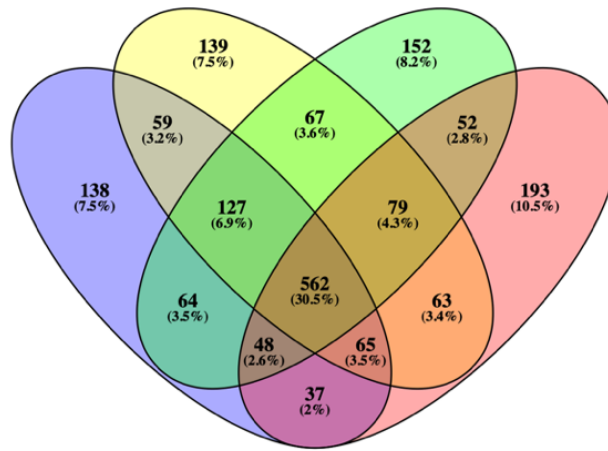


Table S1. Effects of the SARA challenge on the relative abundances of phyla with an abundance above 0.1% by region of the digestive tract.

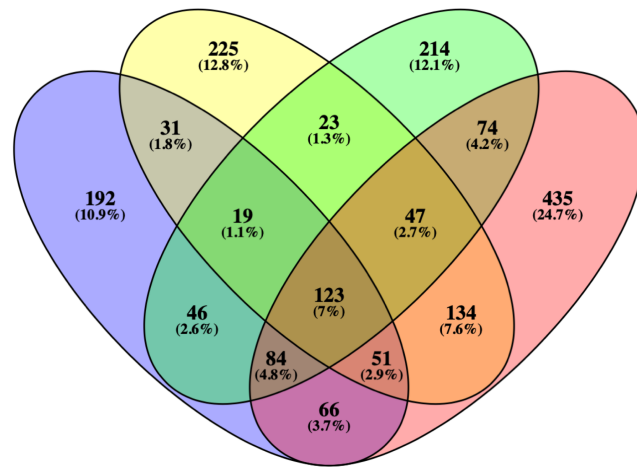
| Rumen | | | | |
|-------------------------|----------------|-------------|------------|---------------------------------|
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 43.0b | 64.8a | 10.2 | 0.05 |
| Bacteroidetes | 33.7a | 16.2b | 5.69 | 0.05 |
| Proteobacteria | 9.0x | 4.2y | 2.32 | 0.08 |
| Spirochaetes | 4.5 | 4.2 | 3.02 | 0.21 |
| Fibrobacteres | 2.7 | 3.4 | 2.46 | 0.29 |
| Tenericutes | 2.4a | 0.5b | 0.77 | 0.005 |
| Euryarchaeota | 0.79a | 0.24b | 0.096 | 0.01 |
| Verrucomicrobia | 0.36a | 0.08b | 0.037 | 0.002 |
| Actinobacteria | 0.31b | 5.54a | 1.34 | 0.005 |
| Chloroflexi | 0.30x | 0.13y | 0.056 | 0.08 |
| Cyanobacteria | 0.029 | 0.13 | 0.041 | 0.13 |
| Duodenum | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 60.00 | 59.00 | 7.08 | 0.88 |
| Bacteroidetes | 18.90 | 11.50 | 4.76 | 0.32 |
| Proteobacteria | 9.34 | 14.90 | 5.93 | 0.88 |
| Actinobacteria | 4.90y | 11.90x | 2.34 | 0.06 |
| Euryarchaeota | 1.60a | 0.32b | 0.39 | 0.04 |
| Tenericutes | 1.57 | 0.90 | 0.43 | 0.27 |
| Spirochaetes | 1.41 | 0.53 | 0.71 | 0.22 |
| Cyanobacteria | 0.52a | 0.07b | 0.13 | 0.02 |
| Verrucomicrobia | 0.43a | 0.05b | 0.11 | 0.02 |
| Fibrobacteres | 0.33a | 0.12b | 0.06 | 0.03 |
| Chloroflexi | 0.07 | 0.07 | 0.05 | 0.96 |
| Proximal jejunum | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 66.1 | 54.7 | 8.43 | 0.42 |
| Bacteroidetes | 10.6x | 6.7y | 1.23 | 0.07 |
| Proteobacteria | 10.4 | 11.2 | 2.18 | 0.85 |
| Actinobacteria | 6.2y | 25.1x | 7.78 | 0.07 |
| Euryarchaeota | 2.0a | 0.4b | 0.65 | 0.10 |
| Tenericutes | 2.0a | 0.6b | 0.37 | 0.03 |
| Spirochaetes | 0.92a | 0.14b | 0.143 | 0.005 |
| Cyanobacteria | 0.48x | 0.14y | 0.114 | 0.08 |
| Verrucomicrobia | 0.34x | 0.14y | 0.067 | 0.08 |
| Fibrobacteres | 0.26 | 0.11 | 0.088 | 0.37 |
| Chloroflexi | 0.033 | 0.12 | 0.0522 | 0.31 |
| Middle jejunum | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 59.0 | 62.8 | 5.83 | 0.63 |
| Proteobacteria | 20.0 | 13.8 | 3.89 | 0.29 |
| Bacteroidetes | 9.8 | 7.3 | 1.69 | 0.33 |
| Actinobacteria | 4.7b | 13.4a | 2.91 | 0.05 |
| Tenericutes | 2.0 | 1.3 | 0.44 | 0.36 |
| Euryarchaeota | 1.40x | 0.41y | 0.37 | 0.08 |
| Cyanobacteria | 0.69x | 0.10y | 0.22 | 0.08 |
| Spirochaetes | 0.62 | 0.2 | 0.17 | 0.13 |
| Verrucomicrobia | 0.35 | 0.13 | 0.212 | 0.75 |
| Fibrobacteres | 0.18 | 0.062 | 0.078 | 0.34 |
| Chloroflexi | 0.17x | 0.033y | 0.044 | 0.05 |
| Distal jejunum | | | | |

