

1 **Diabetes prevalence in NZO females depends on estrogen action on**  
2 **liver fat content**

3 Running head: Estrogen modulates T2DM prevalence by influencing liver fat

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## Abstract

In humans and rodents risk of metabolic syndrome is sexually dimorphic, with an increased incidence in males. Additionally, the protective role of female gonadal hormones is ostensible as prevalence of type 2 diabetes mellitus (T2DM) increases after menopause. Here, we investigated the influence of estrogen (E2) on the onset of T2DM in female New Zealand Obese (NZO) mice. Diabetes prevalence (defined as blood glucose levels >16.6 mmol/l) of NZO females on high-fat diet (60kcal% fat) at week 22 was 43%. This was markedly dependent on liver fat content in week 10, as detected by computed tomography. Only mice with a liver fat content >9% in week 10 plus glucose levels >10 mmol/l in week 9 developed hyperglycaemia by week 22. In addition, at 11 weeks diacylglycerols were elevated in livers of diabetes-prone mice compared to controls. Hepatic expression profiles obtained from diabetes-prone and -resistant mice at 11 weeks revealed increased abundance of two transcripts in diabetes-prone mice: *Mogat1* which catalyzes the synthesis of diacylglycerols from monoacylglycerol and fatty acyl-CoA and the fatty acid transporter *Cd36*. E2-treatment of diabetes-prone mice for 10 weeks prevented any further increase in liver fat content, reduced diacylglycerols and the abundance of *Mogat1* and *Cd36* leading to a reduction of diabetes prevalence and an improved glucose tolerance compared to untreated mice. Our data indicates that early elevation of hepatic *Cd36* and *Mogat1* associates with increased production and accumulation of triglycerides and diacylglycerols, presumably resulting in reduced hepatic insulin sensitivity and leading to later onset of T2DM.

## Keywords

type 2 diabetes, hepatic steatosis, diacylglycerol, estrogen, NZO mice

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## Key messages

65

66 • Early liver fat combined with early blood glucose can be used as a predictor for later  
67 onset of T2DM in NZO mice.

68 • Estrogen supplementation averts fat accumulation in the liver under HFD and  
69 prevents from T2DM.

70 • Diabetes-prone animals have increased abundance of transcripts involved in hepatic  
71 fatty acid metabolism (MOGAT1 and CD36) prior to the onset of T2DM.

## Introduction

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73

74 Type 2 diabetes mellitus (T2DM) is a chronic metabolic disease characterized by an impaired  
75 glucose homeostasis. The prevalence of this disease has been increasing rapidly in recent  
76 decades and with 382 million people affected worldwide it is already considered pandemic  
77 (21). Several studies indicated that men have slightly higher prevalence for T2DM than  
78 women. However, if premenopausal women are compared with age-matched men the  
79 differences are striking (6, 50). In rodents, a sexual dimorphism in T2DM development can  
80 also be observed (37, 39). The New Zealand Obese (NZO) mouse, a model of polygenic  
81 obesity and T2DM (25), shows that females are protected from T2DM unless fed with an  
82 extremely high-fat diet (40, 52). Moreover, ovariectomy of NZO females increased their  
83 diabetes prevalence to the level of male mice (52). Collectively, these data indicate the  
84 importance of gonadal hormones as a protective factor against the development of T2DM in  
85 females, however, the exact mechanisms are yet to be elucidated.

86

87 Obesity is a major risk factor for the development of the metabolic syndrome and related  
88 diseases such as T2DM, fatty liver and cardiovascular complications (14). However,  
89 increased fat accumulation in the visceral compared to the subcutaneous compartment  
90 correlates better with overt T2DM than the total amount of fat (33). Fat distribution is also  
91 sexually dimorphic, with an increased accumulation of intra-abdominal fat in men compared  
92 to women (13). When the deposition of excess fat in visceral fat depots exceeds its capacity  
93 and insulin resistance develops, lipids are stored in other organs and tissues such as liver  
94 and muscle (35, 51) which further deteriorates the insulin sensitivity of these organs (41).  
95 However, it is still not clear how early the differences in fat distribution occur and if they can  
96 be used as a predictor for later onset of T2DM.

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98 The aim of this study was to compare diabetic and non-diabetic NZO females in respect to  
99 their fat distribution, in order to establish criteria for an early prediction of the onset of T2DM.  
100 Additionally, the goal was to clarify the impact of estrogen on the development of T2DM. We  
101 show that the early liver fat content and the expression of *Mogat1* and *Cd36* play an  
102 important role for the later onset of the disease. Furthermore, we demonstrate that E2  
103 reduces hepatic fat accumulation and thereby contributes to improved insulin sensitivity.

## Material and Methods

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105

106 **Animals.** Female NZO/HIBomDife mice (R. Kluge, German Institute of Human Nutrition,  
107 Nuthetal, Germany) from our own colony were housed in Sealsafe™-VC Type 1284L cages  
108 (Tecniplast, Buguggiate, Italy) at a temperature of  $20 \pm 2$  °C with a 12-h light-dark cycle  
109 (lights on at 06:00 h) and had free access to water and diet. All experiments were approved  
110 by the ethics committee of the State Agency of Environment, Health and Consumer  
111 Protection (State of Brandenburg, Germany).

112

113 **Diets.** After weaning animals were kept on standard diet (SD; V153x R/M-H, Ssniff, Soest,  
114 Germany) until the age of 5 weeks when some of the mice were switched to high-fat diet  
115 (HFD; 60 kcal% fat, D12492, Research Diets, New Brunswick, USA) (**Figure 1A**). To  
116 generate plasma and tissue samples mice were sacrificed either at 11 or at 22 weeks of age.  
117 From week 11 estradiol-treated groups received 17 $\beta$ -estradiol (E2) orally over 10 weeks (800  
118  $\mu$ g/kg HFD, Sigma Aldrich, Munich, Germany) (**Figure 1B**).

119

120 **Computed tomography.** Body fat distribution and liver fat content were measured by CT  
121 (Hitachi-Aloka LCT-200, Tokyo, Japan) as described earlier (31). The correlation between  
122 liver fat content, body fat distribution and onset of T2DM was assessed by CT scans at  
123 weeks 10, 16 and 22 (**Figure 1A**). Influence of E2 treatment on accumulation of liver fat was  
124 examined by CT scans of the liver at weeks 10 and 20 (**Figure 1B**). During measurements  
125 animals were anesthetized by isoflurane.

126

127 **Transcriptome analysis.** Total RNA was isolated from snap-frozen livers of 11-weeks old  
128 mice by RNeasy Mini Kit (Qiagen, Venlo, the Netherlands). Before labeling, the integrity of  
129 the samples was checked using an Agilent 2100 Bioanalyzer. Microarray analysis of mRNA  
130 was performed using SurePrint G3 Mouse GE 8x60K Microarray gene chips (Agilent

131 Technologies, Santa Clara, CA, USA). The human study was conducted in accordance with  
132 the Declaration of Helsinki as reflected in a priori approval by the institution's human  
133 research committee. 16 subjects from the cross-sectional INSIGHT (German Clinical Trials-  
134 Register: DRKS00005450) study who gave written informed consent were included. Subject  
135 characteristics are given in table 3. Blood samples were obtained after overnight fasting and  
136 clinical chemistry was assessed using standard methods in certified Clinical Chemistry  
137 laboratories (9). Liver specimens were harvested during hepatic surgery. Samples were  
138 flash-frozen in liquid nitrogen and stored at -80 °C until RNA extraction. A part of the liver  
139 sample was used for histopathological analysis after fixing in 4% formalin (Histofix, Roth,  
140 Germany), embedding in paraffin, and staining with hematoxylin & eosin. NAFLD was  
141 diagnosed according to standard criteria (24). Exclusively healthy liver tissue was used for  
142 analyses, as a blinded clinical expert pathologist considered all harvested liver samples to be  
143 histologically normal with respect to pathologies except for NAFLD.

144

145 **Real time PCR.** Real time PCRs (RT-qPCR) were performed with TaqMan<sup>®</sup> assays, as  
146 described earlier (26). The expression level of target genes was normalized to the  
147 housekeeping reference gene TATA-Box Binding Protein (*Tbp*) by the  $\Delta\Delta C_t$  method (30).  
148 The following TaqMan<sup>®</sup> gene expressions assays were used *Cd36* (Mm01135198\_m1), *Fasn*  
149 (Mm00662319\_m1), *G6pc* (Mm00491176\_m1), *Mogat1* (Mm00503358\_m1), *Pepck*  
150 (Mm01247058\_m1), *Pparg* (Mm00440945\_m1) and *Scd1* (Mm01197142\_m1).

151

152 **Western blotting.** MOGAT1 and CD36 were analyzed in liver (50 mg) homogenates by  
153 Western blotting that was performed as described earlier (4) with an anti-MOGAT1 antibody  
154 (Novus Biologicals, Littleton, USA) in a dilution of 1:1000 and an anti-CD36 antibody (R&D  
155 Systems, Minneapolis, USA; 1:1000) in combination with horseradish peroxidase-labeled  
156 secondary antibodies. PKC- $\epsilon$  activity was determined as PKC- $\epsilon$  association with plasma  
157 membranes as described earlier (BD Transduction Laboratories, Heidelberg, Germany;  
158 1:2000; (22)).

159 **Quantification of diacylglycerols and ceramides.** Liver samples were prepared as  
160 described earlier (34). The procedure included lipid extraction with MeOH/CHCl<sub>3</sub> (2:1, v/v),  
161 homogenization and incubation for 12 h at 48°C. After centrifugation (10 min, 5°C, 3.500 x g)  
162 supernatant was separated and vacuum dried. Subsequently, the pellet was resolved in  
163 eluent for liquid chromatography and the mixture was injected into the LC column, Kinetex  
164 XBC18 (Phenomenex, Aschaffenburg, Germany). Separation of compounds was performed  
165 by UPLC, Ultimate 3000 System (Dionex, Idstein, Germany). Upon separation single  
166 components were detected by mass spectrometer ESI-qToF, maXis<sup>®</sup> 3G (Bruker, Bremen,  
167 Germany).

168

169 **Glucose tolerance.** Oral glucose tolerance tests were performed after overnight fasting as  
170 previously described (43). Insulin measurements were performed by ELISA (DRG  
171 Diagnostics, Marburg, Germany) according to manufacturer's instruction.

172

173 **Statistical analysis.** Data, if not indicated otherwise, are presented as means ± standard  
174 error of the mean (SEM). Statistical analysis and graphical presentation of results were  
175 performed by GraphPad Prism version 6.05 for Windows (GraphPad Software, San Diego,  
176 USA).

177



## Results

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### 180 **Early liver fat content as a predictor for the development of hyperglycemia**

181 NZO females on HFD (n = 42) had significantly higher body weight (week 22:  $76.6 \pm 1.3$  g vs.  
182  $44.6 \pm 2.1$  g,  $p < 0.001$ ) and random blood glucose values ( $14.8 \pm 0.9$  mmol/l vs.  $7.2 \pm 0.4$   
183 mmol/l,  $p < 0.001$ ) than animals on SD (n = 9). Diabetes prevalence (defined as blood  
184 glucose levels  $> 16.6$  mmol/l for at least three weeks) after 22 weeks reached 43 % in the  
185 HFD-fed group (blood glucose concentration:  $20.3 \pm 0.7$  mmol/l) while none of the mice on  
186 SD became diabetic during this period ( $10.8 \pm 0.6$  mmol/l,  $p < 0.001$ ) (**Figure 2**). The body  
187 weight of diabetic and non-diabetic females within the HFD group did not show significant  
188 differences ( $78.0 \pm 2.1$  g vs.  $75.6 \pm 1.6$  g, n.s.).

