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PDGF-BB carried by endothelial cell-derived extracellular vesicles reduces vascular smooth muscle cell apoptosis in diabetes

Gabriele Togliatto¹, Patrizia Dentelli¹, Arturo Rosso¹, Giusy Lombardo¹, Maddalena Gili¹, Sara Gallo¹, Chiara Gai¹, Anna Solini², Giovanni Camussi^{1*}, Maria Felice Brizzi^{1*}

¹Department of Medical Sciences, University of Torino, Italy

²Department of Surgical, Medical, Molecular and Critical Area Pathology, University of Pisa, Italy

GT and PD equally contributed

*Address correspondence to:

Maria Felice Brizzi and Giovanni Camussi, Department of Medical Sciences, University of Turin, Corso Dogliotti 14, 10126, Turin

mariafelice.brizzi@unito.it

giovanni.camussi@unito.it

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1 ABSTRACT

Endothelial cell-derived extracellular vesicles (CD31EVs) are a new entity for therapeutic/prognostic
purposes. The roles of CD31EVs as mediators of smooth muscle cell (VSMC) dysfunction in type 2
diabetes (T2D) is investigated herein.

We demonstrated that, unlike non-diabetic, diabetic serum-derived-EVs (D-CD31EVs) boosted 5 apoptosis resistance of VSMCs cultured in hyperglycaemic condition. Biochemical analysis revealed 6 7 that this effect relies on changes in the balance between anti-apoptotic/pro-apoptotic signals: increase of bcl-2 and decrease of bak/bax. D-CD31EV cargo analysis demonstrated that D-CD31EVs are 8 enriched in membrane-bound-platelet-derived-growth-factor-BB (mbPDGF-BB). Thus, we 9 postulated that mbPDGF-BB transfer by D-CD31EVs could account for VSMC resistance to 10 apoptosis. By depleting CD31EVs of PDGF-BB or blocking the PDGF-BB-receptorβ on VSMCs, we 11 12 demonstrated that mbPDGF-BB contributes to D-CD31EV-mediated bak/bax and bcl-2 levels. Moreover, we found that bak expression is under the control of PDGF-BB-mediated miR-296-5p 13 expression. In fact, while PDGF-BB-treatment recapitulated D-CD31EV-mediated anti-apoptotic 14 program and VSMC resistance to apoptosis, PDGF-BB-depleted CD31EVs failed. D-CD31EVs also 15 increased VSMC migration and recruitment to neovessels, by means of PDGF-BB. Finally, we found 16 17 that VSMCs, from human atherosclerotic arteries of T2D individuals, express low bak/bax and high bcl-2 and miR-296-5p levels. This study identifies the mbPDGF-BB in D-CD31EVs as a relevant 18 19 mediator of diabetes-associated VSMC resistance to apoptosis.

21 INTRODUCTION

22 Cardiovascular complications are a leading cause of morbidity and premature mortality in diabetes (1,2). Structural alterations to vessel walls result in intima-media thickening which marks 23 individuals at high risk to develop acute cardiovascular events (3,4). Moreover, restenosis is still a 24 major complication in the diabetic setting. A main-cause of re-occlusion is intimal hyperplasia which 25 is due to the migration and/or excessive growth of vascular smooth muscle cells (VSMCs). A 26 dysregulated balance between apoptosis and the proliferation of VSMCs seems to play a crucial role 27 in intima-media thickening in diabetic individuals (5,6). Indeed, in vitro studies have suggested that 28 high glucose (HG) induces the expression of bcl-2 family members and inhibits the apoptotic protein 29 Inhibitor of Apoptosis Protein 1, (IAP-1) in VSMCs (7). In addition, Ruiz et al. (8) have demonstrated 30 that VSMCs, recovered from diabetic patients, showed a resistance to apoptosis which was possibly 31 due to bcl-2 over-expression. Although circulating high glucose concentration might per se induce 32 VSMC dysfunction, additional events can contribute to this process in vivo. 33

Several studies have focused on extracellular RNA (exRNA) transporters, indicating that they 34 may be present in biological fluids in the form of vesicles, which have been denoted microvesicles, 35 exosomes, membrane particles and apoptotic bodies (9,10). Despite the lack of consensus on vesicle 36 classification, the presence of overlapping characteristics and biological activity has evoked the use 37 of the inclusive term; "extracellular vesicles" (EVs) (11,12). The paracrine/endocrine effects of EVs 38 have recently gained significant attention (13,14). Indeed, EV biological activity has been linked to 39 the transfer of bioactive molecules, including proteins and microRNA (miRs) (10-14). EVs are widely 40 distributed in human body fluids, while circulating EV cargo usually reflects the cell of origin in its 41 physiological and/or pathological condition (9-15). Indeed, the number and cargo of circulating EVs 42 43 have been suggested as a means to predict the presence of disease and even the risk of developing disease (16,17). 44

Increased levels of circulating platelet- and endothelial cell- (EC) derived microparticles have
been proposed as "biomarkers" of cell dysfunction (18,19). However, EVs might also deliver specific
drivers of disease, as they behave as diffusible vectors of biological activity and participate in
exchanging information. This study therefore investigates the role of EC-derived EVs as mediators
of VSMC fate in type 2 diabetes (T2D).

51 RESEARCH DESIGN AND METHODS

52 Reagents and antibodies are reported in Supplemental Table 1.

Patients and Controls. 11 T2D and 6 non-diabetic individuals (controls), who had undergone carotid endoarteriectomy surgery in our clinic, were included in the study. Clinical characteristics are reported in Supplemental Table 2. All diabetic individuals were under statin and metformin treatment. Ethical approval was obtained from Azienda Ospedaliero-Universitaria (AOU), Città della Salute e della Scienza di Torino, Italy. Informed consent was obtained from all individuals in accordance with the Declaration of Helsinki. We had no direct contact with the participants.

