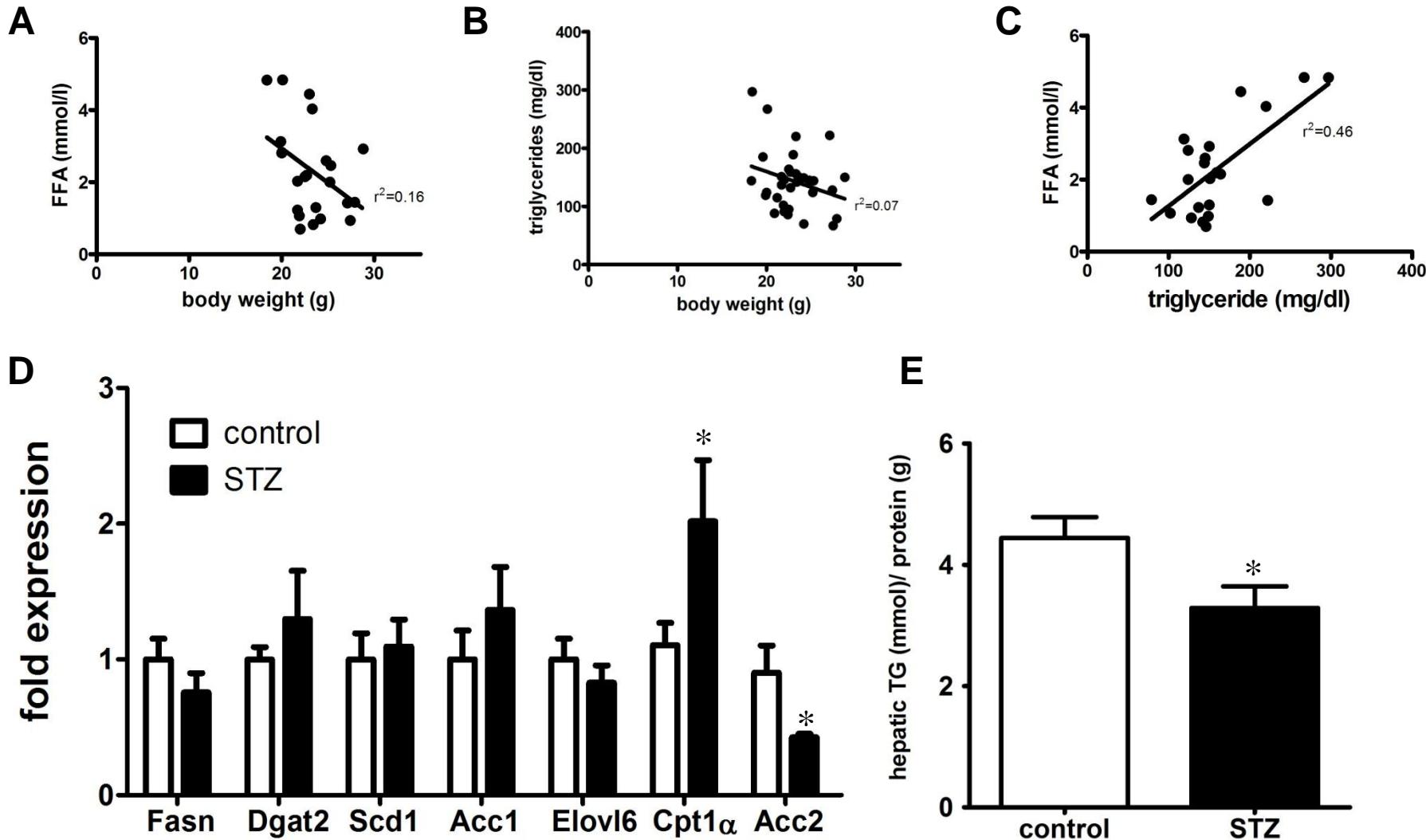


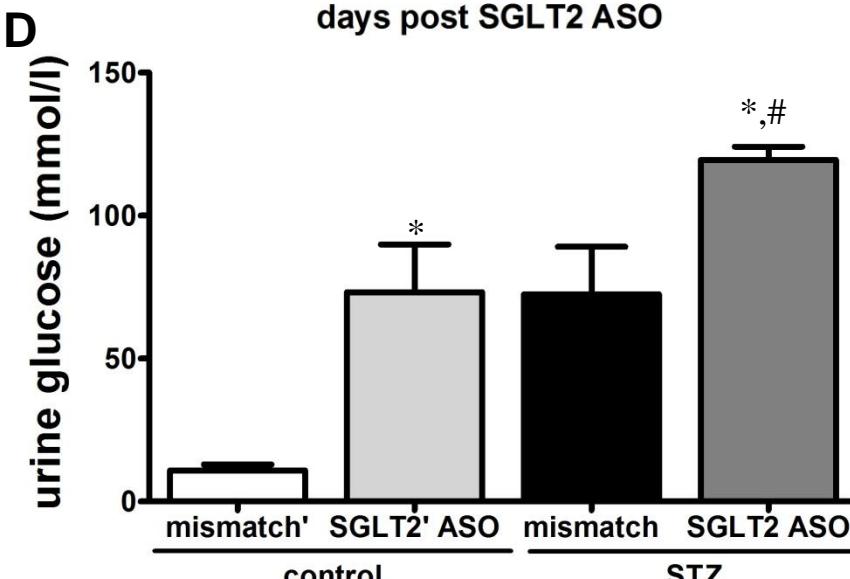
