**Table 3**. Differentially expressed microbiota (genera) associated with T1D identified in the assessed sample types (**A-F**). The log2FoldChange values show the direction of change in pregnant women with T1D (under- or overrepresentation). All presented genera showed significant (padj value) variation in relative abundance.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 1. **Vaginal introitus** | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | | | | baseMean | | | | log2FoldChange | | | | lfcSE | | | | stat | | | | pvalue | | | padj |
| *Gemella* | | | | 7.791854732 | | | | 21.37686055 | | | | 1.594903 | | | | 13.40323 | | | | 5.79E-41 | | | 1.32E-38 |
| *Citrobacter* | | | | 13.1186876 | | | | 15.31044525 | | | | 1.496272 | | | | 10.2324 | | | | 1.42E-24 | | | 1.62E-22 |
| *Terrisporobacter* | | | | 2.507782593 | | | | 14.70171656 | | | | 1.528636 | | | | 9.617539 | | | | 6.74E-22 | | | 5.12E-20 |
| *Enhydrobacter* | | | | 2.725316164 | | | | -5.10656261 | | | | 0.868546 | | | | -5.87944 | | | | 4.12E-09 | | | 2.35E-07 |
| *Klebsiella* | | | | 110.8625127 | | | | 7.790694435 | | | | 1.360577 | | | | 5.726023 | | | | 1.03E-08 | | | 4.69E-07 |
| *Staphylococcus* | | | | 11942.16678 | | | | 2.430468841 | | | | 0.578343 | | | | 4.202468 | | | | 2.64E-05 | | | 0.001003 |
| 1. **Vaginal canal in the middle** | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | | | | baseMean | | | | log2FoldChange | | | | lfcSE | | | | stat | | | | pvalue | | | padj |
| *Sneathia* | | | | 0.91355325 | | | | 49.75205694 | | | | 3.13553 | | | | 15.86719 | | | | 1.07E-56 | | | 2.44E-54 |
| *Intestinibacter* | | | | 2.25394947 | | | | 14.81940553 | | | | 1.300908 | | | | 11.39159 | | | | 4.61E-30 | | | 5.25E-28 |
| *Atopobium* | | | | 96.63138911 | | | | 6.817629914 | | | | 1.005162 | | | | 6.782617 | | | | 1.18E-11 | | | 8.97E-10 |
| *Megasphaera* | | | | 3.663975758 | | | | 7.795750046 | | | | 1.382241 | | | | 5.639935 | | | | 1.70E-08 | | | 9.70E-07 |
| *Streptococcus* | | | | 1247.347326 | | | | -3.575171258 | | | | 0.710685 | | | | -5.0306 | | | | 4.89E-07 | | | 2.23E-05 |
| *Gemella* | | | | 7.791854732 | | | | 7.025311314 | | | | 1.569641 | | | | 4.475743 | | | | 7.61E-06 | | | 0.000289 |
| *Prevotella\_6* | | | | 30.81174732 | | | | 3.78113307 | | | | 0.950575 | | | | 3.977733 | | | | 6.96E-05 | | | 0.002266 |
| 1. **Cervix** | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | | | | baseMean | | | | log2FoldChange | | | | lfcSE | | | | stat | | | | pvalue | | | padj |
| *Enhydrobacter* | | | | 2.725316164 | | | | 18.47318766 | | | | 0.920473 | | | | 20.06924 | | | | 1.37E-89 | | | 2.03E-87 |
| *Parabacteroides* | | | | 10.16690706 | | | | 16.90968828 | | | | 0.981441 | | | | 17.22944 | | | | 1.60E-66 | | | 1.18E-64 |
| *Collinsella* | | | | 5.822141559 | | | | -15.18735083 | | | | 1.050767 | | | | -14.4536 | | | | 2.38E-47 | | | 1.17E-45 |
| *Intestinibacter* | | | | 2.25394947 | | | | 17.91541358 | | | | 1.314871 | | | | 13.62523 | | | | 2.84E-42 | | | 1.05E-40 |
| *Sneathia* | | | | 0.91355325 | | | | 42.94575628 | | | | 3.185337 | | | | 13.48233 | | | | 1.99E-41 | | | 5.88E-40 |
| *Fusicatenibacter* | | | | 4.220114744 | | | | 14.23939158 | | | | 1.11886 | | | | 12.7267 | | | | 4.20E-37 | | | 1.04E-35 |
| *Terrisporobacter* | | | | 2.507782593 | | | | 14.19701848 | | | | 1.528636 | | | | 9.287377 | | | | 1.58E-20 | | | 3.34E-19 |
| *Bacteroides* | | | | 325.9301607 | | | | 6.338634935 | | | | 0.836282 | | | | 7.579545 | | | | 3.47E-14 | | | 6.42E-13 |
| *Jonquetella* | | | | 1.868206931 | | | | 15.34681861 | | | | 2.035424 | | | | 7.539862 | | | | 4.70E-14 | | | 7.74E-13 |
| *Atopobium* | | | | 96.63138911 | | | | 6.622227482 | | | | 1.020744 | | | | 6.487647 | | | | 8.72E-11 | | | 1.29E-09 |
| *Bifidobacterium* | | | | 521.8067153 | | | | -5.863567853 | | | | 0.969993 | | | | -6.04496 | | | | 1.49E-09 | | | 2.01E-08 |
