Supplementary Material

Host genetics is associated with gut microbial community membership rather than structure

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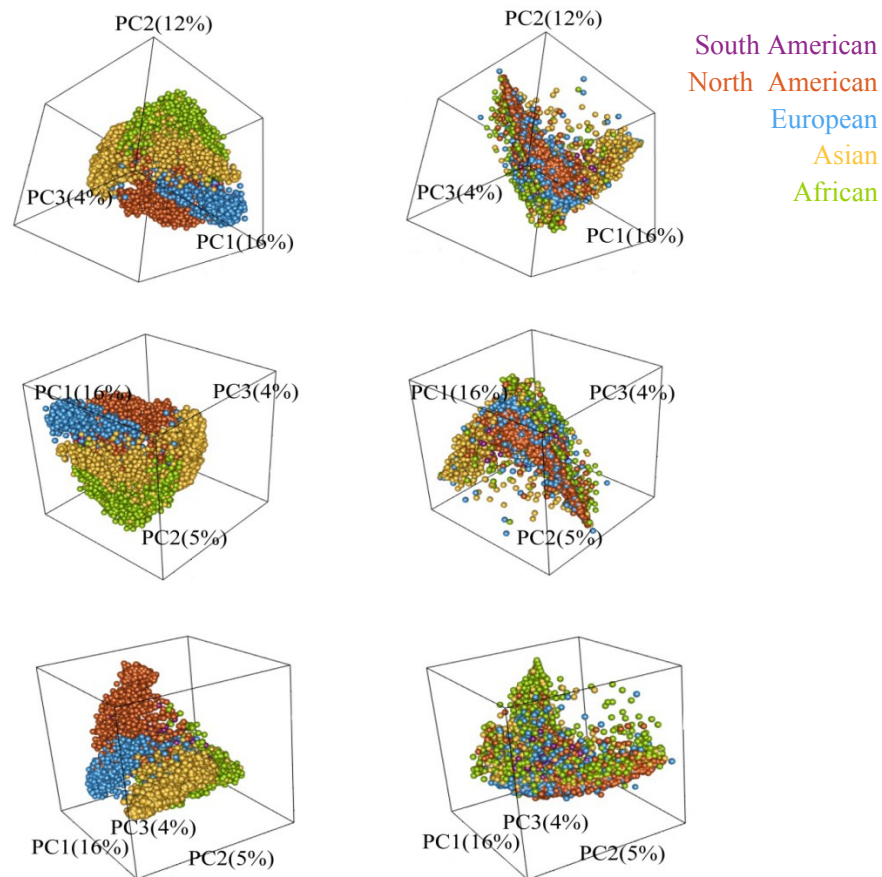
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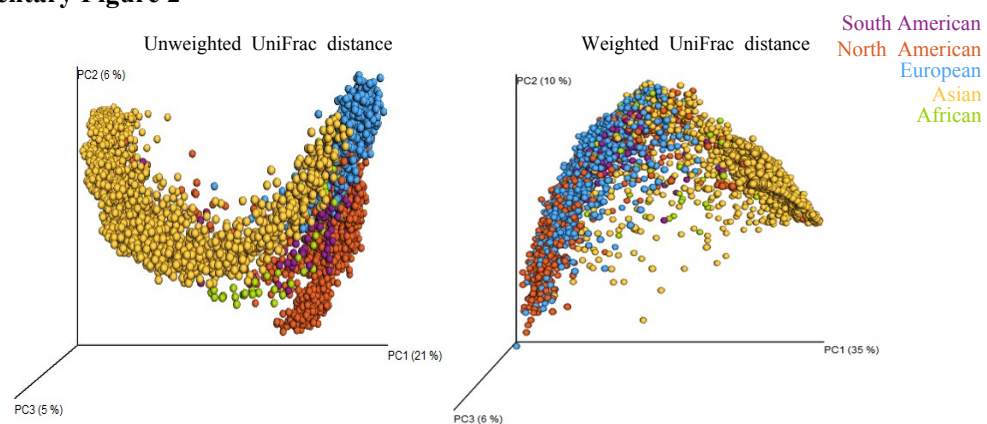*** Correspondence:** Corresponding Author: ddong.ecnu@gmail.com