Isolation of VSMCs from human atherosclerotic plaque specimens. Human atherosclerotic 59 60 plaque specimens were recovered from the above reported subjects (T2D: D; non-diabetic: ND) and processed as previously described (20). Vascular tissue was rinsed 3 times with phosphate-buffered 61 saline (PBS) and intima was removed in order to furnish the VSMCs. Tunica media were finely cut 62 into 2-3 mm pieces and subjected to enzymatic digestion using collagenase type I (0.1mg/ml) in a 63 Dulbecco's Modified Eagle Medium (DMEM) for 1.5h at 37°C. Digestion media were collected and 64 filtered through nylon mesh cell strainers (100µm) to remove the undigested explants. The resulting 65 supernatants were centrifuged at 1200 rpm for 10 min and cells were plated at 2.5×10⁴ cells/cm² and 66 cultured with Modified Eagle Medium (MEM) supplemented with 20% (v/v) foetal bovine serum 67 (FBS), 1% penicillin-streptomycin. Fluorescence-activated cell sorting (FACS) analysis was 68 performed on D-VSMCs and ND-VSMCs to characterize them, as indicated in (20), using antibodies 69 directed to CD31 and alpha-smooth muscle actin (a-SMA), directly or indirectly conjugated with 70 71 fluorescein isothiocyanate (FITC) fluorochrome. FITC mouse non-immune isotypic IgG (BD Bioscience Pharmingen) was used as control. 72

Cell cultures. Primary macrovascular endothelial cells (ECs) and VSMCs were purchased from
Lonza (Basel, Switzerland) and cultured as described by the manufacturer's instructions. VSMCs and

ECs were used at II-III cell-culture passage. To collect the EVs, ECs were starved under either low 75 76 (LG, 5mmol/l) or high glucose (HG, 25 mmol/l) and 24h deprived of bovine calf serum (BCS). Cell viability was evaluated. siRNA technology was also performed in HG-cultured ECs using siRNA 77 negative control or the Platelet-Derived Growth Factor (PDGF-BB) siRNA (Applied Biosystems) 78 (21). EV isolation was obtained from HG-cultured ECs depleted of PDGF-BB. In selected 79 experiments, VSMCs were cultured in LG or HG and then treated in the presence of ND-CD31EVs, 80 D-CD31EVs or EC-derived-EVs (5×10³ EVs/target cell), or stimulated with PDGF-BB. In selected 81 experiments, HG-cultured VSMCs were pre-incubated with a blocking PDGF-Receptor- β (PDGFR β) 82 antibody (5µg/ml). Details are reported in Supplemental Materials. All experiments were performed 83 in accordance with European Guidelines and policies and approved by the Ethical Committee of the 84 University of Turin. 85

Isolation and characterization of CD31EVs from sera of T2D and non-diabetic individuals. 86 Human serum from all above T2D and non-diabetic individuals was obtained before surgery and after 87 informed consent. EVs from each participant were obtained by centrifuging serum as previously 88 89 described (22). The supernatant was subsequently submitted to differential ultracentrifugation at 10k and 100k g for 2h at 4°C. EV pellets were then re-suspended in DMEM and stored at -80°C. FACS 90 91 analysis of D-EVs and ND-EVs was performed as indicated in (23), using anti-CD31allophycocyanin (APC), anti-CD14-phycoerythrin (PE) and anti-CD42b-FITC antibodies. FITC, PE 92 or APC mouse non-immune isotypic IgG (BD Bioscience Pharmingen) were used as controls. FACS 93 analysis was performed using a Guava easyCyteTM Flow Cytometer (Millipore, Germany). 94 Fluorochrome conjugated antibodies were added to a suspension of EVs $(2.5 \times 10^6 \text{ particles}/100 \text{ µl})$ 95 96 for 15 min at 4°C. Surface marker expression is reported in the representative histograms as the percentage of expression±SD. The CD31 microbead kit (Miltenyi Biotec, Auburn, CA, USA) was 97 used to isolate CD31EVs from the sera of T2D (D-CD31EVs) and non-diabetic individuals (ND-98 99 CD31EVs) (24). Briefly, 0,5 ml of freshly-thawed plasma was incubated with 100 µl of CD31

microbeads for 4h at 4°C. EVs captured on CD31 Ab-coated magnetic beads were recovered from
the magnetic column (MS column) as described in the manufacturer's instructions. EV-bound beads
were submitted to differential ultracentrifugation (Beckman Coulter Optima L-90K ultracentrifuge;
Beckman Coulter, Fullerton, CA) for 3h at 4°C. CD31EVs were either used fresh or were stored at 80°C and then processed for transmission electron microscopy (TEM), biological effects, western
blot and q-RT-PCR analysis. CD63 content in CD31EVs was analyzed by western blot. Details are
reported in Supplemental Materials.

Transmission electron microscopy. TEM was performed on CD31EVs that had been isolated by ultracentrifugation and re-suspended in PBS, placed on 200 mesh nickel formvar carbon coated grids (Electron Microscopy Science, Hatfield, PA) and left to adhere for 20 min. Grids were then processed as previously described (25) and observed under a Jeol JEM 1010 electron microscope (Jeol, Tokyo, Japan). Details are reported in Supplemental Materials.

Isolation of EC-derived EVs. ECs were cultured in LG or HG DMEM without BCS for 24h, in order to collect the EVs from supernatants as previously described (21,22) and detailed in Supplemental Materials. EV number and size distribution analysis was performed using a NanoSight LM10 (NanoSight Ltd, Minton Park UK). Results were displayed as number per ml and as a frequency size distribution graph, outputted to a spreadsheet. EC-derived-EVs (LG-EVs or HG-EVs) were processed for biological, western blot and q-RT-PCR analysis (21,22).

Western blot analysis. Cells and EVs were lysed and protein concentrations were obtained, as
previously described (25). Protein levels were normalized to α-SMA, β-actin, or CD63 content.
Details are reported in Supplemental Materials.

121 EV internalization. The internalization of EVs was evaluated using confocal microscopy (LSM5-

122 PASCAL; Zeiss, Oberkochen, Germany) as previously described (25). EV pellets were added to HG-

cultured VSMCs (2x10⁴) pre-treated or not with a blocking PDGFRβ antibody. Z-stack confocal
 microscopy VSMC images were also obtained (25). Details are reported in Supplemental Materials.

