

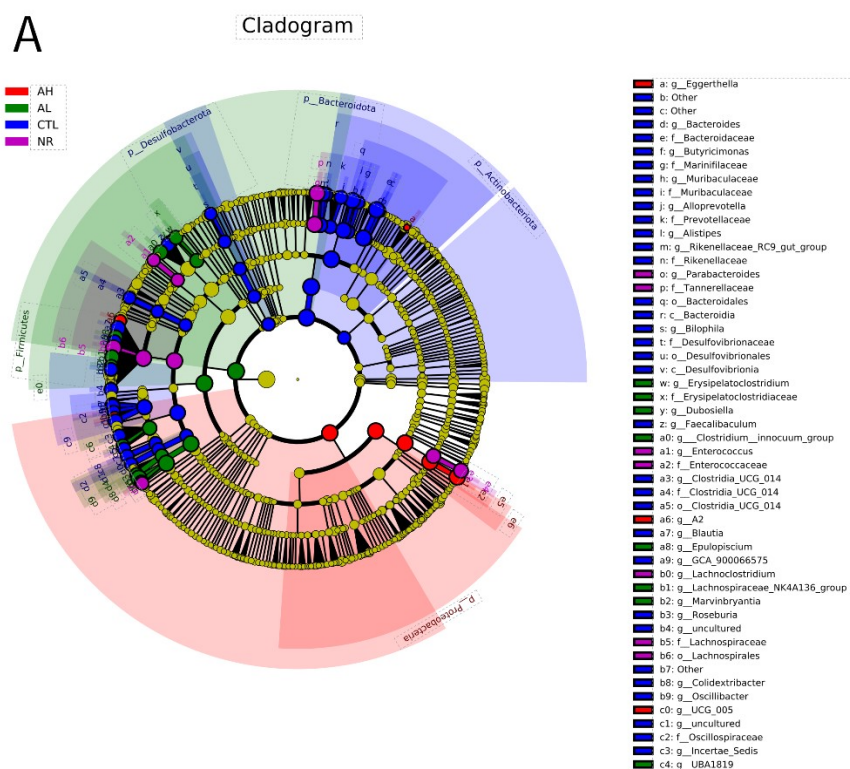
## Supporting Information

**Table S1 The primer sequences for RT-qPCR**

| Primer     | Sequence (5'-3')      |
|------------|-----------------------|
| Claudin1-F | TCTCTGGGATGGATCGGCTC  |
| Claudin1-R | TGTATCTGCCCCGGTGCTTTG |
| ZO-1-F     | TGTTCCGGGTCGTGGATACT  |
| ZO-1-R     | CCCGCTGTCTTTGGAAGTGT  |
| GAPDH-F    | ATGTGTCCGTCGTGGATCTG  |
| GAPDH-R    | AAGTCGCAGGAGACAACCTG  |

**Table S2 The primers sequences during analysis of gut microbiota**

| Primer | Sequence (5'-3') |
|--------|------------------|
| 343-F  | TACGGRAGGCAGCAG  |
| 798-R  | AGGGTATCTAATCCT  |