| | Control | SARA | SEM | Effects, <i>P</i> values |
|-----------------|---------|--------|--------|--------------------------|
| Firmicutes | 79.8a | 53.3b | 6.62 | 0.03 |
| Proteobacteria | 6.5 | 21.5 | 5.01 | 0.13 |
| Bacteroidetes | 4.9 | 3.6 | 1.41 | 0.65 |
| Actinobacteria | 3.8b | 21a | 4.78 | 0.05 |
| Euryarchaeota | 1.7 | 0.12 | 0.36 | 0.005 |
| Tenericutes | 1.6 | 0.27 | 0.378 | 0.036 |
| Spirochaetes | 0.47 | 0.023 | 0.183 | 0.14 |
| Cyanobacteria | 0.32a | 0.02b | 0.074 | 0.02 |
| Verrucomicrobia | 0.21 | 0.11 | 0.077 | 0.26 |
| Fibrobacteres | 0.18 | 0.041 | 0.08 | 0.2 |
| Chloroflexi | 0.13a | 0.025b | 0.02 | 0.01 |
| Ileum | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 78.0a | 52.2b | 7.97 | 0.05 |
| Proteobacteria | 7.8 | 20.2 | 7.79 | 0.95 |
| Bacteroidetes | 5.4 | 10.4 | 2.16 | 0.12 |
| Actinobacteria | 3.4b | 15.8a | 3.92 | 0.04 |
| Euryarchaeota | 2.0a | 0.13b | 0.306 | 0.01 |
| Tenericutes | 1.9x | 0.6y | 0.433 | 0.09 |
| Cyanobacteria | 0.51x | 0.09y | 0.17 | 0.09 |
| Spirochaetes | 0.28 | 0.15 | 0.088 | 0.39 |
| Verrucomicrobia | 0.23x | 0.094y | 0.053 | 0.10 |
| Chloroflexi | 0.13 | 0.026 | 0.05 | 0.18 |
| Fibrobacteres | 0.11 | 0.033 | 0.063 | 0.42 |
| Cecum | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 54.2 | 63.0 | 6.47 | 0.19 |
| Bacteroidetes | 27.2 | 18.8 | 5.15 | 0.12 |
| Spirochaetes | 13.6 | 14.2 | 5.93 | 0.82 |
| Verrucomicrobia | 0.95 | 0.16 | 0.40 | 0.13 |
| Proteobacteria | 0.86a | 0.53b | 0.079 | 0.02 |
| Tenericutes | 0.79 | 0.70 | 0.125 | 0.62 |
| Euryarchaeota | 0.37a | 0.03b | 0.047 | 0.01 |
| Actinobacteria | 0.20 | 1.70 | 0.54 | 0.05 |
| Fibrobacteres | 0.16a | 0.004b | 0.035 | 0.01 |
| Cyanobacteria | 0.15a | 0.012b | 0.044 | 0.03 |
| Chloroflexi | 0.011 | 0.004 | 0.0033 | 0.18 |
| Colon | | | | |
| | Control | SARA | SEM | Effects, <i>P</i> values |
| Firmicutes | 47.8b | 70.3a | 5.38 | 0.02 |
| Bacteroidetes | 32.2a | 19.4b | 5.24 | 0.05 |
| Spirochaetes | 14.2a | 0.88b | 2.28 | 0.001 |
| Proteobacteria | 1.3 | 0.88 | 0.177 | 0.10 |
| Tenericutes | 0.83a | 0.27b | 0.157 | 0.04 |
| Verrucomicrobia | 0.66 | 0.37 | 0.29 | 0.23 |
| Euryarchaeota | 0.55a | 0.06b | 0.061 | 0.002 |
| Cyanobacteria | 0.35a | 0.02b | 0.074 | 0.006 |
| Fibrobacteres | 0.31a | 0.00b | 0.0356 | 0.0002 |
| Actinobacteria | 0.12b | 7.50a | 1.66 | 0.002 |
| Chloroflexi | 0.0068 | 0.0184 | 0.0077 | 0.34 |