RNA isolation and quantitative real-time PCR (gRT-PCR) for miRs. Total RNA was isolated 125 from the VSMCs of atherosclerotic plaque specimens and from human VSMCs, that had been treated 126 as indicated or left untreated, using the TRIzol reagent (Invitrogen) as previously described (26). 127 RNA from cells and EVs was then reverse-transcribed using a TaqMan microRNA RT kit, specific 128 for miR-24-3p, miR-221, miR-222 and miR-296-5p, or a Syber Green microRNA RT Kit specific for 129 miR-21-5p, miR-29a and miR-145, as indicated. miR expression was normalized to the small nuclear 130 RNA, RNU6B. Loss- and gain-of-function experiments were performed in VSMCs that had been 131 transfected with the antago-miR control, the antago-miR-296-5p, pre-miR control or pre-miR-296-132 133 5p oligonucleotides (Applied Biosystem), according to manufacturer's instructions (26). Details are reported in Supplemental Materials. 134

Luciferase miRNA target reporter assay. The luciferase reporter assay was performed using a
construct generated by subcloning the PCR products amplified from the full-length 3'UTR of human *BAK1* DNA into the Xba restriction site of the luciferase reporter vector pGL3 (Promega, Madison,
WI, USA). The PCR products were obtained using the primers for *BAK1* and reported in detail in
Supplemental Materials (26).

Cell proliferation and apoptosis assay. Proliferative activity was assayed as previously described
(27). For the apoptosis assay, VSMCs were subjected to Muse Annexin V and the cell dead assay
(Merck, Darmstadt, Germany) in accordance with manufacturer's instructions. Details are reported
in Supplemental Materials.

Tubule-like structure formation assay. To analyze the EC/VSMC interaction, 24-well-plates were
coated with growth factor-reduced Matrigel matrix (BD Biosciences) (28). Briefly, HG-cultured ECs
and VSMCs were pre-treated, for 24h, with either D-CD31EVs, ND-CD31EVs or HG-EVs that had
either been depleted, or not, of PDGF-BB. 4.5x10⁴ red labeled ECs (PKH26 vital dye) were placed

in HG medium on top of the polymerized matrix. 2x10⁴ green labeled VSMCs (PKH67 vital dye)
were then added to ECs. Details are reported in Supplemental Materials.

Scratch assay on VSMCs. Scratch assays were performed on HG-cultured VSMCs, treated as indicated, to evaluate cell migration activity. VSMCs were seeded to a final density of 100,000 cells per well for 24h in order to allow cell adhesion and the formation of a confluent monolayer to occur. Details are reported in Supplemental Materials.

ELISA Assays. PDGF-BB concentration in D-CD31EVs were measured using a commercially available competitive enzyme immunoassay (ELISA) kit (R&D Systems, MN, USA), according to manufacturer's instructions. To evaluate mbPDGF-BB, intact or lysates D-CD31EVs (2.5x10⁸ particles) were compared. The same samples were pre-treated with trypsin (0.25%) for 1h (negative control). Details are reported in Supplemental Materials.

Statistical analysis. All data are presented as mean \pm SEM, unless otherwise reported. The 159 D'Agostino-Pearson test was used to test normality. Data on in vitro angiogenesis, cell proliferation, 160 ELISA, apoptosis and scratch assays, on qRT-PCR-miR expression, loss- and gain-of-function 161 experiments, characterization of recovered EVs and, lastly, on the densitometric analysis for Western 162 blots were analyzed using the Student t tests for 2-group comparison and using 1-way ANOVA, 163 followed by Tukey's multiple comparison test, for ≥ 3 groups. All western blot experiments were 164 performed in triplicate. The minimum sample size was four experiments performed in triplicate, thus 165 ensuring 90% statistical power among experimental groups, and a probability level of 0.05, two-tailed 166 hypothesis. The cut-off for statistical significance was set at P < 0.05. All statistical analyses were 167 168 carried out using GraphPad Prism version 5.04 (Graph Pad Software, Inc).

170 **RESULTS**

171 D-CD31EVs potentiate VSMCs resistance to apoptosis in high glucose (HG) conditions

Circulating EVs are able to modulate cell fate (9,10,13). It was therefore decided to investigate 172 173 whether and how circulating EVs, derived from ECs of T2D-individuals (D-EVs), may impact on VSMC fate. Guava analysis was used to demonstrate the presence of a high percentage of EVs of 174 endothelial origin in the sera of non-diabetic (ND-EVs) and T2D individuals (Figure 1A). A 175 significant reduction of EVs from T2D individuals was detected (Figure 1A). EC-derived EVs from 176 sera were therefore isolated using CD31-coated magnetic beads (ND-CD31EVs and D-CD31EVs) 177 178 and analyzed using transmission electron microscopy (Figure 1B) and western blot (Figure 1C). Functional studies were then performed to evaluate the biological relevance of D-CD31EVs in 179 mediating VSMC dysfunction in hyperglycaemic condition (HG-culture condition). LG-conditioned 180 181 VSMCs served as control. Consistent with data provided by Ruiz et al. (8), we found that, unlike LG, HG treatment was associated with a significant up-regulation of bcl-2 and down-regulation of bak/bax 182 (Supplemental Figure S1A). By contrast the expression of another member of the bcl-2 protein 183 family, bcl2l2, did not change (Supplemental Figure S1B). Moreover, HG treatment per se 184 significantly decreased the number of apoptotic cells, without affecting VSMC proliferation 185 186 (Supplemental Figure S1C-S1D). Functional studies were then performed on VSMCs cultured in HG conditions and treated with CD31EVs. As shown in Figure 1D, D-CD31EVs, unlike ND-CD31EVs, 187 were able to further reduce both the number of apoptotic VSMCs and bak/bax content and increase 188 189 bcl-2 level (Figure 1E).

D-CD31EVs are enriched in PDGF-BB

The transfer of proteins and/or genetic information into recipient cells is the main mechanism of EV action (9,10,13,14). CD31EV protein cargo and, in particular, the content of well-known VSMC proliferation/survival factor, PDGF-BB, were therefore analyzed in both CD31EVs and EVs recovered from LG- and HG-treated ECs. Supplemental Figure S2A shows Nanosight analysis of EVs recovered from LG- or HG-cultured ECs (LG-EVs or HG-EVs). No differences in EV size and number between LG-EVs and HG-EVs were detected (data not shown). Conversely, PDGF-BB was found to be enriched only in D-CD31EVs (Figure 2A) and in HG-EVs (Supplemental Figure S2B).

