



Bacterial load in meconium

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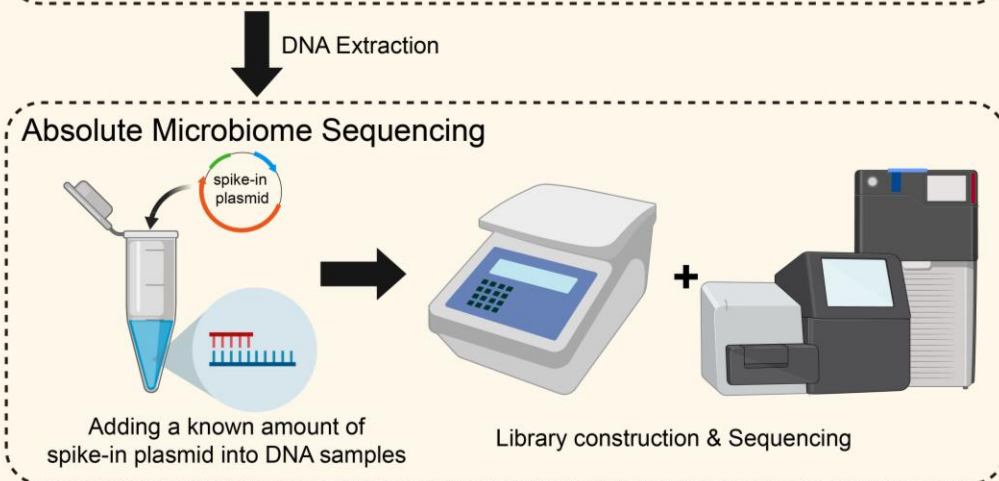
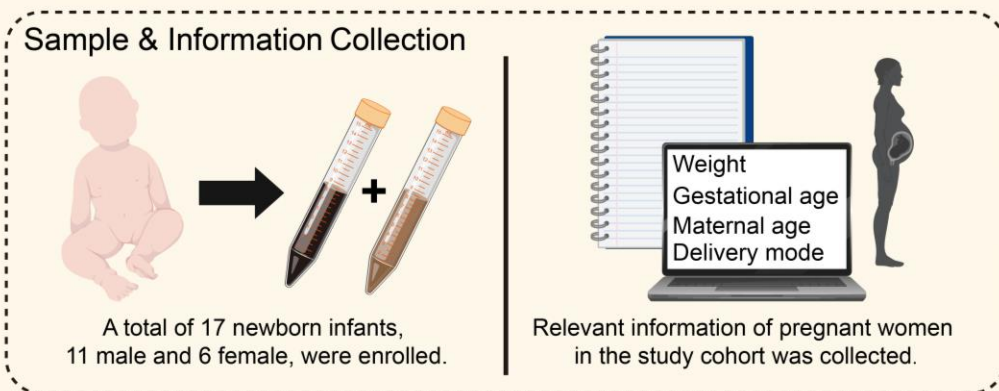
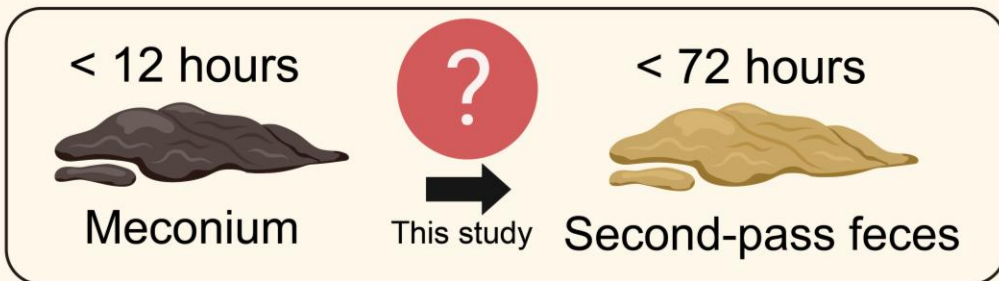
