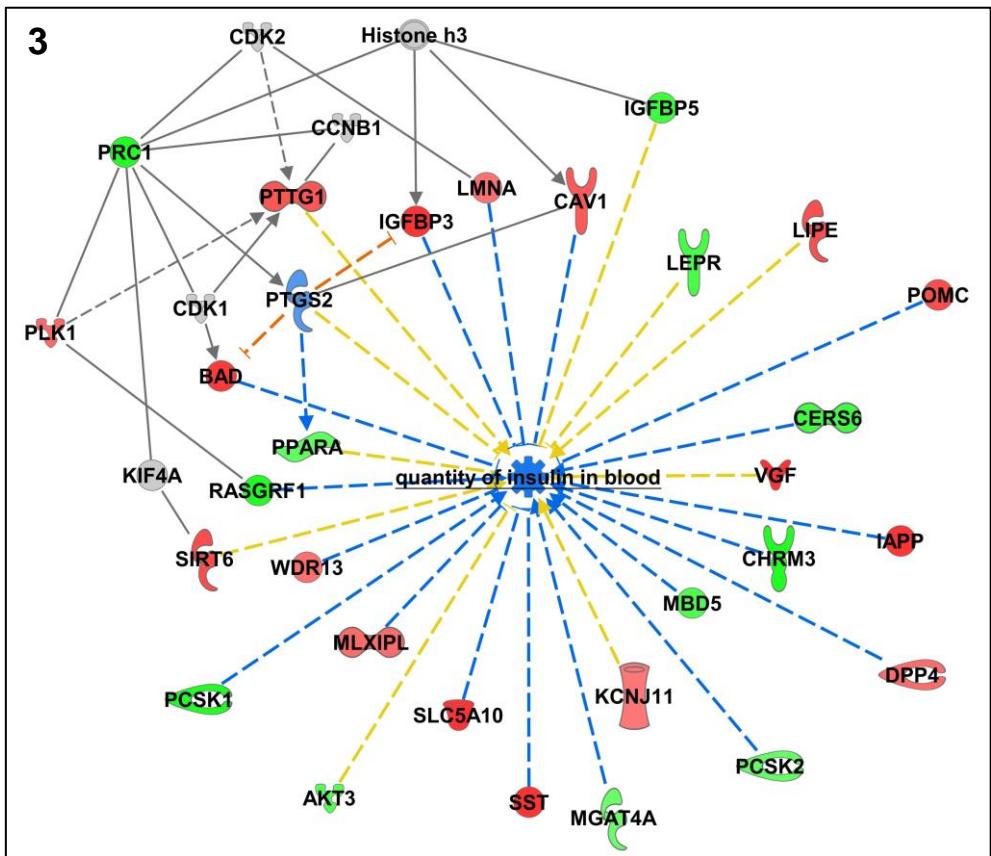
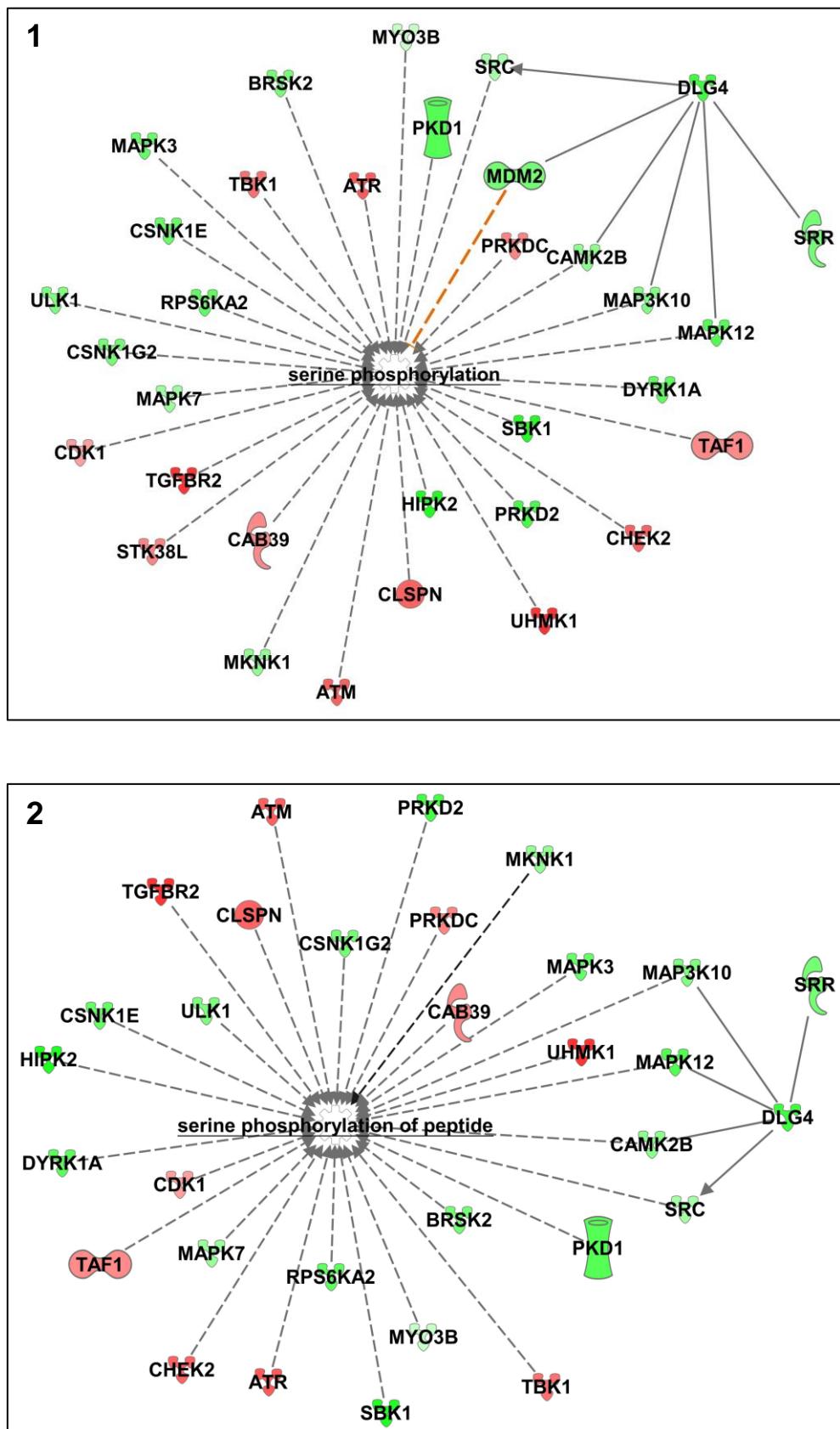


Figure M. Decreased SRR expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network related to serine phosphorylation; (2) a network related to serine phosphorylation of peptide; (3) a network related to endoplasmic reticulum stress response; (4) a network related to congenital disorders of glycosylation. The legends used in each figure are denoted in Figure 7.