189 In order to test if differences in fat distribution were responsible for diabetes development in  
190 NZO females, fat distribution was quantified by CT at the weeks 10, 16 and 22 (**Figure 1A**).  
191 No differences in amounts of total and visceral fat in the abdominal region were detected  
192 between diabetic and non-diabetic mice within the HFD group (**Figure 3A and 3B**). However,  
193 quantification of ectopic fat accumulation in the liver showed more intrahepatic fat in diabetic  
194 than in non-diabetic mice, at all three time points (**Figure 3C**). Earlier CT measurements at  
195 week 5 indicated no initial differences in mice that were later defined as diabetes-prone or  
196 resistant (DR:  $3.37 \pm 0.49$  % vs. DP:  $3.74 \pm 0.48$  %, n = 5, n.s.). A positive correlation was  
197 found between early liver fat content at week 10, prior to the onset of T2DM, and later  
198 random blood glucose values at week 22 ( $r^2 = 0.303$ , **Figure 3F**). We determined a threshold  
199 for liver fat content of 9 % at week 10 that could predict later onset of diabetes with 70 %  
200 probability. Combining the increased liver fat content at week 10 with blood glucose values at  
201 week 9 ( $> 10$  mmol/l), which itself predicts later hyperglycemia with 63 % probability, resulted  
202 in an even more precise prediction quotient of 79 %. Early total (**Figure 3D**) and visceral fat  
203 (**Figure 3E**) mass, however, was not related to later hyperglycemia.

204

205 **Livers of diabetes-prone mice exhibited higher diacylglycerol levels and elevated**  
206 **expression of lipogenic enzymes**

207 Diacylglycerol species were measured in livers of designated diabetes-prone or -resistant  
208 mice as determined by our pre-defined criteria at the age of 11 weeks. Diabetes-prone mice  
209 exhibited a significantly elevated diacylglycerol concentration compared to the diabetes-  
210 resistant group (**Figure 4A**). However, the increase was not specific for individual  
211 diacylglycerol species (**Figure 4B**). In contrast, hepatic ceramides were not altered between  
212 diabetes-prone and -resistant mice (DR:  $365.46 \pm 27.15$  nmol/g, n = 5; DP:  $350.84 \pm 23.70$   
213 nmol/g, n = 6). In order to clarify whether alterations in the expression of lipogenic enzymes  
214 are responsible for elevated hepatic triglycerides and diacylglycerols, the transcriptome of  
215 the livers of the same animals that were used for diacylglycerol analysis (diabetes-prone n =  
216 5; diabetes-resistant n = 6) was analyzed by microarray analysis. We identified 28  
217 significantly (Student's t-test:  $p < 0.05$ ) differentially expressed genes exhibiting  $|\log_2(\text{fold}$   
218  $\text{change})| > 0.7$  (**Table 1**). Among these genes two (*Mogat1* and *Cd36*) could be linked to  
219 hepatic triglyceride synthesis according to their known function (16, 19). MOGAT1 catalyzes  
220 the synthesis of diacylglycerols (8), as an intermediate product of triglyceride synthesis.  
221 CD36, also known as fatty acid translocase, has been suggested to act as a fatty acid  
222 transporter in various tissues (20, 56). Their differential expression could be confirmed by  
223 RT-qPCR analysis (**Figure 5 A, B**, upper panels). Moreover, Western blot analysis confirmed  
224 the higher abundance of MOGAT1 and CD36 proteins in livers DP mice (**Figure 5 A, B**,  
225 lower panels). Furthermore, a closer look on the expression of other genes involved in the  
226 generation and degradation of lipid stores revealed no further relevant alterations of mRNA  
227 levels between diabetes-resistant and diabetes-prone mice (**Table 2**). Besides these  
228 alterations in lipogenic transcripts, the expression of *Pck1* and *G6pc* was elevated in livers of  
229 diabetes-prone mice (**Figures 6**) pointing towards an elevated hepatic glucose production in  
230 response to insulin resistance. In order to test if MOGAT and/or CD36 expression are altered  
231 in human subjects with a fatty liver we analyzed microarray data obtained from human liver  
232 biopsies of controls and patients from the cross-sectional INSIGHT study suffering from non-

233 alcoholic fatty liver disease (NAFLD). In contrast to mice not *MOGAT1* but *MOGAT2*  
234 revealed a significantly higher expression ( $p = 0.05$ ) in livers of NAFLD patients. The two  
235 other genes, *MOGAT1* and *MOGAT3* showed only a tendency towards elevated expression  
236 (**Figure 7**). However, *CD36* expression appeared not to be different between the patients  
237 and controls.

238

### 239 **Treatment with E2 suppresses the development of T2D and prevents fat accumulation** 240 **in the liver**

241 In order to test if estrogen exhibits protective potential and prevents T2DM we treated female  
242 diabetes-prone mice with E2 from the age of 11 weeks (**Figure 1B**). Ten weeks of dietary  
243 supplementation with E2 (800  $\mu\text{g}/\text{kg}$  HFD) did not result in any significant differences in body  
244 weight compared to control groups (week 22:  $81.1 \pm 1.9$  g vs.  $80.5 \pm 1.1$  g, n.s.). However,  
245 E2-treated mice exhibited significantly lower random blood glucose values than control mice  
246 ( $15.0 \pm 2.2$  mmol/l vs.  $27.7 \pm 1.1$  mmol/l, Student's t-test,  $p < 0.01$ ). As expected, all  
247 diabetes-prone control mice developed T2DM, whereas E2 treatment reduced diabetes  
248 prevalence from 100 % to 42 % at week 21 (**Figure 8A**). Prior to E2 treatment the liver fat  
249 content was similar in both groups at week 10 (E2-treated mice:  $11.4 \pm 0.3$  % vs. control  
250 mice:  $11.8 \pm 0.7$  %, n.s). We next tested whether the protective effects of estrogen against  
251 T2DM could be mediated by a limited hepatic lipid accumulation. In fact, supplementation of  
252 E2 completely prevented the increase in liver fat with  $11.4 \pm 0.9$  % fat in week 20, whereas  
253 liver fat content increased to  $26.5 \pm 0.8$  % in the control group (Student's t-test,  $p < 0.001$ )  
254 (**Figure 8B**). In addition, E2-treated mice exhibited significantly lower total diacylglycerol  
255 concentrations in the liver (**Figure 8C**), which was caused by a general reduction in  
256 diacylglycerol species (**Figure 8D**). To clarify a possible mechanism by which E2 can prevent  
257 the impairment of insulin sensitivity in the liver, PKC- $\epsilon$  activity was assessed by isolation of  
258 plasma membranes and its detection by Western blotting. Livers from DP-E2 mice showed a  
259 reduced plasma membrane localization of PKC- $\epsilon$  in comparison with DP-C livers indicating a

260 reduced PKC- $\epsilon$  activity (**Figure 8E**). In order to test if E2 treatment influences the expression  
261 of *Mogat1* and *Cd36* we analyzed their mRNA in E2- and non-treated NZO females. After E2  
262 treatment we detected a reduced mRNA expression of both genes (**Figures 8F and 8G**),  
263 which could contribute to lower hepatic triglyceride and diacylglycerol levels in these livers.  
264 These results were also confirmed on protein level by Western blot analysis (**Figures 8F and**  
265 **8G**, lower panels).

266

### 267 **E2 treatment improves glucose tolerance and prevents $\beta$ -cell loss**

268 Oral glucose tolerance tests (oGTT) at week 13 displayed a slightly but significantly  
269 increased glucose tolerance of E2-treated mice in comparison to diabetes-prone control  
270 animals. This was demonstrated by reduced blood glucose and increased plasma insulin  
271 levels at all time-points in the E2-supplemented group (**Figure 9 A, C, E**). At week 18,  
272 glucose tolerance had further deteriorated in diabetes-prone control mice; their plasma  
273 insulin levels during the test dropped markedly in comparison to the test performed in week  
274 13, indicating  $\beta$ -cell loss. In contrast, oGTT results of diabetes-prone E2 treated mice were  
275 unchanged in comparison to week 13 (**Figure 9 B, D, F**). Furthermore, random plasma  
276 insulin levels at week 22 were markedly reduced in diabetes-prone control ( $3.4 \pm 0.8 \mu\text{g/l}$ )  
277 compared to diabetes-prone E2-treated mice ( $23.6 \pm 5.5 \mu\text{g/l}$ , Student's t-test,  $p < 0.01$ ). One  
278 other proposed mechanism for the amelioration of glucose homeostasis is the estrogen-  
279 induced reduction of the expression of lipogenic genes such as *Scd1*, *Fasn* and *Pparg* (3,  
280 12). The effect of E2 on *Fasn* and *Pparg* expression could not be confirmed in our  
281 experiment, whereas *Scd1* was significantly increased in E2-treated animals (**Figure 10**).

## Discussion

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284 The present study demonstrates that **(1)** early elevated liver fat content is a valuable  
285 prediction marker for T2DM, **(2)** this parameter associated with increased hepatic *Mogat1*  
286 and *Cd36* levels, and **(3)** E2 treatment prevented an increase in liver fat and the  
287 development of T2DM in NZO mice. The accumulation of ectopic fat in the liver and the  
288 development of NAFLD in humans are associated with up to four times increased risk of  
289 developing T2DM (5, 28, 29, 38). Several studies in rodents also support these findings (1,  
290 53). The elevated amount of intrahepatic fat in NZO females that later become diabetic was  
291 accompanied by increased diacylglycerol concentrations which have been shown to disrupt  
292 the insulin signaling pathway (2, 47). As a consequence of insulin resistance in hepatocytes,  
293 expression of enzymes involved in gluconeogenesis (glucose-6-phosphatase (*G6pc*) and  
294 phosphoenolpyruvate carboxykinase (*Pepck*)) are not efficiently suppressed by the insulin-  
295 activated transcription factor FoxO1 (55). This leads to increased gluconeogenesis and an  
296 elevated glucose concentration in plasma (36). Indeed, the expression of both enzymes,  
297 *G6pc* and *Pepck* was increased in livers of diabetes-prone mice at week 11 (**Table 1** and  
298 **Figure 6**).

299 Transcriptome analysis of livers at week 11 revealed the increased expression of two genes  
300 involved in hepatic lipid metabolism (*Mogat1* and *Cd36*). *Mogat1* encodes for a liver-specific  
301 monoacylglycerol O-acyltransferase 1 (MOGAT1), an enzyme which is involved in the  
302 alternative triglyceride synthesis pathway where it catalyzes the formation of diacylglycerols  
303 from monoacylglycerols (8), which were elevated in diabetic NZO females in our study. *Cd36*  
304 encodes for the membrane protein fatty acid translocase (CD36) which is responsible for the  
305 uptake of long-chain fatty acids into hepatocytes (57). Two recent studies indicated the  
306 importance of *Mogat1* for insulin sensitivity in the liver. They showed that silencing of hepatic  
307 *Mogat1* expression by siRNA results in significant improvement in glucose tolerance and  
308 hepatic insulin signaling, as well as a reduction of hepatic fat as well as body weight (19, 46).