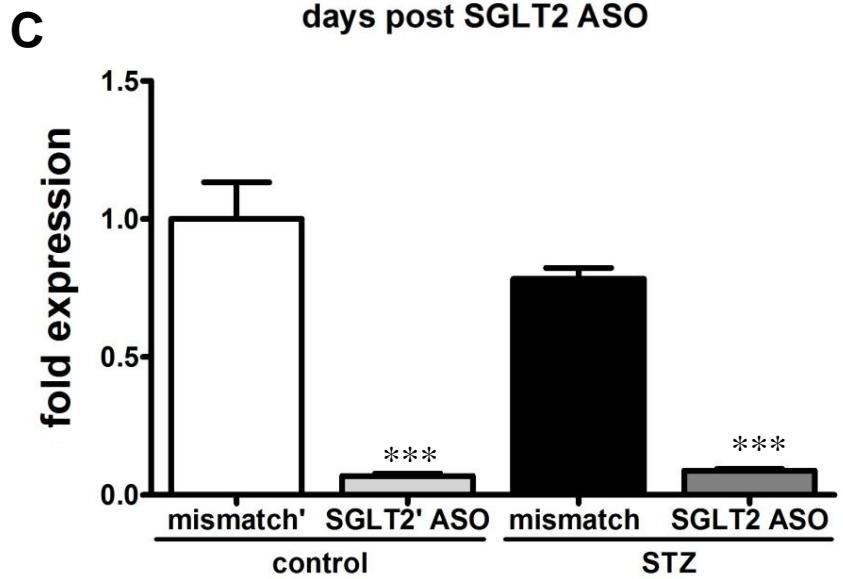
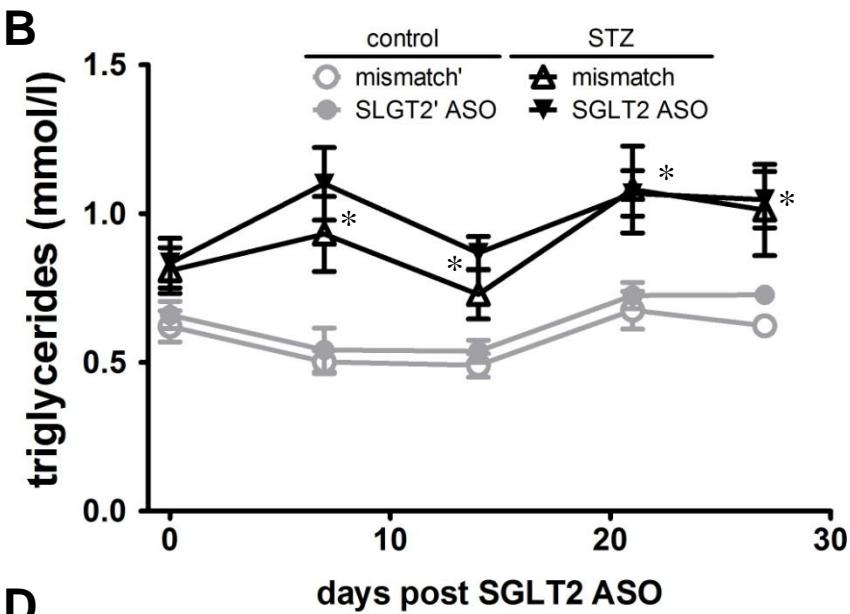