198 Membrane bound-PDGF-BB drives D-CD31EV anti-apoptotic cues

LG- and HG-cultured VSMCs were treated with PDGF-BB in order to investigate the contribution of 199 PDGF-BB in mediating D-CD31EV biological effects. In fact, PDGF-BB further increased bcl-2 200 content, while reducing the number of apoptotic cells and bak/bax content in HG-conditioned 201 VSMCs. Conversely, these effects were not detected in VSMCs cultured in LG conditions (Figure 202 2B-2C). siRNA technology was therefore harnessed to abrogate PDGF-BB expression in EVs (Figure 203 2D-2E) and validate the role of PDGF-BB in regulating D-CD31EV survival signals in HG 204 205 conditions. As expected, PDGF-BB-depleted EVs were no longer able to either increase bcl-2, or decrease bak/bax expression (Figure 2F) and the number of apoptotic cells (Figure 2G). To investigate 206 whether different mechanisms might account for free PDGF-BB and D-CD31EV-PDGF-BB-induced 207 effects, HG-cultured VSMCs were pre-treated with a blocking PDGFRß antibody, stimulated with 208 209 D-CD31EVs or free PDGF-BB, and analyzed for bak/bax and bcl-2 expression. As shown in Figure 3A PDGFRß blockade impacts on both free PDGF-BB and D-CD31EVs-mediated bak/bax and bcl-210 2 expression. To rule out the possibility that this effect depended on inhibition of PDGFRβ-mediated 211 EV internalization, Z-stack analysis was performed. Figure 3B shows that PDGFRβ blockade did not 212 213 hamper EV internalization. Of note, the ELISA assay led to the discovery that PDGF-BB was anchored to the membrane of D-CD31EVs (Figure 3C) indicating that EV-mbPDGF-BB, by binding 214 to the PDGFR β , might drive D-CD31EV biological effects. 215

D-CD31EVs induce VSMC migration and recruitment to neovessels via PDGF-BB-mediated effects

CD31EVs were also evaluated in an EC/VSMC co-culture assay. A reduced number of vessels was detected in HG-cultured ECs (data not shown) and D-CD31EVs were nevertheless able to promote VSMC recruitment to neo-formed tubule-like structures (Figure 4A-4B), unlike ND-CD31EVs. A scratch assay also highlighted increased VSMC motility upon D-CD31EV treatment (Figure 4C). As shown in Supplemental Figure S2C, these effects did not depend on differences in EV-VEGF content. Furthermore, the contribution of PDGF-BB to both processes was validated in experiments using PDGF-BB-depleted EVs; such EVs failed to induce either effects (Figure 4D-F).

T2D individual-derived VSMCs express high bcl-2 and low bak/bax content

To validate the above results VSMCs isolated from either T2D (D) or non-diabetic (ND) human atherosclerotic plaque specimens were analyzed for bak/bax and bcl-2 expression. As shown in Figure 5A, the majority of the recovered cells express VSMC marker. Moreover, as previously reported by Ruiz et al. (8), it was confirmed that D-VSMCs expressed high bcl-2 levels. In addition, we found that D-VSMCs also expressed low bak/bax content (Figure 5B-5C).

miR-296-5p-post-transcriptionally controls bak level in response to HG and D-CD31EVs

To gain further insight into the mechanisms regulating VSMC fate the expression of miRs potentially 232 involved in this process was first analyzed in D-VSMCs and compared to ND-VSMCs. As shown in 233 Figure 6A, no significant differences were detected in the expression of miR-21-5p, miR-24-3p, miR-234 145, miR-29a (not included in the panel: CT>38), miR-221 and miR-222 between D- and ND-235 236 VSMCs (29-30). Moreover, since bak, unlike bax, is one of miR-296-5p putative target genes (TarBase v7.0) (31) its expression was also analyzed. Indeed, high miR-296-5p levels was detected 237 in D-VSMCs (Figure 6A). In order to validate the role of miR-296-5p in controlling bak expression, 238 239 VSMCs cultured in LG- or HG-conditions were analyzed for miR-296-5p expression. As shown in Figure 6B an increased miR-296-5p expression was detected upon HG treatment. Moreover, the 240 depletion of miR-296-5p in HG-cultured VSMCs (Supplemental Figure S3) led to the decrease of 241

bcl-2 levels, the increase of bak/bax content (Figure 6C) and a consistent increase in the number of
apoptotic cells (Figure 6D). To confirm the role of miR-296-5p in bak post-transcriptional regulation,
the full-length 3'UTR *BAK1* nucleotide sequence was analyzed for miR-296-5p blasting sequences
revealing several base pairings (1138–1158bp) (Figure 7A). The luciferase assay was used to
demonstrate that bak is indeed a direct miR-296-5p target (Figure 7B). This observation was further
validated by gain-of-function experiments (Figure 7C-7D).

In order to investigate the contribution of PDGF-BB in mediating miR-296-5p expression, LG- and
HG-cultured VSMCs were also treated with PDGF-BB. As shown in Figure 6E, PDGF-BB further
increased miR-296-5p only in HG-cultured VSMCs. These results were validated by siRNA
technology (Figure 6F), thus suggesting that VSMC survival may be under the control of miR-2965p.

253 D-CD31EVs are almost depleted of miR-296-5p content

To exclude the possibility that D-CD31EV-mediated effects could also depend on the delivery of miR-296-5p, the miR-296-5p content was also evaluated in CD31EVs and LG- or HG-cultured ECderived EVs (LG-EVs or HG-EVs). Almost undetectable levels of miR-296-5p were found in D-CD31EVs (Supplemental Figure S2D) and in EVs from HG-treated ECs (Supplemental Figure S2E). Thus, the role of mbPDGF-BB-D-CD31EVs in mediating miR-296-5p-driven post-transcriptional regulation of bak and its down-stream events was further strengthened.

261 **DISCUSSION**

Atherosclerosis and its associated complications is a major cause of death worldwide (32). 262 Diabetes accelerates atherosclerosis and restenosis after angioplasty (33,34). Indeed, increased 263 VSMC migration and survival/proliferation are crucial for restenosis, particularly in diabetics (35-264 37). In vitro and ex-vivo studies have shown that the up-regulation of bcl-2/bcl-xl is crucial for VSMC 265 resistance to apoptosis in diabetes (7,8,38,39). Moreover, Li H et al. (7) have reported that, while HG 266 enhances the expression of bcl-2 family members in VSMCs, it reduced the expression of the IAP1. 267 We herein demonstrate that VSMCs, exposed to HG concentrations, up-regulate bcl-2 and down-268 regulate bak/bax, without affecting VSMC proliferation. Moreover, we discovered that these effects 269 are boosted by D-CD31EV treatment. A cell's survival or death depends on the integrity of the 270 271 mitochondrial outer membrane (MOM) (40). In this regard, while the pro-apoptotic proteins, bak and bax, are involved in the permealization of MOM, the anti-apoptotic bcl-2 family members counteract 272 such pro-apoptotic signals by preventing cytochrome c efflux (40). Our results therefore indicate that 273 274 an additional shift in the balance, from apoptotic to anti-apoptotic signals, might be the main mechanism behind - D-CD31EVs-induced resistance to apoptosis in HG conditions, and suggest that 275 hyperglycaemia-mediated cues preferentially translate into VSMC resistance towards apoptosis 276 rather than VSMC proliferation. 277