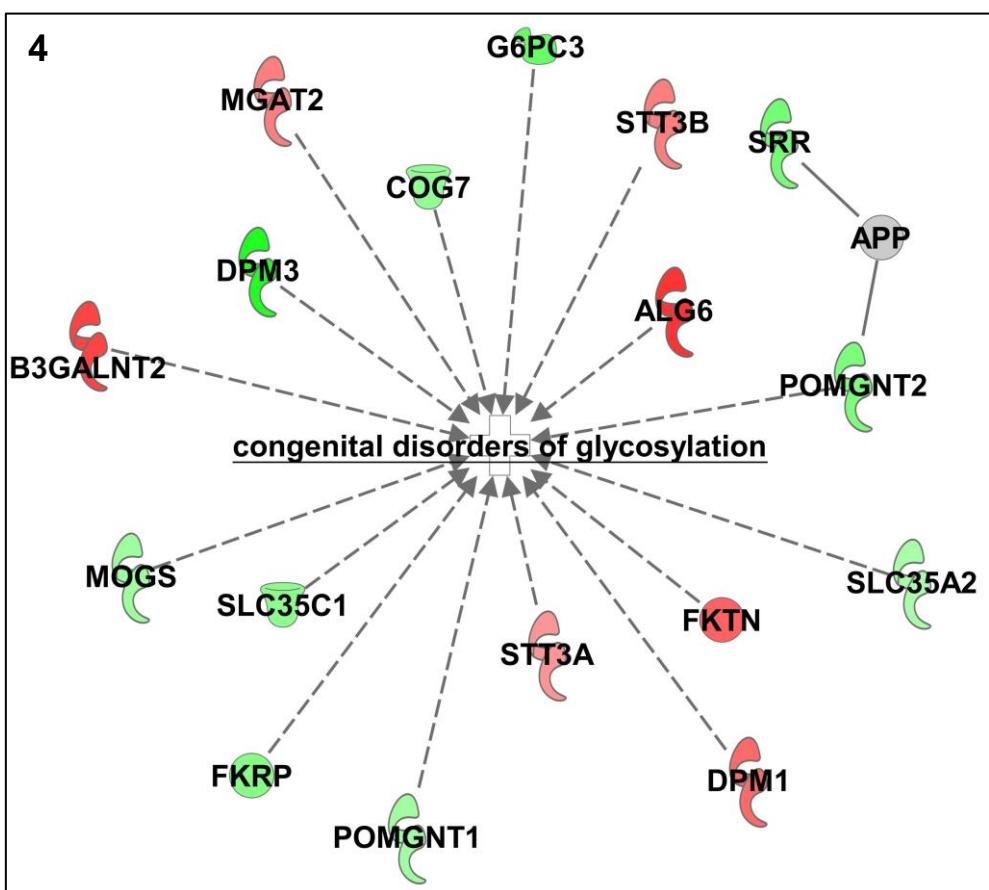
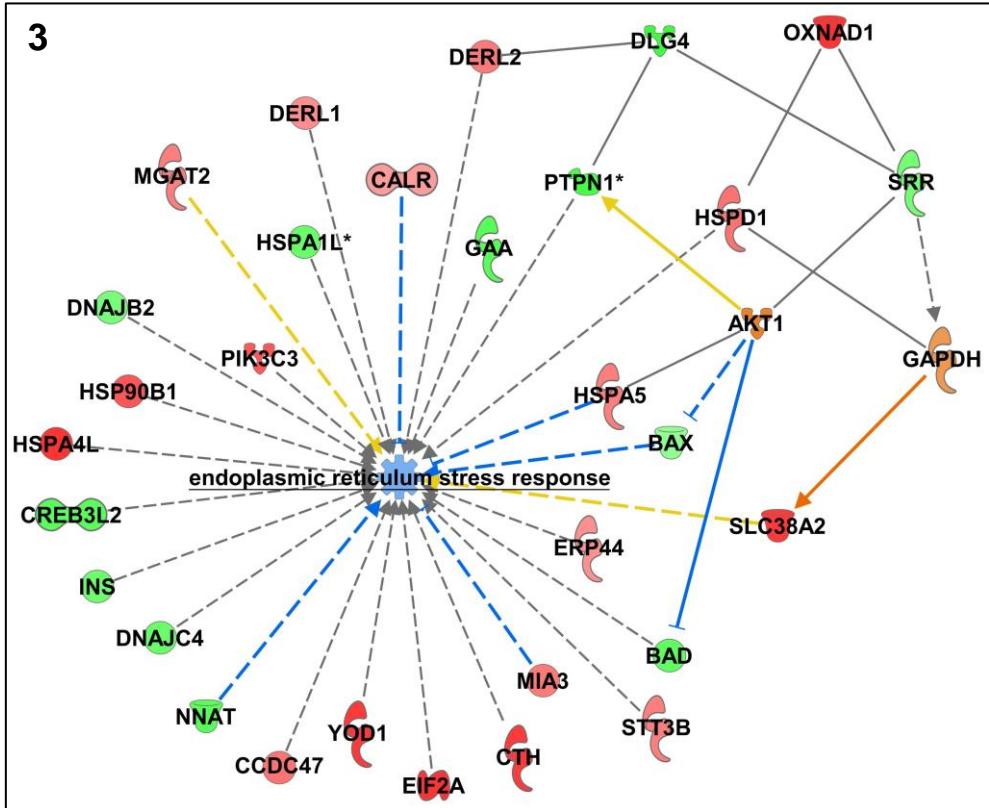
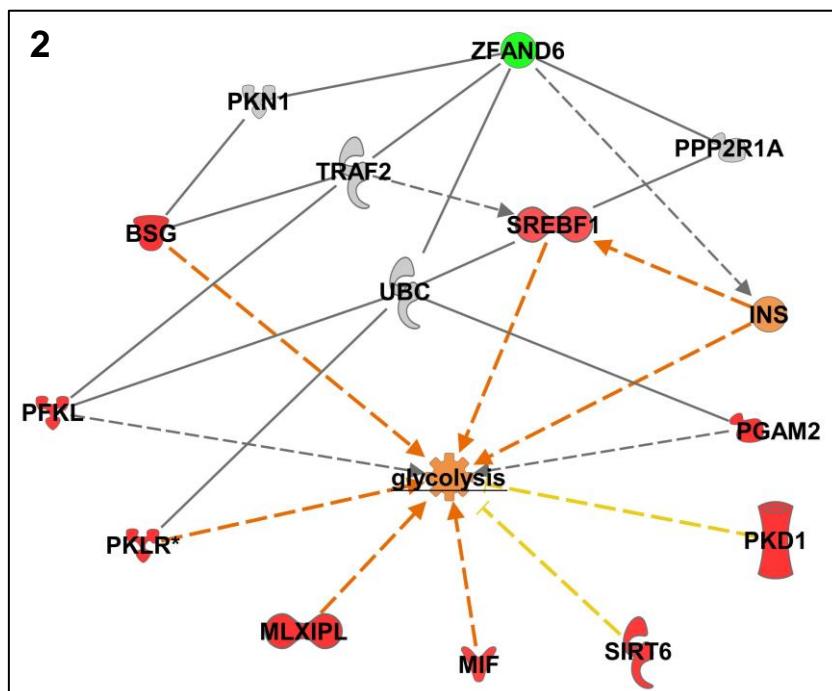
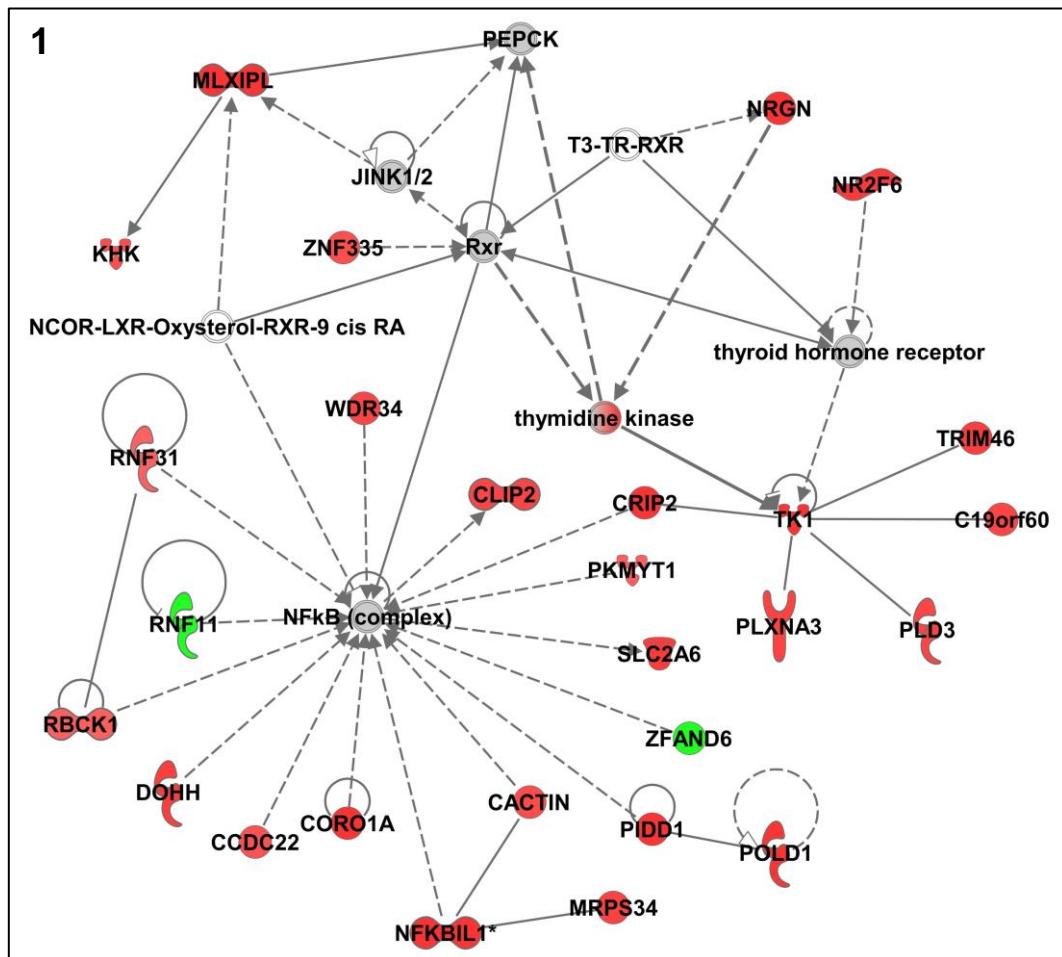


Figure N. Decreased *ZFAND6* expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network of 27 molecules entitled “Cell Signaling, Lipid Metabolism, Small Molecule Biochemistry”; (2) a network related to glycolysis; (3) a network related to the quantity of insulin in blood; (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.



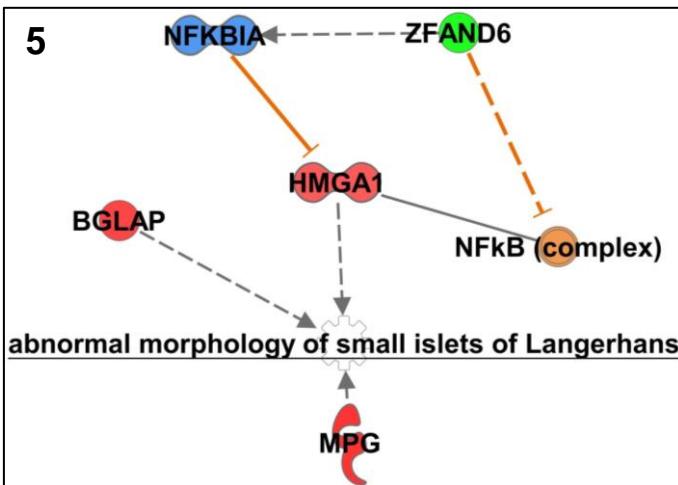
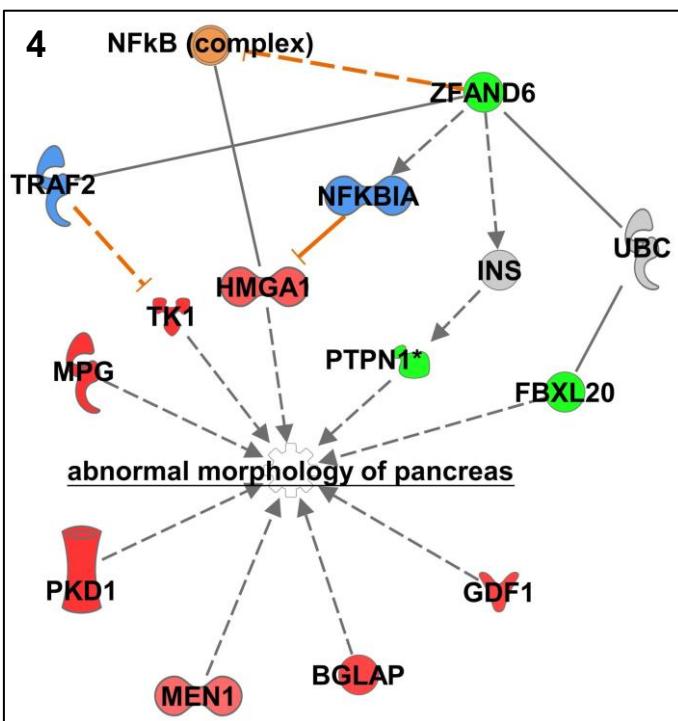
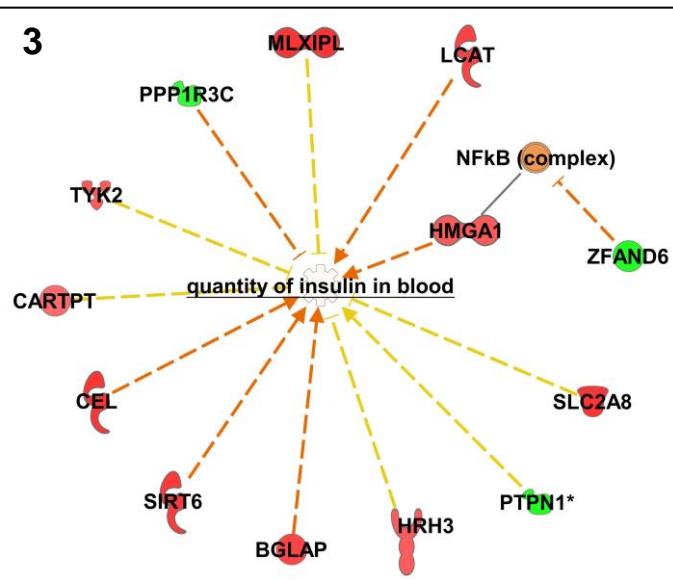


Figure O. Decreased *ZFAND3* expression in EndoC-βH1 cells emphasizes several networks found by IPA: (1) a network of 16 molecules entitled “Cellular Assembly and Organization, Lipid Metabolism, Molecular Transport”; (2) a network related to the transport of alpha-amino acid. The legends used in each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

