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INTEGRATIVE TRANSCRIPTOMIC ANALYSIS OF PANCREATIC ISLETS FROM PATIENTS WITH PREDIABETES/TYPE 2 DIABETES

TRANSCRIPTOMIC ANALYSIS IN DIABETES

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Abbreviations: ND: non-diabetic; PD: prediabetes; T2D: type 2 diabetes; DEG: differential expressed genes.

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ABSTRACT

Aim: to identify new transcriptomic alterations in pancreatic islets associated with metabolic dysfunctions in people with prediabetes (PD)/type 2 diabetes (T2D).

Materials and methods: We collected information from public data repositories T2D related microarray datasets from pancreatic islets. We identified Differential Expressed Genes (DEGs) in non-diabetic (ND) versus people with T2D in each study. To identify relevant DEGs in T2D, we selected those that varied consistently in the different studies for further meta-analysis and functional enrichment analysis. DEGs were also evaluated at the PD stage.

Results: A total of 7 microarray datasets were collected and analyzed to find the DEGs in each study and meta-analysis was performed with 245 ND and 96 T2D cases.

We identified 55 transcriptional alterations potentially associated with specific metabolic dysfunctions in T2D. Meta-analysis showed that 87% of transcripts identified as DEGs (48 out of 55) were confirmed as having statistically significant up- or down-modulation in T2D compared to ND. Notably, 9 of these DEGs have not been previously reported as dysregulated in pancreatic islets from people with T2D. Consistently, the most significantly enriched pathways were related to the metabolism and/or development/maintenance of β-cells. 18 of the 48 selected DEGs (38%) showed an altered expression in islets from people with PD.

Conclusions: These results provide new evidence to interpret the pathogenesis of T2D and the transition from PD to T2D. Further studies are necessary to validate its potential use for the development/implementation of efficient new strategies for the prevention, diagnosis/prognosis and treatment of T2D.

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INTRODUCTION

Type 2 diabetes (T2D) is a worldwide, continuously increasing disease characterized by metabolic dysfunction diagnosed from persistent hyperglycemia resulting from impaired insulin secretion or/and action[1]. It represents a serious public health problem due to its frequent association with other cardiovascular risk factors and the development/progression of chronic complications that decrease the quality of life of the patients and significantly increase their cost of care[2]. Although they can be prevented, these complications result mainly from delayed diagnosis and poor metabolic control of the disease[3].

The clinical manifestations of T2D are preceded by a period of metabolic dysfunction known as prediabetes (PD), characterized by impaired fasting glucose, impaired glucose tolerance, or the association of these alterations[4]. The transition from PD to T2D can be significantly prevented (up to 58%) by adopting healthy lifestyles[5,6].

A key factor in the pathogenesis of T2D is the early and progressive decrease in pancreatic β-cell mass and function which results in deficient insulin secretion frequently associated with decreased response of target tissues to this hormone's action[7,8]. Although several molecular alterations have been identified in the pancreatic β-cells of people with T2D[9], its gene expression profiling and the underlying molecular alterations of its pathogenia are still subjects of active research.

In recent years, comprehensive assessments of molecular alterations have been obtained by studying the transcriptomic features of isolated islets by microarray or RNA-sequencing. However, these studies require high technology and economic resources not always easily available. In this regard, some databases compile data from these types of assays, such as ArrayExpress (https://www.ebi.ac.uk/arrayexpress/) and GEO (https://www.ncbi.nlm.nih.gov/gds). These data are freely available for utilization by

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the research community, and their adequate integration/interpretation facilitates elucidation of significant biological alterations.

On account of this situation we have currently collected, integrated, and analyzed datasets of microarray studies attempting to identify new relevant transcriptomic alterations in pancreatic islets/ β-cells from people without diabetes (ND), with T2D and with PD. We assume that these data may provide new evidence to understand the pathogenesis of PD/T2D, facilitating the development of effective strategies for early diagnosis of both diseases, and also prevent the transition of PD to T2D.

MATERIALS AND METHODS

Selection of microarray datasets from GEO and ArrayExpress

T2D related microarray datasets from pancreatic islets were collected from public data repositories: Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/) and ArrayExpress (http://www.ebi.ac.uk/arrayexpress/). The keywords used to perform the search were "type 2 diabetes" and "pancreatic islets/pancreatic β-cells" and "homo sapiens".

We selected only those studies from transcription profiling by array in which both ND and T2D people were included and each group contained more than five samples. The search was expanded using PubMed with the same selection criteria mentioned above. In the case of PD, we also searched related microarray datasets from pancreatic islets using the keywords: "prediabetes/impaired glucose tolerance/impaired fasting glucose", "pancreatic islets/pancreatic β-cells", and "homo sapiens". These searches were updated in April 2019.

Using the GEO and ArrayExpress databases and the keywords mentioned above, we found 22 different studies containing samples of people without (ND) and with T2D.

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Although 6 of them were array-based transcriptomics studies, one was excluded because it included only one patient with diabetes. Therefore, we used 5 studies from this source: GSE50397 (Fadista J et al[10], Taneera J 2014 et al[11], Taneera J 2019 et al[12]), GSE38642 (Taneera J 2012 et al[13], Taneera J 2013 et al[14], Kanatsuna N et al[15]), GSE25724 (Dominguez V et al[16]), GSE20966 (Marselli L et al[17]), E-CBIL-20 (Gunton JE et al[18]), plus two others from PubMed search: GSE76894 and GSE76895 (Solimena M et al[19]). Their main data characteristics are summarized in Table 1.

Identification of Differential Expressed Genes (DEGs) across T2D studies

Raw data (CEL. format files) of the following studies were downloaded from GEO/ArrayExpress: GSE50397[10–12], GSE38642[13–15], GSE25724[16], GSE20966[17], E-CBIL-20[18], GSE76894 and GSE76895[19]. These datasets were preprocessed using R/Bioconductor package Oligo[20] (GSE50397, GSE38642) or Affy[21]R packages (GSE25724, GSE20966, E-CBIL-20, GSE76894, GSE76895) according to the platform of each dataset.

Data were subjected to background correction, normalization and calculation of expression values using the robust multi-array average algorithm[22].

Differential Expressed Genes (DEGs) between ND and T2D people were detected employing the LIMMA package (Linear Models for Microarray data)[23]. *P* value <0.05 was considered statistically significant and fold change (FC) >1.5 was considered biologically significant. Genes that met both criteria were considered DEGs in this study. Those that varied consistently in the same direction (down- or up-regulated) in at least 3 studies were considered relevant DEGs in T2D. This identification was effected using Venn diagrams (http://bioinformatics.psb.ugent.be/webtools/Venn/). To integrate the information of the different studies, a random effect size meta-analysis for each

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relevant DEG identified across the seven studies was performed using Comprehensive Meta-Analysis Software (https://www.meta-analysis.com/). Since more than one probe can map a gene, to perform this analysis we choose the probe that presented expression level values with the greatest variance (among the significant ones, if there were).

Pathway and molecular interaction analysis

Pathway analysis of the relevant DEGs in T2D were performed using the resource InnateDB (https://www.innatedb.com)[24], one of the most comprehensive sources of pathways available. This type of analysis allows determination of those biological pathways that are significantly over-represented (represented more than expected by chance) in a list of certain genes/proteins.

Since molecular interactions are important for studies of regulation of biological systems, we have built, visualized, and analyzed molecular interactions among proteins encoded by the relevant DEGs using the platform NetworkAnalyst (http://www.networkanalyst.ca)[25]. Specifically, a protein-protein interaction network was done with IMEx Interactoma database (International Molecular Exchange Consortium), a non-redundant set of physical molecular interaction data from a broad taxonomic range of organisms. The proteins involved in the most interactions were key nodes in the network.

