

Supplementary information of the studied metagenome - rarefaction curves

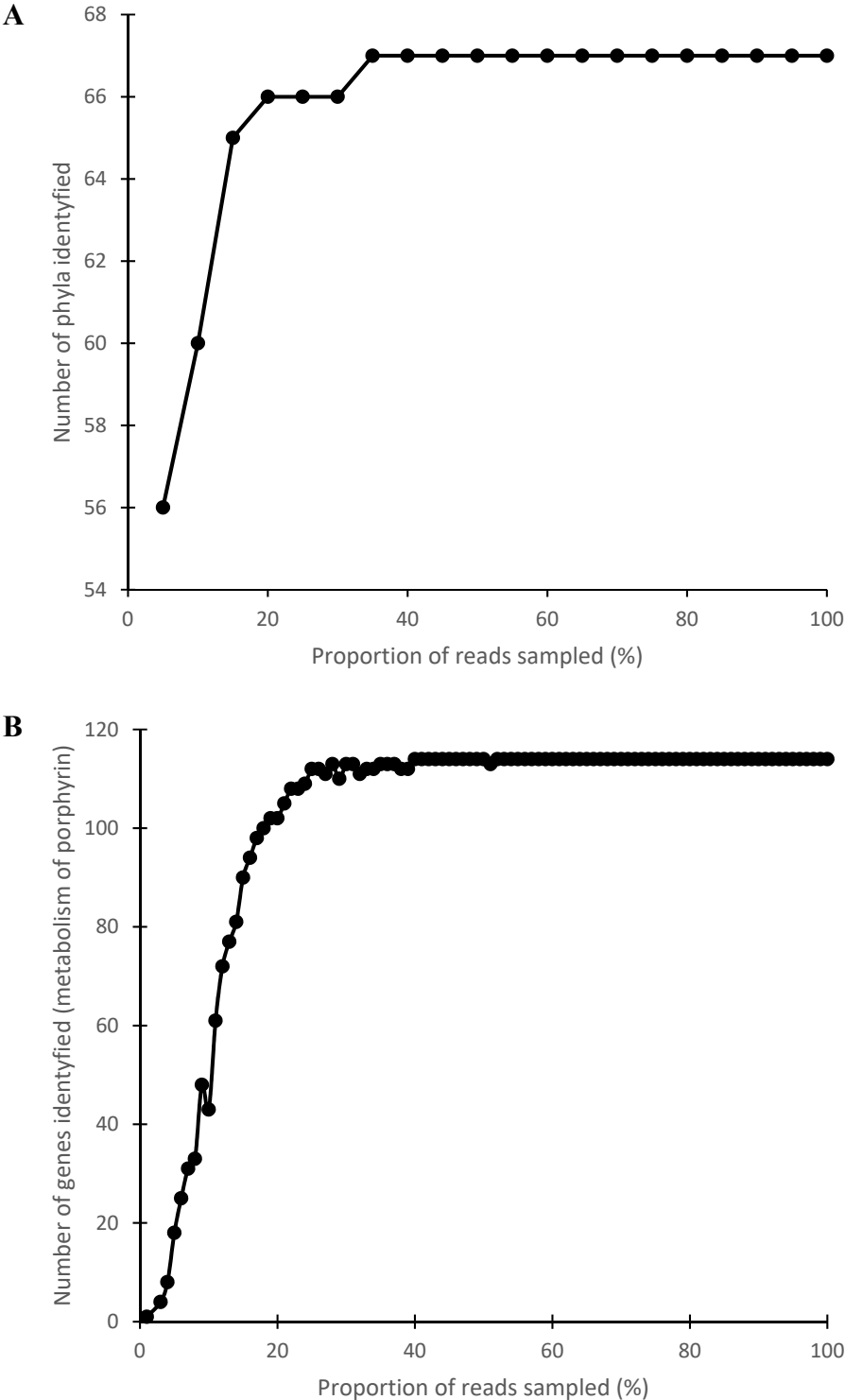


Figure S9. Rarefaction curves representing the relationship between the number of taxa (A) and genes (B) as a function of sequencing depth (proportion of reads sampled). Rarefaction analysis showed that sequencing saturation was achieved in both cases.