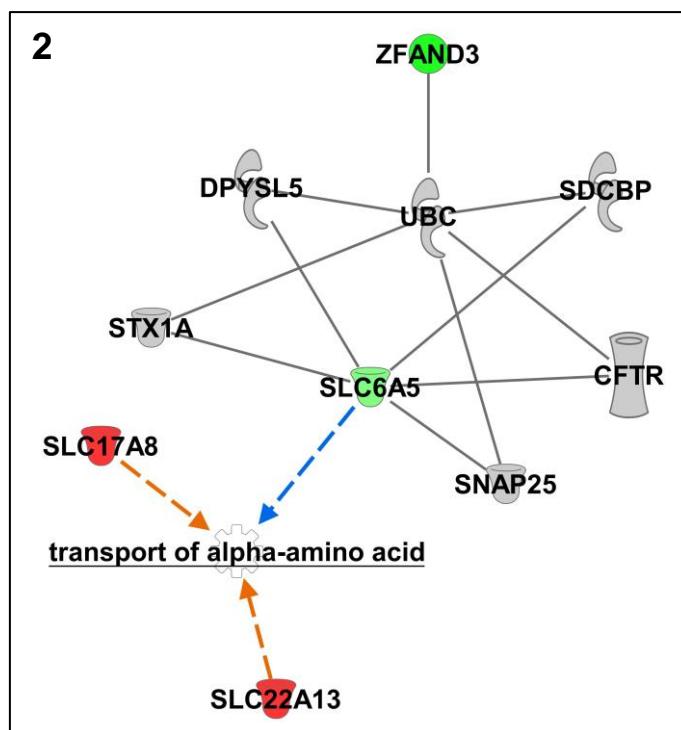
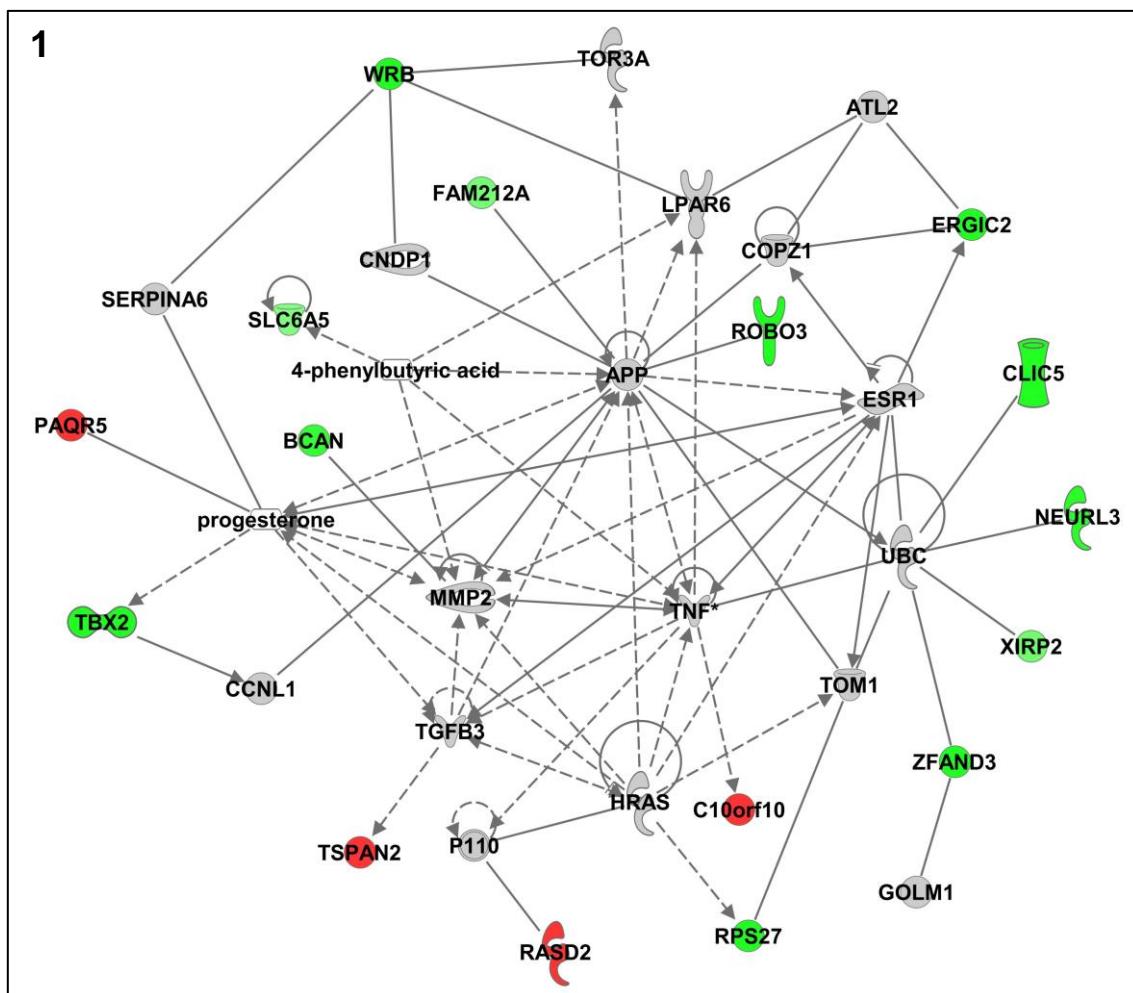


Figure P. Positive correlation between the expression of *Ins2* and the expression of *Prc1*, *Srr*, *Zfand6* and *Zfand3* in mouse pancreatic islets with altered beta-cell function. The expression of the five genes were investigated through quantitative RT-PCR (housekeeping genes: *Actb*) in pancreatic 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.

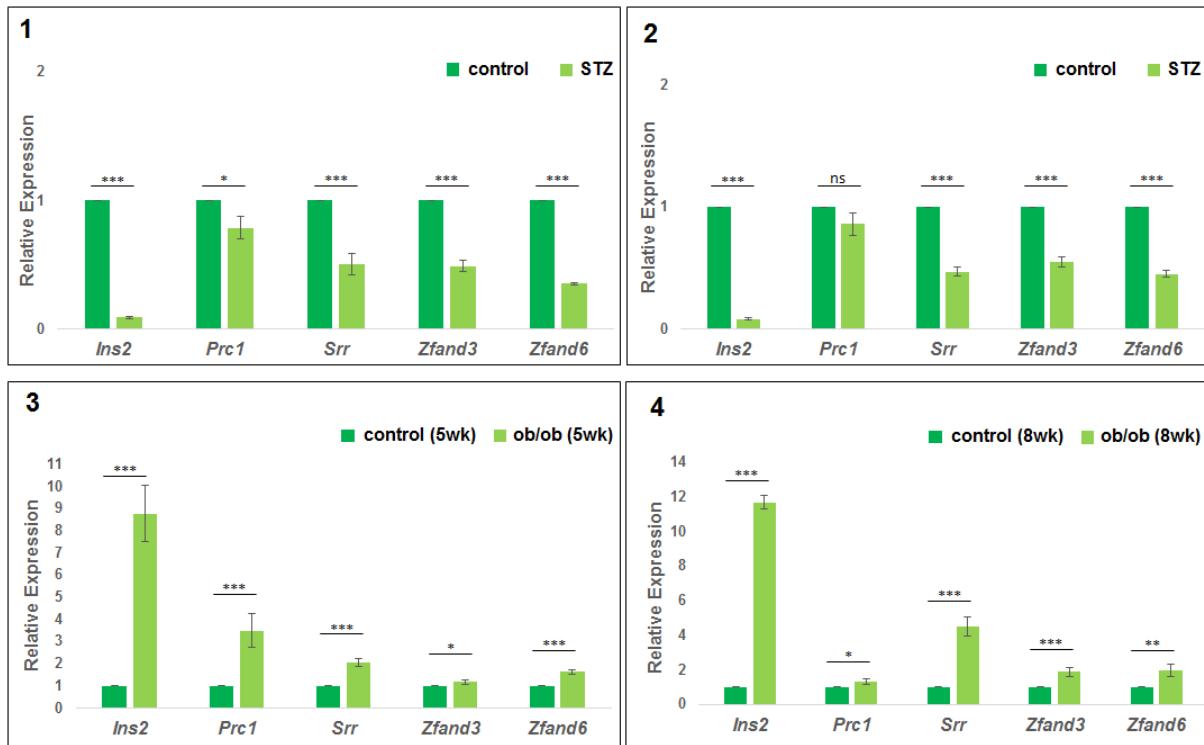
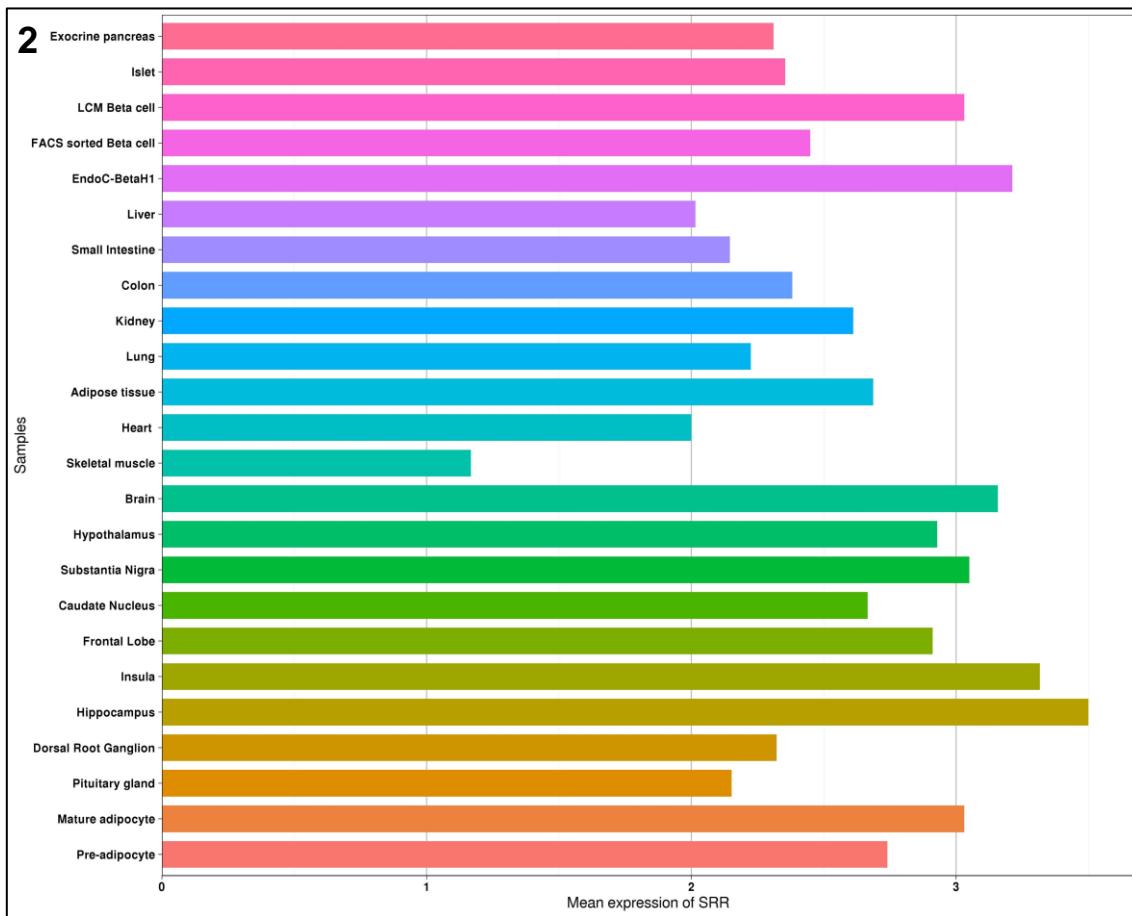
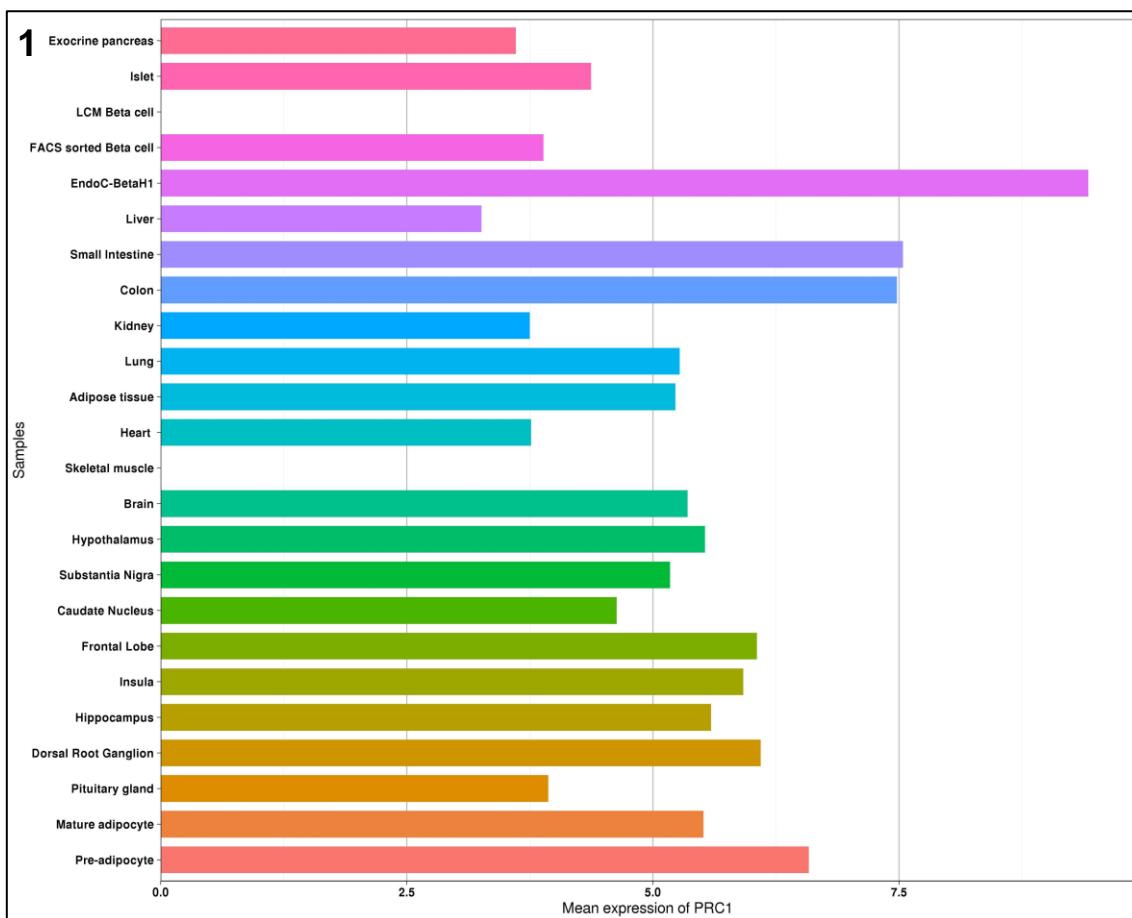


