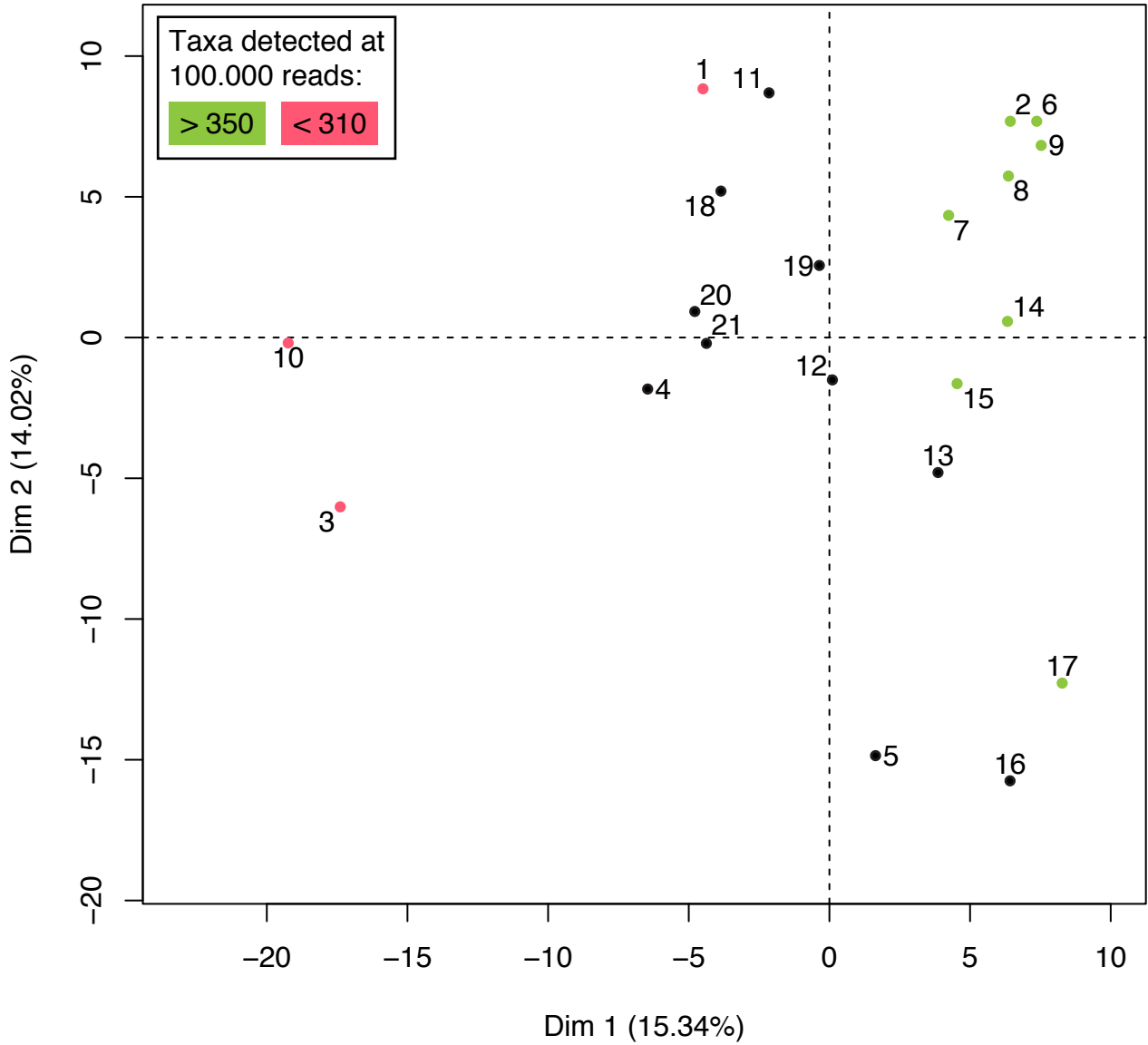


# Individuals factor map (PCA)



**Figure S13:** Prcinpal Component analysis for the mock sample metabarcoded with 21 primer combinations. Sequencing depth was normalised to 100.000 reads for each primer sets (reads below 0.001% abundance discarded).