309 Furthermore, in our own human samples and data by Hall (17) the expression of *MOGAT2*  
310 was associated with non-alcoholic fatty liver disease (NAFLD). Increased expression of  
311 *CD36* in humans and rodents is associated with obesity, insulin resistance and T2DM (27,  
312 44). The abundance of *CD36* is increased in patients with NAFLD (15) and is postulated as a  
313 cause of an increased flux of free fatty acids into hepatocytes (57). However, our own data  
314 did not show this trend for *CD36*, which might be caused by the low sample size.

315 Diacylglycerols are not only intermediates in triglyceride synthesis but also important  
316 signaling molecules in the cell (8). In hepatocytes diacylglycerols can bind to cytosolic PKC- $\epsilon$   
317 to form a complex that is translocated to the plasma membrane where it binds to and inhibits  
318 the insulin receptor tyrosine kinase. This leads to decreased insulin-stimulated glycogen  
319 synthesis and a reduced insulin suppression of hepatic gluconeogenesis (45) and can  
320 thereby contribute to the development of T2DM. Increased abundance of *Mogat1* and *Cd36*  
321 in livers of diabetes-prone mice might explain the increase in hepatic diacylglycerols. In  
322 addition, E2 treatment of diabetes-prone NZO females resulted in a lower expression of  
323 *Mogat1* and *Cd36*, lower hepatic diacylglycerols as well as in a reduced PKC- $\epsilon$  activity which  
324 can contribute to the amelioration of T2DM prevalence in this group. In contrast to our data  
325 Hall and colleagues detected an elevated diacylglycerol concentration in the liver after  
326 suppression of *Mogat1* expression by siRNA treatment (18). This discrepancy might be  
327 explained by a compensatory decreased diacylglycerol O-acyltransferase (*Dgat*) expression  
328 that occurred simultaneously to a decreased *Mogat1* expression in the Hall study.

329 Interestingly, E2 treatment of females that exhibit elevated blood glucose and liver fat levels  
330 at week 9 and 10, respectively, reduced diabetes prevalence by almost 60%, confirming that  
331 estrogen mediates beneficial effects on glucose homeostasis. These results are in  
332 accordance with previous studies where E2 administration was shown to decrease insulin  
333 resistance and diabetes prevalence in rodents (5, 48), whereas ovariectomy increased  
334 insulin resistance and the risk of developing T2DM (49, 52, 54). Human data also suggest  
335 that hormone replacement therapy in menopausal women is associated with a decreased  
336 risk of developing insulin resistance and T2DM (7, 42).

337 Improved glucose homeostasis detected after E2 treatment might be a consequence of  
338 reduced ectopic fat accumulation in the liver (**Figures 8B and 8C**). This phenomenon was  
339 previously observed in postmenopausal women receiving hormone-replacement therapy (11,  
340 32) and estrogen-treated mice (5, 23).

341 As E2 treatment suppressed the expression of *Mogat1* and *Cd36* it is possible that E2 acts  
342 via these two targets resulting in a reduced uptake of long-chain fatty acids and decreased  
343 hepatic triglyceride synthesis by the alternative monoacylglycerol pathway. The analysis of  
344 the promoter region of *Mogat1* and *Cd36* by the transcription factor binding analysis tool  
345 Matinspector (<http://www.genomatix.de/matinspector.html>) revealed the presence of 10 and  
346 2 putative estrogen responsive elements (EREs), respectively (10). This fact indicates that  
347 the expression of *Mogat1* and *Cd36* is at least partially controlled by estrogen.

348 In summary, we conclude that an increase in early liver fat content combined with a slight  
349 increase in plasma glucose concentrations can be used as a valuable predictor for the later  
350 onset of T2DM in NZO females. Moreover, estrogen treatment reduced the abundance of  
351 *Mogat1* and *Cd36*, leading to a triglyceride and diacylglycerol accumulation in the liver and  
352 finally to the prevention of T2DM. However, as estrogens cannot be used systematically over  
353 a long period of time due to their tumor promoting action on the uterus it will be important to  
354 develop novel therapeutic approaches by which estrogen could be target-delivered only into  
355 the liver.

356

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363

364

## **Disclosure**

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366 The authors declare that they have no conflict of interest.



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539

540

## Figure legends

### 541 **Figure 1:**

542 Experimental design. **(A)** Female NZO mice were either fed with a standard diet (SD, n = 9) during the  
543 whole experiment or were switched to HFD (n = 42) at week 5. Body fat distribution and liver fat  
544 content were measured by computed tomography at the indicated time points (CT1, CT2, CT3). **(B)**  
545 Female NZO mice received HFD from week 5. After applying prediction criteria for later onset of T2DM  
546 selected diabetes prone animals were divided into control (DP-C, n = 12) and estradiol-treated (DP-E,  
547 n = 12, 800 µg/kg HFD) groups. Five diabetes-prone and six diabetes-resistant mice were sacrificed at  
548 week 11 and livers were taken for further analysis (microarray, diacylglycerol/ceramide content).  
549 oGTT1 and oGTT2 – oral glucose tolerance tests. CT1 and CT2 – Quantification of hepatic fat content  
550 by computed tomography. Body weight and blood glucose were measured weekly.

551

### 552 **Figure 2:**

553 Female NZO mice exhibit heterogeneous diabetes prevalence. Animals fed with standard diet (SD) (n  
554 = 9) did not develop T2DM. However, feeding with high-fat diet (HFD) that contains 60 kcal% fat (n =  
555 42, diet switch at week 5) causes T2DM from 10 weeks of age and results in diabetes prevalence of  
556 43 % at week 22.

557

### 558 **Figure 3:**

559 Distribution of abdominal white adipose tissue was measured by computed tomography at week 10,  
560 16 and 22. There were no significant differences in amounts of total **(A)** and visceral **(B)** fat in  
561 abdominal region (lumbar vertebrae L4-L5) between diabetic and non-diabetic animals. **(C)** Liver fat  
562 content at week 10, 16 and 22 as measured by computed tomography. Early total **(D)** and visceral  
563 abdominal fat **(E)** at week 10, as measured by computed tomography, did not correlate with later blood  
564 glucose values in non-fasted animals at week 22 and therefore cannot be used as predictors for onset  
565 of T2DM. Accumulation of liver fat was increased in diabetic animals at all three time points and  
566 correlates with later blood glucose values in non-fasted animals at week 22 **(F)**. Data are presented as  
567 mean fat weight per CT-slice (600 µm). Student's t-test: \* p < 0.05, \*\*\* p < 0.001. Mice: NZO females  
568 on HFD (60 kcal% fat), n = 41.  $r^2$  = Pearson's correlation coefficient.

569

570 **Figure 4:**

571 **(A)** LC-MS/MS quantification of diacylglycerols in livers of 11 weeks old NZO female mice indicated  
572 increased diacylglycerol levels in diabetes-prone (DP, n = 5) compared to diabetes-resistant (DR, n =  
573 6) NZO females. **(B)** Diacylglycerol profile of livers from 11 weeks old diabetes-prone (DP, n = 5) and  
574 diabetes-resistant (DR, n = 6) NZO females revealed a general increase of diacylglycerol species in  
575 diabetes-prone group compared to diabetes-resistant animals. Student's t-test: \* p < 0.05.

576

577 **Figure 5:**

578 Expression of *Mogat1* **(A)** and *Cd36* **(B)** mRNA was increased in livers of diabetes-prone (DP, n = 5)  
579 female NZO mice at week 11 compared to diabetes-resistant (DR, n = 6) females. MOGAT1 and  
580 CD36 protein abundance indicated the same trend, as identified by Western blot analysis. Student's t-  
581 test: \* p < 0.05, \*\* p < 0.01.

582

583 **Figure 6:**

584 Expression of genes encoding for gluconeogenic enzymes *Pck1* and *G6pc* was increased in diabetes-  
585 prone (DP, n = 5) compared to diabetes-resistant (DR, n = 6) females at week 11. Student's t-test: \* p  
586 < 0.05.

587

588 **Figure 7:**

589 Microarray expression data for *Cd36* and *Mogat* isoformes of liver biopsies from patients with non-  
590 alcoholic fatty liver disease (NAFLD, n = 8) and controls (n = 8). Student's t-test.

591

592 **Figure 8:**

593 **(A)** At week 22 all diabetes-prone control mice (DP-C, n = 12) suffered from T2DM while only 41.7 %  
594 of estrogen-treated diabetes-prone (DP-E, n = 12) animals became diabetic. Both groups received  
595 high-fat diet containing 60 kcal% fat from the age of 5 weeks; E2-treated animals received the same  
596 diet supplemented with 800 µg estradiol per kg diet from the age of 11 weeks. **(B)** Estrogen treatment  
597 averts ectopic accumulation of fat in livers of diabetes-prone NZO females. Liver fat content was

598 quantified by CT at weeks 10 and 20. **(C)** LC-MS/MS quantification of diacylglycerols in livers of 22  
599 weeks old diabetes-prone mice by LC-MS/MS indicated reduced diacylglycerol levels after estrogen  
600 treatment (DP-E, n = 11) compared to control (DP-C, n = 10) NZO females. **(D)** Estrogen  
601 supplementation of diabetes-prone (DP-E) mice resulted in a reduction of all hepatic diacylglycerol  
602 species compared to controls (DP-C). **(E)** PKC- $\epsilon$  activity was higher in control livers (DP-C) compared  
603 to estrogen treated mice. PKC- $\epsilon$  activity was determined by localization of PKC- $\epsilon$  to the plasma  
604 membrane in DP-C and DP-E livers (n = 4). Expression of *Mogat1* **(F)** and *Cd36* **(G)** mRNA was lower  
605 in livers of estrogen-treated (DP-E, n = 6) female NZO mice at week 22 compared to controls (DP-C, n  
606 = 6). MOGAT1 and CD36 protein abundance indicated the same trend, as determined by Western blot  
607 analysis. Student's t-test: \* p < 0.05, \*\* p < 0.01, \*\*\* p < 0.001.

608

609 **Figure 9:**

610 Estrogen treatment improved glucose tolerance in diabetes-prone mice at the age of 13 and 18 weeks.  
611 Left panel - oGTT at week 13; right panel – oGTT at week 18; blood glucose **(A, B)** and plasma insulin  
612 **(C, D)** concentrations during oGTT; area under the **(E)** glucose and **(F)** insulin curves during oGTT  
613 was calculated using the trapezoidal rule. DP-C: diabetes-prone controls (n = 12); DP-E: diabetes-  
614 prone estrogen-treated mice (n = 12). Student's t-test: \* p < 0.05, \*\* p < 0.01, \*\*\* p < 0.001.

615

616 **Figure 10:**

617 RT-qPCR analysis could not confirm earlier findings that estrogen reduces hepatic expression of  
618 lipogenic genes *Fasn* **(C)** and *Pparg* **(D)**, while the expression of *Scd1* **(E)** was slightly increased at  
619 week 22 upon E2 treatment. DP-C: diabetes-prone control mice, n = 6; DP-E: diabetes-prone E2-  
620 treated mice, n = 6; Student's t-test: \* p < 0.05, **n.s.** – non-significant (p > 0.05).

