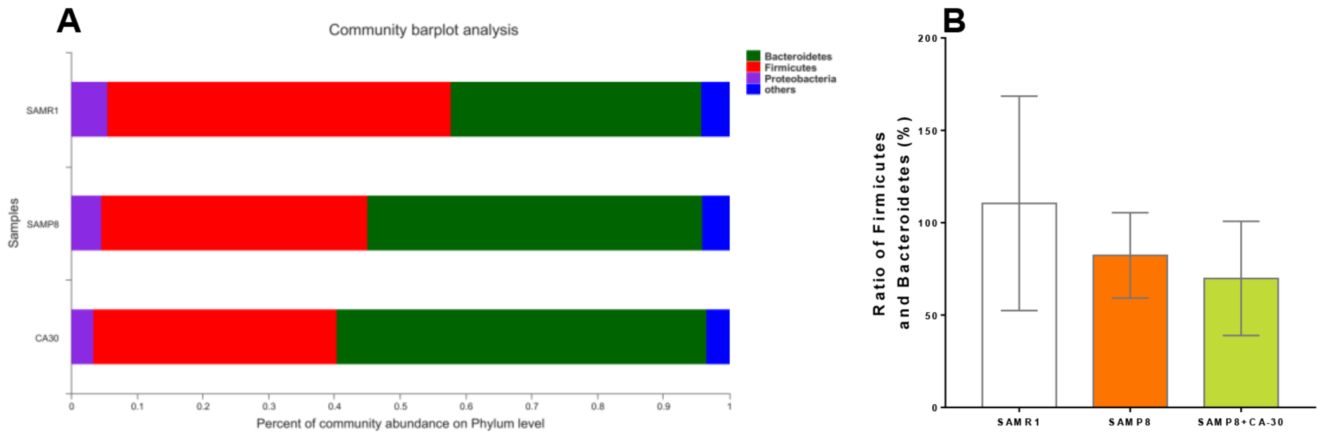
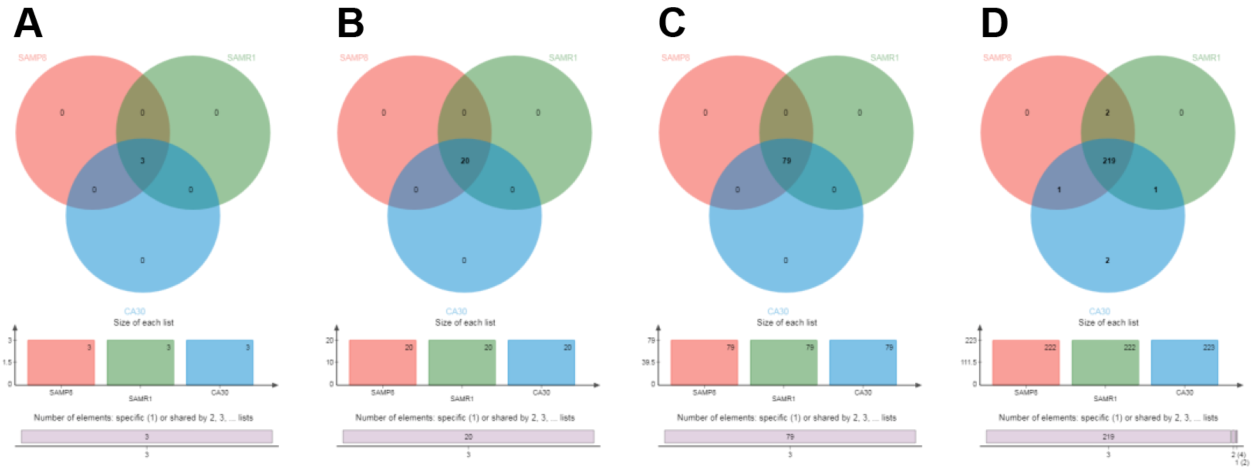
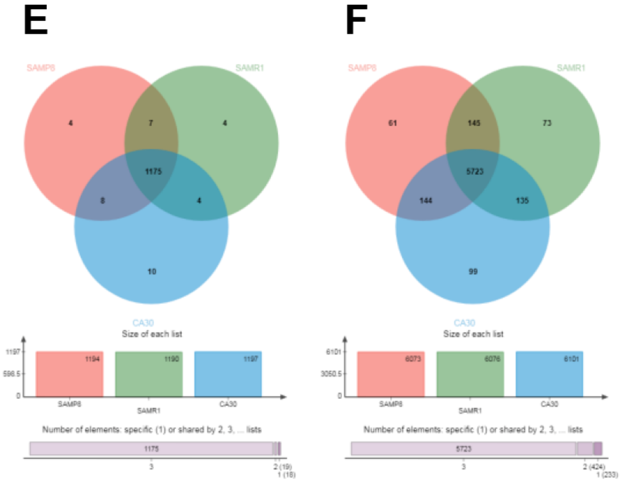
## SUPPLEMENTARY FIGURES



**Supplementary Figure 1.** Dominant bacteria taxa at the Phylum (**A**) level and abundant ratio of Firmicutes and Bacteroidetes (**B**) from all samples.



