

SUPPLEMENTARY MATERIAL

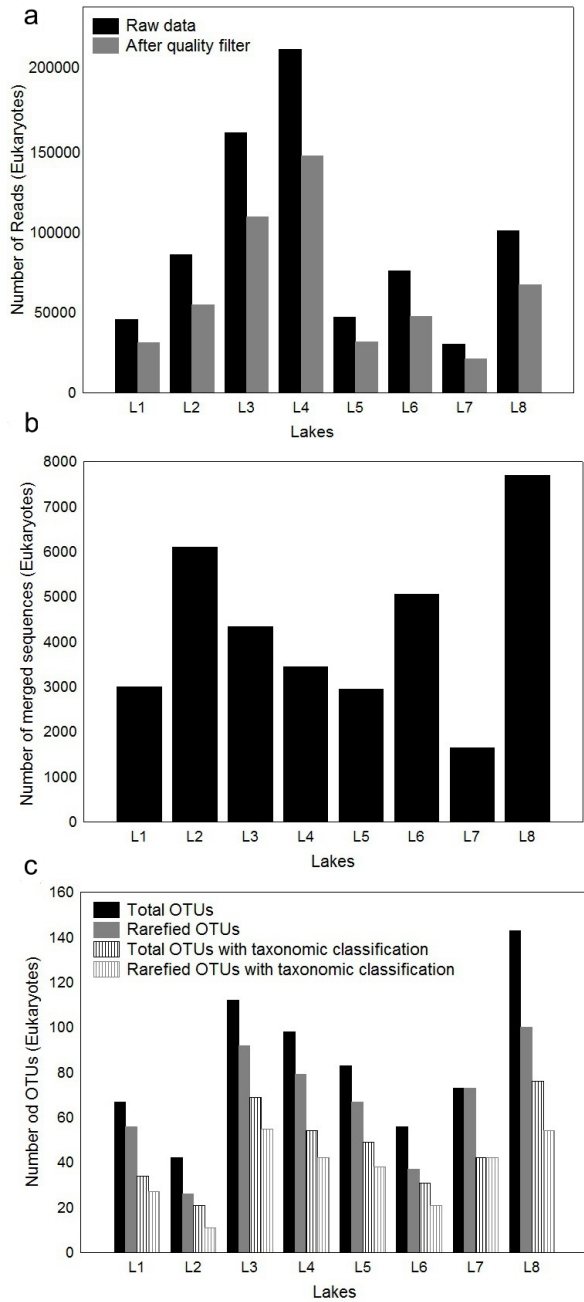


Figure S1. Graphs showing the amount of reads obtained from the sequence of the eukaryotic amplicons of each sampled site before and after quality filter (a), total numbers of merged sequences from each site (b) and the total numbers of OTU and the OTUs classified for each site (c) before and after rarefaction.

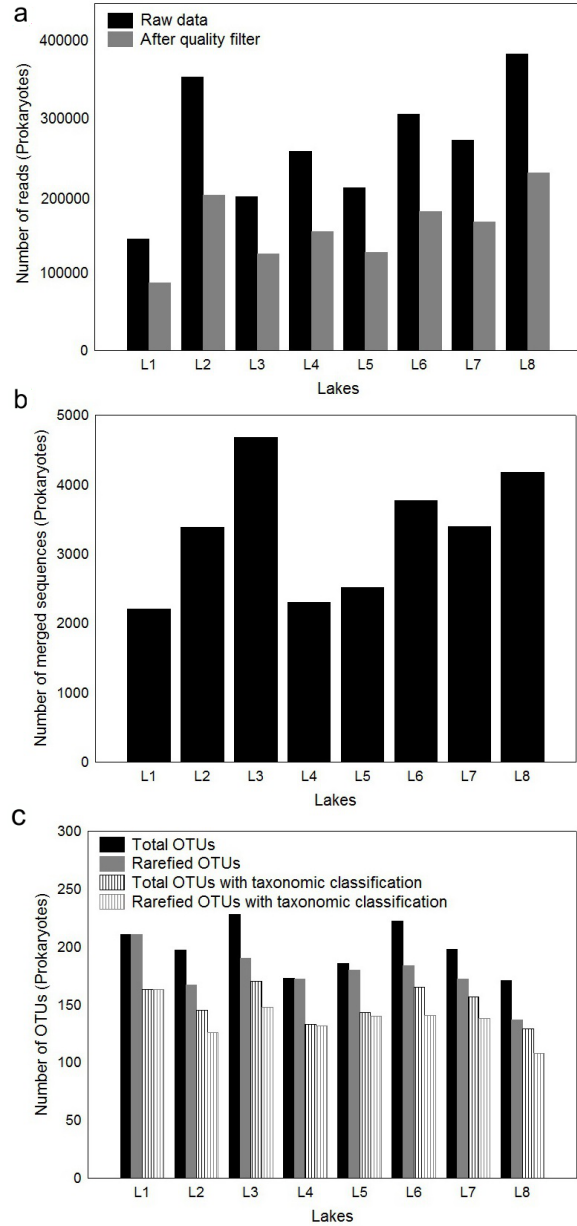


Figure S2. Graphs showing the amount of reads obtained from the sequence of the prokaryotic amplicons of each sampled site before and after quality filter (a), total numbers of merged sequences from each site (b) and the total numbers of OTU and the OTUs classified for each site (c) before and after rarefaction.

