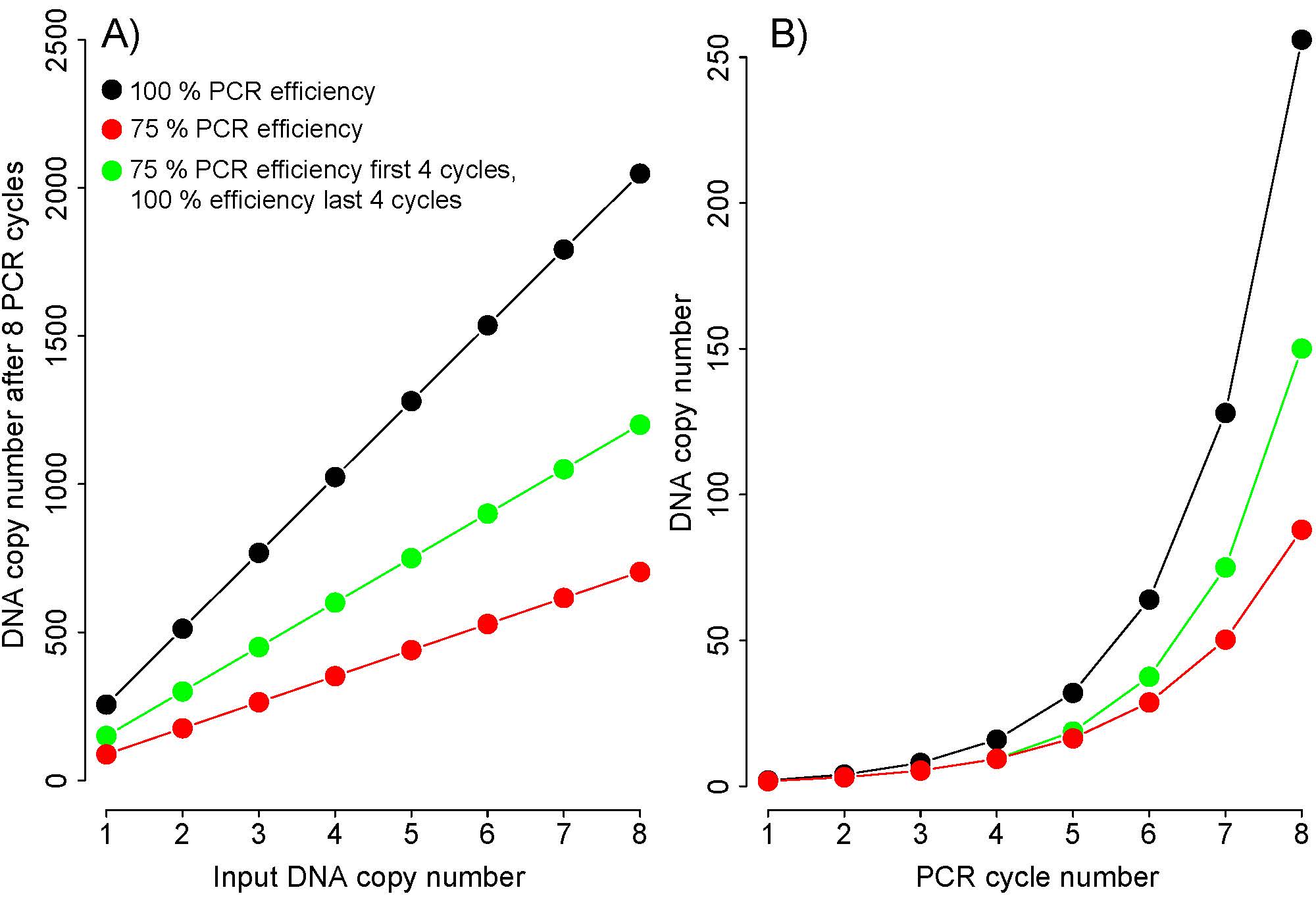
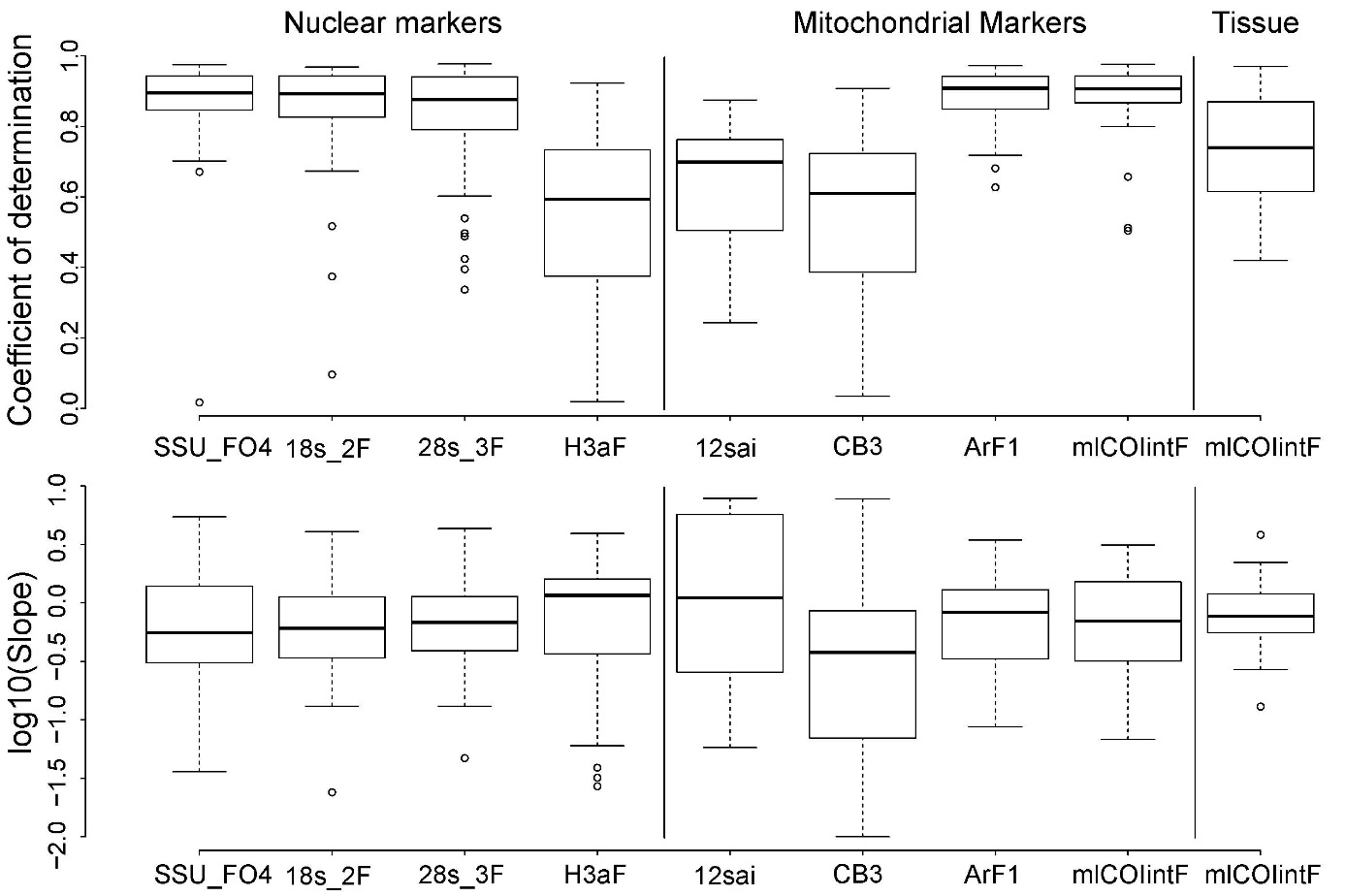
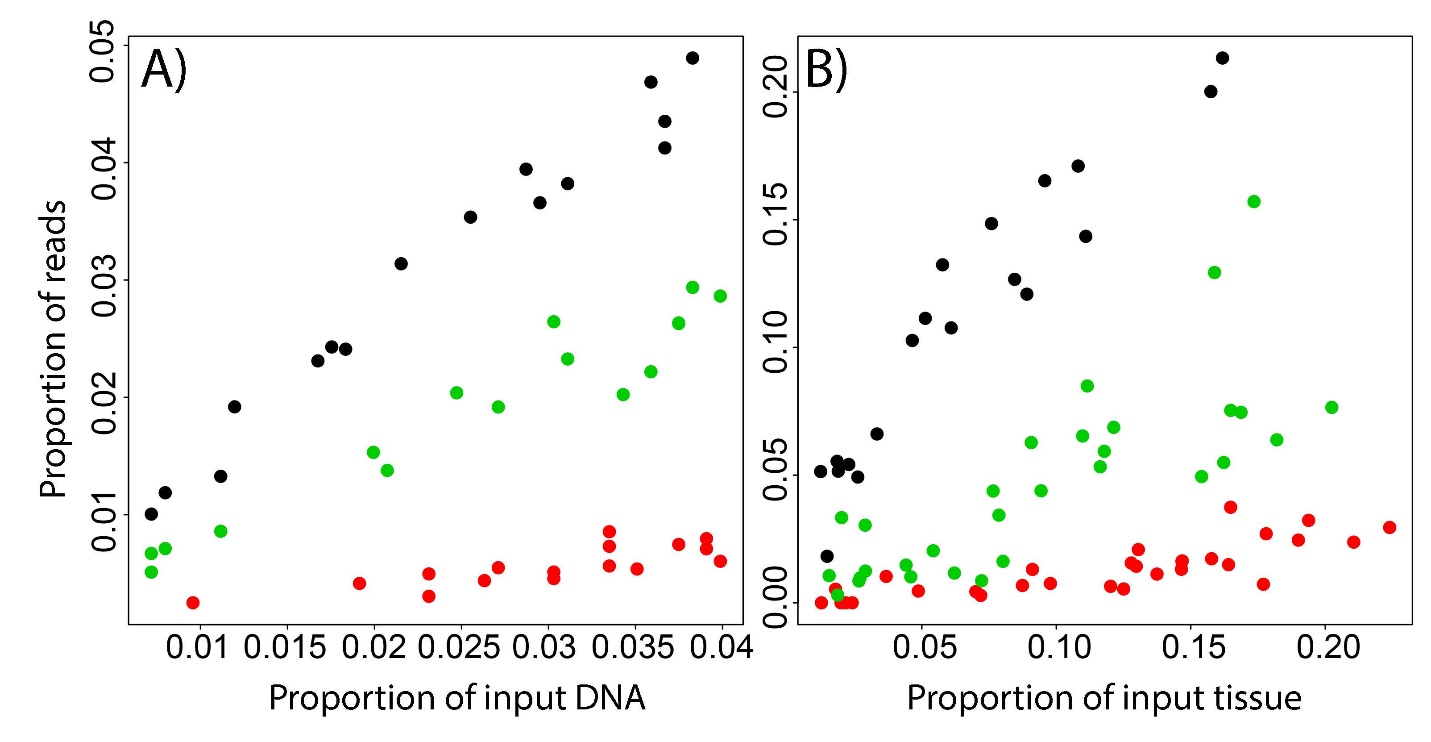
**Supplementary material**



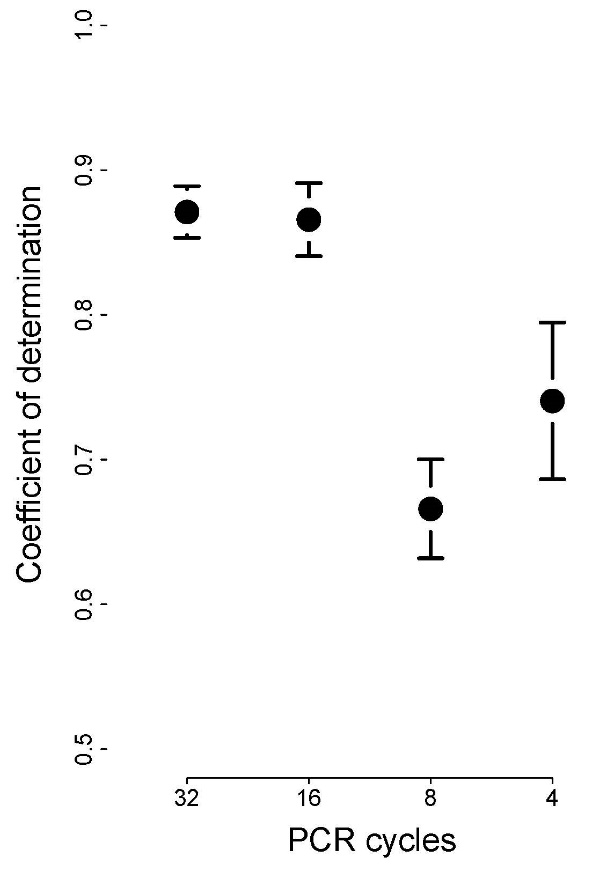
**Supplementary Figure 1 A)** Hypothetical association of input DNA copy number and recovered DNA copy number after 8 PCR cycles for two taxa with a difference in PCR efficiency of 25 % (red and black circles). By using a nested PCR on conserved priming sites after 4 cycles, the recovered copy number is corrected (green circles), leading to less biased abundance estimates. **B)** Association of PCR cycle number and DNA copy number for the same taxa. By removing PCR bias after four cycles, the difference in copy number between the two taxa is reduced.



***Supplementary Figure 2 A)*** *Coefficients of determination and* ***B)*** *slopes of the associations between read count and taxon abundance for nuclear markers, mitochondrial markers and for tissue pools. The forward primer for the targeted marker is shown on the x-axis.*



**Supplementary Figure 3 A)** Association of the proportion of input DNA and recovered reads for three arthropod species (Porcellio scaber, Proteirulus fuscus, Tomocerus minor) and **B)** for the same three species based on tissue pools.



**Supplementary Figure 4** Average coefficient of determination for the association of input DNA and recovered read count for 44 arthropod taxa amplified for mitochondrial COI at four different PCR cycle numbers. Bars depict the 95 % confidence interval.