

Figure S1. Rarefaction curves.

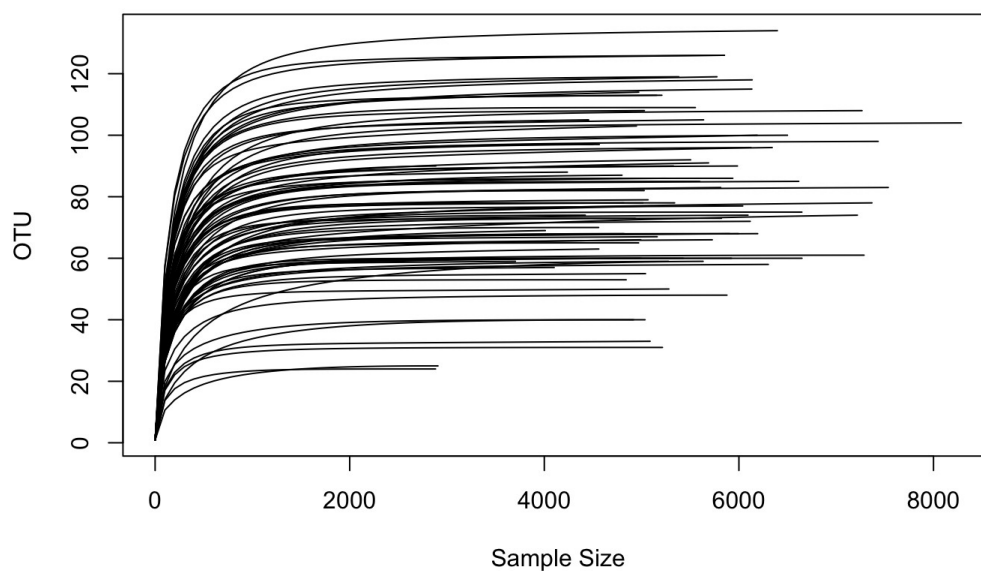


Table S1. Relative abundance of top phyla at pre- and post-treatment stages in all experimental groups.

| | Control | | Vehicle | | CoQ10 | |
|-------------------|----------------|----------------|----------------|----------------|--------------|----------------|
| | Pre | Post | Pre | Post | Pre | Post |
| Firmicutes | 65,1535 | 75,50571428571 | 73,6765 | 79,18025 | 66,1734375 | 68,9211875 |
| Bacteroidota | 27,37571428571 | 19,19233571428 | 17,00275 | 13,18883333333 | 20,2915625 | 22,8609375 |
| Actinobacteriota | 1,975428571429 | 1,248928571428 | 1,625166666666 | 1,26725 | 2,371625 | 1,6203125 |
| Proteobacteria | 0,673142857143 | 0,1665 | 0,45475 | 0,574583333333 | 0,5405 | 0,6205 |
| Campilobacterota | 0,823857142857 | 0,958071428571 | 1,881416666666 | 1,217166666666 | 2,4218125 | 0,6204375 |
| Desulfobacterota | 1,324928571428 | 0,723357142857 | 3,410666666666 | 1,455083333333 | 5,551 | 2,8890625 |
| Spirochaetota | 2,291642857142 | 1,945428571428 | 1,373916666666 | 2,838583333333 | 2,0198 | 1,8905 |
| Unclassified taxa | 0,381785714285 | 0,259664285714 | 0,574833333333 | 0,278249999999 | 0,41499999 | 0,577062500000 |

Table S2. Analysis of differential abundance at genera level.

