# Composition of gut microbiota in infants in China and global comparison

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Figure S1: Bacterial composition, at the phylum level, in infants' gut microbiota from 6 different countries. The world map was generated using R software 3.2.1 package "maps" (https://cran.r-project.org/web/packages/maps )[1]
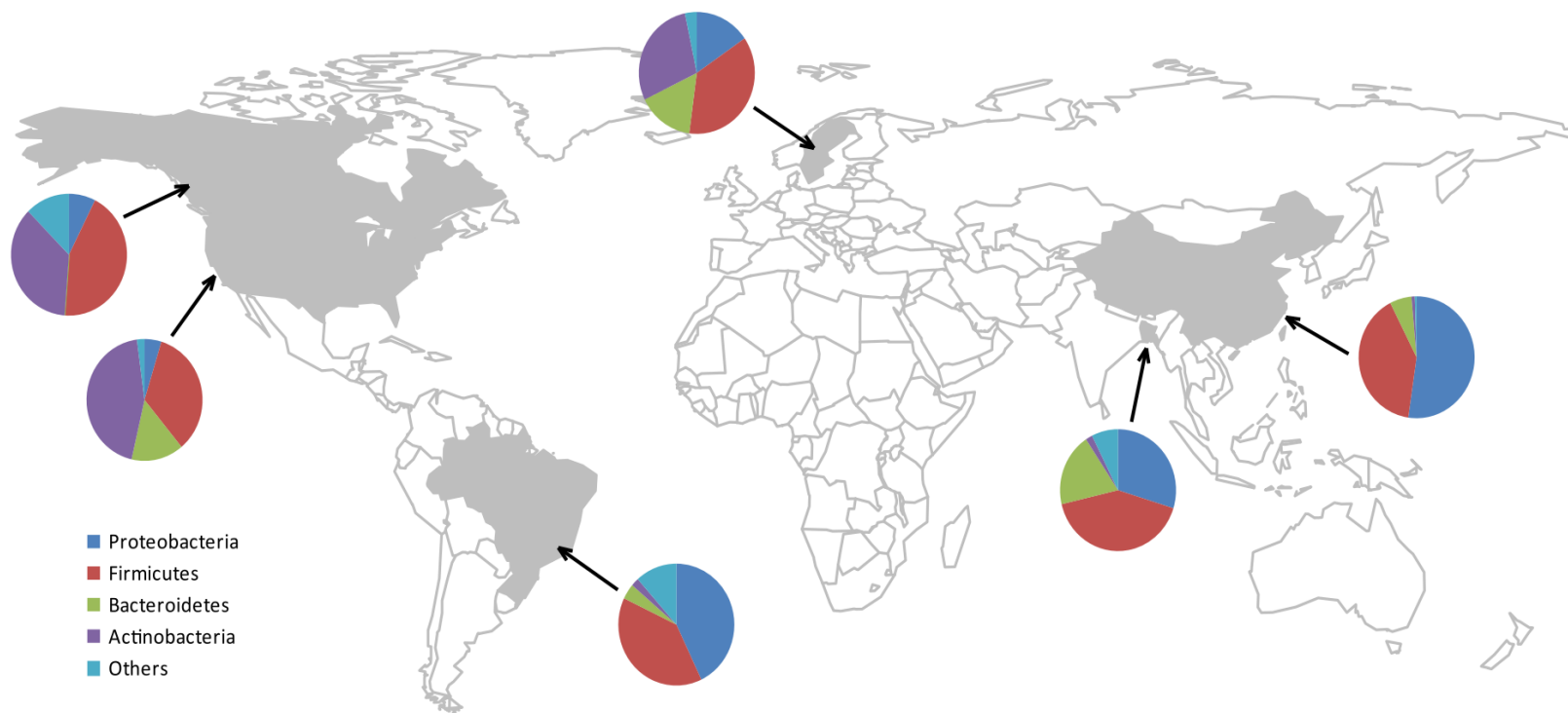
Figure S2: Effects of read depth on principal component analysis of the phylum profiles in infant gut microbiota among 6 countries. (a) (b) Taxonomic relative abundance profiles at the phylum level were also generated based on OTU annotation for each country separately. (c) (d)filtering all OTUs having an abundance lower than 3 reads.(e)(f)and randomly selected 1000 sequences from each sample.
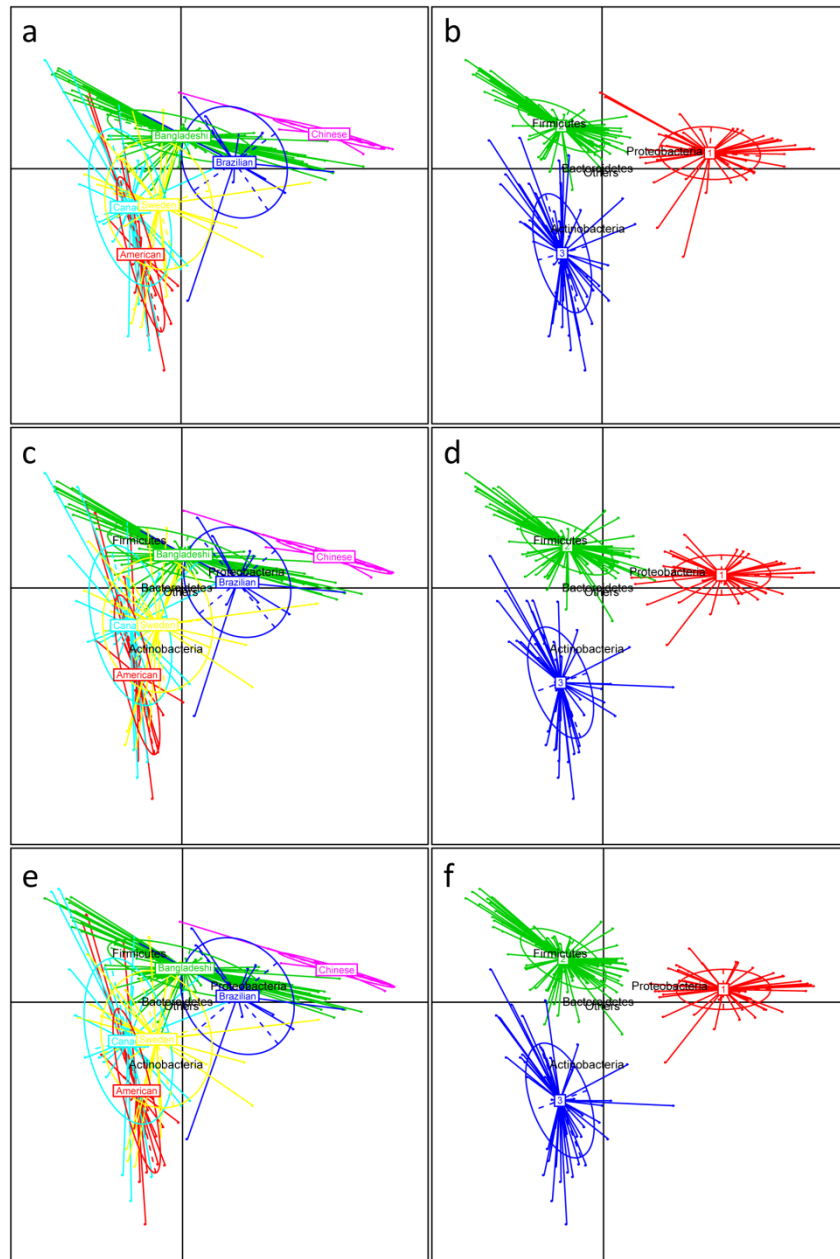
# Reference

1. R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org/