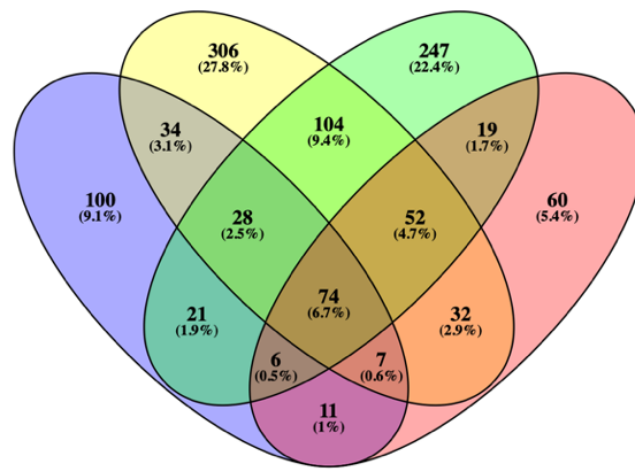
^{a, b} Lsmeans with different superscripts in a row differ ($P < 0.05$), ^{x, y} Lsmeans with different superscripts in a row tend to differ ($P < 0.10$).



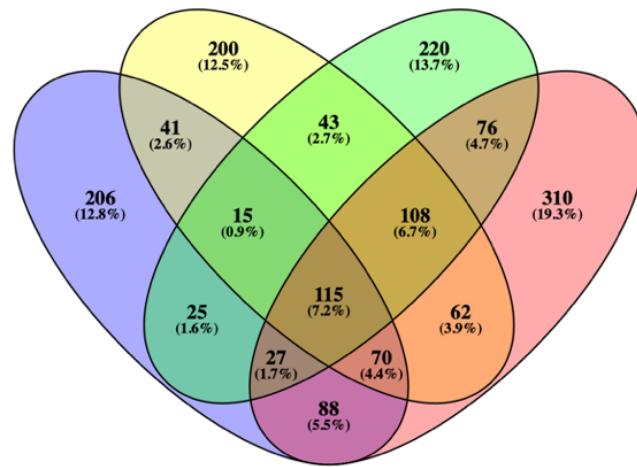
Supplementary figure 1A. Venn diagram of shared OTU in epimural microbiota in the rumen of control cows.



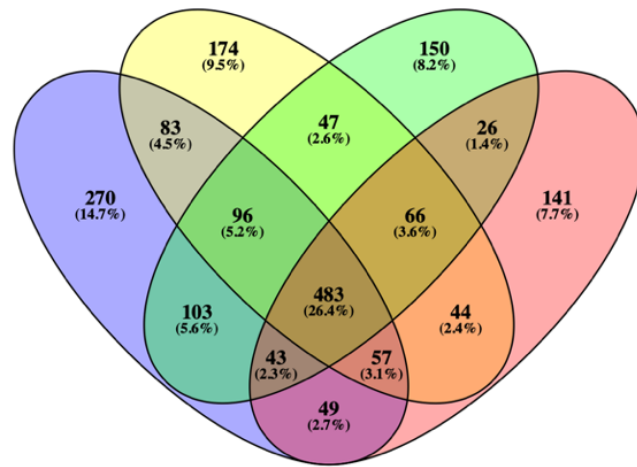
Supplementary figure 1B. Venn diagram of shared OTU in epimural microbiota in the duodenum of control cows.



