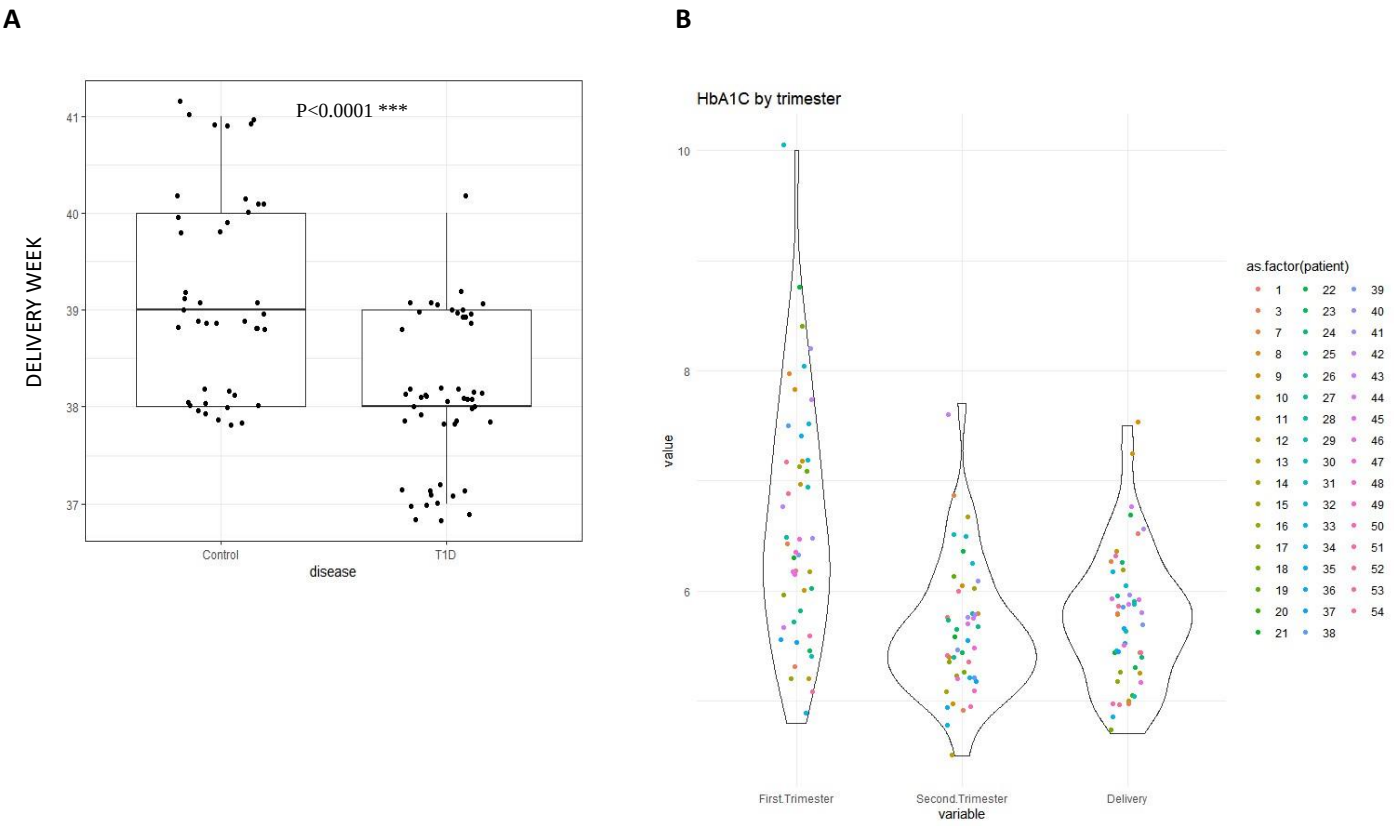
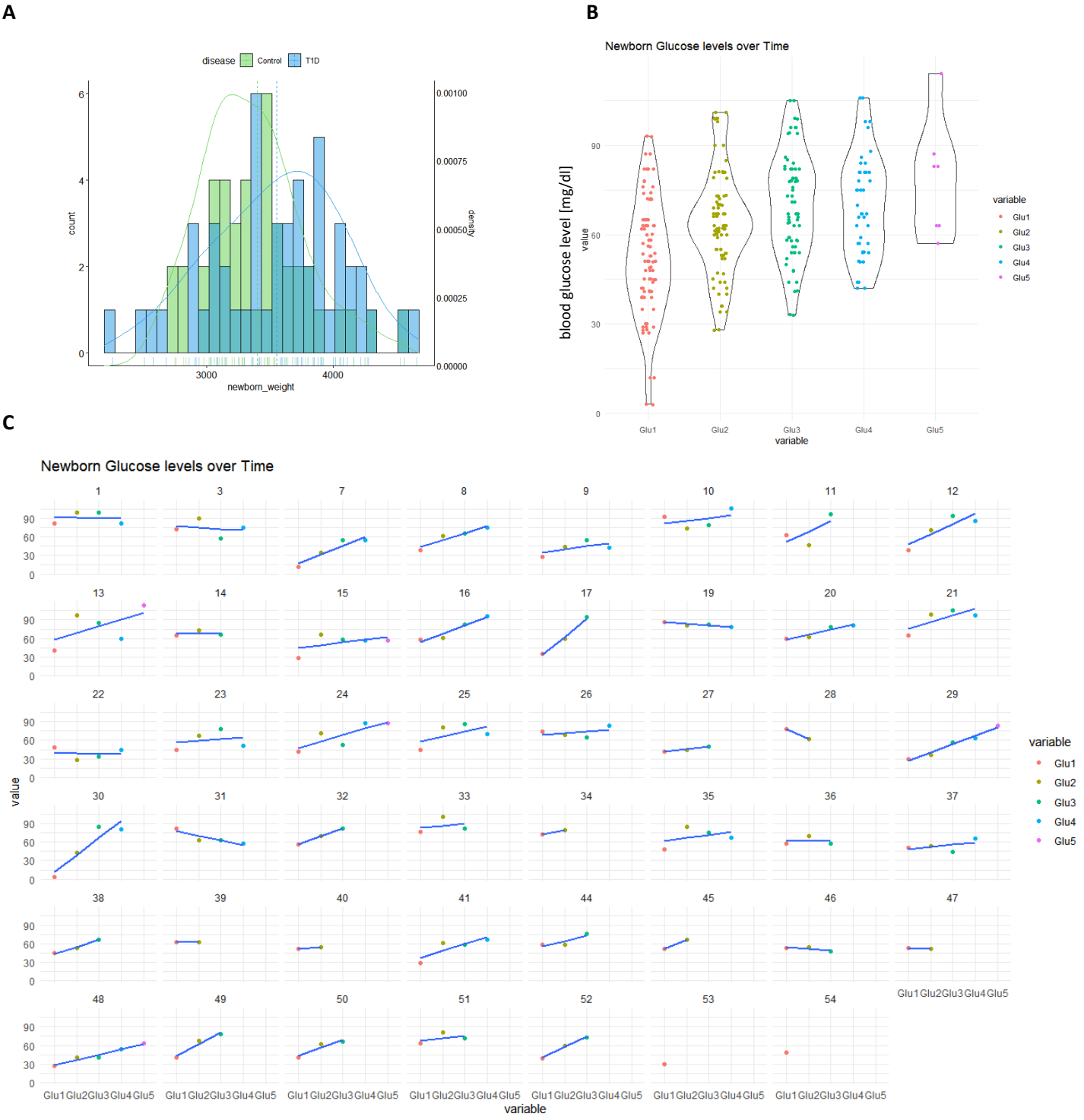
