Supplementary Figure S4: **Boxplot displaying assembly statistics by two assemblers on twelve metagenomes using HiSeq3000 and BGISEQ-500 unprocessed and preprocessed sequence reads**. BGISEQ-500 generated reads sequences are represented in blue, while HiSeq3000 in red. Statistical transformation of data was performed using the default *geom_boxplot* option in R (ggplot2). **A.** Largest contig, **B.** GC (%) of assemblies, **C.** N50. **D.** L50.