

Change in dissolved oxygen of water bodies is the major driver of alteration in intestinal bacterial community of the bottom-feeding fish *Cirrhinus mrigala*

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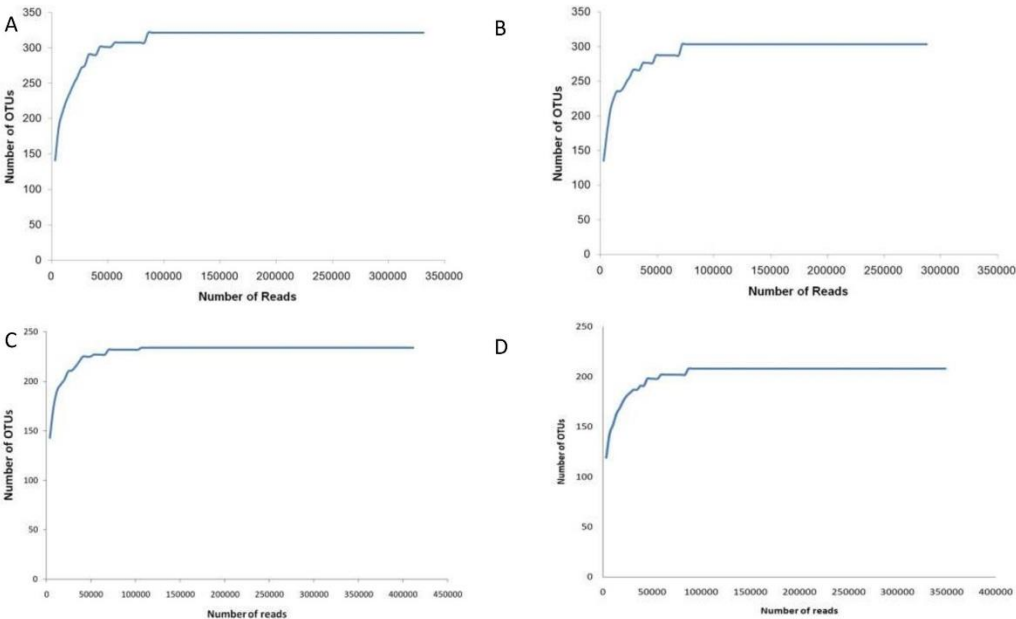
Supplementary data:

Fig. S1 Rarefaction curves showing the proportionality between OTU-level diversity and the number of V3 regions in 16S rRNA gene sequence reads analyzed for (A) MCA, (B)MCP, (C) MTA or (D) MTP samples. For each sample, number of reads used in OTU-clustering is plotted along the X-axis, while number of OTUs is plotted along the Y-axis

Fig. S2 Dendrogram analysis of control and experimental samples of *C. mrigala* at phylum level in MicrobiomeAnalyst using the Bray-Curtis distance method. MCA: Anterior gut of *C. mrigala* under control condition, MCP: Posterior gut of *C. mrigala* under control condition, MTA: Anterior gut of *C. mrigala* under test condition, MTP: Posterior gut of *C. mrigala* under test condition

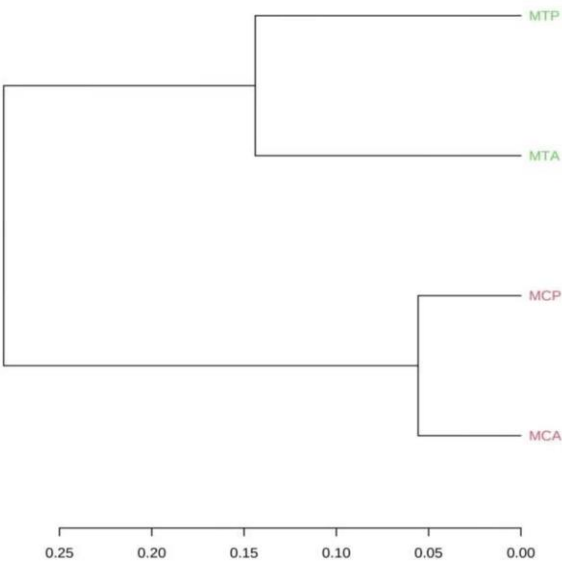
Fig. S3 Stacked bar depicting abundance of diverse bacteria at order level in anterior and posterior gut samples of *C. mrigala* under control and experimental conditions. Here X axis showing the name of bacterial order while number of OTUs is plotted along the Y-axis

Figure S1_ Supplementary data



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Figure S2_ Supplementary data



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Figure S3_ Supplementary data