The genetic material in EV cargo has sparked considerable interest. The role of miRs as 278 mediators of epigenetic changes has been extensively reported, particularly in diabetes (41,42). The 279 transfer of miRs into recipient cells has been described as a relevant mechanism of EV biological 280 281 action (9-14). As a matter of fact, Gu et al. (43) recently reported that the transfer of miR-195 from EC-derived EVs to VSMCs regulates VSMC proliferation. Despite the ability of D-CD31EVs to 282 283 induce functional changes in VSMCs, our results demonstrate that D-CD31EV-mediated VSMC dysfunction relies on a mechanism independent of the delivery of miRs. Indeed, EVs also transport 284 and deliver proteins which can affect VSMC fate, including PDGF-BB. PDGF-BB is a growth factor 285

known to regulate VSMC outcomes (44,45). In this regard, PDGF-BB derived from platelet and EC 286 287 is considered a relevant mediator of VSMC dysfunction and restenosis (46). As a matter of fact, we demonstrate that D-CD31EVs are enriched in PDGF-BB and that PDGF-BB enriched D-CD31EVs 288 may contributes to VSMC dysfunction in diabetic setting. Several lines of evidence indicate that 289 downstream signaling events, activated by PDGF-BB, trigger various biological processes, including 290 291 VSMC migration and recruitment to neo-formed vessels (44,45). It is worth noting that PDGF-BB 292 depleted EVs failed to induce both VSMC migration and recruitment to neovessels. This suggests that CD31EV-PDGF-BB cargo might play a crucial role in accelerating VSMC dysfunction and 293 restenosis in T2D. 294

295 PDGF-BB synthesis and release can increase in response to various stimuli including intima damage 296 (47). As shown herein, in diabetic setting, CD31EVs are a relevant circulating PDGF-BB reservoir 297 and contribute to VSMC fate. We established that PDGF-BB is bound to the membrane of CD31EVs, and is required for their biological action but not for their internalization. As a proof of concept, 298 299 PDGFRβ blockade completely hampers CD31EV-mediated bak/bax expression, without impeding their entry into the cell. This indicates that, along with free PDGF-BB, mbPDGF-BB enriched D-300 CD31EVs contribute to PDGF-BB paracrine effects (48). A co-operative action between CD31EVs 301 and platelets-derived EVs could be postulated in vivo. In fact, EVs released from platelets accumulate 302 in human atherosclerotic plaques and can induce major biological pathways by transferring their 303 PDGF-BB content (49). In line with the results presented herein, it has been recently reported that 304 EC- and platelet-derived EVs are enriched in PDGF-BB in patients with cardiovascular diseases (50). 305

miRs are key regulators of gene expression, mainly at the post-transcriptional level (51). We herein
demonstrate, both *ex vivo* and *in vitro*, that the hyperglycaemia milieu enhances miR-296-5p
expression and modulates bak content in VSMCs, and that these effects are strictly dependent on DCD31EV-PDGF-BB cargo, rather than EV-miR-296-5p delivery. In addition, a shift between antiapoptotic to pro-apoptotic signals after PDGFRβ blockade (down-regulation of bcl-2 expression) was

observed. This suggests that PDGF-BB directly, or indirectly by changing the balance of cellular
 miRs, might transcriptionally or post-transcriptionally regulate its expression. Mutually, these events
 translate in VSMC resistance to apoptosis.

Emerging evidence suggests that EVs can serve as specific diagnostic/prognostic biomarkers 314 since they can provide intercellular state information on a given disease condition (52). Increased 315 levels of "small (submicroscopic) membranous particles" of endothelial origin, such as 316 CD31⁺/annexin V⁺ and CD31⁺/CD42⁻, have been detected in circulation in patients with coronary 317 artery disease (CAD), suggesting that they may be an additional risk stratification factor (18,19). A 318 significant reduction in CD31EVs (CD31^{high}/CD42b^{low}/CD14^{low}) has been found in T2D individuals 319 in the present study. The phenotype of the "small membrane particles", which also includes apoptotic 320 321 bodies, and the lack of exosome refining (18,19) in CAD patient studies could explain the discrepancy with our results. However, increasing amounts of evidence indicate that healthy subjects and diseased 322 individuals release EVs with different cargo. 323

Our *ex vivo* and *in vitro* results, reinforce the notion that D-CD31EV cargo, rather than D-CD31EV number, is the crucial determinant of their biological activity.

The present study reports that hyperglycaemia *per se* induces epigenetic mechanisms in VSMCs by enriching the circulating CD31EV cargo with mbPDGF-BB which translates into VSMC resistance to apoptosis (Figure 8). We are also the first to demonstrate that EV-mbPDGF-BBmediated miR-296-5p overexpression and the post-transcriptional regulation of bak is a relevant mechanism of D-CD31EV action. Overall, these results identify D-CD31EV-mbPDGF-BB as a novel driver of VSMC dysfunction in diabetic setting.

332

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339	
340	DUALITY OF INTEREST
341	The authors declare that there is no duality of interest associated with this manuscript.
342	AUTHOR CONTRIBUTIONS
343	GT: performed ex vivo and in vitro experiments, EC-EV-miRs and protein analysis; PD: performed
344	in vitro angiogenesis assay and FACS analysis; GL: performed in vitro experiments and EV isolation;
345	AR: generated constructs and performed transfections; MG: performed loss- and gain-of-function
346	approaches; SG: performed Western blot analysis; CG: performed EV isolation and characterization;
347	AS: contributed to data interpretation and revised the manuscript; GC: contributed to the study
348	conception and revised the manuscript; MFB: performed the study conception design and wrote the
349	manuscript.