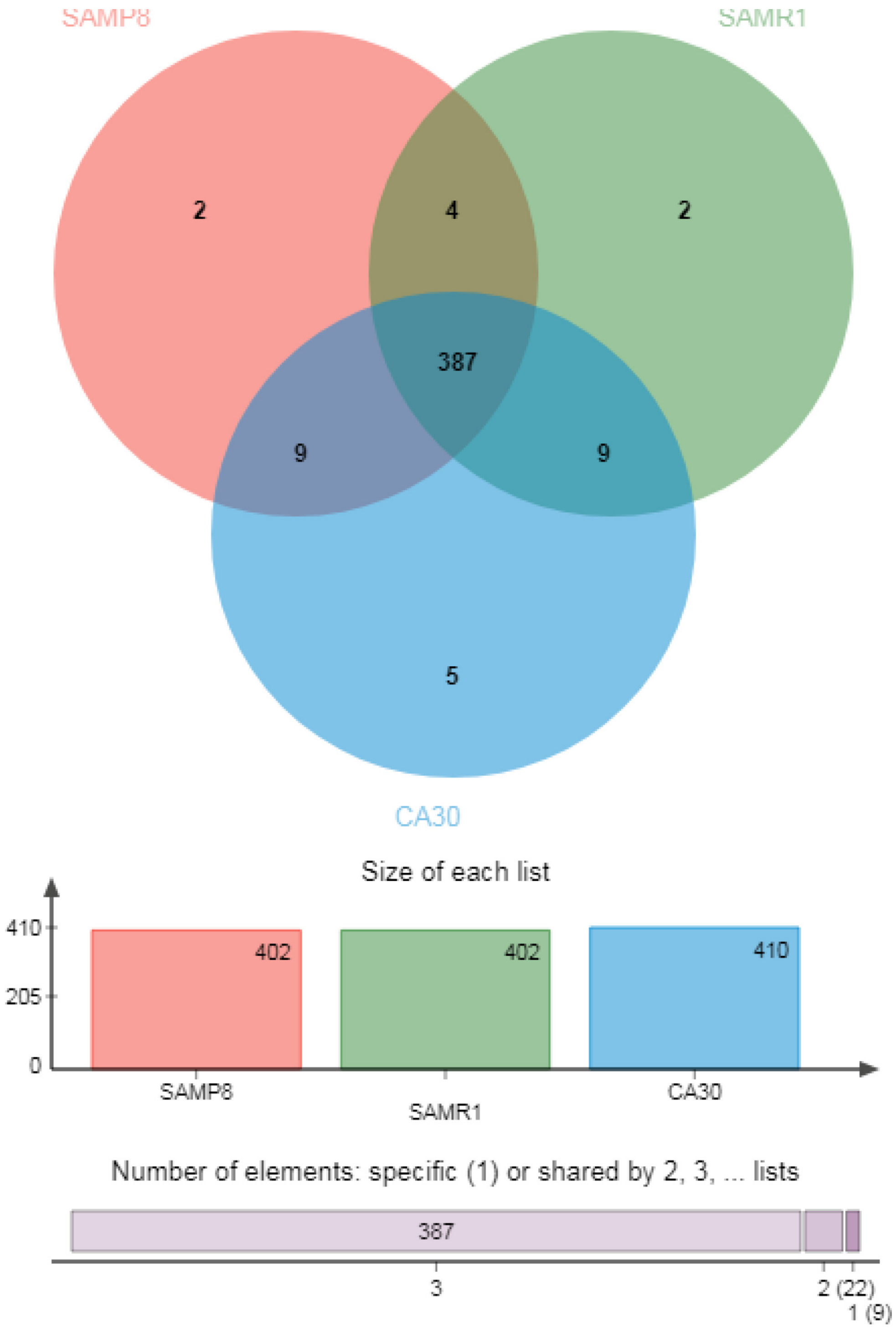


**G**

**Table 1 Summary of gut microbiota composition in all mice**

| Group Label | Number |  |  |  |  |  |
|---|---|---|---|---|---|---|
|  | Phylum | Class | Order | Family | Genus | Species |
| SAMR1 & SAMP8 & CA30 | 3 | 20 | 79 | 219 | 1175 | 5723 |
| SAMR1 & SAMP8 | 3 | 20 | 79 | 221 | 1182 | 5868 |
| SAMR1 & CA30 | 3 | 20 | 79 | 220 | 1179 | 5858 |
| SAMP8 & CA30 | 3 | 20 | 79 | 220 | 1183 | 5867 |
| SAMR1 only | 0 | 0 | 0 | 0 | 4 | 73 |
| SAMP8 only | 0 | 0 | 0 | 0 | 4 | 61 |
| CA30 only | 0 | 0 | 0 | 2 | 10 | 99 |

**Supplementary Figure 2.** Venn diagram of bacteria taxa at the Phylum (**A**), Class (**B**), Order (**C**), Family (**D**), Genus (**E**) and Species (**F**) level from all samples, and the summary of gut microbiota composition in all mice.



**Supplementary Figure 3. Venn diagram of microbial carbohydrate-active enzymes in all mice.** A total of 402, 402, and 410 non-redundant microbial carbohydrate-active enzymes were assigned for metaproteomes of SAMR1, SAMP8, and CA-30 group, respectively.