Dietary acrylamide intake alters gut microbiota in mice and increases its susceptibility to Salmonella Typhimurium infection

Table S1. Primer sequences.

Gene	Forward primer	Reverse primer
IL-6	5′-GCTACCAAACTGGATA-TAATCAGGA-3′	5′-CCAGGTAGCTATGG-TACTCCAGAA-3′
IL-1β	5′-TTGACGGACCCCAAAAGAT-3′	5′-AGCTGGATGCTCTCATCAGG-3′
TNF-α	5′-TCTTCTCATTCCTGCTTGTGG-3′	5′-GGTCTGGGCCATAGAACTGA-3′
Mucin2	5′-TCATGACGTCTGGTGGAATGG-3′	5′-AGCTTGTCGTGGCAGCTTGA-3′
E-cadherin	5′-GCCAATCCTGATGAAATT-GGAAAC-3′	5′-CCACTGCCCTCGTAATCGAAC-3′
Occludin	5′-GGCAAGCGATCATACCCAGAG-3′	5′-AGGCTGCCTGAAGTCATCCAC-3′
ZO-1	5′-GACCAATAGCTGATGTT-GCCAGAG-3′	5′-TATGAAGGCGAATGATGCCAGA-3′
Claudin-1	5′-AGTGCATGAGGTGCCTGGAAG-3′	5′-TGGCCACTAATGTCGCCAGA-3′
GAPDH	5′-ACAGTCCATGCCATCACTGCC-3′	5′-GCCTGCTTCACCACCTTCTTG-3′

Table S2. Diversity and richness of fecal microbiota in NC and AA groups

Groups	Richness		Diversity		Observed_Species	Goods_Coverage
	Chao1	ACE	Shannon	Simpson		
Control	487.977±36.948[a]	475.698±38.079[a]	5.886±0.133[a]	0.963±0.005[a]	375.500±6.985[a]	0.999±0.0001[a]
AA	334.236±47.104[b]	326.063±41.678[b]	5.743±0.130[a]	0.960±0.004[a]	255.333±11.885[b]	0.999±0.0001[a]

The means with different superscript letters (a and b) respresent statistically signinficant results ($p < 0.001$) based on Two-way ANOVA with Bonferroni multiple comparisons test, whereas means labeled with the same superscript correspond to results that show no statistically significant differences. The results were shown as means ± SEM.
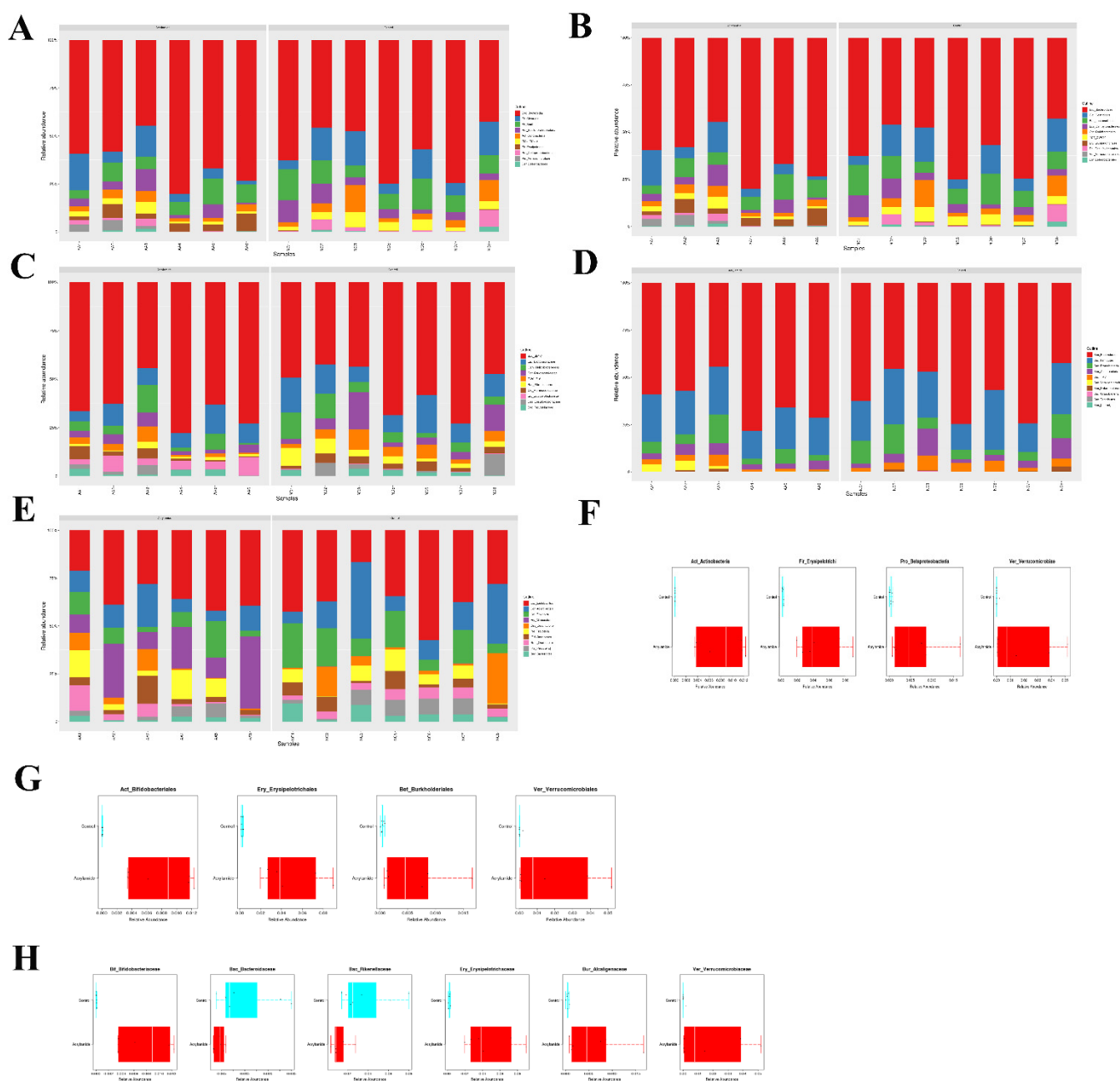
Figure S1. The difference analysis of fecal microbiota between two groups in different levels. (A) Relative abundance of fecal microbiota in each sample at class level. (B) Relative abundance of fecal microbiota in each sample at order level. (C) Relative abundance of fecal microbiota in each sample at family level. (D) Relative abundance of fecal microbiota in each sample at phylum level. (E) Relative abundance of fecal microbiota in each sample at genus level. (F) Comparison of relative abundance of significant bacteria taxa between two groups at class level. (G) Comparison of relative abundance of significant bacteria taxa between two groups at order level. (H) Comparison of relative abundance of significant bacteria taxa between two groups at family level.