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Data Article

# Impact of monocarbonyl analogs of curcumin (MACs) C66 and B2BrBC on the expression of diabetes-associated genes in streptozotocin-treated rat pancreatic RIN-m cells—Quantitative RT-PCR array data

Radoslav Stojchevski[a,b,c], Sara Velichkovikj[d], Jane Bogdanov[e], Nikola Hadzi-Petrushev[f], Mitko Mladenov[f], Leonid Poretsky[a,b,c], Dimiter Avtanski[a,b,c,*]

[a] Friedman Diabetes Institute, Lenox Hill Hospital, Northwell Health, New York, NY, USA
[b] Donald and Barbara Zucker School of Medicine at Hofstra/Northwell, Hempstead, NY, USA
[c] Feinstein Institutes for Medical Research, Manhasset, NY, USA
[d] Department of Medicine, Lenox Hill Hospital, Northwell Health, New York, NY, USA
[e] Faculty of Natural Sciences and Mathematics, Institute of Chemistry, Ss. Cyril and Methodius University, Skopje, North Macedonia
[f] Faculty of Natural Sciences and Mathematics, Institute of Biology, Ss. Cyril and Methodius University, Skopje, North Macedonia

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ABSTRACT

This paper presents a dataset obtained from an RT$^2$-qPCR array analysis of rat pancreatic RIN-m cells treated with two monocarbonyl analogs of curcumin (MACs), C66 and B2BrBC in the presence or absence of streptozotocin (STZ). The array quantified the expression of 84 genes associated with the onset, development, and progression of diabetes. This dataset provides information on the gene expression profiles of pancreatic cells modulated by two specific MACs in a diabetic context. The data can serve as a foundation for developing new hypotheses, designing follow-up experiments, and

* Corresponding author at: Friedman Diabetes Institute, Lenox Hill Hospital, Northwell Health, 110E 59th Street, Suite 8B, Room 837, New York, NY 10022, USA.
*E-mail address:* davtanski@northwell.edu (D. Avtanski).
*Social media:* @DimiterAvtanski (D. Avtanski)

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identifying novel targets for treatment. It can be used to investigate further the molecular mechanisms underlying the therapeutic effects of these MACs and in comparative studies using other experimental antidiabetic compounds.


Specifications Table

| | |
|---|---|
| Subject | Biological Sciences |
| Specific subject area | Gene expression analysis |
| Data format | Raw and analyzed |
| Type of data | Tables |
| Data collection | Rat pancreatic RIN-m cells were cultured *in vitro* and treated with monocarbonyl analogs of curcumin (MACs) C66 or B2BrBC (50 µM) for 72 h, followed by streptozotocin (STZ) treatment (1.5 mM) for 24 h. RNA was extracted using TRIzol reagent and chloroform, quantified using a NanoDrop One spectrophotometer, normalized to 1 µg, and converted to cDNA using the qScript cDNA SuperMix and SimpliAmp thermocycler. Quantitative PCR was performed using the $RT^2$ Profiler PCR Array (Rat Diabetes Panel Kit) and QuantStudio 3 Real-Time PCR System. Data were analyzed using the GeneGlobe Data Analysis Center. |
| Data source location | • Institution: Friedman Diabetes Institute, Northwell Health<br>• City/Town/Region: New York, NY<br>• Country: USA |
| Data accessibility | Repository name: Mendeley Data<br>Data identification number: 10.17632/vdgz7pk6vh.1<br>Direct URL to data: https://data.mendeley.com/datasets/vdgz7pk6vh/1 |
| Related research article | Monocarbonyl analogs of curcumin C66 and B2BrBC modulate oxidative stress, JNK activity, and pancreatic gene expression in rats with streptozotocin-induced diabetes<br>Data identification number: 10.1016/j.bcp.2024.116491<br>Direct URL to data: https://www.sciencedirect.com/science/article/pii/S000629522400474X?via%3Dihub |

## 1. Value of the Data

By providing a thorough gene expression profile, this data supports further research into the pharmacological properties of curcumin derivatives in diabetes treatment, making it valuable for both basic and translational research. Researchers can leverage this dataset to design follow-up experiments or conduct comparative studies using other antidiabetic compounds, particularly those aimed at oxidative stress and inflammatory pathways.

## 2. Background

Curcumin, a bioactive compound derived from turmeric (*Curcuma longa*), has been recognized for its anti-diabetic actions related to its antioxidant and anti-inflammatory properties [1–5]. However, its poor bioavailability limits its clinical applications [6]. Consequently, monocarbonyl analogs of curcumin (MACs) lacking $\beta$-diketone moiety were synthesized to enhance the therapeutic efficacy of curcumin [7]. This $RT^2$-qPCR array dataset was generated to deepen our understanding of the mechanisms of action of the two experimental MACs, C66 and B2BrBC, focusing particularly on diabetes. The motivation behind this study stems from the need to explore novel

interventions that can reduce the negative effects of dysregulated gene expression associated with diabetes. This approach allowed for simultaneous assessment of the expression of multiple genes, providing an overview of the preventive anti-diabetic effects of C66 and B2BrBC. This data article complements a research study by offering a detailed repository of gene expression changes, which can serve as a resource for researchers seeking to understand the genetic landscape of diabetes and the impact of curcumin-based therapies.