Figure Q. *PRC1* (1), *SRR* (2), *ZFAND6* (3) and *ZFAND3* (4) are ubiquitously expressed in our panel of human tissues.



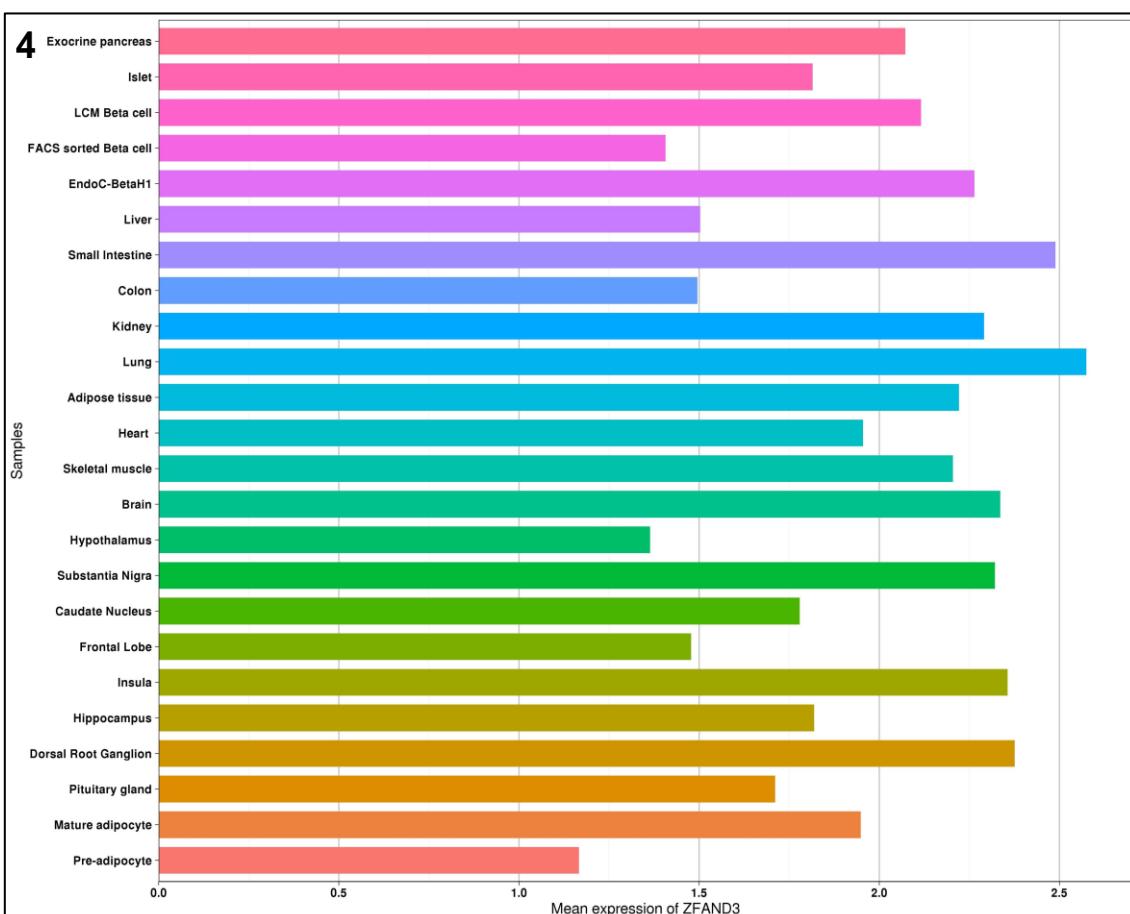
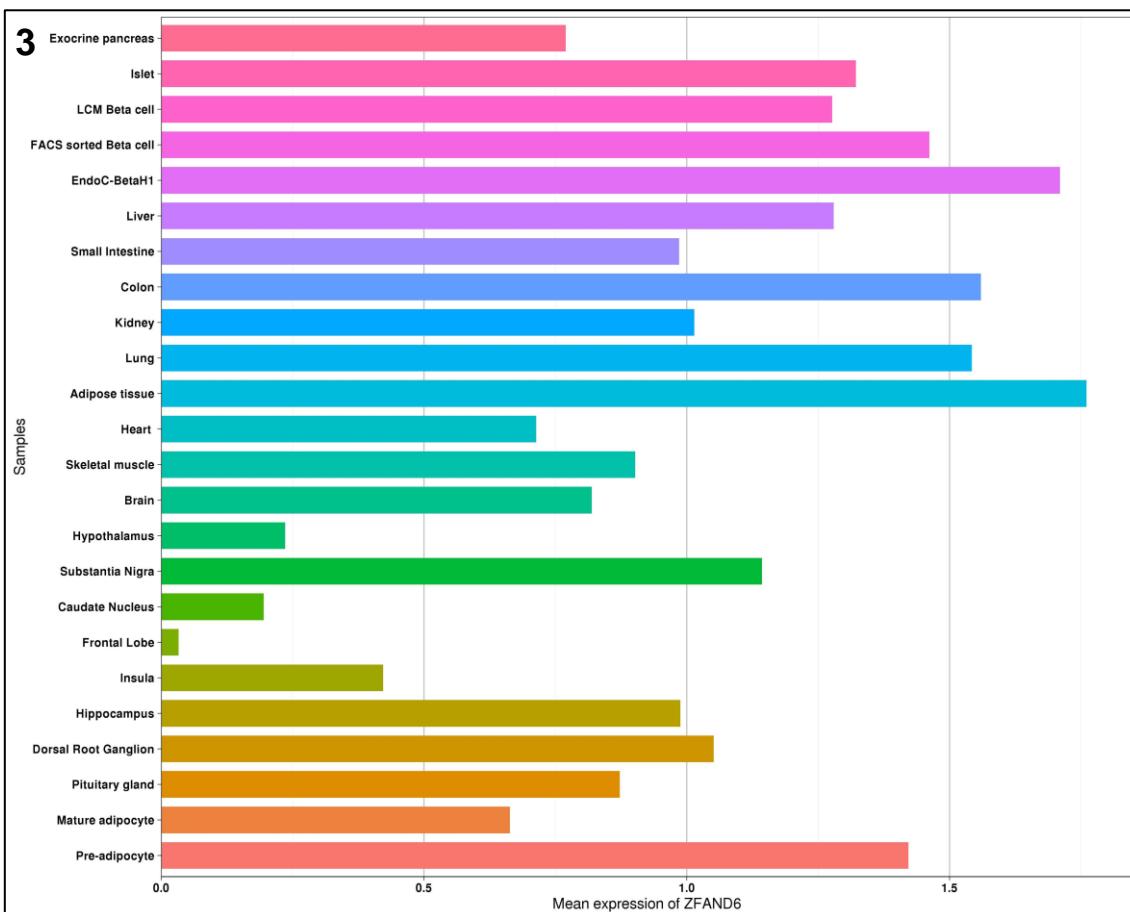


Table A. Probe design and selection for the expression study.