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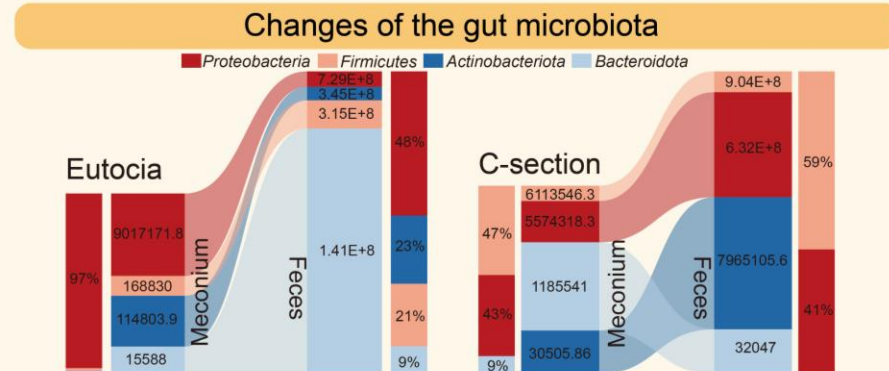
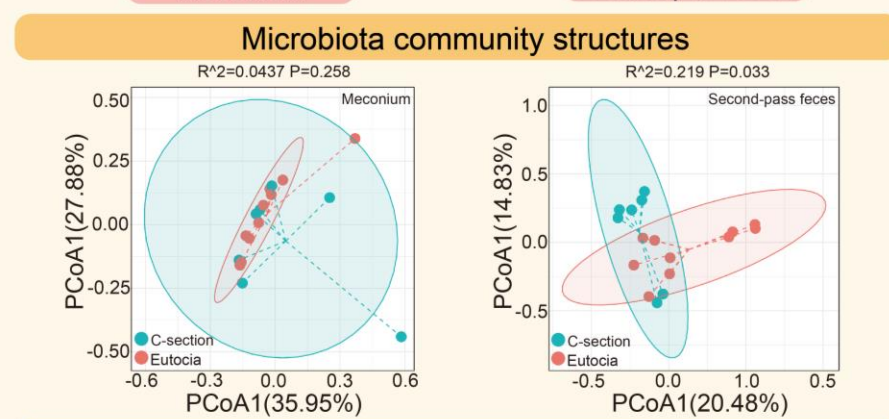
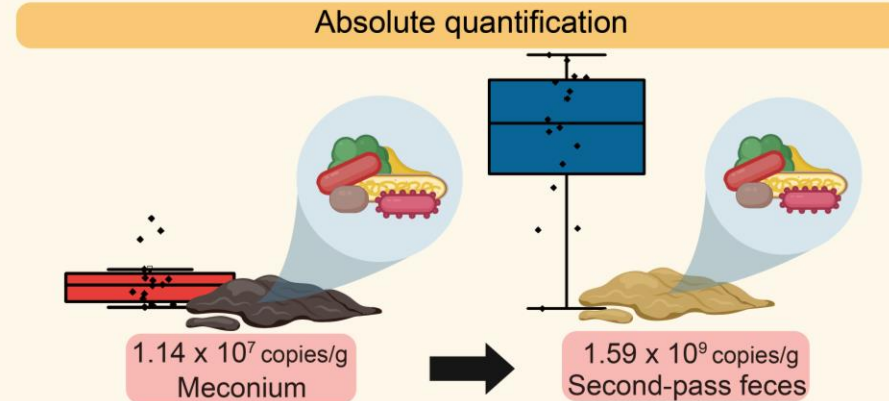


