Supplementary Material

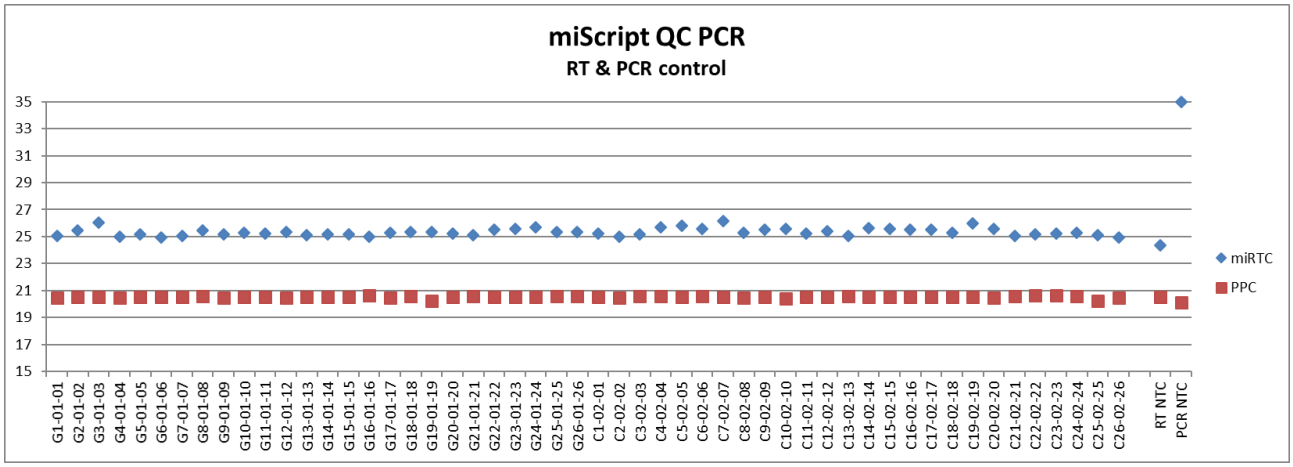
Supplementary Tables

Supplementary Table 1: Pearson's correlation test of miRNAs and HbA_{1c} in the mothers with type 1 diabetes (n=26), two-tailed correlation(r); $p<0.05$ and with correction for multiple testing using Benjamini-Hochberg procedure (adj. p-value).

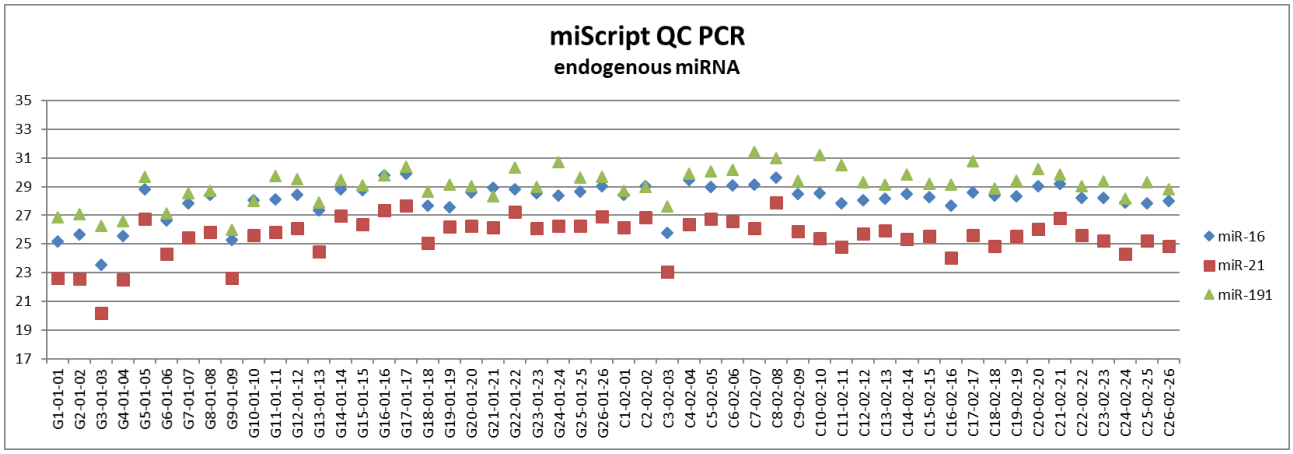
miRNA correlation to HbA_{1c} in mothers with type 1 diabetes			
miRNA name	**Correlation (r)**	**p-value**	**Adj p-value**
hsa-miR-6839-5p	0.710	0.00005	0.0086
hsa-miR-891a-5p	0.657	0.00027	0.0238
hsa-miR-1260a	0.656	0.00027	0.0161
hsa-miR-7977	0.637	0.00047	0.0208
hsa-miR-874-3p	0.633	0.00052	0.0183