Supplementary Figures
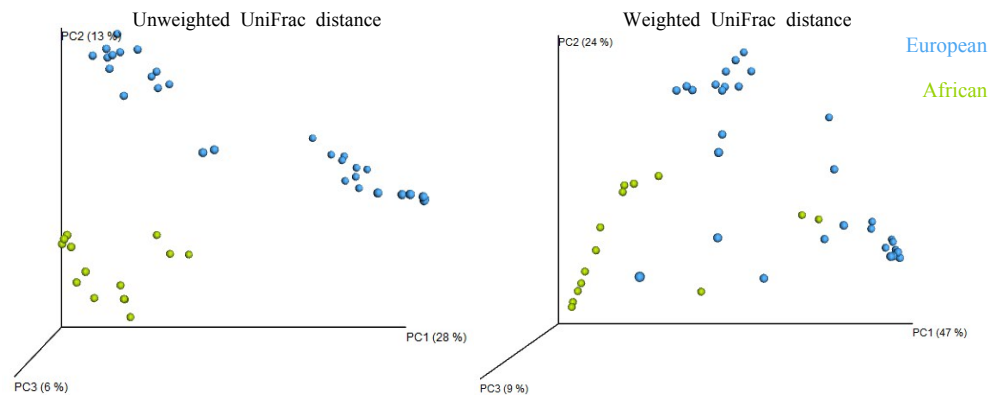
Supplementary Figure 1

Supplementary Figure 1 Different views of the PCoA plot, with each row showing the same view angle, left (unweighted) and right (weighted).

Supplementary Figure 2

Supplementary Figure 2 PCoA plots of the unweighted and weighted UniFrac distances of samples generated from the V4 region. (P < 0.001 for the unweighted and weighted UniFrac distances, ANOSIM).

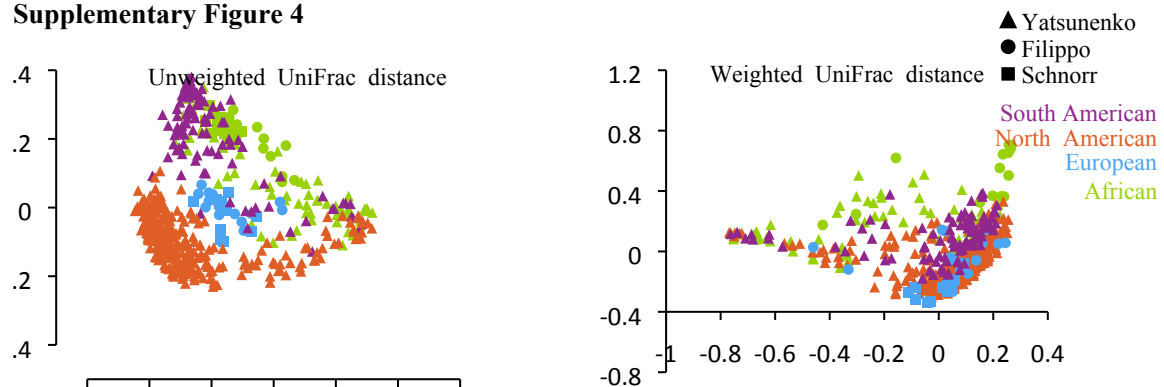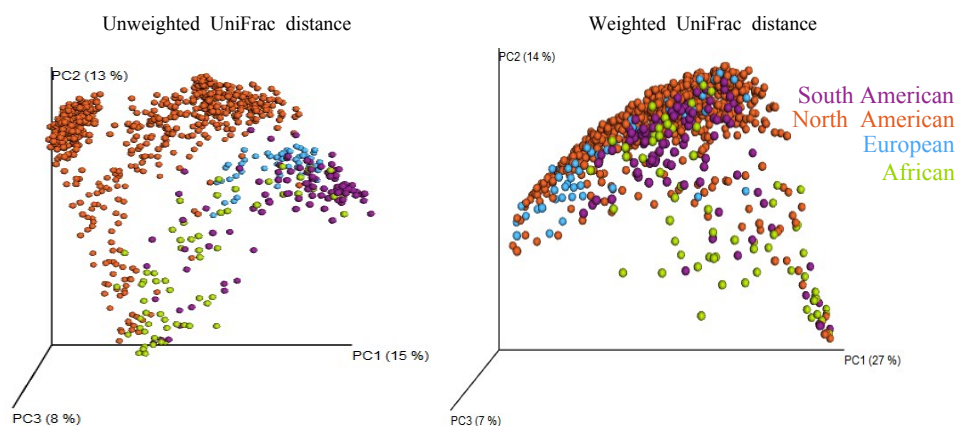**Supplementary Figure 3**