Gene	Accession	Target sequence	Tm CP	Tm RP	PN (CP;RP)	Group
<i>ABCC8</i>	NM_000352.3	ACCTCCGTGGTCACTATCACA ACATCGAGACTTCCAACCTCCC CAAGCTGCTAATTGCCCTGCTG GTGTATTGGACCCCTGGCCTTC TCACCAAGACCA	81	82	309041; 209041	Monogenic diabetes gene
<i>ADAMTS9</i>	NM_182920.1	AGTGAAATTATTAGAGACCTGA GCGAACATCGAAATCGTCTCC CATCCGAGTGACGCTCTCGGA GAACCCTTCCCACGAACGTCC ACTTCAAAGAGA	80	83	350001; 250001	T2D gene
<i>ADCY5</i>	NM_183357.2	CCCACTCCATATTCATGCTCAGC TTCTACCTGACCTGTTCCCTGCT GCTGACCTTGGTGGTGTGTTG TCTGTGATCTACTCCTCGTAA GCTCTTCCC	83	80	350002; 250002	T2D gene
<i>ALPI</i>	NM_001631.3	CAGCAAGGCTCAGGACAGCAAA GCCTACACGTCCATCCTGTACG GCAATGGCCCGGGCTACGTGTT CAACTCAGGCGTGCACCGAC GTGAATGAGAGC	85	85	386252; 286252	Marker of gut
<i>ANK1</i>	NM_020477.2	CAGGGTACTTTTCCCAACCTCA TCTGTAGAAATCCATGTGGGC TTCTGGAAAGAAAAAAA AAGAAAACTAGGCATGAAATCA GTTAACACC	80	79	374572; 274572	T2D gene
<i>ANKRD55</i>	NM_024669.2	GCACAGCAGCAGAAGAGAGTGA ACATTCTGCCAACCCCCACCA GATGAAAATTAACTGTGGGCC CTCGCTGCAGAAATGTAGATGA ATATGTATTTTC	85	77	351314; 251314	T2D gene
<i>AP3S2</i>	NM_005829.4	GGTGCTAGGGCTCGTGAGCGC CGGGGCCAAGTTCCGAGTGCC GCTCTCAGCAGCGCACCAACCG GAAGTGTACGTGTTGGCGGA AGGAGGAGCTTTC	85	85	355827; 255827	T2D gene
<i>AQP2</i>	NM_000486.5	GTCTCACAGGTAGTATATGGTG GAGCCAACACTTGAACTCAGAC CTTTTACACAAAATCCCATGAT TTTCCACTGAGACAAATCCTAG GCTCCTGGGA	80	82	365408; 265408	Marker of kidney
<i>ARAP1</i>	NM_001040118.2	GGCCACAGTGAAGGCCCTTATC AGCCACCTGTACTGTGTTAGT GCTTCTCAGACACGAACCGAGAT GAACGTGCACAACCTGGCAATT GTGTTGGGCC	83	83	370135; 270135	T2D gene
<i>ARL15</i>	NM_019087.2	AATGCCATCTTGAATGTAAAAGA ACTTGGAGGGGCTGATAACATC CGGAAATACTGGAGCCGCTACT ACCAAGGATCTCAAGGGTAAT ATTGTATTAG	84	81	300047552; 200047552	T2D gene
<i>BCAR1</i>	NM_001170717.1	CTGGCCCCGGGCACCCGTACG ATGTGCCCGCTGAAACGGGTGCT TCCCTCTGAGGTGGCTGATGGT GGCGTGGTCGACAGTGGTGTG ATGCGGTGCTCC	85	86	374085; 274085	T2D gene
<i>BCL11A</i>	NM_022893.3	TACACATGTACAACCTGCAAACAC GCCATTACCAAGTGCATGGTT CTCTGCAACACGACAGAAC CTCATGGATTAAGAACATCTACTTA GAAAGCGAAC	79	83	335334; 235334	T2D gene
<i>BLK</i>	NM_001715.2	AGCTTCTGCTCCAATCAACAAAG GCCGGCTCCTTCTTATCAGAG AGAGTGAACCAACAAAGGTGC CTTCTCCCTGTCTGTGAAGGAT GTCACCAACCCA	78	81	304841; 204841	Monogenic diabetes gene
<i>C1orf43</i>	NM_015449.2	ATTCGACTCTCAGGGTTCAGG ATATCAAGTATGAGCCCCAGCT CCTTGCAGATGATGATGCTAGA CTACTACAACGGAAACCCAGG GAAATCAAAGTT	84	84	300000629; 200000629	Housekeeping gene

C2CD4A	NM_207322.2	GCATTTGTTAACGGACCCGGAT AAGAAAATGAGGGCAAAAGAGG TGAAGTGACTTGTCCAAGATCA ACAGTGAATTATTAGTTGGAACG CCAGCCTGAT	81	80	310209; 210209	T2D gene
C2CD4B	NM_001007595.2	AGGATGCCGCTCTCGAGAAC TCTGTTCTCGGCCAGGCAG CTCCGCCGAAGGCCGCTTC GCCAAAGTGCTCACGCCGAATC GCATCCCCGAAT	86	86	335228; 235228	T2D gene
CAMK1D	NM_020397.2	AAAGAGACCCCTCGAACCGGG GCCTTTCCGAAGTGGTTTAGC TGAAGAGAAAGGCAACTGGCAAG CTCTTGCTGTGAAGTGTATCCC TAAGAAGGCCG	79	81	305079; 205079	T2D gene
CCND2	NM_001759.3	TGTGAGGAACAGAACAGTCGAAG AAGAGGTCTCCCTCTGGCCAT GAATTACCTGGACCCTTCTG GCTGGGGTCCCAGTCCGAAGT CCCATCTGCAAC	85	86	340263; 240263	T2D gene
CDC123	NM_006023.2	TTGGTGAAGTCACAGATTCACT GCTGTTCACCTGGGAAGAACTG ATATCTGAGAACAACTAAACGG CGATTTAGTGAAGTTGACGCTC AAGAGCAGGA	83	81	300039699; 200039699	T2D gene
CDH16	NM_004062.2	GCCACGTGAACACATAATCCCC GTGGTGGTCAGCCACAATGCC AGATGTGGCAGCTCCTGGTTG AGTGATCGTGTGTCGCTGCAAC GTGGAGGGGCAG	82	81	308452; 208452	Marker of kidney
CDKAL1	NM_017774.2	GGTCACTCTGTGAGACTGCTGG GTCAGAAAAGGATAATGGAAG GCGGCTGGGGGAGCACGATT GGATTTGCCGAAGATTAGGAAG AATCCACTGATAG	82	82	306459; 206459	T2D gene
CDKN2A	NM_000077.3	AAGCGCACATTCATGTGGGCAT TTCTTGCAGCCTCGCAGCCTC CGGAAGCTGTCGACTTCATGAC AAGCATTGTGAACTAGGGAA GCTCAGGGGGGT	82	81	302810; 202810	T2D gene
CDKN2B	NM_004936.3	CACTGGGTGACGGCAGTCGAT GCGTTCACTCCAATGTCTGCTG AGGAGTTATGGTGAACCCACAA CTTAGGCCCTAGCGGCAGAAAG GAAAACCTGAAG	82	81	301731; 201731	T2D gene
CEL	NM_001807.3	GGTCGTGGAAGCGTCAATAA GAAGCTCGGCCTCTGGTGAC TCTGTGGACATCTTCAGGGCA TCCCCTTCAGCTCCCACCAA GGCCCTGGAAAA	85	84	348673; 248673	Monogenic diabetes gene
CHCHD2P9	ENST0000046172 6.1	CTTCTATGGATCAACAGTTTC TGGAGTGTGCCAGAACAG GCGACATCAAGCTGTGAGGA TTTCAGTAAGGTGCTGAAACAG TGGCGACTTGCA	86	84	300093539; 200093539	T2D gene
CIDEc	NM_022094.2	GACAAGGATGGAATACGCCATG AAGTCCCTTAGCCTCTCTACCC CAAGTCCCTCTCCAGGCATGTG TCAGTGCCTACCTCTGTGGTGA CCCAGCAGCTG	84	85	343264; 243264	Marker of adipose tissue
CILP2	NM_153221.2	CCGCTCCCGACTCAGAACGG CTCTGACTTCTCGTGCAGT GACCCGATTCAATCTTCTACC CTTGGGAGTTCTGGCGTTGGC ACAAAGTCCC	83	79	300060271; 200060271	T2D gene
COBL1	NM_014900.3	AGTTTTTCAACGAGTAAGAA AAAGCGAGACCAACTGCAAGT GCCCTGCAACCCCTAGTAA ATAAGCACCAGCCAACTTTACA AGGTCCAATA	80	82	313525; 213525	T2D gene
DGKB	NM_004080.1	TCCACTTCTGTGCTCTGGGC TTAGAAAATAACGTGAAGGATG ATGGACAGCACGTGTGGCGACT GAAGCAGTAAACAAACCTGCC TATTGCAACCTT	78	79	302687; 202687	T2D gene

<i>DNER</i>	NM_139072.3	CCTCTACATCATCATTGGAGCC CTCTGCGTGGCCTTCATCCTTAT GCTGATCATCCTGATCGTGGGG ATTGCGGCATCAGCCGATTG AATACCAGGGT	82	83	350100; 250100	T2D gene
<i>DUSP9</i>	NM_001395.2	CCCATCTCGACCACCTGGAGCC AGAACCTGTCGCGGTTCTTC GGAGGCCATTGAGTCATTGAT GAGGCCTTGTCCCAGAACTGCG GGGTGCTCGTCC	85	84	347657; 247657	T2D gene
<i>FABP4</i>	NM_001442.2	GGTGGAAATGCGTCATGAAAGGC GTCACTTCCACGAGAGTTATG AGAGAGCATAAGCCAAGGGACG TTGACCTGGACTGAAGTTCGCA TTGAACACTCTACA	83	83	311558; 211558	Marker of adipose tissue
<i>FAF1</i>	NM_007051.2	GCTTTTCAAGAGGCCCTTCTATGT GAAAGCCCGAGATAGAAAGCTT CTTGCTATCTACCTCCACCATGA TGAAAGTGTGTTAACCAACGTG TTCTGCTCAC	81	80	314945; 214945	T2D gene
<i>FITM2</i>	NM_001080472.1	CTTGTCCAGAAGGGTGTG ACCTTGTGTTGGTTGCTGAGCTG GTACGGGACATACGGGTTTG TATCCGAAAGCCTTCCCCAG GACTTCTCTCC	79	82	300022375; 200022375	T2D gene
<i>FOXP3</i>	NM_014009.3	GGGCCATCCTGGAGGGCTCCAG AGAACGCGGGACACTCAATGA GATCTACCACTGGTCACACGC ATGTTGCTTCTTCAGAAACCA TCCTGCCACCTG	81	79	310104; 210104	Monogenic diabetes gene
<i>FTO</i>	NM_001080432.2	AAAGTGAGGATGACTCTCATCT CGAAGGCAGGGATCCTGATATT TGGCATGTTGGTTTAAGATCTC ATGGGACATAGAGACACCTGGT TTGGCGATAAC	84	80	344638; 244638	T2D gene
<i>GATA4</i>	NM_002052.3	GACTTCTTCCCAAGATGTCCTT GTCCCCTCGCTTCCCCACTGTG GCCTAGACCGTGGGTTTGAT TGTGTTCTAGCACCGAGGATC TGAGAACAAAGC	83	81	311568; 211568	Monogenic diabetes gene
<i>GATA6</i>	NM_005257.3	GACAGTGGCGACTCGCCTGACA GAACGTGATTCTCGCCTTAT TTTGAAAGAGATGTTTCCAA 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	TGGACTCCAGGCCTGCCAAGA TTTTGTGCAGTGGTTGATGAATA CCAAGAGGAACAGGAATAACAT TGCCAAACGTCACGATGAATT GAGAGACATGC	84	83	311569; 211569	Marker of pancreatic islet
<i>GCK</i>	NM_000162.3	CCACCTTCTCGCTGGAAATCAAT TTCCCAGAAGGGAGTTGCTCAC TCAGGACTTTGATGCTATTCCAC ACTGTCAGAGCTGTTGGCCTCG CCTGGGCCCA	82	83	311750; 211750	T2D gene & Monogenic diabetes gene
<i>GCKR</i>	NM_001486.3	TGGGTGCTGAATACAGTGAGTA CAGGTGCTCATGTGCTTCTGG TAAGATCCTACAAAACCACATGT TGGACCTCGGATTAGCAACTC CAAGCTCTCT	84	82	349899; 249899	T2D gene
<i>GIPR</i>	NM_000164.2	CCCTGTCTCGCCACACTGCT GCTAGCCCTGCTCATCTTGAGT TTGTTCAGGCCTACATTGCA CTAGAAACTATATCCACATCAAC CTGTTCACGTC	82	79	302954; 202954	T2D gene
<i>GLIS3</i>	NM_001042413.1	CCCGGGACATCCATGTCCAGCA ATAGTGTCTCTAACCTATTACCA TCCTACCTTTGGCACGGAAA GTAGCCACTCTCCTTACCCTAGT CCTCGGCACT	82	83	300021627; 200021627	T2D gene & Monogenic diabetes gene