621

622 **Table 1:**

623 Differentially expressed annotated genes from transcriptome analysis. Microarray analysis was  
624 performed in livers of 11 weeks old diabetes-prone and diabetes-resistant NZO females and genes  
625 were selected according to the stringent criteria: p < 0.05, |log<sub>2</sub>(fold change)| > 0.7; mean signal  
626 intensity > 90 (in at least one group); DR - mean signal intensity in diabetes resistant group (n = 6), DP  
627 - mean signal intensity in diabetes prone group (n = 5), p-value - according to the Student's t-test.



628

629 **Table 2:**

630 Expression of transcripts involved in hepatic lipid metabolism as determined by microarray analysis in  
631 livers of 11 weeks old diabetes-prone and diabetes-resistant NZO females. Genes were regarded as  
632 significantly altered according to these criteria:  $p < 0.05$ ,  $|\log_2(\text{fold change})| > 0.7$ ; mean signal  
633 intensity  $> 90$  (in at least one group); DR - mean signal intensity in diabetes resistant group ( $n = 6$ ), DP  
634 - mean signal intensity in diabetes prone group ( $n = 5$ ), p-value - according to the Student's t-test.

635

636 **Table 3:**

637 Characteristics of human study subjects. Subjects were paired according to clinical parameters of  
638 NAFLD or no NAFLD for microarray data analysis. mean  $\pm$  SD.

Figure 1

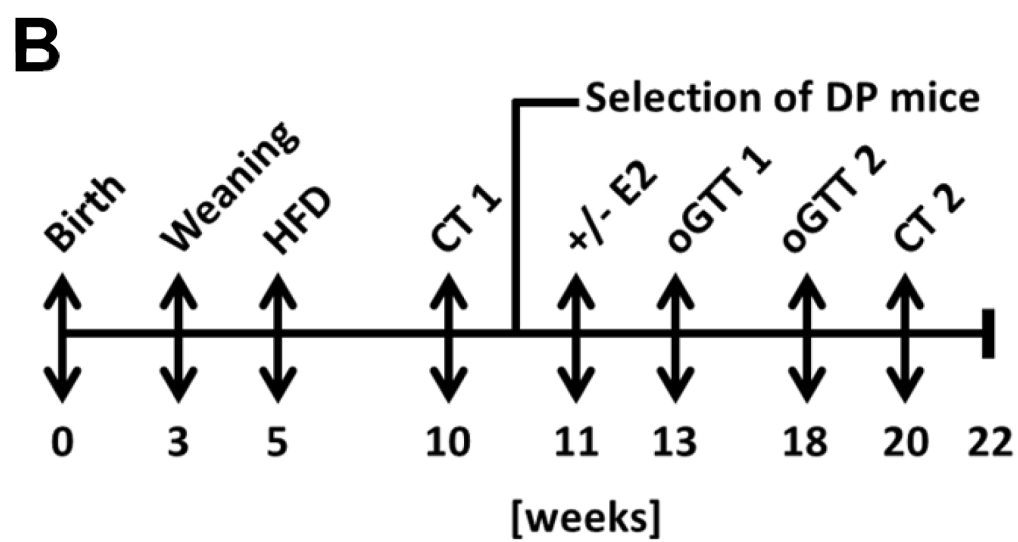
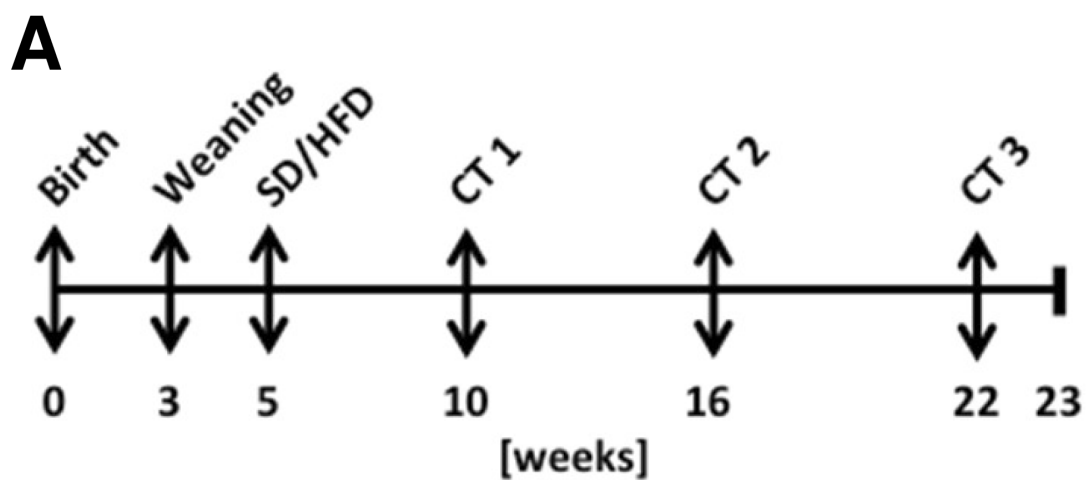