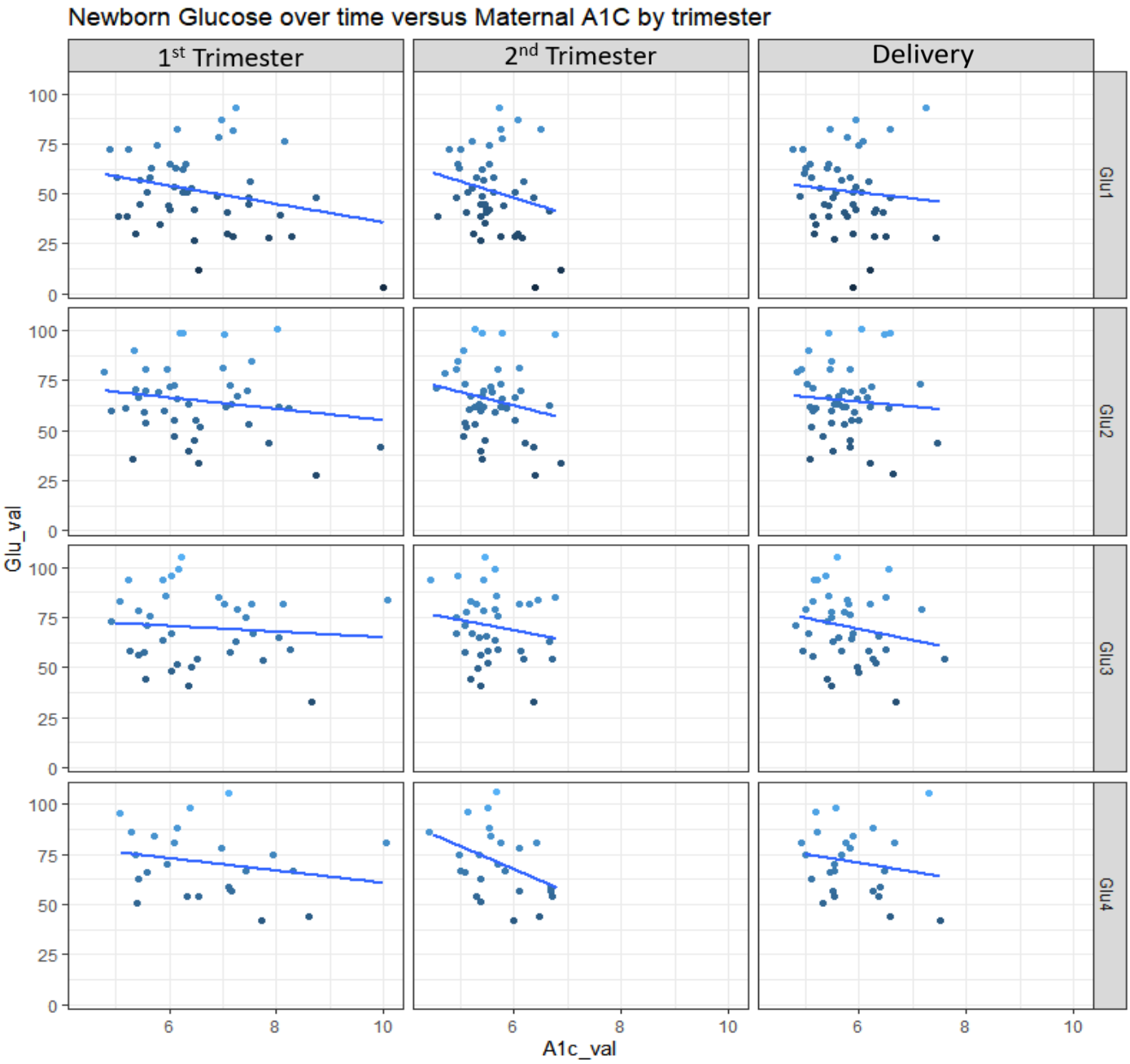


