

Supplementary Material

Polysaccharide metabolic pattern of *Cytophagales* and *Flavobacteriales*: a comprehensive genomics approach

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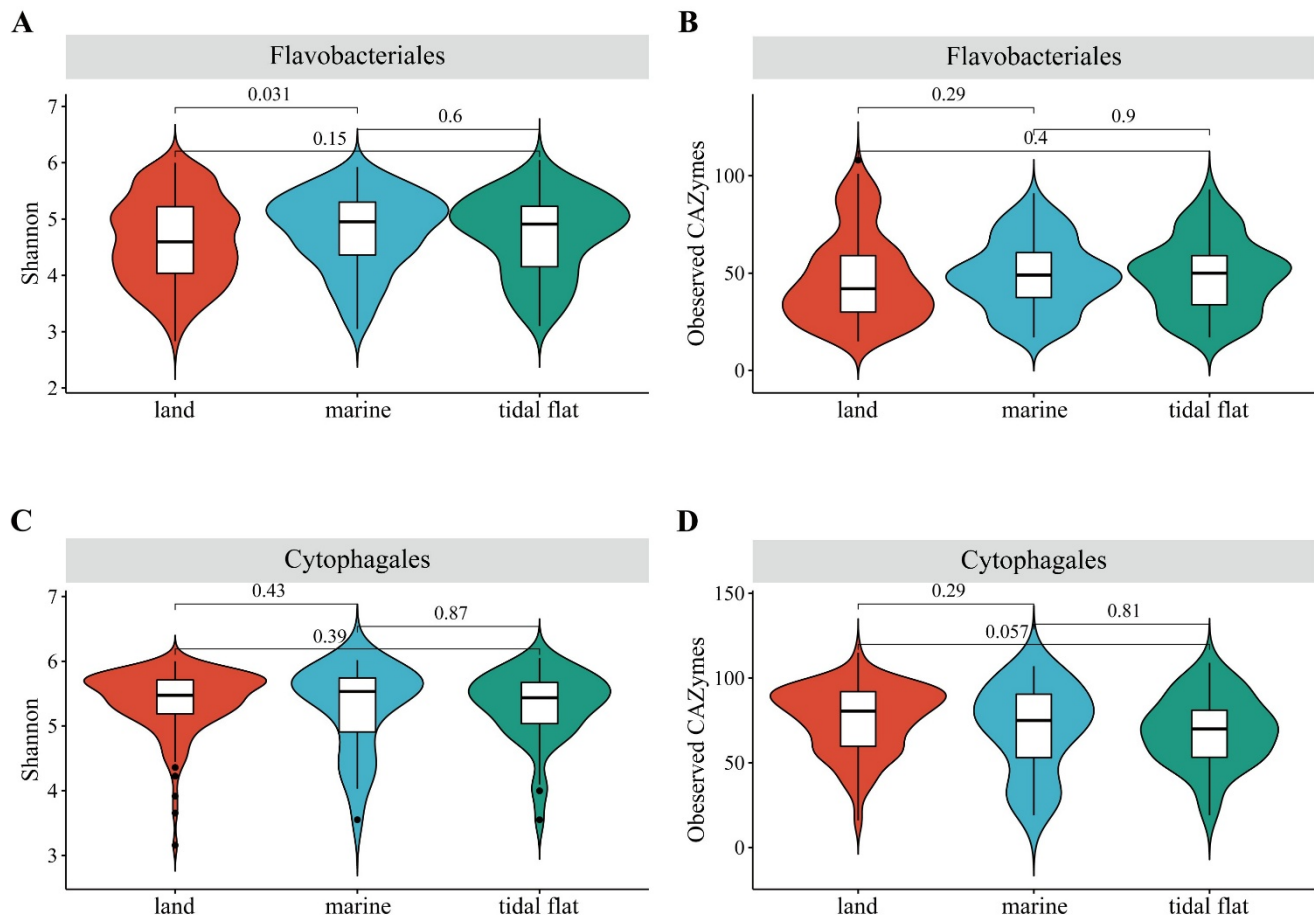