## 3. Data Description

The present dataset comprises the effects of C66 and B2BrBC in the presence or absence of STZ on the expression of 84 diabetes-related genes in rat pancreatic RIN-m cells. The genes included in the PCR panel and their functions are listed in Tables 1 and 2. Individual *Ct* values obtained from the array have been previously published in a data repository [8]. This paper shows the gene expression levels presented as a fold-change of treatment relative to the control or STZ (Tables 3 and 4). Preliminary analysis of the gene expression data suggests that C66 and B2BrBC modulate the expression of several key genes involved in $\beta$-cell function and survival and the pathogenesis of diabetes. For instance, altered expression of *Ins* is directly related to glucose homeostasis and the regulation of $\beta$-cell function [9]. The MACs also influenced genes involved in oxidative stress and inflammatory responses, commonly associated with diabetes, including *Retn, Ccr2, Ccl5, Igfbp5, Srebf1, Gpd1, Slc2a4, Agt, Icam1, Serpine1, Dpp4, Fpb1, Cebpa, and Ctla4*. Moreover, the ability of C66 and B2BrBC to alter *Tnfrsf1a* and *Mapk8* expression, both involved in the JNK signaling pathway, further highlights the therapeutic potential of these analogs, as JNK signaling has been shown to be involved in insulin resistance and $\beta$-cell apoptosis [10,11]. Overall, our findings highlight the potential of MACs to target multiple pathways relevant to diabetes development and progression. Further studies are required to validate these molecular targets and explore their therapeutic significance.

## 4. Experimental Design, Materials and Methods

C66 and B2BrBC were synthesized by cross-aldol condensation [12,13]; STZ was purchased from MilliporeSigma (Cat. # S0130); RIN-m cells were purchased from ATCC (Cat. # CRL-2057). The cells were grown in RPMI-1640 medium (ATCC, Cat. # 30-2001), supplemented with 10 % fetal bovine serum (FBS) (VWR International, Cat. # 89510-186) and antibiotic/antimycotic solution (MP Biomedicals, Cat. # 1674049), and incubated at 37 °C with 5 % $CO_2$. For experiments, cells were initially seeded in 6-well plates in complete medium ($0.3 \times 10^6$ cells/well) for 24 h, then treated with C66 or B2BrBC (50 µM) for 72 h, followed by streptozotocin (STZ) treatment (1.5 mM) for 24 h. Control cells were incubated with the corresponding concentration of DMSO. At the end of the experiment, the cells were washed twice with PBS, and total RNA was extracted using TRIzol reagent (Ambion, Cat. # 5596018) and chloroform. The extracted RNA fraction was quantified using a NanoDrop One spectrophotometer (Thermo Fisher Scientific), normalized to 1 µg, and converted to cDNA using the qScript cDNA SuperMix (Quantabio, Cat. # 95048) and a SimpliAmp thermocycler (Thermo Fisher Scientific) under the following conditions: 5 min/25 °C, 30 min/42 °C, 5 min/85 °C. Quantitative PCR array was performed using the $RT^2$ Profiler PCR Array (Rat Diabetes Panel Kit) (QIAGEN, GeneGlobe ID # PARN-023ZA, Cat. # 330231) and QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific) under the following conditions: 10 min/95 °C, 15 s/95 °C and 1 min/60 °C (40 cycles), and 15 s/95 °C, 1 min/60 °C, 15 s/95 °C. Data were calculated using the $\Delta\Delta Ct$ method and the housekeeping genes *Actb, B2m, Hprt1, Ldha*, and *Rplp1,* and presented as fold-changes of treatment relative to the control or STZ. Statistical analysis was performed using the online-based GeneGlobe Data Analysis Center (https://geneglobe.qiagen.com/us/analyze) (QIAGEN). Statistical differences between the treatment groups were assessed using Student's *t*-test. Data were considered statistically significant at $p < 0.05$.

