



**Figure S9:** Sequencing depth for the mock sample metabarcoding (A) and malaise trap metabarcoding run (B) plotted against amplicon length including illumina adapters. Red lines indicate linear regression lines. **A:** Data from sequencing the mock sample with 21 primer pairs, amplicons pooled equimollary. Sequence depth for each marker can be described with the following formula:  $-0.002462 \times \text{Amplicon size in bp} + 2.288913$ , which was used in successive runs to account for length bias. **B:** Metabarcoding run on a complete malaise sample, amplicons equimolar pooled for sequencing, but concentration additionally adjusted to account length bias, according to the formula in A. Outliers LCO1490 + HCO2198 and dgLCO1490 + dgHCO2198 where excluded for calculating the linear regression.