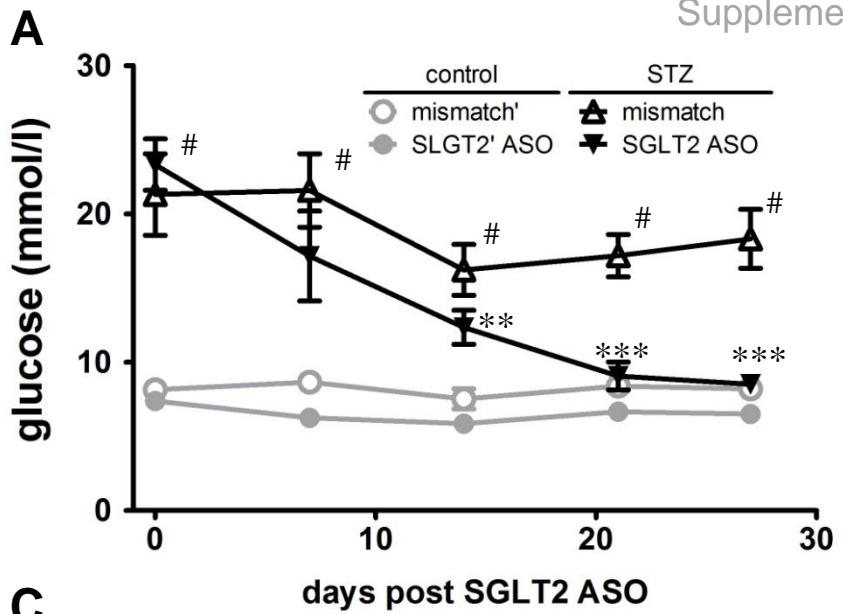
Supplement Material