Supplementary Figure 3 PCoA plots of the unweighted and weighted UniFrac distances of samples generated from the V5-V6 region. (P < 0.001 for the unweighted and weighted UniFrac distances, ANOSIM).
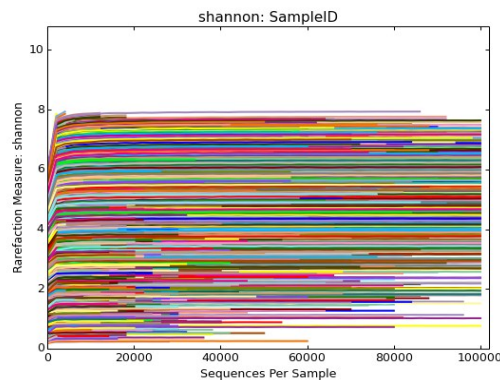
Supplementary Figure 4

Supplementary Figure 4 PCoA plots of the unweighted and weighted UniFrac distances of the samples from the combination of the Yatsunenko, Filippo and Schnorr studies. (P < 0.001 for the unweighted and weighted UniFrac distances, ANOSIM).
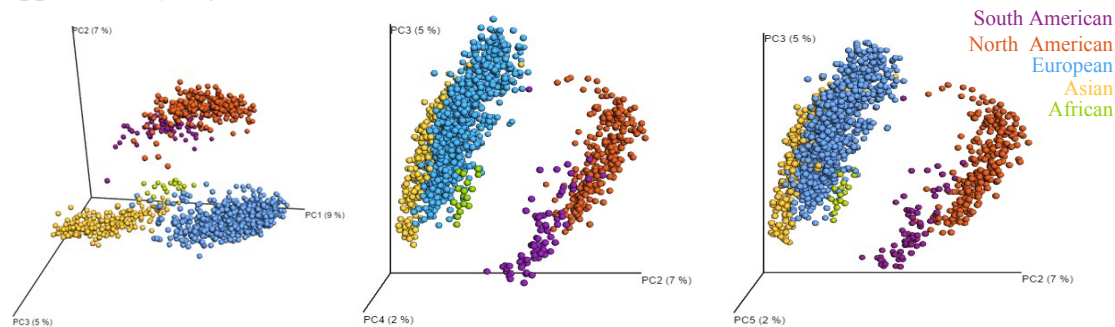
Supplementary Figure 5

Supplementary Figure 5 The rarefaction level of 100,000 was used to perform Principal coordinate analysis. (P < 0.001 for the unweighted and weighted UniFrac distances, ANOSIM).
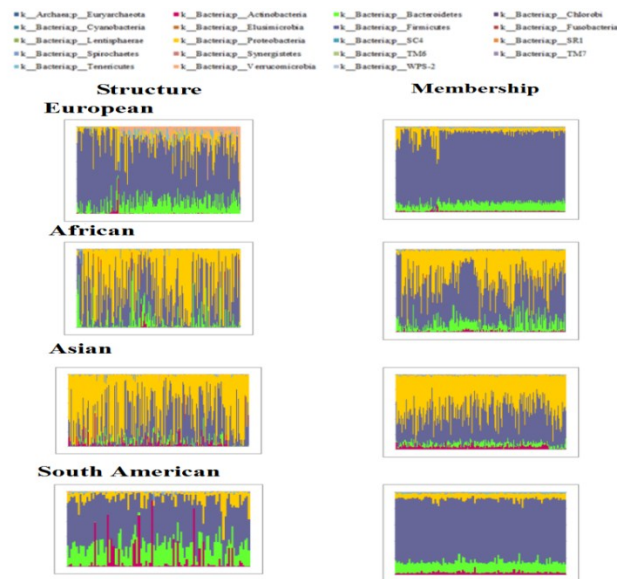
Supplementary Figure 6

Supplementary Figure 6 Alpha rarefaction curves of all samples with a rarefaction depth of 100,000.

