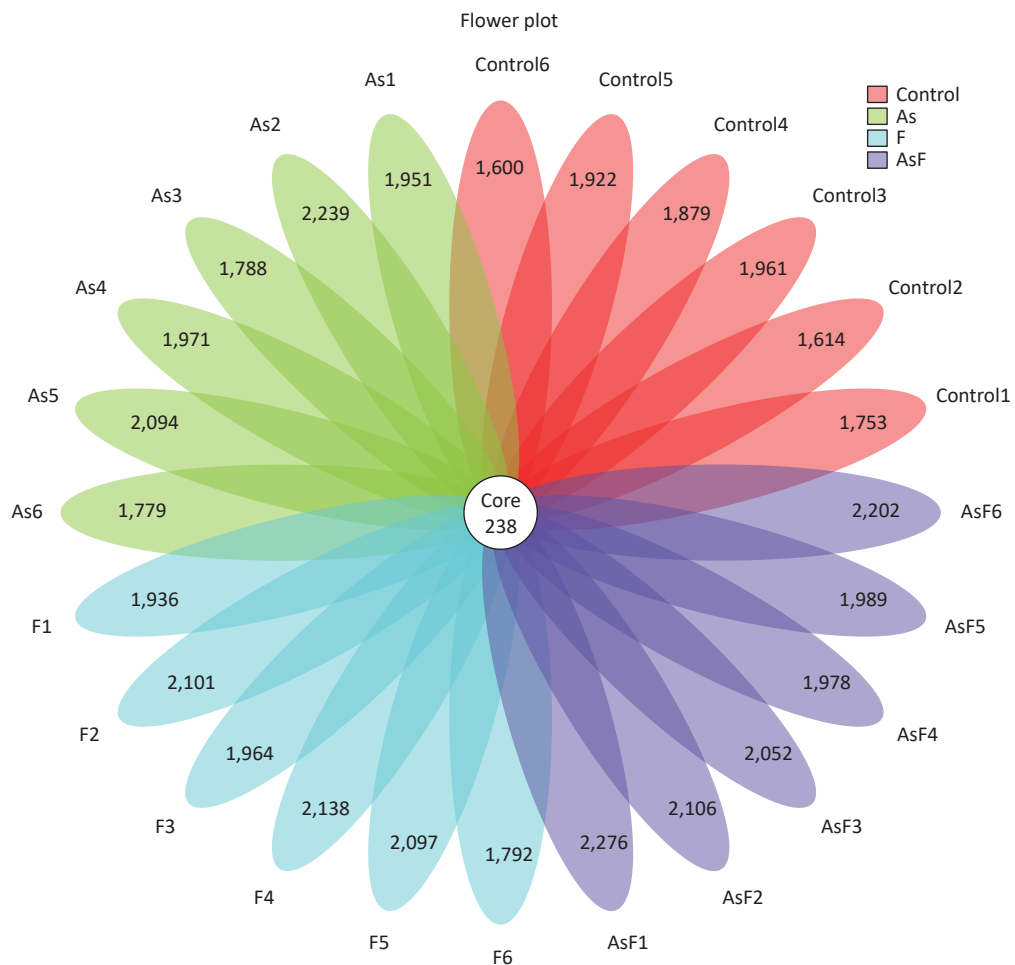


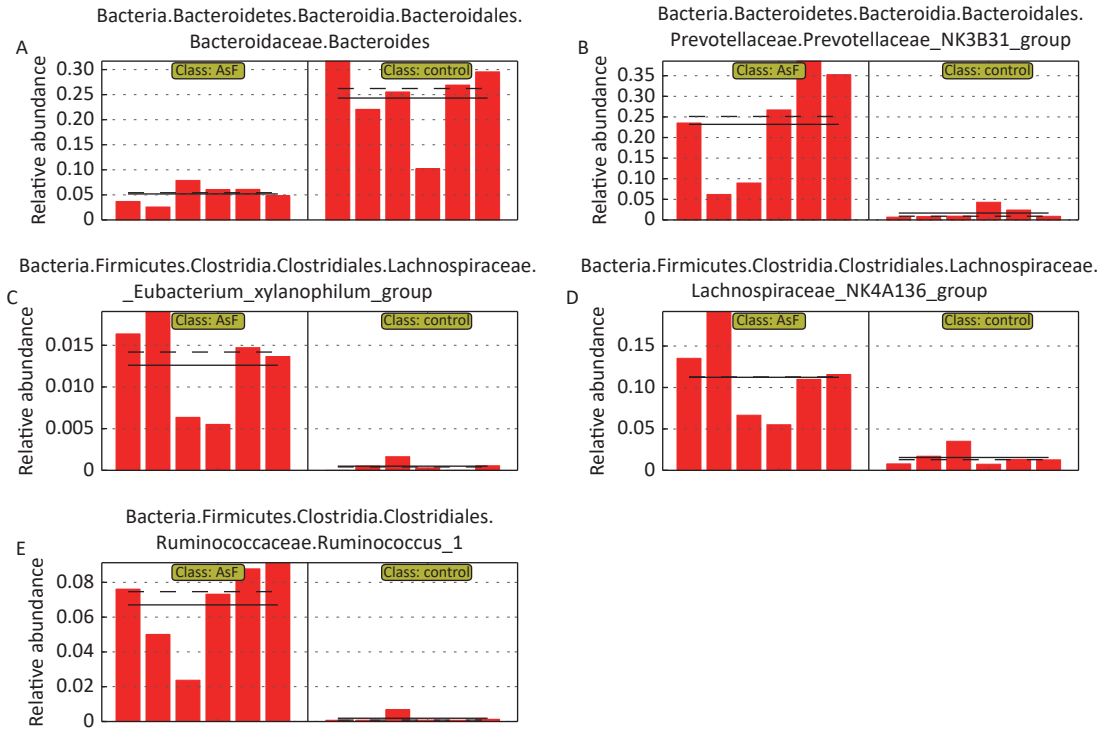
Supplementary Table S1. Elution gradient of mobile phase

Time	A%	B%
0.01	95	5
2	95	5
4	70	30
8	50	50
10	20	80
14	0	100
15	0	100
15.1	95	5
16	95	5

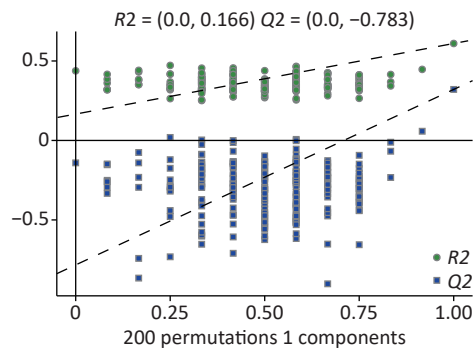
Note. A-water (0.1% formic acid), B-acetonitrile (0.1% formic acid).



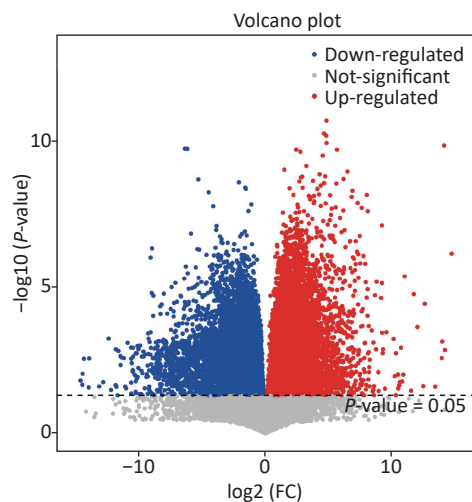
Supplementary Figure S1. Flower plot of OTUs for each sample. The 238 in Core represents the OTUs common to all samples (Core OTUs), and the number on the flower petal represents the total OTUs of each sample minus the number of common OTUs.