Supplement I



Supplemental Figure I: Multivariate analysis comparing **(A)** FFA and body weight, **(B)** TG and body weight and **(C)** TG and FFA. **(D)** Hepatic gene expression of *Fasn*, *Dgat2*, *Scd1*, *Acc1*, *Elovl6*, *Cpt1 α* and *Acc2* was assessed in mice with 8 weeks of STZ-diabetes using quantitative real-time PCR. Gene expression is expressed relative to fed non-diabetic control mice ($n = 5-8/\text{group}$) **(E)** TG content in livers of 8 weeks STZ-diabetic mice ($n = 5-8/\text{group}$). *: $p \leq 0.05$ vs. control. Results are presented as mean \pm SEM.

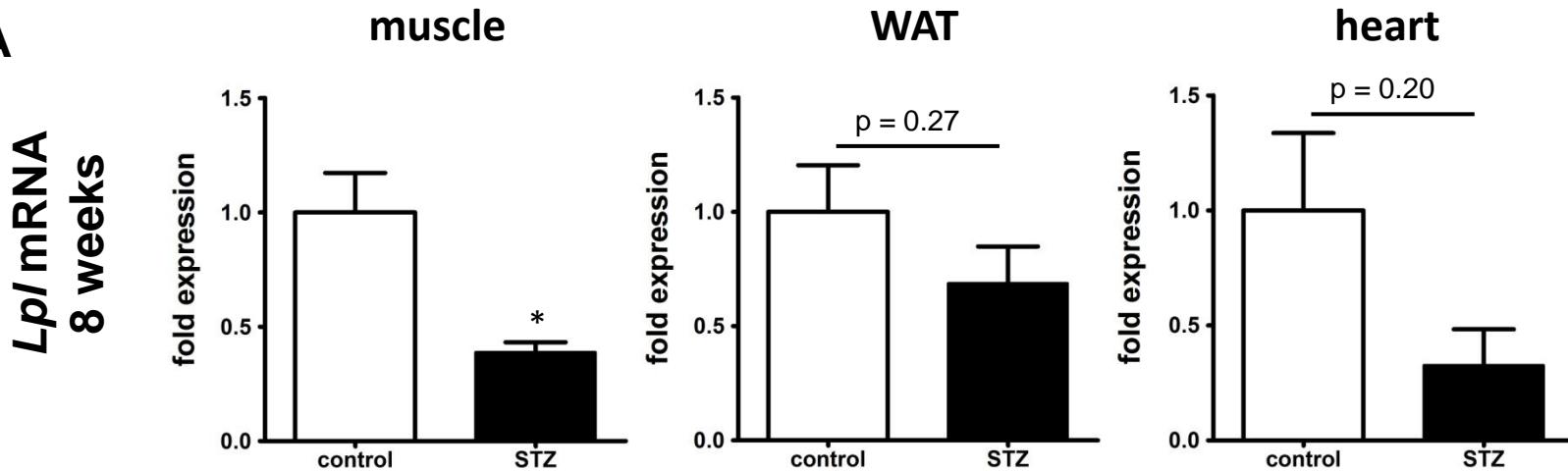
Supplement II



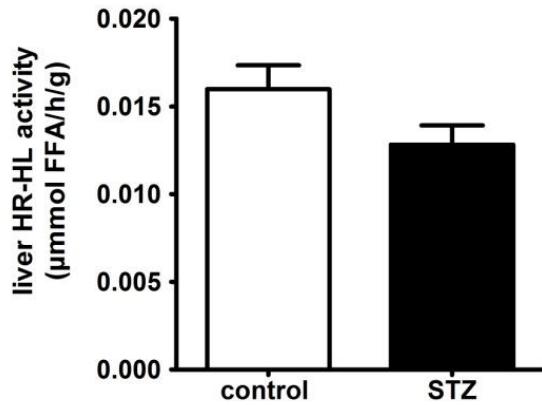
Supplemental Figure II: Glucose reduction in STZ-diabetic mice by SGLT2-antisense does not reduce plasma TG levels (A)
 Course of 4 hours fasting glucose levels over 28 days. **: p ≤ 0.01, ***: p ≤ 0.001 vs. STZ + mismatch, #: p ≤ 0.001 vs. control + mismatch. **(B)** Course of 4 hours fasting TG levels, *: p ≤ 0.05 STZ-diabetic groups vs. respective non-diabetic control groups. **(C)** Gene expression of SGLT2 in the kidney of the different treatment groups, ***: p ≤ 0.001 vs. respective mismatch group. **(D)** Glucose levels in the urine of the different treatment groups. *: p ≤ 0.05 SGLT2-ASO mice vs. respective mismatch mice, #: p ≤ 0.001 vs. control + mismatch. (n = 5-8/group for all panels). Results are presented as mean ± SEM.