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Highlights



Bioinformatics Analysis





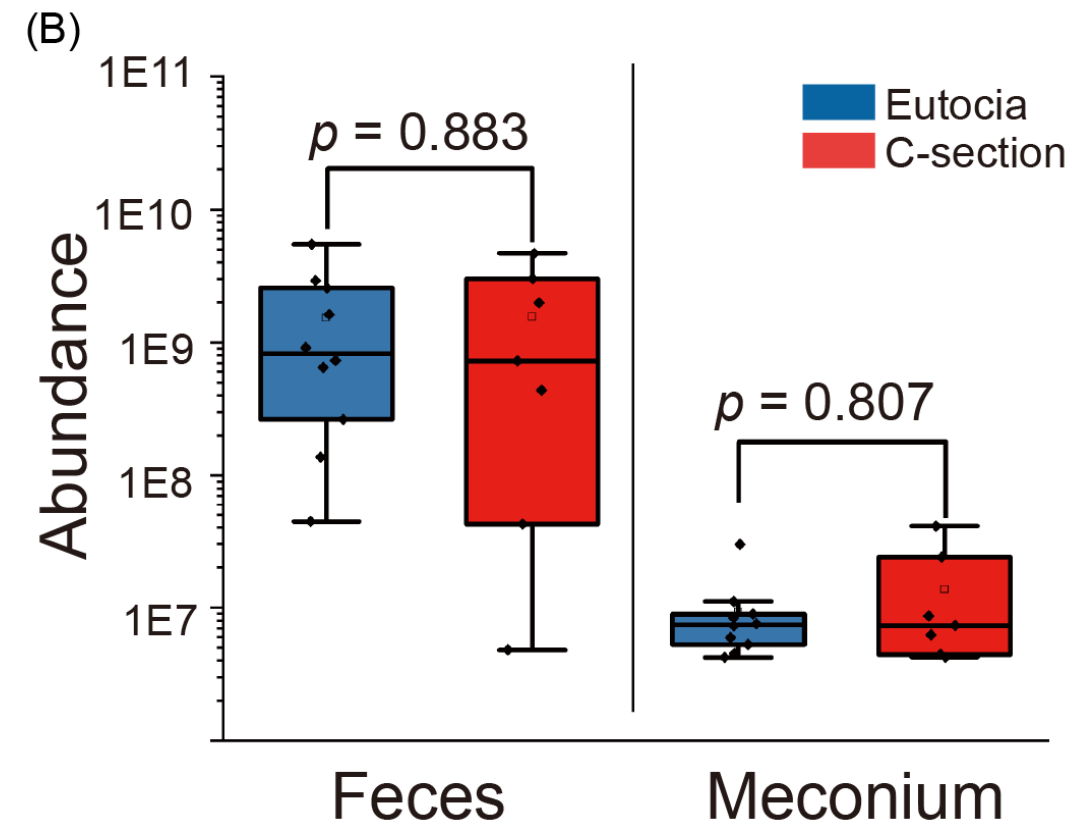
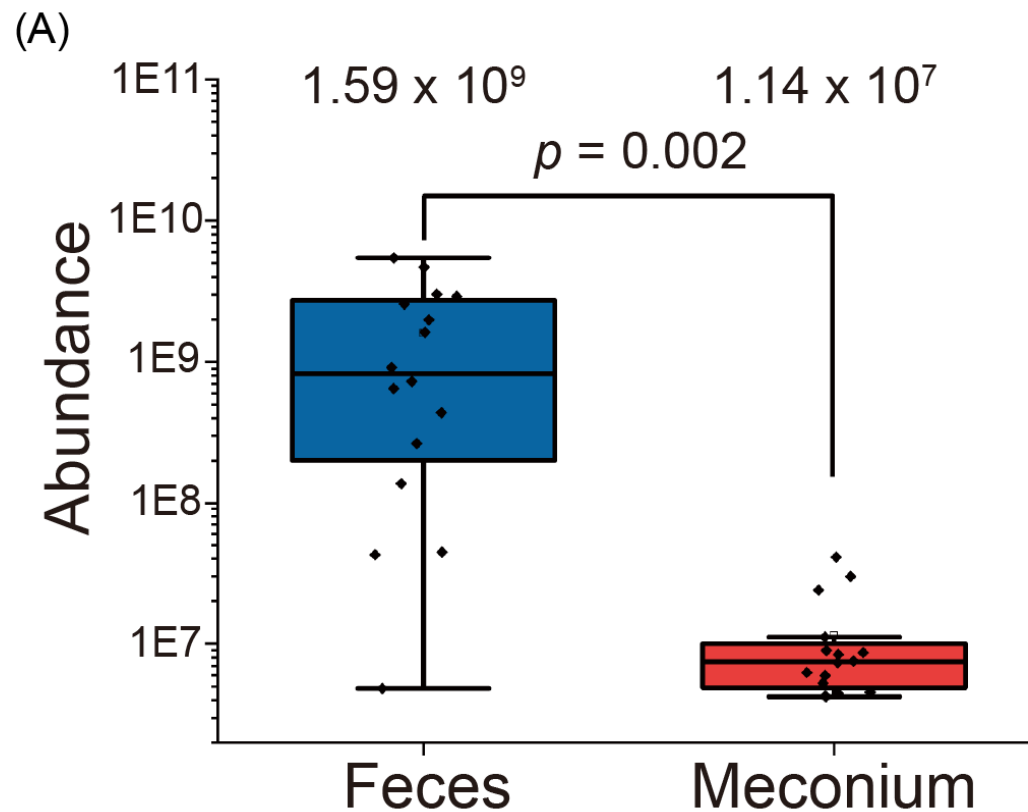
Study Cohort