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511 FIGURE LEGENDS

Figure 1. D-CD31EVs increase VSMC survival. (A) Representative FACS analysis of EVs 512 recovered from sera of T2D (D, n=11) and ND individuals (ND, n=6); CD42b-FITC, CD14-PE and 513 CD31-APC were analyzed. All data are reported in the histograms (mean of percentage \pm SD) (p < 0.01, 514 D-EVs vs ND-EVs for all markers). Isotype controls were included. (B) Representative transmission 515 electron microscopy (TEM) imaging of D- and ND-CD31EVs negatively stained with NanoVan. 516 JEOL Jem 1010 electron microscope was used (black bars= 100 nm). (C) CD31EVs were lysed and 517 518 evaluated for CD31 content (CD31+), normalized to CD63. CD31EV negative (CD31-) fraction was used as the negative control. The results are representative of all samples (D, n=11; ND, n=6) 519 (p < 0.001, CD31 + vs CD31 - fraction of T2D and non-diabetic individuals). (D) Apoptosis assay was 520 applied to HG-cultured VSMCs, treated as indicated (percentage±SEM of total apoptotic cells, n=6). 521 Doxorubicin (1 μ mol/l) was used as positive control (c+) (p < 0.001, all experimental conditions vs 522 control (c+); p < 0.001, D-CD31EVs vs ND-CD31EVs and none). (E) Cell extracts from HG-cultured 523 524 VSMCs, treated with D-CD31EVs or ND-CD31EVs, were analyzed for bak/bax and bcl-2 content, normalized to α -SMA (p < 0.001, D-CD31EVs vs ND-CD31EVs and none for bak; p < 0.05, D-525 CD31EVs vs ND-CD31EVs and none for bax and bcl-2, n=6). 526

527 Figure 2. D-CD31EVs enriched in PDGF-BB induce anti-apoptotic signals (A). Negative and positive fractions of CD31EVs were analyzed by western blot for PDGF-BB, normalized to CD63. 528 The results are representative of all samples (D, n=11; ND, n=6) (p < 0.001, CD31EVs+ vs CD31EVs-529 of D and ND; p<0.001, D-CD31EVs+ vs ND-CD31EVs+ for PDGF-BB). (B) Cell extracts from LG-530 531 and HG-cultured VSMCs untreated or treated with PDGF-BB (10 ng/ml), were analyzed for bak/bax and bcl-2 content, normalized to α -SMA (PDGF-BB vs none in HG-cultured VSMCs, p < 0.001 for 532 533 bak and bax, p=0.04 for bcl-2, n=5). (C) Apoptosis assay was applied to VSMCs, treated as above (percentage±SEM of total apoptotic cells, n=6). Doxorubicin (1µmol/l) served as positive control 534 (c+) (LG-cultured VSMCs, p=0.05, all experimental conditions vs positive control (c+); HG-cultured 535

VSMCs, p=0.001, all experimental conditions vs positive control (c+), p=0.008, PDGF-BB vs none). 536 537 (D) PDGF-BB content was evaluated in HG-cultured ECs transfected or not for 48h with siRNA empty vector, used as control (control siRNA), or with PDGF-BB siRNA, and normalized to β-actin 538 (p=0.007, PDGF-BB siRNA vs none and p=0.003, PDGF-BB siRNA vs control siRNA). (E) PDGF-539 BB content was evaluated in EVs recovered from HG-cultured ECs, treated as above, and normalized 540 to CD63 (p < 0.001, PDGF-BB siRNA vs control siRNA and none). (F) Cell extracts from HG-541 542 cultured VSMCs, treated as indicated, were analyzed for bak/bax and bcl-2 content, normalized to α -SMA (p < 0.01, HG-EVs PDGF-BB siRNA vs HG-EVs control and none; n=6). (G) Apoptosis assay 543 was performed in HG-cultured VSMCs, treated as indicated (percentage±SEM of total apoptotic 544 545 cells, n=6). Doxorubicin (1 μ mol/l) served as positive control (c+) (p < 0.001, all experimental conditions vs positive control (c+); p=0.02, HG-EVs control siRNA vs none; p=0.009, HG-EVs 546 PDGF-BB siRNA vs HG-EVs control siRNA). 547

Figure 3. PDGFRβ blockade interferes with free PDGF-BB- and D-CD31EV-mediated effects. 548 (A) HG-cultured VSMCs, pre-incubated or not with a blocking PDGFRβ antibody (5µg/ml), were 549 untreated or treated with PDGF-BB (10 ng/ml) or with D-CD31EVs for 24h. Cell extracts were 550 analyzed for bak/bax and bcl-2 content, normalized to α -SMA (p < 0.001, PDGF-BB and D-CD31EVs 551 vs PDGF-BB and D-CD31EVs, pre-treated with anti-PDGFR^β antibody) (n=4). (B) VSMC-D-552 CD31EV up-take. VSMCs, pre-incubated or not with the blocking PDGFRß antibody, were evaluated 553 for the uptake of PKH26-labeled D-CD31EVs and analyzed. DAPI was used as nuclear marker. 554 Representative sections (first-middle-last) of images (Z-stack) obtained on a confocal microscope are 555 reported. Four different experiments performed in triplicate (n=4). Scale bars indicate 10 µm. (C) To 556 evaluate mbPDGF-BB, intact or lysates D-CD31EVs (2.5x10⁸ particles), untreated or treated with 557 trypsin (0,25%) for 1h, were measured using a competitive enzyme immunoassay (ELISA) kit (** 558 p < 0.01, D-CD31EVs intact and lysates vs D-CD31EVs +trypsin) (n=3). 559

Figure 4. D-CD31EVs increase VSMC migration and recruitment to tubule-like structures. (A-560 561 **B)** An *in vitro* angiogenesis assay was performed using pre-labeled ECs (red) and VSMCs (green) co-cultured in HG medium with or without the indicated CD31EVs for 6h (scale bars=20µm, 40X 562 magnification). Data are reported in the histogram as number±SEM of VSMCs per number of tubular 563 structures (p < 0.001, ND-CD31EVs vs none and D-CD31EVs; p < 0.05, D-CD31EVs vs none, n=5). 564 (C) VSMC migration assay was performed in HG conditions and the indicated treatment. (n=5, 20X 565 magnification) (p=0.04, D-CD31EVs vs none; p=0.01, D-CD31EVs vs ND-CD31EVs). (D-E) An in 566 vitro angiogenesis assay was performed, as above, using HG-EVs control siRNA or HG-EVs depleted 567 of PDGF-BB (PDGF-BB siRNA) (scale bars=20µm, 40X magnification). Data are reported in the 568 569 histogram as number±SEM of VSMCs per number of tubular structures (p<0.001, HG-EVs PDGF-BB siRNA vs HG-EVs control siRNA and none, n=5). (F) VSMC migration assay was performed in 570 HG conditions under the indicated treatment (n=5, 20X magnification) (p=0.009, HG-EVs PDGF-571 572 BB siRNA vs HG-EVs control siRNA). Representative images were acquired on a confocal microscope. 573