Analysis of selected DEGs expression in ND versus PD cases

The expression level of the relevant DEGs was determined in ND, people with PD and people with T2D from GSE50397 and GSE76895 studies. Since more than one probe can map a gene, to perform this analysis we choose the probe that presented expression level values with the greatest variance. Scatter dot plots and statistical analyses were

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1 performed using GraphPad Prism version 5.01 (GraphPad Software, USA). Data are
2 presented as the mean ± standard error of the mean (SEM). Analyses between two
3 groups (ND *vs.* PD) were done using one-tailed t-test. P values < 0.05 were considered
4 statistically significant for each comparison.
5
6 **RESULTS**
7 **Identification of relevant differentially expressed genes (DEGs) in T2D**
8 Each selected microarray study was analyzed using R/Bioconductor to find the DEGs
9 comparing islets from people with/out diabetes (ND *vs.* T2D). Following this procedure,
10 we found a total of 756, 576, 492, 381, 246, 196 and 78 DEGs in studies GSE76894,
11 GSE25724, GSE20966, E-CBIL-20, GSE76895, GSE38642 and GSE50397,
12 respectively. Each study showed different proportions of down- or up-regulated genes
13 (Figure 1A). Supplementary table 1 shows all genes (and all probes corresponding to
14 each gene) that have been identified as differently expressed in each study.
15 In order to identify transcriptional alterations associated with metabolic dysfunctions in
16 people with T2D, we selected those DEGs that varied consistently in the same direction
17 (down- or up-regulated) in at least 3 studies. Based on this criterion, we identified 55
18 relevant DEGs: 36 down-regulated and 19 up-regulated as shown in Figure 1B and
19 Table 2. Whereas the 19 upregulated DEGs were simultaneously found in only 3
20 studies, 25 of those downregulated were commonly found in 3 studies, 7 in 4 studies
21 and 4 in 5 studies.
22 Hierarchical clustering analysis showed a separation among the studies and identified
23 two main groups: E-CBIL-20 and GSE25724, GSE38642, GSE50397, GSE76894,
24 GSE20966, GSE76895 (Figure 1B).

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As a result of meta-analysis, 87% of DEGs (48 out of 55) showed a significant alteration by integrating all studies. Notably, 9 of these DEGs have not been previously reported as dysregulated in T2D (Table 2, highlighted in gray); the corresponding *p*-values are also shown in that Table.

Functional enrichment analysis of relevant DEGs in T2D

Attempting to find a functional association between the 55 relevant DEGs in T2D, we performed an analysis of the pathway and the protein-protein interaction network. As shown in Figure 2A, we found that the most significantly enriched pathways were directly related to metabolism and/or development of β-cells.

The protein-protein interaction network represented in Figure 2B showed that among the upregulated DEGs, IL7R and IL6, were involved in the most interactions (12 and 6, respectively), thereby becoming key nodes in the network. Among the downregulated DEGs, NR0B1, SCD and PFKFB2 were involved in 4 interactions each. A principal node in the network was UBC which encodes Polyubiquitin-C, which in turn participates in protein recycling, interacting primarily with several down-regulated DEGs.

Analysis of relevant DEGs in pancreatic islets from PD cases

Based on the identification of the 48 potentially relevant DEGs which could play a role in the pathogenesis of T2D, we attempt thereafter to evaluate whether they could also be manifested at an early stage of the disease, i.e. PD.

For this purpose, we repeated the previous search using the same methodology described above but related to PD without success. However, we found that in the previous search related to T2D, two of the selected studies (GSE50397 and GSE76895)

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had included pancreatic islets from people with PD (Table 1); therefore, we used them for the pertinent analysis.

This analysis demonstrated that 18 of the 48 selected DEGs (38%) showed altered expression in islets from people with PD in at least one of the two available studies (Figure 1B, column PD). These results indicate that some of the transcriptional alterations observed in people with T2D were already present in the PD stage. In fact, data from the GSE50397 study showed significantly reduced expressions of SLC2A2, CHL1, GLRA1, PFKFB2, RASGRP1, CAPN13, TMED6, GLP1R, G6PC2, ROBO2, PLCXD3, RBP4, VATL1 and SLC4A8. Conversely, SV2B expression was significantly increased in islets from PD compared to ND people. Additionally, in the GSE76895 study, we found significantly reduced expressions of PLA1, LINC01933 and TMED6 and significantly increased expression of CD44. Relative expressions of DEGs not previously reported as dysregulated in PD are shown in Figure 3. Supplementary table 2 shows a statistic of differentially expressed genes identified in islets from people with PD in at least one of the two available studies.

DISCUSSION

Using the previously explained methodology and a slightly restrictive cutoff value (p value<0.05 and FC>1.5), we have currently identified 55 genes differentially expressed in islets from people with T2D that exhibited consistent transcriptional alterations among the different datasets. Then, we have performed the meta-analysis using combined data from different studies, thus attaining greater statistical power. As a result, 48 genes were confirmed as having statistically significant up- or down-modulation in T2D *vs.* ND. This integrative approach allowed the identification of some

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transcriptional alterations among these 48 genes that not being reported as relevant in the original studies.

Despite RNA sequencing in recent years has become an important technology for transcriptomic analysis, at the time we performed the dataset search, most of the studies found corresponded to microarray assays. In the next few years however, new studies based on RNA sequencing would allow the identification of novel biomarkers, such as new alternative splicing isoforms, that cannot be identified by closed platforms like microarrays.

Since the studies selected were carried out under variable conditions (different operators, people from different populations, diverse islet extraction and analysis techniques), the signature found represents the more reproducible transcriptional changes. Thus, we assumed that this signature could play an effective active role in the pathogenesis of T2D.

As expected, the pathway analysis of these relevant DEGs showed several over-represented pathways related to carbohydrate metabolism and the regulation of β-cell development and gene expression. Specifically, we found that the FOXA2 and FOXA3 transcription factor network was the most enriched pathway. In this regard, Blodgett DM et al. have shown that several genes involved in early development are highly expressed in fetal islet cells, mainly those that are associated with inflammatory function[26]. Further, FOXA proteins are expressed early in embryonic endoderm playing an important role in the regulation of gene expression in liver and pancreas and in the regulation of several pancreas-specific genes[27]. These genes include Pdx-1, a transcription factor that plays a pivotal role in pancreas development and islet cell ontogeny, being a major regulator of β-cell identity and function[28].

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Thirty-six of the 48 (75%) relevant DEGs currently described have been previously reported as being dysregulated in islets from people with T2D in some of the original microarray studies (SLC2A2, CHL1, PPP1R1A, ARG2, GLRA1, RASGRP1, FFAR4, PPM1E, CAPN13, HHATL, EDN3, ABCC8, RASGRF1, TAGLN3, TMEM37, GLP1R, SCD, HADH, G6PC2, PLCB4, PLCXD3, ELAVL4, ALDOB, CD44, TMED6, NR0B1, RBP4, VAT1L, SLC4A8, IL7R, MYCN, PLA1A, HS6ST2, PFKFB2, IAPP, GAD1)[10–19]. Another 3 genes (6%) were also reported as dysregulated in pancreatic islets from T2D in other experimental studies (IL33, NNMT, SV2B). Altogether, their previous reported identification lends validity support to the methodology currently employed and the results obtained.

