We have developed a qPCR-based array (GUT Low Density Array, GULDA), which simultaneously determine the relative abundance of >30 different bacterial 16S rRNA gene targets in a given DNA-sample covering selected phylogenetic levels. GULDA was applied to fecal DNA from 330 healthy Danish infants (the so called SKOT-cohort), sampled at 9, 18 and 36 months after birth. The resulting data together with previously determined nutritional and anthropometrical parameters were used as input for multivariate statistics. We found significant changes in the composition of the gut microbiota between 9 and 18 months, corresponding to dietary changes during weaning; changes were far less pronounced between 18 and 36 months. Few studies have undertaken similar longitudinal and multiparametric analysis for such numerous participants. GULDA was seen to constitute a sensitive, cost-effective tool for microbial community characterization, which here provides new insights into the interactions between the gut microbiota, diet and physiology in infants.