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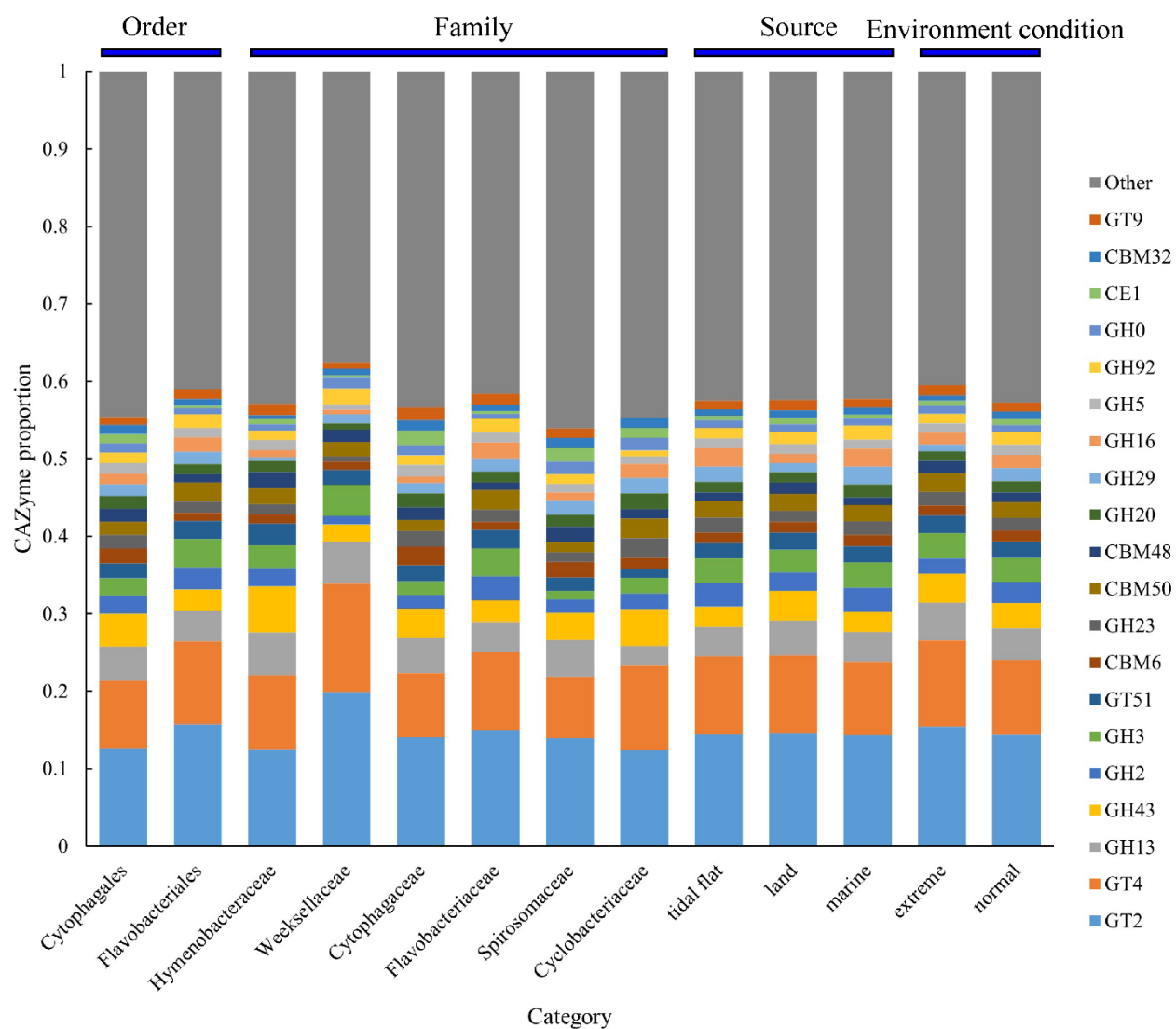
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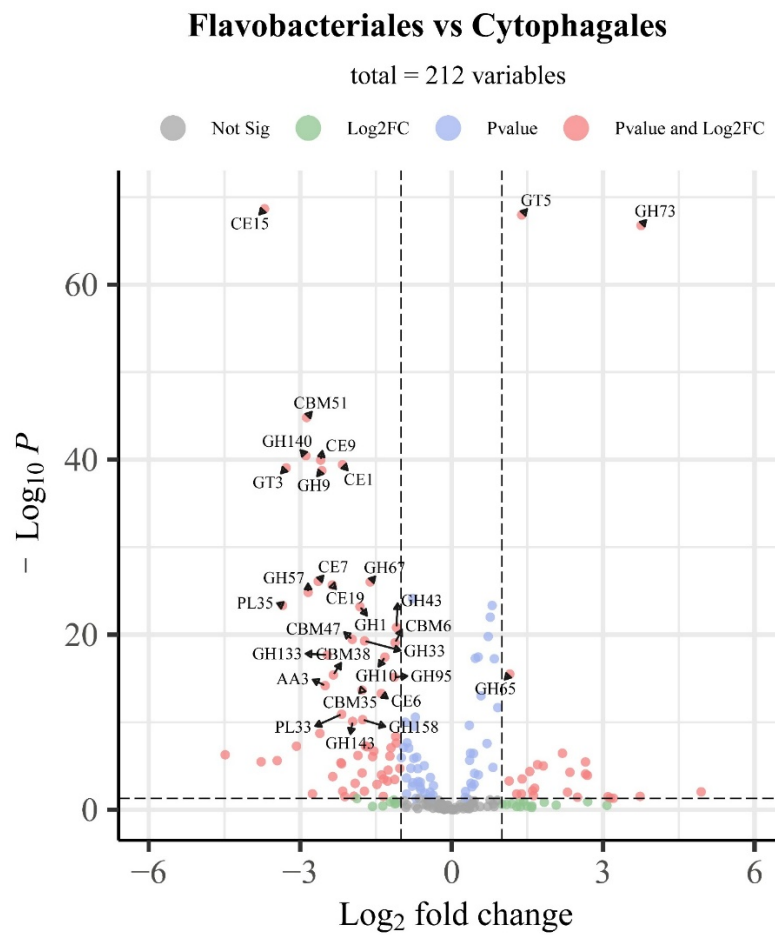
1 Supplementary Figures