On the other hand, as far as we know, 9 genes (19%) of the signature have not been previously reported as dysregulated in islets from people with T2D, namely, LINC01933, LOC101929550, ROBO2, PNLIPRP1, AADAC, CCDC69, TPD52L1, ITIH4 and LINC01116. We discuss some of these genes, as well as other genes of the signature poorly discussed in literature. For that purpose, we will consider them separately according to their dysregulation (either down- or up-regulated) and the mechanisms associated with islet mass and function.

DEGs downregulated in islets from people with T2D: The protein encoded by ROBO2 gene is a transmembrane receptor for the slit homolog 2 protein and its presence becomes essential for endocrine cell type sorting and mature architecture in mice islets[29]. It has also been shown that SLIT-ROBO signaling potentiates insulin secretion and is required for β-cell survival[30].

MYCN, a proto-oncogene that encodes a bHLH transcription factor, has been associated with β-cell mass expansion during pregnancy[31]. Thus, its downregulation might be involved in the long-term impairments of the offspring[32].

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Some other DEGs might be associated with the process of β-cell membrane depolarization which opens the voltage-gated calcium channel raising the cytoplasmic Ca^{2+} concentration that finally triggers exocytosis of insulin-containing granules[33]. For example, the protein encoded by SLC4A8 is a solute carrier that mediates sodium- and carbonate-dependent chloride-HCO3-exchange, an important process for intracellular pH regulation[34] which could control membrane polarization/depolarization process. Therefore, its down regulation may play an active role in the impaired secretion of insulin in T2D.

On the other hand, HS6ST2 (Heparan Sulfate 6-O-Sulfotransferase 2) is related to transferase activity and glycosaminoglycan metabolism. Hs6st2 knockout mice show increased body weight, impaired glucose metabolism and insulin resistance[35].

Since all these genes are related to metabolic and physical processes that promote β-cell function and mass, their downregulation might play a critical role in the pathogenesis of T2D.

DEGs upregulated in islets from people with T2D: SV2B is one of the three homologous isoforms of synaptic vesicle protein 2, which participates in exocytosis process in a Ca^{2+}-dependent manner[36]. Perhaps its upregulation is a compensatory response of β-cells to the higher hormone demand (insulin resistance) in people with T2D[37].

TPD52L1 gene which encodes a member of a family of proteins (D52-like proteins) has been identified as a cell cycle-regulated protein whose impairment affects the cell-mitosis process[38]. Immune system dysregulation and inflammation have been strongly associated with T2D[39,40]. In our case, some of the novel DEGs identified in islets from people with T2D are related to immune response: ITIH4 and ILR7. It has been demonstrated that the protein encoded by ITIH4 gene was dramatically elevated in

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poorly controlled T1D patients[41]. IL7R, is a key regulator of T lymphocyte development and homeostasis[42], associated with adipogenesis and insulin resistance[43-45]. Moreover, based on the results of the protein-protein interaction analysis, IL7R was the molecule with the largest number of interactions, reflecting its crucial role in the regulation of biological systems implicated in T2D pathogenesis. Therefore, IL7R could be considered a novel therapeutic target. Altogether, this evidence shows that upregulation of the genes described strongly suggest that they might play an important role in the pathogenesis of development and progression of T2D.

Others novel DEGs are associated with varied molecular function: lipid metabolism (PLA1A, PNLIPRP1 and AADAC), transcription activity (NR0B1), retinol binding (RBP4). Besides, little is known about the molecular function of the rest of the novel identified genes: CCDC69 (coiled-coil domain containing 69), VATL1 (vesicle amine transport 1 like) and 3 non-coding RNAs (LOC101929550, LINC01933 and LINC01116). Therefore, future studies are necessary to demonstrate their potential role in the islet function dysregulation associated with T2D.

Throughout the identification of relevant DEGs in T2D islets, we aimed to assess whether these dysfunctional genes could be also identified at an early stage of this disease: i.e. prediabetes (PD). Data from GSE50397 and GSE76895 studies - which include analysis of prediabetic pancreatic islets - showed that 2 (SV2B and CD44) of the 13 upregulated genes (15%) and 16 (SLC2A2, CHL1, GLRA1, PFKFB2, RASGRP1, CAPN13, TMED6, GLP1R, G6PC2, ROBO2, PLCXD3, RBP4, VATL1, PLA1A, LINC01933 and SLC4A8) of the 35 downregulated genes (46%), were already present in people with PD.

Some of these DEGs found in PD have not been previously associated with this disease stage in pancreatic islets. Among them, ROBO2, VAT1L, LINC01933, SV2B,

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SLC4A8, PLA1A and RBP4 are discussed above. Otherwise, CD44, PFKFB2, GLP1R and CAPN13 have been reported to be altered in islets from patients with T2D, but not in islets from people with PD. Since they were not reported in PD islets but their effects on β-cell mass and function were already reported, we will not discuss them further[19,46-48]. As for TMED6, it must be stressed that it was down-regulated in both studies performed with islets from people with PD.

Altogether, the results above described suggest that the transcriptional alterations shown in all these genes could have an important role in the development of PD and also perhaps in its progression to T2D.

In summary, we have identified several differentially expressed genes, not previously reported in islets from people with T2D that could potentially play a relevant role in the pathogenesis of the disease. Some of them were also identified in islets from people with an early stage of the disease (PD). It remains to be demonstrated whether their early expression in people with PD can be used as a marker to identify people with higher risk of its fast progression to T2D. Anyhow, these results provide new evidence to interpret T2D pathogenesis and the transition from PD to T2D. Further population studies are necessary to validate the latter hypothesis and its potential use for the development of new strategies to improve the prevention, diagnosis/prognosis and treatment of T2D.

Author Contributions

BM, MCA and JJG conceived and designed the study. Drs. MVM, BM, MA, LEF, and JJG carried out the integrative transcriptomic analysis and the identification of differential expressed genes. All the authors contributed to develop and approve the final manuscript.

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Figure 1. Identification of relevant DEGs in T2D/PD

A. Bar plot representing the number of DEGs (down- or up-regulated genes) in islets from ND versus T2D people of each selected microarray study.

B. HeatMap plot of relevant DEGs in T2D and Hierarchical clustering analysis: each row represents DEGs that vary consistently in the same way (down- or up-regulated) in at least 3 studies, and each column represents a selected microarray study. Blue indicates down-regulated genes, red indicates up-regulated genes, and white indicates unaltered genes. The color intensity is proportional to the fold-change. Gray indicates relevant DEGs that present *p*-value of meta-analysis < 0.05. Black indicates relevant DEGs in islets from ND versus T2D people that also present altered expression in people with PD.

Figure 2. Functional enrichment analysis of relevant DEGs in T2D.

A. Visualization of pathway enrichment analysis of relevant DEGs in T2D.

B. Protein-protein interaction network of relevant DEGs in T2D. Nodes represent the

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genes/proteins inputs as seeds (Green and red nodes), as well as protein added by the platform to obtain a minimum network (Grey nodes). Green indicates down-regulated genes and red indicates up-regulated genes. The color intensity is proportional to the fold-change. Edges indicate interactions between the proteins. This network has 36 seeds, 64 nodes and 95 edges.

Figure 3. Relative expression of novel relevant DEGs in PD.

Expression levels were extracted from the GSE50397 or GSE76895 studies. Data are presented as the mean ± standard error of the mean (SEM). Statistical analyses of two groups were done using one-tailed t-test. *$p<0.05$, **$p<0.01$, ***$p<0.001$.

