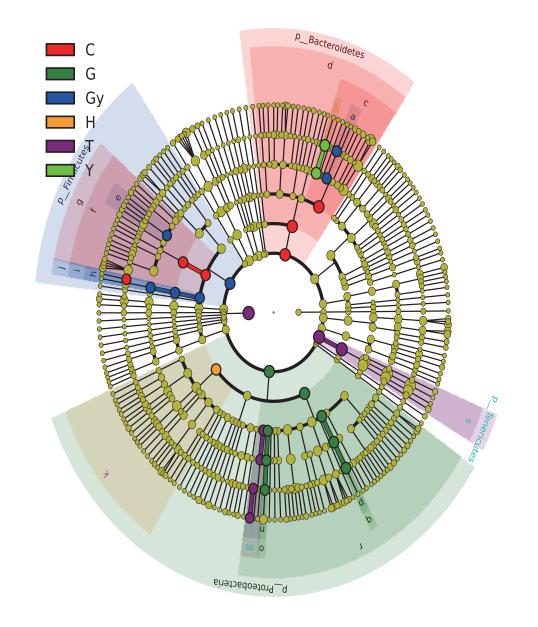
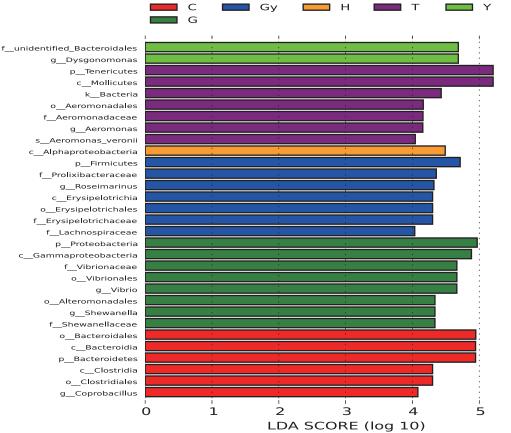
## Cladogram





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g\_\_Dysgonomonas p\_Tenericutes Aeromonadales f\_\_Aeromonadaceae g\_\_Aeromonas Aeromonas\_veronii s c\_\_Alphaproteobacteria p\_\_Firmicutes f\_\_Prolixibacteraceae g\_\_Roseimarinus c\_\_Erysipelotrichia o\_\_Erysipelotrichales f\_Erysipelotrichaceae f\_Lachnospiraceae p\_Proteobacteria \_Gammaproteobacteria C\_ f\_\_Vibrionaceae o\_\_Vibrionales o\_\_Alteromonadales g\_\_Shewanella f\_\_Shewanellaceae o\_\_Bacteroidales c\_\_Bacteroidia p\_\_Bacteroidetes o Clostridiales

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**Supplementary Fig S6** LefSe analysis. (a) The cladogram diagram shows the gut bacteria community species with significant differences in the six crab populations at phylum to genus level. The different colors represent different lakes and their corresponding bacteria. (B) Species with significant difference among the different crab populations have LDA score greater than the estimated value; the default score is 4.0. The length of the histogram is equivalent to the LDA score.