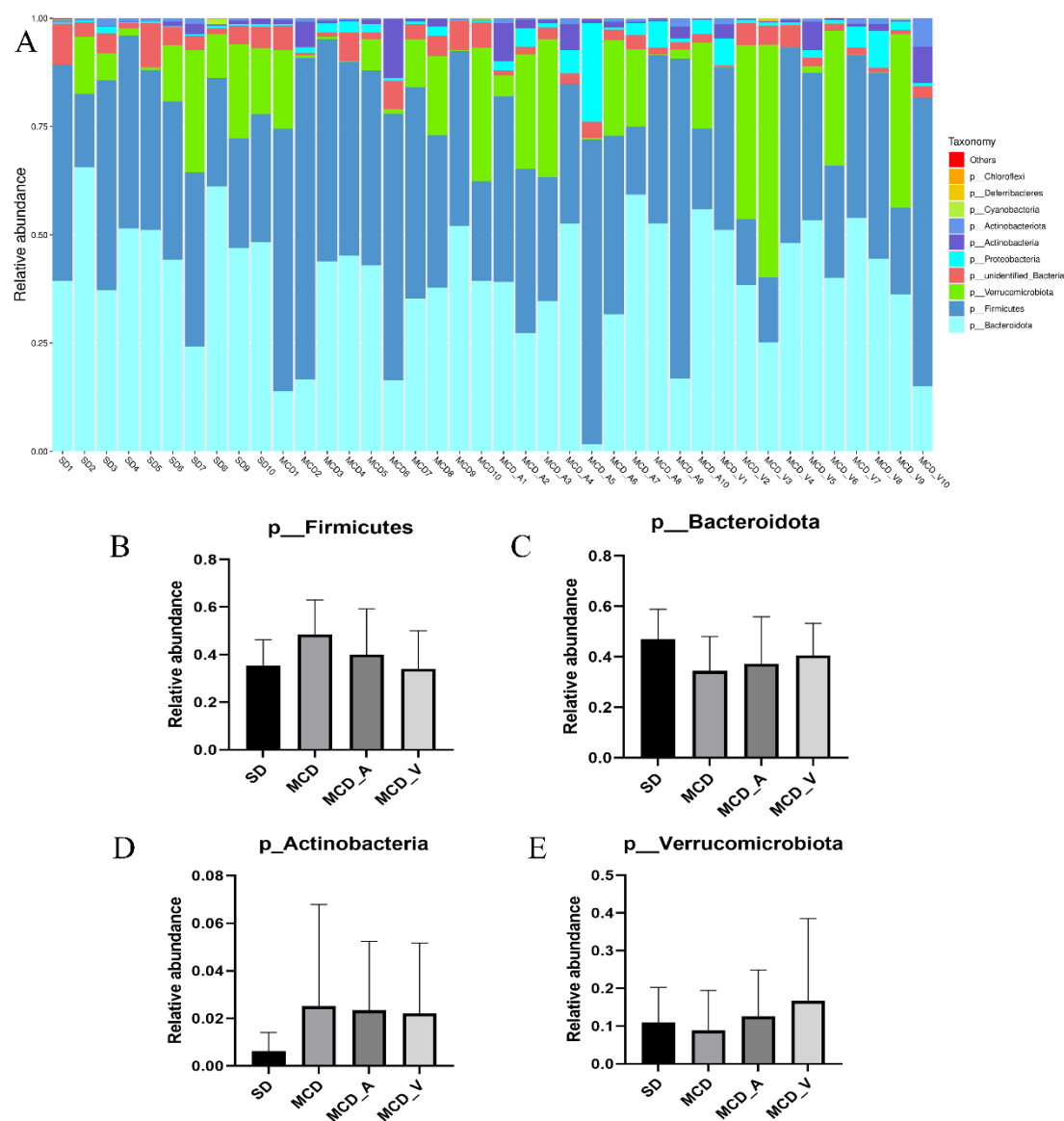
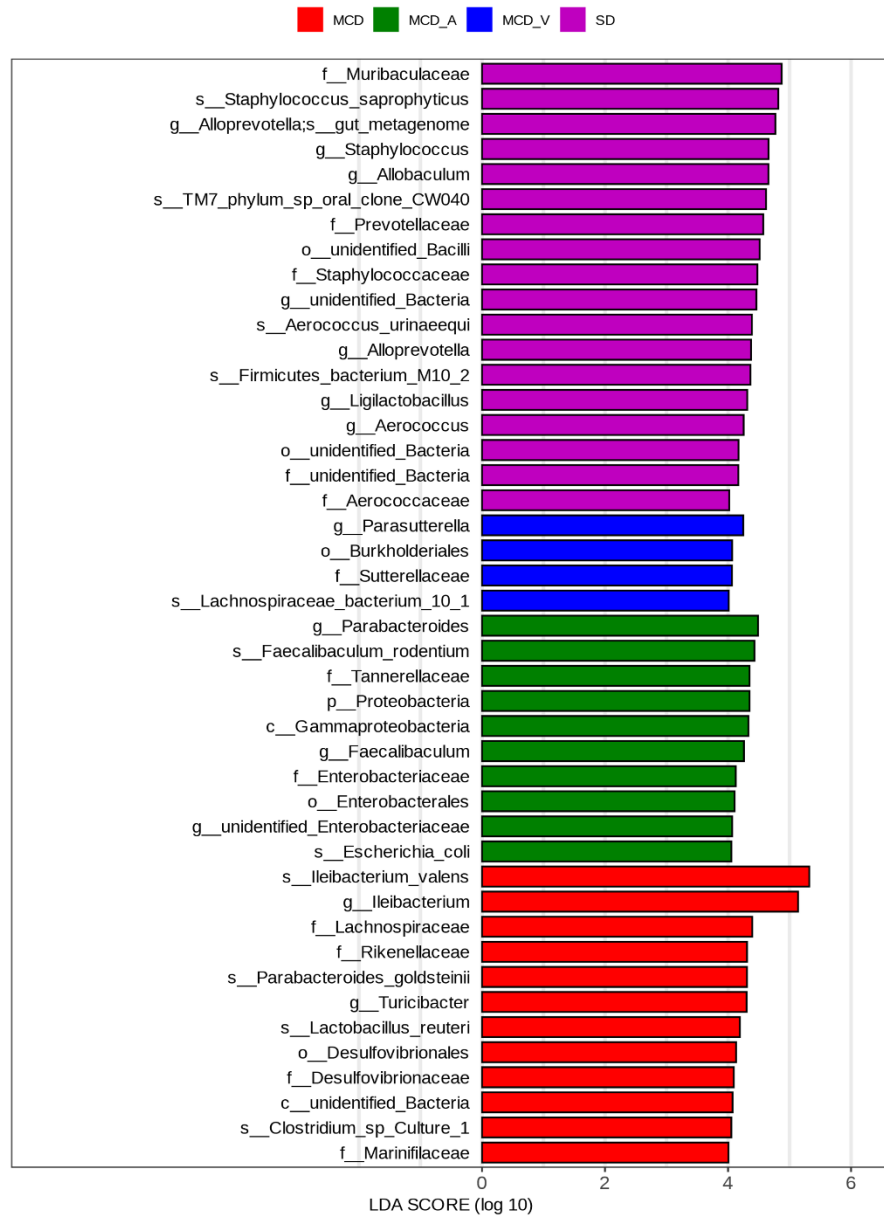


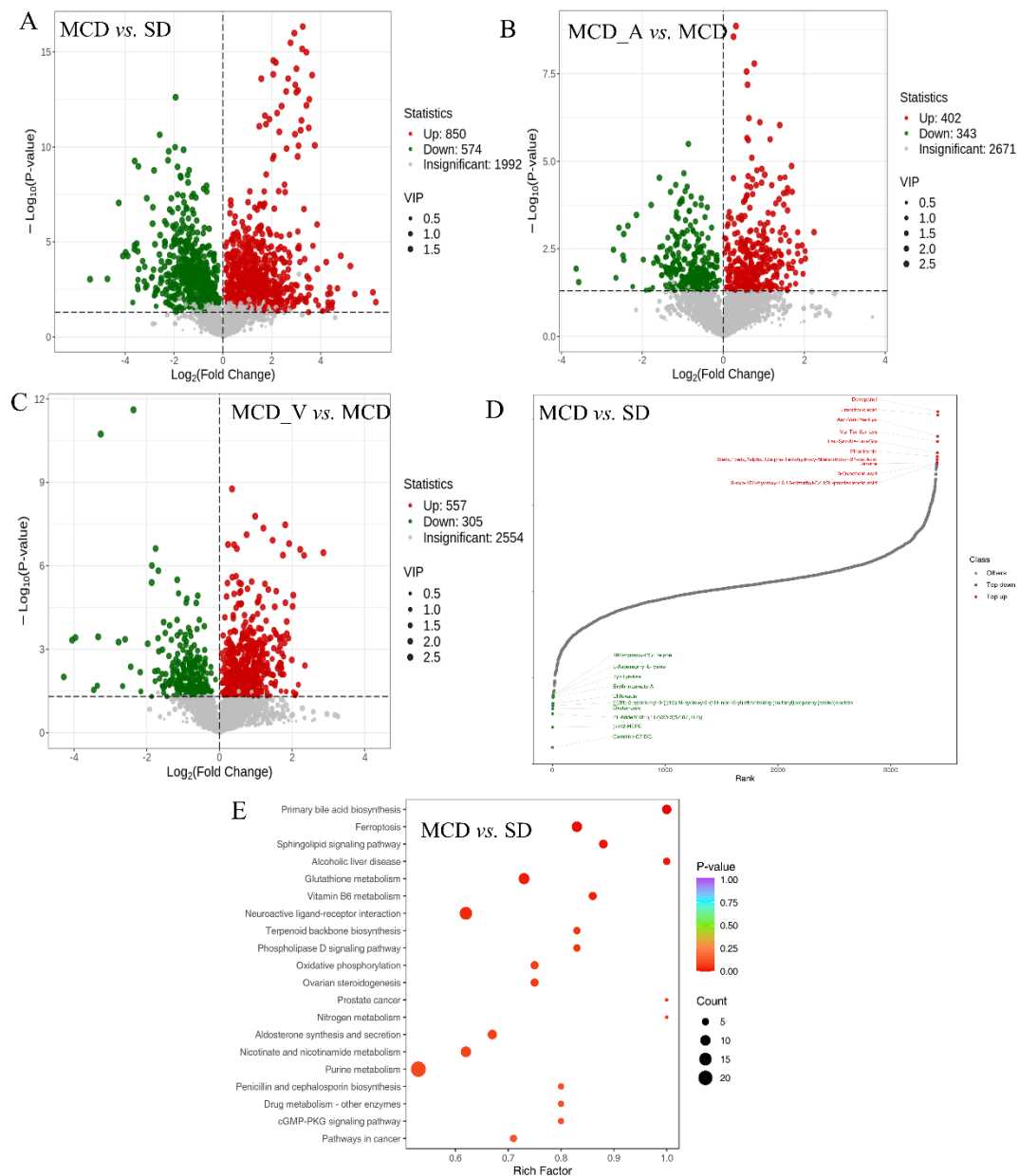
Supplemental Figure S1. The expression of TNF- α and IL-8 in livers or gut of mice. The above values are expressed as mean \pm SD, $n = 10$; ns, no significant difference; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.01$; **** $p < 0.001$.



Supplemental Figure S2. Relative abundances of dominant bacterial at phylum level. (A). Individual relative abundances of dominant bacterial phylum level; (B)-(E): Relative abundance of Firmicutes, Bacteroidetes, Actinobacteria, and Verrucomicrobiota.



Supplemental Figure S3. LEfSe analysis: Histogram showing the LDA scores of genera differentially abundant among the four groups.



Supplemental Figure S4. Metabolic characteristics in four groups. (A)-(C): Volcano plots showing the differential metabolite levels corresponding to the comparison groups, including MCD versus SD, MCD_A versus MCD, and MCD_V versus MCD. (D). Dynamic distribution of metabolite content differences (MCD versus SD); (E). Metabolic analysis based on the KEGG database and enriched pathways were displayed by bubble plots (MCD versus SD).

