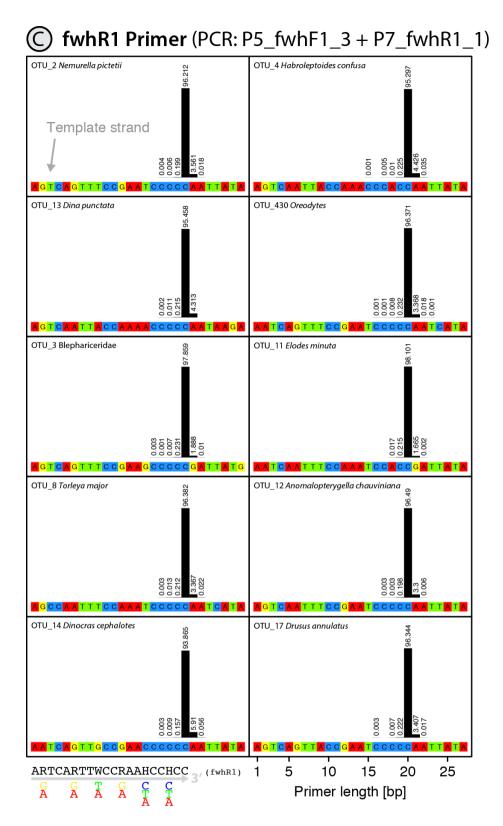
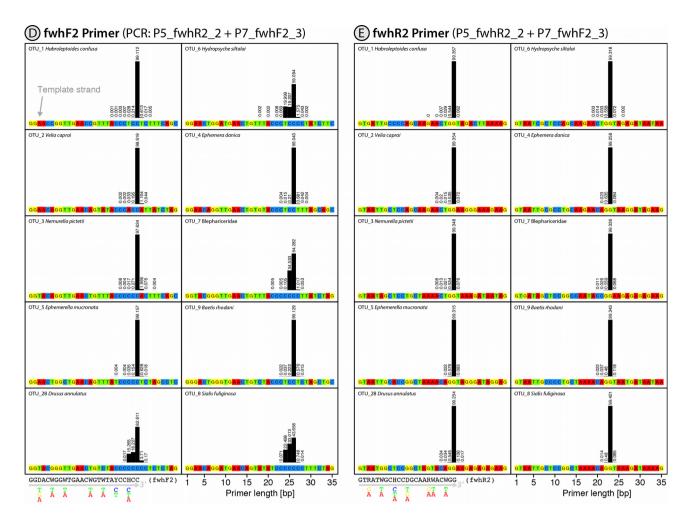


**Figure S1:** Plot of primer binding sites and bar plots depicting length of utilised primers for the 10 most abundant OTUs in mock sample B (sequence data from Elbrecht & Leese 2017). The presence and read abundance for different taxa can vary based on the primer set used, thus while amplifying the same mock samples, the order of and taxa the 10 most abundant specimens is not identical between plots as OTUs are sorted by read abundance. The sample was amplified with the P5\_BF1\_0 + P7\_BR1\_4 and P5\_BF2\_0 + P7\_BR1\_4 primer set, and the length distribution of the incorporated primers is shown for the BR1 primer (A and B). The percentage of amplicons that incorporated a particular length are shown above each bar.

Additional plots for further primer combinations on the next 2 pages (C, D, E).

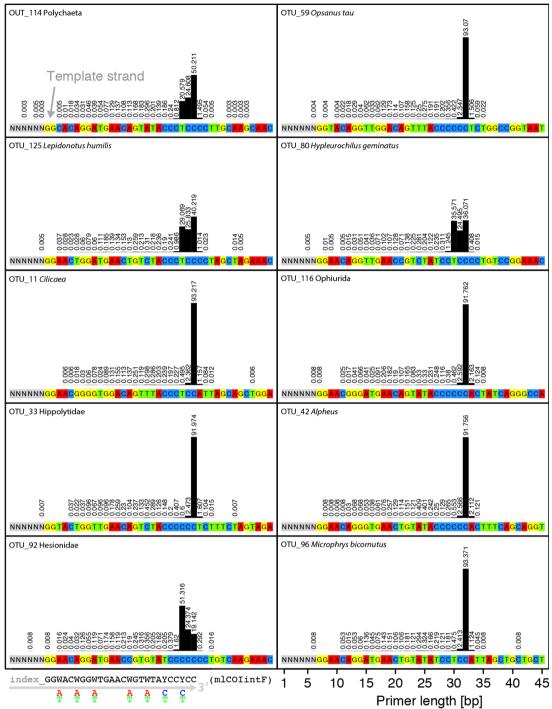


C: Length distribution of the fwhR1 primer (Sample B, P5\_fwhF1\_3 + P7\_fwhR1\_1, Vamos et al. 2017). The fwhF1 primer was not analyzed, as no data about the primer binding site was available (as it binds in the LCO1490 primer binding region which was not sequenced).



**D** & E: Length distribution of the fwhF2 and fwhR2 primer (Sample B, P5\_fwhR2\_2 + P7\_fwhF2\_3, Vamos et al. 2017).

## (F) mlCOlintF Primer (PCR: mlCOlintF + jgHCO2198, run 1)



**F:** Length distribution of the mlCOIintF primer (marine invertebrate sample from Leray & Knowlton 2017, mlCOIintF + jgHCO, run 1). The jgHCO primer was not analyzed, as no data about the primer binding site was available (as it binds in the HCO2198 primer binding region which was not sequenced).