**Figures**

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**Figure 1** **- PLS-DA of 16S bacterial profiles**. Post discharge samples removed. A) Score scatter plot. B) Loadings plot

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**Figure 2 – Box plot of Shannon Diversity Indices**. Significantly lower diversity occurred in during probiotic administration compared to controls and in all groups when compared to samples post discharge (PD).

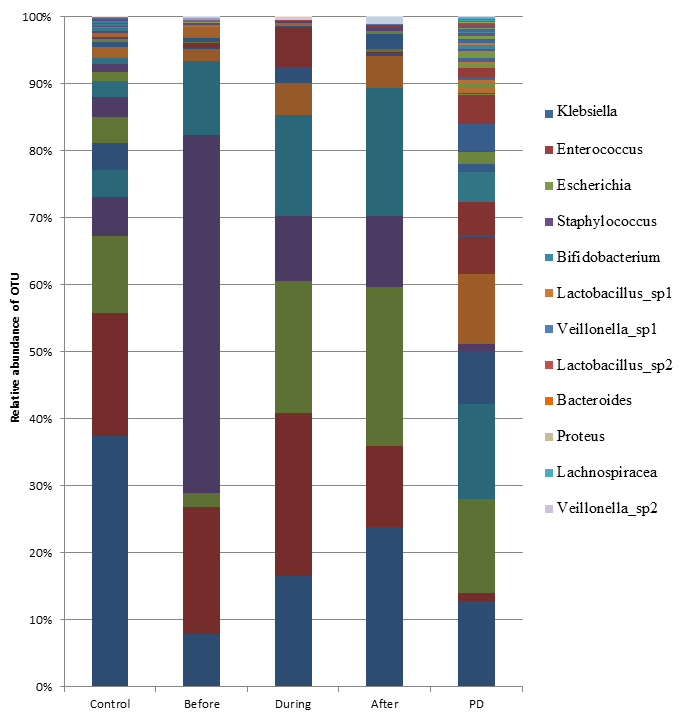
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**Figure 3 - Boxplot of bacterial load determined by qPCR.** \*Asterisks represent the outliers, “a” or “b” represents the grouping by turkey’s family. A)*Bifidobacterium bifidum*. B) *Lactobacillus acidophilus*.

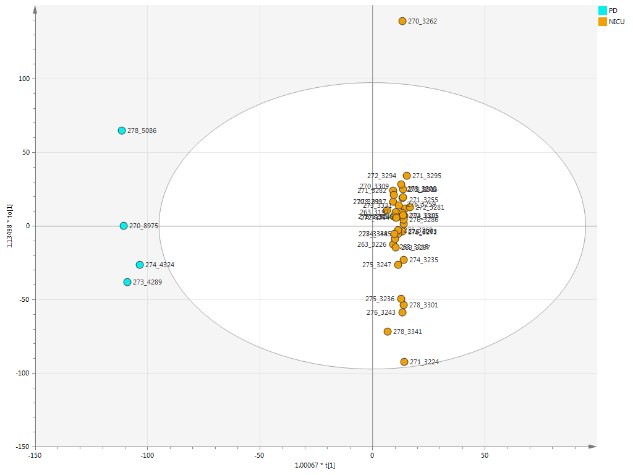
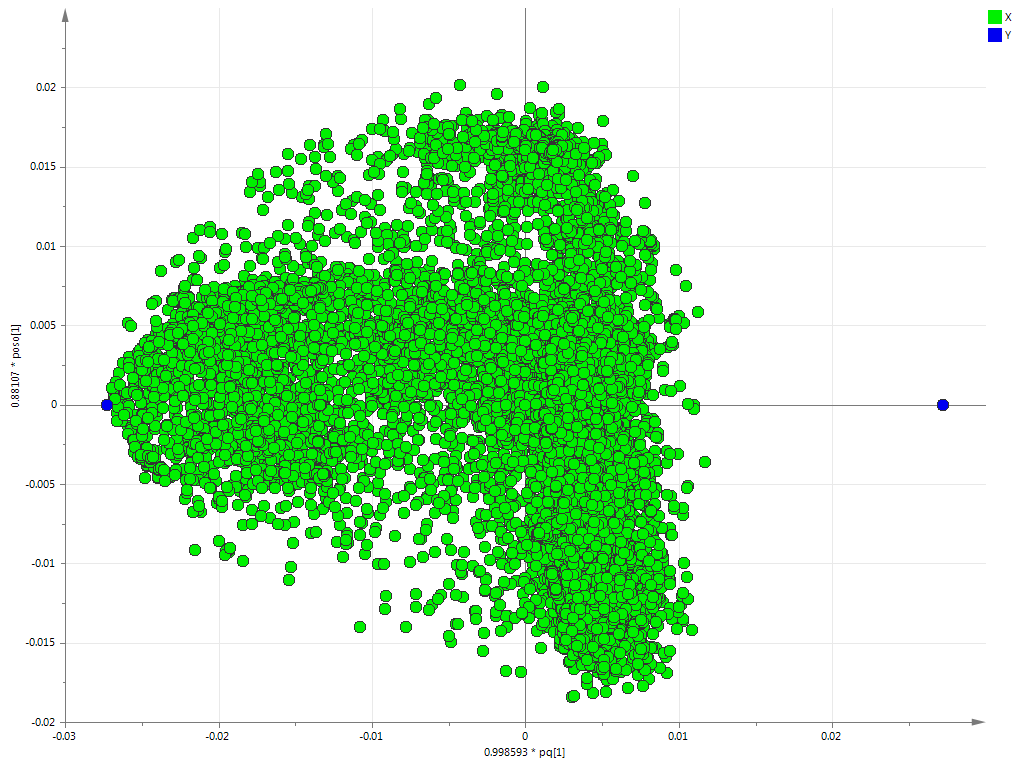
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**Figure 4 -** **PLS-DA of the metabolite profiles**. Before probiotic and post discharge samples excluded. A) Score scatter plot showing the relationship of samples associated with each group (R2Y = 0.62, Q2 = 0.31). B) Loading plot of detected metabolites associated with each group following VIP removal of noise (R2Y = 0.80, Q2 = 0.56). Red metabolites associated with probiotic administration.

**Supplementary Figures**



**Supplementary Figure 1** **- Relative abundance of bacterial OTUs**. Sequences matching other less abundant OTUs are not shown on the legend

**Supplementary Figure 2** **– OPLS-DA of metabolite profiles comparing samples collected on the NICU and post discharge**. R2Y = 0.99, Q2 = 0.8. A) Score scatter plot. B) Loadings plot.