**Table 1**
List of genes included in the rat diabetes panel.

| Gene Symbol | Gene full name | UniGene ID | Accession Number |
|---|---|---|---|
| *Ace* | Angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 | Rn.10149 | NM_012544 |
| *Acly* | ATP citrate lyase | Rn.29771 | NM_016987 |
| *Adra1a* | Adrenergic, alpha-1A-, receptor | Rn.9991 | NM_017191 |
| *Adrb3* | Adrenergic, beta-3-, receptor | Rn.10100 | NM_013108 |
| *Agt* | Angiotensinogen (serpin peptidase inhibitor, clade A, member 8) | Rn.6319 | NM_134432 |
| *Akt2* | V-akt murine thymoma viral oncogene homolog 2 | Rn.87066 | NM_017093 |
| *Aqp2* | Aquaporin 2 (collecting duct) | Rn.90076 | NM_012909 |
| *Ccl5* | Chemokine (C–C motif) ligand 5 | Rn.8019 | NM_031116 |
| *Ccr2* | Chemokine (C–C motif) receptor 2 | Rn.211983 | NM_021866 |
| *Cd28* | Cd28 molecule | Rn.10327 | NM_013121 |
| *Ceacam1* | Carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) | Rn.91235 | NM_031755 |
| *Cebpa* | CCAAT/enhancer binding protein (C/EBP), alpha | Rn.204833 | NM_012524 |
| *Ctla4* | Cytotoxic T-lymphocyte-associated protein 4 | Rn.10259 | NM_031674 |
| *Dpp4* | Dipeptidylpeptidase 4 | Rn.91364 | NM_012789 |
| *Dusp4* | Dual specificity phosphatase 4 | Rn.44407 | NM_022199 |
| *Enpp1* | Ectonucleotide pyrophosphatase/phosphodiesterase 1 | Rn.1199 | NM_053535 |
| *Fbp1* | Fructose-1,6-bisphosphatase 1 | Rn.33703 | NM_012558 |
| *Foxc2* | Forkhead box C2 | Rn.216723 | NM_001101680 |
| *Foxg1* | Forkhead box G1 | Rn.9864 | NM_012560 |
| *Foxp3* | Forkhead box P3 | Rn.177272 | NM_001108250 |
| *G6pc* | Glucose-6-phosphatase, catalytic subunit | Rn.10992 | NM_013098 |
| *Gcg* | Glucagon | Rn.54383 | NM_012707 |
| *Gcgr* | Glucagon receptor | Rn.11225 | NM_172092 |
| *Gck* | Glucokinase | Rn.10447 | NM_012565 |
| *Glp1r* | Glucagon-like peptide 1 receptor | Rn.11408 | NM_012728 |
| *Gpd1* | Glycerol-3-phosphate dehydrogenase 1 (soluble) | Rn.44452 | NM_022215 |
| *Gsk3b* | Glycogen synthase kinase 3 beta | Rn.10426 | NM_032080 |
| *Hmox1* | Heme oxygenase (decycling) 1 | Rn.3160 | NM_012580 |
| *Hnf1b* | HNF1 homeobox B | Rn.11342 | NM_013103 |
| *Hnf4a* | Hepatocyte nuclear factor 4, alpha | Rn.44442 | NM_022180 |
| *Icam1* | Intercellular adhesion molecule 1 | Rn.12 | NM_012967 |
| *Ide* | Insulin degrading enzyme | Rn.45029 | NM_013159 |
| *Ifng* | Interferon gamma | Rn.10795 | NM_138880 |
| *Igfbp5* | Insulin-like growth factor binding protein 5 | Rn.1593 | NM_012817 |
| *Ikbkb* | Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta | Rn.19222 | NM_053355 |
| *Il10* | Interleukin 10 | Rn.9868 | NM_012854 |
| *Il12b* | Interleukin 12b | Rn.48686 | NM_022611 |
| *Il4ra* | Interleukin 4 receptor, alpha | Rn.10471 | NM_133380 |
| *Il6* | Interleukin 6 | Rn.9873 | NM_012589 |
| *Inppl1* | Inositol polyphosphate phosphatase-like 1 | Rn.42902 | NM_022944 |
| *Ins1* | Insulin 1 | Rn.962 | NM_019129 |
| *Irs1* | Insulin receptor substrate 1 | Rn.10476 | NM_012969 |
| *Irs2* | Insulin receptor substrate 2 | Rn.10718 | NM_001168633 |
| *Mapk14* | Mitogen activated protein kinase 14 | Rn.88085 | NM_031020 |
| *Mapk8* | Mitogen-activated protein kinase 8 | Rn.4090 | XM_341399 |
| *Neurod1* | Neurogenic differentiation 1 | Rn.44289 | NM_019218 |
| *Nfkb1* | Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 | Rn.2411 | XM_342346 |
| *Nkx2-1* | NK2 homeobox 1 | Rn.34265 | NM_013093 |
| *Nos3* | Nitric oxide synthase 3, endothelial cell | Rn.44265 | NM_021838 |
| *Nrf1* | Nuclear respiratory factor 1 | Rn.17159 | NM_001100708 |
| *Nsf* | N-ethylmaleimide-sensitive factor | Rn.13345 | NM_021748 |
| *Parp1* | Poly (ADP-ribose) polymerase 1 | Rn.11327 | NM_013063 |
| *Pdx1* | Pancreatic and duodenal homeobox 1 | Rn.54603 | NM_022852 |
| *Pik3cd* | Phosphoinositide-3-kinase, catalytic, delta polypeptide | Rn.11530 | NM_001108978 |
| *Pik3r1* | Phosphoinositide-3-kinase, regulatory subunit 1 (alpha) | Rn.10599 | NM_013005 |

(*continued on next page*)

**Table 1** (*continued*)

| Gene Symbol | Gene full name | UniGene ID | Accession Number |
|---|---|---|---|
| *Ppara* | Peroxisome proliferator activated receptor alpha | Rn.9753 | NM_013196 |
| *Pparg* | Peroxisome proliferator-activated receptor gamma | Rn.23443 | NM_013124 |
| *Ppargc1a* | Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha | Rn.19172 | NM_031347 |
| *Ptpn1* | Protein tyrosine phosphatase, non-receptor type 1 | Rn.11317 | NM_012637 |
| *Pygl* | Phosphorylase, glycogen, liver | Rn.21399 | NM_022268 |
| *Rab4a* | RAB4A, member RAS oncogene family | Rn.3016 | NM_013019 |
| *Retn* | Resistin | Rn.16746 | NM_144741 |
| *Sell* | Selectin L | Rn.10461 | NM_019177 |
| *Serpine1* | Serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type1), member 1 | Rn.29367 | NM_012620 |
| *Slc14a2* | Solute carrier family 14 (urea transporter), member 2 | Rn.10157 | NM_019347 |
| *Slc2a4* | Solute carrier family 2 (facilitated glucose transporter), member 4 | Rn.1314 | NM_012751 |
| *Snap23* | Synaptosomal-associated protein 23 | Rn.14789 | NM_022689 |
| *Snap25* | Synaptosomal-associated protein 25 | Rn.107689 | NM_030991 |
| *Sod2* | Superoxide dismutase 2, mitochondrial | Rn.10488 | NM_017051 |
| *Srebf1* | Sterol regulatory element binding transcription factor 1 | Rn.221929 | XM_213329 |
| *Stx4* | Syntaxin 4 | Rn.33218 | NM_031125 |
| *Stxbp1* | Syntaxin binding protein 1 | Rn.80843 | NM_013038 |
| *Stxbp2* | Syntaxin binding protein 2 | Rn.10121 | NM_031126 |
| *Stxbp4* | Syntaxin binding protein 4 | Rn.49449 | NM_001107038 |
| *Tgfb1* | Transforming growth factor, beta 1 | Rn.40136 | NM_021578 |
| *Tnf* | Tumor necrosis factor (TNF superfamily, member 2) | Rn.2275 | NM_012675 |
| *Tnfrsf1a* | Tumor necrosis factor receptor superfamily, member 1a | Rn.11119 | NM_013091 |
| *Tnfrsf1b* | Tumor necrosis factor receptor superfamily, member 1b | Rn.83633 | NM_130426 |
| *Trib3* | Tribbles homolog 3 (Drosophila) | Rn.22325 | NM_144755 |
| *Ucp2* | Uncoupling protein 2 (mitochondrial, proton carrier) | Rn.13333 | NM_019354 |
| *Vamp2* | Vesicle-associated membrane protein 2 | Rn.12939 | NM_012663 |
| *Vamp3* | Vesicle-associated membrane protein 3 | Rn.219999 | NM_057097 |
| *Vapa* | VAMP (vesicle-associated membrane protein)-associated protein A | Rn.162275 | NM_031631 |
| *Vegfa* | Vascular endothelial growth factor A | Rn.1923 | NM_031836 |
| *Actb* | Actin, beta | Rn.94978 | NM_031144 |
| *B2m* | Beta-2 microglobulin | Rn.1868 | NM_012512 |
| *Hprt1* | Hypoxanthine phosphoribosyltransferase 1 | Rn.47 | NM_012583 |
| *Ldha* | Lactate dehydrogenase A | Rn.107896 | NM_017025 |
| *Rplp1* | Ribosomal protein, large, P1 | Rn.973 | NM_001007604 |