Characteristics	N=17
Gender	
Male	11
Female	6
Birth Weight(g)	3300.5±476.2
Gestational age (weeks)	38.3±1.5
Age of the mothers (years)	32.2±3.5
Time of the first-pass meconium	<12h
Mode of delivery	
Eutocia	10(58.8%)
C-seaction	7(41.2%)

Result

(A) The absolute abundance of meconium and second-pass feces. ($p = 0.002$)

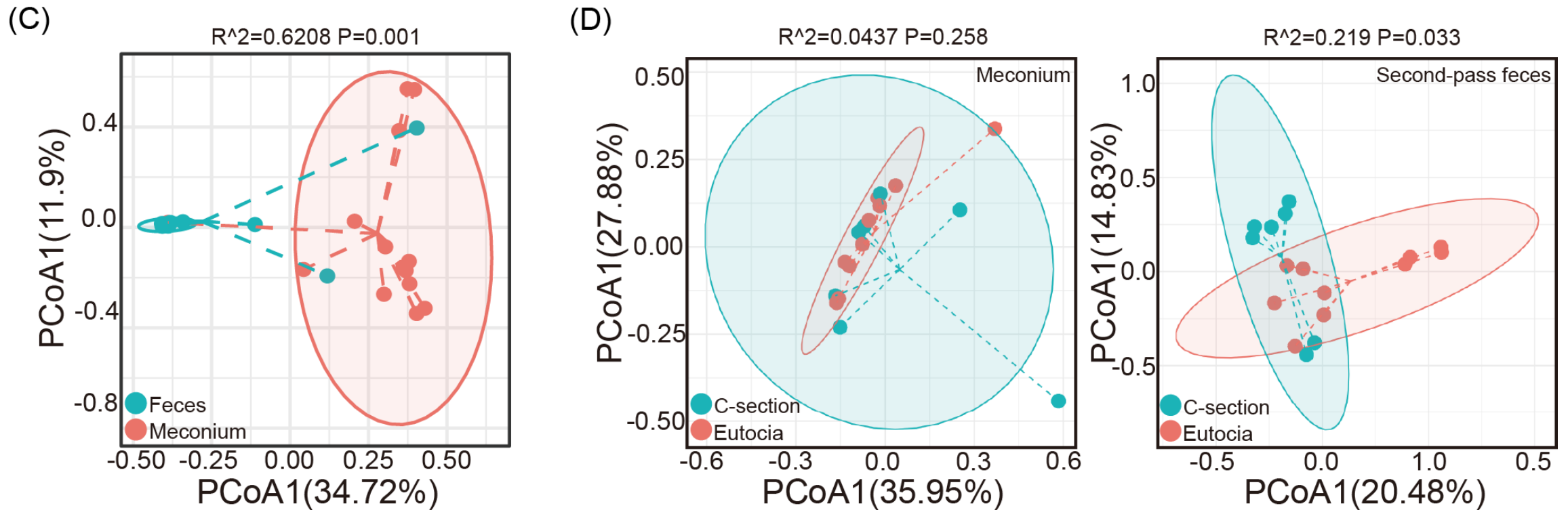
(B) The absolute abundance of eutocia group and C-section group in meconium and second-pass feces.
There is no significant difference between two groups in meconium and second-pass feces.