| *Anaerococcus* | | | | 218.5977436 | | | | -3.201892621 | | | | 0.630139 | | | | -5.08125 | | | | 3.75E-07 | | | 4.62E-06 |
| *Gemella* | | | | 7.791854732 | | | | 7.914833526 | | | | 1.58885 | | | | 4.981487 | | | | 6.31E-07 | | | 7.18E-06 |
| *Enterococcus* | | | | 11413.42655 | | | | -2.766598003 | | | | 0.685799 | | | | -4.03412 | | | | 5.48E-05 | | | 0.000579 |
| *Escherichia/Shigella* | | | | 9056.503563 | | | | 2.792875562 | | | | 0.73106 | | | | 3.82031 | | | | 0.000133 | | | 0.001315 |
| *Staphylococcus* | | | | 11942.16678 | | | | -2.088343619 | | | | 0.580015 | | | | -3.6005 | | | | 0.000318 | | | 0.002938 |
| *Fusobacterium* | | | | 8.180647569 | | | | -3.9099907 | | | | 1.201969 | | | | -3.25299 | | | | 0.001142 | | | 0.009942 |
| 1. **Rectum swabs** | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | | baseMean | | | | | log2FoldChange | | | | lfcSE | | | stat | | | | pvalue | | | padj | | |
| *Staphylococcus* | | 11942.16678 | | | | | 3.133243112 | | | | 0.56915 | | | 5.505127 | | | | 3.69E-08 | | | 8.41E-06 | | |
| *Sneathia* | | 0.91355325 | | | | | 13.85718931 | | | | 3.134176 | | | 4.421318 | | | | 9.81E-06 | | | 0.001118 | | |
| 1. **Ear-skin swabs** | | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | | | baseMean | | | log2FoldChange | | | | lfcSE | | | | | stat | | | | pvalue | | | padj | | |
| *Rothia* | | | 104.7048 | | | -7.754220456 | | | | 0.944265916 | | | | | -8.2119 | | | | 2.18E-16 | | | 4.96E-14 | | |
| *Micrococcus* | | | 34.24541 | | | -3.706357826 | | | | 0.738726707 | | | | | -5.01722 | | | | 5.24E-07 | | | 5.98E-05 | | |
| *Escherichia/Shigella* | | | 9056.504 | | | -3.049190658 | | | | 0.743220907 | | | | | -4.10267 | | | | 4.08E-05 | | | 0.003103903 | | |
| *Kocuria* | | | 7.549618 | | | -3.286509007 | | | | 0.821777475 | | | | | -3.99927 | | | | 6.35E-05 | | | 0.003621694 | | |
| 1. **Stool samples** | | | | | | | | | | | | | | | | | | | | | | | | |
| Genus | baseMean | | | | log2FoldChange | | | | lfcSE | | | | stat | | | | pvalue | | | | padj | | | |
| *Fusicatenibacter* | 4.220115 | | | | 26.4382456 | | | | 1.231132084 | | | | 21.47474 | | | | 2.68E-102 | | | | 3.03E-100 | | | |
| *Fusobacterium* | 8.180648 | | | | 20.08683224 | | | | 1.35277147 | | | | 14.84865 | | | | 7.10E-50 | | | | 4.01E-48 | | | |
| *Megasphaera* | 3.663976 | | | | 15.61100439 | | | | 1.620942737 | | | | 9.630818 | | | | 5.93E-22 | | | | 2.23E-20 | | | |
| *Anaeroglobus* | 2.730555 | | | | 19.46259187 | | | | 2.232914701 | | | | 8.716227 | | | | 2.88E-18 | | | | 8.13E-17 | | | |
| *Pseudomonas* | 5.238713 | | | | 7.50531745 | | | | 0.927683487 | | | | 8.090386 | | | | 5.95E-16 | | | | 1.34E-14 | | | |
| *Collinsella* | 5.822142 | | | | -8.766264106 | | | | 1.128939518 | | | | -7.76504 | | | | 8.16E-15 | | | | 1.54E-13 | | | |
| *Romboutsia* | 2.192765 | | | | 6.40497023 | | | | 1.202747682 | | | | 5.325282 | | | | 1.01E-07 | | | | 1.63E-06 | | | |
| *Peptoniphilus* | 132.7484 | | | | 3.420168182 | | | | 0.746132643 | | | | 4.583861 | | | | 4.56E-06 | | | | 6.45E-05 | | | |
| *Terrisporobacter* | 2.507783 | | | | -7.662802823 | | | | 1.690229063 | | | | -4.53359 | | | | 5.80E-06 | | | | 7.28E-05 | | | |
| *Sutterella* | 3.176991 | | | | -5.191498608 | | | | 1.197334093 | | | | -4.33588 | | | | 1.45E-05 | | | | 0.00016405 | | | |
| *Dialister* | 33.95076 | | | | 3.498783559 | | | | 0.957451276 | | | | 3.654268 | | | | 0.000258 | | | | 0.002649509 | | | |
| *Bacteroides* | 325.9302 | | | | -3.032249963 | | | | 0.875592579 | | | | -3.46308 | | | | 0.000534 | | | | 0.005028719 | | | |
| *Actinomyces* | 7.449215 | | | | 2.884909904 | | | | 0.849028514 | | | | 3.397895 | | | | 0.000679 | | | | 0.005902636 | | | |
| *Lachnoclostridium* | 1.616491 | | | | 3.844592112 | | | | 1.188055273 | | | | 3.236038 | | | | 0.001212 | | | | 0.009782669 | | | |
|  |  | | | |  | | | |  | | | |  | | | |  | | | |  | | | |