Supplement III

A

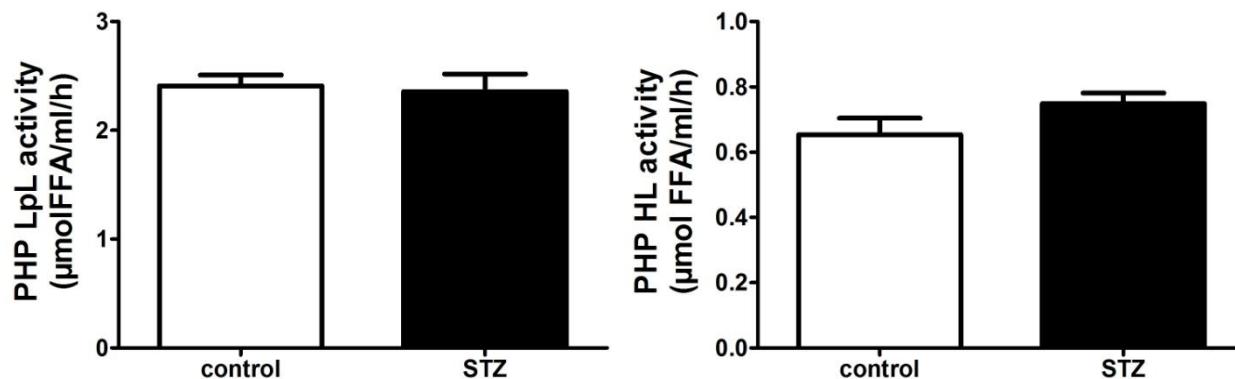


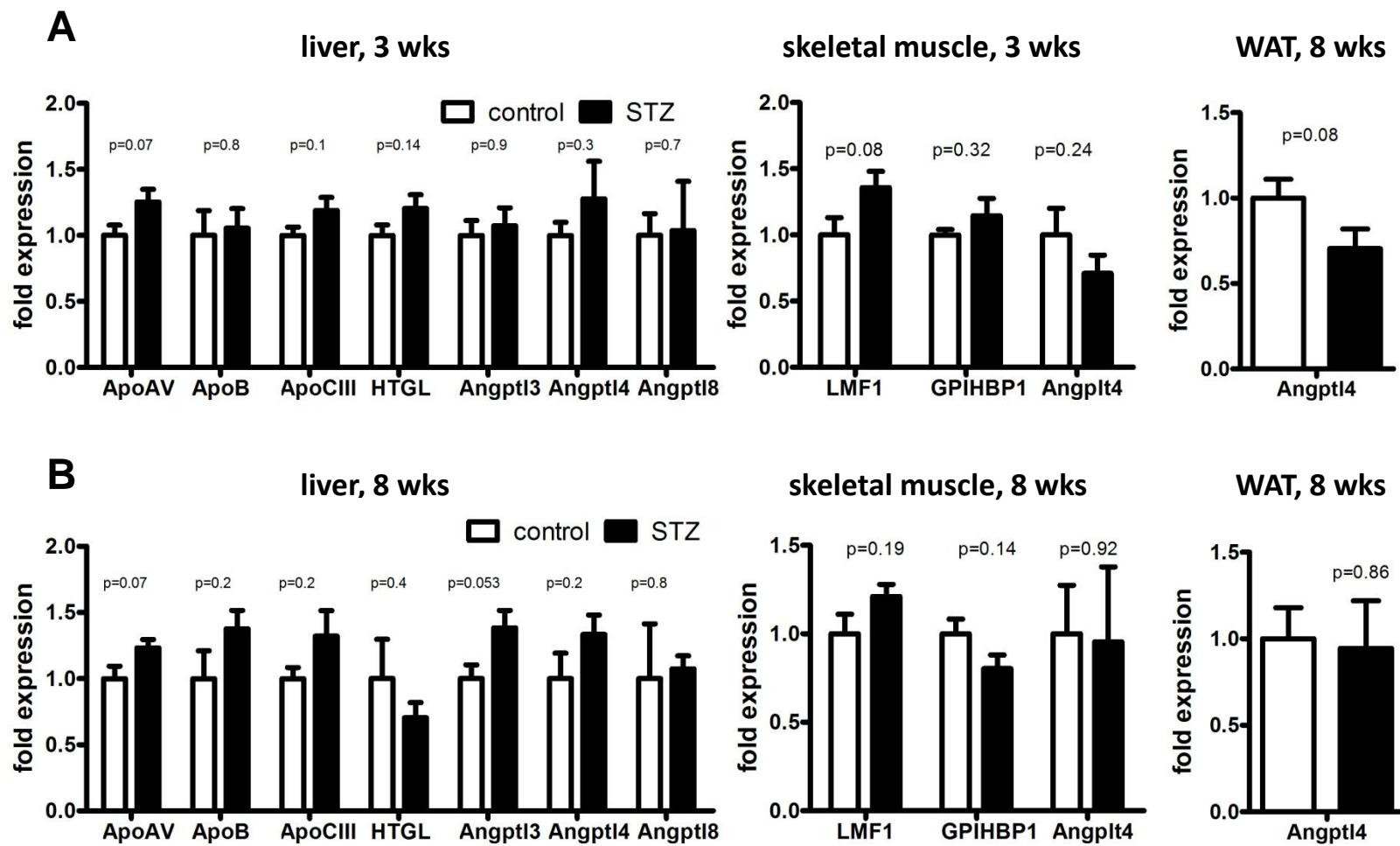
B



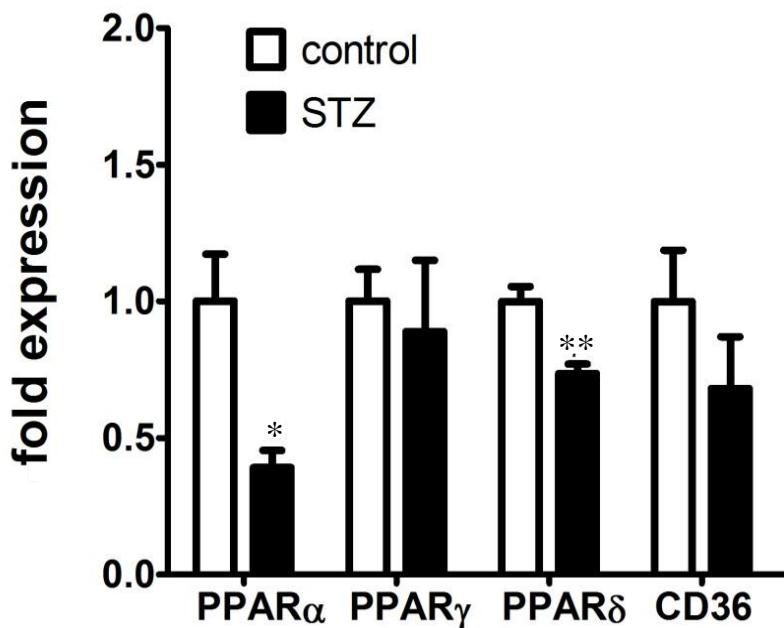
Supplemental Figure III: (A) *LpI* mRNA analysis by quantitative PCR in skeletal muscle, WAT and heart at 8 weeks of diabetes. *: $p \leq 0.05$ vs. non-diabetic control ($n = 5-8/\text{group}$). (B) heparin-releasable hepatic lipase (HL) activity from liver tissue. (C) Post-heparin plasma (PHP) LpL and hepatic lipase (HL) activity at 3 weeks of diabetes ($n = 5/\text{group}$). Results are presented as mean \pm SEM.

C





Supplemental Figure IV: Gene expression of apolipoproteins and regulators of lipolysis in liver, skeletal muscle and WAT after 3 (**A**) and 8 weeks (**B**) of STZ-diabetes using quantitative real-time PCR (n = 5/group for 3 weeks and 5-8/group for 8 weeks). Results are presented as mean \pm SEM.



Supplemental Figure V: Gene expression of *PPAR α* , *PPAR δ* , *PPAR γ* and *CD36* was assessed in the skeletal muscle after 8 weeks of STZ-diabetes using quantitative real-time PCR ($n = 5$ -8/group). *: $p \leq 0.05$, **: $p \leq 0.01$. Results are presented as mean \pm SEM.

Supplemental table I

Supplemental Table I: Primer sequences used for RT-PCR

gene	forward primer	reverse primer
