**Supplementary Figure 1: (Left)** The genus-like bacterial groups with significant Spearman correlations in Ghanaian infants when evaluating the height of the post-vaccination IgA response. (**Middle**) Correlation index between the genus-like group and IgA height and heat map of the correlation: red is positively correlated with vaccine response and blue is negatively correlated with vaccine response. **+** indicates a significant correlation (p<0.05, FDR<0.2). **(Right):** Significance, expressed as adjusted-p level.

**Supplementary Figure 2**: Redundancy analysis (RDA) of matched pre-vaccination samples taken from 39 Ghanaian non-responders (red dots, NR) and 39 responders (green boxes, R) showing the 50 best fitting genus-like groups influencing the plot. The first and second ordination axes are plotted explaining 6.1 and 4% of the variability in the data set. The environmental variables rotavirus vaccine seroconversion is the only environmental variable influencing the plot as calculated by Monte Carlo Permutation Testing **(**p= 0.014, FDR= 0.12.