574 Figure 5. VSMCs from T2D individuals express high levels of bcl-2 and low bak/bax content.

(A) Representative FACS analysis of CD31 and alpha-smooth muscle cell (α -SMA) surface markers expressed by VSMCs recovered from T2D (D, n=11) and non-diabetic (ND) individuals (ND, n=6). All data are reported in the Table (mean percentage±SD). Isotype control was included. (B) bak/bax and bcl-2 content was analyzed on all ND- or D-VSMC samples, normalized to α -SMA content. The statistical analysis of all samples (D, n=11; ND, n=6) is reported in (C) (p<0.01, D vs ND for bak, p<0.001, D vs ND for bax, p<0.05, D vs ND for bcl-2).

Figure 6. VSMC miR-296-5p expression is increased in hyperglycaemic condition and boosted by PDGF-BB (A) The indicated miRs were evaluated by qRT-PCR in VSMCs recovered from T2D (D) and ND human atherosclerotic plaque specimens. Data normalized to RNU6B are representative of all samples (D, n=11; ND, n=6) (p=0.02, D vs ND for miR-296-5p). (B) miR-296-5p was evaluated

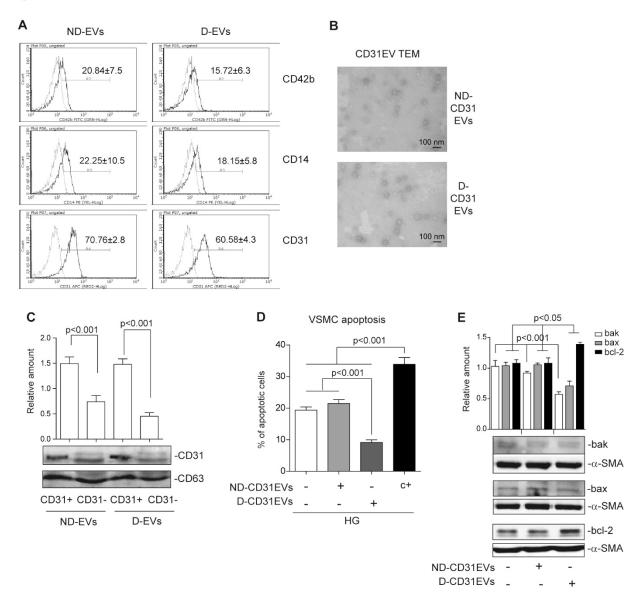
by qRT-PCR on LG- or HG-treated VSMCs and normalized to RNU6B (p=0.03, HG- vs LG-treated 585 VSMCs, n=6). (C) Loss-of-function experiments were performed on LG- and HG-cultured VSMCs 586 for 48h, using antago-miR control or antago-miR-296-5p oligonucleotides. After 48h cells were lysed 587 and analyzed for bak/bax and bcl-2 content, normalized to α -SMA (p < 0.001, LG-antago-miR control 588 and LG-anti-miR-296-5p vs HG-antago-miR control for bak/bax and bcl-2; p<0.001, HG-antago-589 miR control vs HG-antago-miR-296-5p for bak and bcl-2; p < 0.05, HG-antago-miR control vs HG-590 antago-miR-296-5p for bax, n=3). (D) Apoptosis assay was performed on VSMCs cultured and 591 treated as in (C). Doxorubicin (1µmol/l) served as positive control (c+). Data are expressed as 592 percentage \pm SEM (n=5) of total apoptotic cells (p < 0.001, LG-antago-miR control vs HG- antago-miR 593 594 control, HG- antago-miR control vs HG-antago-miR-296-5p; p<0.001, all experimental conditions 595 vs control, c+). (E) miR-296-5p expression, normalized to RNU6B, was evaluated by qRT-PCR in 596 LG and HG-cultured VSMCs both with and without PDGF-BB (10 ng/ml) (p=0.002, PDGF-BB vs 597 none in HG-treated VSMCs, n=6). (F) miR-296-5p expression, normalized to RNU6B, was evaluated by qRT-PCR in HG-cultured VSMCs, treated as indicated (p=0.007, HG-EVs control siRNA vs 598 none; p=0.002, HG-EVs PDGF-BB siRNA vs HG-EVs control siRNA, n=6). 599

Figure 7. miR-296-5p post-transcriptionally regulates bak expression. (A) Blast analysis of hsa-600 miR-296-5p sequence and BAK1 3'UTR full-length shows a base pairing from 1138 to 1158 bp. (B) 601 pGL3 empty vector and pGL3-3'UTR BAK1 luciferase constructs were transfected into LG- and HG-602 cultured VSMCs. Relative luciferase activity is reported (p < 0.001 HG vs LG in pGL3–3'UTR BAK1-603 transfected cells, n=5). (C) pGL3 and pGL3-3'UTR BAK1 constructs were transfected into LG-604 cultured VSMCs previously transfected with pre-miR control or with pre-miR-296-5p. Relative 605 luciferase activity is reported (p<0.001 pre-miR-296-5p vs pre-miR control in pGL3-3'UTR BAK1 606 transfected cells, n=5). (D) Bak content was analyzed on cell extracts from VSMCs overexpressing 607 miR-296-5p (pre-miR-296-5p), not transfected or transfected with pGL3 or pGL3-3'UTR BAK1 608

609 constructs and normalized to α -SMA (p < 0.001 VSMCs/pre-miR-296-5p none and pGL3 vs 610 VSMCs/pre-miR-296-5p+pGL3-3'UTR *BAK1*, n=5).

Figure 8. Schematic representation of HG and D-CD31EV mechanism of action. ND-CD31EVs

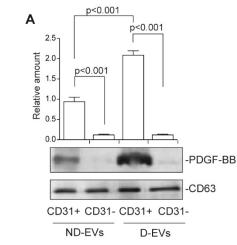
- do not affect VSMC fate due to their low mbPDGF-BB content (left panel). In the diabetic setting,
- 613 D-CD31EVs enriched in mbPDGF-BB content affect VSMC fate by promoting resistance to 614 apoptosis (right panel).