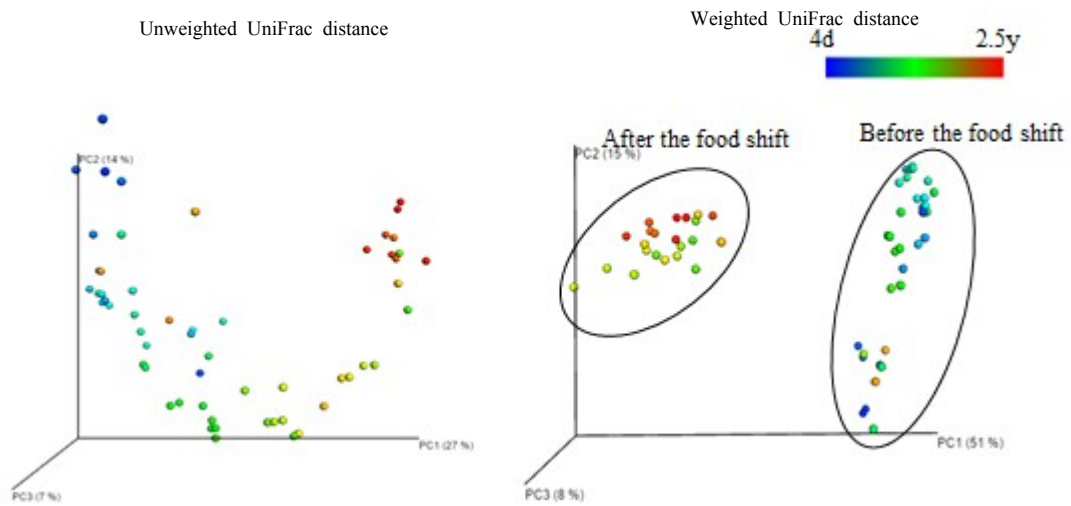**Supplementary Figure 7**

Supplementary Figure 7 PCoA plots of the unweighted UniFrac distances of samples that are normal, generated from V4 region and collected from individuals that are more than 3 years old.

Supplementary Figure 8

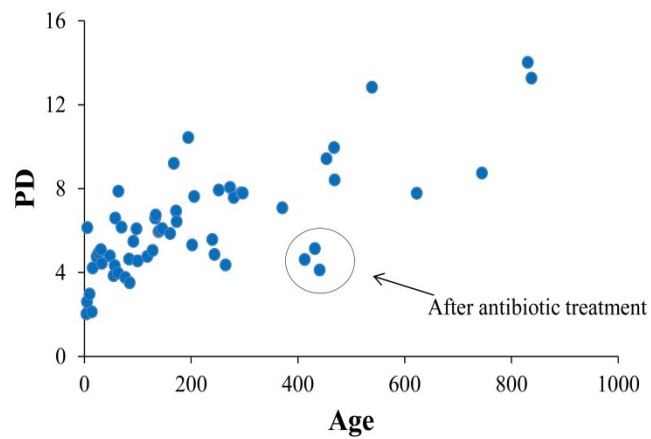**Supplementary Figure 8 Membership and structure of the microbial microbiota in different populations (Asian, European, African, South American).**

Supplementary Figure 9

Supplementary Figure 9 PCoA plot of the unweighted and weighted UniFrac distances in a 2.5 y infant.

Supplementary Figure 10

Supplementary Figure 10 Bacterial PD of an infant gut microbiota over time.

Supplementary table

Table S1 List of studies used.

Study (PMID)	Population	Regions	Sequence platform	Ref
23599893	North American	V2	Illumina GAIIx	Song et al. 2013
24995464	African,Asian	V1-V2	454 FLX	Pop et al. 2014
24336217	North American	V4	Illumina HiSeq	David et al. 2013
22606315	European	V6-V8	454 FLX Titanium	Turroni et al. 2012
24736369	African,European	V4	454 FLX Titanium	Schnorr et al. 2014
25146375	North American	V4	Illumina GAIIx	David et al. 2014
22863002	European	V1-V2	454 FLX Titanium	Koren et al. 2012
25417156	European	V4	Illumina MiSeq	Goodrich et al. 2014
22699611	African, North American, South American	V4	Illumina HiSeq 2000	Yatsunenko et al. 2012
20679230	African,European	V5-V6	454 FLX Titanium	Filippo et al. 2010
20847294	North American	V1-V3	454 FLX Titanium	Dethlefsen et al. 2011
24112053	European	V3-V4	454 FLX Titanium	Avershina et al. 2013
22957008	European	V5-V6	454 FLX Titanium	Jost et al. 2012
24896187	Asian	V4	Illumina MiSeq	Subramanian et al. 2014
20668239	North American	V2	454 FLX	Koenig et al. 2011
21596990	NA	V2	454 FLX	Muegge et al. 2011