



Figure S1: Overview of obtained spots per sample and amount of sequences lost in bioinformatic processing. **A:** Number of PE reads obtained for each sample, and proportion of PhiX and COI sequences without matching tags. Numbers above bars give the proportion of reads in percentage. **B:** Amount of sequences excluded in each major bioinformatics processing step for each sample. Size of the amplified region (not the fragment size) is given below in boxes for each primer combination.