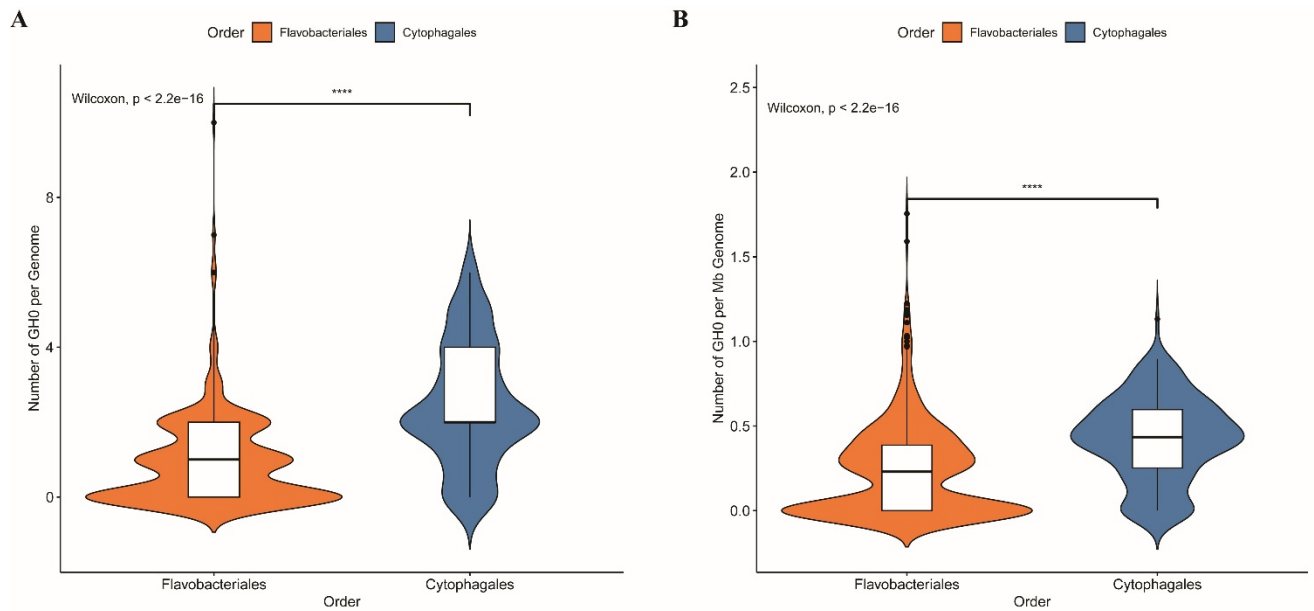
Supplementary Figure 1. Alpha diversity characterized by Shannon index and observed CAZymes index in different environments for each order. The violin plot showed the distribution of Shannon index of CAZymes among species from *Flavobacteriales* (A), *Cytophagales* (C), observed CAZymes index of CAZymes among species from *Flavobacteriales* (B) and *Cytophagales* (D). Two-sided T-Test was used to analyze the significance of difference between different groups. Inner box plots showed median and quartiles.