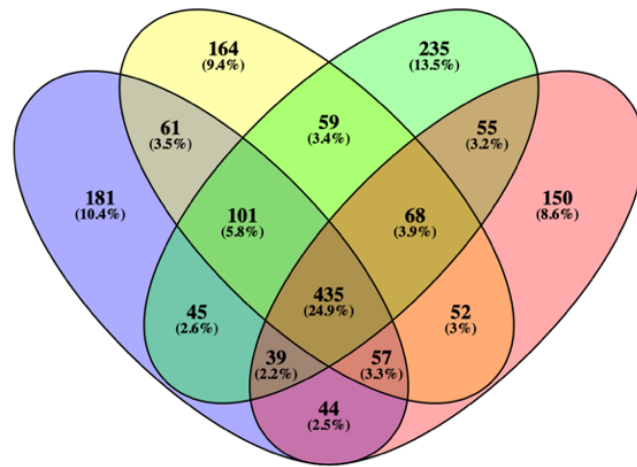
Supplementary figure 1C. Venn diagram of shared OTU in epimural microbiota in the jejunum of control cows.



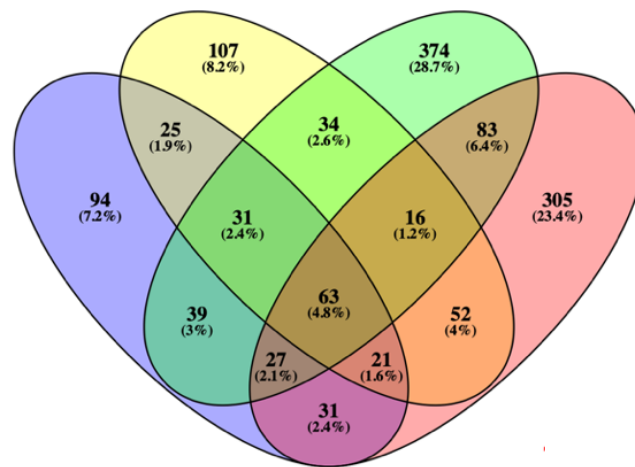
Supplementary figure 1D. Venn diagram of shared OTU in epimural microbiota in the ileum of control cows.



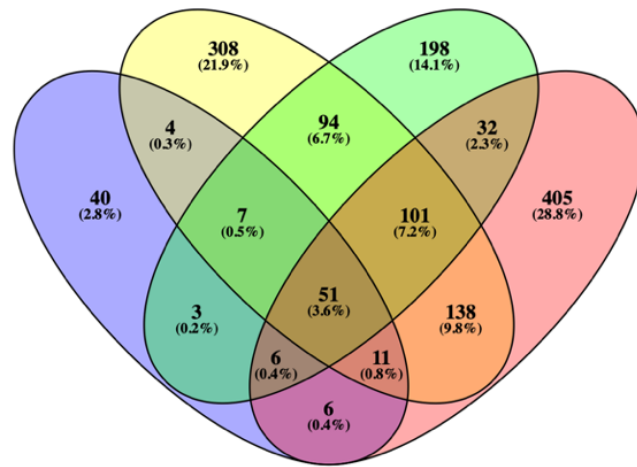
Supplementary figure 1E. Venn diagram of shared OTU in epimural microbiota in the cecum of control cows.



