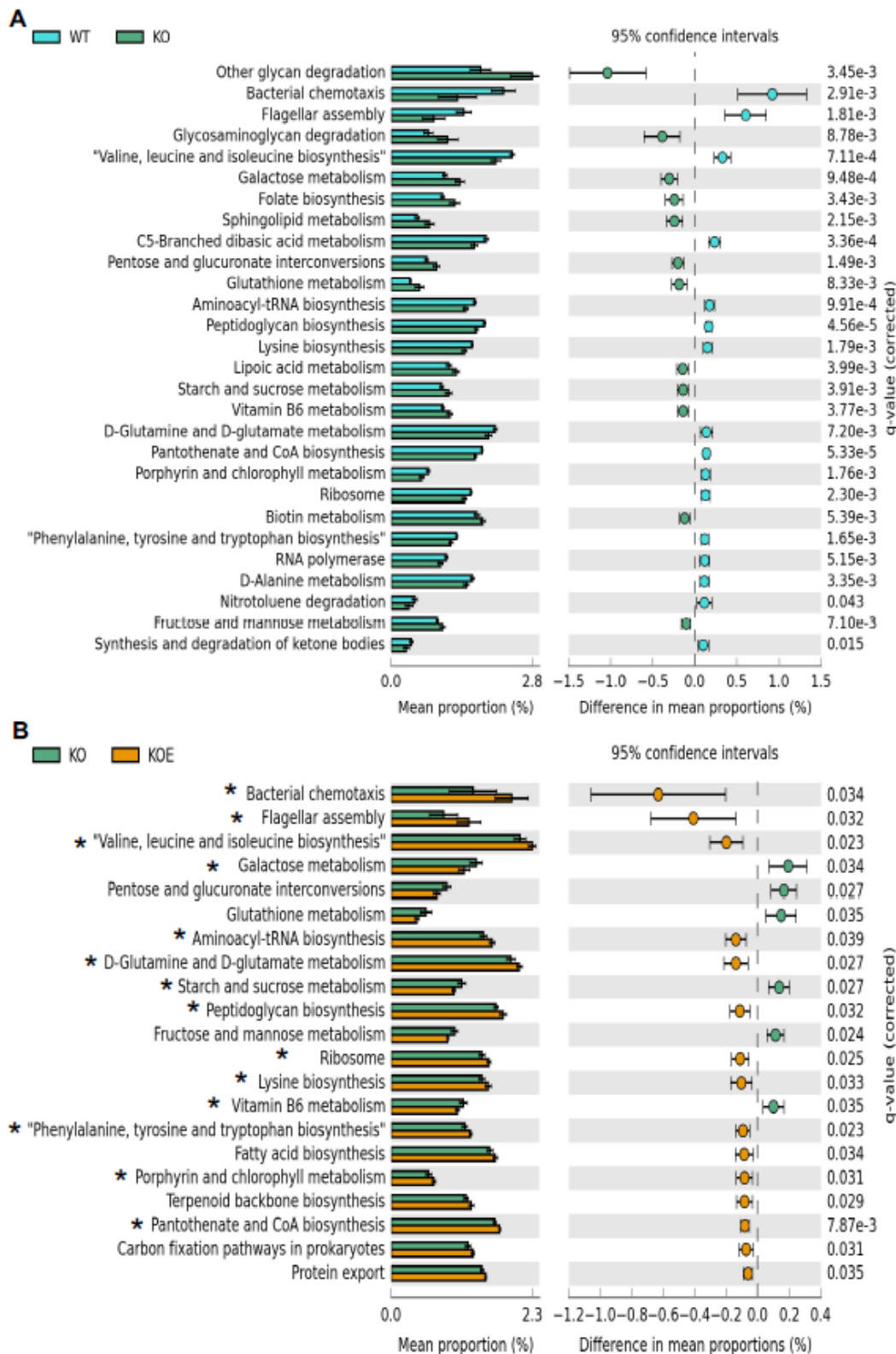


Supplementary Material



Supplementary Figure 1. Prediction of bacterial genes functions to make inferences from KEGG annotated databases using PICRUST analysis (WT: n = 8, KO and KOE: n = 7, respectively). (A) Collectively, 28 KEGG pathways were statistically altered in the WT group compared to that in KO group. (B) In total, 14 KEGG pathways (marked with *) were recovered by ESM treatment. The mean proportion of each pathway is displayed in the bar graphs on the left.