Diagram

Description automatically generated with medium confidenceDiagram

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**PERMANOVA = 0.0406 \***

A)

Vaginal Introitus

MidVaginal

Cervix

Rectum

A picture containing chart

Description automatically generatedA picture containing diagram

Description automatically generatedA picture containing diagram

Description automatically generatedA picture containing background pattern

Description automatically generated

**Figure X.** PCoA plot comparisons of maternal microbiome community composition by disease state(left), delivery mode (center), and maternal 1st trimester hemoglobin A1c values across rectum, cervix, midvaginal, and vaginal introitus sample types (top to bottom). PCoA plots coordinates are based on **A)** Weighted and **B)** Unweighted UniFrac dissimilarity indices obtained from VST transformed ASV counts. Trendlines are derived from fitting generalized linear models for each factor and statistical significance annotations are based on adonis2 permutational analysis of variance scores (permutations = 9999)

Vaginal Introitus

MidVaginal

Cervix

Rectum

**PERMANOVA = 0.0034 \*\***

**PERMANOVA = 0.0216 \***

B)

Weighted UniFrac

A screenshot of a computer

Description automatically generated with medium confidenceA picture containing chart

Description automatically generatedA picture containing diagram

Description automatically generatedA screenshot of a computer

Description automatically generated with medium confidence

Ear

**PERMANOVA = 0.0027 \*\***

**PERMANOVA < 0.0001 \*\*\***

**PERMANOVA = 0.0034 \*\***

Stool

Ear

**PERMANOVA = 0.0508 \***

**PERMANOVA = 0.0076 \*\***

A)

B)

**PERMANOVA = 0.0544 \***

Stool

**PERMANOVA < 0.0001 \*\*\***

**Figure X.** PCoA plot comparisons of neonatal microbiome community composition by disease state(left), delivery mode (center), and maternal 1st trimester hemoglobin A1c values across stool and ear sample types (top to bottom). PCoA plots coordinates are based on **A)** Weighted and **B)** Unweighted UniFrac dissimilarity indices obtained from VST transformed ASV counts. Trendlines are derived from fitting generalized linear models for each factor and statistical significance annotations are based on adonis2 permutational analysis of variance scores (permutations = 9999)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Weighted UniFrac | | | |  | Unweighted UniFrac | | | |  |
| Host | Sample Type | Variable | SumOfSqs | R2 | statistic | p.value |  | SumOfSqs | R2 | statistic | p.value |  |
| Maternal | Anus | Type 1 Diabetes | 0.01 | 0.03 | 2.57 | 0.0406 | \* | 0.72 | 0.02 | 1.84 | 0.0034 | \*\* |
| Delivery Mode | 0.00 | 0.01 | 0.51 | 0.7685 |  | 0.46 | 0.01 | 1.15 | 0.1833 |  |
| 1st Tri HbA1C | 0.00 | 0.01 | 0.97 | 0.3855 |  | 0.59 | 0.02 | 1.49 | 0.0216 | \* |
| Cervix | Type 1 Diabetes | 0.00 | 0.01 | 0.78 | 0.5825 |  | 0.52 | 0.01 | 1.17 | 0.2411 |  |
| Delivery Mode | 0.00 | 0.01 | 1.03 | 0.3906 |  | 0.38 | 0.01 | 0.85 | 0.6525 |  |
| 1st Tri HbA1C | 0.00 | 0.01 | 0.79 | 0.556 |  | 0.38 | 0.01 | 0.87 | 0.6371 |  |
| Introitus | Type 1 Diabetes | 0.00 | 0.02 | 1.44 | 0.1824 |  | 0.60 | 0.01 | 1.32 | 0.0746 |  |
| Delivery Mode | 0.00 | 0.02 | 1.67 | 0.112 |  | 0.61 | 0.02 | 1.36 | 0.0611 |  |
| 1st Tri HbA1C | 0.00 | 0.02 | 1.75 | 0.0946 |  | 0.54 | 0.01 | 1.19 | 0.1703 |  |
| Vagina | Type 1 Diabetes | 0.00 | 0.01 | 1.14 | 0.3226 |  | 0.58 | 0.01 | 1.31 | 0.1028 |  |
| Delivery Mode | 0.00 | 0.02 | 1.73 | 0.1034 |  | 0.47 | 0.01 | 1.06 | 0.3484 |  |
| 1st Tri HbA1C | 0.00 | 0.00 | 0.45 | 0.8508 |  | 0.57 | 0.01 | 1.27 | 0.1299 |  |
| Neonatal | Ear | Type 1 Diabetes | 0.01 | 0.02 | 1.76 | 0.0831 |  | 0.53 | 0.01 | 1.23 | 0.0954 |  |
| Delivery Mode | 0.01 | 0.02 | 2.00 | 0.0508 | \* | 0.74 | 0.02 | 1.72 | 0.0027 | \*\* |
| 1st Tri HbA1C | 0.01 | 0.04 | 3.20 | 0.0076 | \*\* | 0.57 | 0.02 | 1.31 | 0.0567 |  |
| Stool | Type 1 Diabetes | 0.00 | 0.03 | 2.27 | 0.0544 | \* | 0.99 | 0.03 | 2.30 | 0.0034 | \*\* |
| Delivery Mode | 0.00 | 0.10 | 8.16 | 0.0001 | \*\*\*\* | 2.15 | 0.07 | 5.16 | 0.0001 | \*\*\*\* |
| 1st Tri HbA1C | 0.00 | 0.01 | 0.63 | 0.6338 |  | 0.36 | 0.01 | 0.81 | 0.7286 |  |

**Table X.** adonis2 permutational analysis of variance scores (permutations = 9999) comparisons of maternal and neonatal microbiome community beta diversity by disease state, delivery mode, and maternal 1st trimester hemoglobin A1c values across rectum, cervix, midvaginal, vaginal introitus, stool and ear sample types. Missing 1st trimester hemoglobin A1c values were either imputed using a KNN based model from the remaining metadata values for T1D patients or generated based on a norm distribution derived from average 1st Trimester HbA1C values for nondiabetic mothers (4.96 ± 0.53).