Result

(C) PCoA analysis in meconium and feces. ($p = 0.001$)

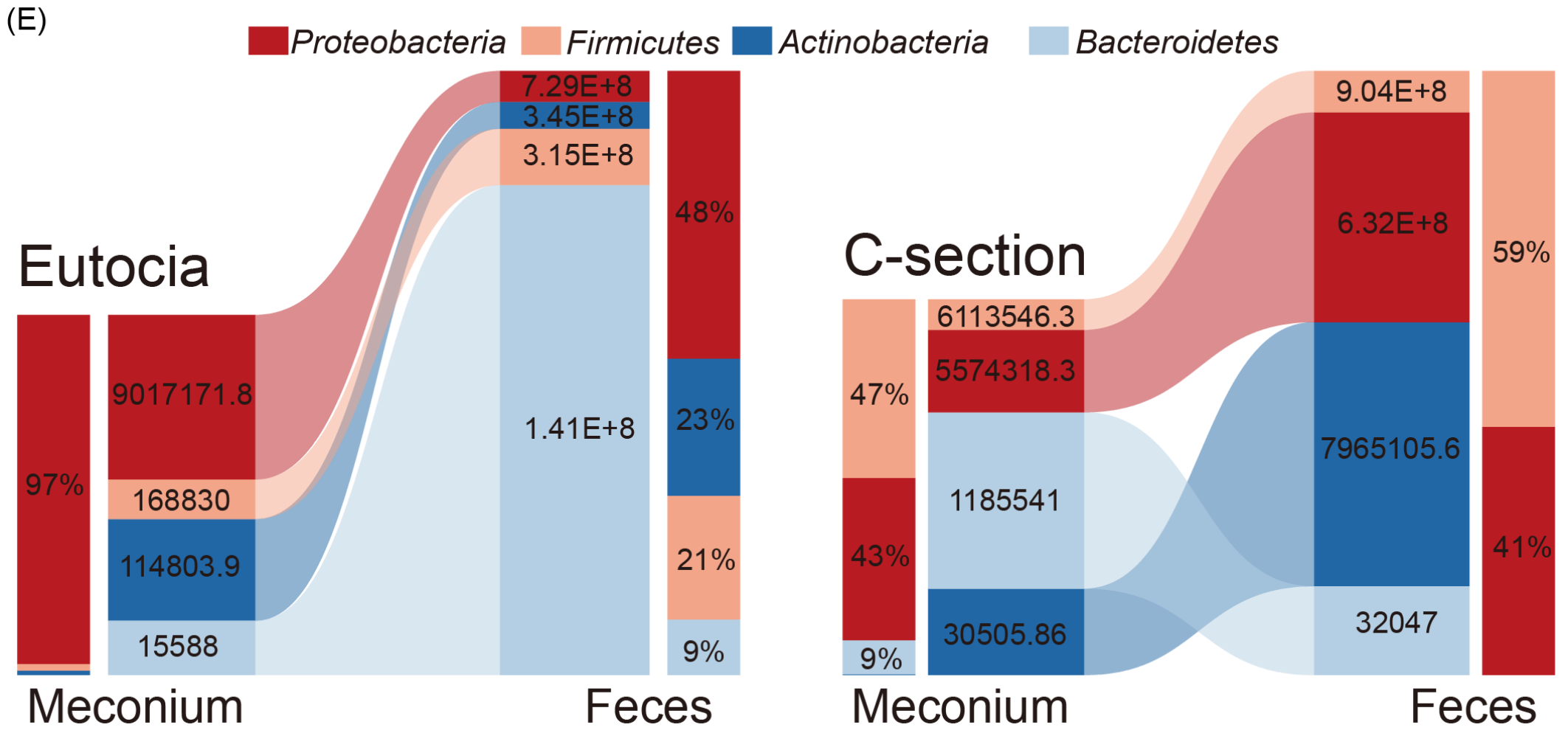
(D) PCoA analysis in eutocia group and C-section group in meconium (left). ($p = 0.258$) and PCoA analysis in eutocia group and C-section group in second-pass feces (right). ($p = 0.033$).