Supplementary Figures

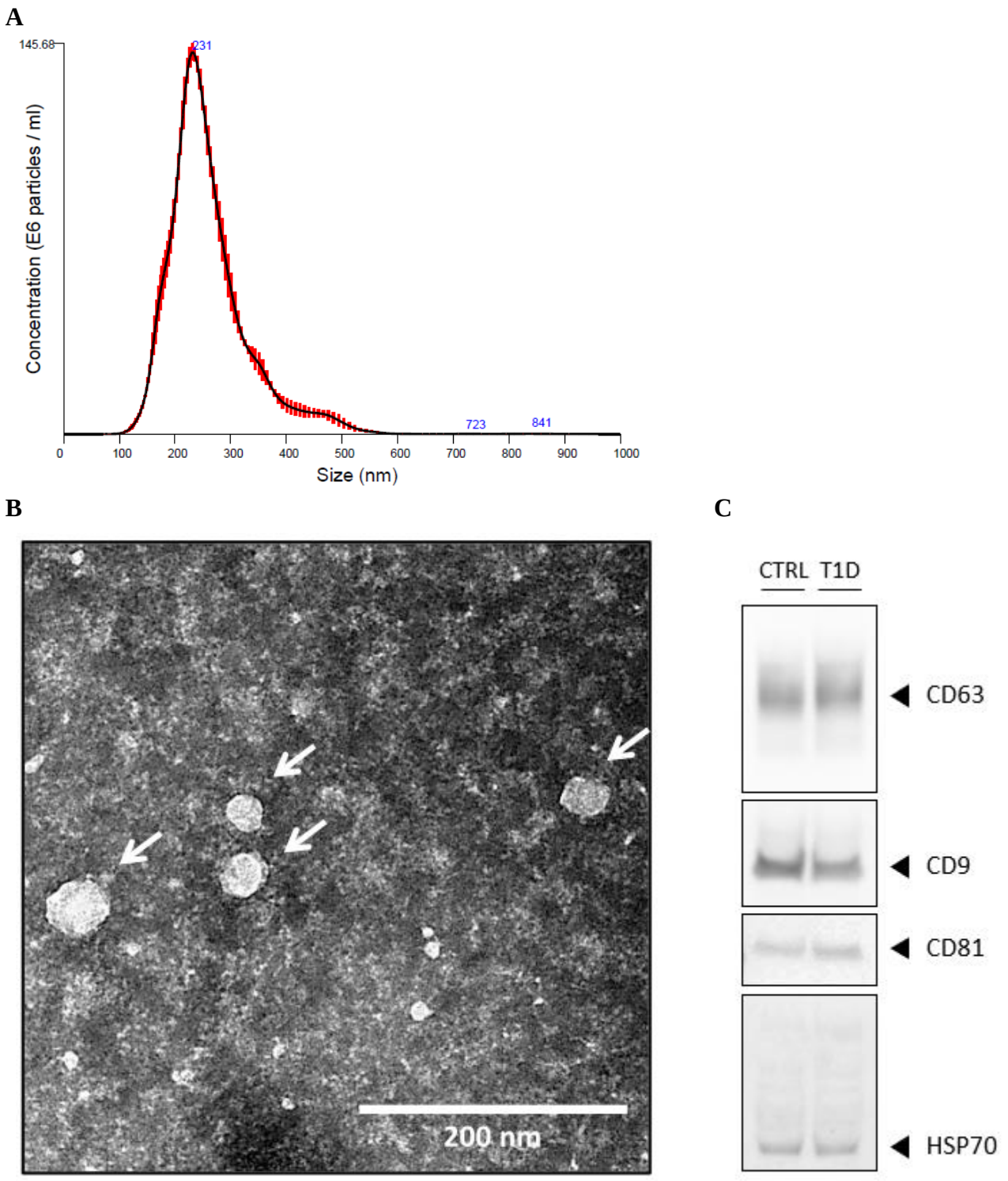
A



B

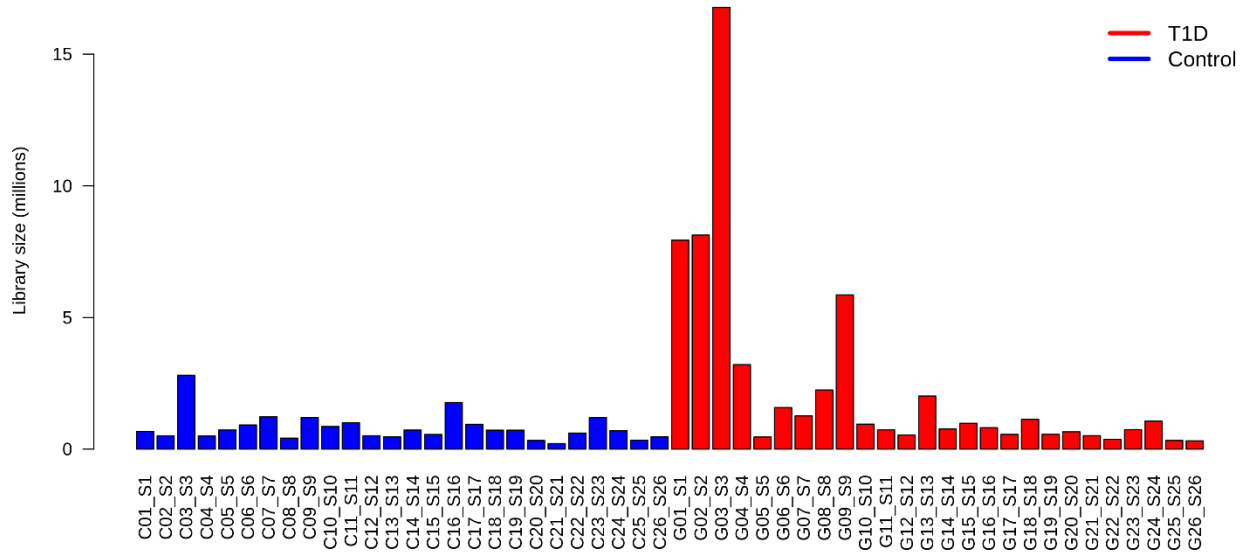


Supplementary Figure 1. The assessment of RNA extracted from exosome-enriched extracellular vesicles. (A) Quality control (QC) of RNA extracted from exosome-enriched extracellular vesicles by assessment of reverse transcription (RT) and PCR performances using miRTC miScript Primer Assay and positive PCR control (PPC) assay. (B) The RNA sample quality was further assessed by measured expression of ubiquitously expressed miR-16, miR-21, and miR-191 using miScript miRNA QC PCR Array. These miRNAs are known to be ubiquitously expressed in a wide range of cells, tissues and body fluid samples (including whole blood, serum, and plasma).



Supplementary Figure 2. Characterization of exosome-enriched extracellular vesicles derived from plasma samples. (A) Particle concentration per ml and size distribution (nm) +/- 1 standard error of the mean (red) analyzed by Nanosight NTA analysis. (B) Transmission electron microscopy of freshly prepared plasma-derived extracellular vesicles (indicated by arrows) by staining with 2% phosphotungstic acid. (C) Western blots of CD63 (30-60 kDa), CD9 (25 kDa), CD81 (26 kDa) and HSP70 (70 kDa) on plasma-derived extracellular vesicles from healthy control mothers (CTRL) or mothers with type 1 diabetes (T1D).