Table 1. Characteristics of selected microarray for analysis

All the studies were performed on human pancreatic islets obtained from cadaverous donors except for the GSE76895 study that used material from pancreatectomized patients while the study GSE20966 was performed specifically on β-cell enriched tissue. Genders are expressed as males/females. Ages are expressed as mean±standard deviation (SD) in years. BMI are expressed as mean±SD in Kg/m^2.

Table 2. List of relevant DEGs in TD2

The novel relevant DEGs are highlighted in gray. Hits are the number of studies that share the specific DEG. The average fold-change (FC) for a certain gene was calculated by averaging the specific FC for each study.

Supplementary table 1. DEGs in each selected study.

Expression levels and statistics (for comparison ND *vs* T2D) of DEGs in each study (all

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1 differentially expressed probes for each gene are shown).

2

3 **Supplementary table 2. Statistics for comparison ND *vs.* PD of relevant DEGs.**

4 The DEGs that show the same variation identified in T2D in at least one of the two

5 available studies are shown (p-value<0.05).

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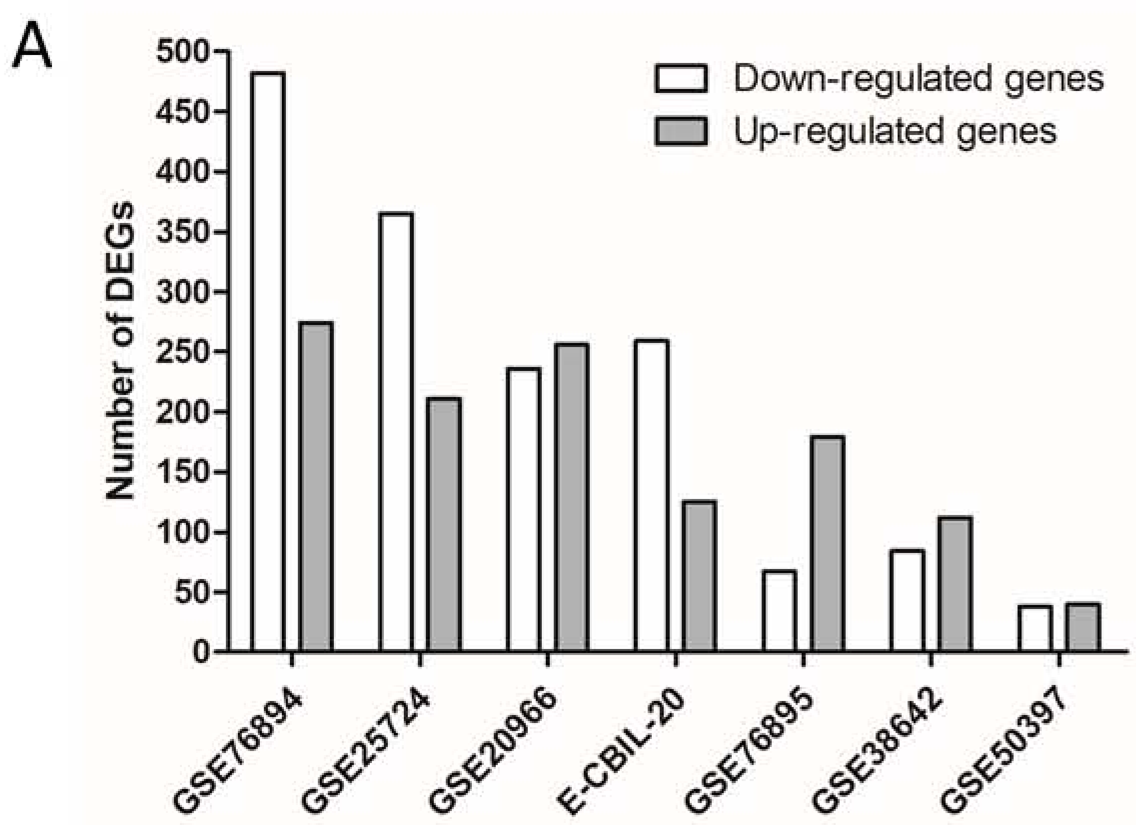

B
E-CBIL-20
GSE25724
GSE38642
GSE50397
GSE76894
GSE20966
GSE76895
PD
Meta-analysis (p<0.05)
CHL1
SLC2A2
PPP1R1A
ARG2
PFKFB2
GLRA1
RASGRP1
FFAR4
PPM1E
CAPN13
IAPP
MYCN
LINC01933
HHATL
PLA1A
EDN3
LOC101929550
TMEM37
HS6ST2
ABCC8
RASGRF1
GLP1R
TMED6
TAGLN3
SCD
NR0B1
HADH
G6PC2
PLCB4
RBP4
ELMO1
PLCXD3
ELAVL4
VAT1L
ROBO2
SLC4A8
ALDOB
PNLIPRP1
GAD1
MMP3
IL6
AADAC
IL33
CCDC69
TPD52L1
SV2B
TMPRSS2
IL24
NNMT
ITIH4
LINC01116
IL7R
LIF
CD44
PDGFRA
Up
Down

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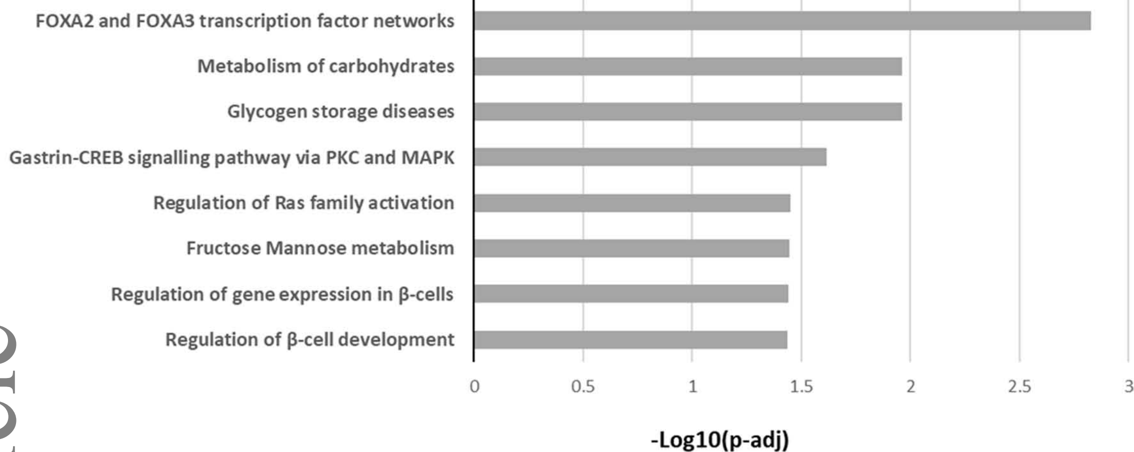

