



Figure S2. Number of sequences obtained per sample after library demultiplexing (A) and percentage of sequences excluded in different bioinformatic analysis steps (B). **A:** Library demultiplexing; Numbers above bars indicate the relative contribution (in percent) to the total number of sequences obtained for each sample. Sequencing started with Ins_F (white) or Ins_R (black) is indicated by bar color. **B:** Number of reads excluded in data processing steps. Mean percentage of sequence abundance in each processing step is written in brackets. Ins_F / Ins_R primer bias was tested with a t-test.