Metagenomics (MGX)

Sample processing

Whole genome fragment libraries were prepared as follows. Metagenomic DNA samples were quantified by Quant-iT PicoGreen dsDNA Assay (Life Technologies) and normalized to a concentration of 50pg/uL. Illumina sequencing libraries were prepared from 100-250pg of DNA using the Nextera XT DNA Library Preparation kit (Illumina) according to the manufacturer's recommended protocol, with reaction volumes scaled accordingly. Prior to sequencing, libraries were pooled by collecting equal volumes (200 nl) of each library from batches of 96 samples. Insert sizes and concentrations for each pooled library were determined using an Agilent Bioanalyzer DNA 1000 kit (Agilent Technologies). Libraries were sequenced on HiSeq 2x101 to yield ~10 million PE reads.

Post-sequencing de-multiplexing and generation of BAM and Fastq files are generated using the Picard suite (https://broadinstitute.github.io/picard/command-line-overview.html).