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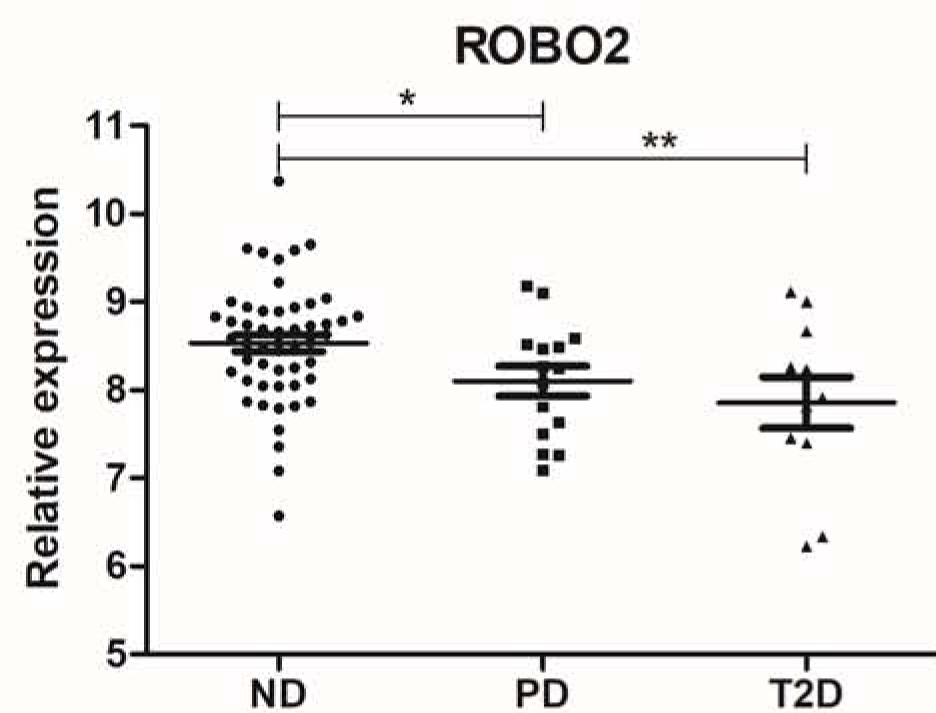