Supplemental Figure 1. Additional clinical findings in women with T1D. (**A)** Disease and week of delivery. The box plot presents the differences in the gestation (weeks) between women with T1D and unaffected women (P<0.0001). Each dot represents one woman. **(B)** Glycaemic control during first, second and third (before delivery) trimesters in women with T1D The HbA1C levels measured during first, second and third (before delivery) trimesters in women with T1D. Each dot represents one woman with T1D. The glycaemic control was found to be satisfactory in second and third trimesters (in accordance with the recommendations of the Polish Diabetes Association, HbA1C ≤ 6.1% (43 mmol/mol)). The Tukey multiple comparisons of means show that no substantial difference in the results of diabetes control when comparing the data of the second and third trimesters of pregnancy (P= 0.682) was found.

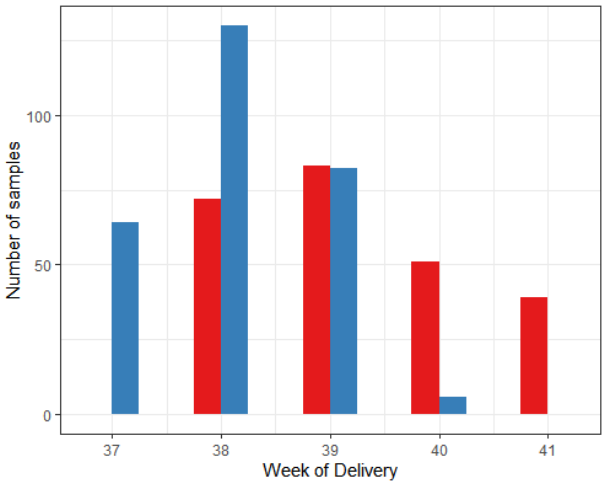


Supplemental Figure 2. Additional clinical findings in newborns delivered by the women with T1D. **(A)** Newborn weight distribution. Newborns born to mothers with T1D had higher body weight (in grams), which is indicated by the Gaussian curve shift to the right (P=0.0947). **(B)** The measurements of plasma glucose level [mg/dl] in two to five time points (the number of measurements depended on the condition of the newborn), performed in newborns born to women with T1D. **(C)** Glucose level measurements over time in particular newborns of women with T1D, presented in 50 individual graphs corresponding to 50 newborns of women with T1D [If a figure 2.C. is selected for this publication, it will be changed to 50 neonates reported in this ms]