**Table 2**
List of genes included in the rat diabetes panel organized by their function.

| Function | Gene |
|---|---|
| Receptors, Transporters & Channels | *Adra1a, Adrb3, Aqp2, Ccr2, Cd28, Ceacam1, Ctla4, Gcgr, Glp1r, Icam1, Il4r, Nsf, Rab4a, Sell (Lecam-1), Slc14a2, Slc2a4 (Glut4), Snap23, Snap25, Stx4, Stxbp1, Stxbp2, Stxbp4, Tnfrsf1a (Tnfr1), Tnfrsf1b, Vamp2, Vamp3, Vapa* |
| Nuclear Receptors | *Ppara, Pparg* |
| Metabolic Enzymes | *Ace, Acly, Dpp4, Enpp1, Fbp1, G6pc, Gck, Gpd1, Gsk3b, Hmox1, Ide, Nos3 (eNOS), Parp1 (Adprt1), Pygl, Sod2* |
| Cytokines & Growth Factors | *Agt, Ccl5 (Rantes), Gcg, Ifng, Il10, Il12b, Il6, Ins1, Retn, Tgfb1, Tnf, Vegfa* |
| Signal Transduction | *Akt2, Dusp4, Igfbp5, Ikbkb (IKK2), Inppl1 (SHIP2), Irs1, Irs2, Mapk14 (p38alpha), Mapk8 (Jnk1), Pik3cd, Pik3r1 (PI3KA), Ptpn1 (Ptp), Trib3 (Skip3)* |
| Transcription Factors | *Cebpa, Foxc2, Foxg1, Foxp3, Hnf1b, Hnf4a, Neurod1, Nfkb1, Nkx2-1, Nrf1, Pdx1 (Ipf1), Ppargc1a, Srebf1* |
| Other Diabetes-associated Genes | *Serpine1 (Pai-1), Ucp2* |

**Table 3**
Modulation of diabetes-associated genes in RIN-m cells. Data are calculated as fold-change of treatment (C66, B2BrBC, STZ, C66+STZ, or B2BrBC+STZ) compared to the control (vehicle-treated) group. Fold-change values > 2 or < 0.5 and *p* values < 0.5 are presented in bold.