Figure 2

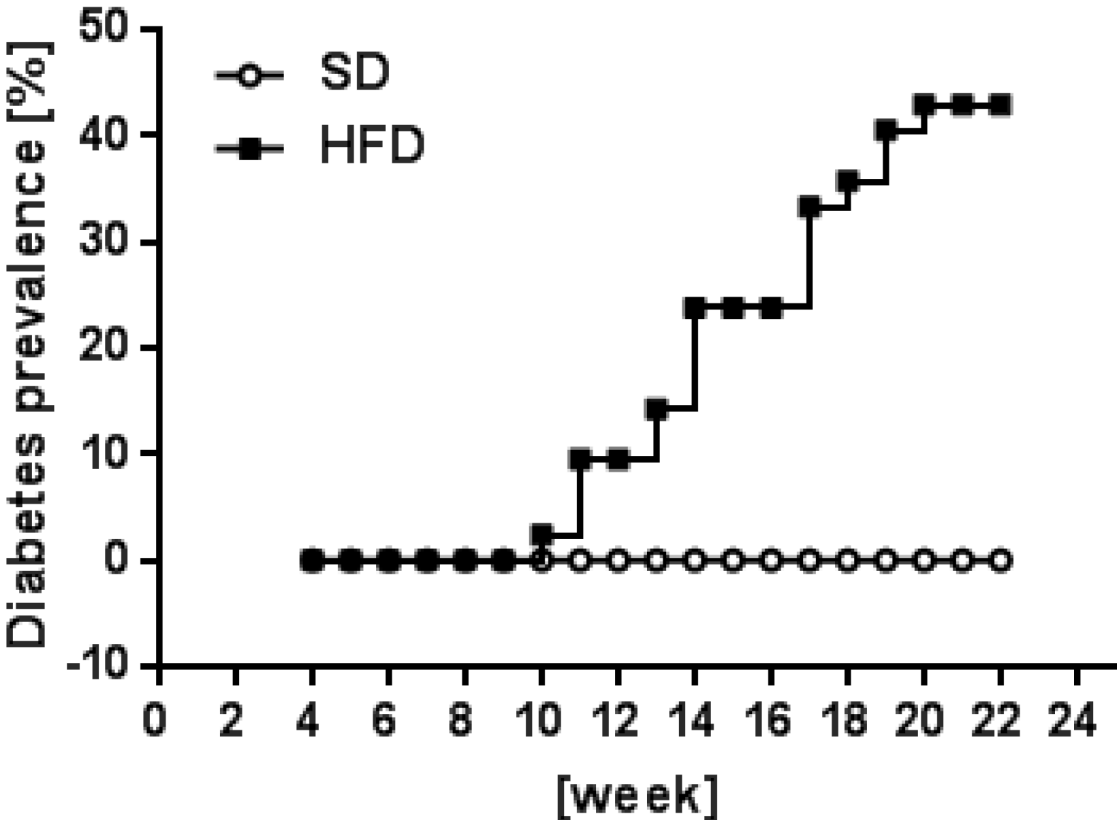


Figure 3

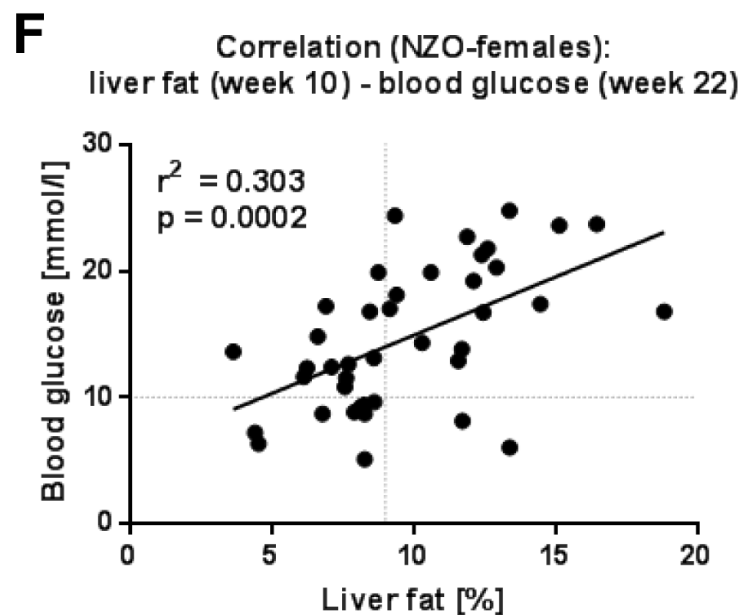
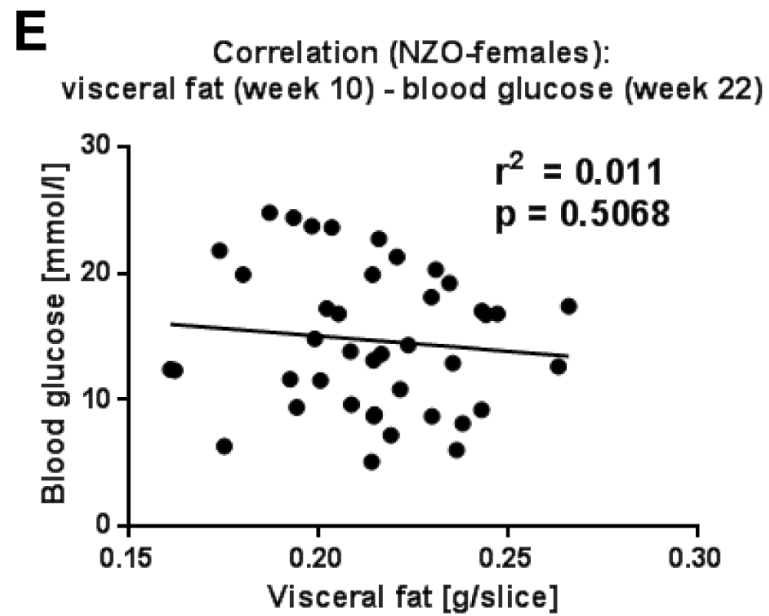
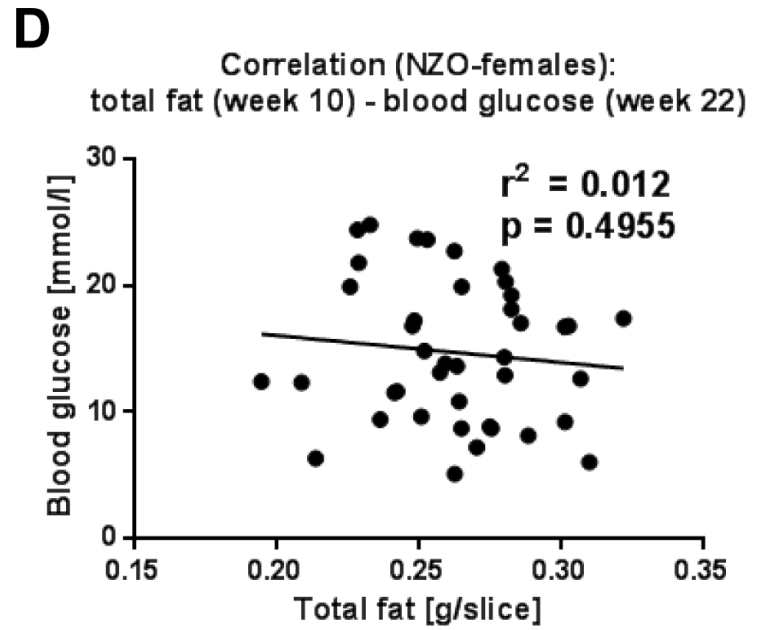
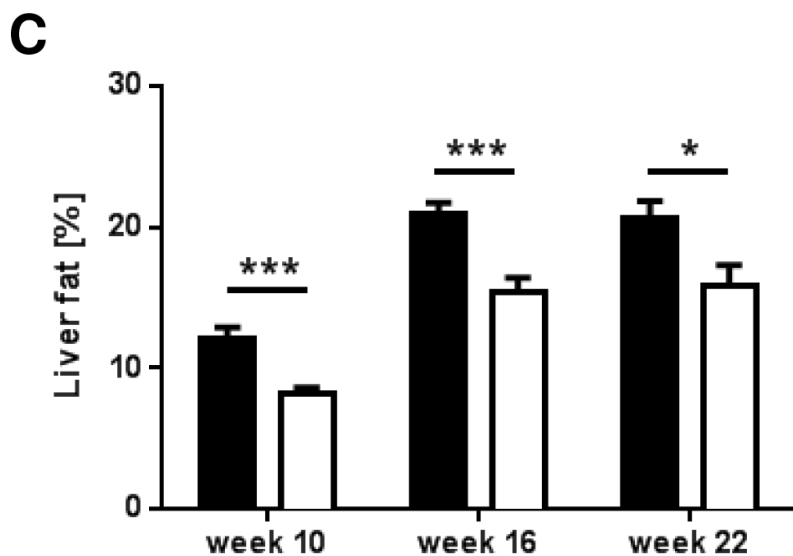
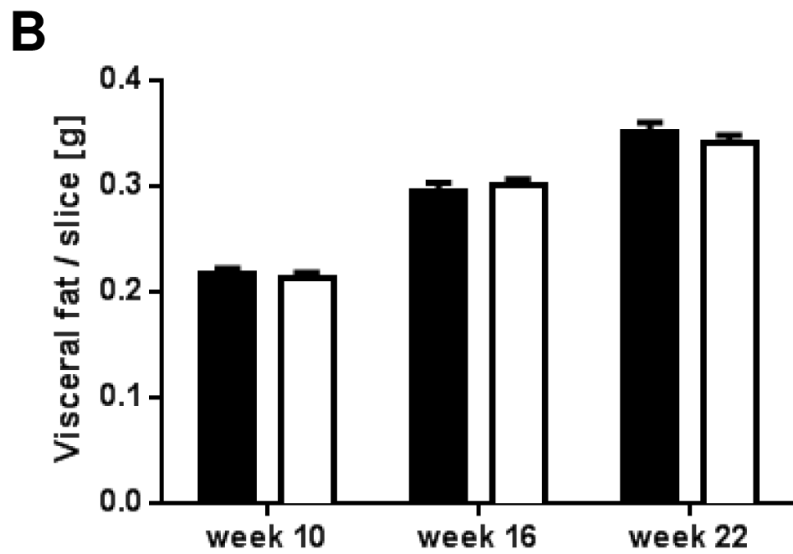
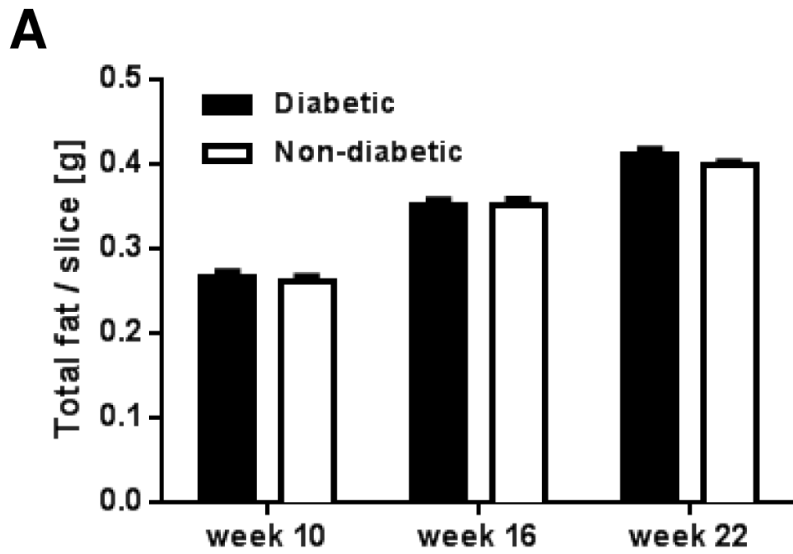


Figure 4

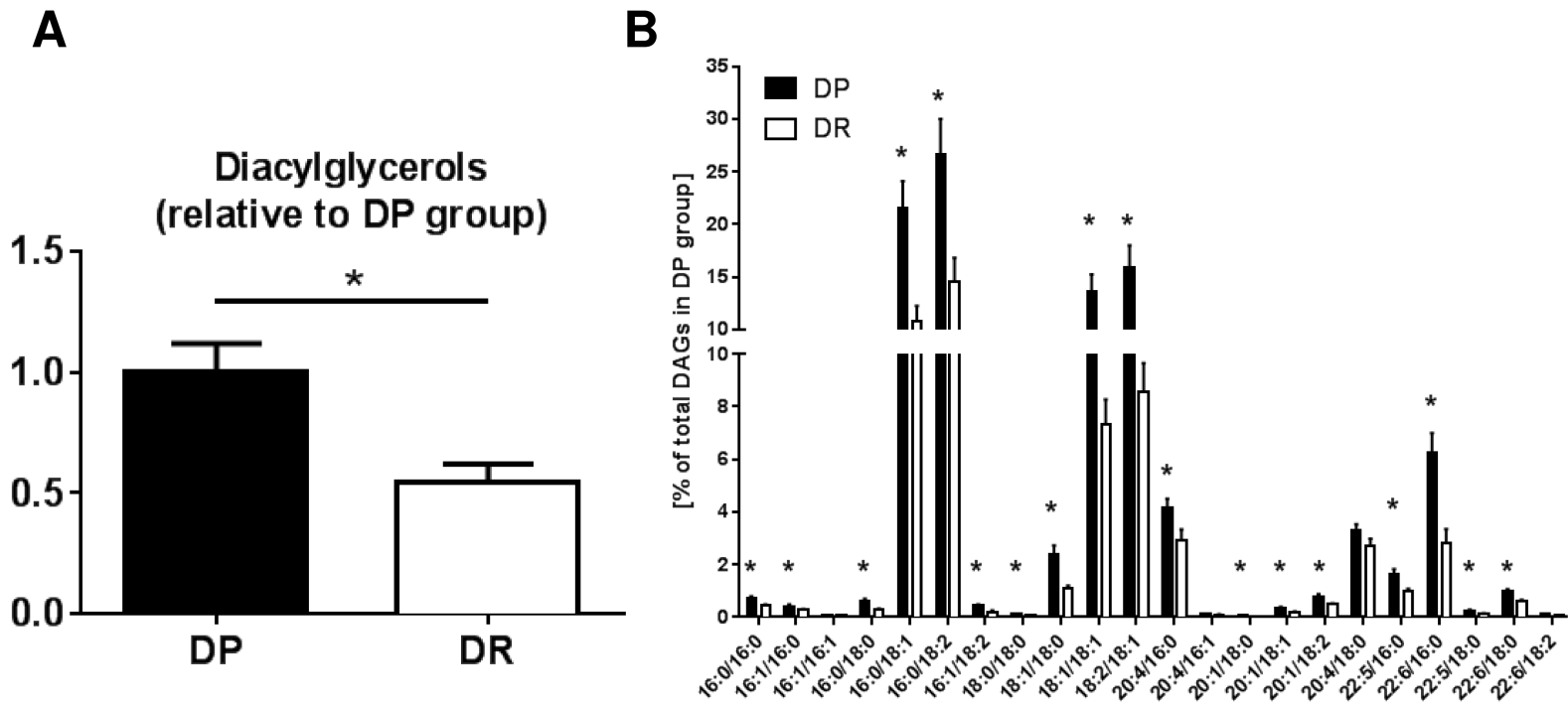
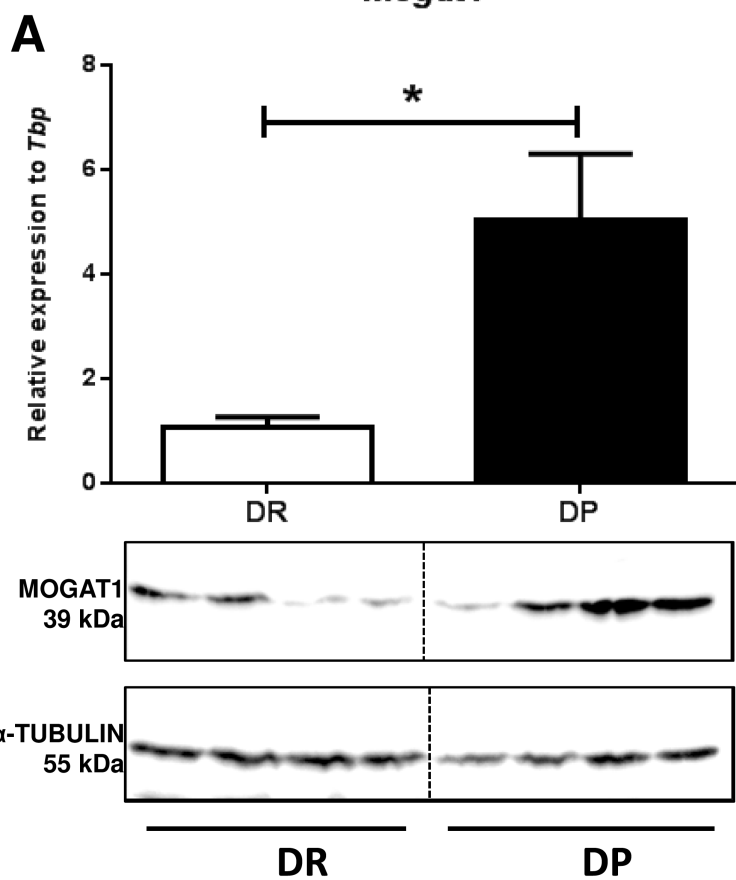


