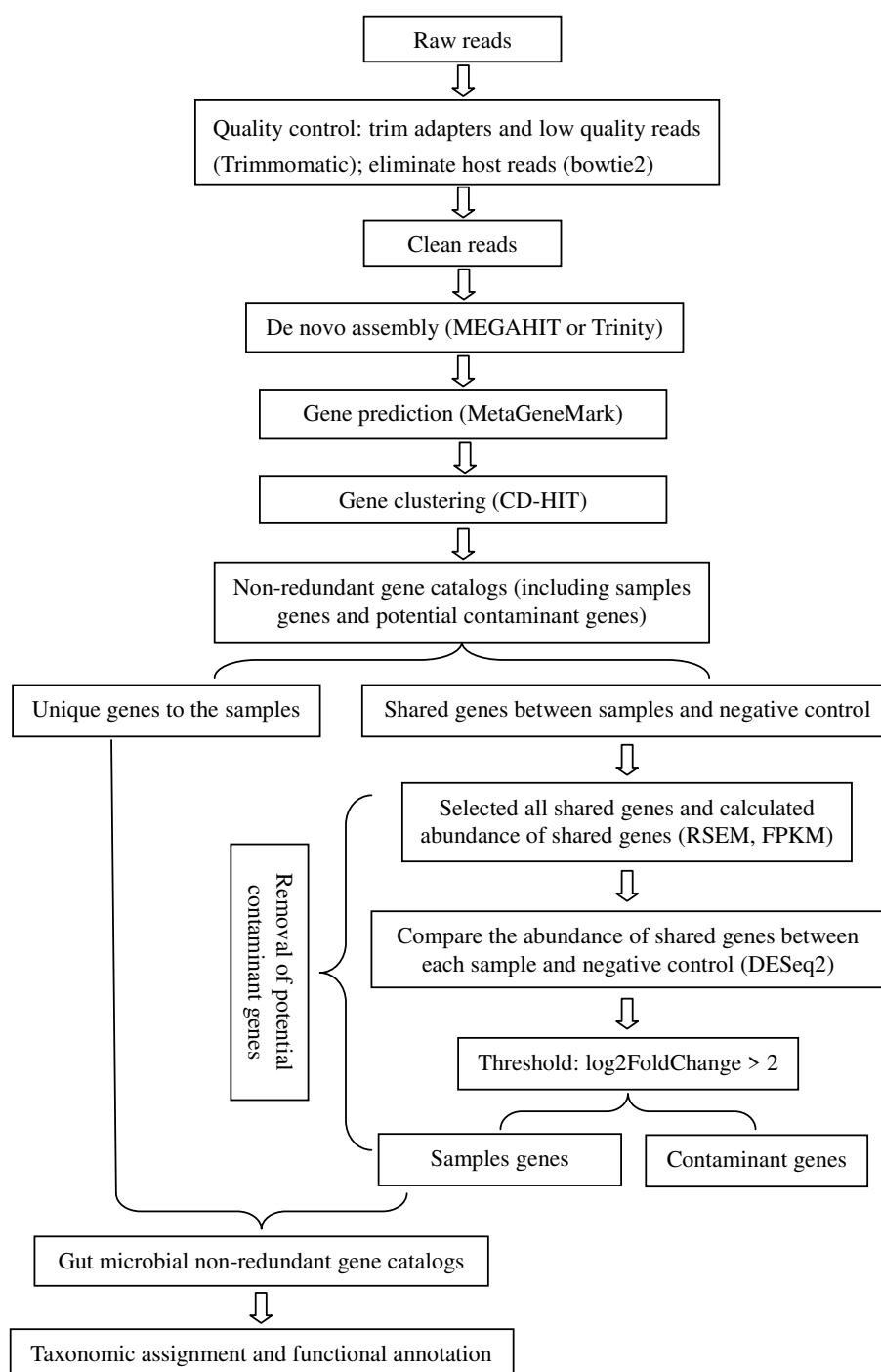


1

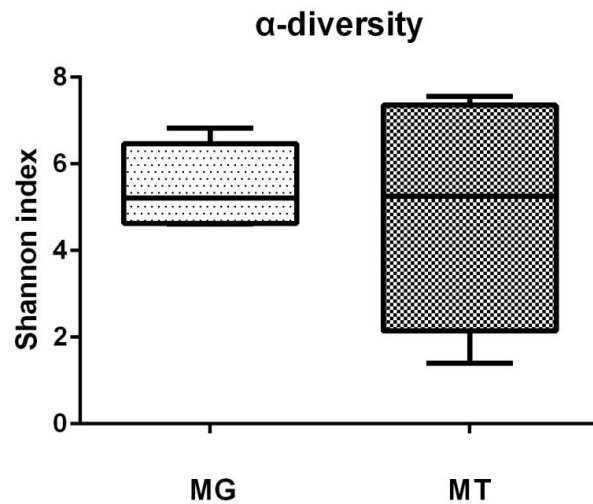
**Supplementary Figures**

2

3 **Supplementary Figure S1** The flow scheme of processing of sequencing data and

4 removal of potential contaminating genes.

5

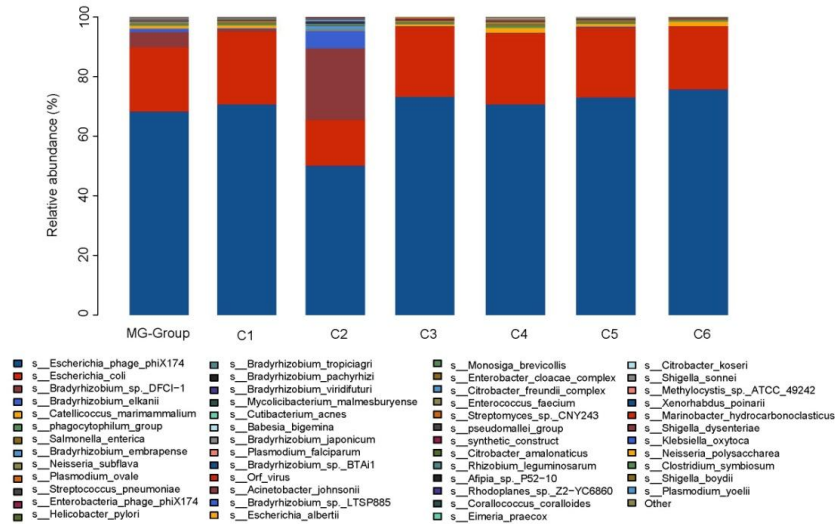


6

7 **Supplementary Figure S2** Alpha diversity of microbial metagenome (MG) and  
8 metatranscriptome (MT) in the fetal gut. Boxes represent interquartile ranges (IQRs)  