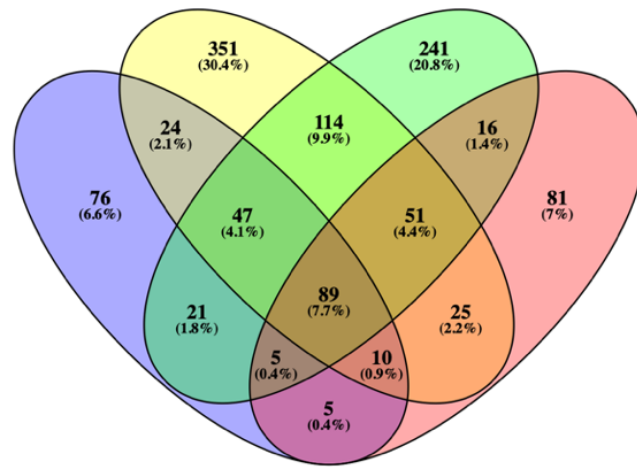
Supplementary figure 1E. Venn diagram of shared OTU in epimural microbiota in the colon of control cows.



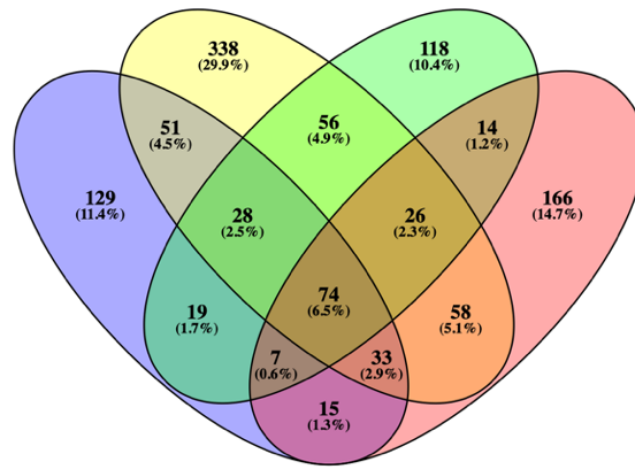
Supplementary figure 1F. Venn diagram of shared OTU in epimural microbiota in the rumen of SARA cows.



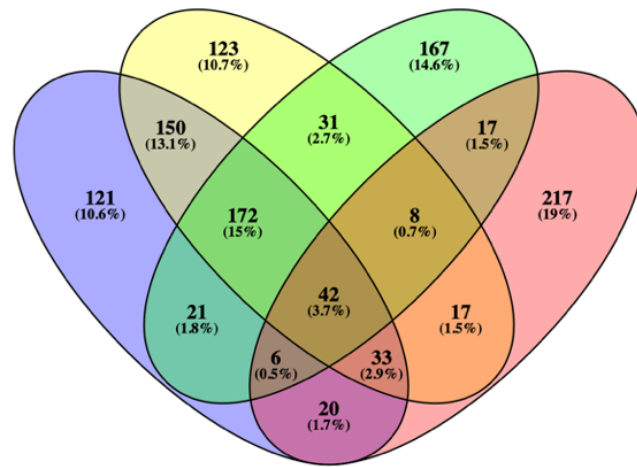
Supplementary figure 1G. Venn diagram of shared OTU in epimural microbiota in the duodenum of SARA cows.



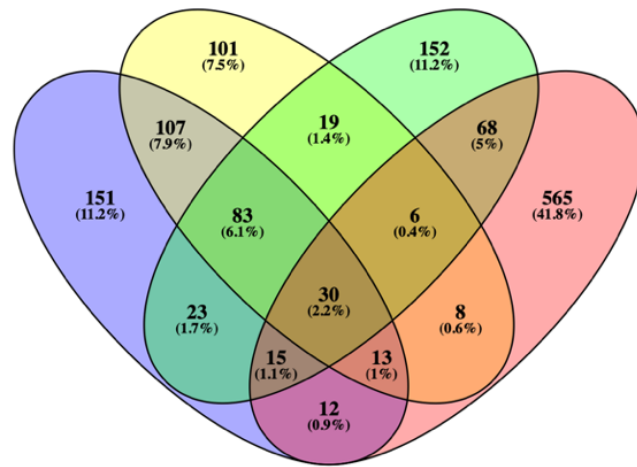
Supplementary figure 1H. Venn diagram of shared OTU in epimural microbiota in the jejunum of SARA cows.



Supplementary figure 1I. Venn diagram of shared OTU in epimural microbiota in the ileum of SARA cows.



Supplementary figure 1J. Venn diagram of shared OTU in epimural microbiota in the cecum of SARA cows.



Supplementary figure 1K. Venn diagram of shared OTU in epimicrobial microbiota in the colon of SARA cows.