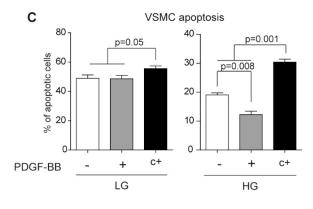


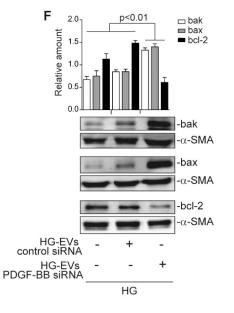
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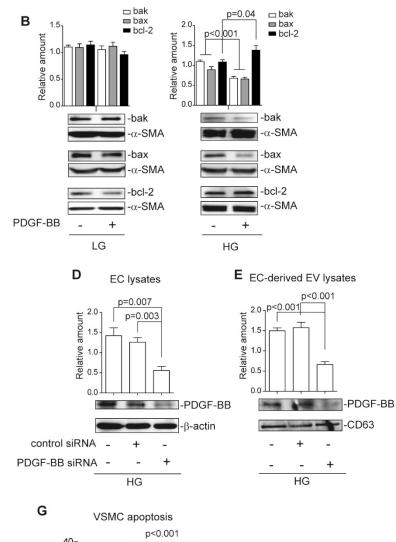
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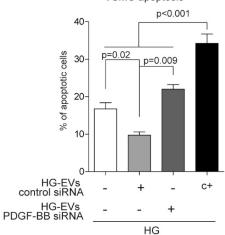








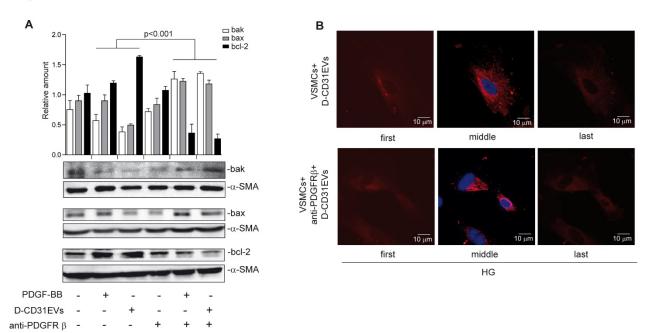












С

HG

PDGF-BB (pg/ml)			
D-CD31EVs	25±4.7		
D-CD31EV lysates	27±6.2		
D-CD31EVs + trypsin	<15**		

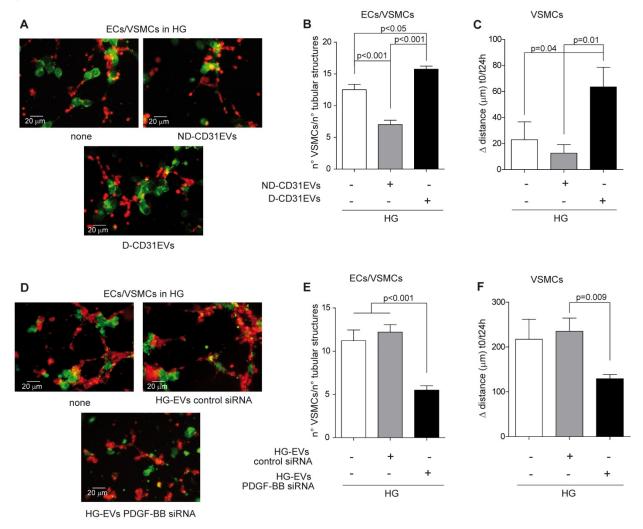
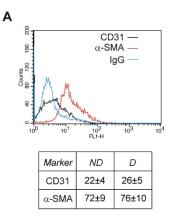
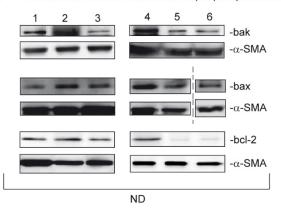
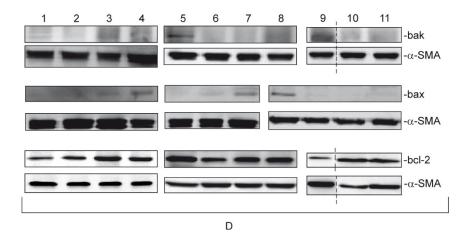


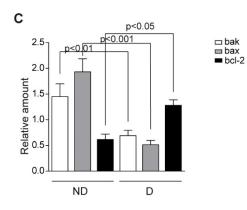
Figure 5



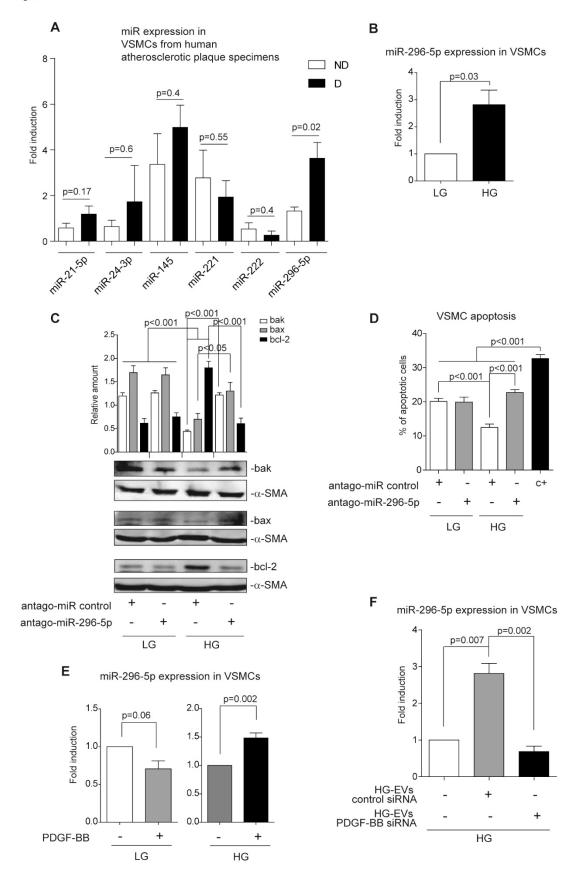
B VSMCs from human atherosclerotic plaque specimens











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