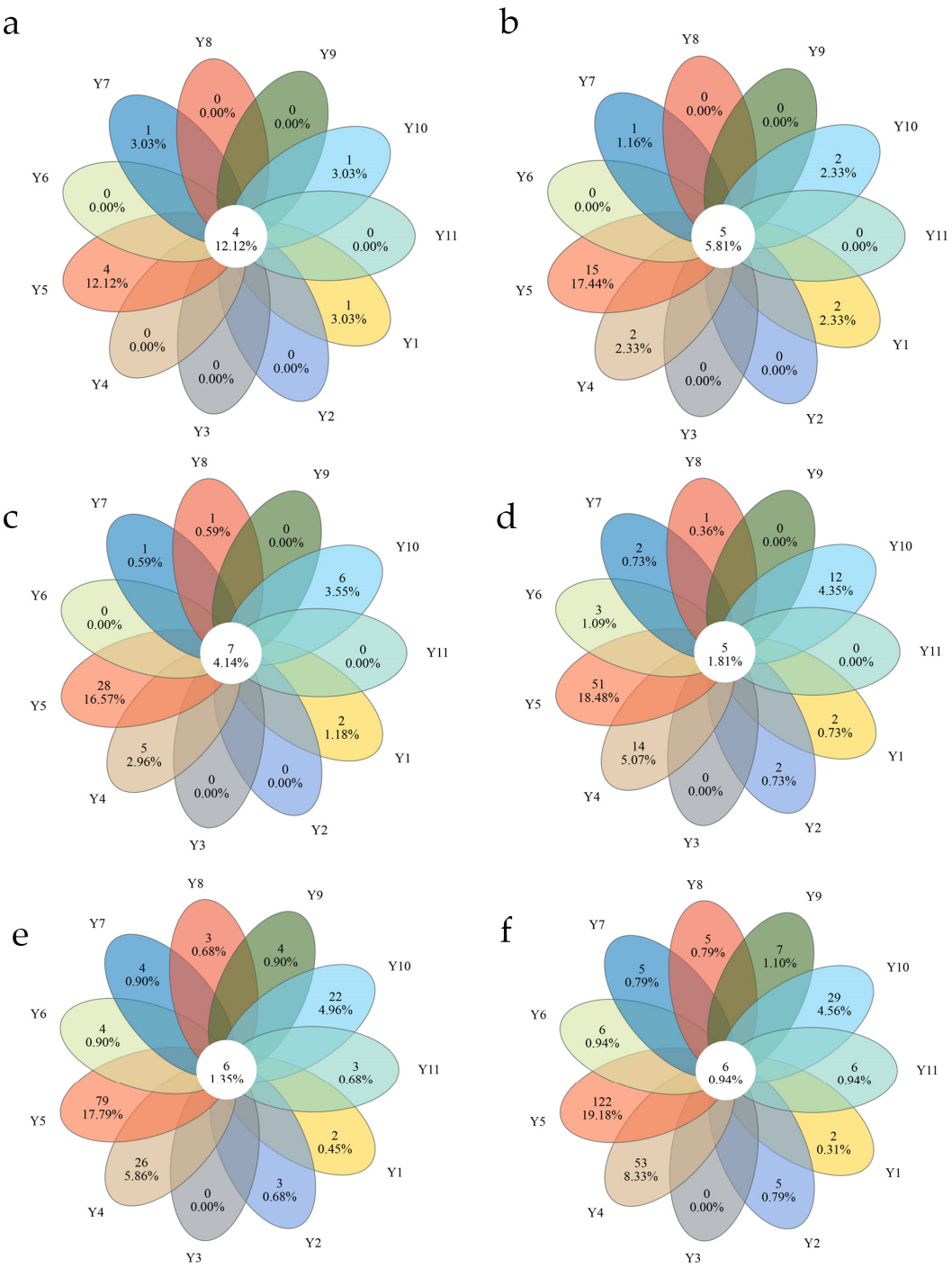


Figure S1. Venn analysis: Venn diagram of oriental storks at phylum level (a), class level (b), order level (c), family level (d), genus level (e), and species level (f).