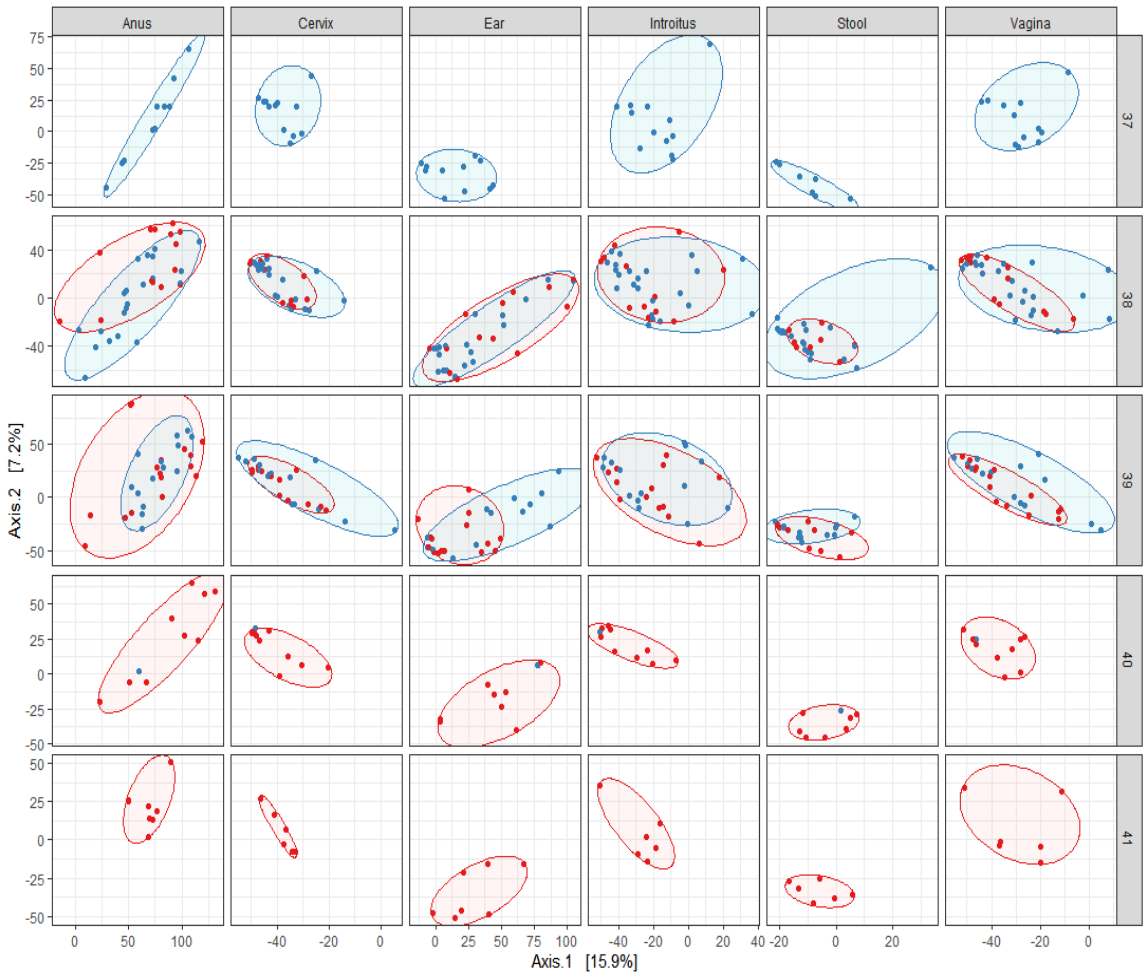


Supplemental Figure 3. The correlation between the glycated hemoglobin level in women with T1D measured before delivery, and the level of glucose in newborns born to these women. No correlations using Pearson's product-moment test were found regarding HbA1C levels of mothers with T1D, in first, second and third (delivery) trimesters, and first measurement of glucose level in newborns (t = -0.62595. df = 45. p-value = 0.5345).

