

Alterations of the expression levels of glucose and iron metabolism related miRNAs and their target genes in the hypothalamus of STZ-induced rat diabetes model

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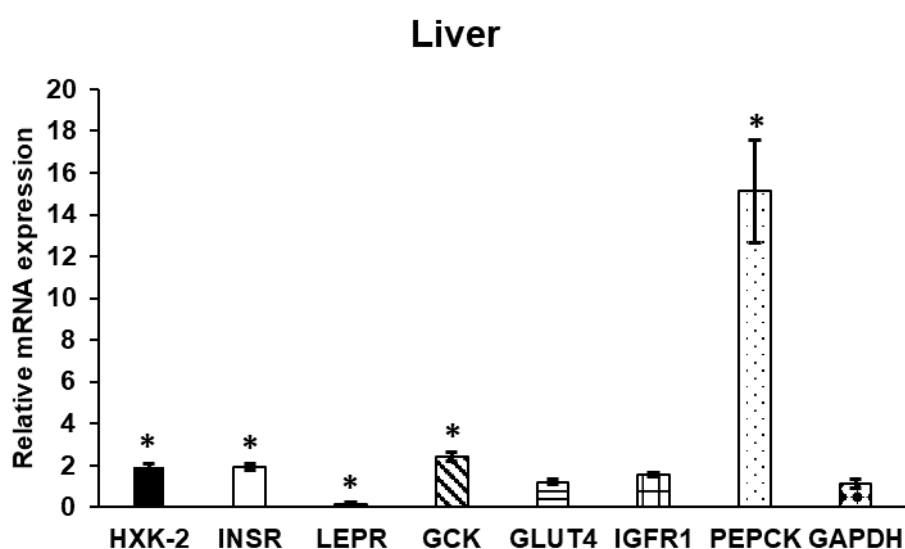
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Supplementary Table 1. Expression level of glucose metabolism-related miRNAs

miRNA	Expression (±SD)	Target genes
rno-miR-135b-5p	1.205 (0.044)	GLUT4 Hexokinase 2
rno-miR-194-5p	0.606 (0.022)	Insulin receptor
rno-miR-21-5p	1.085 (0.031)	GLUT4
rno-miR-200a-3p	0.107 (0.011)	Leptin receptor Insulin receptor
rno-miR-152-3p	0.689 (0.021)	Glucokinase
rno-miR-96-5p	0.072 (0.023)	IGF1R
rno-miR-29a-3p	1.476 (0.049)	PEPCK



Supplementary figure 1. mRNA analysis of the target genes of glucose metabolism related miRNAs. Real time PCR was carried out using a SYBR Green protocol. β -actin housekeeping gene was used as

internal control for the normalization of the reaction. The relative gene expression of the control liver samples was regarded as 1. Real time polymerase chain reactions were carried out in triplicate in each independent experiment. The columns represent mean values, error bars show standard deviation (SD) of three independent determinations (n = 3). Asterisk indicates $p < 0.05$ compared to the control. Abbreviations: HXK-2-hexokinase-2; INSR-insulin receptor; LEPR-leptin receptor; GCK-glucokinase; GLUT4-glucose transporter 4; IGFR1-insulin-like growth factor receptor 1; PEPCK-phosphoenolpyruvate carboxykinase; GAPDH- glyceraldehyde 3-phosphate dehydrogenase; STZ-streptozotocin.