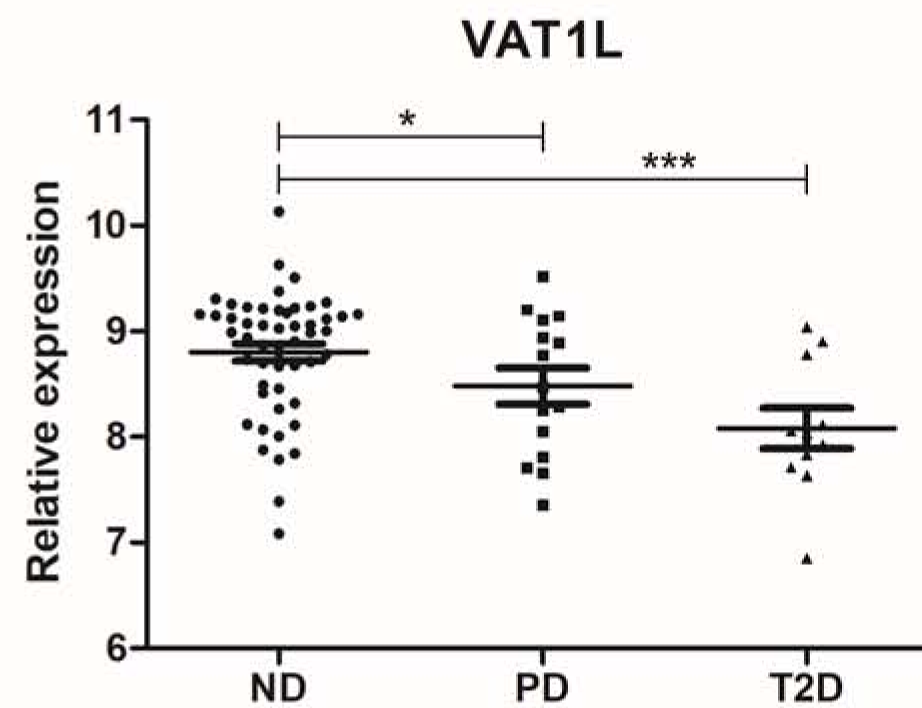

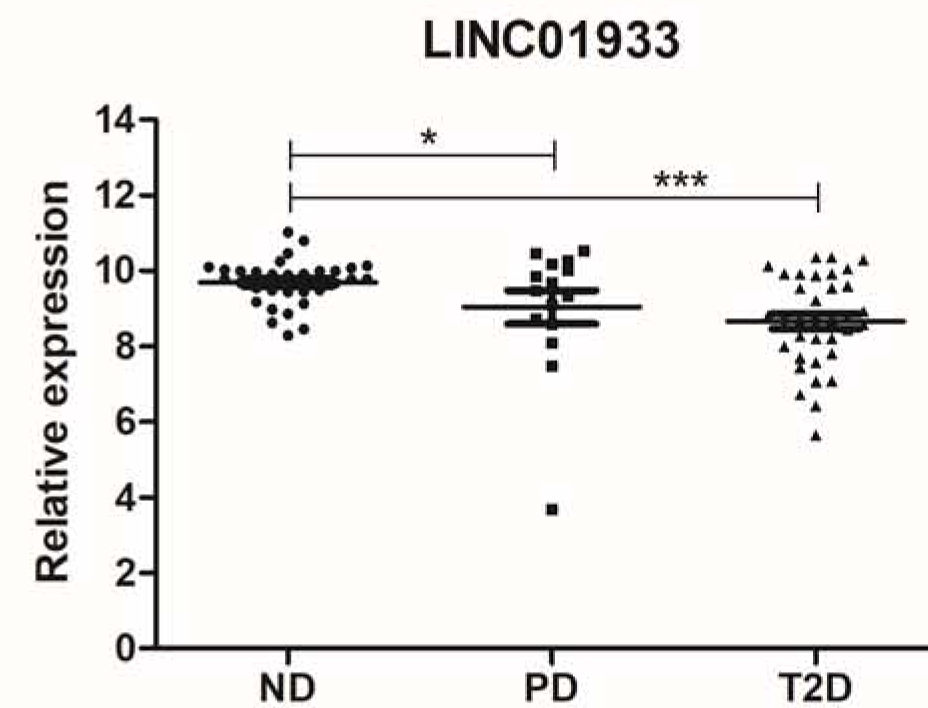

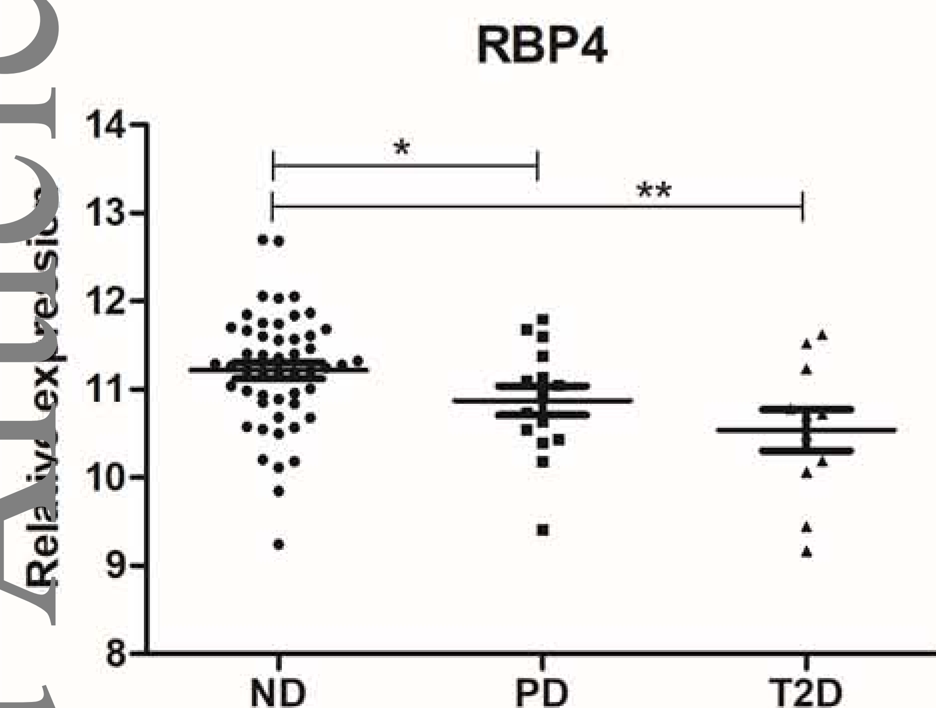

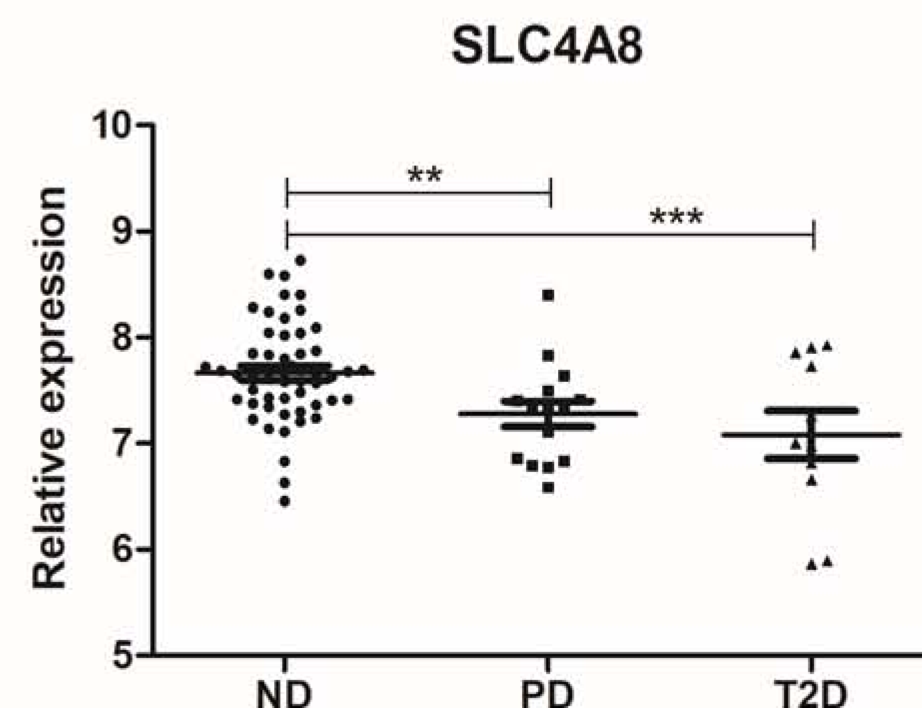

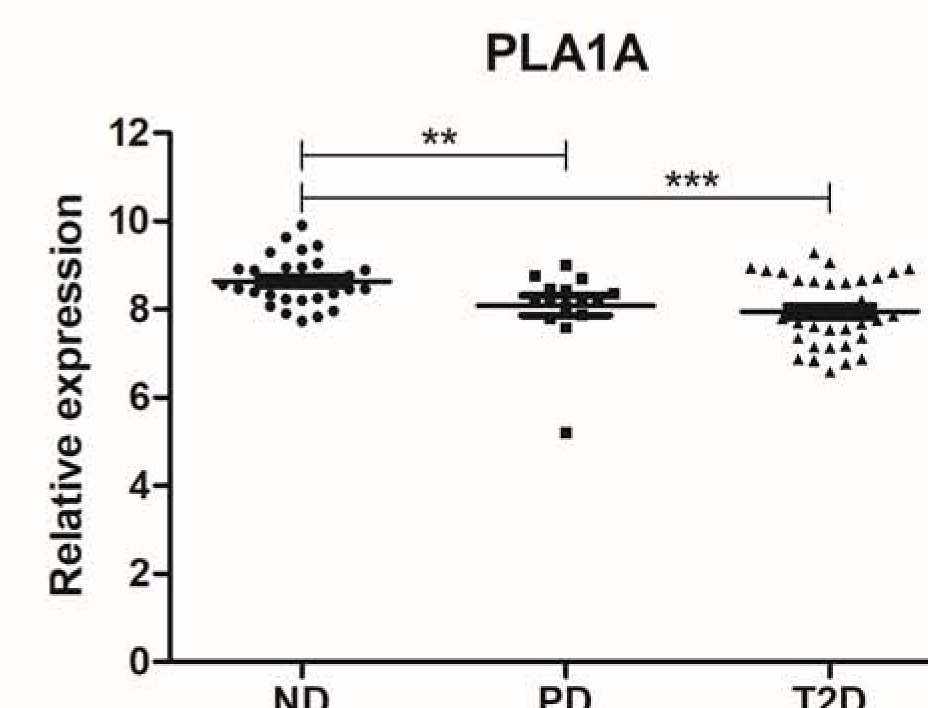

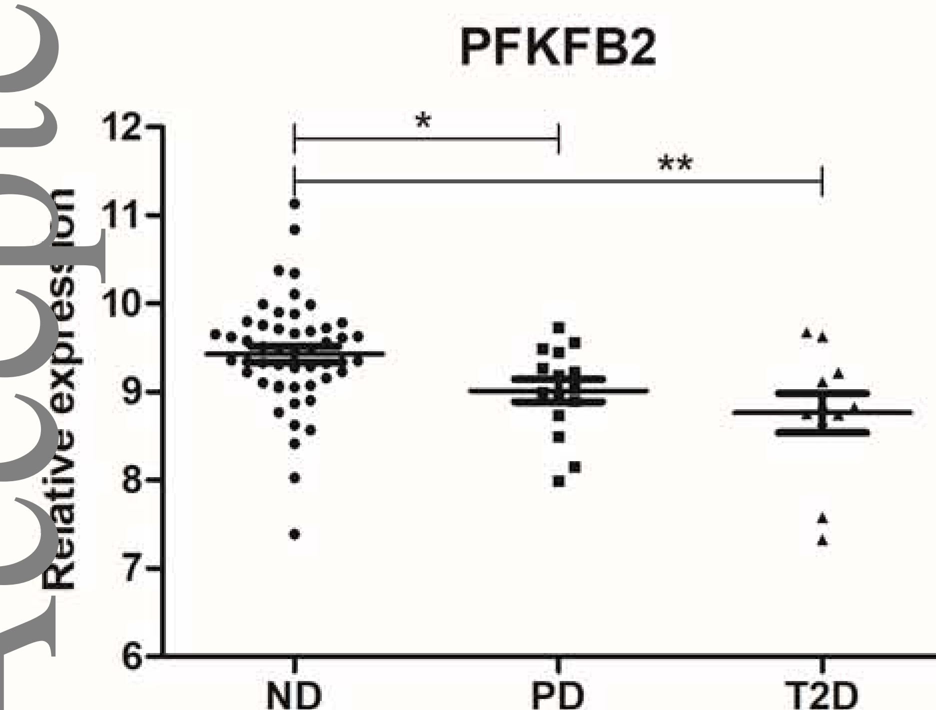

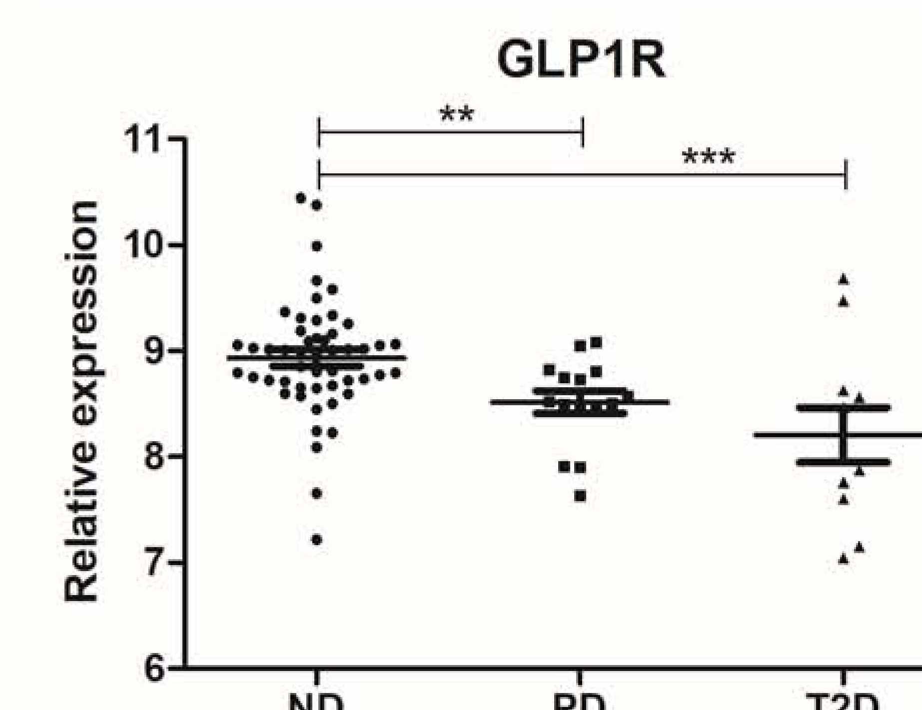

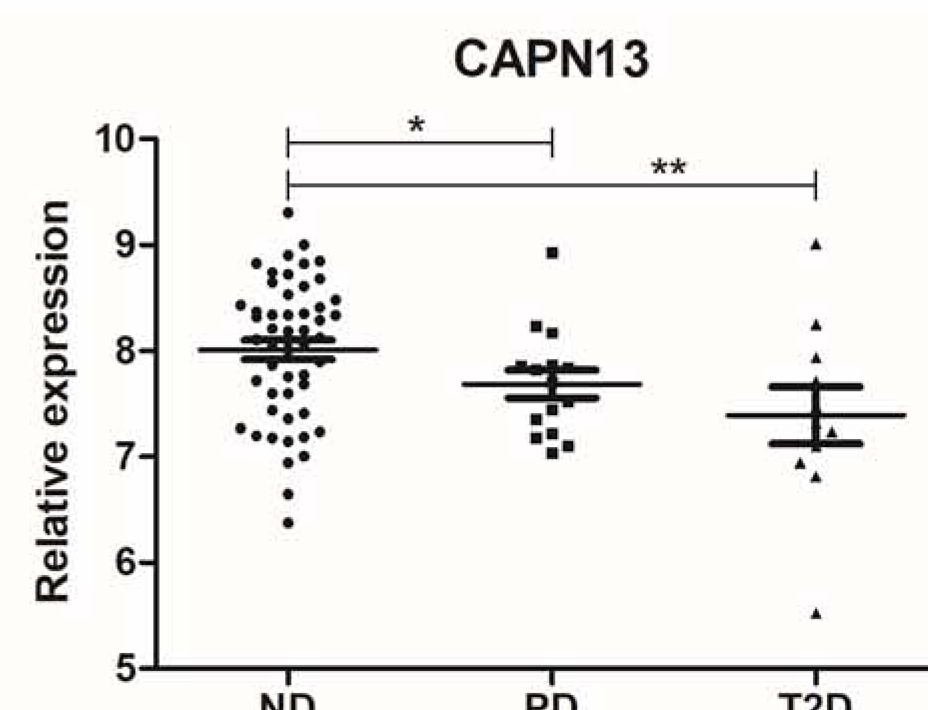

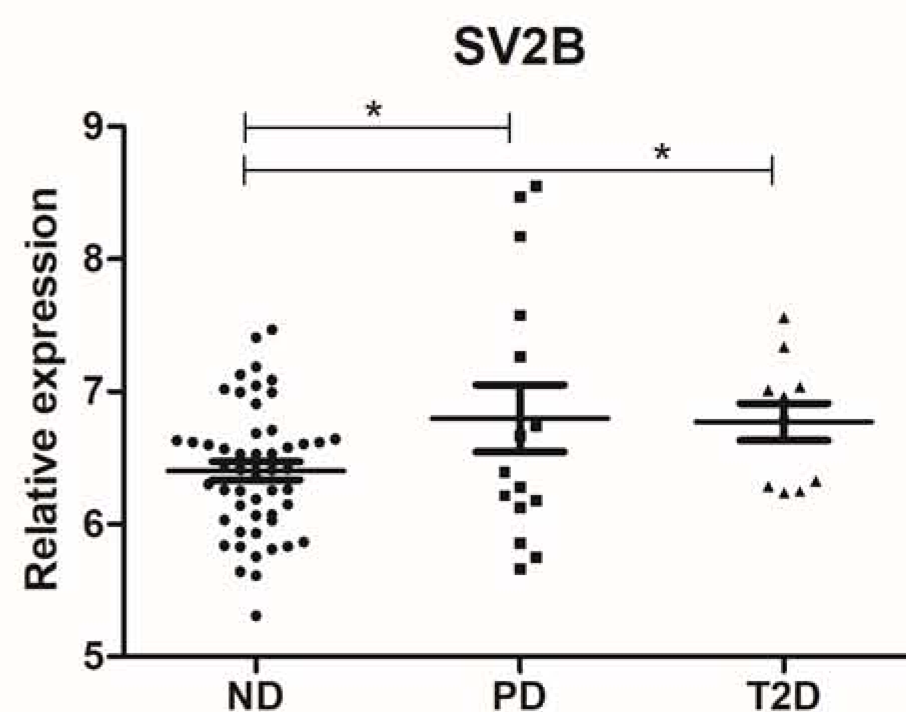

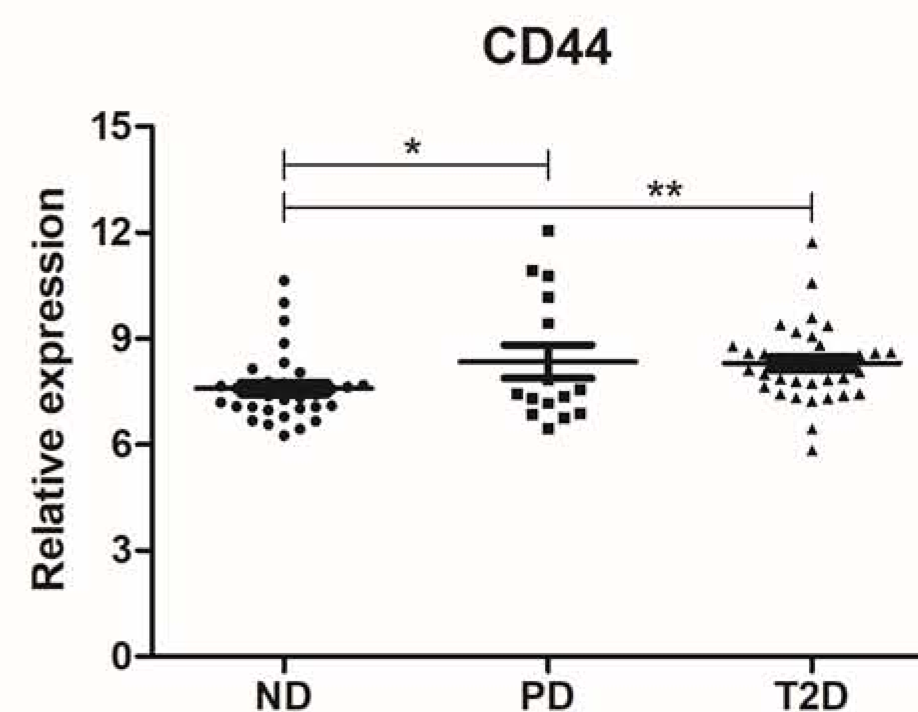

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Study information		Patient information			
Serie Accession	**Platform**	**Characteristics**	**ND**	**PD**	**DT2**
GSE25724 (GEO)	GPL96	n	7	-	6
(reference 16)		Gender	4/3	-	3/3
		Age	58±17	-	71±9
		BMI	24.8±2.5	-	26.0±2.2
E-CBIL-20 (ArrayExpress)	GPL96	n	7	-	5
(reference 18)		Gender	2/5	-	0/5
		Age	48±13 (n=6)	-	47±8 (n=4)
		BMI	-	-	-
GSE38642 (GEO)	GPL6244	n	54	-	9
(reference 13, 14 and 15)		Gender	25/29	-	4/5
		Age	59±9	-	57±4
		BMI	25.9±3.5	-	28.5±4.5
GSE20966 (GEO)	GPL1352	n	10	-	10
(reference 17)		Gender	6/4	-	7/3
		Age	60±5	-	67±7
		BMI	30.5±6.5	-	30.9±6.2 (n=9)
GSE76894 (GEO)	GPL570	n	84	-	19
(reference 19)		Gender	38/46	-	13/6
		Age	60±16	-	72±7
		BMI	25.8±4.2 (n=83)	-	26.5±3.6
GSE50397 (GEO)	GPL6244	n	51	15	11
(reference 10, 11 and 12)		Gender	33/18	9/6	5/6
		Age	56±12	62±7	61±11
		BMI	25.6±2.2	25.6±3.4	29.8±3.1
GSE76895 (GEO)	GPL570	n	32	15	36
(reference 19)		Gender	16/16	9/6	23/13
		Age	60±14	63±13	66±12
		BMI	24.9±3.4	25.7±3.5	25.8±5.0

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N°	Gene symbol	Entrez ID	Full name	Hits	Average FC	*p*-value meta-analysis
	DOWNREGULATED DEGs					
1	**CHL1**	10752	cell adhesion molecule L1 like		-2,78	<0.001
2	**SLC2A2**	6514	solute carrier family 2 member 2	5	-2,74	<0.001