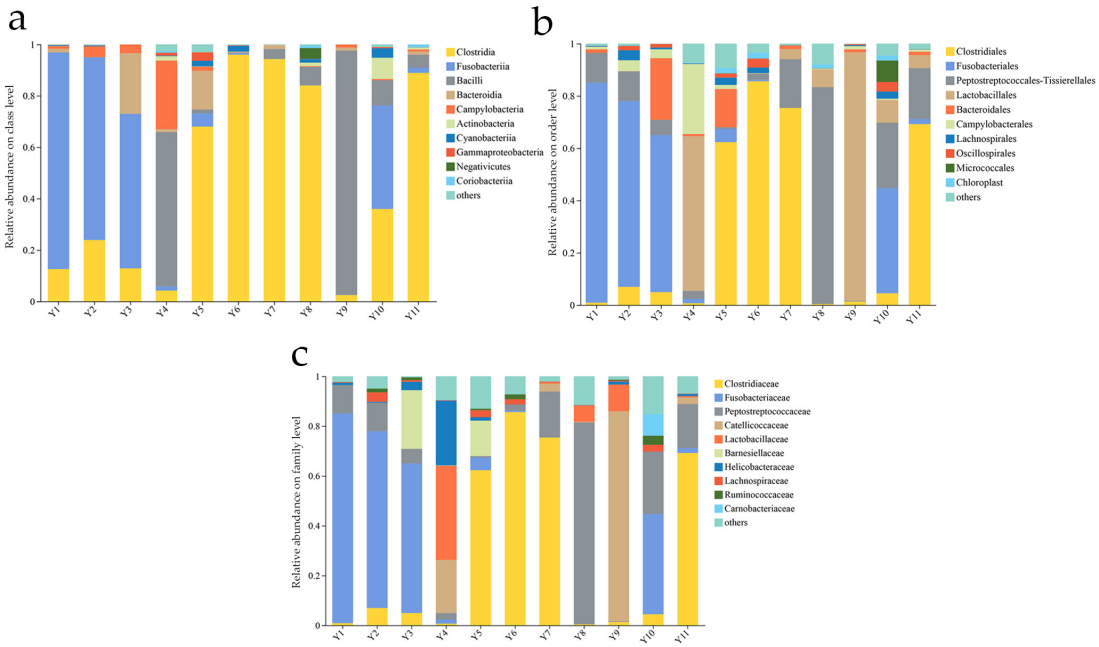


Figure S2. The relative abundance of top 10 classes(a), orders(b), and families(c).