**Table 4.** Beta Diversity Bray Curtis adonis permanova of VST transformed counts versus Delivery mode (**A**) and Antibiotics administration in the women (**B**), stratified by sample type.

**A.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |  |
| disease | 1 | 17149 | 17149 | 1.4868 | 0.00968 | 0.0248 |  |
| Delivery | 1 | 23172 | 23172 | 2.009 | 0.01309 | 0.0008 |  |
| disease:Delivery | 1 | 11811 | 11811 | 1.024 | 0.00667 | 0.2259 |  |
| Residuals | 149 | 1718543 | 11534 |  | 0.97056 |  |  |
| Total | 152 | 1770674 |  |  | 1 |  |  |
|  |  |  |  |  |  |  |  |
| **B.**   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | |  | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |  | | disease | 1 | 23963 | 23963 | 1.926 | 0.00377 | 0.0003 | \*\*\* | | Antibiotics\_2 | 1 | 19261 | 19261 | 1.5482 | 0.00303 | 0.0013 | \*\* | | disease:Antibiotics\_ | 1 | 17335 | 17335 | 1.3933 | 0.00273 | 0.0064 | \*\* | | Residuals | 506 | 6295371 | 12441 |  | 0.99047 |  |  | | Total | 509 | 6355930 |  |  | 1 |  |  | | --- |  |  |  |  |  |  |  | | Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1 | | | | | | | | | | | | | | | |

**Table 5.** Metagenomic pathways predicted as exclusively shared within unaffected mother-neonatal dyads (**A**), and within mother with T1D-neonatal dyads (**B**). These pathways were predicted regardless of the type of neonatal sample type, out of 283 predicted pathways common to all dyads

|  |  |  |  |
| --- | --- | --- | --- |
| 1. **Exclusively shared in unaffected dyads** | | | |
| **pathway** | **class** | **superclass** | **neonatal sample type** |
| mycothiol biosynthesis | Cofactor, Carrier,  and Vitamin Biosynthesis | Biosynthesis | Unaffected\_VaginalEar-skin swabs |
| mono-trans, poly-cis decaprenyl phosphate biosynthesis | Cofactor, Carrier,  and Vitamin Biosynthesis | Biosynthesis | Unaffected\_VaginalEar-skin swabs |
| CMP-legionaminate biosynthesis I | Carbohydrate Biosynthesis | Biosynthesis | Unaffected\_Csection\_Ear-skin swabs |

|  |  |  |  |
| --- | --- | --- | --- |
| 1. **Exclusively shared in T1D dyads** | | | |
| **pathway** | **class** | **superclass** | **neonatal sample type** |
| 2-nitrobenzoate degradation I | Aromatic Compound Degradation | Degradation/ Utilization/  Assimilation | T1D\_Csection  Ear-skin swabs |
| 2-amino-3-carboxymuconate semialdehyde degradation to 2-oxopentenoate | Carboxylase degradation | Degradation/  Utilization/  Assimilation | T1D\_Csection  Ear-skin swabs |
| superpathway of polyamine biosynthesis II | Amine and Polyamine Biosynthesis | Biosynthesis | T1D\_Csection  Ear-skin swabs |