acc1	aac atc ccc acg cta aac ag	agg tcc gga aag aga cca tt
acc2	tgg agtc cat ctt cct gtc c	gga cgc cat aca gac aac ct
angptl3	aca tgt ggc tga gat tgc tg	gct gga gca tca ttt tgg at
angptl4	gga aaa gat gca ccc ttc aa	tgc tgg atc ttg ctg ttt tg
angptl8	gtg ctg caa gga aca ctg aa	tcc aca ggg ctc tgt ctt ct
apoAIV	gag tcg agt gct gca cca ta	acg tgt gag ttt gtg gga ca
apob	aag cac ctc cga aag tac gtg	ctc cag ctc tac ctt aca gtt ga
apocIII	agc gtg cag gag tcc gat ata gc	aga atc cca gaa gcc ggt gaa c
cpt1β	tcg tca cct ctt ctg cct tt	aca cac cat agc cgt cat ca
dgat2	ctgtcacctggctcaacaga	tat cag cca gca gtc tgt gc
elovl6	aca acc tcc ggg cat agg ta	cag agt gtg gtg gag tct gg
fasn	tac caa gcc aag cac att cg	tgg ctt cgg cga tga ga
gpihbp1	ggg cac aag aag atg gtg at	ctg gag cag ctc tgt gtc tg
htgl	gac tgg atc tcc ctg gca ta	agg tga act ttg ctc cga ga
lmf1	ctc agc gta ccc gtg gtt at	cgg tag tgg tat ggc gag at
lpl	atc aac tgg atg gag gag gtt	ttg gtc aga ctt cct gct acg c
opara	tgc aaa ctt gga ctt gaa cg	gatcagcatcccgtcttgt
ppary	gag tgt gac gac aag att tg	ggtgggccagaatggcatct
pparδ	tgg agc tcga tga cag tgac	gta ctg gct gtc agg gtg gt
scd1	ctc ctg ctg atg tgc ttc atc c	agt gta tcg caa gaa ggt gct aac
sglt-2	att gtc tcg ggc tgg tatt g	tta gag cag ccc acc tca gt