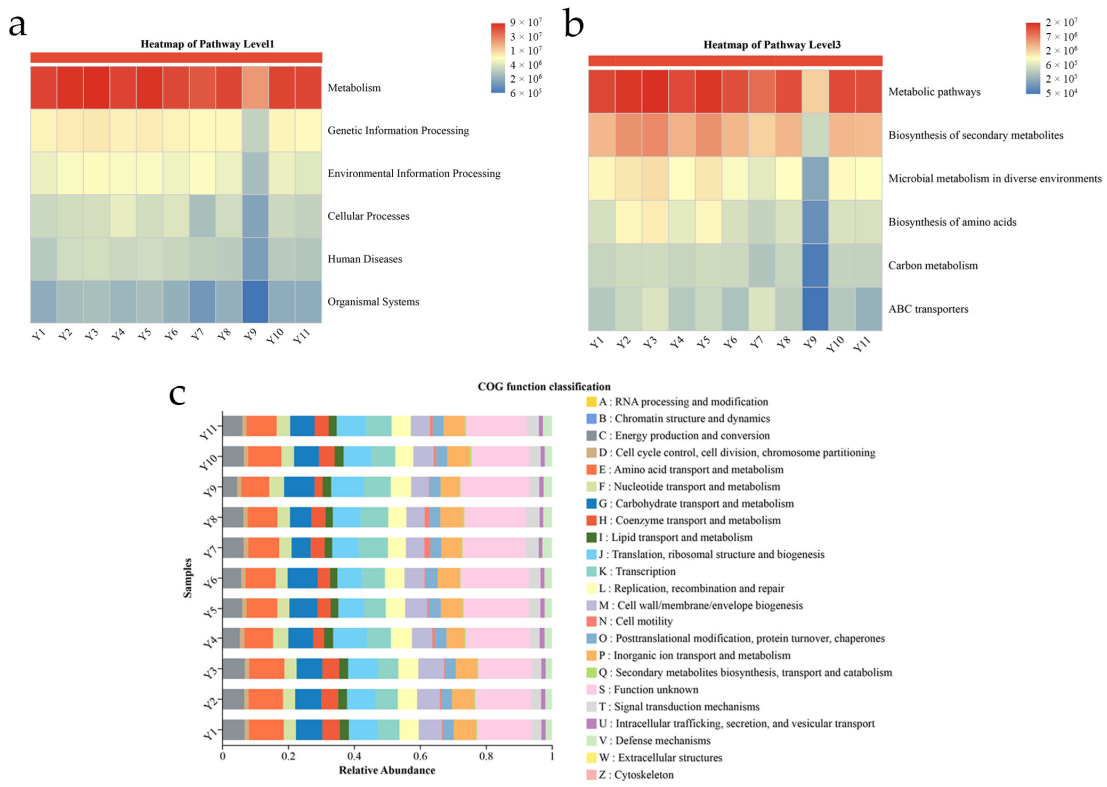


Figure S3. Function prediction: (a) KEGG pathway distribution at Level 1 categories, (b) KEGG pathway distribution at Level 3 categories, and (c) COG function classification.

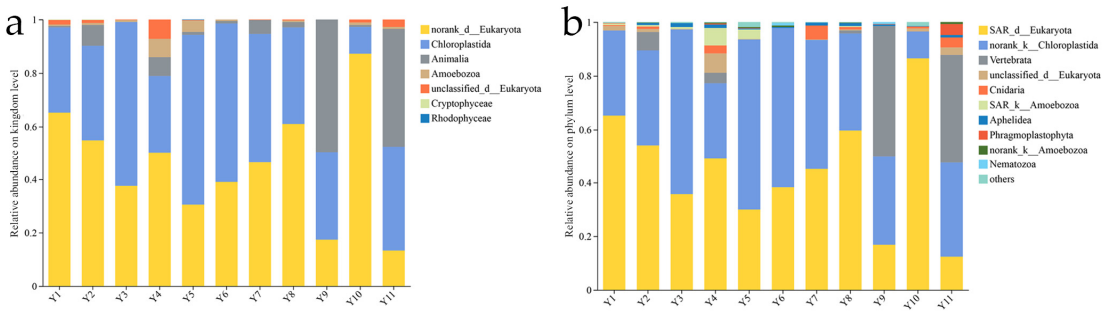


Figure S4. High-throughput sequencing technology of the 18S rRNA at kingdom-level (a) and phylum-level(b).