3	**PPP1R1A**	5502	protein phosphatase 1 regulatory inhibitor subunit 1A	5	-1,98	<0.001
4	**ARG2**	384	arginase 2	5	-1,83	<0.001
5	**PFKFB2**	5208	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	4	-2,06	<0.001
6	**GLRA1**	2741	glycine receptor alpha 1	4	-2,01	0,001
7	**RASGRP1**	10125	RAS guanyl releasing protein 1	4	-1,88	0,003
8	**FFAR4**	338557	free fatty acid receptor 4	4	-1,81	<0.001
9	**PPM1E**	22843	protein phosphatase, Mg2+/Mn2+ dependent 1E	4	-1,79	<0.001
10	**CAPN13**	92291	calpain 13	4	-1,64	<0.001
11	**IAPP**	3375	islet amyloid polypeptide	4	-1,59	<0.001
12	**MYCN**	4613	MYCN proto-oncogene, bHLH transcription factor	3	-2,24	<0.001
13	**LINC01933**	101927115	long intergenic non-protein coding RNA 1933	3	-2,15	<0.001
14	**HHATL**	57467	hedgehog acyltransferase like	3	-2,14	<0.001
15	**PLA1A**	51365	phospholipase A1 member A	3	-2,01	<0.001
16	**EDN3**	1908	endothelin 3	3	-2,00	0,045
17	**LOC101929550**	101929550	ncRNA uncharacterized	3	-1,95	0,003
18	**TMEM37**	140738	transmembrane protein 37	3	-1,91	<0.001
19	**HS6ST2**	90161	heparan sulfate 6-O-sulfotransferase 2	3	-1,90	<0.001
20	**ABCC8**	6833	ATP binding cassette subfamily C member 8	3	-1,89	0,003
21	**RASGRF1**	5923	Ras protein specific guanine nucleotide releasing factor 1	3	-1,83	0,001
22	**GLP1R**	2740	glucagon like peptide 1 receptor	3	-1,81	0,01
23	**TMED6**	146456	transmembrane p24 trafficking protein 6	3	-1,80	<0.001
24	**TAGLN3**	29114	transgelin 3	3	-1,79	<0.001
25	**SCD**	6319	stearoyl-CoA desaturase	3	-1,74	0,004
26	**NR0B1**	190	nuclear receptor subfamily 0 group B member 1	3	-1,68	0,008
27	**HADH**	3033	hydroxyacyl-CoA dehydrogenase	3	-1,65	<0.001
28	**G6PC2**	57818	glucose-6-phosphatase catalytic subunit 2	3	-1,64	<0.001
29	**PLCB4**	5332	phospholipase C beta 4	3	-1,64	0,003