Supplementary Figure 2. Relative abundance of the top 20 CAZyme families across different orders, families, sources, and environment conditions.

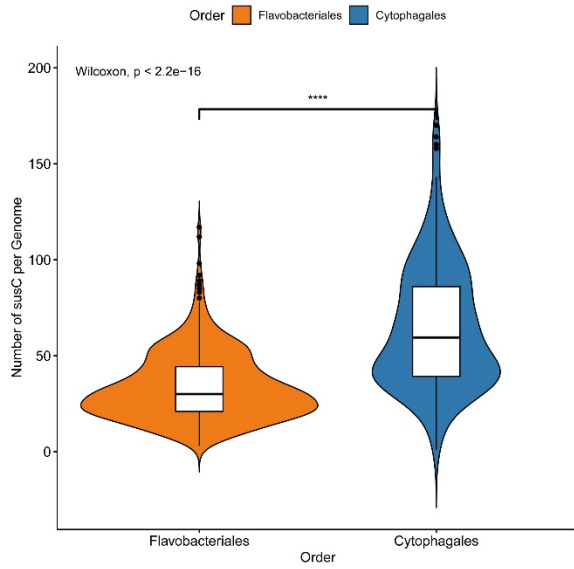


Supplementary Figure 3. Differences in CAZyme family composition between *Flavobacteriales* and *Cytophagales*.

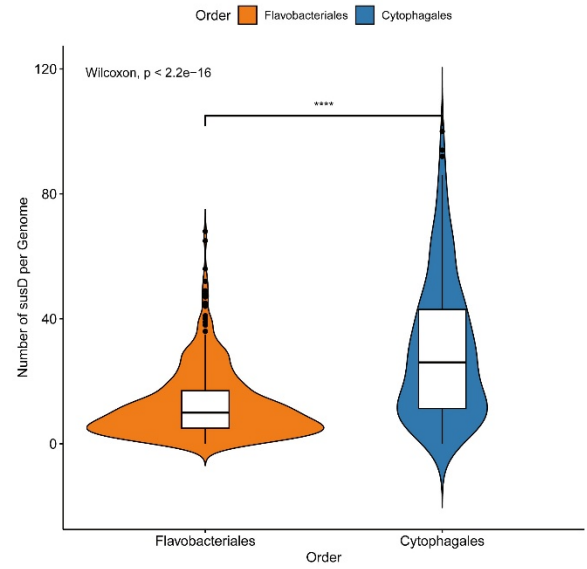


Supplementary Figure 4. Number of GH0 per genome (A) and per Mb genome (B) in *Flavobacteriales* and *Cytophagales*.