A



B



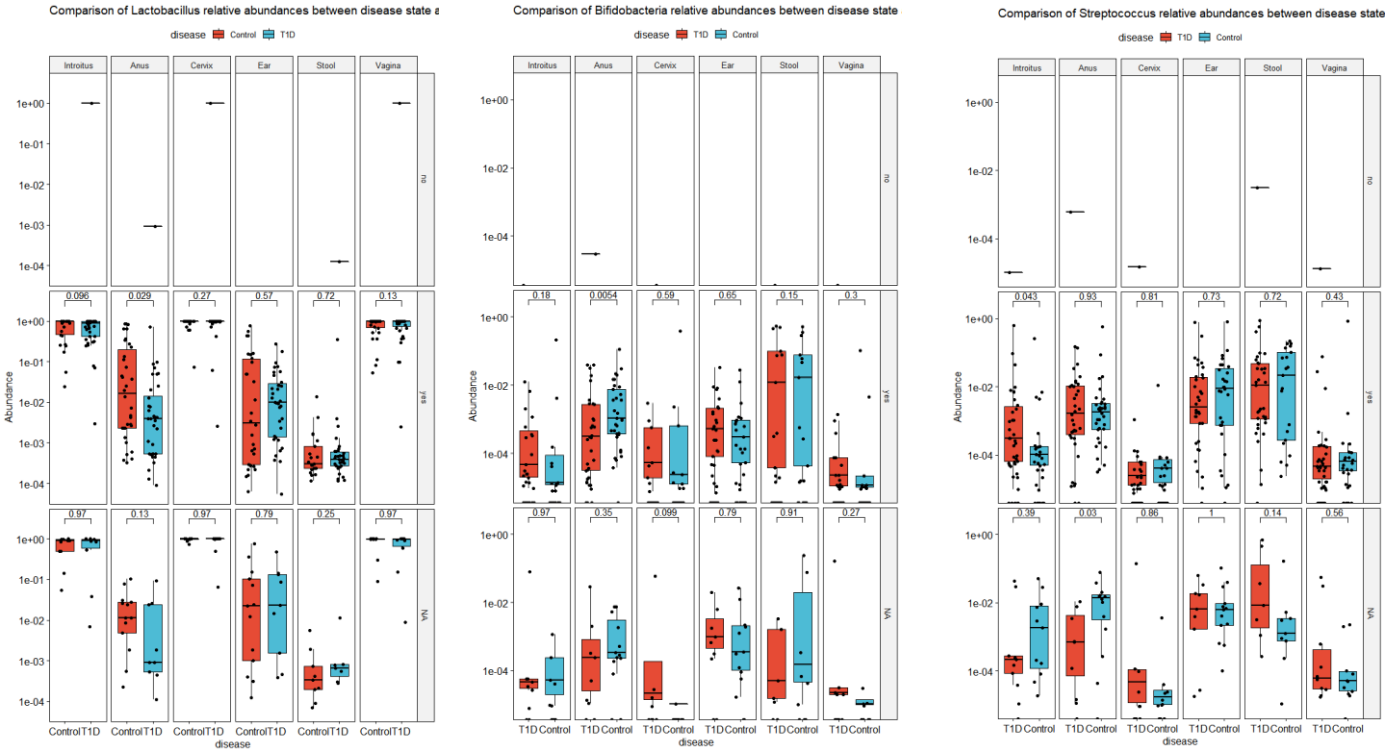
Supplemental Figure 4. The Beta Diversity PCoA plots presenting the T1D and control samples' microbial composition across all studied sample types regarding delivery week. (**A**) The number of samples analyzed, taking into account the given week of labor. (**B**) The influence of delivery week was found to affect the microbial composition (P=0.0024) in the assessed samples (Beta Diversity Bray Curtis adonis permanova of VST transformed counts versus week of delivery stratified by sample type). The T1D disease status also influenced the microbial composition (P=0.002).