| Gene Symbol | C66 *vs.* Control | | B2BrBC *vs.* Control | | STZ *vs.* Control | | C66+STZ *vs.* Control | | B2BrBC+STZ *vs.* Control | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value |
| *Ace* | 0.86 | 0.442730 | 0.68 | **0.012600** | 0.77 | 0.088935 | 0.76 | **0.033801** | 0.54 | **0.006141** |
| *Acly* | 0.66 | **0.010746** | 1.02 | 0.787558 | 0.69 | **0.000010** | 0.61 | **0.000211** | 0.66 | **0.004857** |
| *Adra1a* | 1.03 | 0.895608 | 1.28 | 0.416634 | 1.06 | 0.751310 | 0.85 | 0.520616 | 1.46 | 0.440154 |
| *Adrb3* | 0.56 | 0.255969 | 0.82 | 0.329247 | 0.77 | 0.225980 | 0.76 | 0.279399 | 0.68 | 0.134059 |
| *Agt* | **0.38** | 0.061079 | 0.62 | **0.046934** | 0.78 | 0.138387 | **0.40** | **0.020520** | **0.39** | 0.071851 |
| *Akt2* | 0.67 | 0.180275 | 1.15 | 0.569651 | 1.03 | 0.946601 | 0.84 | 0.339196 | 0.86 | 0.518625 |
| *Aqp2* | 1.60 | 0.177404 | 1.44 | 0.287388 | 1.07 | 0.723052 | 1.06 | 0.595892 | 1.88 | 0.050260 |
| *Ccl5* | **2.06** | 0.158953 | **3.41** | **0.018704** | 1.56 | 0.510847 | 1.80 | 0.393150 | **2.07** | 0.289077 |
| *Ccr2* | **2.41** | 0.145952 | 1.55 | 0.166872 | 0.98 | 0.976489 | 1.26 | 0.519646 | 1.41 | 0.325768 |
| *Cd28* | 1.03 | 0.895608 | 1.28 | 0.416634 | 1.05 | 0.780693 | 0.99 | 0.879266 | 0.88 | 0.655995 |
| *Ceacam1* | 0.70 | 0.054003 | 1.08 | 0.556547 | 0.93 | 0.355188 | 0.73 | **0.011859** | 0.83 | 0.058206 |
| *Cebpa* | 0.52 | 0.057725 | 0.70 | 0.074138 | 0.69 | 0.208656 | **0.49** | **0.030348** | 0.57 | 0.199810 |
| *Ctla4* | 0.96 | 0.881290 | 1.34 | 0.342002 | 0.81 | 0.453545 | 1.84 | **0.033671** | 0.88 | 0.477402 |
| *Dpp4* | 0.95 | 0.757496 | **2.27** | **0.002681** | 1.36 | 0.167585 | 1.67 | **0.004910** | 1.39 | 0.057787 |
| *Dusp4* | 0.59 | 0.197469 | 1.38 | 0.316701 | 1.84 | **0.020897** | 0.94 | 0.715062 | 1.15 | 0.585580 |
| *Enpp1* | 0.82 | 0.120572 | 1.07 | 0.362132 | 0.96 | 0.408696 | 0.82 | 0.082091 | 0.91 | 0.532341 |
| *Fbp1* | 1.19 | 0.544938 | **3.13** | **0.028969** | 1.06 | 0.801672 | 0.87 | 0.640388 | 1.62 | 0.235060 |
| *Foxc2* | 1.41 | 0.287076 | 1.93 | 0.127156 | 1.44 | 0.212590 | 1.18 | 0.547068 | 1.66 | 0.248656 |
| *Foxg1* | 1.13 | 0.333362 | 1.21 | **0.047722** | 0.91 | 0.379301 | 0.98 | 0.884438 | 0.96 | 0.811652 |
| *Foxp3* | 0.76 | 0.349245 | 1.14 | 0.702804 | 1.13 | 0.731756 | 0.99 | 0.820356 | 1.03 | 0.988344 |
| *G6pc* | 1.09 | 0.720966 | 1.32 | 0.478108 | 1.49 | 0.354522 | 1.14 | 0.585436 | 1.29 | 0.453643 |
| *Gcg* | 0.87 | 0.683739 | 0.87 | 0.737765 | 1.19 | 0.432981 | 1.41 | 0.255120 | 1.45 | **0.016324** |
| *Gcgr* | 0.64 | **0.001088** | 0.96 | 0.649863 | 0.71 | **0.000149** | 0.55 | **0.000306** | 0.64 | **0.007554** |
| *Gck* | 0.69 | 0.099628 | 1.19 | 0.355280 | 0.73 | **0.022677** | 0.71 | **0.034491** | 0.68 | 0.097336 |
| *Glp1r* | 0.65 | 0.050496 | 1.03 | 0.746911 | 0.67 | **0.008319** | 0.69 | **0.018188** | 0.70 | **0.012411** |
| *Gpd1* | **0.41** | **0.011142** | 0.85 | 0.537167 | 0.82 | 0.169227 | **0.45** | **0.008268** | 0.54 | **0.047204** |
| *Gsk3b* | 0.75 | **0.010919** | 1.15 | 0.290661 | 0.92 | 0.372670 | 0.86 | 0.119423 | 0.88 | 0.121921 |
| *Hmox1* | 0.60 | 0.353025 | 1.00 | 0.927224 | 1.49 | **0.007334** | 0.82 | 0.188128 | 1.24 | 0.296712 |
| *Hnf1b* | 0.72 | 0.125941 | 1.03 | 0.797553 | 0.97 | 0.786766 | 0.77 | 0.142314 | 0.85 | 0.447554 |
| *Hnf4a* | 0.66 | 0.064131 | 1.03 | 0.855754 | 1.32 | 0.142394 | 1.03 | 0.895824 | 1.09 | 0.667833 |
| *Icam1* | **0.47** | 0.065303 | 0.67 | 0.114651 | 1.99 | **0.030221** | 0.59 | 0.084799 | 0.71 | 0.328419 |
| *Ide* | 0.90 | **0.048591** | 1.12 | **0.018722** | 1.03 | 0.559083 | 1.04 | 0.211721 | 1.05 | 0.097344 |
| *Ifng* | 1.21 | 0.408012 | 1.85 | 0.120916 | 1.11 | 0.622035 | 0.98 | 0.850364 | 1.70 | 0.059380 |
| *Igfbp5* | **0.46** | **0.007832** | 0.69 | 0.060393 | 0.53 | **0.009323** | **0.32** | **0.001818** | **0.25** | **0.001006** |
| *Ikbkb* | 0.69 | 0.063061 | 1.02 | 0.859011 | 1.10 | 0.400231 | 0.79 | 0.087519 | 0.85 | 0.388303 |
| *Il10* | 1.76 | 0.086002 | 1.81 | 0.114208 | 1.24 | 0.260525 | 1.85 | **0.012202** | 1.25 | 0.304901 |
| *Il12b* | 0.84 | **0.001794** | 1.67 | **0.009517** | 1.39 | **0.009219** | 1.08 | 0.459828 | 1.38 | 0.125741 |
| *Il4ra* | 0.60 | 0.230954 | 1.03 | 0.929777 | 1.14 | 0.473680 | 0.70 | 0.144839 | 0.76 | 0.337653 |
| *Il6* | 1.31 | 0.460621 | 1.38 | 0.348874 | 1.53 | 0.221830 | 1.50 | 0.290750 | 1.95 | 0.239274 |
| *Inppl1* | 0.65 | 0.179018 | 1.21 | 0.397048 | 1.09 | 0.691200 | 0.93 | 0.582236 | 0.91 | 0.659664 |
| *Ins1* | 0.98 | 0.889111 | 1.18 | 0.155963 | **0.49** | **0.006242** | 0.65 | **0.022350** | 0.77 | 0.159863 |
| *Irs1* | 0.72 | **0.022272** | 1.19 | 0.125545 | 0.95 | 0.474317 | 0.94 | 0.565200 | 1.05 | 0.460706 |
| *Irs2* | 0.69 | 0.156438 | 0.91 | 0.453617 | 0.78 | 0.126648 | 0.77 | 0.117451 | 0.74 | 0.193982 |
| *Mapk14* | 0.68 | 0.052746 | 1.00 | 0.975839 | 0.93 | 0.609653 | 0.78 | **0.033741** | 0.74 | 0.085597 |
| *Mapk8* | 0.65 | 0.146601 | 1.01 | 0.909926 | 0.54 | **0.014762** | 0.85 | 0.947477 | 1.23 | 0.360564 |
| *Neurod1* | 0.74 | 0.059552 | 1.17 | 0.387047 | 0.64 | **0.006813** | 0.78 | **0.016862** | 0.77 | **0.036818** |
| *Nfkb1* | 0.59 | **0.047018** | 0.89 | 0.311464 | 0.93 | 0.492048 | 0.63 | **0.013998** | 0.63 | 0.082886 |
| *Nkx2–1* | 0.89 | 0.997843 | 1.57 | **0.016983** | 0.76 | 0.138025 | 0.69 | 0.223792 | 0.63 | 0.059658 |
| *Nos3* | 0.98 | 0.823836 | 1.38 | 0.060441 | 1.26 | 0.248340 | 1.07 | 0.603255 | 1.16 | 0.327359 |
| *Nrf1* | 0.77 | 0.178845 | 1.19 | 0.206341 | 0.81 | 0.252873 | 0.82 | 0.308709 | 0.90 | 0.599837 |
| *Nsf* | 0.83 | 0.191326 | 1.24 | 0.077846 | 0.91 | 0.208471 | 0.99 | 0.918093 | 0.92 | 0.331094 |
| *Parp1* | 0.93 | 0.078363 | 1.16 | 0.251165 | 0.81 | **0.008695** | 0.83 | 0.057211 | 0.81 | 0.074437 |
| *Pdx1* | 0.92 | 0.483720 | 1.40 | 0.157848 | 0.80 | **0.015305** | 0.87 | 0.160912 | 0.94 | 0.702784 |

