



Supplementary Figure S5: Boxplot depicting computational resource usage in terms of memory and time required by two taxonomic classifiers (A-C) and assembly (D). All results are from twelve metagenomic reads sequences generated from two sequencing platforms. BGISEQ-500 generated reads sequences are shown in blue, while HiSeq3000 is in red. Statistical transformation of data was performed using the default *geom_boxplot* option in R (*ggplot2*). **A.** CPU resources utilization (Taxonomic classification), **B.** Total Run-Time (Taxonomic classification), **C.** Peak Memory usage (Taxonomic classification), **D.** Peak Memory usage (Assembly).