<i>GPSM1</i>	NM_001145638.1	GGCCACGGCGAGCCCCAGGAG CCGGGGGACGACTCTTCACA TGCTCATCAAGTACCAGTCCTC CAGGATCGATGACCAAGCGCTGC CCGCCACCTGACG	84	84	374380; 274380	T2D gene
<i>GRB14</i>	NM_004490.2	ACAGCTGGACCCTTTGAGCA CCTGCCTCACATAGGTGTAGAA AGAACATAAGAAGACCACGAAC TGGTGATTGAAGTGTCTATCCAA CTGGGGGATAGA	83	82	302690; 202690	T2D gene
<i>GRK5</i>	NM_005308.2	GTTCTCCACGGGCTCTGTGTC ATCCCAGGCAAAACAGAGATGA TAGAACAGAACATGCTTAAGGA GCTGAACGTGTTGGACCTAAT GGTACCCCTCCCG	79	78	303130; 203130	T2D gene
<i>HHEX</i>	NM_002729.4	GCACTATCACTTAGTACCTGTT GACCAAGGTGTTAAGGGATAG TACCTCCAATTCAAGCAGAGA AACTGACCTGACTAAAGTTAAC GCAGATGAAC	82	83	311692; 211692	T2D gene
<i>HLA-B</i>	NM_005514.6	CCCTGAGATGGGAGCCGTCTTC CCAGTCCACCGTCCCCATCGT GGCATTGTTGCTGGCCTGGCTG TCCTAGCAGTTGTGGTCATCGG AGCTGTGGTCGC	86	86	329226; 229226	T2D gene
<i>HMG20A</i>	NM_018200.2	TATACATCTCCATTTCTGACCT CTGGACTAACTGGTGCTCAGC AAGGTTCTGAAGGAGAGTTCT TGCATTGGACAGGCCAGTCCT CTCCCCATCATT	81	80	348437; 248437	T2D gene
<i>HMGA2</i>	NM_003484.1	GAGGAGGAATTCTTCCCCGCC TAACATTCAGGGACACAATT ACTCCAAGTCTCTTCCCTTCCA AGCGCTTCCGAAGTGCTCCCG GTGCCCGCAA	81	85	370307; 270307	T2D gene
<i>HNF1A</i>	NM_000545.4	GGGGGTCGTGGAGAGCTAGGA GCAAAGCCTGTTCATGGCAGAT GTAGGAGGGACTGTCGCTGCTT CGTGGGATACAGTCTTCTTACTT GGAACTGAAGGG	82	82	310561; 210561	T2D gene & Monogenic diabetes gene
<i>HNF1B</i>	NM_000458.1	ACGTCCCTGCTGGCACCTCAGAC AATCCACTCTCAGGAGCGCAGC CCGAAGCCCAGTTCCCTTCTAT GCAGTATTGCCACAATGCCTCT CCCACGATGTC	82	79	300034; 200034	T2D gene & Monogenic diabetes gene
<i>HNF4A</i>	NM_178850.1	CCTTGAGAGCATCACCTGGCA GATGATCGAGCAGATCCAGTTC ATCAAGCTTCTGGCATGGCCA AGATTGACAACCTGTTGCAGGA GATGCTGCTGGG	83	83	360741; 260741	T2D gene & Monogenic diabetes gene
<i>IAPP</i>	NM_000415.1	ATTCTCTCATCTACCAACGTGG ATCCAATACATATGGCAAGAGG AATGCAGTAGAGGTTAAAGA GAGAGCCACTGAATTACTTGCC CCTTAGAGGA	83	81	311536; 211536	Marker of pancreatic islet
<i>IDE</i>	NM_004969.3	AAACTGATCGCACAGAAGAGTG GTATGGAACCCAGTACAAACAA GAAGCTATACCGGATGAAGTCA TCAAGAAATGGCAAAATGCTGA CCTGAATGGGAA	83	83	300039130; 200039130	T2D gene
<i>IER3IP1</i>	NM_016097.3	GGGAACAGACCAGGGAATTGGT GGATTTGGAGAAGAGGCCGGGAA TTAAATCACAGCTAATGAACCTT ATTGATCTGTAAGAACCGTGAT GAGAGTGCCA	84	81	343083; 243083	Monogenic diabetes gene
<i>IGF2</i>	NM_001127598.1	ACACACACTCATGCGCAGCAC TACATGAACACAGCTCACAGCA CACAAACACGCGAGCACACAGT TGCACACGGCAAGCACCCACCTG CACACACACATG	87	88	322178; 222178	T2D gene
<i>IGF2BP2</i>	NM_001007225.1	GAACAAAAGCGAAACACACAAA CCAGCCTCAACTTACACTTGGTT ACTAAAGAACAAAGAGTCAT GGTACTTGTCCCTAGCGTTTGG AAGAGGAAAAAC	84	81	366890; 266890	T2D gene

<i>INS</i>	NM_000207.2	GGGTCCCTGCAGAACCGTGGC ATTGTGAAACAATGCTGTACCA GCATCTGCTCCCTTACCAAGCT GGAGAACTACTGCAACTAGACG CAGCCCGCAGGCA	85	86	350253; 250253	T2D gene & Monogenic diabetes gene & Marker of pancreatic islet
<i>INSM1</i>	NM_002196.2	AAGCCTCCCTTGCGGGGAG AAGCTTTTTCTTGTAGTATT CGCTGTGTCATGGTCTAGAAAT GCGGTCTGGTCTGCCTGCCT ACCAATCTCTG	79	83	311571; 211571	Marker of pancreatic islet
<i>IRS1</i>	NM_005544.2	CCCTGGGCAGCGGGAGAGCA GCTCCACCCGCCGCTCAAGTGA GGATTTAAGCGCCTATGCCAGC ATCAGTTCCAGAACAGCAGCCAG AGGACCGTCAGTA	83	83	300093750; 200093750	T2D gene
<i>ISL1</i>	NM_002202.2	CTTACAGGCTAACCCAGTGGAA GTACAAAGTTACCAGCCACCTT GGAAAGTACTGAGCGACTTCGC CTTGCAGAGTGACATAGATCAG CCTGCTTTTCAG	79	83	308799; 208799	Marker of pancreatic islet
<i>JAZF1</i>	NM_175061.3	CCTGGACACAGAGAGTGCCAT CAGCTCCGAAGCCATCCTCAGC TCCATGTGCATGAATGGAGGG AAGAGAACGCCTTGCCTGCC AGTTCTGGATG	82	82	310734; 210734	T2D gene
<i>KCNJ11</i>	NM_000525.3	CTCATCCAGGGTGTACAAGGC ACTTGTCACTATGCTATTCTGG CCTCAGCAGGAACCTGTACTGG GTTATTTGTCCCTGCTCCTCC CAACCCAATT	81	81	349841; 249841	T2D gene & Monogenic diabetes gene
<i>KCNK16</i>	NM_001135105.1	CTGGTCATTCTCATCTTCCCACC CATGGTCTTCAGCCATGTGGAG GGCTGGAGCTTCAGCGAGGGC TTCTACTTGTCTTCATCACTCT CAGCACCAATTG	83	80	300029232; 200029232	T2D gene
<i>KCNQ1</i>	NM_181798.1	CAGACGTGGGTGGGAAGACC ATCGCCTCTGCTTCTGTCTT TGCCATCTCCTCTTGCCTCC CAGCGGGGATTCTGGCTCGGG GTTTGCCTGA	83	83	311680; 211680	T2D gene
<i>KLF11</i>	NM_001177716.1	TCATCACCTCTAGCCAAAAGTGT GTCCTCAGGTAGACTTTCCC GAAGGAGGAACATGTTGCAG CTTCCCAGGTTGCCCGAACACC TACTTCAAAAG	83	83	349892; 249892	Monogenic diabetes gene
<i>KLF14</i>	NM_138693.2	CAGGCCGTTGTCCTGCTTCT CTCTGCCATCCTCTTCCCAG AGTCATTACACCAAGGCACAGA CTGGTTCTCTGCTCTGAGGGT GGGTCCAGGCA	80	86	349984; 249984	T2D gene
<i>KLHDC5</i>	NM_020782.1	CCACCGCTTTTAAGGAGGCA TTATGAATGAGTGCAGCATTCT GTCCTCTGTGCCAGGATTGGT CTTAGAATCCATGTCAGATTGGT GCTTCCAGAC	78	79	300533; 200533	T2D gene
<i>LAMA1</i>	NM_005559.2	CAGTTGCACCAAAATGCCACCC TTGAACCTAAGGCTGCTGAAGA TTTATTGTCACAAATTCAAGGAAA ATTACCAAGGCCGCTGGAAGA ATTGGAGGTAT	81	82	311620; 211620	T2D gene
<i>LEP</i>	NM_000230.2	GTAGTTCTTGCTGATTGGCTCA CCCAAGCAAGGCCAAATTACC AAAAATCTGGGGGGTTTTACT CCAGTGGTGAAGAAAACCTCCTT TAGCAGGTGG	80	81	316749; 216749	T2D gene
<i>LGALS4</i>	NM_006149.3	AGAAGATCACCCACAACCCATT TGGTCCCCGGACAGTTCTTGAT CTGTCCTTCGCTGTGGCTTG ATCGCTTCAAGGTTACGCCAAT GGCCAGCACCT	82	84	344872; 244872	Marker of gut
<i>LGR5</i>	NM_003667.2	CTTATGCTTACCAAGTGTGTGCA TTTGGAGGTGTGAGAAATGCCT ATAAGATTCTAATCAATGGAAAT AAAGGTGACAACAGCAGTATGG ACGACCTTCA	79	79	344720; 244720	T2D gene

