Fig S1 | The summary of the workflow.

a



Metagenomic data

82 subjects, 246 samples

42 girl and 40 boys

Bacterial community

Contigs

CRISPRs

1882 cCRISPR arrays

23894 spacers

Bacterial host

Target Phages



b

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描述已自动生成

(a) Clean metagenomic data from 246 samples were assembled into contigs using MEGAHIT. Then CRISPRCasFinder was applied to identify CRISPR arrays. Bacterial hosts and target phages by spacers were assigned by BLASTn. Meanwhile, the bacterial communities were investigaed by MetaPhlAn2.

(b) The quality of assemblies. (a) The number of contigs (K), (b) the community size (Mbp) and (c) the N50 (Kbp) in one sample. The difference in community size between girls and boys at 12 months was significant (Mann-Whitney U test, W = 1195, P = 0.00891).

Fig S2 | Bacterial expansion with age

a b

Chart

Description automatically generated Shape

Description automatically generated with medium confidence

(a) The rarefaction curve of bacterial richness.

(b) Bacterial community size increased with age