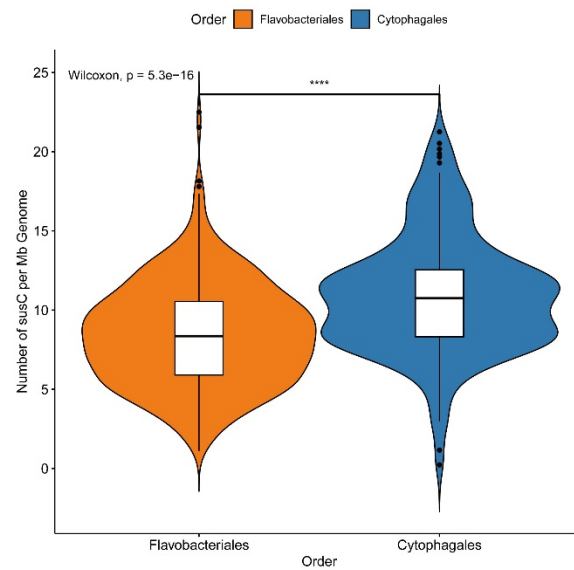
A



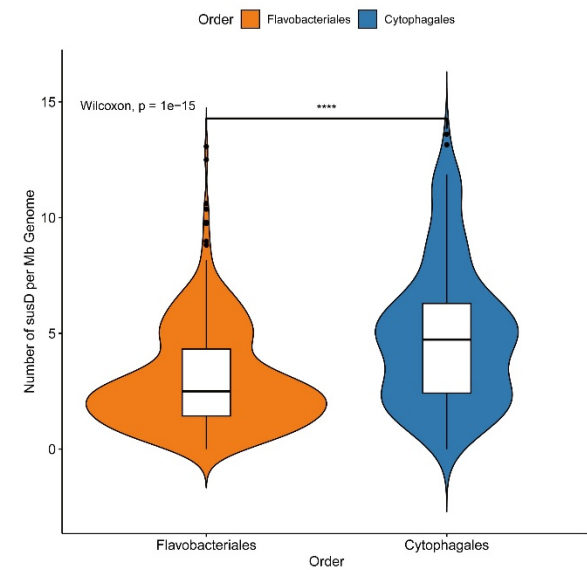
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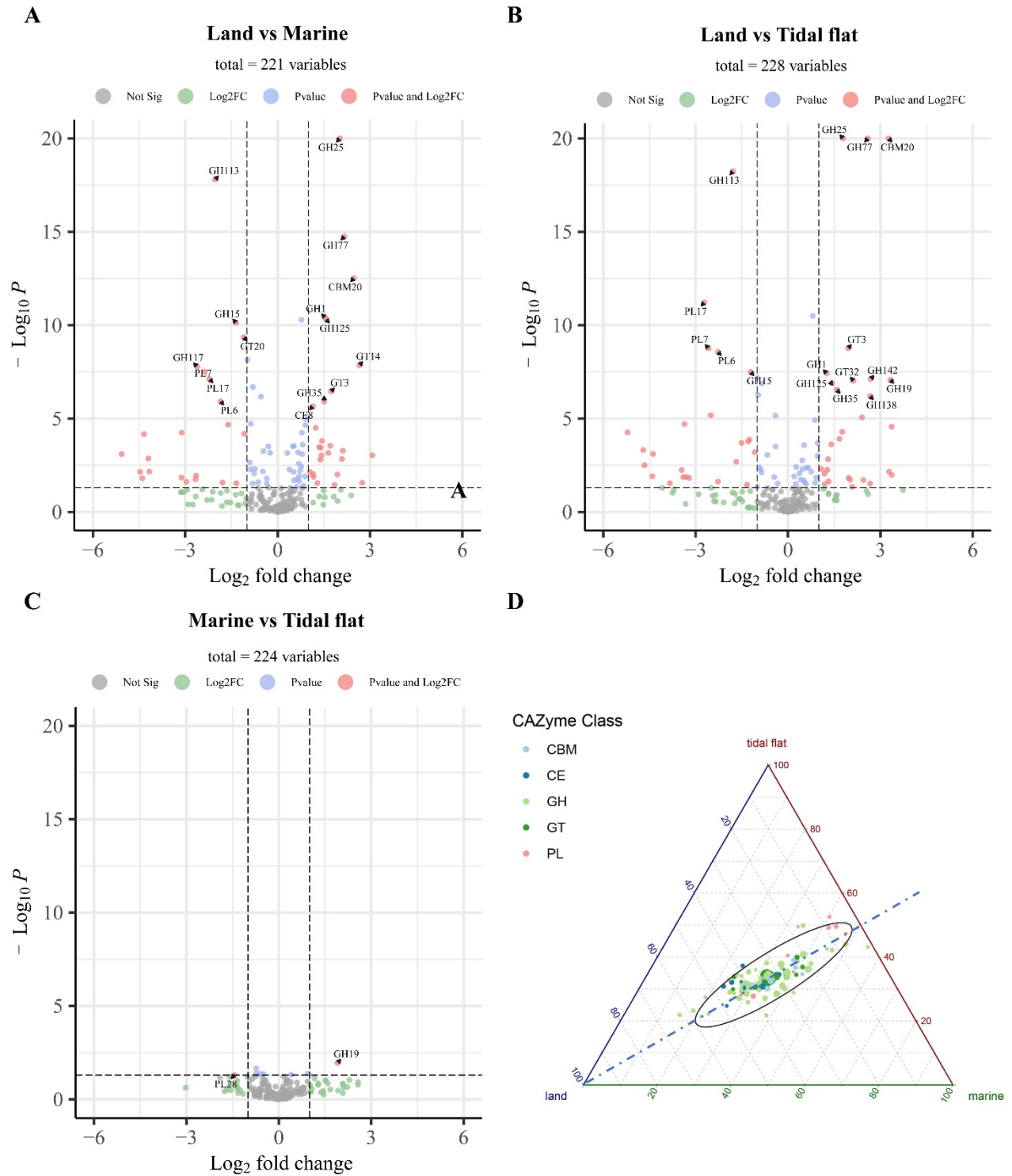
C



D



Supplementary Figure 5. Abundance differences of susC (A, C) and susD (B, D) between *Flavobacteriales* and *Cytophagales*.



Supplementary Figure 6. Differences in CAZyme family (A-C) and class (D) composition across different sources.