<i>LIPF</i>	NM_001198828.1	AGAAGCAGCTACACTATGTTGG CCATTCCCAGGGCACCAACCATT GGTTTTATTGCCTTTCCACCAA TCCCAGCCTGGCTAAAAGAAC AAAACCTTCTA	84	79	387771; 287771	Marker of gut
<i>LPP</i>	NM_005578.2	GCTGTATGACATGGAAAATCCA CCTGCTGACGAATACTTGGCC GCTGTGCTCGCTGTGGAGAAAA CGTAGTTGGGAAGGTACAGGA TGCACGCCATG	81	82	308346; 208346	T2D gene
<i>MACF1</i>	NM_012090.5	CATGGATGAAAAGGAGCAGCTT ATACAGTCCAAGAGTTCCGTTG CCAGTCTCGTTGGGAGATCAA AACCATCGTTCAGCTAAAACCA CGCAGTCCAGAC	83	83	300043617; 200043617	T2D gene
<i>MAEA</i>	NM_001017405.2	CCCTGCCCATGGCCCCTGTGC CAACTCCCGCCTGGTCTGCAAG ATTCTGGCGACGTGATGAACG AGAACAACTCGCCCCATGATGCT GCCCAACGGCTA	83	83	300089574; 200089574	T2D gene
<i>MAFA</i>	NM_201589.2	AGCTGCCAGCAGCCGCTGG CCATCGAGTACGTCAACGACTT CGACCTGATGAAGTTCGAGGTG AAGAAGGAGCCTCCGAGGCC GAGCGCTTCTGCCA	85	86	311743; 211743	Marker of pancreatic islet
<i>MC4R</i>	NM_005912.1	TGGAGGGTGTACGAGCAACTT TTTGTCTCTCTGAGGTGTTTG GACTCTGGGTGTCACTAGCTTG TTGGAGAATATCTTAGTGATTGT GGCAATAGCC	80	78	303291; 203291	T2D gene
<i>MNX1</i>	NM_005515.3	CCTGGCGCTCCCTTTAAGC AAGGGCGCCTCACCTGCTCTTC AAGAAACAGCGAGAGGGAGAC CCAGGGGCTGAAACTTGAACCT CTGGTTCTTTAA	80	82	310646; 210646	Monogenic diabetes gene
<i>MOB2</i>	NM_053005.3	CCACATCAACCTGAGTATAGC ACCATCTGGAGTCTGCACAG GAGAGACGTGTCAGACGATGGC CGTGTGCAACACACAGTACTAC TGGTATGACGAG	84	84	340815; 240815	T2D gene
<i>MPHOSPH9</i>	NM_022782.3	AGCCTGGGAGAAGAATAATCA GTTAGCTACGAACAGTGTAAAGC CGGTTTCAGTCACTCCACAGGG GAATGATTGAAATATACAGCAA AAATTCCGGACC	83	80	300049787; 200049787	T2D gene
<i>MTNR1B</i>	NM_005959.3	ATCCCTGAGGGGCTATTGTCA CTAGCTACTTAAGGCTTATTTC AACAGCTGCCTGAATGCCATTG TCTATGGCTTGAACCAAAA CTTCCGCAGGG	78	79	302238; 202238	T2D gene
<i>NEUROD1</i>	NM_002500.2	GTGCCAGCTCAATGCCATT CATGATTAGAGGCACGCCAGTT TCACCATTCGGGAAACGAAC CCACTGTGCTTACAGTGA CGTGTAA	81	79	311578; 211578	Monogenic diabetes gene & Marker of pancreatic islet
<i>NEUROG3</i>	NM_020999.2	CGCGCGAAGTGGGCATTGCAA GTGCGCTCATTAGGCCTCCT CTCTGCCACCACCCATAATCT CATTCAAAGAAATACAGAATGGT AGCACTACCCG	83	82	311658; 211658	Monogenic diabetes gene
<i>NKX2-2</i>	NM_002509.3	TAATTATTATTATGGAGTCGAGT TGACTCTCGGCTCCACTAGGG GGCGCCGGGAGGGTGCCTGCG TCTCCTGGAGTGGCAGATTCC ACCCACCCAGCT	82	83	383978; 283978	Monogenic diabetes gene
<i>NKX6-1</i>	NM_006168.2	CTGGCCTGTACCCCTCATCAAG GATCCATTGTTGGACAAAGAC GGGAAGAGAAAACACAGGAGAC CCACTTTTCCGGACAGCAGAT CTTCGGCCCTGG	84	83	311629; 211629	Marker of pancreatic islet
<i>NOTCH2</i>	NM_024408.3	AAGAGTCACCAAATTGAGAGT TATACTTGCTTGTGCTCTGG CTGGCAAGGTCAAGGGTGTACC ATTGACATTGACGAGTGTATCTC CAAGCCCTG	79	83	347789; 247789	T2D gene

PAM	NM_000919.2	TCATATATACCAGGCTTGCTCTT TGCAGTGAATGGGAAGCCTCAT TTGGGGACCAAGAACCTGTAC AAGGATTGTGATGAACCTTTCC AATGGGGAAA	79	82	335097; 235097	T2D gene
PAX4	NM_006193.2	TGTCCAGCCCTTGGCTGGG AAATCCAACGCCAGCTTG TGAAGGGCTTGCAACCGAGAC AAGACTCCCAGTGTCTCCTCCA TCAACCGAGTCC	83	84	300039793; 200039793	T2D gene & Monogenic diabetes gene
PAX6	NM_000280.3	GAACATCCTTACCCAAGAGCA AATTGAGGCCCTGGAGAAAGAG TTTGAGAGAACCCATTATCCAGA TGTGTTGCCCGAGAAAGACTA GCAGCCAAAAT	84	83	366937; 266937	Marker of pancreatic islet
PCBD1	NM_000281.2	GGGCTGTGGGGTGGAATGAGC TGGAAAGGCCGTATGCCATCTT CAAGCAGTTCATTTCAAAGACT TCAACAGGGCTTGGGTTCAT GACAAGAGTGGC	83	78	300015261; 200015261	Monogenic diabetes gene
PDX1	NM_000209.3	TGACCTCTTCTTCTCCTCCTC CTCCTTCTACCTCCCTTCTCAT CCCTCCTTCCTCTCTAGC TGCACACTTCACTACTGCACATC TTATAACT	78	79	311526; 211526	T2D gene & Monogenic diabetes gene & Marker of pancreatic islet
PEPD	NM_000285.3	ACGATCCAGAACATGGGGATATGT GCCTGTTGACATGGGCGGTGA GTATTACTGCTTCGCTTCCGACA TCACCTGCTCCTTCCCGCCAA CGGCAAGTTCA	83	82	300015263; 200015263	T2D gene
PLIN1	NM_001145311.1	CATCTCCACCCGCCCTCCGAGT GCCAGAAACAGCAGTCAGCGTT CCATCGCGAGCACCTCAGACAA GGTCCTGGGGGCCGCTTGGC CGGGTGCAGCTT	82	84	362927; 262927	Marker of adipose tissue
POU5F1	NM_002701.4	AAGTTCTTCATTCACTAAGGAAG GAATTGGGAACACAAAGGGTGG GGGCAGGGGAGTTGGGGCAA CTGGTTGGAGGGAGGTGAAGT TCAATGATGCTC	78	82	308193; 208193	T2D gene
PPARG	NM_015869.3	GAGCAAAGAGGTGCCATCCG CATCTTCAGGGCTGCCAGTT CGCTCCGTGGAGGGCTGTGCAG GAGATCACAGAGTATGCCAAA GCATTCTGGTTTT	81	81	300811; 200811	T2D gene
PRC1	NM_199413.1	ACAGAAAGTCTGCTCCAGCTCC ACGATGCTGAGATTGTGCGGTT AAAAAAACTACTATGAAGTTACA AGGAACCTTTGAAGGTGTCCA GAAGTGGGAAG	84	82	336825; 236825	T2D gene
PROX1	NM_002763.3	TCTCCTGTCGCTCATAAAGTCC GAGTGCAGCGATCTTCAAGATA TGTCTGAAATATCACCTTATTG GGAAGTGCAATGCAGGAAGGAT TGTCACCCCAA	79	82	311583; 211583	T2D gene
PSMB2	NM_002794.4	AGCAATATTGTCAGATGAAGG ACGATCATGACAAGATGTTAAG ATGAGTGGAAAGATATTACTCT GTGTGTTGGAGAGGCTGGAGAC ACTGTACAGT	79	85	300093536; 200093536	Housekeeping gene
PSMB4	NM_002796.2	GGACACAGCTATAGCCTAGAG CTATTCAATTGCGTGCAGCAG GGCCATGTACAGCCGGCGCTC GAAGATGAACCCCTTGTGGAAC ACCATGGTCATCG	87	86	300093534; 200093534	Housekeeping gene
PSMD6	NM_001271780.1	ATAGGTCAATTAAACCCCTGGCTAT ATGGCAGAAGCGTTGGTGTG GTGTGGAATTCAATTGATCAGGA ACTGTCCAGGTTATTGCTGCC GGGAGACTACA	79	81	365106; 265106	T2D gene
PTF1A	NM_178161.2	CAACAGCAAATCTCCTCAACA ACATAGAAAACGAACCAACATT GAGTTTGTGCTGAGAAGTCC CAGACTCGGCTGAAGATCTGAT TATGTCTCTG	78	82	311732; 211732	Monogenic diabetes gene