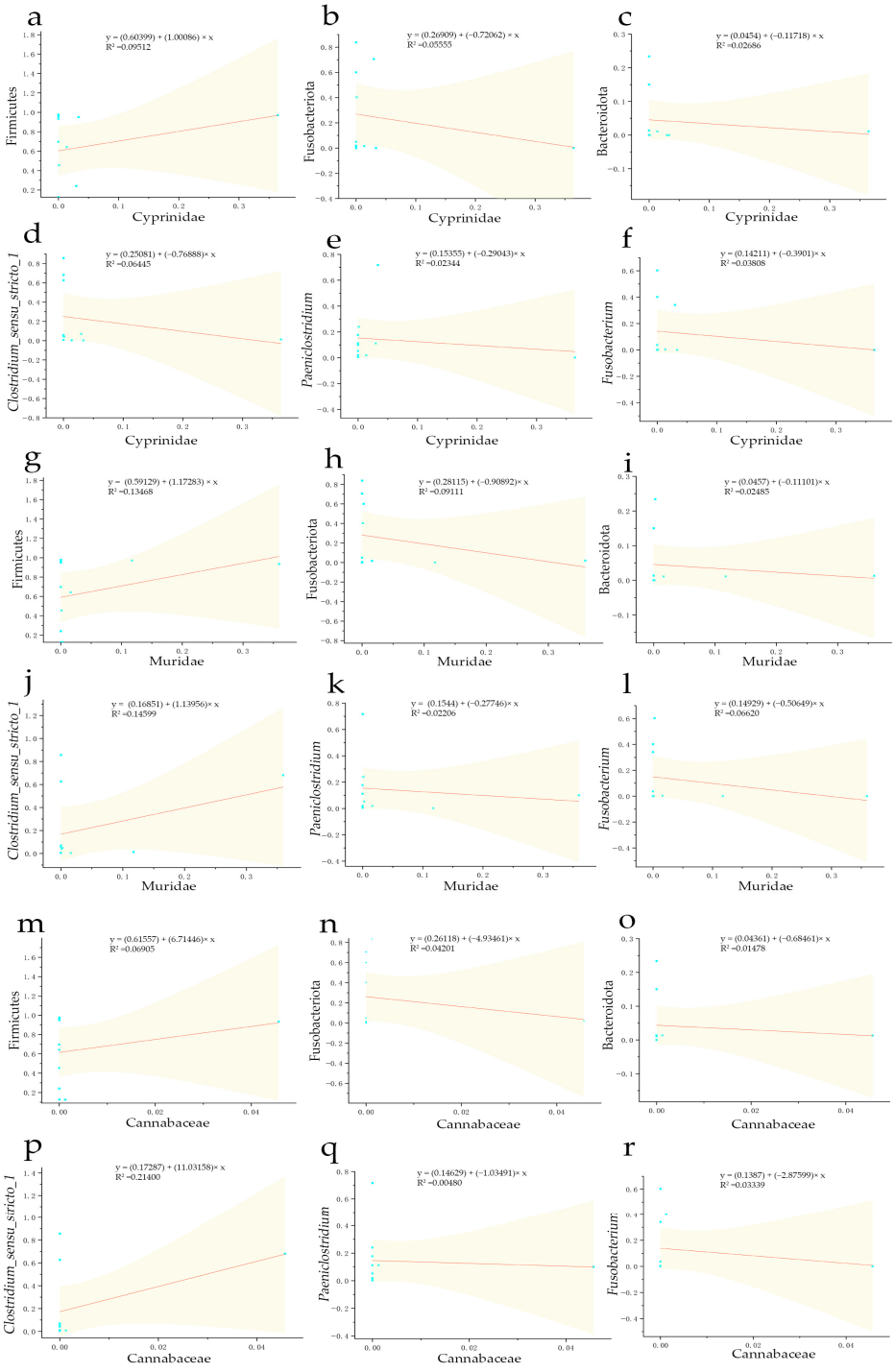


Figure S5. Fitted curves showing potential correlations between the top three food items (family level) and the top three bacterial phyla and genera.

Cyprinidae with Firmicutes (a), Fusobacteriota (b), Bacteroidota (c), *Clostridium_sensu_stricto_1* (d), *Paeniclostridium* (e), and *Fusobacterium* (f); Muridae with Firmicutes (g), Fusobacteriota (h), Bacteroidota (i), *Clostridium_sensu_stricto_1* (j), *Paeniclostridium* (k), and *Fusobacterium* (l); Cannabaceae with Firmicutes (m), Fusobacteriota (n), Bacteroidota (o), *Clostridium_sensu_stricto_1* (p), *Paeniclostridium* (q), and *Fusobacterium* (r).