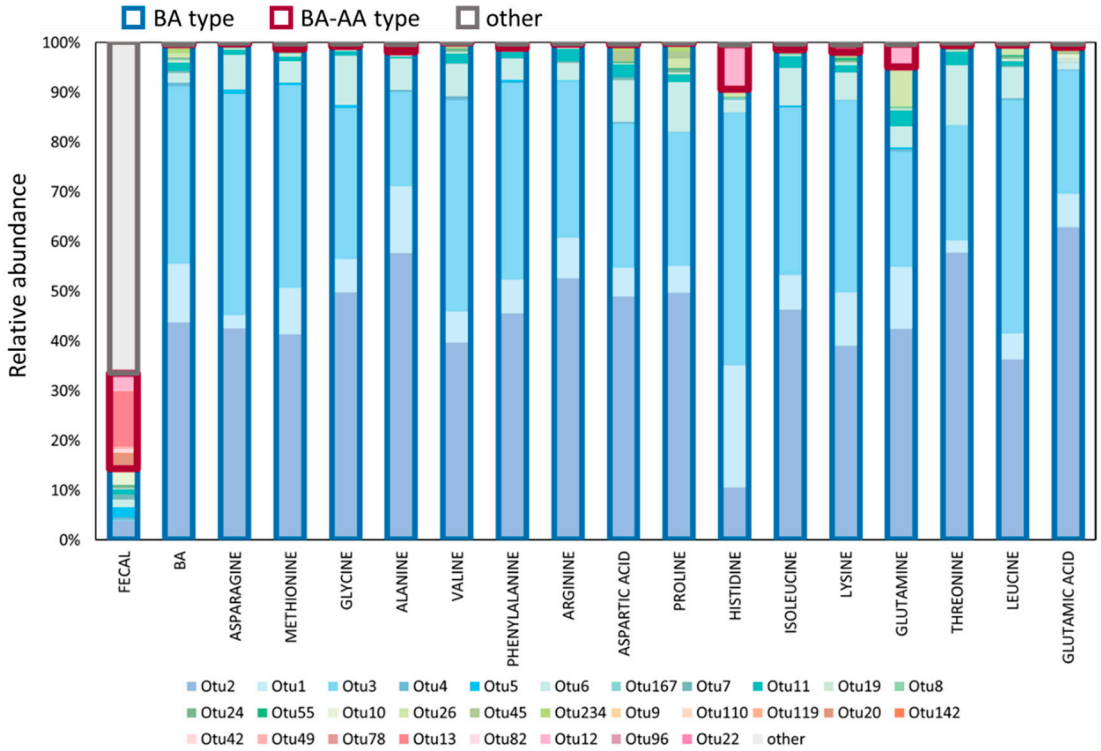
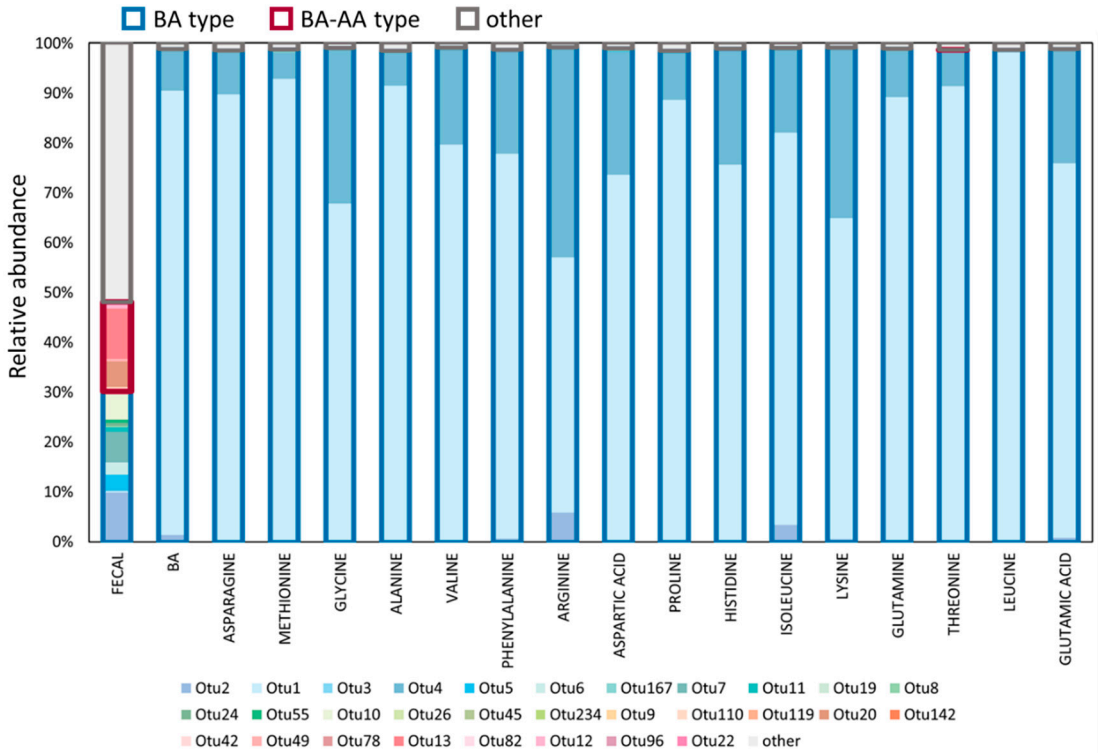
Supplementary Materials