Figure 5

*Mogat1*



*Cd36*

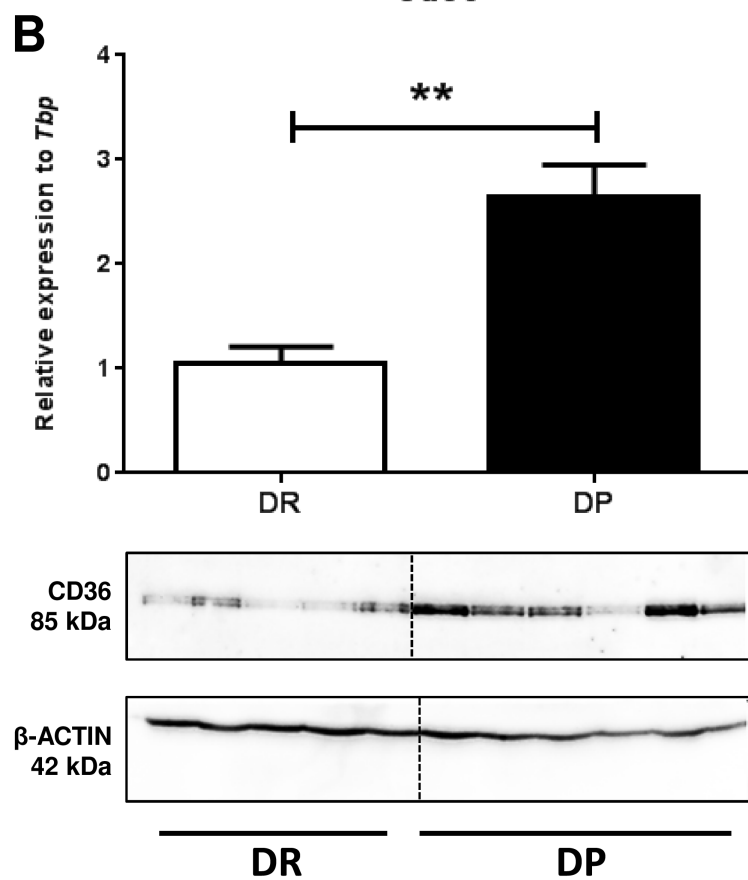


Figure 6

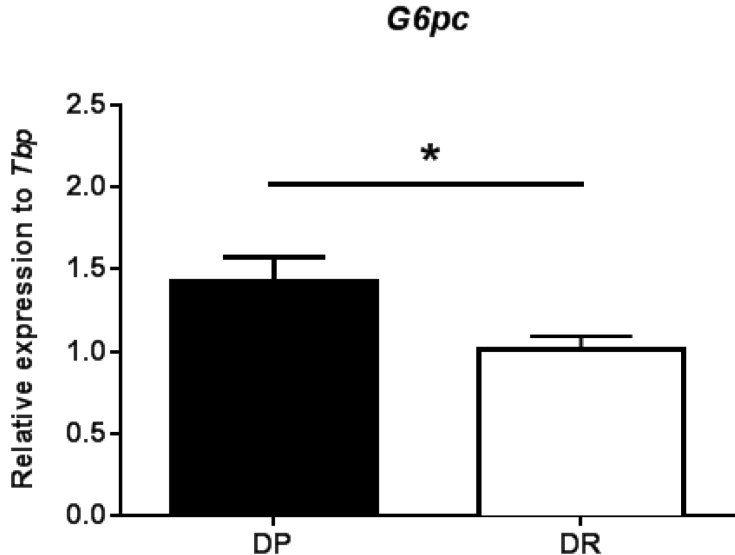
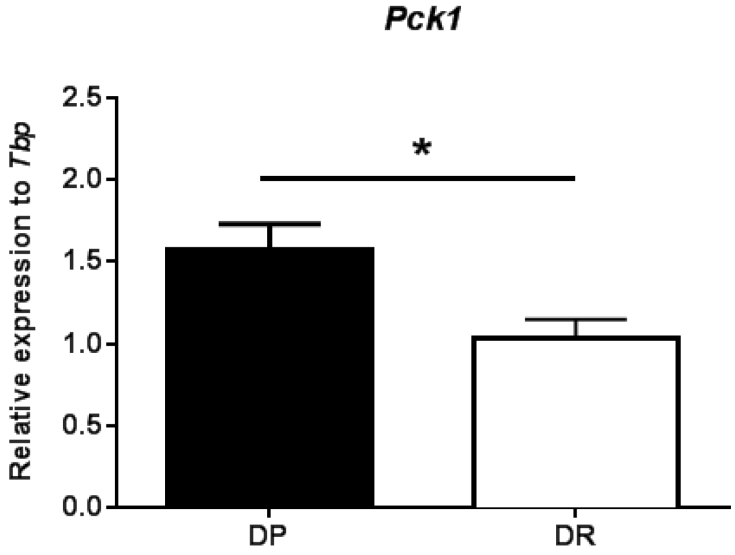


Figure 7

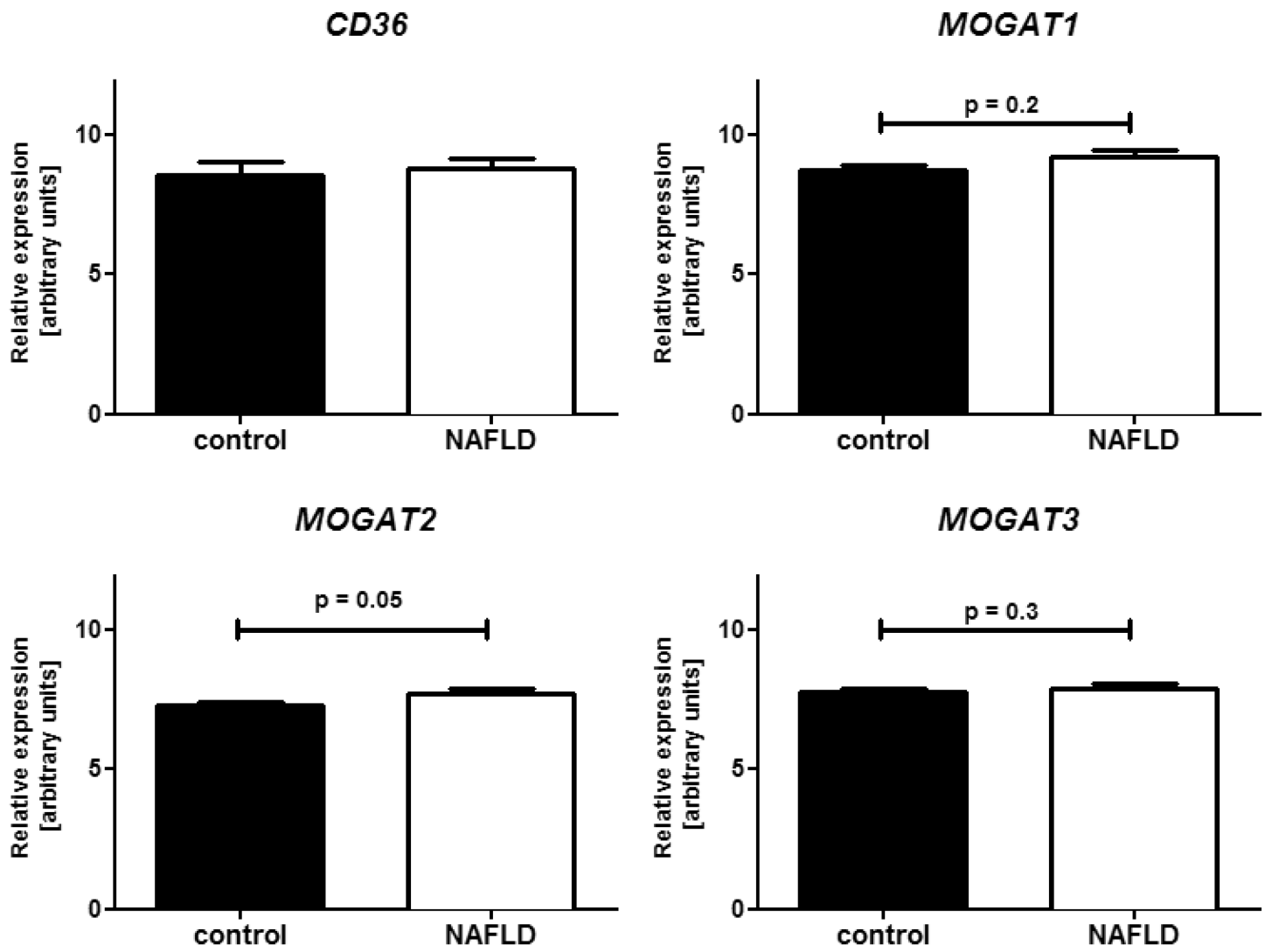
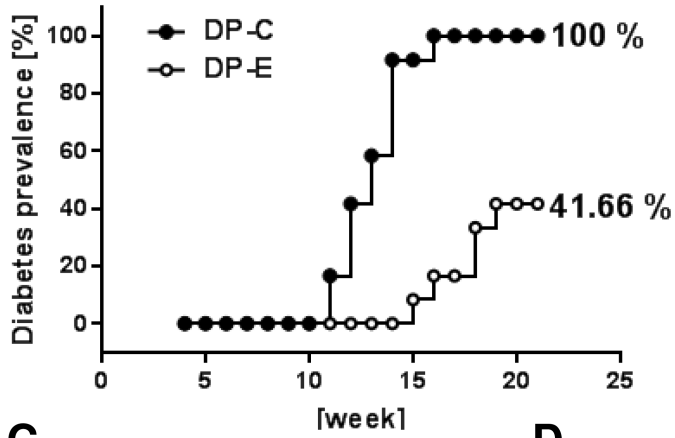