| Taxon | control | | | vehicle | | | coenzyme Q10 | | |
|---|---------|--------|----------|---------|--------|----------|--------------|--------|----------|
| | ancombc | deseq2 | wilcoxon | ancombc | deseq2 | wilcoxon | ancombc | deseq2 | wilcoxon |
| [Eubacterium] hallii group | + | | | | | | | + | |
| [Eubacterium] siraeum group | + | | | | | | | | |
| [Ruminococcus] torques group | | | | | | | + | | |
| Alistipes | | | | | | + | + | | |
| Allobaculum | | | | + | + | + | | | |
| Anaerobiospirillum | + | | | | | | | | |
| Anaerovibrio | | | | | | | | + | |
| Bifidobacterium | + | + | + | | | | | + | |
| Blautia | | | | | | + | | | |
| Butyrivibrio | | | | | | + | | | |
| Campylobacter | | | | + | | | | | |
| Catenisphaera | | | | | | | | | |
| Chlamydia | + | | | | | + | | | |
| Christensenellaceae R-7 group | | + | | | + | | | | |
| Clostridia UCG-014 | | | | | + | | | | |
| Clostridium sensu stricto 1 | | + | | | | | | + | |
| Colidextribacter | + | | + | | | | | | |
| Coprococcus | + | | | | | + | | | |
| Desulfovibrio | | | | | | | | + | |
| Dorea | | | | | | | + | + | |
| Dubosiella | | | | | | | + | | |
| Enterorhabdus | | | | + | + | | + | | |
| Erysipelatoclostridium | + | + | + | | + | | + | | + |
| Erysipelotrichaceae UCG-006 | | | | + | | | | | |
| Eubacterium xylanophilum group | | | | | | + | | | |
| Faecalibacterium | | | | | | | | + | |
| Faecalibaculum | + | | | | | | | | |
| GWE2-31-10 | + | | | | | | + | | |
| Helicobacter | | | | | | | + | + | + |
| Incertae Sedis | + | | | | | | | | |
| Lachnospiraceae AC2044 group | + | | + | + | | | + | | + |
| Lachnospiraceae NK3A20 group | | | | + | | | | | |
| Lachnospiraceae ND3007 group | | | | | | + | | | |
| Lawsonia | + | | | + | | | + | + | |
| Methanobrevibacter | | | | + | + | | + | + | + |
| Mogibacterium | | | | + | | | | | |
| Monoglobus | | | | + | | + | | | + |
| Mucispirillum | | | | + | | + | | | + |
| Mycoplasma | + | | | | | | | | |
| Negativibacillus | | | | + | | | | | |
| Olsenella | | | | | | + | | | |
| Oscillibacter | + | | | + | | | + | | |
| Oscillospira | + | | | | | + | + | | |
| Parasutterella | + | | | + | | | | | |
| Peptoclostridium | + | | | + | | + | | + | |
| Peptococcus | + | | | + | + | + | + | | |
| Prevotellaceae UCG-001 group | | | | | | | + | | |
| Prevotellaceae Ga6A1 group | | | | | | + | | | |
| Pygmaibacter | | | | + | | | + | + | + |
| Rikenellaceae RC9 gut group | | | | | | | | + | |
| Roseburia | | | | | | | + | | |
| Ruminococcus | | | | | | | + | + | |
| Senegalimassilia | + | | | + | + | | + | | |
| Shuttleworthia | + | | | | | | + | | |
| Solobacterium | | | + | | | | + | | |
| Staphylococcus | | | | + | | | | | |
| Streptococcus | | | | | | + | | | |
| Subdoligranulum | | | | | | | | + | |
| Sutterella | + | | | | | | | | |
| Turicibacter | + | + | | + | | | | + | + |
| Erysipelatoclostridiaceae UCG-004 group | | | | | | + | | | |
| Oscillospiraceae UCG-005 group | | + | | | + | + | | | |
| Ureaplasma | | | | + | | | | | + |

'+' means that adjusted p-value for the chosen method is < 0.05; '+*' means that unadjusted p-value for the method is < 0.05, while adjusted is > 0.05; blank cells - both adjusted and unadjusted p-values > 0.05; taxa for which at least to algorythms showed differential abundance before and after treatment ara highlighted with pale green