30	**RBP4**	5950	retinol binding protein 4	3	-1,62	0,002
31	**ELMO1**	9844	engulfment and cell motility 1	3	-1,62	0,129
32	**PLCXD3**	345557	phosphatidylinositol specific phospholipase C X domain containing 3	3	-1,62	<0.001
33	**ELAVL4**	1996	ELAV like RNA binding protein 4	3	-1,61	<0.001
34	**VAT1L**	57687	vesicle amine transport 1 like	3	-1,59	<0.001
35	**ROBO2**	6092	roundabout guidance receptor 2	3	-1,59	0,012
36	**SLC4A8**	9498	solute carrier family 4 member 8	3	-1,53	0,001
	UPREGULATED DEGs					
37	**ALDOB**	229	aldolase, fructose-bisphosphate B	3	6,07	0,041
38	**PNLIPRP1**	5407	pancreatic lipase related protein 1	3	2,72	0,01
39	**GAD1**	2571	glutamate decarboxylase 1	3	2,10	0,023
40	**MMP3**	4314	matrix metallopeptidase 3	3	2,09	0,071
41	**IL6**	3569	interleukin 6	3	2,02	0,321
42	**AADAC**	13	arylacetamide deacetylase	3	1,99	<0.001
43	**IL33**	90865	interleukin 33	3	1,91	<0.001
44	**CCDC69**	26112	coiled-coil domain containing 69	3	1,85	0,028
45	**TPD52L1**	7164	TPD52 like 1	3	1,84	0,01
46	**SV2B**	9899	synaptic vesicle glycoprotein 2B	3	1,79	<0.001
47	**TMPRSS2**	7113	transmembrane serine protease 2	3	1,78	0,136
48	**IL24**	11009	interleukin 24	3	1,78	0,101
49	**NNMT**	4837	nicotinamide N-methyltransferase	3	1,77	0,046
50	**ITIH4**	3700	inter-alpha-trypsin inhibitor heavy chain 4	3	1,76	<0.001
51	**LINC01116**	375295	long intergenic non-protein coding RNA 1116	3	1,75	0,005
52	**IL7R**	3575	interleukin 7 receptor	3	1,71	0,001
53	**LIF**	3976	LIF interleukin 6 family cytokine	3	1,71	0,55
54	**CD44**	960	CD44 molecule (Indian blood group)	3	1,68	0,021
55	**PDGFRA**	5156	platelet derived growth factor receptor alpha	3	1,67	0,096

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