(*continued on next page*)

**Table 3** (*continued*)

| Gene Symbol | C66 *vs.* Control | | B2BrBC *vs.* Control | | STZ *vs.* Control | | C66+STZ *vs.* Control | | B2BrBC+STZ *vs.* Control | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value | Fold Change | *p*-value |
| *Pik3cd* | 0.62 | 0.243153 | 1.68 | 0.115791 | 1.24 | 0.402723 | 0.94 | 0.841720 | 1.00 | 0.975893 |
| *Pik3r1* | 0.94 | 0.742685 | 1.40 | **0.043085** | 1.01 | 0.977925 | 1.14 | 0.272004 | 1.23 | 0.096017 |
| *Ppara* | 0.87 | 0.057084 | 1.25 | 0.098647 | 0.82 | **0.047848** | 0.89 | **0.009824** | 0.91 | 0.184816 |
| *Pparg* | 0.87 | 0.726373 | 1.26 | 0.092874 | 0.87 | 0.408909 | 0.85 | 0.460622 | 1.08 | 0.660362 |
| *Ppargc1a* | 1.06 | 0.509539 | 1.30 | **0.031855** | 0.84 | **0.008754** | 1.18 | **0.030581** | 1.37 | **0.006090** |
| *Ptpn1* | 0.77 | **0.007293** | 1.00 | 0.985874 | 0.95 | 0.394977 | 0.88 | 0.070411 | 0.81 | **0.040062** |
| *Pygl* | 0.88 | 0.258615 | 0.91 | 0.332646 | 0.73 | **0.013445** | 0.75 | **0.013689** | 0.76 | 0.136160 |
| *Rab4a* | 1.09 | 0.514078 | 1.21 | 0.142778 | 0.79 | 0.068140 | 1.03 | 0.814686 | 1.01 | 0.928856 |
| *Retn* | **2.01** | **0.003905** | **2.16** | **0.045615** | 1.60 | 0.057052 | 1.65 | 0.069623 | **2.48** | 0.050720 |
| *Sell* | 1.35 | 0.436817 | 1.69 | 0.138067 | 1.05 | 0.780693 | 1.91 | 0.219637 | 1.90 | 0.129263 |
| *Serpine1* | **0.41** | 0.214996 | **0.48** | 0.072792 | 1.24 | 0.461237 | **0.23** | **0.030061** | **0.43** | 0.069495 |
| *Slc14a2* | 1.22 | 0.489476 | 1.48 | 0.137891 | 0.76 | 0.787523 | 1.38 | 0.170504 | 1.47 | 0.087868 |
| *Slc2a4* | **0.45** | **0.012590** | 0.75 | 0.220971 | 0.93 | 0.661803 | 0.55 | **0.024100** | 0.52 | 0.072572 |
| *Snap23* | 1.18 | 0.144446 | 1.25 | **0.007938** | 0.93 | 0.356643 | 1.12 | 0.257316 | 1.17 | 0.085628 |
| *Snap25* | 1.12 | 0.206643 | 1.82 | **0.029822** | 0.87 | 0.116280 | 1.16 | 0.166500 | 1.39 | **0.036873** |
| *Sod2* | 1.00 | 0.959722 | 1.18 | **0.022647** | 0.90 | 0.179794 | 1.05 | 0.326960 | 1.01 | 0.843811 |
| *Srebf1* | **0.46** | **0.009925** | 0.71 | 0.116093 | 0.69 | 0.125908 | 0.50 | **0.016544** | **0.39** | **0.008837** |
| *Stx4* | 0.83 | **0.015986** | 1.16 | 0.092330 | 0.99 | 0.747363 | 0.88 | **0.027464** | 0.99 | 0.795585 |
| *Stxbp1* | 0.64 | **0.016286** | 1.11 | 0.454667 | 0.80 | 0.089751 | 0.70 | **0.013669** | 0.71 | **0.030191** |
| *Stxbp2* | 0.91 | 0.248381 | 1.18 | 0.067470 | 0.95 | 0.312381 | 0.98 | 0.809537 | 0.94 | 0.665842 |
| *Stxbp4* | 0.86 | 0.269574 | 1.31 | 0.082042 | 0.74 | 0.097190 | 0.80 | 0.227806 | 1.00 | 0.932379 |
| *Tgfb1* | 0.62 | 0.194598 | 0.64 | **0.022367** | 0.98 | 0.795431 | 0.58 | **0.035384** | 0.52 | 0.053447 |
| *Tnf* | 1.11 | 0.942151 | **2.34** | 0.221168 | **2.25** | 0.266468 | 1.36 | 0.764550 | 1.62 | 0.488268 |
| *Tnfrsf1a* | 0.69 | 0.287684 | 0.97 | 0.710123 | 0.95 | 0.577966 | 0.71 | 0.112078 | 0.67 | 0.309384 |
| *Tnfrsf1b* | **0.41** | 0.075302 | 0.71 | 0.141067 | 1.12 | 0.647023 | 0.63 | 0.116084 | 0.62 | 0.254798 |
| *Trib3* | 0.66 | 0.301035 | 0.87 | 0.326694 | 1.08 | 0.361411 | 0.75 | **0.019842** | 0.79 | 0.219030 |
| *Ucp2* | 0.61 | **0.013221** | 1.10 | 0.509814 | 1.07 | 0.362418 | 0.73 | **0.010536** | 0.67 | **0.026954** |
| *Vamp2* | 0.98 | 0.960239 | 1.35 | 0.088734 | 0.85 | **0.006724** | 1.02 | 0.673251 | 0.96 | 0.903868 |
| *Vamp3* | 0.99 | 0.979856 | 1.21 | **0.035102** | 0.79 | **0.029184** | 0.89 | 0.347198 | 1.05 | 0.625692 |
| *Vapa* | 1.08 | 0.487961 | 1.28 | **0.006550** | 0.87 | 0.097195 | 1.05 | 0.622438 | 1.21 | 0.280580 |
| *Vegfa* | 0.78 | 0.378512 | 0.93 | 0.416924 | 0.59 | **0.002975** | 0.65 | **0.014474** | 0.70 | **0.023679** |