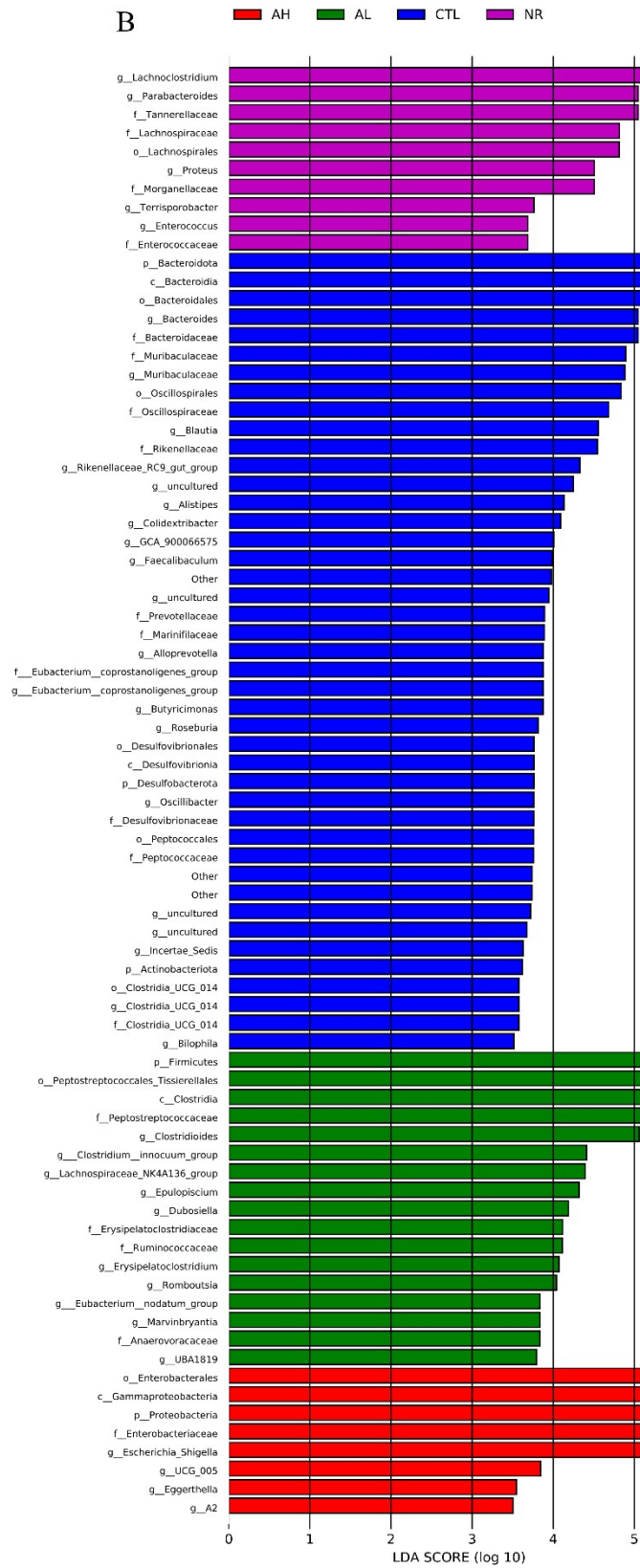


Figure S1. LEfSe analysis of microbiota: (A) taxonomic cladogram obtained from LEfSe analysis of 16S sequences, (B) LDA scores of the differentially abundant taxa.

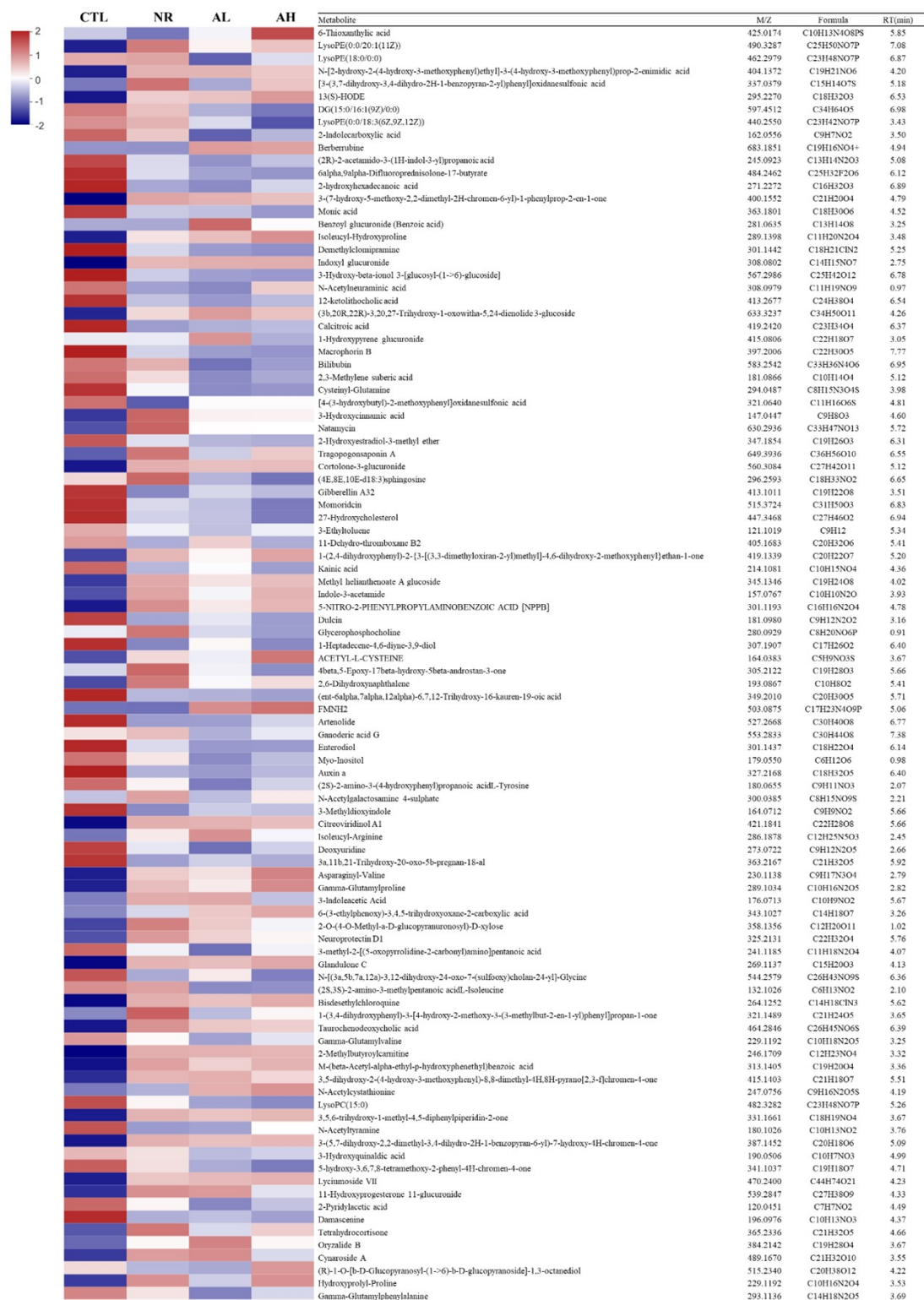


Figure S2. Identification of potential biomarkers (positive ion combined with negative ion) for the effect of tangeretin on antibiotics consumption based on the differently expressed metabolites.