(Donor A:35 y, male)



(Donor B:23 y, female)



(Donor C:25 y, female)

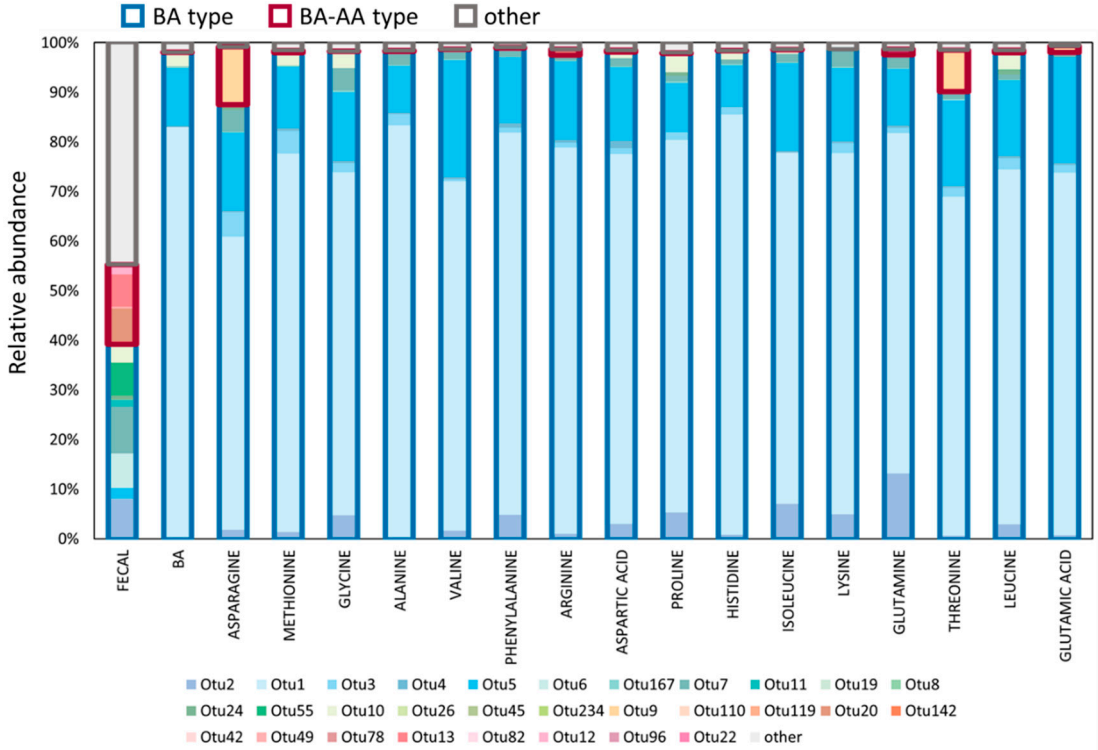


Figure S1. The population of the OTUs in each plate. Each panel shows the relative abundance of each OTU observed in each fecal sample (left end) and bacteria colonies recovered from each donor fecal samples treated by each amino acid. Colonies on the plate were pooled and subjected to the 16S rRNA gene amplicon sequencing. Also, to capture the microbiome of original fecal samples, total bacterial DNA was subjected to the 16S rRNA gene amplicon sequencing. OTUs belonging to the BA type are shown in blue, and those belonging to the BA-AA type are shown in red.

Table S1. Structural information on bile acids used in this study.

Code	Name	Structure
GCA	glycocholic acid	N-(3α,7α,12α-trihydroxy-5β-cholan-24-oyl)glycine
GCDCA	glycochenodeoxycholic acid	N-(3α,7α-dihydroxy-5β-cholan-24-oyl)glycine
GDCA	glycodeoxycholic acid	N-(3α,12α-dihydroxy-5β-cholan-24-oyl)glycine
TCA	taurocholic acid	2-[(3α,7α,12α-trihydroxy-24-oxo-5β-cholan-24-yl)amino]ethanesulfonic acid
TCDCA	taurochenodeoxycholic acid	2-[(3α,7α-dihydroxy-24-oxo-5β-cholan-24-yl)amino]ethanesulfonic acid