**Table 4**
Modulation of diabetes-associated genes in RIN-m cells. Data are calculated as fold-change of treatment (C66+STZ, or B2BrBC+STZ) compared to the STZ group. Fold-change values > 2 or < 0.5 and p values < 0.5 are presented in bold.

| Gene symbol | C66+STZ *vs.* STZ | | B2BrBC+STZ *vs.* STZ | |
|---|---|---|---|---|
| | Fold change | *p*-Value | Fold change | *p*-value |
| *Ace* | 0.98 | 0.782438 | 0.70 | 0.056778 |
| *Acly* | 0.88 | 0.067158 | 0.96 | 0.759243 |
| *Adra1a* | 0.80 | 0.429704 | 1.37 | 0.472744 |
| *Adrb3* | 0.99 | 0.989412 | 0.88 | 0.410985 |
| *Agt* | 0.51 | **0.040259** | 0.50 | 0.191418 |
| *Akt2* | 0.81 | 0.115918 | 0.83 | 0.351331 |
| *Aqp2* | 0.99 | 0.842351 | 1.75 | 0.196464 |
| *Ccl5* | 1.16 | 0.674455 | 1.33 | 0.464351 |
| *Ccr2* | 1.28 | 0.519685 | 1.44 | 0.334970 |
| *Cd28* | 0.94 | 0.951886 | 0.84 | 0.546277 |
| *Ceacam1* | 0.78 | **0.012352** | 0.89 | 0.116948 |
| *Cebpa* | 0.71 | 0.308948 | 0.82 | 0.764824 |
| *Ctla4* | **2.26** | **0.014371** | 1.09 | 0.782794 |
| *Dpp4* | 1.22 | 0.360294 | 1.02 | 0.995298 |
| *Dusp4* | 0.51 | **0.007186** | 0.63 | 0.078481 |

(*continued on next page*)

