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ANALYSIS OF BLOOD LNCRNA EXPRESSION PROFILES IN TYPE 2 DIABETES INDIVIDUALS WITH DYSLIPIDEMIA

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INTRODUCTION
Long noncoding RNAs (lncRNAs) are large RNA transcripts present in the blood without protein-coding capacity, with specific expression profiles for type 2 diabetes (T2D) and other conditions such as dyslipidemia (DLP). The objective of this study was to identify blood lncRNAs associated with well- and poorly-controlled T2D with DLP.

METHODOLOGY
Previous data of the T2D studies (GSE156993 and GSE15932) were retrieved from the NCBI GEOdatasets website and re-analyzed for the differential lncRNA expression for these groups: (1) healthy controls (CON, n=14), (2) T2D well-controlled without DLP (T2D, n=8), (3) DLP without T2D (DLP, n=6), (4) T2D well-controlled with DLP (T2D-DLPW, n=6), and (5) T2D poorly-controlled with DLP (T2D-DLPP, n=6). MicroRNAs predicted to bind to the significant lncRNAs (miRNet) were determined and continued with biological pathway analyses (KEGG).

RESULTS
The first two comparisons (T2D/CON and DLP/CON) resulted in 33 dysregulated lncRNAs [-1.5<log2 Fold Change (log2FC) >1.5, adjusted p-value<0.05. Among these, seven lncRNAs were specific to T2D, and nine specific to DLP. Another three comparisons (T2D-DLPW/T2D, T2D-DLPP/T2D and T2D-DLPP/T2D-DLPW) resulted in 308 dysregulated lncRNAs. From these, 37 were specific to T2D-DLPP and 87 specific to T2D-DLPW. Two lncRNAs, XIST and LINC01857, were upregulated only in T2D-DLPP compared to T2D (log2FC=5.86, adjusted p-value=0.002 and log2FC=1.73, adjusted p-value<0.001, respectively) and T2D-DLPW (log2FC=3.71, adjusted p-value=0.037 and log2FC=2.50, adjusted p-value=0.022, respectively). The biological pathway analyses showed that lncRNA XIST and LINC01857 might be involved in insulin resistance, apoptosis and inflammation pathways. Both lncRNAs are predicted to interact with miR-146b-5p, found to be associated with HbA1C level.

CONCLUSION
Blood lncRNA XIST and LINC01857 may be involved in poor glucose control of T2D with DLP.