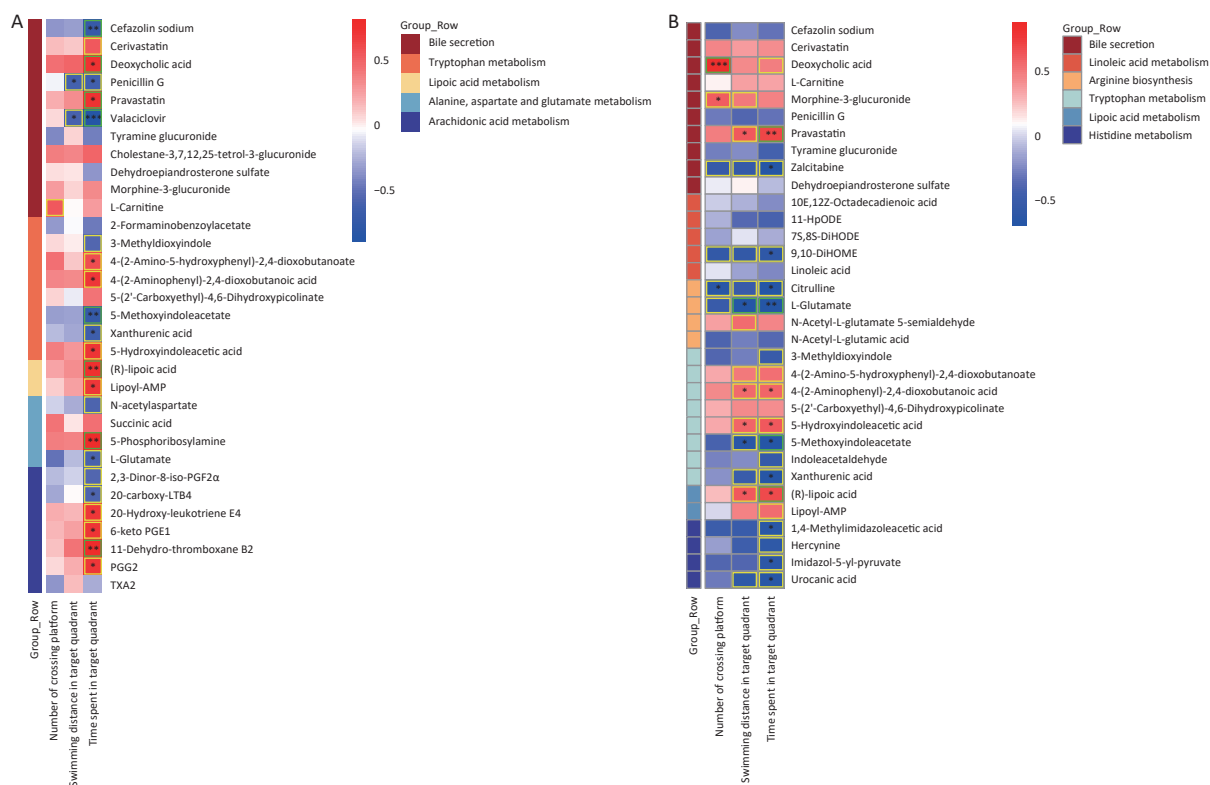
Supplementary Figure S2. Plot of relative abundance of differential bacteria based on group AsF and Con. The bars represent the relative abundance of each sample, and the solid and dashed lines indicate the mean and median values, respectively.



Supplementary Figure S3. Permutation of differential metabolites based on all groups. $R2$, $Q2$: parameter of Permutation test to measure whether the model is overfitted.



Supplementary Figure S4. Volcano plot of differential metabolites based on group AsF and Con. Red and blue dots indicate the differential metabolites that are significantly up- and down-regulated in the two groups of comparisons, respectively, and gray dots represent metabolites that are not significantly different.



Supplementary Figure S5. Correlation between metabolomic alterations and behavioral indicators. Heat map of correlation matrix generated based on control group and As exposure group (A). Heat map of correlation matrix generated based on control group and F exposure group (B). Moderate correlations ($0.5 \leq |r| < 0.7$) are highlighted as yellow-outline squares; strong correlations ($|r| \geq 0.7$) are highlighted as green-outline squares. *, **, and *** *P*-values < 0.05, 0.01, and 0.001, respectively, versus the C group.