9 between the first and third quartiles, and the horizontal line inside the box indicates  
10 the median; whiskers represent the minima or maxima within  $1.5 \times$  IQR from the first  
11 or third quartiles.

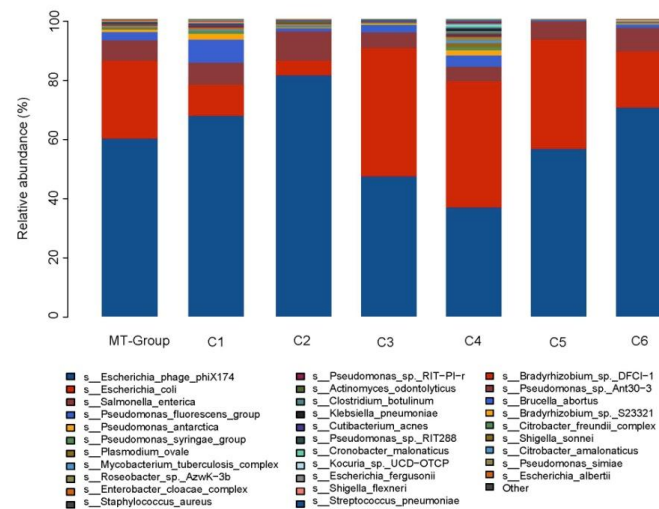
12

A



13

B



14

15 **Supplementary Figure S3** Microbial composition of metagenome (A) and  
 16 metatranscriptome (B) in the fetal gut. C1-C6 represent cecal content samples. Groups  
 17 represent average relative abundance of microbial composition in all samples.