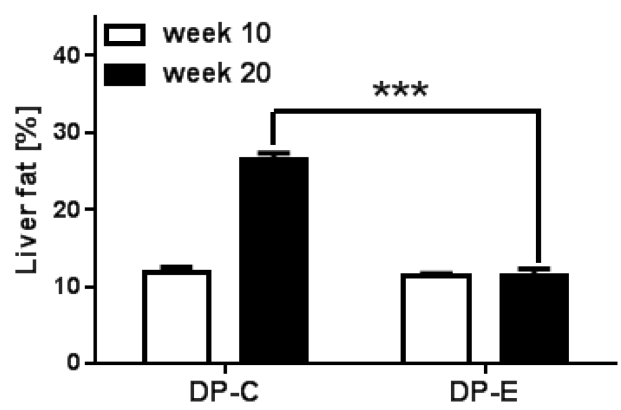


Figure 8

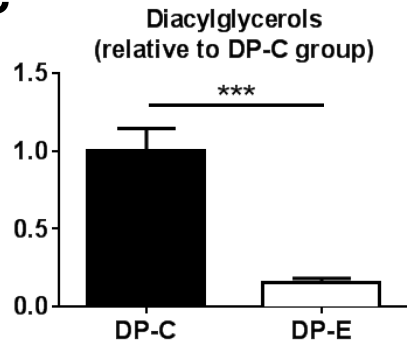
**A**



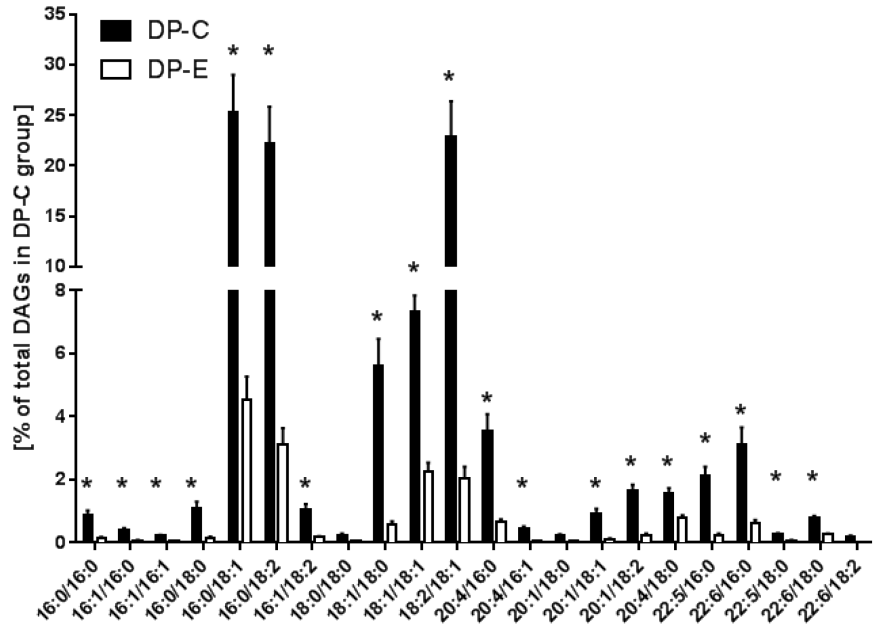
**B**



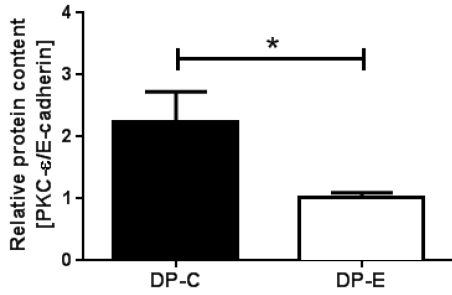
**C**



**D**

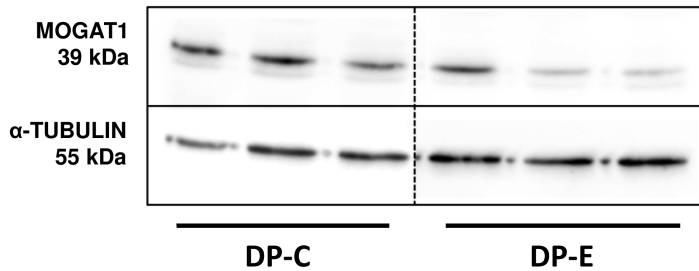
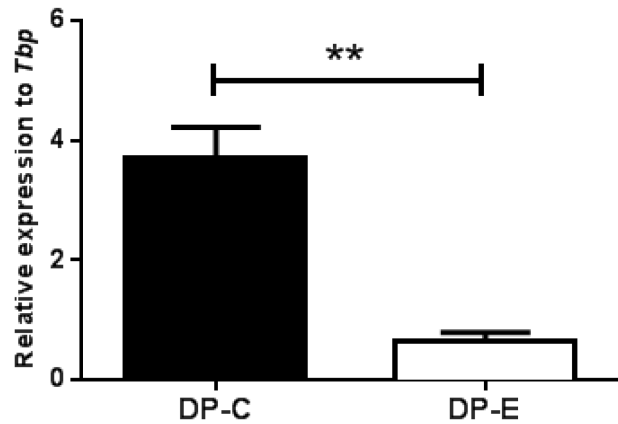


**E**



**F**

*Mogat1*



**G**

*Cd36*

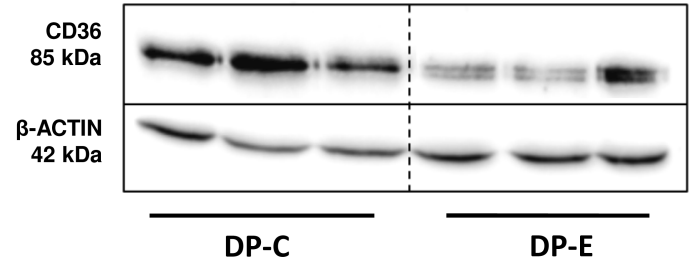
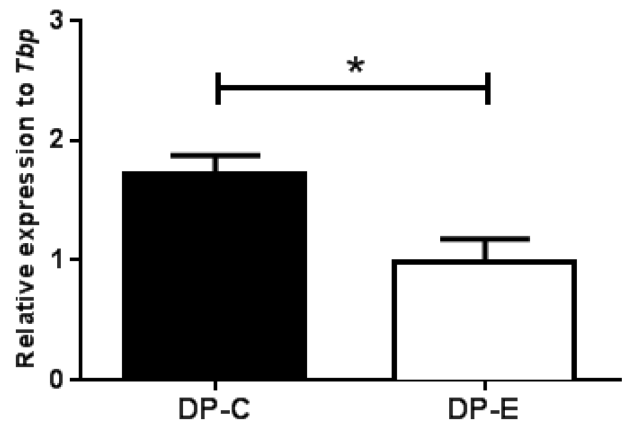