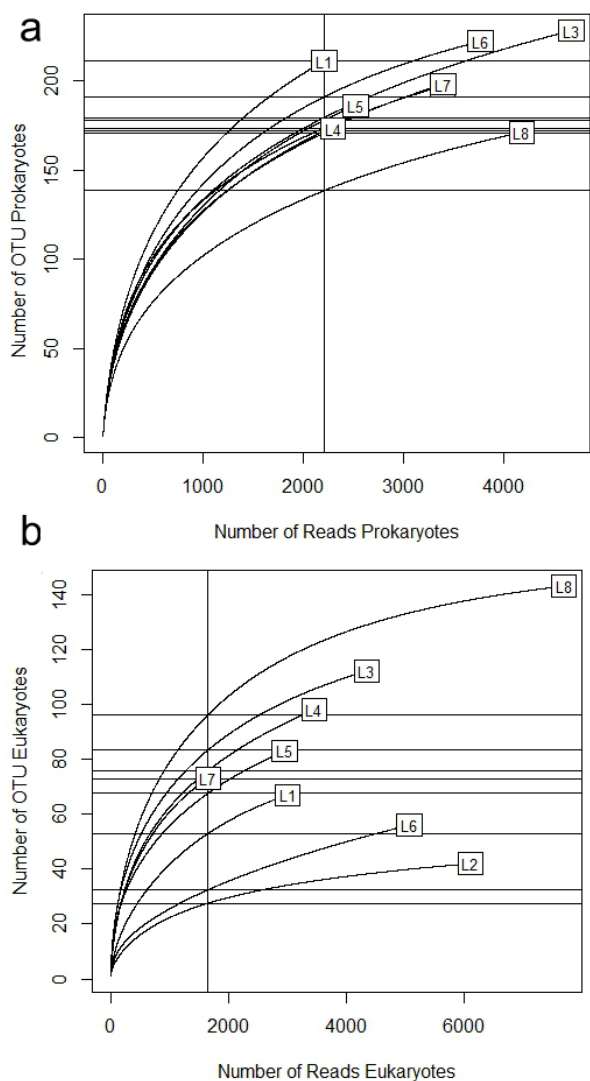


Figure S3. Rarefy curve of Prokaryotes (a) and Eukaryotes (b) community for the 8 floodplain lakes in Araguaia River.

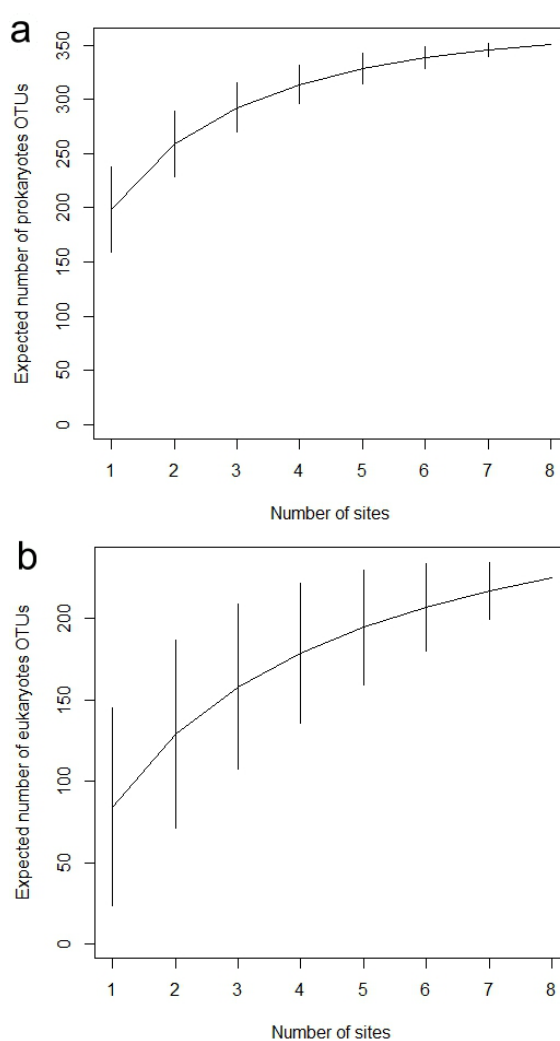


Figure S4. Species accumulation curve of Prokaryotes (a) and Eukaryotes (b) community for the 8 floodplain lakes in Araguaia River.