

Correction

Correction: Meconium Microbiome Analysis Identifies Bacteria Correlated with Premature Birth



The *PLOS ONE* Staff

The title of Figure 3 is incorrect. Please see the corrected Figure 3 here.

Citation: The *PLOS ONE* Staff (2014) Correction: Meconium Microbiome Analysis Identifies Bacteria Correlated with Premature Birth. *PLOS ONE* 9(6): e101399. doi:10.1371/journal.pone.0101399

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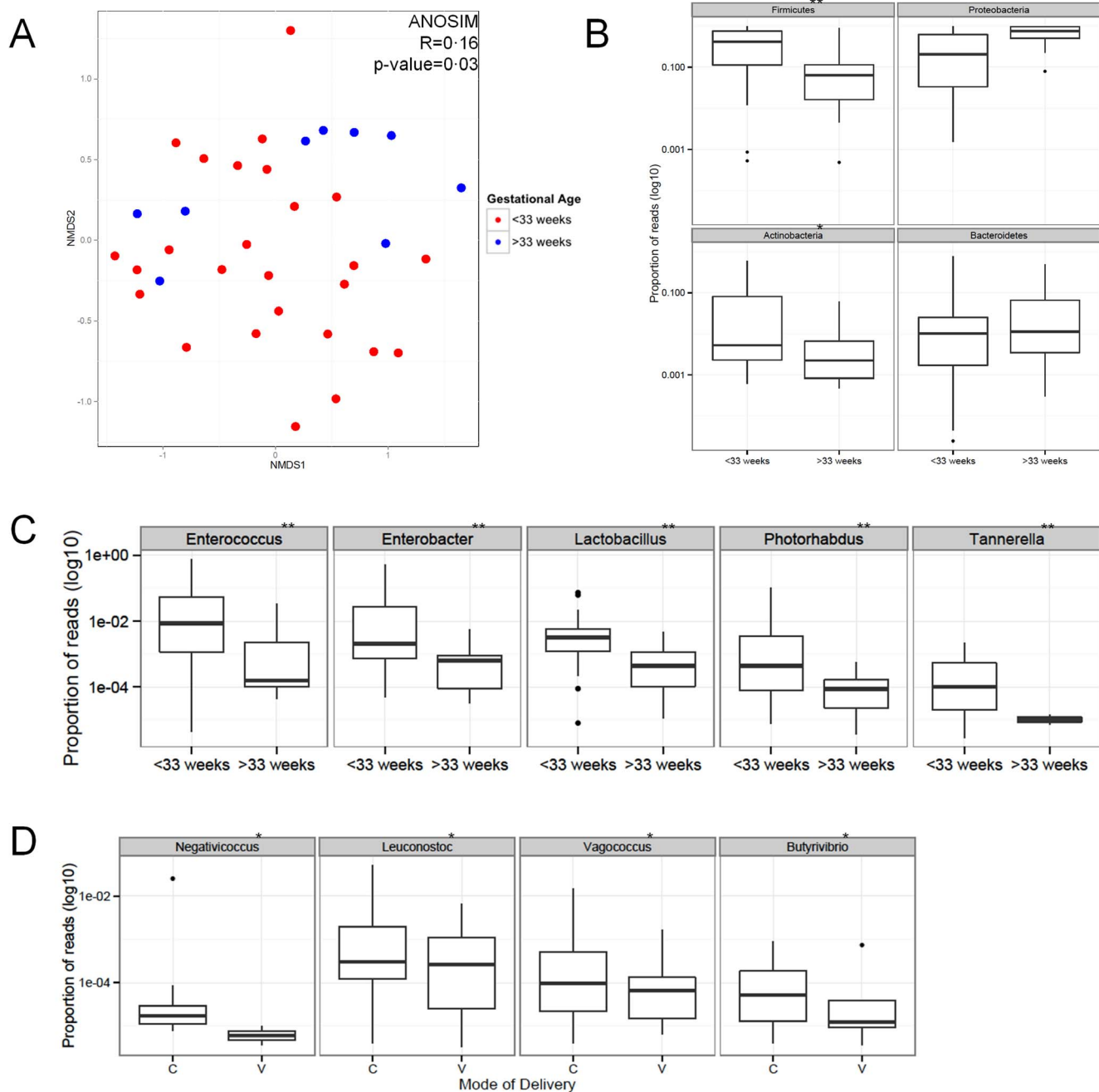


Figure 3. Meconium microbiome correlations with gestational age and mode of delivery. (A) Non-metric multidimensional scaling ordination plot depicting the relatedness of the bacterial communities from all meconium samples; communities from >33 week infants (blue) clustered more closely than those from <33 week infants (red). Analysis of similarity (ANOSIM) revealed that gestational age (<33 and >33 weeks) had the largest effect on meconium microbial structure ($R = 0.16$; $p\text{-value} = 0.03$). (B) Of the four predominant phyla, the relative abundance of Firmicutes and Actinobacteria was correlated with low gestational age (** $p < 0.01$ & * $p < 0.05$, respectively). (C) Genera negatively correlated with gestational age (** $p < 0.01$) are presented. (D) Genera associated with mode of delivery (* $p < 0.05$) were observed, though these differences are not as pronounced as the genera associated with gestational age. doi:10.1371/journal.pone.0090784.g003

Reference

1. Ardisson AN, de la Cruz DM, Davis-Richardson AG, Rechcigl KT, Li N, et al. (2014) Meconium Microbiome Analysis Identifies Bacteria Correlated with Premature Birth. *PLoS ONE* 9(3): e90784. doi:10.1371/journal.pone.0090784