Figure 9

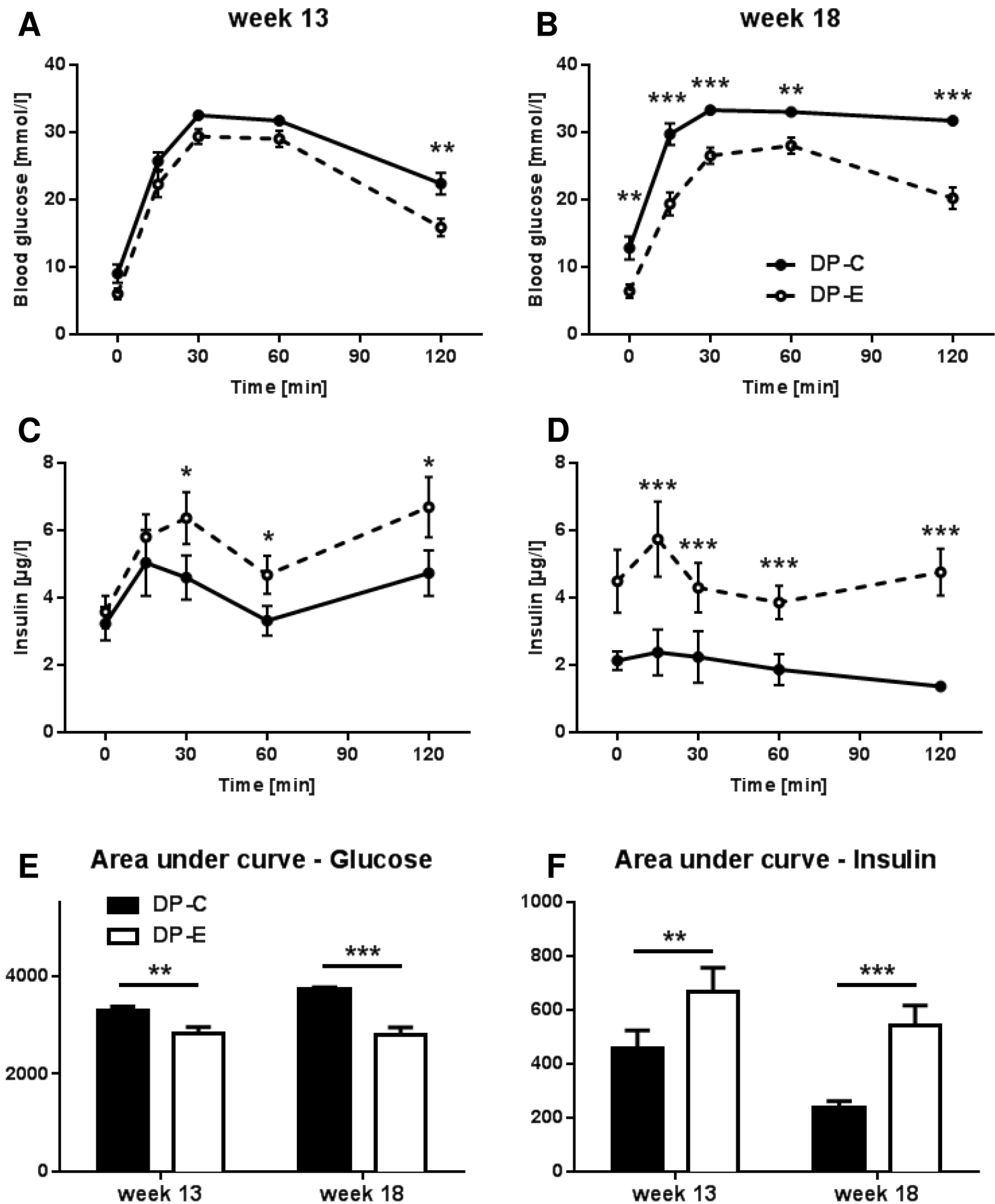


Figure 10

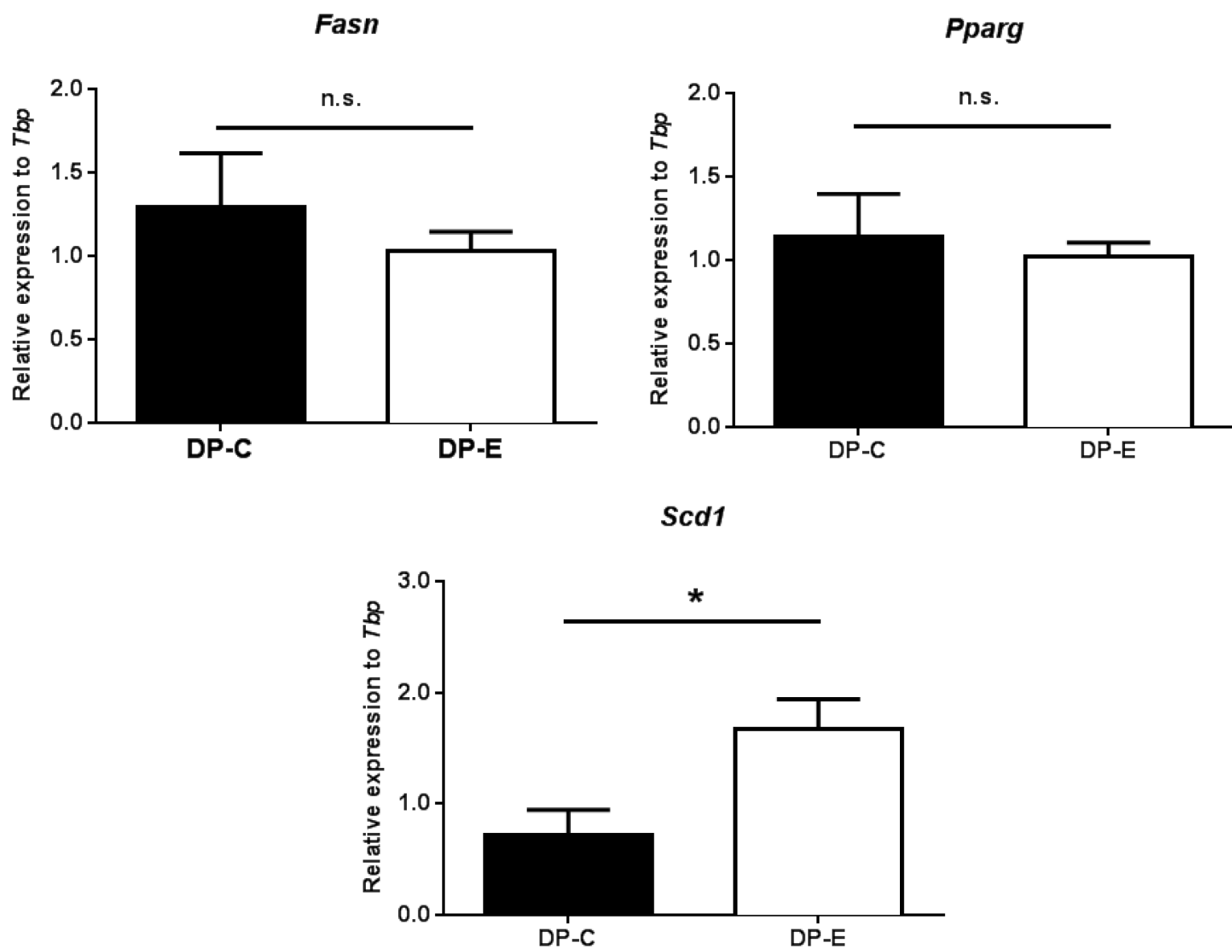


Table 1

GeneSymbol	Gene-ID	mean DR	mean DP	log2fold	fold change	pval
<i>Mogat1</i>	NM_026713	52.6	170.13	1.6935	3.2345	0.0497
<i>Ly6d</i>	NM_010742	88.54	271.76	1.6179	3.0695	0.0491
<i>Cml5</i>	NM_023493	69.79	187.82	1.4283	2.6912	0.0319
<i>Cyp4a14</i>	NM_007822	13963.23	35024.81	1.3267	2.5084	0.0213
<i>Shbg</i>	NM_011367	138.15	58.62	-1.2368	-2.3567	0.0154
<i>Cyp3a44</i>	NM_177380	6954.4	3023.32	-1.2018	-2.3003	0.0062
<i>Atp6v0d2</i>	NM_175406	253.49	117.87	-1.1047	-2.1506	0.0025
<i>Dlx6as2</i>	NR_002839	58.6	125.84	1.1026	2.1475	0.0336
<i>Apoa4</i>	NM_007468	5183.6	10956.2	1.0797	2.1136	0.0184
<i>Cyp4a31</i>	NM_001252539	1102.77	2289.74	1.0541	2.0764	0.0133
<i>A4gnt</i>	NM_001077424	65.74	132.14	1.0072	2.0101	0.0359
<i>Scn4b</i>	NM_001013390	50.73	100.5	0.9863	1.981	0.0264
<i>Atp1b2</i>	NM_013415	92.39	46.83	-0.9803	-1.9731	0.0068
<i>Col5a3</i>	NM_016919	103.29	203.35	0.9773	1.9687	0.032
<i>Fmo3</i>	NM_008030	6890.9	3596.3	-0.9382	-1.9161	0.019
<i>Cyp4a32</i>	NM_001100181	1816.31	3478.7	0.9375	1.9153	0.0183
<i>Igfbp1</i>	NM_008341	1540.36	2912.48	0.9190	1.8908	0.0317
<i>Slc22a26</i>	NM_146232	1855.37	1019.67	-0.8636	-1.8196	0.0022
<i>Clstn3</i>	NM_153508	169.73	307.72	0.8584	1.8131	0.0239
<i>Hamp</i>	NM_032541	15203.45	8411.96	-0.8539	-1.8074	0.0201
<i>Fitm1</i>	NM_026808	179.29	316.07	0.8179	1.7629	0.0218
<i>Cyp2g1</i>	NM_013809	1027.7	583.95	-0.8155	-1.7599	0.0021
<i>Cyp4a10</i>	NM_010011	13392.05	22618.64	0.7561	1.689	0.0369
<i>Gpr110</i>	NM_133776	131.09	79.27	-0.7257	-1.6537	0.0394
<i>Trpm1</i>	NM_001039104	246.44	149.11	-0.7249	-1.6528	0.0155
<i>Cmya5</i>	NM_023821	158.88	96.16	-0.7244	-1.6522	0.0289
<i>Cd36</i>	NM_007643	476.48	787.15	0.7242	1.652	0.0101
<i>Aym1</i>	NM_001012726	80.7	131.4	0.7033	1.6283	0.0149
<b> log2(fold change)  &lt; 0.7</b>						
<i>Pck1</i>	NM_011044	20341.13	30161.63	<b>0.5683</b>	1.4828	0.0041
<i>G6pc</i>	NM_008061	8137	12600.82	<b>0.6309</b>	1.5486	0.0352

Table 2

GeneSymbol	Gene-ID	mean DR	mean DP	log2fold	fold change	pval
<b>TG Synthesis</b>						
<i>Gpam</i>	NM_008149	110.69	133.27	0.26785	1.2040	0.1090
<i>Gpat2</i>	NM_001081089	106.39	93.07	-0.19297	-1.1431	0.1400
<i>Agpat1</i>	NM_001163379	171.76	152.99	-0.16696	-1.1227	0.0371
<i>Agpat2</i>	NM_026212	3652.35	4547.19	0.31615	1.2450	0.0638
<i>Agpat3</i>	NM_053014	10694.07	9935.12	-0.10620	-1.0764	0.1966
<i>Agpat4</i>	NM_026644	128.21	109.79	-0.22374	-1.1678	0.0224
<i>Agpat5</i>	NM_026792	545.48	562.14	0.04339	1.0305	0.3869
<i>Agpat6</i>	NM_018743	6038.75	6277.38	0.05591	1.0395	0.5717
<i>Lclat1</i>	NM_001081071	621.42	661.12	0.08934	1.0639	0.1564
<i>Agpat9</i>	NM_172715	1661.60	1776.97	0.09685	1.0694	0.1581
<i>Lpin1</i>	NM_001130412	229.23	254.89	0.15307	1.1119	0.5038
<i>Lpin2</i>	NM_001164885	331.23	375.52	0.18107	1.1337	0.3089
<i>Mogat1</i>	NM_026713	52.60	170.13	1.69353	3.2345	0.0497
<i>Mogat2</i>	NM_177448	42.47	50.06	0.23719	1.1787	0.3215
<i>Ppap2c</i>	NM_015817	1318.62	1022.74	-0.36660	-1.2893	0.0029
<i>Dgat1</i>	NM_010046	492.49	513.58	0.06051	1.0428	0.3985
<i>Dgat2</i>	NM_026384	46458.21	43908.51	-0.08143	-1.0581	0.2643
<b>Fatty Acid Synthesis</b>						
<i>Fasn</i>	NM_007988	703.00	876.13	0.3176	1.2463	0.3106
<i>Acaca</i>	NM_133360	1248.97	1246.13	-0.0033	-1.0023	0.9811
<i>Scd1</i>	NM_009127	5984.96	10108.73	0.7562	1.6890	0.0858
<i>Acacb</i>	NM_133904	891.01	1185.03	0.4114	1.3300	0.0364
<i>Mcat</i>	NM_001030014	1704.97	1702.39	-0.0022	-1.0015	0.9576
<i>Pdha1</i>	NM_008810	533.03	703.05	0.3994	1.3190	0.0104
<i>Pdha2</i>	NM_008811	1.72	1.89	0.1315	1.0954	0.3976
<i>Pdhb</i>	NM_024221	6677.90	6498.61	-0.0393	-1.0276	0.6408
<i>Pdk1</i>	NM_172665	172.67	181.83	0.0746	1.0531	0.4737
<i>Pdk2</i>	NM_133667	2327.40	2249.41	-0.0492	-1.0347	0.6635
<i>Pdk3</i>	NM_145630	7.15	7.22	0.0134	1.0094	0.9613
<i>Pdk4</i>	NM_013743	195.02	296.48	0.6044	1.5203	0.0728
<i>Pdp1</i>	NM_001098230	35.41	29.61	-0.2580	-1.1958	0.1277
<i>Pdp2</i>	NM_001024606	596.14	609.19	0.0312	1.0219	0.7094
<i>Dlat</i>	NM_145614	323.16	313.22	-0.0451	-1.0318	0.6138
<i>Did</i>	NM_007861	1265.16	1519.55	0.2643	1.2011	0.0017
<i>Elovl6</i>	NM_130450	1437.22	2468.09	0.7801	1.7173	0.0589
<b>TG Hydrolysis</b>						
<i>Lipe</i>	NM_010719	37.07	33.49	-0.1465	-1.1069	0.4359
<i>Pnpla2</i>	NM_001163689	1498.10	1365.47	-0.1337	-1.0971	0.0948
<b>Transcription factors</b>						
<i>Srebf1</i>	NM_011480	703.60	718.77	0.0308	1.0216	0.8345
<i>Ppara</i>	NM_011144	4685.93	4631.22	-0.0169	-1.0764	0.9104
<i>Pparg</i>	NM_011146	367.85	535.41	0.5415	1.4555	0.0461
<b>Fatty acid transporters</b>						
<i>Slc27a2</i>	NM_011978	46096.47	41158.16	-0.1635	-1.0764	0.4849
<i>Slc27a5</i>	NM_009512	70194.59	68594.14	-0.0333	-1.0764	0.3783
<i>Cd36</i>	NM_007643	476.48	787.15	0.7242	1.6520	0.0101
<i>Fabp1</i>	NM_017399	135958.71	143369.63	0.0766	1.0545	0.1785
<i>Acsl1</i>	NM_007981	15340.11	16955.73	0.14446	1.1053	0.0317
<i>Acsl4</i>	NM_207625	1792.81	1696.05	-0.0800	-1.0764	0.4999
<i>Acsl5</i>	NM_027976	3822.18	4252.40	0.1539	1.1126	0.0777

**Table 3**

	<b>NAFLD</b>	<b>No NAFLD</b>	<b>P-value</b>
<i>n (male) (n)</i>	8 (3)	8 (5)	-
<i>Age (years)</i>	57 ± 5	49 ± 5	0.33
<i>BMI (kg/m<sup>2</sup>)</i>	30.5 ± 3.7	24.7 ± 1.5	0.28
<i>CRP (mg/dl)</i>	1.9 ± 0.9	1.6 ± 0.6	0.85
<i>Fasting glucose (mg/dl)</i>	91.5 ± 6.2	90.7 ± 2.2	0.80
<i>HbA1c (%)</i>	5.4 ± 0.2	5.6 ± 0.2	0.61
<i>Triglycerides (mg/dl)</i>	126.6 ± 0.4	93.3 ± 8.3	0.05
<i>High density lipoprotein (mg/dl)</i>	45.9 ± 2.7	44.0 ± 4.1	0.88
<i>NAFLD activity score (0-8)</i>	2.9 ± 0.4	-	0.01
<i>Histological liver steatosis (%)</i>	38.7 ± 8.1	1.2 ± 1.2	<0.001