Result

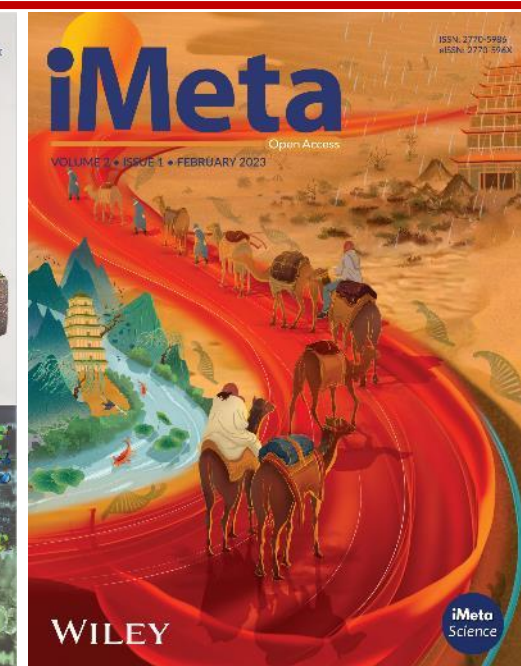
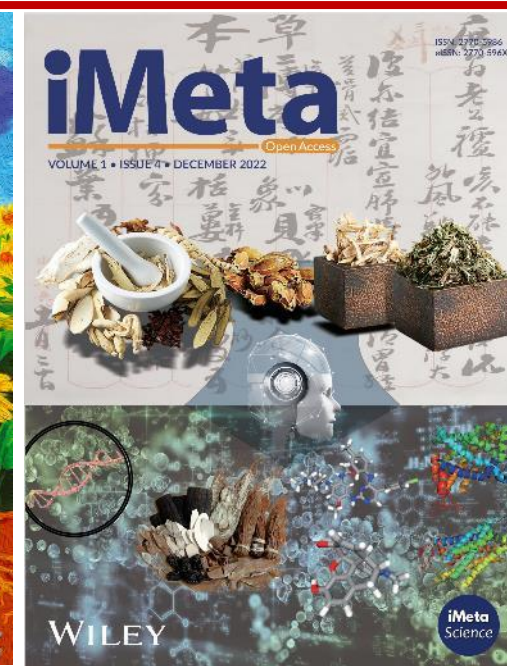
(E) The absolute abundance and relative abundance changing of *Bacteroidetes*, *Proteobacteria*, *Actinobacteria* and *Firmicutes* in the eutocia group (left) and C-section group (right).





Summary

- ❑ In this investigation, we employed the spike-in plasmid method to conduct relative and absolute quantitative analysis of the meconium and the second-pass feces. The abundance of bacteria in meconium samples and second-pass fecal samples was found to be 1.14×10^7 CFU/g and 1.59×10^8 CFU/g respectively
- ❑ We determined that the similarity of meconium was unaffected by the mode of delivery, whereas a notable distinction was evident between the second-pass feces of infants delivered via eutocia and those delivered through C-section.
- ❑ We found an intermediate state (10^6 - 10^7 CFU/g) between fetuses and adults (10^{10} - 10^{11} CFU/g)



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