A


T1D
Control
Library size (millions)
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5
10
15
C01_S1
C02_S2
C03_S3
C04_S4
C05_S5
C06_S6
C07_S7
C08_S8
C09_S9
C10_S10
C11_S11
C12_S12
C13_S13
C14_S14
C15_S15
C16_S16
C17_S17
C18_S18
C19_S19
C20_S20
C21_S21
C22_S22
C23_S23
C24_S24
C25_S25
C26_S26
G01_S1
G02_S2
G03_S3
G04_S4
G05_S5
G06_S6
G07_S7
G08_S8
G09_S9
G10_S10
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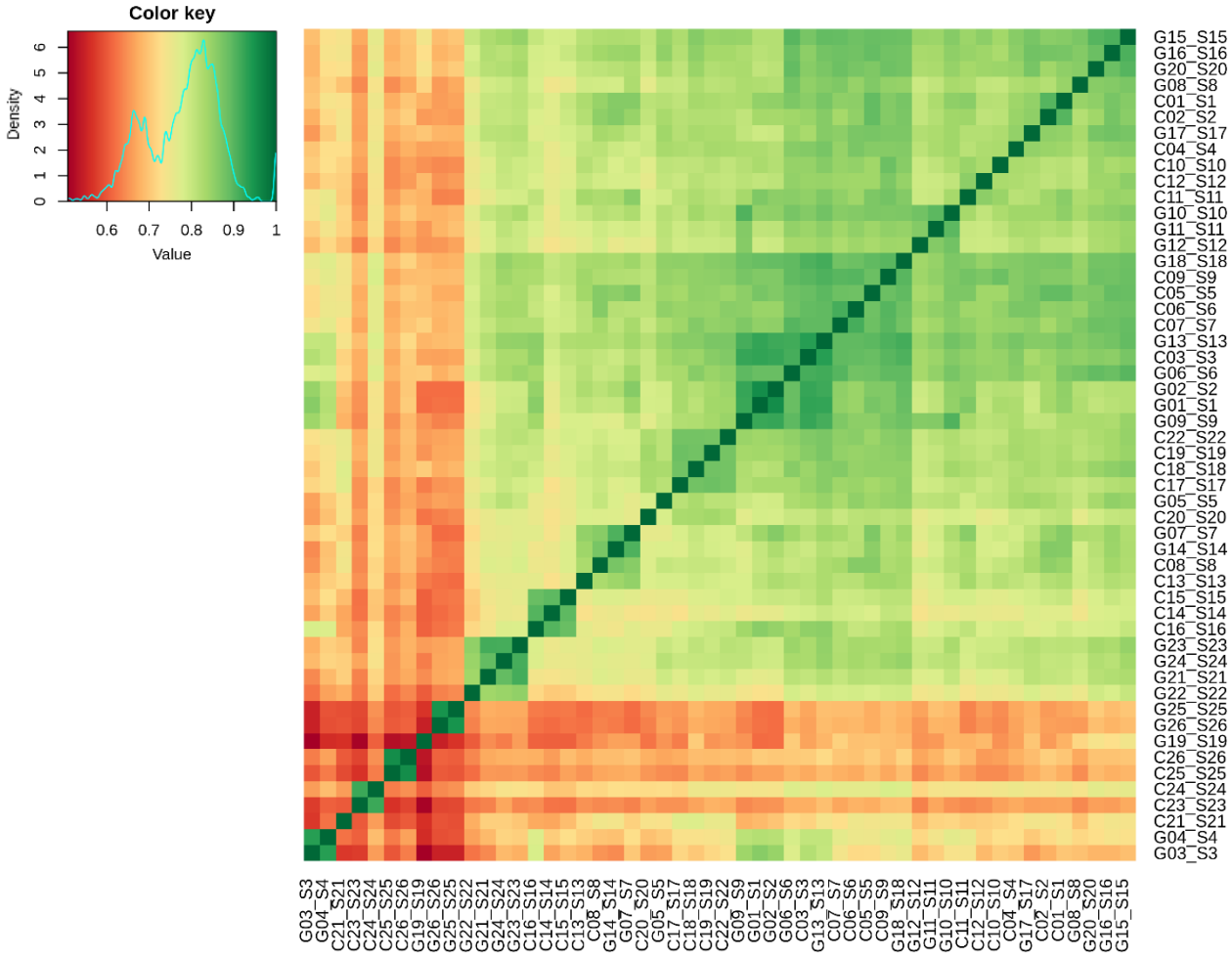
B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G20_S20
G08_S8
C01_S1
C02_S2
G17_S17
C04_S4
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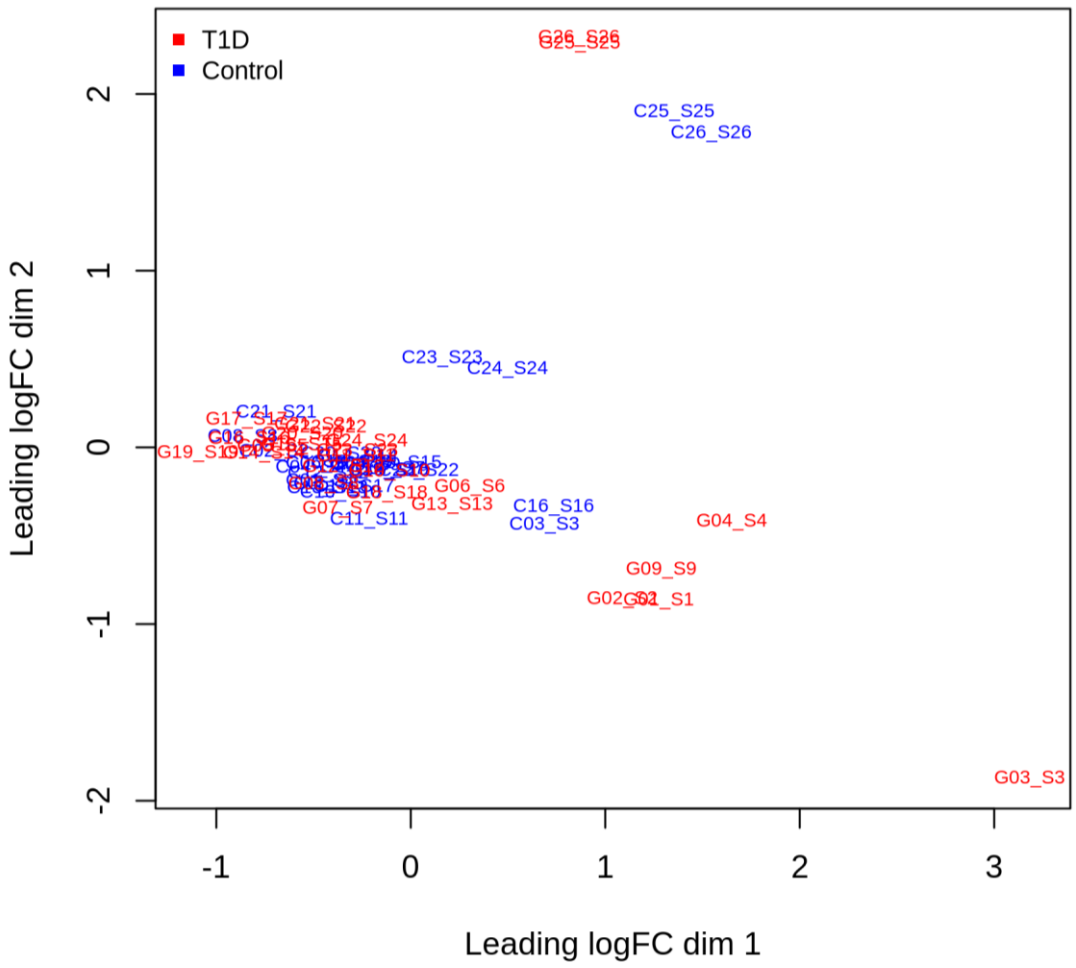
C



Supplementary Figure 3. Library size and sample correlations. (A) The bar plot shows the UMI reads distribution after small RNA sequencing for each sample. The type 1 diabetes (T1D) and control libraries are denoted by red and blue bars, respectively. (B) The correlation heatmap illustrates the relationship between each library for both T1D and control groups. Green indicates a close correlation while red indicates a more distant correlation in the data. (C) Multidimensional scaling (MDS) plot shows biological variability between the T1D and control group libraries.