To be changed into a heat map – Supp Figure 5

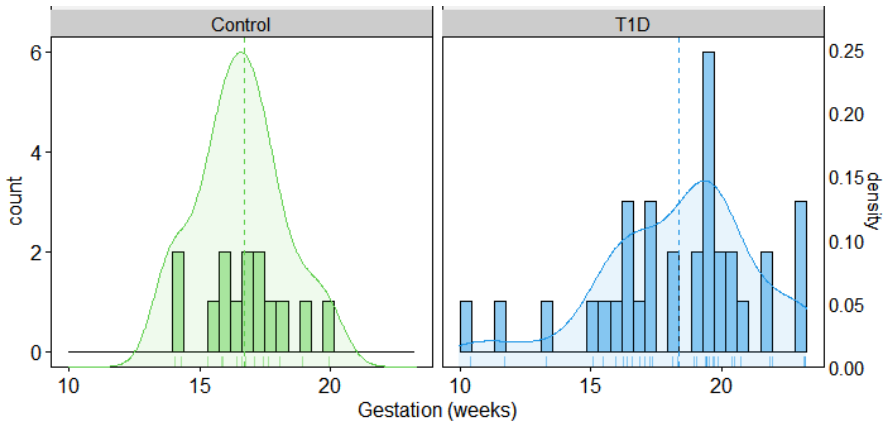
Pathway	Class	Superclass	p-values	Control_Mother _rectum swabs: mean rel. freq. (%)	T1D_Mother _rectum swabs: mean rel. freq. (%)
O-antigen building blocks biosynthesis (E. coli)	Carbohydrate Biosynthesis	Biosynthesis	0.0470	0.249910945	0.164627901
superpathway of UDP-N-acetylglucosamine-derived O-antigen building blocks biosynthesis	Carbohydrate Biosynthesis	Biosynthesis	0.0100	0.039896485	0.019957394
mycolyl-arabinogalactan-peptidoglycan complex biosynthesis	Cell Structure Biosynthesis	Biosynthesis	0.0402	0.001313419	0.000356375
N10-formyl-tetrahydrofolate biosynthesis	Cofactor, Carrier, and Vitamin Biosynthesis	Biosynthesis	0.0378	0.150952768	0.098406784
hexitol fermentation to lactate, formate, ethanol and acetate	Fermentation	Degradation/Utilization/Assimilation	0.0172	0.533944913	0.409494584
acetyl-CoA fermentation to butanoate II	Fermentation	Degradation/Utilization/Assimilation	0.0398	0.041396621	0.024461715
purine nucleobases degradation I (anaerobic)	Nucleoside and Nucleotide Degradation	Degradation/Utilization/Assimilation	0.0142	0.112009051	0.061909494
purine nucleotides degradation II (aerobic)	Nucleoside and Nucleotide Degradation	Degradation/Utilization/Assimilation	0.0407	0.127467766	0.07821811
superpathway of hexitol degradation (bacteria)	Secondary Metabolite Degradation	Degradation/Utilization/Assimilation	0.0018	0.544588477	0.405867128
superpathway of glycolysis and Entner-Doudoroff	Generation of Precursor Metabolites and Energy	Generation of Precursor Metabolites and Energy	0.0281	0.624650598	0.510670746

Supplemental Figure 5. The predicted differently represented pathways in the rectum swabs of women with T1D. The 10 pathways were recognised including 2 pathways from the carbohydrate biosynthesis class. In women with T1D decreased folate biosynthesis (N10-formyl-tetrahydrofolate biosynthesis) was noticed. The SCFA production in the rectum swabs of women with T1D was found lowered (acetyl-CoA fermentation to butanoate II, purine nucleobases degradation I (anaerobic)). The Generation of Precursor Metabolites and Energy (from superpathway of glycolysis and Entner-Doudoroff) was also decreased.

Supp Figure 6 will be modified:



Supplemental Figure 6. Comparison of *Lactobacillus*, *Bifidobacterium*, and *Streptococcus* genera relative abundances by disease and probiotic food products consumed during pregnancy. The relative abundances of the selected genera *Lactobacillus*, *Bifidobacterium*, and *Streptococcus* estimated in the particular maternal and neonatal samples. The differences in the relative abundance of the genera of *Lactobacillus* (P=0.029) and *Bifidobacterium* (P=0.0054) in rectal swabs as well as *Streptococcus* (P=0.043) in the vaginal introitus samples between women with T1D and unaffected women which declared consumption of the probiotic food products during pregnancy were found [the Figure 6 will be modified].



Supplemental Figure 7. The Beta Diversity PCoA plots presenting the T1D and control samples' microbial composition across all studied sample types regarding the percentage of energy derived from protein. The influence of the percentage of energy derived from protein on maternal and neonatal microbiota composition was found, regardless of the T1D disease status (P=0.002). Also, combined, the disease and energy derived from proteins, influenced the microbiota composition (P=0.0027) (Beta Diversity Bray Curtis adonis permanova of VST transformed counts versus the percentage of energy derived from protein, stratified by sample type).