<i>PTPRD</i>	NM_001040712.2	TTTTAGTTAACAAAGGGGGTCA GACAGACATTGCATCATCCAGA CATGCCCTGTGGACATGTAGA ATCCGATGGAGCACTGCACACC AGAATGATTGG	80	84	341816; 241816	T2D gene
<i>R3HDM1</i>	NM_178491.2	CCAGGTACCGCCCGAAGCGCC ACATCTCTGTGAGAGACATGAA TGCCCTACTGGATTATCACAAACC ACATCCGGGCCAGTGTGTACCC ACCTCCCCCAA	84	84	325372; 225372	T2D gene
<i>RASGRP1</i>	NM_005739.3	ACGATCTCATTGACAGCTGCATT CAATCTTTGATGCAGATGGAAA CCTGTGTCGAAGTAACCAACTG TTGCAAGTCATGCTGACCATGC ACCGAATTGT	78	82	335283; 235283	T2D gene
<i>RBM43</i>	NM_198557.2	CAGCAATATAAGTCATAAGGGCT GCTTTCTTGTGCTGAGCAGTGA CCATTGCATGAATGAGGCTAG CTTTACACACCGTATCTCATGAA TCCTTATAAGTC	81	78	355924; 255924	T2D gene
<i>RBMS1</i>	NM_016839.2	ATCTGTCACTAGGCAGCACCGG AACATACATGCCTGCAACGTC GCTATGCAAGGAGCCTACTTGC CACAGTATGCACATATGCAGAC GACAGCGGTTCC	82	82	309308; 209308	T2D gene
<i>RFX6</i>	NM_173560.2	AGCAGTGCATATTACCACTCCG TTTATTCTGGAAAGGGCTTGACA AGGTTTCTGGAAAGCAAGCTAA AGAATGAGGGTGGCTTCACTCG TAAATATTTCG	80	82	336282; 236282	Monogenic diabetes gene & Marker of pancreatic islet
<i>RND3</i>	NM_005168.3	GGAACAAATCACAGAGAGCCAC AAAGCGGATTTCACACATGCCT AGCAGACCAGAACTCTCGGCAG TTGCTACGGACTTACGAAAGGA CAAAGCGAAGAG	82	80	308797; 208797	T2D gene
<i>RREB1</i>	NM_001003698.2	TTCGAACACATCGAGGACTGCT GCGTCACAACGCGCTTGTCCAC AAACAACCTCCCAGGGATGCAA 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	CACACACAGGATCTCTCGAGC AGCAATTCCCCATT CCTCTCCCC TATTGCTGGCTCTGCAGGGCTC TGATCAAGCGGATCCAAGCCAT GATTCCCAAGG	83	86	344205; 244205	Marker of lung
<i>SFTPC</i>	NM_003018.2	TTCCCTGCTGCCAGTGCACCT GAAACGCCCTTCTATCGTGGTG GTGGTGGTGGCTCTCATCGTCG TGGTGATTGTGGGAGCCCTGCT CATGGGTCTCCA	81	81	301927; 201927	Marker of lung
<i>SGCG</i>	NM_000231.2	ACACTGAGTGTGAGTTGCCGT GTGGAGTTAATGTATGACGCTC CACTGTGGATATCTAATGCCCT GTTGAGAGTAGCCTTGCTCAGT ACTAAAATGCC	82	84	345859; 245859	T2D gene
<i>SLC12A1</i>	NM_000338.2	CCAAGTTCGACTGAATGAACTC TTACAGGAGCACTCCAGAGCTG CTAATCTCATTGCTGTGAGCCTT CCCGTGGCAAGAAAGGGATCCA TATCGGATTTG	83	81	300015293; 200015293	Marker of kidney
<i>SLC16A11</i>	NM_153357.1	CGGCCTGAGTCTGTTCACACGC CGGGCCTTCTCAATCTTGCTCT AGGCACAGCCCTGGTGGGGGG CGGGTACTCGTCTTACGTG CACTGGCTCCC	82	83	365403; 265403	T2D gene
<i>SLC16A13</i>	NM_201566.2	GGTGCTCTCAGCCTTCTTCAG TCGGCGCTTGTGTTGGGTGC TCCGCTCCTTGGGGTCTTCTC GTGGAGTTGTGGCGGCGTTG AGGAGCAGGCA	84	82	365405; 265405	T2D gene

<i>SLC19A2</i>	NM_006996.1	CCTGTGGGAGAAAGTGTGCCT TCTCGCTATGCTGCTATCTATAA TGGTGGCGTGGAGGCCGTTCA ACCTTACTGGGTGCTGTTGCTG TGTTTGAGCTT	80	80	300323; 200323	Monogenic diabetes gene
<i>SLC22A2</i>	NM_003058.2	CTAACATCGCTTGAGCTCCC GCTGATGGTTTCGGCGTGCTT GGCTTGGTTGCTGGAGGTCTGG TGCTGTTGCTTCCAGAAAATCAA GGGAAAGCTTT	82	84	320257; 220257	Marker of kidney
<i>SLC2A2</i>	NM_000340.1	CAATTATGGAATATAGTCTGA TGGGTCCAAAAGCTTAGCAGG GTGCTAACGTATCTCTAGGCTG TTTCTCCACCAACTGGAGCACT GATCAATCCT	81	82	311532; 211532	Monogenic diabetes gene
<i>SLC30A8</i>	NM_173851.2	CAGATGCAACCAATTCAATTCA CCACGAGCATGATGTGAGCACT GCTTTGTGCTAGACATTGGCT TAGCATTGAAACTATAAGAGGA ATCAGACGCA	80	83	349995; 249995	T2D gene & Marker of pancreatic islet
<i>SPRY2</i>	NM_005842.2	GCCGTTTTAACTGATATGCTTGT TAGAACTCAGCTATGGAGCTC AAAGTATGAGATACAGAACTTG GTGACCCATGTATTGCATAAGC TAAGCAACAC	77	84	368417; 268417	T2D gene
<i>SRR</i>	NM_021947.1	ACAATTGCCCTGGAAGTGTGA ACCAGGTTCCCTTGGTGGATGC ACTGGTGGTACCTGTAGGTGGA GGAGGAATGCTTGTGGAATAG 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 CCTGAAGATCTGTCCCAGGCTG CTGAGCAGGATGAAATGAGGCT TGAGCTGCAGAG	82	82	301249; 201249	Marker of pancreatic islet
<i>ST6GAL1</i>	NM_003032.2	ATGATGACGCTGTGACCAGG TGGATATTATGAGTTCTCCCA TCCAAGCGCAAGACTGACGTGT GCTACTACTACCAGAAAGTTCTC GATAGTGCCT	81	82	361087; 261087	T2D gene
<i>TBC1D4</i>	NM_014832.2	GCAGTTCTGGCTTACAGTACC GAATCAGACACAGATTGCCCTAA TAAACAAACAGCCTCTGACATAT CCTATAAGGAACCTTGTGAAAGCA GCTCACTGCT	81	83	344936; 244936	T2D gene
<i>TCF19</i>	NM_001077511.1	TTGCAAGTCGGCTTAACCAATT TGCATTGAGTCCTAGGCTGCTT GCACTCTGAATTGGGCTATTCA GGTAGTGTGCTCAAAGTTGAAA CCGCATACAG	79	79	300022149; 200022149	T2D gene
<i>TCF7L2</i>	NM_001146274.1	ATATGGCCCCACACATCATAC GCTACACACGACGGGCATTCCG CATCCGGCCATAGTCACACCAA CAGTCAAACAGGAATCGTCCCA GAGTGATGTCGG	86	86	362160; 262160	T2D gene
<i>THADA</i>	NM_001083953.1	CCAGAACTTCTGTGGATTATT GACGGTGGAGCAGGTAAAGAA ATAGGAGATTACTTTAAACAAACA CCTTTGAGTCCAGGCACAGA GGAGCATTG	81	78	329955; 229955	T2D gene
<i>TLE1</i>	NM_005077.3	CCGACTCACATGACAGCCCCATT CTTCTTCTGGGTGATCTGGG GATCACGCCCTGCCAACAGTGTG AGATTACCTTCTGTTCTTGCA GTTCACCTCAC	82	79	311859; 211859	T2D gene
<i>TLE4</i>	NM_007005.3	AAAACAAGGACAGCAGAGGAGG GTTTGCAGAGACCTCCCTCTGA AAAACACAAAGAATGGACTCTCT CCTGGGATGAGGACTTGCTTT TTTACCTCCGG	81	79	309013; 209013	T2D gene

<i>TMEM154</i>	NM_152680.2	GCGCAGCCCTAGTCTTCGCCCT GGTGATC CGCGCTCGTCCCCTC GGCCGGGGTAATTATGAGGAAT TAGAAAACTCAGGAGATACAAC TGTGGAATCTGA	85	81	373634; 273634	T2D gene
<i>TMEM163</i>	NM_030923.4	TGGGGGTGATATTCCCTCTGTC ATCCATATGTATAGTGGTCAAAG CCATCCATGACCTCTCAACTAG GCTGCTCCCAGAAGTGGACGAT TTCCTGTTCA	79	83	388351; 288351	T2D gene
<i>TP53INP1</i>	NM_033285.3	CCAAGAGCTTCGCCCTTCCA GTGGATAAAAGAACACAGTGAA AGACAGCCTCTAACAGAAATA GCCTTCGTCGCCAAAATCTTAC CAGGGATTGCCA	83	80	348825; 248825	T2D gene
<i>TRMT10A</i>	NM_001134665.1	CCCACAGACAAAGCCTGTGAAA GTGCTTCTCATGACAAATCAGTCT GTCAGGATGGAGGAAGGTGGAT CGGACAGTGATTCCAGTGAGGA GGAATATAGCA	84	83	383028; 283028	Monogenic diabetes gene
<i>TSPAN8</i>	NM_004616.2	CTGGCTATGTGGTATCTTGATCC TAGCATTAGCAATATGGGTACG AGTAAGCAATGACTCTCAAGCA ATTTTGGTTCTGAAGATGTAGG CTCTAGCTCC	79	79	317600; 217600	T2D gene
<i>UBE2E2</i>	NM_152653.3	GTGAAAGTGTTCAGCAAGAAC AGAAAGAGAACAGTTCAGCCC AAGAAAAAAGGAGGGAAAAATAT CCAGCAAAACCGCTGCTAAATT GTCAACTAGTGC	84	83	368035; 268035	T2D gene
<i>VCP</i>	NM_007126.3	AGATGGATCTCATTGACCTAGA GGATGAGACCATTGATGCCGAG GTCATGAACTCTCTAGCAGTTAC TATGGATGACTTCCGGTGGGCC TTGAGGCCAGAG	85	87	300093533; 200093533	Housekeeping gene
<i>VPS26A</i>	NM_004896.3	TGGCACTTGATAAAATGGTCA GGAACCAACTTACTGGCAAAA GGGTCCATGTACCACCATGTGC TGGAGCATCTGTTCTACATGTG GATATCTATGAA	84	81	300039091; 200039091	T2D gene
<i>VPS29</i>	NM_016226.4	AGTGGTCACCTATGTGTATCAG CTAATTGGAGATGATGTGAAAG TAGAACGAATCGAACATACAAAAAA CCTTAAAGCCAGGCCTGTCTTG ATGATTTTGG	81	76	300093535; 200093535	Housekeeping gene
<i>WFS1</i>	NM_006005.3	GTCAGCACCTCACCATCGACT TCTTCGCCCTCTTCATCCCGCTG GTCATCTTCTACCTGTCTTCTAT CTCCATGGTGTATGCAACCCCTC AAGGTGTTCC	80	81	326714; 226714	T2D gene & Monogenic diabetes gene
<i>ZBED3</i>	NM_032367.2	GGGCTGGGAACCGAACCTGG TGACTTTGAAAGGATAGAGCTT CATTCCATACCAAAGACTTATCA CACCATGTGCCTATACACCCAG CAGCCCCAAGGTG	83	83	349968; 249968	T2D gene
<i>ZFAND3</i>	NM_021943.2	ACAGCCAGACGATGATTCCGCT CCAAGTACAAGTAACAGCCAAT CAGATTGTTTCCGAAGAGAC CACCA GTGACAAACAACAAATACC TCGATAACCAACG	84	83	343067; 243067	T2D gene
<i>ZFAND6</i>	NM_001242919.1	AAGTGCCTATGCTTGTCCACT GGCTGTGGATTTATGGAAACC CTCGTACAAATGGCATGTGTT AGTATGCTATAAGAACATCTTC AAAGACAGAA	79	78	363380; 263380	T2D gene
<i>ZMIZ1</i>	NM_020338.3	CCACGGTCAACATGGGGCAGTA TTACAAGCCAGAACAGTTAATG GACAAAATAACACGTTCTCGGG AAGCAGCTACAGTAACACAGC CAAGGGAATGT	84	83	300048334; 200048334	T2D gene

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

Table B. List of deregulated genes emphasized by the decreased expression of *PRC1* in EndoC-βH1 cells, within the network related to apoptosis.

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