**Table 4** (*continued*)

| Gene symbol | C66+STZ *vs.* STZ | | B2BrBC+STZ *vs.* STZ | |
|---|---|---|---|---|
| | Fold change | *p*-Value | Fold change | *p*-value |
| *Enpp1* | 0.86 | 0.128236 | 0.95 | 0.769316 |
| *Fbp1* | 0.83 | 0.509380 | 1.54 | 0.268827 |
| *Foxc2* | 0.82 | 0.797415 | 1.15 | 0.648132 |
| *Foxg1* | 1.08 | 0.669006 | 1.05 | 0.697111 |
| *Foxp3* | 0.87 | 0.127724 | 0.91 | 0.668050 |
| *G6pc* | 0.77 | 0.457808 | 0.87 | 0.867046 |
| *Gcg* | 1.18 | 0.615479 | 1.21 | 0.495689 |
| *Gcgr* | 0.77 | **0.008918** | 0.89 | 0.364340 |
| *Gck* | 0.97 | 0.783192 | 0.92 | 0.789639 |
| *Glp1r* | 1.04 | 0.649724 | 1.05 | 0.485572 |
| *Gpd1* | 0.55 | **0.006428** | 0.66 | 0.119709 |
| *Gsk3b* | 0.94 | 0.471547 | 0.95 | 0.523059 |
| *Hmox1* | 0.55 | **0.002303** | 0.83 | 0.361476 |
| *Hnf1b* | 0.79 | 0.129962 | 0.88 | 0.509003 |
| *Hnf4a* | 0.78 | 0.087534 | 0.82 | 0.392577 |
| *Icam1* | **0.30** | **0.004890** | **0.36** | **0.013435** |
| *Ide* | 1.01 | 0.918710 | 1.02 | 0.701508 |
| *Ifng* | 0.89 | 0.905658 | 1.54 | 0.129612 |
| *Igfbp5* | 0.60 | **0.048454** | **0.48** | **0.015412** |
| *Ikbkb* | 0.72 | **0.008403** | 0.77 | 0.141287 |
| *Il10* | 1.50 | 0.078304 | 1.01 | 0.929047 |
| *Il12b* | 0.78 | 0.096056 | 1.00 | 0.904880 |
| *Il4ra* | 0.62 | **0.005662** | 0.67 | 0.076250 |
| *Il6* | 0.98 | 0.967015 | 1.27 | 0.506446 |
| *Inppl1* | 0.85 | 0.208833 | 0.83 | 0.364745 |
| *Ins1* | 1.33 | **0.002043** | 1.57 | **0.031862** |
| *Irs1* | 0.99 | 0.943609 | 1.10 | 0.299811 |
| *Irs2* | 0.99 | 0.846850 | 0.96 | 0.884641 |
| *Mapk14* | 0.84 | 0.165783 | 0.80 | 0.216964 |
| *Mapk8* | 1.58 | 0.297950 | **2.27** | 0.059805 |
| *Neurod1* | 1.22 | **0.038389** | 1.21 | 0.115533 |
| *Nfkb1* | 0.68 | **0.032327** | 0.68 | 0.147947 |
| *Nkx2–1* | 0.90 | 0.801834 | 0.82 | 0.309017 |
| *Nos3* | 0.85 | 0.327970 | 0.92 | 0.592540 |
| *Nrf1* | 1.01 | 0.950017 | 1.11 | 0.592199 |
| *Nsf* | 1.09 | 0.313035 | 1.00 | 0.970572 |
| *Parp1* | 1.02 | 0.756985 | 1.00 | 0.980363 |
| *Pdx1* | 1.09 | 0.317388 | 1.17 | 0.253820 |
| *Pik3cd* | 0.76 | 0.277712 | 0.81 | 0.473043 |
| *Pik3r1* | 1.12 | 0.099242 | 1.22 | **0.024235** |
| *Ppara* | 1.09 | 0.312078 | 1.11 | 0.310441 |
| *Pparg* | 0.98 | 0.964359 | 1.24 | 0.313684 |
| *Ppargc1a* | 1.40 | **0.002691** | 1.63 | **0.001441** |
| *Ptpn1* | 0.93 | 0.321868 | 0.86 | 0.133497 |
| *Pygl* | 1.02 | 0.766786 | 1.04 | 0.757399 |
| *Rab4a* | 1.31 | 0.070675 | 1.27 | 0.146886 |
| *Retn* | 1.03 | 0.856782 | 1.55 | 0.184355 |
| *Sell* | 1.82 | 0.249638 | 1.81 | 0.162207 |
| *Serpine1* | **0.19** | **0.000536** | **0.34** | **0.002054** |
| *Slc14a2* | 1.81 | 0.255999 | 1.92 | 0.186128 |
| *Slc2a4* | 0.59 | **0.016313** | 0.56 | 0.083723 |
| *Snap23* | 1.20 | 0.160331 | 1.25 | 0.065766 |
| *Snap25* | 1.33 | **0.046461** | 1.60 | **0.016673** |
| *Sod2* | 1.17 | 0.077522 | 1.12 | 0.133450 |
| *Srebf1* | 0.73 | 0.178899 | 0.57 | 0.067244 |
| *Stx4* | 0.89 | **0.036290** | 1.00 | 0.950339 |
| *Stxbp1* | 0.88 | 0.170383 | 0.88 | 0.302448 |
| *Stxbp2* | 1.03 | 0.630033 | 0.99 | 0.969908 |
| *Stxbp4* | 1.08 | 0.607812 | 1.35 | 0.187497 |

(*continued on next page*)

**Table 4** (*continued*)

| Gene symbol | C66+STZ *vs.* STZ | | B2BrBC+STZ *vs.* STZ | |
|---|---|---|---|---|
| | Fold change | *p*-Value | Fold change | *p*-value |
| *Tgfb1* | 0.60 | **0.017564** | 0.53 | **0.040951** |
| *Tnf* | 0.60 | 0.264906 | 0.72 | 0.459048 |
| *Tnfrsf1a* | 0.75 | 0.191680 | 0.71 | 0.406916 |
| *Tnfrsf1b* | 0.57 | 0.111778 | 0.56 | 0.192562 |
| *Trib3* | 0.70 | **0.001330** | 0.73 | 0.095757 |
| *Ucp2* | 0.68 | **0.004035** | 0.63 | **0.013637** |
| *Vamp2* | 1.20 | **0.033369** | 1.13 | 0.396985 |
| *Vamp3* | 1.13 | 0.247775 | 1.33 | **0.030829** |
| *Vapa* | 1.20 | 0.119955 | 1.39 | 0.121049 |
| *Vegfa* | 1.10 | 0.329474 | 1.17 | 0.145781 |

## Limitations

This study is limited by its use of an *in vitro* model of rat pancreatic RIN-m cells, which may not fully replicate the gene expression patterns found in diabetic patients or animal models. Furthermore, while the data provide insights into gene modulation by MACs, C66 and B2BrBC, the translation of these findings to clinical applications requires further validation through *in vivo* studies.

## Ethics Statement

The authors have read and followed the ethical requirements for publication in Data in Brief and confirmed that the current work does not involve human subjects, animal experiments, or any data collected from social media platforms.

## Credit Author Statement

Conceptualization: R.S., N.H.-P., J.B., M.M., D.A.; Data curation: R.S., S.V.; Formal analysis: R.S., D.A.; Resources: D.A., L.P.; Writing - original draft, R.S., D.A., N.H.-P.; Writing - review & editing, R.S., D.A., N.H.-P., L.P.

## Data Availability

Expression of diabetes-related genes in rodent $\beta$-cell line (RIN-m) treated with monocar bonyl curcumin analogues (C66 and B2BrBC) in presence or absence of streptozotocin – PCR array data (Original data) (Mendeley Data).

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## Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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